



wwPDB X-ray Structure Validation Summary Report ⓘ

May 31, 2016 – 04:27 AM EDT

PDB ID : 5IY4
Title : Crystal structure of human PCNA in complex with the PIP box of DVC1
Authors : Jiang, T.; Xu, M.; Wang, Y.
Deposited on : 2016-03-24
Resolution : 2.94 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027674
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027674

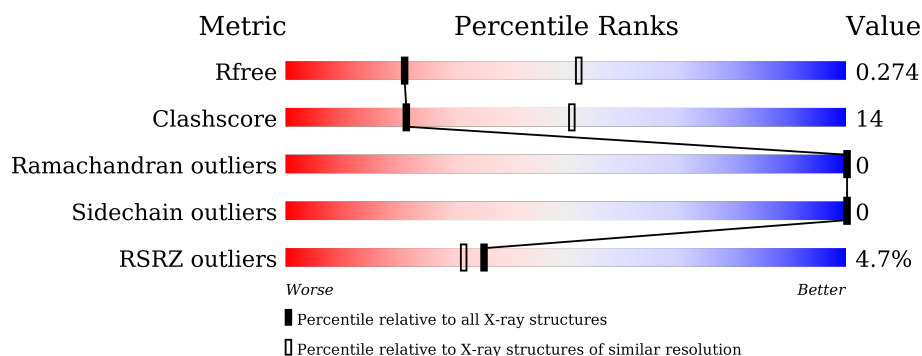
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.94 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}	91344	2057 (2.98-2.90)
Clashscore	102246	2308 (2.98-2.90)
Ramachandran outliers	100387	2245 (2.98-2.90)
Sidechain outliers	100360	2247 (2.98-2.90)
RSRZ outliers	91569	2065 (2.98-2.90)

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. 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	270	<div> <div>2%</div> <div>71% 21% 7%</div> </div>
1	C	270	<div> <div>2%</div> <div>73% 20% 7%</div> </div>
1	E	270	<div> <div>5%</div> <div>72% 20% 7%</div> </div>
2	B	16	<div> <div>81% 6% 13%</div> </div>
2	D	16	<div> <div>6%</div> <div>56% 31% 13%</div> </div>
2	F	16	<div> <div>69%</div> <div>19% 50% 31%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6099 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	250	Total	C	N	O	S	0	0	0
			1922	1209	315	382	16			
1	C	251	Total	C	N	O	S	0	0	0
			1931	1214	316	385	16			
1	E	250	Total	C	N	O	S	0	0	0
			1922	1209	315	382	16			

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	262	LEU	-	expression tag	UNP P12004
A	263	GLU	-	expression tag	UNP P12004
A	264	HIS	-	expression tag	UNP P12004
A	265	HIS	-	expression tag	UNP P12004
A	266	HIS	-	expression tag	UNP P12004
A	267	HIS	-	expression tag	UNP P12004
A	268	HIS	-	expression tag	UNP P12004
A	269	HIS	-	expression tag	UNP P12004
A	270	HIS	-	expression tag	UNP P12004
C	262	LEU	-	expression tag	UNP P12004
C	263	GLU	-	expression tag	UNP P12004
C	264	HIS	-	expression tag	UNP P12004
C	265	HIS	-	expression tag	UNP P12004
C	266	HIS	-	expression tag	UNP P12004
C	267	HIS	-	expression tag	UNP P12004
C	268	HIS	-	expression tag	UNP P12004
C	269	HIS	-	expression tag	UNP P12004
C	270	HIS	-	expression tag	UNP P12004
E	262	LEU	-	expression tag	UNP P12004
E	263	GLU	-	expression tag	UNP P12004
E	264	HIS	-	expression tag	UNP P12004
E	265	HIS	-	expression tag	UNP P12004
E	266	HIS	-	expression tag	UNP P12004

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Chain	Residue	Modelled	Actual	Comment	Reference
E	267	HIS	-	expression tag	UNP P12004
E	268	HIS	-	expression tag	UNP P12004
E	269	HIS	-	expression tag	UNP P12004
E	270	HIS	-	expression tag	UNP P12004

