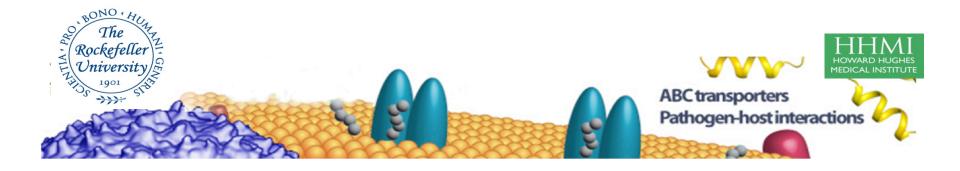
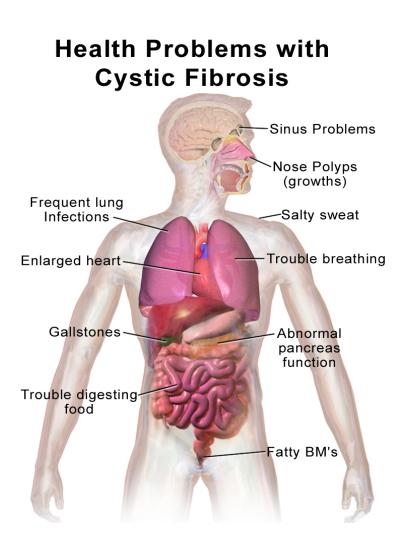
# CFTR, the odd ABC transporter responsible for cystic fibrosis

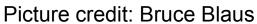
Jue Chen

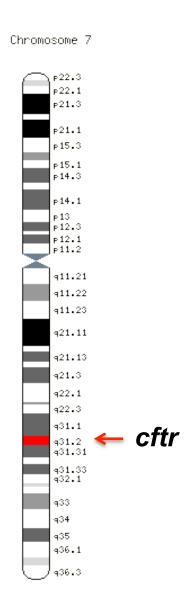
Laboratory of Membrane Biology and Biophysics



### Cystic Fibrosis is a genetic disease

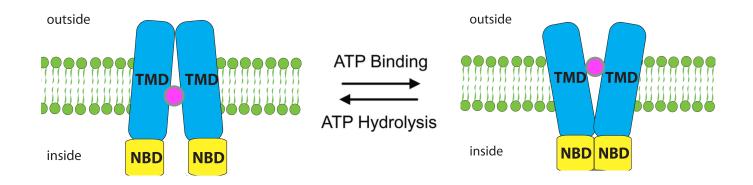




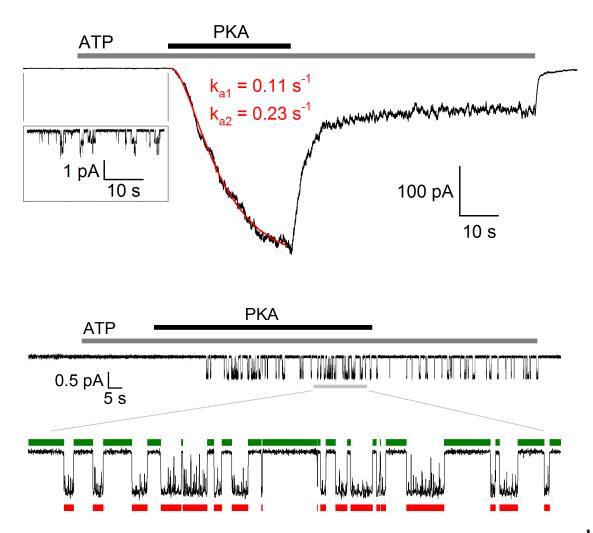


### **CFTR**, an odd **ABC** transporter

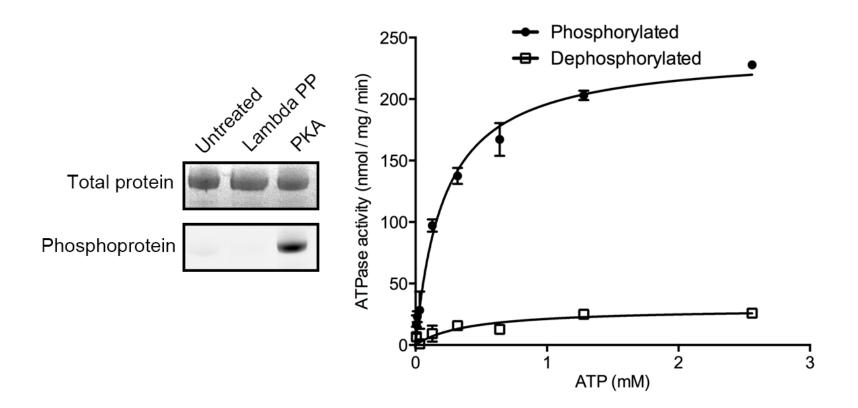
#### **Typical ABC transporters: ATP-powered pumps**



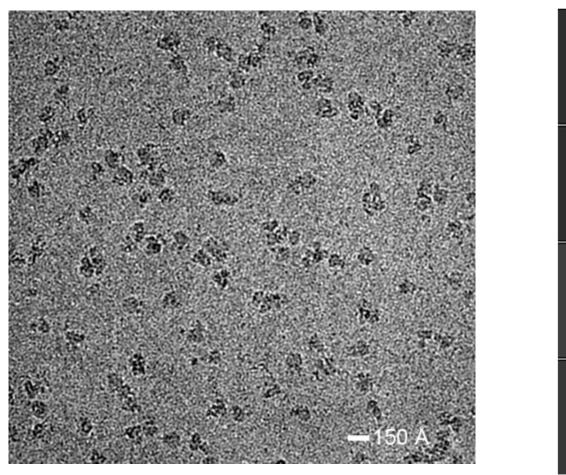
### Phosphorylation gates the CFTR channel

