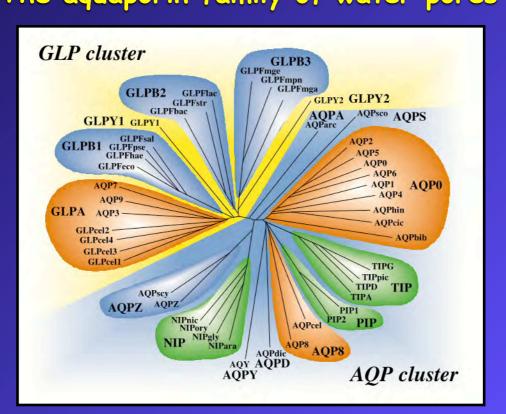
Lipid-Protein Interactions in Aquaporin-0 Membrane Junction

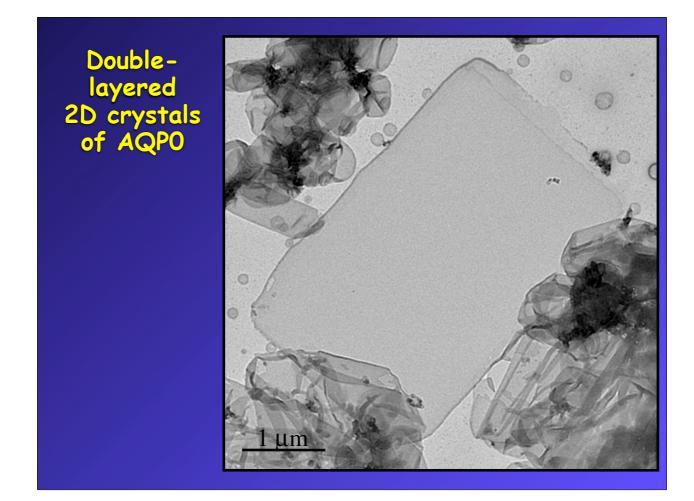
Tom Walz

HHMI & Department of Cell Biology Harvard Medical School

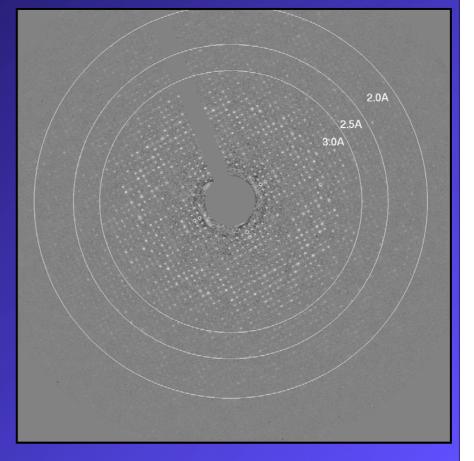
2dx Workshop C-CINA, Biozentrum, University of Basel Basel, August 2010

