WORLDWIDE PDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 5, 2024 – 12:56 am GMT

PDB ID	:	5F99
Title	:	X-ray Structure of the MMTV-A Nucleosome Core Particle
Authors	:	Frouws, T.D.; Richmond, T.J.
Deposited on	:	2015-12-09
Resolution	:	2.63 Å(reported)

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

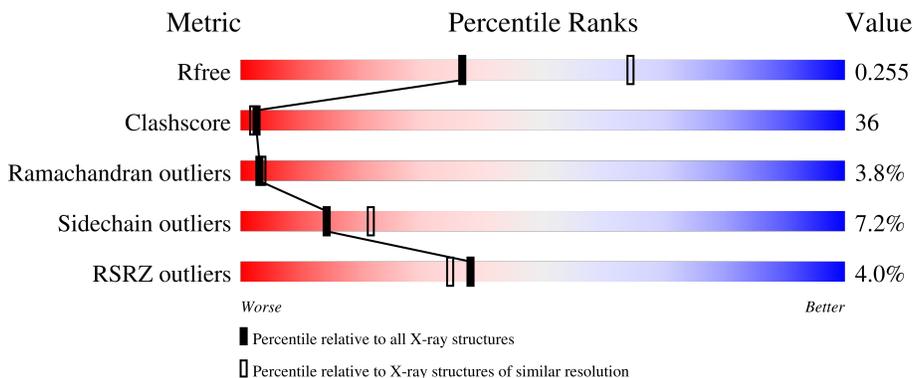|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.63 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	Percentile Ranks	Value
Rfree		0.255
Clashscore		36
Ramachandran outliers		3.8%
Sidechain outliers		7.2%
RSRZ outliers		4.0%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1426 (2.66-2.62)
Clashscore	141614	1472 (2.66-2.62)
Ramachandran outliers	138981	1446 (2.66-2.62)
Sidechain outliers	138945	1446 (2.66-2.62)
RSRZ outliers	127900	1408 (2.66-2.62)

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 <=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	4% 27% 39% 7% 26%
1	E	135	.% 45% 25% • 27%
2	B	103	3% 44% 34% • 19%
2	F	103	2% 62% 22% 5% 11%
3	C	129	2% 57% 24% 5% 14%

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Mol	Chain	Length	Quality of chain
3	G	129	10% · 41% · 40% · 11% · 6%
4	D	122	4% · 52% · 24% · 6% · 18%
4	H	122	2% · 30% · 43% · 7% · 20%
5	I	147	3% · 23% · 75% ·
6	J	147	3% · 23% · 76% ·

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	CL	A	201	-	-	X	-

2 Entry composition ⓘ

There are 9 unique types of molecules in this entry. The entry contains 13349 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	100	Total 825	C 521	N 160	O 142	S 2	0	0	0
1	E	99	Total 816	C 515	N 158	O 141	S 2	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	102	ALA	GLY	conflict	UNP P84233
A	110	ALA	CYS	conflict	UNP P84233
E	102	ALA	GLY	conflict	UNP P84233
E	110	ALA	CYS	conflict	UNP P84233

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	83	Total 662	C 418	N 129	O 114	S 1	0	0	0
2	F	92	Total 730	C 457	N 149	O 123	S 1	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	18	ARG	HIS	engineered mutation	UNP P62799
F	18	ARG	HIS	engineered mutation	UNP P62799

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	111	Total 859	C 540	N 169	O 150	0	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	121	Total 931	C 583	N 183	O 165	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	99	ARG	GLY	conflict	UNP P06897
C	123	SER	ALA	conflict	UNP P06897
G	99	ARG	GLY	conflict	UNP P06897
G	123	SER	ALA	conflict	UNP P06897

- Molecule 4 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	100	Total 789	C 495	N 147	O 145	S 2	0	0	0
4	H	97	Total 767	C 481	N 142	O 142	S 2	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	32	THR	SER	conflict	UNP P02281
H	32	THR	SER	conflict	UNP P02281

- Molecule 5 is a DNA chain called DNA (147-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	147	Total 2972	C 1417	N 506	O 902	P 147	0	0	0

- Molecule 6 is a DNA chain called DNA (147-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	J	147	Total 3057	C 1439	N 607	O 864	P 147	0	0	0

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total 1	Cl 1	0	0
7	C	1	Total 1	Cl 1	0	0
7	E	1	Total 1	Cl 1	0	0
7	G	1	Total 1	Cl 1	0	0

• Molecule 8 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	E	1	Total 1	Mg 1	0	0

• Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	42	Total 42	O 42	0	0
9	B	40	Total 40	O 40	0	0
9	C	85	Total 85	O 85	0	0
9	D	90	Total 90	O 90	0	0
9	E	95	Total 95	O 95	0	0
9	F	102	Total 102	O 102	0	0
9	G	60	Total 60	O 60	0	0
9	H	56	Total 56	O 56	0	0
9	I	176	Total 176	O 176	0	0
9	J	190	Total 190	O 190	0	0

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.
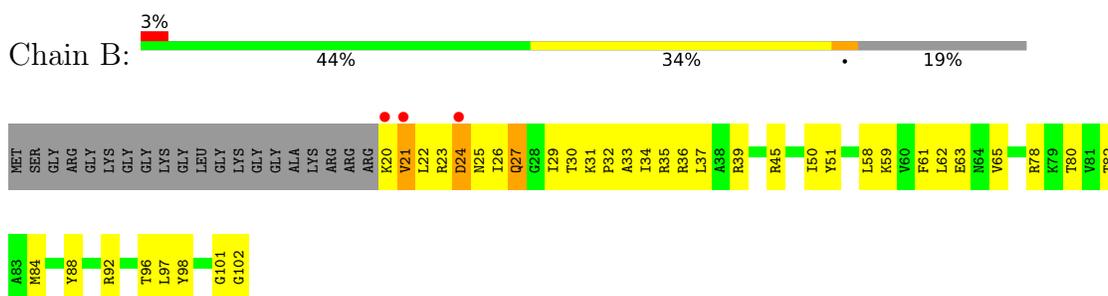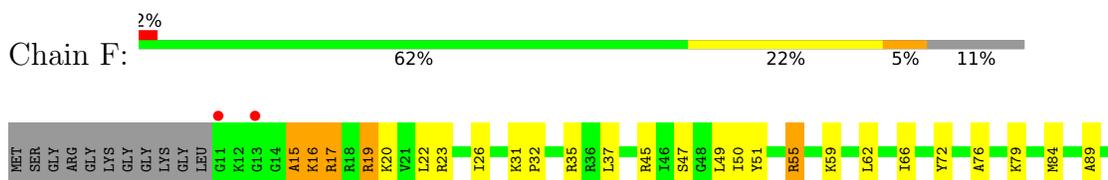
- Molecule 1: Histone H3.2
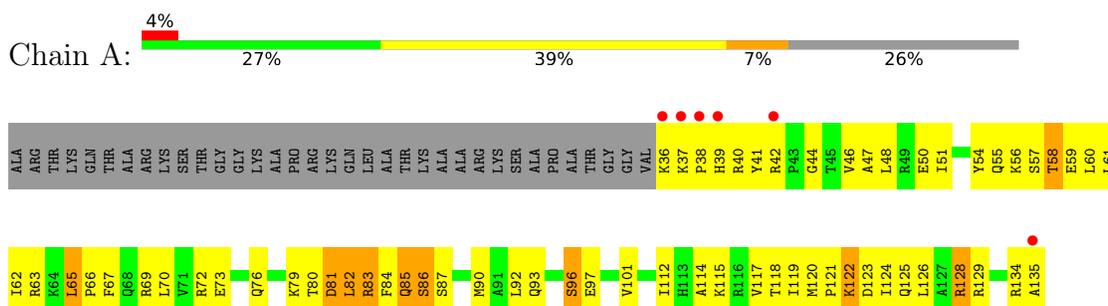
- Molecule 1: Histone H3.2

- Molecule 2: Histone H4
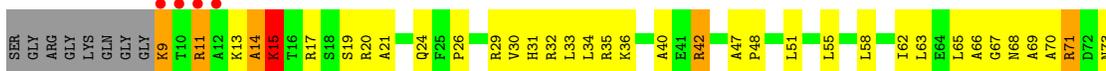

- Molecule 2: Histone H4

R92 Q93 G102

• Molecule 3: Histone H2A type 1

2%
Chain C: 57% 24% 5% 14%

SER GLY ARG GLY LYS GLN GLY LYS THR R11 K15 T16 R17 S18 S19 R20 P26 V27 G28 R29 V30 H31 R32 L33 L34 R35 K36 Y39 R42 V43 G44 G67 R71 D72 N73 K74 K75 T76 R77 I78 I79 P80 R81 H82 L83 Q84 R99 A103 Q104 G105

N110 K118 K119 T120 E121 SER LYS SER ALA LYS SER LYS

• Molecule 3: Histone H2A type 1

10%
Chain G: 41% 40% 11% 6%

SER GLY ARG GLY LYS GLN GLY K9 T10 R11 A12 K13 A14 K15 T16 R17 S18 S19 R20 A21 Q24 F25 P26 R29 V30 H31 R32 L33 L34 R35 K36 A40 E41 R42 A47 P48 L51 L55 L58 I62 L63 E64 L65 A66 G67 N68 A69 A70 R71 D72 N73

