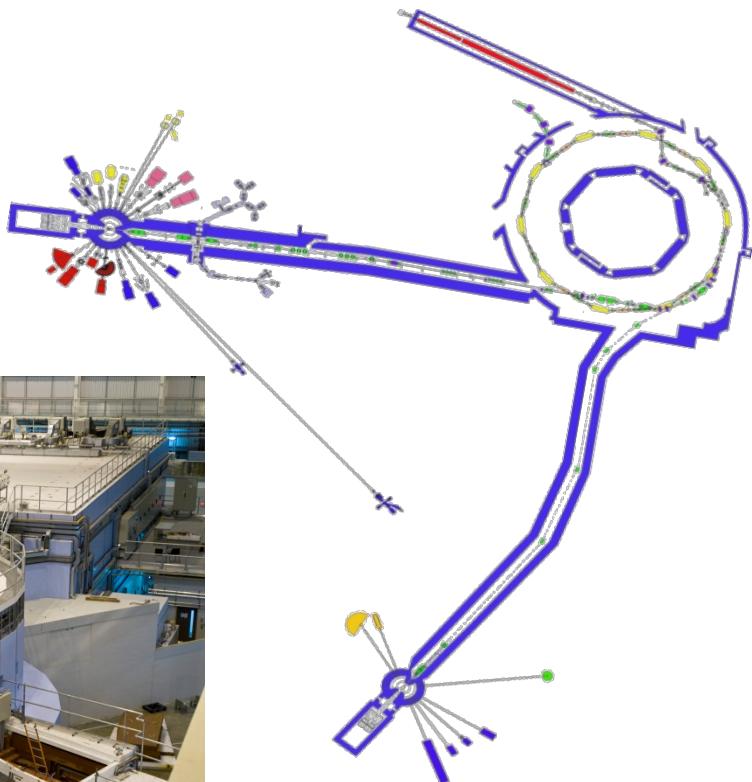
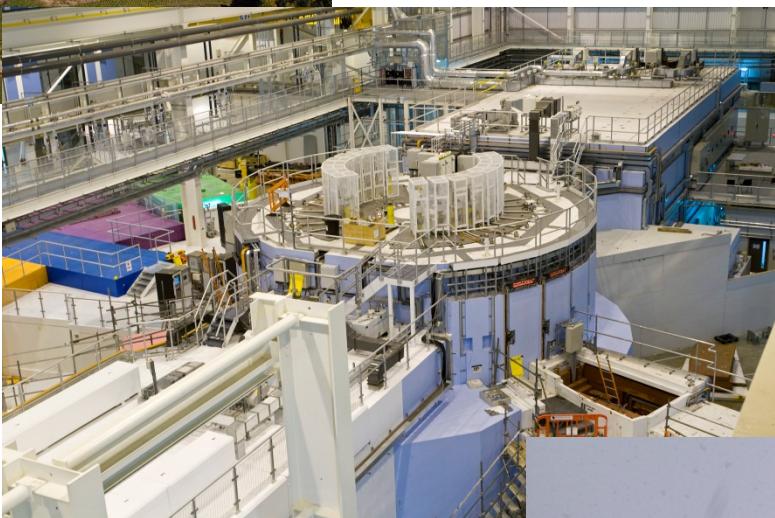


The Interaction of Thionins with Model Pathogen Membranes

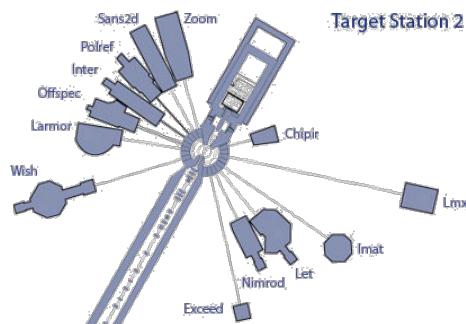
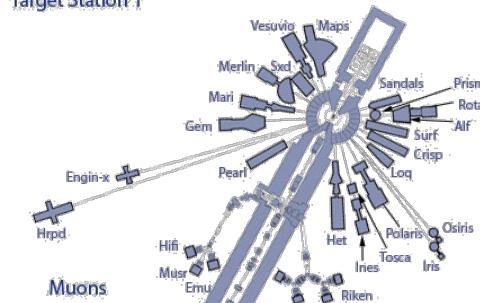
Luke Clifton
[\(luke.clifton@stfc.ac.uk\)](mailto:luke.clifton@stfc.ac.uk)

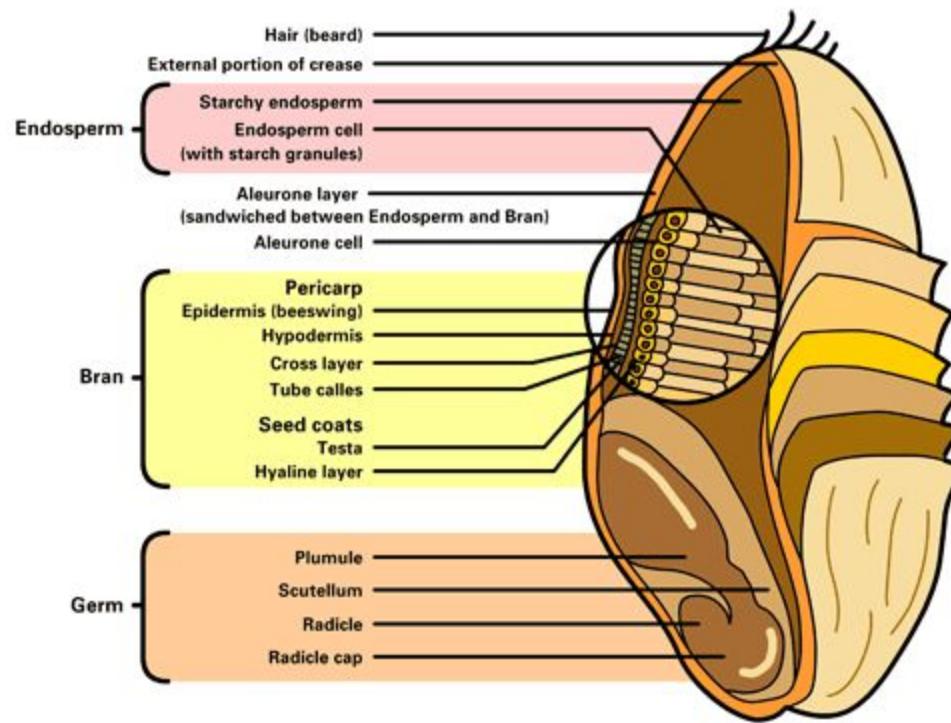


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Target Station 1

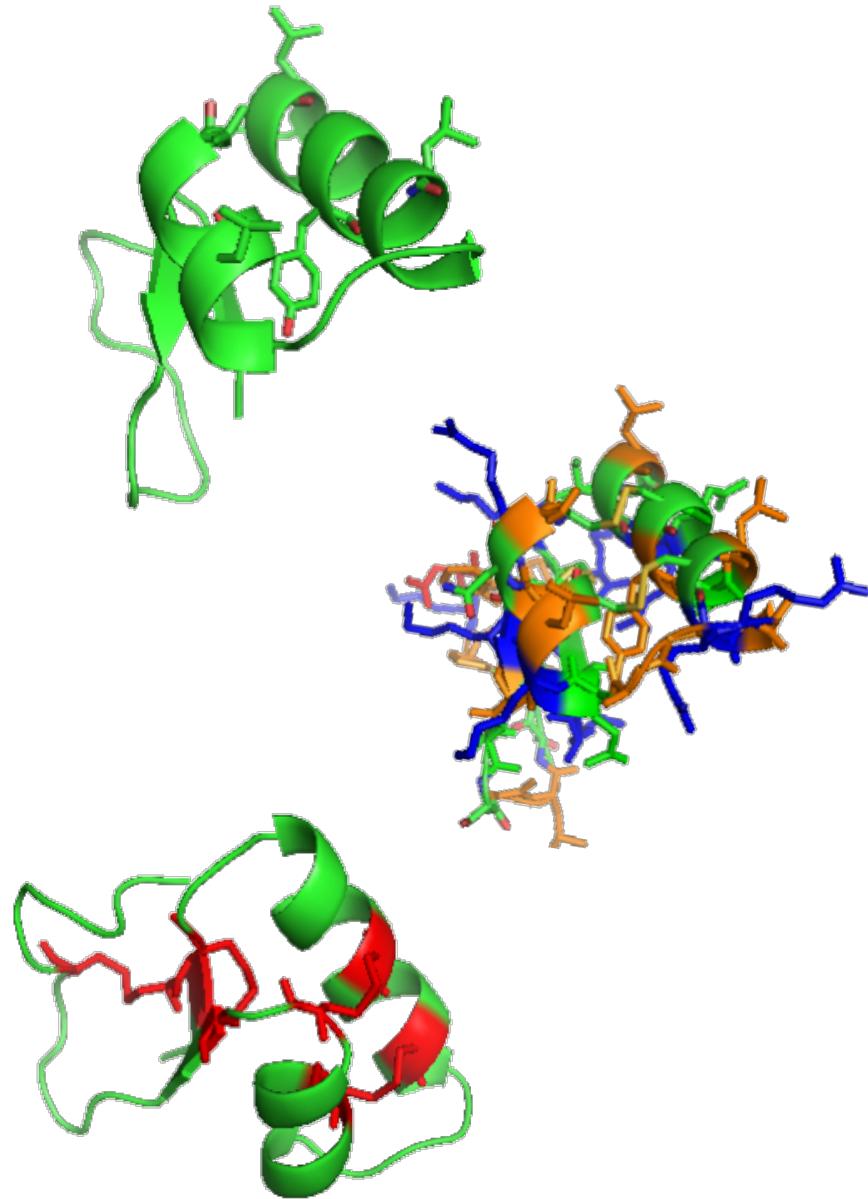




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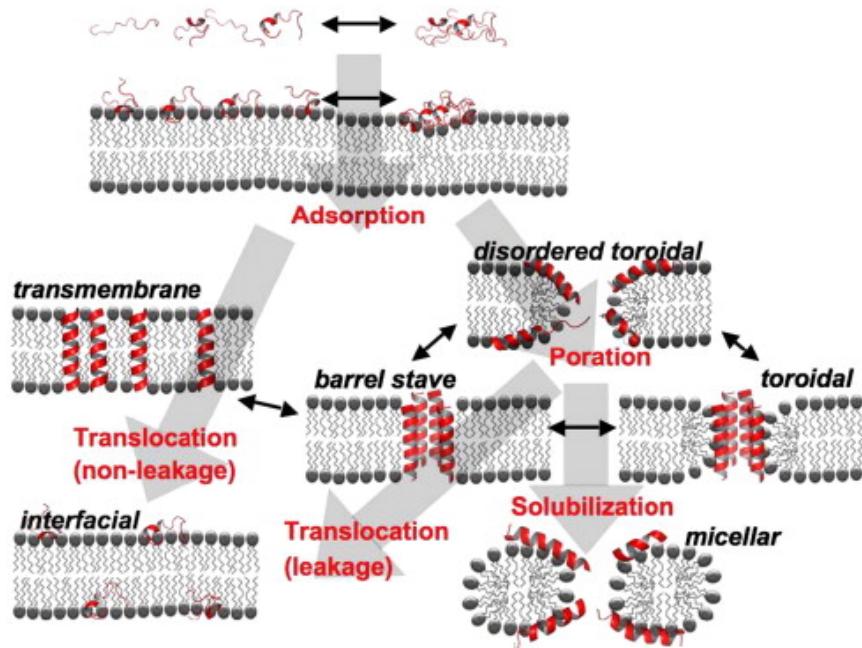
Thionins

- Thionins are small (<5KDa) proteins produced as part of plants innate immune response system.
- All members are highly cationic (pI 9-11) which enables interactions with the anionic bacterial and fungal membranes.
- Most are also amphiphilic allowing partition into the hydrophobic core of the membrane.
- Thionins are cysteine rich, they contain between 8 and 10 cysteine residues forming 4-5 disulphide bonds per protein. Making these proteins structurally stable.

