



## wwPDB EM Validation Summary Report ⓘ

Oct 12, 2024 – 08:30 AM EDT

PDB ID : 6VZ7  
EMDB ID : EMD-21486  
Title : Escherichia coli transcription-translation complex C1 (TTC-C1) containing a 27 nt long mRNA spacer, NusG, and fMet-tRNAs at P-site and E-site  
Authors : Molodtsov, V.; Wang, C.; Su, M.; Ebright, R.H.  
Deposited on : 2020-02-27  
Resolution : 7.00 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

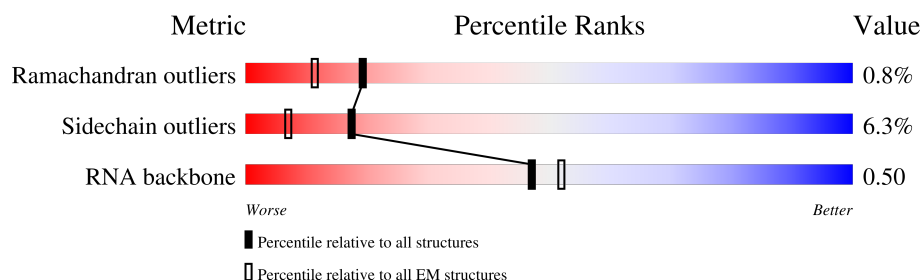
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 7.00 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.







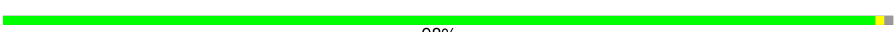







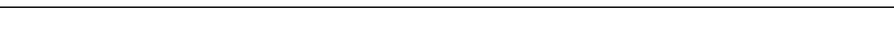

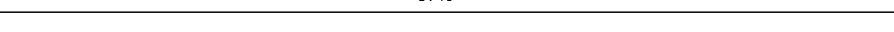
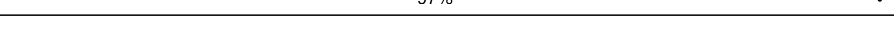
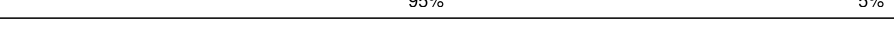
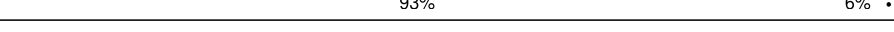
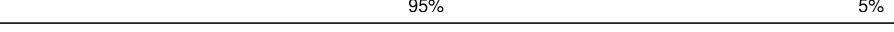
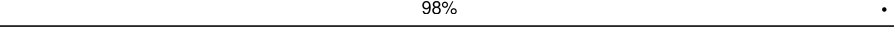
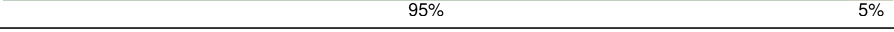

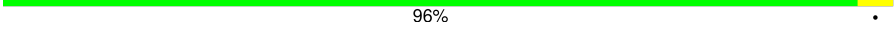

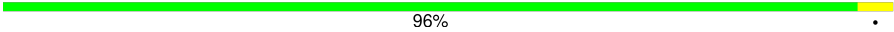
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	0	103	93% 7%
2	1	110	92% 8%
3	2	94	95% 5%
4	3	103	92% 8%
5	4	94	96% .
6	5	27	63% 22% 15%
7	6	27	85% 15%
8	7	16	44% 44% 12%
9	A	76	58% 38% .


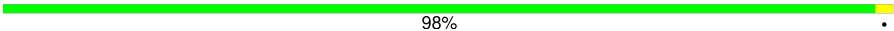
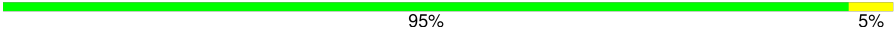



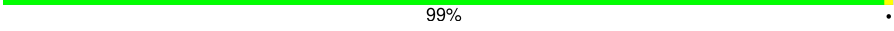
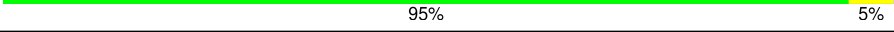

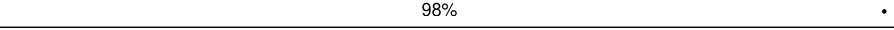
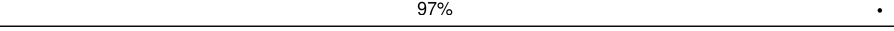
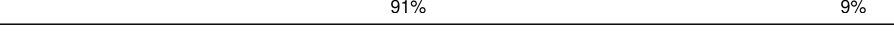
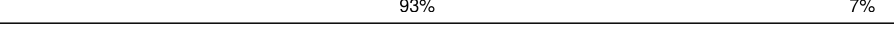

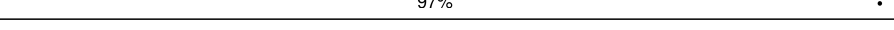
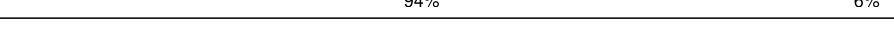
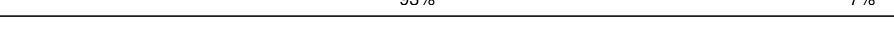
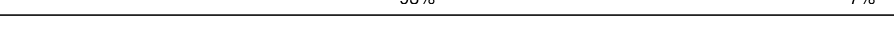

