Full wwPDB X-ray Structure Validation Report (i)

May 14, 2020 – 09:06 pm BST

PDB ID	:	4XIB
Title	:	Crystal structure of the MZM-REP domains of Mind bomb 1 in complex with fly Delta N-box peptide
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Deposited on	:	2015-01-06
Resolution	:	2.15 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 following versions of software and data (see references (1)) were used in the production of this report:

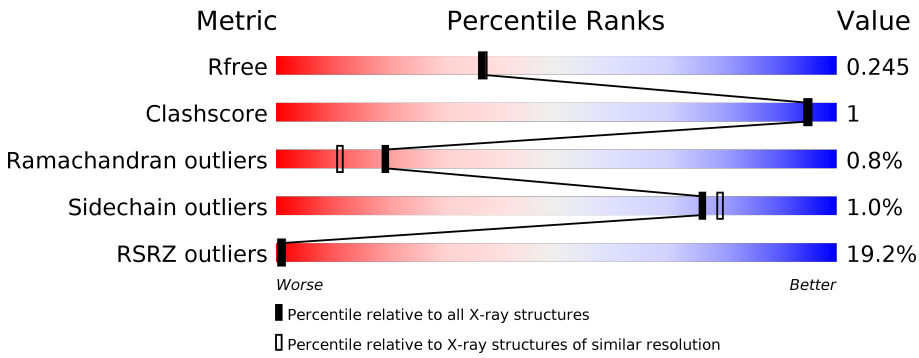
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.15 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	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)
RSRZ outliers	127900	2485 (2.16-2.12)

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 on 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	380	17%, 91%, 5%, 5%
2	C	11	55%, 64%, 36%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5784 atoms, of which 2776 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 E3 ubiquitin-protein ligase MIB1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	362	5543	1763	2714	516	533	17	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	SER	-	expression tag	UNP Q86YT6

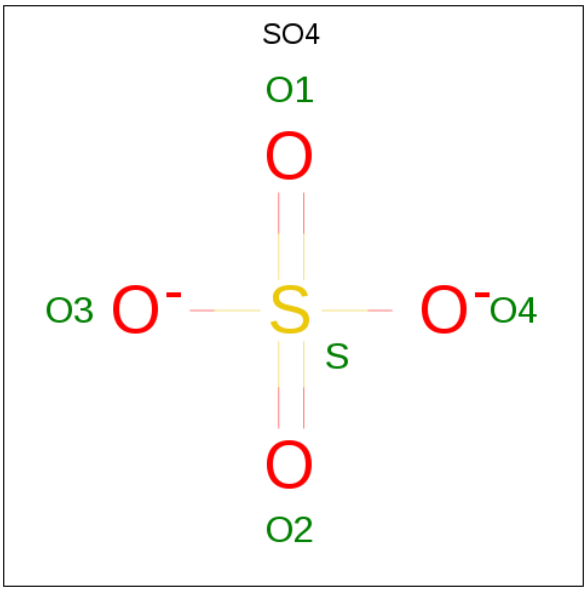
- Molecule 2 is a protein called Delta N-box peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
2	C	7	121	40	62	10	9	0	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
3	A	2	2	2	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0

- Molecule 5 is water.

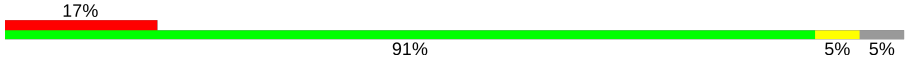
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	108	Total O 108 108	0	0

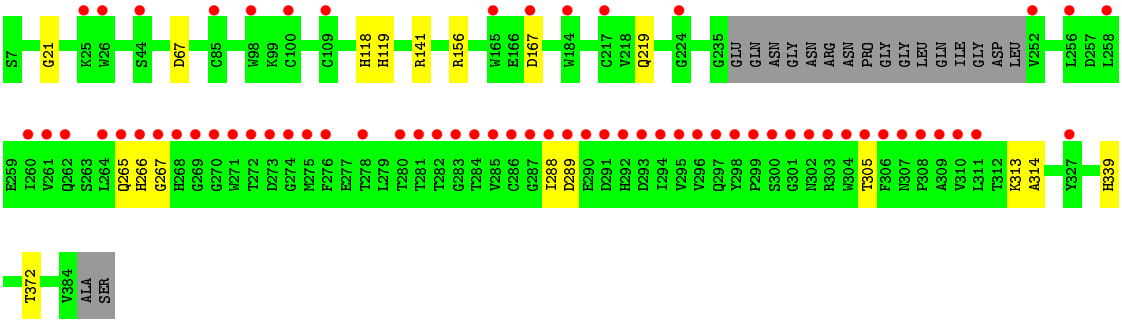
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: E3 ubiquitin-protein ligase MIB1

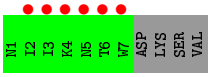
Chain A:





- Molecule 2: Delta N-box peptide

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants a, b, c, α, β, γ	74.13Å 74.13Å 170.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.05 – 2.15 45.05 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.9 (45.05-2.15) 99.9 (45.05-2.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	13.68 (at 2.14Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.209 , 0.244 0.210 , 0.245	Depositor DCC
R_{free} test set	1995 reflections (7.45%)	wwPDB-VP
Wilson B-factor (Å^2)	34.1	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 47.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5784	wwPDB-VP
Average B, all atoms (Å^2)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.83% 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)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SO4

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	0.23	0/2894	0.43	0/3921
2	C	0.97	0/60	0.49	0/81
All	All	0.27	0/2954	0.43	0/4002

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2829	2714	2714	7	0
2	C	59	62	62	0	0
3	A	2	0	0	0	0
4	A	10	0	0	0	0
5	A	108	0	0	0	0
All	All	3008	2776	2776	7	0

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 1.

