



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 29, 2020 – 05:24 PM BST

PDB ID : 6K1K  
Title : Human nucleosome core particle with H2A.X S139E variant  
Authors : Sharma, D.; De Falco, L.; Davey, C.A.  
Deposited on : 2019-05-10  
Resolution : 2.20 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	:	2.13
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)	:	2.13

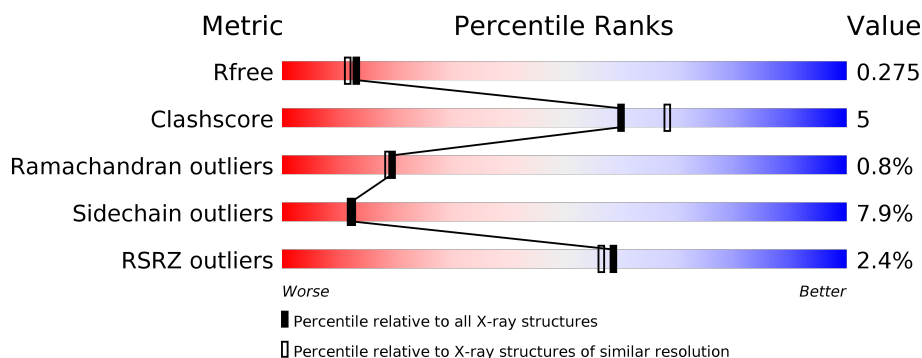
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	139	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>%</span> <span>67%</span> <span>29%</span> </div> </div>
1	E	139	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>2%</span> <span>61%</span> <span>7%</span> <span>30%</span> </div> </div>
2	B	106	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>%</span> <span>71%</span> <span>8%</span> <span>18%</span> </div> </div>
2	F	106	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>%</span> <span>67%</span> <span>9%</span> <span>24%</span> </div> </div>
3	C	146	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>5%</span> <span>64%</span> <span>10%</span> <span>24%</span> </div> </div>
3	G	146	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>6%</span> <span>62%</span> <span>16%</span> <span>22%</span> </div> </div>

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Mol	Chain	Length	Quality of chain
4	D	129	<div><div><div>%</div><div><div></div><div>60%</div><div>13%</div><div>•</div><div>26%</div></div></div></div>
4	H	129	<div><div><div>2%</div><div><div></div><div>64%</div><div>9%</div><div>•</div><div>25%</div></div></div></div>
5	I	145	<div><div><div></div><div><div></div><div>65%</div><div>34%</div><div>•</div></div></div></div>
6	J	145	<div><div><div></div><div><div></div><div>74%</div><div>25%</div><div>•</div></div></div></div>

## 2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 12240 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	98	Total	C	N	O	S	0	0	0
			807	508	156	139	4			
1	E	97	Total	C	N	O	S	0	0	0
			801	505	155	137	4			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP P68431
A	-2	SER	-	expression tag	UNP P68431
A	-1	HIS	-	expression tag	UNP P68431
E	-3	GLY	-	expression tag	UNP P68431
E	-2	SER	-	expression tag	UNP P68431
E	-1	HIS	-	expression tag	UNP P68431

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	87	Total	C	N	O	S	0	0	0
			703	442	142	118	1			
2	F	81	Total	C	N	O	S	0	0	0
			646	407	126	112	1			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP P62805
B	-2	SER	-	expression tag	UNP P62805
B	-1	HIS	-	expression tag	UNP P62805
F	-3	GLY	-	expression tag	UNP P62805
F	-2	SER	-	expression tag	UNP P62805
F	-1	HIS	-	expression tag	UNP P62805

- Molecule 3 is a protein called Histone H2AX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	111	Total	C	N	O	0	0	0
			844	533	163	148			
3	G	114	Total	C	N	O	0	0	0
			869	548	171	150			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	expression tag	UNP P16104
C	-2	SER	-	expression tag	UNP P16104
C	-1	HIS	-	expression tag	UNP P16104
C	139	GLU	SER	variant	UNP P16104
G	-3	GLY	-	expression tag	UNP P16104
G	-2	SER	-	expression tag	UNP P16104
G	-1	HIS	-	expression tag	UNP P16104
G	139	GLU	SER	variant	UNP P16104

