



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 11, 2021 – 07:17 PM EDT

PDB ID : 2OCA  
Title : The crystal structure of T4 UvsW  
Authors : Kerr, I.D.; White, S.W.  
Deposited on : 2006-12-20  
Resolution : 2.70 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](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 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	:	2.23.2
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)	:	2.23.2

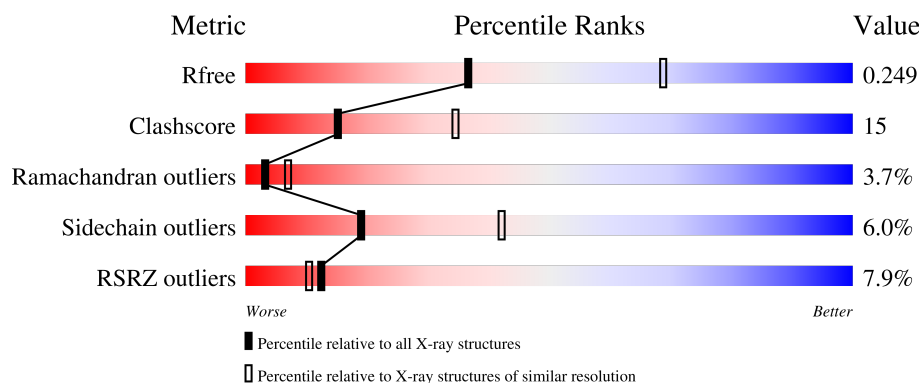
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	510	<div> <div>8%</div> <div>70%</div> <div>21%</div> <div>5% ..</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4123 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 ATP-dependent DNA helicase uvsW.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	494	Total	C	N	O	S	70	0	0
			4017	2591	692	718	16			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	141	ARG	LYS	engineered mutation	UNP P20703
A	457	ASP	SER	variant	UNP P20703
A	503	LEU	-	expression tag	UNP P20703
A	504	GLU	-	expression tag	UNP P20703
A	505	HIS	-	expression tag	UNP P20703
A	506	HIS	-	expression tag	UNP P20703
A	507	HIS	-	expression tag	UNP P20703
A	508	HIS	-	expression tag	UNP P20703
A	509	HIS	-	expression tag	UNP P20703
A	510	HIS	-	expression tag	UNP P20703

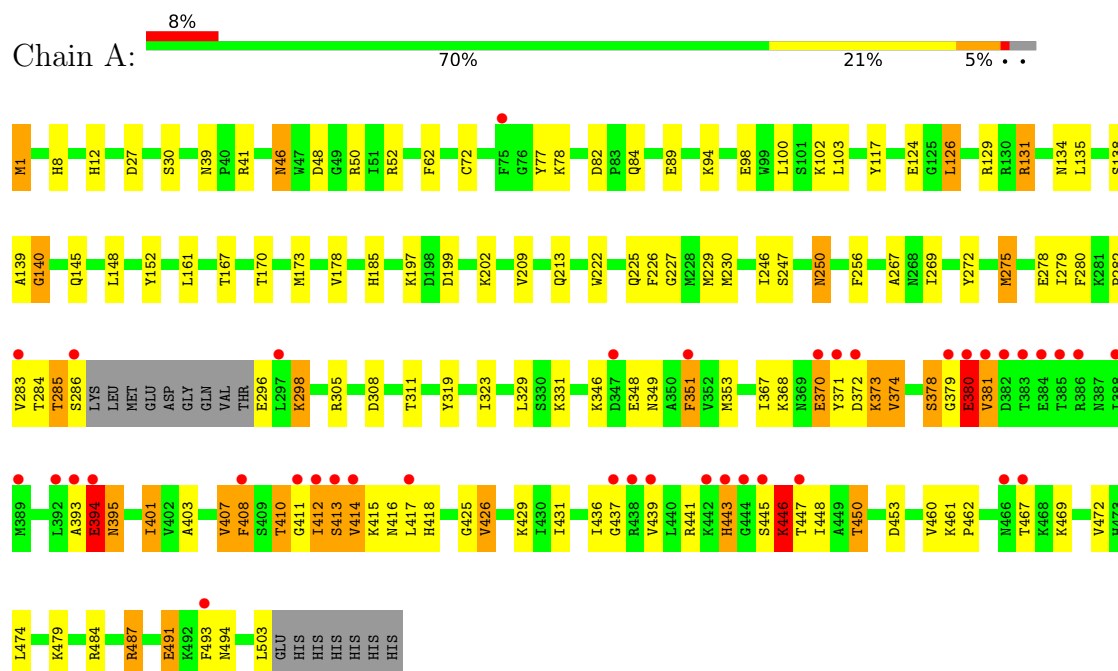
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	106	Total	O	0	0
			106	106		

