



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 12:57 PM UTC

PDB ID : 6AE8 / pdb\_00006ae8  
Title : Structure insight into histone chaperone Chz1-mediated H2A.Z recognition and replacement  
Authors : Wang, Y.Y.; Shan, S.; Zhou, Z.  
Deposited on : 2018-08-03  
Resolution : 1.65 Å (reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

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<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 : 4-5-2 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

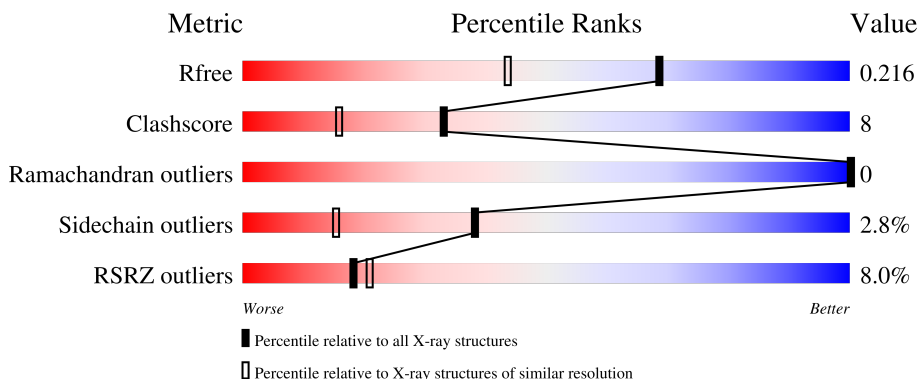
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.65 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	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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	193	 7% 79% 13% •• 6%
1	B	193	 8% 79% 13% • 6%
2	C	120	 2% 10% 90%
2	D	120	 8% • 90%

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
3	BCN	A	201	-	-	X	-
3	BCN	B	201	-	X	X	-

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3178 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 Histone H2B.1,Histone H2A.Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	182	1415	887	261	266	1	0	0	0
1	B	182	1416	888	261	265	2	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP P02293
B	0	MET	-	initiating methionine	UNP P02293

- Molecule 2 is a protein called Histone H2A.Z-specific chaperone CHZ1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	12	104	59	13	32	0	0	0
2	D	12	104	59	13	32	0	0	0

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-29	MET	-	initiating methionine	UNP P40019
C	-28	GLY	-	expression tag	UNP P40019
C	-27	SER	-	expression tag	UNP P40019
C	-26	SER	-	expression tag	UNP P40019
C	-25	HIS	-	expression tag	UNP P40019
C	-24	HIS	-	expression tag	UNP P40019
C	-23	HIS	-	expression tag	UNP P40019
C	-22	HIS	-	expression tag	UNP P40019
C	-21	HIS	-	expression tag	UNP P40019
C	-20	HIS	-	expression tag	UNP P40019

