



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 21, 2023 – 04:38 PM JST

PDB ID : 7W3R  
Title : USP34 catalytic domain  
Authors : Xu, G.L.; Ming, Z.H.  
Deposited on : 2021-11-26  
Resolution : 1.92 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 types of validation reports are described at

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

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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 : 2.36  
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) : 2.36

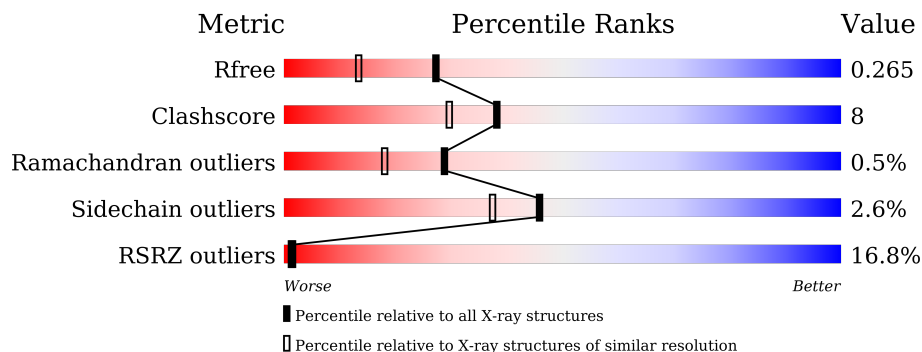
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.92 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	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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	384	
1	B	384	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5683 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 Ubiquitin carboxyl-terminal hydrolase 34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	340	2781	1776	445	532	28	0	0	0
1	B	326	2681	1718	426	511	26	0	0	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

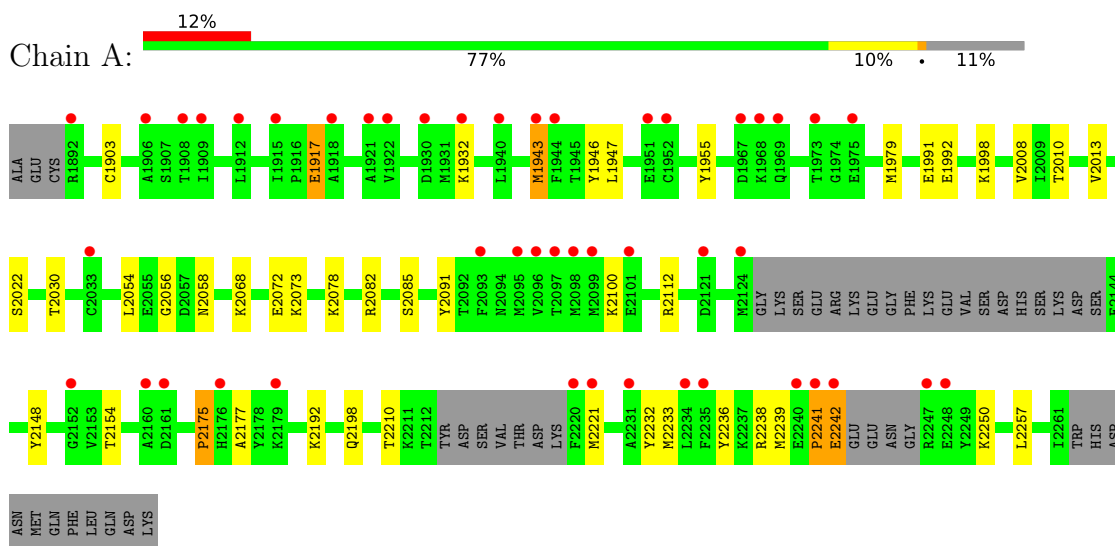
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	116	Total	O	0	0
			116	116		
3	B	104	Total	O	0	0
			104	104		

