

Table S3: Data collection and refinement statistics.

Data collection	
X-ray generator	Rigaku
Space group	H3
Cell dimensions	
a, b, c (Å)	103.63, 103.63, 49.29
α, β, γ (°)	90.000, 90.000, 120.000
Wavelength (Å)	1.54187
Resolution (Å)	25.91~2.60 (2.64~2.60)
Observed reflections	34065
Unique reflections	6039 (281)
R_{sym} (%)	0.14(0.83)
$I/\sigma(I)$	14.5(2.4)
Completeness (%)	99.9(100)
Redundancy	5.6(5.6)

Refinement	
Resolution Range (Å)	25.9~2.6 (3.27~2.60)
No. reflections	6,026
R_{work} (%)	18.2
R_{free} (%)	24.9
No. atoms	
protein	1348
water	50
B-factors (Å ²)	
protein	34.3
water	33.0
R.m.s. deviations	
Bond lengths (Å)	0.010
Bond angles (°)	1.146
Ramachandran plot	
Most favored and allowed regions	100.0
Disallowed regions	0

Values in parentheses are for highest-resolution shell.