DESCRIPTION
   Protein Query-Translated Subject BLAST 2.14.0+

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 = `-'
    * Incompatible with:  in_pssm
 -query_loc <String>
   Location on the query sequence in 1-based offsets (Format: start-stop)
    * Incompatible with:  in_pssm

 *** General search options
 -task <String, Permissible values: 'tblastn' 'tblastn-fast' >
   Task to execute
   Default = `tblastn'
 -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
 -word_size <Integer, >=2>
   Word size for wordfinder algorithm
 -gapopen <Integer>
   Cost to open a gap
 -gapextend <Integer>
   Cost to extend a gap
 -db_gencode <Integer, values between: 1-6, 9-16, 21-31, 33>
   Genetic code to use to translate database/subjects (see user manual for
   details)
   Default = `1'
 -max_intron_length <Integer, >=0>
   Length of the largest intron allowed in a translated nucleotide sequence
   when linking multiple distinct alignments
   Default = `0'
 -matrix <String>
   Scoring matrix name (normally BLOSUM62)
 -threshold <Real, >=0>
   Minimum word score such that the word is added to the BLAST lookup table
 -comp_based_stats <String>
   Use composition-based statistics:

D or d: default (equivalent to 2 )
    0 or F or f: No composition-based statistics
    1: Composition-based statistics as in NAR 29:2994-3005, 2001
    2 or T or t : Composition-based score adjustment as in Bioinformatics
  21:902-911,
    2005, conditioned on sequence properties
    3: Composition-based score adjustment as in Bioinformatics 21:902-911,
    2005, unconditionally
  Default = `2'

*** BLAST-2-Sequences options
-subject <File_In>
  Subject sequence(s) to search
   * Incompatible with:  db, gilist, seqidlist, negative_gilist,
  negative_seqidlist, taxids, taxidlist, negative_taxids, negative_taxidlist,
  db_soft_mask, db_hard_mask
-subject_loc <String>
  Location on the subject sequence in 1-based offsets (Format: start-stop)
   * Incompatible with:  db, gilist, seqidlist, negative_gilist,
  negative_seqidlist, taxids, taxidlist, negative_taxids, negative_taxidlist,
  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,
   18 = Organism Report

  Options 6, 7 and 10 can be additionally configured to produce
  a custom format specified by space delimited format specifiers,
  or by a token specified by the delim keyword.
   E.g.: "10 delim=@ qacc sacc score".
  The delim keyword must appear after the numeric output format
  specification.
  The supported format specifiers are:
          qseqid means Query Seq-id

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           qgi means Query GI
         qacc means Query accesion
      qaccver means Query accesion.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'
   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
 -seg <String>
   Filter query sequence with SEG (Format: 'yes', 'window locut hicut', or
   'no' to disable)
   Default = `12 2.2 2.5'
 -soft_masking <Boolean>
   Apply filtering locations as soft masks
   Default = `false'
 -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:  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:  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:  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:  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
 (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
 (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
  * 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
  * Incompatible with:  gilist, seqidlist, taxids, taxidlist,
 negative_gilist, negative_seqidlist, negative_taxids, remote, 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
-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

*** Statistical options
-dbsize <Int8>
  Effective length of the database
-searchsp <Int8, >=0>
  Effective length of the search space
-sum_stats <Boolean>
  Use sum statistics

*** 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
-ungapped
  Perform ungapped alignment only?
-window_size <Integer, >=0>
  Multiple hits window size, use 0 to specify 1-hit algorithm

*** 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 =<1)>
 Multi-thread mode to use in BLAST search:
  0 (auto) split by database
  1 split by queries
 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, in_pssm
-use_sw_tback
 Compute locally optimal Smith-Waterman alignments?

*** PSI-TBLASTN options
-in_pssm <File_In>
 PSI-TBLASTN checkpoint file
  * Incompatible with:  remote, query, query_loc