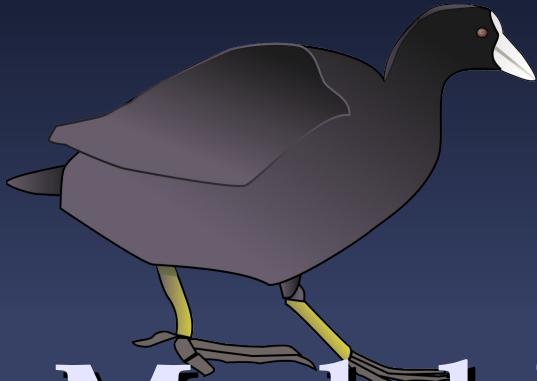




Eurasian Coot
(*Fulica atra*)

January 2010 Nottingham



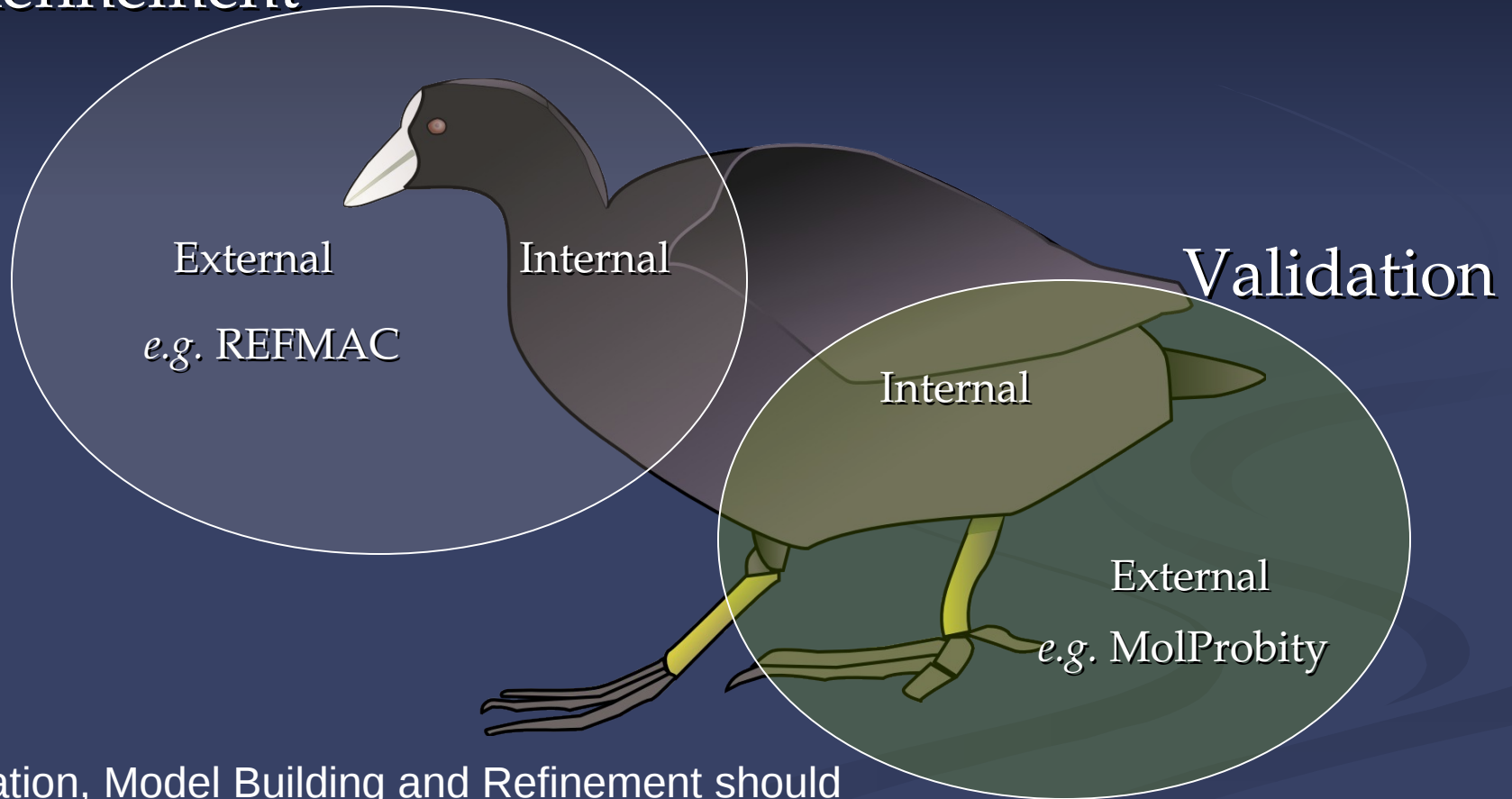
Model-Building with Coot

Hints & Tips

Paul Emsley
University of Oxford

Feature Integration

Refinement



Validation, Model Building and Refinement should be used together

Real Space Refinement

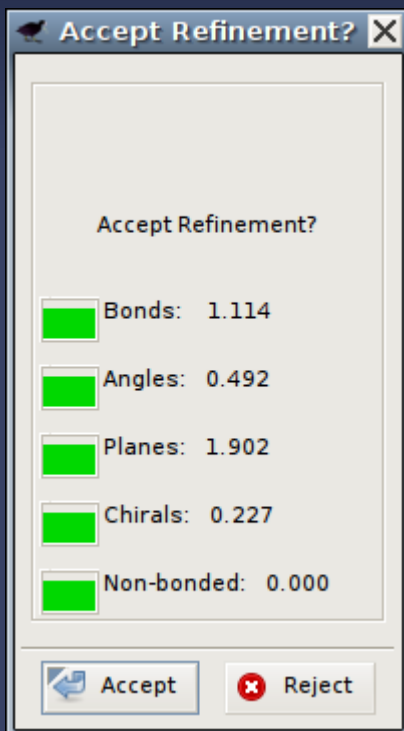
Diamond, R. (1971). *Acta Cryst. A*
27, 436-452.

- Major feature of Coot
 - Gradient minimizer (BFGS derivative)
 - Based on mmCIF standard dictionary
 - Minimizing bonds, angles, planes, non-bonded contacts, torsions, chiral volumes
 - `link_list` and `chem_link` data items
- Provides “interactive refinement”
- Different minimizer to Refmac...
 - Chi squareds

Refinement has been extended in several ways...

Refinement “Traffic Lights”

“Traffic Lights” represent the chi-squared values for each of the refined geometry types



Accept Refinement?

Bonds: 1.114

Angles: 0.492

Planes: 1.902


Chirals: 0.227

Non-bonded: 0.000

Accept Reject

This dialog box displays refinement statistics with green traffic light indicators for all categories, indicating good refinement. The values are: Bonds: 1.114, Angles: 0.492, Planes: 1.902, Chirals: 0.227, and Non-bonded: 0.000. The 'Accept' button is highlighted with a blue arrow icon.

Good refinement



Accept Refinement?

Bonds: 44.705

Angles: 8.964

Planes: 5.654

Chirals: 4.975

Non-bonded: 0.000

Accept Reject

This dialog box displays refinement statistics with red and orange traffic light indicators for most categories, indicating bad refinement. The values are: Bonds: 44.705, Angles: 8.964, Planes: 5.654, Chirals: 4.975, and Non-bonded: 0.000. The 'Accept' button is highlighted with a blue arrow icon.

Bad refinement

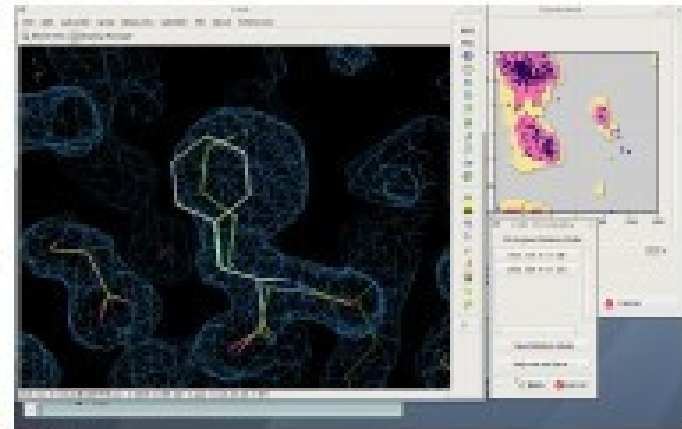
Real Space Refinement (technical note)

- Auto-Zone mechanism
 - The “A” key:
 - Typically have a range of 3 residues to refine, with the middle of the 3 at the centre of the screen
 - Click central atom and “A” key to start the refinement
 - No need to click 2 atoms away from centre

Refinement Techniques

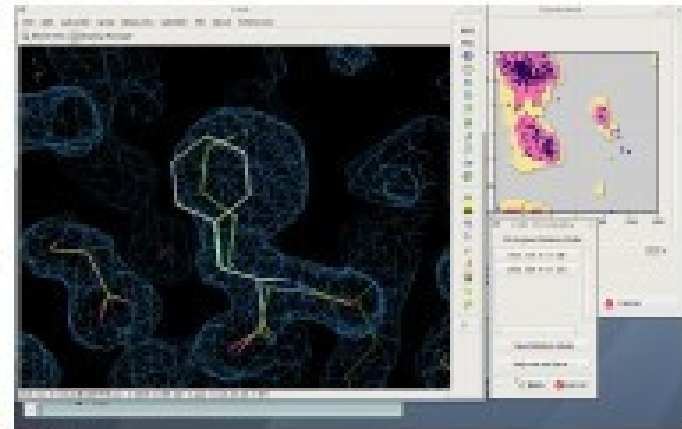
- Auto-zone
- Single-Atom Drag
- Sphere Refinement
- Key-bindings:
 - Triple Refine
 - Single Residue Refine with Auto-accept
- Ramachandran Refinement
- Coming Soon..?
 - Wii Refinement

Wii Refinement?

