Table I. Crystallographic Data and Refinement Statistics

Data Collection	**GRASP55 1-208**
Space group	$P4_12_12$
Unit cell dimensions (Å)	a = b = 88.0
	c = 61.2
Resolution (Å)	62.25-1.65
Outer shell (Å)	1.68-1.65
Number of reflections	
unique	26,966
total	356,291
Mean $I/\sigma_{(I)}$	57.9 (2.40)
Completeness (%)	96.0 (75.8)
R_{sym} (%)	5.0 (52.4)
Refinement	
R factor/R_{free} [b,c]	17.6/22.2
Nonhydrogen atoms	
Total	1877
Solvent	252
Rmsd from ideal geometry	
Bond lengths (Å)	0.026
Bond angles (°)	2.11
Average isotropic B values ($Å^2$)	24.4
Ramachandran plot	
Most favorable region (%)	84.5
Additional allowed region (%)	14.3
Generous allowed region (%)	0.0
Disallowed region (%)	1.2

Values in parenthesis correspond to those in the outer resolution shell.

[a] $R_{sym} = (|(\Sigma I - \langle I \rangle)|)/(\Sigma I)$, where $\langle I \rangle$ is the average intensity of multiple measurements.

[b] R factor = $\Sigma_{hkl}||F_{obs}(hkl)| - |F_{calc}(hkl)||/ \Sigma_{hkl}|F_{obs}(hkl)|$.

[c] R_{free} = the cross validation of R factor for 5% of reflections against which the model was not refined.