



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 2, 2023 – 05:09 PM EDT

PDB ID : 3W99  
Title : Crystal Structure of Human Nucleosome Core Particle lacking H4 N-terminal region  
Authors : Iwasaki, W.; Miya, Y.; Horikoshi, N.; Osakabe, A.; Tachiwana, H.; Shibata, T.; Kagawa, W.; Kurumizaka, H.  
Deposited on : 2013-04-01  
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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

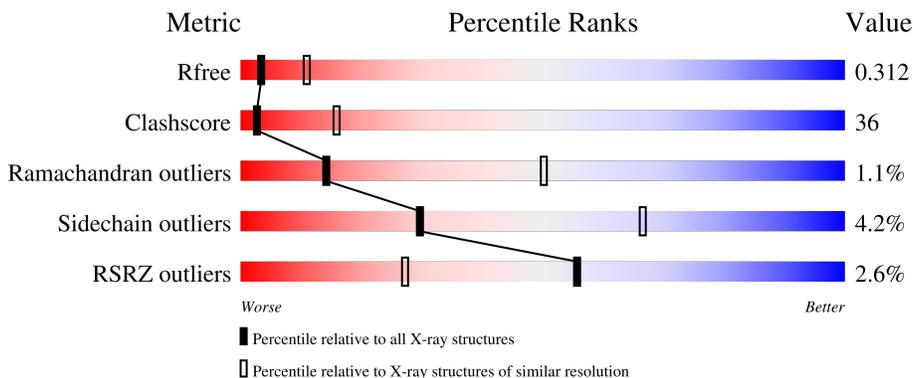
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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.



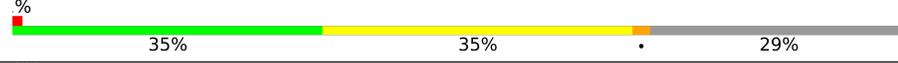
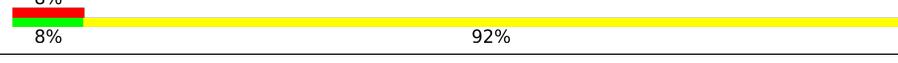
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	139	 31% 34% 2% 1% 30%
1	E	139	 37% 35% 1% 1% 29%
2	B	105	 45% 28% 1% 1% 26%
2	F	105	 42% 34% 1% 1% 20%
3	C	133	 47% 29% 1% 1% 21%

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Mol	Chain	Length	Quality of chain
3	G	133	
4	D	129	
4	H	129	
5	I	146	
5	J	146	

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 11912 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	97	801	505	155	137	4	0	0	0
1	E	99	816	514	158	140	4	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

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

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	78	619	391	120	107	1	0	0	0
2	F	84	673	424	133	115	1	0	0	0

There are 36 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
B	0	HIS	-	expression tag	UNP P62805
B	1	MET	-	expression tag	UNP P62805
B	2	VAL	-	expression tag	UNP P62805
B	3	ASP	-	expression tag	UNP P62805

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Chain	Residue	Modelled	Actual	Comment	Reference
B	4	LEU	-	expression tag	UNP P62805
B	5	GLN	-	expression tag	UNP P62805
B	6	ALA	-	expression tag	UNP P62805
B	7	ALA	-	expression tag	UNP P62805
B	8	ALA	-	expression tag	UNP P62805
B	9	ASN	-	expression tag	UNP P62805
B	10	SER	-	expression tag	UNP P62805
B	11	LEU	-	expression tag	UNP P62805
B	12	VAL	-	expression tag	UNP P62805
B	13	ILE	-	expression tag	UNP P62805
B	14	HIS	-	expression tag	UNP P62805
B	15	MET	-	expression tag	UNP P62805
F	-2	GLY	-	expression tag	UNP P62805
F	-1	SER	-	expression tag	UNP P62805
F	0	HIS	-	expression tag	UNP P62805
F	1	MET	-	expression tag	UNP P62805
F	2	VAL	-	expression tag	UNP P62805
F	3	ASP	-	expression tag	UNP P62805
F	4	LEU	-	expression tag	UNP P62805
F	5	GLN	-	expression tag	UNP P62805
F	6	ALA	-	expression tag	UNP P62805
F	7	ALA	-	expression tag	UNP P62805
F	8	ALA	-	expression tag	UNP P62805
F	9	ASN	-	expression tag	UNP P62805
F	10	SER	-	expression tag	UNP P62805
F	11	LEU	-	expression tag	UNP P62805
F	12	VAL	-	expression tag	UNP P62805
F	13	ILE	-	expression tag	UNP P62805
F	14	HIS	-	expression tag	UNP P62805
F	15	MET	-	expression tag	UNP P62805

