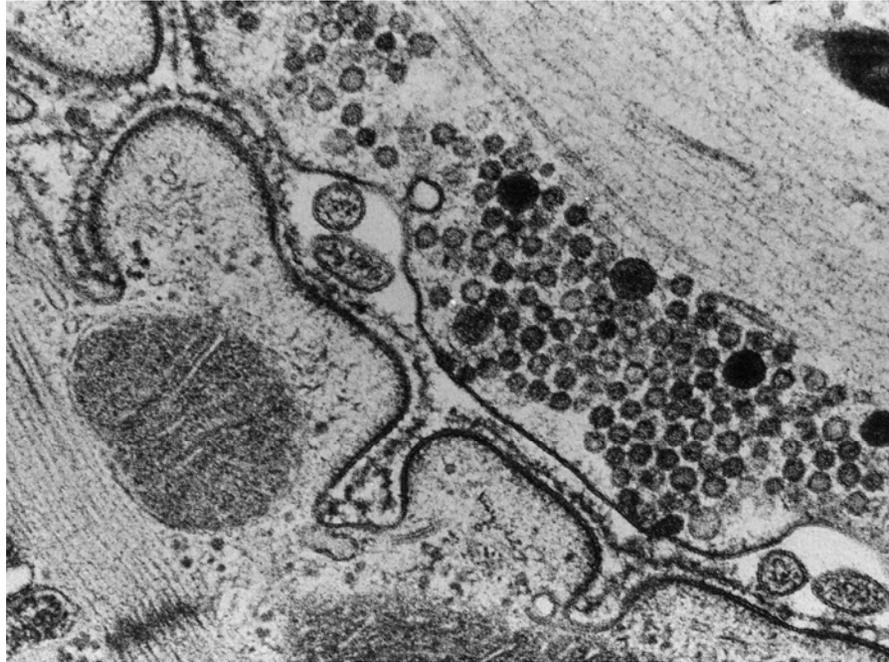


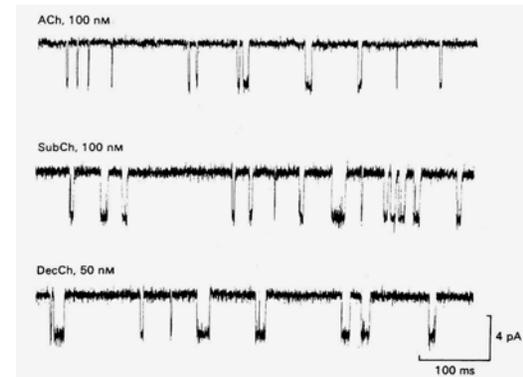
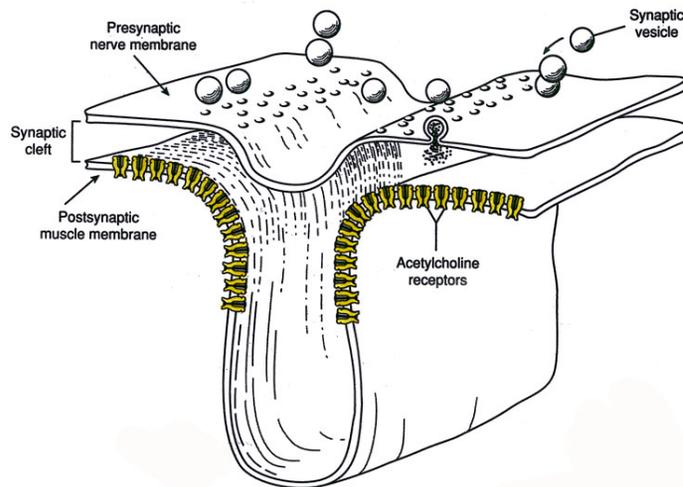
# Electron crystallography of tubes: nicotinic acetylcholine receptor

Nigel Unwin,  
MRC Lab of Molecular  
Biology,  
Cambridge, UK

# The nerve-muscle synapse



John Heuser, 1975



Colquhoun and Sakmann, 1985

## Fundamental questions:

How does the transmitter initiate the movements which open the channel?

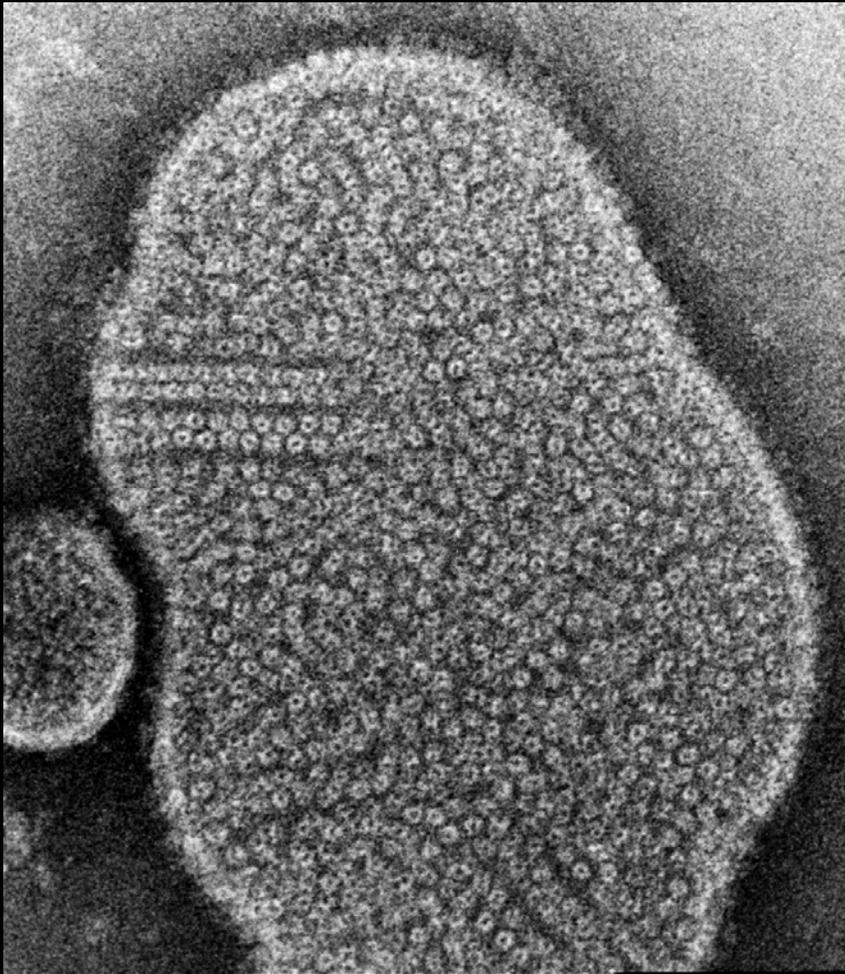
How does the structure change between closed and open states?

How is ion selectivity achieved?

