



wwPDB EM Validation Summary Report ⓘ

May 13, 2024 – 09:21 pm BST

PDB ID : 8RPZ
EMDB ID : EMD-19427
Title : Escherichia coli 50S subunit in complex with the antimicrobial peptide Api88
- conformation I
Authors : Lauer, S.; Nikolay, R.; Spahn, C.
Deposited on : 2024-01-17
Resolution : 2.44 Å(reported)

This is a wwPDB EM Validation Summary 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/EMValidationReportHelp>

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>.

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

EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

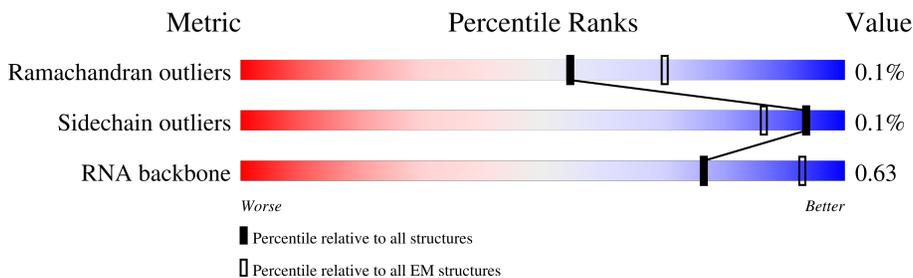
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.44 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)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	0	56	
2	1	50	
3	2	46	
4	3	64	
5	4	38	
6	6	66	
7	A	2903	
8	B	120	
9	C	271	

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Mol	Chain	Length	Quality of chain
10	D	209	100%
11	E	201	100%
12	F	177	100%
13	G	176	99%
14	H	149	100%
15	J	142	100%
16	K	122	100%
17	L	143	100%
18	M	136	100%
19	N	120	100%
20	O	116	100%
21	P	114	100%
22	Q	117	100%
23	R	103	99%
24	S	110	99%
25	T	93	100%
26	U	102	100%
27	V	94	100%
28	W	75	100%
29	X	77	100%
30	Y	63	100%
31	Z	58	100%
32	x	18	67% 6% 28%
32	y	18	83% 17%
32	z	18	89% 11%

2 Entry composition [i](#)

There are 32 unique types of molecules in this entry. The entry contains 90661 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	56	444	269	94	80	1	0	0

- Molecule 2 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	1	50	409	263	75	71	0	0

- Molecule 3 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	46	377	228	90	57	2	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	64	504	323	105	74	2	0	0

- Molecule 5 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	38	302	185	65	48	4	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	6	43	333	206	59	62	6	0	0

- Molecule 7 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	A	2900	62282	27783	11462	20136	2901	1	0

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	B	120	2572	1145	471	836	120	0	0

- Molecule 9 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	C	271	2082	1288	423	364	7	0	0

- Molecule 10 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	D	209	1565	979	288	294	4	0	0

- Molecule 11 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	E	201	1552	974	283	290	5	0	0

- Molecule 12 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	F	177	1410	899	249	256	6	0	0

- Molecule 13 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	G	176	1323	832	243	246	2	0	0

- Molecule 14 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	H	149	1111	699	197	214	1	0	0

- Molecule 15 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	J	142	1129	714	212	199	4	0	0

- Molecule 16 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	K	122	938	587	180	165	6	0	0

- Molecule 17 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	L	143	1045	649	206	189	1	0	0

- Molecule 18 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	M	136	1074	686	205	177	6	0	0

- Molecule 19 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	N	120	960	593	196	166	5	0	0

- Molecule 20 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
20	O	116	892	552	178	162	0	0

- Molecule 21 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	P	114	917	574	179	163	1	0	0

- Molecule 22 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	Q	117	947	604	192	151		0	0

- Molecule 23 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	R	103	816	516	153	145	2	0	0

- Molecule 24 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	S	110	868	538	170	157	3	1	0

- Molecule 25 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	T	93	738	466	139	131	2	0	0

- Molecule 26 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	U	102	779	492	146	141		0	0

