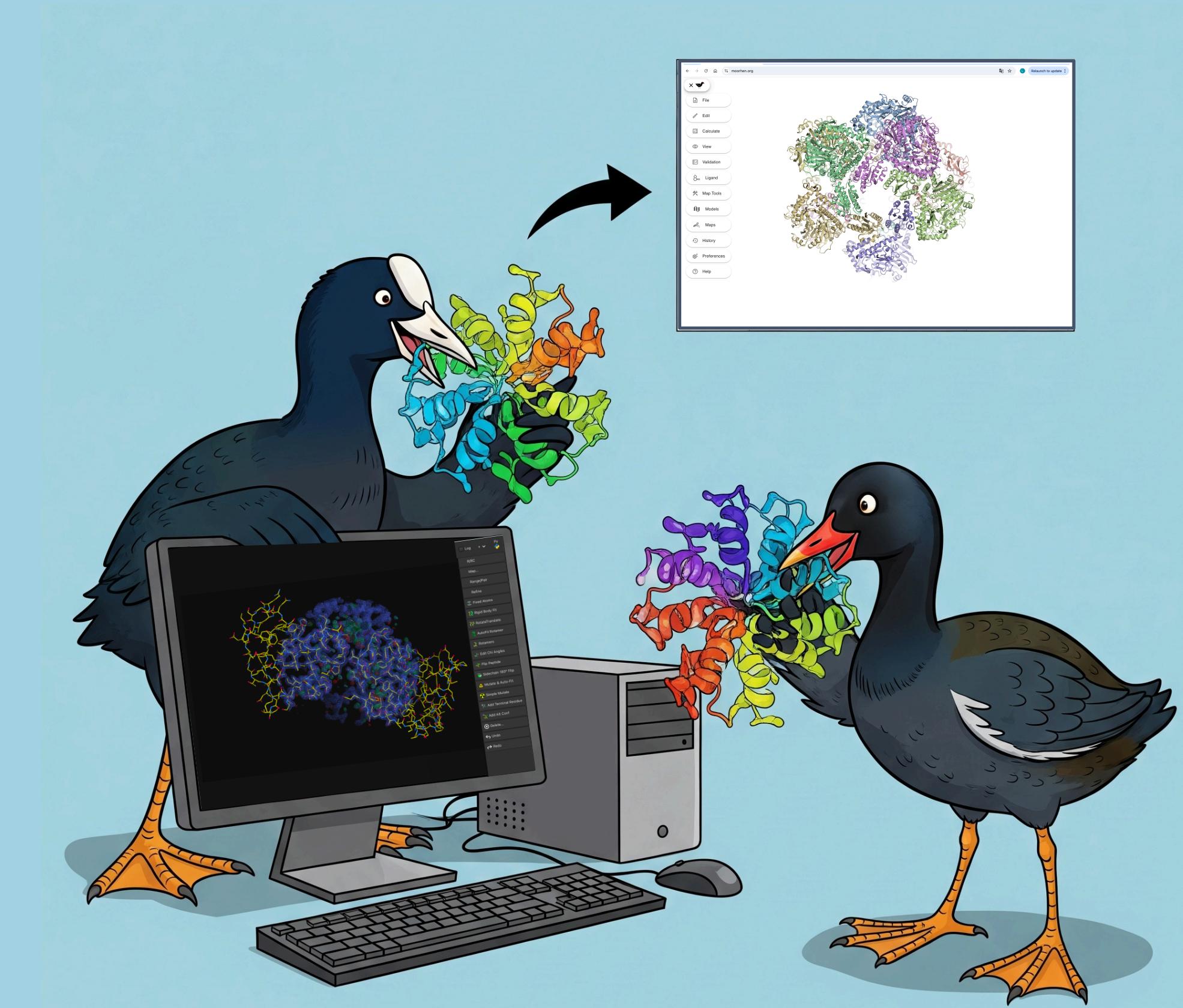


Coot & Moorhen

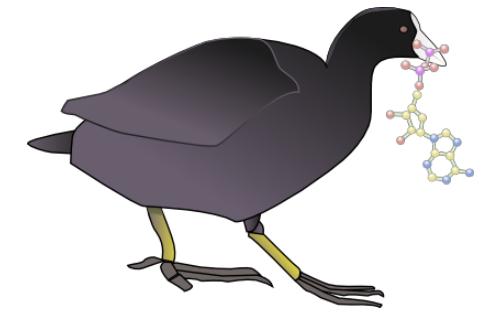
Model building, Real-space refinement & Graphics



Lucrezia Catapano, MRC-LMB

DLS/CCP4 Workshop 2025

Coot



- Coot was born **21 years ago**, on April 1st



Model-building with Coot

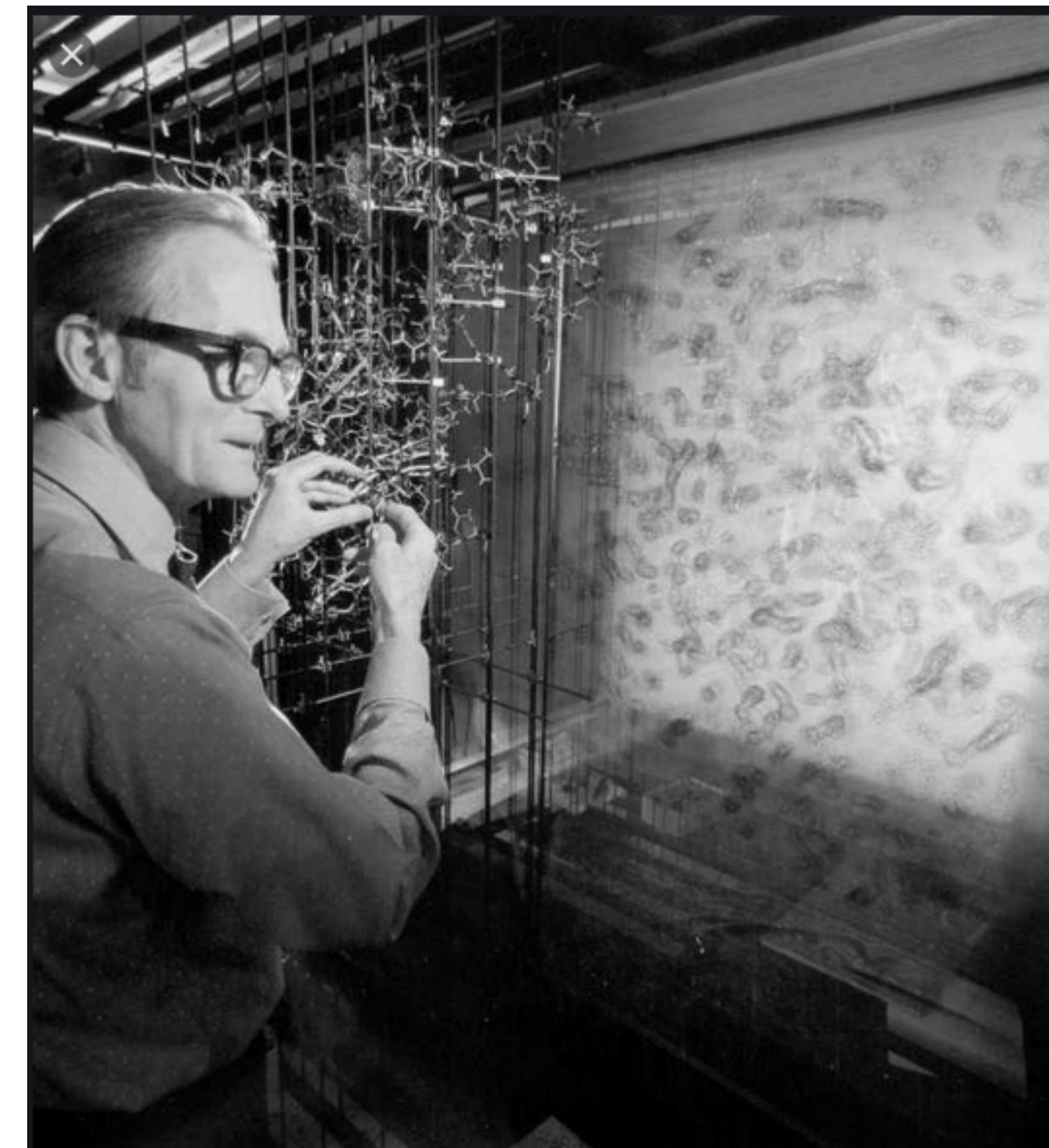
Tools to help improve the quality of the macromolecular model:

- Mutations
- Addition/Deletions/Merging
- Refinement tools
- Tools for ligand analysis and presentation
- Tools for Cryo-EM fitting

On “Manual Model Building”



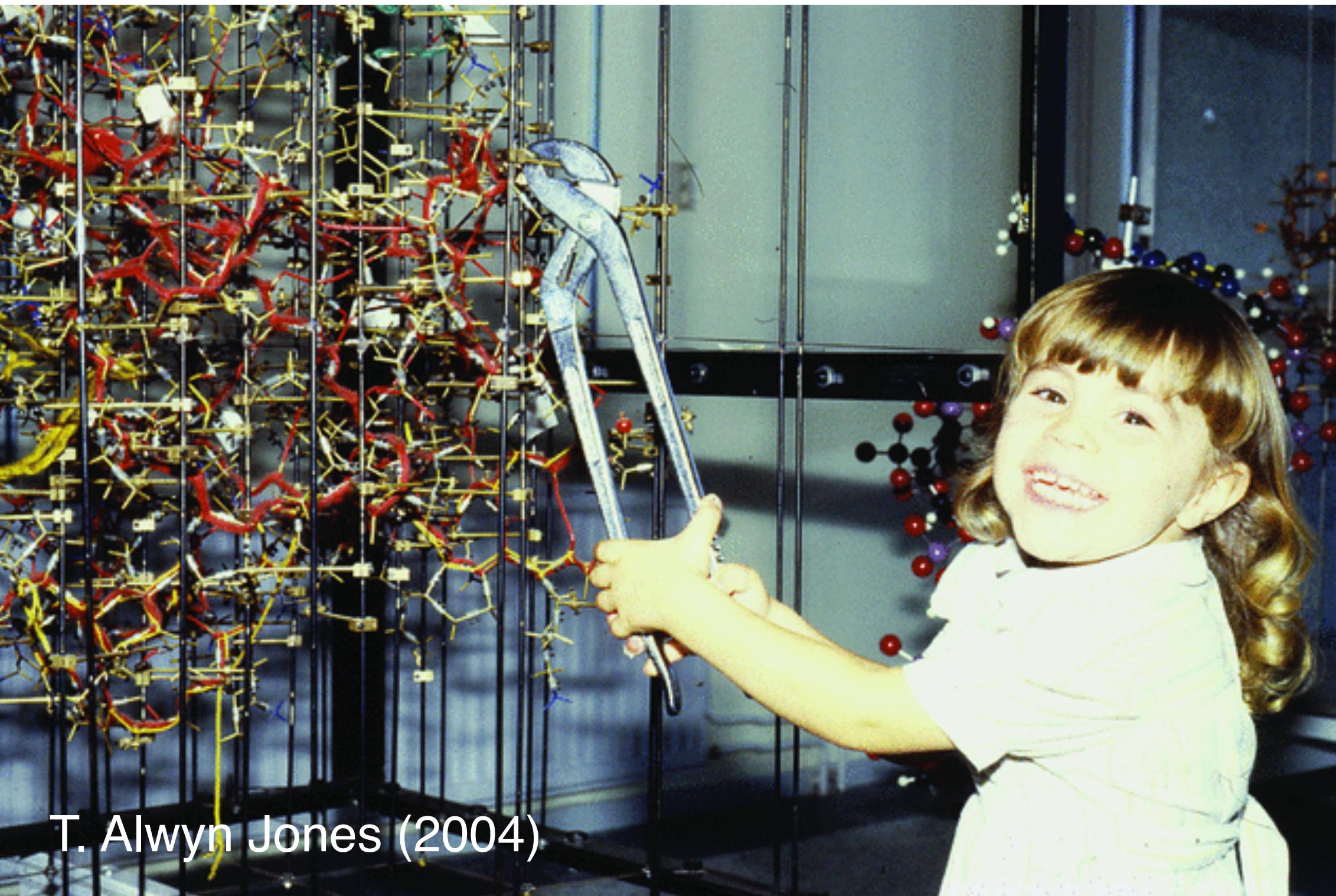
DCH building the first insulin model



William Lipscomb, model of carboxypeptidase

*This is “Manual Model-Building” :
“twisting physical brass models held together
by screws”*

Kendrew wire model of alcohol dehydrogenase that is about to undergo a round of rebuilding by Maelle Cambillau



T. Alwyn Jones (2004)

“Manual” implies that you are deciding where the atoms go – in fact you aren't... Coot is.

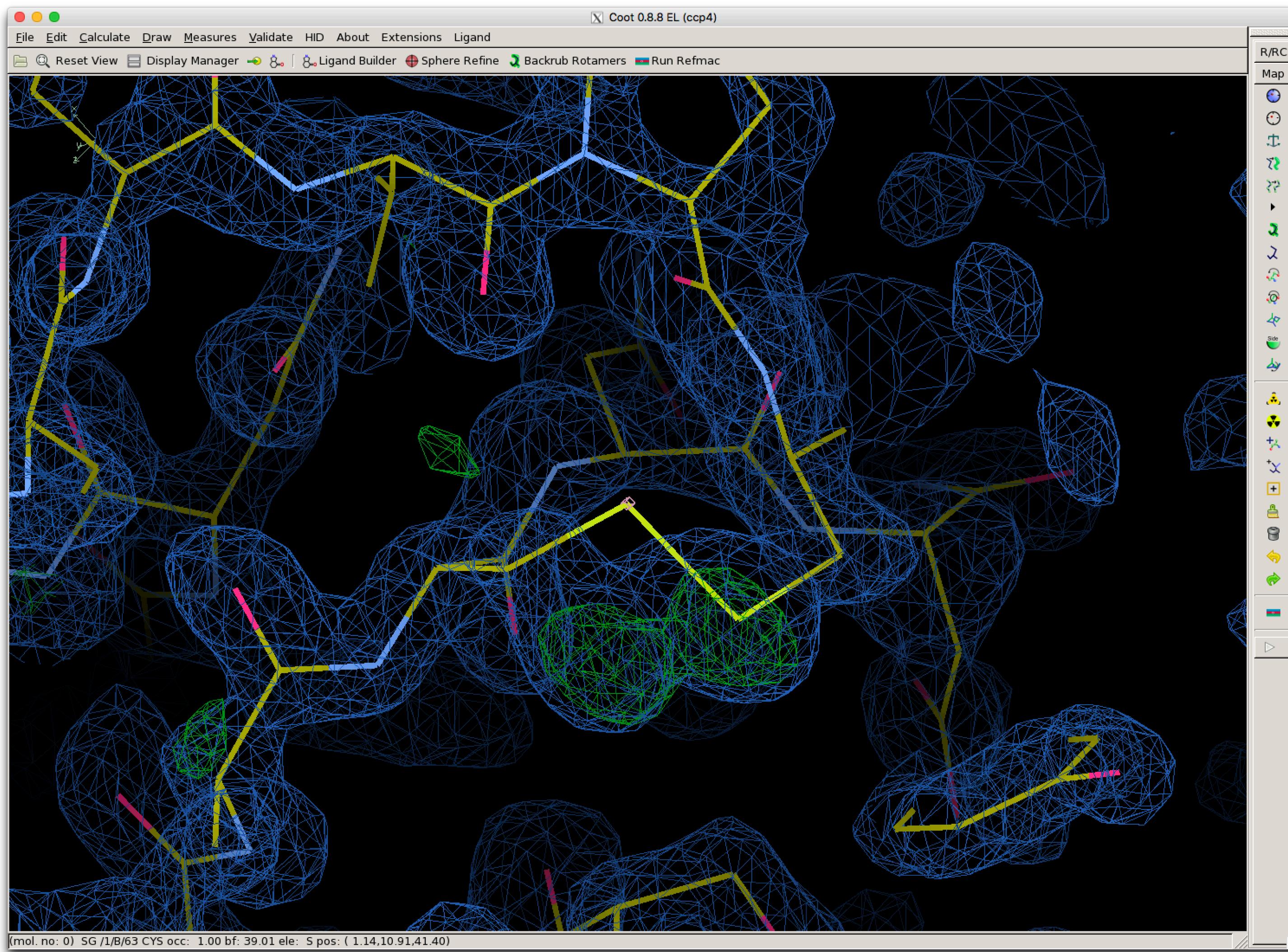
**Using Coot is not like this:
Coot fitting tools are fast and automated**

Coot is (typically) local, automated and interactive.

Coot

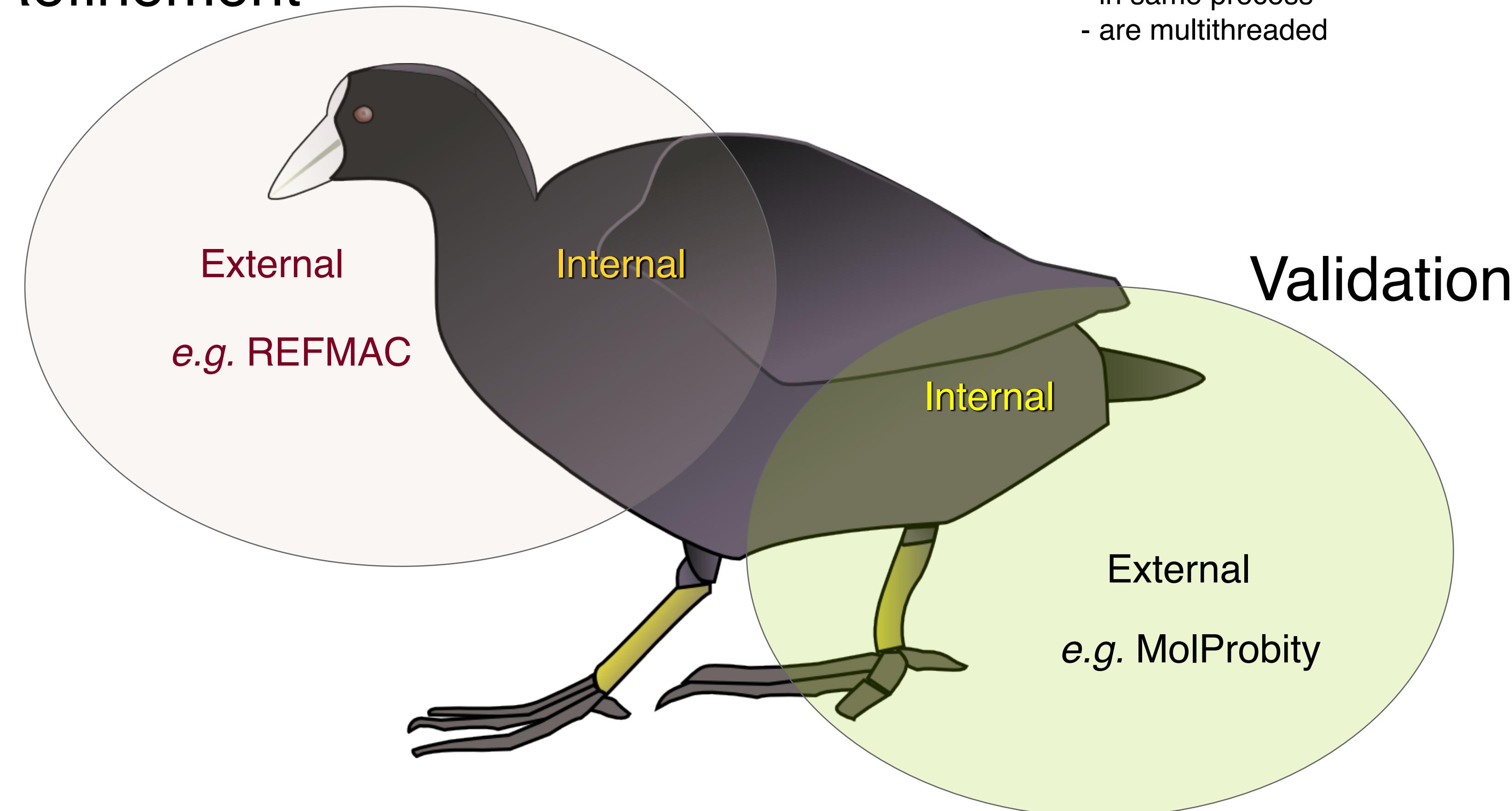
- Molecular Graphics application
- Protein Crystallographic **model-building** tools
- Designed to “fill the gap” where automatic methods fail
- (generally, we don't use molecular graphics programs to do what non-interactive methods can do)
- Interface to other programs: SHELXL, Refmac, Libcheck, Probe&Reduce (Molprobity), EBI, EDS, Povray... and others

Fixing what auto-building doesn't get right



Feature Integration

Refinement



Validation, Model Building and Refinement
should be used together

Rapid Updates of Model, Maps and Validation
considerably expedites
the process

Real Space Refinement

Diamond, R. (1971). Acta Cryst. A
27, 436–452.

Major Feature of Coot

- Gradient-based minimiser (BFGS derivative)
- Geometry library is the standard CIF-based **CCP4 Monomer Library**
- Minimise deviations in bond length, angles, torsions, planes, chiral volume, non-bonded contacts
- Including links and modifications
- Provides “interactive” refinement
- Subject to substantial extension

What prior geometric information do we have?

- We know chemistry....
- We know **bond lengths** and uncertainties
- We know **bond angles** and uncertainties
- We know the **chiral centres**
- We know which atoms should lie in a **plane**
- We know (more or less) about **torsions**
- We combine the gradients from the data with those from molecular mechanics in the minimisation

CCP4 Monomer Library

chem_comp_bond

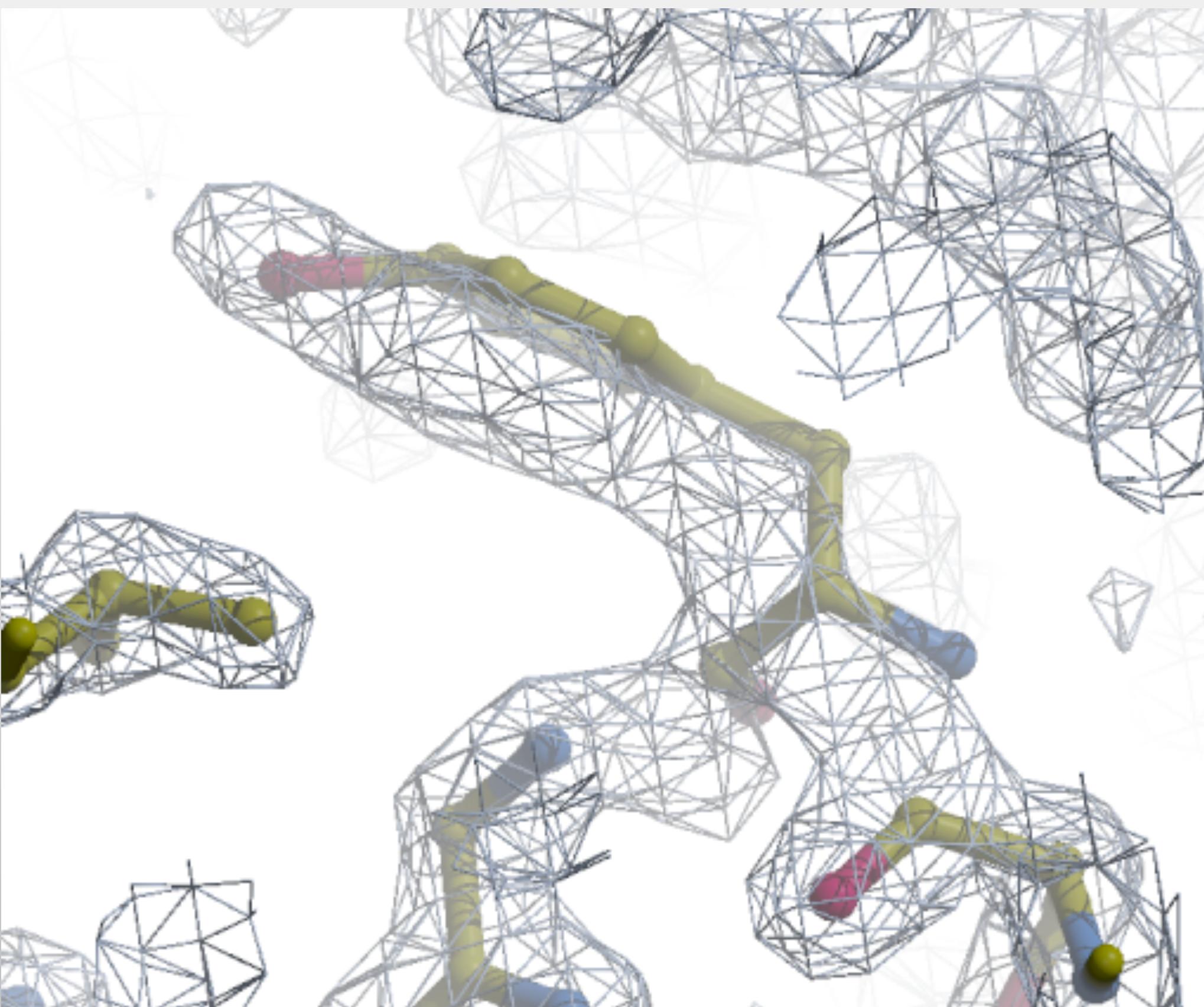
```
data_comp_list
loop_
  _chem_comp.id
  _chem_comp.three_letter_code
  _chem_comp.name
  _chem_comp.group
  _chem_comp.number_atoms_all
  _chem_comp.number_atoms_nh
  _chem_comp.desc_level
  ATP      ATP      "ADENOSINE-5'-TRIPHOSPHATE"      NON-POLYMER    43      31      .
loop_
  _chem_comp_bond.comp_id
  _chem_comp_bond.atom_id_1
  _chem_comp_bond.atom_id_2
  _chem_comp_bond.type
  _chem_comp_bond.aromatic
  _chem_comp_bond.value_dist_nucleus
  _chem_comp_bond.value_dist_nucleus_esd
  _chem_comp_bond.value_dist
  _chem_comp_bond.value_dist_esd
  ATP      "C5'"      "H5'1"      SINGLE      n      1.087      0.0100      0.989      0.0200
  ATP      "C5'"      "H5'2"      SINGLE      n      1.087      0.0100      0.989      0.0200
  ATP      "C4'"      "H4'"      SINGLE      n      1.087      0.0100      0.981      0.0200
  ATP      "C3'"      "H3'"      SINGLE      n      1.087      0.0100      0.992      0.0200
  ATP      "O3'"      "H03'"     SINGLE      n      0.969      0.0180      0.849      0.0200
  ATP      "C2'"      "H2'"      SINGLE      n      1.087      0.0100      0.994      0.0200
  ATP      "O2'"      "H02'"     SINGLE      n      0.969      0.0180      0.849      0.0200
  ATP      "C1'"      "H1'"      SINGLE      n      1.087      0.0100      0.984      0.0200
  ATP      C8          H8          SINGLE      n      1.083      0.0150      0.942      0.0170
  ATP      N6          HN61        SINGLE      n      1.014      0.0120      0.877      0.0200
  ATP      N6          HN62        SINGLE      n      1.014      0.0120      0.877      0.0200
  ATP      C2          H2          SINGLE      n      1.083      0.0150      0.945      0.0200
```

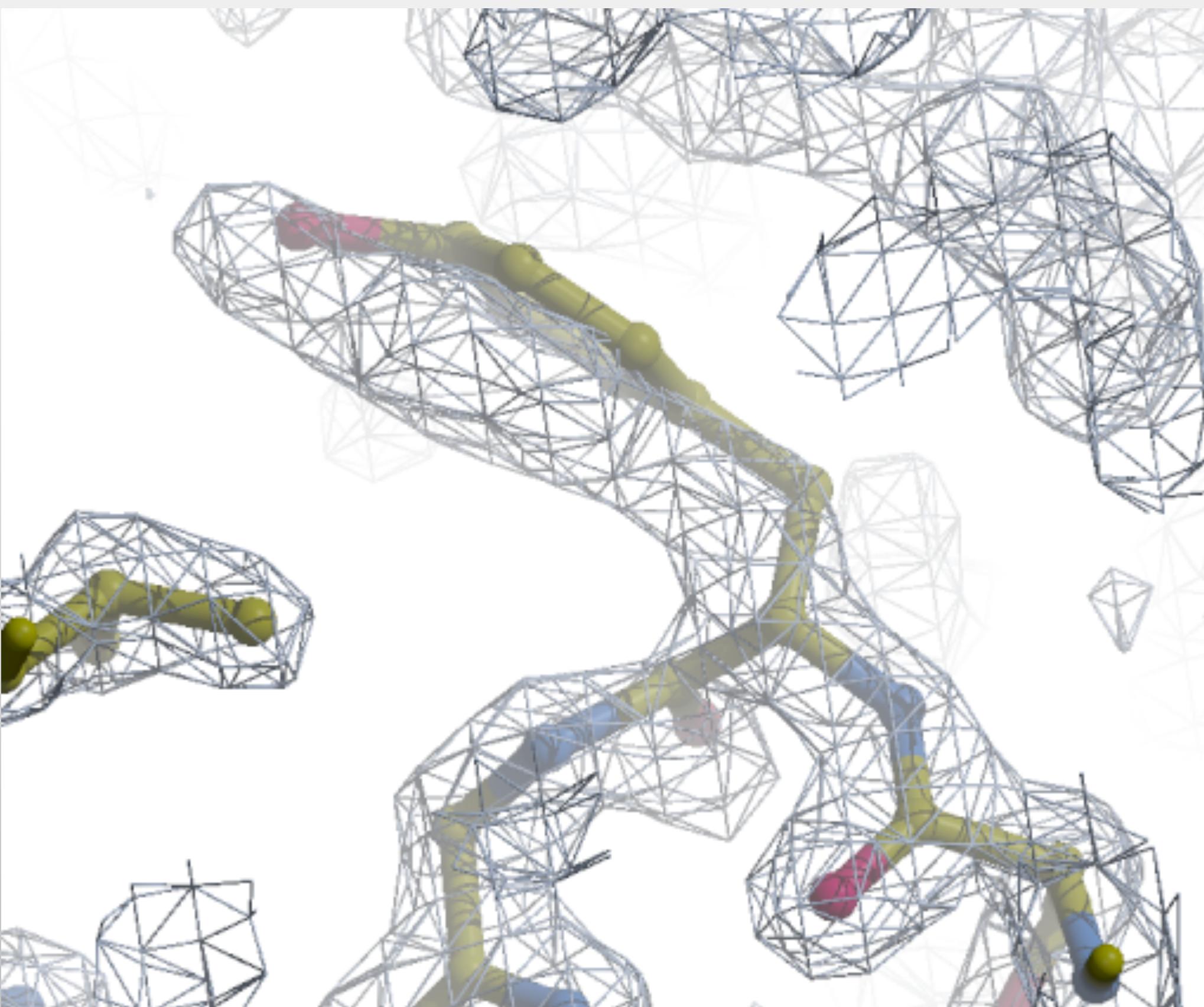
APPENDIX A

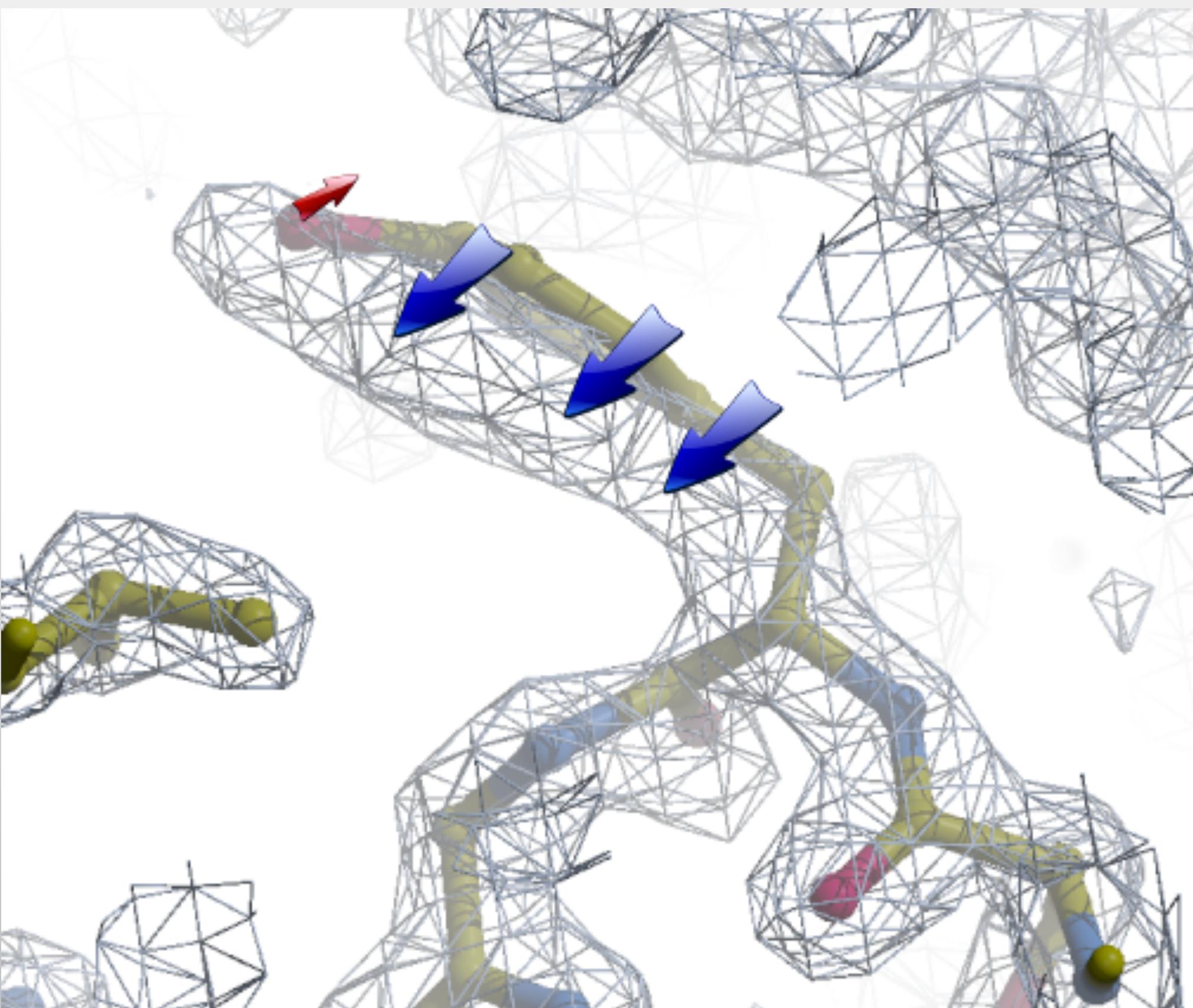
Regularization and refinement derivatives

