



## wwPDB EM Validation Summary Report ⓘ

Mar 31, 2025 – 06:00 PM JST

PDB ID : 5ZEP / pdb\_00005zep  
EMDB ID : EMD-6921  
Title : M. smegmatis hibernating state 70S ribosome structure  
Authors : Mishra, S.; Ahmed, T.; Tyagi, A.; Shi, J.; Bhushan, S.  
Deposited on : 2018-02-27  
Resolution : 3.40 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>.

---

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

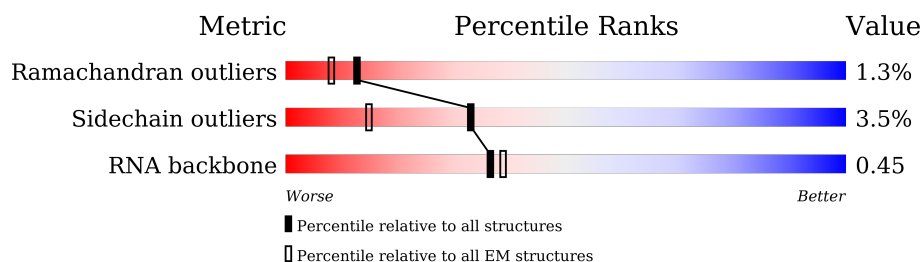
EMDB validation analysis : 0.0.1.dev117  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.42

# 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 3.40 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.



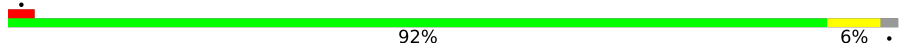
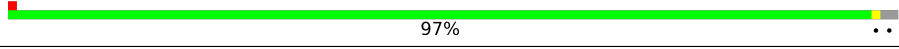
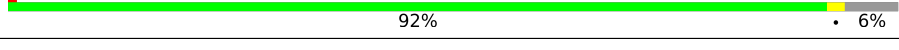
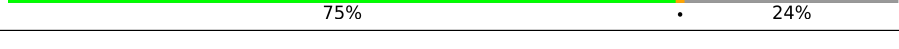
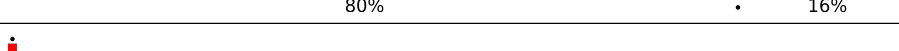
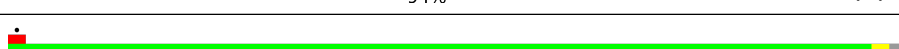

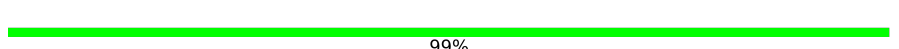
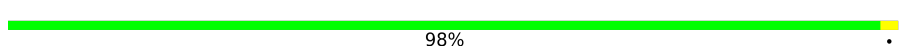
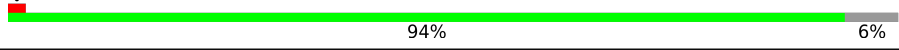


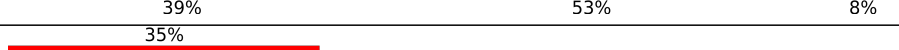

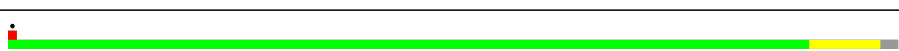
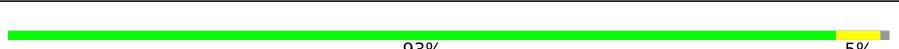


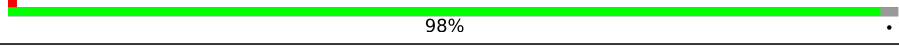
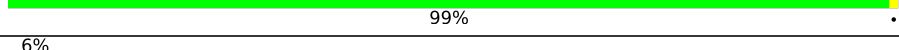

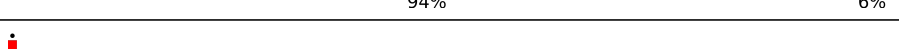
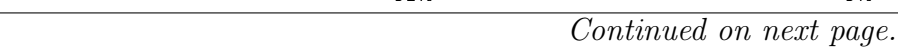


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	a	1528	
2	c	275	
3	e	214	
4	g	156	
5	h	132	
6	i	150	
7	j	101	
8	k	138	

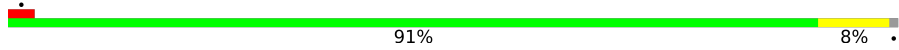
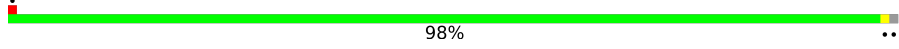
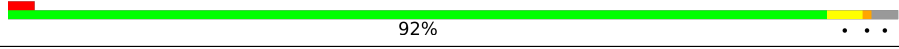
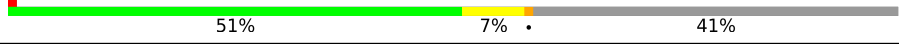
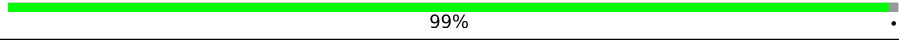
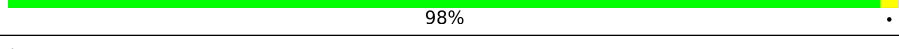
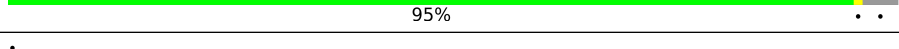
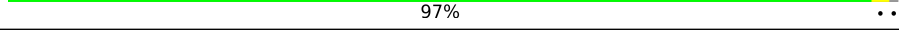
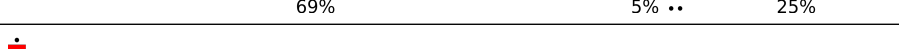
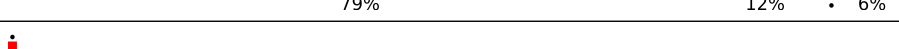
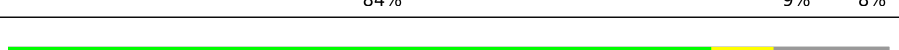

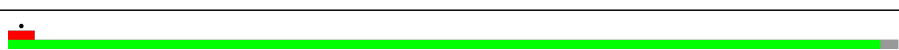

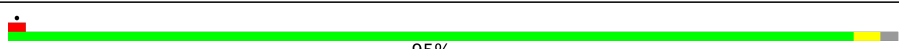

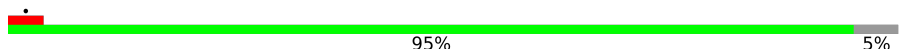


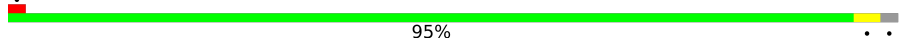
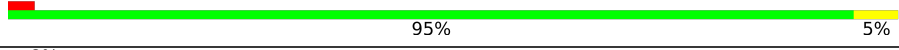
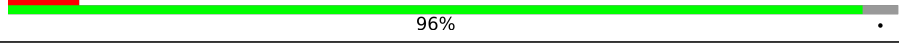



*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	l	124	
10	o	89	
11	q	98	
12	r	84	
13	s	93	
14	t	86	
15	n	61	
16	b	277	
17	d	201	
18	f	96	
19	m	124	
20	p	156	
21	u	33	
22	w	77	
23	x	230	
24	0	479	
25	C	278	
26	D	217	
27	E	215	
28	F	187	
29	G	179	
30	H	151	
31	I	175	
32	J	142	
33	K	147	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	L	122	
35	M	147	
36	N	138	
37	O	199	
38	P	127	
39	Q	113	
40	R	129	
41	S	103	
42	T	153	
43	U	100	
44	V	105	
45	W	215	
46	X	88	
47	Y	64	
48	Z	77	
49	v	61	
50	y	75	
51	z	57	
52	1	55	
53	2	47	
54	3	64	
55	4	37	
56	5	24	
57	B	118	
58	A	3120	

## 2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 152451 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 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1506	Total	C	N	O	P	0	0
			32341	14404	5921	10510	1506		

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	210	Total	C	N	O	S	0	0
			1672	1043	324	300	5		

- Molecule 3 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	e	198	Total	C	N	O	S	0	0
			1433	885	282	262	4		

- Molecule 4 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	g	156	Total	C	N	O	S	0	0
			1240	773	242	222	3		

- Molecule 5 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	h	130	Total	C	N	O	S	0	0
			1003	629	188	185	1		

- Molecule 6 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	i	126	Total	C	N	O		0	0
			994	630	194	170			

- Molecule 7 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	j	97	Total	C	N	O	S	0	0
			775	488	143	141	3		

- Molecule 8 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	k	117	Total	C	N	O	S	0	0
			871	539	173	158	1		

- Molecule 9 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	l	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 10 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	o	87	Total	C	N	O	0	0
			709	443	143	123		

- Molecule 11 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	q	92	Total	C	N	O	S	0	0
			730	458	138	132	2		

- Molecule 12 is a protein called 30S ribosomal protein S18 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	r	64	Total	C	N	O	S	0	0
			512	319	102	88	3		

- Molecule 13 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	s	78	Total	C	N	O	S	0	0
			630	405	117	107	1		

- Molecule 14 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	t	84	Total	C	N	O	0	0
			655	399	138	118		

- Molecule 15 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	n	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

- Molecule 16 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	b	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 17 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	d	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 18 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	f	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 19 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	m	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 20 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	p	113	Total	C	N	O	0	0
			891	570	162	159		

- Molecule 21 is a protein called Conserved domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

- Molecule 22 is a RNA chain called E-tRNA<sup>f</sup>Met.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	w	77	Total	C	N	O	P	0	0
			1643	732	297	537	77		

- Molecule 23 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	x	100	Total	C	N	O	S	0	0
			831	513	167	149	2		

- Molecule 24 is a protein called bS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	0	262	Total	C	N	O	S	0	0
			1310	786	262	262			

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	C	273	Total	C	N	O	S	0	0
			2097	1290	435	368	4		

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	E	207	Total	C	N	O	S	0	0
			1553	959	292	300	2		

- Molecule 28 is a protein called 50S ribosomal protein L5.



Mol	Chain	Residues	Atoms					AltConf	Trace
28	F	181	Total	C	N	O	S	0	0
			1437	903	269	259	6		

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 30 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 31 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 32 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 33 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	K	147	Total	C	N	O	S	0	0
			1138	727	208	201	2		

- Molecule 34 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L	121	Total	C	N	O	S	0	0
			930	580	178	169	3		

- Molecule 35 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	N	134	Total	C	N	O	S	0	0
			1074	680	211	181	2		

- Molecule 37 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	O	117	Total	C	N	O	S	0	0
			919	577	178	162	2		

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	P	126	Total	C	N	O		0	0
			956	586	199	171			

- Molecule 39 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 40 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	R	124	Total	C	N	O		0	0
			988	613	203	172			

- Molecule 41 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S	102	Total	C	N	O		0	0
			768	487	140	141			

- Molecule 42 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 43 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	U	94	Total	C	N	O	0	0
			739	469	135	135		

- Molecule 44 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	V	97	Total	C	N	O	S	0	0
			731	456	137	136	2		

- Molecule 45 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	W	186	Total	C	N	O	0	0
			1389	859	249	281		

- Molecule 46 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	X	82	Total	C	N	O	0	0
			604	372	127	105		

- Molecule 47 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 48 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Z	63	Total	C	N	O	S	0	0
			527	322	102	102	1		

- Molecule 49 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	v	60	Total	C	N	O	0	0
			483	298	97	88		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	y	66	Total	C	N	O	S	0	0
			510	316	93	96	5		

- Molecule 51 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	z	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 52 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	1	50	Total	C	N	O	S	0	0
			416	254	86	72	4		

- Molecule 53 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	2	45	Total	C	N	O	S	0	0
			372	222	96	53	1		

- Molecule 54 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	3	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 55 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	4	37	Total	C	N	O	S	0	0
			298	181	66	46	5		

- Molecule 56 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	5	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 57 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	B	117	Total	C	N	O	P	0	0
			2501	1116	462	806	117		

