Full wwPDB X-ray Structure Validation Report (i)

Jun 23, 2024 – 04:54 AM EDT

PDB ID	:	6FCN
Title	:	Crystal structure of human PCNA soaked with p47phox(106-127) peptide
Authors	:	Housset, D.; Frachet, P.
Deposited on	:	2017-12-20
Resolution	:	3.22 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:

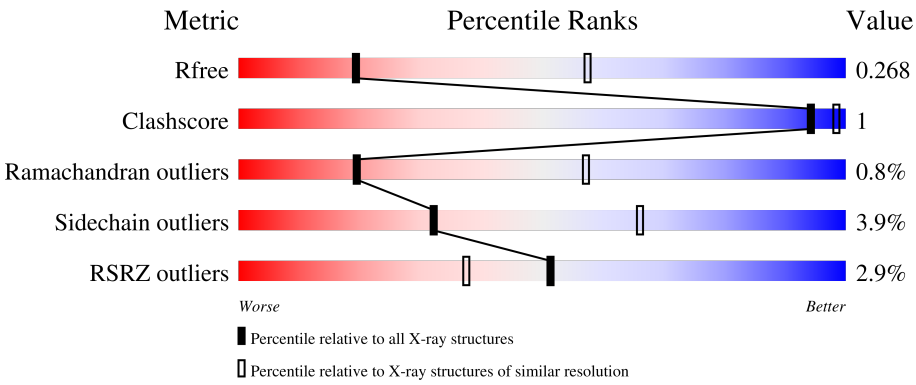
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 3.22 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	1335 (3.24-3.20)
Clashscore	141614	1460 (3.24-3.20)
Ramachandran outliers	138981	1437 (3.24-3.20)
Sidechain outliers	138945	1436 (3.24-3.20)
RSRZ outliers	127900	1291 (3.24-3.20)

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	282	2% 85% • • 11%
1	C	282	% 85% • • 11%
1	E	282	5% 82% 6% • 11%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 5784 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 Proliferating cell nuclear antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	252	1932	1217	318	381	16	0	0	0
1	C	252	1928	1213	318	381	16	0	0	0
1	E	251	1917	1206	316	379	16	0	0	0

There are 63 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	initiating methionine	UNP P12004
A	-19	GLY	-	expression tag	UNP P12004
A	-18	SER	-	expression tag	UNP P12004
A	-17	SER	-	expression tag	UNP P12004
A	-16	HIS	-	expression tag	UNP P12004
A	-15	HIS	-	expression tag	UNP P12004
A	-14	HIS	-	expression tag	UNP P12004
A	-13	HIS	-	expression tag	UNP P12004
A	-12	HIS	-	expression tag	UNP P12004
A	-11	HIS	-	expression tag	UNP P12004
A	-10	SER	-	expression tag	UNP P12004
A	-9	SER	-	expression tag	UNP P12004
A	-8	GLY	-	expression tag	UNP P12004
A	-7	LEU	-	expression tag	UNP P12004
A	-6	VAL	-	expression tag	UNP P12004
A	-5	PRO	-	expression tag	UNP P12004
A	-4	ARG	-	expression tag	UNP P12004
A	-3	GLY	-	expression tag	UNP P12004
A	-2	SER	-	expression tag	UNP P12004
A	-1	HIS	-	expression tag	UNP P12004
A	0	MET	-	expression tag	UNP P12004
C	-20	MET	-	initiating methionine	UNP P12004
C	-19	GLY	-	expression tag	UNP P12004

