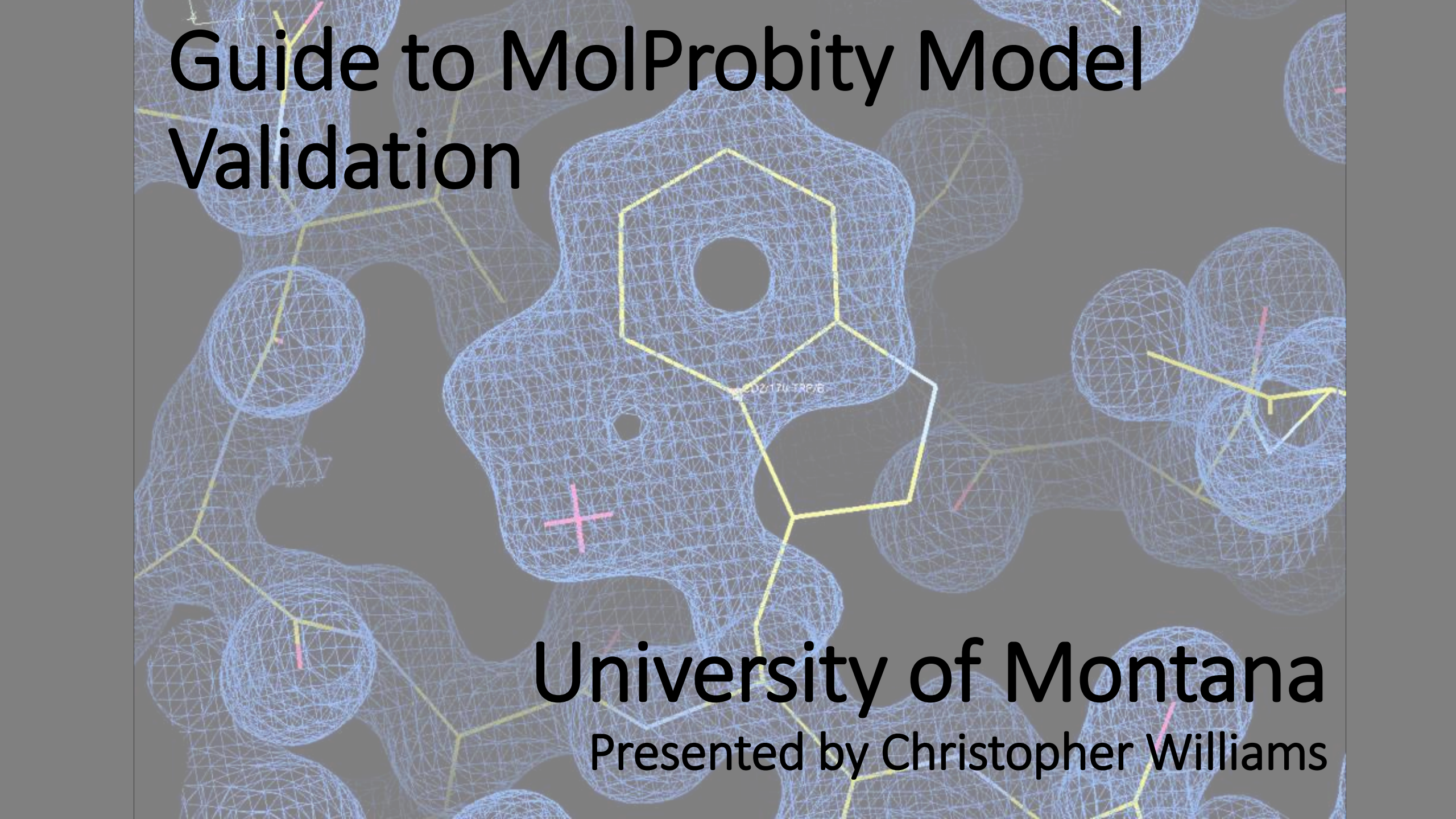
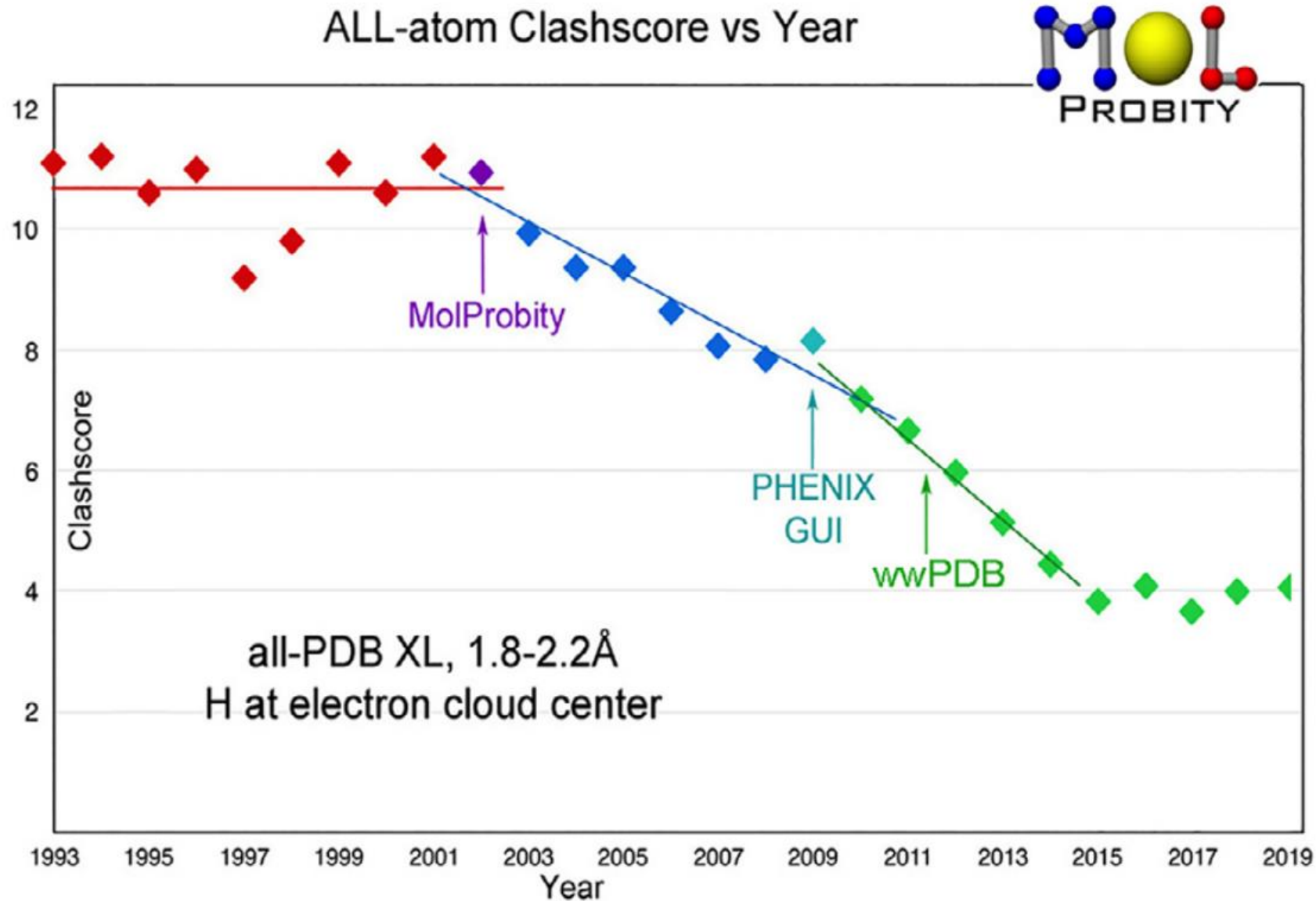


# Guide to MolProbity Model Validation



University of Montana  
Presented by Christopher Williams

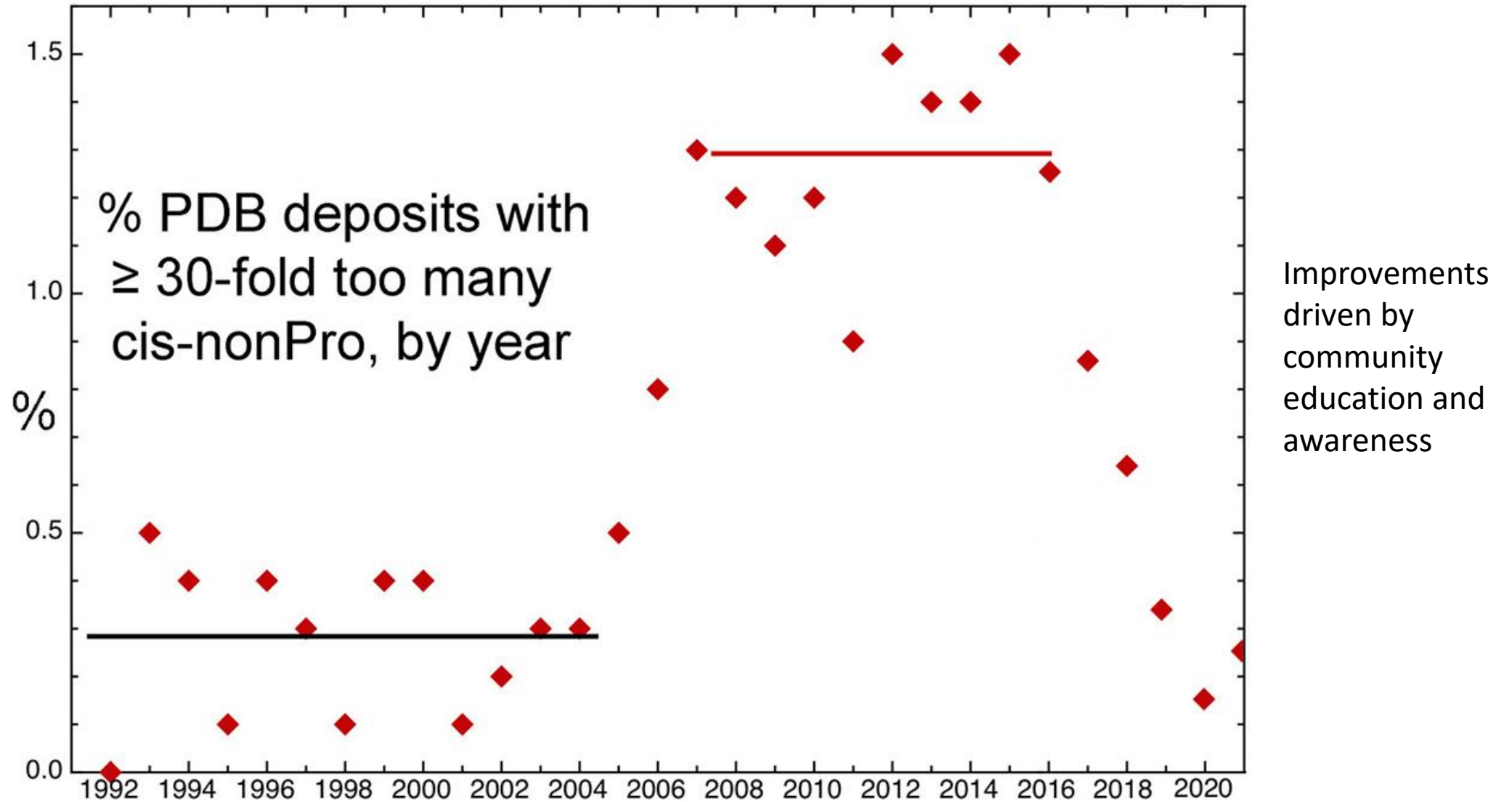
# Validation can make a difference



Improvements  
driven by availability  
of validation tools



# You can make a difference



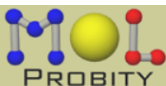
# Validation Philosophy

- Visualizations > statistics
- Local conformations > structure-level averages
- “Outlier” thresholds are set statistically
  - Expect to see experimentally justified statistical outliers sometimes, especially at functional sites
  - Cherish these! You found something cool!

# Intervention Philosophy

- Refinement is great at details, bad at escaping local minima
- Human interventions should
  - Find the right local minimum
  - Preserve interesting features
  - Not sweat the details

# MolProbity



Main page



Main page  
About hydrogens  
Evaluate X-ray  
Evaluate NMR  
Fix up structure  
Work with kins

View & download files  
Lab notebook  
Feedback & bugs  
Site map

Save session  
Log out

You are using 0% of  
your 200 Mb of disk  
space.

We reserve the right to bar access to users who violate our usage guidelines:

In particular, users making burst submissions of large number of structures should **download and install** their own local instance of MolProbity for this purpose. Once again, recent abuse of our server originating from a single institution has caused downtime and denial of service to our broader community. Regrettably, we will need to bar these users if this abuse continues.

Looking at deposited SARS-CoV-2 related structures? Check PDB for updated versions as well as new structures. (Our Fetch > always returns the latest version.)

Solving or improving them? Look at MolProbity's CaBLAM outliers, and at sparse H-bonds.

FILE UPLOAD/RETRIEVAL (MORE OPTIONS)

PDB/NDB code:  type: PDB coords

No file selected. type: PDB coords

Molprobity sites:

Duke (US) | Manchester (UK)

Usage Guidelines:

These web services are provided for analysis of individual structures.

For batch runs, please [download and install](#) your own copy of MolProbity.

## Walkthroughs, tutorials, and usage FAQs:

**Evaluate X-ray structure:** Typical steps for a published X-ray crystal structure or one still undergoing refinement.

**Evaluate NMR structure:** Typical steps for a published NMR ensemble or one still undergoing refinement.

**Fix up structure:** Rebuild the model to remove outliers as part of the refinement cycle.

**Work with kinemages:** Create and view interactive 3-D graphics from your web browser.

**Guide to Reduce options:** Learn about adding hydrogens to a structure for all-atom contact analysis.

**Guide to summary statistics:** Interpret structure-level validation statistics.

**Guide to validation options:** Choose validations appropriate to a structure.

What's new in 4.5.1

## Citations, science, and technical FAQs:

**Cite MolProbity:** Williams et al. (2018) MolProbity: More and better reference data for improved all-atom structure validation. Protein Science 27: 293-315.

**Cite KiNG:** Chen et al. (2009) KiNG (Kinemage, Next Generation): A versatile interactive molecular and scientific visualization program. Protein Science 18:2403-2409.

**Cite CCTBX:** Grosse-Kunstleve et al. (2002) The Computational Crystallography Toolbox: crystallographic algorithms in a reusable software framework. J. Appl. Cryst. 35:126-136.

**Cite NGL:** Rose et al. (2018) NGL viewer: web-based molecular graphics for large complexes. Bioinformatics. 34:3755-3758.

**About hydrogens:** Why have the hydrogen bondlengths changed?

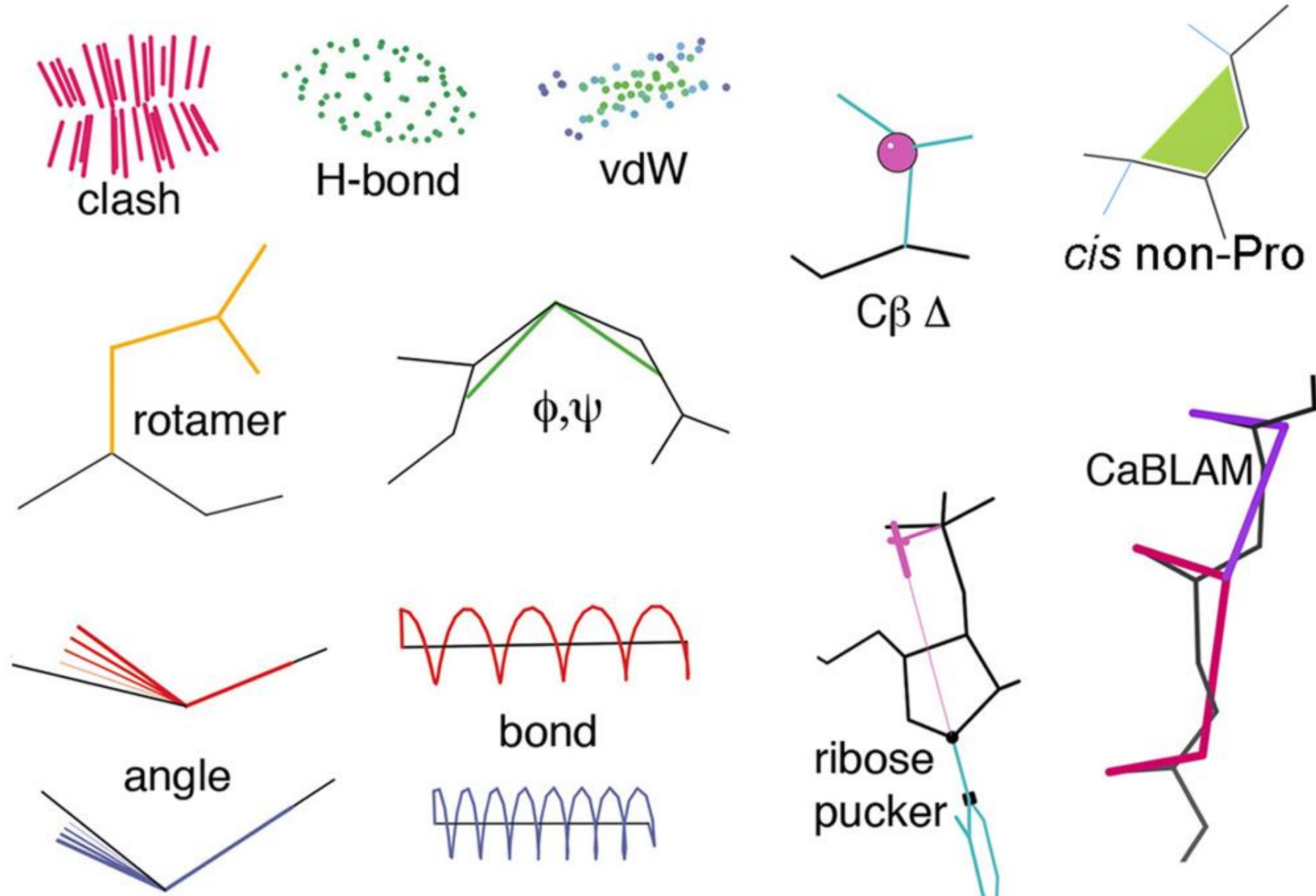
**Installing Java:** how to make kinemage graphics work in your browser.

**Download MolProbity:** how can I run a private MolProbity server, or run from the command line?

<http://molprobity.biochem.duke.edu/index.php>

- Free, online structure validation server
  - Also built into Phenix
- Confidential
  - Files are automatically deleted
- Open-source
  - <https://github.com/rlduke>

More  
tutorials



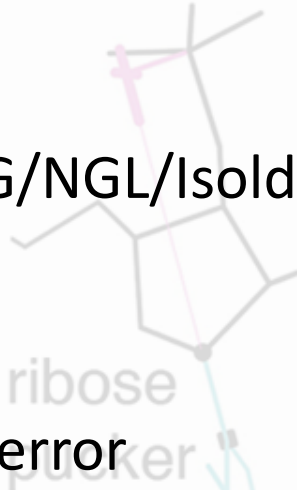
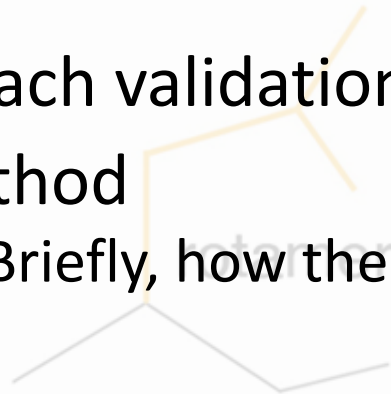
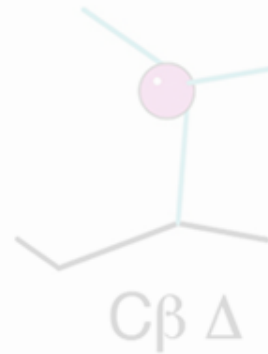
MolProbity markup (KiNG, NGL viewers)

# Outline

For each validation

- Method
  - Briefly, how the underlying idea or math works
- Visualization
  - How outliers are visually represented in KiNG/NGL/Isolde
- Probable causes
  - Example of a common or interesting type of error
  - Not comprehensive!

MolProbity markup

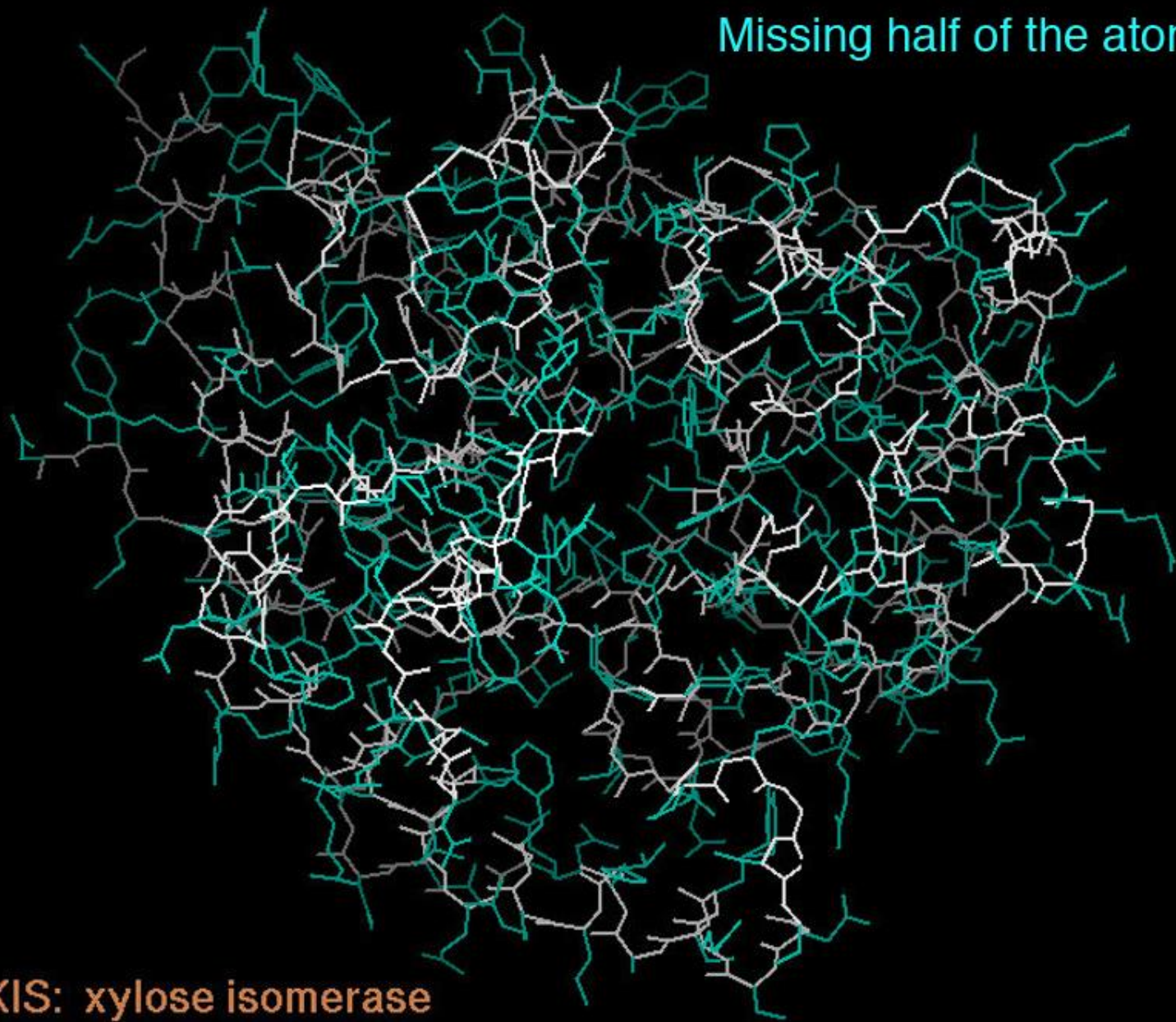




# All-Atom Clashes and Contacts

Add hydrogens  
(phenix.reduce or MolProbity website)

Missing half of the atoms!

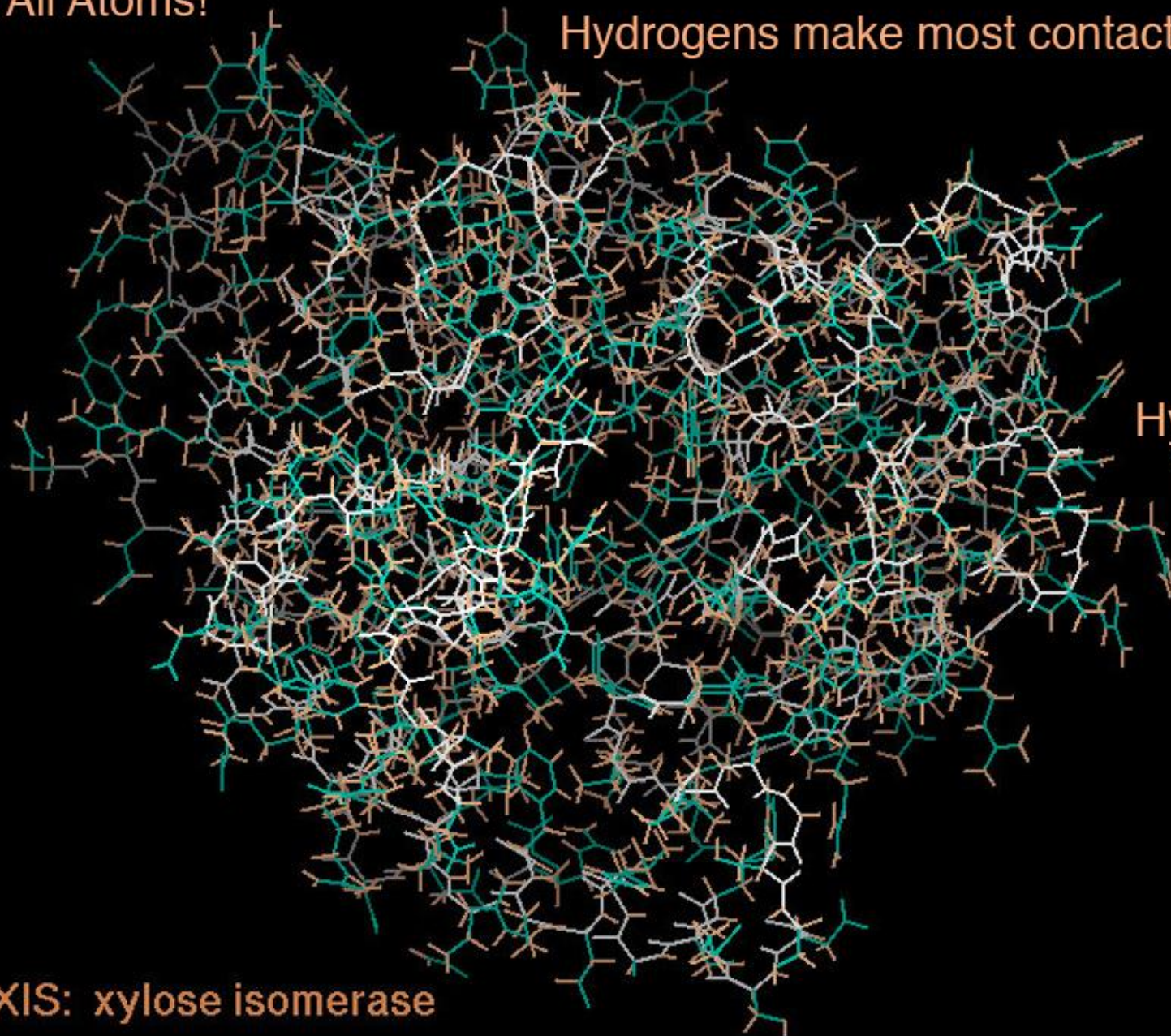


4XIS: xylose isomerase



All Atoms!

