



## wwPDB EM Validation Summary Report ⓘ

Mar 6, 2025 – 06:31 pm GMT

PDB ID : 6HRM  
EMDB ID : EMD-0261  
Title : E. coli 70S d2d8 stapled ribosome  
Authors : Schmied, W.H.; Tnimov, Z.; Uttamapinant, C.; Rae, C.D.; Fried, S.D.; Chin, J.W.  
Deposited on : 2018-09-27  
Resolution : 2.96 Å(reported)  
Based on initial model : 5MDZ

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.dev117  
Mogul : 1.8.4, CSD as541be (2020)  
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) : 2.41

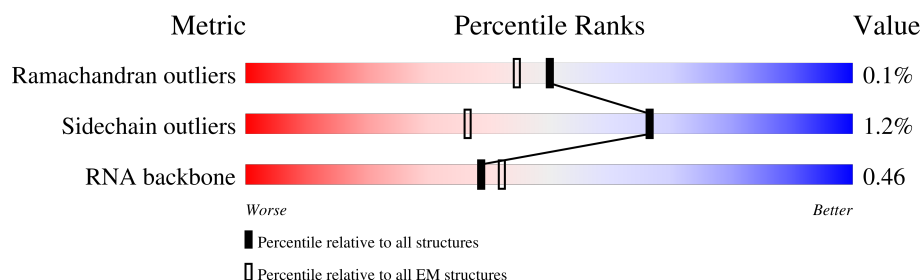
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.96 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.



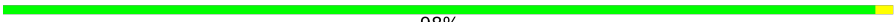
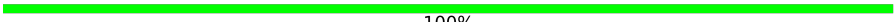
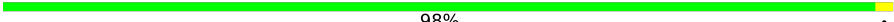
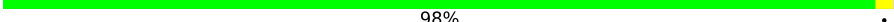


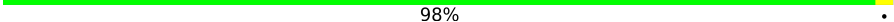
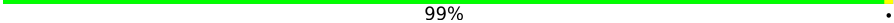
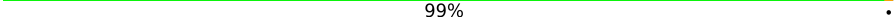
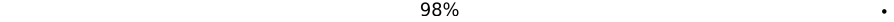
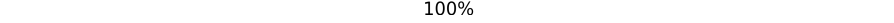
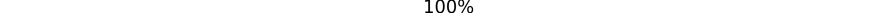
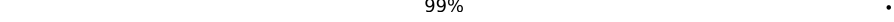
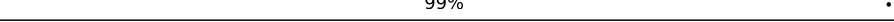
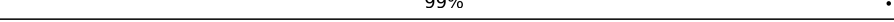
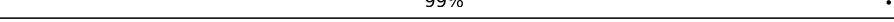
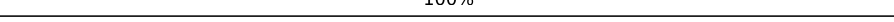
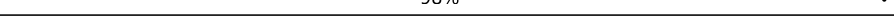
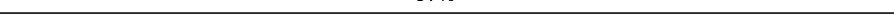






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	1	4458	72% 25% .
2	3	120	75% 23% .
3	B	271	98% .
4	C	209	99% .
5	D	201	99% .
6	E	177	98% .
7	F	175	98% .
8	G	149	98% ..
9	H	130	98% .

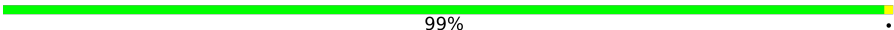
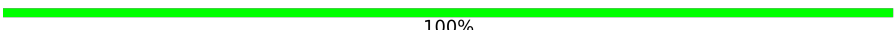
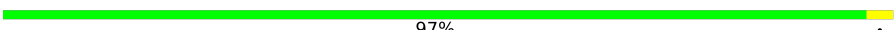
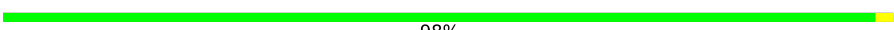
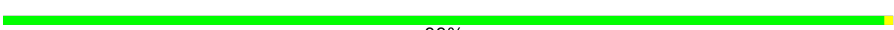





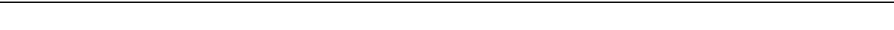

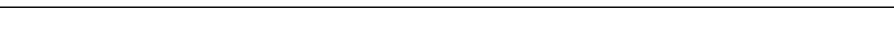

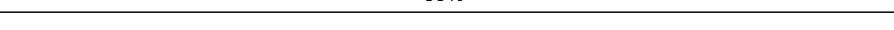
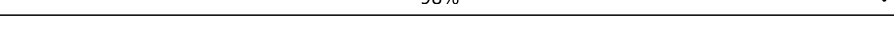
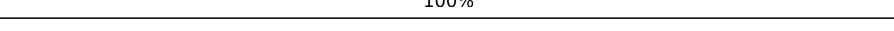
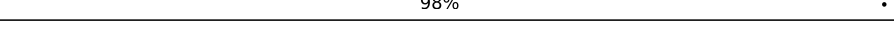
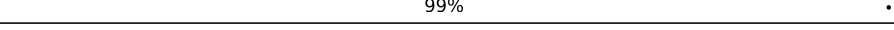
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Mol	Chain	Length	Quality of chain
10	I	135	 98% .
11	J	142	 100%
12	K	123	 98% .
13	L	144	 98% .
14	M	136	 100%
15	N	119	 100%
16	O	116	 98% .
17	P	114	 99% .
18	Q	117	 99% .
19	R	103	 98% .
20	S	110	 100%
21	T	94	 100%
22	U	103	 99% .
23	V	94	 99% .
24	W	76	 99% .
25	X	77	 99% .
26	Y	62	 100%
27	Z	58	 98% .
28	a	66	 97% .
29	b	56	 98% .
30	c	52	 98% .
31	d	46	 98% .
32	e	64	 95% 5%
33	f	38	 100%
34	g	225	 100%

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Mol	Chain	Length	Quality of chain
35	h	208	 99%
36	i	205	 100%
37	j	156	 97%
38	k	104	 98%
39	l	151	 99%
40	m	129	 98%
41	n	127	 98%
42	o	99	 99%
43	p	117	 98%
44	q	123	 98%
45	r	116	 100%
46	s	100	 100%
47	t	88	 95% 5%
48	u	82	 99%
49	v	80	 98%
50	w	66	 100%
51	x	83	 98%
52	y	86	 99%
53	z	70	 100%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	4OC	1	1402	X	-	-	-
1	1MG	1	2251	X	-	-	-
1	PSU	1	2252	X	-	-	-
1	5MU	1	2253	X	-	-	-
1	PSU	1	2461	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	6MZ	1	3124	X	-	-	-
1	PSU	1	3417	X	-	-	-
1	3TD	1	3421	X	-	-	-
1	PSU	1	3423	X	-	-	-
1	5MU	1	3445	X	-	-	-
1	6MZ	1	3536	X	-	-	-
1	G7M	1	3575	X	-	-	-
1	OMG	1	3757	X	-	-	-
1	PSU	1	3963	X	-	-	-
1	OMC	1	4004	X	-	-	-
1	2MA	1	4009	X	-	-	-
1	PSU	1	4010	X	-	-	-
1	OMU	1	4058	X	-	-	-
1	PSU	1	4086	X	-	-	-
1	PSU	1	4111	X	-	-	-
1	PSU	1	516	X	-	-	-
1	7MG	1	527	X	-	-	-

