



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 28, 2020 – 07:47 pm BST

PDB ID : 1ID3  
Title : CRYSTAL STRUCTURE OF THE YEAST NUCLEOSOME CORE PARTICLE REVEALS FUNDAMENTAL DIFFERENCES IN INTER-NUCLEOSOME INTERACTIONS  
Authors : White, C.L.; Suto, R.K.; Luger, K.  
Deposited on : 2001-04-03  
Resolution : 3.10 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.

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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	:	2.11
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)	:	2.11

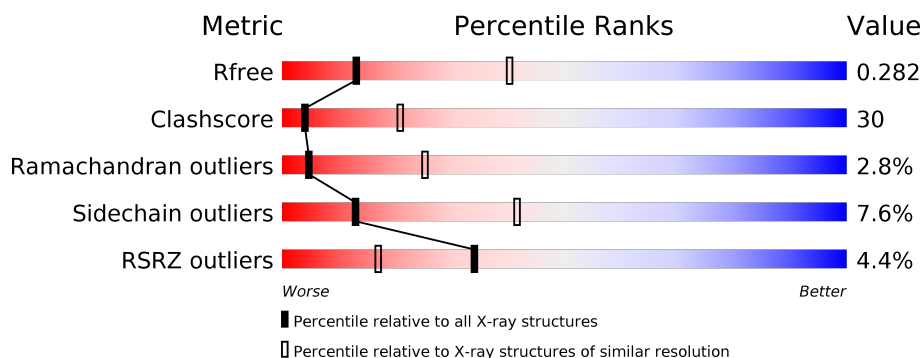
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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 on 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	I	146	<div> <div>12%</div> <div>28%</div> <div>72%</div> </div>
1	J	146	<div> <div>11%</div> <div>22%</div> <div>78%</div> </div>
2	A	135	<div> <div>%</div> <div>36%</div> <div>32%</div> <div>28%</div> </div>
2	E	135	<div> <div>%</div> <div>39%</div> <div>32%</div> <div>28%</div> </div>
3	B	102	<div> <div>32%</div> <div>42%</div> <div>23%</div> </div>
3	F	102	<div> <div>3%</div> <div>35%</div> <div>38%</div> <div>10%</div> <div>17%</div> </div>

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Mol	Chain	Length	Quality of chain
4	C	131	<div><div><div></div><div></div><div></div><div></div></div><div><div>%</div><div>46%</div><div>35%</div><div>•</div><div>16%</div></div></div>
4	G	131	<div><div><div></div><div></div><div></div><div></div></div><div><div>2%</div><div>40%</div><div>39%</div><div>•</div><div>18%</div></div></div>
5	D	130	<div><div><div></div><div></div><div></div><div></div></div><div><div>2%</div><div>37%</div><div>25%</div><div>8%</div><div>•</div><div>28%</div></div></div>
5	H	130	<div><div><div></div><div></div><div></div><div></div></div><div><div>%</div><div>27%</div><div>41%</div><div>6%</div><div>26%</div></div></div>

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 12124 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 DNA chain called PALINDROMIC 146BP DNA FRAGMENT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	I	146	Total	C	N	O	P	0	0	0
			2990	1430	541	874	145			
1	J	146	Total	C	N	O	P	0	0	0
			2990	1430	541	874	145			

- Molecule 2 is a protein called HISTONE H3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	A	97	Total	C	N	O	0	0	0
			802	509	155	138			
2	E	97	Total	C	N	O	0	0	0
			802	509	155	138			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	123	GLU	ASP	CONFLICT	UNP P61830
E	123	GLU	ASP	CONFLICT	UNP P61830

- Molecule 3 is a protein called HISTONE H4.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	B	79	Total	C	N	O	0	0	0
			627	395	120	112			
3	F	85	Total	C	N	O	0	0	0
			684	431	135	118			

- Molecule 4 is a protein called HISTONE H2A.1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	C	110	Total	C	N	O	0	0	0
			845	530	166	149			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	108	Total	C	N	O	0	0	0
			833	523	164	146			

