Microsoft Windows [Version 6.3.9600]

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C:\Users\Alex\Desktop\Work\Research\Lettuce>cd C:\Program Files\NCBI\blast-2.2.2

9+\db\extract

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out ~\Users\Alex\Desktop\

Work\Research\Lettuce\SampleBlast2.csv -outfmt 10 qseqid sseqid pident length mi

smatch gapopen qstart qend sstart send evalue bitscore stitle -query ~\Users\Ale

x\Desktop\Work\Research\Lettuce\Samplesequence.fasta -db refseqplant -evalue 0.0

01

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

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

[-searchsp int\_value] [-max\_hsps int\_value] [-sum\_statistics]

[-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] [-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] [-html] [-max\_target\_seqs num\_sequences]

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

DESCRIPTION

Nucleotide-Nucleotide BLAST 2.2.29+

Use '-help' to print detailed descriptions of command line arguments

========================================================================

Error: Too many positional arguments (1), the offending value: qseqid

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out ~\Users\Alex\Desktop\

Work\Research\Lettuce\SampleBlast2.csv -outfmt "10 qseqid sseqid pident length m

ismatch gapopen qstart qend sstart send evalue bitscore stitle" -query ~\Users\A

lex\Desktop\Work\Research\Lettuce\Samplesequence.fasta -db refseqplant -evalue 0

.001

Command line argument error: Argument "query". File is not accessible: `~\Users

\Alex\Desktop\Work\Research\Lettuce\Samplesequence.fasta'

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out ~\Users\Alex\Desktop\

Work\Research\Lettuce\SampleBlast2.csv -outfmt "10 qseqid sseqid pident length m

ismatch gapopen qstart qend sstart send evalue bitscore stitle" -query C:\Users\

Alex\Desktop\Work\Research\Lettuce\Samplesequence.fasta -db refseqplant -evalue

0.001

Command line argument error: Argument "query". File is not accessible: `C:\User

s\Alex\Desktop\Work\Research\Lettuce\Samplesequence.fasta'

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out ~\Users\Alex\Desktop\

Work\Research\Lettuce\SampleBlast2.csv -outfmt "10 qseqid sseqid pident length m

ismatch gapopen qstart qend sstart send evalue bitscore stitle" -query ~\Users\A

lex\Desktop\Work\Research\Lettuce\Samplesequence.fasta -db refseqplant -evalue 0

.001

Command line argument error: Argument "query". File is not accessible: `~\Users

\Alex\Desktop\Work\Research\Lettuce\Samplesequence.fasta'

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out ~\Users\Alex\Desktop\

Work\Research\Lettuce\SampleBlast2.csv -outfmt "10 qseqid sseqid pident length m

ismatch gapopen qstart qend sstart send evalue bitscore stitle" -query ~\Users\A

lex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.0

01

Command line argument error: Argument "query". File is not accessible: `~\Users

\Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt'

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out ~\Users\Alex\Desktop\

Work\Research\Lettuce\SampleBlast2.csv -outfmt "10 qseqid sseqid pident length m

ismatch gapopen qstart qend sstart send evalue bitscore stitle" -query C:\Users\

Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.

001

Command line argument error: Argument "out". File is not accessible: `~\Users\A

lex\Desktop\Work\Research\Lettuce\SampleBlast2.csv'

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast2.csv -outfmt "10 qseqid sseqid pident length

mismatch gapopen qstart qend sstart send evalue bitscore stitle" -query C:\Users

\Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0

.001

Error: (1431.1) FASTA-Reader: Warning: FASTA-Reader: Ignoring FASTA modifier(s)

found because the input was not expected to have any.

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast3.csv -outfmt "10 qseqid sseqid pident length

mismatch gapopen qstart qend sstart send evalue bitscore" -query C:\Users\Alex\D

esktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.001

Error: (1431.1) FASTA-Reader: Warning: FASTA-Reader: Ignoring FASTA modifier(s)

found because the input was not expected to have any.

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast4.csv -outfmt "10 qseqid sseqid pident length

mismatch gapopen qstart qend sstart send evalue bitscore salltitles scinames sal

lseqid sgi sallgi sacc sallacc stitle" -query C:\Users\Alex\Desktop\Work\Researc

h\Lettuce\Samplesequence.fasta -db refseqplant -evalue 0.001

Command line argument error: Argument "query". File is not accessible: `C:\User

s\Alex\Desktop\Work\Research\Lettuce\Samplesequence.fasta'

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast4.csv -outfmt "10 qseqid sseqid pident length

mismatch gapopen qstart qend sstart send evalue bitscore salltitles scinames sal

lseqid sgi sallgi sacc sallacc stitle" -query C:\Users\Alex\Desktop\Work\Researc

h\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.001

Error: (1431.1) FASTA-Reader: Warning: FASTA-Reader: Ignoring FASTA modifier(s)

found because the input was not expected to have any.

