



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 04:11 AM GMT

PDB ID : 3MVB
Title : Crystal structure of a triple RFY mutant of human MTERF1 bound to the termination sequence
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Deposited on : 2010-05-03
Resolution : 2.79 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

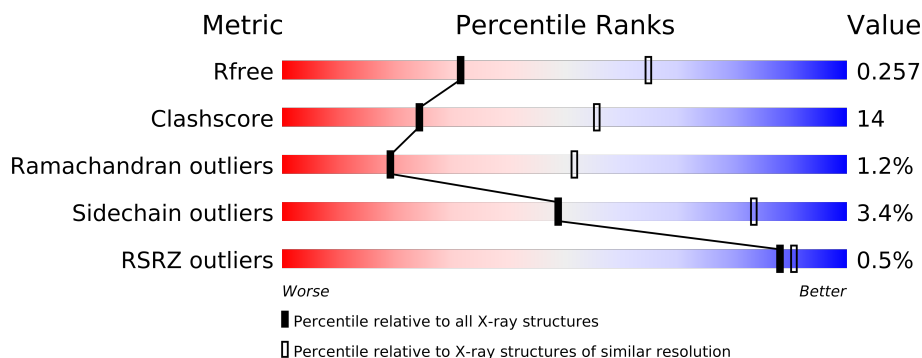
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance


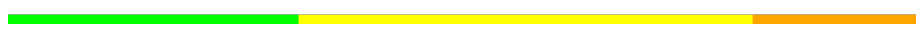
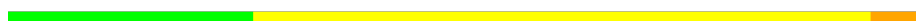
The reported resolution of this entry is 2.79 Å.

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}	66092	2193 (2.80-2.76)
Clashscore	79885	2751 (2.80-2.76)
Ramachandran outliers	78287	2699 (2.80-2.76)
Sidechain outliers	78261	2701 (2.80-2.76)
RSRZ outliers	66119	2196 (2.80-2.76)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	O	343	
2	D	22	
3	E	22	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3522 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Transcription termination factor, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	O	324	Total	C	N	O	S	0	0	0
			2588	1645	451	480	12			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	54	GLY	-	EXPRESSION TAG	UNP Q99551
O	55	HIS	-	EXPRESSION TAG	UNP Q99551
O	56	MET	-	EXPRESSION TAG	UNP Q99551
O	162	ALA	ARG	ENGINEERED	UNP Q99551
O	243	ALA	PHE	ENGINEERED	UNP Q99551
O	288	ALA	TYR	ENGINEERED	UNP Q99551

- Molecule 2 is a DNA chain called 5'-D(*AP*TP*TP*AP*CP*CP*GP*GP*GP*CP*TP*C
P*TP*GP*CP*CP*AP*TP*CP*TP*TP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	22	Total	C	N	O	P	0	0	0
			442	213	75	133	21			

- Molecule 3 is a DNA chain called 5'-D(*TP*AP*AP*GP*AP*TP*GP*GP*CP*AP*GP*A
P*GP*CP*CP*CP*GP*GP*TP*AP*AP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	22	Total	C	N	O	P	0	0	0
			454	216	90	127	21			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	O	24	Total	O	0	0
			24	24		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	10	Total	O	0	0
			10	10		
4	E	4	Total	O	0	0
			4	4		

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	87.53Å 91.43Å 159.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.76 – 2.79 49.49 – 2.79	Depositor EDS
% Data completeness (in resolution range)	94.1 (39.76-2.79) 94.2 (49.49-2.79)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.87 (at 2.77Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.202 , 0.263 0.195 , 0.257	Depositor DCC
R_{free} test set	1213 reflections (7.91%)	DCC
Wilson B-factor (Å ²)	44.5	Xtriage
Anisotropy	0.555	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 17.2	EDS
Estimated twinning fraction	0.041 for -k,-h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 16155 reflections (0.006%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3522	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.32% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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	O	0.39	0/2625	0.54	0/3536
2	D	0.71	0/493	1.70	14/758 (1.8%)
3	E	0.73	0/511	1.50	12/788 (1.5%)
All	All	0.51	0/3629	0.99	26/5082 (0.5%)

There are no bond length outliers.

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	10	DC	O4'-C1'-N1	11.08	115.76	108.00
2	D	22	DA	O4'-C1'-N9	8.74	114.12	108.00
2	D	10	DC	C3'-C2'-C1'	-7.64	93.33	102.50
2	D	15	DC	O4'-C4'-C3'	-7.57	101.46	106.00
3	E	6	DT	N3-C4-O4	7.43	124.36	119.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	O	2588	0	2691	73	0
2	D	442	0	251	12	0
3	E	454	0	248	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	10	0	0	0	0
4	E	4	0	0	0	0
4	O	24	0	0	0	0
All	All	3522	0	3190	94	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 14.

The worst 5 of 94 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:O:265:LEU:CD1	1:O:269:GLU:HB2	1.97	0.95
1:O:265:LEU:HD11	1:O:269:GLU:HB2	1.56	0.85
3:E:3:DA:H2'	3:E:4:DG:C8	2.13	0.84
1:O:103:ASN:HA	1:O:105:GLN:HE22	1.42	0.83
1:O:360:LYS:HA	1:O:363:ILE:HD12	1.61	0.82

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	O	322/343 (94%)	297 (92%)	21 (6%)	4 (1%)	19 52

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	O	370	GLY
1	O	373	LEU
1	O	231	ALA
1	O	226	GLY

5.3.2 Protein sidechains ⓘ

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	O	295/313 (94%)	285 (97%)	10 (3%)	49 83

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	O	274	ILE
1	O	287	ASP
1	O	351	VAL
1	O	265	LEU
1	O	323	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	O	78	ASN
1	O	105	GLN
1	O	227	HIS

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	O	324/343 (94%)	-0.09	2 (0%) 86 88	23, 39, 67, 87	1 (0%)
2	D	22/22 (100%)	-0.52	0 100 100	28, 37, 50, 56	0
3	E	22/22 (100%)	-0.45	0 100 100	30, 37, 49, 54	0
All	All	368/387 (95%)	-0.14	2 (0%) 88 90	23, 39, 67, 87	1 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	O	376	LEU	3.1
1	O	90	ARG	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.