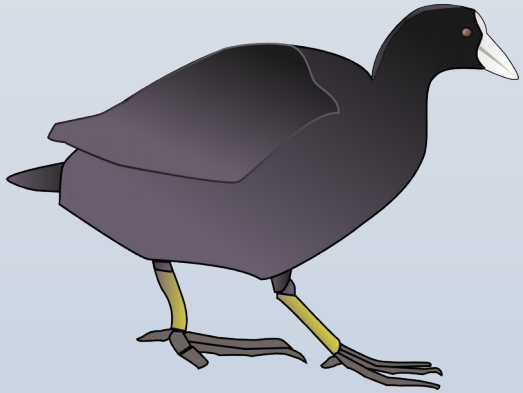
# *Coot*, pyrogen & CCP4 SRS



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June 2015

# *Coot* Updates

- JED-Flip (as it's currently known) added
  - Torsion-spec-dependent rotation of ligand fragment about rotatable bonds
- “Go to Ligand” View is perpendicular now

- Static Analysis: clang and checker
  - Cleaned up the code
  - Now can link with CCP4 SRS

- `coot.available-comp-id JE 20`

```
JEA  JEB  JEC  JED  JEE  JEG  JEH  JEI  JEJ  JEK
JEL  JEM  JEO  JEP  JEQ  JER  JES  JET  JEU  JEV
```

# build-for-scan-build-with-ccp4srs - scan-build results

| | |
|---|---|
| **User:** | pemsley@hector.local |
| **Working Directory:** | /Users/pemsley/Projects/build-for-scan-build-with-ccp4srs |
| **Command Line:** | make -j 4 |
| **Clang Version:** | clang version 3.5 (tags/checker/checker-276) |
| **Date:** | Tue Jun 23 22:59:43 2015 |
| **Version:** | checker-276 (2014-02-18 22:53:01) |

## Bug Summary

Results in this analysis run are based on analyzer build **checker-276**.

| Bug Type | Quantity | Display? |
|---|---|---|
| **All Bugs** | **460** | ☑ |
| **Dead store** | | |
| Dead assignment | 226 | ☑ |
| Dead initialization | 232 | ☑ |
| **Logic error** | | |
| Dangerous variable-length array (VLA) declaration | 1 | ☑ |
| Dereference of undefined pointer value | 1 | ☑ |

## Reports

| Bug Group | Bug Type ▾ | File | Line | Path Length | |
|---|---|---|---|---|---|
| Logic error | Dangerous variable-length array (VLA) declaration | surface/CXXSurface.cpp | 904 | 4 | View Report |
| Dead store | Dead assignment | lbg/wmolecule.cc | 1181 | 1 | View Report |
| Dead store | Dead assignment | src/gtk2-interface.c | 24235 | 1 | View Report |

```
841     vector<int, CXX::CXXAlloc<int> > uniqueAndDrawn(theSphere.nVertices());
842
843     int nDrawn = 0;
```

1 'nDrawn' initialized to 0 →

```
844     for (unsigned  i=0; i< theSphere.nVertices(); i++){
```

2 ← Loop condition is false. Execution continues on line 854 →

```
845         CXXCoord comp1(theSphere.vertex(i).vertex());
846         uniqueAndDrawn[i] = 0;
847         if (theSphere.vertex(i).doDraw()){
848             uniqueAndDrawn[i] = 1;
849             if (uniqueAndDrawn[i]){
850                 equivalence[i] = nDrawn++;
851             }
852         }
853     }
854     static const std::string vertexName("vertices");
855     static const std::string accessiblesName("accessibles");
856     static const std::string normalsName("normals");
857     {
858         oldVertexCount = numberOfVertices();
859         vertices.resize(oldVertexCount+nDrawn);
860         int verticesHandle = getVectorHandle(vertexName);
861         int accessiblesHandle = getVectorHandle(accessiblesName);
862         int normalsHandle = getVectorHandle(normalsName);
863         int iDraw = 0;
864         for (unsigned int i=0; i< theSphere.nVertices(); i++){
```

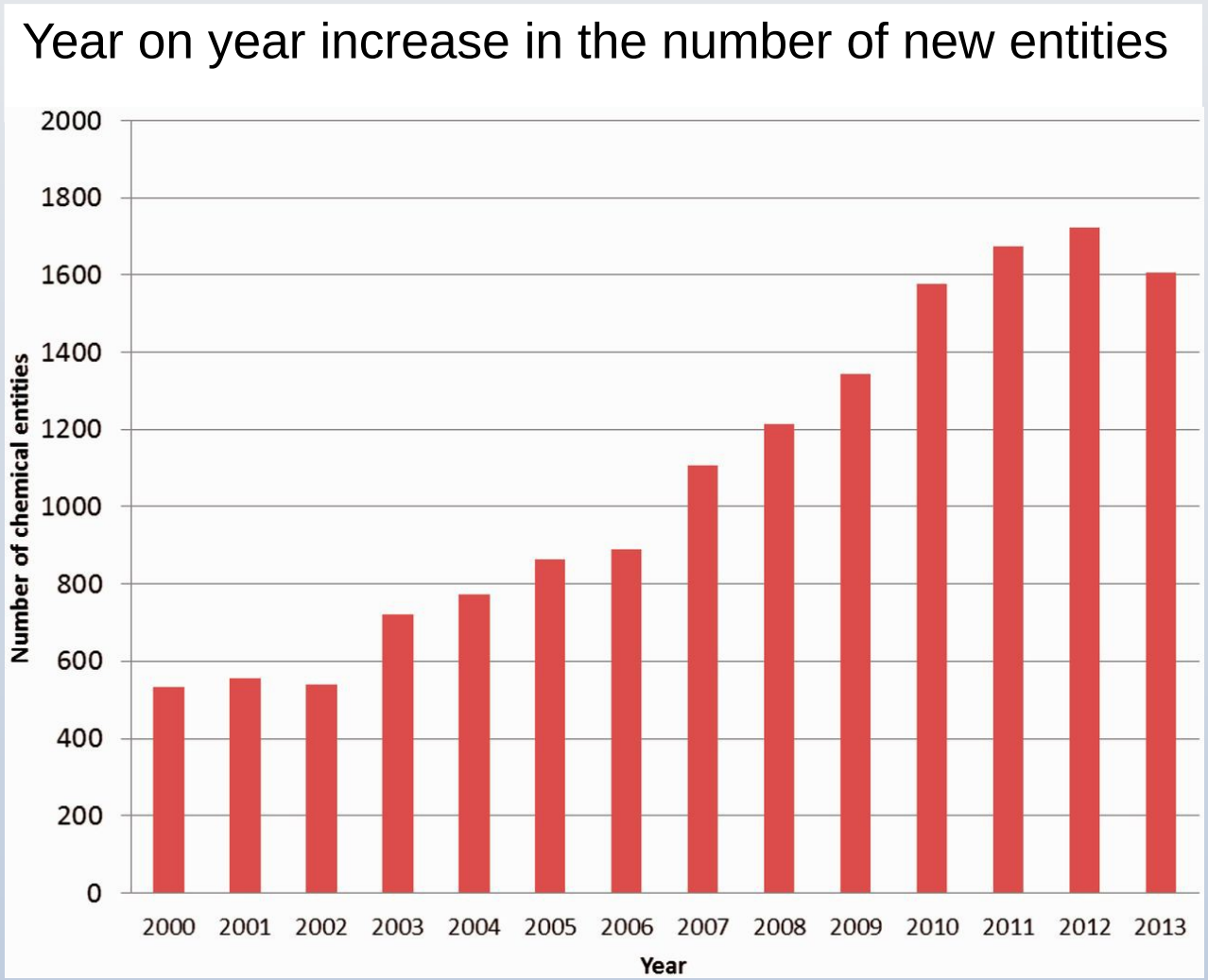
3 ← Loop condition is false. Execution continues on line 904 →

```
865             if (uniqueAndDrawn[i]){
866                 CXXCoord vertexCoord = theSphere.vertex(i).vertex();
```

# Resolving Links in Sphere Refine

- When linking carbohydrate monomers (2 pyranoses) *Coot* used link-by-distance
  - because I believed that the LINK definitions in the input file were often wrong
  - each potential pyranose link was tested against the current model geometry and the closest one selected
- This causes problems when we know what the linking should be
  - as is the case in the N-linked carbohydrate builder (LO/Carb)
- Now we specify the link using LINK record – and optionally pass the link type (as in LINKR)

# wwPDB Ligands




acceleration is
~120 entities/year/year

Sen *et al.* (2014) doi: 10.1093/database/bau116

# Pyrogen

- Based on Coot dictionaries (and thereby mmdb)
- Combine that with the RDKit
  - To create components for a dictionary generator
  - From SMILES and mol files
  - Can do depictions

# Testing pyrogen

- Pyrogen takes a Refmac or wwPDB ligand description, and tries to make a chemically sane representation of with them
  - It gets most of them right
  - but some of them wrong
  - I wanted to decrease the failure rate
  - I needed a list of monomers to test
- So, use CCP4 SRS to do this
  - `test-ccp4srs --list`
  - Filter out polymers
  - (Filter out obsolete?)

# SRS Frankensteination

- I couldn't (simply) fill a dictionary restraints container from an SRS Monomer
  - although the code is there to do it
  - because SRS is the Chemical Components Library with Refmac monomers merged on top
  - It has phosphate hydrogens with delocalized P-O bonds

# SRS Frankensteination

wwPDB:

```
AMP P     O1P    DOUB N N 1
AMP P     O2P    SING N N 2
AMP P     O3P    SING N N 3
AMP P     "O5'"  SING N N 4
AMP O2P   HOP2   SING N N 5
AMP O3P   HOP3   SING N N 6
```

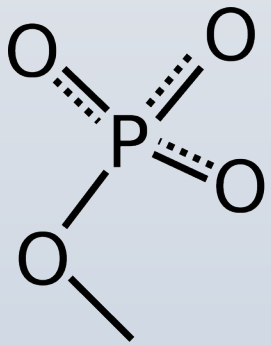
Refmac:

```
AMP  O1P    P   deloc   1.510    0.020
AMP  O2P    P   deloc   1.510    0.020
AMP  P      O3P deloc   1.510    0.020
AMP  "O5'"  P   single  1.610    0.020
```

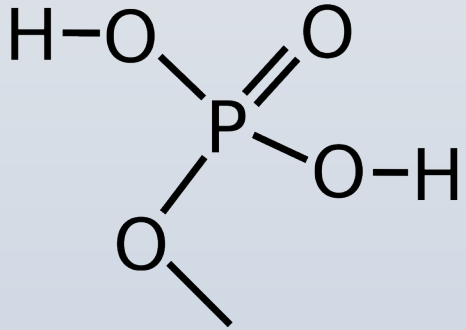
CCP4 SRS:

```
AMP O1P    P     deloc  1.51  0.02
AMP O2P    P     deloc  1.51  0.02
AMP P      O3P   deloc  1.51  0.02
AMP "O5'"  P     single 1.61  0.02
AMP O2P    HOP2  single 0     0
AMP O3P    HOP3  single 0     0
```

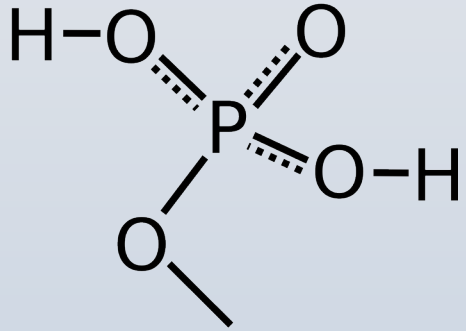
# SRS Frankensteination




Refmac




wwPDB CCD




CCP4 SRS

# SRS Frankensteination

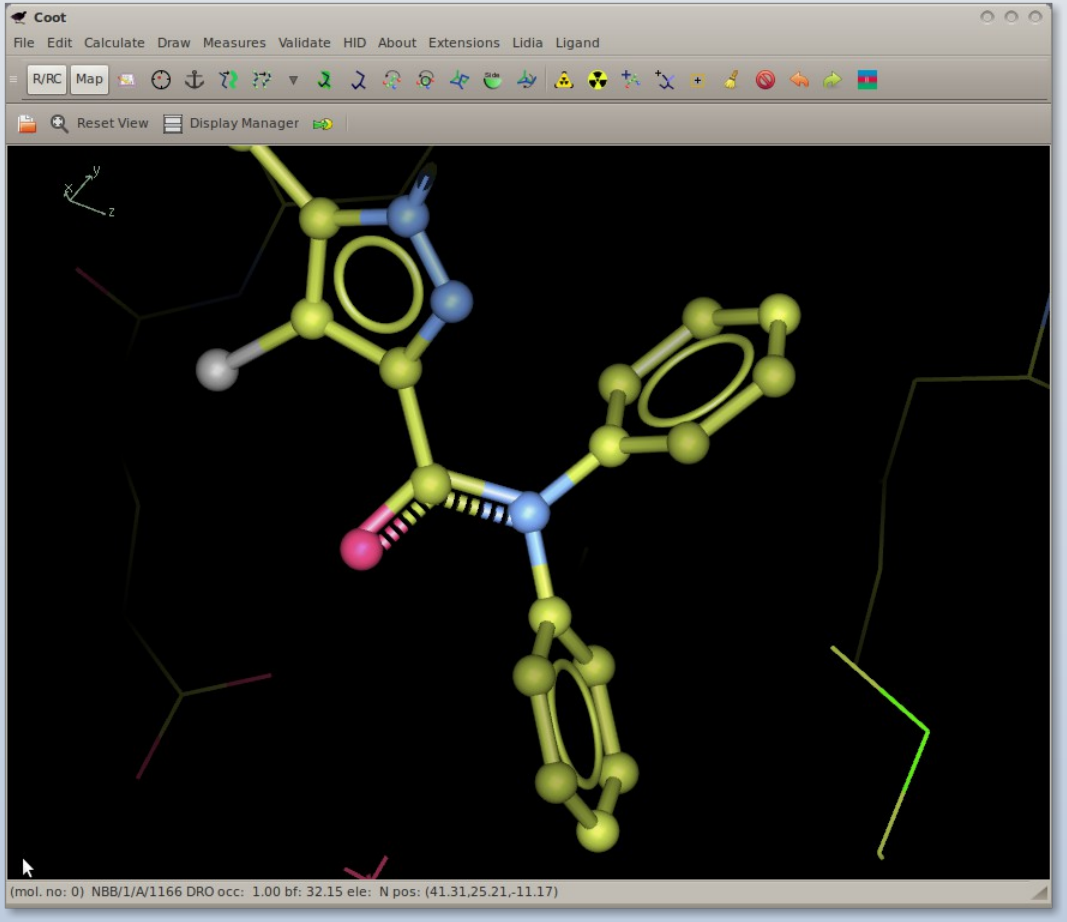
- Recommendation:
  - If the chemical formula doesn't match then completely **overwrite** the Chemical Component Dictionary entry with that from the Refmac library

