



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 12, 2021 – 06:10 PM JST

PDB ID : 6LAB
Title : 169 bp nucleosome, harboring cohesive DNA termini, assembled with linker histone H1.0
Authors : Adhireksan, Z.; Sharma, D.; Lee, P.L.; Bao, Q.; Padavattan, S.; Davey, C.A.
Deposited on : 2019-11-12
Resolution : 3.20 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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	:	2.23.1
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)	:	2.23.1

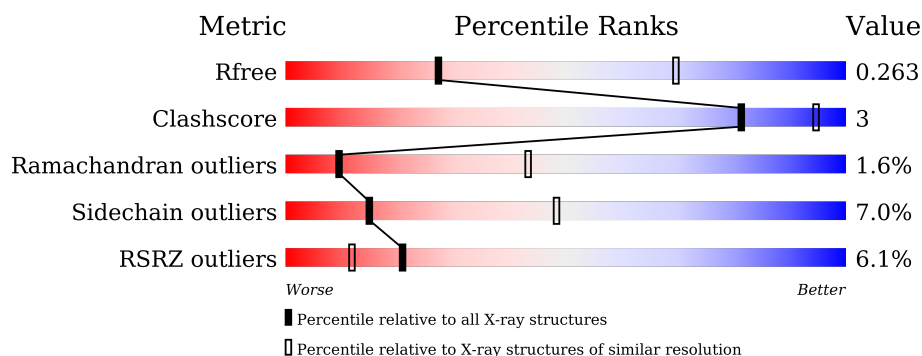
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	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	136	<div> <div></div> <div>63%9%28%</div> </div>
1	E	136	<div> <div></div> <div>63%8%28%</div> </div>
1	K	136	<div> <div></div> <div>63%10%28%</div> </div>
1	O	136	<div> <div></div> <div>65%7%28%</div> </div>
2	B	103	<div> <div></div> <div>72%6%22%</div> </div>
2	F	103	<div> <div>4%</div> <div>72%11%17%</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	169	
5	S	169	
6	J	169	
6	T	169	
7	U	194	
7	V	194	

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 27663 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	98	Total	C	N	O	S	0	0	0
			807	508	156	139	4			
1	K	98	Total	C	N	O	S	0	0	0
			807	508	156	139	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	80	Total	C	N	O	S	0	0	0
			638	401	125	111	1			
2	F	85	Total	C	N	O	S	0	0	0
			683	430	136	116	1			
2	L	83	Total	C	N	O	S	0	0	0
			662	418	129	114	1			
2	P	86	Total	C	N	O	S	0	0	0
			694	436	140	117	1			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	105	Total	C	N	O	0	0	0
			810	511	158	141			
3	G	103	Total	C	N	O	0	0	0
			796	502	155	139			
3	M	106	Total	C	N	O	0	0	0
			819	517	160	142			
3	Q	103	Total	C	N	O	0	0	0
			796	502	155	139			

- 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 (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 H1.0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	U	104	Total	C	N	O	S	0	0	0
			806	505	152	148	1			
7	V	109	Total	C	N	O	S	0	0	0
			841	528	158	154	1			

- Molecule 8 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	C	1	Total K 1 1	0	0
8	M	1	Total K 1 1	0	0

- Molecule 9 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	D	1	Total 1	Ca 1	0	0
9	I	6	Total 6	Ca 6	0	0
9	J	2	Total 2	Ca 2	0	0
9	N	1	Total 1	Ca 1	0	0
9	S	7	Total 7	Ca 7	0	0
9	T	3	Total 3	Ca 3	0	0