## 2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 145179 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 RNA chain called stapled 16S-23S rRNA,stapled 16S-23S rRNA,stapled 16S-23S rRNA,stapled 16S-23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	4450	Total	C	N	O	P	0	0
			95544	42634	17562	30898	4450		

There are 153 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1450	G	-	linker	GB 1370526422
1	1451	G	-	linker	GB 1370526422
1	1452	U	-	linker	GB 1370526422
1	1453	C	-	linker	GB 1370526422
1	1454	A	-	linker	GB 1370526422
1	1455	A	-	linker	GB 1370526422
1	1456	C	-	linker	GB 1370526422
1	1457	A	-	linker	GB 1370526422
1	1458	G	-	linker	GB 1370526422
1	1459	C	-	linker	GB 1370526422
1	1460	C	-	linker	GB 1370526422
1	1461	G	-	linker	GB 1370526422
1	1462	U	-	linker	GB 1370526422
1	1463	U	-	linker	GB 1370526422
1	1464	U	-	linker	GB 1370526422
1	1465	G	-	linker	GB 1370526422
1	1466	A	-	linker	GB 1370526422
1	1467	G	-	linker	GB 1370526422
1	1468	C	-	linker	GB 1370526422
1	1469	U	-	linker	GB 1370526422
1	1470	A	-	linker	GB 1370526422
1	1471	A	-	linker	GB 1370526422
1	1472	C	-	linker	GB 1370526422
1	1473	C	-	linker	GB 1370526422
1	1474	G	-	linker	GB 1370526422
1	1475	G	-	linker	GB 1370526422
1	1476	U	-	linker	GB 1370526422

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Chain	Residue	Modelled	Actual	Comment	Reference
1	1477	A	-	linker	GB 1370526422
1	1478	C	-	linker	GB 1370526422
1	1479	U	-	linker	GB 1370526422
1	1480	A	-	linker	GB 1370526422
1	1481	A	-	linker	GB 1370526422
1	1482	U	-	linker	GB 1370526422
1	1483	G	-	linker	GB 1370526422
1	1484	A	-	linker	GB 1370526422
1	1485	A	-	linker	GB 1370526422
1	1486	C	-	linker	GB 1370526422
1	1487	C	-	linker	GB 1370526422
1	1488	G	-	linker	GB 1370526422
1	1489	U	-	linker	GB 1370526422
1	1490	G	-	linker	GB 1370526422
1	1491	A	-	linker	GB 1370526422
1	1492	G	-	linker	GB 1370526422
1	1493	G	-	linker	GB 1370526422
1	1494	C	-	linker	GB 1370526422
1	1495	U	-	linker	GB 1370526422
1	1496	U	-	linker	GB 1370526422
1	1497	A	-	linker	GB 1370526422
1	1498	A	-	linker	GB 1370526422
1	1499	C	-	linker	GB 1370526422
1	1500	C	-	linker	GB 1370526422
1	1504	A	U	conflict	GB 1063812051
1	4358	A	-	expression tag	GB 1063812051
1	4359	C	-	expression tag	GB 1063812051
1	4360	G	-	expression tag	GB 1063812051
1	4361	G	-	expression tag	GB 1063812051
1	4362	A	-	expression tag	GB 1063812051
1	4363	C	-	expression tag	GB 1063812051
1	4364	A	-	expression tag	GB 1063812051
1	4365	U	-	expression tag	GB 1063812051
1	4366	G	-	expression tag	GB 1063812051
1	4367	G	-	expression tag	GB 1063812051
1	4368	U	-	expression tag	GB 1063812051
1	4369	U	-	expression tag	GB 1063812051
1	4370	G	-	expression tag	GB 1063812051
1	4371	G	-	expression tag	GB 1063812051
1	4372	A	-	expression tag	GB 1063812051
1	4373	G	-	expression tag	GB 1063812051
1	4374	G	-	expression tag	GB 1063812051

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Chain	Residue	Modelled	Actual	Comment	Reference
1	4375	G	-	expression tag	GB 1063812051
1	4376	C	-	expression tag	GB 1063812051
1	4377	G	-	expression tag	GB 1063812051
1	4378	C	-	expression tag	GB 1063812051
1	4379	U	-	expression tag	GB 1063812051
1	4380	U	-	expression tag	GB 1063812051
1	4381	A	-	expression tag	GB 1063812051
1	4382	C	-	expression tag	GB 1063812051
1	4383	C	-	expression tag	GB 1063812051
1	4384	A	-	expression tag	GB 1063812051
1	4385	C	-	expression tag	GB 1063812051
1	4386	U	-	expression tag	GB 1063812051
1	4387	U	-	expression tag	GB 1063812051
1	4388	U	-	expression tag	GB 1063812051
1	4389	G	-	expression tag	GB 1063812051
1	4390	U	-	expression tag	GB 1063812051
1	4391	G	-	expression tag	GB 1063812051
1	4392	A	-	expression tag	GB 1063812051
1	4393	U	-	expression tag	GB 1063812051
1	4394	U	-	expression tag	GB 1063812051
1	4395	C	-	expression tag	GB 1063812051
1	4396	A	-	expression tag	GB 1063812051
1	4397	U	-	expression tag	GB 1063812051
1	4398	G	-	expression tag	GB 1063812051
1	4399	A	-	expression tag	GB 1063812051
1	4400	C	-	expression tag	GB 1063812051
1	4401	U	-	expression tag	GB 1063812051
1	4402	G	-	expression tag	GB 1063812051
1	4403	G	-	expression tag	GB 1063812051
1	4404	G	-	expression tag	GB 1063812051
1	4405	G	-	expression tag	GB 1063812051
1	4406	U	-	expression tag	GB 1063812051
1	4407	G	-	expression tag	GB 1063812051
1	4408	A	-	expression tag	GB 1063812051
1	4409	A	-	expression tag	GB 1063812051
1	4410	G	-	expression tag	GB 1063812051
1	4411	U	-	expression tag	GB 1063812051
1	4412	C	-	expression tag	GB 1063812051
1	4413	G	-	expression tag	GB 1063812051
1	4414	UR3	-	expression tag	GB 1063812051
1	4415	A	-	expression tag	GB 1063812051
1	4416	A	-	expression tag	GB 1063812051