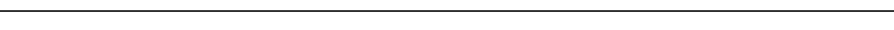

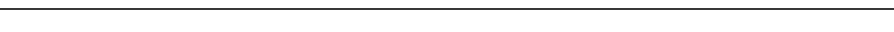
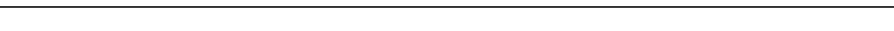


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Mol	Chain	Length	Quality of chain
9	B	76	 46%49%5%
10	AA	1341	 89%8%..
11	AB	112	 86%12%.
12	AC	230	 93%7%
12	AD	230	 98%..
13	AE	1358	 92%6%..
14	AF	83	 99%.
15	C	66	 97%.
16	D	1542	 78%20%..
17	E	86	 94%6%
18	F	70	 96%.
19	G	225	 96%.
20	H	557	 41%54%..
21	I	208	 97%.
22	J	205	 97%.
23	K	156	 95%5%
24	L	104	 93%6%.
25	M	151	 95%5%.
26	N	129	 98%.
27	O	127	 95%5%
28	P	99	 91%9%
29	Q	117	 96%.
30	R	123	 93%6%.
31	S	100	 96%.
32	T	88	 86%14%

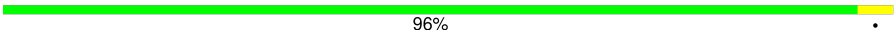
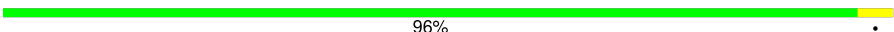


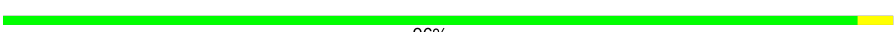

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Mol	Chain	Length	Quality of chain
33	U	82	 94% 6%
34	V	80	 98% .
35	W	83	 95% 5%
36	X	116	 90% 10%
37	Y	3	 33% 67%
38	a	2903	 81% 18% .
39	b	76	 99% .
40	c	77	 95% 5%
41	d	120	 86% 14%
42	e	62	 98% .
43	f	58	 97% .
44	g	66	 91% 9%
45	h	271	 93% 7%
46	i	56	 89% 11%
47	j	209	 97% .
48	k	52	 94% 6%
49	l	201	 93% 7%
50	m	46	 93% 7%
51	n	177	 90% 10%
52	o	64	 92% 8%
53	p	175	 98% .
54	q	38	 95% 5%
55	r	149	 93% 7%
56	s	142	 96% .
57	t	123	 95% 5%

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Mol	Chain	Length	Quality of chain
58	u	144	 96% .
59	v	136	 96% .
60	w	119	 93% 7%
61	x	116	 95% 5%
62	y	114	 96% .
63	z	117	 97% .

## 2 Entry composition

There are 65 unique types of molecules in this entry. The entry contains 299447 atoms, of which 125488 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 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	0	103	Total	C	H	N	O	S	0	0
			1655	516	839	153	145	2		

- Molecule 2 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1	110	Total	C	H	N	O	S	0	0
			1779	532	922	166	156	3		

- Molecule 3 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	2	94	Total	C	H	N	O	S	0	0
			1557	470	811	140	134	2		

- Molecule 4 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	3	103	Total	C	H	N	O		0	0
			1632	498	844	148	142			

- Molecule 5 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	4	94	Total	C	H	N	O	S	0	0
			1533	479	780	137	134	3		

- Molecule 6 is a DNA chain called NT DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	5	23	Total	C	H	N	O	P	0	0
			732	225	260	87	137	23		

- Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	6	27	Total	C	H	N	O	P	0	0
			848	259	306	89	167	27		

- Molecule 8 is a RNA chain called mRNA with 27 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	16	Total	C	H	N	O	P	0	0
			515	154	168	62	115	16		

- Molecule 9 is a RNA chain called E-site and P-site tRNA (fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
9	A	76	Total	C	H	N	O	P	0	0
			2446	723	826	295	527	75		
9	B	76	Total	C	H	N	O	P	0	0
			2433	723	813	295	527	75		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	U	deletion	GB 1848954948
B	?	-	U	deletion	GB 1848954948

- Molecule 10 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	AA	1322	Total	C	H	N	O	S	0	0
			20852	6539	10427	1817	2026	43		

- Molecule 11 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	AB	98	Total	C	H	N	O	S	0	0
			1573	505	783	139	140	6		

- Molecule 12 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AC	230	Total	C	H	N	O	S	0	0
			3599	1112	1813	317	351	6		

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Mol	Chain	Residues	Atoms						AltConf	Trace
12	AD	228	Total	C	H	N	O	S	0	0
			3556	1100	1789	312	349	6		

- Molecule 13 is a protein called DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AE	1335	Total	C	H	N	O	S	0	0
			20999	6526	10611	1854	1958	50		

- Molecule 14 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AF	83	Total	C	H	N	O	S	0	0
			1318	399	663	123	132	1		

- Molecule 15 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	C	66	Total	C	H	N	O	S	0	0
			1103	344	559	102	97	1		

- Molecule 16 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	D	1524	Total	C	H	N	O	P	0	0
			49126	14585	16423	6003	10591	1524		

- Molecule 17 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	E	86	Total	C	H	N	O	S	0	0
			1388	414	719	138	114	3		

- Molecule 18 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	F	70	Total	C	H	N	O	S	0	0
			1218	366	629	125	97	1		

- Molecule 19 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	G	225	Total	C	H	N	O	S	0	0
			3545	1113	1785	316	323	8		

- Molecule 20 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	H	259	Total	C	H	N	O	S	0	0
			3184	1073	1454	305	349	3		

- Molecule 21 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	I	208	Total	C	H	N	O	S	0	0
			3346	1036	1710	307	290	3		

