The New BLAST® Results Page

Enhanced graphical presentation and added functionality

https://blast.ncbi.nlm.nih.gov/

National Center for Biotechnology Information • National Library of Medicine • National Institutes of Health • Department of Health and Human Services

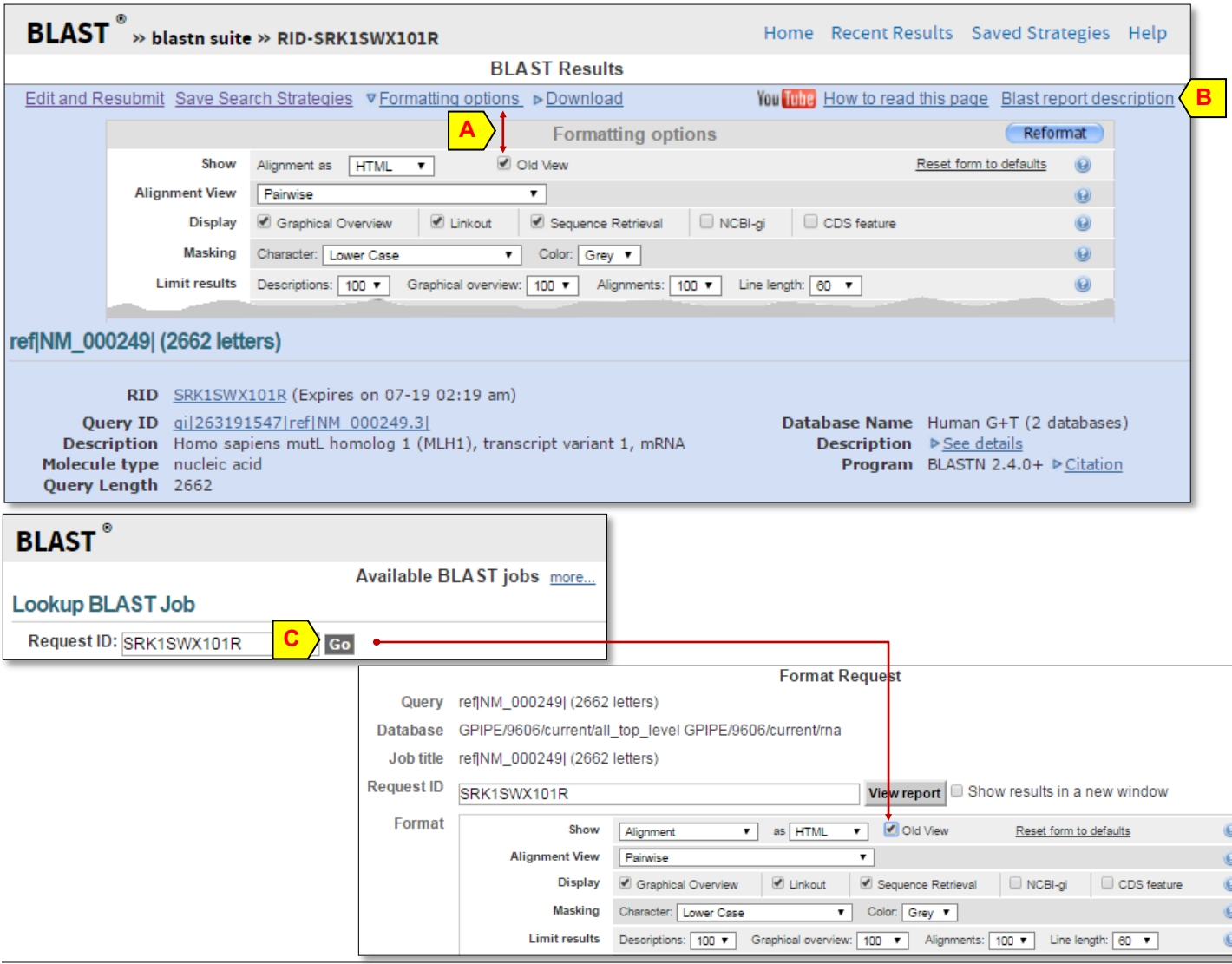
Scope

NCBI has introduced an enhanced report for search results generated by the BLAST® web service, which supersedes the default display first introduced in April, 2006. This report format provides access to displays of the alignment results in the NCBI Sequence Viewer and adds a function for downloading sequences for the aligned regions. It also provides easily accessible links to related information for matched sequences and a Description table with additional columns for extra alignment statistics. It also allows users to customize the columns shown in the result pages. An added benefit of this update is the optimization of BLAST result delivery, which allows the browser to stay responsive to user input while the alignment data is being rendered. This is especially beneficial for displaying results containing large numbers of matches.