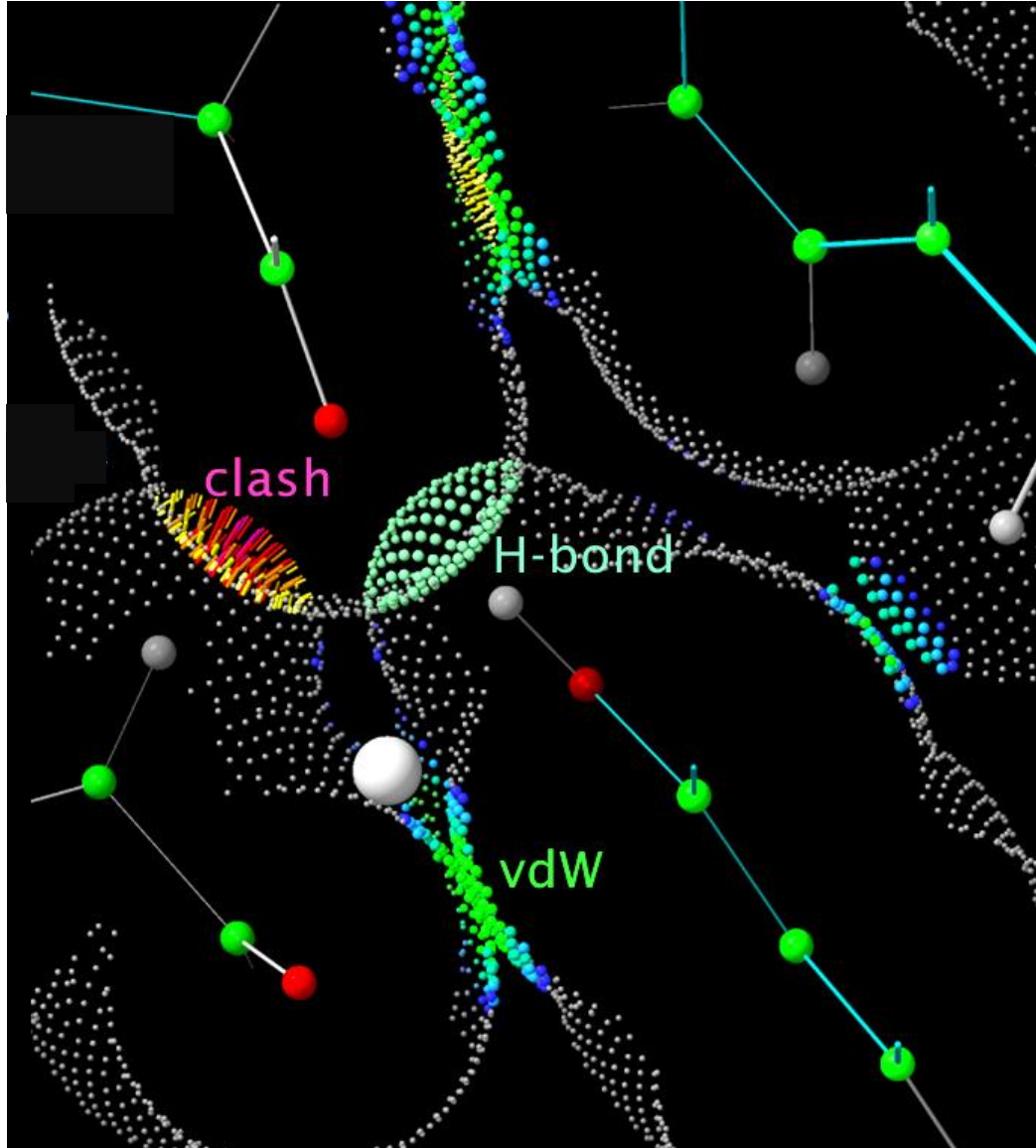
Hydrogens make most contacts



Hydrogens:  
“twigs  
on the  
tree”

4XIS: xylose isomerase

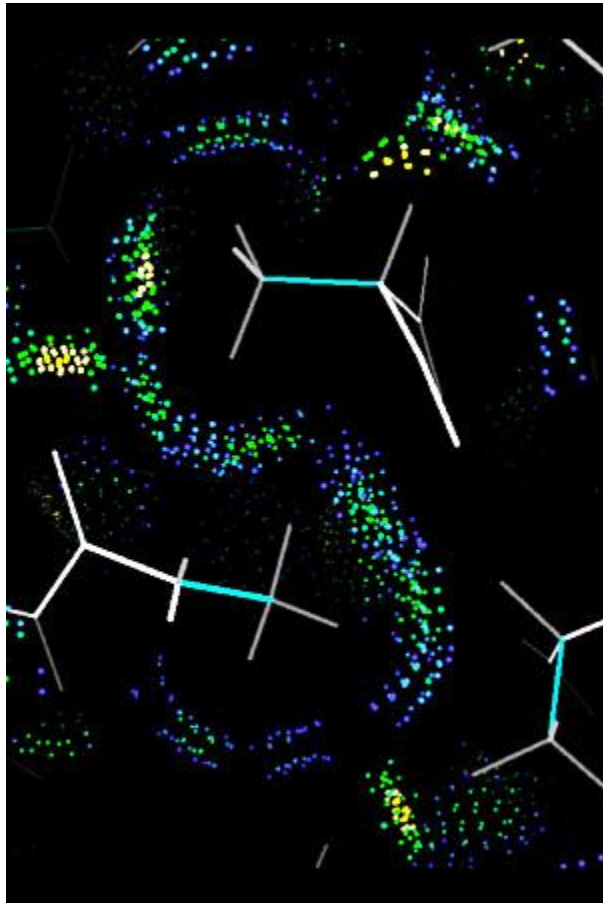
# All-Atom Contacts and Clashes: Method



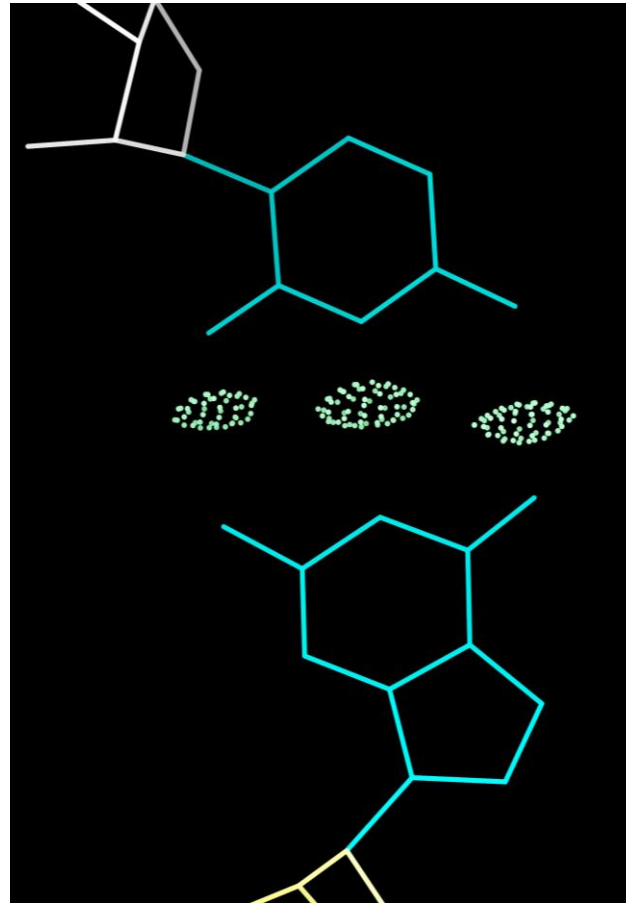
- Roll a 0.25Å radius “Probe” sphere over the van der Waals surface of each atom
- Mark where the probe touches or overlaps with another van der Waals surface
- Note that hydrogen atom surfaces can shield heavy atom surfaces



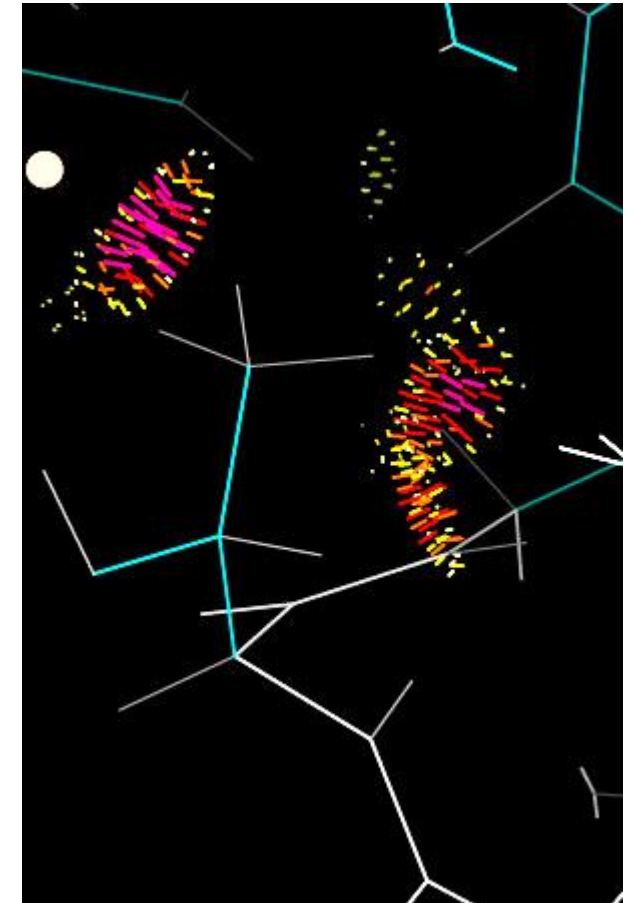
# All-Atom Contacts and Clashes: Visualization



Favorable vdW packing in greens and blues



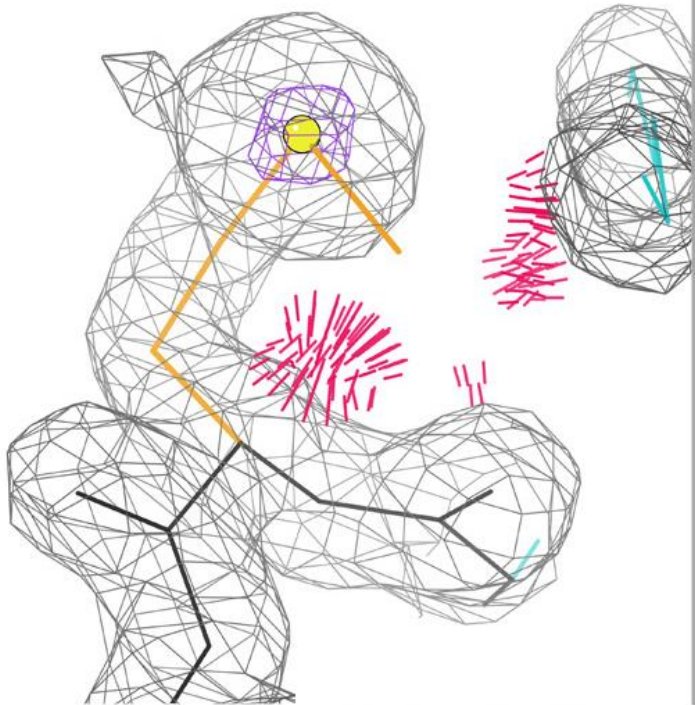
Favorable hydrogen bonding as light green pillows



Steric overlaps, aka "clashes", as hot pink spikes

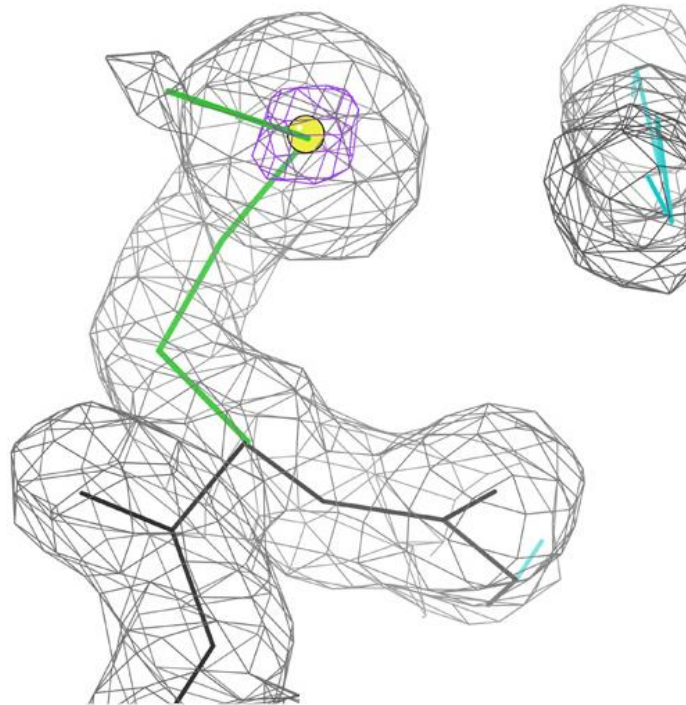
# All-Atom Contacts and Clashes: Probable causes

original: !!



1j58 MSe 351

rebuilt: mmm

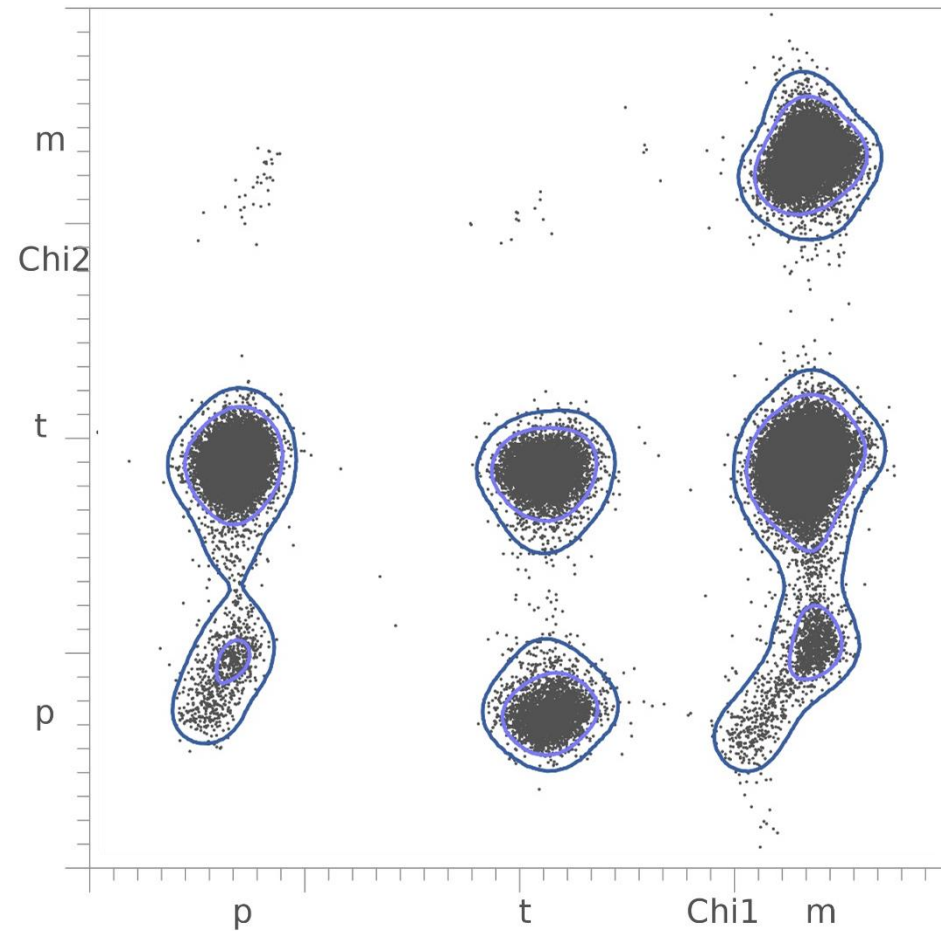


## Other outliers

- Clashes usually occur alongside other outliers
- Emphasize modeling errors
  - *Real* rare features are less likely to have clashes
- Can imply direction for fixups

# Sidechain Rotamers

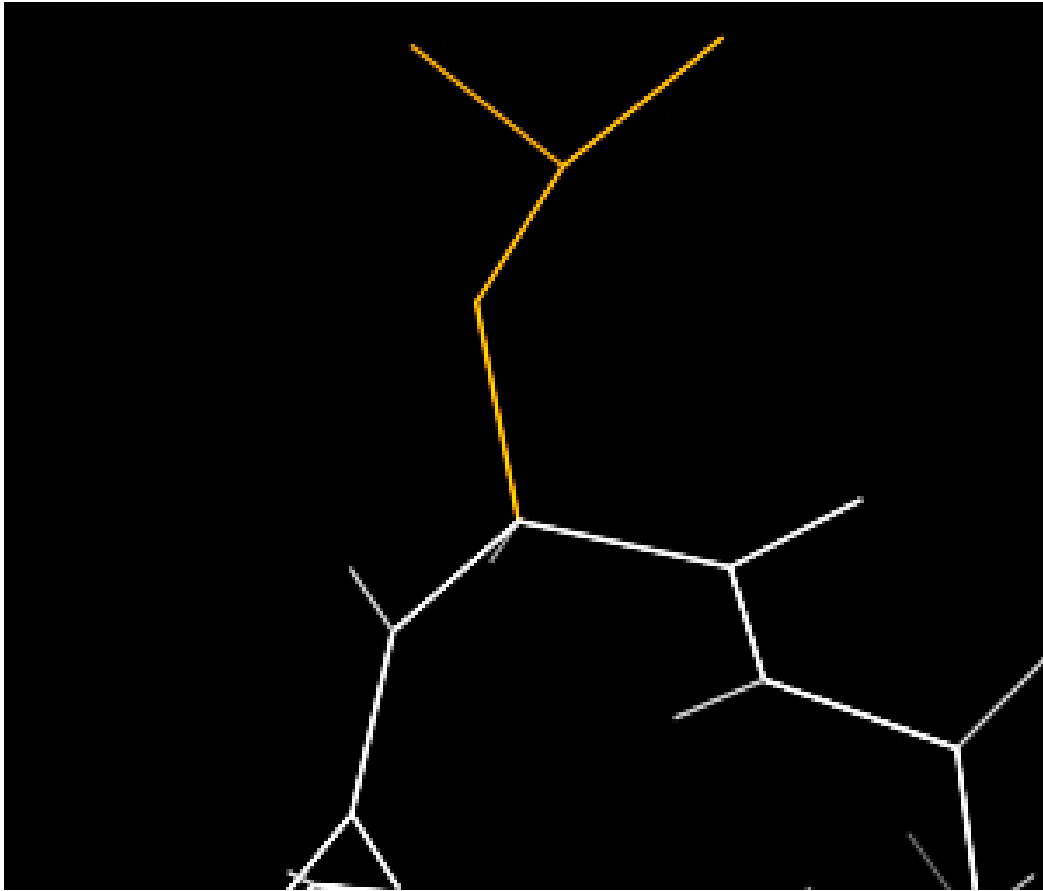
# Sidechain Rotamers: Method



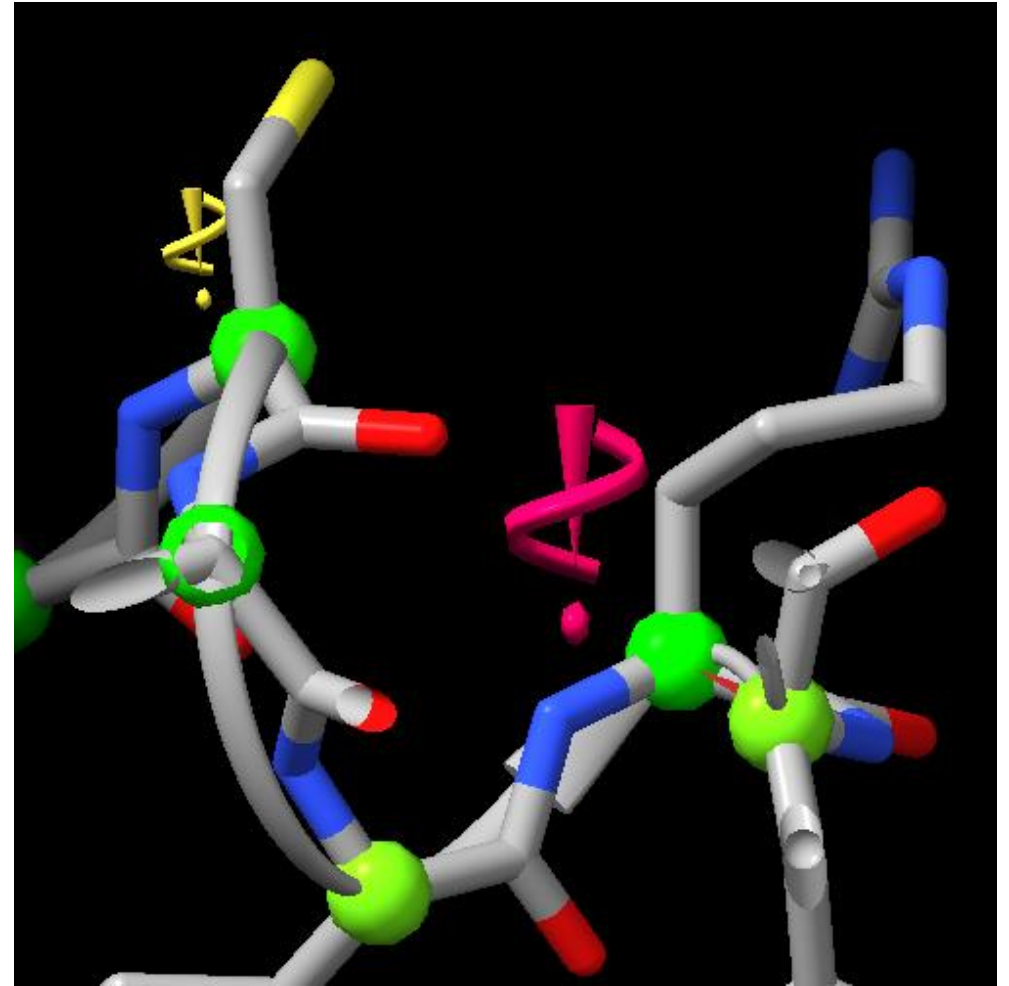
Rotamer distribution for  
Isoleucine in  $\chi_1/\chi_2$  space

- Sidechain conformations are described by a series of  $\chi$  (Chi) torsions
- Rotamers are statistically expected combinations of  $\chi$  values
- For tetrahedral atom centers, this means staggered
  - p +60°
  - t 180°
  - m -60°
- For planar atom centers, rotamers are much more continuous
  - Rotamers are named with a central value
  - e.g m90 or p-80 for Histidine

# Sidechain Rotamers: Visualization



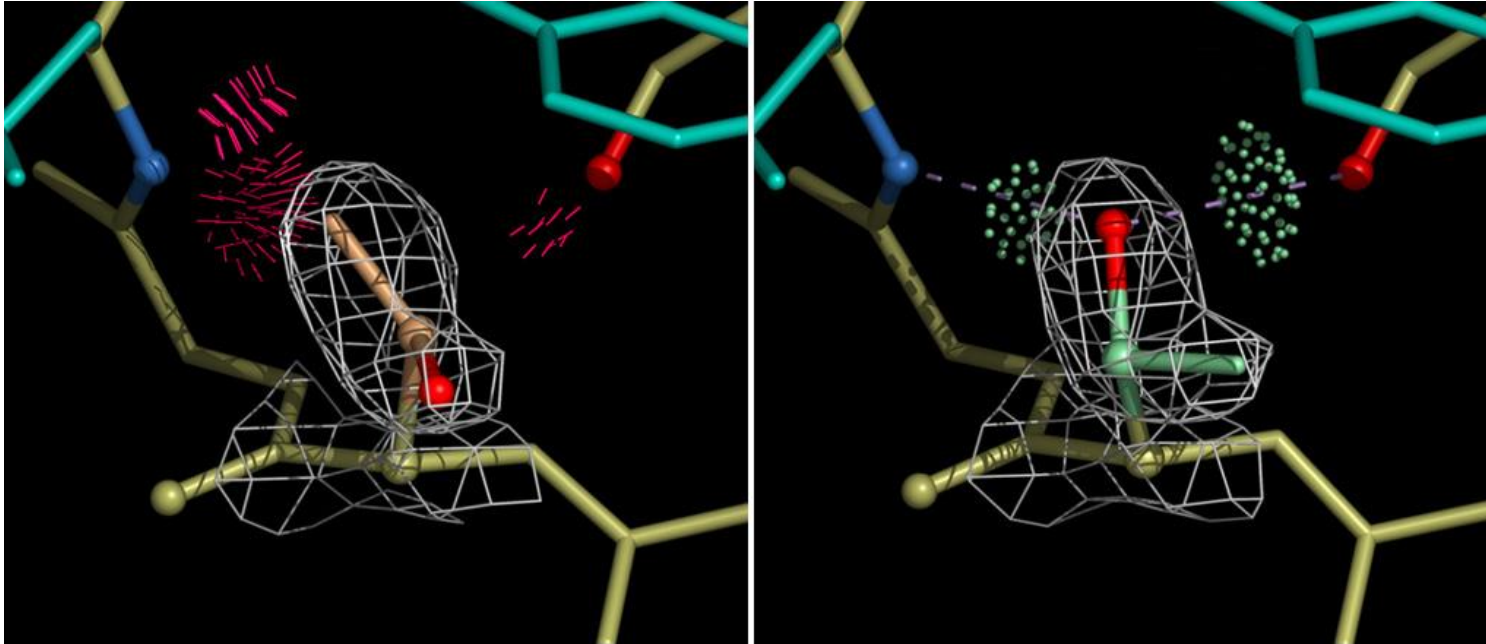
In KiNG, Rotamer outliers are traced in gold over the modeled sidechain



