



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:36 AM UTC

PDB ID : 6CFI / pdb_00006cfi
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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

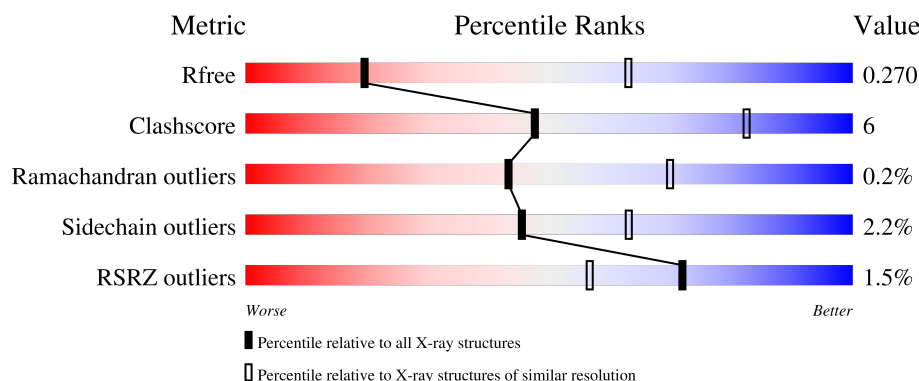
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.36 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}	180053	1099 (3.40-3.32)
Clashscore	190562	1116 (3.40-3.32)
Ramachandran outliers	187476	1101 (3.40-3.32)
Sidechain outliers	187428	1101 (3.40-3.32)
RSRZ outliers	180081	1099 (3.40-3.32)

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 $\leq 5\%$. 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	538	% 81% 10% 8%
2	X	171	2% 24% 7% 69%
3	W	24	67% 33%
4	Y	23	26% 70% .

2 Entry composition

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
1	A	496	Total	C	H	N	O	S	0	0	0
			8248	2608	4162	734	717	27			

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
2	X	53	Total	C	H	N	O	S	0	0	0
			827	260	418	69	78	2			

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

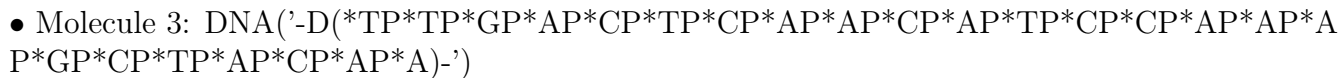
- Molecule 3 is a DNA chain called DNA('D(*TP*TP*GP*AP*CP*TP*CP*AP*AP*CP*A P*TP*CP*CP*AP*AP*AP*GP*CP*TP*AP*CP*AP*A)-').

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

- 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
4	Y	23	Total	C	H	N	O	P	0	0	0
			769	238	275	86	147	23			

- Molecule 1: DNA repair protein RAD4



A1	T5	A6	G7	C8	T649	T10	G11	G12	A13	T14	G15	T16	T17	G18	A19	G20	T21	C22	A23
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4 Data and refinement statistics

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
$\langle I/\sigma(I) \rangle$ ¹	1.17 (at 3.33Å)	Xtriage
Refinement program	PHENIX 1.12rc1_2801	Depositor
R, R_{free}	0.219 , 0.268 0.216 , 0.270	Depositor DCC
R_{free} test set	964 reflections (4.84%)	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)	0.37 , 64.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	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.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

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	0.23	0/4175	0.51	0/5611
2	X	0.21	0/415	0.54	0/565
3	W	0.31	0/543	0.67	0/834
4	Y	0.32	0/508	0.70	0/782
All	All	0.25	0/5641	0.55	0/7792

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	4086	4162	4172	33	1
2	X	409	418	418	7	0
3	W	484	271	271	9	0
4	Y	494	275	276	17	0
All	All	5473	5126	5137	59	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 6.

All (59) 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
2:X:307:GLU:O	2:X:308:ALA:C	2.60	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:OD1	1:A:436:ASP:N	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
2:X:299:GLU:CD	2:X:299:GLU:H	2.30	0.40
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 ⓘ

5.3.1 Protein backbone ⓘ

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%)	43 70
2	X	51/171 (30%)	50 (98%)	1 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	543/709 (77%)	516 (95%)	26 (5%)	1 (0%)	43 70

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	603	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	447/480 (93%)	438 (98%)	9 (2%)	48 65
2	X	46/129 (36%)	44 (96%)	2 (4%)	26 52
All	All	493/609 (81%)	482 (98%)	11 (2%)	45 63

