wwPDB X-ray Structure Validation Summary Report (i)

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PDB ID	:	2XIT
Title	:	Crystal structure of monomeric MipZ
Authors	:	Kiekebusch, D.; Michie, K.A.; Essen, L.O.; Lowe, J.; Thanbichler, M.
Deposited on	:	2010-06-30
Resolution	:	1.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

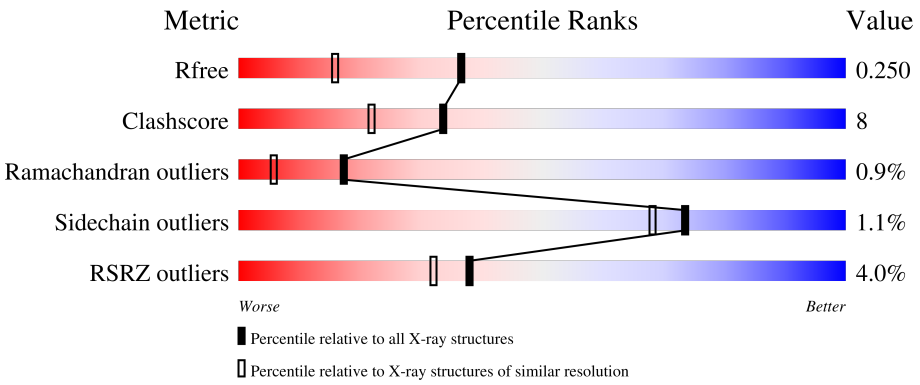
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	294	5% 82% 11% • 6%
1	B	294	3% 82% 12% • 5%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4701 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called MIPZ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	277	2114	1330	389	388	7	0	0	1
1	B	279	2167	1363	398	398	8	0	4	1

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	279	ALA	-	expression tag	UNP B8GY04
A	280	VAL	-	expression tag	UNP B8GY04
A	281	ASP	-	expression tag	UNP B8GY04
A	282	LYS	-	expression tag	UNP B8GY04
A	283	LEU	-	expression tag	UNP B8GY04
A	284	ALA	-	expression tag	UNP B8GY04
A	285	ALA	-	expression tag	UNP B8GY04
A	286	ALA	-	expression tag	UNP B8GY04
A	287	LEU	-	expression tag	UNP B8GY04
A	288	GLU	-	expression tag	UNP B8GY04
A	289	HIS	-	expression tag	UNP B8GY04
A	290	HIS	-	expression tag	UNP B8GY04
A	291	HIS	-	expression tag	UNP B8GY04
A	292	HIS	-	expression tag	UNP B8GY04
A	293	HIS	-	expression tag	UNP B8GY04
A	294	HIS	-	expression tag	UNP B8GY04
B	279	ALA	-	expression tag	UNP B8GY04
B	280	VAL	-	expression tag	UNP B8GY04
B	281	ASP	-	expression tag	UNP B8GY04
B	282	LYS	-	expression tag	UNP B8GY04
B	283	LEU	-	expression tag	UNP B8GY04
B	284	ALA	-	expression tag	UNP B8GY04
B	285	ALA	-	expression tag	UNP B8GY04
B	286	ALA	-	expression tag	UNP B8GY04
B	287	LEU	-	expression tag	UNP B8GY04

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Chain	Residue	Modelled	Actual	Comment	Reference
B	288	GLU	-	expression tag	UNP B8GY04
B	289	HIS	-	expression tag	UNP B8GY04
B	290	HIS	-	expression tag	UNP B8GY04
B	291	HIS	-	expression tag	UNP B8GY04
B	292	HIS	-	expression tag	UNP B8GY04
B	293	HIS	-	expression tag	UNP B8GY04
B	294	HIS	-	expression tag	UNP B8GY04

- Molecule 2 is water.

