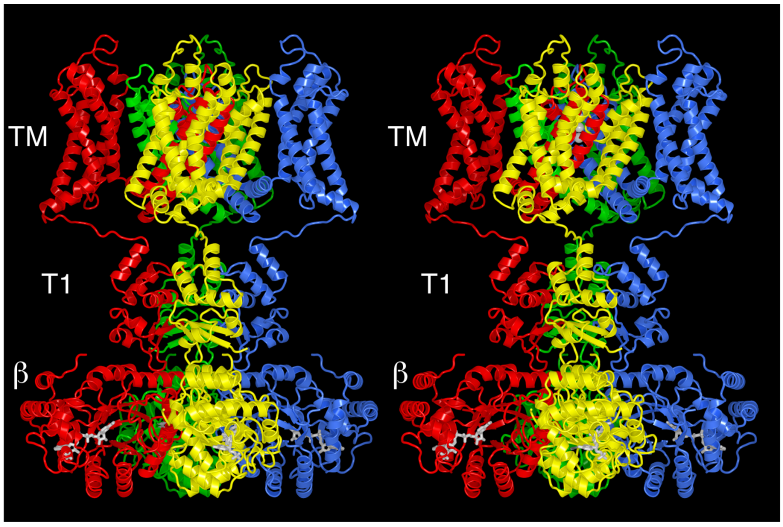
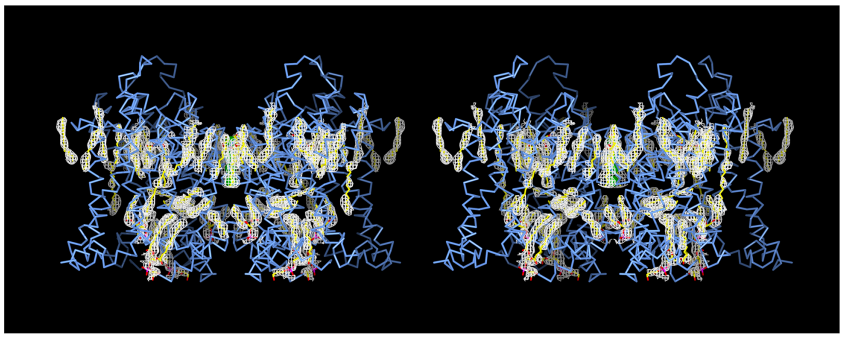
SUPPLEMENTARY INFORMATION



Supplementary Figure 1. | Overall structure of the channel-β subunit complex. A ribbon representation from the side with the extracellular solution 'above' and the intracellular solution 'below', shown in stereo. Each subunit of the channel is colored uniquely. The β subunits are colored according to the channel subunit they contact. The NADP+ cofactor bound to each β subunit is drawn as gray sticks. TM indicates the integral membrane component of the complex.



Supplementary Figure 2. | Electron density for lipid molecules. The view is of the transmembrane region of the channel from the side (extracellular solution 'above' and the intracellular solution 'below'), in stereo. The channel is drawn as blue α-carbon trace. Electron density for lipid molecules is drawn as white mesh. The lipid molecules are shown as sticks and colored according to atom type (carbon, yellow; oxygen, red; phosphorous, magenta). Phases for the map were calculated by removing the lipid molecules from the coordinates and refining these modified coordinates using a simulated annealing protocol in the program CNS (38). This procedure, which is used to generate a 'simulated annealing omit map', minimizes bias in the map. The map has Fourier coefficients 3F(observed) - 2F(calculated), and was calculated from 50-2.4 Å, contoured at 1.0σ, and drawn around the lipid molecules.

Supplementary Table | Data collection and refinement statistics

Data collection			
Spacegroup	$P42_12$		
Cell parameters (Å)	144.0, 144.0, 284.4		
Source	NSLS X-29		
Resolution (Å)	50.0 – 2.4		
Wavelength (Å)	1.08 Å		
No. of reflections (total)	278,768		
No. of reflections (unique)	112,726		
Completeness (%)	96.0 (86.3) ‡		
R_{sym} (%) *	6.4 (43.6)		
I/σ	13.8 (1.4)		
Refinement (50-2.4 Å)			
No. of reflections	104,891	No. of atoms	11,816
No. of molecules/ASU	2	R_{work}/R_{free} (%) §	21.2/24.4
Bond lengh / angle †	0.01 Å /1.4 ^{o}		
Ramachandran	99.8 % (allowed region) / 0.02% (disallowed region)		
Average protein B-factors			
T1/β	molecule 1: 37.2 $Å^2$; molecule 2: 41.2 $Å^2$		
pore	molecule 1: 45.8 $Å^2$; molecule 2: 71.0 $Å^2$		
voltage sensor	molecule 1: 64.0 $Å^2$; molecule 2: 148.0 $Å^2$		
No. and average B-factors			
waters	molecule 1: 193 waters, 41.9 $Å^2$		
	molecule 2: 126 waters, 39.0 $Å^2$		
lipid molecules	molecule 1: 16 lipids (210 atoms), 84.1 $Å^2$		
	molecule 2: 1 lipid (22 atoms), 88.4 $Å^2$		

* $R_{sym} = \Sigma \mid I_i - < I_i > \mid / \Sigma I_i$, where $< I_i >$ is the average intensity of symmetry-equivalent reflections

§ R factor = $\Sigma \mid F(obs) - F(calc) \mid / \Sigma F(obs)$; 5% of the data that were excluded from refinement were used in the R_{free} calculation.

† r.m.s.d of bond is the root-mean-square-deviation of bond angle and length

‡ parentheses indicate outer resolution shell (2.5 - 2.4Å).