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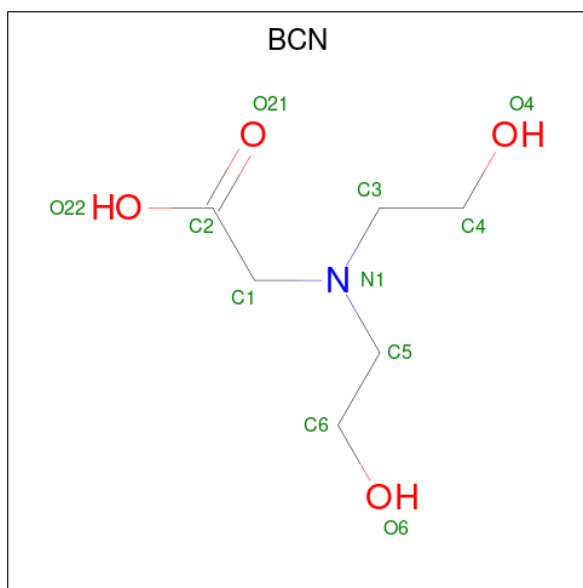
Chain	Residue	Modelled	Actual	Comment	Reference
C	-19	TYR	-	expression tag	UNP P40019
C	-18	PRO	-	expression tag	UNP P40019
C	-17	TYR	-	expression tag	UNP P40019
C	-16	ASP	-	expression tag	UNP P40019
C	-15	VAL	-	expression tag	UNP P40019
C	-14	PRO	-	expression tag	UNP P40019
C	-13	ASP	-	expression tag	UNP P40019
C	-12	TYR	-	expression tag	UNP P40019
C	-11	ALA	-	expression tag	UNP P40019
C	-10	SER	-	expression tag	UNP P40019
C	-9	SER	-	expression tag	UNP P40019
C	-8	GLY	-	expression tag	UNP P40019
C	-7	LEU	-	expression tag	UNP P40019
C	-6	VAL	-	expression tag	UNP P40019
C	-5	PRO	-	expression tag	UNP P40019
C	-4	ARG	-	expression tag	UNP P40019
C	-3	GLY	-	expression tag	UNP P40019
C	-2	SER	-	expression tag	UNP P40019
C	-1	HIS	-	expression tag	UNP P40019
C	0	MET	-	expression tag	UNP P40019
D	-29	MET	-	initiating methionine	UNP P40019
D	-28	GLY	-	expression tag	UNP P40019
D	-27	SER	-	expression tag	UNP P40019
D	-26	SER	-	expression tag	UNP P40019
D	-25	HIS	-	expression tag	UNP P40019
D	-24	HIS	-	expression tag	UNP P40019
D	-23	HIS	-	expression tag	UNP P40019
D	-22	HIS	-	expression tag	UNP P40019
D	-21	HIS	-	expression tag	UNP P40019
D	-20	HIS	-	expression tag	UNP P40019
D	-19	TYR	-	expression tag	UNP P40019
D	-18	PRO	-	expression tag	UNP P40019
D	-17	TYR	-	expression tag	UNP P40019
D	-16	ASP	-	expression tag	UNP P40019
D	-15	VAL	-	expression tag	UNP P40019
D	-14	PRO	-	expression tag	UNP P40019
D	-13	ASP	-	expression tag	UNP P40019
D	-12	TYR	-	expression tag	UNP P40019
D	-11	ALA	-	expression tag	UNP P40019
D	-10	SER	-	expression tag	UNP P40019
D	-9	SER	-	expression tag	UNP P40019
D	-8	GLY	-	expression tag	UNP P40019

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-7	LEU	-	expression tag	UNP P40019
D	-6	VAL	-	expression tag	UNP P40019
D	-5	PRO	-	expression tag	UNP P40019
D	-4	ARG	-	expression tag	UNP P40019
D	-3	GLY	-	expression tag	UNP P40019
D	-2	SER	-	expression tag	UNP P40019
D	-1	HIS	-	expression tag	UNP P40019
D	0	MET	-	expression tag	UNP P40019

- Molecule 3 is BICINE (CCD ID: BCN) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			11	6	1	4		
3	B	1	Total	C	N	O	0	0
			11	6	1	4		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	50	Total	O	0	0
			50	50		
4	C	5	Total	O	0	0
			5	5		
4	B	59	Total	O	0	0
			59	59		

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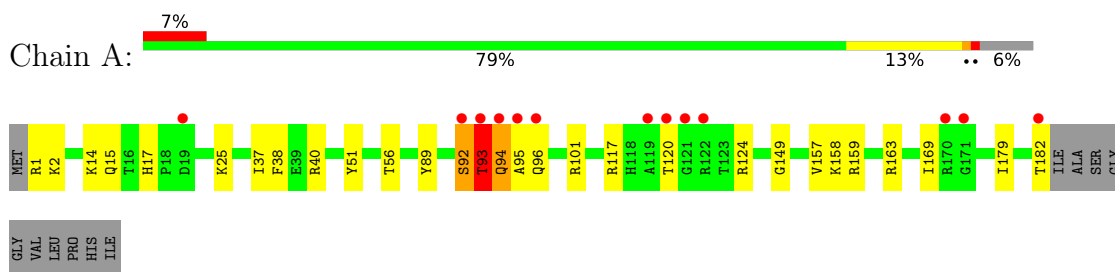
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	D	3	Total	O	0	0
			3	3		

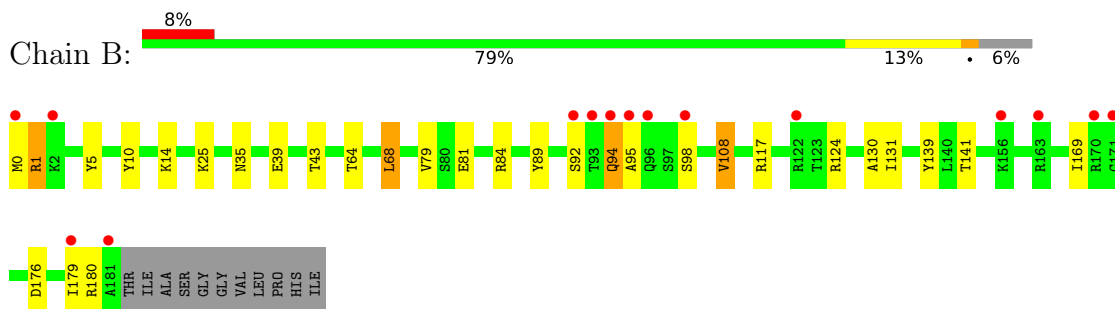
### 3 Residue-property plots [i](#)

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.

