Supplementary Table 1. Data collection and refinement statistics. Highest resolution shell is shown in parentheses.

Structure	SANT1	AntaXV	SAG1.5
Data collection			
Wavelength (Å)	1.0332	1.0332	1.0332
Space group	$C222_1$	$P2_12_12_1$	C2
Unit cell parameters *a,b,c* (Å) β	84.64, 110.88, 145.21	42.83, 79.84, 170.07	72.22, 158.93, 60.02 β=90.26°
Number of crystals	4	6	35
Number of reflections measured	67,988	133,741	353,034
Number of unique reflections	16,010	17,421	18,991
Resoltuion (Å)	50 – 2.80 (2.90– 2.80)	50 – 2.60 (2.69 – 2.60)	50 – 2.60 (2.69 -2.60)
R_{merge} (%)	12.0 (64.1)	9.1 (72.3)	12.9 (>100)
Mean I/σ(I)	11.8 (1.4)	35.0 (2.0)	21.4 (1.8)
Completeness (%)	94.5 (92.3)	94.4 (80.6)	87.5 (53.6)**
Redundancy	4.2 (4.3)	7.7 (6.3)	18.6 (14.3)
Refinement			
Resolution (Å) Number of reflections (test set)	50 – 2.80 15,986 (776)	50 – 2.61 17,377 (901)	50 – 2.60 (2.9, 2.5, 3.3)** 15,154 (755)
Rwork / Rfree	0.204 / 0.253	0.223 / 0.264	0.225 / 0.260
Number of atoms Protein Ligand Zn Lipids and other	 3,570 28 2 57	 3,519 33 1 23	 3,411 36 0 7
Mean Overall B value (Å^2) SMO BRIL Ligand Zn Lipids and other	 80.6 82.2 73.6 71.5 96.9	 90.9 123.4 71.7 129.2 85.3	 53.7 87.6 41.0 n/a 58.1
R.m.s. deviations Bond lengths (Å) Bond angles (°)	 0.010 1.08	 0.010 0.97	 0.010 1.07
Ramanchandran plot statistics (%)*			
Favored regions Allowed regions Disallowed regions	94.7 5.3 0	97.1 2.9 0	94.8 5.2 0

* As defined in MolProbity

** Due to the anisotropic diffraction data, the completeness of the highest resolution shell is low. The resolution limits here are for the a*, b* and c* axes.