# Valence Model

- wwPDB ligands are (mostly?) neutral, kekulized
- Refmac ligands are (implicitly) charged, aromatic and delocalized
  - As is ener-lib.cif
- What's the PDB policy on this?
- Either way, pyrogen and Acedrg need to cope with both forms
  - There's quite a bit of hand-coding chemistry to sort this out
- Pyrogen deletes/adds hydrogens and charges the following:
  - -NH2, -COOH, -PO4H2, -SO4H2

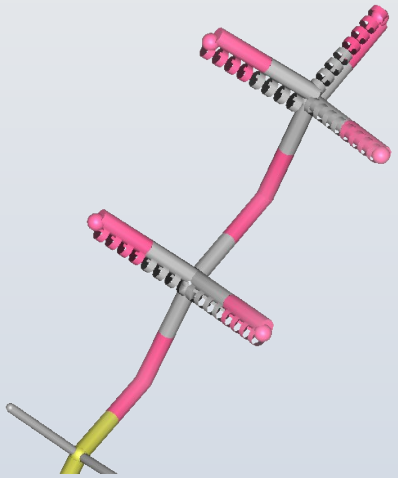
# Undelocalize

Typical Bond Orders from `cprodrg`

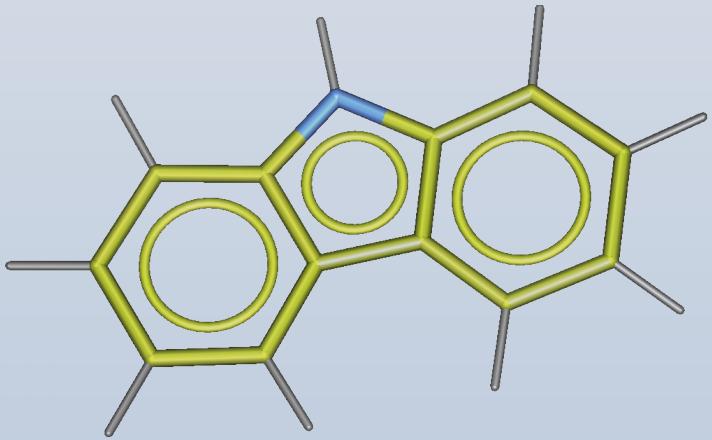


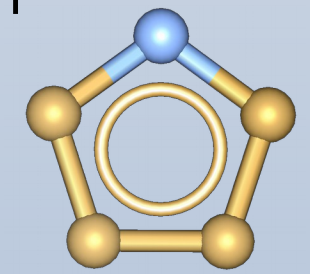
# undelocalize()

- What are the problems?
  - Amino groups



  - Phosphates: `deloc` oxygens
    - 1½ + 1½ + 1½ + 1 → 6 ⇒ P valency problem!
  - Carbazole, indol, pyrrole N
    - 2 x `arom` + H
    - → single bonds and no H





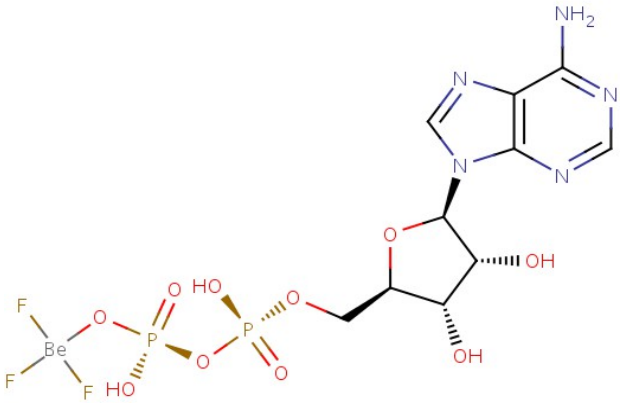
# Testing pyrogen

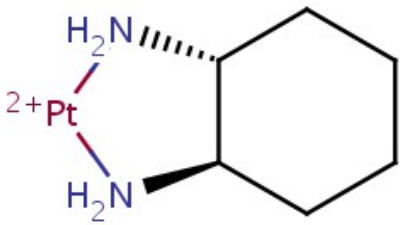
- `geometry.get_residue(`*`comp-id`*`)` used `.model_Cartn_{xyz}`. I should have used `.pdbx_model_Cartn_{xyz}`
  - Why? Because covalently-attached ligands
  - This has since been updated

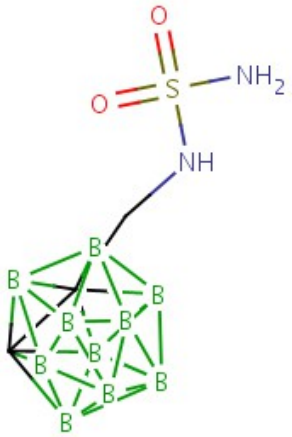
# Testing pyrogen

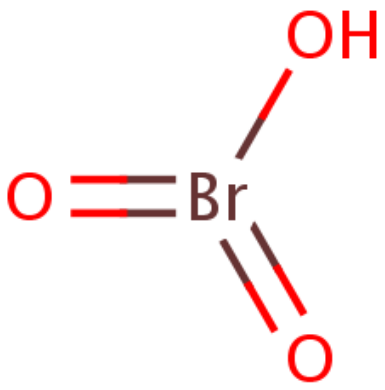
- So, merely use SRS to get a list of non-polymer monomers
- One by one download the wwPDB definition mmcif
  - Total: 15168
  - *e.g.* `pyrogen -w -n -r AMP`
- Decreased the sanitization failure rate:
  - was: 532 (3.5%)
  - now: 198 (1.3%)

# A Sample of Remaining Problem Cases

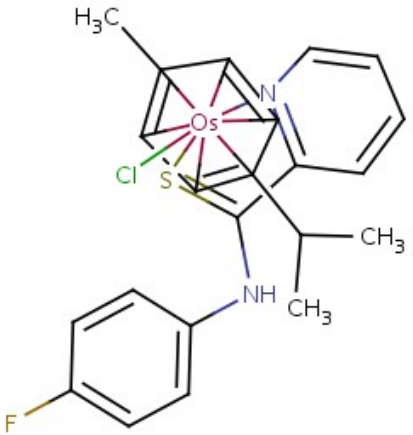


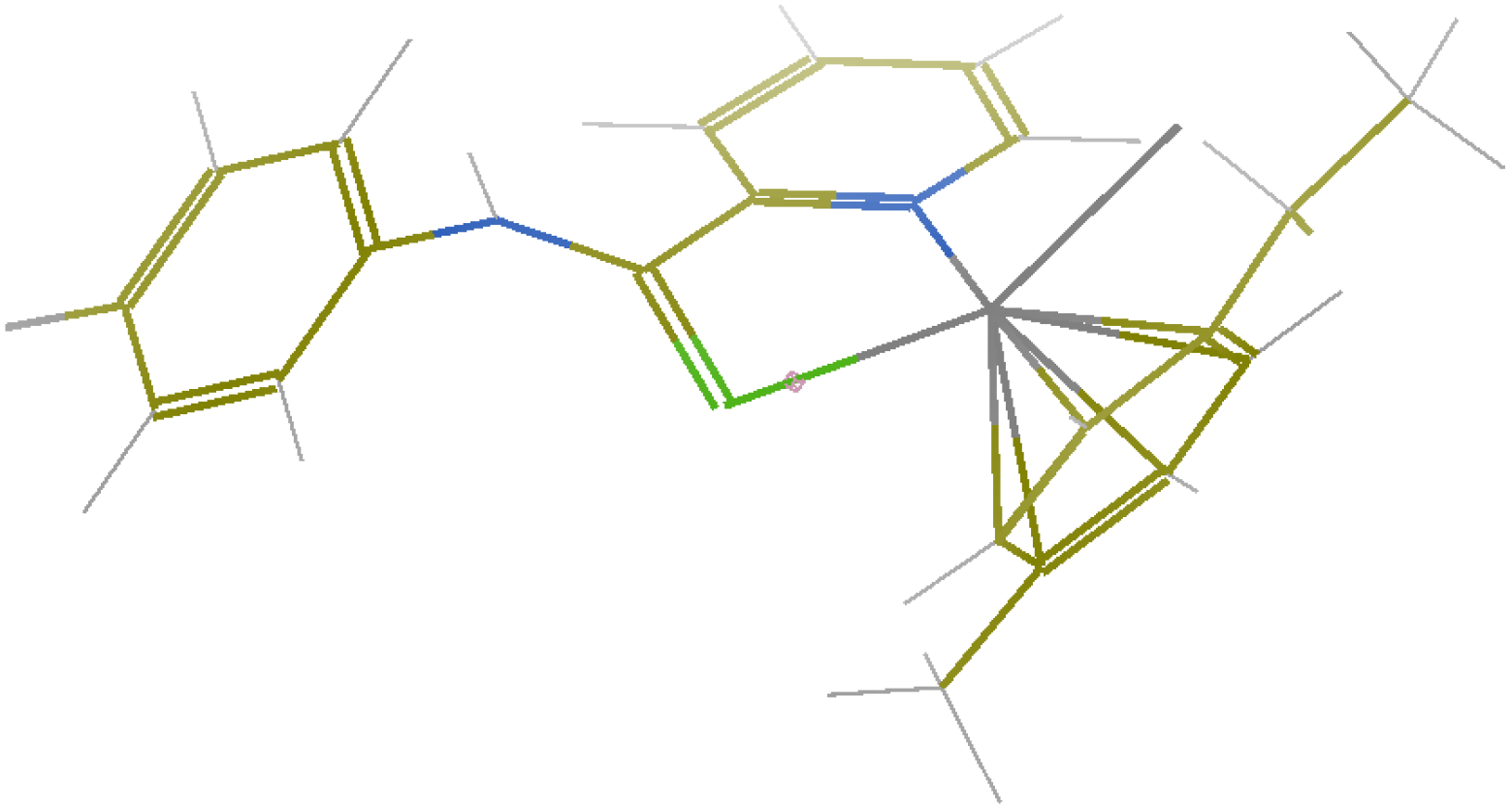





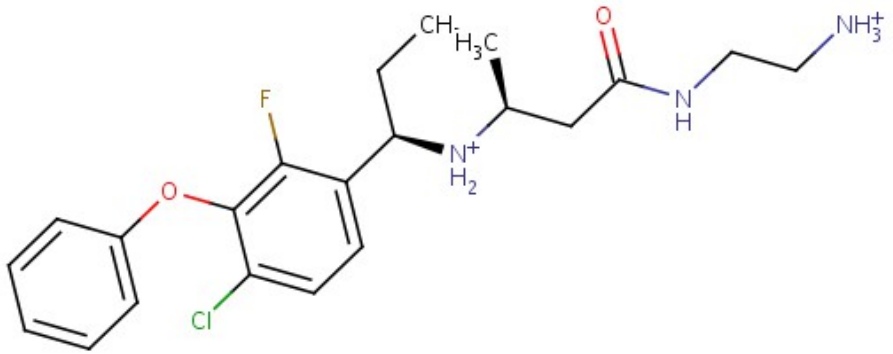


# 1MK in 3D



Fail

# An Organic Failure




- The amine test found $sp^3$ hybridized nitrogen atoms with 2 hydrogen atoms, charged the nitrogen and added a third hydrogen atom.
  - The test has since been amended to additionally check the degree.
  - Formal charge is now parsed from the wwPDB description mmcif.

# Next Steps

- Dictionary parsing is needed to generate sanitized representations of molecules
- Sanitized representations of molecules are needed to generate MDL input for Mogul
  - So we can run pyrogen in "Mogul-mode"
  - And use Mogul to score chemistry distortion of the output of Refmac refinement – using Acedrg (and others)

- Ligand Fitting: "Unknown Chirality" attribute needs to be added to a user-defined set of atoms for use in molecule conformer generation

# Acedrg Tests

- The Refmac Monomer Library has not been updated since ~2012
- Many missing entries
- What do you have to do if you want to refine a structure with a ligand that's not in the Refmac Monomer Library?
- Can today's Acedrg fill the gaps?

