Refinement:
The BUSTER perspective

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Global Phasing Ltd.

DLS/CCP4 2021

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Quality of final (complex) structure depends on:

- Good **crystals** (co-crystallisation or soaking)
- Well designed **data collection**
- Correct **data processing**

- Careful **refinement** of (initial) protein model
- Assessment of ligand density: "***Is there any ligand bound?***"

- Ligand/cofactor **restraints-dictionary** based on correct chemistry
- Correct **fit** of ligand to density
- Final **refinement** of ligand-protein complex

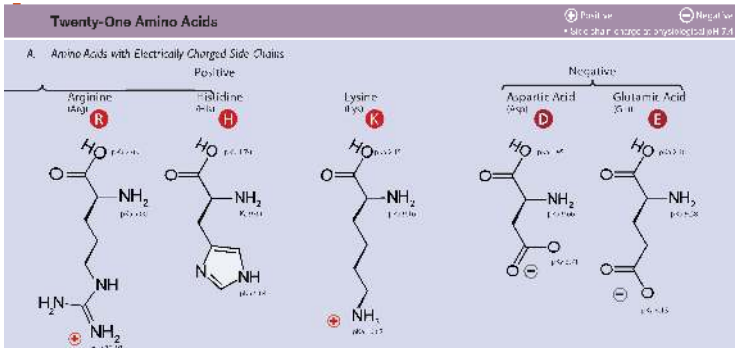
- **A mistake in any one of these can lead to poor ligand-protein complex structures**

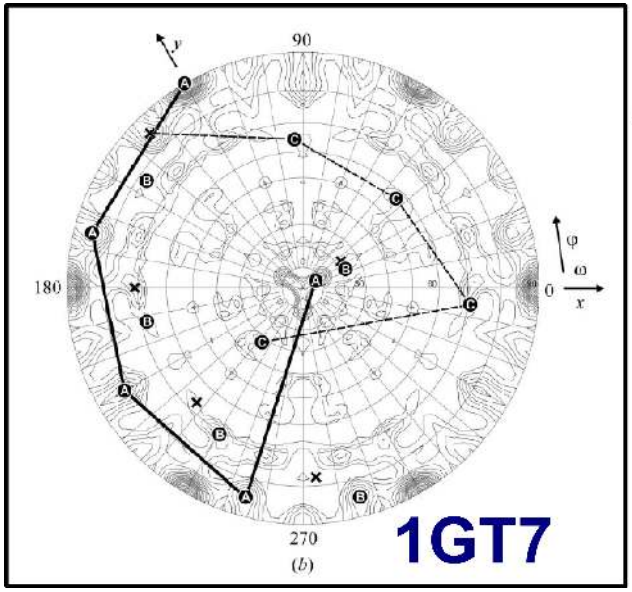
All steps need to be done (in fully automated mode**) for large number of structures**

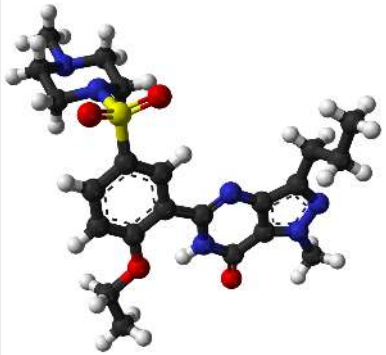
⇨ **We need validation at every step along the way.**

Refinement

- Combines prior knowledge and observed (X-Ray) data
- Chemistry (bonds, angles, ...)
  - Protein (Engh & Huber)
  - Compound/Ligand
  - ...
- Similarity
  - Within the crystal (NCS)
  - To other structures ("targeting")
- Occupancy, disorder (alternate conformations), ...

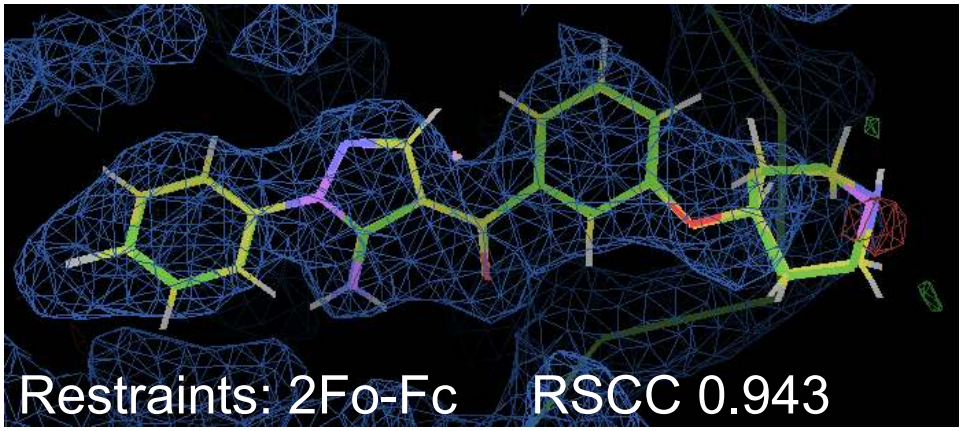






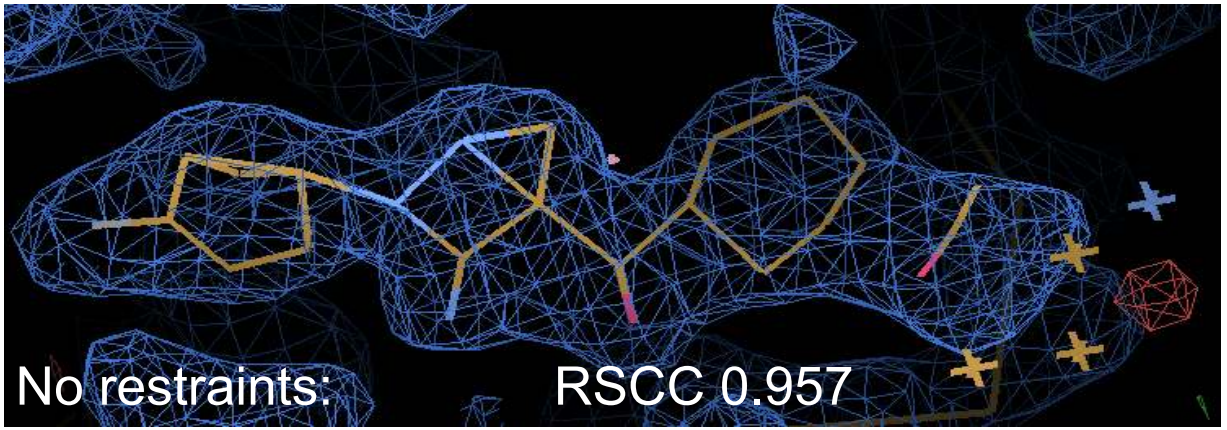
Prior knowledge is essential

2bal kinase 2.1Å resolution.



RSCC is a poor validation criteria here: it tells us that ligand model and map agree, but not if we have a good ligand model that also follows prior chemical knowledge

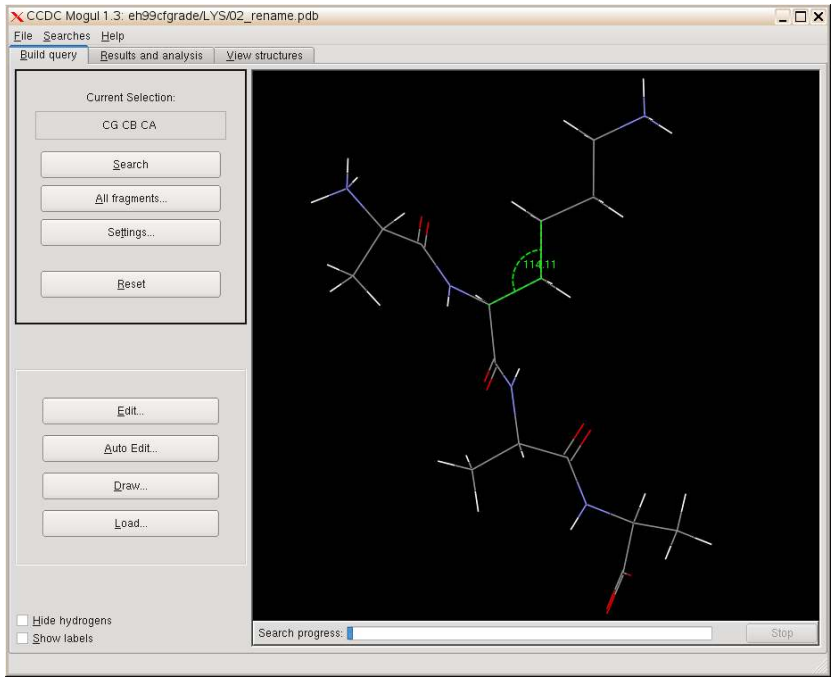
→ pick your quality criteria carefully!

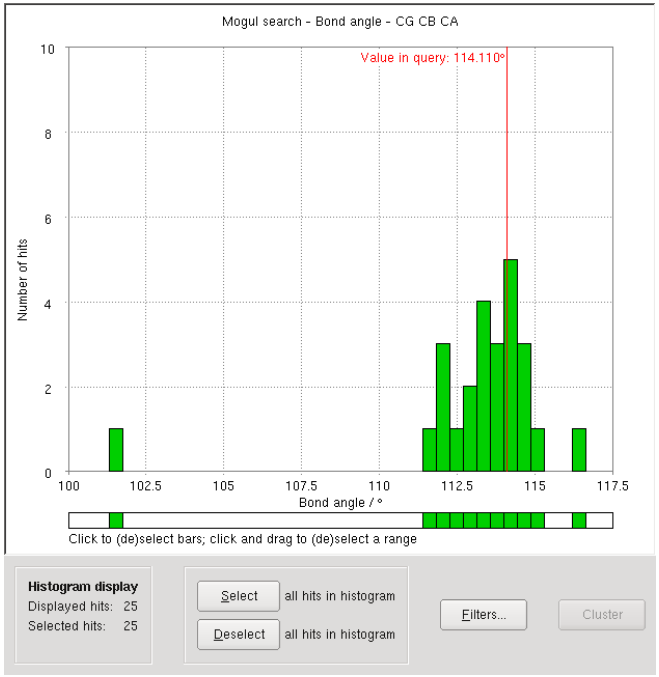


RSCC = real-space correlation coefficient

Grade (2011): ligand dictionaries based on CSD

- Use CCDC **mogul** program to survey **CSD**





- Use CSD as **source of information for restraints** (not only in validation)
- Also: AceDRG (Long et al, 2017: COD), eLBOW (Moriarty et al, 2011: CSD)

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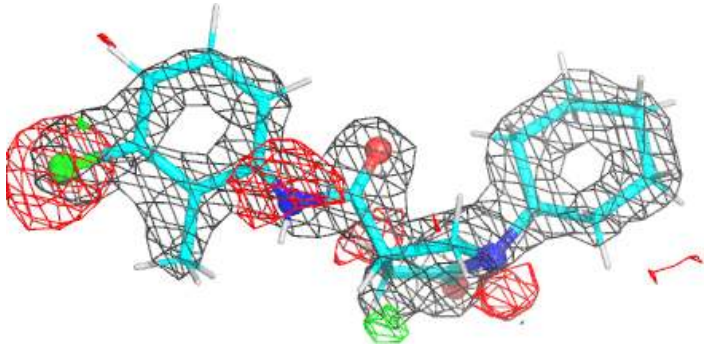
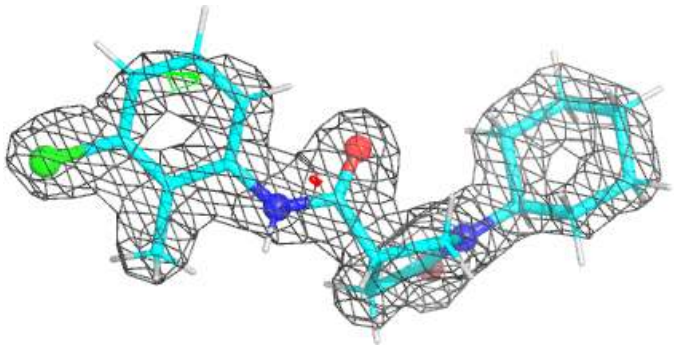
Grade: ligand dictionaries based on CSD

- Dictionaries based on
  - Cambridge Structural Database (CSD) = small molecule crystal structures
  - QM

http://grade.globalphasing.org/



2h7p (residue 468)



After BUSTER refinement with grade dictionary

Grade2 (rewrite, 20210716 release):
https://www.globalphasing.com/buster/manual/grade2/manual/

Reporting

CellPress

Structure
Meeting Report

Outcome of the First wwPDB/CCDC/D3R Ligand Validation Workshop

Paul D. Adams,[1] Kathleen Aertgeerts,[2] Cary Bauer,[3] Jeffrey A. Bell,[4] Helen M. Berman,[5,6] Talapady N. Bhat,[7] Jeff M. Blaney,[8] Evan Bolton,[9] Gerard Bricogne,[10] David Brown,[11,12] Stephen K. Burley,[5,6,13,*] David A. Case,[6] Kirk L. Clark,[14] Tom Darden,[15] Paul Emsley,[16] Victoria A. Feher,[17,*] Zukang Feng,[5,6] Colin R. Groom,[18,*] Seth F. Harris,[8] Jorg Hendle,[19] Thomas Holder,[4] Andrzej Joachimiak,[20] Gerard J. Kleywegt,[21]

502 Structure *24*, April 5, 2016 ©2016 Elsevier Ltd All rights reserved

Figure

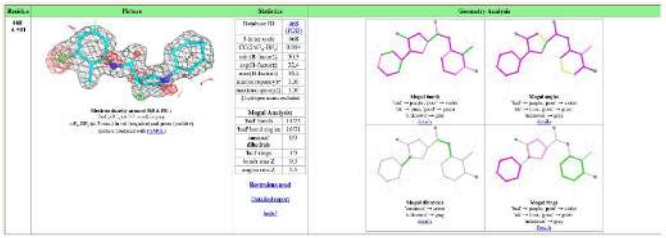


Figure 1. Example highlighting the value of presenting ligand electron density model fit and geometrical analysis from CCDC Mogul from the Global Phasing Buster Report (PDB ID: 2H7P, later superseded by entry 4TZT (He et al., 2006); CCD ID: 468).

- REMARK 3 header
- **buster-report** tool
- Part of BUSTER distribution

Reporting

July 2019: Buster-report now part of wwPDB validation suite

06/11/2019

Improvements to visualization of ligand validation and electron density maps in the wwPDB validation report

Our recent update to the wwPDB validation reports provides much clearer validation information for ligands.

We now include 2-dimensional diagrams of ligands, highlighting geometric validation criteria and, for structures determined by crystallography, 3-dimensional views of electron density.

We also provide calculated electron density map coefficients which were used to generate the analysis in the validation reports.

Ligand Validation

We have collaborated with **Global Phasing Ltd** to integrate the ligand visualization from **buster-report** into the wwPDB validation report, as recommended by the **wwPDB/CCDC/D3R Ligand Validation Workshop**. The ligand visualization will be available for ligands that have been designated as "Ligand of Interest" by the depositor and ligands with a molecular weight greater than 250 Daltons that have outliers.

The following ligand instance of NAP was chosen intentionally as a representative of sub-optimal quality in both the ligand model and its agreement with the X-ray data.

Geometric analysis provided by CCDC Mogul will be highlighted on a 2D diagram of the ligand, as shown below.

RCSB PDB News Image

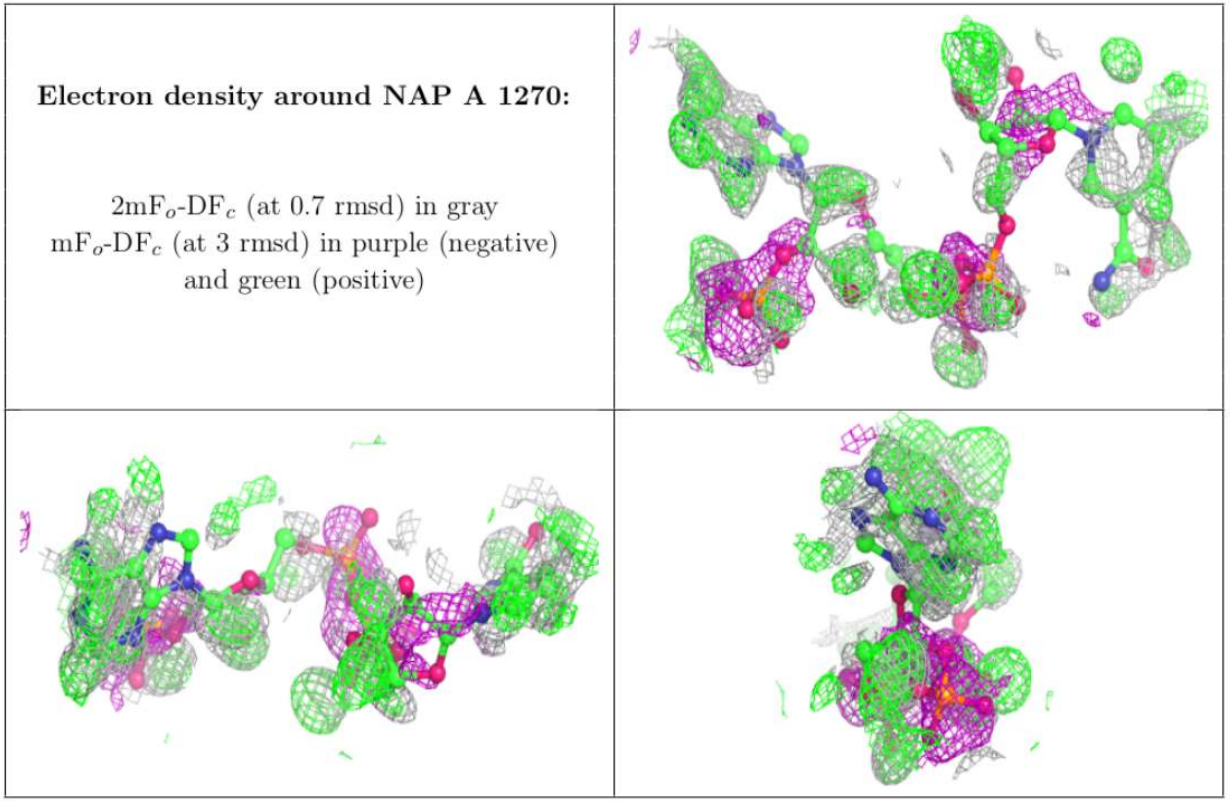
In addition to geometric validation for ligands, for X-ray diffraction PDB entries the wwPDB validation report also presents images displaying the ligand and the surrounding electron density map.

