

Molecular Visualization

Marina Pak
PhD-4

Skoltech
2024

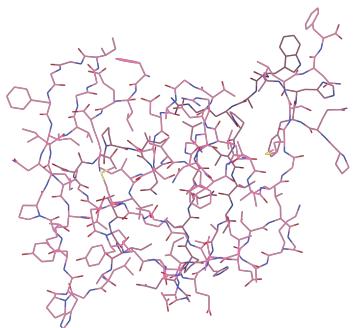
Outline

- Molecular representations
- Objects and scenes
- Color
- Molecular graphics software
- *History of molecular visualization*

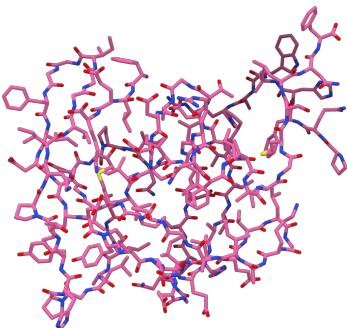
Practice: visualization of ligand-bound receptor

Molecular representations

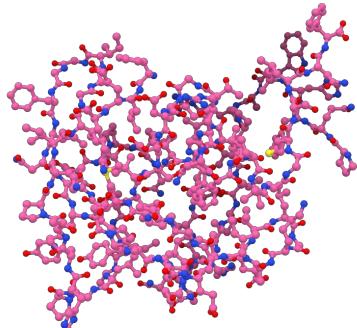
wire (lines)



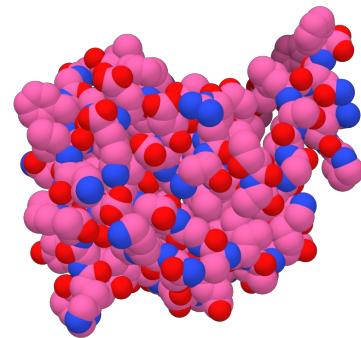
sticks



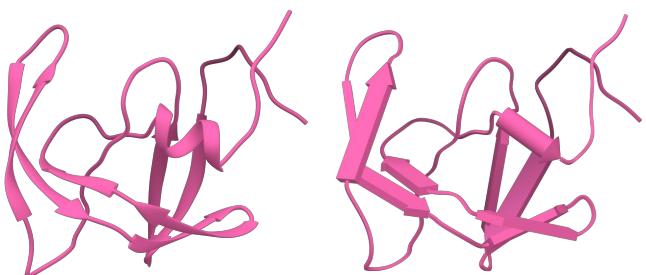
ball-and-stick



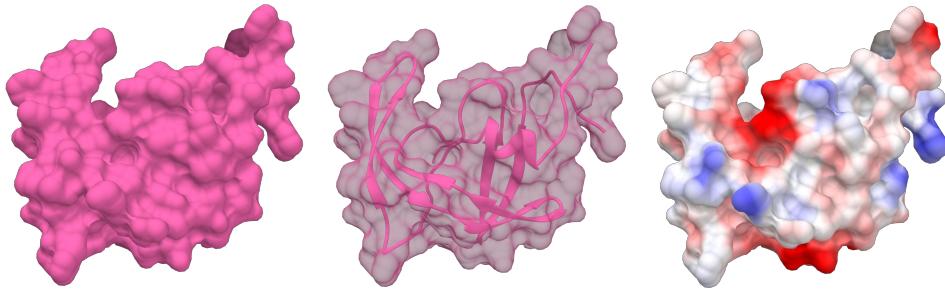
spheres
(space-filled, CPK, vdW)

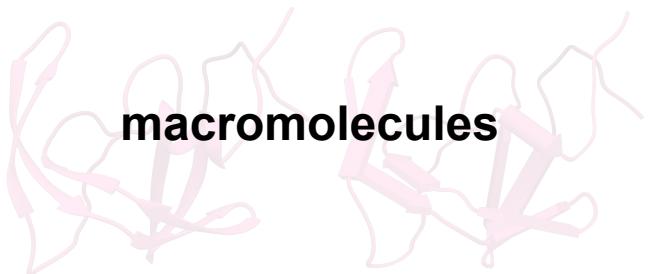
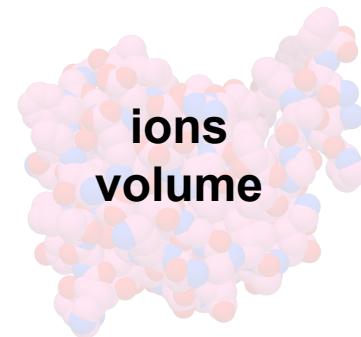
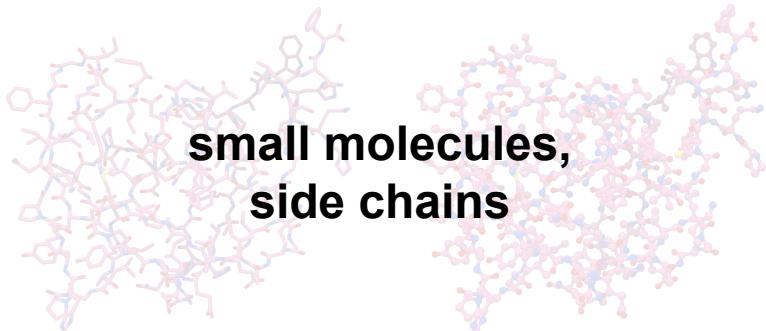


ribbon (cartoon)



surfaces

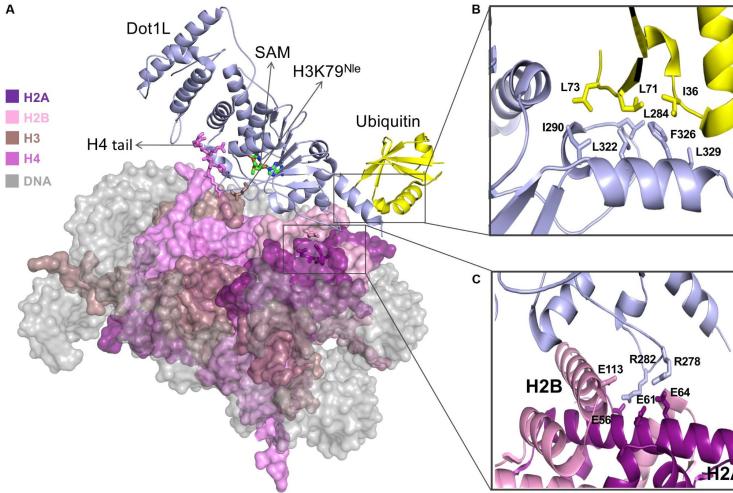




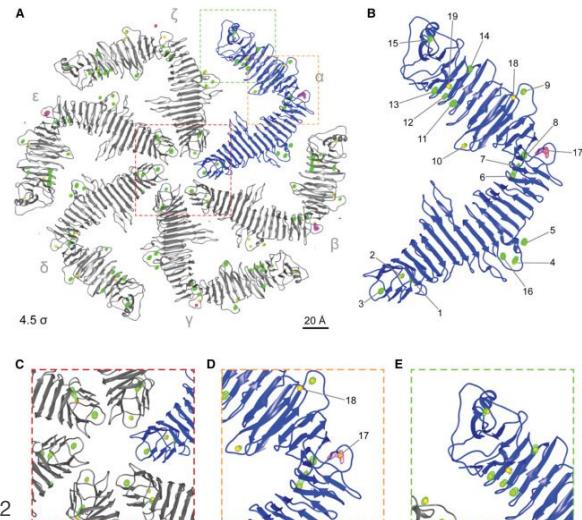
Objects & Scenes

Objects & Scenes: showing details

- zoom box:
 - *upper image*: small rectangle pointing to the zoomed-in area conned with a larger rectangle with zoomed-in picture
 - *bottom image*: pointing areas and zoomed-in rectangles are related by colors
- coloring: color an object of interest with a distinguished color, the rest of the scene with pale color or make transparent.