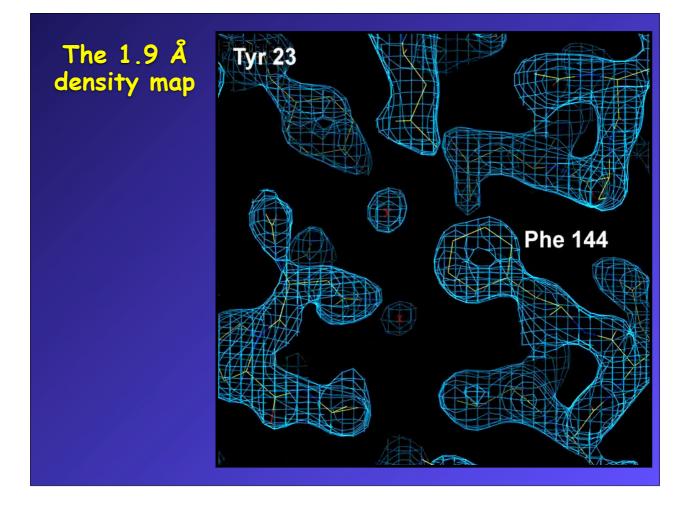


The aquaporin family of water pores

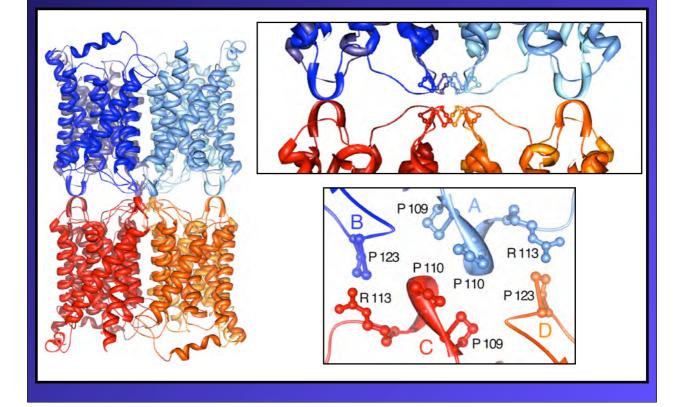


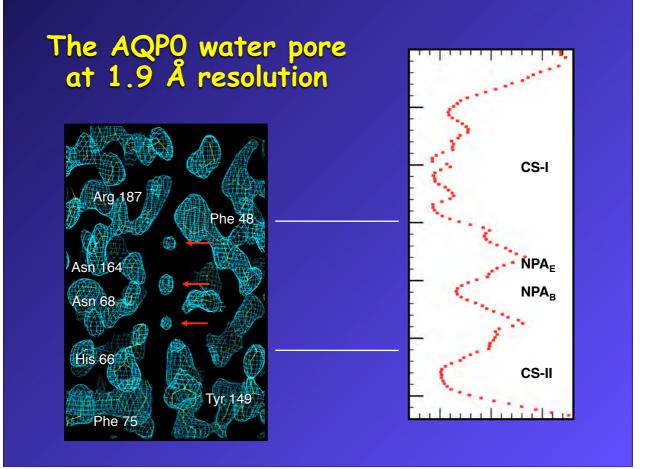
Electron diffraction at liquid He temperature