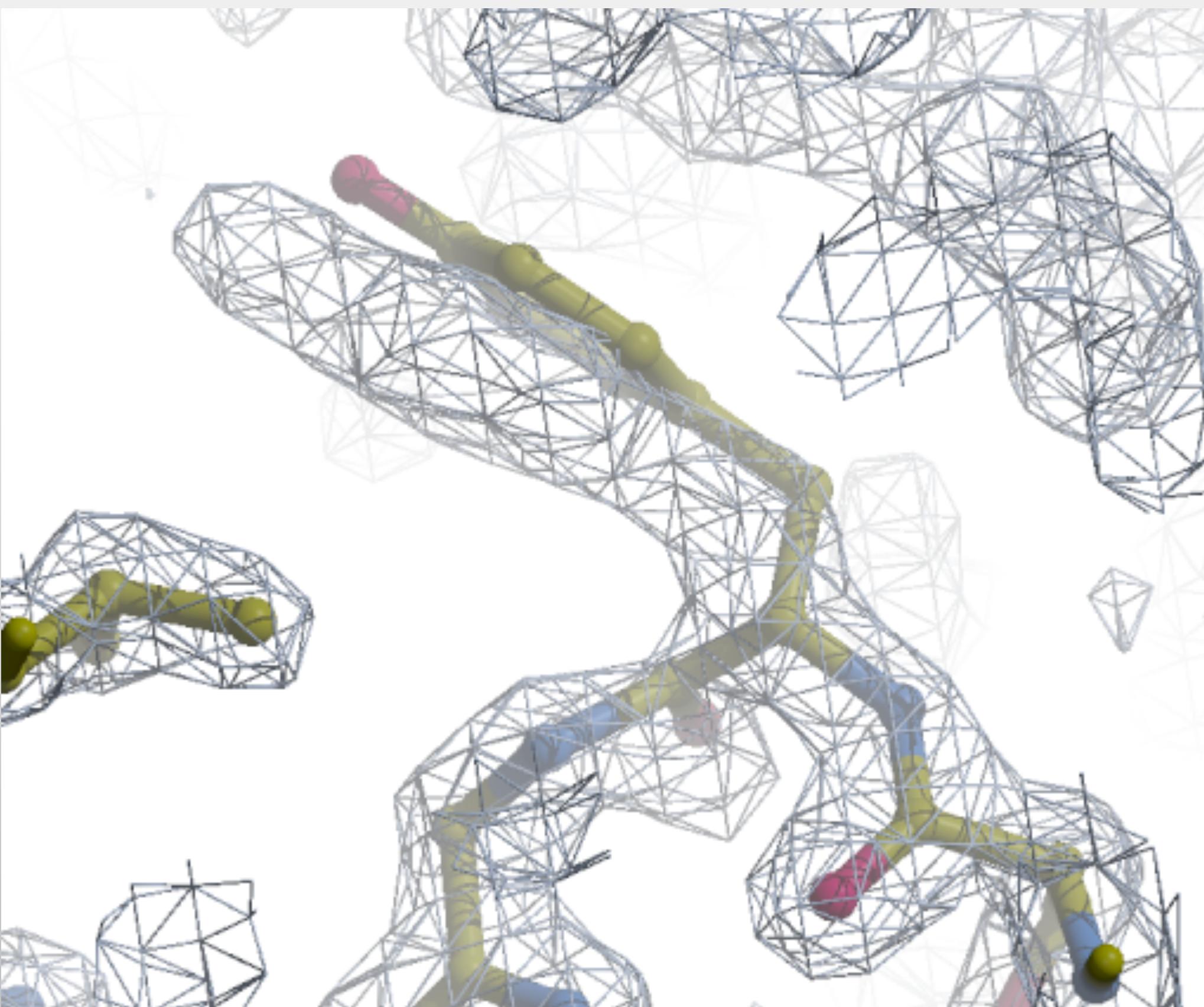
The function that we are trying to minimize is S , where

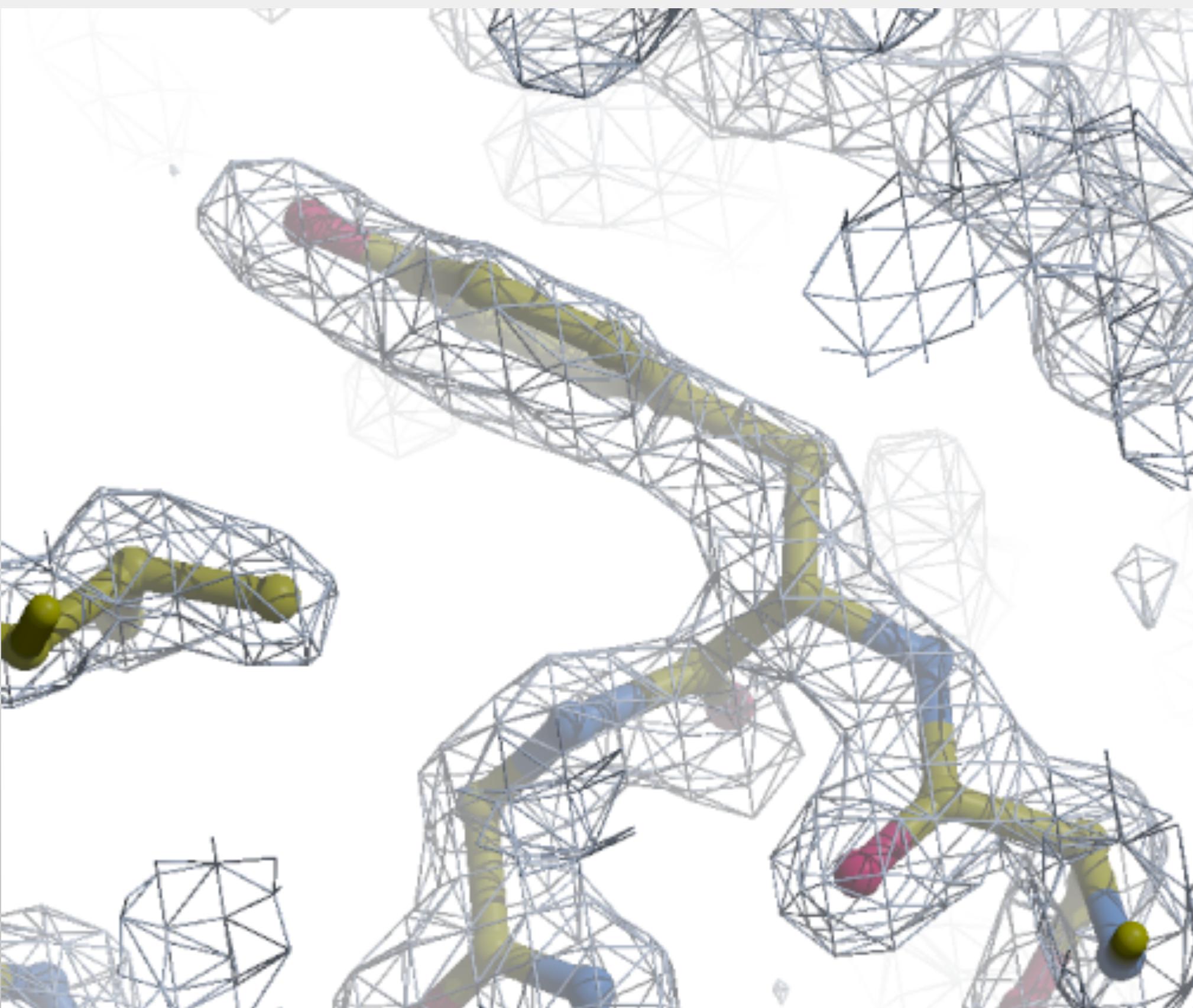
$$S = S_{\text{bond}} + S_{\text{angle}} + S_{\text{torsion}} + S_{\text{plane}} - S_{\text{density}}$$

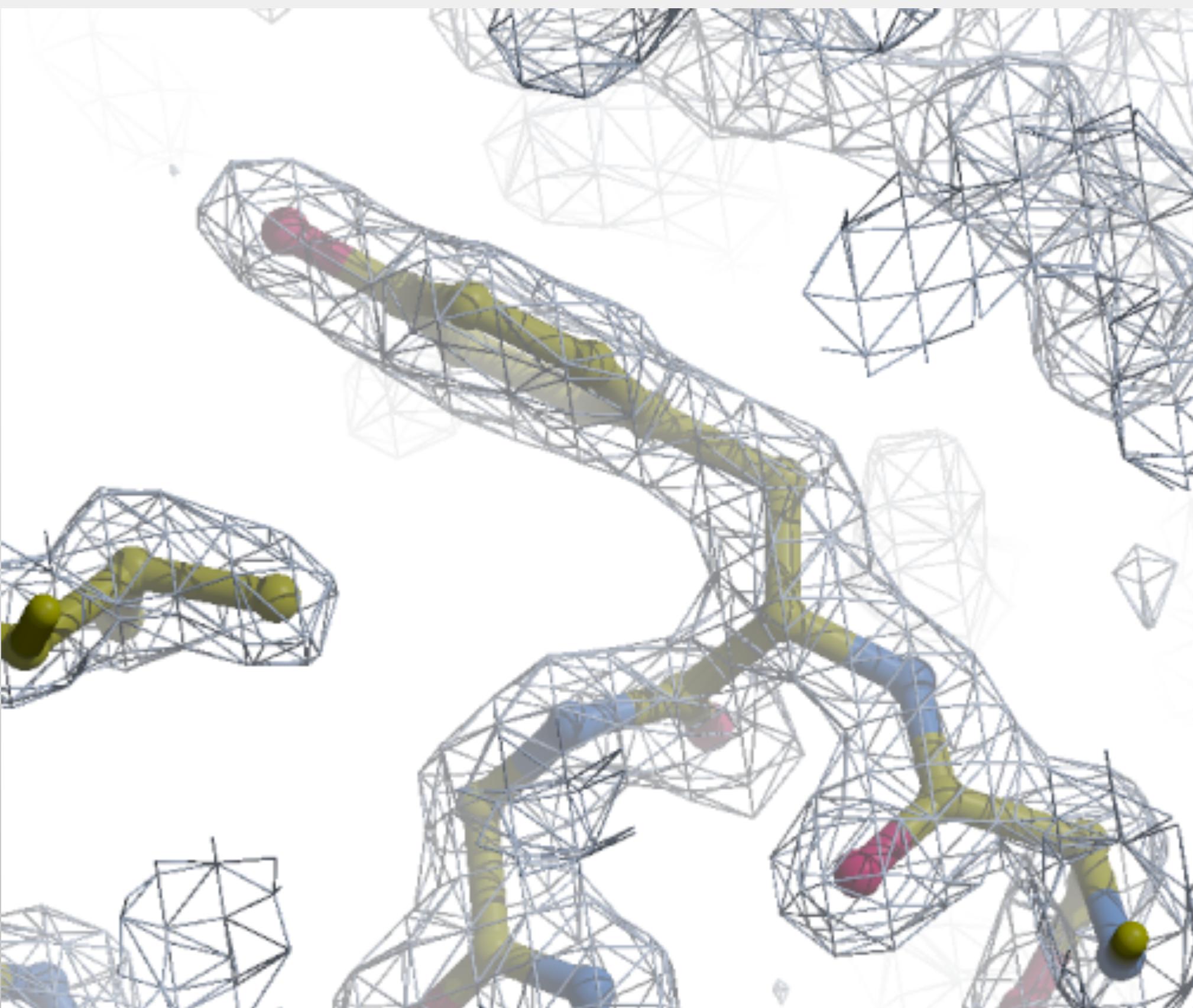












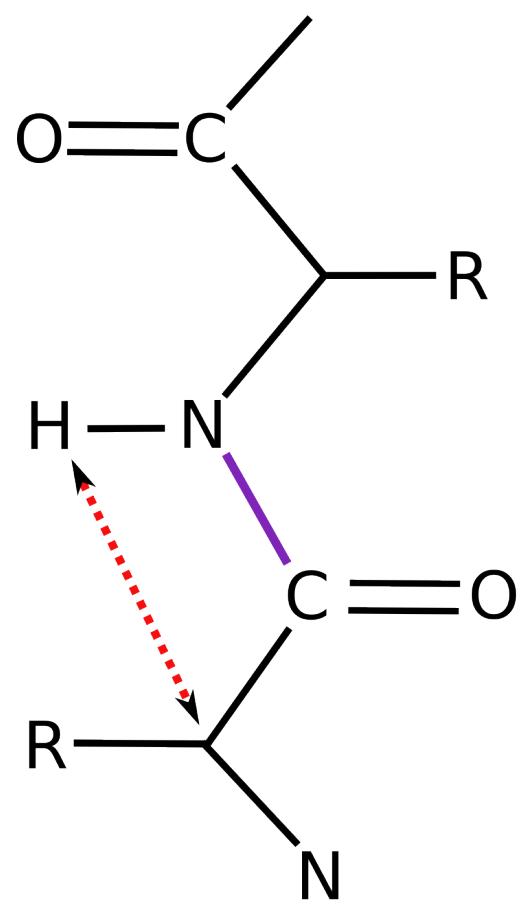
cis-Peptides

A number of papers have been published some time ago highlighting the unusually large number of cis-peptides in some structures:

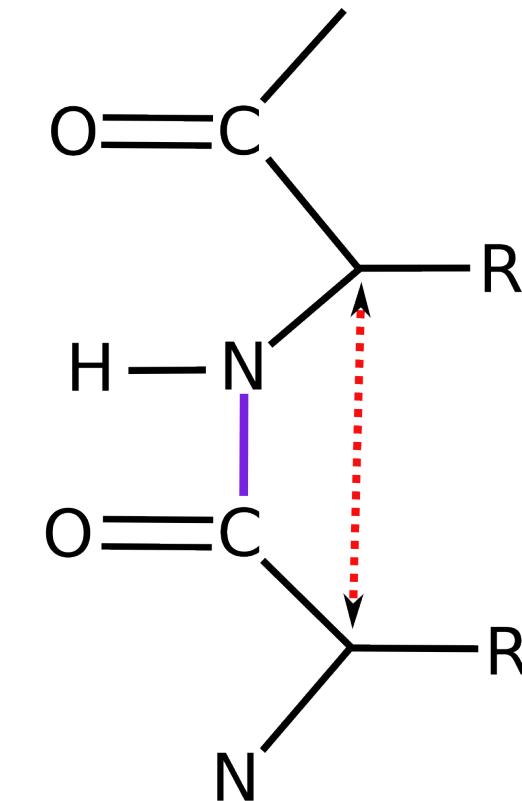
Croll: The rate of cis-trans conformation errors is increasing in low-resolution crystal structures Acta Cryst. (2015). D71, 706-709

Touw et al.: Detection of trans-cis flips and peptide-plane flips in protein structures Acta Cryst. (2015). D71, 1604-71614

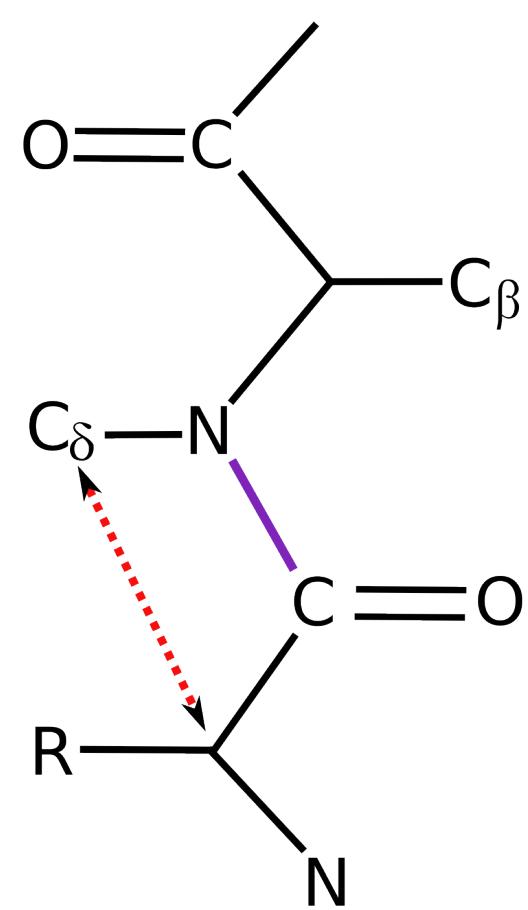
cis-Peptides



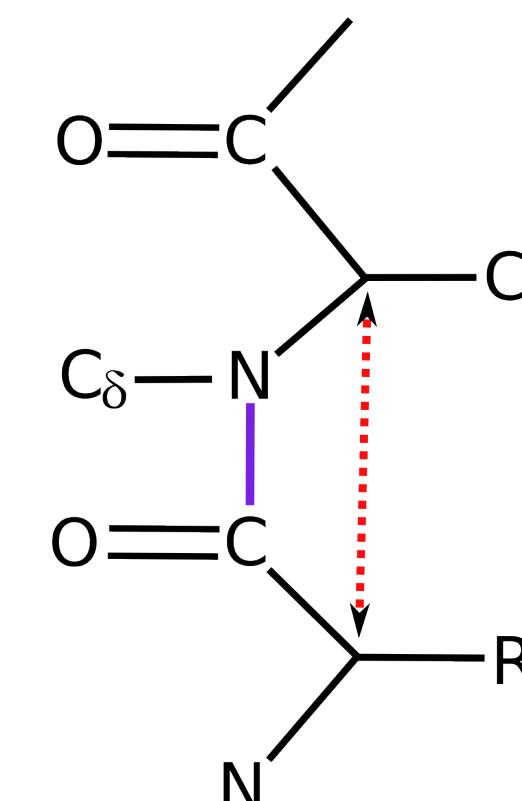
trans-peptide



cis-peptide

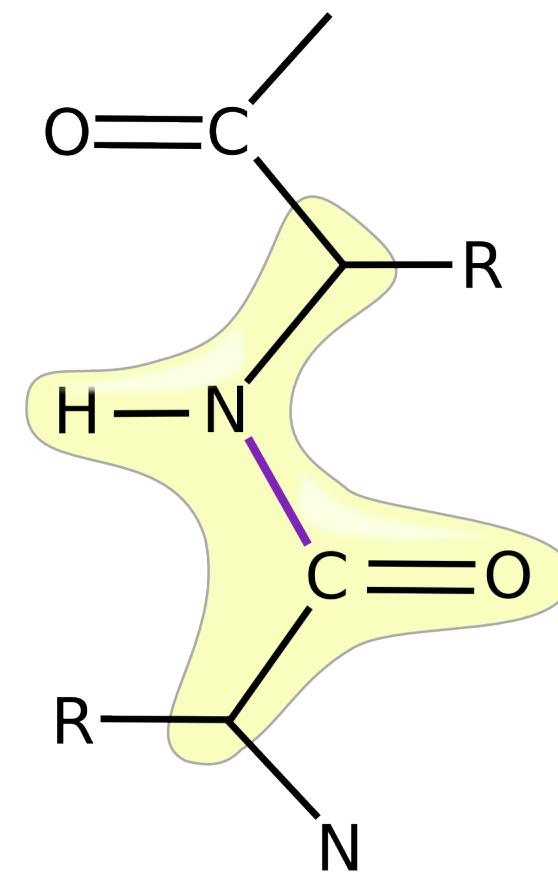


PRO *trans-peptide*

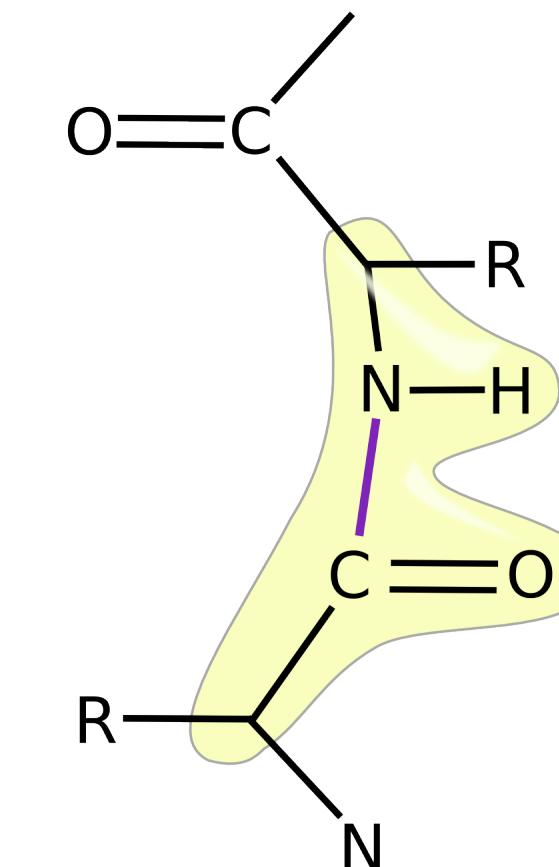


PRO *cis-peptide*

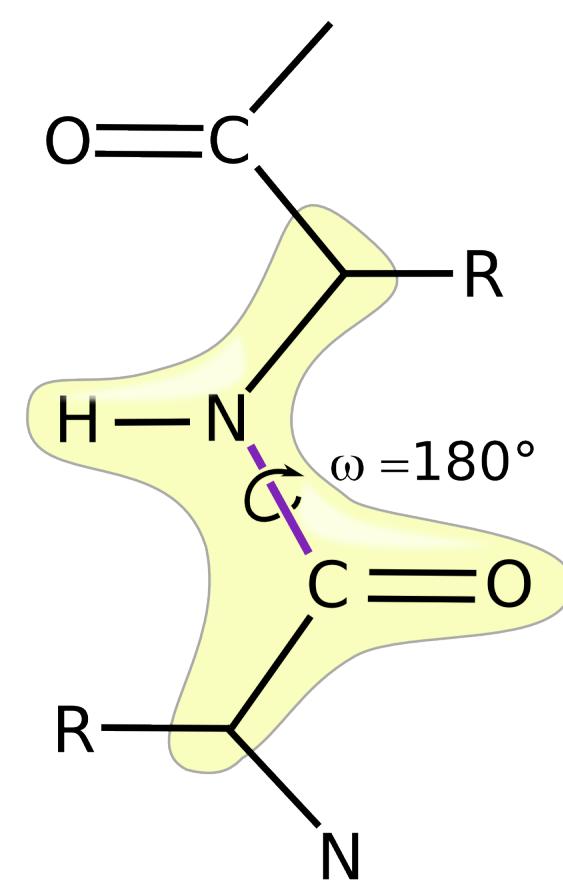
cis-Peptides



trans-peptide
with plane restraints

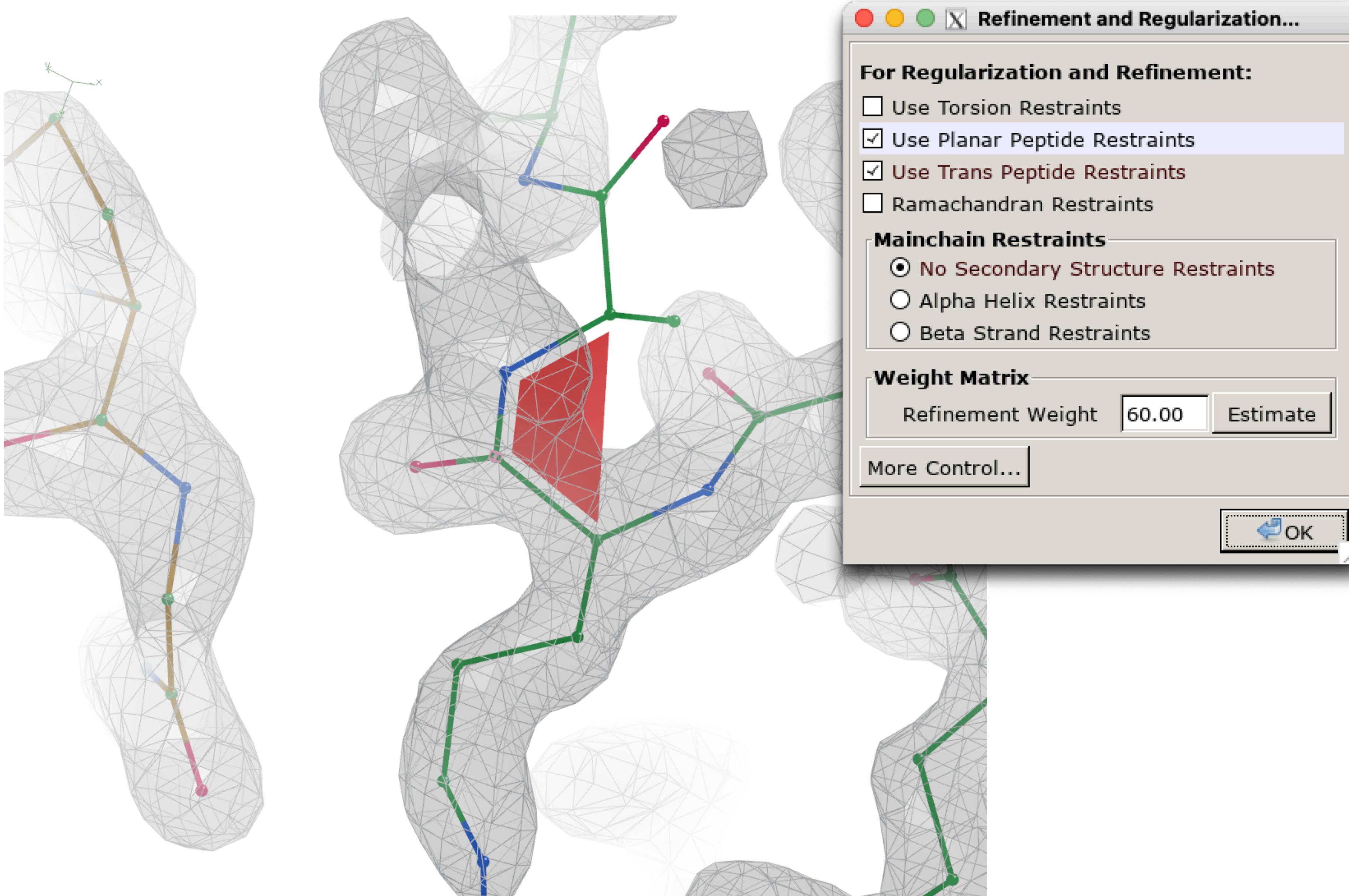


cis-peptide
with plane restraints



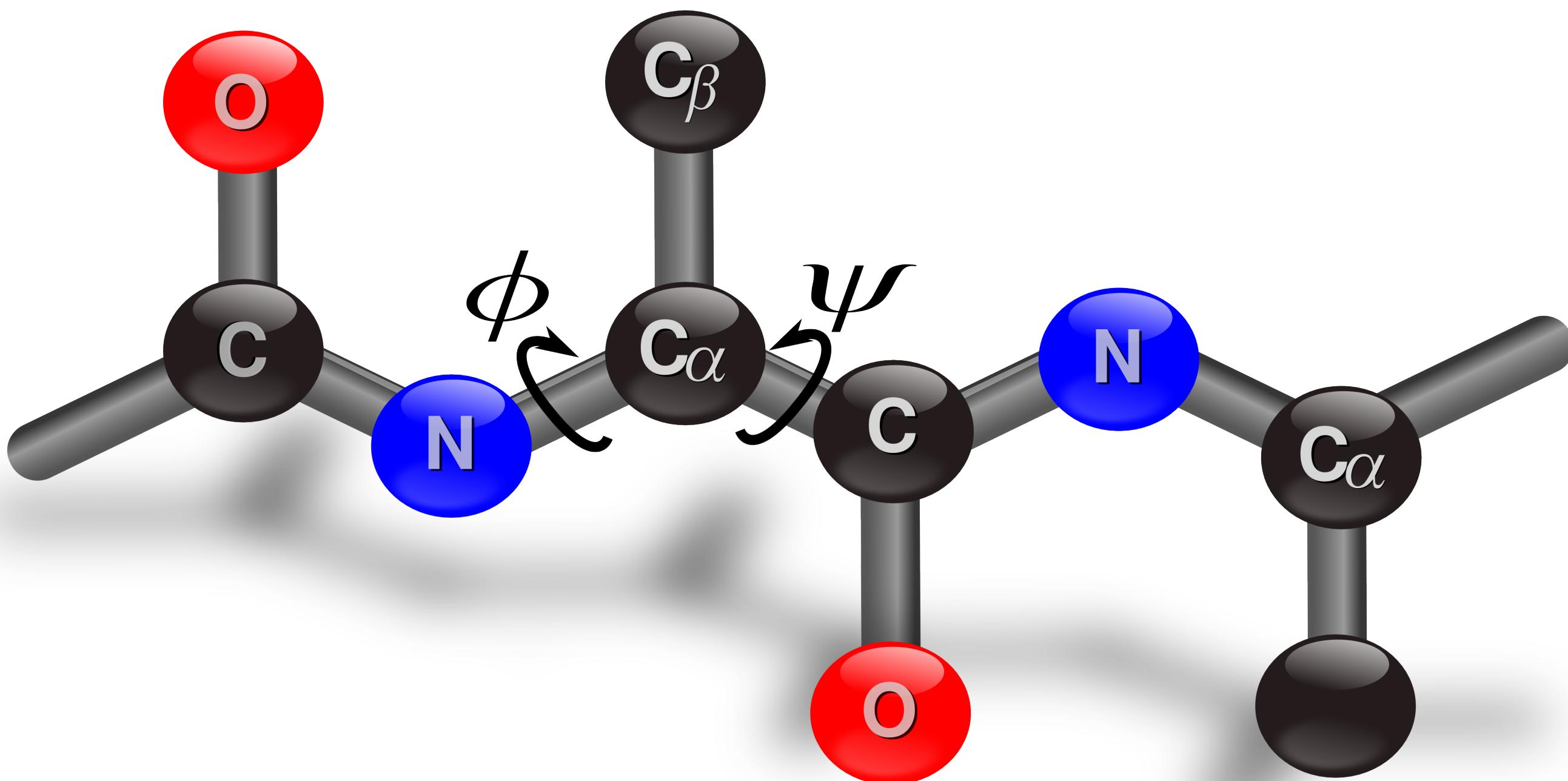
trans-peptide
with plane and trans restraints