In ISOLDE, Rotamer allowed/outliers are marked with a spiral, color coded by prior probability



# Sidechain Rotamers: Probable causes

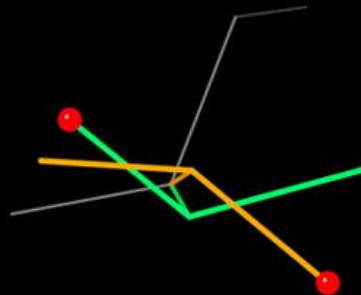


Backwards Valine,  
Leucine, Threonine

- May find terminal atoms fit into density at the expense of the branch atom
- Simple to fix with a flip (then re-refinement)

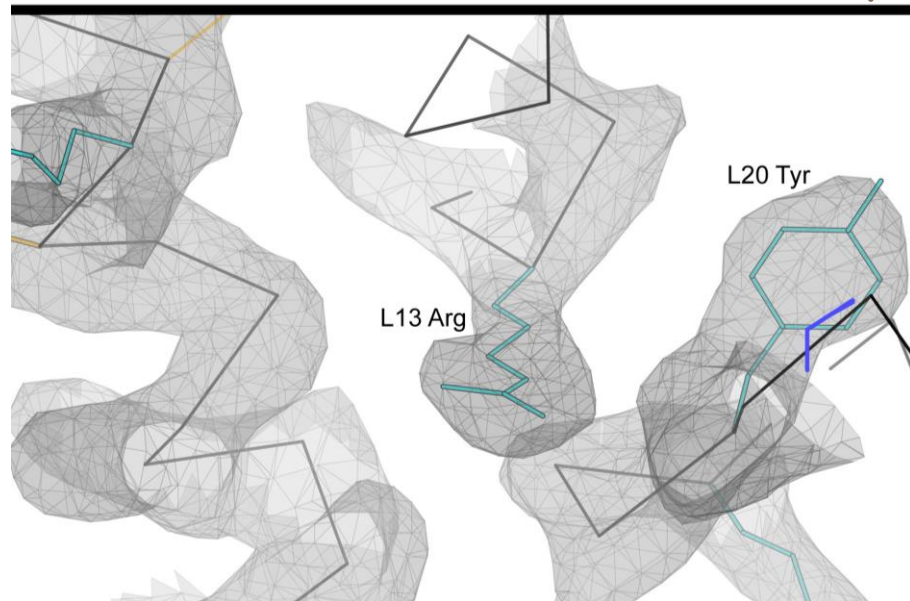
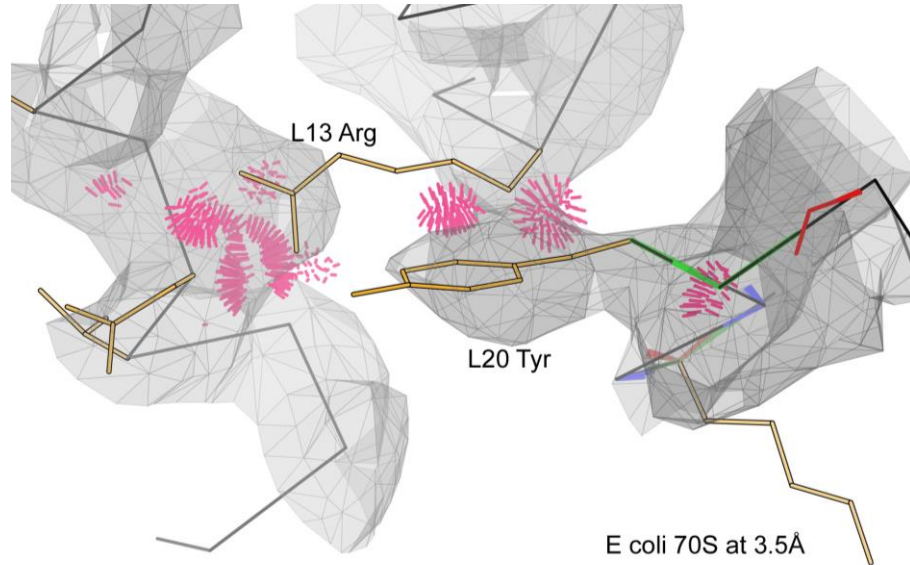
1sbp, 1.7Å

Cbdev = .39 Å  
Chi1 = -109°  
N-Ca-Cb = 98°  
3 bad clashes  
no H-bonds  
C in > density



Cbdev = 0  
Chi1 = 73°  
N-Ca-Cb = 110°  
no bad clashes  
2 H-bonds  
O in > density

# Sidechain Rotamers: Probable causes



Sidechains in wrong density

- Sidechains can get stuck in the density for other features
  - Other sidechains
  - Ligands
  - Backbone in  $\sim 3\text{\AA}$  maps
- Have to fix the whole network of misplacements

# Protein Backbone Validation

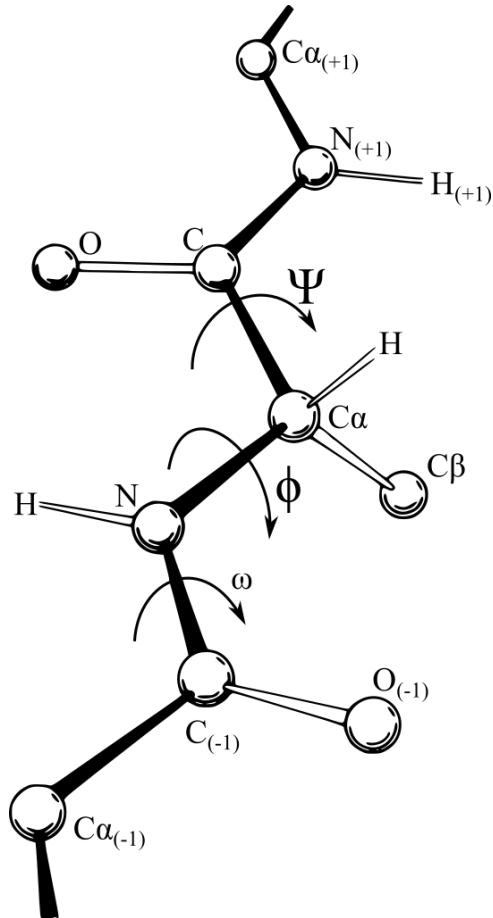
Ramachandran

CaBLAM

Rama-Z

Ramachandran

# Ramachandran: Method



- Phi and Psi torsions describe local protein backbone conformation
- Phi  $\phi$  = C $_{i-1}$ -N-C $\alpha$ -C
- Psi  $\psi$  = N-C $\alpha$ -C-N $_{i+1}$
- Each residue's  $\phi/\psi$  pair is converted into cartesian coordinates and checked against contours of expected behavior



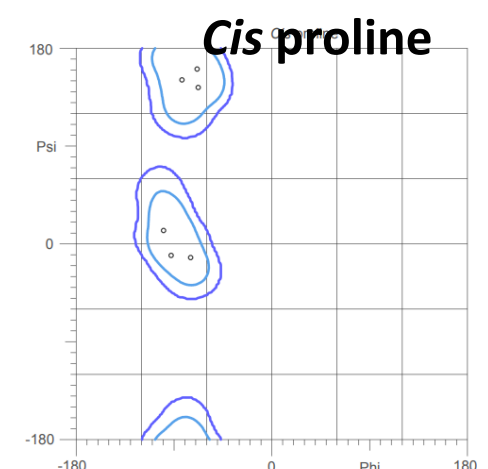
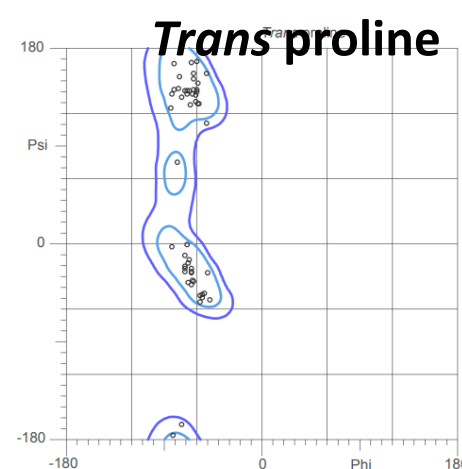
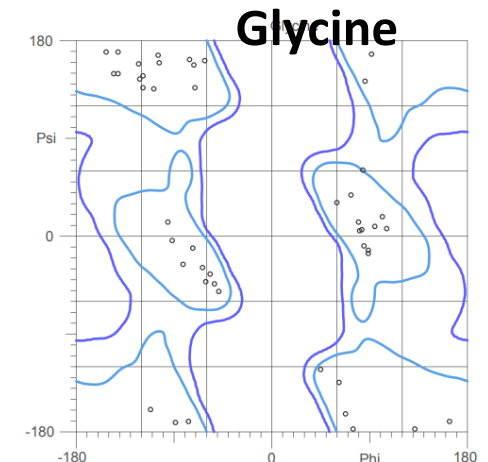
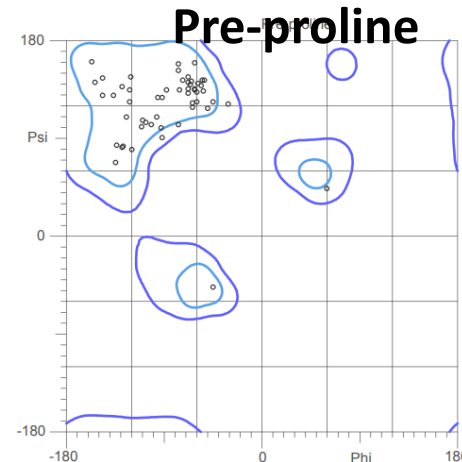
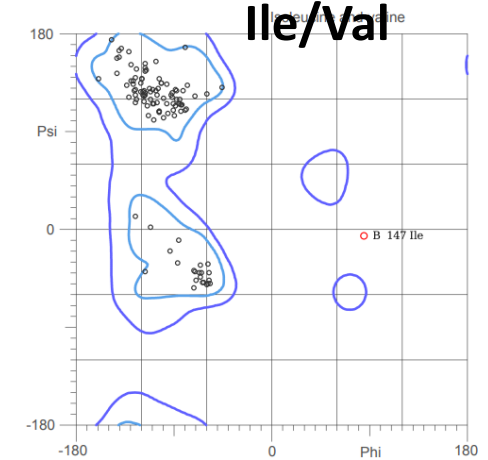
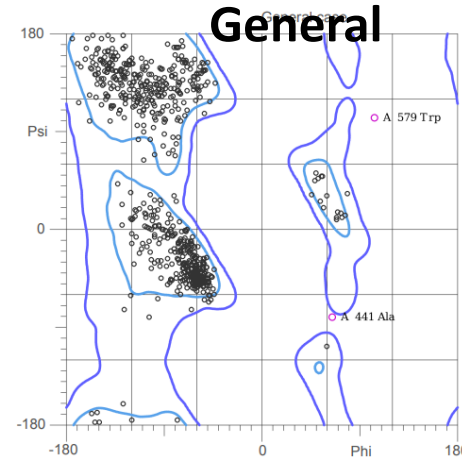
# Ramachandran: Visualization

Ramachandran plots shows location of each residue relative to contours of expected behavior

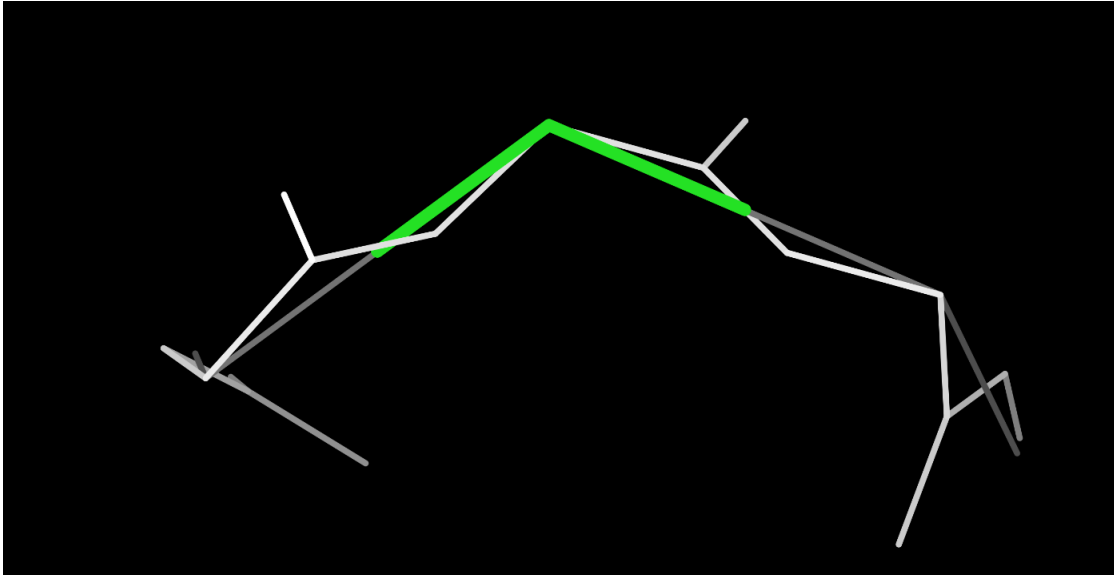
Different residue categories have very different expectations!

Glycine is permissive and symmetrical  
Proline is restrictive

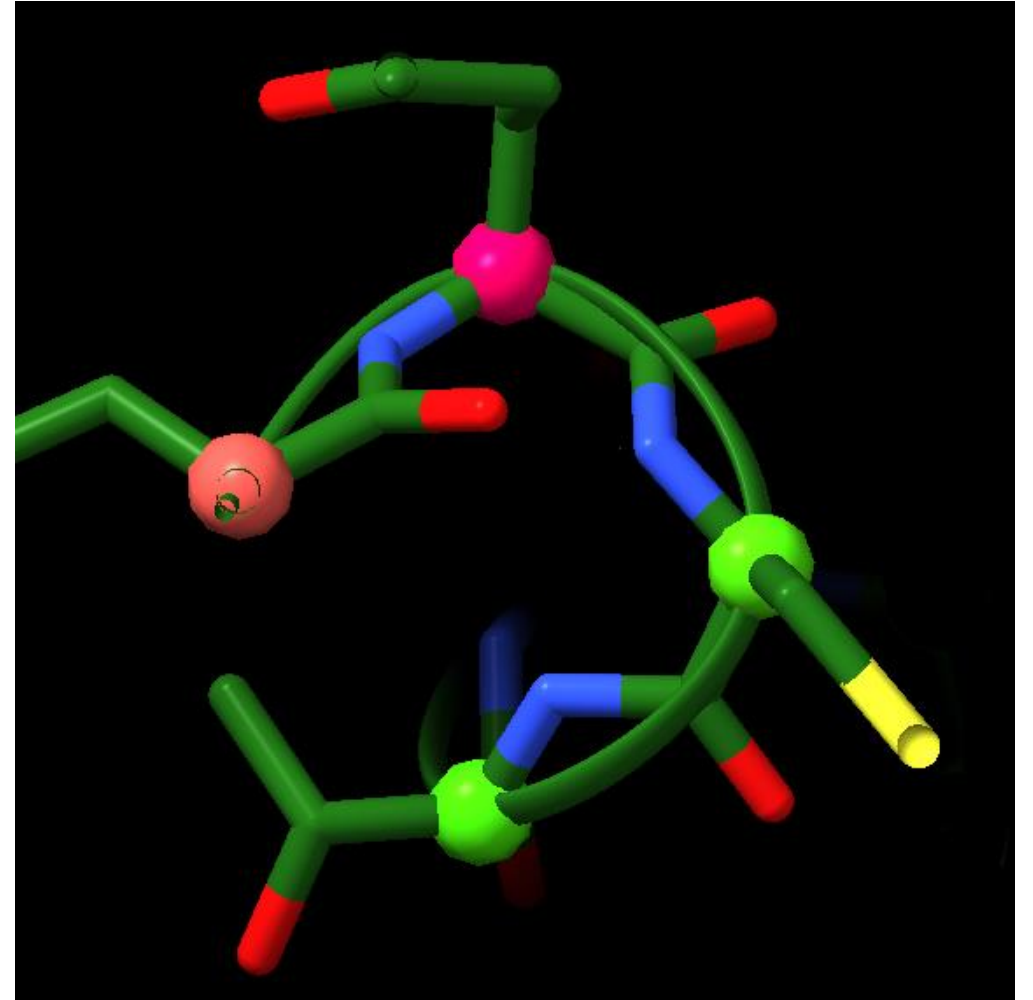
Branched C-Beta sidechain (Ile,Val) affect distribution



# Ramachandran: Visualization



KiNG markup highlights an outlier residue's CA in green, and extends to the peptide bonds on either side, along the CA-CA-trace

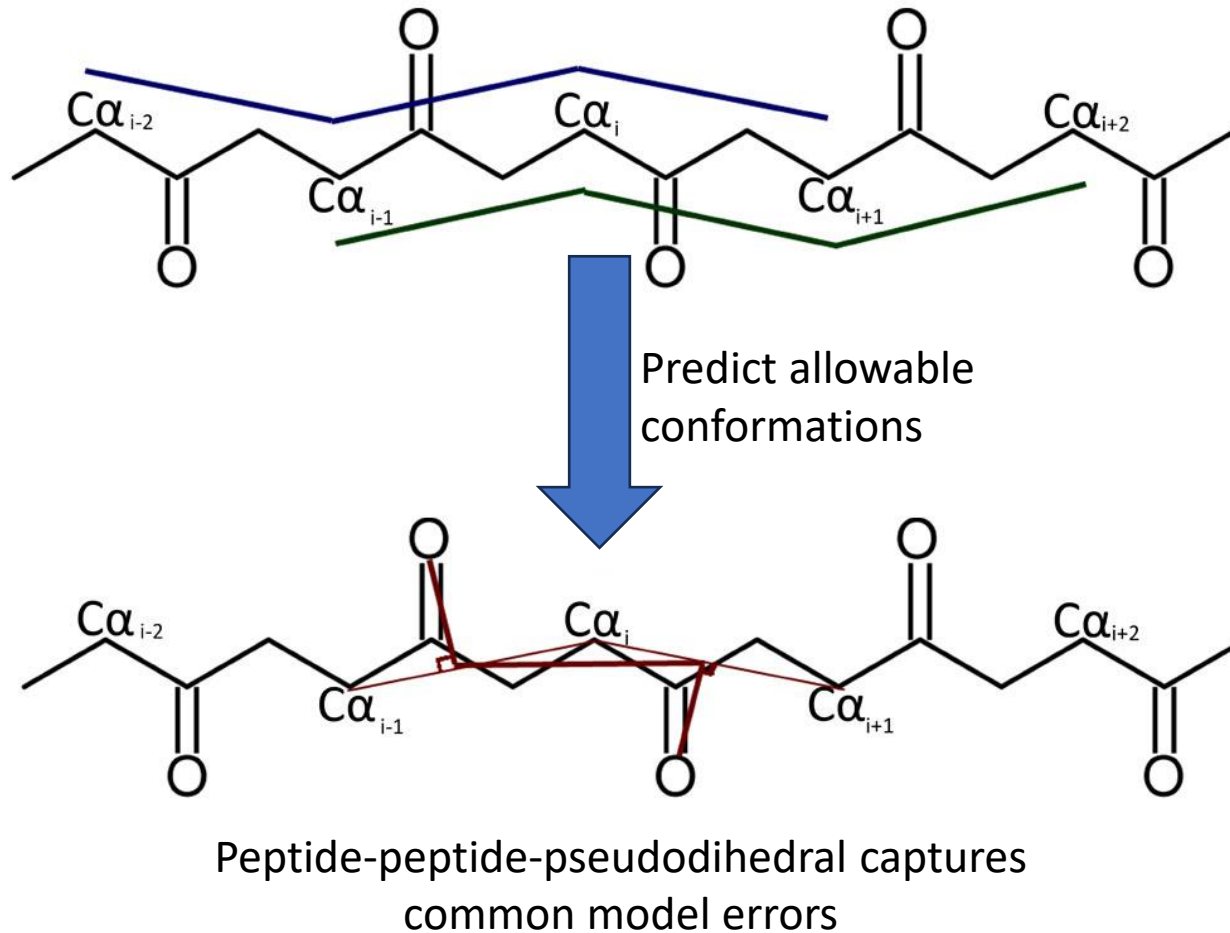


ISOLDE markup places a ball at each CA, color-coded by Ramachandran favorability.

CaBLAM

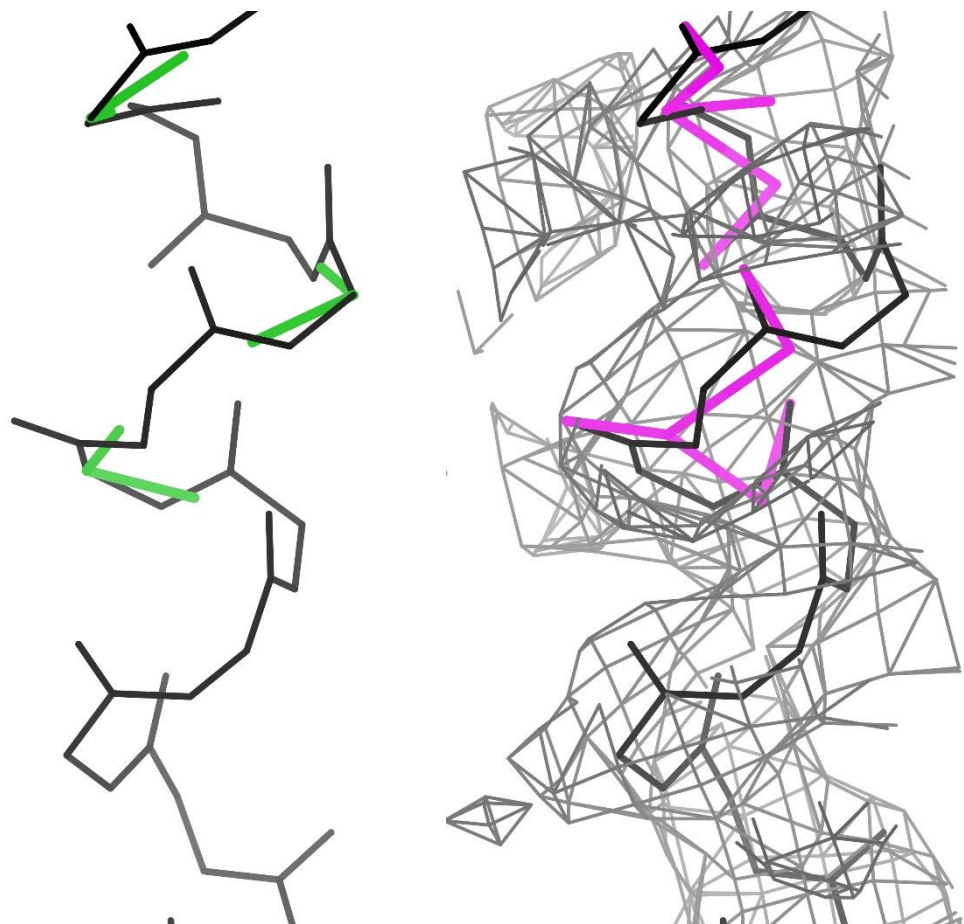
# CaBLAM: Method

CA-pseudodihedrals capture model “intent”



- At low resolution, the backbone CA trace is modeled better than the backbone details
- Common model errors involve wrong peptide plane orientation
- CaBLAM uses modeled CA trace geometry to predict likely peptide plane orientation, and marks the discrepancies

# Rama/CaBLAM: Probable causes



Rama markup

CaBLAM markup  
(magenta bars)

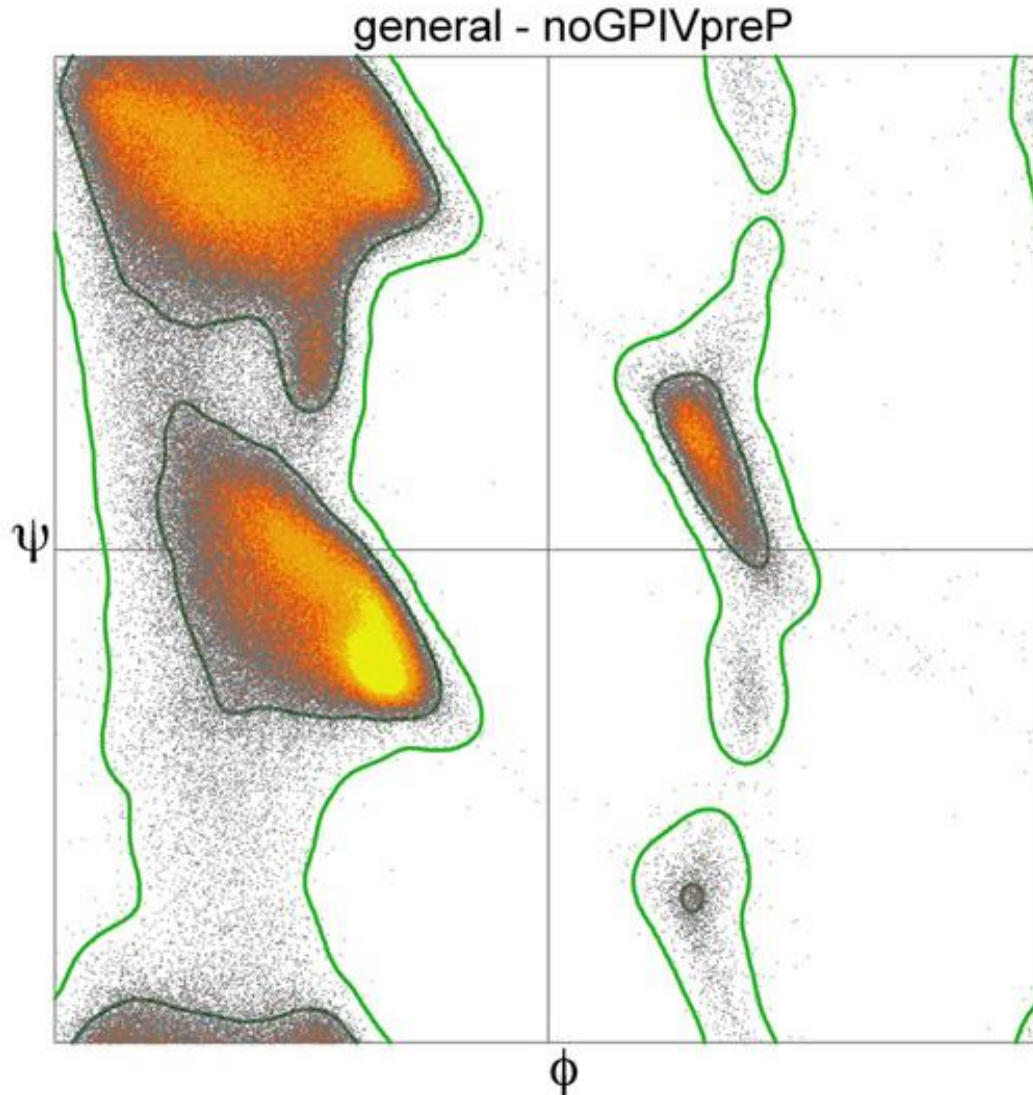
## Misplaced carbonyl oxygens

- At resolutions worse than  $\sim 2.5\text{\AA}$ , carbonyl oxygen density disappears
  - O may be fit in arbitrary orientation
- Low-resolution density envelope allows multiple models
  - Not everything that fits is protein-like
  - Data doesn't have enough information to choose among models



