

Supplementary information, Table S1
Summary of diffraction data and structure refinement statistics

Data Collection Statistics

Beam Line	Beam line BL17U1, SSRF
Space Group	P1
Wavelength (Å)	1.0
Number of Reflections	62,721 (3,132)
Cell dimensions	a=43.19 Å, b=50.51 Å, c=61.84 Å α=98.85°, β=108.74°, γ=108.10°
Resolution (Å)	1.55 (1.58-1.55)
R _{sym} (%)	6.2 (45.4)
I/σ(I)	20.8 (3.0)
Completeness (%)	96.0 (94.3)
Redundancy	3.9

Refinement Statistics

Resolution (Å)	50.0-1.55 (1.57-1.55)
No. Reflections	62,714 (2,486)
Rwork/Rfree %	16.9/19.0 (24.5/29.2)
All protein atoms	3214
R.m.s deviations	
Bond lengths (Å)	0.004
Bond angles (°)	0.987
Ramachandran (%) (from COOT)	
Preferred region	93.13
Allowed region	6.87

Highest resolution shell is shown in parenthesis