



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:49 PM UTC

PDB ID : 8UZG / pdb_00008uzg
EMDB ID : EMD-42840
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 : 2023-11-15
Resolution : 3.70 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:

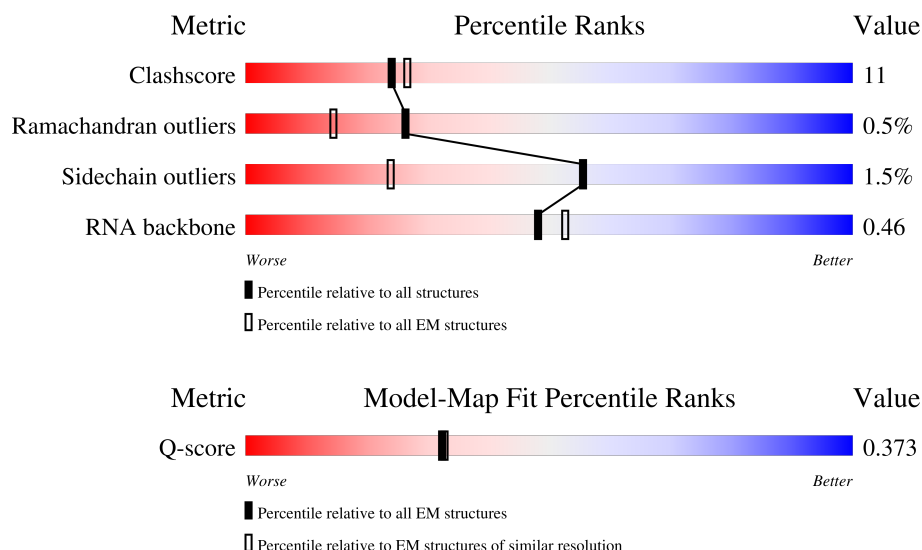
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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.



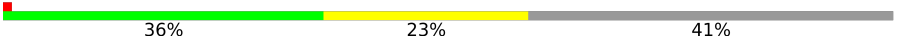
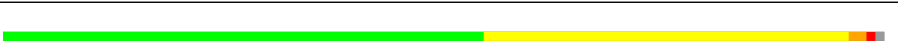
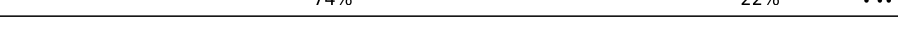
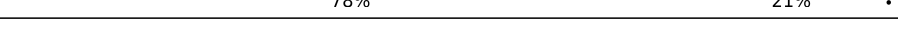
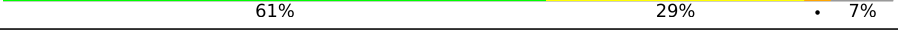
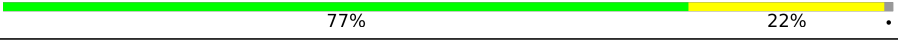
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	
2	2	1540	
3	3	120	

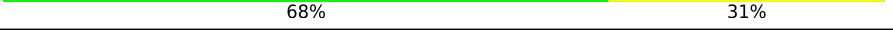
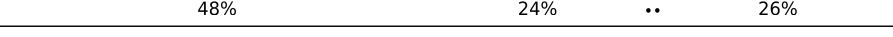
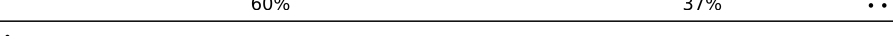
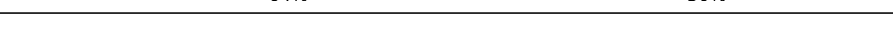
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Mol	Chain	Length	Quality of chain
4	4	18	 22% 78%
5	5	77	 55% 29% 16%
6	A	229	 36% 23% 41%
7	B	273	 74% 25%
8	C	209	 73% 26%
9	D	201	 74% 25%
10	E	179	 63% 35%
11	F	177	 83% 16%
12	G	149	 81% 19%
13	J	142	 73% 25%
14	K	123	 54% 41%
15	L	144	 74% 23%
16	M	136	 81% 19%
17	N	127	 57% 35% 6%
18	O	117	 74% 22%
19	P	115	 78% 21%
20	Q	118	 68% 31%
21	R	103	 76% 24%
22	S	110	 74% 25%
23	T	100	 61% 29% 7%
24	U	104	 69% 29%
25	V	94	 69% 30%
26	W	84	 74% 15% 11%
27	X	78	 77% 22%
28	Y	63	 87% 13%

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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	g	71	
36	h	206	
37	i	206	
38	j	167	
39	k	135	
40	l	179	
41	m	130	
42	n	130	
43	o	103	
44	p	129	
45	q	124	
46	r	118	
47	s	101	
48	t	89	
49	u	82	
50	v	84	
51	w	75	
52	x	92	
53	y	87	

2 Entry composition [i](#)

There are 55 unique types of molecules in this entry. The entry contains 144183 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	S	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	S	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 S2.

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

- Molecule 36 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 37 is a protein called 30S ribosomal protein S4.

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

- Molecule 38 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 39 is a protein called 30S ribosomal protein S6.

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

- Molecule 40 is a protein called 30S ribosomal protein S7.

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

- Molecule 41 is a protein called 30S ribosomal protein S8.

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

- Molecule 42 is a protein called 30S ribosomal protein S9.

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

- Molecule 43 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 44 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 45 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 46 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	r	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 47 is a protein called 30S ribosomal protein S14.

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

- Molecule 48 is a protein called 30S ribosomal protein S15.

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

- Molecule 49 is a protein called 30S ribosomal protein S16.

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

- Molecule 50 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	v	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 51 is a protein called 30S ribosomal protein S18.

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

- Molecule 52 is a protein called 30S ribosomal protein S19.

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

- Molecule 53 is a protein called 30S ribosomal protein S20.

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

- 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	72	Total 72	Mg 72	0
54	3	8	Total 8	Mg 8	0
54	4	1	Total 1	Mg 1	0
54	B	2	Total 2	Mg 2	0
54	E	1	Total 1	Mg 1	0
54	J	1	Total 1	Mg 1	0
54	N	1	Total 1	Mg 1	0
54	Q	1	Total 1	Mg 1	0
54	S	2	Total 2	Mg 2	0
54	b	1	Total 1	Mg 1	0
54	m	1	Total 1	Mg 1	0
54	r	1	Total 1	Mg 1	0

- Molecule 55 is water.

Mol	Chain	Residues	Atoms		AltConf
55	1	478	Total 478	O 478	0
55	2	309	Total 309	O 309	0
55	3	7	Total 7	O 7	0
55	5	3	Total 3	O 3	0
55	A	16	Total 16	O 16	0
55	B	4	Total 4	O 4	0
55	C	2	Total 2	O 2	0

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Mol	Chain	Residues	Atoms		AltConf
55	D	2	Total 2	O 2	0
55	E	16	Total 16	O 16	0
55	F	4	Total 4	O 4	0
55	G	5	Total 5	O 5	0
55	J	2	Total 2	O 2	0
55	K	2	Total 2	O 2	0
55	L	2	Total 2	O 2	0
55	M	2	Total 2	O 2	0
55	N	1	Total 1	O 1	0
55	O	2	Total 2	O 2	0
55	Q	2	Total 2	O 2	0
55	T	2	Total 2	O 2	0
55	U	3	Total 3	O 3	0
55	V	2	Total 2	O 2	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	c	1	Total 1	O 1	0
55	f	1	Total 1	O 1	0
55	g	4	Total 4	O 4	0
55	h	5	Total 5	O 5	0

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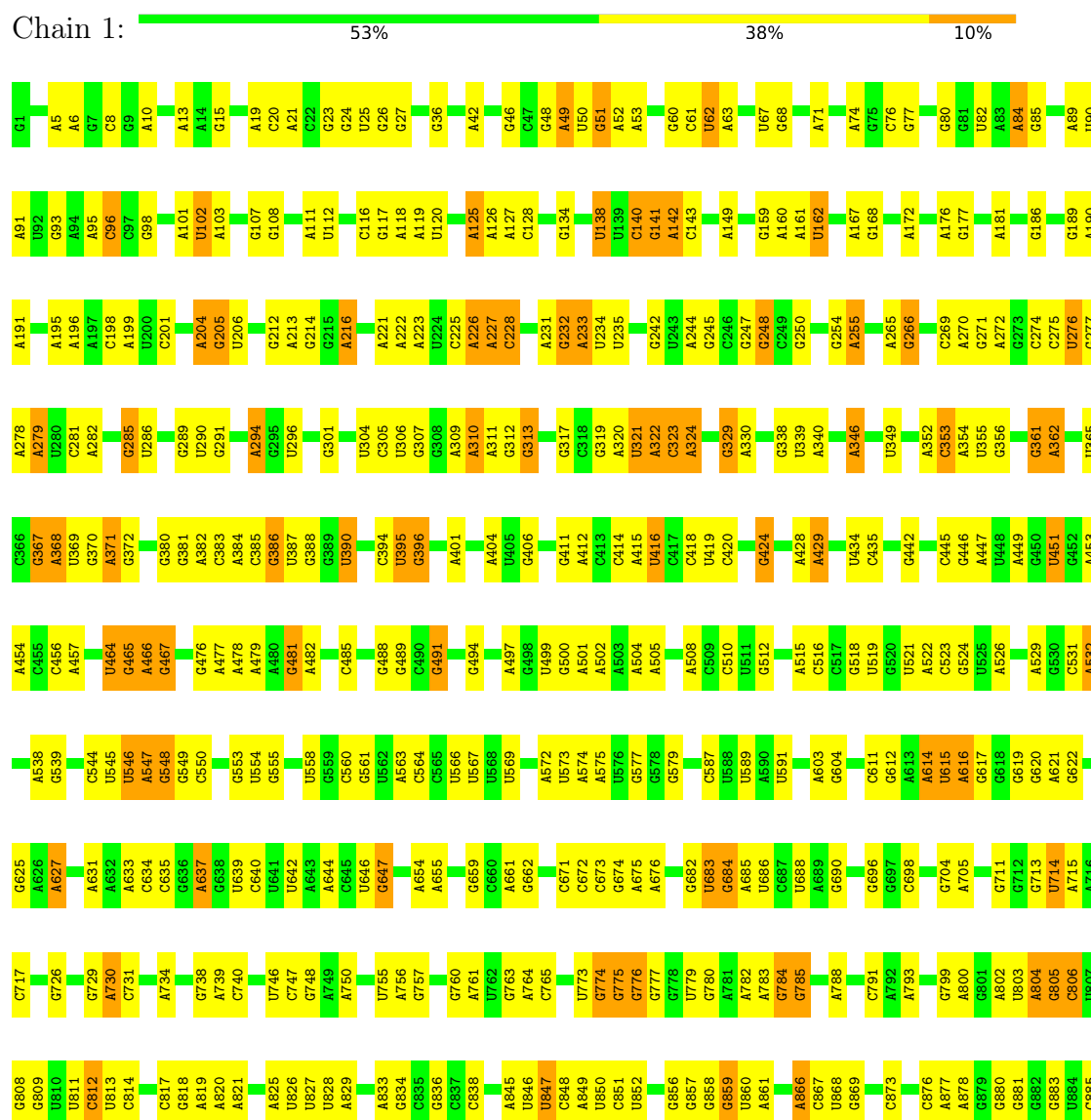
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Mol	Chain	Residues	Atoms		AltConf
55	i	10	Total 10	O 10	0
55	j	3	Total 3	O 3	0
55	k	7	Total 7	O 7	0
55	l	11	Total 11	O 11	0
55	m	3	Total 3	O 3	0
55	n	3	Total 3	O 3	0
55	o	4	Total 4	O 4	0
55	p	4	Total 4	O 4	0
55	q	2	Total 2	O 2	0
55	r	6	Total 6	O 6	0
55	s	2	Total 2	O 2	0
55	t	2	Total 2	O 2	0
55	v	4	Total 4	O 4	0
55	w	4	Total 4	O 4	0
55	x	7	Total 7	O 7	0
55	y	3	Total 3	O 3	0