### 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: ATP-dependent DNA helicase uvsW



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	118.64Å 155.20Å 101.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.70 47.42 – 2.69	Depositor EDS
% Data completeness (in resolution range)	97.5 (30.00-2.70) 97.3 (47.42-2.69)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.30 (at 2.69Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.217 , 0.250 0.217 , 0.249	Depositor DCC
$R_{free}$ test set	1302 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	63.7	Xtriage
Anisotropy	0.620	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 54.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4123	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% 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 [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	0.38	0/4107	0.62	1/5526 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	446	LYS	N-CA-C	-5.22	96.91	111.00

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	4017	0	4061	118	0
2	A	106	0	0	3	0
All	All	4123	0	4061	118	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 15.

All (118) 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:349:ASN:H	1:A:418:HIS:CD2	1.86	0.92

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:349:ASN:H	1:A:418:HIS:HD2	0.98	0.92
1:A:414:VAL:HG11	1:A:417:LEU:HD22	1.54	0.88
1:A:410:THR:HG23	1:A:411:GLY:H	1.36	0.88
1:A:349:ASN:N	1:A:418:HIS:HD2	1.77	0.82
1:A:487:ARG:HB2	1:A:487:ARG:NH1	1.95	0.82
1:A:126:LEU:HD13	1:A:148:LEU:HD23	1.67	0.76
1:A:487:ARG:HB2	1:A:487:ARG:HH11	1.49	0.75
1:A:401:ILE:HD11	1:A:403:ALA:HB2	1.69	0.74
1:A:46:ASN:H	1:A:46:ASN:HD22	1.36	0.72
1:A:412:ILE:HB	1:A:439:VAL:HG13	1.71	0.72
1:A:351:PHE:CD2	1:A:353:MET:HE1	2.24	0.72
1:A:446:LYS:O	1:A:448:ILE:N	2.20	0.72
1:A:250:ASN:N	1:A:250:ASN:HD22	1.89	0.71
1:A:319:TYR:CZ	1:A:323:ILE:HD11	2.25	0.71
1:A:462:PRO:HB3	1:A:472:VAL:HG23	1.73	0.70
1:A:138:SER:O	1:A:139:ALA:HB3	1.90	0.70
1:A:412:ILE:CD1	1:A:443:HIS:HB2	2.22	0.69
1:A:414:VAL:HG12	1:A:417:LEU:HB2	1.73	0.69
1:A:282:PRO:O	1:A:284:THR:N	2.25	0.69
1:A:491:GLU:HB3	1:A:493:PHE:CE2	2.27	0.68
1:A:250:ASN:HD22	1:A:250:ASN:H	1.43	0.66
1:A:367:ILE:HG22	1:A:374:VAL:HG21	1.79	0.64
1:A:346:LYS:HE3	1:A:348:GLU:OE1	1.97	0.63
1:A:135:LEU:HD21	1:A:282:PRO:HG3	1.81	0.62
1:A:48:ASP:OD1	1:A:52:ARG:NH2	2.32	0.62
1:A:305:ARG:HH12	1:A:461:LYS:HE3	1.65	0.62
1:A:30:SER:OG	1:A:50:ARG:NH1	2.33	0.62
1:A:331:LYS:HD3	1:A:503:LEU:HD21	1.83	0.61
1:A:311:THR:CG2	1:A:460:VAL:HG22	2.30	0.61
1:A:425:GLY:HA2	2:A:594:HOH:O	2.02	0.60
1:A:351:PHE:HE2	1:A:408:PHE:HB2	1.68	0.59
1:A:126:LEU:HD13	1:A:148:LEU:CD2	2.33	0.58
1:A:319:TYR:OH	1:A:323:ILE:HD11	2.02	0.58
1:A:408:PHE:CZ	1:A:436:ILE:HG12	2.40	0.57
1:A:378:SER:HA	1:A:407:VAL:CG2	2.34	0.57
1:A:145:GLN:HE22	1:A:173:MET:HE1	1.69	0.57
1:A:410:THR:HG23	1:A:411:GLY:N	2.15	0.57
1:A:161:LEU:HB2	1:A:226:PHE:CD2	2.40	0.56
1:A:311:THR:HG23	1:A:460:VAL:HG22	1.86	0.56
1:A:446:LYS:C	1:A:448:ILE:H	2.08	0.56
1:A:100:LEU:HD12	1:A:103:LEU:HD12	1.89	0.54

