



# 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](https://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)

**BLAST®** » **blastn suite** » **RID-SRK1SWX101R** Home Recent Results Saved Strategies Help

**BLAST Results**

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#) [YouTube](#) [How to read this page](#) [Blast report description](#) **B**

**Formatting options** [Reformat](#)

Show Alignment as: **HTML** ☒ Old View [Reset form to defaults](#)

Alignment View: **Pairwise**

Display: ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☐ NCBI-gi ☐ CDS feature

Masking: Character: **Lower Case** Color: **Grey**

Limit results: Descriptions: **100** Graphical overview: **100** Alignments: **100** Line length: **80**

**ref|NM\_000249| (2662 letters)**

RID [SRK1SWX101R](#) (Expires on 07-19 02:19 am)

Query ID [qi|263191547|ref|NM\\_000249.3|](#)

Description [Homo sapiens mutL homolog 1 \(MLH1\), transcript variant 1, mRNA](#)

Molecule type [nucleic acid](#)

Query Length [2662](#)

Database Name [Human G+T \(2 databases\)](#)

Description [See details](#)

Program [BLASTN 2.4.0+](#) [Citation](#)

**BLAST®** Available BLAST jobs [more...](#)

**Lookup BLAST Job**

Request ID: **SRK1SWX101R** **C** [Go](#)

**Format Request**

Query [ref|NM\\_000249| \(2662 letters\)](#)

Database [GPIPE/9606/current/all\\_top\\_level GPIPE/9606/current/rna](#)

Job title [ref|NM\\_000249| \(2662 letters\)](#)

Request ID [SRK1SWX101R](#) [View report](#) ☐ Show results in a new window

Format

Show Alignment as: **HTML** ☒ Old View [Reset form to defaults](#)

Alignment View: **Pairwise**

Display: ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☐ NCBI-gi ☐ CDS feature

Masking: Character: **Lower Case** Color: **Grey**

Limit results: Descriptions: **100** Graphical overview: **100** Alignments: **100** Line length: **80**

## 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).

**Available columns**  
☒ Description  
☒ Max Score  
☒ Total Score  
☒ Coverage  
☒ E-value  
☒ Ident  
☒ Accession  
 Restore Defaults Ok Cancel

Descriptions

Sequences: All None Selected: 7  
 Select: Alignments Download GenPept Graphics Distance tree of results Multiple alignment

Description	Max score	Total score	Query coverage	E value	Max ident	Accession
<a href="#">creatine kinase B-type [Homo sapiens] &gt;gi332843151ref XP_510185.3  PREDICTED: creatine kinase</a>	639	639	100%	0.0	100%	<a href="#">NP_001814.2</a>
<input checked="" type="checkbox"/> <a href="#">creatine kinase B-type [Macaca mulatta]</a>	637	637	100%	0.0	99%	<a href="#">NP_001253960.1</a>
<input checked="" type="checkbox"/> <a href="#">creatine kinase B-type [Bos taurus]</a>	630	630	100%	0.0	97%	<a href="#">NP_001015613.1</a>
<input checked="" type="checkbox"/> <a href="#">creatine kinase, brain [Sus scrofa]</a>	629	629	100%	0.0	97%	<a href="#">NP_001230504.1</a>
<input checked="" type="checkbox"/> <a href="#">creatine kinase B-type [Oryctolagus cuniculus]</a>	626	626	100%	0.0	97%	<a href="#">NP_001075730.1</a>
<input checked="" type="checkbox"/> <a href="#">creatine kinase B-type [Mus musculus]</a>	625	625	100%	0.0	97%	<a href="#">NP_067248.1</a>
<input checked="" type="checkbox"/> <a href="#">creatine kinase B-type [Rattus norvegicus]</a>						
<input type="checkbox"/> <a href="#">putative creatine kinase B variant 1 [Taeniopogon outgroups]</a>						

Select: All None Selected: 0  
 Alignments Download GenBank Graphics Distance tree of results