# Acedrg Tests

- Take the wwPDB Chemical Component Dictionary
- Remove entries already in the Refmac Monomer Library
  - 7904 missing entries
- Download all these minimal descriptions and run Acedrg
  - 7360 cif files generated (93% coverage)
- Use a PDBe Web Service to find which accession codes use each of these ligands and refine them
  - 6010 successful runs of Refmac (82% coverage)

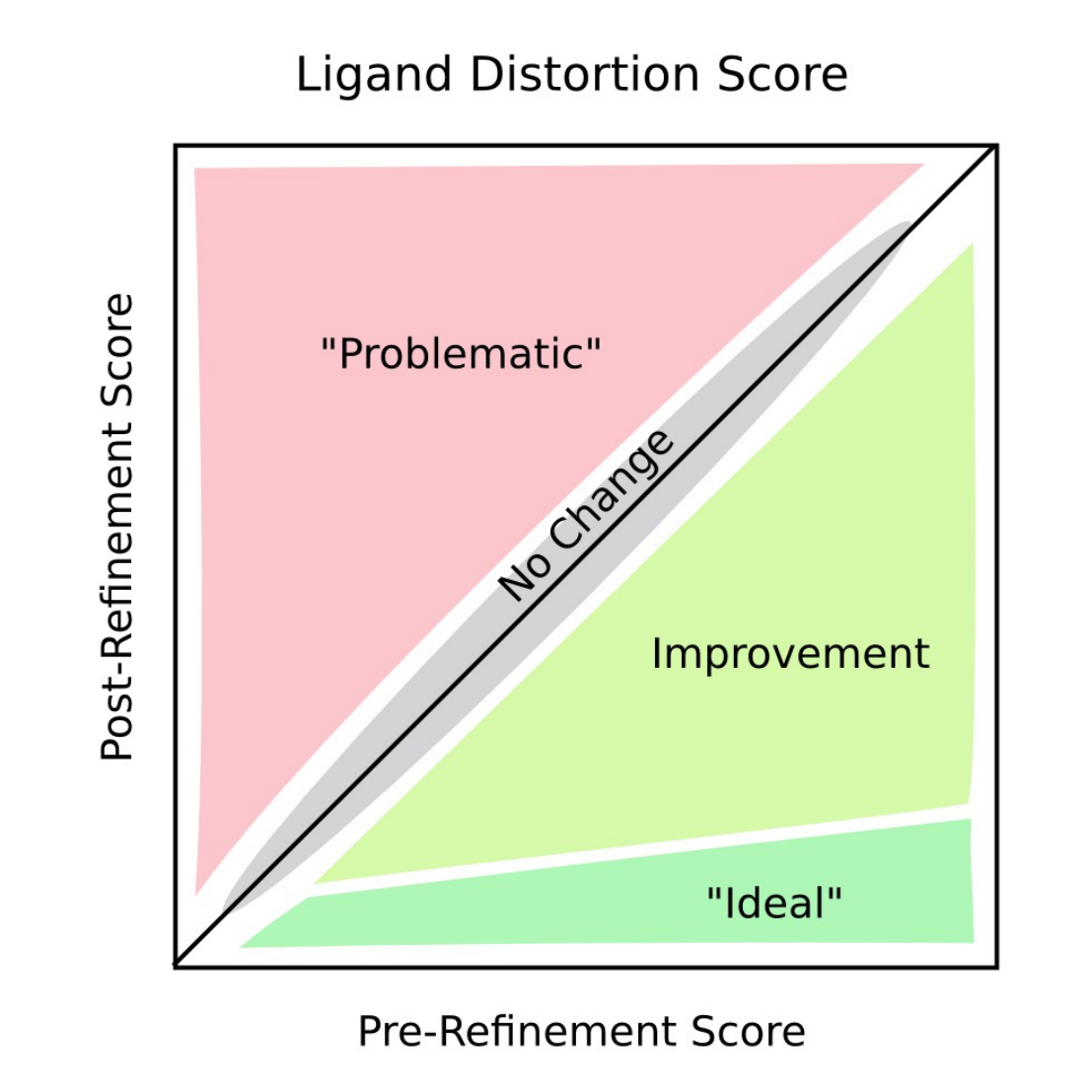
# How Well Did Acedrg Do?

- How much did the atoms move on refinement with Refmac?
- Did refinement with Refmac reduce the distortion of the ligand?
  - distortion score ~ "strain energy"
  - (compared to the Acedrg dictionary?)
- Did refinement with Refmac improve the correlation of the ligand...
  - ...to the depositors map?
- Did Acedrg reduce the Total Mogul Distortion Score?
  - $S_{post}$ *vs.* $S_{pre}$
- Additional: The tests were limited to non-polymers
  - 6943 new ligand types (88%) are non-polymers
  - LINKed ligands excluded

# Example Coot Ligand Distortion Score

```
  Residue Distortion List:
   plane  O3   C19  C20  C18  C16  C15  C17  C13  C14  N2   C4   C5   O1   C3   C6   O2  penalty-score:  36.51
   plane  C2   C7   C8   C9   C10  C11  C12                                              penalty-score:   8.82
   bond  C13 to  C4  target_value:   1.490 d:   1.432 sigma:   0.020 length-devi  -0.058 penalty-score:   8.44
   bond  C4  to  C3  target_value:   1.490 d:   1.436 sigma:   0.020 length-devi  -0.054 penalty-score:   7.21
   bond  O3  to  C19 target_value:   1.362 d:   1.318 sigma:   0.020 length-devi  -0.044 penalty-score:   4.75
   bond  C19 to  C20 target_value:   1.390 d:   1.433 sigma:   0.020 length-devi   0.043 penalty-score:   4.67
   bond  C1  to  C2  target_value:   1.390 d:   1.428 sigma:   0.020 length-devi   0.038 penalty-score:   3.70
   bond  C4  to  C5  target_value:   1.490 d:   1.454 sigma:   0.020 length-devi  -0.036 penalty-score:   3.26
   bond  C13 to  C14 target_value:   1.490 d:   1.456 sigma:   0.020 length-devi  -0.034 penalty-score:   2.91
   bond  C15 to  C13 target_value:   1.490 d:   1.458 sigma:   0.020 length-devi  -0.032 penalty-score:   2.57
   bond  C16 to  C15 target_value:   1.490 d:   1.459 sigma:   0.020 length-devi  -0.031 penalty-score:   2.45
   angle  C13 -  C4  -  C5   target: 108.00 model_angle: 133.80 sigma:  3.00 angle-devi 25.80 penalty-score:  73.93
   angle  O1  -  C5  -  C4   target: 108.00 model_angle: 126.59 sigma:  3.00 angle-devi 18.59 penalty-score:  38.38
   angle  C13 -  C15 -  C16  target: 120.00 model_angle: 102.30 sigma:  3.00 angle-devi 17.70 penalty-score:  34.83
   angle  O2  -  C6  -  N1   target: 108.00 model_angle: 122.80 sigma:  3.00 angle-devi 14.80 penalty-score:  24.34
   angle  O2  -  C6  -  C3   target: 108.00 model_angle: 122.76 sigma:  3.00 angle-devi 14.76 penalty-score:  24.19
   angle  C13 -  C15 -  C17  target: 120.00 model_angle: 133.33 sigma:  3.00 angle-devi 13.33 penalty-score:  19.76
   angle  C4  -  C13 -  C15  target: 120.00 model_angle: 132.99 sigma:  3.00 angle-devi 12.99 penalty-score:  18.76
   angle  N1  -  C5  -  O1   target: 108.00 model_angle: 120.48 sigma:  3.00 angle-devi 12.48 penalty-score:  17.32
   angle  C15 -  C13 -  C14  target: 120.00 model_angle: 110.43 sigma:  3.00 angle-devi -9.57 penalty-score:  10.18
   angle  N1  -  C6  -  C3   target: 108.00 model_angle: 114.28 sigma:  3.00 angle-devi  6.28 penalty-score:   4.38
   angle  C6  -  C3  -  C4   target: 108.00 model_angle: 101.75 sigma:  3.00 angle-devi -6.25 penalty-score:   4.34
Residue Distortion Summary:
   29 bond restraints
   44 angle restraints
   sum of bond  distortions penalties:  59.5697
   sum of angle distortions penalties:  300.405
   average bond  distortion penalty:    2.05413
   average angle distortion penalty:    6.82739
   total distortion penalty:            405.304
   average distortion penalty:          4.93116
```

