

Full wwPDB X-ray Structure Validation Report (i)

Mar 21, 2024 – 02:10 PM EDT

PDB ID	:	8T2D
Title	:	Ubiquitin variant i53:Mutant T12Y.T14E.L67R with 53BP1 Tudor domain
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Deposited on		
Resolution	:	1.75 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 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:

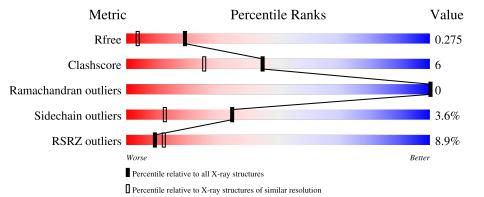
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.75 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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 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	В	78	6% 77%	17%	•••
2	А	124	10%	15%	• 7%



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1573 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 Ubiquitin variant i53.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	В	75	Total 602	C 381	N 105	0 115	S 1	0	0	0

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	-3	GLY	-	expression tag	UNP J3QS39
В	-2	PRO	-	expression tag	UNP J3QS39
В	-1	GLY	-	expression tag	UNP J3QS39
В	0	SER	-	expression tag	UNP J3QS39
В	2	LEU	GLN	conflict	UNP J3QS39
В	12	TYR	THR	engineered mutation	UNP J3QS39
В	14	GLU	THR	engineered mutation	UNP J3QS39
В	44	ALA	ILE	conflict	UNP J3QS39
В	49	SER	GLN	conflict	UNP J3QS39
В	62	LEU	GLN	conflict	UNP J3QS39
В	64	ASP	GLU	conflict	UNP J3QS39
В	66	LYS	THR	conflict	UNP J3QS39
В	67	ARG	LEU	engineered mutation	UNP J3QS39
В	69	PRO	LEU	conflict	UNP J3QS39
В	70	LEU	VAL	conflict	UNP J3QS39

• Molecule 2 is a protein called Tumor protein p53 binding protein 1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	А	115	Total 933	C 598	N 155	0 177	${ m S} { m 3}$	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

	residue	Modelled	Actual	Comment	Reference
A	1480	GLY	-	expression tag	UNP A6NNK5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1481	PRO	-	expression tag	UNP A6NNK5
А	1482	GLY	-	expression tag	UNP A6NNK5
А	1483	SER	-	expression tag	UNP A6NNK5

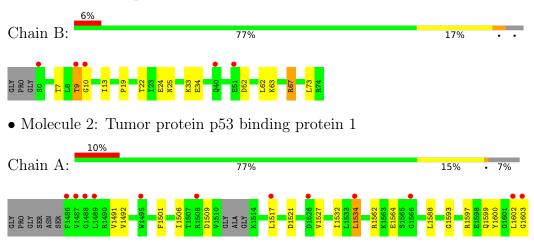
• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	12	Total O 12 12	0	0
3	А	26	Total O 26 26	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: Ubiquitin variant i53



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	39.51Å 46.85 Å 91.12 Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.85 - 1.75	Depositor
	29.85 - 1.75	EDS
% Data completeness	98.9 (29.85-1.75)	Depositor
(in resolution range)	98.9(29.85-1.75)	EDS
R _{merge}	0.06	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.06 (at 1.75 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0411	Depositor
R, R_{free}	0.222 , 0.273	Depositor
It, Itfree	0.229 , 0.275	DCC
R_{free} test set	843 reflections (4.82%)	wwPDB-VP
Wilson B-factor $(Å^2)$	33.2	Xtriage
Anisotropy	0.321	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.39 , 47.1	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	0.96	EDS
Total number of atoms	1573	wwPDB-VP
Average B, all atoms $(Å^2)$	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.57% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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 Chair		Bond	lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	В	0.39	0/610	0.69	0/819	
2	А	0.44	0/951	0.74	0/1275	
All	All	0.42	0/1561	0.72	0/2094	

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	В	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	В	67	ARG	Sidechain

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	В	602	0	630	9	0
2	А	933	0	920	12	0
3	А	26	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	В	12	0	0	0	0
All	All	1573	0	1550	20	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 6.

