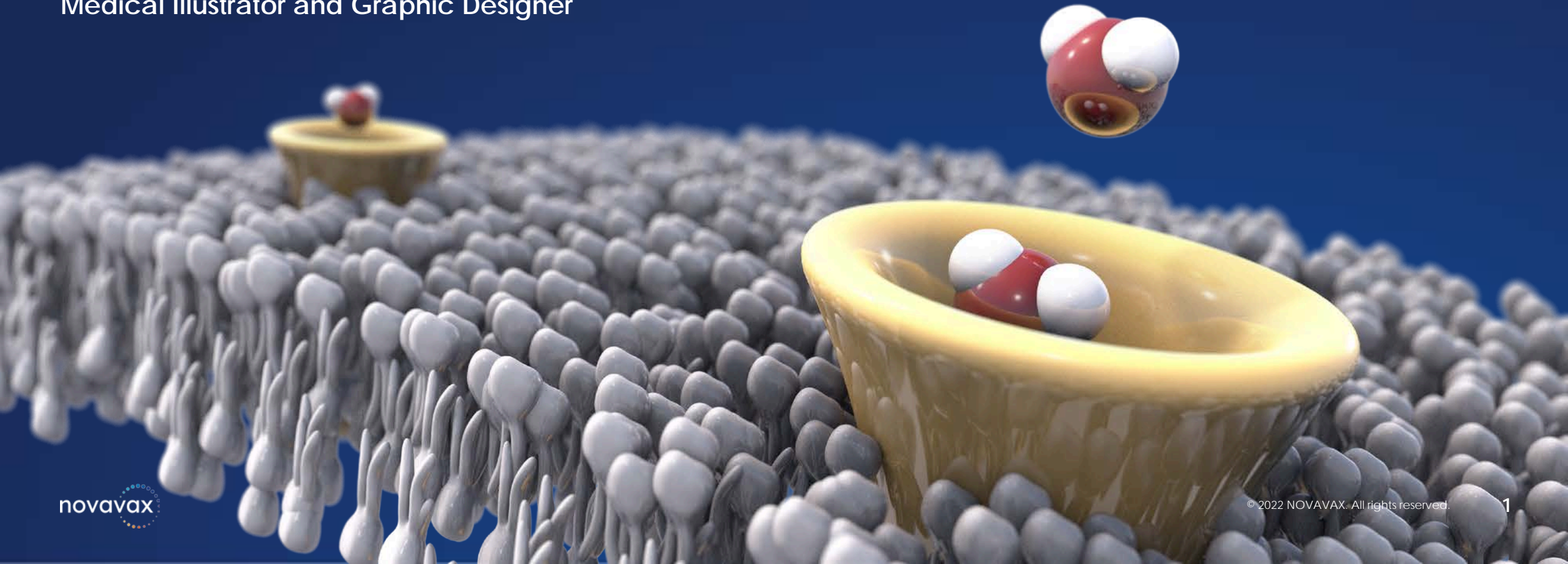


Leveraging the Protein Databank

Creating effective molecular 3D models for improving scientific communication

Emily Adams | eadams@novavax.com
Medical Illustrator and Graphic Designer



Downloads

Pymol

Molecular model editing

<https://pymol.org/2/>

Chimera

Molecular model editing

<https://www.cgl.ucsf.edu/chimera/download.html>

Blender

Whole 3D pipeline (modelling, animating, lighting, etc.)

<https://www.blender.org/download/>

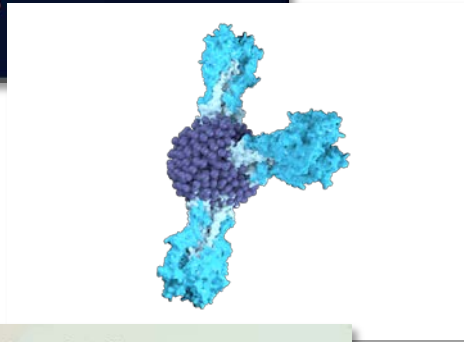
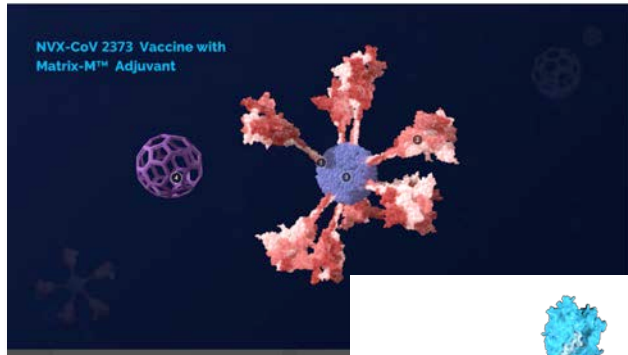
Overview

By the end of this workshop you should:

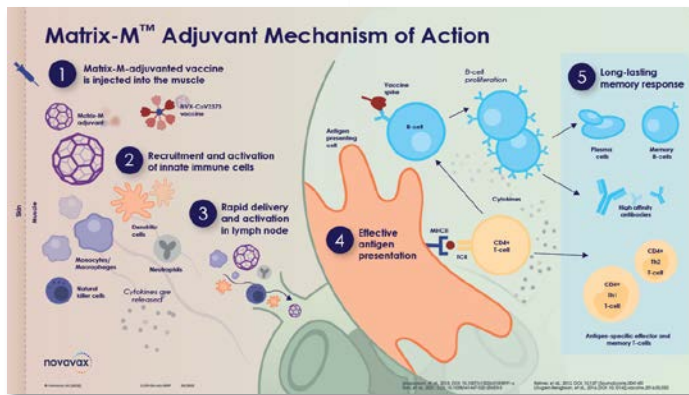
- Have a better understanding of what an accurate protein is and why different representations might be used
- How to export a file from the Protein Databank to use in 3D graphics software
- How to manipulate the file in other software to select and export different elements for use in 3D modeling

Why visualize molecular structures?

Communication with the public, subject matter experts, students and more



- Explain complex biological processes to a general audience, including patient communication
- Help people using the technology (ie. Healthcare providers, public) understand how it works
- Provide internal experts with visual materials they can use to explain the scientific concepts to external stakeholders
- Enhance understanding for employees, scientists and others for training and improved productivity



What is the protein databank?

Public databank of molecularly accurate proteins:

- **File Type:** PDBs (can be converted to other types of 3D data)
- **License:** CC0 1.0 Universal Public Domain Dedication
- **Number of available Files:** ~190,000
- Citation instructions are available on the website

[RCSB PDB: Homepage](https://www.rcsb.org/)



What is a protein?

Molecules that compose one or more long chains of amino acids

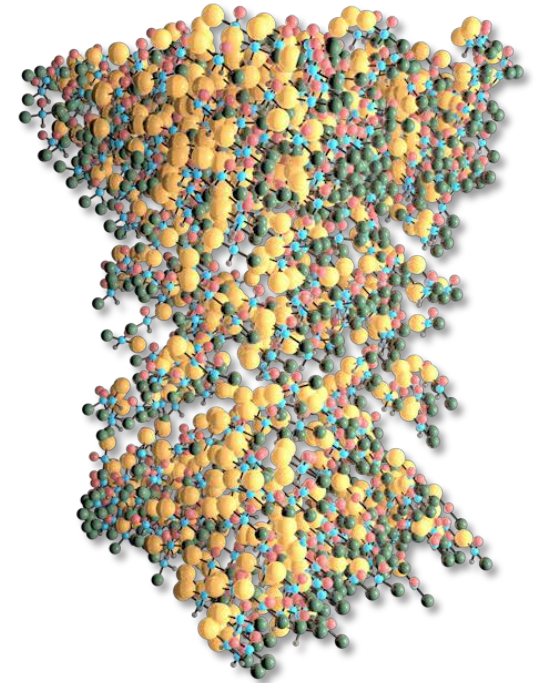
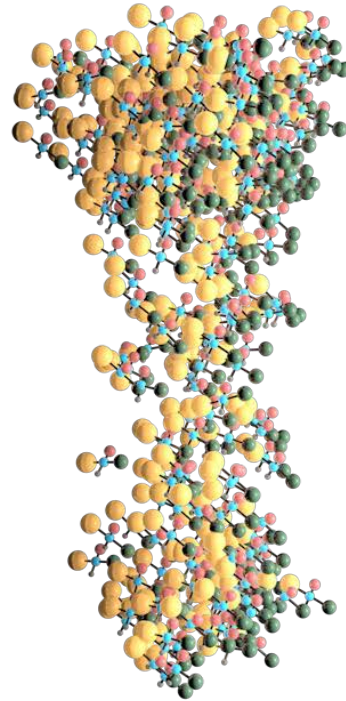
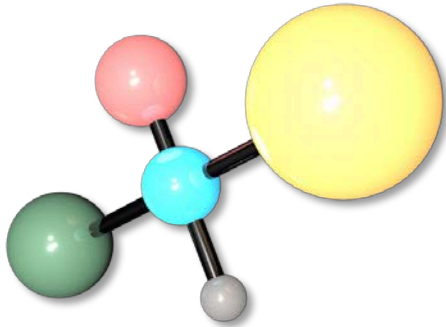
Amino Acid (AA)



Protein (many AAs)



Oligomer (several of the same protein together)



Proteins (of all sizes) do much of **the work of the cell**: growth, structure, signaling, transport, etc.

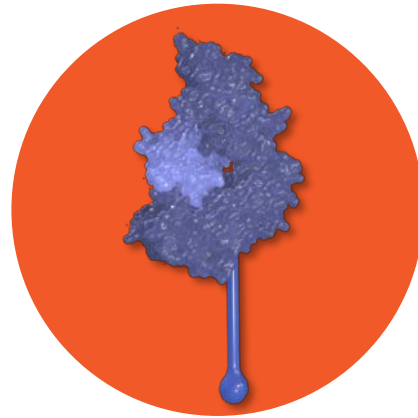
Visualizing Proteins



Ribbon Diagram

The overall path of the protein's backbone

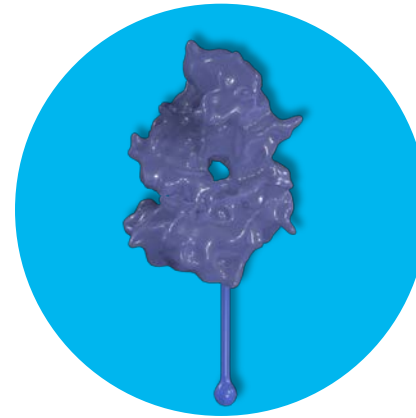
Allows you to include important features at key locations



Surface Structures

The combined shapes of the electrostatic potential of the molecules

Can help to show protein interactions and fit



Reduced

A less detailed surface diagram



Abstract

Represents subunits or important parts of a protein using generic shapes

Illustrating larger-scale pathways and mechanisms

Hands-on:

Go to the link below to access a PDB in the protein databank and work through the following slides to learn the basics of working in molecular editors such as the Protein Databank Editor, PyMol, and Chimera.