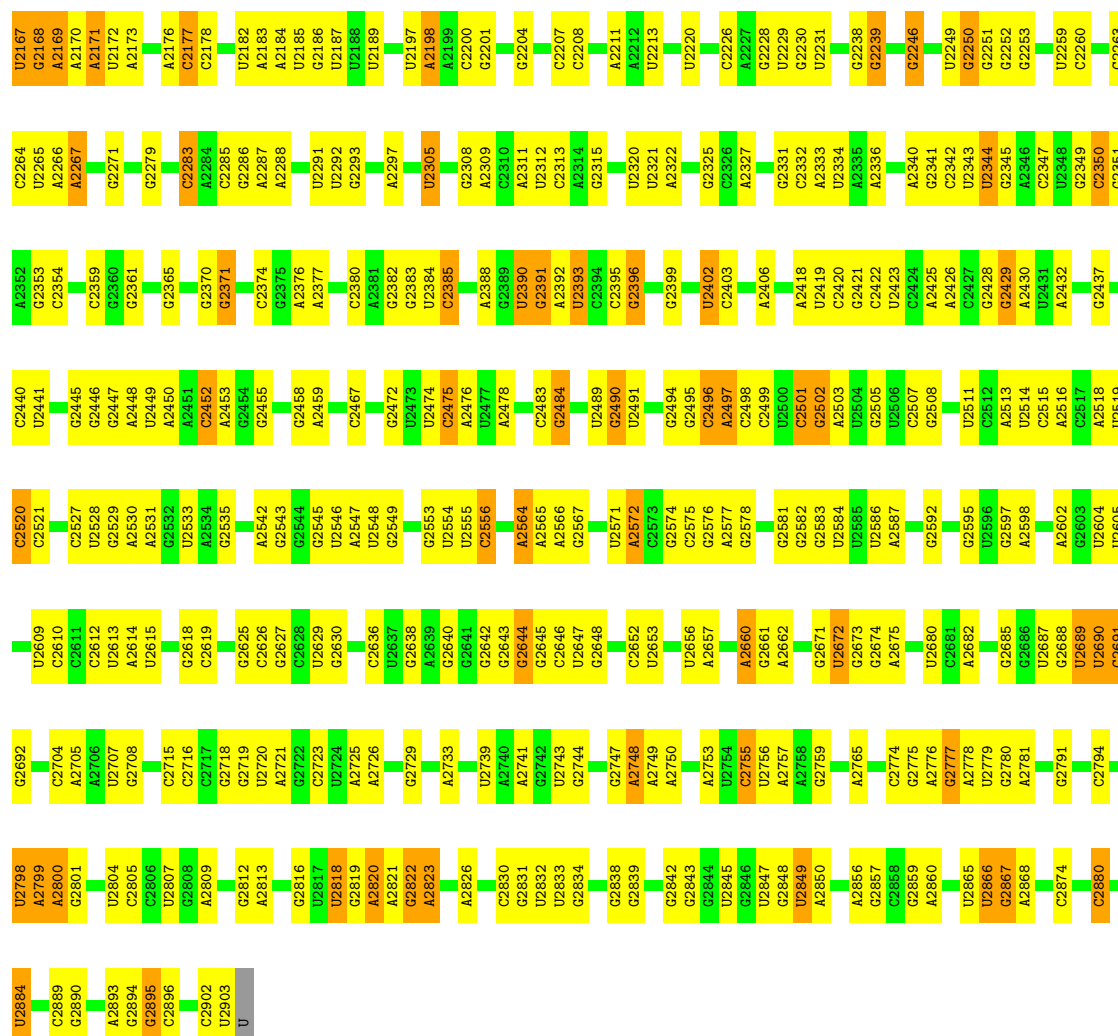
3 Residue-property plots [i](#)

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.

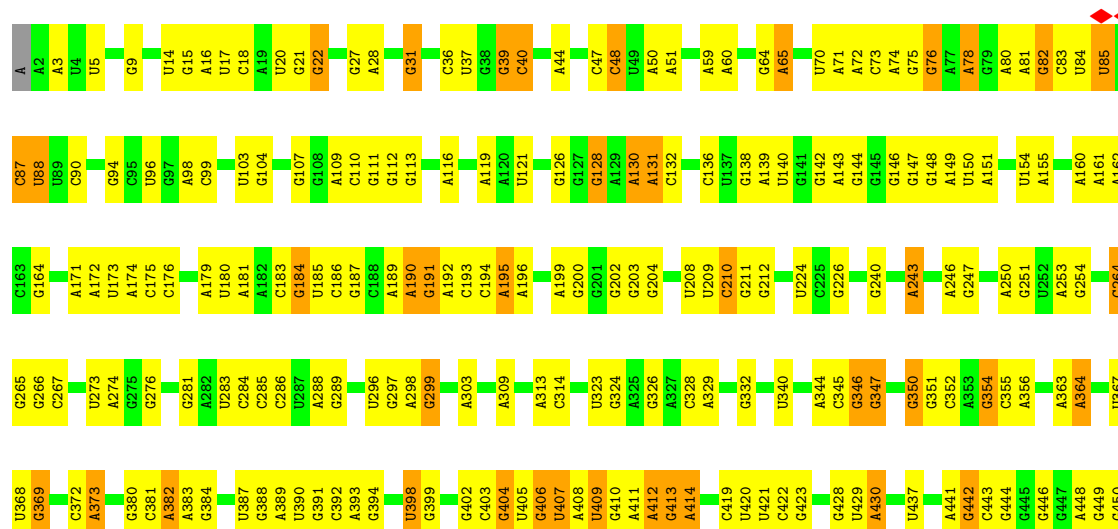
• Molecule 1: 23S ribosomal RNA

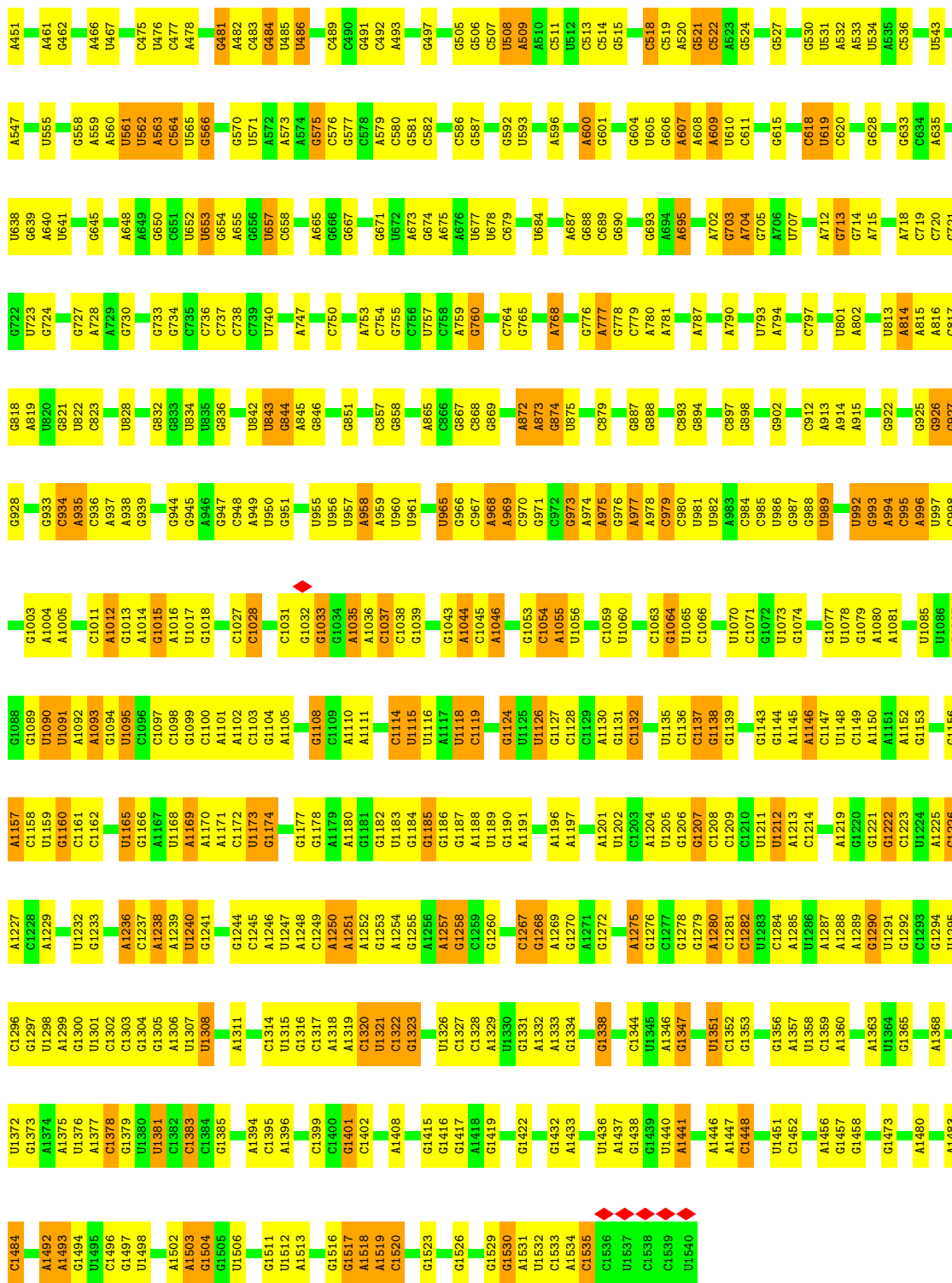


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U2105	G2027	A1938	G1828	G1734	G1645	C1532	G1432	G1341	G1236	C1135	U1061	A973	U887
U2106	A2030	A1939	A1829	A1735	C1646	C1533	A1433	A1342	A1247	G1136	G1062	G974	C388
A2108	G2031	U1940	G1830	U1736	U1647	U1533	A1434	A1343	G1248	G1137	C1063	A975	C389
U2109	G2032	C1941	G1835	G1738	G1649	U1535	G1435	U1344	U1249	C1140	C1064	G976	C390
G2110	A2033	C1942	G1836	A1739	A1650	C1536	G1436	C1345	G1250	U1141	U1066	A890	G891
U2111	U2034	U1943	C1837	U1743	G1651	G1537	C1437	G1346	C1251	A1142	A1067	A891	A892
G2112	C2036	C1838	G1839	G1743	A1652	U1538	U1438	C1347	G1252	A1147	G1068	A892	C393
U2113	U2037	C1839	G1840	G1753	A1653	C1541	G1441	C1348	A1253	G1153	A1069	A893	U895
A2114	G2038	U1841	A1654	A1754	A1655	U1542	U1442	A1353	A1254	C1154	A1070	A896	A896
G2116	U2039	G1842	A1656	G1756	A1656	A1544	C1447	A1354	G1256	A1155	G1071	A897	C397
A2117	C2043	C1843	U1662	A1757	U1663	G1555	C1451	C1357	A1265	G1162	C1072	A898	C398
U2118	C2044	U1844	G1666	U1758	A1667	G1558	A1452	G1360	G1266	G1075	A900	A899	A900
A2119	C2045	A1847	G1667	A1759	C1668	C1559	A1453	U1361	G1267	U1078	G907	G907	G907
U2122	G2048	A1848	A1669	A1762	A1669	G1560	C1454	A1367	A1268	C1079	A910	A910	A910
G2123	G2049	G1854	A1670	G1764	U1671	U1562	G1456	G1368	A1269	A1080	A911	A911	A911
A2124	A2051	U1857	A1672	U1769	U1673	U1563	C1461	G1374	C1270	U1081	C912	C912	C912
G2125	G2055	A1858	G1674	A1773	G1677	C1564	U1466	A1378	A1276	U1082	G914	G914	G914
A2126	C2056	U1864	A1678	U1777	A1678	A1566	U1467	U1379	A1277	A1084	C915	C915	C915
G2127	G2059	G1869	A1679	U1778	G1679	G1567	U1468	A1383	G1281	A1085	G916	G916	G916
G2128	A2060	U1888	A1686	A1781	G1696	U1577	U1469	A1384	G1282	A1086	A917	A917	A917
U2131	C2066	A1889	A1699	U1782	G1697	A1579	G1482	A1395	U1287	A1087	U932	U932	U932
U2132	G2067	A1890	G1700	A1783	A1699	U1580	G1483	A1396	C1288	A1088	A933	A933	A933
G2133	U2068	A1897	A1701	A1785	A1699	C1581	A1490	U1397	C1289	A1089	U934	U934	U934
A2134	G2069	A1899	G1702	U1789	G1699	C1582	A1496	C1399	U1294	U1099	G941	G941	G941
U2137	C2072	G1897	A1703	C1790	A1700	U1583	A1497	U1400	C1295	U1101	G942	G942	G942
G2138	G2073	U1898	A1704	A1791	A1701	C1585	U1498	G1401	G1296	C1102	A945	A945	A945
U2139	U2074	A1901	G1707	U1798	G1702	G1587	C1499	A1403	C1297	A1103	C946	C946	C946
C2140	G2075	G1906	G1707	G1799	G1707	U1588	G1500	C1404	G1300	U1104	A947	A947	A947
G2141	A2076	G1907	U1712	C1800	G1707	A1588	G1501	U1405	A1301	G1105	C948	C948	C948
A2142	C2077	A1912	A1713	A1801	U1712	U1602	A1504	U1406	A1302	U1106	G949	G949	G949
C2143	G2078	A1913	U1714	A1802	A1713	G1606	A1505	G1407	G1303	U1108	G953	G953	G953
G2144	U2079	A1914	U1715	A1808	U1715	C1607	A1506	C1414	A1304	G1109	G954	G954	G954
C2145	A2080	G1915	G1720	A1809	U1720	A1608	A1507	U1415	G1309	A1111	U955	U955	U955
U2146	G2082	U1916	G1721	A1810	G1721	A1608	A1508	U1416	G1322	U1112	C956	C956	C956
A2147	A2083	A1916	G1721	G1811	G1721	A1614	A1515	C1417	A1323	U1217	G961	G961	G961
G2150	C2084	C1920	G1724	G1814	G1724	C1615	G1516	G1418	C1323	U1218	C962	C962	C962
C2151	U2081	G1921	U1725	A1815	U1725	A1616	G1517	A1419	G1324	U1219	G965	G965	G965
G2152	G2085	C1924	G1726	C1816	G1726	C1617	G1518	A1420	U1325	G1125	C966	C966	C966
A2153	A2086	G1925	G1727	G1817	G1727	A1618	G1519	A1421	U1326	G1126	C967	C967	C967
C2154	U2087	A1926	G1728	U1818	G1728	A1626	G1520	G1422	A1327	U1224	G1055	G1055	G1055
U2155	G2088	A1927	U1729	U1819	U1729	G1627	G1521	G1423	U1328	G1125	G1056	G1056	G1056
G2156	A2089	A1928	G1730	A1821	G1730	U1627	A1522	G1424	U1329	A1129	C968	C968	C968
C2157	C2090	G1929	G1731	U1820	G1731	G1643	G1523	G1425	C1330	U1130	U969	U969	U969
A2158	U2091	U1931	C1732	A1821	C1732	G1643	G1524	A1427	G1331	G1131	U970	U970	U970
G2159	G2092												
C2160	U2093												
U2161	A2094												
G2162	C2095												
A2163	U2096												
C2164	G2097												
U2165	A2100												
G2166	G2100												