cis-Peptide Representation



Rotamers

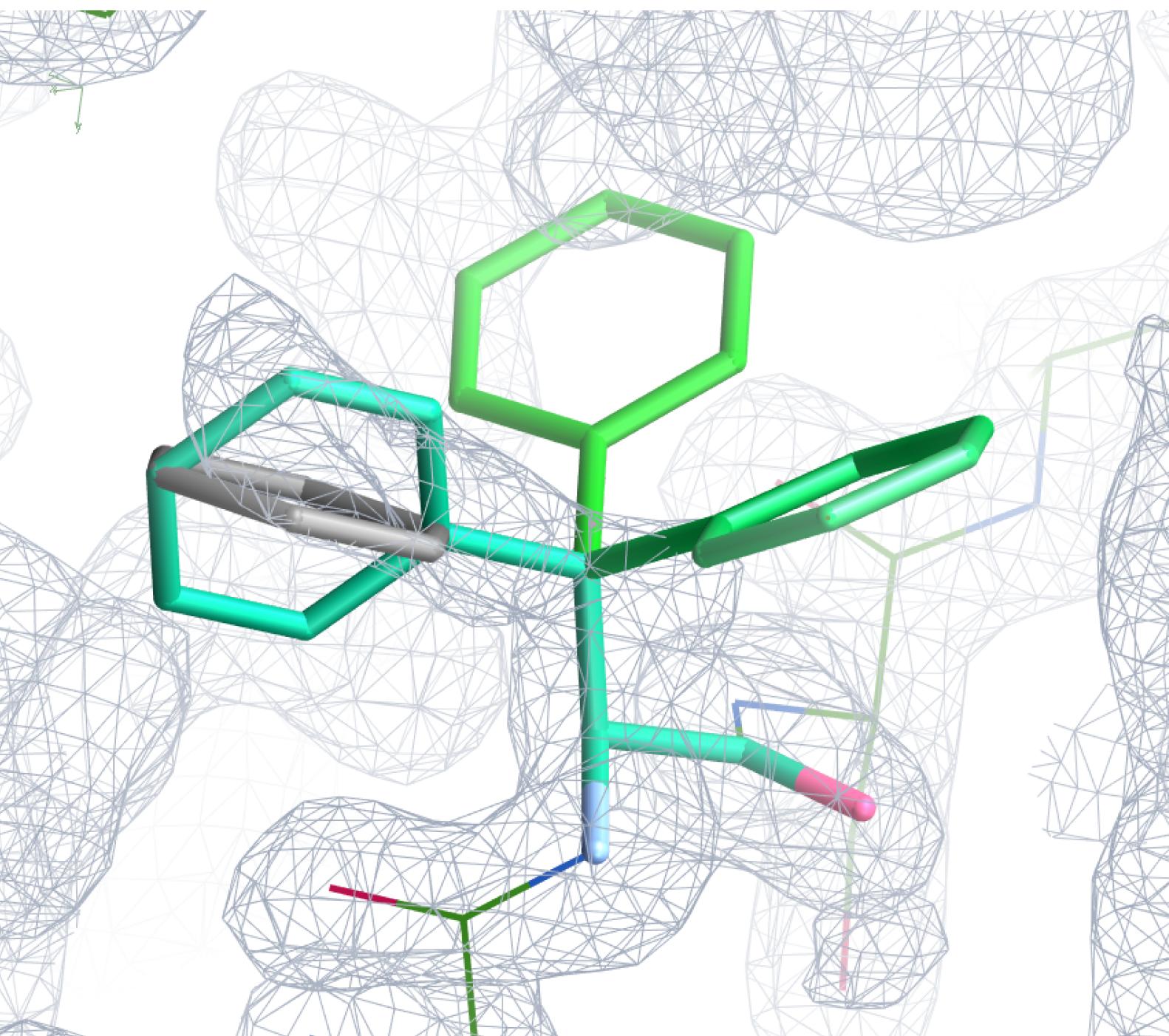
Peptide Backbone Geometry



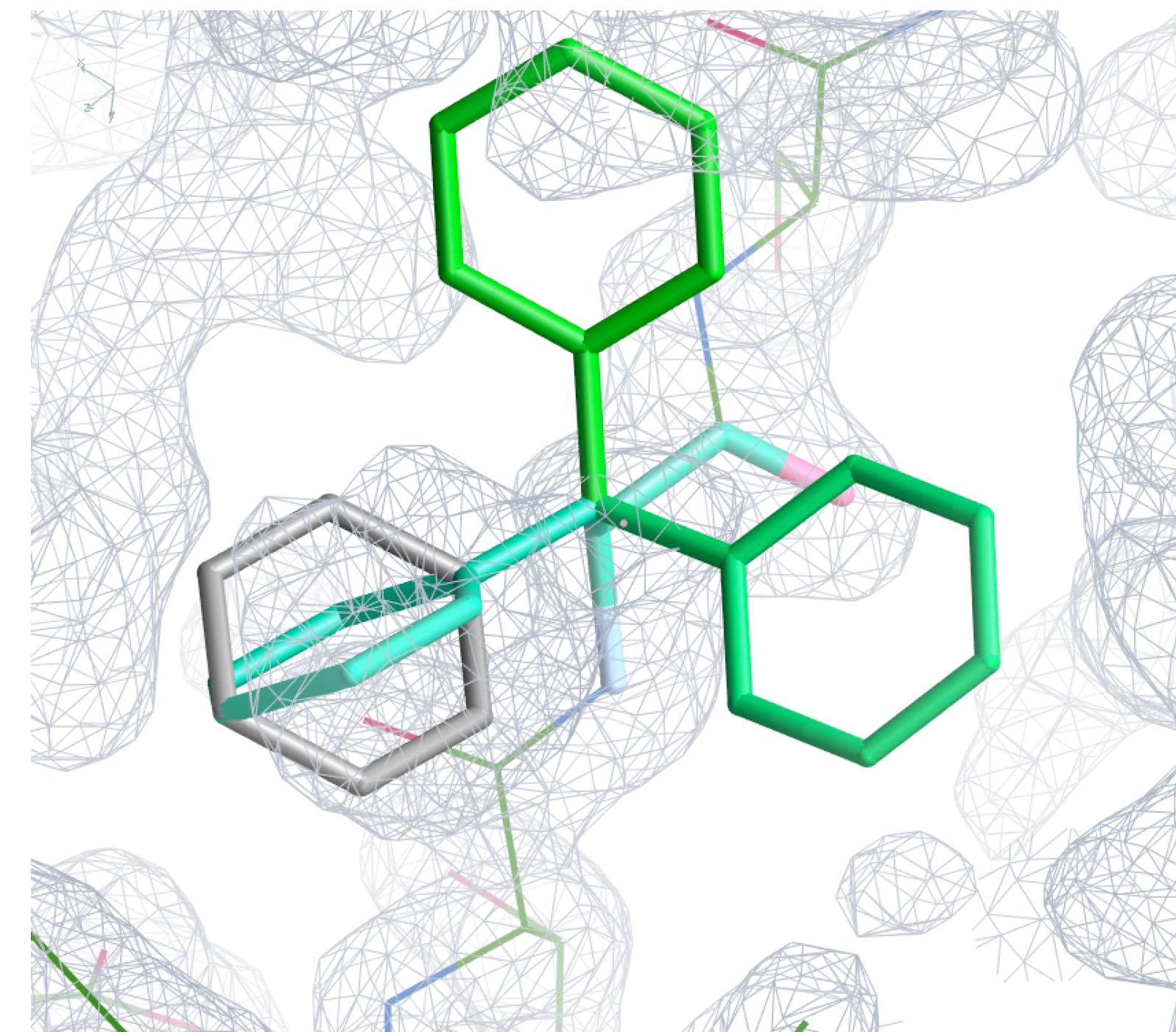
Rotamers

- Rotamers are preferred configurations of a **side-chains rotatable bonds**
- where “preferred” means these configurations occur more frequently in a set of reference protein structures
- “preferred” because they are low-energy conformations
- Several Rotamer “databases” exist
- (Son of) Penultimate Rotamer Library (**Richardson Lab**)

4 PHE Rotamers

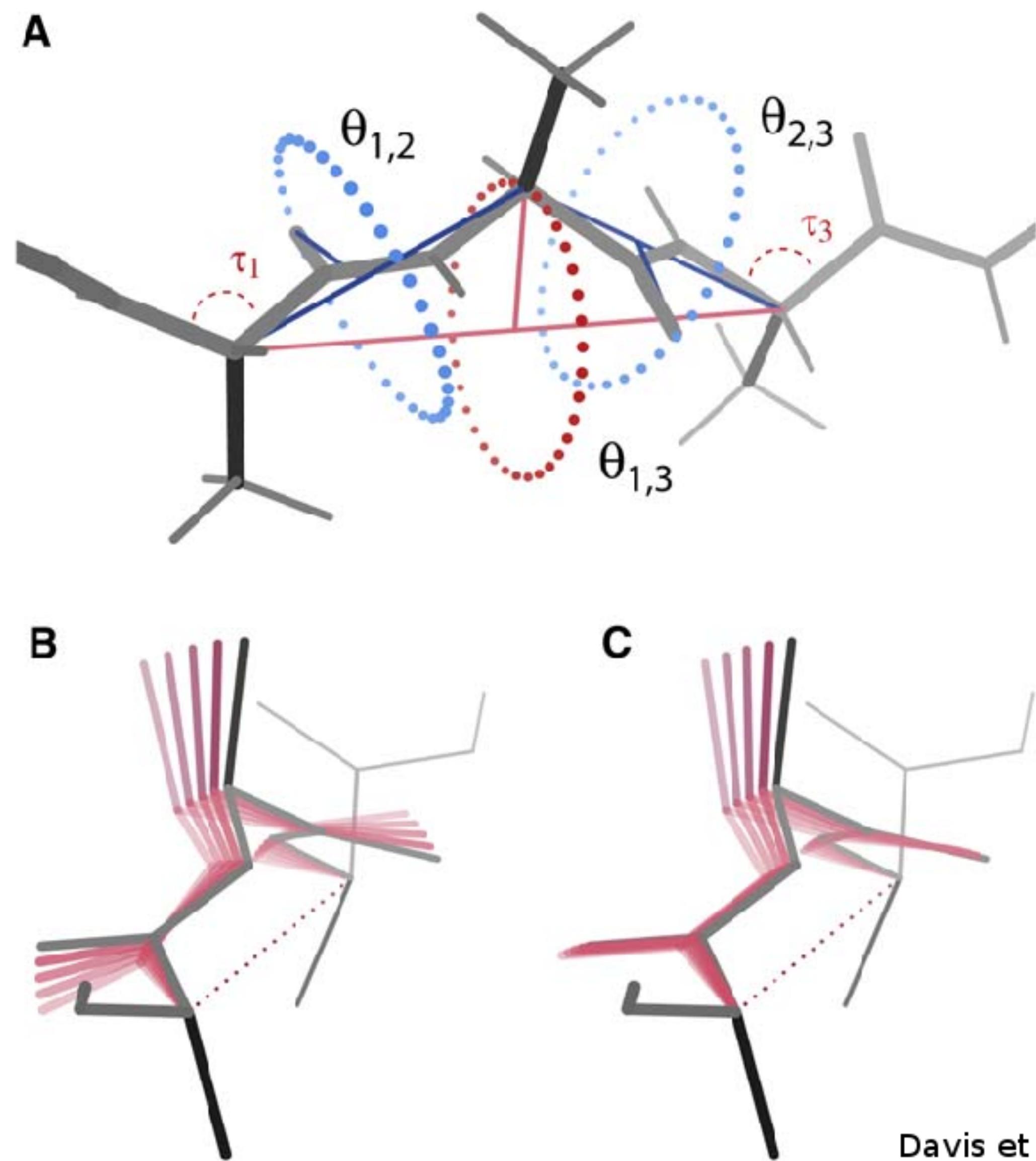


Side view

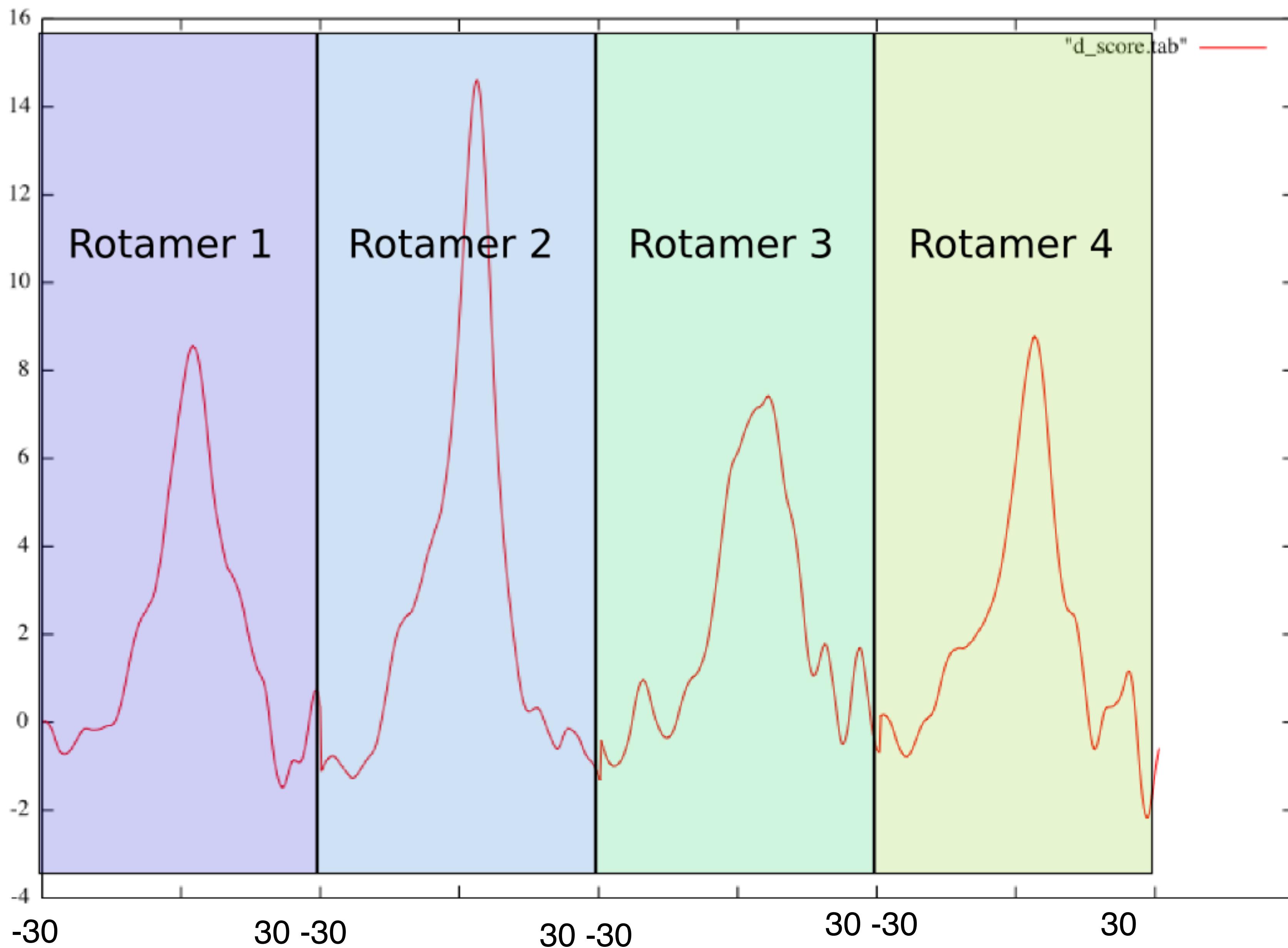


Top view

Backrub rotamer algo



Davis et al. (2006) Structure



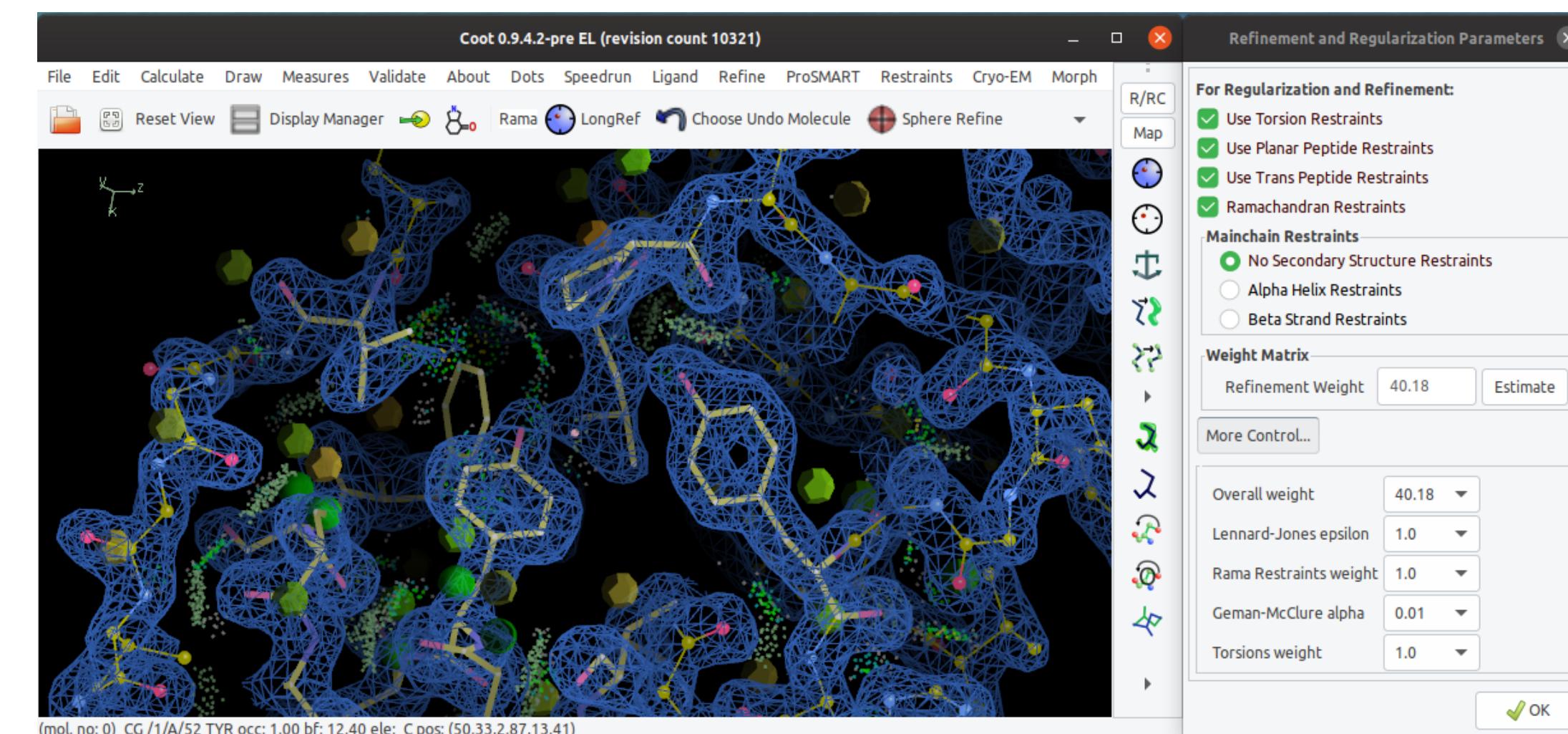
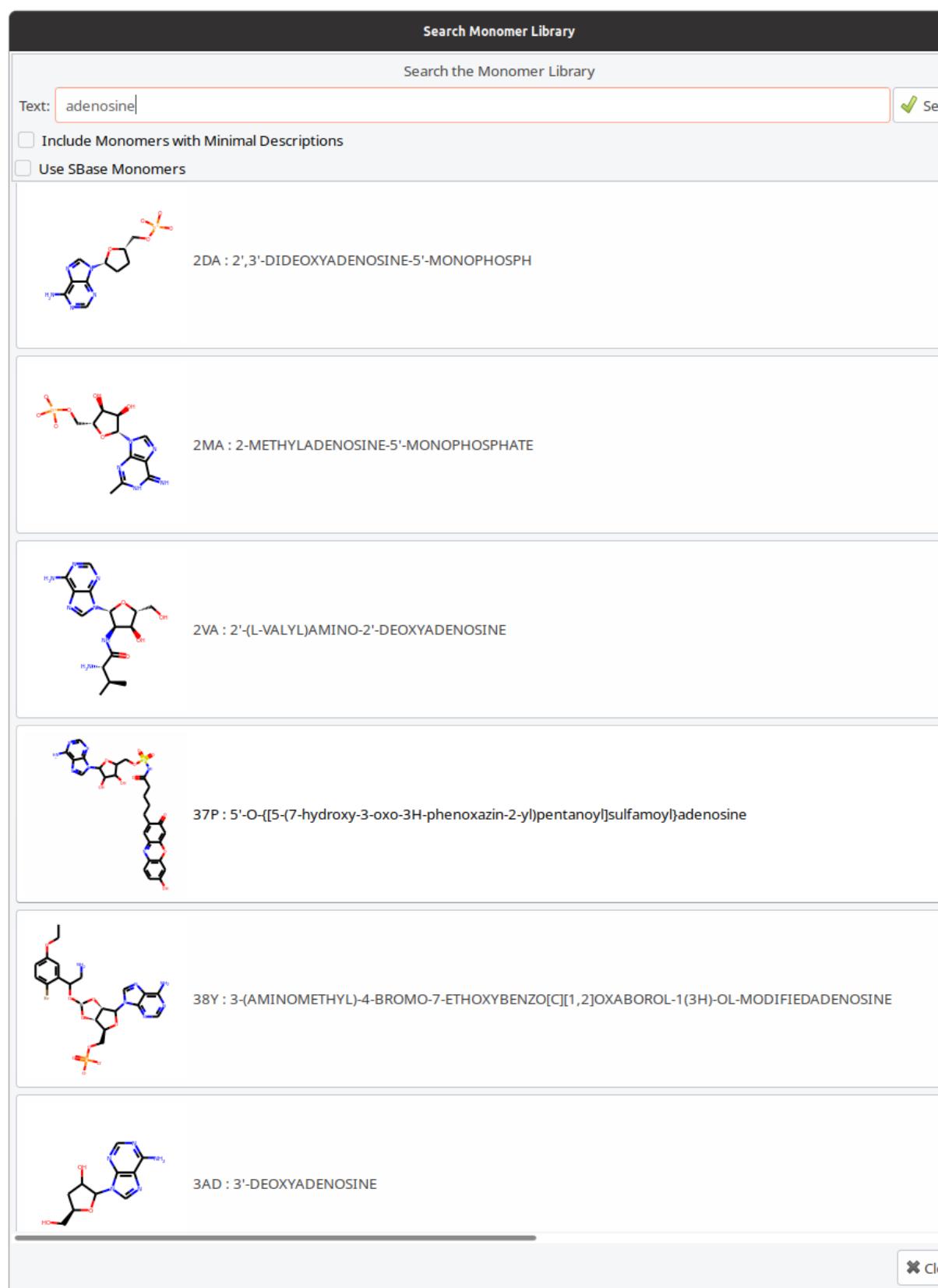
Coot 0.9.x and 1.1

coot-ligand-validation

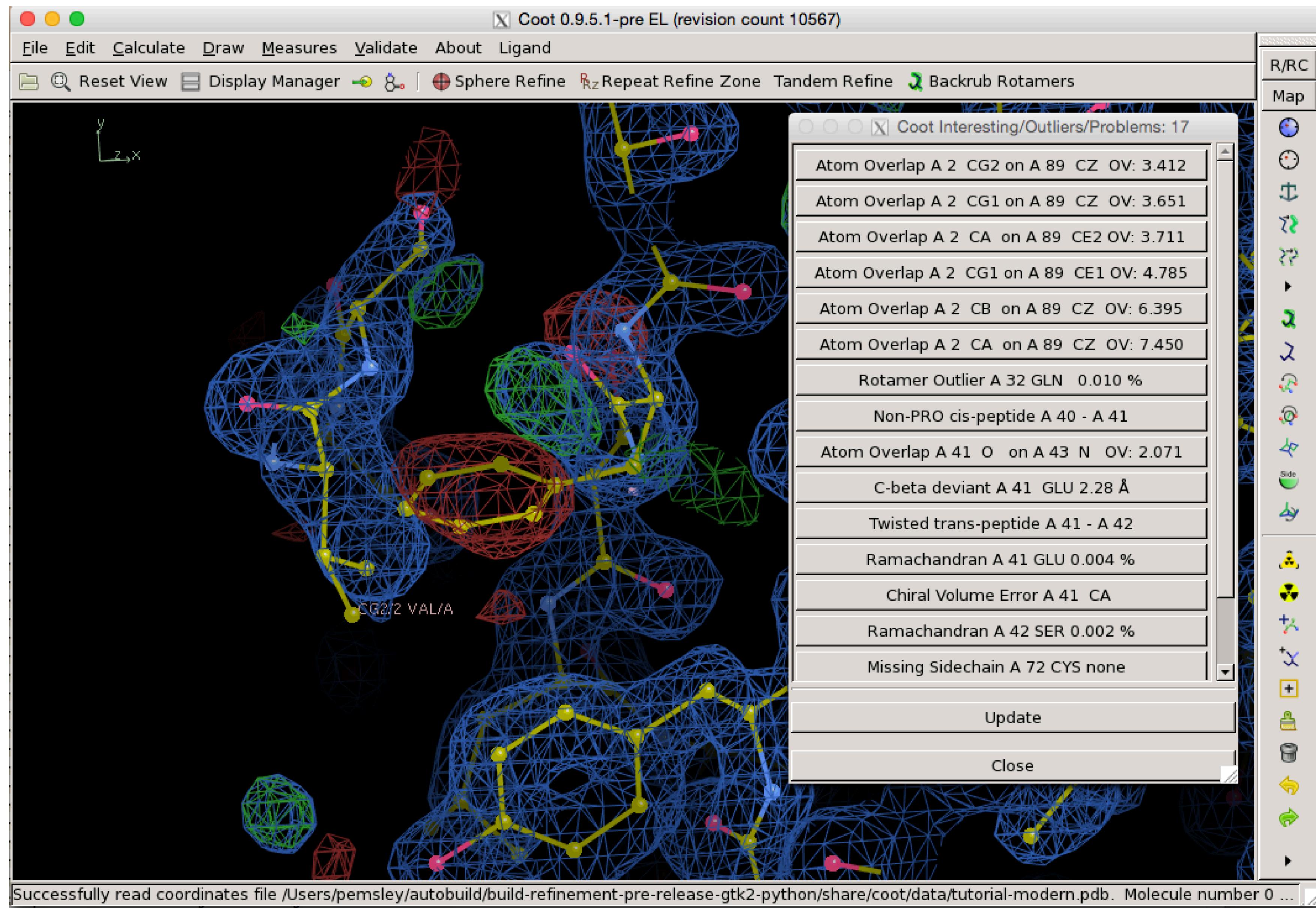
API torsion restraint weights

Dynamic Weights

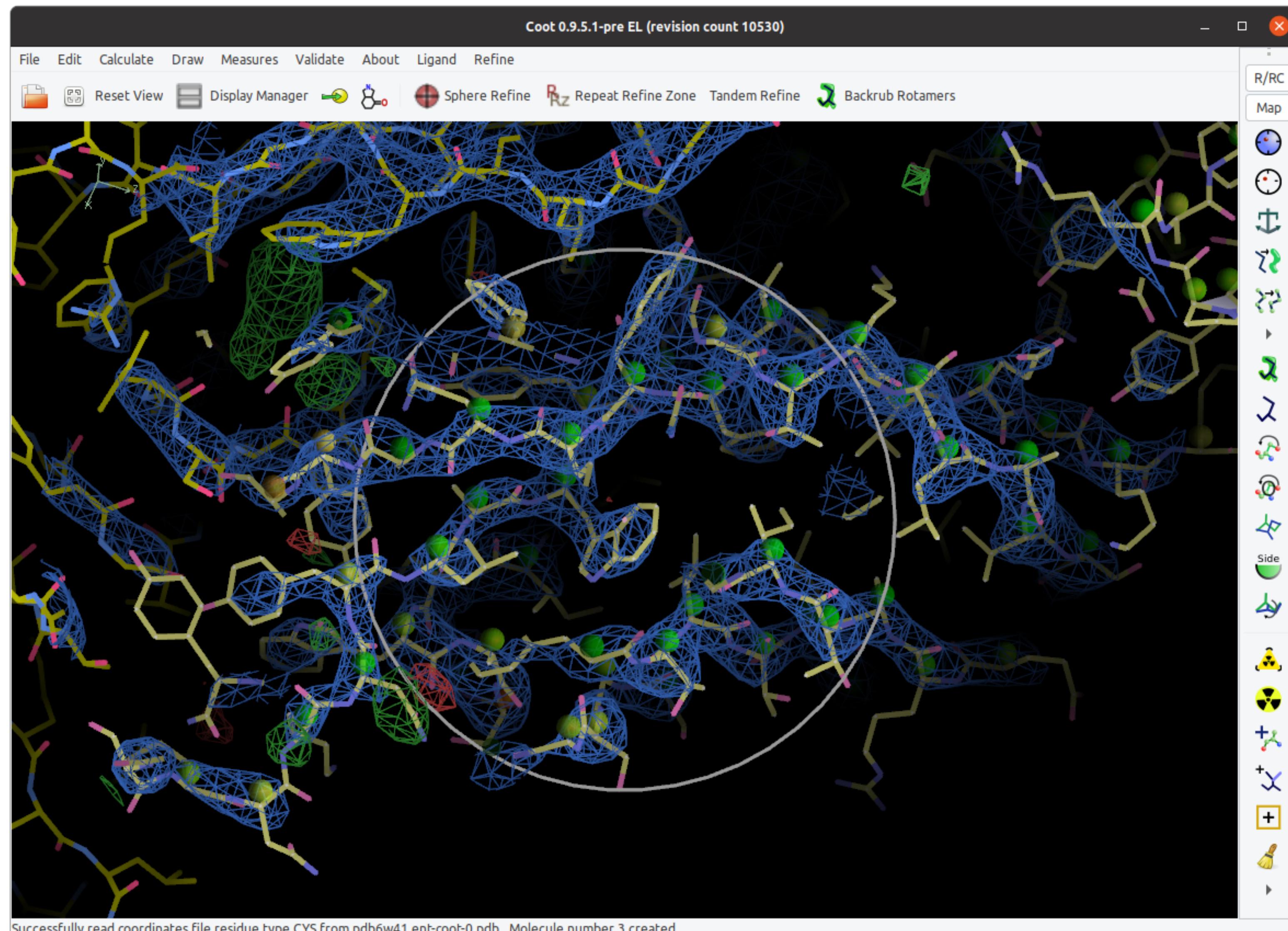
Parses Nuclear Hydrogen Atom Positions



Interactive Validation



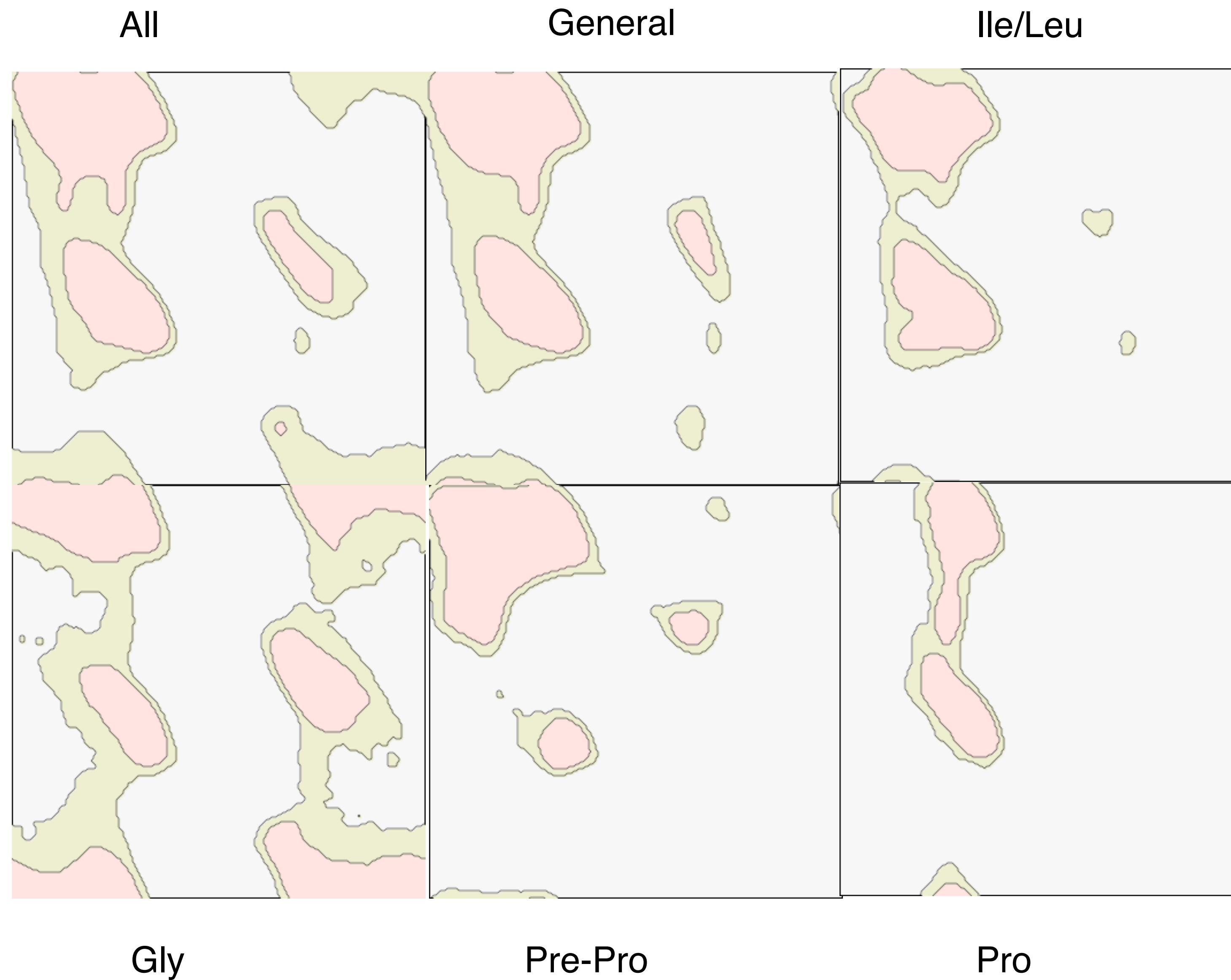
Real-Space Refinement Proportional Editing