Description	Max score	Total score	Query coverage	E value	Max ident
<a href="#">Mus musculus predicted gene 9191 (Gm9191) pseudogene on chromosome 16, complete cds</a>	2582	2582	94%	0.0	96%
<a href="#">Human DNA sequence from clone RP11-276H19 on chromosome 9 Contains the 3' end of gene 1 (CDC20f)</a>	2582	2582	94%	0.0	96%
<a href="#">Rhesus Macaque BAC CH250-38L3 () complete sequence</a>	2230	2230	80%	0.0	96%
<a href="#">Homo sapiens CDC20 cell division cycle 20 homolog (CDC20) gene, complete cds</a>	2215	2215	80%	0.0	96%
<a href="#">Homo sapiens chromosome 1 clone RP11-282K6, complete sequence</a>	2213	2213	80%	0.0	96%
<a href="#">Human DNA sequence from clone RP1-92Q14 on chromosome 1p33-34.2 Contains</a>	2200	2200	78%	0.0	96%
<a href="#">Mus musculus BAC clone RP23-497H15 from chromosome 17, complete sequence</a>	2198	2198	80%	0.0	96%
<a href="#">Human DNA sequence from clone RP1-92Q14 on chromosome 1p33-34.2 Contains</a>	1476	1476	89%	0.0	84%
<a href="#">Mus musculus BAC clone RP23-497H15 from chromosome 17, complete sequence</a>	1476	1476	89%	0.0	84%
<a href="#">Mus musculus predicted gene 9191 (Gm9191) pseudogene on chromosome 16, complete cds</a>	1173	1173	81%	0.0	82%
<a href="#">Mouse DNA sequence from clone RP23-87H12 on chromosome 17, complete sequence</a>	1173	1173	81%	0.0	82%
<a href="#">Mouse DNA sequence from clone RP23-89D4 on chromosome X Contains the 3' end of gene 16</a>	922	922	66%	0.0	82%
<a href="#">Rhesus Macaque BAC CH250-38L3 () complete sequence</a>	433	3077	96%	3e-117	100%
<a href="#">Homo sapiens CDC20 cell division cycle 20 homolog (CDC20) gene, complete cds</a>	411	2786	92%	1e-110	100%
<a href="#">Homo sapiens chromosome 1 clone RP11-282K6, complete sequence</a>	411	2792	92%	1e-110	100%
<a href="#">Human DNA sequence from clone RP1-92Q14 on chromosome 1p33-34.2 Contains</a>	411	2786	92%	1e-110	100%

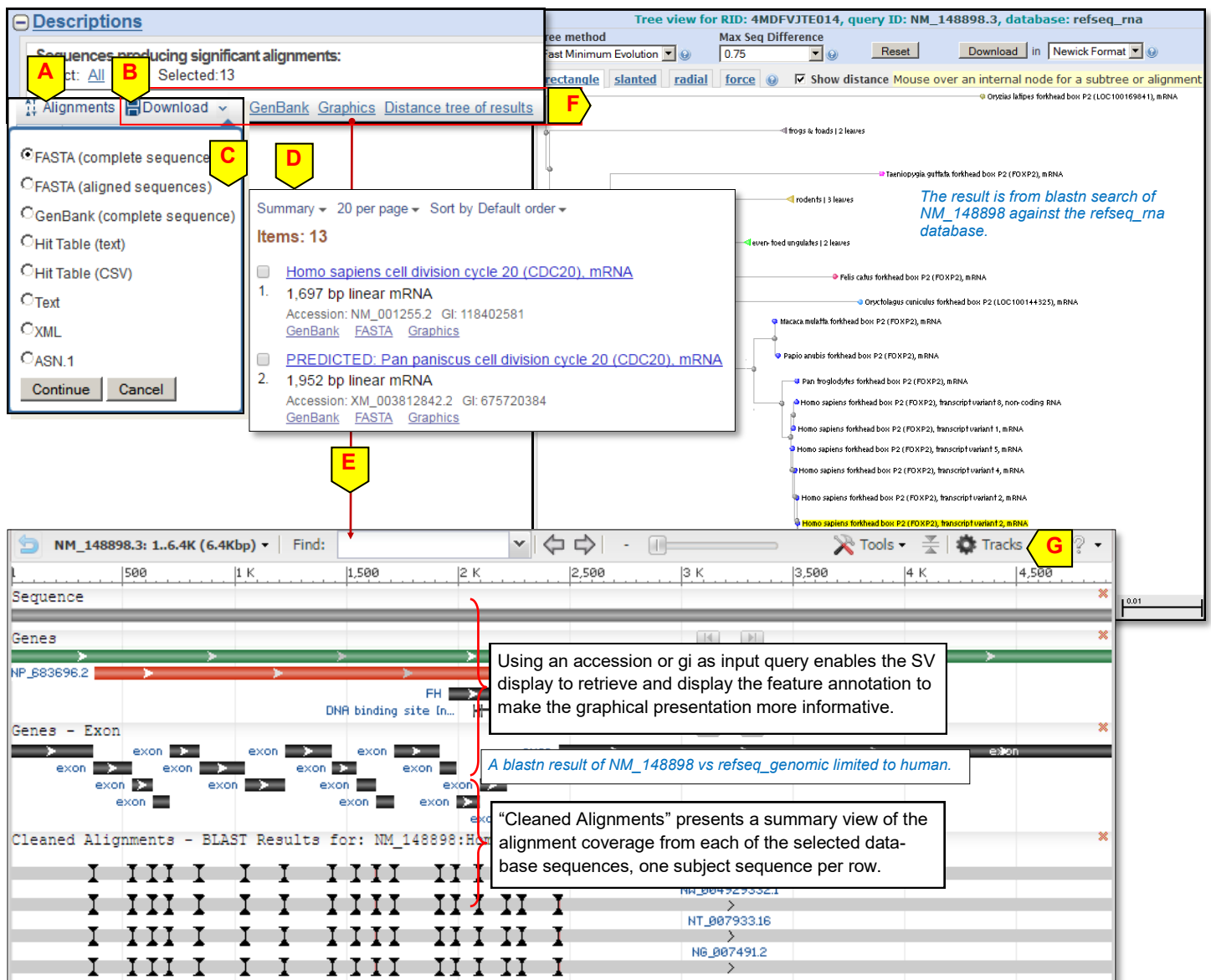
In the table body, clicking a sequence title (G) quickly scrolls the page to display to the alignment section for that sequence where details of the alignment can be examined. Clicking an accession (H) retrieves that record from the corresponding sequence database.