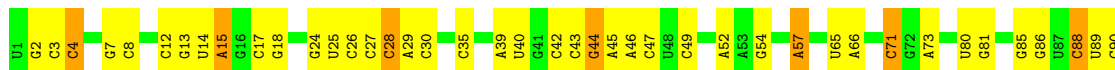
• Molecule 2: 16S ribosomal RNA





• Molecule 3: 5S ribosomal RNA

Chain 3: 58% 35% 8%





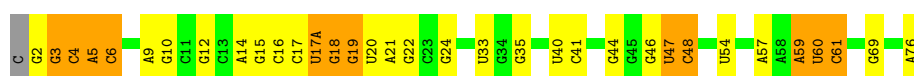
- Molecule 4: mRNA

Chain 4: 22% 78%



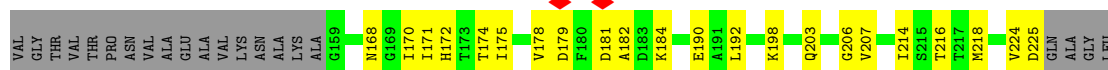
- Molecule 5: tRNA ProL(GGG)

Chain 5: 55% 29% 16%



- Molecule 6: 50S ribosomal protein L1

Chain A: 36% 23% 41%



- Molecule 7: 50S ribosomal protein L2

Chain B: 74% 25%

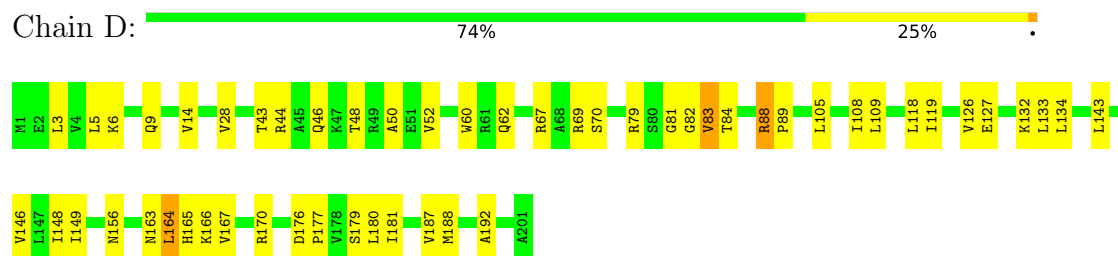


- Molecule 8: 50S ribosomal protein L3

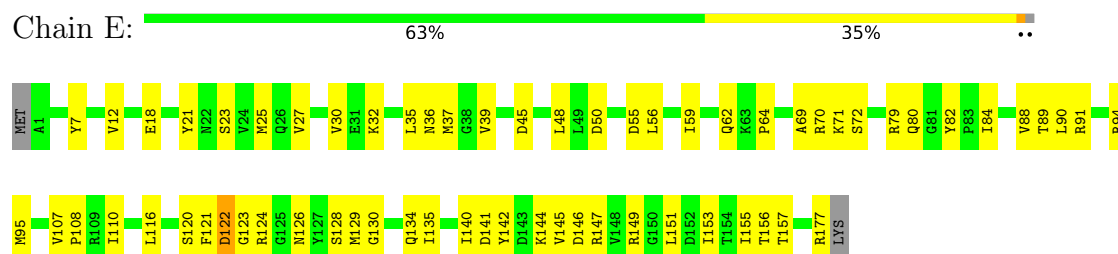
Chain C: 73% 26%



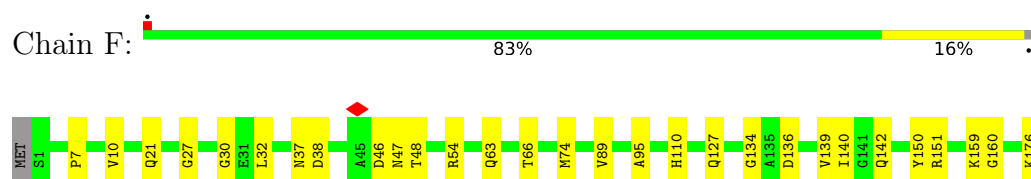
- Molecule 9: 50S ribosomal protein L4



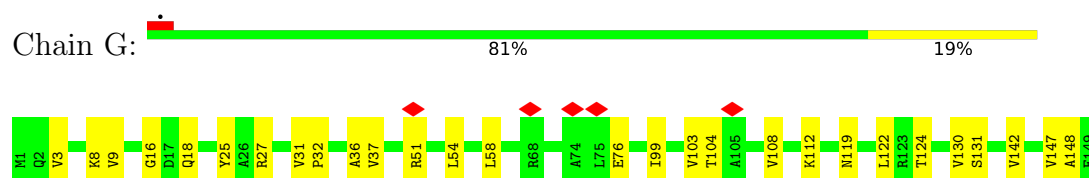
- Molecule 10: 50S ribosomal protein L5



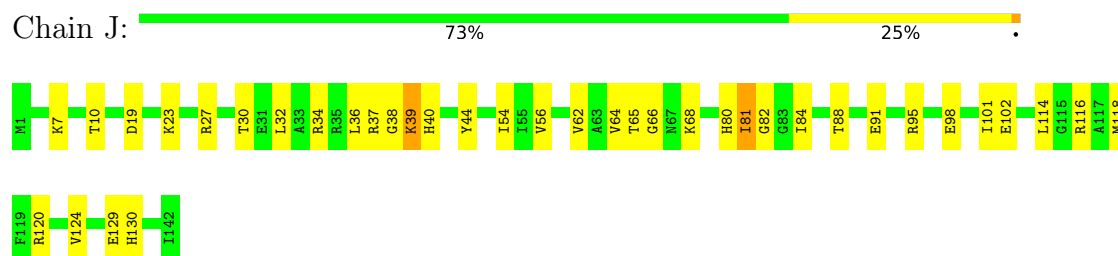
- Molecule 11: 50S ribosomal protein L6



- Molecule 12: 50S ribosomal protein L9

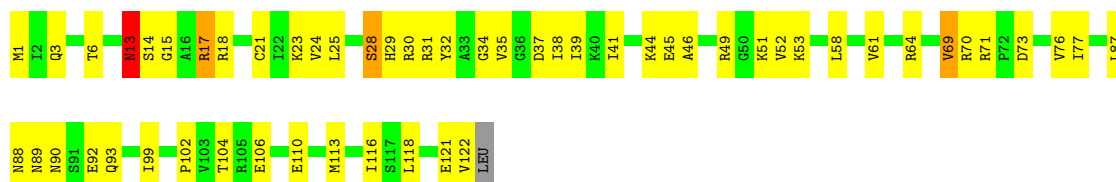


- Molecule 13: 50S ribosomal protein L13

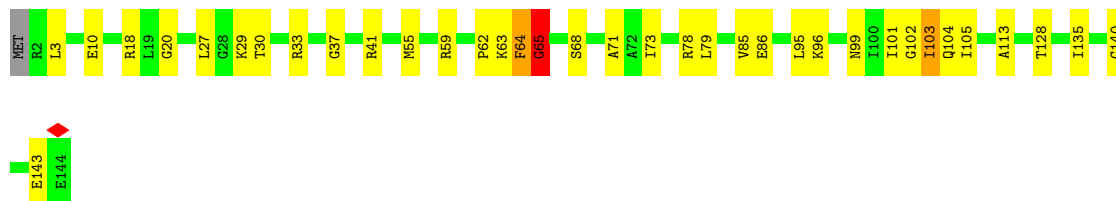


- Molecule 14: 50S ribosomal protein L14

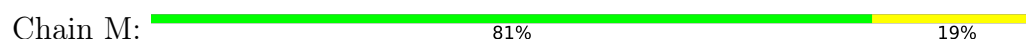




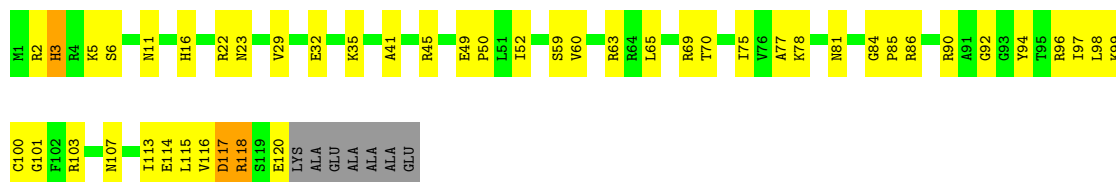
- Molecule 15: 50S ribosomal protein L15



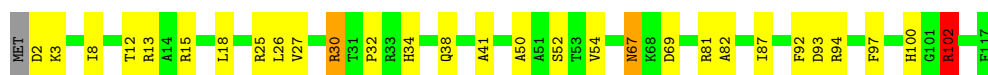
- Molecule 16: 50S ribosomal protein L16



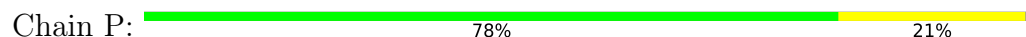
- Molecule 17: 50S ribosomal protein L17



- Molecule 18: 50S ribosomal protein L18



- Molecule 19: 50S ribosomal protein L19



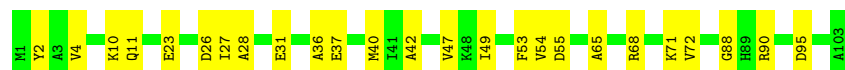
- Molecule 20: 50S ribosomal protein L20

Chain Q:  68% 31%



- Molecule 21: 50S ribosomal protein L21

Chain R:  76% 24%



- Molecule 22: 50S ribosomal protein L22

Chain S:  74% 25%



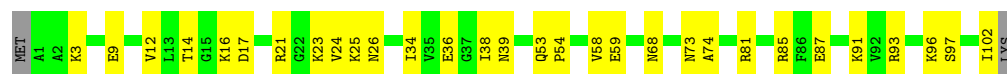
- Molecule 23: 50S ribosomal protein L23

Chain T:  61% 29% 7%



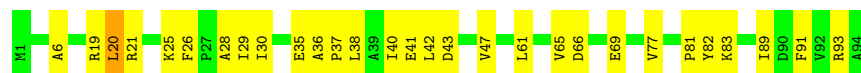
- Molecule 24: 50S ribosomal protein L24

Chain U:  69% 29%



- Molecule 25: 50S ribosomal protein L25

Chain V:  69% 30%



- Molecule 26: 50S ribosomal protein L27

Chain W:  74% 15% 11%



- Molecule 27: 50S ribosomal protein L28

Chain X:  77% 22%



- Molecule 28: 50S ribosomal protein L29

Chain Y:  87% 13%



- Molecule 29: 50S ribosomal protein L30

Chain Z:  61% 34%



- Molecule 30: 50S ribosomal protein L32

Chain b:  65% 33%



- Molecule 31: 50S ribosomal protein L33

Chain c:  76% 15% 9%



- Molecule 32: 50S ribosomal protein L34

Chain d:  67% 33%



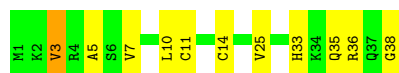
- Molecule 33: 50S ribosomal protein L35

Chain e:  63% 34%



- Molecule 34: 50S ribosomal protein L36

Chain f:  71% 26% .



