



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 26, 2026 – 03:01 PM EDT

PDB ID : 5OY7 / pdb_00005oy7
Title : Structure of the 4_601_157 tetranucleosome (P1 form)
Authors : Ekundayo, B.; Richmond, T.J.; Schalch, T.
Deposited on : 2017-09-07
Resolution : 5.77 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

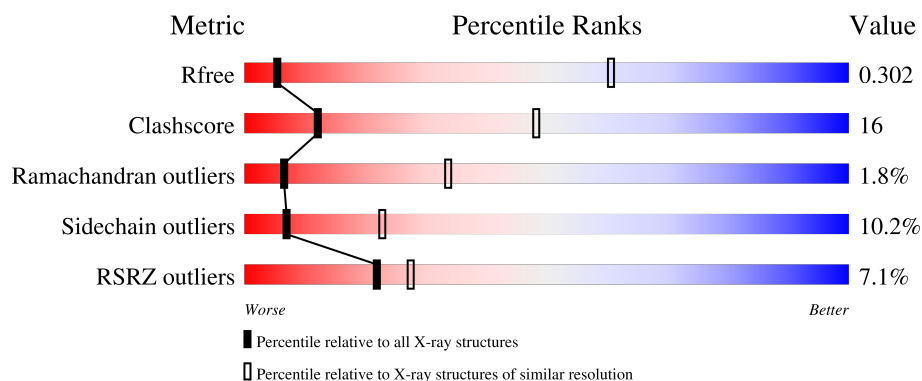
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.77 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1122 (7.56-4.00)
Clashscore	190562	1187 (7.56-4.00)
Ramachandran outliers	187476	1016 (7.54-4.00)
Sidechain outliers	187428	1007 (7.58-3.98)
RSRZ outliers	180081	1115 (7.56-4.00)

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	D	126	9% 45% 24% 6% 25%
1	H	126	7% 40% 29% • 26%
1	L	126	8% 44% 25% 6% 25%
1	P	126	6% 42% 27% • 26%
1	T	126	7% 44% 25% 6% 25%

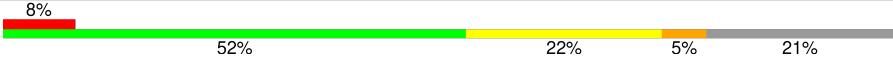
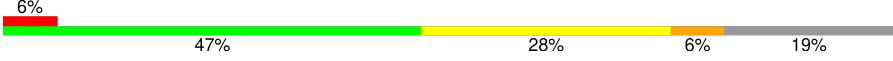
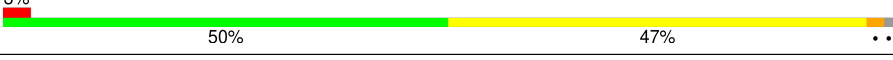
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Mol	Chain	Length	Quality of chain
1	X	126	
1	b	126	
1	f	126	
2	A	135	
2	E	135	
2	I	135	
2	M	135	
2	Q	135	
2	U	135	
2	Y	135	
2	c	135	
3	B	102	
3	F	102	
3	J	102	
3	N	102	
3	R	102	
3	V	102	
3	Z	102	
3	d	102	
4	C	130	
4	G	130	
4	K	130	
4	O	130	
4	S	130	
4	W	130	

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Mol	Chain	Length	Quality of chain
4	a	130	 8% 52% 22% 5% 21%
4	e	130	 6% 47% 28% 6% 19%
5	g	634	 3% 51% 44% . .
6	h	628	 3% 50% 47% . .

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 49215 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 H2B 1.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	95	Total	C	N	O	S	0	0	0
			745	469	134	140	2			
1	P	93	Total	C	N	O	S	0	0	0
			726	457	130	137	2			
1	D	95	Total	C	N	O	S	0	0	0
			745	469	134	140	2			
1	H	93	Total	C	N	O	S	0	0	0
			726	457	130	137	2			
1	T	95	Total	C	N	O	S	0	0	0
			745	469	134	140	2			
1	X	93	Total	C	N	O	S	0	0	0
			726	457	130	137	2			
1	b	95	Total	C	N	O	S	0	0	0
			745	469	134	140	2			
1	f	93	Total	C	N	O	S	0	0	0
			726	457	130	137	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	29	THR	SER	conflict	UNP P02281
P	29	THR	SER	conflict	UNP P02281
D	29	THR	SER	conflict	UNP P02281
H	29	THR	SER	conflict	UNP P02281
T	29	THR	SER	conflict	UNP P02281
X	29	THR	SER	conflict	UNP P02281
b	29	THR	SER	conflict	UNP P02281
f	29	THR	SER	conflict	UNP P02281

- Molecule 2 is a protein called Histone H3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	97	Total	C	N	O	S	0	0	0
			801	504	155	139	3			
2	Q	97	Total	C	N	O	S	0	0	0
			802	506	155	138	3			
2	I	97	Total	C	N	O	S	0	0	0
			802	506	155	138	3			
2	A	97	Total	C	N	O	S	0	0	0
			802	506	155	138	3			
2	E	97	Total	C	N	O	S	0	0	0
			801	504	155	139	3			
2	U	97	Total	C	N	O	S	0	0	0
			801	504	155	139	3			
2	Y	97	Total	C	N	O	S	0	0	0
			802	506	155	138	3			
2	c	97	Total	C	N	O	S	0	0	0
			801	504	155	139	3			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	102	ALA	GLY	conflict	UNP Q92133
M	111	ALA	GLY	conflict	UNP Q92133
Q	102	ALA	GLY	conflict	UNP Q92133
Q	111	ALA	GLY	conflict	UNP Q92133
I	102	ALA	GLY	conflict	UNP Q92133
I	111	ALA	GLY	conflict	UNP Q92133
A	102	ALA	GLY	conflict	UNP Q92133
A	111	ALA	GLY	conflict	UNP Q92133
E	102	ALA	GLY	conflict	UNP Q92133
E	111	ALA	GLY	conflict	UNP Q92133
U	102	ALA	GLY	conflict	UNP Q92133
U	111	ALA	GLY	conflict	UNP Q92133
Y	102	ALA	GLY	conflict	UNP Q92133
Y	111	ALA	GLY	conflict	UNP Q92133
c	102	ALA	GLY	conflict	UNP Q92133
c	111	ALA	GLY	conflict	UNP Q92133

