






What's new in the 2.7 release of KoriBlast

Summary

1. Query NCBI major databanks and get sequences of interest using the Document Viewer's NCBI DataBase Explorer Tool. Sequence retrieval can be done interactively or in batch mode.
2. Export data in plain text files. Text format includes extended hit table and/or pairwise sequence alignments.
3. View protein sequences using the Hydrophobic Cluster Analysis (HCA) drawing system
4. Benefit from an extended display of summaries in the Search Module.
5. When creating local Blast databanks, KoriBlast now gets Fasta sequences out of these banks, instead of querying the NCBI.
6. For proteomics studies, KoriBlast computes theoretical pI and molecular weight.


The following sections give more details about all the novelties of KoriBlast 2.7.

A. Search Module


- Extended display of data in the Job Results table. This table now displays a full set of information for each best hit (Blast scores, alignment data, query vs. hit sequence positions, number of hits and Hsp, etc). Check the upper right corner of the Job Results table () to display all that information .
- Extended text export from the Job Results table. It is now possible to export a text file (Blast text format) containing the whole set (or selected subsets) of Blast hits available for each job. This new text format export is available from the command  .
- The Filter Summary Result table (command ) now displays a full set of information for each best hit (Blast scores, alignment data, query vs. hit sequence positions, number of hits and Hsp, etc). From this table it is also possible to save the table content in a text file (Blast text format).

B. Analyse Module


Transferring hits data to the Document Viewer

When opening a hit's entry from the Analyse Module to the Document Viewer (command ), the corresponding hit data are now transferred to the Document Viewer too. There you can see a feature of type 'BlastHit' in the Feature table associated to the entry.

Export Hit Table in a text file

It is now possible to export a text file (Blast text format) containing the whole set (or selected subsets) of Blast hits displayed in the Hit table (command ).

Export an entire Blast result in a text file

It is now possible to export a text file containing an entire Blast results (command  located at the bottom of the list of open results).

Hit List-SeqAlign Viewer

Theoretical pI and molecular weight are now computed for protein hits.

Graphic Map

Four new data columns have been added to display query vs. hit sequence positions.

C. Filter Manager Module

- The data filtering system provides a new numeric operator: 'is in the range'. This operator enables more sophisticated filters enabling you to query numerical values using ranges of values.

