

**Antibody binding to anthrax edema factor  
determined by RosettaDock (v2.3)  
using flexible loop modeling**

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**NIH**

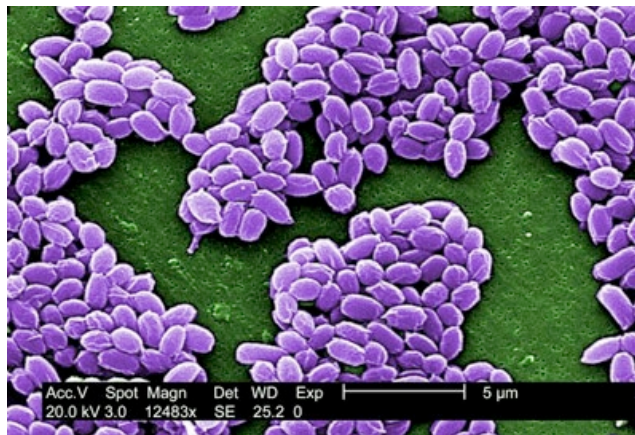
**Office of Cyber Infrastructure and Computational Biology  
National Institute of Allergy and Infectious Diseases  
U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES  
National Institutes of Health**



**Anthrax (band) = ✓**



# Anthrax (bacterium) =

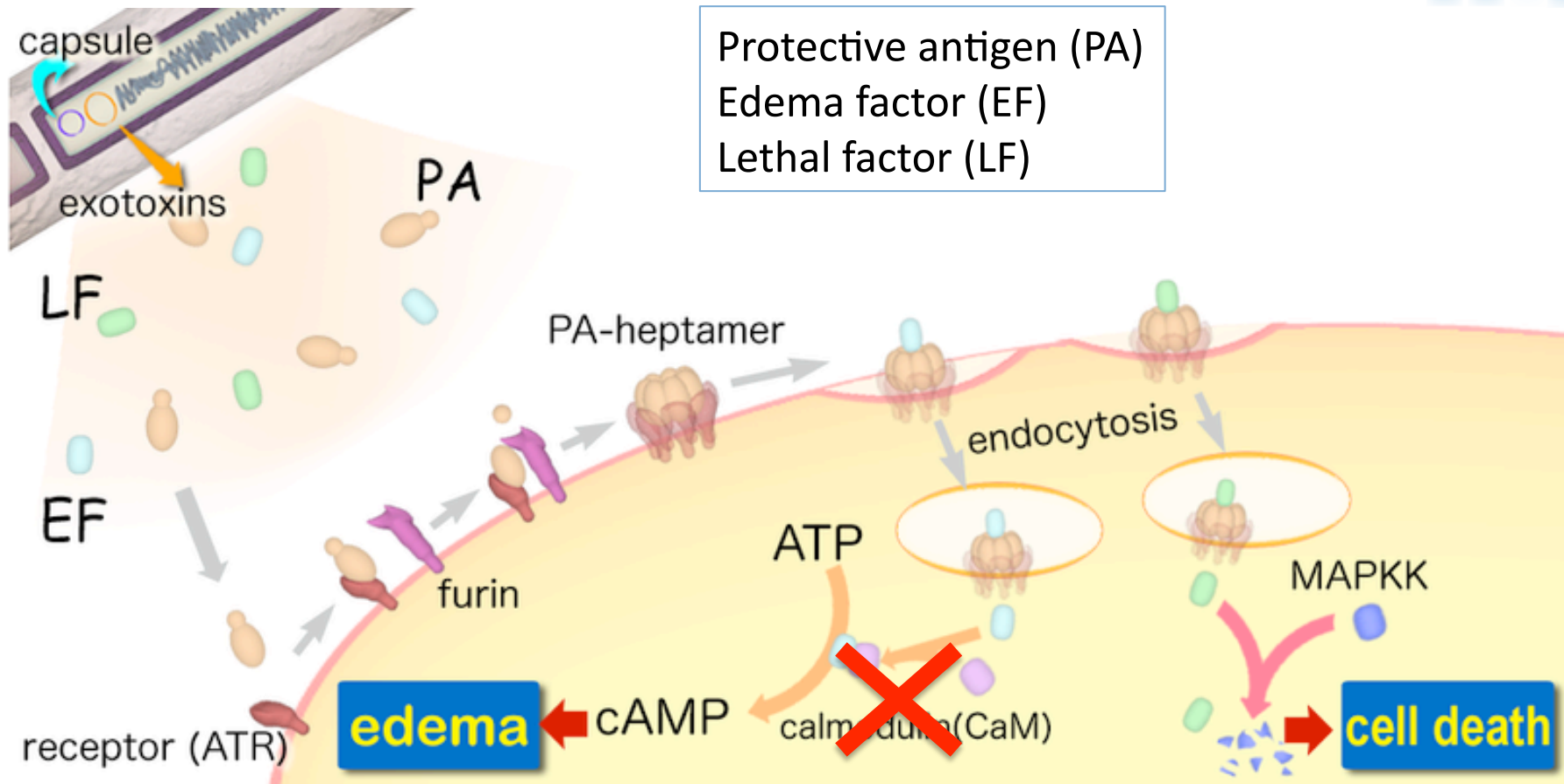


“Less than a  $\mu\text{g}$  of inhaled anthrax is invariably fatal within five days to a week after exposure.”

