

Molecular replacement experiences

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Correct MR solution

Initial	Final		
	R factor	0.5443	0.4863
	R free	0.5425	0.5063
Rms	BondLength	0.0454	0.0110
Rms	BondAngle	2.9234	1.9581
Rms	ChirVolume	0.8050	0.6442

R-free > 0.5 but going down

Graph Data

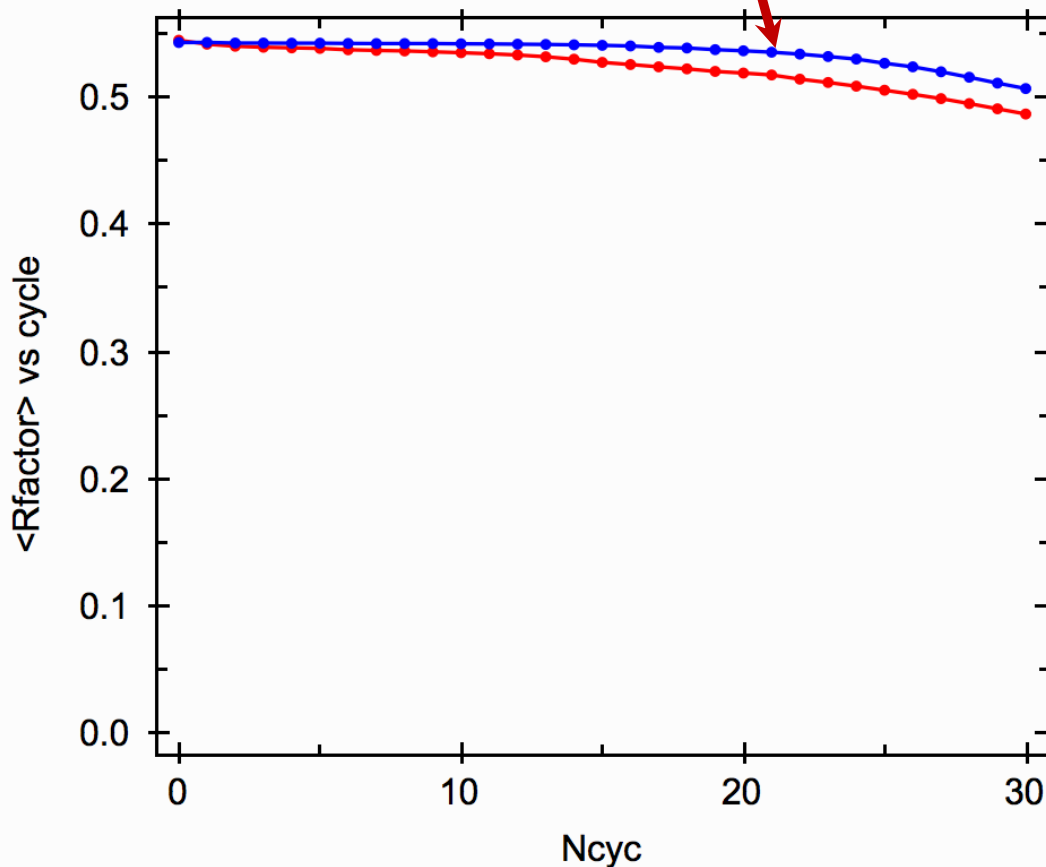
- ▶ Cycle 1. Rfactor analysis, F distribution v resln
- ▶ Cycle 1. FSC and Fom(<cos(DelPhi)>-acentric, ...
- ▶ Cycle 30. Rfactor analysis, F distribution v resln
- ▶ Cycle 30. FSC and Fom(<cos(DelPhi)>-acentric...
- ▶ Cycle 31. Rfactor analysis, F distribution v resln
- ▶ Cycle 31. FSC and Fom(<cos(DelPhi)>-acentric...
- ▼ Rfactor analysis, stats vs cycle
 - ▼ <Rfactor> vs cycle
 - Rfact**
 - Rfree**
 - ▶ FOM vs cycle
 - ▶ -LL vs cycle
 - ▶ -LLfree vs cycle
 - ▶ Geometry vs cycle

☐ raw data

Print

Export

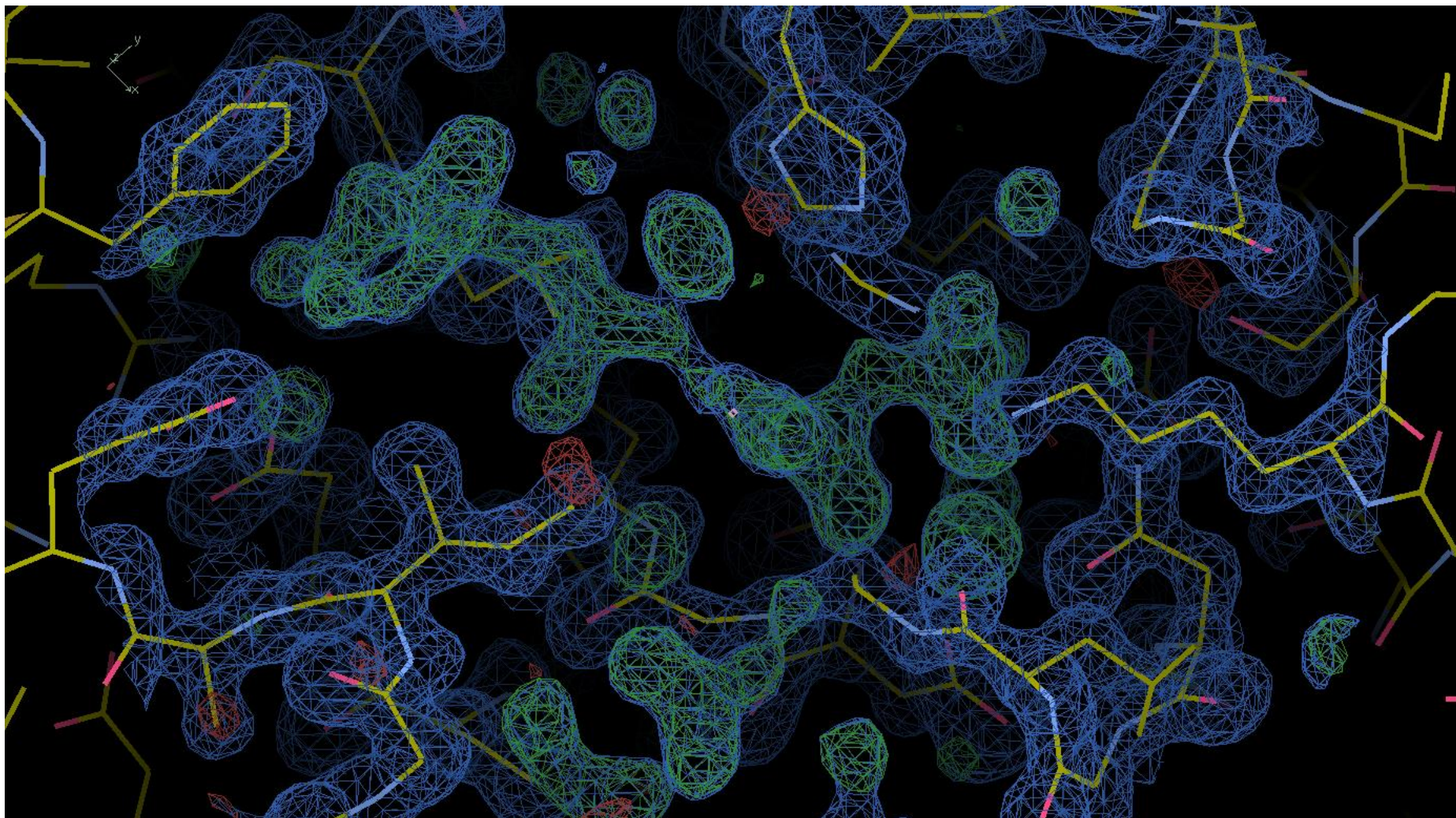
Copy



Correct MR solution map (1.4 Å; 100 %)

Missing side chains are visible

New features (ligands and solvent molecules).



Correct solution at 1.6Å, very remote model.

Result

Initial	Final		
	R factor	0.5575	0.5368
	R free	0.5492	0.5451
	Rms BondLength	0.0148	0.0081
	Rms BondAngle	1.7169	1.8411
	Rms ChirVolume	0.1337	0.0684

R-free > 0.5 and going down very slowly

Graph Data

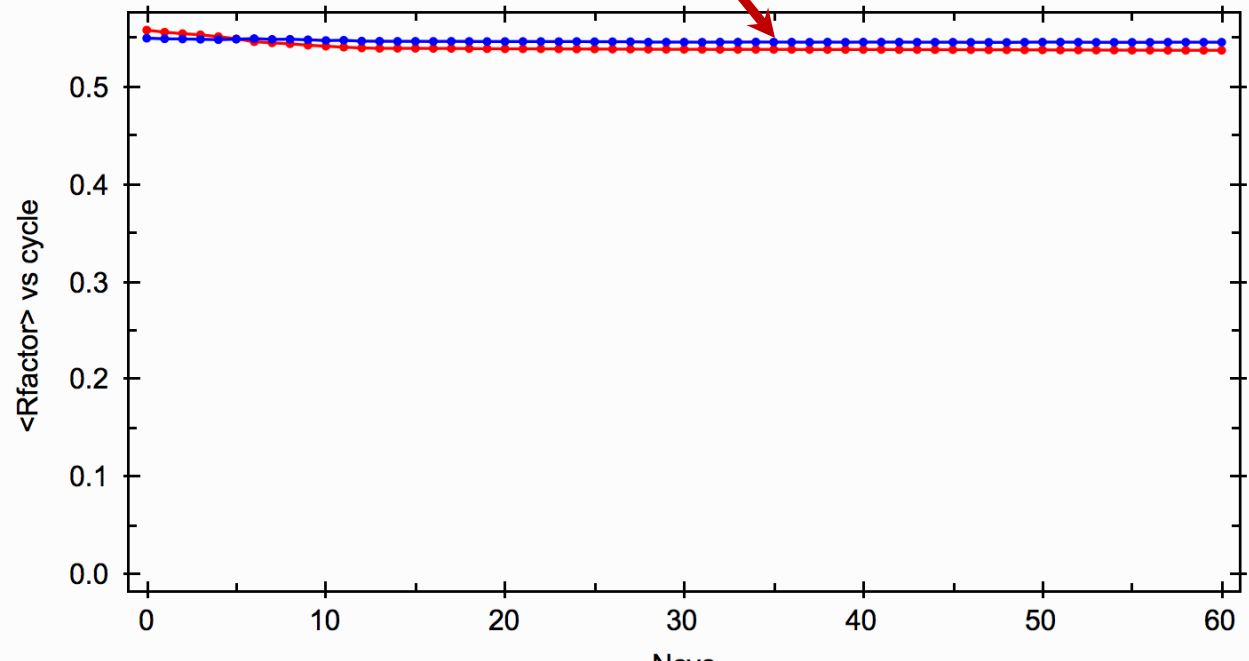
- ▶ Cycle 1. Rfactor analysis, F distribution v resln
- ▶ Cycle 1. FSC and Fom(<cos(DelPhi)>-acentric, ...
- ▶ Cycle 60. Rfactor analysis, F distribution v resln
- ▶ Cycle 60. FSC and Fom(<cos(DelPhi)>-acentric...
- ▶ Cycle 61. Rfactor analysis, F distribution v resln
- ▶ Cycle 61. FSC and Fom(<cos(DelPhi)>-acentric...
- ▼ Rfactor analysis, stats vs cycle

<Rfactor> vs cycle

Rfact

Rfree

- ▶ FOM vs cycle
- ▶ -LL vs cycle
- ▶ -LLfree vs cycle
- ▶ Geometry vs cycle



☐ raw data

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Very remote model initial map

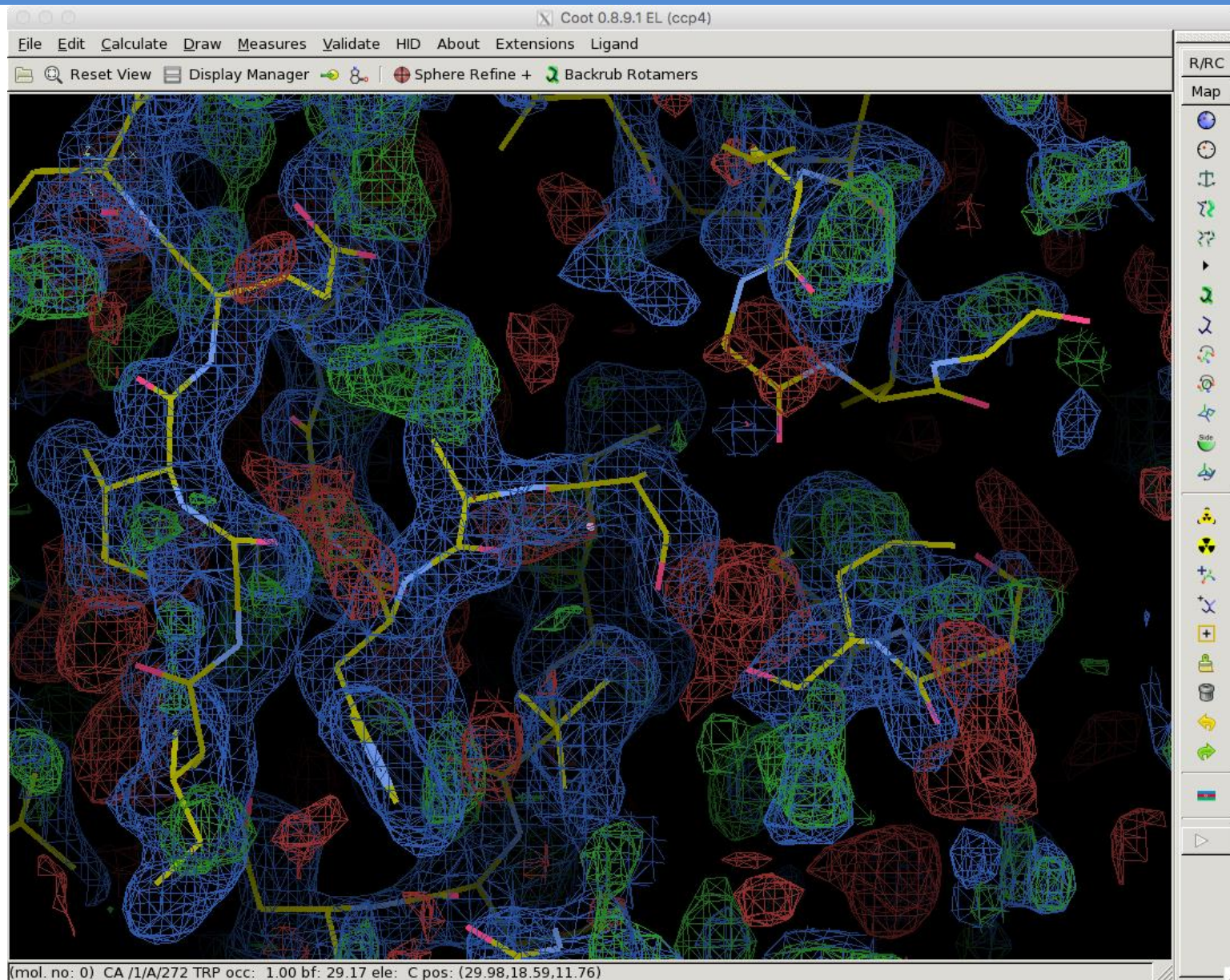
ED maps:

- Good long fragments with smoothly shaped density
- Clearly bad fragments with model in red density
- Clear green density for extension of main chain and building side chains

Refinement:

- R-free does not grow (or drops and slowly grows not higher than initial value)

Very remote model initial map



Wrong MR solution at 1.6 Å resolution.