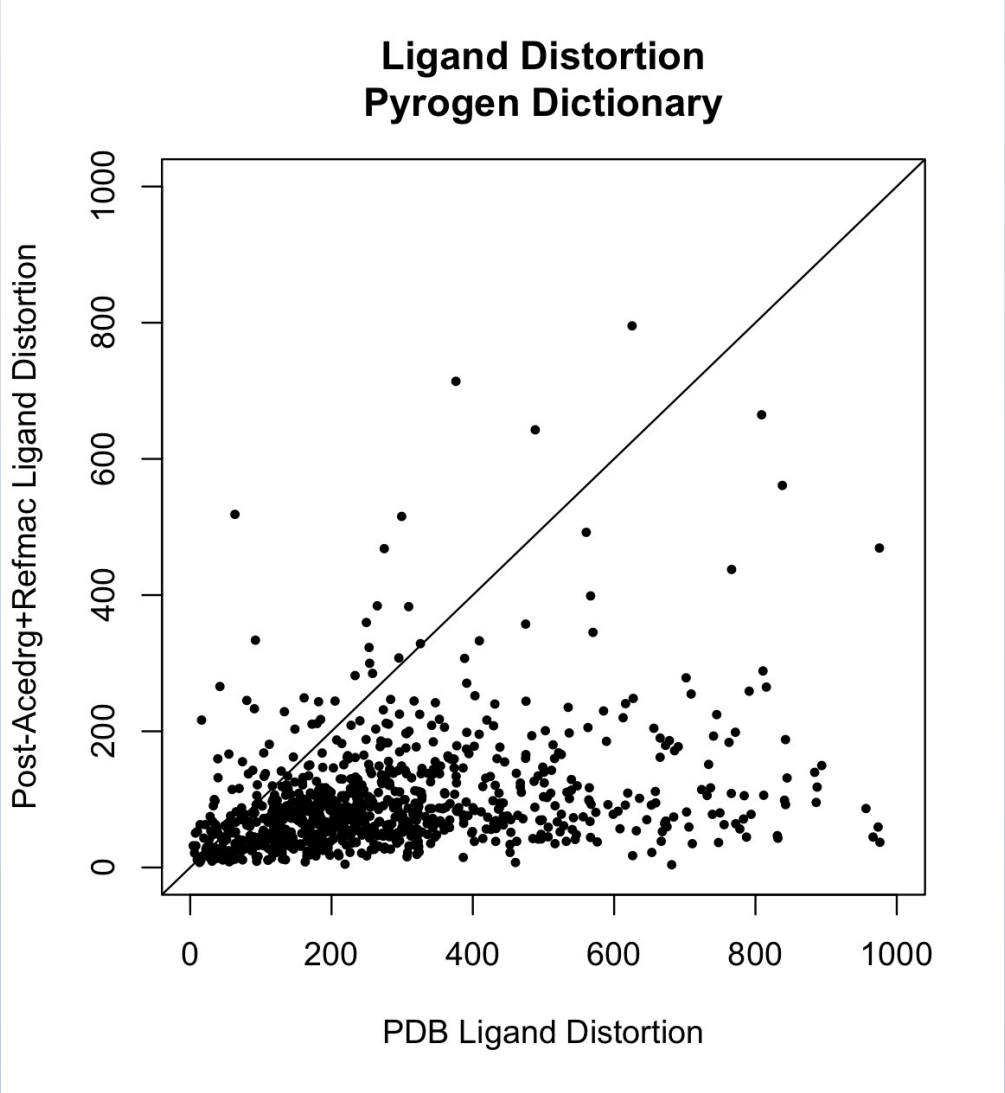
# Ligand Distortion Graph Primer



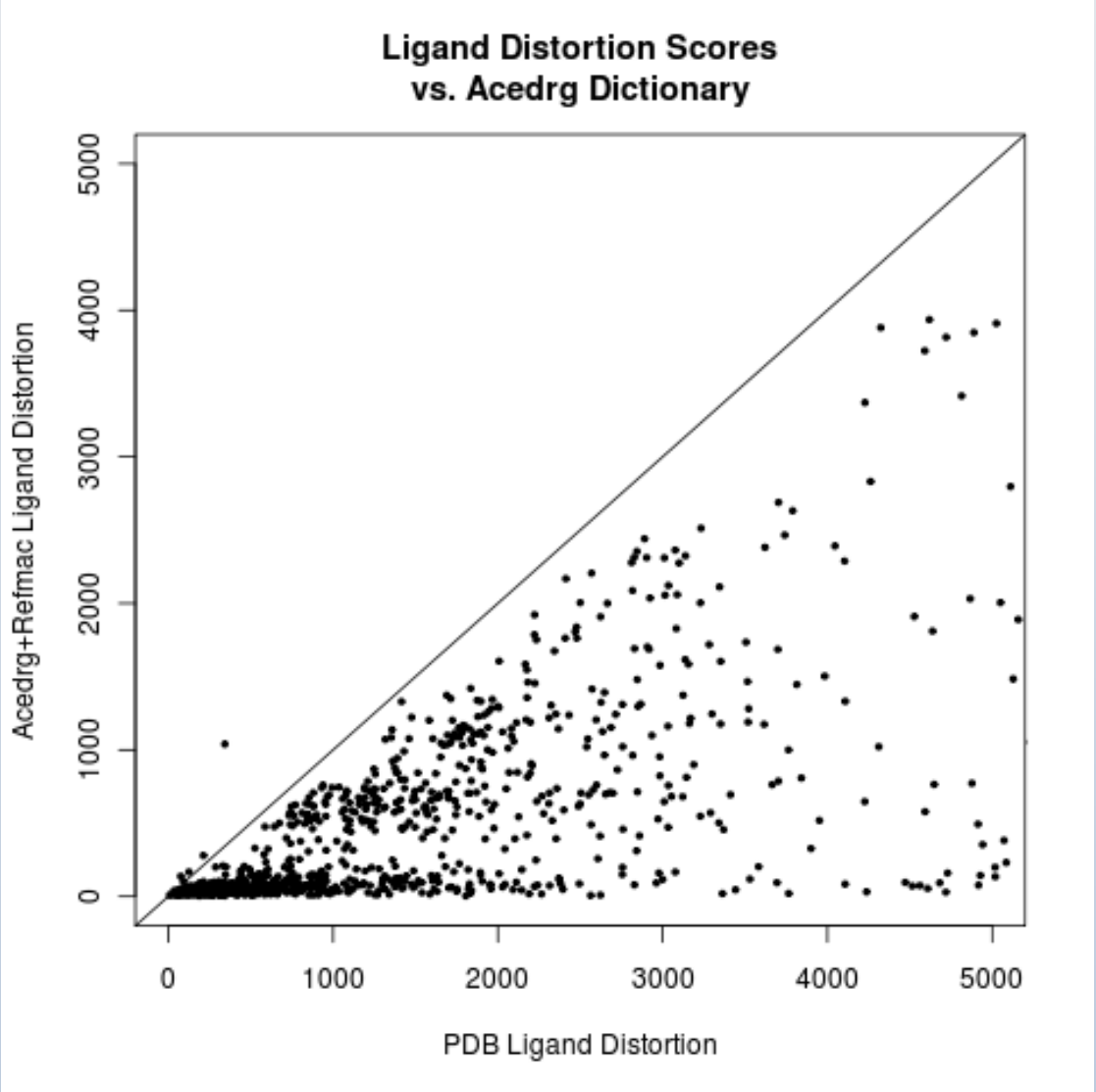
# Testing Acedrg

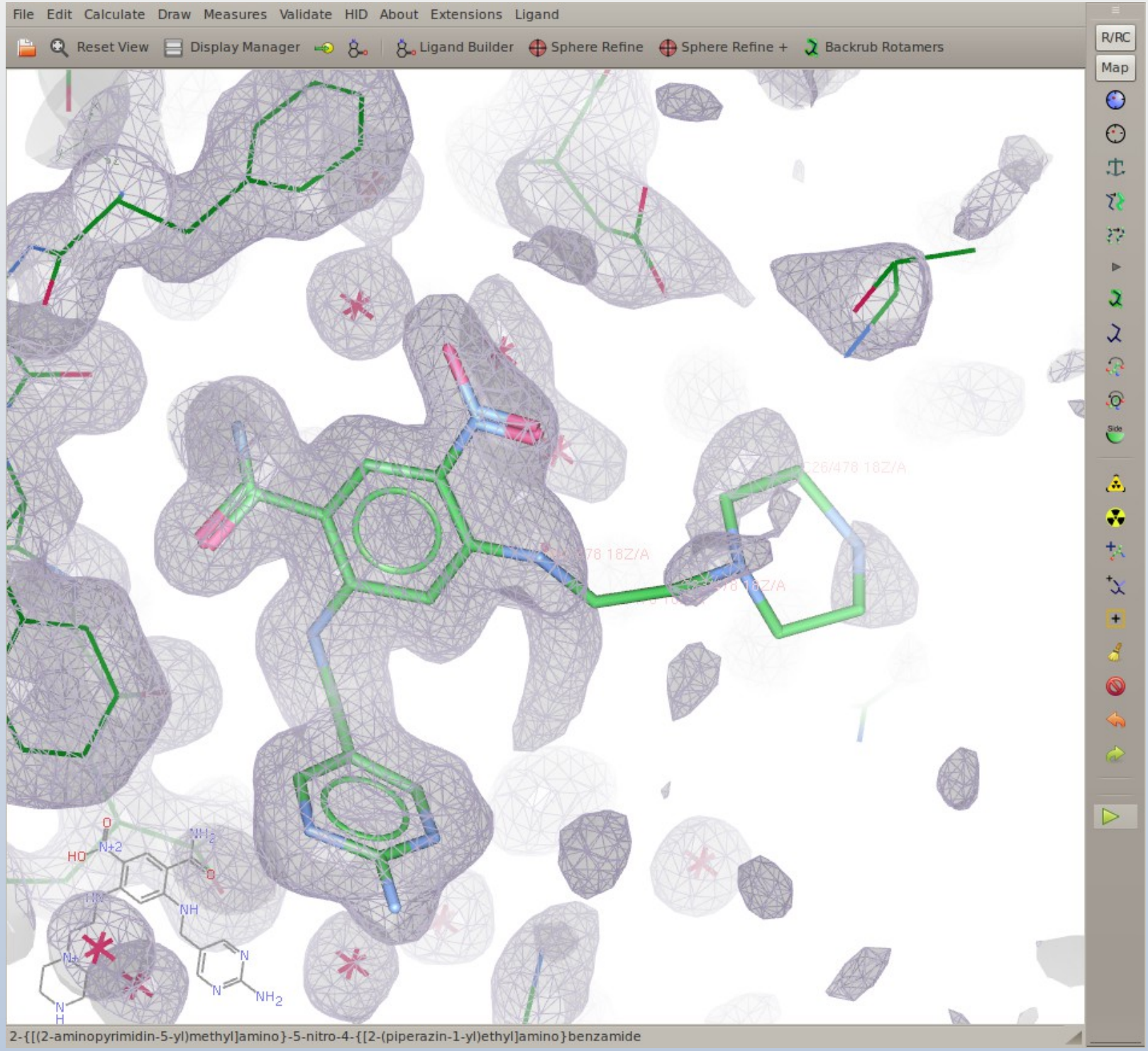
- Redo the tests from a few months ago
  - Using an updated Acedrg
  - Test vs. Internal consistency to dictionary
  - Test vs Mogul average z-score
  - Test vs Mogul worst z-score

# Distortion: using Pyrogen dictionary to score ligand

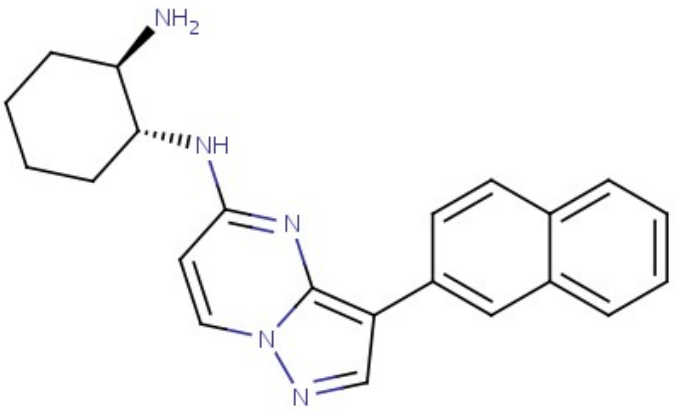


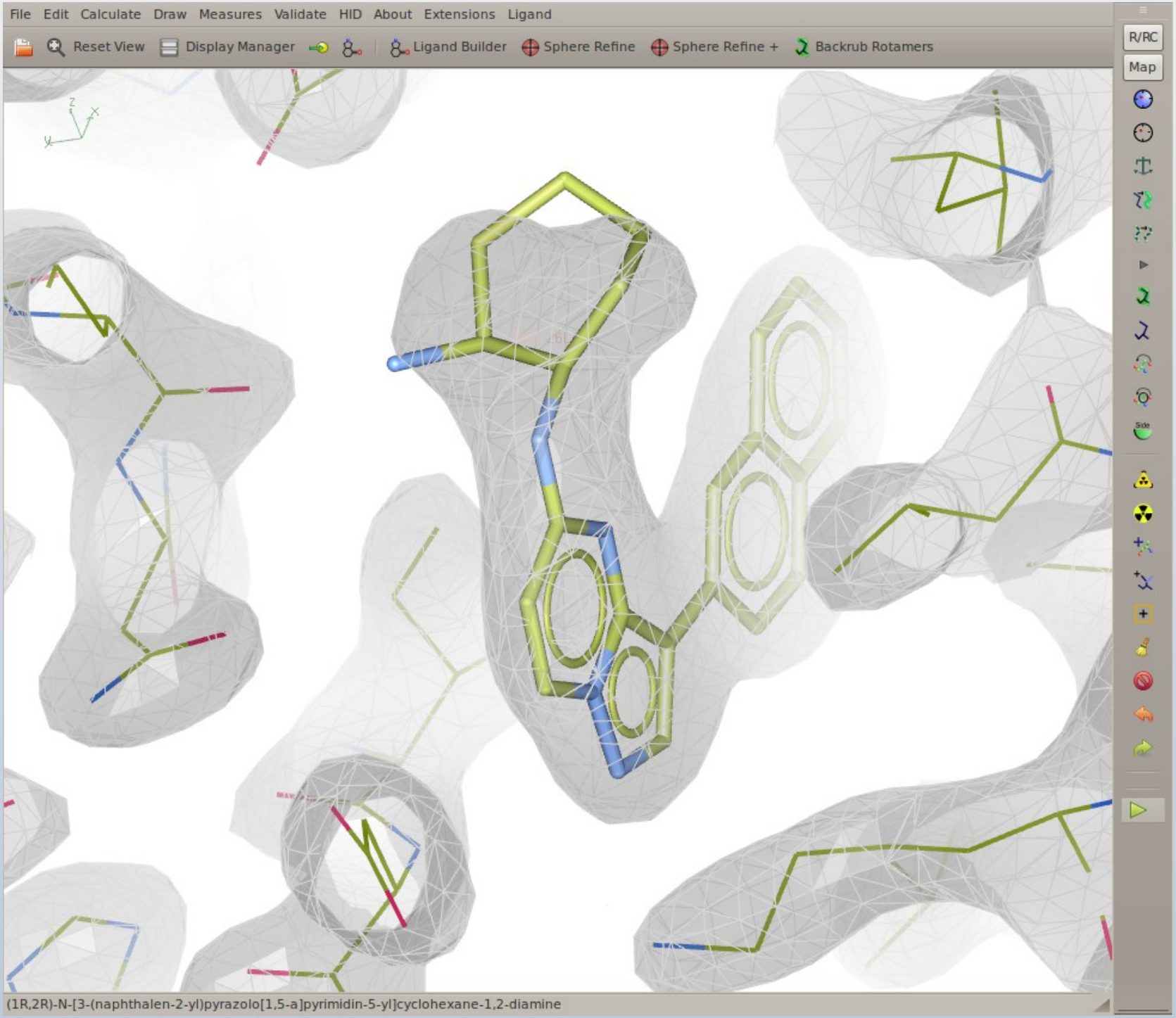
# Distortion: using Acedrg dictionary to score ligand

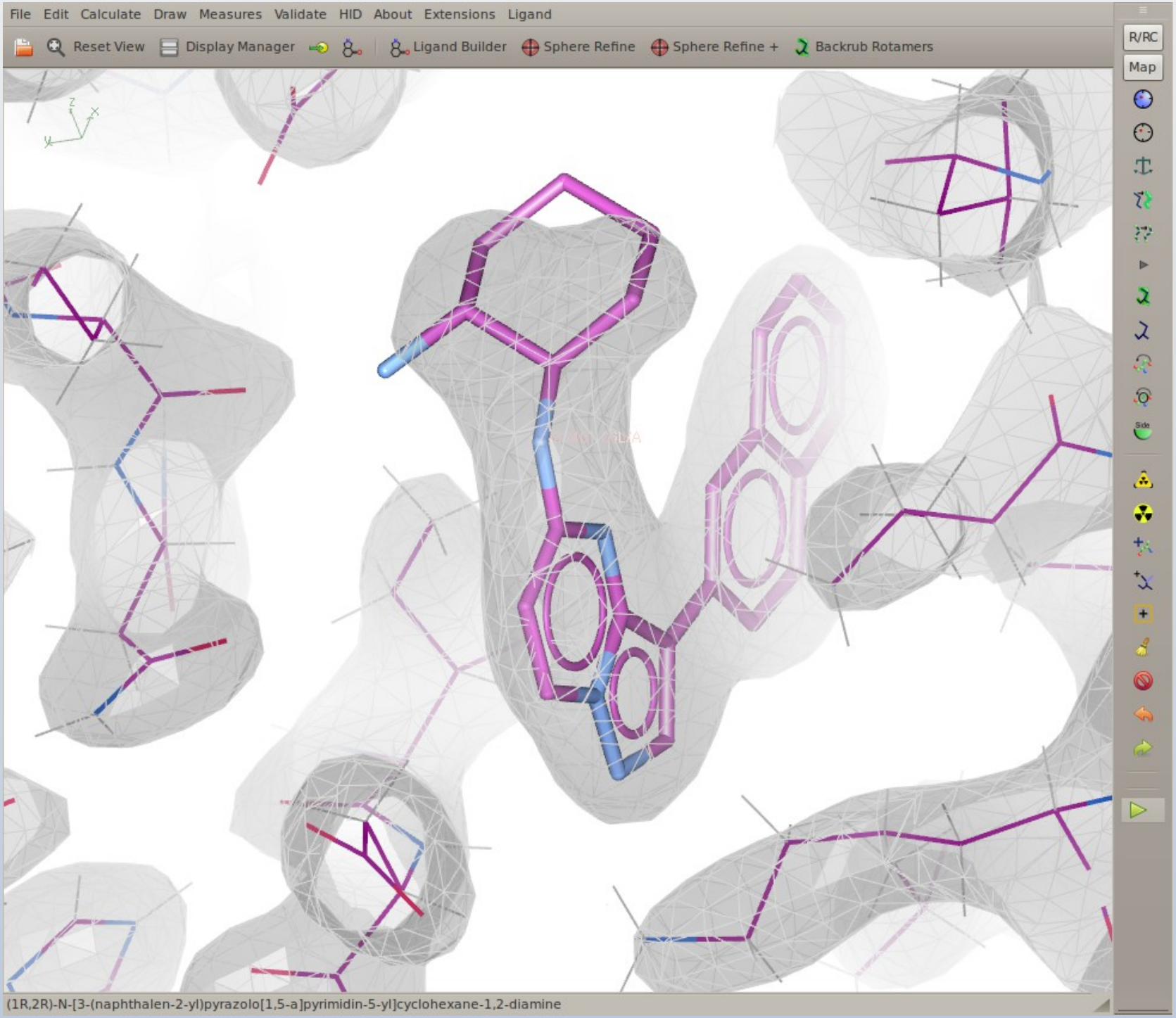



File Edit Calculate Draw Measures Validate HID About Extensions Ligand
Reset View
Display Manager
Ligand Builder
Sphere Refine
Sphere Refine +
Backrub Rotamers
R/RC
Map
Side
2-{[(2-aminopyrimidin-5-yl)methyl]amino}-5-nitro-4-{[2-(piperazin-1-yl)ethyl]amino}benzamide

# 26L




File Edit Calculate Draw Measures Validate HID About Extensions Ligand
Reset View
Display Manager
Ligand Builder
Sphere Refine
Sphere Refine +
Backrub Rotamers
R/RC
Map
(1R,2R)-N-[3-(naphthalen-2-yl)pyrazolo[1,5-a]pyrimidin-5-yl]cyclohexane-1,2-diamine


