

# Cryo-EM studies of Membrane proteins in Peptidiscs & Nanodiscs

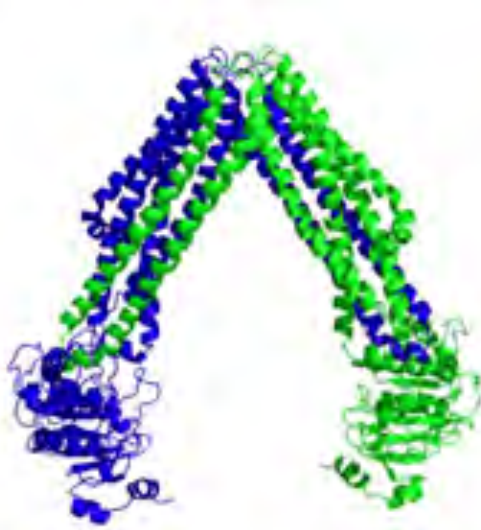
Tom Walz

The Rockefeller University

International  
SMALP Conference

New York, March 2020

# Crystal structures of ABC transporter MsbA in detergent



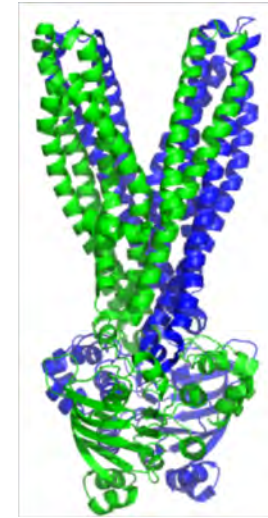
*E. coli*  
5.3 Å

Inward wide open  
No nucleotide



*V. cholerae*  
5.5 Å

Inward twisted open  
No nucleotide



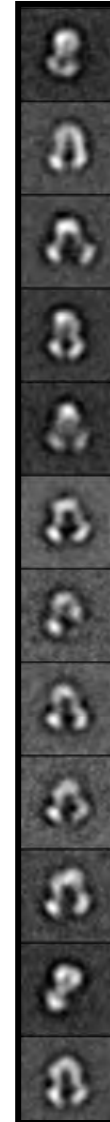
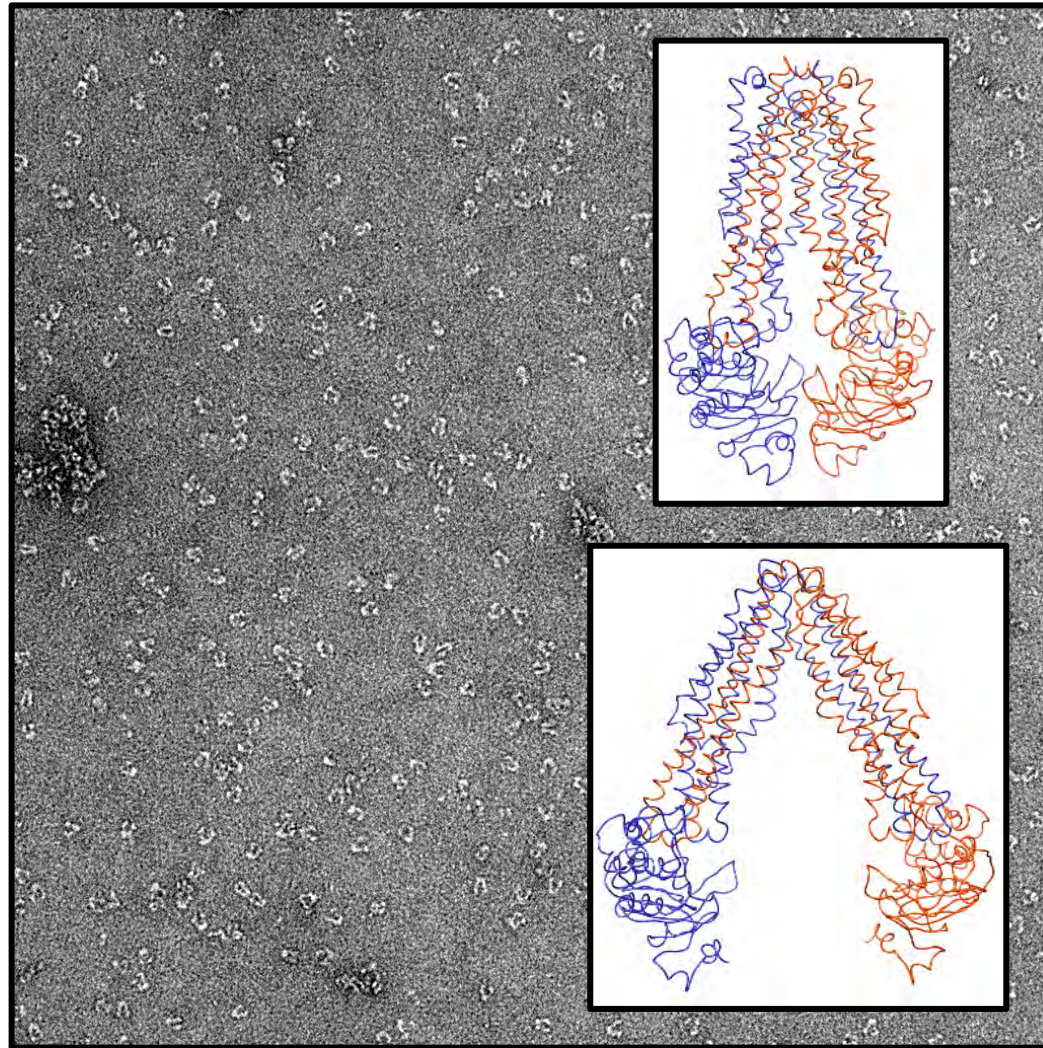
*S. typhimurium*  
3.7 Å

Outward open  
AMPPNP

Are all conformations meaningful ?  
Does the lipid bilayer have an effect ?  
How does MsbA specifically recognize LPS ?  
How does MsbA flip LPS ?



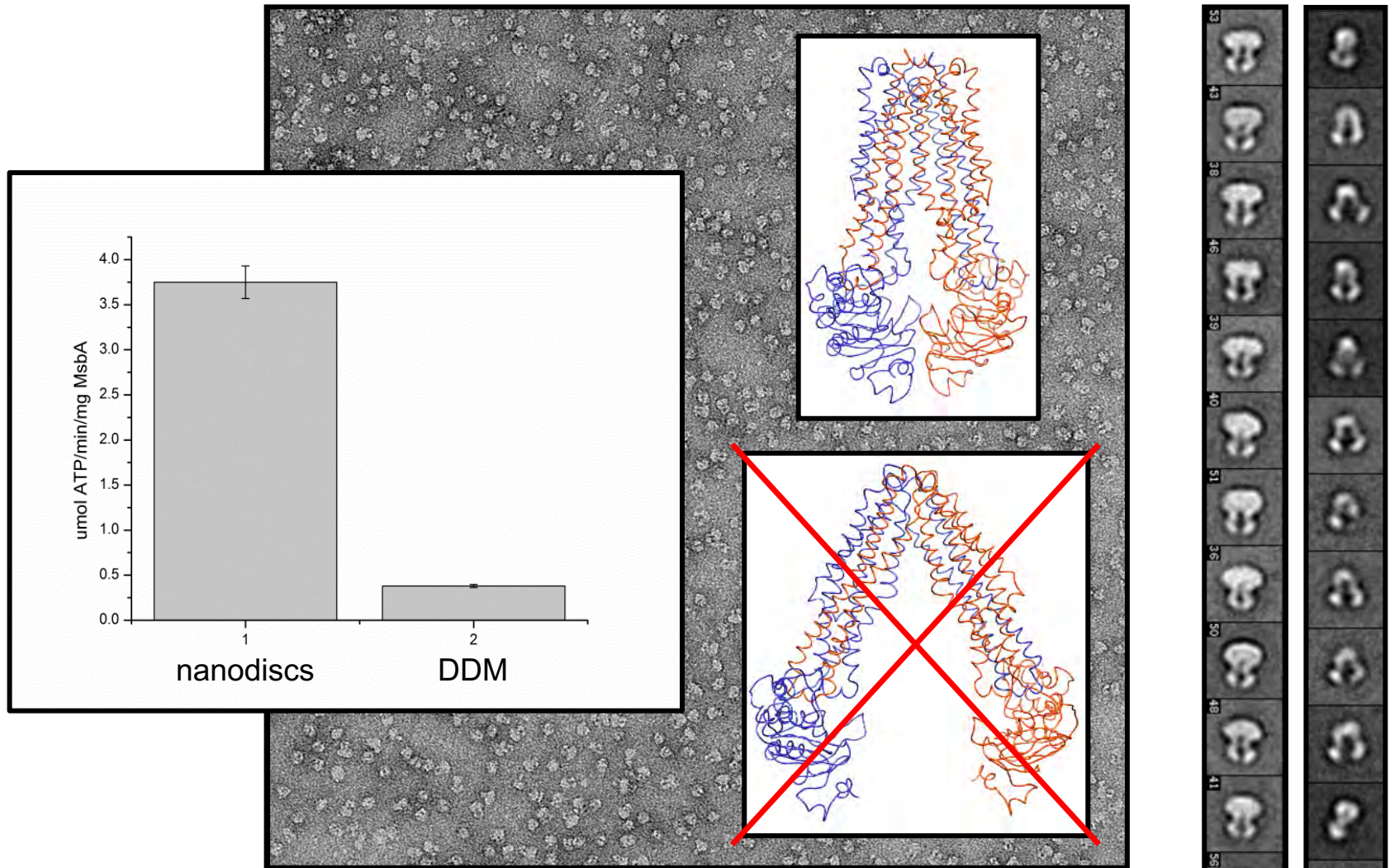
# Nucleotide-free MsbA in detergent (dodecyl maltoside)



