



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 22, 2023 – 11:08 PM JST

PDB ID : 7XX5
Title : Crystal Structure of Nucleosome-H1.3 Linker Histone Assembly (sticky-169a DNA fragment)
Authors : Adhireksan, Z.; Qiuye, B.; Lee, P.L.; Sharma, D.; Padavattan, S.; Davey, C.A.
Deposited on : 2022-05-28
Resolution : 3.19 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

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>.

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 : 2.36
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) : 2.36

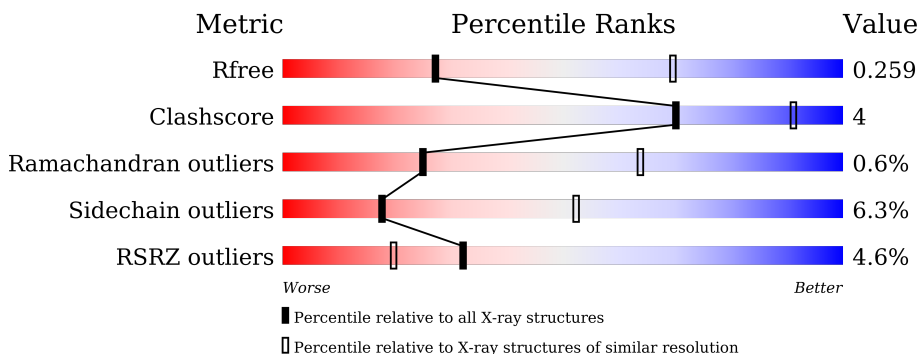
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.19 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	138	
1	E	138	
1	K	138	
1	O	138	
2	B	105	
2	F	105	

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Mol	Chain	Length	Quality of chain
2	L	105	<p>63% 13% 24%</p>
2	P	105	<p>70% 6% 24%</p>
3	C	132	<p>75% 5% 20%</p>
3	G	132	<p>67% 9% 22%</p>
3	M	132	<p>72% 7% 20%</p>
3	Q	132	<p>70% 8% 21%</p>
4	D	128	<p>67% 10% 22%</p>
4	H	128	<p>66% 10% 22%</p>
4	N	128	<p>70% 8% 22%</p>
4	R	128	<p>62% 15% 22%</p>
5	I	169	<p>85% 15%</p>
5	S	169	<p>72% 27%</p>
6	J	169	<p>88% 11%</p>
6	T	169	<p>80% 19%</p>
7	U	222	<p>19% 12% 65%</p>

2 Entry composition i

There are 8 unique types of molecules in this entry. The entry contains 26617 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
			Total	C	N	O	S			
1	A	99	816	514	158	140	4	0	0	0
1	E	99	816	514	158	140	4	0	0	0
1	K	99	816	514	158	140	4	0	0	0
1	O	100	825	520	160	141	4	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

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

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	80	638	401	125	111	1	0	0	0
2	F	80	638	401	125	111	1	0	0	0
2	L	80	638	401	125	111	1	0	0	0
2	P	80	638	401	125	111	1	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	105	810	511	158	141	0	0	0
3	G	103	796	502	155	139	0	0	0
3	M	105	810	511	158	141	0	0	0
3	Q	104	805	508	157	140	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	expression tag	UNP P04908
C	-1	SER	-	expression tag	UNP P04908
G	-2	GLY	-	expression tag	UNP P04908
G	-1	SER	-	expression tag	UNP P04908
M	-2	GLY	-	expression tag	UNP P04908
M	-1	SER	-	expression tag	UNP P04908
Q	-2	GLY	-	expression tag	UNP P04908
Q	-1	SER	-	expression tag	UNP P04908

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	100	788	494	147	145	2	0	0	0
4	H	100	788	494	147	145	2	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	N	100	Total	C	N	O	S	0	0	0
			788	494	147	145	2			
4	R	100	Total	C	N	O	S	0	0	0
			788	494	147	145	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	GLY	-	expression tag	UNP P06899
D	-1	SER	-	expression tag	UNP P06899
H	-2	GLY	-	expression tag	UNP P06899
H	-1	SER	-	expression tag	UNP P06899
N	-2	GLY	-	expression tag	UNP P06899
N	-1	SER	-	expression tag	UNP P06899
R	-2	GLY	-	expression tag	UNP P06899
R	-1	SER	-	expression tag	UNP P06899