- Molecule 3 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	N	78	Total	C	N	O	S	0	0	0
			619	391	120	107	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	R	82	Total	C	N	O	S	0	0	0
			654	412	128	113	1			
3	J	83	Total	C	N	O	S	0	0	0
			662	418	129	114	1			
3	B	83	Total	C	N	O	S	0	0	0
			662	418	129	114	1			
3	F	78	Total	C	N	O	S	0	0	0
			619	391	120	107	1			
3	V	78	Total	C	N	O	S	0	0	0
			619	391	120	107	1			
3	Z	83	Total	C	N	O	S	0	0	0
			662	418	129	114	1			
3	d	78	Total	C	N	O	S	0	0	0
			619	391	120	107	1			

- Molecule 4 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	O	105	Total	C	N	O	0	0	0
			809	510	158	141			
4	C	103	Total	C	N	O	0	0	0
			795	501	155	139			
4	G	105	Total	C	N	O	0	0	0
			809	510	158	141			
4	K	103	Total	C	N	O	0	0	0
			795	501	155	139			
4	S	103	Total	C	N	O	0	0	0
			795	501	155	139			
4	W	105	Total	C	N	O	0	0	0
			809	510	158	141			
4	a	103	Total	C	N	O	0	0	0
			795	501	155	139			
4	e	105	Total	C	N	O	0	0	0
			809	510	158	141			

- Molecule 5 is a DNA chain called DNA (619-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	g	619	Total	C	N	O	P	0	0	0
			12605	5987	2278	3721	619			

- Molecule 6 is a DNA chain called DNA (619-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	h	619	Total	C	N	O	P	0	0	0
			12774	6041	2407	3707	619			

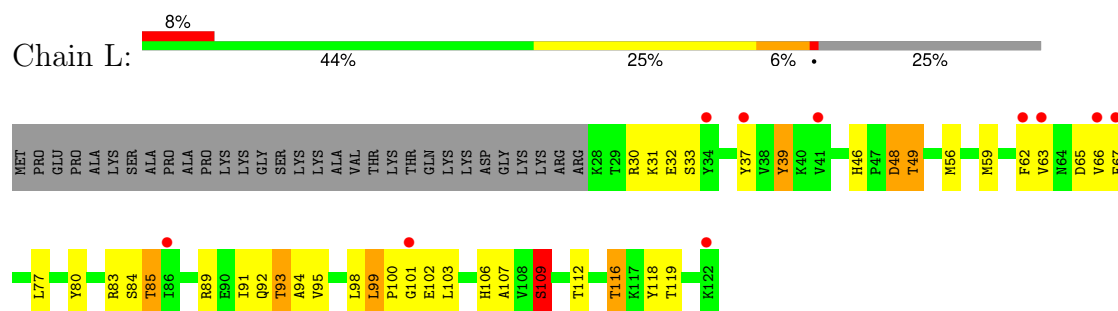
- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	O	1	Total	Cl	1	0
			1	1		
7	C	1	Total	Cl	1	0
			1	1		
7	G	1	Total	Cl	1	0
			1	1		
7	K	1	Total	Cl	1	0
			1	1		
7	S	1	Total	Cl	1	0
			1	1		
7	W	1	Total	Cl	1	0
			1	1		
7	a	1	Total	Cl	1	0
			1	1		
7	e	1	Total	Cl	1	0
			1	1		

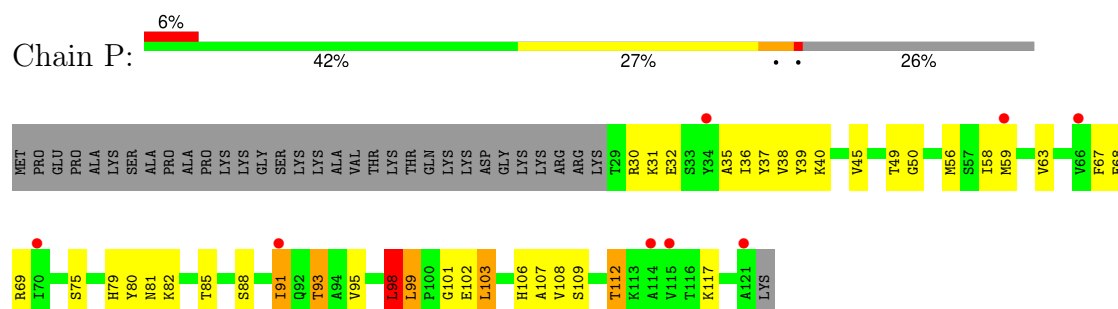
3 Residue-property plots [i](#)

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.

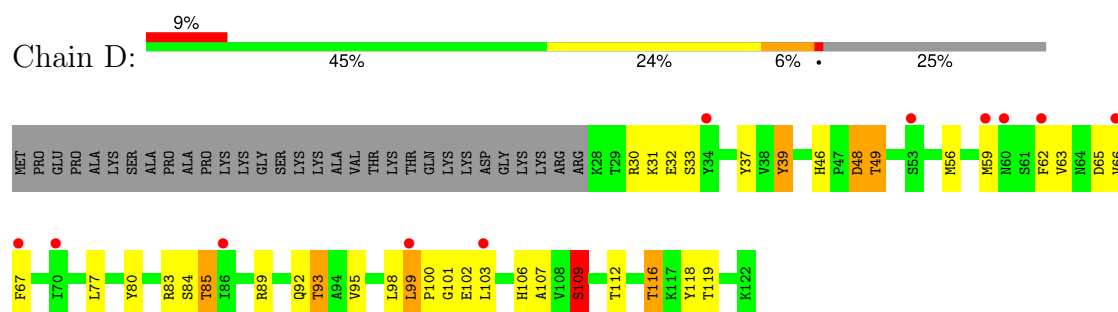
• Molecule 1: Histone H2B 1.1



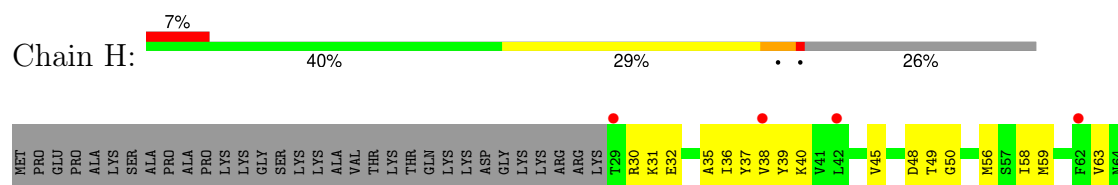
• Molecule 1: Histone H2B 1.1

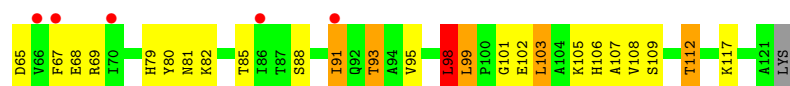


• Molecule 1: Histone H2B 1.1

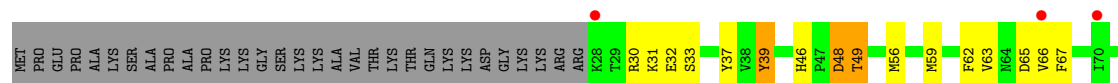
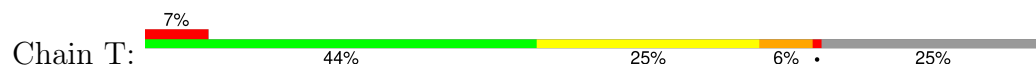