Mi *et al.* (2017) *Nature* 549: 233-237



# Nucleotide-free MsbA in nanodiscs (MSP1D1 & *E. coli* polar lipids)

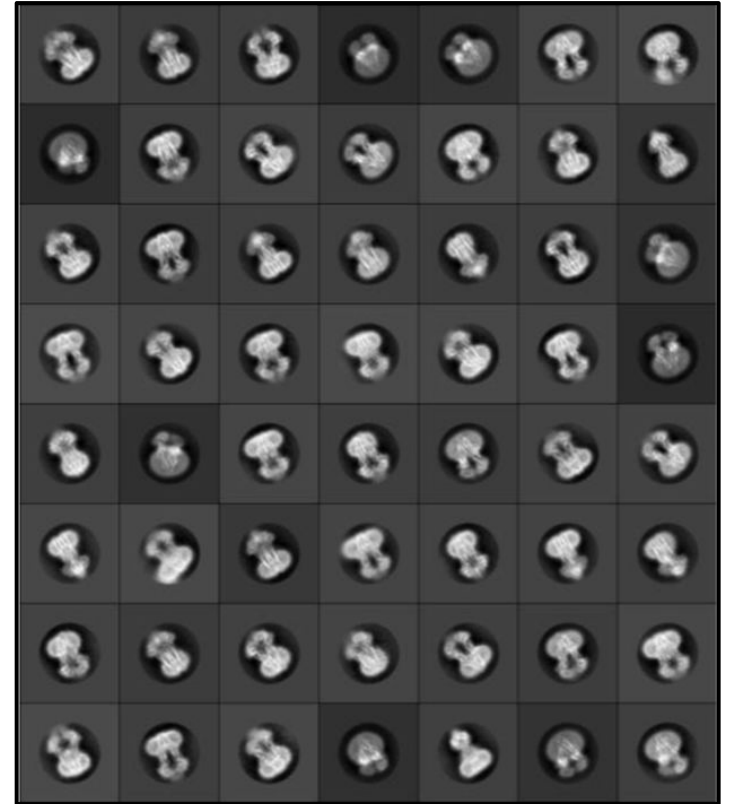
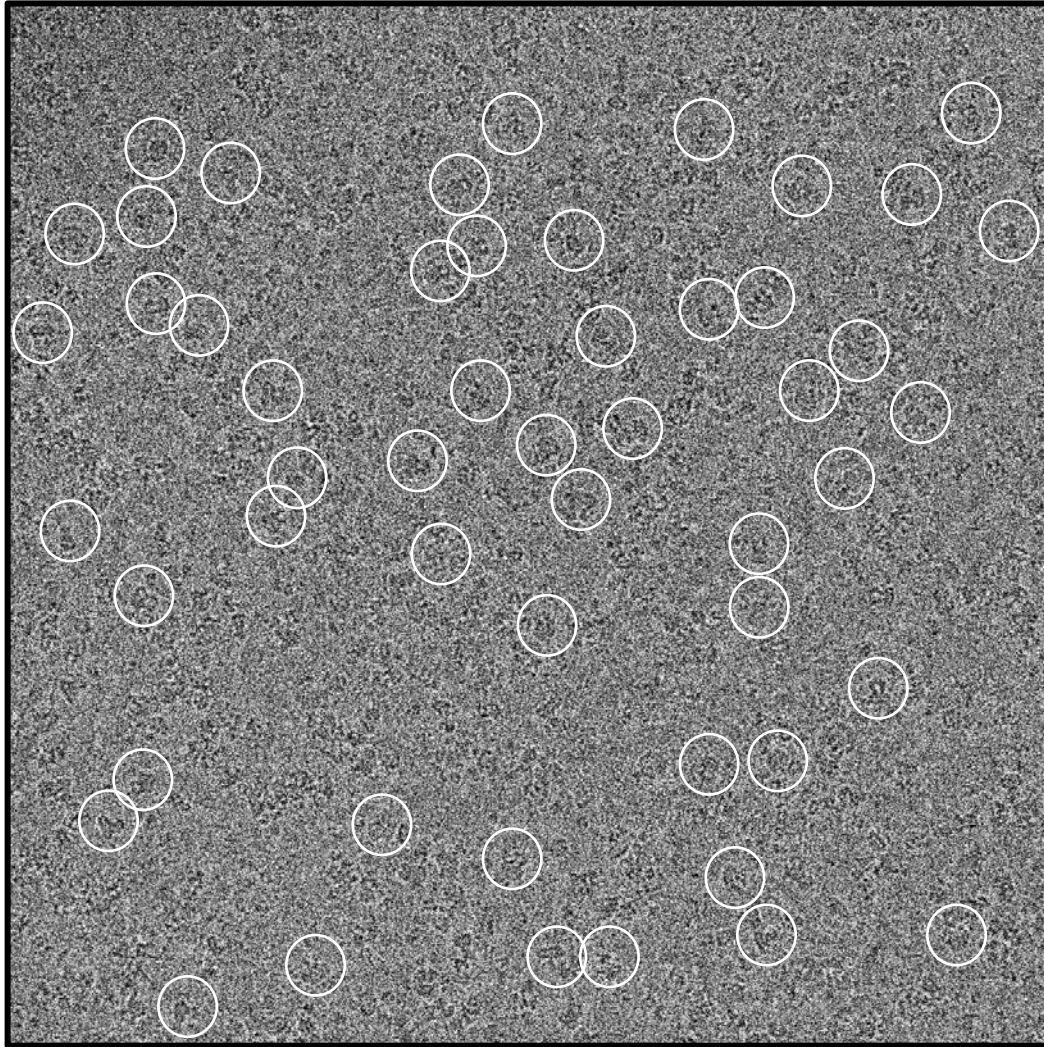


Mi *et al.* (2017) *Nature* 549: 233-237



# Nucleotide-free MsbA in nanodiscs

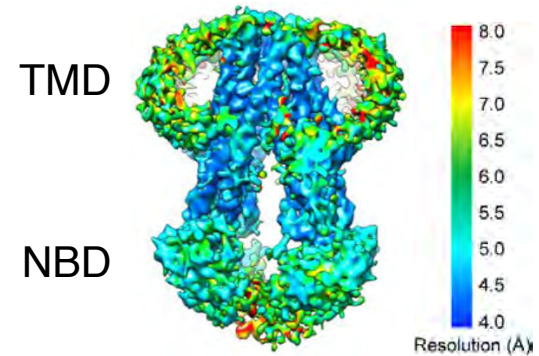
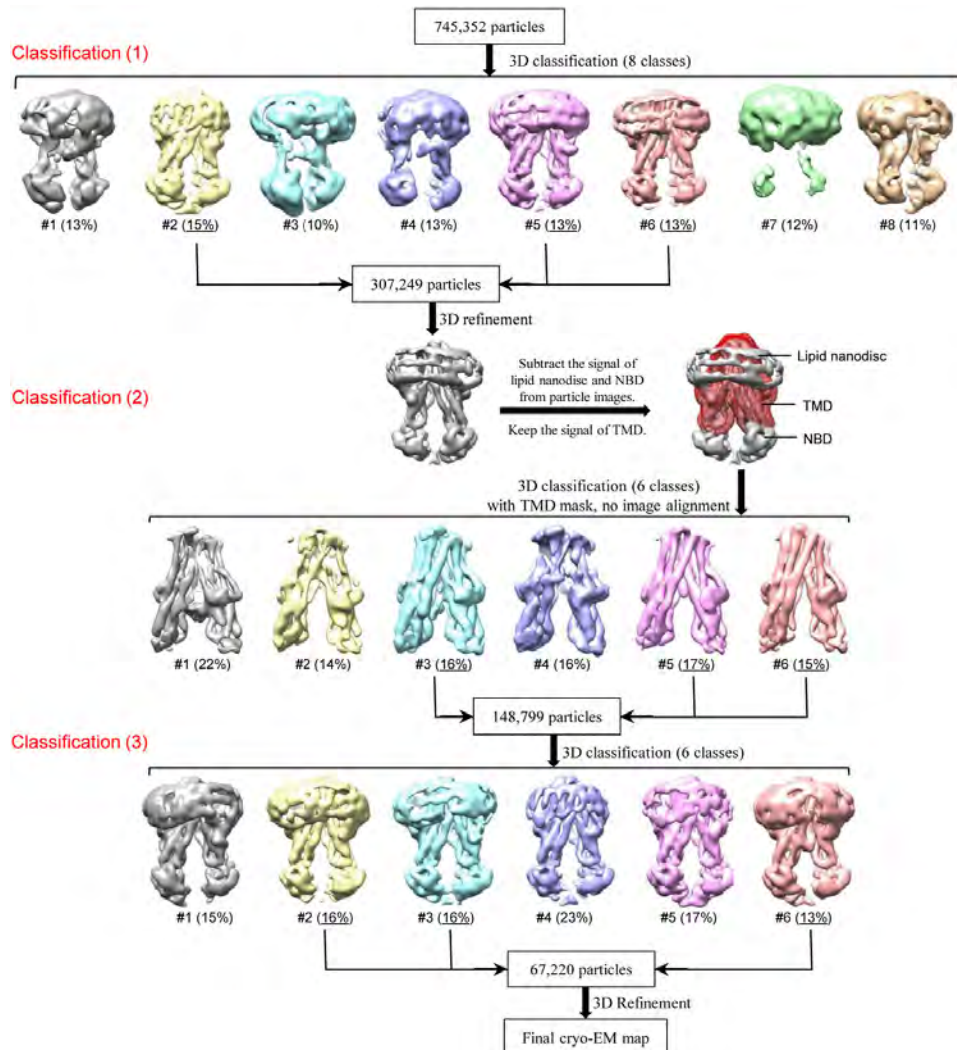
## Cryo-EM and image processing



