Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 05:16 pm BST

PDB ID	:	1W60
Title	:	NATIVE HUMAN PCNA
Authors	:	Kontopidis, G.; Wu, S.; Zheleva, D.; Taylor, P.; Mcinnes, C.; Lane, D.; Fischer, P.; Walkinshaw, M.
Deposited on	:	2004-08-11
Resolution	:	3.15 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 ⓘ symbol.

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

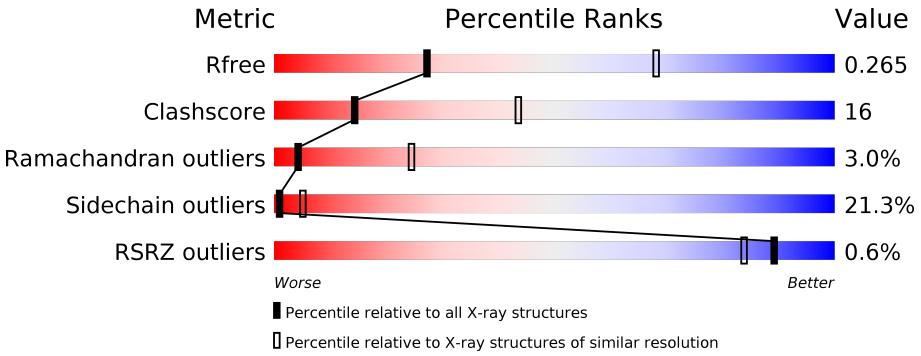
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 3.15 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	1665 (3.20-3.12)
Clashscore	141614	1804 (3.20-3.12)
Ramachandran outliers	138981	1770 (3.20-3.12)
Sidechain outliers	138945	1769 (3.20-3.12)
RSRZ outliers	127900	1616 (3.20-3.12)

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	261	66% 25% 7%
1	B	261	% 57% 29% 9%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3984 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	0	0
			1963	1233	322	392	16			
1	B	255	Total	C	N	O	S	0	0	0
			1963	1233	322	392	16			

- Molecule 2 is water.

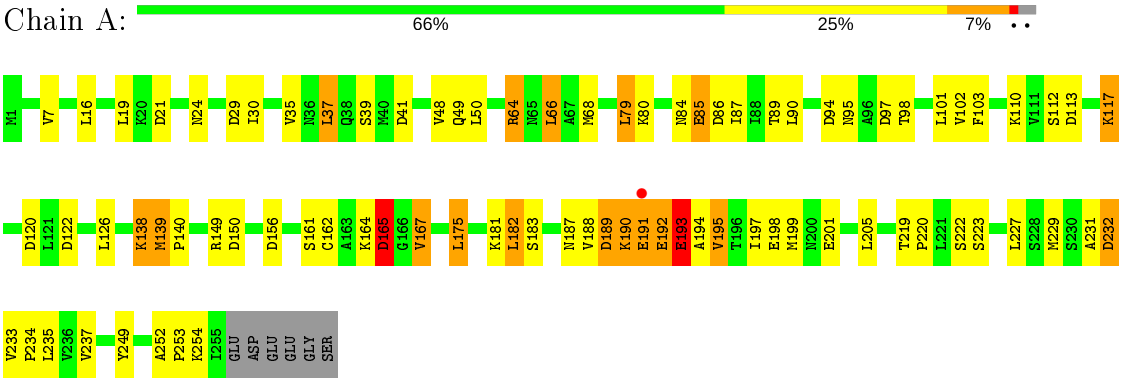
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	26	Total	O	0	0
			26	26		
2	B	32	Total	O	0	0
			32	32		

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 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.

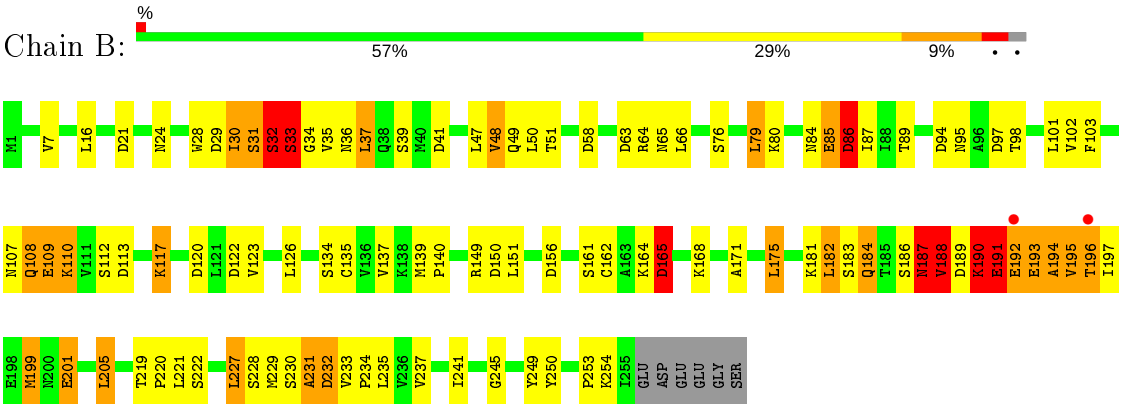
- Molecule 1: PROLIFERATING CELL NUCLEAR ANTIGEN