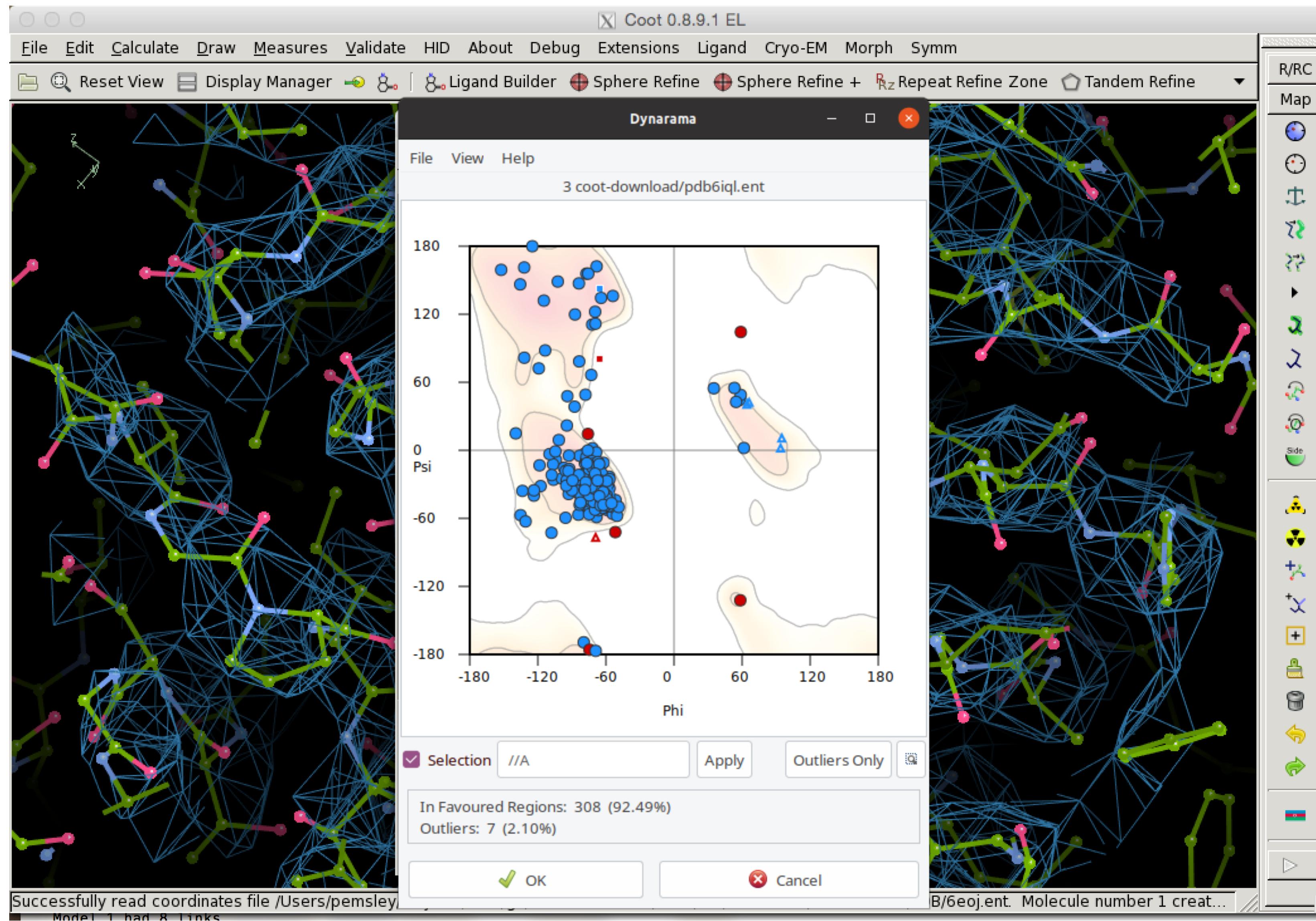
Activate/Change with Ctrl Middle-mouse scroll

Improved Ramachandran Plot(s)

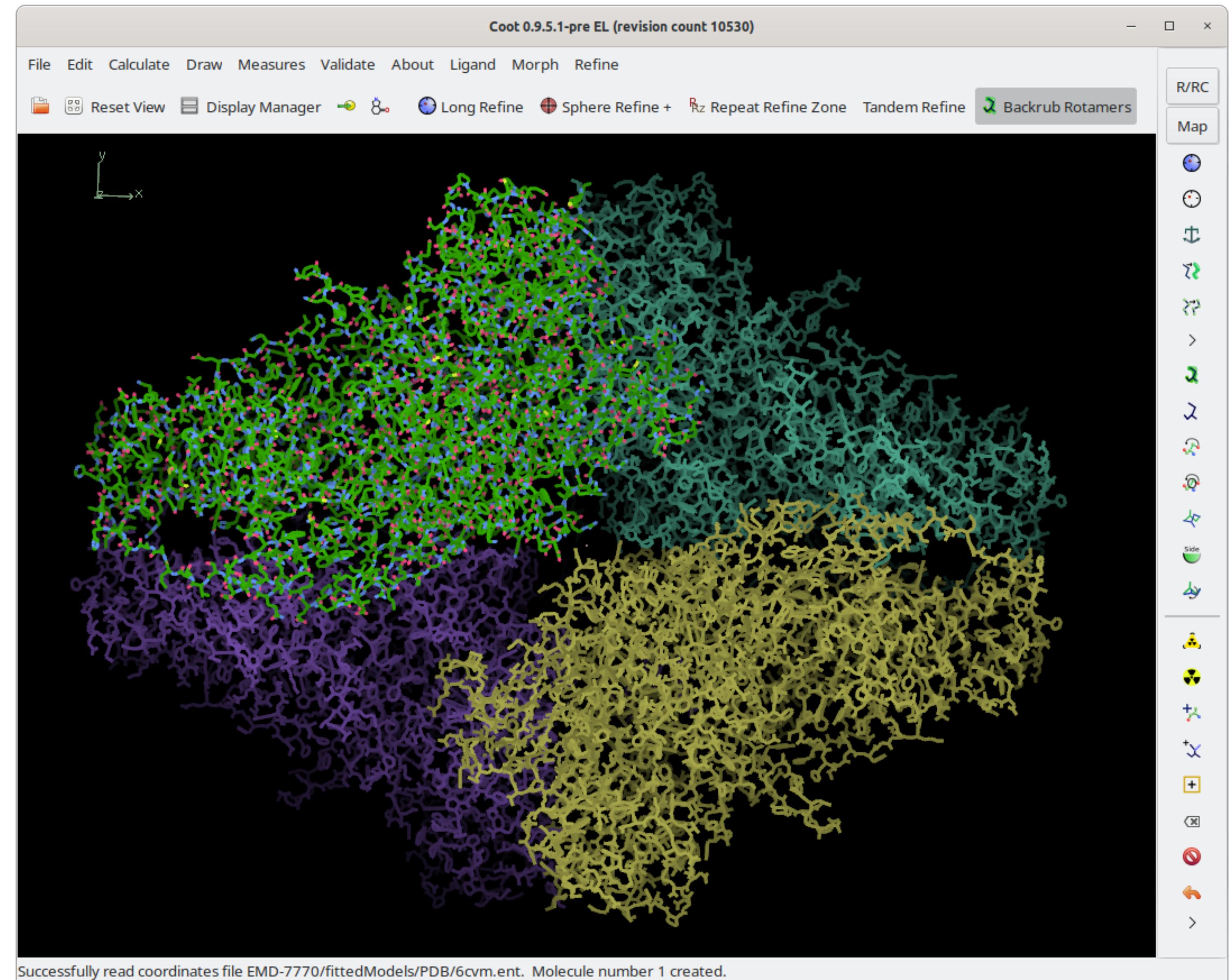
A. Thorn
B. Lohkamp



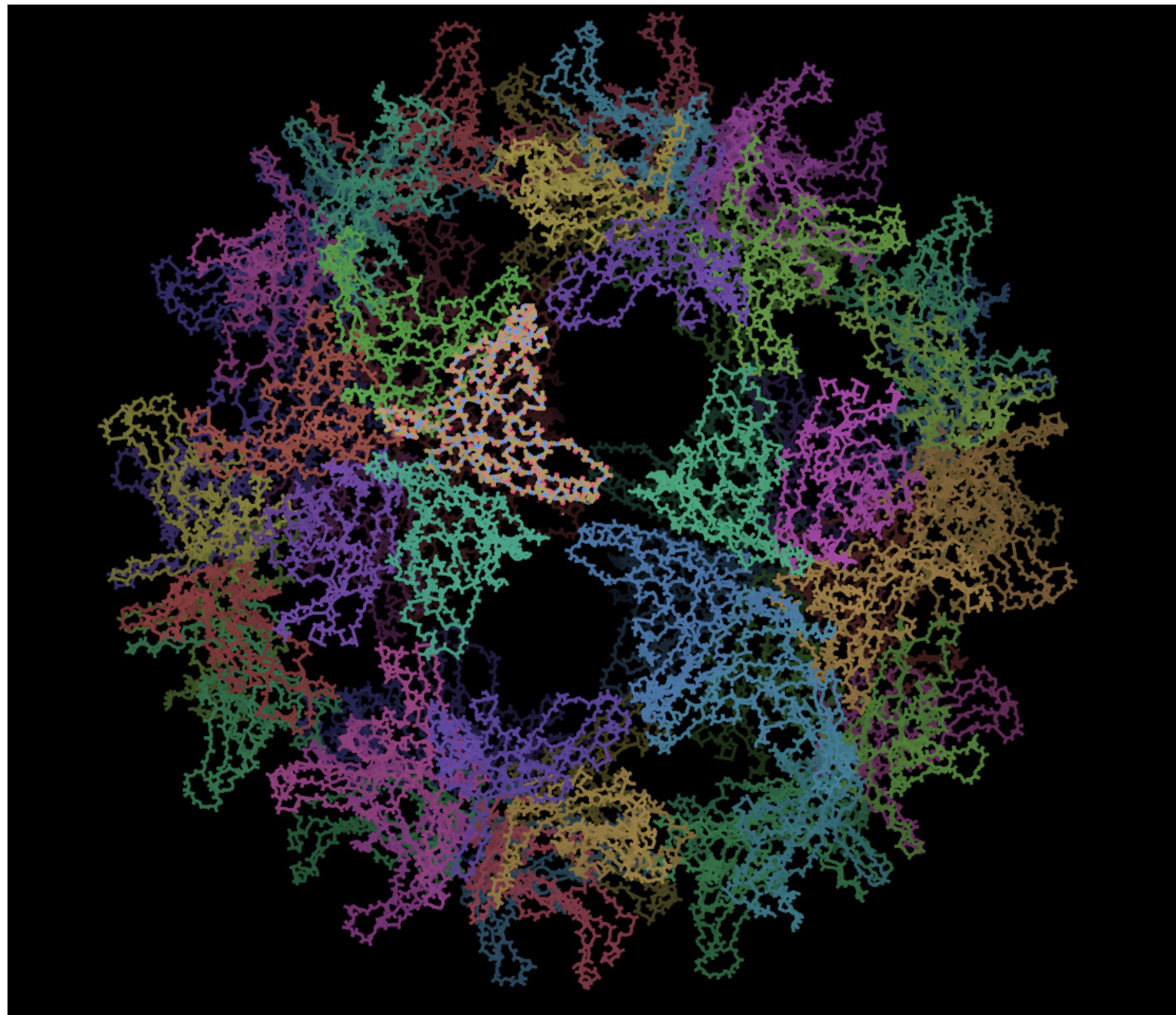
The New Ramachandran Plot



Molecular Symmetry



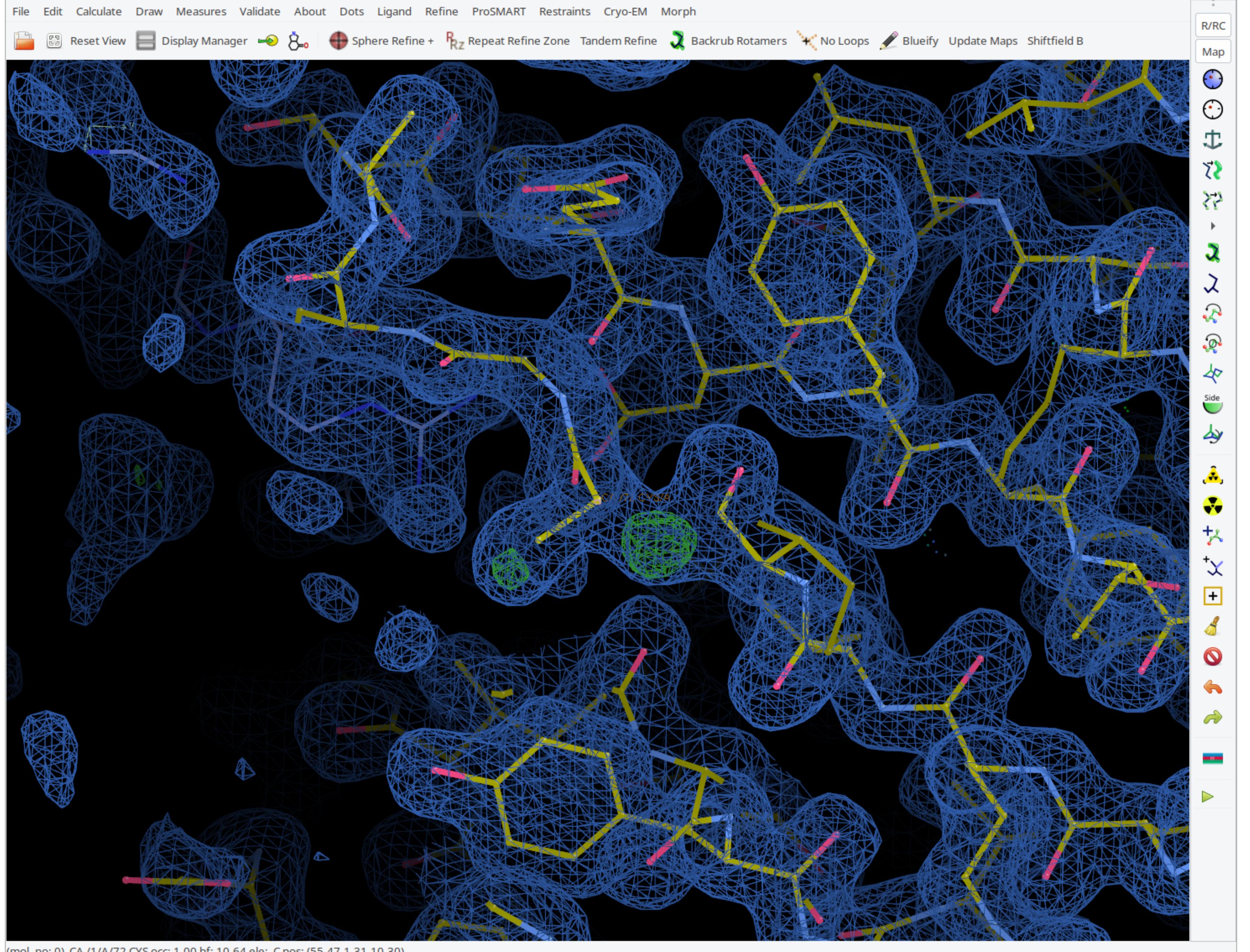
Molecular Symmetry

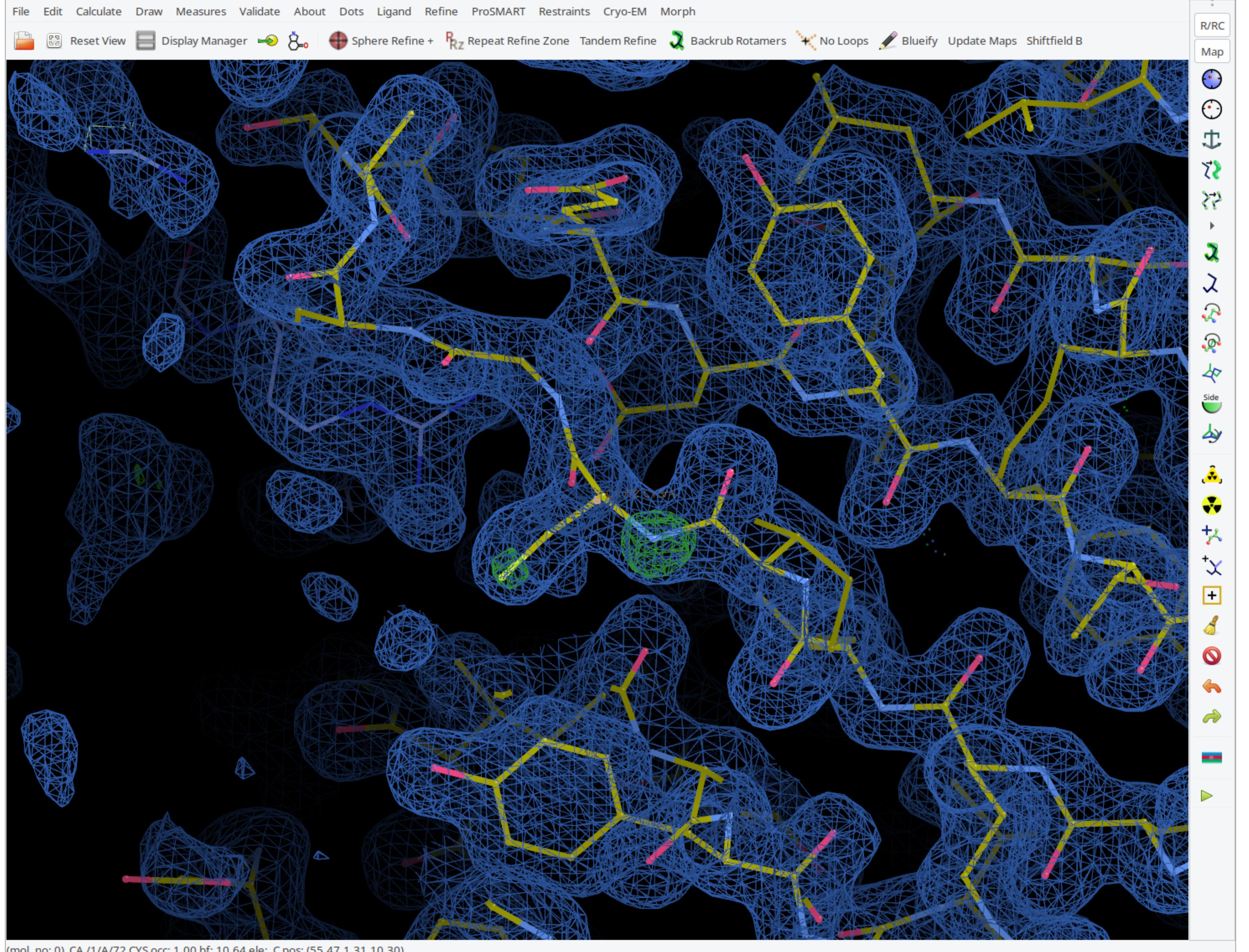


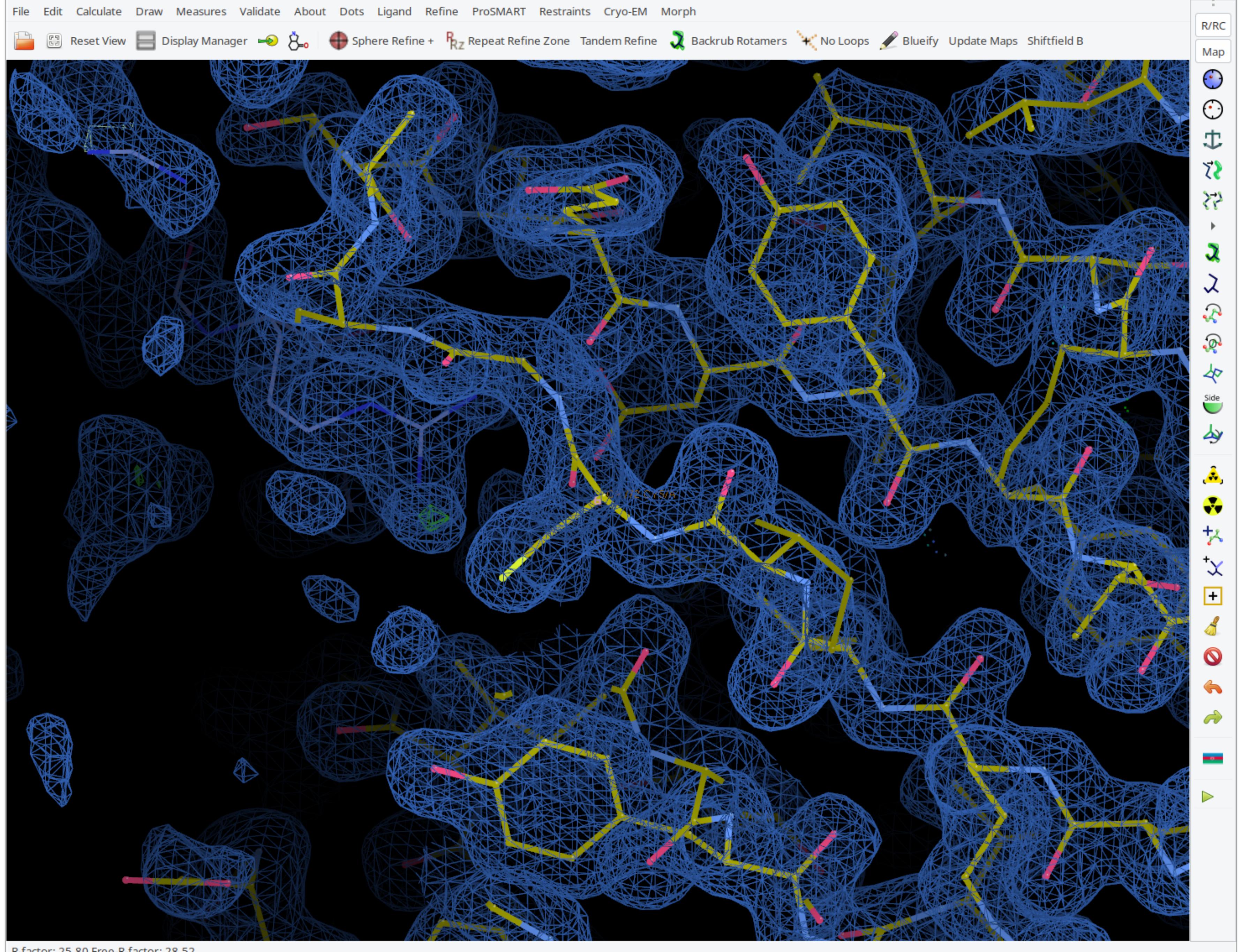
Updating Maps

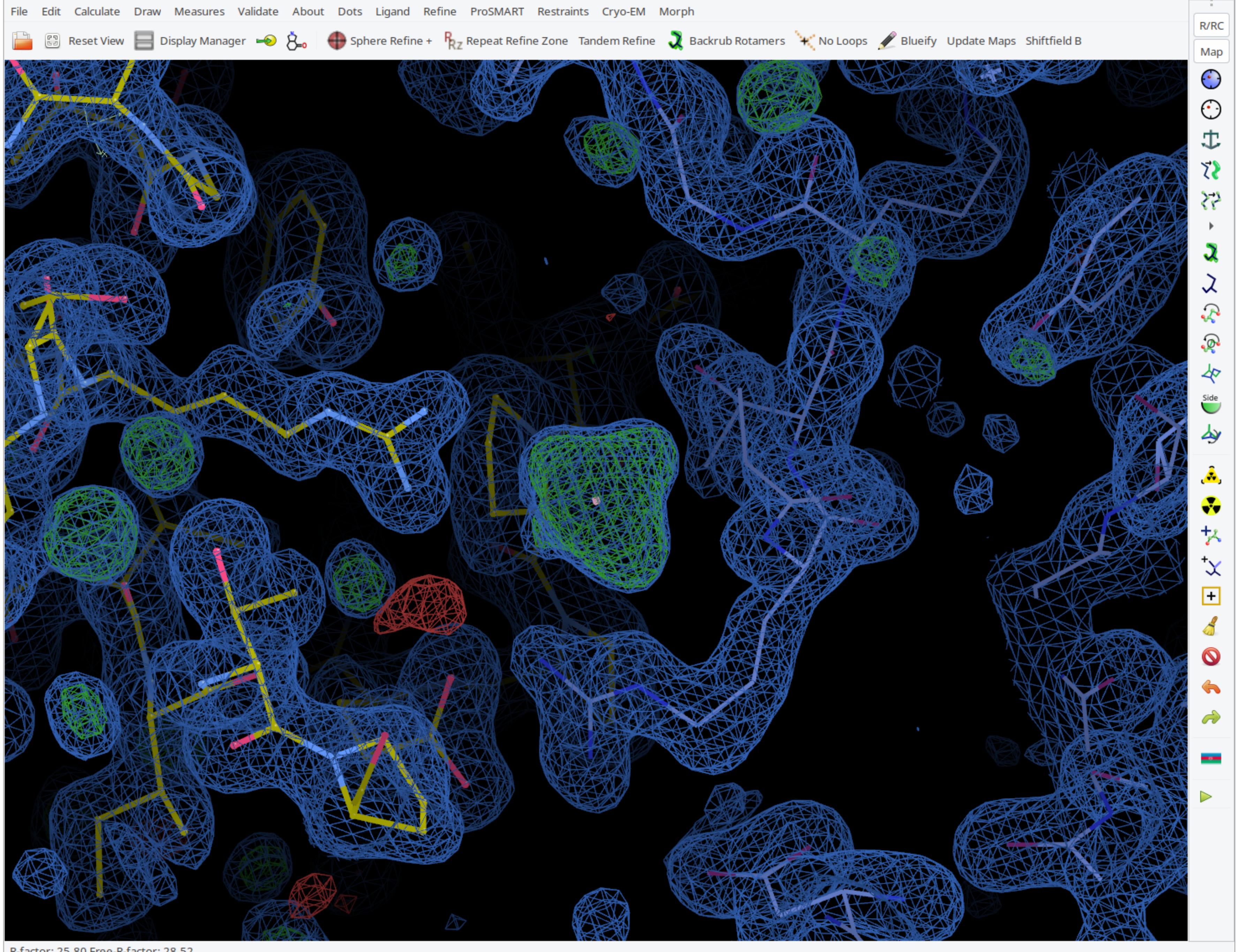
Thanks to **Tristan Croll** who implemented this in Isolde and inspired Paul to add it to Coot. Thanks to **Kathryn Cowtan** for help in doing so

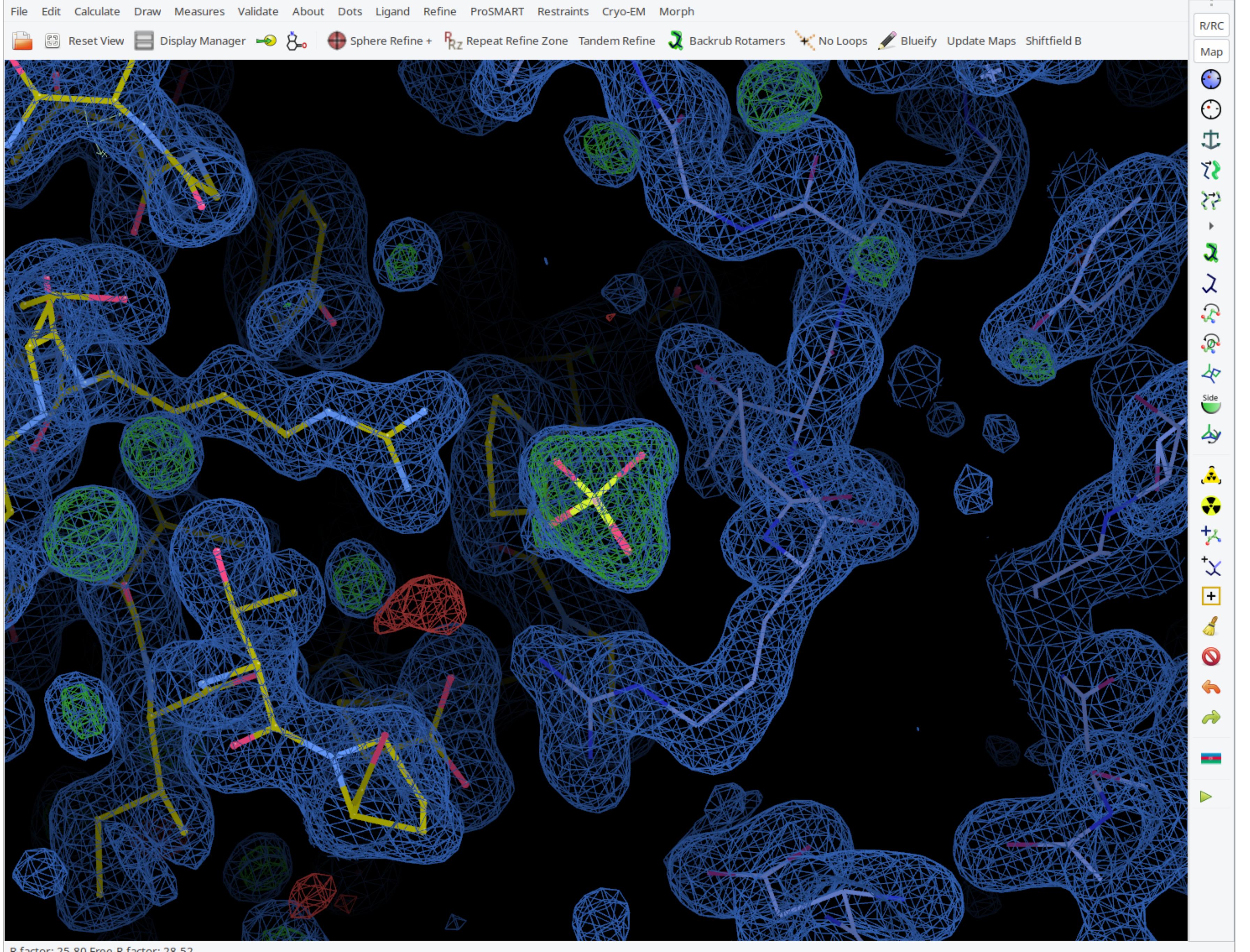
Note: updating maps takes ~0.7s for 200 AA and 1.8A data