File Edit Calculate Draw Measures Validate HID About Extensions Ligand
Reset View
Display Manager
Ligand Builder
Sphere Refine
Sphere Refine +
Backrub Rotamers
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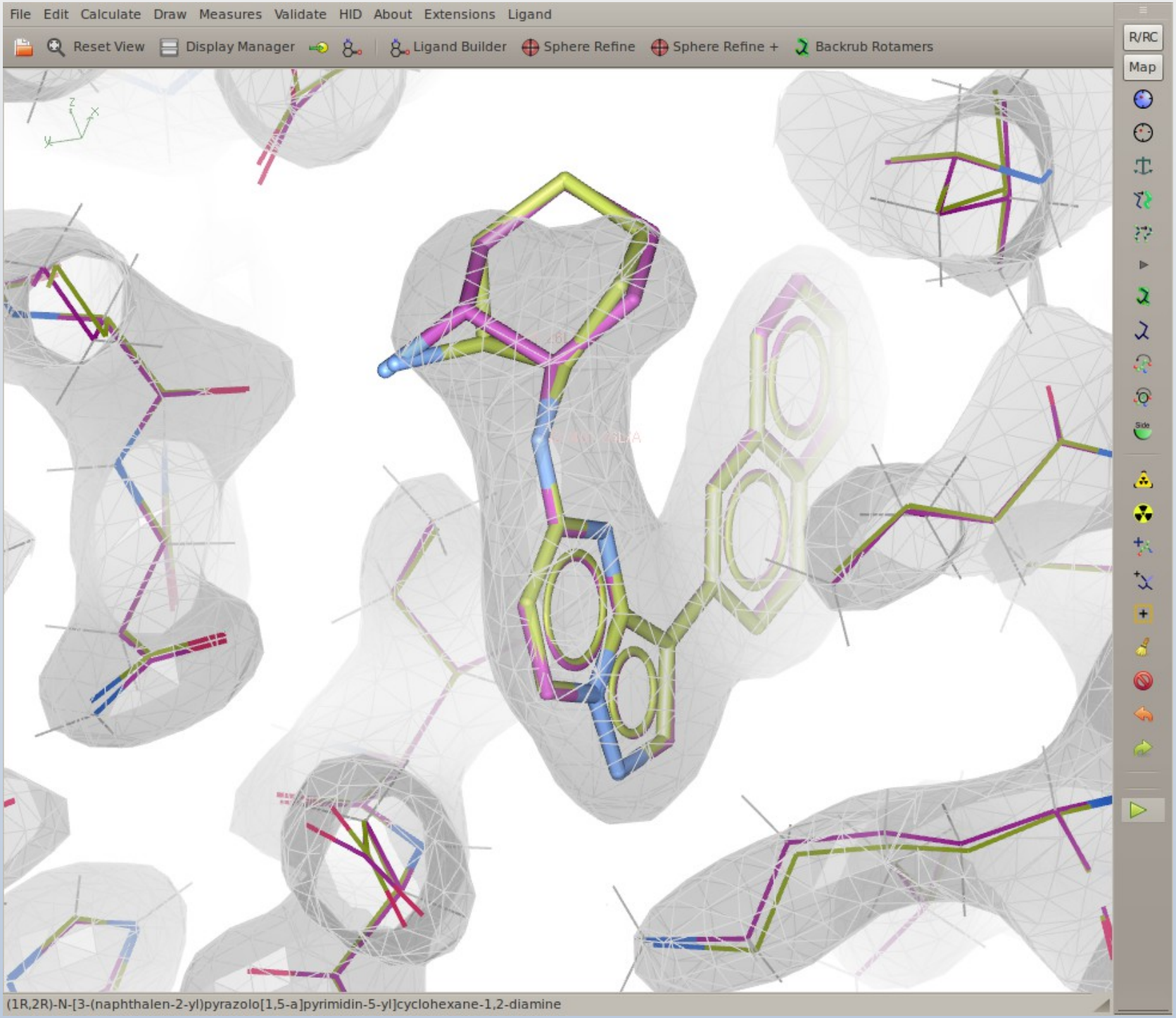
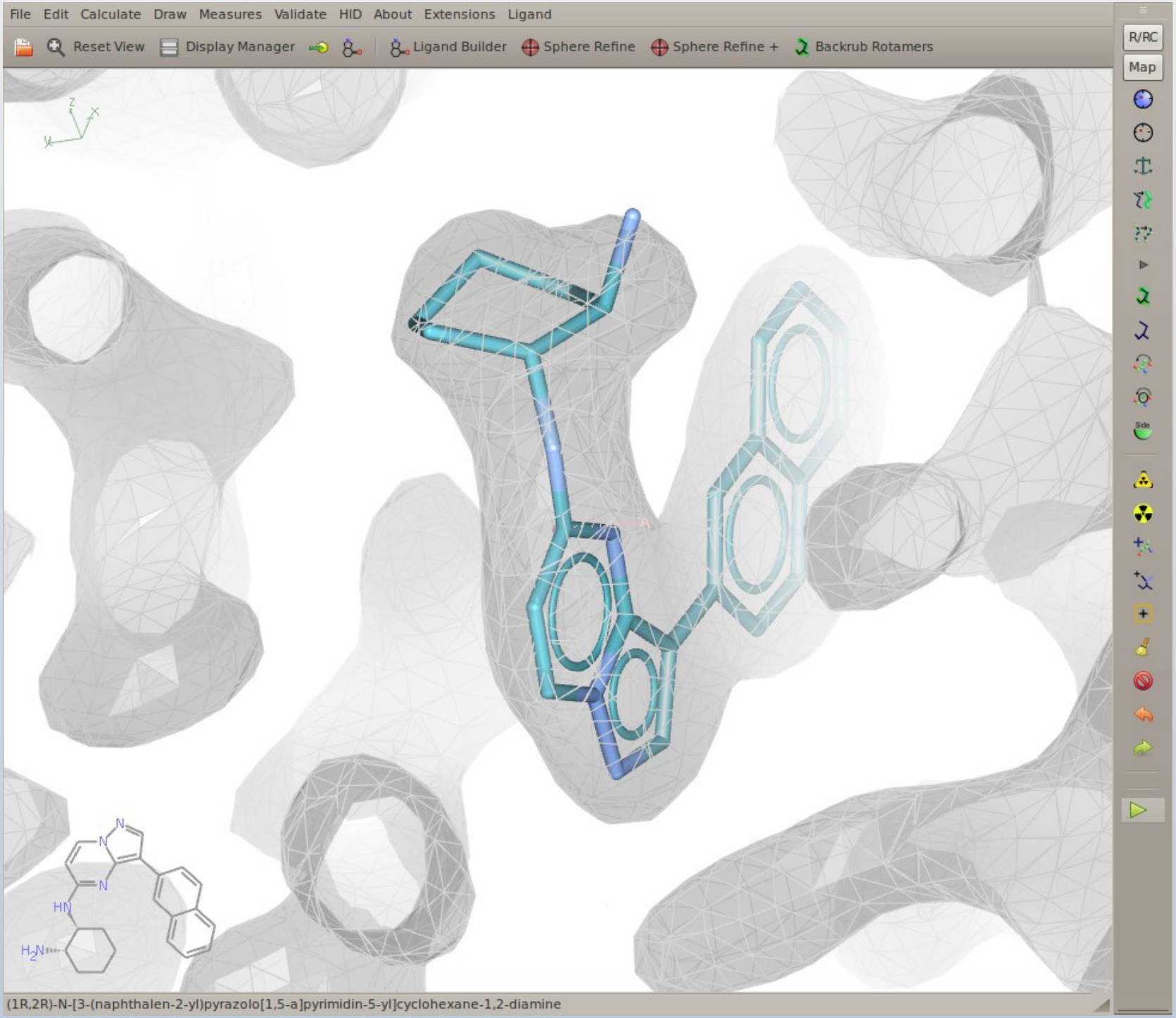
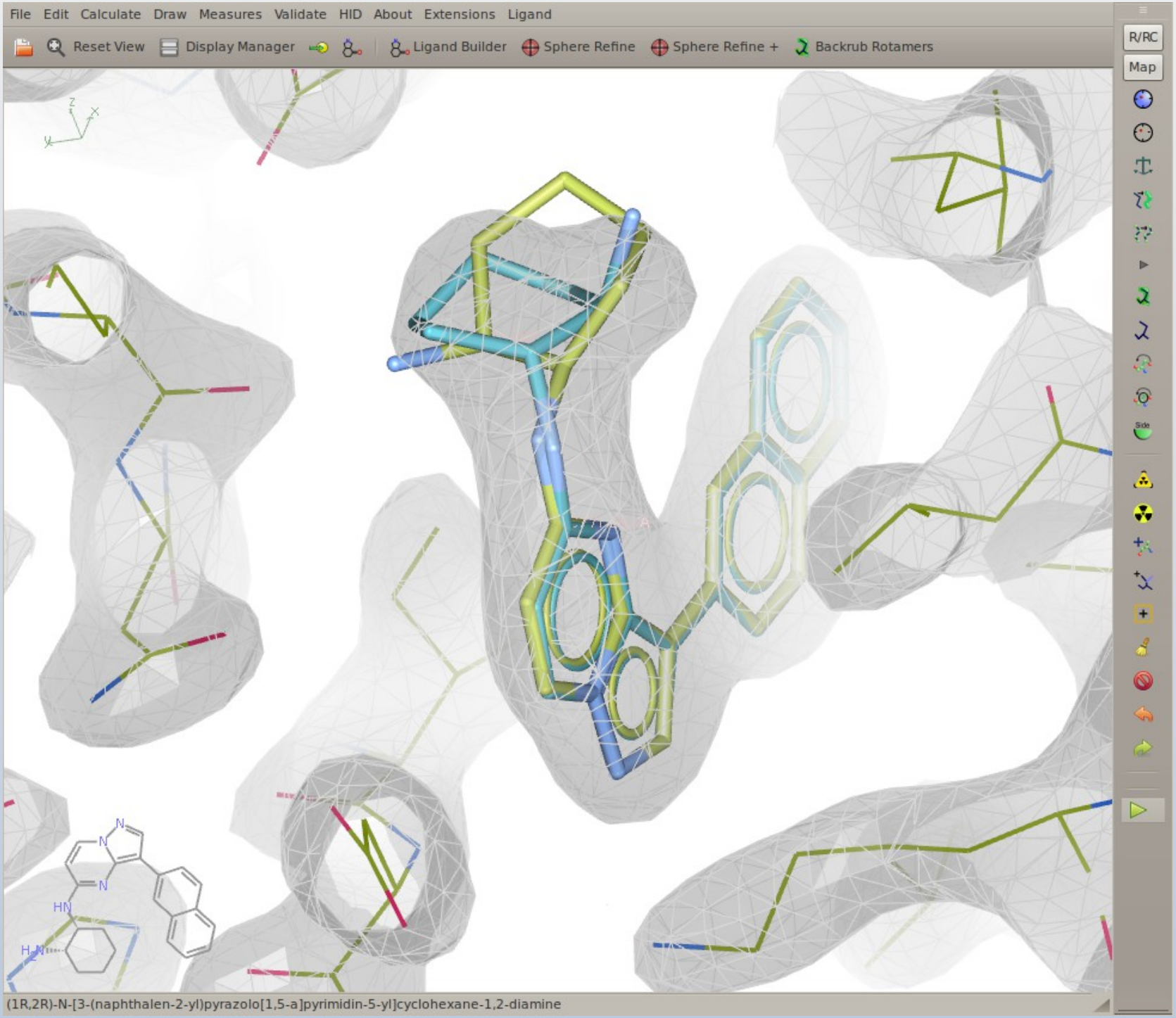
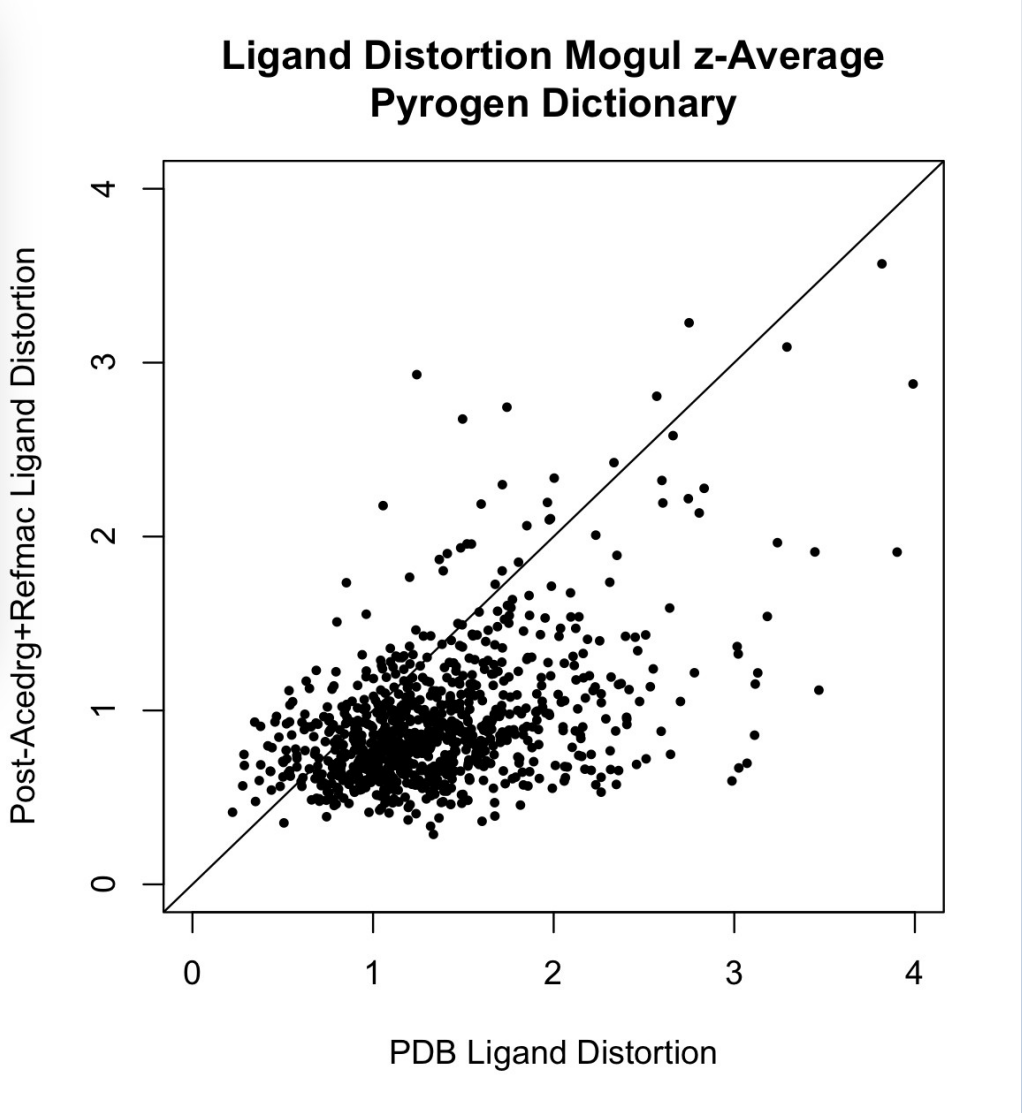
Map
(1R,2R)-N-[3-(naphthalen-2-yl)pyrazolo[1,5-a]pyrimidin-5-yl]cyclohexane-1,2-diamine


File Edit Calculate Draw Measures Validate HID About Extensions Ligand
Reset View
Display Manager
Ligand Builder
Sphere Refine
Sphere Refine +
Backrub Rotamers
R/RC
Map
(1R,2R)-N-[3-(naphthalen-2-yl)pyrazolo[1,5-a]pyrimidin-5-yl]cyclohexane-1,2-diamine

