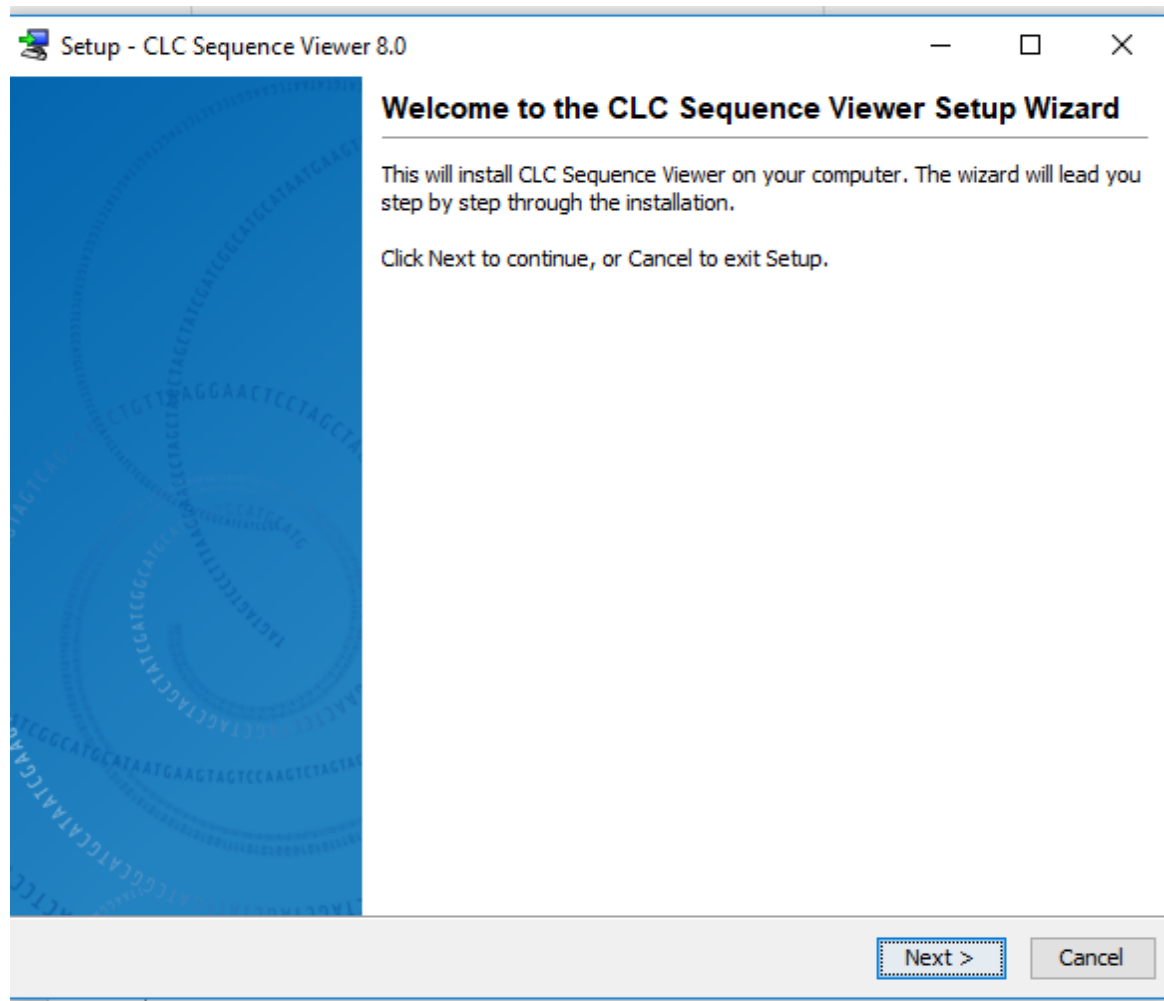
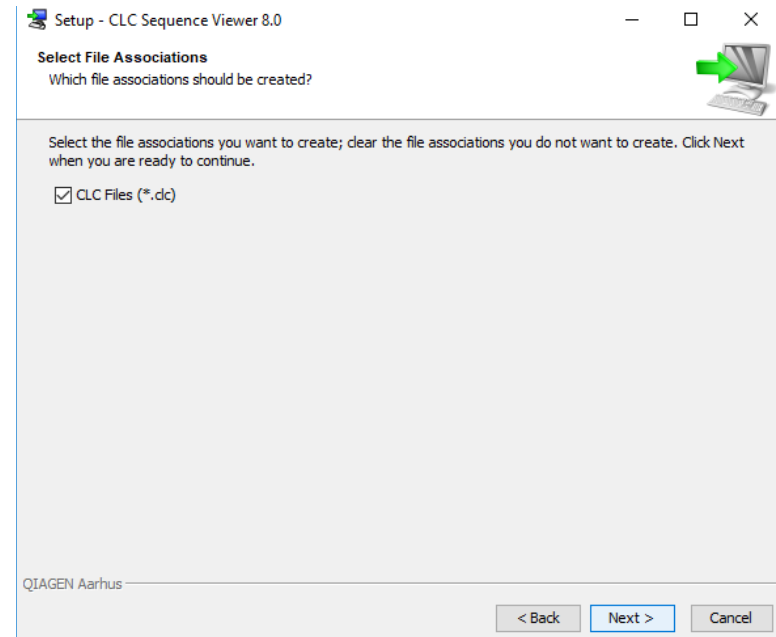
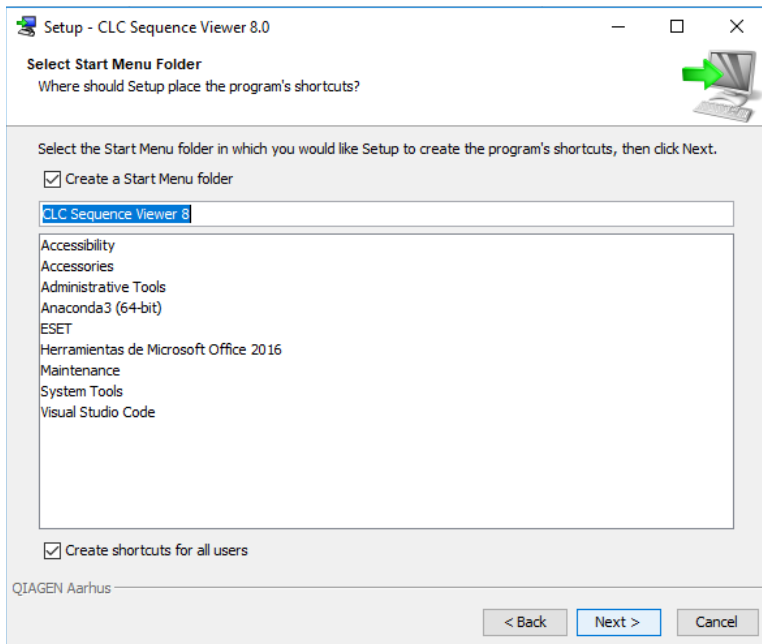