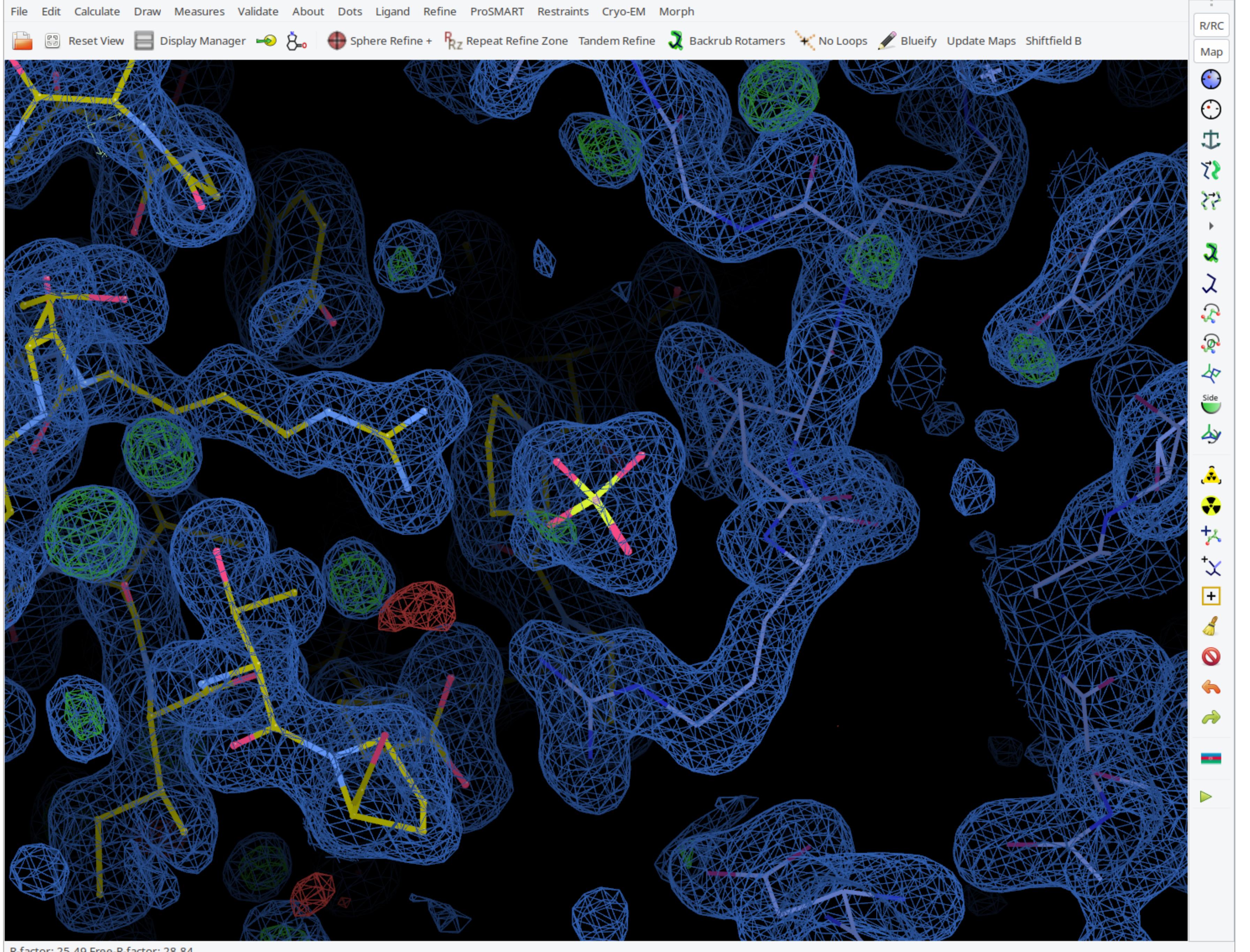












-

□

X

R/RC

Map

○

●

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

◆

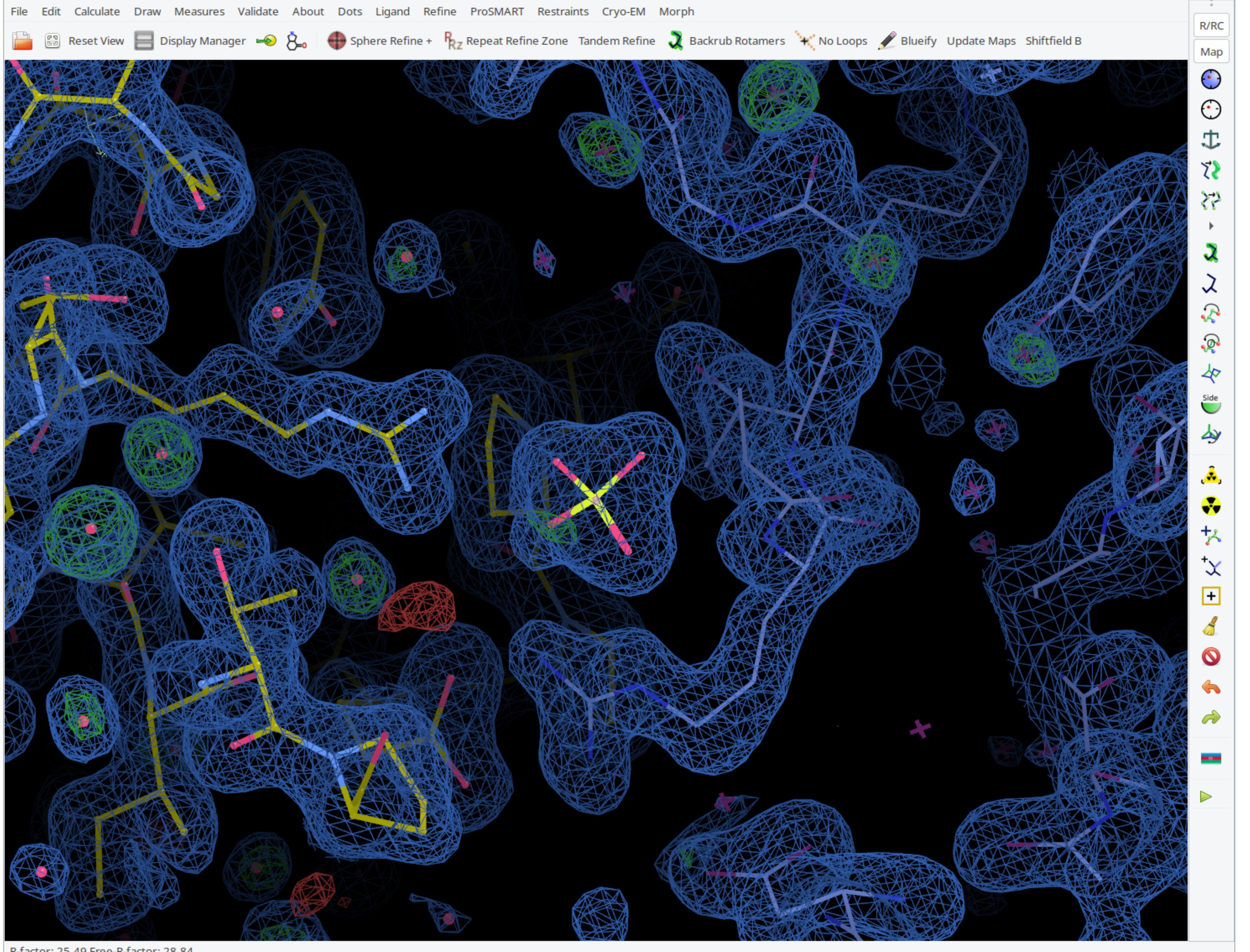
◆

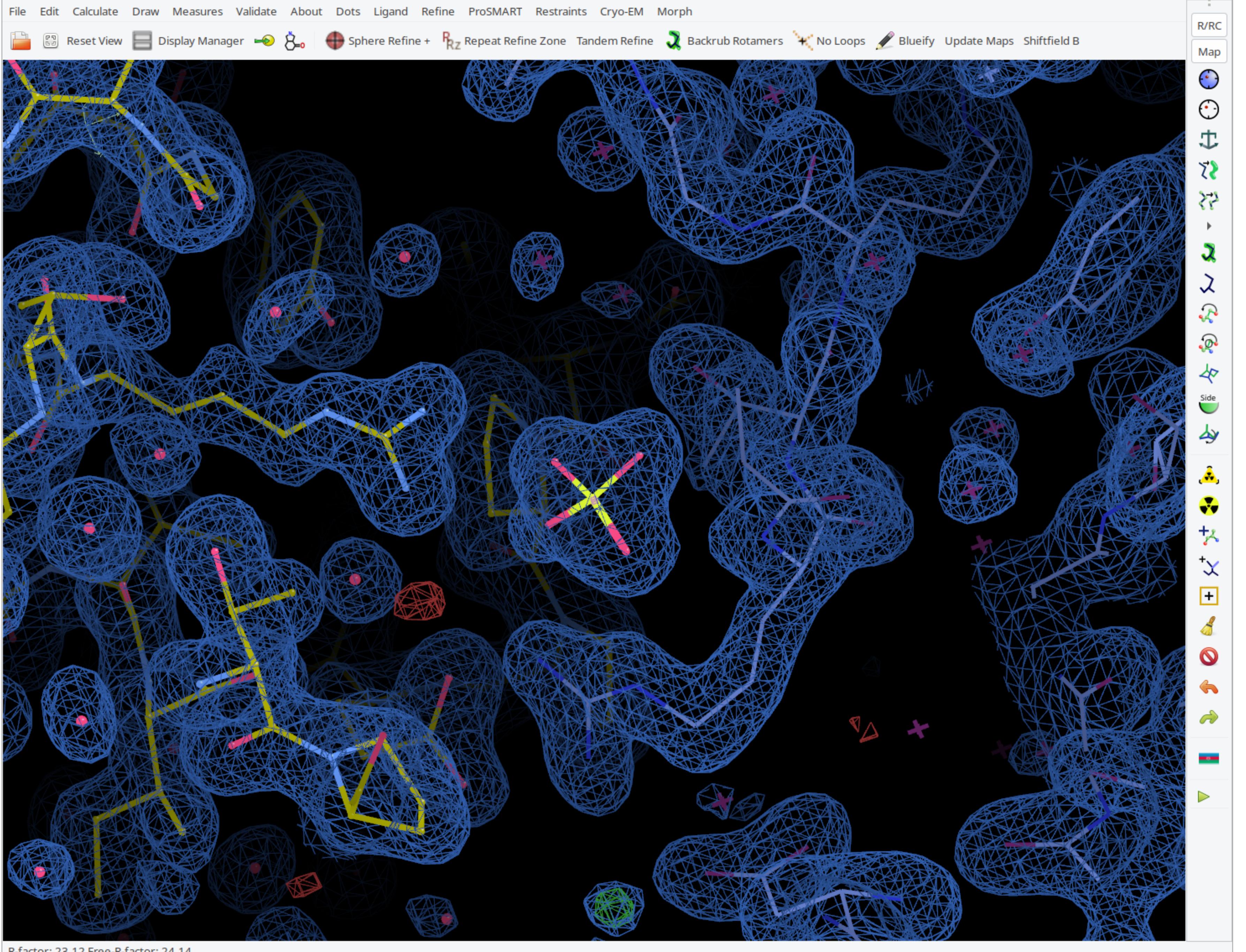
◆

◆

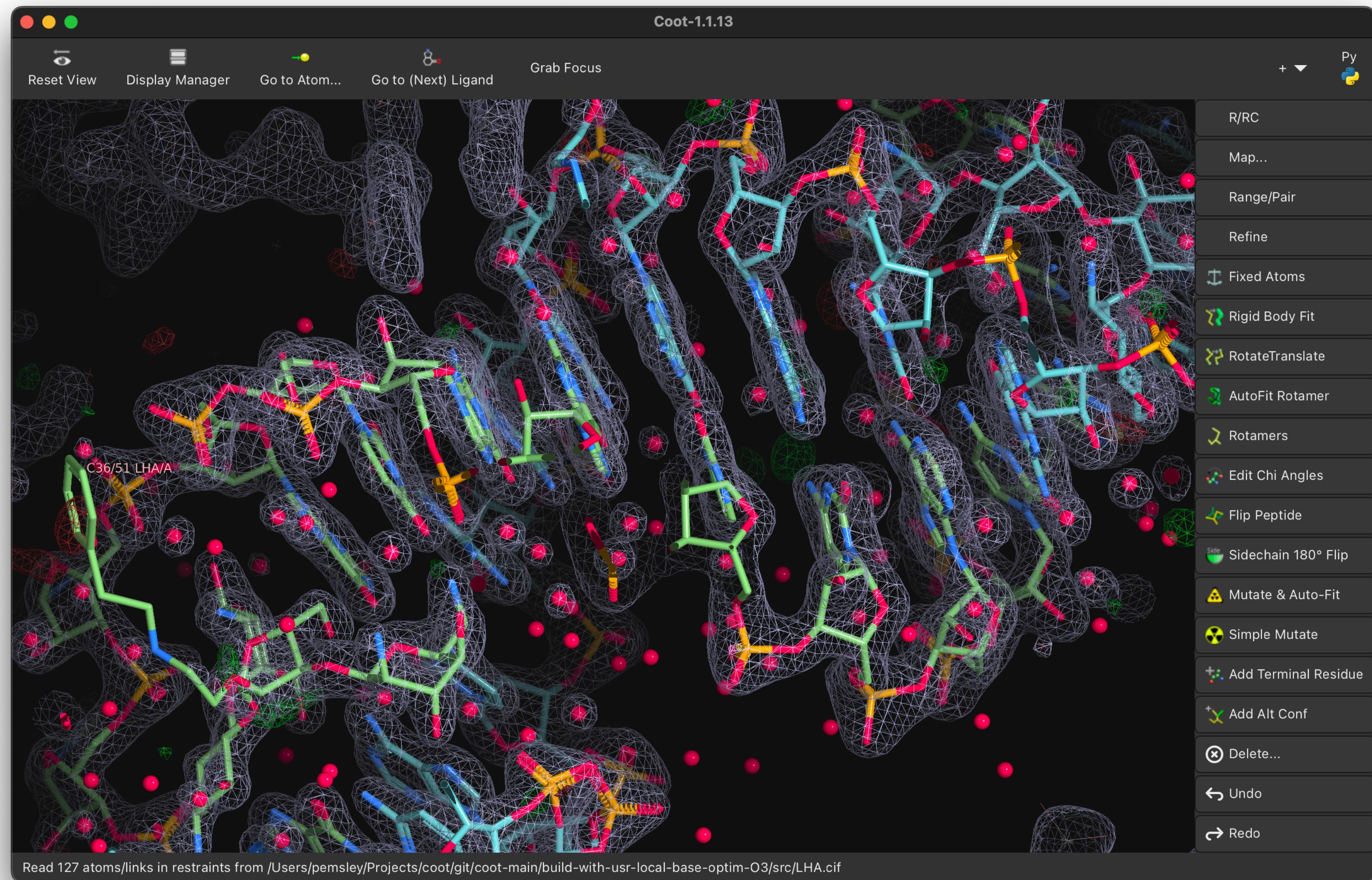
◆

◆





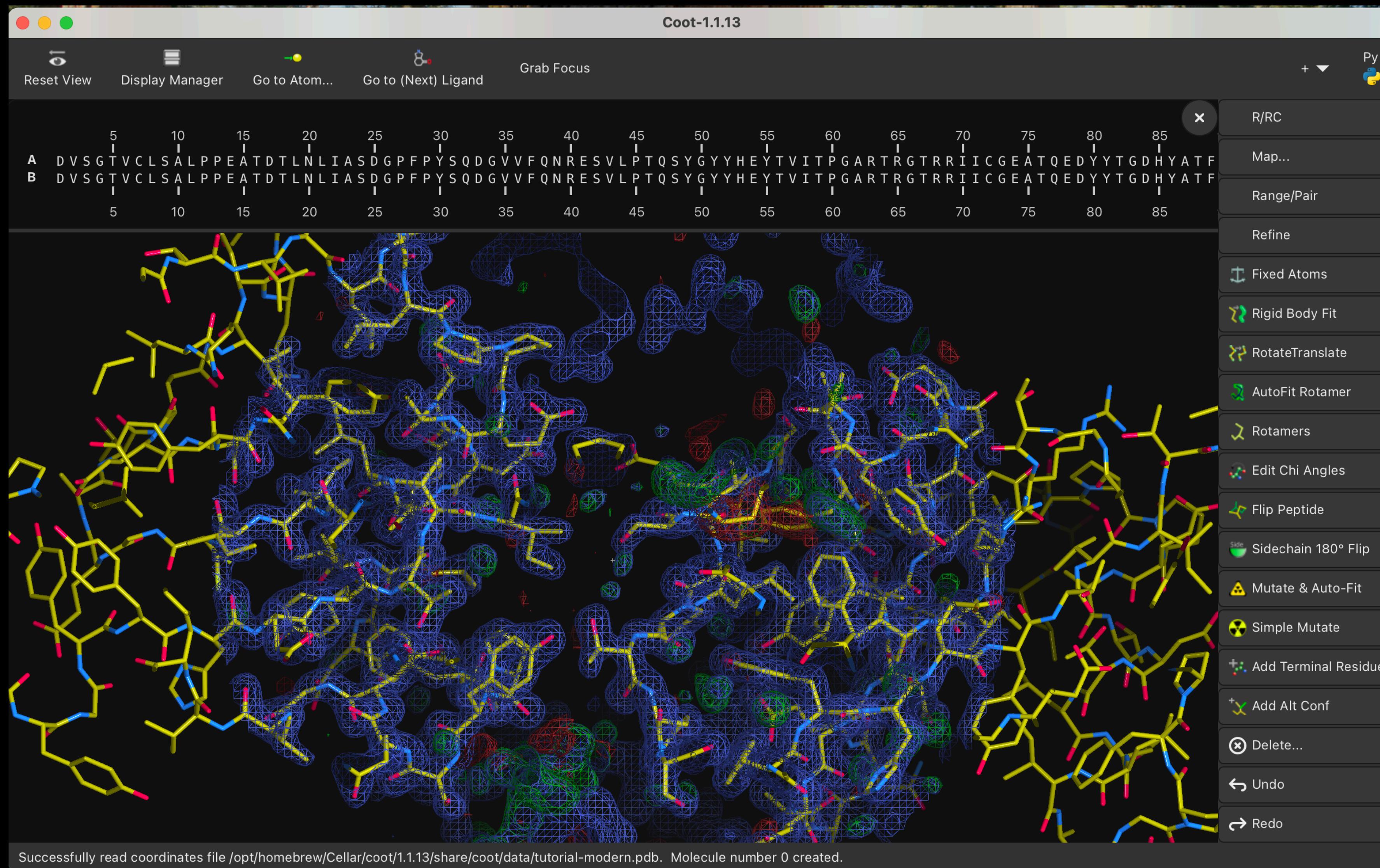
Coot 1.1



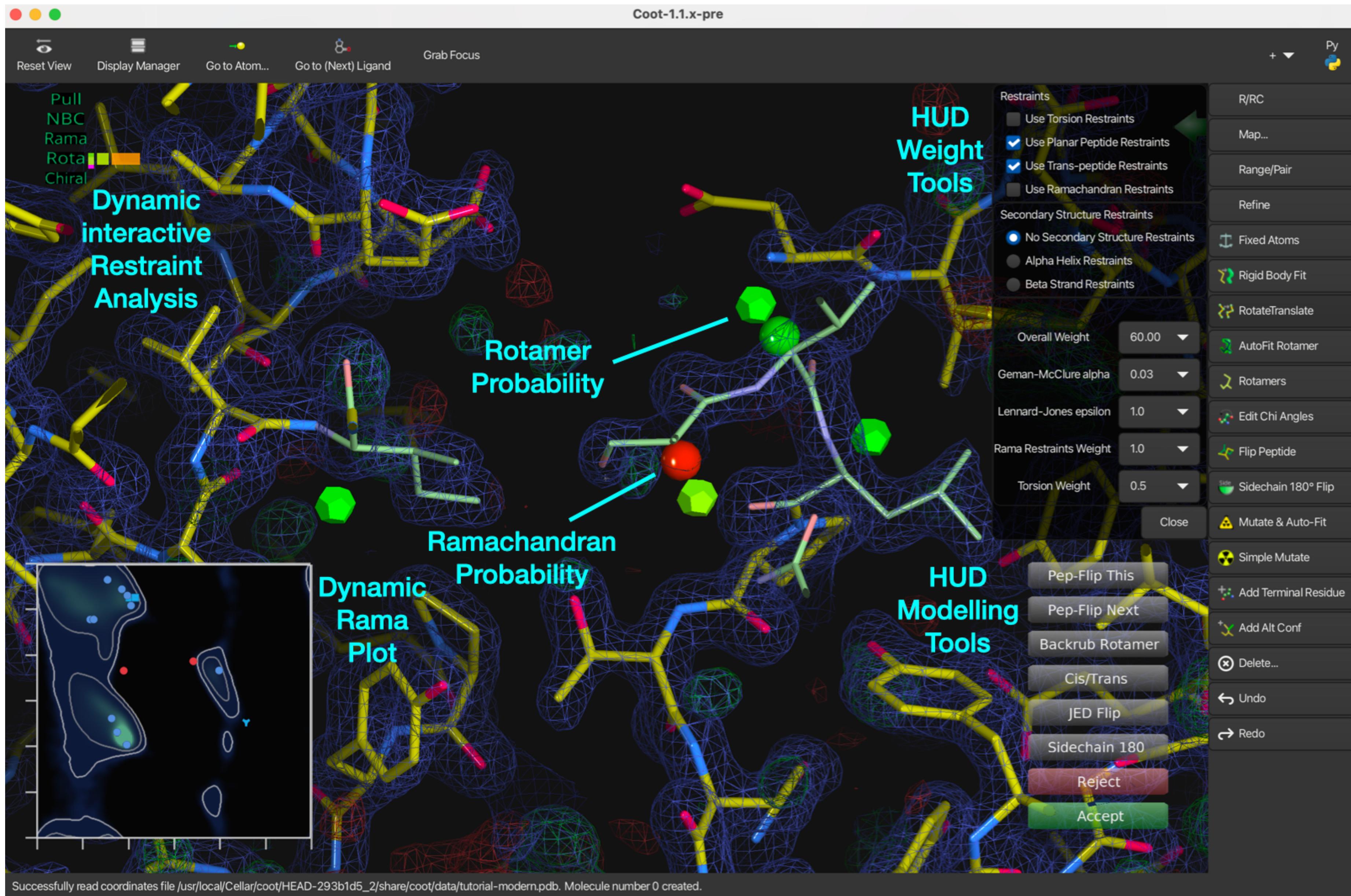
Major Changes

- “Single Panel View”
 - Sequence view
 - Ramachandran plot
 - Geometry analysis
 - Chimera → ChimeraX underwent a similar transformation some years ago
- Lighting/Representation improvements
- Real Space Refinement
- Improved analysis and navigation

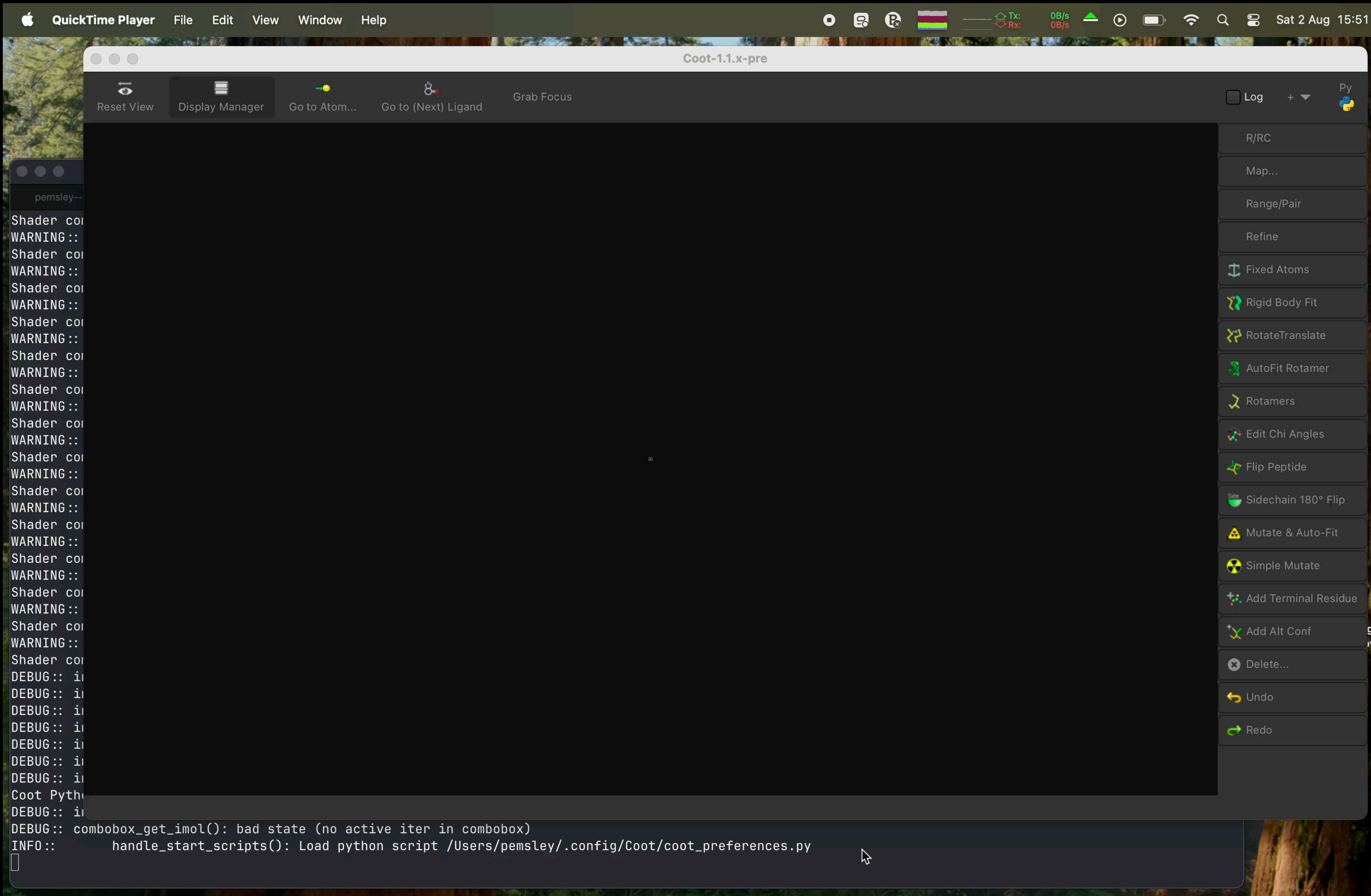
“Sequence View” is Now Embedded



Interactive real space refinement

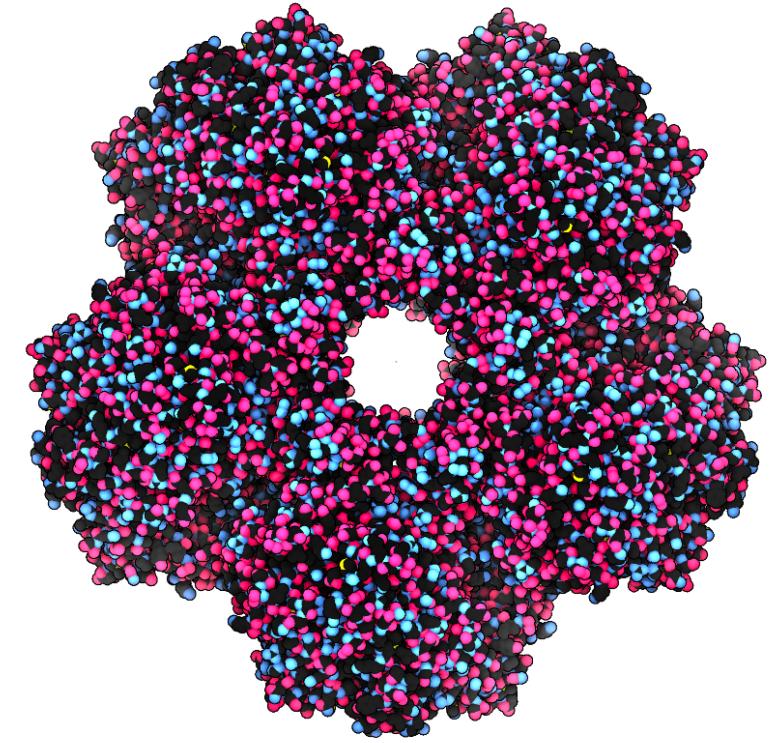
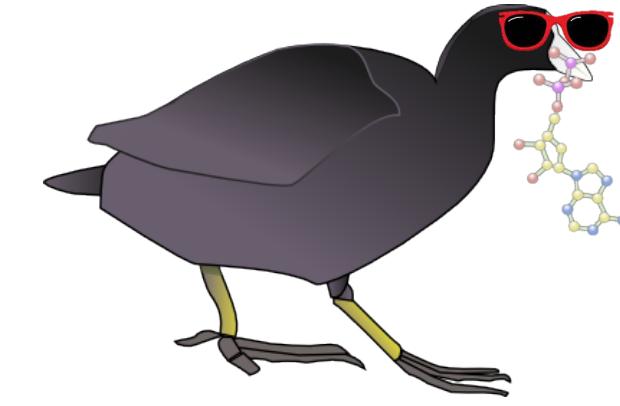


Interactive real space refinement

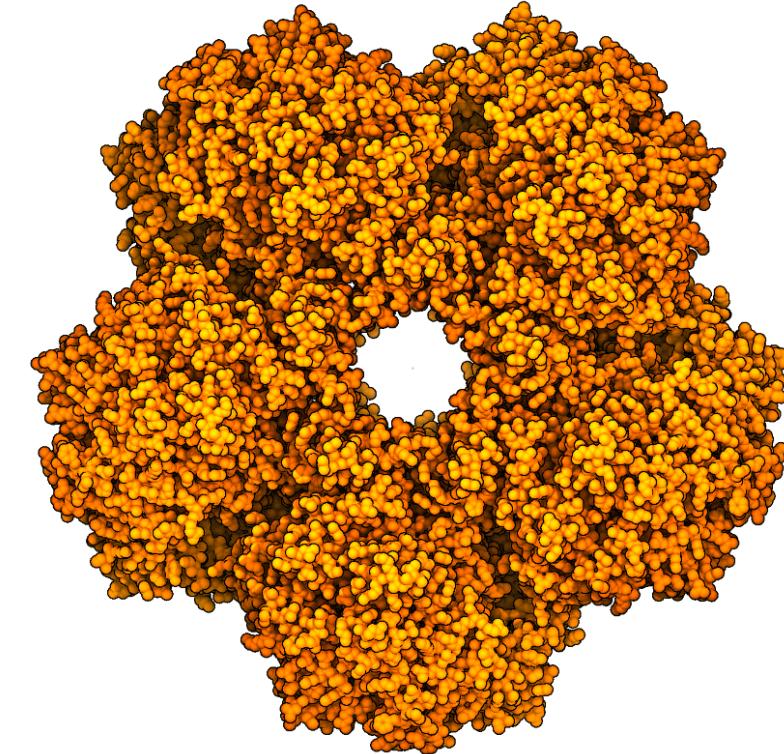


Coot 1.1

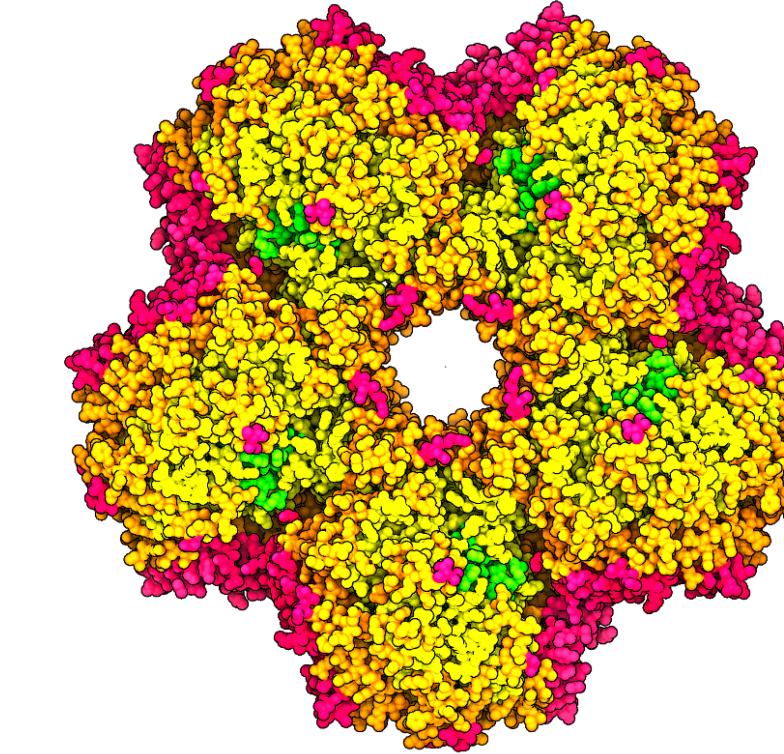
Attractive Graphics



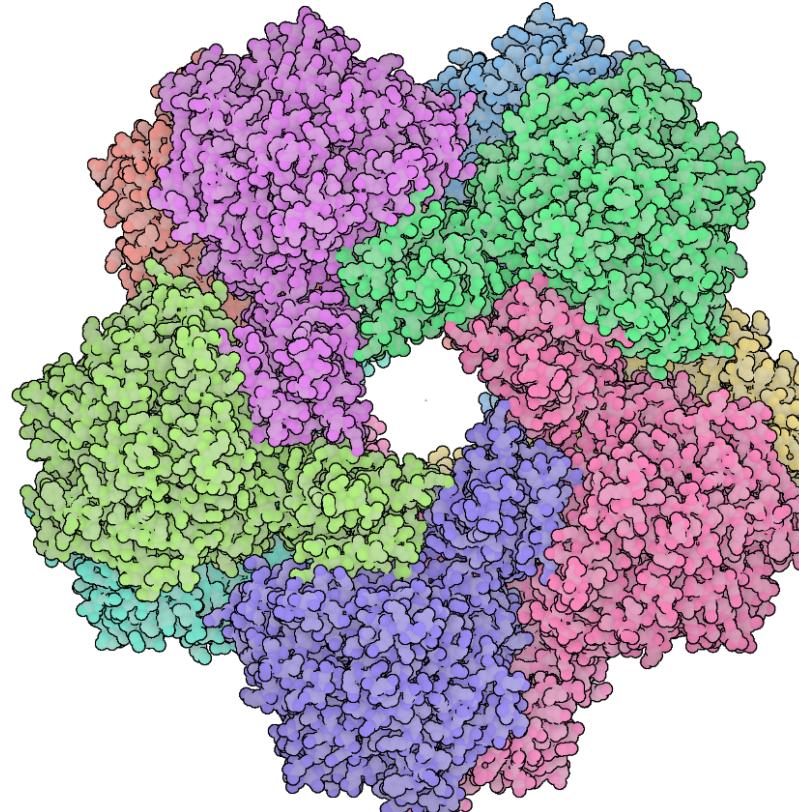
colour by atoms



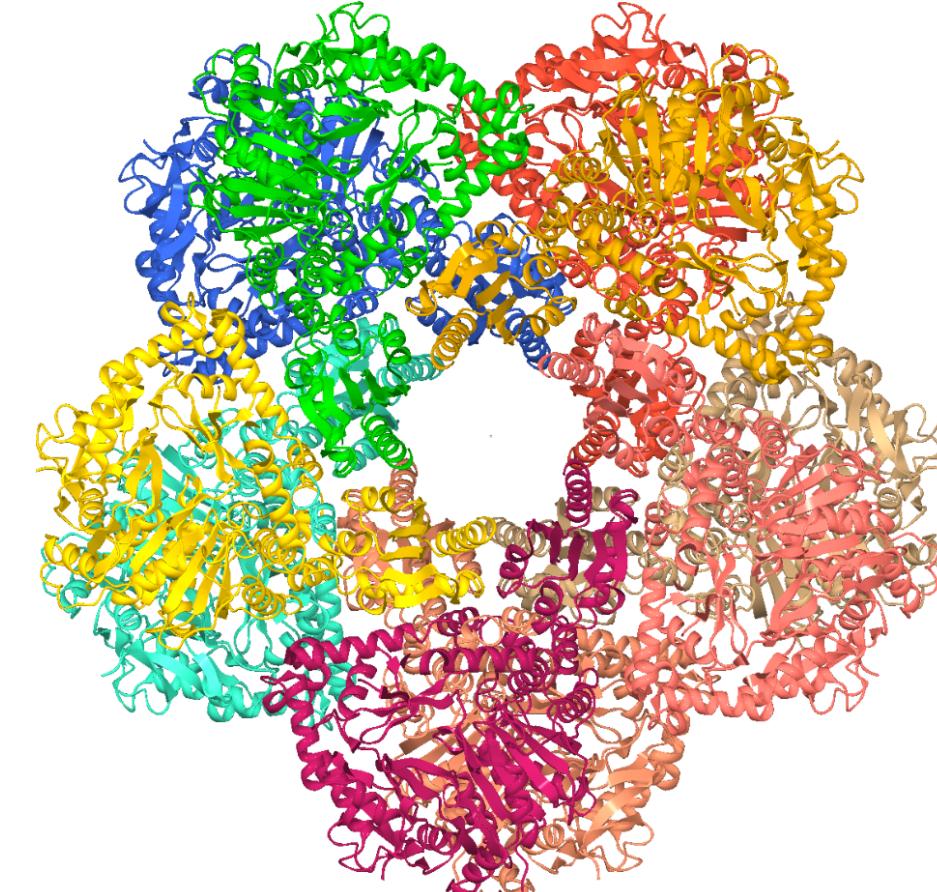
colour by molecule



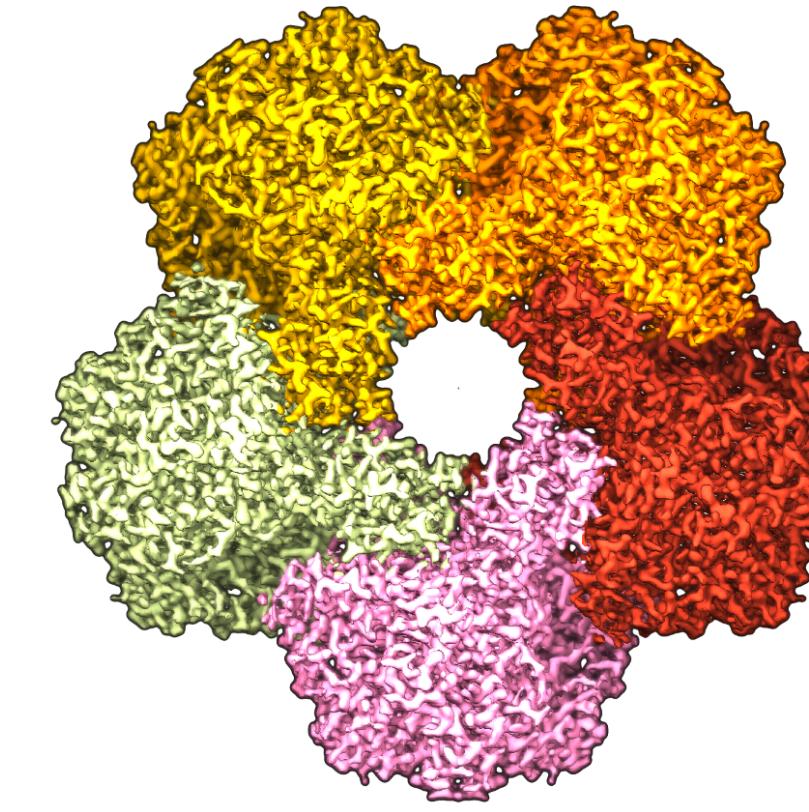
colour by B factors



Goodsell colours



ribbons



masked map

More Sophisticated Lighting in Coot

Old Lighting Model:

Ambient

New lighting:

Ambient, Diffuse, Specular, Key and Fill lights (Basic)

Depth of Field

Shadows

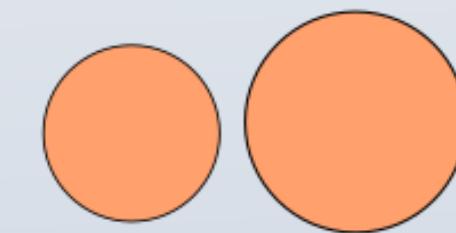
Ambient Occlusion

Approximation, so artefacts

Textures (something other than shiny plastic)

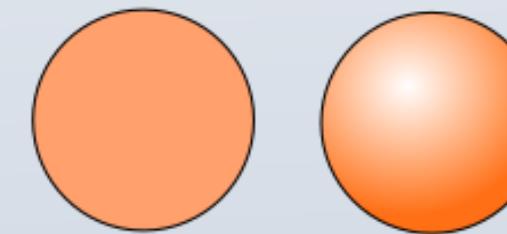
Visual Cues for Depth

Relative Size



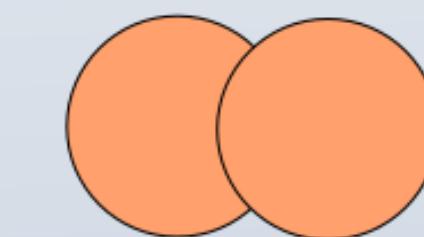
Old Coot:✗
New Coot:✓

Shading



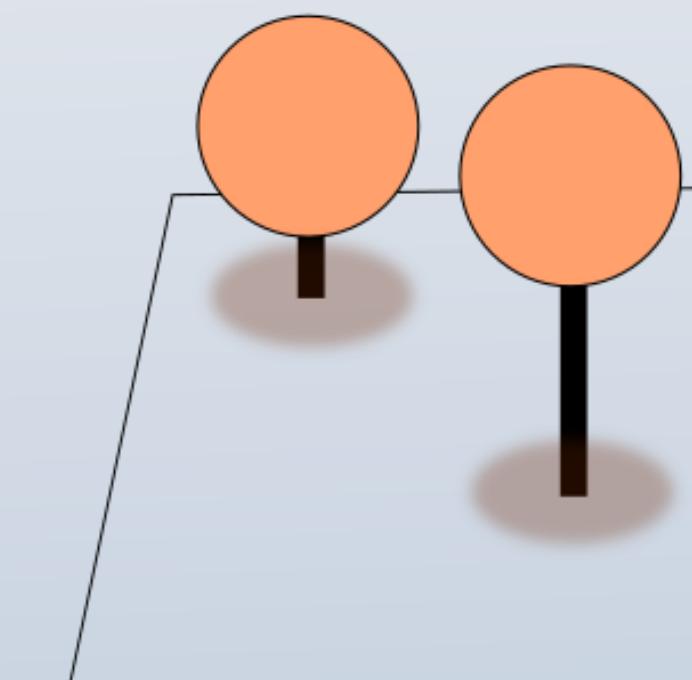
Old Coot:✗
New Coot:✓

Occlusion



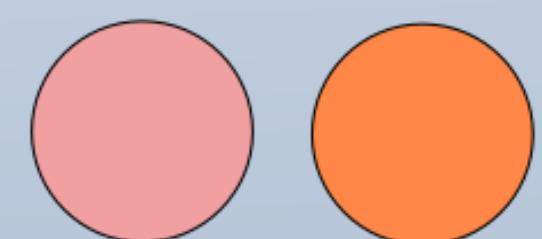
Old Coot:✗
New Coot:✓

Shadows



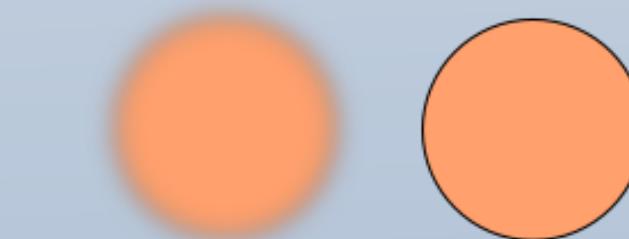
Old Coot:✗
New Coot:✓

Colour



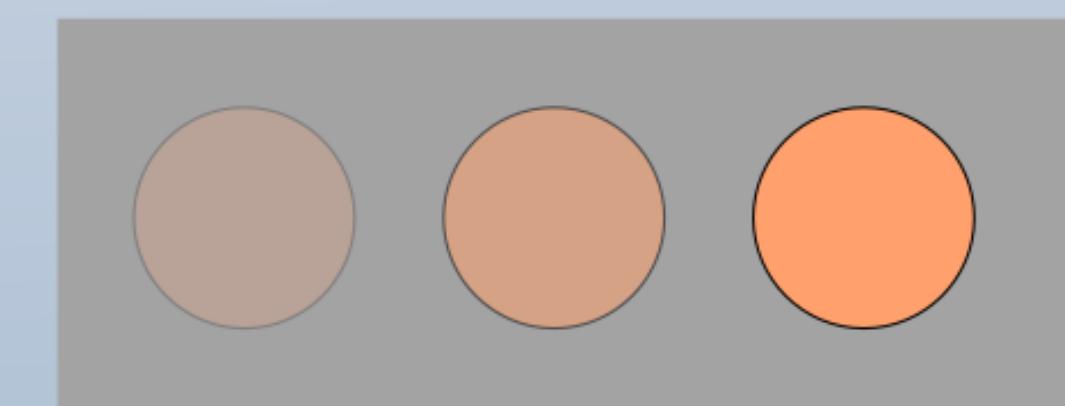
Old Coot:✗
New Coot:✓

Focus/Blur



Old Coot:✗
New Coot:✓

Fog Depth



Old Coot:✓
New Coot:✓

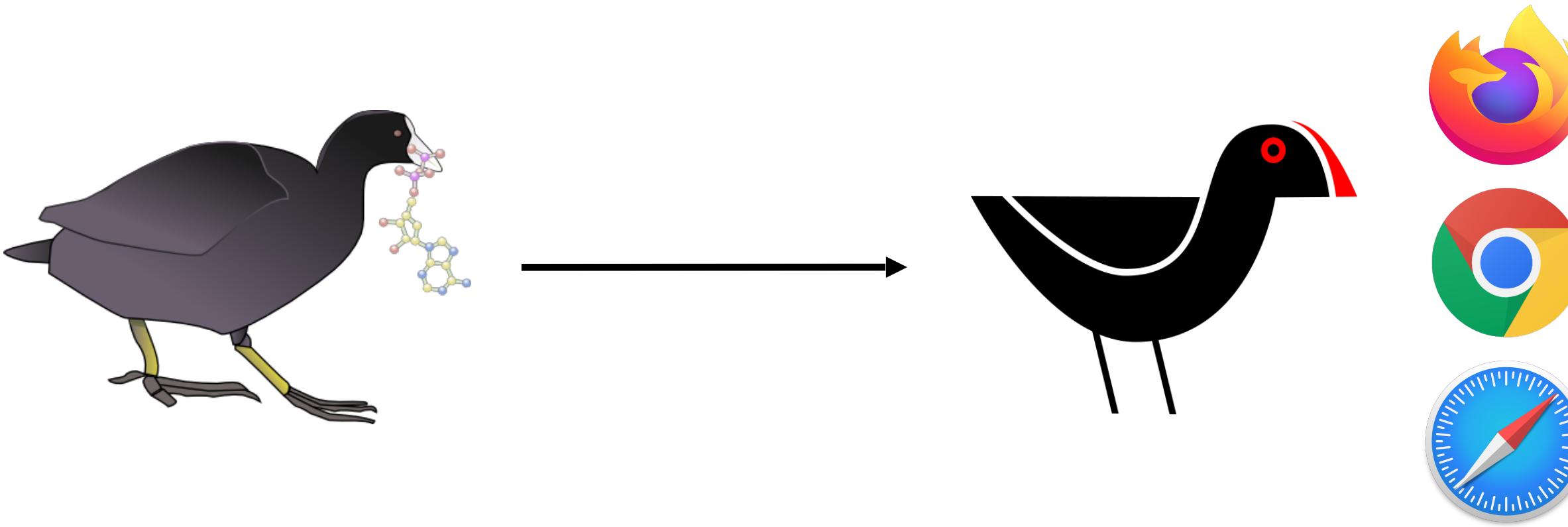
Moorhen

Web-based Interactive Model building



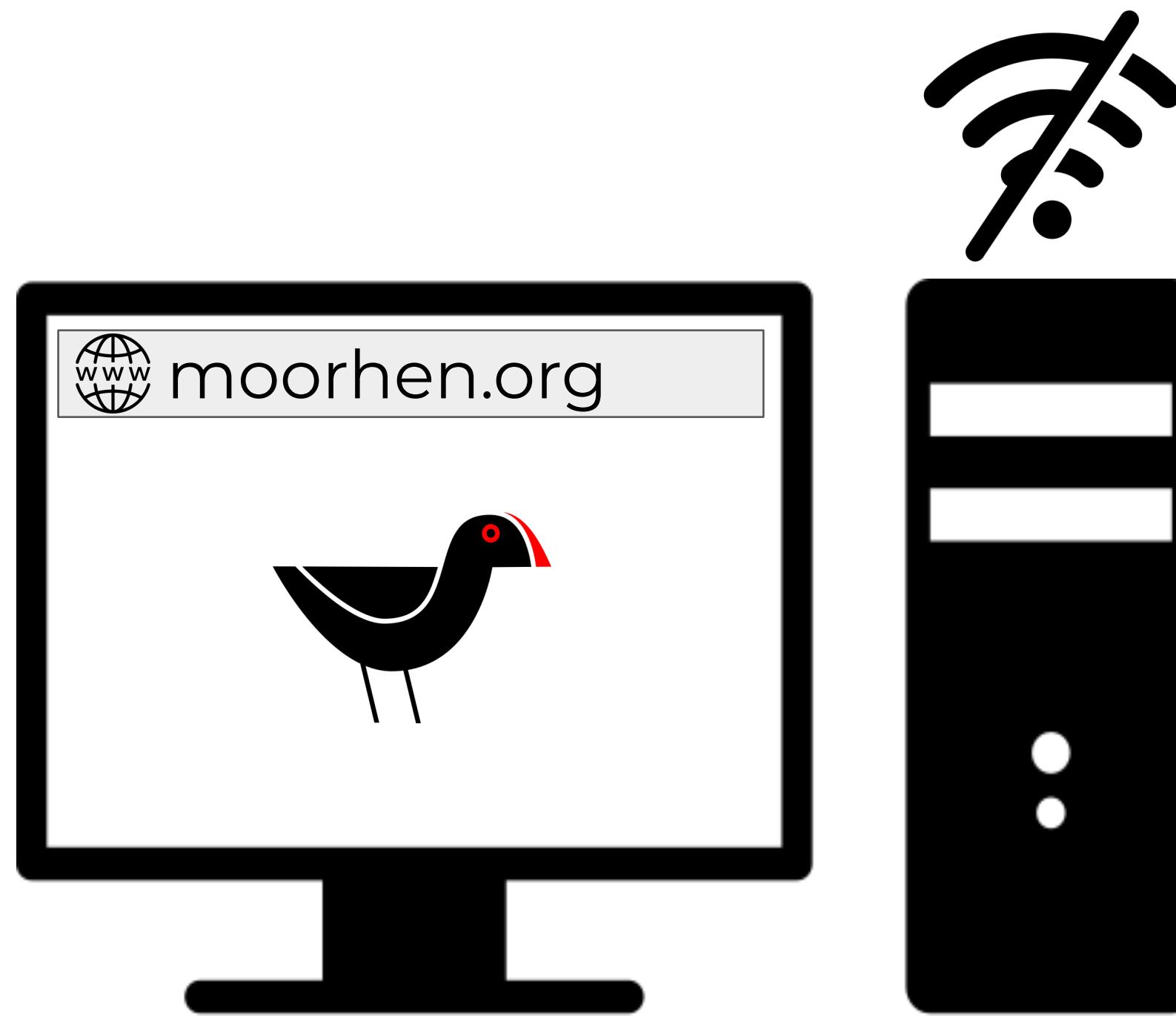
What is Moorhen?

- Moorhen is a next-generation web-based application for the visualisation and manipulation of molecules in structure determination and analysis
 - In short, Coot on the web browser

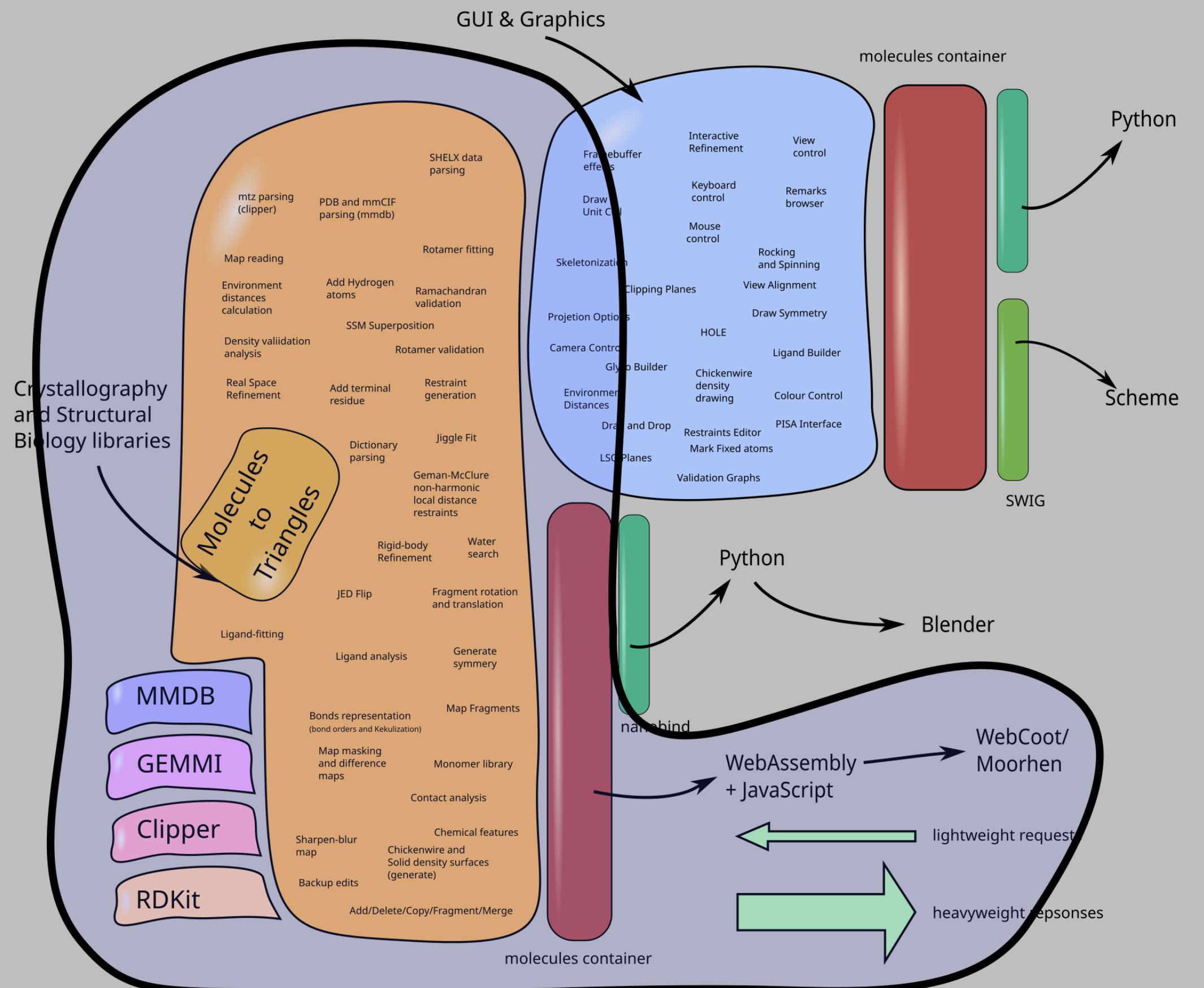


What is Moorhen?

- Moorhen is a client-side-only app.
This means **there is no server-side computation**



Moorhen infrastructure



Moorhen
React-based UI

Coot
API

** shared with Coot **

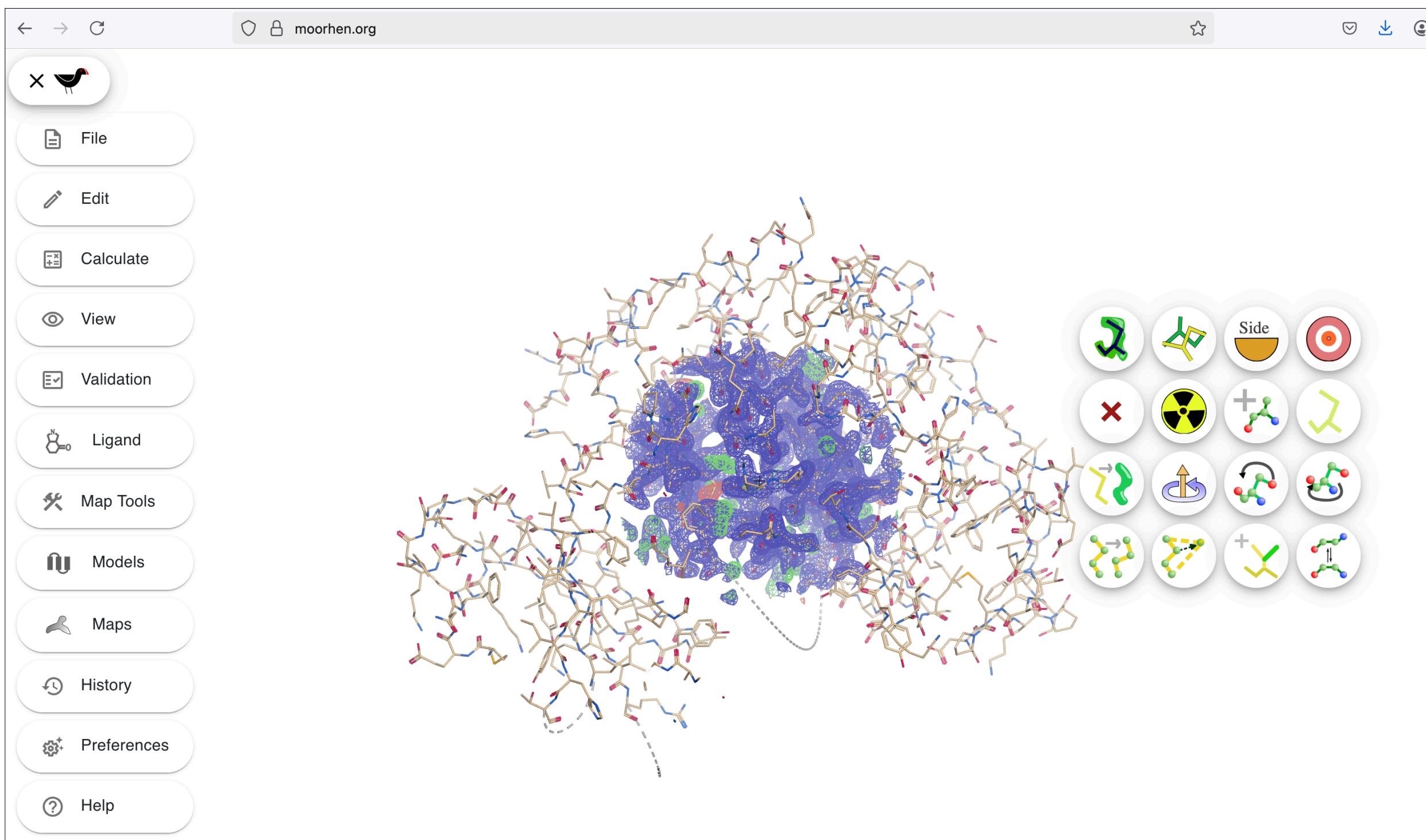
Model-Building
Refinement
Model Validation



Current state of Moorhen

Model Editing Features

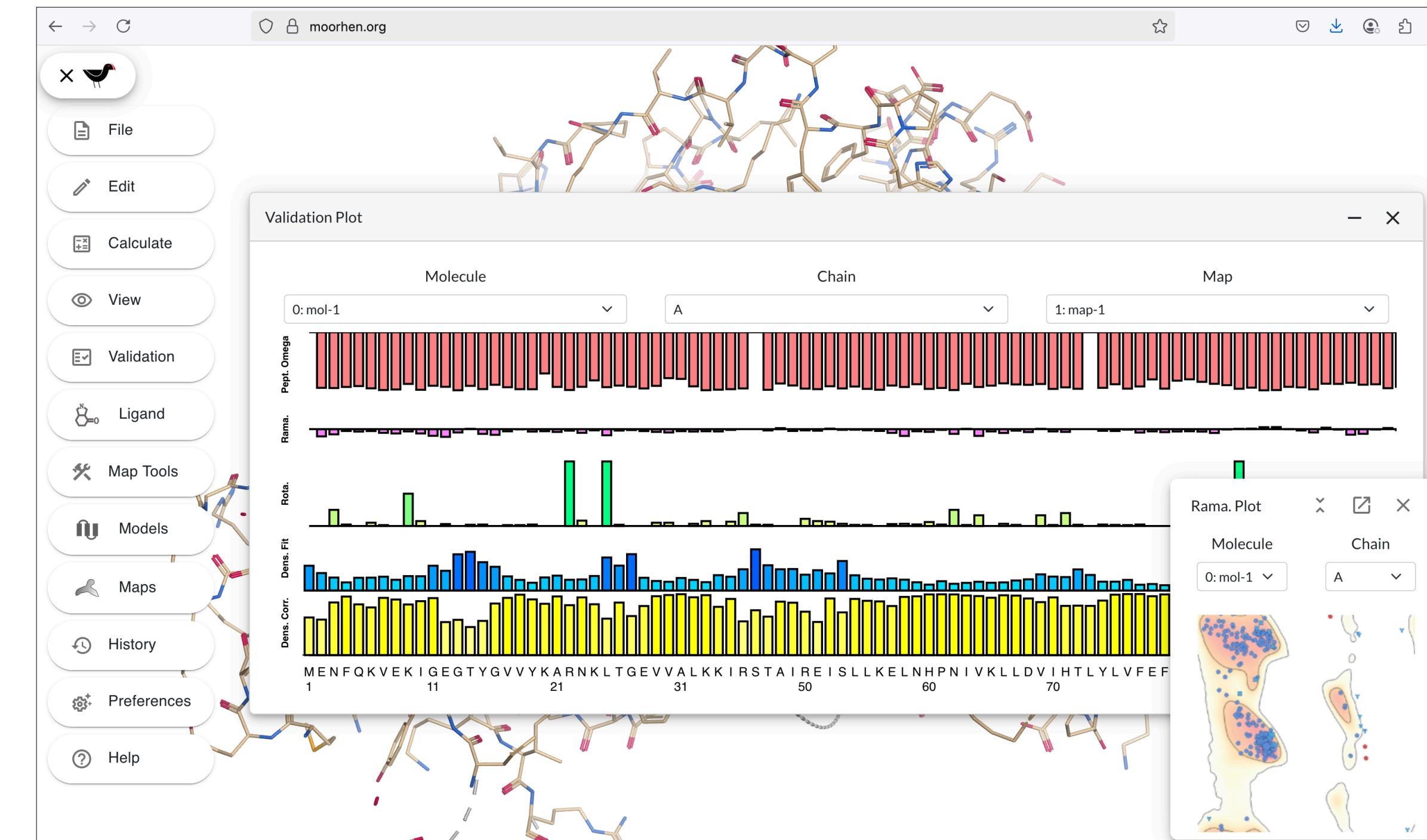
Mutate Residue	Peptide Flip
Real Space Refinement	Auto-fit Rotamer
JED Flip	Add Residue
Check/Delete Waters	Rotate/Translate Residue
Delete Item	Drag Atoms
Edit Chi Angles	Fill Sidechain



Current state of Moorhen

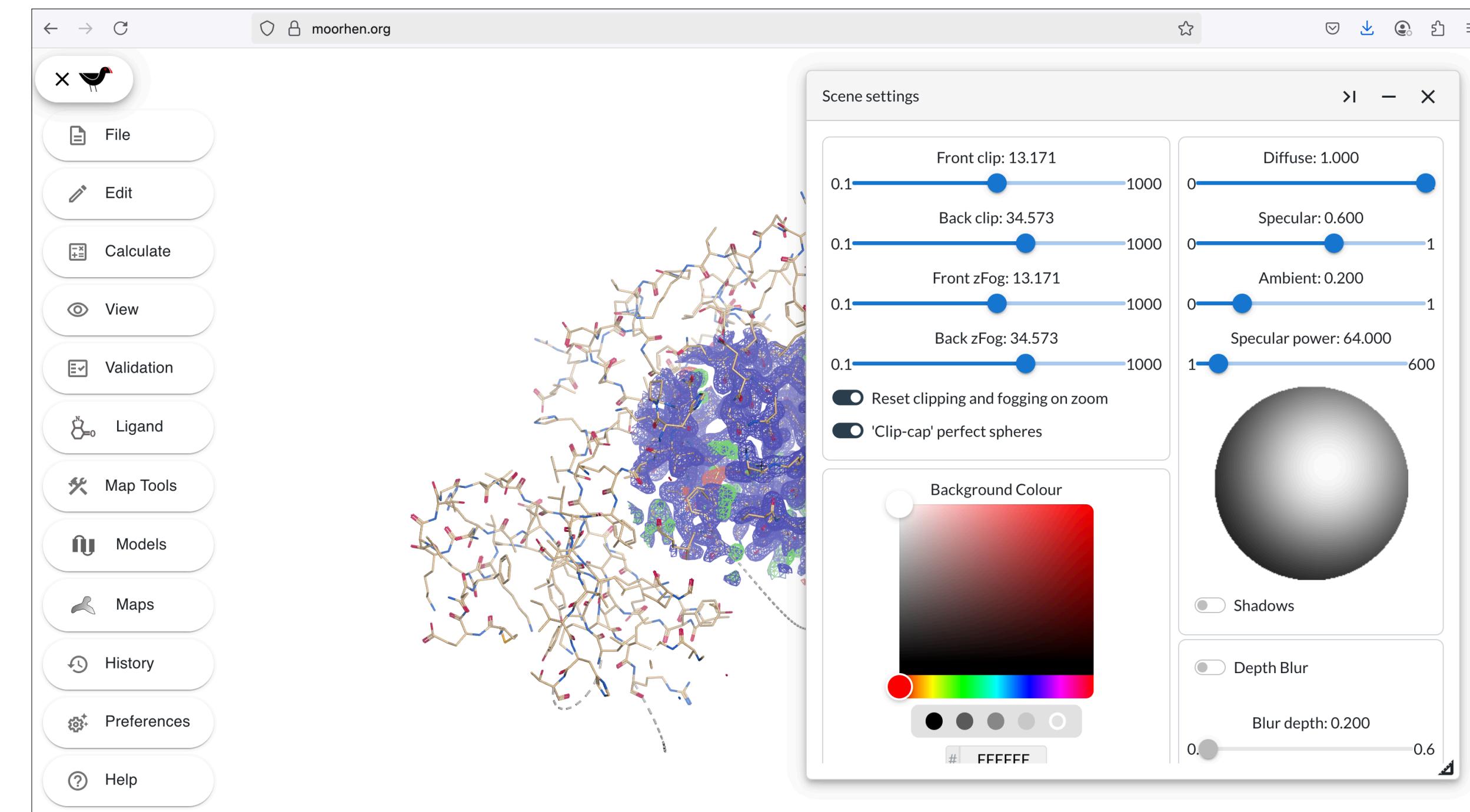
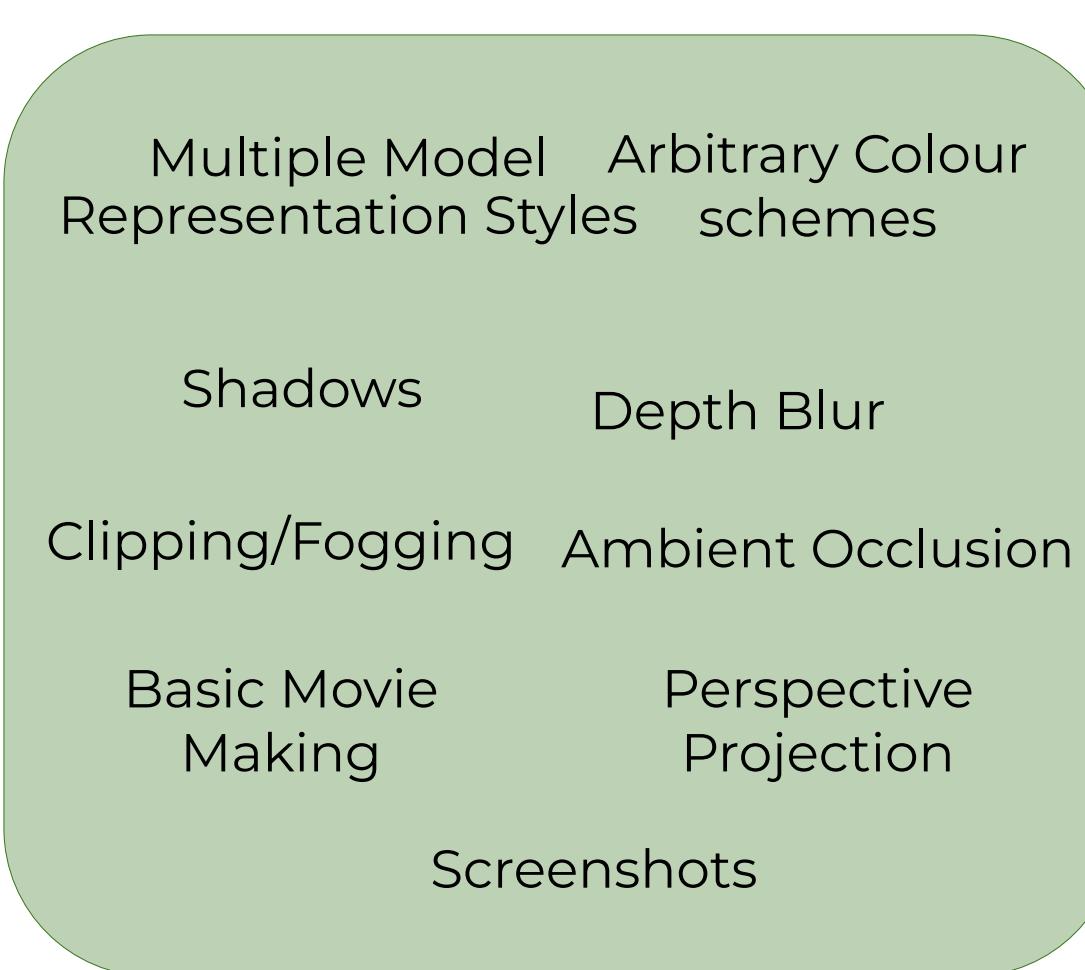
Validation Features

