



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 01:59 PM UTC

PDB ID : 8UZ3 / pdb_00008uz3
EMDB ID : EMD-42832
Title : E. coli 70S ribosome with unmodified e*/E-tRNAPro(GGG) bound to slippery P-site CCC-C codon
Authors : Kimbrough, E.M.; Dunham, C.M.; Nguyen, H.A.
Deposited on : 2023-11-14
Resolution : 3.20 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

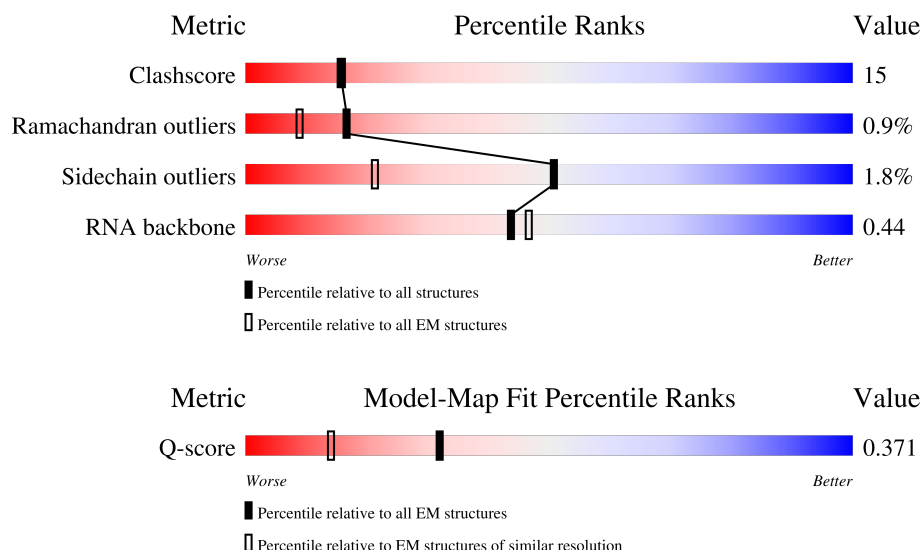
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



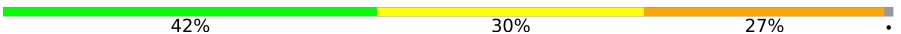
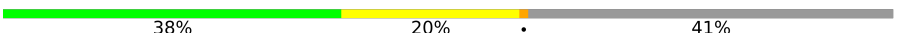
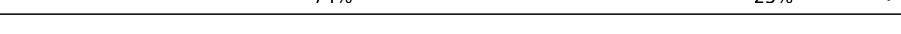
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	1	2904	38% 52% 10%
2	2	1540	32% 56% 12%
3	3	120	48% 47% 5%

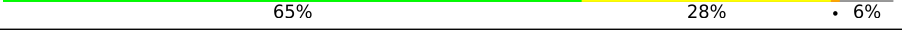
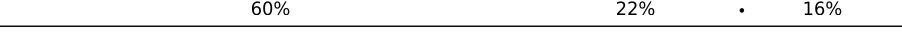
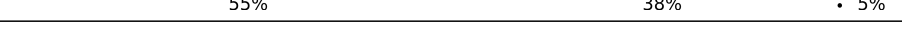
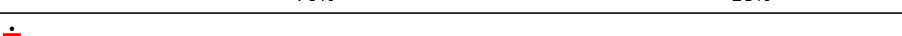
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Mol	Chain	Length	Quality of chain
4	4	18	
5	5	77	
6	A	229	
7	B	273	
8	C	209	
9	D	201	
10	E	179	
11	F	177	
12	G	149	
13	J	142	
14	K	123	
15	L	144	
16	M	136	
17	N	127	
18	O	117	
19	P	115	
20	Q	118	
21	R	103	
22	S	110	
23	T	100	
24	U	104	
25	V	94	
26	W	84	
27	X	78	
28	Y	63	

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Mol	Chain	Length	Quality of chain
29	Z	59	
30	b	57	
31	c	55	
32	d	46	
33	e	65	
34	f	38	
35	h	206	
36	i	206	
37	j	167	
38	k	135	
39	l	179	
40	m	130	
41	n	130	
42	o	103	
43	p	129	
44	q	124	
45	r	118	
46	s	101	
47	t	89	
48	u	82	
49	v	84	
50	w	75	
51	x	92	
52	y	87	
53	z	71	

2 Entry composition [i](#)

There are 55 unique types of molecules in this entry. The entry contains 144496 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 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1109114233

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	120	A	U	conflict	GB 1370526515

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	4	Total	C	N	O	P	0	0
			80	36	12	28	4		

- Molecule 5 is a RNA chain called tRNA ProL(GGG).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	76	Total	C	N	O	P	0	0
			1628	724	294	534	76		

- Molecule 6 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

- Molecule 7 is a protein called 50S ribosomal protein L2.

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

- Molecule 8 is a protein called 50S ribosomal protein L3.

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

- Molecule 9 is a protein called 50S ribosomal protein L4.

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

- Molecule 10 is a protein called 50S ribosomal protein L5.

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

- Molecule 11 is a protein called 50S ribosomal protein L6.

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

- Molecule 12 is a protein called 50S ribosomal protein L9.

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

- Molecule 13 is a protein called 50S ribosomal protein L13.

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

- Molecule 14 is a protein called 50S ribosomal protein L14.

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

- Molecule 15 is a protein called 50S ribosomal protein L15.

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

- Molecule 16 is a protein called 50S ribosomal protein L16.

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

- Molecule 17 is a protein called 50S ribosomal protein L17.

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

- Molecule 18 is a protein called 50S ribosomal protein L18.

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

- Molecule 19 is a protein called 50S ribosomal protein L19.

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

- Molecule 20 is a protein called 50S ribosomal protein L20.

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

- Molecule 21 is a protein called 50S ribosomal protein L21.

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

- Molecule 22 is a protein called 50S ribosomal protein L22.

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

- Molecule 23 is a protein called 50S ribosomal protein L23.

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

- Molecule 24 is a protein called 50S ribosomal protein L24.

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

- Molecule 25 is a protein called 50S ribosomal protein L25.

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

- Molecule 26 is a protein called 50S ribosomal protein L27.

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

- Molecule 27 is a protein called 50S ribosomal protein L28.

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

- Molecule 28 is a protein called 50S ribosomal protein L29.

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

- Molecule 29 is a protein called 50S ribosomal protein L30.

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

- Molecule 30 is a protein called 50S ribosomal protein L32.

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

- Molecule 31 is a protein called 50S ribosomal protein L33.

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

- Molecule 32 is a protein called 50S ribosomal protein L34.

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

- Molecule 33 is a protein called 50S ribosomal protein L35.

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

- Molecule 34 is a protein called 50S ribosomal protein L36.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	206	Total	C	N	O	S	0	0
			1625	1028	305	289	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	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- 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	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	116	Total	C	N	O	S	0	0
			869	535	173	158	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
			955	590	196	165	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	114	Total	C	N	O	S	0	0
			883	546	178	156	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
			648	411	121	113	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
52	y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
53	z	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	1	306	Total 306	Mg 306	0
54	2	78	Total 78	Mg 78	0
54	3	7	Total 7	Mg 7	0
54	4	1	Total 1	Mg 1	0
54	5	1	Total 1	Mg 1	0
54	B	2	Total 2	Mg 2	0
54	D	1	Total 1	Mg 1	0
54	E	1	Total 1	Mg 1	0
54	J	1	Total 1	Mg 1	0
54	K	1	Total 1	Mg 1	0
54	L	1	Total 1	Mg 1	0
54	M	1	Total 1	Mg 1	0
54	N	1	Total 1	Mg 1	0
54	Q	1	Total 1	Mg 1	0
54	R	1	Total 1	Mg 1	0
54	S	3	Total 3	Mg 3	0
54	W	1	Total 1	Mg 1	0
54	Z	1	Total 1	Mg 1	0
54	b	1	Total 1	Mg 1	0
54	m	1	Total 1	Mg 1	0
54	p	1	Total 1	Mg 1	0
54	q	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
54	r	1	Total 1	Mg 1	0
54	w	1	Total 1	Mg 1	0

- Molecule 55 is water.

Mol	Chain	Residues	Atoms		AltConf
55	1	812	Total 812	O 812	0
55	2	288	Total 288	O 288	0
55	3	13	Total 13	O 13	0
55	4	1	Total 1	O 1	0
55	5	5	Total 5	O 5	0
55	A	5	Total 5	O 5	0
55	B	1	Total 1	O 1	0
55	C	2	Total 2	O 2	0
55	E	2	Total 2	O 2	0
55	F	4	Total 4	O 4	0
55	G	8	Total 8	O 8	0
55	J	11	Total 11	O 11	0
55	K	3	Total 3	O 3	0
55	M	6	Total 6	O 6	0
55	N	1	Total 1	O 1	0
55	O	3	Total 3	O 3	0
55	P	2	Total 2	O 2	0

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Mol	Chain	Residues	Atoms		AltConf
55	Q	1	Total 1	O 1	0
55	R	1	Total 1	O 1	0
55	T	5	Total 5	O 5	0
55	U	4	Total 4	O 4	0
55	V	3	Total 3	O 3	0
55	W	3	Total 3	O 3	0
55	X	3	Total 3	O 3	0
55	Y	1	Total 1	O 1	0
55	Z	5	Total 5	O 5	0
55	c	6	Total 6	O 6	0
55	d	1	Total 1	O 1	0
55	h	9	Total 9	O 9	0
55	i	1	Total 1	O 1	0
55	j	4	Total 4	O 4	0
55	k	4	Total 4	O 4	0
55	l	4	Total 4	O 4	0
55	m	1	Total 1	O 1	0
55	o	1	Total 1	O 1	0
55	p	11	Total 11	O 11	0
55	r	1	Total 1	O 1	0
55	t	7	Total 7	O 7	0

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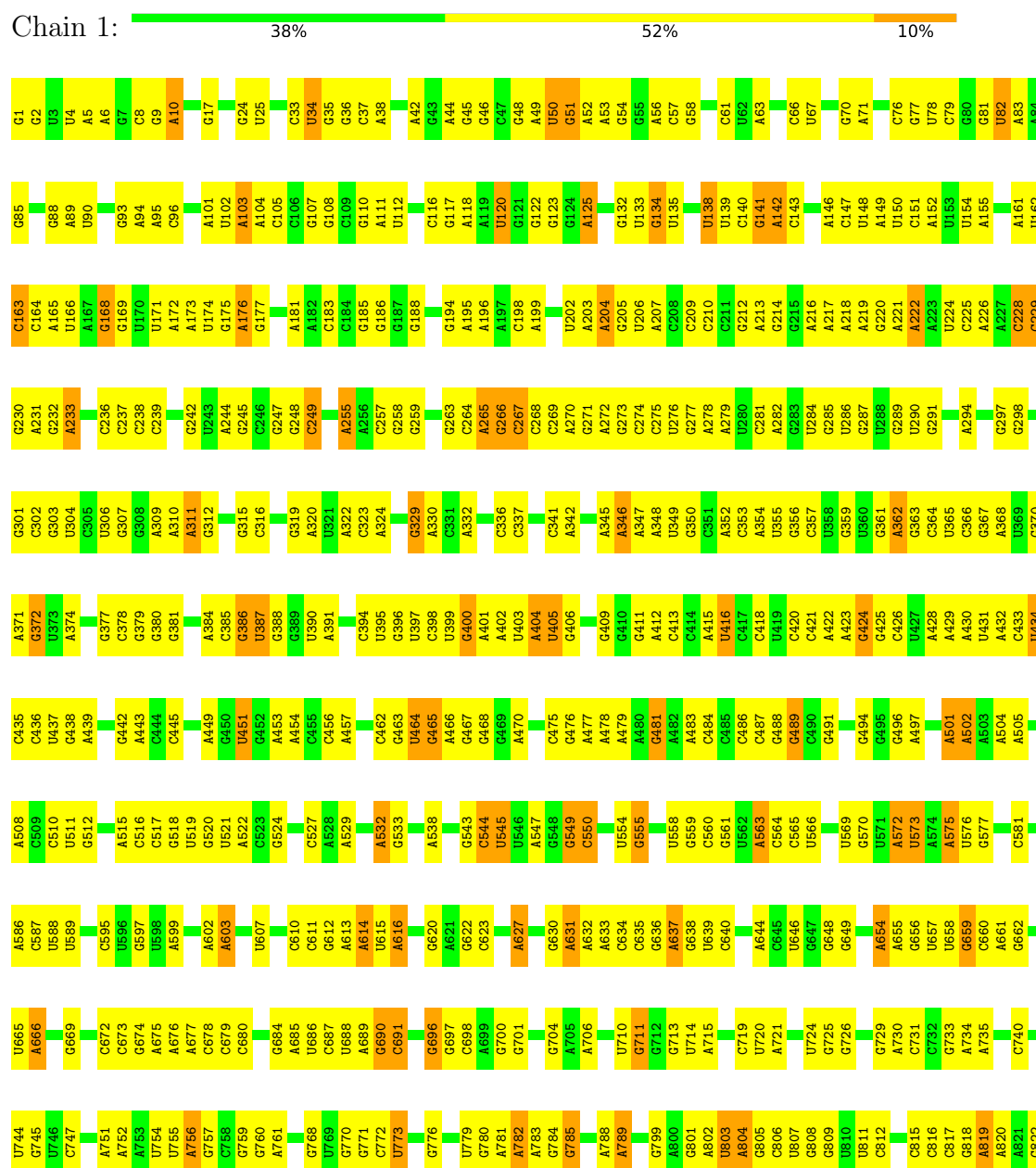
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Mol	Chain	Residues	Atoms		AltConf
55	w	4	Total	O	0
			4	4	
55	z	8	Total	O	0
			8	8	