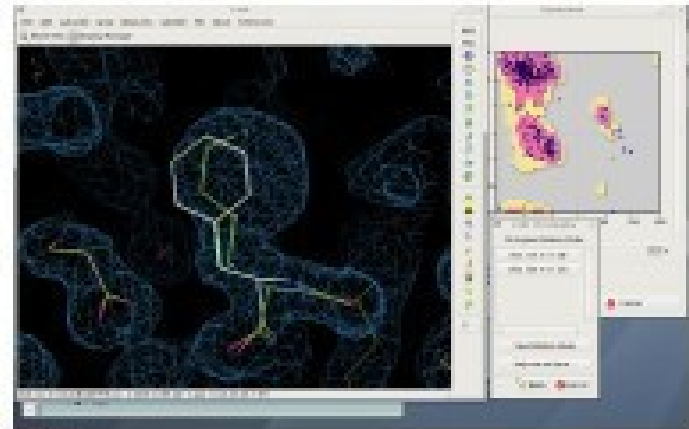




Wii Refinement?



Wii Refinement?



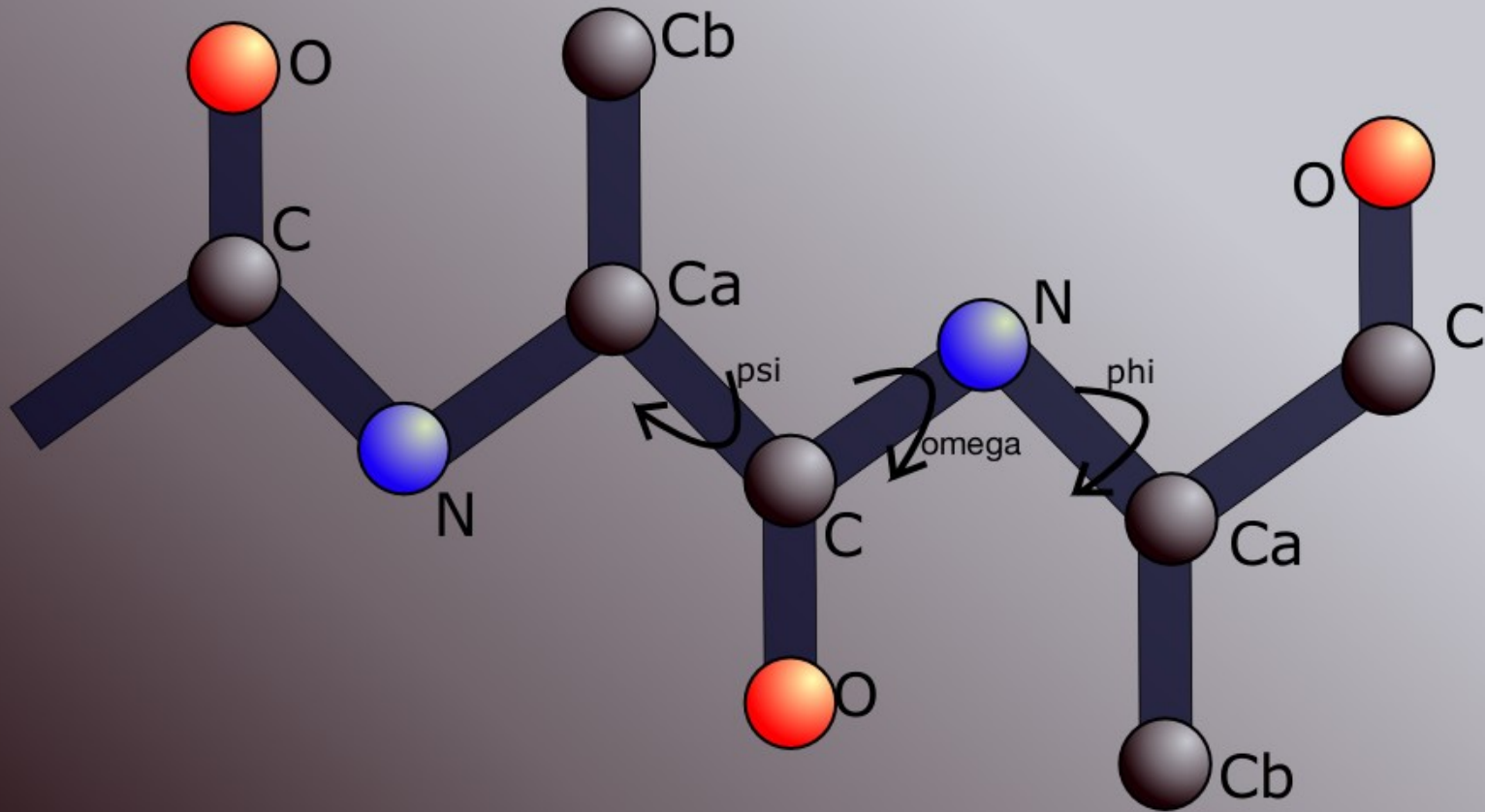
“Sphere” Refinement

- Given an “Active” Residues
 - (The one at the centre of the screen)
 - Fine a sphere of residues around it and use them all for refinement
 - NOT just a linear selection
 - Residues from different chains (or different parts of the same chain) interact
 - Make CYS-CYS or glycosylation links as you find them
 - Use the group and link_list chem_link in the dictionary

Ramachandran Restraints

- Scenario:
 - I have a loop, with poor density, I know the atoms are there somewhere and I want to provide a “reasonable” model
- Controversial Feature?
 - Ramachandran Plots have been used for “validation” - but here we are deliberately optimizing them
- Ramachandran Plots can be added to the geometry target function

