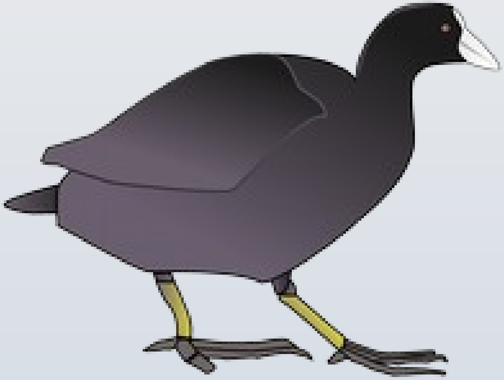


Coot Tools for Cryo-EM

Paul Emsley
MRC Laboratory of Molecular Biology

October 2018

Outline

- New Tools for Cryo-EM reconstructions
- Context (experiments)
- Large-scale movement (morph and jiggle)
- Alpha Helix fitting
- Restraints
- Refinement
- Back-rub Rotamers
- cis-peptides
- Filaments
- New visualizations

Coot & Cryo-EM Model-building

- Coot was originally designed to build and edit protein molecule using x-ray data
  - interactive model-building tool
  - refinement and validation built in
  - and became more sophisticated over the years
- Typically, we need to move more atoms that one does for crystallography
- the maps are lower resolution and the starting model is further from where you want them to be – usually systematically so
- addressing these needs has been the focus of my work extending/changing *Coot* for cryo-EM

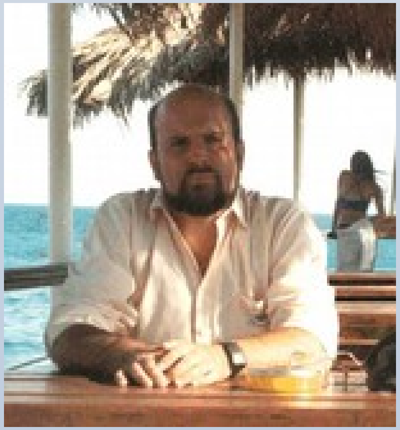
Acknowledgements, Collaborators

Martin
Noble

Alexei
Vagin

Bernhard
Lohkamp

Kevin
Cowtan



Eugene
Krissinel

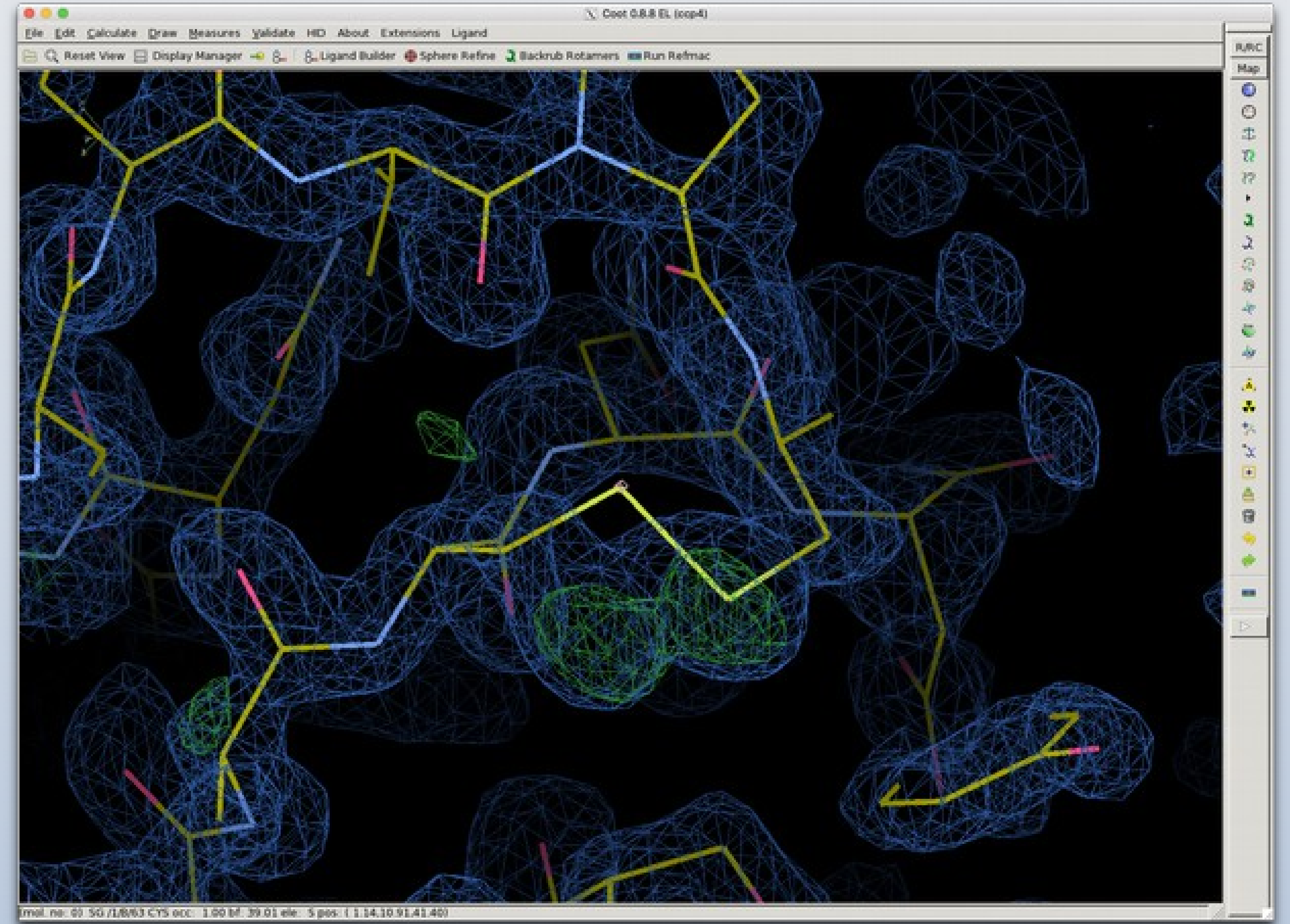
Stuart
McNicholas

+ Rob Nicholls
Richardsons, Duke

But Why Bother?

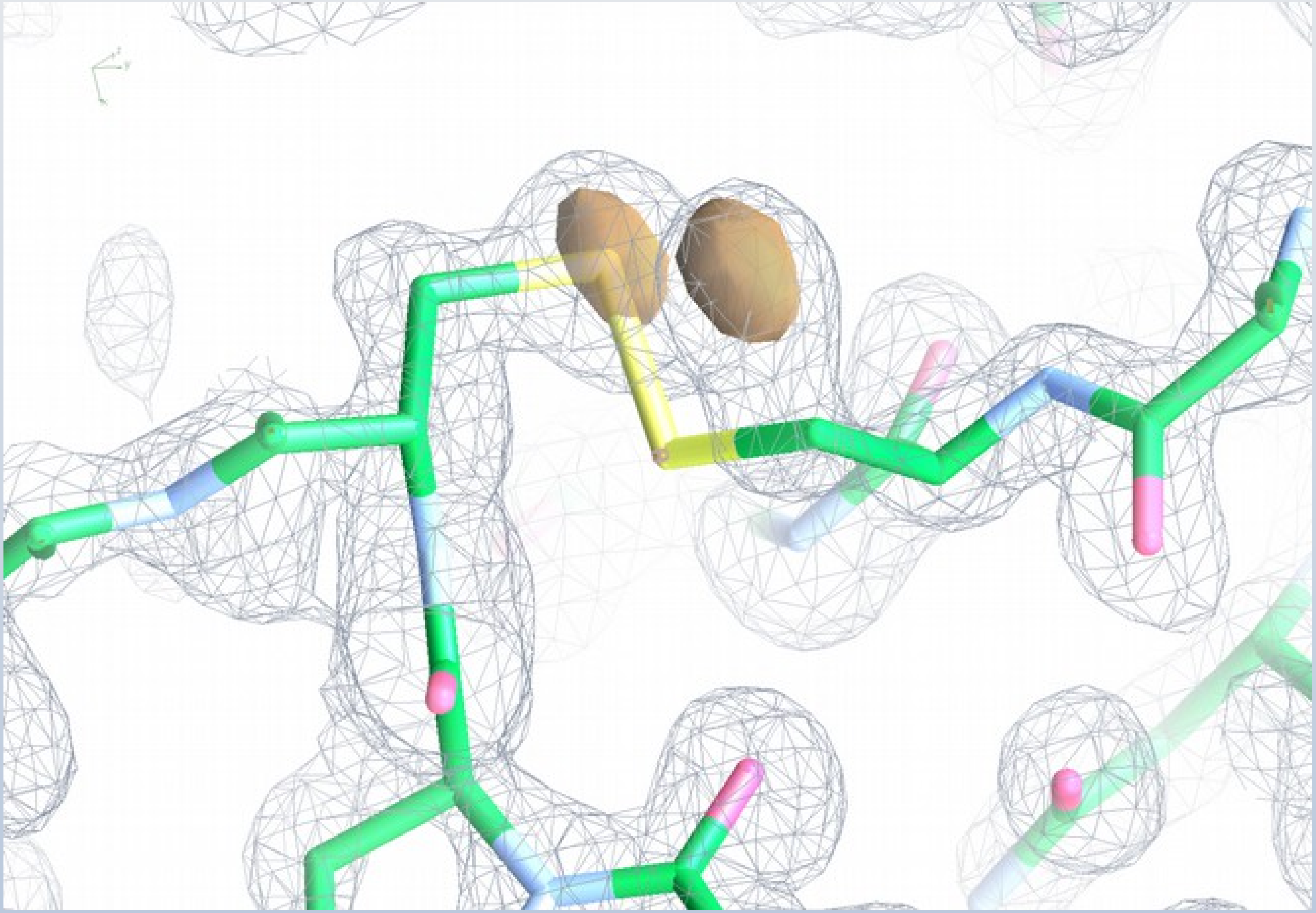
- Automated model-building for complete models is still impossible
  - It takes a brain to validate
- Concerted correction/improvement of a model is difficult on the larger scale

Fixing what auto-building doesn't get right

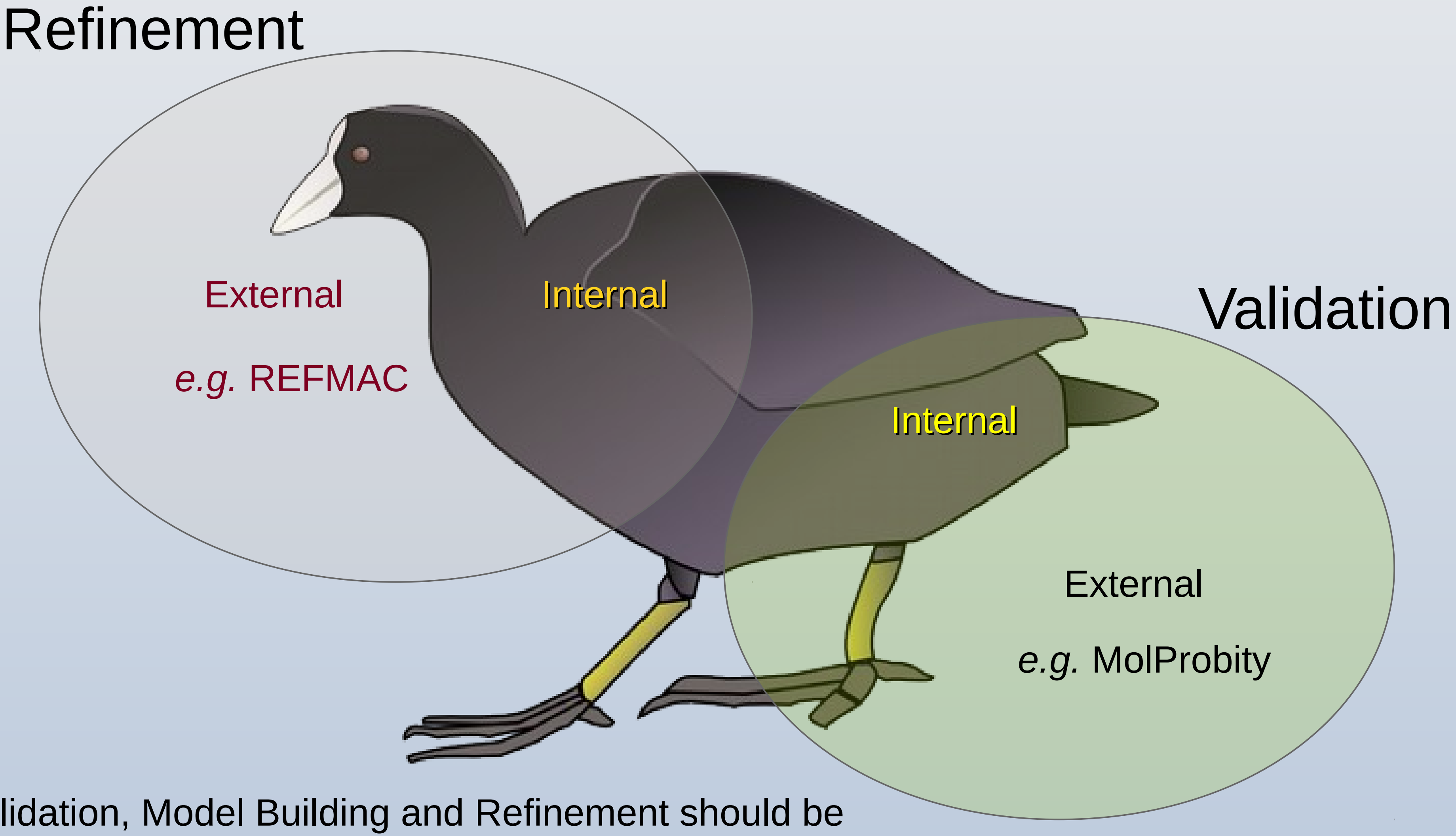


```
(mol. no: 0) SG /1/B/63 CYS occ: 1.00 bf: 39.01 ele: S pos: ( 1.14,10.91,41.40)
```

Fixing what auto-building doesn't get right



Feature Integration



Refinement

External

e.g. REFMAC

Internal

Validation

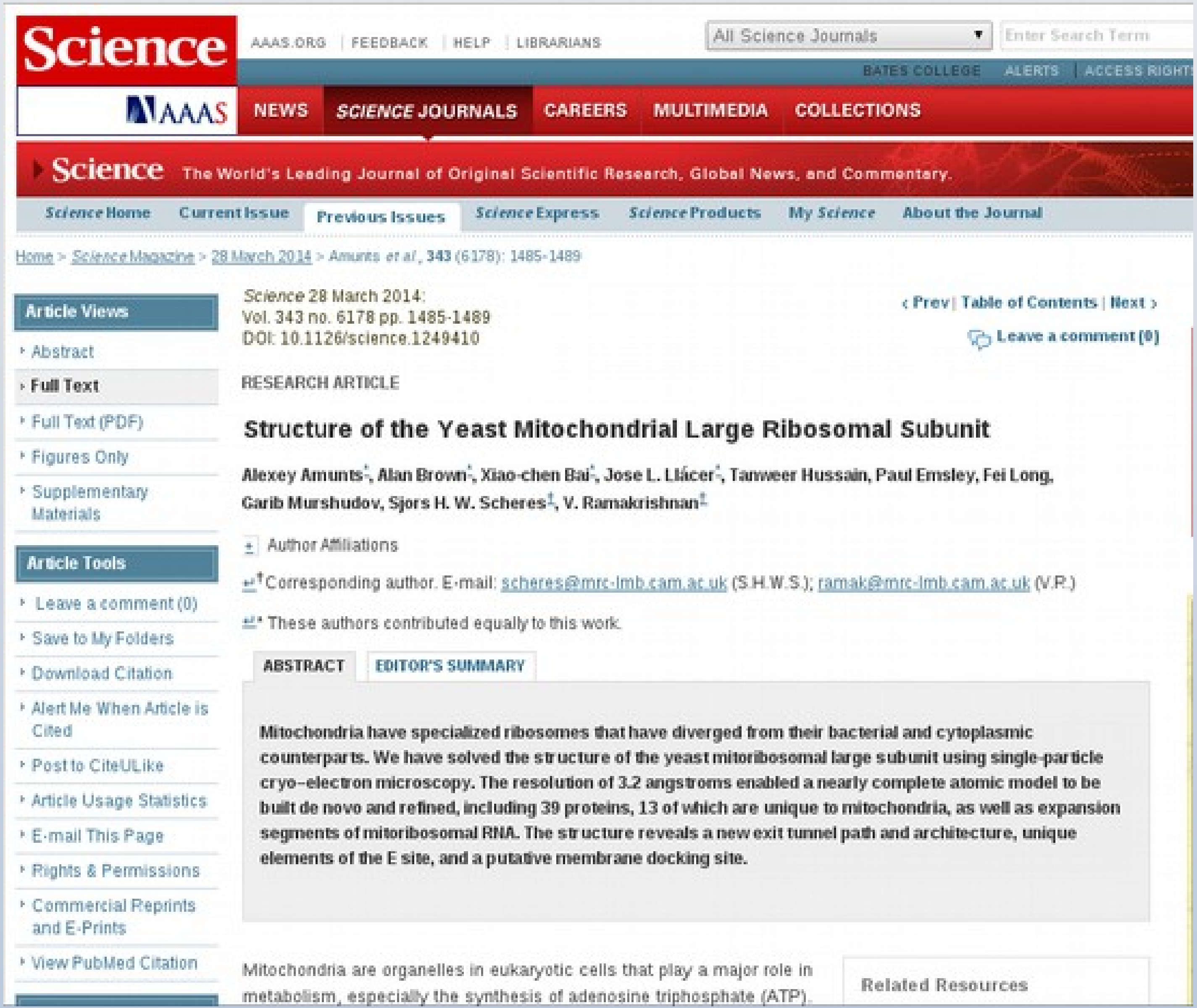
Internal

External

e.g. MolProbity

Validation, Model Building and Refinement should be used together

Yeast Mitochondrial Large Ribosomal Subunit



Science 28 March 2014:
Vol. 343 no. 6178 pp. 1485-1489
DOI: 10.1126/science.1249410

RESEARCH ARTICLE

Structure of the Yeast Mitochondrial Large Ribosomal Subunit

Alexey Amunts*, Alan Brown*, Xiao-chen Bai*, Jose L. Llácer*, Tanweer Hussain, Paul Emsley, Fei Long, Garib Murshudov, Sjors H. W. Scheres†, V. Ramakrishnan†

± Author Affiliations

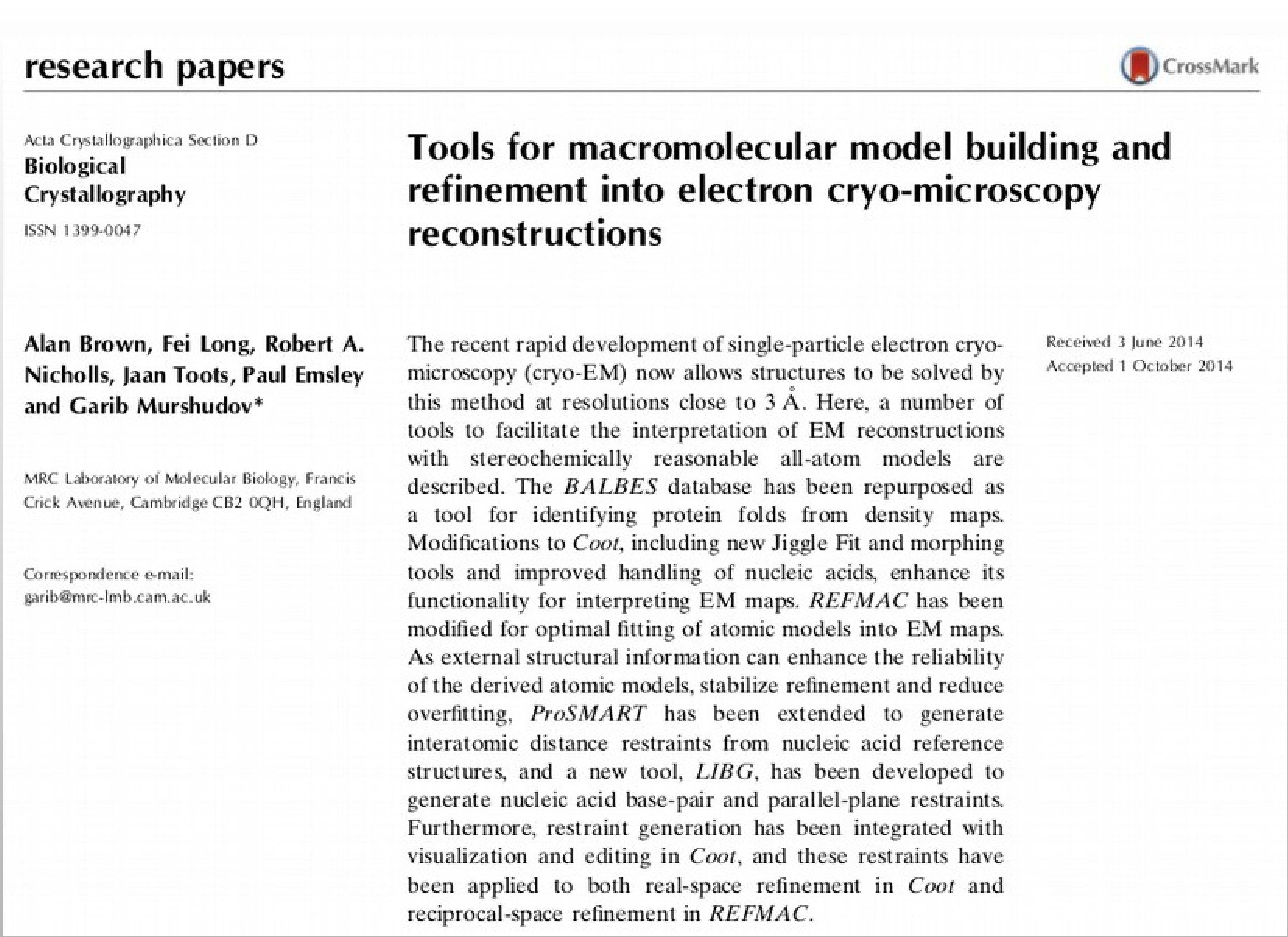
†Corresponding author. E-mail: scheres@mrc-lmb.cam.ac.uk (S.H.W.S.); ramak@mrc-lmb.cam.ac.uk (V.R.)

* These authors contributed equally to this work.

ABSTRACT | EDITOR'S SUMMARY

Mitochondria have specialized ribosomes that have diverged from their bacterial and cytoplasmic counterparts. We have solved the structure of the yeast mitoribosomal large subunit using single-particle cryo–electron microscopy. The resolution of 3.2 angstroms enabled a nearly complete atomic model to be built de novo and refined, including 39 proteins, 13 of which are unique to mitochondria, as well as expansion segments of mitoribosomal RNA. The structure reveals a new exit tunnel path and architecture, unique elements of the E site, and a putative membrane docking site.

Mitochondria are organelles in eukaryotic cells that play a major role in metabolism, especially the synthesis of adenosine triphosphate (ATP).



research papers

CrossMark

Acta Crystallographica Section D
Biological Crystallography
ISSN 1399-0047

Tools for macromolecular model building and refinement into electron cryo-microscopy reconstructions

Alan Brown, Fei Long, Robert A. Nicholls, Jaan Toots, Paul Emsley and Garib Murshudov*

MRC Laboratory of Molecular Biology, Francis Crick Avenue, Cambridge CB2 0QH, England

Correspondence e-mail:
garib@mrc-lmb.cam.ac.uk

Received 3 June 2014
Accepted 1 October 2014

The recent rapid development of single-particle electron cryo-microscopy (cryo-EM) now allows structures to be solved by this method at resolutions close to 3 Å. Here, a number of tools to facilitate the interpretation of EM reconstructions with stereochemically reasonable all-atom models are described. The *BALBES* database has been repurposed as a tool for identifying protein folds from density maps. Modifications to *Coot*, including new Jiggle Fit and morphing tools and improved handling of nucleic acids, enhance its functionality for interpreting EM maps. *REFMAC* has been modified for optimal fitting of atomic models into EM maps. As external structural information can enhance the reliability of the derived atomic models, stabilize refinement and reduce overfitting, *ProSMART* has been extended to generate interatomic distance restraints from nucleic acid reference structures, and a new tool, *LIBG*, has been developed to generate nucleic acid base-pair and parallel-plane restraints. Furthermore, restraint generation has been integrated with visualization and editing in *Coot*, and these restraints have been applied to both real-space refinement in *Coot* and reciprocal-space refinement in *REFMAC*.

Science

REPORTS

Cite as: A. Casañal *et al.*, *Science*
10.1126/science.aao6535 (2017).

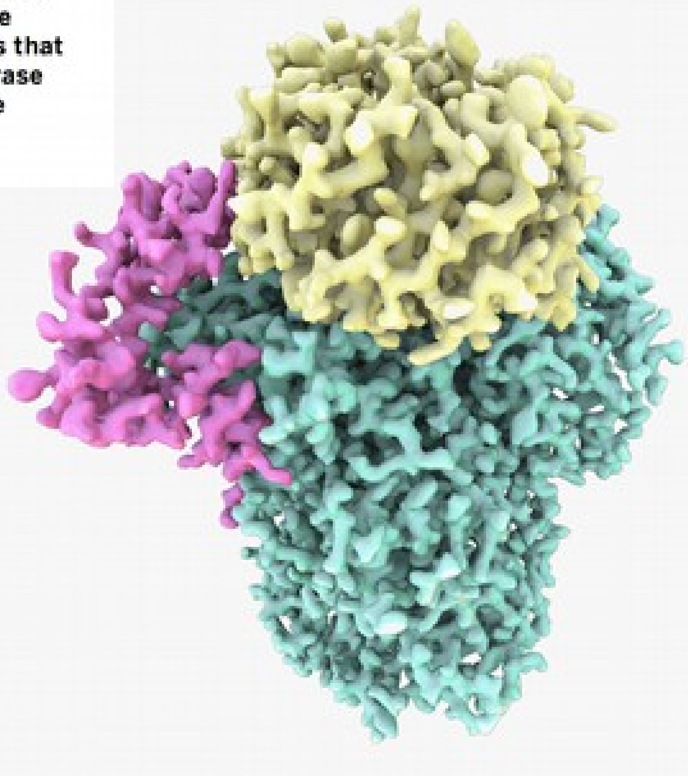
Architecture of eukaryotic mRNA 3′-end processing machinery

Ana Casañal,[1]* Ananthanarayanan Kumar,[1]* Chris H. Hill,[1] Ashley D. Easter,[1] Paul Emsley,[1] Gianluca Degliesposti,[1] Yuliya Gordiyenko,[1,2] Balaji Santhanam,[1] Jana Wolf,[1] Katrin Wiederhold,[1] Gillian L. Dornan,[1] Mark Skehel,[1] Carol V. Robinson,[2] Lori A. Passmore[1]†

[1]MRC Laboratory of Molecular Biology, Cambridge UK. [2]Chemistry Research Laboratory, University of Oxford, Oxford, UK.

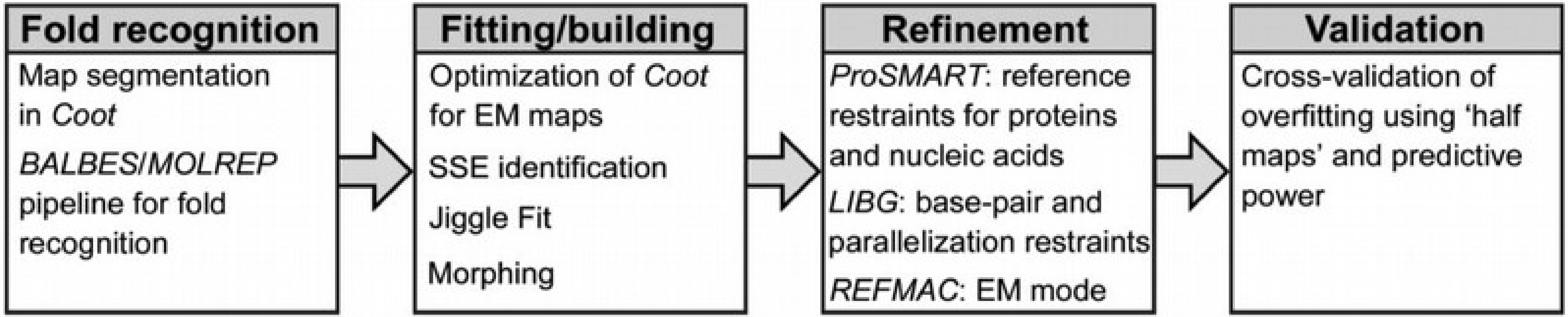
***These authors contributed equally to this work. †Corresponding author. Email: passmore@mrc-lmb.cam.ac.uk**

Newly transcribed eukaryotic pre-mRNAs are processed at their 3′-ends by the ~1 MDa multiprotein cleavage and polyadenylation factor (CPF). CPF cleaves pre-mRNAs, adds a poly(A) tail and triggers transcription termination but it is unclear how its different enzymes are coordinated and assembled. Here, we show that the nuclease, polymerase and phosphatase activities of yeast CPF are organized into three modules. Using cryo-EM, we determine a 3.5 Å resolution structure of the ~200 kDa polymerase module. This reveals four beta propellers in an assembly strikingly similar to other protein complexes that bind nucleic acid. Combined with in vitro reconstitution experiments, our data show that the polymerase module brings together factors required for specific and efficient polyadenylation, to help coordinate mRNA 3′-end processing.



Model-Building Tools

Recent Developments



Fold recognition

Map segmentation in *Coot*

BALBES/*MOLREP* pipeline for fold recognition

Fitting/building

Optimization of *Coot* for EM maps

SSE identification

Jiggle Fit

Morphing

Refinement

ProSMART: reference restraints for proteins and nucleic acids

LIBG: base-pair and parallelization restraints

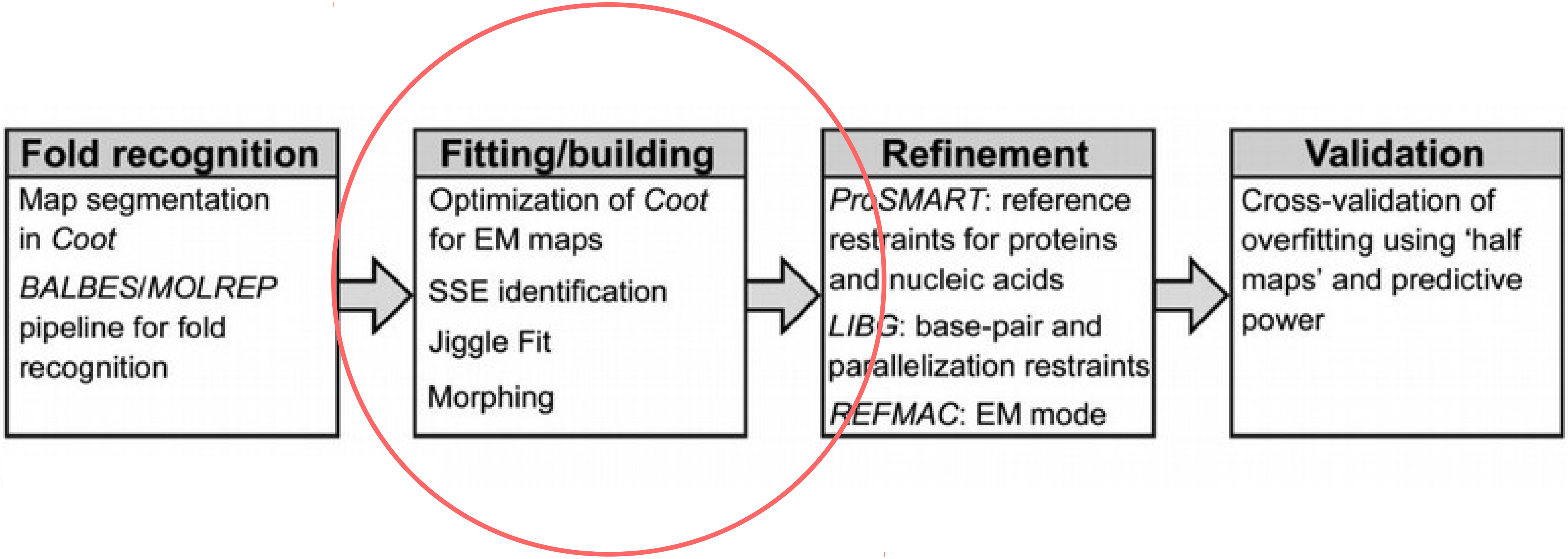
REFMAC: EM mode

Validation

Cross-validation of overfitting using ‘half maps’ and predictive power

Model-Building Tools

Recent Developments



Fold recognition

Map segmentation in *Coot*

BALBES/MOLREP pipeline for fold recognition

Fitting/building

Optimization of *Coot* for EM maps

SSE identification

Jiggle Fit

Morphing

Refinement

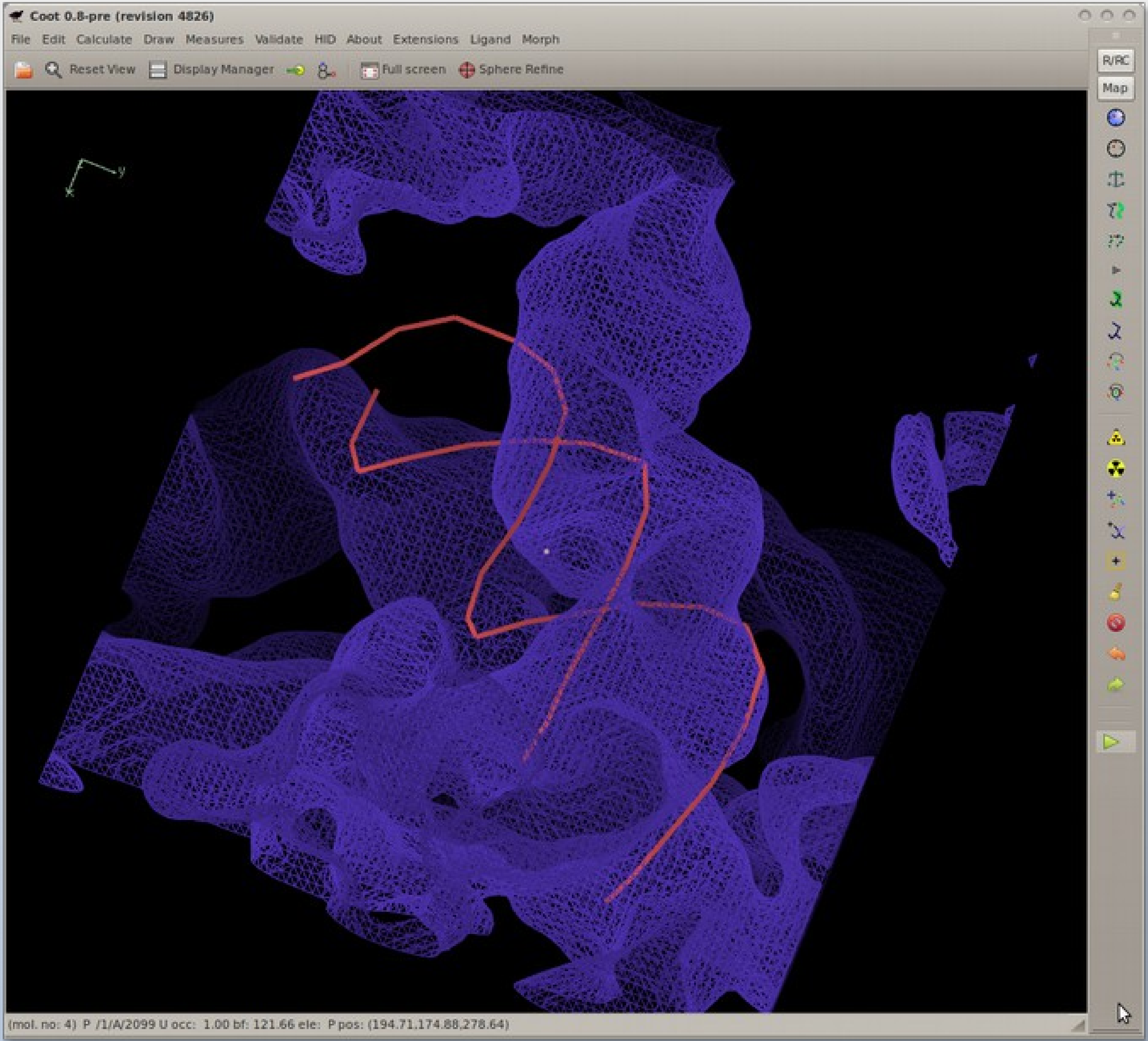
ProSMART: reference restraints for proteins and nucleic acids

