

Supplemental information

**Structural basis for channel conduction
in the pump-like channelrhodopsin ChRmine**

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Table S1. Cryo-EM data collection and refinement statistics, Related to STAR Methods

	ChRmine PDB: 7W9W EMDB: EMD-32377	ChRmine-Fab02 EMDB: EMD-32378
Data collection and processing		
Microscope		Krios
Magnification		105,000
Voltage (kV)		300
Electron exposure (e ⁻ /Å ²)		46
Defocus range (μm)		0.8 – 1.6
Pixel size at detector (Å/pixel)		0.83
Symmetry imposed		C3
Initial particle images (no.)		2,958,159
Final particle images (no.)		185,895
Map resolution (Å)	2.02	2.12
FSC threshold	0.143	0.143
Map sharpening <i>B</i> factor (Å ²)	-35.7	-38.1
Refinement		
Initial model used (PDB code)	3UG9	
Model composition (monomer)		
Protein residues	2204	
Retinal	20	
Lipids	128	
Waters	48	
<i>B</i> factors (Å ²)		
Protein	58.4	
Retinal	46.8	
Lipids	109	
Water	52.9	
R.m.s. deviations		
Bond lengths (Å)	0.015	
Bond angles (°)	2.02	
Validation		
MolProbity score	0.85	
Clashscore	1.27	
Poor rotamers (%)	0.88	
Ramachandran plot		
Favored (%)	98.51	
Allowed (%)	1.49	
Outlier (%)	0	