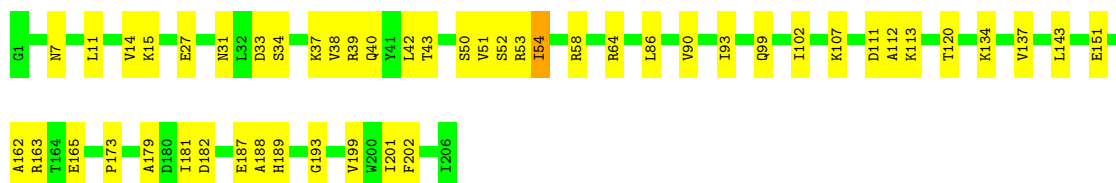
- Molecule 35: 30S ribosomal protein S2

Chain g:  62% 27% . 8%



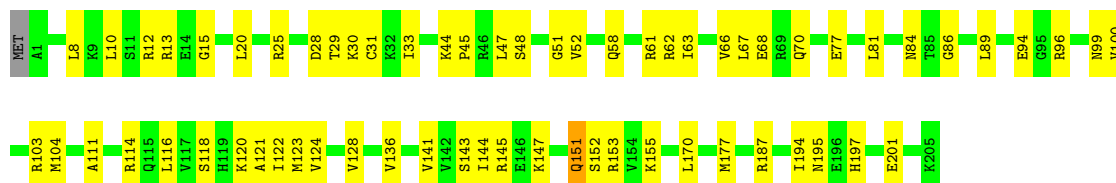
- Molecule 36: 30S ribosomal protein S3

Chain h:  76% 23%



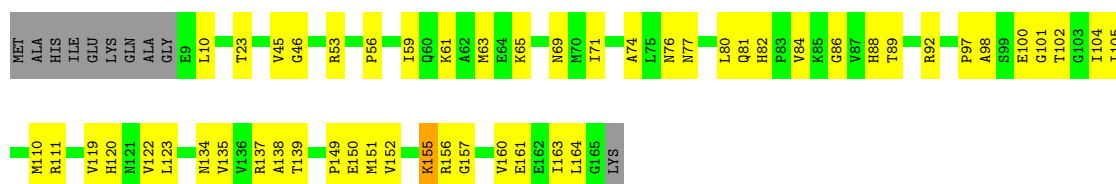
- Molecule 37: 30S ribosomal protein S4

Chain i:  68% 31%



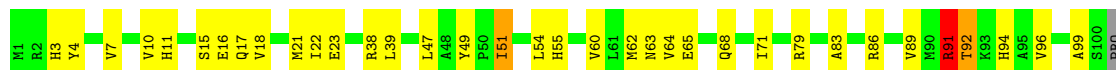
- Molecule 38: 30S ribosomal protein S5

Chain j:  63% 31% . 6%



- Molecule 39: 30S ribosomal protein S6

Chain k:  48% 24% . 26%



MET VAL LYS LYS LYS ASP GLU ARG ARG ARG ARG ASP ASP PHE ALA ALA ASN GLU THR ALA ASP ASP ASP ALA GLU ALA GLY ASP SER GLU GLU GLU GLU

• Molecule 40: 30S ribosomal protein S7

Chain l:  55% 29% 16%

MET P1 R2 R3 R4 V5 I6 L12 L13 G18 K24 M30 K34 K35 S36 T37 A38 E39 V42 A45 L49 G54 K55 S56 E57 L58 E59 A60 F61 A64 V68 S76 R77 R78 V79 G80 G81 S82 T83 Y84 E89 V90 R91 R94 R95

L98 A99 M100 R101 R110 M115 A116 L117 L118 L119 L123 S124 D125 K130 R137 E138 D139 R142 N147 A151 HIS TYR ARG TRP LEU LEU ARG SER PHE SER HIS GLN ALA GLY ALA SER SER LYS GLN PRO ALA LEU TYR LEU ASN

• Molecule 41: 30S ribosomal protein S8

Chain m:  67% 32%

MET S1 D4 P5 I6 A7 D8 M9 L10 T11 R12 T13 R14 A22 A23 V24 T25 N26 P27 S28 S29 K30 I31 K32 E46 K49 K55 L58 E59 L60 T61 L62 I74 Q75 R76 V77 S78 T84 Y85 K86 L91 V94 I100 V103 D112 A115

R116 G119 L120 I124 I125 C126 Y127 V128 A129

• Molecule 42: 30S ribosomal protein S9

Chain n:  60% 37% ..

MET ALA GLU R3 V6 R10 R11 R12 S13 S14 A15 A16 R17 V18 F19 I20 N24 G25 V28 I29 R32 S33 L34 E35 G39 R40 Q49 V54 D55 H56 V57 E58 K59 L60 D61 L62 T63 T64 V65 V66 G69 Q74 A77 I78 T82 T83 R84

Y89 D90 L97 R98 K99 F102 V103 T104 R108 E111 K114 L117 A120 R121 R122 R129

• Molecule 43: 30S ribosomal protein S10

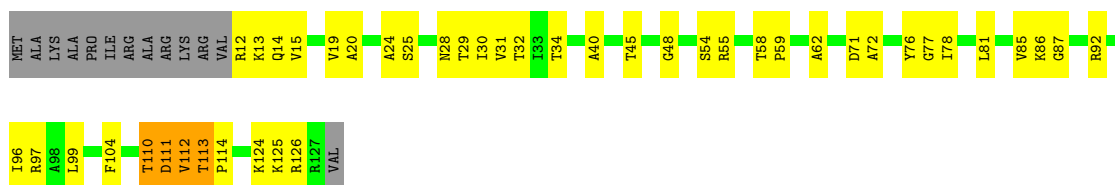
Chain o:  60% 32% 5%

MET GLN ASN GLN R5 I6 R7 I8 R9 L10 D14 H15 R16 V26 E27 T28 A29 K30 V36 R37 G38 P39 I40 P41 L42 P43 T44 R45 R48 I53 S54 P55 H56 E66 H70 L71 R72 L73 V74 D75 I76 T80 T83 A86 L87 M88 R89 L90 V98

S101 L102 GLY

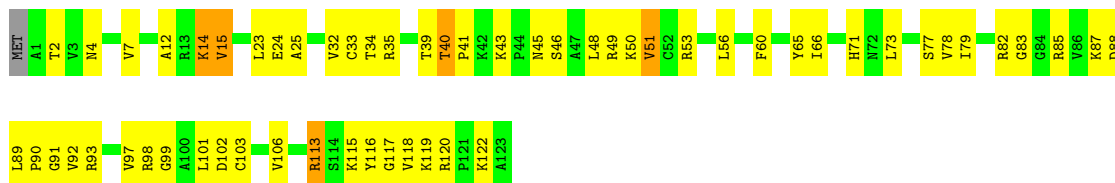
• Molecule 44: 30S ribosomal protein S11

Chain p:  56% 31% 10%



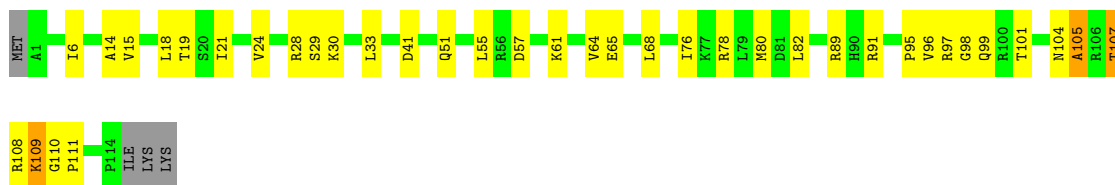
- Molecule 45: 30S ribosomal protein S12

Chain q: 52% 43% ..



- Molecule 46: 30S ribosomal protein S13

Chain r: 64% 30% ..



- Molecule 47: 30S ribosomal protein S14

Chain s: 64% 30% ..



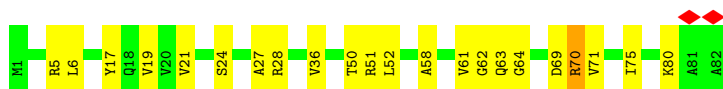
- Molecule 48: 30S ribosomal protein S15

Chain t: 69% 30% .



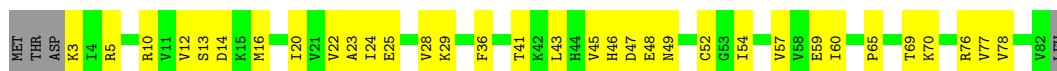
- Molecule 49: 30S ribosomal protein S16

Chain u: 73% 26% .



- Molecule 50: 30S ribosomal protein S17

Chain v: 



- Molecule 51: 30S ribosomal protein S18

Chain w: 



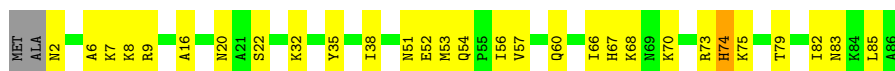
- Molecule 52: 30S ribosomal protein S19

Chain x: 



- Molecule 53: 30S ribosomal protein S20

Chain y: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	71502	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 ($e^-/\text{\AA}^2$)	56.07	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	0.109	Depositor
Minimum map value	-0.021	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0198	Depositor
Map size (Å)	547.3792, 547.3792, 547.3792	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	0.18	0/69796	0.33	11/108888 (0.0%)
2	2	0.20	0/36963	0.36	4/57662 (0.0%)
3	3	0.16	0/2872	0.26	0/4479
4	4	0.09	0/87	0.16	0/132
5	5	0.11	0/1819	0.24	0/2836
6	A	0.15	0/1033	0.39	0/1387
7	B	0.43	1/2121 (0.0%)	0.56	2/2852 (0.1%)
8	C	0.45	0/1586	0.61	1/2134 (0.0%)
9	D	0.65	1/1571 (0.1%)	0.82	9/2113 (0.4%)
10	E	0.23	0/1434	0.50	1/1926 (0.1%)
11	F	0.18	0/1343	0.39	0/1816
12	G	0.14	0/1122	0.35	0/1515
13	J	0.36	0/1152	0.43	0/1551
14	K	0.57	1/947 (0.1%)	0.71	2/1268 (0.2%)
15	L	0.51	0/1054	0.70	2/1403 (0.1%)
16	M	0.18	0/1093	0.38	0/1460
17	N	0.50	0/973	0.71	5/1301 (0.4%)
18	O	0.54	0/902	0.73	2/1209 (0.2%)
19	P	0.18	0/929	0.39	0/1242
20	Q	0.42	0/960	0.48	1/1278 (0.1%)
21	R	0.35	0/829	0.46	0/1107
22	S	0.62	0/864	0.75	5/1156 (0.4%)
23	T	0.61	0/744	0.77	5/994 (0.5%)
24	U	0.18	0/787	0.39	0/1051
25	V	0.47	0/766	0.52	0/1025
26	W	0.26	0/582	0.48	0/769
27	X	0.36	0/635	0.51	0/848
28	Y	0.19	0/510	0.43	0/677
29	Z	0.52	1/453 (0.2%)	0.81	3/605 (0.5%)
30	b	0.33	0/450	0.54	0/599
31	c	0.45	1/416 (0.2%)	0.62	1/554 (0.2%)
32	d	0.20	0/380	0.47	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.28	0/513	0.61	1/676 (0.1%)
34	f	0.54	0/303	0.65	1/397 (0.3%)
35	g	0.55	1/550 (0.2%)	0.89	3/728 (0.4%)
36	h	0.29	0/1652	0.57	4/2225 (0.2%)
37	i	0.39	0/1665	0.55	1/2227 (0.0%)
38	j	0.38	0/1169	0.58	4/1573 (0.3%)
39	k	0.43	0/835	0.84	4/1128 (0.4%)
40	l	0.21	0/1195	0.48	0/1602
41	m	0.25	0/989	0.44	0/1326
42	n	0.24	0/1034	0.53	2/1375 (0.1%)
43	o	0.35	0/796	0.68	2/1077 (0.2%)
44	p	0.30	0/885	0.53	0/1195
45	q	0.59	0/969	0.98	9/1300 (0.7%)
46	r	0.37	1/892 (0.1%)	0.68	5/1193 (0.4%)
47	s	0.57	0/817	0.95	7/1088 (0.6%)
48	t	0.18	0/722	0.36	0/964
49	u	0.49	0/659	0.67	3/884 (0.3%)
50	v	0.19	0/657	0.50	0/881
51	w	0.17	0/544	0.35	0/731
52	x	0.16	0/652	0.45	0/877
53	y	0.49	0/671	0.64	3/888 (0.3%)
All	All	0.26	7/155342 (0.0%)	0.42	103/232670 (0.0%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	r	105	ALA	CA-C	-6.76	1.45	1.53
9	D	133	LEU	CA-C	-6.49	1.44	1.52
7	B	259	ASN	CA-C	-5.46	1.45	1.52
35	g	11	PHE	CA-C	-5.44	1.47	1.52
31	c	25	ASN	CA-C	-5.38	1.46	1.53

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	D	82	GLY	N-CA-C	14.01	146.38	113.18
39	k	92	THR	N-CA-C	13.81	130.32	111.54
22	S	2	GLU	N-CA-C	11.46	123.85	111.36
47	s	30	ILE	N-CA-C	11.12	120.98	110.53
39	k	91	ARG	N-CA-C	9.56	125.32	109.06

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	865	0
2	2	33012	0	16617	498	0
3	3	2568	0	1303	33	0
4	4	80	0	45	0	0
5	5	1628	0	823	16	0
6	A	1026	0	1092	50	0
7	B	2082	0	2157	58	0
8	C	1565	0	1616	39	0
9	D	1552	0	1619	37	0
10	E	1410	0	1447	56	0
11	F	1323	0	1374	23	0
12	G	1111	0	1148	20	0
13	J	1129	0	1162	33	0
14	K	938	0	1012	39	0
15	L	1045	0	1117	33	0
16	M	1074	0	1157	22	0
17	N	960	0	1000	34	0
18	O	892	0	923	25	0
19	P	917	0	965	21	0
20	Q	947	0	1022	36	0
21	R	816	0	839	18	0
22	S	857	0	922	24	0
23	T	738	0	807	20	0
24	U	779	0	834	19	0
25	V	753	0	780	26	0
26	W	575	0	592	10	0
27	X	625	0	655	20	0
28	Y	509	0	543	8	0
29	Z	449	0	491	13	0
30	b	444	0	461	14	0
31	c	409	0	440	6	0
32	d	377	0	418	12	0
33	e	504	0	574	26	0
34	f	302	0	343	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	g	544	0	579	19	0
36	h	1625	0	1699	27	0
37	i	1643	0	1710	53	0
38	j	1156	0	1199	43	0
39	k	817	0	808	27	0
40	l	1181	0	1240	47	0
41	m	979	0	1034	34	0
42	n	1022	0	1070	52	0
43	o	786	0	828	28	0
44	p	869	0	878	44	0
45	q	955	0	1019	46	0
46	r	883	0	944	50	0
47	s	805	0	847	36	0
48	t	714	0	737	22	0
49	u	649	0	666	13	0
50	v	648	0	691	28	0
51	w	535	0	552	19	0
52	x	637	0	665	34	0
53	y	665	0	714	20	0
54	1	306	0	0	0	0
54	2	72	0	0	0	0
54	3	8	0	0	0	0
54	4	1	0	0	0	0
54	B	2	0	0	0	0
54	E	1	0	0	0	0
54	J	1	0	0	0	0
54	N	1	0	0	0	0
54	Q	1	0	0	0	0
54	S	2	0	0	0	0
54	b	1	0	0	0	0
54	m	1	0	0	0	0
54	r	1	0	0	0	0
55	1	478	0	0	59	0
55	2	309	0	0	39	0
55	3	7	0	0	0	0
55	5	3	0	0	0	0
55	A	16	0	0	11	0
55	B	4	0	0	1	0
55	C	2	0	0	2	0
55	D	2	0	0	0	0
55	E	16	0	0	13	0
55	F	4	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	G	5	0	0	1	0
55	J	2	0	0	1	0
55	K	2	0	0	0	0
55	L	2	0	0	0	0
55	M	2	0	0	3	0
55	N	1	0	0	1	0
55	O	2	0	0	5	0
55	Q	2	0	0	2	0
55	T	2	0	0	1	0
55	U	3	0	0	0	0
55	V	2	0	0	0	0
55	W	3	0	0	0	0
55	X	3	0	0	3	0
55	Y	1	0	0	0	0
55	c	1	0	0	0	0
55	f	1	0	0	0	0
55	g	4	0	0	1	0
55	h	5	0	0	3	0
55	i	10	0	0	4	0
55	j	3	0	0	4	0
55	k	7	0	0	5	0
55	l	11	0	0	11	0
55	m	3	0	0	1	0
55	n	3	0	0	4	0
55	o	4	0	0	3	0
55	p	4	0	0	4	0
55	q	2	0	0	2	0
55	r	6	0	0	7	0
55	s	2	0	0	2	0
55	t	2	0	0	1	0
55	v	4	0	0	3	0
55	w	4	0	0	8	0
55	x	7	0	0	4	0
55	y	3	0	0	2	0
All	All	144183	0	95521	2467	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 11.