Chain A:



- Molecule 1: PROLIFERATING CELL NUCLEAR ANTIGEN

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, α, β, γ	82.89Å 82.89Å 70.86Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	11.00 – 3.15 25.21 – 3.14	Depositor EDS
% Data completeness (in resolution range)	98.1 (11.00-3.15) 97.6 (25.21-3.14)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.98 (at 3.17Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.193 , 0.278 0.213 , 0.265	Depositor DCC
R_{free} test set	444 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å^2)	63.9	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 21.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	0.470 for -h,-k,l 0.116 for h,-h-k,-l 0.115 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	3984	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.69% 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	0.32	0/1989	0.65	13/2687 (0.5%)
1	B	0.46	1/1989 (0.1%)	0.73	13/2687 (0.5%)
All	All	0.39	1/3978 (0.0%)	0.69	26/5374 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	28	TRP	NE1-CE2	8.64	1.48	1.37

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	58	ASP	CB-CG-OD2	5.28	123.05	118.30
1	A	86	ASP	CB-CG-OD2	5.27	123.05	118.30
1	A	156	ASP	CB-CG-OD2	5.25	123.03	118.30
1	A	122	ASP	CB-CG-OD2	5.25	123.02	118.30
1	B	122	ASP	CB-CG-OD2	5.24	123.01	118.30
1	A	94	ASP	CB-CG-OD2	5.23	123.01	118.30
1	A	97	ASP	CB-CG-OD2	5.23	123.01	118.30
1	A	113	ASP	CB-CG-OD2	5.23	123.01	118.30
1	B	97	ASP	CB-CG-OD2	5.23	123.00	118.30
1	B	94	ASP	CB-CG-OD2	5.22	123.00	118.30
1	B	156	ASP	CB-CG-OD2	5.22	123.00	118.30
1	B	63	ASP	CB-CG-OD2	5.21	122.99	118.30
1	A	150	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	232	ASP	CB-CG-OD2	5.20	122.98	118.30
1	B	21	ASP	CB-CG-OD2	5.19	122.97	118.30
1	B	86	ASP	CB-CG-OD2	5.19	122.97	118.30
1	A	120	ASP	CB-CG-OD2	5.18	122.97	118.30
1	B	165	ASP	CB-CG-OD2	5.18	122.96	118.30
1	B	41	ASP	CB-CG-OD2	5.18	122.96	118.30
1	A	21	ASP	CB-CG-OD2	5.17	122.95	118.30
1	A	29	ASP	CB-CG-OD2	5.17	122.95	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	113	ASP	CB-CG-OD2	5.15	122.94	118.30
1	B	120	ASP	CB-CG-OD2	5.15	122.94	118.30
1	A	165	ASP	CB-CG-OD2	5.14	122.93	118.30
1	B	150	ASP	CB-CG-OD2	5.13	122.92	118.30
1	A	41	ASP	CB-CG-OD2	5.09	122.88	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1963	0	1973	37	0
1	B	1963	0	1973	85	0
2	A	26	0	0	0	0
2	B	32	0	0	1	0
All	All	3984	0	3946	122	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 16.