- Molecule 22 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	J	205	Total	C	H	N	O	S	0	0
			3350	1026	1707	315	298	4		

- Molecule 23 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	K	156	Total	C	H	N	O	S	0	0
			2348	717	1196	217	212	6		

- Molecule 24 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	L	104	Total	C	H	N	O	S	0	0
			1694	536	846	153	152	7		

- Molecule 25 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	M	151	Total	C	H	N	O	S	0	0
			2416	735	1235	227	215	4		

- Molecule 26 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	N	129	Total	C	H	N	O	S	0	0
			2010	616	1031	173	184	6		

- Molecule 27 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	O	127	Total	C	H	N	O	S	0	0
			2092	634	1070	206	179	3		

- Molecule 28 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	P	99	Total	C	H	N	O	S	0	0
			1621	495	831	151	143	1		

- Molecule 29 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	Q	117	Total	C	H	N	O	S	0	0
			1764	540	887	174	160	3		

- Molecule 30 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	R	121	Total	C	H	N	O	S	0	0
			1940	580	1001	194	161	4		

- Molecule 31 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	S	100	Total	C	H	N	O	S	0	0
			1649	499	844	164	139	3		

- Molecule 32 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	T	88	Total	C	H	N	O	S	0	0
			1448	439	734	144	130	1		

- Molecule 33 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	U	82	Total	C	H	N	O	S	0	0
			1315	406	666	128	114	1		

- Molecule 34 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	V	80	Total	C	H	N	O	S	0	0
			1339	411	691	121	113	3		

- Molecule 35 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	W	83	Total	C	H	N	O	S	0	0
			1351	424	688	126	111	2		

- Molecule 36 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	X	116	Total	C	H	N	O	S	0	0
			1864	558	964	181	158	3		

- Molecule 37 is a RNA chain called mRNA in the ribosomal RNA entrance pore.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	Y	3	Total	C	H	N	O	P	0	0
			90	27	30	6	24	3		

- Molecule 38 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	a	2880	Total	C	H	N	O	P	0	0
			92918	27587	31077	11398	19976	2880		

- Molecule 39 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	b	76	Total	C	H	N	O	S	0	0
			1181	360	599	117	104	1		

- Molecule 40 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	c	77	Total	C	H	N	O	S	0	0
			1277	388	652	129	106	2		

- Molecule 41 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	d	120	Total	C	H	N	O	P	0	0
			3870	1144	1301	468	837	120		

- Molecule 42 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	e	62	Total	C	H	N	O	S	0	0
			1032	308	531	98	94	1		

- Molecule 43 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	f	58	Total	C	H	N	O	S	0	0
			936	281	488	87	78	2		

- Molecule 44 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	g	66	Total	C	H	N	O	S	0	0
			1042	323	520	99	94	6		

- Molecule 45 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	h	271	Total	C	H	N	O	S	0	0
			4236	1288	2154	423	364	7		

- Molecule 46 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	i	56	Total	C	H	N	O	S	0	0
			903	269	459	94	80	1		

- Molecule 47 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	j	209	Total	C	H	N	O	S	0	0
			3182	979	1617	288	294	4		

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	k	52	Total	C	H	N	O		0	0
			890	275	464	78	73			

- Molecule 49 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	l	201	Total	C	H	N	O	S	0	0
			3171	974	1619	283	290	5		

- Molecule 50 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	m	46	Total	C	H	N	O	S	0	0
			795	228	418	90	57	2		

- Molecule 51 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	n	177	Total	C	H	N	O	S	0	0
			2853	899	1443	249	256	6		

- Molecule 52 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	o	64	Total	C	H	N	O	S	0	0
			1076	323	572	105	74	2		

- Molecule 53 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	p	175	Total	C	H	N	O	S	0	0
			2671	826	1358	241	244	2		

- Molecule 54 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	q	38	Total	C	H	N	O	S	0	0
			645	185	343	65	48	4		

- Molecule 55 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	r	149	Total	C	H	N	O	S	0	0
			2259	699	1148	197	214	1		

- Molecule 56 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	s	142	Total	C	H	N	O	S	0	0
			2291	714	1162	212	199	4		

- Molecule 57 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	t	123	Total	C	H	N	O	S	0	0
			1969	593	1023	181	166	6		

- Molecule 58 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	u	144	Total	C	H	N	O	S	0	0
			2182	654	1129	207	190	2		

- Molecule 59 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	v	136	Total	C	H	N	O	S	0	0
			2231	686	1157	205	177	6		

- Molecule 60 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	w	119	Total	C	H	N	O	S	0	0
			1945	588	994	195	163	5		

- Molecule 61 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	x	116	Total	C	H	N	O	0	0
			1815	552	923	178	162		

- Molecule 62 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	y	114	Total	C	H	N	O	S	0	0
			1879	574	962	179	163	1		

- Molecule 63 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	z	117	Total	C	H	N	O	0	0
			1967	604	1020	192	151		

- Molecule 64 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
64	7	1	Total	Mg	0
			1	1	

- Molecule 65 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
65	AA	2	Total	Zn	0
			2	2	