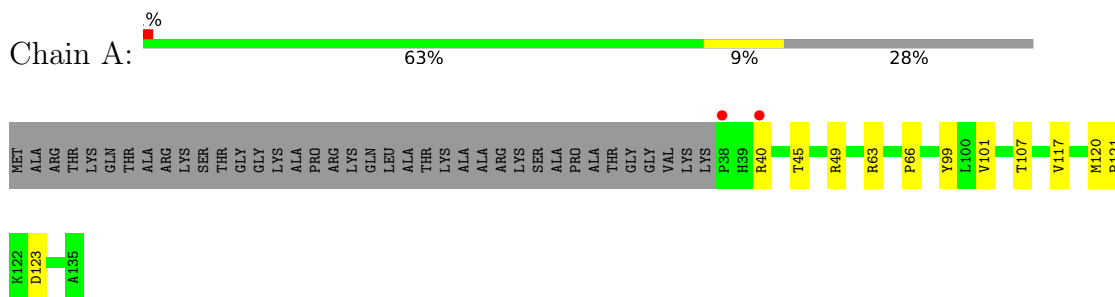
- Molecule 10 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	M	1	Total 1	Cl 1	0	0
10	Q	1	Total 1	Cl 1	0	0

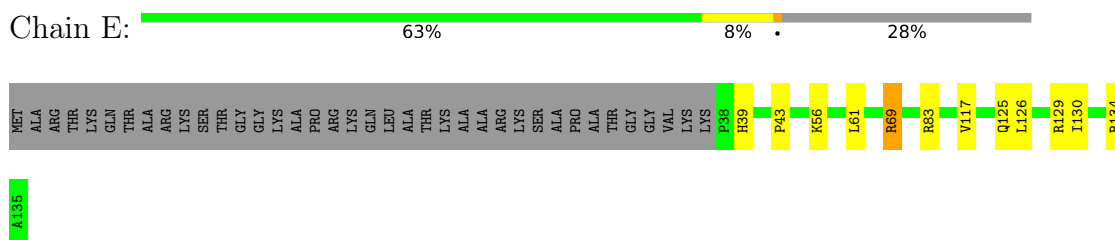
3 Residue-property plots [i](#)

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.