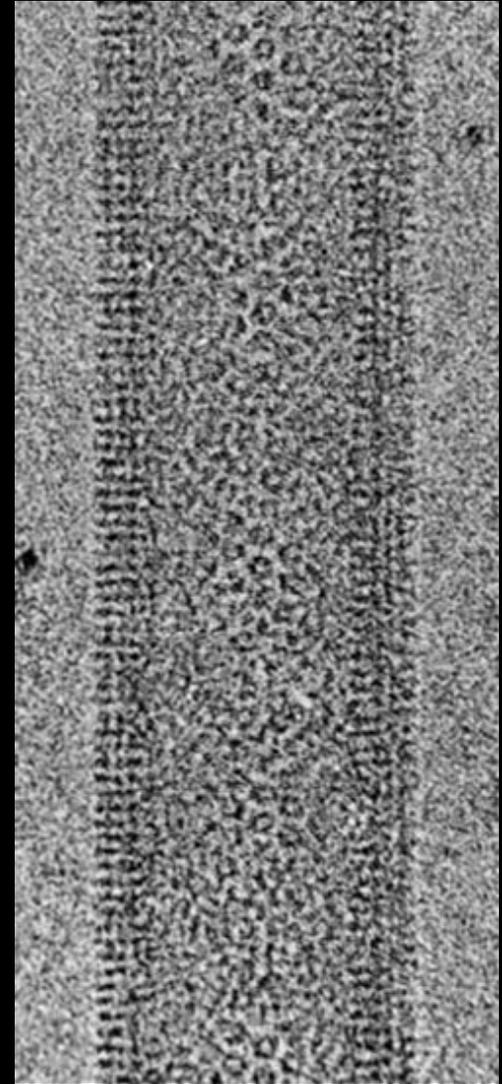
# The electric ray: *Torpedo marmorata*



# Postsynaptic membranes from the Torpedo ray

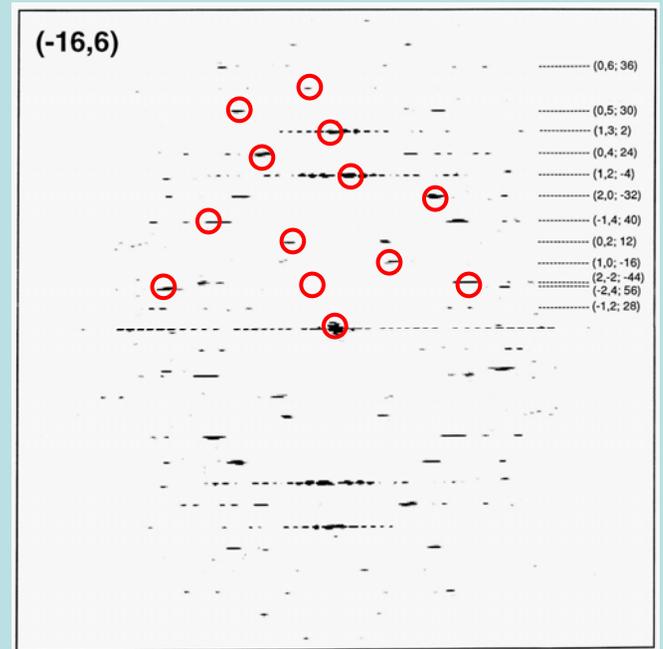
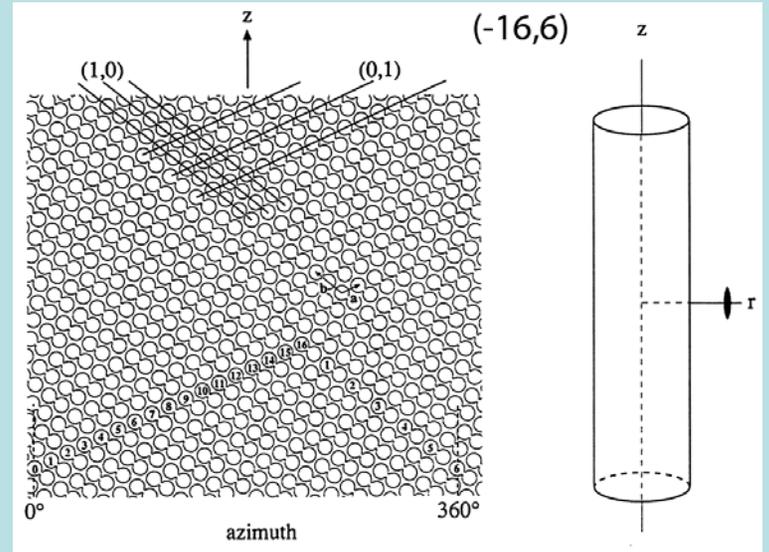
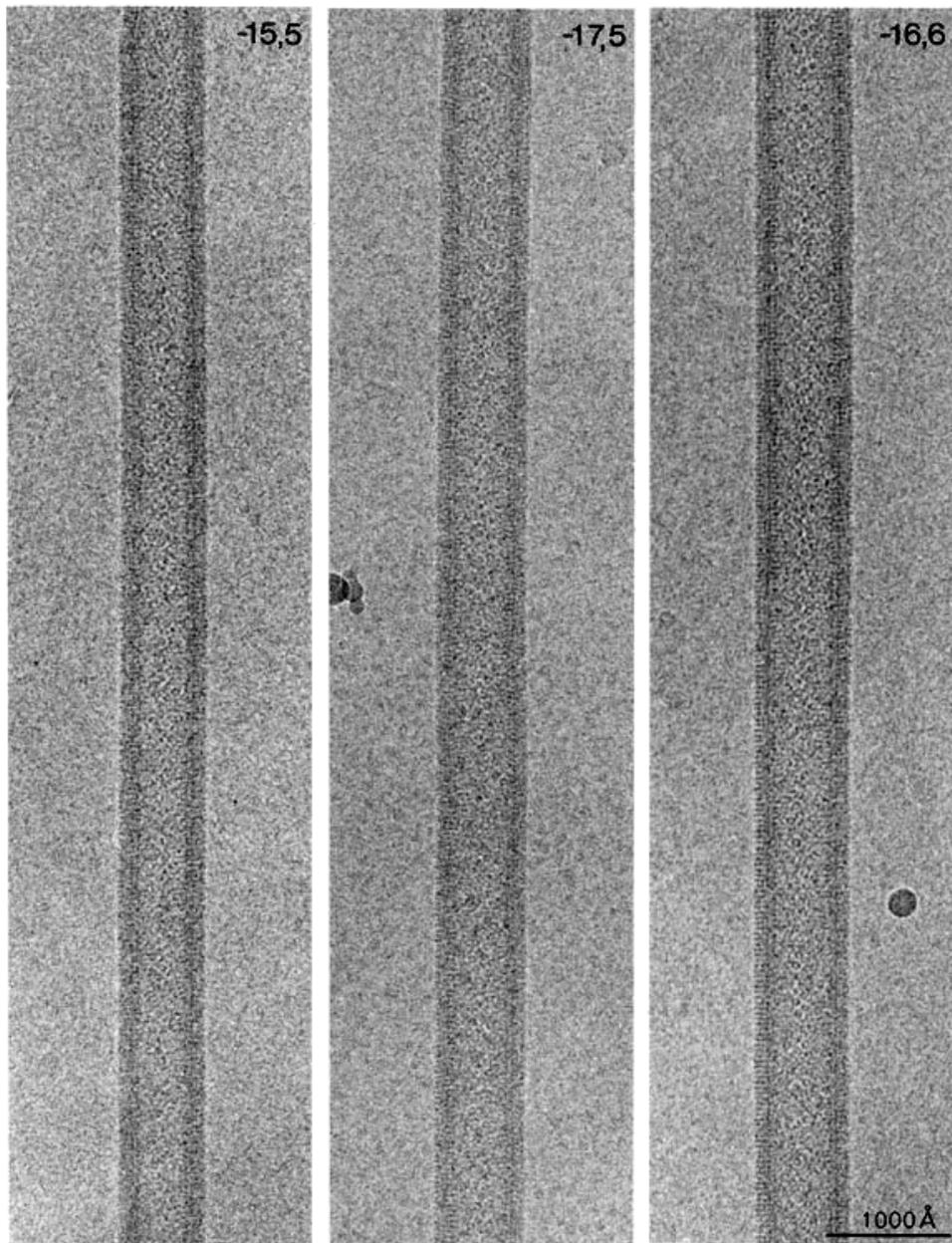


Vesicle (neg. stain)

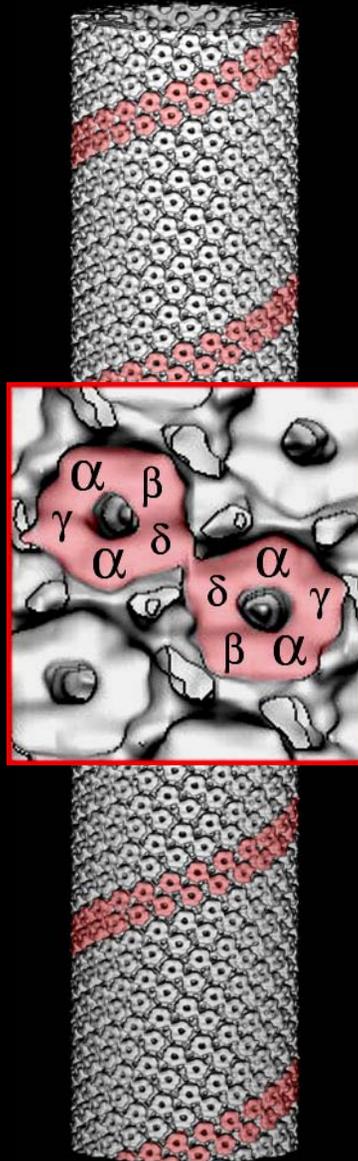


Tube (ice)

# Different helical families



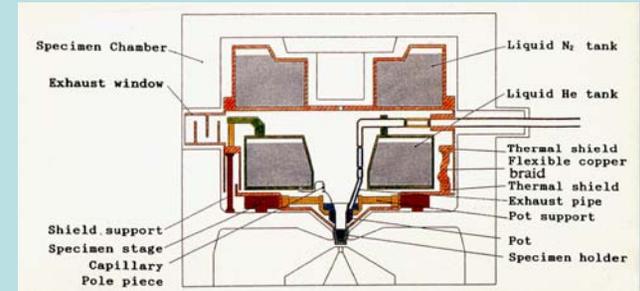
# Reconstruction of a (-16,6) tube



# Important Techniques

## Electron microscopy at liquid helium temperatures

(Fujiyoshi et al., Ultramicroscopy, **38**, 241-251;1991)



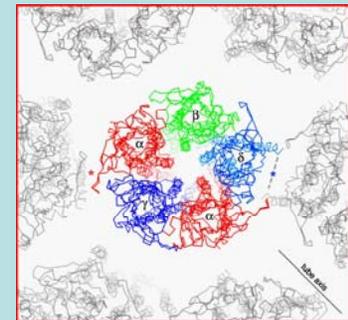
## Undistorting tube images by alignment of short segments to a reference structure

(Beroukhim & Unwin, Ultramicroscopy, **70**, 57-81;1997)



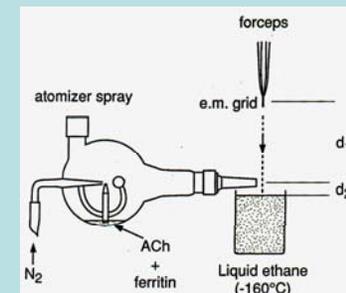
## Structural refinement by R-factor minimisation and comparison of calculated with experimental phases

(Unwin, J. Mol.Biol., **346**, 967-989; 2005)