Mi *et al.* (2017) *Nature* 549: 233-237



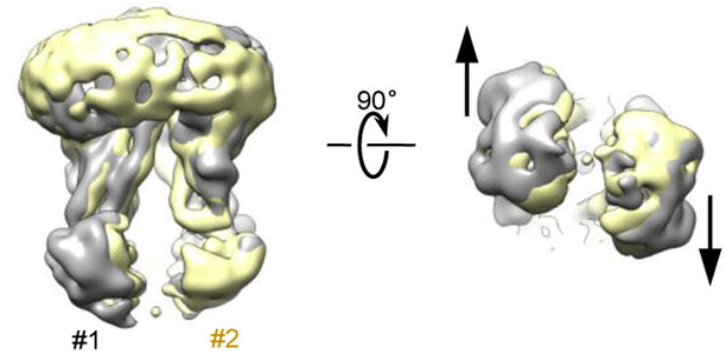
# Nucleotide-free MsbA in nanodiscs Cryo-EM and image processing



Resolution:

TMD+NBD = 4.7 Å

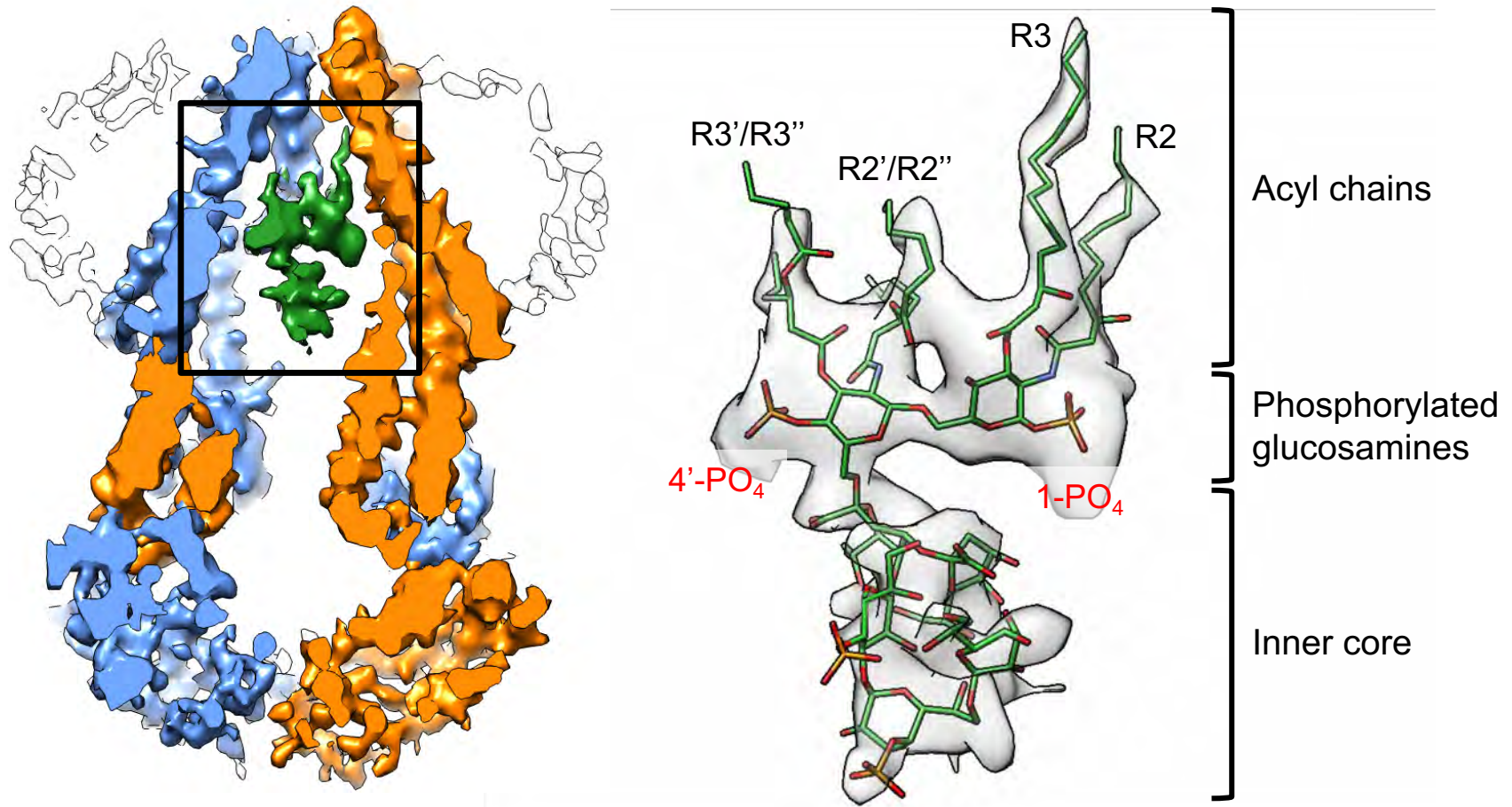
NBD only = 4.2 Å



Mi *et al.* (2017) *Nature* 549: 233-237

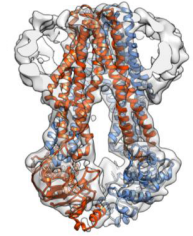
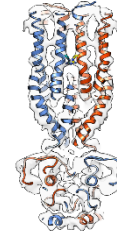
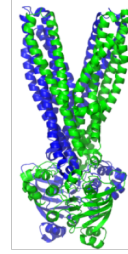
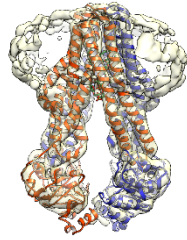
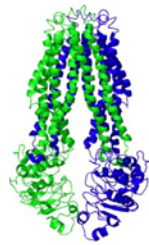


# Map of nucleotide-free MsbA in nanodiscs shows density for LPS in the TMD



Mi *et al.* (2017) *Nature* 549: 233-237

# Structures of MsbA in different functional states and mechanism of LPS flipping across membrane



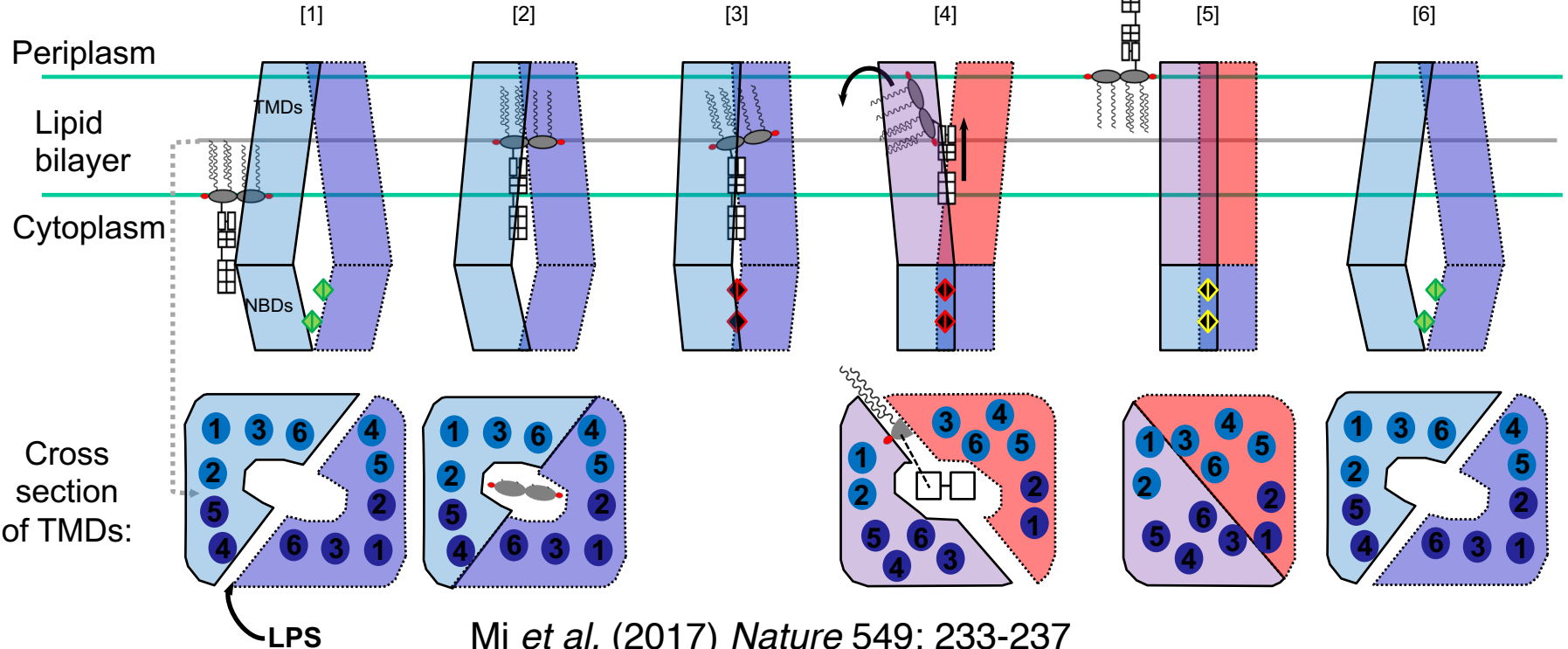
Nucleotide state:

◆ ADP or nucleotide-free

◆ ATP

◆ ADP-Pi

◆ ADP





# The peptidisc – a new membrane mimetic



TOOLS AND RESOURCES



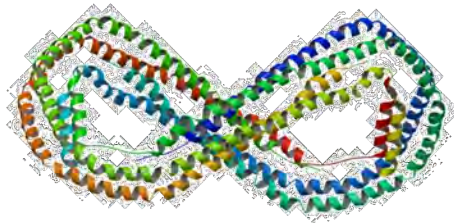
## The Peptidisc, a simple method for stabilizing membrane proteins in detergent-free solution

**Michael Luke Carlson<sup>1</sup>, John William Young<sup>1</sup>, Zhiyu Zhao<sup>1</sup>, Lucien Fabre<sup>1</sup>, Daniel Jun<sup>2,3</sup>, Jianing Li<sup>4</sup>, Jun Li<sup>4</sup>, Harveer Singh Dhupar<sup>1</sup>, Irvin Wason<sup>1</sup>, Allan T Mills<sup>1</sup>, J Thomas Beatty<sup>3</sup>, John S Klassen<sup>4</sup>, Isabelle Rouiller<sup>2</sup>, Franck Duong<sup>1\*</sup>**

<sup>1</sup>Department of Biochemistry and Molecular Biology, Faculty of Medicine, Life Sciences Institute, University of British Columbia, Vancouver, Canada; <sup>2</sup>Department of Anatomy and Cell Biology, McGill University, Montreal, Canada; <sup>3</sup>Department of Microbiology and Immunology, University of British Columbia, Vancouver, Canada; <sup>4</sup>Glycomics Centre and Department of Chemistry, University of Alberta, Alberta, Canada

# Evolution of the peptidisc peptide

Apolipoprotein A1



Peptide 18A

DWLKAFYDKVAEKLKEAF

Model amphipathic peptide with similar lipid-associating properties as apolipoprotein A1

linked two 18A peptides with a proline residue

efficiently displaces apo-A1 from intact HDL

Peptide 18A-P-18A

DWLKAFYDKVAEKLKEAF**P**DWLKAFYDKVAEKLKEAF

Chung *et al.* (1985) *J. Biol. Chem.* 260: 10256-10262

substitute two leucines with phenylalanines

interacts better with lipids forms nanodiscs

NSP (Nanodisc Scaffold Peptide)

DWLKAFYDKVAEKLKEA**A**PDW**F**KAFYDKVAEK**F**KEAF

Kariyazono *et al.* (2016) *J. Pept Sci.* 22: 116-122

reverse amino acid sequence

increased solubility of the peptide

NSPr (Reversed NSP)

= Peptidisc peptide

FAEK**F**KEAVKDYFAK**F**WDPAEKLKEAVKDYFAKLWD

Carlson *et al.* (2018) *eLife* 7: e34085



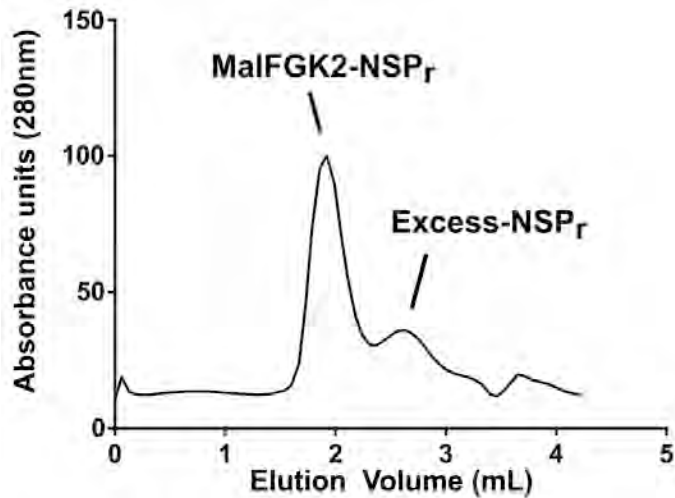
# 'On column' reconstitution of ABC transporter MalFGK<sub>2</sub> into peptidiscs

Approaches to reconstitute membrane proteins into peptidiscs:

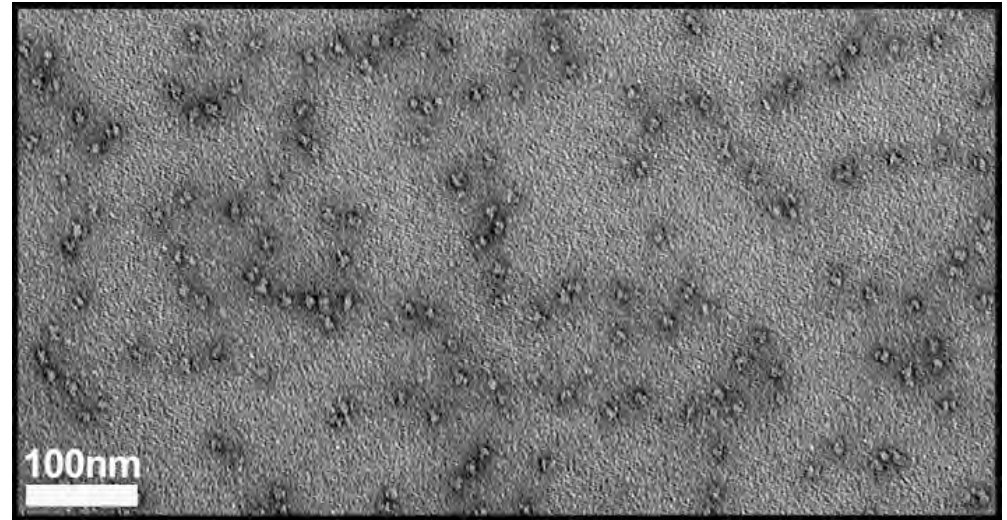
- on column
- on beads
- on gradient

# 'On column' reconstitution of ABC transporter MalFGK<sub>2</sub> into peptidiscs

Size-exclusion chromatogram

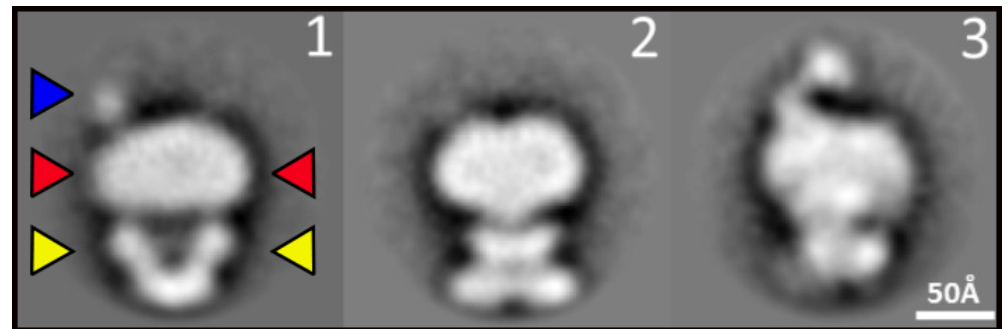


Negative-stain EM image



2D class averages

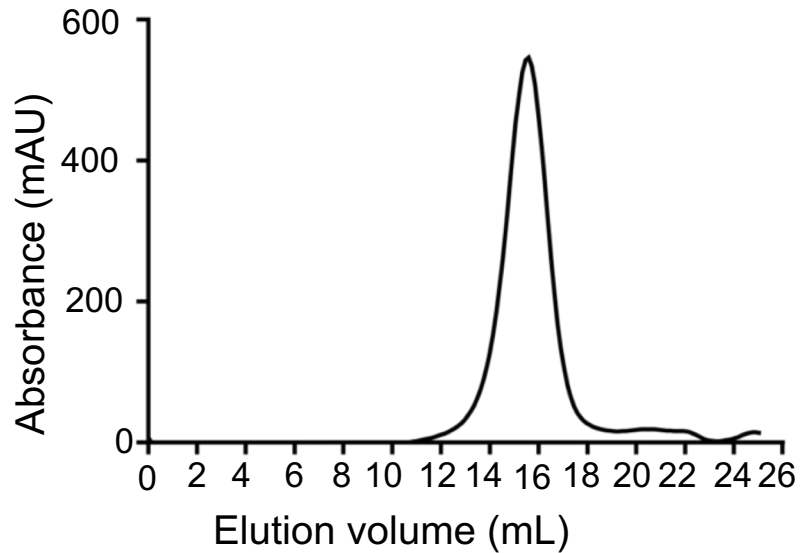
Periplasmic P2 loop  
Transmembrane domain (MalFG)  
Nucleotide-binding domain (MalK2)