All (122) 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:B:187:ASN:O	1:B:188:VAL:HG12	1.33	1.22
1:B:184:GLN:HB2	1:B:195:VAL:HG11	1.16	1.16
1:A:194:ALA:O	1:A:195:VAL:HG23	1.47	1.12
1:B:182:LEU:O	1:B:183:SER:OG	1.69	1.09
1:B:140:PRO:HG2	1:B:193:GLU:HG3	1.33	1.09
1:B:230:SER:O	1:B:231:ALA:O	1.68	1.08
1:B:187:ASN:C	1:B:188:VAL:HG12	1.65	1.08
1:A:192:GLU:OE1	1:A:192:GLU:HA	1.30	1.06
1:B:187:ASN:O	1:B:188:VAL:CG1	2.09	0.99
1:B:135:CYS:SG	1:B:199:MET:HB2	2.01	0.98
1:B:195:VAL:HG13	1:B:196:THR:N	1.78	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:184:GLN:HB2	1:B:195:VAL:CG1	1.93	0.97
1:B:195:VAL:HG13	1:B:196:THR:H	1.28	0.93
1:B:188:VAL:CG2	1:B:188:VAL:O	2.19	0.91
1:B:140:PRO:CG	1:B:193:GLU:HG3	2.00	0.90
1:B:188:VAL:HG22	1:B:188:VAL:O	1.70	0.90
1:B:189:ASP:O	1:B:191:GLU:N	2.03	0.90
1:A:192:GLU:OE1	1:A:192:GLU:CA	2.15	0.89
1:B:189:ASP:C	1:B:191:GLU:H	1.76	0.88
1:B:195:VAL:CG1	1:B:196:THR:H	1.86	0.87
1:B:231:ALA:O	1:B:232:ASP:HB2	1.73	0.87
1:A:195:VAL:O	1:A:195:VAL:HG12	1.75	0.85
1:A:188:VAL:HG23	1:A:188:VAL:O	1.78	0.81
1:B:187:ASN:C	1:B:188:VAL:CG1	2.39	0.81
1:B:205:LEU:CD2	1:B:231:ALA:HA	2.10	0.81
1:B:195:VAL:O	1:B:196:THR:O	2.00	0.80
1:B:108:GLN:O	1:B:109:GLU:HB3	1.81	0.80
1:A:187:ASN:ND2	1:A:189:ASP:OD2	2.16	0.78
1:B:108:GLN:O	1:B:109:GLU:CB	2.32	0.78
1:A:194:ALA:O	1:A:195:VAL:CG2	2.30	0.76
1:B:184:GLN:CB	1:B:195:VAL:HG11	2.08	0.74
1:B:205:LEU:HD21	1:B:231:ALA:HA	1.71	0.72
1:A:188:VAL:CG2	1:A:188:VAL:O	2.40	0.70
1:B:103:PHE:HB2	1:B:112:SER:HB2	1.74	0.69
1:B:187:ASN:O	1:B:188:VAL:CB	2.41	0.69
1:B:182:LEU:C	1:B:183:SER:HG	1.92	0.68
1:B:31:SER:HB2	1:B:65:ASN:ND2	2.11	0.65
1:B:134:SER:HB3	1:B:201:GLU:HG3	1.78	0.64
1:B:237:VAL:O	1:B:249:TYR:N	2.30	0.63
1:A:192:GLU:O	1:A:193:GLU:O	2.16	0.63
1:B:32:SER:O	1:B:33:SER:C	2.35	0.62
1:B:195:VAL:CG1	1:B:196:THR:N	2.44	0.62
1:B:189:ASP:C	1:B:191:GLU:N	2.45	0.62
1:B:190:LYS:O	1:B:191:GLU:C	2.39	0.60
1:B:31:SER:O	1:B:32:SER:C	2.40	0.60
1:B:189:ASP:O	1:B:191:GLU:HG2	2.02	0.59
1:A:195:VAL:O	1:A:195:VAL:CG1	2.49	0.59
1:B:205:LEU:HD23	1:B:231:ALA:HA	1.83	0.59
1:A:191:GLU:O	1:A:192:GLU:OE1	2.21	0.59
1:B:107:ASN:O	1:B:108:GLN:O	2.21	0.59
1:B:135:CYS:SG	1:B:199:MET:CB	2.87	0.58
1:B:237:VAL:HB	1:B:249:TYR:HB2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:MET:HB3	1:A:195:VAL:HG22	1.86	0.58
1:B:205:LEU:HD21	1:B:231:ALA:CA	2.34	0.58
1:A:189:ASP:N	1:A:189:ASP:OD1	2.37	0.58
1:B:219:THR:HB	1:B:220:PRO:HD3	1.85	0.57
1:B:31:SER:O	1:B:33:SER:N	2.38	0.57
1:B:187:ASN:HD22	1:B:188:VAL:H	1.53	0.56
1:A:219:THR:HB	1:A:220:PRO:HD3	1.88	0.56
1:B:234:PRO:HA	1:B:253:PRO:HD3	1.87	0.56