- FAS (Federation of American Scientists), "Biological Warfare Agents (Partial List)," [www.fas.org/nuke/intro/bw/agent.htm](http://www.fas.org/nuke/intro/bw/agent.htm), (28 March 2005).

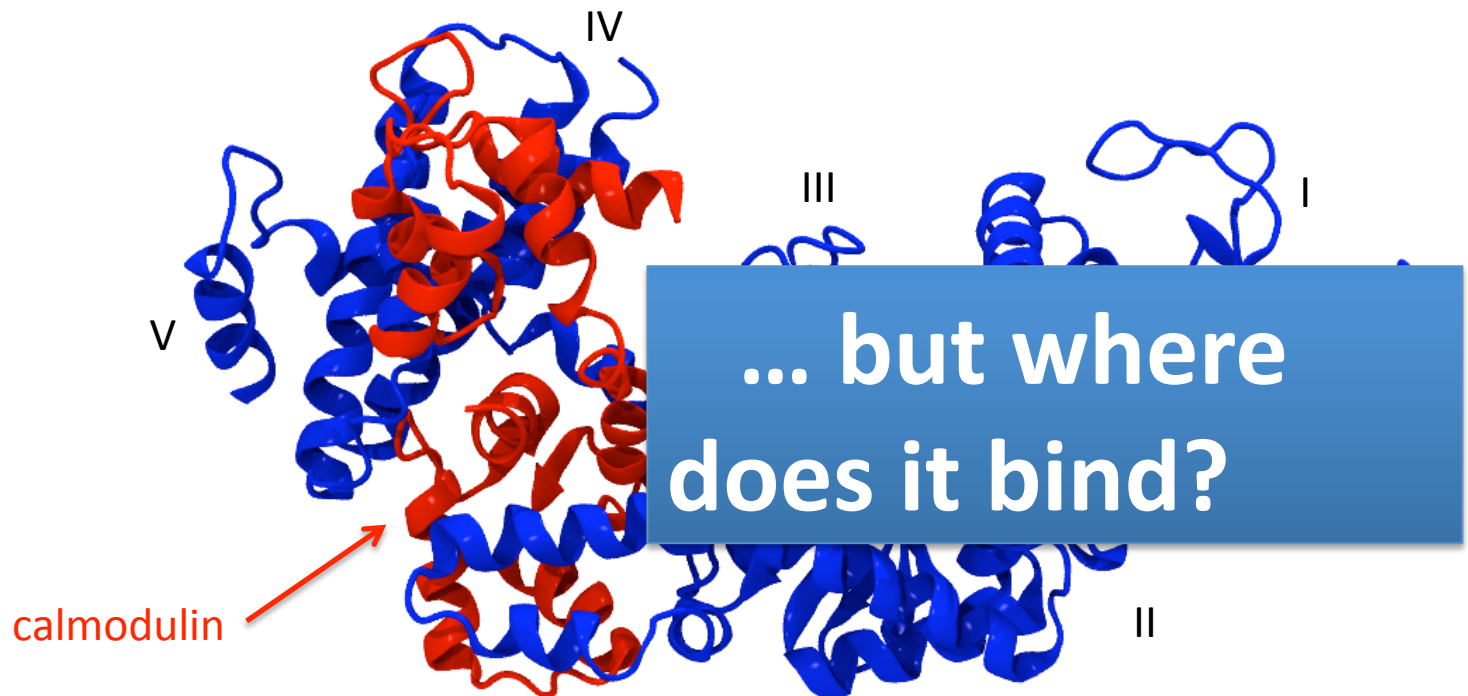


# A three-protein exotoxin

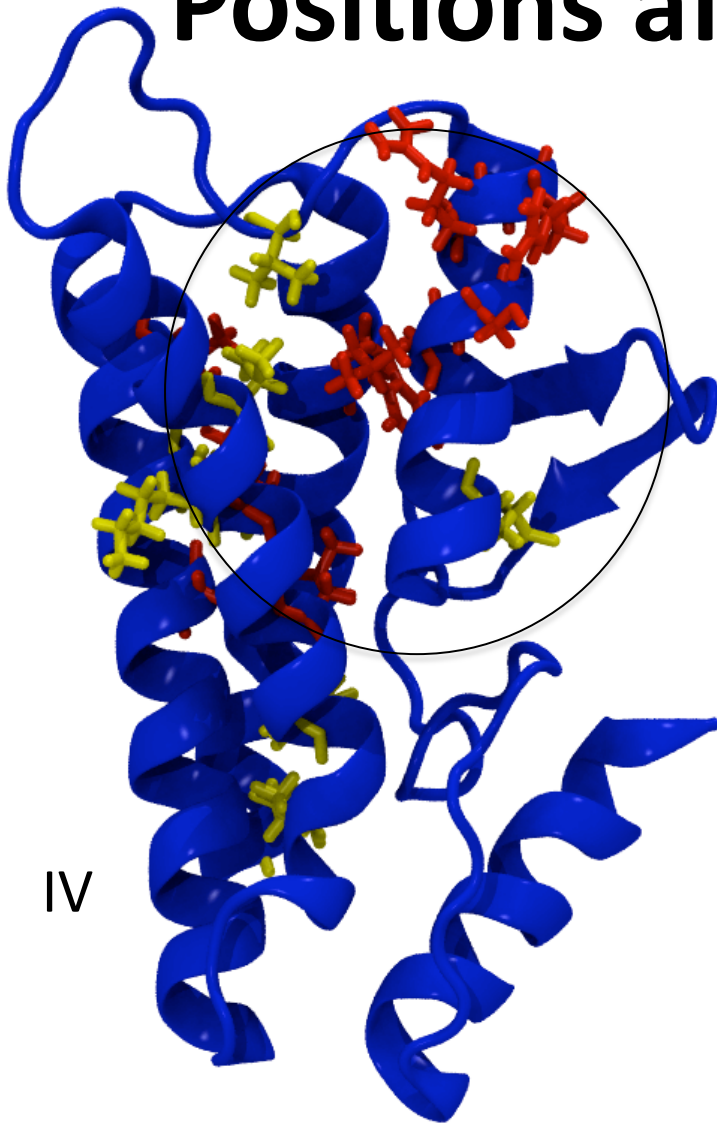


# Monoclonal Ab binds to Edema factor

Chen Z.C., *et al* (2009) Potent neutralization of anthrax edema toxin by a humanized monoclonal antibody that competes with calmodulin for edema factor binding. *Proc Natl Acad Sci USA* **106(32): 13487-13492**



