



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:27 PM UTC

PDB ID : 5XM1 / pdb_00005xm1
Title : The mouse nucleosome structure containing H2A, H2B type3-A, H3mm7, and H4
Authors : Taguchi, H.; Horikoshi, N.; Kurumizaka, H.
Deposited on : 2017-05-12
Resolution : 3.45 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

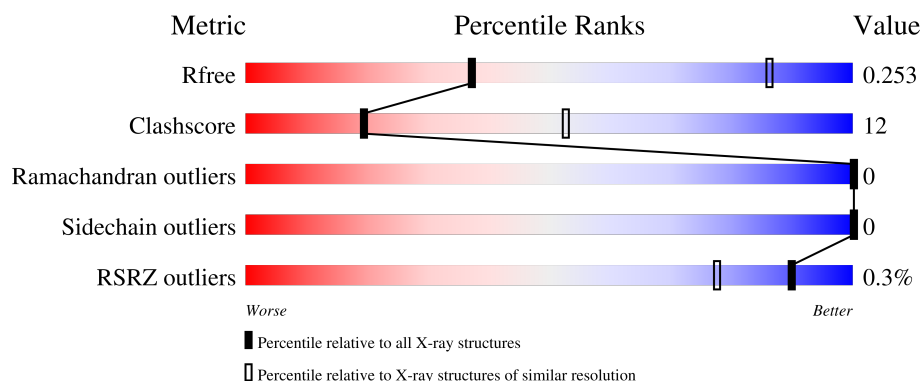
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.45 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	1070 (3.50-3.42)
Clashscore	190562	1128 (3.50-3.42)
Ramachandran outliers	187476	1101 (3.50-3.42)
Sidechain outliers	187428	1102 (3.50-3.42)
RSRZ outliers	180081	1070 (3.50-3.42)

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	139	
1	E	139	
2	B	106	
2	F	106	
3	C	133	

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Mol	Chain	Length	Quality of chain
3	G	133	 58% 20% 22%
4	D	129	 51% 22% 27%
4	H	129	 55% 16% 29%
5	I	146	 51% 49% 0%
5	J	146	 48% 52% 0%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 11920 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 H3mm7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	97	Total	C	N	O	S	0	0	0
			796	503	155	136	2			
1	E	98	Total	C	N	O	S	0	0	0
			802	506	156	138	2			

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	78	Total	C	N	O	S	0	0	0
			619	391	120	107	1			
2	F	83	Total	C	N	O	S	0	0	0
			662	418	129	114	1			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP P62806
B	-2	SER	-	expression tag	UNP P62806
B	-1	HIS	-	expression tag	UNP P62806
F	-3	GLY	-	expression tag	UNP P62806
F	-2	SER	-	expression tag	UNP P62806
F	-1	HIS	-	expression tag	UNP P62806

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	105	Total	C	N	O	0	0	0
			810	511	158	141			
3	G	104	Total	C	N	O	0	0	0
			805	508	157	140			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	expression tag	UNP C0HKE1
C	-2	SER	-	expression tag	UNP C0HKE1
C	-1	HIS	-	expression tag	UNP C0HKE1
G	-3	GLY	-	expression tag	UNP C0HKE1
G	-2	SER	-	expression tag	UNP C0HKE1
G	-1	HIS	-	expression tag	UNP C0HKE1

- Molecule 4 is a protein called Histone H2B type 3-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	94	Total	C	N	O	S	0	0	0
			736	461	134	139	2			
4	H	91	Total	C	N	O	S	0	0	0
			710	447	125	136	2			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	GLY	-	expression tag	UNP Q9D2U9
D	-2	SER	-	expression tag	UNP Q9D2U9
D	-1	HIS	-	expression tag	UNP Q9D2U9
H	-3	GLY	-	expression tag	UNP Q9D2U9
H	-2	SER	-	expression tag	UNP Q9D2U9
H	-1	HIS	-	expression tag	UNP Q9D2U9

- Molecule 5 is a DNA chain called DNA (146-MER).

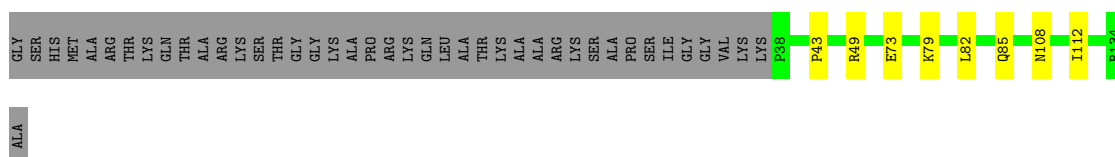
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	146	Total	C	N	O	P	0	0	0
			2990	1431	540	874	145			
5	J	146	Total	C	N	O	P	0	0	0
			2990	1431	540	874	145			

3 Residue-property plots

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.