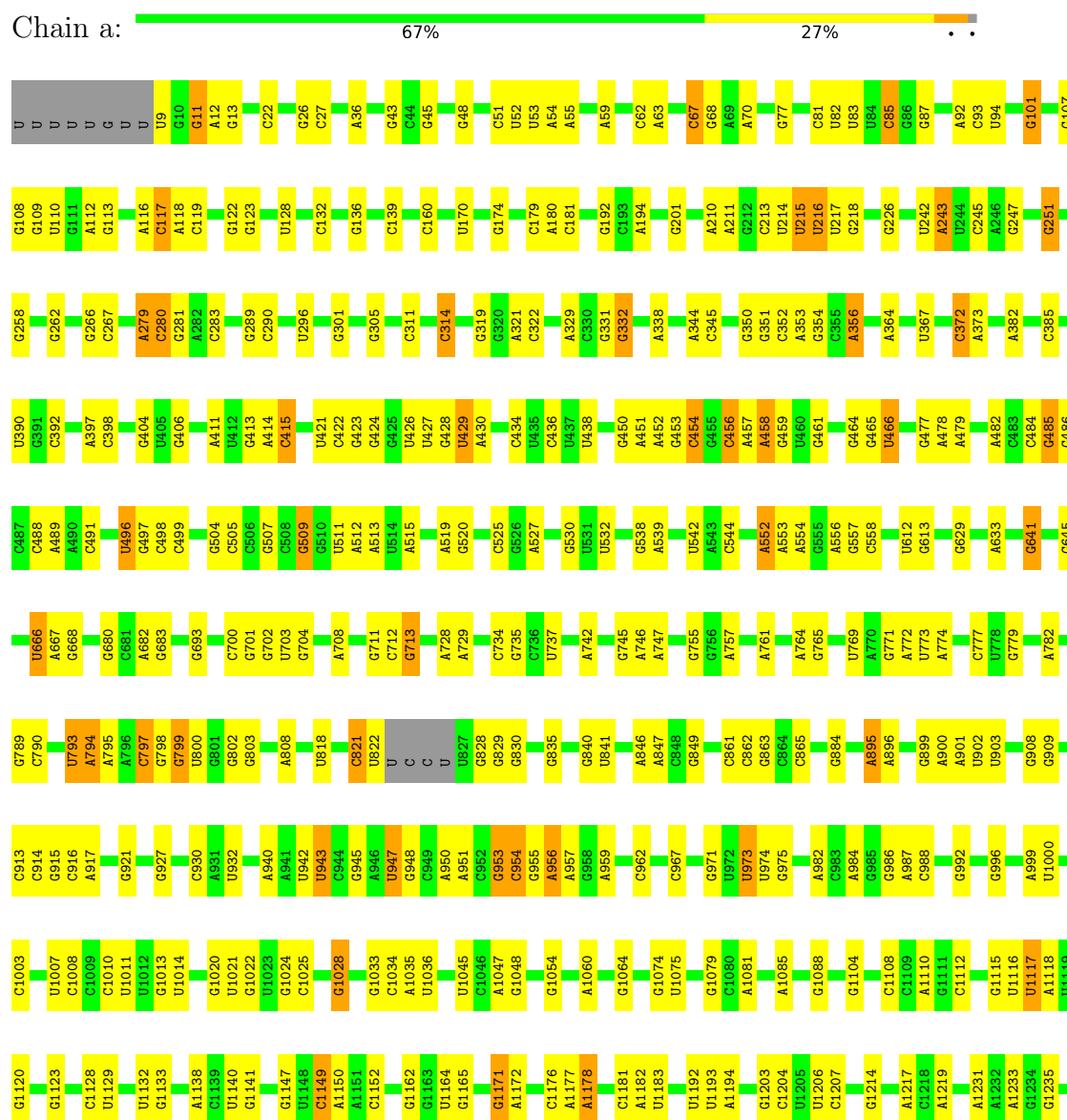
- Molecule 58 is a RNA chain called 23S rRNA.

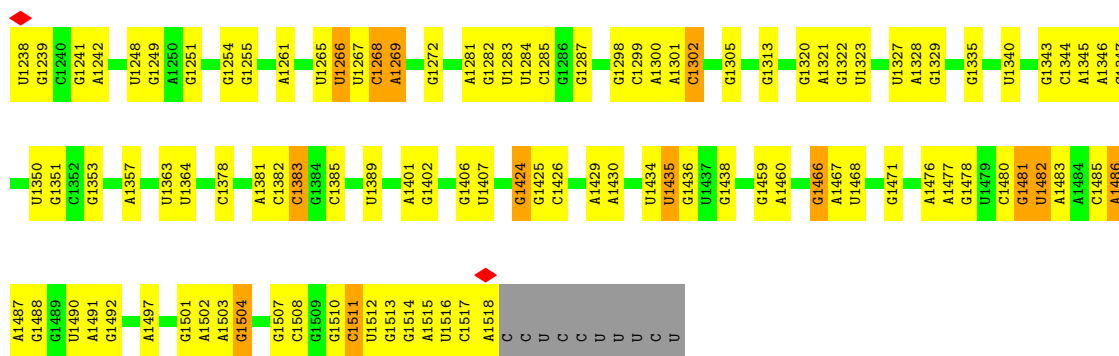
Mol	Chain	Residues	Atoms					AltConf	Trace
58	A	3102	Total	C	N	O	P	0	0
			66623	29694	12253	21574	3102		

### 3 Residue-property plots [i](#)

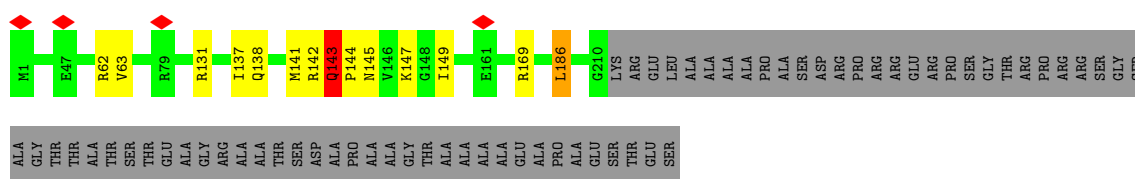
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: 16S rRNA

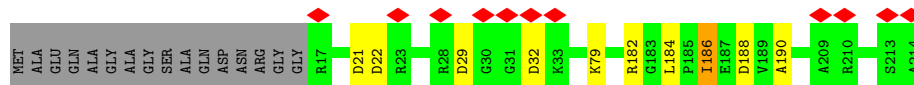
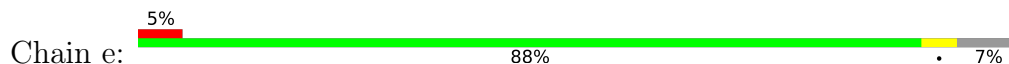




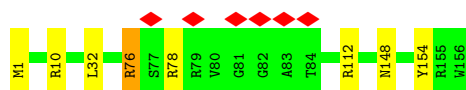
• Molecule 2: 30S ribosomal protein S3



• Molecule 3: 30S ribosomal protein S5



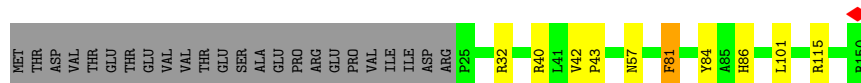
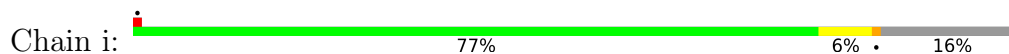
• Molecule 4: 30S ribosomal protein S7




• Molecule 5: 30S ribosomal protein S8

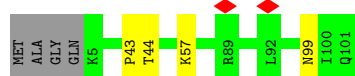


• Molecule 6: 30S ribosomal protein S9




- Molecule 7: 30S ribosomal protein S10

Chain j:  92%



- Molecule 8: 30S ribosomal protein S11

Chain k:  78% 7% 15%



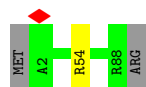
- Molecule 9: 30S ribosomal protein S12

Chain l:  92% 6%

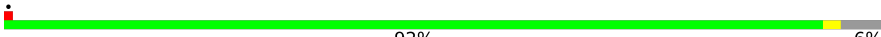


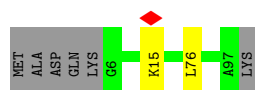
- Molecule 10: 30S ribosomal protein S15

Chain o:  97%



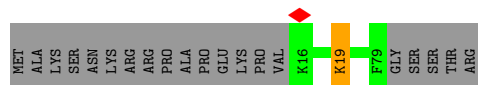
- Molecule 11: 30S ribosomal protein S17

Chain q:  92% 6%




- Molecule 12: 30S ribosomal protein S18 2

Chain r:  75% 24%



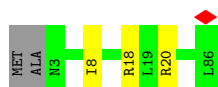
- Molecule 13: 30S ribosomal protein S19

Chain s:  80% 16%

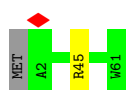




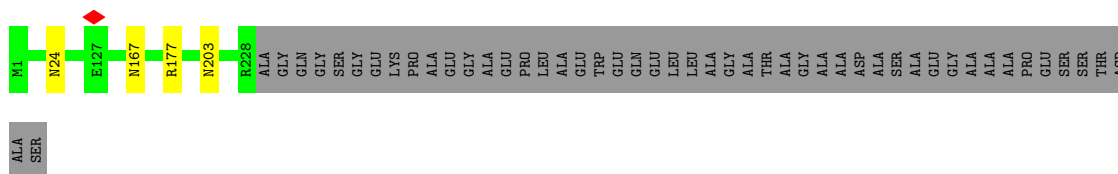
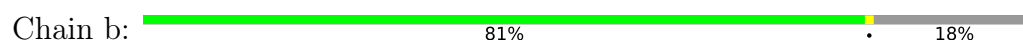
- Molecule 14: 30S ribosomal protein S20



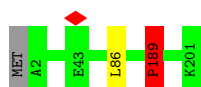
- Molecule 15: 30S ribosomal protein S14 type Z



- Molecule 16: 30S ribosomal protein S2



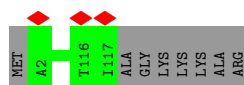
- Molecule 17: 30S ribosomal protein S4



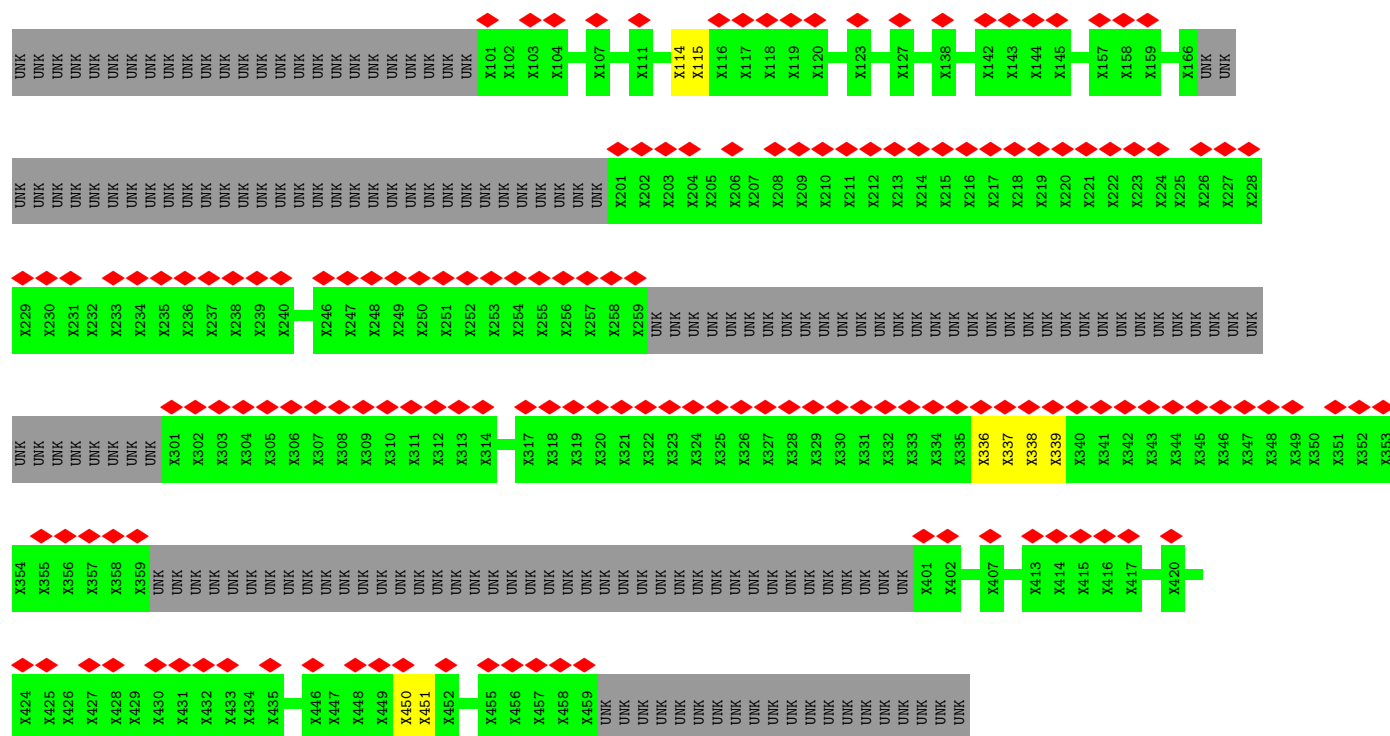
- Molecule 18: 30S ribosomal protein S6



- Molecule 19: 30S ribosomal protein S13



- [illegible]



• Molecule 25: 50S ribosomal protein L2

Chain C: 90% 8% .



