



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 29, 2020 – 02:12 PM JST

PDB ID : 6LA8  
Title : 349 bp di-nucleosome harboring cohesive DNA termini assembled with linker histone H1.0  
Authors : Adhireksan, Z.; Lee, P.L.; Sharma, D.; Davey, C.A.  
Deposited on : 2019-11-12  
Resolution : 3.40 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.

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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	:	2.14.6
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)	:	2.14.6

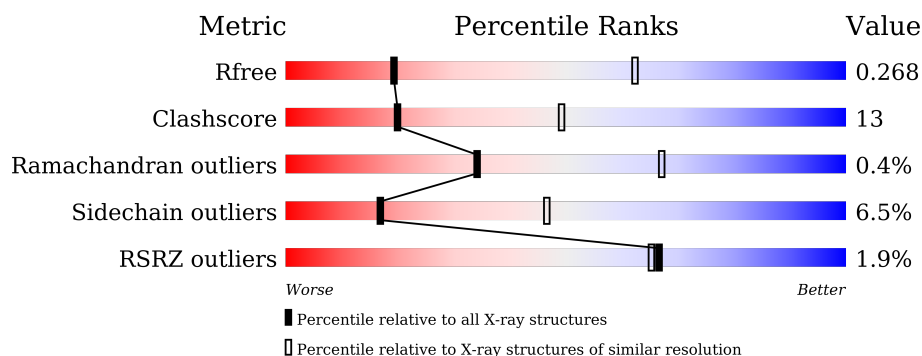
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.40 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	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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 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	136	<div> <div></div> <div>58%</div> <div>15%</div> <div>26%</div> </div>
1	E	136	<div> <div>%</div> <div>60%</div> <div>13%</div> <div>27%</div> </div>
1	K	136	<div> <div>60%</div> <div>13%</div> <div>27%</div> </div>
1	O	136	<div> <div>3%</div> <div>63%</div> <div>10%</div> <div>28%</div> </div>
2	B	103	<div> <div>66%</div> <div>13%</div> <div>21%</div> </div>
2	F	103	<div> <div>70%</div> <div>10%</div> <div>20%</div> </div>

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Mol	Chain	Length	Quality of chain
2	L	103	
2	P	103	
3	C	130	
3	G	130	
3	M	130	
3	Q	130	
4	D	126	
4	H	126	
4	N	126	
4	R	126	
5	I	349	
6	J	349	
7	S	194	

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 27058 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 H3.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	100	Total	C	N	O	S	0	0	0
			825	520	160	141	4			
1	E	99	Total	C	N	O	S	0	0	0
			816	514	158	140	4			
1	K	99	Total	C	N	O	S	0	0	0
			816	514	158	140	4			
1	O	98	Total	C	N	O	S	0	0	0
			807	508	156	139	4			

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	81	Total	C	N	O	S	0	0	0
			646	407	126	112	1			
2	F	82	Total	C	N	O	S	0	0	0
			653	412	127	113	1			
2	L	80	Total	C	N	O	S	0	0	0
			638	401	125	111	1			
2	P	80	Total	C	N	O	S	0	0	0
			638	401	125	111	1			

- Molecule 3 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	110	Total	C	N	O	0	0	0
			849	535	168	146			
3	G	105	Total	C	N	O	0	0	0
			810	511	158	141			
3	M	106	Total	C	N	O	0	0	0
			819	517	160	142			
3	Q	105	Total	C	N	O	0	0	0
			812	512	158	142			

- Molecule 4 is a protein called Histone H2B type 1-J.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	96	Total	C	N	O	S	0	0	0
			755	474	138	141	2			
4	H	96	Total	C	N	O	S	0	0	0
			755	474	138	141	2			
4	N	96	Total	C	N	O	S	0	0	0
			755	474	138	141	2			
4	R	96	Total	C	N	O	S	0	0	0
			755	474	138	141	2			

- Molecule 5 is a DNA chain called DNA (349-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	349	Total	C	N	O	P	0	0	0
			7149	3389	1357	2054	349			

- Molecule 6 is a DNA chain called DNA (349-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	J	349	Total	C	N	O	P	0	0	0
			7162	3407	1270	2136	349			

- Molecule 7 is a protein called Histone H1.0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	S	74	Total	C	N	O	S	0	0	0
			568	354	107	106	1			

- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

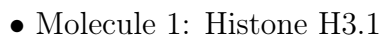
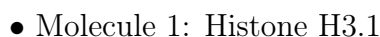
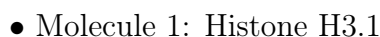
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	G	1	Total	Ca	0	0
			1	1		
8	J	10	Total	Ca	0	0
			10	10		
8	I	11	Total	Ca	0	0
			11	11		
8	M	1	Total	Ca	0	0
			1	1		

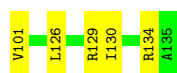
- Molecule 9 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	J	5	Total 5	K 5	0	0
9	I	2	Total 2	K 2	0	0



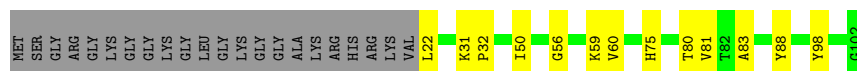
- Molecule 1: Histone H3.1





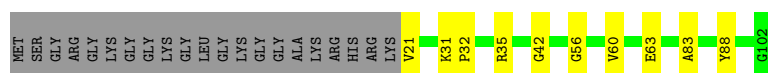
- Molecule 2: Histone H4

Chain B: 66% 13% 21%



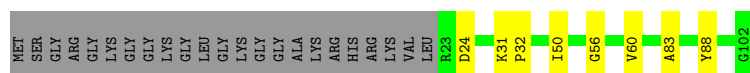
- Molecule 2: Histone H4

Chain F: 70% 10% 20%



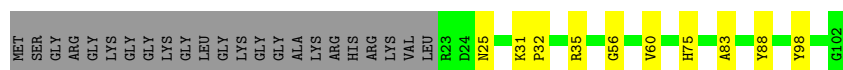
- Molecule 2: Histone H4

Chain L: 70% 8% 22%



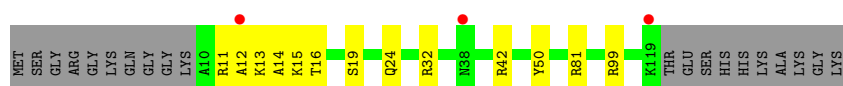
- Molecule 2: Histone H4

Chain P: 68% 10% 22%



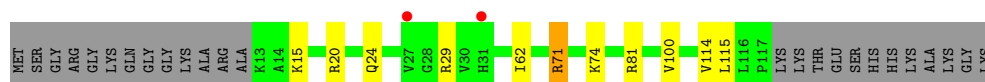
- Molecule 3: Histone H2A type 1-B/E

Chain C: 2% 75% 10% 15%



- Molecule 3: Histone H2A type 1-B/E

Chain G: 2% 72% 8% 19%



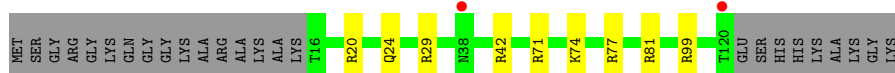
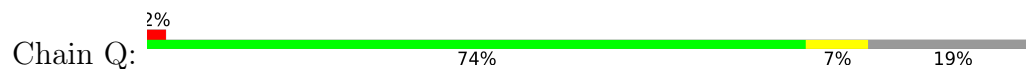
- Molecule 3: Histone H2A type 1-B/E