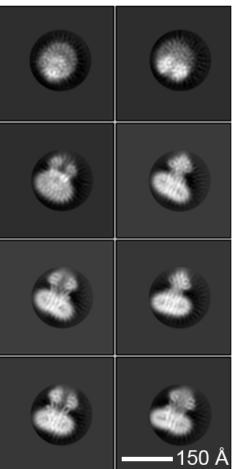


### Phosphorylation also regulates ATPase activity



### **Cryo-EM** analysis of CFTR



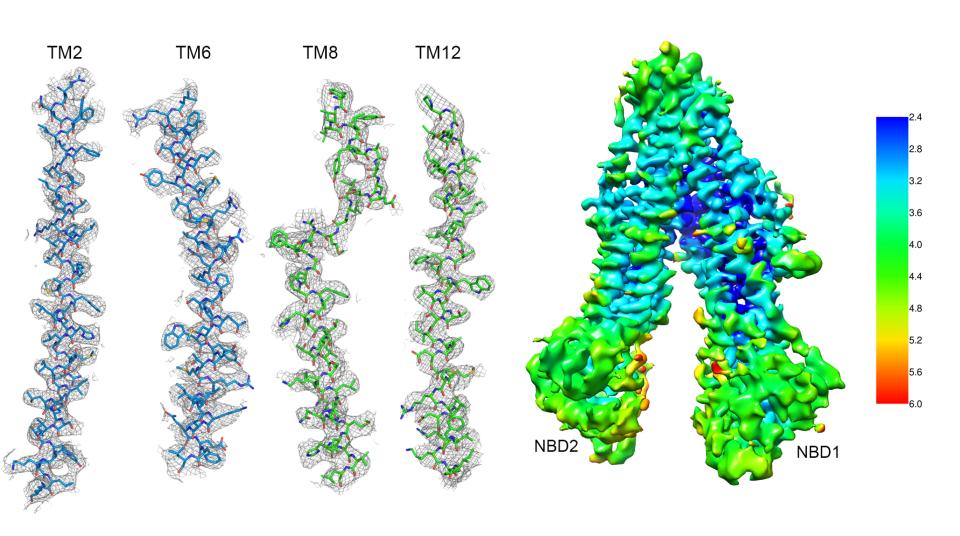


Zhe Zhang

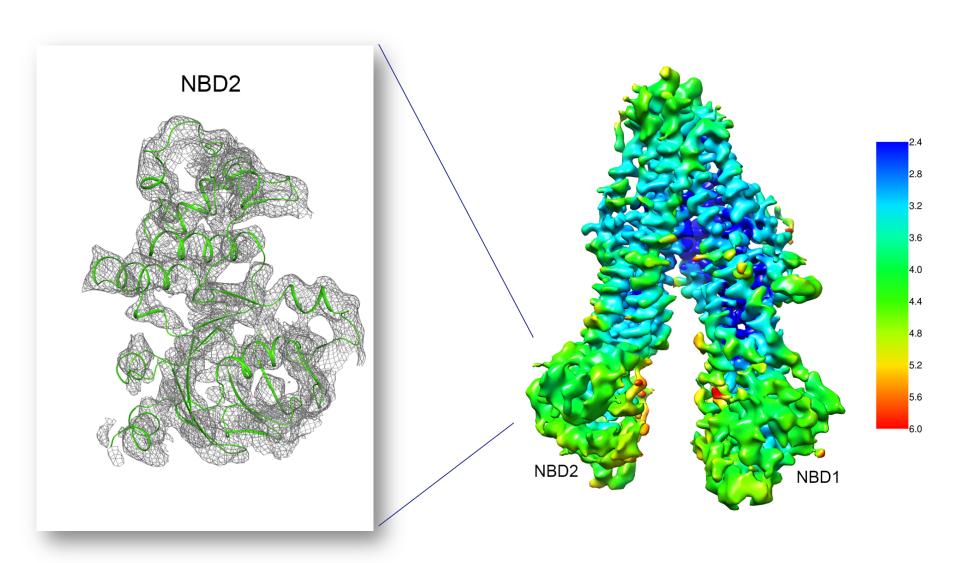
### **Cryo-EM analysis of CFTR**

- Movie alignment and exposure filter
  - -- **Unblur**: Grant & Grigorieff, eLIFE, 2015
- Particle alignment
  - -- alignparts\_Imbfgs: Rubinstein & Brubaker, J Struct Biol. 2014
- Estimate defocus parameters
  - -- CTFFND4: Rohou & Grigorieff, J Struct Biol. (2015)
- Particle picking and subsequent processing
  - -- **Relion**: Scheres, J Struct Biol. 2015
- Final runs of 3D refinement
  - -- Frealign: Lyumkis & Grigorieff, J Struct Biol. 2013

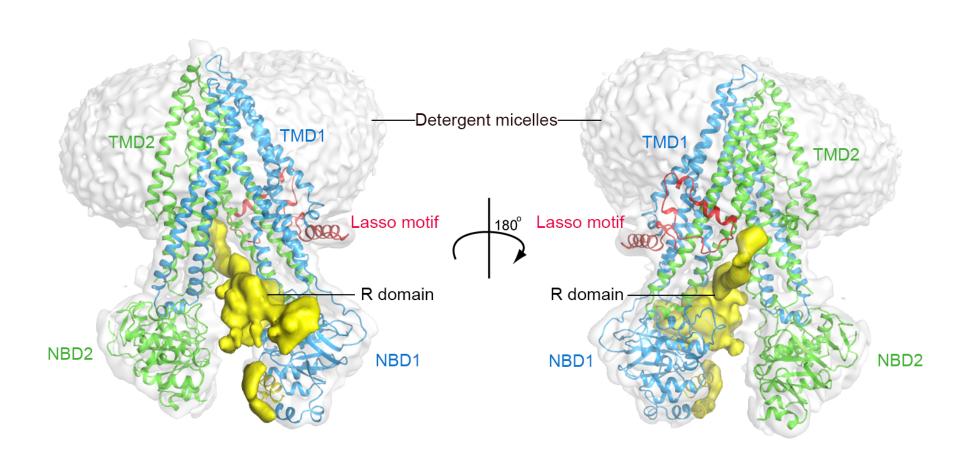
### **Cryo-EM** analysis of zebrafish CFTR



