New host factor study data and capability for cross experiment comparison

ViPR has released another four gene expression microarray studies including influenza A/CA/04/09 (H1N1) infection of mice and human Calu3 cell lines, A/Vietnam/1203-CIP048_RG1/2004 (H5N1) infection of mice, and SARS coronavirus infection of Calu3 cell lines. To access the data, mouse-over the “Search Data” menu and click the “Host Factor Data” option.

Besides providing host factor data, ViPR also allows for customized data-mining analyses. In this release, ViPR has added the capability to compare significant host factor lists from multiple biosets/experiments. This facilitates the identification of subsets of differentially expressed genes that are shared or unique under different experimental conditions or across different experiments.

To do so, on the host factor data landing page, click on next to one or more studies to show the experiments associated with the study, then check the box next to one or more experiment names and click the “View Associated Biosets” button to load the Host Factor Bioset Information page. On the next page, select two desired biosets, mouse-over the “Run Analysis” button located above the bioset list table and click one of the Boolean analysis options: “Find shared factors”, “Find all factors”, or “Find unique factors”. This will generate a list of genes found to be significantly up- or down-regulated across your selected experiment(s).

Spinning 3D protein structure movie

ViPR imports experimentally-determined virus protein structures from the Protein Data Bank and provides various visualization options that include: highlighting sequence features, ligands, immune epitopes, and specific residues on the structure. Now you can generate and download a movie of a spinning 3D protein structure of your interest. Check out the tutorial for details.

Human clinical data search options for rhinovirus

ViPR captures clinical metadata about patients and samples associated with viral sequences whenever possible; currently ~100 rhinovirus strains have associated clinical metadata in ViPR. On the Picornaviridae Genome Search page accessible from the “Search Data” menu, ViPR provides options to search for genomic sequences by host and/or sample attributes. Uncheck the “Exclude partially sequenced genomes” checkbox at the top of the sequence search page in order to retrieve partial sequences, select search criteria and click “Search” to run the query. All clinical data is linked to virus strains with sequence records.

Questions? Problems? Suggestions?
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