wwPDB X-ray Structure Validation Summary Report (i)

May 27, 2020 – 12:34 am BST

PDB ID	:	6EHT
Title	:	Modulation of PCNA sliding surface by p15PAF suggests a suppressive mechanism for cisplatin-induced DNA lesion bypass by pol eta holoenzyme
Authors	:	De March, M.; Barrera-Vilarmau, S.; Mentegari, E.; Merino, N.; Bressan, E.; Maga, G.; Crehuet, R.; Onesti, S.; Blanco, F.J.; De Biasio, A.
Deposited on	:	2017-09-15
Resolution	:	3.20 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

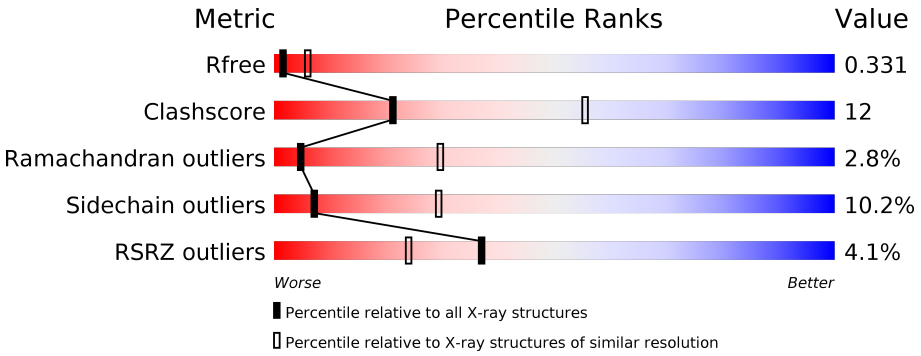
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 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	254	4% 73% 21% 6%
1	B	254	% 77% 19% .
2	C	256	2% 72% 23% .
3	D	20	80% 20%
3	E	20	15% 70% 25% 5%
4	F	10	80% 80% 20%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	G	10	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5925 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
1	A	254	Total	C	N	O	S	0	0	0
			1733	1102	289	328	14			
1	B	253	Total	C	N	O	S	0	0	0
			1652	1050	278	311	13			

- Molecule 2 is a protein called Proliferating cell nuclear antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	256	Total	C	N	O	S	0	0	0
			1844	1161	312	355	16			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	HIS	-	expression tag	UNP P12004

- Molecule 3 is a protein called PCNA-associated factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	20	Total	C	N	O	S	0	0	0
			145	98	22	24	1			
3	E	19	Total	C	N	O	S	0	0	0
			132	88	22	21	1			

- Molecule 4 is a DNA chain called DNA (5'-D(P*AP*TP*AP*CP*GP*AP*TP*GP*GP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	10	Total	C	N	O	P	0	0	0
			210	99	42	59	10			

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

3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	G	10	Total	C	N	O	P	0	0	0
			200	96	33	61	10			

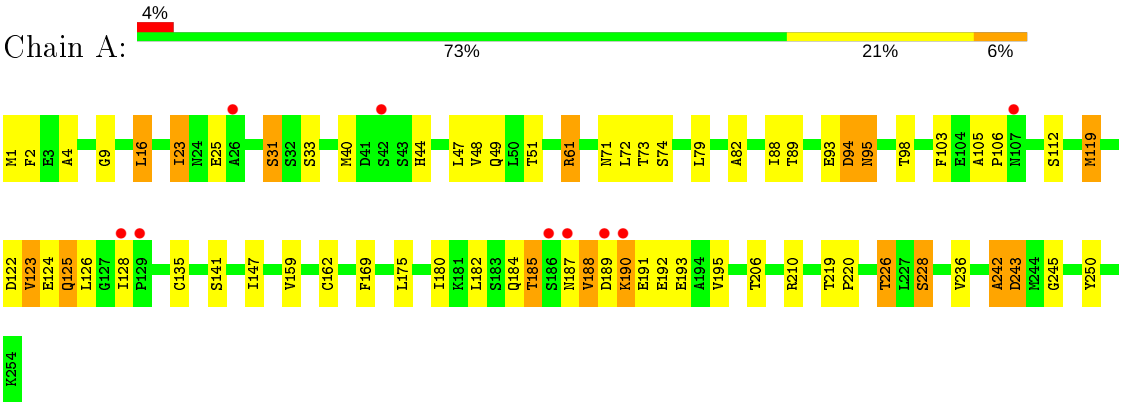
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	3	Total	O	0	0
			3	3		
6	B	1	Total	O	0	0
			1	1		
6	C	5	Total	O	0	0
			5	5		

