



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:47 PM GMT

PDB ID : 3UTB
Title : Crystal Structure of Nucleosome Core Particle Assembled with the 146b Alpha-Satellite Sequence (NCP146b)
Authors : Chua, E.Y.D.; Vasudevan, D.; Davey, G.E.; Wu, B.; Davey, C.A.
Deposited on : 2011-11-25
Resolution : 2.20 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

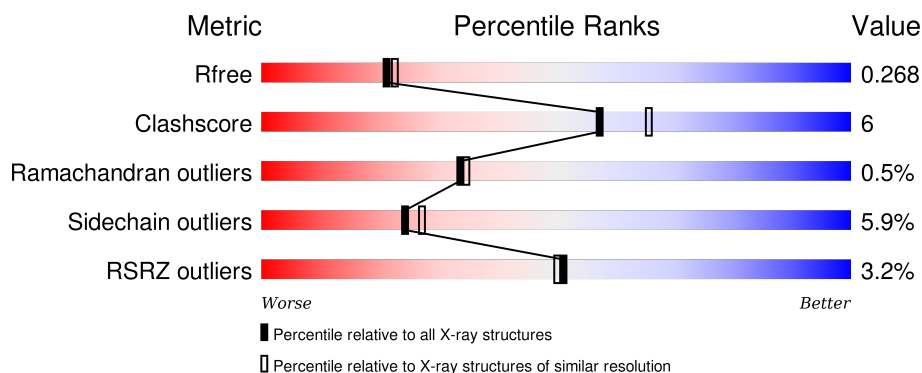
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	135	<div> <div>4%</div> <div>64%</div> <div>8%</div> <div>27%</div> </div>
1	E	135	<div> <div>66%</div> <div>5%</div> <div>28%</div> </div>
2	B	102	<div> <div>71%</div> <div>10%</div> <div>19%</div> </div>
2	F	102	<div> <div>4%</div> <div>67%</div> <div>9%</div> <div>24%</div> </div>
3	C	129	<div> <div>4%</div> <div>64%</div> <div>14%</div> <div>20%</div> </div>

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Mol	Chain	Length	Quality of chain
3	G	129	
4	D	125	
4	H	125	
5	I	146	
5	J	146	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	SO4	C	1102	-	-	-	X
7	SO4	D	1101	-	-	-	X
7	SO4	G	1103	-	-	X	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 12430 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 H3.2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	98	Total	C	N	O	S	0	0	0
			808	509	156	140	3			
1	E	97	Total	C	N	O	S	0	0	0
			801	504	155	139	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	102	ALA	GLY	SEE REMARK 999	UNP P84233
E	102	ALA	GLY	SEE REMARK 999	UNP P84233

- Molecule 2 is a protein called Histone H4.

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

- Molecule 3 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	103	Total	C	N	O		0	0	0
			795	501	155	139				
3	G	105	Total	C	N	O		0	0	0
			809	510	158	141				

- Molecule 4 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	99	Total	C	N	O	S	0	0	0
			785	493	146	144	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	94	Total	C	N	O	S	0	0	0
			736	463	132	139	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	29	THR	SER	SEE REMARK 999	UNP P02281
H	29	THR	SER	SEE REMARK 999	UNP P02281

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

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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	I	9	Total	Mn	0	0
			9	9		
6	A	1	Total	Mn	0	0
			1	1		
6	D	1	Total	Mn	0	0
			1	1		
6	J	9	Total	Mn	0	0
			9	9		
6	E	1	Total	Mn	0	0
			1	1		

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	O	S	0	0
			5	4	1		
7	D	1	Total	O	S	0	0
			5	4	1		
7	G	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	62	Total	O	0	0
			62	62		
8	B	41	Total	O	0	0
			41	41		
8	C	31	Total	O	0	0
			31	31		
8	D	16	Total	O	0	0
			16	16		
8	E	37	Total	O	0	0
			37	37		
8	F	28	Total	O	0	0
			28	28		
8	G	52	Total	O	0	0
			52	52		
8	H	35	Total	O	0	0
			35	35		
8	I	50	Total	O	0	0
			50	50		

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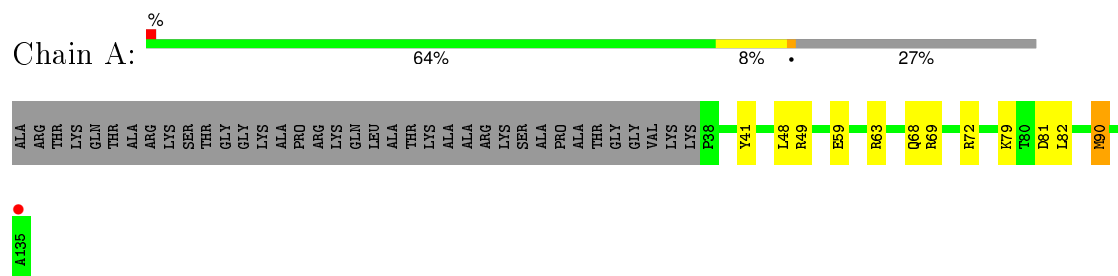
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	J	47	Total	O	0	0
			47	47		