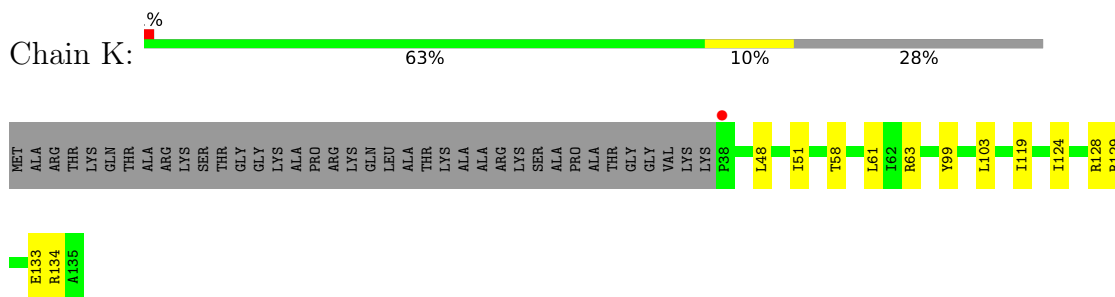
- Molecule 1: Histone H3.1



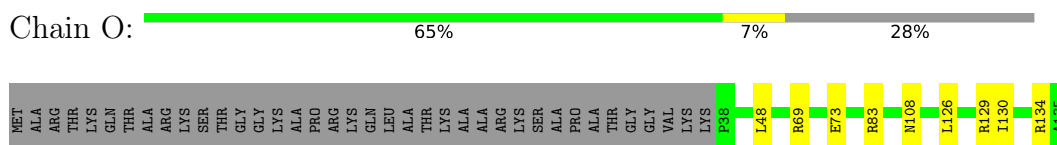
- Molecule 1: Histone H3.1



- Molecule 1: Histone H3.1

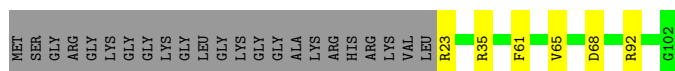


- Molecule 1: Histone H3.1



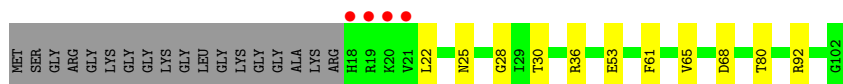
- Molecule 2: Histone H4

Chain B:  72% 6% 22%



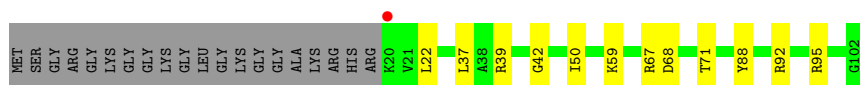
- Molecule 2: Histone H4

Chain F:  4% 72% 11% 17%



- Molecule 2: Histone H4

Chain L:  0% 69% 12% 19%



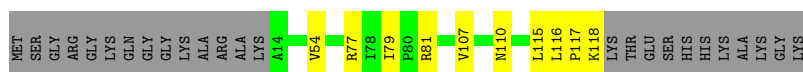
- Molecule 2: Histone H4

Chain P:  3% 71% 12% 17%



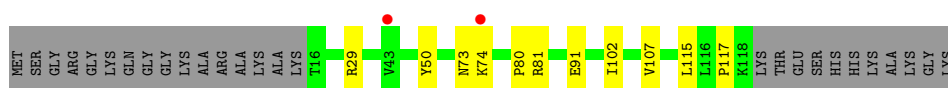
- Molecule 3: Histone H2A type 1-B/E

Chain C:  73% 8% 19%



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

Chain G:  2% 71% 8% 21%



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

Chain M:  68% 12% 18%



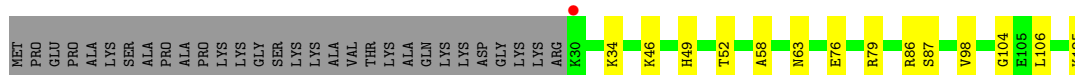
- Molecule 3: Histone H2A type 1-B/E

Chain Q:  70% 9% 21%



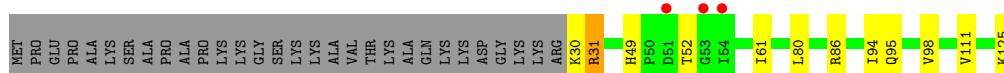
- Molecule 4: Histone H2B type 1-J

Chain D:  65% 11% 24%



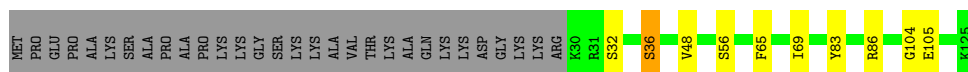
- Molecule 4: Histone H2B type 1-J

Chain H:  67% 9% 24%



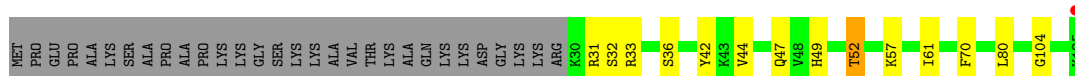
- Molecule 4: Histone H2B type 1-J

Chain N:  68% 7% 24%

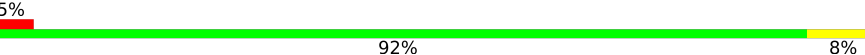


- Molecule 4: Histone H2B type 1-J

Chain R:  65% 10% 24%




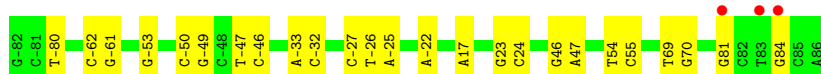
- Molecule 5: DNA (169-MER)

Chain I:  92% 5% 8%

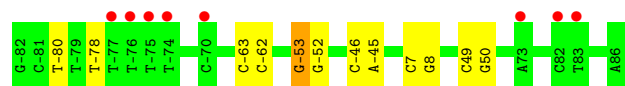
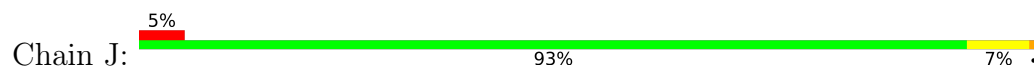


