



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 29, 2021 – 12:33 AM JST

PDB ID : 7D8O
Title : Crystal structure of E. coli ToxIN type III toxin-antitoxin complex
Authors : Manikandan, P.; Rothweiler, U.; Singh, M.
Deposited on : 2020-10-08
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 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	:	2.25
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)	:	2.25

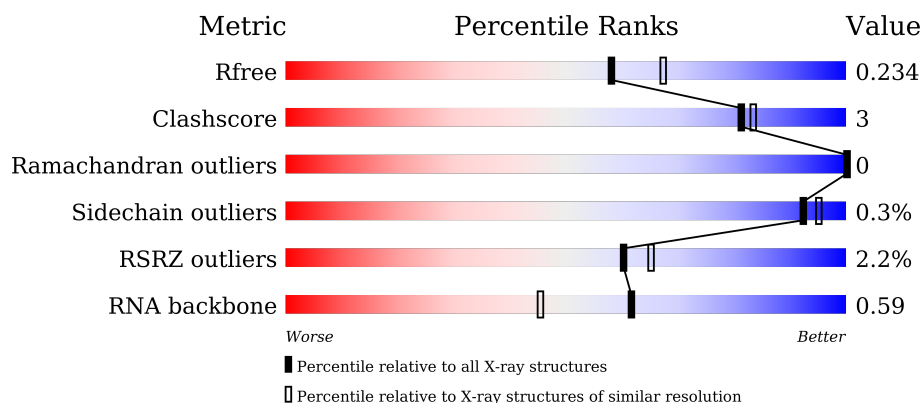
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)
RNA backbone	3102	1000 (2.54-1.66)

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	187	<div> <div>4%</div> <div> <div></div> <div>82%</div> <div>5%</div> <div>13%</div> </div> </div>
1	C	187	<div> <div>3%</div> <div> <div></div> <div>81%</div> <div>6%</div> <div>13%</div> </div> </div>
1	E	187	<div> <div>2%</div> <div> <div></div> <div>82%</div> <div>5%</div> <div>13%</div> </div> </div>
1	G	187	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>•</div> <div>13%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	I	187	<div><div><div></div><div></div><div></div></div><div><div>2%</div><div>80%</div><div>7%</div><div>13%</div></div></div>
1	K	187	<div><div><div></div><div></div><div></div></div><div><div>%</div><div>82%</div><div>5%</div><div>13%</div></div></div>
2	B	37	<div><div><div></div><div></div><div></div></div><div><div></div><div>81%</div><div>19%</div><div></div></div></div>
2	D	37	<div><div><div></div><div></div><div></div></div><div><div></div><div>62%</div><div>35%</div><div></div></div></div>
2	F	37	<div><div><div></div><div></div><div></div></div><div><div></div><div>84%</div><div>14%</div><div></div></div></div>
2	H	37	<div><div><div></div><div></div><div></div></div><div><div><div>3%</div></div><div>65%</div><div>32%</div><div></div></div></div>
2	J	37	<div><div><div></div><div></div><div></div></div><div><div><div>3%</div></div><div>76%</div><div>22%</div><div></div></div></div>
2	L	37	<div><div><div></div><div></div><div></div></div><div><div></div><div>78%</div><div>22%</div><div></div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13509 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 Type III toxin-antitoxin system ToxN/AbiQ family toxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	163	Total	C	N	O	S	0	0	0
			1314	851	215	243	5			
1	C	163	Total	C	N	O	S	0	0	0
			1318	854	216	243	5			
1	E	163	Total	C	N	O	S	0	0	0
			1317	853	215	243	6			
1	G	163	Total	C	N	O	S	0	0	0
			1321	856	216	243	6			
1	I	163	Total	C	N	O	S	0	0	0
			1314	851	215	243	5			
1	K	163	Total	C	N	O	S	0	0	0
			1321	856	216	243	6			

- Molecule 2 is a RNA chain called Antitoxin RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	37	Total	C	N	O	P	0	4	0
			851	381	148	282	40			
2	D	37	Total	C	N	O	P	0	4	0
			851	381	148	282	40			
2	F	37	Total	C	N	O	P	0	4	0
			851	381	148	282	40			
2	H	37	Total	C	N	O	P	0	4	0
			851	381	148	282	40			
2	J	37	Total	C	N	O	P	0	4	0
			851	381	148	282	40			
2	L	37	Total	C	N	O	P	0	4	0
			851	381	148	282	40			