- Molecule 27 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	V	94	753	479	137	134	3	0	0

- Molecule 28 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 29 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 30 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 31 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 32 is a protein called Apidaecins type 88.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	x	13	Total	C	N	O	0	0
			112	74	24	14		
32	y	15	Total	C	N	O	0	1
			121	80	26	15		
32	z	18	Total	C	N	O	0	1
			148	94	34	20		

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. 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. 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: Large ribosomal subunit protein bL32

Chain 0:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: Large ribosomal subunit protein bL33

Chain 1:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Large ribosomal subunit protein bL34

Chain 2:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: Large ribosomal subunit protein bL35

Chain 3:  100%

There are no outlier residues recorded for this chain.

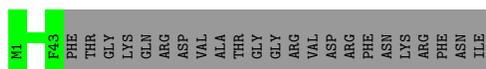
- Molecule 5: Large ribosomal subunit protein bL36A

Chain 4:  100%

There are no outlier residues recorded for this chain.

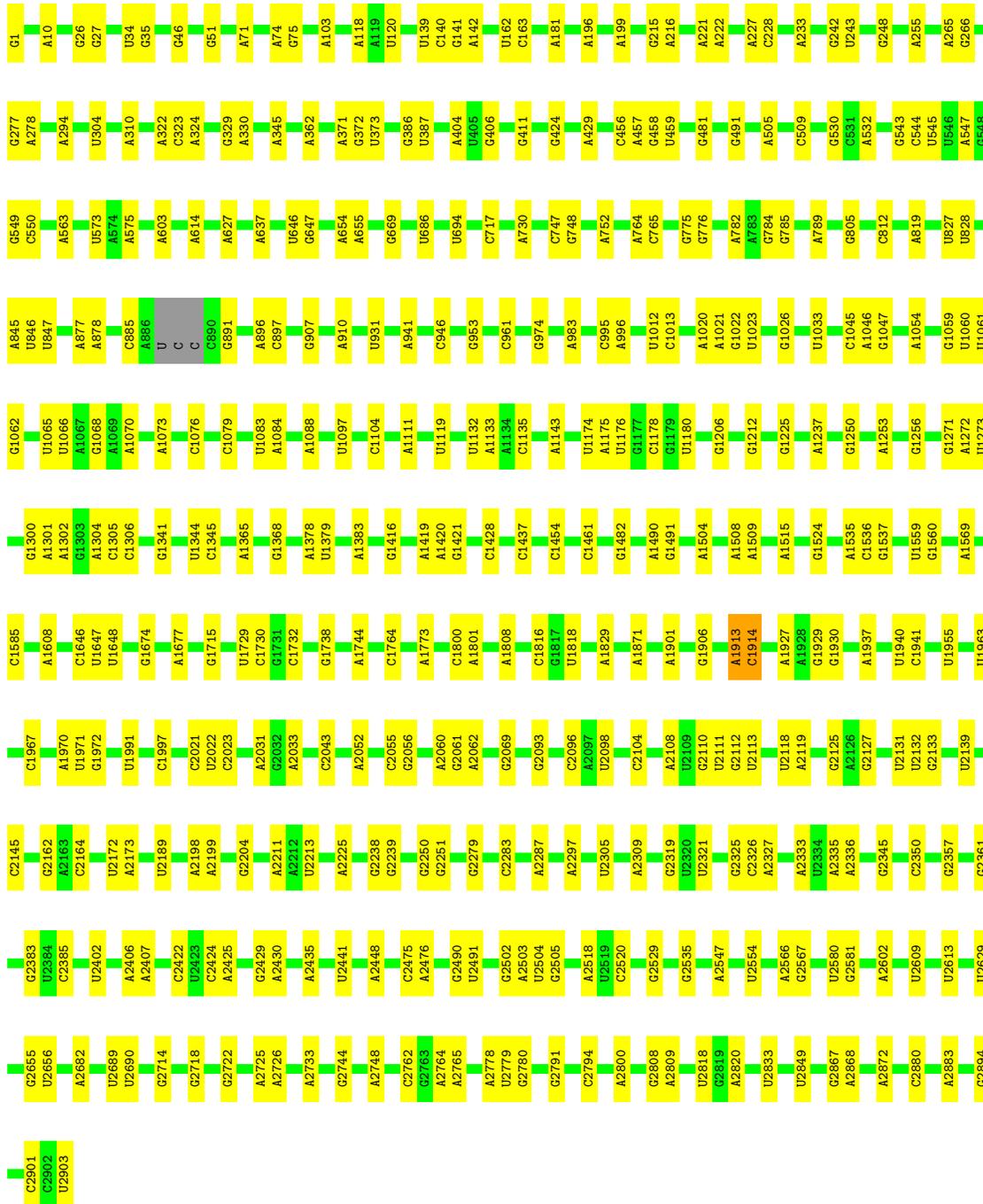
- Molecule 6: Large ribosomal subunit protein bL31