• Molecule 26: 50S ribosomal protein L3

Chain D: 93% 5% .



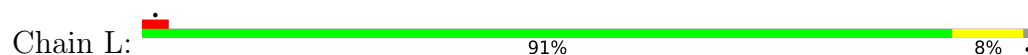
• Molecule 27: 50S ribosomal protein L4

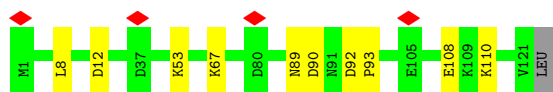
Chain E: 87% 8% . .



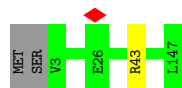
• Molecule 28: 50S ribosomal protein L5

Chain F: 88% 9% .

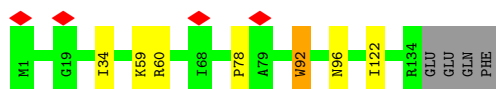




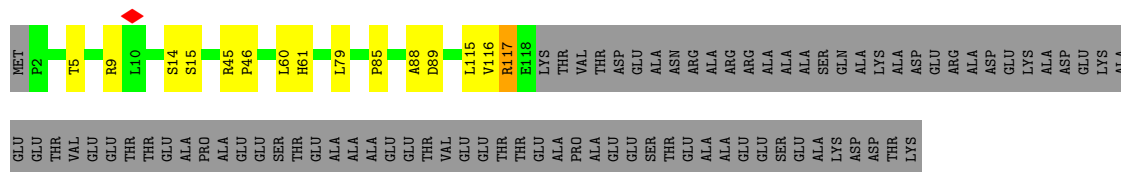
- Molecule 35: 50S ribosomal protein L15



- Molecule 36: 50S ribosomal protein L16



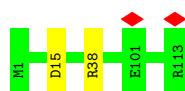
- Molecule 37: 50S ribosomal protein L17



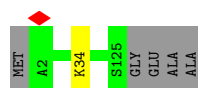
- Molecule 38: 50S ribosomal protein L18



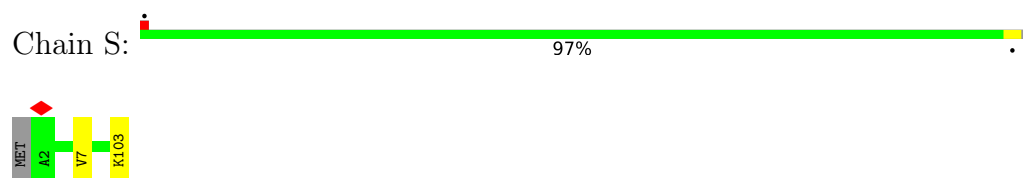
- Molecule 39: 50S ribosomal protein L19



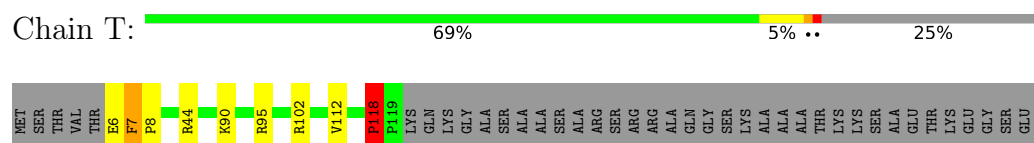
- Molecule 40: 50S ribosomal protein L20



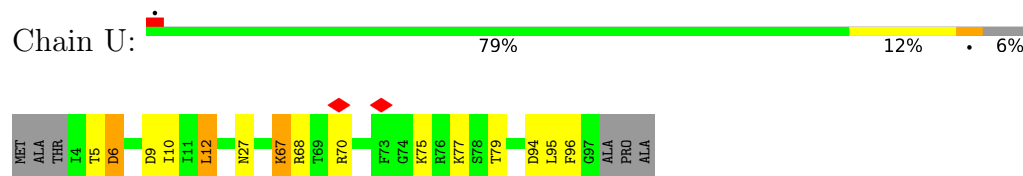
- Molecule 41: 50S ribosomal protein L21



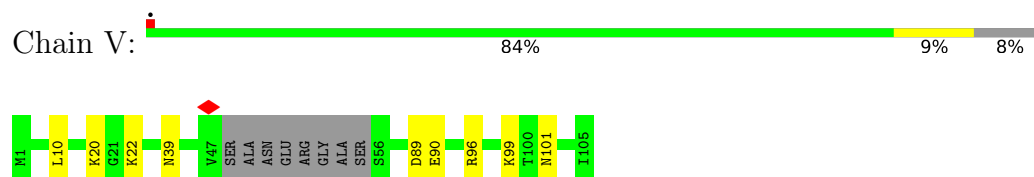
- Molecule 42: 50S ribosomal protein L22



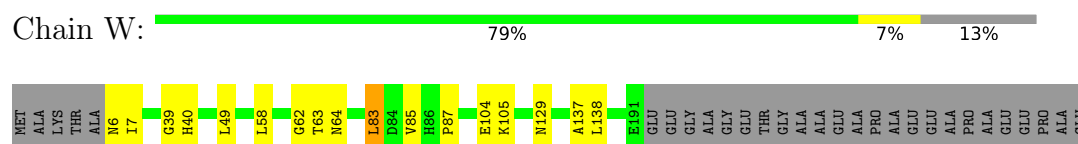
- Molecule 43: 50S ribosomal protein L23



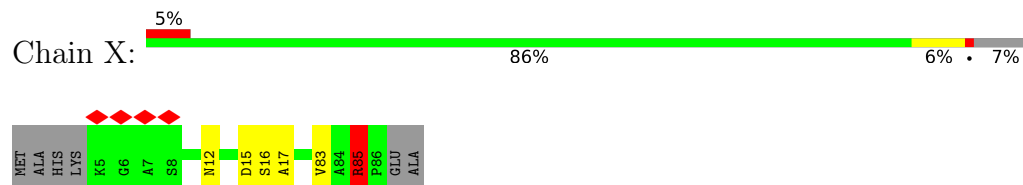
- Molecule 44: 50S ribosomal protein L24



- Molecule 45: 50S ribosomal protein L25



- Molecule 46: 50S ribosomal protein L27

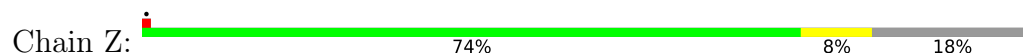


- Molecule 47: 50S ribosomal protein L28





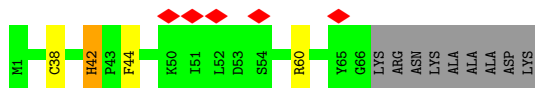
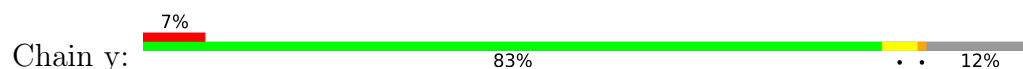
- Molecule 48: 50S ribosomal protein L29



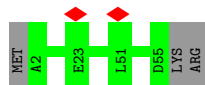
- Molecule 49: 50S ribosomal protein L30



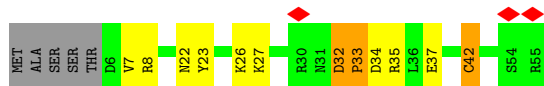
- Molecule 50: 50S ribosomal protein L31



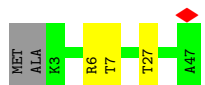
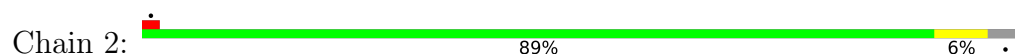
- Molecule 51: 50S ribosomal protein L32



- Molecule 52: 50S ribosomal protein L33 1

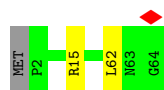


- Molecule 53: 50S ribosomal protein L34



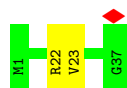
- Molecule 54: 50S ribosomal protein L35