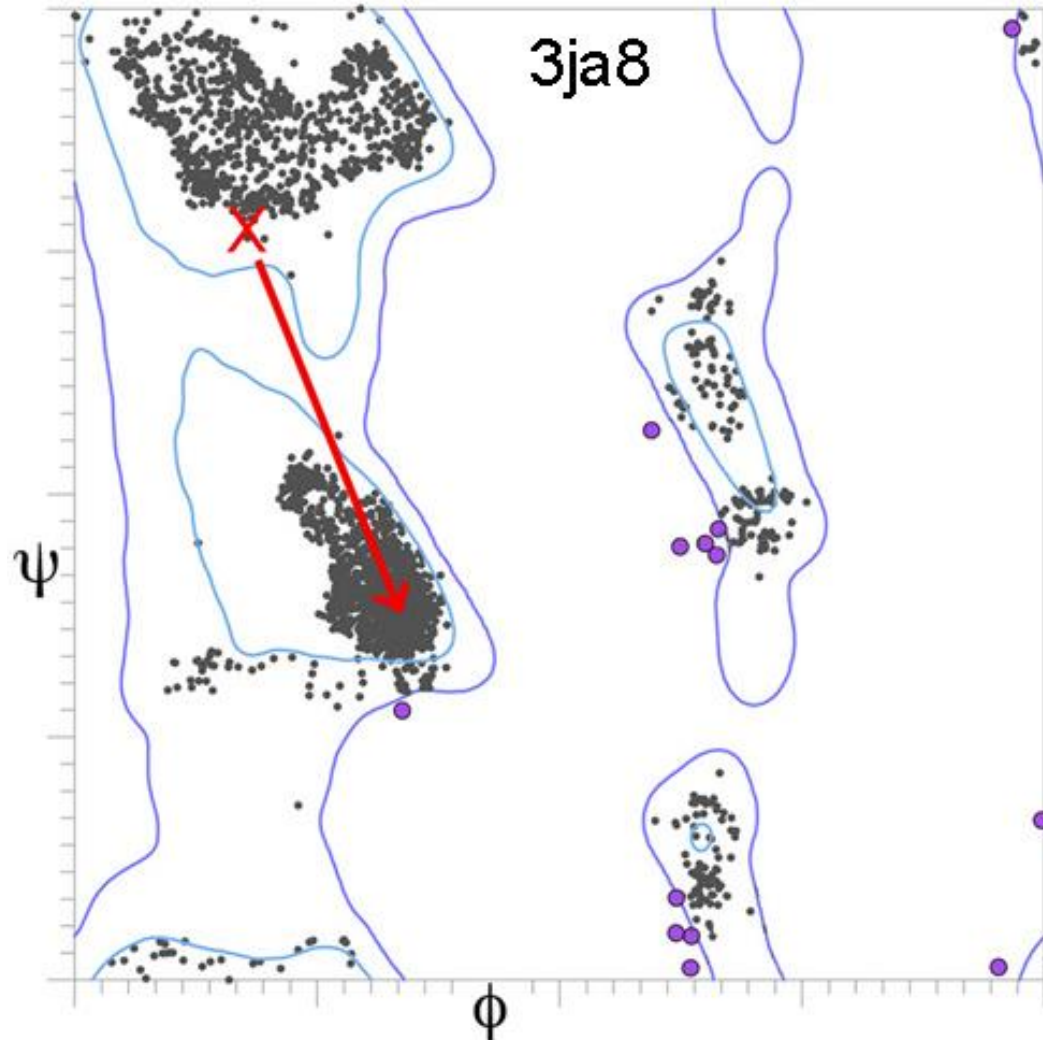
Ramachandran Z-score

# Ramachandran Z-score: Method



- Compare observed Ramachandran distribution against expected distribution (shown)
- Assign statistical Z-score based on distance from expectation
- $|Z\text{-score}| \leq 2$  indicates a realistic distribution
- $|Z\text{-score}| > 3$  indicates a highly unrealistic distribution

# Ramachandran: Probable causes



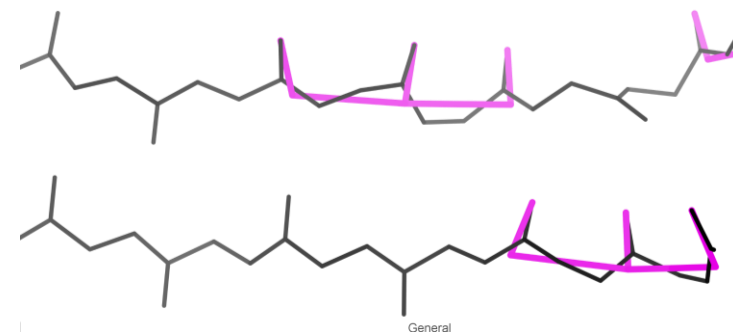
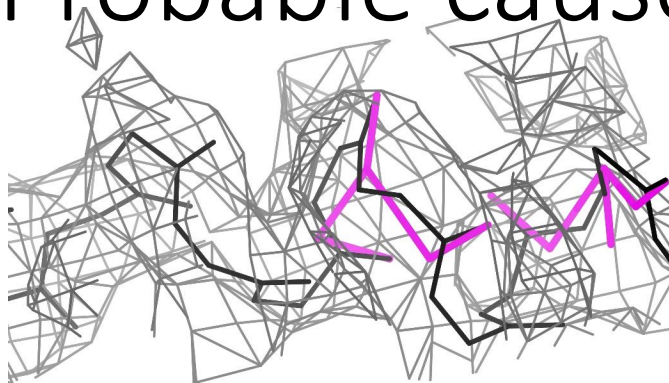
Rama Z-score  $-4.26 \pm 0.10$

## Overfitting to Rama criteria

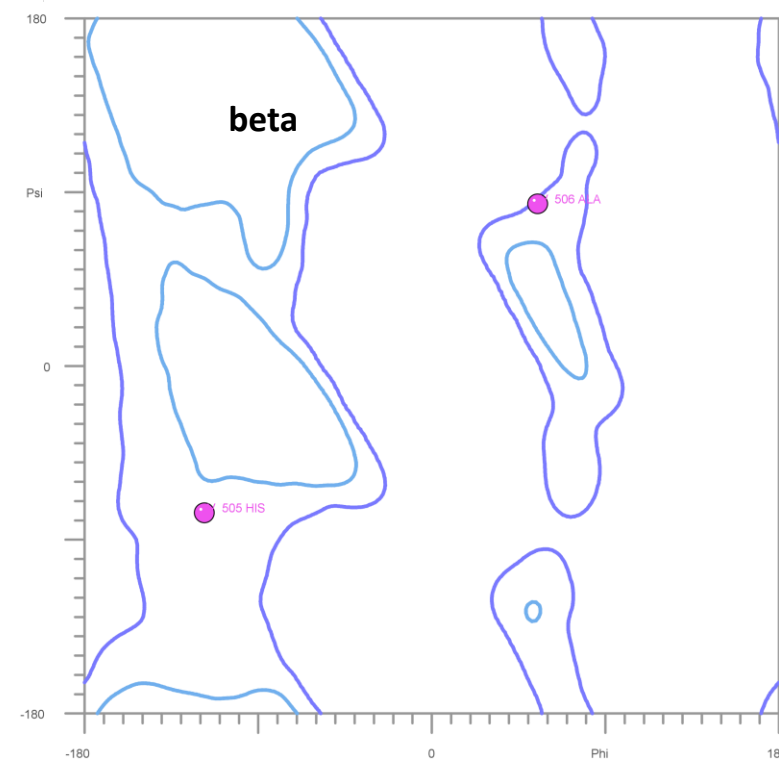
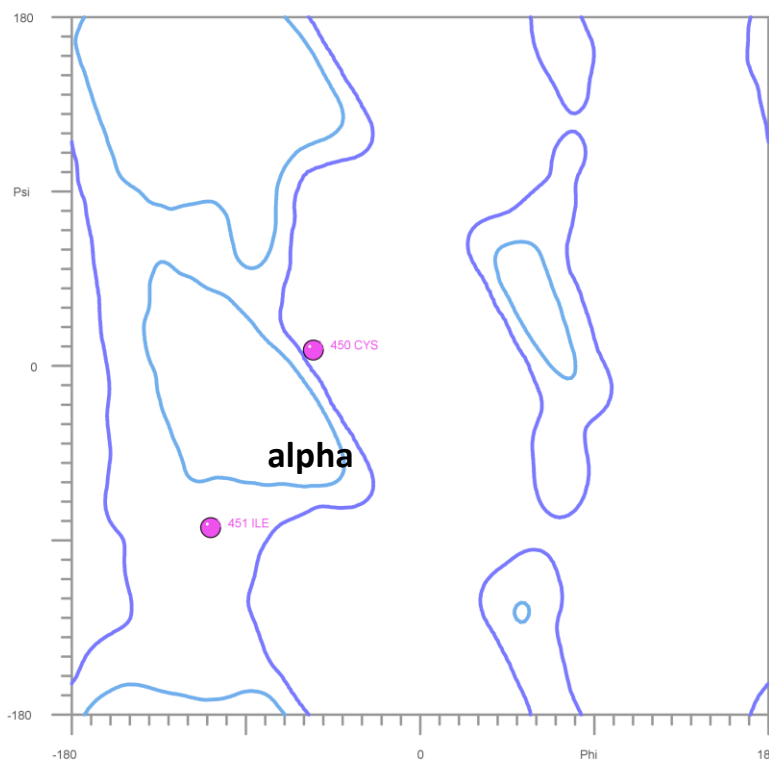
- Some programs allow refinement of the Ramachandran plot
  - Hides/compounds rather than fixes errors, if used carelessly
  - Artificially improves Ramachandran and MolProbity scores
- Over-idealized distribution may be detectible by Rama Z-Score
- Use other methods to fix model errors
- Then (maybe) Rama restraints to hold good structure in place

# Rama/CaBLAM: Probable causes

Current Rama position  
does not predict  
*Correct* Rama position

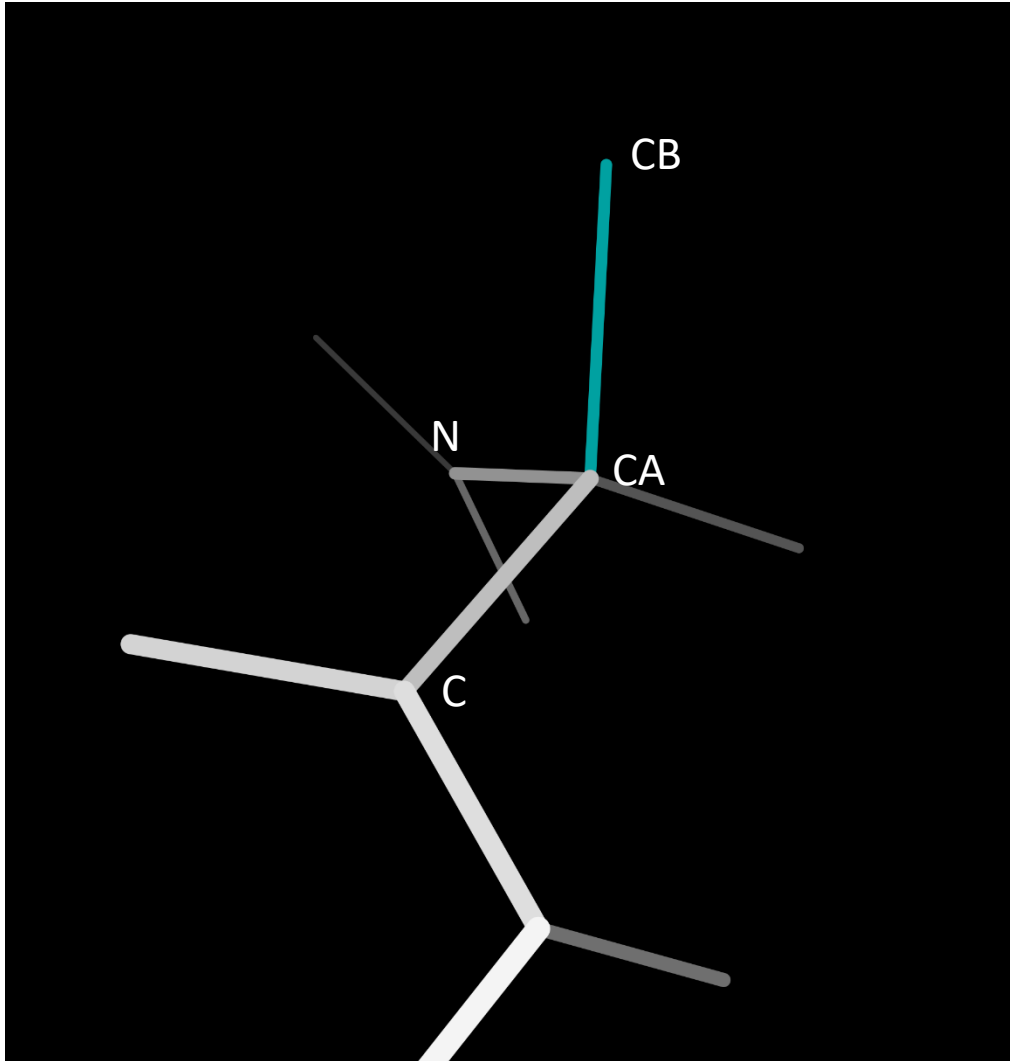


- If model errors are large, points in Rama space are displaced far from their intended regions
- 90° or even 180° peptide orientation errors are possible in low-resolution maps!



C-Beta Deviation

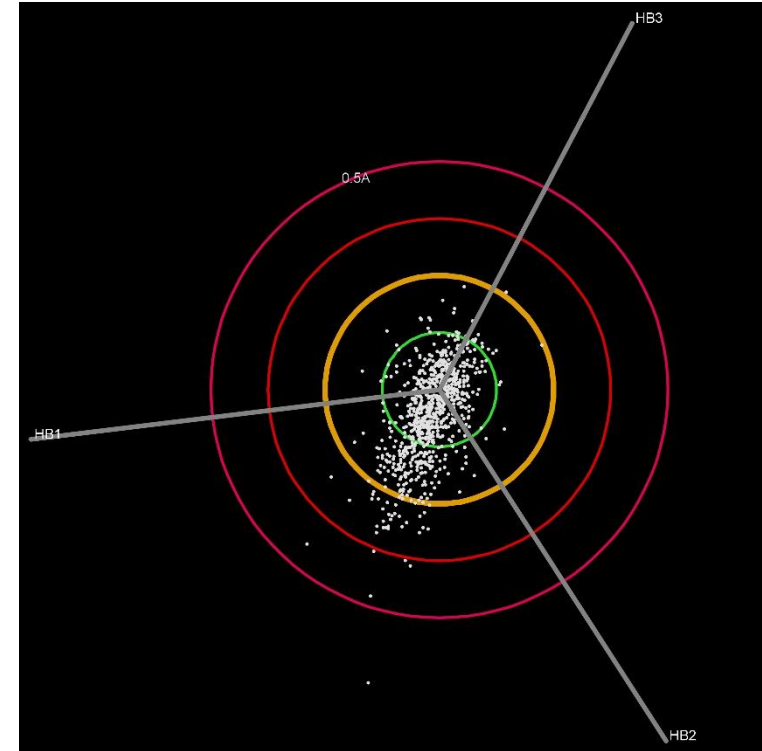
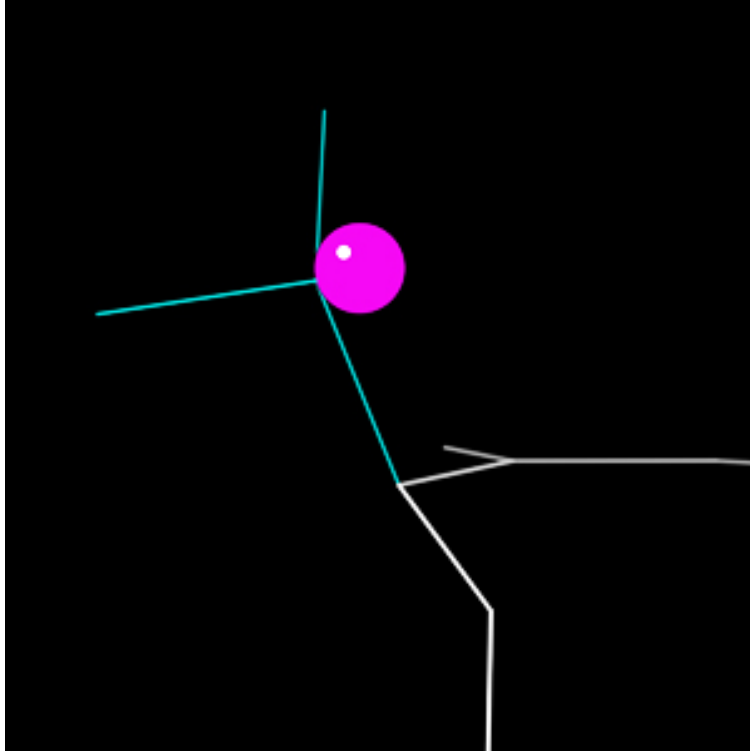
# C-Beta Deviation: Method



- Ideal CB position is defined by backbone geometry
- Calculate ideal position using average of two torsions
  - N-C-CA-CB
  - C-N-CA-CB
- CBs modeled  $>0.25\text{\AA}$  from ideal position are outliers



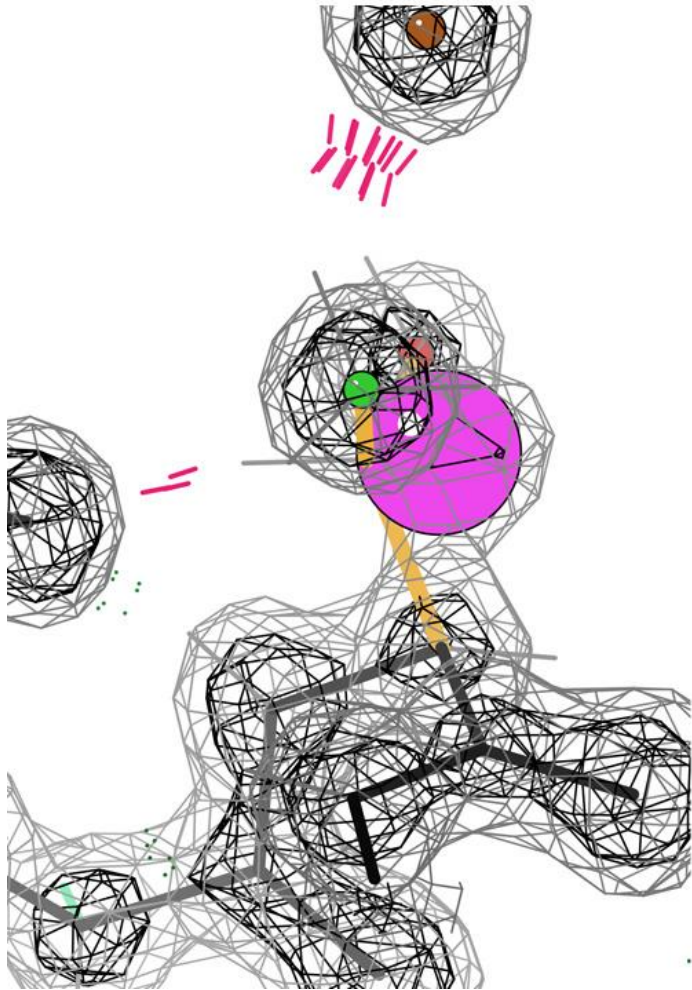
# C-Beta Deviation: Visualization



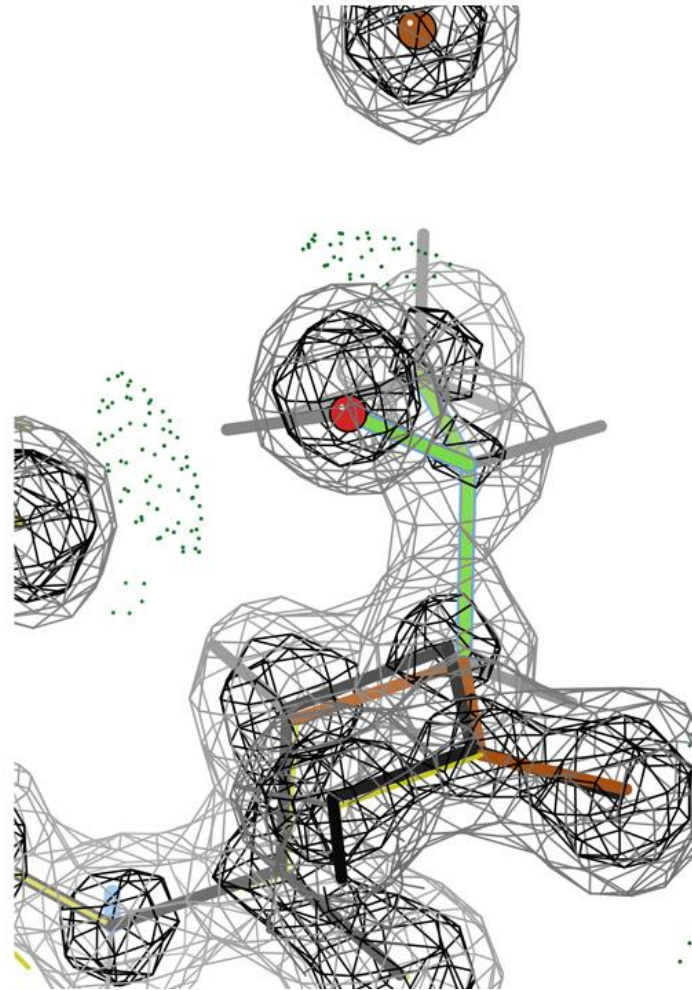
- In KiNG, a magenta sphere is drawn
  - Center at ideal CB position
  - Edge tangent to modeled position
  - Size of sphere proportional to severity of outlier
- Bullseye kinemage shows distribution and direction of all CB positions.
- Yellow circle is 0.25Å outlier cutoff

# C-Beta Deviation: Probable causes

1bkr Thr101, 0.63Å C $\beta$ dev



refit, clashes now H-bonds



## Misplaced sidechains

- CB deviation outliers are usually caused by misplaced sidechains
  - Especially branched sidechains fit backwards, like this Thr

## Chirality errors

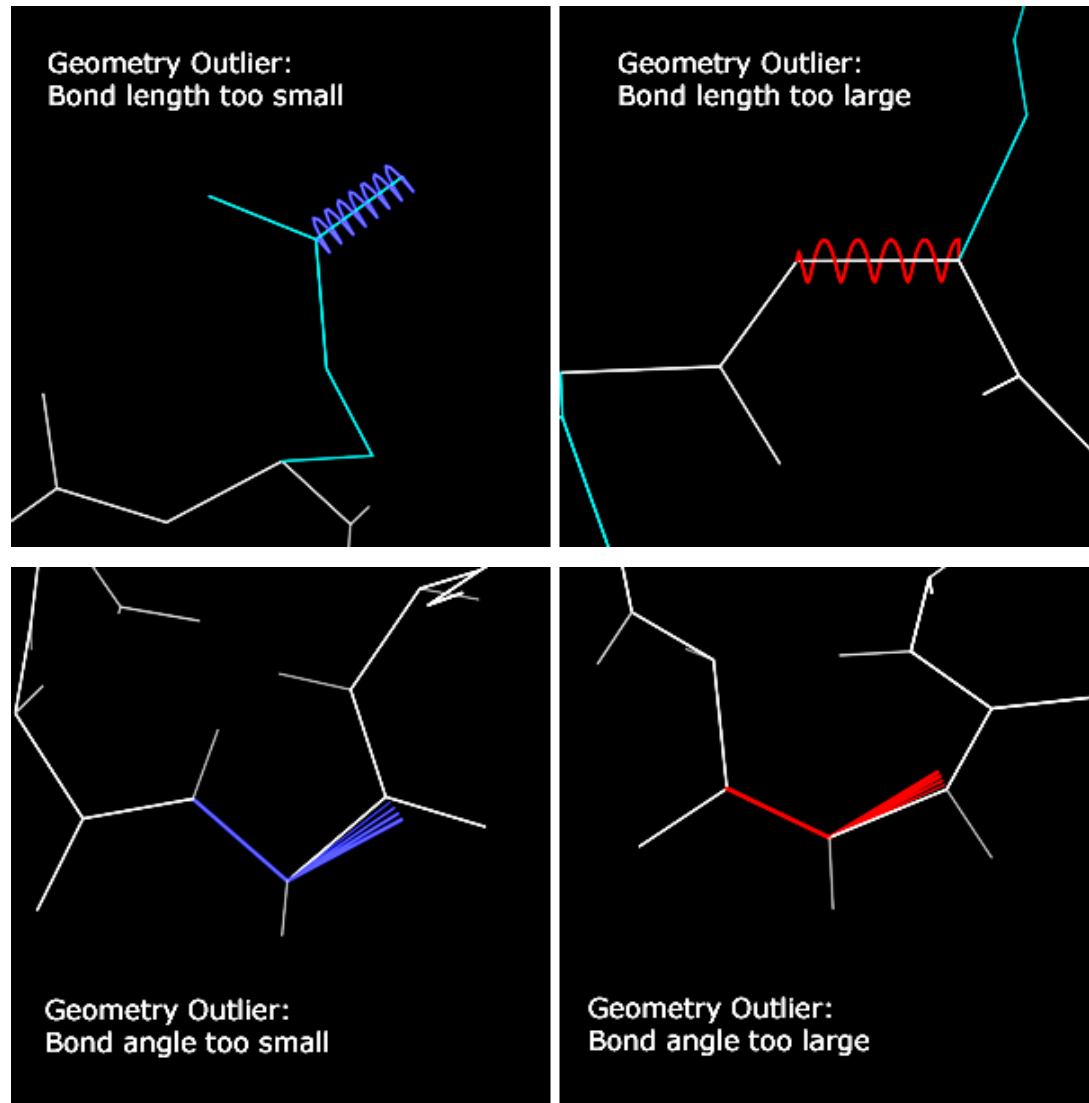
- If D amino acids are misnamed as L amino acids (e.g. ALA for DAL), or vice versa, very large C $\beta$ devs result