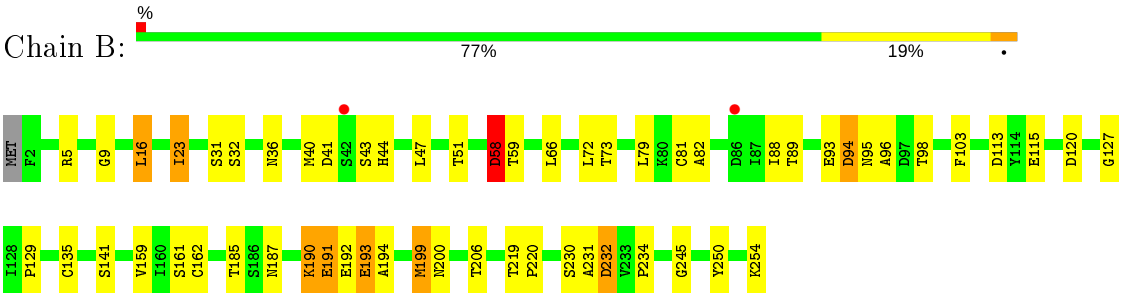
3 Residue-property plots

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.

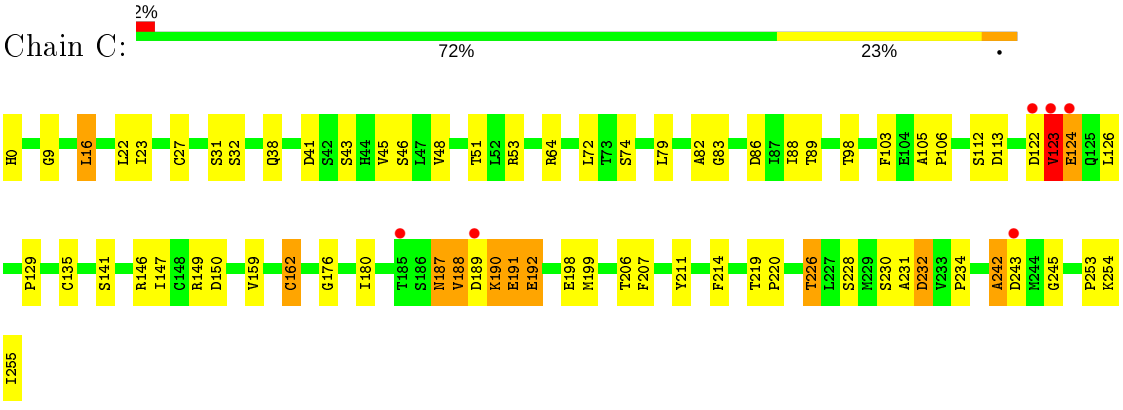
- Molecule 1: Proliferating cell nuclear antigen



- Molecule 1: Proliferating cell nuclear antigen



- Molecule 2: Proliferating cell nuclear antigen

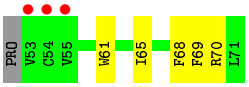


- Molecule 3: PCNA-associated factor

Chain D:

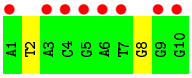
• Molecule 3: PCNA-associated factor

Chain E:



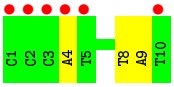
• Molecule 4: DNA (5'-D(P*AP*TP*AP*CP*GP*AP*TP*GP*GP*G)-3')

Chain F:



• Molecule 5: DNA (5'-D(P*CP*CP*CP*AP*TP*CP*GP*TP*AP*T)-3')

Chain G:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	75.99Å 42.30Å 141.83Å 90.00° 102.70° 90.00°	Depositor
Resolution (Å)	40.48 – 3.20 40.45 – 3.20	Depositor EDS
% Data completeness (in resolution range)	94.2 (40.48-3.20) 94.3 (40.45-3.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.21 (at 3.18Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.261 , 0.327 0.259 , 0.331	Depositor DCC
R_{free} test set	716 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	70.8	Xtriage
Anisotropy	0.580	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.17 , 63.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.36$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.85	EDS
Total number of atoms	5925	wwPDB-VP
Average B, all atoms (Å^2)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.22% 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