• Molecule 1: Histone H2B 1.1

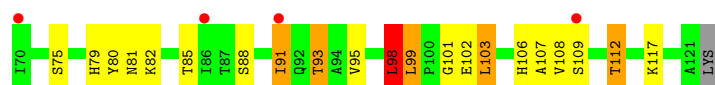
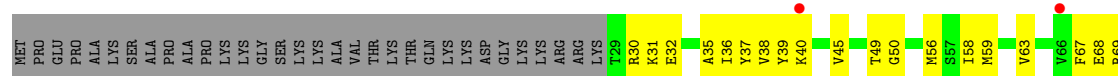
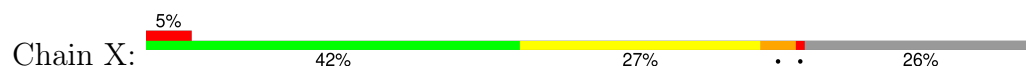




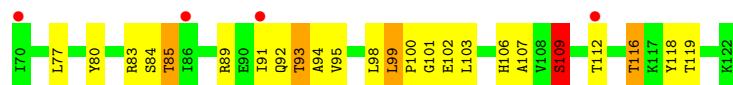
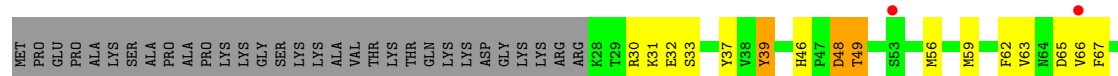
• Molecule 1: Histone H2B 1.1



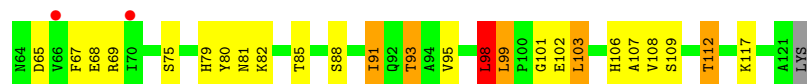
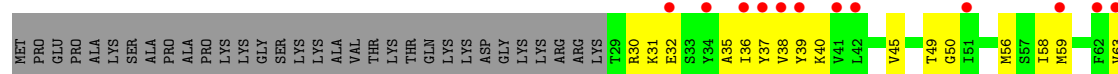
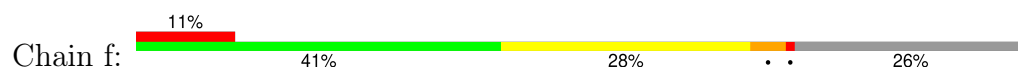
• Molecule 1: Histone H2B 1.1



• Molecule 1: Histone H2B 1.1

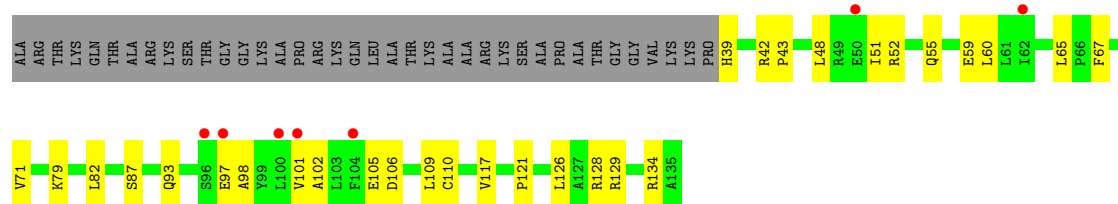


• Molecule 1: Histone H2B 1.1

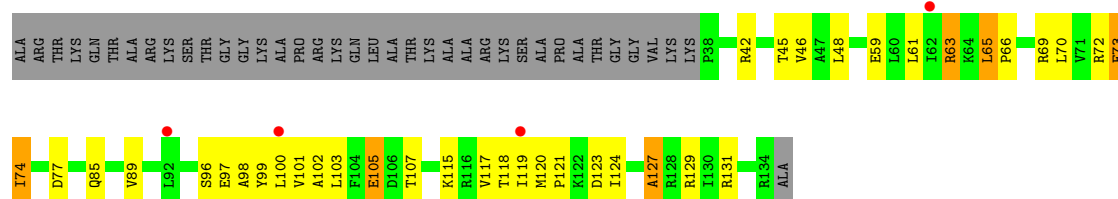
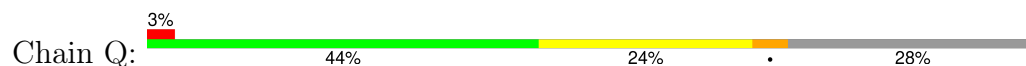


• Molecule 2: Histone H3

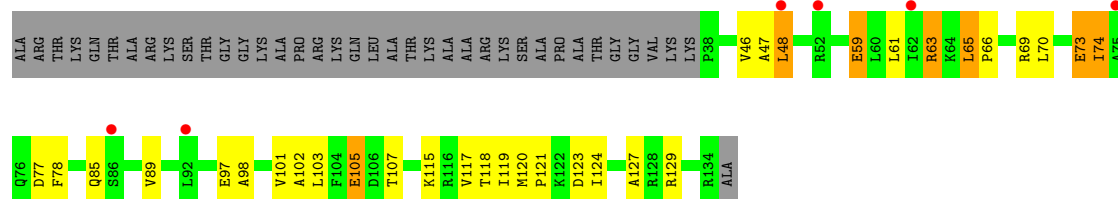




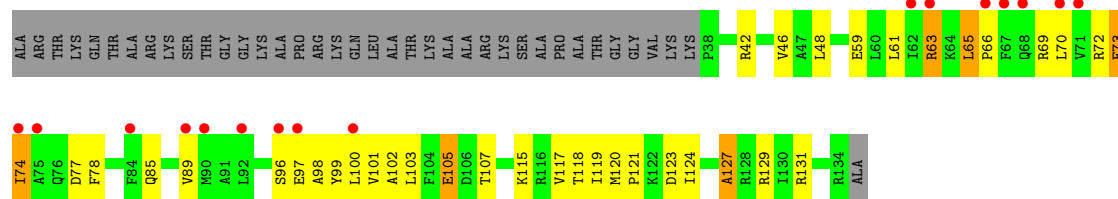
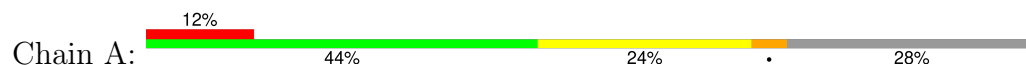
• Molecule 2: Histone H3