[RCSB PDB - 1IGT: STRUCTURE OF IMMUNOGLOBULIN](#)

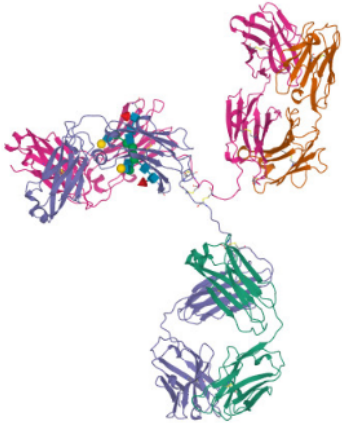
Accessing the Structure in the Databank Editor

RCSB PDBDepositSearchVisualizeAnalyzeDownloadLearnMoreDocumentationCareers

MyPDB

Structure Summary3D ViewAnnotationsExperimentSequenceGenomeVersions

Biological Assembly 1



3D View: Structure | 1D-3D View | Validation Report

Global Symmetry: Asymmetric - C1
Global Stoichiometry: Hetero 4-mer - A2B2

1IGT

STRUCTURE OF IMMUNOGLOBULIN

PDB DOI: 10.2210/pdb1IGT/pdb

Classification: IMMUNOGLOBULIN

Organism(s): Mus musculus

Mutation(s): No




Deposited: 1996-10-25 Released: 1997-07-07

Deposition Author(s): Harris, L.J., Larson, S.B., Hasel, K.W., McPherson, A.

Experimental Data Snapshot

Method: X-RAY DIFFRACTION
Resolution: 2.80 Å
R-Value Free: 0.297
R-Value Work: 0.209
R-Value Observed: 0.209

wwPDB Validation

Metric	Percentile Ranks	Value
Clashscore		21
Ramachandran outliers		3.7%
Sidechain outliers		9.7%

WorseBetter

Percentile relative to all X-ray structures
Percentile relative to X-ray structures of similar resolution

This is version 2.0 of the entry. See complete history.

Display FilesDownload Files

Adding a molecular surface in the PDB Editor

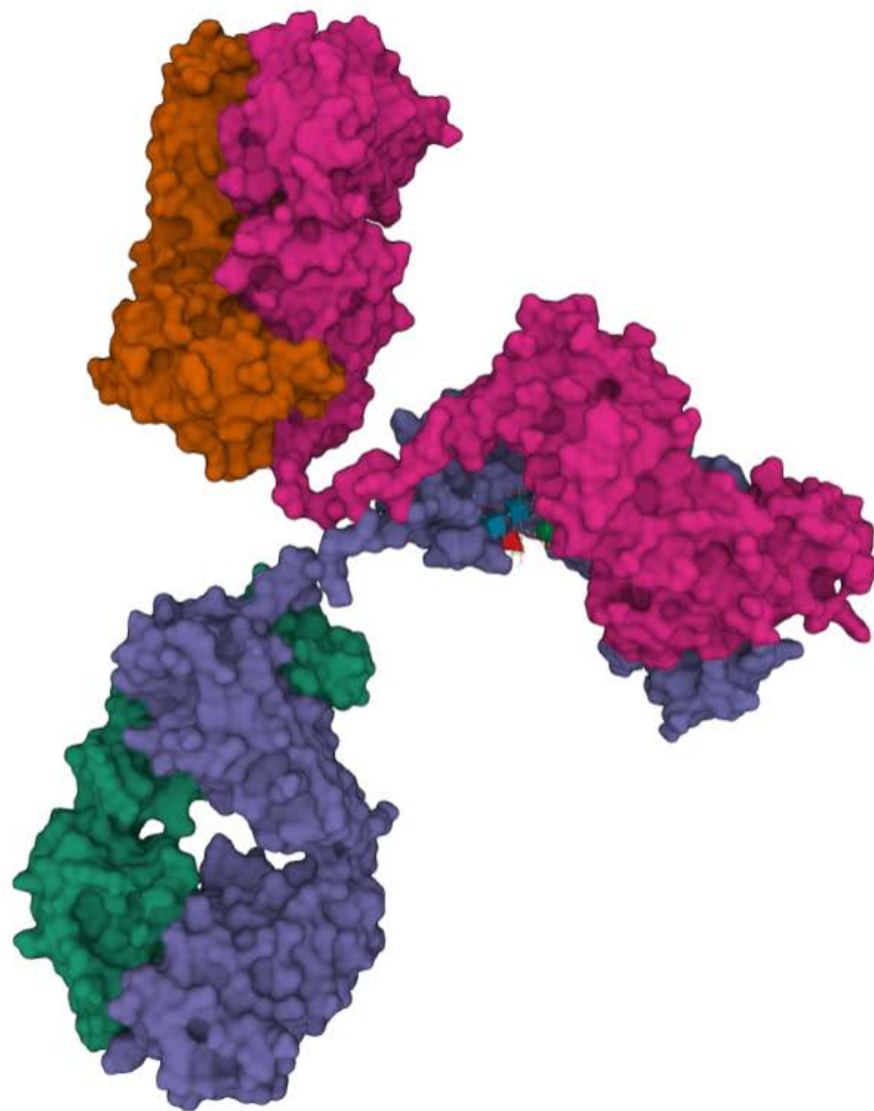
Instructions: Polymer > Add Representation > Molecular Surface

The image illustrates the steps to add a molecular surface representation in the PDB Editor. It shows three sequential screenshots of the software interface, connected by blue arrows.

Step 1: The 'Components' panel for protein 1IGT is shown. The 'Polymer' component is currently set to 'Cartoon'. A blue arrow points to the next step.

Step 2: The 'Add Representation' dropdown menu is open, showing various representation options. The 'Molecular Surface' option is highlighted. A blue arrow points to the final step.

Step 3: The 'Molecular Surface' option is selected in the dropdown menu.



⌕

🔑

📐

📊

🔍

Dynamic Bonds

× Off

Nothing Focused

📐

✂ Measurements

🔍 Structure Motif Search

📦 Components

1IGT

📖 Preset

+ Add

📐

🔄

Polymer

2 reprs

👁

🗑

⋮

Carbohydrate

2 reprs

👁

🗑

⋮

Unit Cell P 1

👁

⋮

📊 Density

🛡 Quality Assessment

🔗 Assembly Symmetry

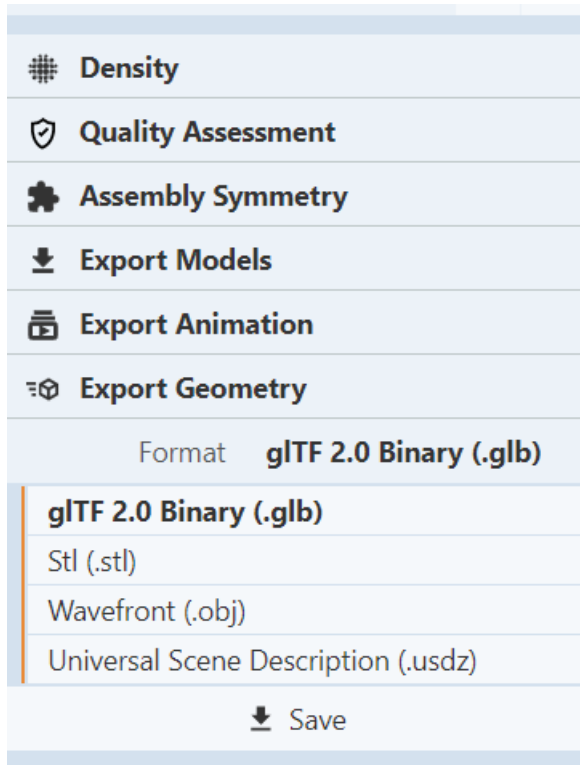
📄 Export Models

📹 Export Animation

📐 Export Geometry

Downloading the Geometry

Instructions: Export Geometry > glTF 2.0 Binary > Select File Type > Save



glTF, STL, and OBJ

Compatible with Blender

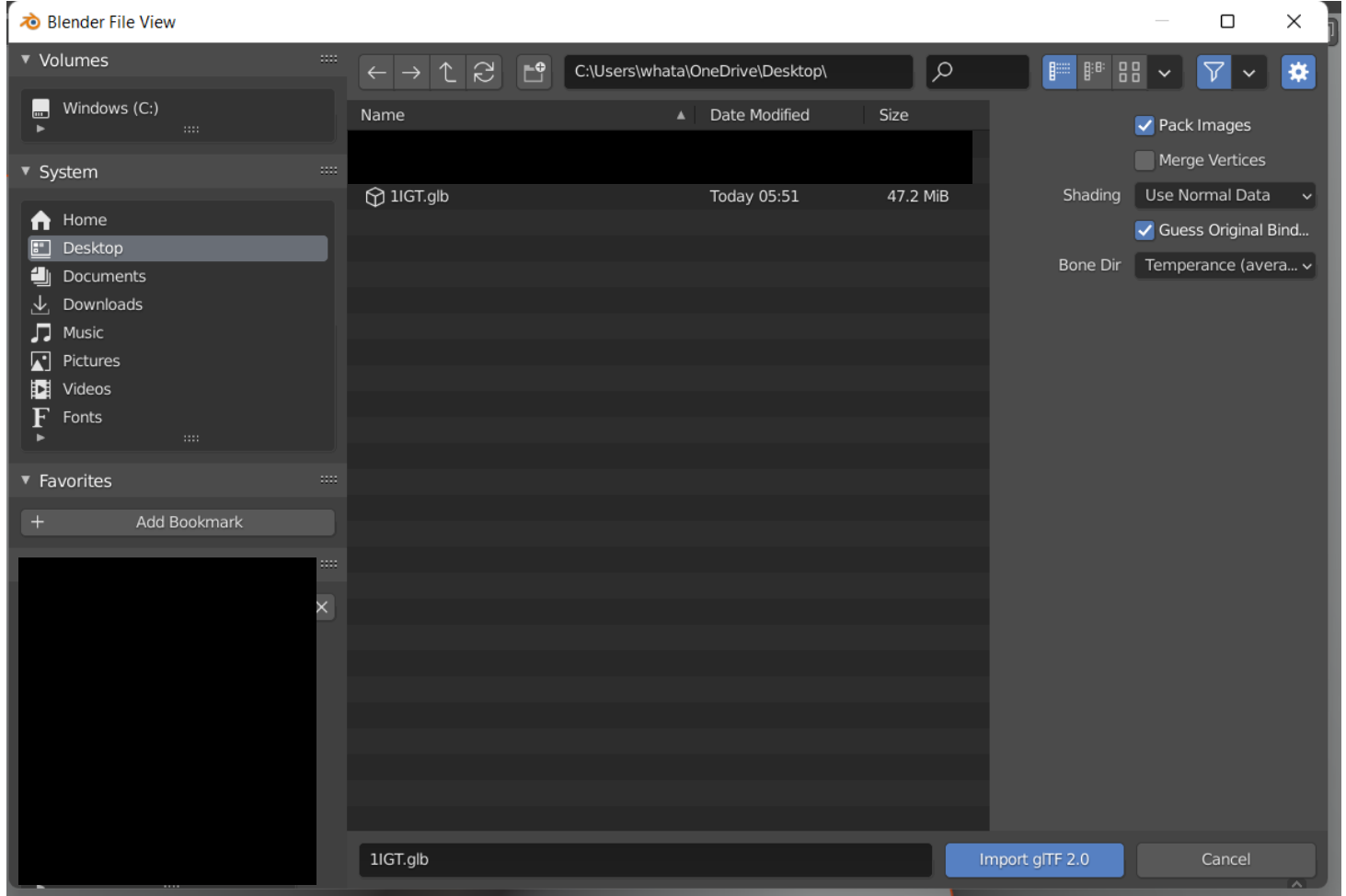
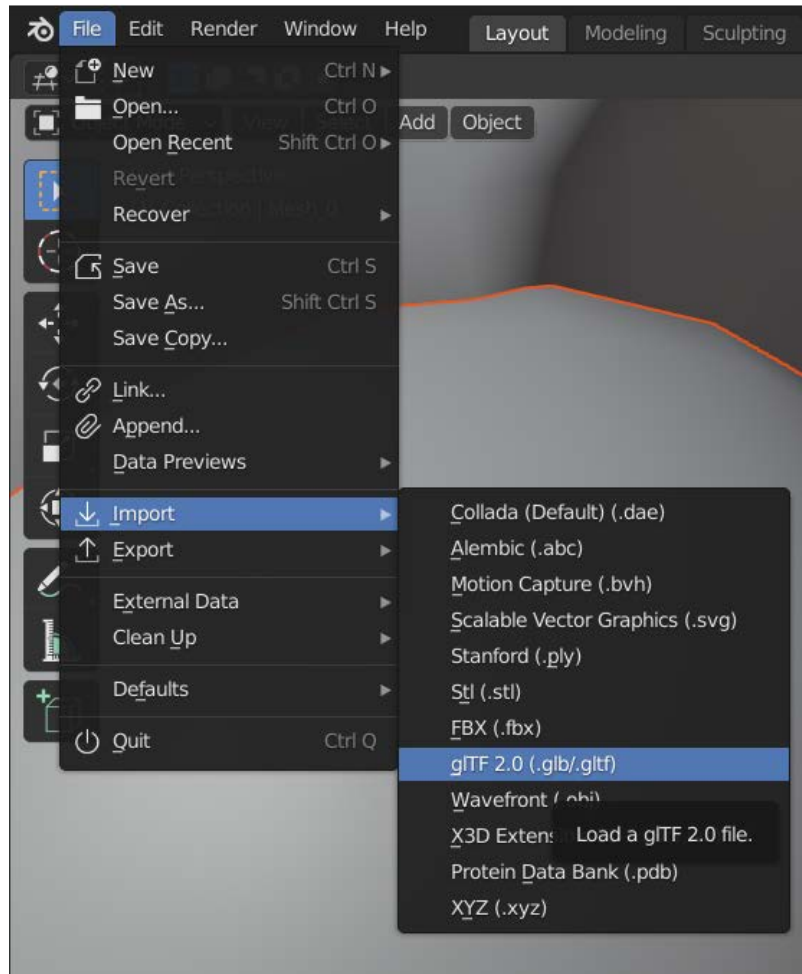
Download a .glb

