Table S1. Data collection and refinement statistics for $ALIX_{Bro1}$–CHMP4 complexes

Statistic	CHMP4A	CHMP4B	CHMP4C
Data collection			
Space group	C2	C2	C2
Cell dimensions			
a, *b*, *c*, Å	120.7, 62.7, 76.1	120.5, 62.6, 76.1	120.9, 62.4, 76.4
b, deg.	122.1	121.5	121.6
Resolution, Å	50.0–2.15 (2.23–2.15)	50.0–2.1 (2.18–2.10)	50.0–2.02 (2.09–2.02)
R_{sym}	0.063 (0.334)	0.067 (0.413)	0.066 (0.596)
$I/\sigma(I)$	19 (1.8)	14 (1.7)	9 (1.5)
Completeness, %	94.9 (75.1)	92.3 (67.6)	95.5 (81.0)
Redundancy	9.5 (3.8)	7.2 (4.6)	6.6 (4.4)
Refinement			
Resolution, Å	50.0–2.15 (2.21–2.15)	50.0–2.10 (2.154–2.10)	50.0–2.02 (2.07–2.02)
Reflections, no.	25,024	26,458	30,381
R_{work}	0.214 (0.305)	0.228 (0.326)	0.243 (0.333)
R_{free}	0.284 (0.344)	0.290 (0.386)	0.291 (0.411)
Number of atoms			
Protein	2911	2953	2905
Ligand/ion	6	6	6
Water	127	90	56
$\langle B \rangle$-factors			
Protein	33.2	35.3	34.0
Ligand/ion	82.5	78.9	85.8
Water	49.9	55.0	51.3
rmsd			
Bond lengths, Å	0.019	0.017	0.016
Bond angles, deg.	1.710	1.653	1.542
Ramachandran plot, %			
Most favored	89.7	88.0	90.6
Additionally allowed	9.7	10.8	8.6
Generously allowed	0.3 (Q27)	1.2 (K207,Q27,S31,C40)	0.3 (K207)
Disallowed	0.3 (Q88)	0.0	0.6 (Y29, E34)

Diffraction data from one crystal were used to determine each structure. This includes the CHMP4A complex, for which data were collected in two separate sweeps from different beamlines. Values in parentheses refer to the high-resolution shell.