Access to BLAST and the New BLAST Result Page

Access to NCBI BLAST web services through its homepage (blast.ncbi.nlm.nih.gov) remains the same as before. The change is in the layout of the results, which are displayed after a search is run.

The enhanced report format is the default display. The “old view” option under the “Formatting options” (**A**) at the top provides a convenient way to convert the display back to the old format, should such need arises. The YouTube link (**B**) at the top right points to a video tutorial explaining this new report format, with a link to this document to the right. Another way to set the result display back to the old format is to check the “Old view” checkbox in the “Form request” form, which can be reached after entering a valid RID in the “Recent Results” tab and clicking the “Go” button (**C**)



Contact: blast-help@ncbi.nlm.nih.gov

The New BLAST Result Pages

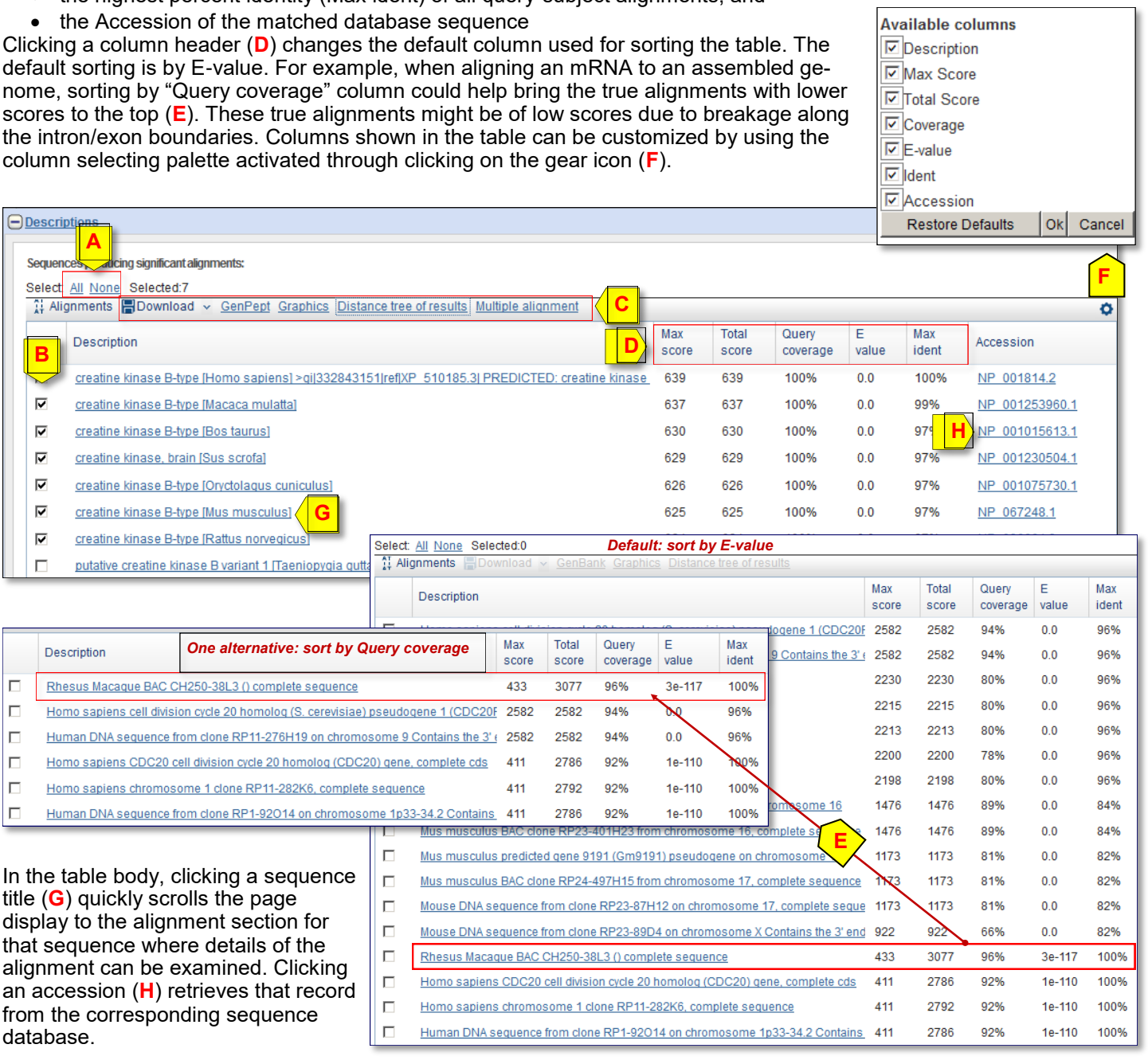
The general structure of the BLAST result page stays the same, which contains the Summary, Graphical Overview, Descriptions table, and Alignments sections. The changes are predominantly in how the Descriptions table and the Alignments are presented.