All (7) 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:118:HIS:CG	1:A:119:HIS:H	2.33	0.46
1:A:156:ARG:HB2	1:A:219:GLN:HB3	1.97	0.45
1:A:141:ARG:O	1:A:141:ARG:HD3	2.17	0.44
1:A:141:ARG:HD2	1:A:339:HIS:CD2	2.52	0.44
1:A:21:GLY:N	1:A:67:ASP:O	2.47	0.42
1:A:288:ILE:HG22	1:A:289:ASP:N	2.35	0.41
1:A:265:GLN:O	1:A:267:GLY:N	2.53	0.41

There are no symmetry-related clashes.

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	358/380 (94%)	339 (95%)	16 (4%)	3 (1%)	19 11
2	C	5/11 (46%)	5 (100%)	0	0	100 100
All	All	363/391 (93%)	344 (95%)	16 (4%)	3 (1%)	19 11

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	313	LYS
1	A	266	HIS
1	A	314	ALA

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	300/314 (96%)	297 (99%)	3 (1%)	76 79
2	C	6/11 (54%)	6 (100%)	0	100 100
All	All	306/325 (94%)	303 (99%)	3 (1%)	76 79

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	167	ASP
1	A	305	THR
1	A	372	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	SO4	A	403	-	4,4,4	0.15	0	6,6,6	0.06	0
4	SO4	A	404	-	4,4,4	0.15	0	6,6,6	0.08	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	362/380 (95%)	1.21	65 (17%) 1 1	23, 43, 116, 156	0
2	C	7/11 (63%)	3.17	6 (85%) 0 0	72, 81, 87, 100	0
All	All	369/391 (94%)	1.25	71 (19%) 1 1	23, 44, 116, 156	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	286	CYS	10.2
1	A	294	ILE	9.2
1	A	285	VAL	9.1
1	A	271	TRP	8.9
1	A	261	VAL	7.5
1	A	306	PHE	7.3
1	A	262	GLN	6.9
1	A	287	GLY	6.5
1	A	270	GLY	6.4
1	A	288	ILE	6.4
1	A	258	LEU	6.0
1	A	304	TRP	5.7
1	A	267	GLY	5.7
1	A	308	PRO	5.6
1	A	269	GLY	5.6
1	A	296	VAL	5.5
1	A	284	THR	5.5
1	A	264	LEU	5.3
1	A	268	HIS	5.3
1	A	298	TYR	5.3
1	A	272	THR	5.3
1	A	292	HIS	5.2
1	A	283	GLY	5.0
1	A	290	GLU	5.0

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Mol	Chain	Res	Type	RSRZ
2	C	4	LYS	4.3
1	A	293	ASP	4.0
1	A	276	PHE	4.0
1	A	303	ARG	4.0
1	A	289	ASP	4.0
1	A	274	GLY	3.9
1	A	252	VAL	3.9
1	A	256	LEU	3.9
1	A	275	MET	3.9
1	A	305	THR	3.7
2	C	6	THR	3.6
2	C	5	ASN	3.6
2	C	7	TRP	3.4
2	C	2	ILE	3.4
1	A	266	HIS	3.4
1	A	299	PRO	3.4
1	A	291	ASP	3.1
1	A	273	ASP	3.0
1	A	297	GLN	2.9
1	A	44	SER	2.9
1	A	224	GLY	2.8
1	A	300	SER	2.7
1	A	26	TRP	2.7
1	A	278	THR	2.7
1	A	167	ASP	2.7
1	A	301	GLY	2.7
2	C	3	ILE	2.6
1	A	100	CYS	2.4
1	A	260	ILE	2.4
1	A	165	TRP	2.4
1	A	280	THR	2.4
1	A	282	THR	2.4
1	A	98	TRP	2.4
1	A	311	LEU	2.3
1	A	307	ASN	2.3
1	A	310	VAL	2.3
1	A	265	GLN	2.2
1	A	302	ASN	2.2
1	A	25	LYS	2.2
1	A	184	TRP	2.2
1	A	327	TYR	2.2
1	A	109	CYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	309	ALA	2.0
1	A	217	CYS	2.0
1	A	281	THR	2.0
1	A	85	CYS	2.0
1	A	295	VAL	2.0

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 carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	SO4	A	403	5/5	0.98	0.11	47,54,56,59	0
4	SO4	A	404	5/5	0.99	0.21	29,31,37,37	0
3	ZN	A	402	1/1	1.00	0.18	26,26,26,26	0
3	ZN	A	401	1/1	1.00	0.16	32,32,32,32	0

6.5 Other polymers (i)

There are no such residues in this entry.