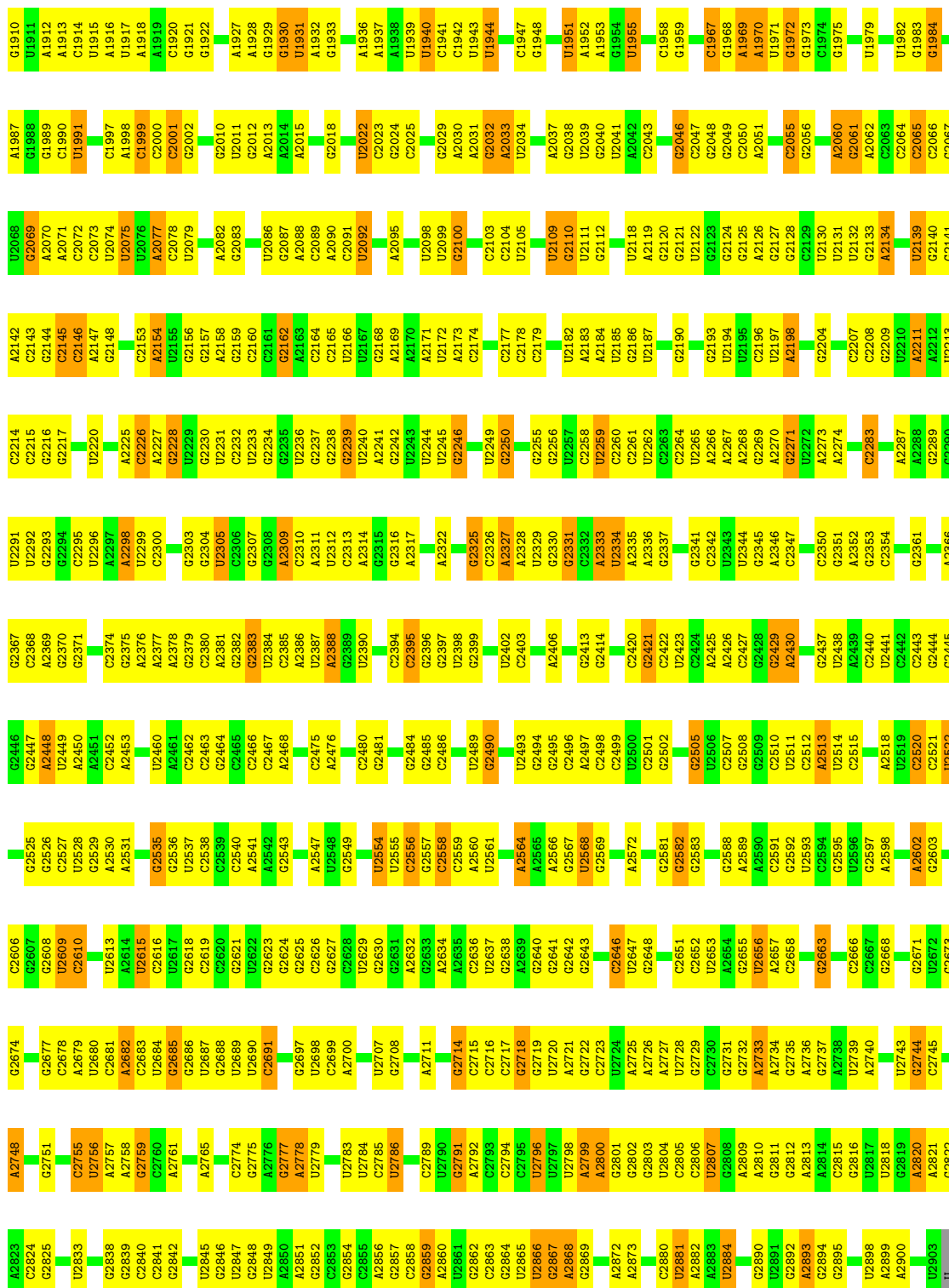
3 Residue-property plots

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 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: 23S ribosomal RNA

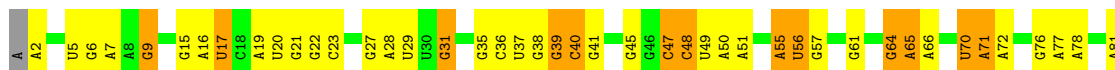


G1823	A1759	G1619	G1543	G1475	U1400	G1331	A1254	G1187	G1121	G1059	C982	U827
G1824	C1760	G1620	A1544	G1478	G1401	G1332	U1255	U1188	G1122	U1060	A983	U828
U1825	G1763	U1621	A1545	G1479	U1402	G1333	U1256	A1189	G1123	U1061	C915	A829
G1826	G1697	A1626	C1547	U1481	C1403	G1334	G1259	G1192	G1124	G1062	C989	A830
U1827	U1655	G1627	C1548	U1482	U1404	G1338	A1260	U1193	G1125	G1063	A990	G831
G1828	G1698	G1699	A1549	G1483	U1405	G1339	G1261	A1194	A1127	G1064	C993	A919
A1829	A1700	A1700	C1550	U1484	U1406	U1340	C1261	G1195	G1128	U1065	C994	A920
C1830	G1701	G1630	A1551	U1484	G1407	U1341	A1268	G1196	G1129	U1066	C995	G836
G1835	A1771	G1631	A1552	U1484	G1408	G1342	A1269	U1197	U1132	A1067	C996	A845
C1836	C1772	A1632	A1553	C1489	U1409	A1343	C1270	G1198	U1133	G1068	A996	U846
C1837	C1773	G1633	U1554	C1489	G1410	G1343	C1271	U1199	A1134	A1069	G997	G924
C1838	C1774	U1636	U1555	G1490	U1411	U1344	G1271	U1200	G1135	A1070	C998	A925
G1839	U1775	A1637	C1556	G1492	A1413	C1345	A1272	U1201	C1135	G1071	U999	U847
U1840	G1776	G1638	C1557	U1495	C1414	G1347	A1275	U1202	G1138	C1072	A1000	C848
U1841	U1777	C1639	U1558	A1496	U1415	A1348	G1278	G1203	G1139	A1073	A928	A849
G1842	U1778	A1640	U1559	U1497	G1416	C1349	C1279	U1204	G1140	G1074	U1001	U850
C1843	G1779	A1641	U1560	C1498	C1417	G1350	U1278	G1205	U1141	C1075	G930	G855
	A1780	G1642	U1561	C1499	G1418	C1351	U1282	G1206	A1142	C1076	C1005	G856
	U1781	G1643	U1562	C1499	A1419	U1352	U1282	C1207	A1143	U1077	C1006	G857
	U1782	G1644	A1563	C1499	A1500	A1353	G1283	C1208	A1144	U1078	C1007	G858
A1848	A1783	G1645	A1566	G1501	G1421	G1357	A1284	U1209	U1145	A1080	C1079	G859
G1849	U1784	U1646	G1567	A1502	G1422	C1363	A1285	G1210	C1146	U1083	U1012	U860
G1857	A1785	U1647	A1568	C1498	G1423	G1364	A1286	C1211	A1147	U1084	C1013	C865
	U1786	U1648	A1569	C1499	G1424	U1359	A1287	G1212	U1148	A1085	A1020	A866
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G1878	G1799	A1665	A1583	G1517	G1444	G1374	A1301	G1227	A1165	U1101	G1037	A886
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A1899	C1810	A1678	C1595	A1532	G1459	C1386	G1317	G1239	G1179	U1112	G1051	A899
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G1901	G1813	U1683	A1603	C1534	C1461	G1388	A1321	A1245	U1181	G1115	A1054	C901
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C1908	A1819	A1690	G1617	C1541	G1471	C1399	C1330					
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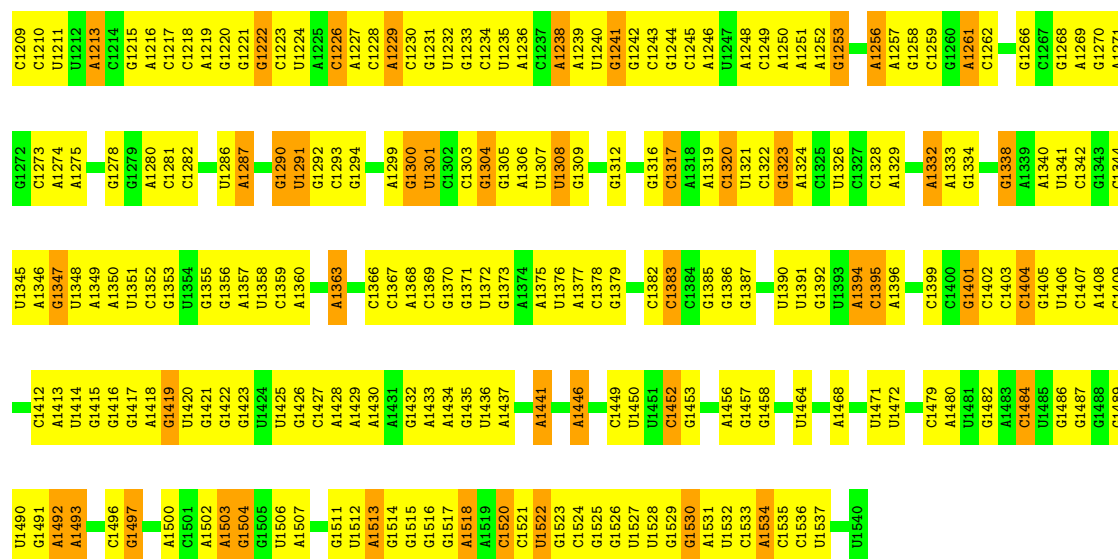