Contact: [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)

NCBI Handout Series | New BLAST | Last Updated on September 8, 2016

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](http://www.ncbi.nlm.nih.gov/projects/sviewer/help.html)
- Sequence Viewer handout [ftp.ncbi.nih.gov/pub/factsheets/Factsheet\\_Graphical\\_SV.pdf](http://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.

The screenshot displays the NCBI BLAST Results page for a query against the Homo sapiens chromosome 7, GRCh38.p7 Primary Assembly. The interface includes several key sections:

- Top Navigation:** Buttons for Download, GenBank, Graphics, and a Sort by menu (set to E value). Navigation links for Next, Previous, and Descriptions are also present.
- Alignment Summary:** Shows the query sequence (Homo sapiens chromosome 7, GRCh38.p7 Primary Assembly) and the database sequence (ref|NC\_000007.14|). Statistics include Score (7371 bits), Expect (0.0), Identities (3993/3994 (99%)), Gaps (0/3994 (0%)), and Strand (Plus/Plus).
- Related Information:** A sidebar on the right provides links to PubChem BioAssay, bioactivity screening, and Map Viewer-aligned genomic context.
- Alignment Details:** The main section shows the pairwise alignment between the query and the database sequence. The query sequence is 2450 bp, and the database sequence is 114689779 to 114693772 bp. The alignment is sorted by E value.
- FASTA Download:** A dropdown menu (B) allows users to download the FASTA (complete sequence), FASTA (aligned sequences), or GenBank (complete sequence).
- Sort by Menu:** A dropdown menu (D) allows users to sort the alignments by E value, Score, Percent identity, Query start position, or Subject start position.
- Statistics Table:** A table (H) summarizes the alignment statistics for each HSP. The table includes columns for Range, Score, Expect, Identities, Gaps, and Strand. The first HSP has a range of 114689779 to 114693772, a score of 7371 bits, and an expect value of 0.0.
- Genomic Context:** A section at the bottom shows the query sequence aligned to the genomic context of the database sequence. The query sequence is 2450 bp, and the database sequence is 114689779 to 114693772 bp. The alignment is sorted by E value.
- Feedback:** A section at the bottom right encourages users to send questions, comments, and bug reports to the blast-help group at NCBI.

## Feedback

Please send questions, comments, and bug reports to blast-help group at NCBI  
[blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)