

X-Ray data collection and structure determination statistics

Parameter	Overall (Highest shell)	Overall (Highest shell)
Protein	MHF1 (1-110) + MHF2	MHF1(1-110) + MHF2 + MID(669 - 800)
Beamline	APS-23-ID-B	APS-23-ID-B
Collection date	09-Mar-2011	09-Mar-2011
Space Group	P12 ₁ 1	P12 ₁ 1
Unit Cell	a=40.78Å b=91.93Å, c=61.43 Å β=96.30°	a=110.98Å b=69.97Å, c=116.05Å β=91.60°
Solvent content	56.8%	57.7%
V _m	2.84 Å ³ /Da	2.90 Å ³ /Da
Resolution	45.97-2.10 Å (2.15-2.10) *	49.51-2.00 Å (2.05-2.00)
I/σ	11.71 (3.52)	14.90 (3.04)
Completeness	96.6% (96.9%)	98.9% (99.7%)
R _{merge}	0.066 (0.548)	0.052 (0.512)
Multiplicity	2.70 (2.73)	3.50 (3.56)
Reflections	26336 (1931)	120454 (8895)
Mosaicity	0.30	0.15
R	0.200 (0.236)	0.202 (0.286)
R _{free}	0.231 (0.288)	0.245 (0.334)
Ramachandran		
Favored	99.13%	98.77%
Allowed	100.0%	100.0%
Molprobit Score	100 th percentile	99 th percentile

*parentheses indicate values for highest resolution shell.