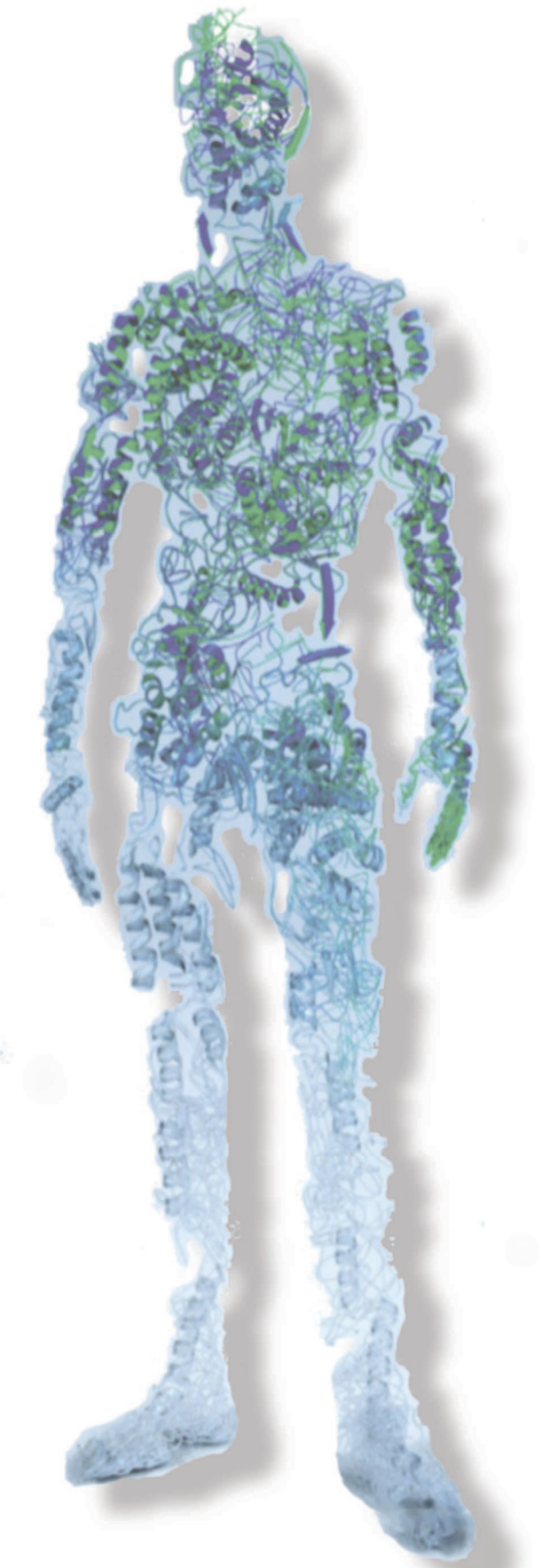




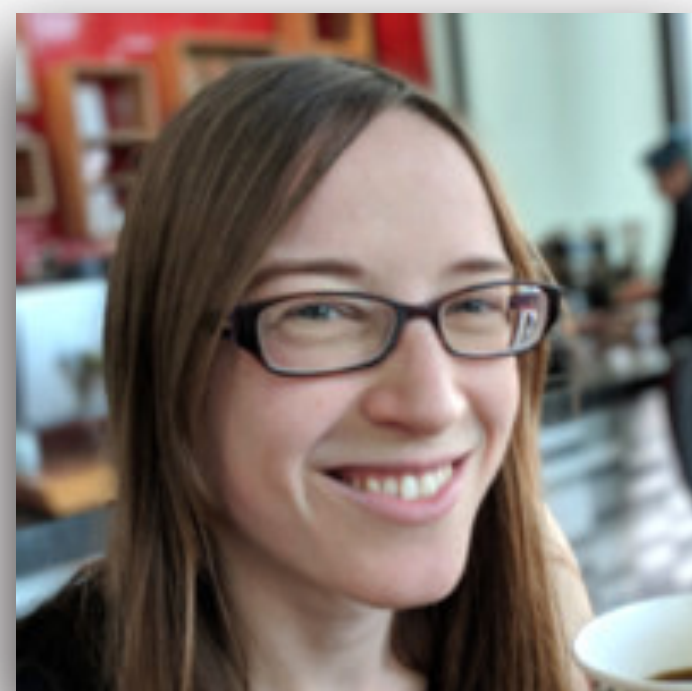
*MAX IV Structural Biology Workshop 211021*