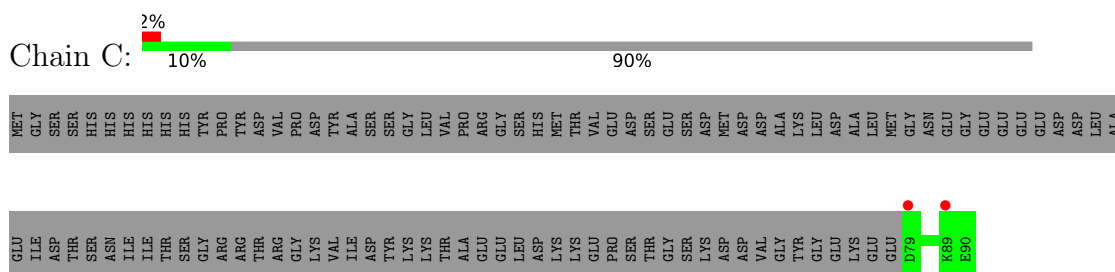
- Molecule 1: Histone H2B.1,Histone H2A.Z



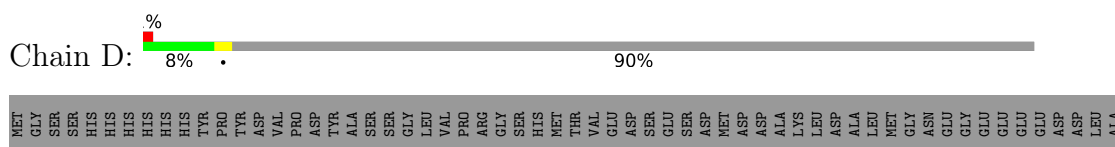
- Molecule 1: Histone H2B.1,Histone H2A.Z



- Molecule 2: Histone H2A.Z-specific chaperone CHZ1



- Molecule 2: Histone H2A.Z-specific chaperone CHZ1



GLU	ILE	ASP	THR	SER	ASN	ILE	ILE	THR	SER	GLY	ARG	ARG	THR	ARG	GLY	LYS	VAL	ILE	ASP	TYR	LYS	LYS	THR	ALA	GLU	GLU	LEU	ASP	LYS	LYS	GLU	PRO	SER	THR	GLY	SER	LYS	ASP	ASP	VAL	GLY	TYR	GLY	GLU	LYS	GLU	E78	E84	F89	GLU
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	42.08Å 46.21Å 56.66Å 72.37° 70.92° 70.60°	Depositor
Resolution (Å)	50.00 – 1.65 50.00 – 1.65	Depositor EDS
% Data completeness (in resolution range)	96.2 (50.00-1.65) 96.2 (50.00-1.65)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.93 (at 1.65Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, $R_{free}$	0.181 , 0.216 0.185 , 0.216	Depositor DCC
$R_{free}$ test set	2158 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.9	Xtrriage
Anisotropy	0.376	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 31.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3178	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.21% 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: BCN

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	1.28	1/1433 (0.1%)	1.18	6/1930 (0.3%)
1	B	1.30	4/1434 (0.3%)	1.18	5/1930 (0.3%)
2	C	0.92	0/104	0.95	0/138
2	D	1.13	0/104	1.01	0/138
All	All	1.28	5/3075 (0.2%)	1.17	11/4136 (0.3%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	10	TYR	N-CA	6.06	1.53	1.46
1	B	141	THR	N-CA	-5.84	1.39	1.46
1	B	124	ARG	C-O	-5.38	1.16	1.23
1	B	1	ARG	C-O	-5.26	1.17	1.23
1	A	95	ALA	CA-C	-5.24	1.47	1.53

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	94	GLN	N-CA-C	10.77	126.96	108.76
1	A	95	ALA	N-CA-C	-7.85	98.65	109.71
1	A	120	THR	N-CA-C	6.71	120.10	110.24
1	B	94	GLN	N-CA-C	-5.46	99.18	110.80
1	B	108	VAL	N-CA-C	5.36	115.57	110.42

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	1415	0	1483	30	3
1	B	1416	0	1485	17	4
2	C	104	0	69	0	0
2	D	104	0	69	1	0
3	A	11	0	10	10	0
3	B	11	0	11	6	0
4	A	50	0	0	0	1
4	B	59	0	0	0	0
4	C	5	0	0	0	0
4	D	3	0	0	1	0
All	All	3178	0	3127	48	4

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.