# Covalent Bond Geometry

# Bond Geometry: Method

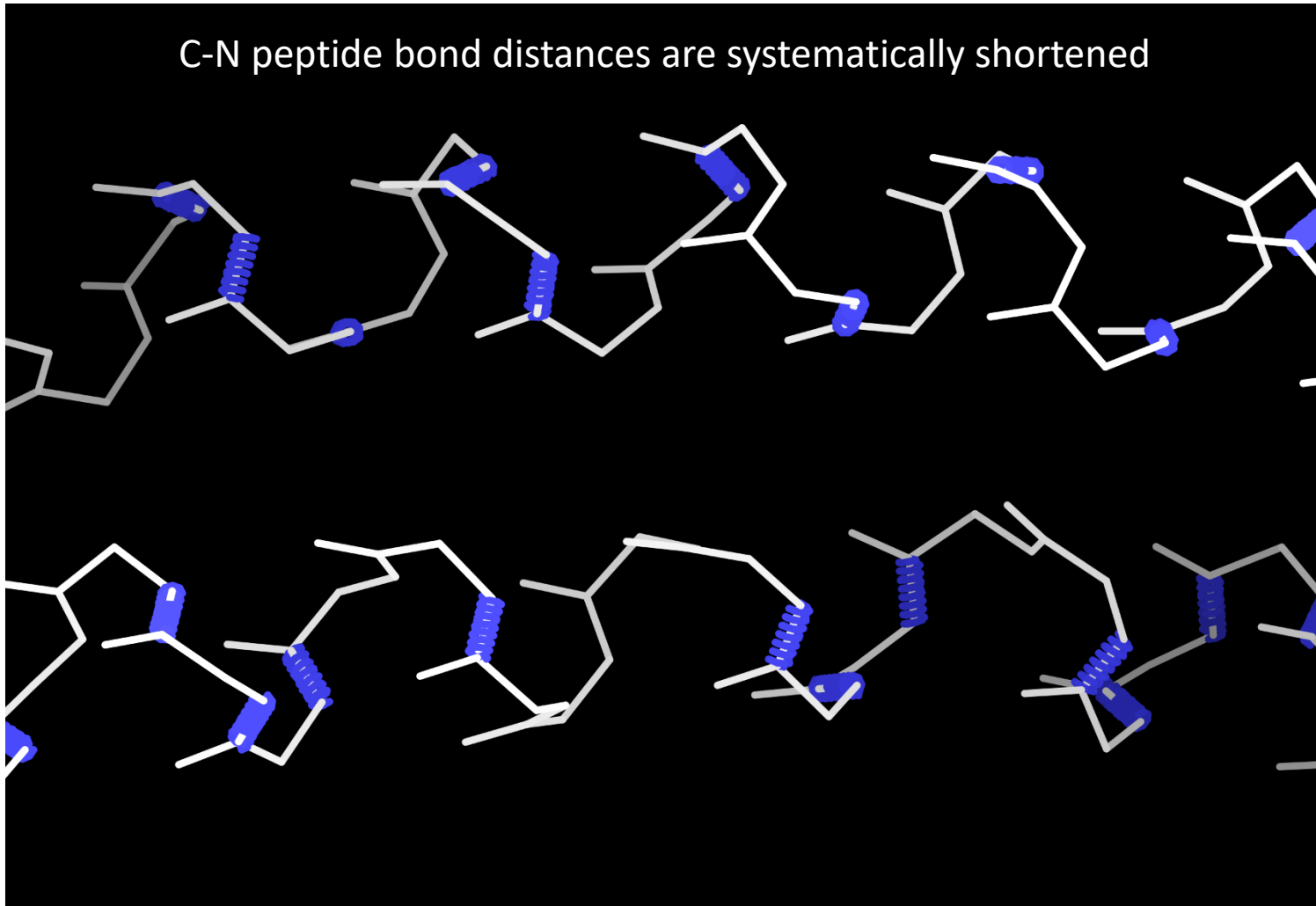
- Measure bond lengths and angles
- Check against a library of expected values
  - $>4\sigma$  deviation from expected = outlier
- Standard reference library has 1 value per bond or angle
- Derived from Engh and Huber
  - <https://doi.org/10.1107/S0108767391001071>
- Conformation-Dependent Library (CDL) has values that depend on local Ramachandran conformation
- Phenix default
- Derived from Karplus et al.
  - <https://doi.org/10.1107/S2059798315022408>

# Bond Geometry: Visualization



- Bond length outliers are drawn as springs
- Bond angle outliers are drawn as fans
- Color-coded
  - Red-shift = too far
  - Blue-shift = too close

# Bond Geometry: Probable causes



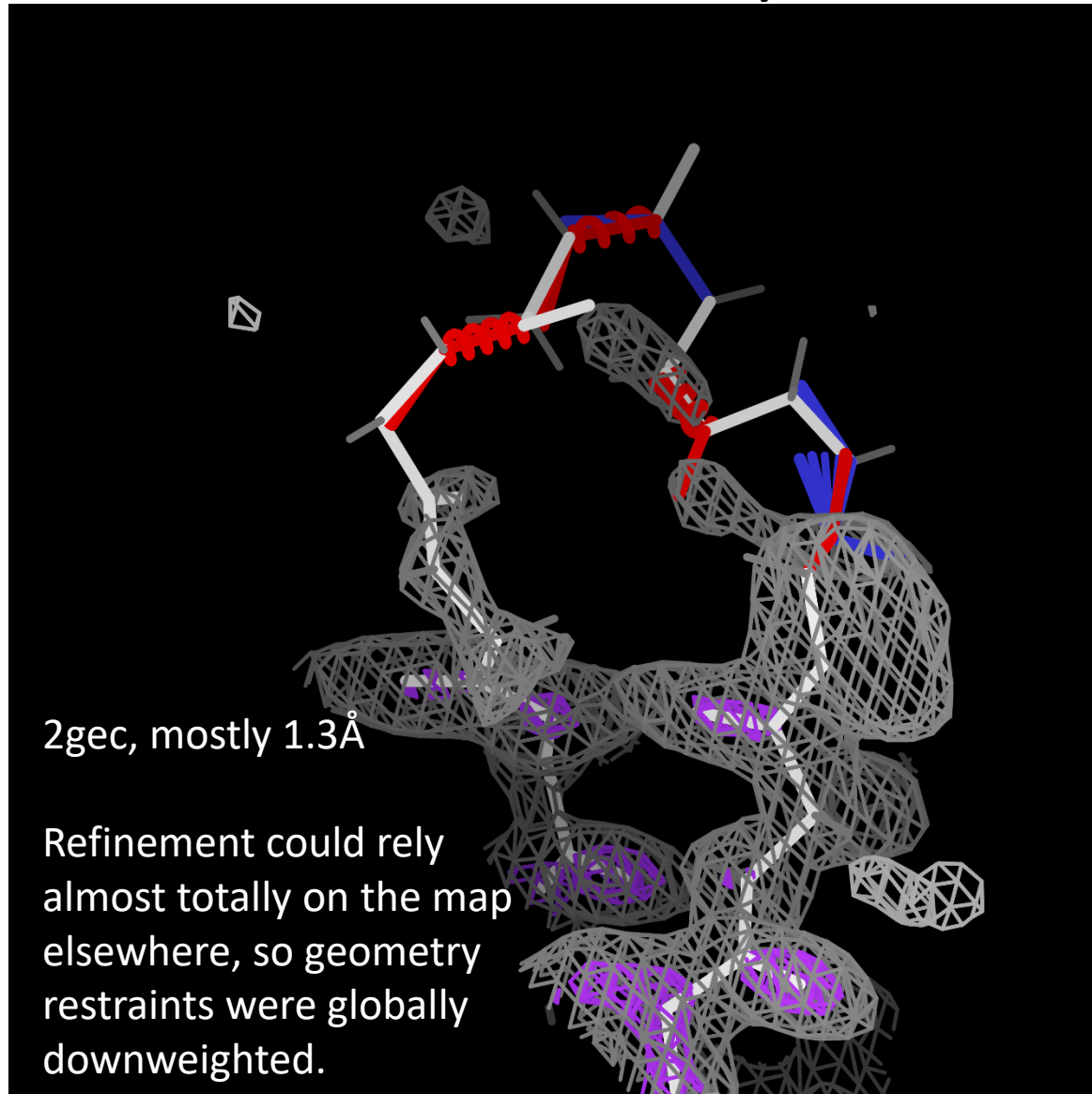
## Systematic

- Systematic geometry errors occur in programs with different libraries or expectations
- Be aware of what you import
- Do geometry minimization and/or re-refine.

OmegaFold prediction for p81313, as of Sept 2022



# Bond Geometry: Probable causes

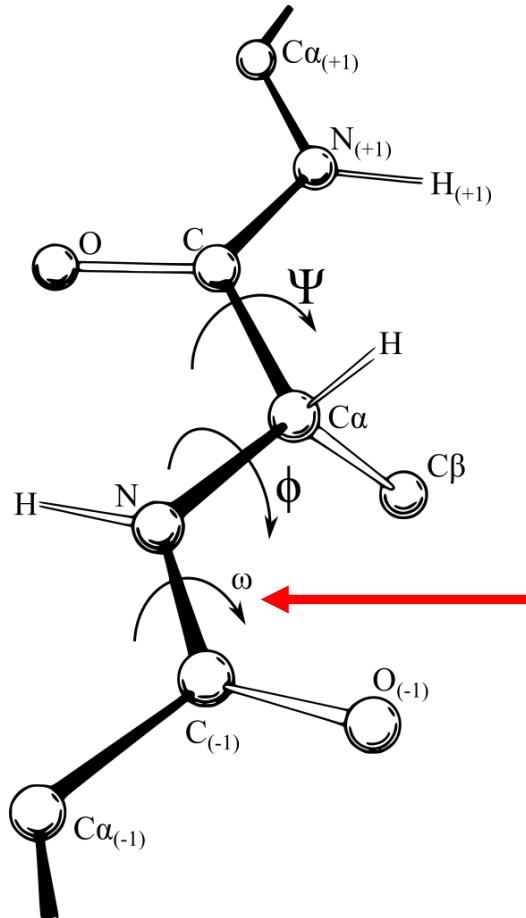


## Localized

- Localized geometry outliers result from conformational strain and/or missing density
- Fix the source of strain
- Manually apply more restraints to low-data regions
- Leave it unmodeled if a good solution is impossible

# *Cis* Peptides

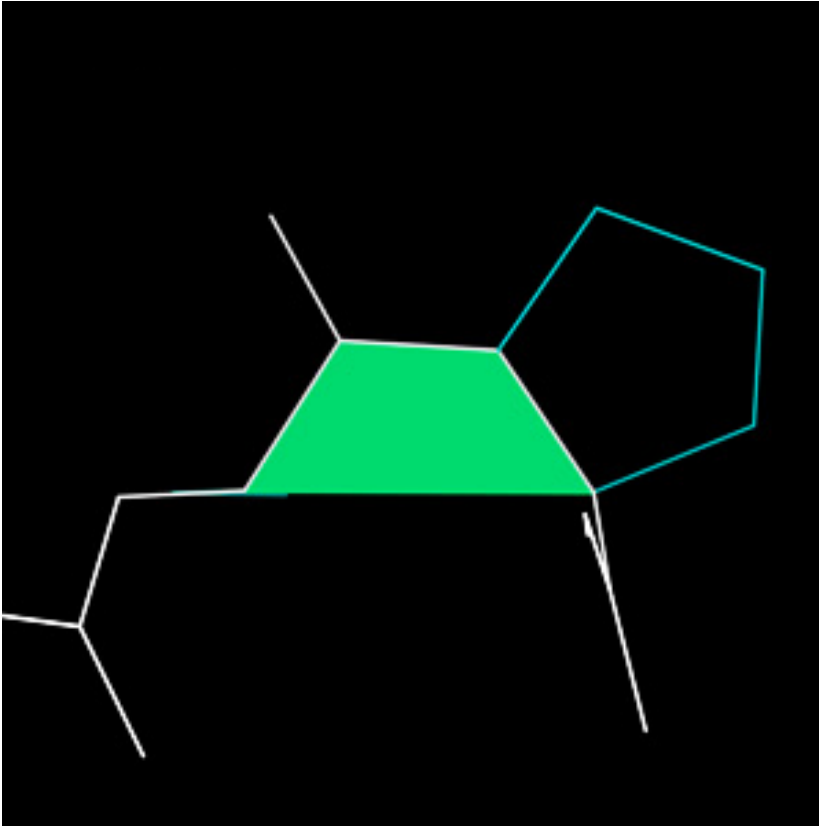
# Cis Peptides: Method



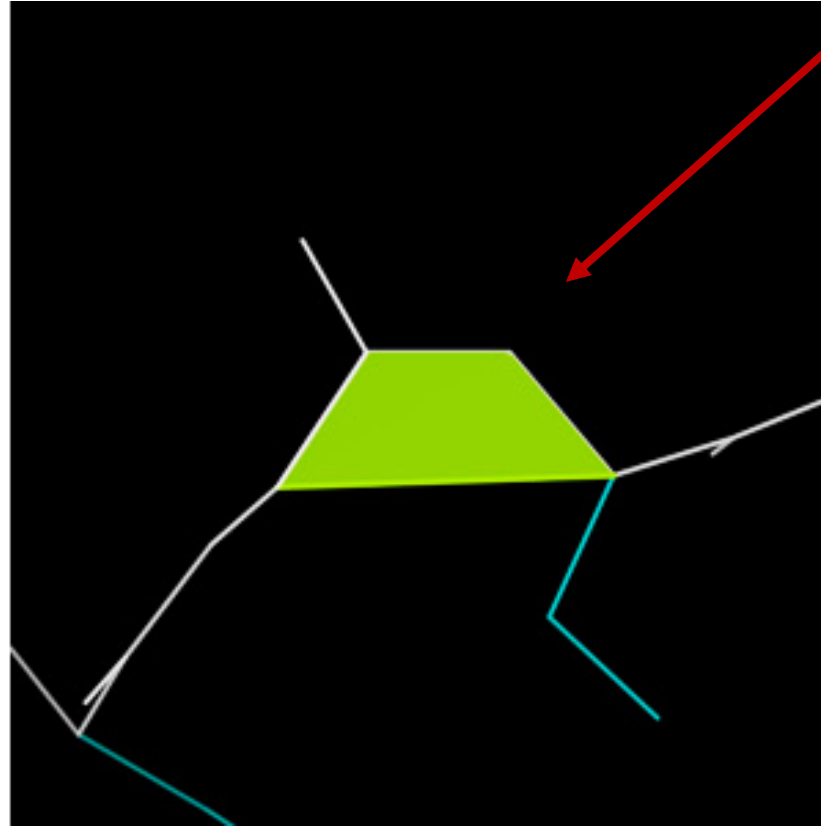
- The peptide bond that joins amino acids has partial double bond character and does not rotate freely
- CA-C-N-CA torsion
  - “Omega”
- Usually *trans* (CA on opposite sides)
- Rarely *cis* (both CA on same side)

# *Cis* Peptides: Visualization (KiNG)

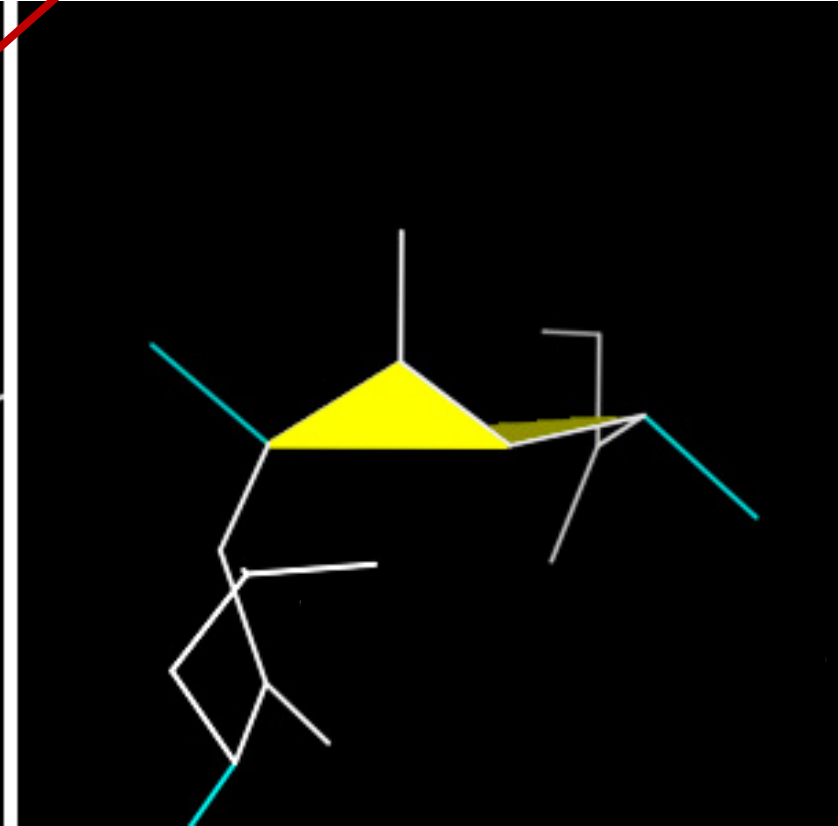
These are red in Coot!



- *Cis* peptide bond is much more common preceding Proline
  - ~5% of **Proline**
- Gentle green trapezoid fills the characteristic CA-CA space

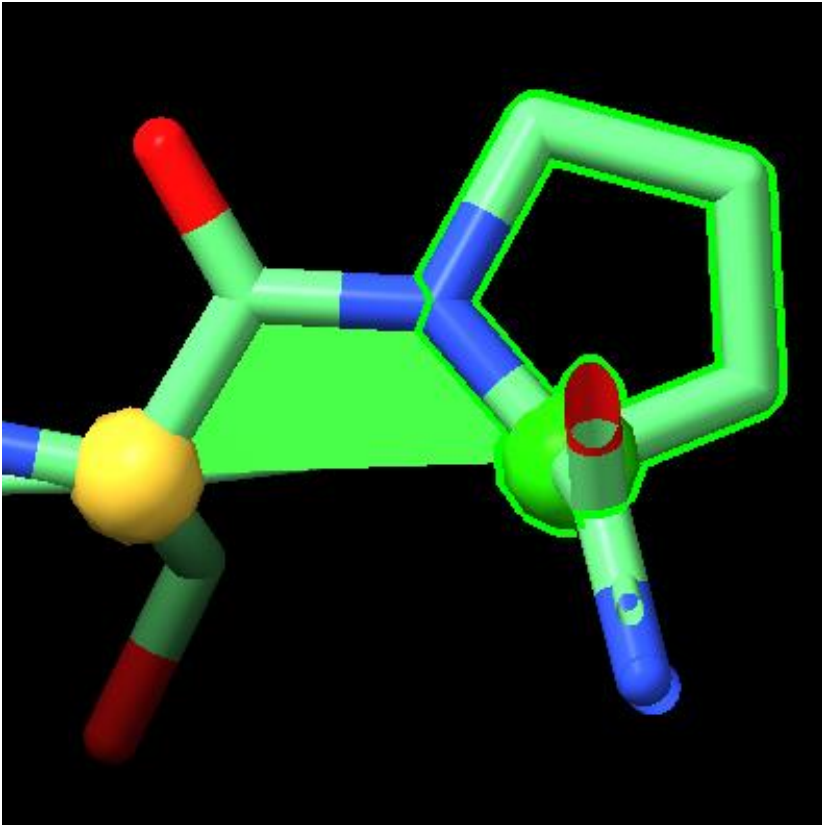


- *Cis* peptide bond is extremely rare preceding other residues
  - ~0.03% of **non-Proline**
- Unpleasantly lime trapezoid fills the characteristic CA-CA space

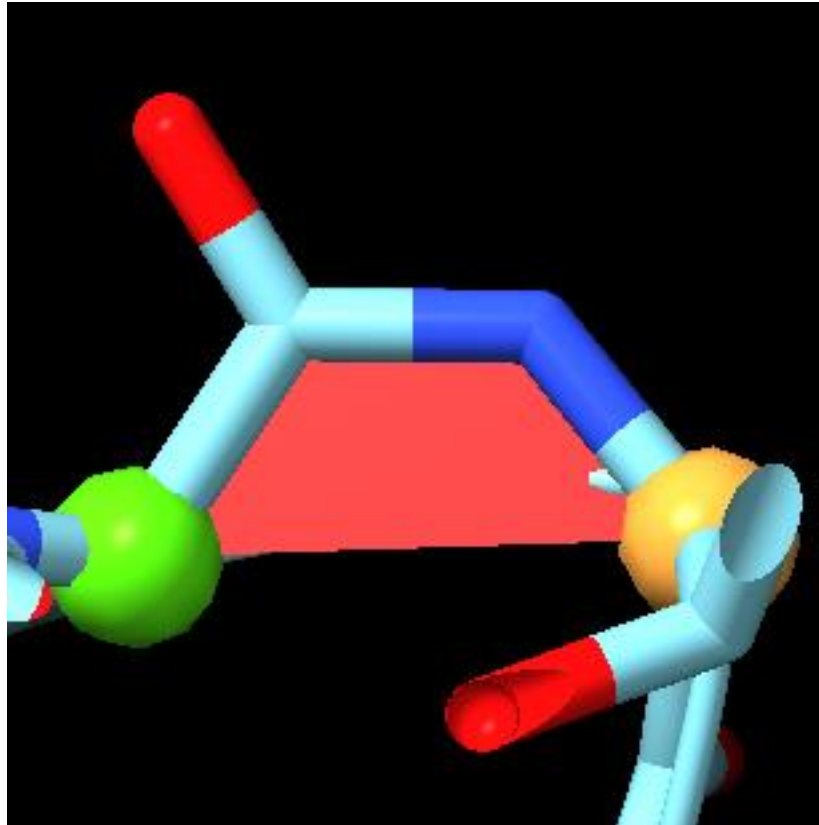


- Peptides **twisted** >30 from planar are severe geometry distortions
- Space is filled with yellow, angle between component planes approximates severity

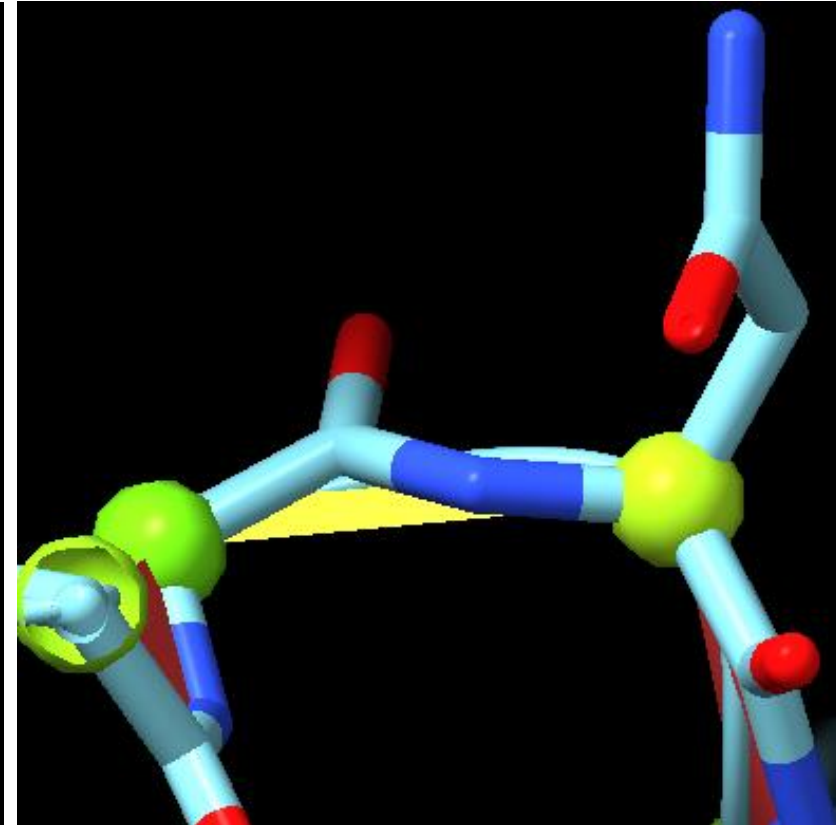
# Cis Peptides: Visualization (ISOLDE)



- *Cis* peptide bond is much more common preceding Proline
  - ~5% of **Proline**
- Gentle green trapezoid fills the characteristic CA-CA space



