

# ClustalW

<http://www.clustal.org/clustal2/>



**Clustal W / Clustal X**  
Multiple alignment of nucleic acid and protein sequences

**Webservers**  
You don't necessarily have to go through the hassle to install Clustal on your computer. Instead, you can run Clustal online on several servers on the web:

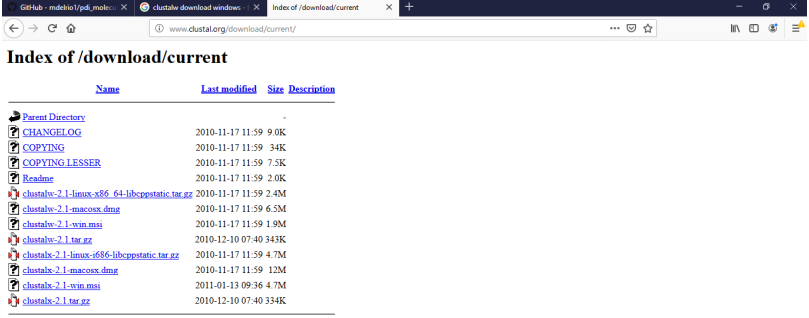
- EBI web server
- Swiss Institute of Bioinformatics

**Download Clustal W/X**  
Clustal 2 comes in two flavors: the command-line version Clustal W and the graphical version Clustal X. Precompiled executables for Linux, Mac OS X and Windows (incl. XP and Vista) of the most recent version (currently 2.1) along with the source code are [available for download here](#). You can also [browse for older versions](#) (Clustal W 1.81, Clustal V etc.). The current version of Clustal 2 is also mirrored on the [EBI ftp site](#). Clustal 2.1 is released under the [GNU Lesser GPL](#).

**Documentation**  
**Help**  
Please have a look at Clustal X's builtin help menu or if you are using Clustal W use `clustalw2 -h` or `clustalw2 --help` (depending on your platform and version of Clustal). Online versions (which might be out of date) can be found here: [Clustal W](#) and [Clustal X](#). There are a couple of references on how to use Clustal W/X on the net. A very nice tutorial which also covers advanced features like using secondary structures for profile alignment is ["Using Clustal X for multiple sequence" by Jarno Tuimala \(local mirror\)](#).

**References**  
Escriba aquí para buscar

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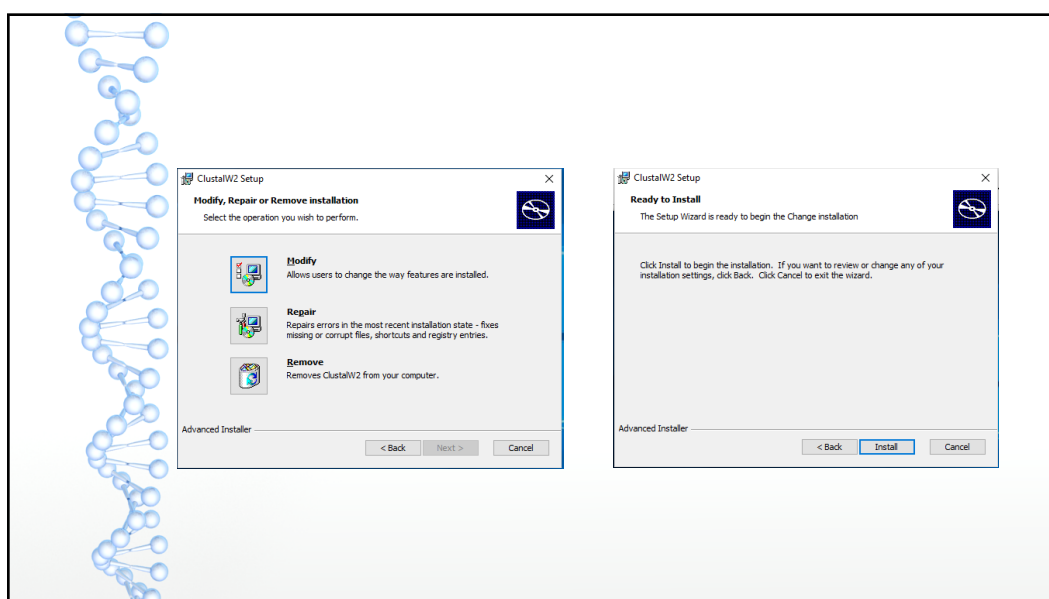
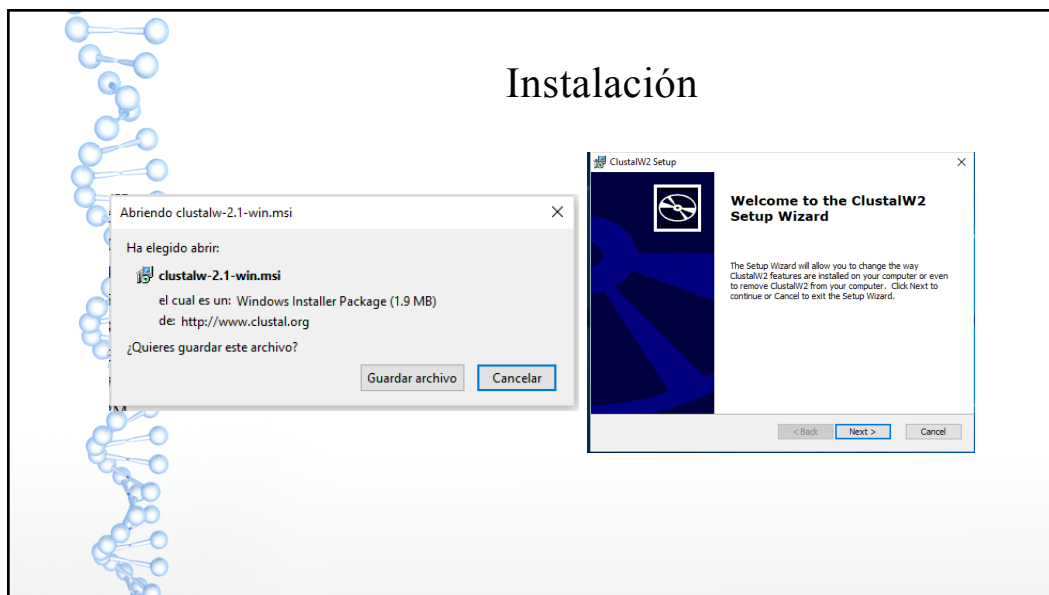


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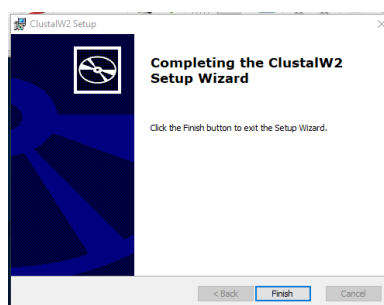
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Apache/2.4.7 (Ubuntu) Server at www.clustal.org Port 80

# Instalación



## Termino de la instalación



## Verificar el directorio en donde quedó instalado