Result

Initial	Final		
	R factor	0.5154	0.4637
	R free	0.5084	0.5232
	Rms BondLength	0.0089	0.0510
	Rms BondAngle	1.3596	7.1730
	Rms ChirVolume	0.0929	0.6472

Graph Data

▼ Rfactor analysis, stats vs cycle

▼ <Rfactor> vs cycle

Rfact

Rfree

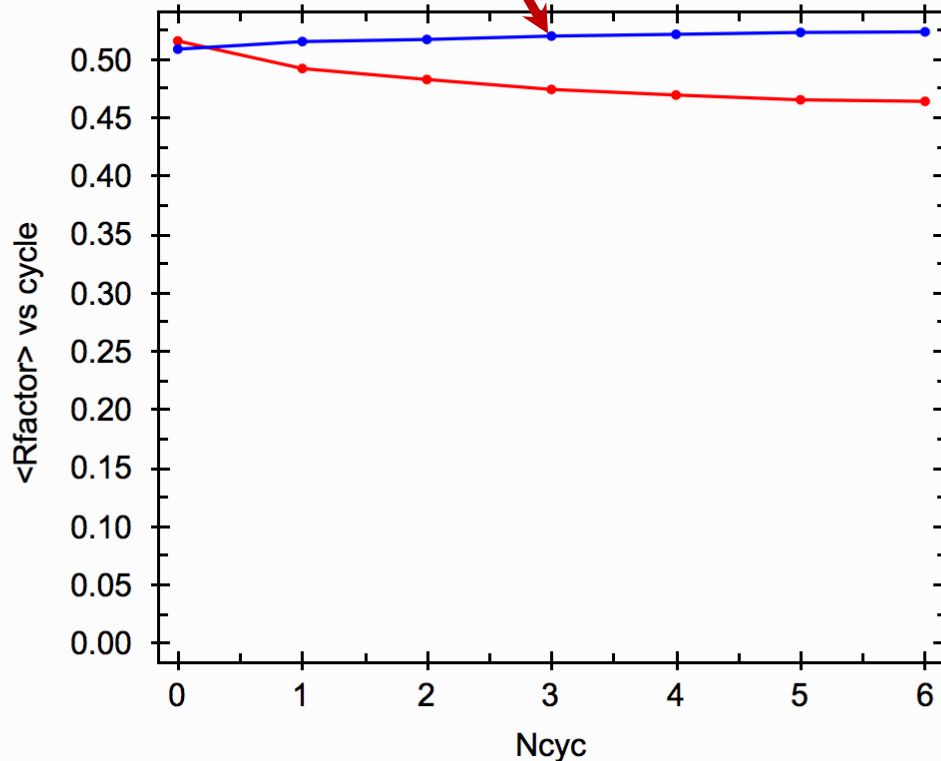
- ▶ FOM vs cycle
- ▶ -LL vs cycle
- ▶ -LLfree vs cycle
- ▶ Geometry vs cycle

☐ raw data

Print

Export

Copy

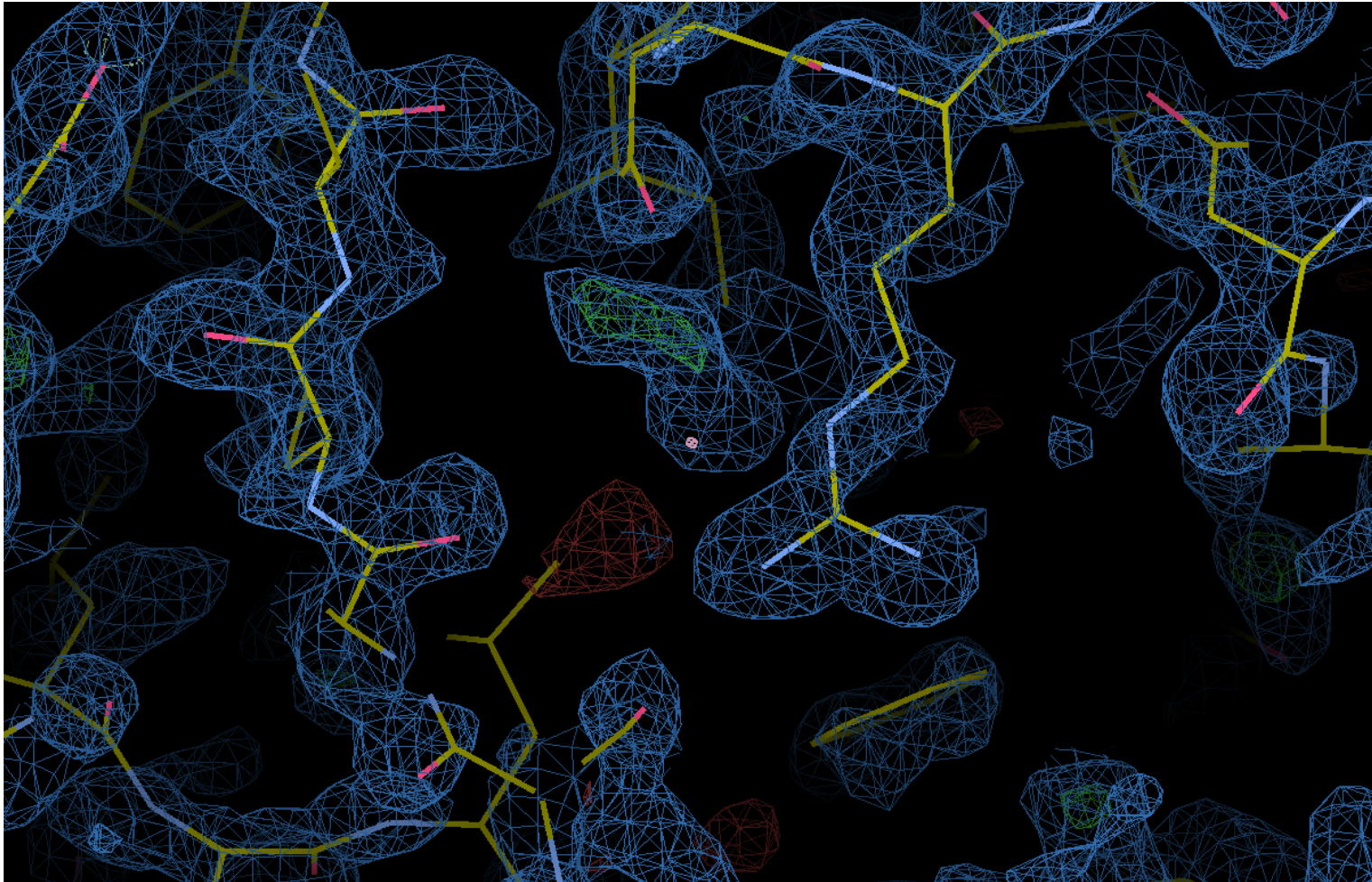


How does wrong MR solution map looks like at 1.6Å?

The maps look more similar to the model the lower the resolution 'Model bias'

Main chain breaks

No useful features for rebuilding



35 % complete model at 2.5 Å resolution.

Initial	Final		
	R factor	0.5059	0.4899
	R free	0.5063	0.5018
Rms BondLength		0.0134	0.0041
Rms BondAngle		1.5788	1.0578
Rms ChirVolume		0.1075	0.0943

**R-free > 0.5 and slowly
going down**

Graph Data

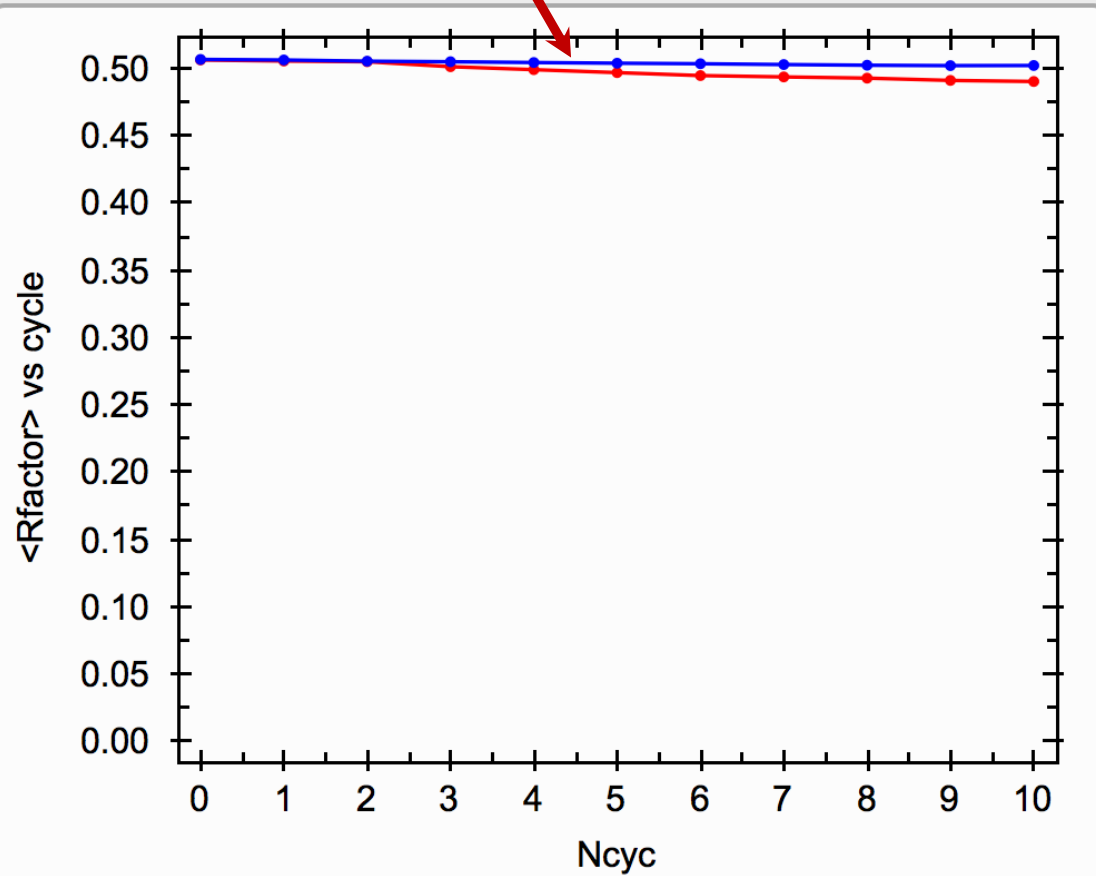
- ▶ Cycle 1. Rfactor analysis, F distribution v resln
- ▶ Cycle 1. FSC and Fom(<cos(DelPhi)>-acentric, ...
- ▶ Cycle 10. Rfactor analysis, F distribution v resln
- ▶ Cycle 10. FSC and Fom(<cos(DelPhi)>-acentric...
- ▶ Cycle 11. Rfactor analysis, F distribution v resln
- ▶ Cycle 11. FSC and Fom(<cos(DelPhi)>-acentric...
- ▼ Rfactor analysis, stats vs cycle
 - ▼ <Rfactor> vs cycle
 - Rfact
 - Rfree
 - ▶ FOM vs cycle
 - ▶ -LL vs cycle
 - ▶ -LLfree vs cycle
 - ▶ Geometry vs cycle

☐ raw data

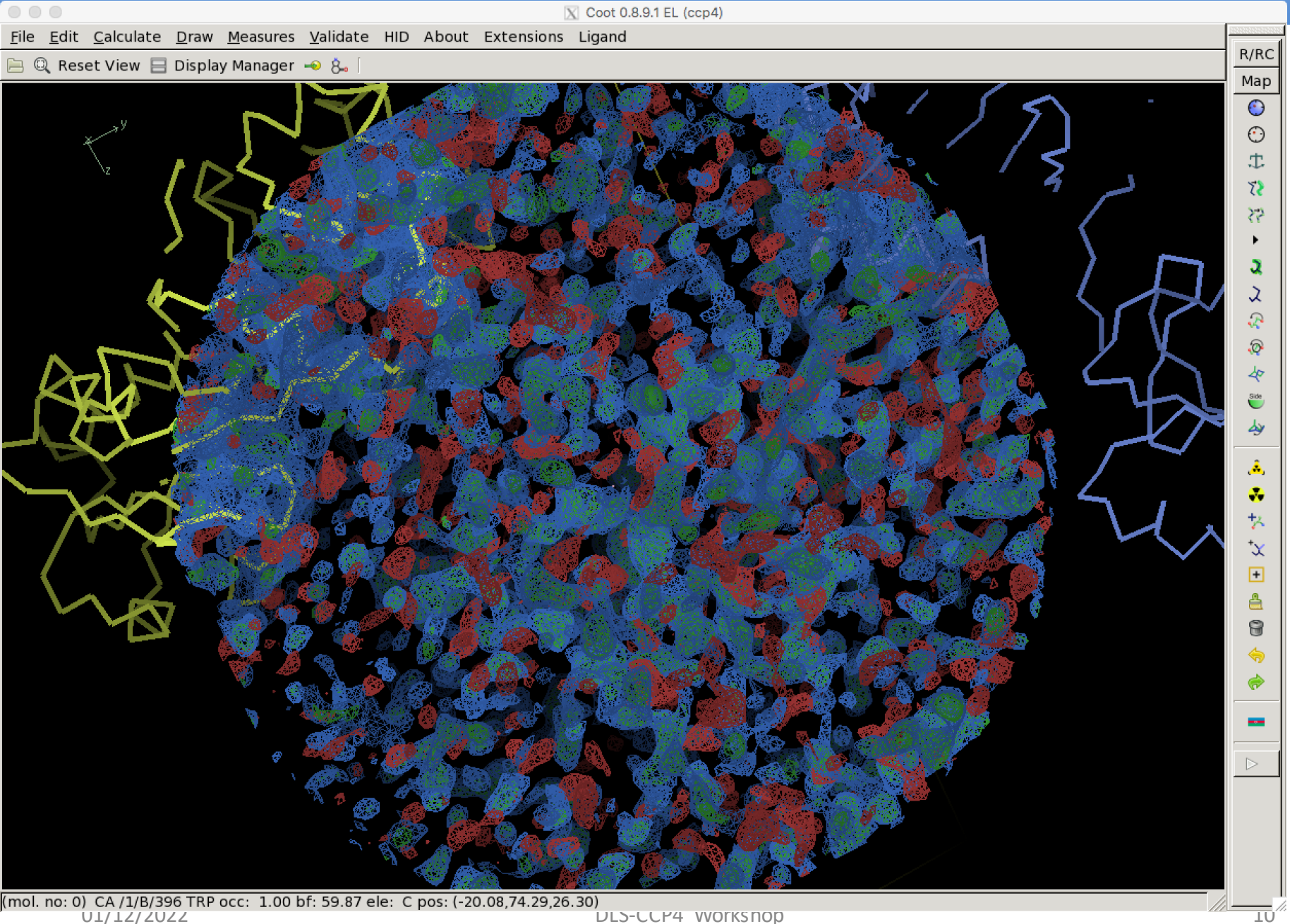
Print

Export

Copy



35 % complete model at 2.5 Å resolution

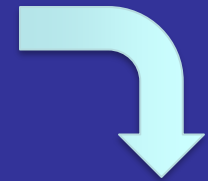
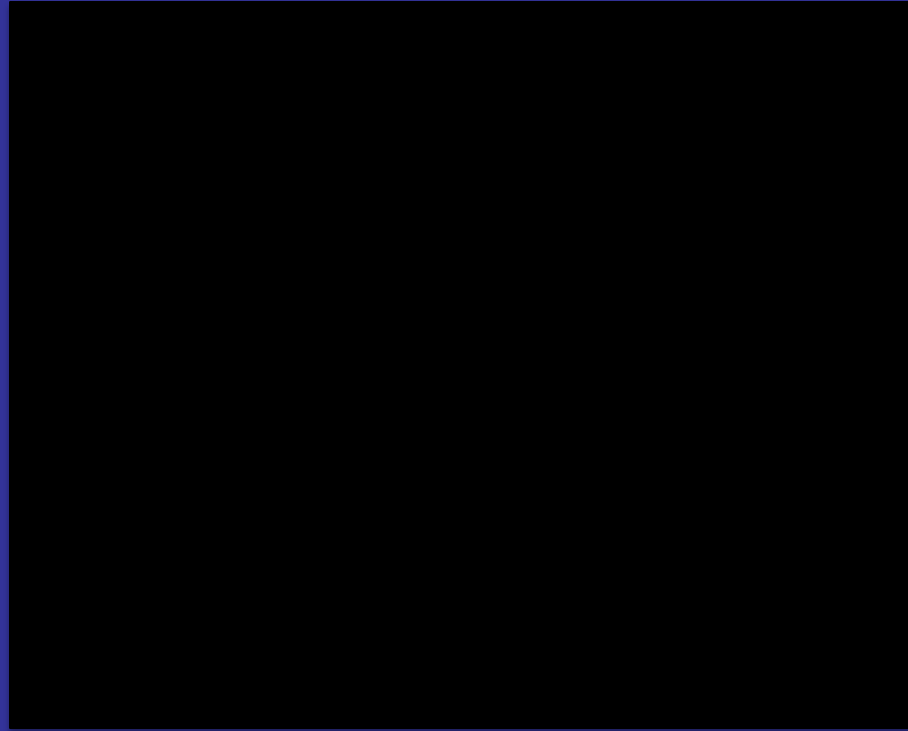


Outline of this talk

- **Molecular replacement approaches when pipelines fail**
- **Simple steps in conventional MR search**
- **Phased MR examples**
- **Density modification**
- **Crystal anisotropy**
- **Self-rotation function and examples**
- **Conserved molecular symmetry use example**

A Black Box crystallography pipeline

Data,
sequence

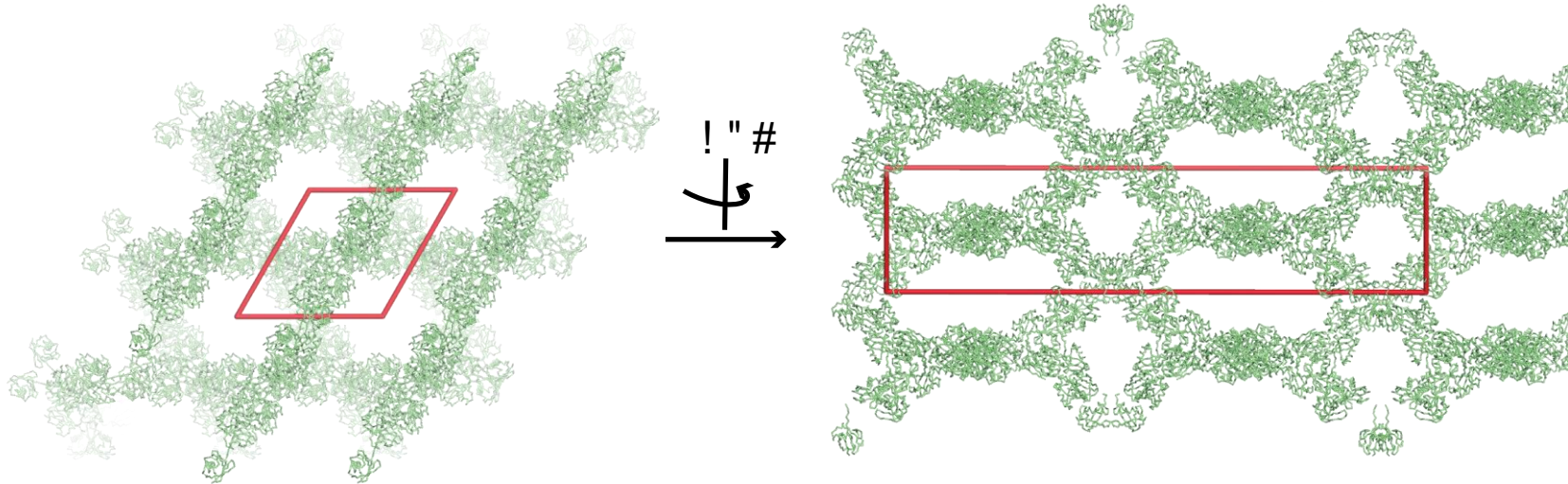
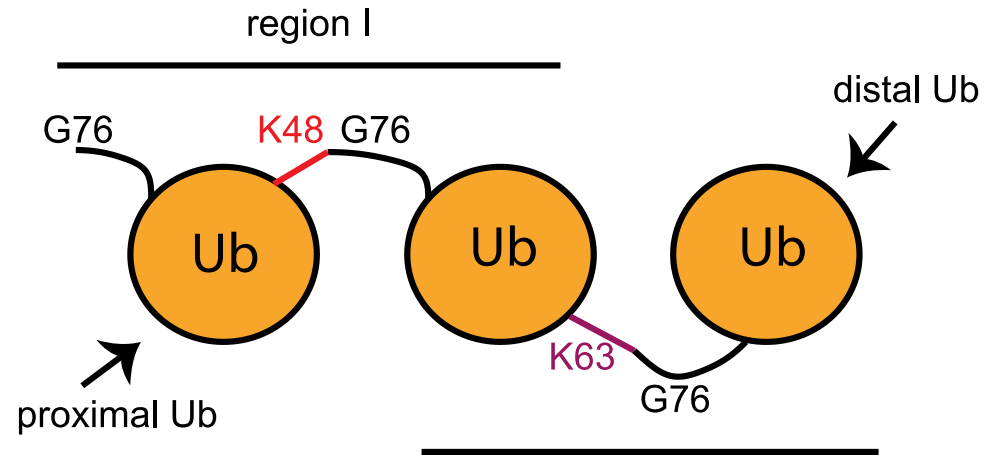


Refined
Model

User does not have to know what is inside

Tri-ubiquitin with Dr Reuven Wiener (number of RF peaks).

