Supplementary Table S1. X-ray Data Collection and Refinement Statistics for StScsC

Data collection	*ScsC*
Wavelength (Å)	1.5419
Resolution range (Å)	48.7 – 1.98 (2.05 – 1.98)
Space group	$P2_1$
Unit cell dimensions (Å)	$a = 53.1$, $b = 91.0$, $c = 83.3$ $\alpha = \gamma = 90$, $\beta = 102.23$
Observed reflections	790723
Unique reflections	106172
R_{merge}[a*]	0.06 (0.48)
Completeness (%)*	100 (100)
$<I>/\sigma(I)>$ *	13.0 (2.4)
Redundancy[c]	7.5 (7.3)
Refinement	
Resolution (Å)	48.7 – 2.04
Completeness for range (%)	99.8
R_{factor}[b] (%)*	*19.9 (43.7)*
R_{free}[c] (%)*	*25.3 (47.9)*
Number of non-H protein atoms	*5503*
Number of waters	*411*
Wilson B	*35.41*
Average B factor (Å^2)–All atoms	45.32
Average B factor (Å^2)–Water	46.28
Average B factor (Å^2)–Nonsolvent	45.25
R.m.s.d. from ideal geometry	
Bonds (Å)	0.008
Angles (°)	1.003
Molprobity analysis	
Residues in most favored/ additionally allowed regions (%)	98.7/1.3
Residues with bad angles (%)	0
Poor rotamers (%)	2
Clashscore (percentile)	11.55 (76th)
Molprobity score (percentile)	1.81 (87th)

*Values in parentheses refer to the highest resolution shell.

[a] $R_{merge} = \sum |I - <I>| / \sum <I>$, where I is the intensity of individual reflections.

[b] $R_{fac} = \sum_h |F_o - F_c| / \sum_h |F_o|$, where F_o and F_c are the observed and calculated structure-factor amplitudes for each reflection "h."

[c] R_{free} was calculated with 5% of the diffraction data selected randomly and excluded from refinement.