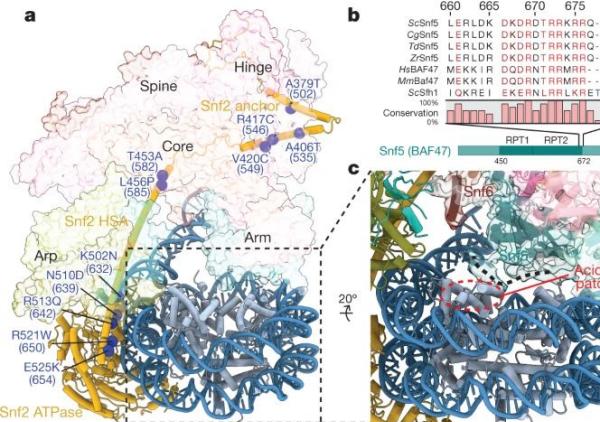


<https://www.frontiersin.org/articles/10.3389/fcell.2020.00600/full>

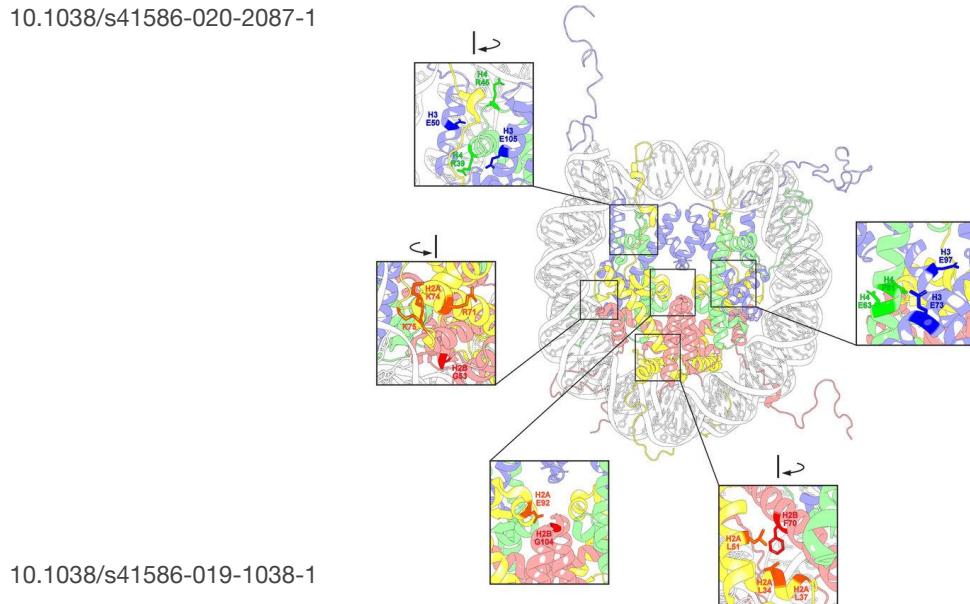


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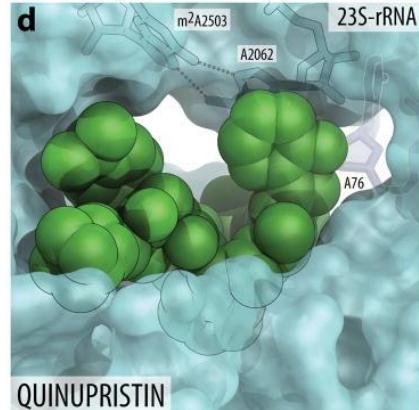
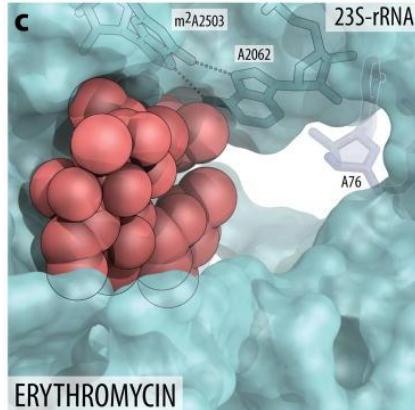
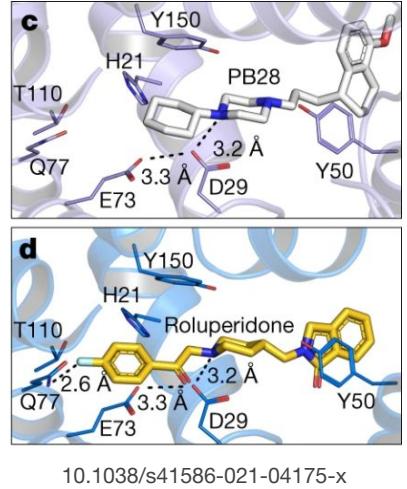
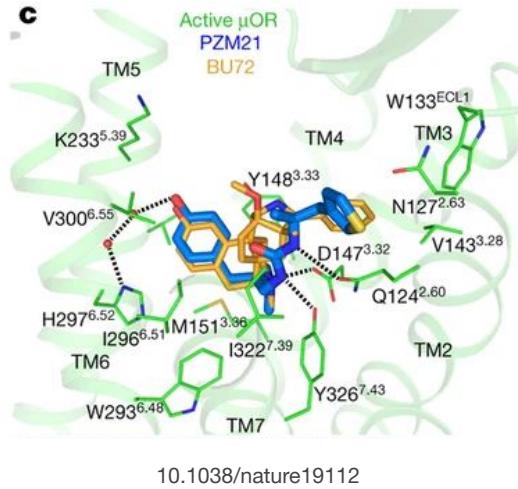


10.1038/s41586-020-2087-1



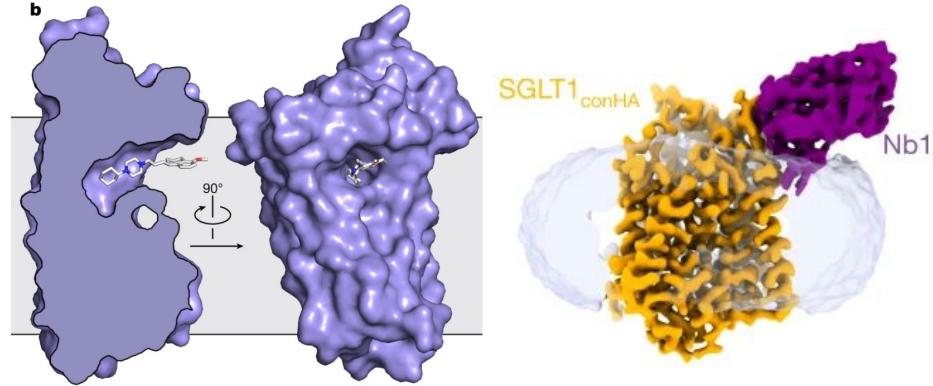
Objects & Scenes: binding site

- distances between atoms with dashed lines
- residue labels (can be drawn in external tool)
- transparent protein ribbons
- sticks representation of side chains of interacting residues
- surfaces to illustrate cavities
- superposition of ligands



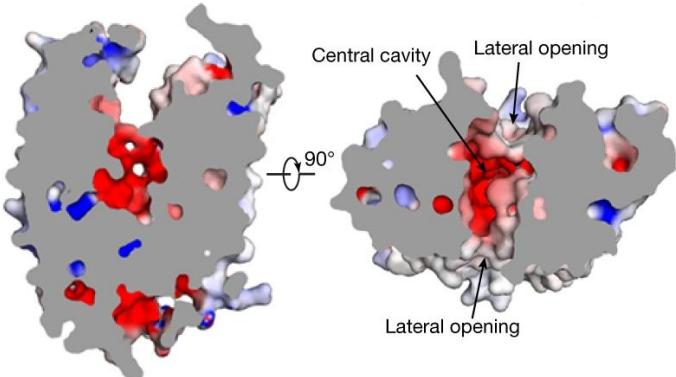
Objects & Scenes: surfaces

- clipping planes
- transparency
- coloring by property



10.1038/s41586-021-04175-x

10.1038/s41586-021-04211-w



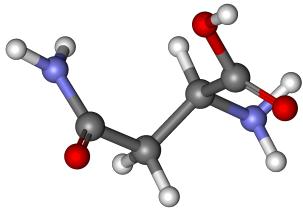
10.1038/s41586-021-03782-y

Color

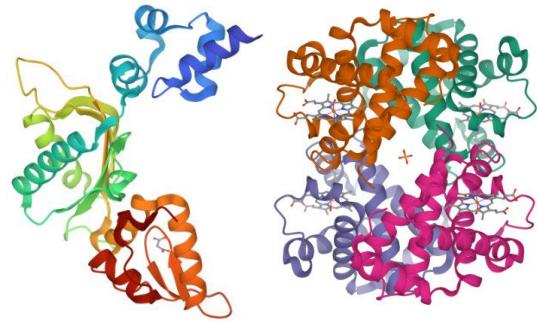
Color

Color should convey information.