The worst 5 of 2467 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)
27:X:75:GLU:HG3	55:X:101:HOH:O	1.39	1.19
55:2:1752:HOH:O	41:m:27:PRO:HB3	1.42	1.18
2:2:84:U:H4'	55:2:1882:HOH:O	1.47	1.12
1:1:2104:C:H1'	55:1:3577:HOH:O	1.51	1.11
42:n:49:GLN:HG3	55:n:202:HOH:O	1.47	1.10

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%)	121 (93%)	9 (7%)	0	100	100
7	B	269/273 (98%)	232 (86%)	34 (13%)	3 (1%)	11	42
8	C	207/209 (99%)	179 (86%)	26 (13%)	2 (1%)	12	43
9	D	199/201 (99%)	178 (89%)	20 (10%)	1 (0%)	24	56
10	E	175/179 (98%)	154 (88%)	20 (11%)	1 (1%)	21	52
11	F	174/177 (98%)	161 (92%)	13 (8%)	0	100	100
12	G	147/149 (99%)	142 (97%)	5 (3%)	0	100	100
13	J	140/142 (99%)	130 (93%)	8 (6%)	2 (1%)	9	37
14	K	120/123 (98%)	101 (84%)	17 (14%)	2 (2%)	7	34
15	L	141/144 (98%)	111 (79%)	27 (19%)	3 (2%)	5	31
16	M	134/136 (98%)	118 (88%)	16 (12%)	0	100	100
17	N	118/127 (93%)	97 (82%)	19 (16%)	2 (2%)	7	34
18	O	114/117 (97%)	101 (89%)	13 (11%)	0	100	100
19	P	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
20	Q	115/118 (98%)	109 (95%)	6 (5%)	0	100	100
21	R	101/103 (98%)	88 (87%)	13 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	S	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
23	T	91/100 (91%)	81 (89%)	9 (10%)	1 (1%)	11	42
24	U	100/104 (96%)	91 (91%)	9 (9%)	0	100	100
25	V	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
26	W	73/84 (87%)	66 (90%)	7 (10%)	0	100	100
27	X	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
28	Y	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
29	Z	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
30	b	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
31	c	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
32	d	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
33	e	62/65 (95%)	55 (89%)	6 (10%)	1 (2%)	7	35
34	f	36/38 (95%)	29 (81%)	7 (19%)	0	100	100
35	g	63/71 (89%)	48 (76%)	14 (22%)	1 (2%)	7	35
36	h	204/206 (99%)	192 (94%)	12 (6%)	0	100	100
37	i	203/206 (98%)	182 (90%)	21 (10%)	0	100	100
38	j	155/167 (93%)	141 (91%)	14 (9%)	0	100	100
39	k	98/135 (73%)	89 (91%)	9 (9%)	0	100	100
40	l	149/179 (83%)	140 (94%)	9 (6%)	0	100	100
41	m	127/130 (98%)	115 (91%)	12 (9%)	0	100	100
42	n	125/130 (96%)	114 (91%)	11 (9%)	0	100	100
43	o	96/103 (93%)	80 (83%)	13 (14%)	3 (3%)	3	26
44	p	114/129 (88%)	101 (89%)	12 (10%)	1 (1%)	14	45
45	q	121/124 (98%)	92 (76%)	28 (23%)	1 (1%)	16	48
46	r	112/118 (95%)	99 (88%)	13 (12%)	0	100	100
47	s	98/101 (97%)	85 (87%)	12 (12%)	1 (1%)	12	43
48	t	86/89 (97%)	79 (92%)	7 (8%)	0	100	100
49	u	80/82 (98%)	72 (90%)	8 (10%)	0	100	100
50	v	78/84 (93%)	61 (78%)	17 (22%)	0	100	100
51	w	63/75 (84%)	59 (94%)	4 (6%)	0	100	100
52	x	77/92 (84%)	65 (84%)	11 (14%)	1 (1%)	9	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	y	83/87 (95%)	83 (100%)	0	0	100	100
All	All	5428/5803 (94%)	4852 (89%)	550 (10%)	26 (0%)	26	56

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	B	260	LYS
14	K	28	SER
17	N	3	HIS
35	g	10	PRO
7	B	259	ASN

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%)	110 (100%)	0	100	100
7	B	216/218 (99%)	212 (98%)	4 (2%)	50	65
8	C	164/164 (100%)	160 (98%)	4 (2%)	43	61
9	D	165/165 (100%)	161 (98%)	4 (2%)	43	61
10	E	148/150 (99%)	147 (99%)	1 (1%)	76	77
11	F	137/138 (99%)	137 (100%)	0	100	100
12	G	114/114 (100%)	114 (100%)	0	100	100
13	J	116/116 (100%)	114 (98%)	2 (2%)	53	67
14	K	103/104 (99%)	100 (97%)	3 (3%)	37	57
15	L	102/103 (99%)	101 (99%)	1 (1%)	68	74
16	M	109/109 (100%)	109 (100%)	0	100	100
17	N	100/103 (97%)	98 (98%)	2 (2%)	48	64
18	O	86/87 (99%)	82 (95%)	4 (5%)	23	48
19	P	99/100 (99%)	99 (100%)	0	100	100
20	Q	89/90 (99%)	88 (99%)	1 (1%)	65	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	R	84/84 (100%)	84 (100%)	0	100	100
22	S	93/93 (100%)	89 (96%)	4 (4%)	26	50
23	T	80/84 (95%)	78 (98%)	2 (2%)	42	61
24	U	83/85 (98%)	83 (100%)	0	100	100
25	V	78/78 (100%)	76 (97%)	2 (3%)	40	60
26	W	57/62 (92%)	57 (100%)	0	100	100
27	X	67/68 (98%)	67 (100%)	0	100	100
28	Y	55/55 (100%)	55 (100%)	0	100	100
29	Z	48/49 (98%)	45 (94%)	3 (6%)	16	43
30	b	47/48 (98%)	47 (100%)	0	100	100
31	c	45/49 (92%)	45 (100%)	0	100	100
32	d	38/38 (100%)	38 (100%)	0	100	100
33	e	51/52 (98%)	49 (96%)	2 (4%)	28	53
34	f	34/34 (100%)	34 (100%)	0	100	100
35	g	55/61 (90%)	53 (96%)	2 (4%)	31	54
36	h	170/170 (100%)	167 (98%)	3 (2%)	51	67
37	i	172/173 (99%)	172 (100%)	0	100	100
38	j	119/126 (94%)	119 (100%)	0	100	100
39	k	87/116 (75%)	82 (94%)	5 (6%)	18	45
40	l	124/147 (84%)	122 (98%)	2 (2%)	55	68
41	m	104/105 (99%)	104 (100%)	0	100	100
42	n	105/107 (98%)	105 (100%)	0	100	100
43	o	86/90 (96%)	84 (98%)	2 (2%)	44	62
44	p	89/99 (90%)	85 (96%)	4 (4%)	24	49
45	q	103/104 (99%)	96 (93%)	7 (7%)	14	42
46	r	92/96 (96%)	92 (100%)	0	100	100
47	s	83/84 (99%)	80 (96%)	3 (4%)	31	54
48	t	76/77 (99%)	76 (100%)	0	100	100
49	u	65/65 (100%)	63 (97%)	2 (3%)	35	57
50	v	74/78 (95%)	74 (100%)	0	100	100
51	w	56/65 (86%)	56 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	x	70/79 (89%)	70 (100%)	0	100	100
53	y	65/66 (98%)	65 (100%)	0	100	100
All	All	4513/4725 (96%)	4444 (98%)	69 (2%)	55	68

5 of 69 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	q	2	THR
45	q	40	THR
47	s	50	LEU
18	O	102	ARG
18	O	69	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
26	W	42	HIS
52	x	13	HIS
36	h	18	ASN
51	w	53	GLN
53	y	74	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2904 (99%)	637 (21%)	39 (1%)
2	2	1538/1540 (99%)	379 (24%)	10 (0%)
3	3	119/120 (99%)	20 (16%)	1 (0%)
4	4	3/18 (16%)	0	0
5	5	76/77 (98%)	25 (32%)	3 (3%)
All	All	4638/4659 (99%)	1061 (22%)	53 (1%)

5 of 1061 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	8	C
1	1	10	A
1	1	36	G
1	1	42	A

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Mol	Chain	Res	Type
1	1	46	G

5 of 53 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1829	A
1	1	2168	G
3	3	14	U
1	1	1857	G
1	1	2109	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](#)

Of 398 ligands modelled in this entry, 398 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.

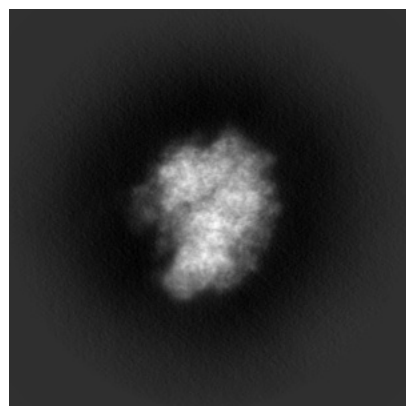
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42840. These allow visual inspection of the internal detail of the map and identification of artifacts.

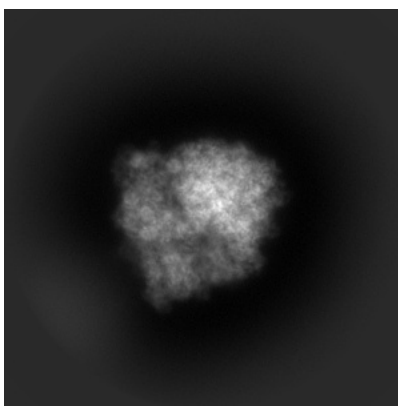
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

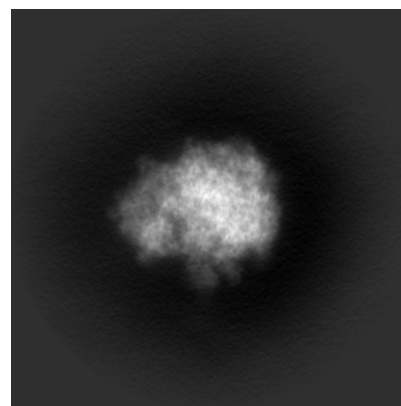
6.1.1 Primary map



X

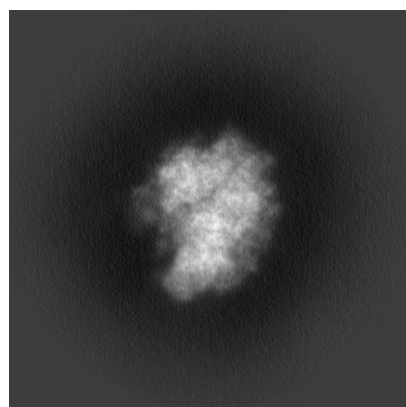


Y

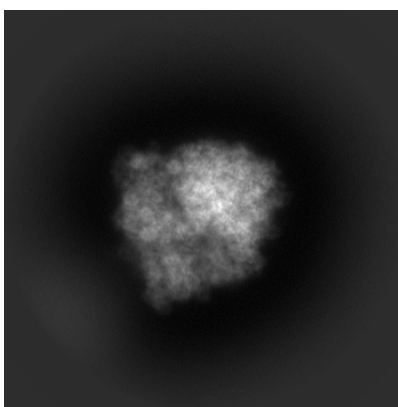


Z

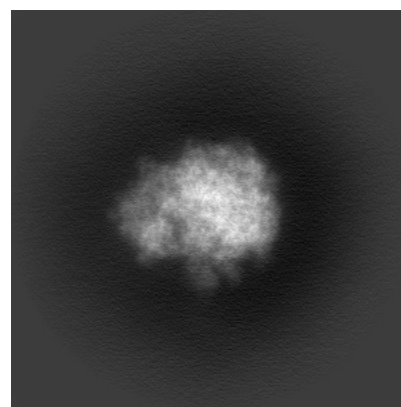
6.1.2 Raw map



X



Y

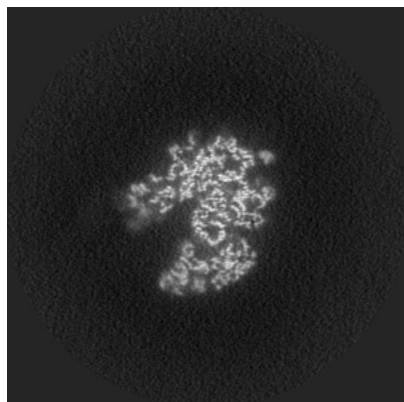


Z

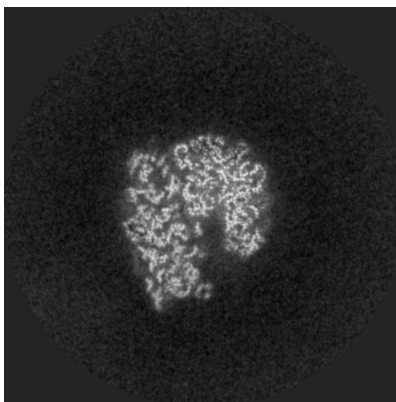
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

