Table S1 related to Figure 3 Data collection and refinement statistics

	Apo-RUMGNA_01526	S-aFMT-RUMGNA_01526
Wavelength (Å)		
Resolution range (Å)	79.37 - 2.804 (2.905 - 2.804)	52.44 - 2.84 (2.942 - 2.84)
Space group	P 1	P 41 21 2
Unit cell	58.63 145.77 165.07 72.85 88.84 88.3	135.03 135.03 249.8 90 90 90
Total reflections	218936 (22174)	730528 (73919)
Unique reflections	121102 (12262)	55248 (5448)
Multiplicity	1.8 (1.8)	13.2 (13.6)
Completeness (%)	94.70 (96.28)	99.97 (99.96)
Mean I/sigma(I)	9.54 (2.09)	25.80 (3.80)
Wilson B-factor	41.16	54.76
R-merge	0.08033 (0.363)	0.119 (0.8652)
R-meas	0.1136	0.1238
CC1/2	0.99 (0.73)	0.999 (0.881)
CC*	0.998 (0.919)	1 (0.968)
R-work	0.2311 (0.3077)	0.2098 (0.2745)
R-free	0.2568 (0.3623)	0.2423 (0.3494)
Number of atoms	29598	15146
macromolecules	29064	14886
ligands	120	184
water	414	0
Protein residues	3696	1889
RMS(bonds)	0.002	0.007
RMS(angles)	0.67	0.64
Ramachandran favored (%)	96	95
Ramachandran outliers (%)	0	0.053
Clashscore	3.03	3.04
Average B-factor	21.2	36.4
macromolecules	21.3	36.2
ligands	41.8	47.9
solvent	9.7	

Statistics for the highest-resolution shell are shown in parentheses.