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Chain	Residue	Modelled	Actual	Comment	Reference
1	4417	C	-	expression tag	GB 1063812051
1	4418	A	-	expression tag	GB 1063812051
1	4419	A	-	expression tag	GB 1063812051
1	4420	G	-	expression tag	GB 1063812051
1	4421	G	-	expression tag	GB 1063812051
1	4422	U	-	expression tag	GB 1063812051
1	4423	A	-	expression tag	GB 1063812051
1	4424	A	-	expression tag	GB 1063812051
1	4425	C	-	expression tag	GB 1063812051
1	4426	C	-	expression tag	GB 1063812051
1	4427	G	-	expression tag	GB 1063812051
1	4428	U	-	expression tag	GB 1063812051
1	4429	A	-	expression tag	GB 1063812051
1	4430	G	-	expression tag	GB 1063812051
1	4431	G	-	expression tag	GB 1063812051
1	4432	2MG	-	expression tag	GB 1063812051
1	4433	G	-	expression tag	GB 1063812051
1	4434	MA6	-	expression tag	GB 1063812051
1	4435	MA6	-	expression tag	GB 1063812051
1	4436	C	-	expression tag	GB 1063812051
1	4437	C	-	expression tag	GB 1063812051
1	4438	U	-	expression tag	GB 1063812051
1	4439	G	-	expression tag	GB 1063812051
1	4440	C	-	expression tag	GB 1063812051
1	4441	G	-	expression tag	GB 1063812051
1	4442	G	-	expression tag	GB 1063812051
1	4443	U	-	expression tag	GB 1063812051
1	4444	U	-	expression tag	GB 1063812051
1	4445	G	-	expression tag	GB 1063812051
1	4446	G	-	expression tag	GB 1063812051
1	4447	A	-	expression tag	GB 1063812051
1	4448	U	-	expression tag	GB 1063812051
1	4449	C	-	expression tag	GB 1063812051
1	4450	A	-	expression tag	GB 1063812051
1	4451	C	-	expression tag	GB 1063812051
1	4452	C	-	expression tag	GB 1063812051
1	4453	U	-	expression tag	GB 1063812051
1	4454	C	-	expression tag	GB 1063812051
1	4455	C	-	expression tag	GB 1063812051
1	4456	U	-	expression tag	GB 1063812051
1	4457	U	-	expression tag	GB 1063812051
1	4458	A	-	expression tag	GB 1063812051

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 4 is a protein called 50S ribosomal protein L3.

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

- Molecule 5 is a protein called 50S ribosomal protein L4.

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

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 8 is a protein called 50S ribosomal protein L9.

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

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	130	Total	C	N	O	S	0	0
			980	620	174	182	4		

- Molecule 10 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	135	Total	C	N	O	S	0	0
			984	622	171	185	6		

- Molecule 11 is a protein called 50S ribosomal protein L13.

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

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 13 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 14 is a protein called 50S ribosomal protein L16.

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

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 16 is a protein called 50S ribosomal protein L18.

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

- Molecule 17 is a protein called 50S ribosomal protein L19.

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

- Molecule 18 is a protein called 50S ribosomal protein L20.

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

- Molecule 19 is a protein called 50S ribosomal protein L21.

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

- Molecule 20 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	U	103	Total	C	N	O	0	0
			788	498	148	142		

- Molecule 23 is a protein called 50S ribosomal protein L25.

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

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 25 is a protein called 50S ribosomal protein L28.

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

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 29 is a protein called 50S ribosomal protein L32.

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

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 31 is a protein called 50S ribosomal protein L34.

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

- Molecule 32 is a protein called 50S ribosomal protein L35.

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

- Molecule 33 is a protein called 50S ribosomal protein L36.

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

- Molecule 34 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 36 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 40 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	m	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 41 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	n	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 46 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 47 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	t	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 51 is a protein called 30S ribosomal protein S19.



Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	y	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 53 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	z	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 54 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	1	422	Total	Mg	0
			422	422	
54	3	8	Total	Mg	0
			8	8	
54	N	1	Total	Mg	0
			1	1	
54	P	1	Total	Mg	0
			1	1	
54	Q	1	Total	Mg	0
			1	1	
54	U	1	Total	Mg	0
			1	1	
54	b	1	Total	Mg	0
			1	1	
54	i	1	Total	Mg	0
			1	1	

- Molecule 55 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	a	1	Total	Zn	0
			1	1	
55	f	1	Total	Zn	0
			1	1	

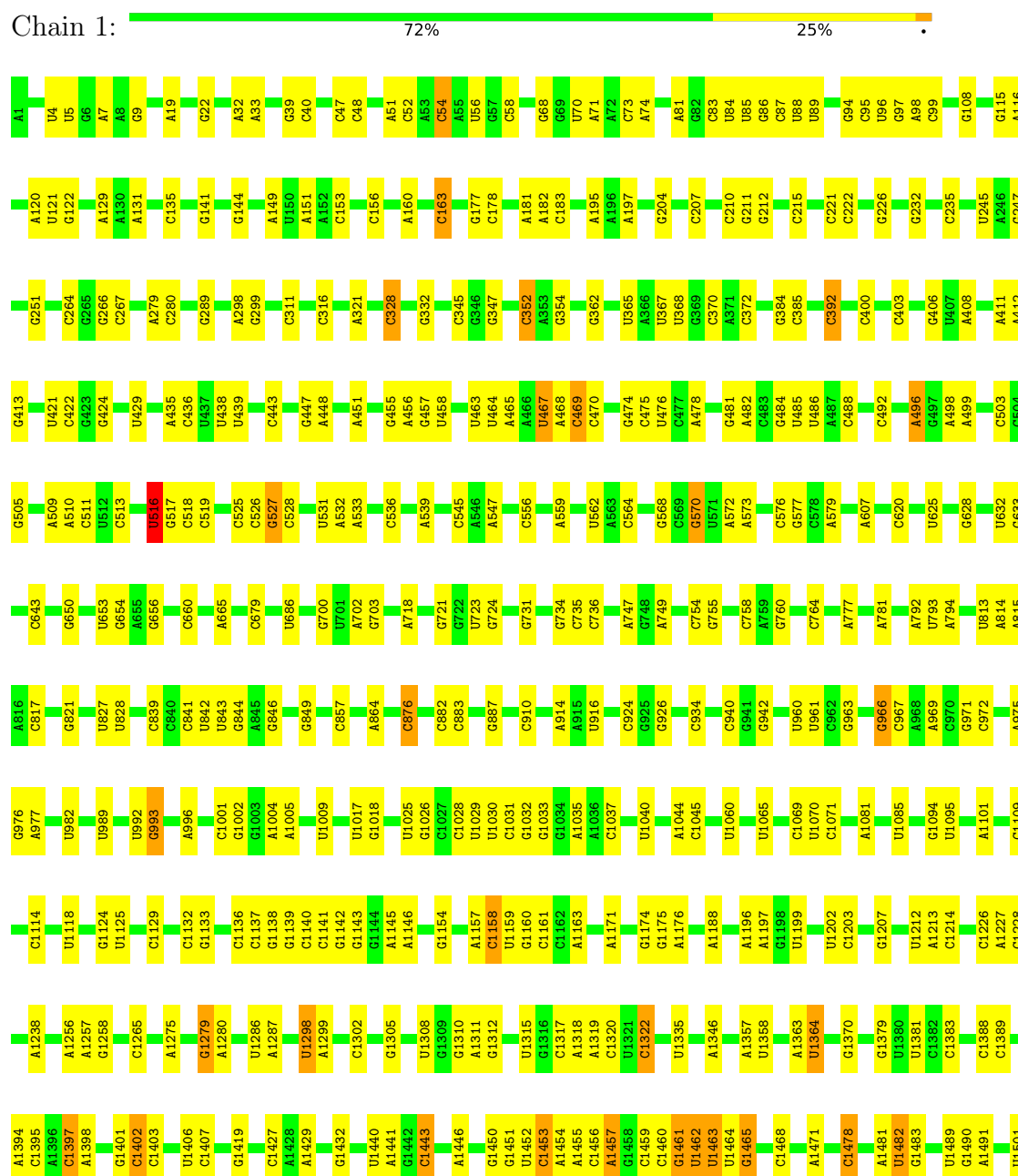
- Molecule 56 is water.