# Six Months of AlphaPhasing



**Luca Jovine**

*Karolinska Institutet, Stockholm*



Kathryn  
Tunyasuvunakool



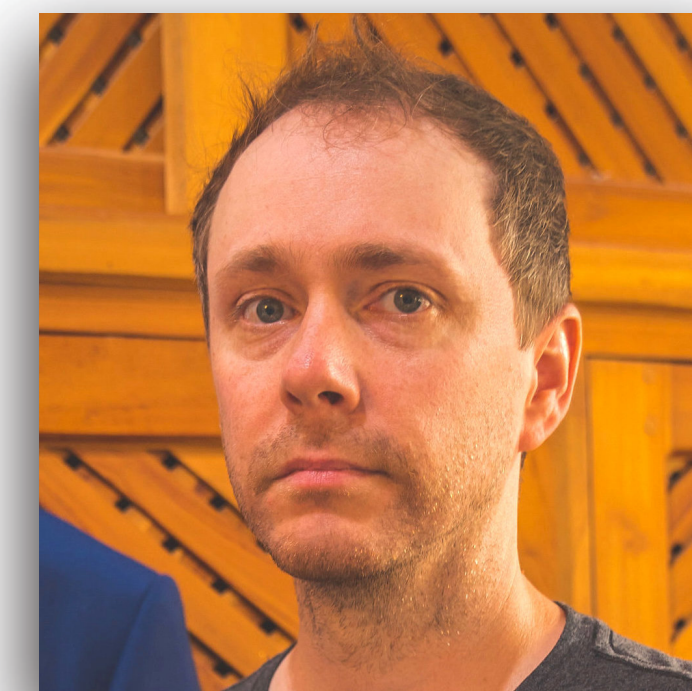
John  
Jumper



Alena  
Stsiapanava



Shunsuke  
Nishio



Benjamin  
Wiseman



**Karolinska  
Institutet**

Target	Homologs in PDB	kDa/AU	SG	Resolution	Issue(s)	LLG	TFZ	Rfree	GDT_TS
1	NO	38	P1	1.9	Significant disorder in one direction	1268	31.6	0.28	94.9
2	NO	171	C2	2.3	No heavy atom binding, not enough S atoms	876	23.1	0.24	74.7, 94.6
				3.5	Low resolution	361	13.5	0.48 (initial)	
3	NO	200	P2 <sub>1</sub>	2.7	Twinning	427	18.4	0.26	
4	YES (avg 29% ID)	72	P3 <sub>1</sub> 21	4.0	Low resolution, bad data quality	95	11.5	0.35	



**bioRxiv**  
THE PREPRINT SERVER FOR BIOLOGY

bioRxiv posts many COVID19-related papers. A reminder: they have not been formally peer-reviewed and should not guide health-related behavior or be reported in the press as conclusive.