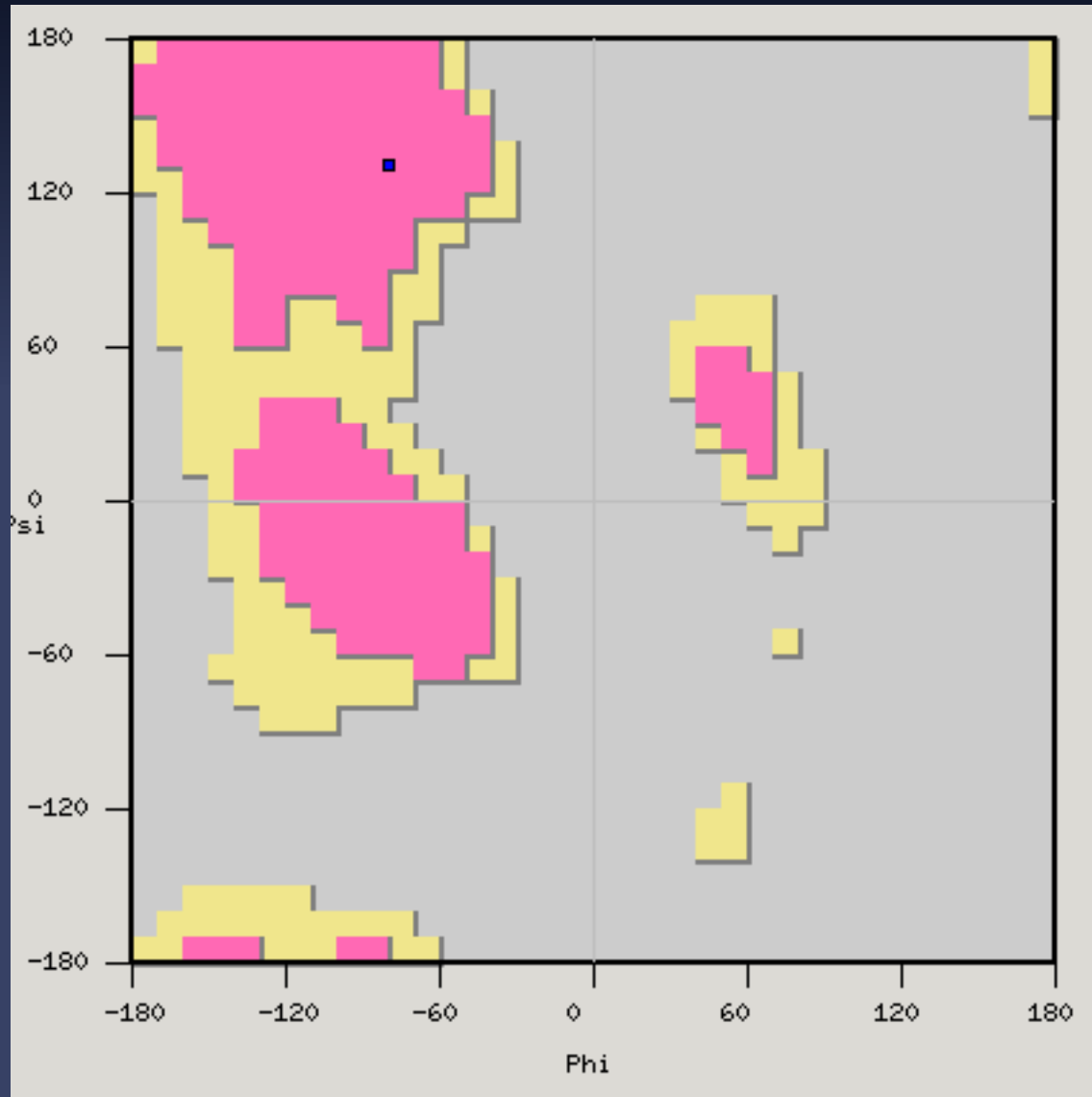
Peptide Torsion Angles



Ramachandran Distributions

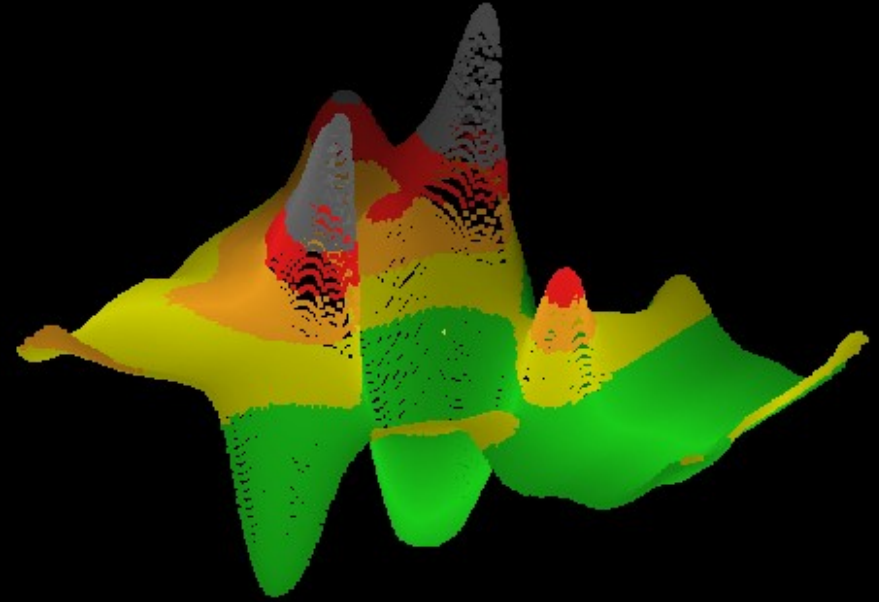
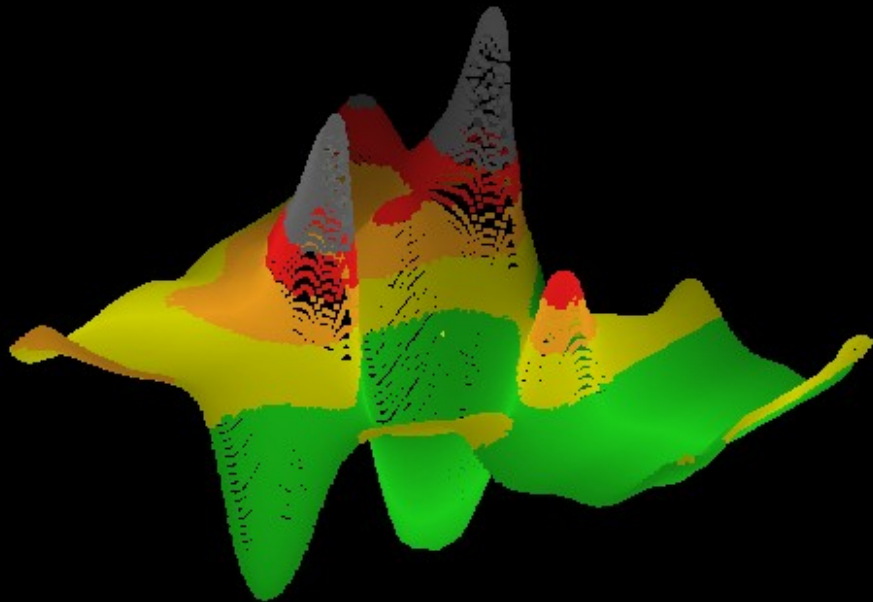
- Using Cowtan distribution only included currently
 - Log-likelihood, “negatively enhance disallowed”
 - Secondary-structure-type independent

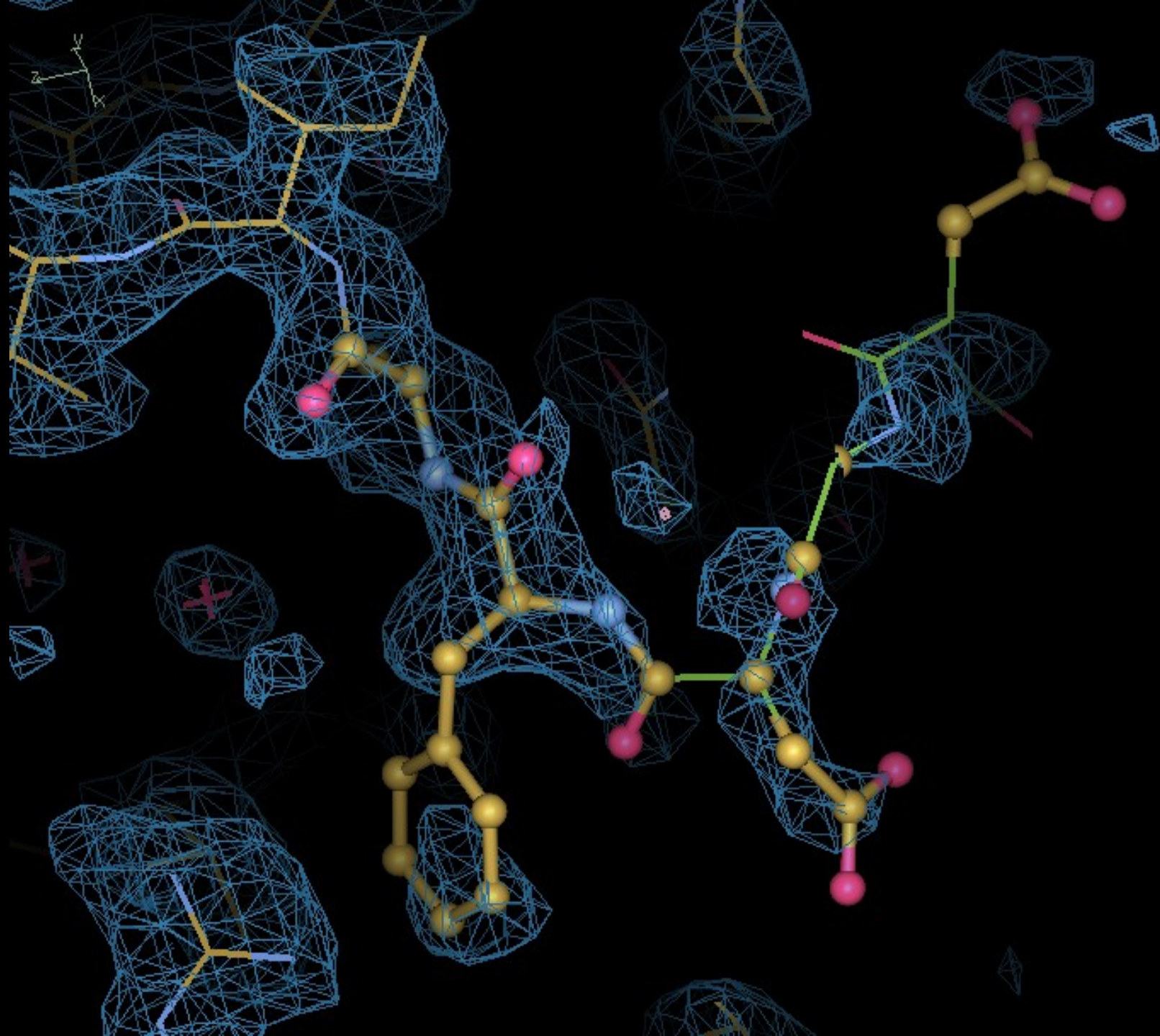
Conventional Ramachandran Plot As Rendered by Coot