# Positions affecting Ab binding



Total loss Ab binding  
Partial loss Ab binding

EF position	Amino Acid	PARTIAL BINDING	LOSS OF BINDING
662	GLU	x	
667	LEU		x
668	SER		x
671	ARG		x
672	ARG		x
678	VAL	x	
694	VAL	x	
696	LYS	x	
697	ILE		x
701	LEU		x
704	TYR	x	
728	ALA		x
732	ILE	x	
736	LEU		x
748	TYR		x
763	LEU	x	
797	ILE	x	



# Rosetta docking



- Ab constructed  
F<sub>v</sub> Homology M

- Perturbation, fl  
loop modeling:

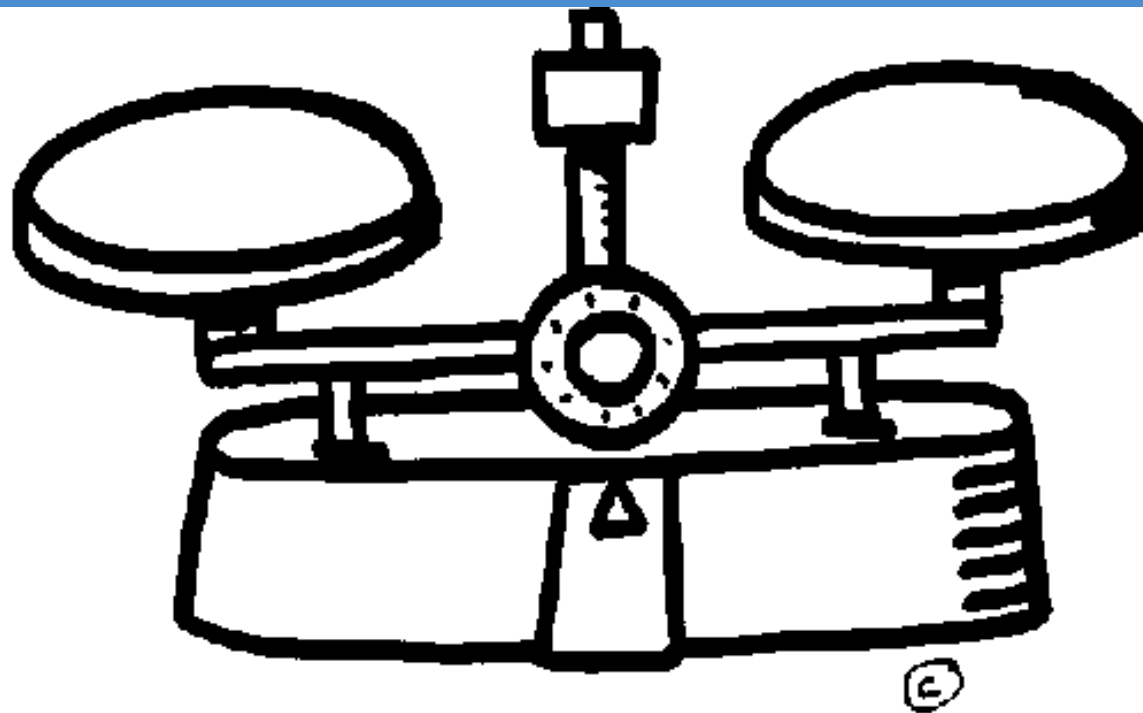
1. H3
2. L1,L2,L3 a
3. L1,L2,L3 a
4. 5. 6. – as