- Molecule 5 is a DNA chain called DNA (169-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	169	Total	C	N	O	P	0	0	0
			3462	1646	637	1011	168			
5	S	169	Total	C	N	O	P	0	0	0
			3462	1646	637	1011	168			

- Molecule 6 is a DNA chain called DNA (169-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	J	169	Total	C	N	O	P	0	0	0
			3461	1646	634	1013	168			
6	T	169	Total	C	N	O	P	0	0	0
			3461	1646	634	1013	168			

- Molecule 7 is a protein called Histone H1.3.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace	
7	U	78	Total	C	N	O	0	0	0
			560	351	104	105			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	0	SER	-	expression tag	UNP P16402

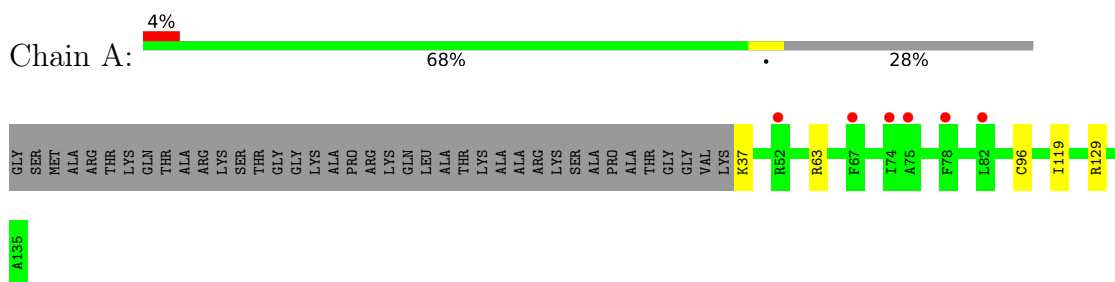
- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	G	1	Total Ca 1 1	0	0
8	I	3	Total Ca 3 3	0	0
8	J	1	Total Ca 1 1	0	0
8	Q	3	Total Ca 3 3	0	0
8	S	2	Total Ca 2 2	0	0
8	T	3	Total Ca 3 3	0	0

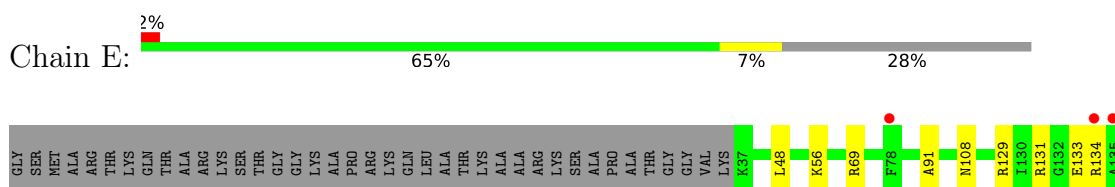
3 Residue-property plots [i](#)

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.