The Descriptions Table

The Descriptions table (shown below) provides a summary of the database sequences identified by BLAST to be similar to the input query. Two selection controls at the top of the table, "All" and "None" (**A**), allow for the quick selection and de-selection of matched database sequences. Individual sequences in the table can be selected/de-selected using the checkboxes to the left (**B**). Selecting database sequences activates links (**C**) at the top (see details on p.3). From left to right, the Descriptions table columns provide the following information:

- the description/title of matched database sequence
- the highest alignment score (Max score) from that database sequence
- the total alignment scores (Total score) from all alignment segments
- the percentage of query covered by alignment to the database sequence
- the best (lowest) Expect value (E value) of all alignments from that database sequence
- the highest percent identity (Max ident) of all query-subject alignments, and
- the Accession of the matched database sequence

Clicking a column header (**D**) changes the default column used for sorting the table. The default sorting is by E-value. For example, when aligning an mRNA to an assembled genome, sorting by "Query coverage" column could help bring the true alignments with lower scores to the top (**E**). These true alignments might be of low scores due to breakage along the intron/exon boundaries. Columns shown in the table can be customized by using the column selecting palette activated through clicking on the gear icon (**F**).

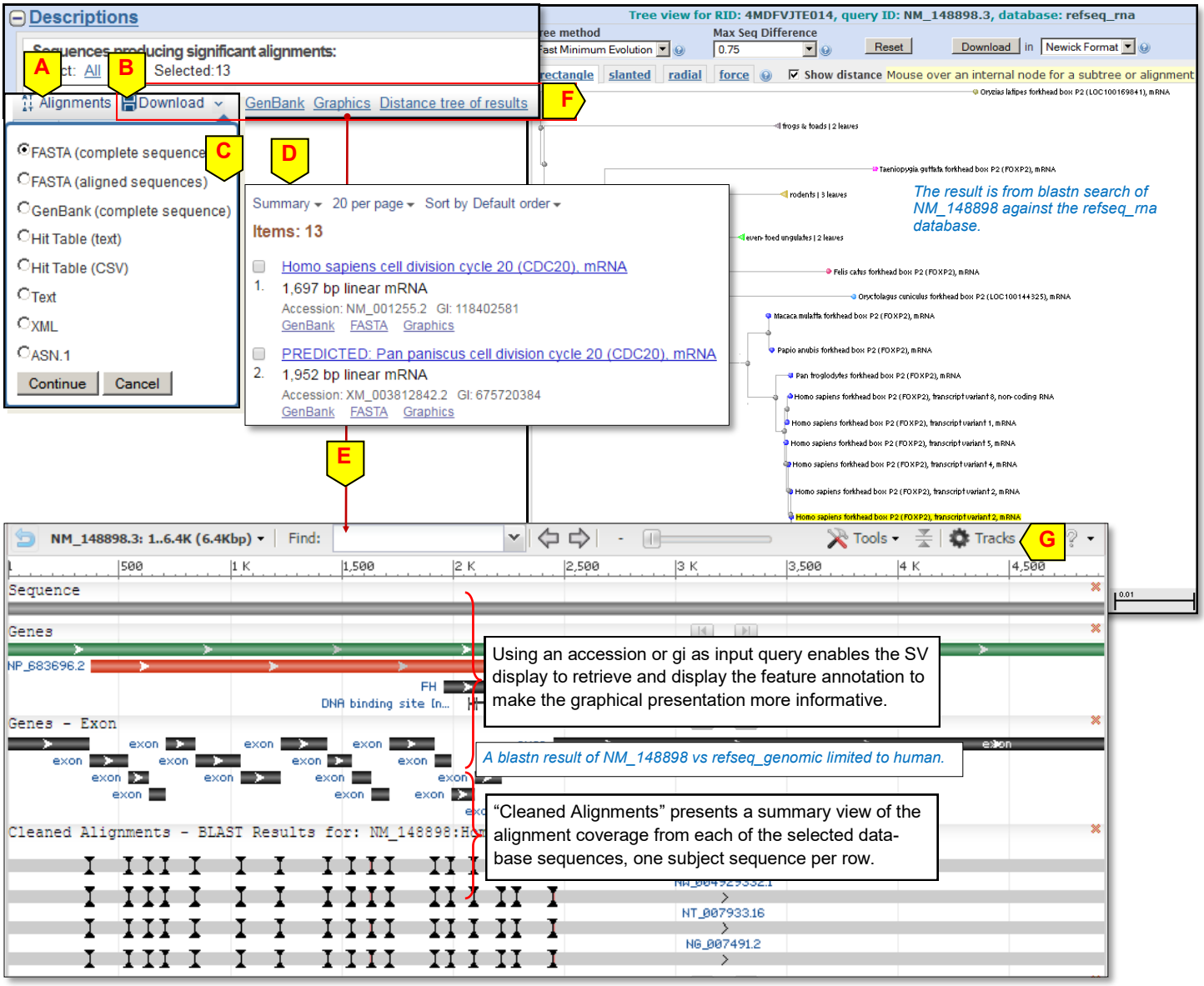


In the table body, clicking a sequence title (**G**) quickly scrolls the page display to the alignment section for that sequence where details of the alignment can be examined. Clicking an accession (**H**) retrieves that record from the corresponding sequence database.