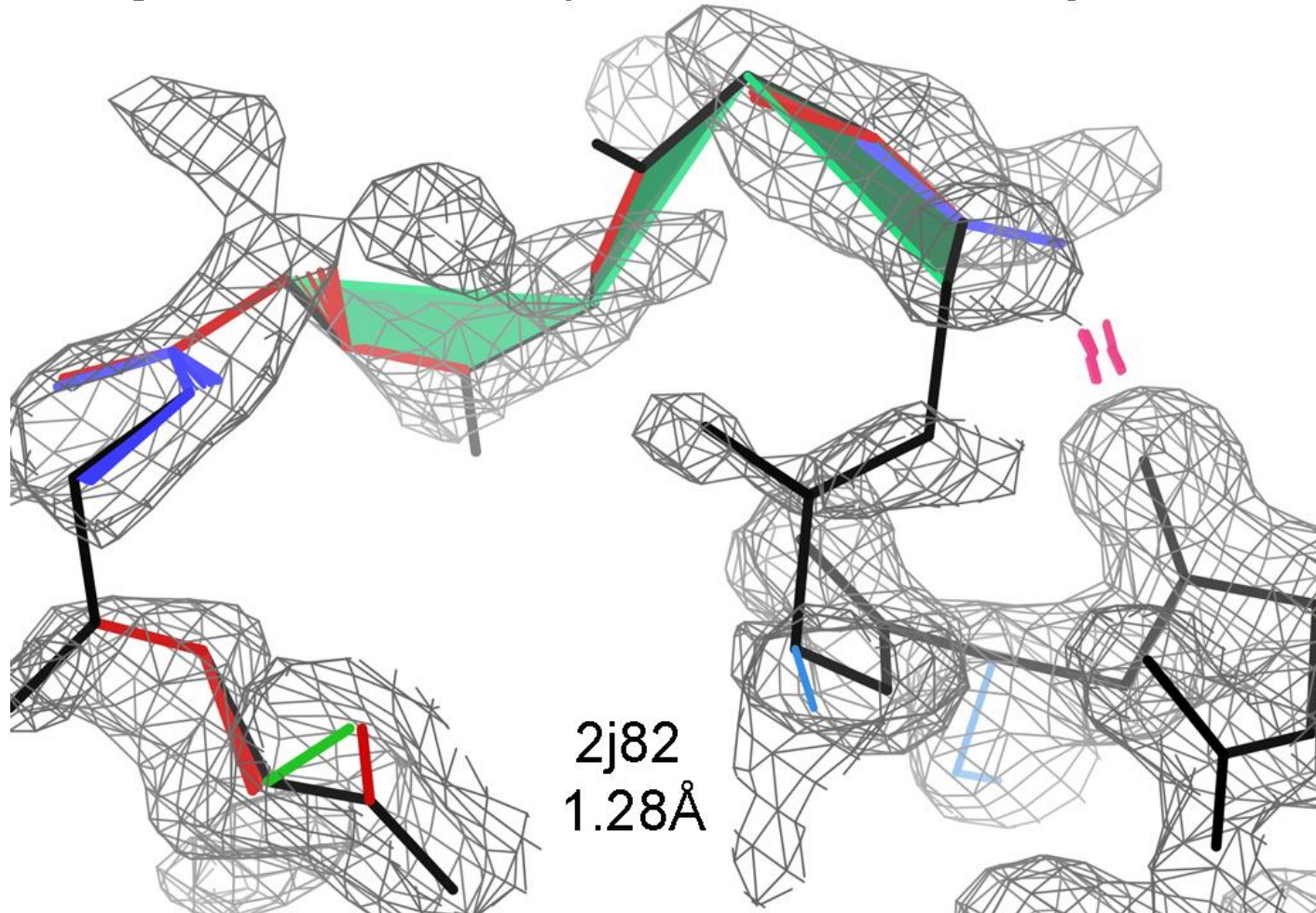
- *Cis* peptide bond is extremely rare preceding other residues
  - ~0.03% of **non-Proline**
- Warning red trapezoid fills the characteristic CA-CA space



- Peptides **twisted** >30 from planar are severe geometry distortions
- Space is filled with yellow, angle between component planes approximates severity

# Cis Peptides: Probable causes

Arg-Gln-Asn-Ser triple *cis*-nonPro -- unjustified



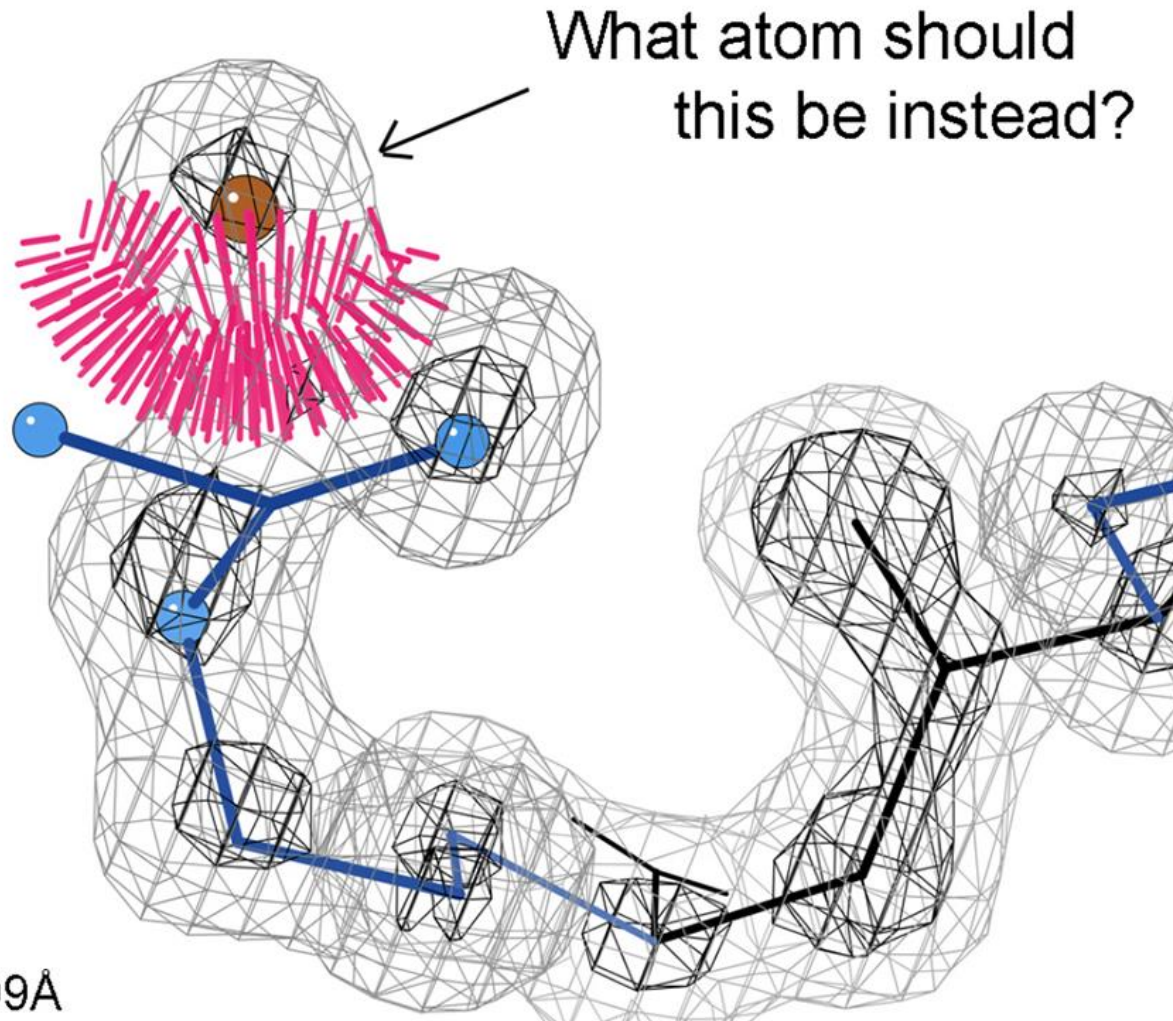
## Fit to small density

- The *cis* CA-CA distance is shorter and **seems** to fit better into fragmented density
- A conformation this rare requires more justification than a marginally better fit
- Flip it to *trans* unless density, chemistry, homology, or another source gives you clear support



# UnDowser Water Validation

# UnDowser: Method



- Undowser is a tool for finding incorrect waters
- Use all-atom contact analysis to find waters with steric clashes
- Identify probable substitutions for each problem water
  - Ions
  - Ligands
  - Sidechain alternates
  - Nothing!

# UnDowser: Visualization

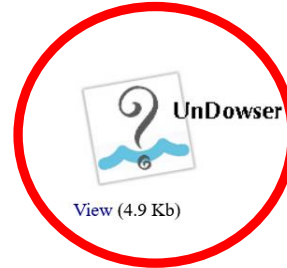
## Multi-criterion visualizations



[View in KiNG](#) | [View in NGL](#) | [Download \(294 Kb\)](#)



[View \(135 Kb\)](#)



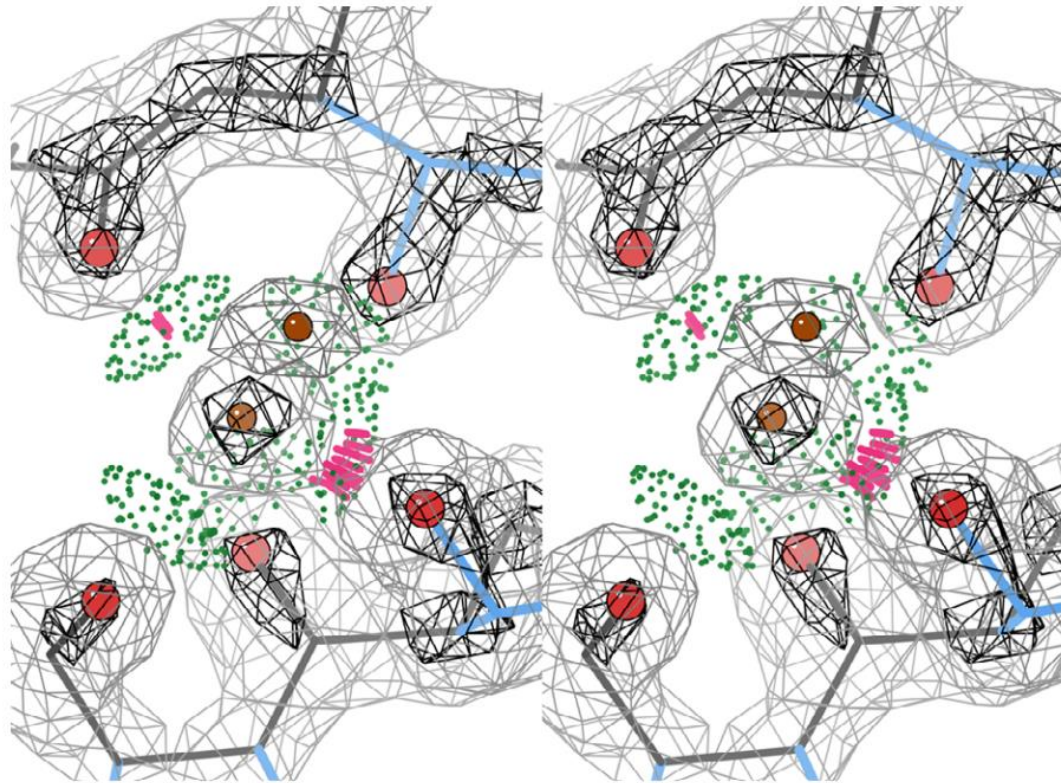
[View \(4.9 Kb\)](#)

SUMMARY: 6 waters out of 58 have clashes (10.34%)

Water ID	Clashes with	Water B	Contact B	Clash Severity	Clash with Polar May be ion	Clash with non-polar Unmodeled alt or noise	Clash with water Occ <1 or ligand	Clash with altloc Add or rename alts
A: 125 :HOH:	CG of A: 51 :GLU:	26.53	26.06	0.506		×		
	HG3 of A: 51 :GLU:	26.53	26.06	0.503		×		
A: 107 :HOH:	HA2 of A: 10 :GLY:	23.36	18.74	0.736		×		
A: 100 :HOH:	HE3 of A: 48 :LYS:	24.10	20.04	0.501		×		
	CE of A: 48 :LYS:	24.10	20.04	0.425		×		
A: 114 :HOH:	O of A: 122 :HOH:	27.11	26.13	0.651			×	
A: 122 :HOH:	O of A: 114 :HOH:	26.13	27.11	0.651			×	
A: 80 :HOH:	HB3 of A: 39 :ASP:	22.27	24.16	0.426		×		

- MolProbity has a dedicated chart for water analysis
- Each clashing water is listed
  - Colored by severity
  - Possible causes marked in table
- Recently added to Phenix commandline
  - *phenix.undowser\_validation*
  - Coming soon to GUI

# A water that should be an ion

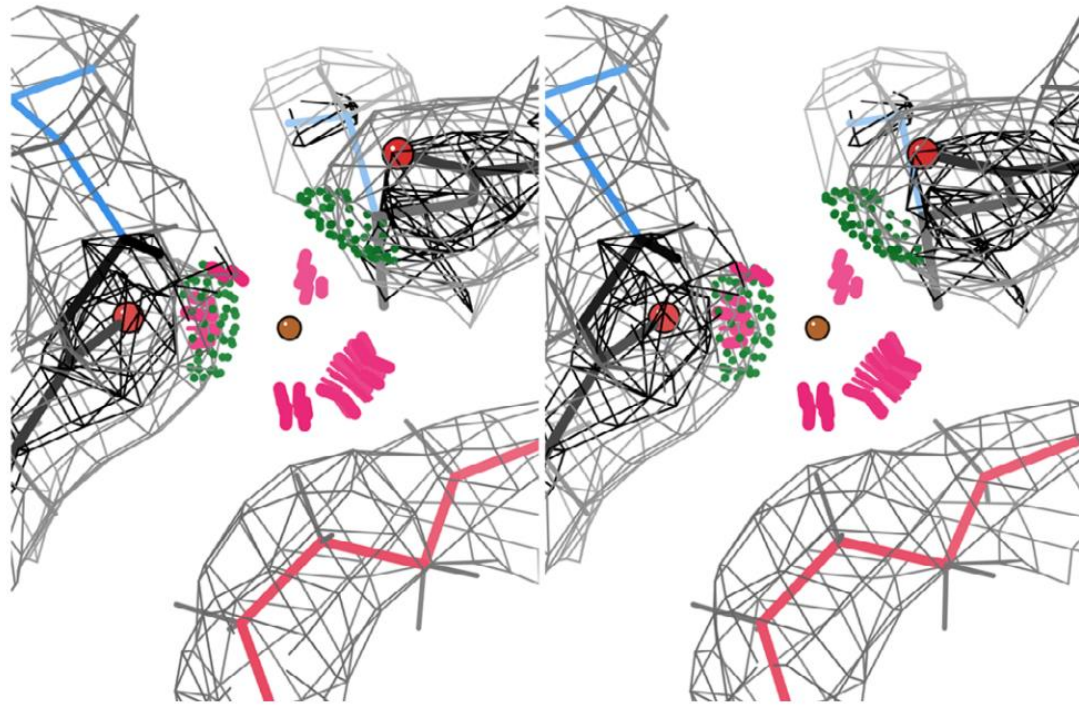


(Stereo image)  
HOH 606 from 6hhm, 1.23 Å

- Very strong density peak
- Octahedral contact geometry
  - (water is tetrahedral)
- Contacts are all polar groups ( $\delta^-$ )
- This actually a + ion, probably  $\text{Na}^+$



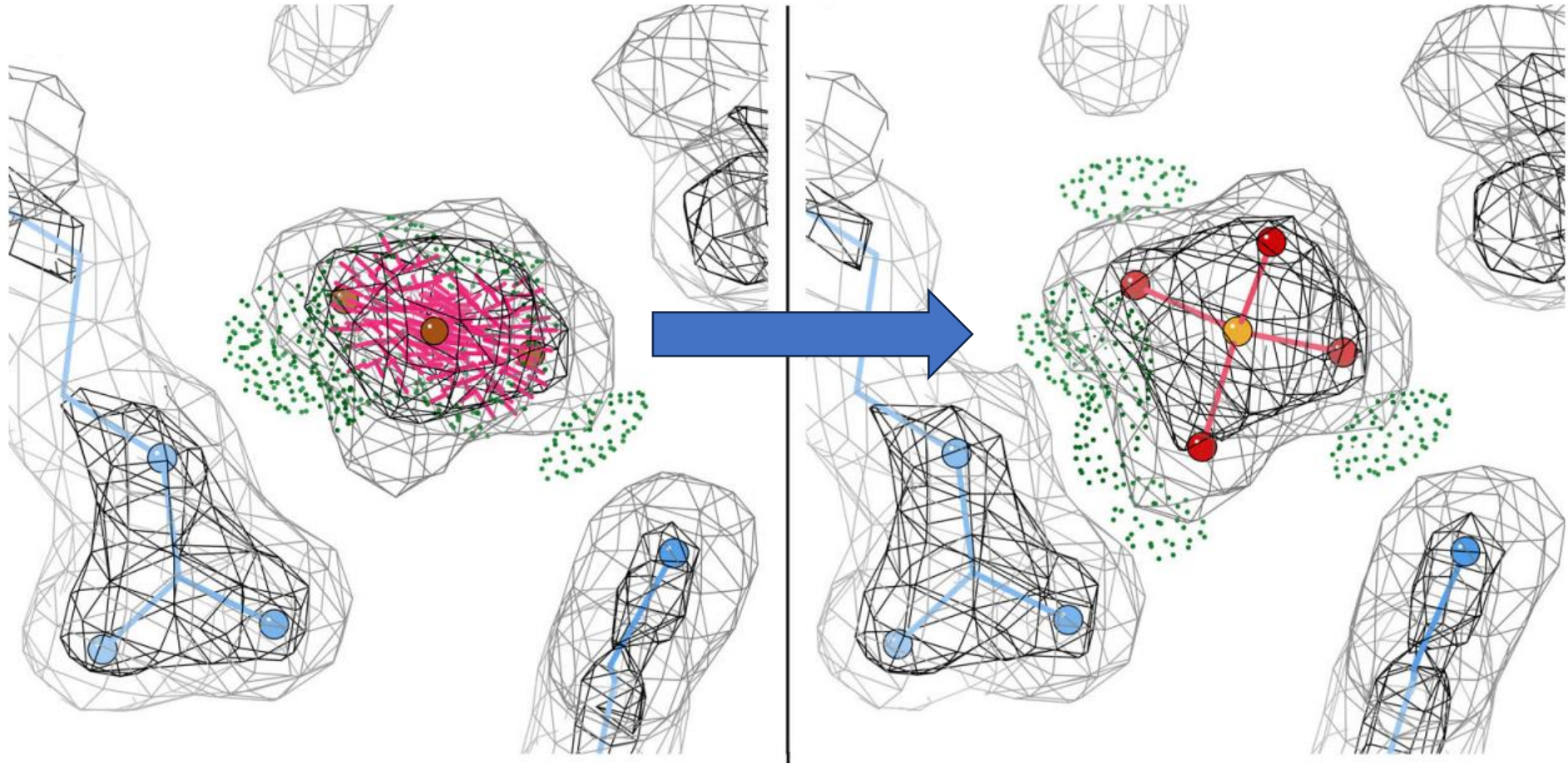
# A water that should not be



(Stereo image)  
HOH 504 from 5onu, 2.22 Å

- No density peak
- Mix of polar and non-polar contacts
  - So unlikely to be a coordinated ion
- This water doesn't really exist

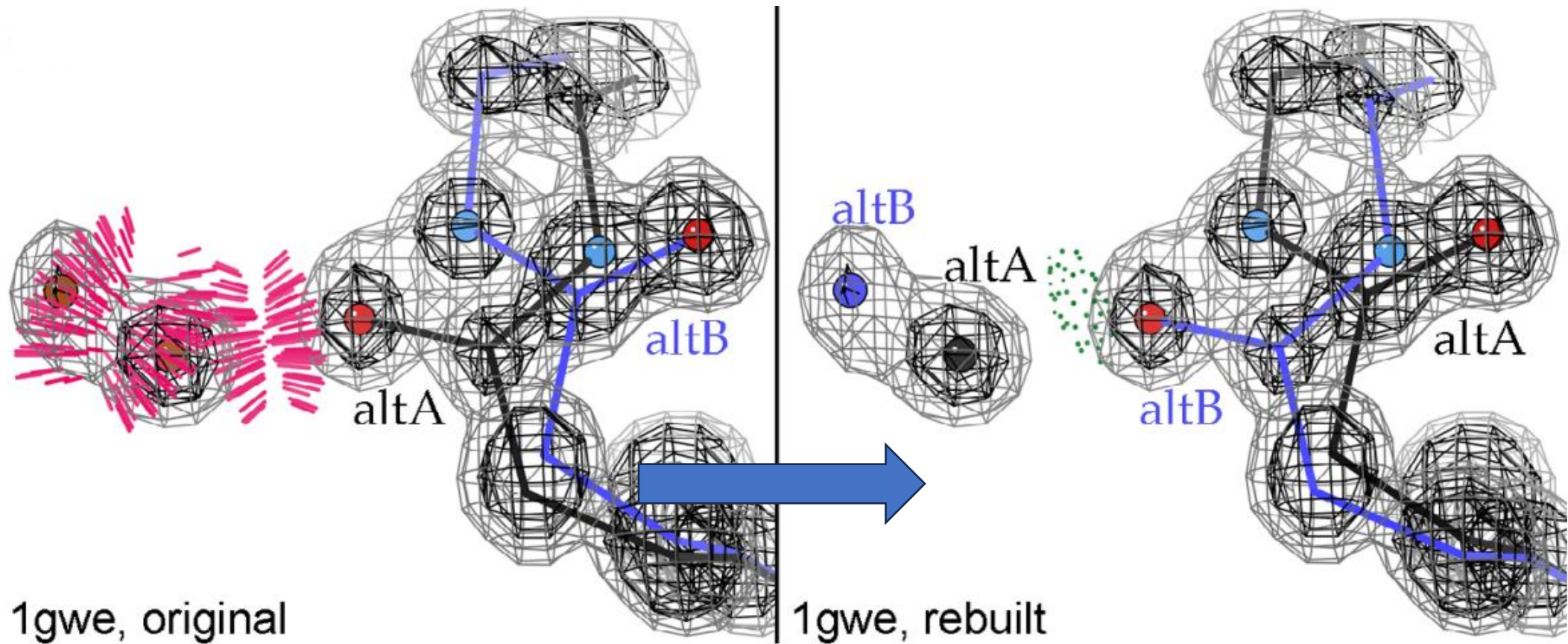
# Waters that should be ligands



- Densely-clashing waters may actually be a ligand

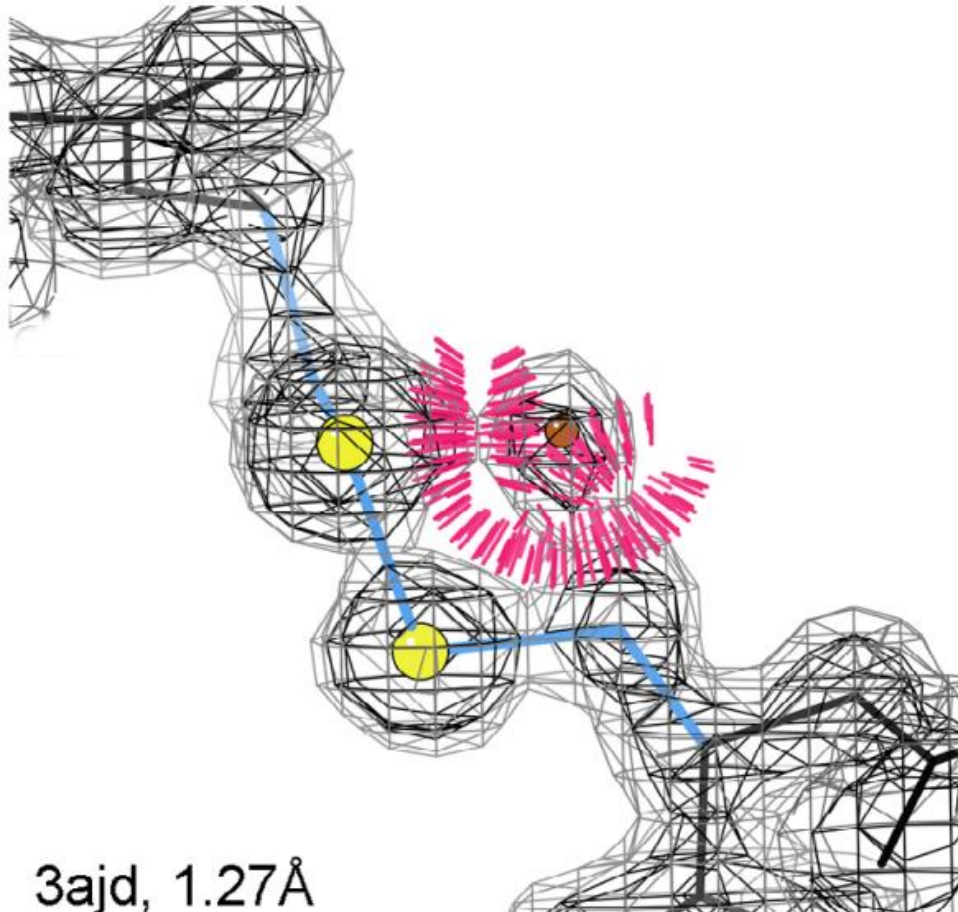


# Waters that should be ligands



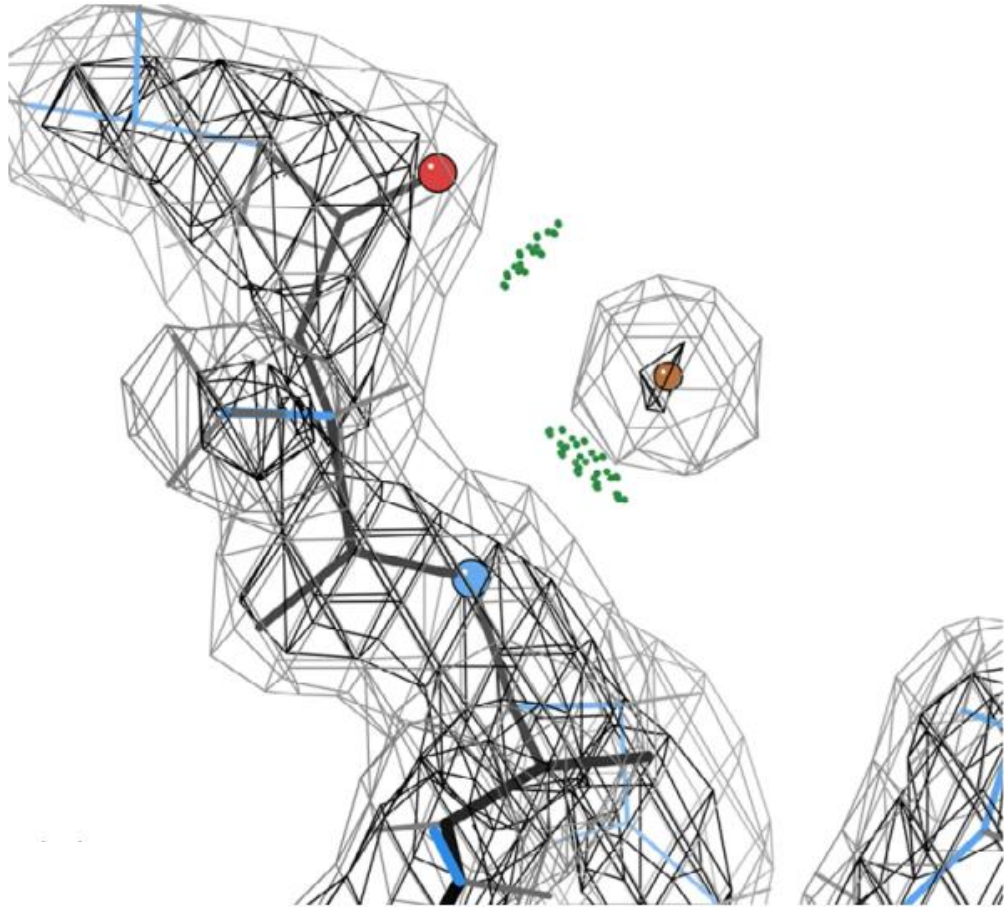
- Densely-clashing waters may actually be part of an alternate conformation network

# Waters that replace alternates



- Very close contacts
  - (Covalent bond distance)
- Clash with non-terminal sidechain atoms
- Could be an unmodeled alternate conformation

# Waters can be real, too!



- Clear density peak
  - Weaker than macromolecule density is fine
- Hydrogen bonds
- Contacts with both  $\delta+$  and  $\delta-$  polar partners, so an ion is unlikely

# More on water

- For more, see
  - <https://doi.org/10.1002/pro.3786>
  - [https://phenix-online.org/phenixwebsite\\_static/mainsite/files/newsletter/CCN\\_2019\\_07.pdf#page=2](https://phenix-online.org/phenixwebsite_static/mainsite/files/newsletter/CCN_2019_07.pdf#page=2)
- Important update: interaction distance for  $\delta^-$  ions is generally too far to see a clash when HOH replaces one
  - Clashes with  $\delta^+$  polar partners probably indicate alternates or other unmodeled structure
- Pavel and I plan to develop more water validation tools once I get clear of some RNA work.