- 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
			756	474	140	140	2			
4	H	97	Total	C	N	O	S	0	0	0
			766	480	142	142	2			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-6	GLY	-	expression tag	UNP P06899
D	-5	SER	-	expression tag	UNP P06899
D	-4	HIS	-	expression tag	UNP P06899
H	-6	GLY	-	expression tag	UNP P06899
H	-5	SER	-	expression tag	UNP P06899
H	-4	HIS	-	expression tag	UNP P06899

- Molecule 5 is a DNA chain called DNA (145-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	145	Total	C	N	O	P	0	0	0
			2970	1409	550	867	144			

- Molecule 6 is a DNA chain called DNA (145-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	J	145	Total	C	N	O	P	0	0	0
			2969	1409	547	869	144			

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	G	1	Total	Cl	0	0
			1	1		
7	C	1	Total	Cl	0	0
			1	1		

- Molecule 8 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	H	1	Total	Mn	0	0
			1	1		
8	J	16	Total	Mn	0	0
			16	16		
8	I	16	Total	Mn	0	0
			16	16		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	J	1	Total	K	0	0
			1	1		
9	I	1	Total	K	0	0
			1	1		

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	12	Total	O	0	0
			12	12		
10	B	10	Total	O	0	0
			10	10		
10	C	5	Total	O	0	0
			5	5		
10	D	3	Total	O	0	0
			3	3		

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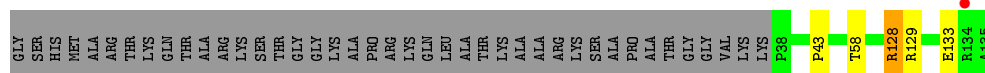
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	E	11	Total 11	O 11	0	0
10	F	7	Total 7	O 7	0	0
10	G	8	Total 8	O 8	0	0
10	H	7	Total 7	O 7	0	0
10	I	5	Total 5	O 5	0	0
10	J	4	Total 4	O 4	0	0

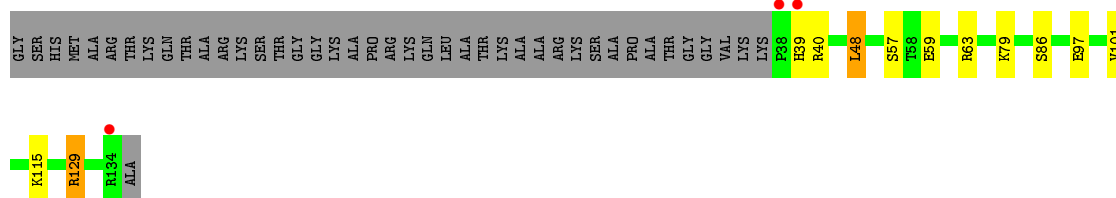
### 3 Residue-property plots [i](#)

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.