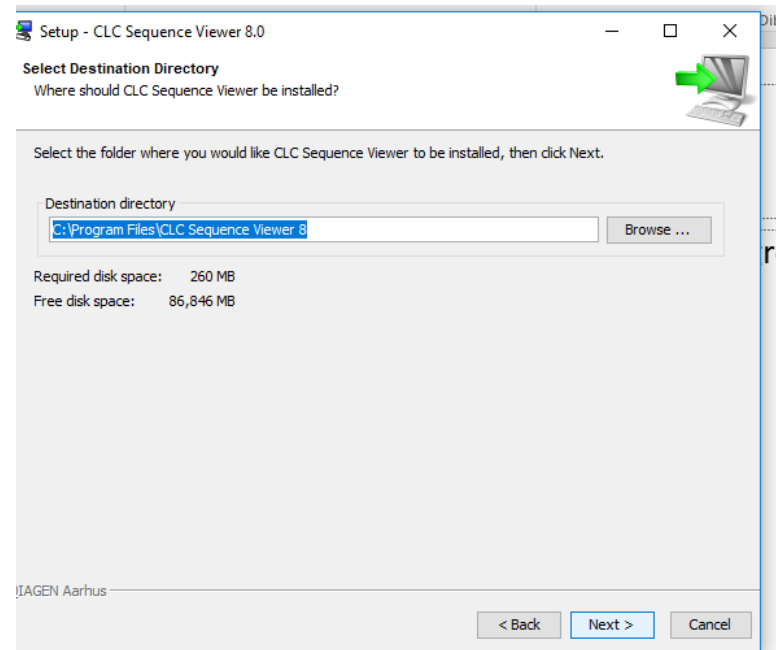
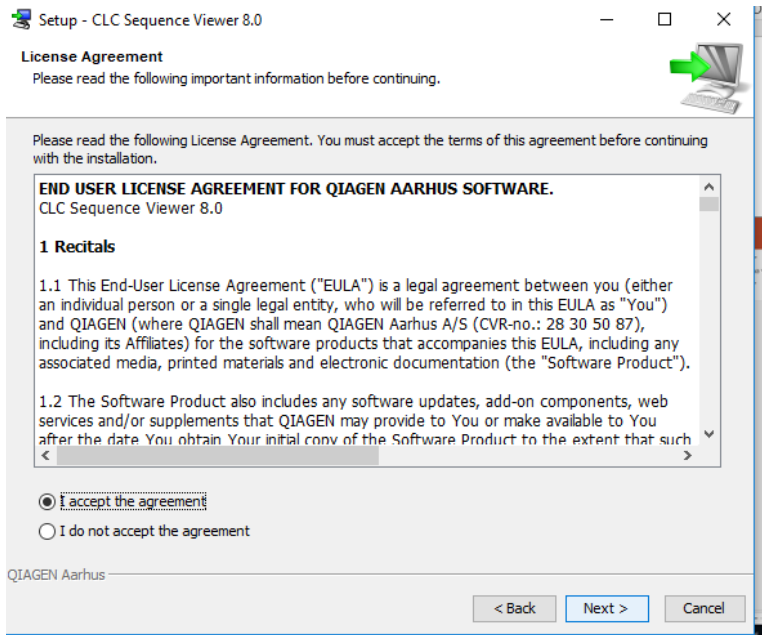