MolProbity Score

# MolProbity Score

- The MolProbity Score combines validations and scales the result to look like a resolution
  - Clashscore
  - Ramachandran
  - Rotamers
- MolProbity better than model resolution is good
- MolProbity worse than model resolution is bad



# MolProbity Score



**A single statistic cannot explain a whole structure's quality!**

**Don't rely on it!  
Especially at low resolution!**

**You now know enough to look at the other statistics  
You now know enough to look at your model and the markup in detail**

# Useful links

- For the quick-and-dirty webpage version of this material:
  - [http://molprobity.biochem.duke.edu/help/validation\\_options/validation\\_options.html](http://molprobity.biochem.duke.edu/help/validation_options/validation_options.html)
  - This also includes links to many of the relevant publications
- I deliberately skipped over structure-level statistics, but if you want to see the target values for Ramachandran Favored, CaBLAM Outliers, etc:
  - [http://molprobity.biochem.duke.edu/help/validation\\_options/summary\\_table\\_guide.html](http://molprobity.biochem.duke.edu/help/validation_options/summary_table_guide.html)

# Bonus Content

Here are a few more examples of interesting model errors associated with certain validations.

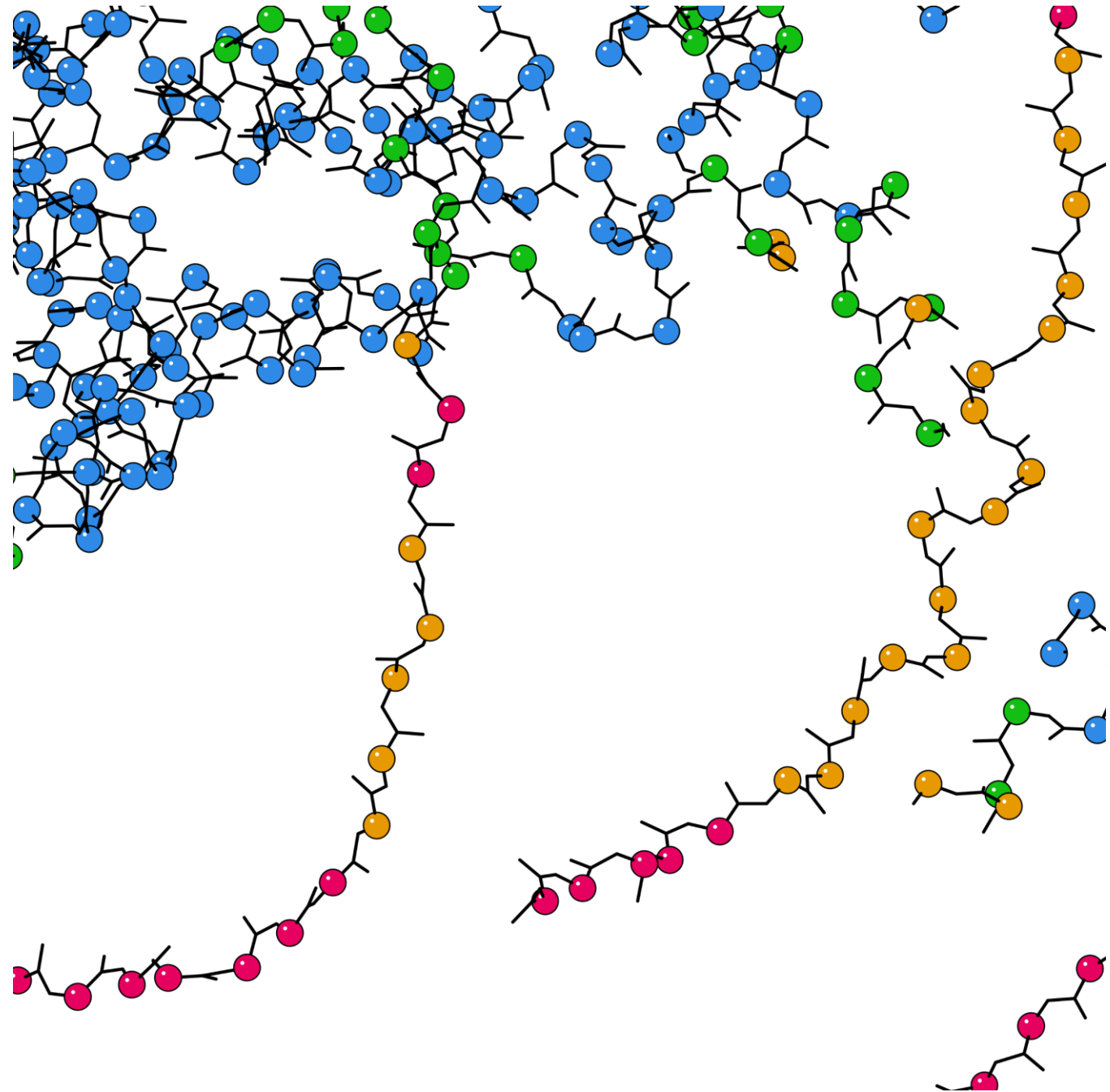
These didn't fit in the main presentation, but you should still get to see them.

# AlphaFold validation

`phenix.barbed_wire_analysis output.type=kin`  
(under development)

# Validation tool

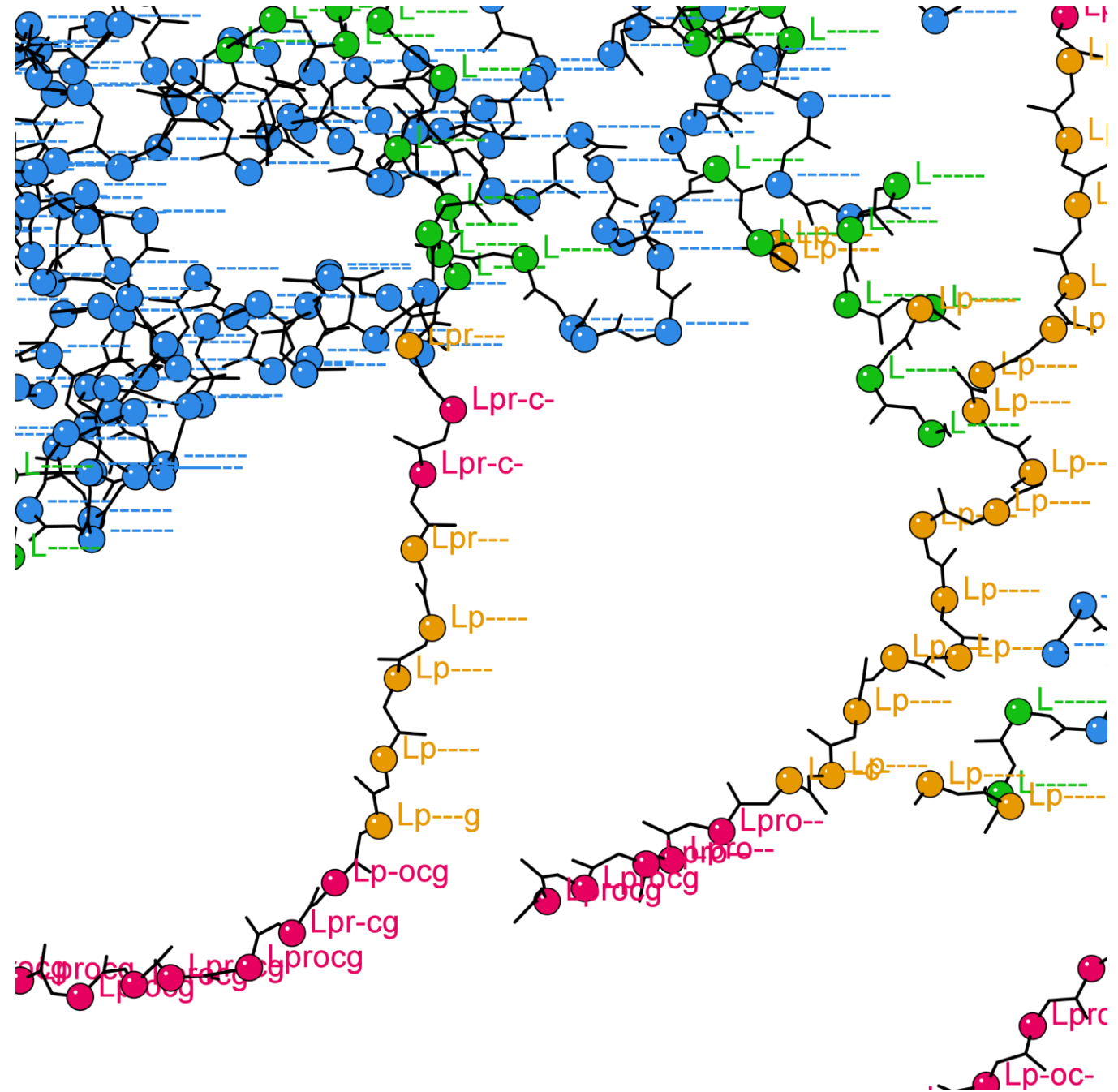
- Predictive (blue)
  - Unpacked high pLDDT (gray)
  - Near-predictive (green)
  - Unpacked possible (gold)
  - Barbed wire (hot pink)
- 
- Note barbed wire/unpacked possible transitions





# Validation tool

- Letter codes show assessment of each residue
- More letters = more barbed-wire-like
  - L = low pLDDT
  - p = low packing
  - r = bad Rama
  - o = bad omega (cis)
  - c = bad CaBLAM
  - g = bad bond geometry

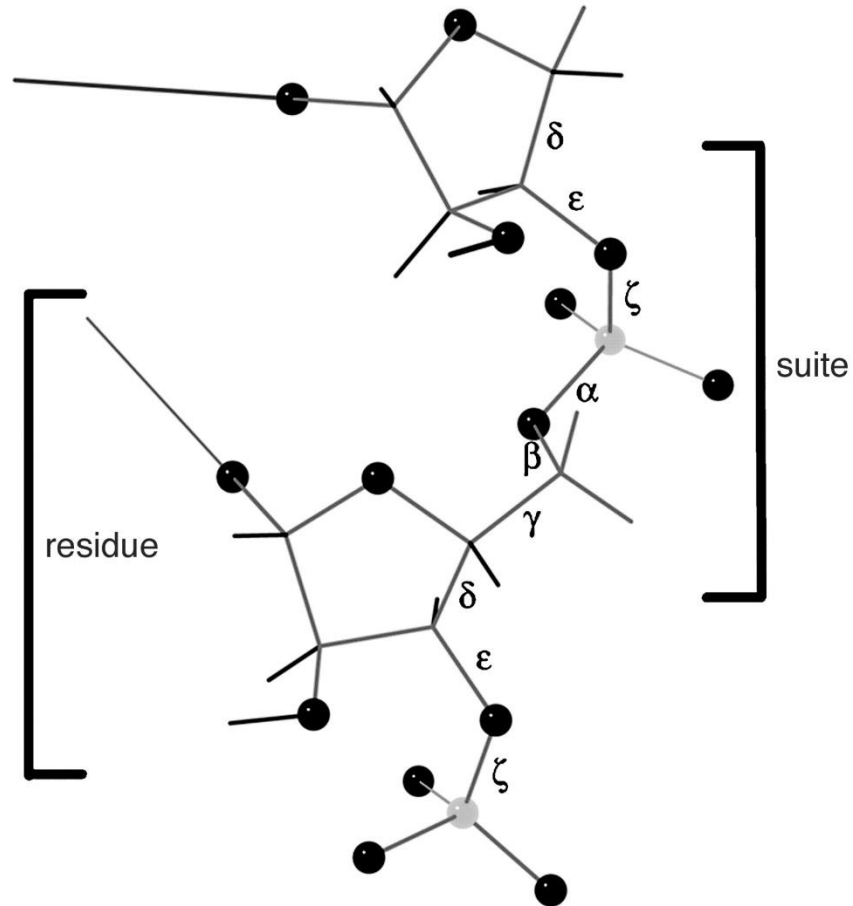


(In KiNG, press “w” for larger font)



# RNA Suites

# RNA Suites: Method

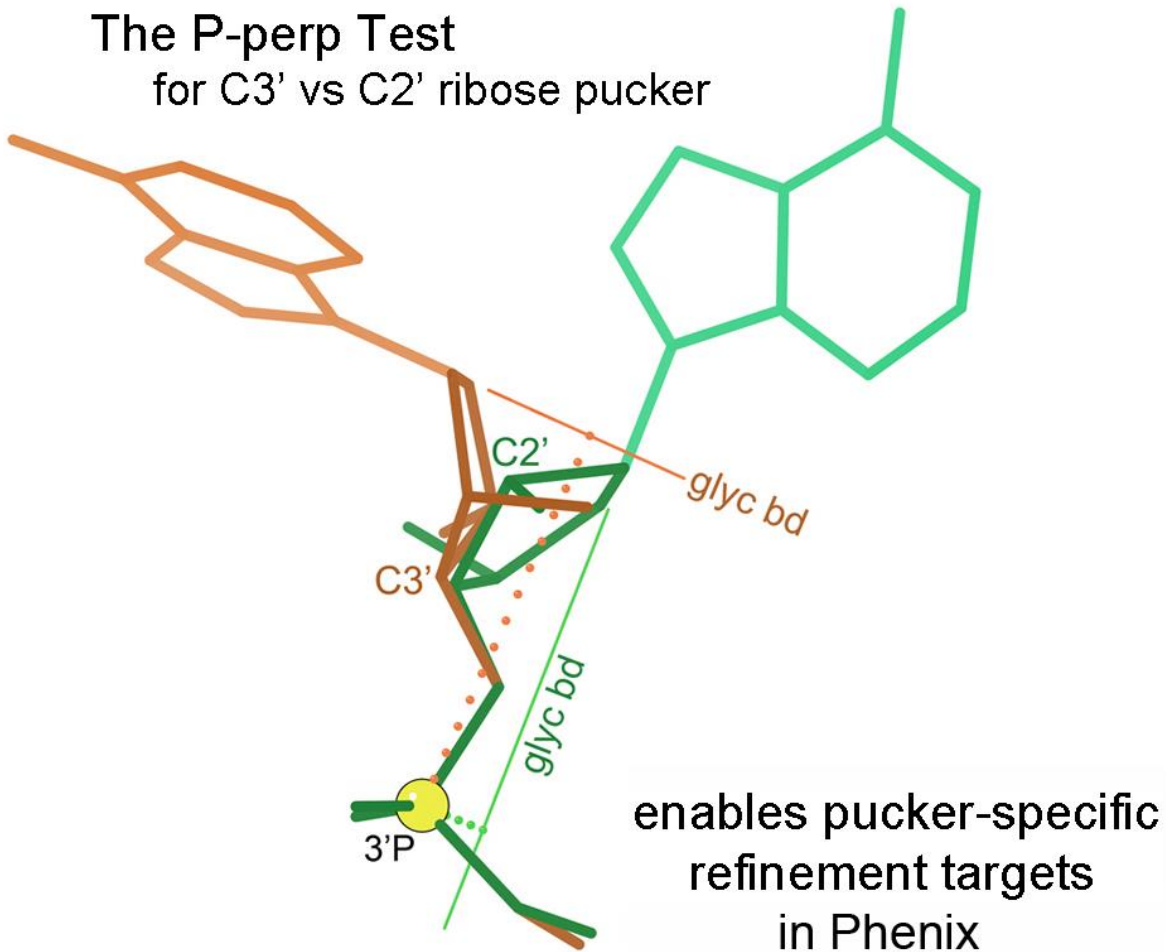


- Useful RNA backbone division is sugar-to-sugar suite, not P-to-P residue
- Suite conformation names are a combination of a number and a letter/character
  - e.g. 1A is the most common A-form helix conformation
- Outliers are named as !!
  - Pronounced “bang, bang”
  - Many !!’s are real, rare conformations

RNA Ribose Puckers

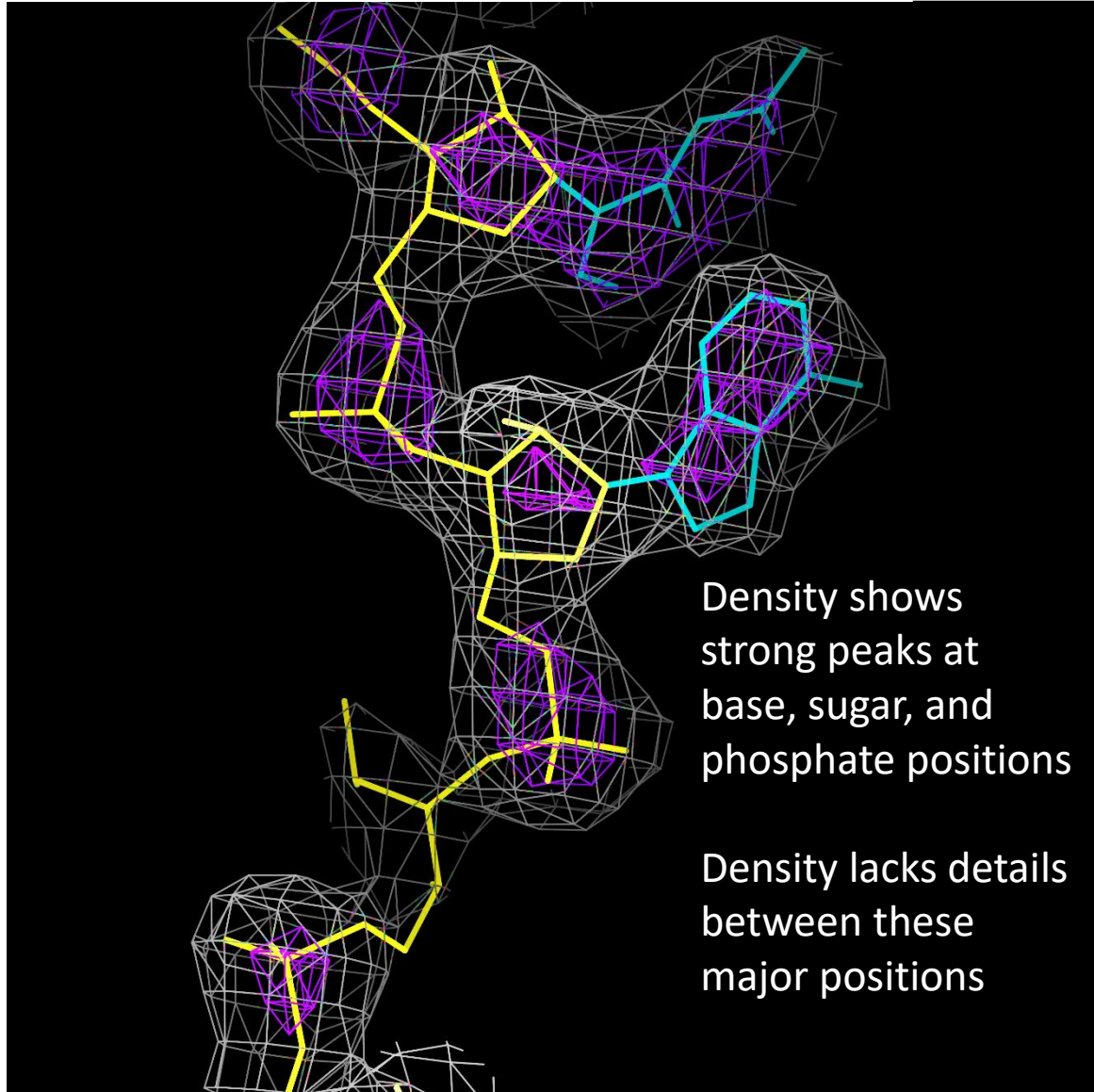
# RNA Ribose Puckers: Method

The P-perp Test  
for C3' vs C2' ribose pucker



- The backbone ribose in RNA can have one of two pucker states
  - C2' endo
  - C3' endo
- Ribose pucker correlates very strongly with perpendicular distance from the 3' phosphate to the glycosidic bond vector
  - Glycosidic bond joins ribose sugar to nucleobase
- At low resolution, perpendicular distance is easy to see, ribose pucker is hard to see
- If there's a mismatch, the pucker is probably wrong

# RNA Errors: Probable Causes



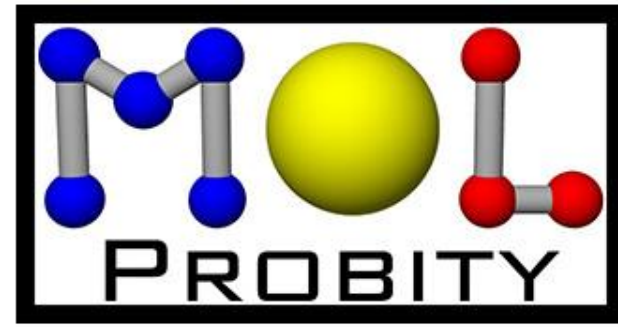
- RNA backbone has many degrees of freedom
- Electron density often leaves RNA backbone underdetermined
  - Even when bases are better resolved
- More tools to help with this are in development

# Resolution and the Limits of Validation



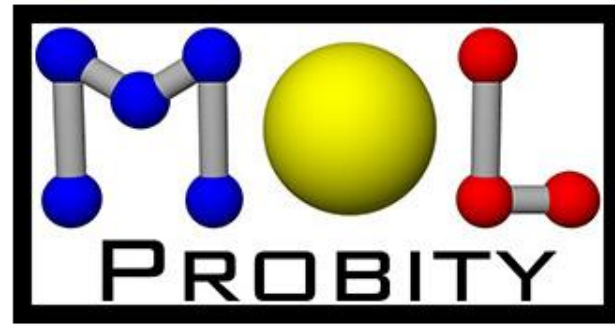
At 1.5Å to 2.5Å

MolProbity is still very effective.



The density contains enough specific information  
that where your model fits the density,  
the simple validations (geometry, Rama, rotamers),  
**and** the explicit-H all-atom contacts

**then it's pretty sure to be accurate !**



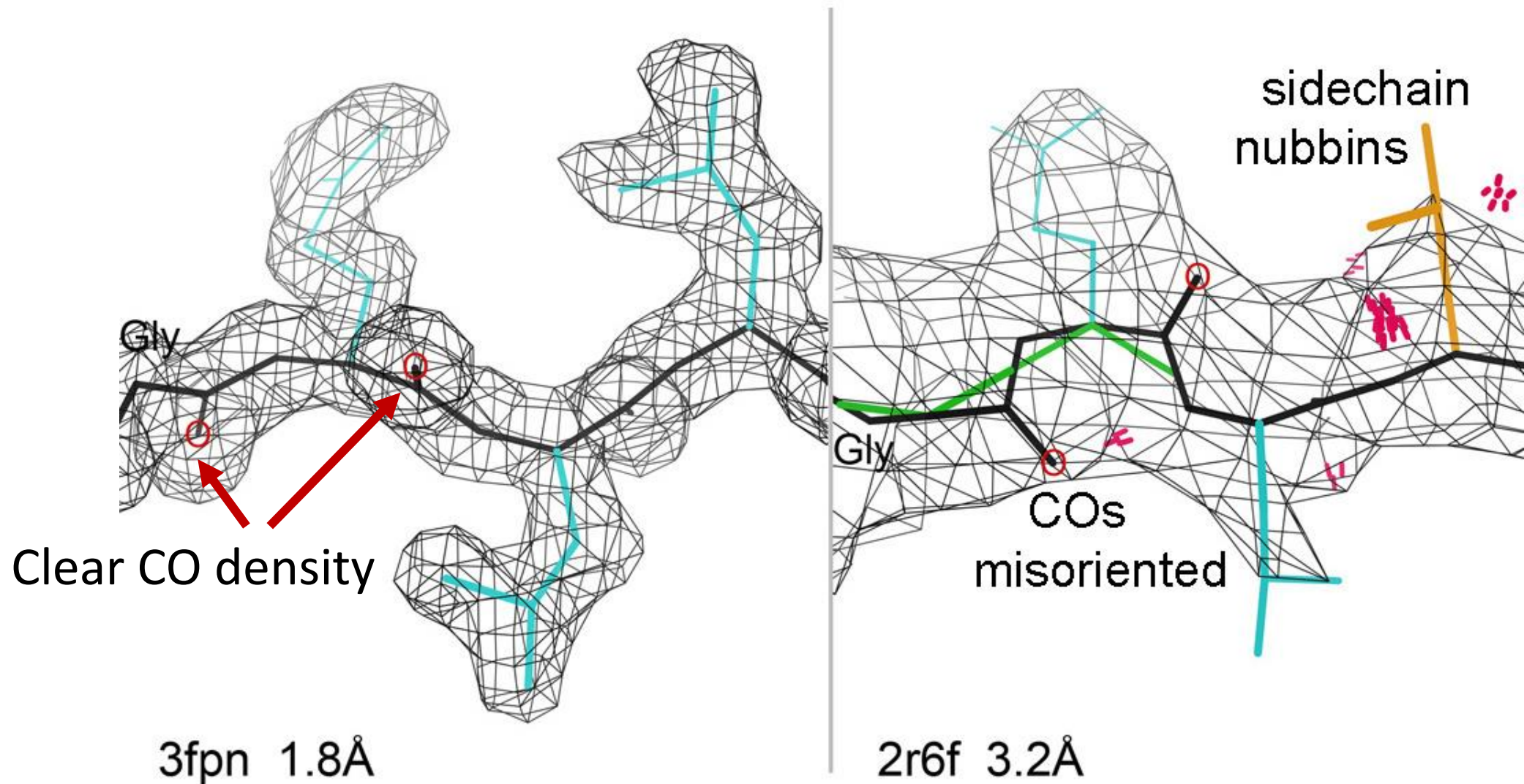
But that's not true at 3 to 4Å !!

