

CRBS summer bootcamp

Exploring Protein Structures and Interactions using PyMol

Instructor: Jean-François Trempe

Date: Tuesday, June 30, 2020

Time: 1 – 4 PM

<https://mcgill.zoom.us/j/96031899180>

Meeting ID: 960 3189 9180

Password: CRBS2020

In this boot camp seminar, you will learn how to use PyMOL to 1) inspect protein structures, with a focus on X-ray crystallography and NMR, 2) analyze protein:ligand interactions, and 3) produce high quality figures and movies.

In preparation for the seminar, please download and install PyMOL. It can be installed on Windows/MacOS/Linux. You can download the latest version (2.4) here:

<https://pymol.org>

The software requires a license, but you can use it in “for evaluation only”. PyMOL 2.4 requires

- 64-bit Windows 10 or newer
- 64-bit macOS 10.12+
- 64-bit Linux, including CentOS 7+, Ubuntu 18.04+, and others (glibc 2.12+)

If you have an older system (Windows 7 or MacOS 10.10+), you can download v2.0 here:

<https://pymol.org/installers/>

The session will take about 2 hours, but it may overflow to 3 hours depending on how many questions we get. We will follow the tutorial slides available here:

https://www.dropbox.com/s/fkcqxclfvqwhss3/CRBS_Bootcamp_30june2020_PyMol.pptx?dl=0

Looking forward to seeing you tomorrow!

Jean-François Trempe