



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 04:51 pm GMT

PDB ID : 4EVT  
Title : Crystal Structure of Mouse Catenin beta-59 in 8.3M urea  
Authors : Wang, C.; Zhang, G.Y.  
Deposited on : 2012-04-26  
Resolution : 2.34 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

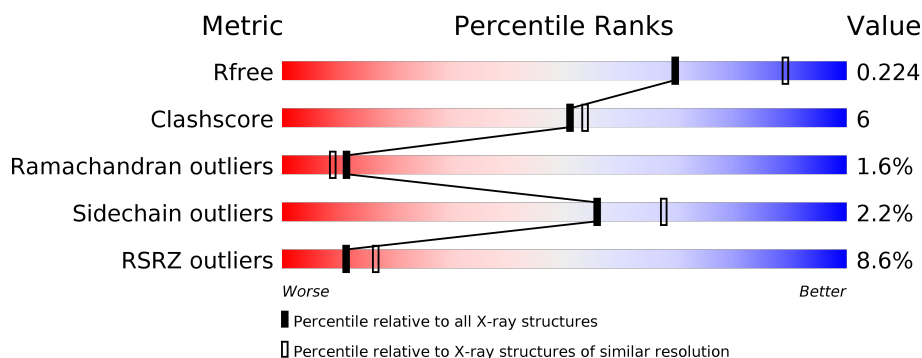
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.34 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))
$R_{free}$	100719	1570 (2.36-2.32)
Clashscore	112137	1673 (2.36-2.32)
Ramachandran outliers	110173	1654 (2.36-2.32)
Sidechain outliers	110143	1655 (2.36-2.32)
RSRZ outliers	101464	1576 (2.36-2.32)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>8%</div> <div>77%</div> <div>12%</div> <div>9%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	URE	A	702	-	-	-	X
2	URE	A	703	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	URE	A	705	-	-	-	X
2	URE	A	706	-	-	-	X
2	URE	A	708	-	-	-	X
2	URE	A	710	-	-	-	X
2	URE	A	719	-	-	X	X
2	URE	A	721	-	-	-	X
2	URE	A	722	-	-	-	X
2	URE	A	727	-	-	-	X
2	URE	A	728	-	-	-	X
2	URE	A	729	-	-	-	X
2	URE	A	731	-	-	-	X
2	URE	A	737	-	-	-	X
2	URE	A	741	-	-	X	X
2	URE	A	743	-	-	-	X
2	URE	A	746	-	-	-	X
2	URE	A	748	-	-	-	X
2	URE	A	749	-	-	-	X
2	URE	A	751	-	-	-	X
2	URE	A	752	-	-	-	X

## 2 Entry composition [i](#)

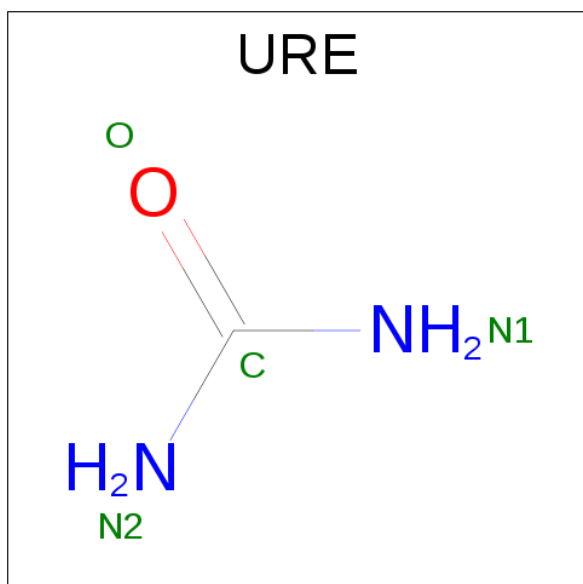
There are 3 unique types of molecules in this entry. The entry contains 4036 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Catenin beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	490	Total	C	N	O	S	0	1	0
			3727	2342	683	676	26			