LIBG: base-pair and parallelization restraints

REFMAC: EM mode

Validation

Cross-validation of overfitting using ‘half maps’ and predictive power



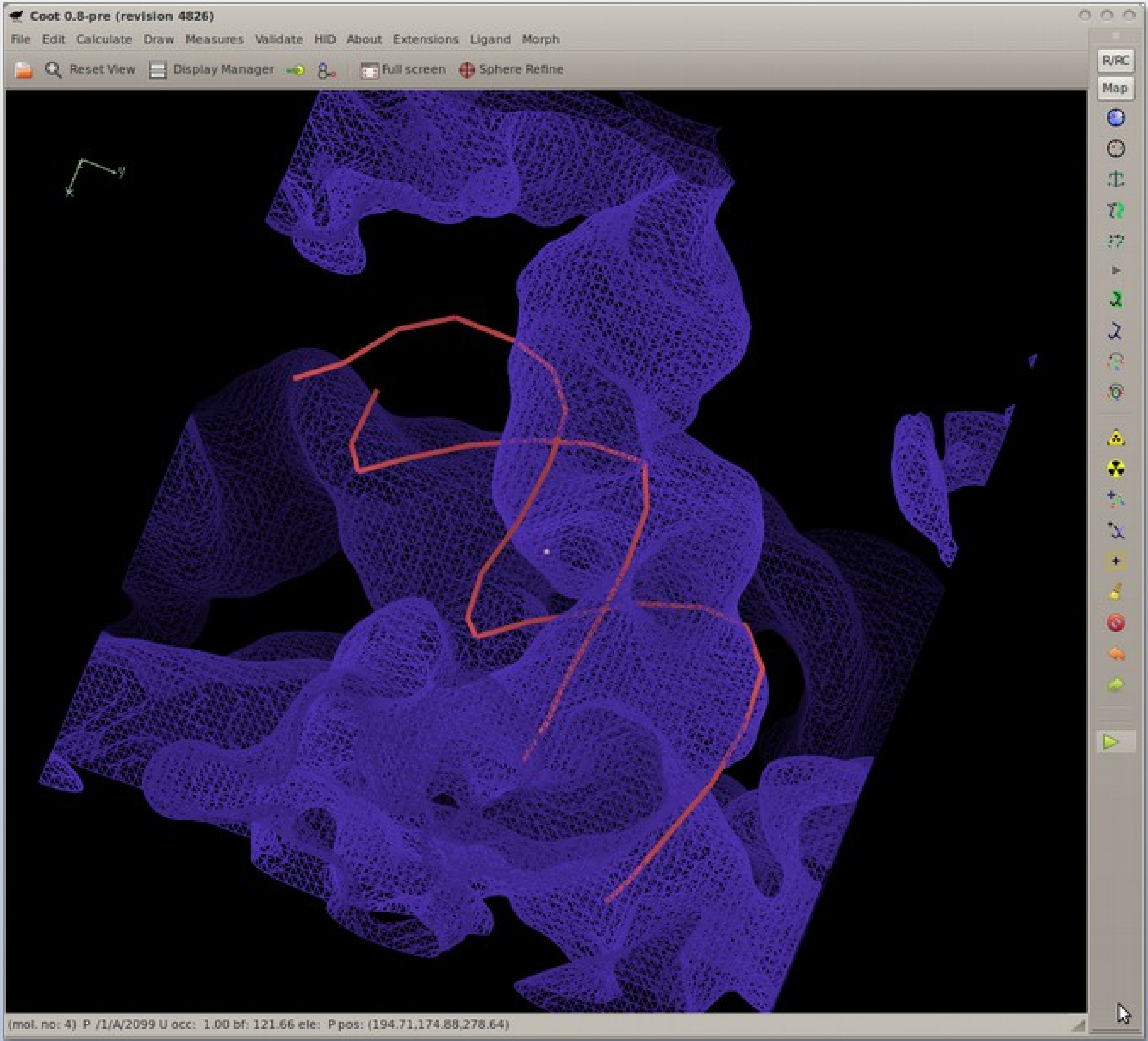
```
(mol. no: 4)  P  /1/A/2099 U occ:  1.00 bf: 121.66 ele:  P pos: (194.71,174.88,278.64)
```

Jiggle Fit

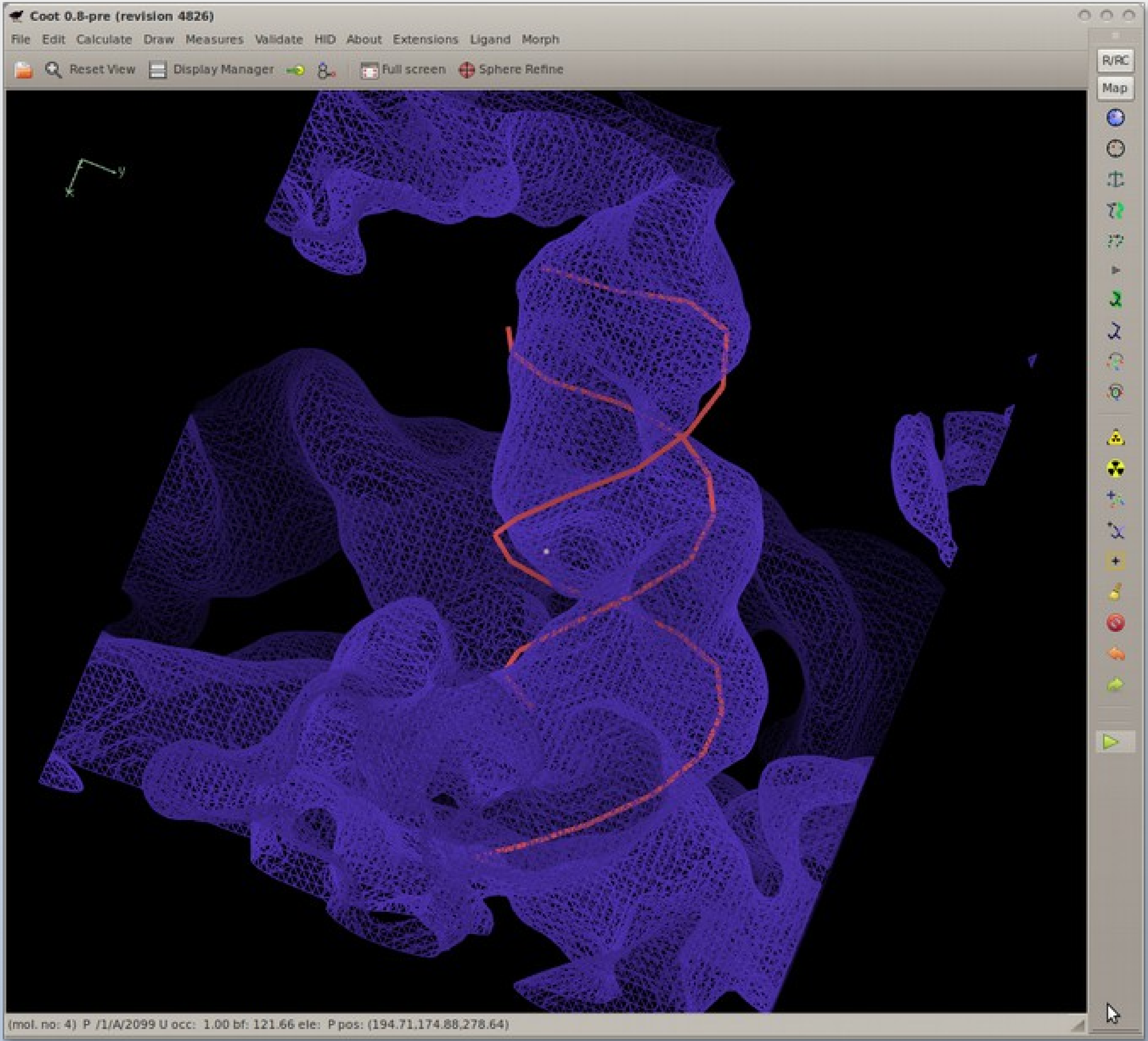
- How do I rotate and translate these atoms to fit the density?
  - 6-dimensional problem
- Originally used to fit simple ligands/solvent molecules to blobs of density
- Now extended to fit arbitrary atom selections
  - *e.g.* by Chain

Jiggle Fit: How it Works

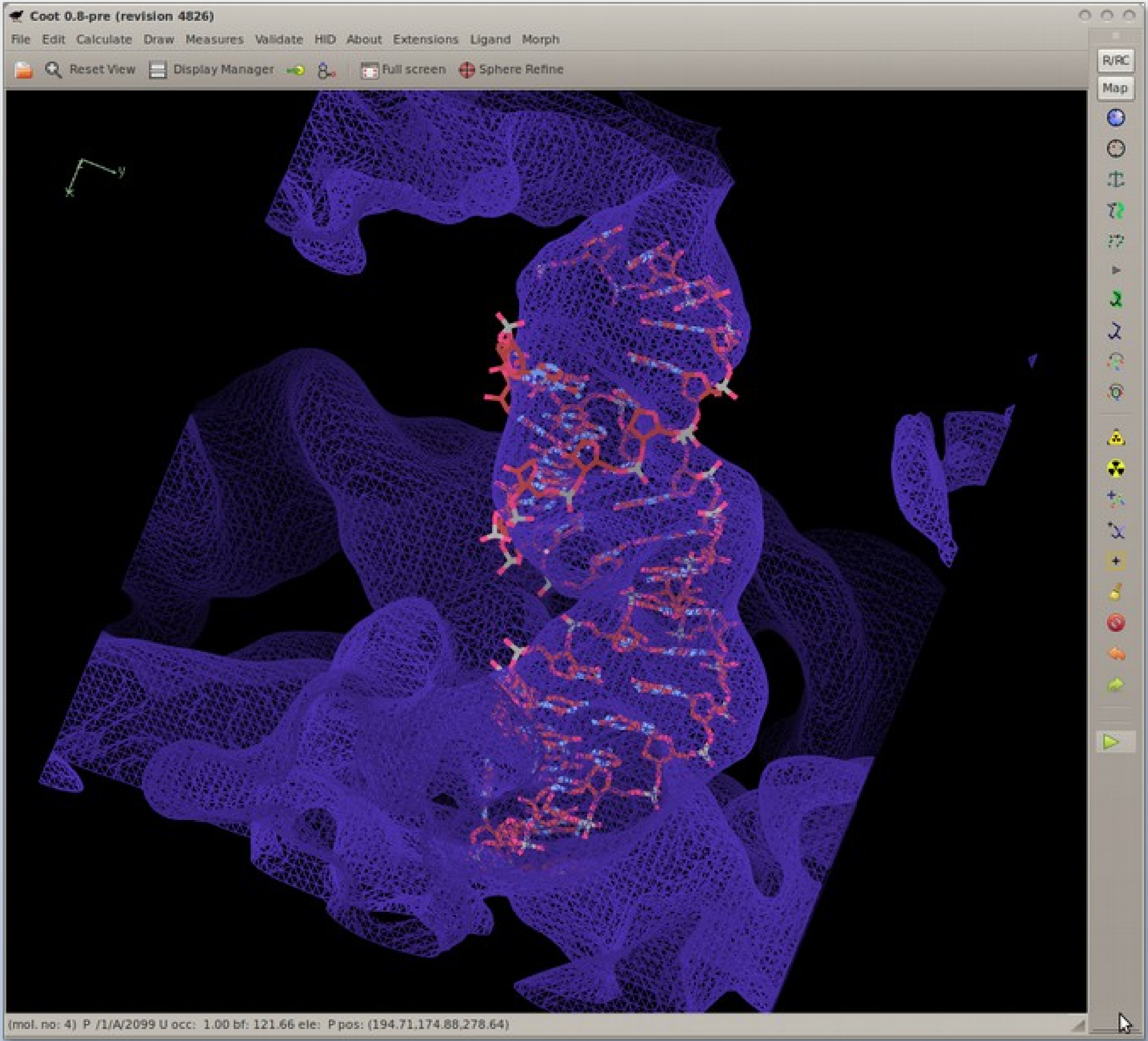
- Loop *n* (say 1000) times:
  - Generate sample angles and translations
  - Transform atom selection by these rotations and translation
  - Score and store the fit to density
- Rank density fit scores,
  - Pick top 10 solution, for each of them
    - Rigid body fit and score solutions
    - Pick the highest scoring solution if it's better than the starting model)
- Radius of Convergence is larger when using a low-pass map
- Reimplementing the algorithm using CUDA



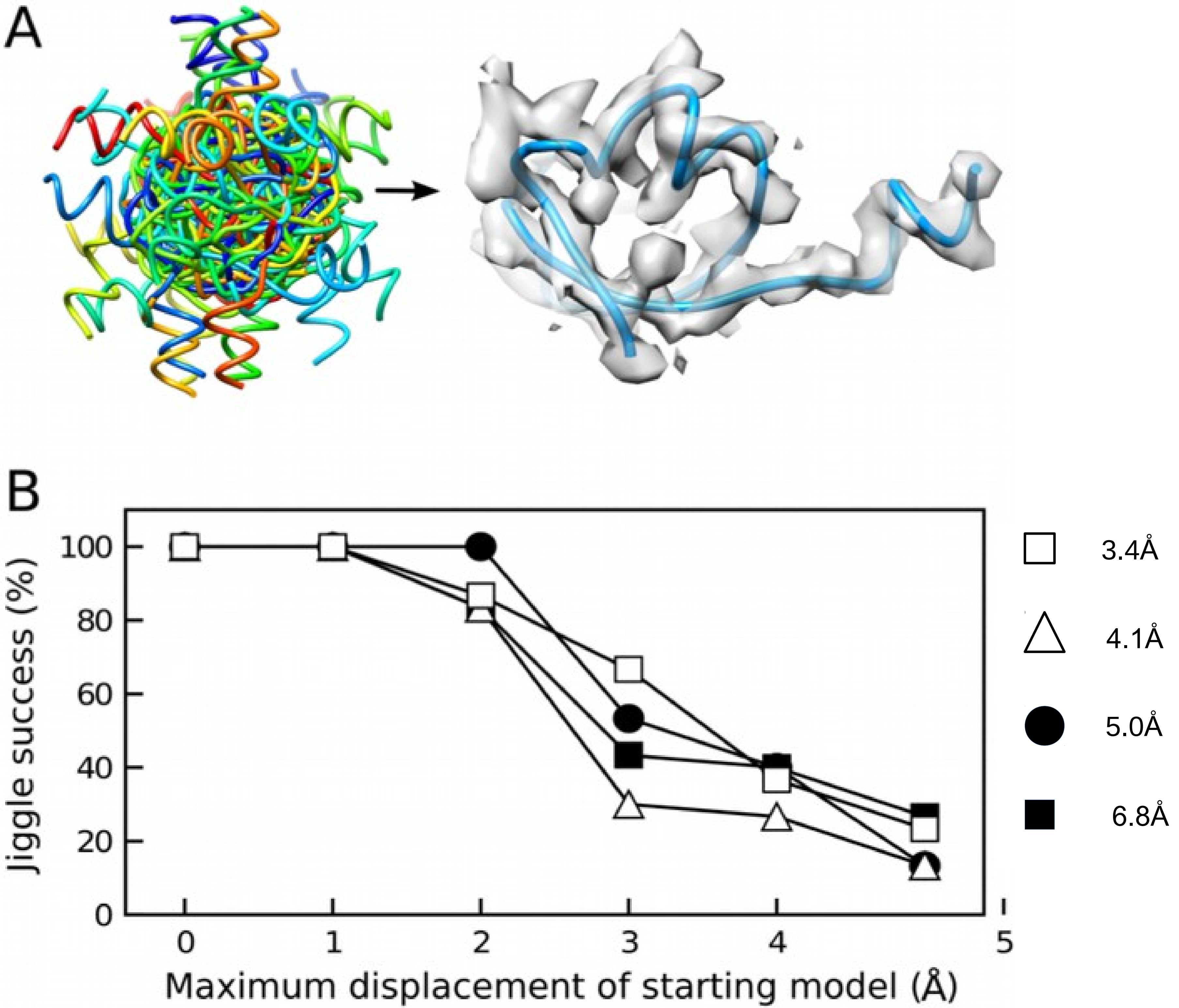
```
(mol. no: 4)  P  /1/A/2099 U occ:  1.00 bf: 121.66 ele:  P pos: (194.71,174.88,278.64)
```



```
(mol. no: 4)  P /1/A/2099 U occ:  1.00 bf: 121.66 ele:  P pos: (194.71,174.88,278.64)
```



```
(mol. no: 4)  P  /1/A/2099 U occ:  1.00 bf: 121.66 ele:  P pos: (194.71,174.88,278.64)
```


A
B
Jiggle success (%)
0
20
40
60
80
100
0
1
2
3
4
5
Maximum displacement of starting model (Å)
□ 3.4Å
△ 4.1Å
● 5.0Å
■ 6.8Å

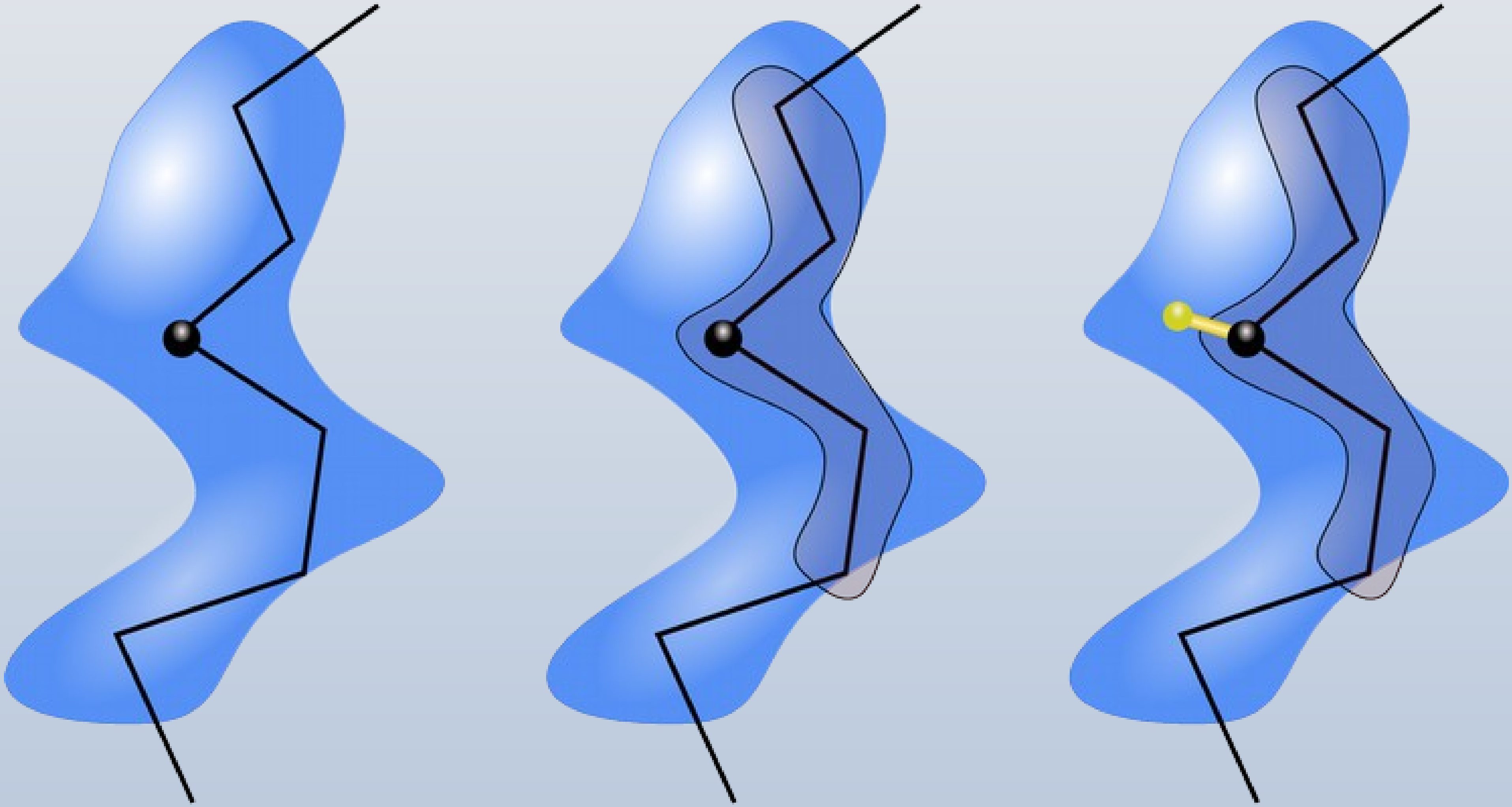
So we have our ideal RNA or homologous protein sitting roughly in the density

(not a great fit)

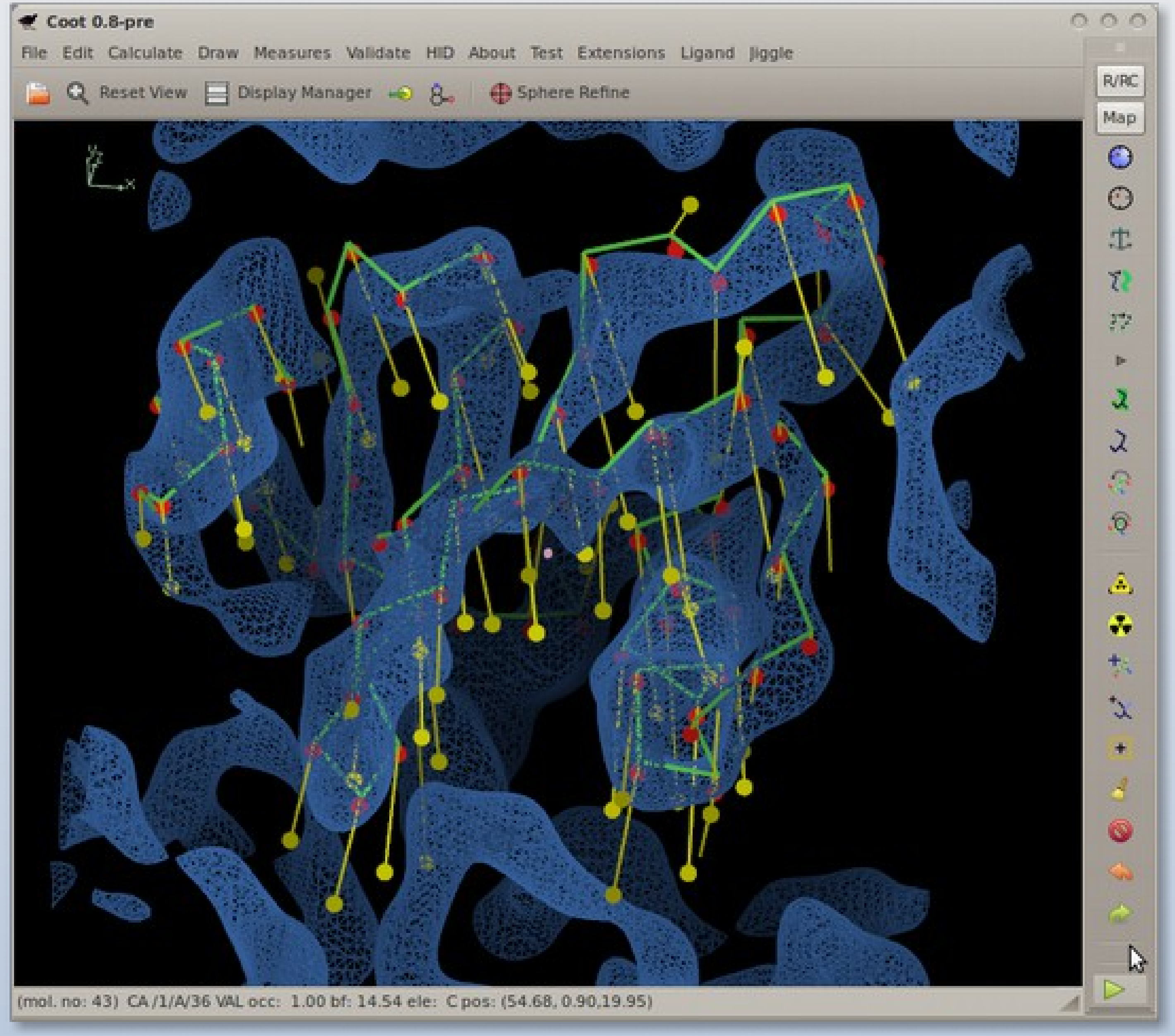
Model Morphing: How it Works

- For each residue in a chain, we ask:
  - where does a small fragment centred on this residue want to go?
  - (Robust) average the transformations and apply them on a per-residue basis
- Repeat

Model Morphing: Generating the Raw RTs



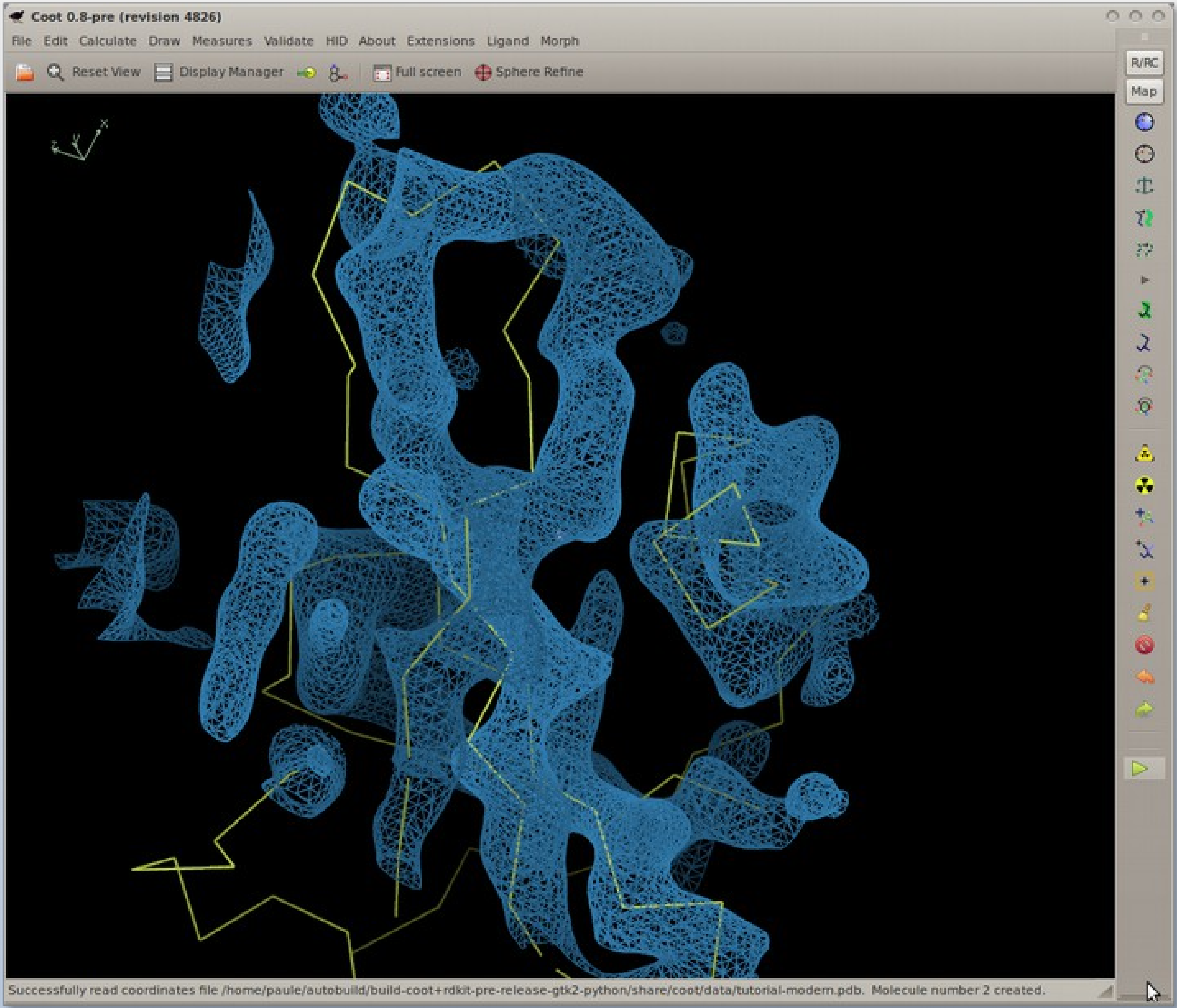
Model Morphing: Example



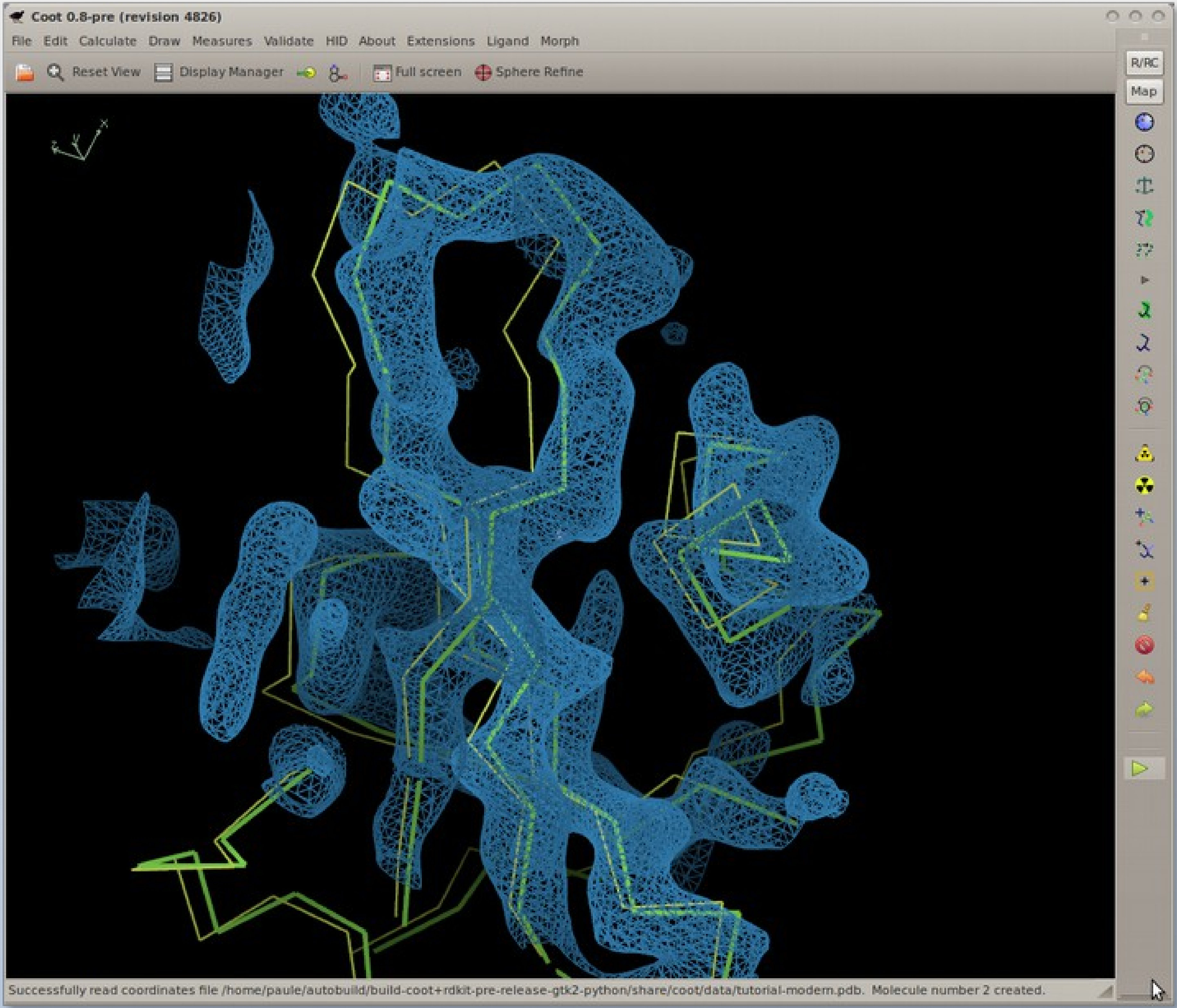
```
(mol. no: 43)  CA /1/A/36 VAL occ:   1.00 bf: 14.54 ele:   C pos: (54.68, 0.90,19.95)
```

Model Morphing: Robust Averaging

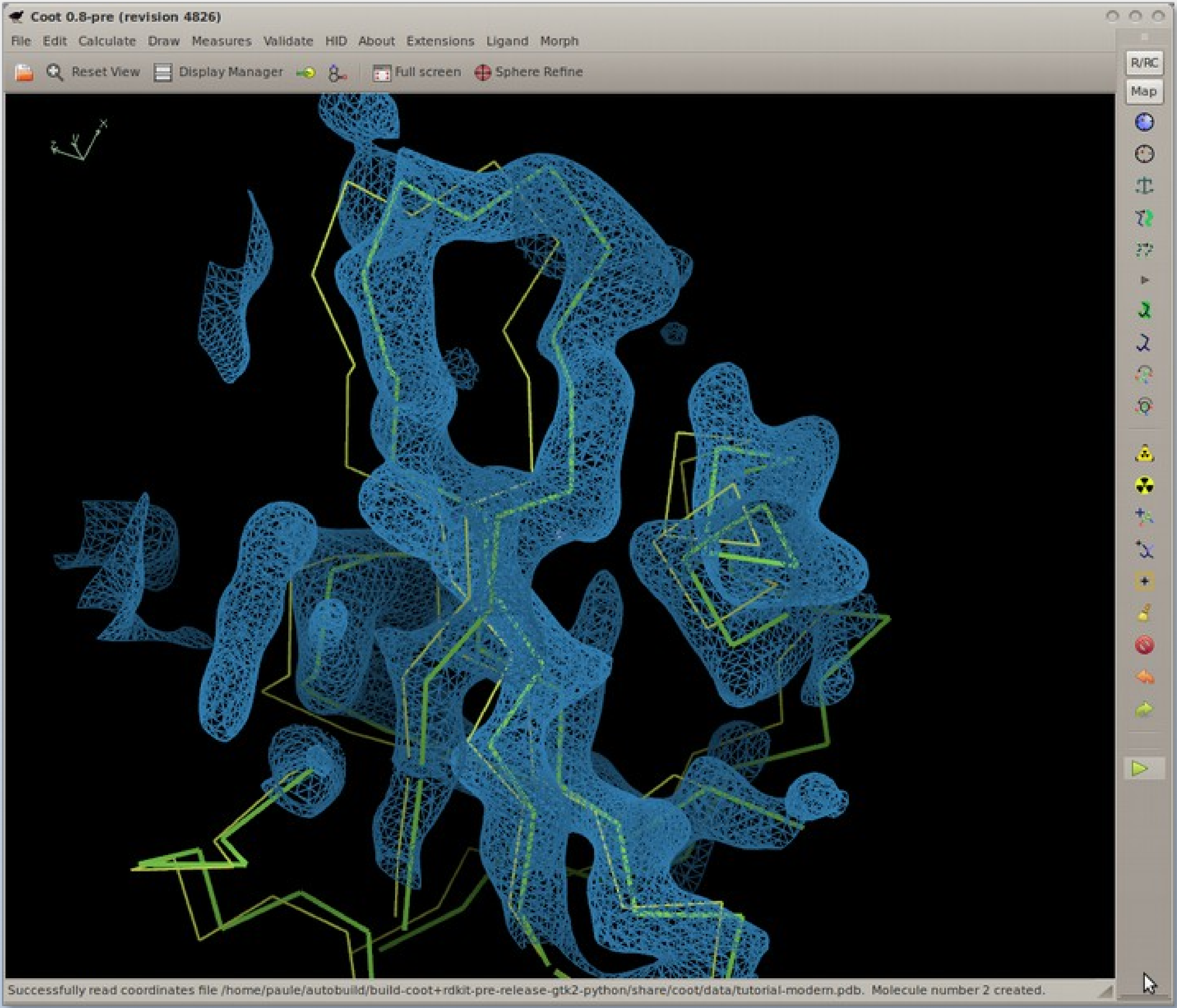
- What are the residues in the environment of a residue?
  - What are their RTs?
  - Create a metric 'distance', sort on that
  - Discard the top and bottom 25%
  - Use remaining RTs to generate average
  - ...which is then applied to central residue
- Repeat for all residues
- Larger environment radii make the shifts smaller/more conservative
  - More cycles needed



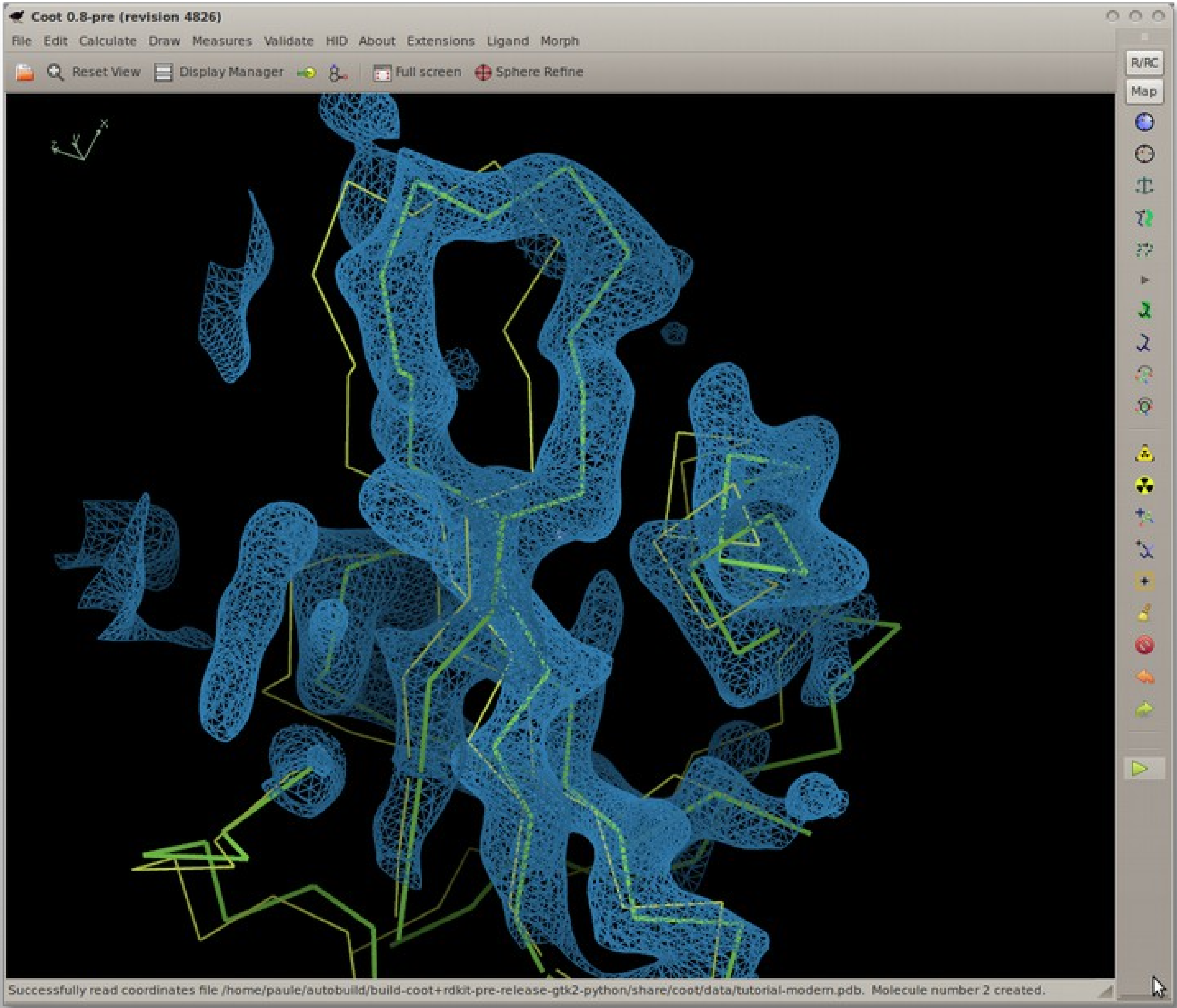
Successfully read coordinates file /home/paule/autobuild/build-coot+rdkit-pre-release-gtk2-python/share/coot/data/tutorial-modern.pdb. Molecule number 2 created.