- Only 1 calculati  
agreed with ben

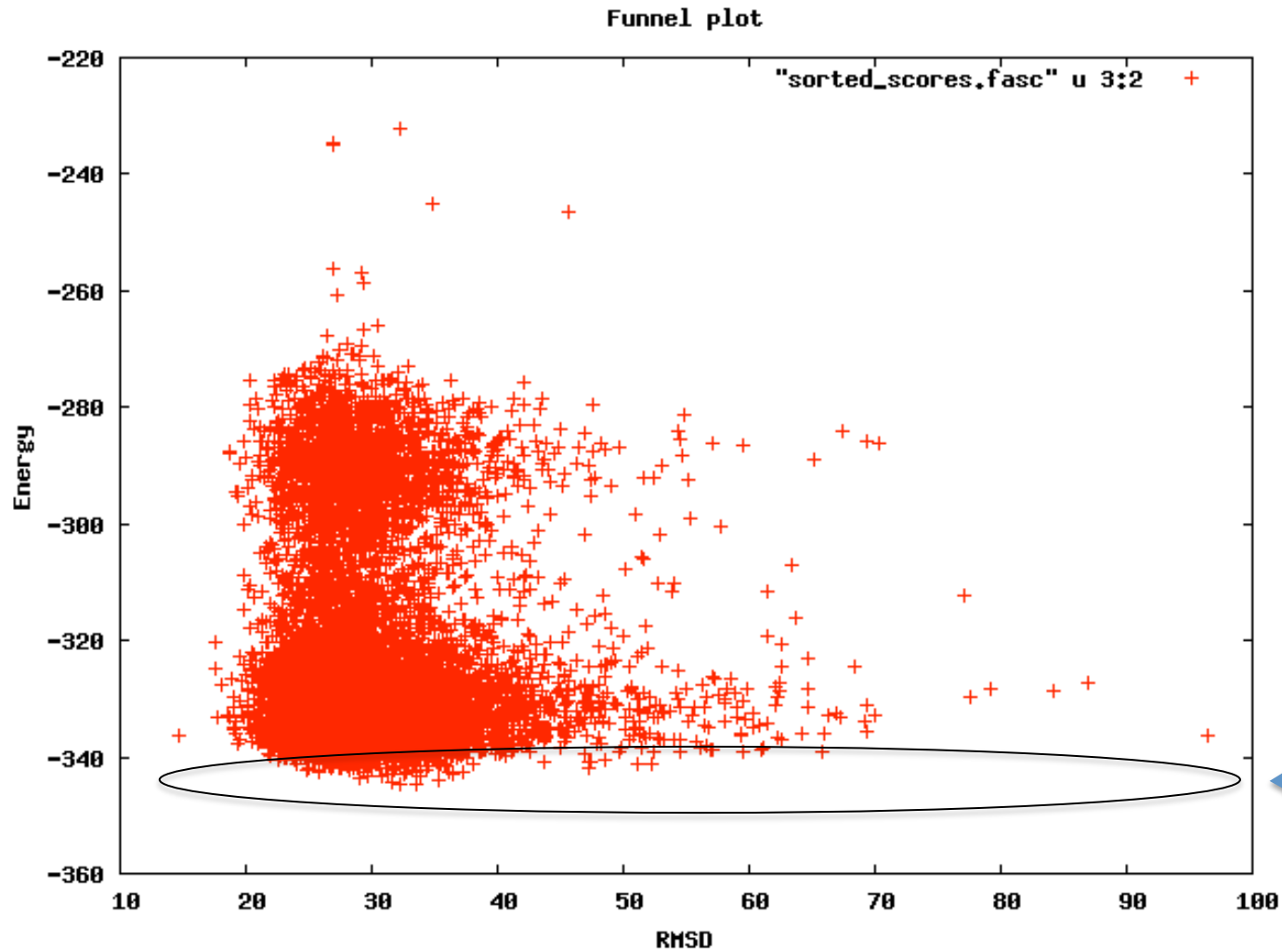
Underscores need  
interpreting resu  
the trick.)