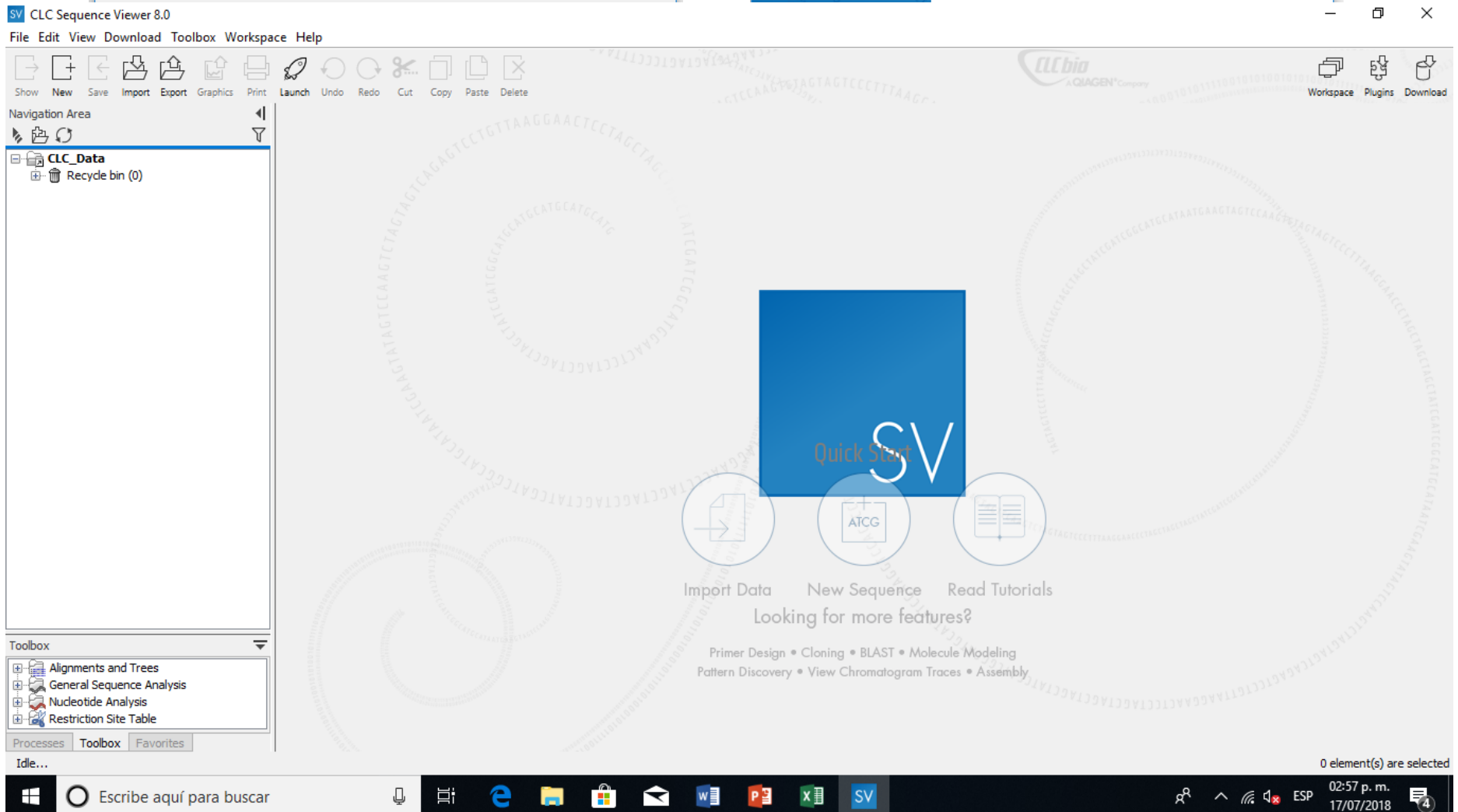
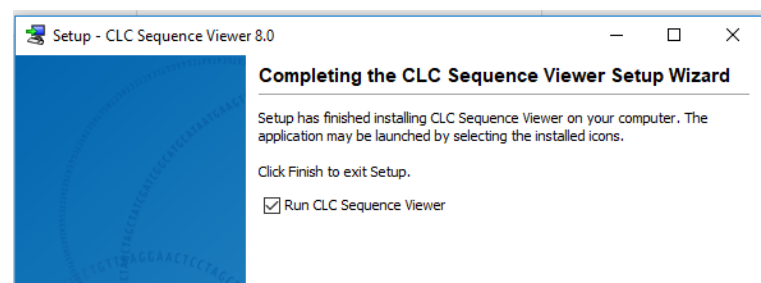
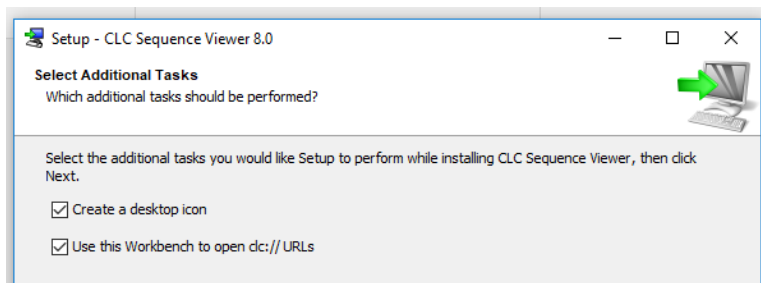
# CLC Sequence Viewer