K74 K75 T76 R77 I78 I79 P80 R81 H82 L83 Q84 L85 E92 L93 N94 K95 T101 I102 A103 Q104 V107 L108 P109 N110 I111 Q112 S113 V114 L115 L116 P117 K118 K119 T120 E121 S122 S123 K124 S125 A126 K127 S128 K129

• Molecule 4: Histone H2B 1.1

4%
Chain D: 52% 24% 6% 18%

ALA LYS SER ALA PRO ALA PRO LYS LYS GLY SER LYS LYS ALA VAL THR LYS THR GLN LYS LYS ASP G26 K27 K28 R29 R30 K31 T32 R33 K34 E35 Y40 V44 L45 K46 Q47 V48 H49 T52 K57 A58 R72 S78 H82 Y83 N84 K85 R86 S87 T88 I89

R99 L100 L101 L102 P103 G104 E105 L106 K116 A117 V118 T119 K120 S123 A124 K125

• Molecule 4: Histone H2B 1.1

2%
Chain H: 30% 43% 7% 20%

ALA LYS SER ALA PRO ALA PRO LYS LYS GLY SER LYS LYS ALA VAL THR LYS THR GLN LYS LYS ASP GLY LYS LYS R29 R30 K31 T32 R33 K34 E35 Y40 V41 Y42 K43 V44 L45 K46 Q47 V48 H49 P50 G53 I54 S55 S56 K57 A58 I61 S64 F65 V66 N67 D68 V69

F70 E71 R79 N84 S87 T88 I89 T90 S91 R92 E93 I94 Q95 V98 L102 P103 G104 E105 L106 A107 K108 H109 A110 V111 S112 E113 G114 T115 K116 A117 V118 T119 K120 Y121 T122 S123 A124 K125

• Molecule 5: DNA (147-MER)

3%
Chain I: 23% 75% •

• Molecule 6: DNA (147-MER)

Chain J:
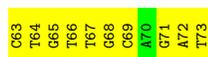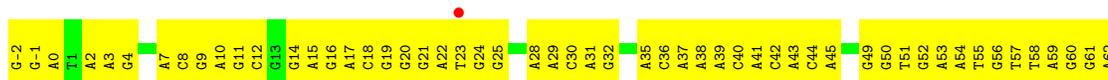
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	107.87Å　　178.91Å　　109.06Å 90.00°　　90.00°　　90.00°	Depositor
Resolution (Å)	29.68　–　2.63 29.63　–　2.63	Depositor EDS
% Data completeness (in resolution range)	94.2 (29.68-2.63) 94.5 (29.63-2.63)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.29 (at 2.64Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.175　,　0.252 0.178　,　0.255	Depositor DCC
R_{free} test set	3008 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	61.5	Xtriage
Anisotropy	0.628	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 77.2	EDS
L-test for twinning[2]	$< |L| > = 0.46, < L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.027 for l,-k,h	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	13349	wwPDB-VP
Average B, all atoms (Å^2)	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: MG, 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	A	0.56	0/837	0.76	0/1121
1	E	0.77	0/828	0.89	0/1110
2	B	0.58	0/669	0.77	0/894
2	F	0.80	0/737	0.92	0/980
3	C	0.65	0/869	0.79	0/1171
3	G	0.50	0/941	0.73	0/1264
4	D	0.78	2/800 (0.2%)	0.80	0/1070
4	H	0.62	0/778	0.76	1/1043 (0.1%)
5	I	0.47	1/3318 (0.0%)	0.72	1/5109 (0.0%)
6	J	0.47	1/3444 (0.0%)	0.70	0/5320
All	All	0.57	4/13221 (0.0%)	0.75	2/19082 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
5	I	0	2
6	J	0	2
All	All	0	5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	-73	DA	OP3-P	-7.11	1.52	1.61
5	I	-73	DA	OP3-P	-7.02	1.52	1.61
4	D	105	GLU	CG-CD	5.58	1.60	1.51
4	D	58	ALA	CA-CB	-5.38	1.41	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	H	104	GLY	N-CA-C	5.76	127.50	113.10
5	I	17	DG	OP2-P-O3'	5.54	117.38	105.20

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	41	TYR	Sidechain
5	I	26	DG	Sidechain
5	I	28	DA	Sidechain
6	J	-12	DG	Sidechain
6	J	-13	DT	Sidechain

