Supplementary information, Table S1 Crystallographic data collection and refinement statistics for Scp1-WD40

Data	Scp1-WD40 Native	Scp1-WD40 Se-SAD
Integration Package	HKL2000	HKL2000
Space Group	$P2_1$	$P2_1$
Unit Cell (Å)	38.01, 109.71, 103.45	37.92,109.76,103.26
Unit Cell (°)	90.00, 100.46, 90.00	90.00, 100.39, 90.00
Wavelength (Å)	1.0000	0.9793
Resolution (Å)	40~2.05 (2.12~2.05)	50~2.62 (2.71~2.62)
R_{merge} (%)	8.5 (39.1)	9.2 (39.9)
I/sigma	20.0 (4.5)	34.2 (6.0)
Completeness (%)	99.0 (98.9)	98.9 (90.4)
Number of measured reflections	192,570	186,374
Number of unique reflections	51,784	25,071
Redundancy	3.7 (3.5)	7.4 (7.1)
R_{work} / R_{free} (%)	17.72/22.93	
No. atoms		
Protein	6754	
main chain	3403	
side chain	3351	
Water	307	
Others	26	
Average B value (Å^2)		
Protein	40.44	
main chain	36.78	
side chain	44.15	
Water	43.61	
Others	46.56	
R.m.s. deviations		
Bonds (Å)	0.017	
Angle (°)	1.836	
Ramachandran plot statistics (%)		
Most favourable	89.4	
Additionally allowed	9.9	
Generously allowed	0.7	
Disallowed	0.0	

Values in parentheses are for the highest resolution shell. $R_{merge}=\Sigma_h\Sigma_i|I_{h,i}-I_h|/\Sigma_h\Sigma_i I_{h,i}$, where I_h is the mean intensity of the i observations of symmetry related reflections of h. $R=\Sigma|F_{obs}-F_{calc}|/\Sigma F_{obs}$, where F_{calc} is the calculated protein structure factor from the atomic model (R_{free} was calculated with 5% of the reflections selected).