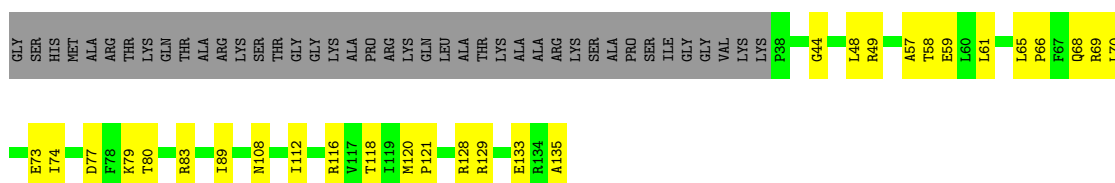
- Molecule 1: Histone H3mm7

Chain A: 



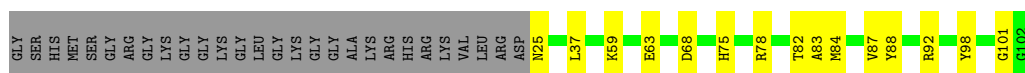
- Molecule 1: Histone H3mm7

Chain E: 



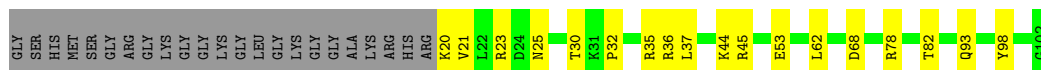
- Molecule 2: Histone H4

Chain B: 



- Molecule 2: Histone H4

Chain F: 



- Molecule 3: Histone H2A type 1-B

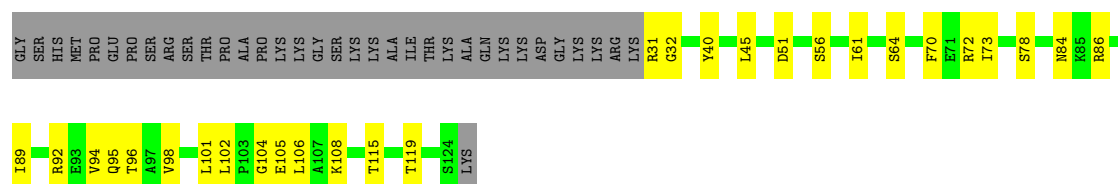
Chain C: 



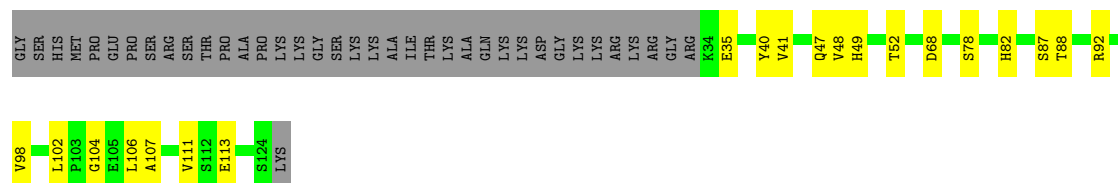
- Molecule 3: Histone H2A type 1-B



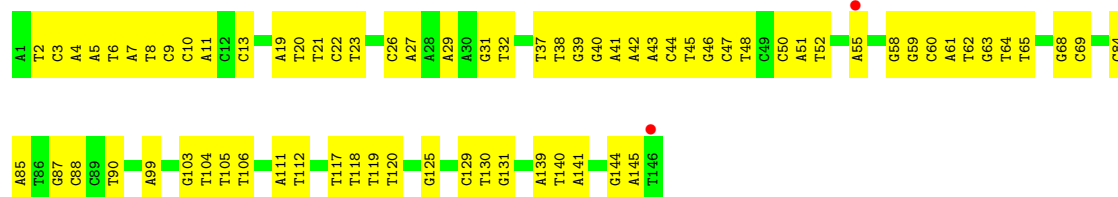
- Molecule 4: Histone H2B type 3-A



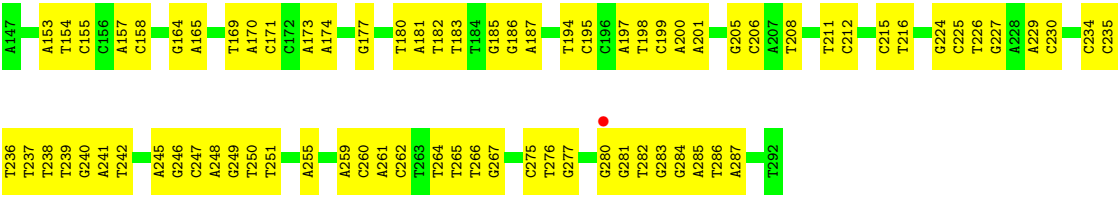
- Molecule 4: Histone H2B type 3-A



- Molecule 5: DNA (146-MER)



- Molecule 5: DNA (146-MER)