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:412:ILE:HD11	1:A:443:HIS:HB2	1.88	0.54
1:A:408:PHE:HZ	1:A:436:ILE:HG12	1.71	0.54
1:A:410:THR:O	1:A:412:ILE:HG23	2.07	0.54
1:A:462:PRO:HB3	1:A:472:VAL:CG2	2.38	0.54
1:A:131:ARG:HG3	1:A:278:GLU:O	2.08	0.54
1:A:138:SER:O	1:A:139:ALA:CB	2.56	0.54
1:A:378:SER:HA	1:A:407:VAL:HG21	1.90	0.53
1:A:474:LEU:HD23	1:A:479:LYS:HG2	1.90	0.53
1:A:412:ILE:HD12	1:A:413:SER:N	2.24	0.53
1:A:135:LEU:CD2	1:A:282:PRO:HG3	2.38	0.53
1:A:429:LYS:HB3	1:A:431:ILE:HD13	1.91	0.53
1:A:491:GLU:HB3	1:A:493:PHE:CD2	2.44	0.53
1:A:431:ILE:N	1:A:431:ILE:HD12	2.24	0.52
1:A:296:GLU:OE1	1:A:441:ARG:HD2	2.10	0.52
1:A:445:SER:O	1:A:446:LYS:CB	2.56	0.52
1:A:269:ILE:HD11	1:A:279:ILE:HD11	1.91	0.52
1:A:308:ASP:O	1:A:311:THR:HB	2.10	0.51
1:A:311:THR:HG21	1:A:460:VAL:HA	1.92	0.51
1:A:487:ARG:HH11	1:A:487:ARG:CB	2.21	0.50
1:A:453:ASP:OD1	1:A:484:ARG:NH2	2.42	0.50
1:A:351:PHE:CE1	1:A:401:ILE:HG12	2.46	0.50
1:A:213:GLN:NE2	1:A:213:GLN:H	2.09	0.50
1:A:401:ILE:O	1:A:401:ILE:HG13	2.11	0.50
1:A:408:PHE:CD2	1:A:408:PHE:C	2.85	0.49
1:A:46:ASN:H	1:A:46:ASN:ND2	2.09	0.49
1:A:82:ASP:OD1	1:A:84:GLN:HG2	2.13	0.49
1:A:1:MET:HB2	1:A:78:LYS:O	2.12	0.49
1:A:152:TYR:OH	1:A:227:GLY:HA3	2.13	0.49
1:A:379:GLY:O	1:A:380:GLU:C	2.51	0.48
1:A:199:ASP:HA	1:A:202:LYS:HE3	1.94	0.48
1:A:296:GLU:CD	1:A:441:ARG:HD2	2.34	0.48
1:A:412:ILE:HD12	1:A:443:HIS:HB2	1.93	0.48
1:A:197:LYS:HG3	2:A:537:HOH:O	2.13	0.48
1:A:285:THR:HG21	1:A:494:ASN:HB2	1.96	0.48
1:A:39:ASN:OD1	1:A:41:ARG:HB2	2.14	0.48
1:A:250:ASN:H	1:A:250:ASN:ND2	2.10	0.47
1:A:140:GLY:HA2	2:A:556:HOH:O	2.14	0.47
1:A:267:ALA:HB3	1:A:272:TYR:CZ	2.49	0.47
1:A:445:SER:O	1:A:446:LYS:HB2	2.15	0.47
1:A:246:ILE:HG23	1:A:247:SER:N	2.31	0.46
1:A:431:ILE:CD1	1:A:431:ILE:H	2.29	0.46