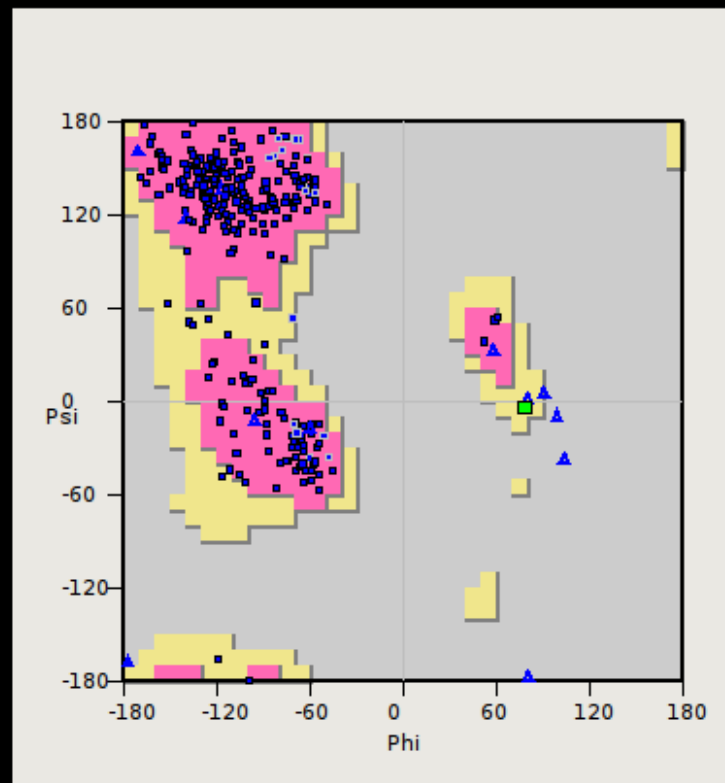
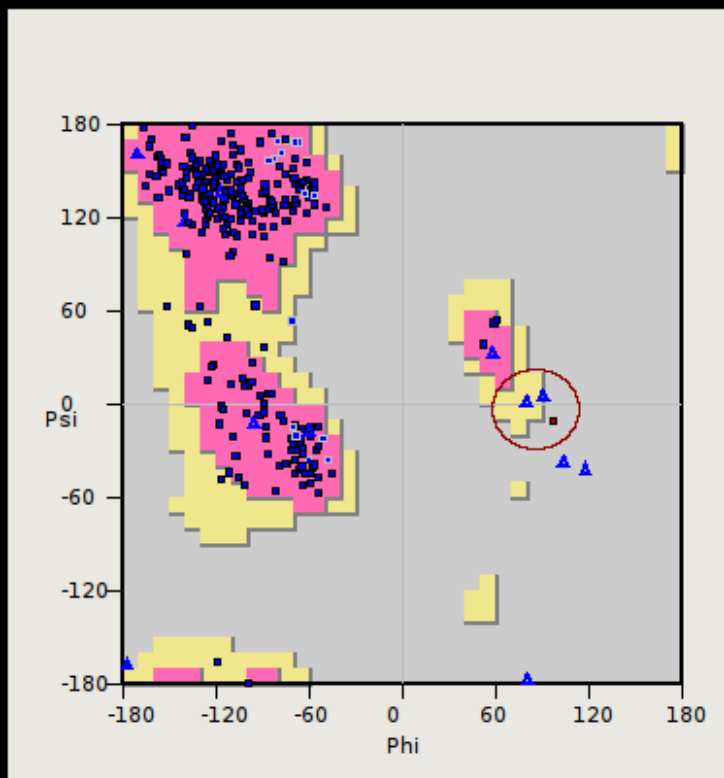
Based on
Richardson's
"Top500"

Negatively enhanced disallowed regions

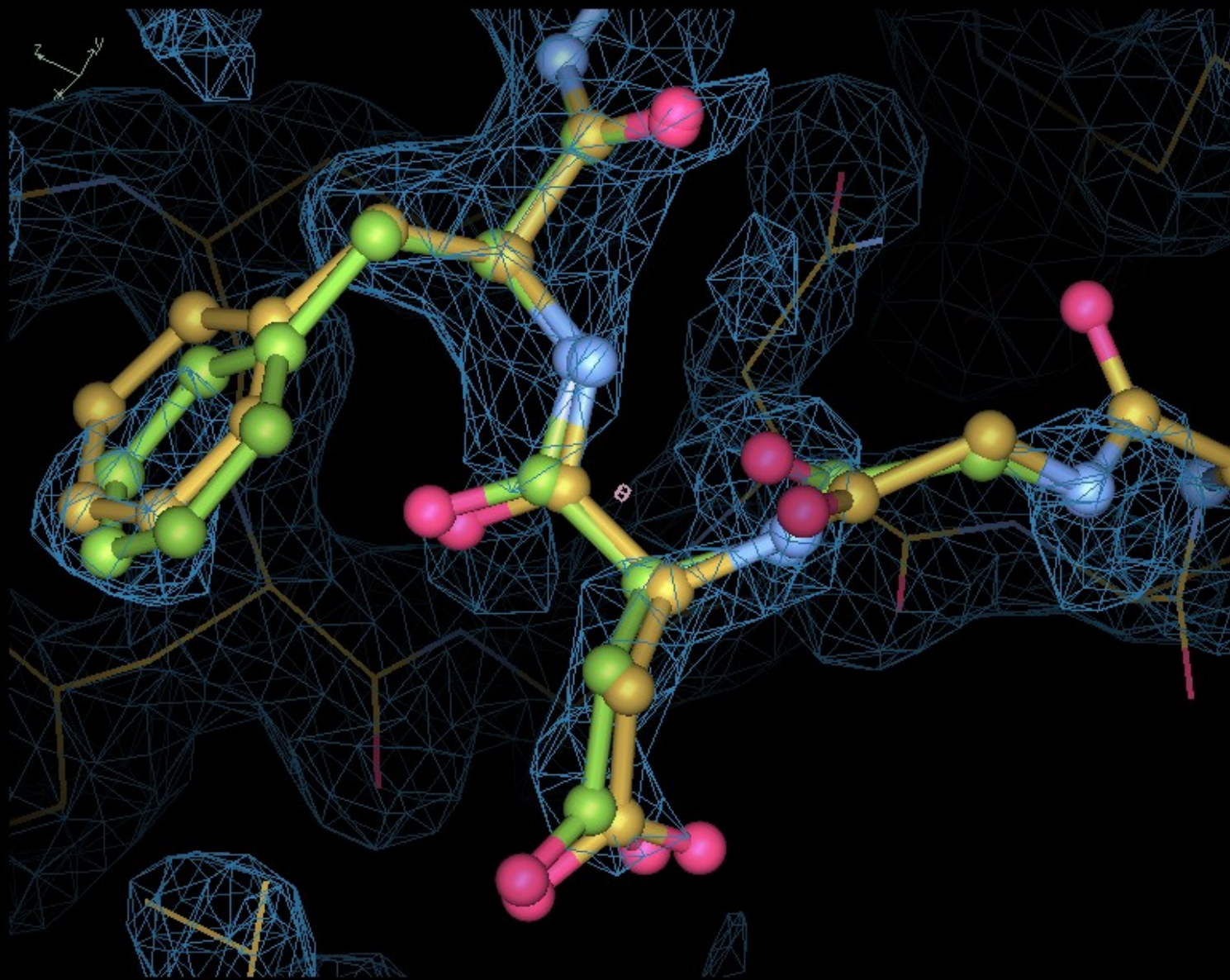




Tweaking a Ramachandran Outlier



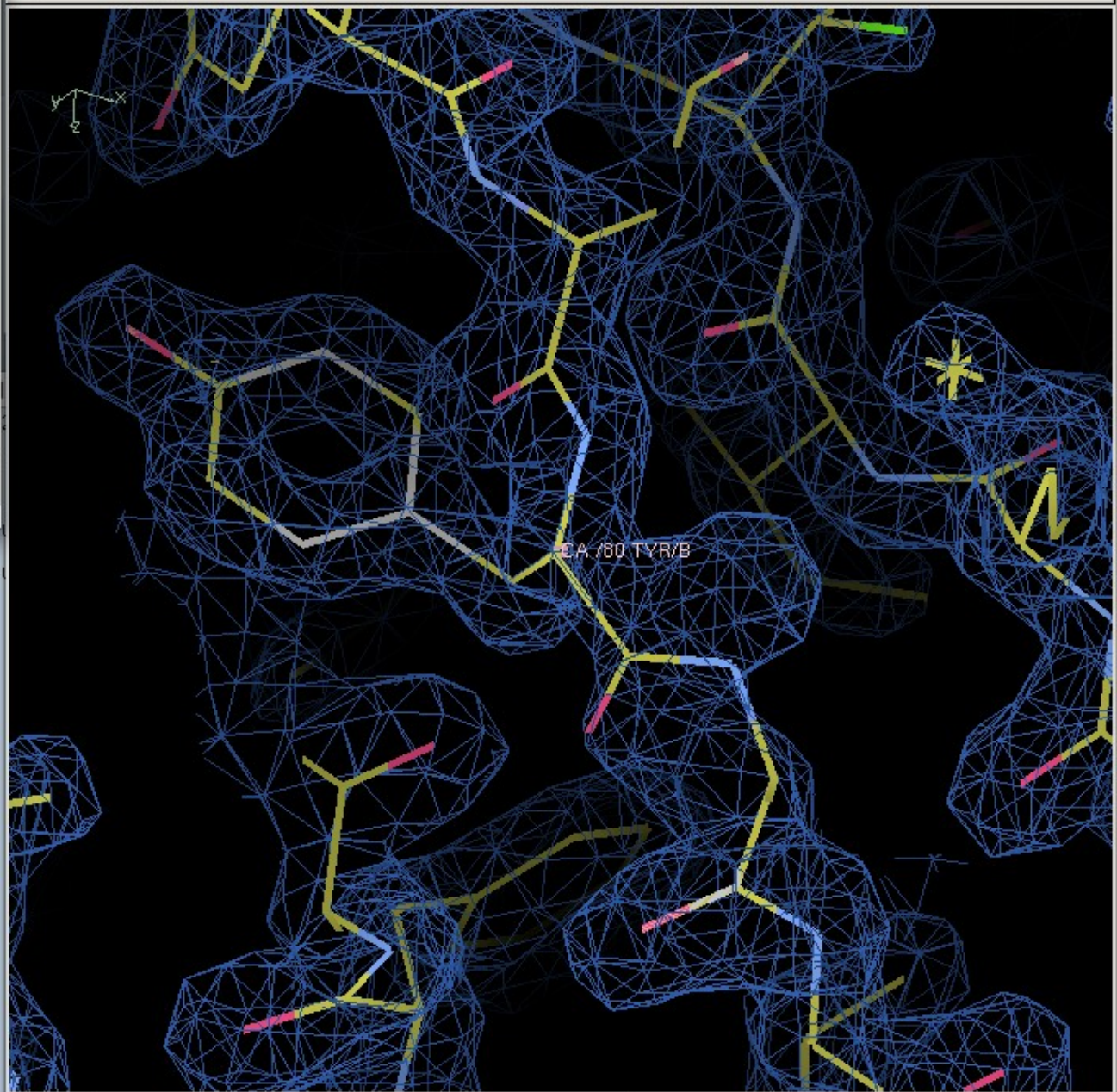
Tweaking Phi and Psi



Accept Refinement?