Chain 6:  65% 35%

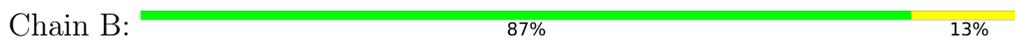


- Molecule 7: 23S ribosomal RNA

Chain A:  87% 13%



• Molecule 8: 5S ribosomal RNA



• Molecule 9: Large ribosomal subunit protein uL2



There are no outlier residues recorded for this chain.

- Molecule 10: Large ribosomal subunit protein uL3

Chain D:  100%

There are no outlier residues recorded for this chain.

- Molecule 11: Large ribosomal subunit protein uL4

Chain E:  100%

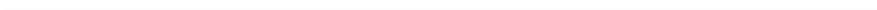


- Molecule 12: Large ribosomal subunit protein uL5

Chain F:  100%

There are no outlier residues recorded for this chain.

- Molecule 13: Large ribosomal subunit protein uL6

Chain G:  99%

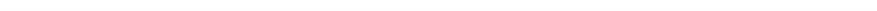


- Molecule 14: Large ribosomal subunit protein bL9

Chain H:  100%

There are no outlier residues recorded for this chain.

- Molecule 15: Large ribosomal subunit protein uL13

Chain J:  100%

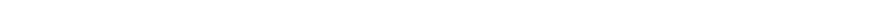
There are no outlier residues recorded for this chain.

- Molecule 16: Large ribosomal subunit protein uL14

Chain K:  100%

There are no outlier residues recorded for this chain.

- Molecule 17: Large ribosomal subunit protein uL15

Chain L:  100%

There are no outlier residues recorded for this chain.

- Molecule 18: Large ribosomal subunit protein uL16

Chain M:  100%

There are no outlier residues recorded for this chain.

- Molecule 19: Large ribosomal subunit protein bL17

Chain N:  100%

There are no outlier residues recorded for this chain.

- Molecule 20: Large ribosomal subunit protein uL18

Chain O:  100%

There are no outlier residues recorded for this chain.

- Molecule 21: Large ribosomal subunit protein bL19

Chain P:  100%

There are no outlier residues recorded for this chain.

- Molecule 22: Large ribosomal subunit protein bL20

Chain Q:  100%

There are no outlier residues recorded for this chain.

- Molecule 23: Large ribosomal subunit protein bL21

Chain R:  99%



- Molecule 24: Large ribosomal subunit protein uL22

Chain S:  99%



- Molecule 25: Large ribosomal subunit protein uL23

Chain T:  100%

There are no outlier residues recorded for this chain.

- Molecule 26: Large ribosomal subunit protein uL24

Chain U:  100%

There are no outlier residues recorded for this chain.

- Molecule 27: Large ribosomal subunit protein bL25

Chain V:  100%

There are no outlier residues recorded for this chain.

- Molecule 28: Large ribosomal subunit protein bL27

Chain W:  100%

There are no outlier residues recorded for this chain.

- Molecule 29: Large ribosomal subunit protein bL28

Chain X:  100%

There are no outlier residues recorded for this chain.