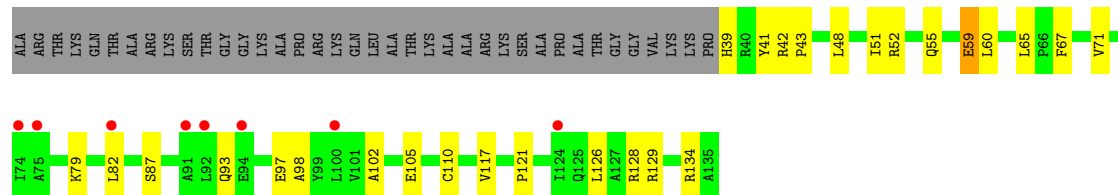
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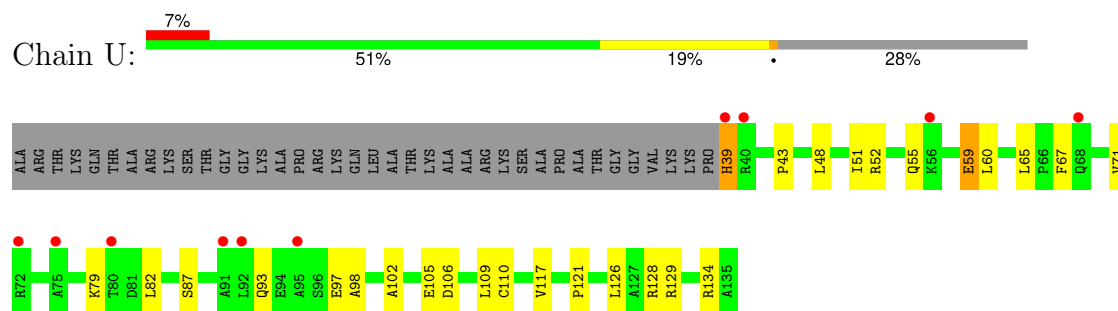
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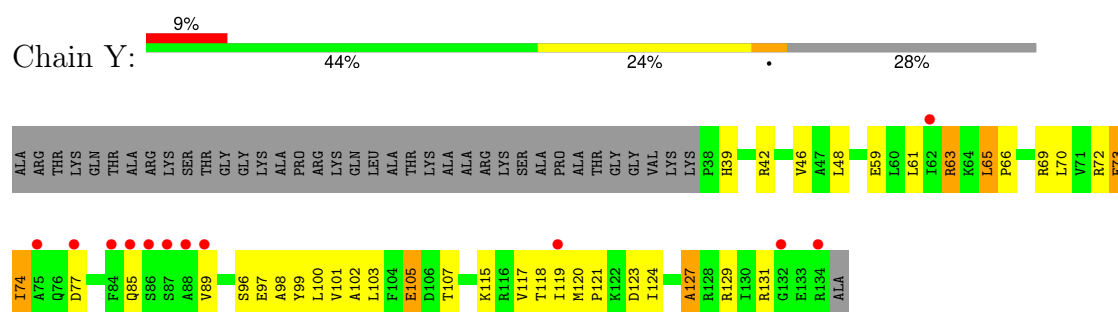
• Molecule 2: Histone H3