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:GLU:O	1:A:395:ASN:HB2	2.14	0.45
1:A:8:HIS:HB3	1:A:12:HIS:O	2.17	0.45
1:A:98:GLU:HG3	1:A:102:LYS:HE3	1.99	0.45
1:A:170:THR:HG23	1:A:209:VAL:HG12	1.99	0.45
1:A:446:LYS:O	1:A:448:ILE:HG13	2.17	0.45
1:A:222:TRP:O	1:A:225:GLN:HG2	2.17	0.44
1:A:246:ILE:HD13	1:A:275:MET:SD	2.57	0.44
1:A:167:THR:O	1:A:170:THR:HB	2.18	0.43
1:A:124:GLU:HG3	1:A:280:PHE:CE2	2.53	0.43
1:A:413:SER:HA	1:A:443:HIS:HB3	2.01	0.43
1:A:124:GLU:HG3	1:A:280:PHE:CZ	2.53	0.43
1:A:298:LYS:O	1:A:450:THR:HA	2.17	0.43
1:A:412:ILE:O	1:A:413:SER:HB3	2.19	0.43
1:A:117:TYR:CE1	1:A:139:ALA:HB1	2.55	0.42
1:A:230:MET:HA	1:A:256:PHE:O	2.19	0.42
1:A:213:GLN:H	1:A:213:GLN:CD	2.22	0.42
1:A:379:GLY:O	1:A:381:VAL:N	2.52	0.42
1:A:89:GLU:HG2	1:A:129:ARG:HE	1.84	0.42
1:A:437:GLY:O	1:A:441:ARG:HD3	2.20	0.42
1:A:372:ASP:O	1:A:374:VAL:N	2.50	0.41
1:A:72:CYS:HB3	1:A:77:TYR:O	2.20	0.41
1:A:431:ILE:HD12	1:A:431:ILE:H	1.84	0.41
1:A:139:ALA:O	1:A:140:GLY:C	2.58	0.41
1:A:431:ILE:N	1:A:431:ILE:CD1	2.83	0.41
1:A:467:THR:HG22	1:A:469:LYS:H	1.85	0.41
1:A:296:GLU:O	1:A:448:ILE:HA	2.20	0.41
1:A:368:LYS:C	1:A:370:GLU:H	2.23	0.41
1:A:413:SER:OG	1:A:414:VAL:N	2.54	0.41
1:A:135:LEU:CG	1:A:282:PRO:HG3	2.52	0.40
1:A:178:VAL:HG11	1:A:185:HIS:CD2	2.56	0.40
1:A:311:THR:CG2	1:A:460:VAL:HA	2.51	0.40
1:A:393:ALA:HA	1:A:415:LYS:HB2	2.03	0.40
1:A:319:TYR:CZ	1:A:323:ILE:CD1	3.01	0.40
1:A:446:LYS:C	1:A:448:ILE:N	2.72	0.40
1:A:371:TYR:CE2	1:A:373:LYS:HB2	2.57	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	490/510 (96%)	453 (92%)	19 (4%)	18 (4%)	<b>3</b> <b>7</b>

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	283	VAL
1	A	378	SER
1	A	381	VAL
1	A	394	GLU
1	A	395	ASN
1	A	413	SER
1	A	414	VAL
1	A	447	THR
1	A	140	GLY
1	A	416	ASN
1	A	426	VAL
1	A	446	LYS
1	A	410	THR
1	A	370	GLU
1	A	373	LYS
1	A	285	THR
1	A	380	GLU
1	A	407	VAL

### 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	434/449 (97%)	408 (94%)	26 (6%)	19	42

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	27	ASP
1	A	46	ASN
1	A	62	PHE
1	A	94	LYS
1	A	126	LEU
1	A	131	ARG
1	A	134	ASN
1	A	229	MET
1	A	250	ASN
1	A	275	MET
1	A	286	SER
1	A	298	LYS
1	A	329	LEU
1	A	351	PHE
1	A	374	VAL
1	A	380	GLU
1	A	394	GLU
1	A	401	ILE
1	A	408	PHE
1	A	412	ILE
1	A	426	VAL
1	A	443	HIS
1	A	450	THR
1	A	487	ARG
1	A	491	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	ASN
1	A	134	ASN
1	A	145	GLN
1	A	213	GLN
1	A	250	ASN
1	A	418	HIS
1	A	480	HIS

### 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 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<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	494/510 (96%)	0.43	39 (7%) 12 10	44, 64, 100, 100	23 (4%)

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	443	HIS	8.6
1	A	408	PHE	6.4
1	A	393	ALA	6.0
1	A	412	ILE	5.4
1	A	413	SER	5.2
1	A	389	MET	4.8
1	A	392	LEU	4.8
1	A	351	PHE	4.6
1	A	442	LYS	4.6
1	A	447	THR	4.3
1	A	466	ASN	4.3
1	A	394	GLU	3.8
1	A	444	GLY	3.8
1	A	379	GLY	3.7
1	A	439	VAL	3.6
1	A	372	ASP	3.6
1	A	286	SER	3.4
1	A	445	SER	3.3
1	A	381	VAL	3.2
1	A	386	ARG	3.2
1	A	283	VAL	3.2
1	A	385	THR	2.7
1	A	414	VAL	2.7
1	A	382	ASP	2.7
1	A	438	ARG	2.7
1	A	380	GLU	2.5
1	A	388	ILE	2.5

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	437	GLY	2.4
1	A	411	GLY	2.4
1	A	347	ASP	2.3
1	A	384	GLU	2.2
1	A	75	PHE	2.2
1	A	371	TYR	2.2
1	A	370	GLU	2.2
1	A	297	LEU	2.1
1	A	493	PHE	2.1
1	A	383	THR	2.1
1	A	417	LEU	2.0
1	A	467	THR	2.0

## 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.