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	217	THR
1	A	294	MET
1	A	361	ARG
1	A	364	ILE
1	A	377	ARG
1	A	429	ASP
1	A	441	LEU
1	A	451	GLN
1	A	630	GLU
2	X	262	LEU
2	X	265	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	222	ASN

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Mol	Chain	Res	Type
1	A	558	ASN
2	X	297	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	41,44,45	4.23	18 (43%)	53,69,72	2.15	17 (32%)

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	-	11/22/76/77	0/3/5/5

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Y	9	T64	C6T-N1T	11.85	1.58	1.38
4	Y	9	T64	C6-C4T	10.33	1.64	1.51
4	Y	9	T64	C6T-C5T	9.94	1.50	1.34
4	Y	9	T64	C2-N3	8.34	1.52	1.38
4	Y	9	T64	C2-N1	7.97	1.51	1.36
4	Y	9	T64	C2T-N3T	6.73	1.49	1.36
4	Y	9	T64	C4-N3	6.37	1.47	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Y	9	T64	C5A-C5	5.97	1.62	1.52
4	Y	9	T64	C2T-N1T	5.82	1.52	1.40
4	Y	9	T64	PB-O3R	4.37	1.72	1.59
4	Y	9	T64	C4T-N3T	4.12	1.44	1.31
4	Y	9	T64	C1'-N1	3.83	1.50	1.45
4	Y	9	T64	C5M-C5T	2.68	1.57	1.50
4	Y	9	T64	C2'-C3R	-2.43	1.47	1.52
4	Y	9	T64	PB-O5R	2.33	1.68	1.59
4	Y	9	T64	C6-N1	2.12	1.50	1.46
4	Y	9	T64	O2T-C2T	-2.07	1.19	1.23
4	Y	9	T64	O4-C4	-2.04	1.19	1.22

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	Y	9	T64	C6T-N1T-C2T	-6.24	112.64	120.95
4	Y	9	T64	C6-C5-C4	5.23	117.86	109.70
4	Y	9	T64	C5T-C4T-N3T	-4.31	119.90	123.61
4	Y	9	T64	C4-N3-C2	-4.11	120.46	126.67
4	Y	9	T64	C2T-N3T-C4T	4.08	122.71	119.02
4	Y	9	T64	C5M-C5T-C4T	3.63	122.26	118.28
4	Y	9	T64	C5M-C5T-C6T	-3.44	118.20	122.85
4	Y	9	T64	C5-C4-N3	3.31	119.58	115.23
4	Y	9	T64	C1R-N1T-C6T	3.19	126.09	120.74
4	Y	9	T64	O4-C4-C5	-3.10	120.31	123.13
4	Y	9	T64	N3-C2-N1	2.94	119.86	116.78
4	Y	9	T64	O5P-PB-O3R	2.64	117.46	106.70
4	Y	9	T64	PB-O5R-C5R	-2.29	108.24	121.35
4	Y	9	T64	O2-C2-N1	-2.28	120.02	123.44
4	Y	9	T64	O2T-C2T-N3T	-2.27	118.75	122.33
4	Y	9	T64	O5P-PB-O5R	2.12	117.19	107.57
4	Y	9	T64	N1T-C2T-N3T	2.10	122.45	118.80

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	Y	9	T64	C5R-O5R-PB-O4P
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	C2R-C1R-N1T-C6T

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Mol	Chain	Res	Type	Atoms
4	Y	9	T64	O4'-C4R-C5'-O5'
4	Y	9	T64	C4R-C5'-O5'-P
4	Y	9	T64	C2R-C1R-N1T-C2T
4	Y	9	T64	O4R-C1R-N1T-C6T
4	Y	9	T64	O4R-C1R-N1T-C2T
4	Y	9	T64	C3R-O3R-PB-O5P

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 oligosaccharides 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, 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	496/538 (92%)	-0.04	5 (1%) 79 66	47, 98, 159, 269	0
2	X	53/171 (30%)	0.62	4 (7%) 20 16	88, 142, 189, 205	0
3	W	24/24 (100%)	0.09	0 100 100	105, 136, 176, 178	0
4	Y	22/23 (95%)	0.06	0 100 100	110, 148, 173, 195	0
All	All	595/756 (78%)	0.03	9 (1%) 72 57	47, 103, 174, 269	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	129	ARG	3.6
2	X	256	GLY	3.3
1	A	517	VAL	3.3
2	X	308	ALA	2.9
2	X	257	LEU	2.6
1	A	130	ASN	2.4
2	X	285	ALA	2.3
1	A	146	LEU	2.3
1	A	516	THR	2.2

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, 95th 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	0.28	0.16	177,227,263,279	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.