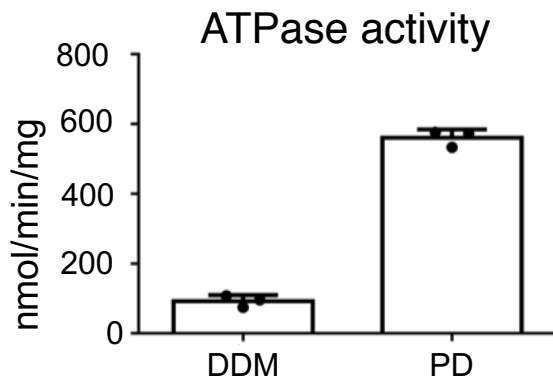
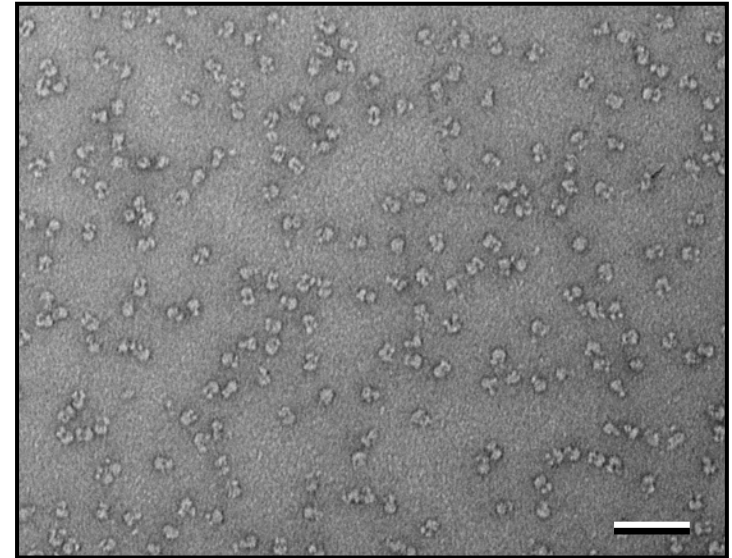


# 'On column' reconstitution of nucleotide-free MsbA into peptidiscs

Size-exclusion chromatogram

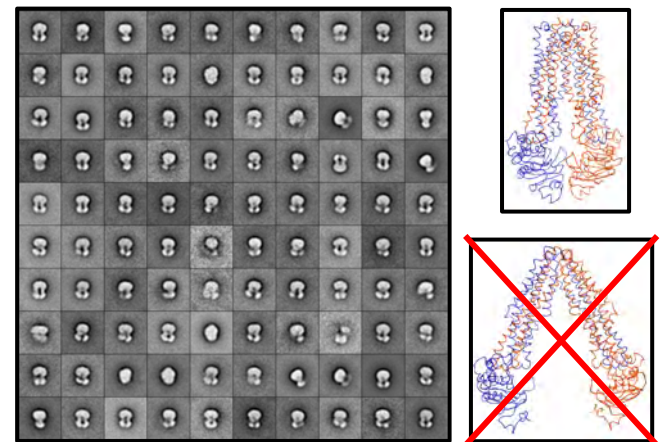


Negative-stain EM image



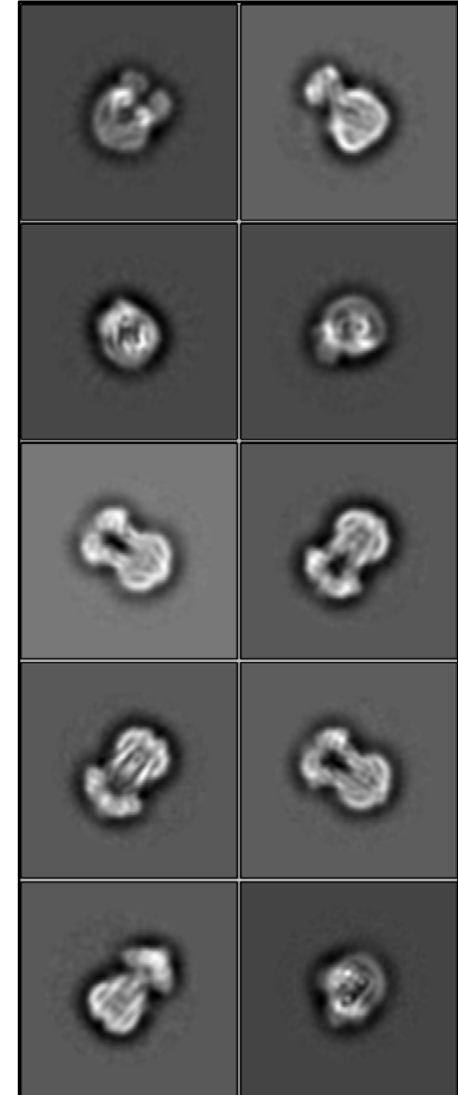
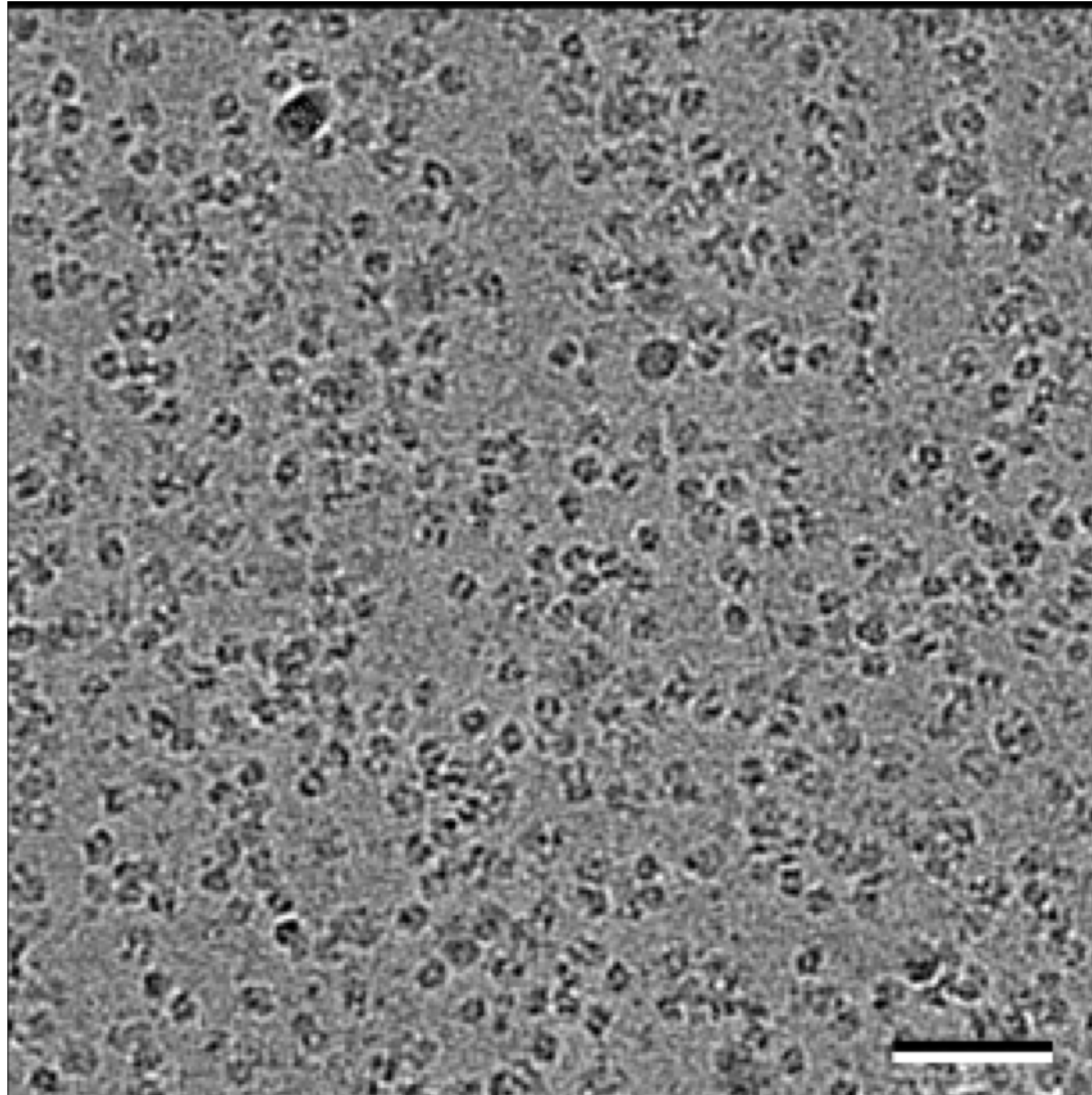
Peptidiscs stabilize MsbA as well as nanodiscs

2D class averages



# Nucleotide-free MsbA in peptidiscs

## Cryo-EM and image processing

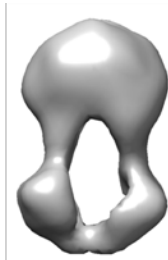




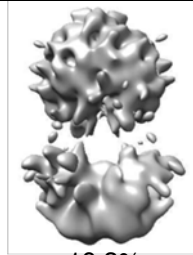
# Nucleotide-free MsbA in peptidiscs Cryo-EM and image processing

363,126  
particles

Initial model  
generation



3D classification  
C2 symmetry



10.3%



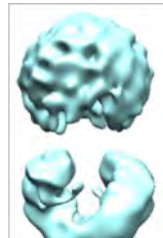
9.8%



36.5%



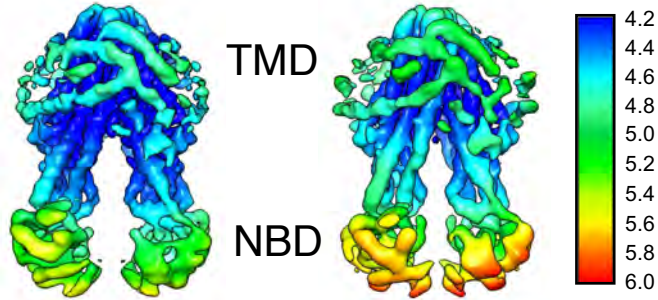
15.3%



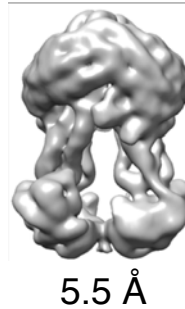
6.6%



21.5%

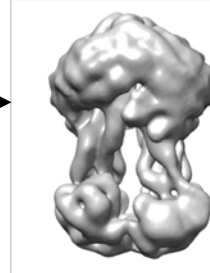


3D refinement  
C2 symmetry



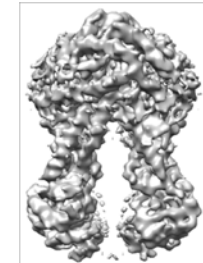
5.5 Å

5.8 Å



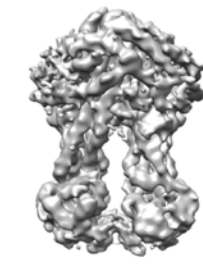
Refinement  
Post-processing  
CTF refinement  
Bayesian polishing