Mol	Chain	Residues	Atoms		AltConf
56	B	2	Total	O	0
			2	2	

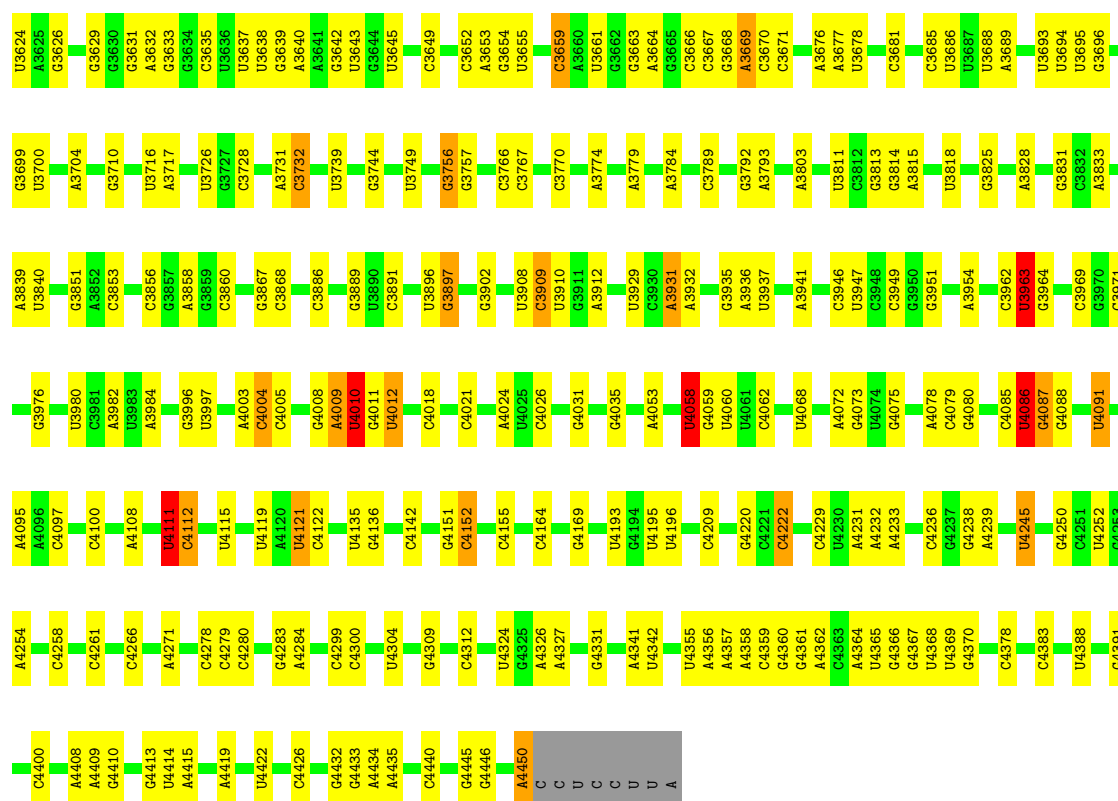
### 3 Residue-property plots

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: stapled 16S-23S rRNA, stapled 16S-23S rRNA, stapled 16S-23S rRNA, stapled 16S-23S rRNA



C3503	C3411	C3236	G3046	A2889	G2762	U2611	U2518	U2390	C2246	U2086	U1911	C1770	C1612	U1502
G3508	G3412	G3237	C3053	G2900	C2763	G2612	C2619	C2391	G2251	A2092	G1917	A1771	U1620	G1503
C3512	G3413	G3239	G3066	U2900	G2772	U2614	A2527	A2392	U2252	A2086	G1918	G1772	C1621	A1504
C3527	G3416	G3244	A3072	U2902	G2773	A2617	G2528	C2394	U2253	A2108	G1930	C1781	G1622	A1506
U3528	A3417	A3263	A3075	U2903	A2774	G2618	G2532	A2398	G2254	A2109	U1937	U1782	G1624	G1514
C3529	A3418	C3287	A3075	U2904	G2777	G2621	U2539	U2400	A2258	A2115	U1950	G1783	A1625	G1515
G3533	A3419	C3287	U3084	C2905	A2778	G2622	G2544	U2401	C2264	A2119	C1950	A1788	U1626	A1516
A3536	A3420	C3270	A3089	G2922	A2780	C2624	A2545	A2416	A2270	U2121	U1954	U1791	A1631	U1518
A3537	A3421	C3274	U3090	C2923	A2781	G2626	G2547	A2417	C2271	U2122	U1957	U1792	C1635	G1521
G3538	A3422	C3279	A3091	G2924	A2790	G2628	G2548	U2418	G2281	G2130	U1957	G1793	U1644	C1522
U3540	A3423	A3279	A3092	A2925	A2791	G2628	C2549	C2419	G2282	A2133	A1963	U1810	U1645	U1535
G3541	A3424	C3281	U3095	C2934	A2792	A2632	C2550	C2420	U2285	G2133	U1963	A1816	C1646	G1537
C3542	A3425	G3282	A3096	C2943	C2795	U2636	A2552	C2421	G2286	C2140	G1987	A1817	U1664	C1536
C3549	A3426	U3285	C3113	C2943	C2803	G2637	G2553	A2433	A2287	C2141	C1990	A1828	C1669	C1539
C3550	A3427	C3286	A3114	G2968	C2804	U2638	G2557	U2437	A2288	C2142	C1991	U1829	U1540	G1541
C3551	A3428	A3290	A3115	A2969	G2805	A2639	C2558	U2437	A2289	A2143	C1992	A1830	A1671	G1552
G3552	A3429	C3301	A3116	C2967	G2806	A2640	C2559	A2447	G2291	U2151	C1993	G1831	C1564	
C3553	A3430	G3282	A3096	C2968	A2807	G2642	A2560	C2482	C2292	G2152	C1996	U1676	U1677	A1555
C3561	A3431	U3286	C3113	C2969	U2819	U2636	G2561	A2483	A2295	G2153	G1997	G1835	A1585	U1596
G3562	A3432	C3307	A3114	C2969	C2820	A2648	A2562	A2483	U2296	C2156	G2002	A1836	A1687	U1596
C3563	A3433	A3308	A3115	G2984	C2821	A2648	G2563	U2461	C2297	U2159	G2002	A1838	A1687	A1588
C3566	A3434	C3314	A3116	C2987	A2807	A2642	G2564	U2462	A2298	U2160	A2009	A1840	C1698	G1564
G3567	A3435	G3317	A3140	G2988	A2827	G2642	C2565	C2487	C2299	A2161	A2010	C1849	A1702	C1567
A3568	A3436	C3322	C3150	A2996	U2830	A2675	U2572	C2470	G2311	A2174	A2014	A1850	A1703	C1572
G3575	A3437	G3323	C3150	C2999	U2835	G2676	A2573	C2471	C2312	G2175	C2015	A1851	A1705	C1572
C3578	A3438	C3328	U3153	C3003	C2836	G2677	G2574	G2480	C2318	A2176	C2016	G1862	G1711	C1575
C3579	A3439	C3339	U3154	U3004	U2846	C2678	A2576	A2489	C2321	C2186	U2017	G1867	C1715	G1576
G3599	A3440	A3335	G3155	C3004	U2850	U2679	G2577	A2490	C2322	A2191	G2018	A1868	C1716	A1577
C3602	A3441	C3340	G3156	C3009	C2851	A2681	A2579	C2491	C2323	U2192	A2035	G1869	C1717	U1578
U3605	A3442	U3340	G3157	A3009	C2854	U2682	U2584	C2492	A2325	C2193	G2037	G1876	G1721	A1579
G3606	A3443	C3342	C3173	C3013	C2855	G2684	C2585	C2493	U2333	G2202	A2038	A1877	A1722	A1580
A3607	A3444	A3353	A3175	A3015	C2858	C2684	G2589	A2495	U2334	U2208	C2050	G1878	C1722	G1581
G3608	A3445	A3354	C3176	G3016	U2858	G2692	A2590	C2496	C2343	U2216	U2051	A1881	A1728	C1582
C3611	A3446	A3354	C3176	A3021	C2868	A2710	A2590	C2497	C2344	U2216	U2052	G1881	C1728	C1585
U3612	A3447	U3370	G3180	A3022	C2874	G2718	A2601	C2501	U2352	G2232	A2069	C1889	C1745	G1586
G3613	A3448	C3376	C3181	A3028	G2874	G2742	A2602	A2502	A2351	C2233	C2071	G1892	C1745	A1590
A3614	A3449	C3377	C3197	U3029	G2874	G2744	A2603	G2503	U2352	G2236	A2069	C1899	C1745	G1594
G3616	A3450	C3378	G3221	C3030	G2880	U2745	A2604	C2504	U2353	G2236	C2071	G1902	G1754	C1603
U3619	A3451	G3379	U3040	C3039	G2881	G2746	A2605	G2505	U2354	A2236	C2071	G1902	G1754	A1607
A3620	A3452	C3380	C3232	A3041	C2882	U2746	G2605	C2512	A2383	C2242	U2079	U1905	G1755	U1608
G3621	A3453	C3385	C3233	A3042	C2882	G2756	C2606	C2513	A2388	G2243	A2080	G1756	G1756	U1609
G3622	A3454	C3386	C3234	C3043	U2885	G2756	U2607	A2514	G2388	G2244	A2081	C1759	C1759	A1610
A3623	A3455	A3406	U3235	C3043	G2886	A2759	C2610	A2515	G2389	A2245				C1611