- Molecule 2 is UREA (three-letter code: URE) (formula:  $\text{CH}_4\text{N}_2\text{O}$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			4	1	2	1		
2	A	1	Total	C	N	O	0	0
			4	1	2	1		
2	A	1	Total	C	N	O	0	0
			4	1	2	1		
2	A	1	Total	C	N	O	0	0
			4	1	2	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			4	1	2	1		
2	A	1	Total	C	N	O	0	0
			4	1	2	1		
2	A	1	Total	C	N	O	0	0
			4	1	2	1		
2	A	1	Total	C	N	O	0	0
			4	1	2	1		
2	A	1	Total	C	N	O	0	0
			4	1	2	1		
2	A	1	Total	C	N	O	0	0
			4	1	2	1		
2	A	1	Total	C	N	O	0	0
			3	1	1	1		

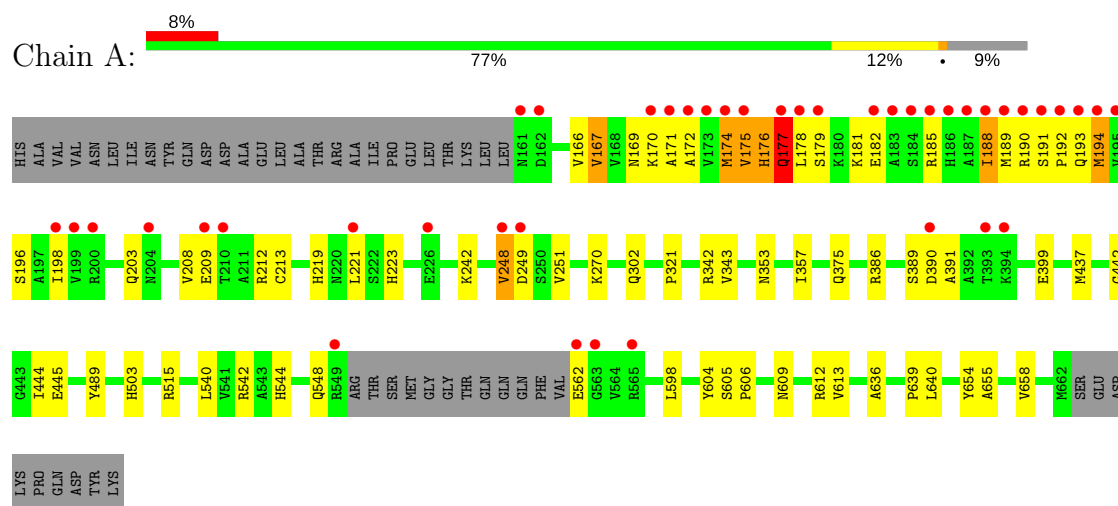
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	86	Total	O	0	0
			86	86		

### 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: Catenin beta-1





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.75Å 102.61Å 187.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.99 – 2.34 47.28 – 2.26	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.99-2.34) 98.8 (47.28-2.26)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.17 (at 2.27Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.191 , 0.225 0.222 , 0.224	Depositor DCC
$R_{free}$ test set	1341 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	39.6	Xtriage
Anisotropy	0.436	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 62.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4036	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.54% 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: URE

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	0.22	0/3779	0.42	0/5127

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	3727	0	3864	52	0
2	A	223	0	222	13	0
3	A	86	0	0	1	0
All	All	4036	0	4086	52	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 6.