### 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. 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.

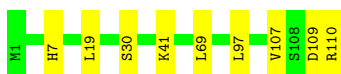
- Molecule 1: 50S ribosomal protein L21

Chain 0:  93% 7%



- Molecule 2: 50S ribosomal protein L22

Chain 1:  92% 8%



- Molecule 3: 50S ribosomal protein L23

Chain 2:  95% 5%



- Molecule 4: 50S ribosomal protein L24

Chain 3:  92% 8%



- Molecule 5: 50S ribosomal protein L25


Chain 4:  96% 4%

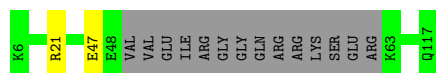


- Molecule 6: NT DNA

Chain 5:  63% 22% 15%



Chain AB:  86% 12%



- Molecule 12: DNA-directed RNA polymerase subunit alpha

Chain AC:  93% 7%



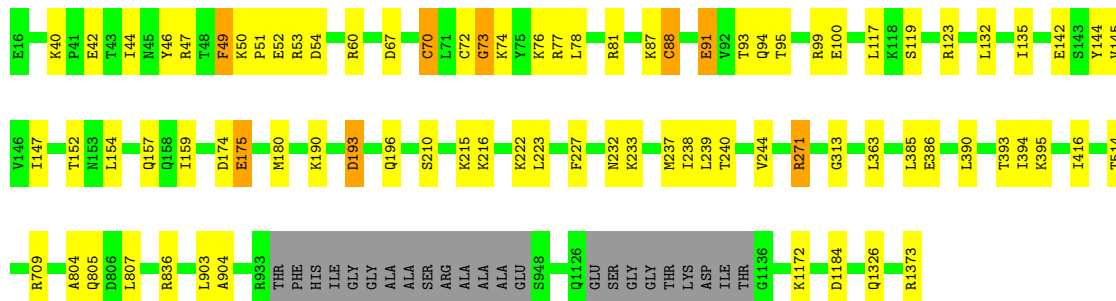
- Molecule 12: DNA-directed RNA polymerase subunit alpha

Chain AD:  98% ..



- Molecule 13: DNA-directed RNA polymerase subunit

Chain AE:  92% 6% ..



- Molecule 14: DNA-directed RNA polymerase subunit omega

Chain AF:  99% .




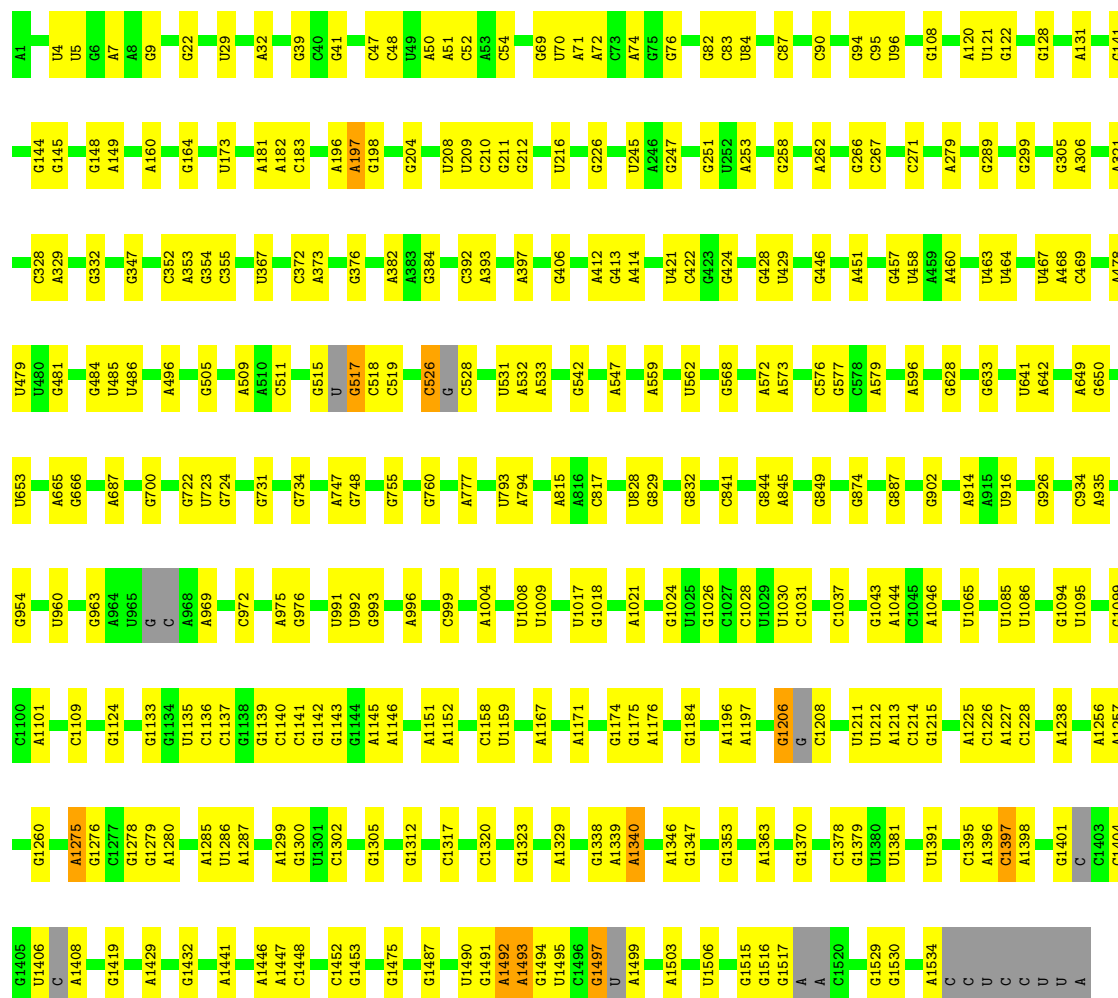
- Molecule 15: 30S ribosomal protein S18

Chain C:  97% .



- Molecule 16: 16S rRNA

Chain D:  78% 20% ..