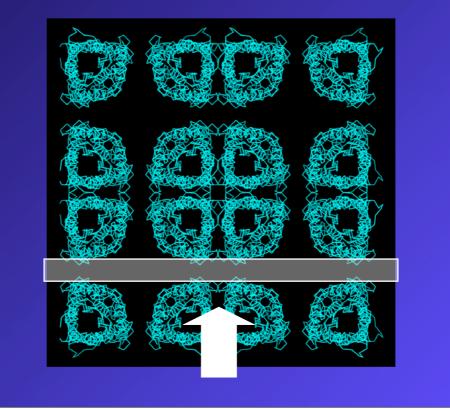


Junction interactions

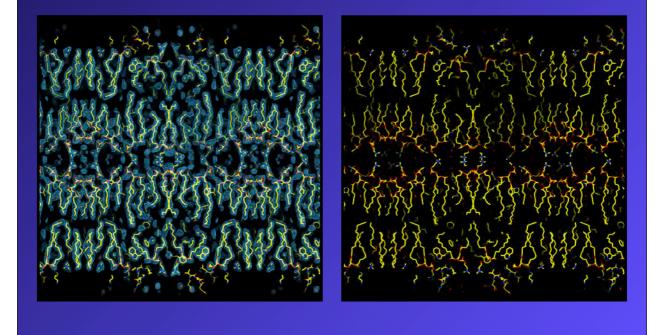




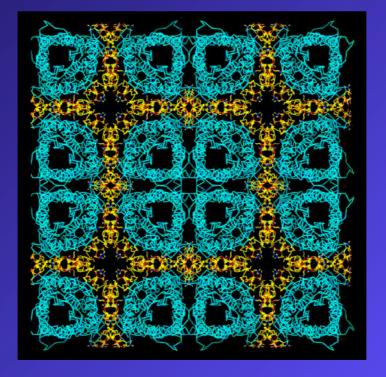
The packing of AQPO in the 2D crystals



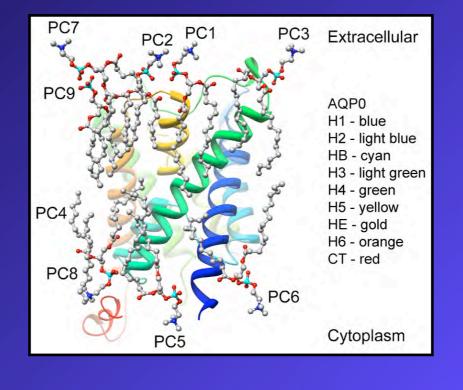
The packing of AQPO in the 2D crystals



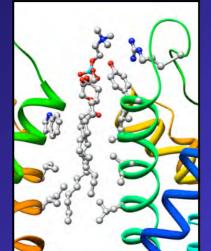
The packing of AQPO in the 2D crystals



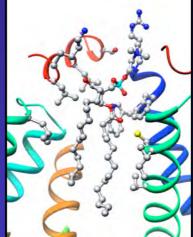
The lipids surrounding an AQPO monomer



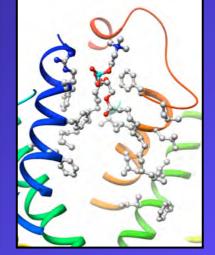
Protein-lipid interactions



PC 1

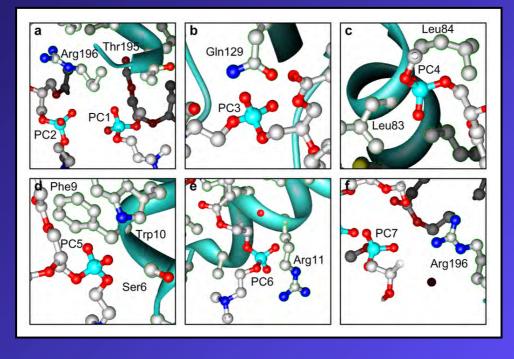


PC 5



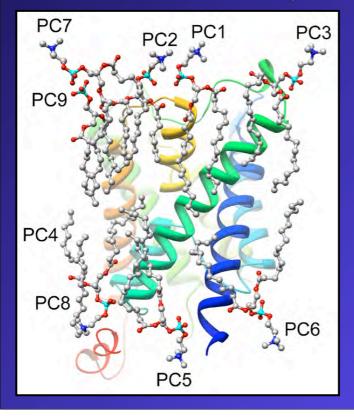
PC 6

Lipid binding motifs



No obvious binding motif for PC phosphodiester group

Protein-lipid interactions



Different lipids

Head group interactions? Lipid-binding motifs?

Acyl chain positions?

Bilayer thickness? Acyl chain interactions?

Protein conformation?