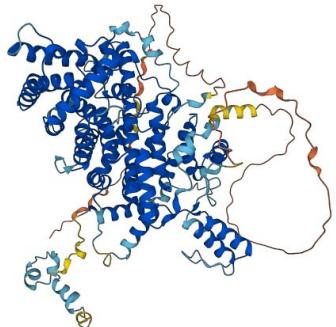
- distinct components (atoms, protein chains)
- N- to C-terminus
- properties (scores, charge, etc)



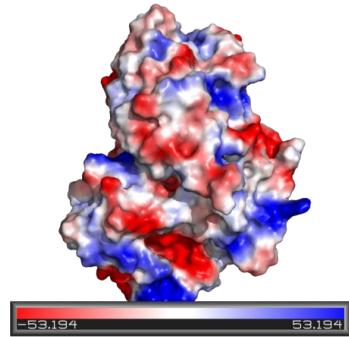
CPK coloring of atoms



PDB: N-to-C rainbow for a single chain,
different colors for distinct chains



AlphaFold models colored
by pLDDT

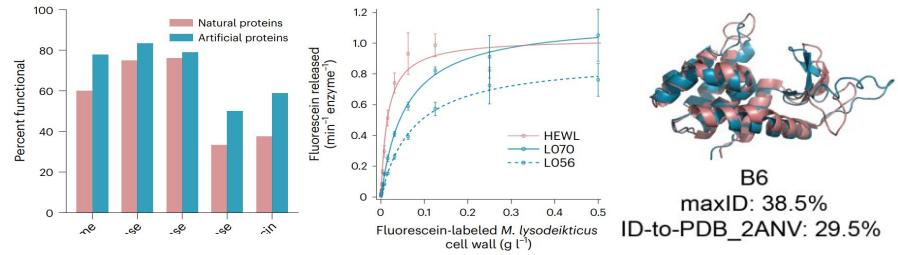


Electrostatic surface

Color

Good practices.

- Nice color combinations, fancy colors instead of default magenta and cyan.
- A single color scheme for plots and molecular graphics.

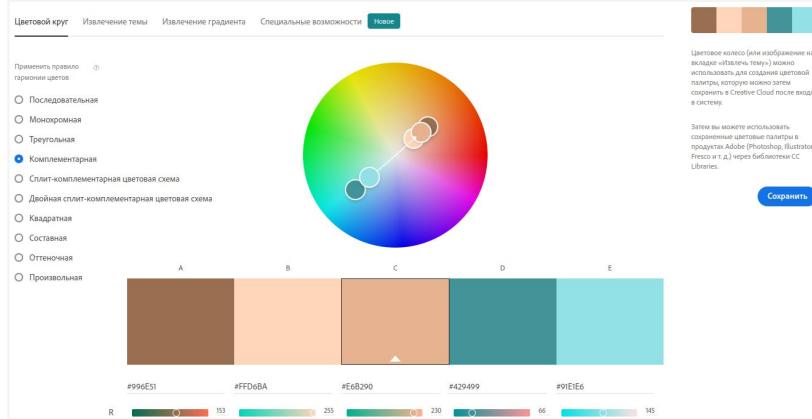


- Colors that are easy to distinguish and refer to: it might be troublesome to distinguish purple from violet or salmon from pink.

Color resources

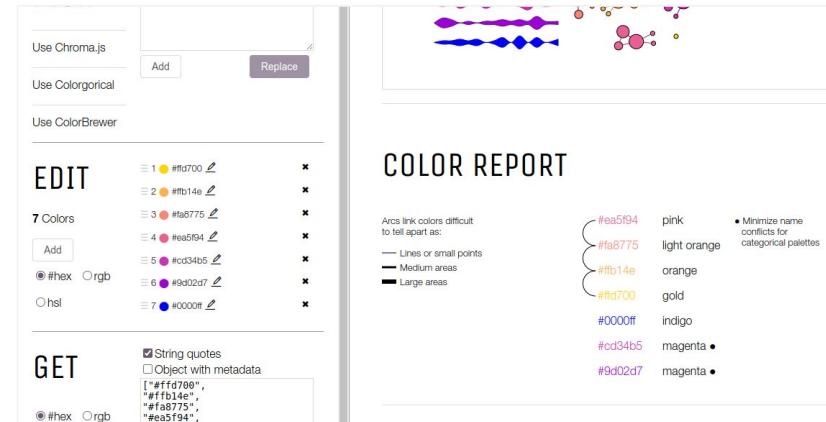
Create / find color schemes:

- colors.co/palettes/trending
- color-hex.com/color-palettes
- color.adobe.com/ru/trends
- color.adobe.com/ru/create/color-wheel
- davidmathlogic.com/colorblind



Analyse your color scheme:

projects.susielu.com/viz-palette



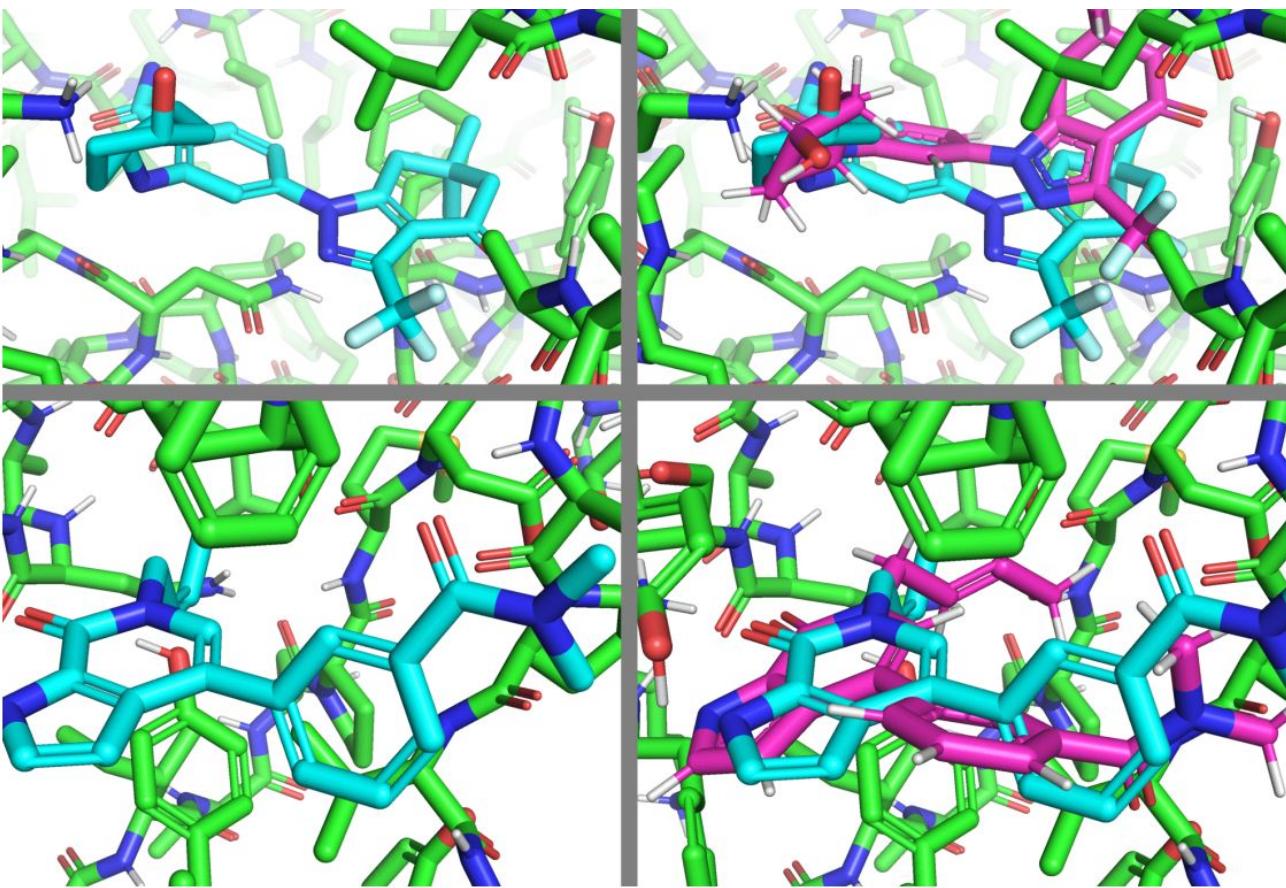


Figure 14. Three cherry-picked example predictions of EQUIBIND (cyan) on the left with the same image on the right, including the true bound conformer in pink.

Protein atoms overload the view and obstruct conformers:

- hide backbone atoms / display protein as transparent ribbons / display side chains only

Too many details overload the scene:

- hydrogen atoms
- double bonds
- mixed representation of aromaticity
- different sticks radius

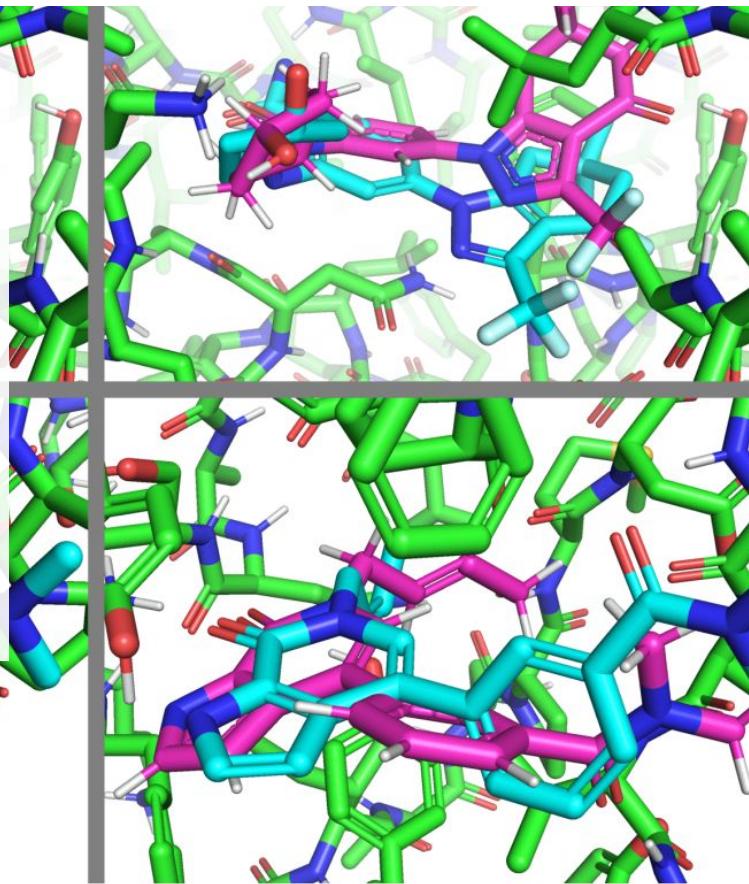
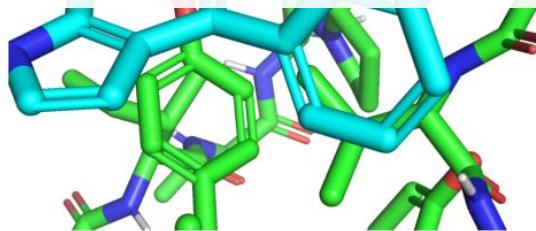
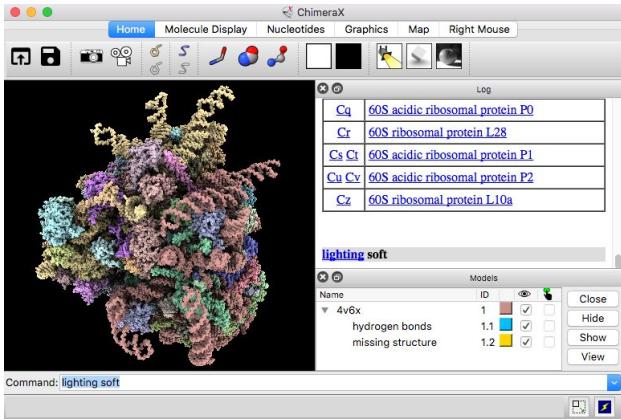


Figure 14. Three cherry-picked example predictions of EQUIBIND (cyan) on the left with the same image on the right, including the true bound conformer in pink.

Molecular graphics software

Chimera, PyMol



Chimera / Chimera X

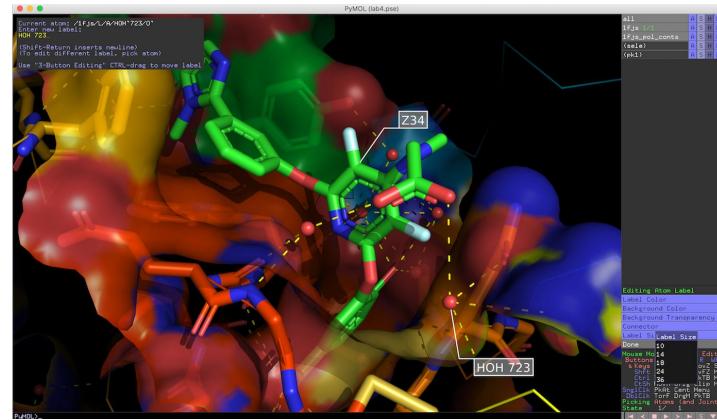
Extensible molecular modeling system

[Download \(VPN needed\)](#)

[Download \(from my cloud\)](#)

[Gallery](#)

[Documentation](#)



PyMol

[Download](#)

[Gallery](#)

[Documentation:](#)

https://pymolwiki.org/index.php/Command_Line_Options

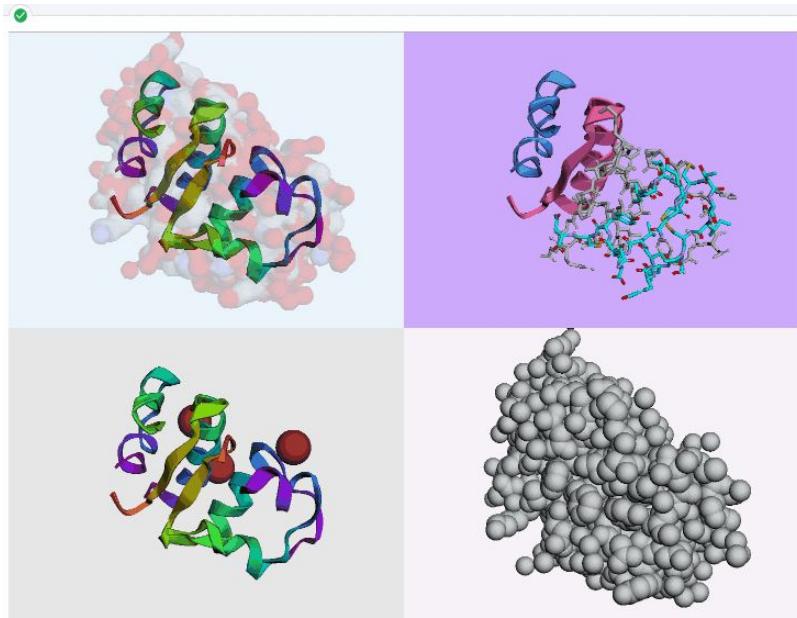
<https://pymol.org/pymol-command-ref.html>