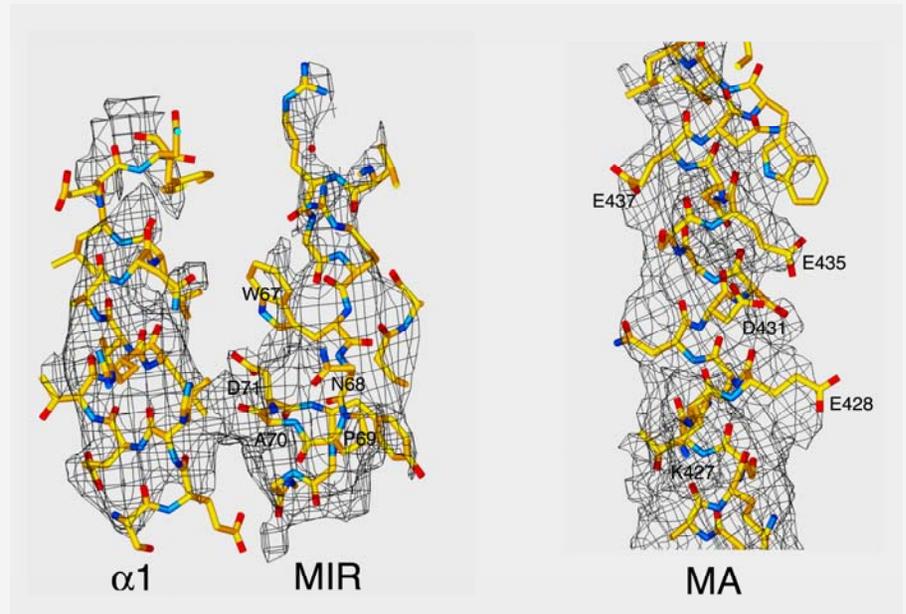
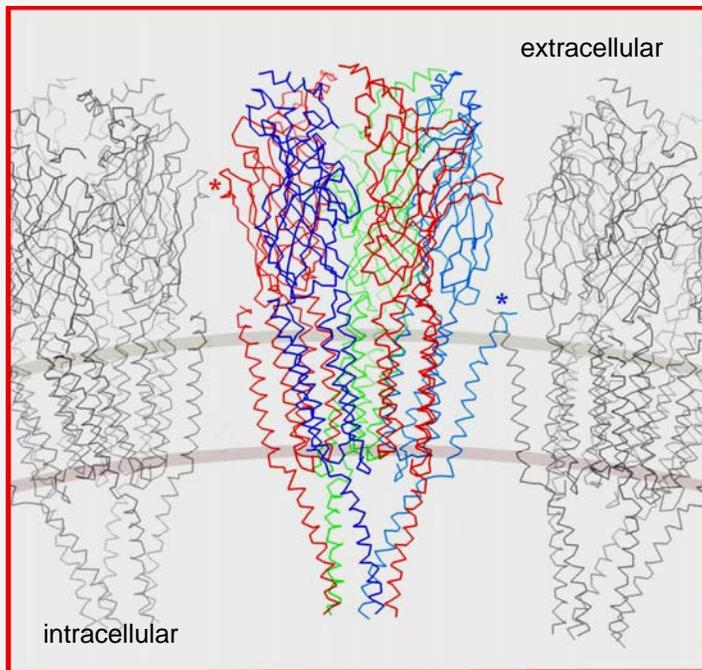
## Freeze-trapping to image gating movements

(Berriman & Unwin, Ultramicroscopy, **56**, 241-252; 1994)



# 3D map at 4Å resolution

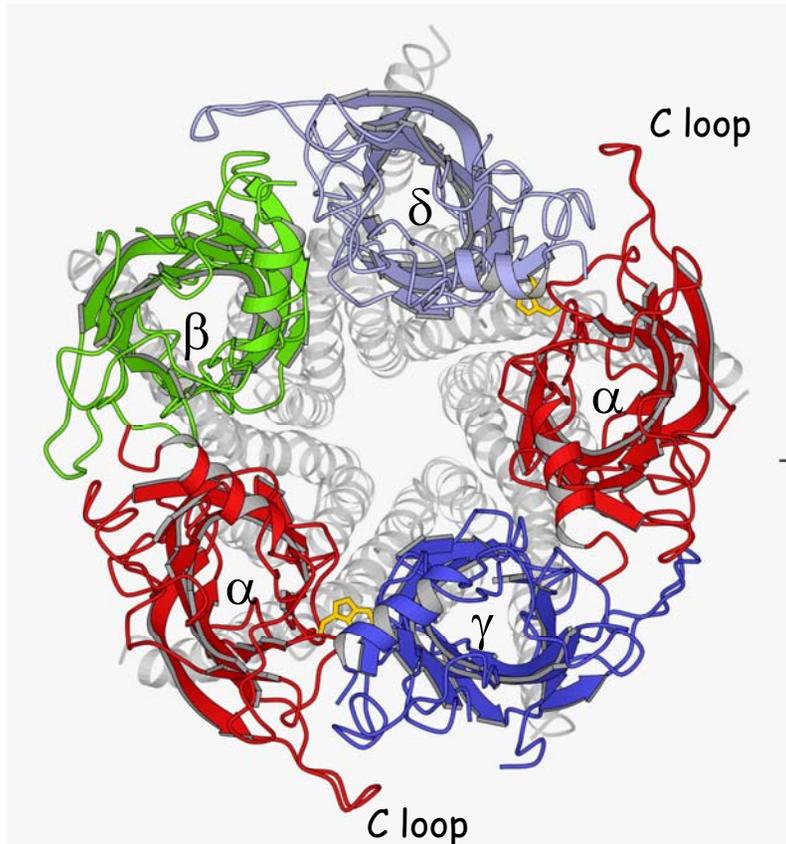
Number of images	342
Number of receptors	$\sim 10^6$
No. Fourier terms	$\sim 10^5$
Amp. wted phase error	$51^\circ$
R-factor	36.7%
( $R_{\text{free}}$ )	37.9%



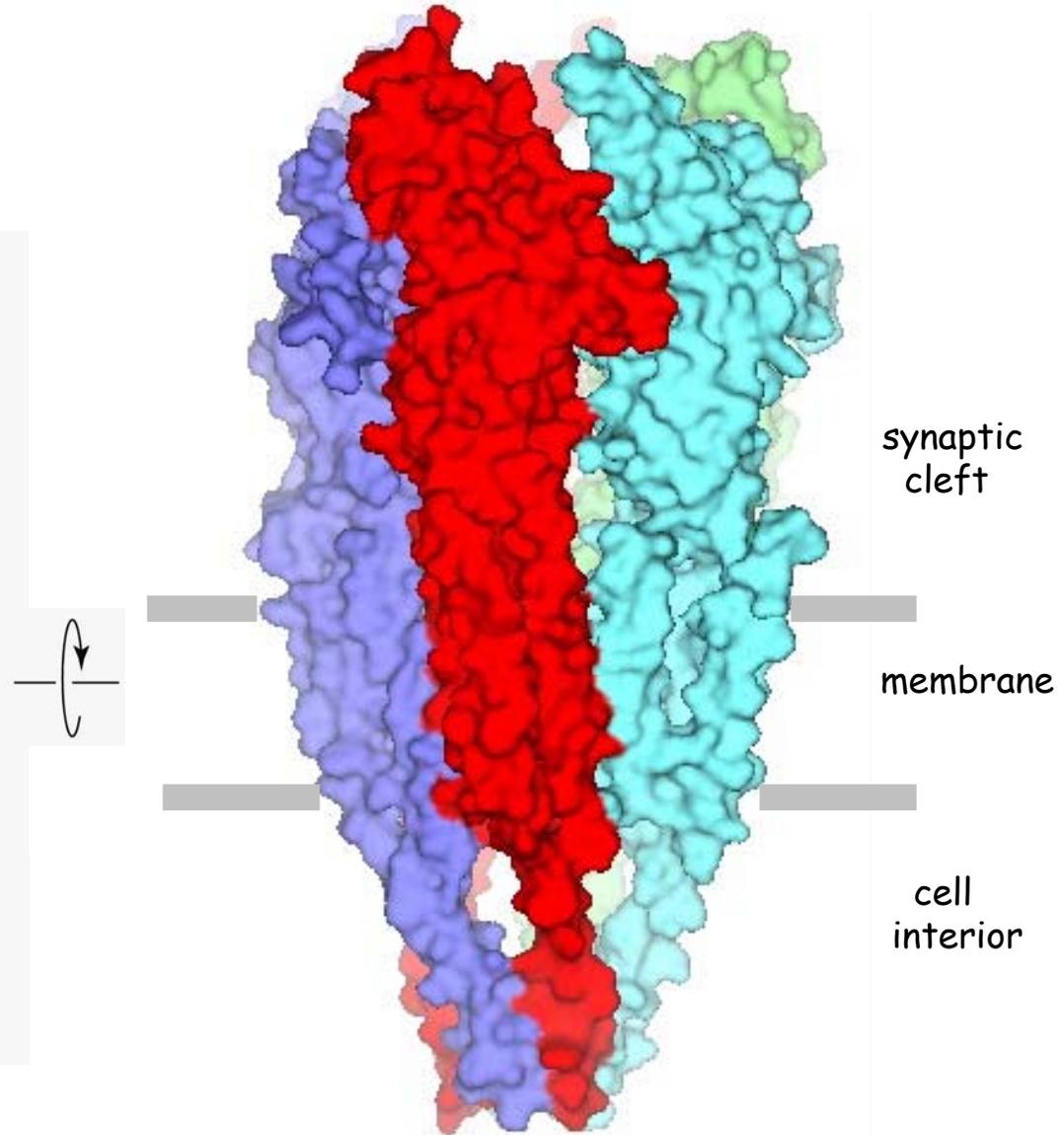
top,  $\alpha$  subunit

bottom,  $\gamma$  subunit

# Structure of the closed channel



Viewed from synaptic cleft



Viewed from the side

# Fit of mouse $\alpha$ subunit ligand-binding domain to Torpedo ACh receptor



$\beta$ -sheet core  
r.m.s deviations ( $\text{\AA}$ ):