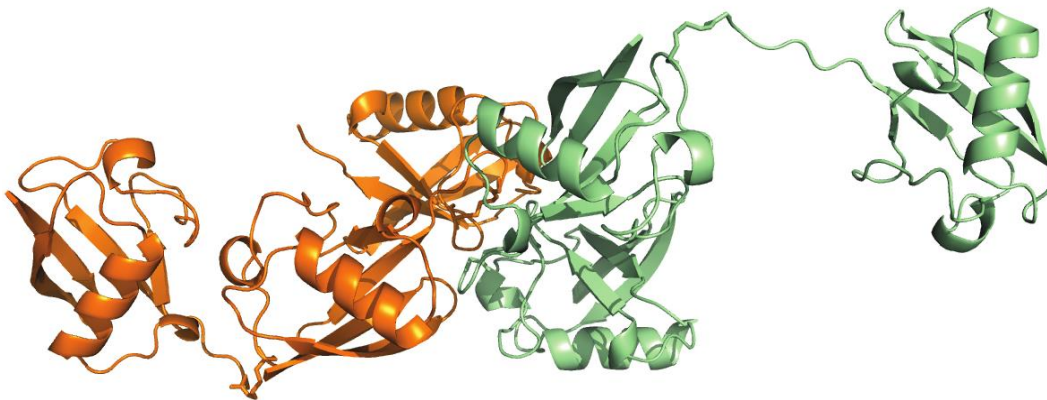
Space group $P6_122$
Cell 110.8, 110.8, 417.0 Å
Resolution 3.2 Å
Solvent content 82 %



Padala et al. (2017) JMB 429, 3801-3813.

MORDA located 3 Ub monomers in P6₁22 with good contrast, however the partial structure did not refine, probably due to low resolution of the data.

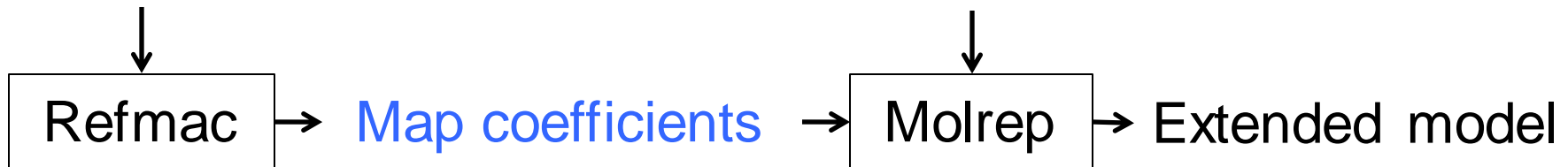
Increasing number of RF peaks to 200 (instead of default 30) in MOLREP gave clear solution for 6 Ub monomers (2 trimers), this model refined to FreeR below 28 %. Two of the correct peaks were in the second hundred of RF peaks list.



Search in the electron density map

Partial structure

Search model



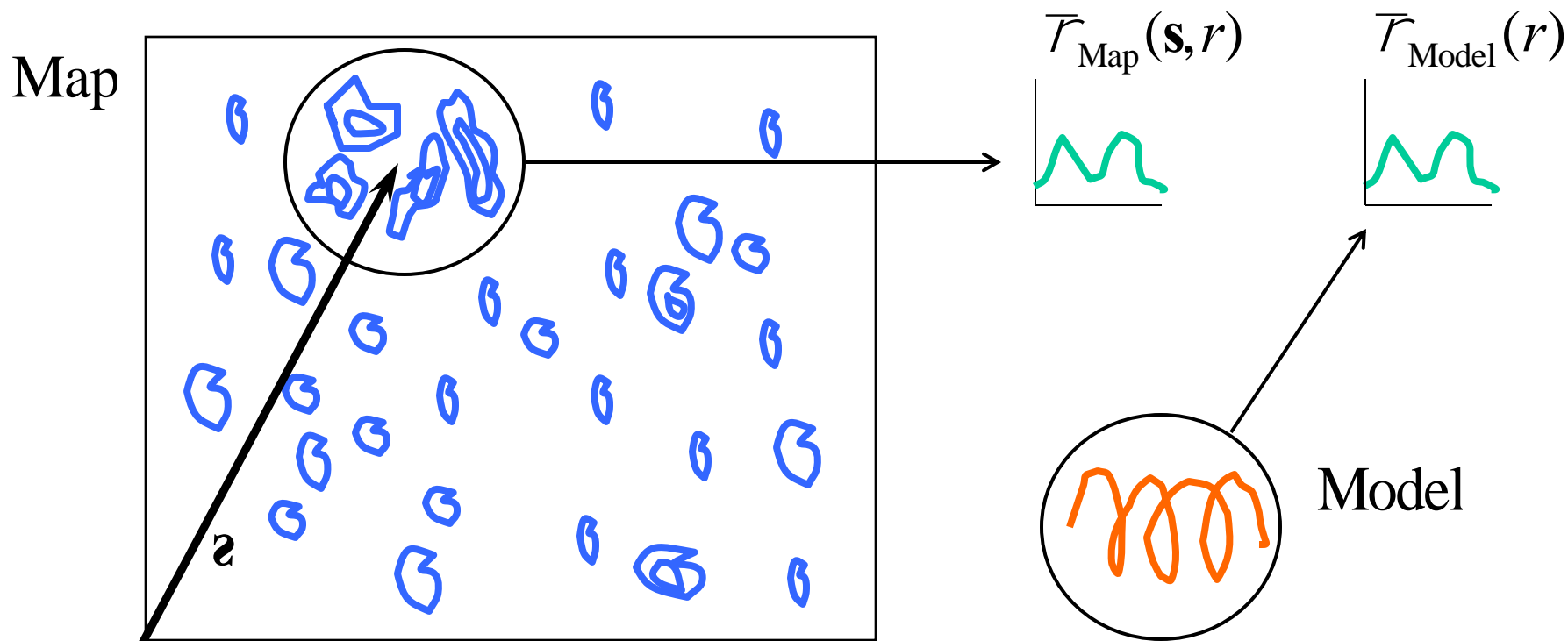
Search in the map

- Calculate 2-1 or 1-1 maps after restrained refinement of partial structure
- Flatten the **map** which corresponding to the known substructure
- Calculate structure amplitudes from the modified map
- Use these **modified amplitudes** in Rotation Function
- And finally – **Phased TF**

Molrep: SAPTF

Spherically Averaged Phased Translation Function
(FFT based algorithm)

$$\text{SAPTF}(\mathbf{s}) = \int_0^\infty \bar{T}_{\text{Map}}(\mathbf{s}, r) \bar{T}_{\text{Model}}(r) r^2 dr$$



Molrep: Search in the map with SAPTF

1. Find approximate position:

Spherically Averaged **Phased** Translation Function

2. Find orientation:

Local Rotation Function

– Structure amplitudes from the density within the SAPTF sphere

3. Verify and adjust position:

Phased Translation Function

- Local RF is less sensitive than Phased RF to inaccuracy of the model position

Phased MR options in MOLREP

Molrep

Job title

Do **MR Using Phases**

Use MAP files for ☐ observed data ☐ search model

Data

a temp_b.mtz Browse View

F PHI FWT PHWT

Obs not used

Model

Full path.. /Users/misha/work/biomex/9_biomex/mod2.pdb Browse View

Sequence

a Browse View

Fixed

a f24.pdb Browse View

☐ Automatic output filename

Solution

a mod2_molrep1.pdb Browse View

Search Options

Search protocol **RF + Phased TF**

Number of copies RF + Phased TF

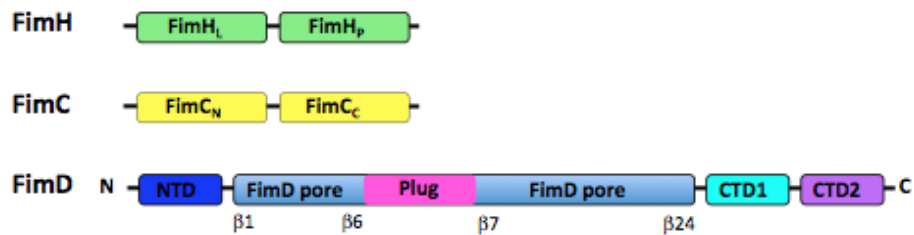
Number of RF pe SAPTF + Local Phased RF + Phased TF

Diameter of sear SAPTF + Local RF + Phased TF

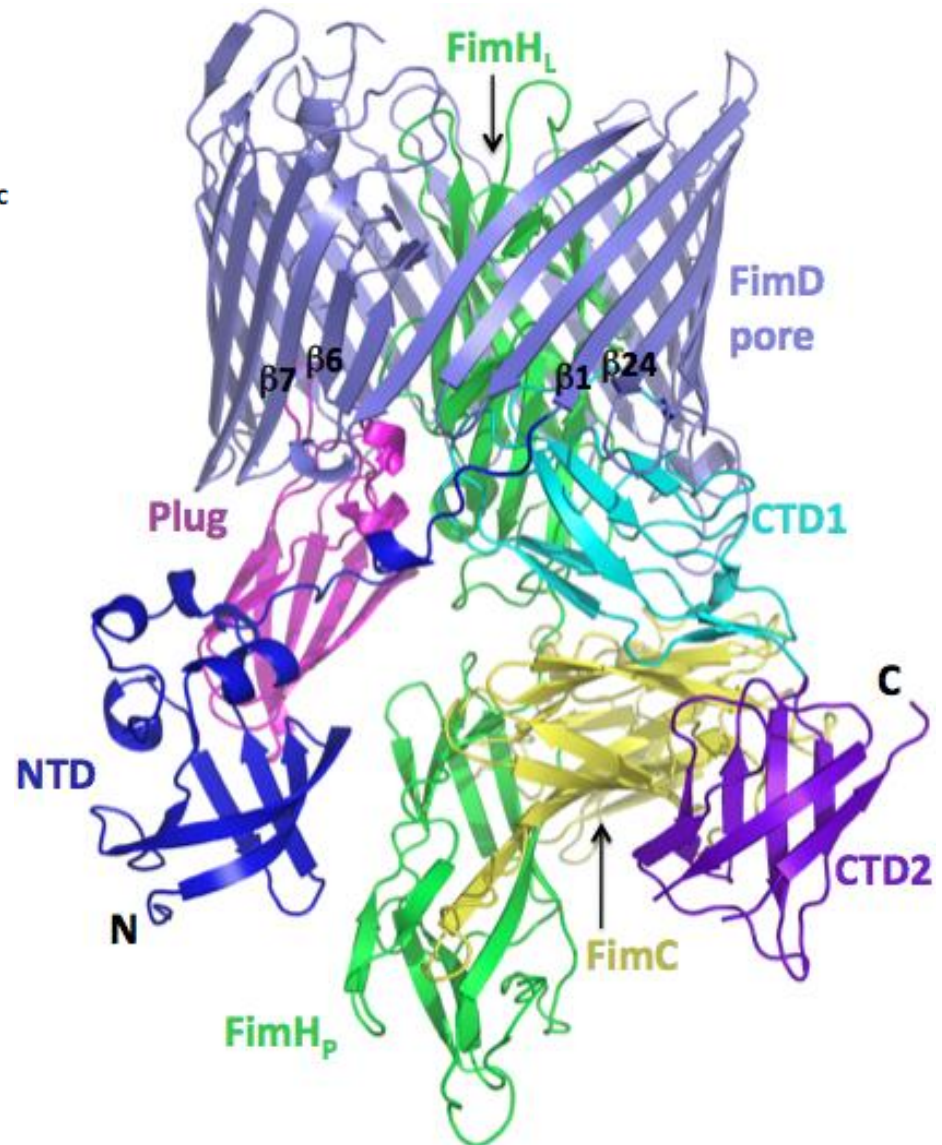
Pseudo-Translation: **Auto**

Experimental Data

Usher complex *E. coli*



- Asymmetric unit two copies
- Resolution 2.8 Å

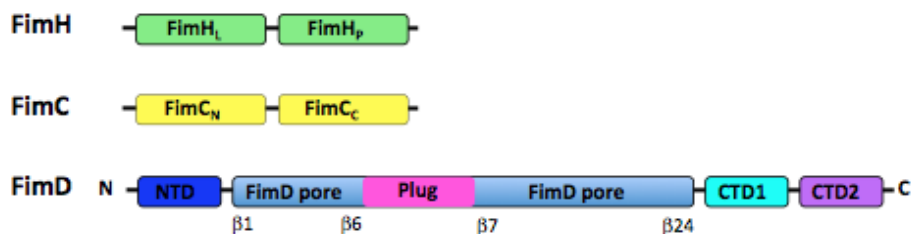


Phan et. al (2011) Nature, 474, 50-53

Usher complex structure solution

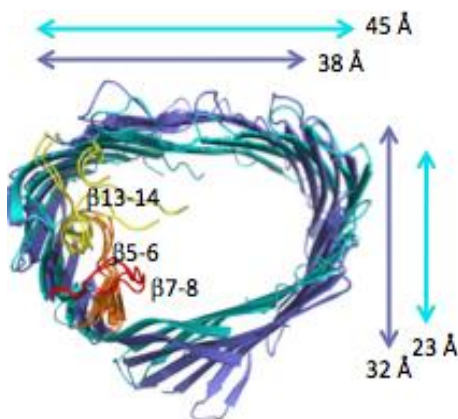
1. Conventional MR

- FimC-N + FimC-C
- FimH-L + FimH-P
- FimD-Pore



2. Jelly body refinement (Refmac)

- FimD-Pore



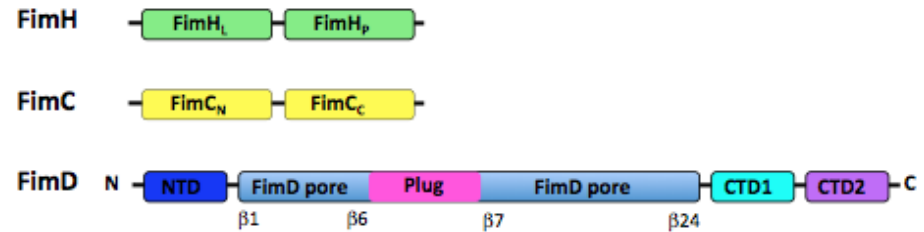
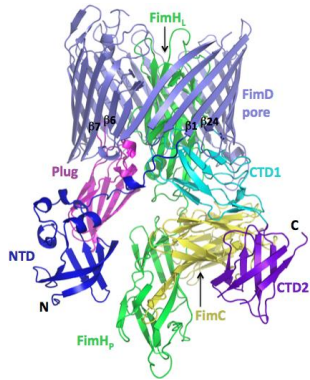
3. Fitting into the electron density

- FimD-Plug
- FimD-NTD
- FimD-CTD-2

4. Manual building

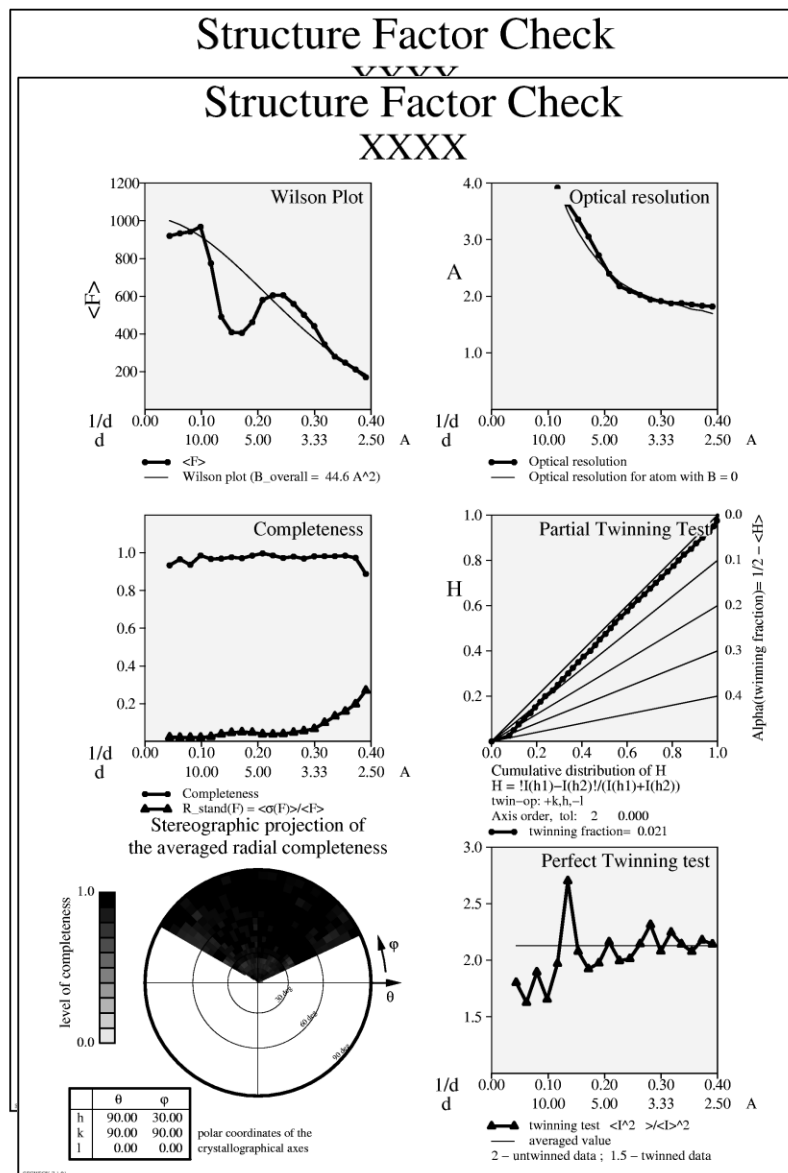
- FimD-CTD-1

Performance of fitting methods

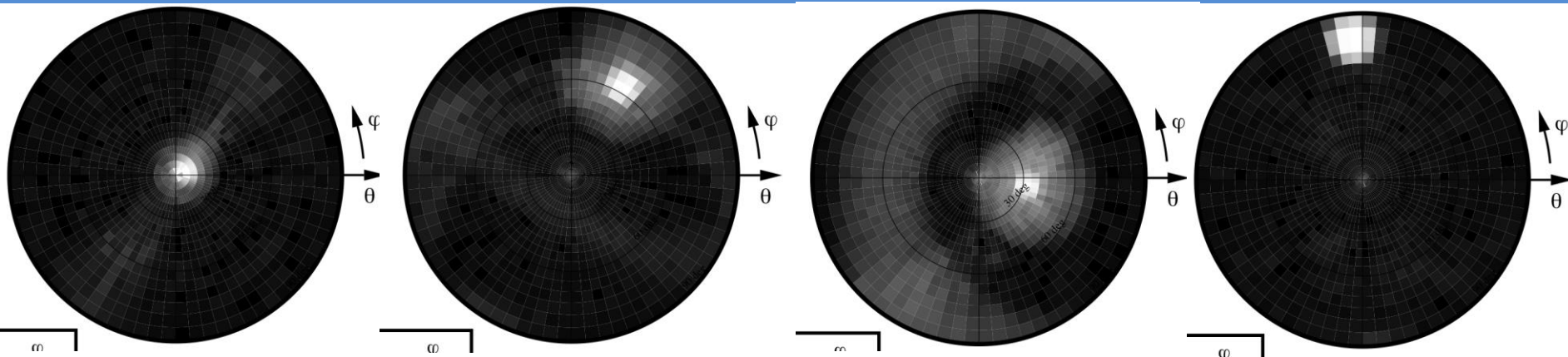


	search model	sequence identity	"Masked" RF PTF	SAPTF PRF PTF	SAPTF Local RF PTF
FimD-Plug	3fip_A	38.5%	2	—	1
FimD-NTD	1ze3_D	100%	2	1	2
FimD-CTD-2	3l48_A	33.3%	—	2	—

Trying several methods is a good practice (also a way of cross-validation)



Multicrystal averaging: the same lattice.



