USAGE

blastn [-h] [-help] [-import\_search\_strategy filename]

[-export\_search\_strategy filename] [-task task\_name] [-db database\_name]

[-dbsize num\_letters] [-gilist filename] [-seqidlist filename]

[-negative\_gilist filename] [-negative\_seqidlist filename]

[-taxids taxids] [-negative\_taxids taxids] [-taxidlist filename]

[-negative\_taxidlist filename] [-no\_taxid\_expansion]

[-entrez\_query entrez\_query] [-db\_soft\_mask filtering\_algorithm]

[-db\_hard\_mask filtering\_algorithm] [-subject subject\_input\_file]

[-subject\_loc range] [-query input\_file] [-out output\_file]

[-evalue evalue] [-word\_size int\_value] [-gapopen open\_penalty]

[-gapextend extend\_penalty] [-perc\_identity float\_value]

[-qcov\_hsp\_perc float\_value] [-max\_hsps int\_value]

[-xdrop\_ungap float\_value] [-xdrop\_gap float\_value]

[-xdrop\_gap\_final float\_value] [-searchsp int\_value] [-penalty penalty]

[-reward reward] [-no\_greedy] [-min\_raw\_gapped\_score int\_value]

[-template\_type type] [-template\_length int\_value] [-dust DUST\_options]

[-filtering\_db filtering\_database]

[-window\_masker\_taxid window\_masker\_taxid]

[-window\_masker\_db window\_masker\_db] [-soft\_masking soft\_masking]

[-ungapped] [-culling\_limit int\_value] [-best\_hit\_overhang float\_value]

[-best\_hit\_score\_edge float\_value] [-subject\_besthit]

[-window\_size int\_value] [-off\_diagonal\_range int\_value]

[-use\_index boolean] [-index\_name string] [-lcase\_masking]

[-query\_loc range] [-strand strand] [-parse\_deflines] [-outfmt format]

[-show\_gis] [-num\_descriptions int\_value] [-num\_alignments int\_value]

[-line\_length line\_length] [-html] [-sorthits sort\_hits]

[-sorthsps sort\_hsps] [-max\_target\_seqs num\_sequences]

[-num\_threads int\_value] [-mt\_mode int\_value] [-remote] [-version]

DESCRIPTION

Nucleotide-Nucleotide BLAST 2.15.0+

OPTIONAL ARGUMENTS

-h

Print USAGE and DESCRIPTION; ignore all other parameters

-help

Print USAGE, DESCRIPTION and ARGUMENTS; ignore all other parameters

-version

Print version number; ignore other arguments

\*\*\* Input query options

-query <File\_In>

Input file name

Default = `-'

-query\_loc <String>

Location on the query sequence in 1-based offsets (Format: start-stop)

-strand <String, `both', `minus', `plus'>

Query strand(s) to search against database/subject

Default = `both'

\*\*\* General search options

-task <String, Permissible values: 'blastn' 'blastn-short' 'dc-megablast'

'megablast' 'rmblastn' >

Task to execute

Default = `megablast'

-db <String>

BLAST database name

\* Incompatible with: subject, subject\_loc

-out <File\_Out, file name length < 256>

Output file name

Default = `-'

-evalue <Real>

Expectation value (E) threshold for saving hits. Default = 10 (1000 for

blastn-short)

-word\_size <Integer, >=4>

Word size for wordfinder algorithm (length of best perfect match)

-gapopen <Integer>

Cost to open a gap

-gapextend <Integer>

Cost to extend a gap

-penalty <Integer, <=0>

Penalty for a nucleotide mismatch

-reward <Integer, >=0>

Reward for a nucleotide match

-use\_index <Boolean>

Use MegaBLAST database index

Default = `false'

-index\_name <String>

MegaBLAST database index name (deprecated; use only for old style indices)

\*\*\* BLAST-2-Sequences options

-subject <File\_In>

Subject sequence(s) to search

\* Incompatible with: no\_taxid\_expansion, db, gilist, seqidlist,

negative\_gilist, negative\_seqidlist, taxids, taxidlist, negative\_taxids,

negative\_taxidlist, no\_taxid\_expansion, db\_soft\_mask, db\_hard\_mask

-subject\_loc <String>

Location on the subject sequence in 1-based offsets (Format: start-stop)