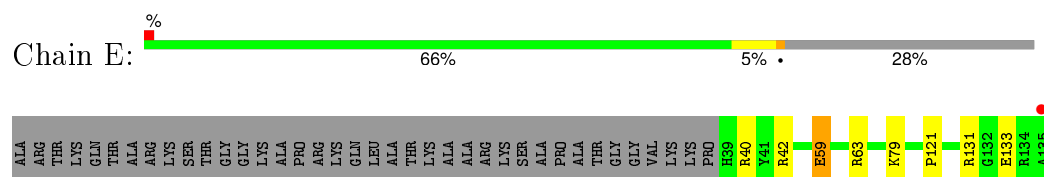
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

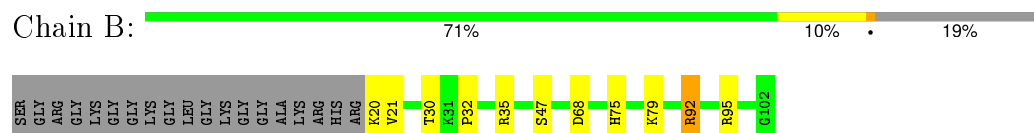
- Molecule 1: Histone H3.2



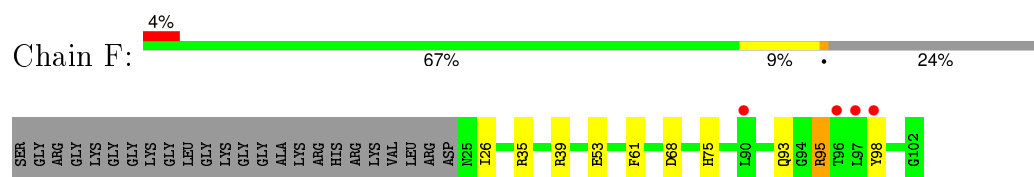
- Molecule 1: Histone H3.2



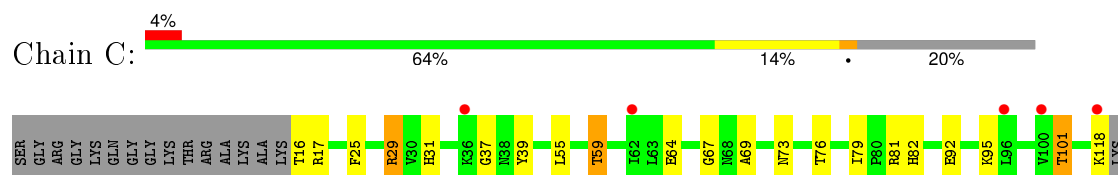
- Molecule 2: Histone H4



- Molecule 2: Histone H4



- Molecule 3: Histone H2A



THR
GLU
SER
SER
LYS
LYS
SER
ALA
LYS
SER
LYS

• Molecule 3: Histone H2A



SER
GLY
GLY
GLY
LYS
GLN
GLY
GLY
LYS
THR
ARG
LYS
LYS
ALA
LYS
K114
R17
F25
R31
R38
R42
V43
V43
G44
A45
G46
V54
L55
T59
I62
L63
E64
R71
D72
N73
T76
R77
T78
F79
F80
R81
R82
L83
Q84
R88
I102
K118
LYS
THR
GLU

SER
SER
LYS
LYS
SER
ALA
LYS
LYS
SER
LYS

• Molecule 4: Histone H2B 1.1



PRO
GLU
PRO
ALA
LYS
LYS
SER
SER
ALA
PRO
ALA
PRO
LYS
LYS
LYS
GLY
SER
K24
K25
R26
R27
K28
T29
R30
K31
E32
S33
Y34
A35
Y39
K43
H46
M56
S61
F67
E73
L77
A78
H79
T87
S88
R89
T93
R96
L97
L98
L99
P100
E101
E102
L103
A104
S109
V115
T119
A120
A121
K122

• Molecule 4: Histone H2B 1.1



PRO
GLU
PRO
ALA
LYS
LYS
SER
SER
ALA
PRO
ALA
PRO
LYS
LYS
LYS
GLY
SER
T29
R30
Y34
A35
V38
V45
H46
M56
S57
I58
M59
N60
S61
F62
E68
N81
K82
R83
S84
T85
T93
A94
V95
L98
G101
A104
V108
S120
A121
K122