STL and OBJ

Compatible with Cinema 4D

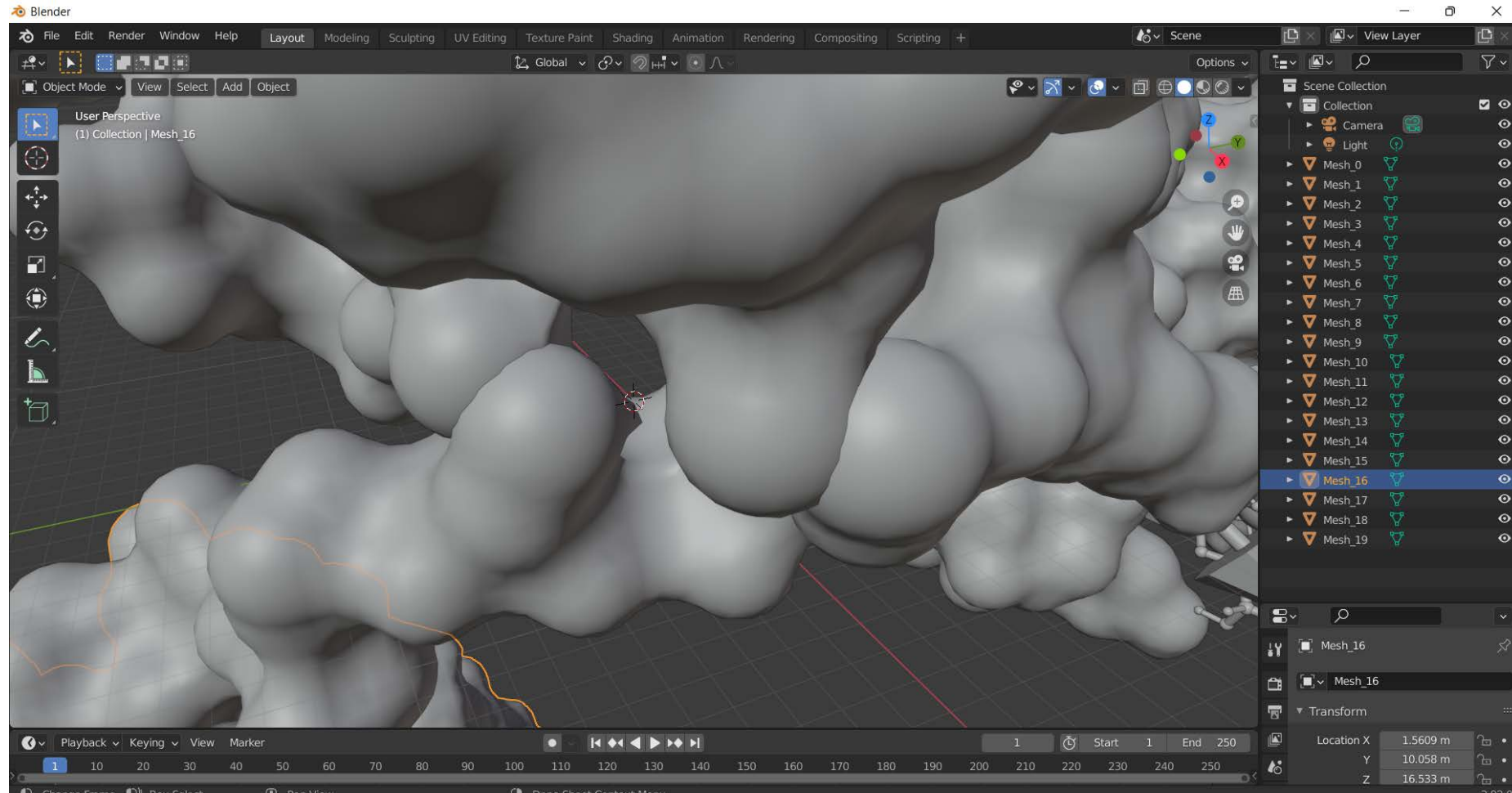
Bringing a Protein Into Blender

Instructions: File > Import > [File Type] > Select File > Import



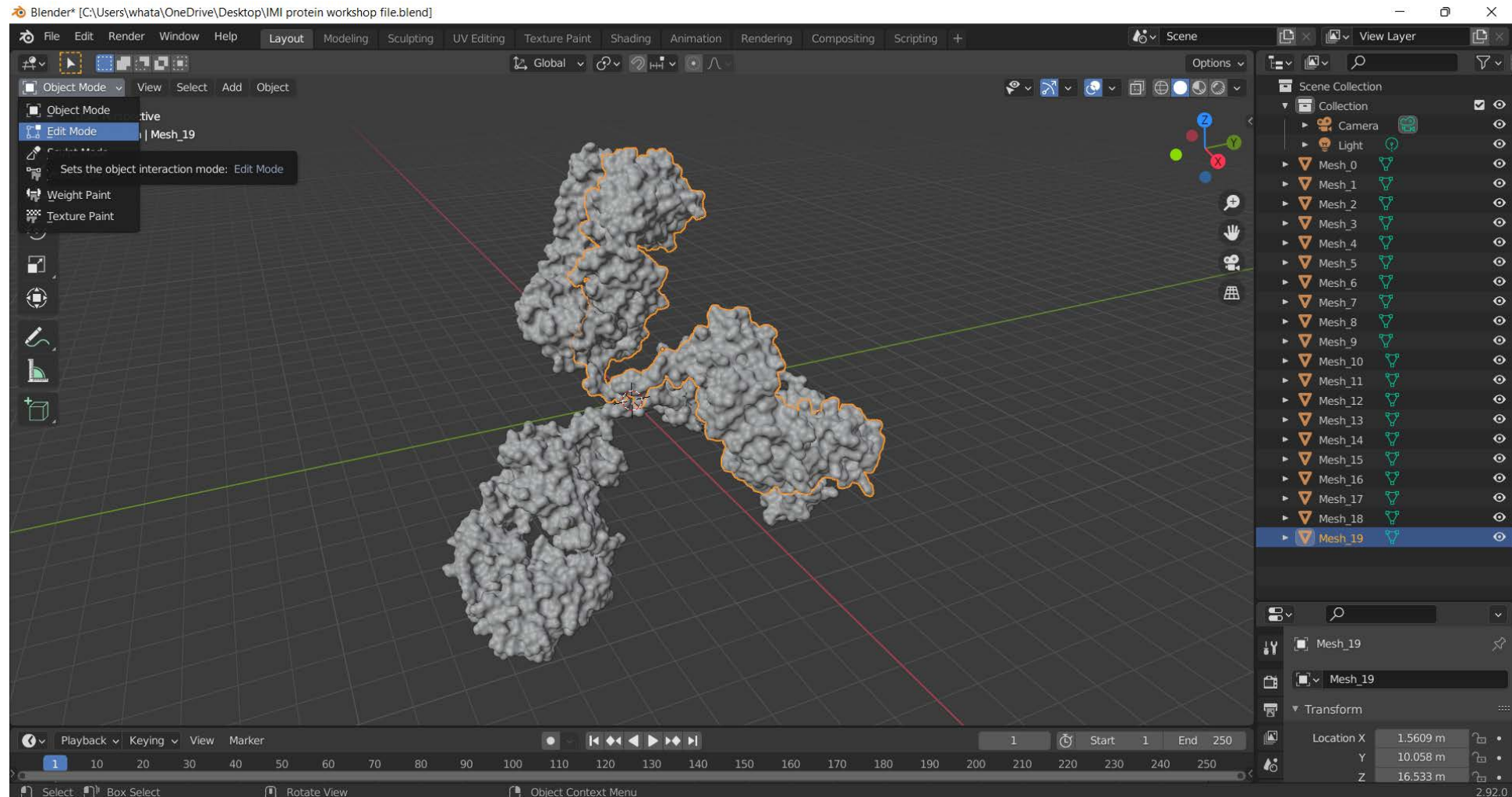
Protein Enters Scene

Protein may not be visible when it first comes into scene or may be very zoomed in