Reporting

WORLDWIDE PDB PROTEIN DATA BANK VALIDATION ▾ DEPOSITION ▾ DICTIONARIES ▾ DOCUMENTATION ▾ TASK FORCES ▾ FTP ▾ STATISTICS ▾ ABOUT ▾ wwPDB Foundation

Electron density around NAP A 1270:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Take care in restraint dictionary generation and in (over-)interpreting density features

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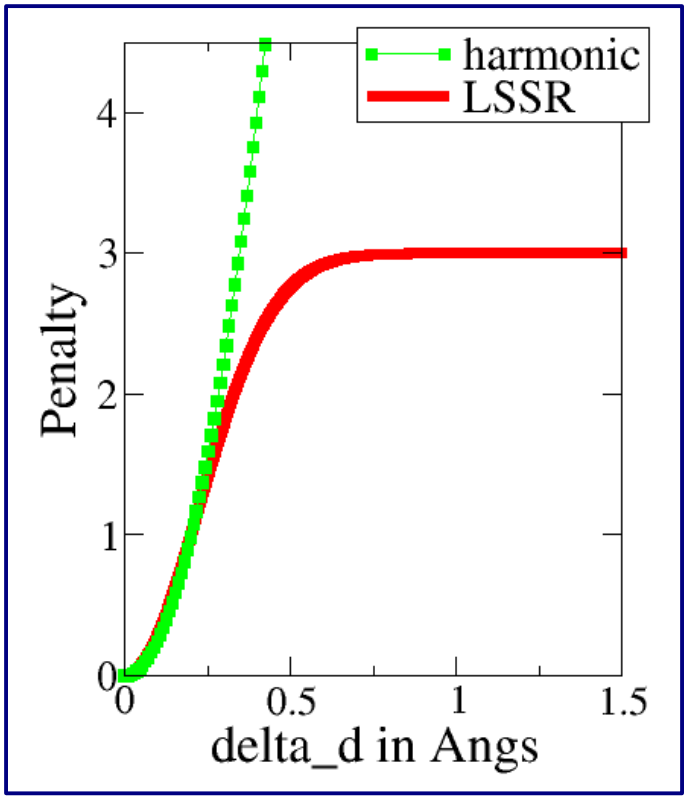
Local Structural Similarity Restraints (LSSR)

- Conventional superposition-based restraints are laborious to use.
- LSSR is a much easier to use approach to NCS restraints:
  - "involves" local contact distances
  - "softer" than superposition-based methods – violations entail only a fixed cost
- method in BUSTER fully automated (detection and application): ***-autoncs***
- ***Always use NCS restraints***



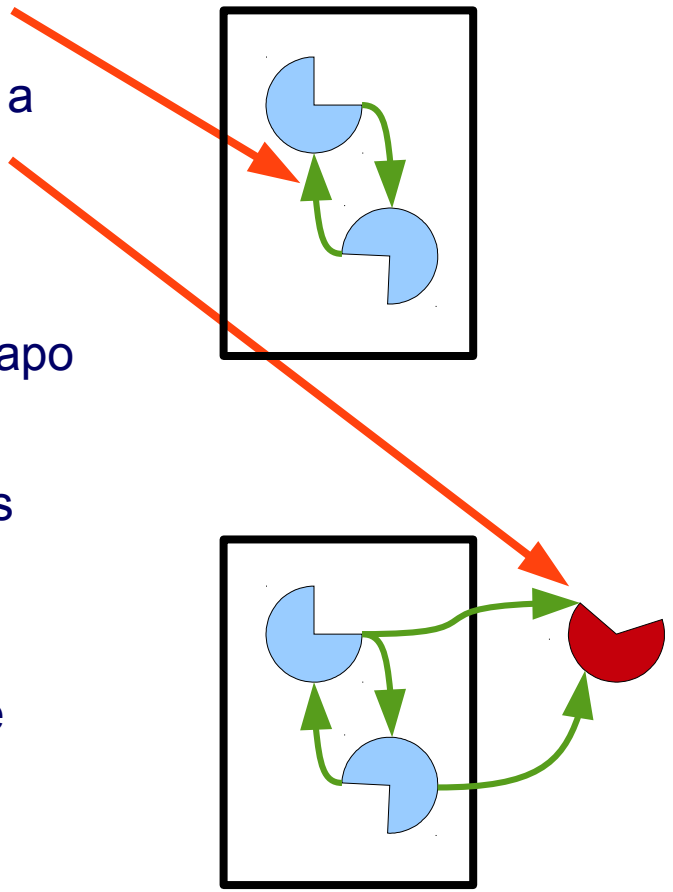
Smart et al (2008). Abstr. Annu. Meet. Am. Crystallogr. Assoc., Abstract TP139, p. 117.

Murshudov et al (2011). Acta D67, 355-367.

Smart et al (2012). Acta D68, 368-380

LSSR Target Restraints

- NCS restraints: between chains within the same model
- Often, the chain being refined is similar to a structure that has already been solved



- For example:
  - ligand complex with higher resolution apo
  - two crystal forms of the same protein
  - partial datasets from non-isomorphous crystals
  - following radiation damage
- The already solved structure becomes the "target"
- Apply LSSR restraints to the fixed target structure supplied as pdb file (**`-target some.pdb`**)

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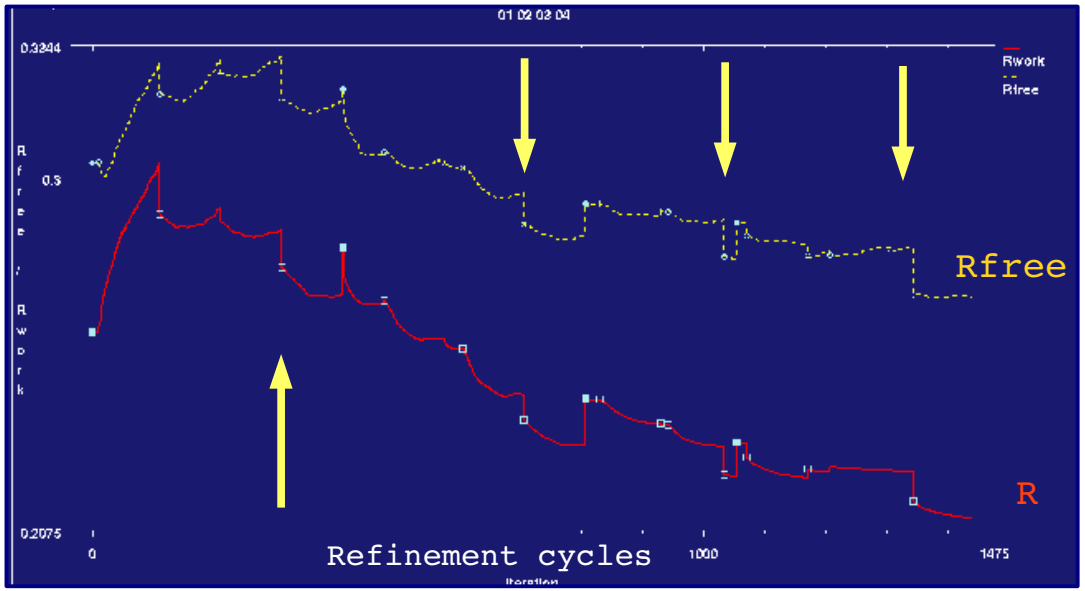
BUSTER - void correction

- Structures often have voids/cavities filled neither by ordered nor by disordered solvent
  - "filled" by vacuum
  - mask-based bulk solvent correction needs to take this into accout
- Before the last big cycle, BUSTER will try and detect such voids and exclude them automatically from the bulk solvent area

- This can often bring a 'jump' in R/Rfree at the last big cycle (switch off with `AnalyseVoids=no`)

- But main effect is to clean-up difference (mFo-DFc) map … especially if using usual rms-based cutoff to decide on significance of difference map

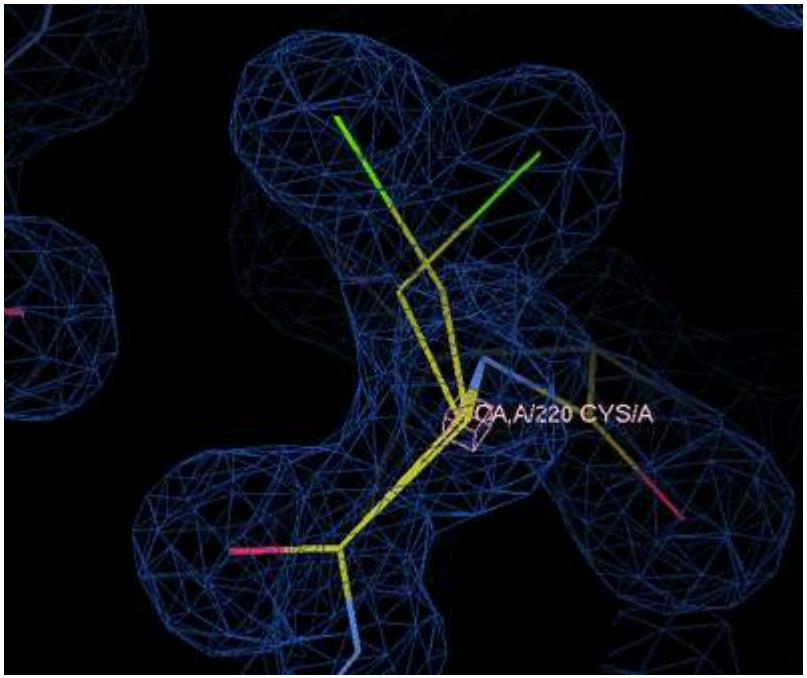


Alternate conformations

Alternate conformation

- Atoms with altConf “A” see atoms with no altConf or with altConf “A”
- Atoms with different altConf don’t see one another

- Set occupancies you want refined to something not equal to 1.0, and then run
  - **pdb2occ** -p model.pdb -o occ.gelly
  - **refine** -Gelly occ.gelly ...
- If occ(A)+occ(B)=1 in input, **pdb2occ** will restrain occupancy sum (to 1)



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Additional restraints

- **E.g. using powerful and flexible utility restraints (Gelly) in BUSTER**
- **Example: $Mg^{2+}\cdot(H_2O)_6$**

Crystal structure of class I ligase ribozyme self-ligation product, in complex with U1A RBD

3HHN Display Files ▾ Download Files ▾ Download Citation ▾

DOI:10.2210/pdb3hhn/pdb **NDB ID:** PR0381

Primary Citation

Crystal structure of the catalytic core of an RNA-polymerase ribozyme.

Shechner, D.M., Grant, R.A., Bagby, S.C., Koldobskaya, Y., Piccirilli, J.A., Bartel, D.P.

Journal: (2009) Science **326:** 1271-1275

PubMed: 19965478
PubMedCentral: PMC3978776
DOI: 10.1126/science.1174676
Search Related Articles in PubMed

PubMed Abstract:

Primordial organisms of the putative RNA world would have required polymerase ribozymes able to replicate RNA. Known ribozymes with polymerase activity best approximating that needed for RNA replication contain at their catalytic core the class I RNA ligase, an artificial... [Read More & Search PubMed Abstracts]

Molecular Description Hide

Biological Assembly

3.0 Å

3D View: JSmol or PV More Images

Symmetry: **C2** view
Stoichiometry: **Homo 2-mer - A2**

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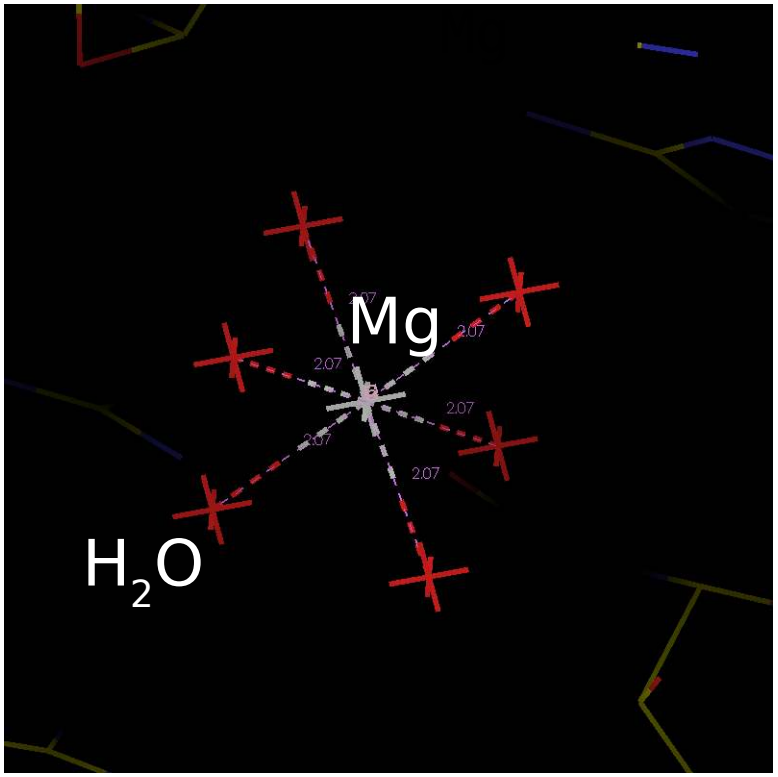
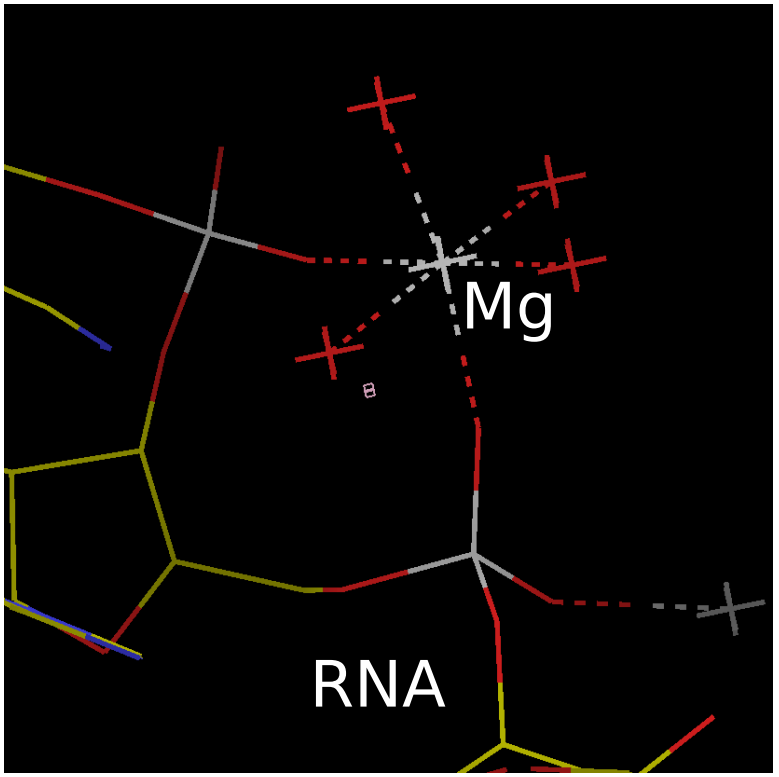
3HHN





Marcus (1988). Chem. Rev. 88, 1475.	2.09 Å ± 0.04
Ohtaki & Radnai (1993). Chem Rev 93, 1157-1204.	2.07 Å
Caminiti et al (1979). J Appl Crystallogr 12, 34-38.	2.11 Å

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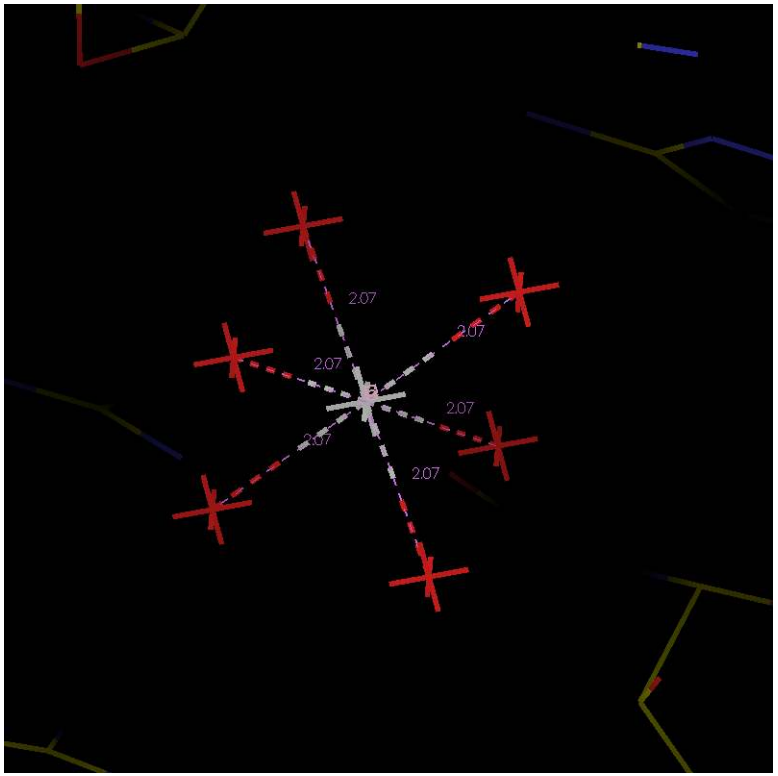
3HHN: BUSTER refinement



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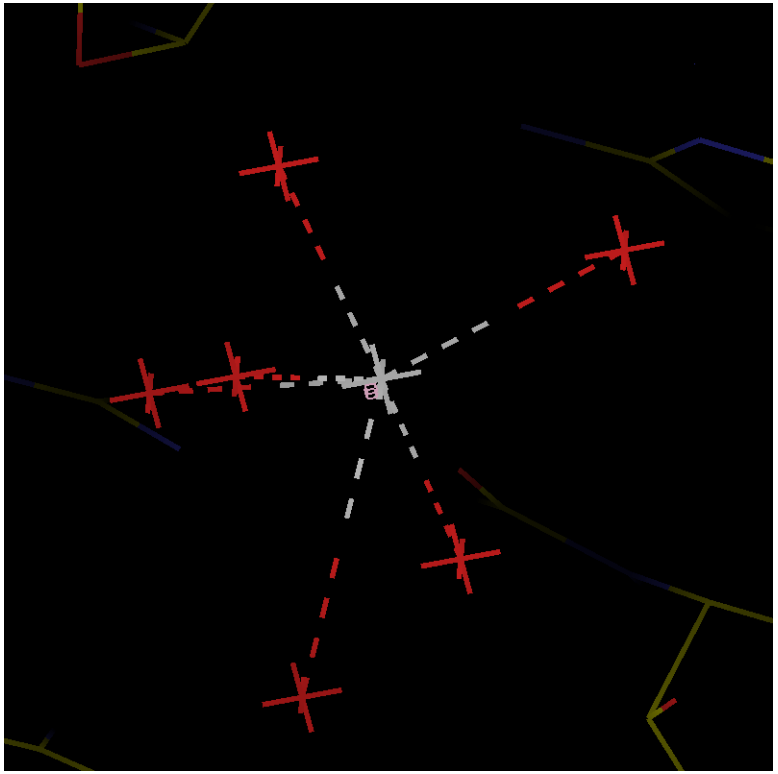

no restraints

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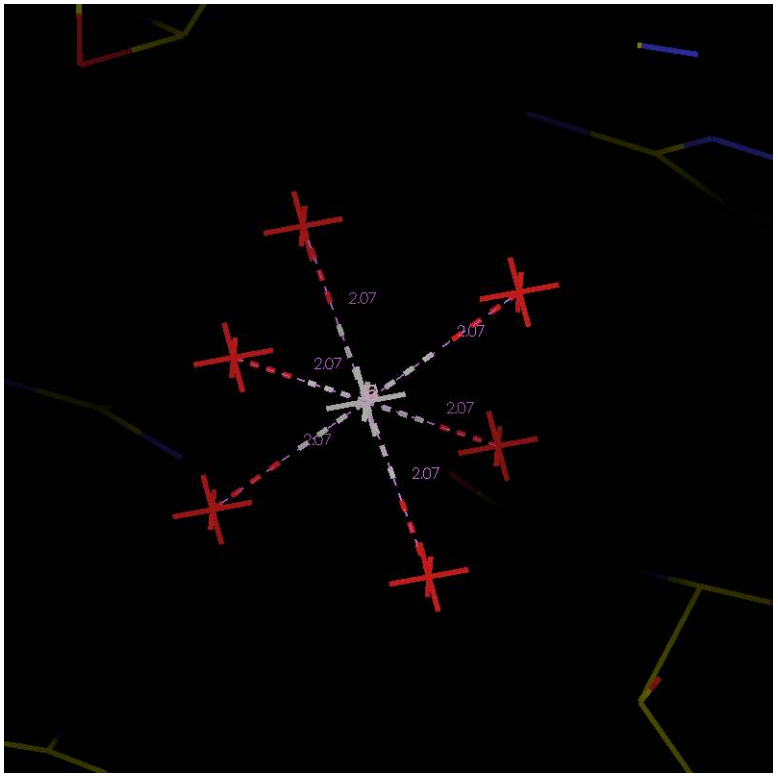
3HHN: BUSTER refinement