• Molecule 2: 5S ribosomal RNA

Chain 3: 75% 23%



• Molecule 3: 50S ribosomal protein L2

Chain B: 98%



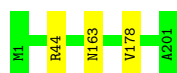
• Molecule 4: 50S ribosomal protein L3

Chain C: 99%



• Molecule 5: 50S ribosomal protein L4

Chain D: 99%



- Molecule 6: 50S ribosomal protein L5

Chain E:  98% .



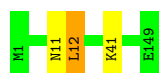
- Molecule 7: 50S ribosomal protein L6

Chain F:  98% .



- Molecule 8: 50S ribosomal protein L9

Chain G:  98% ..



- Molecule 9: 50S ribosomal protein L10

Chain H:  98% .



- Molecule 10: 50S ribosomal protein L11

Chain I:  98% .



- Molecule 11: 50S ribosomal protein L13

Chain J:  100%

There are no outlier residues recorded for this chain.

- Molecule 12: 50S ribosomal protein L14

Chain K:  98% .



- Molecule 13: 50S ribosomal protein L15

Chain L:  98%



- Molecule 14: 50S ribosomal protein L16

Chain M:  100%

There are no outlier residues recorded for this chain.

- Molecule 15: 50S ribosomal protein L17

Chain N:  100%

There are no outlier residues recorded for this chain.

- Molecule 16: 50S ribosomal protein L18

Chain O:  98%



- Molecule 17: 50S ribosomal protein L19

Chain P:  99%



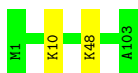
- Molecule 18: 50S ribosomal protein L20

Chain Q:  99%



- Molecule 19: 50S ribosomal protein L21

Chain R:  98%



- Molecule 20: 50S ribosomal protein L22

Chain S:  100%

There are no outlier residues recorded for this chain.

- Molecule 21: 50S ribosomal protein L23

Chain T:  100%

There are no outlier residues recorded for this chain.

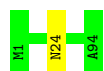
- Molecule 22: 50S ribosomal protein L24

Chain U:  99%



- Molecule 23: 50S ribosomal protein L25

Chain V:  99%



- Molecule 24: 50S ribosomal protein L27

Chain W:  99%



- Molecule 25: 50S ribosomal protein L28

Chain X:  99%



- Molecule 26: 50S ribosomal protein L29

Chain Y:  100%

There are no outlier residues recorded for this chain.

- Molecule 27: 50S ribosomal protein L30

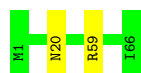
Chain Z:  98%



- Molecule 28: 50S ribosomal protein L31



Chain a:  97% .



- Molecule 29: 50S ribosomal protein L32

Chain b:  98% .



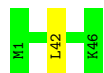
- Molecule 30: 50S ribosomal protein L33

Chain c:  98% .



- Molecule 31: 50S ribosomal protein L34

Chain d:  98% .



- Molecule 32: 50S ribosomal protein L35

Chain e:  95% 5%



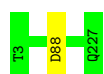
- Molecule 33: 50S ribosomal protein L36

Chain f:  100%

There are no outlier residues recorded for this chain.

- Molecule 34: 30S ribosomal protein S2

Chain g:  100%



- Molecule 35: 30S ribosomal protein S3

Chain h:  99% .



- Molecule 36: 30S ribosomal protein S4

Chain i:  100%

There are no outlier residues recorded for this chain.

- Molecule 37: 30S ribosomal protein S5

Chain j:  97%



- Molecule 38: 30S ribosomal protein S6

Chain k:  98%



- Molecule 39: 30S ribosomal protein S7

Chain l:  99%



- Molecule 40: 30S ribosomal protein S8

Chain m:  98%



- Molecule 41: 30S ribosomal protein S9

Chain n:  98%



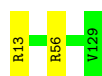
- Molecule 42: 30S ribosomal protein S10

Chain o:  99%



- Molecule 43: 30S ribosomal protein S11

Chain p:  98%



- Molecule 44: 30S ribosomal protein S12

Chain q:  98%



- Molecule 45: 30S ribosomal protein S13

Chain r:  100%

There are no outlier residues recorded for this chain.