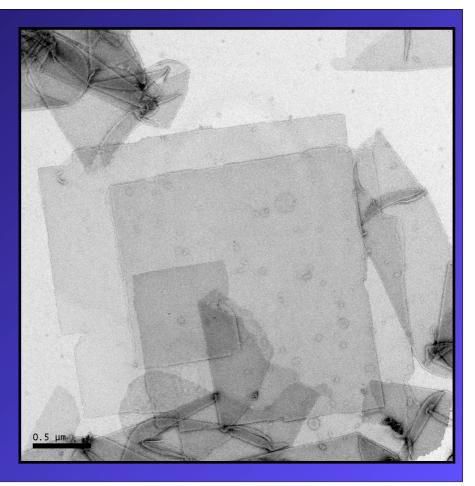


Rich Hite

Doublelayered 2D crystals of AQPO

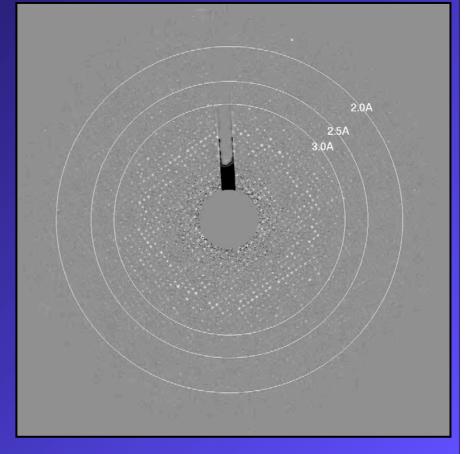
AQP0 in *E. coli* polar lipids

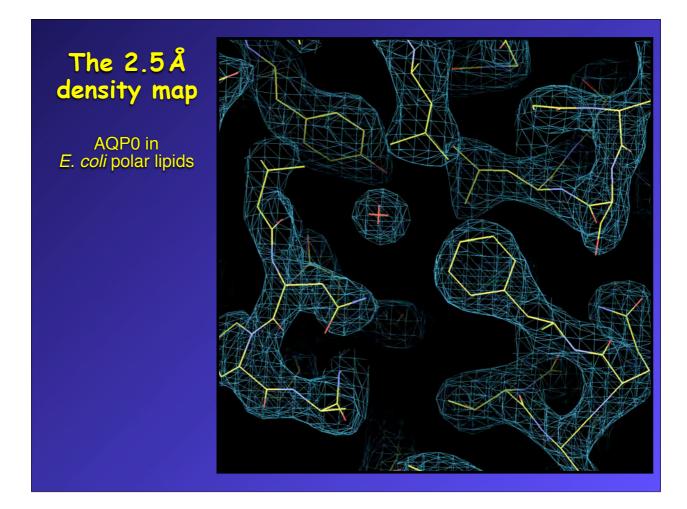
67% PE 23% PG 10% cardiolipin



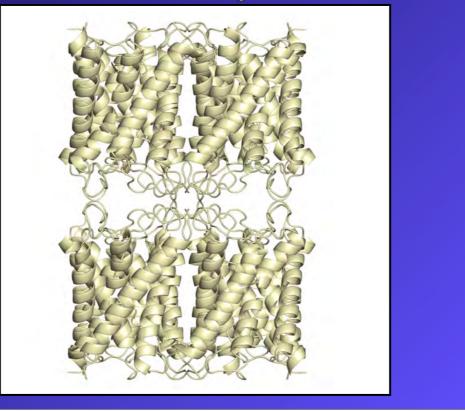
Electron diffraction at liquid He temperature