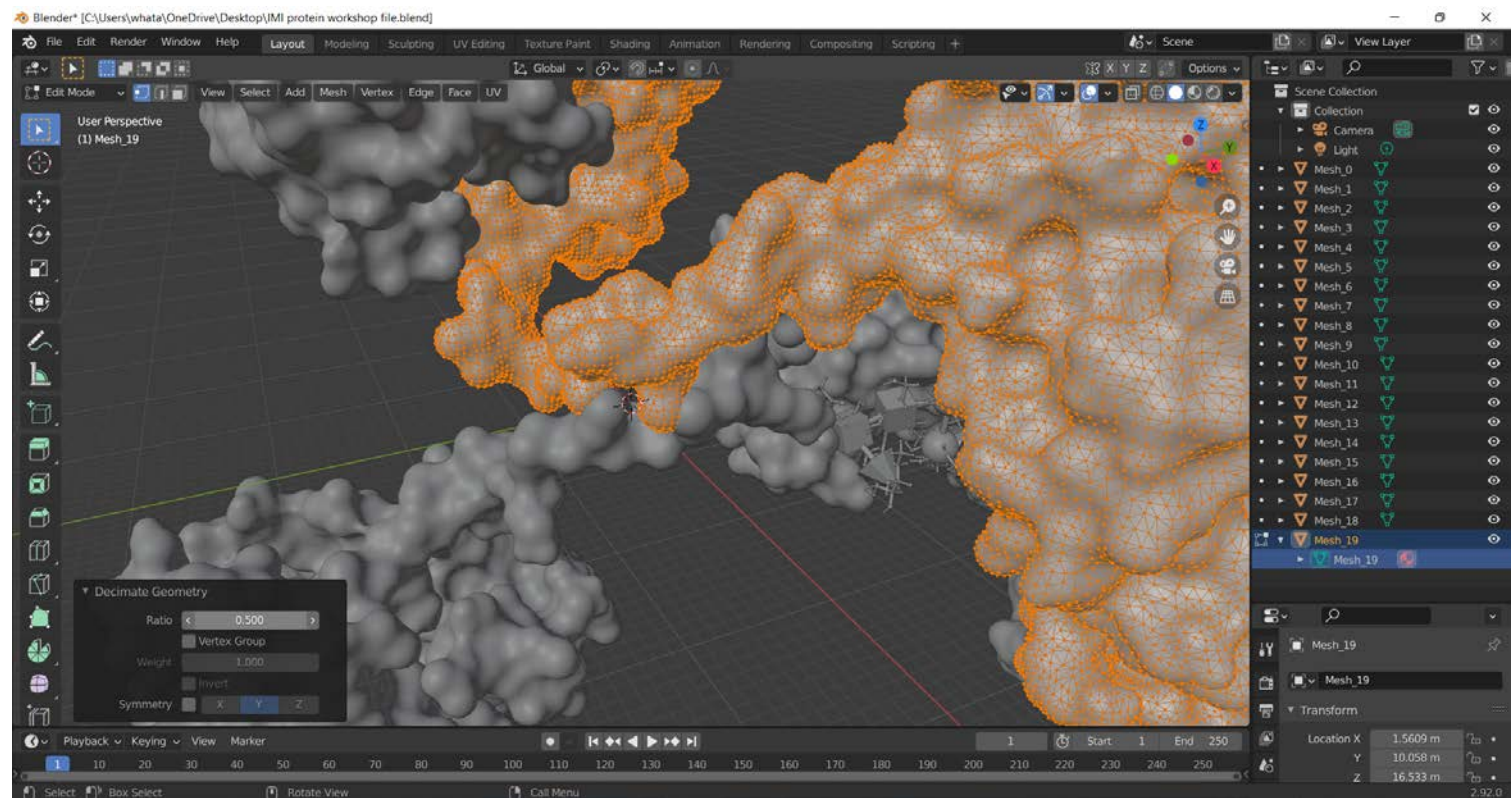
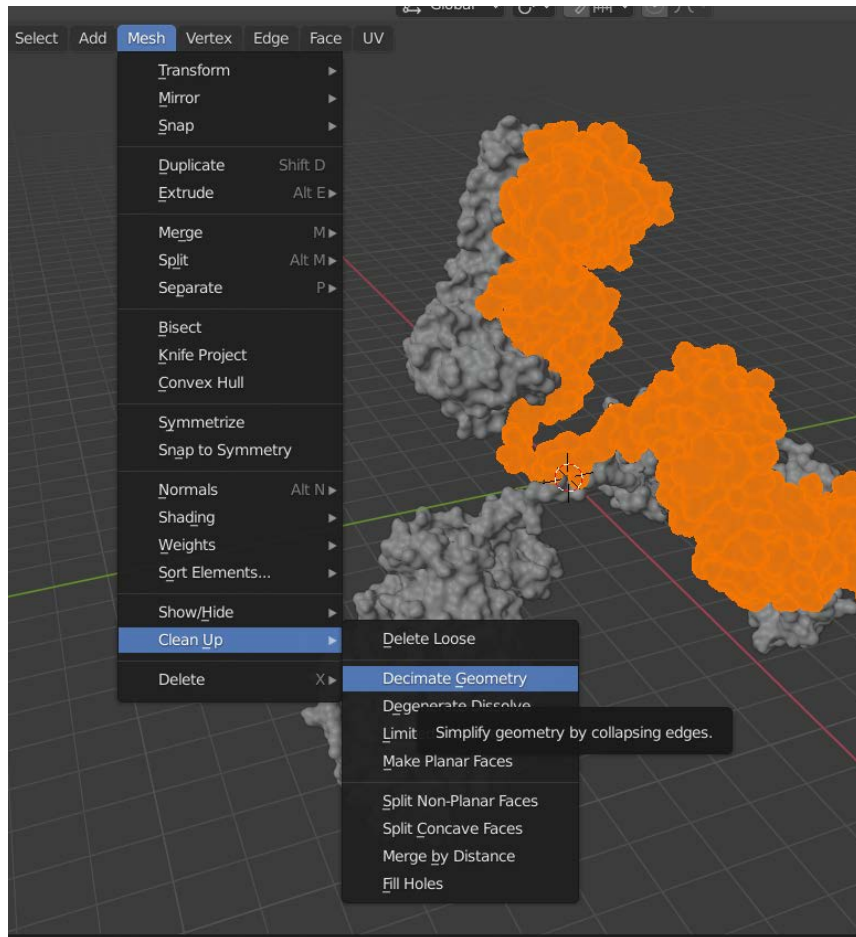
Object Mode to Edit Mode

Instructions: Object Mode > Edit Mode



Decimate Geometry

Instructions: Mesh > Clean Up > Decimate Geometry > Adjust number in ratio slider

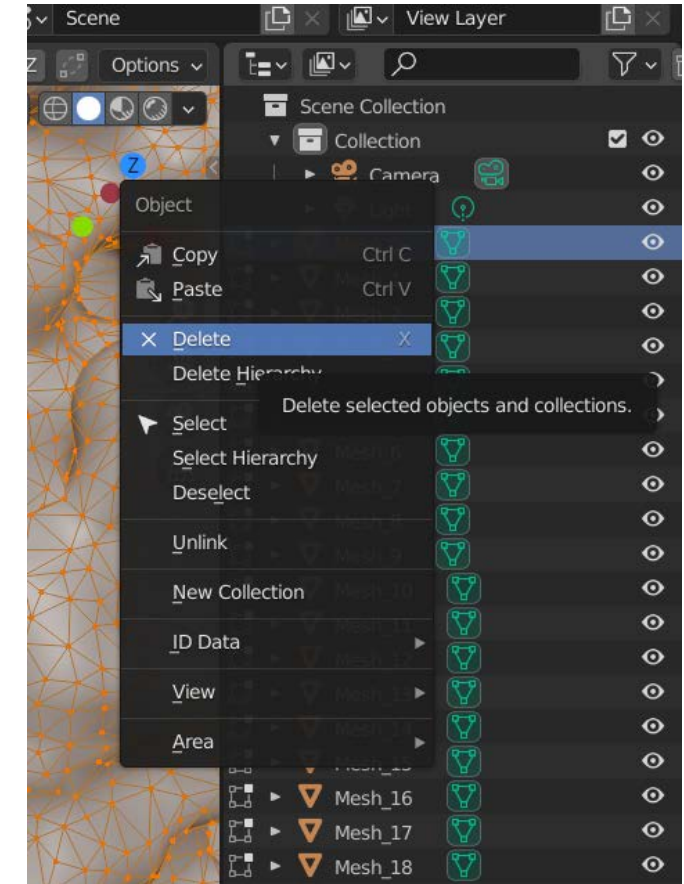
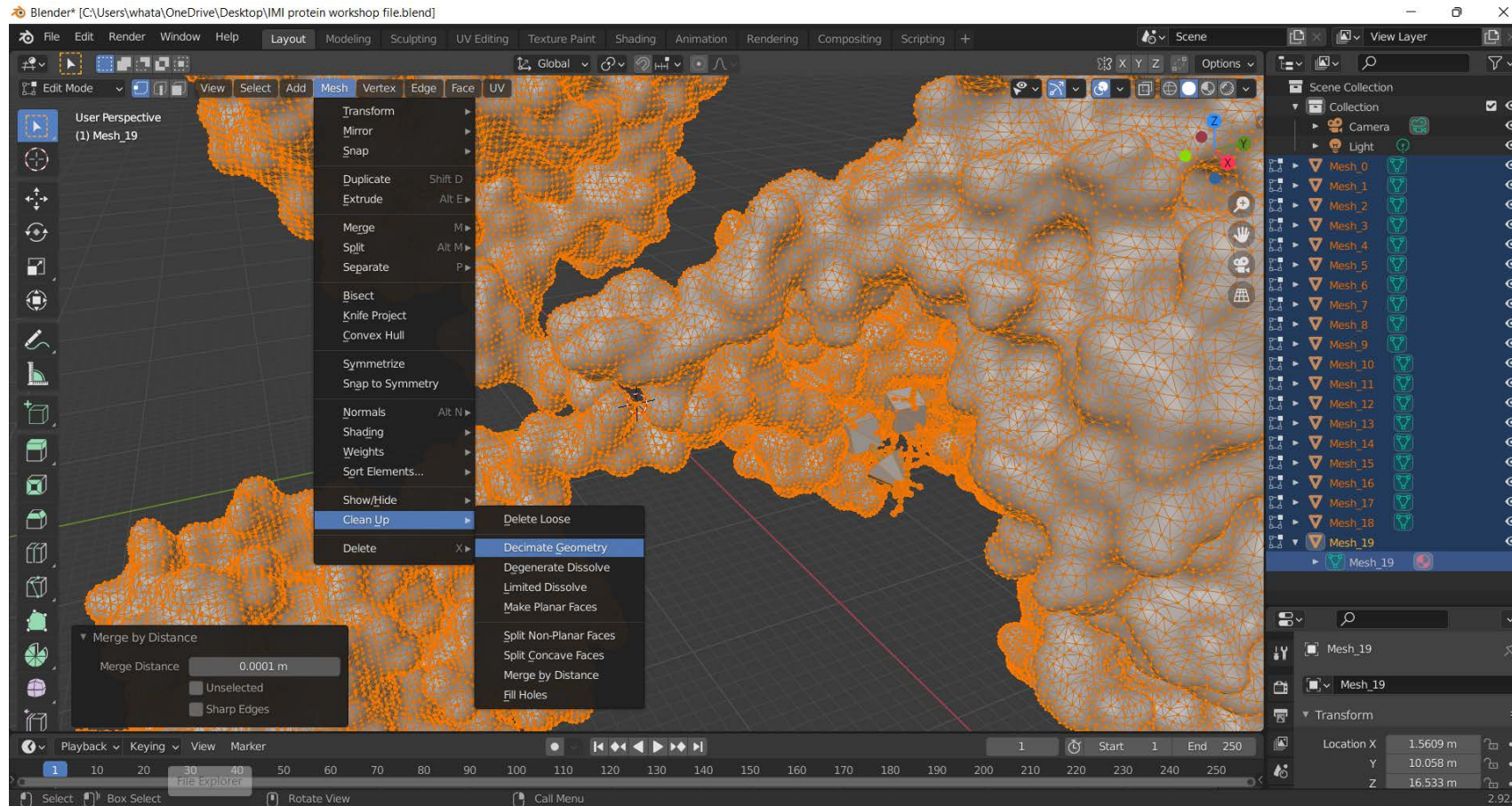


