



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 24, 2024 – 12:35 AM EDT

PDB ID : 6QC0  
Title : PCNA complex with Cdt2 C-terminal PIP-box peptide  
Authors : Perrakis, A.P.; von Castelmur, E.  
Deposited on : 2018-12-25  
Resolution : 3.50 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) 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

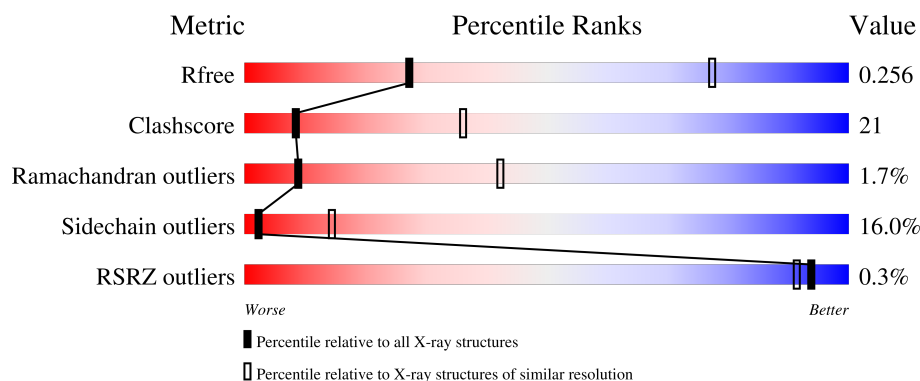
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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  $\geq 3$ , 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	263	<div> <div>55%</div> <div>35%</div> <div>6%</div> <div>.</div> </div>
1	C	263	<div> <div>%</div> <div>60%</div> <div>31%</div> <div>6%</div> <div>.</div> </div>
1	E	263	<div> <div>51%</div> <div>40%</div> <div>6%</div> <div>.</div> </div>
2	B	14	<div> <div>14%</div> <div>36%</div> <div>29%</div> <div>21%</div> </div>
2	D	14	<div> <div>36%</div> <div>29%</div> <div>14%</div> <div>21%</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	14	<div><div></div><div></div><div></div><div></div></div> <div><div>14%</div><div>21%</div><div>43%</div><div>21%</div></div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6173 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
			1950	1225	320	389	16			
1	C	255	Total	C	N	O	S	0	0	0
			1963	1233	322	392	16			
1	E	255	Total	C	N	O	S	0	0	0
			1963	1233	322	392	16			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P12004
A	0	PRO	-	expression tag	UNP P12004
C	-1	GLY	-	expression tag	UNP P12004
C	0	PRO	-	expression tag	UNP P12004
E	-1	GLY	-	expression tag	UNP P12004
E	0	PRO	-	expression tag	UNP P12004

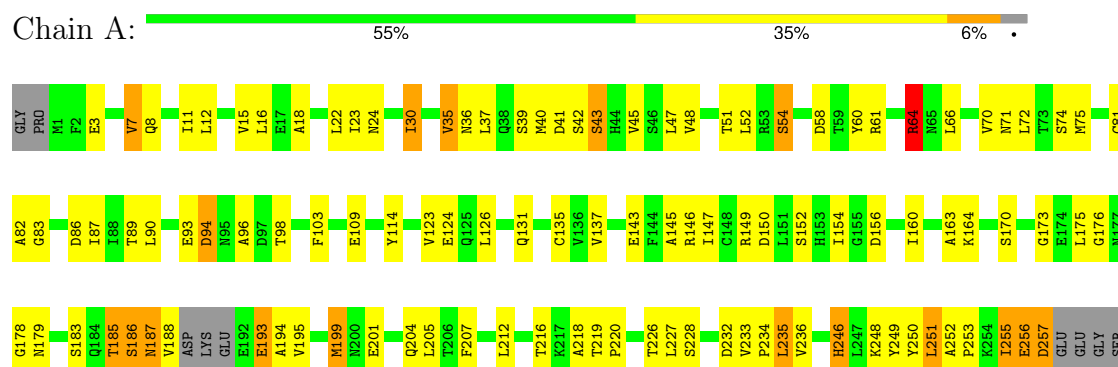
- Molecule 2 is a protein called Denticless protein homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	11	Total	C	N	O	S	0	0	0
			99	63	20	14	2			
2	D	11	Total	C	N	O	S	0	0	0
			99	63	20	14	2			
2	F	11	Total	C	N	O	S	0	0	0
			99	63	20	14	2			