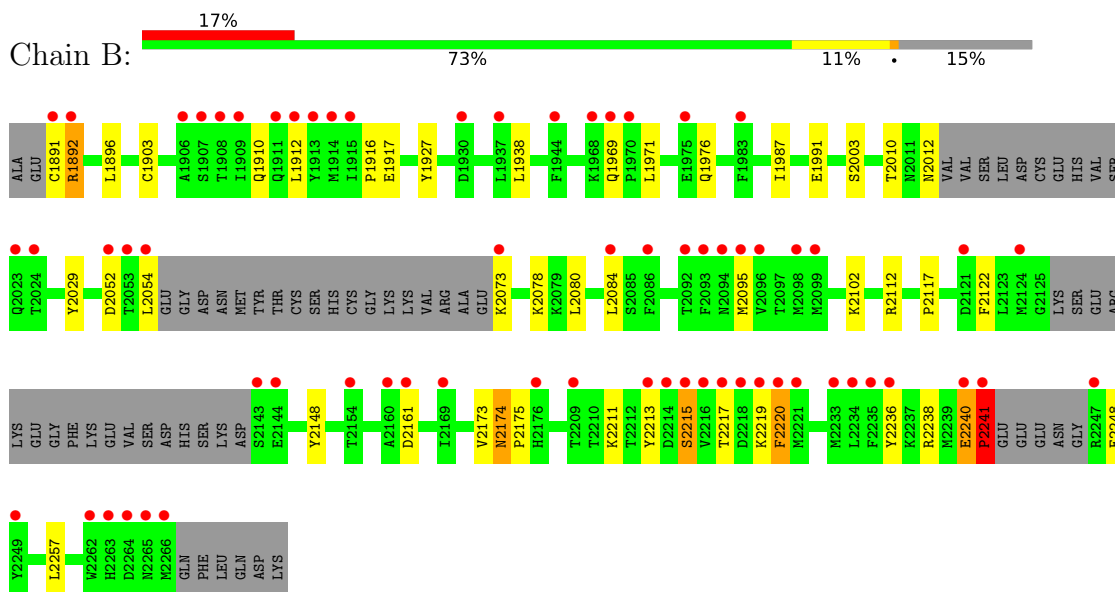
### 3 Residue-property plots [i](#)

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: Ubiquitin carboxyl-terminal hydrolase 34



- Molecule 1: Ubiquitin carboxyl-terminal hydrolase 34



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	50.12Å 128.06Å 64.40Å 90.00° 93.49° 90.00°	Depositor
Resolution (Å)	25.01 – 1.92 32.47 – 1.92	Depositor EDS
% Data completeness (in resolution range)	97.9 (25.01-1.92) 97.9 (32.47-1.92)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.72 (at 1.92Å)	Xtrriage
Refinement program	PHENIX 1.15_3459	Depositor
R, $R_{free}$	0.226 , 0.262 0.230 , 0.265	Depositor DCC
$R_{free}$ test set	2993 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.0	Xtrriage
Anisotropy	0.341	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 47.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5683	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.01% 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](#)

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

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	0.45	1/2843 (0.0%)	0.60	0/3829
1	B	0.41	0/2743	0.57	1/3695 (0.0%)
All	All	0.43	1/5586 (0.0%)	0.58	1/7524 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1917	GLU	CG-CD	5.10	1.59	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2241	PRO	CA-N-CD	-5.61	103.64	111.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	2215	SER	Peptide

## 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	2781	0	2695	50	0
1	B	2681	0	2593	33	0
2	A	1	0	0	0	0
3	A	116	0	0	7	0
3	B	104	0	0	9	0
All	All	5683	0	5288	82	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.