*you may need to zoom in to see the polygons, reduce it based on your needs

Selecting > 1 Object and Deleting Objects

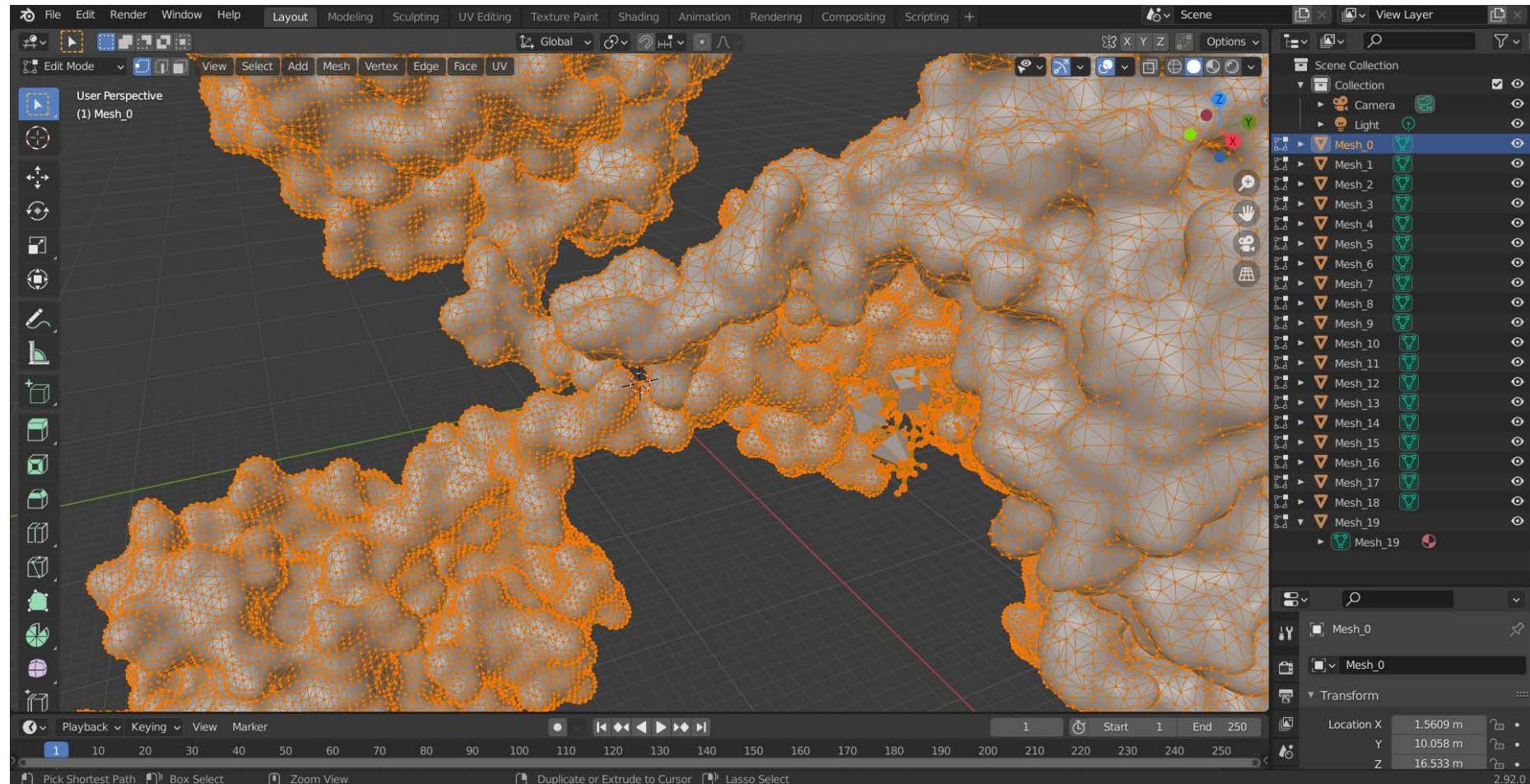
Instructions: Select one object > Shift > Select the number of objects you want

Right click > Select delete



Exporting Object

Click: File > Export > Select file type



Pymol

An open source molecular visualization software, it uses Python-based commands to control, select, and highlight the protein in the software

<https://pymol.org/2/>

Downloading a PDB

Instructions: Double-click file to open in Pymol

Structure Summary3D ViewAnnotationsExperimentSequenceGenomeVersions

Biological Assembly 1 ?

1IGT

STRUCTURE OF IMMUNOGLOBULIN

PDB DOI: [10.2210/pdb1IGT/pdb](https://doi.org/10.2210/pdb1IGT/pdb)

Classification: IMMUNOGLOBULIN

Organism(s): [Mus musculus](#)

Mutation(s): No ⓘ

Deposited: 1996-10-25 **Released:** 1997-07-07

Deposition Author(s): [Harris, L.J.](#), [Larson, S.B.](#), [Hasel, K.W.](#), [McPherson, A.](#)

Experimental Data Snapshot

Method: X-RAY DIFFRACTION

Resolution: 2.80 Å

R-Value Free: 0.297

R-Value Work: 0.209

R-Value Observed: 0.209

wwPDB Validation ⓘ

Metric	Worse	Percent
Clashscore	<div></div>	
Ramachandran outliers	<div></div>	
Sidechain outliers	<div></div>	

Display FilesDownload Files

FASTA Sequence

PDB Format

PDB Format (gz)

PDBx/mmCIF Format

PDBx/mmCIF Format (gz)

PDBML/XML Format (gz)

Validation Full PDF

Validation XML

Biological Assembly 1 (CIF - gz) ⓘ

Biological Assembly 1 (PDB - gz)

3D View: Structure | 1D-3D View | Validation Report

[org/download/1IGT.pdb](https://www.rcsb.org/download/1IGT.pdb)



Fetching a PDB

"Fetch 1IGT"

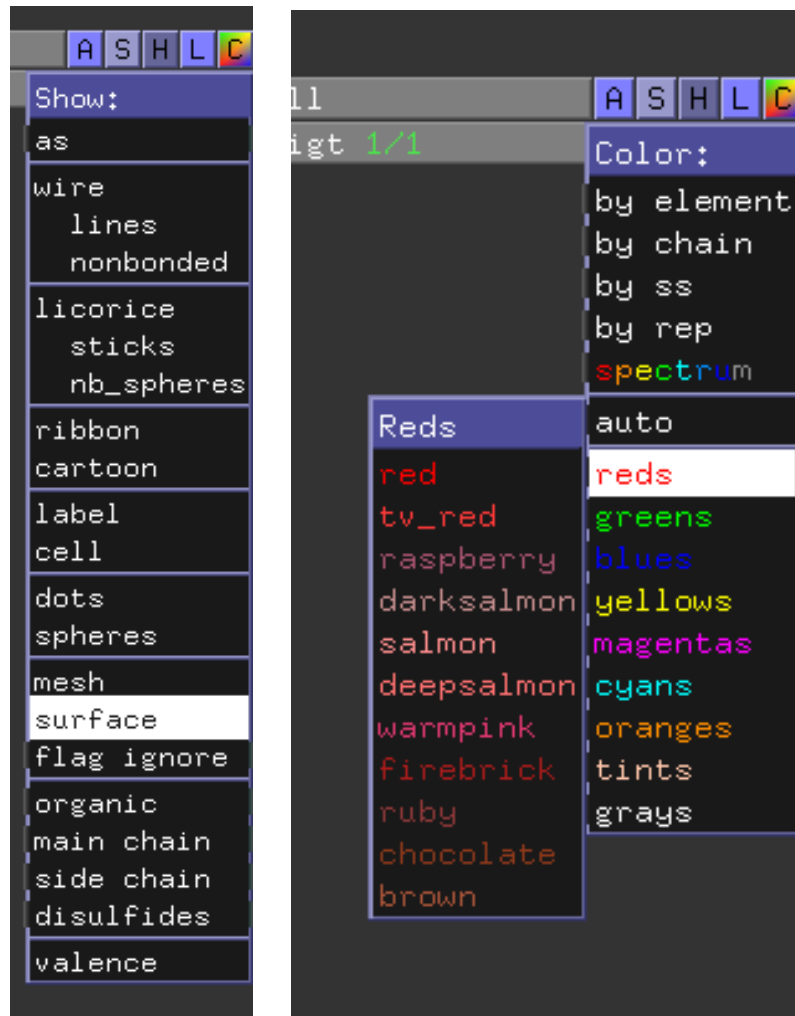


```
File Edit Build Movie Display Setting Scene Mouse Wizard Plugin Help
GL_VERSION: 4.5.0 - Build 24.20.100.6344
No License File - For Evaluation Only (0 days remaining)
Detected 8 CPU cores. Enabled multithreaded rendering.
TITLE      STRUCTURE OF IMMUNOGLOBULIN
ExecutiveLoad-Detail: Detected mmCIF
CmdLoad: "C:\Users\whata\OneDrive\Desktop\1igt.cif" loaded as "1igt".

PyMOL> fetch 1IGT|
```