• Molecule 2: 16S ribosomal RNA

Chain 2: 32% 56% 12%

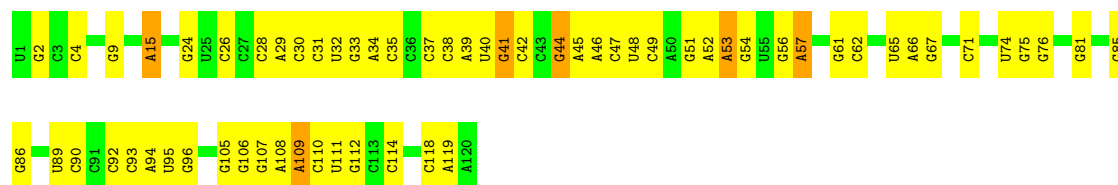


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A1150	A1080	G1013	G951	A878	A794	C720	G577	G515	A448	C385	C311	G159	G83	C83
A1151	A1081	A1014	U952	A878	C795	G721	C578	U516	G449	C386	C312	A160	U84	U84
A1152	A1082	G1015	G953	C879	C796	G722	A579	G517	G450	U387	A313	U245	U85	U85
G1153	U1085	A1016	G954	C880	G799	U723	C580	C518	A451	C388	C314	A162	G86	G86
G1154	U1086	U1017	U955	C881	G799	G724	C581	C519	A452	A389	A315	C163	C87	C87
U1086	G1086	G1018	U956	C882	G800	G724	C582	A520	G453	A393	C316	G247	U88	U88
A1155	U1087	G1018	U957	C883	U801	A728	A583	G521	G454	A393	G324	G165	U89	U89
A1156	G1088	A1021	A958	U884	A807	A729	C586	C522	G455	G394	G324	A171	C90	U91
A1157	U1089	A1022	A959	G885	A807	G730	C587	A523	A456	A397	C328	A253	U91	
C1158	U1090	U1023	U960	C886	C808	G731	C587	G524	G457	U398	A329	G175	G84	G84
U1159	U1091	G1024	U961	C887	G809	C732	C588	C525	U458	U399	A330	C176	C95	C95
G1160	A1092	U1025	C962	G890	C810	G733	U590	C526	A459	G399	C330	G177		
C1161	A1093	G1026	G963	U891	C811	G734	U593	G527	A460	C400	G331	G256		
C1162	G1094	C1027	A964	A892	G812	C735	U593	C528	A461	C401	G332	G257		
A1163	U1095	C1028	U965	C893	U813	C736	U594		A462	G402	U333	G258		
G1164	C1096	G966	A966	G894	A814	C737	A595		U463	C403	C334	G259		
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C1098	U1098	G1032	A968	C896	A816	C738	U598	A532	A465	G405	A336	U261		
A1167	G1099	G1033	A969	C897	C817		C599	A533	A466	U406	A337	G182		
C1168	U1100	G1034	C970	A900	G818	C744	C599	A533	A466	U407	A338	G185		
A1169	A1101	A1035	G971	A901	G818	G745	A600	A535	U467	U407	A338	C186		
C1170		A1036	G972	G902	A819	A746	C536	C536	A468	A408	C339	G187		
A1171	G1104	C1037	G973	G903	U820	A747	G606	G537	C469	U409	U340	G188		
A1105	A1105	C1038	A974	U904	G821	G748	A607	G538	C470	U268	U340	G189		
U1173	G1106		G975	U905	U828	A749	A608	A539		A411	C345	C289		
C1107	C1107	G1041	G976	A906	C879	C750	A609	G540	U476	A412	G346	A270		
C1108	U1108	A1042	A977	A907	U751	G679	U610	G541	C477	G413	G347	G191		
A1176	G1109	G1043	A978	A908	G833	G752	C613	G542	A478	A414	A348	C193		
G1177	A1110	A1044	C979	A908	U834	A753	U613	U543	U479	A415	A349	U273		
A1111	C1111	C1045	C980	A913	U835	C754	C614	G544	U480	C416	G350	A274		
A1178	A1111	A1046	U981	A914	G836	G755	G615	C546	G481	C417	G351	G275		
C1113	C1113	G1047	U982	A915	U837	C756	G616	A546		C418	C352	G276		
G1114	C1114	G1048	U983	U916	G838	C757	G617	A547	G484	C419	A353	C277		
U1115	U1115		C984	G917	U842	C758	C618	G548	U485	U420	G354	C277		
U1116	U1116	G1053	C985	A918	U843	A759	U619	C549	U486	U421	C355	A279		
A1184	A1117	C1054	U986	A919	U844	G760	C620		A487	C422	C355	C280		
C1185	U1118	A1055	G987	A919	G844	A761	U621	U552	C488	G423	U358	G281		
C1119	C1119	U1056	G988	C922	A845	G763	A622	A553	C489	C424	G359	A282		
G1120	G1120	G1057	U989	G922	G846	C764	C623	A554	C490	G425	G360	U209		
U1121	U1121	G1058		G922	G846	G765	C624	U555	C491	U426	C284	C210		
U1122	U1122	C1059	U992	G927	G849	A766	U625	C556	C492	U427	A363	G213		
C1190	U1123	C1059	G993	G928	U850	A767	G626	C557	A493	C428	A364	G214		
G1191	G1124	U1060	G993	C929	G851	A768	G627	A696	G494	U429	U365	C285		
C1192	U1125	C1061	A994	C930	U851	A768	C627	U558	A495	U429	U365	G289		
G1193	U1126	U1062	C995	C931	U855	G771	A630	A560	A496	A430	A366	C290		
C1127	C1193	C1063	C996	C932	C856	C631	U561	U561	G497	A431	U367	U291		
U1194	G1127	G1064	U997	G933	C857	A777	U632	U562	C497	A432	U368	G292		
C1195	C1128	U1065	C998	C934	C858	G778	U633	A563	C501	G433	G369	G293		
A1196		C1066	C999	C935	G859	C779	C634	C564	C501	U434	C372	U294		
A1197	U1136	A1067	A935	A935	U859	C779	C634	A564	A502	A435	C372	G294		
C1200	C1136	G1068	C1001	C936	A864	A780	C637	U565	C503	C436	A373	A298		
C1137	U1137	C1069	G1002	A937	A864	A781	C637	G566	C504	U437	A374	G297		
A1201	G1138	U1070	G1003	G939	A865	A782	U638	G567	U438	U438	U375	G299		
C1139	U1139	G1003	G1003	G939	C858	C783	U638	G568	U439	U439	G376	A300		
U1202	C1140	A1004	A1004	C940	C868	A784	U641	C569	C507	C440	G377	G301		
C1203	C1141	U1005	A1005	C945	G869	A784	A642	G570	U508	A441	G378	G302		
U1205	G1142	U1075	C1006	G945	U870	G713	C643	U571	A509	G442	C379	A303		
G1143	U1076	U1076	U1007	A946	U871	A789	U644	A572	A510	C443	G380	A236		
C1206	C1143	U1076	U1008	G947	A872	A790	C645	A573	C511	G444	C381	G237		
G1144	U1207	G1077	U1009	C948	A873	G791	G646	A574	U512	G445	A382	C307		
A1145	C1145	U1077	U1009	C948	A873	G791	G646	A574	U512	G445	A382	C307		
C1208	U1208	U1077	U1009	C948	A873	G791	G646	A574	U512	G445	A382	C307		



• Molecule 3: 5S ribosomal RNA

Chain 3: 48% 47% 5%



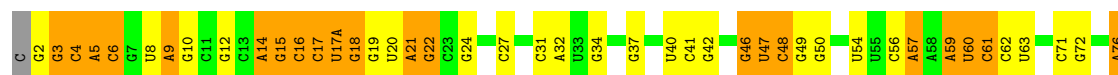
• Molecule 4: mRNA

Chain 4: 17% 6% 78%



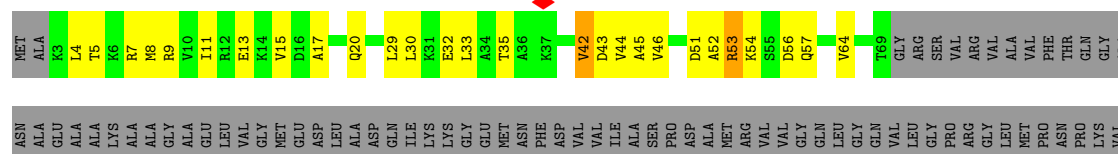
• Molecule 5: tRNA ProL(GGG)

Chain 5: 42% 30% 27%



• Molecule 6: 50S ribosomal protein L1

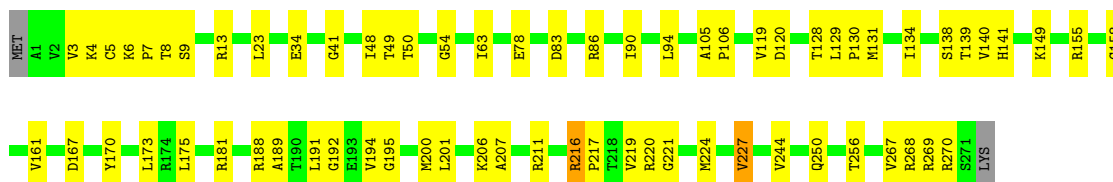
Chain A: 38% 20% 41%





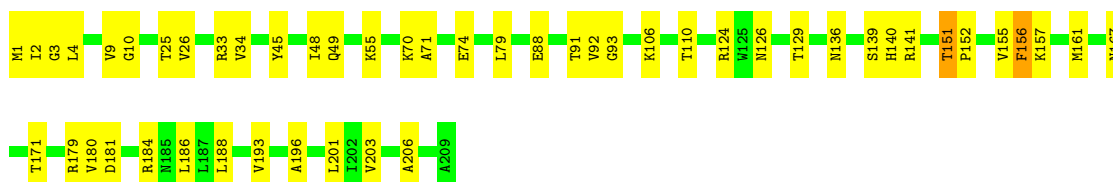
• Molecule 7: 50S ribosomal protein L2

Chain B: 74% 24% ..



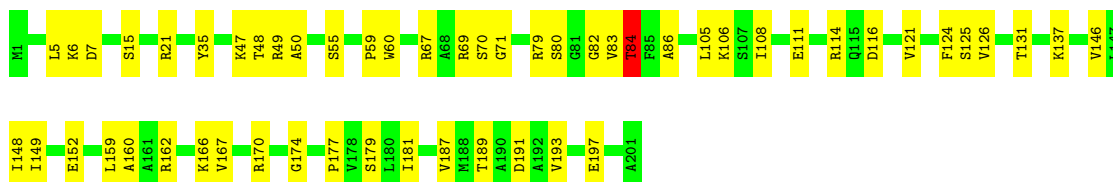
• Molecule 8: 50S ribosomal protein L3

Chain C: 76% 23% .



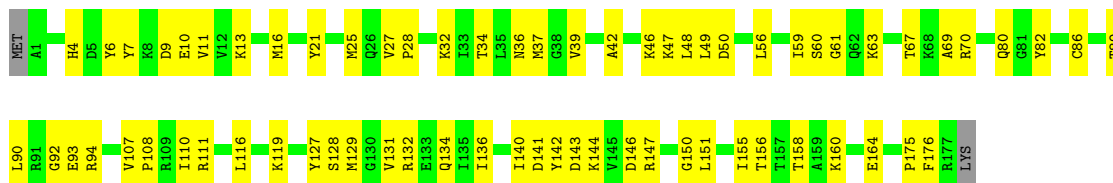
• Molecule 9: 50S ribosomal protein L4

Chain D: 73% 26%



• Molecule 10: 50S ribosomal protein L5

Chain E: 61% 38% .



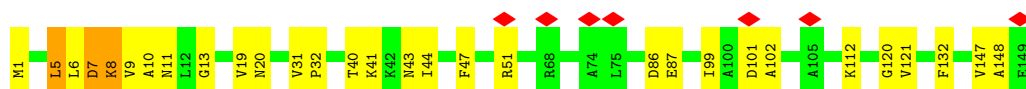
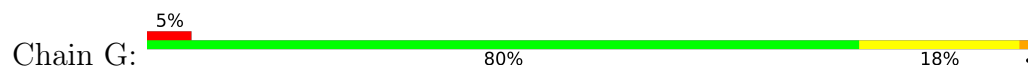
• Molecule 11: 50S ribosomal protein L6

Chain F: 70% 27% ..

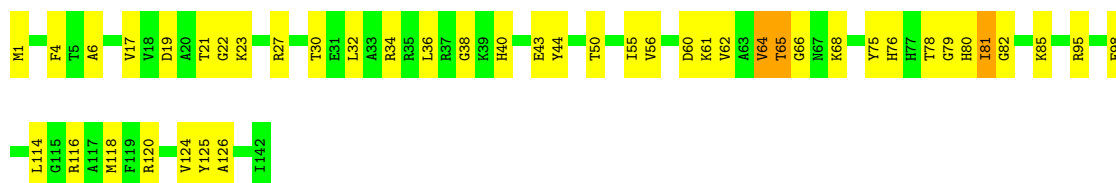




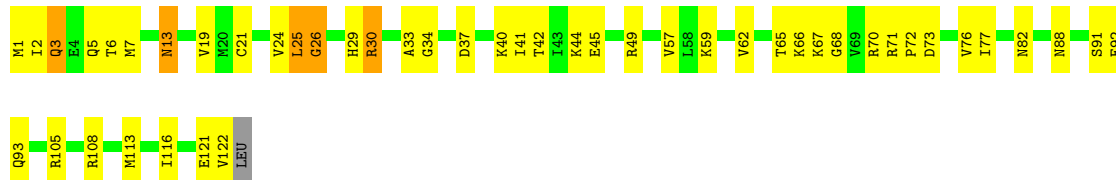
- Molecule 12: 50S ribosomal protein L9



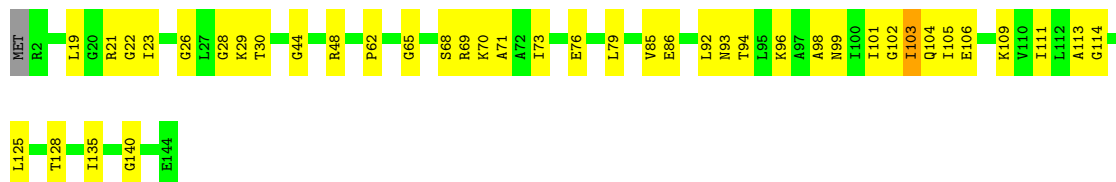
- Molecule 13: 50S ribosomal protein L13



- Molecule 14: 50S ribosomal protein L14



- Molecule 15: 50S ribosomal protein L15

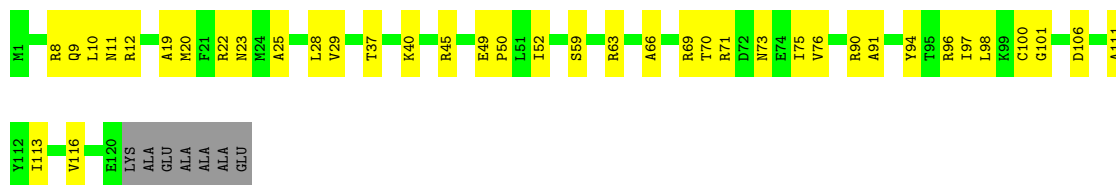


- Molecule 16: 50S ribosomal protein L16



- Molecule 17: 50S ribosomal protein L17

Chain N:  64% 31% 6%



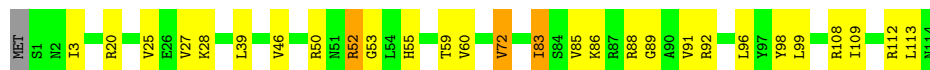
- Molecule 18: 50S ribosomal protein L18

Chain O:  74% 25%



- Molecule 19: 50S ribosomal protein L19

Chain P:  75% 22%



- Molecule 20: 50S ribosomal protein L20

Chain Q:  75% 22%



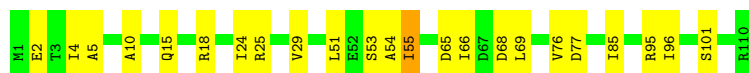
- Molecule 21: 50S ribosomal protein L21

Chain R:  75% 23%



- Molecule 22: 50S ribosomal protein L22

Chain S:  79% 20%



- Molecule 23: 50S ribosomal protein L23

Chain T:  67% 26% 7%



- Molecule 24: 50S ribosomal protein L24

Chain U:  78% 20%



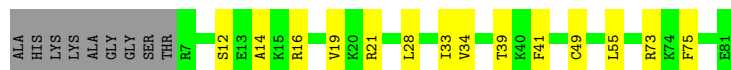
- Molecule 25: 50S ribosomal protein L25