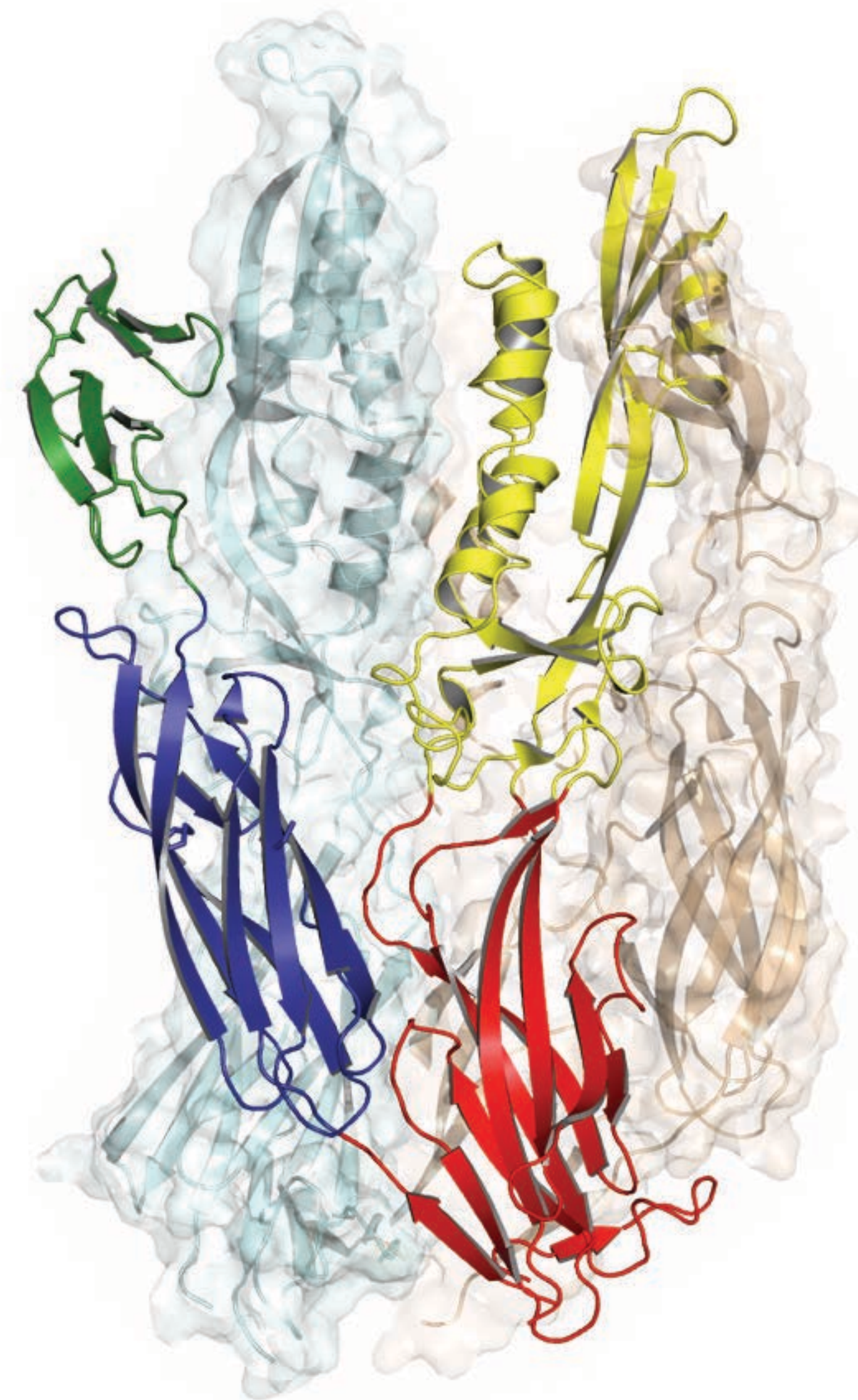
New Results

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## Archaeal origins of gamete fusion