- Molecule 17: 30S ribosomal protein S20

Chain E: 94% 6%



- Molecule 18: 30S ribosomal protein S21

Chain F: 96% 4%



- Molecule 19: 30S ribosomal protein S2

Chain G: 96% 4%





Chain M:  95% 5% •



- Molecule 26: 30S ribosomal protein S8

Chain N:  98% •



- Molecule 27: 30S ribosomal protein S9

Chain O:  95% 5%



- Molecule 28: 30S ribosomal protein S10

Chain P:  91% 9%



- Molecule 29: 30S ribosomal protein S11

Chain Q:  96% •



- Molecule 30: 30S ribosomal protein S12

Chain R:  93% 6% •




- Molecule 31: 30S ribosomal protein S14

Chain S:  96% •



- Molecule 32: 30S ribosomal protein S15

Chain T:  86% 14%



- Molecule 33: 30S ribosomal protein S16

Chain U:  94% 6%



- Molecule 34: 30S ribosomal protein S17

Chain V:  98% .



- Molecule 35: 30S ribosomal protein S19

Chain W:  95% 5%



- Molecule 36: 30S ribosomal protein S13

Chain X:  90% 10%




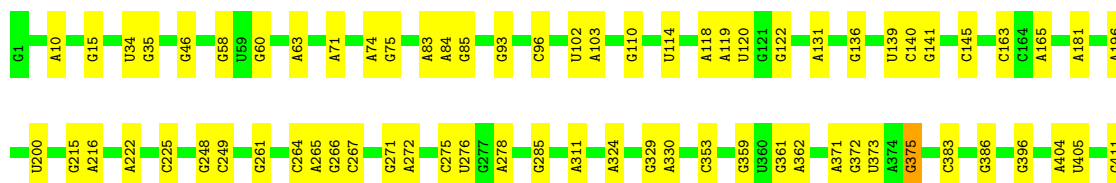
- Molecule 37: mRNA in the ribosomal RNA entrance pore

Chain Y:  33% 67%



- Molecule 38: 23S rRNA

Chain a:  81% 18%



G2722	C2512	U2372	A2198	U2113	A1965	C1833	U1584	A1395	U1119	U999	A819	G617	A412
A2726	A2513	A2376	G2204	G2115	C1967	U1894	U1589	U1406	G1122	C1005	U827	G618	C420
G2744	A2518	A2376	G2204	G2116	A1970	C1836	G1407	G1408	U1132	U1012	U828	A621	G424
A2748	G2383	G2385	U2210	U2117	G1972	A1847	A1508	U1411	A1133	C1013	A845	A627	C435
A2757	C2385	C2385	A2211	A2118	A1987	A1848	A1509	U1411	A1134	G1022	U846	A637	U451
A2758	C2385	C2385	A2212	U2122	A1991	A1868	A1610	C1414	C1136	U1023	U858	C645	C456
A2765	C2385	C2385	A2213	G2123	G1992	A1869	C1617	G1415	U1141	G1026	G859	G647	A457
G2777	C2385	C2385	C2226	G2125	U1993	A1869	6M2	G1416	A1142	U1033	A878	A654	A477
A2778	C2385	C2385	U2229	A2126	C1997	A1869	G1619	G1417	A1169	G1041	A878	A654	A477
A2791	C2385	C2385	U2238	G2127	G2002	A1869	U1647	A1419	C1170	G1045	A881	G664	G481
A2792	C2385	C2385	G2239	G2128	G2002	A1869	U1648	A1420	U1173	G1046	A881	G664	G481
C2793	C2385	C2385	U2243	U2131	U2022	A1870	G1649	C1428	U1174	G1047	A881	A668	G491
U2796	C2385	C2385	U2244	U2132	C2023	A1872	A1651	G1452	A1175	G1047	U884	A685	A501
U2797	C2385	C2385	U2245	G2133	G2027	A1873	G1674	A1453	U1176	G1047	C885	U686	A502
U2798	C2385	C2385	U2250	A2134	U2028	C1905	U1460	U1460	C1177	U1060	C888	U710	A503
A2799	C2385	C2385	U2251	U2139	G2029	C1906	A1677	U1460	C1178	U1061	C888	U710	A504
A2800	C2385	C2385	U2252	G2141	6M2	G1907	G1703	G1478	U1180	G1062	A891	C717	A505
G2801	C2385	C2385	U2252	G2141	G2031	G1907	G1703	G1478	U1180	G1062	A891	C717	A505
U2818	C2385	C2385	U2252	G2141	G2032	G1907	U1714	G1482	G1186	G1063	A892	C717	A505
G2819	C2385	C2385	U2252	G2141	A2033	PSU	G1715	G1482	G1186	G1063	A892	C717	A505
A2820	C2385	C2385	U2252	G2141	A2033	A1912	G1715	G1482	G1186	G1063	A892	C717	A505
A2823	C2385	C2385	U2252	G2141	A2033	A1913	G1715	G1482	G1186	G1063	A892	C717	A505
G2824	C2385	C2385	U2252	G2141	A2033	A1914	G1715	G1482	G1186	G1063	A892	C717	A505
G2825	C2385	C2385	U2252	G2141	A2033	A1915	G1715	G1482	G1186	G1063	A892	C717	A505
U2849	C2385	C2385	U2252	G2141	A2033	A1916	U1729	U1490	G1238	G1063	A892	C717	A505
A2850	C2385	C2385	U2252	G2141	A2033	A1917	C1730	U1490	G1238	G1063	A892	C717	A505
G2859	C2385	C2385	U2252	G2141	A2033	A1918	C1732	U1490	G1238	G1063	A892	C717	A505
U2860	C2385	C2385	U2252	G2141	A2033	A1919	C1732	U1490	G1238	G1063	A892	C717	A505
U2861	C2385	C2385	U2252	G2141	A2033	A1920	G1738	U1490	G1238	G1063	A892	C717	A505
G2867	C2385	C2385	U2252	G2141	A2033	A1921	G1750	U1490	G1238	G1063	A892	C717	A505
C2880	C2385	C2385	U2252	G2141	A2033	A1922	A1755	U1490	G1238	G1063	A892	C717	A505
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C2902	C2385	C2385	U2252	G2141	A2033	A1926	A1791	U1490	G1238	G1063	A892	C717	A505
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	C2385	C2385	U2252	G2141	A2033	A1987		U1490	G1238	G1063	A892	C717	A505
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	C2385	C2385	U2252	G2141	A2033	A1989		U1490	G1238	G1063	A892	C717	A505
	C2385	C2385	U2252	G2141	A2033	A1990		U1490					