All (52) 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:166:VAL:O	1:A:167:VAL:HG12	1.43	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:VAL:O	1:A:167:VAL:CG1	2.30	0.76
1:A:177:GLN:OE1	1:A:178:LEU:N	2.21	0.73
1:A:612:ARG:HE	2:A:741:URE:HN21	1.39	0.69
1:A:270:LYS:NZ	3:A:864:HOH:O	2.28	0.66
1:A:193:GLN:O	1:A:196:SER:OG	2.17	0.62
1:A:174:MET:O	1:A:176:HIS:N	2.36	0.59
1:A:503:HIS:CD2	2:A:754:URE:HN11	2.21	0.58
1:A:169:ASN:O	1:A:172:ALA:N	2.25	0.55
1:A:203:GLN:HG3	1:A:242:LYS:HD2	1.89	0.55
1:A:176:HIS:O	1:A:179:SER:OG	2.25	0.54
1:A:171:ALA:HA	1:A:174:MET:HB3	1.90	0.53
1:A:171:ALA:O	1:A:174:MET:HB3	2.09	0.53
1:A:542:ARG:HG2	2:A:736:URE:HN12	1.73	0.53
1:A:248:VAL:HG13	1:A:249:ASP:HB2	1.92	0.51
1:A:188:ILE:O	1:A:191:SER:OG	2.28	0.51
1:A:386:ARG:HH21	2:A:725:URE:HN12	1.59	0.50
1:A:442:GLY:HA2	2:A:719:URE:HN12	1.76	0.50
1:A:604:TYR:CZ	1:A:639:PRO:HG3	2.47	0.50
1:A:612:ARG:NE	2:A:741:URE:HN21	2.08	0.49
1:A:302:GLN:HB2	1:A:343:VAL:HG22	1.95	0.49
1:A:194:MET:O	1:A:198:ILE:HG12	2.13	0.48
1:A:321:PRO:HB3	1:A:357:ILE:HD13	1.94	0.48
1:A:353:ASN:O	1:A:357:ILE:HG12	2.13	0.48
1:A:185:ARG:O	1:A:189:MET:HG2	2.14	0.48
1:A:185:ARG:O	1:A:188:ILE:HG22	2.15	0.47
1:A:489:TYR:HA	2:A:743:URE:HN22	1.78	0.47
1:A:270:LYS:H	2:A:721:URE:HN12	1.62	0.46
1:A:189:MET:HB3	1:A:221:LEU:HD22	1.97	0.46
1:A:190:ARG:O	1:A:192:PRO:HD3	2.16	0.46
1:A:249:ASP:O	1:A:249:ASP:OD1	2.34	0.45
1:A:444:ILE:HB	2:A:719:URE:HN21	1.82	0.45
1:A:342:ARG:HG2	2:A:727:URE:HN12	1.82	0.44
1:A:540:LEU:HG	1:A:598:LEU:HD21	2.00	0.43
1:A:445:GLU:HG2	2:A:712:URE:N2	2.33	0.43
1:A:604:TYR:OH	1:A:639:PRO:HG3	2.19	0.42
1:A:442:GLY:HA2	2:A:719:URE:N1	2.34	0.42
1:A:209:GLU:O	1:A:213:CYS:HB2	2.20	0.42
1:A:175:VAL:HG13	1:A:188:ILE:HD11	2.02	0.42
1:A:182:GLU:OE1	1:A:185:ARG:NH1	2.52	0.41
1:A:375:GLN:HG2	2:A:726:URE:HN21	1.85	0.41
1:A:640:LEU:HD22	1:A:655:ALA:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:636:ALA:C	1:A:639:PRO:HD2	2.41	0.41
1:A:605:SER:HA	1:A:606:PRO:HD3	1.90	0.41
1:A:389:SER:O	1:A:391:ALA:N	2.53	0.41
1:A:654:TYR:O	1:A:658:VAL:HG23	2.21	0.40
1:A:219:HIS:CD2	1:A:223:HIS:HE1	2.39	0.40
1:A:399:GLU:HG3	1:A:437:MET:SD	2.61	0.40
1:A:609:ASN:O	1:A:613:VAL:HG22	2.21	0.40
1:A:544:HIS:O	1:A:548:GLN:HG2	2.20	0.40
1:A:221:LEU:HA	1:A:221:LEU:HD23	1.88	0.40
1:A:188:ILE:CG2	1:A:221:LEU:HD21	2.52	0.40

There are no symmetry-related clashes.