Chain 3:  95%



- Molecule 55: 50S ribosomal protein L36

Chain 4:  95%



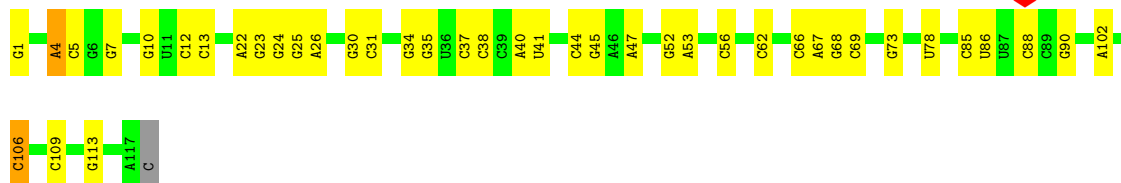
- Molecule 56: Uncharacterized protein

Chain 5:  8% 96%



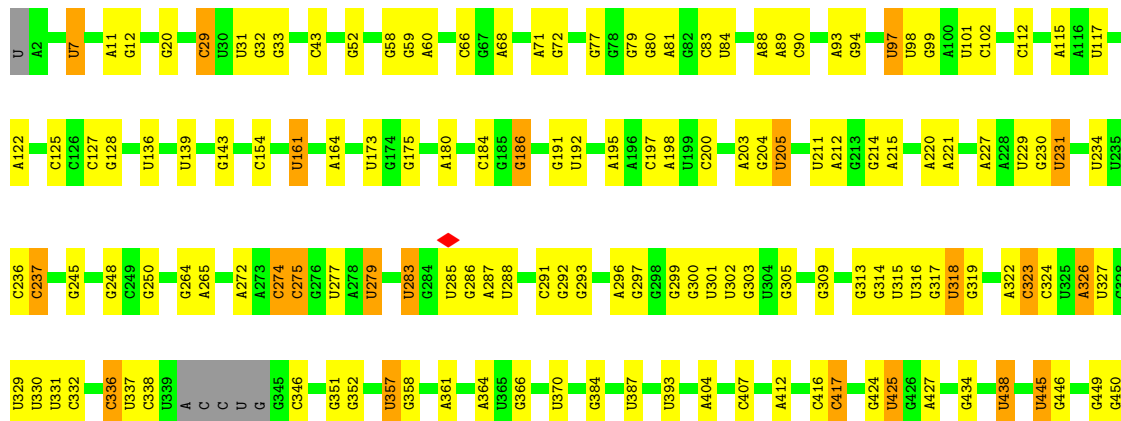
- Molecule 57: 5S rRNA

Chain B:  64% 33%



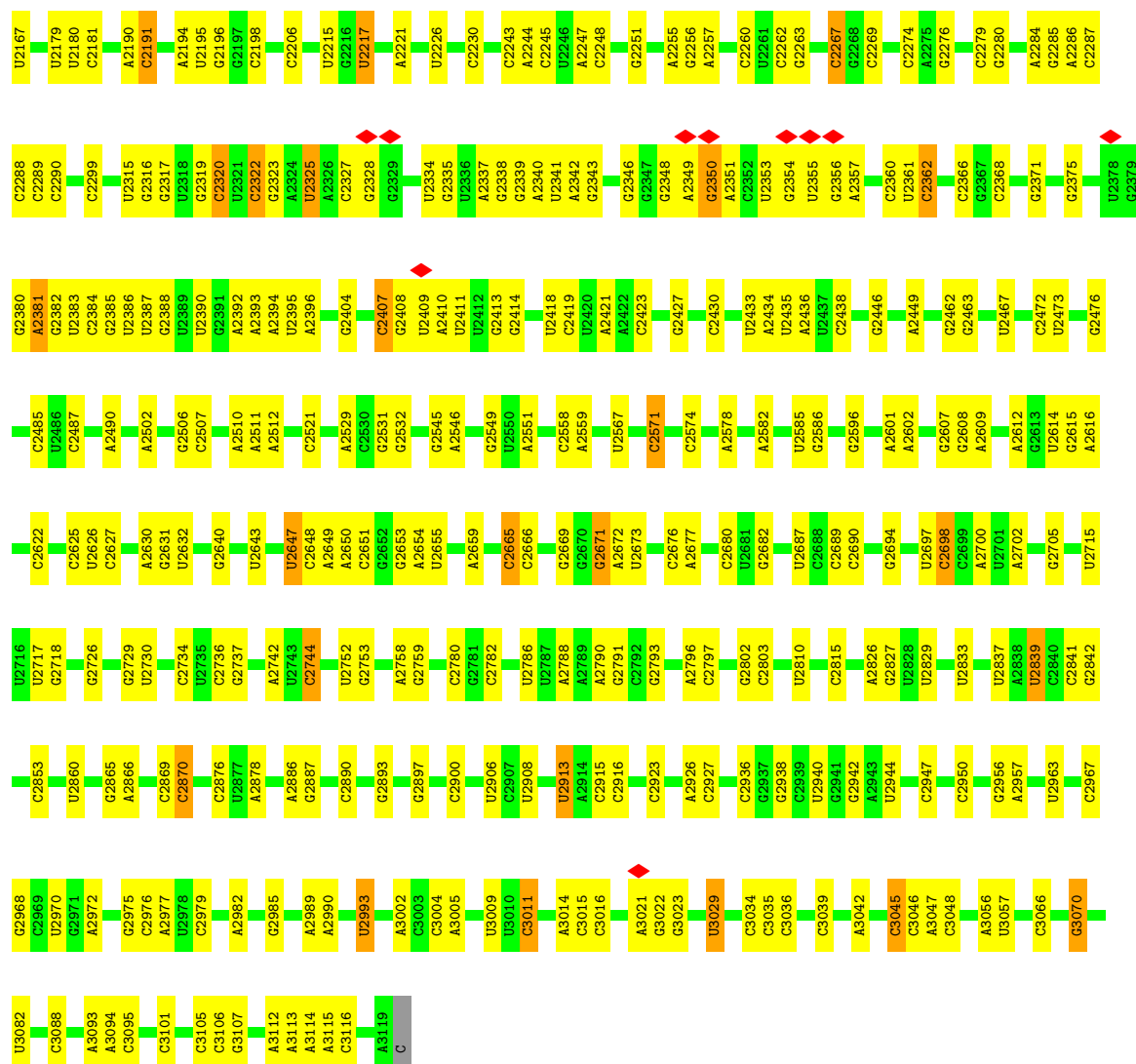
- Molecule 58: 23S rRNA

Chain A:  67% 30%





G2075	A2083	A1787	C1926	G2076	A1679	U1593	C1515	U1370	A1233	A1144	G1043	A944	G838	C703	U451
A2076	A2084	G1788	G1933	A2077	A1680	G1594	C1521	G1371	U1237	U1151	U1044	G945	U839	G706	G452
C2077	C2085	A1789	U1945	C2078	U1681	G1595	G1522	C1372	G1238	U1158	C1045	C952	A590	G707	U453
U2086	U2086	A1792	U1945	U2087	G1688	G1596	U1529	U1382	C1239	U1163	C845	C957	G591	G708	U454
C2088	C2088	U1798	U1945	C2089	G1689	G1597	G1530	G1386	G1240	A1167	U709	C960	G593	U709	C456
C2089	C2089	C1801	U	U2090	U1690	U1598	C1531	U1389	A1244	A1164	C853	U961	U594	G712	A459
U2091	U2091	G1802	A	U2092	G1600	U1599	U1533	U1390	U1245	U1168	U857	U962	G460	G713	U461
U2092	U2092	G1803	C1949	G2093	G1601	G1600	U1534	C1393	A1246	C1167	U862	U963	C596	U714	G599
G2094	G2094	G1804	C1953	G2095	U1602	U1602	C1535	G1403	U1250	A1169	U863	U964	G605	A721	G468
G2096	G2096	C1813	C1958	G2107	G1604	G1604	A1539	C1404	U1251	C1170	U864	U965	C471	A725	C471
U2106	U2106	C1816	C1967	U2110	G1605	G1605	U1540	C1409	G1253	C1171	C1063	U966	C472	A728	C472
G2107	G2107	C1817	U	U2111	G1606	G1606	U1547	C1410	G1254	C1172	A1065	G971	C473	A729	G474
U2110	U2110	C1822	C1973	U2112	U1607	U1607	G1547	C1411	U1260	A1174	C1068	G972	G475	A730	G475
U2111	U2111	A1826	A1974	C2116	U1608	U1608	G1548	A1415	A1261	A1175	G1069	G973	U617	A731	A489
C2117	C2117	U1837	A1975	G2118	C1609	C1609	G1549	A1416	U1266	U1178	G1070	G974	C618	A732	A489
G2119	G2119	G1837	C1977	C2119	C1610	C1610	U1551	A1417	C1266	G1181	A1074	U975	C619	G730	A489
A2120	A2120	G1724	U1981	C2120	U1612	U1612	U1552	U1428	G1270	G1182	U1075	G977	C620	A733	U491
G2130	G2130	C1843	U1990	C2131	C1618	C1618	C1553	C1429	A1275	U1184	A1076	G980	C622	C734	U493
G2131	G2131	A1844	A1991	C2132	G1625	G1625	U1554	C1440	G1276	U1185	A1077	G981	A633	A740	G494
C2133	C2133	G1845	C1991	C2134	G1629	G1629	A1555	C1441	U1292	U1186	G1082	U982	C	A747	C495
G2134	G2134	U1847	U1992	C2135	A1631	A1631	A1556	C1442	G1293	A1187	C1083	G983	G	A748	G498
A2137	A2137	A1852	U1996	C2136	G1632	G1632	C1561	U1444	U1298	A1188	U1085	U984	U	A749	C504
G2138	G2138	C1853	C1997	C2139	U1633	U1633	C1562	C1445	C1298	U1189	U1088	G996	C639	A753	C505
U2140	U2140	A1854	A1998	C2141	U1636	U1636	A1564	C1446	G1302	C1197	A1091	C1001	C640	G757	U509
U2141	U2141	G1855	C1999	C2142	G1637	G1637	C1565	G1456	U1303	A1190	A1092	C1002	G641	A758	G512
G2143	G2143	C1856	U1999	C2143	G1638	G1638	C1566	U1457	U1320	C1198	G1093	C1003	G642	A759	G513
C2144	C2144	A1857	U2005	C2144	G1639	G1639	C1567	C1458	C1321	C1199	A1094	C	G643	A760	C514
U2147	U2147	U1870	C2012	U2148	U1640	U1640	C1569	C1459	U1325	G1201	G1094	A	G644	A761	G530
A2151	A2151	G1878	C2013	U2149	C1641	C1641	C1570	G1460	G1343	A1202	A1098	G1006	U915	G764	G645
G2152	G2152	A1879	C2014	U2150	G1642	G1642	C1571	C1461	U1344	A1203	A1099	G1007	C927	G765	U543
G2153	G2153	U1880	C2015	U2151	U1643	U1643	C1572	C1462	G1345	G1204	A1100	G1008	U928	G766	U544
G2154	G2154	C1887	C2016	U2152	C1644	C1644	C1573	C1463	U1346	A1205	A1101	G1009	A648	A767	A547
U2155	U2155	G1888	C2017	U2153	G1645	G1645	C1574	C1464	G1347	A1206	A1102	U1010	C655	A768	A548
C2158	C2158	U1889	C2018	U2154	C1646	C1646	C1575	C1465	G1348	U1207	A1103	C1012	C656	C549	C549
G2159	G2159	C1903	C2019	U2155	C1647	C1647	C1576	C1466	U1349	G1208	A1098	C1013	U922	C550	C550
A2160	A2160	U1904	C2020	U2156	C1648	C1648	C1577	C1467	G1349	A1209	A1099	U1013	G655	A785	G555
G2161	G2161	G1905	C2021	U2157	C1649	C1649	C1578	C1468	U1350	U1210	A1104	C1014	A666	C786	G561
G2162	G2162	U1906	C2022	U2158	C1650	C1650	C1579	C1469	G1351	A1211	A1105	C1015	A667	C787	G562
U2163	U2163	G1917	C2023	U2159	C1651	C1651	C1580	C1470	G1352	A1212	A1106	C1016	A678	C788	G563
C2166	C2166	U1918	C2024	U2160	C1652	C1652	C1581	C1471	U1353	U1213	A1107	C1017	G679	G794	A566
			C2025	U2161	C1653	C1653	C1582	C1472	U1354	C1214	A1108	U1014	A567	U801	A567
			C2026	U2162	C1654	C1654	C1583	C1473	U1355	A1215	A1109	C1015	A568	C802	A568
			C2027	U2163	C1655	C1655	C1584	C1474	U1356	A1216	A1110	C1016	G685	U802	G569
			C2028	U2164	C1656	C1656	C1585	C1475	U1357	U1217	A1111	C1017	U689	A830	C572
			C2029	U2165	C1657	C1657	C1586	C1476	U1358	U1218	A1112	C1018	A696	A831	G585
			C2030	U2166	C1658	C1658	C1587	C1477	U1359	U1219	A1113	C1019		G832	
			C2031	U2167	C1659	C1659	C1588	C1478	U1360	C1220	A1114	A1025			
			C2032	U2168	C1660	C1660	C1589	C1479	U1361	G1221	A1115	A1026			
			C2033	U2169	C1661	C1661	C1590	C1480	U1362	G1222	A1116	A1027			
			C2034	U2170	C1662	C1662	C1591	C1481	U1363	G1223	A1117	A1028			
			C2035	U2171	C1663	C1663	C1592	C1482	U1364	U1224	A1118	A1029			
			C2036	U2172	C1664	C1664	C1593	C1483	U1365	G1225	A1119	C1030			
			C2037	U2173	C1665	C1665	C1594	C1484	U1366	A1226	A1120	C1031			
			C2038	U2174	C1666	C1666	C1595	C1485	U1367	U1227	A1121	C1032			
			C2039	U2175	C1667	C1667	C1596	C1486	U1368	A1228	A1122	C1033			
			C2040	U2176	C1668	C1668	C1597	C1487	U1369	U1229	A1123	C1034			
			C2041	U2177	C1669	C1669	C1598	C1488	U1370	G1230	A1124	C1035			
			C2042	U2178	C1670	C1670	C1599	C1489	U1371	U1231	A1125	C1036			
			C2043	U2179	C1671	C1671	C1600	C1490	U1372	G1232	A1126	C1037			
			C2044	U2180	C1672	C1672	C1601	C1491	U1373		A1127	C1038			
			C2045	U2181	C1673	C1673	C1602	C1492	U1374		A1128	C1039			
			C2046	U2182	C1674	C1674	C1603	C1493	U1375		A1129	C1040			
			C2047	U2183	C1675	C1675	C1604	C1494	U1376		A1130	C1041			
			C2048	U2184	C1676	C1676	C1605	C1495	U1377		A1131	C1042			
			C2049	U2185	C1677	C1677	C1606	C1496	U1378		A1132	C1043			
			C2050	U2186	C1678	C1678	C1607	C1497	U1379		A1133	C1044			
			C2051	U2187	C1679	C1679	C1608	C1498	U1380		A1134	C1045			
			C2052	U2188	C1680	C1680	C1609	C1499	U1381		A1135	C1046			
			C2053	U2189	C1681	C1681	C1610	C1500	U1382		A1136	C1047			
			C2054	U2190	C1682	C1682	C1611	C1501	U1383		A1137	C1048			
			C2055	U2191	C1683	C1683	C1612	C1502	U1384		A1138	C1049			
			C2056	U2192	C1684	C1684	C1613	C1503	U1385		A1139	C1050			
			C2057	U2193	C1685	C1685	C1614	C1504	U1386		A1140	C1051			
			C2058	U2194	C1686	C1686	C1615	C1505	U1387		A1141	C1052			
			C2059	U2195	C1687	C1687	C1616	C1506	U1388		A1142	C1053			
			C2060	U2196	C1688	C1688	C1617	C1507	U1389		A1143	C1054			
			C2061	U2197	C1689	C1689	C1618	C1508	U1390		A1144	C1055			
			C2062	U2198	C1690	C1690	C1619	C1509	U1391		A1145	C1056			
			C2063	U2199	C1691	C1691	C1620	C1510	U1392		A1146	C1057			
			C2064	U2200	C1692	C1692	C1621	C1511	U1393		A1147	C1058			
			C2065	U2201	C1693	C1693	C1622	C1512	U1394		A1148	C1059			
			C2066	U2202	C1694	C1694	C1623	C1513	U1395		A1149	C1060			
			C2067	U2203	C1695	C1695	C1624	C1514	U1396		A1150	C1061			
			C2068	U2204	C1696	C1696	C1625	C1515	U1397		A1151	C1062			
			C2069	U2205	C1697	C1697	C1626	C1516	U1398		A1152	C1063			
			C2070	U2206	C1698	C1698	C1627	C1517	U1399		A1153	C1064			
			C2071	U2207	C1699	C1699	C1628	C1518	U1400		A1154	C1065			
			C2072	U2208	C1700	C1700	C1629	C1519	U1401		A1155	C1066			
			C2073	U2209	C1701	C1701	C1630	C1520	U1402		A1156	C1067			
			C2074	U2210	C1702	C1702	C1631	C1521	U1403		A1157	C1068			
			C2075	U2211	C1703	C1703	C1632	C1522	U1404		A1158	C1069			
			C2076	U2212	C1704	C1704	C1633	C1523	U1405		A1159	C1070			
			C2077	U2213	C1705	C1705	C1634	C1524	U1406		A1160	C1071			
			C2078	U2214	C1706	C1706	C1635	C1525	U1407						