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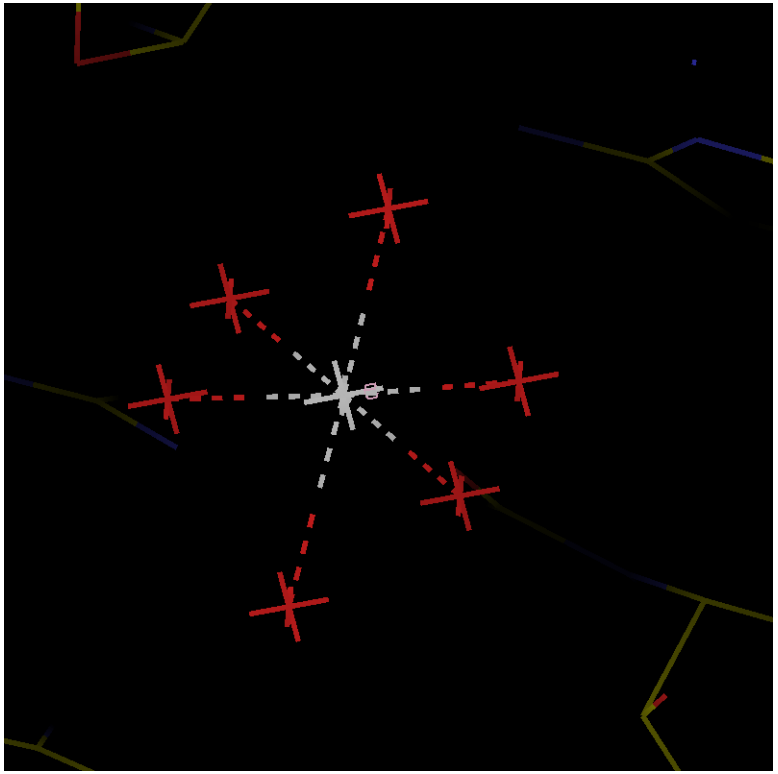

Gelly utility restraints

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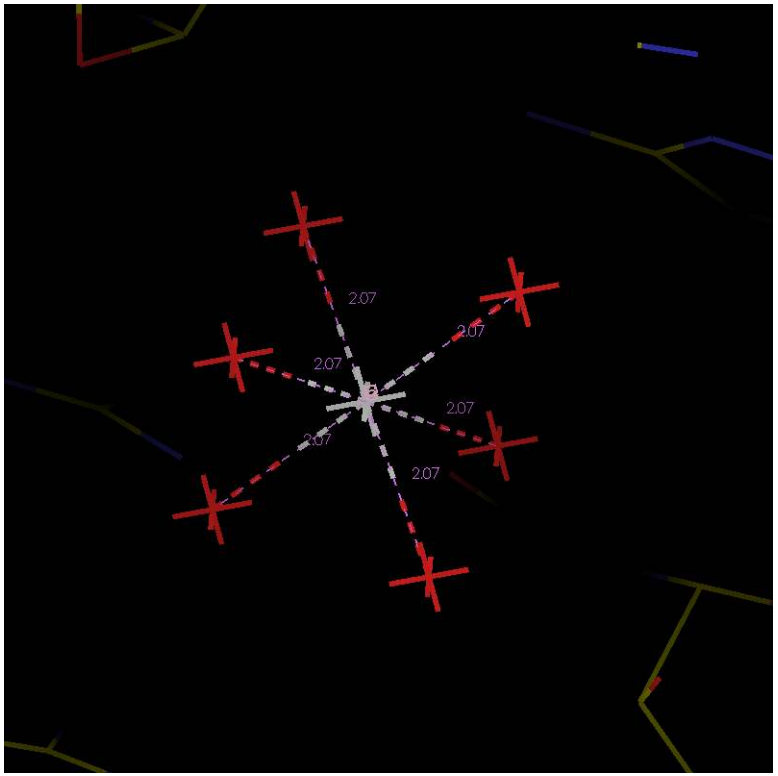
3HHN: BUSTER refinement



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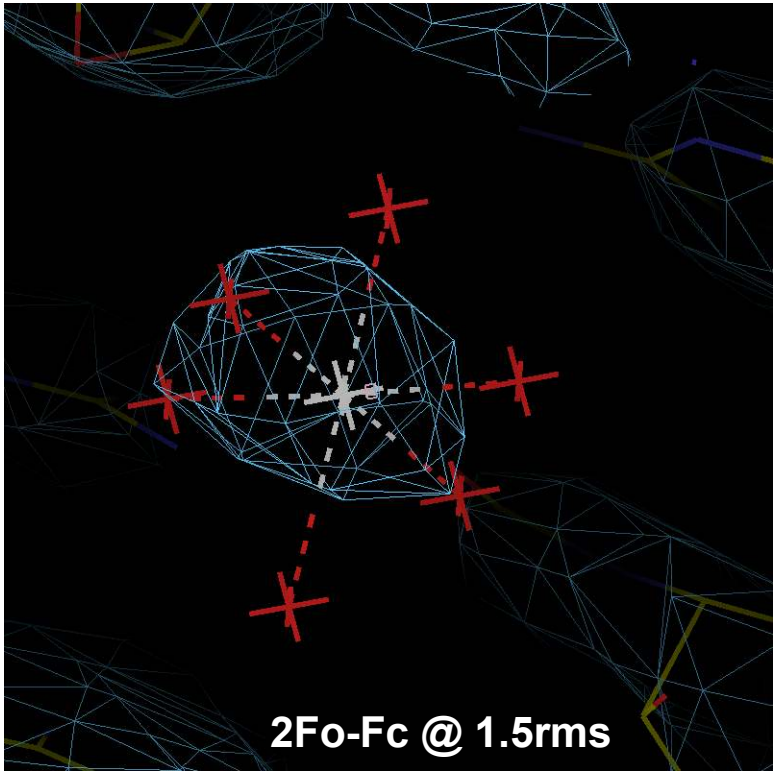

Gelly utility restraints

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BUSTER – additional restraints

- **E.g. using powerful and flexible utility restraints (Gelly) in BUSTER**
- **Example: $Mg^{2+} \cdot (H_2O)_6$**

4U1U

Display Files
Download Files
Usage Note
Download Citation

Entry 4U1U supersedes and combines 4PE9 4PEA 4PEB 4PEC

Primary Citation

Synergy of streptogramin antibiotics occurs independently of their effects on translation.

Noeske, J., Huang, J., Olivier, N.B., Giacobbe, R.A., Zambrowski, M., Cate, J.H.

Journal: (2014) Antimicrob.Agents Chemother. **58:** 5269-5279

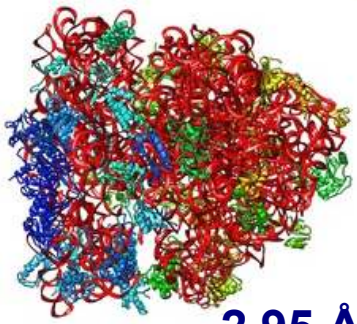
PubMed: 24957822
PubMedCentral: PMC4135883
DOI: 10.1128/AAC.03389-14
Search Related Articles in PubMed

PubMed Abstract:

Streptogramin antibiotics are divided into types A and B, which in combination can act synergistically. We compared the molecular interactions of the streptogramin combinations Synercid (type A, dalfopristin; type B, quinupristin) and NXL 103 (type A, flopristin; type B, linopristin)... [Read More & Search PubMed Abstracts]

Molecular Description Hide

Biological Assembly 1



2.95 Å

3D View: Jmol More Images

Biological assembly 1 assigned by authors

Downloadable viewers:

Simple Viewer Protein Workshop

- **1.1 Mio reflections**
- **290 000 atoms in asymmetric unit**
- **11 000 amino acids, 9000 RNA, 500 Mg, 1700 HOH**

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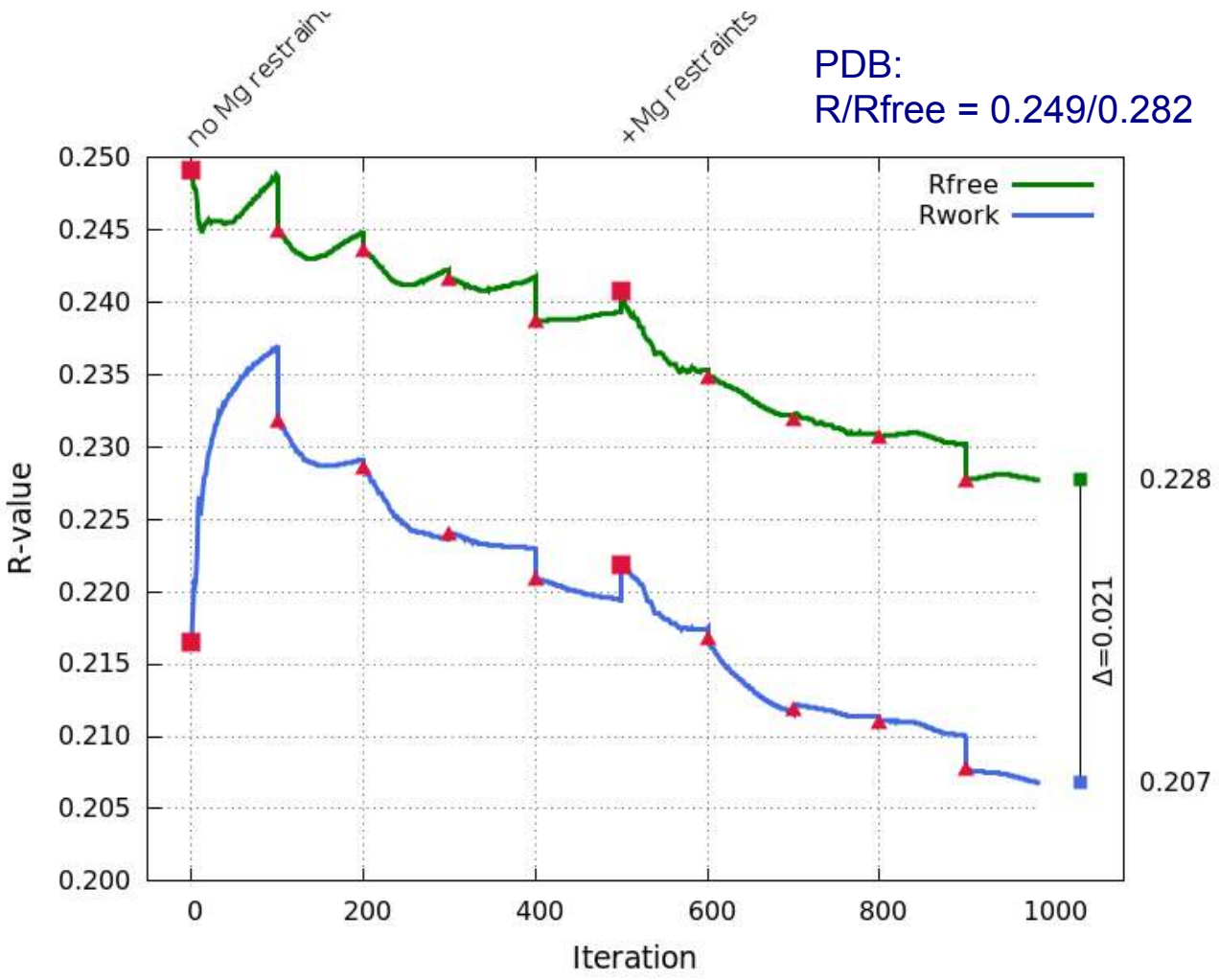
4U1U: BUSTER refinement



CAVEAT:

Comparing R/Rfree from different programs difficult: they use different methods (e.g. bulk solvent model) and scaling.

Sometimes program A gives lower R/Rfree, sometimes program B.

Goal is to get best model - fitting data, chemistry and prior knowledge.

Good to have choice of different approaches and parametrisation!

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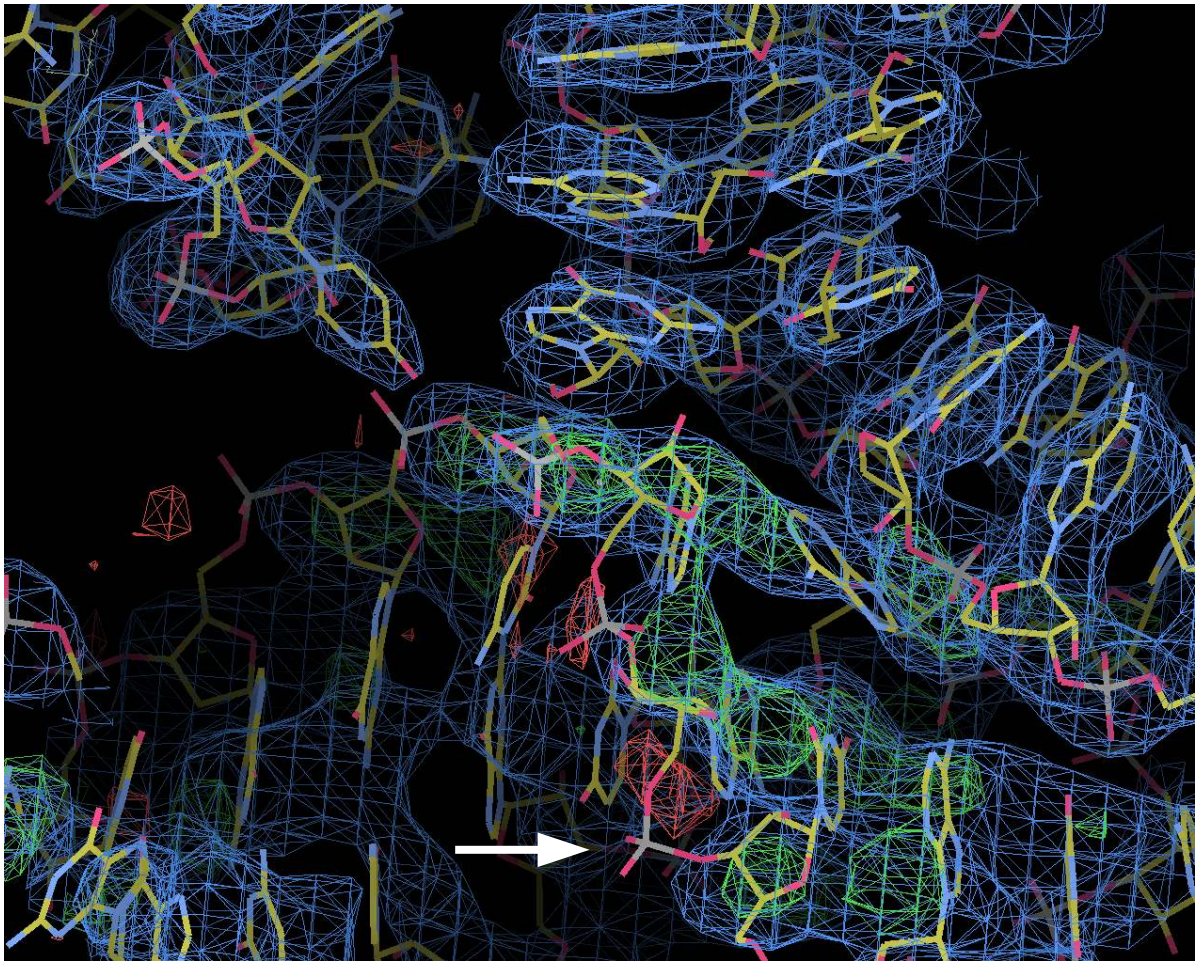
BUSTER: 4U1U



Region-1:

deposited model

Initial map

2Fo-Fc @ 1.5rms
Fo-Fc @ 3.5rms

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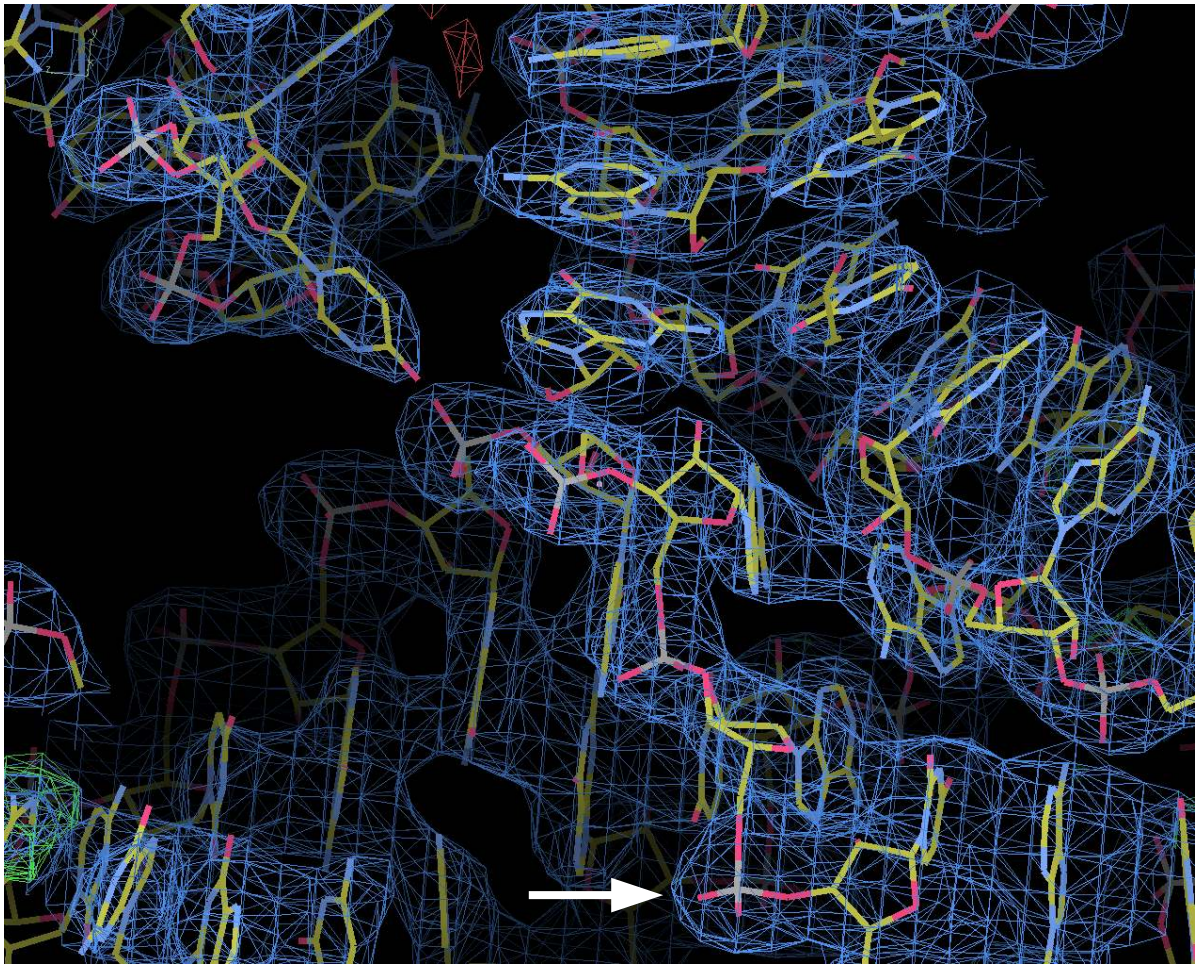
BUSTER: 4U1U



Region-1:

BUSTER model

Final map

2Fo-Fc @ 1.5rms
Fo-Fc @ 3.5rms

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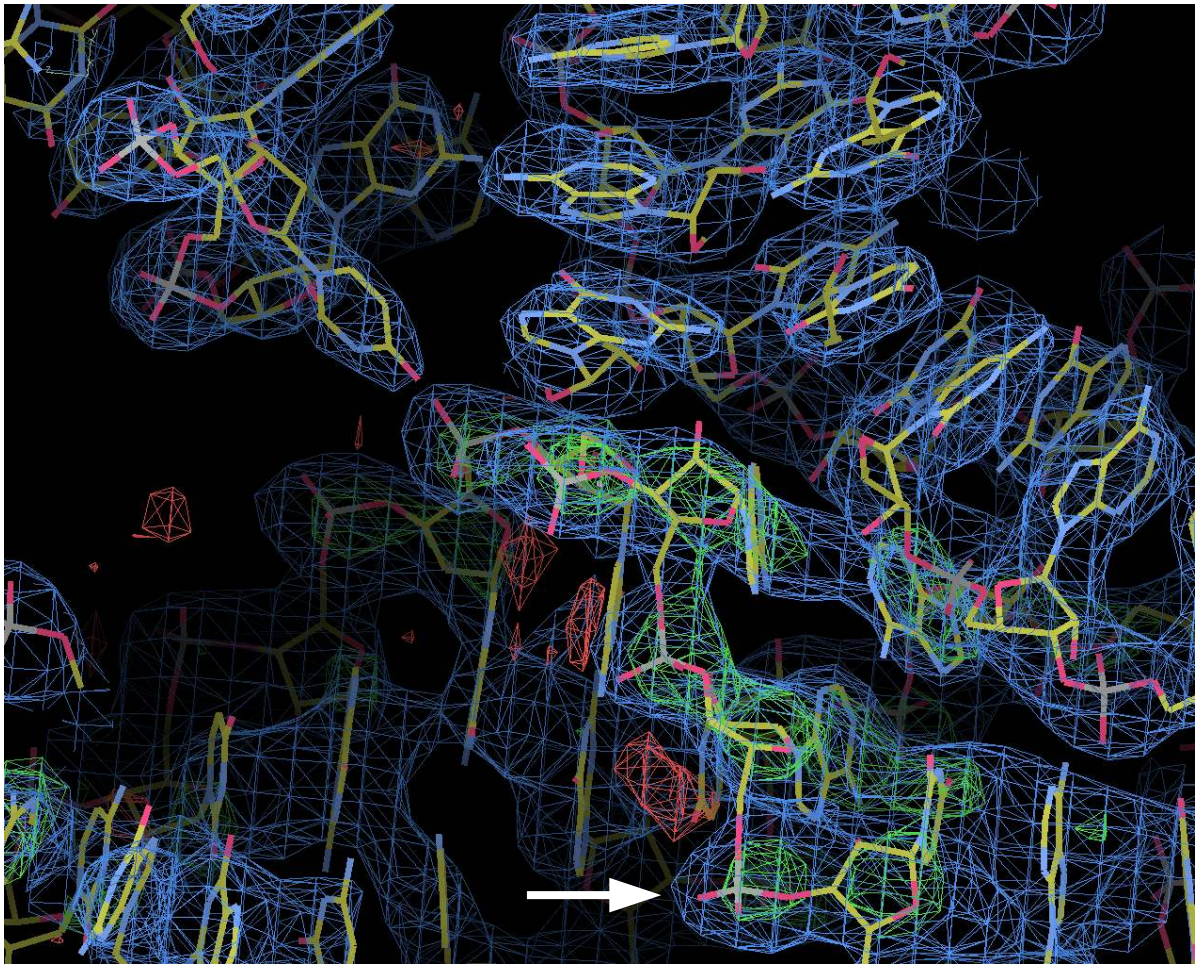
BUSTER: 4U1U



Region-1:

BUSTER model

Initial map

2Fo-Fc @ 1.5rms
Fo-Fc @ 3.5rms

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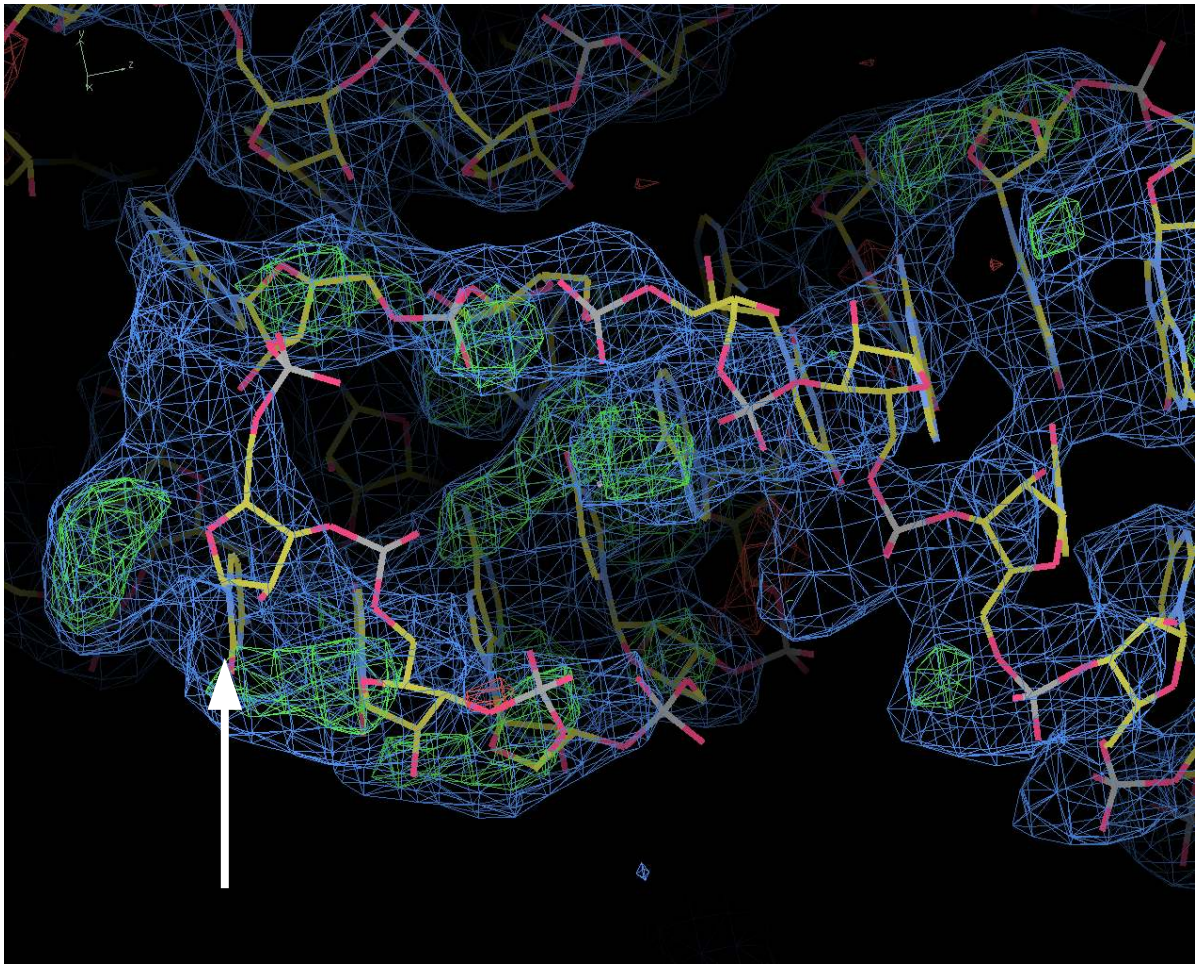
BUSTER: 4U1U



Region-2:

deposited model

Initial map

2Fo-Fc @ 1.5rms
Fo-Fc @ 3.5rms

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BUSTER: 4U1U

Region-2:

BUSTER model

Final map

2Fo-Fc @ 1.5rms
Fo-Fc @ 3.5rms

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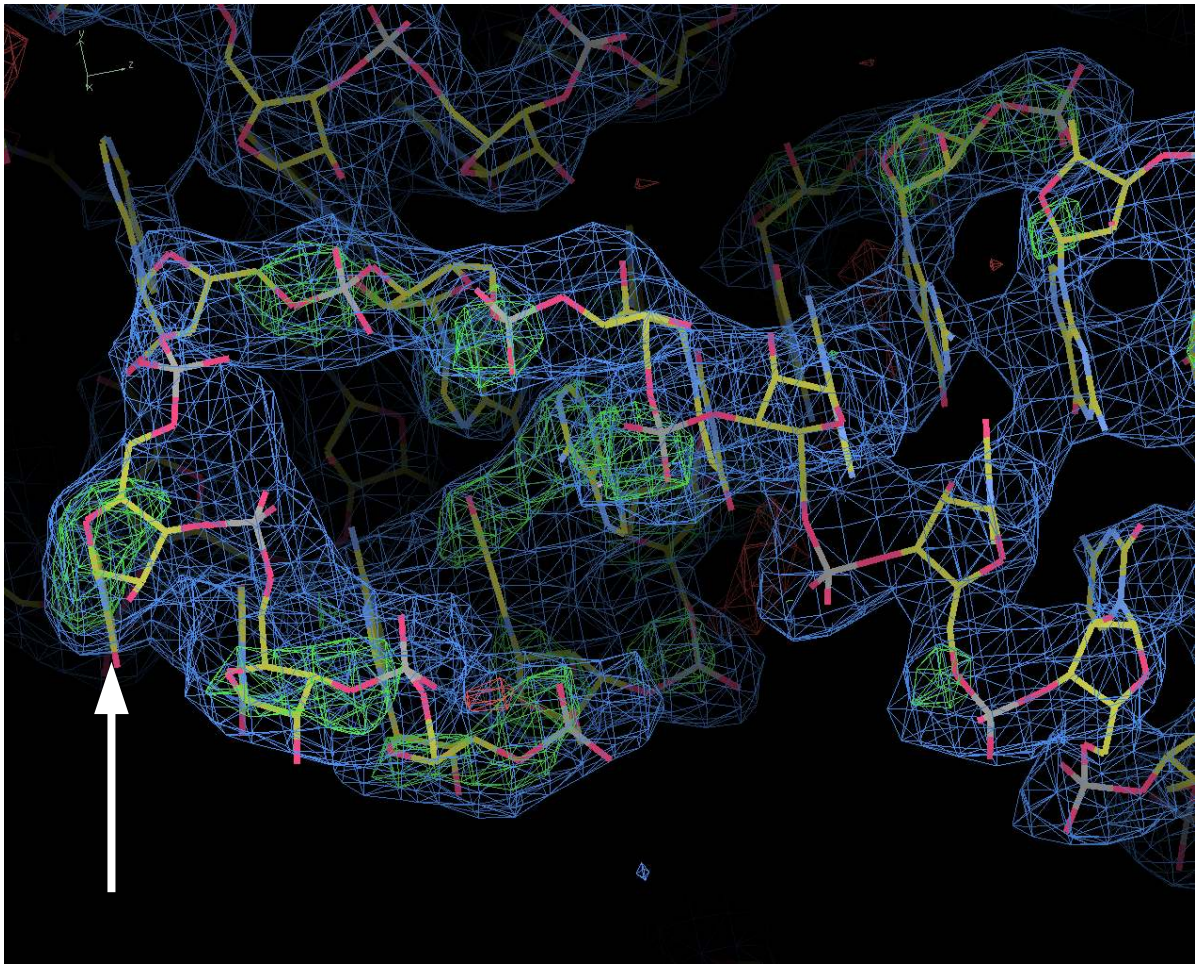
BUSTER: 4U1U



Region-2:

BUSTER model

Initial map

2Fo-Fc @ 1.5rms
Fo-Fc @ 3.5rms

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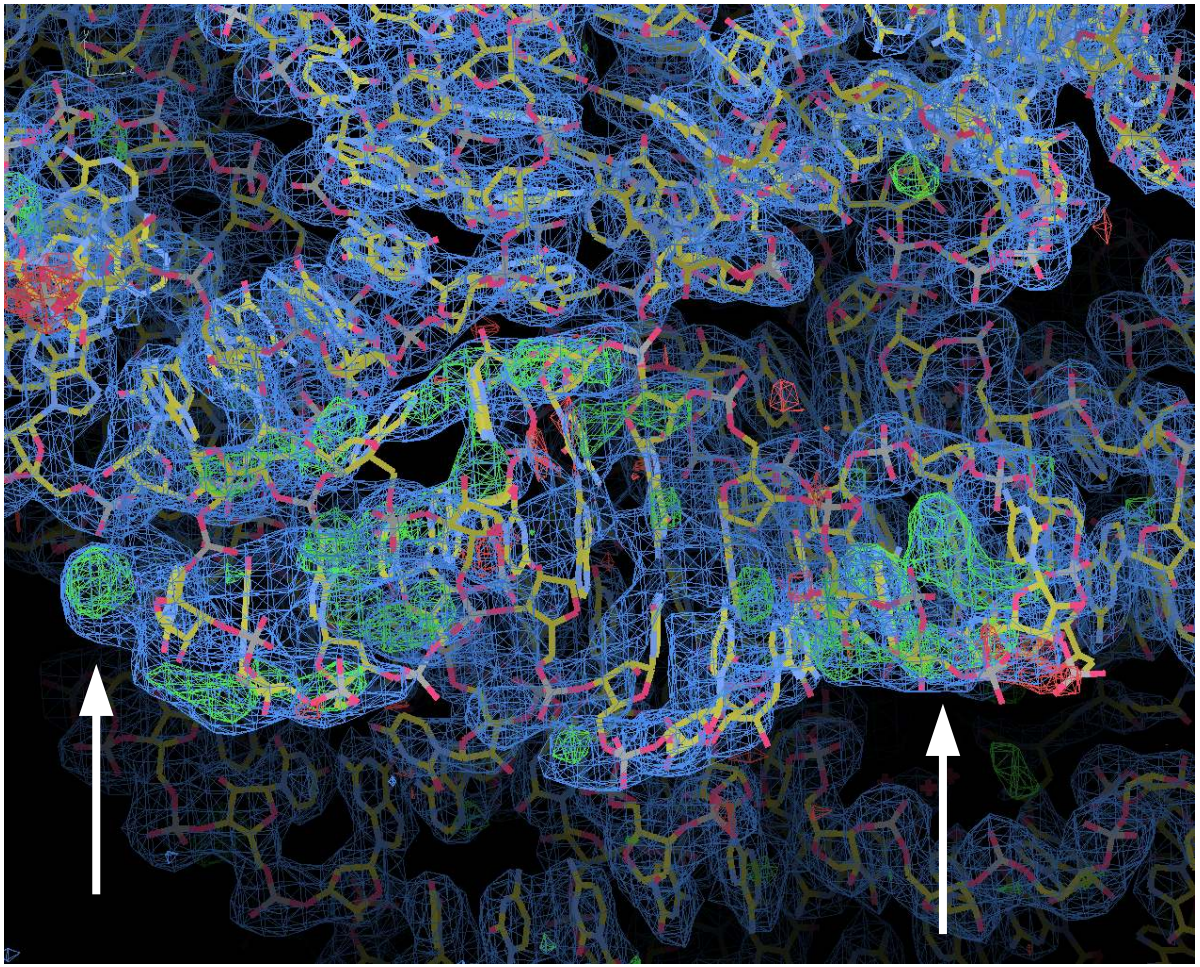
BUSTER: 4U1U



Region-2:

deposited model

Initial map

2Fo-Fc @ 1.5rms
Fo-Fc @ 3.5rms

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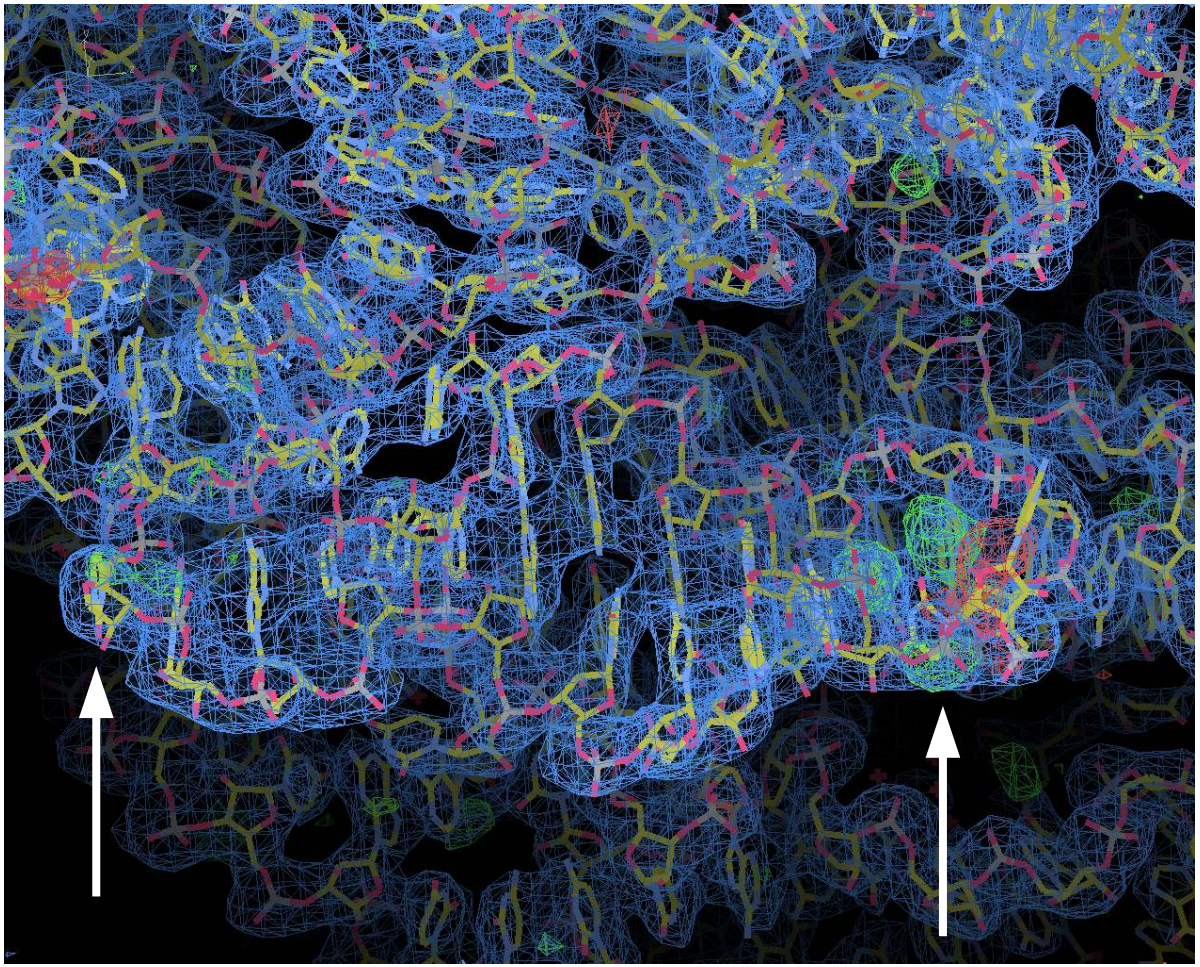
BUSTER: 4U1U



Region-2:

BUSTER model

Final map

2Fo-Fc @ 1.5rms
Fo-Fc @ 3.5rms

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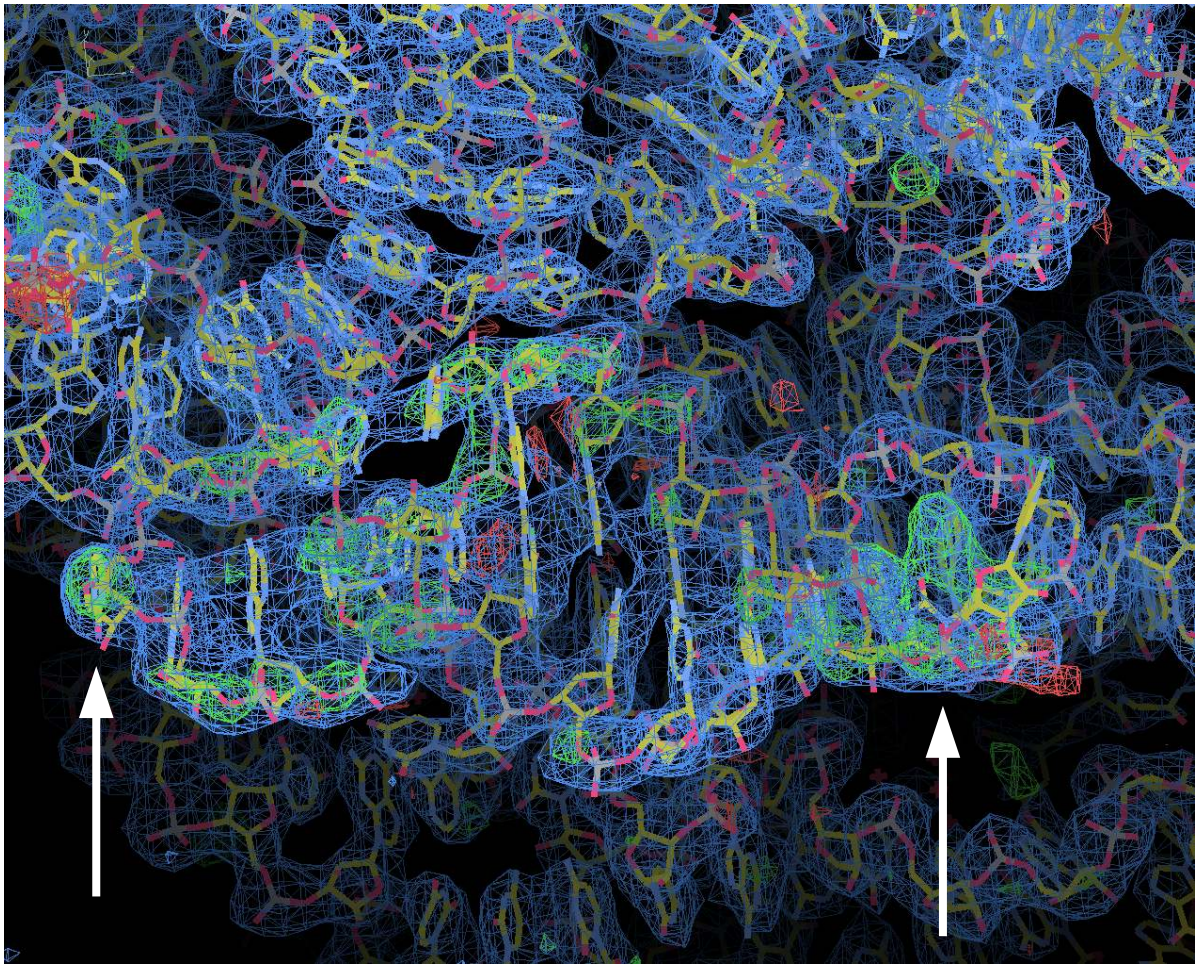
BUSTER: 4U1U



Region-2:

BUSTER model

Initial map

2Fo-Fc @ 1.5rms
Fo-Fc @ 3.5rms

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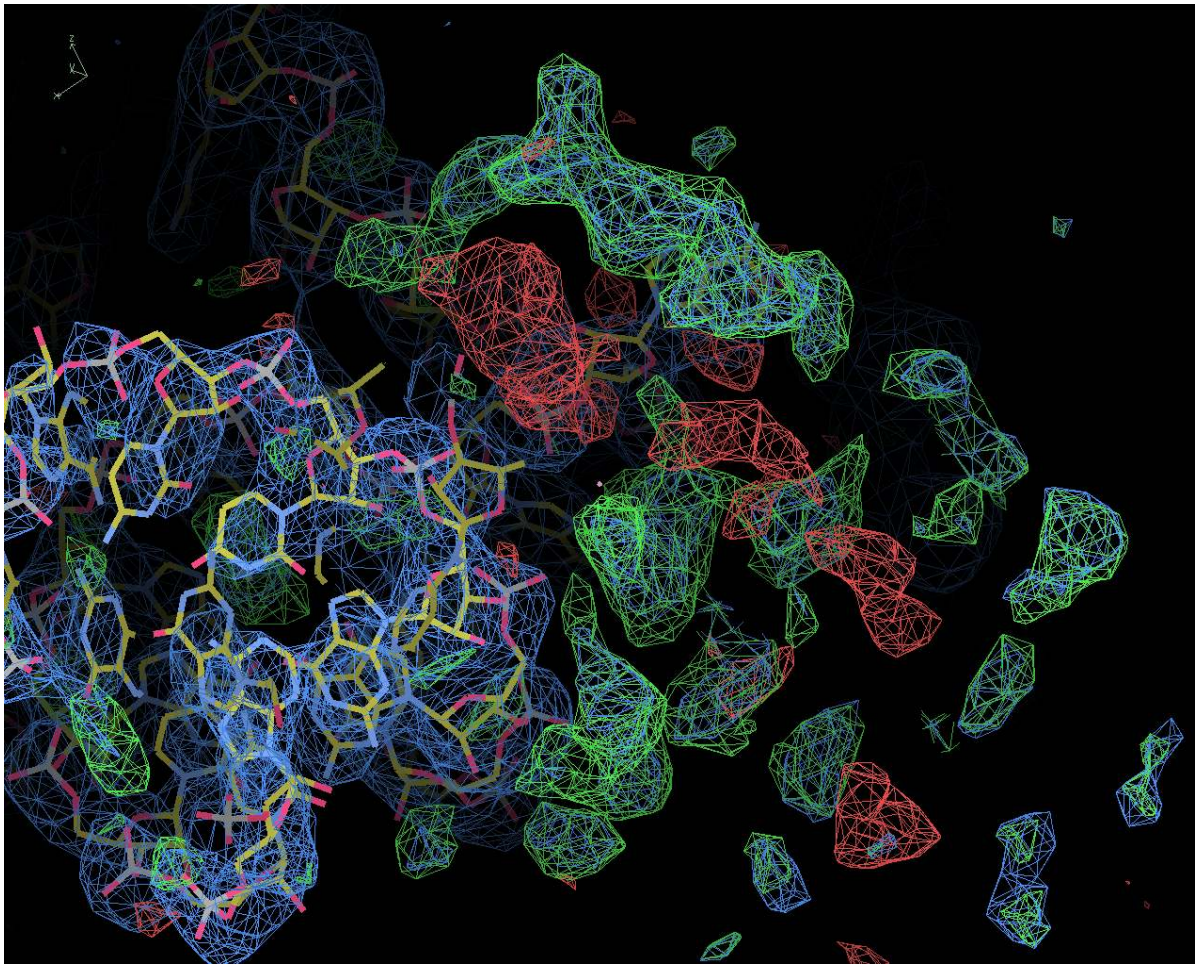
BUSTER: 4U1U



Region-3:

deposited model

Initial map

2Fo-Fc @ 1.5rms
Fo-Fc @ 3.5rms

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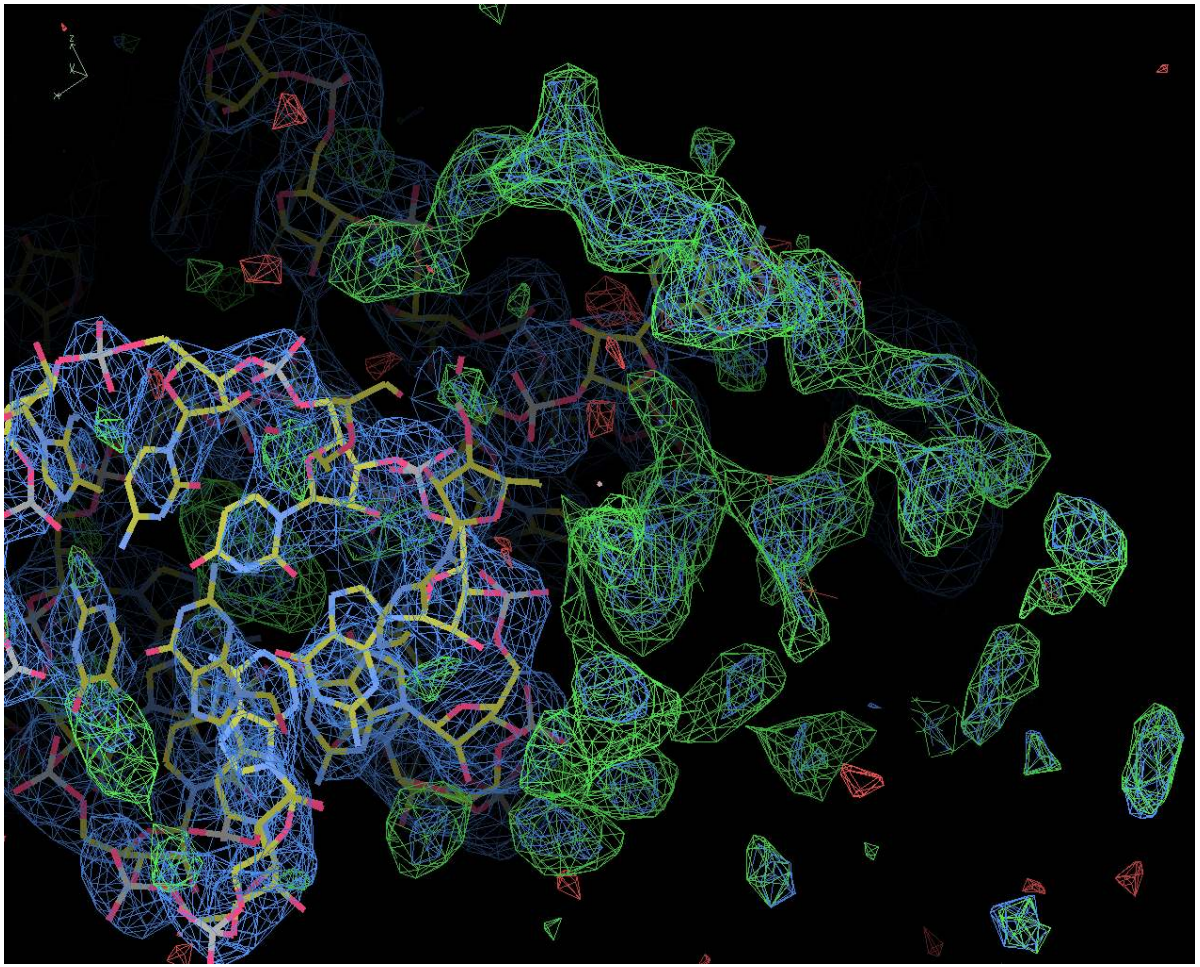
BUSTER: 4U1U



Region-3:

BUSTER model

Final map

2Fo-Fc @ 1.5rms
Fo-Fc @ 3.5rms

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Some notes about rotamers and outliers

- MolProbity rotamer analysis often used as a quality criteria for model
- outliers are considered problematic und highly unlikely (the stated goal is <1% outliers)

6D0E (deposited)

```
  2% A   10  LEU:1.00:0.4:280.2:36.0:::Allowed:mp
  2% A   19  LEU:1.00:0.4:273.1:36.4:::Allowed:mp
  2% A   24  LEU:1.00:0.4:260.6:43.2:::Allowed:mp
  2% A   45  LYS:1.00:0.5:199.5:130.2:301.8:173.9:Allowed:ttmt
    A   50  ILE:1.00:0.0:249.5:205.1:::OUTLIER:OUTLIER
 20% A   82 AVAL:0.33:2.1:311.2::::Favored:m
    A   97  LEU:1.00:0.0:235.3:15.2:::OUTLIER:OUTLIER
 59% B   23  LEU:1.00:0.4:247.2:198.3:::Allowed:mt
  ? B   41  ARG:1.00:0.4:142.9:262.7:191.0:181.3:Allowed:tmt170
  2% B   45  LYS:1.00:0.3:203.2:129.9:301.1:170.3:Allowed:ttmt
  8% B   50  ILE:1.00:0.4:215.5:155.0:::Allowed:tt
 20% B   82  VAL:1.00:1.2:312.5::::Allowed:m
    B   97  LEU:1.00:0.0:236.7:13.8:::OUTLIER:OUTLIER
```

BUSTER

```
A   10  LEU:1.00:0.0:259.1:21.3:::OUTLIER:OUTLIER
A   19  LEU:1.00:0.1:309.3:303.1:::OUTLIER:OUTLIER
A   24  LEU:1.00:0.2:297.4:296.7:::OUTLIER:OUTLIER
A   45  LYS:1.00:0.1:197.6:122.2:308.4:165.6:OUTLIER:OUTLIER
A   50  ILE:1.00:0.0:239.0:174.6:::OUTLIER:OUTLIER
A   82 AVAL:0.33:0.2:320.6::::OUTLIER:OUTLIER
A   97  LEU:1.00:0.0:238.9:5.1:::OUTLIER:OUTLIER
B   23  LEU:1.00:0.0:180.7:193.4:::OUTLIER:OUTLIER
B   41  ARG:1.00:0.1:138.1:266.5:172.2:188.0:OUTLIER:OUTLIER
B   45  LYS:1.00:0.1:197.5:123.2:307.8:166.2:OUTLIER:OUTLIER
B   50  ILE:1.00:0.0:238.2:171.6:::OUTLIER:OUTLIER
B   82  VAL:1.00:0.1:326.1::::OUTLIER:OUTLIER
B   97  LEU:1.00:0.0:238.8:5.0:::OUTLIER:OUTLIER
```

Unlikely – but not classified as “outlier”

- Do we have a problem with rotamers in BUSTER refinements?

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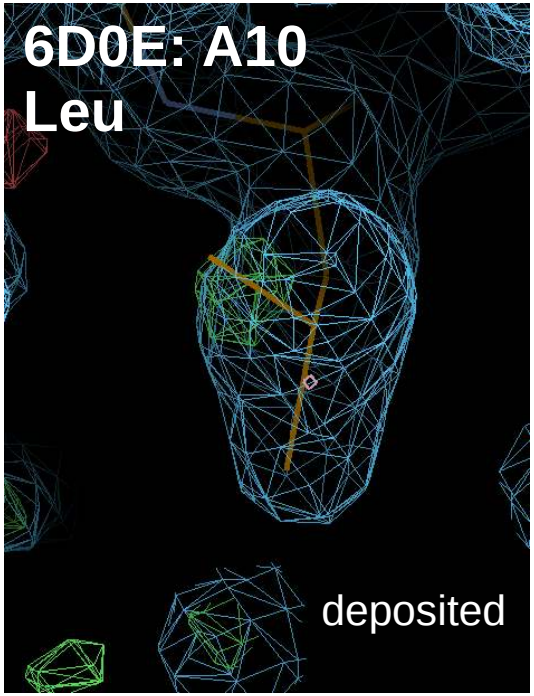
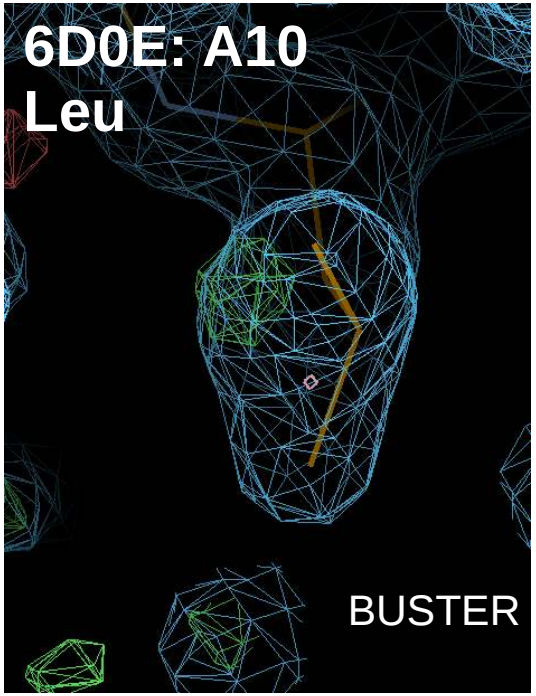
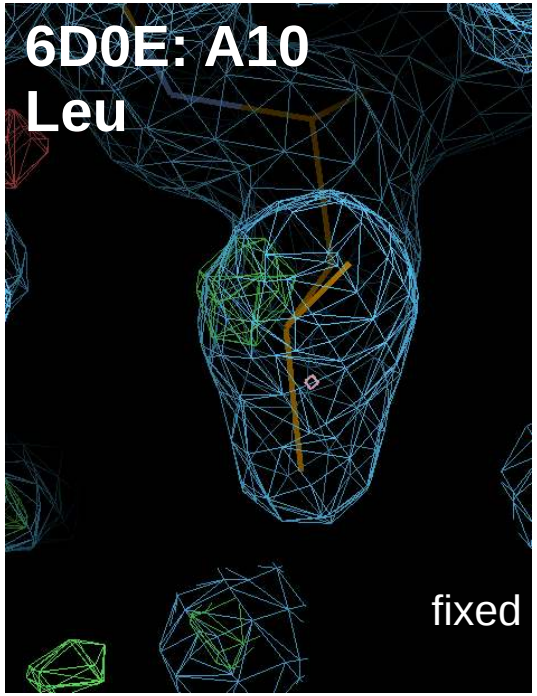
Rotamer has to fit density (for X-Ray crystallographic models)







mp (2%): Allowed **OUTLIER** **mt (59%): favoured**

- small, but significant difference between mt (59%) and mp (2%)
- BUSTER refines model away from poor/wrong rotamer and gives clear indications:
  - positive difference density
  - rotamer now highlighted as outlier
- enforcing rotamer restraints can mask incorrect side-chain conformations

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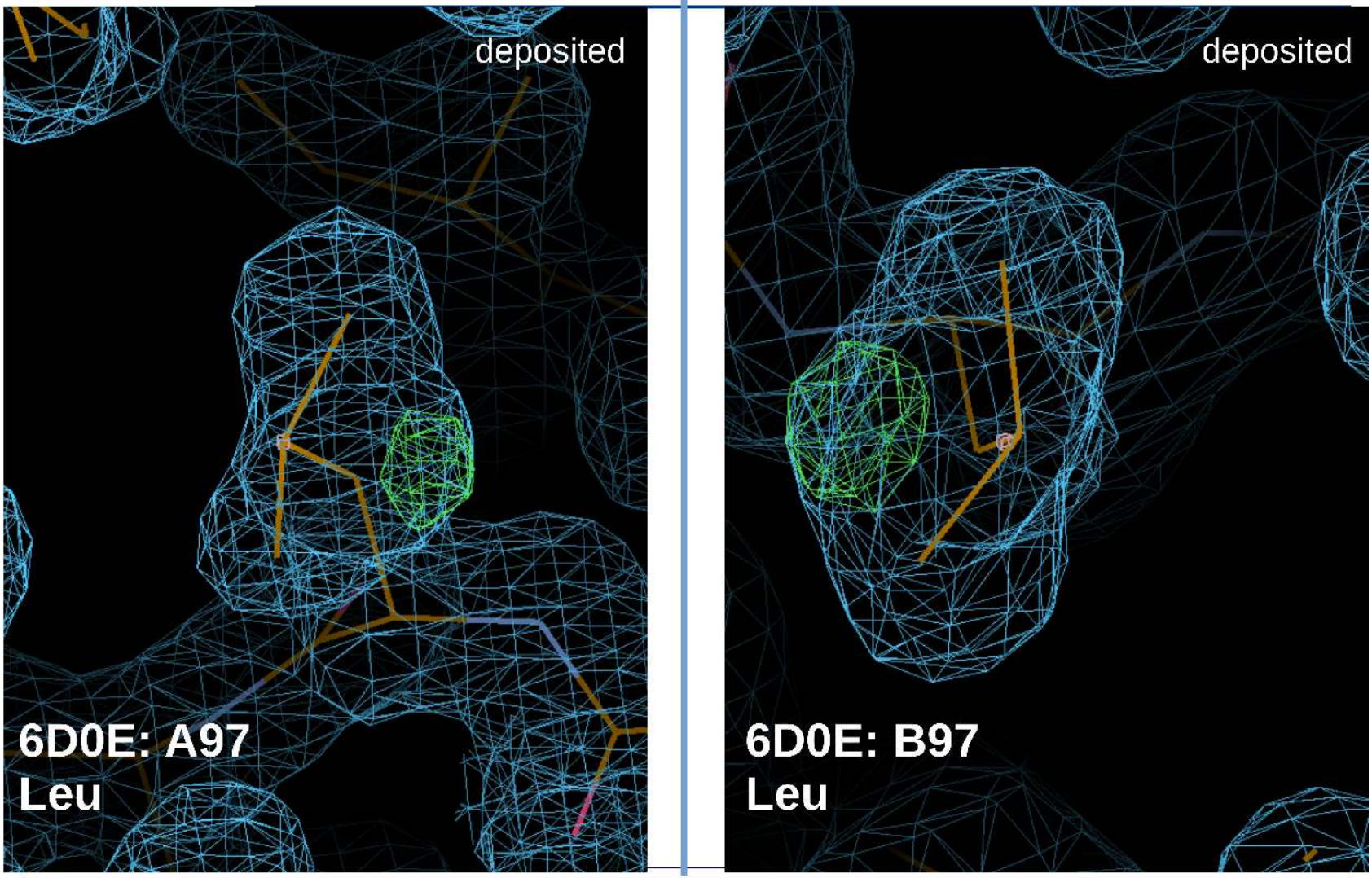
Rotamer outliers are useful markers