- Molecule 30: Large ribosomal subunit protein uL29

Chain Y:  100%

There are no outlier residues recorded for this chain.

- Molecule 31: Large ribosomal subunit protein uL30

Chain Z:  100%

There are no outlier residues recorded for this chain.

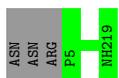
- Molecule 32: Apidaecins type 88

Chain x:  67% 6% 28%



- Molecule 32: Apidaecins type 88

Chain y:  83% 17%



- Molecule 32: Apidaecins type 88

Chain z:  89% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	260475	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	26	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

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: NH2

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	0	0.25	0/450	0.55	0/599
2	1	0.25	0/416	0.50	0/554
3	2	0.25	0/380	0.64	0/498
4	3	0.25	0/513	0.58	0/676
5	4	0.26	0/303	0.56	0/397
6	6	0.25	0/339	0.47	0/454
7	A	0.30	1/69756 (0.0%)	0.67	8/108822 (0.0%)
8	B	0.30	1/2876 (0.0%)	0.66	0/4483
9	C	0.26	0/2121	0.57	0/2852
10	D	0.27	0/1586	0.52	0/2134
11	E	0.25	0/1571	0.50	0/2113
12	F	0.25	0/1434	0.53	0/1926
13	G	0.24	0/1343	0.49	0/1816
14	H	0.25	0/1122	0.49	0/1515
15	J	0.26	0/1152	0.49	0/1551
16	K	0.26	0/947	0.59	0/1268
17	L	0.26	0/1054	0.59	0/1403
18	M	0.26	0/1093	0.55	0/1460
19	N	0.26	0/973	0.61	0/1301
20	O	0.25	0/902	0.54	0/1209
21	P	0.27	0/929	0.55	0/1242
22	Q	0.27	0/960	0.51	0/1278
23	R	0.26	0/829	0.54	0/1107
24	S	0.24	0/875	0.53	0/1170
25	T	0.25	0/744	0.51	0/994
26	U	0.28	0/787	0.53	0/1051
27	V	0.26	0/766	0.50	0/1025
28	W	0.26	0/582	0.56	0/769
29	X	0.25	0/635	0.57	0/848
30	Y	0.24	0/510	0.52	0/677
31	Z	0.25	0/453	0.53	0/605
32	x	0.33	0/119	0.62	0/165

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	y	0.28	0/127	0.58	0/175
32	z	0.39	0/154	0.69	0/212
All	All	0.29	2/98801 (0.0%)	0.64	8/148349 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1	G	OP3-P	-10.62	1.48	1.61
8	B	1	U	OP3-P	-10.59	1.48	1.61

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	1913	A	OP1-P-O3'	-11.07	80.84	105.20
7	A	1913	A	OP2-P-O3'	-9.17	85.03	105.20
7	A	1305	C	P-O3'-C3'	-9.04	108.85	119.70
7	A	1914	C	OP1-P-OP2	7.83	131.34	119.60
7	A	1344	U	P-O3'-C3'	-6.18	112.28	119.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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 PDB entries followed by that with respect to all EM entries.

