



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 7, 2023 – 03:48 PM EDT

PDB ID : 6DCX
Title : iASPP-PP-1c structure and targeting of p53
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Deposited on : 2018-05-08
Resolution : 3.41 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

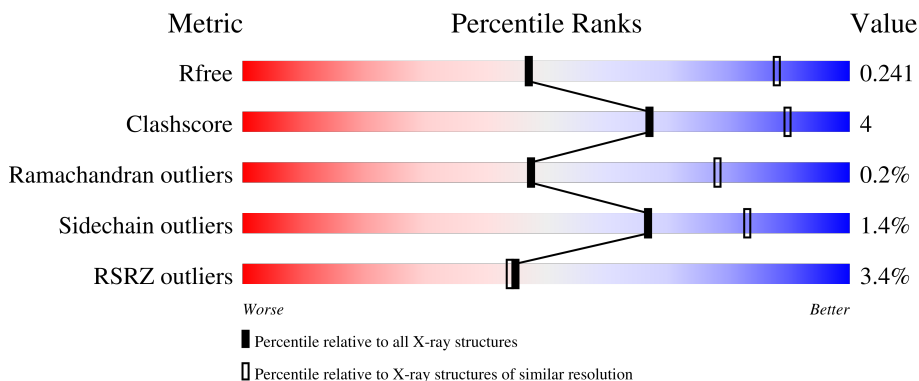
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


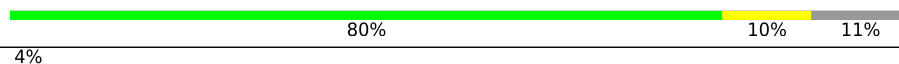
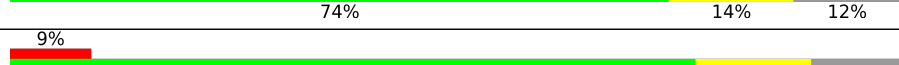

The reported resolution of this entry is 3.41 Å.

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	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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 $\leq 5\%$. 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	339	 82% 6% 12%
1	B	339	 80% 10% 11%
2	C	228	 4% 74% 14% 12%
2	D	228	 9% 77% 13% 10%

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 7972 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 Serine/threonine-protein phosphatase PP1-alpha catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	300	2411	1543	406	444	18	0	0	0
1	B	303	2434	1557	413	446	18	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	GLY	-	expression tag	UNP P62136
A	-7	PRO	-	expression tag	UNP P62136
A	-6	GLY	-	expression tag	UNP P62136
A	-5	TYR	-	expression tag	UNP P62136
A	-4	GLN	-	expression tag	UNP P62136
A	-3	ASP	-	expression tag	UNP P62136
A	-2	PRO	-	expression tag	UNP P62136
A	-1	ASN	-	expression tag	UNP P62136
A	0	SER	-	expression tag	UNP P62136
B	-8	GLY	-	expression tag	UNP P62136
B	-7	PRO	-	expression tag	UNP P62136
B	-6	GLY	-	expression tag	UNP P62136
B	-5	TYR	-	expression tag	UNP P62136
B	-4	GLN	-	expression tag	UNP P62136
B	-3	ASP	-	expression tag	UNP P62136
B	-2	PRO	-	expression tag	UNP P62136
B	-1	ASN	-	expression tag	UNP P62136
B	0	SER	-	expression tag	UNP P62136

- Molecule 2 is a protein called RelA-associated inhibitor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	201	1542	970	259	303	10	0	0	0

