Table S1 (related to Figure 5). Crystallographic Data and Refinement Statistics

Diffraction data	
Wavelength (Å)	1.0
Space group	C2
Unit cell *a*/*b*/*c* (Å)	99.92 / 39.91 / 120.70
Unit cell $\alpha/\beta/\gamma$ (°)	90.00 / 94.82 / 90.00
Resolution (Å)	40.0-2.25 (2.33-2.25)
Completeness (%)	95.6 (80.0)
Redundancy	11.8 (6.2)
R_{merge}[a] (%)	9.1 (34.0)
I/σ	24.1 (3.0)
Refinement	
Resolution (Å)	40.0-2.25
R_{factor}[b] (%)	22.1
R_{free}[c] (%)	27.9
Asymmetric unit content	
Number of residues	440 (dimer)
Number of solvent atoms	283
Rmsd bond lengths (Å)	0.007
Rmsd bond angles (°)	0.957
Average B factors (Å^2)	
All atoms	50.58
Protein atoms	50.57
Solvent	50.84
Residues in Ramachandran plot	
Most favored regions (%)	97.53
Other allowed regions (%)	2.47
PDB code	3OK8

Values in parentheses correspond to highest resolution shell

[a] $R_{merge}=\Sigma_{hkl}(I-\langle I\rangle)/\Sigma I$, where I and $\langle I\rangle$ are the observed and mean intensities of all the observations of reflection *hkl*, including its symmetry-related equivalents

[b] $R_{factor}=\Sigma_{hkl}||F_{obs}| - |F_{calc}||/\Sigma|F_{obs}|$, where F_{obs} and F_{calc} are the observed and calculated structure factors of reflection *hkl*

[c] R_{free}, R_{factor} calculated for a randomly selected subset of reflections (5%) that were not used in refinement