Table S1. Data collection and refinement statistics.

	PDB ID: 5JL4
Wavelength	
Resolution range	43.04 - 1.758 (1.821 - 1.758)
Space group	P 1
Unit cell	45.192 45.346 49.04 63.957 68.045 62.434
Total reflections	154054 (8489)
Unique reflections	29814 (2580)
Multiplicity	5.2 (3.1)
Completeness (%)	0.96 (0.90)
Mean I/sigma(I)	36.27 (9.40)
Wilson B-factor	21.07
R-merge	0.05641 (0.1798)
R-meas	0.06241 (0.2133)
CC1/2	0.998 (0.961)
CC*	1 (0.99)
Reflections used in refinement	28961 (2425)
Reflections used for R-free	1919 (159)
R-work	0.1591 (0.2143)
R-free	0.1918 (0.2872)
CC(work)	0.968 (0.918)
CC(free)	0.957 (0.872)

Number of non-hydrogen atoms	2623
macromolecules	2324
ligands	20
Protein residues	294
RMS(bonds)	0.010
RMS(angles)	0.95
Ramachandran favored (%)	99
Ramachandran allowed (%)	0.67
Ramachandran outliers (%)	0
Rotamer outliers (%)	0.4
Clashscore	4.86
Average B-factor	26.27
macromolecules	24.92
ligands	56.60
solvent	35.34

Statistics for the highest-resolution shell are shown in parentheses.