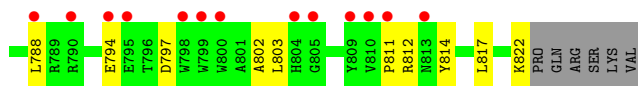
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	206	1585	996	270	309	10	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	601	GLY	-	expression tag	UNP Q8WUF5
C	602	PRO	-	expression tag	UNP Q8WUF5
C	603	GLY	-	expression tag	UNP Q8WUF5
C	604	TYR	-	expression tag	UNP Q8WUF5
C	605	GLN	-	expression tag	UNP Q8WUF5
C	606	ASP	-	expression tag	UNP Q8WUF5
C	607	PRO	-	expression tag	UNP Q8WUF5
D	601	GLY	-	expression tag	UNP Q8WUF5
D	602	PRO	-	expression tag	UNP Q8WUF5
D	603	GLY	-	expression tag	UNP Q8WUF5
D	604	TYR	-	expression tag	UNP Q8WUF5
D	605	GLN	-	expression tag	UNP Q8WUF5
D	606	ASP	-	expression tag	UNP Q8WUF5
D	607	PRO	-	expression tag	UNP Q8WUF5



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	135.46Å 135.46Å 165.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.87 – 3.41 48.87 – 3.41	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.87-3.41) 99.6 (48.87-3.41)	Depositor EDS
R_{merge}	0.30	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 3.40Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.187 , 0.241 0.187 , 0.241	Depositor DCC
R_{free} test set	1113 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	92.0	Xtrriage
Anisotropy	0.277	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 51.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7972	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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	0.29	0/2467	0.46	0/3334
1	B	0.28	0/2490	0.46	0/3364
2	C	0.27	0/1580	0.46	0/2157
2	D	0.27	0/1622	0.46	0/2211
All	All	0.28	0/8159	0.46	0/11066

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	2411	0	2369	13	0
1	B	2434	0	2400	16	0
2	C	1542	0	1447	20	0
2	D	1585	0	1497	18	0
All	All	7972	0	7713	61	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 4.

The worst 5 of 61 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)
2:D:687:ASN:HD21	2:D:718:ALA:H	1.30	0.79
2:D:755:MET:HG2	2:D:817:LEU:HD13	1.70	0.73
1:A:116:GLU:HB3	2:D:609:SER:HB2	1.74	0.68
1:A:270:PRO:HB3	1:A:298:PRO:HD3	1.75	0.68
2:C:640:LEU:HG	2:C:644:GLN:HE21	1.63	0.63

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	296/339 (87%)	280 (95%)	16 (5%)	0	100	100
1	B	299/339 (88%)	282 (94%)	17 (6%)	0	100	100
2	C	199/228 (87%)	193 (97%)	5 (2%)	1 (0%)	29	61
2	D	202/228 (89%)	194 (96%)	7 (4%)	1 (0%)	29	61
All	All	996/1134 (88%)	949 (95%)	45 (4%)	2 (0%)	47	78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	726	ASP
2	D	726	ASP

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	265/295 (90%)	263 (99%)	2 (1%)	81	91
1	B	267/295 (90%)	263 (98%)	4 (2%)	65	82
2	C	160/182 (88%)	159 (99%)	1 (1%)	86	94
2	D	165/182 (91%)	160 (97%)	5 (3%)	41	68
All	All	857/954 (90%)	845 (99%)	12 (1%)	67	83

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	609	SER
2	D	612	ARG
2	D	794	GLU
2	D	641	GLU
1	B	198	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	99	GLN
1	B	99	GLN
2	C	644	GLN
2	C	687	ASN
2	D	687	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, 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	300/339 (88%)	0.21	3 (1%) 82 81	51, 82, 139, 172	0
1	B	303/339 (89%)	0.23	1 (0%) 94 93	53, 85, 131, 172	0
2	C	201/228 (88%)	0.34	10 (4%) 28 29	77, 115, 166, 195	0
2	D	206/228 (90%)	0.74	20 (9%) 7 9	81, 124, 174, 223	0
All	All	1010/1134 (89%)	0.35	34 (3%) 45 44	51, 100, 160, 223	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	799	TRP	4.6
2	D	809	TYR	3.7
2	D	688	SER	3.5
2	D	811	PRO	3.3
1	A	300	ASP	3.1

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.