

Installation

Download `XlinkAnalyzer.zip` from <http://www.beck.embl.de/XlinkAnalyzer.html> and extract it.

Method 1 [recommended]

1. Install UCSF Chimera (version 1.9 or 1.8 recommended). You can download Chimera from <https://www.cgl.ucsf.edu/chimera/download.html>
2. Extract `XlinkAnalyzer.zip` in some directory. The directory can be your Desktop or any directory you use for software.
3. Start Chimera
4. Go to Menu Favorites -> Preferences... -> Category: Tools
5. Click Add... button, which is on the bottom of the window, and browse for directory of Xlink Analyzer.
 - a. So if your unzipped Xlink Analyzer has path:
`/user/Desktop/XlinkAnalyzer/`, add
`/user/Desktop/XlinkAnalyzer`. A line similar to
"XlinkAnalyzer - /user/Desktop/" should appear in Locations section of the Tools window
6. Click Save
7. Close. This configuration will persist and you don't need to repeat it.
Do not remove the `XlinkAnalyzer` directory.

Method 2

This method involves installing Xlink Analyzer in the main Chimera installation directory. This gives advantage of that all users of the computer on which Chimera is installed will have Xlink Analyzer installed by default.

1. Extract `XlinkAnalyzer.zip` in any directory (e.g. Desktop).
2. Open `XlinkAnalyzer` directory
3. In the `XlinkAnalyzer` directory there should be directories:
 1. `xlinkanalyzer`
 2. `pyxlinks`
4. Copy `xlinkanalyzer` and `pyxlinks` directories to Chimera share directory. The share directory may be in different places depending on a platform and where Chimera was installed. A quick way to find the share directory is:
 1. Start Chimera
 2. Start Python command line: Menu Tools -> General Controls -> IDLE
 3. Type: `import os; print os.environ['CHIMERA']`
 4. Press Enter. You should see a path.
 5. On Mac by default:
`/Applications/Chimera.app/Contents/Resources/share`
 6. On Windows: A path like `C:\Program Files\Chimera 1.9\share`
 7. On linux: `installation_path/UCSF-Chimera64-1.9/share`

Quick start

To get quick overview of Xlink Analyzer, and test your installation, you can open an example project for XL-MS analysis of RNA Polymerase I.

1. Download and extract `XlinkAnalyzer_documentation.zip` from <http://www.beck.embl.de/XlinkAnalyzer.html>
2. Go to *Menu Tools -> Utilities -> Xlink Analyzer*
3. To load Pol I project from example directory:
Setup -> Load project
and browse `example/PolI/PolI.json` file.
4. Open Pol I PDB file:
`example/PolI/4C3H.pdb`
5. Color subunits: *Subunits tab -> select 4C3H.pdb -> Color all subunits*
6. Display cross-links: *Xlinks tab -> General tab -> Display cross-links*
7. Set score threshold to 30

You should see the structure with colored subunits and cross-links displayed as blue and red sticks.