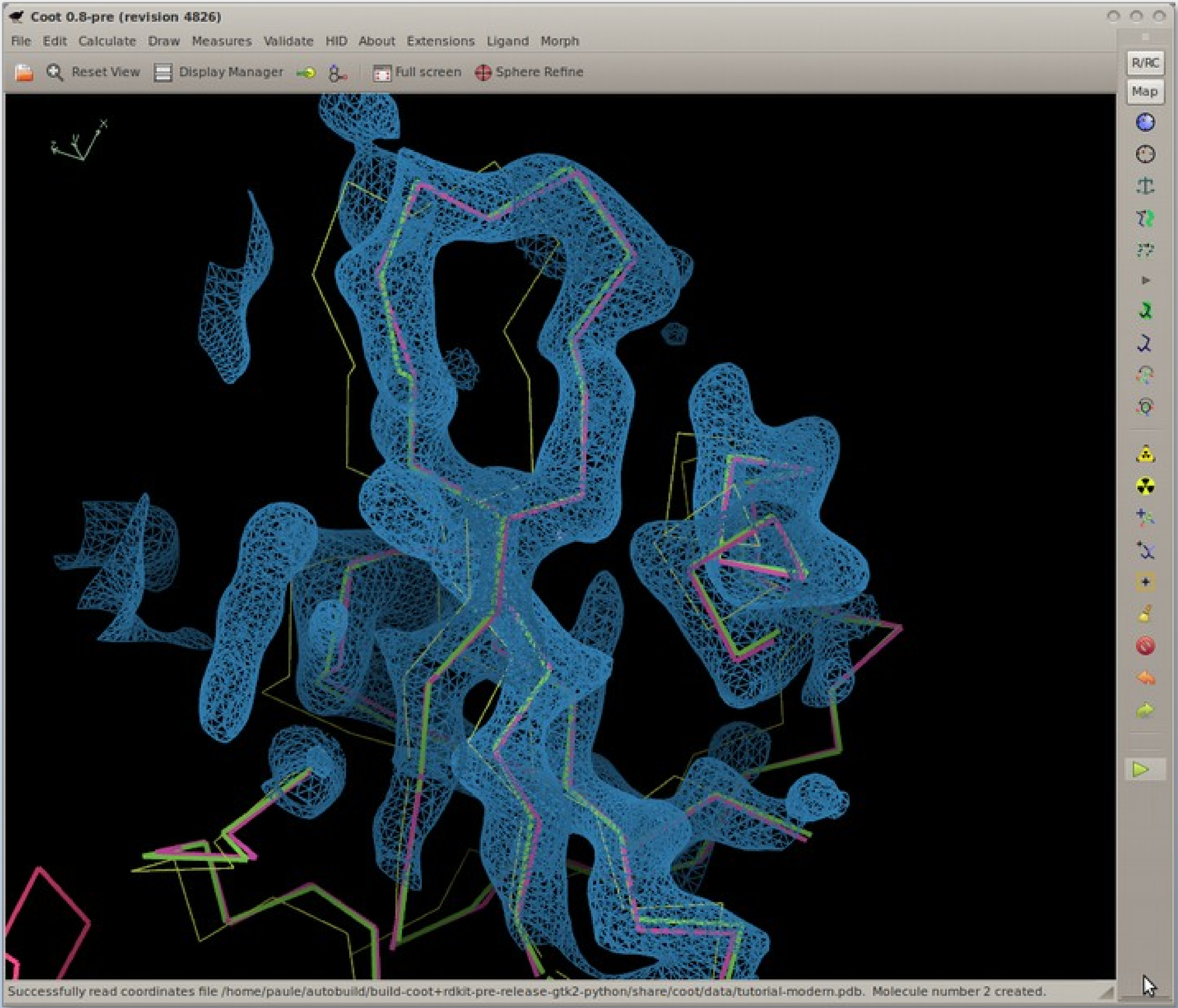
Successfully read coordinates file /home/paule/autobuild/build-coot+rdkit-pre-release-gtk2-python/share/coot/data/tutorial-modern.pdb. Molecule number 2 created.



Successfully read coordinates file /home/paule/autobuild/build-coot+rdkit-pre-release-gtk2-python/share/coot/data/tutorial-modern.pdb. Molecule number 2 created.

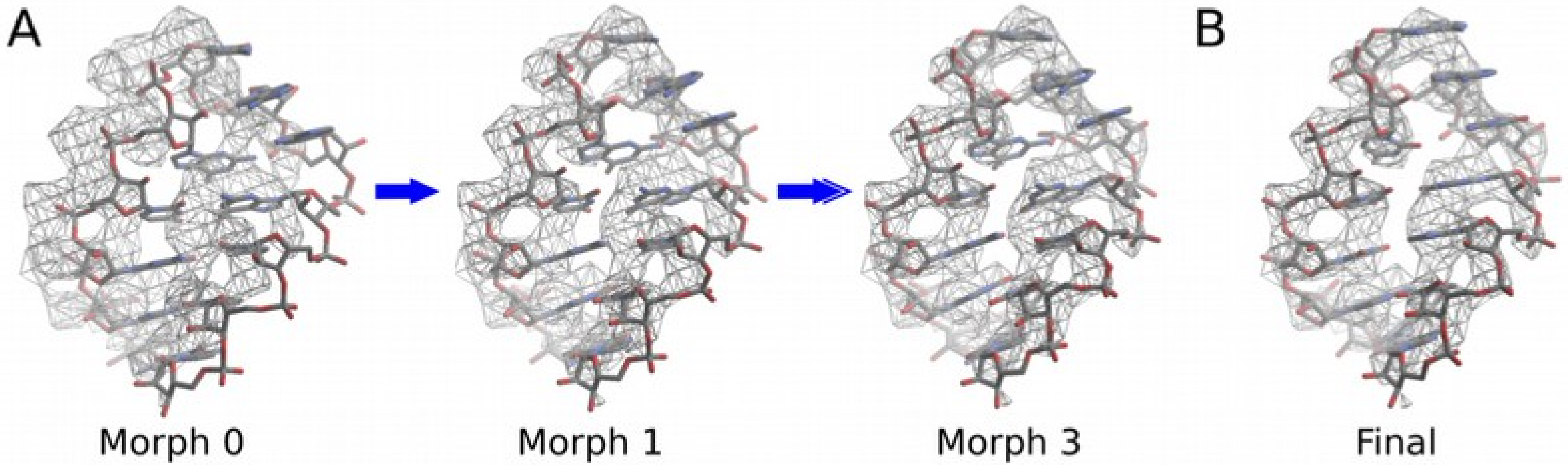


Successfully read coordinates file /home/paule/autobuild/build-coot+rdkit-pre-release-gtk2-python/share/coot/data/tutorial-modern.pdb. Molecule number 2 created.

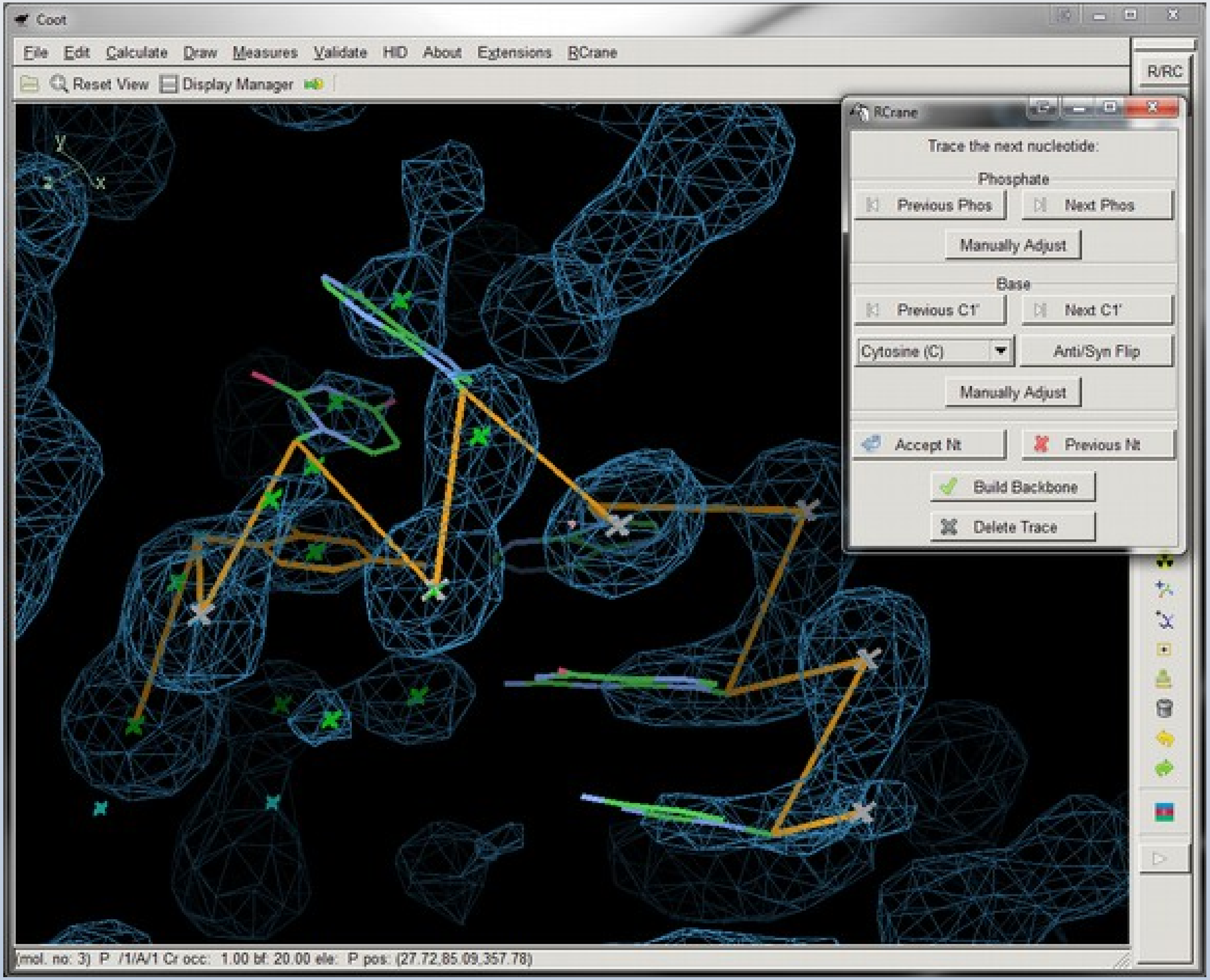


```
Successfully read coordinates file /home/paule/autobuild/build-coot+rdkit-pre-release-gtk2-python/share/coot/data/tutorial-modern.pdb.  Molecule number 2 created.
```

Model Morphing



RCrane: Semi-Automated Building of RNA



Trace the next nucleotide:

```
(mol. no: 3) P /1/A/1 Cr occ:  1.00 bf: 20.00 ele:  P pos: (27.72,85.09,357.78)
```

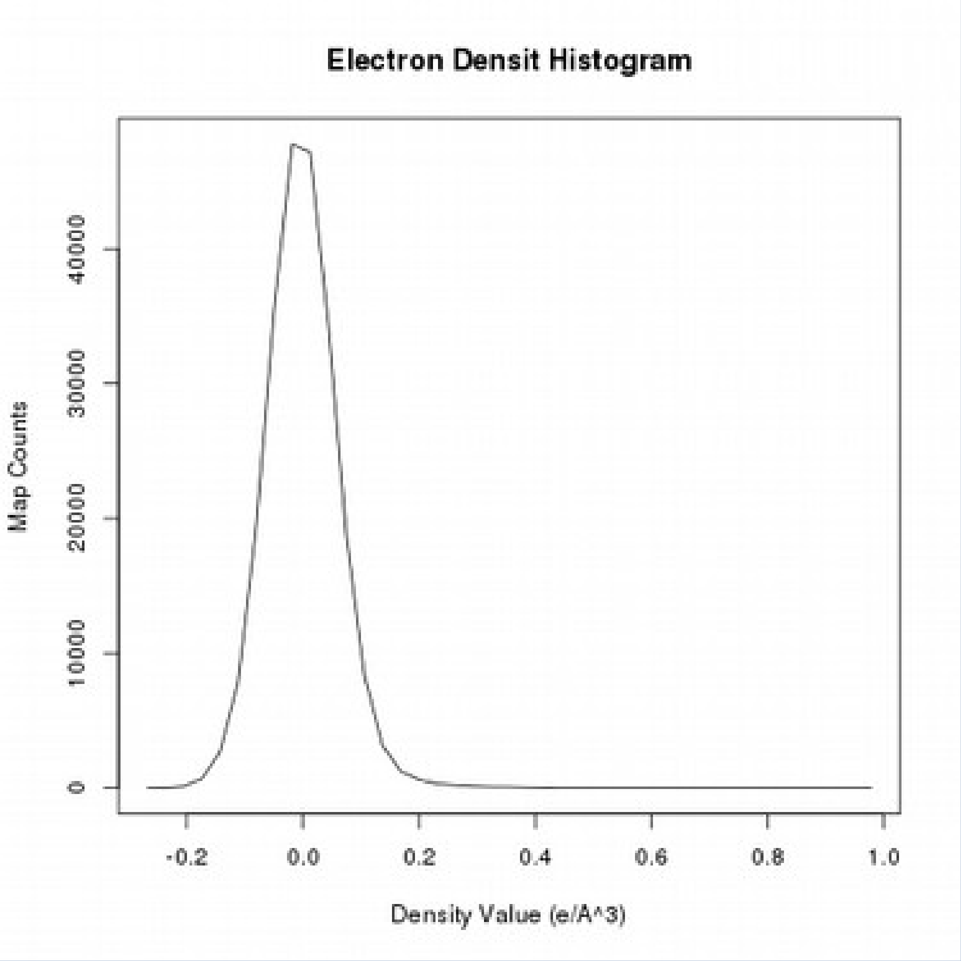
Helix Fitting

- The distribution of electron density is quite unlike that of x-ray maps
  - e.g. You don't see main-chain atoms at 4 rmsd in x-ray maps
    - regions of dense electron density contribute negatively to helix score in x-ray maps

Helix Fitting

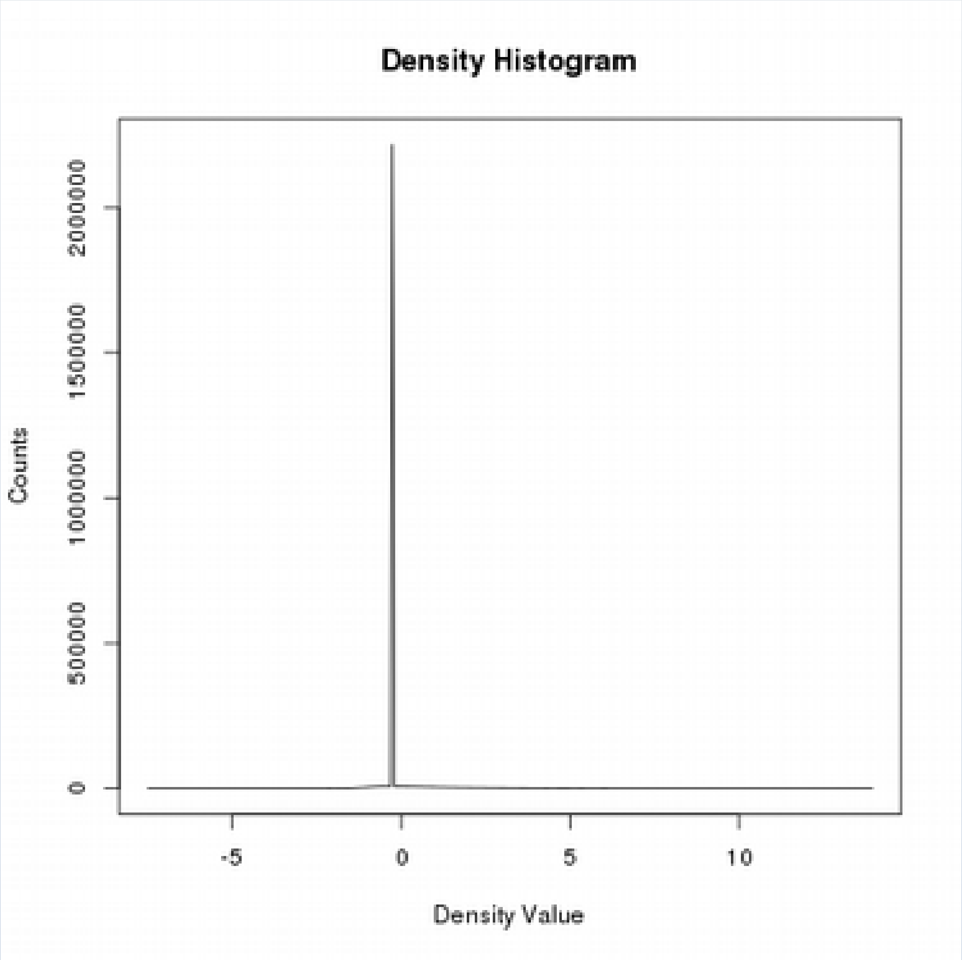
- The distribution of density is quite unlike that of x-ray maps

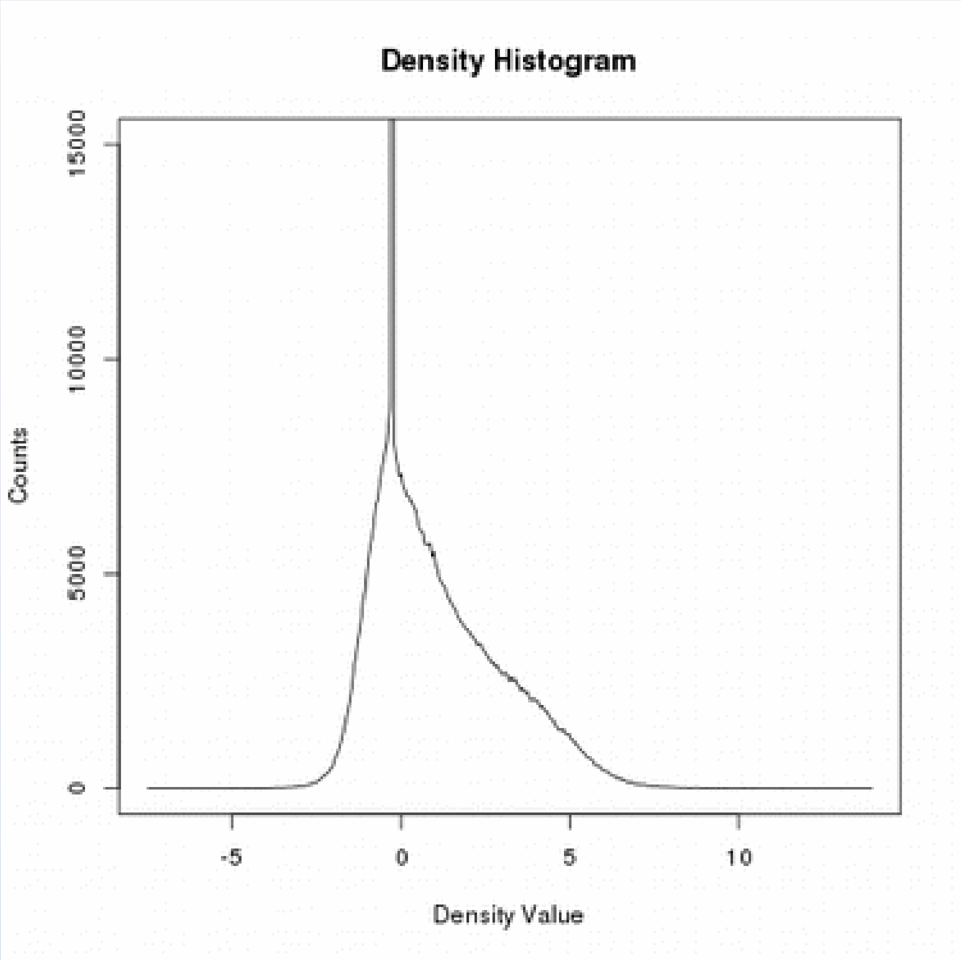
Typical Density Histogram
from an X-ray map



Helix Fitting

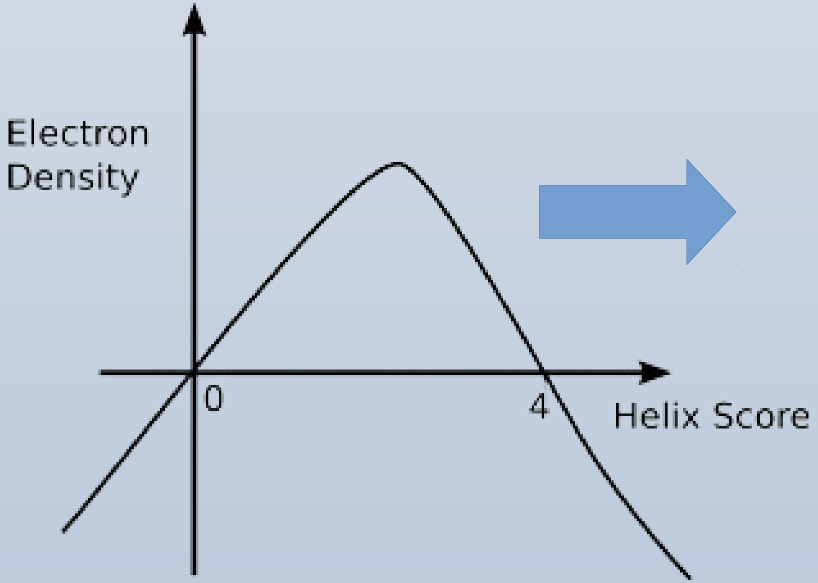
- The distribution of electron density is quite unlike that of x-ray maps





Helix Fitting

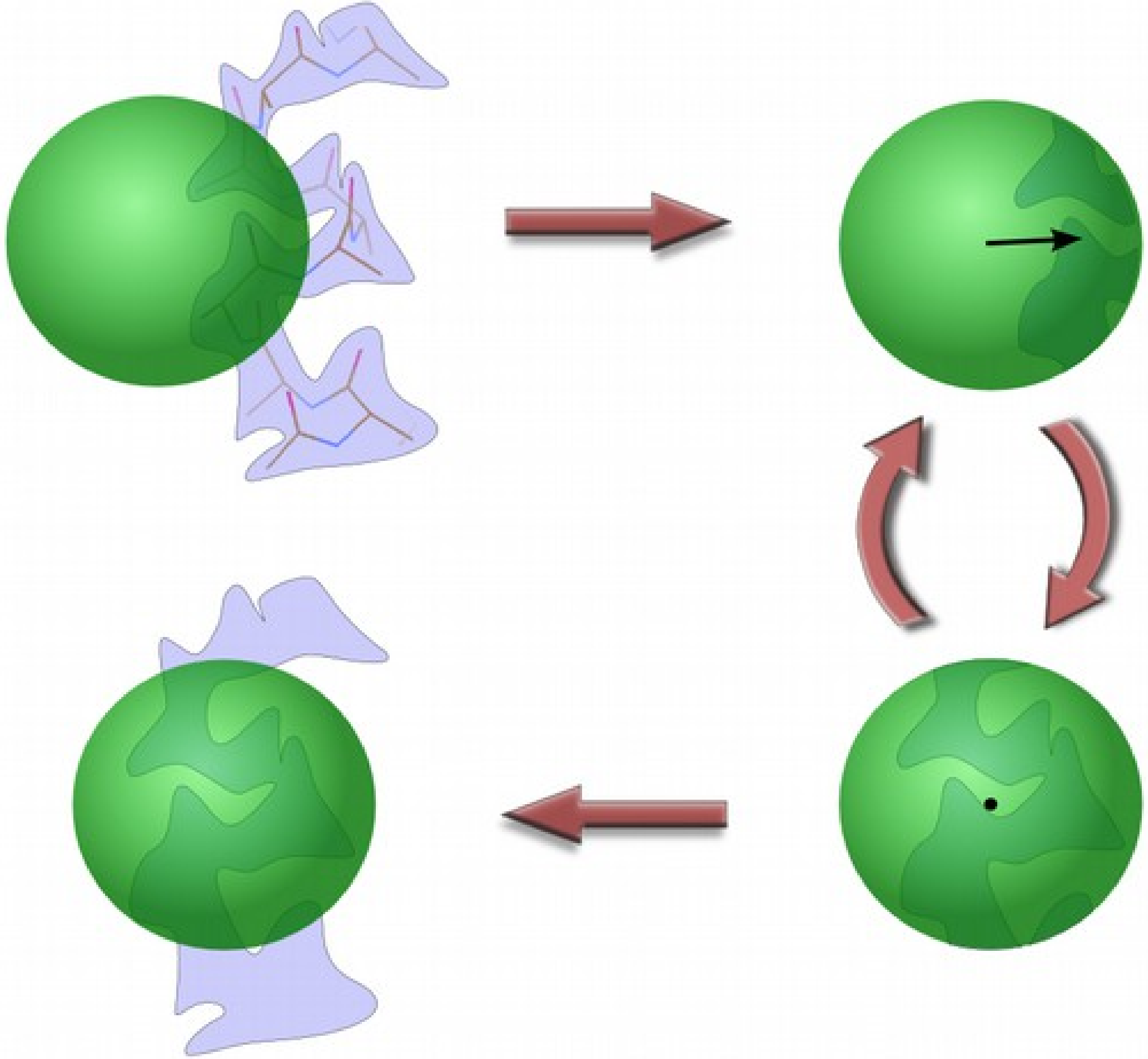
- The distribution of electron density is quite unlike that of x-ray maps
  - e.g. You don't see main-chain atoms at 4 rmsd in x-ray maps
    - regions of dense electron density contribute negatively to helix score
  - These EM maps were sharpened and in a big box of mostly nothing
  - Lots to see at 4 rmsd



Alpha Helix Placement

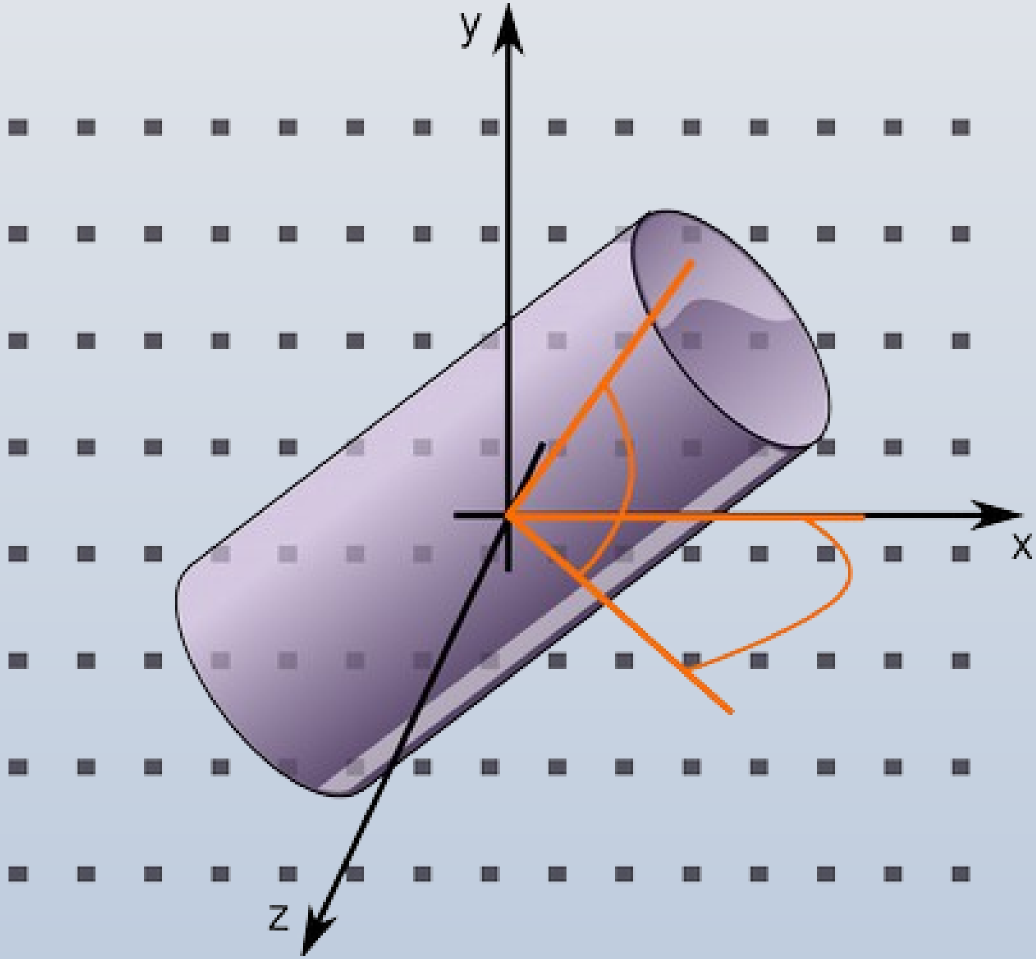
- Scenario: Looking at a new map, not built with automatic tools:
  - "I can see that there's a helix here - build it for me!"
- From a given point:
  - Move to local averaged maximum
  - Do a 2D MR-style orientation search on a cylinder of electron density
  - Build a helix (both directions)
  - 1D Rotation search to find best fit
  - Score based on density at CB positions
  - Trim 'n Grow

Centering the Rotation point

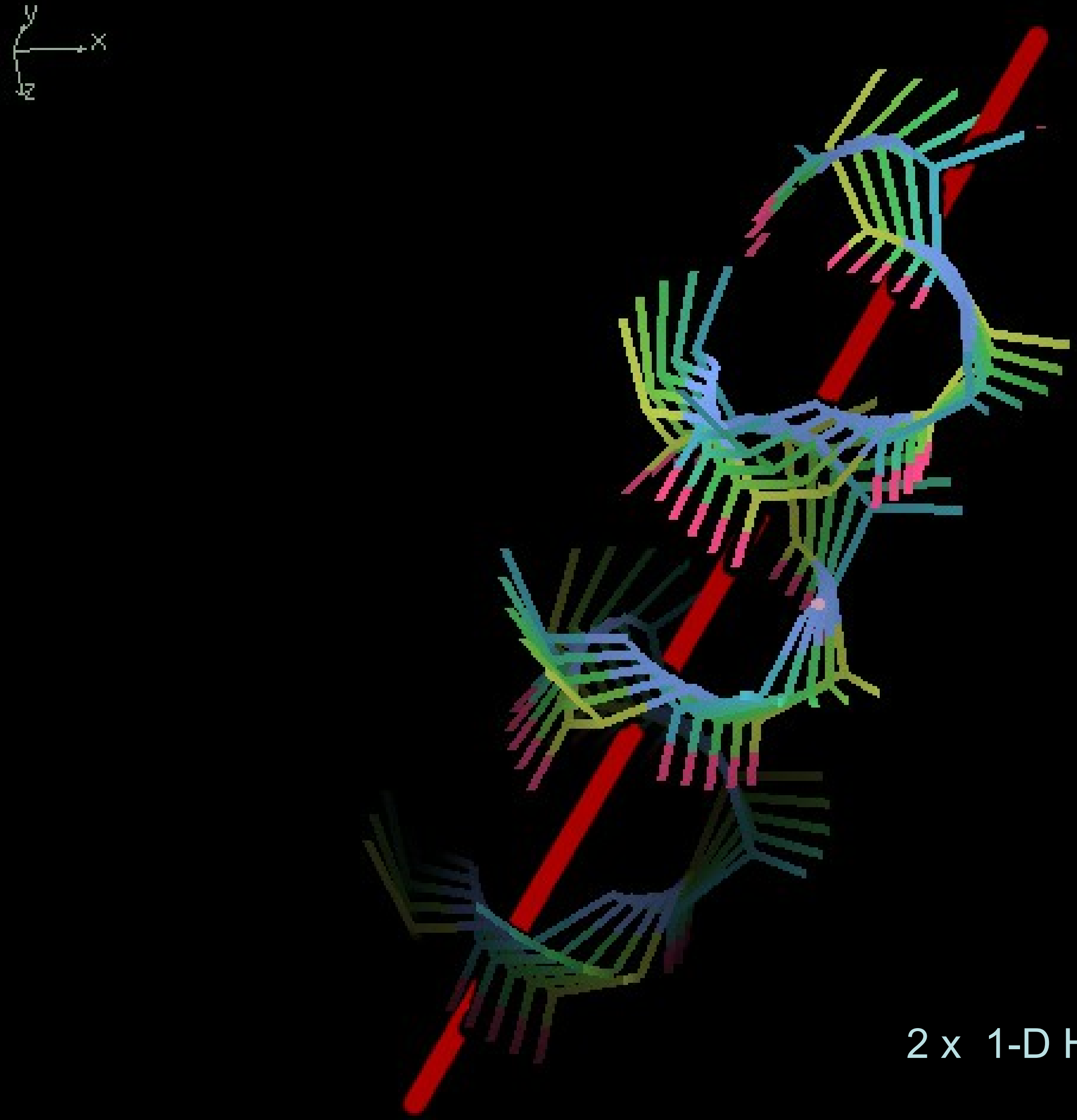


Helix Fitting: Cylinder Search

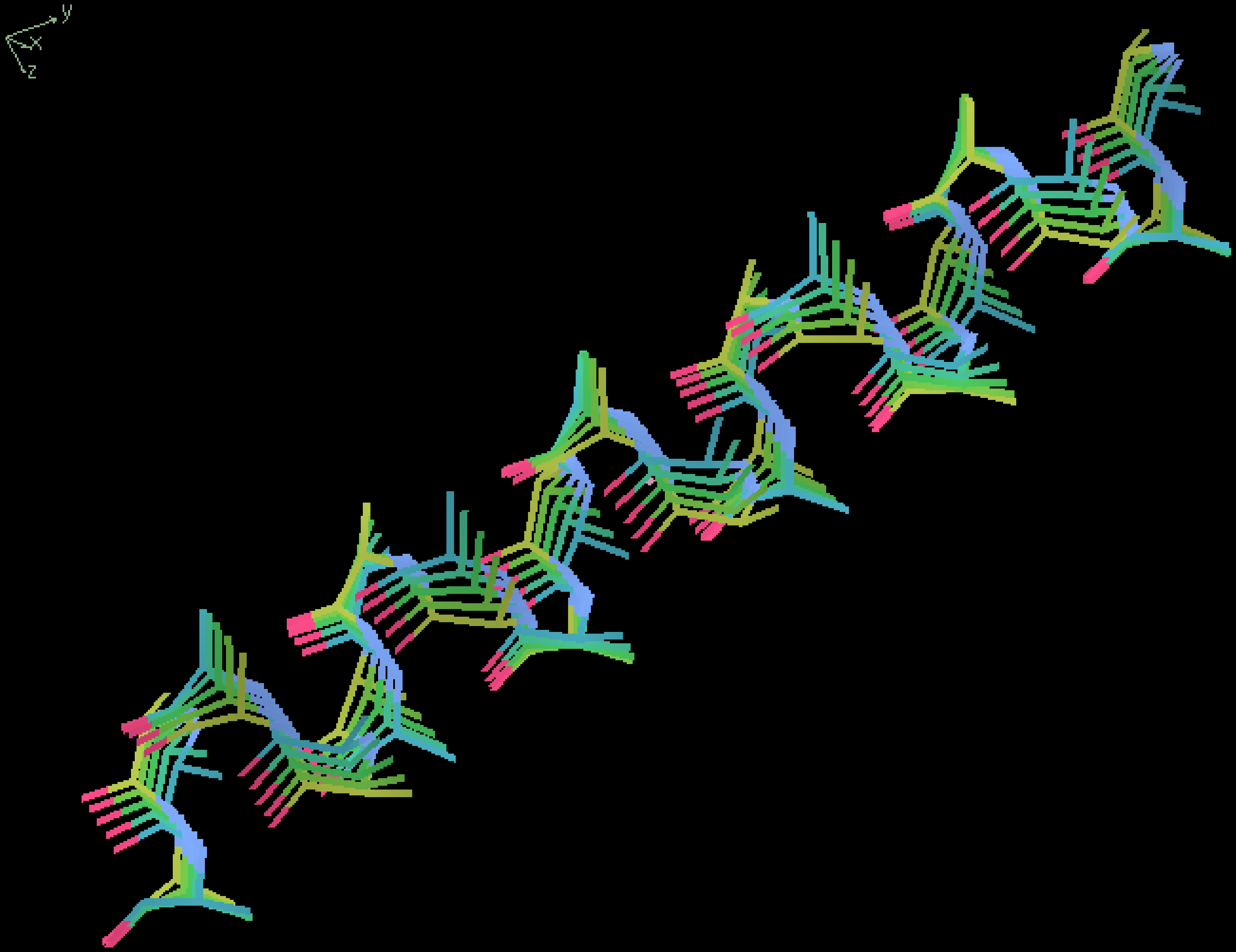
- Pick the orientation that encapsulates the most electron density