FLEXIBILITY

WILL I BE DEAD  
WHEN THE  
CALCULATION FINISHES??

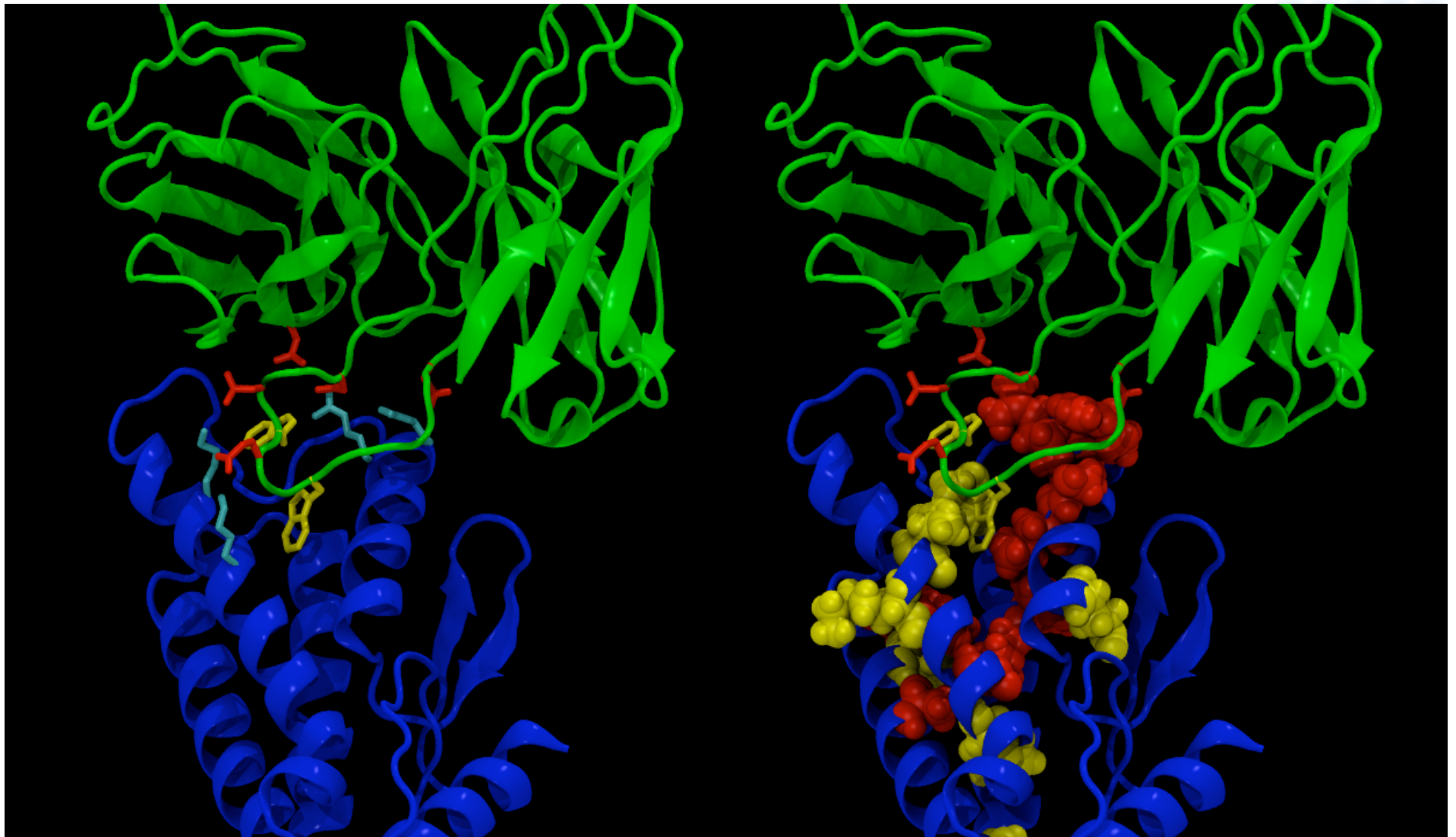