The Descriptions Table: Functions Provided by the Links at the Top

At the top of the Descriptions table, clicking the "Alignments" link (**A**) scrolls the display to the Alignments section. The remaining links (**B**) work on the selected database sequence(s) for which checkboxes have been checked:

- "Download" activates a menu to select download format (**C**). The first three options select full sequence records or their aligned regions. The remaining options select the alignment data for these selected sequences.
- "GenBank" or "GenPept" (**D**) retrieves the selected sequences from the source database.
- "Graphics" (**E**) spawns a new browser window (or tab depending on the browser setting) to display the summary of query-anchored alignments in the NCBI Sequence Viewer (**SV**). It is recommended that an accession or gi (with subsequence range if necessary) be used to help makes this display more informative.
- "Distance tree of results" (**F**) opens a new page depicting the relationship among the selected database sequences and the query in a dendrograph. The distances for the tree view are derived from the pairwise local alignment between query and that of selected database sequences. Functions are available on this page to manipulate the display.
- For results from blastp searches, a "Multiple alignment" link (not shown) will be available within this group. Clicking this link performs multiple sequence alignment for the query protein and selected database sequences using the Constraint -based alignment tool (COBALT).
- The graphical display in Sequence Viewer can be customized using the "Tools" and "Tracks" (**G**) menu and controls.



More information on Sequence Viewer is available through the handout and help document accessible online:

