Release 1.3: New Features

Search Changes
• While we strive to provide all available data to our user community, we are aware that many scientists are only interested in sequences when the whole genome has been sequenced. While we now include all sequence fragments found in GenBank in the ViPR database, we provide a checkbox on the genome and gene/protein searches allowing you to exclude partial genomes from your search results.
• We have been able to assign a subtype to more than half the Hepatitis C genomes found in ViPR using information found on the GenBank record. Flaviviridae genome and gene/protein searches allow you to select specific Hepatitis C subtypes to include in your search results.

Data and Analysis Changes
• The Virus Taxonomy Browser on the ViPR homepage now offers an alternative view - a list of all viruses supported by ViPR.
• Use of the ViPR method for identifying mature peptide products of polyproteins has been extended to include the majority of Flavivirus strains. We will continue to extend the use of this method in the future.
• Mature peptides derived from polyproteins are now linked to 3D protein structures obtained from the Protein Data Bank (PDB).

Work Bench Operations
• To make it easier for you to use ViPR tools for analysis of your own data, you can save files in ViPR that you upload to your workbench for up to 6 months. Saved files are only visible to you or collaborators with which you choose to share the data.
• In the last ViPR release, we introduced a new sharing capability, allowing you to make a working set, search or analysis saved on your workbench “public” or visible to any ViPR user with a workbench. To improve the usability of this feature, the workbench owner must provide a name and institution so you can clearly see the source of public data.
• Collaborator groups defined for one virus family are now available across all virus families in a user’s account, including influenza on the IRD site. This simplifies sharing on the workbench.
• The original owner of an item made public can now revoke its public status.

Best Regards,
The Virus Pathogen Resource (ViPR) team

The May 2010 release of ViPR is now available, visit www.viprbrc.org/

Questions? Problems? Suggestions? Click here

Special Announcement
Major website redesign in progress
The ViPR team has been working on a major redesign of the ViPR web site since December 2009. The next release, in mid-July of this year, will have a totally new look. Based on feedback from you, our user community, we are making it easier to see what you can do in ViPR and to make it easier to search and analyze our data and to use our tools to analyze your own data. All of the features and capabilities that are now part of ViPR will still be there. They will just be easier to find and use. We look forward to your comments on the new look of our web site.