Show Surface

Instructions: S in the right drop down menu > C to change its color

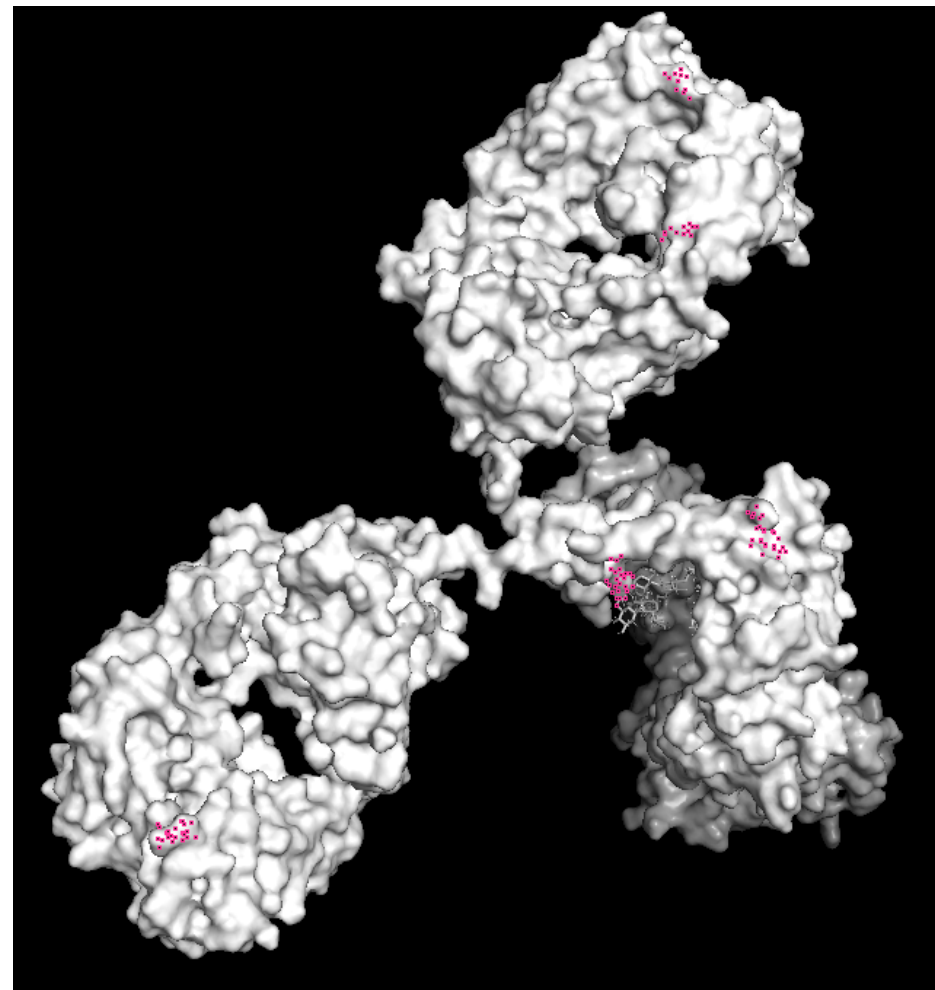


**Magnified view of drop-down bar*

Select Residue

Instructions: Type "Select Resi #"

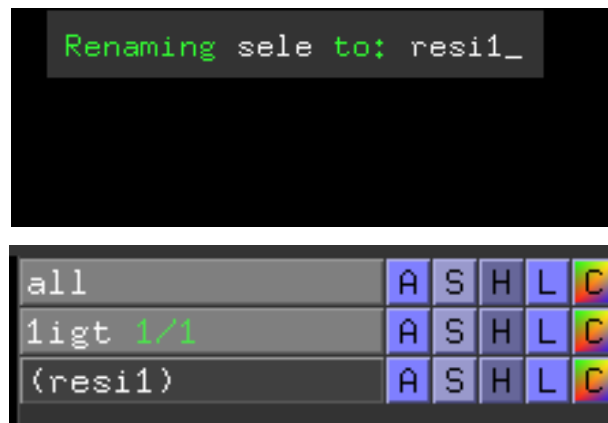
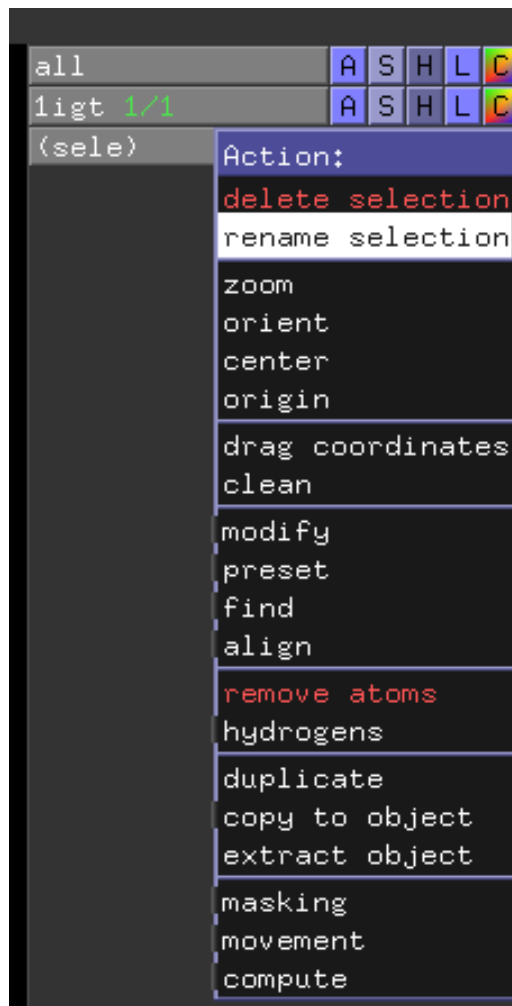
```
PyMOL> select resi 1
```



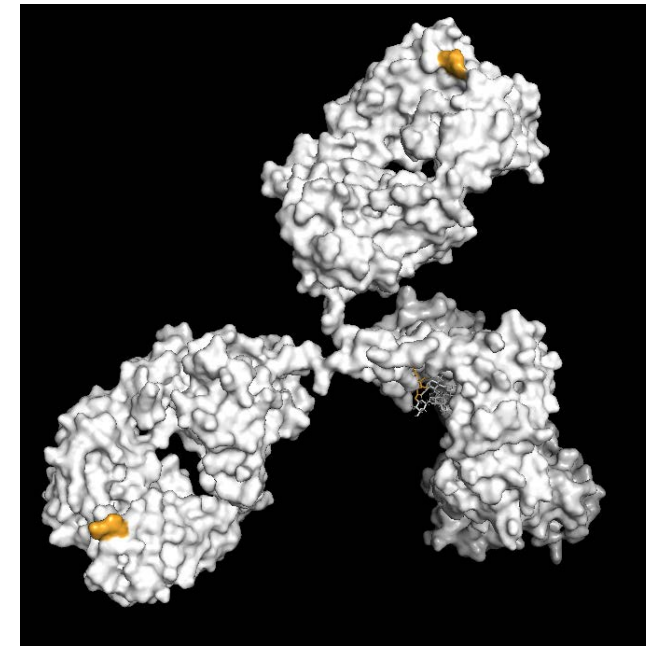
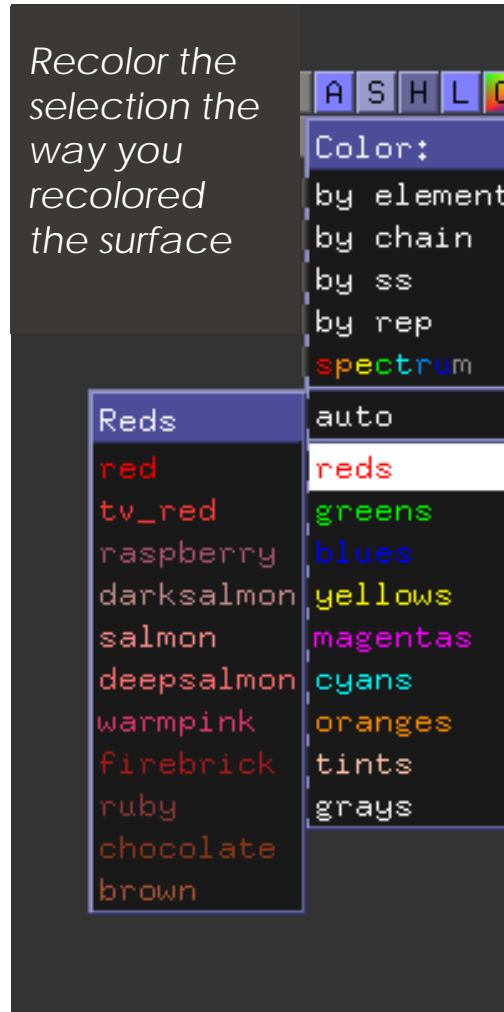
**you should
see pink dots
show up*

Rename and Recolor Selection

Instructions: Type "Select Resi #"

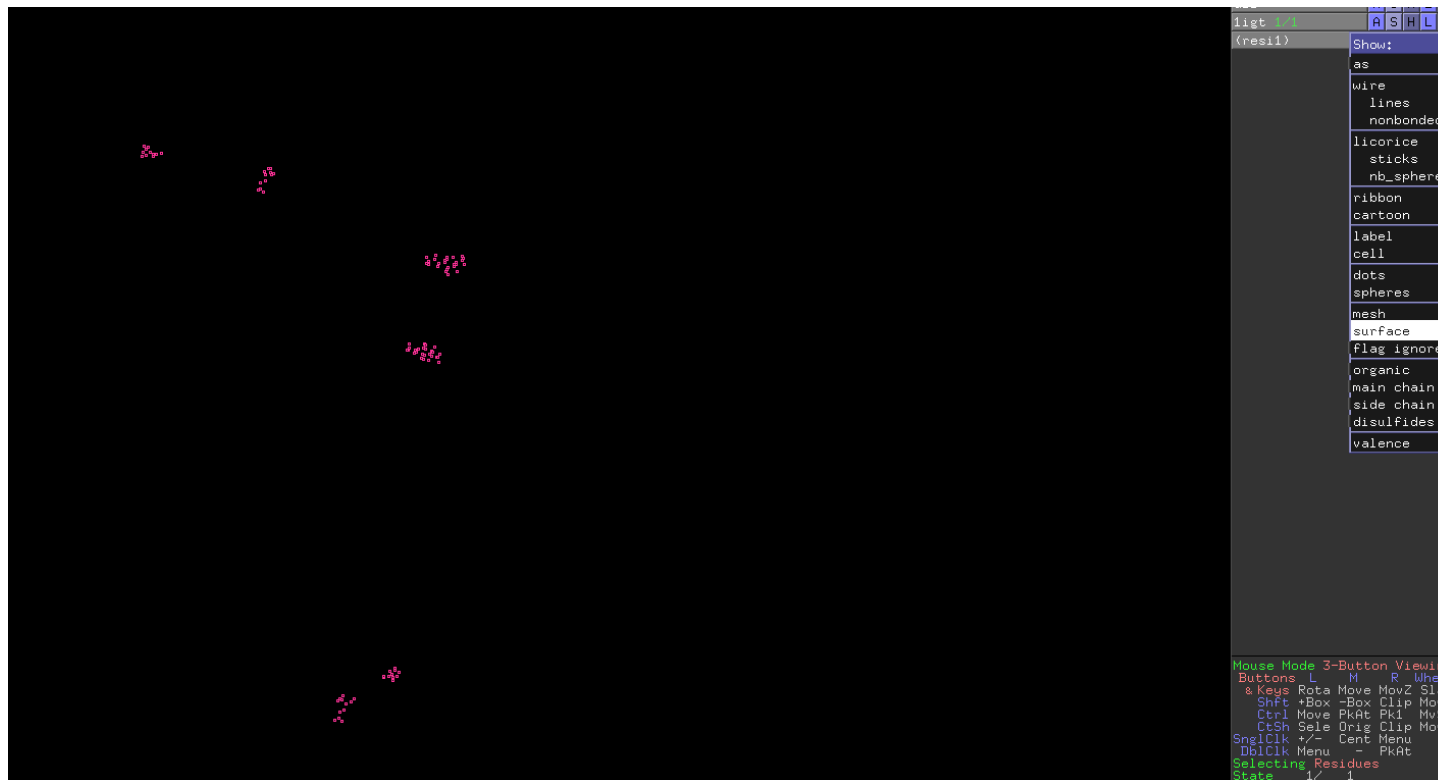
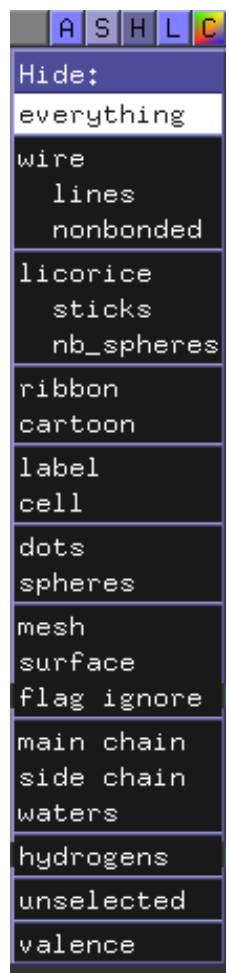