- Molecule 5 is a protein called HISTONE H2B.2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	D	93	Total	C	N	O	S	0	0	0
			726	456	127	142	1			
5	H	96	Total	C	N	O	S	0	0	0
			748	469	131	147	1			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	G	1	Total	Mn	0	0
			1	1		
6	J	7	Total	Mn	0	0
			7	7		
6	D	1	Total	Mn	0	0
			1	1		
6	E	1	Total	Mn	0	0
			1	1		
6	H	1	Total	Mn	0	0
			1	1		
6	I	4	Total	Mn	0	0
			4	4		
6	C	2	Total	Mn	0	0
			2	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	I	12	Total	O	0	0
			12	12		
7	J	7	Total	O	0	0
			7	7		
7	A	5	Total	O	0	0
			5	5		
7	B	7	Total	O	0	0
			7	7		
7	C	4	Total	O	0	0
			4	4		

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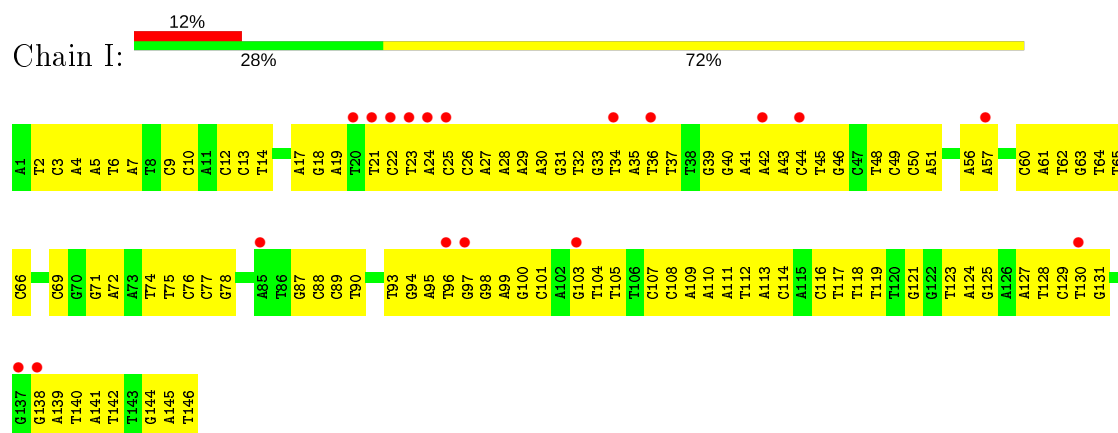
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	7	Total 7	O 7	0	0
7	E	5	Total 5	O 5	0	0
7	F	2	Total 2	O 2	0	0
7	G	6	Total 6	O 6	0	0
7	H	5	Total 5	O 5	0	0

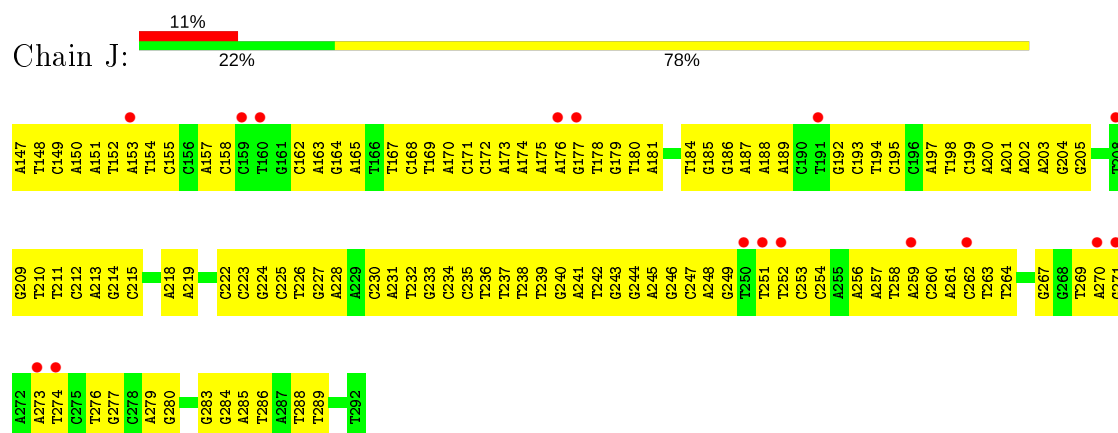
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

