Full wwPDB X-ray Structure Validation Report (i)

May 20, 2021 – 06:03 PM EDT

PDB ID	:	6CFI
Title	:	Crystal structure of Rad4-Rad23 bound to a 6-4 photoproduct UV lesion
Authors	:	Min, J.; Jeffrey, P.D.
Deposited on	:	2018-02-15
Resolution	:	3.36 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 (i) symbol.

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

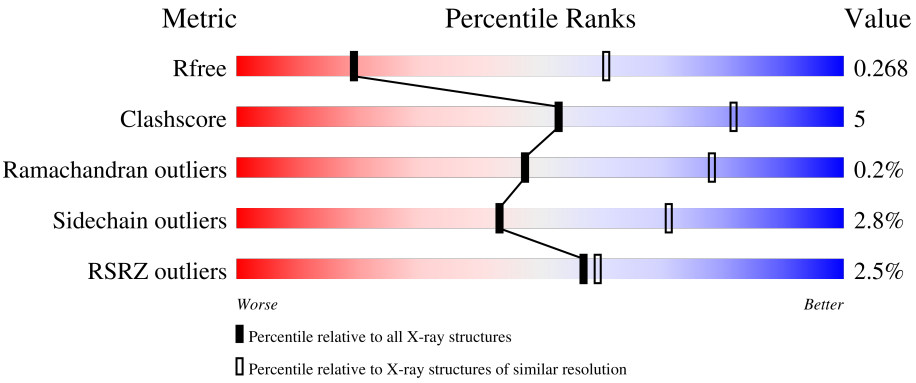
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.18
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.18

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 3.36 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	1558 (3.42-3.30)
Clashscore	141614	1627 (3.42-3.30)
Ramachandran outliers	138981	1599 (3.42-3.30)
Sidechain outliers	138945	1598 (3.42-3.30)
RSRZ outliers	127900	1507 (3.42-3.30)

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 >=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	538	3% 80% 11% • 8%
2	X	171	% 26% 5% 69%
3	W	24	54% 42% •
4	Y	23	26% 65% 9%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 10599 atoms, of which 5126 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 DNA repair protein RAD4.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	496	8248	2608	4162	734	717	27	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	95	GLY	-	expression tag	UNP P14736
A	96	SER	-	expression tag	UNP P14736
A	97	SER	-	expression tag	UNP P14736
A	98	ARG	-	expression tag	UNP P14736
A	99	ALA	-	expression tag	UNP P14736
A	100	MET	-	expression tag	UNP P14736
A	115	THR	LYS	conflict	UNP P14736
A	223	GLU	VAL	conflict	UNP P14736
A	427	ARG	GLN	conflict	UNP P14736

- Molecule 2 is a protein called UV excision repair protein RAD23.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	X	53	827	260	418	69	78	2	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	228	GLY	-	expression tag	UNP P32628
X	229	SER	-	expression tag	UNP P32628

- Molecule 3 is a DNA chain called DNA('-D(*TP*TP*GP*AP*CP*TP*CP*AP*AP*CP*AP*TP*CP*CP*AP*AP*AP*GP*CP*TP*AP*CP*AP*A)-').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	P			
3	W	24	755	233	271	91	137	23	0	0	0

- Molecule 4 is a DNA chain called DNA (5'-D(*AP*TP*TP*GP*TP*AP*GP*CP*(T64)P*TP*GP*GP*AP*TP*GP*TP*TP*GP*AP*GP*TP*CP*A)-3').

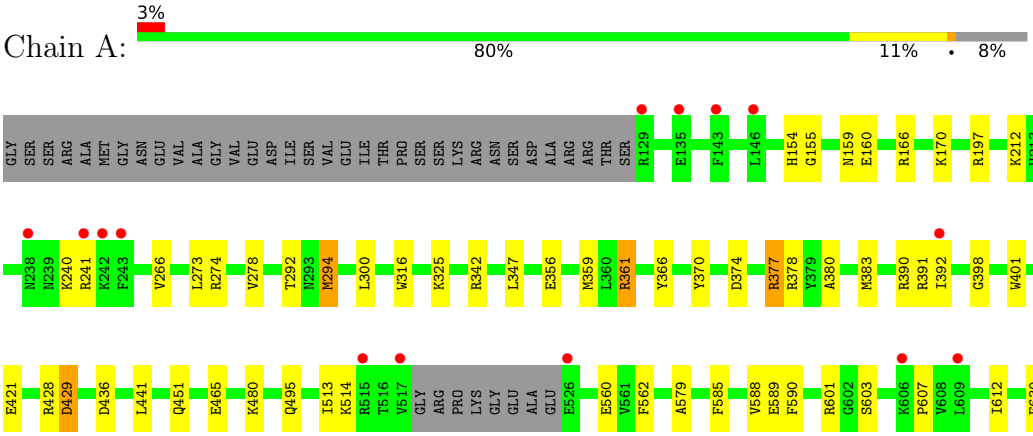
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	P			
4	Y	23	769	238	275	86	147	23	0	0	0

3 Residue-property plots (i)

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.