\* Incompatible with: no\_taxid\_expansion, db, gilist, seqidlist,

negative\_gilist, negative\_seqidlist, taxids, taxidlist, negative\_taxids,

negative\_taxidlist, no\_taxid\_expansion, db\_soft\_mask, db\_hard\_mask, remote

\*\*\* Formatting options

-outfmt <String>

alignment view options:

0 = Pairwise,

1 = Query-anchored showing identities,

2 = Query-anchored no identities,

3 = Flat query-anchored showing identities,

4 = Flat query-anchored no identities,

5 = BLAST XML,

6 = Tabular,

7 = Tabular with comment lines,

8 = Seqalign (Text ASN.1),

9 = Seqalign (Binary ASN.1),

10 = Comma-separated values,

11 = BLAST archive (ASN.1),

12 = Seqalign (JSON),

13 = Multiple-file BLAST JSON,

14 = Multiple-file BLAST XML2,

15 = Single-file BLAST JSON,

16 = Single-file BLAST XML2,

17 = Sequence Alignment/Map (SAM),

18 = Organism Report

Options 6, 7, 10 and 17 can be additionally configured to produce

a custom format specified by space delimited format specifiers,

or in the case of options 6, 7, and 10, by a token specified

by the delim keyword. E.g.: "17 delim=@ qacc sacc score".

The delim keyword must appear after the numeric output format

specification.

The supported format specifiers for options 6, 7 and 10 are:

qseqid means Query Seq-id

qgi means Query GI

qacc means Query accession

qaccver means Query accession.version

qlen means Query sequence length

sseqid means Subject Seq-id

sallseqid means All subject Seq-id(s), separated by a ';'

sgi means Subject GI

sallgi means All subject GIs

sacc means Subject accession

saccver means Subject accession.version

sallacc means All subject accessions

slen means Subject sequence length

qstart means Start of alignment in query

qend means End of alignment in query

sstart means Start of alignment in subject

send means End of alignment in subject

qseq means Aligned part of query sequence

sseq means Aligned part of subject sequence

evalue means Expect value

bitscore means Bit score

score means Raw score

length means Alignment length

pident means Percentage of identical matches

nident means Number of identical matches

mismatch means Number of mismatches

positive means Number of positive-scoring matches

gapopen means Number of gap openings

gaps means Total number of gaps

ppos means Percentage of positive-scoring matches

frames means Query and subject frames separated by a '/'

qframe means Query frame

sframe means Subject frame

btop means Blast traceback operations (BTOP)

staxid means Subject Taxonomy ID

ssciname means Subject Scientific Name

scomname means Subject Common Name

sblastname means Subject Blast Name

sskingdom means Subject Super Kingdom

staxids means unique Subject Taxonomy ID(s), separated by a ';'

(in numerical order)

sscinames means unique Subject Scientific Name(s), separated by a ';'

scomnames means unique Subject Common Name(s), separated by a ';'

sblastnames means unique Subject Blast Name(s), separated by a ';'

(in alphabetical order)

sskingdoms means unique Subject Super Kingdom(s), separated by a ';'

(in alphabetical order)

stitle means Subject Title

salltitles means All Subject Title(s), separated by a '<>'

sstrand means Subject Strand

qcovs means Query Coverage Per Subject

qcovhsp means Query Coverage Per HSP

qcovus means Query Coverage Per Unique Subject (blastn only)

When not provided, the default value is:

'qaccver saccver pident length mismatch gapopen qstart qend sstart send

evalue bitscore', which is equivalent to the keyword 'std'

The supported format specifier for option 17 is:

SQ means Include Sequence Data

SR means Subject as Reference Seq

Default = `0'

-show\_gis

Show NCBI GIs in deflines?