In a recent medium resolution (2.5Å) protein complex case I have built most of the model (2 copies of two proteins in a.u.), however a particular interdomain loop (containing a disulphide) in a larger protein remained poorly defined. Inspection of this P1 crystal data statistics suggested good (for P1) completeness of 93% but low redundancy (1.7).

Multicrystal averaging (DMMULTI) using three additional slightly non-isomorphous datasets (2.7-2.9Å) in the same space group (different blind zones), alongside with data of domain structures of the smaller protein in this crystal from pdb and subsequent phased refinement in REFMAC5 produced a map with interpretable density for the elusive loop.

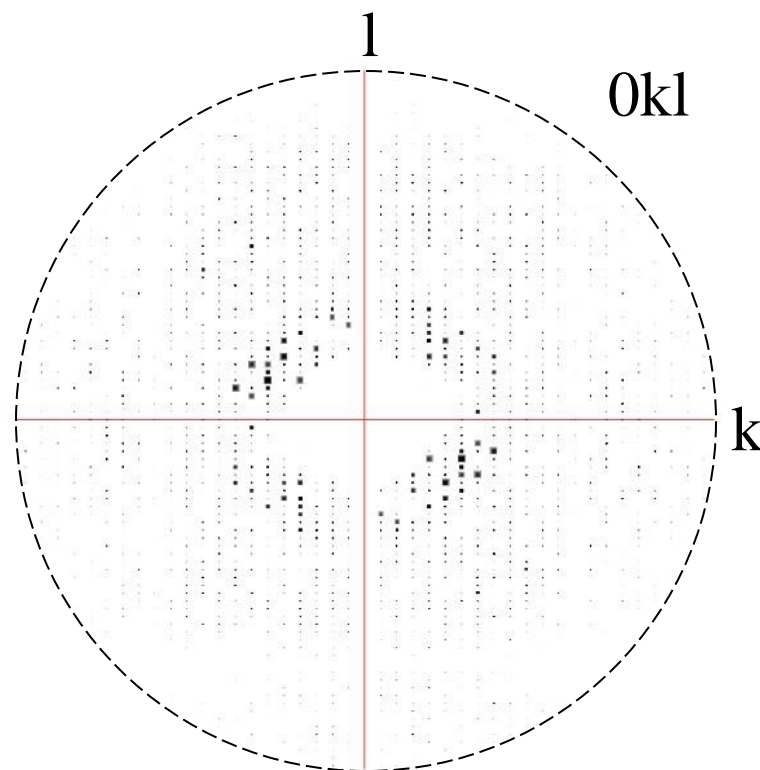
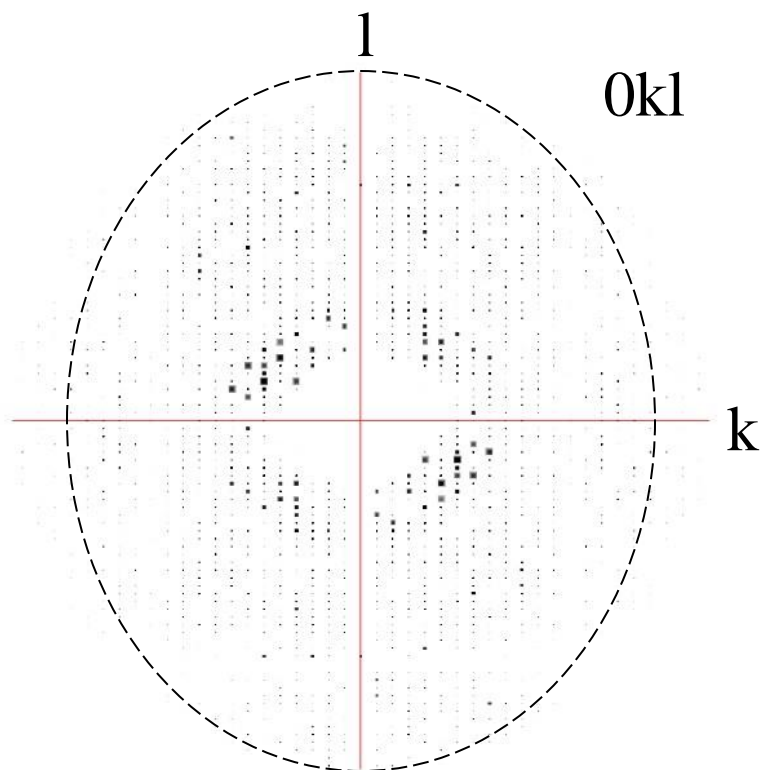
ANISOTROPY CORRECTION OF DATA

MOLREP does anisotropic corrections using structure factor amplitudes.

This may result in raising the noise level in extreme cases

PHASER uses intensities for correction, which appears to give better results.

STARANISO server uses unmerged intensities to produce elliptically complete data, these appear to give better results in MR.



STARANISO corrected data is better in MR phasing

May be better in EP phasing

MR case: F222

RF staraniso

MOLREP

No correct RF

peak in first 40

#Sol_	RF	theta	phi	chi	alpha	beta	gamma	Rf	Rf/sigma
Sol_RF	1	34.27	116.59	99.25	70.77	50.81	17.60	0.3181E-01	4.68
Sol_RF	2	146.36	-62.44	142.75	139.60	63.33	84.48	0.2585E-01	3.81
Sol_RF	3	142.88	-54.87	134.42	152.92	67.60	82.66	0.2470E-01	3.64
Sol_RF	4	143.11	-53.26	131.45	156.16	66.36	82.67	0.2453E-01	3.61
Sol_RF	5	149.71	-68.68	153.17	126.76	58.77	84.12	0.2359E-01	3.47
Sol_RF	6	135.07	-72.35	124.14	144.48	77.22	109.17	0.2220E-01	3.27

	RF	TF	theta	phi	chi	tx	ty	tz	TF/sg	wRfac	Score
1	1	2	34.27	116.59	99.25	0.224	0.190	0.455	6.38	0.606	0.24150
2	10	14	97.18	130.04	50.83	0.007	0.059	0.385	3.66	0.633	0.18717
3	8	3	30.96	-140.81	79.97	0.123	0.159	0.195	3.73	0.634	0.17748
4	9	13	46.43	58.19	119.28	0.409	0.058	0.093	4.08	0.627	0.17734
5	2	7	146.36	-62.44	142.75	0.380	0.060	0.311	3.60	0.633	0.17621
6	5	3	149.71	-68.68	153.17	0.443	0.333	0.254	4.34	0.634	0.17174
7	7	11	149.69	-95.68	174.41	0.286	0.402	0.302	3.32	0.628	0.16794
8	3	1	142.88	-54.87	134.42	0.334	0.046	0.045	3.90	0.639	0.16778

	RF	TF	theta	phi	chi	tx	ty	tz	TF/sg	wRfac	Score
1	1	1	34.27	116.59	99.25	0.475	0.440	0.205	5.15	0.683	0.11021
2	5	13	149.71	-68.68	153.17	0.000	0.147	0.448	4.19	0.687	0.10395
3	7	3	149.69	-95.68	174.41	0.095	0.376	0.204	4.21	0.680	0.10385
4	6	8	135.07	-72.35	124.14	0.018	0.402	0.417	4.79	0.691	0.10316
5	2	5	146.36	-62.44	142.75	0.454	0.422	0.253	4.69	0.688	0.09854
6	9	4	46.43	58.19	119.28	0.252	0.447	0.486	6.46	0.697	0.09835
7	3	14	142.88	-54.87	134.42	0.084	0.296	0.326	4.76	0.701	0.09503
8	4	8	143.11	-53.26	131.45	0.338	0.045	0.066	5.31	0.697	0.09413

TF staraniso

High contrast
solution

MOLREP

No correction

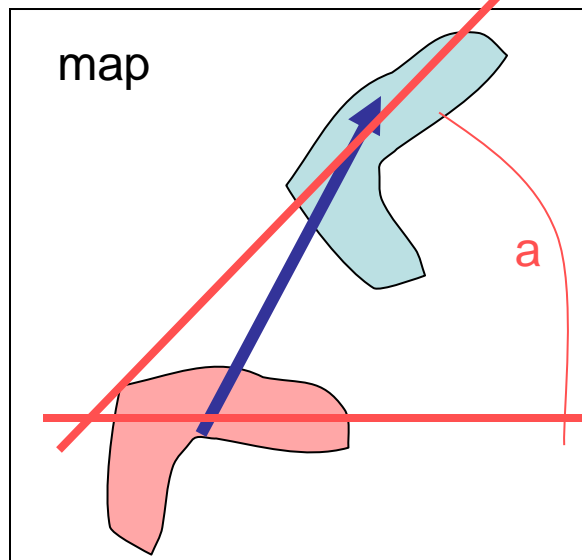
Correct TF

found, very

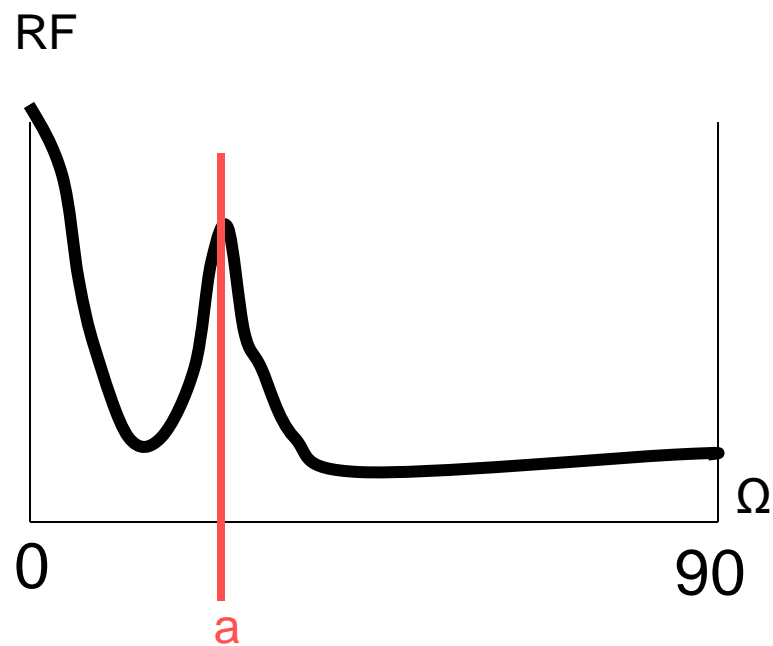
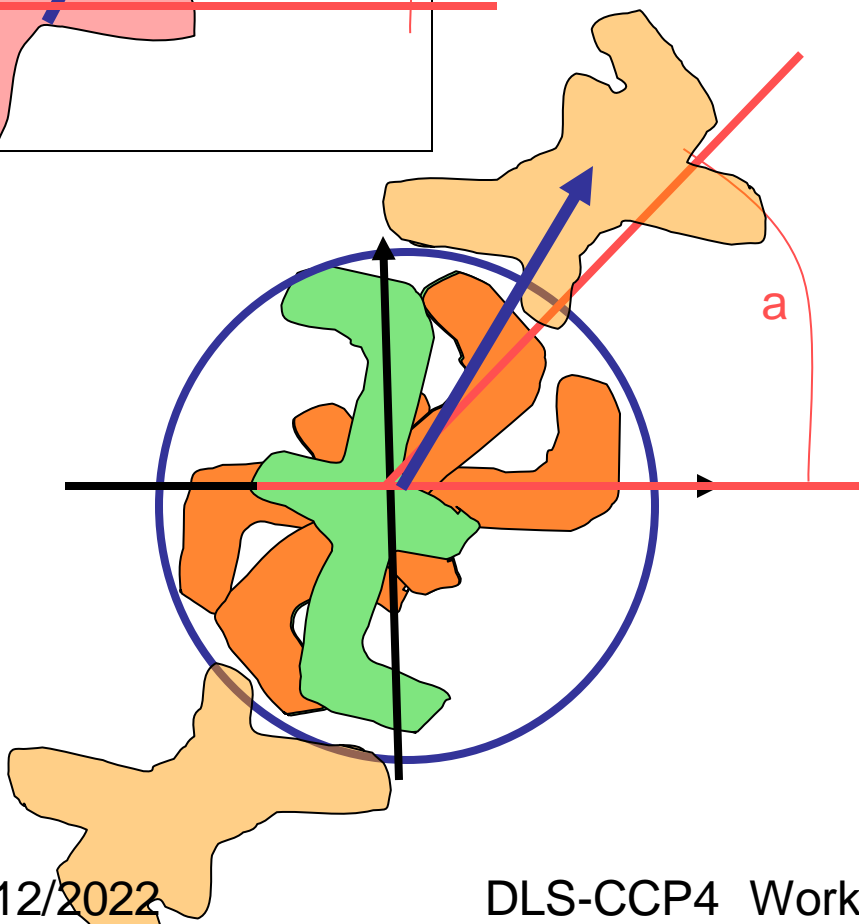
little contrast

PHASER is less
affected

Self Rotation Function

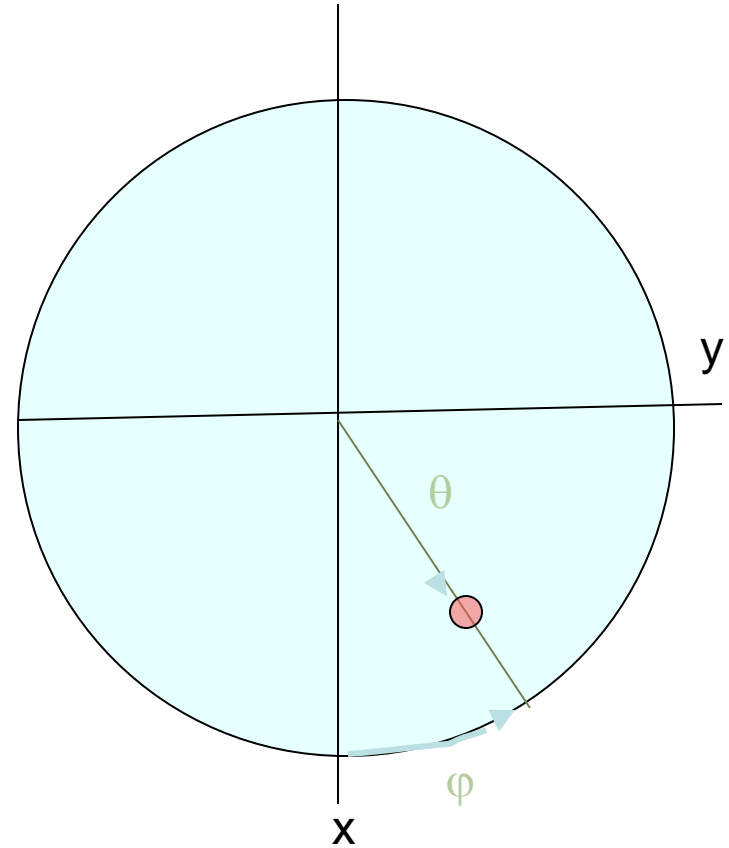
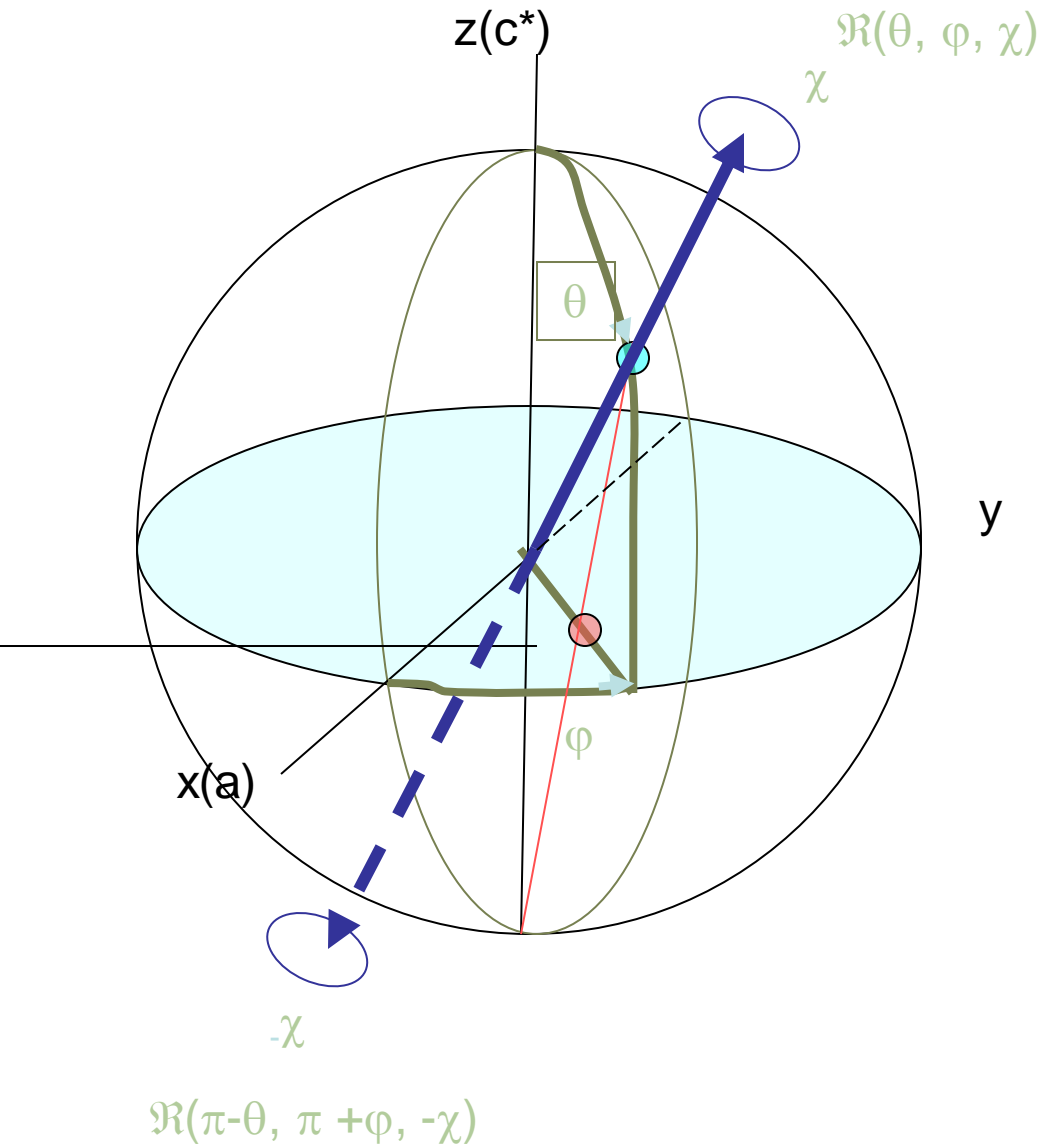


$$\text{RF}(\Omega) = \int P_{\text{obs}}(r) \Re_{\Omega}\{P_{\text{obs}}(r)\} dr$$