# CLC Sequence Viewer, instalación



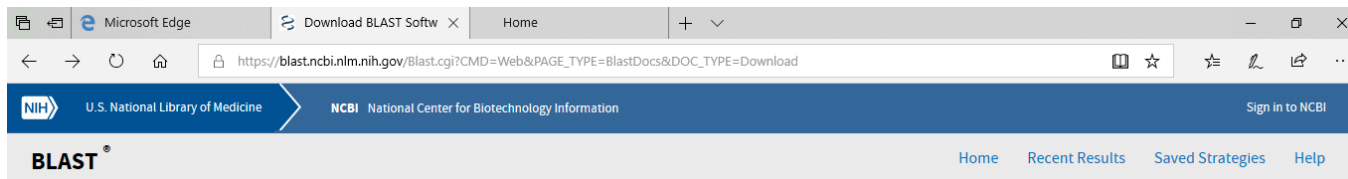




# Blast

[https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Web&PAGE\\_TYPE=BlastDocs&DOC\\_TYPE=Download](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Web&PAGE_TYPE=BlastDocs&DOC_TYPE=Download)

# Blast



## Download BLAST Software and Databases

### BLAST+ executables

Do you have difficulties running high volume BLAST searches? Do you have proprietary sequence data to search and cannot use the NCBI BLAST web site? Do you have access to your own server? Do you have your own research pipeline? Have security or IP concerns about sending searches outside of your organization? If you answered yes to any of these questions, read on!

The NCBI provides a suite of command-line tools to run BLAST called BLAST+. This allows users to perform BLAST searches on their own server without size, volume and database restrictions. BLAST+ can be used with a command line so it can be integrated directly into your workflow.

### What are the next steps?

Download and install BLAST+. Installers and source code are available from <ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/> your own. Start searching.