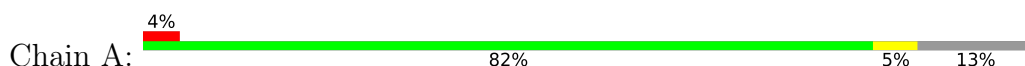
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	36	Total 36	O 36	0	0
3	B	40	Total 40	O 40	0	0
3	C	48	Total 48	O 48	0	0
3	D	30	Total 30	O 30	0	0
3	E	41	Total 41	O 41	0	0
3	F	32	Total 32	O 32	0	0
3	G	44	Total 44	O 44	0	0
3	H	50	Total 50	O 50	0	0
3	I	49	Total 49	O 49	0	0
3	J	33	Total 33	O 33	0	0
3	K	52	Total 52	O 52	0	0
3	L	43	Total 43	O 43	0	0

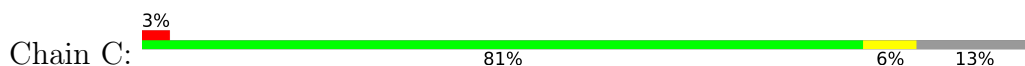
3 Residue-property plots [i](#)

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.

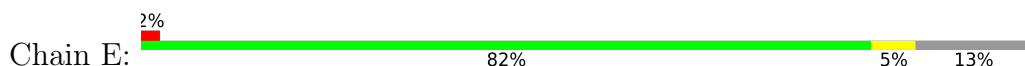
- Molecule 1: Type III toxin-antitoxin system ToxN/AbiQ family toxin



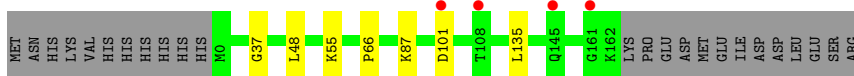
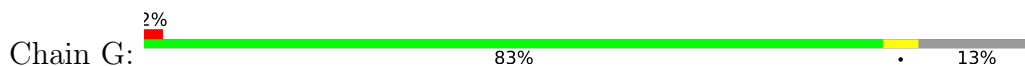
- Molecule 1: Type III toxin-antitoxin system ToxN/AbiQ family toxin



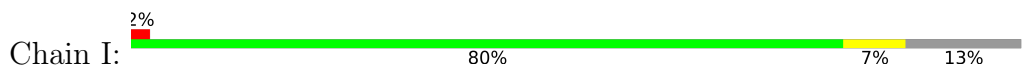
- Molecule 1: Type III toxin-antitoxin system ToxN/AbiQ family toxin



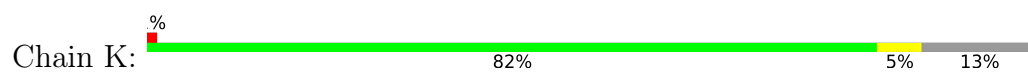
- Molecule 1: Type III toxin-antitoxin system ToxN/AbiQ family toxin



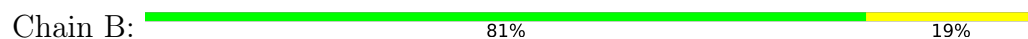
- Molecule 1: Type III toxin-antitoxin system ToxN/AbiQ family toxin



- Molecule 1: Type III toxin-antitoxin system ToxN/AbiQ family toxin



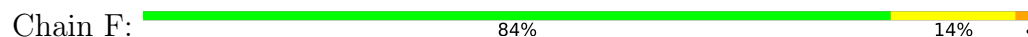
- Molecule 2: Antitoxin RNA



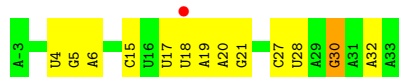
- Molecule 2: Antitoxin RNA



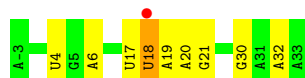
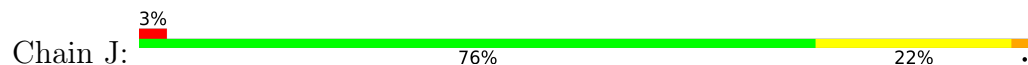
- Molecule 2: Antitoxin RNA