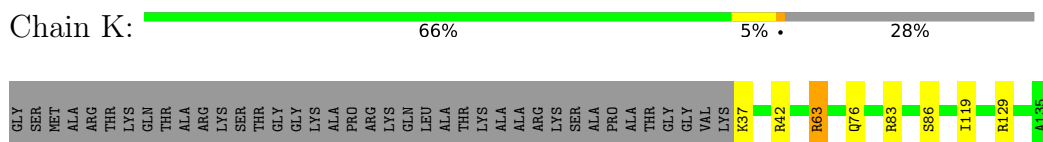
- Molecule 1: Histone H3.1



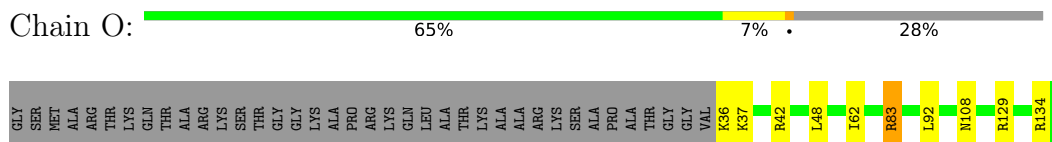
- Molecule 1: Histone H3.1



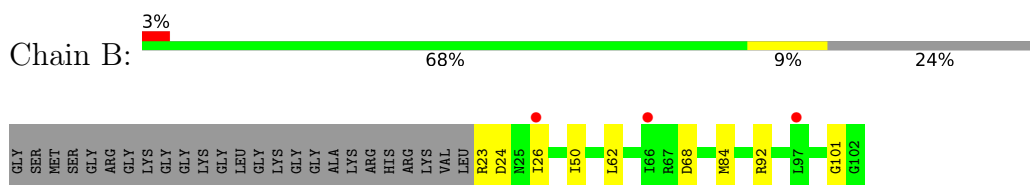
- Molecule 1: Histone H3.1



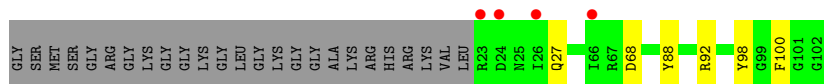
- Molecule 1: Histone H3.1



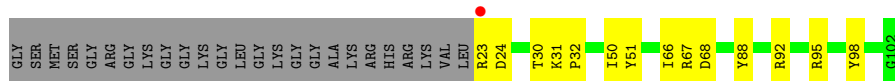
- Molecule 2: Histone H4



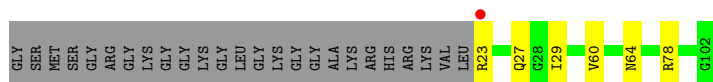
- Molecule 2: Histone H4



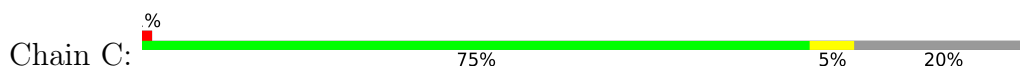
- Molecule 2: Histone H4



- Molecule 2: Histone H4



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



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



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



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

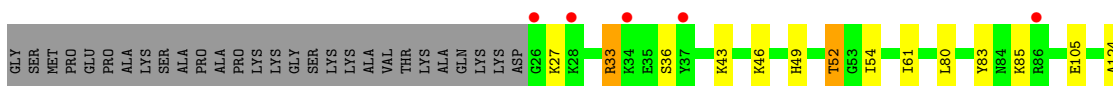




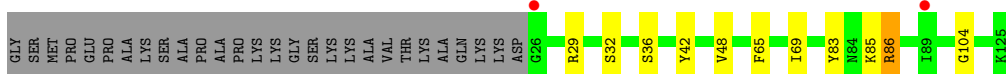
● Molecule 4: Histone H2B type 1-J



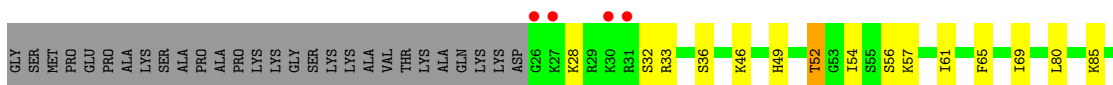
● Molecule 4: Histone H2B type 1-J



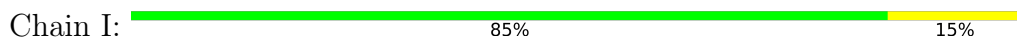
● Molecule 4: Histone H2B type 1-J



● Molecule 4: Histone H2B type 1-J

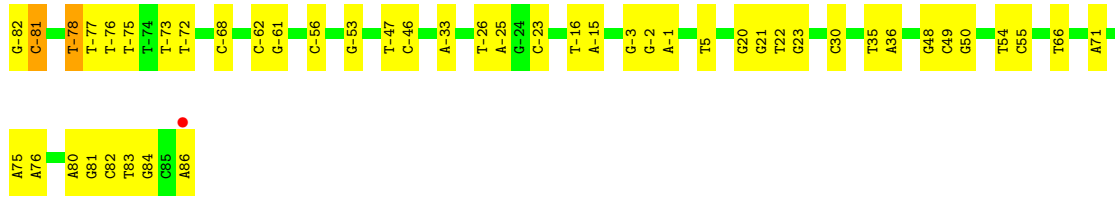


● Molecule 5: DNA (169-MER)

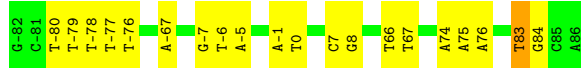
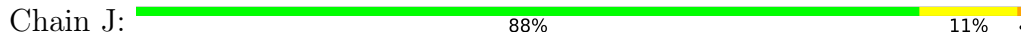