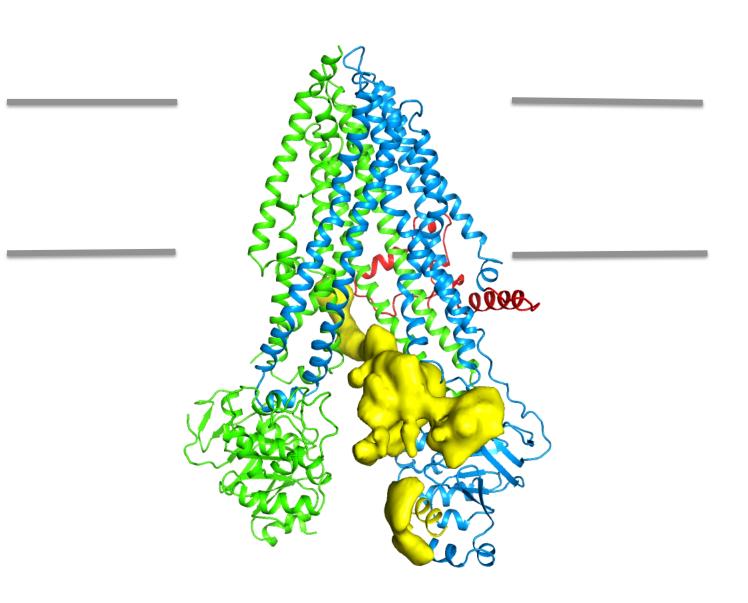
### **Cryo-EM** analysis of zebrafish CFTR



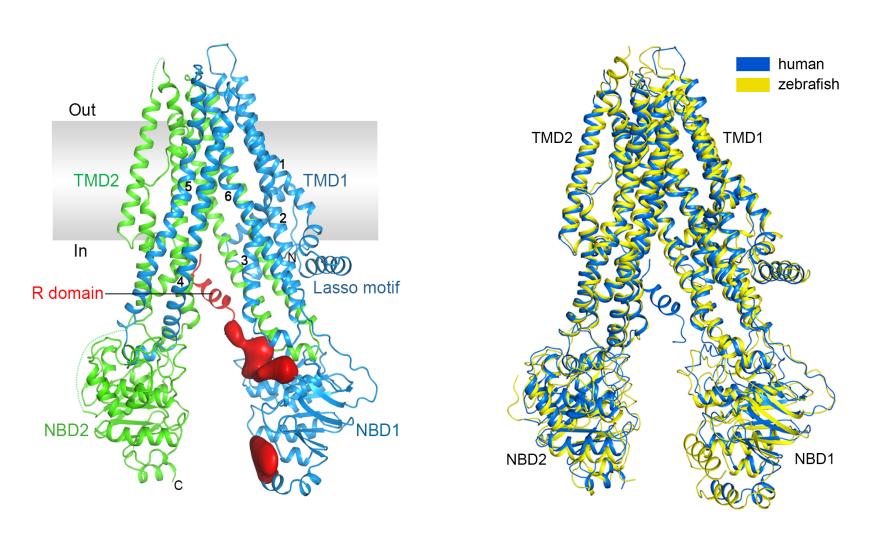
### **Cryo-EM analysis of zebrafish CFTR**