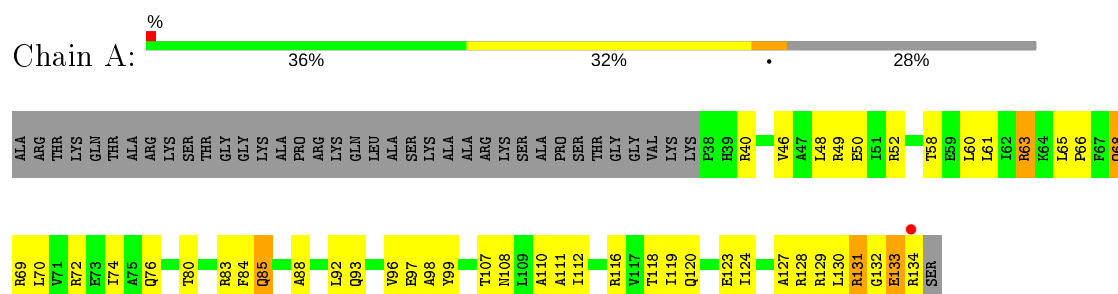
#### • Molecule 1: PALINDROMIC 146BP DNA FRAGMENT



#### • Molecule 1: PALINDROMIC 146BP DNA FRAGMENT



#### • Molecule 2: HISTONE H3



R72	E73	I74	D77	F78	K79	L82	R83	F84	Q85	L92	Q93	E94	S95	V96	D106	T107	M108	I112	H113	A114	K115	R116	V117	T118	I119	Q120	K121	K122	E123	I124	A127	L130	R131	R134	SER																		
ALA	ARG	THR	LYS	GLN	THR	ALA	ARG	LYS	SER	THR	GLY	GLY	ALA	PRO	ARG	LYS	GLN	LEU	ALA	SER	LYS	ALA	ALA	ARG	LYS	SER	ALA	PRO	SER	THR	GLY	GLY	VAL	LYS	P38	A47	L48	R49	E50	I51	Q55	E59	L60	L61	I62	R63	I64	L65	P66	F67	Q68	R69	L70

I66	R67	D68	S69	V70	H75	A76	K77	R78	K79	T80	V81	T82	S83	L84	Y88	R95	T96	L97	Y98	G102																																		
SER	GLY	ARG	GLY	LVS	GLY	GLY	LVS	GLY	LEU	GLY	LVS	GLY	GLY	ALA	ARG	HIS	ARG	LVS	ILE	LEU	ARG	D24	N25	I26	Q27	T30	K31	P32	A33	T34	R35	R36	L37	A38	R39	G42	V43	R44	R45	I46	S47	G48	L49	Y50	I51	E52	E53	V54	R55	A56	V57	L58	K59	L62

SER	GLY	ARG	GLY	LYS	GLY	LYS	GLY	LEU	GLY	LYS	GLY	ALA	LYS	ARG	H18	R19	K20	I21	L22	R23	D24	M25	L26	T30	K31	P32	A33	I34	R35	R36	L37	A38	R39	V43	K44	R45	L46	I50	Y51	E52	E53	V54	V57	L58	K59	S60	F61	L62	E63	I66	R67
S89	V70	T71	T72	E74	H75	A76	K77	R78	K79	T80	V81	T82	S83	L84	D85	V86	V87	Y88	R92	Y98	G102																														

T77	R78	G17	SER
I79	R80	LVS	GLY
I80	R81	LVS	ALA
R82	R82	GLY	LVS
R83	R83	LVS	ALA
L84	L84	GLY	ALA
		GLY	SER
I88	R89	ALA	ALA
R90	R90	LVS	LVS
D91	D92	ALA	ALA
R93	R93	SER	SER
L94	L94	LVS	LVS
N95	N95	LVS	LVS
		LVS	LVS
L98	L98	LVS	LVS
I103	I103	LVS	LVS
I104	I104	LVS	LVS
Q105	Q105	LVS	LVS
G106	G106	LVS	LVS
G107	G107	LVS	LVS
		LVS	LVS
P118	P118	LVS	LVS
K119	K119	LVS	LVS
K120	K120	LVS	LVS
S121	S121	LVS	LVS
A122	A122	LVS	LVS
K123	K123	LVS	LVS
A124	A124	LVS	LVS
T125	T125	LVS	LVS
LVS	LVS	LVS	LVS
ALA	ALA	LVS	LVS
SER	SER	LVS	LVS
GLN	GLN	LVS	LVS
GLU	GLU	LVS	LVS
LEU	LEU	LVS	LVS