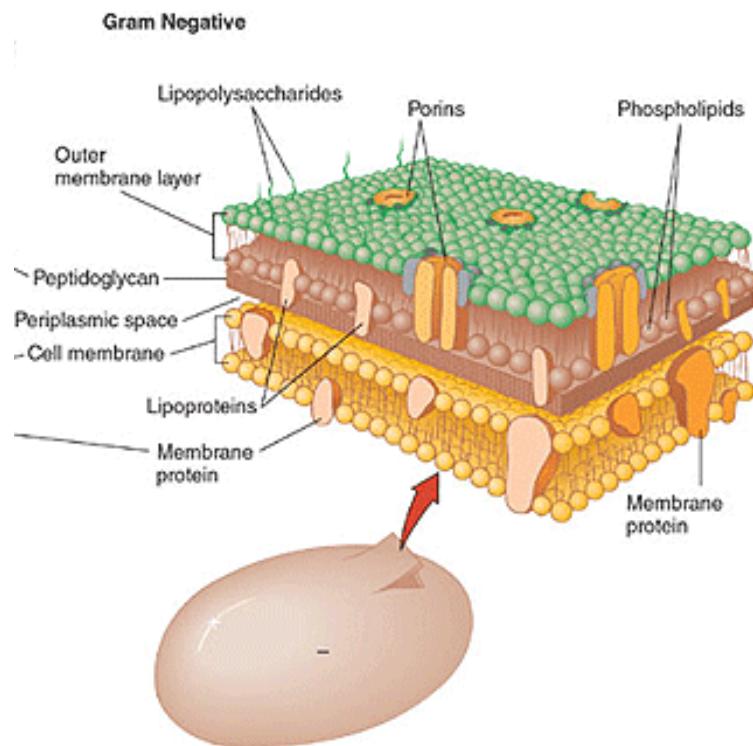
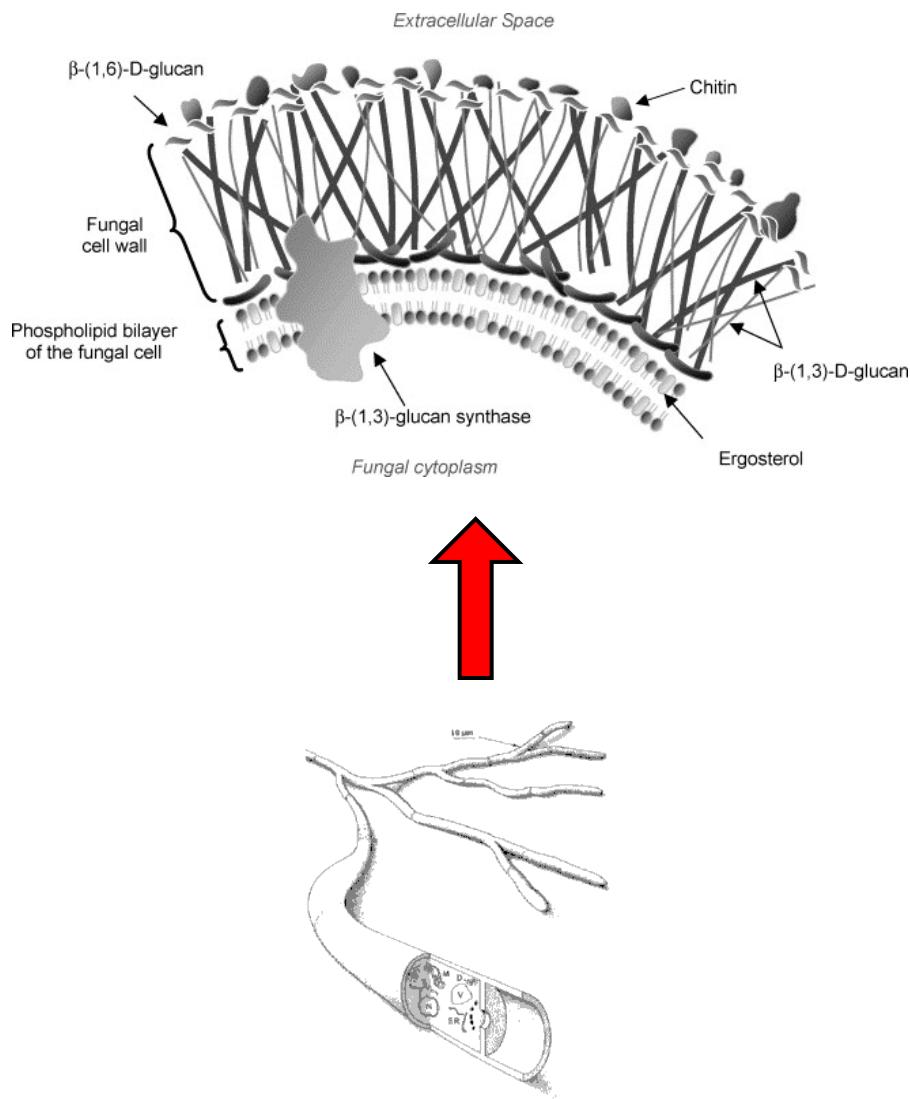


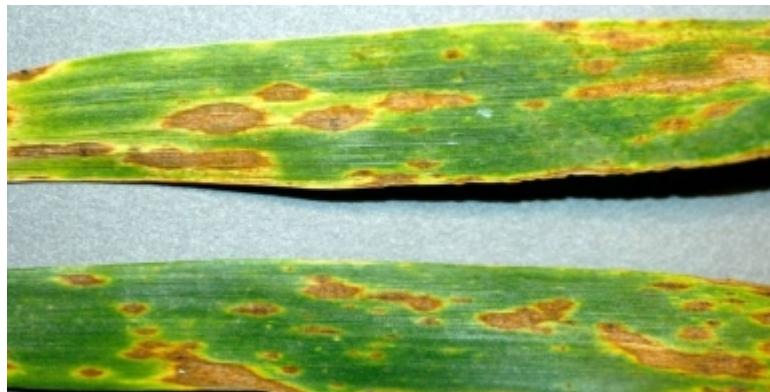
Antimicrobial Proteins which act at the membrane level.

- Charge.
- Hydrophobic and hydrophilic domains (amphiphilicity).
- Hydrophobicity.
- Stable molecular conformation.
- Size.
- The balance of these attributes modulates binding selectivity (prokaryotic/eukaryotic) and activity.



Fungal and bacterial membranes





Tan spot (*Pyrenophora tritici-repentis*)



Glumbe Blotch (*Stagonospora nodorum*)



L.J. Duczek

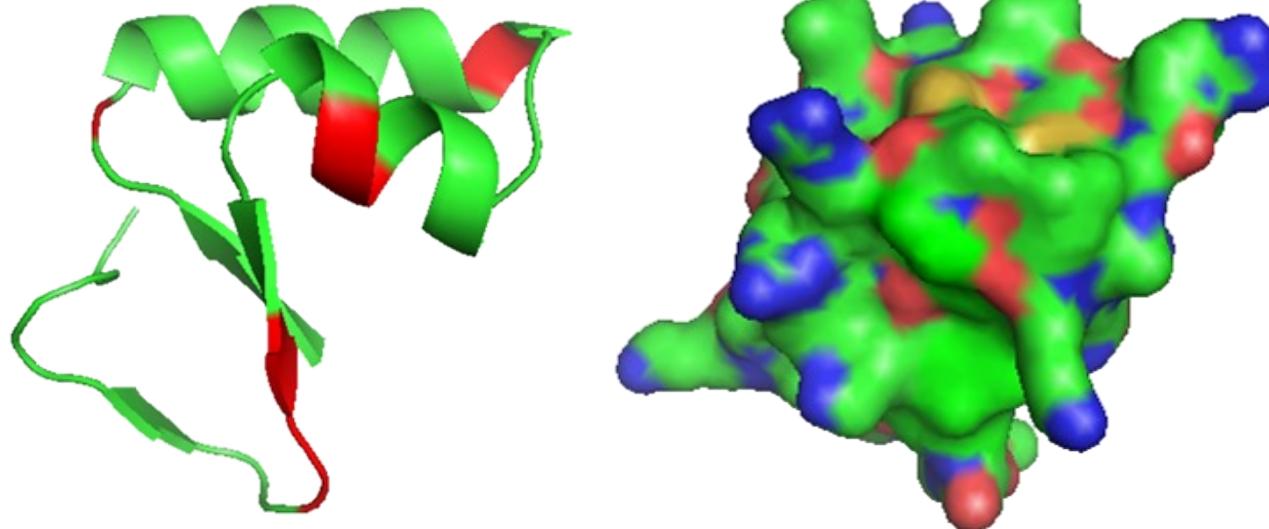
Common Smudge (*Cochliobolus sativus*)