All (82) 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:2072:GLU:OE2	3:A:2401:HOH:O	1.88	0.90
1:B:2248:GLU:OE2	3:B:2301:HOH:O	1.92	0.86
1:B:2012:ASN:ND2	3:B:2302:HOH:O	2.16	0.79
1:B:2240:GLU:HB3	1:B:2241:PRO:CD	2.15	0.77
1:A:2112:ARG:CG	1:A:2239:MET:CE	2.64	0.76
1:B:1916:PRO:HG3	1:B:2173:VAL:HG22	1.68	0.75
1:B:1903:CYS:SG	3:B:2371:HOH:O	2.46	0.74
1:B:2217:THR:HB	1:B:2219:LYS:HD2	1.73	0.69
1:A:1903:CYS:SG	3:A:2499:HOH:O	2.52	0.68
1:A:2112:ARG:HG3	1:A:2239:MET:HE1	1.78	0.65
1:A:2112:ARG:CG	1:A:2239:MET:HE1	2.27	0.64
1:A:2192:LYS:NZ	3:A:2404:HOH:O	2.31	0.63
1:B:1891:CYS:SG	1:B:1892:ARG:NH1	2.73	0.61
1:A:2054:LEU:HB3	1:A:2058:ASN:O	2.00	0.61
1:A:2198:GLN:NE2	3:A:2402:HOH:O	1.99	0.60
1:A:2242:GLU:O	1:A:2242:GLU:HG2	2.02	0.60
1:A:2112:ARG:CG	1:A:2239:MET:HE3	2.33	0.58
1:A:2112:ARG:HG2	1:A:2239:MET:HE3	1.85	0.57
1:B:2174:ASN:HD22	1:B:2175:PRO:HD2	1.69	0.57
1:A:1991:GLU:HG3	1:A:1998:LYS:HG3	1.85	0.56
1:A:2112:ARG:HG2	1:A:2239:MET:CE	2.35	0.56
1:A:2241:PRO:HB2	3:A:2426:HOH:O	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2240:GLU:HB3	1:B:2241:PRO:HD2	1.88	0.56
1:A:1943:MET:HE2	1:A:1955:TYR:HE2	1.70	0.55
1:A:2010:THR:HG23	1:A:2078:LYS:HB2	1.88	0.55
1:A:1917:GLU:CG	1:A:2082:ARG:HH12	2.19	0.54
1:A:1932:LYS:HE2	1:A:1992:GLU:HB3	1.88	0.54
1:B:1976:GLN:HG3	3:B:2319:HOH:O	2.09	0.53
1:A:1917:GLU:HG2	1:A:2082:ARG:HH12	1.73	0.53
1:A:2112:ARG:HD3	1:A:2239:MET:HE1	1.90	0.53
1:B:2213:TYR:HD2	1:B:2220:PHE:CD1	2.26	0.53
1:B:1912:LEU:HD21	1:B:1987:ILE:HD11	1.91	0.53
1:A:2112:ARG:HD3	1:A:2239:MET:CE	2.39	0.52
1:A:2013:VAL:CG1	1:A:2022:SER:HB3	2.40	0.52
1:B:2240:GLU:CB	1:B:2241:PRO:HD2	2.39	0.52
1:B:2112:ARG:HD3	3:B:2310:HOH:O	2.09	0.51
1:B:2073:LYS:N	3:B:2313:HOH:O	2.43	0.51
1:A:2112:ARG:CD	1:A:2239:MET:CE	2.88	0.51
1:A:2210:THR:HG23	1:B:1938:LEU:HD22	1.92	0.51
1:B:2240:GLU:CB	1:B:2241:PRO:CD	2.86	0.50
1:A:2030:THR:HG22	1:A:2085:SER:OG	2.13	0.49
1:B:2010:THR:HG23	1:B:2078:LYS:HB2	1.93	0.49
1:B:2148:TYR:HB3	1:B:2236:TYR:HB3	1.94	0.49