https://pymolwiki.org/index.php/Category:Script_Library

Chimera vs PyMol

	Interface	Molecular modeling	Visualization
Chimera	<ul style="list-style-type: none">- GUI- CMD (Python)- Scripts	<ul style="list-style-type: none">- Basic functionality (building, editing, alignment, etc)- Integration of external tools: Modeller, Autodock Vina, MD, AlphaFold	<ul style="list-style-type: none">- External renders support- Advanced movie making- Does not display double bonds
PyMol	<ul style="list-style-type: none">- CMD (Python)- GUI – limited functionality- Conda- Python API- Scripts	<ul style="list-style-type: none">- Basic functionality (building, editing, alignment, etc)- Mutagenesis- Advanced manual structure editing- Refines PDB file structure (adds TER record, etc)	<ul style="list-style-type: none">- Displays double bonds, dihedral angles

Molecular visualization in Jupyter



insilicochemistry.io/tutorials/foundations/chemistry-visualization-with-py3dmol

py3Dmol

3dmol.org/

github.com/3dmol/3Dmol.js/tree/master/py3Dmol

Tutorials:

william-dawson.github.io/using-py3dmol.html

insilicochemistry.io/tutorials/foundations/chemistry-visualization-with-py3dmol

colab.research.google.com/github/pb3lab/ibm3202/blob/master/tutorials/lab02_molviz.ipynb

NGLview

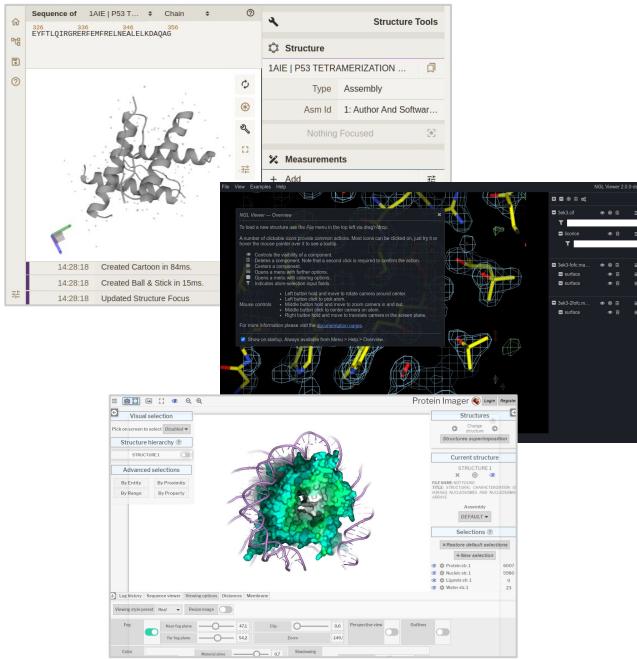
github.com/nglviewer/nglview

Tutorials:

ambermd.org/tutorials/analysis/tutorial_notebooks/nglview_notebook/index.html

projects.volkamerlab.org/teachopencadd/talktutorials/T017_advanced_nglview_usage.html

Web-tools for molecular visualization



Tool	Functionality	Resources that use the tool
Mol* molstar.org	basic visualization and analysis	RCSB PDB
LiteMol litemol.org	basic visualization, embedding into web pages	Uniprot, AlphaFold DB
Protein Imager 3dproteinimaging.com/protein-imager	super advanced beautiful styling	
NGL Viewer nglviewer.org/ngl/ nglviewer.org/ngl/gallery/	seems to be powerful, but complicated in use	
Jmol jmol.sourceforge.net	embedding into web pages	Wiki, Proteopedia
VRMol vrmol.net	VR support	

Practice

Tutorial: tinyurl.com/4axsca25

Ligand-bound transmembrane domain (PDB ID: [4OR2](#)) of metabotropic glutamate receptor 1 aligned to a full-length receptor (PDB ID: [7DGD](#)).

- structure editing
- alignment of structures
- visualize binding site residues
- visualize ligand in the binding site
- publication style image
- + optional tasks

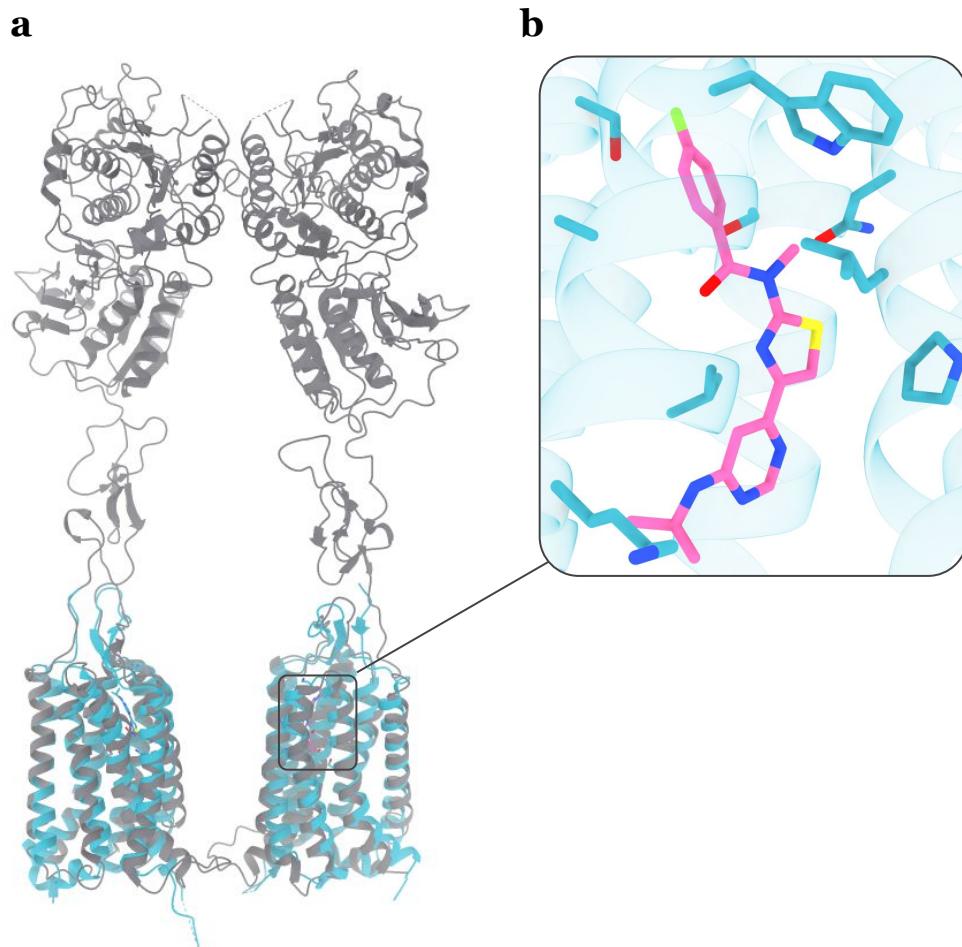
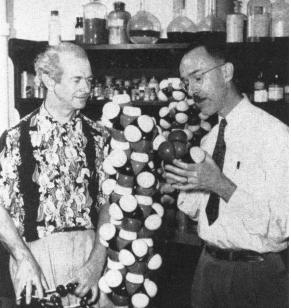
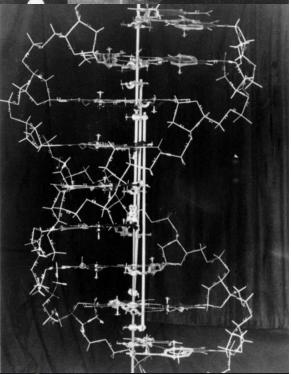