- Molecule 5: DNA (169-MER)

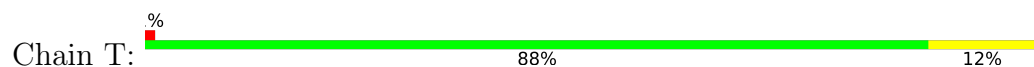
Chain S:  85% 2% 15%



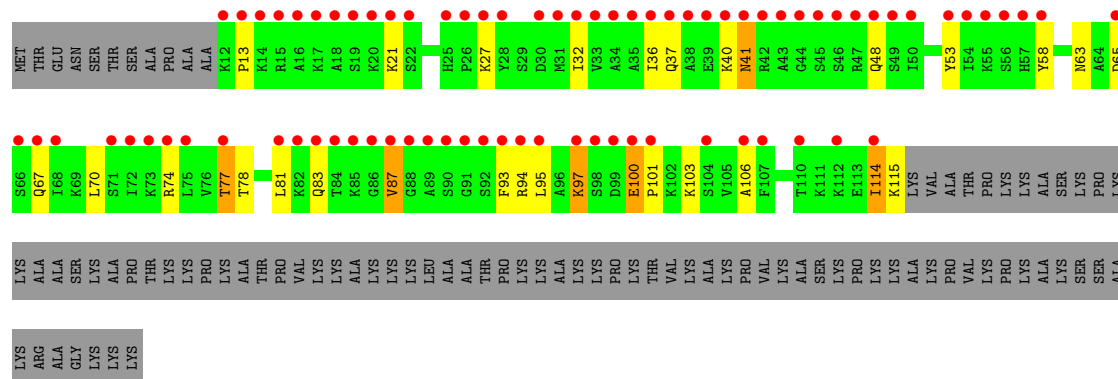
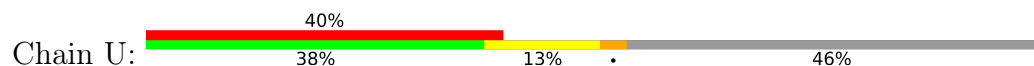
- Molecule 6: DNA (169-MER)



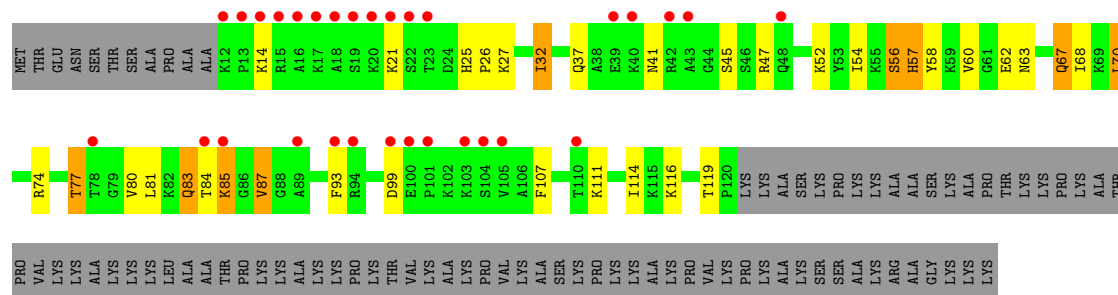
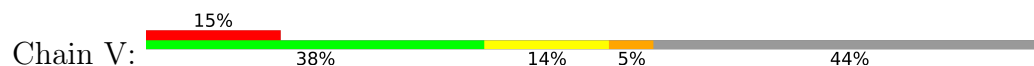
- Molecule 6: DNA (169-MER)