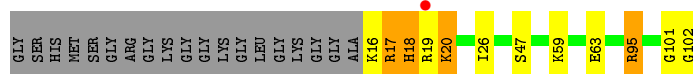
- Molecule 1: Histone H3.1



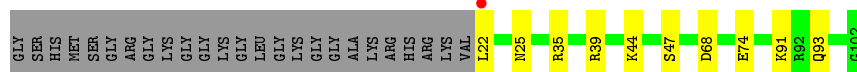
- Molecule 1: Histone H3.1



- Molecule 2: Histone H4



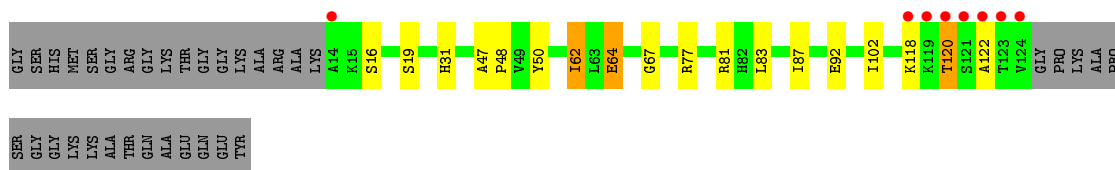
- Molecule 2: Histone H4



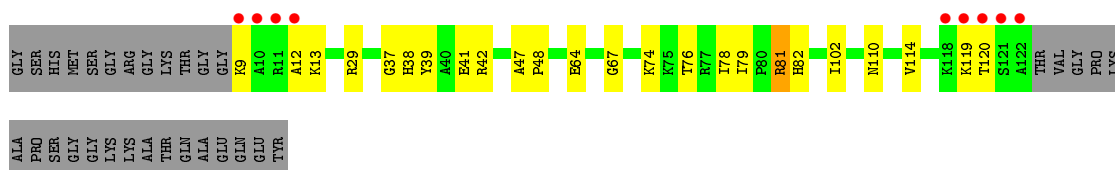
- Molecule 3: Histone H2AX



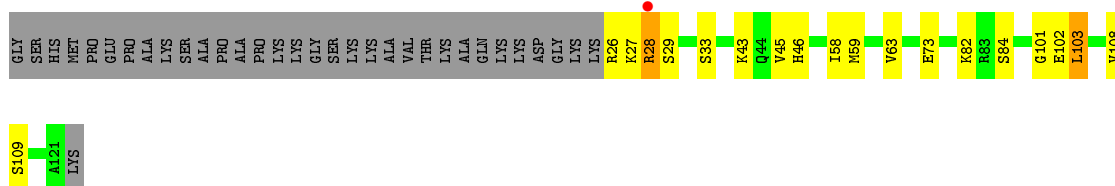




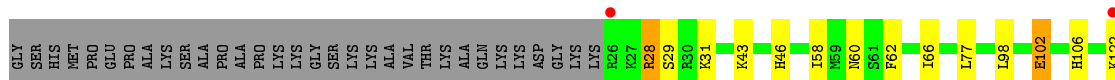
- Molecule 3: Histone H2AX



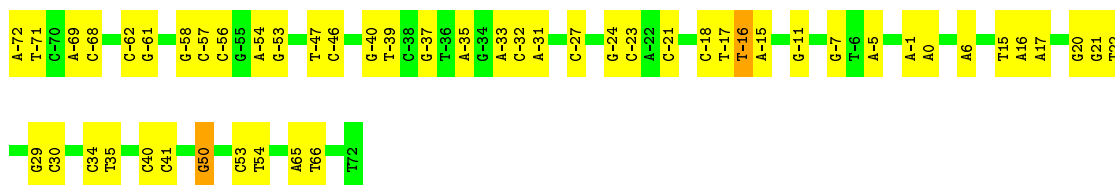
- Molecule 4: Histone H2B type 1-J



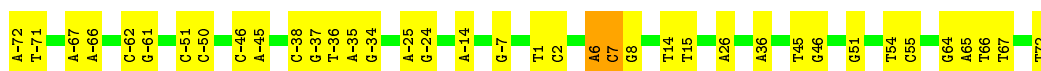
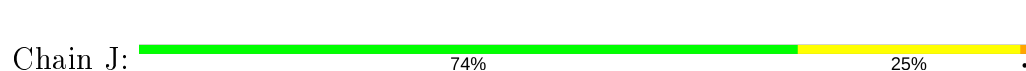
- Molecule 4: Histone H2B type 1-J



- Molecule 5: DNA (145-MER)



- Molecule 6: DNA (145-MER)



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.95Å 109.46Å 183.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	93.20 – 2.20 76.86 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.4 (93.20-2.20) 98.4 (76.86-2.20)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.39 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0232	Depositor
R, $R_{free}$	0.232 , 0.275 0.236 , 0.275	Depositor DCC
$R_{free}$ test set	2154 reflections (1.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	47.8	Xtriage
Anisotropy	0.026	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 35.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.014 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	12240	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% 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, MN, CL

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	0.77	0/819	1.00	2/1097 (0.2%)
1	E	0.69	0/813	0.89	1/1090 (0.1%)
2	B	0.75	0/711	0.94	0/948
2	F	0.70	0/653	0.90	0/873
3	C	0.73	1/855 (0.1%)	0.94	1/1155 (0.1%)
3	G	0.76	0/880	0.87	0/1185
4	D	0.74	0/767	0.86	0/1029
4	H	0.78	0/777	0.89	0/1040
5	I	0.47	1/3332 (0.0%)	0.86	4/5141 (0.1%)
6	J	0.46	2/3330 (0.1%)	0.90	5/5138 (0.1%)
All	All	0.62	4/12937 (0.0%)	0.90	13/18696 (0.1%)

