



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 07:31 PM GMT

PDB ID : 4RJF  
Title : Crystal structure of the human sliding clamp at 2.0 angstrom resolution  
Authors : Kroker, A.J.; Bruning, J.B.  
Deposited on : 2014-10-09  
Resolution : 2.01 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  
<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-20026982  
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-20026982

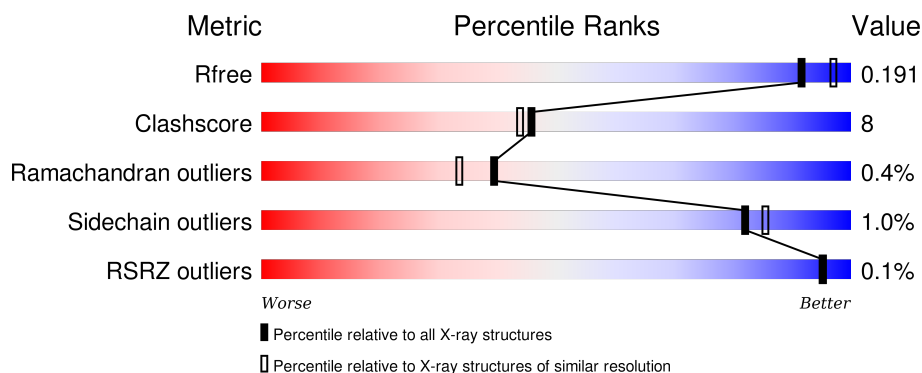
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.01 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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  $\geq 3$ , 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	261	<div> <div>80%</div> <div>18%</div> <div>•</div> </div>
1	C	261	<div> <div>79%</div> <div>17%</div> <div>•</div> </div>
1	E	261	<div> <div>81%</div> <div>14%</div> <div>5%</div> </div>
2	B	22	<div> <div>82%</div> <div>14%</div> <div>5%</div> </div>
2	D	22	<div> <div>73%</div> <div>18%</div> <div>9%</div> </div>

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
2	F	22	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: green (59%), yellow (23%), and grey (18%). The percentages are labeled below each segment.

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8200 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	255	Total	C	N	O	S	0	1	0
			1944	1224	321	383	16			
1	C	253	Total	C	N	O	S	0	3	0
			1934	1217	319	382	16			
1	E	249	Total	C	N	O	S	0	0	0
			1896	1193	311	376	16			

- Molecule 2 is a protein called Cyclin-dependent kinase inhibitor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	21	Total	C	N	O	S	0	0	1
			176	110	36	29	1			
2	D	20	Total	C	N	O	S	0	0	1
			165	104	33	27	1			
2	F	18	Total	C	N	O	S	0	0	0
			158	100	31	26	1			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	151	PHE	TYR	ENGINEERED MUTATION	UNP P38936
D	151	PHE	TYR	ENGINEERED MUTATION	UNP P38936
F	151	PHE	TYR	ENGINEERED MUTATION	UNP P38936

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	555	Total	O	0	0
			555	555		
3	B	49	Total	O	0	0
			49	49		

*Continued on next page...*

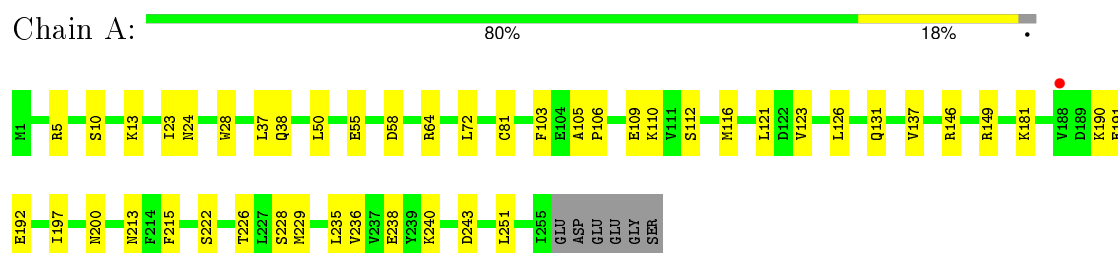
*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	568	Total 568	O 568	0	0
3	D	44	Total 44	O 44	0	0
3	E	615	Total 615	O 615	0	0
3	F	96	Total 96	O 96	0	0

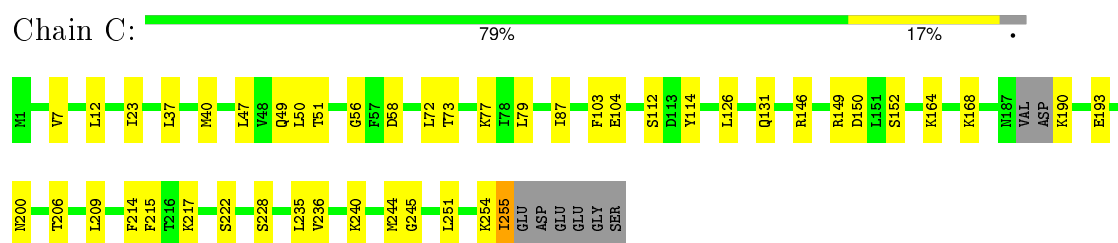
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ( $\text{RSRZ} > 2$ ). 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.

