Supplementary Table 1: Using Image Lab software (Bio-rad), the PE band intensities of MscS samples in Lanes (1-3) of the TLC chromatogram (Fig 2C) were quantified using PE standard (Lane 5). The Quantity toolbox was used to carefully define the PE bands, including the reference band (Lane 5) and to enable for background correction. The signal intensities obtained were used to quantify the PE content in each band. Molar ratios of PE to protein were then calculated.

Lane	Sample	Protein	Volume	PE	Relative	Molar ratio of
no.		content	(Intensity)	(nmoles)	Quantity	PE: MscS
		(nmoles)				monomer
1	238 μg MscS-DDM	7.3	2366980	3.86	2.314035	0.53:1
2*	280 μg MscS-DDM*	8.7	757619	1.24	0.740672	0.14:1
3	305 μg MscS-Fos-	9.5	3042969	4.96	2.974903	0.52:1
	14					
4	-	-	-		-	-
5	1.2 μg PE	-	1022880	1.67	1.000000	-
6	8.0 μg <i>E. coli</i> lipids	-	4050540	6.61	3.959937	-

Supplementary Table 2: Fractional quenching of tryptophan fluorescence. MscS mutants with tryptophan residues at different positions in a tryptophan-free background were reconstituted into either 100% DOPC or 100% BrPC. Fluorescence spectra were recorded and the fractional quenching was calculated from the fluorescence intensities at 340 nm as $FrQ=(F_0-F)/F_0$ where F_0 is the intensity for the DOPC sample and F for the BrPC sample. Data were obtained in the same way for reconstitution in 80% DOPE/20% DOPG or their brominated equivalents (right column). Mean values are given with standard deviations

MscS mutant	Fractional DOPC	quenching Fractional PE/PG	quenching
A103W	0.75 ± 0.08		
V107W	0.57 ± 0.06		
L111W	0.68 ± 0.21	0.80 ± 0.06	
A119W	0.88 ± 0.04	0.90 ± 0.02	
L123W	0.49 ± 0.07	0.56 ± 0.05	
Controls			
M47W	0.64 ± 0.09		
L105W	0.32 ± 0.04		
Q203W	-0.01 ± 0.12		
W240	0.01 ± 0.01		

Lipid headgroup						
(PDB code)	Total number of carbons	Volume (A ³)				
LHG(1JB0)_5001	32	1599				
PE (1P84)_710	32	1480				
PE(1P84)_711	25	1241				
PE(3M9I)_301	13	849				
PE(3M9I)_302	22	1205				
PE(3M9I)_303	27	1318				
PE(3M9I)_304	25	1208				
PE(3M9I)_305	23	1180				
PE(3M9I)_306	33	1496				
PE(3M9I)_307	25	1230				

Supplementary Table 3: Calculated lipid volumes for existing PDB x-ray structures, containing resolved lipids ,using Molspace, a VMD software plug-in