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	A	0.58	0/1759	0.75	0/2403
1	B	0.55	0/1677	0.71	0/2301
2	C	0.70	0/1871	0.82	0/2542
3	D	0.60	0/151	0.72	0/207
3	E	0.39	0/137	0.64	0/187
4	F	0.34	0/236	0.96	1/363 (0.3%)
5	G	0.37	0/222	0.85	0/339
All	All	0.59	0/6053	0.77	1/8342 (0.0%)

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	A	0	1
2	C	0	3
All	All	0	4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	F	2	DT	C1'-O4'-C4'	-5.08	105.02	110.10

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	210	ARG	Sidechain
2	C	0	HIS	Peptide
2	C	53	ARG	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
2	C	64	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	A	1733	0	1546	46	0
1	B	1652	0	1360	38	0
2	C	1844	0	1738	47	0
3	D	145	0	124	3	0
3	E	132	0	105	4	0
4	F	210	0	113	1	0
5	G	200	0	114	2	0
6	A	3	0	0	0	0
6	B	1	0	0	0	0
6	C	5	0	0	0	0
All	All	5925	0	5100	130	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 12.

The worst 5 of 130 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:61:ARG:HH11	1:A:61:ARG:HG3	0.92	1.06
2:C:123:VAL:HG13	2:C:124:GLU:N	1.71	1.04
1:B:254:LYS:HA	3:E:61:TRP:CZ3	1.97	0.99
1:A:61:ARG:NH1	1:A:61:ARG:HG3	1.69	0.94
1:B:199:MET:CE	1:B:200:ASN:O	2.19	0.91

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	252/254 (99%)	224 (89%)	20 (8%)	8 (3%)	4 26
1	B	251/254 (99%)	222 (88%)	23 (9%)	6 (2%)	6 34
2	C	254/256 (99%)	232 (91%)	14 (6%)	8 (3%)	4 26
3	D	18/20 (90%)	17 (94%)	1 (6%)	0	100 100
3	E	17/20 (85%)	14 (82%)	3 (18%)	0	100 100
All	All	792/804 (98%)	709 (90%)	61 (8%)	22 (3%)	5 29

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	94	ASP
1	A	123	VAL
1	A	190	LYS
1	B	190	LYS
1	B	193	GLU

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	151/222 (68%)	136 (90%)	15 (10%)	8 30
1	B	124/222 (56%)	108 (87%)	16 (13%)	4 19
2	C	184/224 (82%)	168 (91%)	16 (9%)	10 37
3	D	13/18 (72%)	12 (92%)	1 (8%)	13 44

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	E	10/18 (56%)	9 (90%)	1 (10%)	7 30
All	All	482/704 (68%)	433 (90%)	49 (10%)	7 29

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	73	THR
1	B	135	CYS
2	C	228	SER
1	B	98	THR
1	B	161	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	ASN
2	C	38	GLN
1	B	246	HIS
1	A	49	GLN
1	A	131	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

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, 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	A	254/254 (100%)	-0.14	9 (3%) 44 28	43, 64, 73, 81	107 (42%)
1	B	253/254 (99%)	-0.13	2 (0%) 86 78	56, 66, 74, 78	137 (54%)
2	C	256/256 (100%)	-0.33	6 (2%) 60 47	32, 53, 76, 113	44 (17%)
3	D	20/20 (100%)	-0.01	0 100 100	58, 70, 88, 106	6 (30%)
3	E	19/20 (95%)	0.92	3 (15%) 2 1	57, 66, 85, 88	19 (100%)
4	F	10/10 (100%)	3.02	8 (80%) 0 0	196, 226, 243, 261	0
5	G	10/10 (100%)	2.27	6 (60%) 0 0	210, 236, 246, 270	0
All	All	822/824 (99%)	-0.10	34 (4%) 37 24	32, 63, 78, 270	313 (38%)

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	G	10	DT	5.9
4	F	4	DC	5.0
2	C	189	ASP	4.4
4	F	6	DA	4.2
3	E	55	VAL	3.7

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.