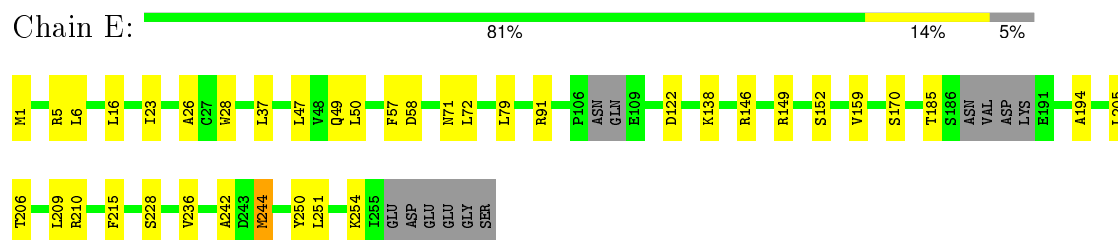
- Molecule 1: Proliferating cell nuclear antigen



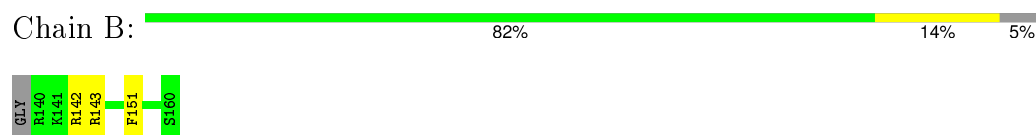
- Molecule 1: Proliferating cell nuclear antigen



- Molecule 1: Proliferating cell nuclear antigen



- Molecule 2: Cyclin-dependent kinase inhibitor 1



- Molecule 2: Cyclin-dependent kinase inhibitor 1

Chain D:  73% 18% 9%



- Molecule 2: Cyclin-dependent kinase inhibitor 1

Chain F:  59% 23% 18%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	142.97Å 142.97Å 41.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.27 – 2.01 41.27 – 2.01	Depositor EDS
% Data completeness (in resolution range)	100.0 (39.27-2.01) 99.3 (41.27-2.01)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.67 (at 2.01Å)	Xtriage
Refinement program	phenix	Depositor
R, $R_{free}$	0.148 , 0.189 0.155 , 0.191	Depositor DCC
$R_{free}$ test set	1962 reflections (3.12%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.2	Xtriage
Anisotropy	0.309	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.16 , 44.0	EDS
Estimated twinning fraction	0.490 for -h,-k,l 0.477 for -h,-k,l 0.129 for h,-h-k,-l 0.130 for -k,-h,-l	Xtriage
Reported twinning fraction	0.490 for -h,-k,l	Depositor
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.36$ , $\langle L^2 \rangle = 0.19$	Xtriage
Outliers	0 of 63386 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8200	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% 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, 0.375 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	0.22	0/1973	0.40	0/2666
1	C	0.22	0/1965	0.40	0/2645
1	E	0.21	0/1920	0.40	0/2593
2	B	0.22	0/179	0.34	0/235
2	D	0.23	0/167	0.35	0/219
2	F	0.22	0/161	0.35	0/212
All	All	0.22	0/6365	0.40	0/8570

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	1944	0	1945	33	0
1	C	1934	0	1951	32	0
1	E	1896	0	1885	23	0
2	B	176	0	173	3	0
2	D	165	0	166	5	0
2	F	158	0	157	5	0
3	A	555	0	0	15	0
3	B	49	0	0	2	0
3	C	568	0	0	7	0
3	D	44	0	0	2	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	615	0	0	8	0
3	F	96	0	0	4	0
All	All	8200	0	6277	96	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 8.

The worst 5 of 96 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:5:ARG:NH1	1:A:58:ASP:OD2	2.24	0.69
1:C:126:LEU:HD23	2:D:153:SER:HB3	1.73	0.69
1:E:228:SER:HB2	1:E:236:VAL:HB	1.81	0.62
1:A:28:TRP:HE1	1:A:72:LEU:HD21	1.63	0.62
1:A:192:GLU:N	3:A:316:HOH:O	2.29	0.62

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	254/261 (97%)	241 (95%)	11 (4%)	2 (1%)	24	15
1	C	250/261 (96%)	242 (97%)	8 (3%)	0	100	100
1	E	243/261 (93%)	232 (96%)	10 (4%)	1 (0%)	39	33
2	B	19/22 (86%)	18 (95%)	1 (5%)	0	100	100
2	D	18/22 (82%)	17 (94%)	1 (6%)	0	100	100
2	F	16/22 (73%)	16 (100%)	0	0	100	100
All	All	800/849 (94%)	766 (96%)	31 (4%)	3 (0%)	39	33

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	109	GLU
1	E	242	ALA
1	A	191	GLU

### 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	216/228 (95%)	215 (100%)	1 (0%)	92	94
1	C	216/228 (95%)	214 (99%)	2 (1%)	84	88
1	E	211/228 (92%)	208 (99%)	3 (1%)	74	77
2	B	19/21 (90%)	19 (100%)	0	100	100
2	D	18/21 (86%)	18 (100%)	0	100	100
2	F	18/21 (86%)	17 (94%)	1 (6%)	26	20
All	All	698/747 (93%)	691 (99%)	7 (1%)	82	85

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	49	GLN
2	F	147	MET
1	E	210	ARG
1	C	235	LEU
1	E	244	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	177	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 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, 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	255/261 (97%)	-0.82	1 (0%) 93 93	16, 22, 29, 40	9 (3%)
1	C	253/261 (96%)	-0.81	0 100 100	18, 23, 31, 36	5 (1%)
1	E	249/261 (95%)	-0.81	0 100 100	21, 26, 32, 41	15 (6%)
2	B	21/22 (95%)	-0.83	0 100 100	17, 22, 29, 31	1 (4%)
2	D	20/22 (90%)	-0.63	0 100 100	23, 29, 34, 35	1 (5%)
2	F	18/22 (81%)	-0.88	0 100 100	25, 28, 31, 33	0
All	All	816/849 (96%)	-0.81	1 (0%) 95 95	16, 24, 32, 41	31 (3%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	188	VAL	2.2

### 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.