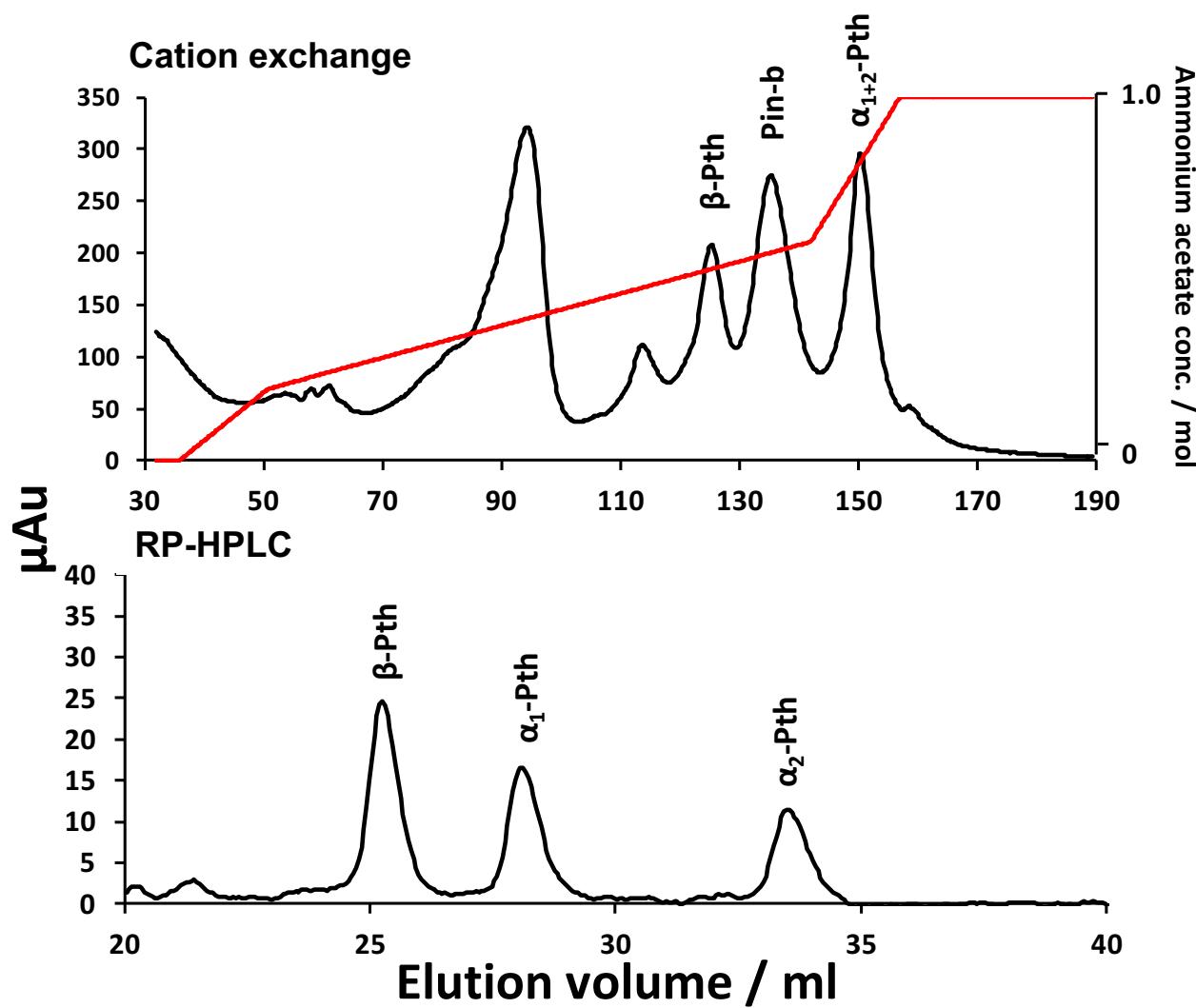
Stripe blight (*Pseudomonas syringiae*)

α -purothioins

α_1 -Pth	KSCCR <u>S</u> TLGR NCYNL <u>C</u> R <u>A</u> RG AQKLC <u>A</u> G <u>V</u> CR CK <u>I</u> <u>S</u> GLSCP KGFPK
α_2 -Pth	KSCCR <u>T</u> TLGR NCYNL <u>C</u> R <u>S</u> RG AQKLC <u>S</u> <u>T</u> VCR CK <u>L</u> <u>T</u> SGLSCP KGFPK



α_1 and α_2 -purothionin – same charge, differing hydrophobicity



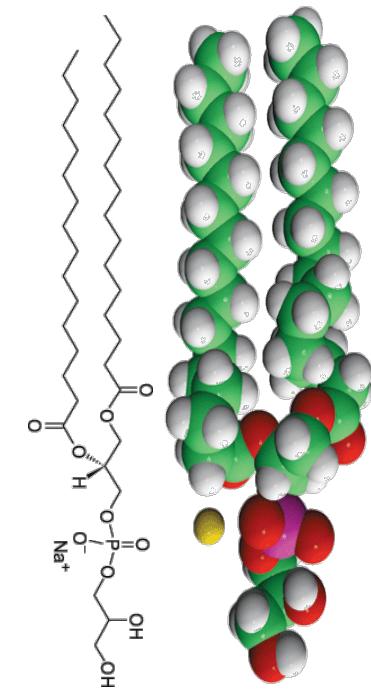
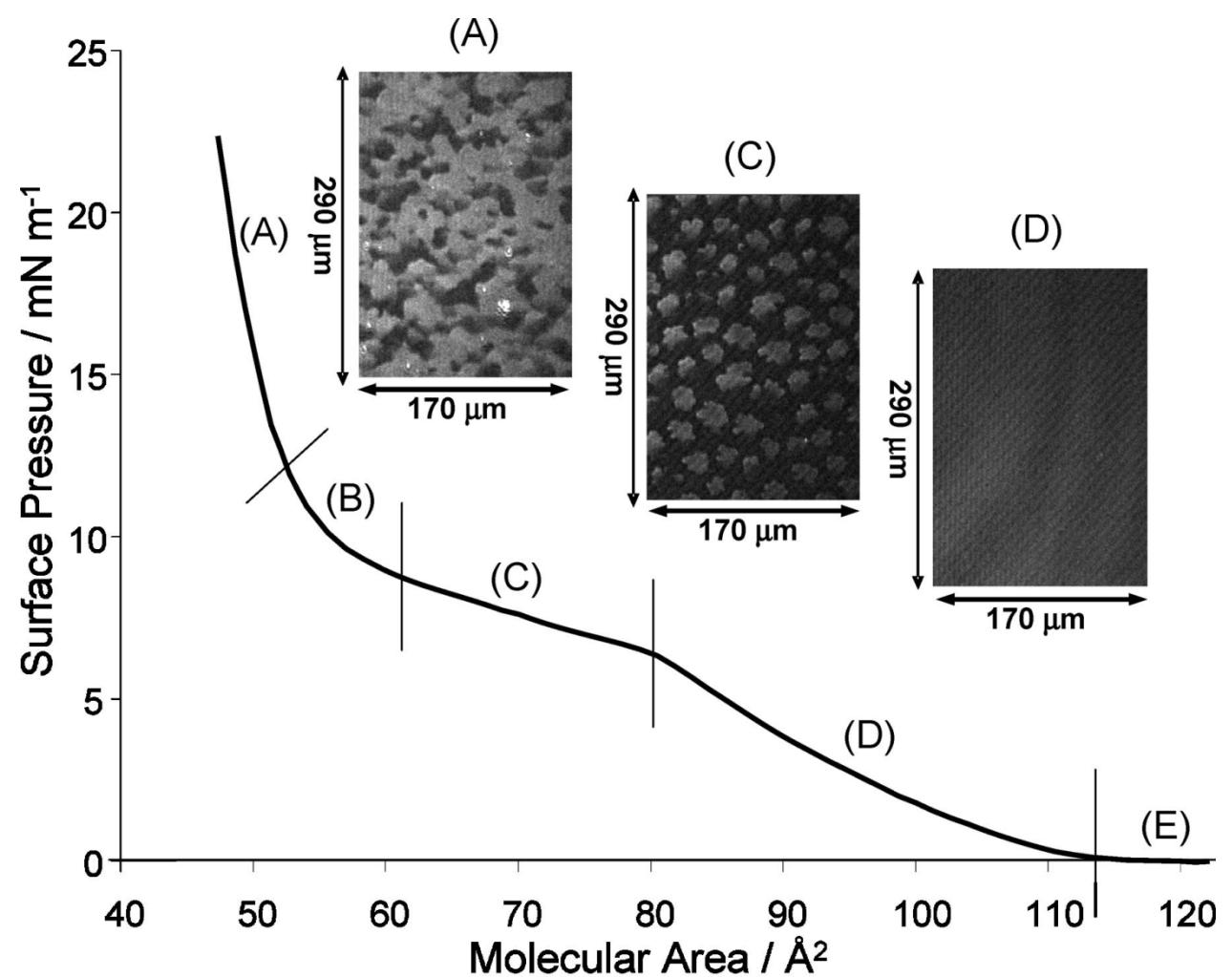
Aim

To determine the method by which thionins exert their seed defence activity, and determine how a difference in antimicrobial protein hydrophobicity effects protein membrane disruptive effects.



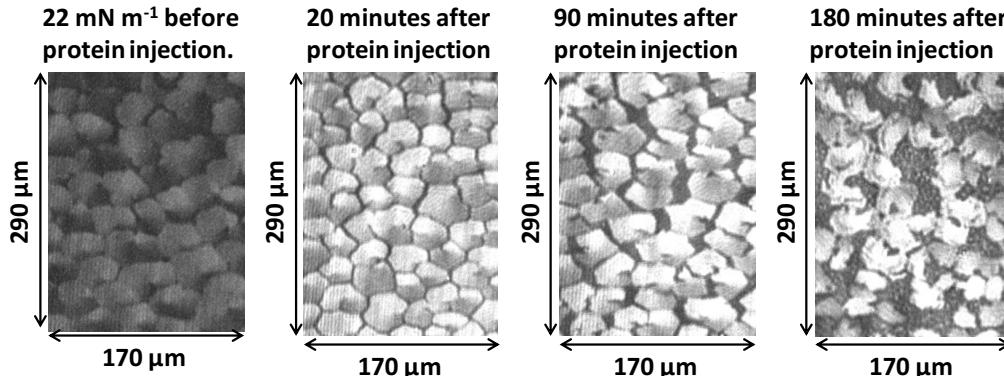
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Comparing defense protein interactions with condense phase anionic phospholipid monolayers.

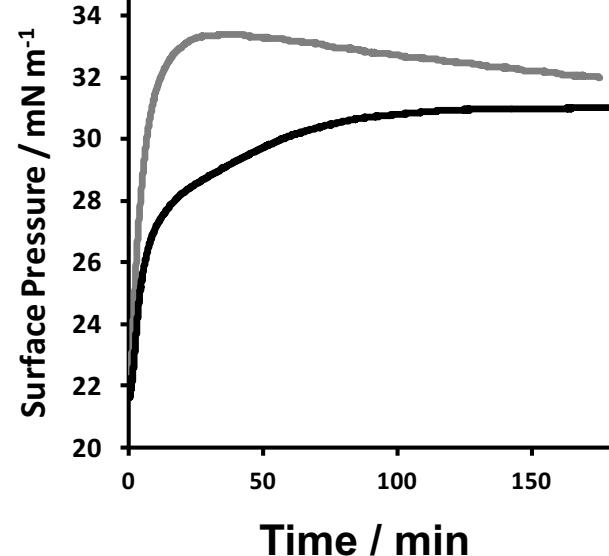
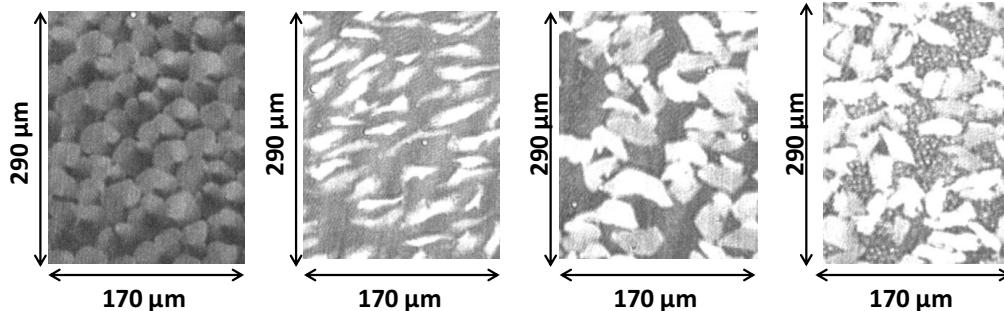