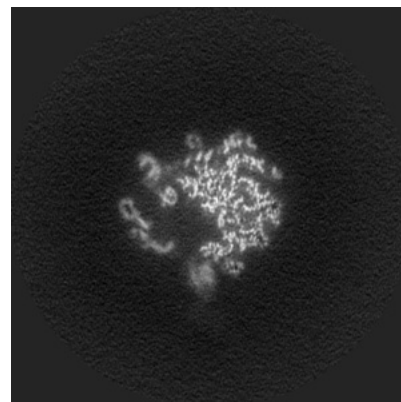
6.2.1 Primary map



X Index: 256

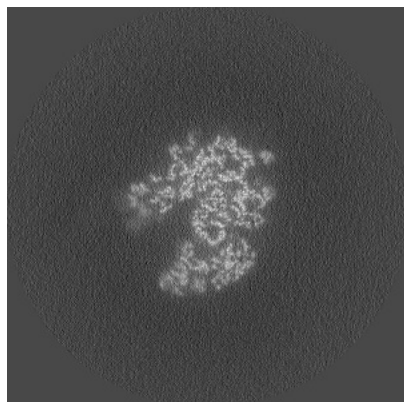


Y Index: 256

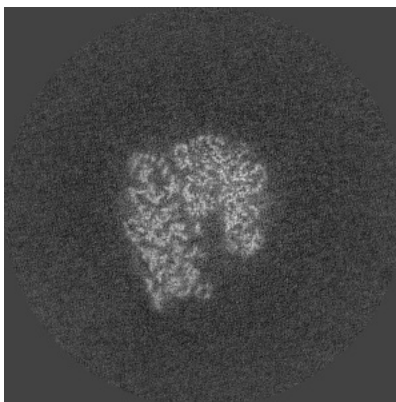


Z Index: 256

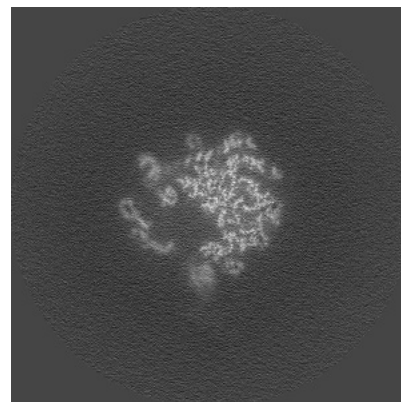
6.2.2 Raw map



X Index: 256



Y Index: 256

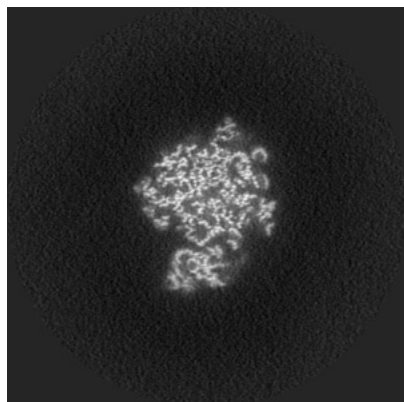


Z Index: 256

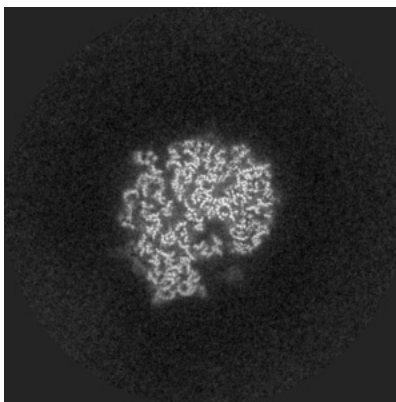
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

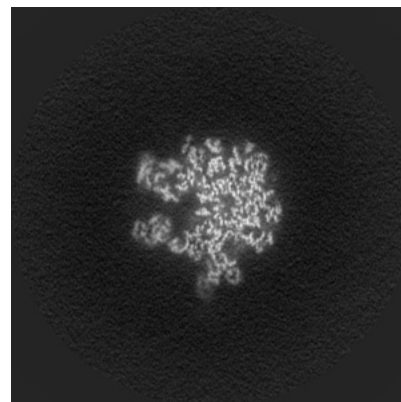
6.3.1 Primary map



X Index: 275

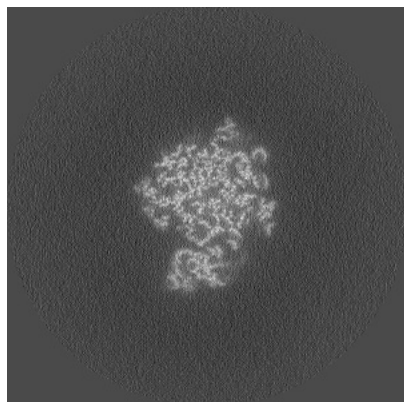


Y Index: 265

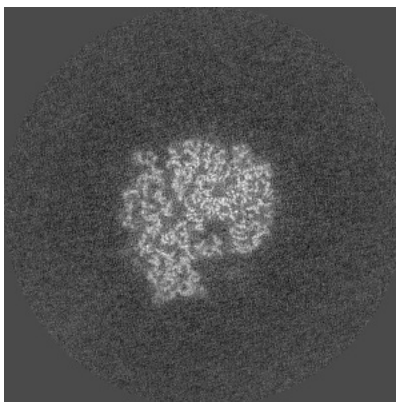


Z Index: 275

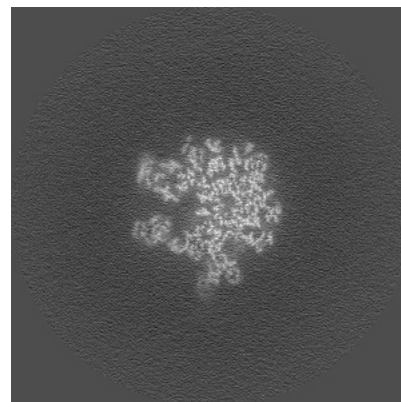
6.3.2 Raw map



X Index: 275



Y Index: 265

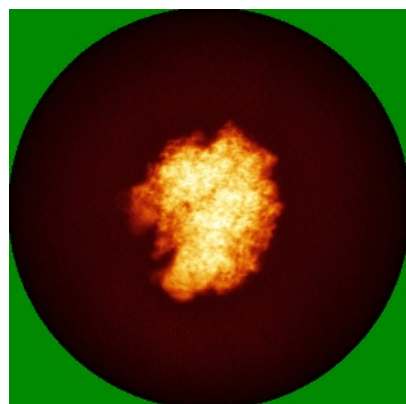


Z Index: 275

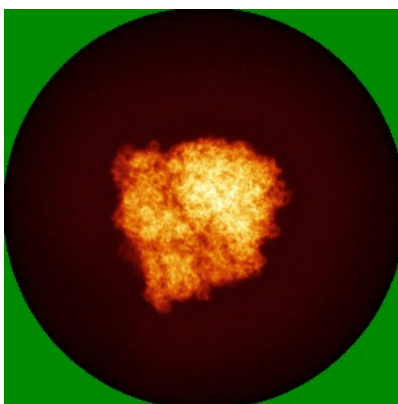
The images above show the largest variance slices of the map in three orthogonal directions.

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

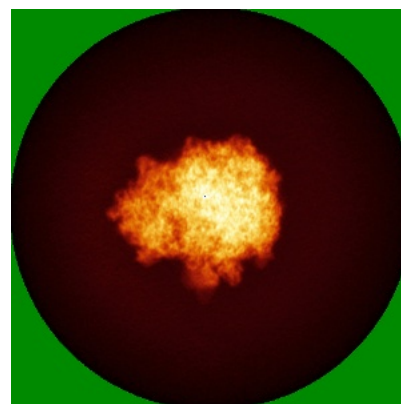
6.4.1 Primary map



X

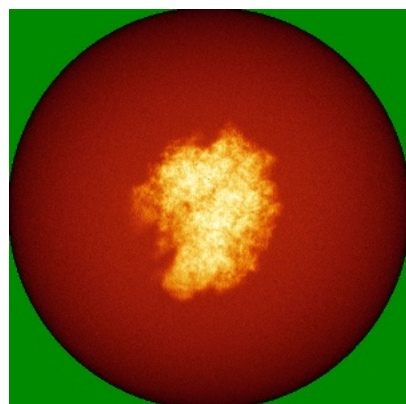


Y

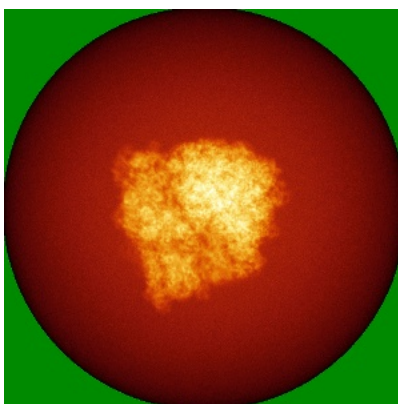


Z

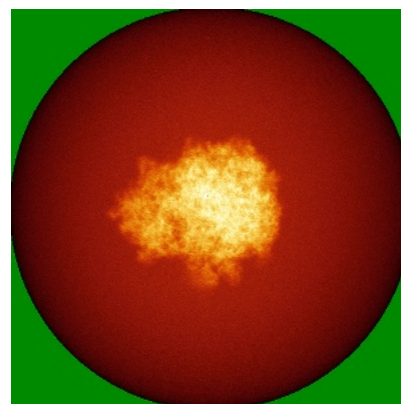
6.4.2 Raw map



X



Y

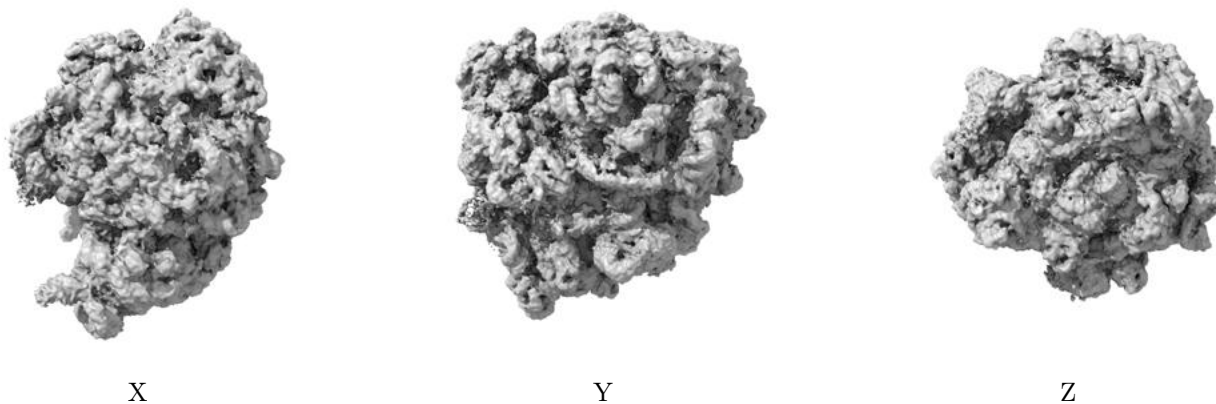


Z

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.

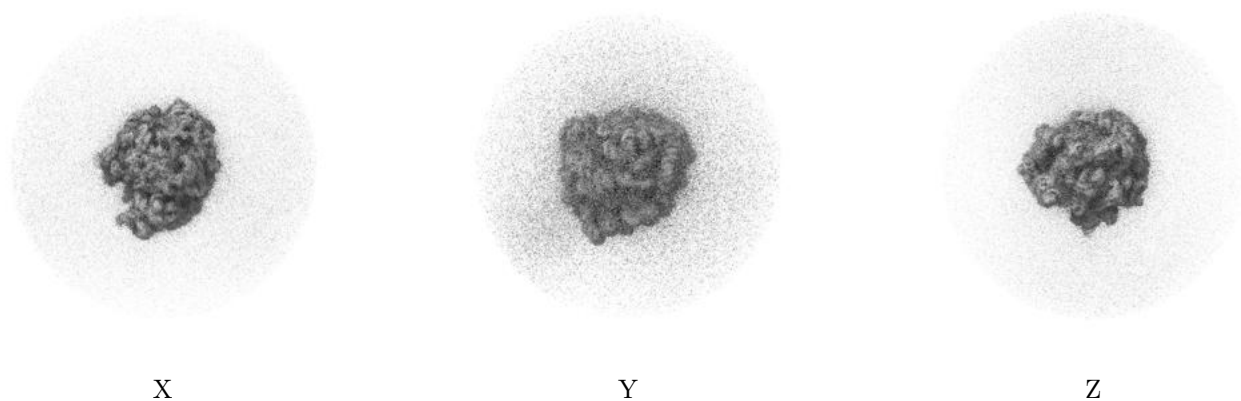
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0198. 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



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.

