Lesson 1: The 3D Viewport and Lighting

**Day:** Jan 18, 2023

**Time:** 10:30 – 11:30AM

**Room:** 56-154

**Lesson Summary**

For many of you, this will be your first introduction to the world of 3D modeling. At first it would feel foreign, and you will likely find yourself wondering, how can I possibly remember all this? Don’t worry! Everyone feels this way when they first start.

**Class Schedule**

* Course Intro - 10 min
* Get a structure – 10 min
* Navigating the viewport - 10 min
* Importing a structure - 10 min
* Adding lighting - 10 min
* Preparing and rendering the scene - 10 min

# Converting a structure to a 3D model

**Time:** 5 min

Before we jump into Blender, we will need a structure. In this lesson, we will be rendering the MHC structure from assignment 2 of 20.420. Some of you may remember it. I model of any structure can be obtained very easily. As this is the first class, many of you won’t have the software downloaded yet so I have provided the file. So, you can sit back and relax for this section as I demo it.

* Download ChimeraX: <https://www.rbvi.ucsf.edu/chimerax/>
* Download the PDB file: <https://files.rcsb.org/download/2BVP.pdb>
* Open the PDB in ChimeraX
  + Delete waters 🡪 delete :HOH
  + Delete everything but the MHC 🡪 delete /B /A:181-274
  + Hide interacting amino acids 🡪 hide /A atoms
  + Increase cartoon width 🡪 cartoon style width 3.5
  + Increase cartoon thickness 🡪 cartoon style thickness 1
  + Update colors 🡪 color byelement
  + Depict peptide as spheres 🡪 style /C sphere
  + Save as a model 🡪 save mhc.glb format gltf instancing true

# Viewing a Structure in Blender

Now that you have a model of your structure, we can open it in Blender and begin practicing with the interface.

* Download Blender: <https://www.blender.org/download/>
* Open Blender
* Delete default cube 🡪 **X** 🡪 **d**
* Import the structure 🡪 **File** 🡪 **Import** 🡪 **glTF (.glb/.gltf)**
* Clean up the structure
  + Create new collection called **MHC** 🡪 **C**
  + Create new collection called **Peptide** 🡪 **C**
  + Create new collection called **Complex** 🡪 **C**
  + Right-click and delete **2bvp.pdb**
  + Move **ribbons** to **MHC**
  + Right-click and delete **Atoms**
  + Move all **atoms** into **Peptide**
  + Move **Peptide** and **MHC** into **Complex**
* Right click **Complex** and **Select Objects**
* Set the origin to your object 🡪 **Object** 🡪 **Set Origin** 🡪 **Origin to Geometry**
* Center the object at World Origin
  + Click on an **orthographic viewpoint**
  + Move the object 🡪 **Move**
  + Repeat with at least two **orthographic viewpoint**