**Special Announcement**

**Major Website Redesign**

- The VIPR July release introduces our totally redesigned website.
- The old side navigation menu has been replaced by drop-down menus, leaving more space for search and analysis results.
- New pages describe each VIPR search and tool, making it easier for you to find the feature you want to use.
- This release is the first of a series meant to improve the usability of VIPR

**New Features to Improve VIPR Usability**

- A page is reached by clicking on each drop-down menu that describes each Search and Analysis tool to help you choose the proper one for your needs.
- A Quick Search capability allows you to input text or public identifiers such as GenBank accession numbers and get a list of genome, gene, and protein data meeting the criteria.

---

**The Virus Pathogen Resource (VIPR) has been totally redesigned to make it easier for you to use. Please try it out and let us know what you think.**

---

**Things to Look for in Our New Release**

**Home Page and Menu Structure**

The new VIPR **Home Page** and menu structure include:

- Menus at the top of each page to provide links to information about the VIPR team as well as announcements and resources of interest
- Dropdown menus on every page to provide direct, easy access to all VIPR features via submenu choices
- A totally new **home page** that provides a visual summary of the VIPR usage paradigm: Search → Analyze → Save to Workbench, with direct links to key searches and tools in each usage area
- A revolving graphic on the new home page highlights key system features
- Computation of mature peptides was completed for St. Louis encephalitis virus (Flaviviridae)

**Workbench**

The VIPR workbench has been totally redesigned to make it easier to use:

- All content types (working sets, searches, analyses) are shown on the same page, but you can easily filter out the types you don’t want to see
- We have introduced the folder concept, allowing you to group together all content types associated with a study you are doing for easy retrieval and sharing
- We have made it easier to share with collaborators
- Uploaded files can be kept on your workbench and combined with other VIPR data for analyses such as sequence alignment

---

Best Regards,
The Virus Pathogen Resource team

**The July 2010 release of ViPR is now available, visit [www.viprbrc.org/brc/](http://www.viprbrc.org/brc/)**