Brewster Angle Microscopy vs. time imaging

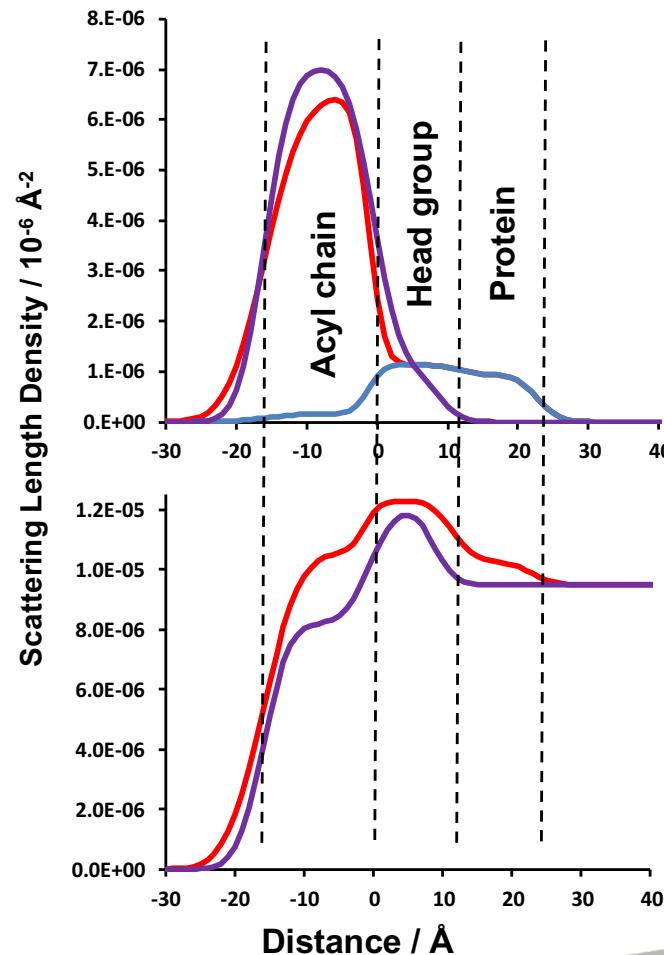
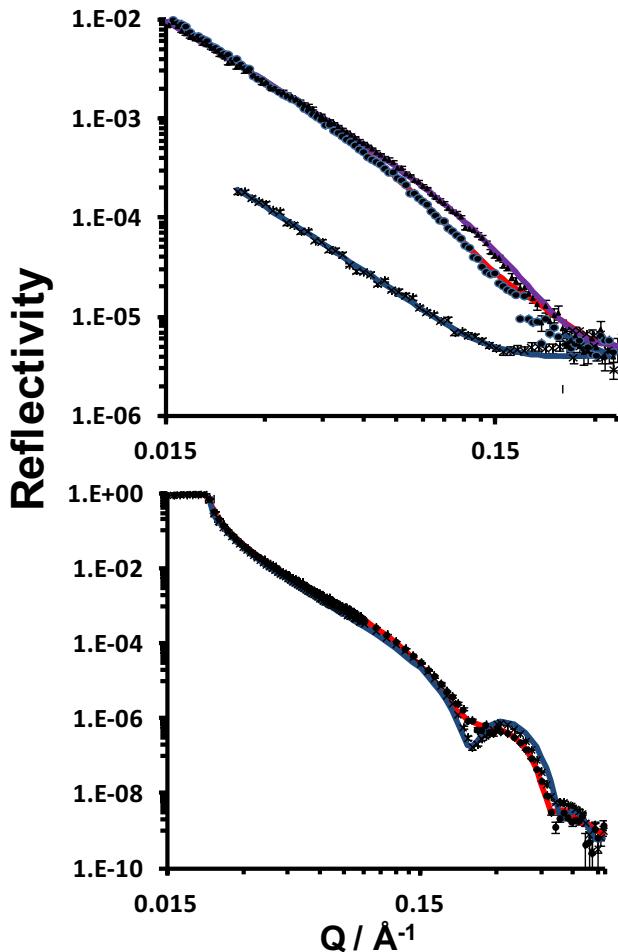
$\alpha 1$ -Pth



$\alpha 2$ -Pth

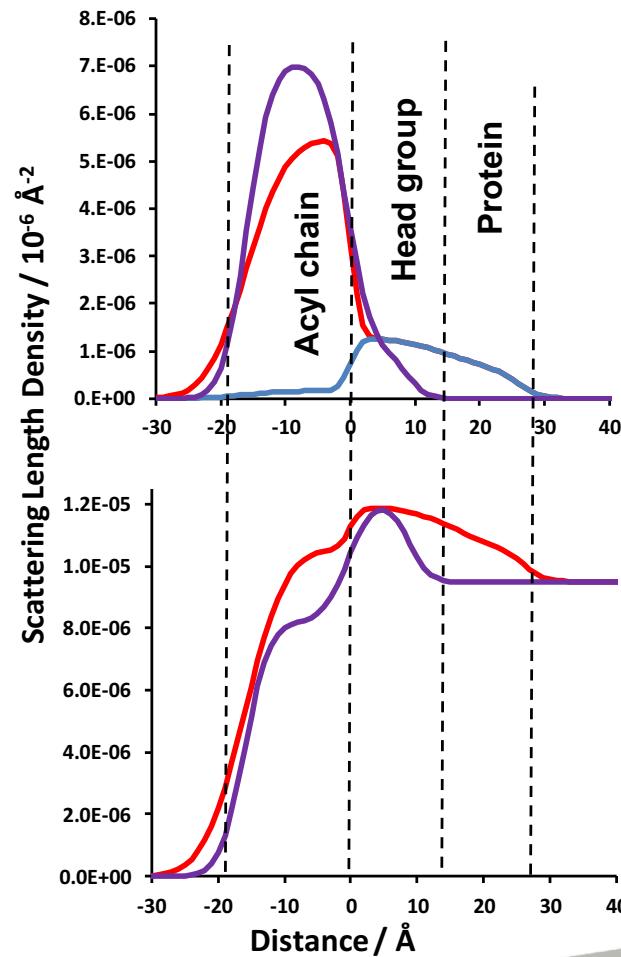
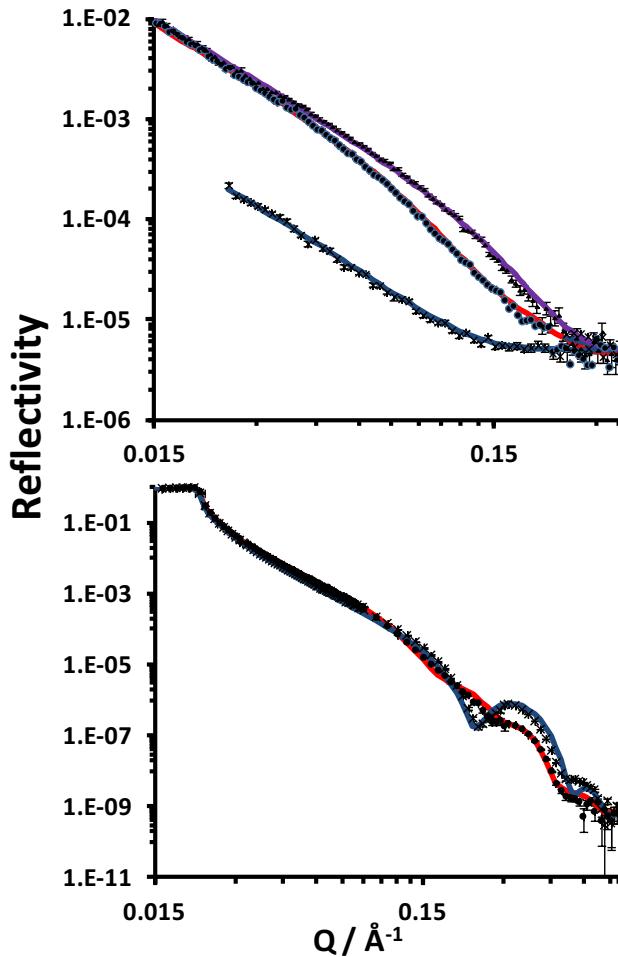


Equilibrium α 1-Pth adsorbed DPPG monolayer



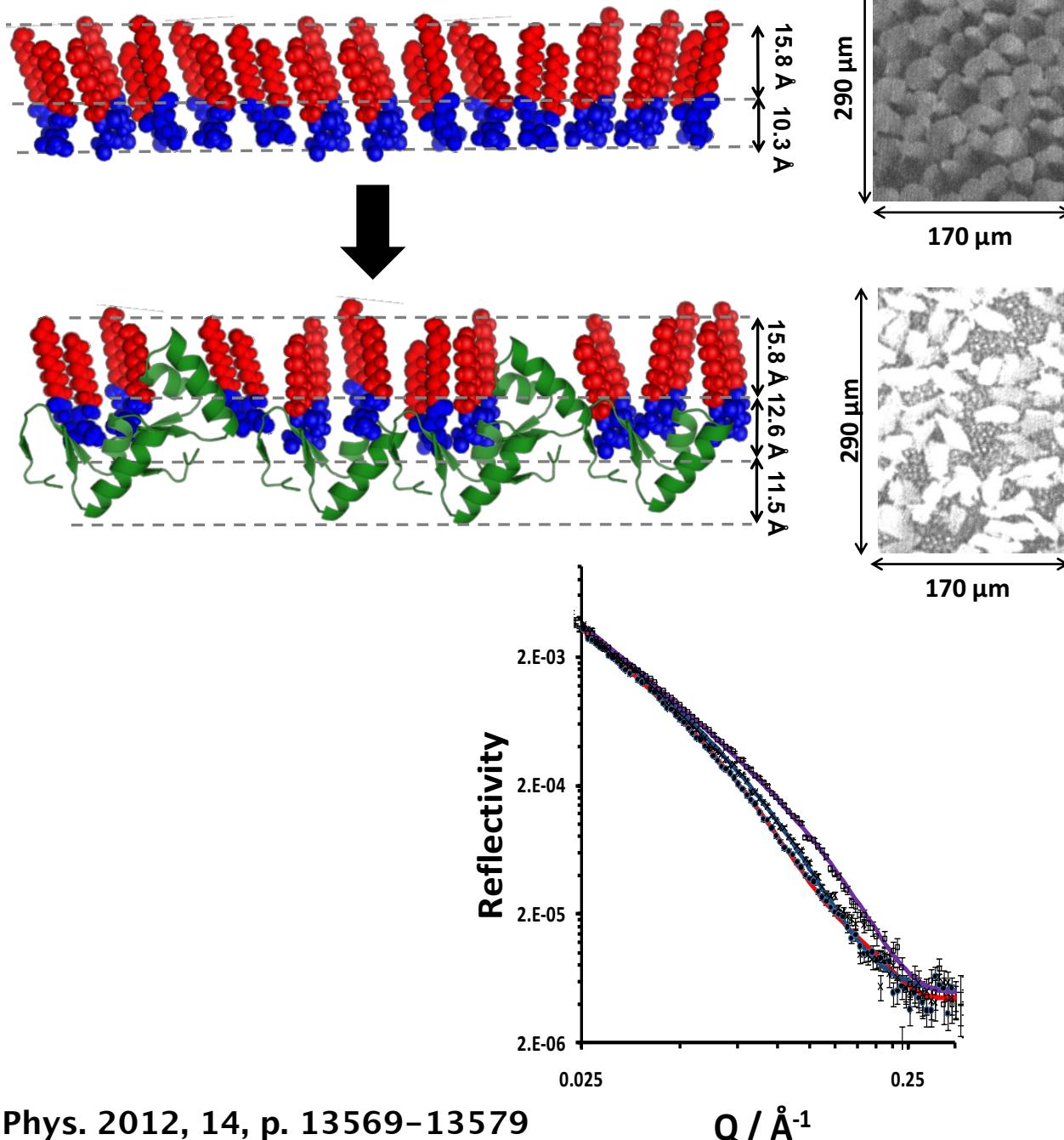
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Equilibrium α 2-Pth adsorbed DPPG monolayer