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast4.csv -outfmt "10 salltitles" -query C:\Users\

Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.

001

Command line argument error: Argument "out". File is not accessible: `C:\Users\

Alex\Desktop\Work\Research\Lettuce\SampleBlast4.csv'

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast5.csv -outfmt "10 salltitles" -query C:\Users\

Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.

001

Error: (1431.1) FASTA-Reader: Warning: FASTA-Reader: Ignoring FASTA modifier(s)

found because the input was not expected to have any.

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast6.csv -outfmt "10 scinames" -query C:\Users\Al

ex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.00

1

Error: (1431.1) FASTA-Reader: Warning: FASTA-Reader: Ignoring FASTA modifier(s)

found because the input was not expected to have any.

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast7.csv -outfmt "10 qseqid sseqid pident length

mismatch qstart sqend sstart send evalue bitscore sgi sacc stitle" -query C:\Use

rs\Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue

0.001

Error: (1431.1) FASTA-Reader: Warning: FASTA-Reader: Ignoring FASTA modifier(s)

found because the input was not expected to have any.

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast7.csv -outfmt "10 qseqid sseqid pident length mismatch qstart sqend sstart send evalue bitscore sgi sacc stitle" -query C:\Use

rs\Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue

0.001

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C:\Users\Alex\Desktop\Work\Research\Lettuce>cd C:\Program Files\NCBI\blast-2.2.2

9+\db\extract

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out ~\Users\Alex\Desktop\

Work\Research\Lettuce\SampleBlast2.csv -outfmt 10 qseqid sseqid pident length mi

smatch gapopen qstart qend sstart send evalue bitscore stitle -query ~\Users\Ale

x\Desktop\Work\Research\Lettuce\Samplesequence.fasta -db refseqplant -evalue 0.0

01

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

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

[-searchsp int\_value] [-max\_hsps int\_value] [-sum\_statistics]

[-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] [-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] [-html] [-max\_target\_seqs num\_sequences]

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

DESCRIPTION

Nucleotide-Nucleotide BLAST 2.2.29+

Use '-help' to print detailed descriptions of command line arguments

========================================================================

Error: Too many positional arguments (1), the offending value: qseqid

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out ~\Users\Alex\Desktop\

Work\Research\Lettuce\SampleBlast2.csv -outfmt "10 qseqid sseqid pident length m

ismatch gapopen qstart qend sstart send evalue bitscore stitle" -query ~\Users\A

lex\Desktop\Work\Research\Lettuce\Samplesequence.fasta -db refseqplant -evalue 0

.001

Command line argument error: Argument "query". File is not accessible: `~\Users

\Alex\Desktop\Work\Research\Lettuce\Samplesequence.fasta'

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out ~\Users\Alex\Desktop\

Work\Research\Lettuce\SampleBlast2.csv -outfmt "10 qseqid sseqid pident length m

ismatch gapopen qstart qend sstart send evalue bitscore stitle" -query C:\Users\

Alex\Desktop\Work\Research\Lettuce\Samplesequence.fasta -db refseqplant -evalue

0.001

Command line argument error: Argument "query". File is not accessible: `C:\User

s\Alex\Desktop\Work\Research\Lettuce\Samplesequence.fasta'

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out ~\Users\Alex\Desktop\

Work\Research\Lettuce\SampleBlast2.csv -outfmt "10 qseqid sseqid pident length m

ismatch gapopen qstart qend sstart send evalue bitscore stitle" -query ~\Users\A

lex\Desktop\Work\Research\Lettuce\Samplesequence.fasta -db refseqplant -evalue 0

.001

Command line argument error: Argument "query". File is not accessible: `~\Users

\Alex\Desktop\Work\Research\Lettuce\Samplesequence.fasta'

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out ~\Users\Alex\Desktop\

Work\Research\Lettuce\SampleBlast2.csv -outfmt "10 qseqid sseqid pident length m

ismatch gapopen qstart qend sstart send evalue bitscore stitle" -query ~\Users\A

lex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.0

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Command line argument error: Argument "query". File is not accessible: `~\Users

\Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt'

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out ~\Users\Alex\Desktop\

Work\Research\Lettuce\SampleBlast2.csv -outfmt "10 qseqid sseqid pident length m

ismatch gapopen qstart qend sstart send evalue bitscore stitle" -query C:\Users\

Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.