Bonds:	3.181
Angles:	3.997
Planes:	2.148
Chirals:	3.772
Non-bonded:	0.006
Rama Plot:	-123.403

Accept Reject



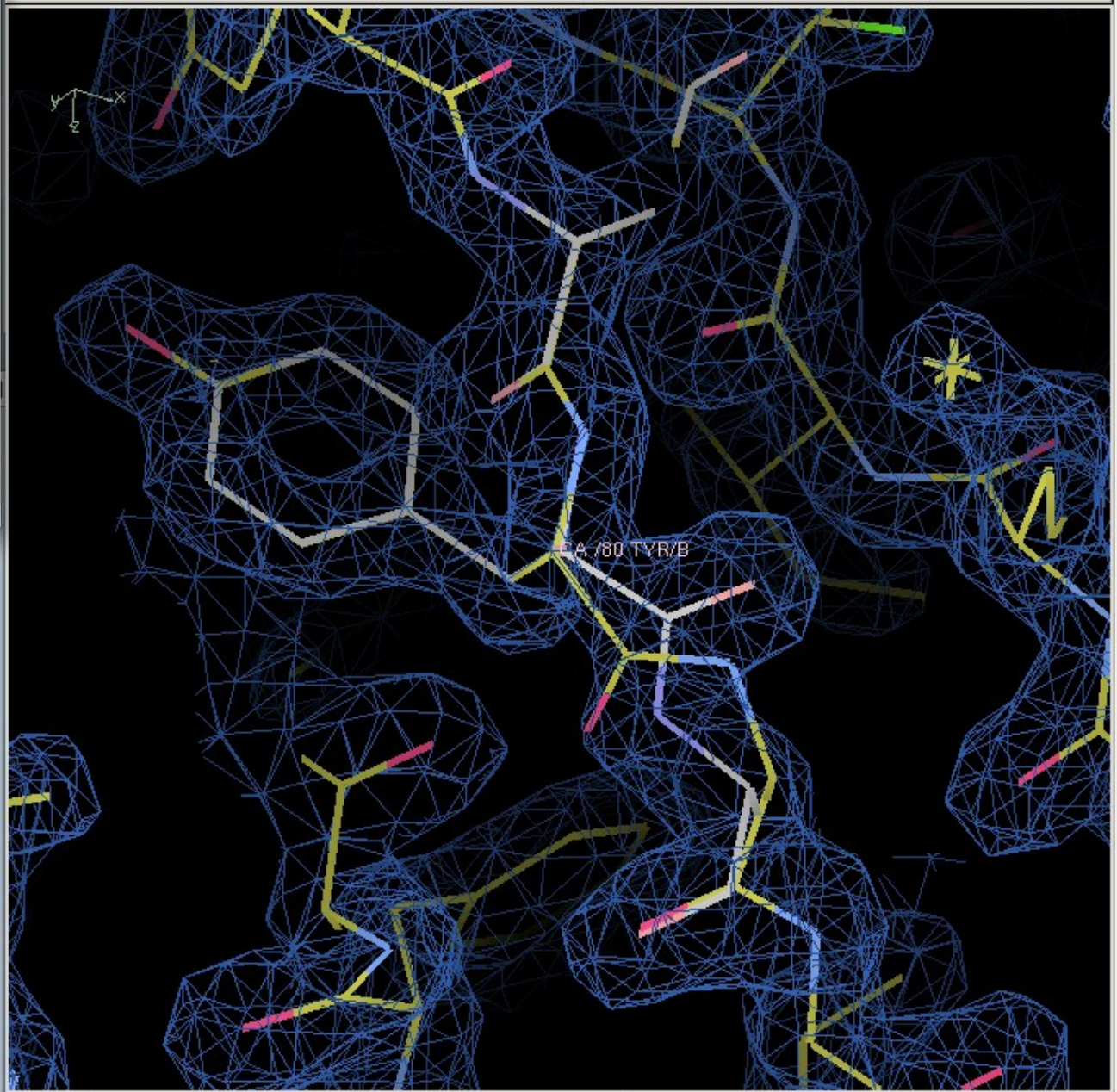
R/R/C
Map
[Navigation icons]

g_atoms_rama_restraints) ret
ints
6
at -14010.6
31

Accept Refinement?

- Bonds: 1.625
- Angles: 0.318
- Planes: 1.671
- Chirals: 0.177
- Non-bonded: 0.000
- Rama Plot: -177.602