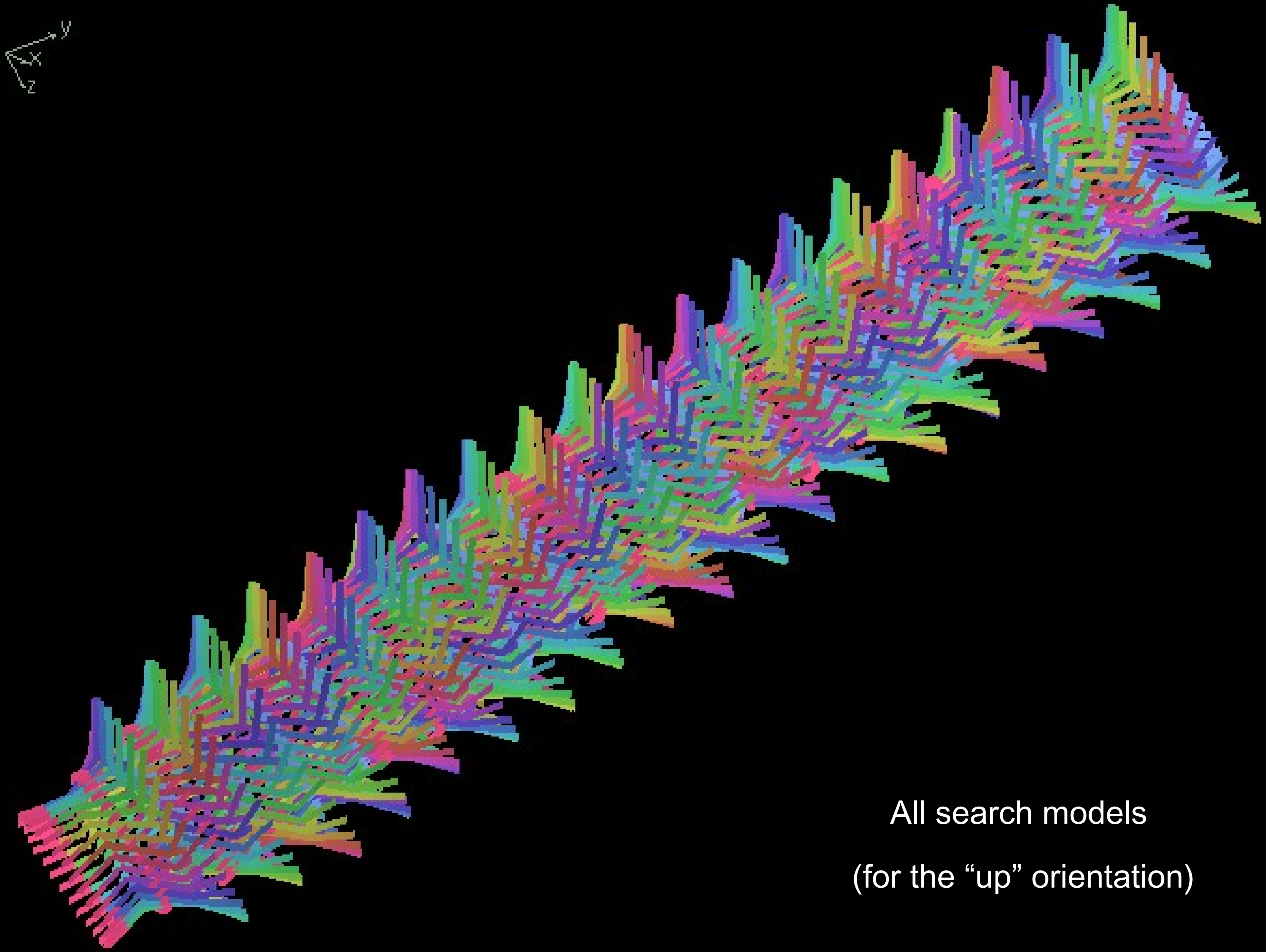


Using 2 rotation axes



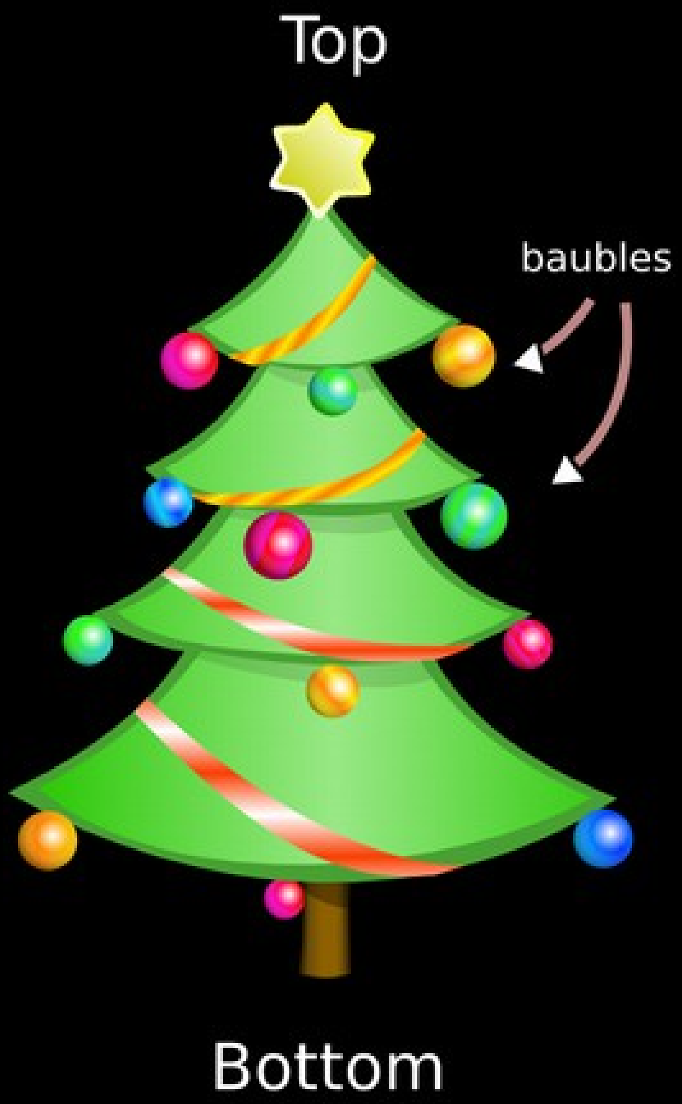
2 x 1-D Helix orientation searches


y
x
z

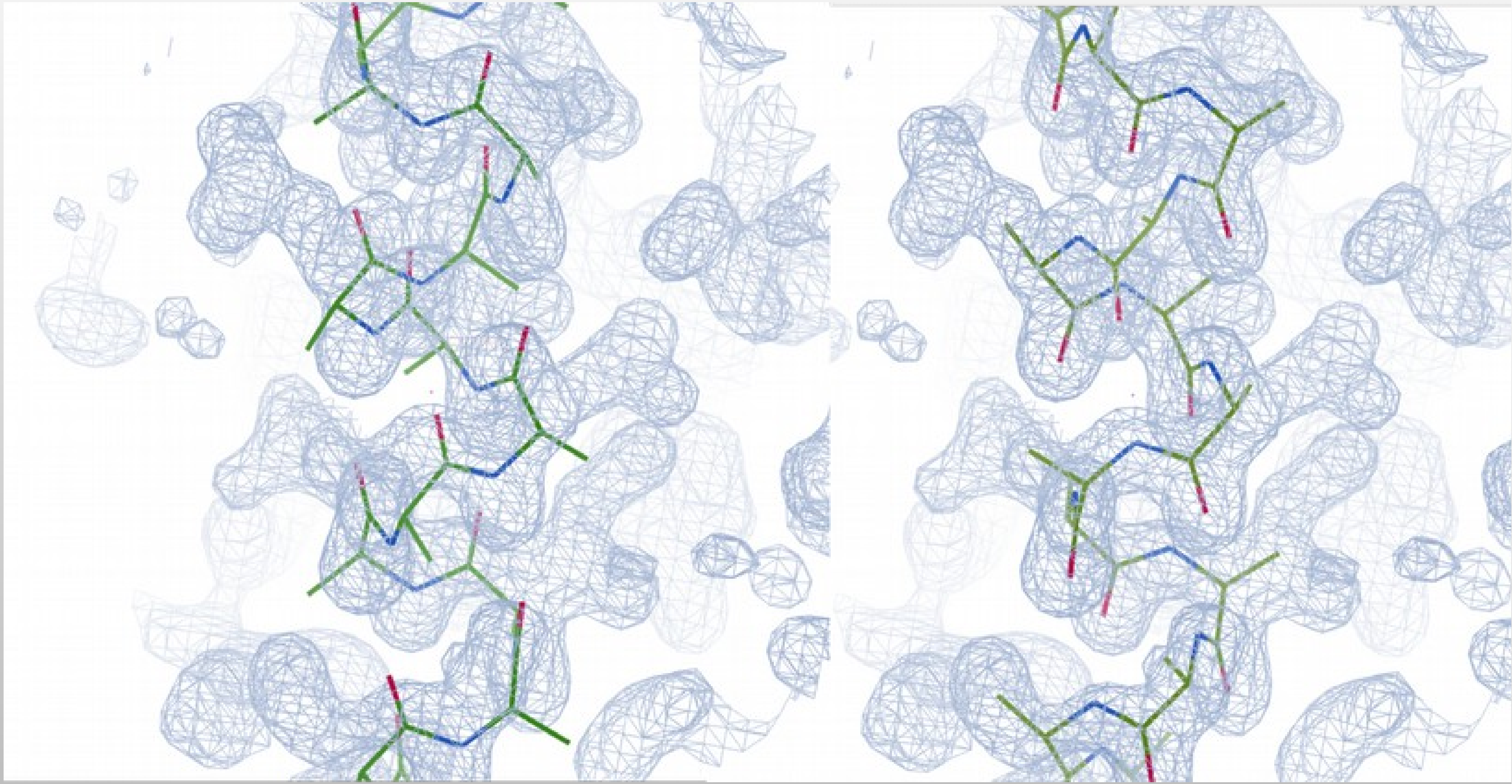


All search models

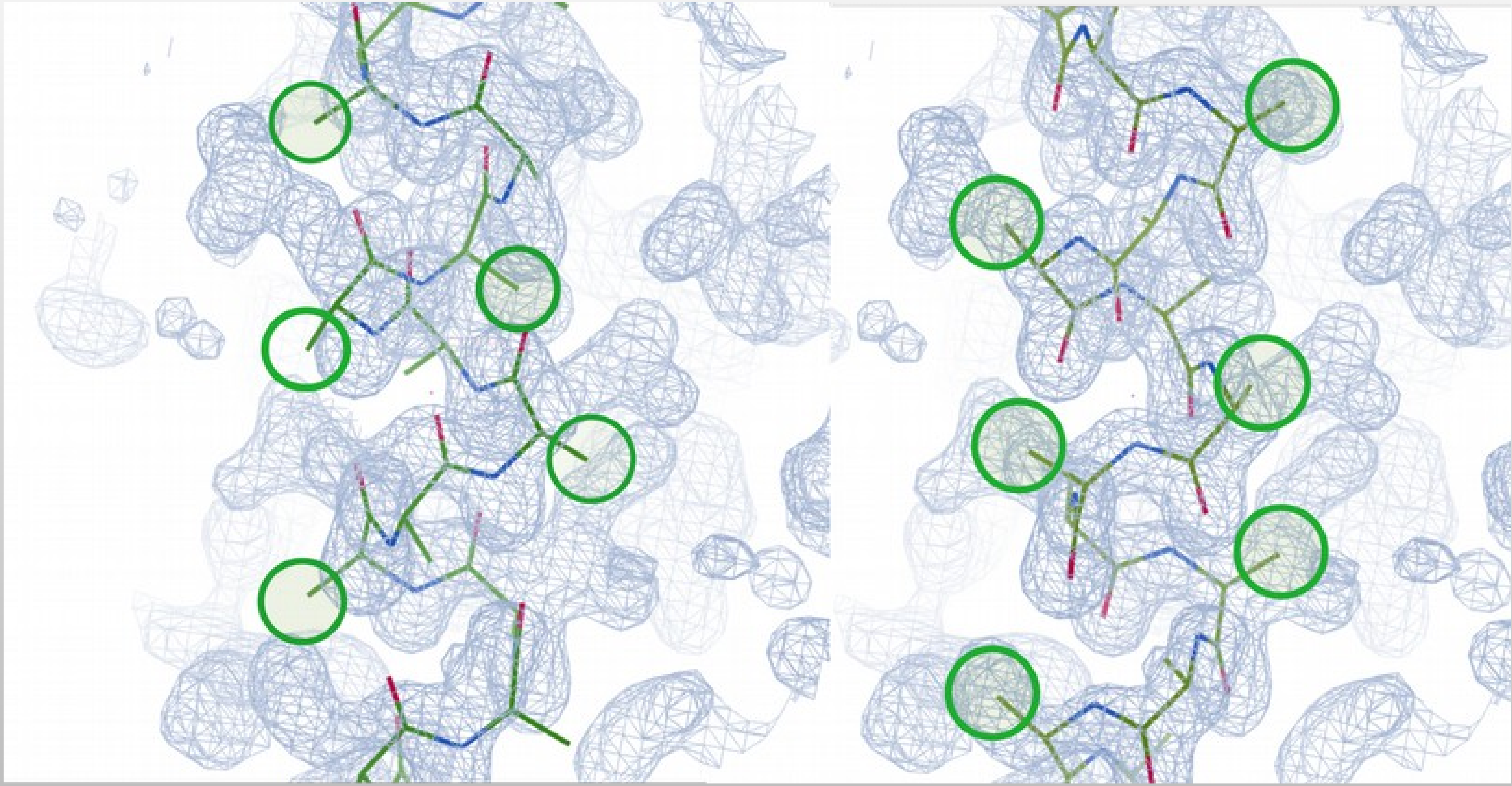
(for the “up” orientation)


Top
baubles
Bottom

Helix Fitting
Comparing orientation hypotheses



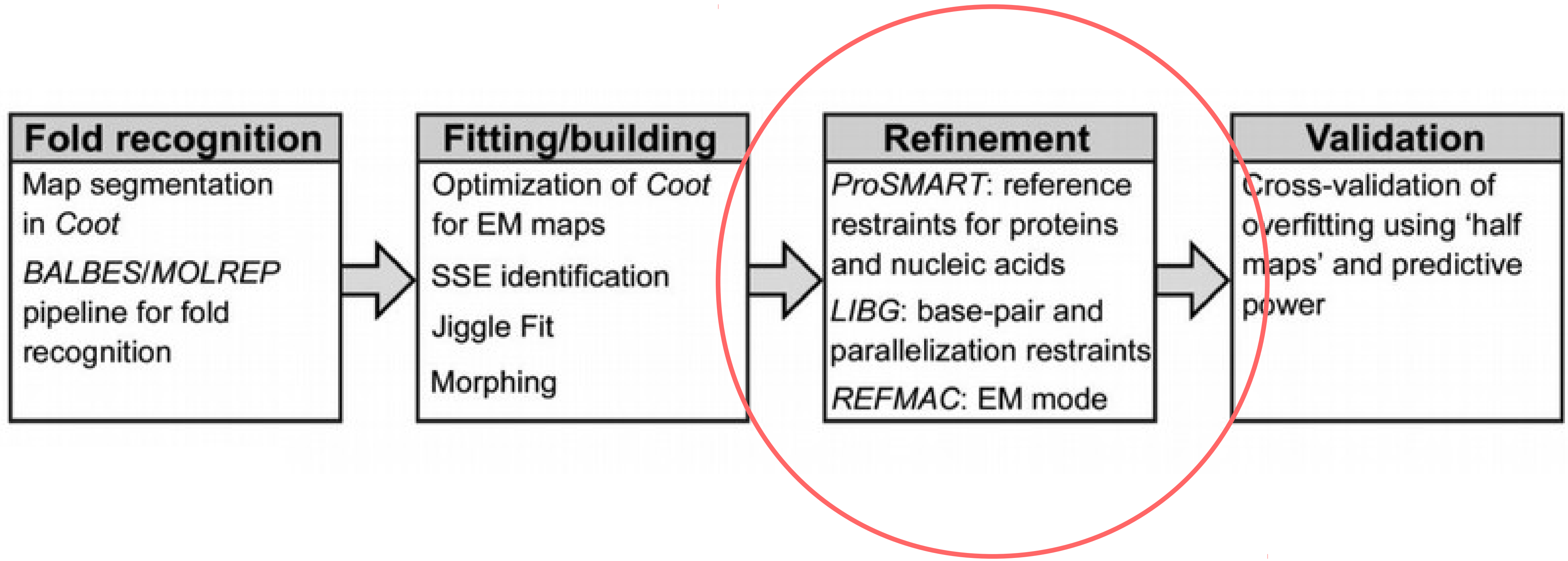
Helix Fitting
Comparing orientation hypotheses



c-betas are not fitted and are used for scoring

Model-Building Tools

Recent Developments



Fold recognition

Map segmentation in *Coot*

BALBES/*MOLREP* pipeline for fold recognition

Fitting/building

Optimization of *Coot* for EM maps

SSE identification

Jiggle Fit

Morphing

Refinement

ProSMART: reference restraints for proteins and nucleic acids

LIBG: base-pair and parallelization restraints

REFMAC: EM mode

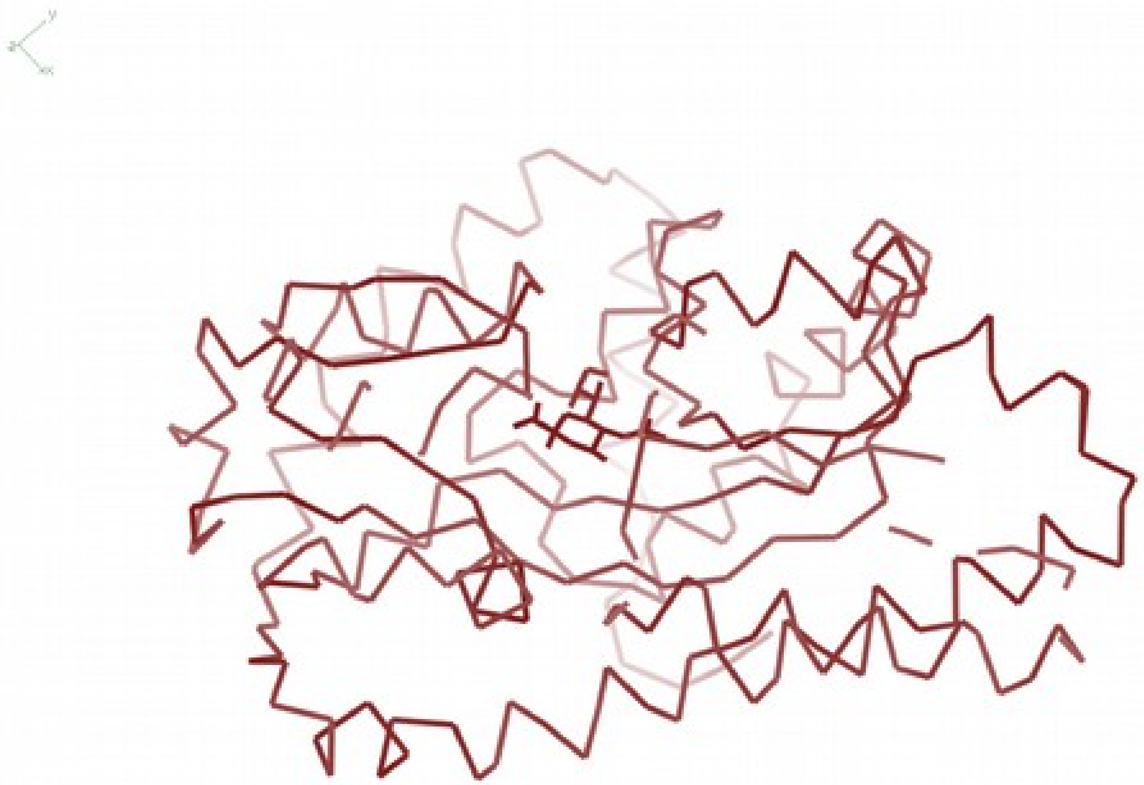
Validation

Cross-validation of overfitting using 'half maps' and predictive power

Local Distance Restraints

- ProSMART:
  - Use previous-solved "template" structures to inform the refinement of the (low resolution) target protein
  - by local-distance of atom pairs restraint generation

Local Distance Restraints: Prior Structure

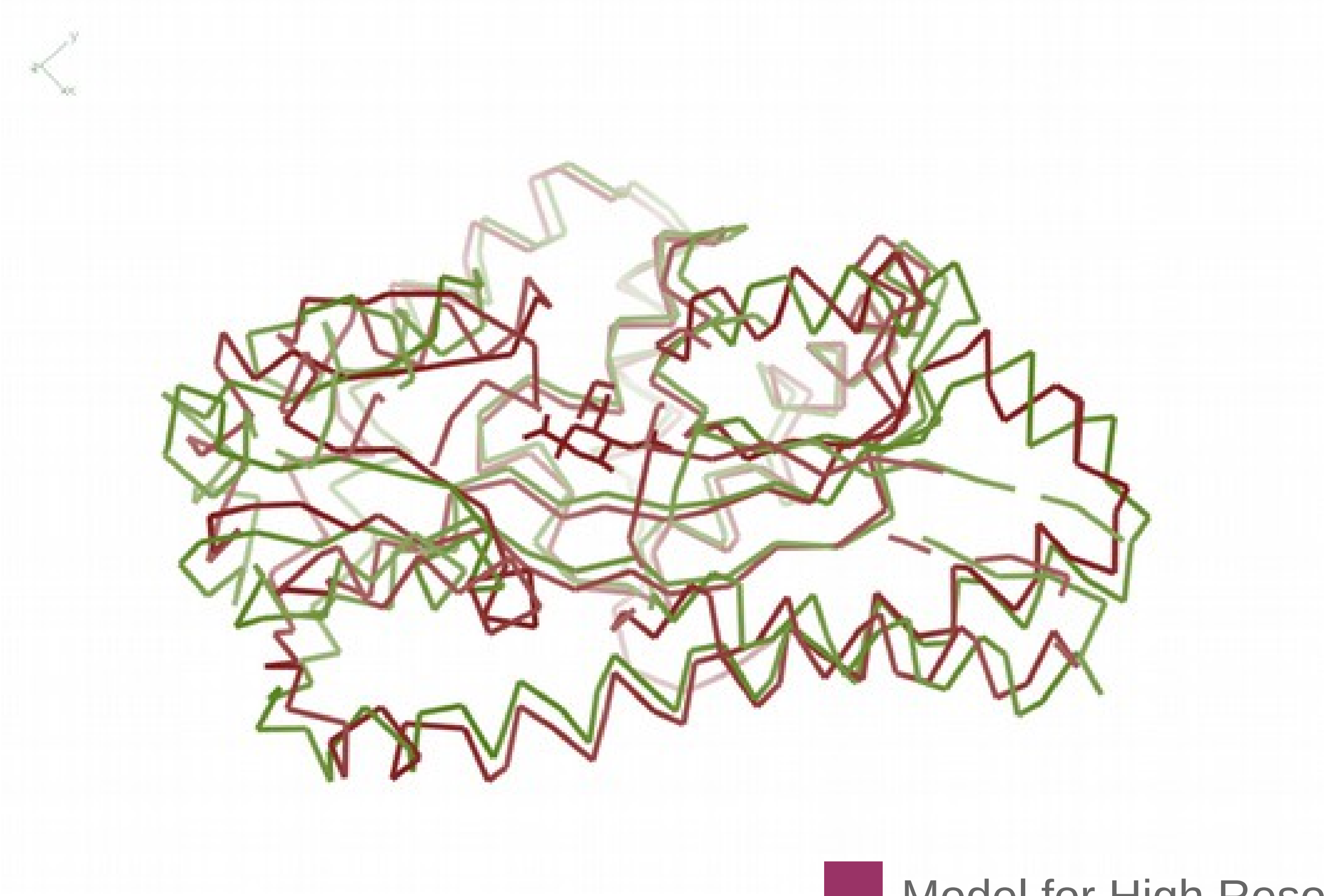


🟪 Model for High Resolution data

Local Distance Restraints: Today's Structure

🟩 Model for Low Resolution data

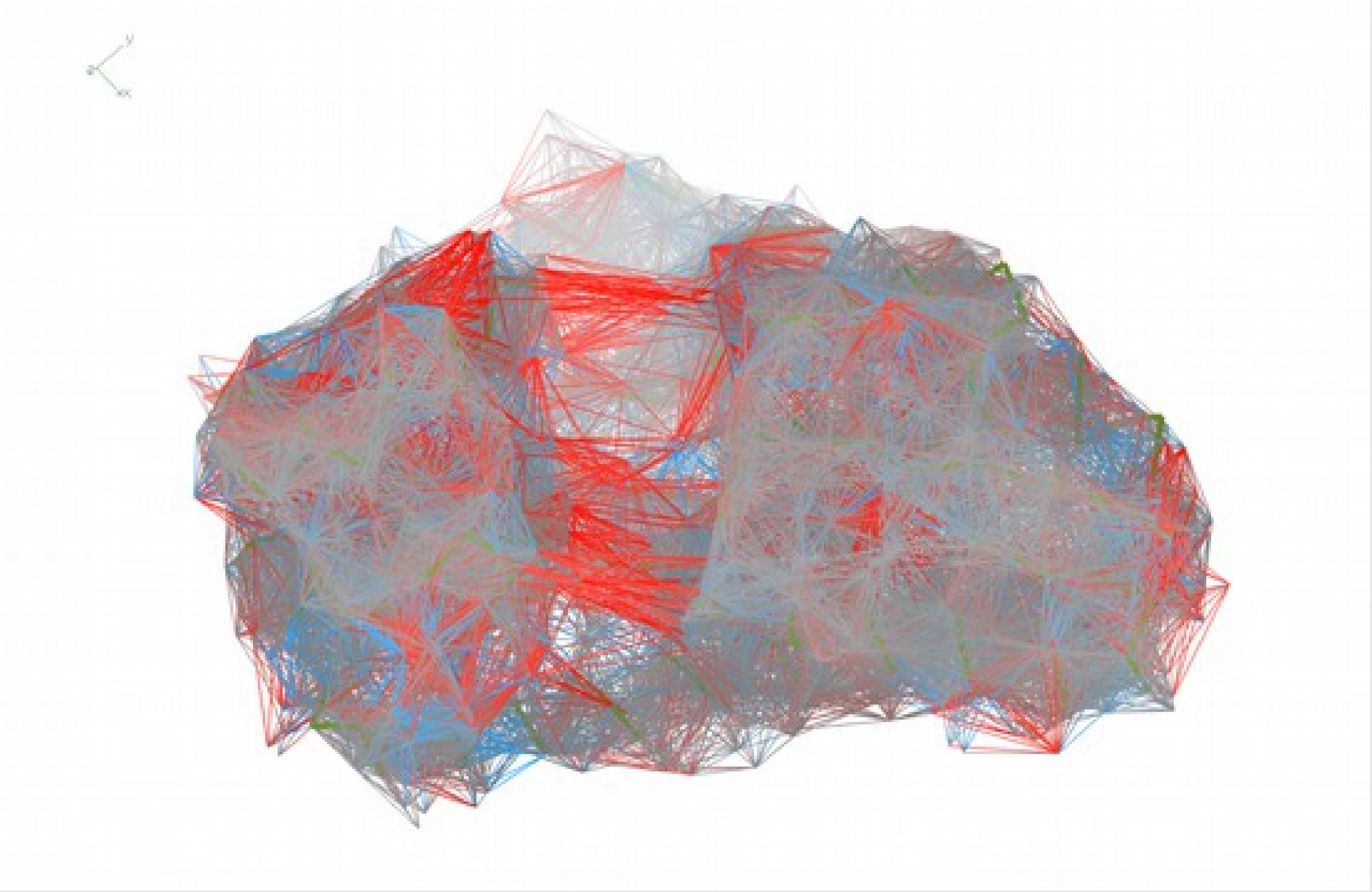
Local Distance Restraints: Structure Comparison



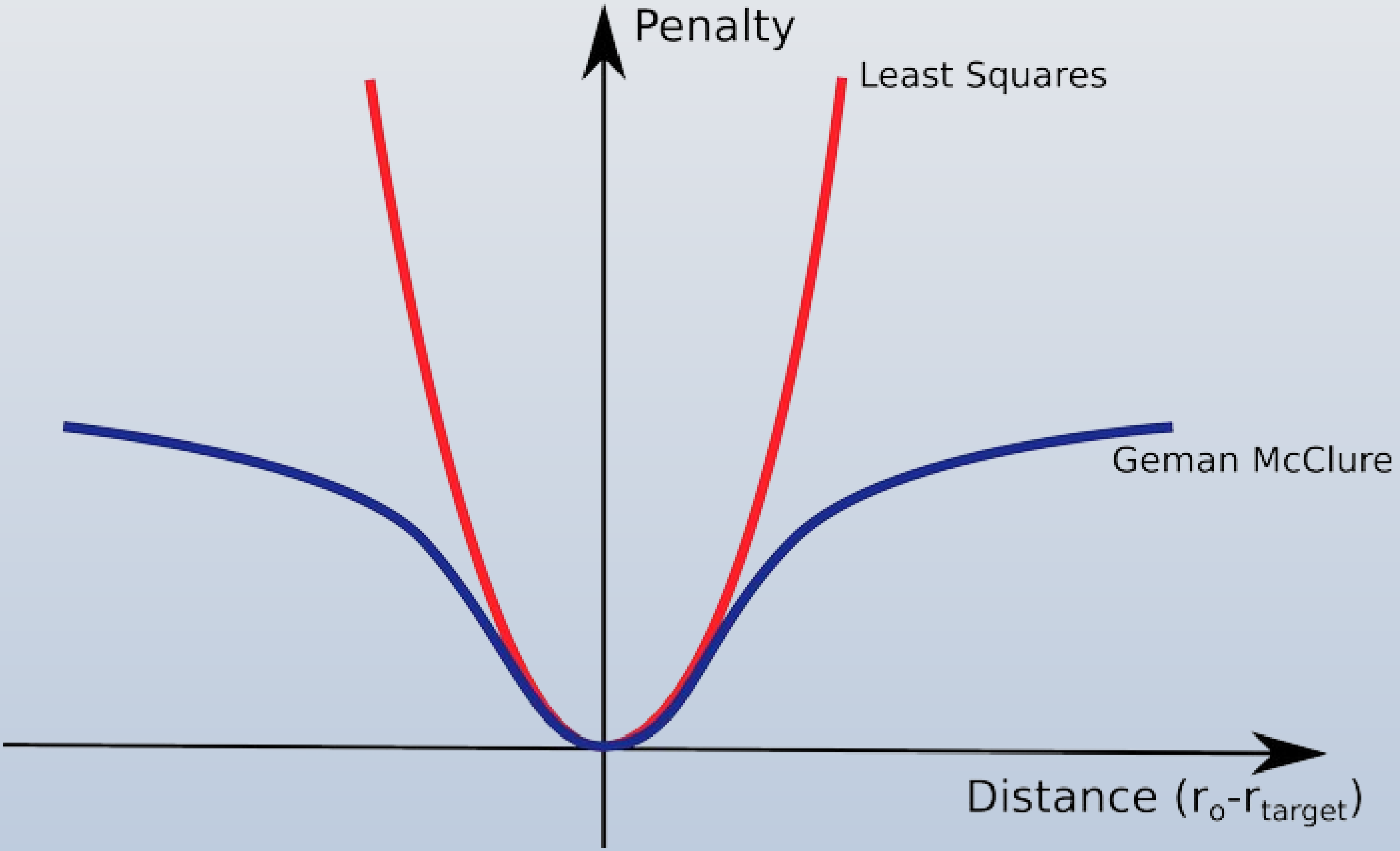
🟪 Model for High Resolution data

🟩 Model for Low Resolution data

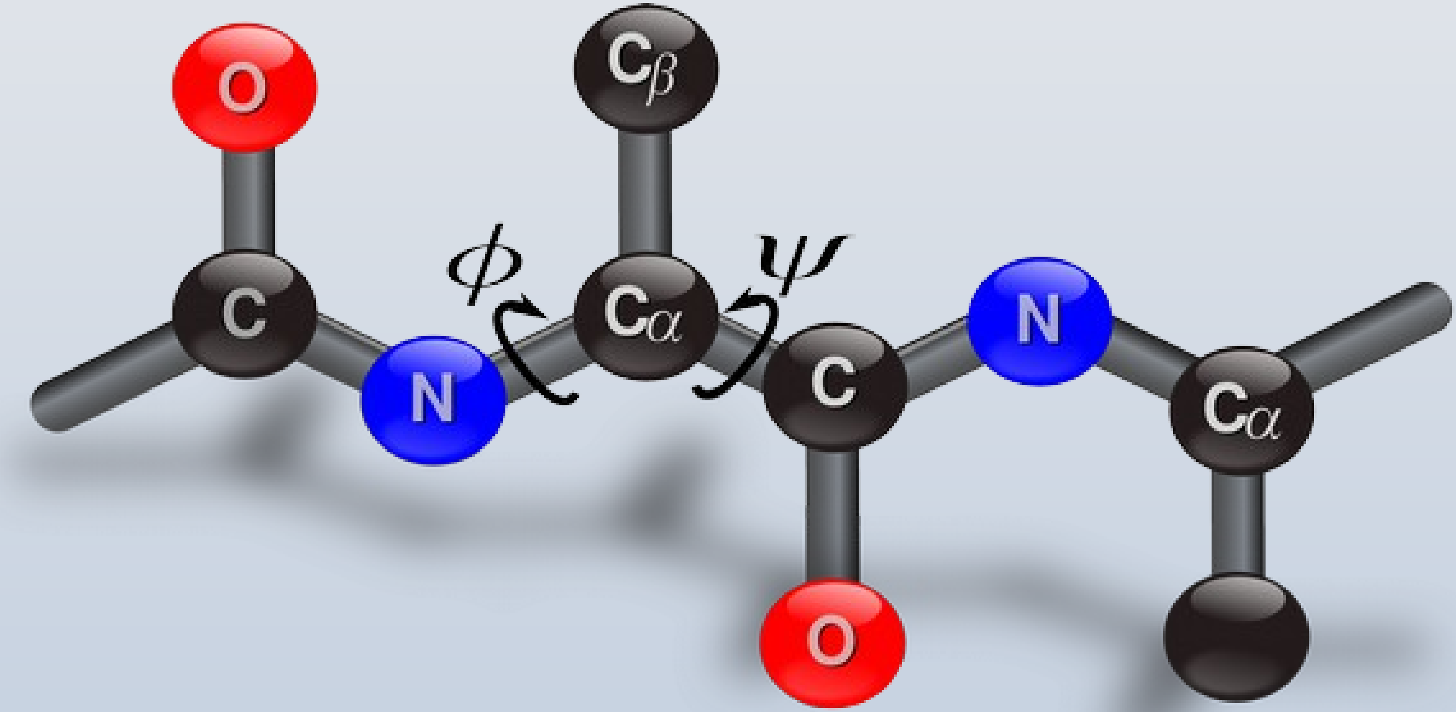
Local Distance Restraints:
ProSMART/Geman McClure Restraints