**hit enter to rename selection*

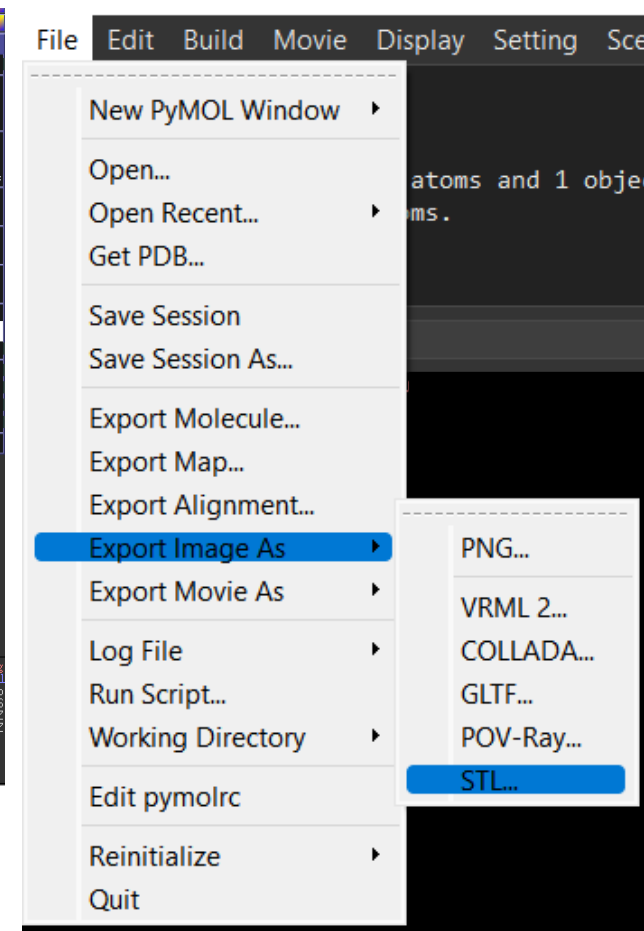


Make selection separate export

Instructions: Click H > Everything > Resi 1 > S > Surface > File > Export Image As



**also export the main antibody by selecting it and exporting it as an stl*



Selecting specific chains on your model

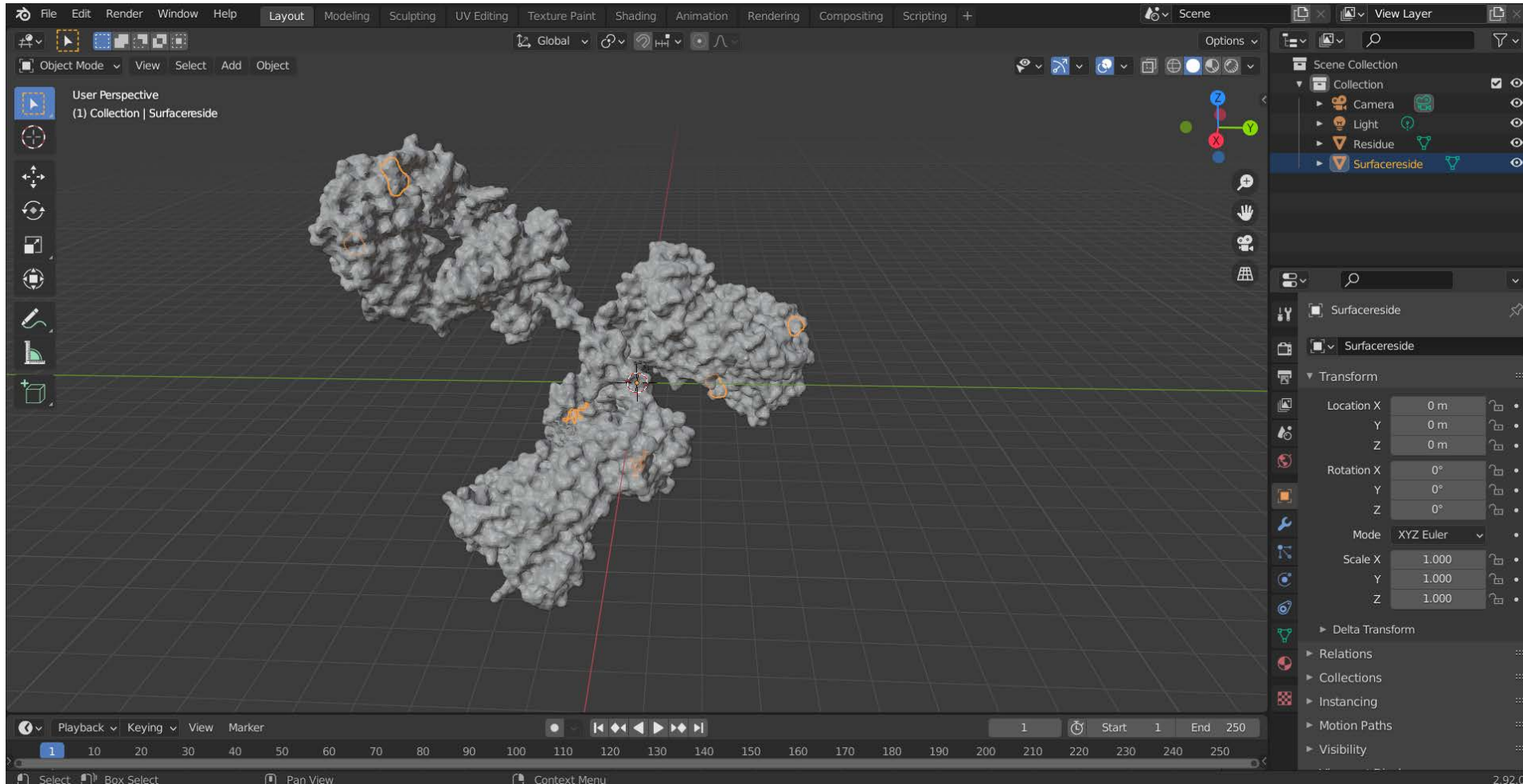
Instructions: Put your cursor in the command box > Type select "select chA, chain A"



**chains can be exported using the same process to export residues, we are not going to do that as a part of this workshop*

Overlay Residue on Blender File

Instructions: Open Blender > File > Import > STL > Select both the antibody and residue



**should come in overlapping as separate objects*

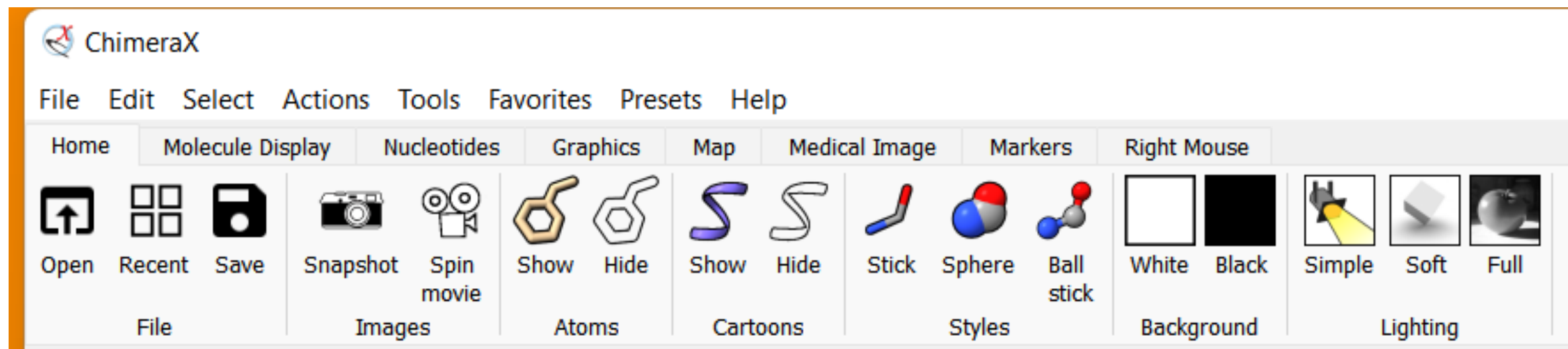
Chimera

Open-source molecular visualization software

<https://www.cgl.ucsf.edu/chimera/download.html>

Opening a File

Instructions: [Open](#) > [Select PDB](#)



Select Chains, Create Surface

Instructions: Select Chains in right hand menu > Go to top menu > Molecule Display > Surface

1igt.cif title:
Structure of immunoglobulin [\[more info...\]](#)

Chain information for 1igt.cif #1	
Chain	Description
A C	IGG2A intact antibody - MAB231
B D	IGG2A intact antibody - MAB231



Non-standard residues in 1igt.cif #1	
BMA	— beta-D-mannopyranose
FUC	— alpha-L-fucopyranose
FUL	— beta-L-fucopyranose (6-deoxy-β-L-galactose)
GAL	— beta-D-galactopyranose
MAN	— alpha-D-mannopyranose
NAG	— 2-acetamido-2-deoxy-beta-D-glucopyranose