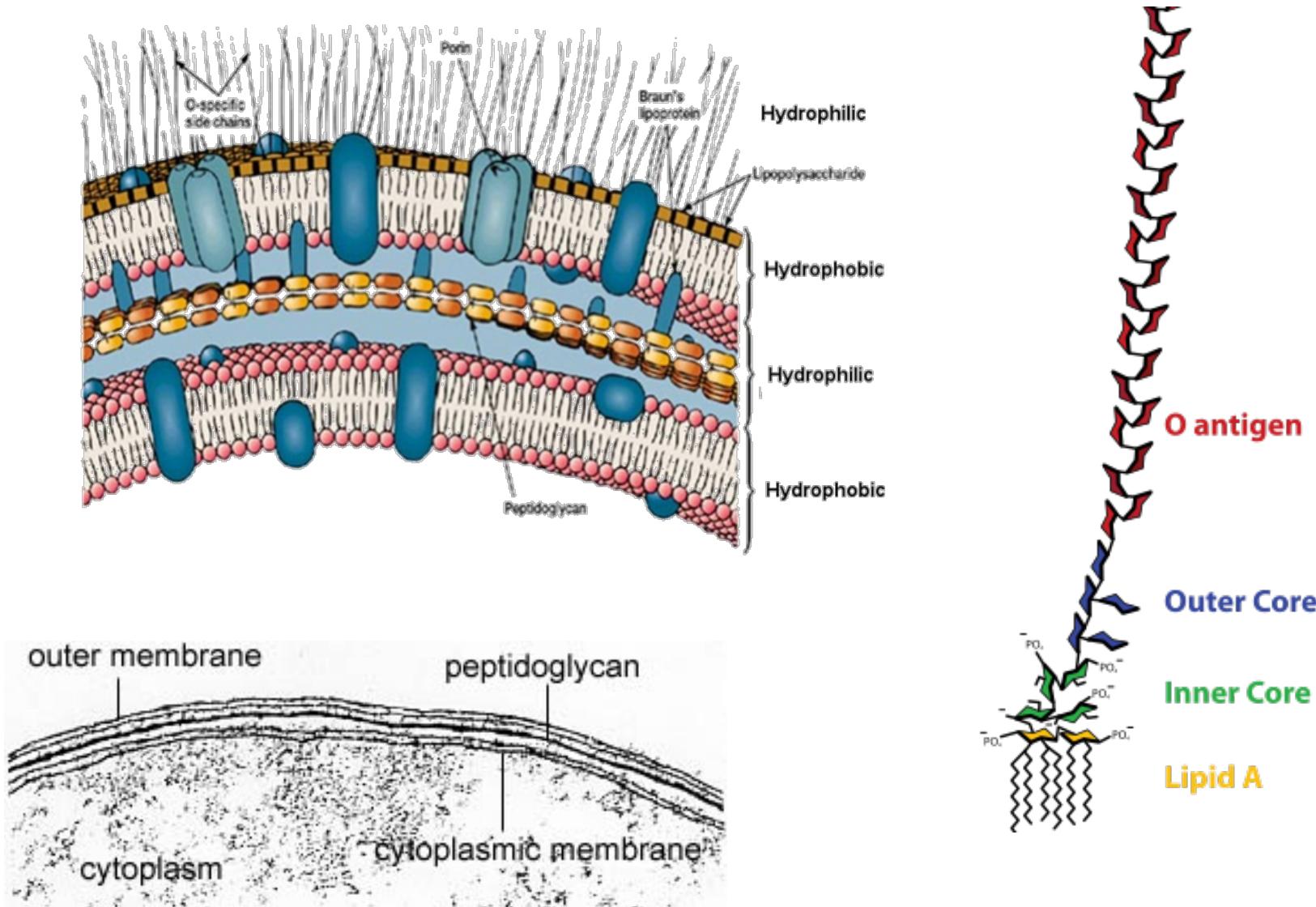


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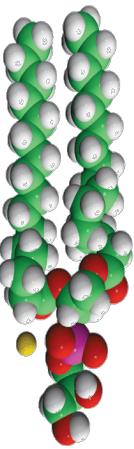
Monolayer results summary



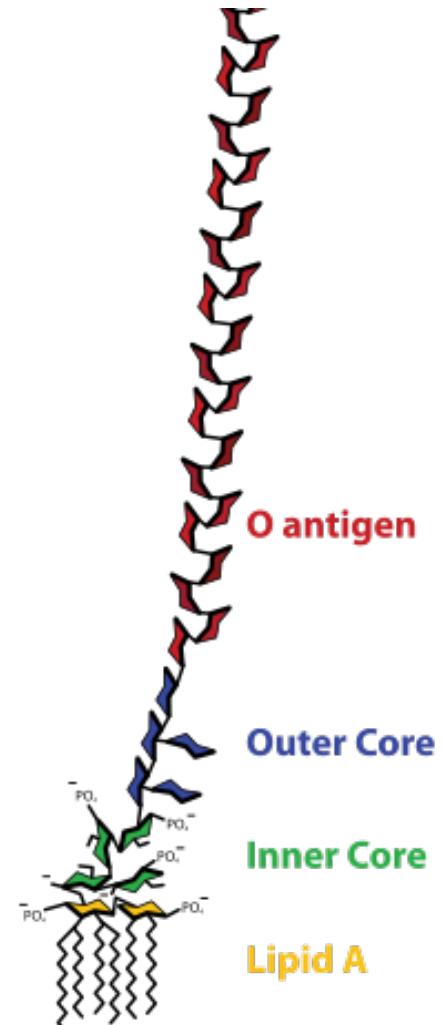
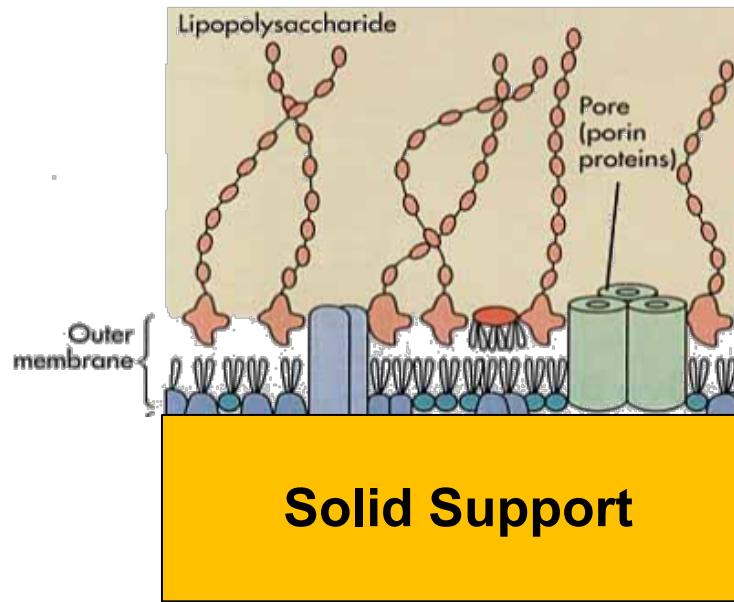
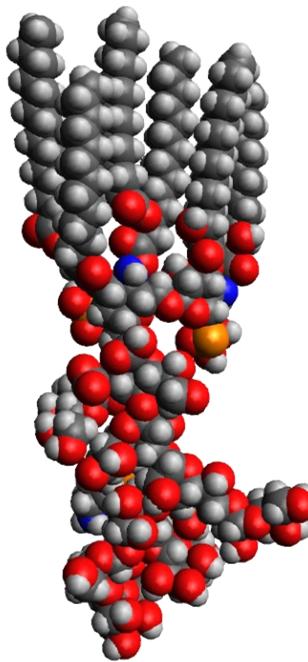
Bilayer models of the Gram negative bacterial outer membrane



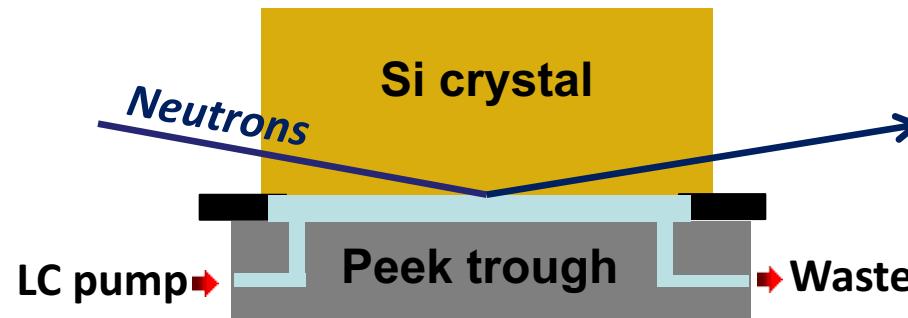
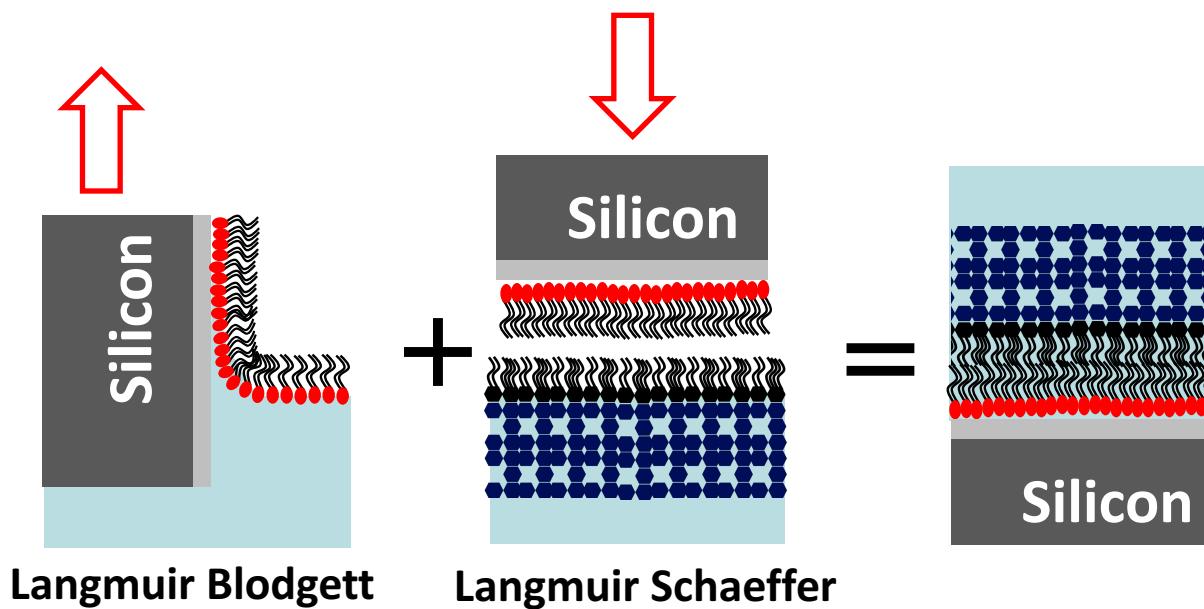
DPPC