Chain V:  70% 29%



- Molecule 26: 50S ribosomal protein L27

Chain W:  73% 17% 11%



- Molecule 27: 50S ribosomal protein L28

Chain X:  63% 36%



- Molecule 28: 50S ribosomal protein L29

Chain Y:  83% 16%



- Molecule 29: 50S ribosomal protein L30

Chain Z:  68% 31%



- Molecule 30: 50S ribosomal protein L32

Chain b:  74% 23%



- Molecule 31: 50S ribosomal protein L33

Chain c:  60% 31% 9%



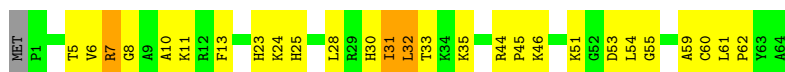
- Molecule 32: 50S ribosomal protein L34

Chain d:  74% 26%



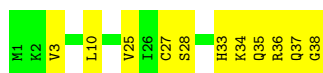
- Molecule 33: 50S ribosomal protein L35

Chain e:  57% 37% 5%



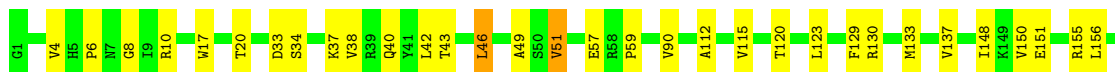
- Molecule 34: 50S ribosomal protein L36

Chain f:  71% 29%



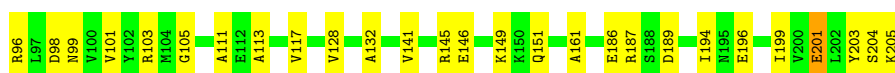
- Molecule 35: 30S ribosomal protein S3

Chain h:  80% 19%



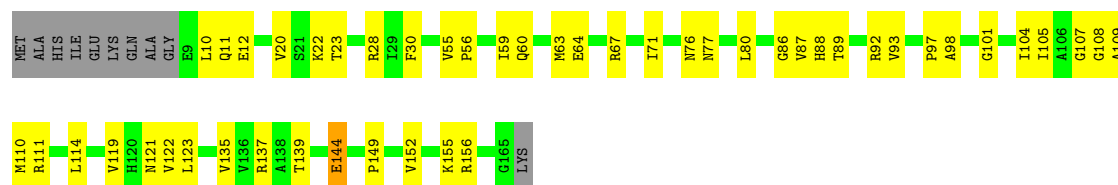
- Molecule 36: 30S ribosomal protein S4

Chain i:  68% 31%



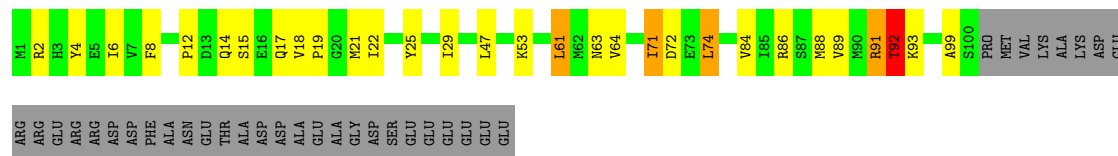
- Molecule 37: 30S ribosomal protein S5

Chain j:  65% 28% 6%



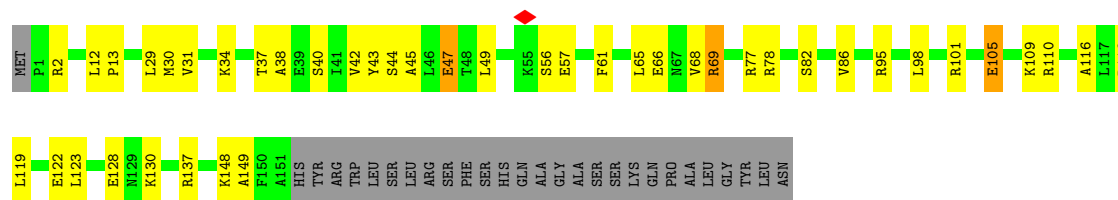
- Molecule 38: 30S ribosomal protein S6

Chain k: 52% 19% 26%



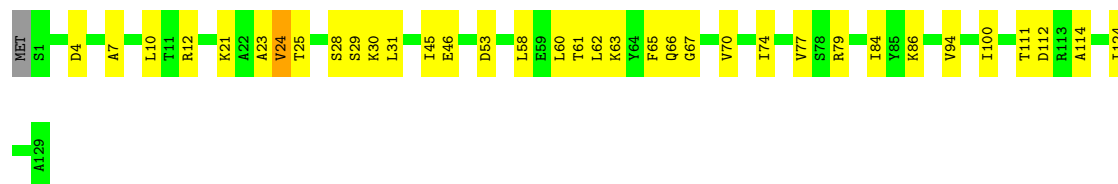
- Molecule 39: 30S ribosomal protein S7

Chain l: 60% 22% 16%



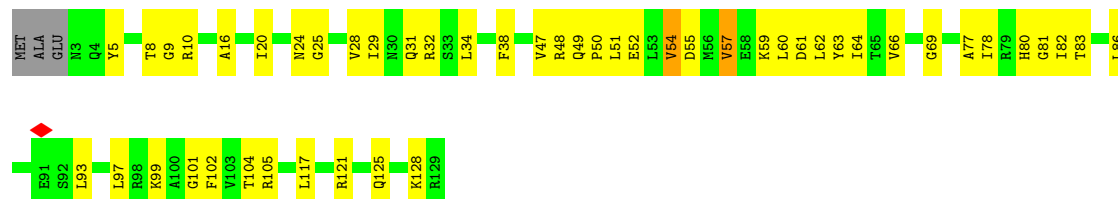
- Molecule 40: 30S ribosomal protein S8

Chain m: 72% 26% 2%



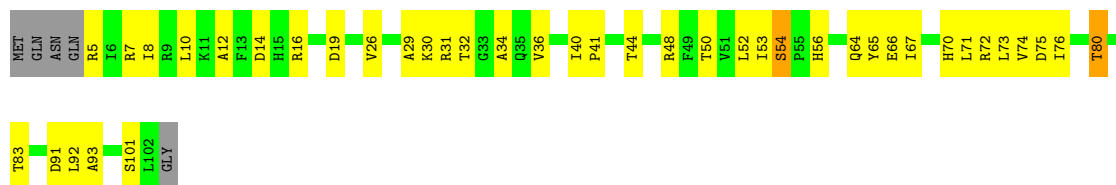
- Molecule 41: 30S ribosomal protein S9

Chain n: 60% 36% 4%



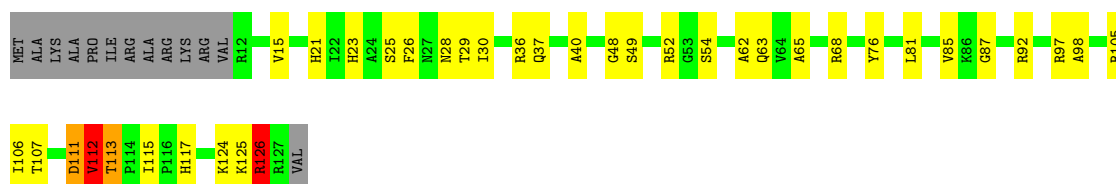
- Molecule 42: 30S ribosomal protein S10

Chain o:  55% 38% • 5%



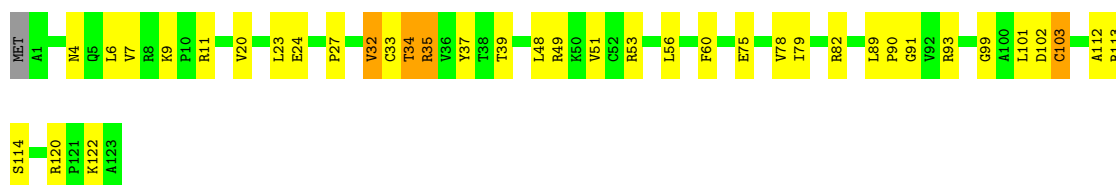
- Molecule 43: 30S ribosomal protein S11

Chain p:  61% 26% • • 10%



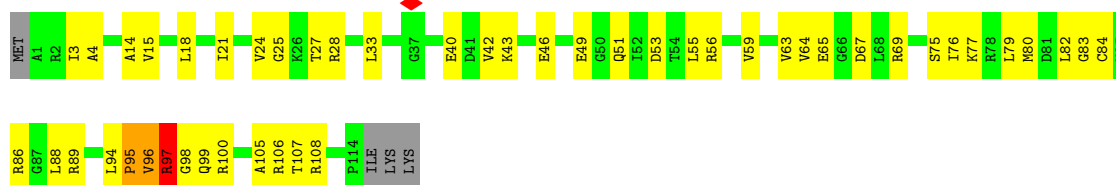
- Molecule 44: 30S ribosomal protein S12

Chain q:  69% 27% • •



- Molecule 45: 30S ribosomal protein S13

Chain r:  56% 38% • • •



- Molecule 46: 30S ribosomal protein S14

Chain s:  76% 23% •

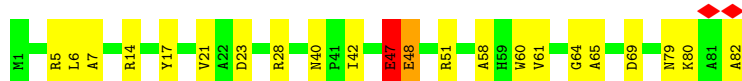


- Molecule 47: 30S ribosomal protein S15

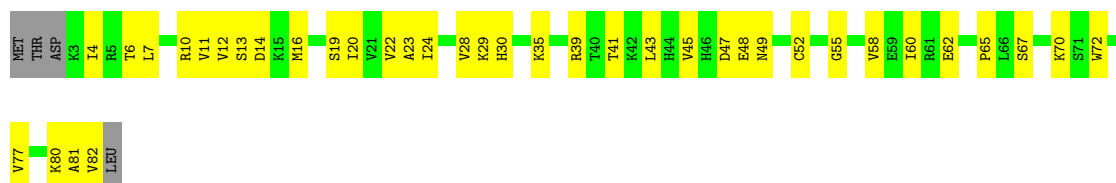
Chain t:  70% 28% • •



- Molecule 48: 30S ribosomal protein S16



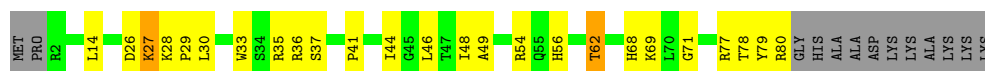
- Molecule 49: 30S ribosomal protein S17



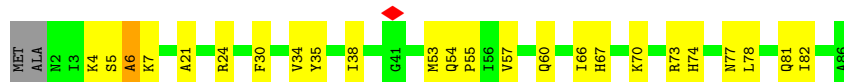
- Molecule 50: 30S ribosomal protein S18



- Molecule 51: 30S ribosomal protein S19



- Molecule 52: 30S ribosomal protein S20



- Molecule 53: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	65321	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	61.23	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.090	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0126	Depositor
Map size ($\text{\AA}$)	427.64, 427.64, 427.64	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0691, 1.0691, 1.0691	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.23	0/69796	0.36	0/108888
2	2	0.20	0/36963	0.37	1/57662 (0.0%)
3	3	0.21	0/2872	0.33	0/4479
4	4	0.49	0/87	0.50	0/132
5	5	0.21	0/1819	0.39	0/2836
6	A	0.20	0/1033	0.44	0/1387
7	B	0.32	0/2121	0.53	1/2852 (0.0%)
8	C	0.30	0/1586	0.50	0/2134
9	D	0.29	0/1571	0.56	2/2113 (0.1%)
10	E	0.23	0/1434	0.47	0/1926
11	F	0.31	0/1343	0.53	1/1816 (0.1%)
12	G	0.22	0/1122	0.43	1/1515 (0.1%)
13	J	0.30	0/1152	0.48	0/1551
14	K	0.39	0/947	0.63	0/1268
15	L	0.34	0/1054	0.73	2/1403 (0.1%)
16	M	0.31	0/1093	0.50	1/1460 (0.1%)
17	N	0.35	0/973	0.51	0/1301
18	O	0.24	0/902	0.45	1/1209 (0.1%)
19	P	0.39	0/929	0.59	0/1242
20	Q	0.38	0/960	0.54	0/1278
21	R	0.40	0/829	0.53	0/1107
22	S	0.35	0/864	0.71	3/1156 (0.3%)
23	T	0.35	0/744	0.48	0/994
24	U	0.29	0/787	0.50	0/1051
25	V	0.27	0/766	0.44	0/1025
26	W	0.33	0/582	0.54	0/769
27	X	0.27	0/635	0.45	0/848
28	Y	0.49	0/510	0.71	0/677
29	Z	0.29	0/453	0.54	0/605
30	b	0.32	0/450	0.51	0/599
31	c	0.38	0/416	0.48	0/554
32	d	0.30	0/380	0.50	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.52	0/513	0.82	1/676 (0.1%)
34	f	0.28	0/303	0.56	0/397
35	h	0.24	0/1652	0.46	1/2225 (0.0%)
36	i	0.25	0/1665	0.53	1/2227 (0.0%)
37	j	0.28	0/1169	0.52	0/1573
38	k	0.36	0/835	0.66	3/1128 (0.3%)
39	l	0.31	0/1195	0.53	1/1602 (0.1%)
40	m	0.30	0/989	0.55	1/1326 (0.1%)
41	n	0.24	0/1034	0.59	1/1375 (0.1%)
42	o	0.23	0/796	0.59	2/1077 (0.2%)
43	p	0.38	0/885	0.65	2/1195 (0.2%)
44	q	0.25	0/969	0.56	1/1300 (0.1%)
45	r	0.30	0/892	0.59	1/1193 (0.1%)
46	s	0.21	0/817	0.44	0/1088
47	t	0.24	0/722	0.43	0/964
48	u	0.30	0/659	0.59	0/884
49	v	0.21	0/657	0.52	0/881
50	w	0.23	0/544	0.42	0/731
51	x	0.17	0/652	0.43	0/877
52	y	0.27	0/671	0.55	1/888 (0.1%)
53	z	0.35	0/550	0.74	1/728 (0.1%)
All	All	0.25	0/155342	0.42	30/232670 (0.0%)

There are no bond length outliers.