- Molecule 40: 50S ribosomal protein L28

Chain c: 95% 5%



- Molecule 41: 5S rRNA

Chain d: 86% 14%



- Molecule 42: 50S ribosomal protein L29

Chain e: 98% .



- Molecule 43: 50S ribosomal protein L30

Chain f: 97% .



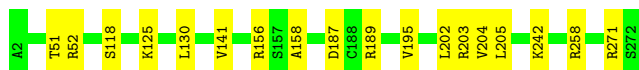
- Molecule 44: 50S ribosomal protein L31

Chain g: 91% 9%



- Molecule 45: 50S ribosomal protein L2

Chain h: 93% 7%



- Molecule 46: 50S ribosomal protein L32

Chain i: 89% 11%



- Molecule 47: 50S ribosomal protein L3

Chain j: 97%



- Molecule 48: 50S ribosomal protein L33

Chain k: 94%



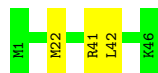
- Molecule 49: 50S ribosomal protein L4

Chain l: 93%



- Molecule 50: 50S ribosomal protein L34

Chain m: 93%



- Molecule 51: 50S ribosomal protein L5

Chain n: 90%



- Molecule 52: 50S ribosomal protein L35

Chain o: 92%



- Molecule 53: 50S ribosomal protein L6

Chain p: 98%



- Molecule 54: 50S ribosomal protein L36

Chain q: 95% 5%



- Molecule 55: 50S ribosomal protein L9

Chain r: 93% 7%



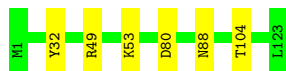
- Molecule 56: 50S ribosomal protein L13

Chain s: 96% .



- Molecule 57: 50S ribosomal protein L14

Chain t: 95% 5%



- Molecule 58: 50S ribosomal protein L15

Chain u: 96% .



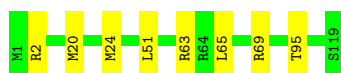
- Molecule 59: 50S ribosomal protein L16

Chain v: 96% .

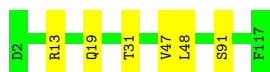


- Molecule 60: 50S ribosomal protein L17

Chain w: 93% 7%



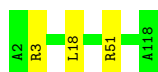
- Molecule 61: 50S ribosomal protein L18



- Molecule 62: 50S ribosomal protein L19



- Molecule 63: 50S ribosomal protein L20



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5979	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 ( $e^-/\text{\AA}^2$ )	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

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	0.38	0/829	0.67	0/1107
2	1	0.48	0/864	0.83	0/1156
3	2	0.42	0/752	0.71	0/1005
4	3	0.35	0/796	0.66	2/1062 (0.2%)
5	4	0.40	0/766	0.68	0/1025
6	5	1.13	6/528 (1.1%)	0.97	1/810 (0.1%)
7	6	1.11	4/603 (0.7%)	0.97	0/926
8	7	0.95	4/388 (1.0%)	1.04	0/604
9	A	0.39	0/1810	0.75	1/2821 (0.0%)
9	B	0.46	1/1810 (0.1%)	0.86	7/2821 (0.2%)
10	AA	0.58	2/10591 (0.0%)	0.77	19/14289 (0.1%)
11	AB	0.43	0/808	0.59	0/1088
12	AC	0.47	0/1808	0.61	1/2450 (0.0%)
12	AD	0.39	0/1789	0.56	0/2425
13	AE	0.52	3/10545 (0.0%)	0.66	5/14236 (0.0%)
14	AF	0.47	0/657	0.67	0/886
15	C	0.48	0/553	0.83	0/743
16	D	0.34	10/36610 (0.0%)	0.74	30/57091 (0.1%)
17	E	0.57	0/675	0.85	0/895
18	F	0.56	0/597	0.87	0/792
19	G	0.49	0/1791	0.71	0/2413
20	H	0.55	1/1746 (0.1%)	1.03	13/2382 (0.5%)
21	I	0.43	0/1663	0.71	0/2241
22	J	0.47	0/1665	0.73	0/2227
23	K	0.45	0/1165	0.75	0/1568
24	L	0.43	0/867	0.75	1/1171 (0.1%)
25	M	0.50	0/1195	0.81	0/1602
26	N	0.41	0/989	0.70	0/1326
27	O	0.43	0/1034	0.75	0/1375
28	P	0.43	0/800	0.75	0/1082
29	Q	0.40	0/893	0.70	0/1205
30	R	0.35	0/952	0.74	0/1274