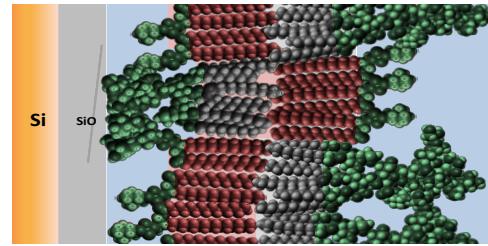
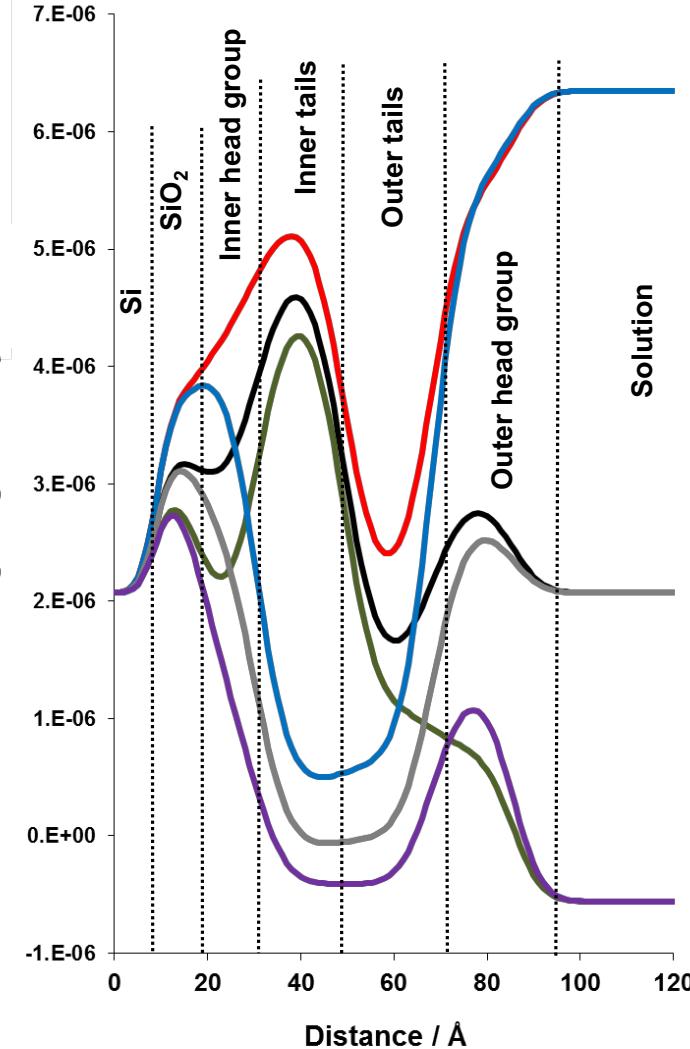
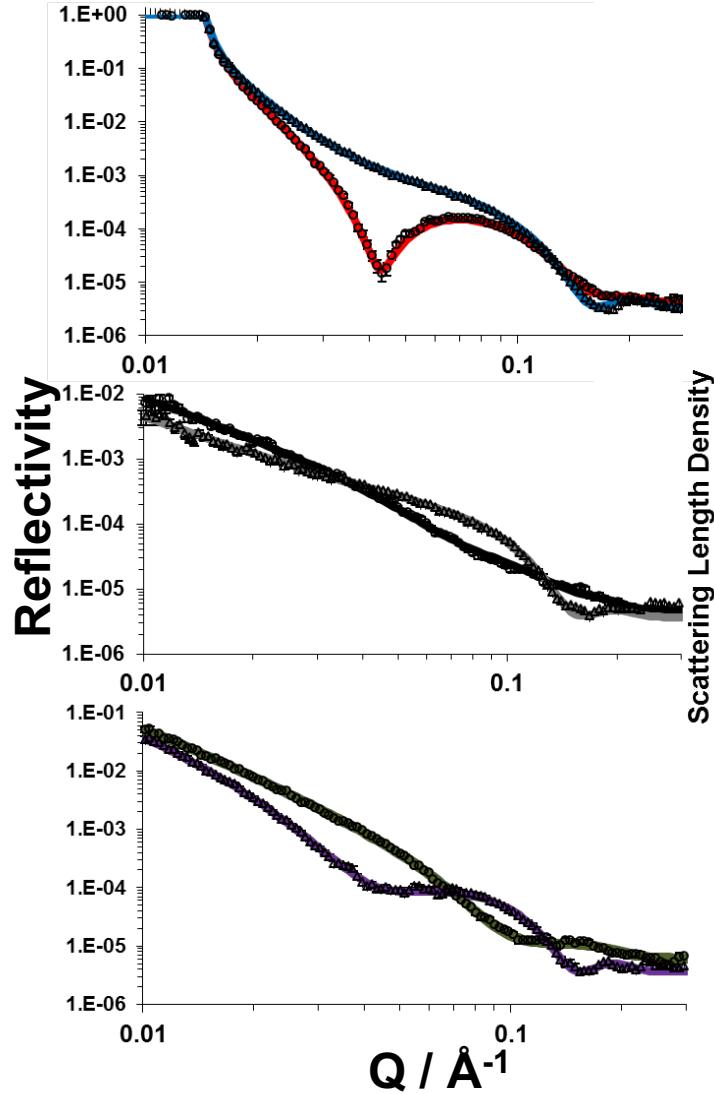
Rough mutant-LPS