Chain M: 69% 12% 18%

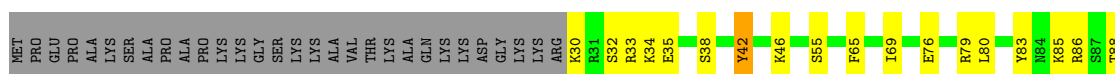




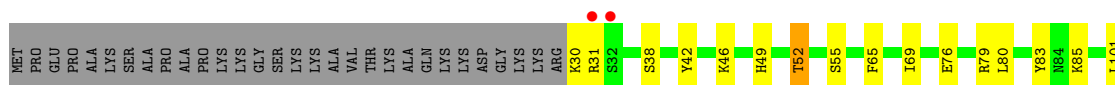
• Molecule 3: Histone H2A type 1-B/E



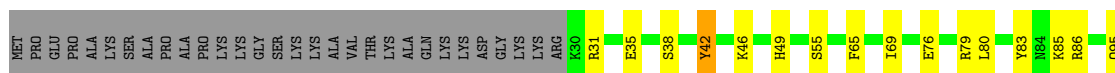
• Molecule 4: Histone H2B type 1-J



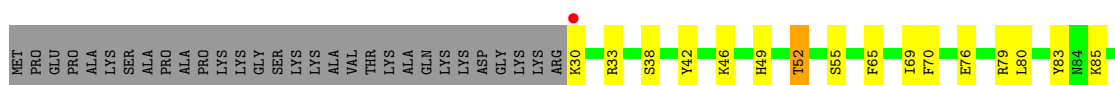
• Molecule 4: Histone H2B type 1-J



• Molecule 4: Histone H2B type 1-J



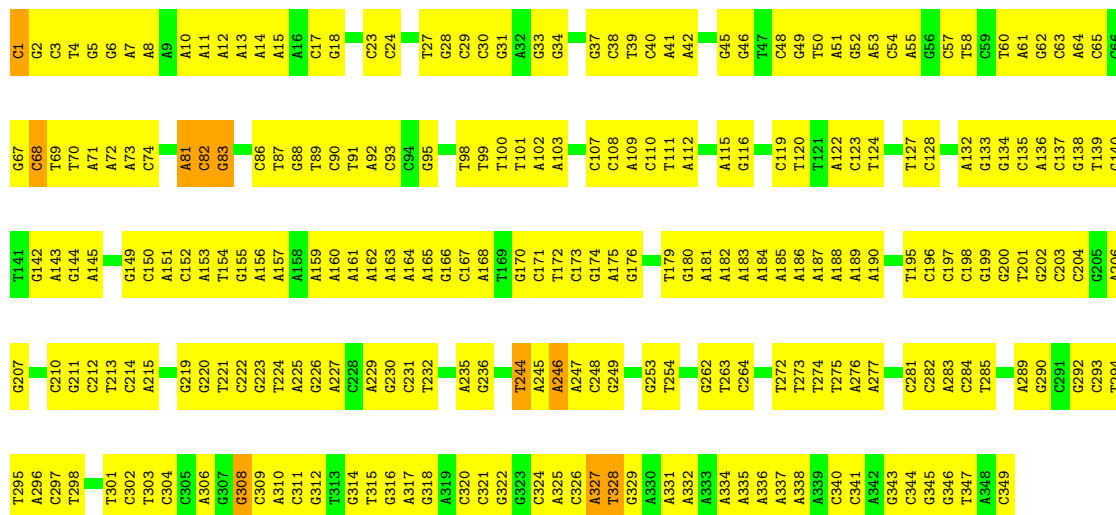
• Molecule 4: Histone H2B type 1-J





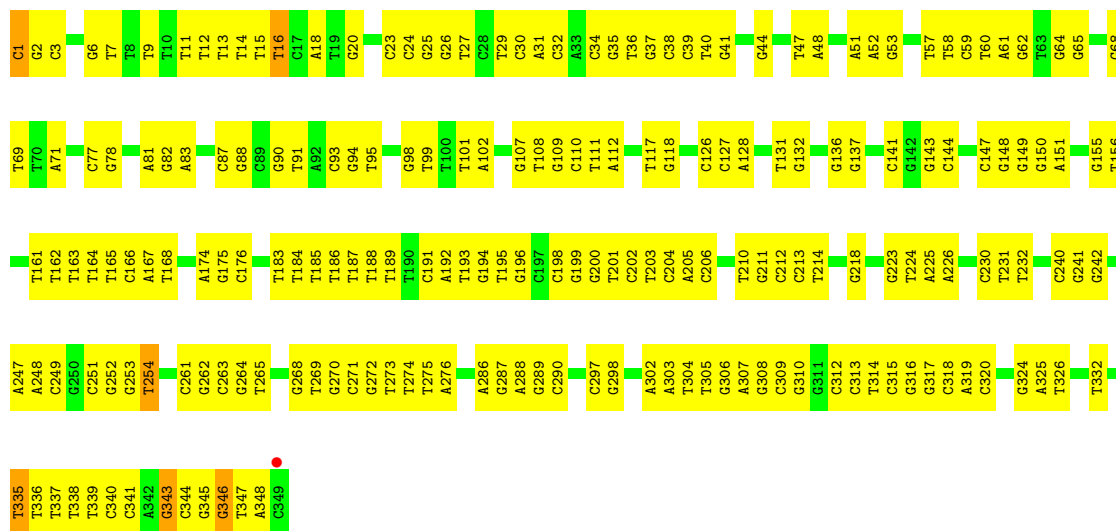
• Molecule 5: DNA (349-MER)

Chain I: 30% 67% .