Accept Reject



R/R/C

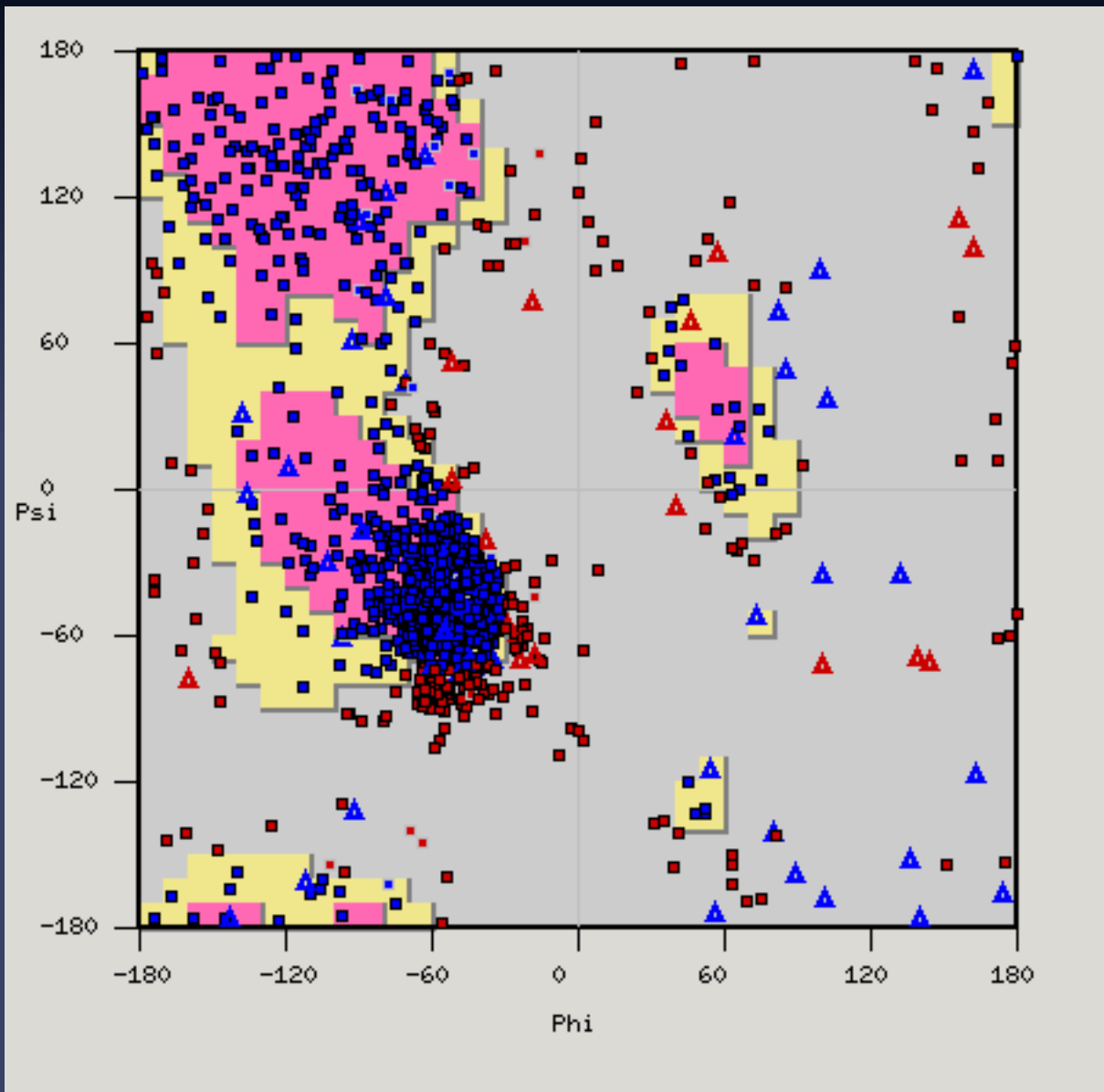
Map

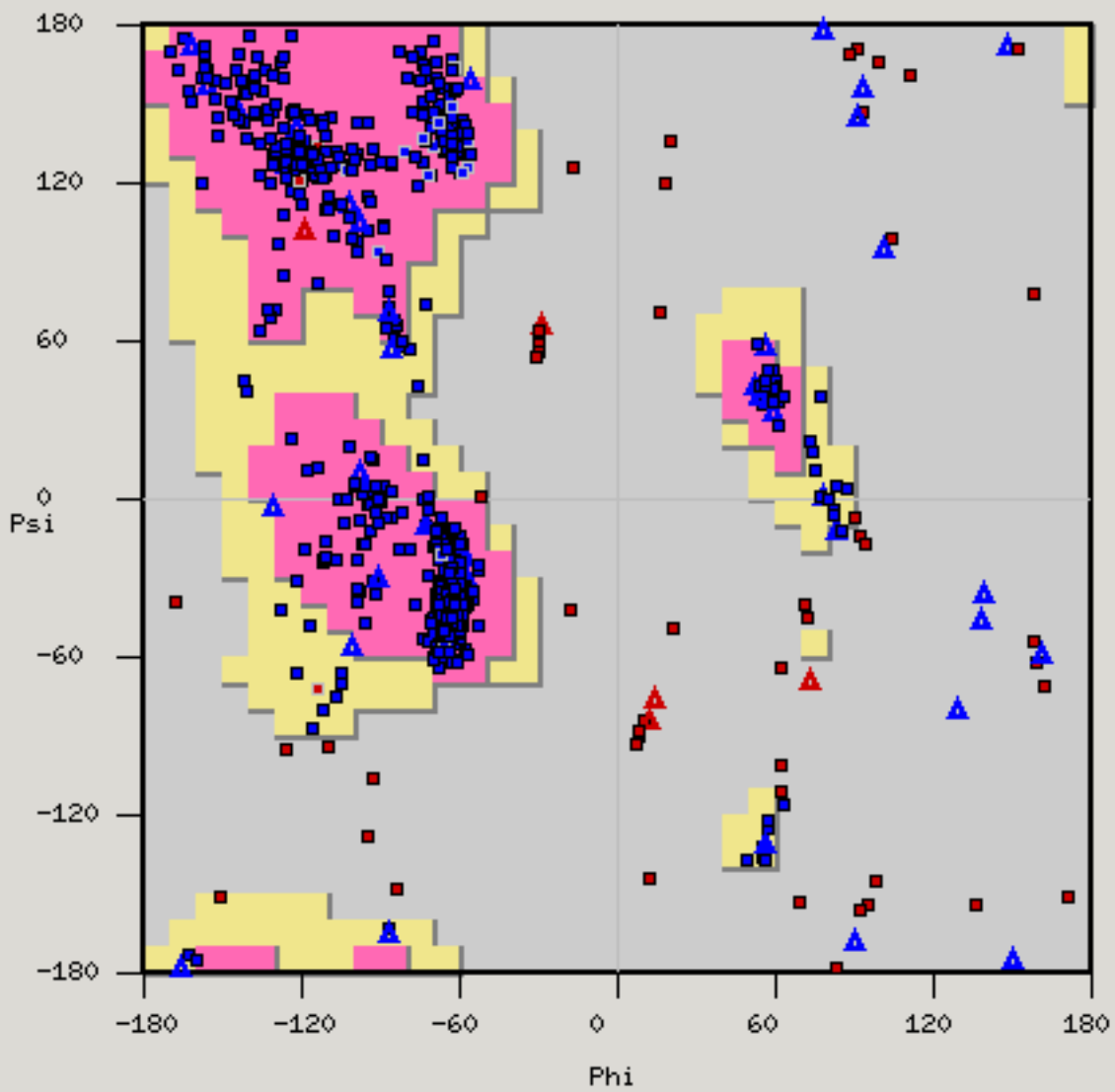
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31