The worst 5 of 48 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:40:ARG:HH21	1:A:182:THR:HG23	1.26	1.01
1:A:40:ARG:HE	1:A:182:THR:HG22	1.28	0.96
1:A:117:ARG:HH21	3:A:201:BCN:C4	1.81	0.93
1:B:5:TYR:OH	3:B:201:BCN:H61	1.67	0.93
1:A:40:ARG:HH21	1:A:182:THR:CG2	1.83	0.91

All (4) 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:B:0:MET:CE	4:A:305:HOH:O[1_554]	1.11	1.09
1:A:51:TYR:CD1	1:B:0:MET:SD[1_456]	1.57	0.63
1:A:15:GLN:O	1:B:0:MET:CE[1_556]	1.91	0.29
1:A:51:TYR:CE1	1:B:0:MET:SD[1_456]	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	180/193 (93%)	176 (98%)	4 (2%)	0	100	100
1	B	180/193 (93%)	176 (98%)	4 (2%)	0	100	100
2	C	10/120 (8%)	10 (100%)	0	0	100	100
2	D	10/120 (8%)	10 (100%)	0	0	100	100
All	All	380/626 (61%)	372 (98%)	8 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	151/159 (95%)	146 (97%)	5 (3%)	33	11
1	B	151/159 (95%)	148 (98%)	3 (2%)	48	26
2	C	12/105 (11%)	12 (100%)	0	100	100
2	D	12/105 (11%)	11 (92%)	1 (8%)	10	1
All	All	326/528 (62%)	317 (97%)	9 (3%)	38	15

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	79	VAL
2	D	84	GLU
1	A	158	LYS

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Mol	Chain	Res	Type
1	A	163	ARG
1	B	25	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	GLN
1	B	15	GLN
1	B	17	HIS
1	B	63	GLN

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

2 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
3	BCN	A	201	-	10,10,10	1.29	1 (10%)	11,11,11	3.07	5 (45%)
3	BCN	B	201	-	10,10,10	1.62	3 (30%)	11,11,11	3.63	6 (54%)

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
3	BCN	A	201	-	-	3/10/10/10	-
3	BCN	B	201	-	-	4/10/10/10	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	201	BCN	C1-C2	3.03	1.57	1.51
3	B	201	BCN	O6-C6	-2.50	1.29	1.42
3	A	201	BCN	O6-C6	-2.41	1.29	1.42
3	B	201	BCN	C3-C4	-2.06	1.43	1.51

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	201	BCN	C5-N1-C3	-6.80	95.25	111.44
3	A	201	BCN	C5-N1-C3	-5.93	97.31	111.44
3	B	201	BCN	O6-C6-C5	-5.90	86.91	111.22
3	A	201	BCN	O6-C6-C5	-5.87	87.04	111.22
3	B	201	BCN	O4-C4-C3	-4.54	92.51	111.22

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	201	BCN	N1-C3-C4-O4
3	A	201	BCN	C2-C1-N1-C5
3	A	201	BCN	C6-C5-N1-C1
3	B	201	BCN	C2-C1-N1-C3
3	B	201	BCN	C4-C3-N1-C5

There are no ring outliers.

2 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	201	BCN	10	0
3	B	201	BCN	6	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	182/193 (94%)	0.18	13 (7%) 22 25	11, 18, 44, 83	0
1	B	182/193 (94%)	0.16	15 (8%) 17 19	11, 19, 44, 97	0
2	C	12/120 (10%)	1.37	2 (16%) 4 4	27, 39, 54, 55	0
2	D	12/120 (10%)	0.85	1 (8%) 17 19	24, 37, 60, 62	0
All	All	388/626 (61%)	0.23	31 (7%) 18 21	11, 19, 51, 97	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	93	THR	11.5
1	B	95	ALA	7.6
1	B	93	THR	6.5
1	B	0	MET	5.6
2	C	79	ASP	5.4

### 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 oligosaccharides 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( $\text{\AA}^2$ )	Q<0.9
3	BCN	A	201	11/11	0.86	0.12	22,31,48,49	0
3	BCN	B	201	11/11	0.88	0.12	22,26,40,40	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.