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	391837	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	1.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.253	Depositor
Minimum map value	-0.087	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.03	Depositor
Map size ( $\text{\AA}$ )	419.84, 419.84, 419.84	wwPDB
Map dimensions	328, 328, 328	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.28, 1.28, 1.28	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	a	0.81	24/36201 (0.1%)	1.27	213/56488 (0.4%)
2	c	0.36	0/1696	0.62	2/2276 (0.1%)
3	e	0.39	0/1449	0.67	5/1949 (0.3%)
4	g	0.35	0/1260	0.58	0/1701
5	h	0.42	0/1018	0.71	2/1375 (0.1%)
6	i	0.36	0/1012	0.74	2/1362 (0.1%)
7	j	0.36	0/789	0.60	0/1069
8	k	0.31	0/889	0.57	0/1201
9	l	0.38	0/969	0.75	0/1294
10	o	0.34	0/718	0.58	0/963
11	q	0.39	0/741	0.67	1/993 (0.1%)
12	r	0.34	0/517	0.56	0/691
13	s	0.34	0/647	0.64	0/871
14	t	0.33	0/658	0.52	0/875
15	n	0.53	0/488	0.57	0/650
16	b	0.31	0/1822	0.54	0/2457
17	d	0.38	0/1672	0.61	1/2251 (0.0%)
18	f	0.38	0/782	0.62	1/1059 (0.1%)
19	m	0.36	0/942	0.62	0/1260
20	p	0.41	0/908	0.60	0/1226
21	u	0.49	0/280	0.67	0/359
22	w	0.78	1/1835 (0.1%)	1.23	20/2857 (0.7%)
23	x	0.56	0/843	0.93	6/1127 (0.5%)
25	C	1.00	5/2140 (0.2%)	0.93	5/2879 (0.2%)
26	D	0.54	0/1609	0.65	2/2165 (0.1%)
27	E	0.84	1/1576 (0.1%)	0.87	4/2132 (0.2%)
28	F	0.58	0/1459	0.79	1/1962 (0.1%)
29	G	0.36	0/1369	0.57	0/1848
30	H	0.33	0/1027	0.61	1/1398 (0.1%)
31	I	0.29	0/925	0.52	0/1246
32	J	0.29	0/1006	0.60	0/1364
33	K	0.76	1/1165 (0.1%)	0.88	4/1578 (0.3%)
34	L	0.92	0/938	0.96	5/1257 (0.4%)
35	M	0.53	0/1091	0.65	0/1457

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
36	N	0.91	1/1100 (0.1%)	0.86	1/1482 (0.1%)
37	O	0.74	0/936	0.95	5/1256 (0.4%)
38	P	0.43	0/966	0.57	0/1298
39	Q	0.51	0/921	0.60	1/1236 (0.1%)
40	R	0.55	0/1000	0.58	0/1341
41	S	0.47	0/778	0.57	0/1048
42	T	0.96	1/887 (0.1%)	0.93	3/1204 (0.2%)
43	U	0.75	0/749	0.87	2/1006 (0.2%)
44	V	0.65	0/737	0.78	1/987 (0.1%)
45	W	0.52	0/1404	0.81	5/1917 (0.3%)
46	X	0.96	0/613	0.87	1/821 (0.1%)
47	Y	0.55	0/478	0.71	0/641
48	Z	0.68	0/530	0.75	0/708
49	v	0.80	0/486	0.88	0/651
50	y	0.37	0/520	0.60	1/698 (0.1%)
51	z	0.55	0/427	0.61	0/572
52	1	0.73	1/424 (0.2%)	0.78	2/567 (0.4%)
53	2	0.84	0/375	1.00	1/493 (0.2%)
54	3	0.92	0/507	0.94	2/672 (0.3%)
55	4	0.82	0/302	0.77	0/401
56	5	0.44	0/191	0.60	0/247
57	B	0.55	1/2797 (0.0%)	1.15	19/4357 (0.4%)
58	A	1.00	1/74597 (0.0%)	1.24	627/116386 (0.5%)
All	All	0.84	37/164166 (0.0%)	1.13	946/245629 (0.4%)

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
2	c	0	1
3	e	0	1
4	g	0	3
5	h	0	2
7	j	0	1
8	k	0	2
9	l	0	2
11	q	0	1
12	r	0	1
13	s	0	2
17	d	0	1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	#Chirality outliers	#Planarity outliers
23	x	0	11
24	0	0	8
25	C	0	5
26	D	0	2
27	E	0	5
28	F	0	1
33	K	0	1
36	N	0	2
37	O	0	2
42	T	0	1
43	U	0	1
45	W	0	2
52	1	0	2
All	All	0	60

The worst 5 of 37 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	w	1	C	OP3-P	-11.11	1.47	1.61
57	B	1	G	OP3-P	-10.43	1.48	1.61
1	a	861	C	N1-C6	-7.36	1.32	1.37
1	a	552	A	N9-C4	-7.21	1.33	1.37
25	C	79	VAL	CB-CG2	-6.93	1.38	1.52

The worst 5 of 946 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	A	323	C	N1-C2-O2	11.58	125.85	118.90
58	A	1130	C	N1-C2-O2	11.12	125.57	118.90
58	A	2245	C	N1-C2-O2	11.04	125.52	118.90
58	A	2245	C	C2-N1-C1'	10.65	130.51	118.80
58	A	323	C	C2-N1-C1'	10.46	130.31	118.80

There are no chirality outliers.

5 of 60 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	c	62	ARG	Peptide
3	e	186	ILE	Peptide
4	g	1	MET	Peptide
4	g	32	LEU	Peptide

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Group
4	g	76	ARG	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	
2	c	208/275 (76%)	184 (88%)	17 (8%)	7 (3%)	3	17
3	e	196/214 (92%)	176 (90%)	19 (10%)	1 (0%)	25	54
4	g	154/156 (99%)	144 (94%)	9 (6%)	1 (1%)	22	50
5	h	128/132 (97%)	119 (93%)	8 (6%)	1 (1%)	16	44
6	i	124/150 (83%)	108 (87%)	13 (10%)	3 (2%)	5	23
7	j	95/101 (94%)	84 (88%)	10 (10%)	1 (1%)	12	37
8	k	115/138 (83%)	103 (90%)	10 (9%)	2 (2%)	7	28
9	l	120/124 (97%)	93 (78%)	26 (22%)	1 (1%)	16	44
10	o	85/89 (96%)	81 (95%)	4 (5%)	0	100	100
11	q	90/98 (92%)	79 (88%)	11 (12%)	0	100	100
12	r	62/84 (74%)	54 (87%)	8 (13%)	0	100	100
13	s	76/93 (82%)	68 (90%)	8 (10%)	0	100	100
14	t	82/86 (95%)	77 (94%)	5 (6%)	0	100	100
15	n	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
16	b	226/277 (82%)	211 (93%)	15 (7%)	0	100	100
17	d	198/201 (98%)	185 (93%)	12 (6%)	1 (0%)	25	54
18	f	94/96 (98%)	90 (96%)	4 (4%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	m	114/124 (92%)	102 (90%)	12 (10%)	0	100	100
20	p	111/156 (71%)	104 (94%)	7 (6%)	0	100	100
21	u	30/33 (91%)	28 (93%)	2 (7%)	0	100	100
23	x	98/230 (43%)	80 (82%)	15 (15%)	3 (3%)	3	18
25	C	271/278 (98%)	234 (86%)	33 (12%)	4 (2%)	8	30
26	D	212/217 (98%)	197 (93%)	10 (5%)	5 (2%)	5	23
27	E	205/215 (95%)	179 (87%)	20 (10%)	6 (3%)	3	19
28	F	179/187 (96%)	163 (91%)	14 (8%)	2 (1%)	12	37
29	G	174/179 (97%)	166 (95%)	8 (5%)	0	100	100
30	H	149/151 (99%)	139 (93%)	9 (6%)	1 (1%)	19	47
31	I	124/175 (71%)	118 (95%)	6 (5%)	0	100	100
32	J	131/142 (92%)	118 (90%)	13 (10%)	0	100	100
33	K	145/147 (99%)	132 (91%)	10 (7%)	3 (2%)	5	24
34	L	119/122 (98%)	106 (89%)	10 (8%)	3 (2%)	4	22
35	M	143/147 (97%)	128 (90%)	15 (10%)	0	100	100
36	N	132/138 (96%)	111 (84%)	20 (15%)	1 (1%)	16	44
37	O	115/199 (58%)	101 (88%)	11 (10%)	3 (3%)	4	22
38	P	124/127 (98%)	119 (96%)	5 (4%)	0	100	100
39	Q	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
40	R	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
41	S	100/103 (97%)	94 (94%)	5 (5%)	1 (1%)	13	39
42	T	112/153 (73%)	103 (92%)	6 (5%)	3 (3%)	4	21
43	U	92/100 (92%)	76 (83%)	11 (12%)	5 (5%)	1	10
44	V	93/105 (89%)	83 (89%)	8 (9%)	2 (2%)	5	24
45	W	184/215 (86%)	156 (85%)	22 (12%)	6 (3%)	3	18
46	X	80/88 (91%)	61 (76%)	14 (18%)	5 (6%)	1	7
47	Y	61/64 (95%)	57 (93%)	4 (7%)	0	100	100
48	Z	61/77 (79%)	59 (97%)	1 (2%)	1 (2%)	8	29
49	v	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
50	y	64/75 (85%)	60 (94%)	3 (5%)	1 (2%)	8	29
51	z	52/57 (91%)	51 (98%)	1 (2%)	0	100	100