Self Rotation Function

Plot for rotation by χ
(stereographic projection)

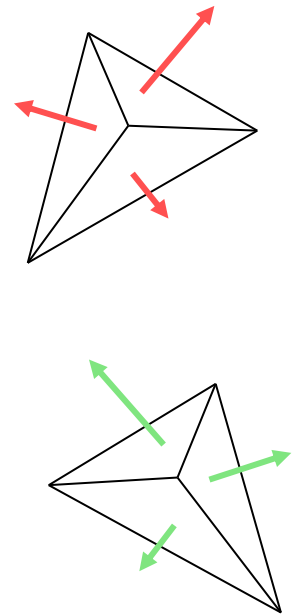
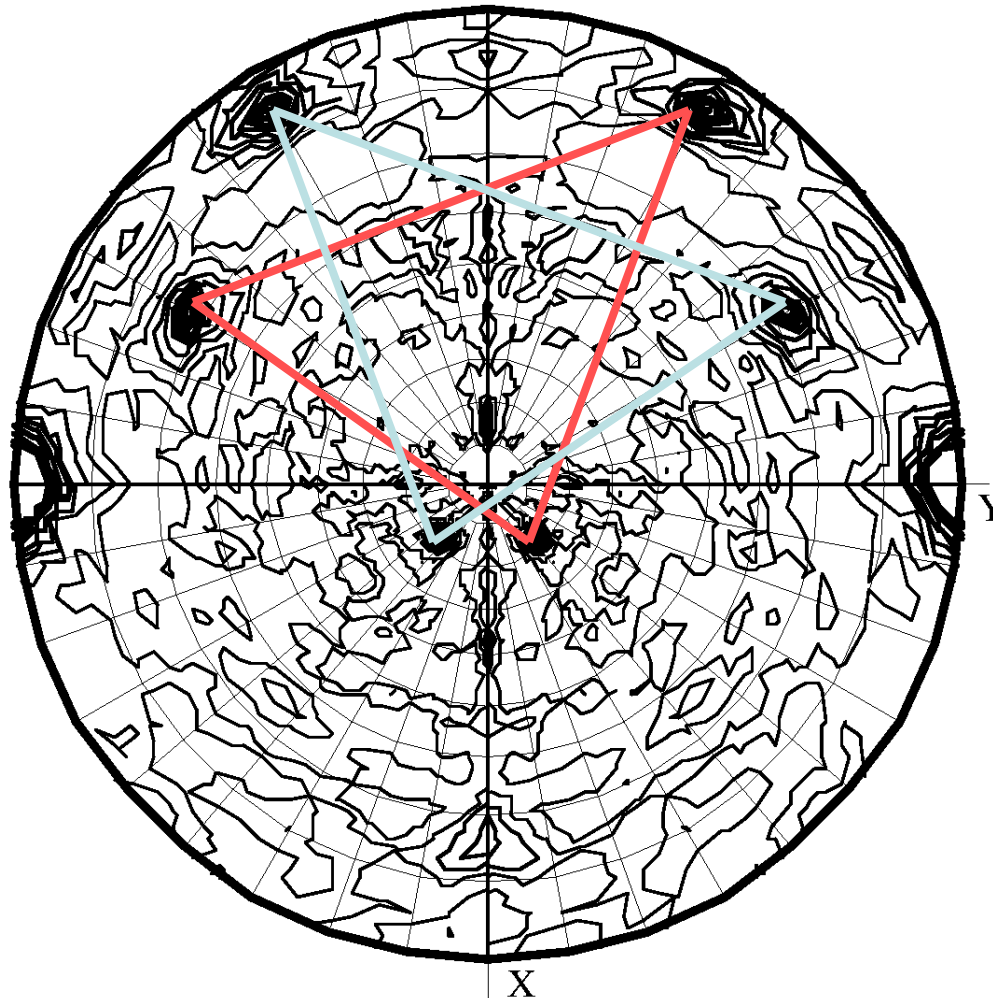


Self Rotation Function

Space group $P2_1$

one tetramer point group symmetry 222 in a.u

Chi = 180.0



In CCP4CLOUD task interface

Task List ✕

Suggested tasksAll tasksWorkflowsA-Z

▸ Density Modification (0)

▸ Refinement and Model Building (0)


▸ Coot (0)

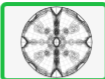
▸ Ligands (1)


▸ Validation, Analysis and Deposition (0)

▼ Toolbox (3)

Reflection data tools

Reflection data diagnostics with Auspex plots
-- detects problems and artifacts in the reflection data

Self-Rotation Function Analysis with Molrep
-- helps to determine the internal symmetry of the reflection data

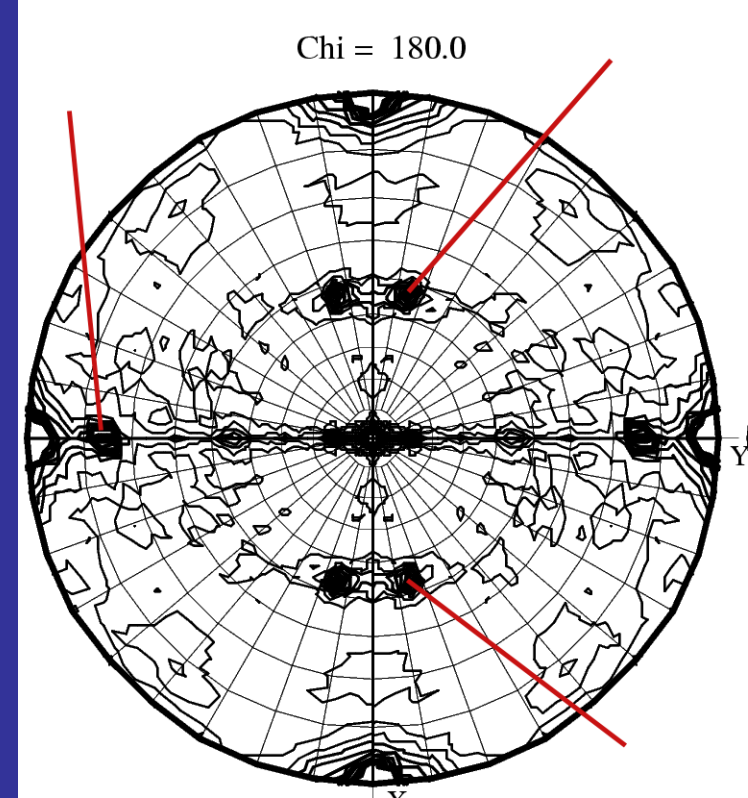
X-ray cross sections and anomalous scattering factors
-- interpolates X-ray cross sections and compute anomalous scattering factors

Help

Cancel

SELF-ROTATION FUNCTION.

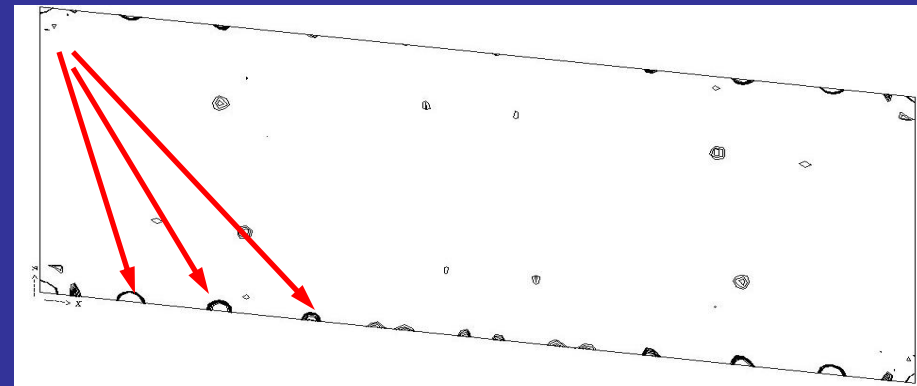
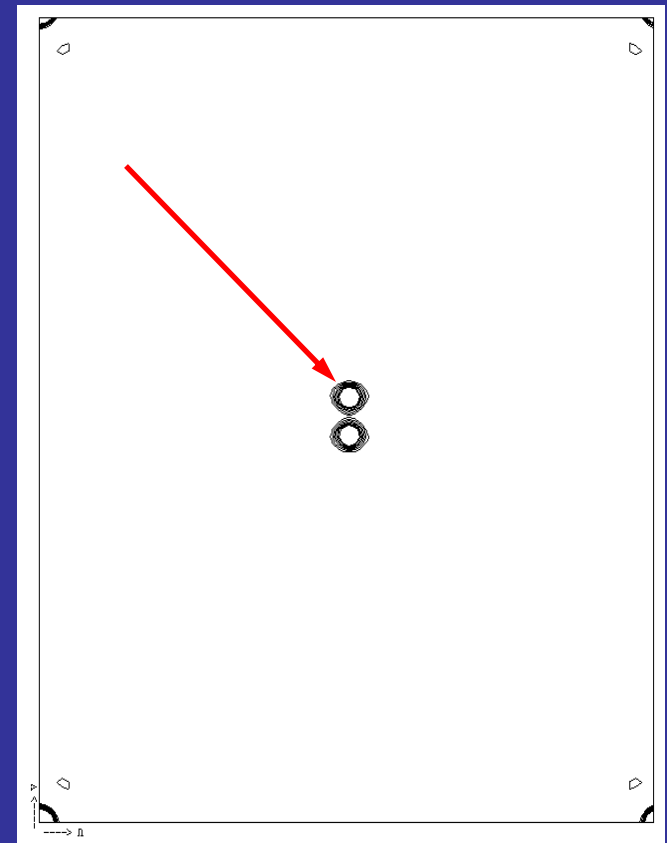
- Can indicate the point group symmetry of the biomolecule.
- Can help to limit the search space for MR.
- SRF calculated using F_{calc} from the putative MR solution should be similar to that of F_{obs} . Otherwise the rotation solution is wrong, provided peaks in SRF are not artefacts.



Section $\text{Chi}=180^\circ$ of self-rotation function of tetrameric tryptophanase indicates molecular symmetry 222 in the space group $P2_12_12_1$.

NATIVE PATTERSON SYNTHESIS INSPECTION

- Peaks with height comparable with origin (in MOLREP 0.15 of origin) are indicative of pseudo-translation which often complicates MR – can give unreasonably high CC for the wrong solution.
- Also may result in the wrong SG assignment.
- May indicate crystal disorder (OD-structure) and occurs in some types of twinning.



Structure solution of the oxygenating subunit of 3,6-diketocamphane monooxygenase from *Pseudomonas putida*

- 42kDa FMN binding enzyme.
- Dimer from size exclusion chromatography.
- No cloned gene.
- Space group $P2_12_12_1$,
- 50% solvent (native crystal).
- Variable cell parameter c.
- Native data to 2 Å resolution. $a=55.0, b=93.4, c=162.0$ Å.
- 1 M NaBr soak. $a=54.9, b=93.3, c=140.8$ Å.
- 3 wavelength MAD data to 2.5 Å.
- No solution for anomalous substructure.

Isupov et al. (2015) Acta D 71, 2344-2353.

- Homologue – bacterial luciferase from *Vibrio harveyi*.

- 17% sequence identity.

- No MR solution for a luciferase monomer.

- $\alpha\beta, \beta_2 \rightarrow \alpha_2$

- MOLREP with α_2 dimeric model, native data.

- No rotation solution.

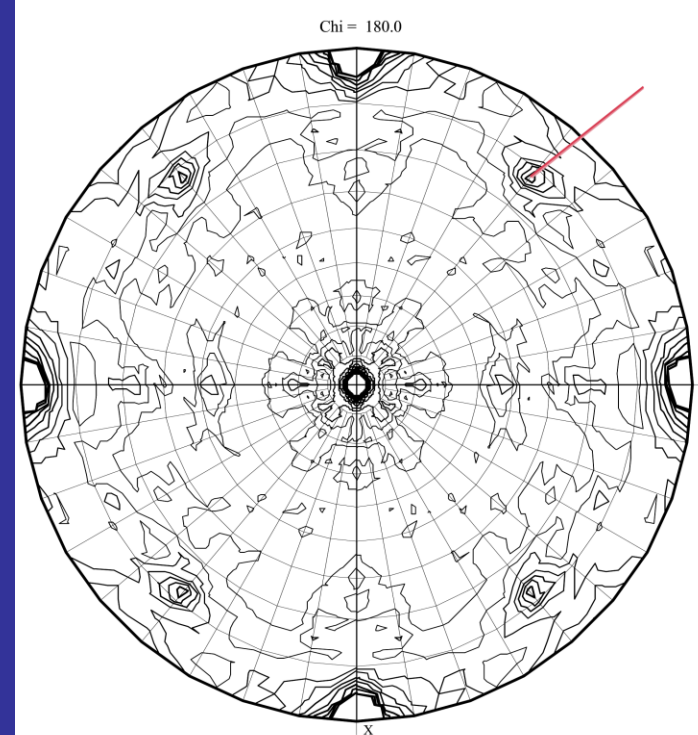
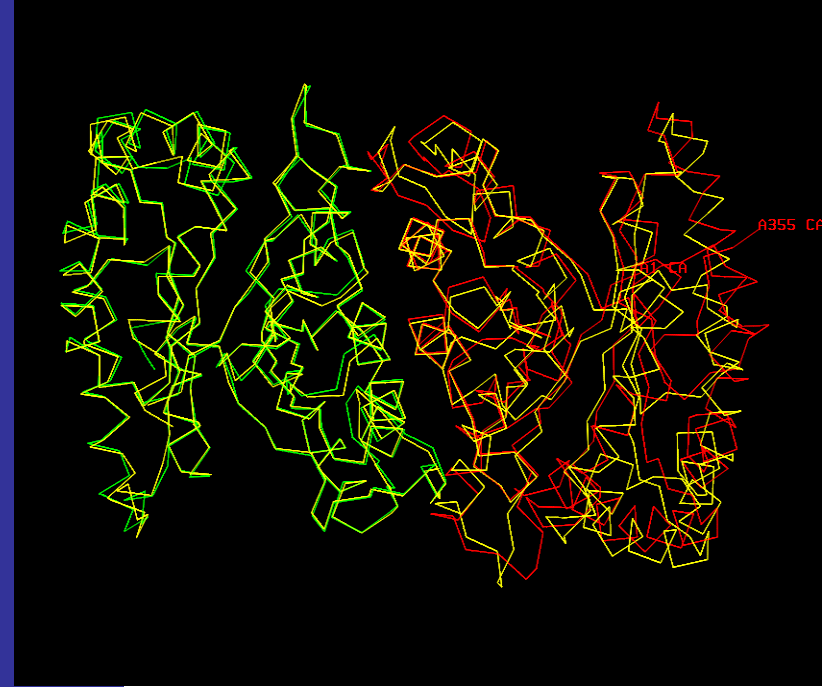
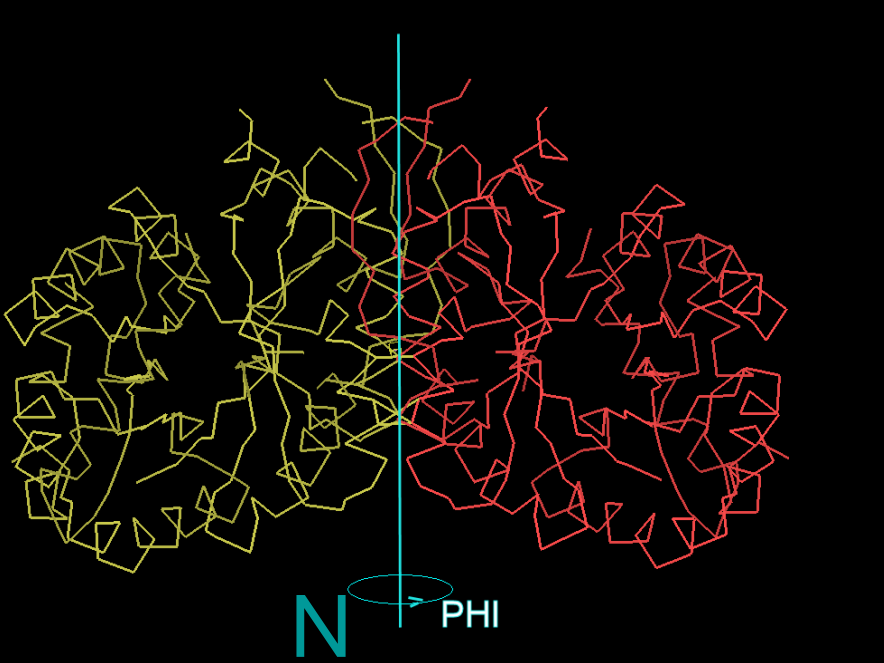
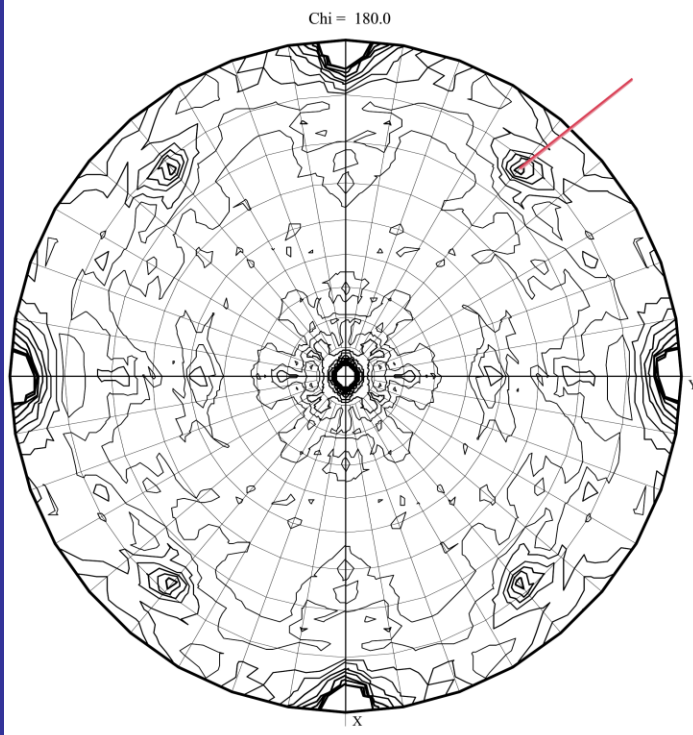


Table of rotation peaks instead of rotation search.