1:A:1979:MET:HE2	1:A:2154:THR:HG21	1.95	0.48
1:B:2117:PRO:HA	1:B:2122:PHE:CD2	2.49	0.48
1:B:1991:GLU:OE1	1:B:2029:TYR:OH	2.20	0.47
1:A:2257:LEU:HA	1:A:2257:LEU:HD23	1.74	0.47
1:A:1917:GLU:HG2	1:A:2082:ARG:NH1	2.30	0.47
1:A:2112:ARG:CD	1:A:2239:MET:HE1	2.45	0.47
1:B:2054:LEU:HD11	1:B:2073:LYS:HE3	1.97	0.46
1:A:1979:MET:HE3	1:A:2233:MET:HB2	1.98	0.46
1:A:1917:GLU:H	1:A:1917:GLU:CD	2.19	0.46
1:A:2073:LYS:HB3	1:A:2073:LYS:HE3	1.76	0.46
1:A:2112:ARG:CD	1:A:2239:MET:HE3	2.45	0.46
1:A:1917:GLU:CD	1:A:2082:ARG:HH12	2.19	0.45
1:A:2091:TYR:HB3	1:A:2100:LYS:CG	2.47	0.45
1:A:2091:TYR:HB3	1:A:2100:LYS:HD2	1.99	0.45
1:A:1946:TYR:CD1	1:A:1955:TYR:HB2	2.51	0.45
1:B:1927:TYR:HB2	3:B:2335:HOH:O	2.16	0.45
1:B:2052:ASP:O	1:B:2073:LYS:N	2.51	0.44
1:A:2112:ARG:HG3	1:A:2239:MET:CE	2.36	0.44
1:B:2102:LYS:HE3	3:B:2321:HOH:O	2.17	0.44
1:A:2148:TYR:HB3	1:A:2236:TYR:HB3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2238:ARG:HD3	3:A:2411:HOH:O	2.16	0.43
1:A:2008:VAL:HG11	1:A:2078:LYS:HE2	1.99	0.43
1:A:2250:LYS:HA	1:A:2250:LYS:HD3	1.75	0.43
1:B:1896:LEU:HD12	1:B:1910:GLN:HG2	2.01	0.43
1:A:2013:VAL:HG13	1:A:2022:SER:HB3	1.99	0.43
1:A:1943:MET:O	1:A:1947:LEU:HG	2.18	0.43
1:A:1979:MET:HB3	1:A:2232:TYR:CE1	2.55	0.42
1:A:2175:PRO:C	1:A:2177:ALA:N	2.73	0.42
1:B:1917:GLU:HA	1:B:2248:GLU:OE2	2.18	0.42
1:B:2080:LEU:O	1:B:2238:ARG:NH2	2.53	0.42
1:B:2240:GLU:HB3	1:B:2241:PRO:HD3	1.96	0.42
1:B:1976:GLN:NE2	3:B:2319:HOH:O	2.52	0.42
1:A:2010:THR:HG21	1:A:2078:LYS:HD3	2.02	0.42
1:A:1943:MET:HE2	1:A:1955:TYR:CE2	2.53	0.41
1:B:2257:LEU:HD23	1:B:2257:LEU:HA	1.92	0.41
1:A:1932:LYS:HG3	3:A:2453:HOH:O	2.21	0.40
1:B:1916:PRO:HB3	1:B:2248:GLU:HB2	2.02	0.40
1:A:2091:TYR:HB3	1:A:2100:LYS:HG2	2.02	0.40
1:B:1971:LEU:HD12	1:B:1971:LEU:HA	1.91	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	332/384 (86%)	317 (96%)	13 (4%)	2 (1%)	25	14
1	B	316/384 (82%)	307 (97%)	8 (2%)	1 (0%)	41	31
All	All	648/768 (84%)	624 (96%)	21 (3%)	3 (0%)	29	18