Modified Target Function



Peptide Backbone Geometry



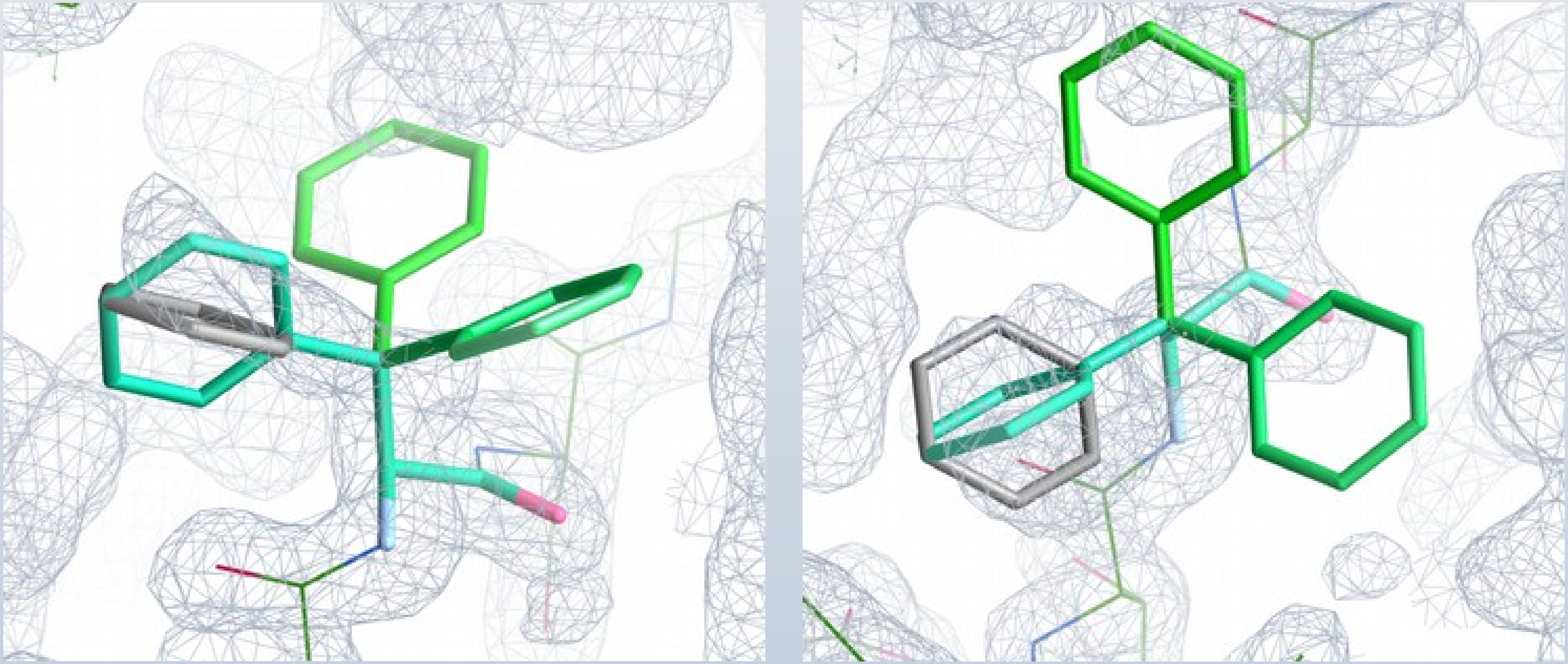
Rotamer Searching

- Two methods
  - Traditional
  - Backrub

Rotamers

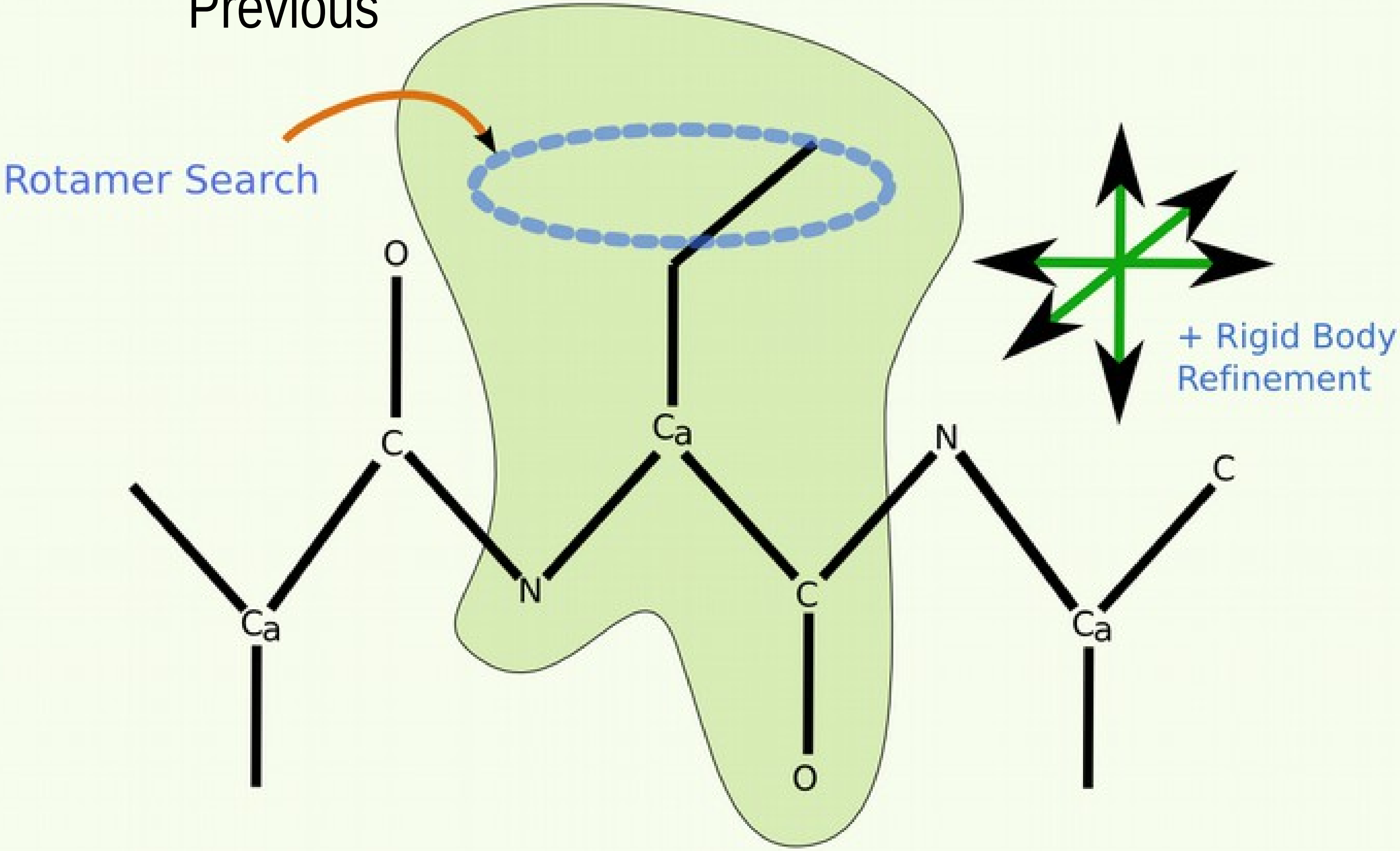
- Rotamers are preferred configurations of a side-chains rotatable bonds
    - where "preferred" means these configurations occur more frequently in a set of reference protein structures
    - "preferred" because they are low-energy conformations
- Several Rotamer "databases" exist
    - best: (Son of)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

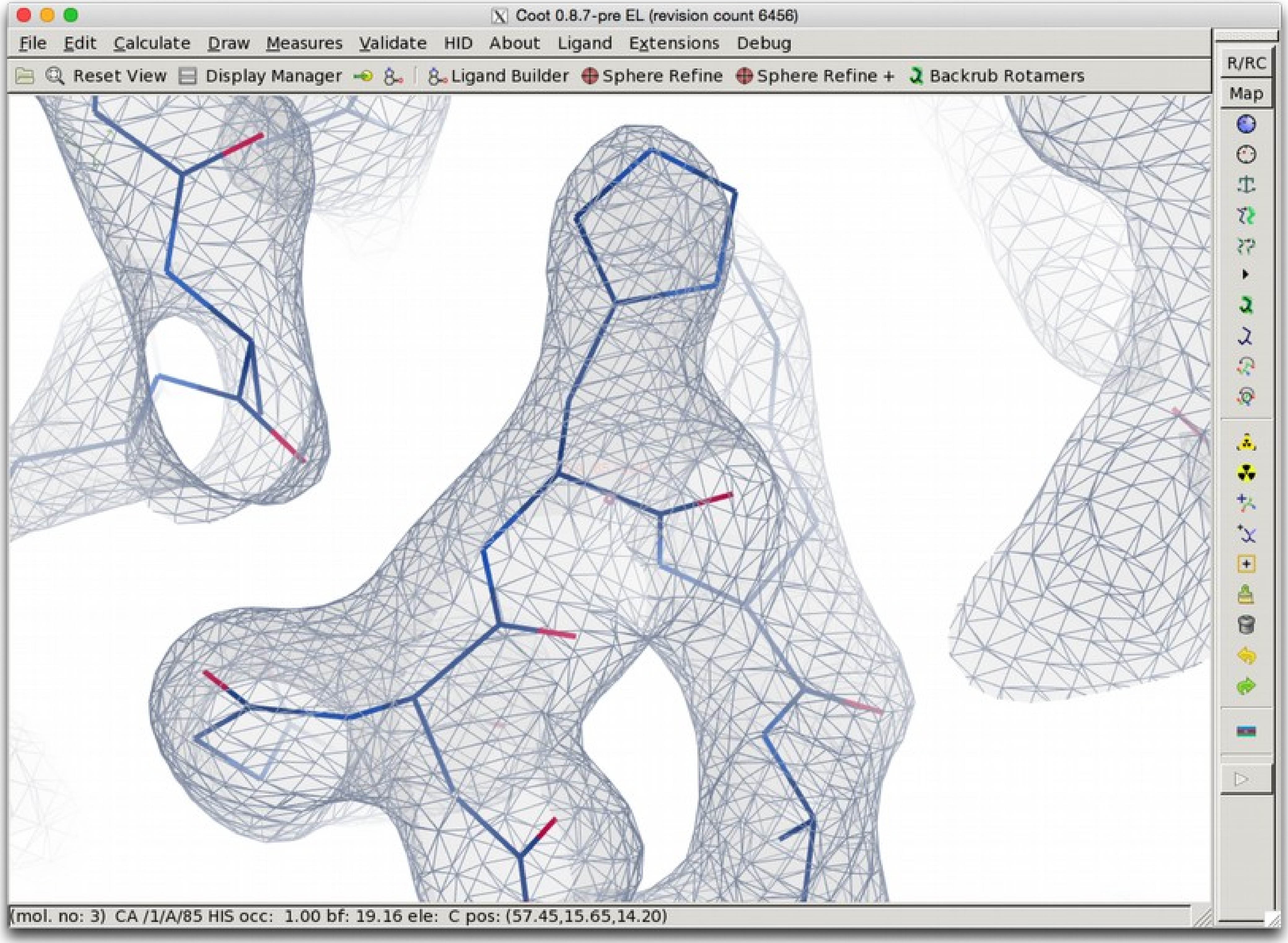
4 PHE Rotamers



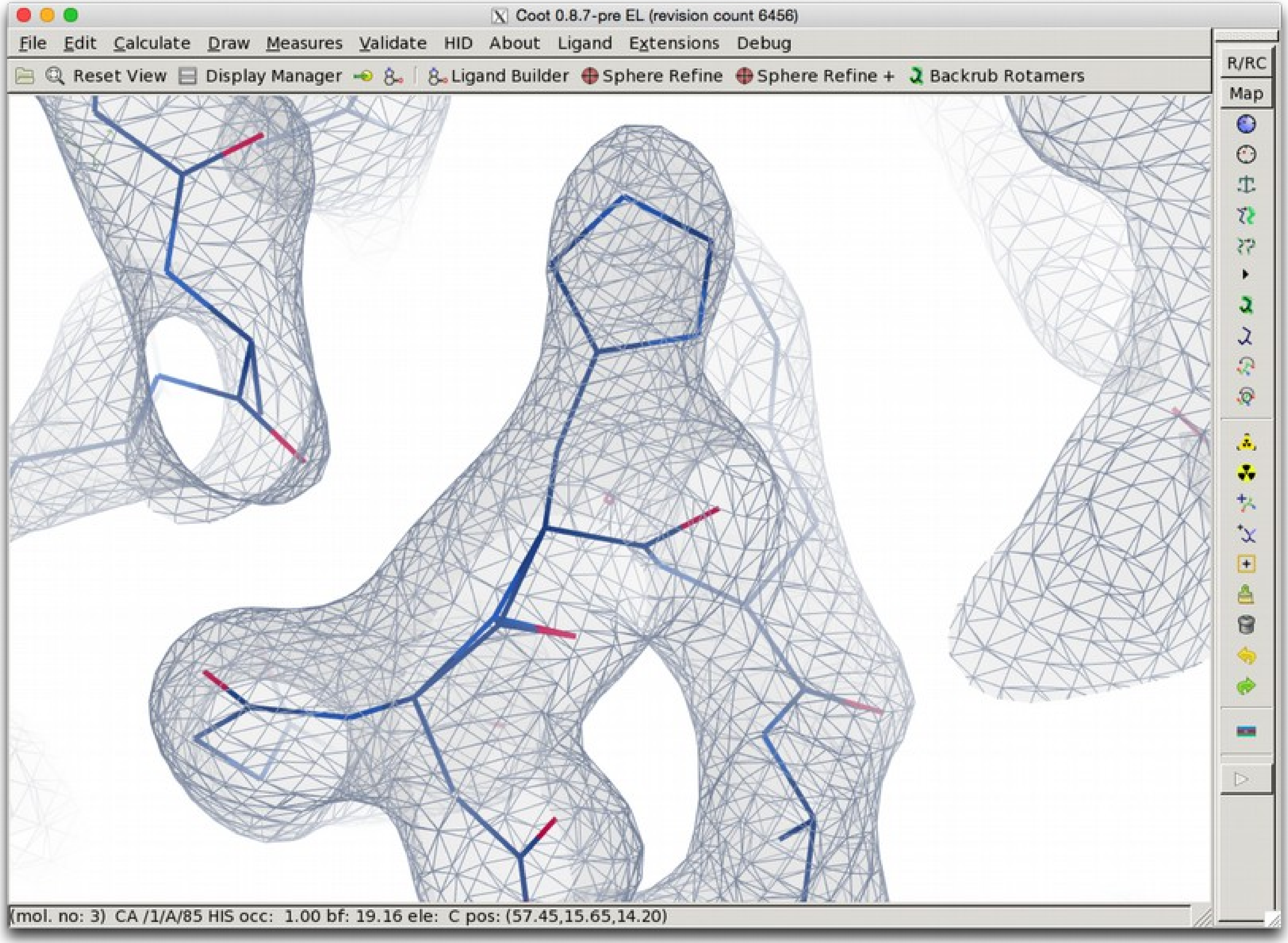
~~Current~~ Low Resolution Rotamer Search

Previous

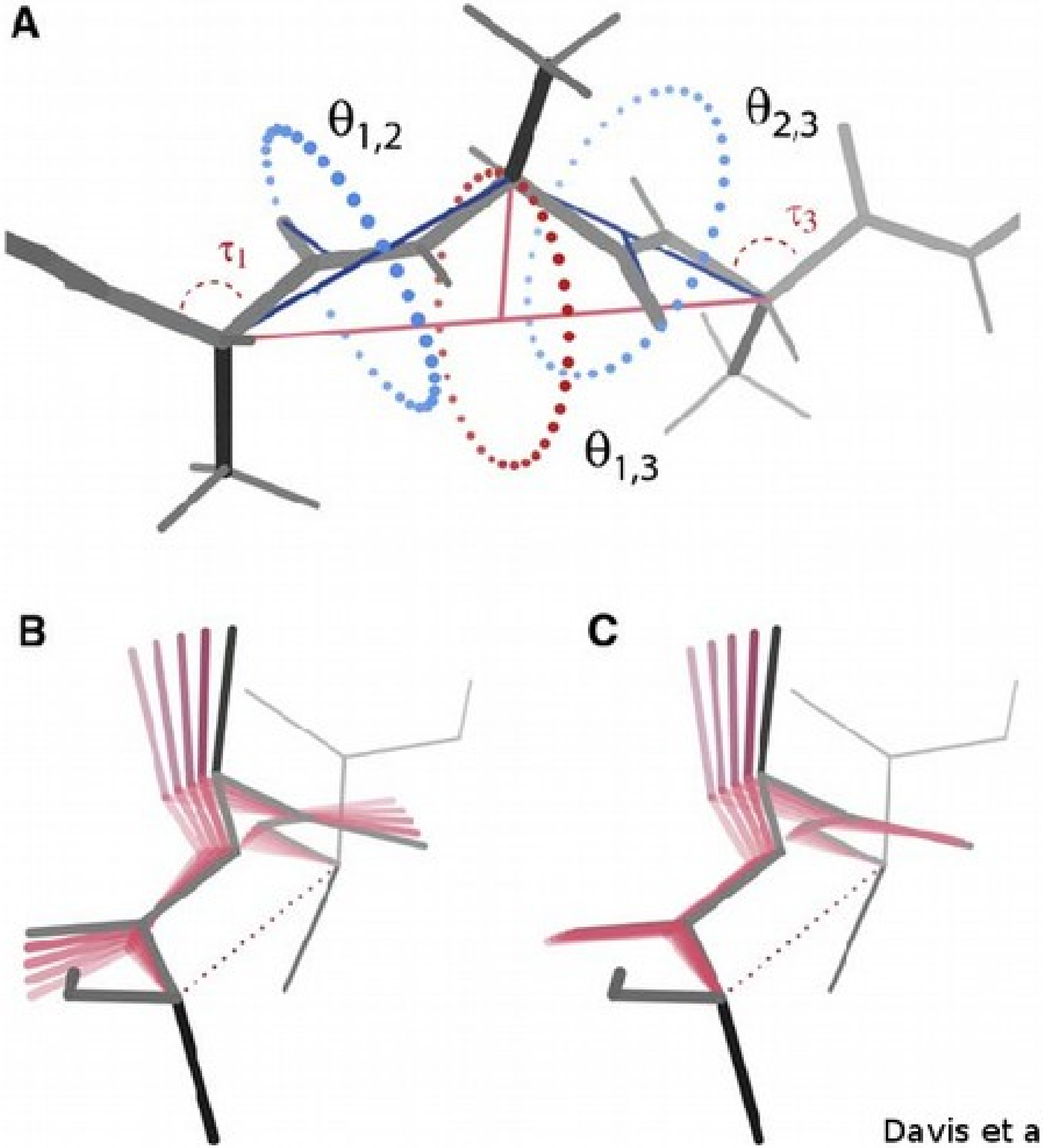




```
(mol. no: 3)  CA /1/A/85 HIS occ:  1.00 bf: 19.16 ele:  C pos: (57.45,15.65,14.20)
```

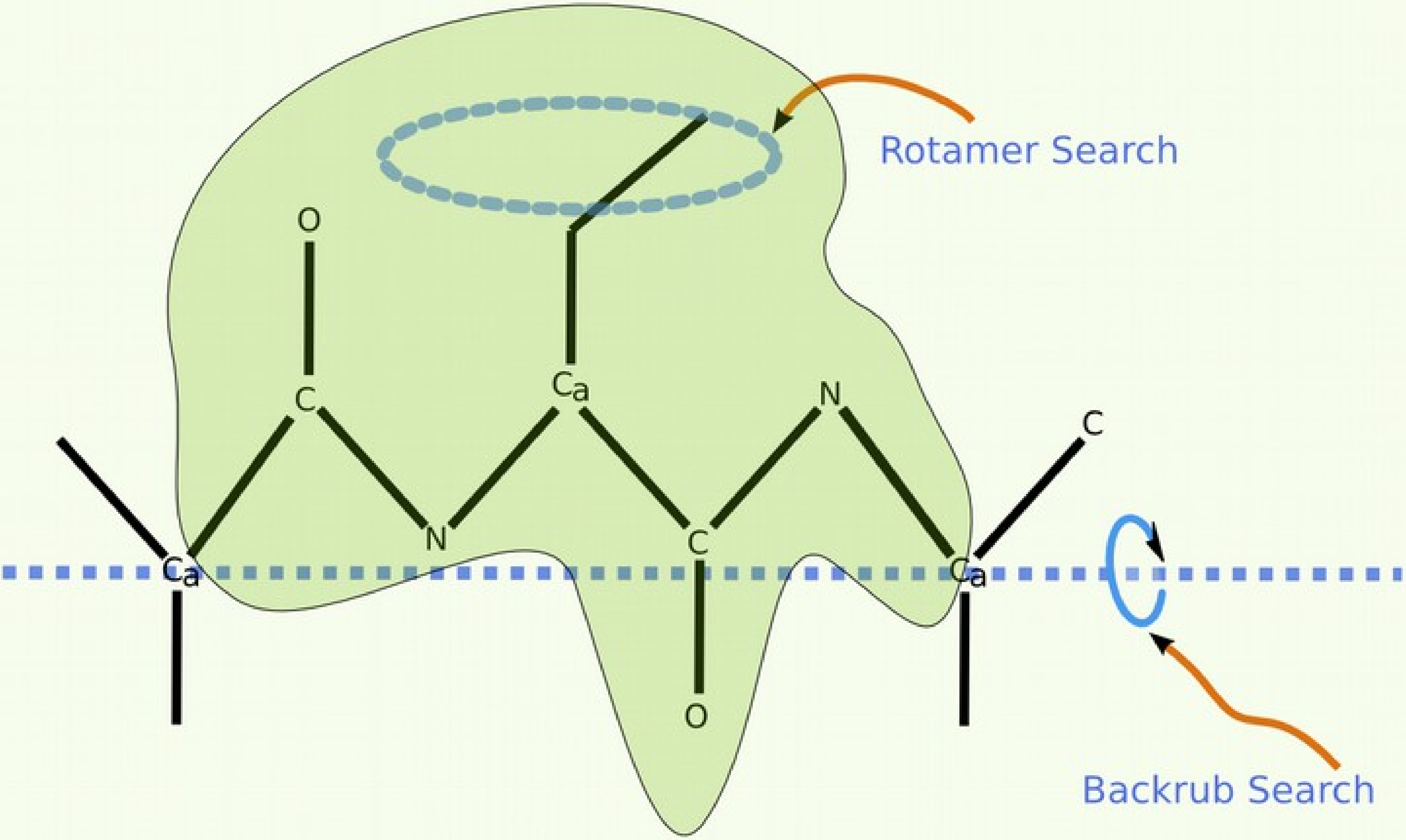


```
(mol. no: 3) CA /1/A/85 HIS occ:  1.00 bf: 19.16 ele:  C pos: (57.45,15.65,14.20)
```

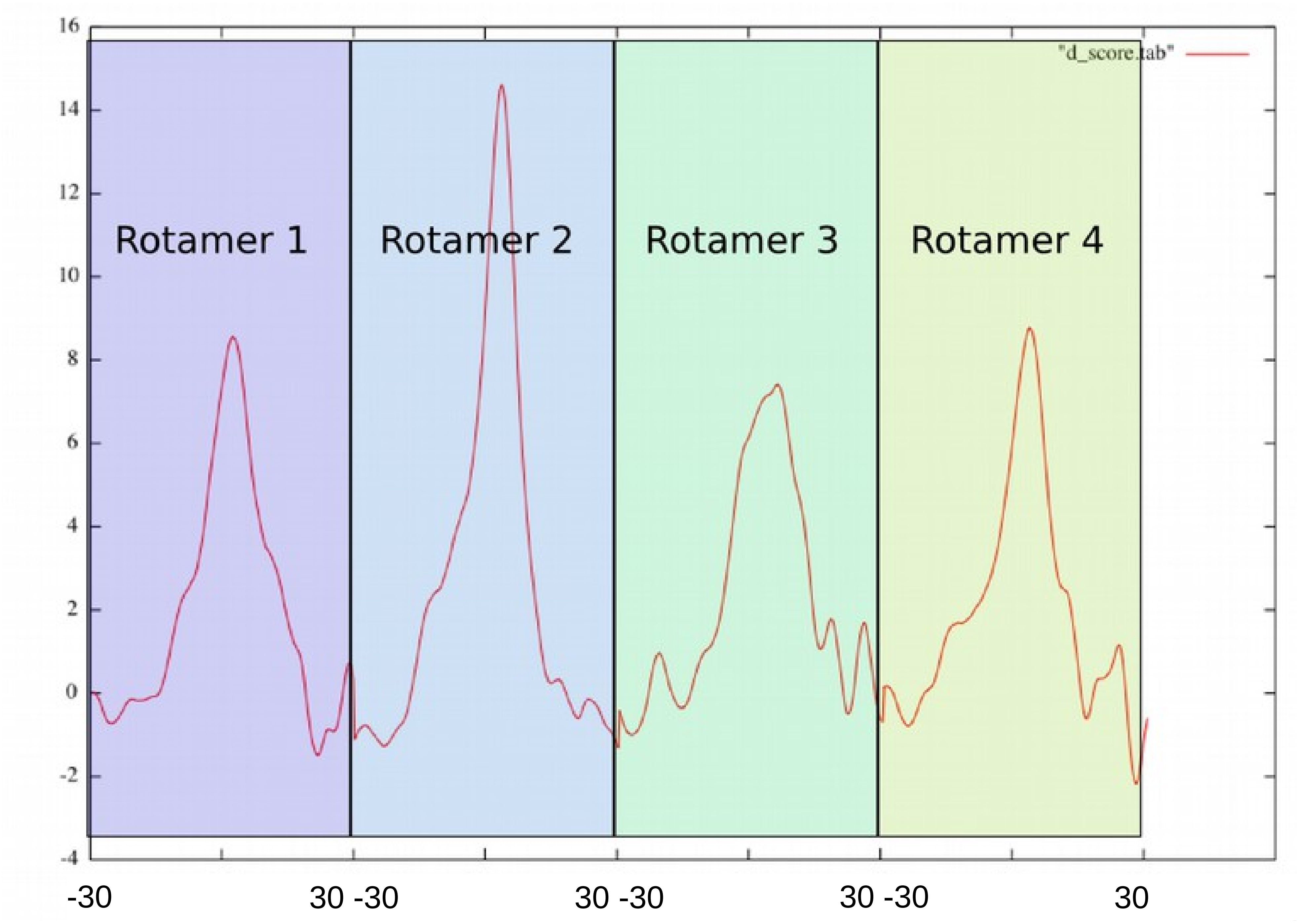


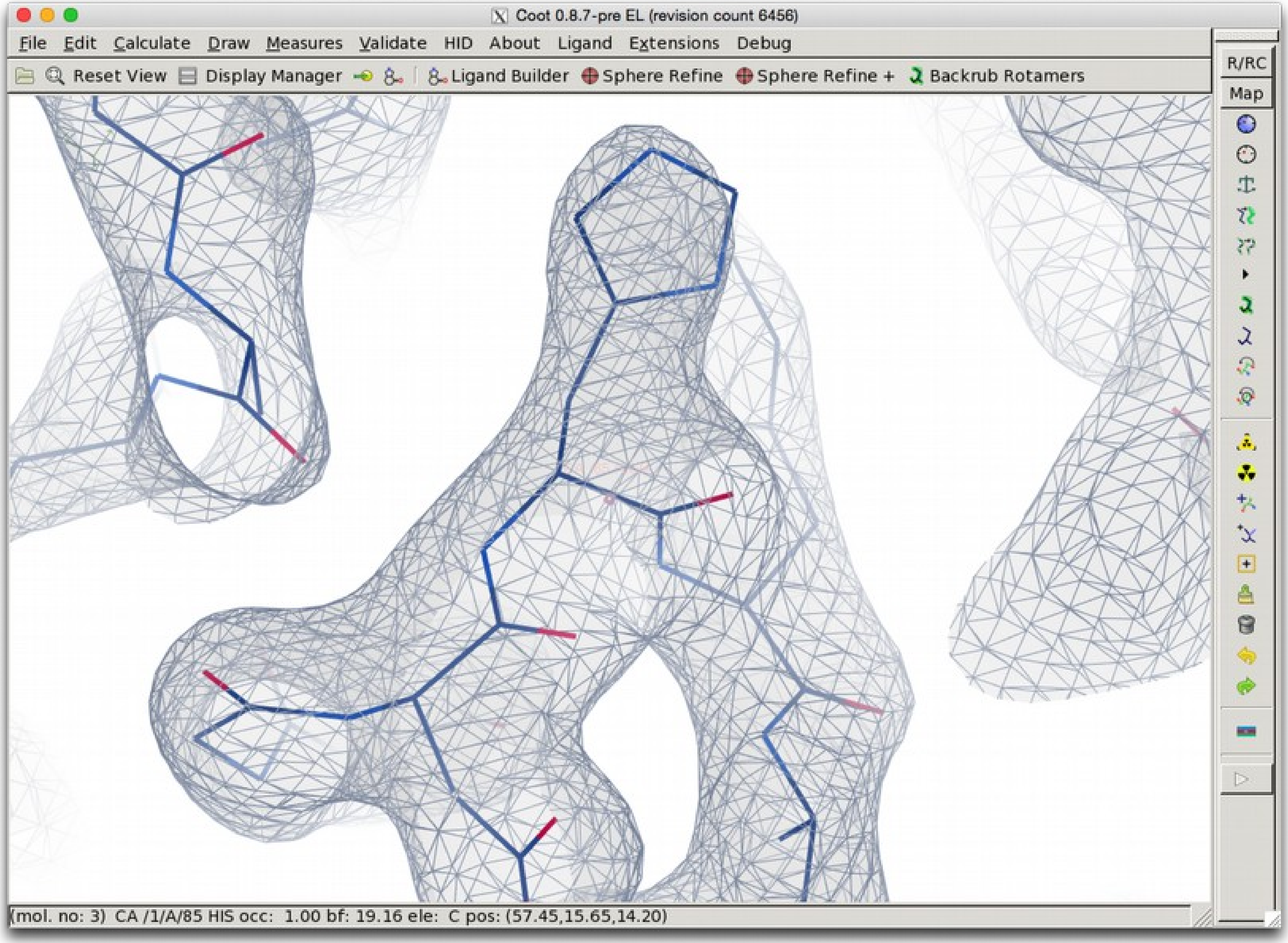
Davis et al. (2006) Structure

New Low Resolution Rotamer Search

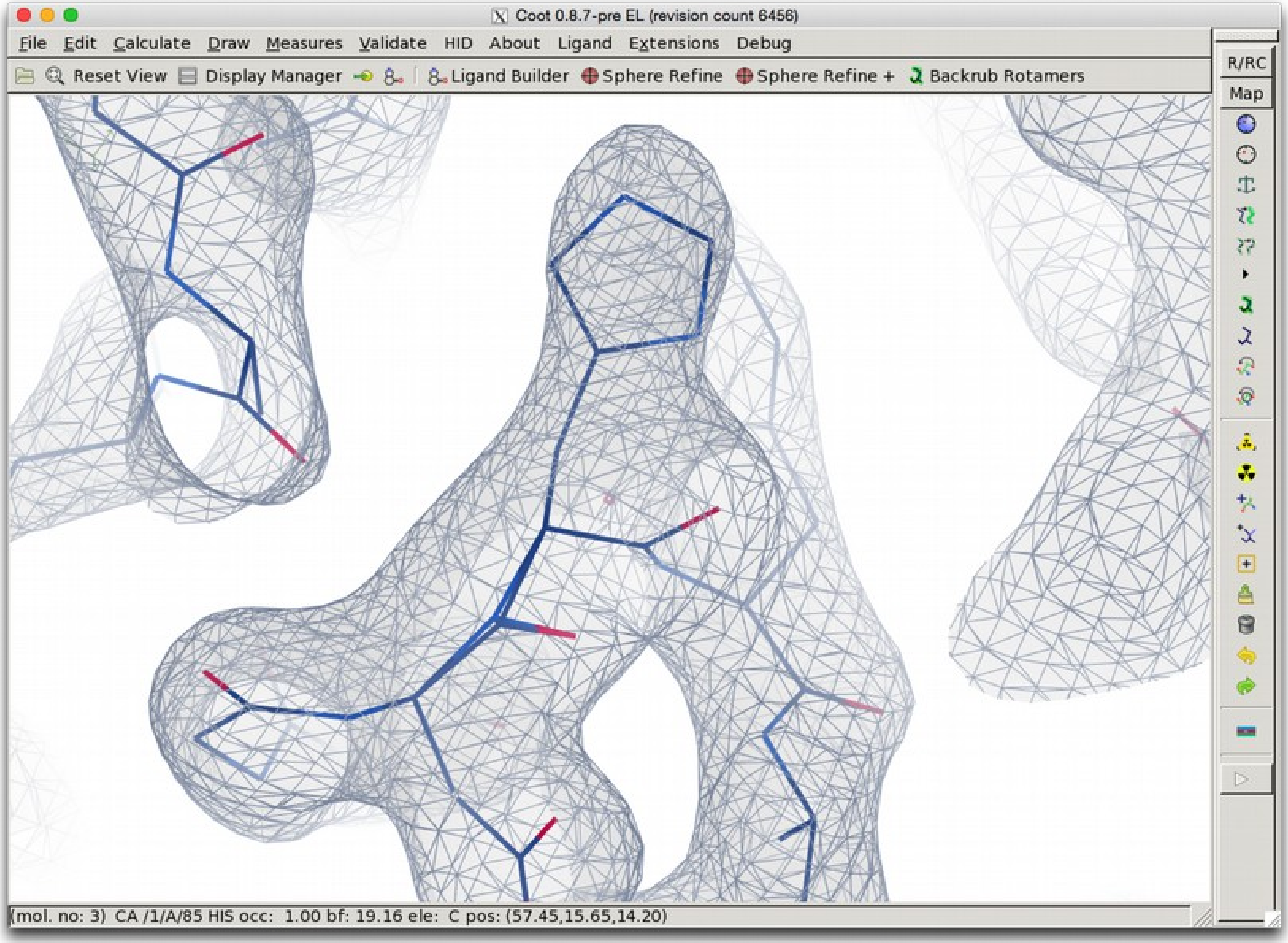


After Fitting Tools in KING/Molprobity

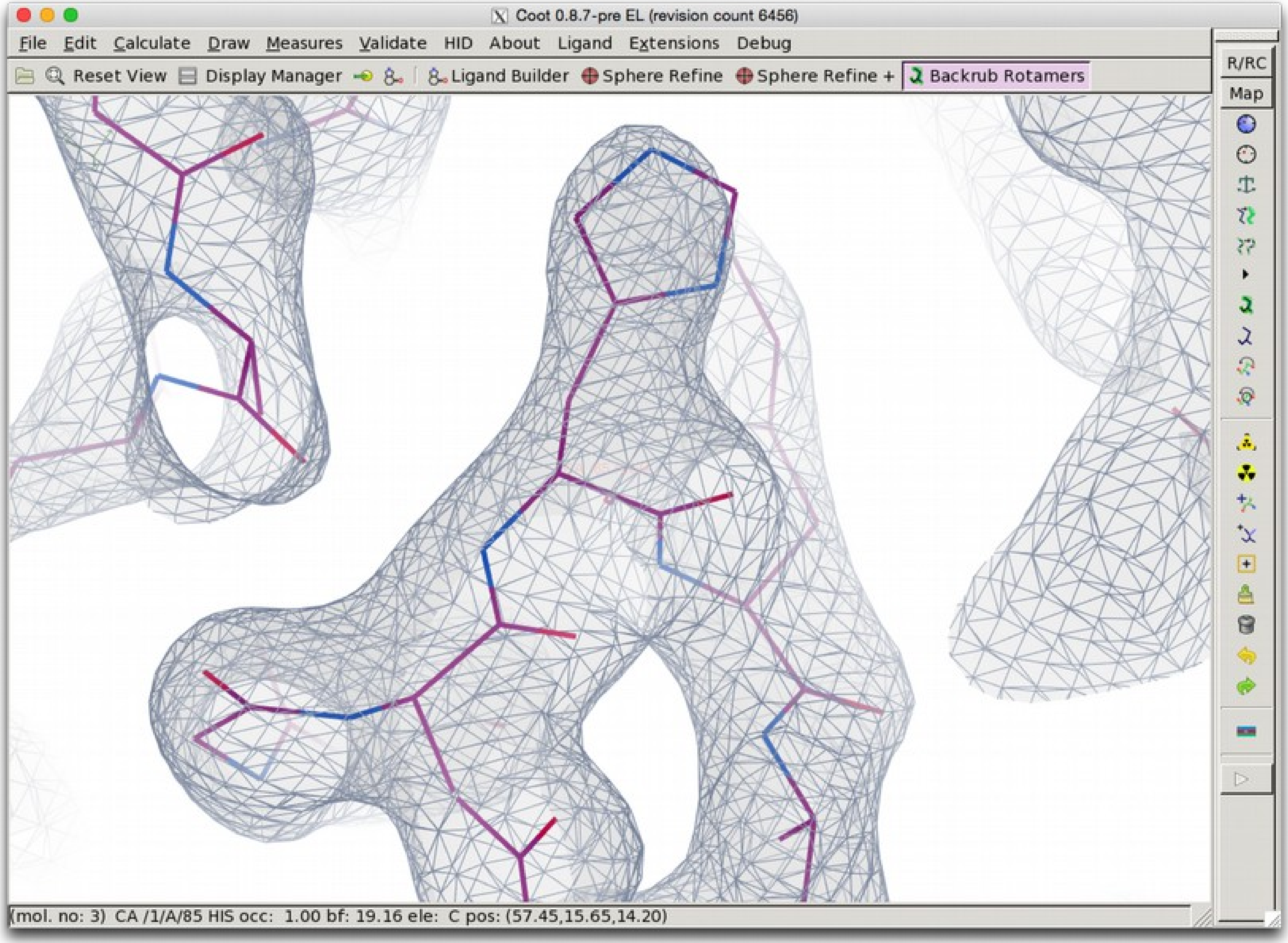

16
14
12
10
8
6
4
2
0
-2
-4
"d_score.tab"
Rotamer 1
Rotamer 2
Rotamer 3
Rotamer 4
-30
30 -30
30 -30
30 -30
30



