



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)

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)	Database Name Human G+T (2 databases)
Query ID qi 263191547 ref NM_000249.3 	Description See details
Description Homo sapiens mutL homolog 1 (MLH1), transcript variant 1, mRNA	Program BLASTN 2.4.0+ Citation
Molecule type nucleic acid	
Query Length 2662	

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

Lookup BLAST Job

Request ID: **C**

Format Request

Query [ref|NM_000249| \(2662 letters\)](#)

Database [GPIPE/9606/current/all_top_level GPIPE/9606/current/mna](#)

Job title [ref|NM_000249| \(2662 letters\)](#)

Request ID: Show results in a new window

Format

Show Alignment as: 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

Select: **All** None Selected: 7

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

Description	Max score	Total score	Query coverage	E value	Max ident	Accession
creatine kinase B-type [Homo sapiens] >qil332843151[ref]XP_510185.3[PREDICTED: creatine kinase	639	639	100%	0.0	100%	NP_001814.2
<input checked="" type="checkbox"/> creatine kinase B-type [Macaca mulatta]	637	637	100%	0.0	99%	NP_001253960.1
<input checked="" type="checkbox"/> creatine kinase B-type [Bos taurus]	630	630	100%	0.0	97%	NP_001015613.1
<input checked="" type="checkbox"/> creatine kinase, brain [Sus scrofa]	629	629	100%	0.0	97%	NP_001230504.1
<input checked="" type="checkbox"/> creatine kinase B-type [Oryctolagus cuniculus]	626	626	100%	0.0	97%	NP_001075730.1
<input checked="" type="checkbox"/> creatine kinase B-type [Mus musculus]	625	625	100%	0.0	97%	NP_067248.1
<input type="checkbox"/> putative creatine kinase B variant 1 [Taeniopygia guttata]						

Select: **All** None Selected: 0 **Default: sort by E-value**

Description	Max score	Total score	Query coverage	E value	Max ident
logene 1 [CDC20]	2582	2582	94%	0.0	96%
9 Contains the 3'	2582	2582	94%	0.0	96%
<input type="checkbox"/> Rhesus Macaque BAC CH250-38L3 () complete sequence	433	3077	96%	3e-117	100%
<input type="checkbox"/> Homo sapiens cell division cycle 20 homolog (S. cerevisiae) pseudoqene 1 (CDC20)	2582	2582	94%	0.0	96%
<input type="checkbox"/> Human DNA sequence from clone RP11-276H19 on chromosome 9 Contains the 3'	2582	2582	94%	0.0	96%
<input type="checkbox"/> Homo sapiens CDC20 cell division cycle 20 homolog (CDC20) gene, complete cds	411	2786	92%	1e-110	100%
<input type="checkbox"/> Homo sapiens chromosome 1 clone RP11-282K6, complete sequence	411	2792	92%	1e-110	100%
<input type="checkbox"/> Human DNA sequence from clone RP1-92O14 on chromosome 1p33-34.2 Contains	411	2786	92%	1e-110	100%
<input type="checkbox"/> Mus musculus BAC clone RP23-40 TH23 from chromosome 16, complete sequence	1476	1476	89%	0.0	84%
<input type="checkbox"/> Mus musculus predicted gene 9191 (Gm9191) pseudoqene on chromosome 16	1173	1173	81%	0.0	82%
<input type="checkbox"/> Mus musculus BAC clone RP24-497H15 from chromosome 17, complete sequence	1173	1173	81%	0.0	82%
<input type="checkbox"/> Mouse DNA sequence from clone RP23-87H12 on chromosome 17, complete sequence	1173	1173	81%	0.0	82%
<input type="checkbox"/> Mouse DNA sequence from clone RP23-89D4 on chromosome X Contains the 3' end	922	922	66%	0.0	82%
<input type="checkbox"/> Rhesus Macaque BAC CH250-38L3 () complete sequence	433	3077	96%	3e-117	100%
<input type="checkbox"/> Homo sapiens CDC20 cell division cycle 20 homolog (CDC20) gene, complete cds	411	2786	92%	1e-110	100%
<input type="checkbox"/> Homo sapiens chromosome 1 clone RP11-282K6, complete sequence	411	2792	92%	1e-110	100%
<input type="checkbox"/> Human DNA sequence from clone RP1-92O14 on chromosome 1p33-34.2 Contains	411	2786	92%	1e-110	100%

One alternative: sort by Query coverage

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.

The screenshot displays the NCBI BLAST interface. At the top, the "Descriptions" table shows search results for query ID NM_148898.3. A dropdown menu is open, showing options for downloading sequences in various formats (FASTA, GenBank, etc.). A distance tree of results is visible, showing the relationship between the query and database sequences. The Sequence Viewer is shown at the bottom, displaying the sequence alignment and feature annotations for the query sequence. Annotations A-G highlight specific features and functions:

- A:** Points to the "Alignments" link in the Descriptions table.
- B:** Points to the "Download" link in the Descriptions table.
- C:** Points to the "FASTA (complete sequence)" option in the download menu.
- D:** Points to the "GenBank" link in the download menu.
- E:** Points to the "Graphics" link in the download menu.
- F:** Points to the "Distance tree of results" link in the Descriptions table.
- G:** Points to the "Tools" and "Tracks" menu in the Sequence Viewer.

Additional annotations in the Sequence Viewer include:

- A box stating: "Using an accession or gi as input query enables the SV display to retrieve and display the feature annotation to make the graphical presentation more informative."
- A box stating: "A blastn result of NM_148898 vs refseq_genomic limited to human."
- A box stating: "“Cleaned Alignments” presents a summary view of the alignment coverage from each of the selected database sequences, one subject sequence per row."

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.nlm.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 BLAST Results Page for a query against the Homo sapiens chromosome 7, GRCh38.p7 Primary Assembly. The interface is annotated with letters A through I, corresponding to the text descriptions provided.

Annotations:

- A:** Sort by: E value
- B:** Download button
- C:** Graphics button
- D:** Sort by menu
- E:** Query start position menu
- F:** Next/Previous navigation buttons
- G:** Related Information section
- H:** Alignment statistics table
- I:** Next Match/Previous Match navigation buttons

Alignment Statistics Table (H):

Range	Score	Expect	Identities	Gaps	Strand
1: 114689779 to 114693772	7371 bits (3991)	0.0	3993/3994 (99%)	0/3994 (0%)	Plus/Plus
2: 114414997 to 114415363	678 (7)	0.0	367/367 (100%)	0/367 (0%)	Plus/Plus
3: 114642408 to 114642623	399 bits (216)	3e-107	216/216 (100%)	0/216 (0%)	Plus/Plus
4: 114426500 to 114426680	335 bits (181)	9e-88	181/181 (100%)	0/181 (0%)	Plus/Plus
5: 114534615 to 114534707	172 bits (93)	7e-39	93/93 (100%)	0/93 (0%)	Plus/Plus

Genomic Context (C): Homo sapiens chromosome 7, GRCh38.p7 Primary Assembly. NCBI Reference Sequence: NC_000007.14. GenBank FASTA. The alignment is shown as a blue bar on a genomic track with coordinates from 114,654 K to 114,664 K.

Related Information (G): PubChem BioAssay - bioactivity screening, Map Viewer - aligned genomic context.

Alignment Details: The alignment shows the query sequence (Query) and the subject sequence (Sbjct) with their respective coordinates. The alignment is sorted by E-value, and the "Query start position" menu (E) is used to sort by query start position.

Feedback

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