Table 1

Crystal	DBM RyR NTD
λ for data collection (Å)	0.9795
Data collection	
Space group	P61
Cell deminsion (Å)	
a, b, c (Å)	170.13，170.13，51.76
α, β, γ, (°)	90.00, 90.00, 120.00
Resolution	44.22-2.84 (2.94-2.84)
Rmerge†	0.082 (1.393)
Average I/σ(I)	18.9 (1.2)
Completeness (%)	99.66(97.24)
Redundancy	6.6(6.5)
Z	2
Refinement	
Resolution	44.24–2.84 Å
No. of reflections	20,497
R_{factor}/R_{free} (10% data)	0.214/0.245
RMSD length (Å)	0.004
RMSD angle (°)	0.702
No. of atoms	
Protein	2559
Ligands	7
Water	1
Ramachandran plot (%)	
Most favored	92.58
Additionally allowed	7.42

Values in parentheses refer to the highest resolution shell.