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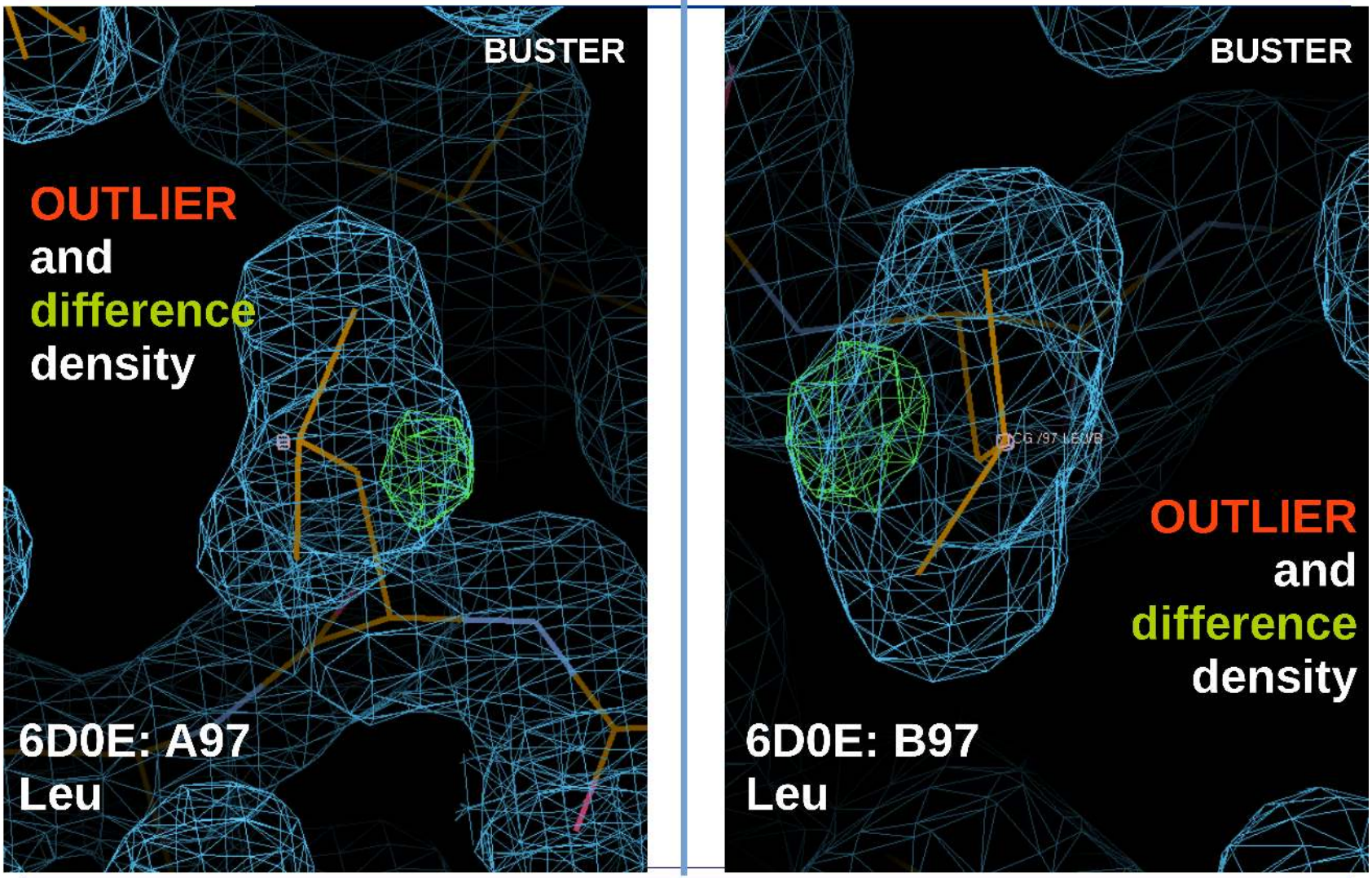
Rotamer outliers are useful markers



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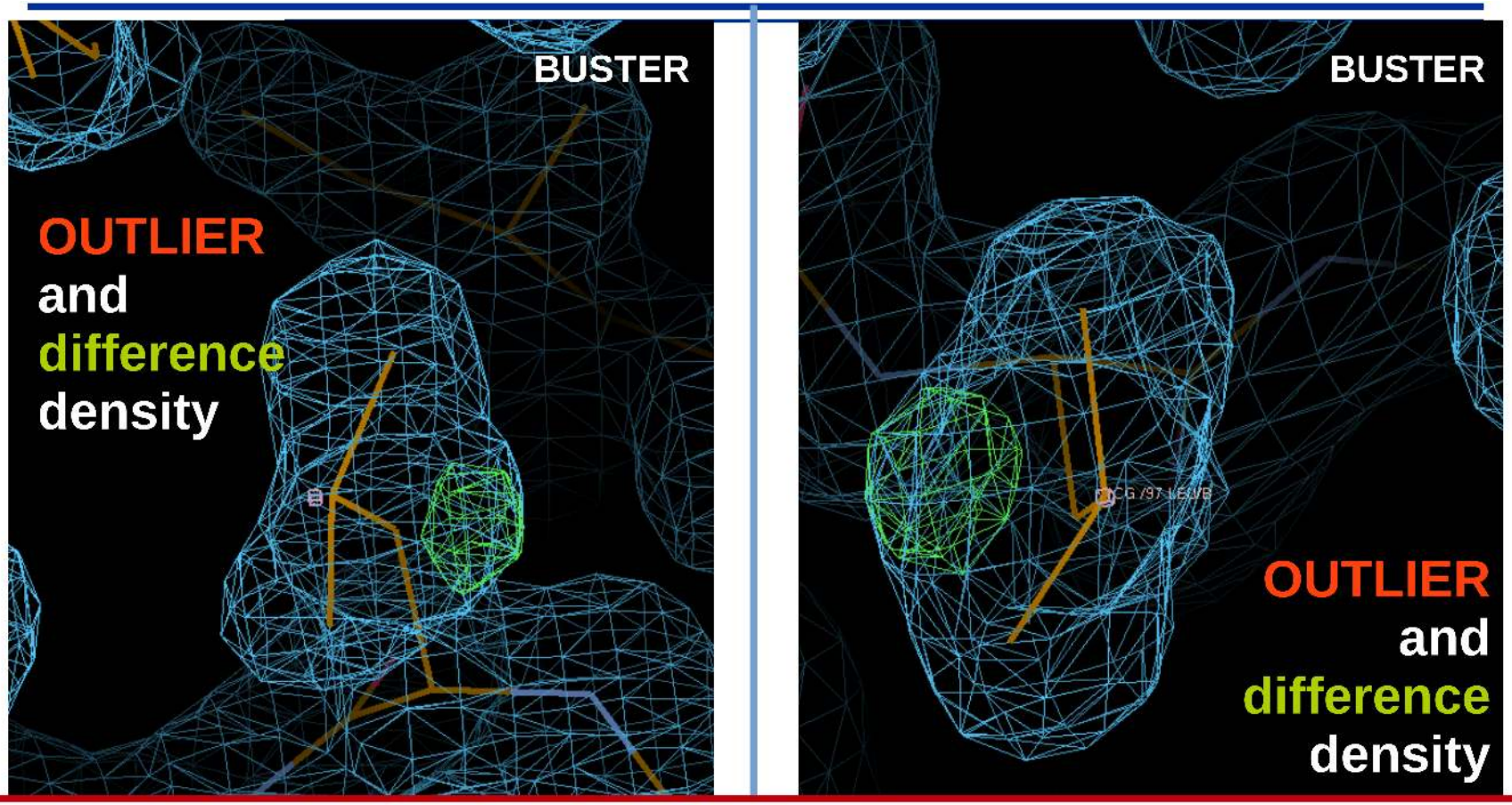
Rotamer outliers are useful markers



Do not use *too many* additional restraints to keep geometry under control if underlying problem is incorrect atomic model - as visible in density!

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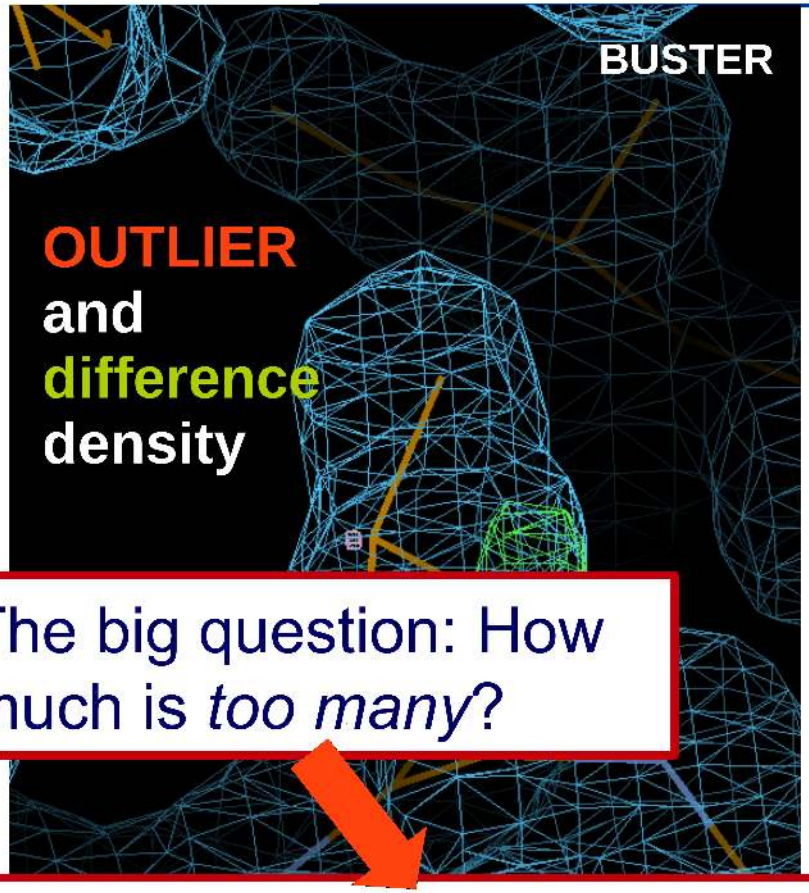
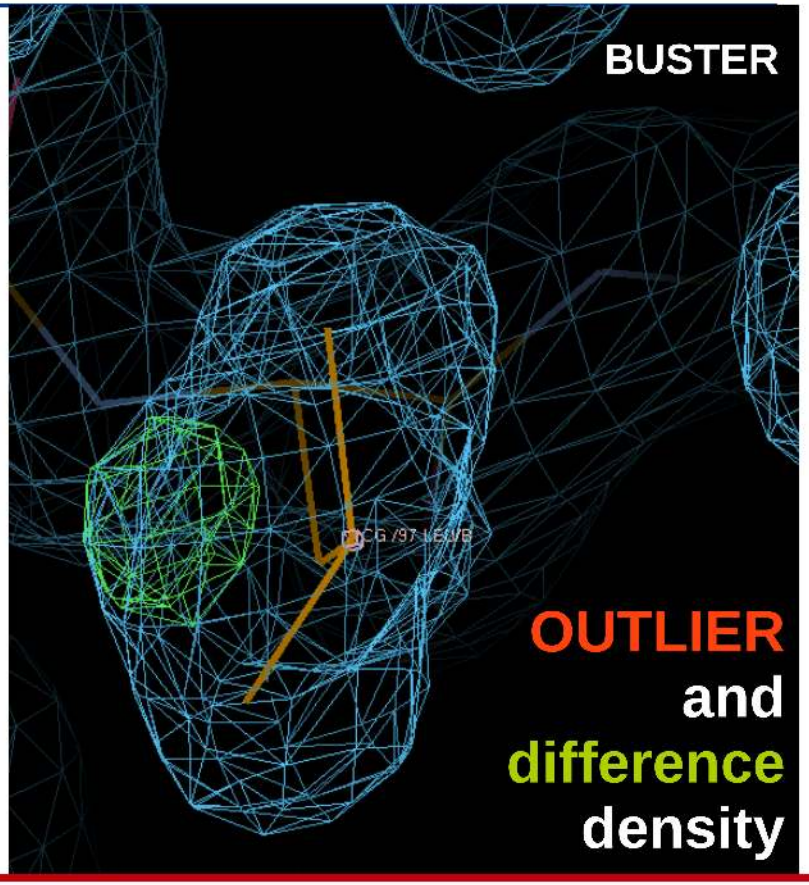
Rotamer outliers are useful markers





The big question: How much is *too many*?

Do not use *too many* additional restraints to keep geometry under control if underlying problem is incorrect atomic model - as visible in density!

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BUSTER: Is there any any ligand bound?

Acta Cryst. (2005). A**61**, C248

Automated Structure Refinement for High-throughput Ligand Detection with BUSTER-TNT

Clemens Vonrhein, Gerard Bricogne, *Global Phasing Ltd., Cambridge, UK.* E-mail: vonrhein@GlobalPhasing.com

The use of crystallography for the discovery of lead compounds often involves a large number of experiments with different soaking or co-crystallization trials. The subsequent refinement and analysis of the resulting datasets can be time-consuming and tedious. Since the crystallographic parameters (resolution, space group, cell parameters) are quite often similar, this task is ideally suited for automation.

We present a method (**autoBUSTER**) that automates the refinement, solvent model update, ligand detection and analysis. Centered around the BUSTER-TNT program [1,2], it requires a minimal amount of user input. Although it can be used at any resolution and for any kind of macromolecular structure, it is tuned to the refinement of protein structures at better than 2.8 Å resolution.

The knowledge of any (possibly) bound ligand can be given (a) explicitly by supplying a PDB file of dummy atoms that describes the assumed binding site, or (b) by letting the system automatically analyze the residual density of difference Fourier maps. A unique feature of BUSTER-TNT is used, where the various masks describing the known fragment, the bulk solvent and the missing part can be given independently from each other. The results show that this can greatly enhance the capability of uniquely defining any bound ligand.

[1] Bricogne G., Irwin J., *Macromolecular Refinement: Proceedings of the CCP4 Study Weekend*, Warrington: Daresbury Laboratory, 1996, 85-92. [2] Blanc E., Roversi P., Vonrhein C., Flensburg C., Lea S. M., Bricogne G., *Acta Cryst.*, 2004, **D60**, 2210-2221.

- BUSTER's '**-L**' feature tries to take an **unbiased look** at data/model to decide **if, where and how** something ***might*** have bound.
- No prior knowledge (bias?) required/used.
- Used since 2003, with first academic release in 2009

Liebschner et al (2017): "Polder maps: improving OMIT maps by excluding bulk solvent.", Acta D 73, 148

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BUSTER: Is there any any ligand bound?

GΦL **LigandDetectionModes**

Favorite? Search Attachments

(You are AnonymousGnome)

Content:

- Introduction
- Unknown location
- Known location
- Caveats
- Summary

Introduction

Apart from the standard procedures for detecting ligands (difference Fourier maps), BUSTER has one particular feature that needs a bit further explanation - to explain what it can do, what it can't do and what potential bias it might introduce.

This feature is triggered by the –L and –Lpdb flags to the `refine` command:

```
% refine -p some.pdb -m some.mtz -L ...
  - or -
% refine -p some.pdb -m some.mtz -Lpdb bindingsite.pdb ...
```

It will treat a certain region of the model differently during the last big cycle of refinement: that region will neither contain an atomic model nor a contribution from the bulk solvent. However, if there is some electron density present in this region, it should show up in difference (`Fo-Fc`) maps as strong positive density. The interpretation, what this electron density might represent (atomic model, bulk solvent or a mixture) is up to the user.

Here we're going to explain the typical usage of this BUSTER feature, their assumptions and caveats.

Unknown location

The least biased assumption is that there might be some ligand bound, but its location is unknown. In that case one would use the

- Unbiased towards “expected” binding (just because the crystal was soaked/co-crystallised with compound doesn’t mean it actualy is bound)
- Unbiased towards binding site (there can be unexpected or new binding sites)
- Unbiased towards binding pose

BUSTER wiki
www.globalphasing.com/buster/wiki/

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Difference Fourier maps

- **Anomalous:**
  - distinguish ion from solvent
  - help difficult sequencing (Cys/Met marker)
  - help placing of compound
  - automatically generated and analysed in BUSTER
- **Early-Late:**
  - show radiation damage effects
  - automatically prepared in autoPROC - then generated and analysed in BUSTER
- **Fo-Fo:**
  - (Compound - Apo) to show compound

```
diff_fourier -h
```

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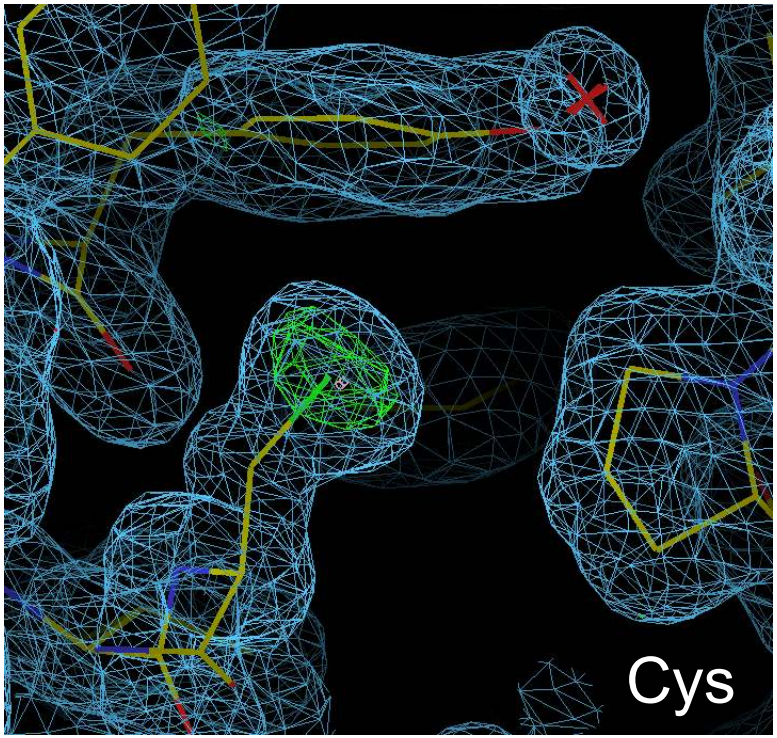
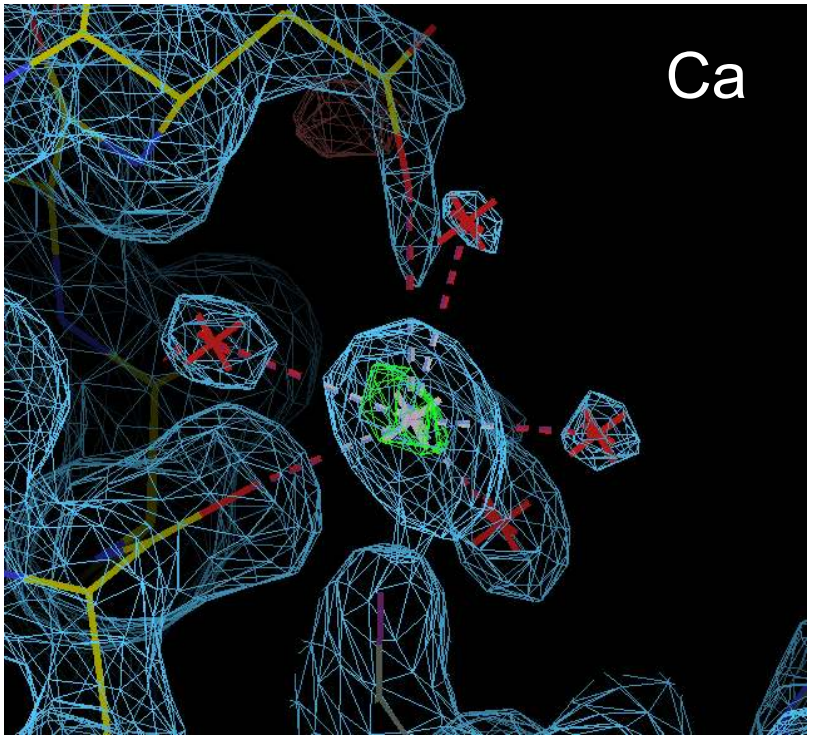
Difference Fourier maps 1: ANO