For more details, please see the [BLAST+ user manual](#), the [BLAST Help manual](#), t

The BLAST+ suite is the currently supported package. The older C toolkit execut

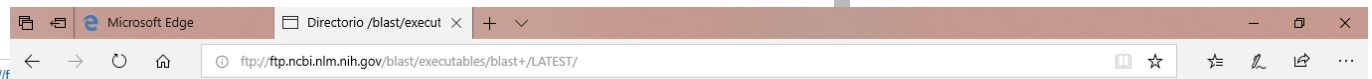
We are always listening and welcome your feedback at [BLAST Support Center](#).

### Magic-BLAST

Magic-BLAST is a tool for mapping large next-generation RNA or DNA sequencing

Installers and source code are available from <ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/>

<ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/>



## Directorio /blast/executables/blast+/LATEST/ de FTP en ftp.ncbi.nlm.nih.gov

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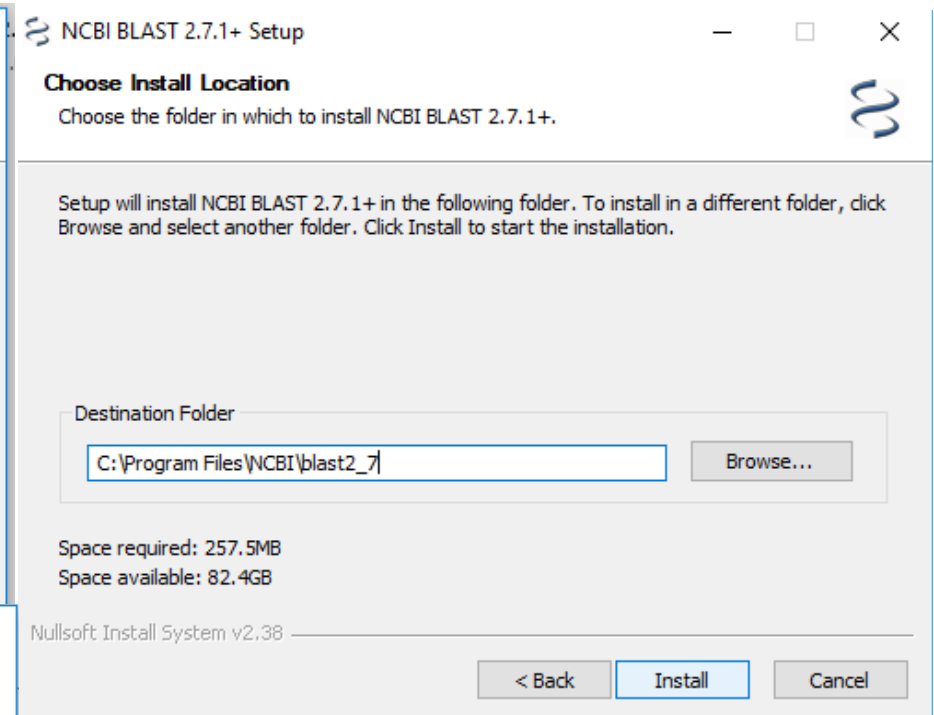
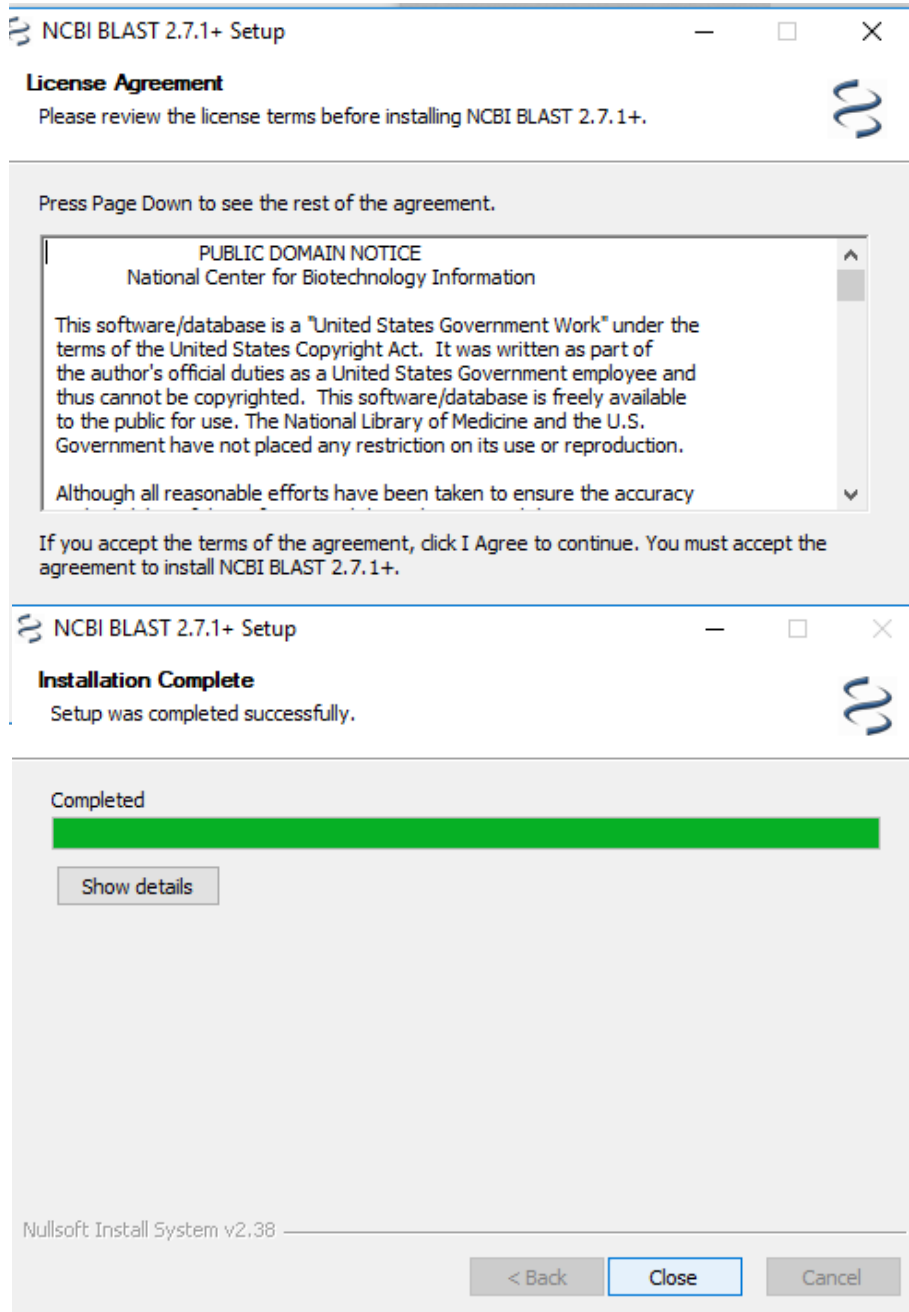
Se han descargado 37.9 MB de ncbi-blast-2.7.1+-win64.exe desde  
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https://www.ncbi.nlm.nih.gov/guide/data-software/