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	G	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	26	DA	O3'-P	6.22	1.68	1.61
3	C	64	GLU	CD-OE2	5.33	1.31	1.25
5	I	-16	DT	O3'-P	-5.17	1.54	1.61
6	J	7	DC	O3'-P	-5.02	1.55	1.61

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	26	DA	P-O3'-C3'	10.89	132.76	119.70
6	J	26	DA	OP2-P-O3'	10.50	128.30	105.20
6	J	26	DA	OP1-P-O3'	-10.16	82.86	105.20
1	A	128	ARG	NE-CZ-NH2	-9.74	115.43	120.30
3	C	64	GLU	OE1-CD-OE2	8.49	133.49	123.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	G	12	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	807	0	844	4	0
1	E	801	0	839	6	0
2	B	703	0	755	5	0
2	F	646	0	687	5	0
3	C	844	0	901	11	0
3	G	869	0	934	9	0
4	D	756	0	784	8	0
4	H	766	0	797	9	0
5	I	2970	0	1628	38	0
6	J	2969	0	1629	25	0
7	C	1	0	0	0	0
7	G	1	0	0	0	0
8	H	1	0	0	0	0
8	I	16	0	0	0	0
8	J	16	0	0	0	0
9	I	1	0	0	0	0
9	J	1	0	0	0	0
10	A	12	0	0	0	0
10	B	10	0	0	1	0
10	C	5	0	0	0	0
10	D	3	0	0	0	0
10	E	11	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	F	7	0	0	0	0
10	G	8	0	0	1	0
10	H	7	0	0	2	0
10	I	5	0	0	1	0
10	J	4	0	0	0	0
All	All	12240	0	9798	98	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 5.

The worst 5 of 98 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)
5:I:-72:DA:C2'	5:I:-71:DT:H5'	2.18	0.73
5:I:-33:DA:H2''	5:I:-32:DC:O5'	1.88	0.72
4:H:102:GLU:CG	10:H:307:HOH:O	2.37	0.71
4:H:102:GLU:HG3	10:H:307:HOH:O	1.88	0.71
6:J:7:DC:H2''	6:J:8:DG:C8	2.27	0.69

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	96/139 (69%)	96 (100%)	0	0	100	100
1	E	95/139 (68%)	93 (98%)	2 (2%)	0	100	100
2	B	85/106 (80%)	82 (96%)	1 (1%)	2 (2%)	6	3
2	F	79/106 (74%)	77 (98%)	2 (2%)	0	100	100
3	C	109/146 (75%)	102 (94%)	5 (5%)	2 (2%)	8	5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	G	112/146 (77%)	107 (96%)	5 (4%)	0	100	100
4	D	94/129 (73%)	89 (95%)	4 (4%)	1 (1%)	14	12
4	H	95/129 (74%)	90 (95%)	4 (4%)	1 (1%)	14	12
All	All	765/1040 (74%)	736 (96%)	23 (3%)	6 (1%)	19	19

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	122	ALA
2	B	17	ARG
4	D	101	GLY
4	H	29	SER
2	B	18	HIS

### 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	85/113 (75%)	85 (100%)	0	100	100
1	E	85/113 (75%)	79 (93%)	6 (7%)	14	16
2	B	72/81 (89%)	67 (93%)	5 (7%)	15	16
2	F	66/81 (82%)	64 (97%)	2 (3%)	41	53
3	C	86/108 (80%)	80 (93%)	6 (7%)	15	16
3	G	87/108 (81%)	74 (85%)	13 (15%)	3	2
4	D	82/107 (77%)	71 (87%)	11 (13%)	4	3
4	H	83/107 (78%)	75 (90%)	8 (10%)	8	8
All	All	646/818 (79%)	595 (92%)	51 (8%)	12	12

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	40	ARG

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Mol	Chain	Res	Type
2	F	47	SER
4	H	98	LEU
1	E	86	SER
2	F	91	LYS