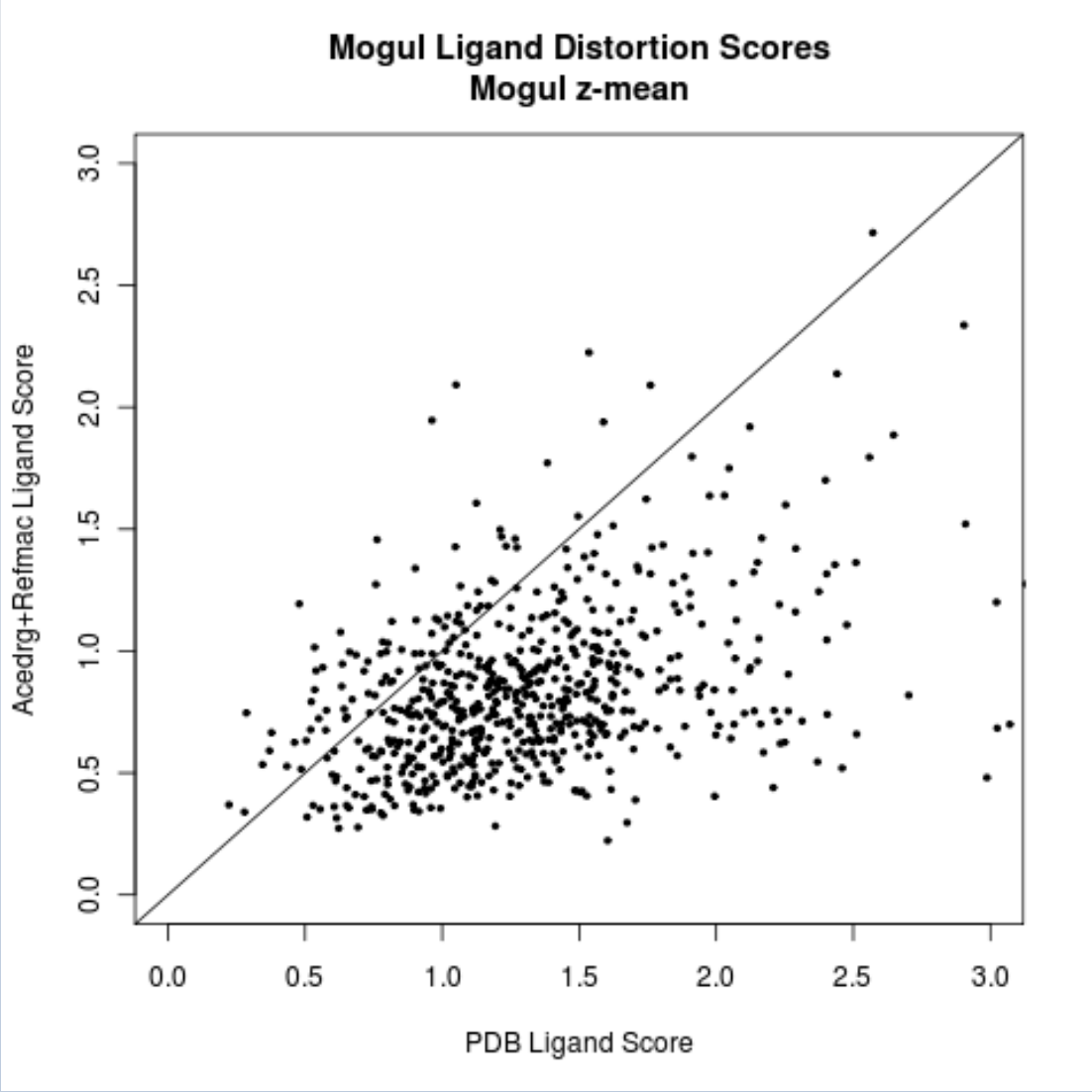

File Edit Calculate Draw Measures Validate HID About Extensions Ligand
Reset View
Display Manager
Ligand Builder
Sphere Refine
Sphere Refine +
Backrub Rotamers
R/RC
Map
Side
(1R,2R)-N-[3-(naphthalen-2-yl)pyrazolo[1,5-a]pyrimidin-5-yl]cyclohexane-1,2-diamine


File Edit Calculate Draw Measures Validate HID About Extensions Ligand
Reset View
Display Manager
Ligand Builder
Sphere Refine
Sphere Refine +
Backrub Rotamers
R/RC
Map
(1R,2R)-N-[3-(naphthalen-2-yl)pyrazolo[1,5-a]pyrimidin-5-yl]cyclohexane-1,2-diamine

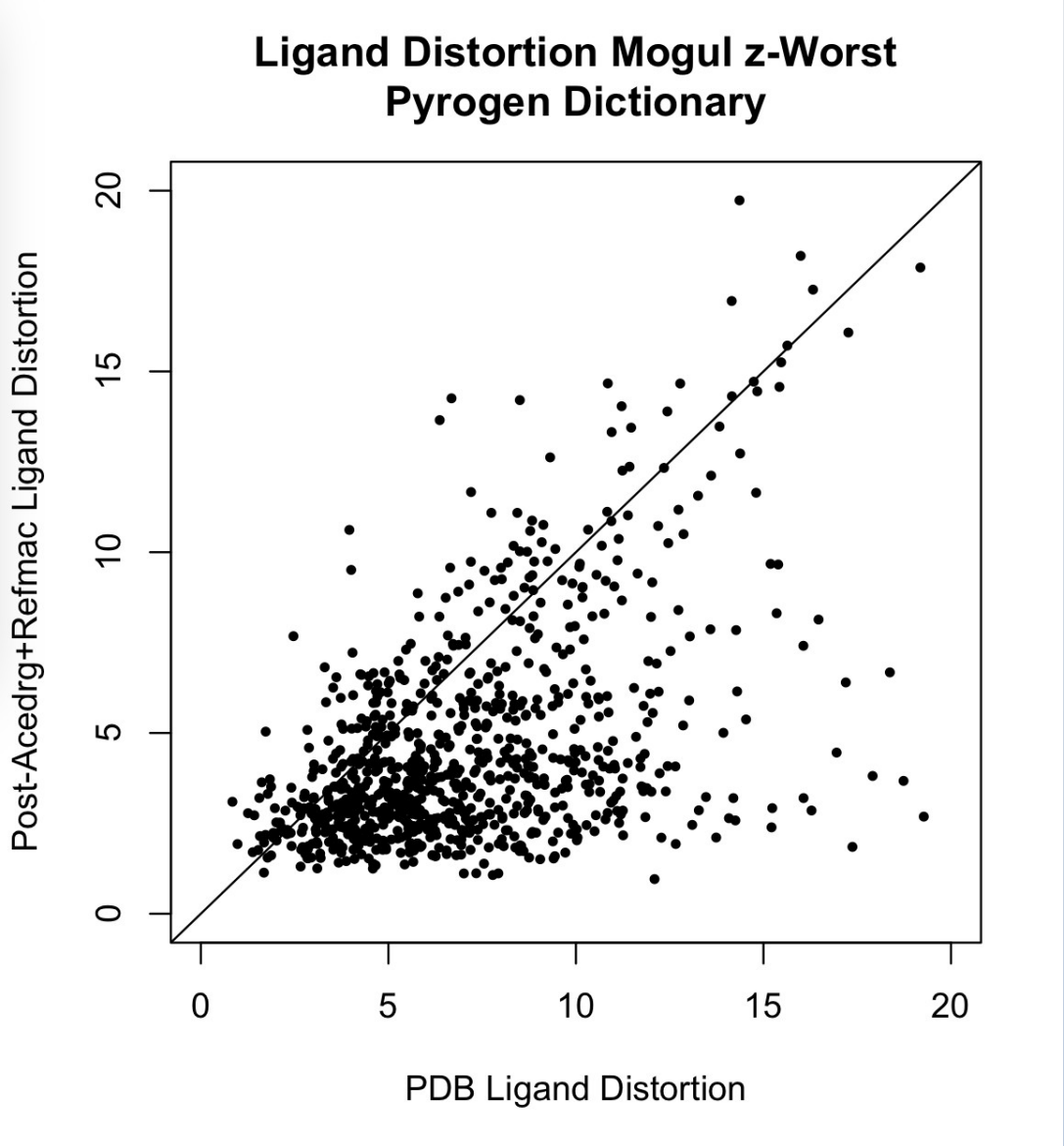
# Ligand Distortion: Pyrogen Scoring vs. Mogul Average z



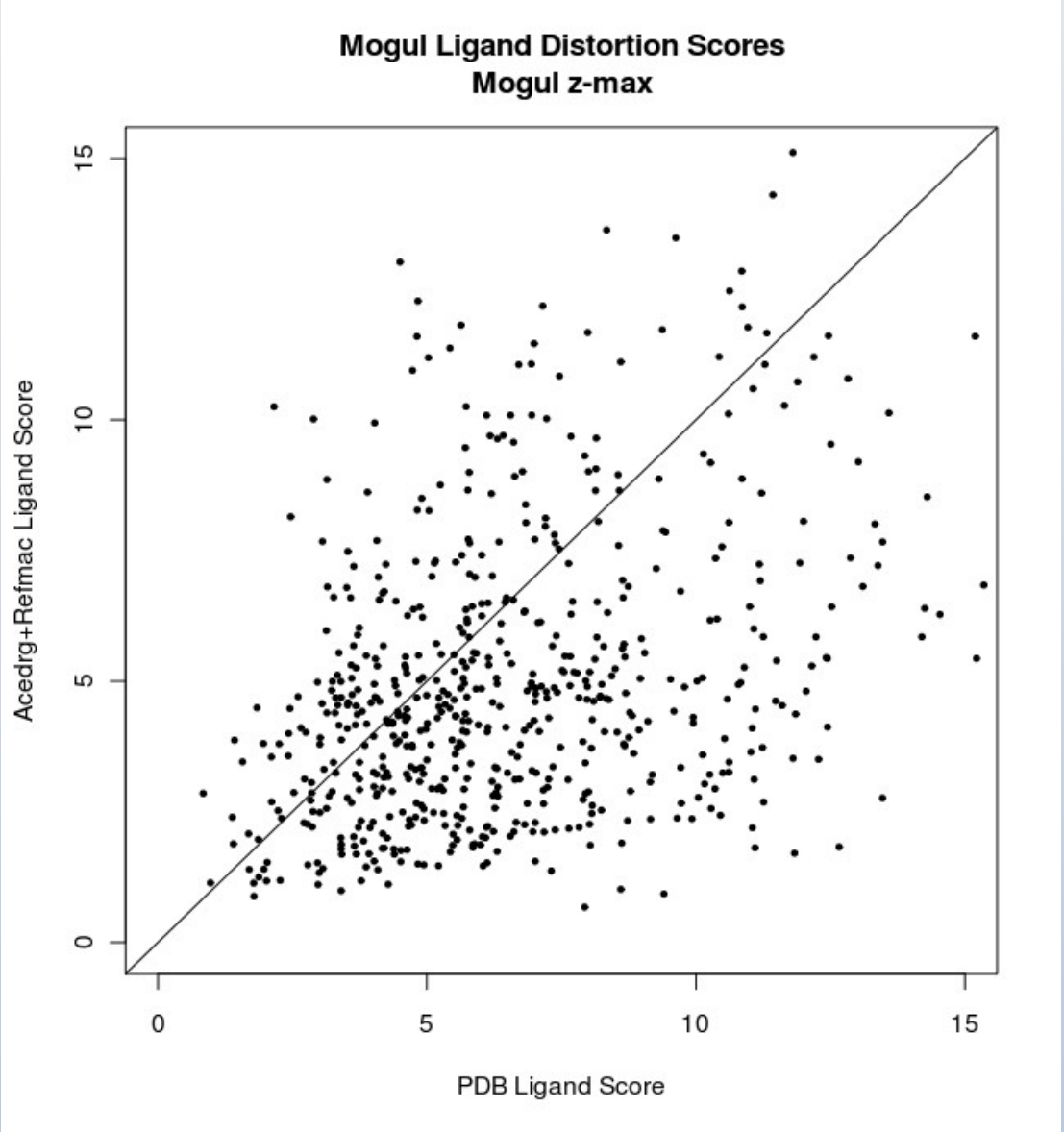
# Ligand Distortion: Acedrg Scoring vs. Mogul Average z