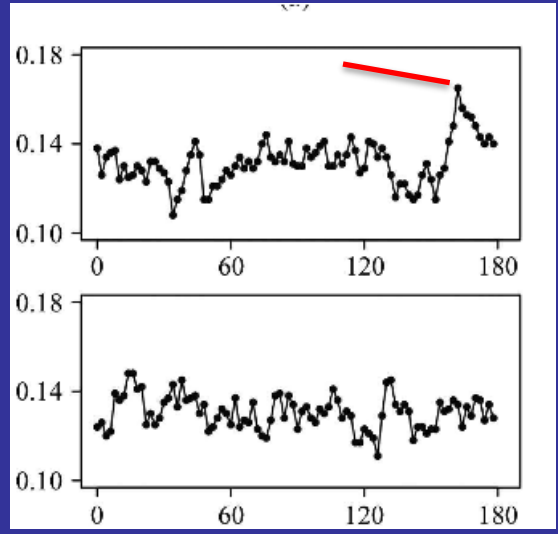
- N-termini top and bottom.
- PHI 0-180° with 2° step – 90x2.
180 translations.

One orientation better for all models
and resolutions – no clear translation.

Clear translation solution after rigid body
refinement of monomers in P₁.



correlation



PHI

Restrained refinement REFMAC,
averaging DM, phased refinement
– difficult electron density.

Successful MR against Br data
with partially refined model.

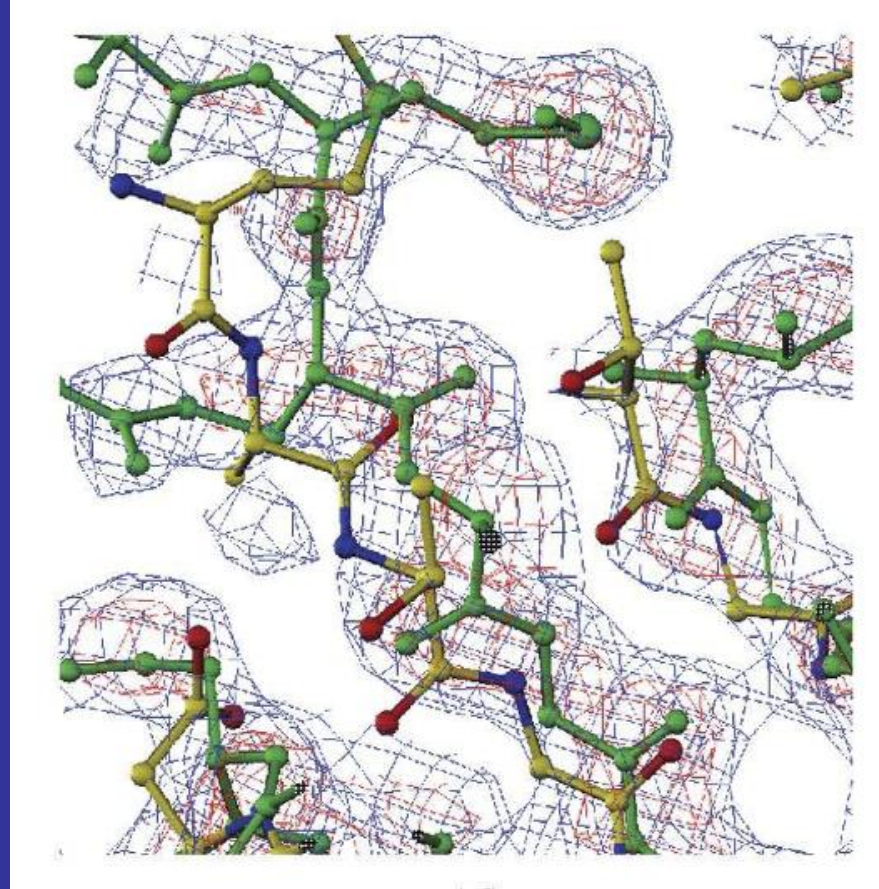
Multicrystal averaging DMMULTI.

18 Br sites 14-6s found in
anomalous difference Fourier at
10-3 Å (peak wavelength).

3 wavelength MAD phasing
MLPHARE FOM 0.26 (2.5 Å)
and 0.63 (6Å).

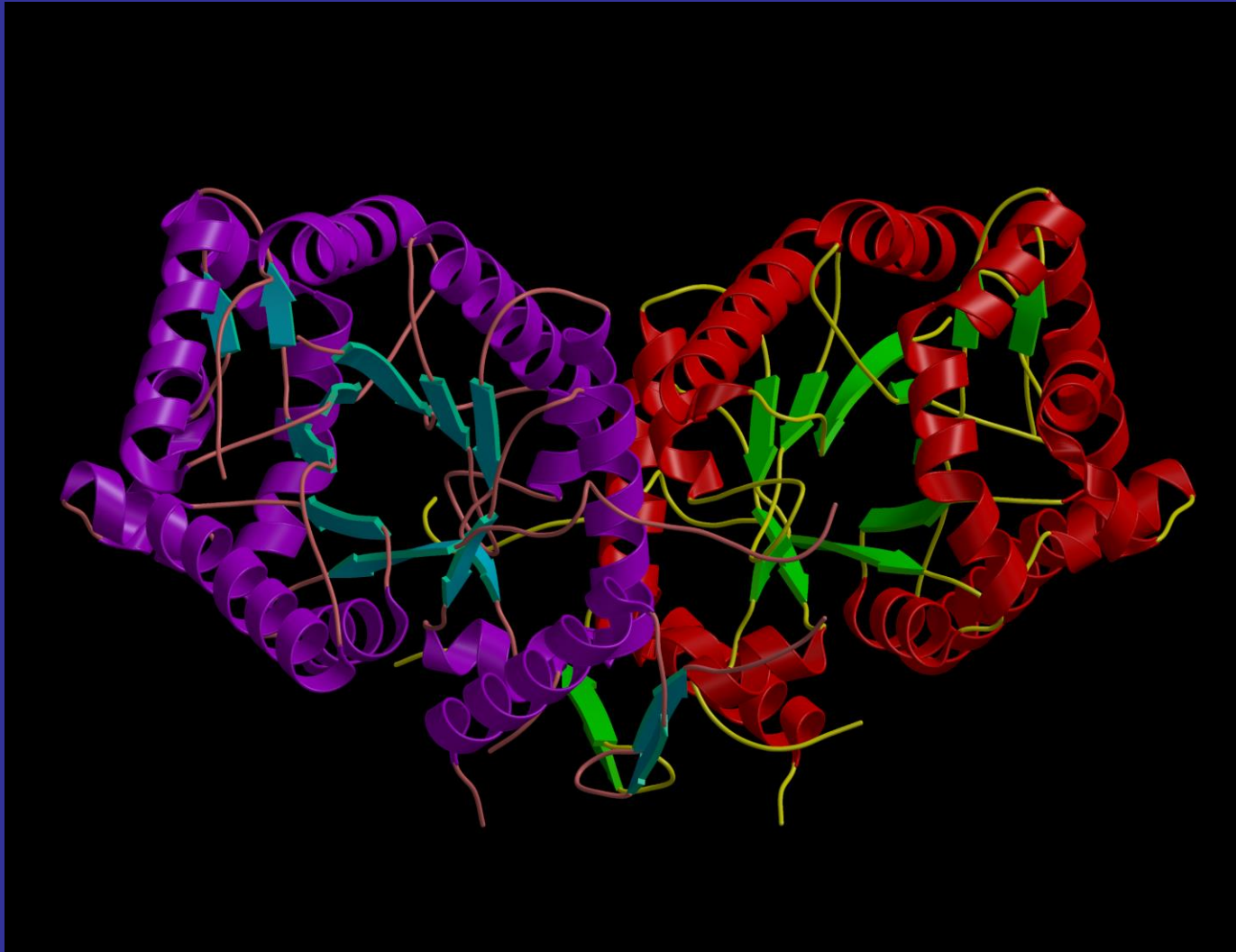
DMMULTI:

Model phases (native xtal),
MAD phases (Br soak).



Electron density after
DMMULTI with input of
model and MAD phases.

Final R-factor 16.3 %, FreeR 23.3 %.



Solution of the structure of anti-TRAP from *Bacillus licheniformis*.

- Anti-TRAP regulates the activity of tryptophan attenuation protein (TRAP) in *Bacilli*.
- 53 amino acids.
- Space group $P2_1$.
- $a=118.5$, $b=99.8$, $c=123.2$ Å, $\beta=117.6^\circ$.
- Data to 2.2 Å.

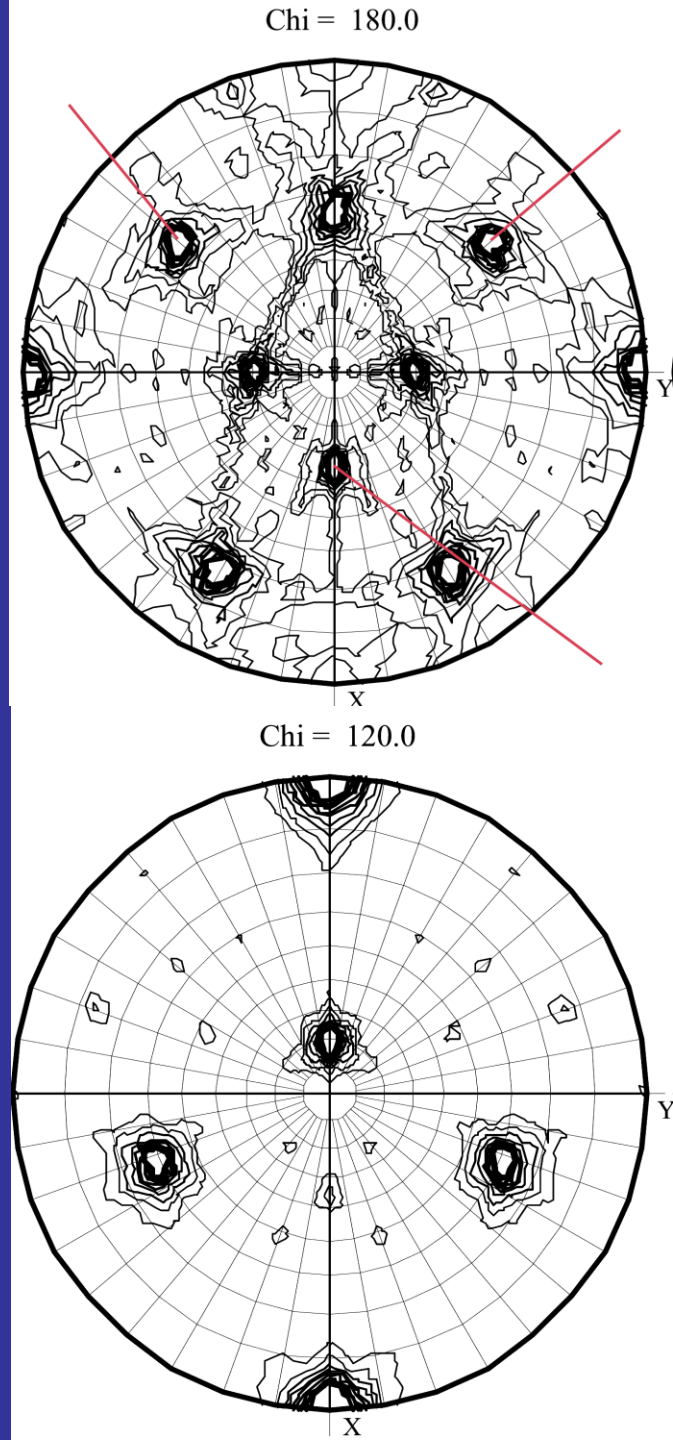
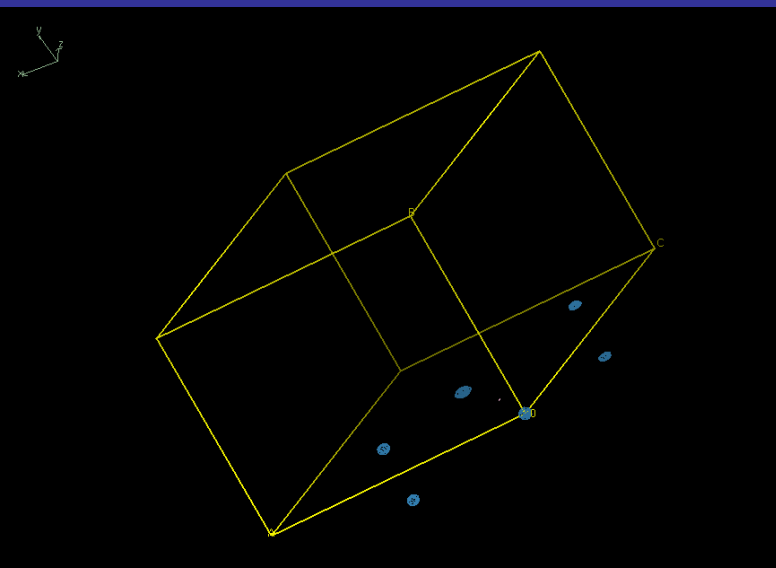
Model

- *Bacillus subtilis* anti-TRAP is a 12-mer with 23 point group symmetry.
- 64 % sequence identity .

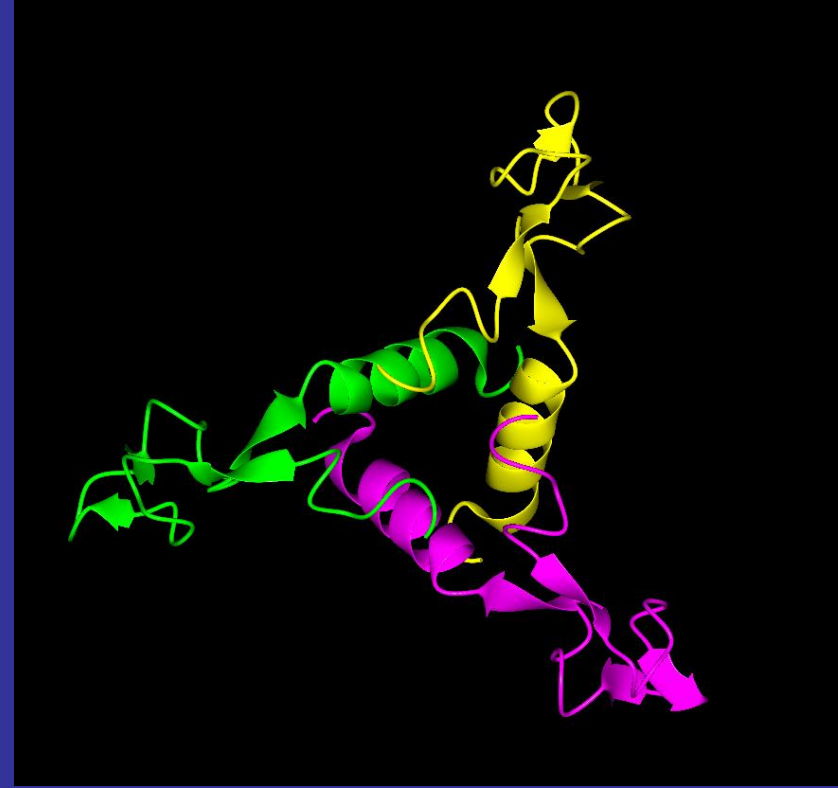


B. subtilis dodecamer
has cubic 23 symmetry.

- Native Patterson peaks.
- (0.5 0.13 0.0) 0.4 origin
- (0.5 0.0 0.5) 0.4 origin
- (0.0 0.13 0.5) 0.16 origin
- SRF – 23 point group symmetry, apparent 432 due to special orientation of 12-mer in relation to crystal dyad.
- A.u. contains 3 or 4 12-mers with 23 point group symmetry related by pseudotranslation.