SER	GLY	GLY	LYS	GLY	GLY	LYS	ALA	GLY	SER	SER	ALA	ALA	K13	K14	A15	A16	A17	A18	A19	A20	T25	F26	F27	V28	V31	H32	R33	L34	L35	R37	G38	N39	Y40	R43	I44	A48	P49	Y50	Y51	Y55	Y58	I63	G67	G68	M69	A70	A71	R72	D73	M74
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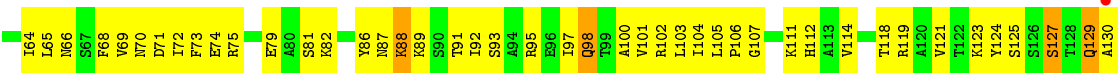




• Molecule 5: HISTONE H2B.2



• Molecule 5: HISTONE H2B.2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	104.92Å 110.40Å 192.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.10 49.06 – 3.13	Depositor EDS
% Data completeness (in resolution range)	92.6 (40.00-3.10) 95.3 (49.06-3.13)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.72 (at 3.12Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.223 , 0.292 0.218 , 0.282	Depositor DCC
$R_{free}$ test set	1966 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	86.2	Xtriage
Anisotropy	0.322	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 103.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	12124	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% 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 [i](#)

### 5.1 Standard geometry [i](#)

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	I	0.31	0/3354	0.67	0/5175
1	J	0.32	0/3354	0.67	0/5175
2	A	0.48	0/813	0.70	0/1087
2	E	0.47	0/813	0.70	0/1087
3	B	0.55	0/634	0.75	0/848
3	F	0.46	0/692	0.80	1/924 (0.1%)
4	C	0.42	0/856	0.73	0/1156
4	G	0.42	0/844	0.68	0/1139
5	D	0.45	0/736	0.69	0/991
5	H	0.46	0/758	0.73	0/1020
All	All	0.39	0/12854	0.69	1/18602 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	25	ASN	N-CA-C	8.44	133.79	111.00

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	I	2990	0	1651	130	0
1	J	2990	0	1651	149	0
2	A	802	0	853	69	0
2	E	802	0	853	63	0
3	B	627	0	664	62	0
3	F	684	0	732	63	0
4	C	845	0	895	53	0
4	G	833	0	883	70	0
5	D	726	0	748	52	0
5	H	748	0	770	77	0
6	C	2	0	0	0	0
6	D	1	0	0	0	0
6	E	1	0	0	0	0
6	G	1	0	0	0	0
6	H	1	0	0	0	0
6	I	4	0	0	0	0
6	J	7	0	0	0	0
7	A	5	0	0	1	0
7	B	7	0	0	2	0
7	C	4	0	0	0	0
7	D	7	0	0	1	0
7	E	5	0	0	1	0
7	F	2	0	0	0	0
7	G	6	0	0	2	0
7	H	5	0	0	1	0
7	I	12	0	0	1	0
7	J	7	0	0	3	0
All	All	12124	0	9700	653	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 30.

The worst 5 of 653 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)
1:J:258:DT:H2''	1:J:259:DA:H5'	1.31	1.12
1:I:93:DT:H2''	1:I:94:DG:H5''	1.20	1.09
3:B:30:THR:HB	3:B:32:PRO:HD2	1.32	1.06
1:J:185:DG:H5''	4:G:43:ARG:HE	1.20	1.01
5:H:38:GLU:HG3	7:H:132:HOH:O	1.67	0.94

There are no symmetry-related clashes.