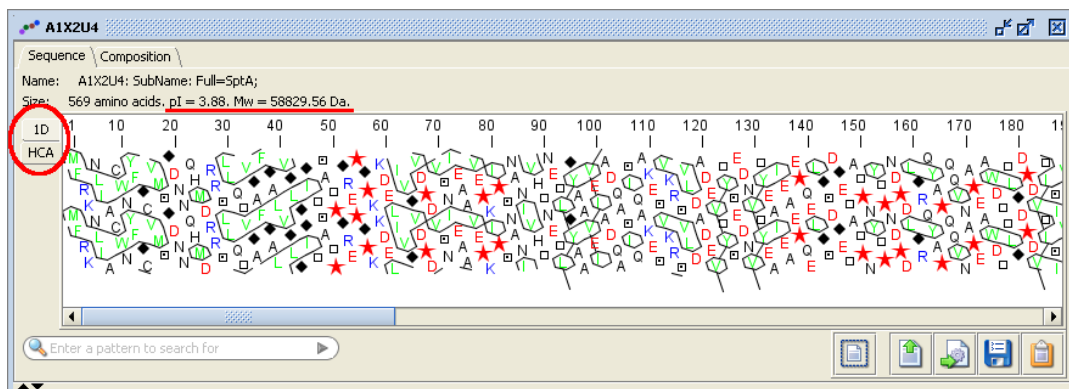
D. Document Viewer Module

Management commands

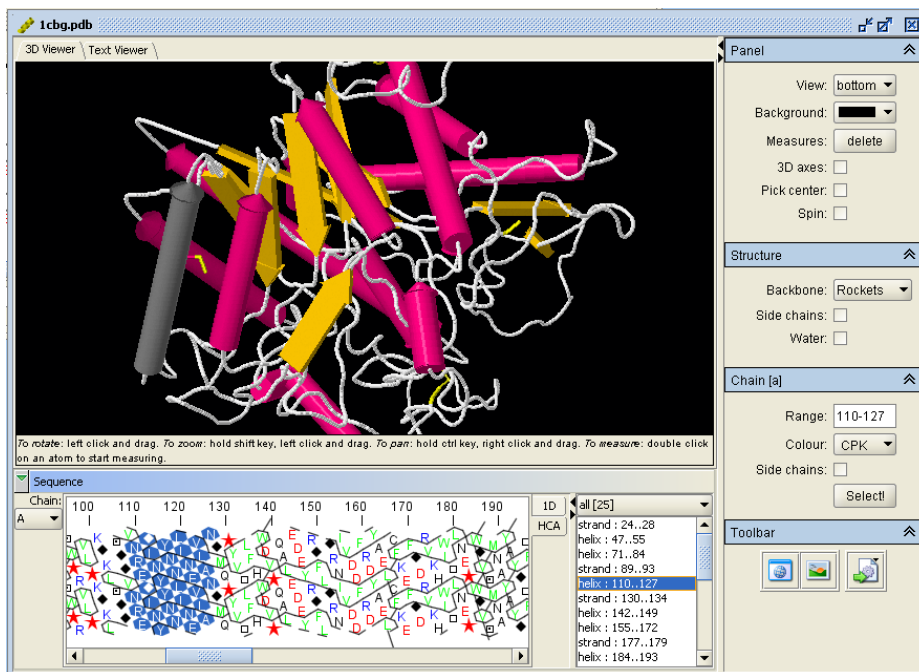
- Within the Sequence and Structure Viewers, the 'Open from cache' panel now accepts multiple selections enabling you to open or delete set of entries.
- The content of the 'Open from cache' panel can be saved using the CSV format that is compatible with spreadsheet applications. This Save command is available from the contextual menu of the 'Open from cache' panel (mouse right click).

E. A brand new viewer available in the Document Viewer Module

- an HCA (Hydrophobic Cluster Analysis) viewer has been added to the Sequence and Structure viewers.

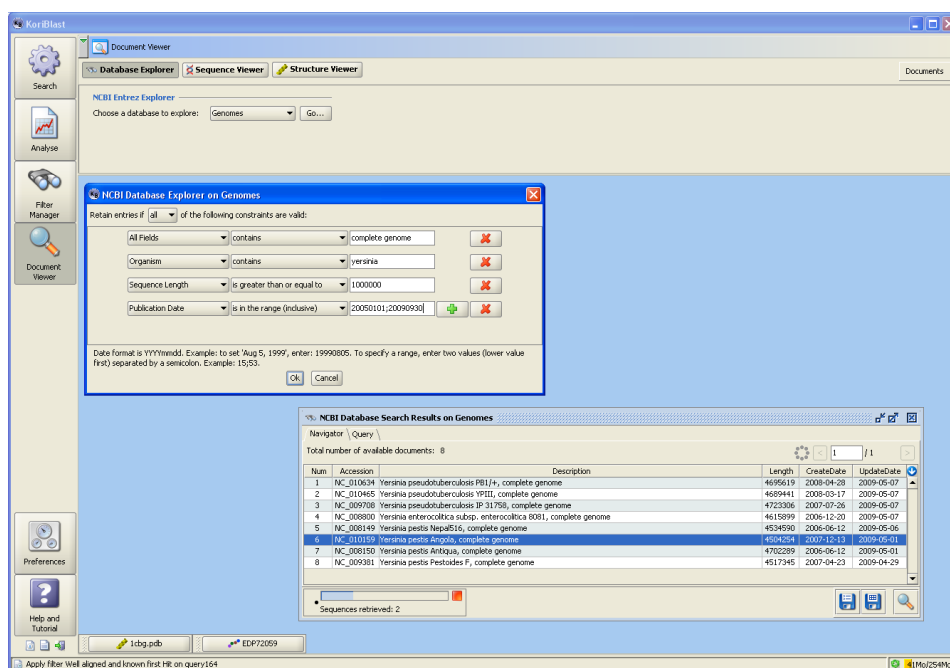


- The sequence viewer now displays theoretical pI and mW for proteins (see above picture)



F. Querying NCBI to get sequences and create personal Blast databanks

The brand new NCBI Entrez Query component enables you to query the major sequence databanks available at the NCBI to get sequences of interest. Sequences can be retrieved as Fasta files that can then be directly used to create personal Blast databanks usable from KoriBlast.



G. Other improvements:

- Export Blast results and pairwise sequence alignments using text reports. This new Save command is available from the Search and the Analyse modules.
- Contextual menu (mouse right click) has been added on several viewers: the Multiple Sequence Alignment Viewer (Analyse module), the 'Open from cache' panel (Sequence/Structure viewers from the Document Viewer).
- Update preparation of Blast databanks to handle update in Uniprot fasta headers.
- Possibility to set a user defined KoriBlast workspace location.