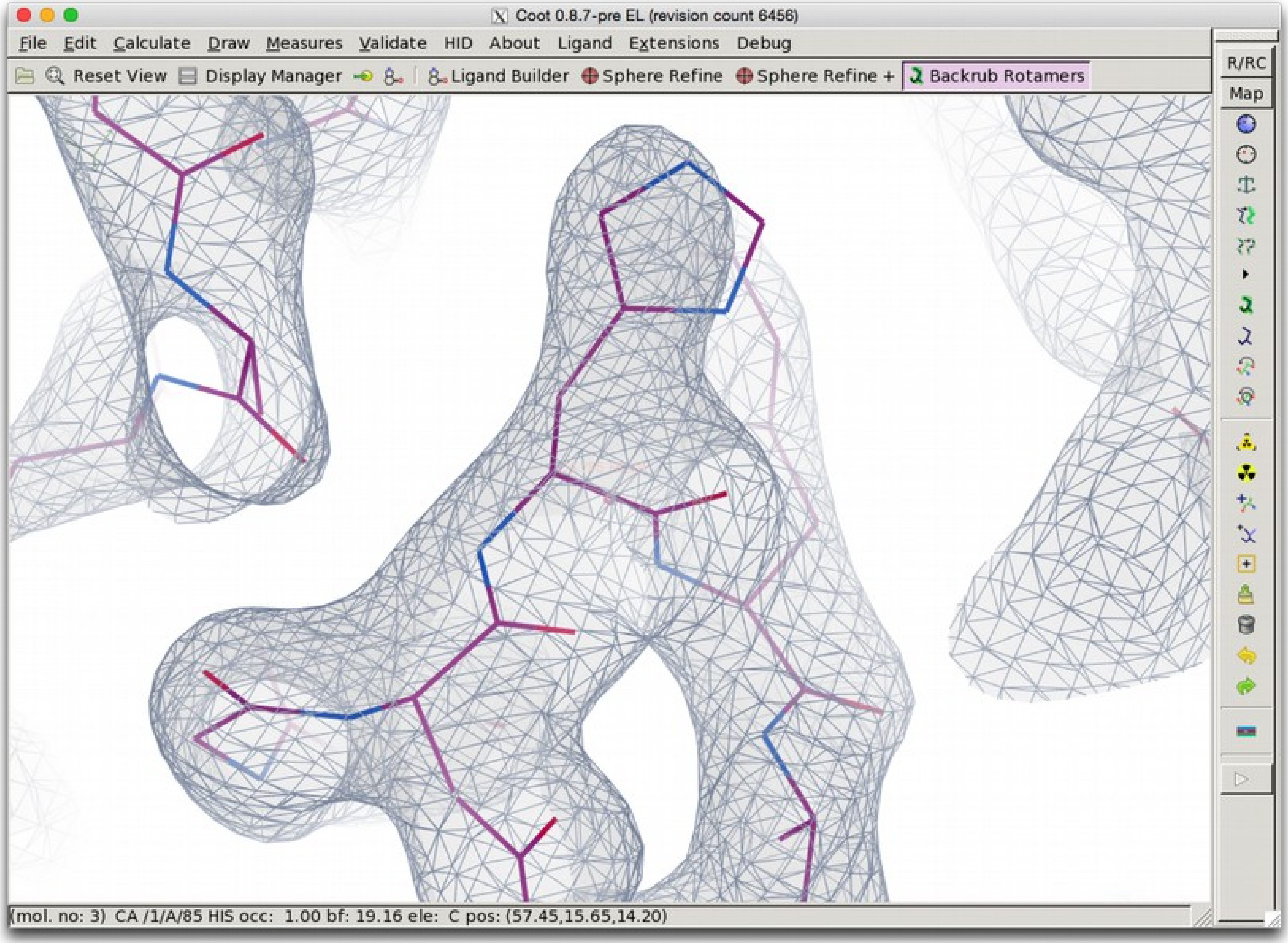
```
(mol. no: 3)  CA /1/A/85 HIS occ:  1.00 bf: 19.16 ele:  C pos: (57.45,15.65,14.20)
```



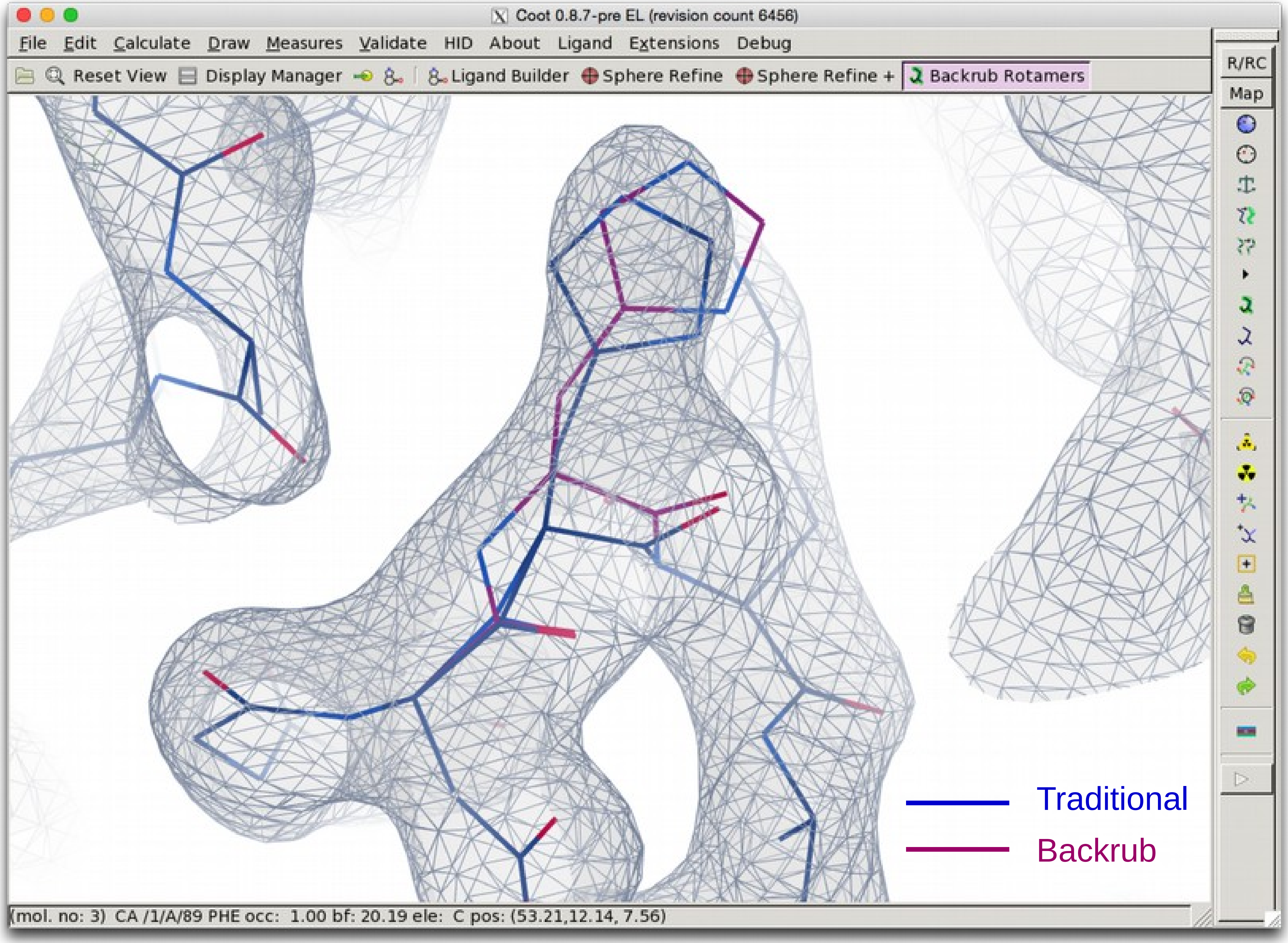
```
(mol. no: 3)  CA /1/A/85 HIS occ:  1.00 bf: 19.16 ele:  C pos: (57.45,15.65,14.20)
```



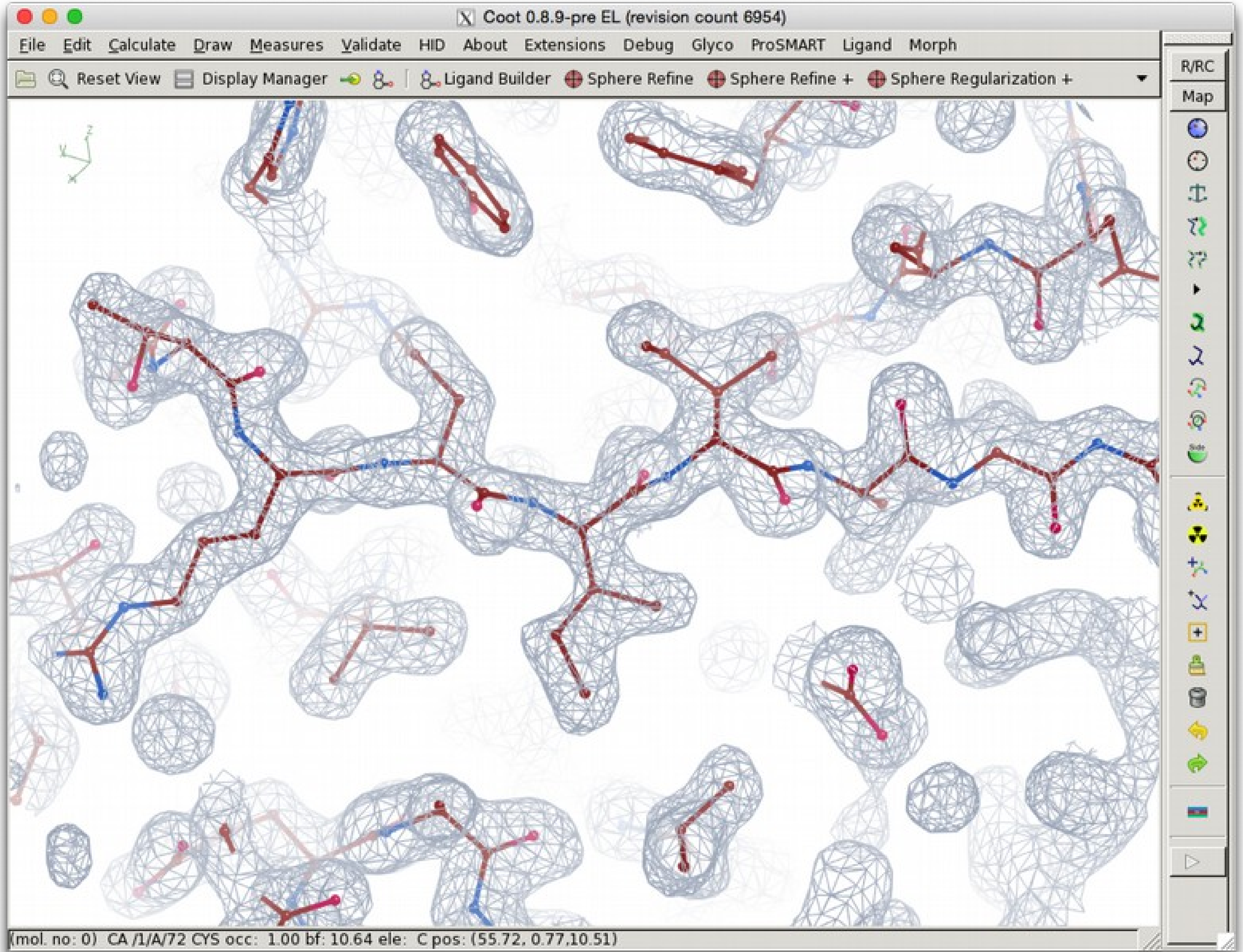
(mol. no: 3) CA /1/A/85 HIS occ: 1.00 bf: 19.16 ele: C pos: (57.45,15.65,14.20)



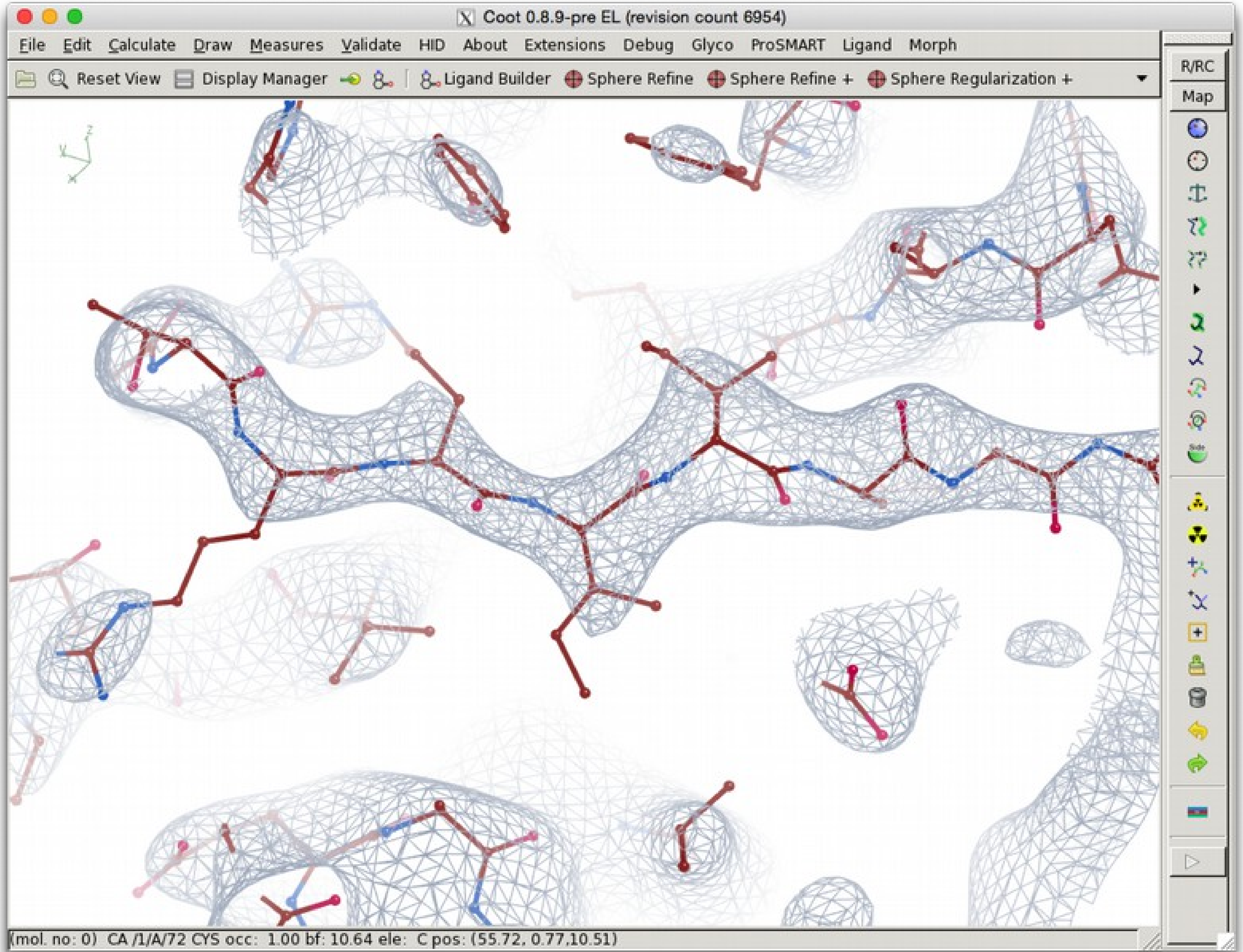
```
(mol. no: 3)  CA /1/A/85 HIS occ:  1.00 bf: 19.16 ele:  C pos: (57.45,15.65,14.20)
```



```
(mol. no: 3) CA /1/A/89 PHE occ:  1.00 bf: 20.19 ele:  C pos: (53.21,12.14, 7.56)
```



```
(mol. no: 0)  CA /1/A/72 CYS occ:  1.00 bf: 10.64 ele:  C pos: (55.72, 0.77,10.51)
```



```
(mol. no: 0)  CA /1/A/72 CYS occ:  1.00 bf: 10.64 ele:  C pos: (55.72, 0.77,10.51)
```

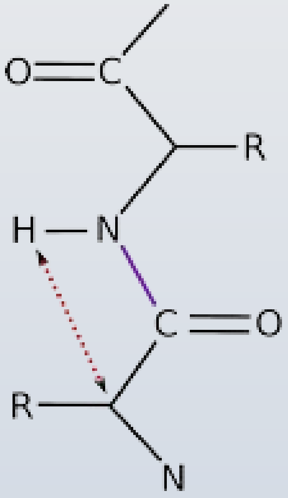
cis-Peptides

- What is a cis-peptide?
- Peptide restraints in Coot 2004-2015

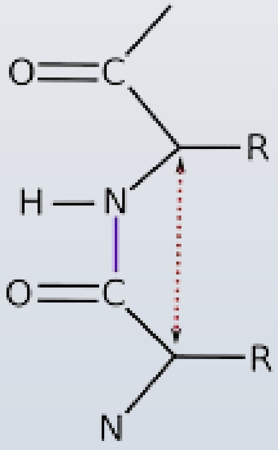
cis-Peptides

- A number of paper have been published recently 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). **D**71, 706-709
  - Touw *et al.*: Detection of trans–cis flips and peptide-plane flips in protein structures *Acta Cryst.* (2015). **D**71, 1604-71614

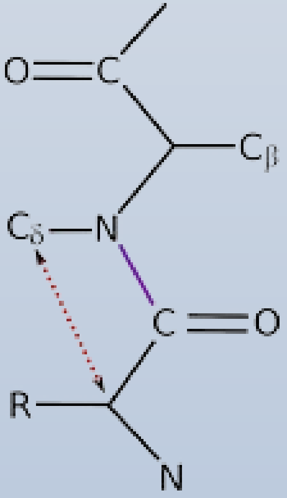
cis-Peptides



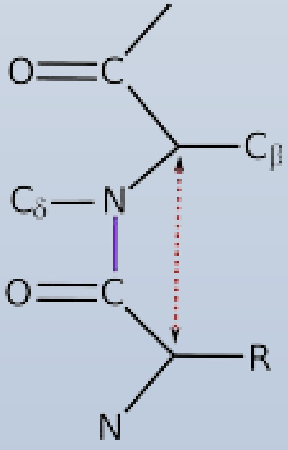
trans-peptide



cis-peptide

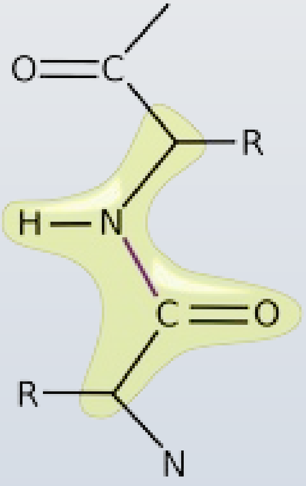


PRO *trans-peptide*

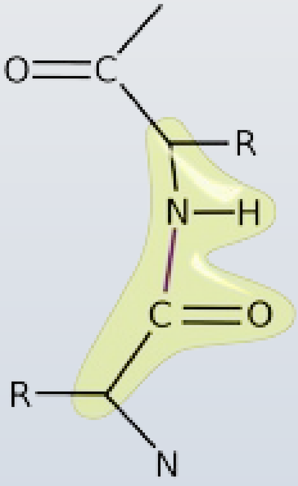


PRO *cis-peptide*

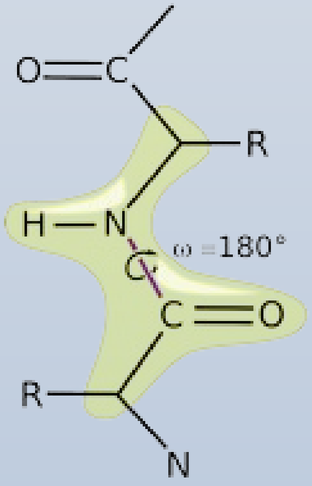
cis-Peptides



trans-peptide
with plane restraints

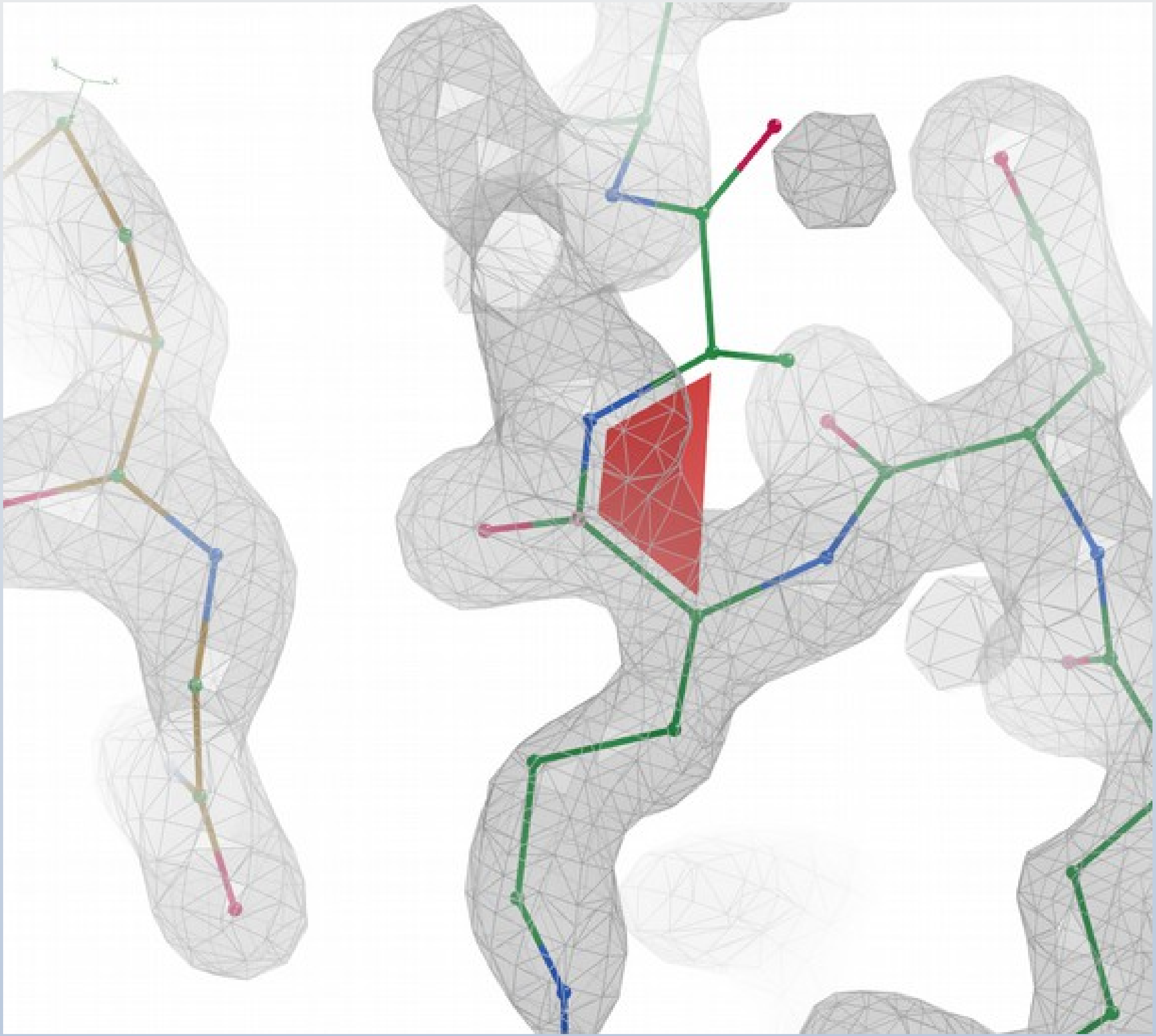


cis-peptide
with plane restraints



trans-peptide
with plane and trans restraints

cis-peptide Representation



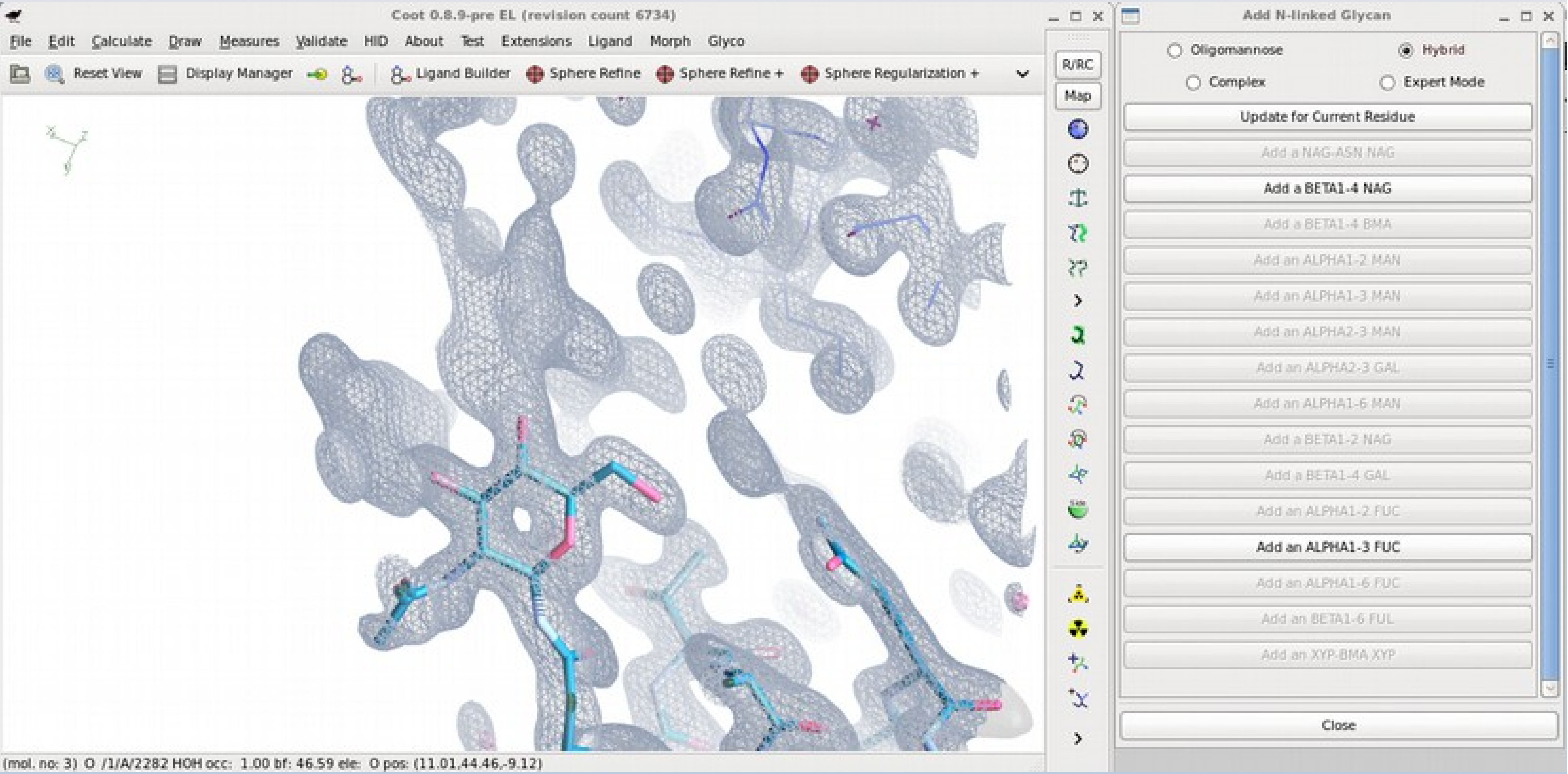
Pre-PRO 🟩

Twisted-trans 🟨

Non-pre-PRO 🟥

N-linked Carbohydrates

- Improved algorithm and re-worked GUI

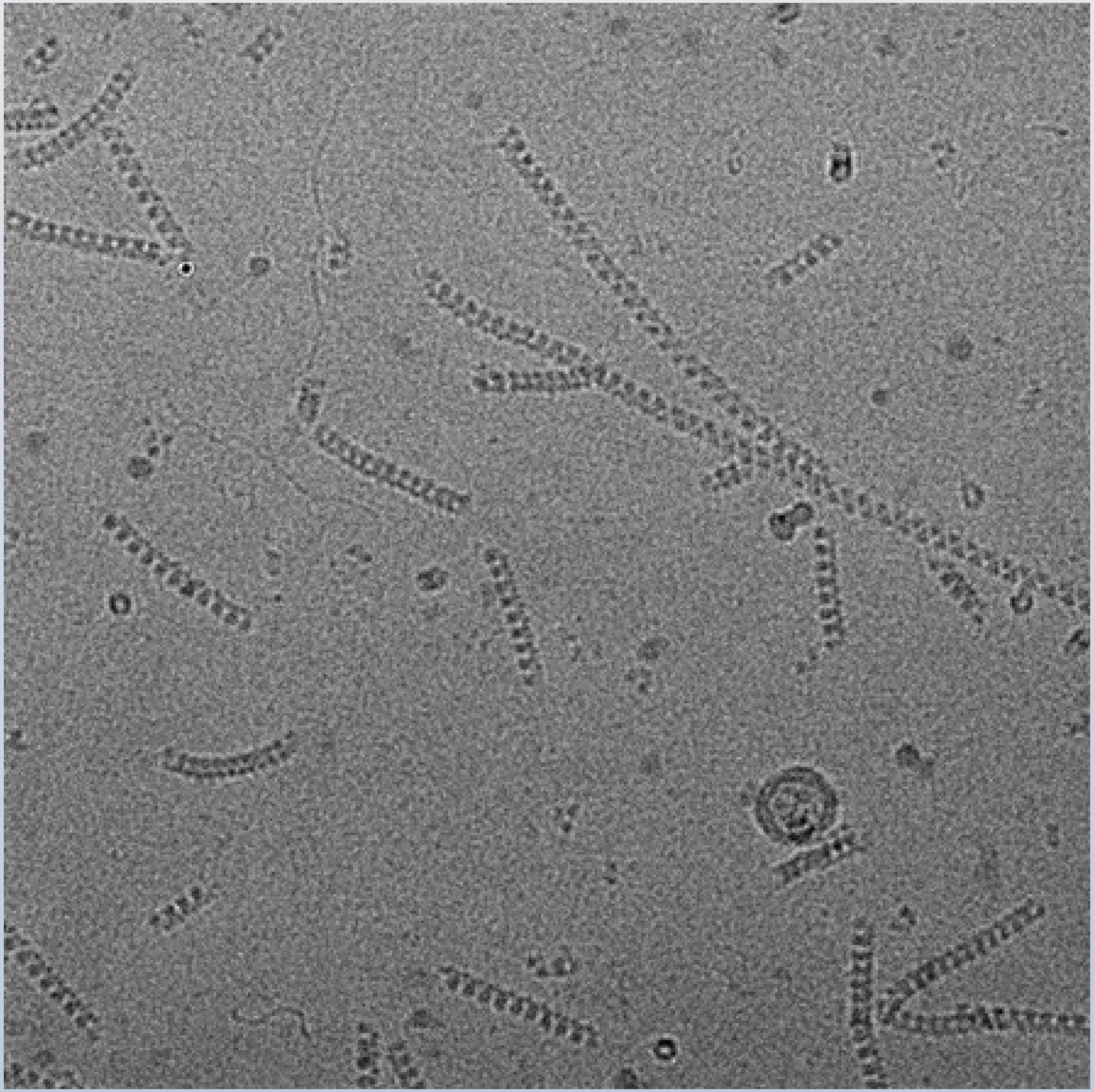


○ Oligomannose ● Hybrid
○ Complex ○ Expert Mode

(mol. no: 3) O /1/A/2282 HOH occ: 1.00 bf: 46.59 ele: O pos: (11.01,44.46,-9.12)

