**Host factor enhancement**

We have added 9 new experiments that identify host factors involved in influenza virus or SARS Coronavirus infections in either human cell lines or mice. Now we provide access to a total of 32 host factor experiments with almost equal amounts of data from transcriptomic and proteomic experiments. The paired transcriptomic and proteomic experiments will facilitate the comparison of host factors at the RNA and protein levels across experiments under different conditions.

The host factor component has been enhanced to include the following features:

- **Compare host factors:** In addition to finding shared (AND), all (OR), or unique (XOR) host factors identified under different experimental conditions, from different experiments, or of different data types, now you can subtract (NOT) overlapping factors from one selected bioset to find exclusive factors from the Set Operations menu. The number of biosets that can be intersected (AND) and union (OR) has also been increased to a maximum of 10.

- **Host Factor Results Finder:** Besides performing a search using different criteria relating to the experimental design and experiment results, a Host Factor Results Finder has been added for finding experiments and biosets in which the user-specified host factor(s) were identified. To do so, click the “Host Factor Results” button on Host Factor Biosets page and search by one (or more) Gene Accession, Entrez Gene ID, Gene Symbol, Gene Name, UniProt ID, Protein Name, or Protein Symbol.

**Comparative Analysis of MERS-CoV Sequences**

As of July 3, 2013, ViPR has 10 genomes of the recently identified MERS-CoV. We have recently completed a comparative genomics analysis of Middle East Respiratory Syndrome Coronavirus (MERS-CoV) whole genome sequences, with implications for viral evolution, performed using the suite of bioinformatics tools available in Virus Pathogen Resource (ViPR).

ViPR provides annotation tracks of protein coding annotations, Pfam domains, experimentally determined epitopes imported from the Immune Epitope Database, and custom user tracks. To view a genome in GBrowse, click the “View in GBrowse” link in the Sequence Annotations section within the Strain Details page. View the GBrowse tutorial to see how to use it.

**View complete genome sequences in GBrowse**

GBrowse offers simultaneous bird’s eye and detailed views of genomes and genome annotations. Now we have made all complete genomes, as well as their annotations, belonging to the Herpesviridae and Poxviridae families viewable in GBrowse. ViPR provides...