Supplementary Table 1: Crystallography data collection and refinement statistics.

Data collection	
Space Group	$P222_1$
Mosaicity	3.43^{o}
Unit Cell **a**, **b**, **c**	122.01 Å, 47.20 Å, 82.25 Å
α, β, γ (^{o})	90.00, 90.00, 90.00
Wavelength	1.5419 Å
Resolution range (Å)	28.92-1.54 (1.59-1.54)[a]
Total reflections	3,35,702
Unique reflections	59,836
Average redundancy	5.61 (1.92)
Completeness (%)[d]	83.4 (19.9)
Rmerge[b]	0.383
Output<I/σI>[c]	2.7 (0.9)
Reduced Chi Squared	1.21
Refinement	
Resolution range	20.99-1.74 Å
R-factor	0.3441
R-free	0.4272
Protein atoms	3,577
Water molecules	134
Unique reflns used	49,194
R.m.s.d.	
Bonds	0.008 Å
Angles	1.376^{o}
Chirality	0.084 $Å^3$
Planarity	0.005 Å
Dihedrals	14.763^{o}
Ramach. Outliers	0.90%
All atom clash score	18

[a] Statistics for the highest resolution bin of reflections in parentheses
[b] Rmerge reported above is for the measured intensities till 1.54 Å; for 1.74 Å resolution, it drops to 0.35, for 2.0 Å data it drops to 0.315, for 2. 5Å data to 0.221
[c] Intensity signal to noise ratio average, increases to ~3.0 for 1.74 Å data
[d] Completeness of data is improved to 99.17% by using 21.0-1.74 Å data, 837 reflections were free reflections amounting to 1.7% of the total unique reflections used