Data Collection	
PDB entry	4OU0
Wavelength (Å)	0.97857
Space group	P 65
Cell dimensions	
a, b, c (Å)	69.556, 69.556, 23.567
α, β, γ (°)	90, 90, 120
Resolution range (Å)	50-1.4
R-merge	0.077 (0.357)
Mean I/sigma(I)	14.46 (4.51)
Completeness (%)	98.41 (89.03)
Redundancy	7.6 (6.1)
Refinement	
Resolution (Å)	30.12-1.4 (1.45-1.4)
Number of reflections	97592
Unique reflections	12921 (1161)
R-work	0.1969 (0.2400)
R-free	0.2380 (0.3095)
Number of non-hydrogen atoms	581
Protein	528
Water	53
Protein residues	66
B-factor ($Å^2$)	
Average B-factor	35.4
Protein	34.8
Water	40.76
Bonds (RMS deviation)	
Bond Lengths (Å)	0.003
Bond Angles (°)	0.8
Ramachandran plot (%)	
Favored (%)	97
Allowed (%)	3
Outliers (%)	0
*Values in parentheses refer to those in the highest-resolution shell	

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