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How To Install and Use NCBI Blast+ on Windows

This page is prepared for the people who want to use NCBI Blast+ on local machines, because we found most of the NCBI Blast+ information available on the Internet is out-dated or inaccurate. You can find a review for several installation instructions available on the Internet here. You will be surprised with the results.
This instruction supports newest version of NCBI Blast+ (ver. 2.7.1) released on 10/18/2017. If you don't like to type blast commands, try web-based NCBI Blast+.

> If you have more than 10,000 query sequences and/or large databases > 10GB, we strongly recommend to use cloud providers such as Amazon Web Services.
> Visit here for instructions.

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If you don't understand any part of the instruction below, we recommend you to try BlastStation2 or BlastStation-Local64 to save time. You can start Blast search in less than five minutes with the intuitive manner of operation, amazing easy-to-use interface, and useful extra functions including summary table exporting in CSV format and hit sequence exporting in FASTA format.

Local Blast Search on Windows with BlastStation-Local

1. Installation

32-bit Windows

NCBI Blast+ 2.3.0 or later does not support 32-bit Windows. Even though 64-bit NCBI Blast+ will not start on 32-bit Windows, it can be installed on 32-bit Windows because of the lack of the OS version check function.
- Click the link to download installer from ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/2.2.30/ncbi-blast-2.2.30+-win32.exe
- Double click ncbi-blast-2.2.30+-win32.exe to launch installer
- Follow the instructions of installer
  All program will be installed under "C:Program Files\NCBI\blast-2.2.30+\bin"
    README.txt which contains the link to he BLAST Help web page will be installed in "C:Program Files\NCBI\blast-2.2.30+\doc". user_manual.pdf is not bundled with the installer anymore.
    Uninstaller is found in "C:Program Files\NCBI\blast-2.2.30+".

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- Double click ncbi-blast-2.7.1+-win64.exe to launch installer
- Follow the instructions of installer
  All program will be installed under "C:Program Files\NCBI\blast-2.7.1+\bin"
    README.txt which contains the link to he BLAST Help web page will be installed in "C:Program Files\NCBI\blast-2.7.1+\doc". user_manual.pdf is not bundled with the installer anymore.
    Uninstaller is found in "C:Program Files\NCBI\blast-2.7.1+".

2. Setup environments

- In order to use NCBI Blast+, Blast database file location should be specfied. One option is ncbi.ini file.
- Make ncbi.ini text file in C:\Windows directory. One example is shown below. Since \ should be escaped with \ in this file, there are two \s instead of one.

  Click to get ncbi.ini file

- Create BLAST database directory.
  1) Open command prompt. If you don't know how to do this, visit http://www.howtogeek.com/235101/10-ways-to-open-the-command-prompt-in-windows-10/
  2) Type "cd C:\"
  3) Type "mkdir blast\db" and type return.

3. Download database

- Click the link to visit NCBI ftp server. ftp://ftp.ncbi.nih.gov/blast/db/
- Double click the database file you want to download, such as nt.00.tar.gz.
- Save the file in C:\blast\db.
- Extract downloaded tar.gz file. If you don't have such a software, 7-zip is convenient.

4. Create database

- Download or create FASTA file. File name is assumed to be testdb.fasta.
- Copy testdb.fasta to C:\blast\db directory using Windows Explorer.
- Open command prompt. If you don't know how to do this, visit http://www.sevenforums.com/tutorials/947-command-prompt.html (Windows 7) or http://www.intowindows.com/how-to-open-command-prompt-as-administrator-in-windows-8-1/ (Windows 8.1) or http://www.howtogeek.com/235101/10-ways-to-open-the-command-prompt-in-windows-10/ (Windows 10)
- Type "cd C:\blast\db" and type return.
- Type "makeblastdb -in testdb.fasta -out testdb -dbtype nucl" for DNA or "makeblastdb -in testdb.fasta -out testdb -dbtype prot" for Protein and type return to get the database named testdb.
- Type "makeblastdb -help" for advanced options.

5. Launch NCBI-Blast+ commands

- Create dna or protein query FASTA file. It can contain multi FASTA data. File name is assumed to be test_dna.fasta and test_protein.fasta here. nt.00 is a dna database file and nr.00 is a protein database

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2) Type "blastn -query test_dna.fasta -db nt.00 -out test.html -html" and type return.
3) Type "blastn -help" for advanced options.
- blastp
  1) Open command prompt.
  2) Type "blastp -query test_protein.fasta -db nr.00 -out test.html -html" and type return.
  3) Type "blastn -help" for advanced options.

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