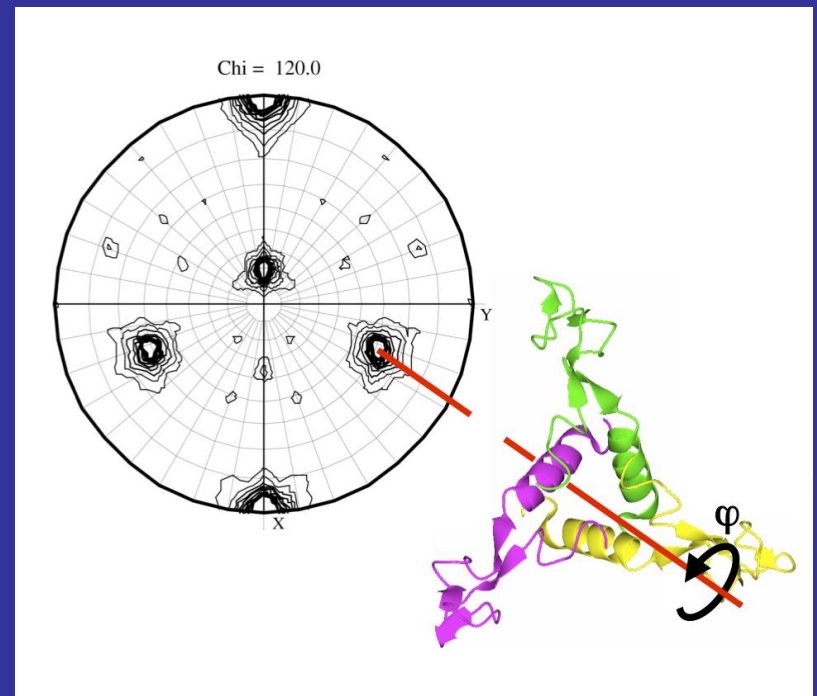


- MOLREP.
- No solution for a dodecamer model.
- No solution for a monomer.
- Evidence of trimeric species from analytical ultracentrifugation.
- No rotation solution for a trimer.

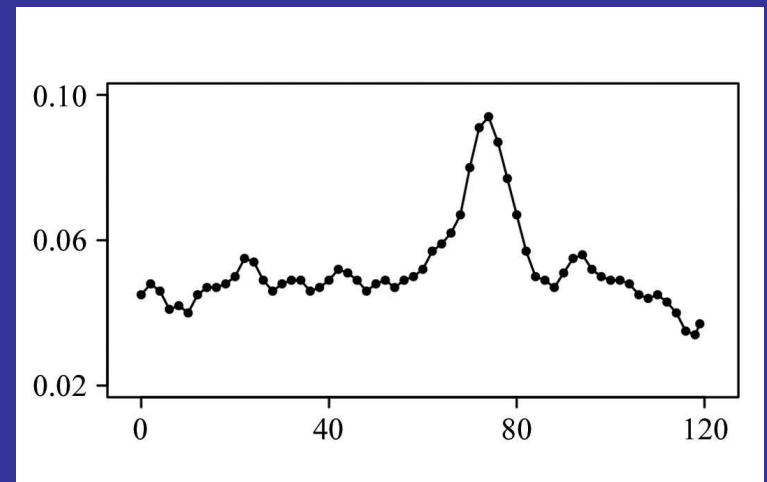


Trimeric model.

- Table of rotation peaks instead of rotation search.
- An increment of 2 degrees in the range 0-120 degrees.
- 60 runs of translation function.
- Due to special orientation of dodecamer in relation to crystallographic 2_1 axis the trimer does not need to be turned over.
- Found solution was fixed and the search repeated for another NCS three-fold until one full dodecamer was built.
- Resulting dodecamer was used as a model for MR.
- Clear translation peaks.

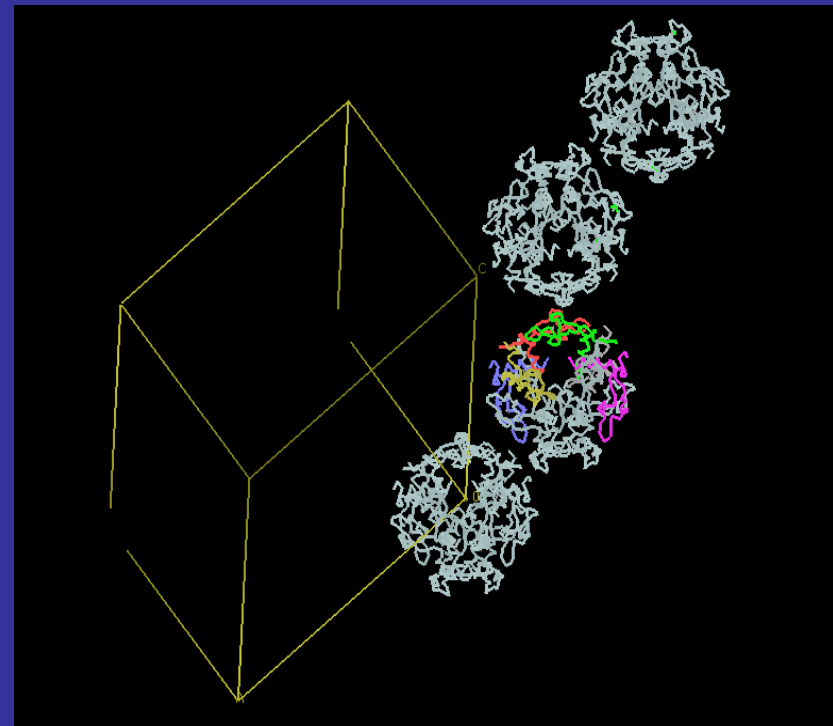


correlation

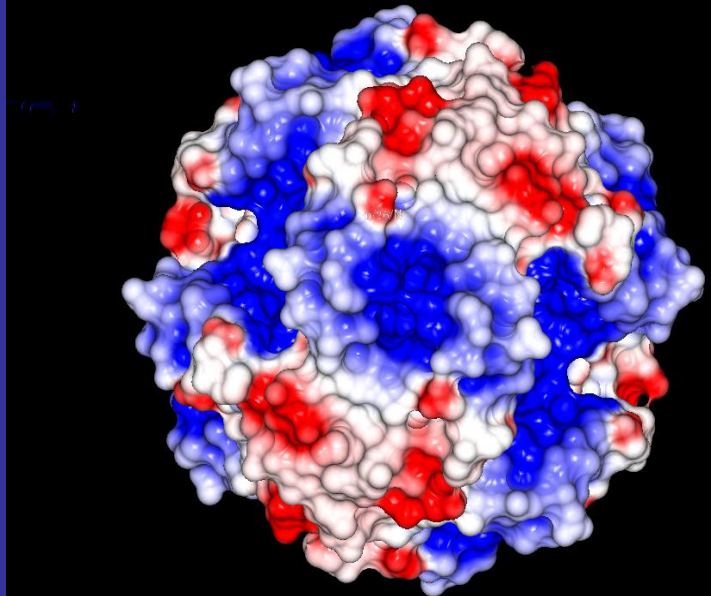
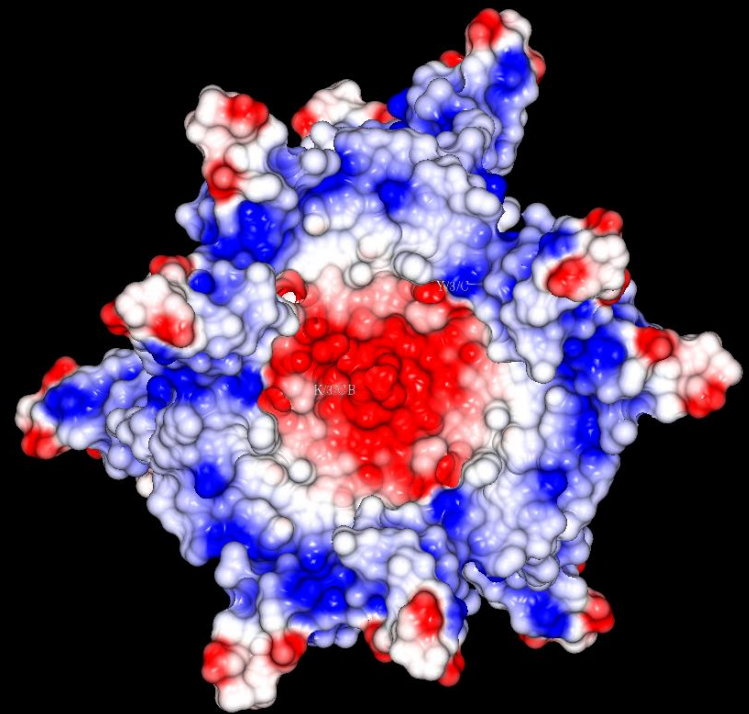


PHI

- Final model contained 4 dodecamers in asymmetric unit, related by pseudotranslation.
 - It was subjected to restrained refinement in REFMAC.
 - However FreeR did not decrease lower than 43 %.
 - Main chain breaks in 2Fo-Fc map.
 - One dodecamer with fewer main chain breaks in the density was resubmitted to MR. The resulting structure easily refined to R_{cryst} 19.7%, FreeR 25.4 %.
-
- ZANUDA later revealed origin assignment – related error in the original TF.



- The resulting 12-mer is different from the original one.
- Later, another crystal form was obtained which contained *B. licheniformis* 12-mer of *B. subtilis* type (Antson and Shevtsov, private communication).
- Depending on yet unknown environmental conditions the two dodecamers appear to interconvert.



Solution of the structure of peroxiredoxin 2 from human erythrocytes

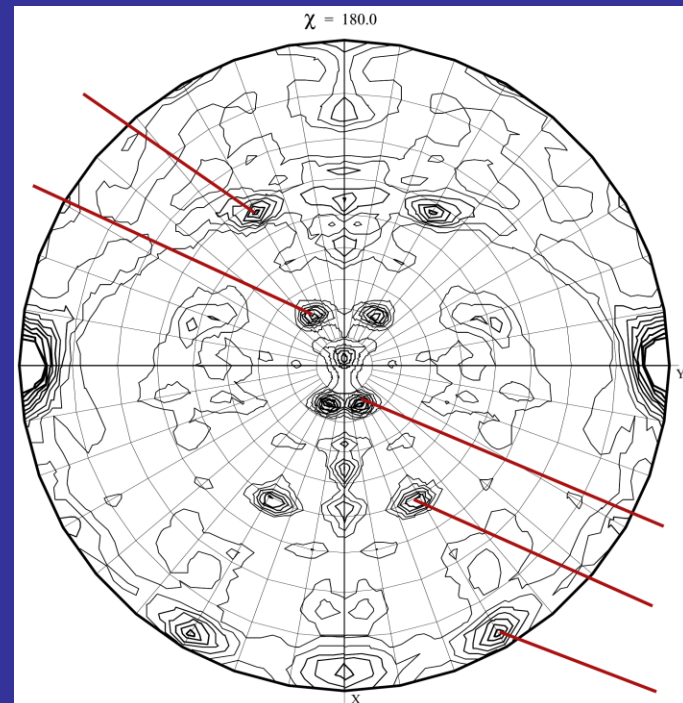
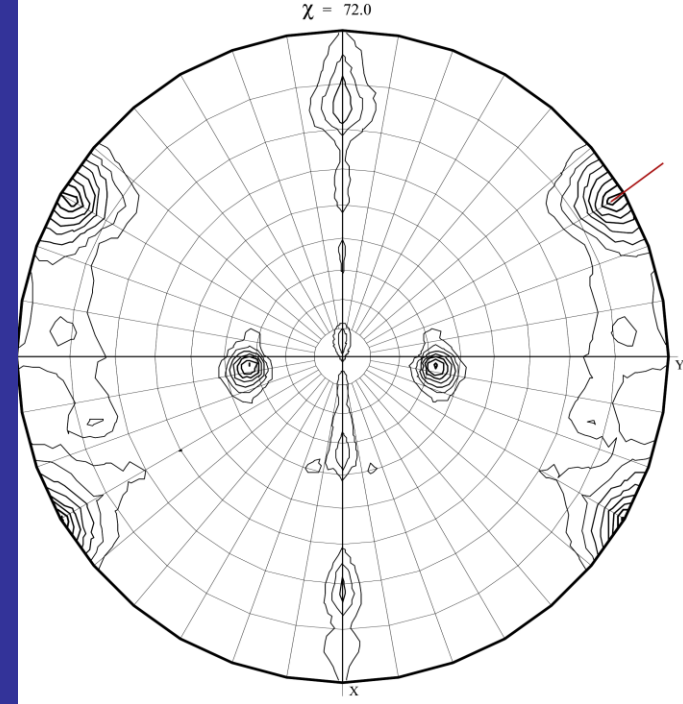
- Antioxidant enzyme, PRX.
- 22 kDa monomer.
- Purified from old blood packs.
- Symmetry $P2_1$.
 $a=88.9$, $b=107.$, $c=119.5\text{\AA}$, $\beta=110.9^\circ$.
- Native data to 1.7 \AA .
- Poor native crystals isomorphism.
- Model - dimeric PRX6.
- 30% sequence identity.
- No MR solution for dimeric model.



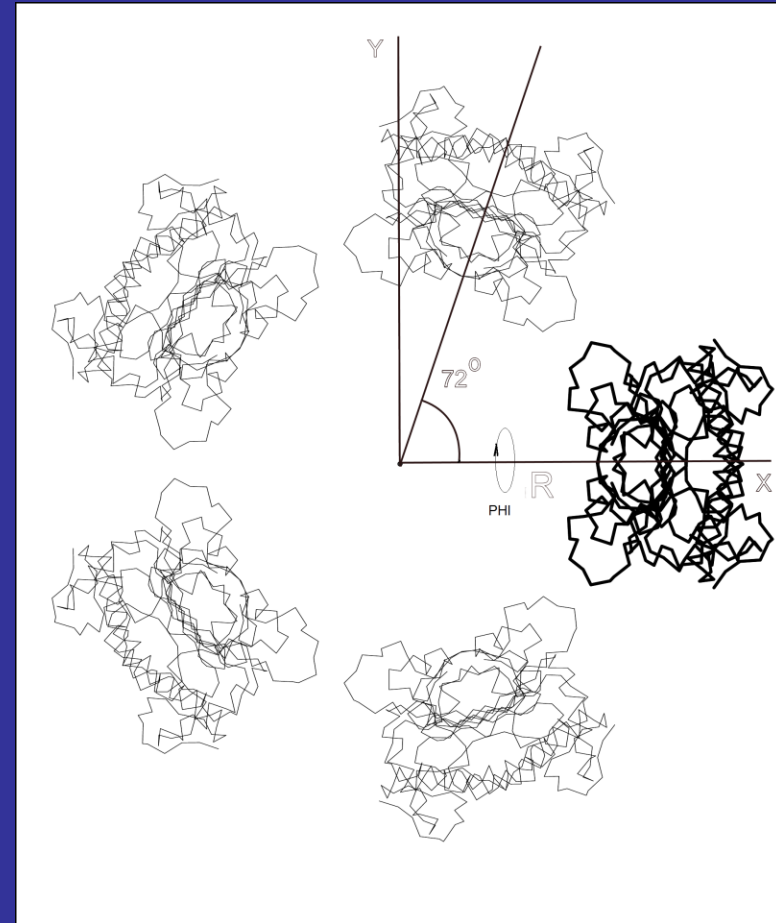
PRX6 dimer

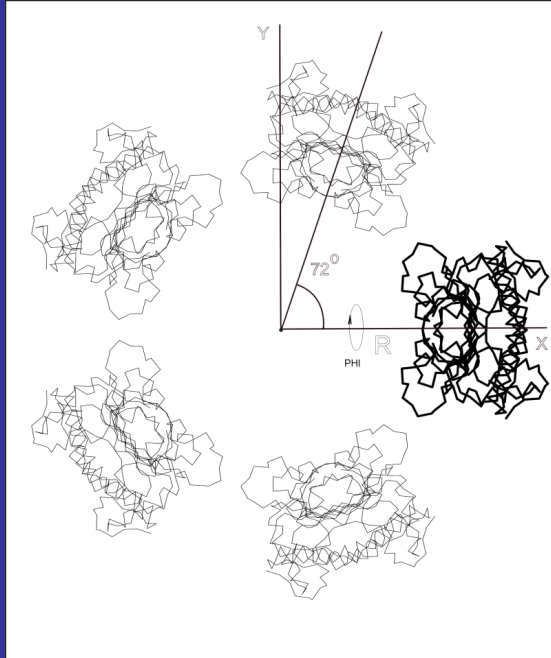
- Analytical ultracentrifugation, size exclusion chromatography and crystal packing results inconclusive: 6-14 subunits.

- Self-rotation (MOLREP) revealed that PRX is a decamer with molecular symmetry 52.

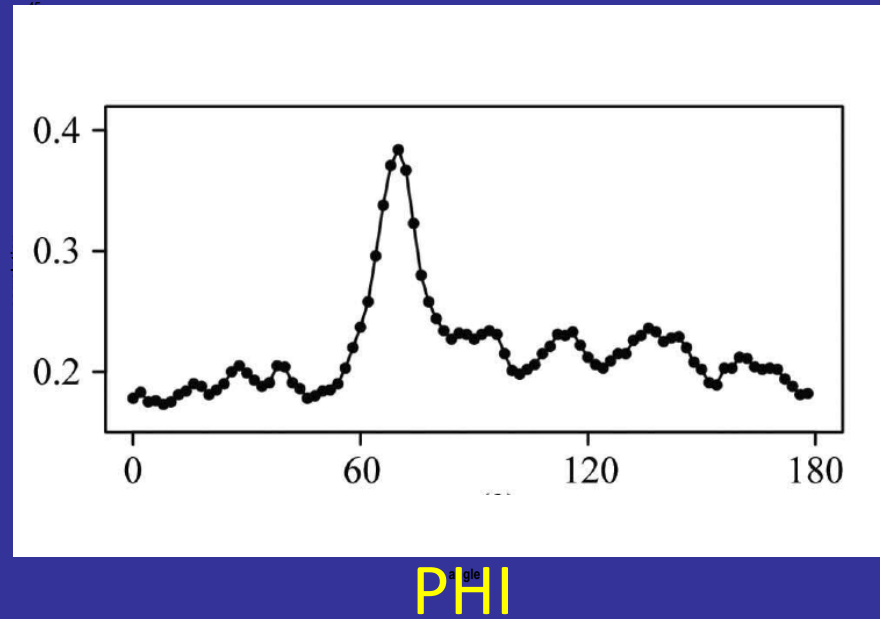


- Polyalanine dimer.
- Amino acids 1-189 out of 224 to cut off poorly conserved domain.
- All possible decamers with point group symmetry 52 were generated using this dimer.
- Radius limits (32-52) and (-52 - -32).
- Angle limits 0-180°
- 3600 models.