$$\alpha_m/\alpha_\gamma = 2.16$$

$$\alpha_m/\alpha_\delta = 2.10$$

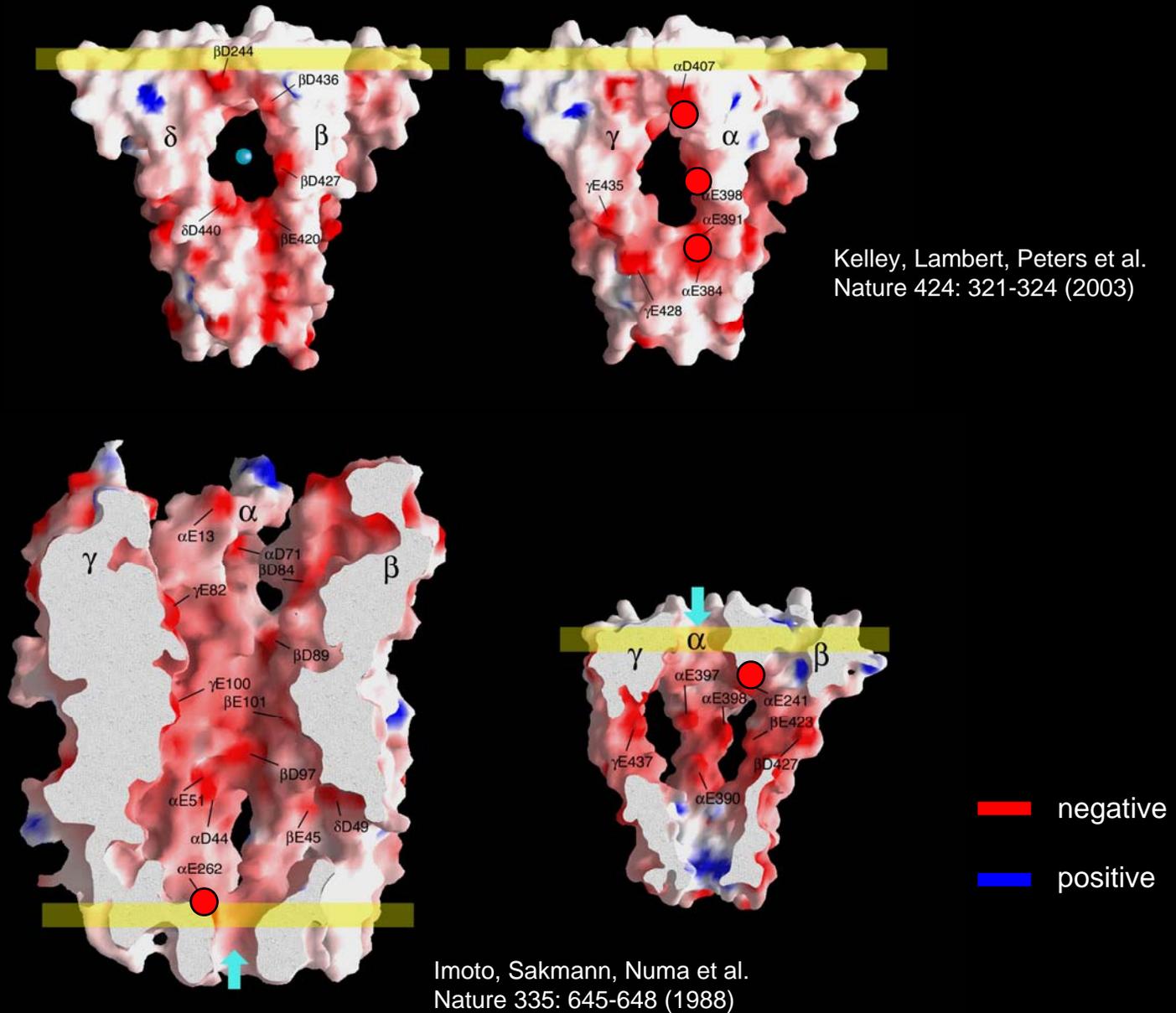
$$\alpha_m/\beta = 2.17$$

$$\alpha_m/\gamma = 1.81$$

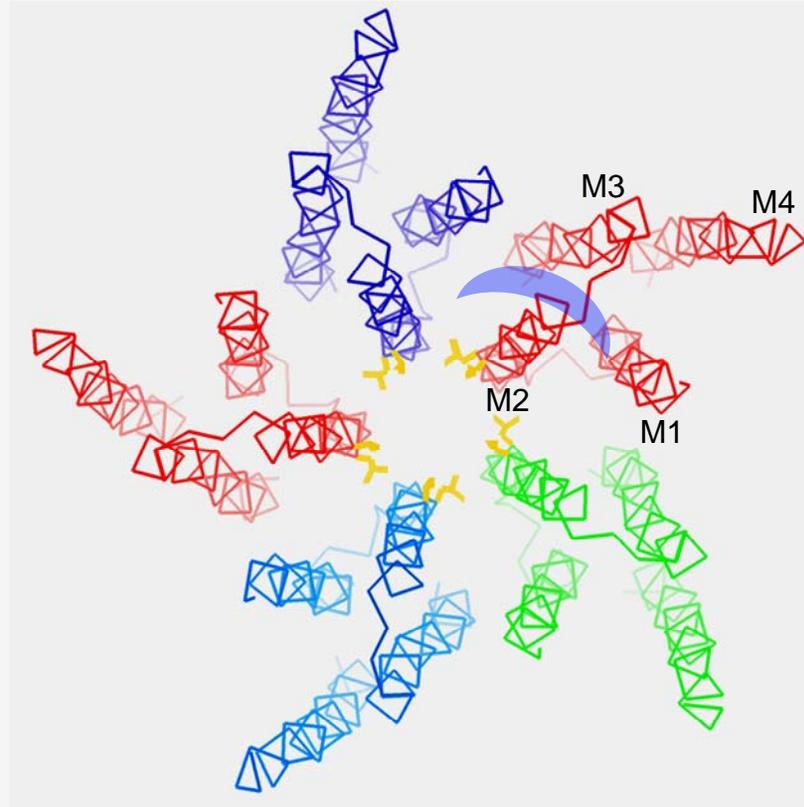
$$\alpha_m/\delta = 1.86$$

$$(\text{AChBP}/\alpha_\gamma = 2.43)$$

# Vestibules are negatively charged

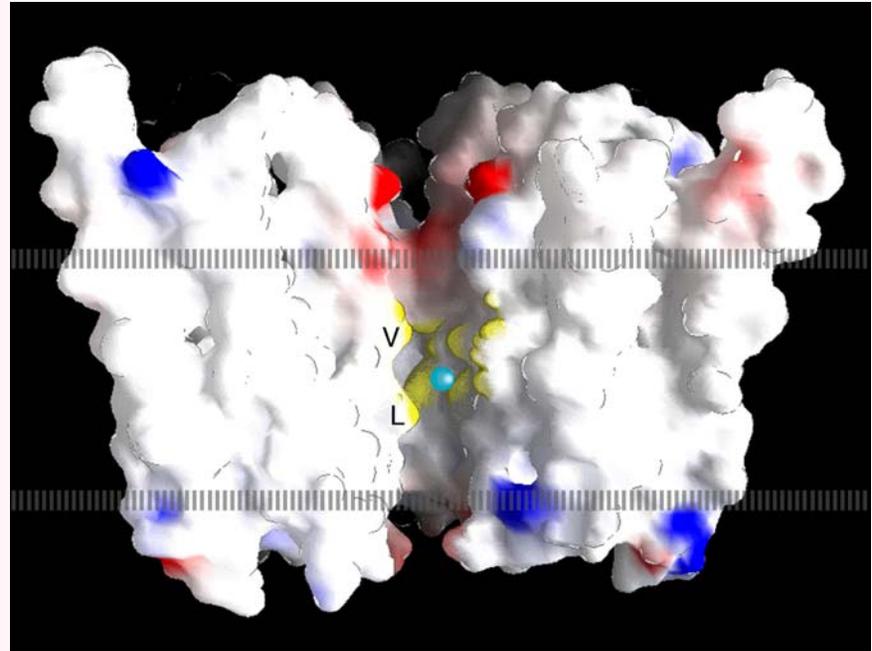
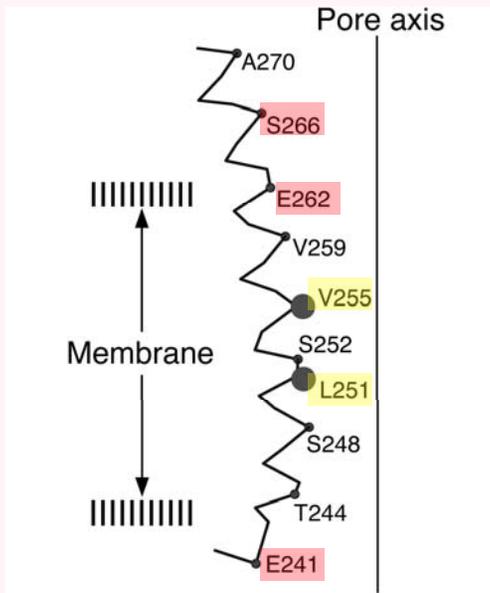


# Membrane-spanning portion

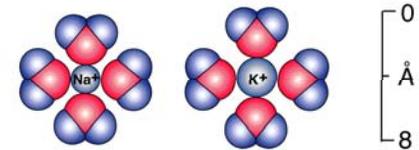
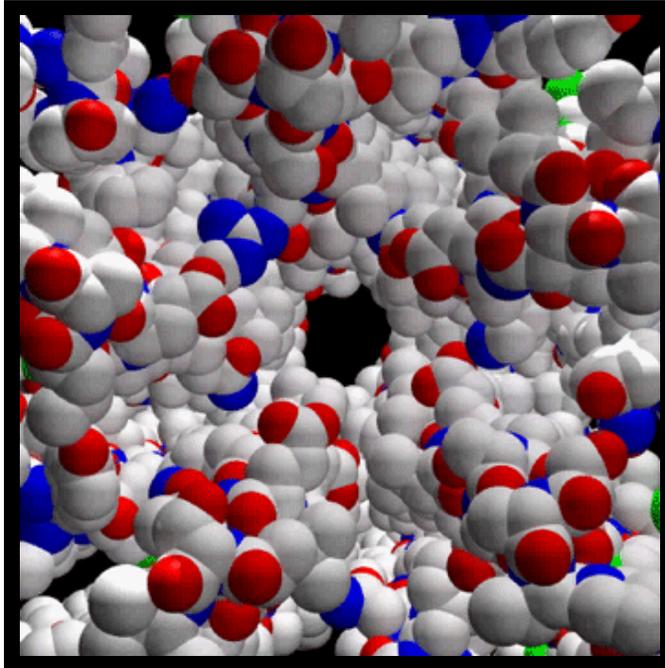