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	S	24	ILE	N-CA-C	14.17	125.61	112.29
15	L	22	GLY	N-CA-C	13.45	128.75	112.48
41	n	57	VAL	N-CA-C	11.51	122.36	110.62
45	r	96	VAL	N-CA-C	8.99	128.05	109.34
42	o	53	ILE	N-CA-C	-8.88	101.88	112.98

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	62317	0	31343	1438	0
2	2	33012	0	16618	874	0
3	3	2568	0	1303	53	0
4	4	80	0	45	1	0
5	5	1628	0	823	40	0
6	A	1026	0	1092	38	0
7	B	2082	0	2157	49	0
8	C	1565	0	1616	38	0
9	D	1552	0	1619	36	0
10	E	1410	0	1447	54	0
11	F	1323	0	1374	34	0
12	G	1111	0	1148	24	0
13	J	1129	0	1161	49	0
14	K	938	0	1012	37	0
15	L	1045	0	1117	33	0
16	M	1074	0	1157	26	0
17	N	960	0	1000	29	0
18	O	892	0	923	24	0
19	P	917	0	965	21	0
20	Q	947	0	1022	23	0
21	R	816	0	839	25	0
22	S	857	0	922	12	0
23	T	738	0	807	21	0
24	U	779	0	834	19	0
25	V	753	0	780	25	0
26	W	575	0	592	11	0
27	X	625	0	655	30	0
28	Y	509	0	543	9	0
29	Z	449	0	491	12	0
30	b	444	0	461	11	0
31	c	409	0	440	14	0
32	d	377	0	418	9	0
33	e	504	0	574	23	0
34	f	302	0	343	6	0
35	h	1625	0	1699	34	0
36	i	1643	0	1710	47	0
37	j	1156	0	1199	42	0
38	k	817	0	808	25	0
39	l	1181	0	1240	34	0
40	m	979	0	1034	24	0
41	n	1022	0	1070	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	o	786	0	828	31	0
43	p	869	0	878	43	0
44	q	955	0	1019	31	0
45	r	883	0	944	46	0
46	s	805	0	847	18	0
47	t	714	0	737	24	0
48	u	649	0	666	16	0
49	v	648	0	691	31	0
50	w	535	0	552	16	0
51	x	637	0	665	22	0
52	y	665	0	714	15	0
53	z	544	0	579	23	0
54	1	306	0	0	0	0
54	2	78	0	0	0	0
54	3	7	0	0	0	0
54	4	1	0	0	0	0
54	5	1	0	0	0	0
54	B	2	0	0	0	0
54	D	1	0	0	0	0
54	E	1	0	0	0	0
54	J	1	0	0	0	0
54	K	1	0	0	0	0
54	L	1	0	0	0	0
54	M	1	0	0	0	0
54	N	1	0	0	0	0
54	Q	1	0	0	0	0
54	R	1	0	0	0	0
54	S	3	0	0	0	0
54	W	1	0	0	0	0
54	Z	1	0	0	0	0
54	b	1	0	0	0	0
54	m	1	0	0	0	0
54	p	1	0	0	0	0
54	q	1	0	0	0	0
54	r	1	0	0	0	0
54	w	1	0	0	0	0
55	1	812	0	0	85	0
55	2	288	0	0	33	0
55	3	13	0	0	5	0
55	4	1	0	0	0	0
55	5	5	0	0	1	0
55	A	5	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	B	1	0	0	0	0
55	C	2	0	0	2	0
55	E	2	0	0	0	0
55	F	4	0	0	1	0
55	G	8	0	0	7	0
55	J	11	0	0	14	0
55	K	3	0	0	0	0
55	M	6	0	0	2	0
55	N	1	0	0	0	0
55	O	3	0	0	2	0
55	P	2	0	0	2	0
55	Q	1	0	0	0	0
55	R	1	0	0	3	0
55	T	5	0	0	4	0
55	U	4	0	0	0	0
55	V	3	0	0	0	0
55	W	3	0	0	4	0
55	X	3	0	0	5	0
55	Y	1	0	0	1	0
55	Z	5	0	0	0	0
55	c	6	0	0	2	0
55	d	1	0	0	0	0
55	h	9	0	0	4	0
55	i	1	0	0	0	0
55	j	4	0	0	4	0
55	k	4	0	0	3	0
55	l	4	0	0	3	0
55	m	1	0	0	2	0
55	o	1	0	0	0	0
55	p	11	0	0	12	0
55	r	1	0	0	1	0
55	t	7	0	0	6	0
55	w	4	0	0	4	0
55	z	8	0	0	7	0
All	All	144496	0	95521	3421	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 15.

The worst 5 of 3421 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:t:34:GLN:HG3	55:t:106:HOH:O	1.26	1.25
26:W:73:ARG:HG3	55:W:202:HOH:O	1.37	1.19
43:p:54:SER:HB2	55:p:310:HOH:O	1.40	1.18
2:2:209:U:H3'	55:2:1725:HOH:O	1.45	1.16
5:5:27:C:H5''	55:5:202:HOH:O	1.44	1.13

There are no symmetry-related clashes.

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	
6	A	130/229 (57%)	118 (91%)	11 (8%)	1 (1%)	16	50
7	B	269/273 (98%)	235 (87%)	33 (12%)	1 (0%)	30	62
8	C	207/209 (99%)	178 (86%)	28 (14%)	1 (0%)	24	59
9	D	199/201 (99%)	175 (88%)	23 (12%)	1 (0%)	24	59
10	E	175/179 (98%)	153 (87%)	22 (13%)	0	100	100
11	F	174/177 (98%)	156 (90%)	17 (10%)	1 (1%)	21	56
12	G	147/149 (99%)	138 (94%)	8 (5%)	1 (1%)	18	52
13	J	140/142 (99%)	124 (89%)	14 (10%)	2 (1%)	9	39
14	K	120/123 (98%)	96 (80%)	19 (16%)	5 (4%)	2	16
15	L	141/144 (98%)	112 (79%)	25 (18%)	4 (3%)	4	25
16	M	134/136 (98%)	116 (87%)	17 (13%)	1 (1%)	18	52
17	N	118/127 (93%)	96 (81%)	21 (18%)	1 (1%)	16	50
18	O	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
19	P	112/115 (97%)	99 (88%)	13 (12%)	0	100	100
20	Q	115/118 (98%)	110 (96%)	5 (4%)	0	100	100
21	R	101/103 (98%)	90 (89%)	11 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	S	108/110 (98%)	102 (94%)	6 (6%)	0	100	100
23	T	91/100 (91%)	83 (91%)	8 (9%)	0	100	100
24	U	100/104 (96%)	92 (92%)	7 (7%)	1 (1%)	12	45
25	V	92/94 (98%)	83 (90%)	8 (9%)	1 (1%)	11	43
26	W	73/84 (87%)	64 (88%)	9 (12%)	0	100	100
27	X	75/78 (96%)	68 (91%)	7 (9%)	0	100	100
28	Y	61/63 (97%)	59 (97%)	1 (2%)	1 (2%)	7	36
29	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
30	b	54/57 (95%)	46 (85%)	8 (15%)	0	100	100
31	c	48/55 (87%)	46 (96%)	2 (4%)	0	100	100
32	d	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
33	e	62/65 (95%)	54 (87%)	4 (6%)	4 (6%)	1	8
34	f	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	25
35	h	204/206 (99%)	191 (94%)	13 (6%)	0	100	100
36	i	203/206 (98%)	183 (90%)	19 (9%)	1 (0%)	24	59
37	j	155/167 (93%)	134 (86%)	21 (14%)	0	100	100
38	k	98/135 (73%)	89 (91%)	7 (7%)	2 (2%)	6	31
39	l	149/179 (83%)	141 (95%)	8 (5%)	0	100	100
40	m	127/130 (98%)	115 (91%)	11 (9%)	1 (1%)	16	50
41	n	125/130 (96%)	110 (88%)	14 (11%)	1 (1%)	16	50
42	o	96/103 (93%)	82 (85%)	13 (14%)	1 (1%)	12	45
43	p	114/129 (88%)	105 (92%)	8 (7%)	1 (1%)	14	47
44	q	121/124 (98%)	96 (79%)	23 (19%)	2 (2%)	7	35
45	r	112/118 (95%)	97 (87%)	13 (12%)	2 (2%)	6	34
46	s	98/101 (97%)	87 (89%)	10 (10%)	1 (1%)	12	45
47	t	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
48	u	80/82 (98%)	69 (86%)	9 (11%)	2 (2%)	4	27
49	v	78/84 (93%)	61 (78%)	17 (22%)	0	100	100
50	w	63/75 (84%)	59 (94%)	3 (5%)	1 (2%)	7	36
51	x	77/92 (84%)	66 (86%)	10 (13%)	1 (1%)	9	40
52	y	83/87 (95%)	79 (95%)	3 (4%)	1 (1%)	10	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	z	63/71 (89%)	49 (78%)	11 (18%)	3 (5%)	2	14
All	All	5428/5803 (94%)	4818 (89%)	563 (10%)	47 (1%)	16	47

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	J	81	ILE
38	k	92	THR
43	p	126	ARG
44	q	35	ARG
52	y	6	ALA

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	
6	A	110/177 (62%)	108 (98%)	2 (2%)	51	74
7	B	216/218 (99%)	214 (99%)	2 (1%)	70	81
8	C	164/164 (100%)	161 (98%)	3 (2%)	51	74
9	D	165/165 (100%)	159 (96%)	6 (4%)	31	63
10	E	148/150 (99%)	148 (100%)	0	100	100
11	F	137/138 (99%)	133 (97%)	4 (3%)	37	67
12	G	114/114 (100%)	110 (96%)	4 (4%)	32	64
13	J	116/116 (100%)	112 (97%)	4 (3%)	32	64
14	K	103/104 (99%)	97 (94%)	6 (6%)	18	51
15	L	102/103 (99%)	102 (100%)	0	100	100
16	M	109/109 (100%)	109 (100%)	0	100	100
17	N	100/103 (97%)	100 (100%)	0	100	100
18	O	86/87 (99%)	85 (99%)	1 (1%)	63	79
19	P	99/100 (99%)	96 (97%)	3 (3%)	36	66
20	Q	89/90 (99%)	87 (98%)	2 (2%)	45	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	R	84/84 (100%)	81 (96%)	3 (4%)	31	63
22	S	93/93 (100%)	89 (96%)	4 (4%)	26	59
23	T	80/84 (95%)	80 (100%)	0	100	100
24	U	83/85 (98%)	82 (99%)	1 (1%)	63	79
25	V	78/78 (100%)	78 (100%)	0	100	100
26	W	57/62 (92%)	56 (98%)	1 (2%)	51	74
27	X	67/68 (98%)	67 (100%)	0	100	100
28	Y	55/55 (100%)	54 (98%)	1 (2%)	51	74
29	Z	48/49 (98%)	47 (98%)	1 (2%)	47	71
30	b	47/48 (98%)	46 (98%)	1 (2%)	47	71
31	c	45/49 (92%)	44 (98%)	1 (2%)	45	71
32	d	38/38 (100%)	38 (100%)	0	100	100
33	e	51/52 (98%)	50 (98%)	1 (2%)	48	72
34	f	34/34 (100%)	34 (100%)	0	100	100
35	h	170/170 (100%)	169 (99%)	1 (1%)	78	84
36	i	172/173 (99%)	170 (99%)	2 (1%)	63	79
37	j	119/126 (94%)	118 (99%)	1 (1%)	73	82
38	k	87/116 (75%)	82 (94%)	5 (6%)	18	51
39	l	124/147 (84%)	121 (98%)	3 (2%)	43	70
40	m	104/105 (99%)	103 (99%)	1 (1%)	68	80
41	n	105/107 (98%)	104 (99%)	1 (1%)	68	80
42	o	86/90 (96%)	85 (99%)	1 (1%)	63	79
43	p	89/99 (90%)	86 (97%)	3 (3%)	32	64
44	q	103/104 (99%)	102 (99%)	1 (1%)	68	80
45	r	92/96 (96%)	90 (98%)	2 (2%)	45	71
46	s	83/84 (99%)	83 (100%)	0	100	100
47	t	76/77 (99%)	75 (99%)	1 (1%)	61	78
48	u	65/65 (100%)	63 (97%)	2 (3%)	35	66
49	v	74/78 (95%)	74 (100%)	0	100	100
50	w	56/65 (86%)	56 (100%)	0	100	100
51	x	70/79 (89%)	69 (99%)	1 (1%)	59	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
52	y	65/66 (98%)	63 (97%)	2 (3%)	35 66
53	z	55/61 (90%)	54 (98%)	1 (2%)	51 74
All	All	4513/4725 (96%)	4434 (98%)	79 (2%)	51 74

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	k	71	ILE
45	r	97	ARG
38	k	92	THR
42	o	80	THR
51	x	62	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
29	Z	8	GLN
36	i	35	GLN
50	w	30	ASN
30	b	18	HIS
32	d	29	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2904 (99%)	568 (19%)	9 (0%)
2	2	1538/1540 (99%)	334 (21%)	8 (0%)
3	3	119/120 (99%)	16 (13%)	0
4	4	3/18 (16%)	0	0
5	5	76/77 (98%)	25 (32%)	3 (3%)
All	All	4638/4659 (99%)	943 (20%)	20 (0%)

5 of 943 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	8	C
1	1	10	A
1	1	34	U
1	1	42	A

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Mol	Chain	Res	Type
1	1	46	G

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	1069	C
5	5	2	G
5	5	59	A
5	5	47	U
1	1	1828	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 415 ligands modelled in this entry, 415 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

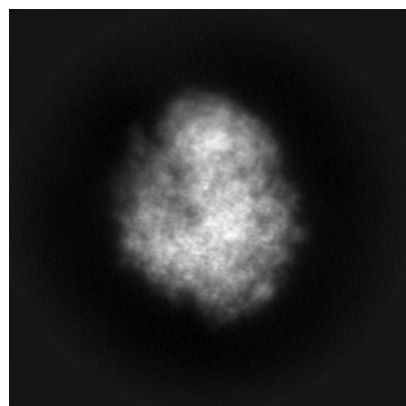
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42832. These allow visual inspection of the internal detail of the map and identification of artifacts.