6) at -15414.1

18



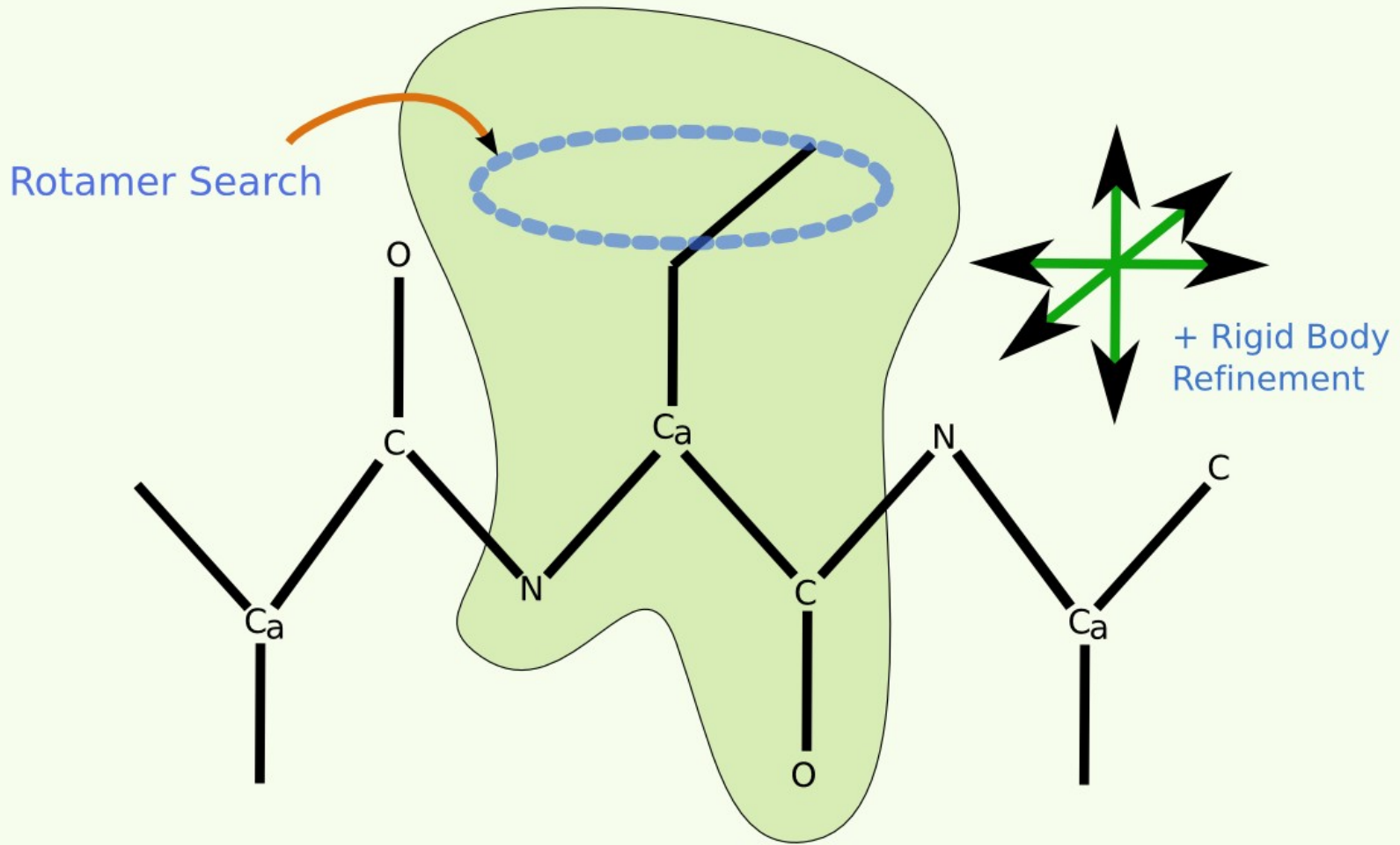




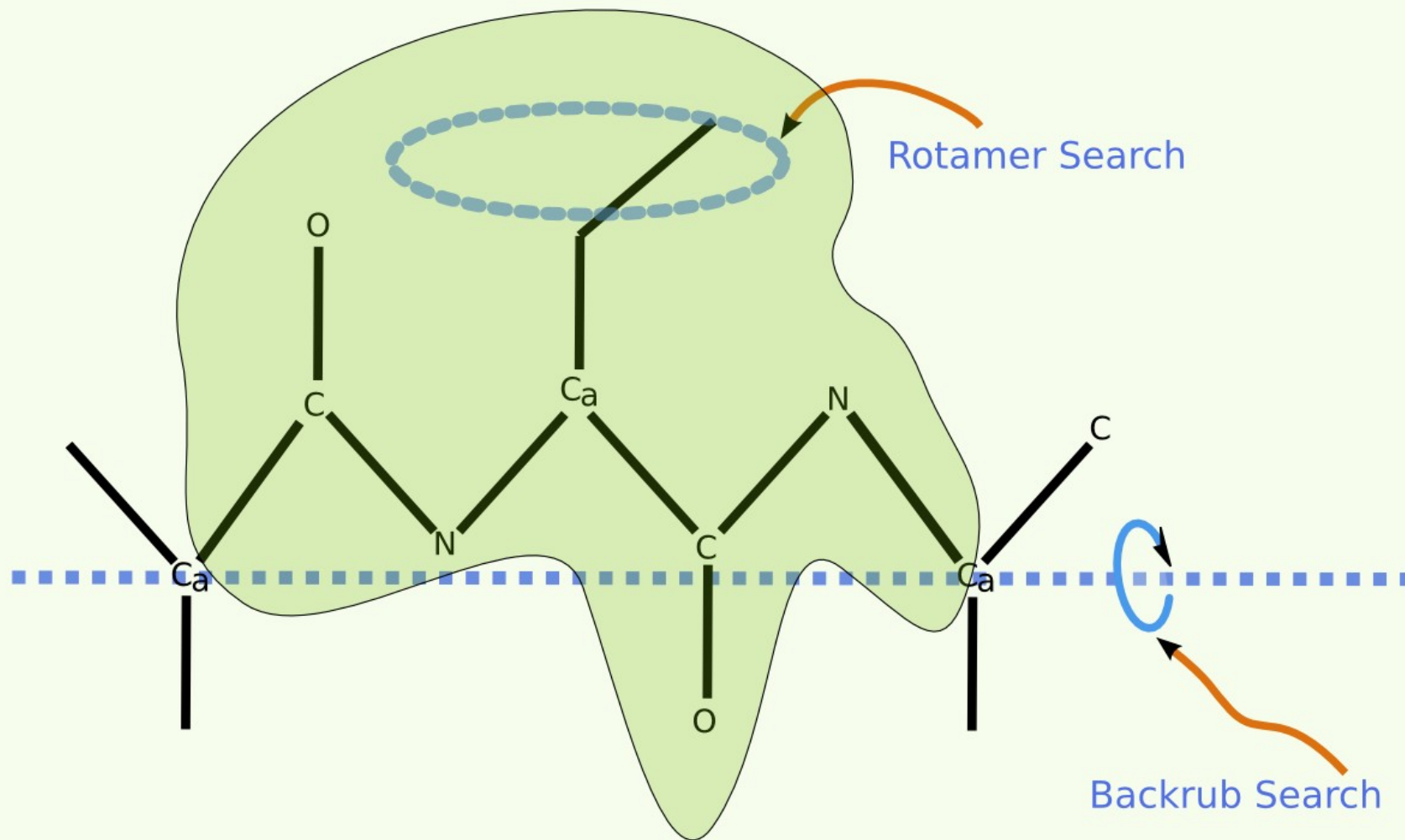
Backrub Rotamers

Previous

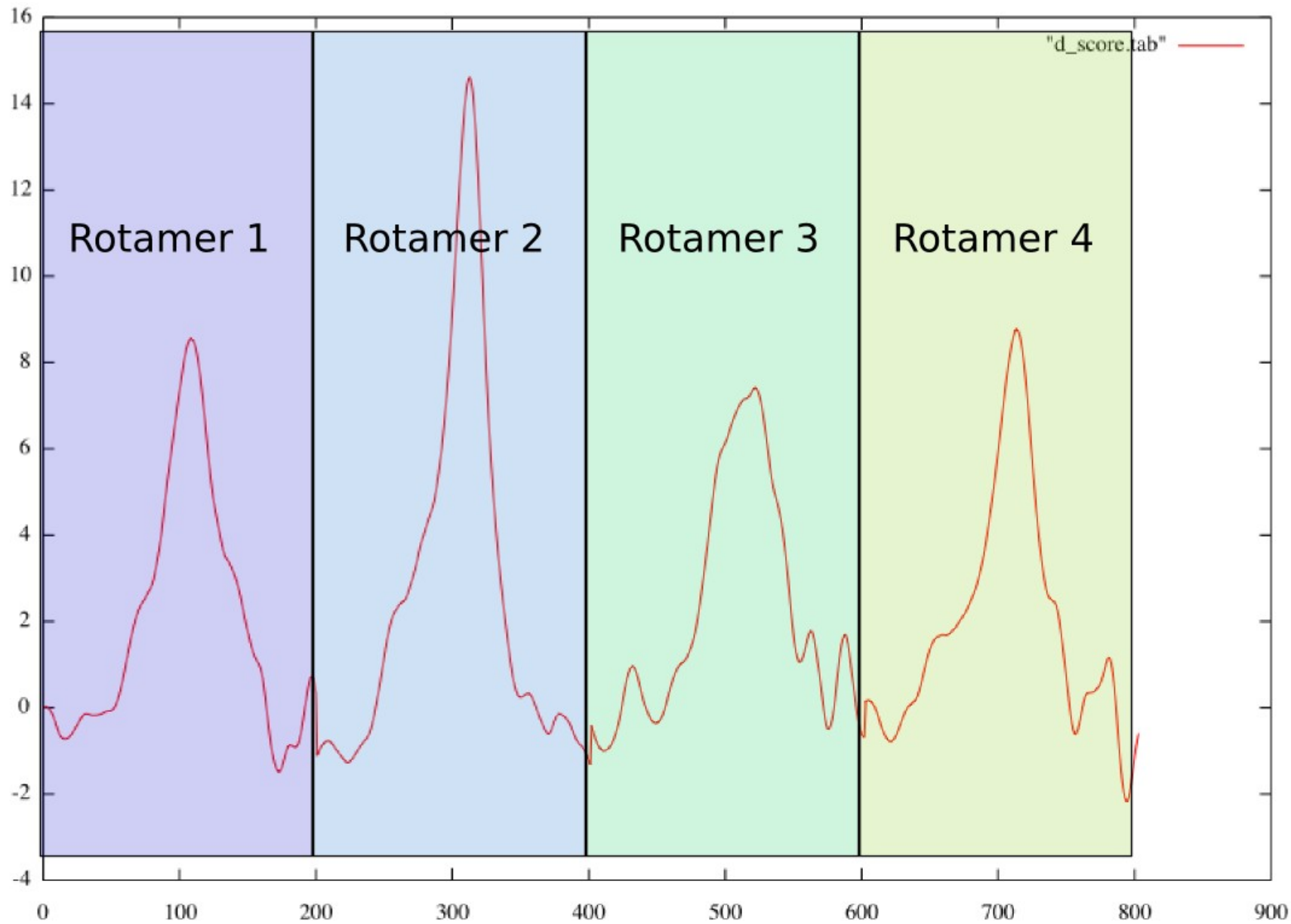
~~Current~~ Low Resolution Rotamer Search