- Molecule 46: 30S ribosomal protein S14

Chain s:  100%

There are no outlier residues recorded for this chain.

- Molecule 47: 30S ribosomal protein S15

Chain t:  95% 5%



- Molecule 48: 30S ribosomal protein S16

Chain u:  99%



- Molecule 49: 30S ribosomal protein S17

Chain v:  98%



- Molecule 50: 30S ribosomal protein S18

Chain w:  100%

There are no outlier residues recorded for this chain.

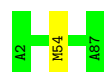
- Molecule 51: 30S ribosomal protein S19

Chain x:  98% .



- Molecule 52: 30S ribosomal protein S20

Chain y:  99% .



- Molecule 53: 30S ribosomal protein S21

Chain z:  100%

There are no outlier residues recorded for this chain.

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	94371	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	27	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (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: OMG, PSU, 5MU, 4OC, 2MA, G7M, 7MG, OMC, 0TD, 5MC, 2MG, ZN, 3TD, UR3, 1MG, 6MZ, MA6, OMU, MG

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	1	0.93	3/106185 (0.0%)	1.13	561/165633 (0.3%)
2	3	0.73	0/2872	1.08	12/4478 (0.3%)
3	B	0.53	0/2122	0.68	1/2852 (0.0%)
4	C	0.50	0/1586	0.66	0/2134
5	D	0.44	0/1571	0.61	0/2113
6	E	0.34	0/1435	0.63	2/1926 (0.1%)
7	F	0.36	0/1333	0.60	0/1805
8	G	0.30	0/1122	0.62	1/1515 (0.1%)
9	H	0.35	0/993	0.72	2/1340 (0.1%)
10	I	0.31	0/998	0.63	0/1348
11	J	0.49	0/1152	0.59	0/1551
12	K	0.50	0/955	0.69	0/1279
13	L	0.47	1/1062 (0.1%)	0.69	0/1413
14	M	0.46	0/1093	0.64	0/1460
15	N	0.49	0/964	0.64	0/1289
16	O	0.37	0/902	0.62	0/1209
17	P	0.47	0/929	0.61	0/1242
18	Q	0.54	0/960	0.65	1/1278 (0.1%)
19	R	0.48	0/829	0.67	0/1107
20	S	0.47	0/864	0.62	0/1156
21	T	0.42	0/752	0.65	0/1005
22	U	0.40	0/796	0.59	1/1062 (0.1%)
23	V	0.41	0/766	0.58	0/1025
24	W	0.47	0/589	0.60	0/779
25	X	0.48	0/635	0.59	0/848
26	Y	0.33	0/502	0.61	0/667
27	Z	0.38	0/452	0.61	0/605
28	a	0.32	0/531	0.55	0/709
29	b	0.48	0/450	0.70	0/599
30	c	0.46	0/433	0.65	0/576
31	d	0.52	0/380	0.72	1/498 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	e	0.48	0/513	0.71	0/676
33	f	0.47	0/303	0.62	0/397
34	g	0.33	0/1791	0.61	1/2413 (0.0%)
35	h	0.33	0/1663	0.58	0/2241
36	i	0.35	0/1665	0.57	0/2227
37	j	0.43	0/1165	0.66	0/1568
38	k	0.38	0/867	0.62	0/1171
39	l	0.31	0/1195	0.61	0/1602
40	m	0.40	0/989	0.62	1/1326 (0.1%)
41	n	0.34	0/1034	0.67	0/1375
42	o	0.36	0/800	0.66	0/1082
43	p	0.39	0/893	0.56	0/1205
44	q	0.44	0/960	0.68	0/1286
45	r	0.30	0/909	0.66	0/1215
46	s	0.32	0/817	0.54	0/1088
47	t	0.38	0/722	0.59	0/964
48	u	0.38	0/659	0.62	0/884
49	v	0.38	0/658	0.67	2/881 (0.2%)
50	w	0.39	0/553	0.57	0/743
51	x	0.31	0/680	0.56	0/915
52	y	0.35	0/675	0.51	0/895
53	z	0.33	0/597	0.56	0/792
All	All	0.81	4/156321 (0.0%)	1.02	586/233447 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	39	0
3	B	0	2
10	I	0	1
12	K	0	1
32	e	0	1
38	k	0	1
All	All	39	6

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2393	U	C1'-N1	6.57	1.58	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	496	A	N9-C4	6.55	1.41	1.37
13	L	60	ARG	C-N	-5.20	1.22	1.34
1	1	1625	A	N9-C4	-5.12	1.34	1.37

The worst 5 of 586 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	467	U	C2-N1-C1'	11.57	131.59	117.70
1	1	1518	U	N3-C2-O2	-10.46	114.88	122.20
1	1	467	U	N1-C2-O2	10.30	130.01	122.80
1	1	2018	G	O4'-C1'-N9	10.21	116.37	108.20
1	1	1518	U	N1-C2-O2	9.83	129.68	122.80

5 of 39 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	1	516	PSU	C4',C3'
1	1	527	7MG	C3'
1	1	1402	4OC	C3',C1'
1	1	2251	1MG	C2',C1'
1	1	2252	PSU	C4',C3'

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	157	SER	Peptide
3	B	195	VAL	Peptide
10	I	116	MET	Peptide
12	K	93	GLN	Peptide
32	e	31	HIS	Peptide

## 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	
3	B	269/271 (99%)	259 (96%)	10 (4%)	0	100	100
4	C	207/209 (99%)	199 (96%)	8 (4%)	0	100	100
5	D	199/201 (99%)	193 (97%)	6 (3%)	0	100	100
6	E	175/177 (99%)	159 (91%)	15 (9%)	1 (1%)	22	46
7	F	173/175 (99%)	163 (94%)	10 (6%)	0	100	100
8	G	147/149 (99%)	134 (91%)	13 (9%)	0	100	100
9	H	128/130 (98%)	105 (82%)	23 (18%)	0	100	100
10	I	133/135 (98%)	120 (90%)	13 (10%)	0	100	100
11	J	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
12	K	121/123 (98%)	116 (96%)	5 (4%)	0	100	100
13	L	142/144 (99%)	137 (96%)	5 (4%)	0	100	100
14	M	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
15	N	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
16	O	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
17	P	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
18	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
19	R	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
20	S	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
21	T	92/94 (98%)	92 (100%)	0	0	100	100
22	U	101/103 (98%)	91 (90%)	10 (10%)	0	100	100
23	V	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
24	W	74/76 (97%)	71 (96%)	3 (4%)	0	100	100
25	X	75/77 (97%)	75 (100%)	0	0	100	100
26	Y	60/62 (97%)	60 (100%)	0	0	100	100
27	Z	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
28	a	64/66 (97%)	58 (91%)	6 (9%)	0	100	100
29	b	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
30	c	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
31	d	44/46 (96%)	43 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	e	62/64 (97%)	56 (90%)	5 (8%)	1 (2%)	8	22
33	f	36/38 (95%)	36 (100%)	0	0	100	100
34	g	223/225 (99%)	212 (95%)	11 (5%)	0	100	100
35	h	206/208 (99%)	190 (92%)	16 (8%)	0	100	100
36	i	203/205 (99%)	200 (98%)	3 (2%)	0	100	100
37	j	154/156 (99%)	136 (88%)	18 (12%)	0	100	100
38	k	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
39	l	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
40	m	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
41	n	125/127 (98%)	112 (90%)	13 (10%)	0	100	100
42	o	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
43	p	115/117 (98%)	104 (90%)	11 (10%)	0	100	100
44	q	120/123 (98%)	113 (94%)	7 (6%)	0	100	100
45	r	114/116 (98%)	103 (90%)	11 (10%)	0	100	100
46	s	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
47	t	86/88 (98%)	82 (95%)	3 (4%)	1 (1%)	11	29
48	u	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
49	v	78/80 (98%)	74 (95%)	4 (5%)	0	100	100
50	w	64/66 (97%)	61 (95%)	3 (5%)	0	100	100
51	x	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
52	y	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
53	z	68/70 (97%)	65 (96%)	3 (4%)	0	100	100
All	All	5869/5972 (98%)	5563 (95%)	303 (5%)	3 (0%)	50	72