AQP0 in *E. coli* polar lipids

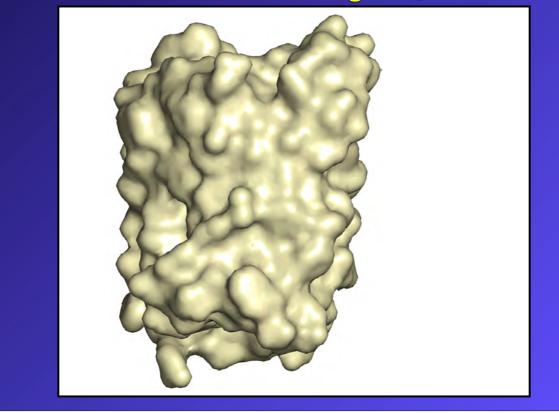


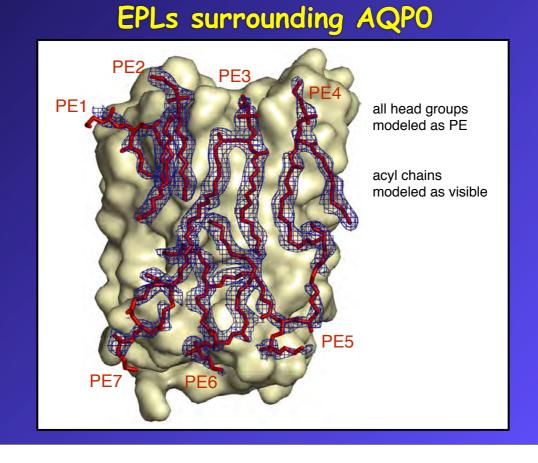


Model of the AQPO junction in EPL



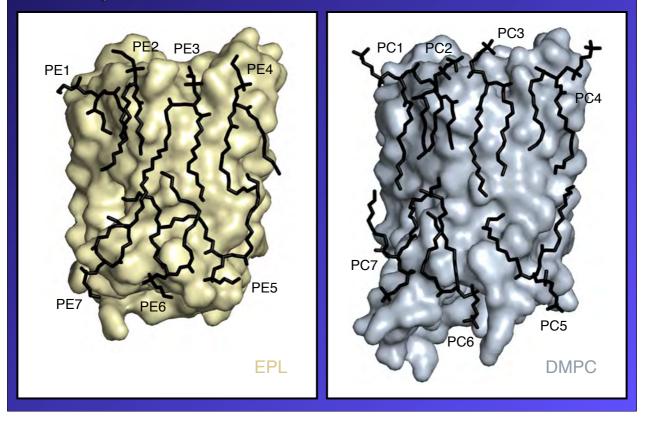
EPLs surrounding AQPO

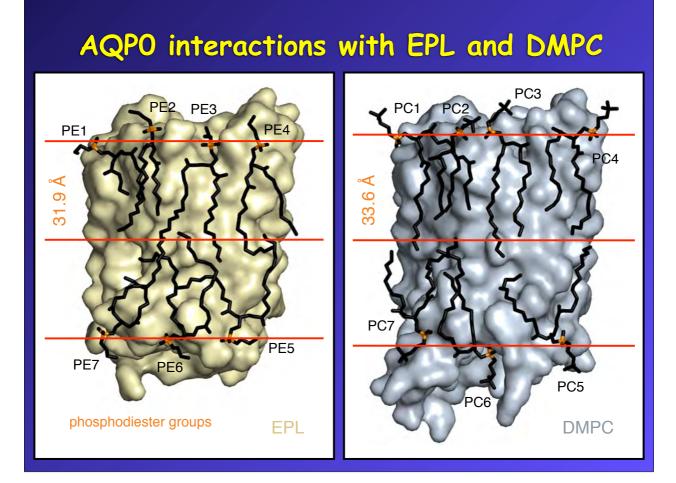




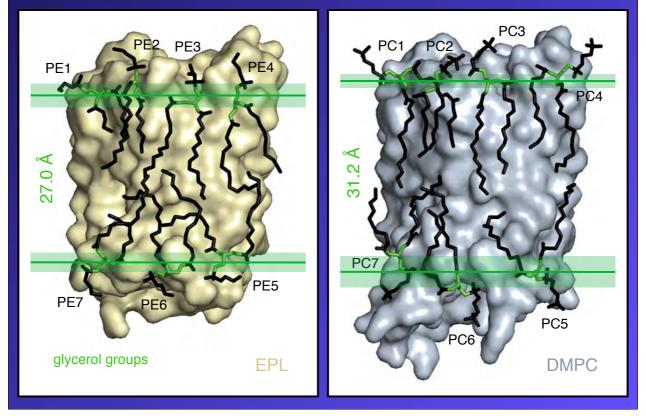
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AQPO interactions with EPL and DMPC