## 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	
2	A	95/135 (70%)	85 (90%)	8 (8%)	2 (2%)	7	30
2	E	95/135 (70%)	81 (85%)	14 (15%)	0	100	100
3	B	77/102 (76%)	65 (84%)	11 (14%)	1 (1%)	12	42
3	F	83/102 (81%)	70 (84%)	12 (14%)	1 (1%)	13	44
4	C	108/131 (82%)	88 (82%)	16 (15%)	4 (4%)	3	19
4	G	106/131 (81%)	91 (86%)	13 (12%)	2 (2%)	8	33
5	D	91/130 (70%)	71 (78%)	13 (14%)	7 (8%)	1	5
5	H	94/130 (72%)	67 (71%)	23 (24%)	4 (4%)	2	16
All	All	749/996 (75%)	618 (82%)	110 (15%)	21 (3%)	5	25

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	C	121	SER
5	H	88	LYS
5	D	39	THR
5	D	107	GLY
5	D	115	SER

### 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	
2	A	85/112 (76%)	82 (96%)	3 (4%)	36	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	85/112 (76%)	82 (96%)	3 (4%)	36	68
3	B	66/80 (82%)	63 (96%)	3 (4%)	27	60
3	F	72/80 (90%)	61 (85%)	11 (15%)	2	12
4	C	87/98 (89%)	82 (94%)	5 (6%)	20	52
4	G	86/98 (88%)	80 (93%)	6 (7%)	15	45
5	D	81/109 (74%)	72 (89%)	9 (11%)	6	24
5	H	83/109 (76%)	74 (89%)	9 (11%)	6	25
All	All	645/798 (81%)	596 (92%)	49 (8%)	13	41

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	77	ASP
3	F	60	SER
5	H	55	THR
3	F	20	LYS
3	F	73	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
4	C	39	ASN
4	C	74	ASN
4	G	74	ASN
3	B	25	ASN
4	C	32	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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 17 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, 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	I	146/146 (100%)	0.77	18 (12%) 4 1	67, 130, 185, 201	0
1	J	146/146 (100%)	0.77	16 (10%) 5 2	62, 130, 182, 201	0
2	A	97/135 (71%)	-0.07	1 (1%) 82 67	26, 50, 102, 200	0
2	E	97/135 (71%)	-0.01	1 (1%) 82 67	25, 56, 110, 197	0
3	B	79/102 (77%)	-0.19	0 100 100	23, 49, 82, 121	0
3	F	85/102 (83%)	0.15	3 (3%) 44 23	26, 53, 145, 193	0
4	C	110/131 (83%)	0.06	1 (0%) 84 69	26, 52, 158, 201	0
4	G	108/131 (82%)	-0.11	3 (2%) 53 30	28, 55, 132, 201	0
5	D	93/130 (71%)	0.11	3 (3%) 47 25	28, 50, 111, 184	0
5	H	96/130 (73%)	-0.08	1 (1%) 82 67	24, 54, 115, 201	0
All	All	1057/1288 (82%)	0.20	47 (4%) 34 17	23, 64, 171, 201	0

The worst 5 of 47 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	159	DC	4.8
5	H	130	ALA	4.7
3	F	23	ARG	4.5
5	D	36	ARG	4.4
1	J	252	DT	3.8

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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



### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

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(Å <sup>2</sup> )	Q<0.9
6	MN	J	103	1/1	0.81	0.07	56,56,56,56	0
6	MN	E	136	1/1	0.81	0.18	56,56,56,56	0
6	MN	J	117	1/1	0.87	0.21	56,56,56,56	0
6	MN	I	148	1/1	0.90	0.08	56,56,56,56	0
6	MN	H	131	1/1	0.90	0.19	56,56,56,56	0
6	MN	I	147	1/1	0.91	0.08	56,56,56,56	0
6	MN	J	113	1/1	0.91	0.18	56,56,56,56	0
6	MN	C	132	1/1	0.92	0.09	56,56,56,56	0
6	MN	I	150	1/1	0.94	0.15	56,56,56,56	0
6	MN	J	111	1/1	0.95	0.19	56,56,56,56	0
6	MN	J	115	1/1	0.96	0.19	56,56,56,56	0
6	MN	I	149	1/1	0.96	0.05	56,56,56,56	0
6	MN	J	108	1/1	0.97	0.10	56,56,56,56	0
6	MN	C	133	1/1	0.98	0.27	56,56,56,56	0
6	MN	G	132	1/1	0.98	0.05	56,56,56,56	0
6	MN	J	114	1/1	0.98	0.18	56,56,56,56	0
6	MN	D	131	1/1	0.99	0.20	56,56,56,56	0

### 6.5 Other polymers ⓘ

There are no such residues in this entry.