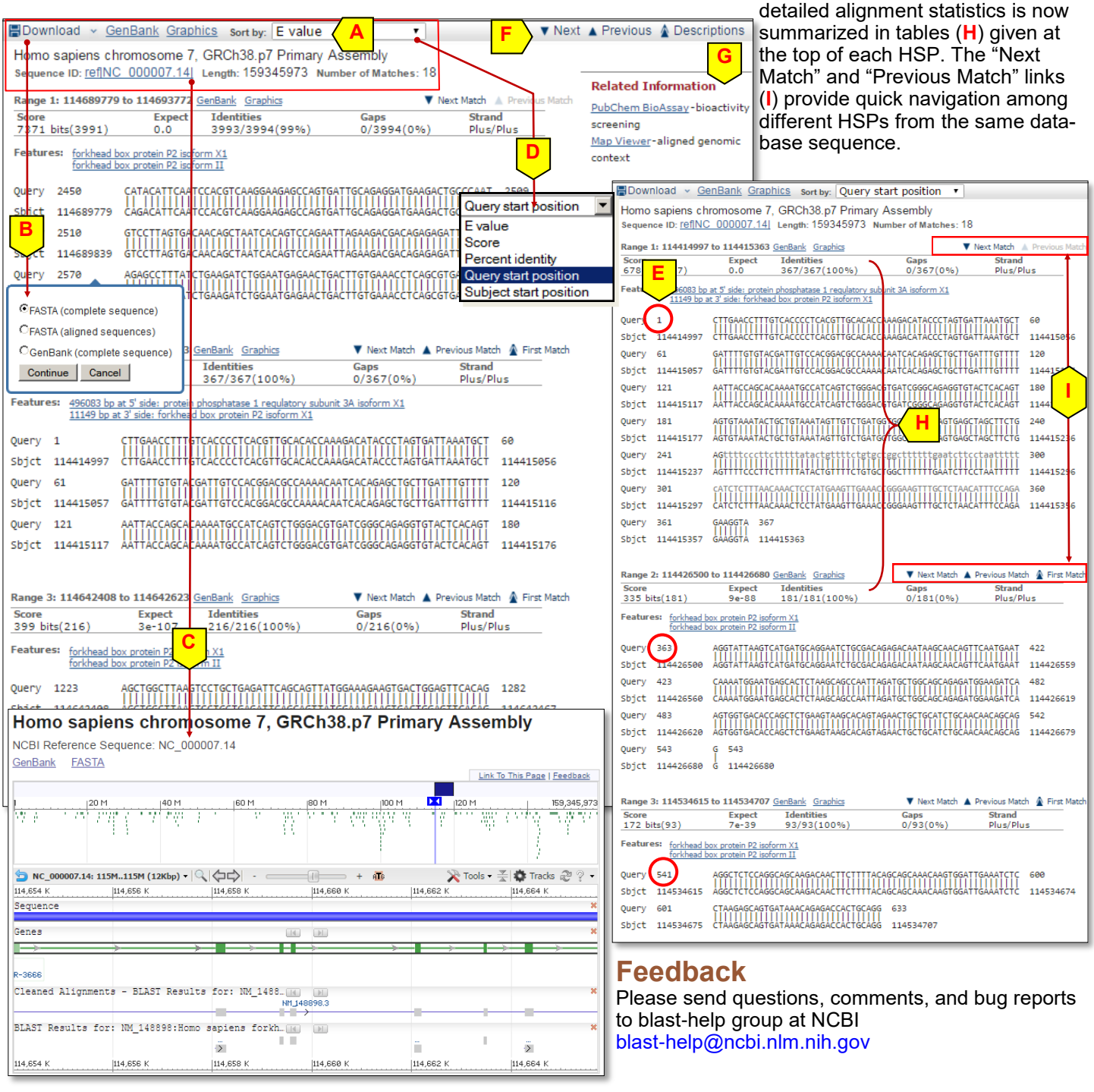
- Sequence Viewer help document www.ncbi.nlm.nih.gov/projects/sviewer/help.html
- Sequence Viewer handout ftp.ncbi.nih.gov/pub/factsheets/Factsheet_Graphical_SV.pdf

The Alignments Section

The Alignments section (below) contains the detailed pairwise alignments between query and database sequences. Segments of alignments, also known as high scoring pairs (HSPs), from the same database sequence are grouped under the same separator (**A**) and are sorted by ascending E-value. Links within the separator, from left to right, provide the following functions:

- "Download" enables downloading the database sequence or its aligned region (**B**).
- "GenBank" retrieves the database sequence record from the source database.
- "Graphics" presents the alignment in SV (**C**) for interactive examination under the context of the annotation of that sequence record.
- "Sort by" (**D**) pull-down menu enables sorting of the HSPs from the same database sequence by specific orders, such as the "Query start position" (**E**) to place mRNAs in the biological natural order to genomic alignments.
- "Next" and "Previous" allows for quick navigation in the Alignments section (**F**).

The "Related Information" section to the right of alignments prominently displays additional information available for each database sequence from NCBI databases such as Gene, UniGene, Map Viewer, GeoProfiles, and Structure (**G**). The detailed alignment statistics is now summarized in tables (**H**) given at the top of each HSP. The "Next Match" and "Previous Match" links (**I**) provide quick navigation among different HSPs from the same database sequence.



Feedback

Please send questions, comments, and bug reports to blast-help group at NCBI
blast-help@ncbi.nlm.nih.gov