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[BLAST \(Stand-alone\)](#)  
BLAST executables for local use are provided for Solaris, LINUX, Windows, and MacOSX systems. See the README file in the ftp directory for more information. Pre-formatted databases for BLAST nucleotide, protein, and translated searches also are available for downloading under the db subdirectory.

[FTP: BLAST Databases](#)  
Sequence databases for use with the stand-alone BLAST programs. The files in this directory are pre-formatted databases that are ready to use with BLAST.

[FTP: CDD](#)  
This site provides full data records for CDD, along with individual Position Specific Scoring Matrices (PSSMs), mFASTA sequences and annotation data for each conserved domain. See the README file for full details.

[FTP: ClinVar Data](#)  
This site provides full data extractions in XML and summary data in VCF format. It contains files with information about standard terms used in [ClinVar](#), [MedGen](#), and [GTR](#).

[FTP: FASTA BLAST Databases](#)  
Sequence databases in FASTA format for use with the stand-alone BLAST programs. These databases must be formatted using formatdb before they can be used with BLAST.

[FTP: GenBank](#)  
This site contains files for all sequence records in GenBank in the default flat file format. The files are organized by GenBank division, and the full contents are described in the README.genbank file.

Quick Links

[BLAST \(Stand-alone\)](#)  
GenBank: BankIt  
GenBank: Sequin  
GenBank: tbl2asn  
SNP Submission Tool  
Basic Local Alignment Search Tool (BLAST)  
Cn3D  
Conserved Domain Search Service (CD Search)  
E-Utilities  
Genome ProtMap  
Genome Workbench  
Primer-BLAST  
ProSplign  
PubChem Structure Search  
Splign  
Vector Alignment Search Tool (VAST)

ftp://ftp.ncbi.nlm.nih.gov/blast/db/

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04:12 p. m. 17/07/2018



# Perl

## <https://www.perl.org/>