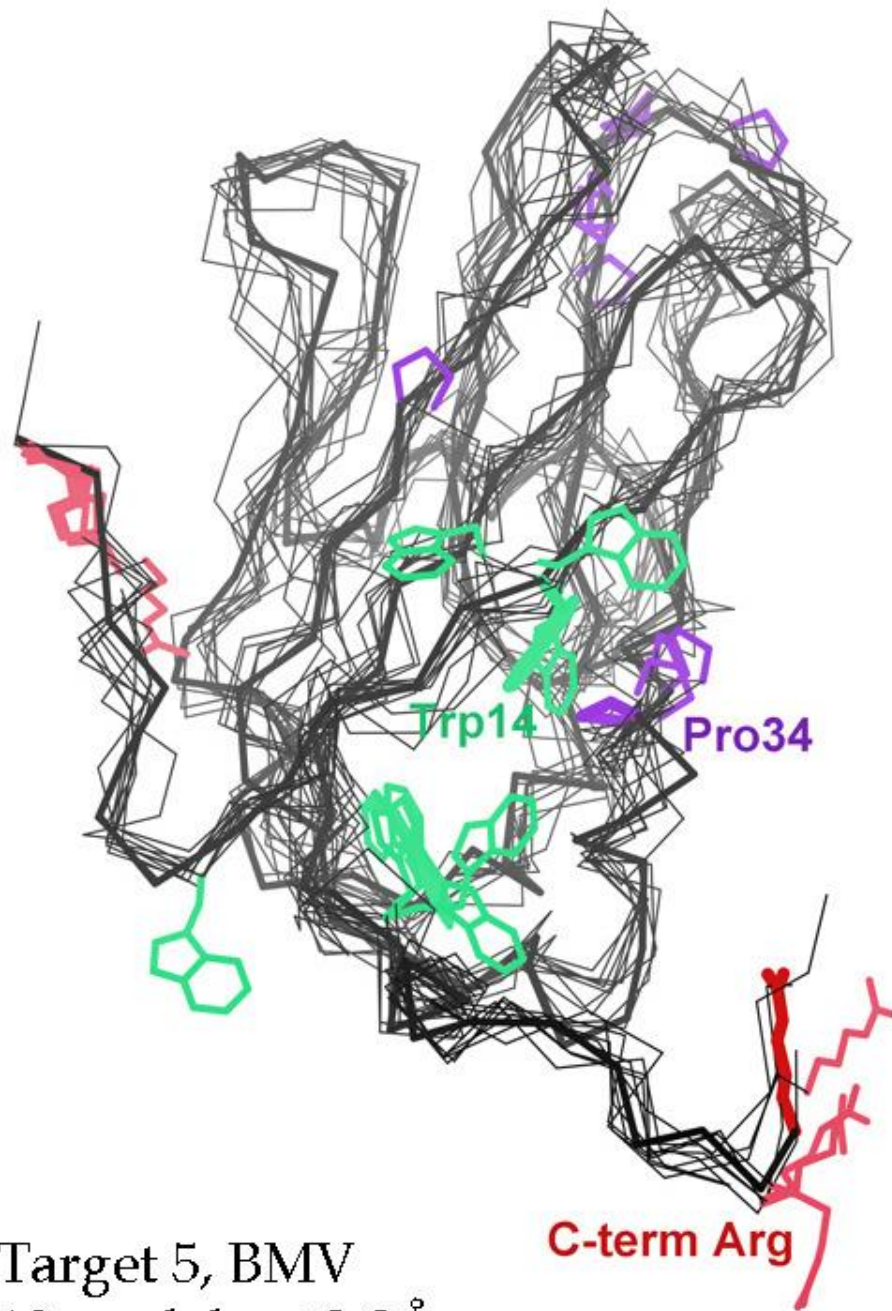
Why does this happen ?

What are we doing about it ?

# Tackling lower resolution (2.5 to 4Å)

Very challenging both for x-ray and for cryoEM





Target 5, BMV  
10 models at 3.8Å

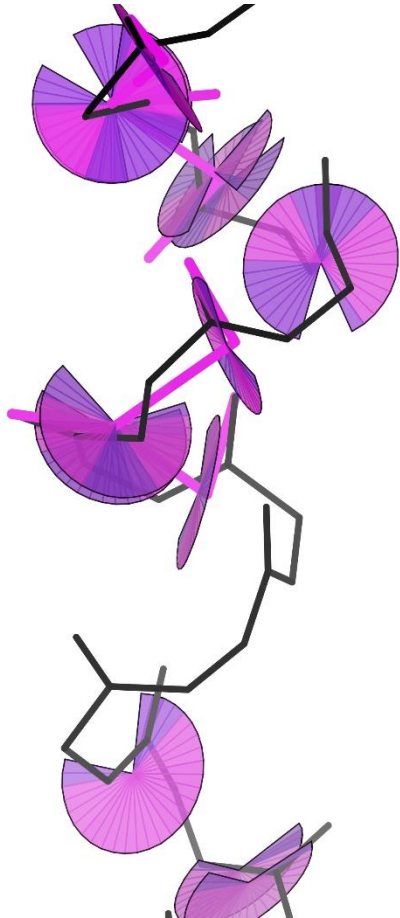
At 3-4Å,  
many distinct  
models are equally  
compatible with  
the broad density

Much other information  
is needed, which can  
lead to overfitting  
and systematic errors



More Visualizations

# CaBLAM: Visualization



- Colored bars are drawn along the dihedral relationship between peptide planes
  - Purple for disfavored
    - Matters in helix/sheet, not in loops
  - Pink for full outlier
    - Matters everywhere
- Colored wheels show CaBLAM evaluation if a peptide plane were rotated



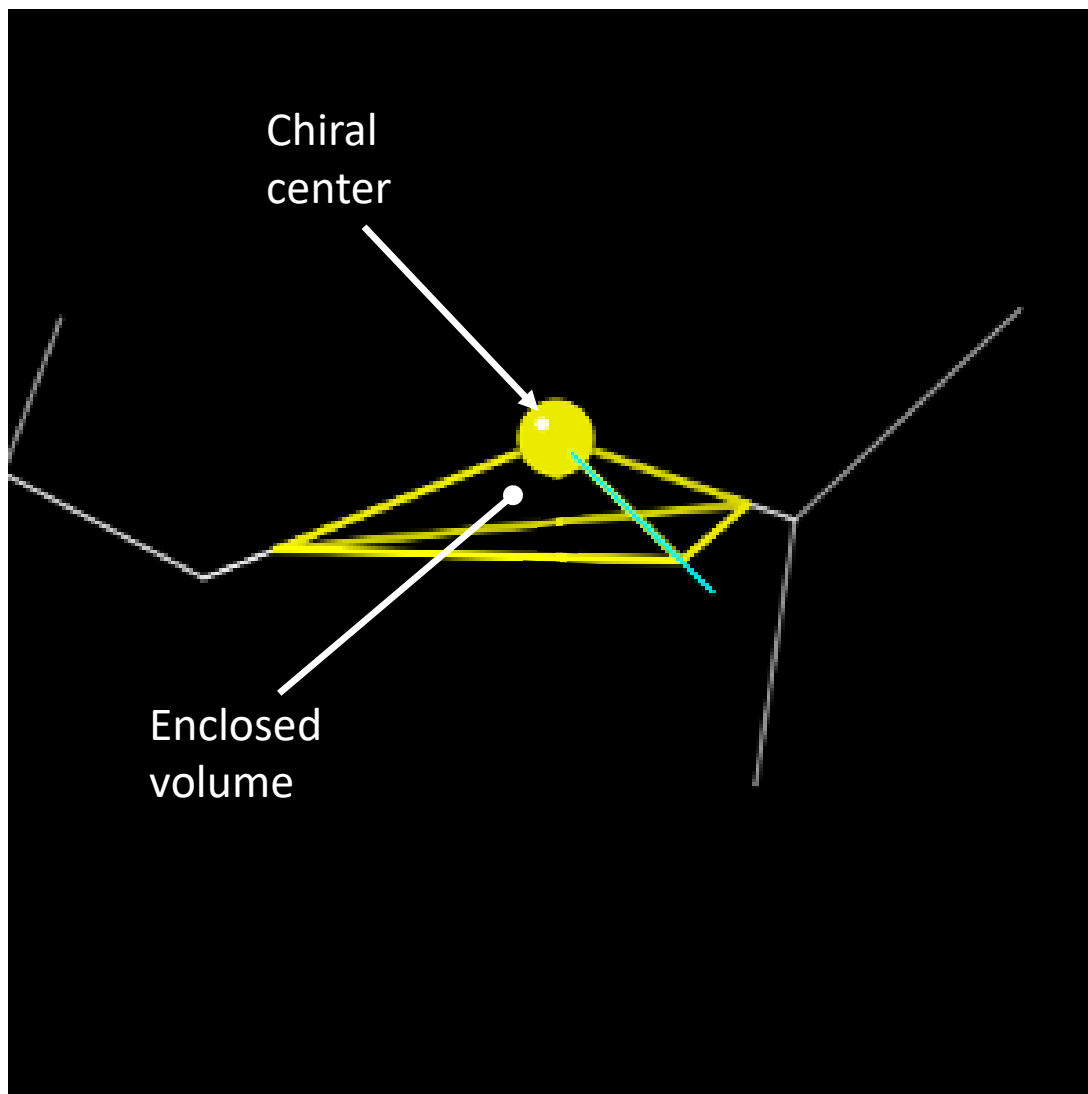
# RNA Ribose Puckers: Visualization



- A magenta cross is drawn for each incorrect ribose pucker
  - Long end of cross points along glycosidic bond vector
  - Cross is connected to 3' phosphate by the perpendicular distance line

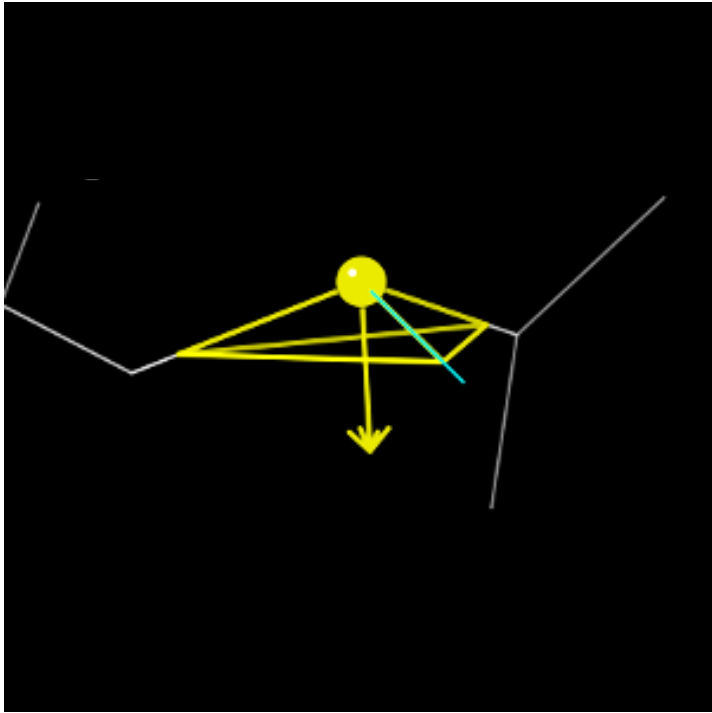
Chiral Volume Outliers  
(Very rare unless something is weird)

# Chiral Volume Outliers: Method



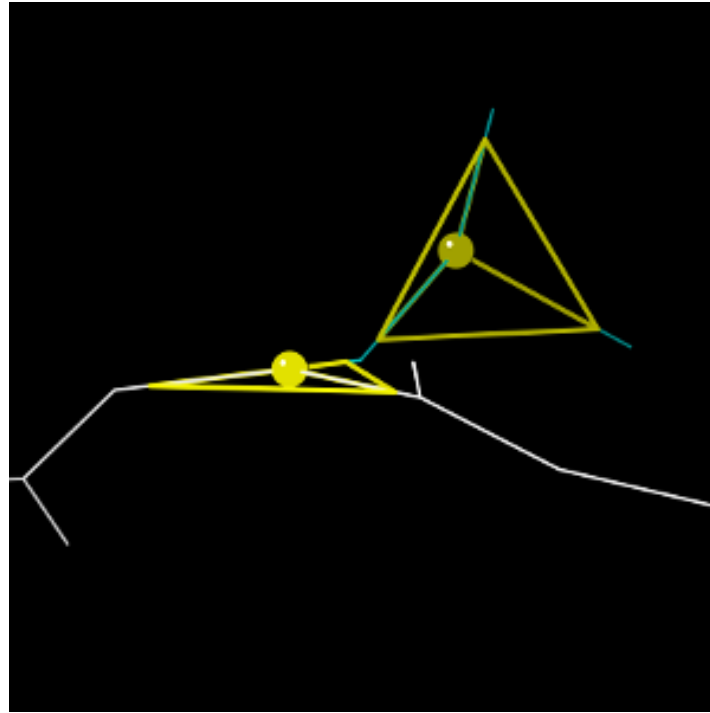
- Tetrahedral atoms with 4 distinct substituents are chiral
- Do a little light vector math to find the volume enclosed by the chiral center and its three heaviest children
  - Magnitude of volume indicates how tetrahedral the bonding is
  - Sign of volume indicates handedness (L vs D)

# Chiral Volume Outliers: Visualization and Causes

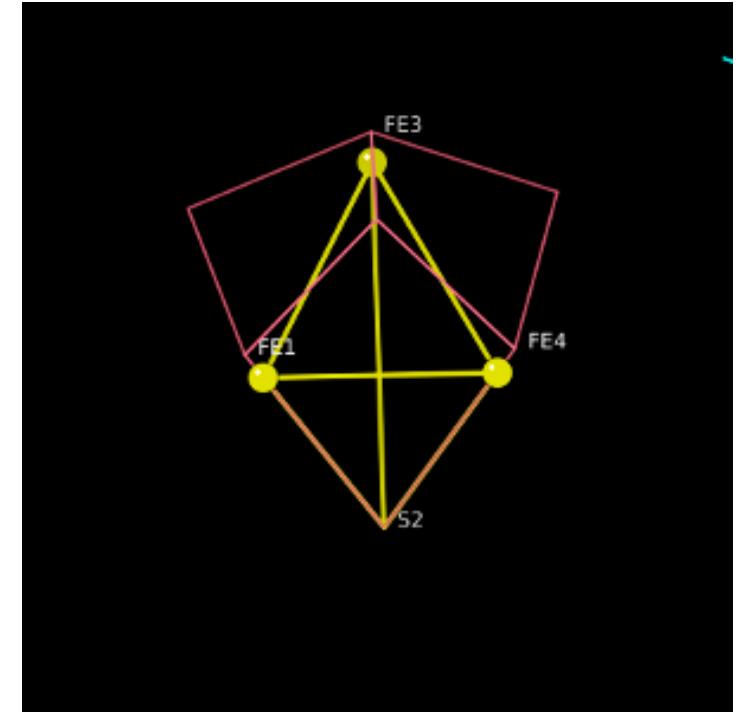


True handedness swaps

- D-amino acids with L names
- L-amino-acids with D names



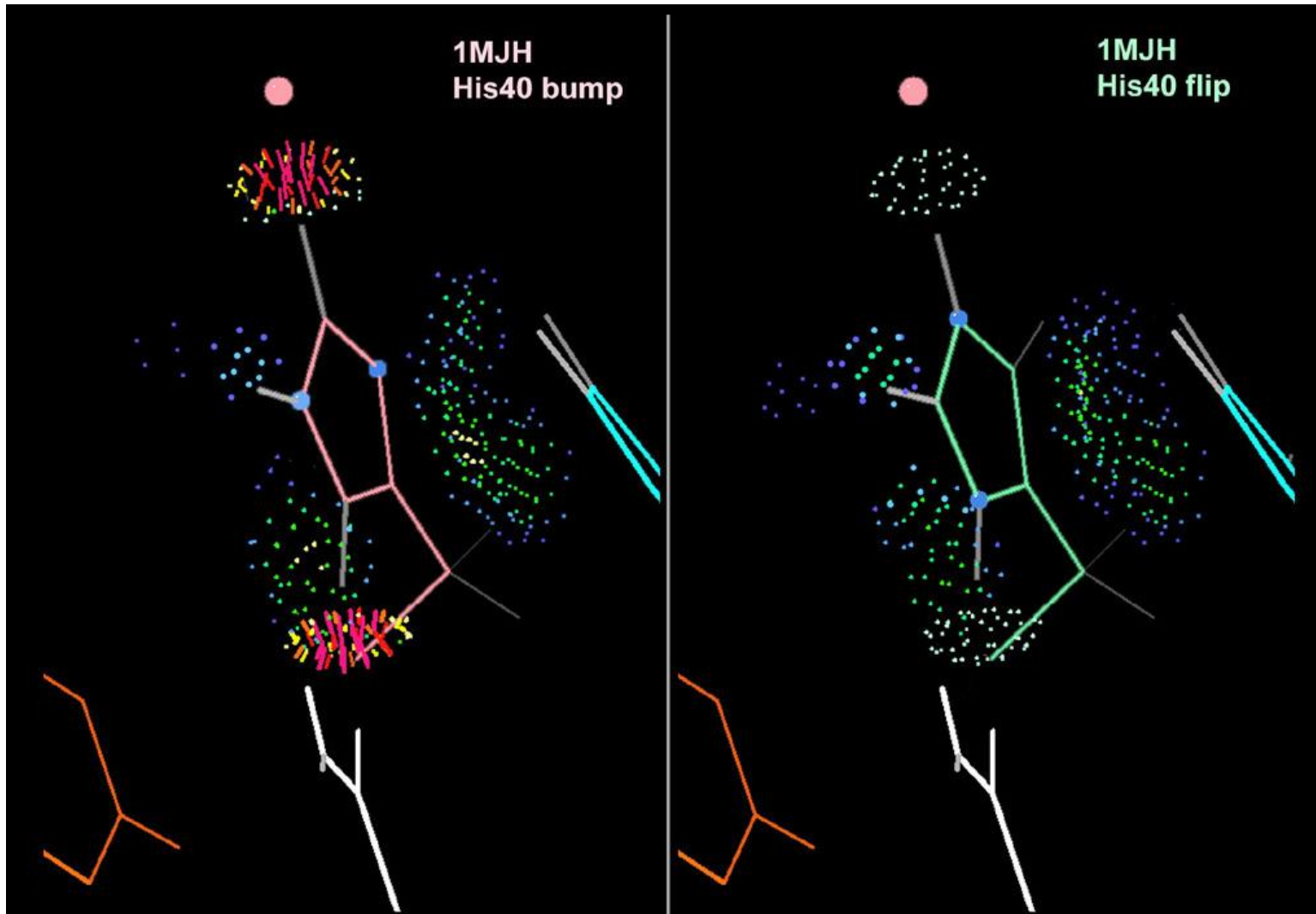
Squished or flattened  
geometry errors



Atom naming errors

- FeS clusters
- Swapping CD1 and CD2 names in Leu

# All-Atom Contacts and Clashes: Probable causes



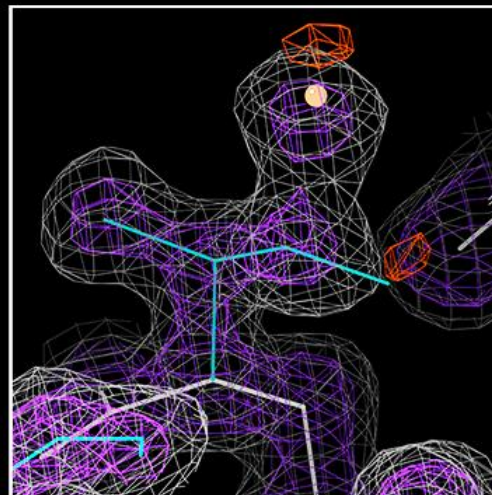
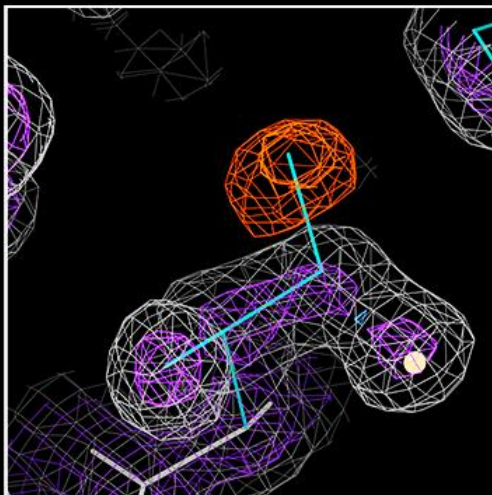
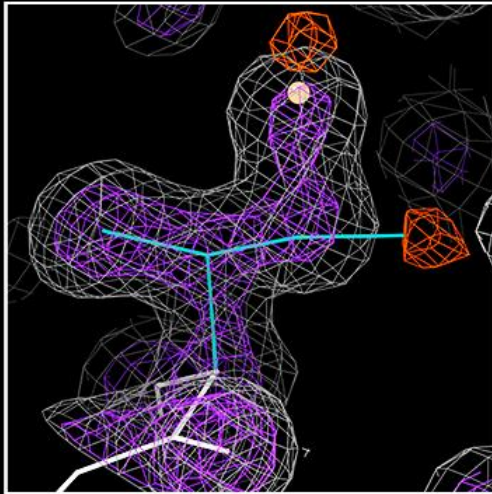
His flips change protonation, H-bonds, & even charge

## Sidechain flips

- Asparagine, Glutamine, and Histidine (N/Q/H) are pseudo-symmetric
- Wrong orientation can produce clashes without other error markup
- Fix with Reduce or Coot tools, then re-refine.

# Sidechain Rotamers: Probable causes

3js8

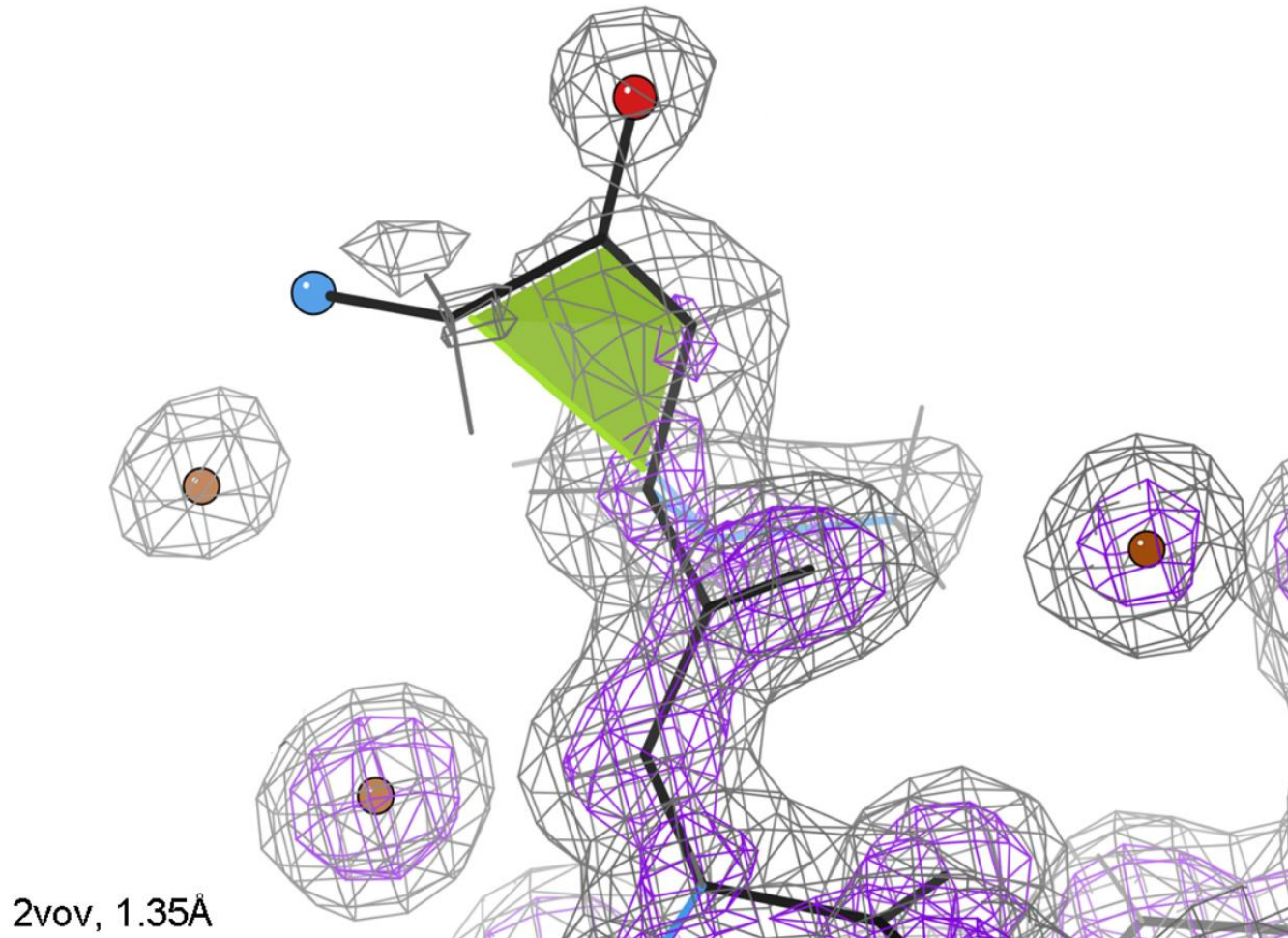


## Water problems

- Modeled water may co-opt sidechain density and create a rotamer outlier
- Isoleucine CD1 is especially vulnerable
- Delete water, rebuild sidechain



# Cis Peptides: Probable causes



## Chain termini

- Non-Pro *cis* peptides at chain ends are always wrong
- Limited density and lack of other constraints *allows* them to be modeled
- But that same lack of constraints means there's nothing to hold an unusual conformation in place