



## Display BLAST search results with custom output format

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The `-outfmt` option permits formatting arbitrary fields from the BLAST tabular and comma-separated-value (CSV) formats. Use the `-help` option on the command-line application (e.g., `blastn`) to see the supported fields. The `max_target_seqs` option should be used with any tabular output to control the number of matches reported.

### Example of custom output format: field selection

The following example shows how to display the results of a BLAST search using a custom output format. The tabular output format with comments is used, but only the query accession, subject accession, evalue, query start, query stop, subject start, and subject stop are requested. For brevity, only the first 10 lines of output are shown:

```
$ echo 1786181 | ./blastn -db ecoli -outfmt "7 qacc sacc evalue
qstart qend sstart send"
# BLASTN 2.2.18+
# Query: gi|1786181|gb|AE000111.1|AE000111
# Database: ecoli
# Fields: query acc., subject acc., evalue, q. start, q. end, s.
start, s. end
# 85 hits found
AE000111      AE000111      0.0      1      10596      1      10596
AE000111      AE000174      8e-30     5565     5671      6928     6821
AE000111      AE000394      1e-27     5587     5671      135      219
AE000111      AE000425      6e-26     5587     5671      8552     8468
AE000111      AE000171      3e-24     5587     5671      2214     2130
$
```

### Example of custom output format: output separator

One can also customize the output separator in the tabular and comma-separated-value output formats using the `delim` token immediately after the numeric output format selector. In the example below `@` is used as a custom output separator:

```
$ echo 1786181 | blastn -db ecoli -outfmt '6 delim=@' | head
AE000111.1@AE000111.1@100.000@10596@0@0@1@10596@1@10596@0.0@19568
AE000111.1@AE000174.1@88.991@109@9@3@5565@5671@6928@6821@7.69e-30@132
AE000111.1@AE000394.1@92.941@85@6@0@5587@5671@135@219@1.29e-27@124
AE000111.1@AE000425.1@91.860@86@5@2@5587@5671@8552@8468@5.99e-26@119
AE000111.1@AE000171.1@90.588@85@8@0@5587@5671@2214@2130@2.78e-24@113
AE000111.1@AE000171.1@90.476@84@8@0@5587@5670@10559@10642@1.00e-23@111
AE000111.1@AE000376.1@88.889@90@7@3@5587@5675@129@42@1.30e-22@108
AE000111.1@AE000268.1@89.412@85@9@0@5587@5671@6174@6090@1.30e-22@108
AE000111.1@AE000112.1@100.000@58@0@0@10539@10596@1@58@1.30e-22@108
```

```
AE000111.1@AE000447.1@89.286@84@9@0@5587@5670@681@598@4.66e-22@106
$
```

## Trace-back operations (BTOP)

The “Blast trace-back operations” (BTOP) string describes the alignment produced by BLAST. This string is similar to the CIGAR string produced in SAM format, but there are important differences. BTOP is a more flexible format that lists not only the aligned region but also matches and mismatches. BTOP operations consist of 1.) a number with a count of matching letters, 2.) two letters showing a mismatch (e.g., “AG” means A was replaced by G), or 3.) a dash (“-”) and a letter showing a gap. The box below shows a blastn run first with BTOP output and then the same run with the BLAST report showing the alignments.

```
$ blastn -query test_q.fa -subject test_s.fa -dust no -outfmt "6
qseqid sseqid btop" -parse_deflines
query1  q_multi 7AG39
query1  q_multi 7A-39
query1  q_multi 6-G-A41
$ blastn -query test_q.fa -subject test_s.fa -dust no -parse_deflines
BLASTN 2.2.24+
```

```
Query= query1
Length=47
```

```
Subject=
Length=142
```

```
Score = 82.4 bits (44), Expect = 9e-22
Identities = 46/47 (97%), Gaps = 0/47 (0%)
Strand=Plus/Plus
```

```
Query 1  ACGTCCGAGACGCGAGCAGCGAGCAGCAGAGCGACGAGCAGCGACGA 47
          ||||||| |||||||||||||||||||||||||||||||||||
Sbjct 47  ACGTCCGGGACGCGAGCAGCGAGCAGCAGAGCGACGAGCAGCGACGA 93
```

```
Score = 80.5 bits (43), Expect = 3e-21
Identities = 46/47 (97%), Gaps = 1/47 (2%)
Strand=Plus/Plus
```

```
Query 1  ACGTCCGAGACGCGAGCAGCGAGCAGCAGAGCGACGAGCAGCGACGA 47
          ||||||| |||||||||||||||||||||||||||||||||||
Sbjct 1  ACGTCCG-GACGCGAGCAGCGAGCAGCAGAGCGACGAGCAGCGACGA 46
```

```
Score = 78.7 bits (42), Expect = 1e-20
Identities = 47/49 (95%), Gaps = 2/49 (4%)
Strand=Plus/Plus
```

```
Query 1  ACGTCC--GAGACGCGAGCAGCGAGCAGCAGAGCGACGAGCAGCGACGA 47
          ||||||| |||||||||||||||||||||||||||||||||||
Sbjct 94  ACGTCCGAGAGACGCGAGCAGCGAGCAGCAGAGCGACGAGCAGCGACGA 142
```