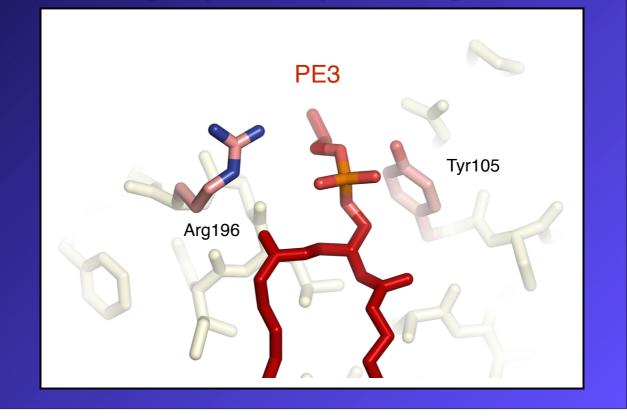


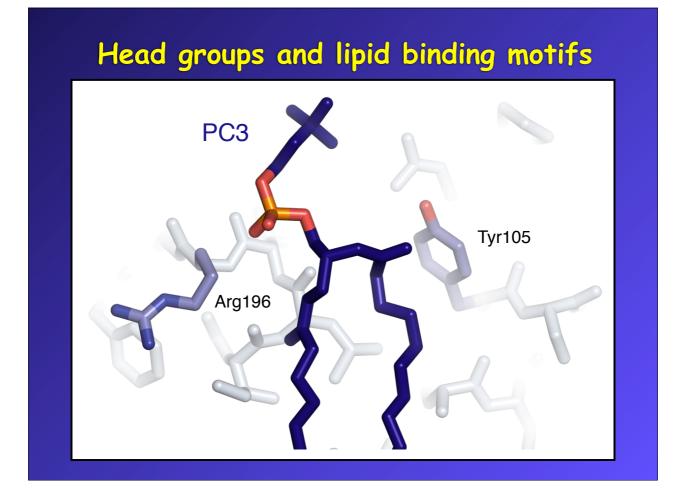


AQPO interactions with EPL and DMPC

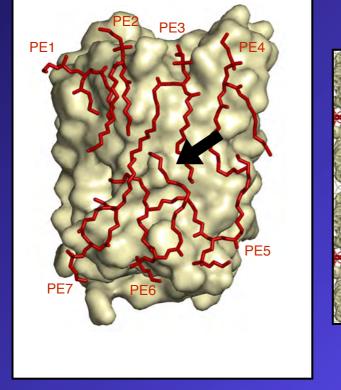


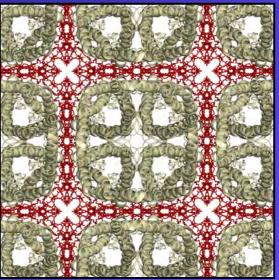
Head groups and lipid binding motifs



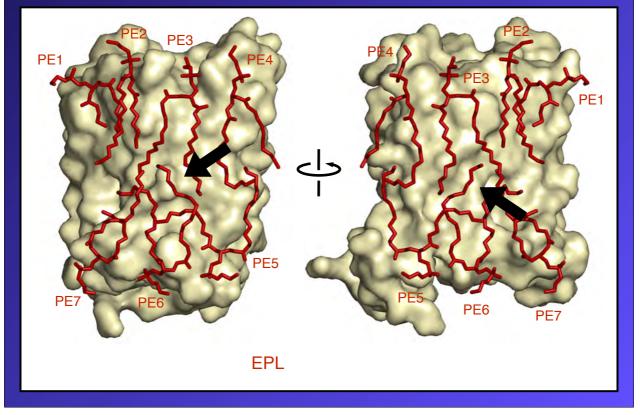


Acyl chain positions

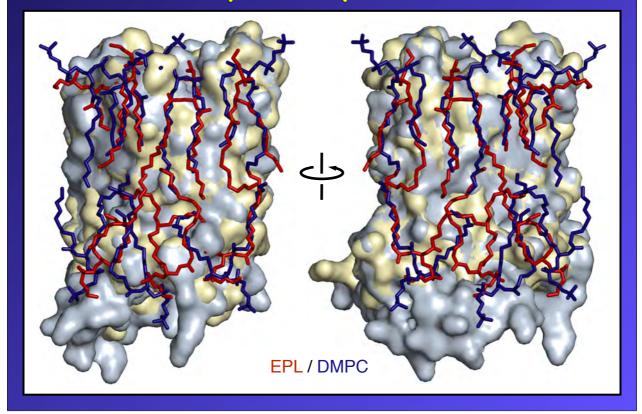


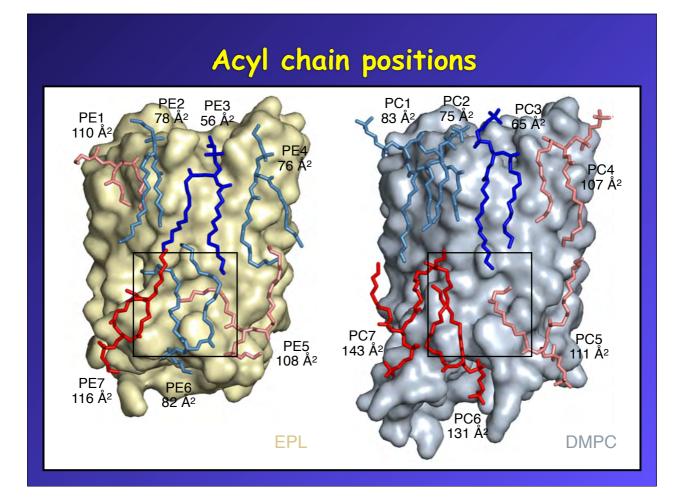


Acyl chain positions

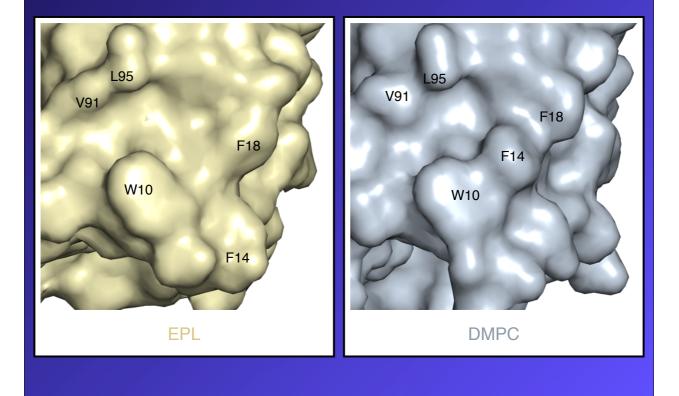


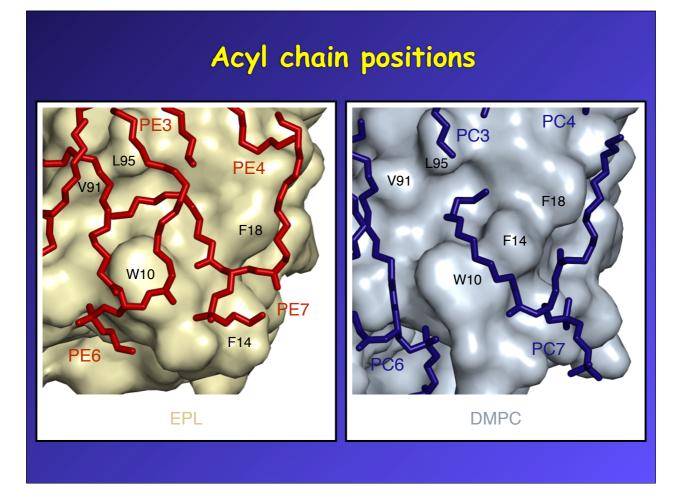
Acyl chain positions



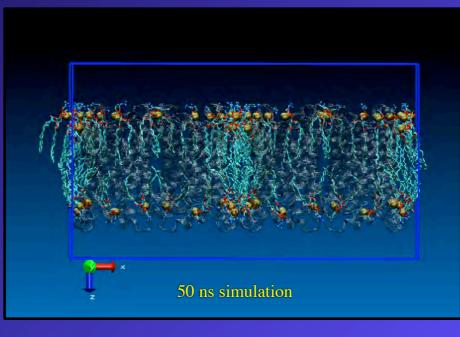


Acyl chain positions





