Host factor data enhancement
ViPR now contains host factor data generated through the NIAID-sponsored Systems Biology for Infectious Diseases Research program. The current release includes four gene expression microarray studies using either human cell lines or mice infected with influenza virus or SARS coronavirus. Besides the basic information about each study and associated experiments, you can also view the experiment results in a matrix as shown in the screenshot below. Each row/column groups host genes based on the same differential expression pattern, and links to the list of the differentially expressed genes. All of the data are available for download. To access host factor data, mouse-over the “Search Data” tab and click “Host Factor Data”.

In the near future, ViPR will add host factor data from siRNA high throughput screens and proteomics and metabolomics experiments, as well as analytical and visualization tools to help further understand the host response to virus infection.

Genotype Determination and Recombination Detection Tool available for Flaviviridae viruses
ViPR has developed a Genotype Determination and Recombination Detection Tool that estimates the most likely genotype for your input sequences and identifies possible sites of recombination. This tool is now available for Flaviviridae viruses, including Hepatitis C virus, Dengue virus, St. Louis Encephalitis virus, West Nile virus, Japanese Encephalitis virus, Tick-borne Encephalitis virus, Yellow Fever virus, Bovine Viral Diarrheal virus, and Murray Valley Encephalitis virus. To access this tool, go to the Flaviviridae family page, mouse-over the “Analyze & Visualize” and click “Genotype Determination and Recombination Detection”.

New clinical data for human rhinovirus isolates
ViPR has added clinical data for human rhinoviruses, including patient demographics and disease symptoms. The clinical data is searchable from the Picornaviridae Genome Search page as well as the Picornaviridae Human Clinical Metadata page. All clinical data is linked to genome sequences.

Search and browse viral protein orthologs
ViPR has developed an ortholog pipeline to identify orthologs across taxonomic branches, varying from a subspecies to a genus or even an entire family. This pipeline processes all protein sequences for a taxon in ViPR and viral protein orthologs into ortholog group clusters. This ortholog component can help you infer gene function and study virus evolution.

For this release, the Ortholog Group component has been implemented for Poxviridae viruses. To access this feature, go to the Poxviridae homepage, mouse-over the “Search Data” tab and click “Ortholog Groups”. Here you can browse all ortholog groups for a specific taxon or search by ortholog group name. Orthologs for other virus families will be implemented in future releases.

New clinical data for human rhinovirus isolates
ViPR has added clinical data for human rhinoviruses, including patient demographics and disease symptoms. The clinical data is searchable from the Picornaviridae Genome Search page as well as the Picornaviridae Human Clinical Metadata page. All clinical data is linked to genome sequences.

The March 2012 release of ViPR is now available, visit www.viprbrc.org/brc/