Supplementary Table S1. Summary of data-collection and refinement statistics

Data collection	
Space group	$P2_12_12$
Unit-cell parameters (Å)	a = 128.8, b = 158.3, c = 68.4
Resolution range (Å)	50.0-3.0 (3.11-3.0)
Number of total reflections	142005 (14055)
Number of unique reflections	28798 (2811)
Data completeness (%)	99.4 (99.6)
$\langle I \rangle / \langle \sigma(I) \rangle$	14.7 (3.7)
R_{merge} (%) [a]	10.6 (42.7)
Refinement	
Resolution range used for refinement (Å)	30.0-3.0
Number of reflections used	28525
R_{cryst} / R_{free} (%) [b]	19.7 / 25.1
r.m.s.d. bond length (Å)	0.006
r.m.s.d. bond angles (°)	1.06
Number of atoms modeled	6806
Mean B factor for protein atoms (Å^2)	19.5
Ramachandran plot statistics	
Residues in most favored region (%)	96.1
Residues in additional allowed region (%)	3.9
Residues in disallowed region (%)	0

[a] $R_{merge} = \sum_{hkl}\sum_i |I_i(hkl) - \langle I(hkl)\rangle| / \sum_{hkl}\sum_i I_i(hkl)$, where $\langle I(hkl)\rangle$ is the main value of $I(hkl)$.

[b] $R_{cryst} = \sum||F_{obs}| - |F_{calc}||/\sum|F_{obs}|$, where F_{obs} and F_{calc} are observed and calculated structure factors.

The free R factor was calculated using 5% of reflections omitted from the refinement.

Numbers in parentheses represent the value for the highest resolution shell.