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

Release 1.2: New Features

Work Bench operations

- In response to user requests for tools to facilitate collaboration, we have made a major enhancement to the ViPR workbench. We now allow sharing of all items saved on your workbench with selected colleagues and collaborators. You can specify one or more working sets, searches, or analysis results for sharing with a single colleague or a group of collaborators.

- You can define any number of collaborator groups to include specific colleagues for sharing saved working sets, searches and analyses.

- You now have the option of making your saved working sets, searches and analyses public for use by the research community.

- Workbench users can now supply their name in addition to email addresses when registering, making it easier for your colleagues to add you to a collaborator group.

Data and Analysis Changes

- An alignment-based protein annotation method is being used to compute mature peptides from their parent polyproteins, using Dengue and West Nile virus as pilot projects. The method provides more accurate polyprotein cleavage junctions, particularly in isolates that existed prior to publication of a RefSeq standard. We plan to expand slowly to all other virus families that generate polyproteins as we verify that the results are valid.

- For Blast of ViPR genomes, the Swiss-Prot virus proteins database has been added for BlastP and BlastX analyses.

- You can construct a position-by-position report of sequence variation (polymorphism) at each coordinate using either nucleotide or amino acid sequences that you either select from the ViPR database or upload in FASTA format.

- The Protein Details page carries ortholog information, with a link to a list of all members of the respective ortholog group. From this list you can launch analyses (e.g. alignments) of some or all members of the ortholog group. Ortholog information was derived from data developed by the VBRC and PATRIC BRC projects.

- ViPR’s installation of GATU (Genome Annotation Transfer Utility) will accept a sequence you provide for annotation and recommend appropriate reference sequences by comparing (using BlastN) your sequence to a database of virus reference sequences selected from the NCBI Ref_Seq database. The reference sequence selected will be used for annotation transfer.

Search Changes

- If search results span several pages, selections are retained when moving between pages of the search results. This greatly streamlines adding selected results to your working set and allows easier selection of results for direct input into an analysis tool.
• When searching experimental epitopes, the Search Results now lists each unique epitope sequence only once. An Occurrence link for each entry shows a table of all proteins/strains in which the epitope is found.

Educational Materials
• An archive of ViPR newsletters is available on the General Information menu.

Performance
• The system has just transitioned to new hardware, which should result in a significant improvement in performance.

ViPR Driving Biological Projects (DBPs)
• The ViPR Scientific Advisory Group is currently evaluating 23 letters of intent submitted in response to the RFP previously posted on ViPR. Two Driving Biological Projects will be funded by the ViPR BRC during 2010 for 2 year periods of performance. Another 2 such projects will be funded in 2012.

Best Regards,
The Virus Pathogen Resource (ViPR) team