- 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	102	Total	C	N	O	0	0	0
			789	498	154	137			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	expression tag	UNP P04908
C	-2	SER	-	expression tag	UNP P04908
C	-1	HIS	-	expression tag	UNP P04908
G	-3	GLY	-	expression tag	UNP P04908
G	-2	SER	-	expression tag	UNP P04908
G	-1	HIS	-	expression tag	UNP P04908

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	95	Total	C	N	O	S	0	0	0
			745	468	136	139	2			
4	H	92	Total	C	N	O	S	0	0	0
			719	453	129	135	2			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	GLY	-	expression tag	UNP P06899
D	-2	SER	-	expression tag	UNP P06899
D	-1	HIS	-	expression tag	UNP P06899
H	-3	GLY	-	expression tag	UNP P06899
H	-2	SER	-	expression tag	UNP P06899
H	-1	HIS	-	expression tag	UNP P06899

- Molecule 5 is a DNA chain called 146-mer DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	145	Total	C	N	O	P	0	0	0
			2970	1421	538	867	144			
5	J	145	Total	C	N	O	P	0	0	0
			2969	1421	535	869	144			

- Molecule 6 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	1	Total	Mn	0	0
			1	1		

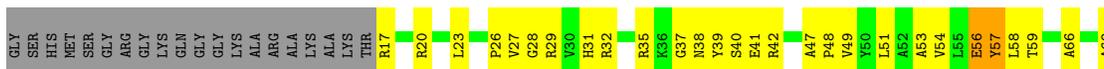




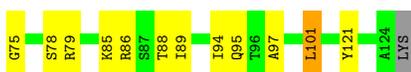
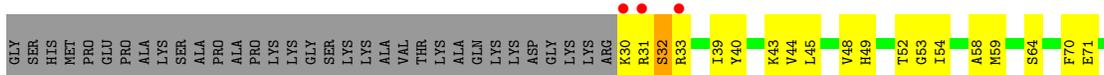
- Molecule 3: Histone H2A type 1-B/E



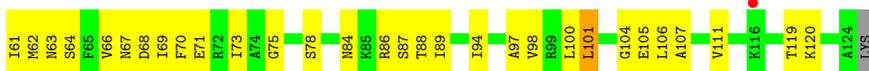
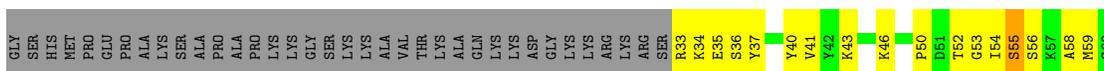
- Molecule 3: Histone H2A type 1-B/E



- Molecule 4: Histone H2B type 1-J



- Molecule 4: Histone H2B type 1-J



- Molecule 5: 146-mer DNA





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.70Å 109.29Å 175.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.54 – 3.00 48.54 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.2 (48.54-3.00) 99.3 (48.54-3.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.43 (at 3.01Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.244 , 0.312 0.244 , 0.312	Depositor DCC
$R_{free}$ test set	2064 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	82.0	Xtrriage
Anisotropy	0.816	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 74.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.026 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	11912	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	120.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.71% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MN

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	0.36	0/813	0.59	0/1090
1	E	0.38	0/828	0.63	0/1109
2	B	0.34	0/626	0.57	0/837
2	F	0.38	0/680	0.64	0/908
3	C	0.33	0/820	0.60	0/1107
3	G	0.30	0/799	0.57	0/1079
4	D	0.35	0/756	0.59	0/1015
4	H	0.33	0/730	0.58	0/982
5	I	0.36	0/3332	0.76	0/5141
5	J	0.36	0/3330	0.78	0/5138
All	All	0.35	0/12714	0.70	0/18406

There are no bond length outliers.

There are no bond angle outliers.

