



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:15 PM UTC

PDB ID : 5JSB / pdb\_00005jsb  
Title : Crystal structure of Mcl1-inhibitor complex  
Authors : Shen, B.W.; Stoddard, B.L.  
Deposited on : 2016-05-07  
Resolution : 2.74 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)

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 : 4-5-2 with Phenix2.0  
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

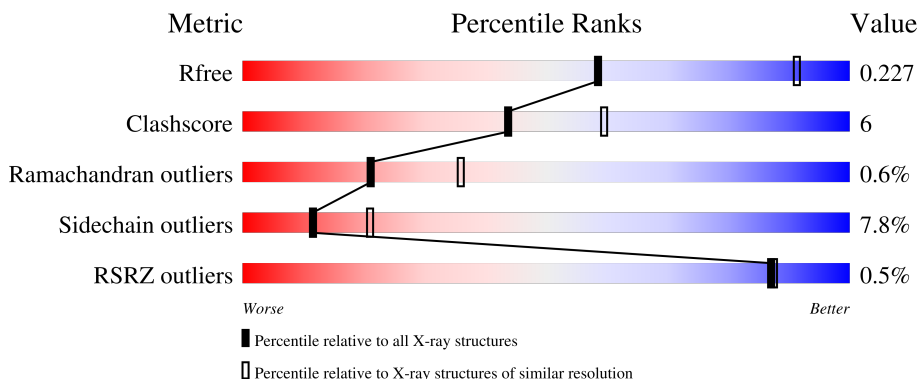
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.74 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	1819 (2.76-2.72)
Clashscore	190562	1866 (2.76-2.72)
Ramachandran outliers	187476	1830 (2.76-2.72)
Sidechain outliers	187428	1831 (2.76-2.72)
RSRZ outliers	180081	1819 (2.76-2.72)

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	179	 % 64% 17% • 16%
1	C	179	 65% 16% • • 16%
1	E	179	 66% 17% • 16%
1	G	179	 % 60% 21% • 16%
1	I	179	 64% 16% • 16%

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Mol	Chain	Length	Quality of chain
1	K	179	<p>%</p> <p>62% 18% 16%</p>
2	B	116	<p>2%</p> <p>84% 16%</p>
2	D	116	<p>%</p> <p>89% 10%</p>
2	F	116	<p>83% 17%</p>
2	H	116	<p>81% 16%</p>
2	J	116	<p>84% 14%</p>
2	L	116	<p>%</p> <p>80% 20%</p>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 13069 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 Induced myeloid leukemia cell differentiation protein Mcl-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	151	1217	764	224	225	4	0	0	0
1	C	151	1217	764	224	225	4	0	0	0
1	E	151	1217	764	224	225	4	0	0	0
1	G	151	1217	764	224	225	4	0	0	0
1	I	151	1217	764	224	225	4	0	0	0
1	K	151	1213	760	224	225	4	0	0	0

- Molecule 2 is a protein called Mcl-1 inhibitor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	116	956	597	175	183	1	0	0	0
2	D	116	966	602	177	186	1	0	1	0
2	F	116	957	597	175	184	1	0	0	0
2	H	116	956	597	175	183	1	0	0	0
2	J	116	957	597	175	184	1	0	0	0
2	L	116	957	597	175	184	1	0	0	0

- Molecule 3 is water.

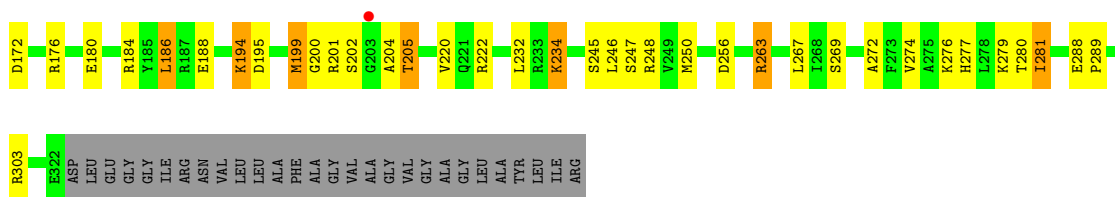
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total O 2 2	0	0
3	B	2	Total O 2 2	0	0
3	C	3	Total O 3 3	0	0
3	D	1	Total O 1 1	0	0
3	E	3	Total O 3 3	0	0
3	F	1	Total O 1 1	0	0
3	G	3	Total O 3 3	0	0
3	H	1	Total O 1 1	0	0
3	I	2	Total O 2 2	0	0
3	K	2	Total O 2 2	0	0
3	L	2	Total O 2 2	0	0