Figure 1. Metabotropic glutamate receptor with a ligand

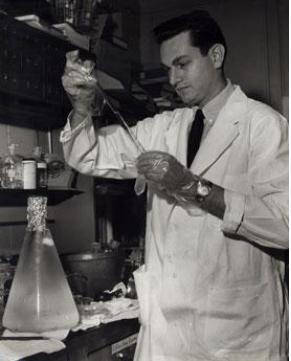
History of molecular visualization



protein structures (1951)



Watson & Crick's DNA model (1953)



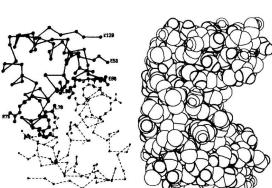
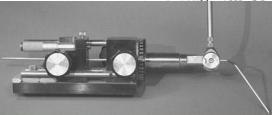
genetic code (1966)



CRYSTALLOGRAPHY

Protein Data Bank

A repository system for protein crystallographic data will be operated jointly by the Crystallographic Data Centre, Cambridge, and the Brookhaven National Laboratory. The system will be responsible for storing atomic coordinates, structure factors and electron density maps and will make these data available on request. Distribution will be on magnetic tape in machine-readable form whenever possible. There will be no charge for the service other than handling costs. Files will be updated as new material is received. The total holding will be

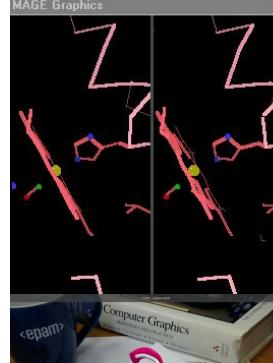
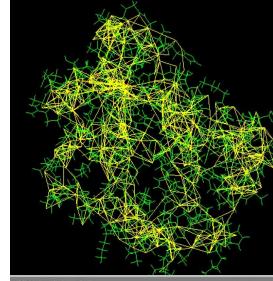


first computer models (1966)

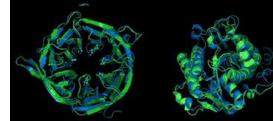
Protein Data Bank (1971)

Byron's Bender (1972)

molecular graphics software (1980s)



T0954 / 6CVZ T0965 / 6D2V



‘It will change everything’: DeepMind’s A
giant leap in solving protein structure

Google’s deep learning program for determining the 3D shapes of proteins stands to transform biology

Even Gaffney

biological NMR spectroscopy (1985)

RasMol Kinemage (1990s)

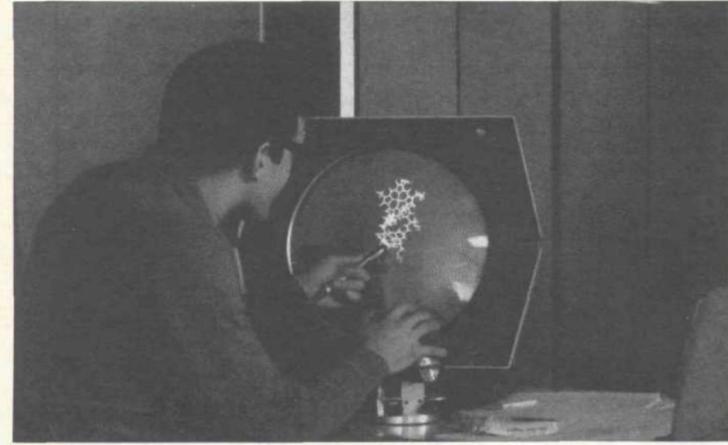
Web/ VR/AR (2010)

accurate structure prediction (2021)

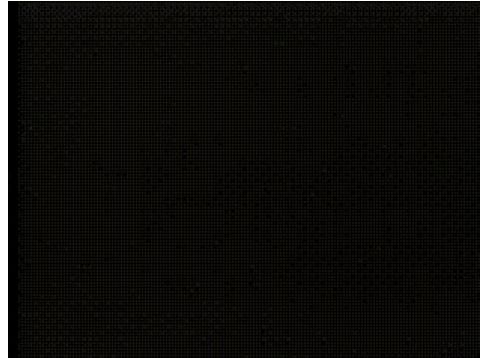
First computer models

- computer controlled oscilloscope
- continuously changing projections - effect of rotation
- rotation rate controlled by globe-shaped device

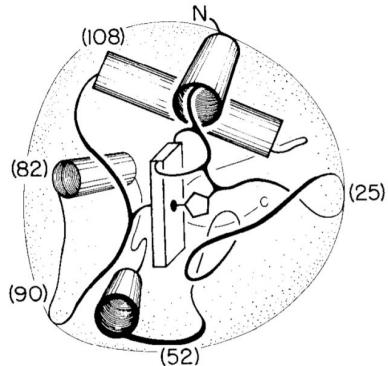
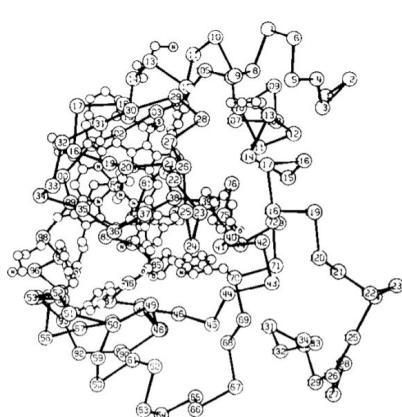
Molecular Model-building by Computer. Levinthal. Scientific American (1966), 214:42



DISPLAY UNIT designed by John Ward and Robert Stotz has access to the large time-shared central computer at the Massachusetts Institute of Technology. The investigator communicates with the computer by typing commands or punching preset buttons on a keyboard or by pointing with the light pen. He regulates the direction and the speed of rotation of the model by moving the gimbaled control on which his right hand rests.