-num\_descriptions <Integer, >=0>

Number of database sequences to show one-line descriptions for

Not applicable for outfmt > 4

Default = `500'

\* Incompatible with: max\_target\_seqs

-num\_alignments <Integer, >=0>

Number of database sequences to show alignments for

Default = `250'

\* Incompatible with: max\_target\_seqs

-line\_length <Integer, >=1>

Line length for formatting alignments

Not applicable for outfmt > 4

Default = `60'

-html

Produce HTML output?

-sorthits <Integer, (>=0 and =<4)>

Sorting option for hits:

alignment view options:

0 = Sort by evalue,

1 = Sort by bit score,

2 = Sort by total score,

3 = Sort by percent identity,

4 = Sort by query coverage

Not applicable for outfmt > 4

-sorthsps <Integer, (>=0 and =<4)>

Sorting option for hps:

0 = Sort by hsp evalue,

1 = Sort by hsp score,

2 = Sort by hsp query start,

3 = Sort by hsp percent identity,

4 = Sort by hsp subject start

Not applicable for outfmt != 0

\*\*\* Query filtering options

-dust <String>

Filter query sequence with DUST (Format: 'yes', 'level window linker', or

'no' to disable) Default = '20 64 1' ('no' for blastn-short)

-filtering\_db <String>

BLAST database containing filtering elements (i.e.: repeats)

-window\_masker\_taxid <Integer>

Enable WindowMasker filtering using a Taxonomic ID

\* Incompatible with: no\_taxid\_expansion

-window\_masker\_db <String>

Enable WindowMasker filtering using this repeats database.

-soft\_masking <Boolean>

Apply filtering locations as soft masks

Default = `true'

-lcase\_masking

Use lower case filtering in query and subject sequence(s)?

\*\*\* Restrict search or results

-gilist <String>

Restrict search of database to list of GIs

\* Incompatible with: no\_taxid\_expansion, seqidlist, taxids, taxidlist,

negative\_gilist, negative\_seqidlist, negative\_taxids, negative\_taxidlist,

remote, subject, subject\_loc

-seqidlist <String>

Restrict search of database to list of SeqIDs

\* Incompatible with: no\_taxid\_expansion, gilist, taxids, taxidlist,

negative\_gilist, negative\_seqidlist, negative\_taxids, negative\_taxidlist,

remote, subject, subject\_loc

-negative\_gilist <String>

Restrict search of database to everything except the specified GIs

\* Incompatible with: no\_taxid\_expansion, gilist, seqidlist, taxids,

taxidlist, negative\_seqidlist, negative\_taxids, negative\_taxidlist, remote,

subject, subject\_loc

-negative\_seqidlist <String>

Restrict search of database to everything except the specified SeqIDs

\* Incompatible with: no\_taxid\_expansion, gilist, seqidlist, taxids,

taxidlist, negative\_gilist, negative\_taxids, negative\_taxidlist, remote,

subject, subject\_loc

-taxids <String>

Restrict search of database to include only the specified taxonomy IDs and

their descendants (multiple IDs delimited by ',')

\* Incompatible with: gilist, seqidlist, taxidlist, negative\_gilist,

negative\_seqidlist, negative\_taxids, negative\_taxidlist, remote, subject,

subject\_loc

-negative\_taxids <String>

Restrict search of database to everything except the specified taxonomy IDs

and their descendants (multiple IDs delimited by ',')