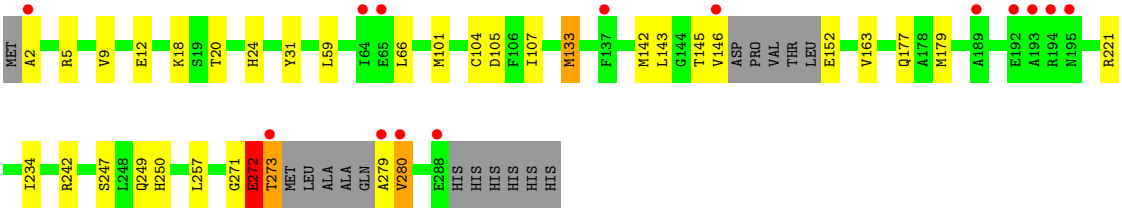
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	187	187	187	0	0
			Total	O		
2	B	233	233	233	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

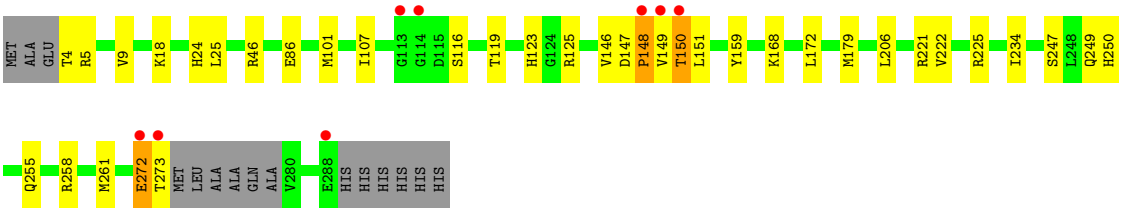
- Molecule 1: MIPZ

Chain A:



- Molecule 1: MIPZ

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	124.67Å 124.67Å 239.05Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.27 – 1.80 49.20 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.27-1.80) 99.8 (49.20-1.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.55 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.184 , 0.230 0.209 , 0.250	Depositor DCC
R_{free} test set	1215 reflections (1.83%)	wwPDB-VP
Wilson B-factor (Å^2)	21.0	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 45.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4701	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.69% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	A	0.52	0/2146	0.67	1/2906 (0.0%)
1	B	0.56	0/2213	0.71	0/2995
All	All	0.54	0/4359	0.69	1/5901 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	133	MET	CG-SD-CE	-5.46	91.47	100.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	272	GLU	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2114	0	2135	29	1
1	B	2167	0	2211	44	0
2	A	187	0	0	1	0
2	B	233	0	0	8	0
All	All	4701	0	4346	73	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 73 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:ALA:HA	1:A:177:GLN:HE22	1.23	1.03
1:B:149:VAL:O	1:B:150:THR:HG23	1.64	0.96
1:A:272:GLU:HA	1:A:272:GLU:OE2	1.75	0.85
1:B:179[A]:MET:SD	2:B:2095:HOH:O	2.35	0.84
1:B:4:THR:N	2:B:2002:HOH:O	2.10	0.82

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:ALA:CB	1:A:2:ALA:CB[17_555]	1.96	0.24

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	271/294 (92%)	264 (97%)	5 (2%)	2 (1%)	22 10
1	B	279/294 (95%)	272 (98%)	4 (1%)	3 (1%)	14 4
All	All	550/588 (94%)	536 (98%)	9 (2%)	5 (1%)	17 6

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	280	VAL
1	B	148	PRO
1	B	150	THR
1	A	272	GLU
1	B	272	GLU

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	216/238 (91%)	213 (99%)	3 (1%)	67	59
1	B	227/238 (95%)	225 (99%)	2 (1%)	78	75
All	All	443/476 (93%)	438 (99%)	5 (1%)	73	68

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	242	ARG
1	A	272	GLU
1	A	273	THR
1	B	5	ARG
1	B	272	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	249	GLN
1	B	250	HIS
1	B	255	GLN
1	A	250	HIS
1	B	24	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	277/294 (94%)	0.23	14 (5%)	28	22	14, 25, 42, 57	4 (1%)
1	B	279/294 (94%)	0.06	8 (2%)	51	46	11, 20, 37, 55	0
All	All	556/588 (94%)	0.14	22 (3%)	38	32	11, 23, 40, 57	4 (0%)

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	149	VAL	7.6
1	A	273	THR	6.5
1	A	193	ALA	5.5
1	A	194	ARG	5.2
1	A	2	ALA	5.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.