

Supporting Table 1. Data Collection and Refinement Statistics for CfAvr4 (PDB ID: 6BN0).

X-ray Source	ALS 8.3.1
Wavelength (Å)	1.11583
Temperature (K)	100
Space group	<i>P2</i> ₁
Unit-cell parameters (Å, °)	a=39.86, b=41.08, c=121.36 α=γ=90, β=97.87
Resolution (Å)	60.11-1.95 (2.00-1.95)
<i>R</i> _{merge} ^a (%)	5.4 (61.2)
<I/σ(I)>	13.69 (2.12)
CC _{1/2} (%)	99.9 (74.8)
No. of reflections	104,460 (7,850)
No. of unique reflections	28,654 (2,110)
Completeness (%)	99.6 (99.8)
Redundancy	3.65 (3.72)
Refinement Statistics	
Resolution (Å)	60.11-1.95 (2.02-1.95)
No. of reflections (F>0) used in refinement	28,641 (2,719)
<i>R</i> _{factor} ^b (%)	16.77
<i>R</i> _{free} ^c (%)	21.40
RMS bond length (Å)	0.013
RMS bond angle (°)	1.261
Overall B Value (Å ²)	44.01
Ramachandran Plot Statistics^d	
Residues	207
Most favored Region	97.7%
Allowed Region	2.3%
Disallowed	0.0%

^a $R_{\text{merge}} = [\sum_h \sum_i |I_h - \bar{I}_h| / \sum_h \sum_i I_h]$ where \bar{I}_h is the mean of I_{hi} observations of reflection h . Numbers in parenthesis represent highest resolution shell. ^b $R_{\text{factor}} = \sum ||F_{\text{obs}}| - |F_{\text{calc}}|| / \sum |F_{\text{obs}}| \times 100$ for 95% of recorded data (R_{factor}) or 5% data (R_{free}). ^d From MolProbity (Chen et al., 2010)