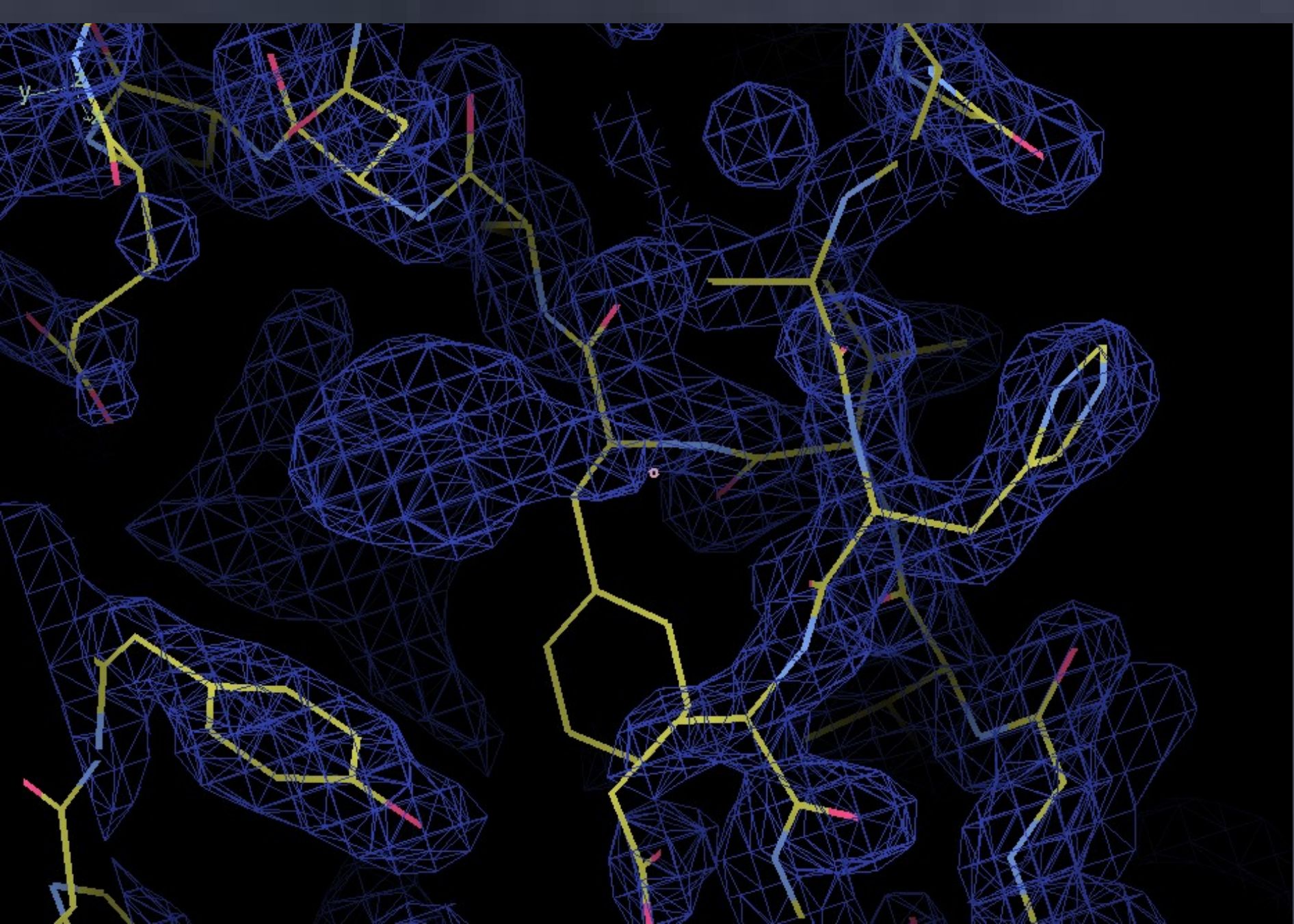


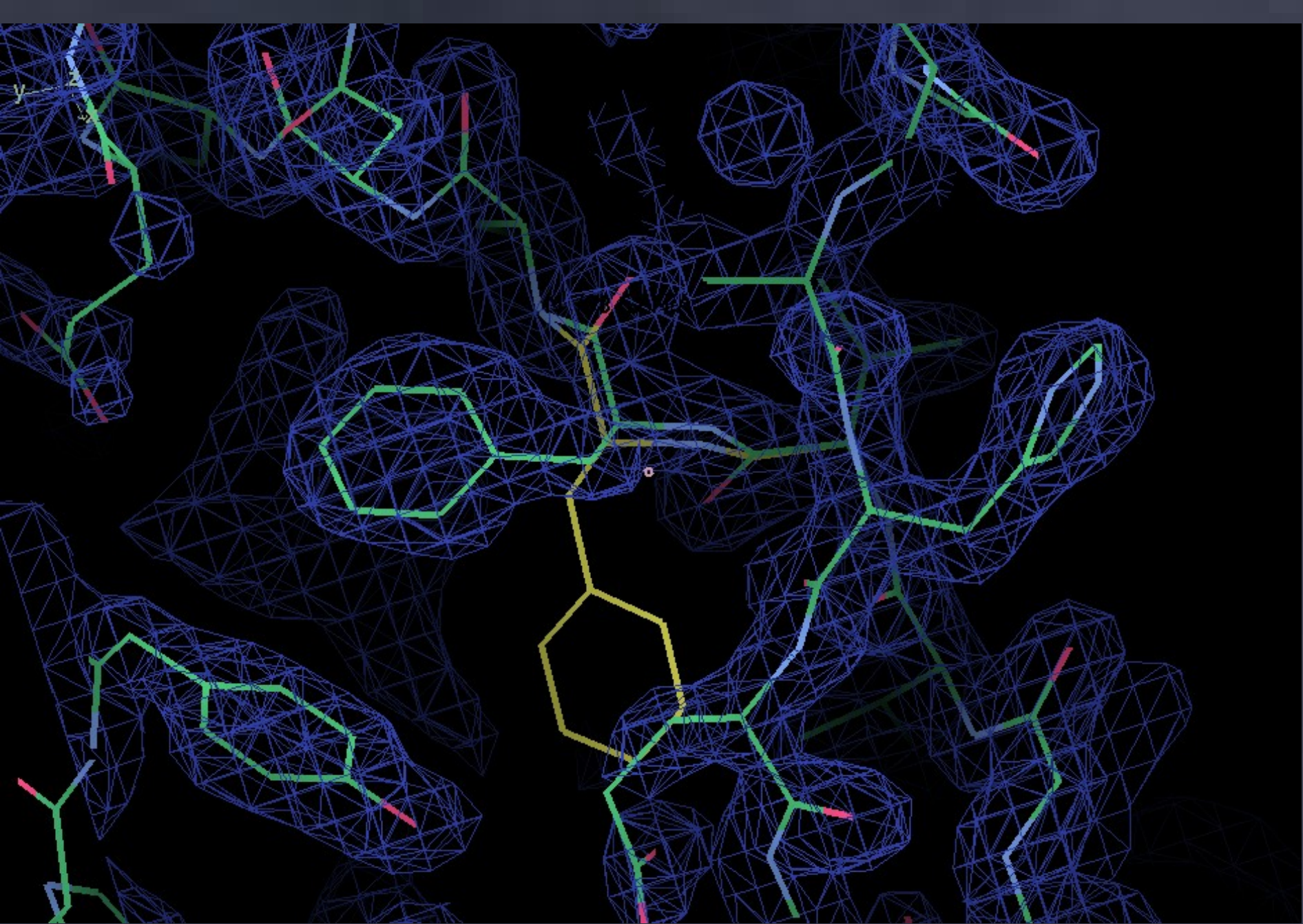
New Low Resolution Rotamer Search

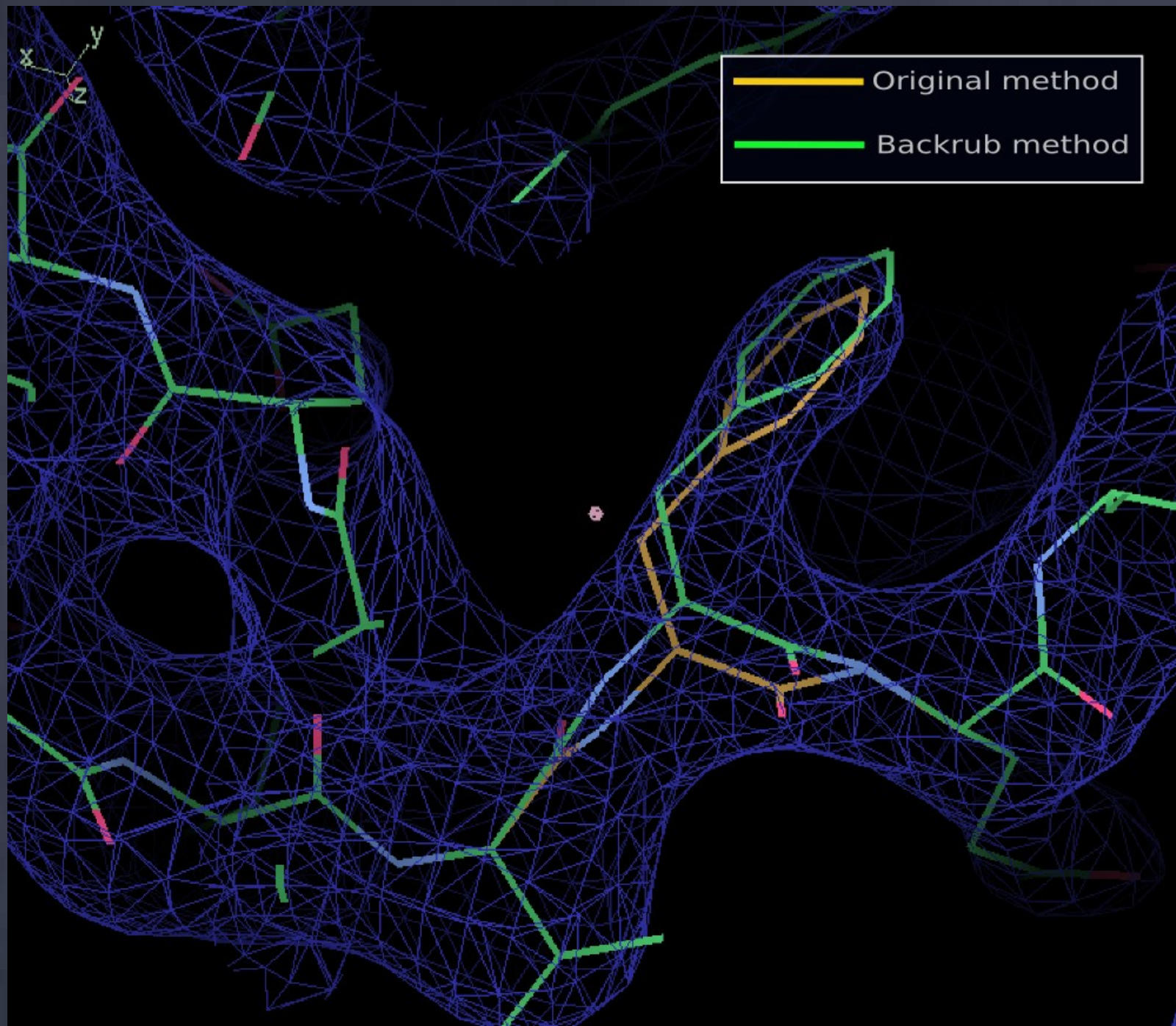


After Fitting Tools in KING/Molprobity









“Ease of Use” vs “Easy to Learn”

“Ease of Use” fights back!

- Any function can be bound to a key
 - Allows for personalization/customization
- Here's how you do it:
 - (add-key-binding *name key function*)
- Makes Coot easy to use
 - (but harder to learn)
- See Coot Wiki for more details

Example Keybindings

- (add-key-binding "Refine Active Residue AA" "x" refine-active-residue)
- (add-key-binding "Refine Active Residue" "r" (lambda () (manual-refine-residues 0)))
- (add-key-binding "Triple Refine" "t" (lambda () (manual-refine-residues 1)))
- (add-key-binding "Triple Refine AA" "h" (lambda () (refine-active-residue-triple)))

Thanks to...

- William Scott, Karen McLuskey, Charlie Bond, Miguel Ortiz Lombardia, Lieven Buts, Adrian Laphorn, Constantina Foteinou, Mike Hartshorn, Ezra Peisash, Dirk Kostrewa, Frank von Delft, Bob Nolte, George Sheldrick, Joel Bard, Randy Read, Roberto Steiner, Jan Dohnalek, Juergen Bosch, Martin Noble, Judit Debreczeni, Gabor Bunkoczi, Ingo Korndoerfer, Tadeusz Skarzynski, Artem Lyubimov, Sabine Schneider, Claudia Schnick, Tim Guene, Garib Murshudov, Phil Evans, Tassos Perrakis, Dug Kuntz, Gideon Davies, Tracey Gloster, Matin Winn, Gerard Kleywegt

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 - Richardsons & team (Duke)

- Funding

<http://www.biop.ox.ac.uk/coot>

or

Google: Coot

