How to query a NCBI database with a fasta file

Purpose: To query a NCBI database with another fasta file. This will determine if any sequences in the fasta file have similarity to sequences in the database.

Source code: Download Blast tools from NCBI to your Desktop:
ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/
The file needed is called "blastn". Drag this file to your Desktop.

Example input file: test2.fna
Note: We will blast the test2.fna against the database we constructed previously (see How to make a blast database)

Example output file: test2_vs_test.txt
Example output file with a header: test2_vs_test.xls

Instructions:
Type the following line command:

./blastn -query test2.fna -db test.fna -out test2_vs_test.txt -outfmt 6 -num_descriptions 1 -num_alignments 1 -max_target_seqs 1