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	2240	GLU
1	A	2056	GLY
1	A	2175	PRO

### 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	311/351 (89%)	306 (98%)	5 (2%)	62	58
1	B	299/351 (85%)	288 (96%)	11 (4%)	34	23
All	All	610/702 (87%)	594 (97%)	16 (3%)	46	37

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1943	MET
1	A	2068	LYS
1	A	2221	MET
1	A	2241	PRO
1	A	2242	GLU
1	B	1892	ARG
1	B	1969	GLN
1	B	2003	SER
1	B	2084	LEU
1	B	2095	MET
1	B	2161	ASP
1	B	2174	ASN
1	B	2211	LYS
1	B	2215	SER
1	B	2220	PHE
1	B	2241	PRO

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

Mol	Chain	Res	Type
1	B	2174	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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

### 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	340/384 (88%)	0.93	46 (13%) <b>3</b> <b>3</b>	28, 48, 71, 96	0
1	B	326/384 (84%)	1.10	66 (20%) <b>1</b> <b>1</b>	33, 49, 77, 92	0
All	All	666/768 (86%)	1.01	112 (16%) <b>1</b> <b>1</b>	28, 48, 73, 96	0

All (112) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2216	VAL	9.7
1	B	2213	TYR	8.2
1	B	2262	TRP	7.5
1	B	2214	ASP	7.4
1	A	2176	HIS	7.2
1	A	2096	VAL	6.6
1	B	2054	LEU	6.4
1	B	2215	SER	6.1
1	A	2241	PRO	6.1
1	A	2242	GLU	6.0
1	A	2247	ARG	6.0
1	B	2266	MET	5.6
1	B	2247	ARG	5.6
1	B	1912	LEU	5.2
1	A	2093	PHE	5.1
1	B	2093	PHE	5.1
1	B	2143	SER	5.0
1	B	2241	PRO	5.0
1	A	2221	MET	4.9
1	B	2221	MET	4.9
1	A	1967	ASP	4.8
1	B	1891	CYS	4.8
1	A	2098	MET	4.5
1	A	2220	PHE	4.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	1892	ARG	4.3
1	B	2218	ASP	4.2
1	A	2095	MET	4.2
1	B	2095	MET	4.2
1	A	1912	LEU	4.2
1	A	2099	MET	4.2
1	B	2217	THR	4.2
1	B	2219	LYS	4.1
1	B	2220	PHE	4.1
1	A	1944	PHE	4.1
1	A	2097	THR	3.9
1	B	2235	PHE	3.9
1	A	2179	LYS	3.8
1	B	2098	MET	3.7
1	B	1908	THR	3.6
1	A	1969	GLN	3.6
1	B	2240	GLU	3.5
1	B	2176	HIS	3.5
1	B	2053	THR	3.5
1	B	2092	THR	3.4
1	B	1909	ILE	3.3
1	B	2161	ASP	3.3
1	A	1909	ILE	3.3
1	A	1952	CYS	3.3
1	A	2124	MET	3.2
1	B	2160	ALA	3.2
1	A	1932	LYS	3.1
1	B	2023	GLN	3.0
1	B	1930	ASP	3.0
1	B	2144	GLU	3.0
1	B	1968	LYS	2.9
1	B	1915	ILE	2.9
1	A	2240	GLU	2.9
1	B	2249	TYR	2.9
1	B	2052	ASP	2.9
1	A	1922	VAL	2.9
1	B	1970	PRO	2.8
1	A	1908	THR	2.8
1	A	1940	LEU	2.8
1	A	1921	ALA	2.8
1	B	2209	THR	2.8
1	B	2233	MET	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	2099	MET	2.7
1	A	2160	ALA	2.7
1	B	1913	TYR	2.7
1	B	2263	HIS	2.7
1	B	2236	TYR	2.7
1	A	2234	LEU	2.6
1	A	1915	ILE	2.6
1	B	2124	MET	2.6
1	B	2084	LEU	2.6
1	A	1968	LYS	2.6
1	A	1973	THR	2.6
1	B	2073	LYS	2.6
1	A	1943	MET	2.5
1	B	2264	ASP	2.5
1	A	2235	PHE	2.5
1	B	2024	THR	2.5
1	B	2086	PHE	2.5
1	B	2154	THR	2.5
1	A	1951	GLU	2.5
1	B	1911	GLN	2.4
1	B	2265	ASN	2.4
1	A	1906	ALA	2.4
1	B	1975	GLU	2.4
1	B	1969	GLN	2.4
1	B	2096	VAL	2.3
1	B	2169	ILE	2.3
1	B	1914	MET	2.3
1	B	1983	PHE	2.3
1	B	1907	SER	2.3
1	A	1975	GLU	2.2
1	A	2121	ASP	2.2
1	B	1944	PHE	2.2
1	A	1918	ALA	2.2
1	B	1937	LEU	2.2
1	B	2234	LEU	2.2
1	A	1930	ASP	2.2
1	A	2161	ASP	2.2
1	A	2101	GLU	2.2
1	B	1906	ALA	2.2
1	A	2248	GLU	2.2
1	B	2094	ASN	2.1
1	B	2121	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	1892	ARG	2.1
1	A	2231	ALA	2.1
1	A	2152	GLY	2.1
1	A	2033	CYS	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](#)

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	ZN	A	2301	1/1	0.99	0.14	41,41,41,41	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.