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-18	SER	-	expression tag	UNP P12004
C	-17	SER	-	expression tag	UNP P12004
C	-16	HIS	-	expression tag	UNP P12004
C	-15	HIS	-	expression tag	UNP P12004
C	-14	HIS	-	expression tag	UNP P12004
C	-13	HIS	-	expression tag	UNP P12004
C	-12	HIS	-	expression tag	UNP P12004
C	-11	HIS	-	expression tag	UNP P12004
C	-10	SER	-	expression tag	UNP P12004
C	-9	SER	-	expression tag	UNP P12004
C	-8	GLY	-	expression tag	UNP P12004
C	-7	LEU	-	expression tag	UNP P12004
C	-6	VAL	-	expression tag	UNP P12004
C	-5	PRO	-	expression tag	UNP P12004
C	-4	ARG	-	expression tag	UNP P12004
C	-3	GLY	-	expression tag	UNP P12004
C	-2	SER	-	expression tag	UNP P12004
C	-1	HIS	-	expression tag	UNP P12004
C	0	MET	-	expression tag	UNP P12004
E	-20	MET	-	initiating methionine	UNP P12004
E	-19	GLY	-	expression tag	UNP P12004
E	-18	SER	-	expression tag	UNP P12004
E	-17	SER	-	expression tag	UNP P12004
E	-16	HIS	-	expression tag	UNP P12004
E	-15	HIS	-	expression tag	UNP P12004
E	-14	HIS	-	expression tag	UNP P12004
E	-13	HIS	-	expression tag	UNP P12004
E	-12	HIS	-	expression tag	UNP P12004
E	-11	HIS	-	expression tag	UNP P12004
E	-10	SER	-	expression tag	UNP P12004
E	-9	SER	-	expression tag	UNP P12004
E	-8	GLY	-	expression tag	UNP P12004
E	-7	LEU	-	expression tag	UNP P12004
E	-6	VAL	-	expression tag	UNP P12004
E	-5	PRO	-	expression tag	UNP P12004
E	-4	ARG	-	expression tag	UNP P12004
E	-3	GLY	-	expression tag	UNP P12004
E	-2	SER	-	expression tag	UNP P12004
E	-1	HIS	-	expression tag	UNP P12004
E	0	MET	-	expression tag	UNP P12004

- Molecule 2 is water.

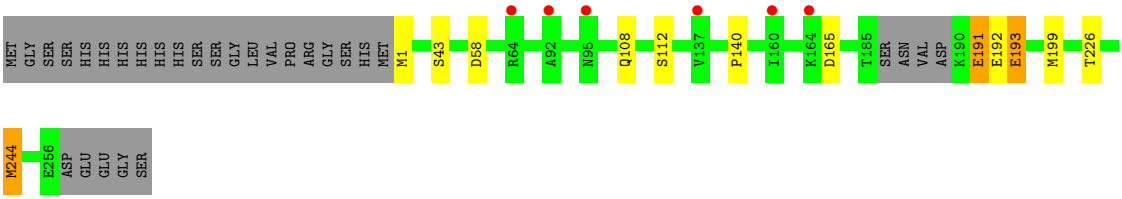
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	2	2	2	0	0
			Total	O		
2	C	3	3	3	0	0
			Total	O		
2	E	2	2	2	0	0

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.

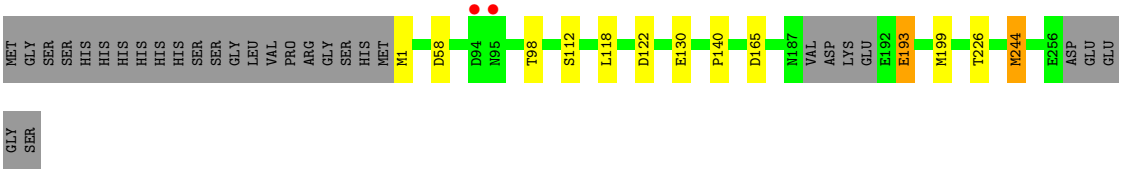
• Molecule 1: Proliferating cell nuclear antigen

Chain A:



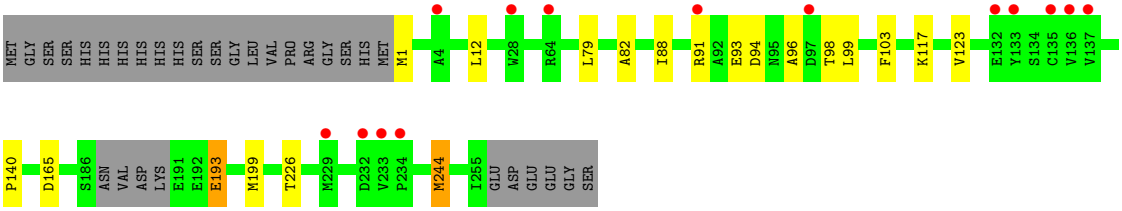
• Molecule 1: Proliferating cell nuclear antigen

Chain C:



• Molecule 1: Proliferating cell nuclear antigen

Chain E:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	39.88Å 140.67Å 171.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.00 – 3.22 41.07 – 3.22	Depositor EDS
% Data completeness (in resolution range)	91.6 (41.00-3.22) 91.7 (41.07-3.22)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.92 (at 3.25Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.209 , 0.272 0.211 , 0.268	Depositor DCC
R_{free} test set	733 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å^2)	105.7	Xtriage
Anisotropy	0.022	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 70.2	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)	121.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.75% 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	0.37	0/1957	0.64	0/2642
1	C	0.38	0/1953	0.63	0/2638
1	E	0.37	0/1942	0.64	0/2623
All	All	0.37	0/5852	0.63	0/7903

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	1932	0	1944	2	1
1	C	1928	0	1936	2	0
1	E	1917	0	1921	11	0
2	A	2	0	0	0	0
2	C	3	0	0	0	0
2	E	2	0	0	0	0
All	All	5784	0	5801	15	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 1.