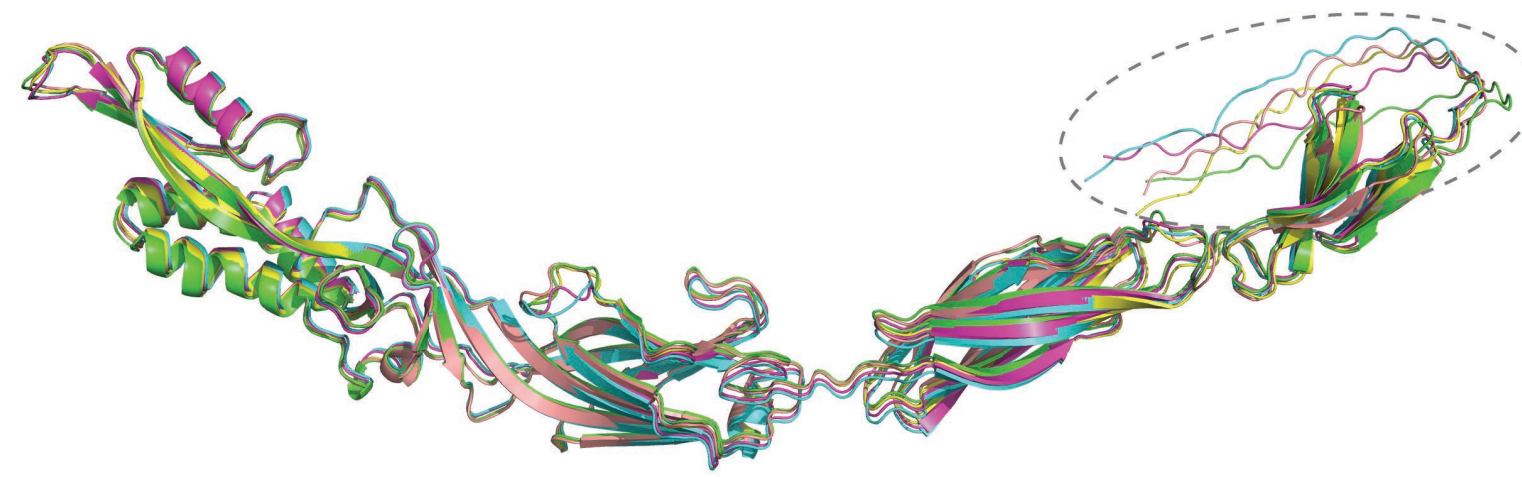
David Moi, Shunsuke Nishio, Xiaohui Li, Clari Valansi, Mauricio Langleib, Nicolas G. Brukman, Kateryna Flyak, Christophe Dessimoz, Daniele de Sanctis, Kathryn Tunyasuvunakool, John Jumper, Martín Graña, Héctor Romero, Pablo S. Aguilar,  Luca Jovine,  Benjamin Podbilewicz

**doi:** <https://doi.org/10.1101/2021.10.13.464100>



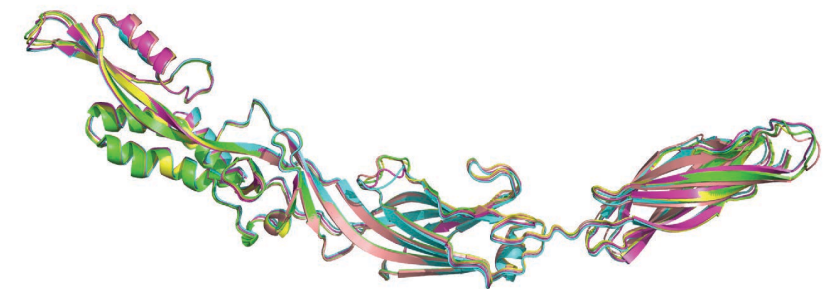


Model generation  
(AlphaFold2)