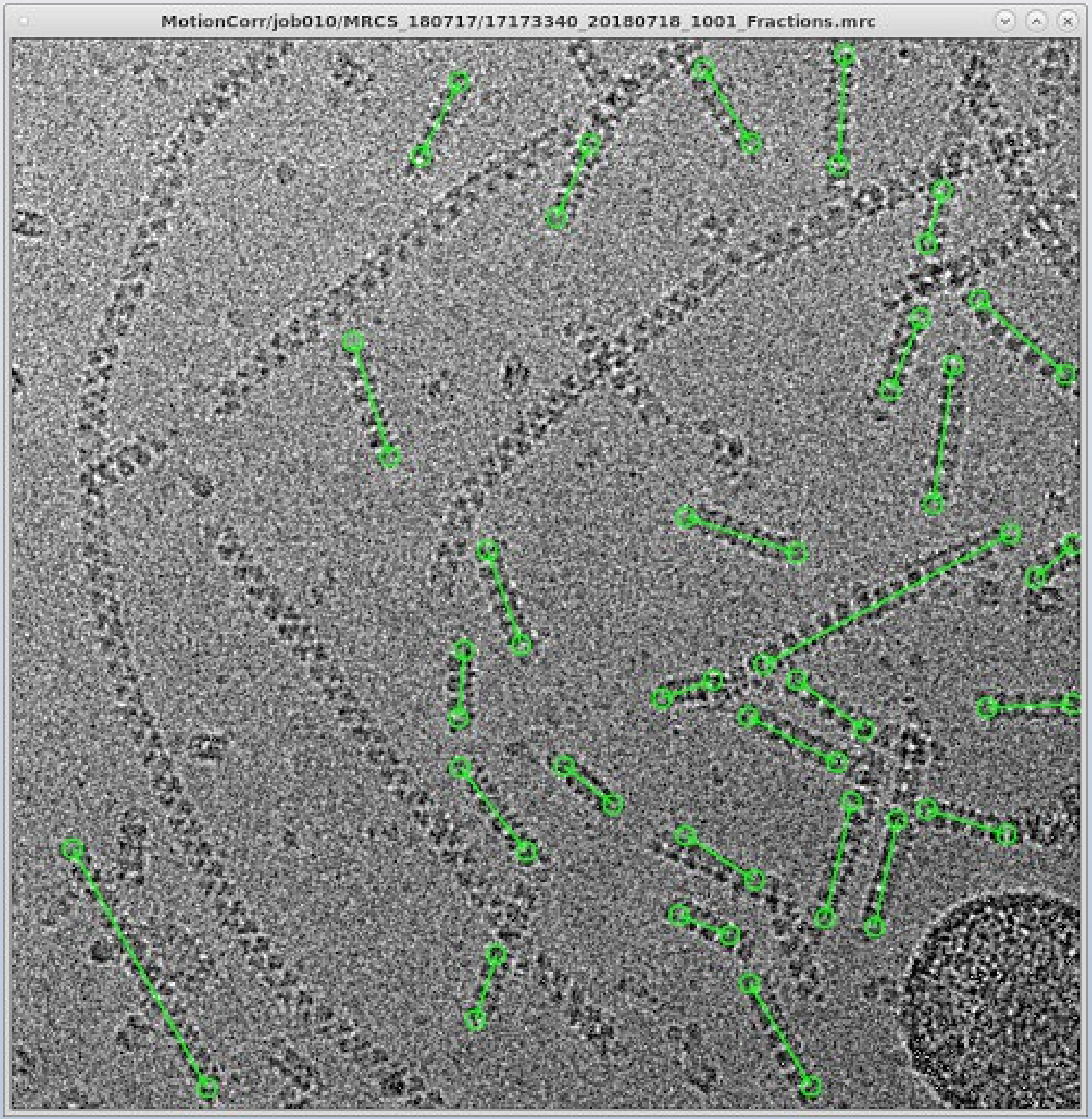
Filaments

Filaments



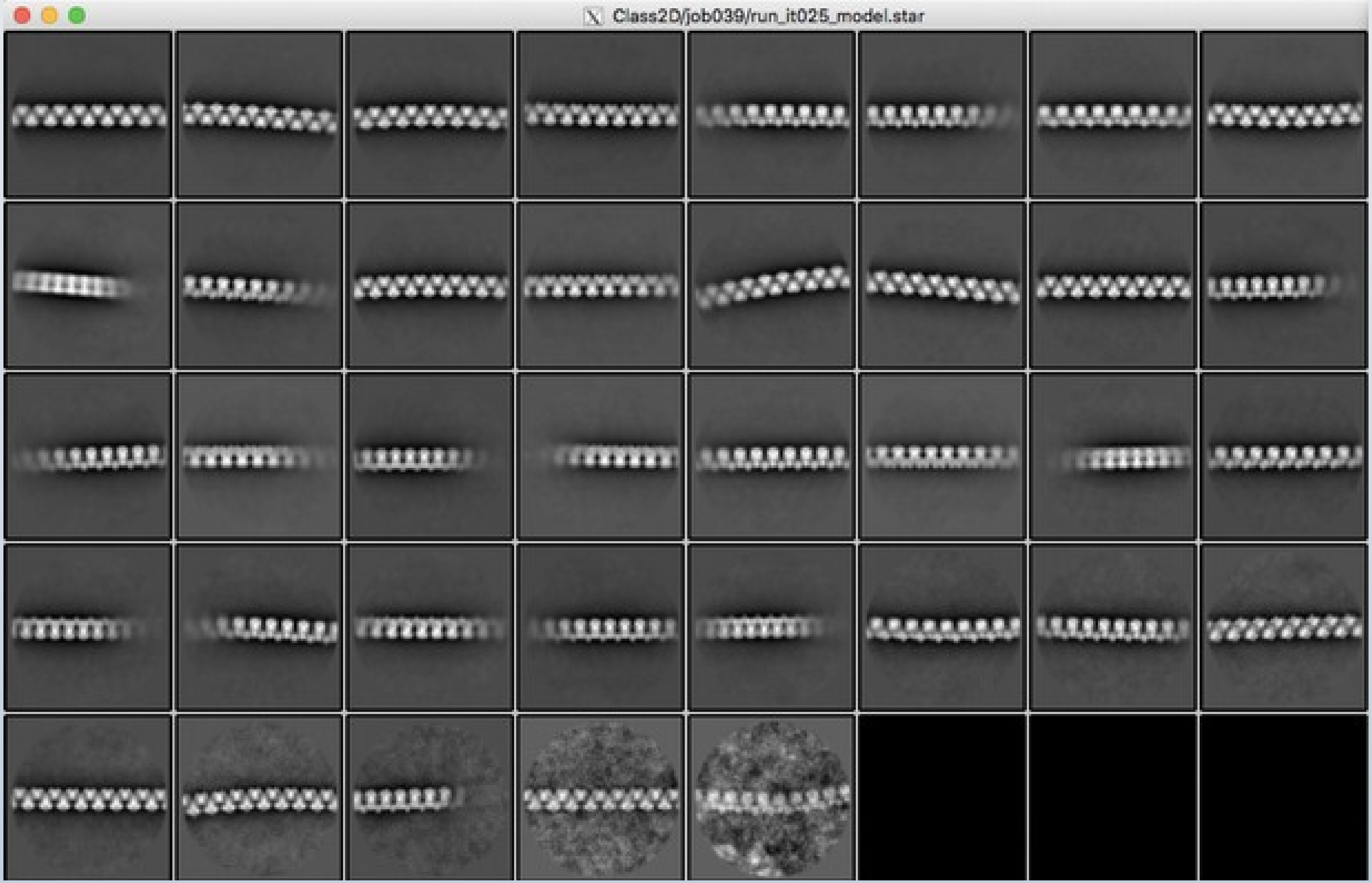
Titan Krios
K2 Detector

Filaments

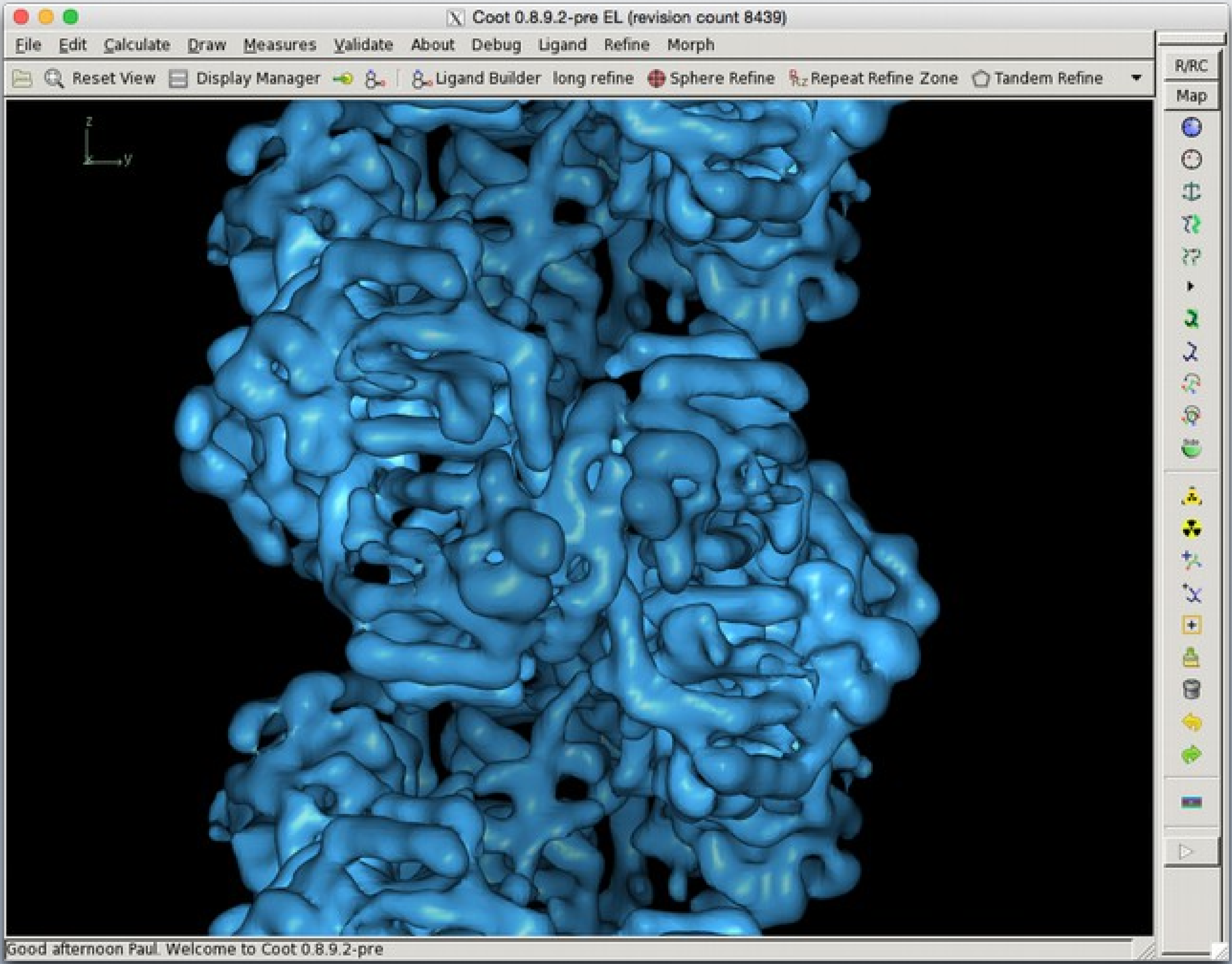


MotionCorr/job010/MRCS_180717/17173340_20180718_1001_Fractions.mrc

Filaments

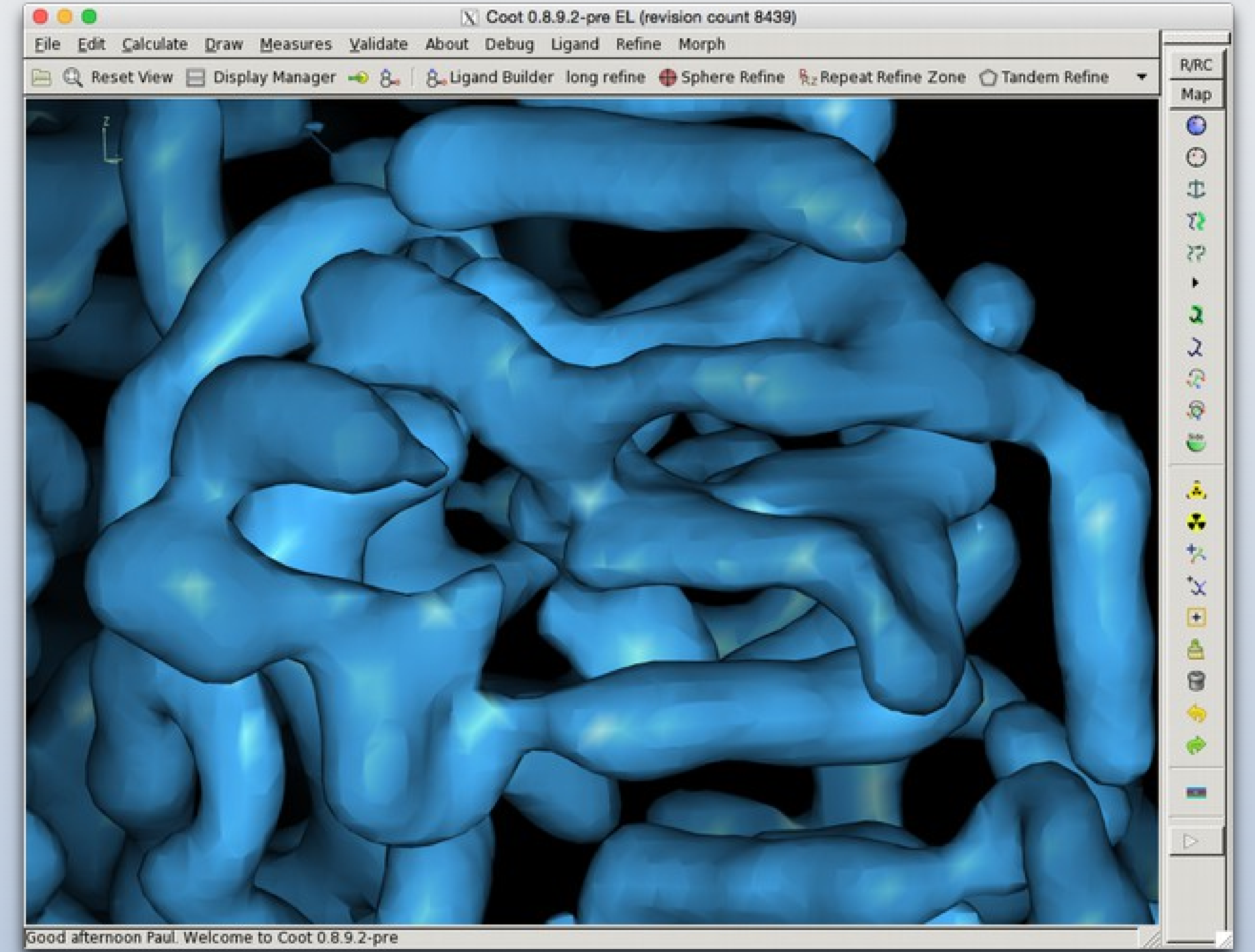


Filaments



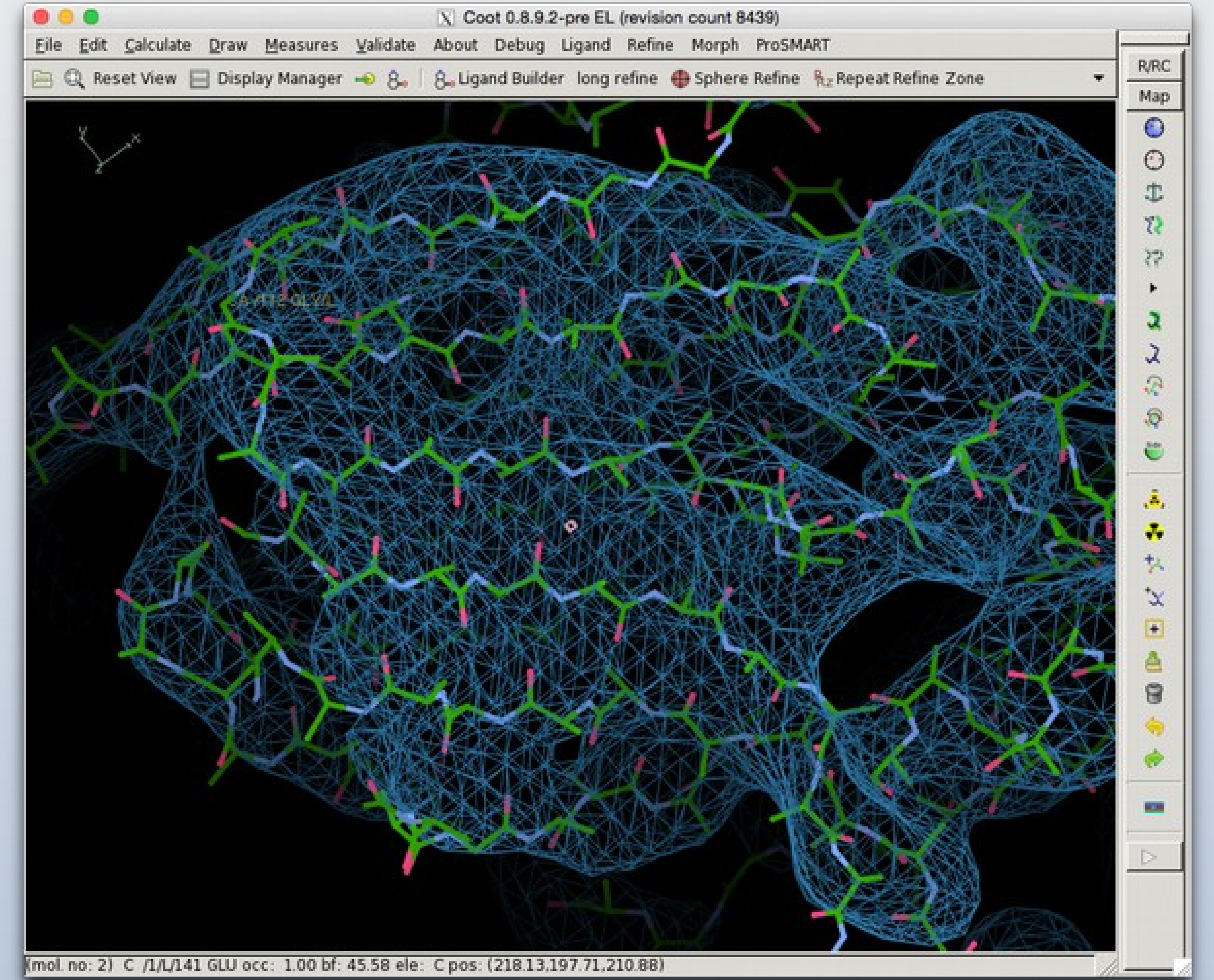
Good afternoon Paul. Welcome to Coot 0.8.9.2-pre

Filaments



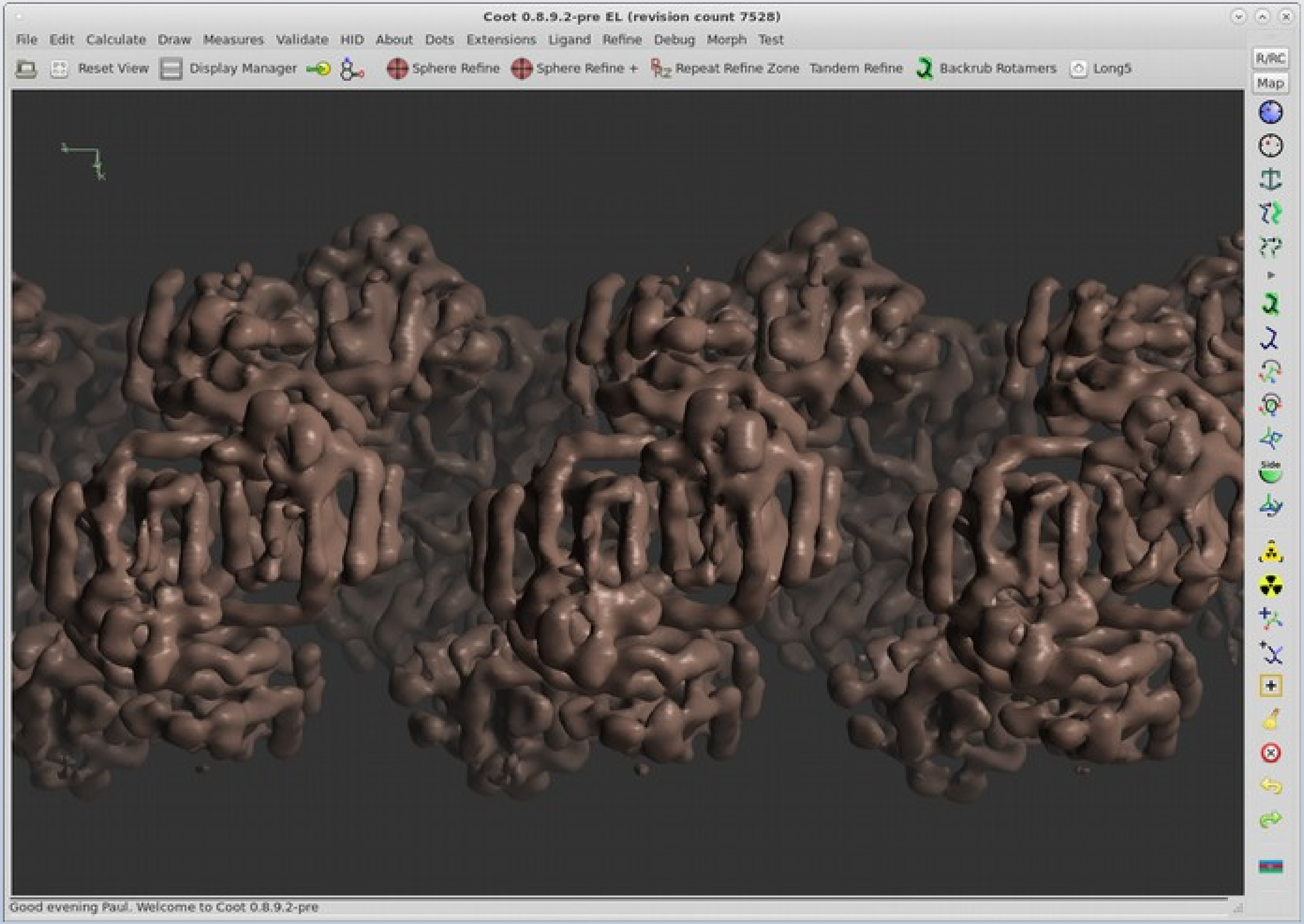
Good afternoon Paul. Welcome to Coot 0.8.9.2-pre

Filaments



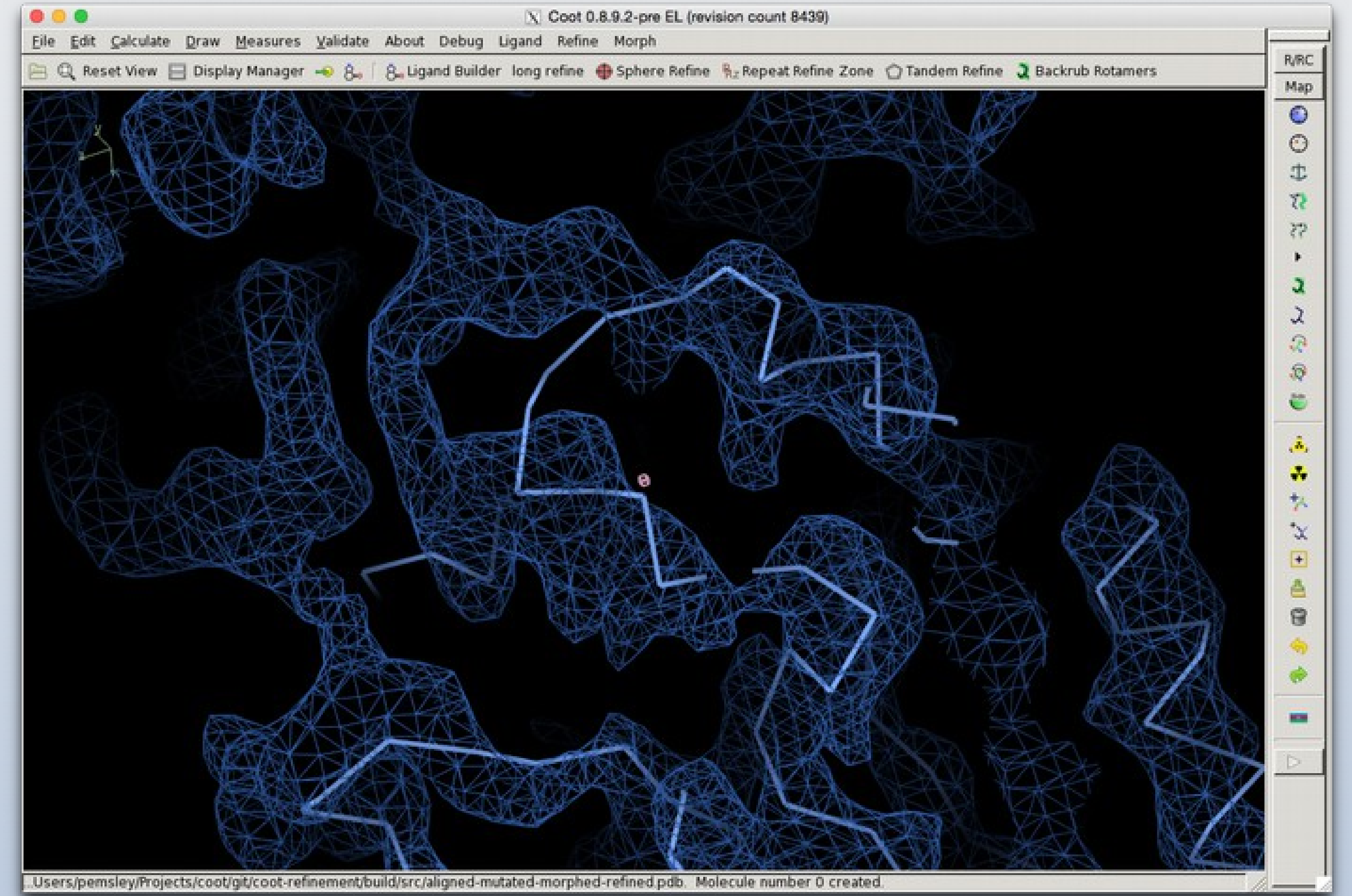
```
(mol. no: 2) C /1/L/141 GLU occ: 1.00 bf: 45.58 ele: C pos: (218.13,197.71,210.88)
```

3D Reconstruction



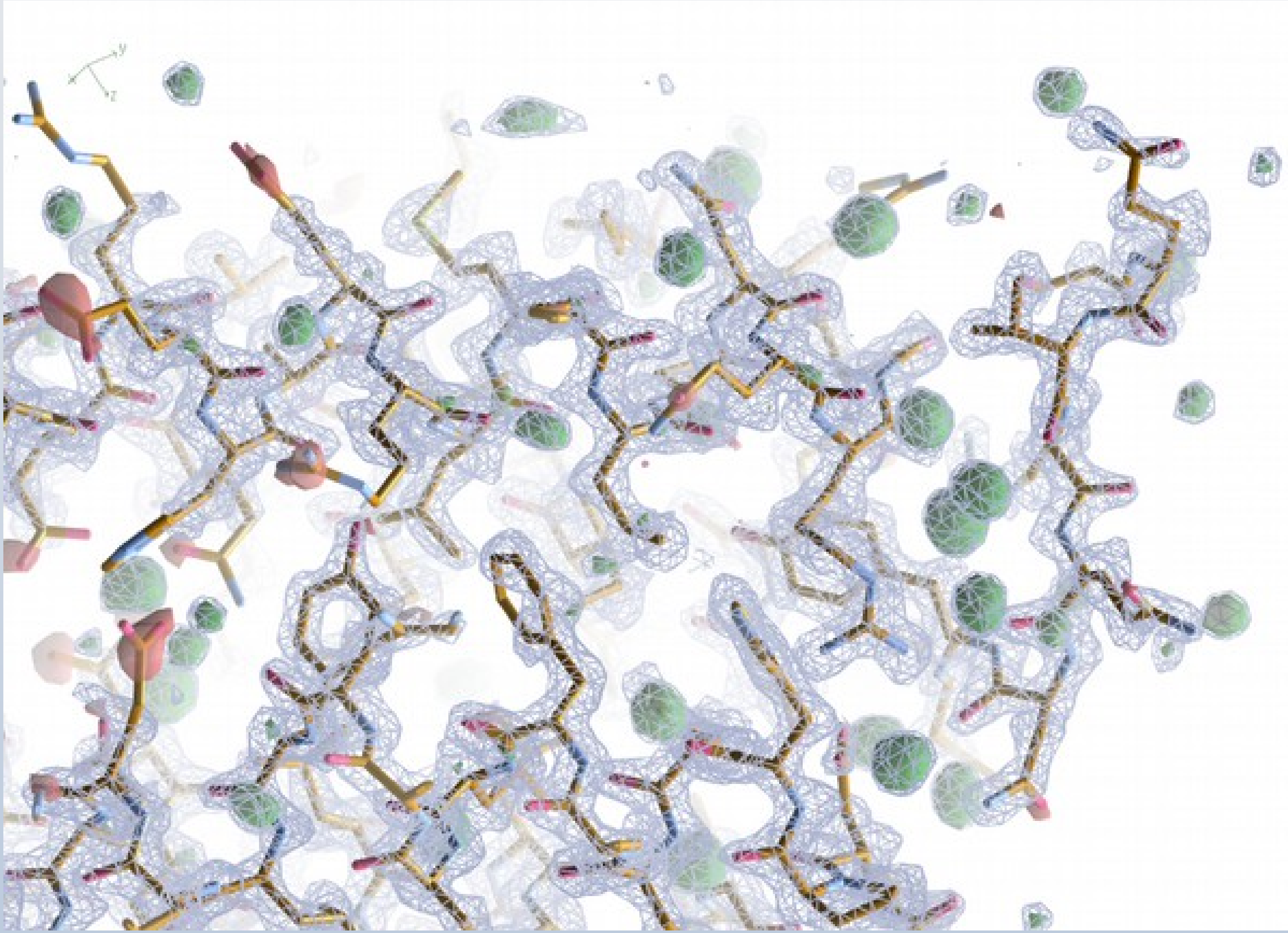
Good evening Paul. Welcome to Coot 0.8.9.2-pre

Filaments

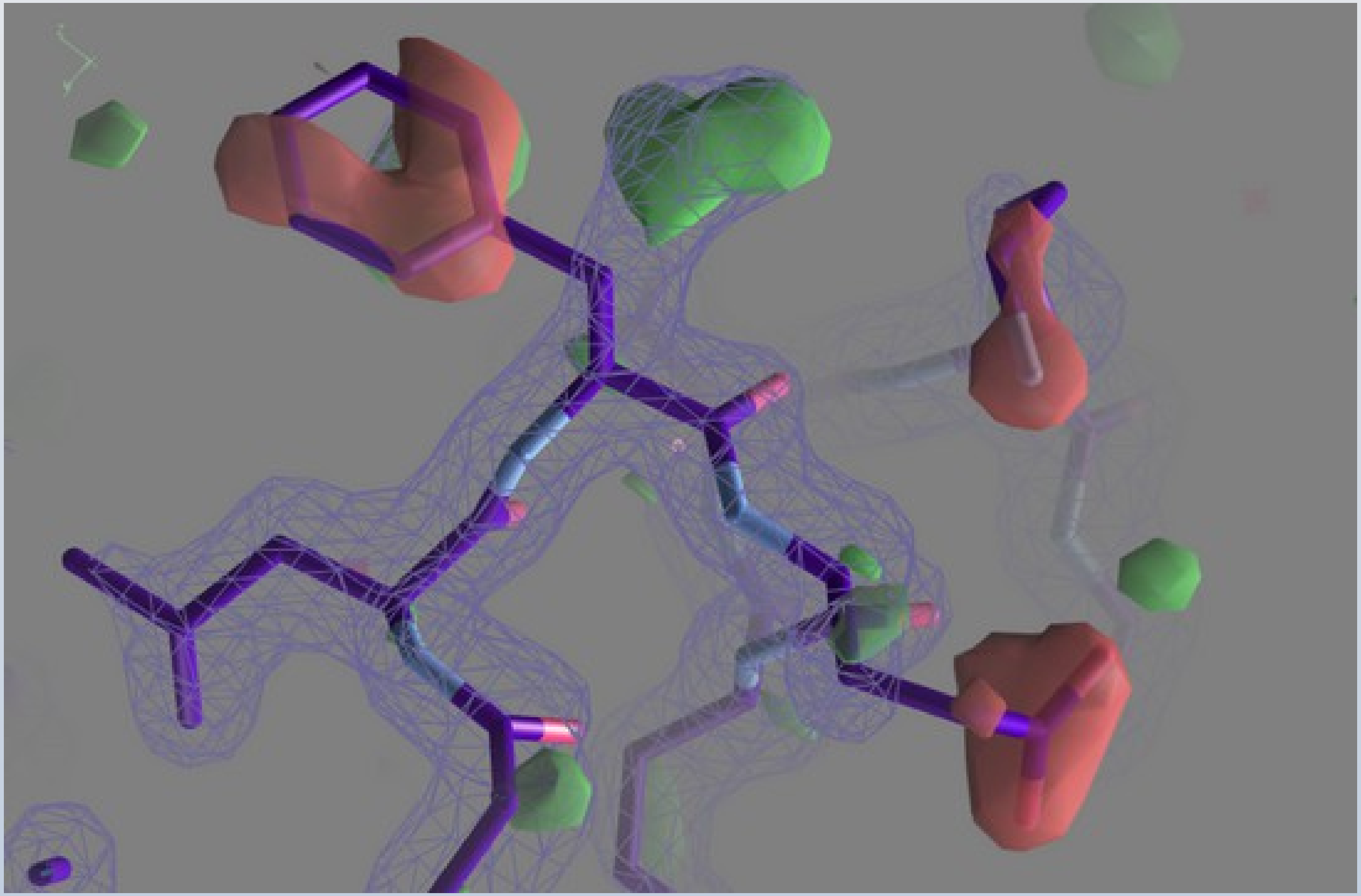


Users/pemsley/Projects/coot/git/coot-refinement/build/src/aligned-mutated-morphed-refined.pdb. Molecule number 0 created.

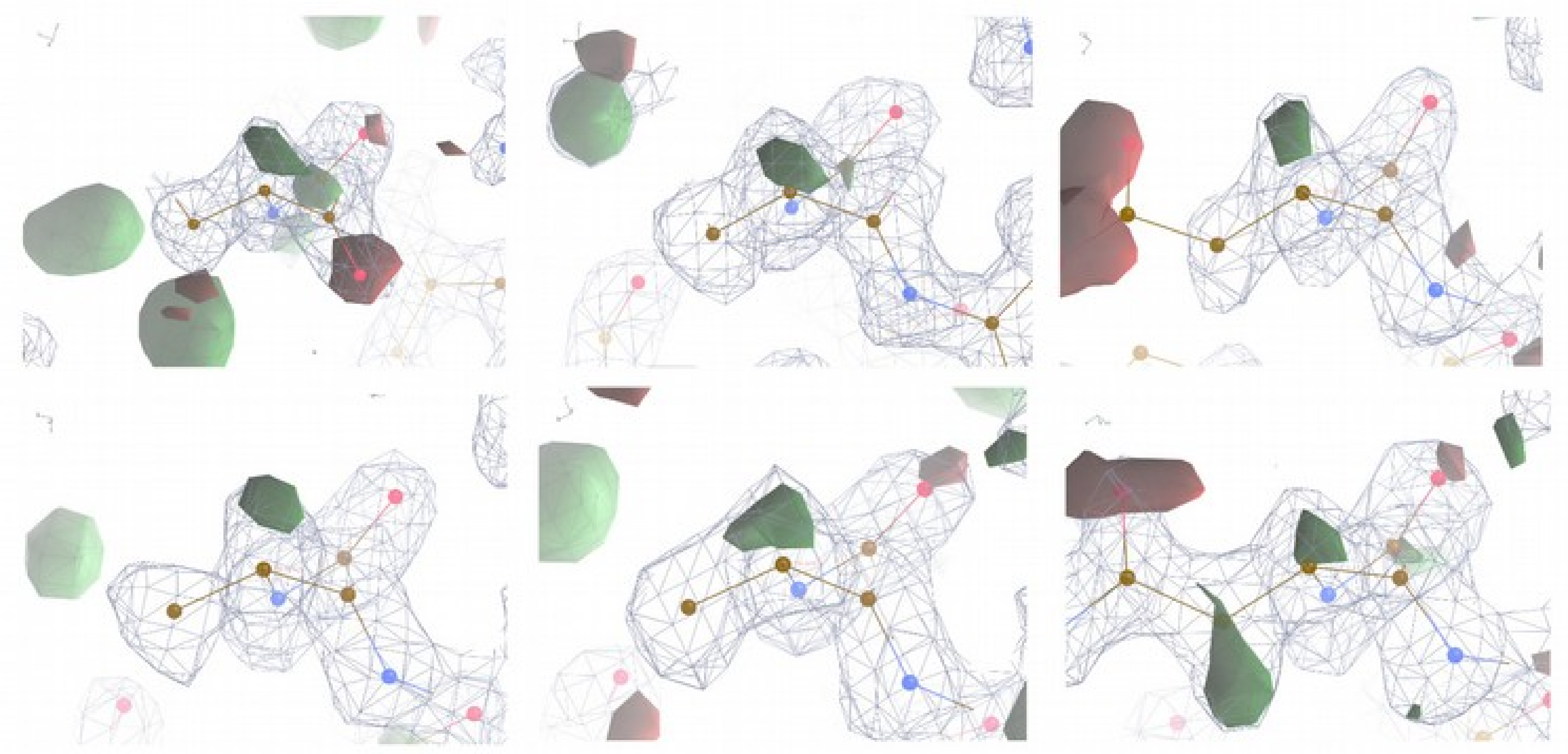
EMD-0144:
1.65 Å Human Apoferritin Relion-3



EMD-0144:
1.65 Å Human Apoferritin Relion-3

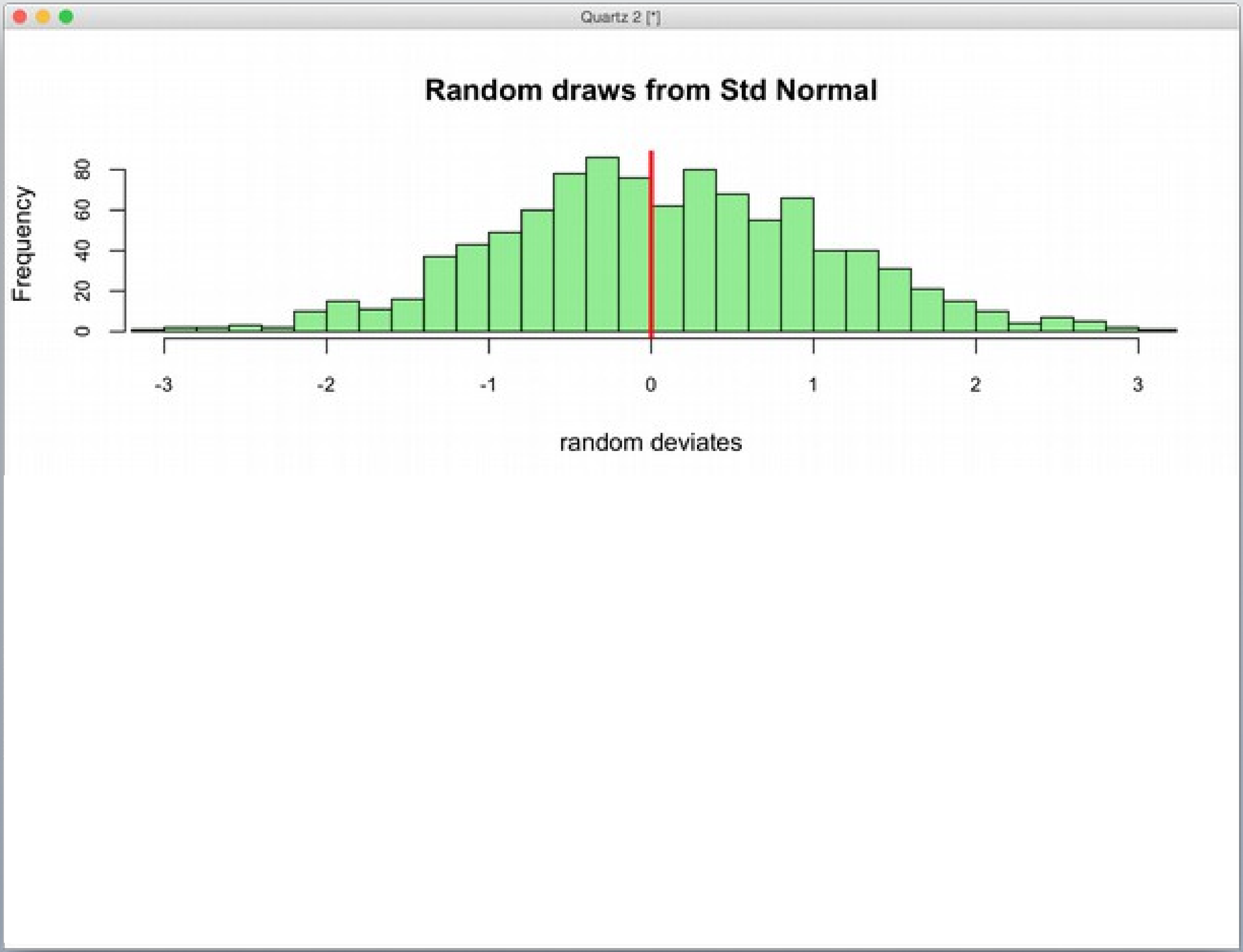


Hydrogen Density?



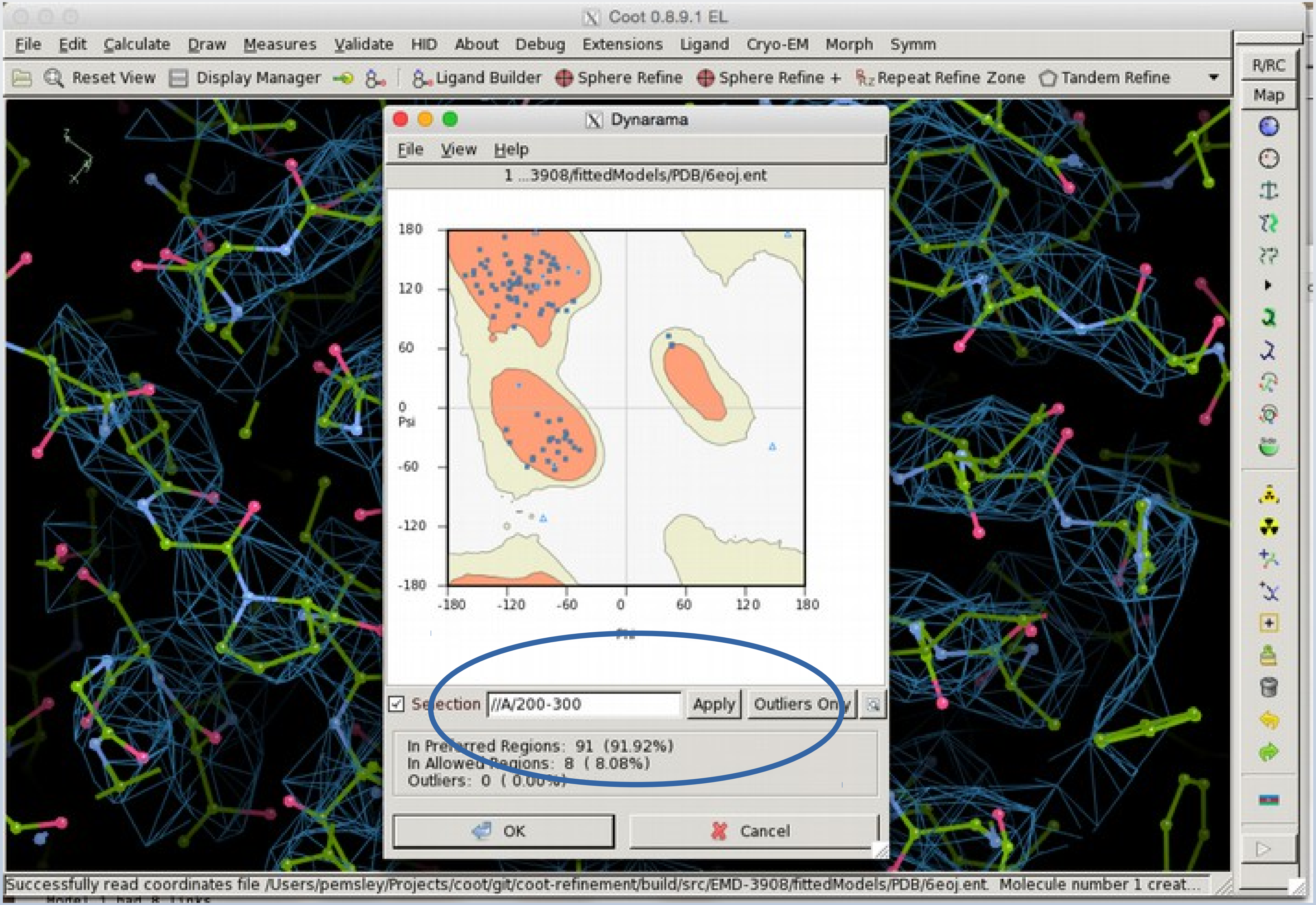
Red/Green is a difference map calculated without Hydrogen atoms being in the model

Hydrogen Density?