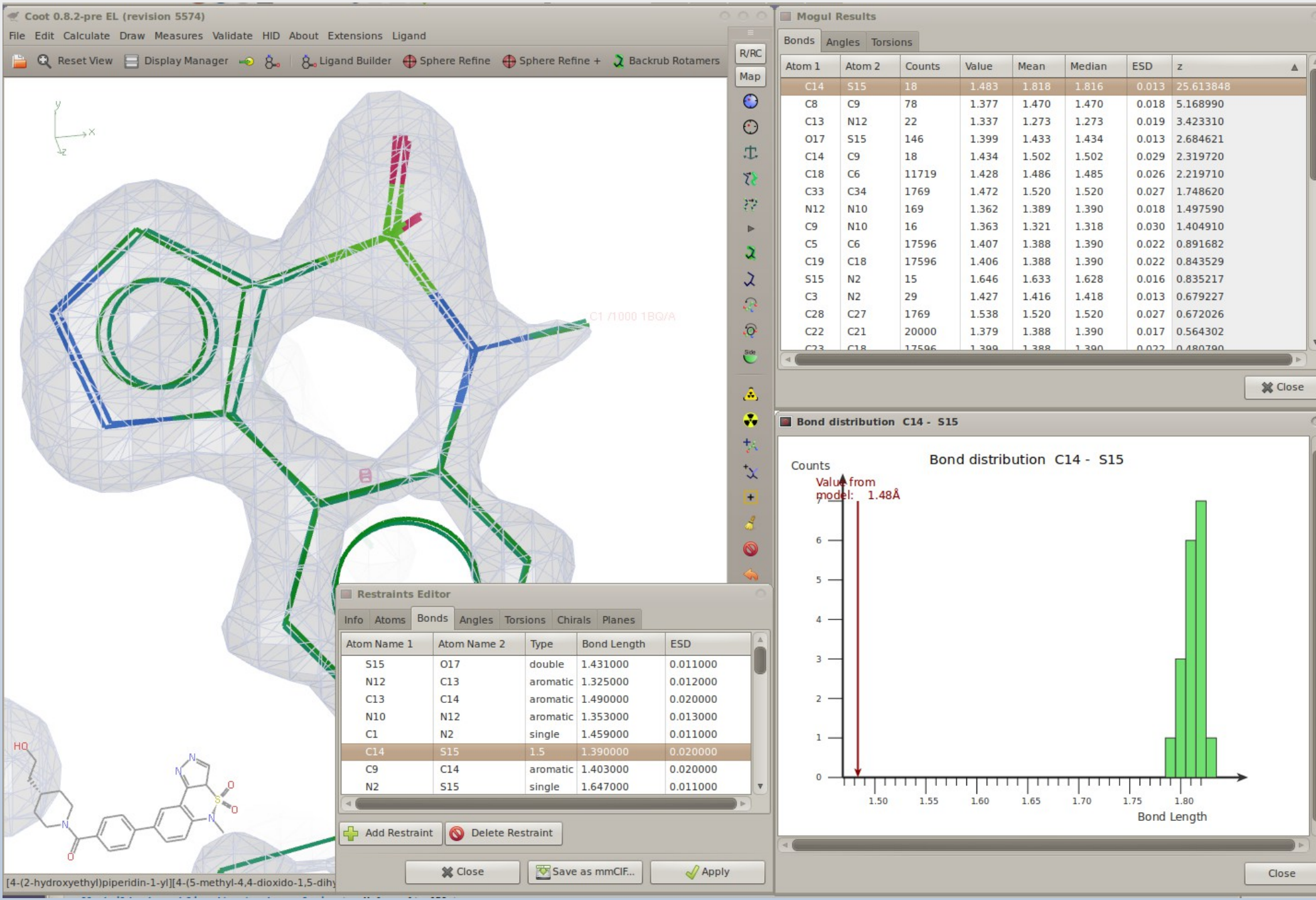


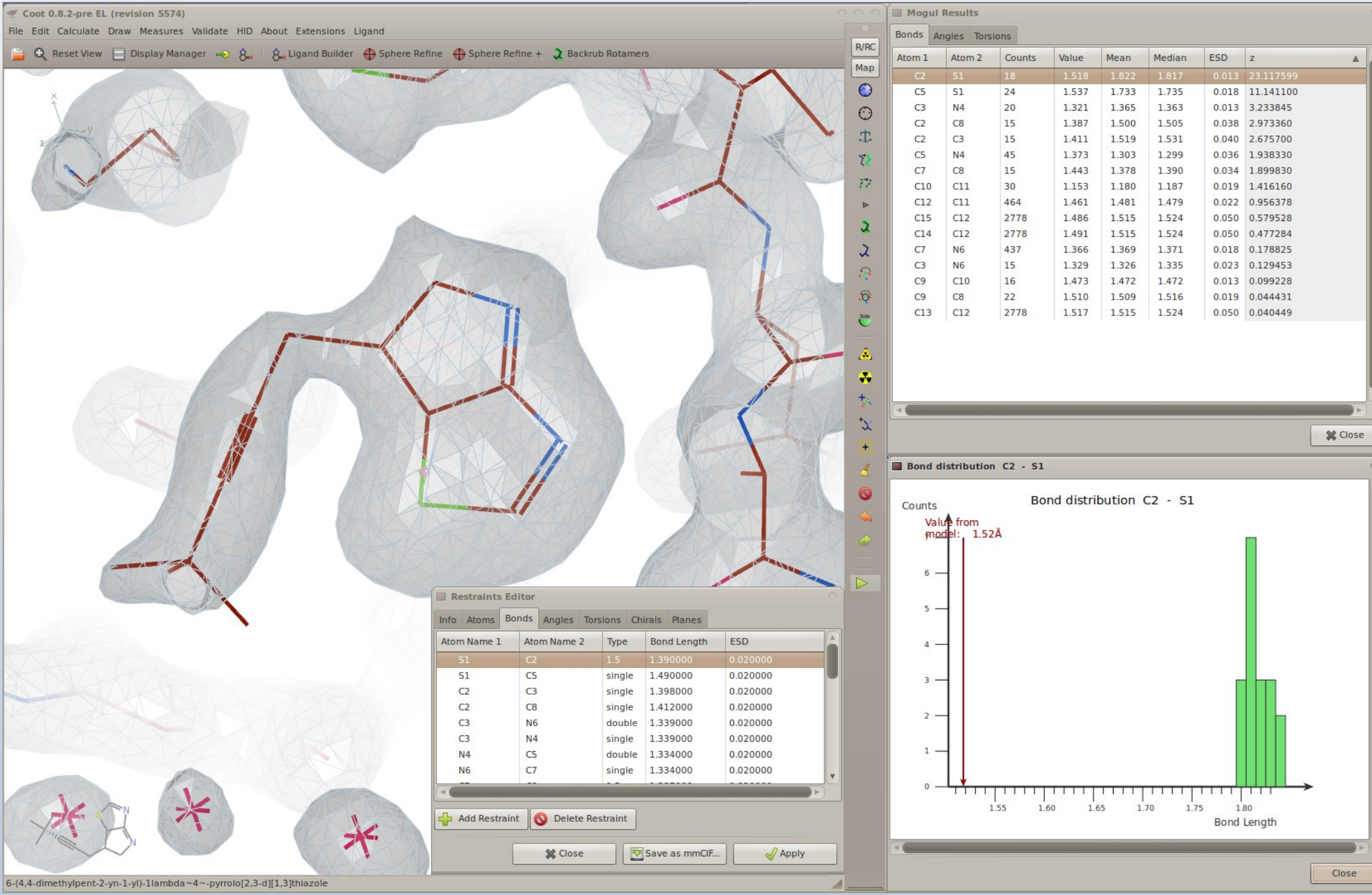
# Ligand Distortion: Pyrogen: Scoring Mogul z-worst



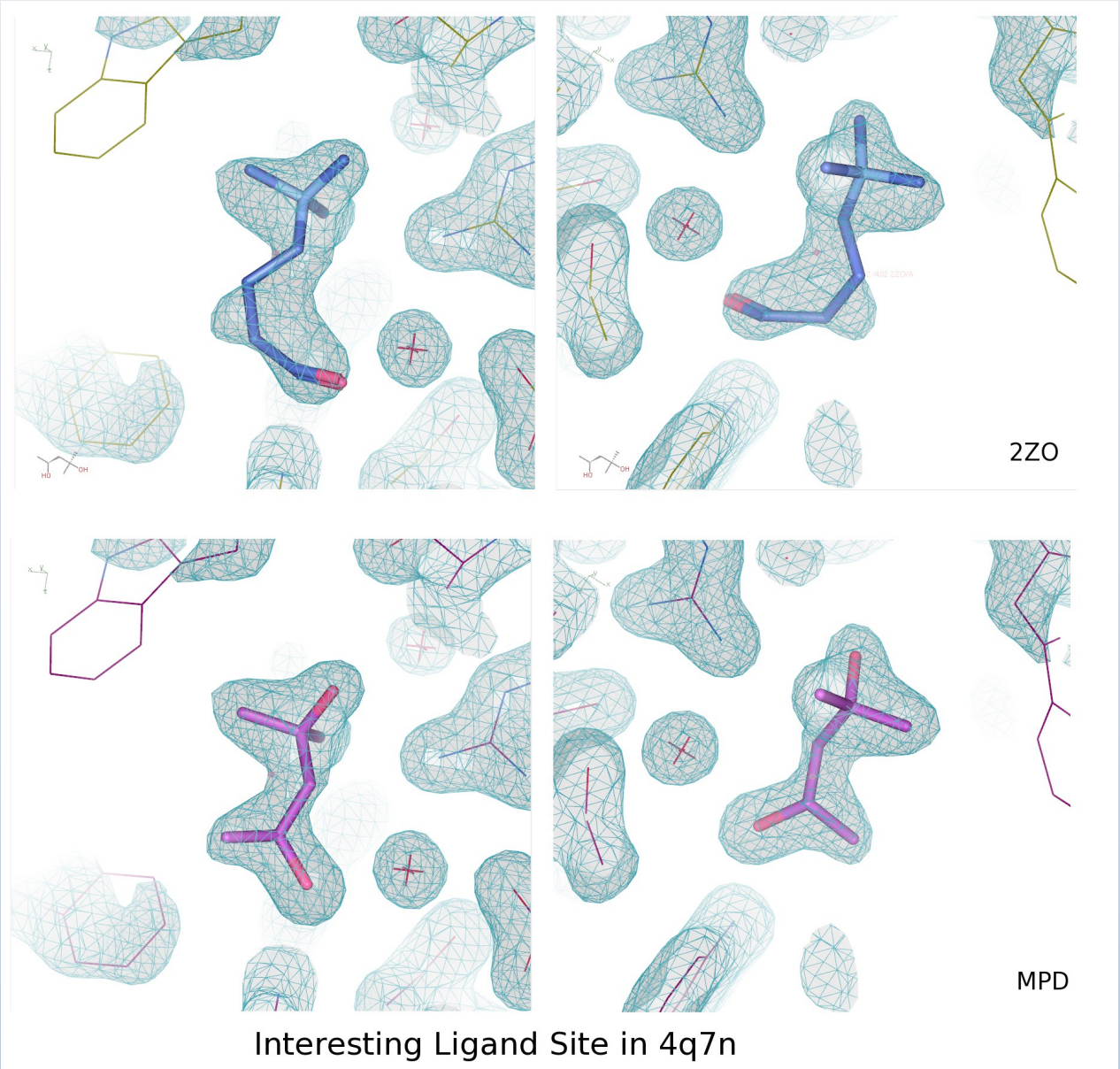
# Ligand Distortion: Acedrg: Scoring Mogul z-worst




Coot 0.8.2-pre EL (revision 5574)
File Edit Calculate Draw Measures Validate HID About Extensions Ligand
Reset View
Display Manager
Ligand Builder
Sphere Refine
Sphere Refine +
Backrub Rotamers
R/RC
Map
C1 /1000 1BQ/A
Mogul Results
Bonds
Angles
Torsions
Atom 1 Atom 2 Counts Value Mean Median ESD z
C14 S15 18 1.483 1.818 1.816 0.013 25.613848
C8 C9 78 1.377 1.470 1.470 0.018 5.168990
C13 N12 22 1.337 1.273 1.273 0.019 3.423310
O17 S15 146 1.399 1.433 1.434 0.013 2.684621
C14 C9 18 1.434 1.502 1.502 0.029 2.319720
C18 C6 11719 1.428 1.486 1.485 0.026 2.219710
C33 C34 1769 1.472 1.520 1.520 0.027 1.748620
N12 N10 169 1.362 1.389 1.390 0.018 1.497590
C9 N10 16 1.363 1.321 1.318 0.030 1.404910
C5 C6 17596 1.407 1.388 1.390 0.022 0.891682
C19 C18 17596 1.406 1.388 1.390 0.022 0.843529
S15 N2 15 1.646 1.633 1.628 0.016 0.835217
C3 N2 29 1.427 1.416 1.418 0.013 0.679227
C28 C27 1769 1.538 1.520 1.520 0.027 0.672026
C22 C21 20000 1.379 1.388 1.390 0.017 0.564302
Close
Bond distribution C14 - S15
Bond distribution C14 - S15
Counts
Value from model: 1.48Å
0 1 2 3 4 5 6
1.50 1.55 1.60 1.65 1.70 1.75 1.80
Bond Length
Close
Restraints Editor
Info
Atoms
Bonds
Angles
Torsions
Chirals
Planes
Atom Name 1 Atom Name 2 Type Bond Length ESD
S15 O17 double 1.431000 0.011000
N12 C13 aromatic 1.325000 0.012000
C13 C14 aromatic 1.490000 0.020000
N10 N12 aromatic 1.353000 0.013000
C1 N2 single 1.459000 0.011000
C14 S15 1.5 1.390000 0.020000
C9 C14 aromatic 1.403000 0.020000
N2 S15 single 1.647000 0.011000
Add Restraint
Delete Restraint
Close
Save as mmCIF...
Apply
[4-(2-hydroxyethyl)piperidin-1-yl][4-(5-methyl-4,4-dioxido-1,5-dihy


Coot 0.8.2-pre EL (revision 5574)
File Edit Calculate Draw Measures Validate HID About Extensions Ligand
Reset View
Display Manager
Ligand Builder
Sphere Refine
Sphere Refine +
Backrub Rotamers
R/RC
Map
Restraints Editor
Info Atoms Bonds Angles Torsions Chirals Planes
Atom Name 1 Atom Name 2 Type Bond Length ESD
S1 C2 1.5 1.390000 0.020000
S1 C5 single 1.490000 0.020000
C2 C3 single 1.398000 0.020000
C2 C8 single 1.412000 0.020000
C3 N6 double 1.339000 0.020000
C3 N4 single 1.339000 0.020000
N4 C5 double 1.334000 0.020000
N6 C7 single 1.334000 0.020000
Add Restraint
Delete Restraint
Close
Save as mmCIF...
Apply
6-(4,4-dimethylpent-2-yn-1-yl)-1lambda~4~-pyrrolo[2,3-d][1,3]thiazole
Mogul Results
Bonds Angles Torsions
Atom 1 Atom 2 Counts Value Mean Median ESD z
C2 S1 18 1.518 1.822 1.817 0.013 23.117599
C5 S1 24 1.537 1.733 1.735 0.018 11.141100
C3 N4 20 1.321 1.365 1.363 0.013 3.233845
C2 C8 15 1.387 1.500 1.505 0.038 2.973360
C2 C3 15 1.411 1.519 1.531 0.040 2.675700
C5 N4 45 1.373 1.303 1.299 0.036 1.938330
C7 C8 15 1.443 1.378 1.390 0.034 1.899830
C10 C11 30 1.153 1.180 1.187 0.019 1.416160
C12 C11 464 1.461 1.481 1.479 0.022 0.956378
C15 C12 2778 1.486 1.515 1.524 0.050 0.579528
C14 C12 2778 1.491 1.515 1.524 0.050 0.477284
C7 N6 437 1.366 1.369 1.371 0.018 0.178825
C3 N6 15 1.329 1.326 1.335 0.023 0.129453
C9 C10 16 1.473 1.472 1.472 0.013 0.099228
C9 C8 22 1.510 1.509 1.516 0.019 0.044431
C13 C12 2778 1.517 1.515 1.524 0.050 0.040449
Close
Bond distribution C2 - S1
Bond distribution C2 - S1
Counts
Value from model: 1.52Å
0 1 2 3 4 5 6
1.55 1.60 1.65 1.70 1.75 1.80
Bond Length
Close