- Molecule 7: Histone H1.0



- Molecule 7: Histone H1.0



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	104.80Å 102.76Å 218.05Å 90.00° 97.40° 90.00°	Depositor
Resolution (Å)	216.23 – 3.20 39.86 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.2 (216.23-3.20) 99.3 (39.86-3.20)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.57 (at 3.18Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.209 , 0.263 0.214 , 0.263	Depositor DCC
R_{free} test set	1469 reflections (1.94%)	wwPDB-VP
Wilson B-factor (Å ²)	90.7	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 78.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	27663	wwPDB-VP
Average B, all atoms (Å ²)	126.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.93% 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: K, CL, 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	0.42	0/819	0.72	0/1097
1	E	0.44	0/819	0.77	1/1097 (0.1%)
1	K	0.53	0/819	0.81	0/1097
1	O	0.50	0/819	0.82	0/1097
2	B	0.44	0/645	0.79	0/862
2	F	0.46	0/691	0.79	0/923
2	L	0.50	0/669	0.87	0/894
2	P	0.56	0/702	0.84	0/937
3	C	0.42	0/820	0.67	0/1107
3	G	0.42	0/806	0.69	0/1089
3	M	0.46	0/829	0.79	1/1118 (0.1%)
3	Q	0.47	0/806	0.79	0/1089
4	D	0.42	0/766	0.62	0/1026
4	H	0.47	0/766	0.73	0/1026
4	N	0.53	0/766	0.74	0/1026
4	R	0.50	0/766	0.78	0/1026
5	I	0.31	0/3884	0.79	0/5993
5	S	0.40	1/3884 (0.0%)	0.82	1/5993 (0.0%)
6	J	0.32	0/3882	0.81	1/5990 (0.0%)
6	T	0.41	0/3882	0.82	2/5990 (0.0%)
7	U	0.60	0/815	0.77	0/1080
7	V	0.56	0/851	0.88	2/1130 (0.2%)
All	All	0.43	1/29506 (0.0%)	0.80	8/42687 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	S	84	DG	P-OP2	5.81	1.58	1.49

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	V	57	HIS	N-CA-C	9.10	135.58	111.00
3	M	81	ARG	NE-CZ-NH1	6.37	123.49	120.30
6	T	-53	DG	C1'-O4'-C4'	-5.71	104.39	110.10
6	J	-53	DG	C1'-O4'-C4'	-5.60	104.50	110.10
5	S	81	DG	C1'-O4'-C4'	-5.54	104.56	110.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	807	0	844	6	0
1	E	807	0	844	6	0
1	K	807	0	844	7	0
1	O	807	0	844	5	0
2	B	638	0	676	3	0
2	F	683	0	729	7	0
2	L	662	0	709	6	0
2	P	694	0	742	8	0
3	C	810	0	866	6	0
3	G	796	0	848	4	0
3	M	819	0	879	9	0
3	Q	796	0	848	3	0
4	D	755	0	784	4	0
4	H	755	0	784	7	0
4	N	755	0	784	5	0
4	R	755	0	784	7	0
5	I	3462	0	1901	8	0
5	S	3462	0	1901	14	0
6	J	3461	0	1902	7	0
6	T	3461	0	1902	12	0
7	U	806	0	874	10	0
7	V	841	0	915	12	0
8	C	1	0	0	0	0
8	M	1	0	0	0	0
9	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	I	6	0	0	0	0
9	J	2	0	0	0	0
9	N	1	0	0	0	0
9	S	7	0	0	0	0
9	T	3	0	0	0	0
10	M	1	0	0	0	0
10	Q	1	0	0	0	0
All	All	27663	0	22204	126	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 3.