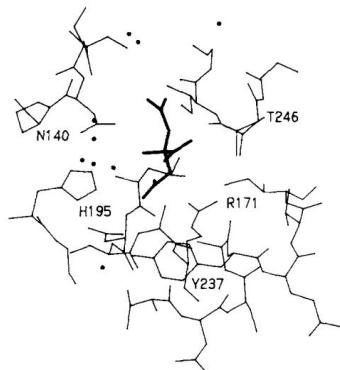


1970s

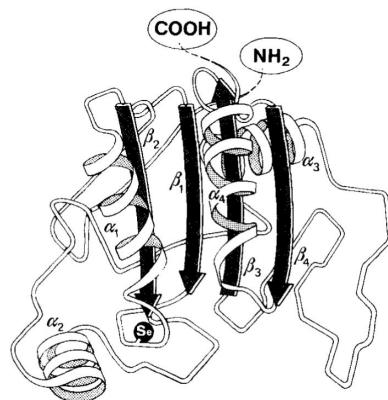


10.1016/S0021-9258(17)33352-5

1980s

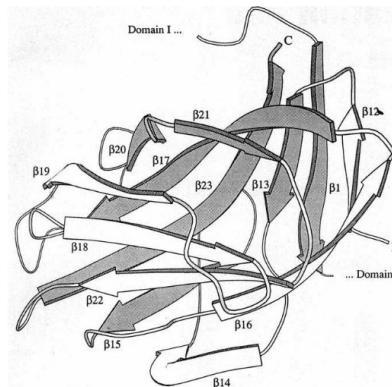


10.1016/0022-2836(87)90293-2



10.1111/j.1432-1033.1983.tb07429.x

1990s

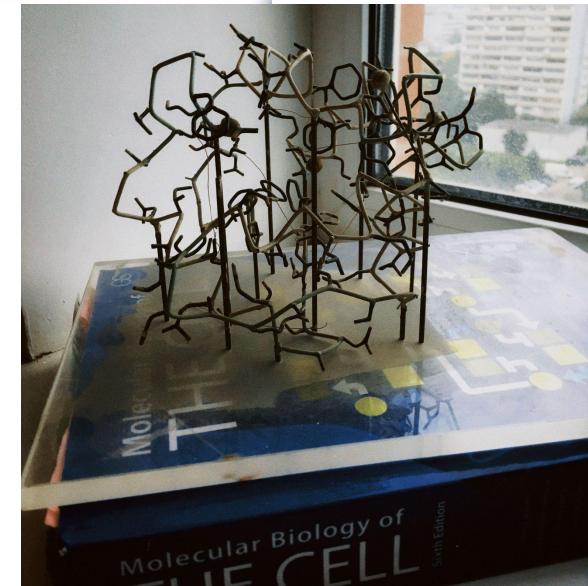
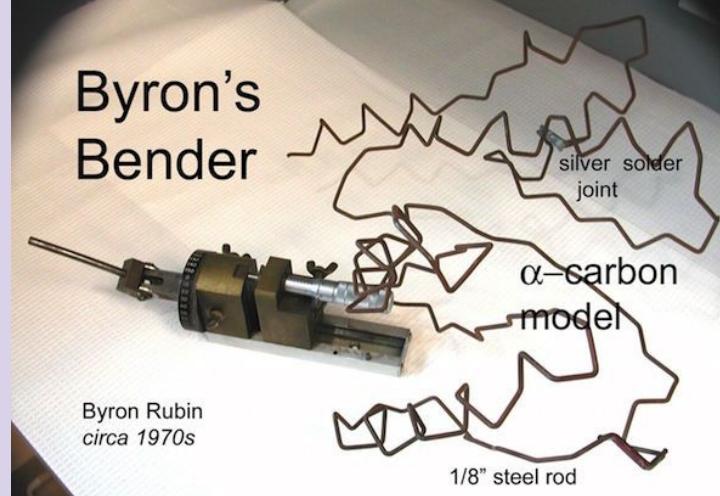


10.1038/353815a0

Physical models of protein structures

widely used till 1980s

<https://onlinelibrary.wiley.com/doi/epdf/10.1002/bip.1972.360111116>
https://proteopedia.org/wiki/index.php/Byron%27s_Bender