- Rama. Plot
- Unmodeled Blobs
- Density Fit
- Diff. Map Peaks
- Geom. Analysis
- Combined Validation Plot
- Rotamers



Current state of Moorhen

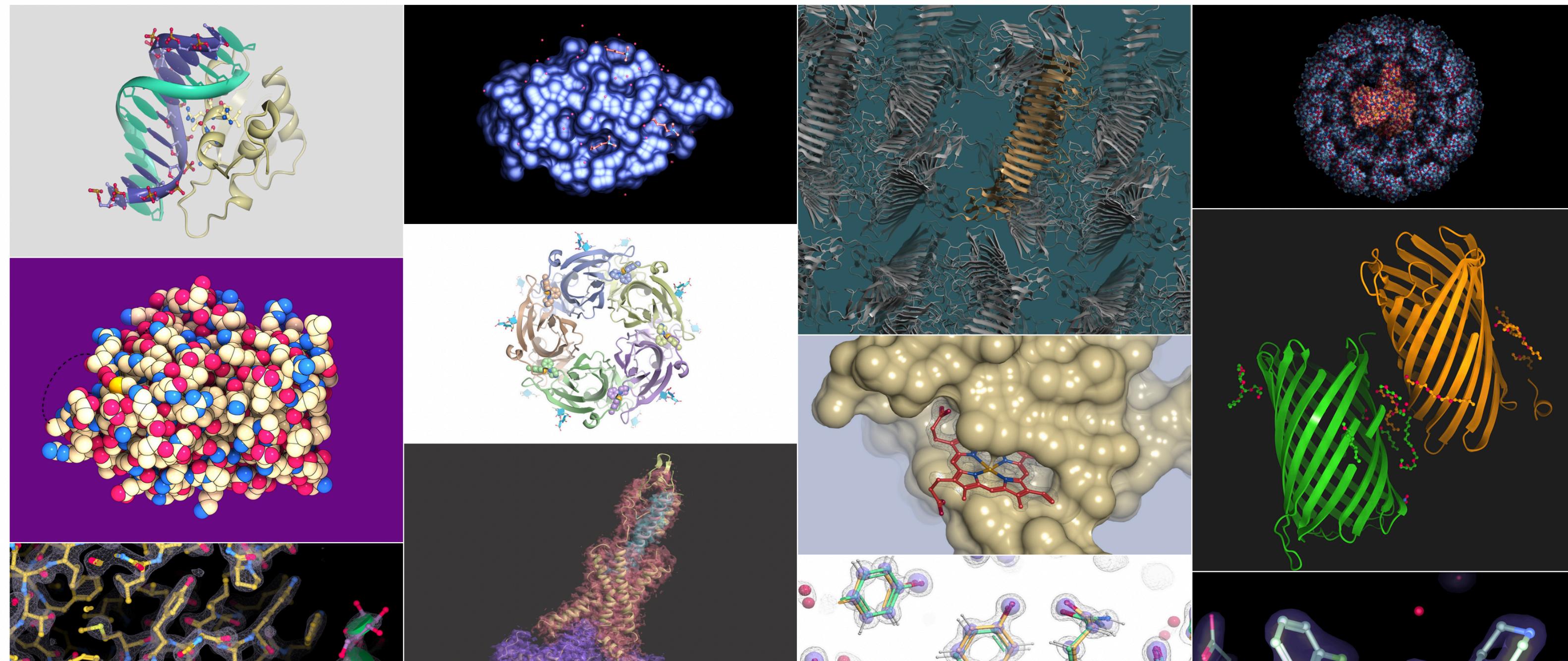
Figure-Making Features

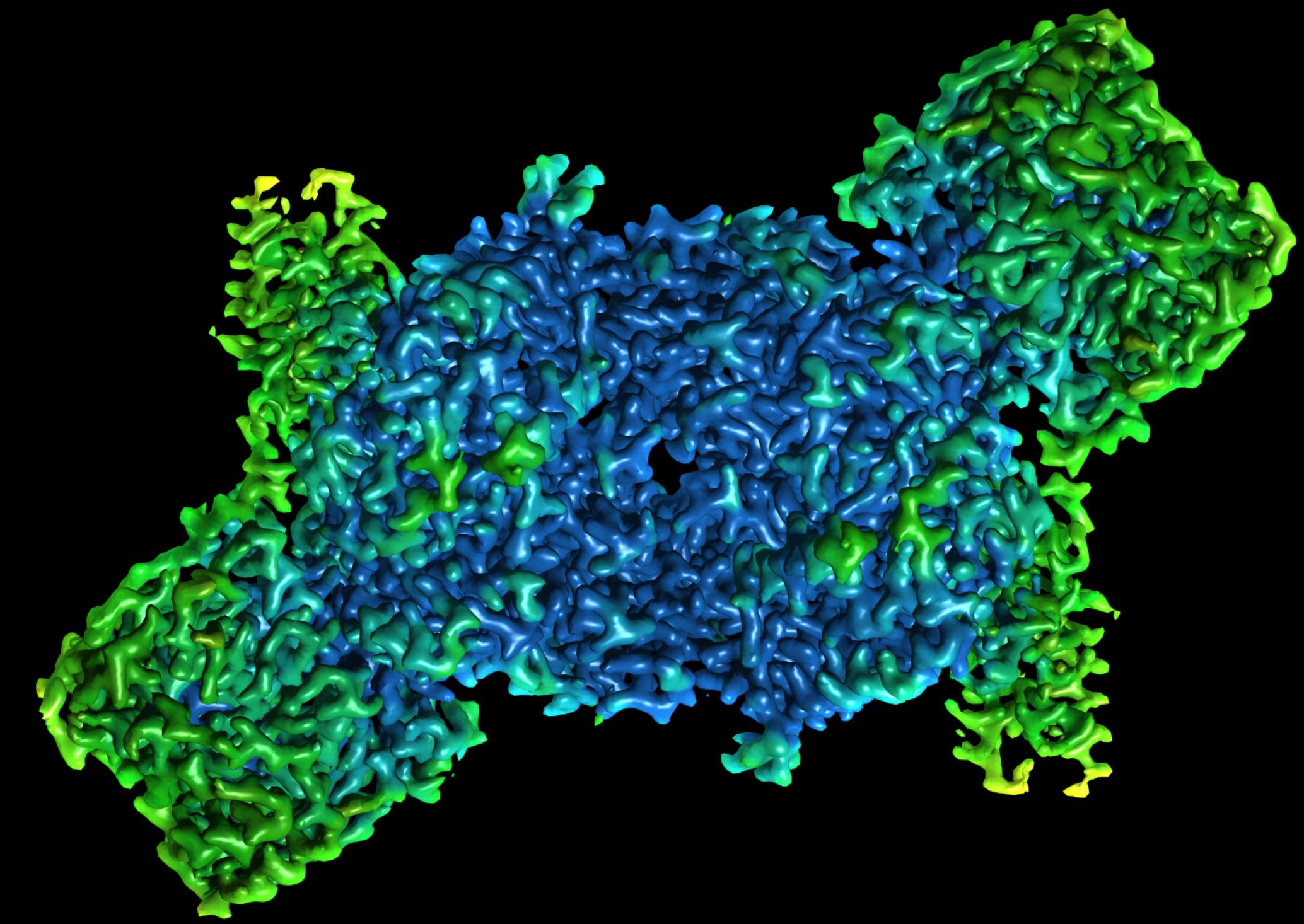


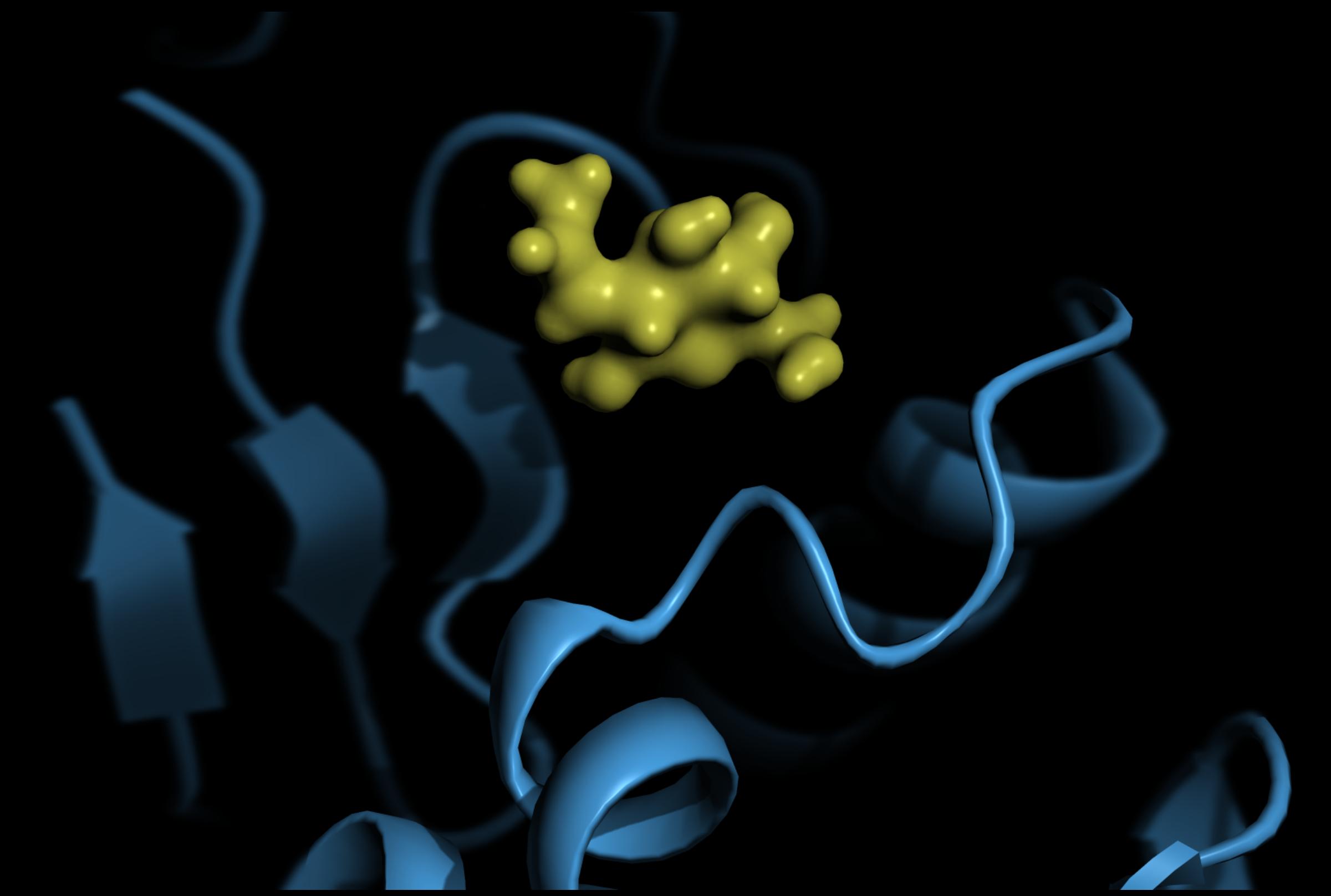


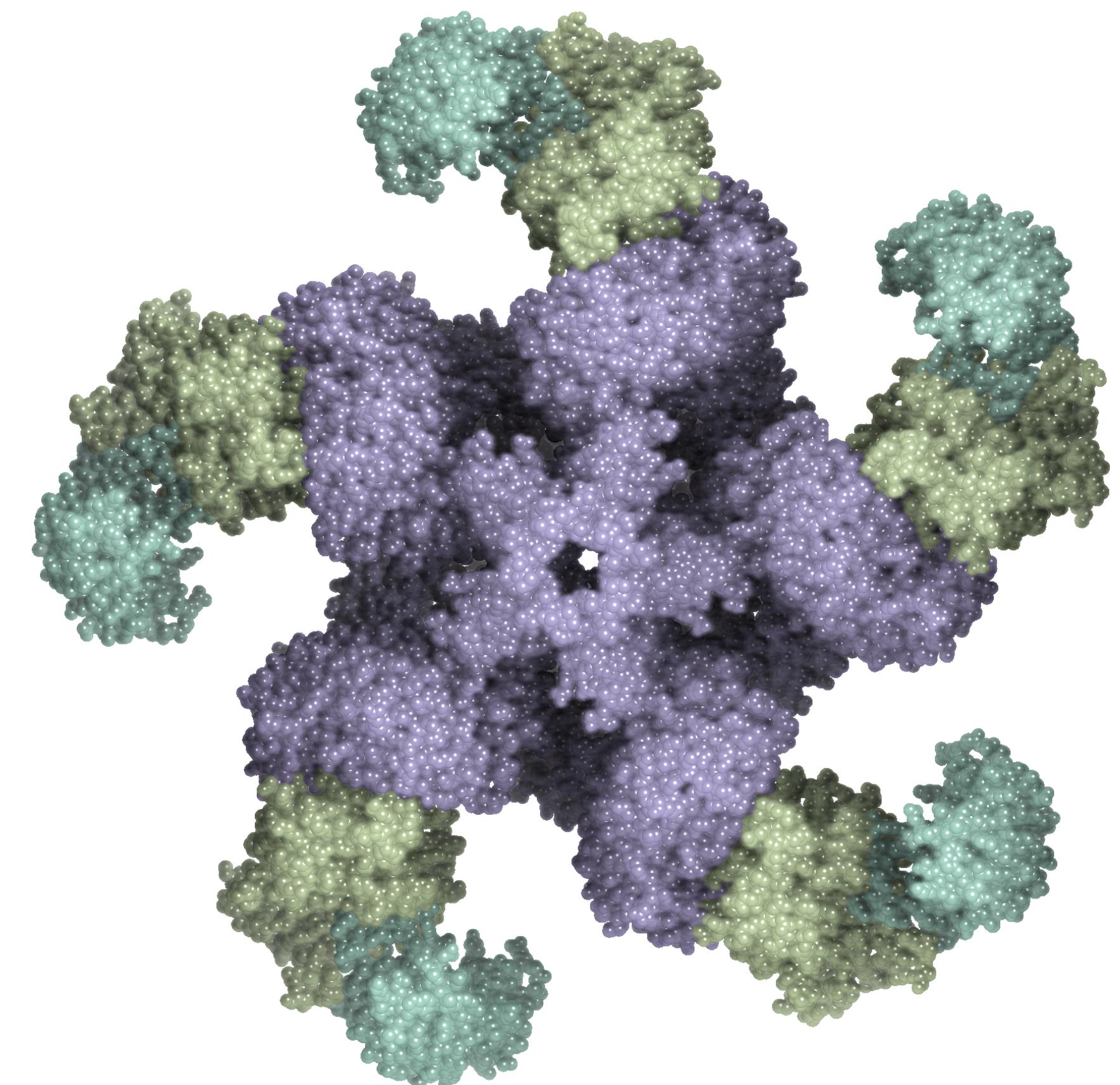
Moorhen Gallery

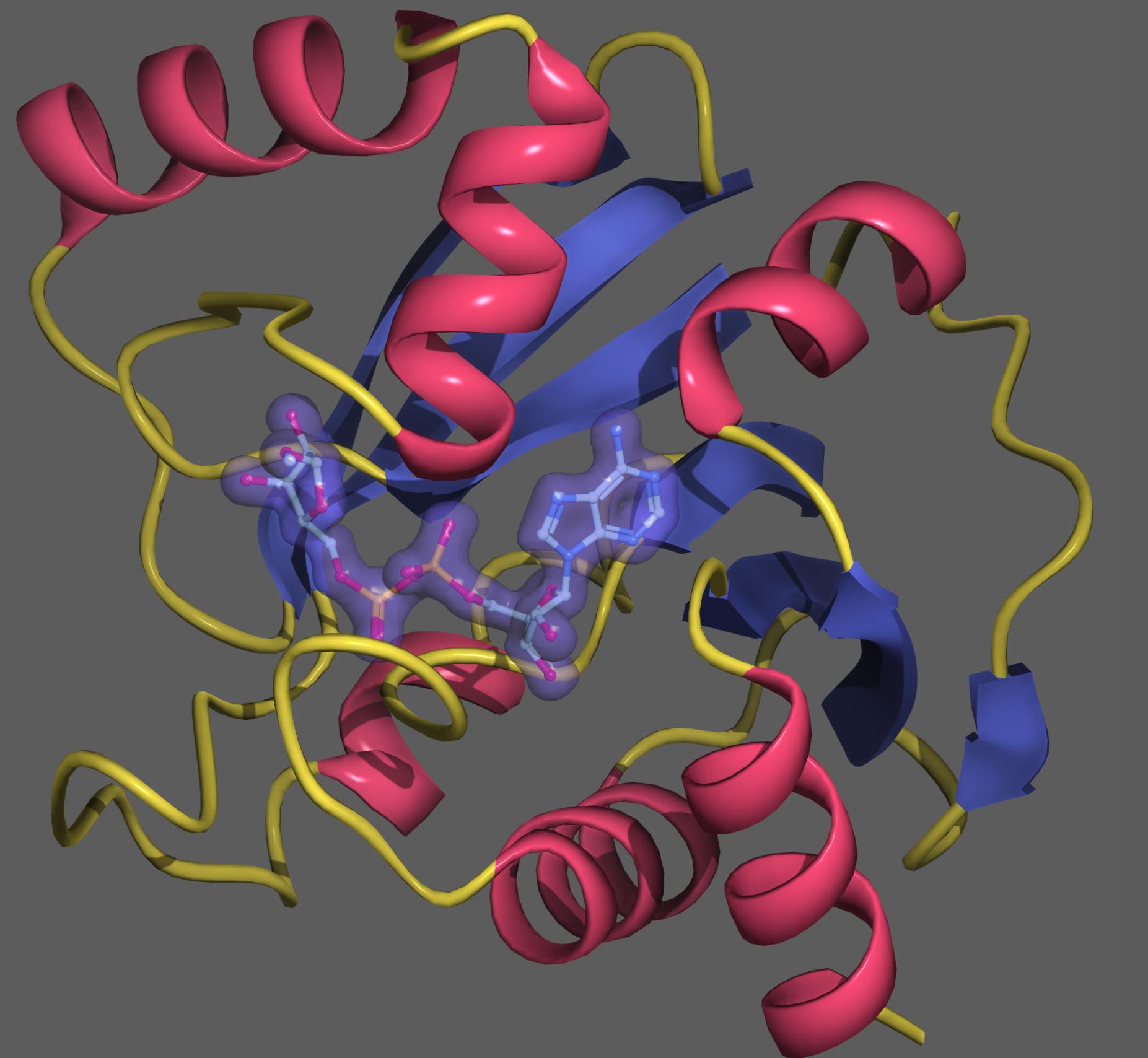
Screenshots created with moorhen.org

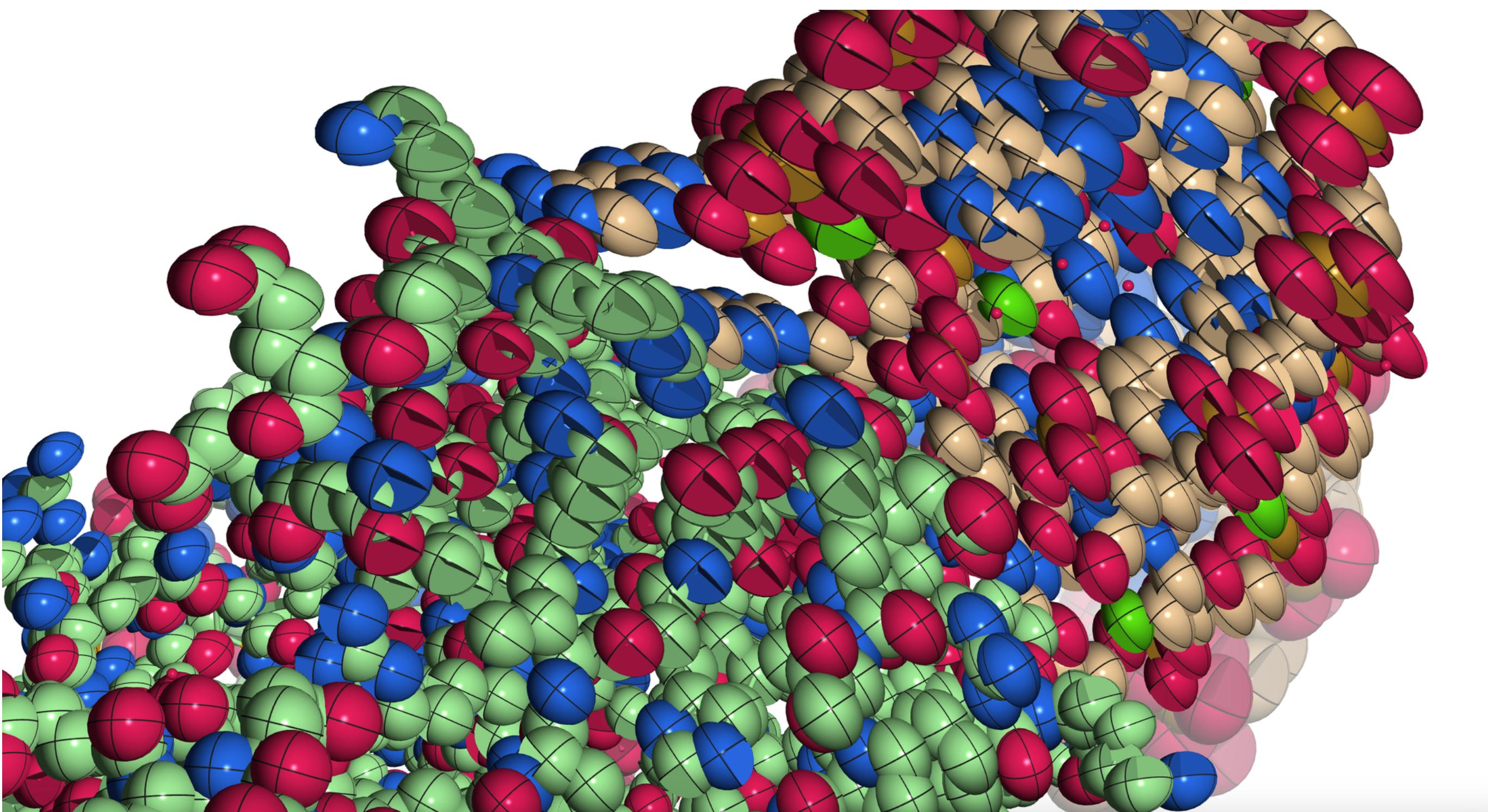












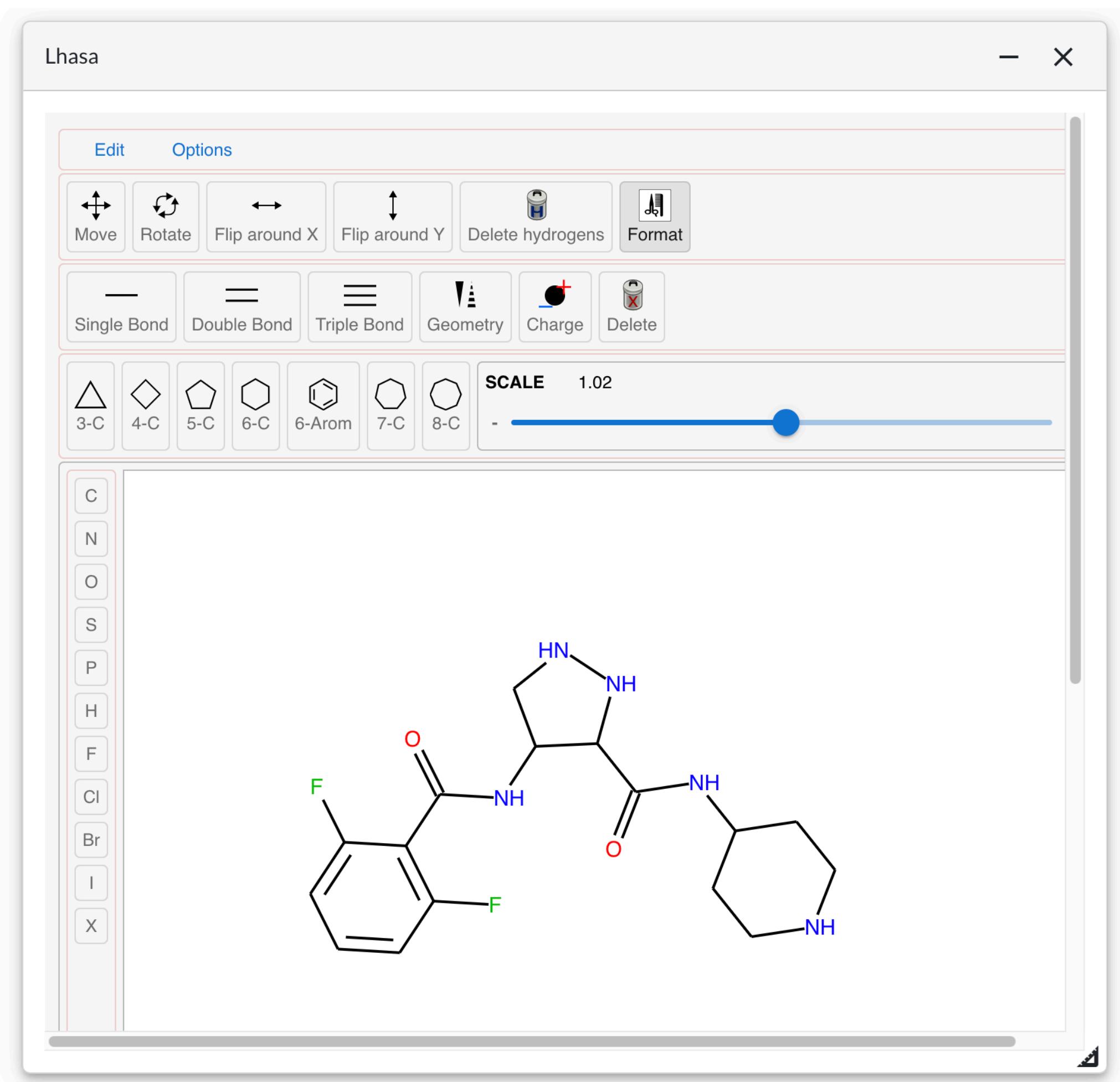
Moorhen - Ligand tools

Jakub
Smulski



GΦL

Global Phasing Limited



Lhasa
Ligand Builder

Moorhen - Ligand tools

Jakub
Smulski



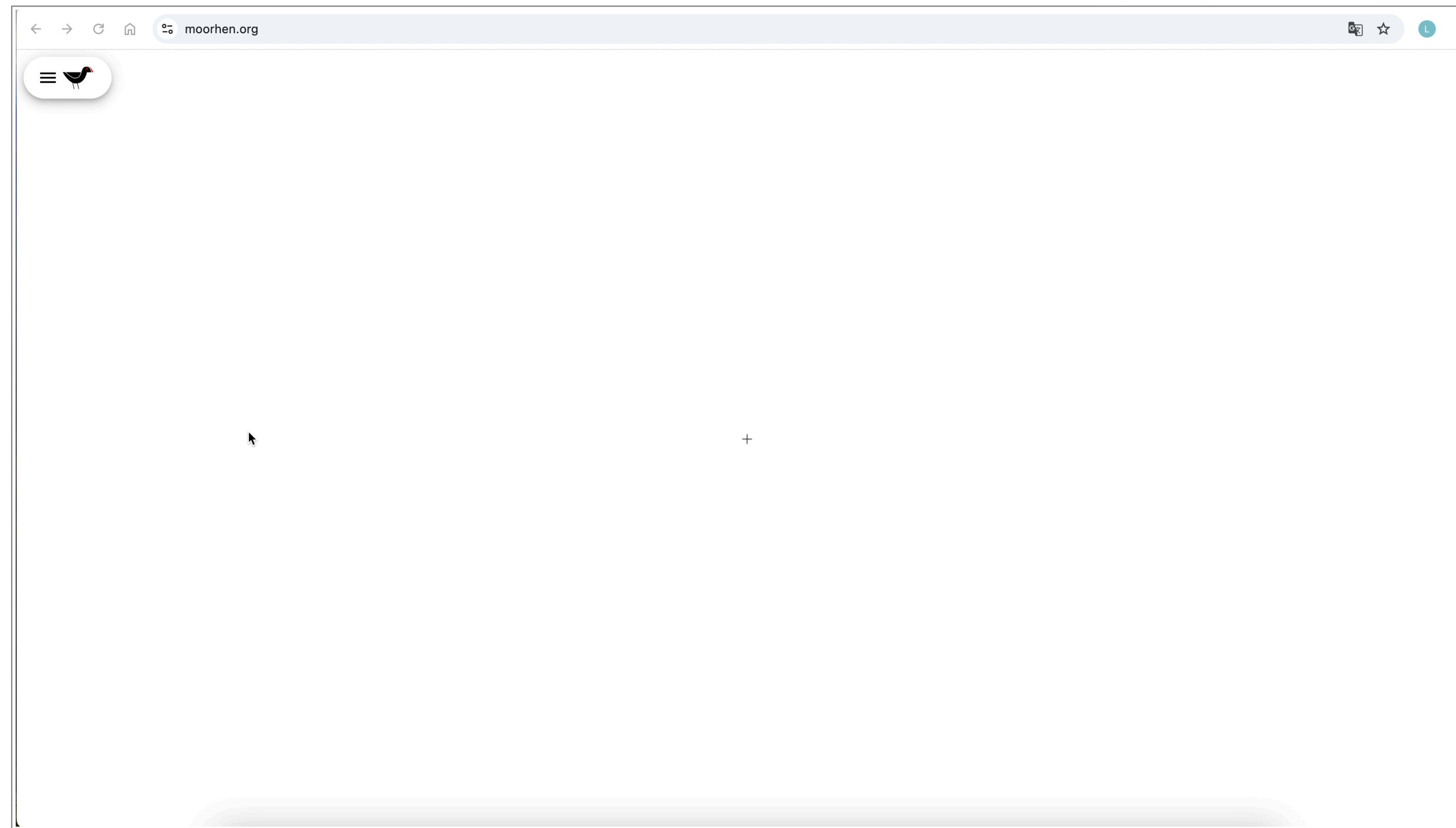
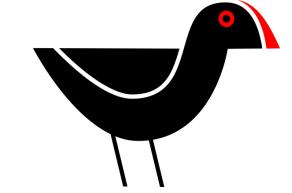
GΦL

Global Phasing Limited

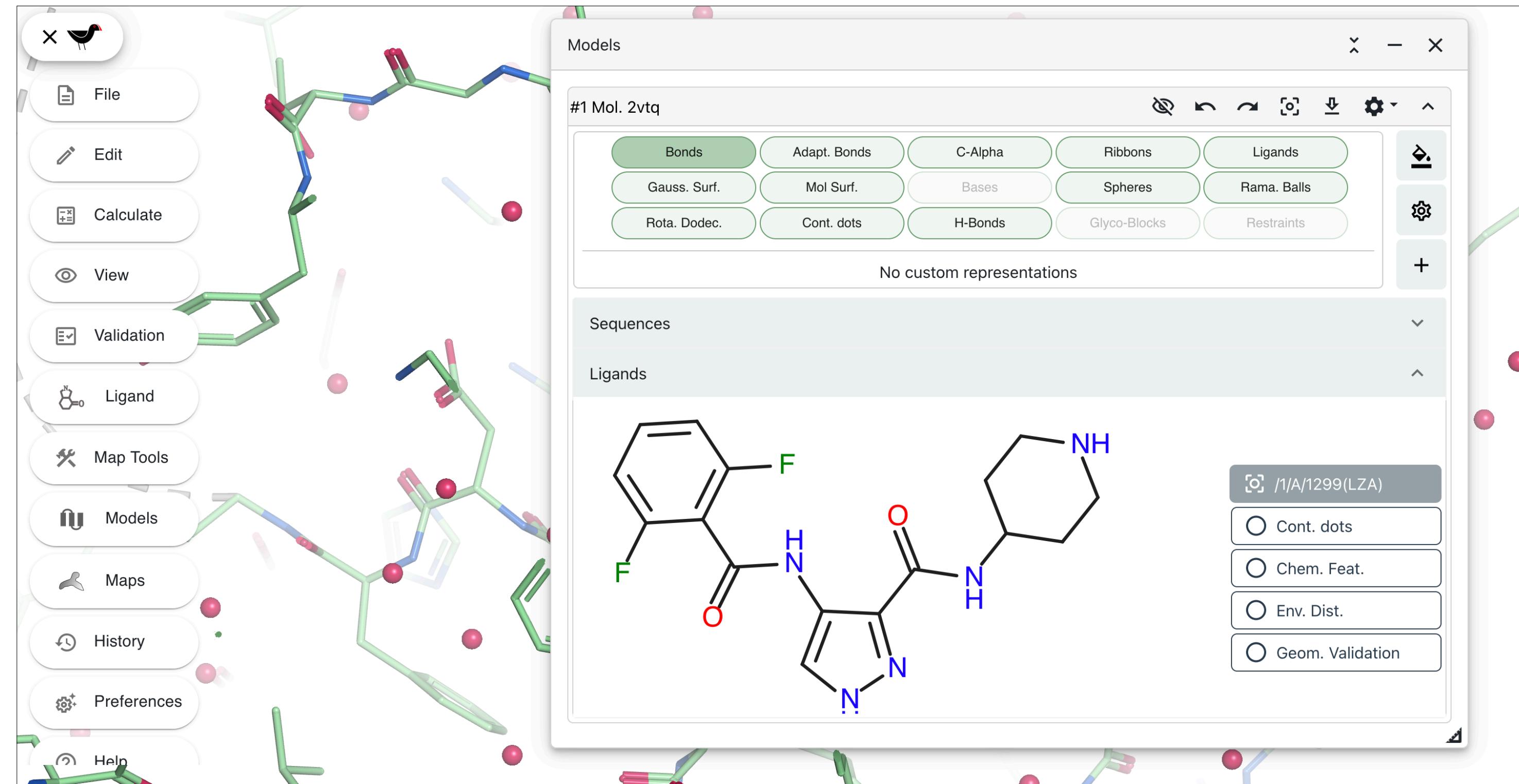
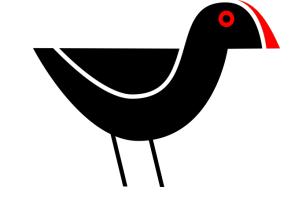
The screenshot shows the Lhasa software interface with a modal dialog box titled "CIF generation via Bansu". The dialog contains a warning message about the security implications of using a non-local instance of Bansu. It includes a checkbox for agreeing to proceed and two buttons: "Cancel" and "Spawn Bansu job". Below the dialog, there is a "SMILES" input field containing the text "O=C(NC1CCNCC1)c1r" and a "Send to Moorhen" button. The main interface features a toolbar with various chemical bond icons and a "SCALE 1.00" slider.