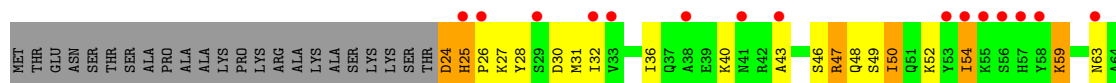
• Molecule 6: DNA (349-MER)

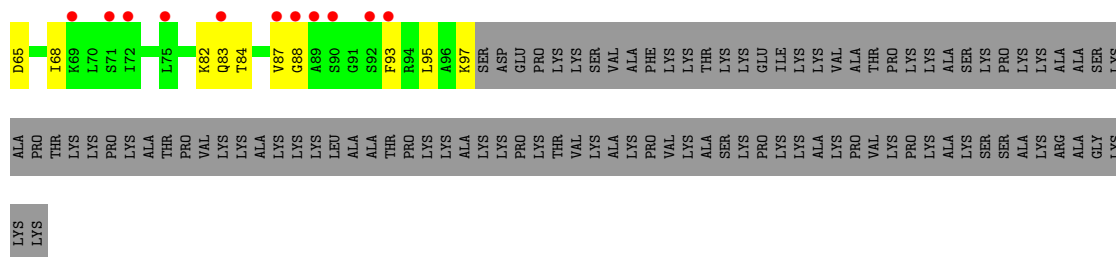
Chain J: 42% 56% .



• Molecule 7: Histone H1.0

Chain S: 13% 23% 12% 62% .





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	121.06Å 184.07Å 223.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.32 – 3.40 49.32 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.32-3.40) 99.8 (49.32-3.40)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.47 (at 3.40Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, $R_{free}$	0.206 , 0.265 0.212 , 0.268	Depositor DCC
$R_{free}$ test set	1381 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	126.8	Xtriage
Anisotropy	0.222	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.25 , 89.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.39$ , $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	27058	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	160.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.07% 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: K, CA

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	0.63	0/837	0.77	0/1120
1	E	0.62	0/828	0.77	0/1109
1	K	0.63	0/828	0.78	0/1109
1	O	0.63	0/819	0.77	0/1097
2	B	0.65	0/653	0.82	0/873
2	F	0.65	0/660	0.81	0/883
2	L	0.65	0/645	0.80	0/862
2	P	0.66	0/645	0.80	0/862
3	C	0.64	0/859	0.78	0/1157
3	G	0.64	0/820	0.78	0/1107
3	M	0.65	0/829	0.77	0/1118
3	Q	0.65	0/822	0.78	0/1110
4	D	0.65	0/766	0.76	0/1026
4	H	0.66	0/766	0.77	0/1026
4	N	0.66	0/766	0.76	0/1026
4	R	0.66	0/766	0.76	0/1026
5	I	0.57	10/8032 (0.1%)	0.85	5/12384 (0.0%)
6	J	0.54	3/8022 (0.0%)	0.85	4/12387 (0.0%)
7	S	0.72	0/574	0.85	0/765
All	All	0.60	13/28937 (0.0%)	0.82	9/42047 (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
3	C	0	1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	1	DC	OP3-P	-10.47	1.48	1.61
5	I	1	DC	OP3-P	-10.20	1.49	1.61
5	I	306	DA	O3'-P	-7.53	1.52	1.61
5	I	327	DA	O3'-P	-5.72	1.54	1.61
5	I	328	DT	O3'-P	-5.52	1.54	1.61

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	343	DG	C1'-O4'-C4'	-6.93	103.17	110.10
6	J	335	DT	C1'-O4'-C4'	-6.41	103.69	110.10
5	I	82	DC	C1'-O4'-C4'	-6.35	103.75	110.10
5	I	308	DG	C1'-O4'-C4'	-6.32	103.78	110.10
6	J	346	DG	N9-C1'-C2'	5.54	123.12	112.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	14	ALA	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	825	0	869	19	0
1	E	816	0	856	14	0
1	K	816	0	856	10	0
1	O	807	0	844	9	0
2	B	646	0	687	15	0
2	F	653	0	696	6	0
2	L	638	0	676	5	0
2	P	638	0	676	8	0
3	C	849	0	915	5	0
3	G	810	0	866	7	0
3	M	819	0	879	11	0
3	Q	812	0	868	4	0
4	D	755	0	784	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	755	0	784	15	0
4	N	755	0	784	13	0
4	R	755	0	784	15	0
5	I	7149	0	3902	245	1
6	J	7162	0	3943	242	1
7	S	568	0	597	22	1
8	G	1	0	0	0	0
8	I	11	0	0	0	0
8	J	10	0	0	0	0
8	M	1	0	0	0	0
9	I	2	0	0	0	0
9	J	5	0	0	0	0
All	All	27058	0	21266	598	2

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 13.