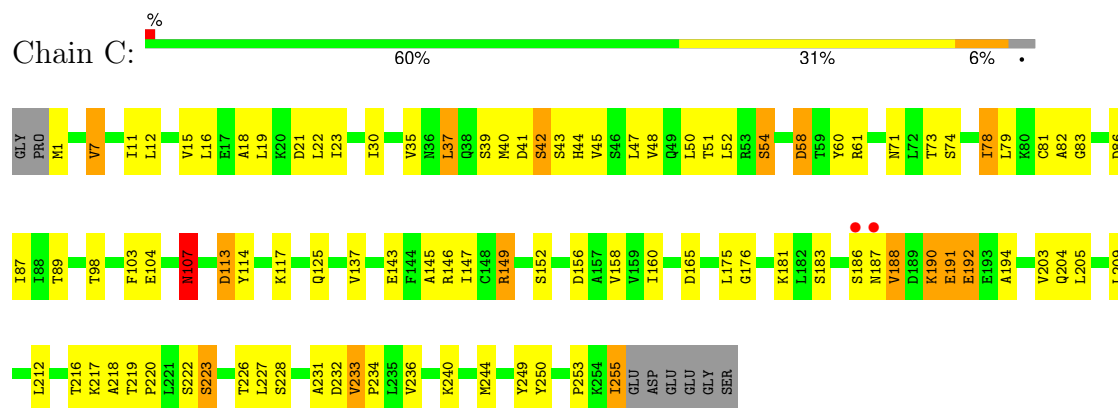
### 3 Residue-property plots

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.

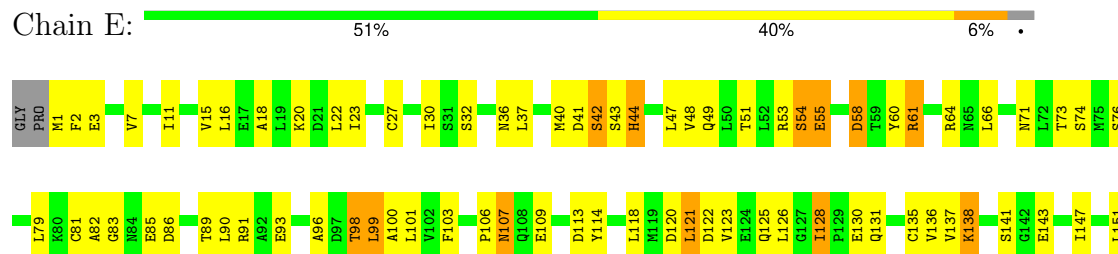
#### • Molecule 1: Proliferating cell nuclear antigen

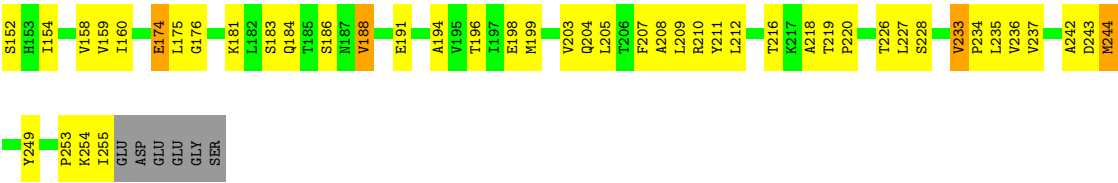


#### • Molecule 1: Proliferating cell nuclear antigen

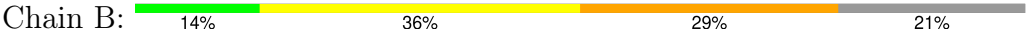


#### • Molecule 1: Proliferating cell nuclear antigen

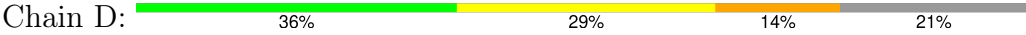




● Molecule 2: Denticleless protein homolog



● Molecule 2: Denticleless protein homolog



● Molecule 2: Denticleless protein homolog



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	151.37Å 151.37Å 91.49Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.73 – 3.50 43.70 – 3.50	Depositor EDS
% Data completeness (in resolution range)	97.2 (43.73-3.50) 97.3 (43.70-3.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.62 (at 3.48Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, $R_{free}$	0.196 , 0.252 0.203 , 0.256	Depositor DCC
$R_{free}$ test set	748 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	63.3	Xtriage
Anisotropy	0.622	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 12.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.055 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	6173	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 ⓘ

