Table S1. X-ray Data Collection and Refinement.

	3TPZ
Data collection	
Resolution	34.65 – 2.10 (2.18 – 2.10)
$I/\sigma(I)$ (highest resolution shell)	12.7 (4.0)
% Completeness (highest resolution shell)	95.8 (93.9)
N_{obs}	33415
Multiplicity (highest resolution shell)	3.98 (3.95)
R_{merge} (highest resolution shell)	0.064 (0.335)
Refinement	
Resolution	28.0 – 2.10 (2.15 – 2.10)
R_{work} (highest resolution shell)	0.211 (0.354)
R_{free} (highest resolution shell)	0.276 (0.374)
N_{work}	30071
N_{free}	3339
N_{atoms}	4195
$<B_{protein}>$	40.2
$<B_{water}>$	40.9
$<B_{ligand}>$	70.8
RMSD from ideal	
Bond length	0.01
Bond angles	1.23
Ramachandran Plot	
residues most in most favored regions	406
residues in additionally allowed regions	38
residues in generously allowed regions	1
residues in forbidden regions	2