### **Zebrafish CFTR**

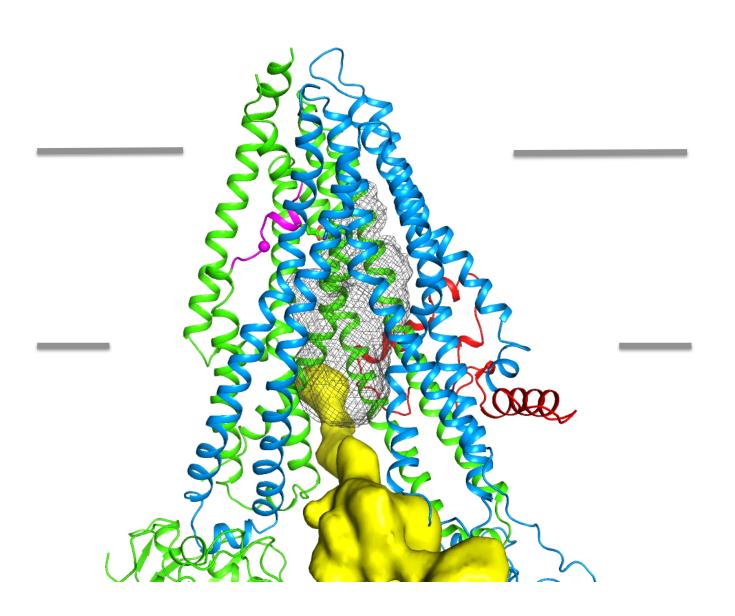


### **Human CFTR**

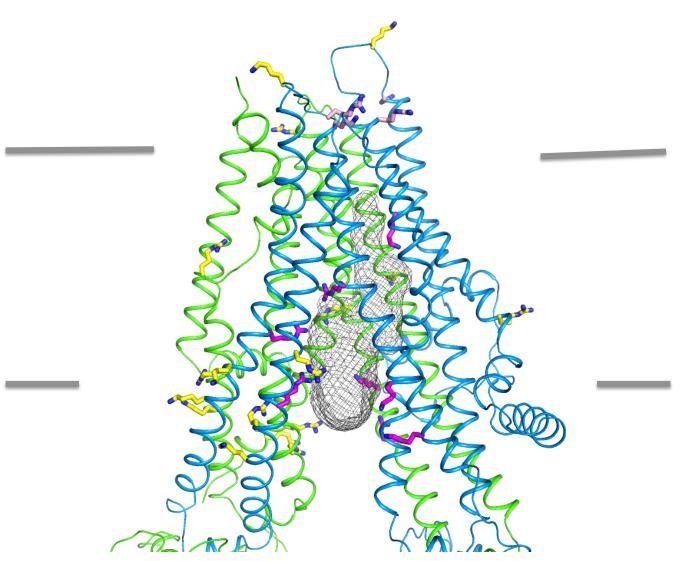


Fangyu Liu and Zhe Zhang

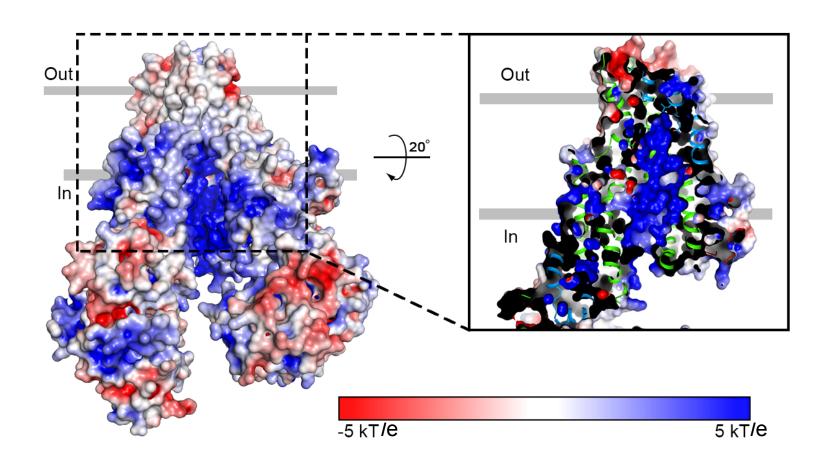
### The ion conduction pathway



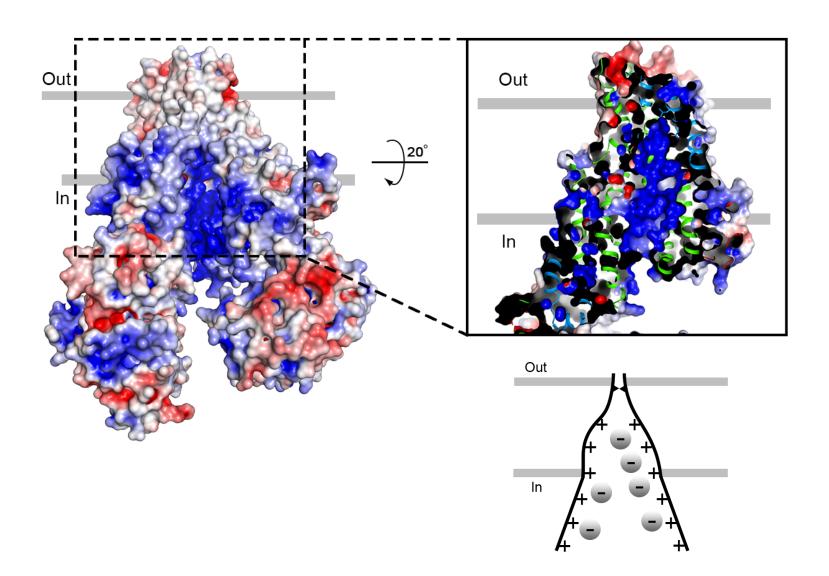