### 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.

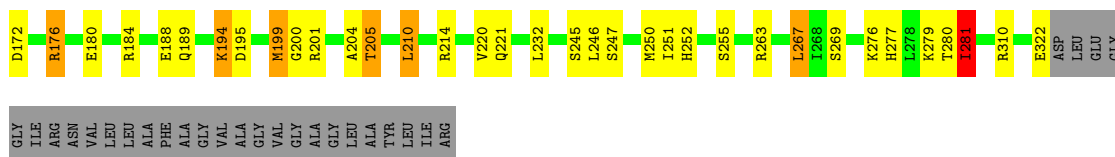
- Molecule 1: Induced myeloid leukemia cell differentiation protein Mcl-1

Chain A: 



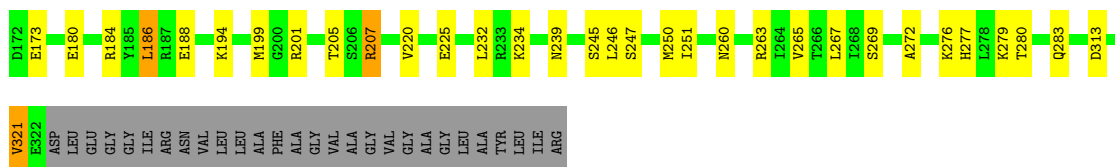
- Molecule 1: Induced myeloid leukemia cell differentiation protein Mcl-1

Chain C: 



- Molecule 1: Induced myeloid leukemia cell differentiation protein Mcl-1

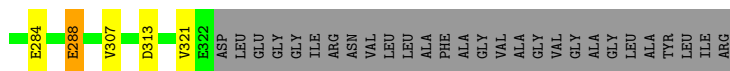
Chain E: 



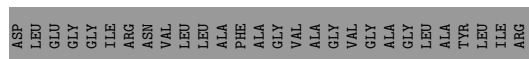
- Molecule 1: Induced myeloid leukemia cell differentiation protein Mcl-1

Chain G: 

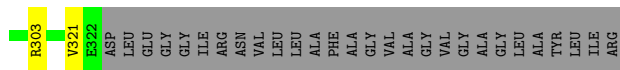




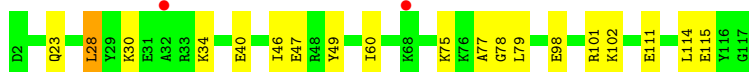
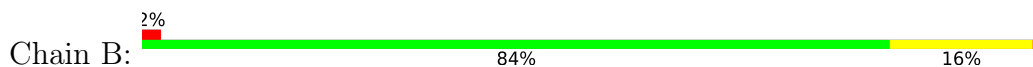
• Molecule 1: Induced myeloid leukemia cell differentiation protein Mcl-1



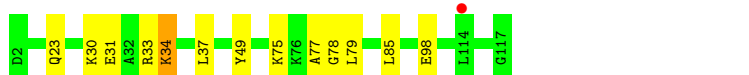
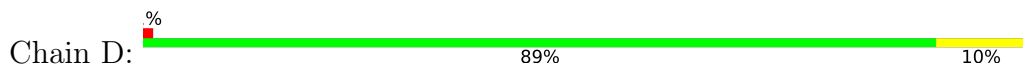
• Molecule 1: Induced myeloid leukemia cell differentiation protein Mcl-1



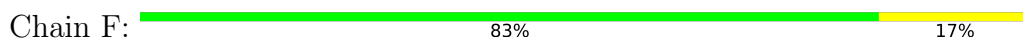
• Molecule 2: Mcl-1 inhibitor



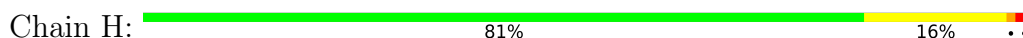
• Molecule 2: Mcl-1 inhibitor

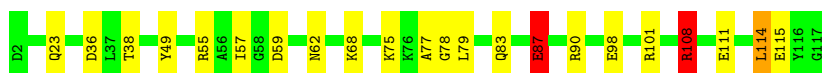


• Molecule 2: Mcl-1 inhibitor

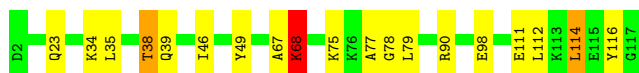
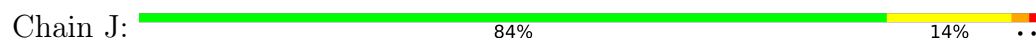