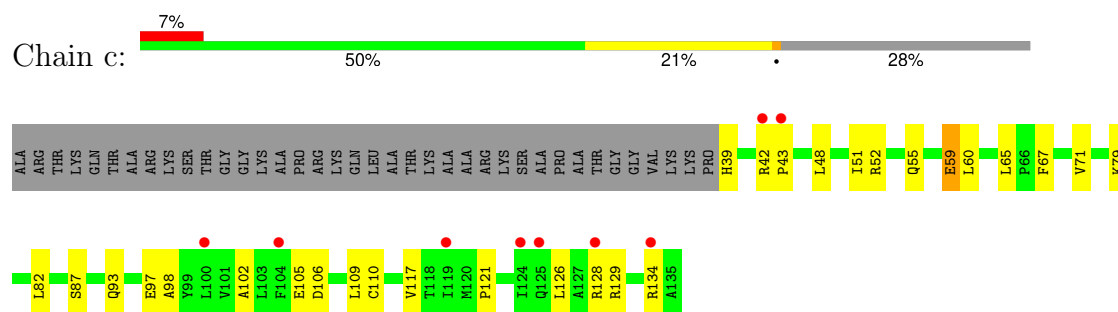
- Molecule 2: Histone H3



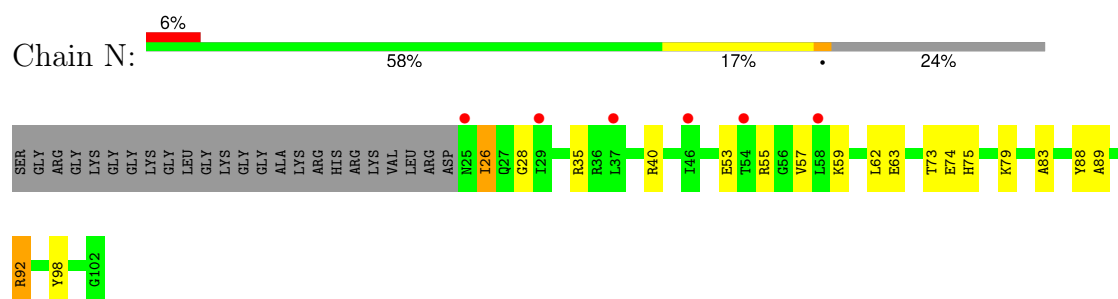
- Molecule 2: Histone H3



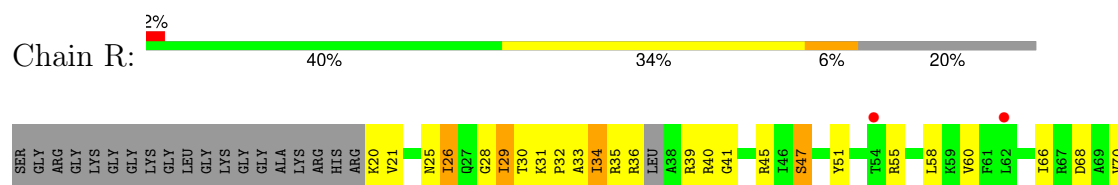
- Molecule 2: Histone H3



- Molecule 3: Histone H4

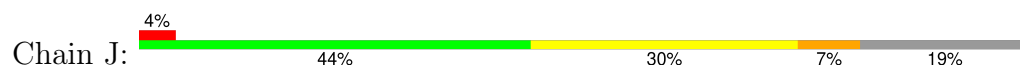


- Molecule 3: Histone H4





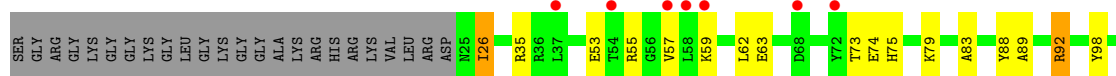
- Molecule 3: Histone H4



- Molecule 3: Histone H4



- Molecule 3: Histone H4

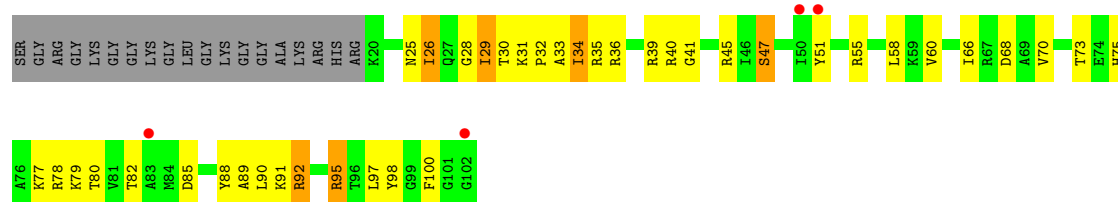


- Molecule 3: Histone H4



- Molecule 3: Histone H4

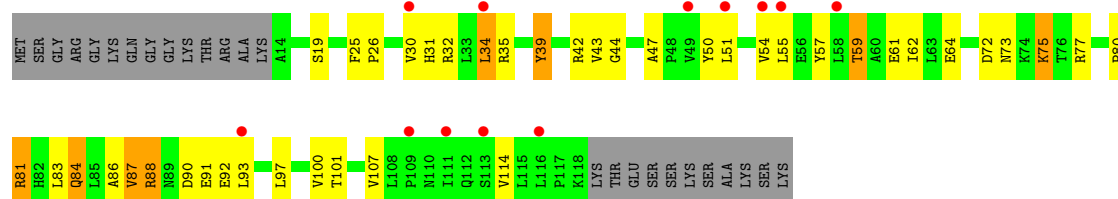




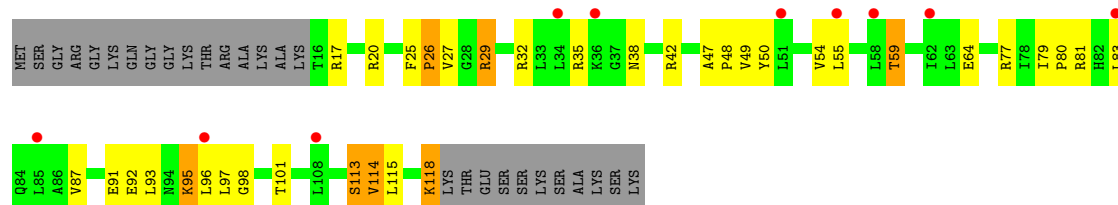
• Molecule 3: Histone H4



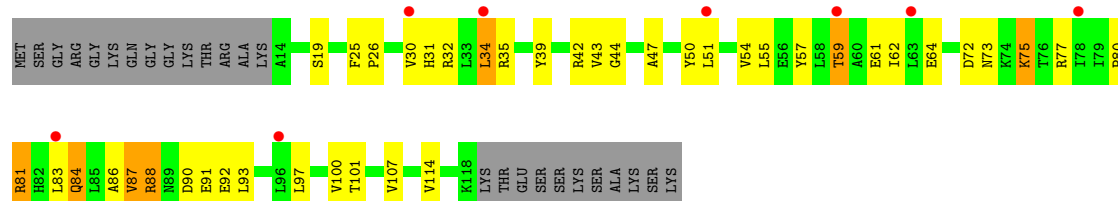
• Molecule 4: Histone H2A



• Molecule 4: Histone H2A



• Molecule 4: Histone H2A



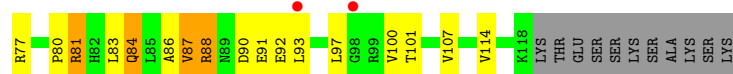
Chain K:



Chain S:



Chain W:



Chain a: 8% 52% 22% 5% 11%

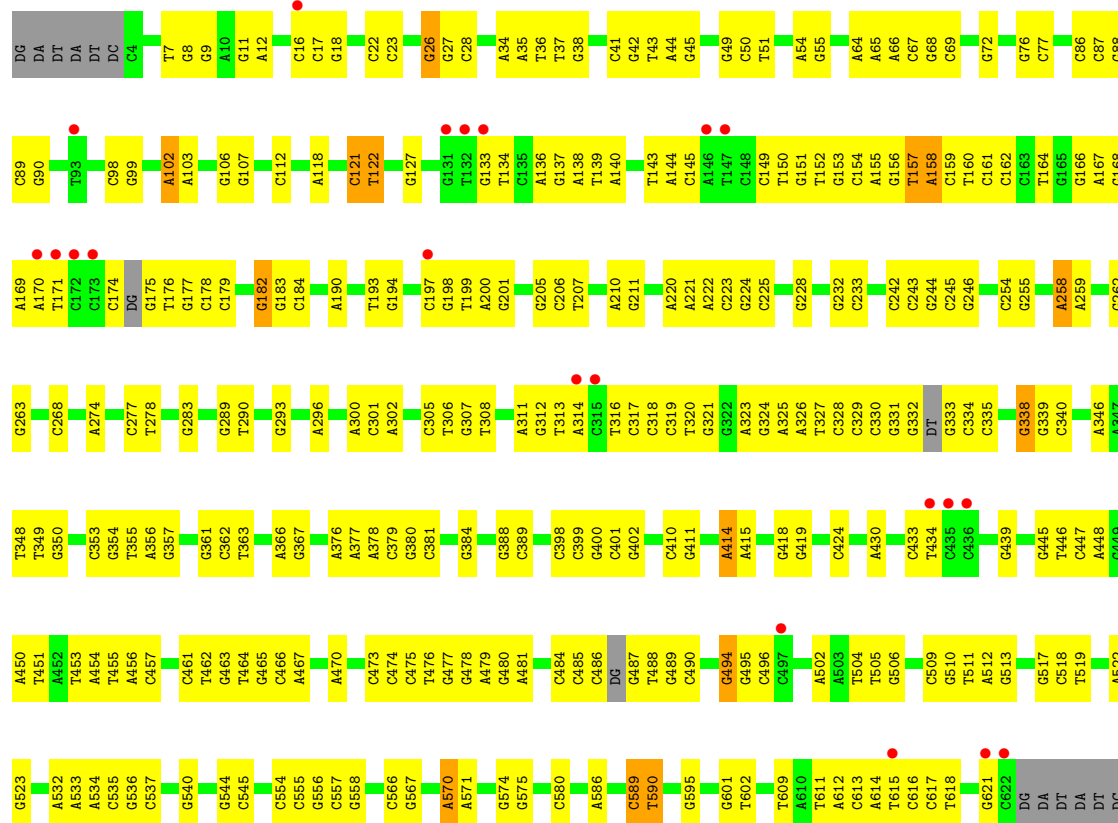


Chain e:

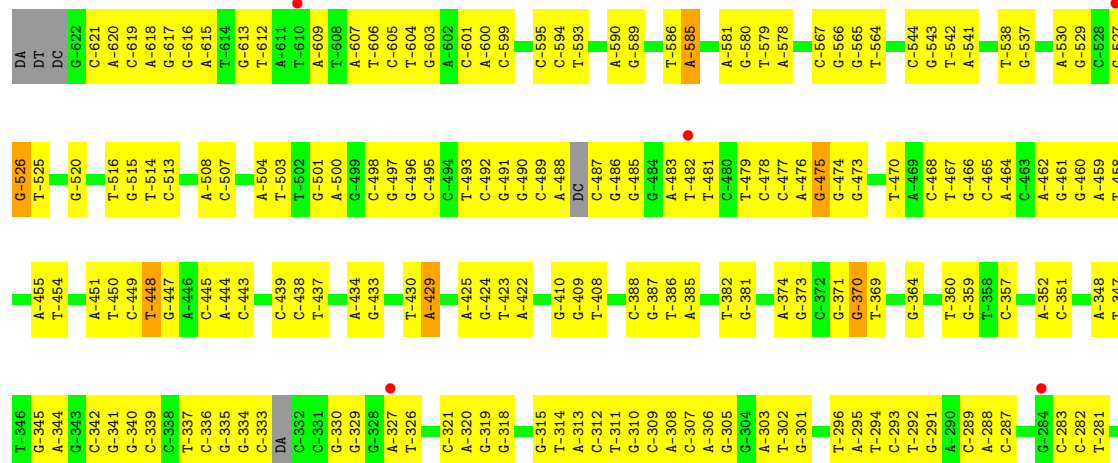




• Molecule 5: DNA (619-MER)



• Molecule 6: DNA (619-MER)





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	66.62Å 161.47Å 227.91Å 78.94° 83.86° 83.74°	Depositor
Resolution (Å)	111.41 – 5.77 111.41 – 5.77	Depositor EDS
% Data completeness (in resolution range)	93.8 (111.41-5.77) 93.8 (111.41-5.77)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 5.77Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.219 , 0.238 0.289 , 0.302	Depositor DCC
R_{free} test set	1226 reflections (4.73%)	wwPDB-VP
Wilson B-factor (Å ²)	222.9	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , 226.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	49215	wwPDB-VP
Average B, all atoms (Å ²)	246.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section:
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	D	0.60	0/756	1.00	2/1015 (0.2%)
1	H	0.77	0/737	1.10	1/993 (0.1%)
1	L	0.61	0/756	1.01	2/1015 (0.2%)
1	P	0.76	0/737	1.10	1/993 (0.1%)
1	T	0.60	0/756	1.00	2/1015 (0.2%)
1	X	0.77	0/737	1.10	1/993 (0.1%)
1	b	0.61	0/756	1.00	2/1015 (0.2%)
1	f	0.77	0/737	1.10	1/993 (0.1%)
2	A	0.84	1/814 (0.1%)	1.02	3/1092 (0.3%)
2	E	0.48	0/812	0.88	0/1088
2	I	0.83	1/814 (0.1%)	1.02	3/1092 (0.3%)
2	M	0.48	0/812	0.88	0/1088
2	Q	0.84	1/814 (0.1%)	1.02	3/1092 (0.3%)
2	U	0.49	0/812	0.88	0/1088
2	Y	0.83	1/814 (0.1%)	1.02	3/1092 (0.3%)
2	c	0.49	0/812	0.87	0/1088
3	B	0.82	0/669	1.12	2/894 (0.2%)
3	F	0.56	0/626	0.89	0/837
3	J	0.83	0/669	1.18	3/894 (0.3%)
3	N	0.56	0/626	0.89	0/837
3	R	0.80	0/660	1.12	2/880 (0.2%)
3	V	0.56	0/626	0.89	0/837
3	Z	0.81	0/669	1.12	2/894 (0.2%)
3	d	0.56	0/626	0.89	0/837
4	C	0.58	0/805	0.96	1/1088 (0.1%)
4	G	0.81	0/819	1.15	5/1106 (0.5%)
4	K	0.59	0/805	0.96	1/1088 (0.1%)
4	O	0.81	0/819	1.15	5/1106 (0.5%)
4	S	0.59	0/805	0.96	1/1088 (0.1%)
4	W	0.81	0/819	1.15	5/1106 (0.5%)
4	a	0.58	0/805	0.96	1/1088 (0.1%)
4	e	0.81	0/819	1.15	5/1106 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	g	0.34	0/14121	0.86	23/21771 (0.1%)
6	h	0.38	2/14351 (0.0%)	0.91	37/22170 (0.2%)
All	All	0.54	6/52615 (0.0%)	0.95	117/76379 (0.2%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	h	-448	DT	O3'-P	21.04	1.92	1.61
6	h	-475	DG	C1'-N9	-5.75	1.34	1.46
2	Q	127	ALA	CA-CB	-5.36	1.45	1.53
2	Y	127	ALA	CA-CB	-5.27	1.45	1.53
2	A	127	ALA	CA-CB	-5.26	1.45	1.53

The worst 5 of 117 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	h	-448	DT	P-O3'-C3'	23.23	155.04	120.20
6	h	-448	DT	O3'-P-O5'	15.28	126.92	104.00
6	h	-371	DG	O3'-P-O5'	-15.24	81.14	104.00
6	h	-215	DG	O3'-P-O5'	-15.17	81.25	104.00
6	h	-59	DG	O3'-P-O5'	-15.14	81.29	104.00