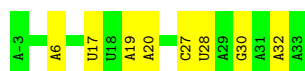
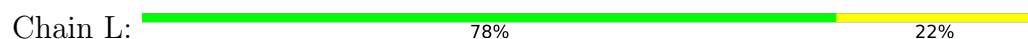
- Molecule 2: Antitoxin RNA



- Molecule 2: Antitoxin RNA



- Molecule 2: Antitoxin RNA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	86.63Å 86.64Å 123.57Å 90.00° 91.66° 90.00°	Depositor
Resolution (Å)	43.30 – 2.10 43.94 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.5 (43.30-2.10) 97.7 (43.94-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.32 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.213 , 0.232 0.213 , 0.234	Depositor DCC
R_{free} test set	2100 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.290	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 41.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -k,-h,-l 0.000 for k,h,-l 0.000 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13509	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 29.11 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.6398e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

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	0/1346	0.52	0/1818
1	C	0.31	0/1350	0.50	0/1822
1	E	0.30	0/1349	0.50	1/1821 (0.1%)
1	G	0.33	0/1353	0.53	0/1825
1	I	0.31	0/1346	0.49	0/1818
1	K	0.33	0/1353	0.51	0/1825
2	B	0.30	0/951	0.79	0/1479
2	D	0.34	0/951	0.89	0/1479
2	F	0.32	0/951	0.82	0/1479
2	H	0.33	0/951	0.86	0/1479
2	J	0.35	0/951	0.86	2/1479 (0.1%)
2	L	0.32	0/951	0.86	0/1479
All	All	0.32	0/13803	0.68	3/19803 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	145	GLN	CA-CB-CG	5.25	124.96	113.40
2	J	18[A]	U	P-O3'-C3'	5.23	125.98	119.70
2	J	18[B]	U	P-O3'-C3'	5.23	125.98	119.70

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	1314	0	1314	6	0
1	C	1318	0	1325	8	0
1	E	1317	0	1321	5	0
1	G	1321	0	1332	3	0
1	I	1314	0	1314	10	0
1	K	1321	0	1332	6	0
2	B	851	0	426	3	0
2	D	851	0	426	9	0
2	F	851	0	426	3	0
2	H	851	0	426	8	0
2	J	851	0	426	4	0
2	L	851	0	426	2	0
3	A	36	0	0	0	0
3	B	40	0	0	0	0
3	C	48	0	0	0	0
3	D	30	0	0	0	0
3	E	41	0	0	0	0
3	F	32	0	0	0	0
3	G	44	0	0	0	0
3	H	50	0	0	1	0
3	I	49	0	0	3	0
3	J	33	0	0	0	0
3	K	52	0	0	1	0
3	L	43	0	0	0	0
All	All	13509	0	10494	61	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 3.