● Molecule 5: DNA (169-MER)

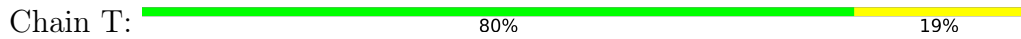




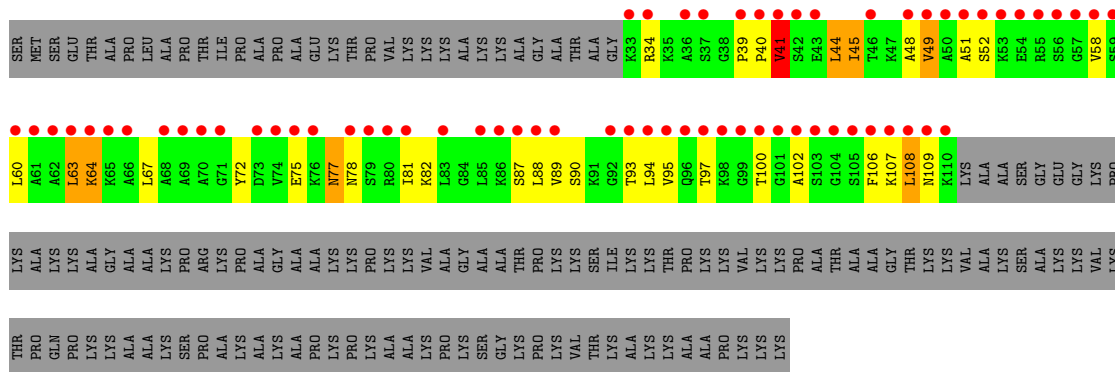
● Molecule 6: DNA (169-MER)



● Molecule 6: DNA (169-MER)



● Molecule 7: Histone H1.3



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.07Å 101.74Å 218.40Å 90.00° 103.52° 90.00°	Depositor
Resolution (Å)	46.57 – 3.19 46.57 – 3.19	Depositor EDS
% Data completeness (in resolution range)	98.4 (46.57-3.19) 98.4 (46.57-3.19)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.44 (at 3.19Å)	Xtrriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.203 , 0.259 0.205 , 0.259	Depositor DCC
R_{free} test set	3677 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	102.2	Xtrriage
Anisotropy	0.291	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 74.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtrriage
Estimated twinning fraction	0.059 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	26617	wwPDB-VP
Average B, all atoms (Å ²)	128.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.60% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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:
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	0.46	0/828	0.73	0/1109
1	E	0.45	0/828	0.76	0/1109
1	K	0.53	0/828	0.84	1/1109 (0.1%)
1	O	0.54	0/837	0.85	0/1120
2	B	0.46	0/645	0.79	0/862
2	F	0.45	0/645	0.81	0/862
2	L	0.50	0/645	0.81	0/862
2	P	0.58	0/645	0.90	1/862 (0.1%)
3	C	0.46	0/820	0.74	0/1107
3	G	0.41	0/806	0.68	1/1089 (0.1%)
3	M	0.49	0/820	0.84	2/1107 (0.2%)
3	Q	0.52	0/815	0.80	1/1100 (0.1%)
4	D	0.48	0/799	0.70	0/1067
4	H	0.44	0/799	0.70	0/1067
4	N	0.51	0/799	0.74	0/1067
4	R	0.52	0/799	0.77	0/1067
5	I	0.36	0/3884	0.82	0/5993
5	S	0.47	1/3884 (0.0%)	0.85	4/5993 (0.1%)
6	J	0.34	0/3882	0.84	2/5990 (0.0%)
6	T	0.46	0/3882	0.84	2/5990 (0.0%)
7	U	0.80	0/563	0.98	1/750 (0.1%)
All	All	0.46	1/28453 (0.0%)	0.82	15/41282 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	S	5	DT	O3'-P	-6.28	1.53	1.61

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	S	-78	DT	C1'-O4'-C4'	-6.20	103.90	110.10
3	M	81	ARG	NE-CZ-NH1	5.95	123.28	120.30
6	J	83	DT	C1'-O4'-C4'	-5.89	104.21	110.10
6	J	-67	DA	C1'-O4'-C4'	-5.72	104.38	110.10
5	S	-81	DC	C1'-O4'-C4'	-5.70	104.40	110.10