### Positively charged residues



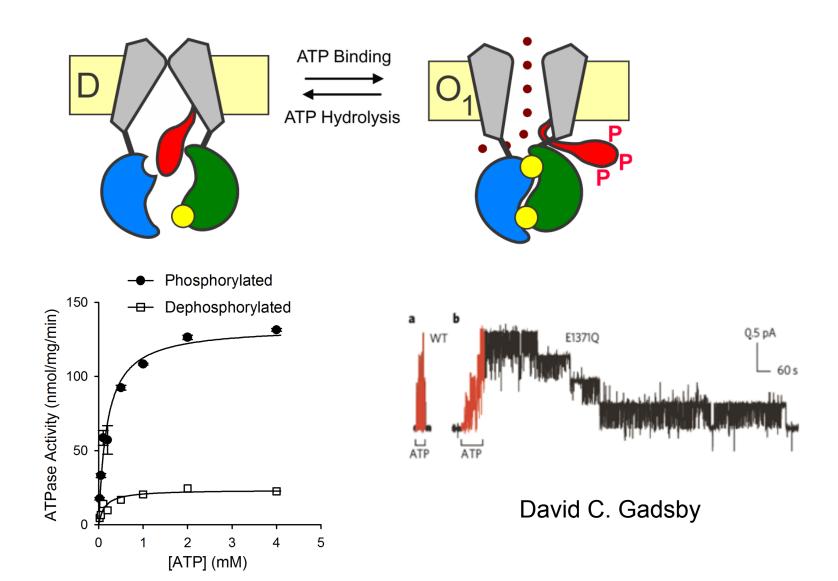
### **Anion selectivity**

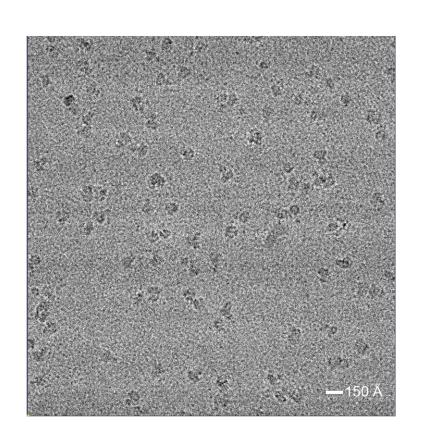


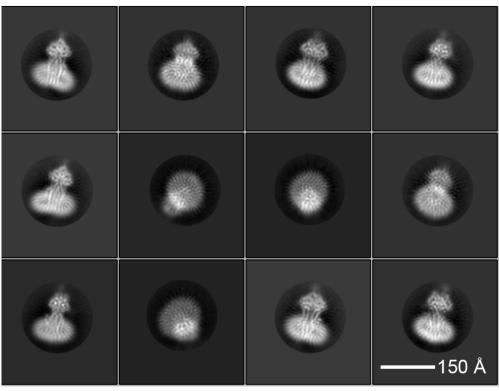
## **Selectivity**

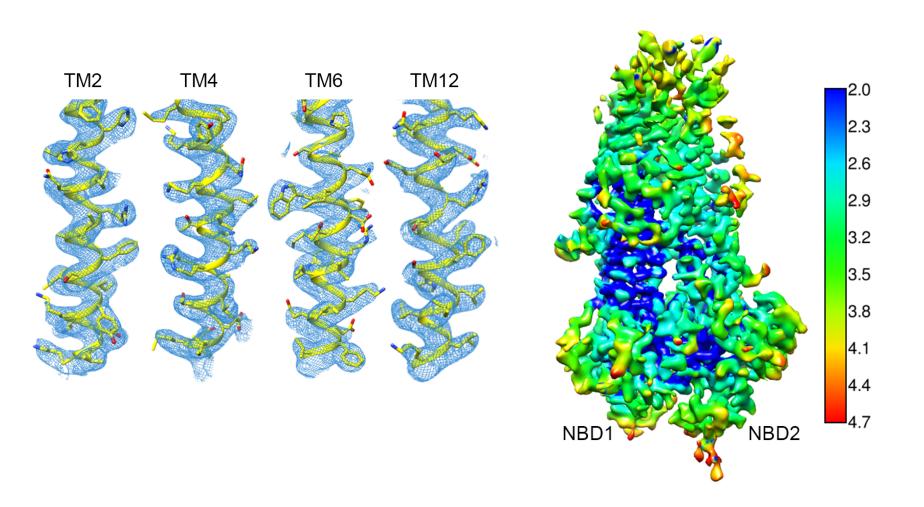


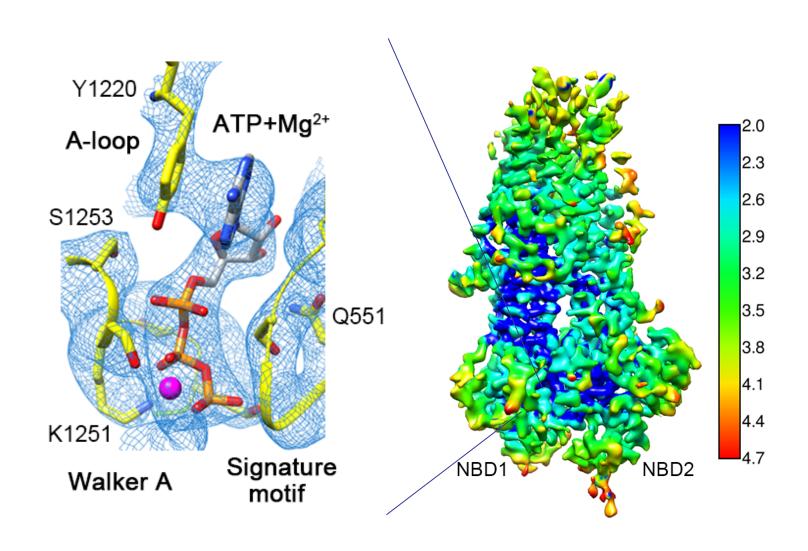
### Towards an open channel conformation

