Supplementary Data Table 1. Data collection and refinement statistics

	RBD-AZD8895	RBD-AZD1061
Data collection		
Space group	$P2_1$	$P2_1$
Cell dimensions		
a, *b*, *c* (Å)	44.12, 81.58, 101.16	97.15, 152.52, 199.24
α, β, γ (°)	90.00,94.60,90.00	90.00,94.74,90.00
Resolution (Å)	43.98(2.50)	35.21(3.00)
R_{merge}	0.046(0.245)	0.231(0.810)
CC1/2	0.0982(0.945)	0.986(0.89)
$I / \sigma I$	19.2(4.8)	6.4(2.3)
Completeness (%)	99.9(99.6)	99.9(100)
Redundancy	3.7(3.7)	7.7(7.7)
Refinement		
Resolution (Å)	43.98-2.50	35.21-3.00
No. reflections	93185	889918
R_{work} / R_{free}	0.185/0.231	0.215/0.273
No. atoms		
Protein	4794	32639
Ligand/ion	50	96
Water	220	144
B-factors		
Protein	47.94	52.23
Ligand/ion	76.52	80.51
Water	42.68	32.83
R.m.s. deviations		
Bond lengths (Å)	0.0030	0.0023
Bond angles (°)	0.563	0.598

*One crystal for each dataset.
*Values in parentheses are for highest-resolution shell.