## 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	487/538 (90%)	467 (96%)	12 (2%)	8 (2%)	11	9

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	167	VAL
1	A	174	MET
1	A	390	ASP
1	A	175	VAL
1	A	177	GLN
1	A	248	VAL
1	A	170	LYS
1	A	176	HIS

### 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	401/447 (90%)	391 (98%)	10 (2%)	53 64

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	177	GLN
1	A	181	LYS
1	A	188	ILE
1	A	194	MET
1	A	208	VAL
1	A	212	ARG
1	A	251	VAL
1	A	515[A]	ARG
1	A	515[B]	ARG
1	A	562	GLU

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

Mol	Chain	Res	Type
1	A	223	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 carbohydrates in this entry.

## 5.6 Ligand geometry

56 ligands are 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	$\# Z  > 2$
2	URE	A	701	-	3,3,3	1.16	0	3,3,3	0.70	0
2	URE	A	702	-	3,3,3	1.13	0	3,3,3	0.69	0
2	URE	A	703	-	3,3,3	1.15	0	3,3,3	0.72	0
2	URE	A	704	-	3,3,3	1.16	0	3,3,3	0.73	0
2	URE	A	705	-	3,3,3	1.15	0	3,3,3	0.67	0
2	URE	A	706	-	3,3,3	1.13	0	3,3,3	0.74	0
2	URE	A	707	-	3,3,3	1.15	0	3,3,3	0.78	0
2	URE	A	708	-	3,3,3	1.15	0	3,3,3	0.70	0
2	URE	A	709	-	3,3,3	1.14	0	3,3,3	0.73	0
2	URE	A	710	-	3,3,3	1.14	0	3,3,3	0.70	0
2	URE	A	711	-	3,3,3	1.14	0	3,3,3	0.75	0
2	URE	A	712	-	3,3,3	1.16	0	3,3,3	0.64	0
2	URE	A	713	-	3,3,3	1.14	0	3,3,3	0.59	0
2	URE	A	714	-	3,3,3	1.16	0	3,3,3	0.76	0
2	URE	A	715	-	3,3,3	1.15	0	3,3,3	0.72	0
2	URE	A	716	-	3,3,3	1.14	0	3,3,3	0.71	0
2	URE	A	717	-	3,3,3	1.13	0	3,3,3	0.73	0
2	URE	A	718	-	3,3,3	1.13	0	3,3,3	0.78	0
2	URE	A	719	-	3,3,3	1.15	0	3,3,3	0.82	0
2	URE	A	720	-	3,3,3	1.14	0	3,3,3	0.68	0
2	URE	A	721	-	3,3,3	1.16	0	3,3,3	0.75	0
2	URE	A	722	-	3,3,3	1.15	0	3,3,3	0.76	0
2	URE	A	723	-	3,3,3	1.14	0	3,3,3	0.70	0
2	URE	A	724	-	3,3,3	1.15	0	3,3,3	0.72	0
2	URE	A	725	-	3,3,3	1.16	0	3,3,3	0.80	0
2	URE	A	726	-	3,3,3	1.14	0	3,3,3	0.71	0
2	URE	A	727	-	3,3,3	1.15	0	3,3,3	0.76	0
2	URE	A	728	-	3,3,3	1.16	0	3,3,3	0.72	0
2	URE	A	729	-	3,3,3	1.14	0	3,3,3	0.73	0
2	URE	A	730	-	3,3,3	1.14	0	3,3,3	0.80	0
2	URE	A	731	-	3,3,3	1.15	0	3,3,3	0.75	0
2	URE	A	732	-	3,3,3	1.14	0	3,3,3	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	URE	A	733	-	3,3,3	1.14	0	3,3,3	0.70	0
2	URE	A	734	-	3,3,3	1.14	0	3,3,3	0.71	0
2	URE	A	735	-	3,3,3	1.14	0	3,3,3	0.70	0
2	URE	A	736	-	3,3,3	1.16	0	3,3,3	0.70	0
2	URE	A	737	-	3,3,3	1.16	0	3,3,3	0.66	0
2	URE	A	738	-	3,3,3	1.14	0	3,3,3	0.72	0
2	URE	A	739	-	3,3,3	1.12	0	3,3,3	0.69	0
2	URE	A	740	-	3,3,3	1.14	0	3,3,3	0.74	0
2	URE	A	741	-	3,3,3	1.17	0	3,3,3	0.71	0
2	URE	A	742	-	3,3,3	1.12	0	3,3,3	0.68	0
2	URE	A	743	-	3,3,3	1.13	0	3,3,3	0.75	0
2	URE	A	744	-	3,3,3	1.13	0	3,3,3	0.71	0
2	URE	A	745	-	3,3,3	1.12	0	3,3,3	0.73	0
2	URE	A	746	-	3,3,3	1.15	0	3,3,3	0.76	0
2	URE	A	747	-	3,3,3	1.14	0	3,3,3	0.72	0
2	URE	A	748	-	3,3,3	1.12	0	3,3,3	0.75	0
2	URE	A	749	-	3,3,3	1.15	0	3,3,3	0.85	0
2	URE	A	750	-	3,3,3	1.15	0	3,3,3	0.73	0
2	URE	A	751	-	3,3,3	1.12	0	3,3,3	0.70	0
2	URE	A	752	-	3,3,3	1.16	0	3,3,3	0.85	0
2	URE	A	753	-	3,3,3	1.15	0	3,3,3	0.73	0
2	URE	A	754	-	3,3,3	1.16	0	3,3,3	0.53	0
2	URE	A	755	-	3,3,3	1.16	0	3,3,3	0.75	0
2	URE	A	756	-	2,2,3	0.82	0	1,1,3	0.73	0