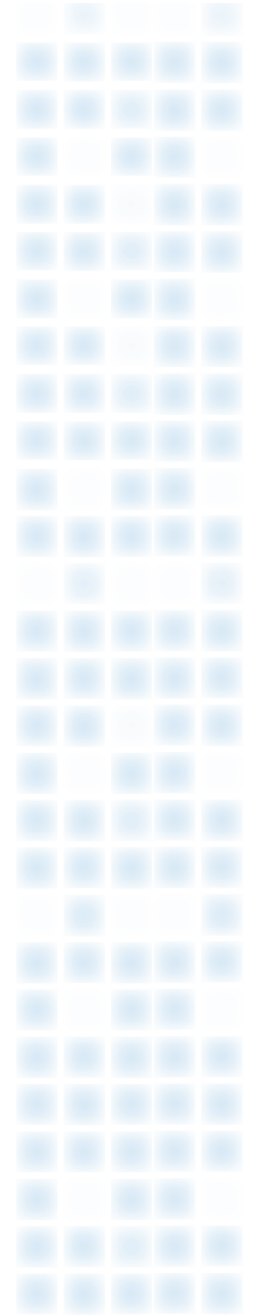
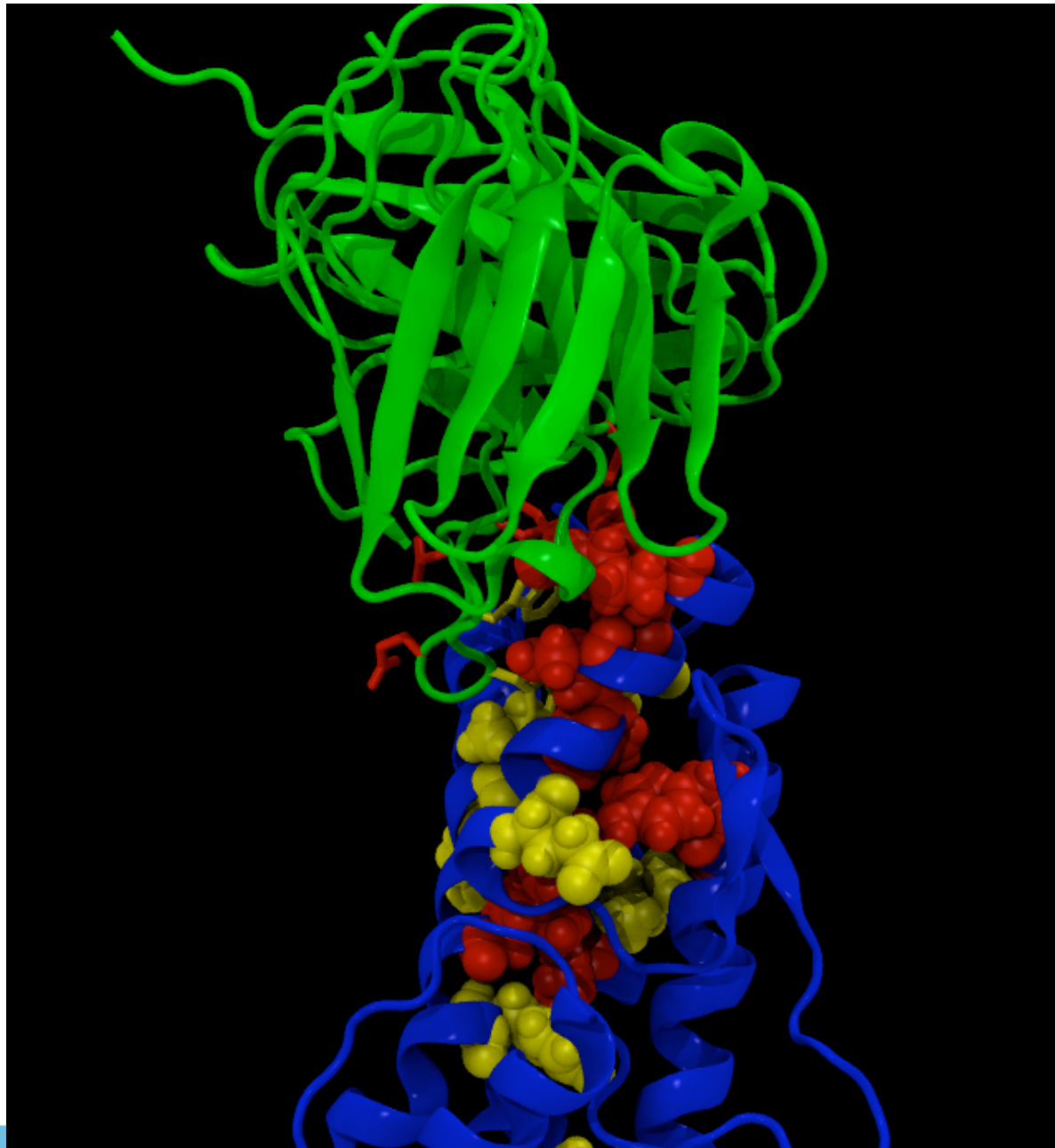
# “Funnel” plot