All (20) 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:B:7:THR:OG1	1:B:9:THR:HG23	1.85	0.75
2:A:1491:VAL:CG1	2:A:1532:ILE:HG23	2.35	0.56
1:B:24:GLU:OE1	1:B:52:ASP:HB3	2.06	0.56
2:A:1491:VAL:HG13	2:A:1532:ILE:HG23	1.89	0.55
2:A:1534:LEU:HD23	2:A:1602:LEU:HG	1.89	0.54
1:B:10:GLY:O	2:A:1521:ASP:HB2	2.12	0.50
2:A:1506:ILE:HG12	2:A:1517:LEU:HD21	1.94	0.49
1:B:63:LYS:HD3	1:B:67:ARG:NH2	2.29	0.48
2:A:1492:VAL:HG12	2:A:1501:PHE:HB3	1.97	0.47
2:A:1602:LEU:HD23	2:A:1603:GLY:N	2.31	0.45
2:A:1501:PHE:HB2	2:A:1588:LEU:HB2	1.99	0.44
1:B:13:ILE:HD11	1:B:34:GLU:HG3	2.00	0.42
1:B:52:ASP:OD1	1:B:52:ASP:N	2.53	0.42
2:A:1562:ARG:HD2	2:A:1564:GLU:OE1	2.19	0.42
2:A:1501:PHE:CE1	2:A:1593:GLY:HA3	2.54	0.42
1:B:19:PRO:HA	1:B:62:LEU:HD12	2.02	0.42
2:A:1509:ASP:OD1	2:A:1509:ASP:C	2.59	0.41
2:A:1534:LEU:HG	2:A:1600:TYR:O	2.20	0.41
1:B:22:THR:H	1:B:25:ASN:HD22	1.69	0.41
1:B:7:THR:HA	1:B:73:LEU:HD12	2.02	0.40

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.



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percer	ntiles
1	В	73/78~(94%)	$71 \ (97\%)$	2 (3%)	0	100	100
2	А	$111/124 \ (90\%)$	108 (97%)	3~(3%)	0	100	100
All	All	184/202~(91%)	179 (97%)	5(3%)	0	100	100

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

There are no Ramachandran outliers to report.

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	В	68/69~(99%)	66~(97%)	2(3%)	42 19
2	А	99/103~(96%)	95~(96%)	4 (4%)	31 10
All	All	167/172~(97%)	161~(96%)	6 (4%)	35 13

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	\mathbf{Res}	Type
1	В	9	THR
1	В	33	LYS
2	А	1527	VAL
2	А	1534	LEU
2	А	1597	ARG
2	А	1599	GLN

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such side chains are listed below:

Mol	Chain	Res	Type
1	В	25	ASN



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, 95^{th} 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	В	75/78~(96%)	0.62	5 (6%) 17 23	27, 47, 70, 79	0
2	А	115/124~(92%)	0.54	12 (10%) 6 9	23, 41, 65, 81	0
All	All	190/202~(94%)	0.57	17 (8%) 9 12	23, 44, 69, 81	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	А	1603	GLY	7.1
2	А	1486	PHE	6.6
2	А	1489	LEU	5.2
2	А	1566	GLY	5.0
1	В	0	SER	3.6
2	А	1495	TRP	3.5
2	А	1526	ASP	3.2
1	В	9	THR	2.7
2	А	1508	ARG	2.7
2	А	1517	LEU	2.3
2	А	1602	LEU	2.3
1	В	40	GLN	2.3
2	А	1487	VAL	2.2
1	В	51	GLU	2.2
1	В	10	GLY	2.2
2	А	1534	LEU	2.1
2	А	1488	GLY	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 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.