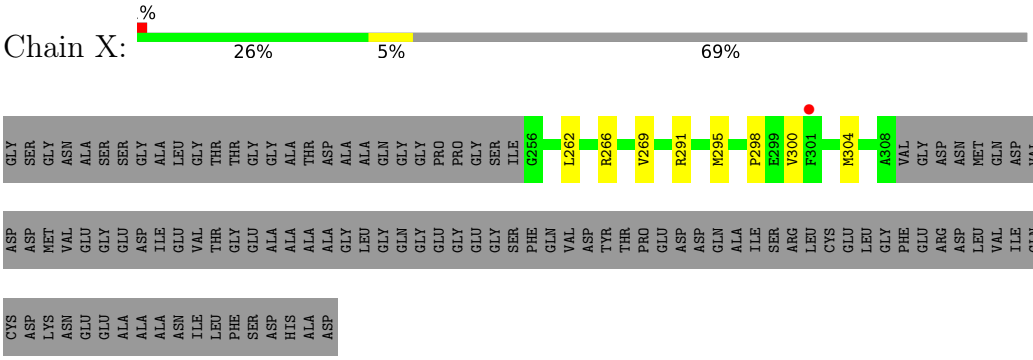
• Molecule 1: DNA repair protein RAD4

Chain A:



• Molecule 2: UV excision repair protein RAD23

Chain X:



• Molecule 3: DNA('-D(*TP*TP*GP*AP*CP*TP*CP*AP*AP*CP*AP*TP*CP*CP*AP*AP*AP*GP*CP*TP*AP*CP*AP*A)-')

Chain W:

• Molecule 4: DNA (5'-D(*AP*TP*TP*GP*TP*AP*GP*CP*(T64)P*TP*GP*GP*AP*TP*GP*TP*TP*GP*AP*GP*TP*CP*A)-3')

Chain Y:


26%
65%
9%
A1
T5
A6
G7
C8
T649
T10
G11
G12
A13
T14
G15
T16
T17
G18
A19
G20
T21
C22
A23

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	80.20Å 80.20Å 405.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	74.57 – 3.36 74.57 – 3.36	Depositor EDS
% Data completeness (in resolution range)	95.9 (74.57-3.36) 95.9 (74.57-3.36)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.17 (at 3.33Å)	Xtriage
Refinement program	PHENIX 1.12rc1_2801	Depositor
R, R_{free}	0.219 , 0.268 0.219 , 0.268	Depositor DCC
R_{free} test set	964 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	100.9	Xtriage
Anisotropy	0.196	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 65.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	10599	wwPDB-VP
Average B, all atoms (Å^2)	113.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.07% 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

Bond lengths and bond angles in the following residue types are not validated in this section: T64

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	0/4175	0.51	0/5611
2	X	0.29	0/415	0.51	0/565
3	W	0.69	0/543	1.10	4/834 (0.5%)
4	Y	0.69	0/508	1.18	1/782 (0.1%)
All	All	0.41	0/5641	0.69	5/7792 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	Y	11	DG	O4'-C1'-N9	6.56	112.59	108.00
3	W	9	DA	O4'-C1'-C2'	-5.83	101.23	105.90
3	W	22	DC	O4'-C1'-C2'	-5.42	101.56	105.90
3	W	3	DG	O4'-C1'-N9	5.34	111.73	108.00
3	W	18	DG	P-O3'-C3'	5.27	126.03	119.70

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	4086	4162	4172	33	1
2	X	409	418	418	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	W	484	271	271	9	0
4	Y	494	275	276	17	0
All	All	5473	5126	5137	57	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 5.