• Molecule 5: 146-mer DNA

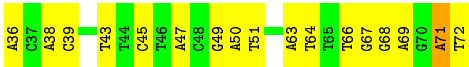


A-72
C-67
A-66
A-62
A-51
A-46
A-43
G-35
C-29
T-28
G-27
T-23
A-22
T-21
C-20
A-19
A-18
G-14
A-13
A-12
G-2
T1
T2
C3
A4
A10
G11
C17
A22
T23
A24
G25
G30
T33
G34
C38
A39
C40
C46
T47
C53
C54
G55
C56
A57
G71
T72
T73

• Molecule 5: 146-mer DNA



A-73
T-70
C-60
T-57
G-56
C-55
G-54
G-53
C-50
G-49
C-34
C-30
T-29
G-28
T-24
C-25
C-21
A-20
A-19
A-18
G-17
G-16
G-15
C-11
T-10
A-6
C-5
T-4
G4
T5
T6
G7
A8
T17
G20
A21
A22
A23
C25
G29
T30
T31
T32
G33



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	105.46Å 109.28Å 175.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	57.46 – 2.20 57.46 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.1 (57.46-2.20) 98.1 (57.46-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.232 , 0.275 0.227 , 0.268	Depositor DCC
R_{free} test set	2034 reflections (2.04%)	DCC
Wilson B-factor (Å ²)	48.2	Xtriage
Anisotropy	0.594	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 43.6	EDS
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 101641 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12430	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, SO4

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	0.67	0/820	0.66	0/1099
1	E	0.54	0/812	0.65	0/1088
2	B	0.73	0/669	0.73	0/894
2	F	0.58	0/626	0.67	0/837
3	C	0.52	0/805	0.62	0/1088
3	G	0.62	0/819	0.71	0/1106
4	D	0.58	0/796	0.67	1/1065 (0.1%)
4	H	0.62	0/747	0.68	0/1004
5	I	0.73	0/3354	1.34	16/5175 (0.3%)
5	J	0.72	0/3354	1.37	25/5175 (0.5%)
All	All	0.67	0/12802	1.10	42/18531 (0.2%)

There are no bond length outliers.

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	J	-30	DC	O4'-C1'-N1	7.85	113.49	108.00
5	I	-14	DG	P-O3'-C3'	7.76	129.01	119.70
5	I	-35	DG	O4'-C1'-N9	-7.47	102.77	108.00
5	J	-19	DA	O4'-C1'-N9	7.44	113.21	108.00
5	J	23	DA	P-O3'-C3'	7.09	128.21	119.70

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	808	0	846	10	0
1	E	801	0	838	4	0
2	B	662	0	709	10	0
2	F	619	0	659	9	0
3	C	795	0	846	16	0
3	G	809	0	864	28	0
4	D	785	0	825	24	0
4	H	736	0	760	25	0
5	I	2990	0	1651	21	0
5	J	2990	0	1651	32	0
6	A	1	0	0	0	0
6	D	1	0	0	0	0
6	E	1	0	0	0	0
6	I	9	0	0	0	0
6	J	9	0	0	0	0
7	C	5	0	0	1	0
7	D	5	0	0	0	0
7	G	5	0	0	3	0
8	A	62	0	0	2	0
8	B	41	0	0	1	0
8	C	31	0	0	0	0
8	D	16	0	0	3	0
8	E	37	0	0	0	0
8	F	28	0	0	2	0
8	G	52	0	0	4	0
8	H	35	0	0	0	0
8	I	50	0	0	0	0
8	J	47	0	0	1	0
All	All	12430	0	9649	130	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 6.

The worst 5 of 130 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:75:HIS:CD2	4:D:93:THR:HG21	1.80	1.17
2:F:75:HIS:CD2	4:H:93:THR:HG21	1.85	1.10
2:B:75:HIS:HD2	4:D:93:THR:HG21	1.18	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:95:ARG:HD2	8:B:502:HOH:O	1.69	0.92
2:F:75:HIS:HD2	4:H:93:THR:HG21	1.28	0.90

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	96/135 (71%)	96 (100%)	0	0	100	100
1	E	95/135 (70%)	94 (99%)	1 (1%)	0	100	100
2	B	81/102 (79%)	81 (100%)	0	0	100	100
2	F	76/102 (74%)	75 (99%)	1 (1%)	0	100	100
3	C	101/129 (78%)	98 (97%)	3 (3%)	0	100	100
3	G	103/129 (80%)	100 (97%)	3 (3%)	0	100	100
4	D	97/125 (78%)	95 (98%)	0	2 (2%)	9	5
4	H	92/125 (74%)	90 (98%)	0	2 (2%)	8	4
All	All	741/982 (76%)	729 (98%)	8 (1%)	4 (0%)	34	35

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	101	GLY
4	H	101	GLY
4	H	120	SER
4	D	25	LYS