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
31	S	0.49	0/817	0.79	0/1088
32	T	0.53	0/722	0.86	0/964
33	U	0.44	0/659	0.79	0/884
34	V	0.34	0/657	0.62	0/881
35	W	0.38	0/680	0.62	0/915
36	X	0.49	0/909	0.87	0/1215
37	Y	0.26	0/65	0.74	0/98
38	a	0.39	3/69247 (0.0%)	0.72	18/107985 (0.0%)
39	b	0.39	0/589	0.70	0/779
40	c	0.48	0/635	0.81	1/848 (0.1%)
41	d	0.30	0/2872	0.70	0/4478
42	e	0.54	0/502	0.83	0/667
43	f	0.45	0/452	0.78	0/605
44	g	0.43	0/531	0.68	0/709
45	h	0.39	0/2121	0.78	0/2852
46	i	0.40	0/450	0.79	0/599
47	j	0.44	0/1586	0.70	0/2134
48	k	0.35	0/433	0.65	0/576
49	l	0.46	0/1571	0.77	0/2113
50	m	0.53	0/380	0.99	0/498
51	n	0.49	0/1434	0.88	3/1926 (0.2%)
52	o	0.45	0/513	0.83	0/676
53	p	0.39	0/1333	0.67	0/1805
54	q	0.37	0/303	0.77	0/397
55	r	0.44	0/1122	0.69	0/1515
56	s	0.50	0/1152	0.75	0/1551
57	t	0.41	0/955	0.78	0/1279
58	u	0.40	0/1062	0.76	0/1413
59	v	0.47	0/1093	0.82	0/1460
60	w	0.52	0/964	0.87	0/1289
61	x	0.46	0/902	0.81	0/1209
62	y	0.41	0/929	0.72	1/1242 (0.1%)
63	z	0.60	0/960	0.91	0/1278
All	All	0.43	34/187139 (0.0%)	0.74	103/276026 (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
9	A	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	B	0	2
10	AA	0	12
13	AE	0	5
14	AF	0	1
20	H	0	3
36	X	0	1
All	All	0	26

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	D	1516	G	O3'-P	-13.47	1.45	1.61
16	D	1339	A	O3'-P	10.59	1.73	1.61
10	AA	374	GLU	C-N	10.38	1.53	1.34
13	AE	88	CYS	CB-SG	-10.14	1.65	1.82
6	5	109	DT	O3'-P	8.59	1.71	1.61

The worst 5 of 103 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	D	1516	G	P-O3'-C3'	-18.97	96.94	119.70
16	D	1516	G	O3'-P-O5'	13.77	130.17	104.00
10	AA	1007	LYS	O-C-N	-13.02	101.87	122.70
10	AA	1250	SER	C-N-CA	11.20	149.69	121.70
38	a	2252	G	N9-C1'-C2'	-10.97	99.74	114.00

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	A	19	G	Sidechain
9	A	7	G	Sidechain
10	AA	205	PRO	Peptide
10	AA	594	VAL	Peptide
10	AA	595	THR	Peptide

## 5.2 Too-close contacts

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

## 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 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	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	13	49
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
4	3	101/103 (98%)	96 (95%)	4 (4%)	1 (1%)	13	49
5	4	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
10	AA	1318/1341 (98%)	1145 (87%)	140 (11%)	33 (2%)	4	26
11	AB	94/112 (84%)	88 (94%)	6 (6%)	0	100	100
12	AC	228/230 (99%)	214 (94%)	12 (5%)	2 (1%)	14	52
12	AD	226/230 (98%)	212 (94%)	14 (6%)	0	100	100
13	AE	1329/1358 (98%)	1198 (90%)	122 (9%)	9 (1%)	19	57
14	AF	81/83 (98%)	74 (91%)	7 (9%)	0	100	100
15	C	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
17	E	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
18	F	68/70 (97%)	68 (100%)	0	0	100	100
19	G	223/225 (99%)	210 (94%)	13 (6%)	0	100	100
20	H	255/557 (46%)	189 (74%)	54 (21%)	12 (5%)	2	16
21	I	206/208 (99%)	196 (95%)	9 (4%)	1 (0%)	25	64
22	J	203/205 (99%)	198 (98%)	5 (2%)	0	100	100
23	K	154/156 (99%)	146 (95%)	7 (4%)	1 (1%)	22	60
24	L	102/104 (98%)	97 (95%)	4 (4%)	1 (1%)	13	49
25	M	149/151 (99%)	144 (97%)	4 (3%)	1 (1%)	19	57
26	N	127/129 (98%)	121 (95%)	5 (4%)	1 (1%)	16	55
27	O	125/127 (98%)	115 (92%)	9 (7%)	1 (1%)	16	55
28	P	97/99 (98%)	88 (91%)	8 (8%)	1 (1%)	13	49
29	Q	115/117 (98%)	104 (90%)	9 (8%)	2 (2%)	7	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	R	117/123 (95%)	116 (99%)	1 (1%)	0	100	100
31	S	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
32	T	86/88 (98%)	82 (95%)	4 (5%)	0	100	100
33	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	10	43
34	V	78/80 (98%)	74 (95%)	4 (5%)	0	100	100
35	W	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
36	X	114/116 (98%)	107 (94%)	5 (4%)	2 (2%)	7	35
39	b	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
40	c	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
42	e	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
43	f	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
44	g	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
45	h	269/271 (99%)	259 (96%)	9 (3%)	1 (0%)	30	68
46	i	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
47	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
48	k	50/52 (96%)	50 (100%)	0	0	100	100
49	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	25	64
50	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
51	n	175/177 (99%)	162 (93%)	11 (6%)	2 (1%)	12	47
52	o	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
53	p	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
54	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
55	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
56	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
57	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
58	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
59	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
60	w	117/119 (98%)	107 (92%)	10 (8%)	0	100	100
61	x	114/116 (98%)	108 (95%)	6 (5%)	0	100	100
62	y	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
63	z	115/117 (98%)	110 (96%)	4 (4%)	1 (1%)	14	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	9136/9618 (95%)	8457 (93%)	604 (7%)	75 (1%)	19	55