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
2	URE	A	701	-	-	0/0/0/0	0/0/0/0
2	URE	A	702	-	-	0/0/0/0	0/0/0/0
2	URE	A	703	-	-	0/0/0/0	0/0/0/0
2	URE	A	704	-	-	0/0/0/0	0/0/0/0
2	URE	A	705	-	-	0/0/0/0	0/0/0/0
2	URE	A	706	-	-	0/0/0/0	0/0/0/0
2	URE	A	707	-	-	0/0/0/0	0/0/0/0
2	URE	A	708	-	-	0/0/0/0	0/0/0/0
2	URE	A	709	-	-	0/0/0/0	0/0/0/0
2	URE	A	710	-	-	0/0/0/0	0/0/0/0
2	URE	A	711	-	-	0/0/0/0	0/0/0/0
2	URE	A	712	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	URE	A	713	-	-	0/0/0/0	0/0/0/0
2	URE	A	714	-	-	0/0/0/0	0/0/0/0
2	URE	A	715	-	-	0/0/0/0	0/0/0/0
2	URE	A	716	-	-	0/0/0/0	0/0/0/0
2	URE	A	717	-	-	0/0/0/0	0/0/0/0
2	URE	A	718	-	-	0/0/0/0	0/0/0/0
2	URE	A	719	-	-	0/0/0/0	0/0/0/0
2	URE	A	720	-	-	0/0/0/0	0/0/0/0
2	URE	A	721	-	-	0/0/0/0	0/0/0/0
2	URE	A	722	-	-	0/0/0/0	0/0/0/0
2	URE	A	723	-	-	0/0/0/0	0/0/0/0
2	URE	A	724	-	-	0/0/0/0	0/0/0/0
2	URE	A	725	-	-	0/0/0/0	0/0/0/0
2	URE	A	726	-	-	0/0/0/0	0/0/0/0
2	URE	A	727	-	-	0/0/0/0	0/0/0/0
2	URE	A	728	-	-	0/0/0/0	0/0/0/0
2	URE	A	729	-	-	0/0/0/0	0/0/0/0
2	URE	A	730	-	-	0/0/0/0	0/0/0/0
2	URE	A	731	-	-	0/0/0/0	0/0/0/0
2	URE	A	732	-	-	0/0/0/0	0/0/0/0
2	URE	A	733	-	-	0/0/0/0	0/0/0/0
2	URE	A	734	-	-	0/0/0/0	0/0/0/0
2	URE	A	735	-	-	0/0/0/0	0/0/0/0
2	URE	A	736	-	-	0/0/0/0	0/0/0/0
2	URE	A	737	-	-	0/0/0/0	0/0/0/0
2	URE	A	738	-	-	0/0/0/0	0/0/0/0
2	URE	A	739	-	-	0/0/0/0	0/0/0/0
2	URE	A	740	-	-	0/0/0/0	0/0/0/0
2	URE	A	741	-	-	0/0/0/0	0/0/0/0
2	URE	A	742	-	-	0/0/0/0	0/0/0/0
2	URE	A	743	-	-	0/0/0/0	0/0/0/0
2	URE	A	744	-	-	0/0/0/0	0/0/0/0
2	URE	A	745	-	-	0/0/0/0	0/0/0/0
2	URE	A	746	-	-	0/0/0/0	0/0/0/0
2	URE	A	747	-	-	0/0/0/0	0/0/0/0
2	URE	A	748	-	-	0/0/0/0	0/0/0/0
2	URE	A	749	-	-	0/0/0/0	0/0/0/0
2	URE	A	750	-	-	0/0/0/0	0/0/0/0
2	URE	A	751	-	-	0/0/0/0	0/0/0/0
2	URE	A	752	-	-	0/0/0/0	0/0/0/0
2	URE	A	753	-	-	0/0/0/0	0/0/0/0
2	URE	A	754	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	URE	A	755	-	-	0/0/0/0	0/0/0/0
2	URE	A	756	-	-	0/0/0/0	0/0/0/0