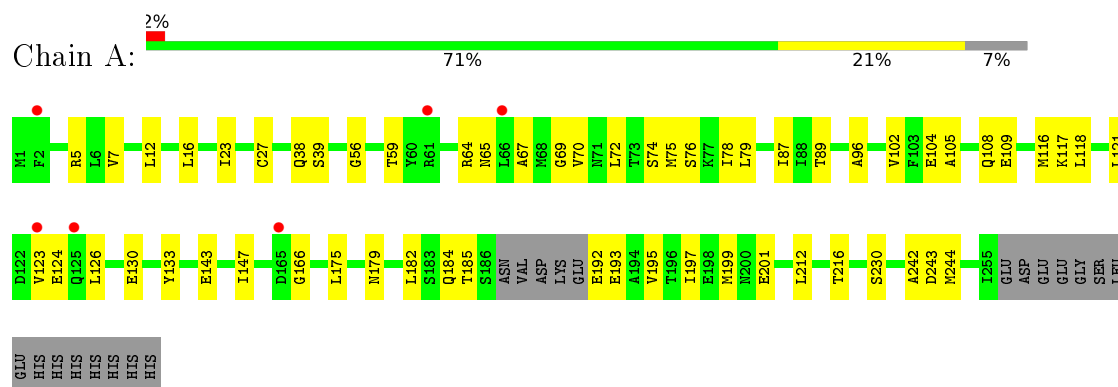
- Molecule 2 is a protein called DVC1 PIP box.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	14	Total	C	N	O	0	0	0
			116	73	22	21			
2	D	14	Total	C	N	O	0	0	0
			116	73	22	21			
2	F	11	Total	C	N	O	0	0	0
			92	59	16	17			

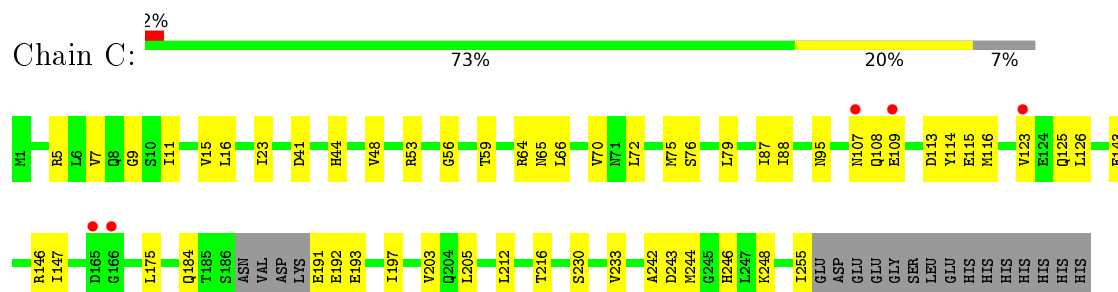
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

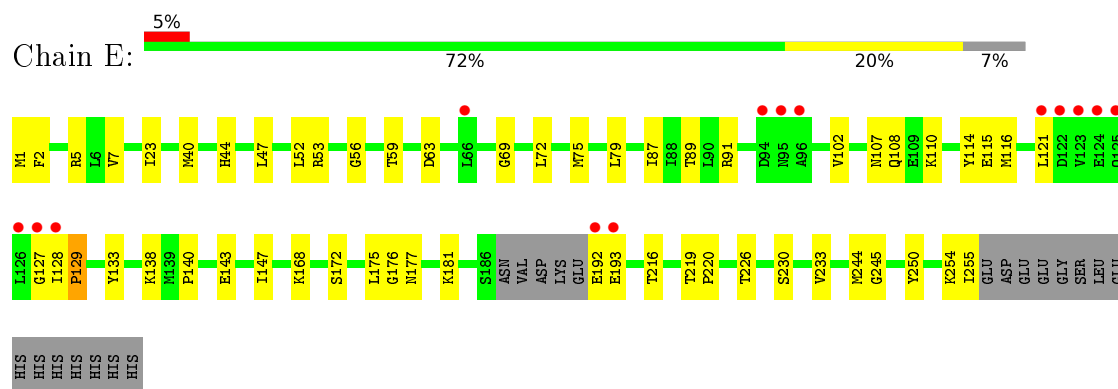
- Molecule 1: Proliferating cell nuclear antigen