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	801	0	839	72	0
1	E	816	0	856	63	0
2	B	619	0	659	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	673	0	722	60	0
3	C	810	0	866	59	0
3	G	789	0	841	68	0
4	D	745	0	771	34	0
4	H	719	0	740	44	0
5	I	2970	0	1640	201	0
5	J	2969	0	1641	247	0
6	E	1	0	0	0	0
All	All	11912	0	9575	773	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 36.

The worst 5 of 773 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)
2:B:78:ARG:HD3	5:J:248:DA:H5'	1.23	1.17
5:J:241:DA:H2''	5:J:242:DT:H5'	1.18	1.13
5:I:128:DT:H2''	5:I:129:DC:H5''	1.10	1.05
5:I:52:DT:H2''	5:I:53:DC:H5'	1.38	1.05
5:I:101:DC:H2''	5:I:102:DA:H5''	1.35	1.05

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	95/139 (68%)	84 (88%)	9 (10%)	2 (2%)	<b>7</b> 33
1	E	97/139 (70%)	88 (91%)	9 (9%)	0	<b>100</b> <b>100</b>
2	B	76/105 (72%)	67 (88%)	8 (10%)	1 (1%)	<b>12</b> 45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F	82/105 (78%)	78 (95%)	4 (5%)	0	100	100
3	C	103/133 (77%)	95 (92%)	8 (8%)	0	100	100
3	G	100/133 (75%)	88 (88%)	10 (10%)	2 (2%)	7	34
4	D	93/129 (72%)	84 (90%)	8 (9%)	1 (1%)	14	50
4	H	90/129 (70%)	77 (86%)	11 (12%)	2 (2%)	6	31
All	All	736/1012 (73%)	661 (90%)	67 (9%)	8 (1%)	14	50

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	H	55	SER
1	A	86	SER
4	H	104	GLY
3	G	56	GLU
3	G	57	TYR

### 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	85/113 (75%)	77 (91%)	8 (9%)	8	32
1	E	86/113 (76%)	86 (100%)	0	100	100
2	B	63/86 (73%)	61 (97%)	2 (3%)	39	74
2	F	69/86 (80%)	65 (94%)	4 (6%)	20	55
3	C	83/102 (81%)	78 (94%)	5 (6%)	19	53
3	G	81/102 (79%)	79 (98%)	2 (2%)	47	79
4	D	81/107 (76%)	79 (98%)	2 (2%)	47	79
4	H	78/107 (73%)	75 (96%)	3 (4%)	33	69
All	All	626/816 (77%)	600 (96%)	26 (4%)	30	66

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	118	LYS
2	F	21	VAL
4	H	101	LEU
4	D	101	LEU
2	F	45	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	104	GLN
3	G	38	ASN
1	E	76	GLN
4	H	95	GLN
2	F	75	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 1 ligands modelled in this entry, 1 is 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, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	97/139 (69%)	0.17	1 (1%) 82 59	59, 92, 125, 160	0
1	E	99/139 (71%)	0.14	2 (2%) 65 36	54, 76, 117, 148	0
2	B	78/105 (74%)	0.18	1 (1%) 77 51	61, 91, 111, 135	0
2	F	84/105 (80%)	0.31	1 (1%) 79 54	48, 74, 95, 133	0
3	C	105/133 (78%)	0.09	0 100 100	57, 83, 114, 145	0
3	G	102/133 (76%)	0.03	1 (0%) 82 59	68, 92, 123, 136	0
4	D	95/129 (73%)	0.21	3 (3%) 47 20	58, 88, 117, 169	0
4	H	92/129 (71%)	0.28	1 (1%) 80 56	68, 92, 125, 139	0
5	I	145/146 (99%)	0.44	5 (3%) 45 19	75, 152, 191, 199	0
5	J	145/146 (99%)	0.53	12 (8%) 11 3	82, 153, 194, 200	0
All	All	1042/1304 (79%)	0.26	27 (2%) 56 27	48, 94, 179, 200	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	37	LYS	4.9
5	J	161	DG	4.6
4	D	31	ARG	4.2
4	D	33	ARG	3.8
5	J	160	DT	3.4

### 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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
6	MN	E	1001	1/1	0.92	0.33	75,75,75,75	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.