All (15) 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:E:82:ALA:HB2	1:E:103:PHE:CD2	2.29	0.67
1:E:98:THR:HG22	1:E:117:LYS:HA	1.78	0.66
1:E:93:GLU:O	1:E:96:ALA:HB2	1.99	0.61
1:E:140:PRO:HG3	1:E:193:GLU:HG2	1.82	0.59
1:E:91:ARG:O	1:E:99:LEU:HD12	2.03	0.58
1:E:88:ILE:HG23	1:E:103:PHE:CE1	2.38	0.58
1:C:140:PRO:HG3	1:C:193:GLU:HG2	1.86	0.57
1:E:88:ILE:HG23	1:E:103:PHE:HE1	1.70	0.56
1:A:191:GLU:HB3	1:A:192:GLU:OE1	2.06	0.56
1:A:140:PRO:HG3	1:A:193:GLU:HG2	1.90	0.53
1:E:82:ALA:HB2	1:E:103:PHE:CE2	2.49	0.47
1:E:88:ILE:HG12	1:E:103:PHE:CD1	2.49	0.47
1:E:79:LEU:HD23	1:E:103:PHE:CZ	2.52	0.44
1:C:98:THR:HA	1:C:118:LEU:HG	2.01	0.43
1:E:12:LEU:HD23	1:E:88:ILE:HG21	2.04	0.40

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:43:SER:CB	1:A:192:GLU:OE2[1_655]	2.10	0.10

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	248/282 (88%)	236 (95%)	10 (4%)	2 (1%)	19 57
1	C	248/282 (88%)	235 (95%)	11 (4%)	2 (1%)	19 57
1	E	247/282 (88%)	234 (95%)	11 (4%)	2 (1%)	19 57
All	All	743/846 (88%)	705 (95%)	32 (4%)	6 (1%)	19 57

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	191	GLU
1	A	244	MET
1	C	244	MET
1	E	244	MET
1	C	130	GLU
1	E	123	VAL

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	217/246 (88%)	208 (96%)	9 (4%)	30	65
1	C	217/246 (88%)	208 (96%)	9 (4%)	30	65
1	E	215/246 (87%)	208 (97%)	7 (3%)	38	70
All	All	649/738 (88%)	624 (96%)	25 (4%)	32	66

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	58	ASP
1	A	108	GLN
1	A	112	SER
1	A	165	ASP
1	A	193	GLU
1	A	199	MET
1	A	226	THR
1	A	244	MET
1	C	1	MET
1	C	58	ASP
1	C	112	SER
1	C	122	ASP
1	C	165	ASP
1	C	193	GLU
1	C	199	MET
1	C	226	THR

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Mol	Chain	Res	Type
1	C	244	MET
1	E	1	MET
1	E	94	ASP
1	E	165	ASP
1	E	193	GLU
1	E	199	MET
1	E	226	THR
1	E	244	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	ASN
1	A	49	GLN
1	A	65	ASN
1	A	108	GLN
1	C	36	ASN
1	C	49	GLN
1	C	65	ASN
1	E	36	ASN
1	E	49	GLN
1	E	65	ASN
1	E	108	GLN

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	252/282 (89%)	0.32	6 (2%)	59	45	81, 112, 161, 195	0
1	C	252/282 (89%)	0.20	2 (0%)	86	79	74, 106, 163, 200	0
1	E	251/282 (89%)	0.44	14 (5%)	24	14	96, 134, 172, 202	0
All	All	755/846 (89%)	0.32	22 (2%)	51	37	74, 117, 165, 202	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	135	CYS	4.7
1	E	4	ALA	3.1
1	C	95	ASN	2.9
1	A	64	ARG	2.9
1	E	132	GLU	2.7
1	E	233	VAL	2.7
1	E	64	ARG	2.7
1	E	97	ASP	2.7
1	E	232	ASP	2.6
1	A	95	ASN	2.6
1	E	137	VAL	2.6
1	E	133	TYR	2.5
1	E	91	ARG	2.5
1	E	229	MET	2.4
1	A	92	ALA	2.3
1	A	164	LYS	2.3
1	E	28	TRP	2.3
1	A	160	ILE	2.3
1	A	137	VAL	2.2
1	E	234	PRO	2.1
1	E	136	VAL	2.0
1	C	94	ASP	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.