The worst 5 of 598 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)
6:J:318:DC:H2''	6:J:319:DA:C8	1.60	1.35
5:I:346:DG:H2''	5:I:347:DT:OP2	1.41	1.14
5:I:153:DA:H2''	5:I:154:DT:OP2	1.51	1.08
4:H:49:HIS:HB3	4:H:52:THR:CG2	1.85	1.05
6:J:35:DG:H2'	6:J:36:DT:H72	1.34	1.04

All (2) 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)
5:I:1:DC:O5'	5:I:349:DC:O3'[4_446]	1.84	0.36
6:J:112:DA:OP1	7:S:52:LYS:NZ[3_555]	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	98/136 (72%)	92 (94%)	6 (6%)	0	100	100
1	E	97/136 (71%)	92 (95%)	5 (5%)	0	100	100
1	K	97/136 (71%)	92 (95%)	5 (5%)	0	100	100
1	O	96/136 (71%)	90 (94%)	6 (6%)	0	100	100
2	B	79/103 (77%)	74 (94%)	5 (6%)	0	100	100
2	F	80/103 (78%)	76 (95%)	4 (5%)	0	100	100
2	L	78/103 (76%)	74 (95%)	4 (5%)	0	100	100
2	P	78/103 (76%)	73 (94%)	5 (6%)	0	100	100
3	C	108/130 (83%)	100 (93%)	8 (7%)	0	100	100
3	G	103/130 (79%)	94 (91%)	9 (9%)	0	100	100
3	M	104/130 (80%)	96 (92%)	8 (8%)	0	100	100
3	Q	103/130 (79%)	95 (92%)	8 (8%)	0	100	100
4	D	94/126 (75%)	82 (87%)	10 (11%)	2 (2%)	7	30
4	H	94/126 (75%)	81 (86%)	12 (13%)	1 (1%)	14	44
4	N	94/126 (75%)	84 (89%)	9 (10%)	1 (1%)	14	44
4	R	94/126 (75%)	82 (87%)	11 (12%)	1 (1%)	14	44
7	S	72/194 (37%)	62 (86%)	9 (12%)	1 (1%)	11	37
All	All	1569/2174 (72%)	1439 (92%)	124 (8%)	6 (0%)	34	67

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	104	GLY
4	H	104	GLY
4	N	104	GLY
4	R	104	GLY
4	D	33	ARG

### 5.3.2 Protein sidechains ⓘ

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	87/111 (78%)	84 (97%)	3 (3%)	37	65
1	E	86/111 (78%)	83 (96%)	3 (4%)	36	65
1	K	86/111 (78%)	83 (96%)	3 (4%)	36	65
1	O	85/111 (77%)	82 (96%)	3 (4%)	36	65
2	B	66/79 (84%)	65 (98%)	1 (2%)	65	82
2	F	67/79 (85%)	65 (97%)	2 (3%)	41	68
2	L	65/79 (82%)	64 (98%)	1 (2%)	65	82
2	P	65/79 (82%)	64 (98%)	1 (2%)	65	82
3	C	86/100 (86%)	81 (94%)	5 (6%)	20	50
3	G	83/100 (83%)	78 (94%)	5 (6%)	19	49
3	M	84/100 (84%)	78 (93%)	6 (7%)	14	44
3	Q	84/100 (84%)	79 (94%)	5 (6%)	19	49
4	D	82/105 (78%)	72 (88%)	10 (12%)	5	18
4	H	82/105 (78%)	71 (87%)	11 (13%)	4	15
4	N	82/105 (78%)	74 (90%)	8 (10%)	8	28
4	R	82/105 (78%)	73 (89%)	9 (11%)	6	23
7	S	61/158 (39%)	50 (82%)	11 (18%)	1	6
All	All	1333/1738 (77%)	1246 (94%)	87 (6%)	17	46

5 of 87 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	H	122	THR
3	M	81	ARG
7	S	50	ILE
1	K	63	ARG
3	M	24	GLN

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

Mol	Chain	Res	Type
3	M	24	GLN
4	N	49	HIS

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Mol	Chain	Res	Type
4	R	95	GLN
4	H	95	GLN
7	S	37	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 monosaccharides in this entry.