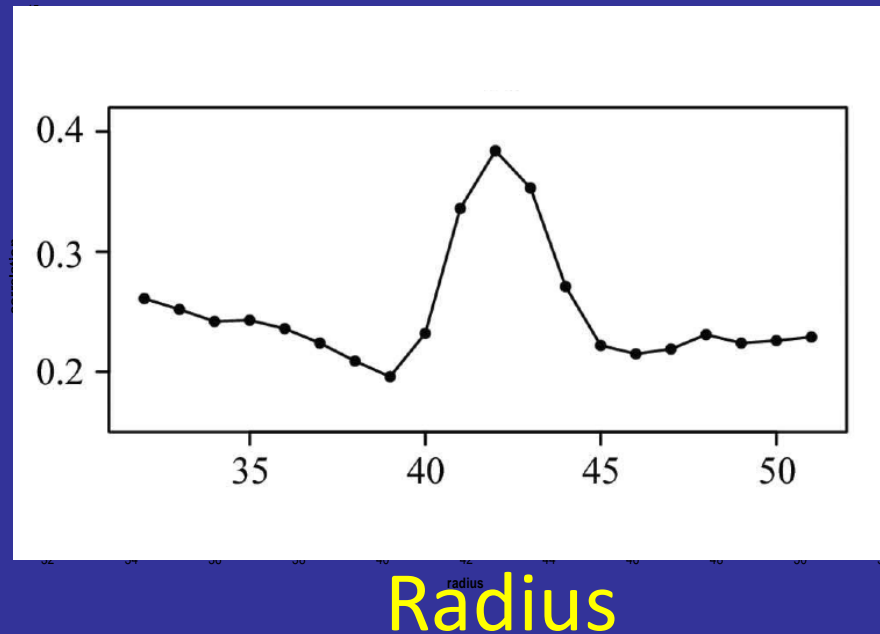
correlation



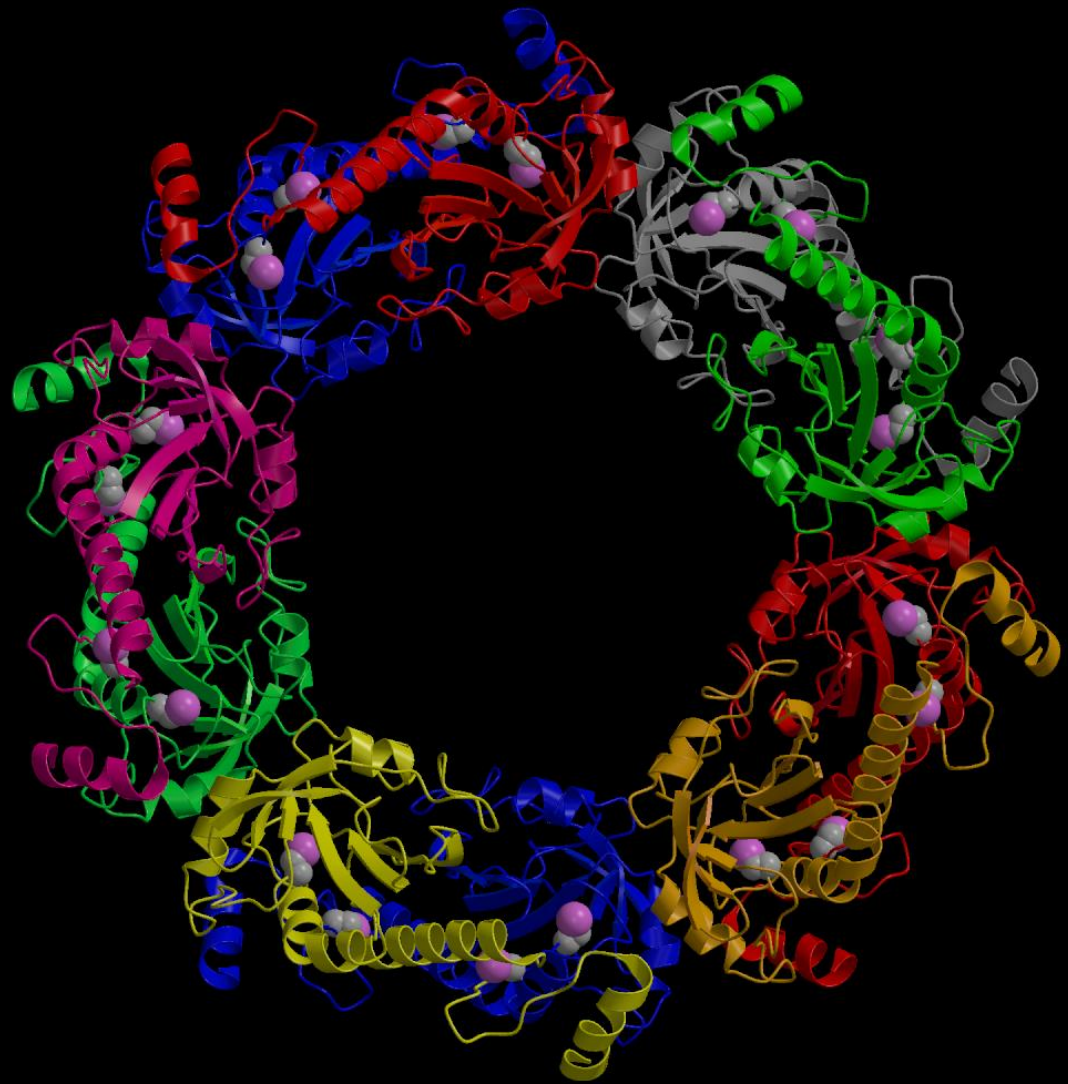
PHI

- Alignment of decamer dyads to NCS dyads.
- Translation search for 3600 models.
- AMORE
- 10-fold averaging by DM.
- Refinement (REFMAC) using external (averaged) phases.

correlation



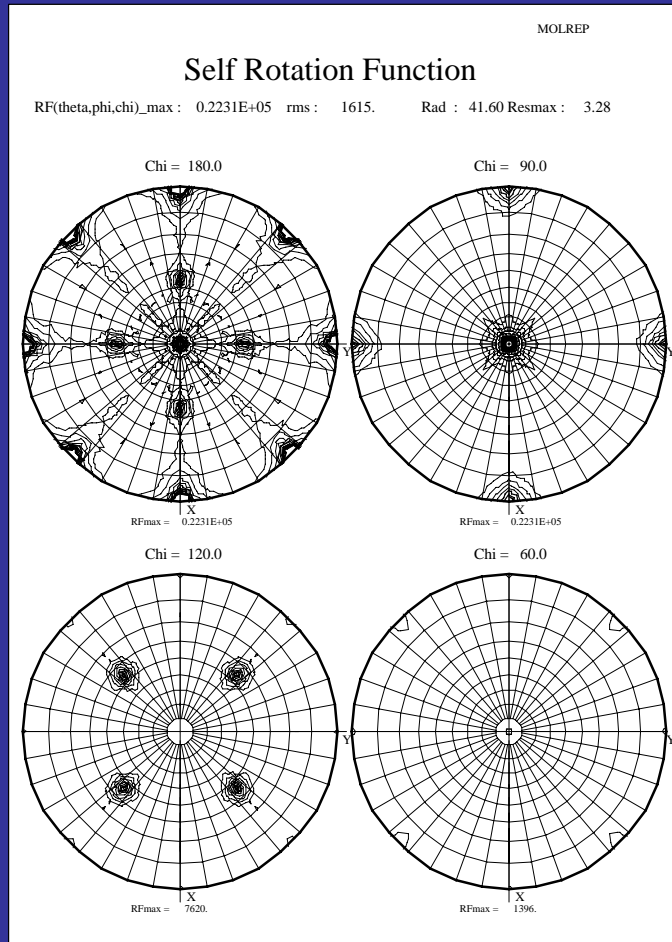
Radius



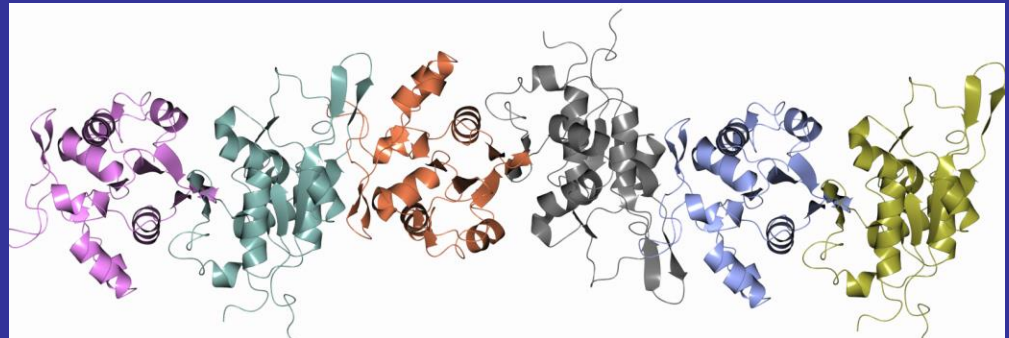
Final Rcryst 19.2 %, FreeR 25.6 %.

Schroder et al. (2000). *Structure with Folding & Design*, 8, 605-615.

Warning: Self-rotation function can be misleading

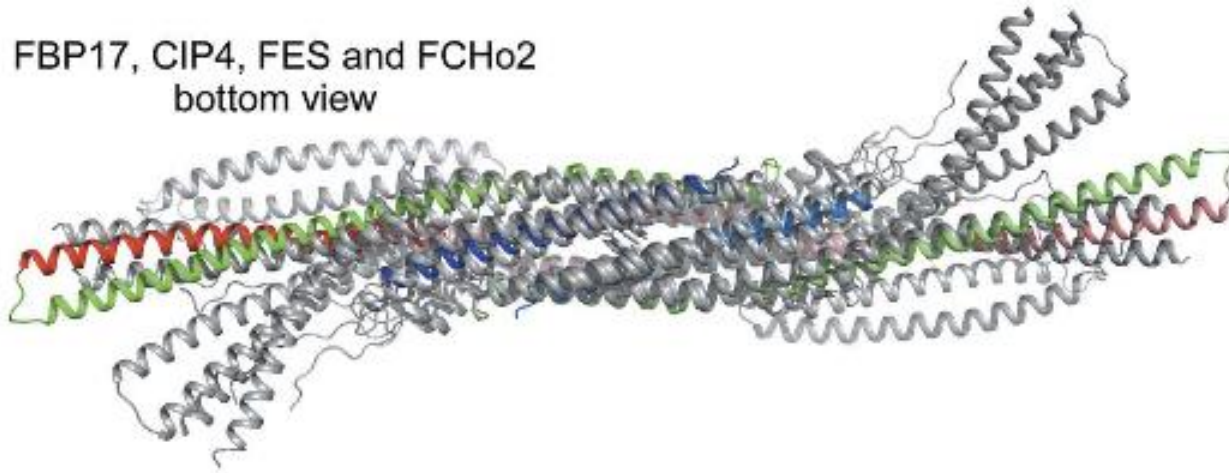


Solvent boundaries can introduce artifacts,
also special arrangement of molecules
Space group $P4_12_12$
Apparent NCS symmetry 432
Impossible due to packing.
2 monomers per a.u. are related by 90°
rotation and $\frac{1}{4}$ fractional translation
creating 4_1 screw columns with symmetry
molecules along a and b crystal axes.



Human SrGAP2 with Dr Yarden Opatowsky

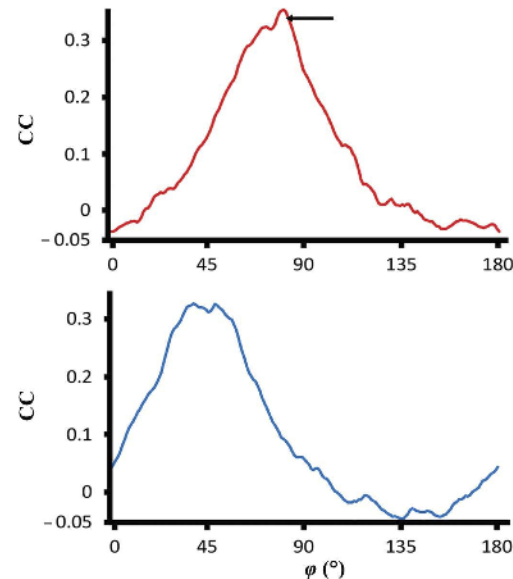
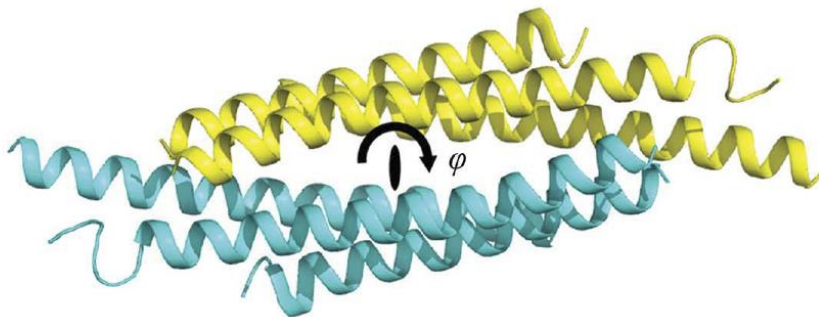
Molecular symmetry without NCS



- Space group C2, one monomer 484 aa per au.
- Coiled coil protein
- Conserved central six-helical core of the dimer.
- Centre of mass fixed, unknown rotation around crystallographic dyad.
- Nearest homologue 19% sequence identity over 60% of length

Sporny et al. (2017) *Mol Biol Evol* **34**, 1463-1478.

Exhaustive search on a crystallographic dyad.



- Easy MR, but difficult refinement
- Space group C2, one monomer per a.u.
- Conserved central six-helical core of the dimer.
- Centre of mass fixed, unknown rotation around crystallographic dyad.
- One-parametric exhaustive search with minimal model using TF as score function (packing function switched off in MOLREP)

Importance of weak anisotropic data

Problem with model rebuilding and refinement starting with partial polyalanine model (171 aa out of 484). Starting mean phase error of 87.6° to 3\AA (84.6° to 5.5\AA).

Multicrystal averaging and phased refinement in REFMAC5.

Data from two poorly isomorphous crystals in space group C2

1) $a = 203.8$, $b = 29.9$, $c = 95.0\text{\AA}$, $\beta = 91.9$ to 2.2\AA ($CC_{1/2}=0.3$)
or 2.7\AA ($\langle I \rangle / \langle \sigma(I) \rangle = 2$)

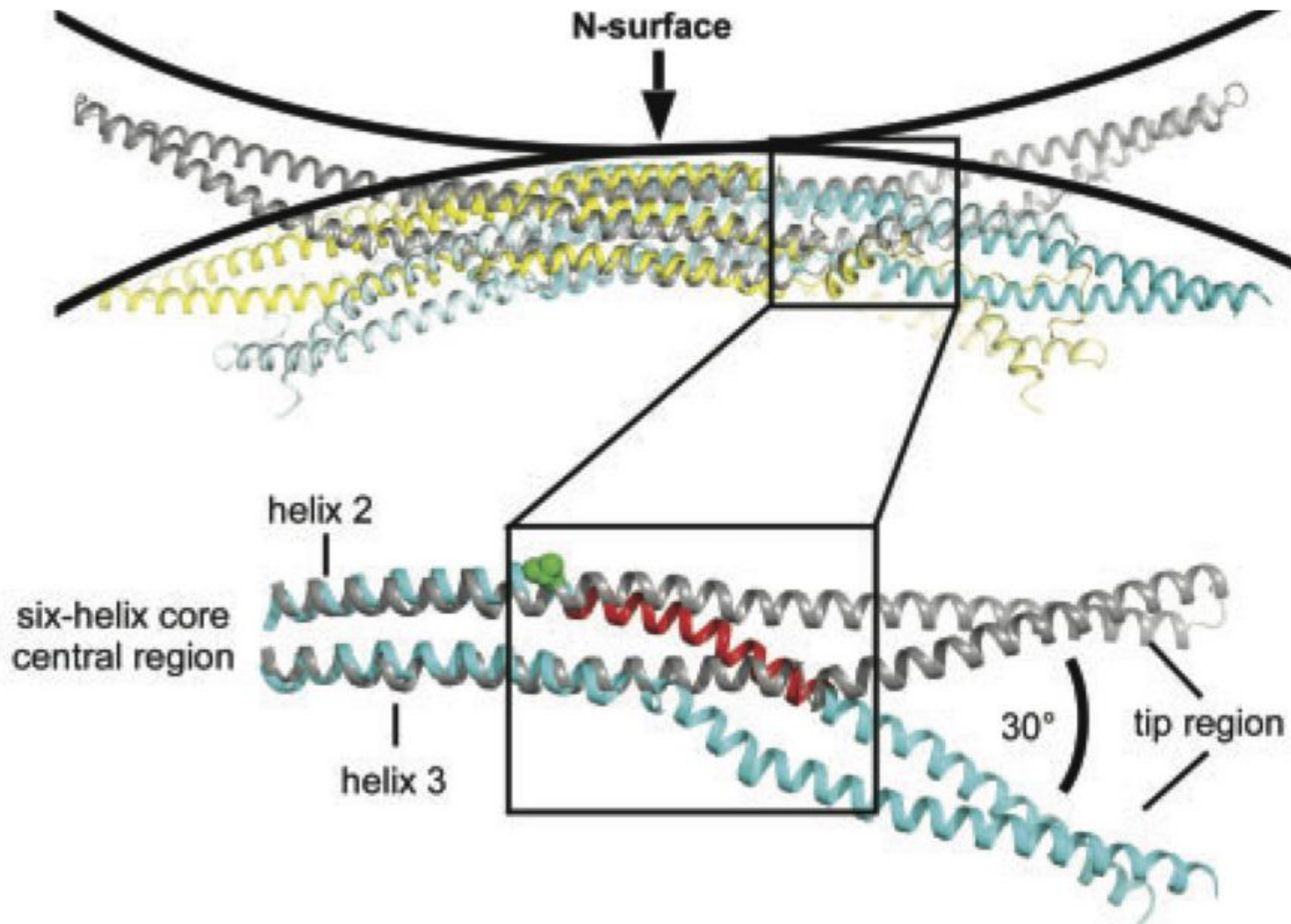
2) $a = 216.9$, $b = 29.6$, $c = 94.7\text{\AA}$, $\beta = 92.0$ to 2.9\AA

Two more helical stretches added - mean phase error 82.4° to 3\AA , after refinement and helix idealization - 75.4° to 3\AA 6 cycles of SHELXE model autotracing at 2.2\AA improved phases to 66° , no improvement was observed for the same run at 2.7\AA

Hierarchy of phase improvement approaches in SRGAP2 case (weak 2.2 Å) good 2.7 Å

- Multicrystal averaging/ phased refinement (DMMULTI/REFMAC) of a partial model is improving phases at any stage, provided initial phases were correct
- SHELXE model autotracing is not as powerful at lower resolution in the beginning of refinement/model improvement, and phase improvement requires better initial phases
- ARP/wARP, Buccaneer, CCP4build, Modelcraft procedures are extremely useful e.g. for sequence assignment but require significantly better starting phases at medium resolution

The structure is unlikely to be solved by a full model.



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