Fabrication of asymmetric phospholipid : LPS membranes on silicon supports



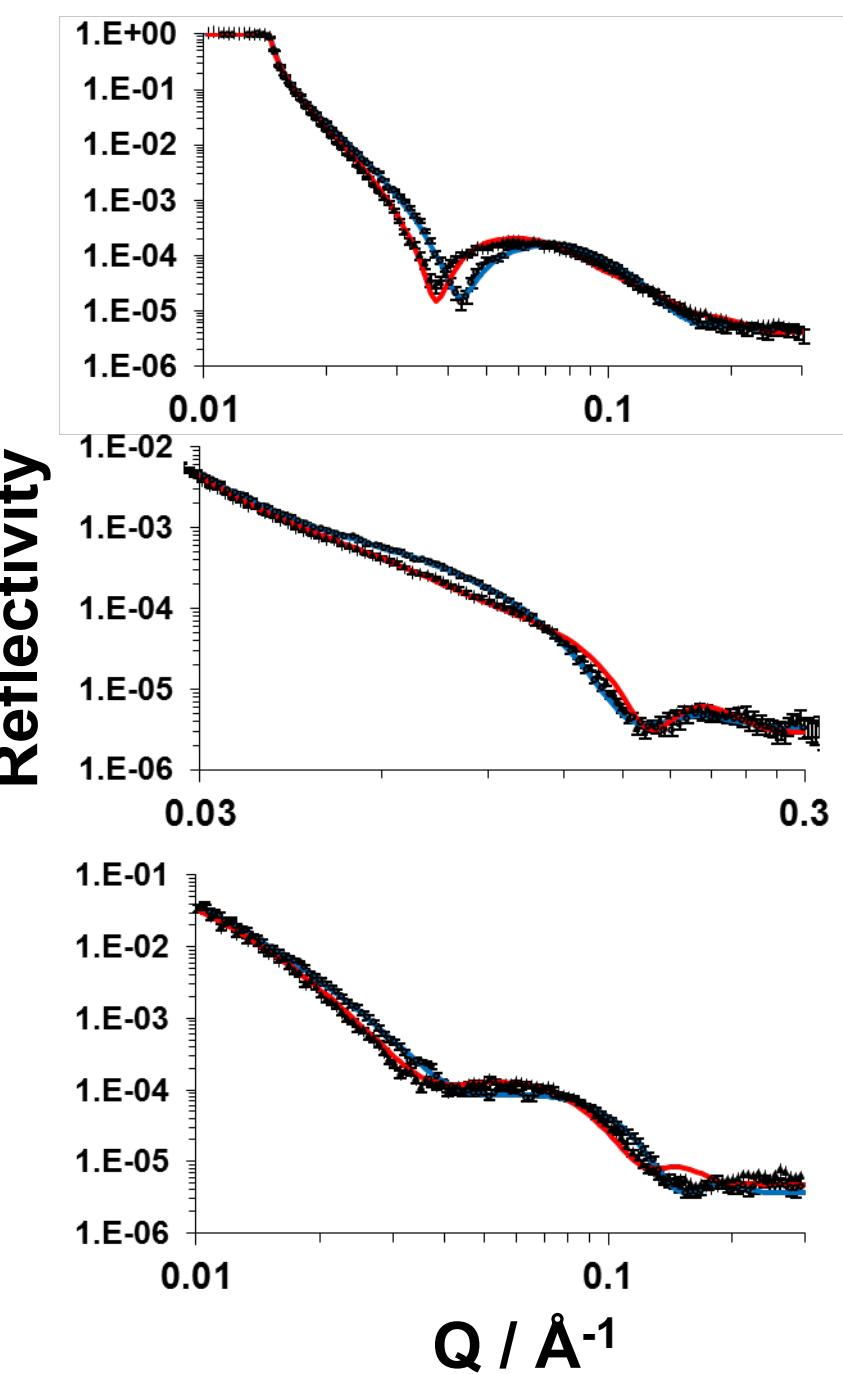
DPPC : Rc-LPS bilayer



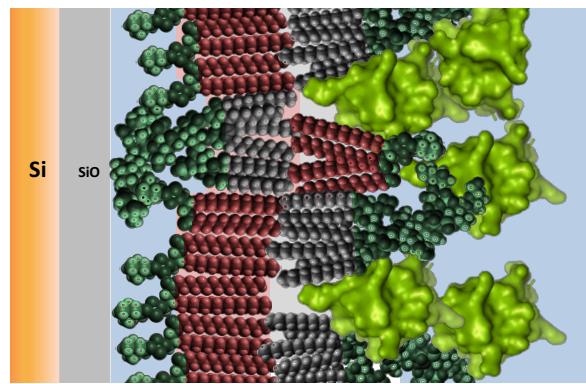
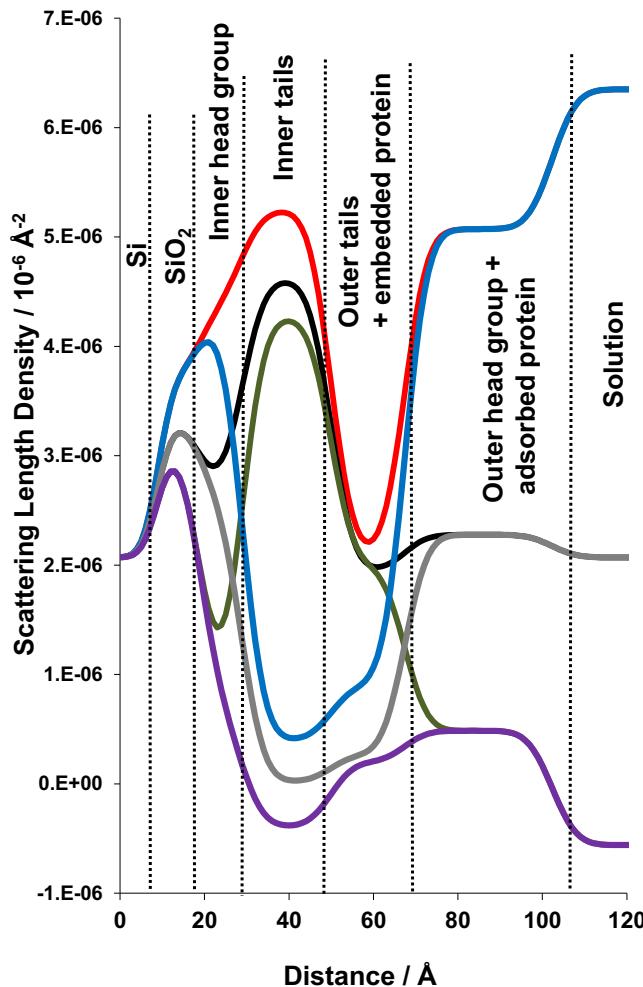
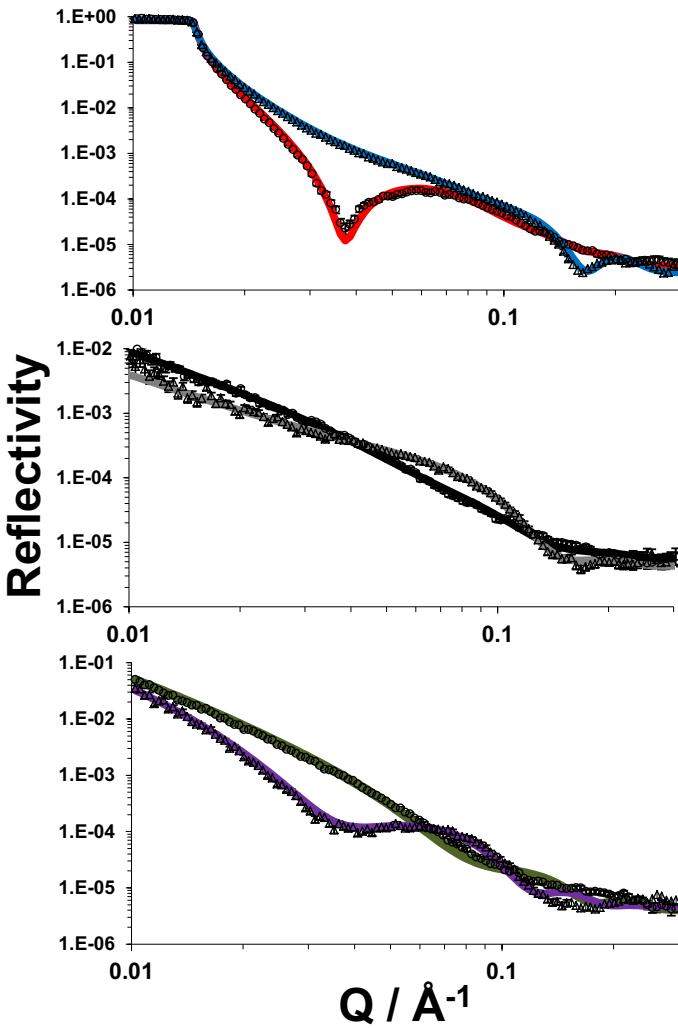
Changes Upon addition of α 1-Pth

— = before protein addition

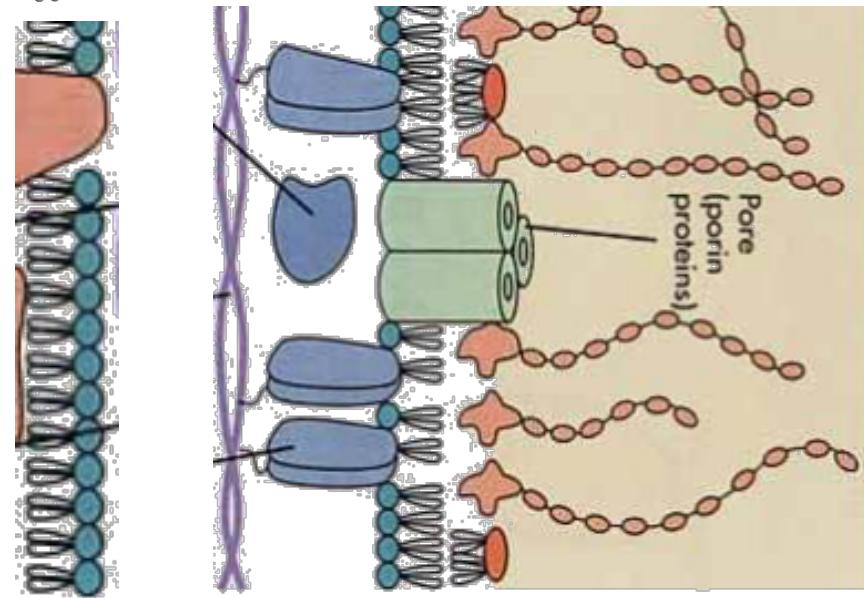
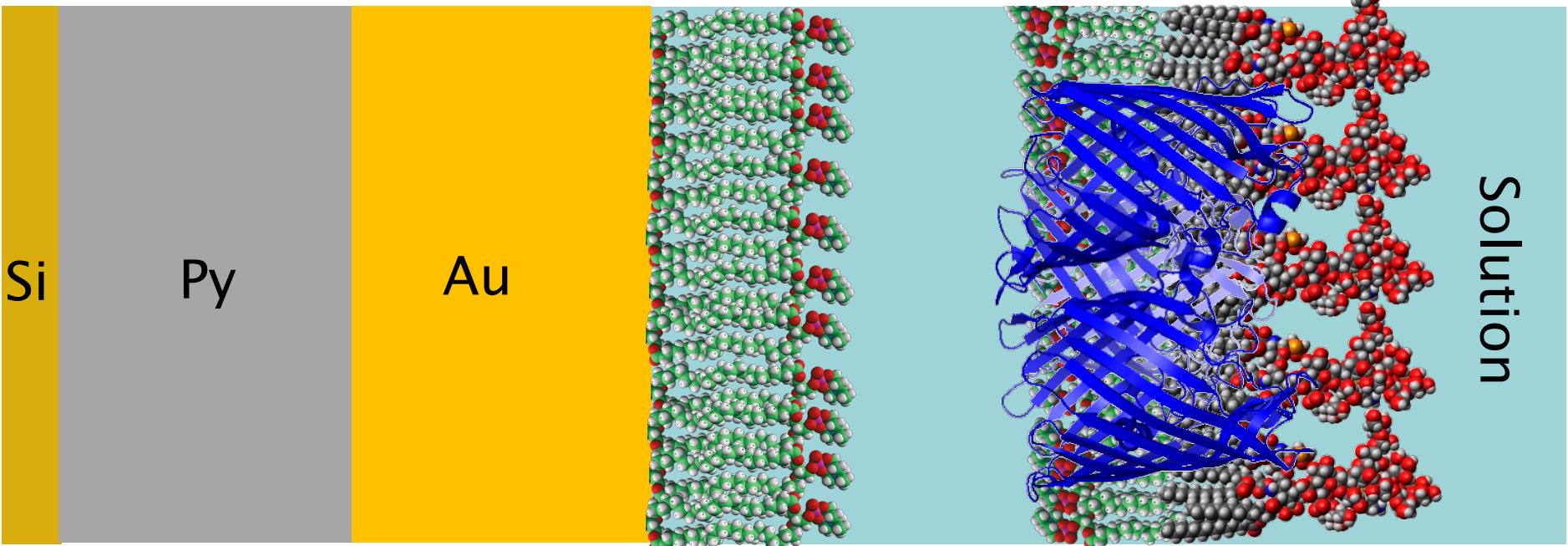
— = after 0.01 mg / ml injected into cell



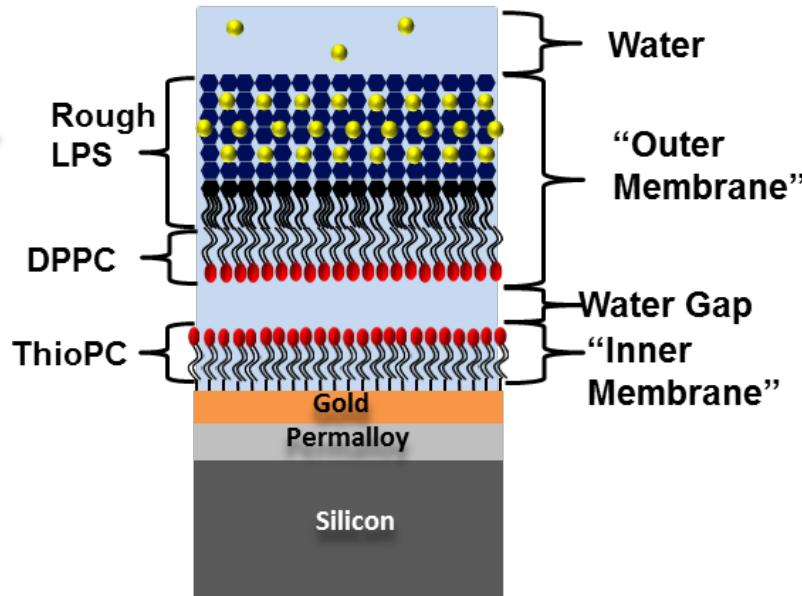
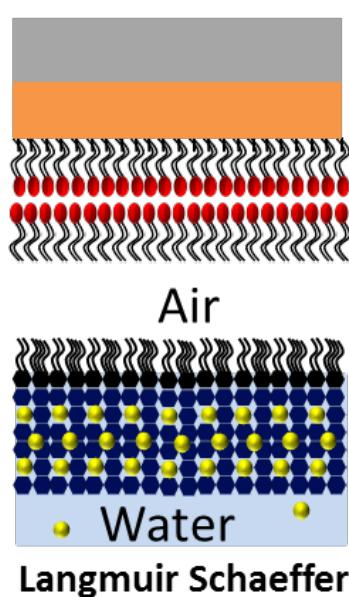
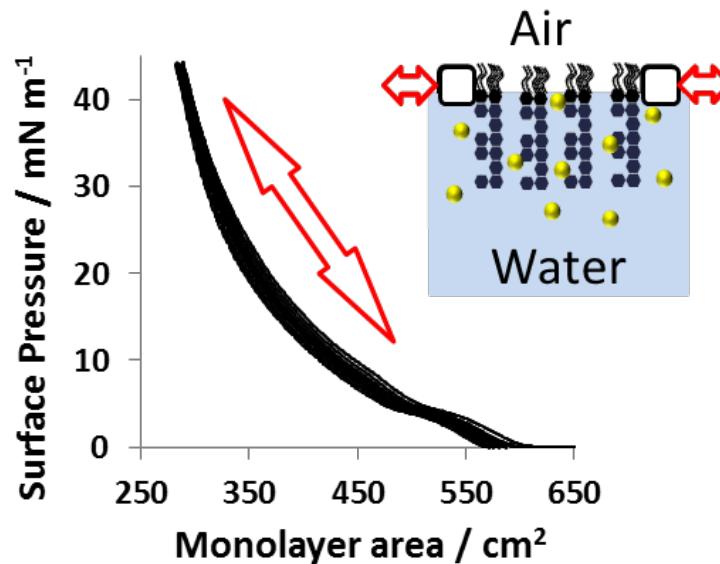
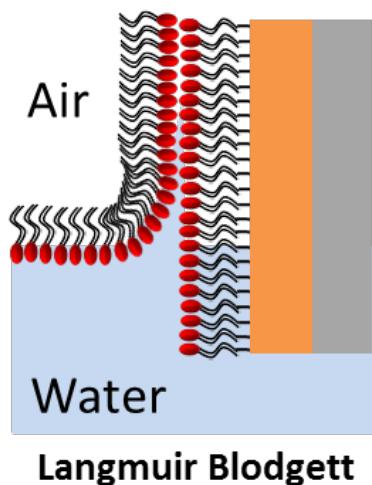
DPPC : Rc-LPS bilayer + α 1-Pth