[select](#) /A:1-214

2033 atoms, 2073 bonds, 214 residues, 1 model selected

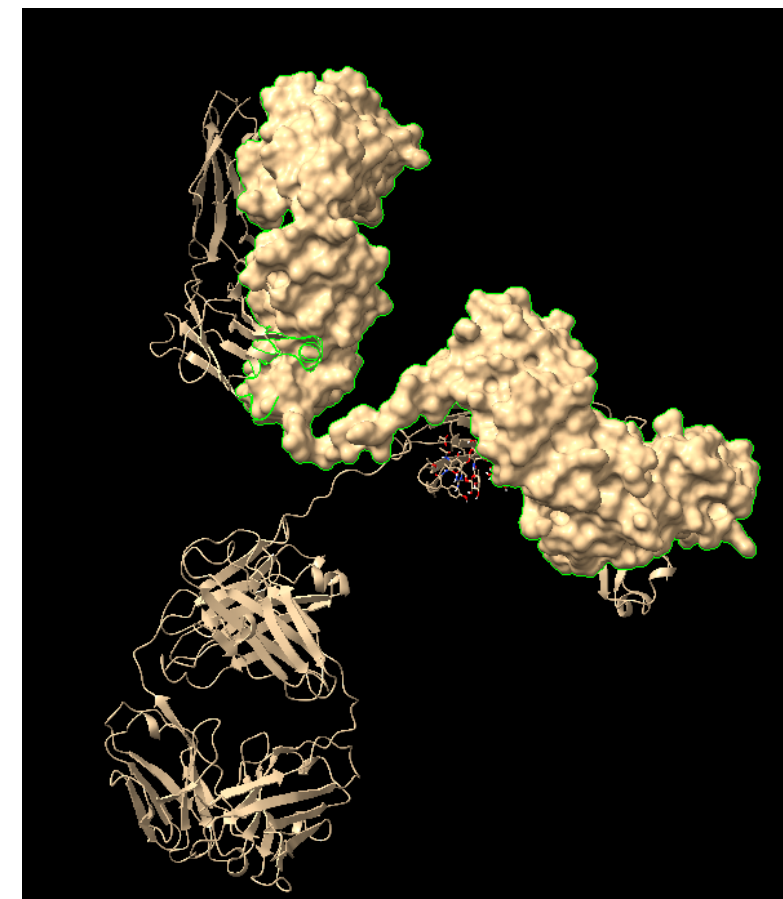
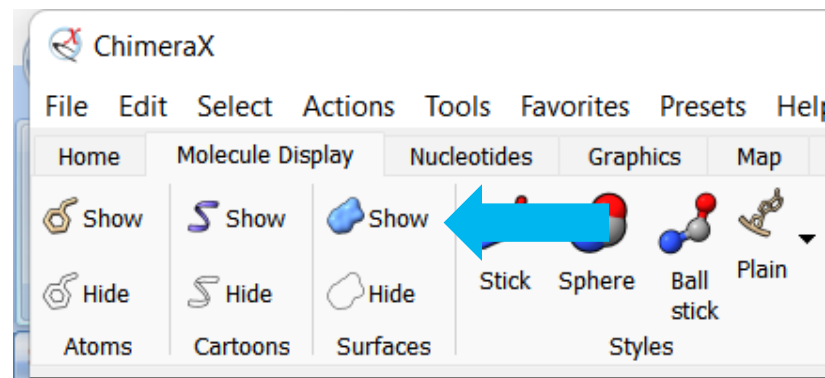
[select](#) /C:1-214

2033 atoms, 2073 bonds, 214 residues, 1 model selected

[select](#) /D:1-474

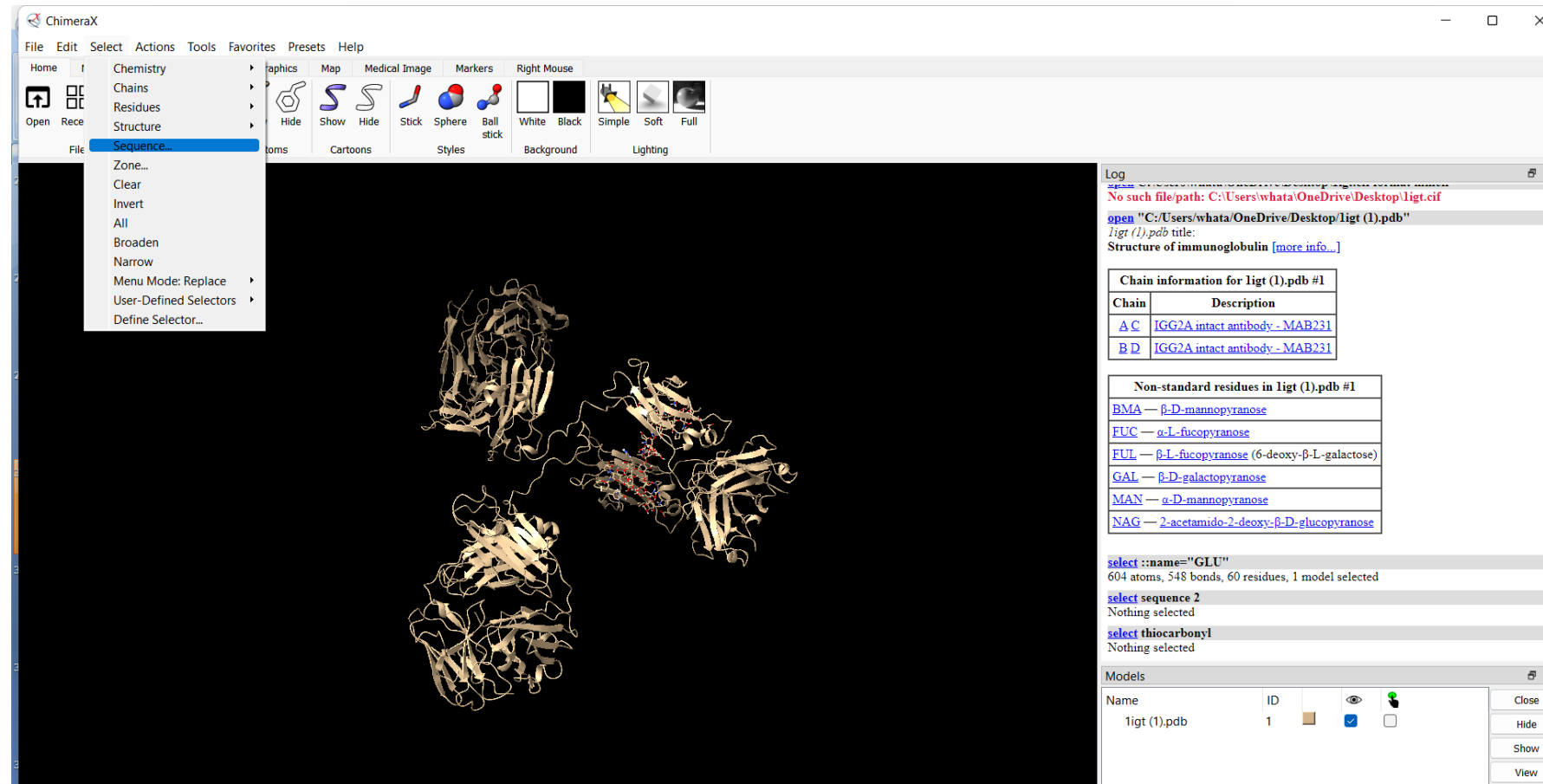
4232 atoms, 4330 bonds, 444 residues, 1 model selected

[show](#) sel surfaces



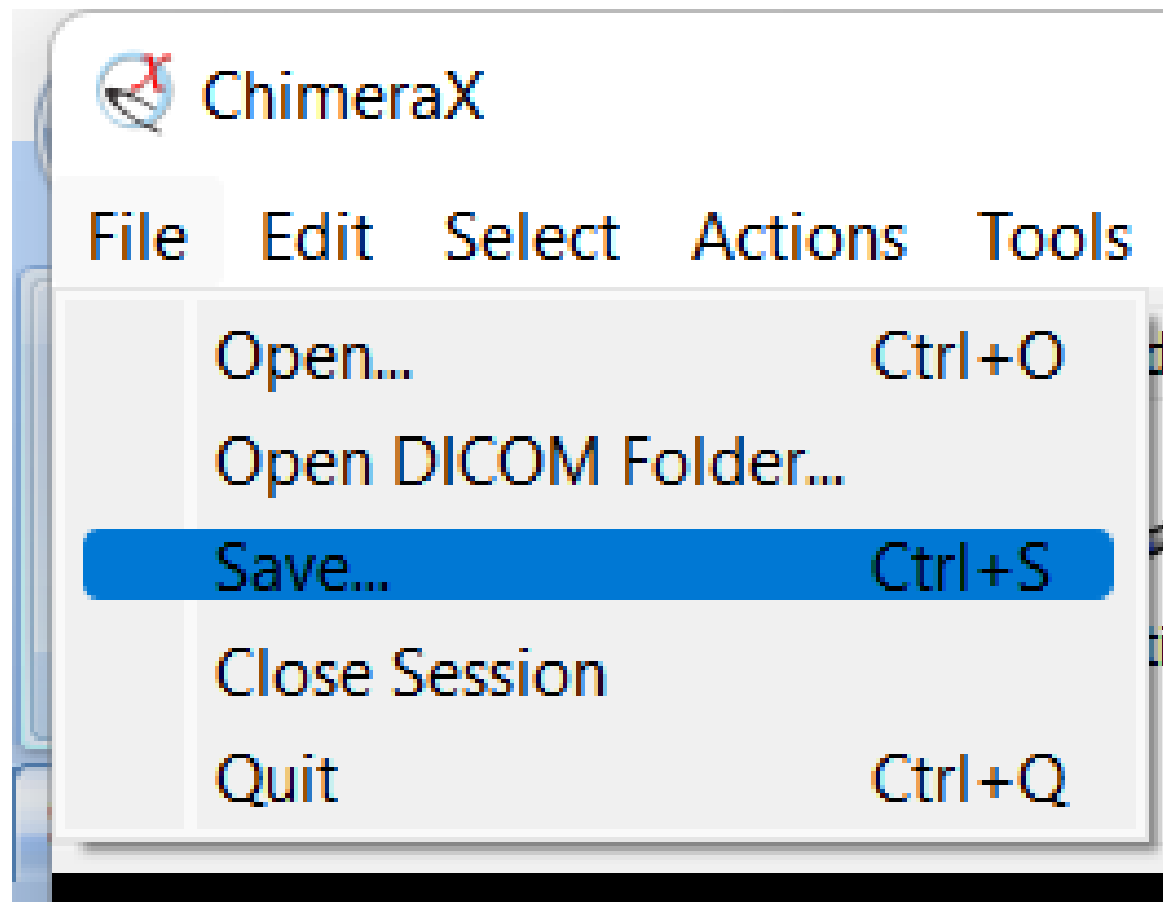
Other types of selections in chimera

Instructions: Select > you will see a list of potential things you can select and highlight on the model



Export a File

Instructions: File > Save



Useful resources to help you get started

- **PyMol Command References:**
<https://pymol.org/pymol-command-ref.html>
- **Additional Proteins:** <https://charmm-gui.org/?doc=archive&lib=covid19>
- **Visualizing Mutations:** <https://pcur.princeton.edu/2021/05/visualizing-covid-19-mutations-using-pymol-a-university-provided-resource/>
- **Blender for Scientists CG Figures YouTube Channel:** <https://www.youtube.com/c/CGFigures/featured>
- **Blender for Biochemists YouTube Channel:** <https://www.youtube.com/c/BradyJohnston>
- **Luminous Labs Blender for Scientists Youtube Channel:** <https://www.youtube.com/c/LuminousLab>
- **Animation in Chimera:** <https://www.youtube.com/watch?v=SpfVA45oAuA>



Thank you!

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Medical Illustrator and Graphic Designer