# “What's my blob?”




Interesting Ligand Site in 4q7n

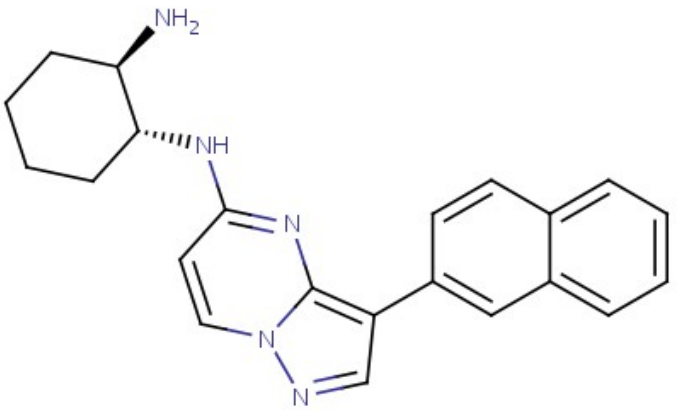
# ValidatorDB: database of up-to-date validation results for ligands and non-standard residues from the PDB

David Sehnal, Radka Svobodová, Vařeková, Lukáš Pravda, Crina-Maria Ionescu, Stanislav Geidl, Vladimír Horský, Deepti Jaiswal, Michaela Wimmerová, and Jaroslav Koča

Nucleic Acids Research, 2014

doi: 10.1093/nar/gku1118

# 26L



# ValidatorDB: database of ligand validations

- Didn't cite Read *et al.* (Validation Task Force), or Twilight Weichenberger, Pozharski & Rupp (2014)
  - No interest in electron density
  - Report on annotation errors
  - Missing atoms and rings
  - “Degenerate motif” (long bonds)
  - Report on chiralities
  - “It's hard to evaluate which molecules are correct” using conventional methods (bonds, angles, planes, *etc.*) so they don't try

# ValidatorDB: Developments Described

- Software to generate reference chiralities from _chem_atom records in the Chemical Components Dictionary
- Software to match wwPDB files to reference chiralities
- A database of these chiralities
- A web-site that accesses this database

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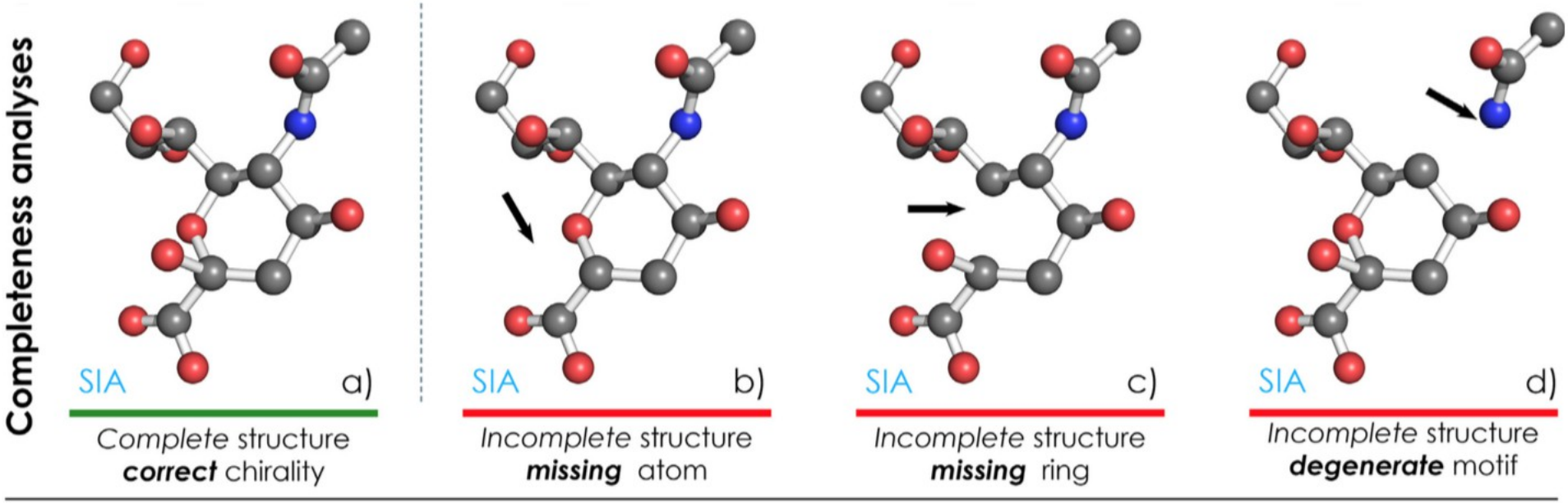
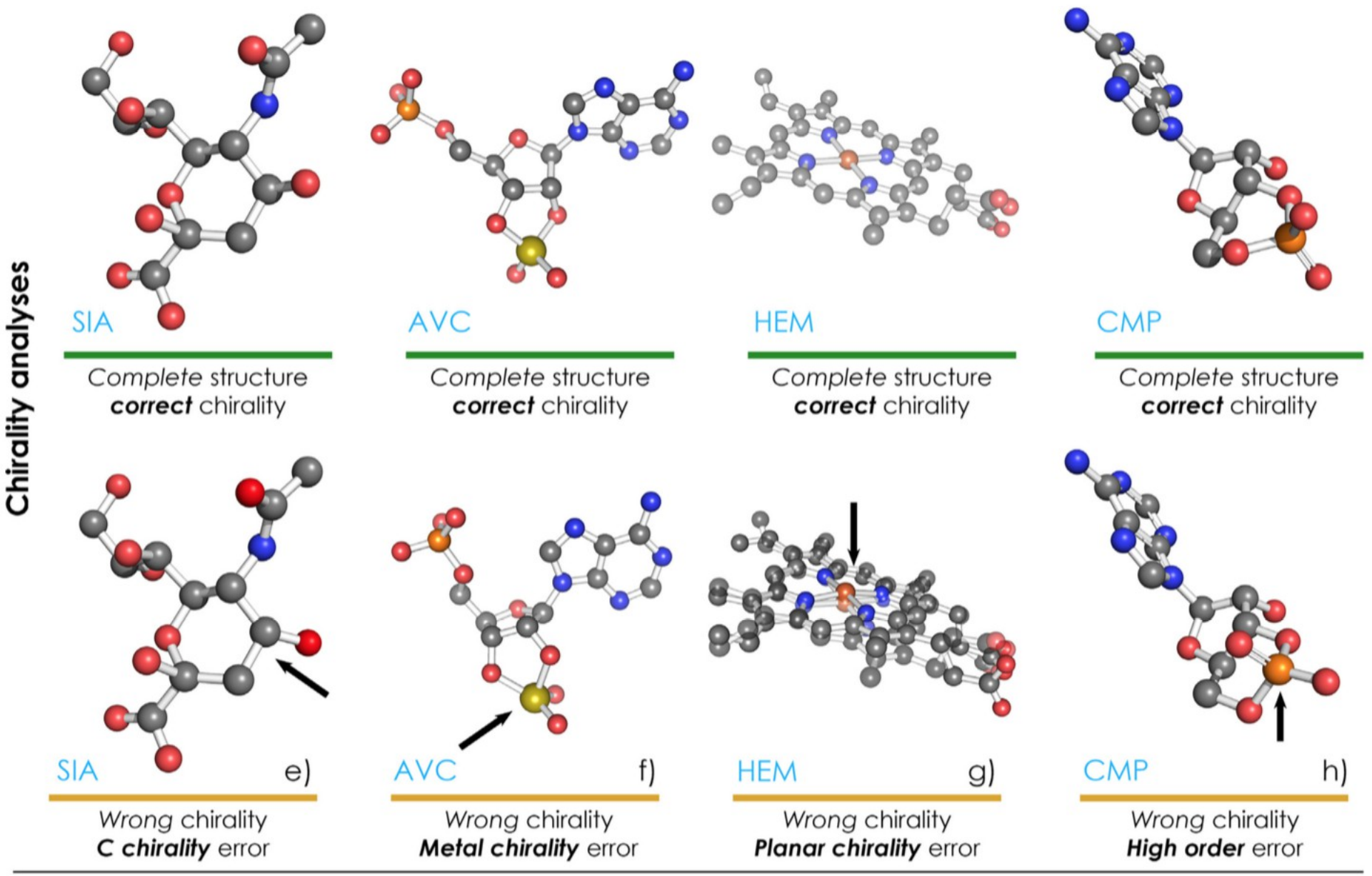
# ValidatorDB: Example Validations




| | | | |
|---|---|---|---|
| Coot Ligand Test: | Fail | Fail | Pass |

# ValidatorDB: Example Validations



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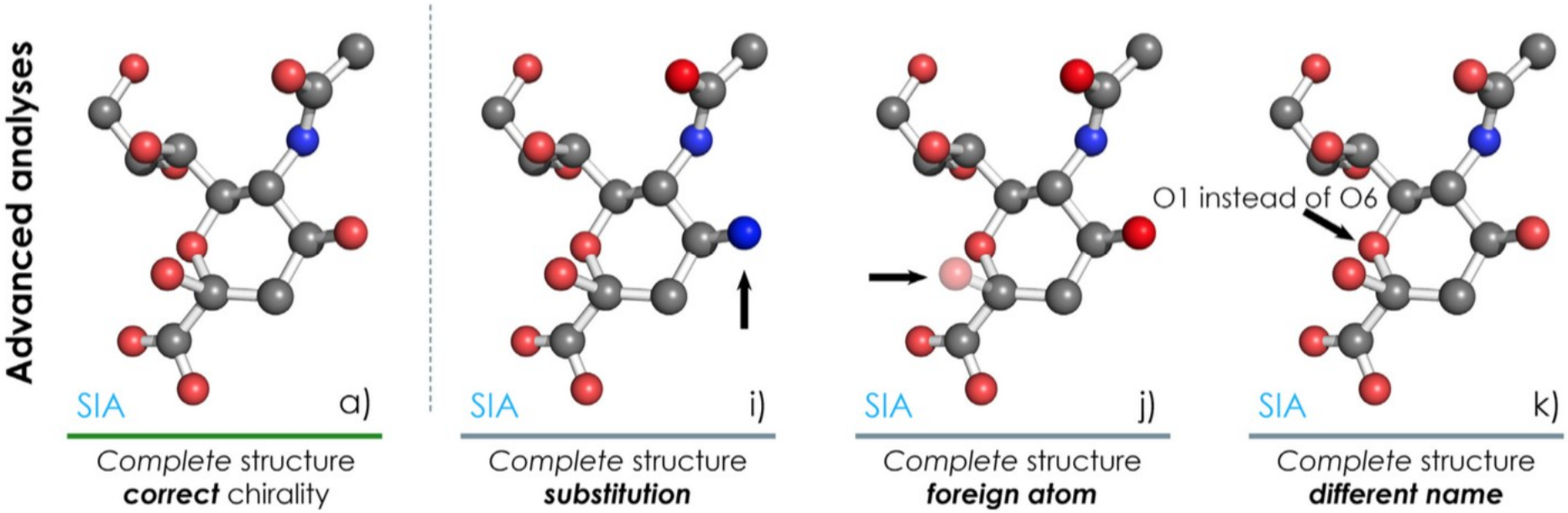
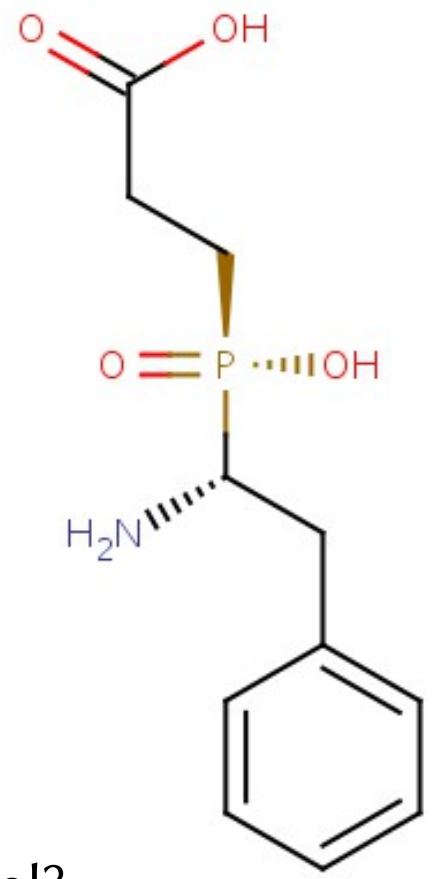



| | | | |
|---|---|---|---|
| Coot Ligand Test: | Fail | Fail | Fail |

# ValidatorDB: Issues

Comp-id: 00H




Is the P atom chiral?

Note to self: What do Acedrg and Pyrogen say?

# ValidatorDB: Issues

| | Completeness analyses | | Chirality analyses | | Advanced analyses | |
|---|---|---|---|---|---|---|
| **Wrong structures** | Incomplete | 8.9 % | Wrong chirality | 7.9 % | - | |
| **Issues found during individual analyses** | Missing only atoms | 5.9 % | Wrong C chirality | 2.4 % | Atom substitution | 20.7 % |
| | Missing rings | 2.6 % | Wrong Metal chirality | 1.4 % | Foreign atom | 34.8 % |
| | Degenerate | 0.5 % | Wrong High order chirality | 4.3 % | Different atom naming | 38.2 % |
| | | | Wrong Planar chirality | 1.1 % | Alternate conformations | 2.4 % |
| **No significant issues** | **Complete** | 91.1 % | **Complete + Correct chirality** | 83.0 % | **Complete + Correct chirality + no Atom substitutions + no Foreign atoms** | 48.0% |
| | | | **Complete + Correct chirality (tolerant)** | 88.3 % | **Complete + Correct chirality (tolerant) + no Atom substitutions + no Foreign atoms** | 53.2% |

# ValidatorDB: database of ligand validations

"It is necessary to ensure that the model serving as reference during validation is indeed correct. This limitation is overcome by using high-quality structures from wwPDB CCD."

- Ligand superposition is sometime compromised as they can't rotate about unexpectedly long bonds and organometallic cages

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# ValidatorDB: database of ligand validations

“Organometals seem to have overall lower quality. Part of the errors is artifacts of our validation algorithm [...]. However, the majority of the reported errors are significant, proving that many challenges remain in the field of structure determination for organometals.

“On the other hand, the overall quality of the structure of experimental drugs is clearly much higher than the PDB-wide statistics for all ligands and non-standard residues.”

# ValidatorDB: What Does it Mean for Us?

- Not much at present
- High-order chirality was previously unknown to me
  - I will add it at some stage
  - Not urgent
  - Because these are organometallic compounds
  - Maybe chiralities could be added to CCP4 SRS?
- Other tests are covered in Coot,
  - but the reporting of the error type leaves something to be desired in comparison
- To the user, it's a web-site not a database
  - CCP4 is more interested in software that we can either use on the CCP4 web server or distribute with the suite

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