The worst 5 of 126 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)
4:R:49:HIS:HB3	4:R:52:THR:CG2	2.14	0.77
7:V:74:ARG:HD2	7:V:81:LEU:HD13	1.70	0.74
1:E:83:ARG:HB3	2:F:80:THR:HG23	1.74	0.68
7:U:81:LEU:HD11	7:U:95:LEU:HD23	1.77	0.67
4:R:49:HIS:HB3	4:R:52:THR:HG23	1.77	0.65

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	96/136 (71%)	93 (97%)	3 (3%)	0	100	100
1	E	96/136 (71%)	90 (94%)	4 (4%)	2 (2%)	7	37
1	K	96/136 (71%)	92 (96%)	4 (4%)	0	100	100
1	O	96/136 (71%)	93 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	78/103 (76%)	71 (91%)	7 (9%)	0	100	100
2	F	83/103 (81%)	79 (95%)	4 (5%)	0	100	100
2	L	81/103 (79%)	69 (85%)	12 (15%)	0	100	100
2	P	84/103 (82%)	79 (94%)	4 (5%)	1 (1%)	13	49
3	C	103/130 (79%)	99 (96%)	4 (4%)	0	100	100
3	G	101/130 (78%)	95 (94%)	4 (4%)	2 (2%)	7	38
3	M	104/130 (80%)	94 (90%)	8 (8%)	2 (2%)	8	39
3	Q	101/130 (78%)	94 (93%)	7 (7%)	0	100	100
4	D	94/126 (75%)	88 (94%)	5 (5%)	1 (1%)	14	51
4	H	94/126 (75%)	90 (96%)	3 (3%)	1 (1%)	14	51
4	N	94/126 (75%)	91 (97%)	2 (2%)	1 (1%)	14	51
4	R	94/126 (75%)	86 (92%)	5 (5%)	3 (3%)	4	26
7	U	102/194 (53%)	76 (74%)	17 (17%)	9 (9%)	1	4
7	V	107/194 (55%)	81 (76%)	20 (19%)	6 (6%)	2	14
All	All	1704/2368 (72%)	1560 (92%)	116 (7%)	28 (2%)	9	43

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	G	91	GLU
7	U	13	PRO
7	U	78	THR
7	U	100	GLU
7	V	85	LYS

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	85/111 (77%)	82 (96%)	3 (4%)	36	69
1	E	85/111 (77%)	82 (96%)	3 (4%)	36	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	85/111 (77%)	81 (95%)	4 (5%)	26	62
1	O	85/111 (77%)	82 (96%)	3 (4%)	36	69
2	B	65/79 (82%)	63 (97%)	2 (3%)	40	72
2	F	70/79 (89%)	69 (99%)	1 (1%)	67	86
2	L	68/79 (86%)	65 (96%)	3 (4%)	28	64
2	P	71/79 (90%)	69 (97%)	2 (3%)	43	74
3	C	83/100 (83%)	81 (98%)	2 (2%)	49	77
3	G	82/100 (82%)	77 (94%)	5 (6%)	18	54
3	M	84/100 (84%)	81 (96%)	3 (4%)	35	69
3	Q	82/100 (82%)	75 (92%)	7 (8%)	10	38
4	D	82/105 (78%)	75 (92%)	7 (8%)	10	38
4	H	82/105 (78%)	77 (94%)	5 (6%)	18	54
4	N	82/105 (78%)	77 (94%)	5 (6%)	18	54
4	R	82/105 (78%)	76 (93%)	6 (7%)	14	46
7	U	88/158 (56%)	70 (80%)	18 (20%)	1	6
7	V	92/158 (58%)	70 (76%)	22 (24%)	0	3
All	All	1453/1896 (77%)	1352 (93%)	101 (7%)	15	48

