

Table S1. Data collection and refinement statistics

	RBD-tr2: aRBD-2-7	RBD: aRBD-5
Data collection	BL02U1	BL19U1
Wavelength (Å)	0.97918	0.97852
Space group	<i>P</i> 6 ₅ 22	<i>P</i> 2 ₁ 2 ₁ 2 ₁
Unit cell parameters		
a, b, c (Å)	154.46, 154.46, 257.92	53.44, 87.70, 89.06
α, β, γ (°)	90, 90, 120	90, 90, 90
Resolution range (Å)	50.00-3.20 (3.37-3.20)	45.82-1.80 (1.85-1.80)
Monomers in an asymmetric unit	2	1
Unique reflections	30769 (4397)	38650 (2755)
Average redundancy	18.5 (19.0)	12.9 (12.4)
Completeness (%)	100 (100)	97.8 (95.4)
<i>R</i> _{merge} (%) ^a	15.3 (126.1)	10.2 (242.4)
<i>I</i> /σ (<i>I</i>)	20.3 (3.2)	13.14 (1.17)
Wilson B factor (Å ²)	84.6	33.1
Refinement Statistics		
Resolution range (Å)	50.00-3.20	45.82-1.80
<i>R</i> _{work} (%) ^b	20.62	18.63
<i>R</i> _{free} (%) ^c	26.22	22.62
RMSD bond lengths (Å)	0.0078	0.016
RMSD bond angles (°)	1.2814	1.370
Mean B factors (Å ²)		
Protein	97.58	48.96
Ligand	136.82	78.43
Water	72.62	52.18
No. of non-hydrogen protein atoms	6945	2536
No. of ligand atoms	75	14
No. of water oxygen atoms	56	175
Ramachandran plot ^d		
Favored (%)	96.0	96.94
Outliers (%)	0	0.31
PDB entry	7FH0	7VOA

^a $R_{\text{merge}} = \sum_{hkl} \sum_i |I_i(hkl) - \langle I(hkl) \rangle| / \sum_{hkl} \sum_i I_i(hkl)$, where $I_i(hkl)$ is the intensity of *i*th observation and $\langle I(hkl) \rangle$ is the mean value for reflection *hkl*.

^b $R_{\text{work}} = \sum_{hkl} ||F_{\text{obs}}| - |F_{\text{calc}}|| / \sum_{hkl} |F_{\text{obs}}|$, where F_{obs} and F_{calc} are the observed and calculated structure-factor amplitudes, respectively.

^c R_{free} is calculated same as R_{work} with 5% reflections, which were selected randomly from the refinement process.

^dThe categories were defined by PROCHECK. The numbers in brackets are the parameters for the “Resolution range,” “Unique reflection,” “Average redundancy,” “Completeness,” “ R_{merge} ,” and “ $I/\sigma(I)$ ” of the highest resolution shell.