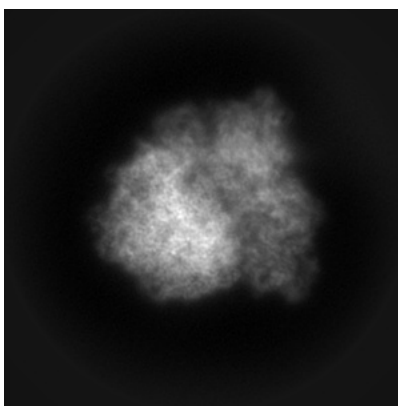
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

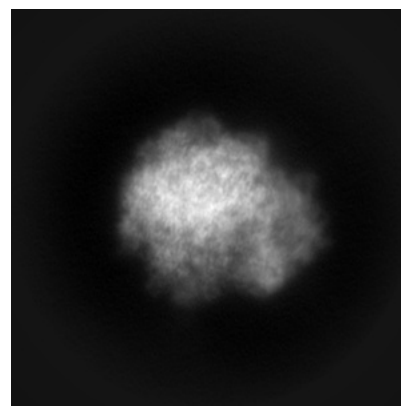
6.1.1 Primary map



X

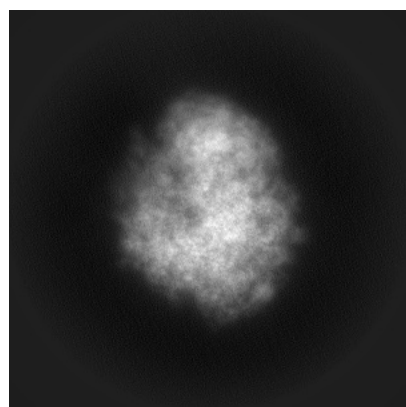


Y

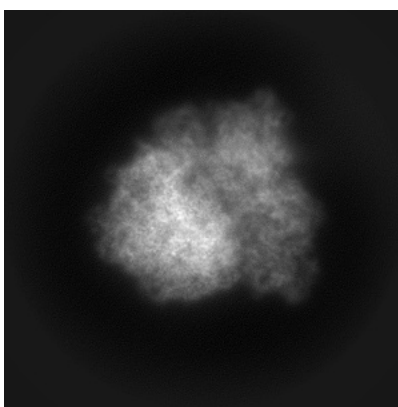


Z

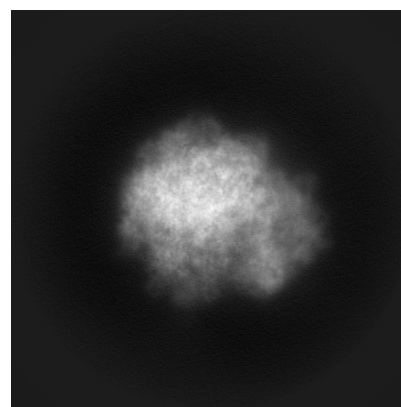
6.1.2 Raw map



X



Y

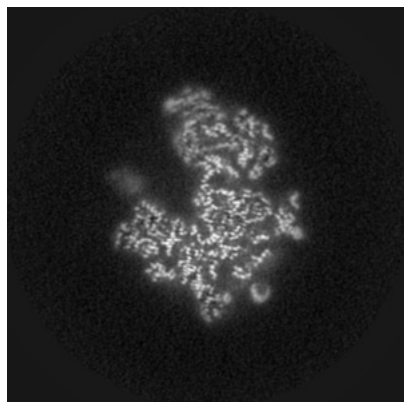


Z

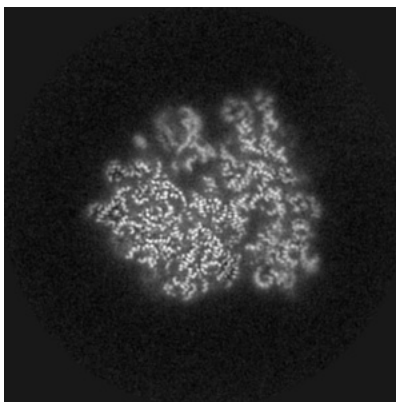
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

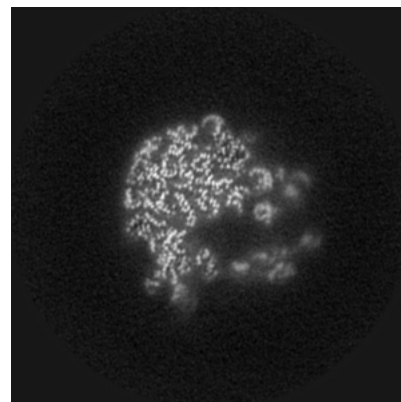
6.2.1 Primary map



X Index: 200

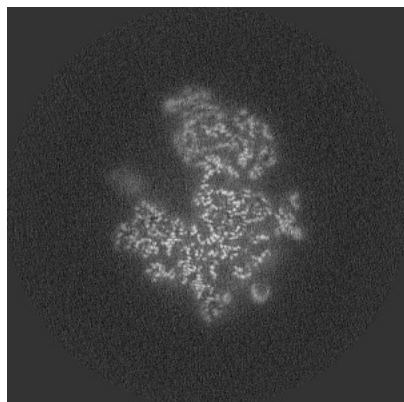


Y Index: 200

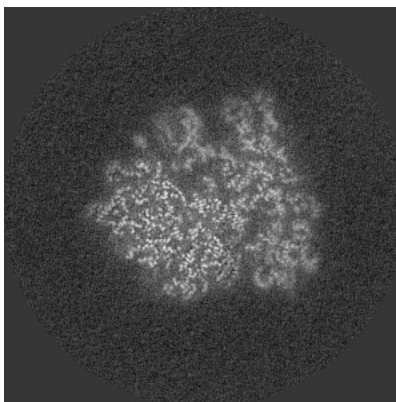


Z Index: 200

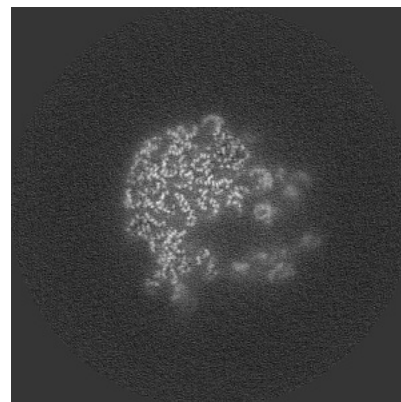
6.2.2 Raw map



X Index: 200



Y Index: 200

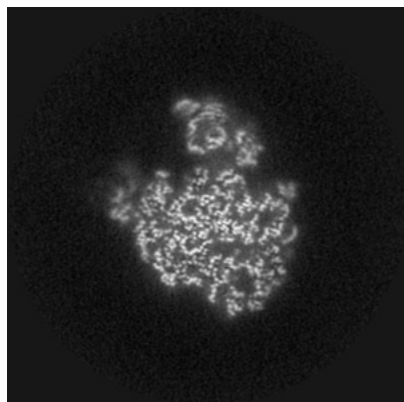


Z Index: 200

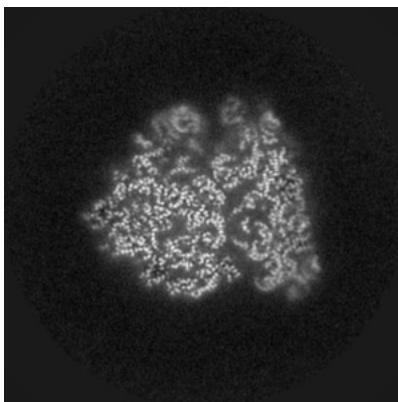
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

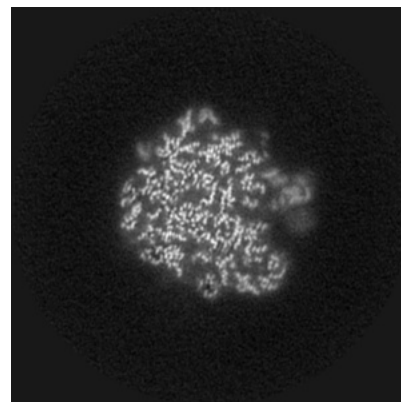
6.3.1 Primary map



X Index: 169

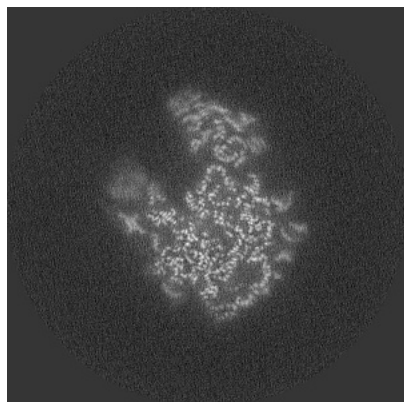


Y Index: 208

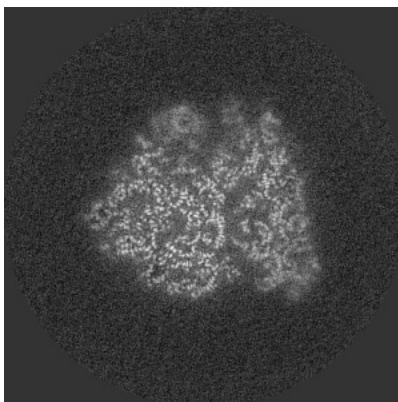


Z Index: 170

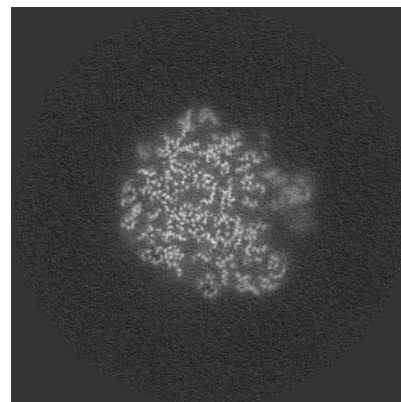
6.3.2 Raw map



X Index: 182



Y Index: 209

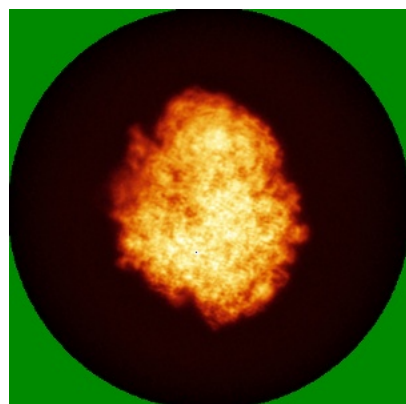


Z Index: 170

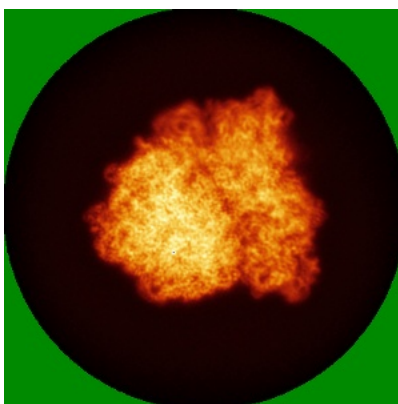
The images above show the largest variance slices of the map in three orthogonal directions.