*Continued on next page...*



Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	1	48/55 (87%)	40 (83%)	5 (10%)	3 (6%)	1	7
53	2	43/47 (92%)	41 (95%)	2 (5%)	0	100	100
54	3	61/64 (95%)	54 (88%)	7 (12%)	0	100	100
55	4	35/37 (95%)	29 (83%)	5 (14%)	1 (3%)	3	19
56	5	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
All	All	6085/6909 (88%)	5493 (90%)	515 (8%)	77 (1%)	13	33

5 of 77 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	c	138	GLN
2	c	143	GLN
2	c	144	PRO
4	g	154	TYR
8	k	116	VAL

### 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	
2	c	171/212 (81%)	164 (96%)	7 (4%)	26	51
3	e	139/147 (95%)	135 (97%)	4 (3%)	37	61
4	g	132/132 (100%)	127 (96%)	5 (4%)	28	54
5	h	106/108 (98%)	103 (97%)	3 (3%)	38	62
6	i	102/125 (82%)	96 (94%)	6 (6%)	16	41
7	j	88/90 (98%)	86 (98%)	2 (2%)	45	67
8	k	91/105 (87%)	85 (93%)	6 (7%)	14	39
9	l	103/105 (98%)	98 (95%)	5 (5%)	21	48
10	o	75/77 (97%)	74 (99%)	1 (1%)	65	78
11	q	78/83 (94%)	78 (100%)	0	100	100
12	r	55/72 (76%)	54 (98%)	1 (2%)	54	73

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	s	69/84 (82%)	67 (97%)	2 (3%)	37	61
14	t	69/70 (99%)	66 (96%)	3 (4%)	25	50
15	n	49/50 (98%)	48 (98%)	1 (2%)	50	70
16	b	191/218 (88%)	187 (98%)	4 (2%)	48	69
17	d	175/176 (99%)	174 (99%)	1 (1%)	84	90
18	f	85/85 (100%)	84 (99%)	1 (1%)	67	80
19	m	99/104 (95%)	99 (100%)	0	100	100
20	p	92/118 (78%)	92 (100%)	0	100	100
21	u	30/31 (97%)	23 (77%)	7 (23%)	0	2
23	x	88/199 (44%)	66 (75%)	22 (25%)	0	1
25	C	214/218 (98%)	208 (97%)	6 (3%)	38	62
26	D	160/163 (98%)	156 (98%)	4 (2%)	42	65
27	E	167/173 (96%)	159 (95%)	8 (5%)	21	48
28	F	150/156 (96%)	138 (92%)	12 (8%)	10	31
29	G	148/150 (99%)	148 (100%)	0	100	100
30	H	90/116 (78%)	90 (100%)	0	100	100
31	I	89/120 (74%)	89 (100%)	0	100	100
32	J	102/108 (94%)	102 (100%)	0	100	100
33	K	120/120 (100%)	116 (97%)	4 (3%)	33	58
34	L	99/100 (99%)	97 (98%)	2 (2%)	50	70
35	M	112/114 (98%)	111 (99%)	1 (1%)	75	86
36	N	112/116 (97%)	109 (97%)	3 (3%)	40	63
37	O	96/158 (61%)	90 (94%)	6 (6%)	15	40
38	P	93/94 (99%)	93 (100%)	0	100	100
39	Q	100/100 (100%)	99 (99%)	1 (1%)	73	83
40	R	97/99 (98%)	96 (99%)	1 (1%)	73	83
41	S	82/83 (99%)	81 (99%)	1 (1%)	67	80
42	T	90/117 (77%)	86 (96%)	4 (4%)	24	50
43	U	82/85 (96%)	72 (88%)	10 (12%)	4	15
44	V	81/86 (94%)	75 (93%)	6 (7%)	11	35
45	W	152/168 (90%)	146 (96%)	6 (4%)	27	53

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	X	59/63 (94%)	57 (97%)	2 (3%)	32	57
47	Y	50/51 (98%)	50 (100%)	0	100	100
48	Z	58/66 (88%)	53 (91%)	5 (9%)	8	29
49	v	53/54 (98%)	51 (96%)	2 (4%)	28	54
50	y	57/63 (90%)	54 (95%)	3 (5%)	19	45
51	z	43/46 (94%)	43 (100%)	0	100	100
52	1	48/52 (92%)	41 (85%)	7 (15%)	2	10
53	2	35/36 (97%)	33 (94%)	2 (6%)	17	43
54	3	53/54 (98%)	53 (100%)	0	100	100
55	4	35/35 (100%)	34 (97%)	1 (3%)	37	61
56	5	18/19 (95%)	18 (100%)	0	100	100
All	All	5032/5574 (90%)	4854 (96%)	178 (4%)	33	56

5 of 178 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	L	8	LEU
43	U	96	PHE
36	N	92	TRP
42	T	6	GLU
45	W	6	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 102 such sidechains are listed below:

Mol	Chain	Res	Type
32	J	119	ASN
40	R	38	GLN
54	3	28	ASN
33	K	132	HIS
35	M	127	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1504/1528 (98%)	397 (26%)	0
22	w	76/77 (98%)	41 (53%)	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
57	B	116/118 (98%)	33 (28%)	1 (0%)
58	A	3096/3120 (99%)	785 (25%)	28 (0%)
All	All	4792/4843 (98%)	1256 (26%)	29 (0%)

5 of 1256 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	11	G
1	a	12	A
1	a	13	G
1	a	26	G
1	a	36	A

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
58	A	1010	U
58	A	2350	G
58	A	1186	G
58	A	2085	C
58	A	1117	U

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

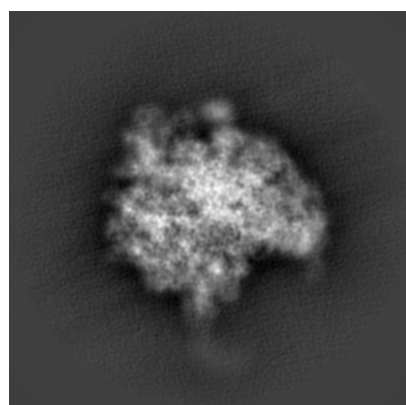
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6921. These allow visual inspection of the internal detail of the map and identification of artifacts.

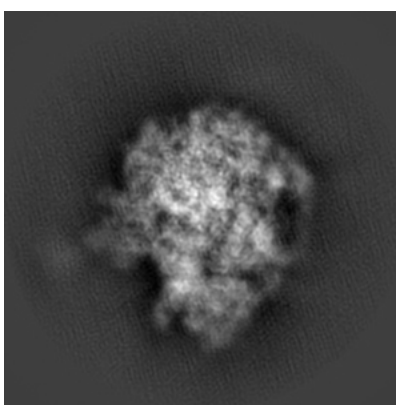
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

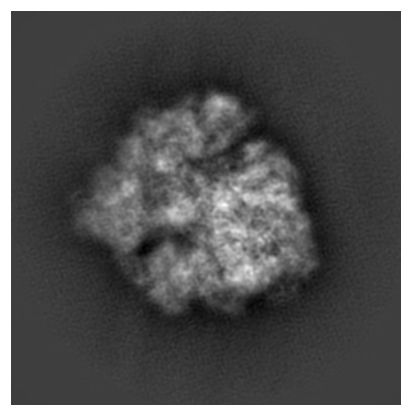
#### 6.1.1 Primary map



X



Y

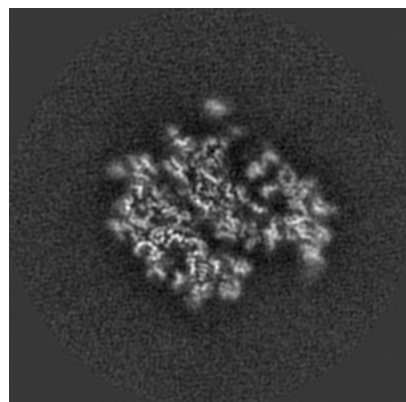


Z

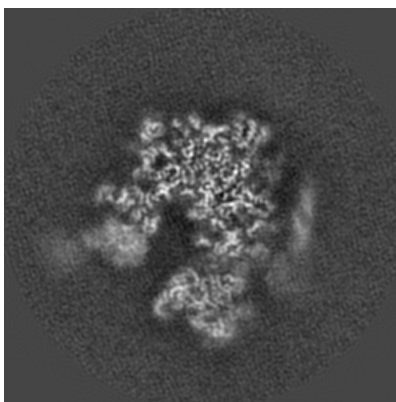
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

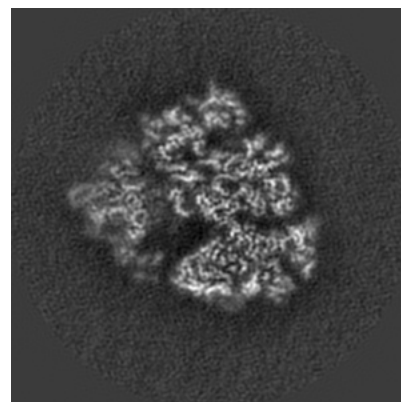
#### 6.2.1 Primary map



X Index: 164



Y Index: 164

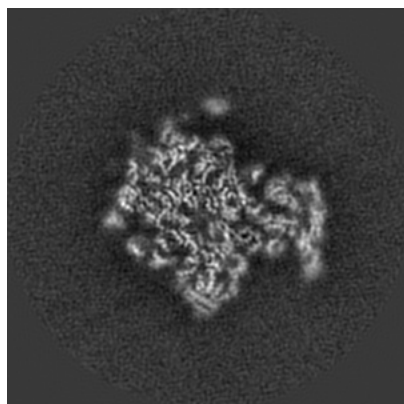


Z Index: 164

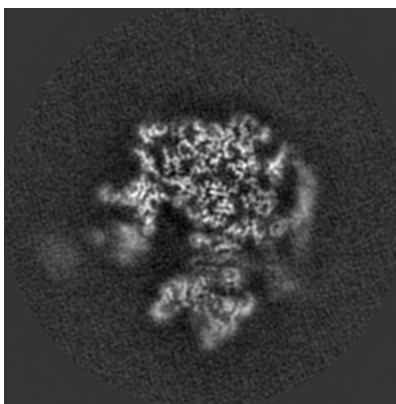
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

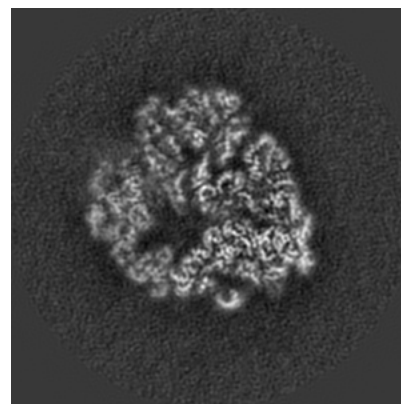
### 6.3.1 Primary map



X Index: 171



Y Index: 169

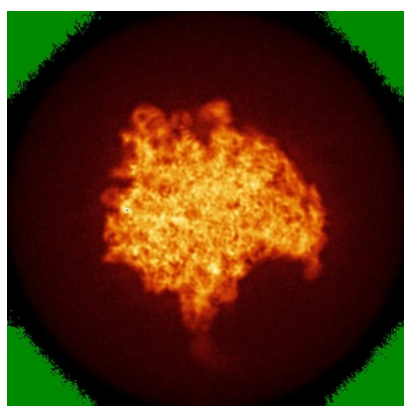


Z Index: 157

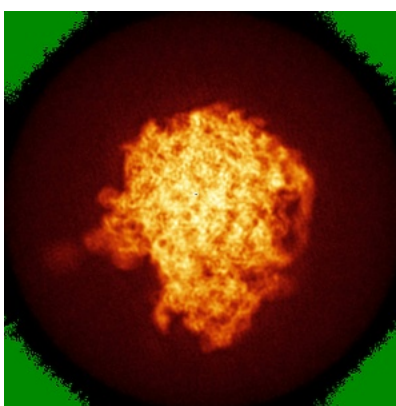
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