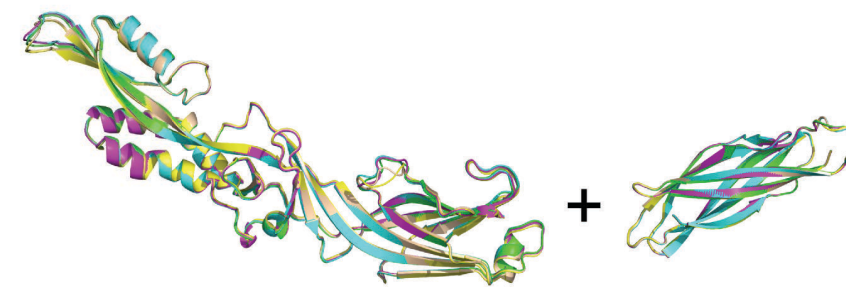


ectodomain model ensemble  
D25-S535  
RMSD 1.4-3.3 Å

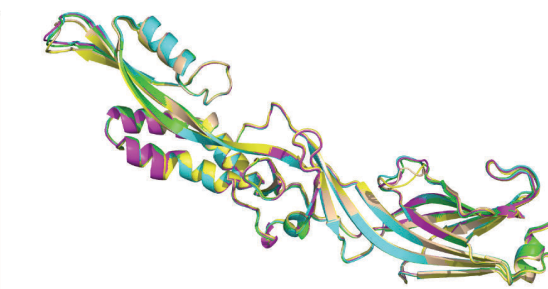
Model postprocessing



**domains I/II/III ensemble**  
D25-Q453 = 418 aa  
(~27% AU scattering mass)  
RMSD 0.6-1.4 Å



**domains I/II + domain III ensembles**  
D25-A335 + P350-Q453 = 311 aa + 104 aa  
(~20% + 7% AU scattering mass)  
RMSD 0.3-0.9 Å + 0.1-0.3 Å



**domains I/II ensemble**  
D25-A335 = 311 aa  
(~20% AU scattering mass)  
RMSD 0.3-0.9 Å



**domain III ensemble**  
P350-Q453 = 104 aa  
(~7% AU scattering mass)  
RMSD 0.1-0.3 Å

7%  
AU !!

Molecular replacement  
(Phaser)

4 solutions  
top LLG 118  
top TFZ 9.6

single solution  
top LLG 876  
top TFZ 23.1

single solution  
top LLG 228  
top TFZ 14.6

single solution  
top LLG 275  
top TFZ 15.1

Initial refinement  
(phenix.refine)