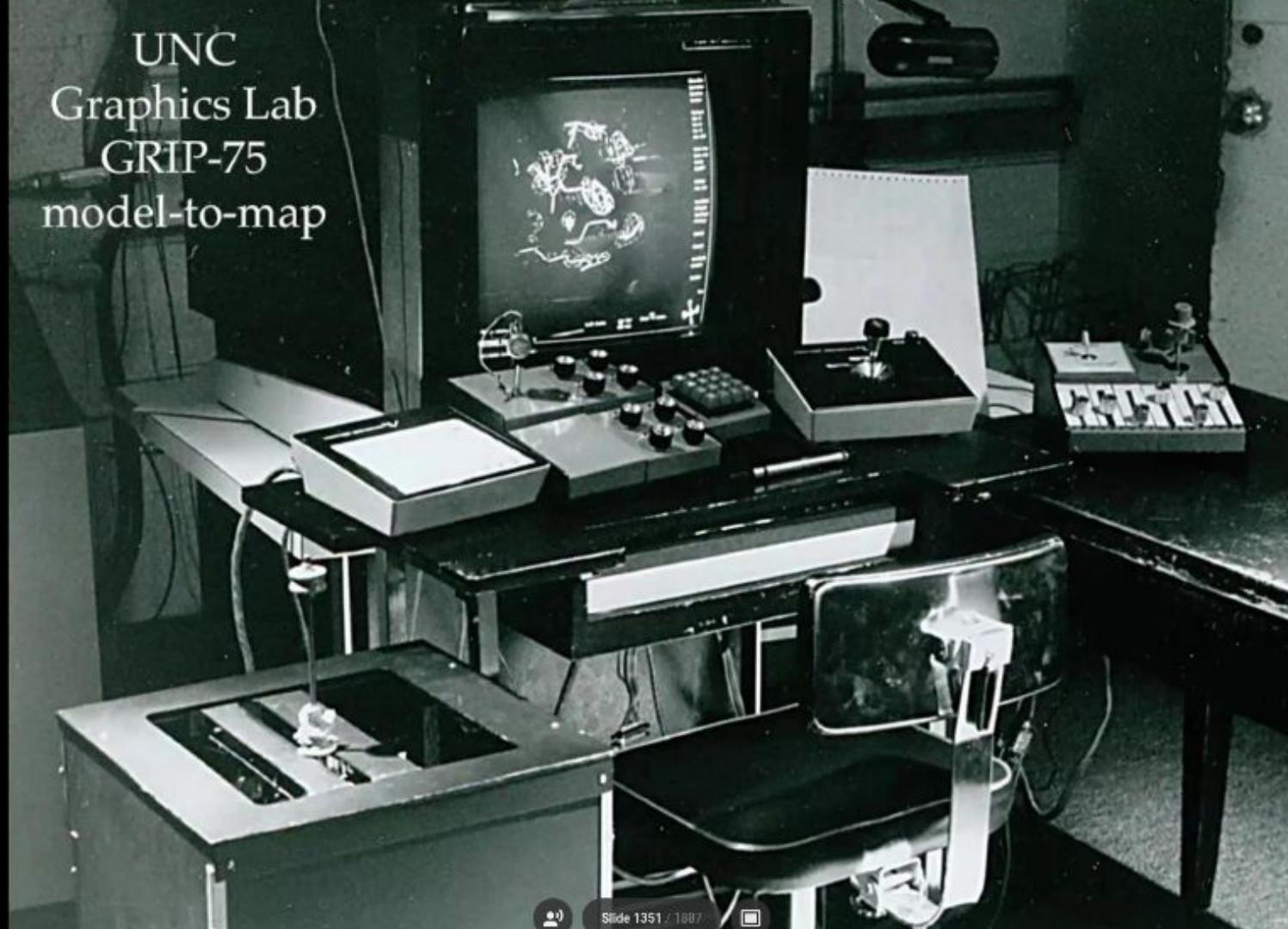


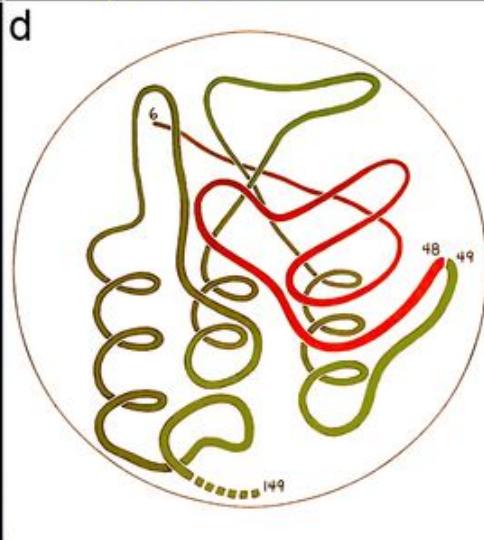
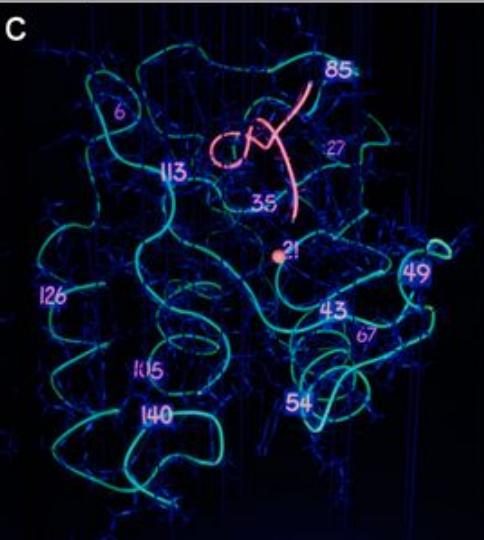
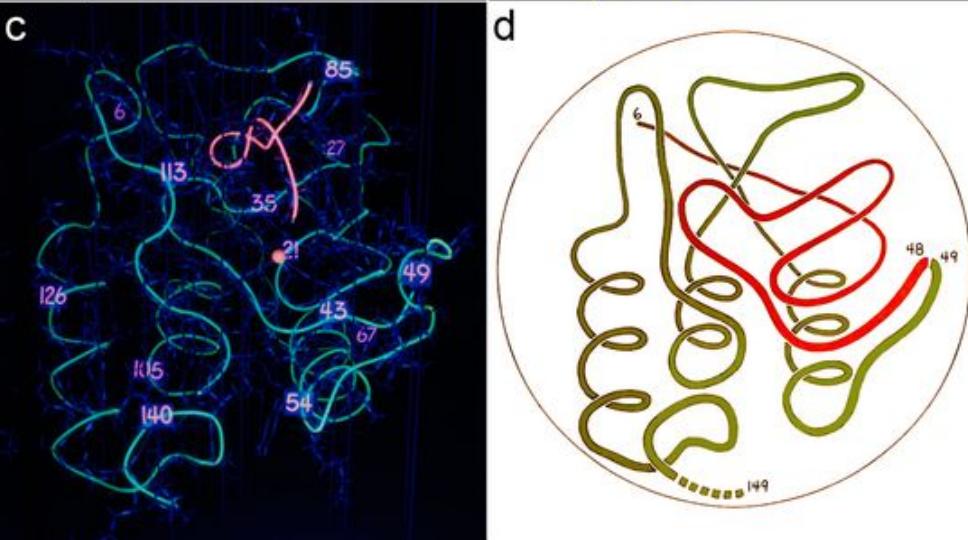
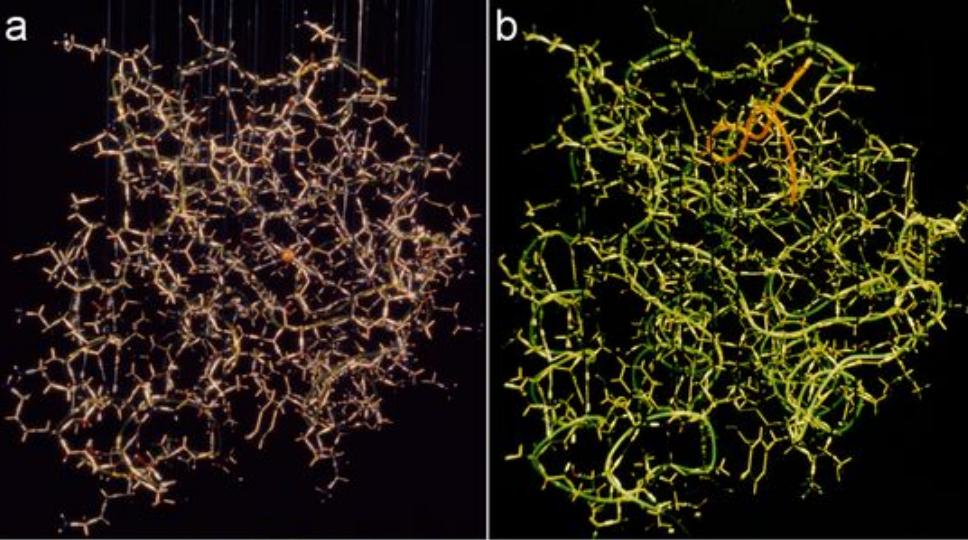
Electron-density contours
hand-drawn on numerical printout,
copied onto big glass sheets

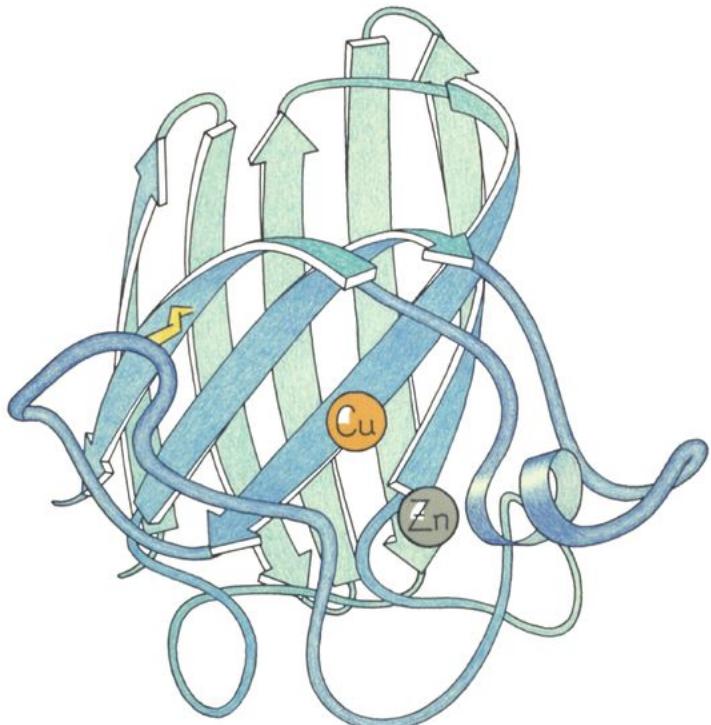
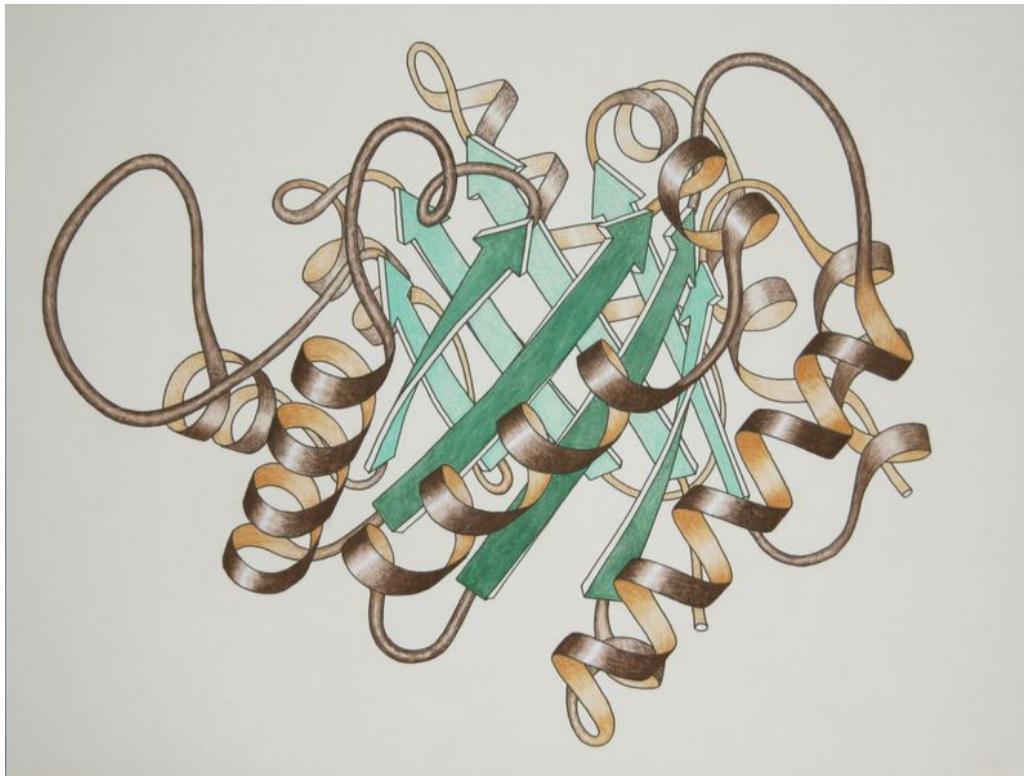
brass Kendrew model
sitting on top:
Phe-Arg bonding inhibitor PO4



UNC
Graphics Lab
GRIP-75
model-to-map







<https://stories.duke.edu/sciences-mother-of-ribbon-diagrams-celebrates-50-years-at-duke>

<https://commons.wikimedia.org/wiki/User:Dcrjsr>