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	D	745	0	773	37	5
1	H	726	0	747	38	5
1	L	745	0	773	39	5
1	P	726	0	747	37	5
1	T	745	0	773	37	5
1	X	726	0	747	37	5
1	b	745	0	773	38	4
1	f	726	0	747	39	4

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	802	0	841	23	0
2	E	801	0	838	18	0
2	I	802	0	841	26	0
2	M	801	0	838	16	0
2	Q	802	0	841	23	0
2	U	801	0	838	17	0
2	Y	802	0	841	23	0
2	c	801	0	838	17	0
3	B	662	0	709	39	1
3	F	619	0	659	17	0
3	J	662	0	709	46	0
3	N	619	0	659	19	0
3	R	654	0	697	43	0
3	V	619	0	659	17	0
3	Z	662	0	709	39	0
3	d	619	0	659	18	0
4	C	795	0	846	27	0
4	G	809	0	864	42	0
4	K	795	0	846	25	0
4	O	809	0	864	44	0
4	S	795	0	846	25	0
4	W	809	0	864	44	0
4	a	795	0	846	25	0
4	e	809	0	864	45	0
5	g	12605	0	6944	402	0
6	h	12774	0	6940	402	1
7	C	1	0	0	0	0
7	G	1	0	0	0	0
7	K	1	0	0	0	0
7	O	1	0	0	0	0
7	S	1	0	0	0	0
7	W	1	0	0	0	0
7	a	1	0	0	0	0
7	e	1	0	0	0	0
All	All	49215	0	38980	1348	20

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 16.

The worst 5 of 1348 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:g:312:DG:C8	5:g:313:DT:H72	1.18	1.67
5:g:8:DG:N2	6:h:-7:DA:C2	1.71	1.55
6:h:-468:DC:N1	6:h:-467:DT:H72	1.26	1.48
5:g:467:DA:C2	6:h:-466:DG:C2	2.10	1.38
3:Z:75:HIS:CD2	1:b:93:THR:HG21	1.58	1.38

The worst 5 of 20 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:48:ASP:OD2	1:H:106:HIS:ND1[1_455]	0.19	2.01
1:L:48:ASP:OD2	1:P:106:HIS:ND1[1_655]	0.47	1.73
1:T:48:ASP:OD2	1:X:106:HIS:ND1[1_655]	0.66	1.54
1:b:48:ASP:OD2	1:f:106:HIS:ND1[1_455]	0.75	1.45
1:D:48:ASP:OD2	1:H:106:HIS:CE1[1_455]	1.30	0.90

5.3 Torsion angles

5.3.1 Protein backbone

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	D	93/126 (74%)	82 (88%)	9 (10%)	2 (2%)	5	28
1	H	91/126 (72%)	80 (88%)	10 (11%)	1 (1%)	11	45
1	L	93/126 (74%)	82 (88%)	9 (10%)	2 (2%)	5	28
1	P	91/126 (72%)	80 (88%)	10 (11%)	1 (1%)	11	45
1	T	93/126 (74%)	81 (87%)	10 (11%)	2 (2%)	5	28
1	X	91/126 (72%)	80 (88%)	10 (11%)	1 (1%)	11	45
1	b	93/126 (74%)	82 (88%)	9 (10%)	2 (2%)	5	28
1	f	91/126 (72%)	80 (88%)	10 (11%)	1 (1%)	11	45
2	A	95/135 (70%)	83 (87%)	9 (10%)	3 (3%)	3	21
2	E	95/135 (70%)	86 (90%)	9 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	I	95/135 (70%)	83 (87%)	9 (10%)	3 (3%)	3	21
2	M	95/135 (70%)	86 (90%)	9 (10%)	0	100	100
2	Q	95/135 (70%)	83 (87%)	9 (10%)	3 (3%)	3	21
2	U	95/135 (70%)	86 (90%)	9 (10%)	0	100	100
2	Y	95/135 (70%)	83 (87%)	9 (10%)	3 (3%)	3	21
2	c	95/135 (70%)	86 (90%)	9 (10%)	0	100	100
3	B	81/102 (79%)	70 (86%)	8 (10%)	3 (4%)	2	19
3	F	76/102 (74%)	67 (88%)	9 (12%)	0	100	100
3	J	81/102 (79%)	70 (86%)	8 (10%)	3 (4%)	2	19
3	N	76/102 (74%)	67 (88%)	9 (12%)	0	100	100
3	R	78/102 (76%)	68 (87%)	7 (9%)	3 (4%)	2	19
3	V	76/102 (74%)	67 (88%)	9 (12%)	0	100	100
3	Z	81/102 (79%)	70 (86%)	8 (10%)	3 (4%)	2	19
3	d	76/102 (74%)	67 (88%)	9 (12%)	0	100	100
4	C	101/130 (78%)	88 (87%)	9 (9%)	4 (4%)	2	18
4	G	103/130 (79%)	88 (85%)	15 (15%)	0	100	100
4	K	101/130 (78%)	88 (87%)	9 (9%)	4 (4%)	2	18
4	O	103/130 (79%)	87 (84%)	16 (16%)	0	100	100
4	S	101/130 (78%)	88 (87%)	9 (9%)	4 (4%)	2	18
4	W	103/130 (79%)	88 (85%)	15 (15%)	0	100	100
4	a	101/130 (78%)	88 (87%)	9 (9%)	4 (4%)	2	18
4	e	103/130 (79%)	88 (85%)	15 (15%)	0	100	100
All	All	2937/3944 (74%)	2572 (88%)	313 (11%)	52 (2%)	6	34

5 of 52 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	101	GLY
2	Q	73	GLU
3	R	29	ILE
2	I	73	GLU
3	J	29	ILE