133,205 particles



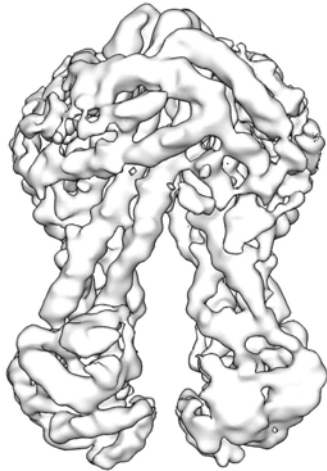
4.2 Å

4.4 Å

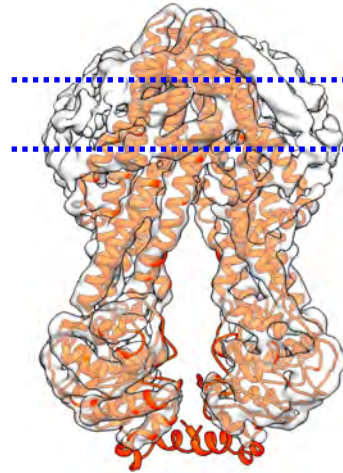


78,589 particles

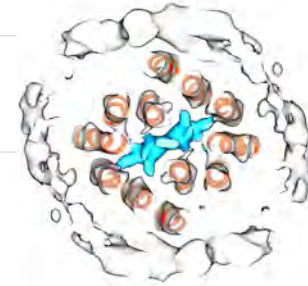
# Nucleotide-free MsbA in peptidiscs Cryo-EM and image processing



MsbA in peptidisc



90°



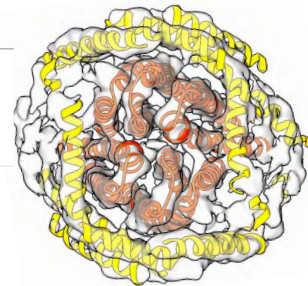
Peptidiscs preserve  
tightly bound lipids



