

Extended Data Table 1. Data collection and refinement statistics

Data Set	SHP2–pPD1 complex PDB:21BJ
Space group	<i>P212121</i>
<i>a</i> , <i>b</i> , <i>c</i> (Å)	65.38, 107.73, 216.68
α , β , γ (°)	90.0, 90.0, 90.0
Resolution (Å)	50.0 - 2.6 (2.69 - 2.60)
R _{sym}	0.049 (0.84)
R _{pim}	0.02 (0.37)
I/ σ (I)	35.1 (1.5)
CC ^{1/2}	0.995 (0.81)
Completeness (%)	98.0 (95.7)
Redundancy	6.2 (5.8)
Refinement	
Resolution (Å)	50 - 2.6
No. of reflections	46,483
R _{work} /R _{free} (%)	23.1/26.1
Protein atoms	8,392
Solvent atoms	6
B factors (Å ²)	99.3
protein	99.4
Rmsd bond lengths (Å)	0.007
Rmsd bond angles (°)	1.06

Ramachandran outliers (%): 0

Ramachandran favored (%): 96.1

Values in parentheses are for the highest-resolution shell.