# Membrane-spanning portion

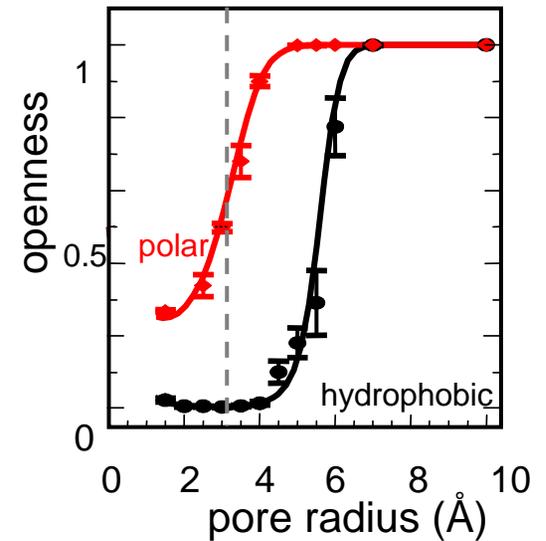
M2 ( $\alpha$  subunit)



# Hydrophobic girdle at middle of membrane

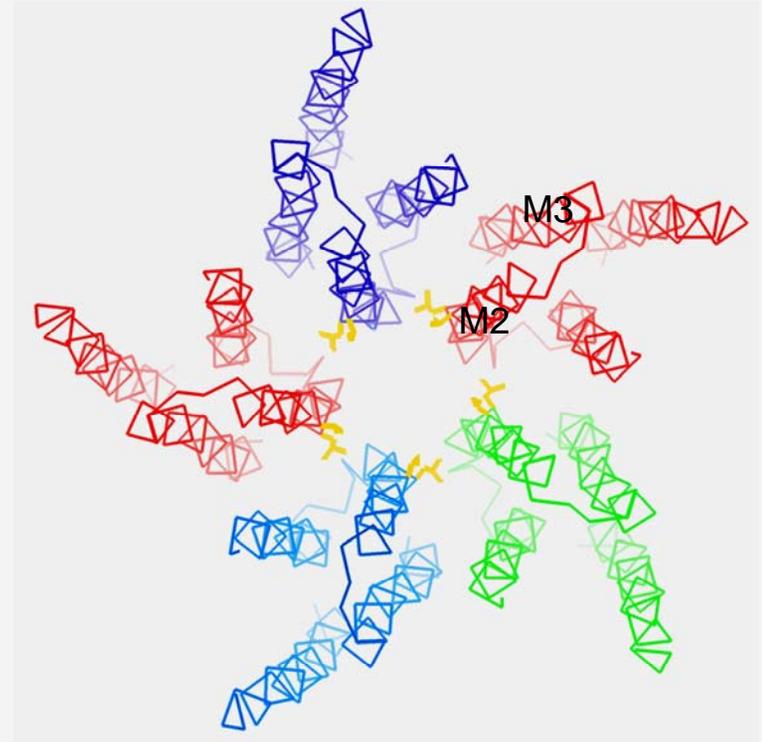
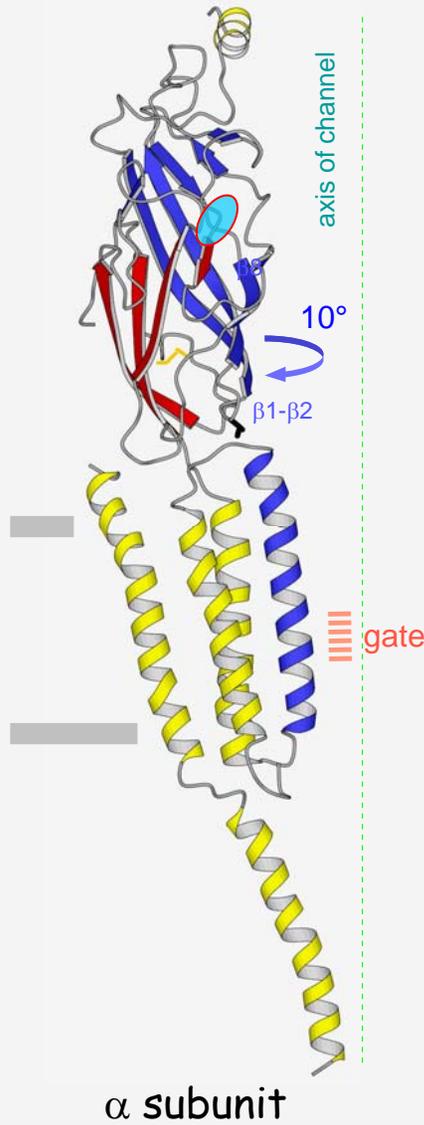


hydrophobic gating

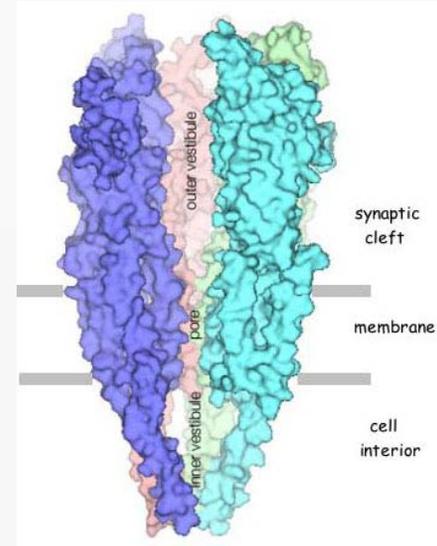
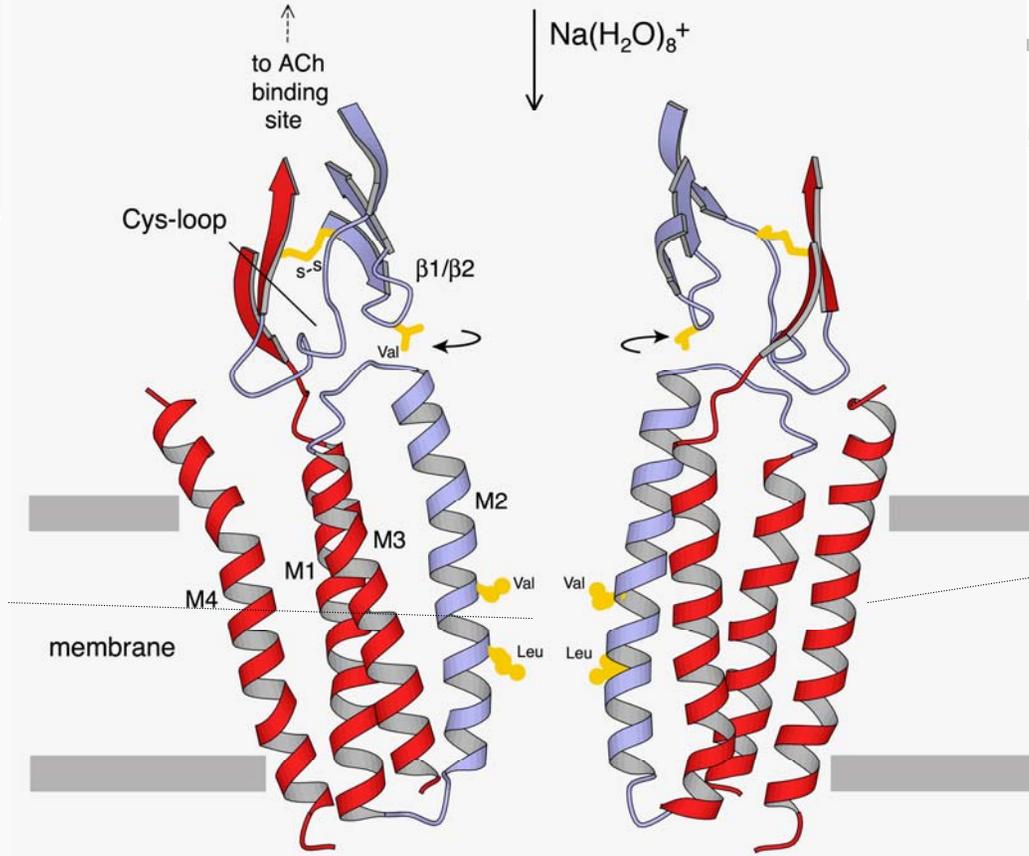
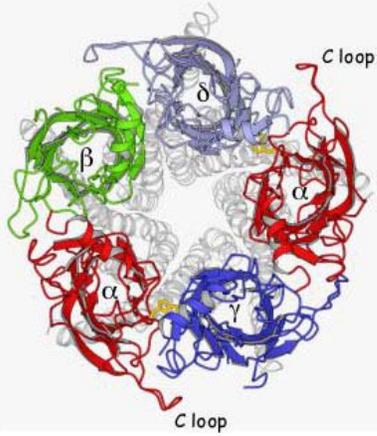