MsbA in nanodisc



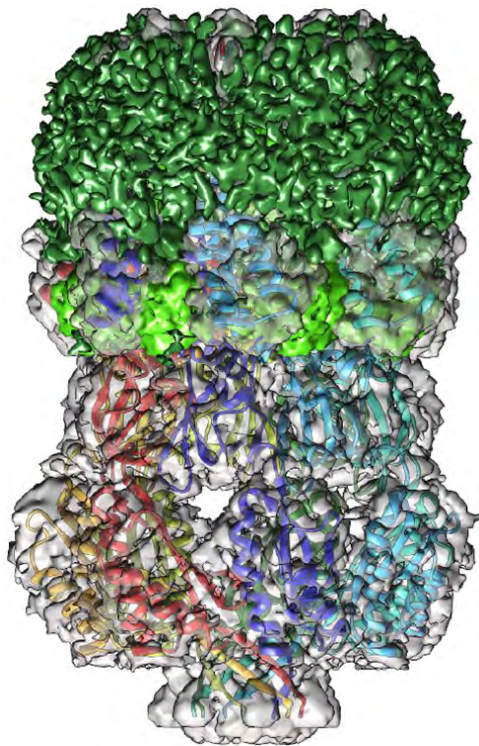
90°



Peptidisc density  
adds to mass for  
image processing

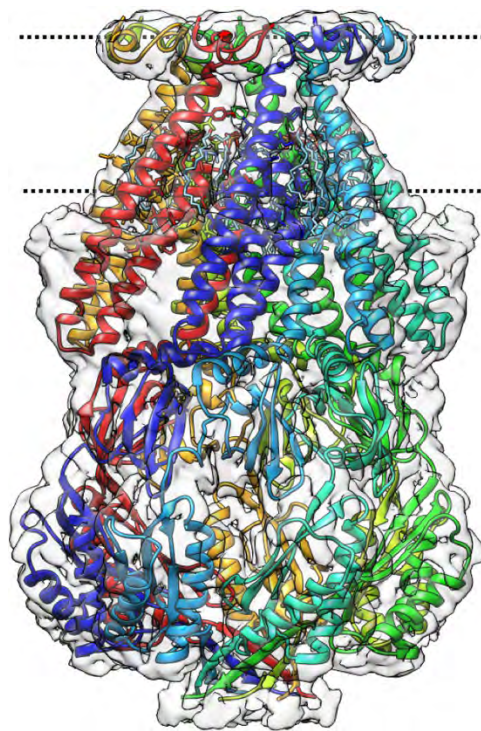


# Structures of *E. coli* MscS in nanodiscs



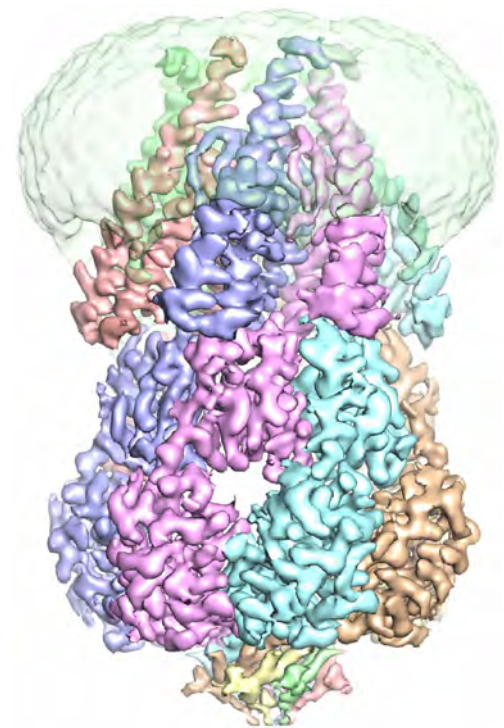
2.9 Å

Rasmussen *et al.* (2019)  
*J. Mol. Biol.* 431: 3081-3090



3.1 Å

Reddy *et al.* (2019)  
*eLife* 8: e50486

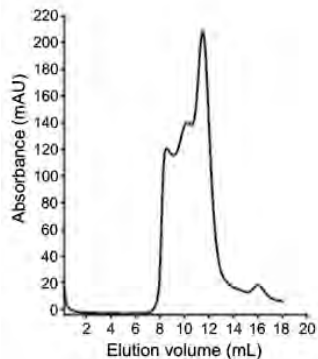


3.2 Å

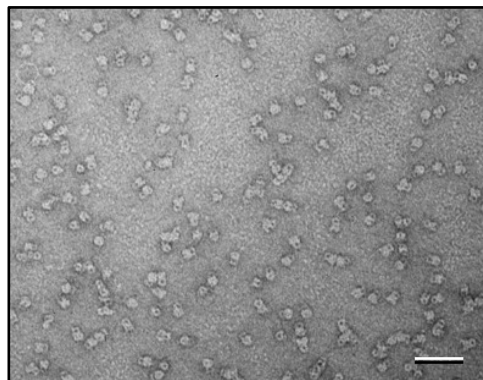


# Reconstitution of MscS into peptidiscs and structural analysis by cryo-EM

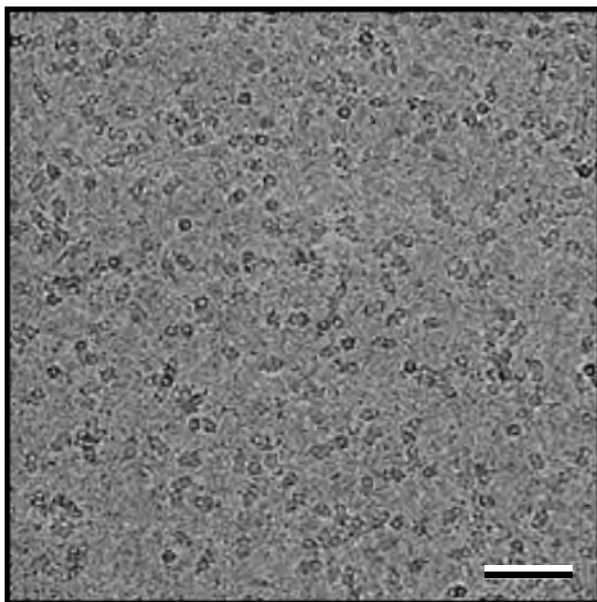
Size-exclusion chromatogram



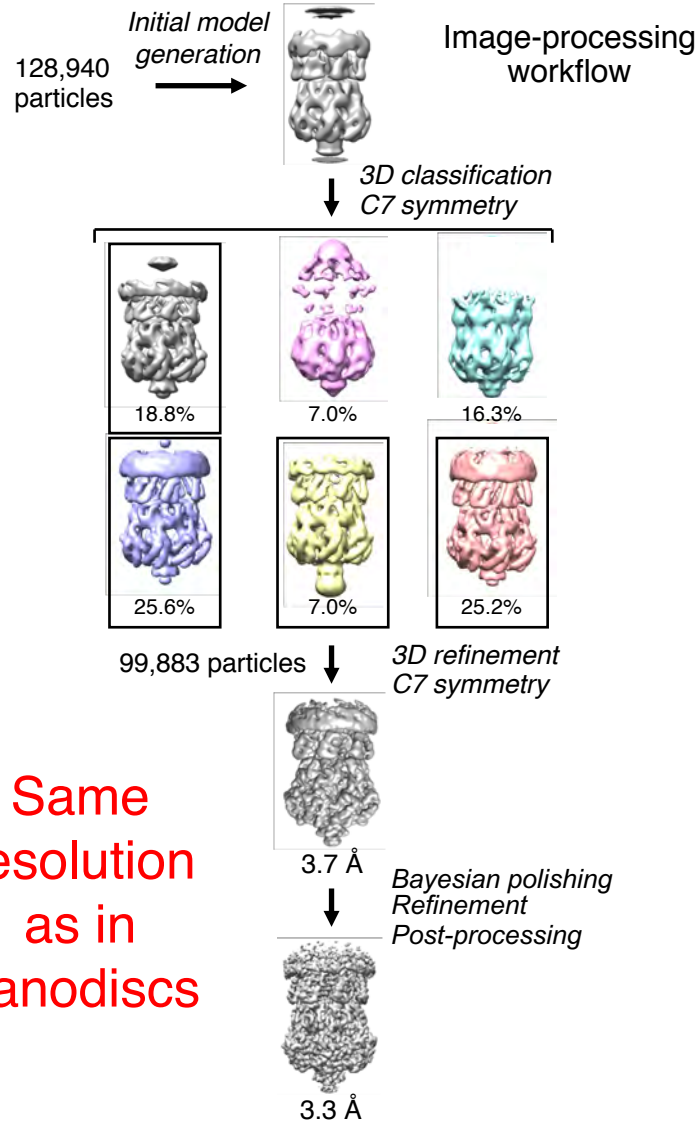
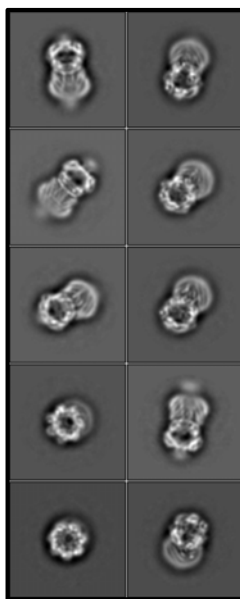
Negative-stain EM image



Cryo-EM image



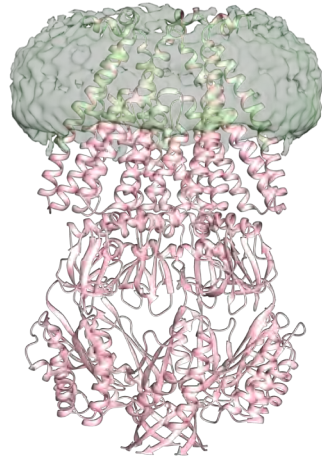
2D averages



# MscS in peptidiscs and nanodiscs

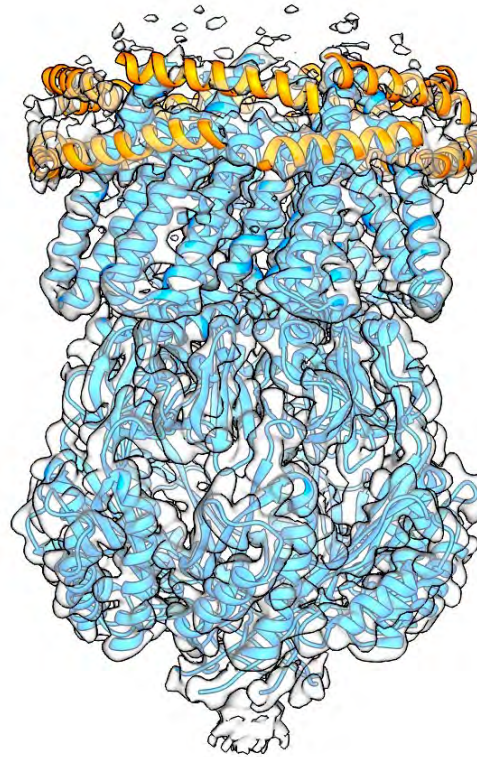


MscS in peptidisc

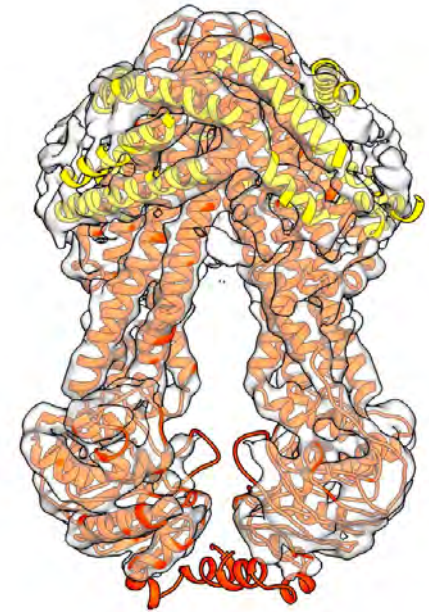


MscS in nanodisc

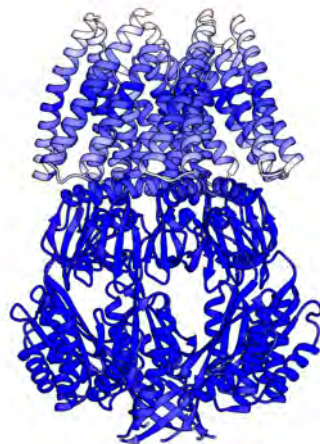
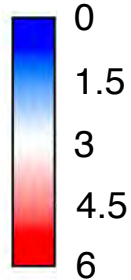
MscS in peptidisc



MsbA in peptidisc



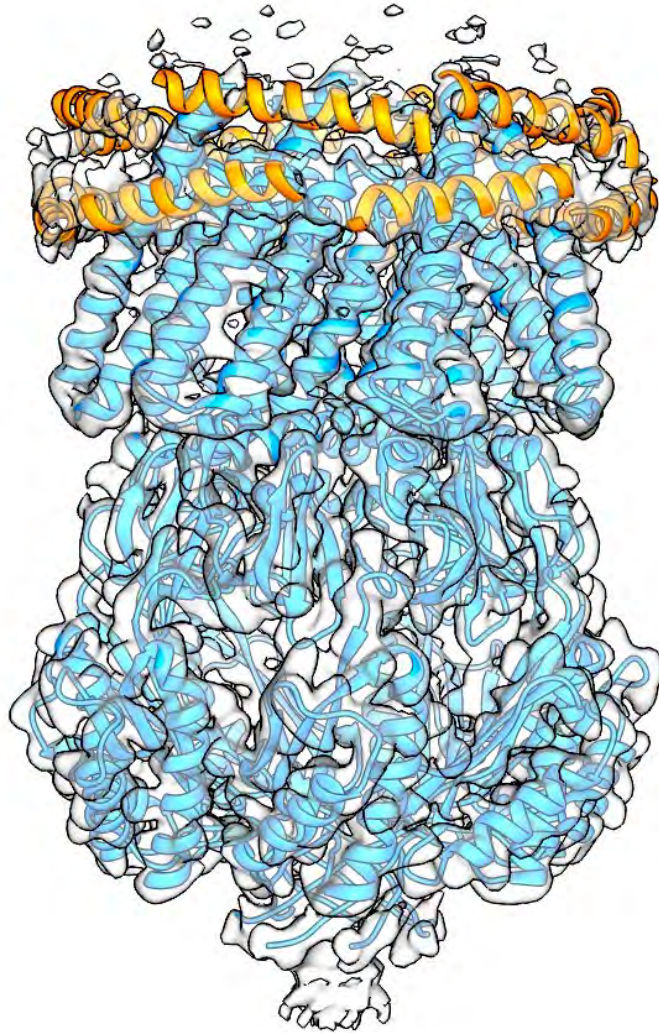
RMSD



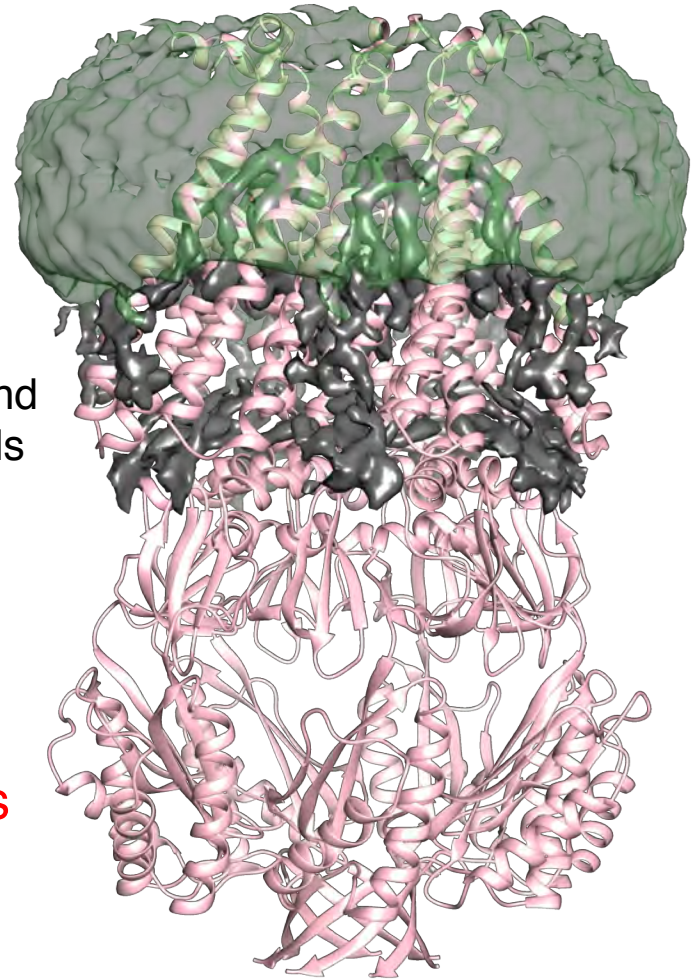
Peptidisc peptides adapt to the TMDs of membrane proteins in different ways