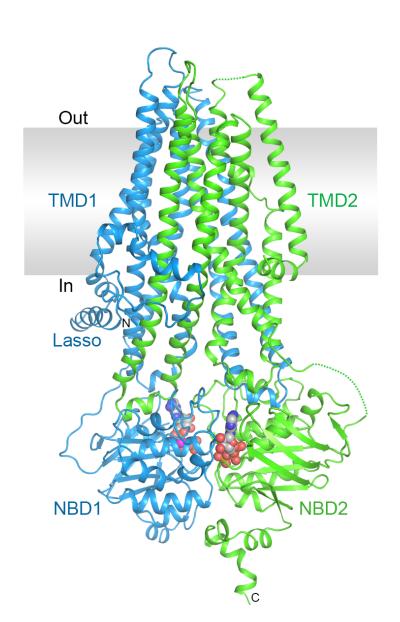


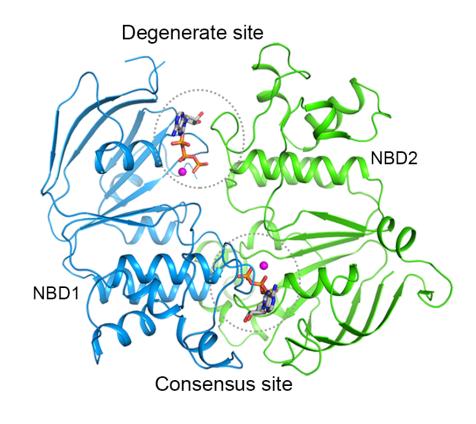






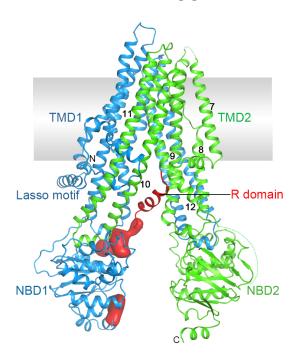


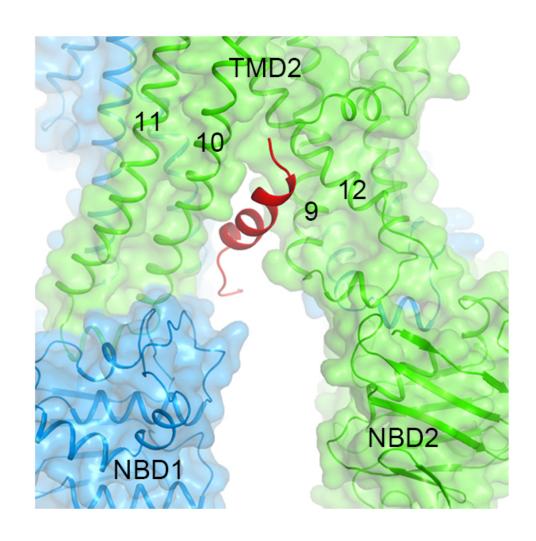




### R domain prevents NBD dimerization

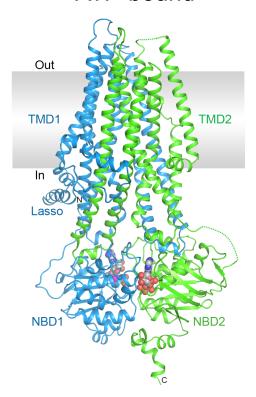
# Dephosphorylated ATP-free

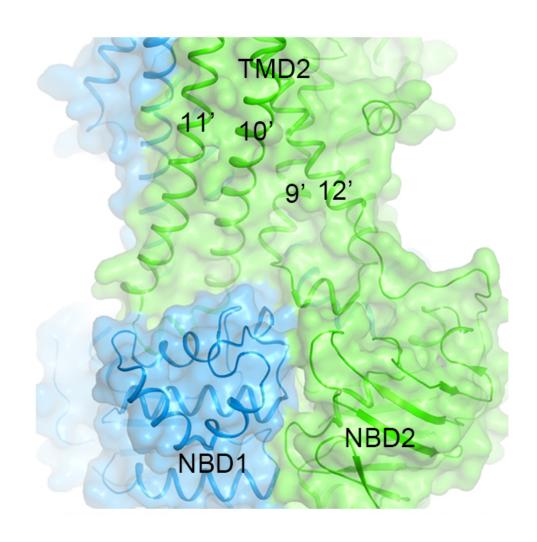




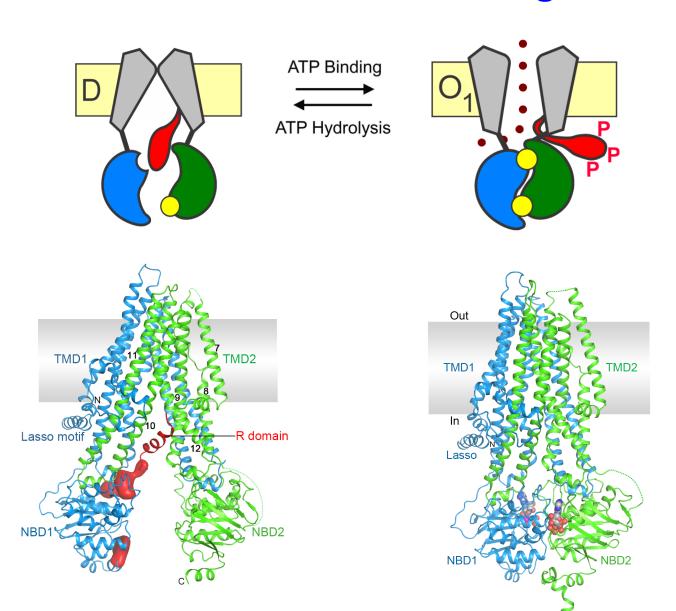
### R domain prevents NBD dimerization

Phosphorylated ATP-bound

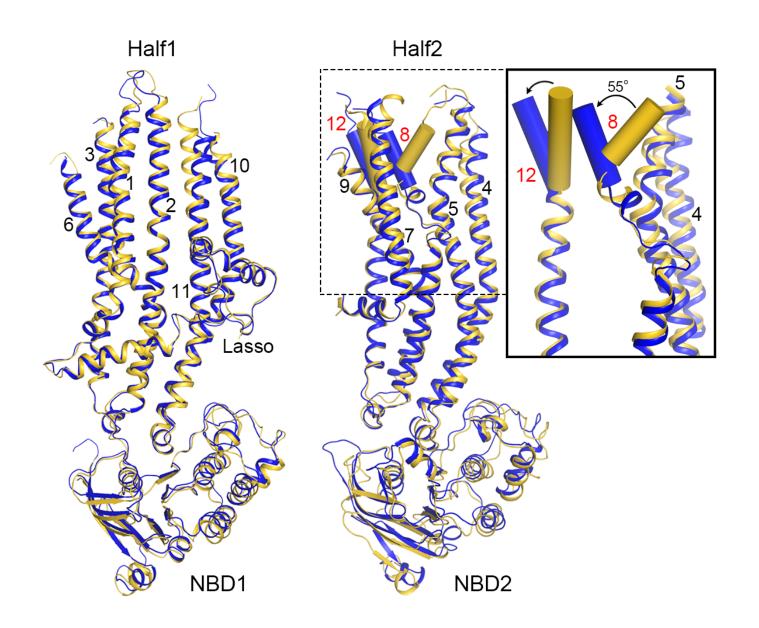




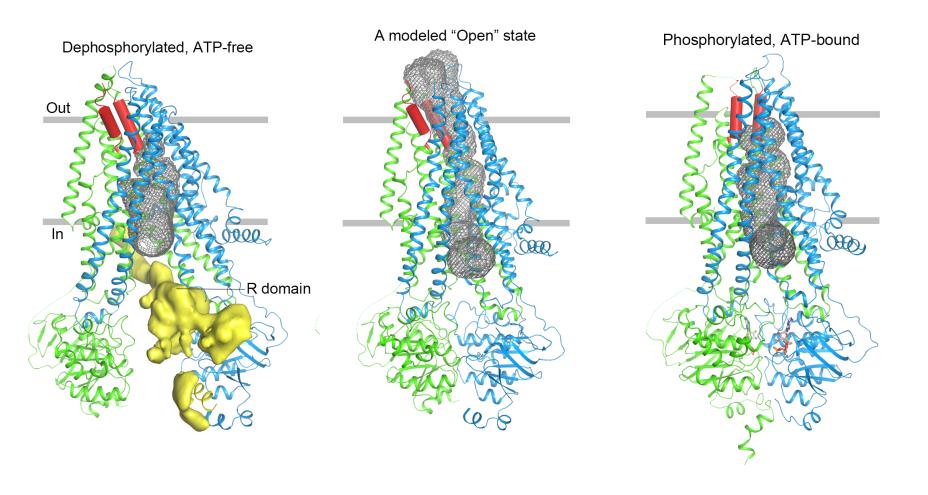
### **Conformational changes**



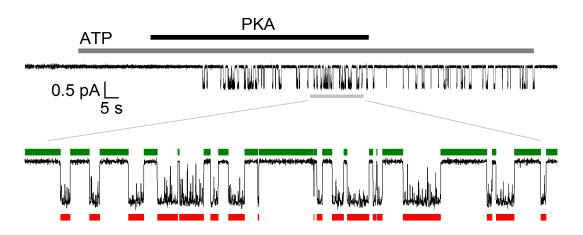
### **Conformational changes**



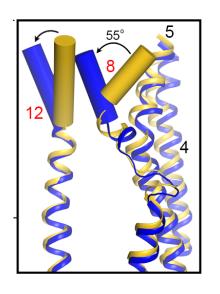
### Local conformations control ion access