• Molecule 2: Mcl-1 inhibitor

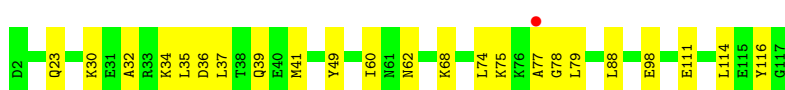
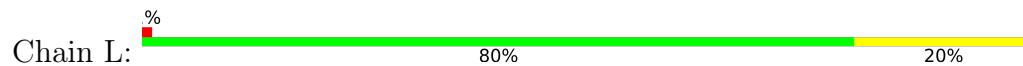




- Molecule 2: Mcl-1 inhibitor



- Molecule 2: Mcl-1 inhibitor



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	61.92Å 92.25Å 162.00Å 90.00° 92.39° 90.00°	Depositor
Resolution (Å)	161.86 – 2.74 161.86 – 2.74	Depositor EDS
% Data completeness (in resolution range)	95.0 (161.86-2.74) 95.0 (161.86-2.74)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.22 (at 2.73Å)	Xtrriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.191 , 0.230 0.194 , 0.227	Depositor DCC
$R_{free}$ test set	2316 reflections (4.61%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	66.5	Xtrriage
Anisotropy	0.399	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 72.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.025 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	13069	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	92.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.61% 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	1.25	1/1237 (0.1%)	1.27	6/1663 (0.4%)
1	C	1.27	2/1237 (0.2%)	1.29	7/1663 (0.4%)
1	E	1.28	3/1237 (0.2%)	1.24	5/1663 (0.3%)
1	G	1.27	5/1237 (0.4%)	1.20	3/1663 (0.2%)
1	I	1.33	3/1237 (0.2%)	1.25	5/1663 (0.3%)
1	K	1.34	7/1233 (0.6%)	1.38	12/1657 (0.7%)
2	B	1.18	2/962 (0.2%)	1.27	5/1280 (0.4%)
2	D	1.16	0/972	1.21	2/1292 (0.2%)
2	F	1.14	3/963 (0.3%)	1.20	2/1280 (0.2%)
2	H	1.14	3/962 (0.3%)	1.24	3/1280 (0.2%)
2	J	1.18	2/963 (0.2%)	1.24	1/1280 (0.1%)
2	L	1.18	1/963 (0.1%)	1.27	4/1280 (0.3%)
All	All	1.24	32/13203 (0.2%)	1.26	55/17664 (0.3%)

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	A	0	1
1	C	0	1
1	K	0	1
All	All	0	3

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	198	PRO	CA-C	14.31	1.72	1.52
1	G	199	MET	CA-C	6.90	1.62	1.52
1	K	199	MET	N-CA	6.17	1.53	1.46
2	B	46	ILE	CA-CB	6.10	1.62	1.54
1	K	202	SER	N-CA	6.10	1.54	1.46

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	199	MET	N-CA-C	20.59	133.80	111.36
1	I	194	LYS	N-CA-C	9.10	124.01	111.55
1	E	265	VAL	N-CA-CB	8.78	122.47	110.54
1	I	194	LYS	CB-CA-C	-8.75	100.11	111.40
1	E	265	VAL	CB-CA-C	-8.70	100.39	112.14

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	199	MET	Peptide
1	C	199	MET	Peptide
1	K	199	MET	Peptide

## 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	1217	0	1226	27	1
1	C	1217	0	1226	35	0
1	E	1217	0	1226	12	1
1	G	1217	0	1226	41	0
1	I	1217	0	1226	23	0
1	K	1213	0	1216	21	1
2	B	956	0	997	11	0
2	D	966	0	1004	6	0
2	F	957	0	997	9	1
2	H	956	0	997	15	0
2	J	957	0	997	13	1
2	L	957	0	997	13	1
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	3	0	0	0	0
3	D	1	0	0	0	0
3	E	3	0	0	0	0
3	F	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	3	0	0	0	0
3	H	1	0	0	0	0
3	I	2	0	0	0	0
3	K	2	0	0	0	0
3	L	2	0	0	0	0
All	All	13069	0	13335	161	3

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.