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	e	32	ILE
6	E	177	PHE
47	t	22	THR

### 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	
3	B	216/216 (100%)	213 (99%)	3 (1%)	62	79
4	C	164/164 (100%)	161 (98%)	3 (2%)	54	75
5	D	165/165 (100%)	162 (98%)	3 (2%)	54	75
6	E	148/148 (100%)	148 (100%)	0	100	100
7	F	136/136 (100%)	133 (98%)	3 (2%)	47	69
8	G	114/114 (100%)	111 (97%)	3 (3%)	41	65
9	H	99/99 (100%)	99 (100%)	0	100	100
10	I	104/104 (100%)	102 (98%)	2 (2%)	52	73
11	J	116/116 (100%)	116 (100%)	0	100	100
12	K	104/104 (100%)	103 (99%)	1 (1%)	73	85
13	L	103/103 (100%)	101 (98%)	2 (2%)	52	73
14	M	109/109 (100%)	109 (100%)	0	100	100
15	N	99/99 (100%)	99 (100%)	0	100	100
16	O	86/86 (100%)	84 (98%)	2 (2%)	45	69
17	P	99/99 (100%)	98 (99%)	1 (1%)	73	85
18	Q	89/89 (100%)	88 (99%)	1 (1%)	70	83
19	R	84/84 (100%)	82 (98%)	2 (2%)	44	68
20	S	93/93 (100%)	93 (100%)	0	100	100
21	T	81/81 (100%)	81 (100%)	0	100	100
22	U	84/84 (100%)	84 (100%)	0	100	100
23	V	78/78 (100%)	77 (99%)	1 (1%)	65	80
24	W	58/58 (100%)	57 (98%)	1 (2%)	56	76
25	X	67/67 (100%)	66 (98%)	1 (2%)	60	78
26	Y	54/54 (100%)	54 (100%)	0	100	100
27	Z	48/48 (100%)	47 (98%)	1 (2%)	48	70
28	a	59/59 (100%)	57 (97%)	2 (3%)	32	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	b	47/47 (100%)	46 (98%)	1 (2%)	48	70
30	c	47/47 (100%)	46 (98%)	1 (2%)	48	70
31	d	38/38 (100%)	38 (100%)	0	100	100
32	e	51/51 (100%)	50 (98%)	1 (2%)	50	72
33	f	34/34 (100%)	34 (100%)	0	100	100
34	g	187/187 (100%)	187 (100%)	0	100	100
35	h	171/171 (100%)	168 (98%)	3 (2%)	54	75
36	i	172/172 (100%)	172 (100%)	0	100	100
37	j	119/119 (100%)	115 (97%)	4 (3%)	32	57
38	k	91/91 (100%)	90 (99%)	1 (1%)	70	83
39	l	124/124 (100%)	122 (98%)	2 (2%)	58	77
40	m	104/104 (100%)	103 (99%)	1 (1%)	73	85
41	n	105/105 (100%)	102 (97%)	3 (3%)	37	61
42	o	86/86 (100%)	85 (99%)	1 (1%)	67	82
43	p	90/90 (100%)	88 (98%)	2 (2%)	47	69
44	q	102/102 (100%)	101 (99%)	1 (1%)	73	85
45	r	94/94 (100%)	94 (100%)	0	100	100
46	s	83/83 (100%)	83 (100%)	0	100	100
47	t	76/76 (100%)	73 (96%)	3 (4%)	27	52
48	u	65/65 (100%)	64 (98%)	1 (2%)	60	78
49	v	74/74 (100%)	74 (100%)	0	100	100
50	w	57/57 (100%)	57 (100%)	0	100	100
51	x	72/72 (100%)	70 (97%)	2 (3%)	38	63
52	y	65/65 (100%)	64 (98%)	1 (2%)	60	78
53	z	60/60 (100%)	60 (100%)	0	100	100
All	All	4871/4871 (100%)	4811 (99%)	60 (1%)	66	82

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	X	27	ARG
47	t	72	ARG
35	h	72	ARG

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Mol	Chain	Res	Type
47	t	70	LEU
52	y	54	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
46	s	43	ASN
47	t	20	ASN
19	R	86	GLN
16	O	38	GLN
47	t	40	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	4435/4458 (99%)	953 (21%)	24 (0%)
2	3	119/120 (99%)	25 (21%)	0
All	All	4554/4578 (99%)	978 (21%)	24 (0%)

5 of 978 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	7	A
1	1	9	G
1	1	19	A
1	1	22	G
1	1	32	A

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	3445	5MU
1	1	3814	G
1	1	3668	G
1	1	3931	A
1	1	2192	U