# MscS in peptidiscs and nanodiscs



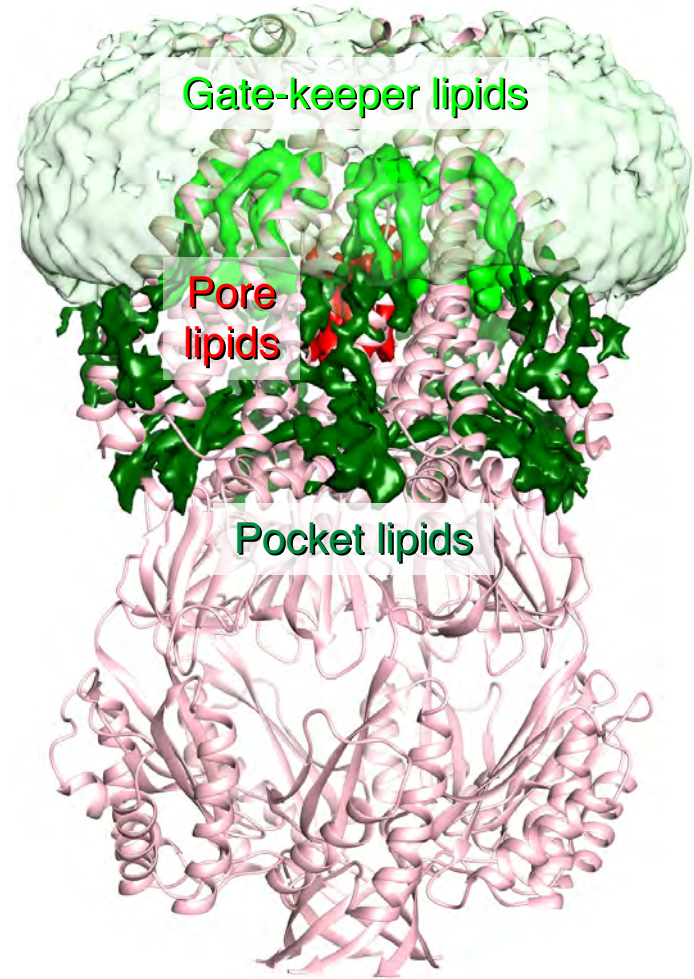
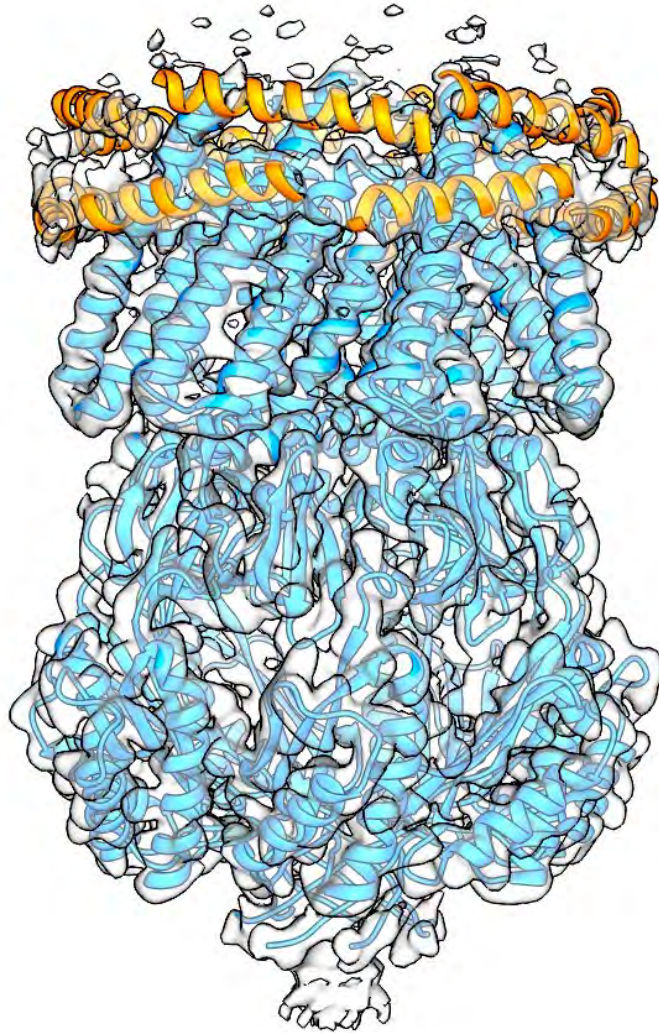
Bound lipids



Peptidiscs  
do not  
preserve  
loosely  
bound lipids

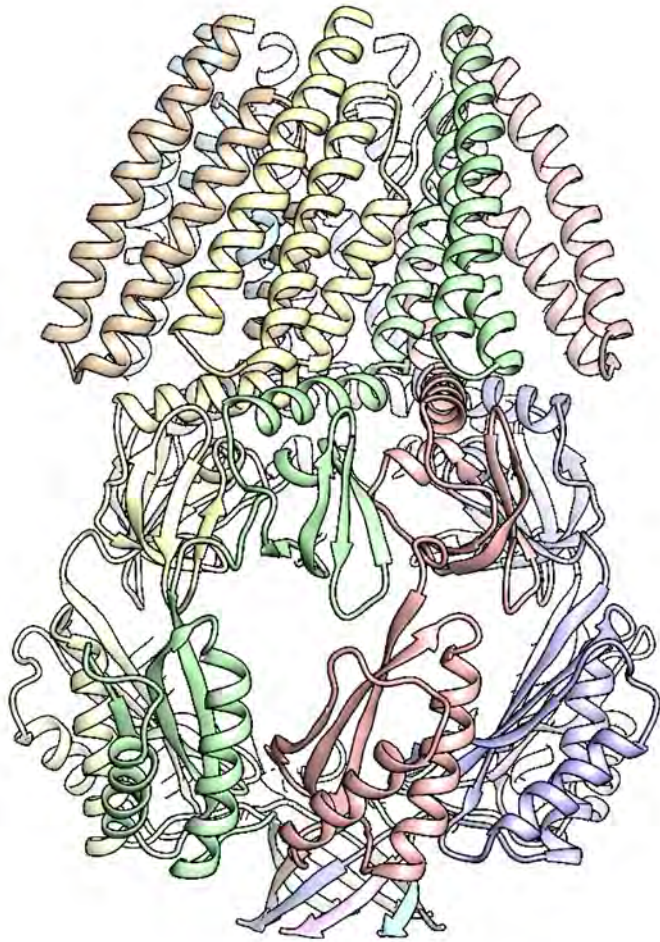


# MscS in peptidiscs and nanodiscs

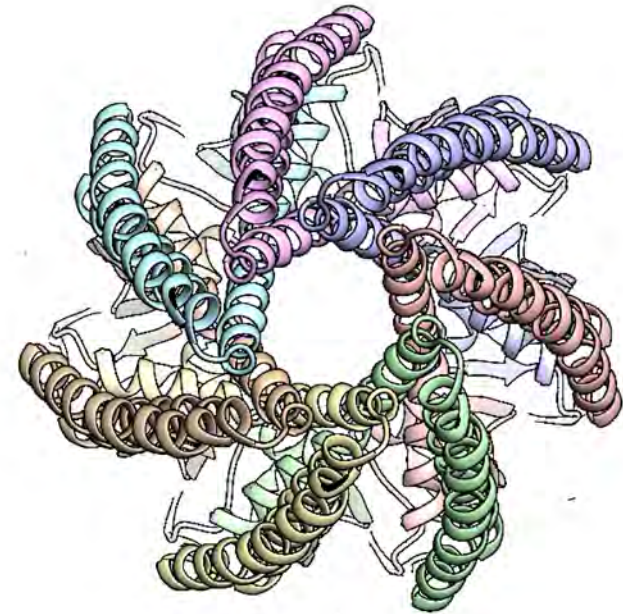


# Conformational cycle of MscS

Closed



Closed





# Membrane mimetics for cryo-EM studies

- Detergents**
  - Most established
  - Risk of affecting MP structure
  - Can be used to modify orientation of particles
- Peptidiscs**
  - Appears to stabilize MPs better than detergents
  - Excellent if only MP structure is of interest
  - Can induce formation of linear aggregates
- Nanodiscs**
  - Excellent mimetic of biological membrane
  - Excellent if membrane characteristics are important
  - Problematic for MPs with little extramembranous mass
- SMALPS**
  - Not much used yet for cryo-EM studies
  - Most native lipid environment
  - Structural heterogeneity ?

# Acknowledgments

*MsbA in  
nanodiscs*

Harvard Medical School

Maofu Liao  
Wei Mi

*MscS in  
nanodiscs*

Yixiao Zhang

*MsbA and MscS  
in peptidiscs*

Gabriella Angiulli  
Hiroshi Suzuki

University of British Columbia

Franck Duong  
Harveer Dhupar  
Irvin Wason