R 0.50  
R<sub>free</sub> 0.53

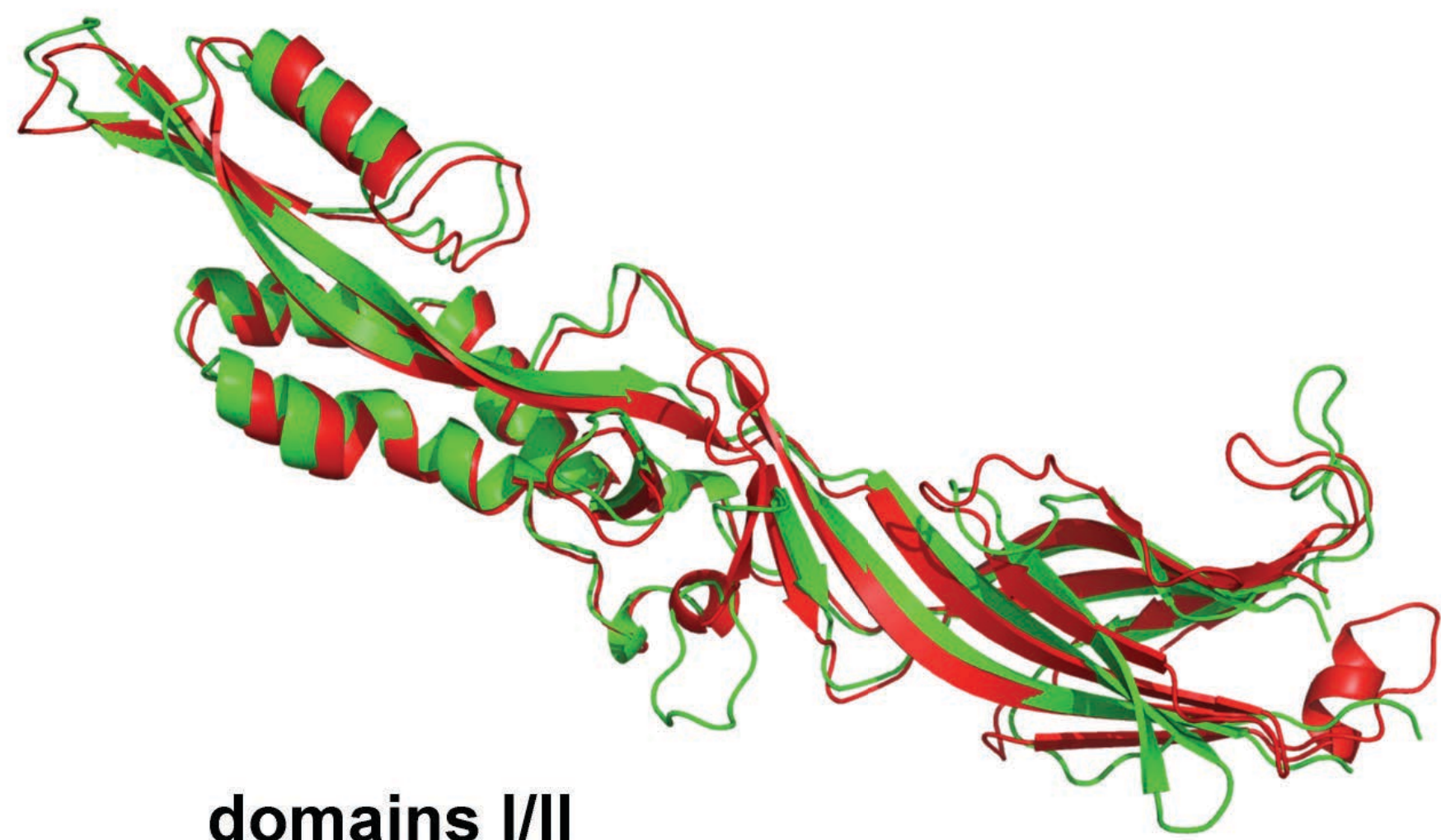
R 0.45  
R<sub>free</sub> 0.46

R 0.48  
R<sub>free</sub> 0.51

R 0.51  
R<sub>free</sub> 0.51

Autobuilding  
(PHENIX AutoBuild/ARP+wARP),  
manual rebuilding  
(Coot/SOLDE),  
refinement  
(phenix.refine)

R 0.21  
R<sub>free</sub> 0.24



**domains I/II**

RMSD 4.2 Å (299 C $\alpha$ )  
[1.1 Å after outlier rejection (222 C $\alpha$ )]

**GDT\_TS 74.7**



**domain III**

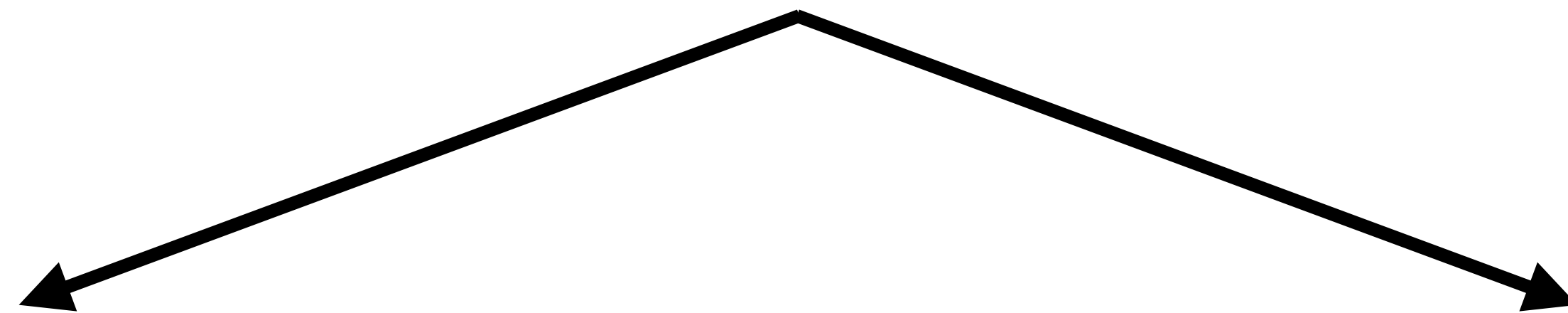
RMSD 0.7 Å (104 C $\alpha$ )  
[0.5 Å after outlier rejection (90 C $\alpha$ )]

**GDT\_TS 97.6**

- AlphaFold2 model
- Refined experimental model

**The protein folding problem is (probably) not solved as such**

**The crystallographic phase problem practically is**



**XR / cryo-EM**

**Will there be any need for more than one tunable beamline per synchrotron?**