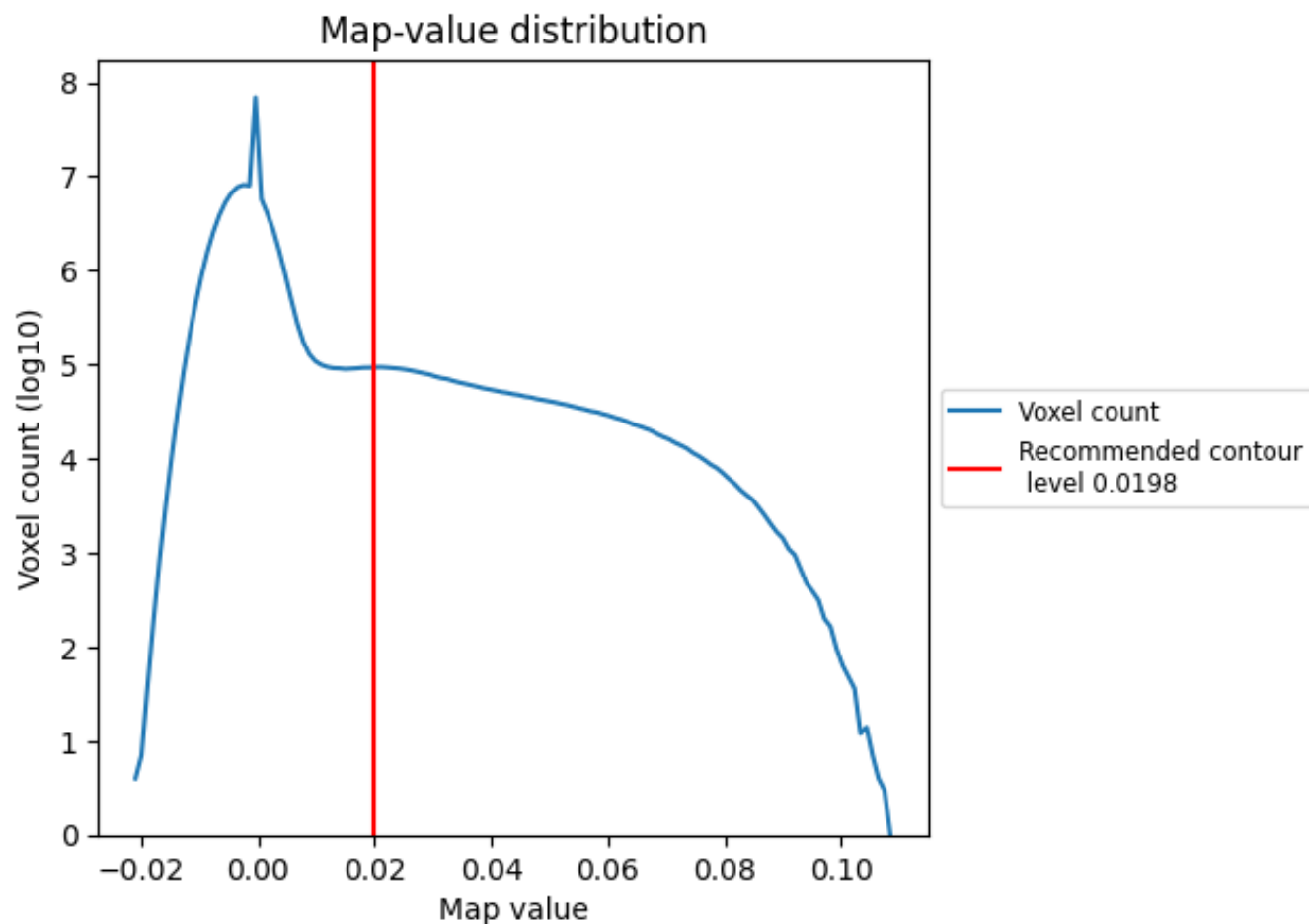
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

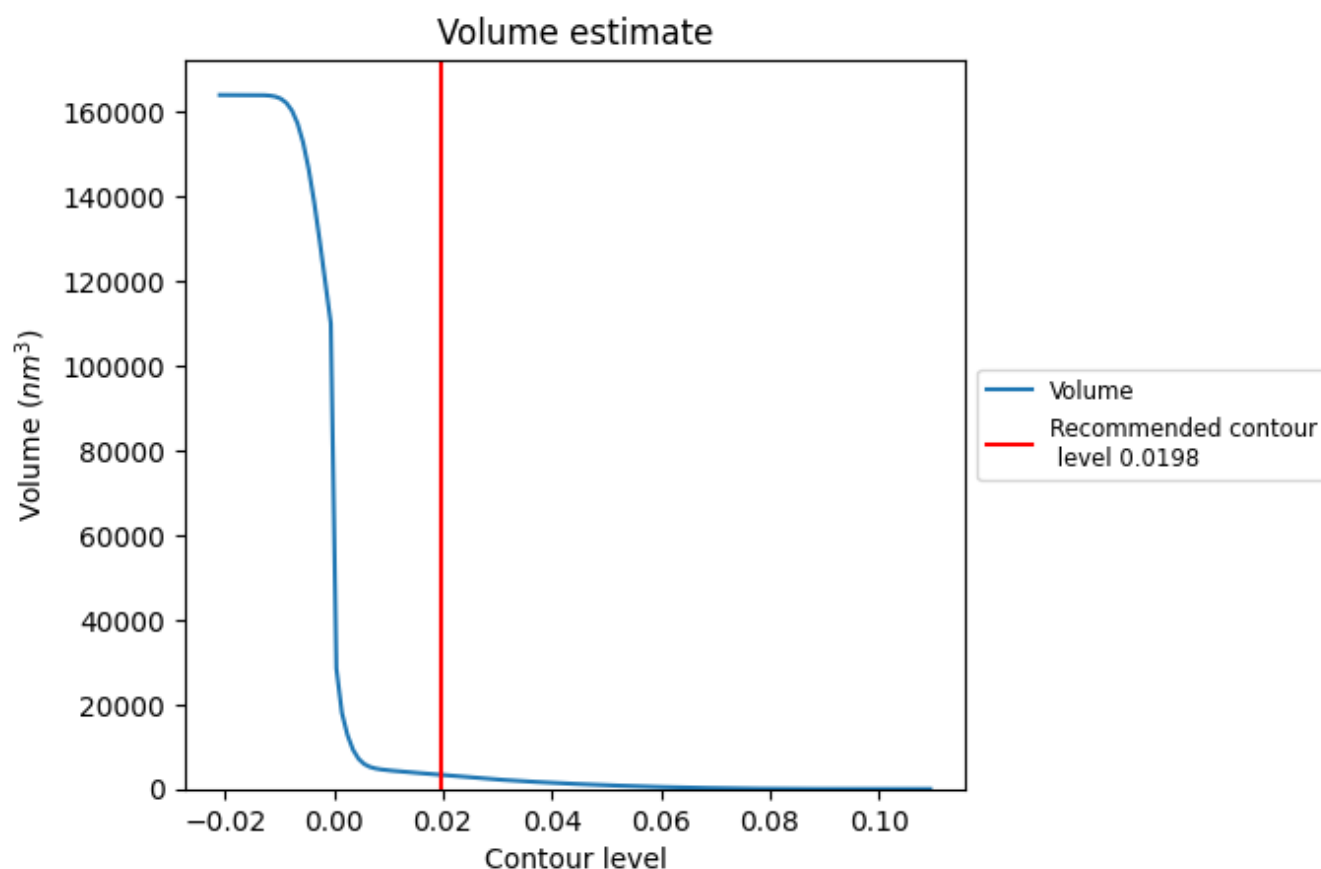
This section contains the results of statistical analysis of the map.

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.

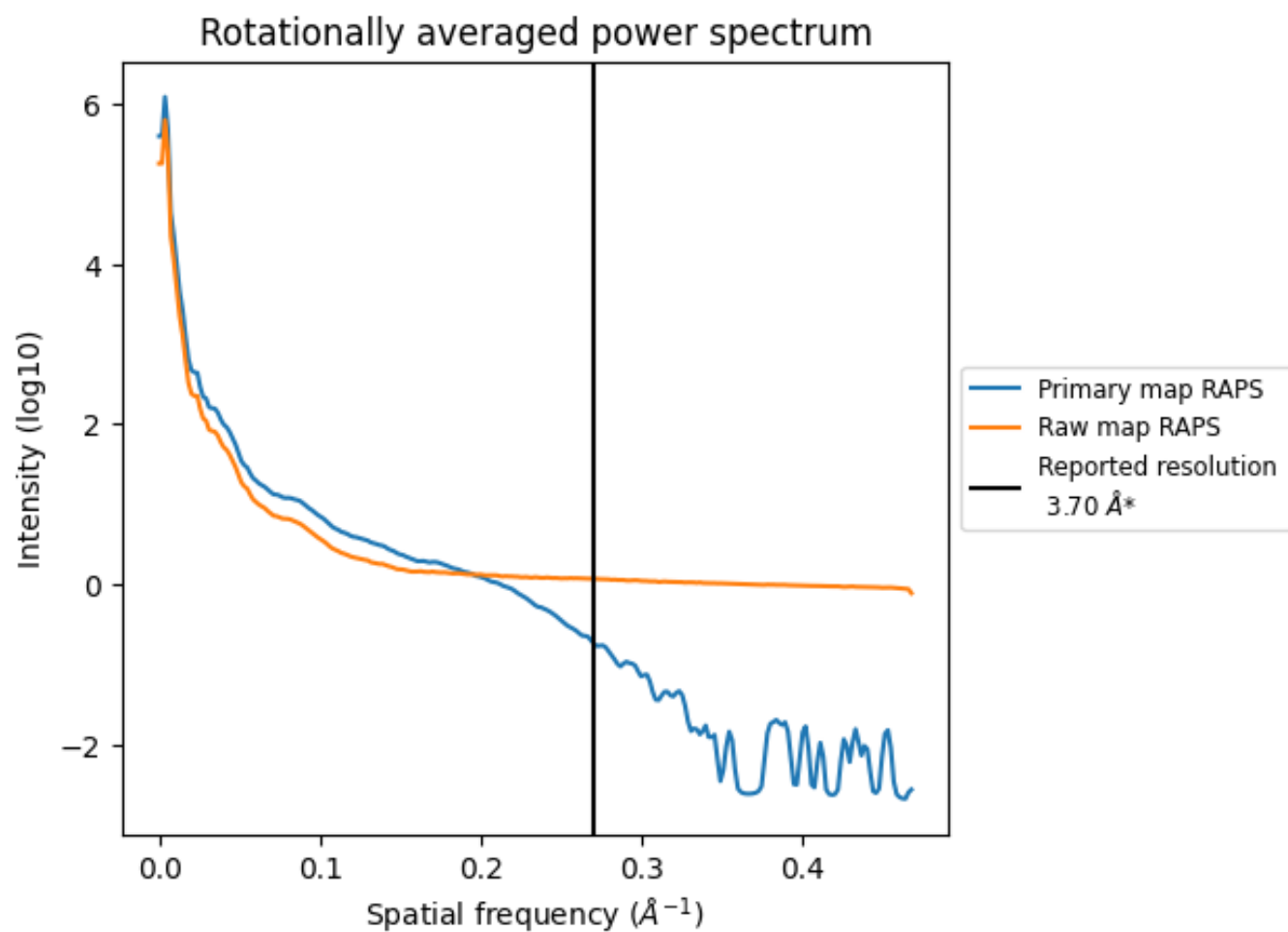
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3313 nm^3 ; this corresponds to an approximate mass of 2992 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 ⓘ