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.

10 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	712	URE	1	0
2	A	719	URE	3	0
2	A	721	URE	1	0
2	A	725	URE	1	0
2	A	726	URE	1	0
2	A	727	URE	1	0
2	A	736	URE	1	0
2	A	741	URE	2	0
2	A	743	URE	1	0
2	A	754	URE	1	0

## 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	490/538 (91%)	0.42	42 (8%) 11 16	40, 61, 138, 156	1 (0%)

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	187	ALA	8.3
1	A	174	MET	7.5
1	A	183	ALA	7.3
1	A	189	MET	6.7
1	A	178	LEU	6.5
1	A	190	ARG	6.1
1	A	185	ARG	5.7
1	A	172	ALA	5.4
1	A	177	GLN	5.3
1	A	170	LYS	4.7
1	A	192	PRO	4.6
1	A	248	VAL	4.0
1	A	226	GLU	3.9
1	A	195	VAL	3.9
1	A	186	HIS	3.8
1	A	562	GLU	3.8
1	A	549	ARG	3.6
1	A	161	ASN	3.6
1	A	175	VAL	3.4
1	A	194	MET	3.2
1	A	193	GLN	3.1
1	A	221	LEU	3.1
1	A	171	ALA	3.0
1	A	162	ASP	3.0
1	A	209	GLU	3.0
1	A	204	ASN	2.9
1	A	191	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	210	THR	2.7
1	A	188	ILE	2.7
1	A	182	GLU	2.6
1	A	390	ASP	2.5
1	A	179	SER	2.5
1	A	249	ASP	2.4
1	A	393	THR	2.4
1	A	200	ARG	2.4
1	A	184	SER	2.4
1	A	173	VAL	2.3
1	A	198	ILE	2.3
1	A	563	GLY	2.3
1	A	199	VAL	2.3
1	A	394	LYS	2.2
1	A	565	ARG	2.1