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	105.55Å 109.38Å 176.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.88 – 3.45 34.88 – 3.45	Depositor EDS
% Data completeness (in resolution range)	96.5 (34.88-3.45) 96.5 (34.88-3.45)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.08 (at 3.39Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.200 , 0.254 0.199 , 0.253	Depositor DCC
R_{free} test set	1987 reflections (6.92%)	wwPDB-VP
Wilson B-factor (Å ²)	90.8	Xtriage
Anisotropy	0.688	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 46.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.027 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11920	wwPDB-VP
Average B, all atoms (Å ²)	112.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.96% 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](#)

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	0.48	0/808	0.71	0/1084
1	E	0.68	1/814 (0.1%)	0.91	0/1091
2	B	0.48	0/626	0.78	0/837
2	F	0.61	0/669	0.85	0/894
3	C	0.59	0/820	0.81	0/1107
3	G	0.48	0/815	0.78	0/1100
4	D	0.58	0/747	0.85	0/1004
4	H	0.53	0/721	0.78	0/971
5	I	0.38	0/3354	0.63	0/5175
5	J	0.40	0/3354	0.64	0/5175
All	All	0.48	1/12728 (0.0%)	0.72	0/18438

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	77	ASP	CB-CG	7.49	1.70	1.52

There are no bond angle outliers.

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	796	0	835	6	0
1	E	802	0	840	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	619	0	659	16	0
2	F	662	0	709	15	1
3	C	810	0	866	23	1
3	G	805	0	861	24	0
4	D	736	0	756	24	0
4	H	710	0	727	21	0
5	I	2990	0	1652	78	0
5	J	2990	0	1652	71	0
All	All	11920	0	9557	238	1

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 12.

The worst 5 of 238 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:125:DG:N2	5:J:169:DT:O2	2.03	0.91
5:I:55:DA:H61	5:J:238:DT:H3	1.18	0.87
1:E:121:PRO:HB3	2:F:53:GLU:HG3	1.62	0.81
2:F:30:THR:HB	2:F:32:PRO:HD2	1.63	0.80
5:I:11:DA:N6	5:J:282:DT:O4	2.16	0.79

All (1) 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)
3:C:56:GLU:OE2	2:F:23:ARG:NH2[3_544]	2.15	0.05

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	95/139 (68%)	92 (97%)	3 (3%)	0	100	100
1	E	96/139 (69%)	90 (94%)	6 (6%)	0	100	100
2	B	76/106 (72%)	74 (97%)	2 (3%)	0	100	100
2	F	81/106 (76%)	79 (98%)	2 (2%)	0	100	100
3	C	103/133 (77%)	99 (96%)	4 (4%)	0	100	100
3	G	102/133 (77%)	97 (95%)	5 (5%)	0	100	100
4	D	92/129 (71%)	88 (96%)	4 (4%)	0	100	100
4	H	89/129 (69%)	87 (98%)	2 (2%)	0	100	100
All	All	734/1014 (72%)	706 (96%)	28 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	82/111 (74%)	82 (100%)	0	100	100
1	E	82/111 (74%)	82 (100%)	0	100	100
2	B	63/81 (78%)	63 (100%)	0	100	100
2	F	68/81 (84%)	68 (100%)	0	100	100
3	C	83/102 (81%)	83 (100%)	0	100	100
3	G	83/102 (81%)	83 (100%)	0	100	100
4	D	81/110 (74%)	81 (100%)	0	100	100
4	H	79/110 (72%)	79 (100%)	0	100	100
All	All	621/808 (77%)	621 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	93	GLN
3	C	24	GLN
3	C	31	HIS
3	C	73	ASN
4	H	82	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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(Å²)	Q<0.9	
1	A	97/139 (69%)	-0.30	0	100	100	64, 83, 118, 151	0
1	E	98/139 (70%)	-0.40	0	100	100	50, 67, 96, 122	0
2	B	78/106 (73%)	-0.49	0	100	100	64, 79, 99, 102	0
2	F	83/106 (78%)	-0.54	0	100	100	50, 64, 78, 120	0
3	C	105/133 (78%)	-0.57	0	100	100	54, 71, 96, 126	0
3	G	104/133 (78%)	-0.41	0	100	100	66, 82, 111, 122	0
4	D	94/129 (72%)	-0.57	0	100	100	54, 74, 100, 143	0
4	H	91/129 (70%)	-0.39	0	100	100	61, 81, 104, 114	0
5	I	146/146 (100%)	-0.18	2 (1%)	73	49	87, 149, 185, 203	0
5	J	146/146 (100%)	-0.15	1 (0%)	84	64	93, 149, 185, 193	0
All	All	1042/1306 (79%)	-0.38	3 (0%)	90	77	50, 82, 168, 203	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	J	280	DG	2.3
5	I	146	DT	2.2
5	I	55	DA	2.0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.