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

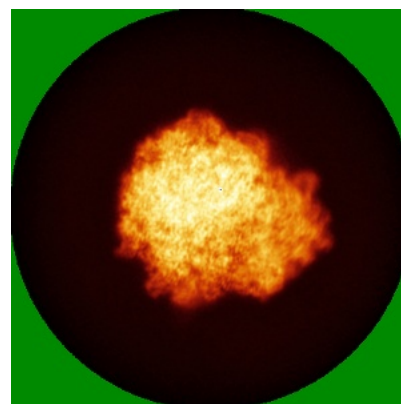
6.4.1 Primary map



X

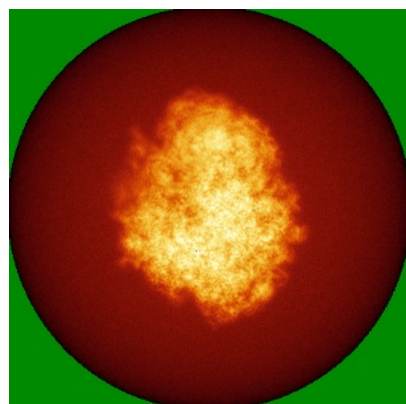


Y

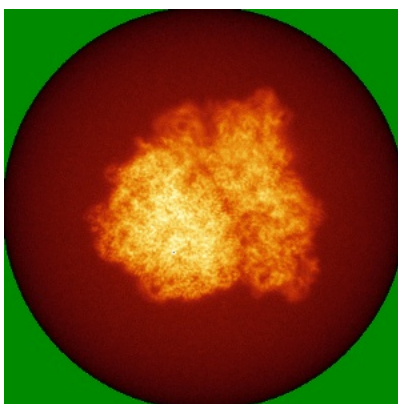


Z

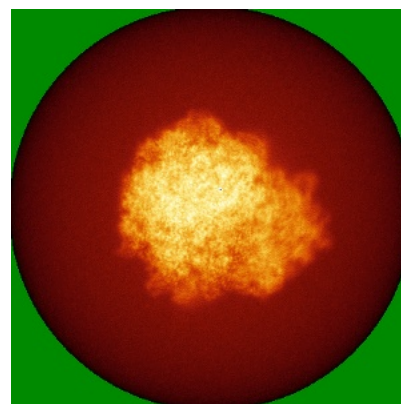
6.4.2 Raw map



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



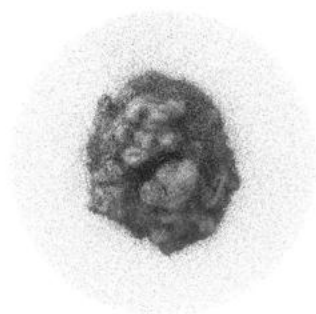
Y



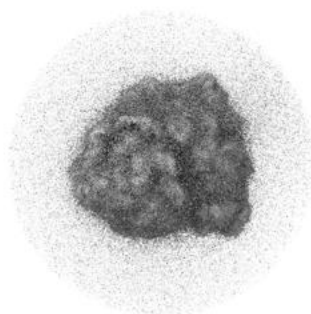
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0126. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

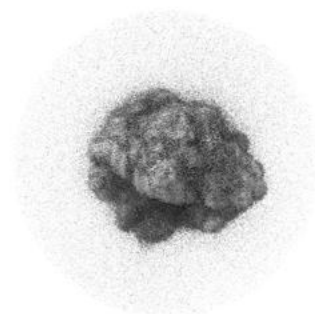
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

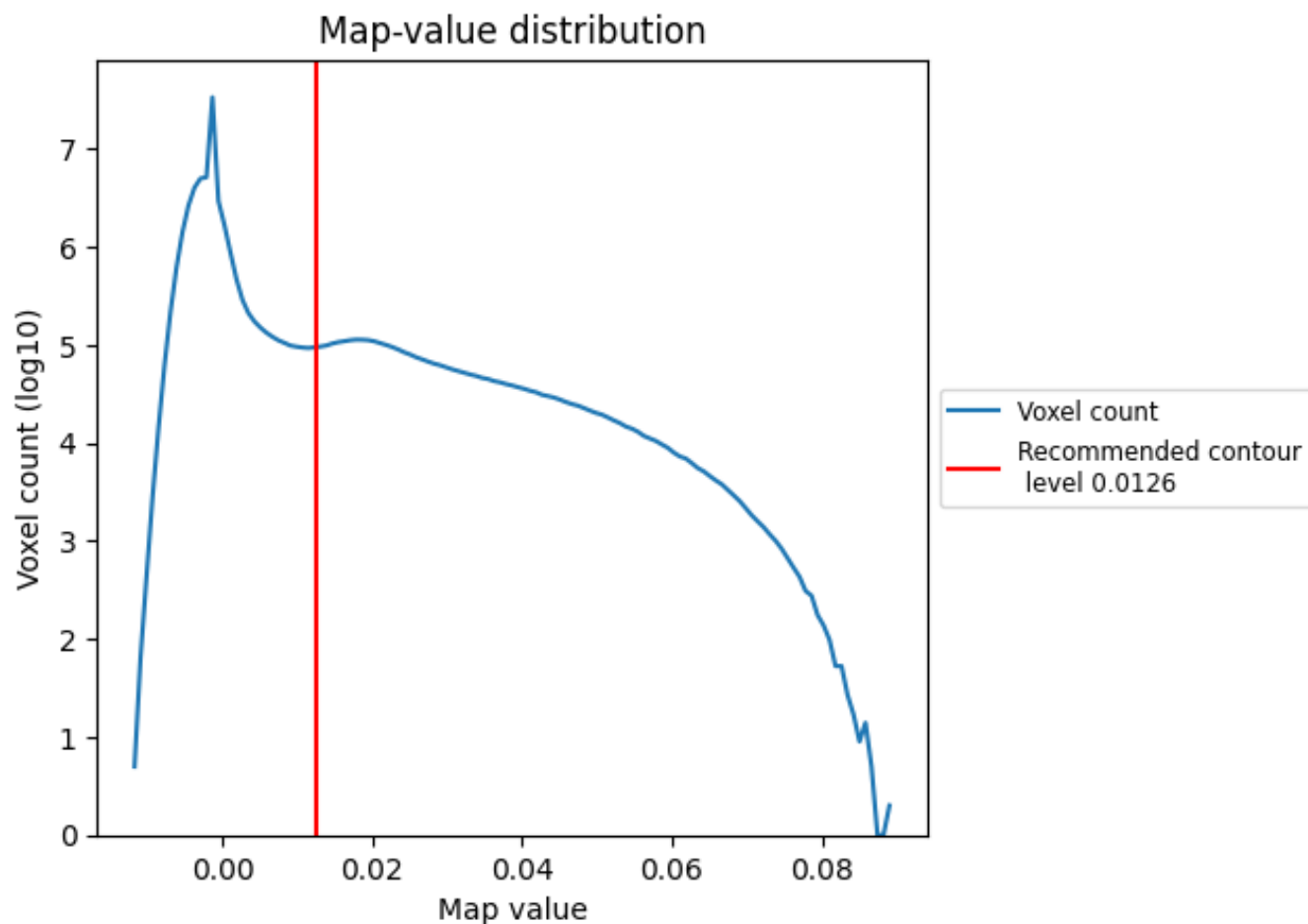
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

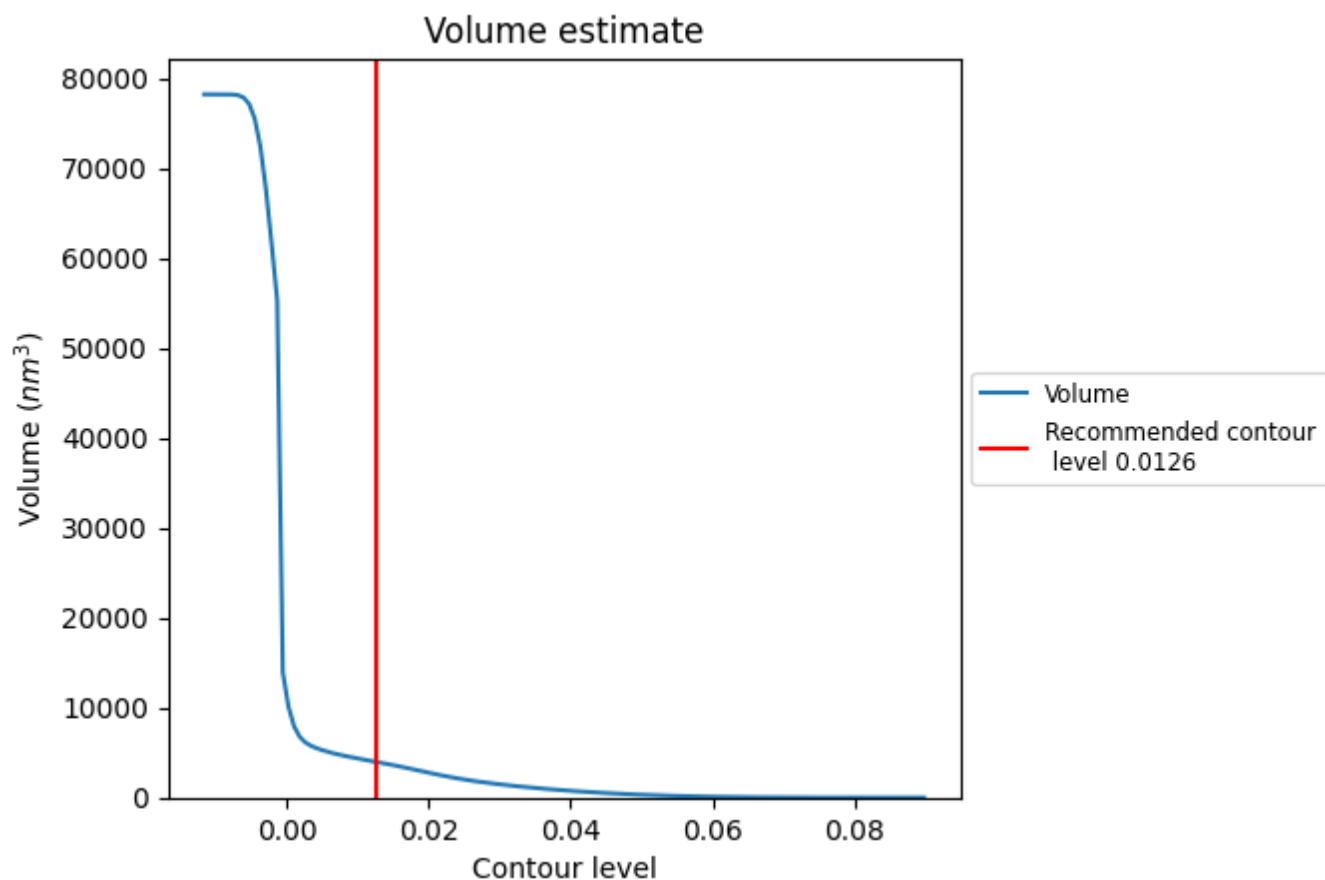
This section contains the results of statistical analysis of the map.

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.

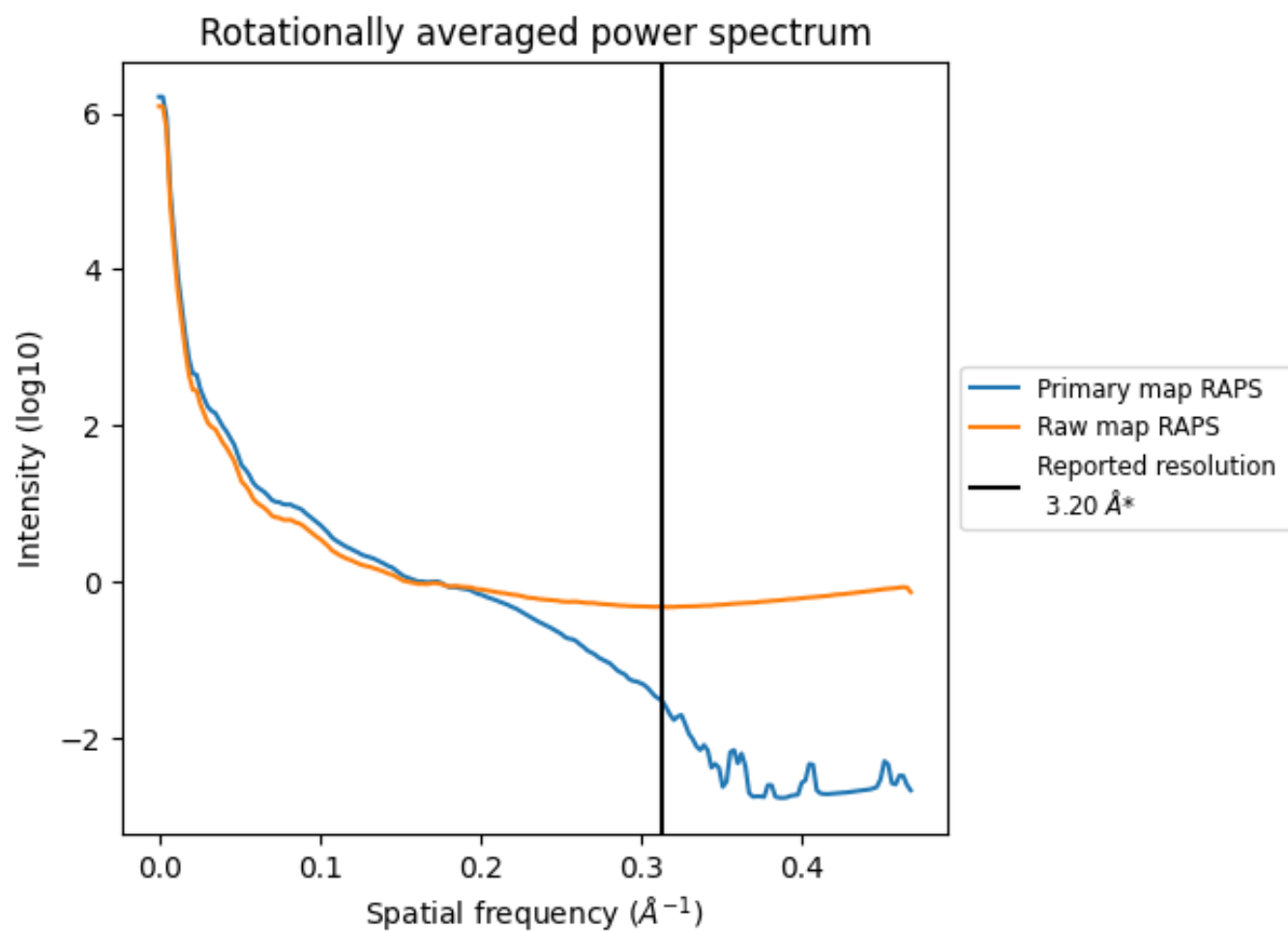
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3966 nm³; this corresponds to an approximate mass of 3583 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 ⓘ