All (57) 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:414:ARG:NH1	1:A:419:ASP:OD1	2.30	0.65
3:W:9:DA:H2"	3:W:10:DC:H5"	1.80	0.64
1:A:495:GLN:NE2	3:W:15:DA:OP1	2.32	0.62
4:Y:11:DG:H2"	4:Y:12:DG:C8	2.40	0.57
4:Y:10:DT:H2"	4:Y:11:DG:C8	2.40	0.56
4:Y:8:DC:H3'	4:Y:9:T64:H4R	1.87	0.56
1:A:214:TRP:O	1:A:215:LYS:HB2	2.05	0.55
1:A:240:LYS:O	1:A:241:ARG:NH1	2.39	0.54
1:A:374:ASP:OD1	1:A:391:ARG:NH2	2.43	0.52
3:W:10:DC:H2"	3:W:11:DA:C8	2.46	0.51
4:Y:12:DG:H2"	4:Y:13:DA:OP2	2.11	0.50
1:A:377:ARG:O	1:A:377:ARG:HD3	2.11	0.49
4:Y:20:DG:C2'	4:Y:21:DT:H71	2.43	0.49
1:A:601:ARG:HG3	4:Y:10:DT:H5"	1.96	0.48
1:A:359:MET:O	1:A:361:ARG:HD3	2.14	0.47
4:Y:17:DT:H2'	4:Y:18:DG:C8	2.49	0.47
4:Y:22:DC:H2"	4:Y:23:DA:C8	2.49	0.47
3:W:11:DA:C2	4:Y:15:DG:C2	3.03	0.47
1:A:377:ARG:HA	1:A:383:MET:HG3	1.96	0.47
3:W:10:DC:H2"	3:W:11:DA:H8	1.79	0.47
1:A:465:GLU:HG2	1:A:480:LYS:HD2	1.96	0.46
1:A:560:GLU:HB3	1:A:562:PHE:CE2	2.51	0.46
1:A:212:LYS:HA	1:A:212:LYS:HE2	1.98	0.46
1:A:392:ILE:O	1:A:398:GLY:HA3	2.16	0.46
2:X:291:ARG:O	2:X:295:MET:HG2	2.16	0.46
4:Y:10:DT:C2'	4:Y:11:DG:C8	2.99	0.46
4:Y:13:DA:H1'	4:Y:14:DT:H5'	1.99	0.45
1:A:377:ARG:NH2	1:A:429:ASP:OD1	2.42	0.45
1:A:380:ALA:HB3	1:A:383:MET:HG2	2.00	0.44
1:A:579:ALA:HB1	1:A:612:ILE:HG12	1.98	0.44
1:A:159:ASN:OD1	1:A:274:ARG:NH1	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:LEU:HB3	1:A:278:VAL:CG1	2.48	0.44
4:Y:12:DG:H1'	4:Y:13:DA:C8	2.53	0.43
1:A:266:VAL:HG21	1:A:316:TRP:HA	1.99	0.43
4:Y:13:DA:H2"	4:Y:14:DT:OP2	2.17	0.43
1:A:300:LEU:HD22	1:A:356:GLU:HG2	2.01	0.43
1:A:160:GLU:HG2	1:A:370:TYR:HE1	1.84	0.42
3:W:14:DC:H2"	3:W:15:DA:C8	2.54	0.42
1:A:377:ARG:HD2	1:A:428:ARG:HB3	2.01	0.42
1:A:378:ARG:NH2	1:A:421:GLU:OE2	2.52	0.42
1:A:401:TRP:CD1	2:X:298:PRO:HG3	2.55	0.42
4:Y:9:T64:H2'	4:Y:9:T64:N3T	2.34	0.42
2:X:300:VAL:O	2:X:304:MET:HG2	2.20	0.42
1:A:154:HIS:ND1	2:X:269:VAL:O	2.52	0.42
1:A:607:PRO:HG3	3:W:17:DA:C8	2.54	0.42
2:X:266:ARG:NH2	2:X:304:MET:O	2.52	0.41
3:W:4:DA:C4	3:W:5:DC:C5	3.07	0.41
1:A:292:THR:HG21	1:A:390:ARG:NH1	2.36	0.41
1:A:294:MET:HG3	4:Y:17:DT:H5"	2.01	0.41
1:A:316:TRP:CD2	1:A:347:LEU:HD23	2.56	0.41
1:A:436:ASP:N	1:A:436:ASP:OD1	2.53	0.41
1:A:513:ILE:HD12	1:A:514:LYS:O	2.20	0.41
4:Y:6:DA:C6	4:Y:7:DG:C6	3.08	0.41
1:A:155:GLY:HA3	1:A:366:TYR:CE2	2.56	0.41
1:A:588:VAL:HG22	1:A:589:GLU:H	1.86	0.41
3:W:4:DA:H2"	3:W:5:DC:H6	1.85	0.40
4:Y:5:DT:H2"	4:Y:6:DA:N7	2.35	0.40

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:342:ARG:NH2	1:A:585:PHE:O[1_455]	2.19	0.01