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	85/110 (77%)	81 (95%)	4 (5%)	32	39
1	E	84/110 (76%)	80 (95%)	4 (5%)	31	37
2	B	68/78 (87%)	65 (96%)	3 (4%)	35	42
2	F	63/78 (81%)	61 (97%)	2 (3%)	46	57
3	C	82/101 (81%)	76 (93%)	6 (7%)	17	18
3	G	83/101 (82%)	77 (93%)	6 (7%)	18	18
4	D	85/105 (81%)	80 (94%)	5 (6%)	24	27
4	H	80/105 (76%)	73 (91%)	7 (9%)	12	12
All	All	630/788 (80%)	593 (94%)	37 (6%)	24	27

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	103	LEU
1	E	59	GLU
4	H	85	THR
4	D	109	SER
1	E	40	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
4	D	79	HIS
2	F	75	HIS
4	H	60	ASN
4	D	46	HIS
4	H	46	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 21 are monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
7	SO4	C	1102	-	4,4,4	0.52	0	6,6,6	0.33	0
7	SO4	D	1101	-	4,4,4	0.25	0	6,6,6	0.10	0
7	SO4	G	1103	-	4,4,4	0.74	0	6,6,6	0.35	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	SO4	C	1102	-	-	0/0/0/0	0/0/0/0
7	SO4	D	1101	-	-	0/0/0/0	0/0/0/0
7	SO4	G	1103	-	-	0/0/0/0	0/0/0/0

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.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	1102	SO4	1	0
7	G	1103	SO4	3	0

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	98/135 (72%)	0.28	1 (1%) 84 83	27, 40, 60, 69	0
1	E	97/135 (71%)	0.26	1 (1%) 84 83	36, 48, 62, 70	0
2	B	83/102 (81%)	0.32	0 100 100	27, 38, 47, 54	0
2	F	78/102 (76%)	0.47	4 (5%) 32 31	37, 44, 55, 59	0
3	C	103/129 (79%)	0.54	5 (4%) 33 33	36, 50, 64, 75	0
3	G	105/129 (81%)	0.46	2 (1%) 70 68	28, 43, 60, 73	0
4	D	99/125 (79%)	0.76	10 (10%) 9 8	39, 52, 87, 100	0
4	H	94/125 (75%)	0.65	3 (3%) 51 50	32, 44, 67, 79	0
5	I	146/146 (100%)	0.21	3 (2%) 67 65	48, 95, 144, 155	0
5	J	146/146 (100%)	0.14	5 (3%) 49 47	52, 93, 129, 142	0
All	All	1049/1274 (82%)	0.39	34 (3%) 51 50	27, 50, 118, 155	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	24	LYS	8.6
1	A	135	ALA	6.7
3	C	118	LYS	6.4
4	H	122	LYS	3.8
5	J	-18	DA	3.5

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
7	SO4	G	1103	5/5	0.97	0.30	5.77	32,37,40,41	5
7	SO4	D	1101	5/5	0.79	0.40	4.40	148,148,148,148	0
7	SO4	C	1102	5/5	0.93	0.22	3.80	45,48,49,51	5
6	MN	A	1001	1/1	1.00	0.18	0.53	37,37,37,37	0
6	MN	J	1009	1/1	0.45	0.12	-	120,120,120,120	0
6	MN	I	1014	1/1	0.95	0.13	-	108,108,108,108	0
6	MN	J	1015	1/1	0.70	0.11	-	124,124,124,124	0
6	MN	I	1017	1/1	0.61	0.12	-	125,125,125,125	0
6	MN	I	1021	1/1	0.74	0.19	-	134,134,134,134	0
6	MN	J	1012	1/1	0.79	0.09	-	121,121,121,121	0
6	MN	E	1002	1/1	0.96	0.20	-	94,94,94,94	0
6	MN	I	1005	1/1	0.87	0.14	-	83,83,83,83	0
6	MN	D	1007	1/1	0.72	0.17	-	130,130,130,130	0
6	MN	J	1011	1/1	0.67	0.18	-	124,124,124,124	0
6	MN	J	1020	1/1	0.79	0.18	-	150,150,150,150	0
6	MN	J	1010	1/1	0.06	0.38	-	188,188,188,188	0
6	MN	I	1013	1/1	-0.58	0.19	-	176,176,176,176	0
6	MN	I	1003	1/1	0.95	0.22	-	77,77,77,77	0
6	MN	J	1016	1/1	0.87	0.19	-	102,102,102,102	0
6	MN	I	1006	1/1	0.92	0.12	-	83,83,83,83	0
6	MN	I	1019	1/1	0.95	0.23	-	118,118,118,118	0
6	MN	J	1018	1/1	0.53	0.15	-	115,115,115,115	0
6	MN	I	1004	1/1	0.80	0.13	-	127,127,127,127	0
6	MN	J	1008	1/1	0.98	0.05	-	147,147,147,147	0

6.5 Other polymers ⓘ

There are no such residues in this entry.