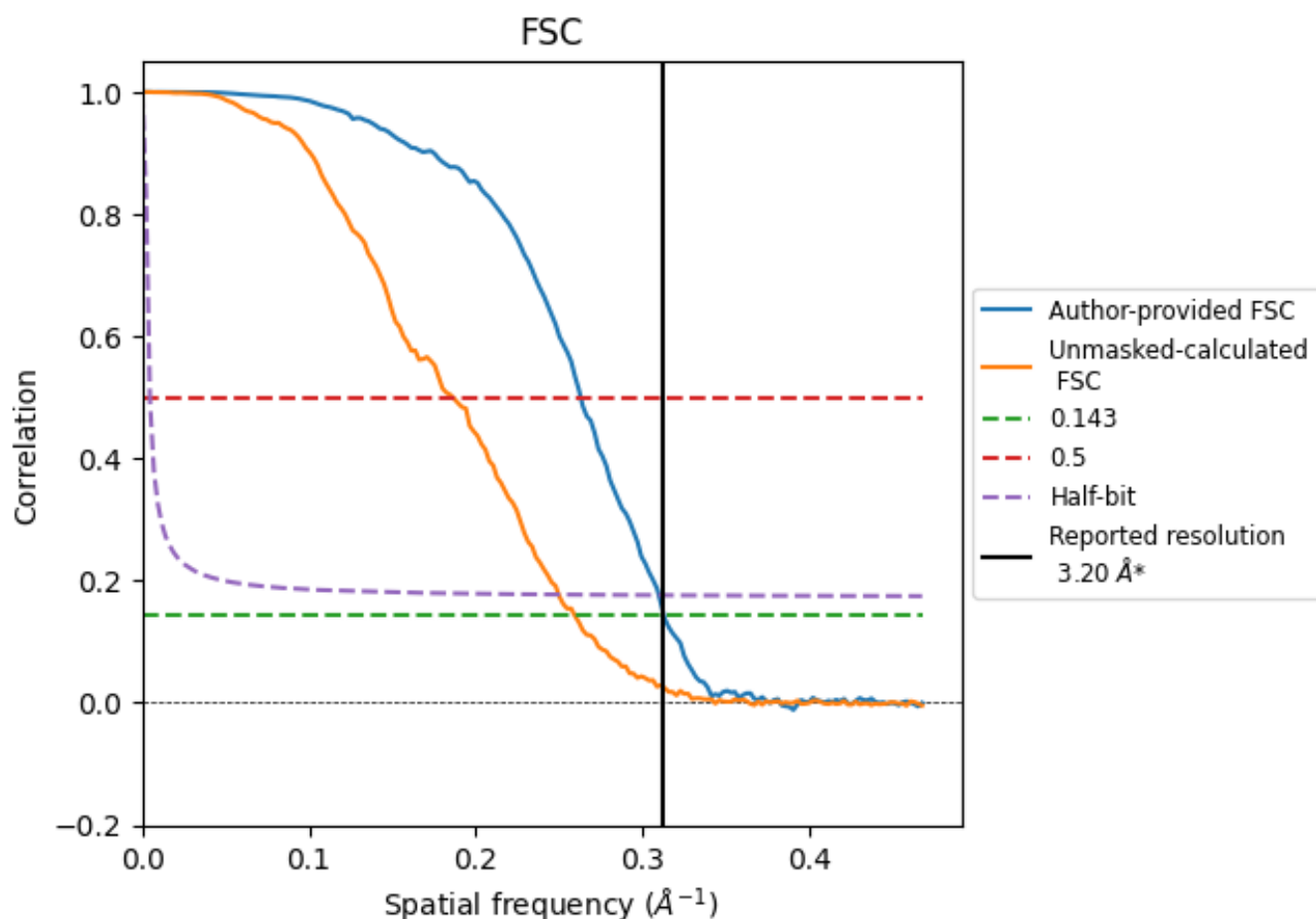


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

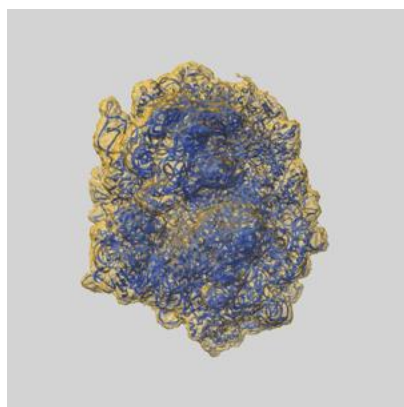
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.20	3.80	3.23
Unmasked-calculated*	3.86	5.37	4.00

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.86 differs from the reported value 3.2 by more than 10 %

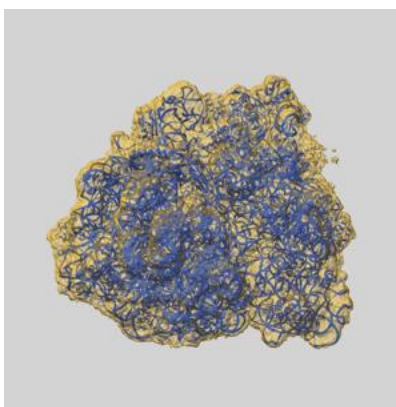
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-42832 and PDB model 8UZ3. Per-residue inclusion information can be found in section [3](#) on page [17](#).

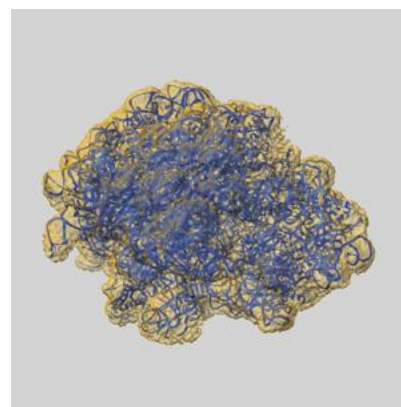
9.1 Map-model overlay [i](#)



X



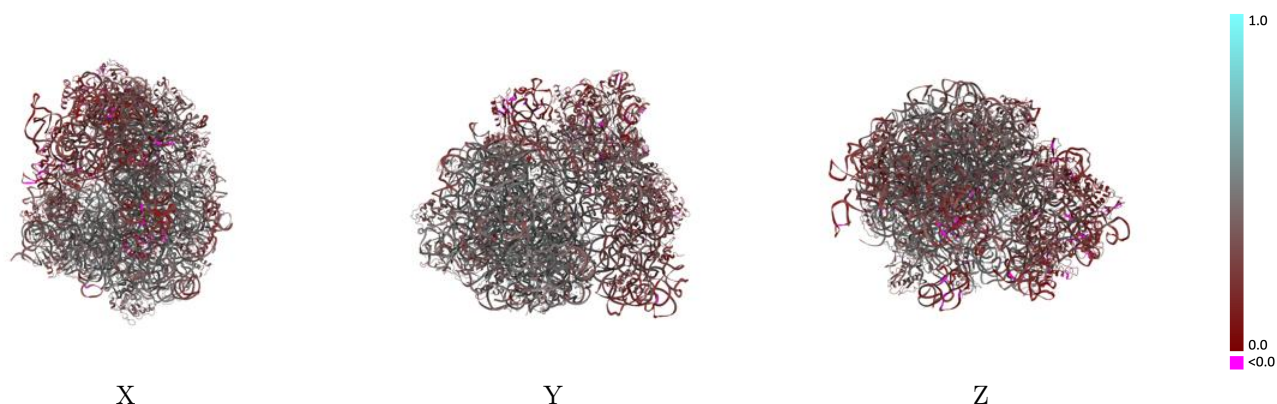
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0126 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](#)

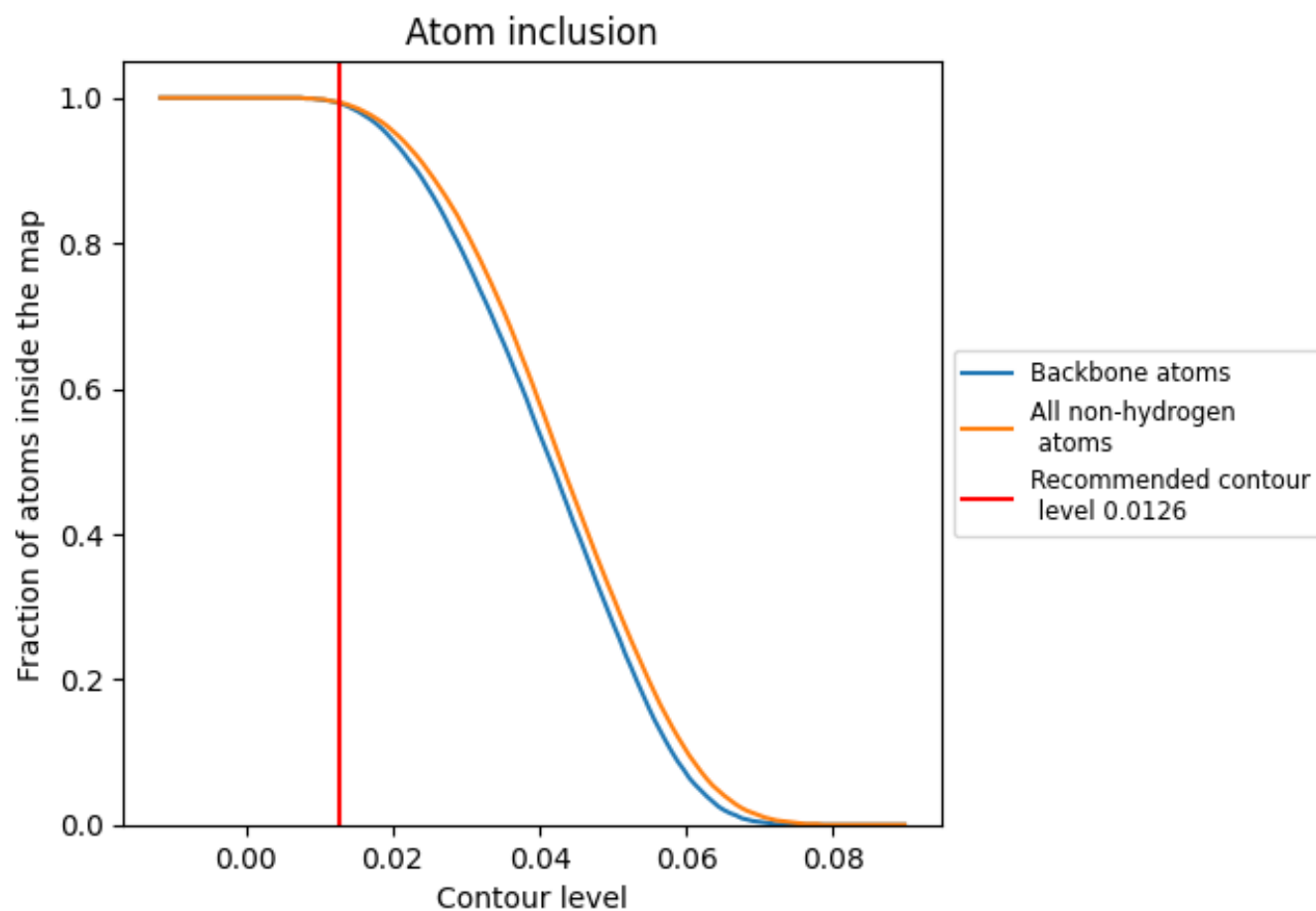


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% 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 (0.0126) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9940	 0.3710
1	 0.9980	 0.4300
2	 0.9960	 0.3240
3	 1.0000	 0.4080
4	 1.0000	 0.3990
5	 1.0000	 0.3860
A	 0.9560	 0.1150
B	 0.9990	 0.4340
C	 0.9950	 0.4030
D	 0.9880	 0.3860
E	 0.9910	 0.2560
F	 0.9880	 0.3210
G	 0.8490	 0.2430
J	 1.0000	 0.4110
K	 1.0000	 0.3950
L	 0.9890	 0.4160
M	 1.0000	 0.3860
N	 0.9970	 0.4240
O	 0.9900	 0.3590
P	 0.9980	 0.3860
Q	 0.9960	 0.4320
R	 0.9950	 0.4210
S	 0.9990	 0.4110
T	 0.9960	 0.3780
U	 0.9870	 0.3730
V	 0.9910	 0.3880
W	 1.0000	 0.4240
X	 1.0000	 0.3890
Y	 0.9820	 0.3200
Z	 0.9910	 0.4040
b	 0.9950	 0.4130
c	 0.9950	 0.3650
d	 1.0000	 0.4410
e	 1.0000	 0.4330
f	 1.0000	 0.3720



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Chain	Atom inclusion	Q-score
h	 0.9920	 0.2520
i	 0.9810	 0.1940
j	 0.9940	 0.2950
k	 0.9820	 0.3090
l	 0.9690	 0.1680
m	 0.9910	 0.3140
n	 0.9730	 0.1960
o	 0.9750	 0.2010
p	 1.0000	 0.3230
q	 0.9950	 0.2060
r	 0.9680	 0.1840
s	 0.9990	 0.2040
t	 0.9860	 0.2980
u	 0.9750	 0.2630
v	 0.9840	 0.2620
w	 0.9920	 0.2990
x	 0.9890	 0.1970
y	 0.9660	 0.2160
z	 0.9830	 0.2120