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	0	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
2	1	48/50 (96%)	48 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	2	44/46 (96%)	44 (100%)	0	0	100	100
4	3	62/64 (97%)	60 (97%)	2 (3%)	0	100	100
5	4	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
6	6	41/66 (62%)	38 (93%)	3 (7%)	0	100	100
9	C	269/271 (99%)	257 (96%)	12 (4%)	0	100	100
10	D	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
11	E	199/201 (99%)	192 (96%)	6 (3%)	1 (0%)	29	34
12	F	175/177 (99%)	166 (95%)	9 (5%)	0	100	100
13	G	174/176 (99%)	167 (96%)	7 (4%)	0	100	100
14	H	147/149 (99%)	139 (95%)	8 (5%)	0	100	100
15	J	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
16	K	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
17	L	141/143 (99%)	128 (91%)	13 (9%)	0	100	100
18	M	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
19	N	118/120 (98%)	112 (95%)	6 (5%)	0	100	100
20	O	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
21	P	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
22	Q	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
23	R	101/103 (98%)	96 (95%)	4 (4%)	1 (1%)	15	16
24	S	109/110 (99%)	105 (96%)	4 (4%)	0	100	100
25	T	91/93 (98%)	88 (97%)	3 (3%)	0	100	100
26	U	100/102 (98%)	93 (93%)	7 (7%)	0	100	100
27	V	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
28	W	73/75 (97%)	72 (99%)	1 (1%)	0	100	100
29	X	75/77 (97%)	75 (100%)	0	0	100	100
30	Y	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
31	Z	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
32	x	11/18 (61%)	10 (91%)	1 (9%)	0	100	100
32	y	13/18 (72%)	10 (77%)	3 (23%)	0	100	100
32	z	16/18 (89%)	15 (94%)	0	1 (6%)	1	0
All	All	3248/3342 (97%)	3115 (96%)	130 (4%)	3 (0%)	54	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	R	54	VAL
11	E	83	VAL
32	z	13	PRO

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 PDB entries followed by that with respect to all EM entries.

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	0	47/47 (100%)	47 (100%)	0	100	100
2	1	45/45 (100%)	45 (100%)	0	100	100
3	2	38/38 (100%)	38 (100%)	0	100	100
4	3	51/51 (100%)	51 (100%)	0	100	100
5	4	34/34 (100%)	34 (100%)	0	100	100
6	6	40/59 (68%)	40 (100%)	0	100	100
9	C	216/216 (100%)	216 (100%)	0	100	100
10	D	164/164 (100%)	164 (100%)	0	100	100
11	E	165/165 (100%)	165 (100%)	0	100	100
12	F	148/148 (100%)	148 (100%)	0	100	100
13	G	137/137 (100%)	136 (99%)	1 (1%)	84	90
14	H	114/114 (100%)	114 (100%)	0	100	100
15	J	116/116 (100%)	116 (100%)	0	100	100
16	K	103/103 (100%)	103 (100%)	0	100	100
17	L	102/102 (100%)	102 (100%)	0	100	100
18	M	109/109 (100%)	109 (100%)	0	100	100
19	N	100/100 (100%)	100 (100%)	0	100	100
20	O	86/86 (100%)	86 (100%)	0	100	100
21	P	99/99 (100%)	99 (100%)	0	100	100
22	Q	89/89 (100%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	R	84/84 (100%)	84 (100%)	0	100	100
24	S	94/93 (101%)	93 (99%)	1 (1%)	73	83
25	T	80/80 (100%)	80 (100%)	0	100	100
26	U	83/83 (100%)	83 (100%)	0	100	100
27	V	78/78 (100%)	78 (100%)	0	100	100
28	W	57/57 (100%)	57 (100%)	0	100	100
29	X	67/67 (100%)	67 (100%)	0	100	100
30	Y	55/55 (100%)	55 (100%)	0	100	100
31	Z	48/48 (100%)	48 (100%)	0	100	100
32	x	13/17 (76%)	12 (92%)	1 (8%)	13	15
32	y	14/17 (82%)	14 (100%)	0	100	100
32	z	17/17 (100%)	16 (94%)	1 (6%)	19	25
All	All	2693/2718 (99%)	2689 (100%)	4 (0%)	93	96

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	G	21	GLN
24	S	110	ARG
32	x	15	HIS
32	z	12	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
7	A	2897/2903 (99%)	371 (12%)	15 (0%)
8	B	119/120 (99%)	13 (10%)	2 (1%)
All	All	3016/3023 (99%)	384 (12%)	17 (0%)

5 of 384 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	10	A

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Mol	Chain	Res	Type
7	A	26	G
7	A	27	G
7	A	34	U
7	A	35	G

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A	2808	G
8	B	66	A
7	A	1022	G
7	A	1378	A
7	A	1940	U

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](#)

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 Map visualisation

This section contains visualisations of the EMDB entry EMD-19427. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution

This section was not generated.

7.2 Volume estimate versus contour level

This section was not generated.

7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.