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

Of 30 ligands modelled in this entry, 30 are 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	100/136 (73%)	-0.25	0 100 100	94, 119, 167, 210	0
1	E	99/136 (72%)	0.11	1 (1%) 82 81	94, 123, 168, 190	0
1	K	99/136 (72%)	-0.02	0 100 100	91, 116, 160, 215	0
1	O	98/136 (72%)	0.10	4 (4%) 37 36	97, 131, 179, 216	0
2	B	81/103 (78%)	-0.26	0 100 100	90, 114, 143, 190	0
2	F	82/103 (79%)	0.07	0 100 100	91, 117, 153, 221	0
2	L	80/103 (77%)	0.00	0 100 100	87, 111, 148, 220	0
2	P	80/103 (77%)	0.07	0 100 100	100, 126, 155, 211	0
3	C	110/130 (84%)	0.12	3 (2%) 54 53	101, 129, 198, 251	0
3	G	105/130 (80%)	0.13	2 (1%) 66 65	96, 127, 183, 202	0
3	M	106/130 (81%)	0.02	0 100 100	95, 127, 173, 227	0
3	Q	105/130 (80%)	0.03	2 (1%) 66 65	90, 127, 177, 196	0
4	D	96/126 (76%)	-0.18	0 100 100	93, 129, 182, 225	0
4	H	96/126 (76%)	0.19	2 (2%) 63 62	98, 135, 185, 245	0
4	N	96/126 (76%)	0.23	1 (1%) 82 81	99, 130, 196, 241	0
4	R	96/126 (76%)	0.02	2 (2%) 63 62	96, 132, 190, 231	0
5	I	349/349 (100%)	-0.97	0 100 100	115, 177, 263, 321	0
6	J	349/349 (100%)	-0.96	1 (0%) 94 93	112, 179, 267, 315	0
7	S	74/194 (38%)	1.75	26 (35%) 0 0	155, 197, 234, 256	1 (1%)
All	All	2301/2872 (80%)	-0.22	44 (1%) 66 65	87, 139, 221, 321	1 (0%)

The worst 5 of 44 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	S	55	LYS	5.2

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Mol	Chain	Res	Type	RSRZ
4	N	125	LYS	5.0
4	R	125	LYS	4.5
7	S	93	PHE	4.5
7	S	58	TYR	4.4

## 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 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
9	K	J	415	1/1	0.51	0.09	156,156,156,156	0
8	CA	J	409	1/1	0.66	0.11	173,173,173,173	0
8	CA	I	411	1/1	0.67	0.12	153,153,153,153	0
8	CA	I	409	1/1	0.71	0.18	190,190,190,190	0
9	K	J	411	1/1	0.73	0.28	146,146,146,146	0
8	CA	J	405	1/1	0.74	0.19	145,145,145,145	0
8	CA	J	410	1/1	0.76	0.15	181,181,181,181	0
8	CA	I	407	1/1	0.84	0.17	145,145,145,145	0
8	CA	I	403	1/1	0.85	0.08	124,124,124,124	0
8	CA	I	405	1/1	0.86	0.10	174,174,174,174	0
8	CA	J	406	1/1	0.86	0.15	159,159,159,159	0
8	CA	I	402	1/1	0.87	0.14	126,126,126,126	0
9	K	I	413	1/1	0.87	0.18	130,130,130,130	0
8	CA	G	201	1/1	0.87	0.29	140,140,140,140	0
8	CA	I	408	1/1	0.87	0.14	191,191,191,191	0
9	K	I	412	1/1	0.87	0.18	153,153,153,153	0
8	CA	J	401	1/1	0.87	0.07	126,126,126,126	0
9	K	J	412	1/1	0.89	0.17	147,147,147,147	0
8	CA	J	407	1/1	0.89	0.06	150,150,150,150	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
8	CA	I	406	1/1	0.90	0.25	175,175,175,175	0
8	CA	I	401	1/1	0.90	0.17	148,148,148,148	0
8	CA	J	404	1/1	0.90	0.69	177,177,177,177	0
9	K	J	413	1/1	0.92	0.15	154,154,154,154	0
9	K	J	414	1/1	0.93	0.12	157,157,157,157	0
8	CA	J	408	1/1	0.94	0.10	160,160,160,160	0
8	CA	I	404	1/1	0.94	0.22	139,139,139,139	0
8	CA	M	201	1/1	0.94	0.25	155,155,155,155	0
8	CA	J	403	1/1	0.95	0.08	135,135,135,135	0
8	CA	J	402	1/1	0.96	0.07	137,137,137,137	0
8	CA	I	410	1/1	0.98	0.09	151,151,151,151	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.