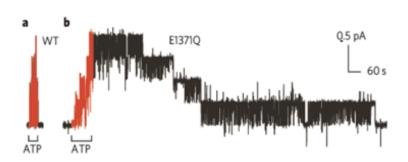


### **Flickering**



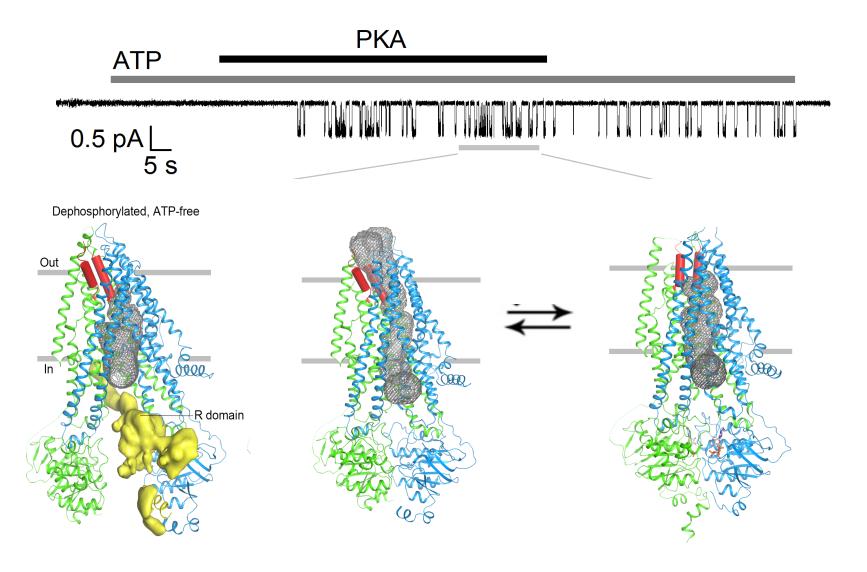
László Csanády





David C. Gadsby

### The CFTR gating cycle

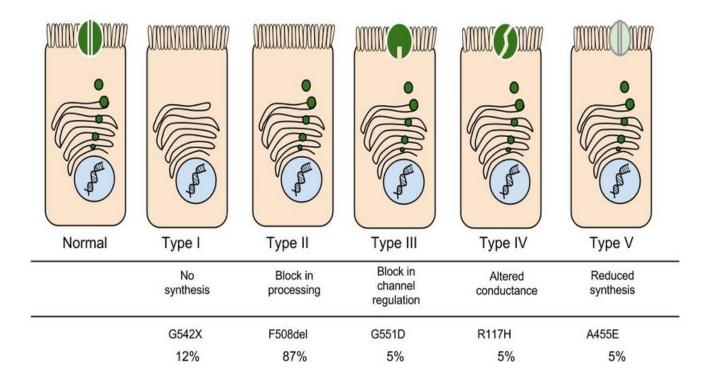


# The CFTR gating cycle

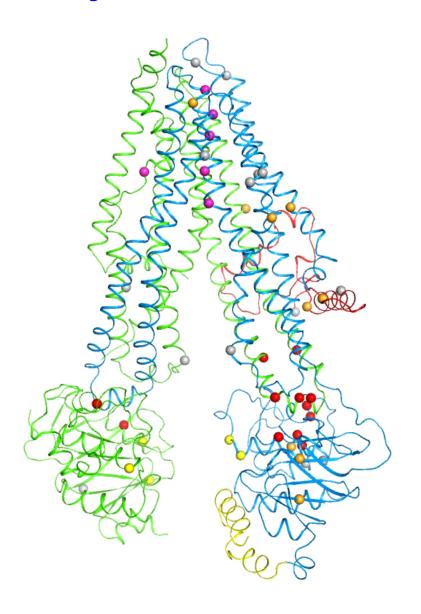


### **Cystic Fibrosis-causing mutations**

- >1000 mutations in CFTR
- 272 mutations causing CF
- 53 missense mutations at 46 positions

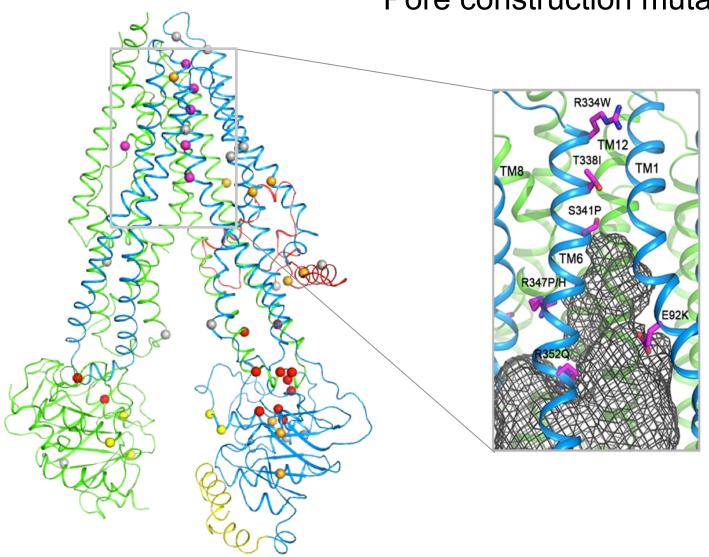


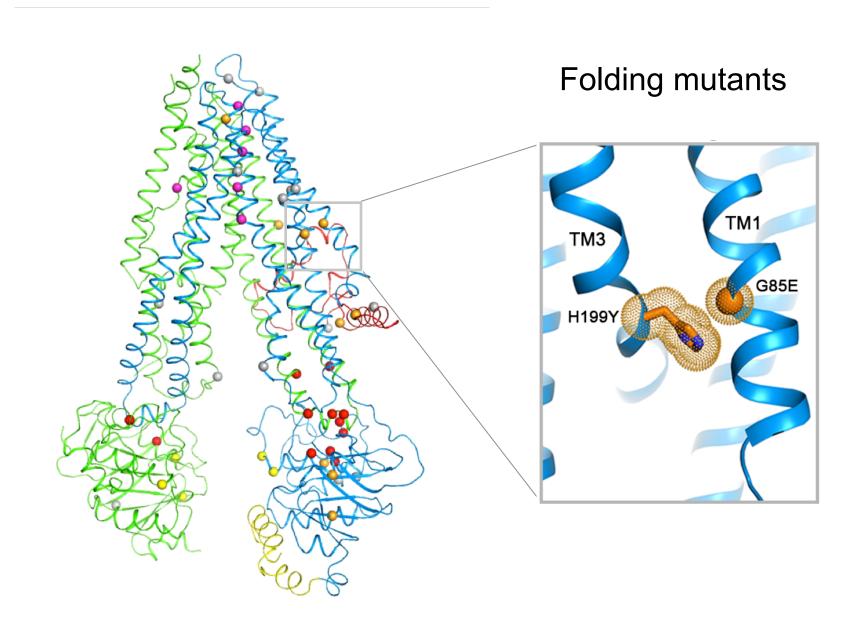
### **Cystic Fibrosis-causing mutations**