All (61) 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:I:106:PRO:O	3:I:201:HOH:O	2.03	0.76
1:I:125:GLU:OE1	3:I:202:HOH:O	2.05	0.74
1:K:74:ASN:ND2	3:K:201:HOH:O	2.22	0.73
1:G:87:LYS:HA	1:G:135:LEU:HD21	1.82	0.61
2:B:33:A:OP2	1:C:55:LYS:NZ	2.34	0.58
1:K:87:LYS:HA	1:K:135:LEU:HD21	1.85	0.57
1:A:87:LYS:HA	1:A:135:LEU:HD21	1.88	0.56
1:K:37:GLY:HA3	1:K:48:LEU:HD22	1.89	0.55
1:E:87:LYS:HA	1:E:135:LEU:HD21	1.88	0.54
1:I:137:ASN:OD1	1:I:141:GLN:NE2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:87:LYS:HA	1:C:135:LEU:HD21	1.87	0.54
2:H:19[B]:A:O2'	2:H:20[B]:A:O4'	2.26	0.52
1:C:37:GLY:HA3	1:C:48:LEU:HD22	1.90	0.52
1:A:67:ALA:HA	1:A:135:LEU:HD13	1.92	0.51
2:J:18[B]:U:O2'	2:J:19[B]:A:OP1	2.24	0.51
1:G:37:GLY:HA3	1:G:48:LEU:HD22	1.92	0.51
1:E:67:ALA:HA	1:E:135:LEU:HD13	1.93	0.51
2:L:19[B]:A:O2'	2:L:20[B]:A:OP2	2.26	0.50
2:D:19[A]:A:H5''	2:D:19[A]:A:H8	1.76	0.50
1:A:37:GLY:HA3	1:A:48:LEU:HD22	1.94	0.50
1:I:87:LYS:HA	1:I:135:LEU:HD21	1.94	0.49
1:I:94:GLU:CD	1:I:94:GLU:H	2.17	0.48
2:D:30:G:C8	1:E:113:MET:HB2	2.49	0.48
2:D:18[B]:U:H3'	2:D:19[B]:A:H5''	1.94	0.48
1:I:62:LYS:NZ	3:I:203:HOH:O	2.07	0.47
2:H:30:G:C8	1:I:113:MET:HB2	2.50	0.47
2:D:15:C:O2'	2:D:19[B]:A:N3	2.41	0.47
1:E:37:GLY:HA3	1:E:48:LEU:HD22	1.96	0.47
1:I:67:ALA:HA	1:I:135:LEU:HD13	1.96	0.47
2:D:18[A]:U:H2'	2:D:18[A]:U:OP1	2.15	0.46
1:K:67:ALA:HA	1:K:135:LEU:HD13	1.97	0.46
2:L:27:C:H2'	2:L:28:U:O4'	2.16	0.45
1:A:135:LEU:HD12	1:A:144:MET:HG3	1.99	0.45
2:F:15:C:O2'	2:F:19[A]:A:N3	2.49	0.45
1:A:24:SER:C	1:A:25:GLU:HG2	2.37	0.45
2:H:4:U:H2'	2:H:21[A]:G:C8	2.53	0.44
1:A:113:MET:HB2	2:F:30:G:C8	2.52	0.44
2:F:15:C:O2'	2:F:19[B]:A:H1'	2.18	0.43
1:G:66:PRO:HB2	1:G:135:LEU:HB2	2.00	0.43
2:H:4:U:H2'	2:H:21[B]:G:C8	2.54	0.43
2:D:23:G:H2'	2:D:24:C:C6	2.53	0.43
1:I:6:ILE:HG12	1:I:97:VAL:HG12	2.01	0.43
2:J:19[B]:A:O2'	2:J:20[B]:A:O4'	2.37	0.43
1:C:11:ILE:HG21	1:C:24:SER:HB3	2.01	0.43
1:C:135:LEU:HD12	1:C:144:MET:HG3	2.01	0.43
1:C:57:TRP:CD2	2:D:-1:U:H4'	2.53	0.43
2:H:5:G:H5'	3:H:102:HOH:O	2.18	0.43
2:H:27:C:H2'	2:H:28:U:O4'	2.19	0.43
2:J:4:U:H2'	2:J:21[B]:G:C8	2.54	0.42
1:K:127:LYS:O	1:K:130:GLU:HB3	2.20	0.42
2:H:15:C:O2'	2:H:19[B]:A:N3	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:18[B]:U:H6	2:H:18[B]:U:OP1	2.02	0.42
2:B:19[B]:A:O2'	2:B:20[B]:A:OP2	2.30	0.42
1:I:11:ILE:HG21	1:I:24:SER:HB2	2.01	0.42
2:B:33:A:OP1	1:C:33:LYS:NZ	2.46	0.41
1:E:41:GLU:HA	1:E:45:HIS:O	2.21	0.41
2:D:10:G:H2'	2:D:11:C:C6	2.55	0.41
2:J:4:U:H2'	2:J:21[A]:G:C8	2.56	0.41
1:K:122:ARG:HA	1:K:125:GLU:HG3	2.02	0.40
2:D:27:C:H2'	2:D:28:U:O4'	2.21	0.40
1:C:67:ALA:HA	1:C:135:LEU:HD13	2.03	0.40