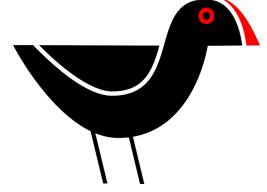
Bansu
cif generation via
AceDRG

Moorhen - Ligand fitting



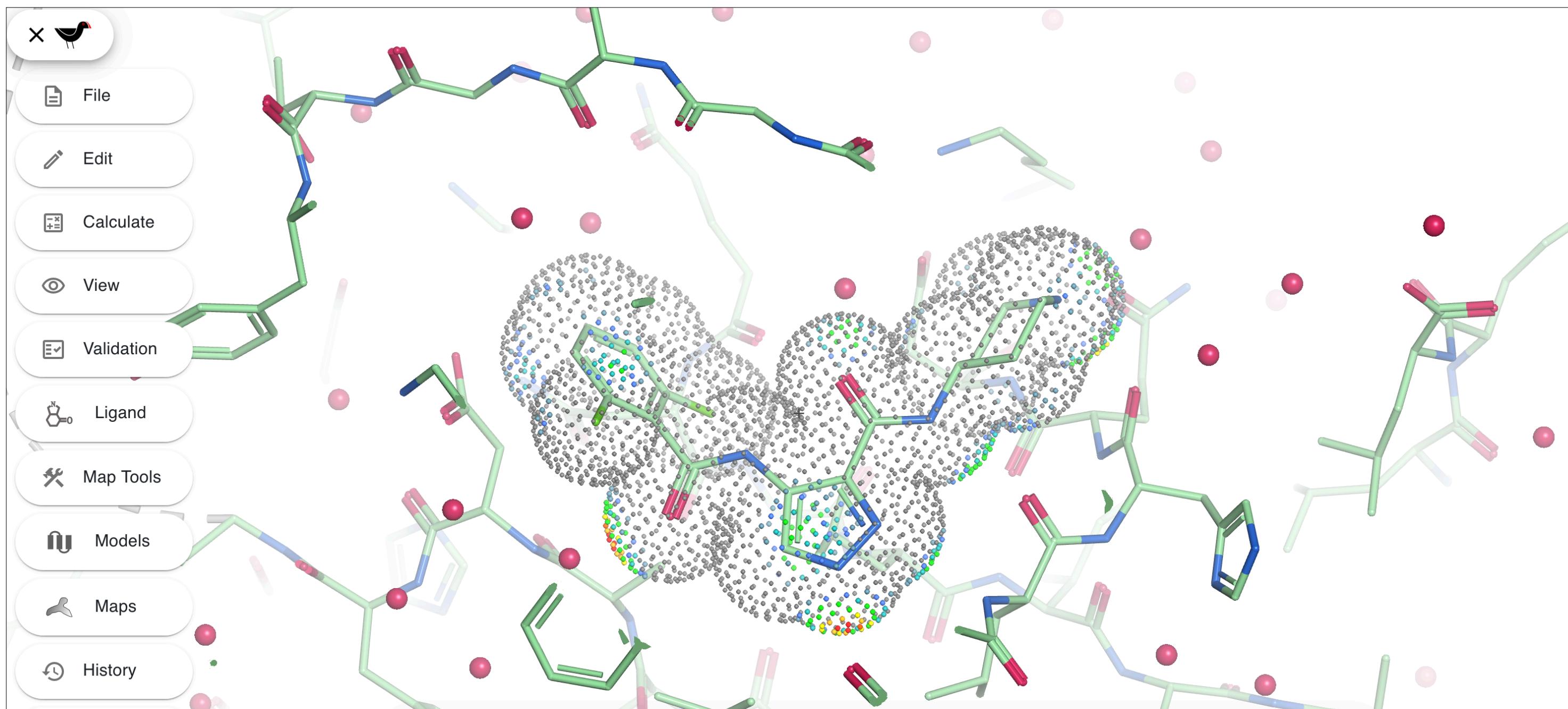
Moorhen – Ligand validation



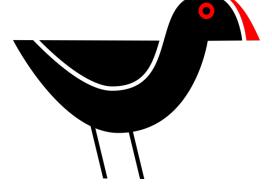


Moorhen - Ligand validation

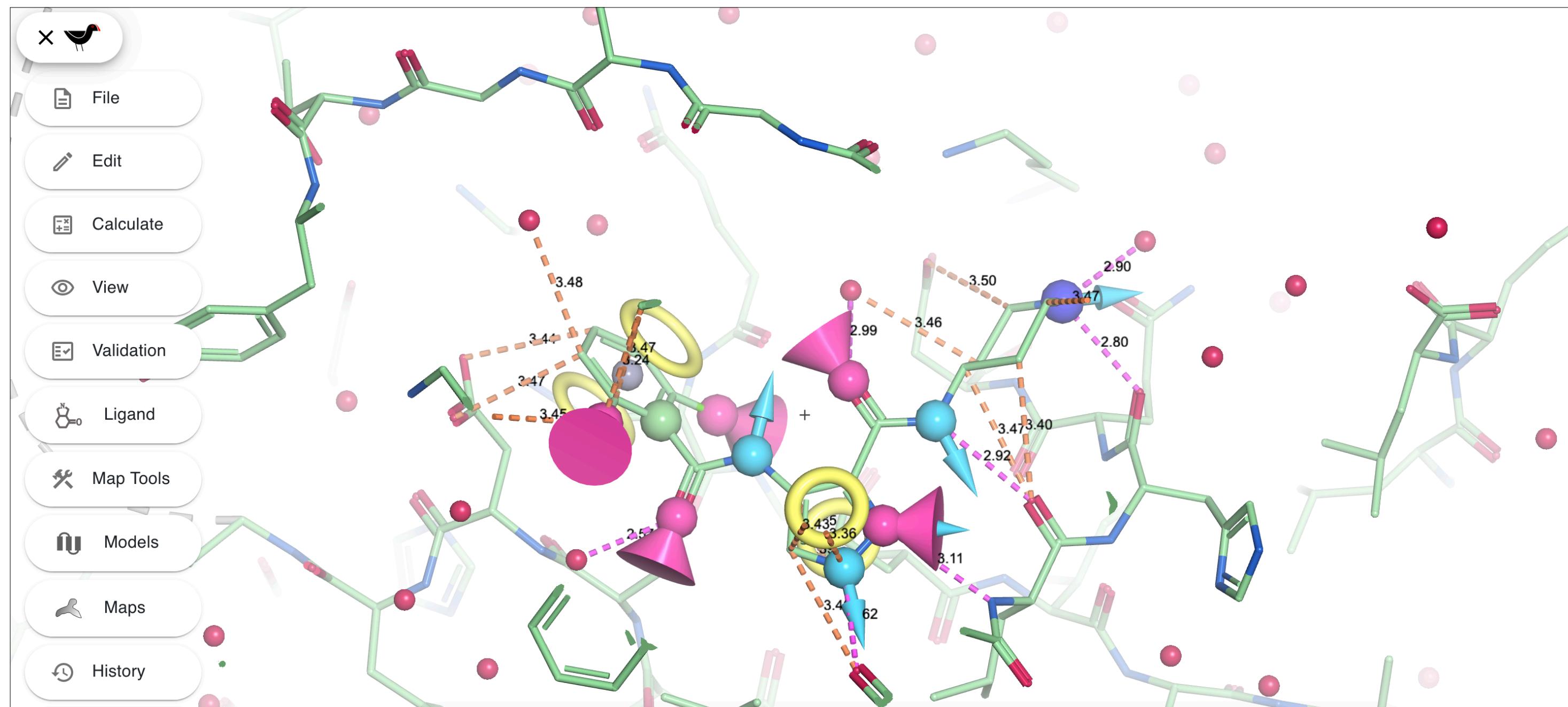
Contact dots

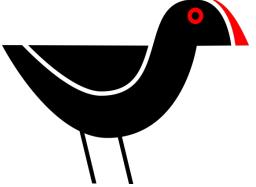


Moorhen - Ligand validation



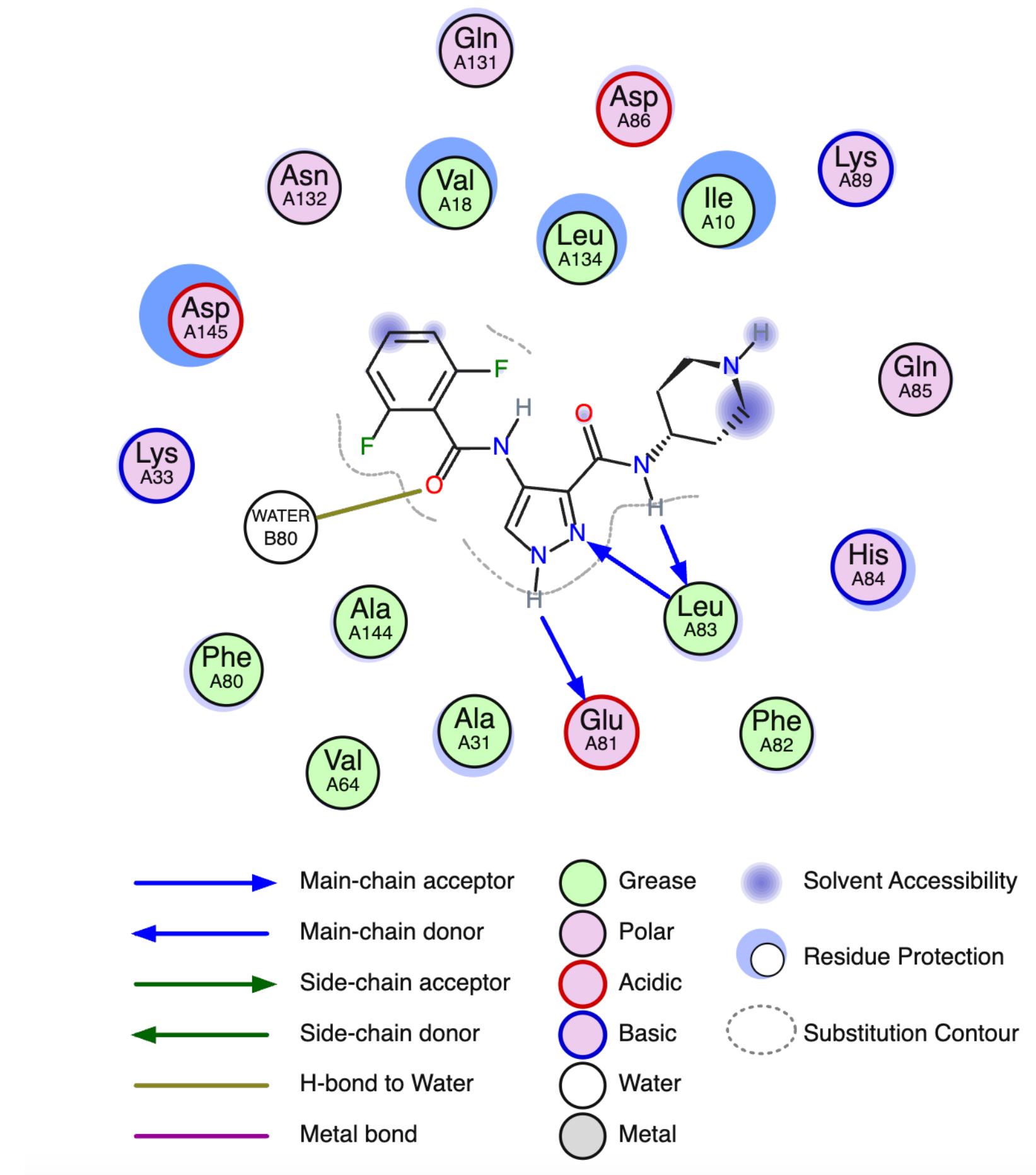
Chemical features & environment distances



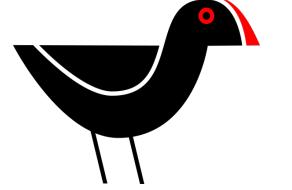


Moorhen - Ligand validation

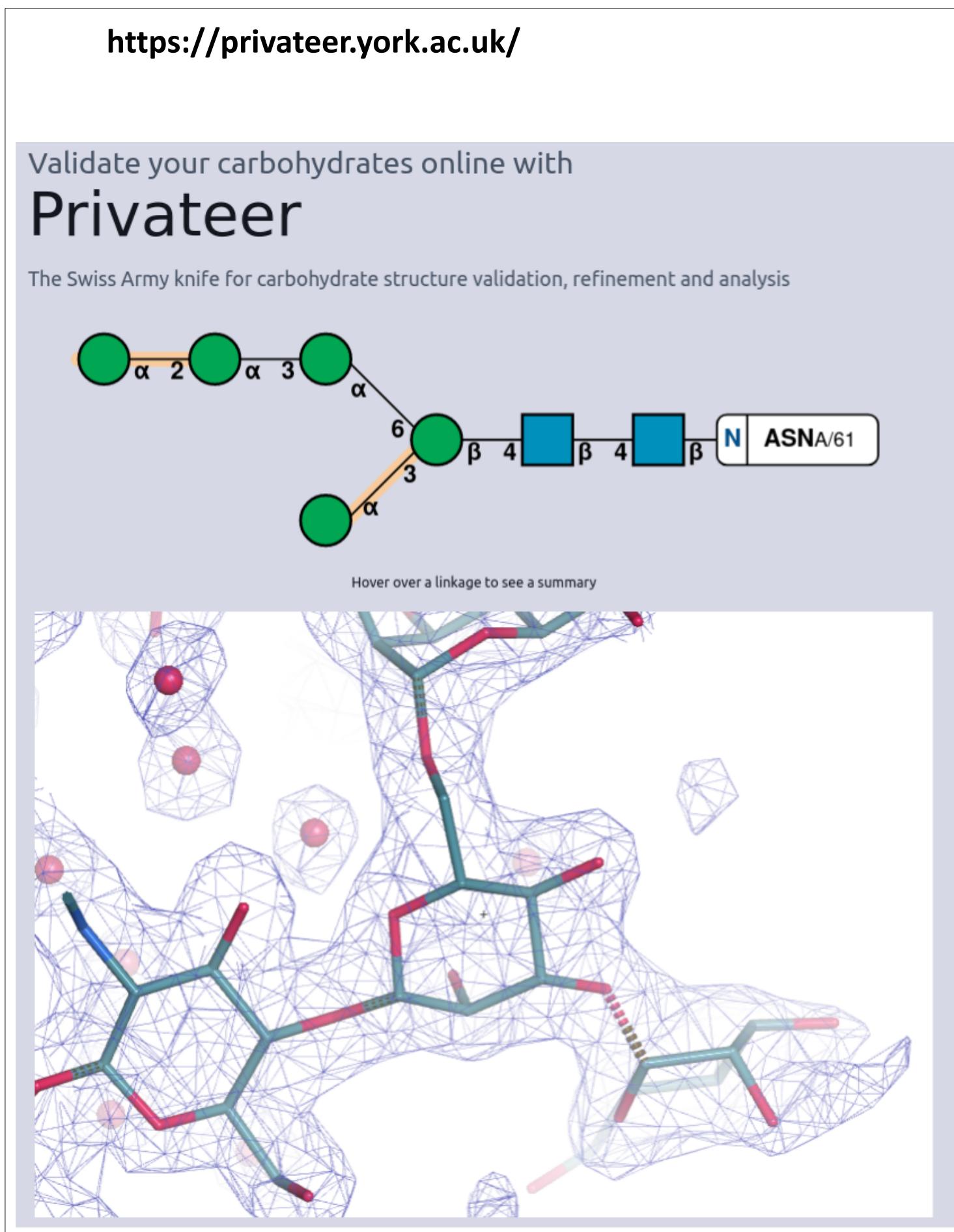
2D environment view



Moorhen as a React component



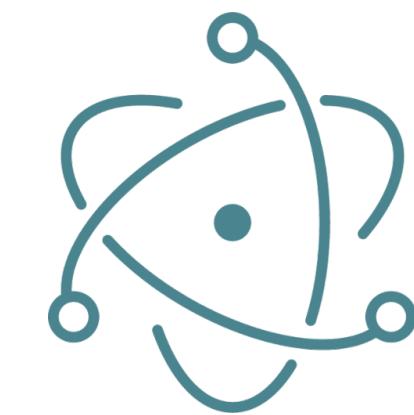
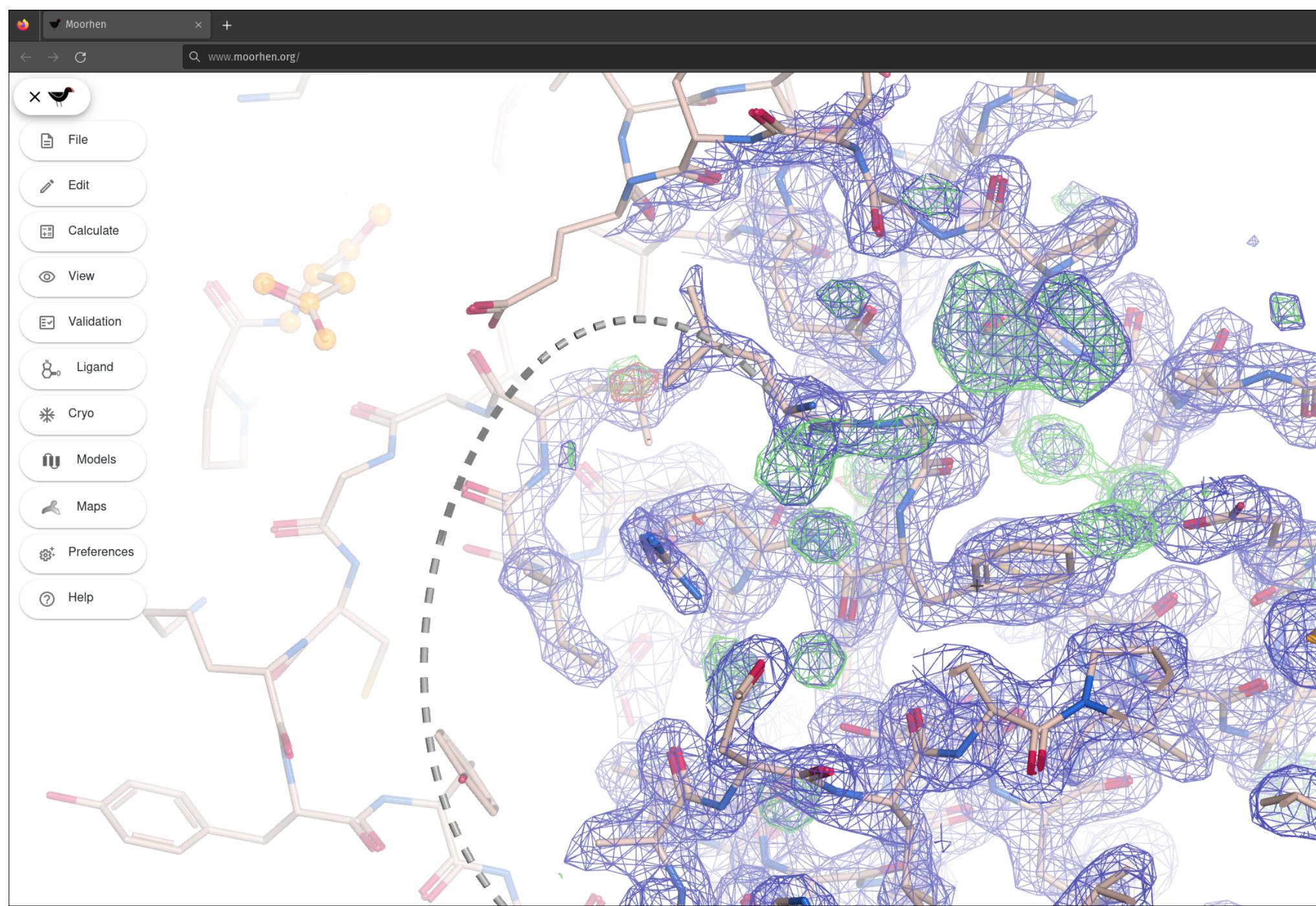
→ Moorhen can be easily integrated to any other website to extends its



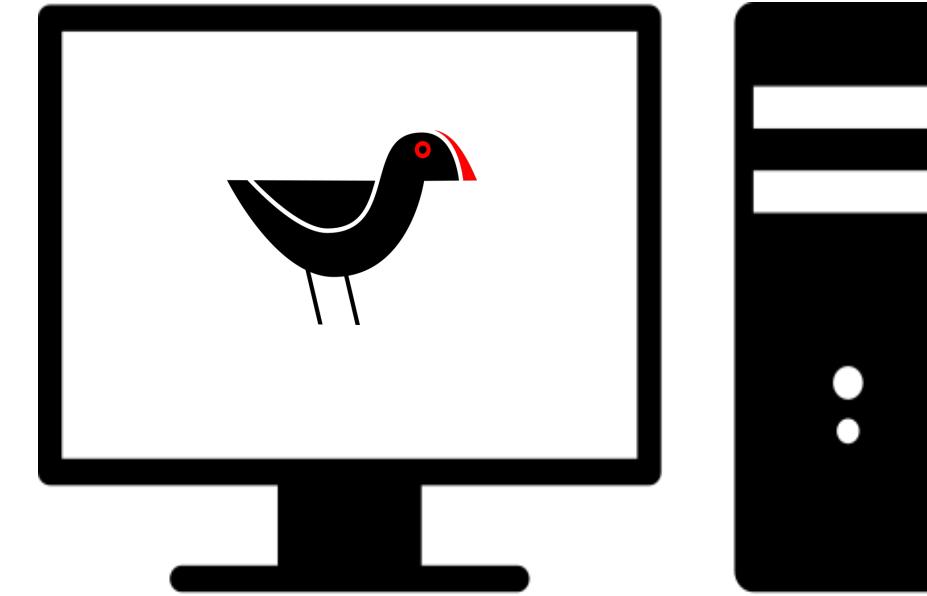
Dialpuri J. et al., (2024). Online carbohydrate 3D structure validation with the Privateer web app. (2024). *Acta Cryst. F* **80**, 30–35

Where is Moorhen available?

www.moorhen.org



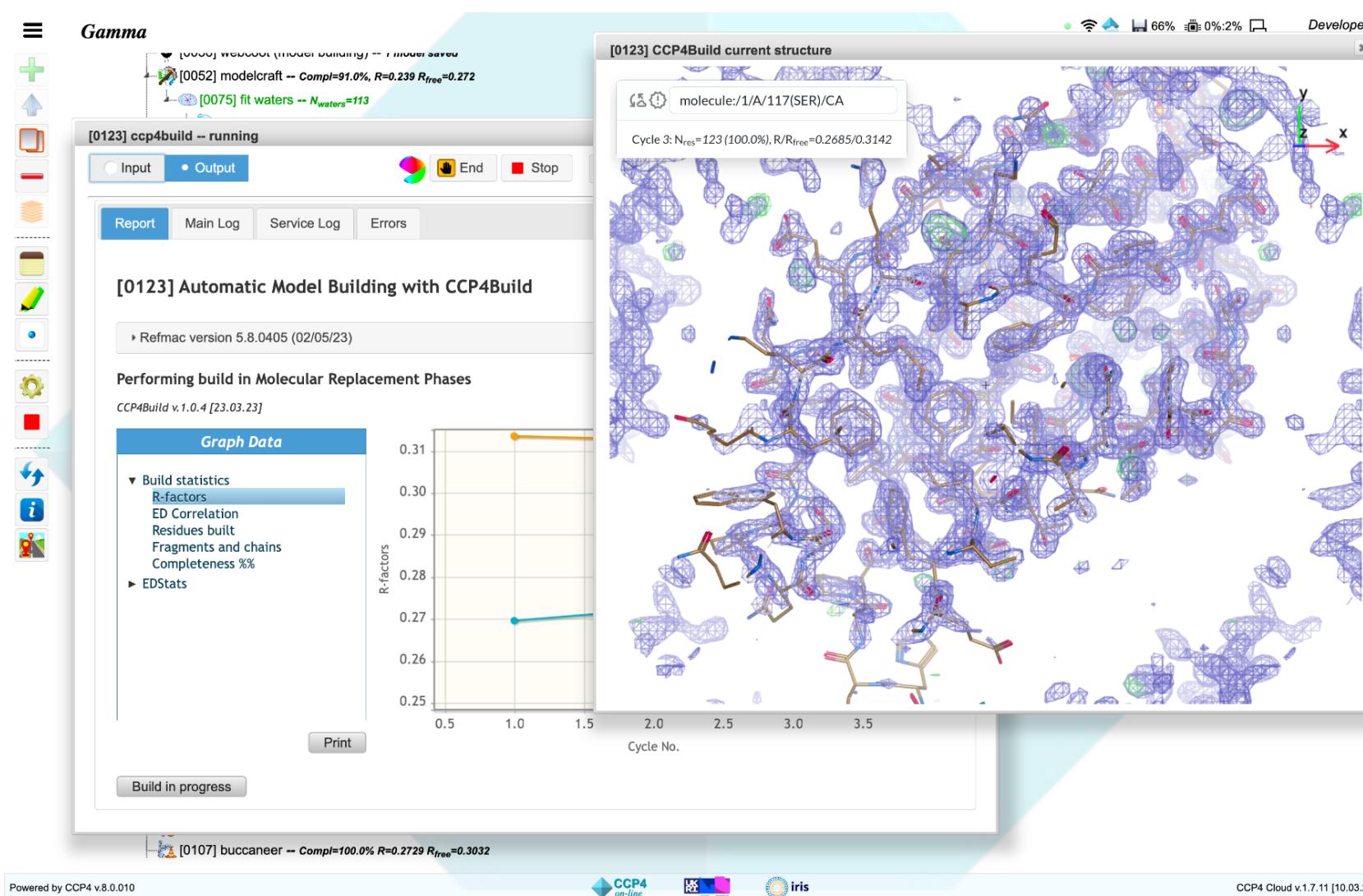
Electron



Where is Moorhen available?



CCP4
Cloud



The screenshot shows the CCP-EM interface with a 'Project: ~/ccpem-project' tab. It displays a list of jobs: '7 - Fetch - coot-em-tutorial' and '6 - Fetch - occupy-16890'. Below the list, there are sections for 'RESULTS', 'LOGS', 'I/O', and 'PARAMS'. Under 'I/O', there are buttons for PDF VIEWER, TEXT EDITOR, UGLYMOL, MOL*, MOORHEN, and TERMINAL. Inputs and outputs for the selected job are also listed.

GitHub

<https://github.com/moorhen-coot/Moorhen>

Moorhen

[npm package 0.8.5](#) [Nightly tests failing](#) [Deploy moorhen.org passing](#) [Dev docs passing](#) [Wiki passing](#)

Moorhen is a web browser molecular graphics program based on the Coot desktop program. It is developed by porting some [CCP4](#) libraries and programs, [Coot](#), [FFTW2](#), [Privateer](#) and the [Gnu Scientific Library](#) to Web Assembly.

The emscripten suite of tools is required to do the compilation.

The sources of CCP4, Coot, Privateer, FFTW, and GSL are not included. They are downloaded and (possibly) patched by the running the `get_sources` script, which is part of the build process of this project.

The following libraries/programs are compiled to Web Assembly:

- libccp4 (8.0.0)
- clipper (20240123)
- ssm (1.4.0)
- mmdb2 (2.0.22)
- gemmi 0.6.4
- Coot 1.0 ('gtk3' git branch)
- fftw 2.1.5
- gsl 2.7.1
- Boost 1.83.0
- glm 0.9.9.8
- RDKit 2023_09_1

Moorhen is available to use at <https://moorhen.org>.

<https://moorhen-coot.github.io/wiki/>

Moorhen Wiki

About

Posts

Jul 8, 2025 [Embedding Moorhen in React, NextJS and Electron](#)

Feb 3, 2025 [Moorhen Gallery](#)

Sep 3, 2024 [Moorhen Tutorial 1: Fix up the Cyclin-Dependent Kinase](#)

May 20, 2024 [Moorhen Cryo-EM Tutorial: Fitting the Nanobody](#)

Nov 3, 2023 [Creating Figures with Moorhen](#)

Nov 2, 2023 [Fetch data from Moorhen in your React app](#)

Jul 6, 2023 [Using Moorhen in a react app](#)

Mar 22, 2023 [What is Moorhen?](#)

Moorhen mailing list:



<https://groups.google.com/a/york.ac.uk/g/moorhen-group>

Acknowledgements

Filo
Sanchez



**Paul
Emsley**



Jakub
Smulski



Martin
Noble



Stuart
McNicholas



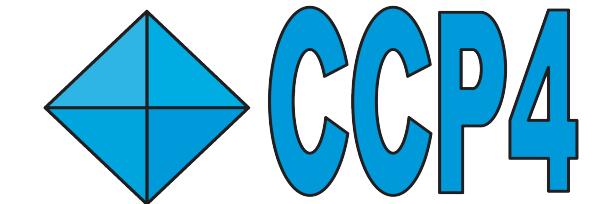
Clement
Degut



Bernard
Lohkamp



MRC Laboratory
of Molecular
Biology



GΦL

Global Phasing Limited

lucrezia@mrc-lmb.cam.ac.uk

... And everyone who has contributed to CCP4

CCP4 Study Weekend 2026

Ligands in Focus: Decoding Ligand Binding in
Modern Structural Biology

EMCC, Nottingham, UK & Virtual

7th - 9th January 2026

<https://studyweekend ccp4.ac.uk/>