## 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	URE	A	727	4/4	0.81	0.34	16.57	79,93,98,113	0
2	URE	A	741	4/4	0.71	0.60	15.66	99,104,111,115	0
2	URE	A	746	4/4	0.72	0.74	12.51	98,109,116,127	0
2	URE	A	749	4/4	0.54	0.64	11.59	76,79,95,97	0
2	URE	A	748	4/4	0.58	0.32	9.39	65,74,107,111	0
2	URE	A	737	4/4	0.95	0.39	7.81	83,84,94,96	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	URE	A	751	4/4	0.57	0.39	7.77	62,96,97,109	0
2	URE	A	721	4/4	0.66	0.34	6.22	92,93,106,112	0
2	URE	A	731	4/4	0.71	0.26	6.07	66,75,81,92	0
2	URE	A	703	4/4	0.56	0.39	5.41	74,79,97,98	0
2	URE	A	729	4/4	0.77	0.56	5.01	91,103,104,104	0
2	URE	A	743	4/4	0.75	0.27	3.60	58,81,96,99	0
2	URE	A	719	4/4	0.72	0.25	3.44	58,82,82,85	0
2	URE	A	706	4/4	0.86	0.31	3.20	69,72,74,94	0
2	URE	A	728	4/4	0.90	0.37	2.92	87,89,98,124	0
2	URE	A	708	4/4	0.96	0.17	2.75	59,59,71,87	0
2	URE	A	722	4/4	0.73	0.24	2.66	77,81,94,102	0
2	URE	A	705	4/4	0.94	0.14	2.27	49,52,53,59	0
2	URE	A	710	4/4	0.90	0.19	2.15	78,87,91,119	0
2	URE	A	702	4/4	0.94	0.13	2.04	44,50,59,60	0
2	URE	A	752	4/4	0.76	0.25	2.03	70,78,91,96	0
2	URE	A	735	4/4	0.92	0.18	0.51	71,81,84,97	0
2	URE	A	704	4/4	0.95	0.13	0.30	49,53,54,62	0
2	URE	A	742	4/4	0.79	0.46	-	70,84,94,99	0
2	URE	A	709	4/4	0.71	0.31	-	78,84,90,100	0
2	URE	A	720	4/4	0.88	0.51	-	67,83,89,101	0
2	URE	A	716	4/4	0.63	0.27	-	95,97,102,117	0
2	URE	A	726	4/4	0.81	0.41	-	85,92,97,99	0
2	URE	A	732	4/4	0.73	0.43	-	79,94,96,97	0
2	URE	A	712	4/4	0.52	0.32	-	77,99,101,103	0
2	URE	A	755	4/4	0.60	0.76	-	97,98,113,119	0
2	URE	A	740	4/4	0.60	0.39	-	88,97,99,106	0
2	URE	A	736	4/4	0.69	0.20	-	69,88,90,96	0
2	URE	A	701	4/4	0.90	0.13	-	46,47,48,52	4
2	URE	A	715	4/4	0.60	0.47	-	75,84,100,107	0
2	URE	A	739	4/4	0.78	0.35	-	64,67,101,102	0
2	URE	A	725	4/4	0.91	0.28	-	83,90,95,96	0
2	URE	A	750	4/4	0.67	0.44	-	99,113,124,132	0
2	URE	A	754	4/4	0.56	0.58	-	86,96,102,116	0
2	URE	A	730	4/4	0.69	0.49	-	87,87,106,113	0
2	URE	A	747	4/4	0.74	0.40	-	85,88,94,103	0
2	URE	A	733	4/4	0.59	0.41	-	88,99,105,112	0
2	URE	A	711	4/4	0.80	0.30	-	73,73,75,87	0
2	URE	A	734	4/4	0.86	0.14	-	78,86,98,101	0
2	URE	A	718	4/4	0.84	0.21	-	67,82,95,103	0
2	URE	A	724	4/4	0.68	0.39	-	84,88,99,101	0
2	URE	A	723	4/4	0.86	0.26	-	64,74,83,87	0
2	URE	A	745	4/4	0.77	0.59	-	85,86,98,106	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	URE	A	714	4/4	0.87	0.27	-	77,80,95,98	0
2	URE	A	738	4/4	0.66	0.45	-	63,90,92,96	0
2	URE	A	707	4/4	0.61	0.24	-	81,84,99,112	0
2	URE	A	744	4/4	0.37	0.35	-	72,82,92,105	0
2	URE	A	717	4/4	0.38	0.37	-	75,83,93,94	0
2	URE	A	713	4/4	0.76	0.66	-	75,101,103,120	0
2	URE	A	753	4/4	0.91	0.23	-	94,96,99,103	0
2	URE	A	756	3/4	0.48	0.24	-	102,102,105,108	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.