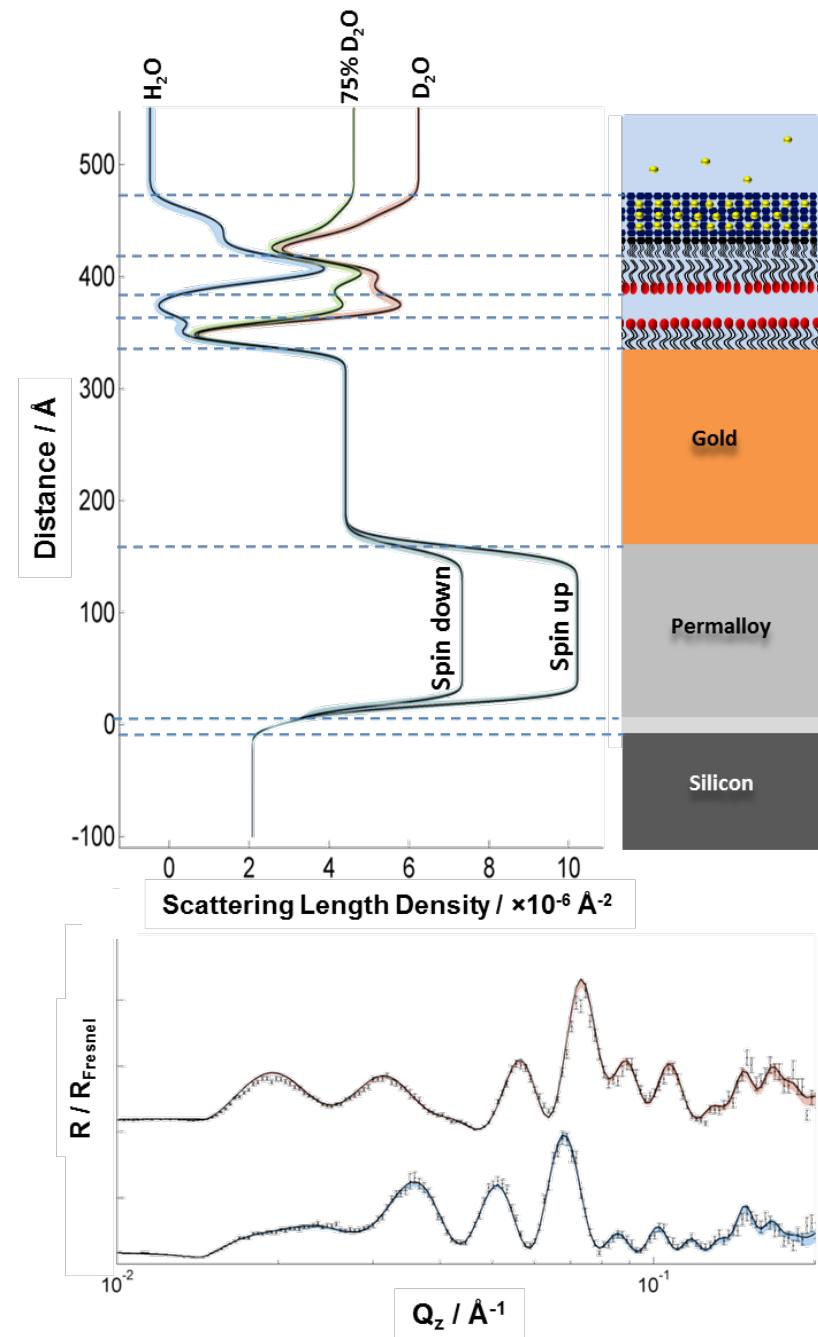
Accurate Model of Bacterial Membranes for Structural Studies



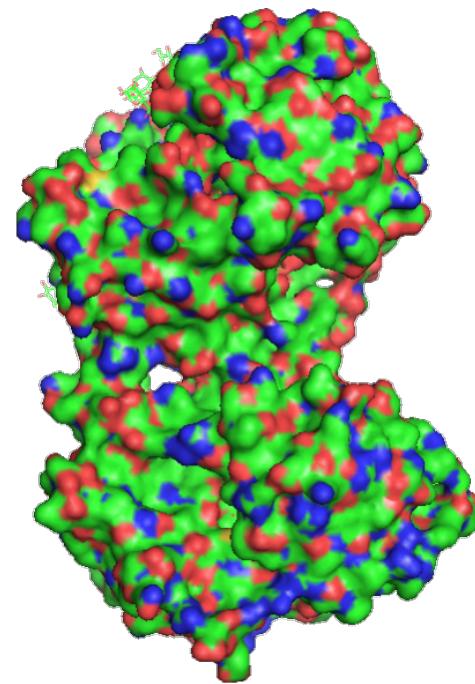
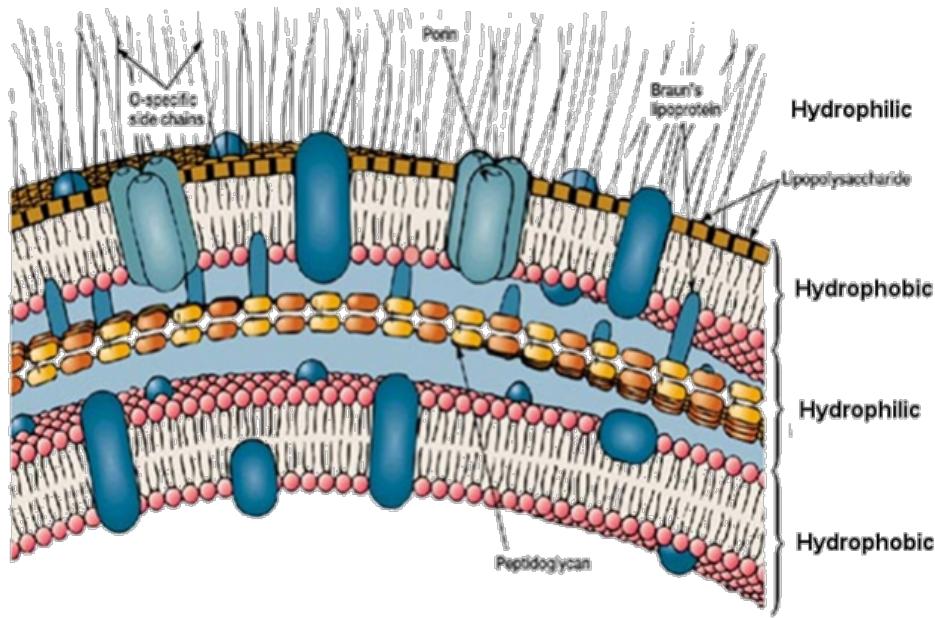
Floating Model Gram Negative Bacterial Membranes : Fabrication



Floating Model Gram Negative Bacterial Membranes



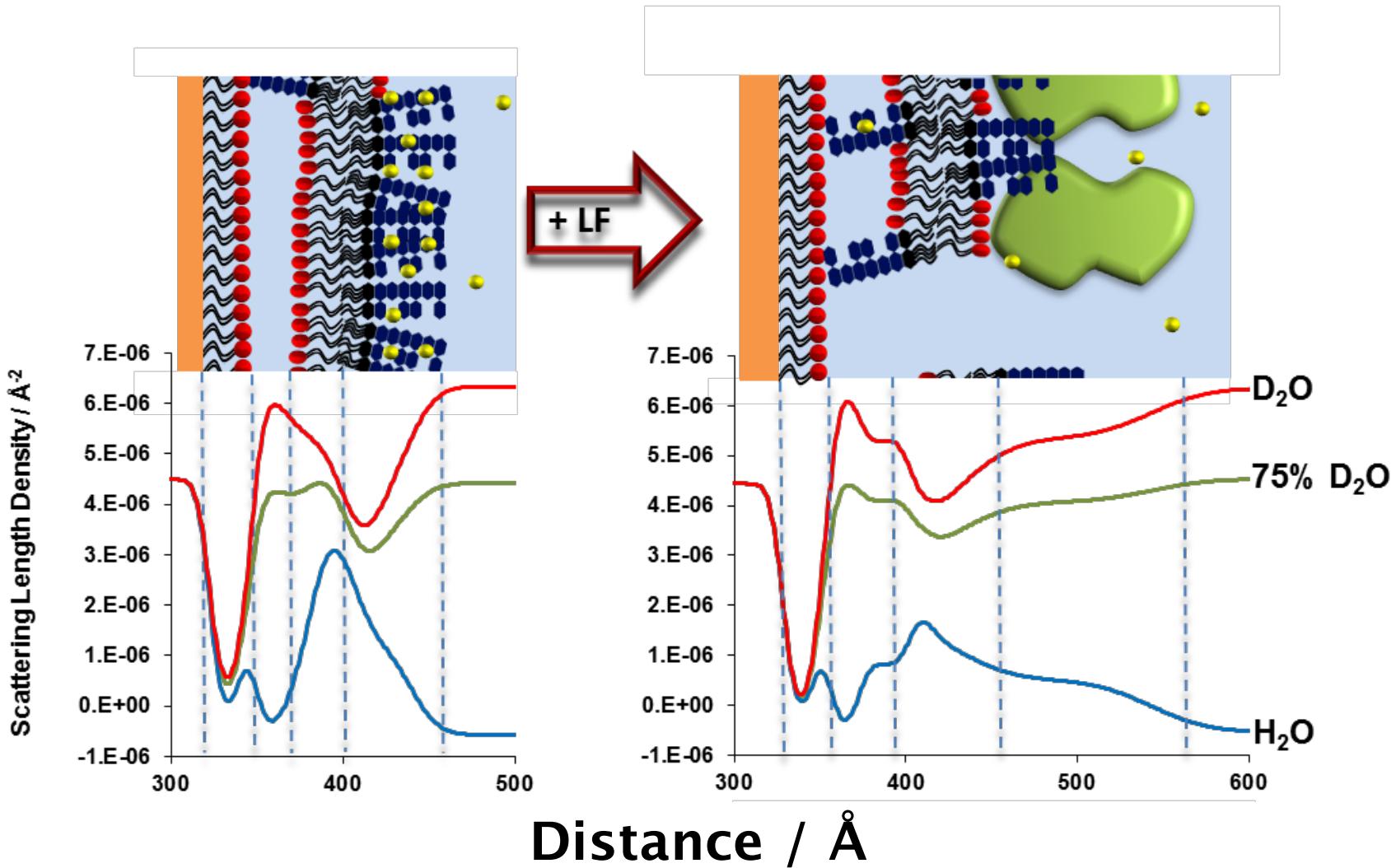
Antimicrobial protein interactions with the OM



**Lactoferrin
pI 8.7**

Floating Model Gram Negative Bacterial Membranes : Interaction Studies

Lactoferrin



Conclusions



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