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	816	0	856	2	0
1	E	816	0	856	5	0
1	K	816	0	856	5	0
1	O	825	0	869	6	0
2	B	638	0	676	6	0
2	F	638	0	676	4	0
2	L	638	0	676	9	0
2	P	638	0	676	2	0
3	C	810	0	866	3	0
3	G	796	0	848	8	0
3	M	810	0	866	4	0
3	Q	805	0	861	4	0
4	D	788	0	826	5	0
4	H	788	0	826	7	0
4	N	788	0	826	5	0
4	R	788	0	826	6	0
5	I	3462	0	1901	21	0
5	S	3462	0	1901	37	0
6	J	3461	0	1902	12	0
6	T	3461	0	1902	21	0
7	U	560	0	619	36	0
8	G	1	0	0	0	0
8	I	3	0	0	0	0
8	J	1	0	0	0	0
8	Q	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	S	2	0	0	0	0
8	T	3	0	0	0	0
All	All	26617	0	21111	166	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 4.

The worst 5 of 166 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:S:-77:DT:H72	7:U:41:VAL:HG23	1.55	0.89
7:U:45:ILE:HD12	7:U:67:LEU:HD21	1.58	0.86
4:R:49:HIS:HB3	4:R:52:THR:HG23	1.59	0.84
1:K:76:GLN:OE1	2:L:23:ARG:NH1	2.14	0.79
5:S:-75:DT:H71	7:U:44:LEU:HD22	1.65	0.76

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	97/138 (70%)	94 (97%)	3 (3%)	0	100	100
1	E	97/138 (70%)	95 (98%)	2 (2%)	0	100	100
1	K	97/138 (70%)	96 (99%)	1 (1%)	0	100	100
1	O	98/138 (71%)	96 (98%)	2 (2%)	0	100	100
2	B	78/105 (74%)	76 (97%)	2 (3%)	0	100	100
2	F	78/105 (74%)	75 (96%)	3 (4%)	0	100	100
2	L	78/105 (74%)	73 (94%)	5 (6%)	0	100	100
2	P	78/105 (74%)	76 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	103/132 (78%)	97 (94%)	6 (6%)	0	100	100
3	G	101/132 (76%)	98 (97%)	3 (3%)	0	100	100
3	M	103/132 (78%)	97 (94%)	6 (6%)	0	100	100
3	Q	102/132 (77%)	97 (95%)	5 (5%)	0	100	100
4	D	98/128 (77%)	93 (95%)	3 (3%)	2 (2%)	7	38
4	H	98/128 (77%)	88 (90%)	8 (8%)	2 (2%)	7	38
4	N	98/128 (77%)	92 (94%)	5 (5%)	1 (1%)	15	54
4	R	98/128 (77%)	92 (94%)	3 (3%)	3 (3%)	4	26
7	U	76/222 (34%)	62 (82%)	12 (16%)	2 (3%)	5	31
All	All	1578/2234 (71%)	1497 (95%)	71 (4%)	10 (1%)	25	64

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	H	124	ALA
7	U	41	VAL
7	U	77	ASN
4	R	104	GLY
4	D	29	ARG

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	86/112 (77%)	83 (96%)	3 (4%)	36	69
1	E	86/112 (77%)	83 (96%)	3 (4%)	36	69
1	K	86/112 (77%)	82 (95%)	4 (5%)	26	62
1	O	87/112 (78%)	82 (94%)	5 (6%)	20	56
2	B	65/80 (81%)	64 (98%)	1 (2%)	65	85
2	F	65/80 (81%)	64 (98%)	1 (2%)	65	85
2	L	65/80 (81%)	63 (97%)	2 (3%)	40	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	P	65/80 (81%)	63 (97%)	2 (3%)	40	72
3	C	83/101 (82%)	81 (98%)	2 (2%)	49	77
3	G	82/101 (81%)	75 (92%)	7 (8%)	10	38
3	M	83/101 (82%)	80 (96%)	3 (4%)	35	69
3	Q	83/101 (82%)	76 (92%)	7 (8%)	11	39
4	D	85/106 (80%)	79 (93%)	6 (7%)	14	47
4	H	85/106 (80%)	77 (91%)	8 (9%)	8	33
4	N	85/106 (80%)	80 (94%)	5 (6%)	19	54
4	R	85/106 (80%)	76 (89%)	9 (11%)	6	27
7	U	59/159 (37%)	43 (73%)	16 (27%)	0	1
All	All	1335/1755 (76%)	1251 (94%)	84 (6%)	18	52