Beckstein, Biggin & Sansom (2001)  
*J. Phys. Chem. B* 105:12902

# ACh-induced rotations in the ligand-binding domain break open the gate



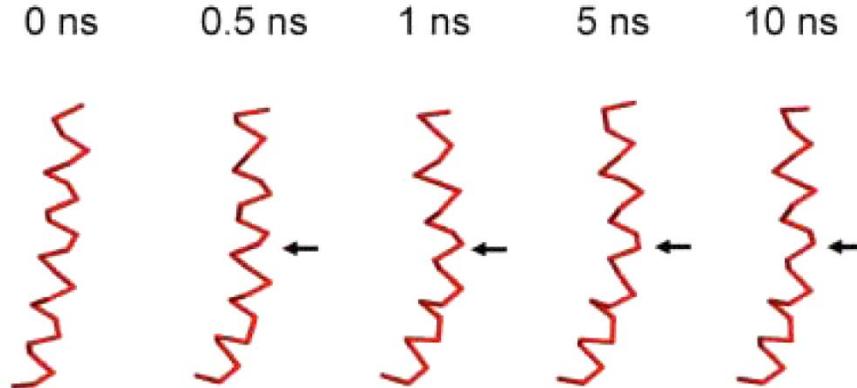
# Summary of proposed gating mechanism



Hydrophobic girdle:  
energetic barrier to  
ion permeation when  
channel is closed

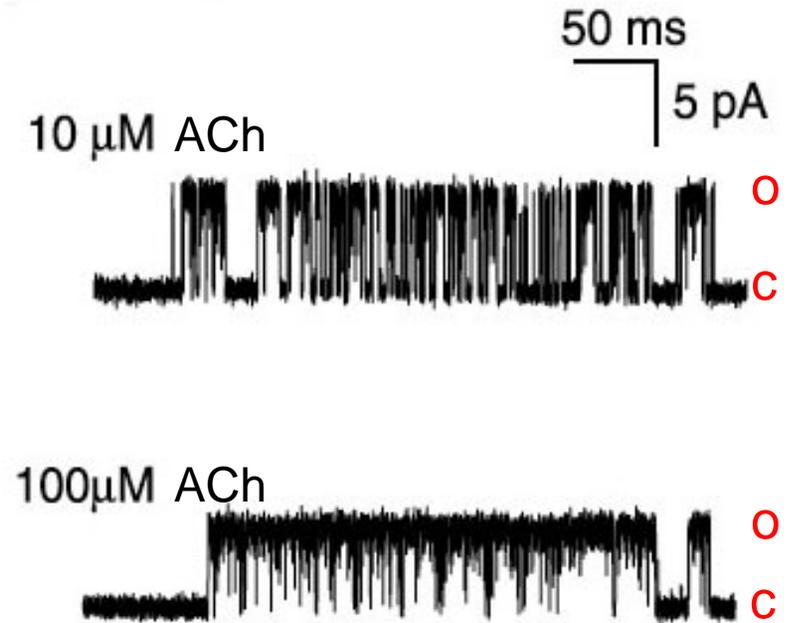
Protein scaffold (M1,  
M3, M4) shielding  
gating motions from  
lipids

# Do gating movements involve helix bending?



MD simulations on membrane-spanning portion of ACh receptor

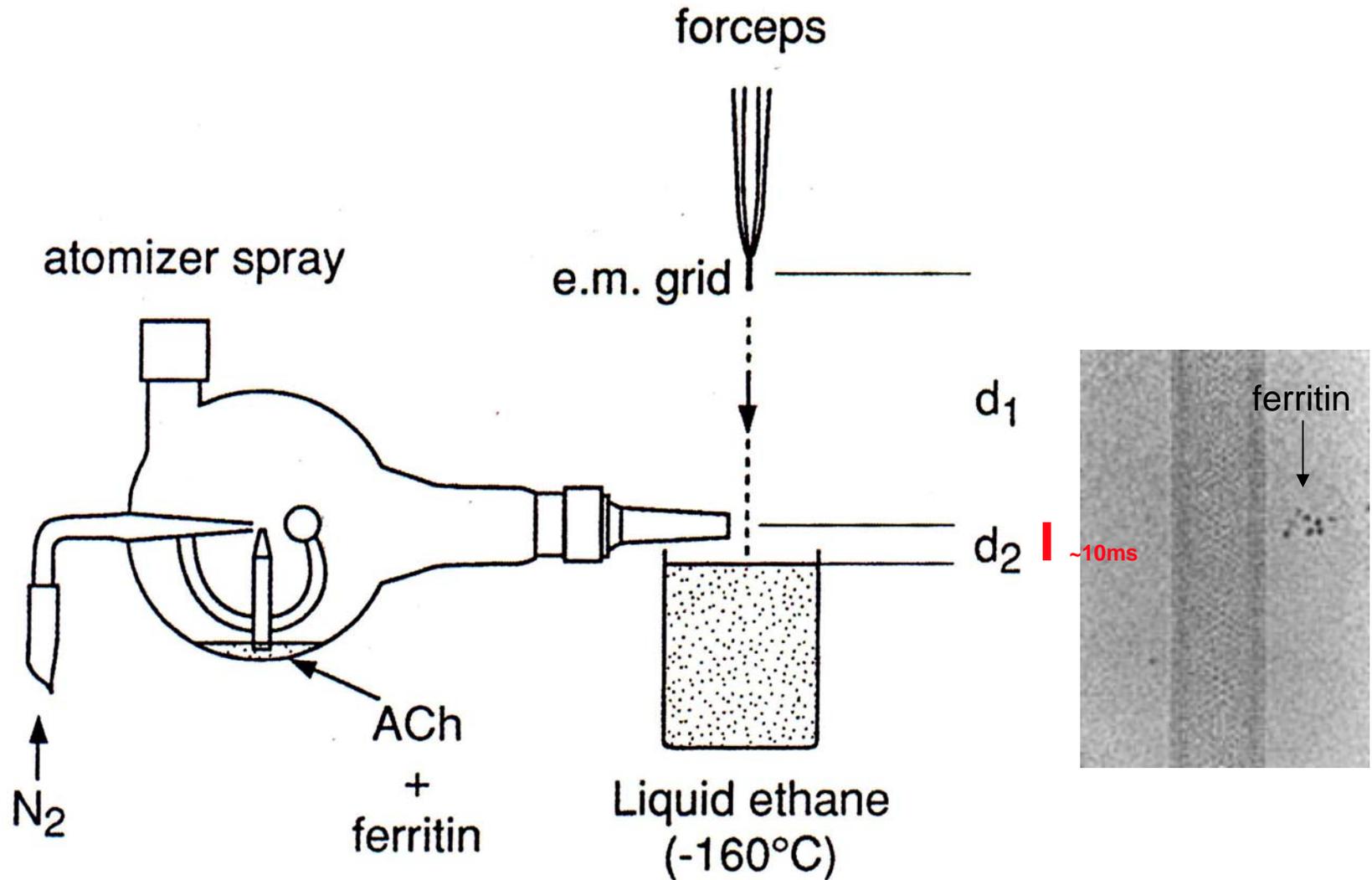
(Hung, Sansom et al., Biophys. J. 88: 3321-3333 (2005))



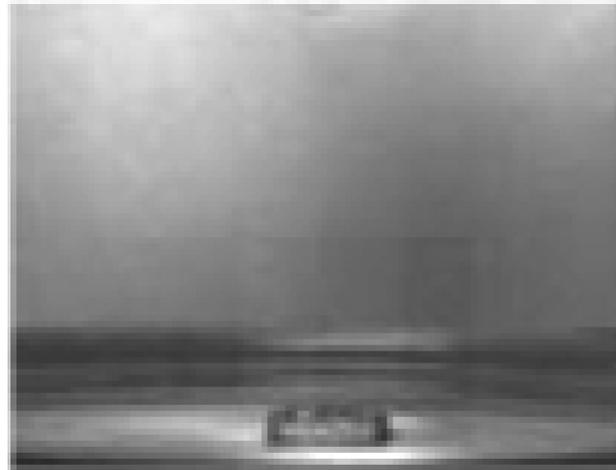
Electrophysiological recordings

Wang, Sine et al., Nat. Neurosc., 2: 226-233 (1999)

# Catching the gating movement by plunge-freezing



# Spread of droplet over a thin aqueous film



Manzello & Yang,  
Exps. in Fluids, 32: 580-589 (2002)

2 ms

Measurements from  $1\ \mu\text{m}$  droplet, after 10 ms:

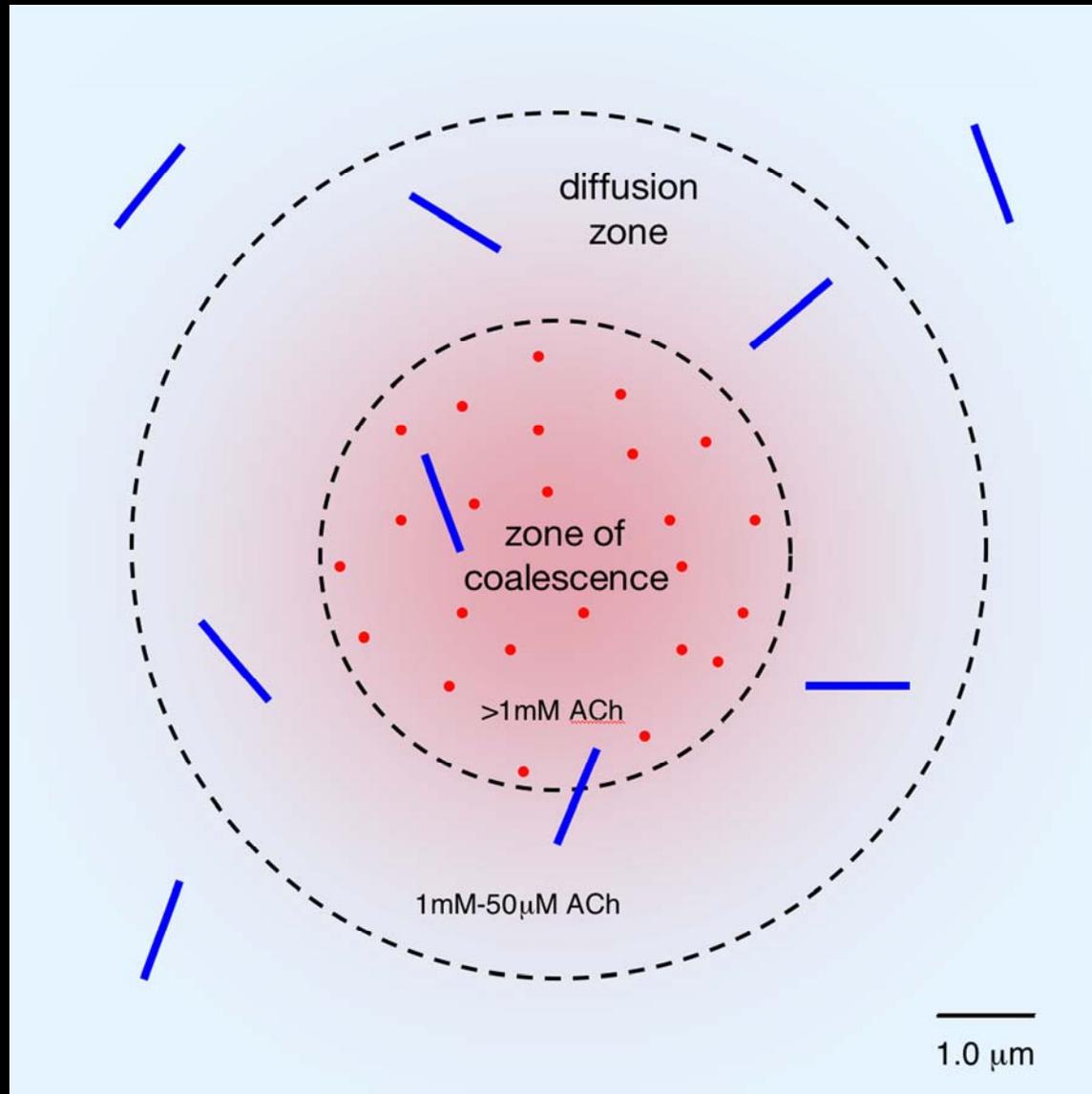
(Berriman & Unwin, Ultramicroscopy 56: 241-252 (1994))

Zone of coalescence extends to radius of  $\sim 3\ \mu\text{m}$

Diffusing ions extend to radius of  $\sim 7\ \mu\text{m}$

Estimated diffusion distance for ions ( $2(Dt)^{1/2}$ ):  $9.0\ \mu\text{m}$

# 1 $\mu\text{m}$ droplet after 10 ms



# Data collection

$P = RISHFP$

R = sample from a suitable *Torpedo* Ray (~1 in 50)

I = good thickness of Ice on em grid ( $\pm 200\text{\AA}$ )

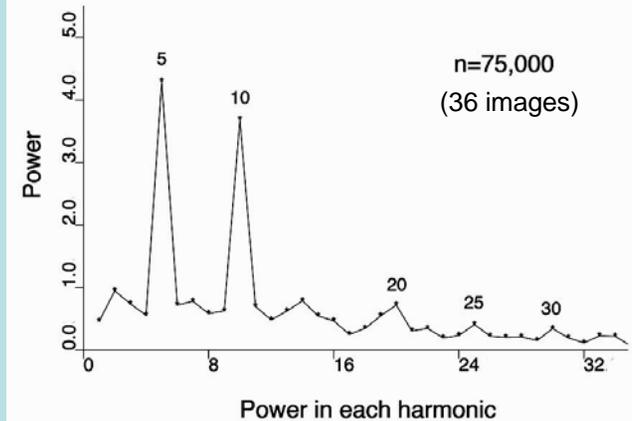
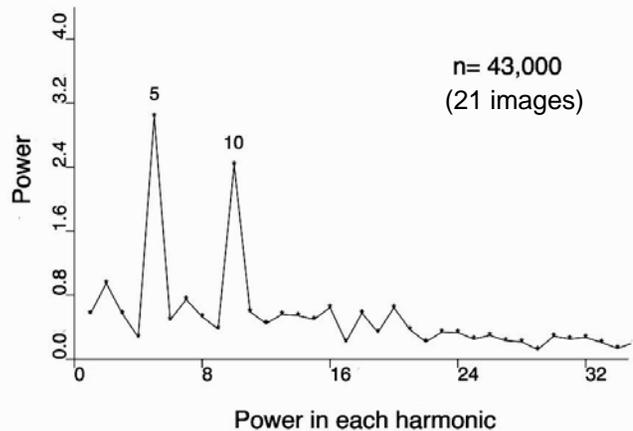
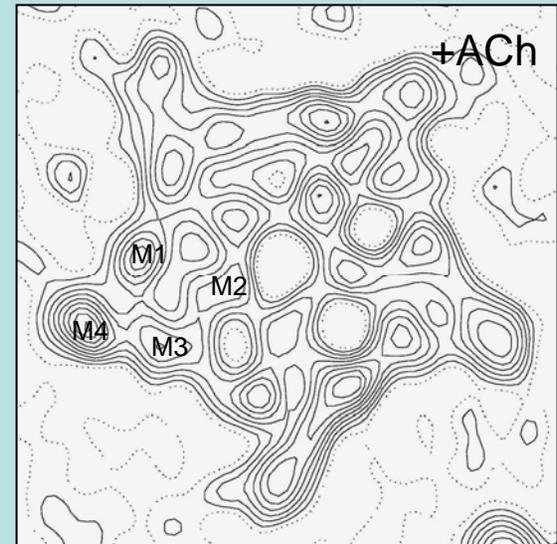
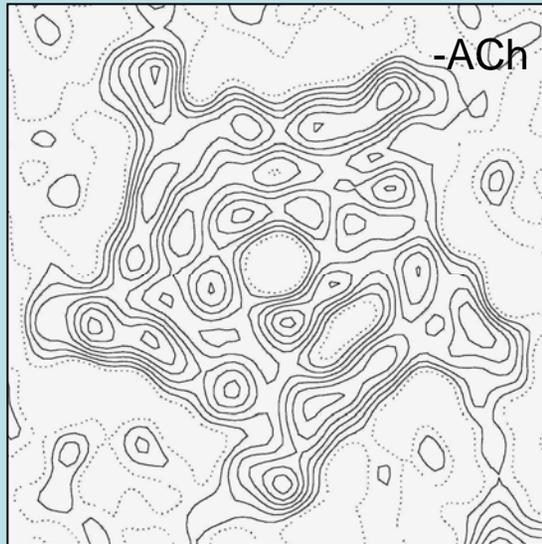
S = Spray droplet lands appropriate distance from tube

H = tube is straight, over a Hole in the support film

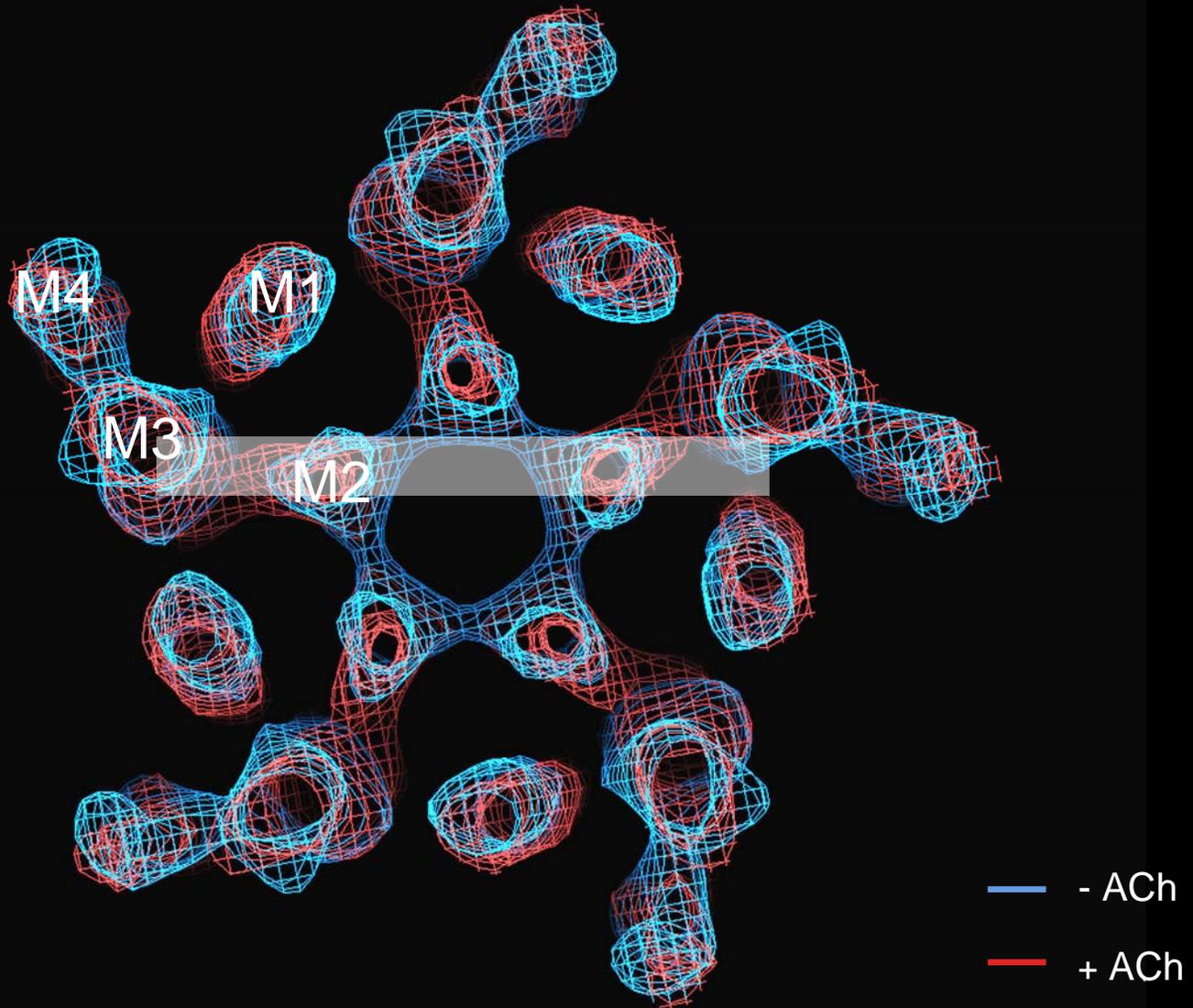
F = tube belongs to a suitable helical Family