Crystal structure of a DNA methyltransferase 1 associated protein 1 (DMAP1) from Homo sapiens at 1.45 A resolution, JCSG (2013)

4IEJ: anomalous Fourier map at 3.5 rms
Wavelength = 0.9795 A f”(S)=0.23 f”(Ca)=0.56

Low dose (rate), high multiplicity, fine-slicing

…. and don’t lose anomalous data columns in output reflection data

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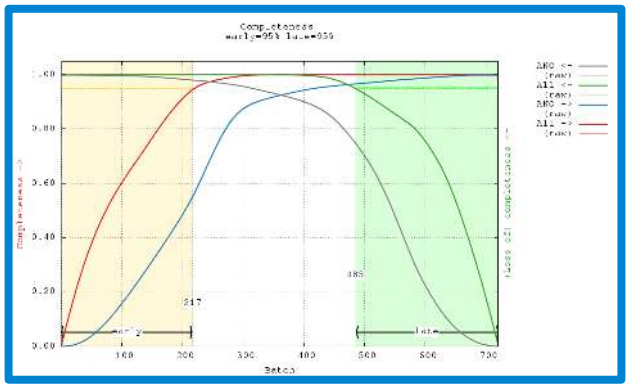
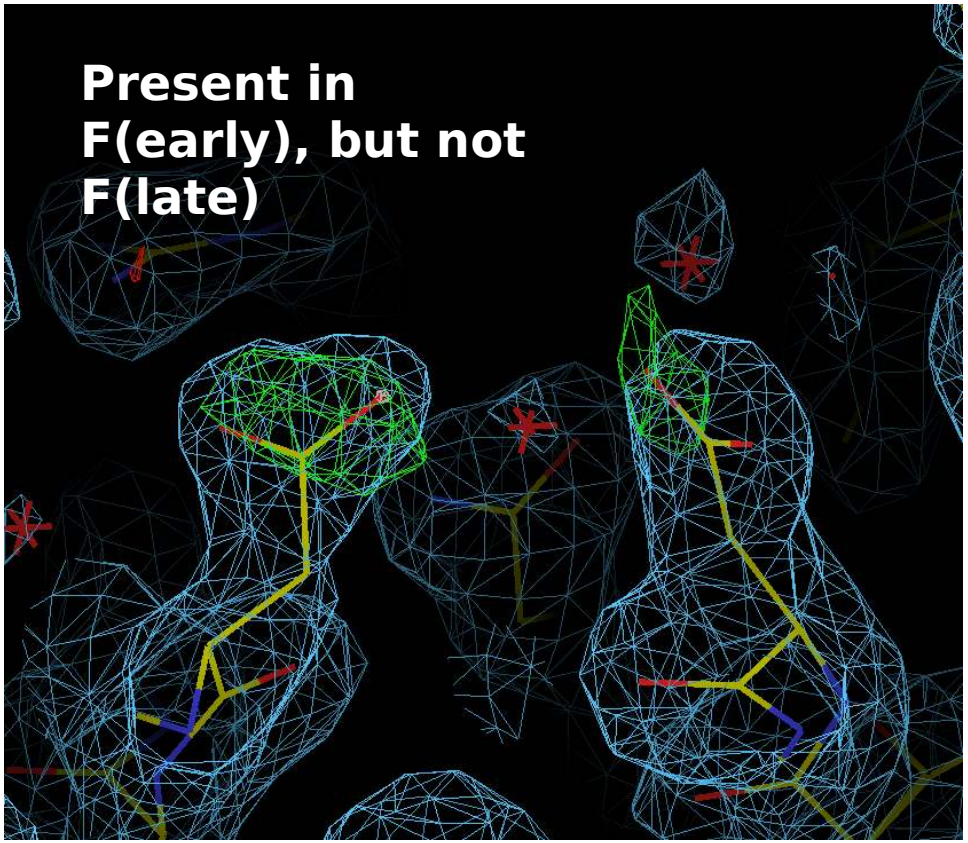
Difference Fourier maps: F(early)-F(late) detecting/describing radiation damage

Typical decarboxylation of ASP/GLU residues

Normal mFo-Dfc maps will show negative peaks.



low dose, high-multiplicity



A novel mode of Gleevec binding is revealed by the structure of spleen tyrosine kinase. Atwell, S. et al.(2004) J.Biol.Chem. 279, 55827-55832.

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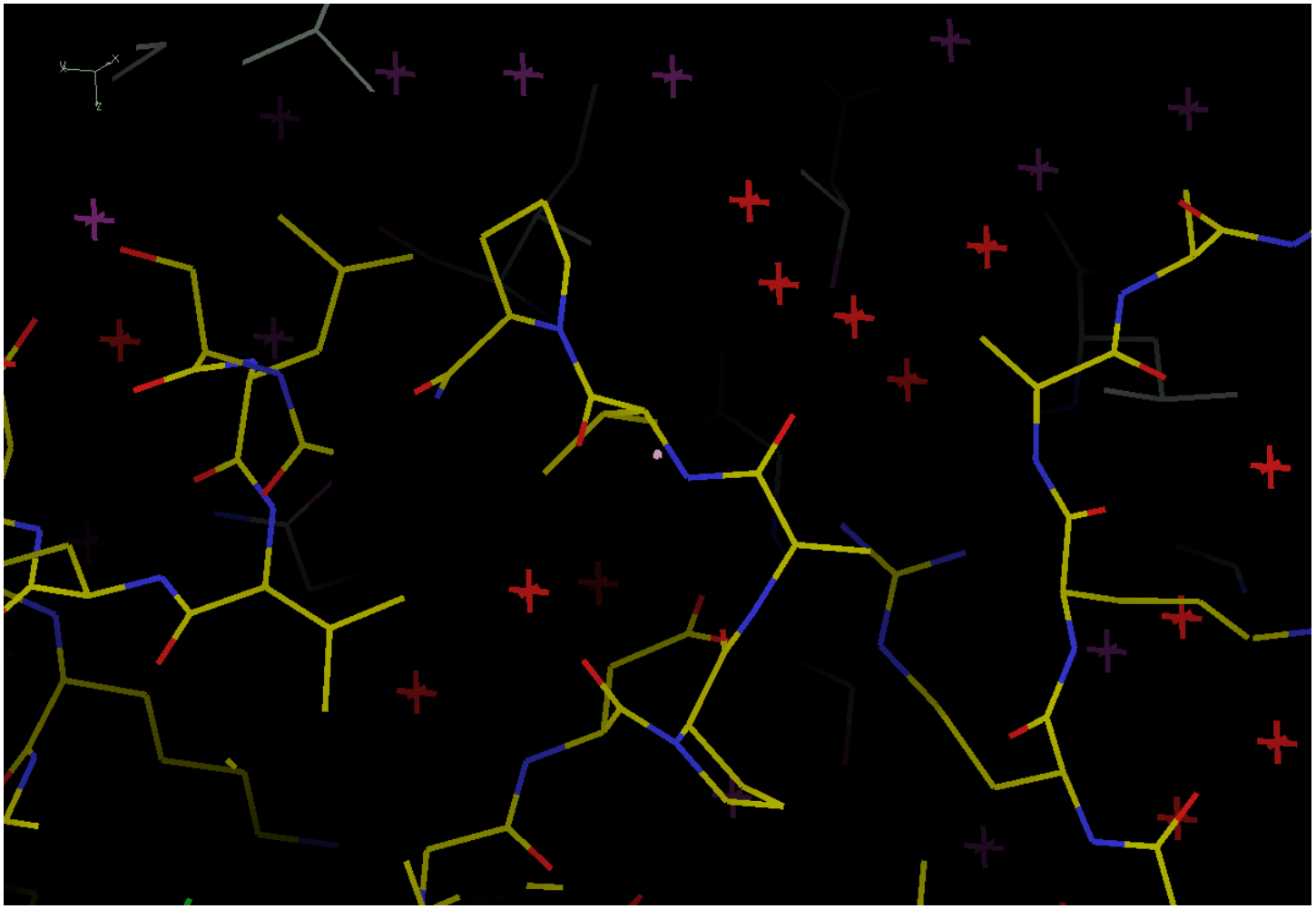
F(early)-F(late): water in crystal contact



4LER

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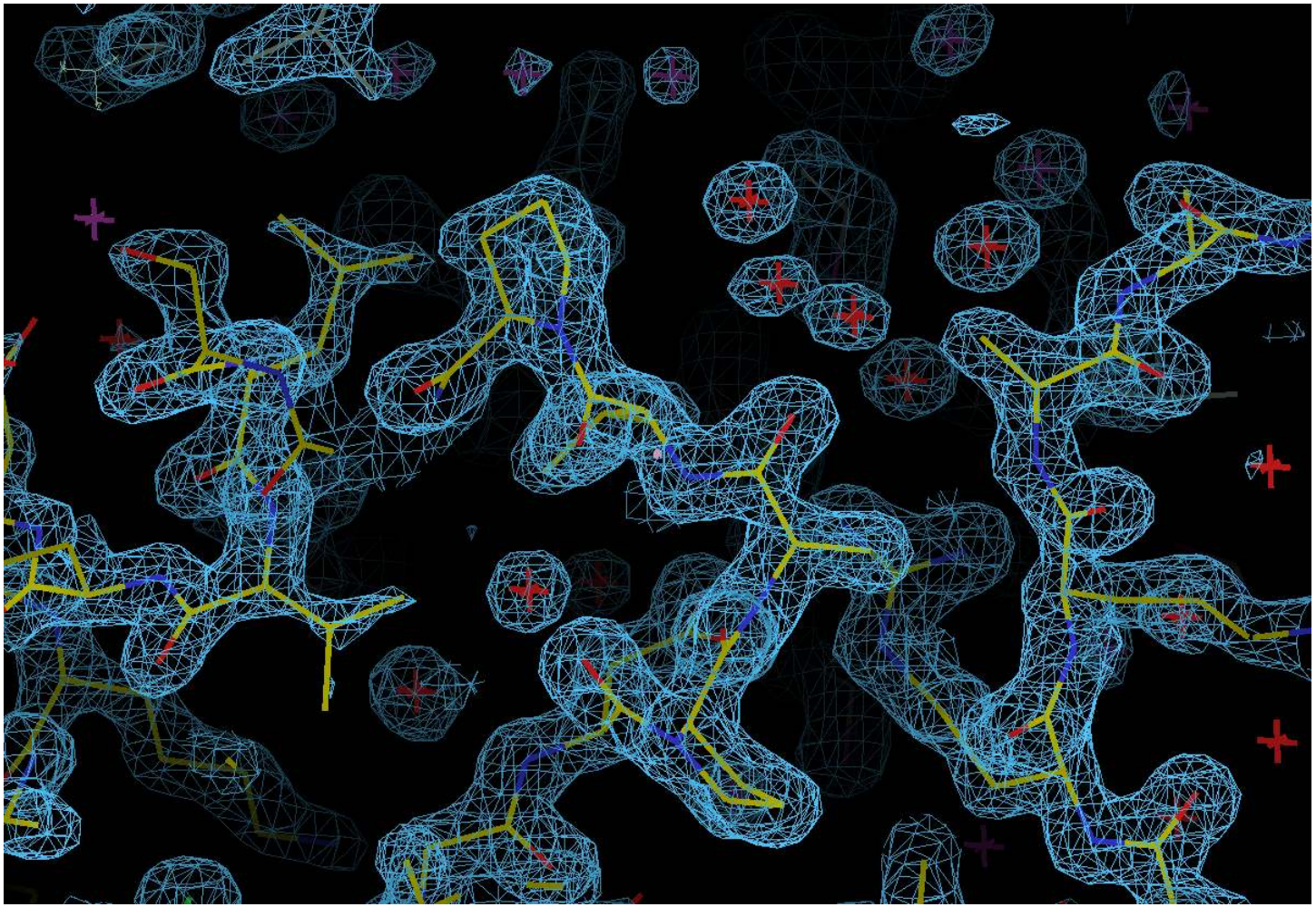
F(early)-F(late): water in crystal contact



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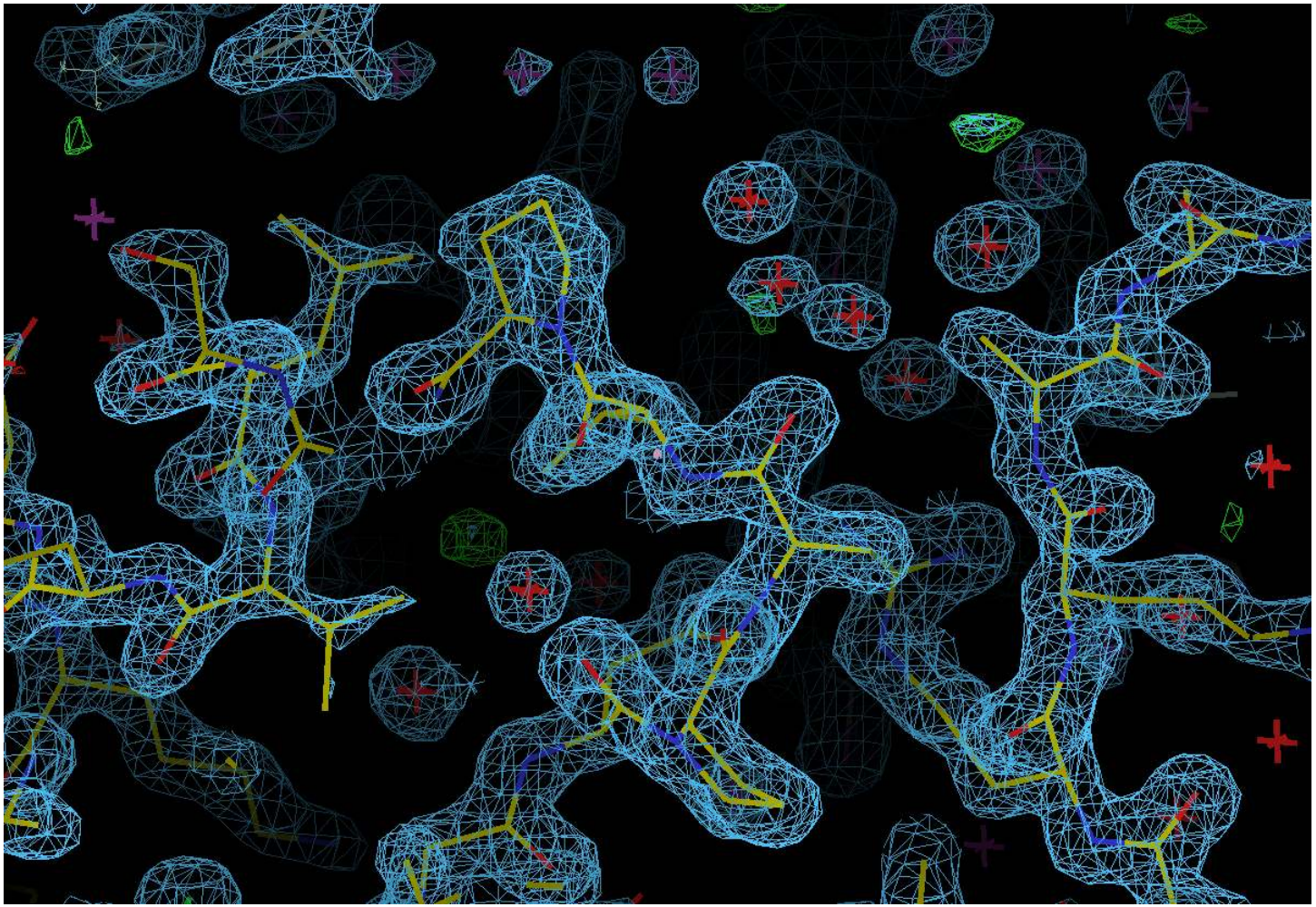
F(early)-F(late): water in crystal contact



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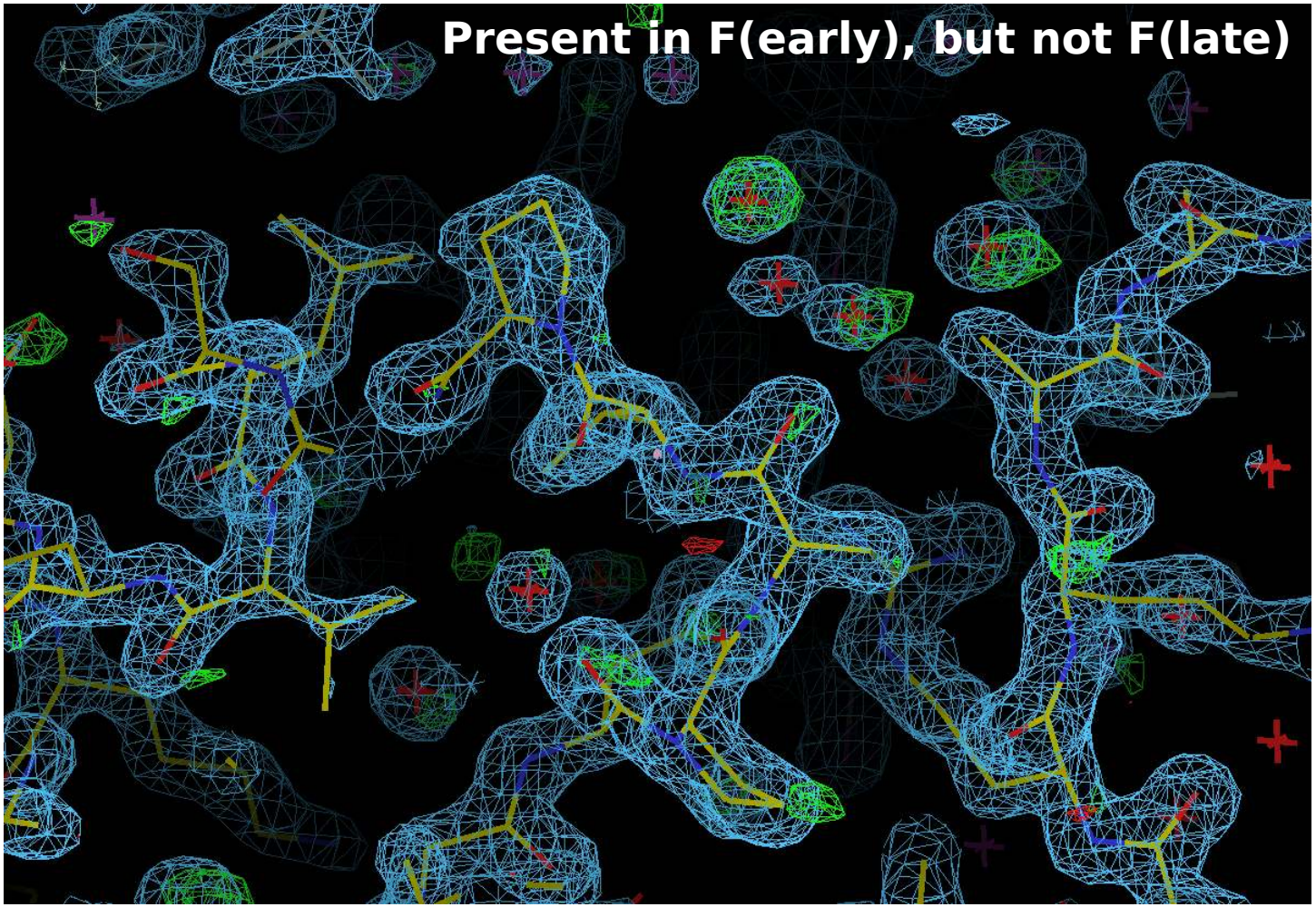
F(early)-F(late): water in crystal contact