5 of 75 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	AA	596	ASP
10	AA	853	ASP
10	AA	859	GLU
10	AA	862	LEU
10	AA	937	ASP

### 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 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	84/84 (100%)	78 (93%)	6 (7%)	12	32
2	1	93/93 (100%)	84 (90%)	9 (10%)	6	22
3	2	81/81 (100%)	76 (94%)	5 (6%)	15	36
4	3	84/84 (100%)	78 (93%)	6 (7%)	12	32
5	4	78/78 (100%)	74 (95%)	4 (5%)	20	41
10	AA	1140/1156 (99%)	1043 (92%)	97 (8%)	8	27
11	AB	86/98 (88%)	84 (98%)	2 (2%)	45	64
12	AC	198/198 (100%)	184 (93%)	14 (7%)	12	32
12	AD	196/198 (99%)	194 (99%)	2 (1%)	73	82
13	AE	1120/1134 (99%)	1051 (94%)	69 (6%)	15	36
14	AF	70/70 (100%)	70 (100%)	0	100	100
15	C	57/57 (100%)	55 (96%)	2 (4%)	31	51
17	E	65/65 (100%)	60 (92%)	5 (8%)	10	30
18	F	60/60 (100%)	57 (95%)	3 (5%)	20	41
19	G	187/187 (100%)	178 (95%)	9 (5%)	21	43
20	H	137/461 (30%)	128 (93%)	9 (7%)	14	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	I	171/171 (100%)	165 (96%)	6 (4%)	31	51
22	J	172/172 (100%)	165 (96%)	7 (4%)	26	47
23	K	119/119 (100%)	112 (94%)	7 (6%)	16	37
24	L	91/91 (100%)	85 (93%)	6 (7%)	14	34
25	M	124/124 (100%)	116 (94%)	8 (6%)	14	35
26	N	104/104 (100%)	102 (98%)	2 (2%)	52	69
27	O	105/105 (100%)	100 (95%)	5 (5%)	21	43
28	P	86/86 (100%)	78 (91%)	8 (9%)	7	23
29	Q	90/90 (100%)	87 (97%)	3 (3%)	33	52
30	R	101/103 (98%)	94 (93%)	7 (7%)	13	33
31	S	83/83 (100%)	79 (95%)	4 (5%)	21	43
32	T	76/76 (100%)	64 (84%)	12 (16%)	2	10
33	U	65/65 (100%)	61 (94%)	4 (6%)	15	36
34	V	74/74 (100%)	72 (97%)	2 (3%)	40	58
35	W	72/72 (100%)	68 (94%)	4 (6%)	17	38
36	X	94/94 (100%)	85 (90%)	9 (10%)	7	22
39	b	58/58 (100%)	57 (98%)	1 (2%)	56	72
40	c	67/67 (100%)	64 (96%)	3 (4%)	23	45
42	e	54/54 (100%)	53 (98%)	1 (2%)	52	69
43	f	48/48 (100%)	46 (96%)	2 (4%)	25	46
44	g	59/59 (100%)	53 (90%)	6 (10%)	6	20
45	h	216/216 (100%)	199 (92%)	17 (8%)	10	29
46	i	47/47 (100%)	41 (87%)	6 (13%)	3	14
47	j	164/164 (100%)	157 (96%)	7 (4%)	25	46
48	k	47/47 (100%)	44 (94%)	3 (6%)	14	35
49	l	165/165 (100%)	151 (92%)	14 (8%)	8	27
50	m	38/38 (100%)	35 (92%)	3 (8%)	10	29
51	n	148/148 (100%)	134 (90%)	14 (10%)	7	22
52	o	51/51 (100%)	46 (90%)	5 (10%)	6	21
53	p	136/136 (100%)	132 (97%)	4 (3%)	37	56
54	q	34/34 (100%)	32 (94%)	2 (6%)	16	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	r	114/114 (100%)	104 (91%)	10 (9%)	8	25
56	s	116/116 (100%)	110 (95%)	6 (5%)	19	40
57	t	104/104 (100%)	98 (94%)	6 (6%)	17	38
58	u	103/103 (100%)	97 (94%)	6 (6%)	17	38
59	v	109/109 (100%)	103 (94%)	6 (6%)	18	39
60	w	99/99 (100%)	91 (92%)	8 (8%)	9	28
61	x	86/86 (100%)	80 (93%)	6 (7%)	12	32
62	y	99/99 (100%)	95 (96%)	4 (4%)	27	47
63	z	89/89 (100%)	87 (98%)	2 (2%)	47	65
All	All	7614/7984 (95%)	7136 (94%)	478 (6%)	17	36

5 of 478 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	G	132	LYS
57	t	80	ASP
28	P	25	ILE
56	s	57	LEU
62	y	27	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
10	AA	1010	GLN
10	AA	1013	GLN
19	G	18	HIS
36	X	105	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	D	1515/1542 (98%)	289 (19%)	35 (2%)
37	Y	2/3 (66%)	2 (100%)	0
38	a	2859/2903 (98%)	531 (18%)	0
41	d	119/120 (99%)	17 (14%)	0
8	7	15/16 (93%)	7 (46%)	0
9	A	75/76 (98%)	29 (38%)	6 (8%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	B	75/76 (98%)	35 (46%)	6 (8%)
All	All	4660/4736 (98%)	910 (19%)	47 (1%)

5 of 910 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	56	U
8	7	57	G
8	7	58	A
8	7	59	U
8	7	60	U

5 of 47 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	D	722	G
16	D	1211	U
16	D	793	U
16	D	1109	C
16	D	1213	A

## 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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 Map visualisation

This section contains visualisations of the EMDB entry EMD-21486. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 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.