New/Bleeding Edge/Still-in-Development

The New Ramachandran Plot



1 ...3908/fittedModels/PDB/6eoj.ent

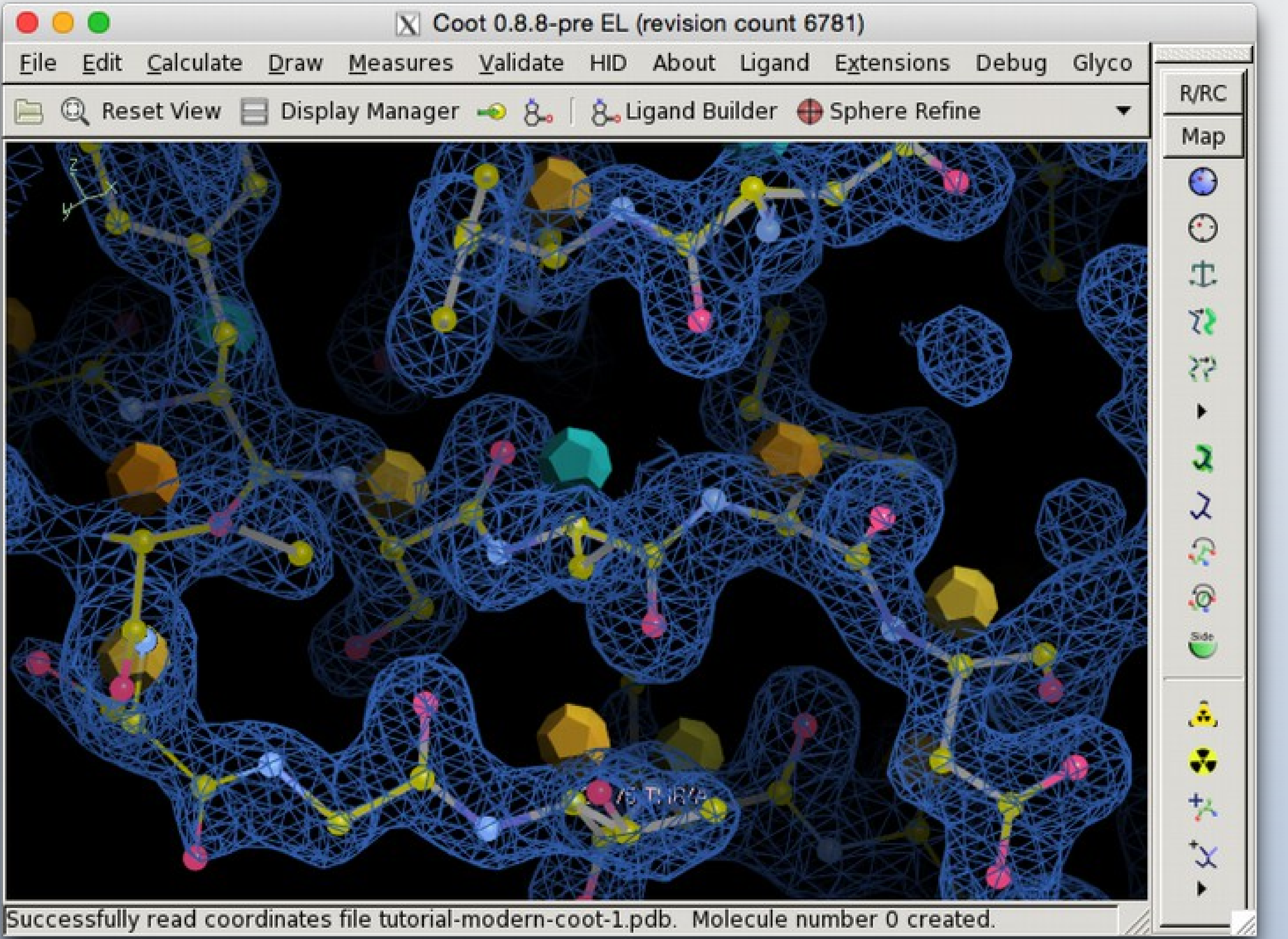
☑ Selection //A/200-300

```
In Preferred Regions:  91  (91.92%)
In Allowed Regions:  8  ( 8.08%)
Outliers:  0  ( 0.00%)
```

```
Successfully read coordinates file /Users/pemsley/Projects/coot/git/coot-refinement/build/src/EMD-3908/fittedModels/PDB/6eoj.ent  Molecule number 1 creat...
Model 1 had 8 links
```

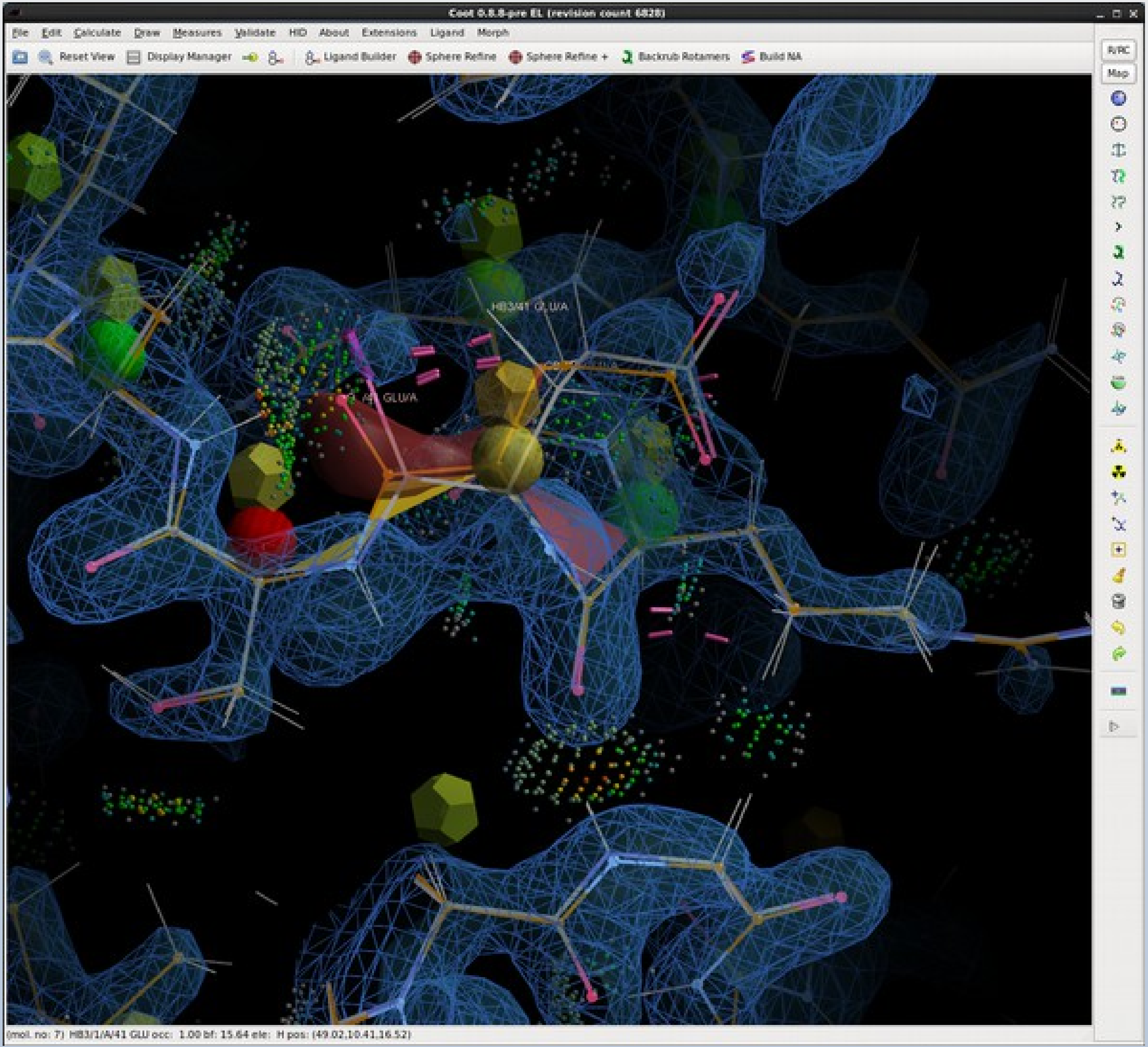
Now with Pre-PRO

Interactive Rotamer Probabilities



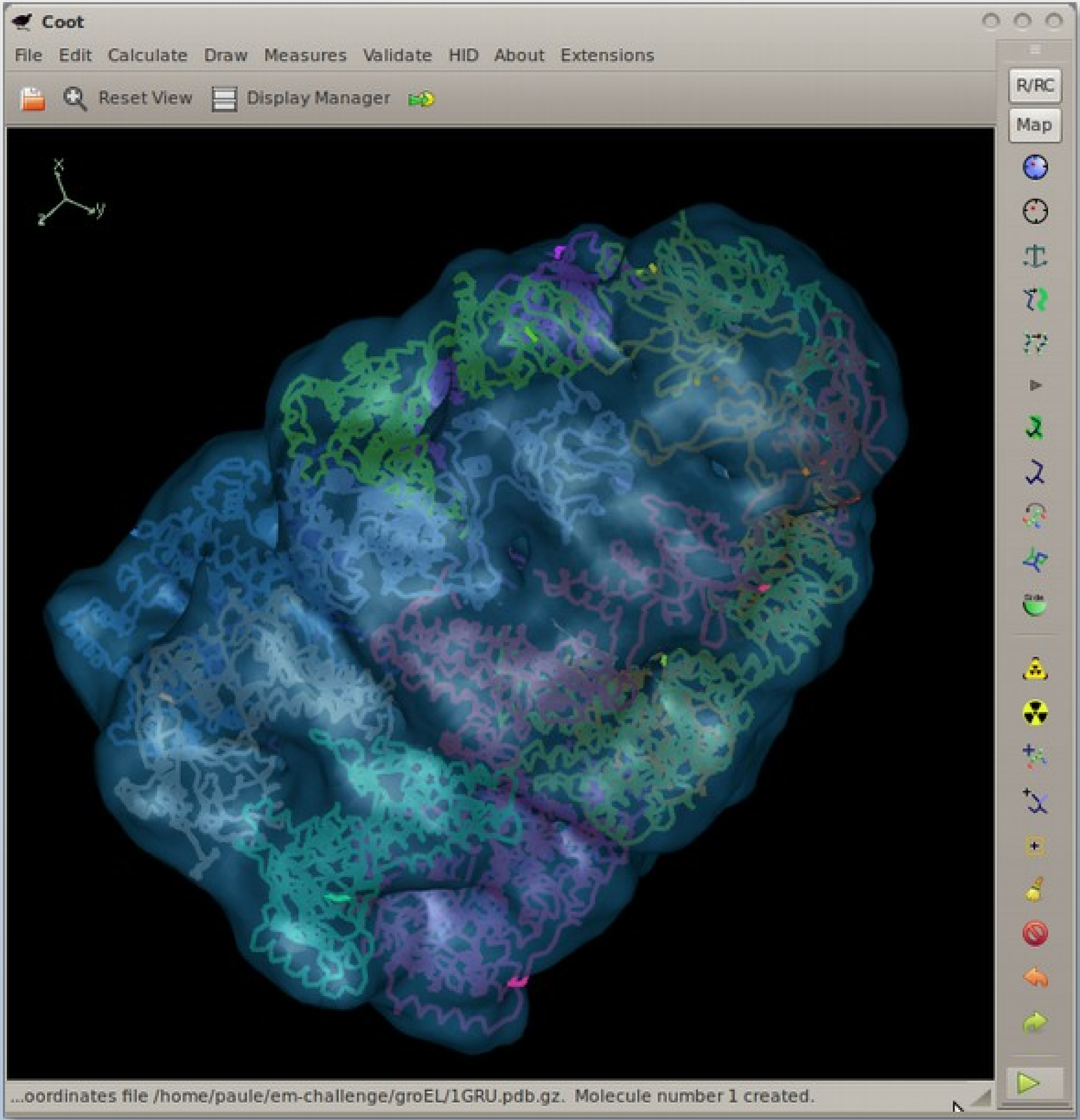
Successfully read coordinates file tutorial-modern-coot-1.pdb. Molecule number 0 created.

Multi-Criteria Markup

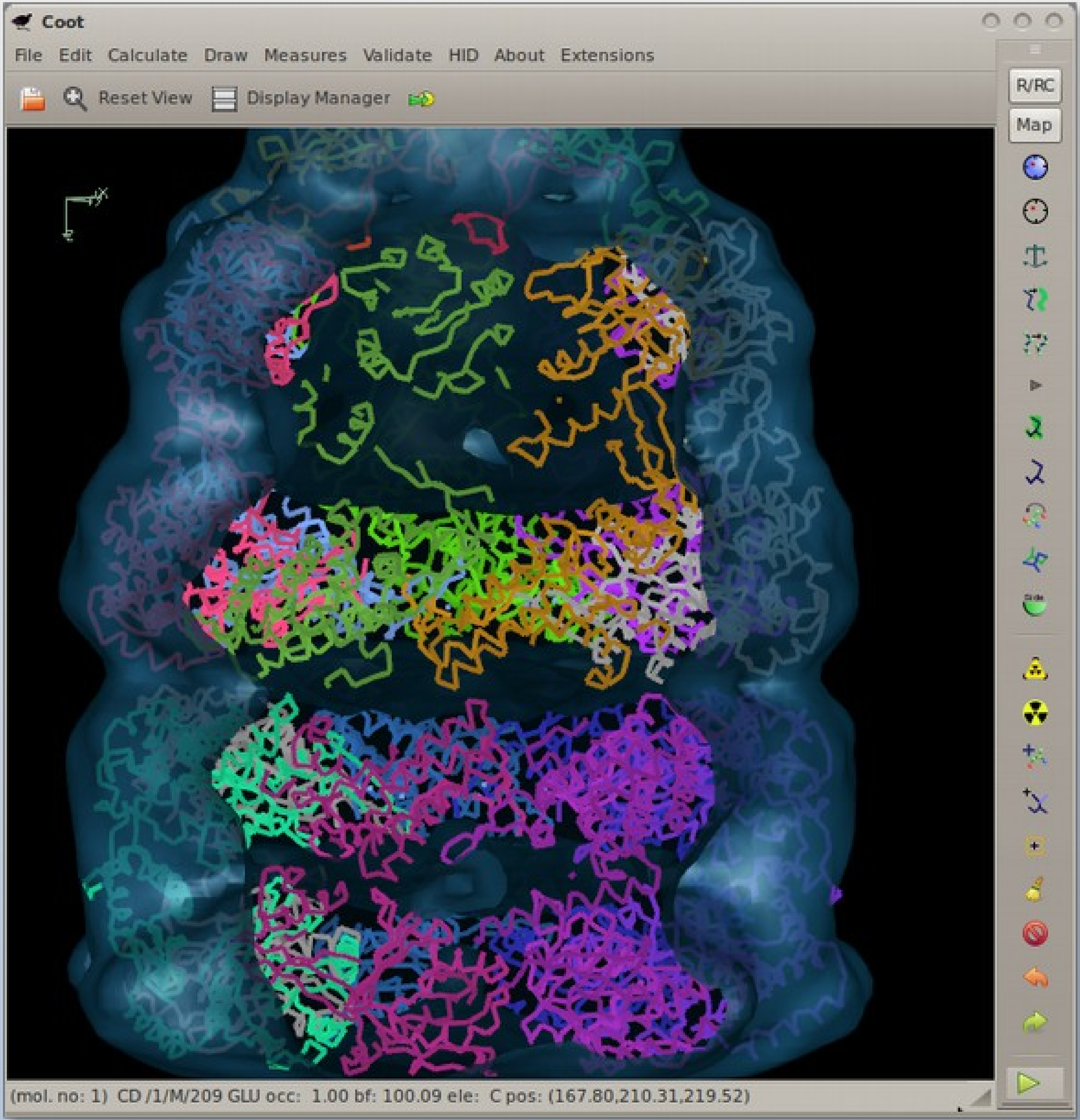


```
(mol. no: 7) HB3/1/A/41 GLU occ:  1.00 bf: 15.64 ele:  H pos: (49.02,10.41,16.52)
```

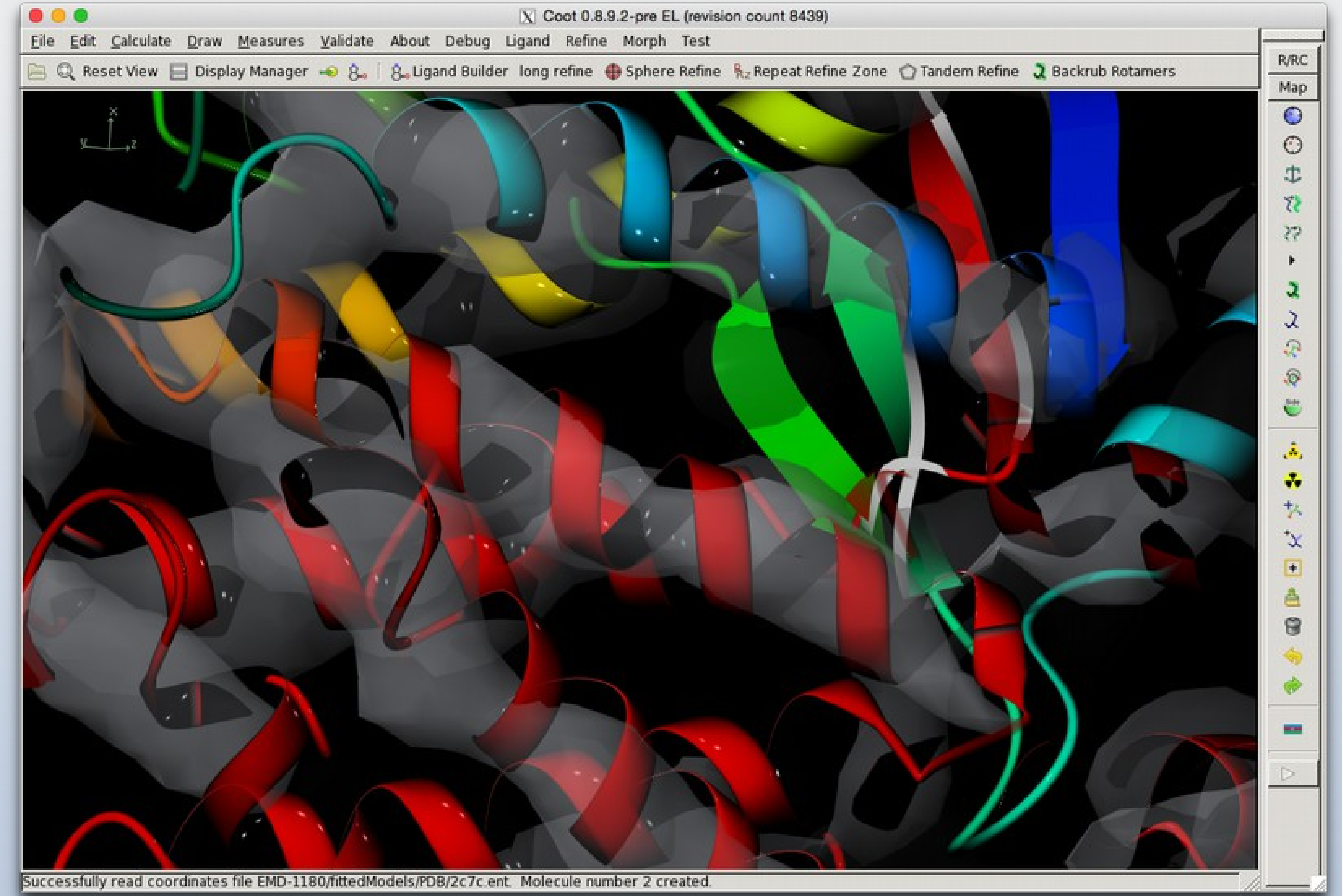
A Few Screenshots



...oordinates file /home/paule/em-challenge/groEL/1GRU.pdb.gz. Molecule number 1 created.

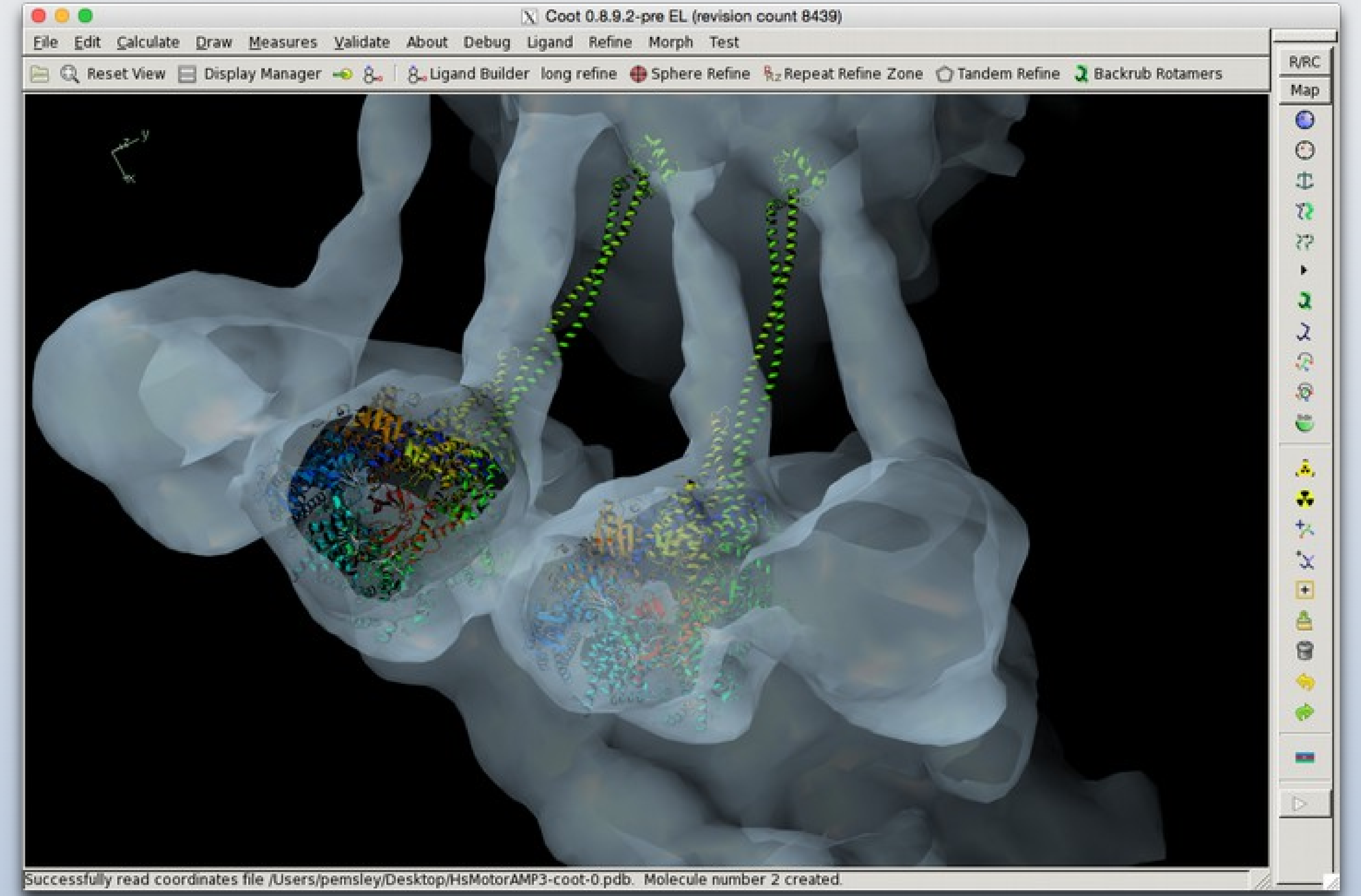


```
(mol. no: 1)  CD /1/M/209 GLU occ:  1.00 bf: 100.09 ele:  C pos: (167.80,210.31,219.52)
```



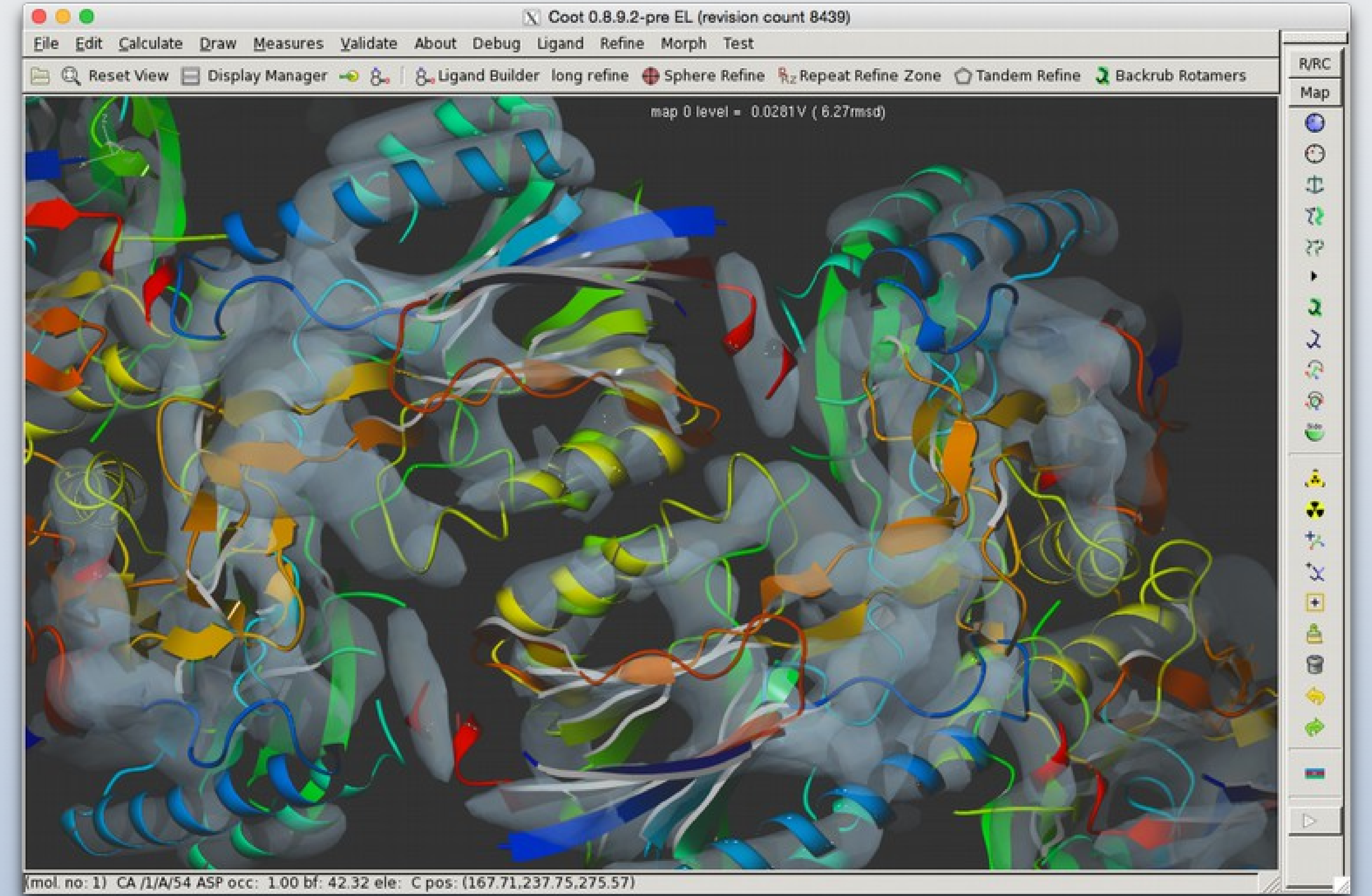
Successfully read coordinates file EMD-1180/fittedModels/PDB/2c7c.ent. Molecule number 2 created.

Screenshots



Successfully read coordinates file /Users/pemsley/Desktop/HsMotorAMP3-coot-0.pdb. Molecule number 2 created.

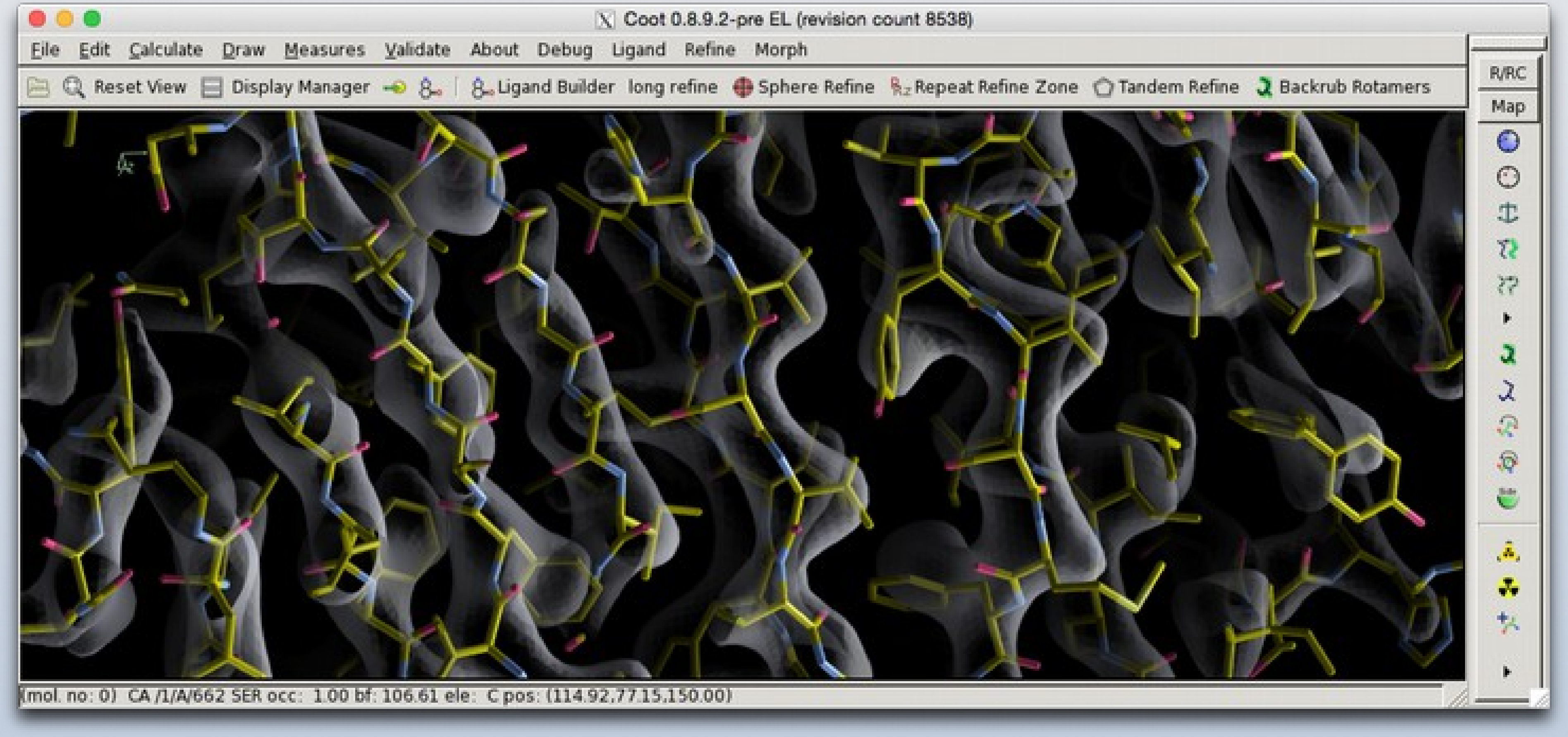
Screenshots



```
map 0 level =  0.0281V ( 6.27rmsd)
```

```
(mol. no: 1)  CA /1/A/54 ASP occ:  1.00 bf: 42.32 ele:  C pos: (167.71,237.75,275.57)
```

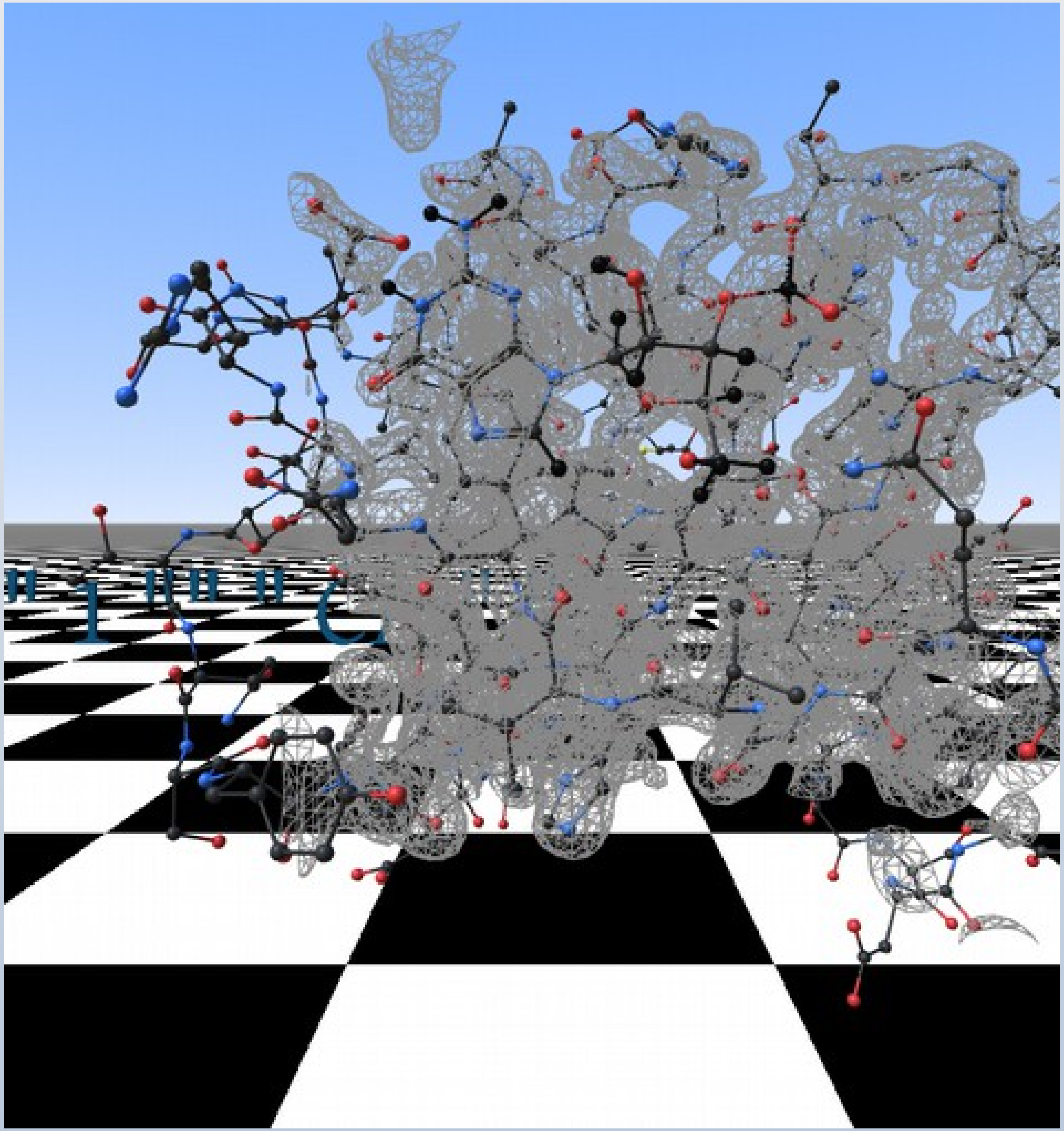
Screenshots



```
(mol. no: 0)  CA /1/A/662 SER occ:  1.00 bf: 106.61 ele:  C pos: (114.92,77.15,150.00)
```

Coot Futures: Virtual Reality

Hamish Todd



- **An Intuitive Interface:**
- Stereoscopic Representation
- Greater Field of View
- 2 Hands with Articulation
- However:
  - current tools are not immediately transferable
  - because: nausea

- Augmented-Reality Coot

Martin Noble

Acknowledgements

- LMB:
  - Garib Murshudov, Rob Nicholls

- Kevin Cowan, Bernhard Lohkamp

- Libraries & Dictionaries:
  - Jane & Dave Richardson
  - Alexei Vagin
  - Eugene Krissinel