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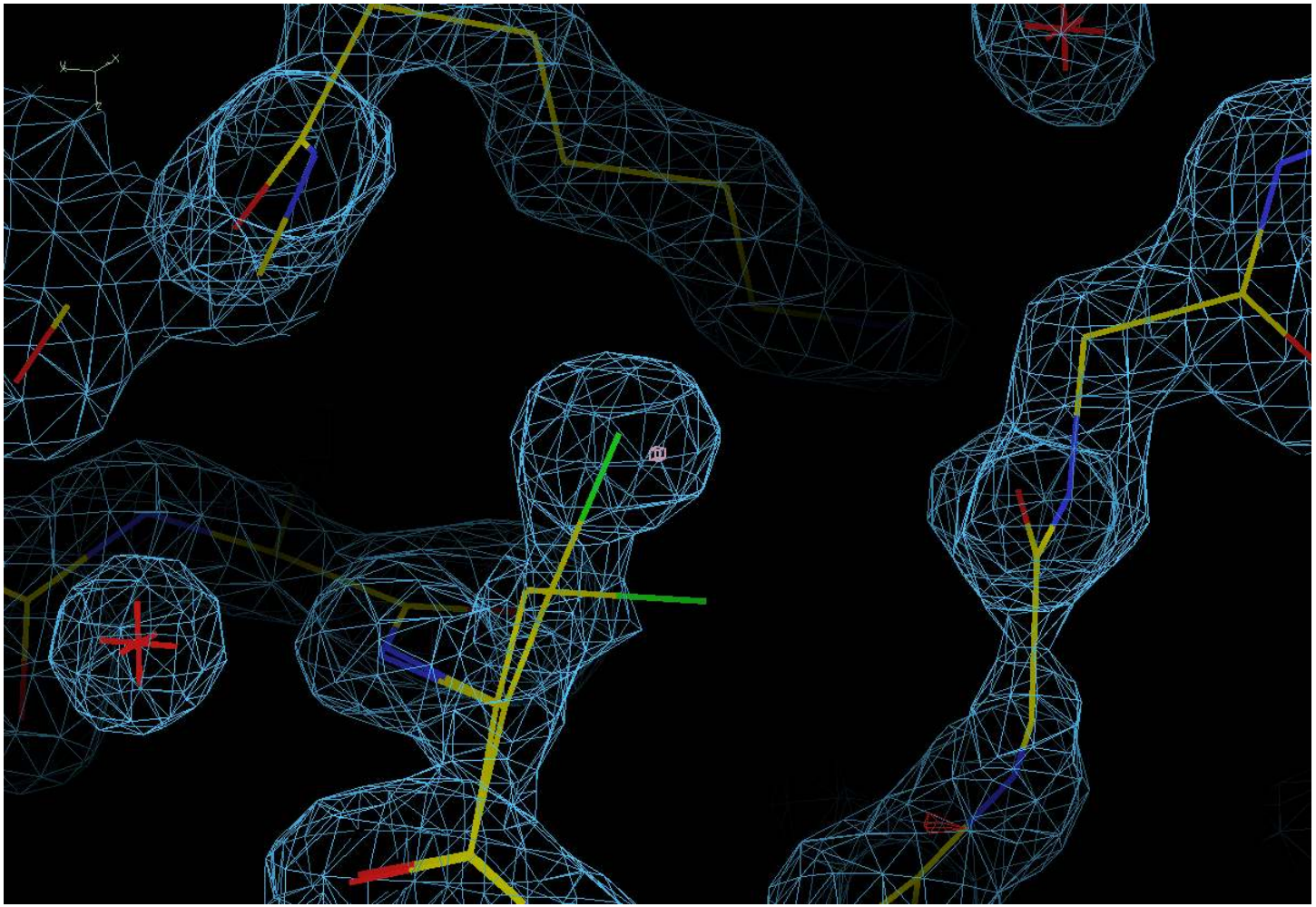
F(early)-F(late): alternate conformation?



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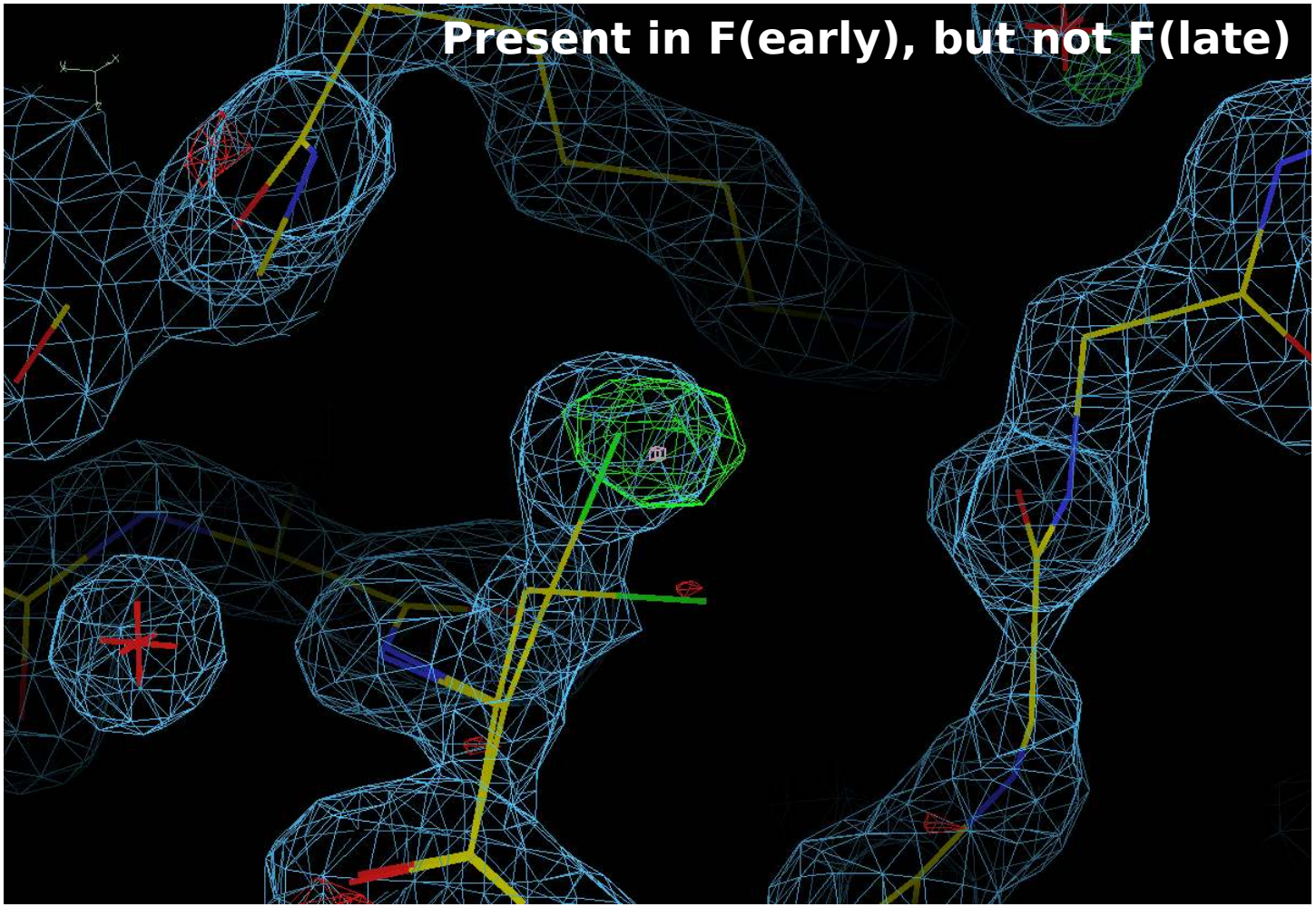
F(early)-F(late): alternate conformation?



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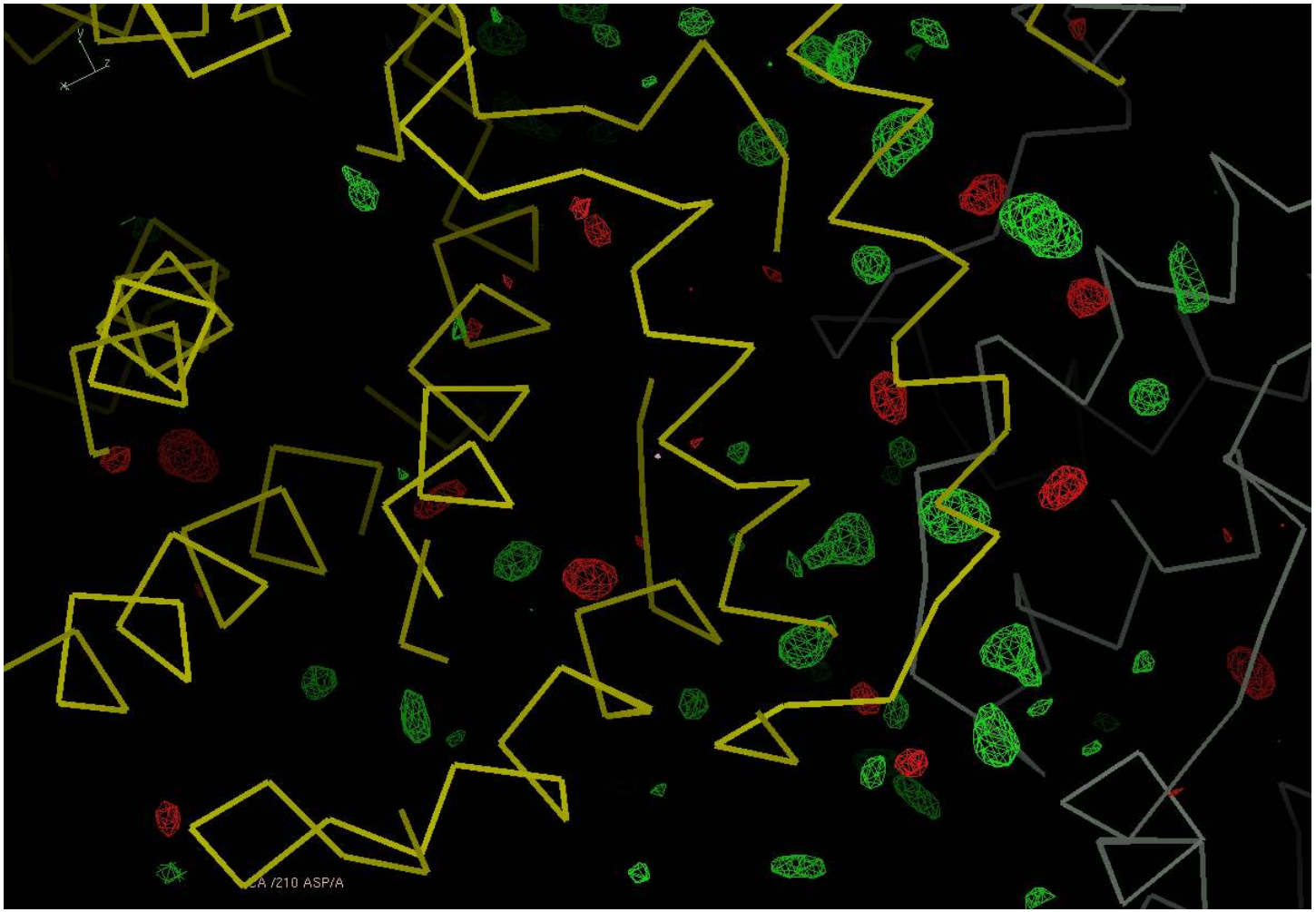
F(early)-F(late): large-scale movements



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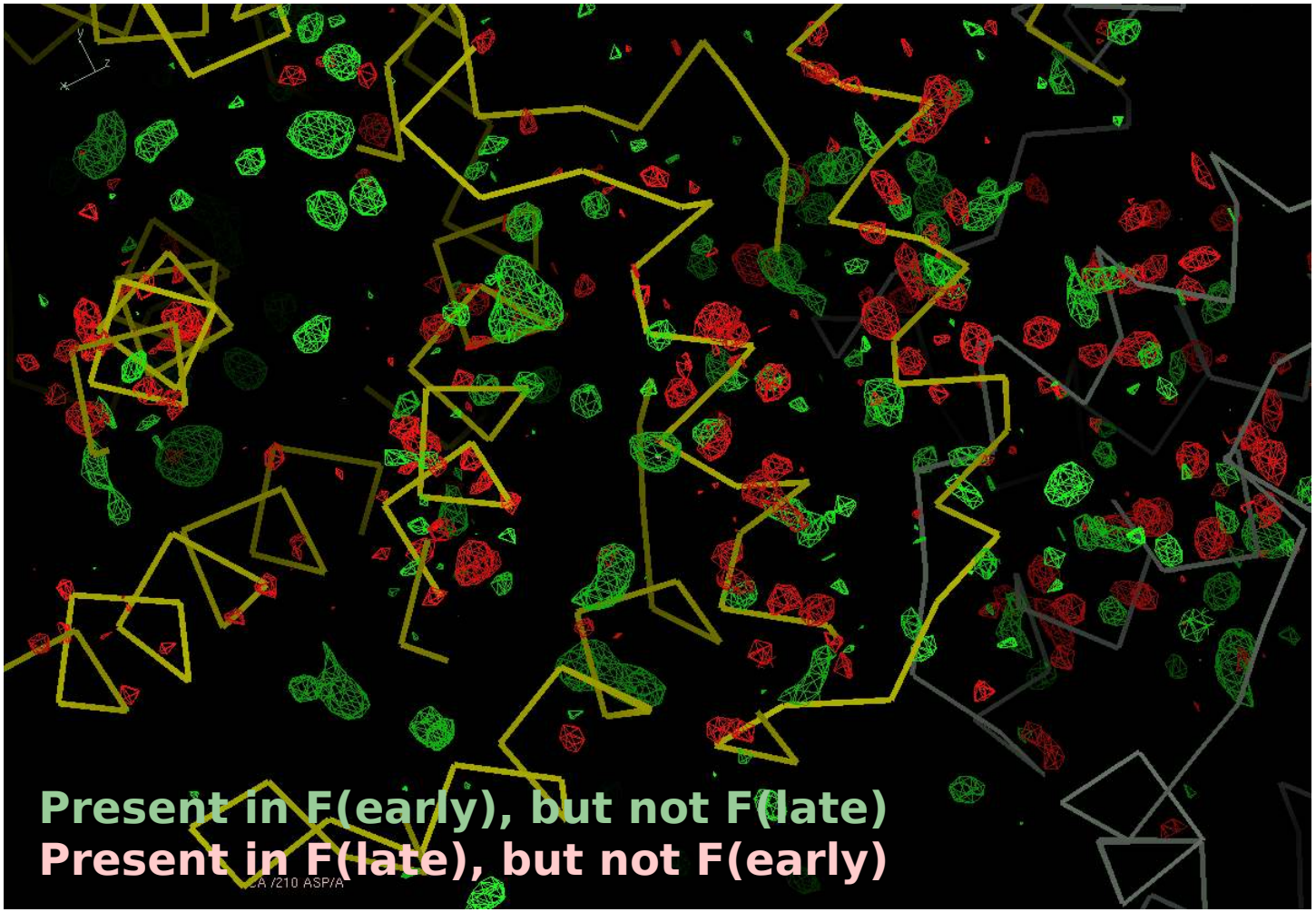
F(early)-F(late): large-scale movements



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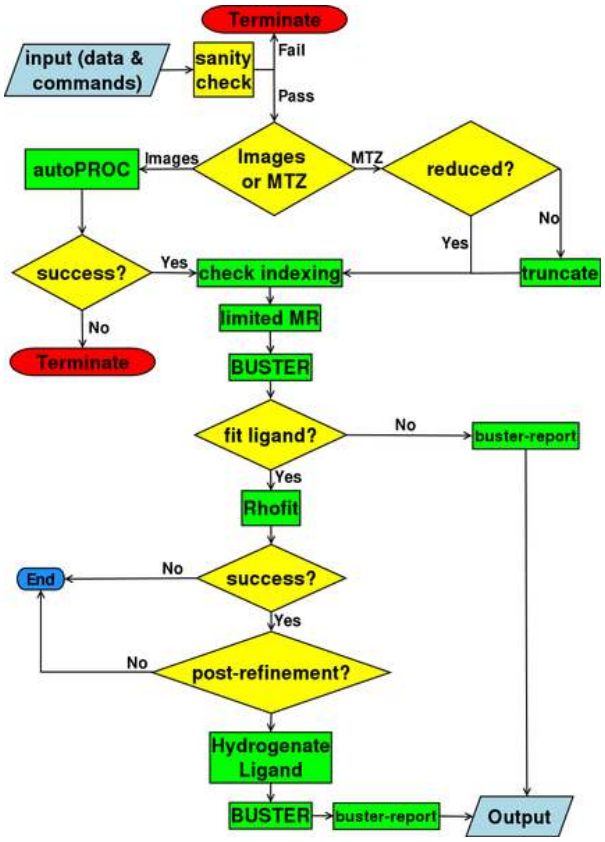
Pipedream - combining all steps



Expert system that links data processing (***autoPROC***), initial refinement & ligand detection (***BUSTER***), ligand fitting (***Rhofit***), final refinement (***BUSTER***) and analysis (***buster-report***) - including **pepflip/SideAide** option.

Used in large-scale operations within commercial and academic environments.

For a given crystal form:

1) Apo model
2) Dataset (directory with images)
3) Ligand dictionary (CIF)

=> refined complex structure

https://www.globalphasing.com/buster/wiki/index.cgi?PipedreamMainpage

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Summary

- **Careful processing of data** can be crucial (not everything is Lysozyme)
  - A **good collection strategy** (that adapts to crystal quality, SG, orientation, detector, beamline, goniostat) will result in better data, better density and better models
- Collect all **prior knowledge**
  - Geometric restraints (good ligand dictionaries)
  - Similarity restraints (NCS, targeting)
  - Occupancy
  - Correct formfactors (fluorescence scan)
- Refine to **convergence**
  - Otherwise difference maps can be hard to interpret
  - And statistics like R/Rfree are (fairly) meaningless
- What happened to crystal during data collection is still (very) important at this stage
  - **Radiation damage**: F(early)-F(late) maps
  - **Anisotropy** (STARANISO)
- Often the defaults (quick click) work well … but to get the correct structure interpretation the **best/correct parametrisation and refinement is important**

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Acknowledgements

- Global Phasing, Cambridge (UK):
  - Gérard Bricogne, Leigh Carter, Claus Flensburg, Rasmus Fogh, Peter Keller, Wlodek Paciorek, Andrew Sharff, Ian Tickle
  - Oliver Smart, Thomas Womack, Eric Blanc, Gwyndaf Evans, Pietro Roversi, John Irwin, Eric de la Fortelle, Marc Schiltz
- Vizier Project FP6
- JCSG
- W. Kabsch, K. Diederichs
- P. Evans
- CCP4
- CCDC
- Martin Field, Alexei Vagin, Garib Murshudov, openbabel developers
- R. Joosten & PDB_REDO team
- Global Phasing Consortium members
- … many, many users & collaborators

https://www.globalphasing.com/
https://www.globalphasing.com/buster/wiki/ (Tutorials etc)