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	D	81/106 (76%)	70 (86%)	11 (14%)	3	14
1	H	79/106 (74%)	65 (82%)	14 (18%)	2	9
1	L	81/106 (76%)	70 (86%)	11 (14%)	3	14
1	P	79/106 (74%)	65 (82%)	14 (18%)	2	9
1	T	81/106 (76%)	70 (86%)	11 (14%)	3	14
1	X	79/106 (74%)	65 (82%)	14 (18%)	2	9
1	b	81/106 (76%)	70 (86%)	11 (14%)	3	14
1	f	79/106 (74%)	65 (82%)	14 (18%)	2	9
2	A	85/110 (77%)	76 (89%)	9 (11%)	6	21
2	E	84/110 (76%)	79 (94%)	5 (6%)	17	38
2	I	85/110 (77%)	76 (89%)	9 (11%)	6	21
2	M	84/110 (76%)	79 (94%)	5 (6%)	17	38
2	Q	85/110 (77%)	76 (89%)	9 (11%)	6	21
2	U	84/110 (76%)	79 (94%)	5 (6%)	17	38
2	Y	85/110 (77%)	76 (89%)	9 (11%)	6	21
2	c	84/110 (76%)	79 (94%)	5 (6%)	17	38
3	B	68/78 (87%)	62 (91%)	6 (9%)	9	28
3	F	63/78 (81%)	59 (94%)	4 (6%)	16	37
3	J	68/78 (87%)	62 (91%)	6 (9%)	9	28
3	N	63/78 (81%)	59 (94%)	4 (6%)	16	37
3	R	67/78 (86%)	61 (91%)	6 (9%)	9	27
3	V	63/78 (81%)	59 (94%)	4 (6%)	16	37
3	Z	68/78 (87%)	62 (91%)	6 (9%)	9	28
3	d	63/78 (81%)	59 (94%)	4 (6%)	16	37
4	C	82/102 (80%)	75 (92%)	7 (8%)	10	29
4	G	83/102 (81%)	75 (90%)	8 (10%)	8	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	K	82/102 (80%)	75 (92%)	7 (8%)	10	29
4	O	83/102 (81%)	75 (90%)	8 (10%)	8	25
4	S	82/102 (80%)	75 (92%)	7 (8%)	10	29
4	W	83/102 (81%)	75 (90%)	8 (10%)	8	25
4	a	82/102 (80%)	75 (92%)	7 (8%)	10	29
4	e	83/102 (81%)	75 (90%)	8 (10%)	8	25
All	All	2499/3168 (79%)	2243 (90%)	256 (10%)	7	23

5 of 256 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	d	35	ARG
4	e	81	ARG
1	D	77	LEU
1	D	39	TYR
1	f	49	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
4	W	84	GLN
1	b	81	ASN
1	X	64	ASN
4	a	38	ASN
4	e	31	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
6	h	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	h	-448:DT	O3'	-447:DG	P	1.92

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	D	95/126 (75%)	0.55	11 (11%) 9 16	204, 214, 234, 244	0
1	H	93/126 (73%)	0.50	9 (9%) 13 20	194, 206, 224, 233	0
1	L	95/126 (75%)	0.56	10 (10%) 11 18	200, 214, 227, 244	0
1	P	93/126 (73%)	0.42	8 (8%) 16 22	199, 214, 230, 243	0
1	T	95/126 (75%)	0.43	9 (9%) 14 20	217, 228, 246, 255	0
1	X	93/126 (73%)	0.41	6 (6%) 25 29	210, 220, 239, 247	0
1	b	95/126 (75%)	0.41	6 (6%) 26 30	236, 250, 274, 297	0
1	f	93/126 (73%)	0.79	14 (15%) 5 13	237, 249, 264, 265	0
2	A	97/135 (71%)	0.73	16 (16%) 4 11	215, 230, 257, 269	0
2	E	97/135 (71%)	0.38	8 (8%) 17 24	202, 221, 259, 288	0
2	I	97/135 (71%)	0.37	6 (6%) 26 31	219, 232, 261, 281	0
2	M	97/135 (71%)	0.15	7 (7%) 21 27	214, 229, 257, 263	0
2	Q	97/135 (71%)	0.08	4 (4%) 41 40	221, 238, 270, 283	0
2	U	97/135 (71%)	0.34	10 (10%) 12 19	230, 248, 287, 324	0
2	Y	97/135 (71%)	0.40	12 (12%) 8 15	235, 254, 287, 297	0
2	c	97/135 (71%)	0.39	9 (9%) 14 21	262, 273, 303, 320	0
3	B	83/102 (81%)	0.32	4 (4%) 35 36	204, 225, 247, 284	0
3	F	78/102 (76%)	0.34	7 (8%) 15 21	192, 207, 229, 242	0
3	J	83/102 (81%)	0.43	4 (4%) 35 36	206, 222, 250, 266	0
3	N	78/102 (76%)	0.45	6 (7%) 19 25	209, 218, 237, 247	0
3	R	82/102 (80%)	0.17	2 (2%) 59 51	209, 229, 253, 272	0
3	V	78/102 (76%)	0.28	6 (7%) 19 25	220, 242, 259, 268	0
3	Z	83/102 (81%)	0.32	4 (4%) 35 36	230, 245, 269, 287	0
3	d	78/102 (76%)	0.73	11 (14%) 6 14	243, 259, 282, 294	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
4	C	103/130 (79%)	0.52	10 (9%) 13 20	202, 213, 239, 250	0
4	G	105/130 (80%)	0.28	8 (7%) 20 25	195, 211, 232, 243	0
4	K	103/130 (79%)	0.74	13 (12%) 8 15	203, 218, 237, 241	0
4	O	105/130 (80%)	0.76	12 (11%) 10 17	201, 215, 240, 250	0
4	S	103/130 (79%)	0.36	6 (5%) 29 33	216, 229, 255, 262	0
4	W	105/130 (80%)	0.37	7 (6%) 24 28	203, 221, 242, 248	0
4	a	103/130 (79%)	0.43	10 (9%) 13 20	238, 256, 275, 288	0
4	e	105/130 (80%)	0.33	8 (7%) 20 25	232, 250, 266, 271	0
5	g	619/634 (97%)	0.44	21 (3%) 48 43	145, 265, 315, 374	0
6	h	619/628 (98%)	0.40	16 (2%) 57 48	150, 266, 316, 381	0
All	All	4241/5206 (81%)	0.43	300 (7%) 22 27	145, 238, 295, 381	0

The worst 5 of 300 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	92	LEU	9.3
5	g	172	DC	8.5
1	D	34	TYR	8.3
1	f	34	TYR	7.9
5	g	171	DT	7.7

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
7	CL	O	201	1/1	-	-	210,210,210,210	1
7	CL	C	1101	1/1	-	-	212,212,212,212	1
7	CL	G	201	1/1	-	-	207,207,207,207	1
7	CL	K	1101	1/1	-	-	207,207,207,207	1
7	CL	S	1101	1/1	-	-	227,227,227,227	1
7	CL	W	201	1/1	-	-	222,222,222,222	1
7	CL	a	1101	1/1	-	-	253,253,253,253	1
7	CL	e	201	1/1	-	-	248,248,248,248	1

6.5 Other polymers [i](#)

There are no such residues in this entry.