Molecular dynamics calculations

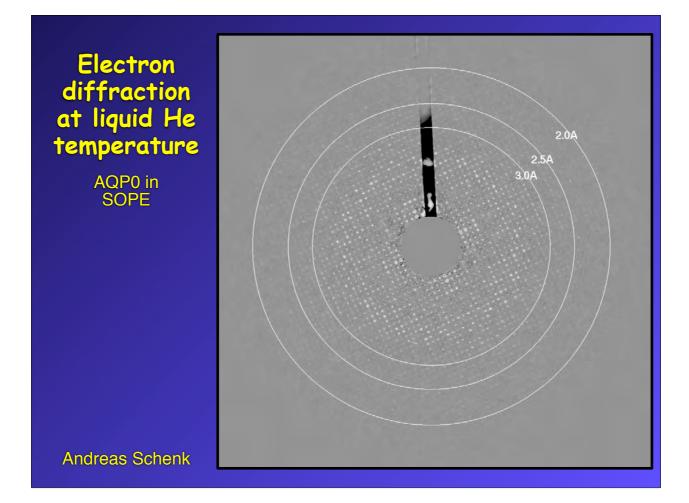


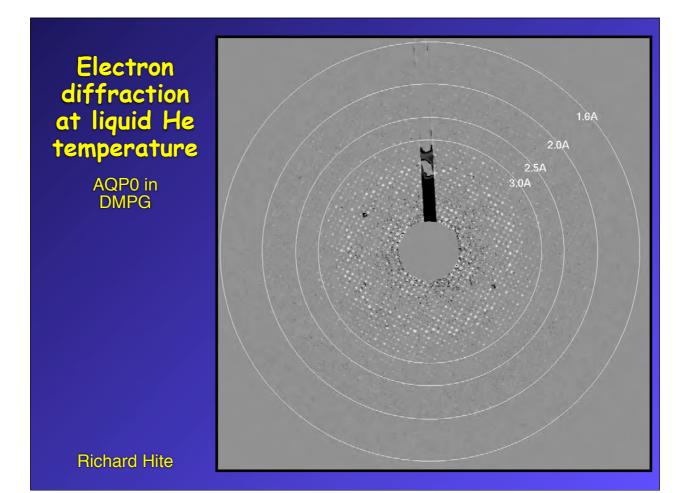
Rodolfo Briones, Camilo Aponte & Bert de Groot MPI for Biophysical Chemistry (Göttingen)

Conclusions

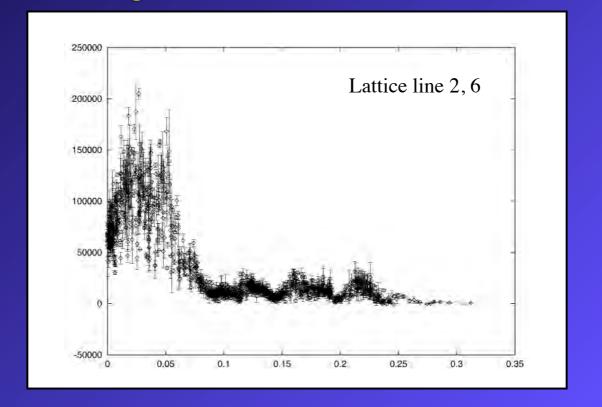
- 1. lipid positions defined by acyl chains – filling in the gaps in protein surface
- 2. further interactions by lipid headgroups

 may lead to stronger (specific) binding
 may define lipid selectivity
- 3. AQP0 forms well-ordered 2D crystals with very different lipids
 - should allow systematic analysis of lipid-protein interactions