- Molecule 1: Proliferating cell nuclear antigen



- Molecule 1: Proliferating cell nuclear antigen



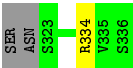
- Molecule 2: DVC1 PIP box

Chain B:

81%

6%

13%



- Molecule 2: DVC1 PIP box

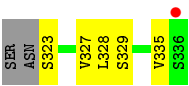
Chain D:

6%

56%

31%

13%



- Molecule 2: DVC1 PIP box

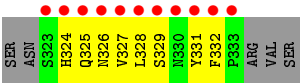
Chain F:

69%

19%

50%

31%



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	71.65Å 71.65Å 322.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.33 – 2.94 48.33 – 2.95	Depositor EDS
% Data completeness (in resolution range)	94.6 (48.33-2.94) 94.7 (48.33-2.95)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.11 (at 2.96Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.207 , 0.270 0.215 , 0.274	Depositor DCC
R_{free} test set	918 reflections (5.15%)	DCC
Wilson B-factor (Å ²)	51.0	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 40.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	6099	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.58	0/1947	0.69	0/2629
1	C	0.61	0/1956	0.72	0/2641
1	E	0.58	1/1947 (0.1%)	0.71	0/2629
2	B	0.39	0/119	0.55	0/161
2	D	0.40	0/119	0.59	0/161
2	F	0.40	0/95	0.58	0/129
All	All	0.58	1/6183 (0.0%)	0.70	0/8350

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	129	PRO	N-CD	5.75	1.55	1.47

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	1922	0	1932	56	1
1	C	1931	0	1938	52	1
1	E	1922	0	1934	66	0
2	B	116	0	108	1	0
2	D	116	0	108	5	0
2	F	92	0	81	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6099	0	6101	172	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 14.

The worst 5 of 172 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:47:LEU:CD2	1:E:128:ILE:HD11	1.42	1.45
1:E:44:HIS:O	2:F:327:VAL:HG13	1.33	1.25
1:E:216:THR:O	1:E:219:THR:HG23	1.45	1.15
1:E:47:LEU:HD22	1:E:128:ILE:HD11	1.23	1.12
1:C:16:LEU:HD22	1:C:79:LEU:HD12	1.30	1.10

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:5:ARG:NH1	1:C:95:ASN:ND2[5_454]	2.15	0.05

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	246/270 (91%)	243 (99%)	3 (1%)	0	100	100
1	C	247/270 (92%)	238 (96%)	9 (4%)	0	100	100
1	E	246/270 (91%)	242 (98%)	4 (2%)	0	100	100
2	B	12/16 (75%)	12 (100%)	0	0	100	100
2	D	12/16 (75%)	11 (92%)	1 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F	9/16 (56%)	4 (44%)	5 (56%)	0	100	100
All	All	772/858 (90%)	750 (97%)	22 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	A	218/237 (92%)	218 (100%)	0	100	100
1	C	219/237 (92%)	219 (100%)	0	100	100
1	E	218/237 (92%)	218 (100%)	0	100	100
2	B	14/16 (88%)	14 (100%)	0	100	100
2	D	14/16 (88%)	14 (100%)	0	100	100
2	F	11/16 (69%)	11 (100%)	0	100	100
All	All	694/759 (91%)	694 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	184	GLN
2	D	324	HIS

5.3.3 RNA ⓘ

There are no RNA molecules 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 [i](#)

There are no carbohydrates 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	250/270 (92%)	0.10	6 (2%) 62 59	23, 38, 64, 78	0
1	C	251/270 (92%)	0.00	5 (1%) 68 66	23, 40, 65, 85	0
1	E	250/270 (92%)	0.36	14 (5%) 28 23	30, 50, 77, 90	0
2	B	14/16 (87%)	0.42	0 100 100	39, 50, 60, 70	0
2	D	14/16 (87%)	0.54	1 (7%) 19 14	46, 52, 72, 74	0
2	F	11/16 (68%)	4.07	11 (100%) 0 0	58, 71, 79, 84	0
All	All	790/858 (92%)	0.22	37 (4%) 35 32	23, 43, 72, 90	0

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	126	LEU	6.8
1	E	124	GLU	6.7
1	E	125	GLN	5.9
2	F	326	ASN	5.8
2	F	329	SER	5.7

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 carbohydrates 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.