The worst 5 of 161 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:C:250:MET:HG2	1:C:267:LEU:HD11	1.54	0.89
1:C:176:ARG:HD2	1:G:196:THR:OG1	1.73	0.88
1:C:201:ARG:NE	1:G:193:ALA:HB2	1.96	0.80
1:C:201:ARG:CD	1:G:193:ALA:HB2	2.16	0.76
1:I:184:ARG:NH1	1:I:199:MET:HG2	2.03	0.74

All (3) 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:288:GLU:OE2	2:J:34:LYS:NZ[1_655]	1.86	0.34
1:E:201:ARG:N	2:F:36:ASP:OD2[2_544]	1.89	0.31
1:K:196:THR:OG1	2:L:36:ASP:OD1[2_455]	2.09	0.11

## 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	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	18	32
1	C	149/179 (83%)	142 (95%)	6 (4%)	1 (1%)	18	32
1	E	149/179 (83%)	142 (95%)	6 (4%)	1 (1%)	18	32
1	G	149/179 (83%)	142 (95%)	6 (4%)	1 (1%)	18	32
1	I	149/179 (83%)	140 (94%)	9 (6%)	0	100	100
1	K	149/179 (83%)	142 (95%)	7 (5%)	0	100	100
2	B	114/116 (98%)	110 (96%)	3 (3%)	1 (1%)	14	26
2	D	115/116 (99%)	111 (96%)	3 (3%)	1 (1%)	14	26
2	F	114/116 (98%)	110 (96%)	3 (3%)	1 (1%)	14	26
2	H	114/116 (98%)	110 (96%)	3 (3%)	1 (1%)	14	26
2	J	114/116 (98%)	110 (96%)	3 (3%)	1 (1%)	14	26
2	L	114/116 (98%)	110 (96%)	3 (3%)	1 (1%)	14	26
All	All	1579/1770 (89%)	1513 (96%)	56 (4%)	10 (1%)	21	36

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	78	GLY
2	D	78	GLY
2	F	78	GLY
2	H	78	GLY
2	J	78	GLY

### 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	132/149 (89%)	120 (91%)	12 (9%)	9	16
1	C	132/149 (89%)	121 (92%)	11 (8%)	10	19
1	E	132/149 (89%)	122 (92%)	10 (8%)	12	22
1	G	132/149 (89%)	120 (91%)	12 (9%)	9	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	132/149 (89%)	120 (91%)	12 (9%)	9	16
1	K	131/149 (88%)	121 (92%)	10 (8%)	12	22
2	B	99/99 (100%)	94 (95%)	5 (5%)	21	39
2	D	100/99 (101%)	95 (95%)	5 (5%)	22	40
2	F	99/99 (100%)	92 (93%)	7 (7%)	13	24
2	H	99/99 (100%)	92 (93%)	7 (7%)	13	24
2	J	99/99 (100%)	90 (91%)	9 (9%)	9	16
2	L	99/99 (100%)	91 (92%)	8 (8%)	11	20
All	All	1386/1488 (93%)	1278 (92%)	108 (8%)	11	21

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	263	ARG
1	I	186	LEU
1	K	281	ILE
1	G	274	VAL
2	H	87	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	66	GLN
1	K	277	HIS
2	L	66	GLN
1	I	277	HIS
1	C	309	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](#)

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 [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	151/179 (84%)	-0.41	1 (0%) 84 84	44, 77, 151, 177	0
1	C	151/179 (84%)	-0.30	0 100 100	39, 82, 166, 223	0
1	E	151/179 (84%)	-0.48	0 100 100	46, 76, 124, 168	0
1	G	151/179 (84%)	-0.35	1 (0%) 84 84	46, 86, 160, 201	0
1	I	151/179 (84%)	-0.41	0 100 100	44, 78, 148, 181	0
1	K	151/179 (84%)	-0.27	2 (1%) 75 74	41, 87, 165, 229	0
2	B	116/116 (100%)	-0.21	2 (1%) 69 66	51, 100, 148, 171	0
2	D	116/116 (100%)	-0.18	1 (0%) 81 81	38, 92, 143, 163	1 (0%)
2	F	116/116 (100%)	-0.24	0 100 100	52, 94, 134, 149	0
2	H	116/116 (100%)	-0.15	0 100 100	49, 95, 149, 165	0
2	J	116/116 (100%)	-0.36	0 100 100	49, 88, 132, 156	0
2	L	116/116 (100%)	-0.28	1 (0%) 81 81	43, 97, 162, 182	0
All	All	1602/1770 (90%)	-0.31	8 (0%) 87 87	38, 87, 149, 229	1 (0%)

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	198	PRO	2.6
2	L	77	ALA	2.5
2	B	68	LYS	2.5
1	K	204	ALA	2.3
1	K	181	ILE	2.3

### 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](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.