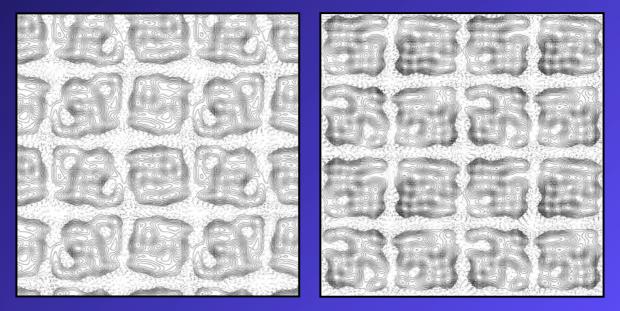




Merged data for AQPO in DMPG



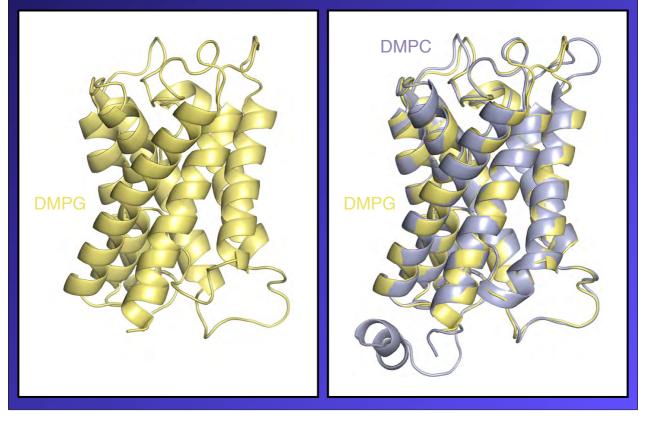
AQPO forms different crystals in DMPG



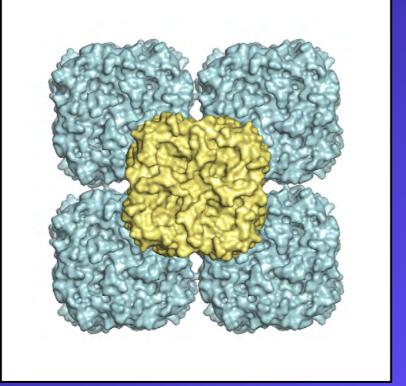
*p*12₁

*p*42₁2

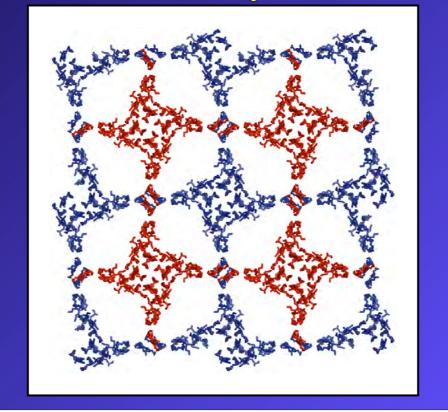
AQPO in DMPG and DMPC



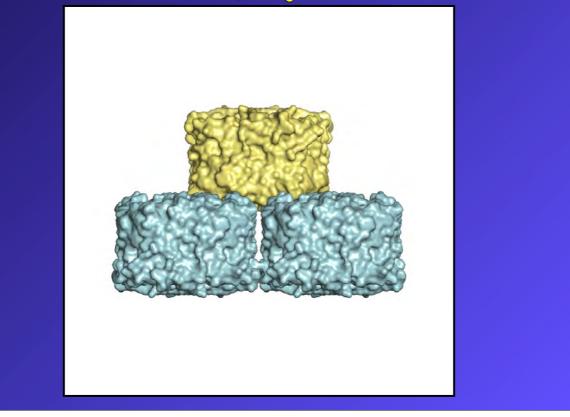
Model of the AQPO junction in DMPG



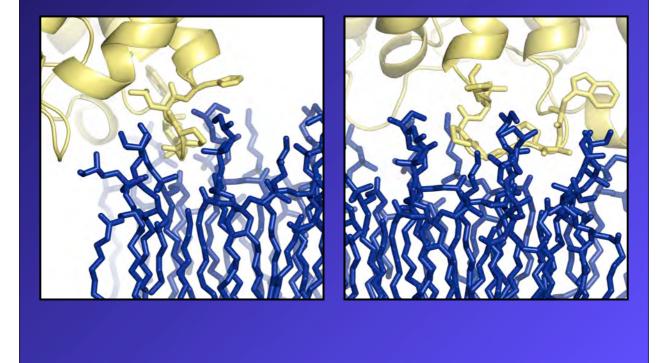
Model of the AQPO junction in DMPG



Model of the AQPO junction in DMPG



Interaction of loop A with lipids



Collaborators

Harvard Medical School Tamir Gonen Yifan Cheng Richard Hite Zongli Li Stephen Harrison Piotr Sliz

University of Auckland Joerg Kistler

> Kyoto University Yoshinori Fujiyoshi Yoko Hiroaki