

Table S3 X-ray data collection and model refinement statistics

M ^{Pro} /GC376 (7tgr)	
<hr/> Data collection <hr/>	
Resolution range (Å)	47.85 - 1.68 (1.72 - 1.68)
Space group	C2
Unit cell	
(<i>a</i> , <i>b</i> , <i>c</i> in Å)	114.56, 52.94, 45.90
(α , β , γ in °)	90, 102.551, 90
Total reflections	111667 (7620)
Unique reflections	30122 (1993)
Multiplicity	3.7 (3.8)
Completeness (%)	97.44 (96.19)
Mean <i>I</i> / σ (<i>I</i>)	11.36 (1.06)
<i>R</i> _{merge}	0.0636 (1.23)
<i>R</i> _{meas}	0.0744 (1.43)
<i>R</i> _{pim}	0.0382 (0.719)
CC _{1/2}	0.998 (0.526)
<hr/> Refinement <hr/>	
No. of Reflections	29949 (1992)
No. of Refl. for <i>R</i> _{free}	1505 (94)
<i>R</i> _{work}	0.179 (0.323)
<i>R</i> _{free}	0.228 (0.347)
Number of non-H atoms	
Macromolecules	2406
Ligands	20
Solvent	167
Average B-factor (Å ²)	
Macromolecules	39.03
Ligands	38.54
Solvent	53.84
Protein residues	45.66
Protein residues	305
R.m.s.d.	
Bond length (Å)	0.018
Bond angles (°)	1.57
Ramachandran plot	
Favored (%)	98.01
Allowed (%)	1.99
Outliers (%)	0.00

Statistics for the highest-resolution shell are shown in parentheses.