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

Mol	Chain	Res	Type
3	C	31	HIS
2	F	25	ASN
3	G	73	ASN
3	G	110	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 37 ligands modelled in this entry, 37 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	98/139 (70%)	0.01	1 (1%) 82 81	28, 39, 71, 120	0
1	E	97/139 (69%)	0.07	3 (3%) 49 47	35, 50, 86, 137	0
2	B	87/106 (82%)	0.08	1 (1%) 80 79	30, 39, 68, 148	0
2	F	81/106 (76%)	-0.12	1 (1%) 79 77	37, 47, 72, 138	0
3	C	111/146 (76%)	0.55	8 (7%) 15 14	38, 54, 134, 188	0
3	G	114/146 (78%)	0.55	9 (7%) 12 11	30, 45, 133, 164	0
4	D	96/129 (74%)	-0.02	1 (1%) 82 81	37, 53, 109, 142	0
4	H	97/129 (75%)	0.06	2 (2%) 63 61	32, 47, 91, 155	0
5	I	145/145 (100%)	-0.39	0 100 100	56, 91, 119, 131	0
6	J	145/145 (100%)	-0.37	0 100 100	50, 92, 126, 137	0
All	All	1071/1330 (80%)	0.02	26 (2%) 59 56	28, 54, 120, 188	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	120	THR	14.6
3	C	123	THR	13.8
3	G	121	SER	13.4
3	C	121	SER	13.1
3	C	122	ALA	11.3

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 6.4 Ligands ⓘ

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
8	MN	I	111	1/1	0.78	0.06	124,124,124,124	0
8	MN	I	110	1/1	0.79	0.08	115,115,115,115	0
8	MN	I	104	1/1	0.81	0.07	104,104,104,104	0
8	MN	J	115	1/1	0.81	0.07	102,102,102,102	0
8	MN	I	101	1/1	0.82	0.15	100,100,100,100	0
8	MN	J	103	1/1	0.82	0.15	119,119,119,119	0
8	MN	I	103	1/1	0.83	0.07	114,114,114,114	0
8	MN	I	107	1/1	0.83	0.05	109,109,109,109	0
8	MN	J	110	1/1	0.85	0.08	120,120,120,120	0
8	MN	I	114	1/1	0.85	0.05	122,122,122,122	0
8	MN	J	106	1/1	0.85	0.06	108,108,108,108	0
8	MN	J	116	1/1	0.86	0.06	115,115,115,115	0
8	MN	J	111	1/1	0.86	0.12	118,118,118,118	0
8	MN	I	116	1/1	0.87	0.07	120,120,120,120	0
8	MN	I	115	1/1	0.87	0.12	96,96,96,96	0
8	MN	J	107	1/1	0.88	0.05	100,100,100,100	0
8	MN	I	109	1/1	0.89	0.04	114,114,114,114	0
8	MN	I	102	1/1	0.89	0.16	89,89,89,89	0
8	MN	J	112	1/1	0.89	0.08	104,104,104,104	0
8	MN	I	113	1/1	0.89	0.09	116,116,116,116	0
8	MN	I	106	1/1	0.90	0.07	106,106,106,106	0
7	CL	G	201	1/1	0.94	0.06	54,54,54,54	0
9	K	J	117	1/1	0.94	0.08	81,81,81,81	0
8	MN	J	113	1/1	0.95	0.07	100,100,100,100	0
8	MN	J	105	1/1	0.96	0.20	85,85,85,85	0
8	MN	I	112	1/1	0.96	0.13	100,100,100,100	0
8	MN	J	102	1/1	0.96	0.16	95,95,95,95	0
7	CL	C	201	1/1	0.97	0.11	51,51,51,51	0
8	MN	J	108	1/1	0.97	0.20	80,80,80,80	0
9	K	I	117	1/1	0.97	0.10	71,71,71,71	0
8	MN	J	109	1/1	0.97	0.07	94,94,94,94	0
8	MN	J	114	1/1	0.98	0.09	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
8	MN	J	101	1/1	0.98	0.17	71,71,71,71	0
8	MN	J	104	1/1	0.99	0.08	103,103,103,103	0
8	MN	I	108	1/1	0.99	0.19	93,93,93,93	0
8	MN	I	105	1/1	0.99	0.21	80,80,80,80	0
8	MN	H	201	1/1	1.00	0.17	35,35,35,35	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.