1:A:16:LEU:HD22	1:A:79:LEU:HD13	1.87	0.56
1:B:16:LEU:HD22	1:B:79:LEU:HD13	1.89	0.55
1:B:32:SER:O	1:B:34:GLY:N	2.41	0.54
1:B:192:GLU:HB3	2:B:2027:HOH:O	2.08	0.53
1:B:182:LEU:C	1:B:183:SER:OG	2.43	0.53
1:A:231:ALA:O	1:A:232:ASP:HB2	2.09	0.52
1:A:219:THR:N	1:A:220:PRO:CD	2.73	0.52
1:A:138:LYS:O	1:A:195:VAL:HA	2.10	0.51
1:A:165:ASP:OD1	1:A:165:ASP:N	2.43	0.51
1:B:37:LEU:HB3	1:B:50:LEU:HB3	1.91	0.51
1:B:188:VAL:HG23	1:B:188:VAL:O	2.09	0.51
1:B:193:GLU:O	1:B:194:ALA:HB2	2.11	0.51
1:B:231:ALA:O	1:B:232:ASP:CB	2.48	0.51
1:A:190:LYS:CG	1:A:191:GLU:N	2.74	0.50
1:B:190:LYS:O	1:B:191:GLU:O	2.29	0.49
1:B:230:SER:O	1:B:231:ALA:C	2.40	0.49
1:B:109:GLU:O	1:B:110:LYS:CB	2.59	0.49
1:B:109:GLU:O	1:B:110:LYS:HB3	2.12	0.49
1:B:219:THR:N	1:B:220:PRO:CD	2.76	0.49
1:B:30:ILE:O	1:B:31:SER:HB3	2.12	0.48
1:B:190:LYS:HA	1:B:190:LYS:HD2	1.49	0.48
1:B:107:ASN:O	1:B:108:GLN:C	2.52	0.48
1:A:237:VAL:HB	1:A:249:TYR:HB2	1.96	0.48
1:B:47:LEU:HB3	1:B:250:TYR:HB2	1.96	0.47
1:A:103:PHE:HB2	1:A:112:SER:HB2	1.96	0.47
1:A:175:LEU:H	1:A:175:LEU:HG	1.40	0.47
1:A:167:VAL:HG13	1:A:182:LEU:HB2	1.96	0.46
1:A:237:VAL:O	1:A:249:TYR:N	2.47	0.46
1:A:7:VAL:HA	1:A:87:ILE:HG23	1.97	0.46
1:B:189:ASP:O	1:B:191:GLU:CG	2.62	0.46
1:A:140:PRO:HG3	1:A:193:GLU:OE2	2.15	0.46
1:A:66:LEU:HD22	1:A:68:MET:HG3	1.97	0.45
1:B:85:GLU:H	1:B:85:GLU:HG2	1.55	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:151:LEU:HD22	1:B:171:ALA:HB3	1.98	0.45
1:A:89:THR:HB	1:A:102:VAL:HB	1.98	0.45
1:B:85:GLU:O	1:B:86:ASP:C	2.54	0.45
1:A:19:LEU:HD22	1:A:48:VAL:HG11	1.99	0.45
1:B:137:VAL:HB	1:B:227:LEU:HD12	1.99	0.44
1:B:221:LEU:HD22	1:B:241:ILE:HG12	1.99	0.44
1:B:186:SER:OG	1:B:186:SER:O	2.33	0.43
1:A:234:PRO:HA	1:A:253:PRO:HD3	1.99	0.43
1:B:165:ASP:OD1	1:B:165:ASP:N	2.51	0.43
1:B:89:THR:HB	1:B:102:VAL:HB	2.01	0.43
1:B:168:LYS:HB2	1:B:181:LYS:HD2	2.01	0.42
1:A:98:THR:HG22	1:A:117:LYS:HA	2.01	0.42
1:B:98:THR:HG22	1:B:117:LYS:HA	2.00	0.42
1:B:175:LEU:HG	1:B:175:LEU:H	1.56	0.42
1:B:29:ASP:HB2	1:B:36:ASN:HB2	2.01	0.42
1:B:187:ASN:ND2	1:B:188:VAL:H	2.16	0.42
1:B:48:VAL:HG13	1:B:249:TYR:CE1	2.55	0.42
1:A:37:LEU:HB3	1:A:50:LEU:HB3	2.01	0.42
1:A:194:ALA:C	1:A:195:VAL:HG23	2.31	0.41
1:B:7:VAL:HA	1:B:87:ILE:HG23	2.02	0.41
1:A:64:ARG:HD3	1:A:64:ARG:HH11	1.66	0.41
1:B:227:LEU:H	1:B:227:LEU:HG	1.59	0.41
1:B:16:LEU:HD23	1:B:76:SER:HA	2.02	0.41
1:A:252:ALA:HA	1:A:253:PRO:HD3	1.91	0.41
1:B:51:THR:O	1:B:245:GLY:HA3	2.21	0.41
1:B:47:LEU:CD1	1:B:126:LEU:HD12	2.51	0.41
1:B:189:ASP:N	1:B:189:ASP:OD2	2.54	0.40
1:B:230:SER:O	1:B:230:SER:OG	2.39	0.40
1:A:85:GLU:HG2	1:A:85:GLU:H	1.52	0.40