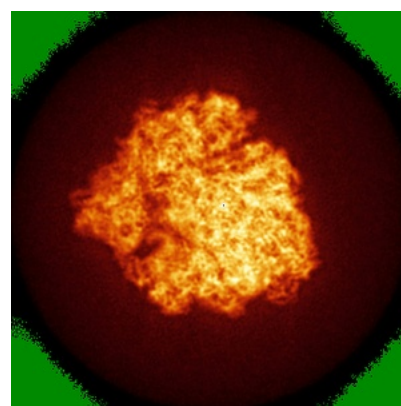
### 6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

## 6.6 Mask visualisation [i](#)

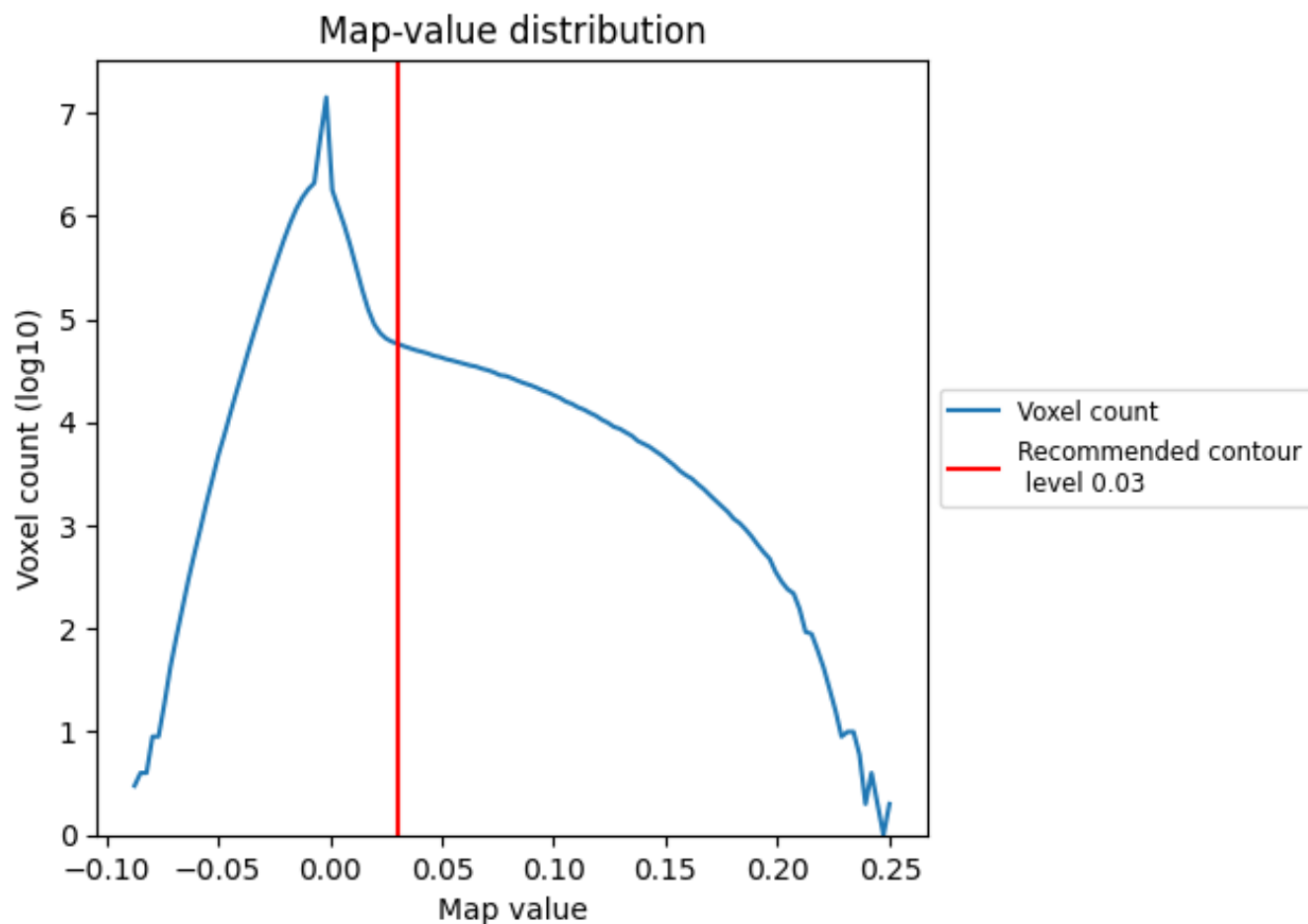
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

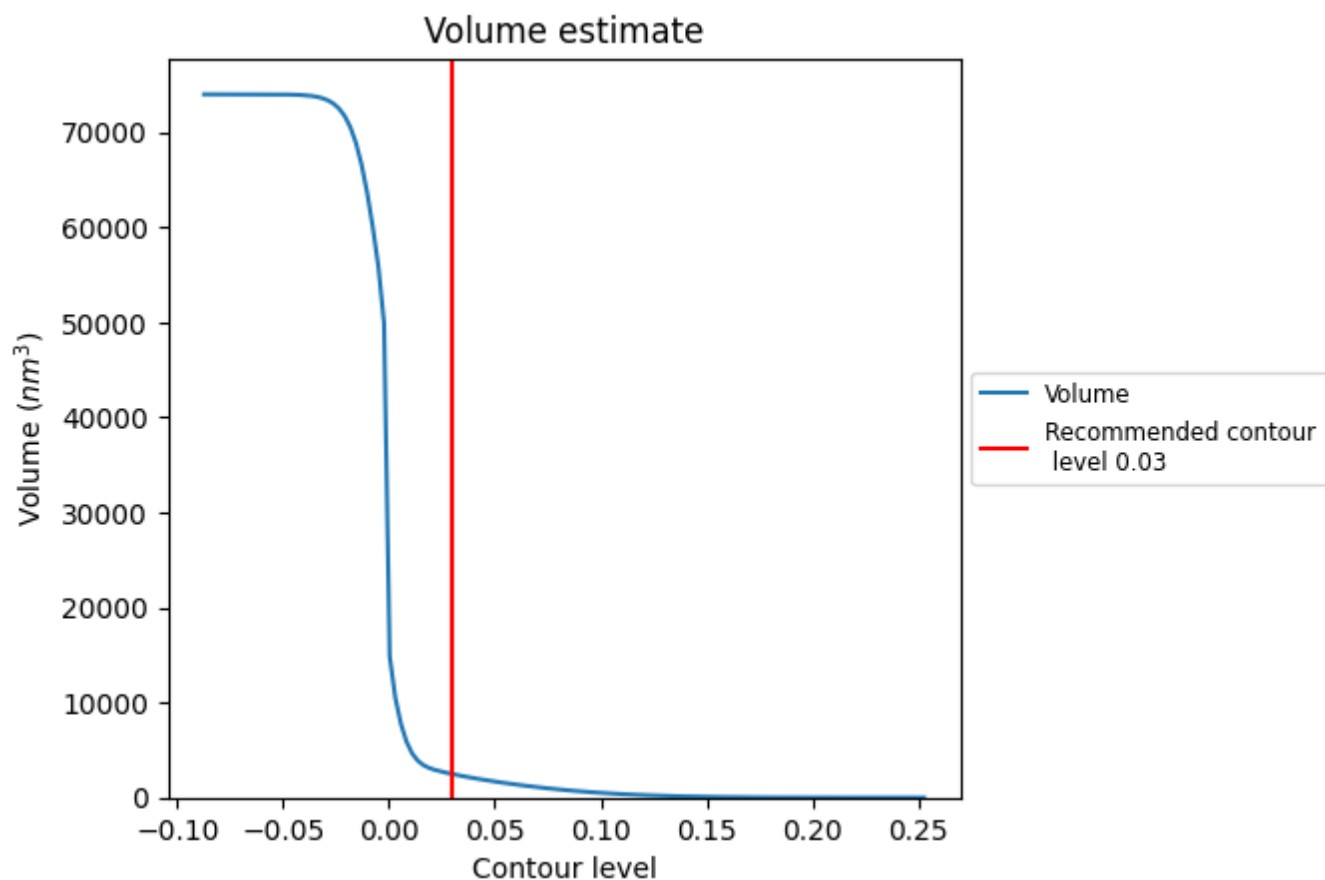
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

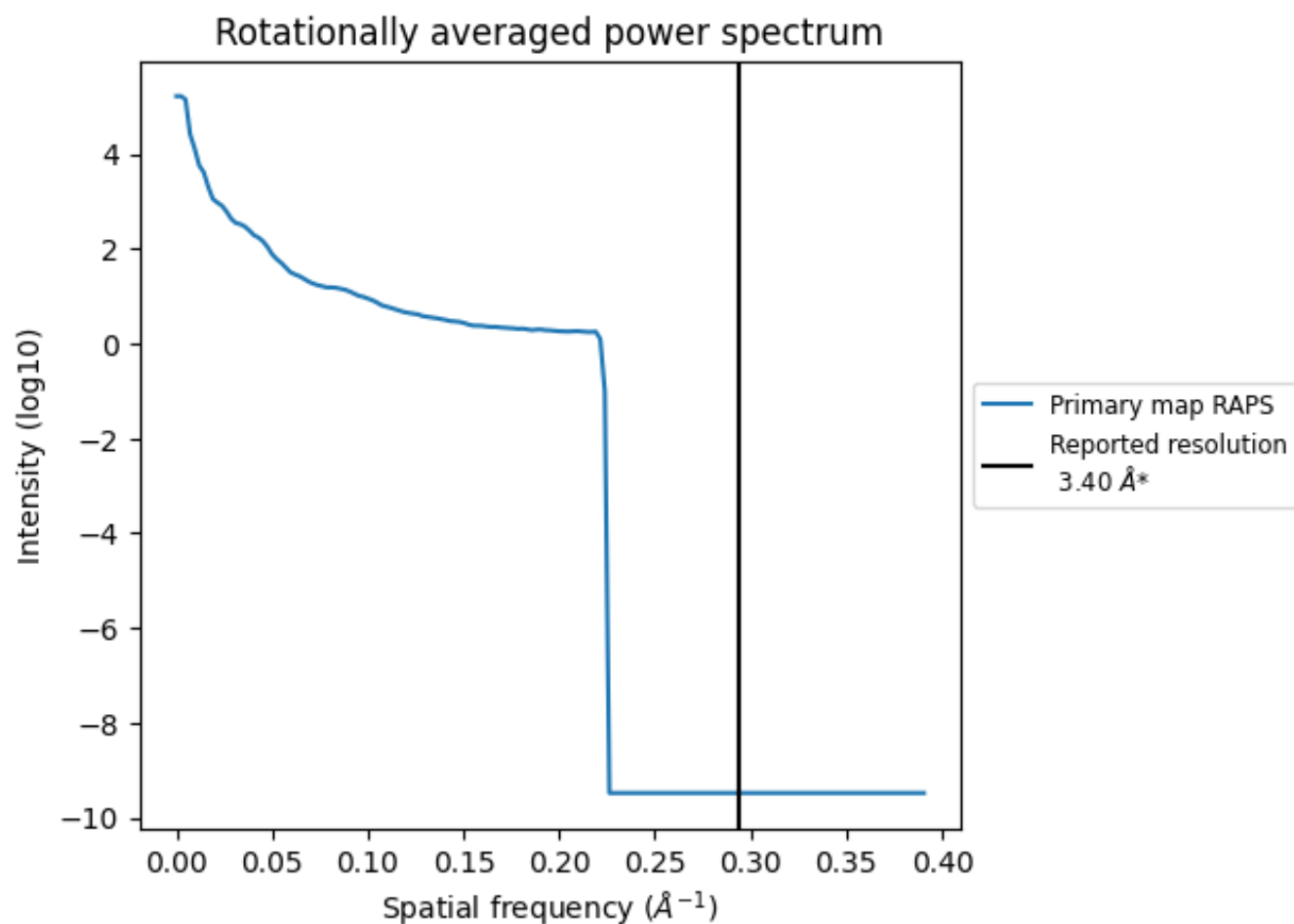
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2473 nm<sup>3</sup>; this corresponds to an approximate mass of 2234 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ



\*Reported resolution corresponds to spatial frequency of 0.294 Å<sup>-1</sup>

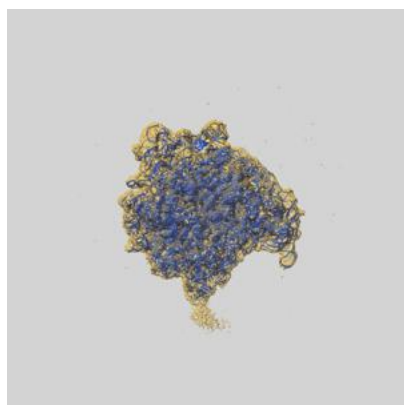
## 8 Fourier-Shell correlation ⓘ

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

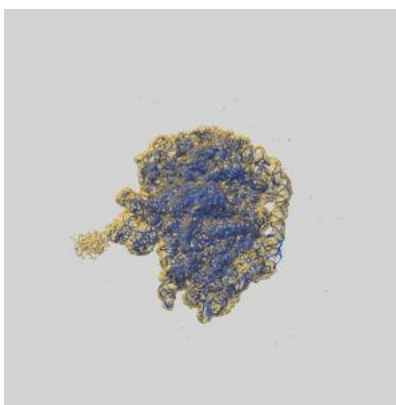
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6921 and PDB model 5ZEP. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

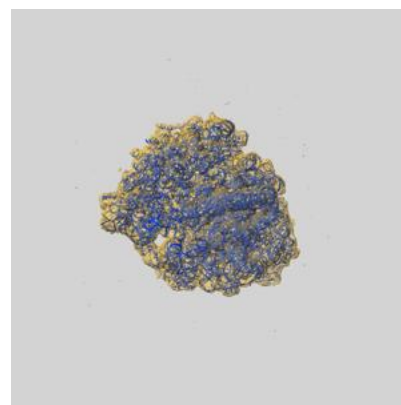
### 9.1 Map-model overlay [i](#)



X



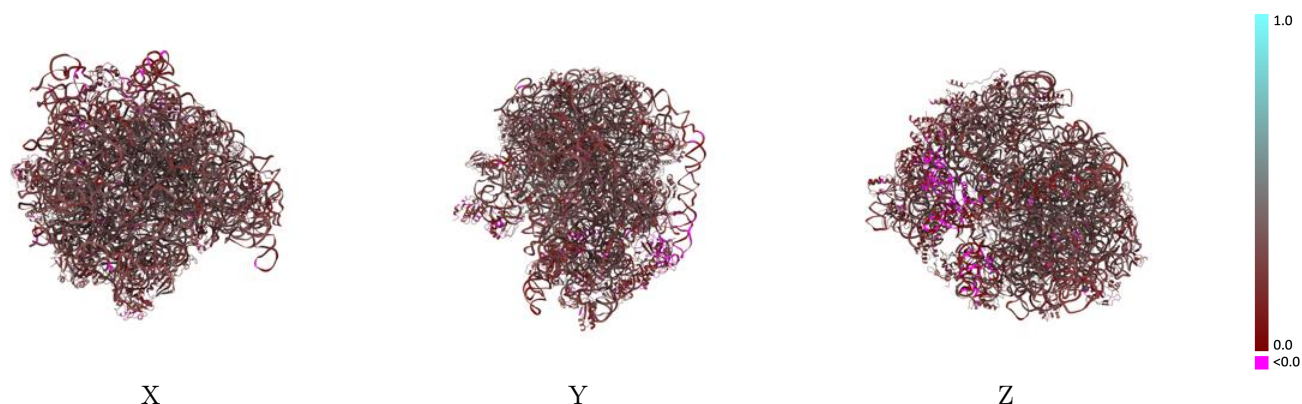
Y



Z

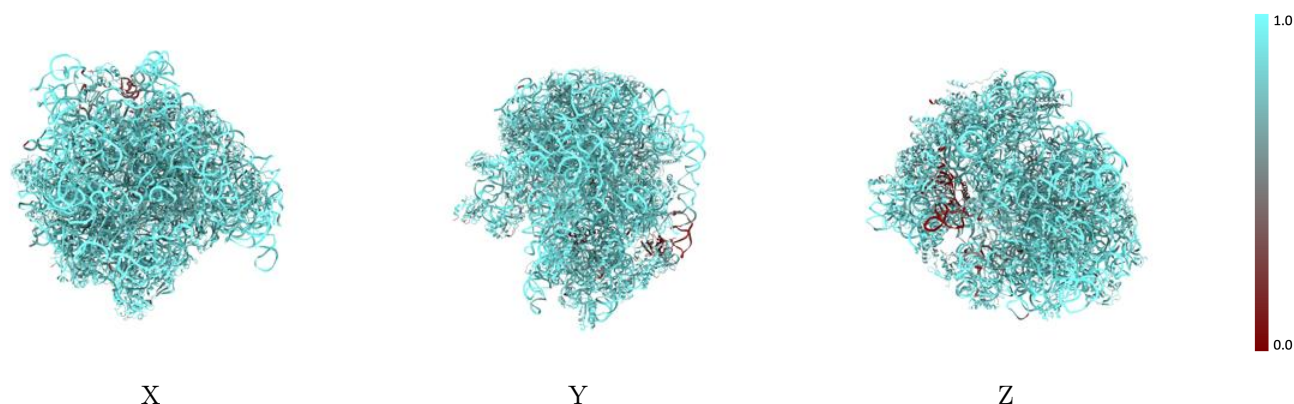
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



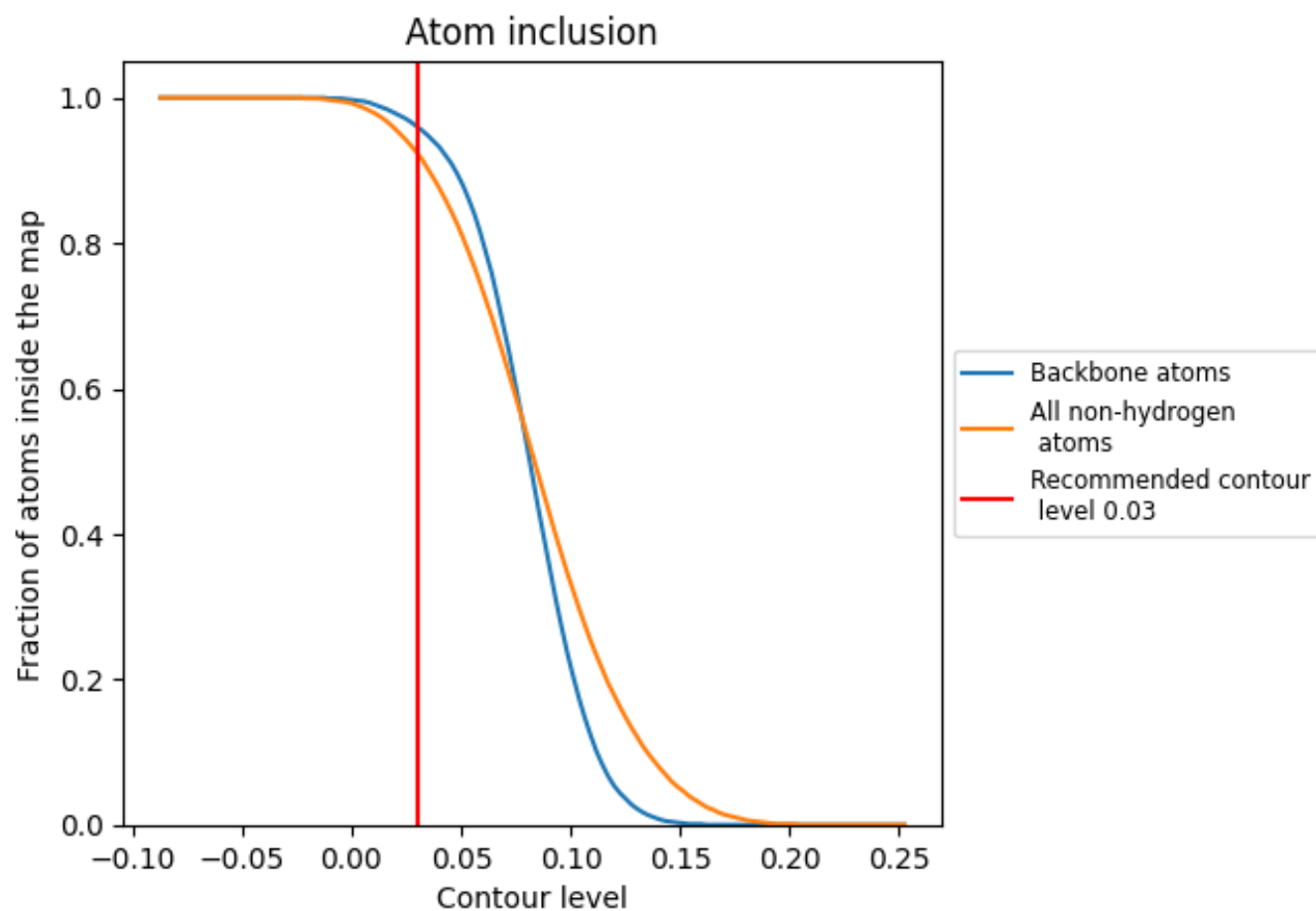
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).







































































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

















































Chain	Atom inclusion	Q-score
All	 0.9240	 0.2750
0	 0.4170	 0.0310
1	 0.8560	 0.2240
2	 0.8370	 0.3070
3	 0.8210	 0.2930
4	 0.8850	 0.2810
5	 0.8270	 0.2680
A	 0.9680	 0.2950
B	 0.9760	 0.2680
C	 0.8200	 0.2850
D	 0.8540	 0.2870
E	 0.8670	 0.2690
F	 0.8780	 0.2420
G	 0.9110	 0.2520
H	 0.8720	 0.2260
I	 0.8400	 0.1300
J	 0.8630	 0.1190
K	 0.8560	 0.2760
L	 0.7560	 0.2780
M	 0.8450	 0.2700
N	 0.8330	 0.2880
O	 0.8120	 0.2510
P	 0.9100	 0.2480
Q	 0.8040	 0.2540
R	 0.8550	 0.2450
S	 0.8680	 0.3080
T	 0.8290	 0.2830
U	 0.8340	 0.2990
V	 0.8780	 0.2290
W	 0.8890	 0.2550
X	 0.8060	 0.2590
Y	 0.8460	 0.3030
Z	 0.8420	 0.2110
a	 0.9860	 0.3000
b	 0.8330	 0.1980



*Continued on next page...*



*Continued from previous page...*

Chain	Atom inclusion	Q-score
c	 0.8420	 0.2040
d	 0.8530	 0.1940
e	 0.8140	 0.2510
f	 0.8650	 0.2630
g	 0.8400	 0.2020
h	 0.8760	 0.2830
i	 0.9170	 0.2300
j	 0.8770	 0.2300
k	 0.8600	 0.2540
l	 0.8090	 0.2680
m	 0.8560	 0.2020
n	 0.8420	 0.2520
o	 0.8440	 0.2410
p	 0.8680	 0.2440
q	 0.8140	 0.2600
r	 0.8850	 0.2500
s	 0.8470	 0.2270
t	 0.8300	 0.1930
u	 0.6830	 0.2450
v	 0.8310	 0.2500
w	 0.6690	 0.1340
x	 0.2420	 -0.0160
y	 0.8460	 0.2190
z	 0.8210	 0.2820