5 of 101 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	R	42	TYR
7	U	83	GLN
7	V	107	PHE
4	R	57	LYS
7	U	53	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
4	N	95	GLN
2	P	64	ASN
2	P	27	GLN
4	R	47	GLN
4	D	84	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 24 ligands modelled in this entry, 24 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, 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	98/136 (72%)	0.13	2 (2%) 65 51	93, 112, 159, 178	0
1	E	98/136 (72%)	-0.02	0 100 100	82, 102, 137, 158	0
1	K	98/136 (72%)	-0.15	1 (1%) 82 72	45, 66, 105, 134	0
1	O	98/136 (72%)	-0.08	0 100 100	48, 67, 113, 139	0
2	B	80/103 (77%)	-0.02	0 100 100	83, 108, 142, 154	0
2	F	85/103 (82%)	0.20	4 (4%) 31 19	80, 96, 146, 193	0
2	L	83/103 (80%)	-0.04	1 (1%) 79 67	44, 66, 125, 158	0
2	P	86/103 (83%)	0.13	3 (3%) 44 28	47, 67, 133, 170	0
3	C	105/130 (80%)	-0.06	0 100 100	80, 100, 129, 145	0
3	G	103/130 (79%)	0.11	2 (1%) 66 53	81, 111, 144, 162	0
3	M	106/130 (81%)	-0.15	0 100 100	55, 72, 104, 133	0
3	Q	103/130 (79%)	-0.10	0 100 100	50, 70, 101, 112	0
4	D	96/126 (76%)	0.04	1 (1%) 82 72	77, 104, 149, 165	0
4	H	96/126 (76%)	0.04	3 (3%) 49 32	83, 110, 154, 177	0
4	N	96/126 (76%)	-0.06	0 100 100	49, 75, 120, 149	0
4	R	96/126 (76%)	-0.06	1 (1%) 82 72	51, 73, 120, 168	0
5	I	169/169 (100%)	0.06	8 (4%) 31 19	106, 166, 247, 276	0
5	S	169/169 (100%)	-0.35	3 (1%) 68 55	73, 114, 229, 261	0
6	J	169/169 (100%)	0.09	8 (4%) 31 19	120, 168, 236, 290	0
6	T	169/169 (100%)	-0.30	2 (1%) 79 67	75, 114, 208, 284	0
7	U	104/194 (53%)	3.70	78 (75%) 0 0	166, 198, 235, 249	1 (0%)
7	V	109/194 (56%)	1.34	30 (27%) 0 0	107, 166, 206, 217	1 (0%)
All	All	2416/3044 (79%)	0.18	147 (6%) 21 12	44, 105, 206, 290	2 (0%)

The worst 5 of 147 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	U	90	SER	12.3
7	U	94	ARG	10.0
7	V	16	ALA	9.1
7	U	68	ILE	9.0
7	U	19	SER	8.6

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
9	CA	I	103	1/1	0.43	0.18	121,121,121,121	0
9	CA	I	104	1/1	0.56	0.13	134,134,134,134	0
9	CA	S	104	1/1	0.60	0.20	118,118,118,118	0
9	CA	J	101	1/1	0.74	0.32	128,128,128,128	0
9	CA	T	101	1/1	0.75	0.25	106,106,106,106	0
9	CA	D	201	1/1	0.78	0.10	121,121,121,121	0
9	CA	S	102	1/1	0.80	0.23	76,76,76,76	0
9	CA	I	102	1/1	0.82	0.12	119,119,119,119	0
9	CA	S	105	1/1	0.82	0.18	105,105,105,105	0
9	CA	S	103	1/1	0.82	0.17	120,120,120,120	0
9	CA	I	105	1/1	0.83	0.14	128,128,128,128	0
9	CA	J	102	1/1	0.84	0.15	125,125,125,125	0
9	CA	S	101	1/1	0.88	0.24	84,84,84,84	0
10	CL	M	202	1/1	0.88	0.23	75,75,75,75	0
9	CA	T	103	1/1	0.90	0.10	111,111,111,111	0
9	CA	I	106	1/1	0.90	0.11	124,124,124,124	0
9	CA	T	102	1/1	0.93	0.25	114,114,114,114	0
9	CA	I	101	1/1	0.93	0.10	102,102,102,102	0
9	CA	N	201	1/1	0.93	0.18	114,114,114,114	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
9	CA	S	107	1/1	0.95	0.19	101,101,101,101	0
9	CA	S	106	1/1	0.97	0.25	102,102,102,102	0
8	K	M	201	1/1	0.97	0.41	102,102,102,102	0
8	K	C	201	1/1	0.97	0.56	114,114,114,114	0
10	CL	Q	201	1/1	0.99	0.11	70,70,70,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.