Table S1. Data Collection and Refinement Statistics

	$ALIX_{Bro1-V}$ [a]	$ALIX_{Bro1}$ [a]	$ALIX_V$ [a]	
Data Collection [b]				
			Crystal 1	Crystal 2
Space Group	C2	C2	$P2_1$	$P2_1$
Cell Parameters (Å)	a = 144.0	a = 120.7	a = 63.9	a = 63.2
	b = 98.5	b = 63.2	b = 50.0	b = 49.8
	c = 72.2	c = 76.4	c = 130.2	c = 129.6
	ß = 105.6	ß = 122.1	ß = 101.1	ß = 101.2
Wavelength (Å)	1.1	1.54180	0.9792	0.9792
Resolution (Å)	30-3.30	30-2.55	50-2.60	50-2.60
Outer Shell (Å)	3.42-3.30	2.64-2.55	2.69-2.60	2.69-2.60
Number of reflections				
Total	727,803	178,235	1,048,903	1,677,930
Unique	14,236	15,487	23,601	22,229
Completeness (%)	94.6 (64.9)	96.5 (79.3)	92.4 (64.0)	89.8 (57.7)
R_{sym} (%)[b]	8.7 (28.8)	5.3 (24.0)	7.8 (20.4)	10.6 (29.7)
Mean I/s(I)	21.1 (3.5)	19.6 (3.6)	12.3 (3.6)	16.1 (3.2)
Refinement				
R factor/R_{free} (%)[c,d]	23.5/31.7	20.8/27.4	22.8/30.2	
Nonhydrogen atoms				
Total	5486	2910	5489	
Solvent	0	79	91	
RMSD from ideal geometry [e]				
Bond lengths (Å)	0.009	0.016	0.010	
Bond angles (º)	1.153	1.544	1.293	
Average B-factor ($Å^2$)	140.7	60.3	48.5	
Ramachandran plot, nonglycine residue in				
Most favorable region (%)	83.7	88.8	93.9	
Additional allowed region (%)	15.7	10.3	6.0	
Generous allowed region (%)	0.6	0.9	0.2	
Disallowed region (%)	0.0	0	0.0	

Values in parenthesis are for the highest resolution shell.

[a] The $ALIX_{Bro1-V}$ construct crystallized comprises ALIX residues Met1-Arg698 preceded by the vector sequence GIDPFTH. Of these, ALIX residues 2-698 are ordered in the refined model. The $ALIX_{Bro1}$ construct comprises ALIX residues Met1-Val359 preceded by MHHHHHHHHHHSGQNLYFQGH, and ALIX residues 1-358 are ordered. The $ALIX_V$ construct comprises ALIX residues Pro360-Arg702 preceded by GIDPFTHM, and ALIX residues 361-702 (molecule A) and 362-702 (molecule B) are ordered.

[b] Data were collected from single crystals at beamline X29 at the National Synchrotron Light Source, Brookhaven National Laboratory ($ALIX_V$ and $ALIX_{Bro1-V}$) or on a rotating anode source ($ALIX_{Bro1}$). Data were integrated and scaled with the HKL package (Otwinowski and Minor, 1997).

[b] $R_{sym} = (|(\sum I - \langle I \rangle)|)/(\sum I)$, where $\langle I \rangle$ is the average intensity of multiple measurements.

[c] R factor = $\sum_{hkl}||F_{obs}(hkl)|| - F_{calc}(hkl)||/\sum_{hkl}|F_{obs}(hkl)|$

[d] R_{free} = the crossvalidation R factor for 5% of reflections against which the model was not refined (7% for $ALIX_{Bro1-V}$).

[e] Geometry was analyzed in PROCHECK (Laskowski et al., 1993)