P = microscope records a perfect Picture

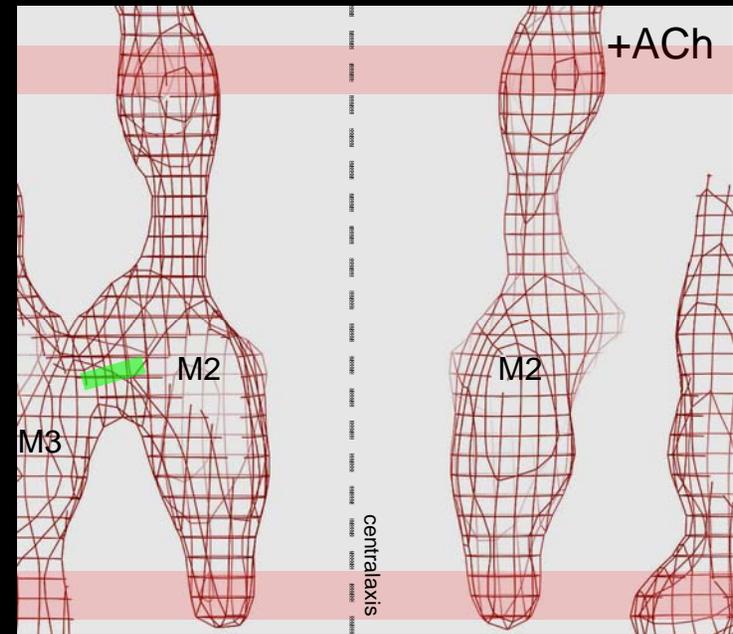
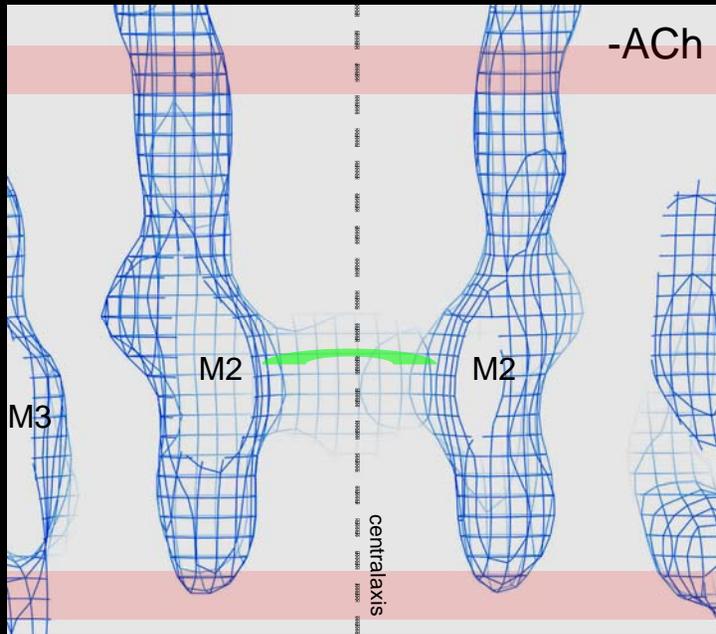
# Comparison of +ACh with -ACh images (so far) (-15,5) family; $\sim 6\text{\AA}$ resolution



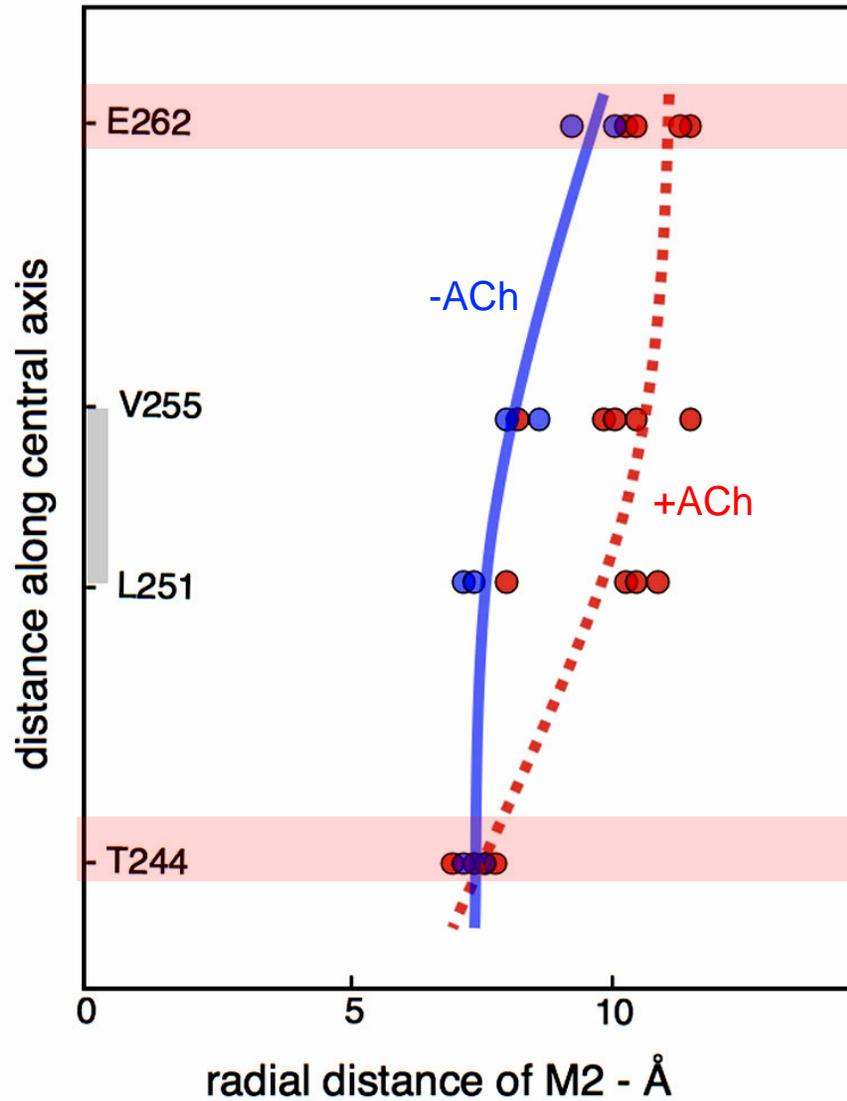
# Slab through upper leaflet of lipid bilayer



# Central sections normal to plane of lipid bilayer

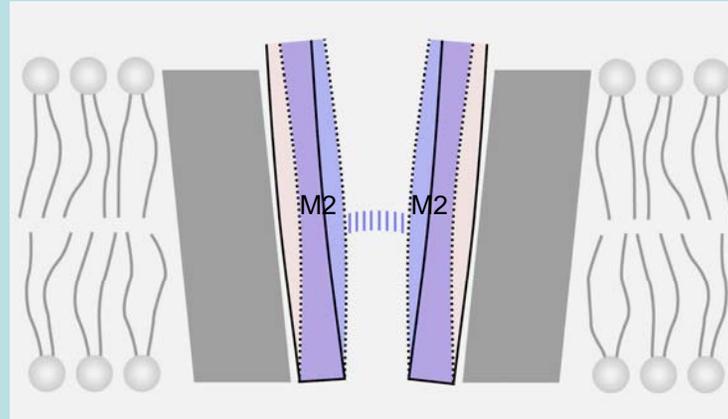


Radial distance of M2 from central axis measured from averages of nine images (n= $\sim$ 18,000)

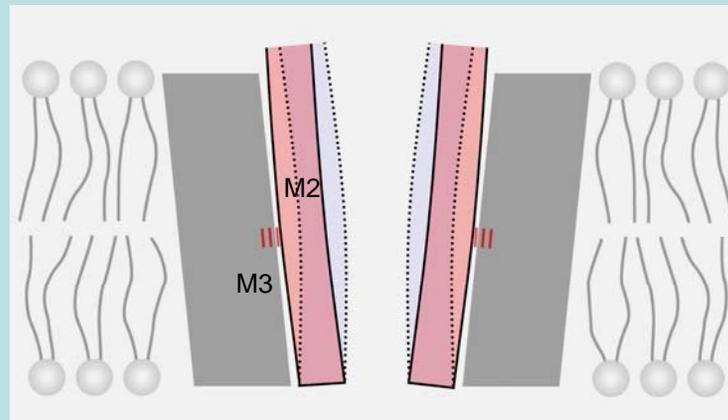


# Tentative Conclusion

Closed channel: stabilised by interactions between inner helices (and by ligand-binding domain)



Open channel: stabilised by interactions between inner helices and outer wall





Rameen  
Beroukhim



Yoshi

Atsuo  
Miyazawa