5 of 84 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	Q	81	ARG
7	U	49	VAL
4	R	28	LYS
4	R	57	LYS
7	U	72	TYR

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

Mol	Chain	Res	Type
3	Q	31	HIS
4	R	95	GLN
7	U	109	ASN
4	R	47	GLN
3	M	31	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 13 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 [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, 95th 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 ²)	Q < 0.9
1	A	99/138 (71%)	0.34	6 (6%) 21 12	99, 119, 148, 165	0
1	E	99/138 (71%)	0.35	3 (3%) 50 34	95, 112, 148, 161	0
1	K	99/138 (71%)	0.04	0 100 100	57, 80, 117, 136	0
1	O	100/138 (72%)	0.06	0 100 100	57, 73, 109, 141	0
2	B	80/105 (76%)	0.36	3 (3%) 40 26	101, 118, 139, 168	0
2	F	80/105 (76%)	0.26	4 (5%) 28 16	96, 110, 132, 154	0
2	L	80/105 (76%)	0.14	1 (1%) 77 65	61, 79, 106, 163	0
2	P	80/105 (76%)	0.21	1 (1%) 77 65	57, 73, 95, 133	0
3	C	105/132 (79%)	0.29	1 (0%) 82 72	98, 117, 148, 156	0
3	G	103/132 (78%)	0.39	6 (5%) 23 13	96, 120, 147, 162	0
3	M	105/132 (79%)	0.12	0 100 100	62, 78, 107, 133	0
3	Q	104/132 (78%)	0.09	0 100 100	64, 80, 114, 140	0
4	D	100/128 (78%)	0.50	3 (3%) 50 34	99, 120, 165, 179	0
4	H	100/128 (78%)	0.37	5 (5%) 28 16	101, 121, 171, 192	0
4	N	100/128 (78%)	0.29	2 (2%) 65 51	67, 83, 143, 171	0
4	R	100/128 (78%)	0.33	4 (4%) 38 25	67, 82, 157, 179	0
5	I	169/169 (100%)	-0.77	0 100 100	122, 163, 219, 253	0
5	S	169/169 (100%)	-0.60	1 (0%) 89 83	83, 125, 211, 260	0
6	J	169/169 (100%)	-0.74	0 100 100	122, 161, 209, 273	0
6	T	169/169 (100%)	-0.59	0 100 100	84, 124, 200, 250	0
7	U	78/222 (35%)	5.13	66 (84%) 0 0	151, 170, 223, 263	0
All	All	2288/2910 (78%)	0.15	106 (4%) 32 20	57, 114, 187, 273	0

The worst 5 of 106 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	U	103	SER	14.1
7	U	100	THR	12.9
7	U	62	ALA	12.9
7	U	59	SER	12.7
7	U	57	GLY	11.3

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 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, 95th 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 ²)	Q<0.9
8	CA	I	103	1/1	0.74	0.29	120,120,120,120	0
8	CA	T	102	1/1	0.74	0.26	126,126,126,126	0
8	CA	S	102	1/1	0.80	0.17	112,112,112,112	0
8	CA	Q	202	1/1	0.80	0.12	116,116,116,116	0
8	CA	G	201	1/1	0.82	0.29	129,129,129,129	0
8	CA	Q	201	1/1	0.90	0.19	96,96,96,96	0
8	CA	T	103	1/1	0.90	0.26	124,124,124,124	0
8	CA	J	101	1/1	0.91	0.30	119,119,119,119	0
8	CA	I	101	1/1	0.94	0.26	112,112,112,112	0
8	CA	I	102	1/1	0.95	0.15	113,113,113,113	0
8	CA	T	101	1/1	0.96	0.31	92,92,92,92	0
8	CA	Q	203	1/1	0.97	0.24	115,115,115,115	0
8	CA	S	101	1/1	0.97	0.13	107,107,107,107	0

6.5 Other polymers [i](#)

There are no such residues in this entry.