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	825	0	871	105	0
1	E	816	0	858	49	0
2	B	662	0	709	67	0
2	F	730	0	788	40	0
3	C	859	0	921	49	0
3	G	931	0	1005	106	0
4	D	789	0	828	44	0
4	H	767	0	799	93	0
5	I	2972	0	1659	194	0
6	J	3057	0	1640	209	0
7	A	1	0	0	3	0
7	C	1	0	0	0	0
7	E	1	0	0	0	0
7	G	1	0	0	0	0
8	E	1	0	0	0	0
9	A	42	0	0	6	0
9	B	40	0	0	10	0
9	C	85	0	0	5	0
9	D	90	0	0	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	E	95	0	0	13	0
9	F	102	0	0	13	0
9	G	60	0	0	10	0
9	H	56	0	0	7	0
9	I	176	0	0	23	0
9	J	190	0	0	15	0
All	All	13349	0	10078	810	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 810 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:24:DC:H2"	5:I:25:DC:H5"	1.23	1.18
6:J:-51:DC:H2"	6:J:-50:DC:H5"	1.20	1.16
5:I:50:DG:H2"	5:I:51:DG:H5"	1.26	1.15
6:J:-48:DA:H2"	6:J:-47:DC:H5"	1.26	1.15
5:I:43:DT:H2"	5:I:44:DC:H5'	1.20	1.14

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	
1	A	98/135 (73%)	81 (83%)	12 (12%)	5 (5%)	2	2
1	E	97/135 (72%)	91 (94%)	6 (6%)	0	100	100
2	B	81/103 (79%)	67 (83%)	13 (16%)	1 (1%)	13	18
2	F	90/103 (87%)	82 (91%)	5 (6%)	3 (3%)	4	4
3	C	109/129 (84%)	92 (84%)	16 (15%)	1 (1%)	17	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	G	119/129 (92%)	85 (71%)	22 (18%)	12 (10%)	0	0
4	D	98/122 (80%)	90 (92%)	6 (6%)	2 (2%)	7	10
4	H	95/122 (78%)	82 (86%)	7 (7%)	6 (6%)	1	1
All	All	787/978 (80%)	670 (85%)	87 (11%)	30 (4%)	3	3

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	85	GLN
1	A	86	SER
4	D	85	LYS
3	G	11	ARG
3	G	14	ALA

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	86/109 (79%)	79 (92%)	7 (8%)	11	17
1	E	85/109 (78%)	80 (94%)	5 (6%)	19	30
2	B	68/79 (86%)	66 (97%)	2 (3%)	42	60
2	F	73/79 (92%)	71 (97%)	2 (3%)	44	63
3	C	88/101 (87%)	80 (91%)	8 (9%)	9	13
3	G	97/101 (96%)	87 (90%)	10 (10%)	7	9
4	D	85/102 (83%)	77 (91%)	8 (9%)	8	12
4	H	83/102 (81%)	77 (93%)	6 (7%)	14	21
All	All	665/782 (85%)	617 (93%)	48 (7%)	14	21

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	65	LEU

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Mol	Chain	Res	Type
3	G	80	PRO
1	E	78	PHE
3	G	9	LYS
3	G	92	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
3	G	73	ASN
4	H	49	HIS
4	H	84	ASN
4	H	47	GLN
4	D	82	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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 5 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	100/135 (74%)	0.22	6 (6%)	21	19	49, 81, 147, 175	0
1	E	99/135 (73%)	0.34	1 (1%)	82	81	36, 53, 98, 144	0
2	B	83/103 (80%)	0.14	3 (3%)	42	39	56, 77, 121, 170	0
2	F	92/103 (89%)	0.05	2 (2%)	62	58	35, 50, 93, 153	0
3	C	111/129 (86%)	0.04	3 (2%)	54	50	35, 57, 128, 190	0
3	G	121/129 (93%)	0.28	13 (10%)	6	4	55, 82, 177, 210	0
4	D	100/122 (81%)	0.14	5 (5%)	28	25	35, 60, 142, 173	0
4	H	97/122 (79%)	-0.23	2 (2%)	63	60	41, 77, 127, 151	0
5	I	147/147 (100%)	-0.19	4 (2%)	54	50	65, 136, 204, 227	0
6	J	147/147 (100%)	0.06	5 (3%)	45	41	64, 139, 200, 232	0
All	All	1097/1272 (86%)	0.08	44 (4%)	38	35	35, 78, 175, 232	0

The worst 5 of 44 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	120	THR	9.5
1	A	135	ALA	7.8
4	D	26	GLY	6.9
3	G	123	SER	6.6
3	G	9	LYS	5.7

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 (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, 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(Å^2)	Q<0.9
7	CL	E	201	1/1	0.89	0.15	54,54,54,54	1
7	CL	A	201	1/1	0.92	0.17	49,49,49,49	1
7	CL	G	201	1/1	0.94	0.18	62,62,62,62	1
7	CL	C	201	1/1	0.95	0.15	67,67,67,67	1
8	MG	E	202	1/1	0.98	0.21	33,33,33,33	0

6.5 Other polymers (i)

There are no such residues in this entry.

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