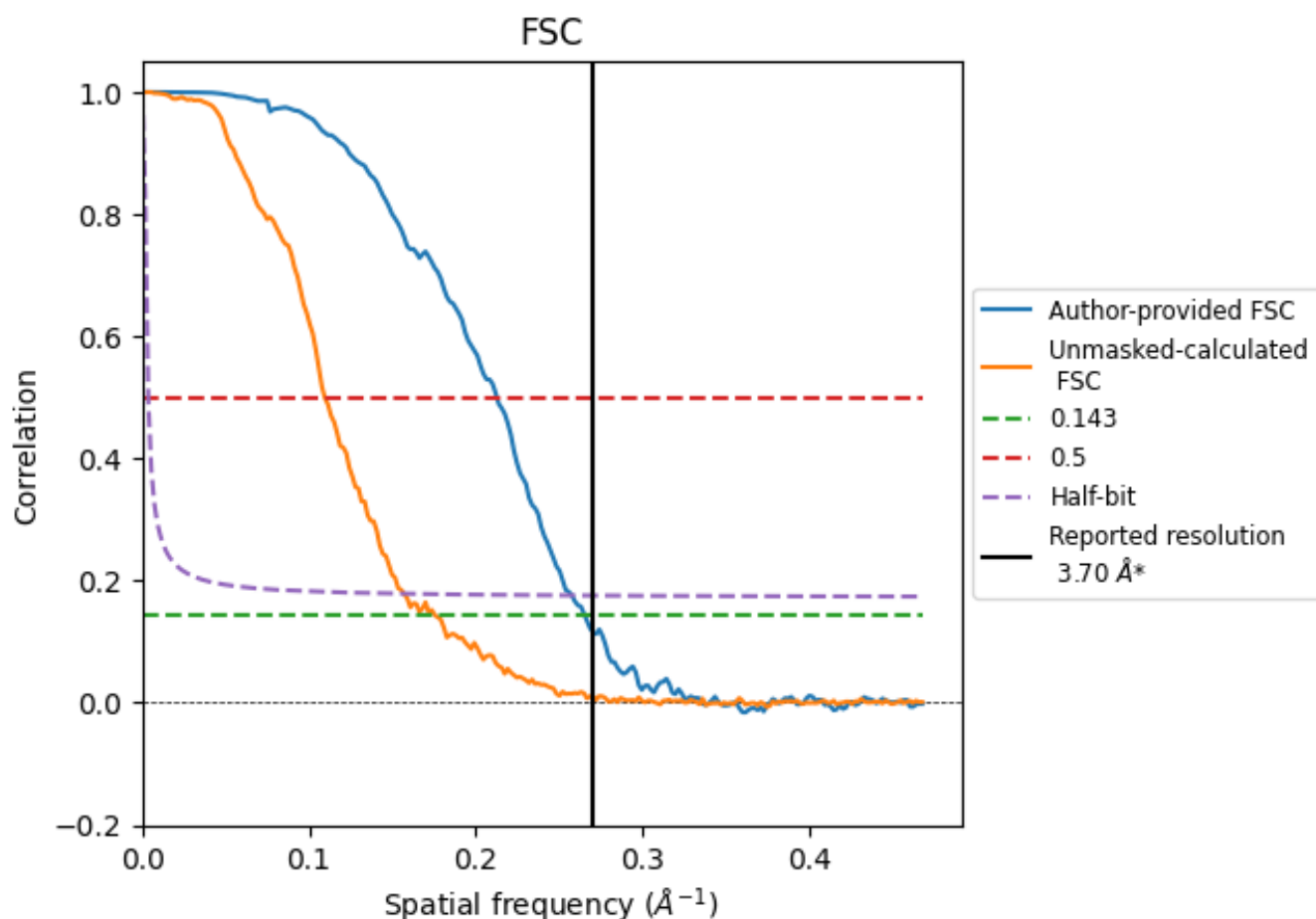


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

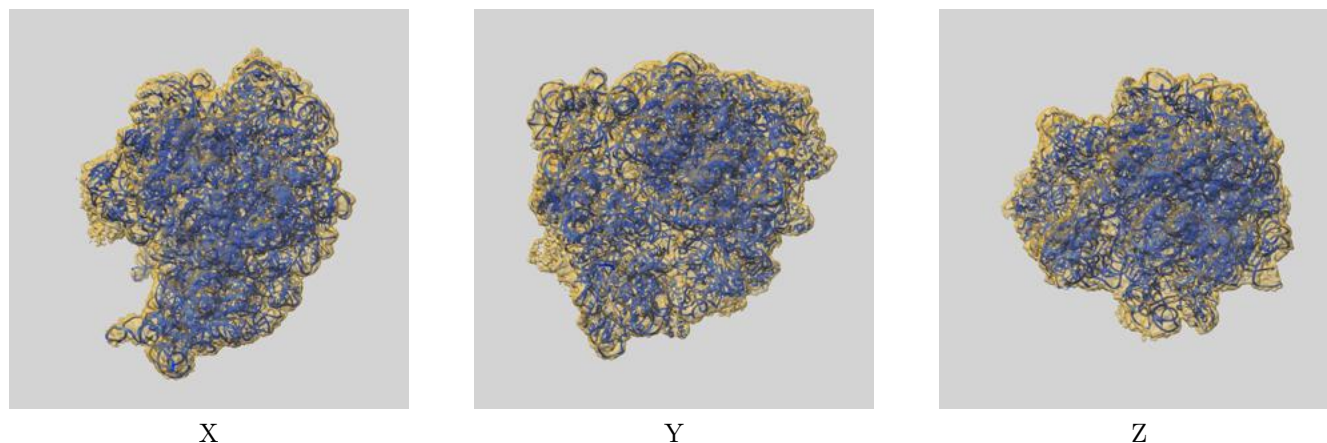
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.77	4.70	3.88
Unmasked-calculated*	5.69	9.13	6.37

*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 5.69 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

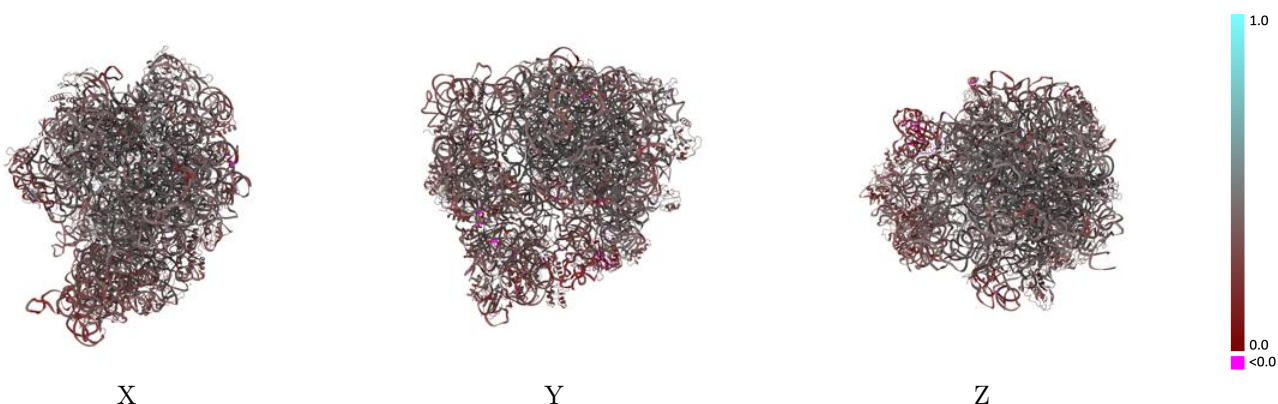
This section contains information regarding the fit between EMDB map EMD-42840 and PDB model 8UZG. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



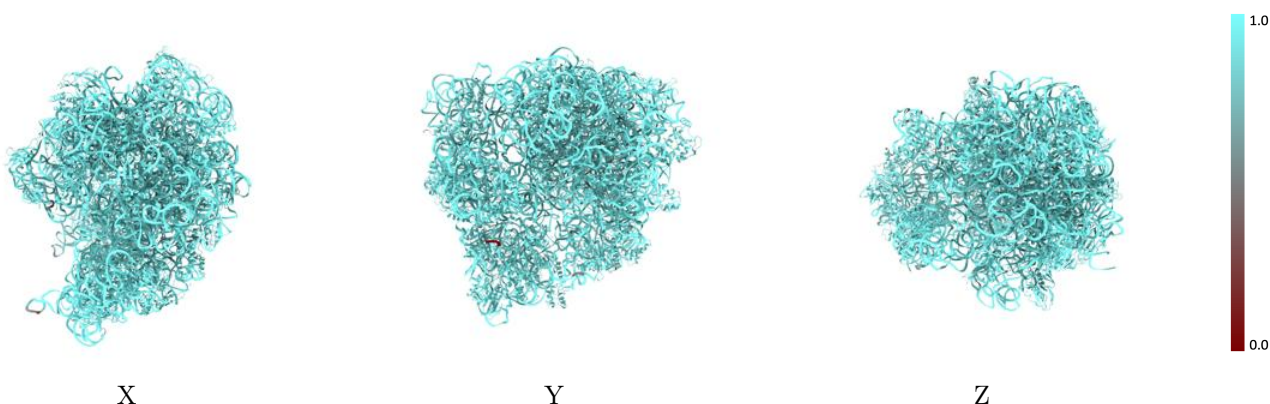
The images above show the 3D surface view of the map at the recommended contour level 0.0198 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



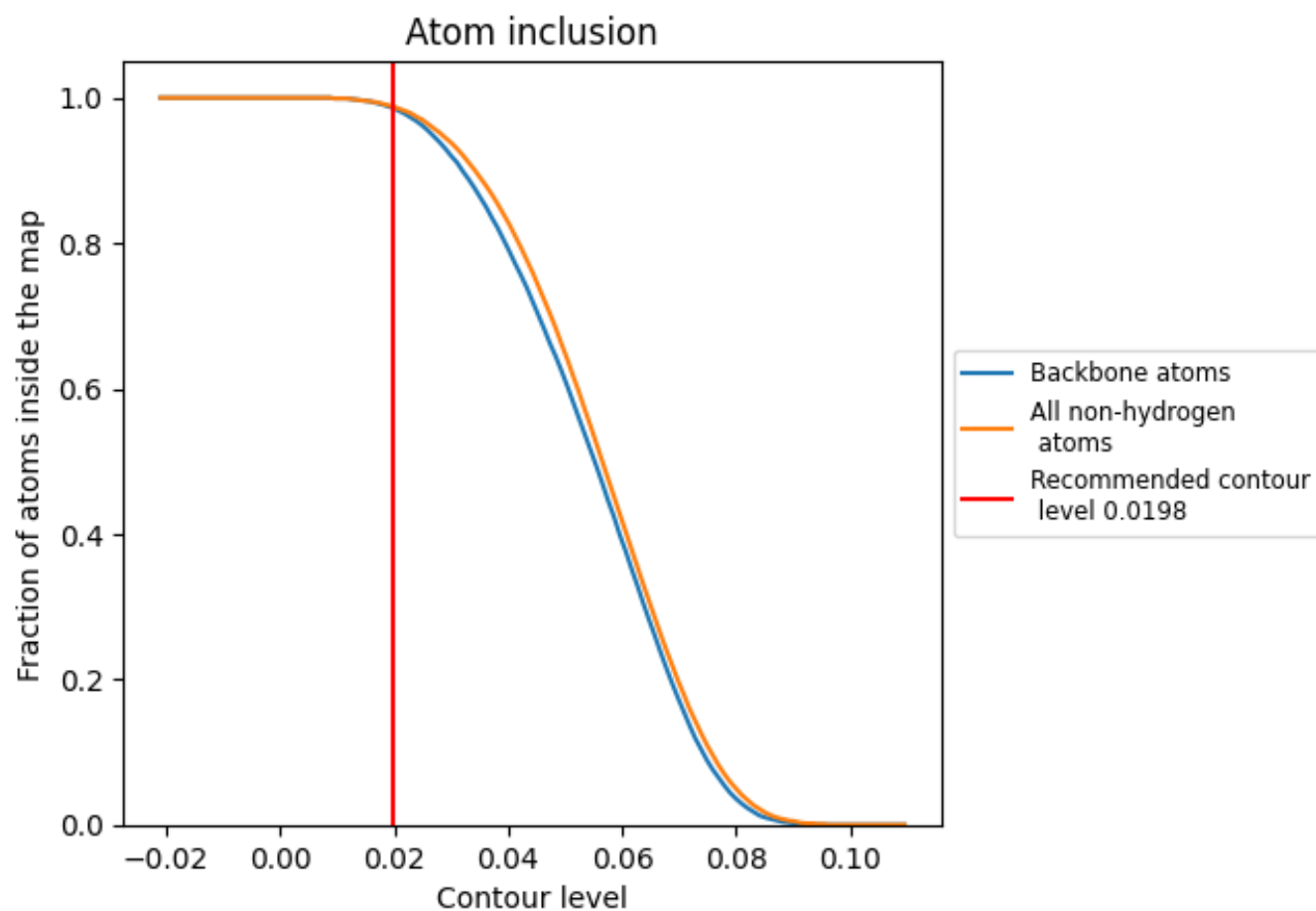
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0198).

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 (0.0198) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9880	 0.3730
1	 0.9970	 0.4010
2	 0.9920	 0.3610
3	 0.9990	 0.3930
4	 1.0000	 0.3290
5	 1.0000	 0.3650
A	 0.9300	 0.1680
B	 0.9990	 0.4270
C	 0.9820	 0.4070
D	 0.9670	 0.3850
E	 0.9590	 0.2750
F	 0.9570	 0.3450
G	 0.8340	 0.2760
J	 0.9950	 0.3980
K	 0.9960	 0.4020
L	 0.9750	 0.4120
M	 0.9930	 0.3930
N	 0.9990	 0.4000
O	 0.9680	 0.3540
P	 0.9910	 0.3970
Q	 0.9900	 0.3830
R	 0.9700	 0.4100
S	 0.9880	 0.3890
T	 0.9820	 0.3850
U	 0.9830	 0.3660
V	 0.9660	 0.3690
W	 0.9950	 0.4140
X	 0.9950	 0.3780
Y	 0.9620	 0.3120
Z	 0.9730	 0.3980
b	 0.9950	 0.4130
c	 0.9930	 0.3960
d	 1.0000	 0.3970
e	 1.0000	 0.4100
f	 1.0000	 0.3710



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Chain	Atom inclusion	Q-score
g	 0.9560	 0.2560
h	 0.9640	 0.2970
i	 0.9550	 0.2650
j	 0.9890	 0.3570
k	 0.9700	 0.3160
l	 0.9520	 0.2210
m	 0.9770	 0.3630
n	 0.9650	 0.2880
o	 0.9590	 0.2850
p	 0.9850	 0.3350
q	 0.9900	 0.2940
r	 0.9390	 0.2290
s	 0.9850	 0.2710
t	 0.9870	 0.3260
u	 0.9710	 0.3240
v	 0.9840	 0.3100
w	 0.9860	 0.3010
x	 0.9780	 0.2700
y	 0.9820	 0.2840