\* Incompatible with: gilist, seqidlist, taxids, taxidlist,

negative\_gilist, negative\_seqidlist, negative\_taxidlist, remote, subject,

subject\_loc

-taxidlist <String>

Restrict search of database to include only the specified taxonomy IDs and

their descendants

\* Incompatible with: gilist, seqidlist, taxids, negative\_gilist,

negative\_seqidlist, negative\_taxids, negative\_taxidlist, remote, subject,

subject\_loc

-negative\_taxidlist <String>

Restrict search of database to everything except the specified taxonomy IDs

and their descendants

\* Incompatible with: gilist, seqidlist, taxids, taxidlist,

negative\_gilist, negative\_seqidlist, negative\_taxids, remote, subject,

subject\_loc

-no\_taxid\_expansion

Do not expand the taxonomy IDs provided to their descendant taxonomy IDs

\* Incompatible with: subject, subject\_loc, window\_masker\_taxid, gilist,

seqidlist, negative\_gilist, negative\_seqidlist, subject, subject\_loc

-entrez\_query <String>

Restrict search with the given Entrez query

\* Requires: remote

-db\_soft\_mask <String>

Filtering algorithm ID to apply to the BLAST database as soft masking

\* Incompatible with: db\_hard\_mask, subject, subject\_loc

-db\_hard\_mask <String>

Filtering algorithm ID to apply to the BLAST database as hard masking

\* Incompatible with: db\_soft\_mask, subject, subject\_loc

-perc\_identity <Real, 0..100>

Percent identity

-qcov\_hsp\_perc <Real, 0..100>

Percent query coverage per hsp

-max\_hsps <Integer, >=1>

Set maximum number of HSPs per subject sequence to save for each query

-culling\_limit <Integer, >=0>

If the query range of a hit is enveloped by that of at least this many

higher-scoring hits, delete the hit

\* Incompatible with: best\_hit\_overhang, best\_hit\_score\_edge

-best\_hit\_overhang <Real, (>0 and <0.5)>

Best Hit algorithm overhang value (recommended value: 0.1)

\* Incompatible with: culling\_limit

-best\_hit\_score\_edge <Real, (>0 and <0.5)>

Best Hit algorithm score edge value (recommended value: 0.1)

\* Incompatible with: culling\_limit

-subject\_besthit

Turn on best hit per subject sequence

-max\_target\_seqs <Integer, >=1>

Maximum number of aligned sequences to keep

(value of 5 or more is recommended)

Default = `500'

\* Incompatible with: num\_descriptions, num\_alignments

\*\*\* Discontiguous MegaBLAST options

-template\_type <String, `coding', `coding\_and\_optimal', `optimal'>

Discontiguous MegaBLAST template type

\* Requires: template\_length

-template\_length <Integer, Permissible values: '16' '18' '21' >

Discontiguous MegaBLAST template length

\* Requires: template\_type

\*\*\* Statistical options

-dbsize <Int8>

Effective length of the database

-searchsp <Int8, >=0>

Effective length of the search space

\*\*\* Search strategy options

-import\_search\_strategy <File\_In>

Search strategy to use

\* Incompatible with: export\_search\_strategy

-export\_search\_strategy <File\_Out>

File name to record the search strategy used

\* Incompatible with: import\_search\_strategy

\*\*\* Extension options

-xdrop\_ungap <Real>

X-dropoff value (in bits) for ungapped extensions

-xdrop\_gap <Real>

X-dropoff value (in bits) for preliminary gapped extensions

-xdrop\_gap\_final <Real>

X-dropoff value (in bits) for final gapped alignment

-no\_greedy

Use non-greedy dynamic programming extension

-min\_raw\_gapped\_score <Integer>

Minimum raw gapped score to keep an alignment in the preliminary gapped and

traceback stages

-ungapped

Perform ungapped alignment only?

-window\_size <Integer, >=0>

Multiple hits window size, use 0 to specify 1-hit algorithm

-off\_diagonal\_range <Integer, >=0>

Number of off-diagonals to search for the 2nd hit, use 0 to turn off

Default = `0'

\*\*\* Miscellaneous options

-parse\_deflines

Should the query and subject defline(s) be parsed?

-num\_threads <Integer, >=1>

Number of threads (CPUs) to use in the BLAST search

Default = `1'

\* Incompatible with: remote

-mt\_mode <Integer, (>=0 and =<2)>

Multi-thread mode to use in BLAST search:

0 auto split by database or queries

1 split by queries

2 split by database

Default = `0'

\* Requires: num\_threads

-remote

Execute search remotely?

\* Incompatible with: gilist, seqidlist, taxids, taxidlist,

negative\_gilist, negative\_seqidlist, negative\_taxids, negative\_taxidlist,

subject\_loc, num\_threads