### 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	0.77	1/1975 (0.1%)	0.97	3/2668 (0.1%)
1	C	0.72	0/1989	0.97	2/2687 (0.1%)
1	E	0.73	0/1989	1.01	1/2687 (0.0%)
2	B	0.87	0/101	1.19	0/132
2	D	0.91	0/101	1.30	0/132
2	F	0.91	0/101	1.29	0/132
All	All	0.75	1/6256 (0.0%)	1.00	6/8438 (0.1%)

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	1	3
1	C	0	4
1	E	2	0
All	All	3	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	64	ARG	CZ-NH2	12.35	1.49	1.33

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	122	ASP	CB-CA-C	10.53	131.46	110.40
1	C	156	ASP	CB-CA-C	-6.44	97.52	110.40
1	A	64	ARG	NE-CZ-NH2	6.22	123.41	120.30
1	A	156	ASP	CB-CA-C	-6.02	98.36	110.40
1	C	107	ASN	CB-CA-C	5.52	121.44	110.40



All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	186	SER	CA
1	E	122	ASP	CA
1	E	188	VAL	CA

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	109	GLU	Peptide
1	A	185	THR	Peptide
1	A	193	GLU	Peptide
1	C	107	ASN	Peptide
1	C	187	ASN	Peptide

## 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	1950	0	1955	79	0
1	C	1963	0	1973	58	0
1	E	1963	0	1973	100	0
2	B	99	0	100	16	0
2	D	99	0	100	8	0
2	F	99	0	100	21	0
All	All	6173	0	6201	257	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 21.

The worst 5 of 257 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:30:ILE:CD1	1:A:66:LEU:HB2	1.85	1.06
1:C:255:ILE:HG23	2:D:705:SER:HB2	1.44	0.98
1:A:35:VAL:HG23	1:A:52:LEU:HB2	1.46	0.97
1:C:192:GLU:HG3	1:C:223:SER:HB2	1.49	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:255:ILE:CG2	2:D:705:SER:HB2	2.01	0.90

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	250/263 (95%)	215 (86%)	30 (12%)	5 (2%)	7	39
1	C	253/263 (96%)	227 (90%)	23 (9%)	3 (1%)	13	50
1	E	253/263 (96%)	225 (89%)	25 (10%)	3 (1%)	13	50
2	B	9/14 (64%)	6 (67%)	2 (22%)	1 (11%)	0	6
2	D	9/14 (64%)	5 (56%)	3 (33%)	1 (11%)	0	6
2	F	9/14 (64%)	7 (78%)	2 (22%)	0	100	100
All	All	783/831 (94%)	685 (88%)	85 (11%)	13 (2%)	9	42

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	188	VAL
1	E	188	VAL
2	B	706	MET
2	D	706	MET
1	A	187	ASN

### 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	221/229 (96%)	190 (86%)	31 (14%)	3	19
1	C	223/229 (97%)	190 (85%)	33 (15%)	3	17
1	E	223/229 (97%)	187 (84%)	36 (16%)	2	14
2	B	11/14 (79%)	7 (64%)	4 (36%)	0	1
2	D	11/14 (79%)	10 (91%)	1 (9%)	9	36
2	F	11/14 (79%)	4 (36%)	7 (64%)	0	0
All	All	700/729 (96%)	588 (84%)	112 (16%)	2	14

5 of 112 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	203	VAL
2	F	714	HIS
1	E	61	ARG
2	F	711	THR
1	E	244	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	38	GLN
1	E	177	ASN
2	D	714	HIS
1	A	131	GLN
1	A	179	ASN

### 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 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	254/263 (96%)	-0.48	0 100 100	51, 71, 102, 116	0
1	C	255/263 (96%)	-0.40	2 (0%) 86 81	48, 71, 112, 149	0
1	E	255/263 (96%)	-0.44	0 100 100	48, 70, 105, 138	0
2	B	11/14 (78%)	-0.34	0 100 100	76, 84, 103, 105	0
2	D	11/14 (78%)	-0.21	0 100 100	85, 95, 106, 115	0
2	F	11/14 (78%)	-0.08	0 100 100	78, 95, 107, 111	0
All	All	797/831 (95%)	-0.43	2 (0%) 94 91	48, 71, 106, 149	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	187	ASN	2.9
1	C	186	SER	2.1

### 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.