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

34 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
1	5MC	1	1407	1	18,22,23	2.05	3 (16%)	26,32,35	1.38	3 (11%)
1	2MG	1	1207	1	18,26,27	2.83	5 (27%)	16,38,41	1.44	3 (18%)
1	5MU	1	3445	1	19,22,23	2.52	7 (36%)	28,32,35	3.54	9 (32%)
1	6MZ	1	3124	1	18,25,26	1.98	1 (5%)	16,36,39	2.36	4 (25%)
1	2MA	1	4009	1,54	19,25,26	1.20	1 (5%)	21,37,40	2.29	4 (19%)
1	PSU	1	4086	1	18,21,22	2.17	5 (27%)	22,30,33	2.14	7 (31%)
1	G7M	1	3575	1	20,26,27	2.81	5 (25%)	17,39,42	1.23	2 (11%)
1	UR3	1	4414	1	19,22,23	2.82	6 (31%)	26,32,35	1.45	3 (11%)
1	4OC	1	1402	1	20,23,24	2.44	5 (25%)	26,32,35	2.32	9 (34%)
1	PSU	1	2461	1	18,21,22	2.25	5 (27%)	22,30,33	2.22	5 (22%)
1	5MC	1	967	1,54	18,22,23	2.01	3 (16%)	26,32,35	1.44	4 (15%)
1	3TD	1	3421	1	18,22,23	2.84	8 (44%)	22,32,35	1.72	2 (9%)
1	7MG	1	527	1	22,26,27	6.31	6 (27%)	29,39,42	2.43	10 (34%)
1	OMC	1	4004	1,54	19,22,23	1.77	6 (31%)	26,31,34	2.10	9 (34%)
1	2MG	1	3951	1	18,26,27	2.97	6 (33%)	16,38,41	1.36	3 (18%)
1	PSU	1	4111	1	18,21,22	2.18	5 (27%)	22,30,33	2.09	4 (18%)
1	1MG	1	2251	1	18,26,27	2.96	6 (33%)	19,39,42	2.37	9 (47%)
1	PSU	1	3963	1	18,21,22	2.29	5 (27%)	22,30,33	2.29	5 (22%)
1	2MG	1	3341	1	18,26,27	2.85	6 (33%)	16,38,41	1.42	4 (25%)
1	PSU	1	2252	1,54	18,21,22	2.25	6 (33%)	22,30,33	2.30	5 (22%)
1	2MG	1	966	1	18,26,27	2.88	5 (27%)	16,38,41	1.39	3 (18%)
1	PSU	1	4010	1	18,21,22	2.35	5 (27%)	22,30,33	2.37	5 (22%)
1	PSU	1	3423	1	18,21,22	2.11	5 (27%)	22,30,33	2.07	5 (22%)
1	PSU	1	3417	1	18,21,22	1.97	5 (27%)	22,30,33	2.12	4 (18%)
44	0TD	q	89	44	7,9,10	1.40	0	6,11,13	2.82	3 (50%)
1	5MC	1	3468	1	18,22,23	2.14	3 (16%)	26,32,35	1.41	4 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	6MZ	1	3536	1	18,25,26	2.12	1 (5%)	16,36,39	3.75	8 (50%)
1	OMU	1	4058	1	19,22,23	2.76	7 (36%)	26,31,34	2.38	12 (46%)
1	MA6	1	4434	1	18,26,27	0.93	1 (5%)	19,38,41	1.59	3 (15%)
1	MA6	1	4435	1	18,26,27	0.88	0	19,38,41	1.67	2 (10%)
1	PSU	1	516	1	18,21,22	2.10	6 (33%)	22,30,33	2.20	5 (22%)
1	OMG	1	3757	1	18,26,27	2.91	8 (44%)	19,38,41	1.76	4 (21%)
1	2MG	1	4432	1	18,26,27	2.89	6 (33%)	16,38,41	1.52	3 (18%)
1	5MU	1	2253	1	19,22,23	2.32	7 (36%)	28,32,35	4.01	13 (46%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MU	1	3445	1	2/2/5/5	1/7/25/26	0/2/2/2
1	2MG	1	1207	1	-	0/5/27/28	0/3/3/3
1	5MC	1	1407	1	-	0/7/25/26	0/2/2/2
1	6MZ	1	3124	1	2/2/5/6	5/5/27/28	0/3/3/3
1	2MA	1	4009	1,54	2/2/5/5	2/3/25/26	0/3/3/3
1	PSU	1	4086	1	2/2/5/5	3/7/25/26	0/2/2/2
1	G7M	1	3575	1	1/1/5/5	2/3/25/26	0/3/3/3
1	UR3	1	4414	1	-	0/7/25/26	0/2/2/2
1	4OC	1	1402	1	2/2/5/6	4/9/29/30	0/2/2/2
1	PSU	1	2461	1	2/2/5/5	3/7/25/26	0/2/2/2
1	3TD	1	3421	1	1/1/5/5	4/7/25/26	0/2/2/2
1	5MC	1	967	1,54	-	0/7/25/26	0/2/2/2
1	7MG	1	527	1	1/1/7/7	3/7/37/38	0/3/3/3
1	OMC	1	4004	1,54	1/1/5/5	4/9/27/28	0/2/2/2
1	2MG	1	3951	1	-	0/5/27/28	0/3/3/3
1	PSU	1	4111	1	2/2/5/5	3/7/25/26	0/2/2/2
1	1MG	1	2251	1	2/2/5/5	1/3/25/26	0/3/3/3
1	PSU	1	3963	1	2/2/5/5	3/7/25/26	0/2/2/2
1	2MG	1	3341	1	-	0/5/27/28	0/3/3/3
1	PSU	1	2252	1,54	2/2/5/5	3/7/25/26	0/2/2/2
1	2MG	1	966	1	-	4/5/27/28	0/3/3/3
1	PSU	1	4010	1	2/2/5/5	3/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	1	3423	1	2/2/5/5	3/7/25/26	0/2/2/2
1	PSU	1	3417	1	2/2/5/5	3/7/25/26	0/2/2/2
44	0TD	q	89	44	-	1/7/12/14	-
1	5MC	1	3468	1	-	0/7/25/26	0/2/2/2
1	6MZ	1	3536	1	2/2/5/6	2/5/27/28	0/3/3/3
1	OMU	1	4058	1	2/2/5/5	3/9/27/28	0/2/2/2
1	MA6	1	4434	1	-	1/7/29/30	0/3/3/3
1	MA6	1	4435	1	-	3/7/29/30	0/3/3/3
1	PSU	1	516	1	2/2/5/5	5/7/25/26	0/2/2/2
1	OMG	1	3757	1	1/1/5/5	2/5/27/28	0/3/3/3
1	2MG	1	4432	1	-	0/5/27/28	0/3/3/3
1	5MU	1	2253	1	2/2/5/5	5/7/25/26	0/2/2/2

The worst 5 of 159 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	527	7MG	C8-N9	-27.11	1.30	1.46
1	1	3575	G7M	O6-C6	9.70	1.43	1.23
1	1	966	2MG	O6-C6	8.88	1.41	1.23
1	1	3757	OMG	O6-C6	8.71	1.41	1.23
1	1	1207	2MG	O6-C6	8.70	1.41	1.23

The worst 5 of 178 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2253	5MU	N3-C2-N1	9.66	127.72	114.89
1	1	2253	5MU	C5M-C5-C4	9.47	129.19	118.77
1	1	3445	5MU	C5M-C5-C4	8.86	128.52	118.77
1	1	3536	6MZ	C9-N6-C6	-8.64	115.43	122.87
1	1	4009	2MA	C2-N3-C4	8.63	122.54	115.52

5 of 39 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	1	516	PSU	C4'
1	1	516	PSU	C3'
1	1	527	7MG	C3'
1	1	1402	4OC	C3'
1	1	1402	4OC	C1'



5 of 76 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	516	PSU	O4'-C1'-C5-C4
1	1	516	PSU	O4'-C1'-C5-C6
1	1	516	PSU	C3'-C4'-C5'-O5'
1	1	516	PSU	O4'-C4'-C5'-O5'
1	1	527	7MG	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 438 ligands modelled in this entry, 438 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	1	5

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	1501:U	O3'	1502:U	P	3.88
1	1	1276:G	O3'	1277:C	P	3.82
1	1	3820:A	O3'	3821:G	P	3.74
1	1	1383:C	O3'	1384:C	P	3.50
1	1	147:G	O3'	148:G	P	3.31

## 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-0261. 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.