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	253/261 (97%)	236 (93%)	15 (6%)	2 (1%)	19 55
1	B	253/261 (97%)	223 (88%)	17 (7%)	13 (5%)	2 13
All	All	506/522 (97%)	459 (91%)	32 (6%)	15 (3%)	4 24

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	193	GLU
1	A	195	VAL
1	B	32	SER
1	B	108	GLN
1	B	187	ASN
1	B	188	VAL
1	B	190	LYS
1	B	196	THR
1	B	231	ALA
1	B	33	SER
1	B	191	GLU
1	B	195	VAL
1	B	109	GLU
1	B	194	ALA
1	B	31	SER

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	223/228 (98%)	176 (79%)	47 (21%)	1 5
1	B	223/228 (98%)	175 (78%)	48 (22%)	1 5
All	All	446/456 (98%)	351 (79%)	95 (21%)	1 5

All (95) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ASN

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Mol	Chain	Res	Type
1	A	30	ILE
1	A	35	VAL
1	A	37	LEU
1	A	39	SER
1	A	49	GLN
1	A	64	ARG
1	A	66	LEU
1	A	79	LEU
1	A	80	LYS
1	A	84	ASN
1	A	85	GLU
1	A	90	LEU
1	A	95	ASN
1	A	101	LEU
1	A	110	LYS
1	A	117	LYS
1	A	126	LEU
1	A	138	LYS
1	A	139	MET
1	A	149	ARG
1	A	161	SER
1	A	162	CYS
1	A	164	LYS
1	A	165	ASP
1	A	167	VAL
1	A	175	LEU
1	A	181	LYS
1	A	182	LEU
1	A	183	SER
1	A	189	ASP
1	A	190	LYS
1	A	191	GLU
1	A	192	GLU
1	A	193	GLU
1	A	197	ILE
1	A	198	GLU
1	A	199	MET
1	A	201	GLU
1	A	205	LEU
1	A	222	SER
1	A	223	SER
1	A	227	LEU

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Mol	Chain	Res	Type
1	A	229	MET
1	A	233	VAL
1	A	235	LEU
1	A	254	LYS
1	B	24	ASN
1	B	30	ILE
1	B	32	SER
1	B	33	SER
1	B	35	VAL
1	B	37	LEU
1	B	39	SER
1	B	48	VAL
1	B	49	GLN
1	B	64	ARG
1	B	66	LEU
1	B	79	LEU
1	B	80	LYS
1	B	84	ASN
1	B	85	GLU
1	B	86	ASP
1	B	95	ASN
1	B	101	LEU
1	B	110	LYS
1	B	117	LYS
1	B	123	VAL
1	B	139	MET
1	B	149	ARG
1	B	161	SER
1	B	162	CYS
1	B	164	LYS
1	B	165	ASP
1	B	175	LEU
1	B	182	LEU
1	B	184	GLN
1	B	187	ASN
1	B	188	VAL
1	B	190	LYS
1	B	191	GLU
1	B	192	GLU
1	B	193	GLU
1	B	197	ILE
1	B	199	MET

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Mol	Chain	Res	Type
1	B	201	GLU
1	B	205	LEU
1	B	222	SER
1	B	227	LEU
1	B	228	SER
1	B	229	MET
1	B	232	ASP
1	B	233	VAL
1	B	235	LEU
1	B	254	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	ASN
1	A	108	GLN
1	A	184	GLN
1	B	65	ASN
1	B	71	ASN
1	B	187	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

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	255/261 (97%)	-0.11	1 (0%)	92	89	17, 45, 87, 144	0
1	B	255/261 (97%)	-0.11	2 (0%)	86	78	17, 45, 87, 144	0
All	All	510/522 (97%)	-0.11	3 (0%)	89	84	17, 46, 87, 144	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	192	GLU	4.0
1	B	196	THR	2.1
1	A	191	GLU	2.1

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.