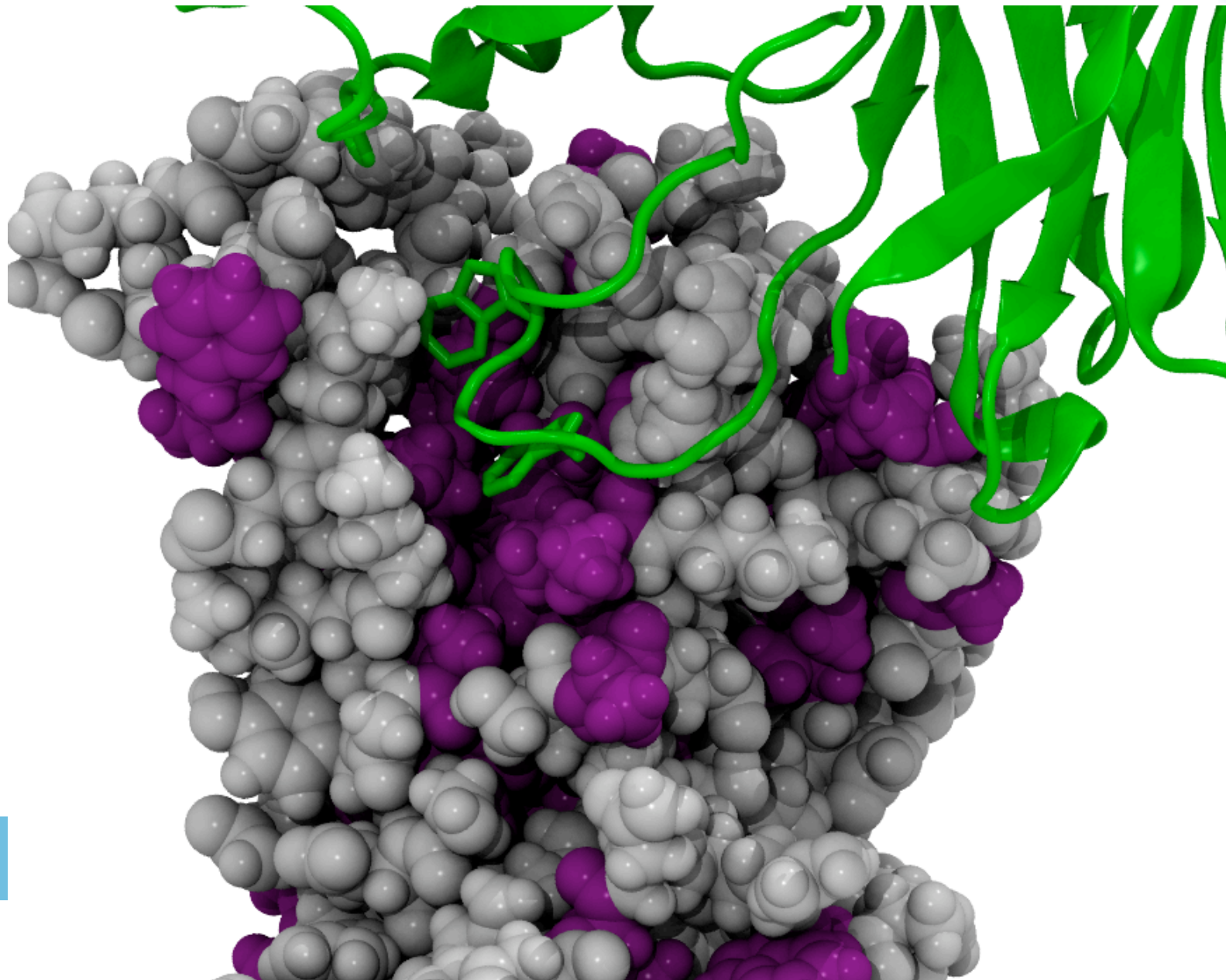


# Detailed contacts



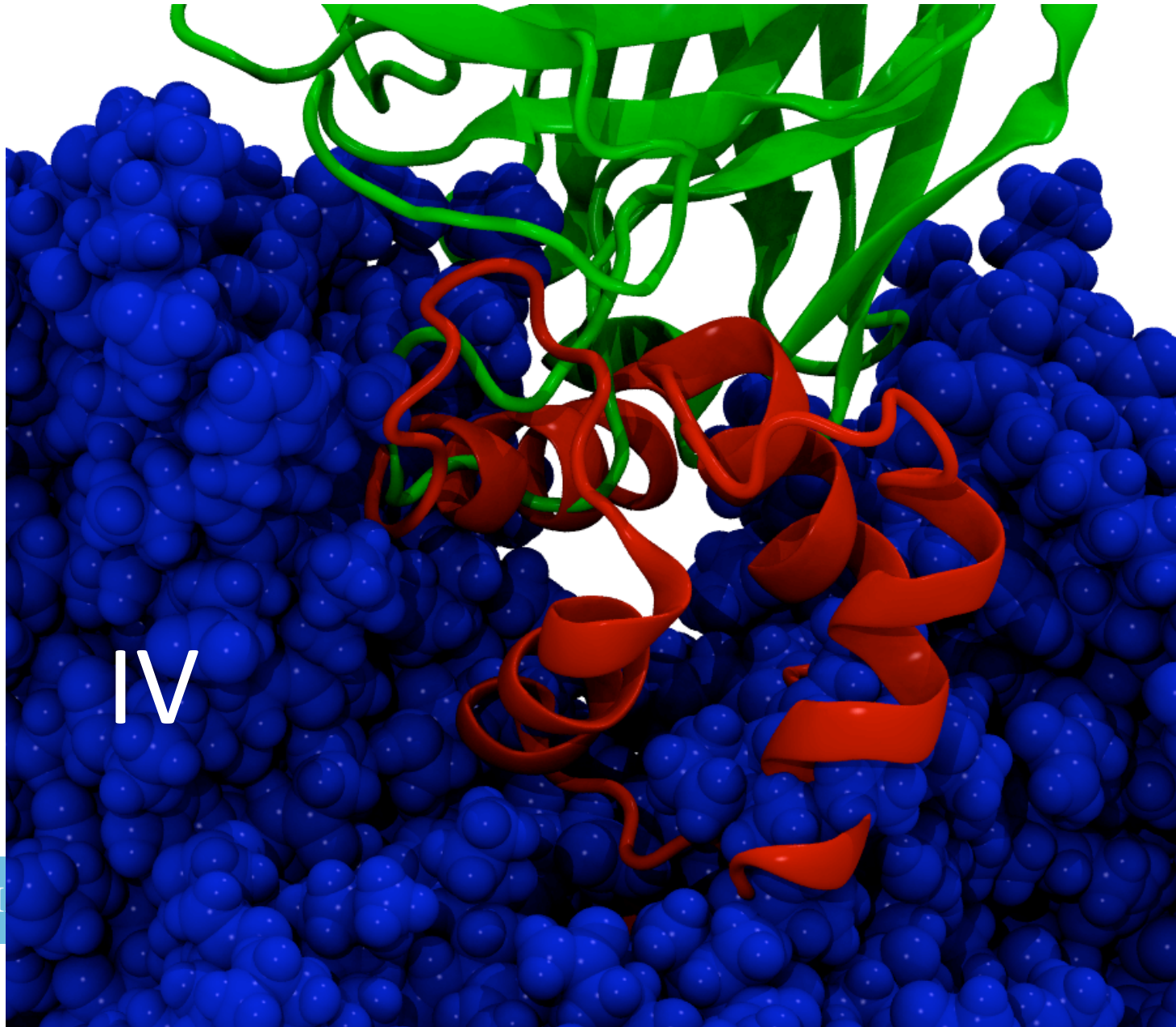


# Post-molecular dynamics





# Anti-EF/calmodulin overlap

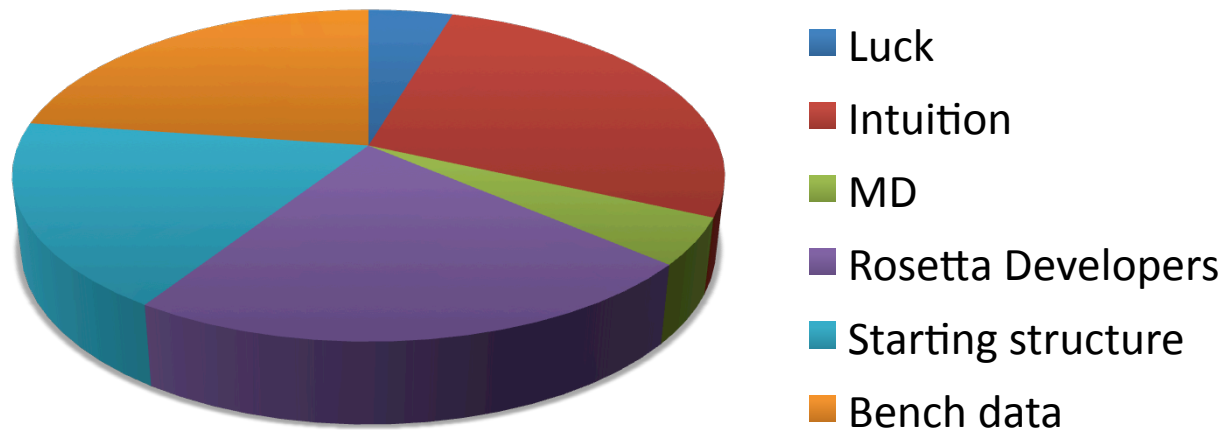


IV

# Conclusions

- A little bit of bench data goes a long way
- Constraints (.cst file) not needed
- MD finds lower energy conformation (more native than Rosetta results?)

## What is needed to produce a good, docked solution



# Future work

Additional EF domain IV and/or anti-EF H3 loop mutations to verify docking results



## Acknowledgements

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