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	161/187 (86%)	159 (99%)	2 (1%)	0	100	100
1	C	161/187 (86%)	161 (100%)	0	0	100	100
1	E	161/187 (86%)	159 (99%)	2 (1%)	0	100	100
1	G	161/187 (86%)	159 (99%)	2 (1%)	0	100	100
1	I	161/187 (86%)	159 (99%)	2 (1%)	0	100	100
1	K	161/187 (86%)	160 (99%)	1 (1%)	0	100	100
All	All	966/1122 (86%)	957 (99%)	9 (1%)	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	145/171 (85%)	145 (100%)	0	100	100
1	C	146/171 (85%)	145 (99%)	1 (1%)	84	88
1	E	146/171 (85%)	146 (100%)	0	100	100
1	G	147/171 (86%)	145 (99%)	2 (1%)	67	73
1	I	145/171 (85%)	145 (100%)	0	100	100
1	K	147/171 (86%)	147 (100%)	0	100	100
All	All	876/1026 (85%)	873 (100%)	3 (0%)	92	95

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	162	LYS
1	G	55	LYS
1	G	101	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	K	30	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	31/37 (83%)	4 (12%)	1 (3%)
2	D	31/37 (83%)	4 (12%)	1 (3%)
2	F	31/37 (83%)	4 (12%)	1 (3%)
2	H	31/37 (83%)	4 (12%)	1 (3%)
2	J	31/37 (83%)	4 (12%)	1 (3%)
2	L	31/37 (83%)	4 (12%)	1 (3%)
All	All	186/222 (83%)	24 (12%)	6 (3%)

All (24) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	6	A
2	B	17	U
2	B	30	G
2	B	32	A
2	D	6	A
2	D	17	U
2	D	30	G
2	D	32	A
2	F	6	A
2	F	17	U
2	F	30	G
2	F	32	A
2	H	6	A
2	H	17	U
2	H	30	G
2	H	32	A
2	J	6	A
2	J	17	U
2	J	30	G
2	J	32	A
2	L	6	A
2	L	17	U
2	L	30	G
2	L	32	A

All (6) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	32	A
2	D	32	A
2	F	32	A
2	H	32	A
2	J	32	A
2	L	32	A

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 monosaccharides 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

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	163/187 (87%)	0.48	7 (4%) 35 41	21, 36, 59, 69	0
1	C	163/187 (87%)	0.55	5 (3%) 49 55	23, 33, 49, 70	0
1	E	163/187 (87%)	0.38	4 (2%) 57 62	24, 35, 53, 66	0
1	G	163/187 (87%)	0.43	4 (2%) 57 62	21, 32, 50, 69	0
1	I	163/187 (87%)	0.28	3 (1%) 68 72	22, 34, 49, 64	0
1	K	163/187 (87%)	0.40	2 (1%) 79 82	20, 32, 50, 66	0
2	B	37/37 (100%)	-0.33	0 100 100	27, 36, 54, 74	0
2	D	37/37 (100%)	-0.24	0 100 100	26, 36, 53, 73	0
2	F	37/37 (100%)	-0.29	0 100 100	28, 38, 56, 72	0
2	H	37/37 (100%)	-0.31	1 (2%) 54 60	27, 34, 56, 71	0
2	J	37/37 (100%)	-0.23	1 (2%) 54 60	29, 38, 59, 73	0
2	L	37/37 (100%)	-0.23	0 100 100	28, 33, 52, 68	0
All	All	1200/1344 (89%)	0.29	27 (2%) 60 65	20, 34, 54, 74	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	159	HIS	5.1
1	A	145	GLN	4.6
1	E	145	GLN	4.5
1	A	159	HIS	3.7
1	I	159	HIS	3.7
1	G	161	GLY	3.6
1	A	161	GLY	3.5
1	G	145	GLN	3.5
2	J	18[A]	U	3.2
1	E	159	HIS	3.1
1	G	101	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	E	17	PHE	3.0
1	C	145	GLN	2.7
1	E	142	GLY	2.6
1	A	28	THR	2.6
1	K	161	GLY	2.5
2	H	18[A]	U	2.4
1	I	160	PHE	2.3
1	C	161	GLY	2.3
1	I	17	PHE	2.2
1	K	143	ARG	2.2
1	C	162	LYS	2.2
1	A	160	PHE	2.1
1	A	29	TYR	2.1
1	G	108	THR	2.0
1	A	25	GLU	2.0
1	C	143	ARG	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 monosaccharides 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.