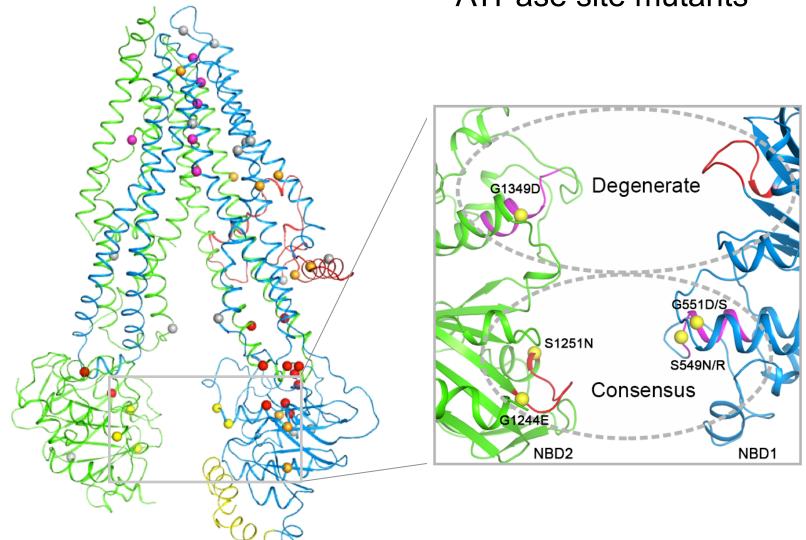
- Pore construction
- Folding
- ATPase site
- NBD/TMD interface
- To be determined

### Pore construction mutants



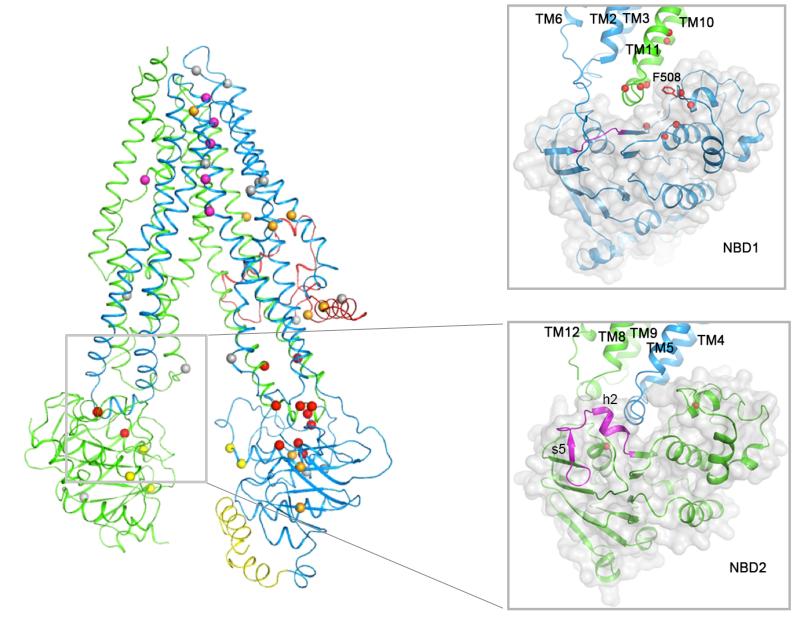


### ATPase site mutants

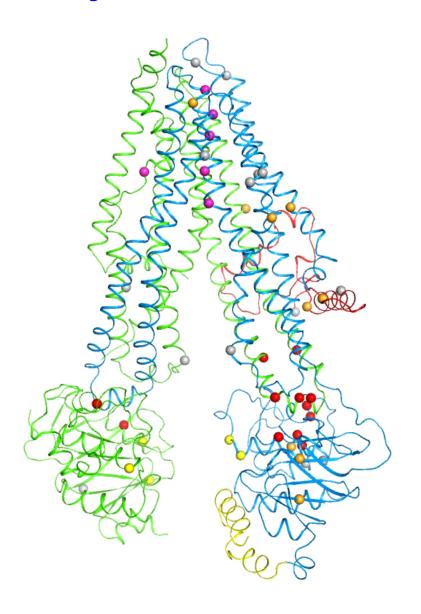


# NBD/TMD interface mutants TM2 TM3 тм6 NBD1 TM11 TM10 TM3 F508 IH4

### NBD/TMD interface mutants

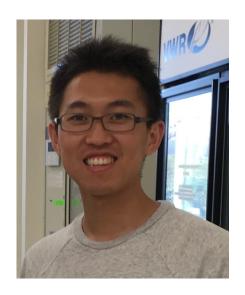


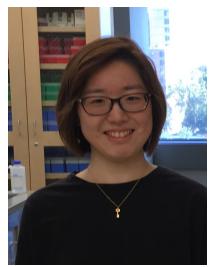
### **Cystic Fibrosis-causing mutations**



- Pore construction
- Folding
- ATPase site
- NBD/TMD interface
- To be determined

### **Acknowledgment**





### **CFTR** project

Zhe Zhang

Fangyu Liu

David C. Gadsby

László Csanády



#### **EM Mentors**

- Tom Walz
- Zongli Li
- Rich Hite
- Nikolaus Grigorieff
- Tim Grant
- Alexis Rohou

#### Staff at RU and Janelia

- Mark Ebrahim
- Johanna Sotiris
- Zhiheng Yu
- Chuang Hong
- Rick Huang

