Supplemental Table I. Crystallographic Data and Refinement Statistics

	Native
PDB ID	1Z5S
Source	APS 31ID
Wavelength (Å)	0.9793
Resolution Limits (Å)	50-3.0
Space Group	$P3_221$
Unit Cell (Å) a, b, c, α, β, γ	157.1, 157.1, 59.6, 90, 90, 120
Number of observations	147869
Number of reflections	16464
Completeness (%)	97.0 (91.8)
Mean I/σI	15.1 (2.1)
R-merge on I [a]	7.5 (46.4)
Cut-off criteria I/σI	0
Refinement Statistics	
Resolution Limits (Å)	30-3.0
Number of reflections	16461
Completeness (%)	96.5 (86.2)
Cutoff Criteria I/σI	0
Protein/water atoms	3564/28
Rcryst [b]	0.247 (0.425)
Rfree (5% of data)	0.290 (0.432)
Bonds (Å) [c]	0.006
Angles (°) [c]	1.2
Bfactor (mc/sc in $Å^2$) [c]	2.27/2.80

a. $Rmerge = \sum hkl \sum i|I(hkl)i - <I(hkl)>|/\sum hkl \sum i <I(hkl)i>$.
b. $Rcryst = \sum hkl\ |Fo(hkl)-Fc(hkl)|/\sum hkl\ |Fo(hkl)|$, where *Fo* and *Fc* are observed and calculated structure factors, respectively.
c. Values indicate root-mean-square deviations in bond lengths, bond angles, and Bfactors of bonded atoms.
Parentheses indicate statistics for the high-resolution data bin for x-ray and refinement data.

Data were processed using DENZO, SCALEPACK[1], and CCP4[2]. The structure was solved by molecular replacement using CCP4[2]. The atomic model was built using O[3] and refined using CNS[4].

1. Otwinowski, Z. & Minor, W. Processing of X-ray Diffraction Data Collected in Oscillation Mode. *Methods in Enzymology* **276**, 307-326 (1997).
2. Collaborative Computational Project. The CCP4 suite: programs for protein crystallography. *Acta Crystallography* **D50**, 760-763 (1994).
3. Jones, T. A., Zou, J. Y., Cowan, S. W. & Kjeldgaard, M. Improved methods for building protein models in electron density maps and the location of errors in these models. *Acta Crystallogr.* **A 47 (Pt 2),** 110-119 (1991).
4. Brunger, A. T. *et al.* Crystallography & NMR system: A new software suite for macromolecular structure determination. *Acta Crystallogr. D. Biol. Crystallogr.* **54 (Pt 5),** 905-921 (1998).