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	492/538 (91%)	466 (95%)	25 (5%)	1 (0%)	47 78
2	X	51/171 (30%)	50 (98%)	1 (2%)	0	100 100
All	All	543/709 (77%)	516 (95%)	26 (5%)	1 (0%)	47 78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	603	SER

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	447/480 (93%)	434 (97%)	13 (3%)	42 70
2	X	46/129 (36%)	45 (98%)	1 (2%)	52 76
All	All	493/609 (81%)	479 (97%)	14 (3%)	43 71

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	166	ARG
1	A	170	LYS
1	A	197	ARG
1	A	217	THR
1	A	294	MET
1	A	325	LYS
1	A	361	ARG
1	A	377	ARG
1	A	429	ASP
1	A	441	LEU
1	A	451	GLN
1	A	590	PHE

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Mol	Chain	Res	Type
1	A	630	GLU
2	X	262	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	T64	Y	9	4	36,44,45	3.45	14 (38%)	47,69,72	1.67	10 (21%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	T64	Y	9	4	-	8/22/76/77	0/3/5/5

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Y	9	T64	C2-N3	8.15	1.52	1.38
4	Y	9	T64	C5T-C4T	7.54	1.47	1.40
4	Y	9	T64	C2-N1	7.51	1.51	1.36
4	Y	9	T64	C4T-N3T	6.91	1.44	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Y	9	T64	C4-N3	6.36	1.47	1.37
4	Y	9	T64	C2T-N3T	5.82	1.49	1.38
4	Y	9	T64	C5A-C5	5.73	1.62	1.52
4	Y	9	T64	PB-O3R	4.59	1.72	1.60
4	Y	9	T64	C6T-C5T	3.87	1.50	1.40
4	Y	9	T64	C1'-N1	3.87	1.50	1.45
4	Y	9	T64	C5M-C5T	3.08	1.57	1.51
4	Y	9	T64	C2'-C3R	-2.30	1.47	1.52
4	Y	9	T64	PB-O5R	2.28	1.68	1.59
4	Y	9	T64	O4-C4	-2.01	1.19	1.22

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	Y	9	T64	C6-C5-C4	5.23	117.86	109.70
4	Y	9	T64	C4-N3-C2	-4.04	120.46	126.67
4	Y	9	T64	C4T-C6-N1	-3.32	106.63	110.23
4	Y	9	T64	C5T-C4T-N3T	-3.09	119.90	123.35
4	Y	9	T64	C6T-N1T-C1R	3.05	126.09	119.24
4	Y	9	T64	N3-C2-N1	3.05	119.86	116.69
4	Y	9	T64	O5P-PB-O3R	2.71	117.46	106.78
4	Y	9	T64	PB-O5R-C5R	-2.29	108.24	121.68
4	Y	9	T64	O2-C2-N1	-2.23	120.02	123.49
4	Y	9	T64	O5P-PB-O5R	2.03	117.19	107.75

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	Y	9	T64	C5R-O5R-PB-O4P
4	Y	9	T64	O4R-C1R-N1T-C6T
4	Y	9	T64	C3'-C4'-C5R-O5R
4	Y	9	T64	O4R-C4'-C5R-O5R
4	Y	9	T64	C3R-C4R-C5'-O5'
4	Y	9	T64	O4'-C4R-C5'-O5'
4	Y	9	T64	C4R-C5'-O5'-P
4	Y	9	T64	C5R-O5R-PB-O3R

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	Y	9	T64	2	0

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

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	496/538 (92%)	0.52	14 (2%) 53 55	43, 88, 144, 234	0
2	X	53/171 (30%)	0.50	1 (1%) 66 70	79, 129, 171, 187	0
3	W	24/24 (100%)	-0.22	0 100 100	97, 126, 165, 167	0
4	Y	22/23 (95%)	-0.14	0 100 100	103, 136, 161, 179	0
All	All	595/756 (78%)	0.47	15 (2%) 57 59	43, 93, 161, 234	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	242	LYS	4.9
1	A	609	LEU	3.0
1	A	238	ASN	2.8
1	A	146	LEU	2.7
1	A	526	GLU	2.7
1	A	241	ARG	2.7
1	A	129	ARG	2.5
1	A	517	VAL	2.4
1	A	143	PHE	2.3
1	A	515	ARG	2.3
1	A	606	LYS	2.2
1	A	243	PHE	2.1
1	A	135	GLU	2.1
2	X	301	PHE	2.0
1	A	392	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column

labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	T64	Y	9	40/41	0.65	0.38	177,227,263,279	0

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.