001

Command line argument error: Argument "out". File is not accessible: `~\Users\A

lex\Desktop\Work\Research\Lettuce\SampleBlast2.csv'

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast2.csv -outfmt "10 qseqid sseqid pident length

mismatch gapopen qstart qend sstart send evalue bitscore stitle" -query C:\Users

\Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0

.001

Error: (1431.1) FASTA-Reader: Warning: FASTA-Reader: Ignoring FASTA modifier(s)

found because the input was not expected to have any.

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast3.csv -outfmt "10 qseqid sseqid pident length

mismatch gapopen qstart qend sstart send evalue bitscore" -query C:\Users\Alex\D

esktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.001

Error: (1431.1) FASTA-Reader: Warning: FASTA-Reader: Ignoring FASTA modifier(s)

found because the input was not expected to have any.

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast4.csv -outfmt "10 qseqid sseqid pident length

mismatch gapopen qstart qend sstart send evalue bitscore salltitles scinames sal

lseqid sgi sallgi sacc sallacc stitle" -query C:\Users\Alex\Desktop\Work\Researc

h\Lettuce\Samplesequence.fasta -db refseqplant -evalue 0.001

Command line argument error: Argument "query". File is not accessible: `C:\User

s\Alex\Desktop\Work\Research\Lettuce\Samplesequence.fasta'

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast4.csv -outfmt "10 qseqid sseqid pident length

mismatch gapopen qstart qend sstart send evalue bitscore salltitles scinames sal

lseqid sgi sallgi sacc sallacc stitle" -query C:\Users\Alex\Desktop\Work\Researc

h\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.001

Error: (1431.1) FASTA-Reader: Warning: FASTA-Reader: Ignoring FASTA modifier(s)

found because the input was not expected to have any.

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast4.csv -outfmt "10 salltitles" -query C:\Users\

Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.

001

Command line argument error: Argument "out". File is not accessible: `C:\Users\

Alex\Desktop\Work\Research\Lettuce\SampleBlast4.csv'

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast5.csv -outfmt "10 salltitles" -query C:\Users\

Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.

001

Error: (1431.1) FASTA-Reader: Warning: FASTA-Reader: Ignoring FASTA modifier(s)

found because the input was not expected to have any.

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast6.csv -outfmt "10 scinames" -query C:\Users\Al

ex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.00

1

Error: (1431.1) FASTA-Reader: Warning: FASTA-Reader: Ignoring FASTA modifier(s)

found because the input was not expected to have any.

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast7.csv -outfmt "10 qseqid sseqid pident length

mismatch qstart sqend sstart send evalue bitscore sgi sacc stitle" -query C:\Use

rs\Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue

0.001

Error: (1431.1) FASTA-Reader: Warning: FASTA-Reader: Ignoring FASTA modifier(s)

found because the input was not expected to have any.

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast7.csv -outfmt "10 qseqid sseqid pident length

mismatch qstart sqend sstart send evalue bitscore sgi sacc stitle" -query C:\Use

rs\Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue

0.001

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast8.csv -outfmt "10 send" -query C:\Users\Alex\D

esktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.001

Error: (1431.1) FASTA-Reader: Warning: FASTA-Reader: Ignoring FASTA modifier(s)

found because the input was not expected to have any.

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast8.csv -outfmt "10 qseqid sseqid pident length

mismatch gapopen qstart qend sstart send evalue bitscore sgi sacc stitle" -query

C:\Users\Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant

-evalue 0.001

Command line argument error: Argument "out". File is not accessible: `C:\Users\

Alex\Desktop\Work\Research\Lettuce\SampleBlast8.csv'

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn -out C:\Users\Alex\Desktop

\Work\Research\Lettuce\SampleBlast9.csv -outfmt "10 qseqid sseqid pident length

mismatch gapopen qstart qend sstart send evalue bitscore sgi sacc stitle" -query

C:\Users\Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant

-evalue 0.001

Error: (1431.1) FASTA-Reader: Warning: FASTA-Reader: Ignoring FASTA modifier(s)

found because the input was not expected to have any.

C:\Program Files\NCBI\blast-2.2.29+\db\extract>blastn –out C:\Users\Alex\Desktop\Work\Research\Lettuce\SampleBlast9.csv -outfmt "10 qseqid sseqid pident length mismatch gapopen qstart qend sstart send evalue bitscore sgi sacc stitle" –query C:\Users\Alex\Desktop\Work\Research\Lettuce\Samplesequence.txt -db refseqplant -evalue 0.001

C:\Program Files\NCBI\blast-2.2.29+\db\extract>