



## wwPDB EM Validation Summary Report ⓘ

Aug 18, 2025 – 02:09 PM EDT

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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

The types of validation reports are described at

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

---

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

EMDB validation analysis : 0.0.1.dev126  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.45.1

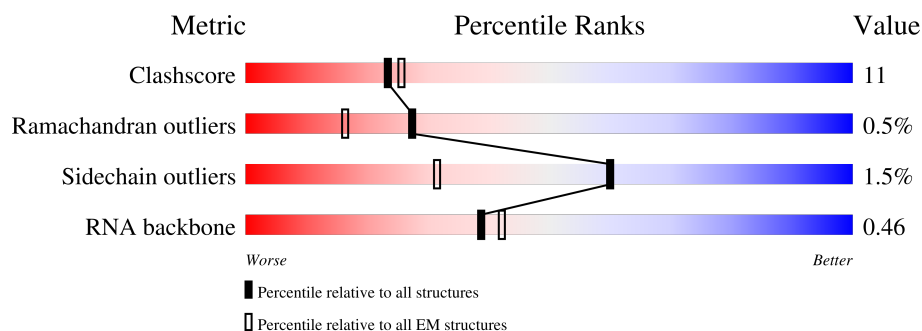
# 1 Overall quality at a glance

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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	2904	53% 38% 10%
2	2	1540	49% 40% 11%
3	3	120	58% 35% 8%
4	4	18	22% 78%
5	5	77	55% 29% 16%
6	A	229	36% 23% 41%
7	B	273	74% 25%







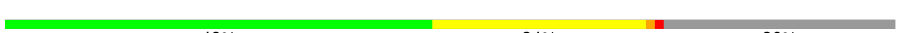







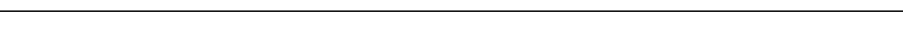
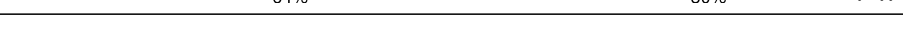





Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
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	
29	Z	59	
30	b	57	
31	c	55	
32	d	46	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
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

*Continued on next page...*

*Continued from previous page...*

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

*Continued on next page...*

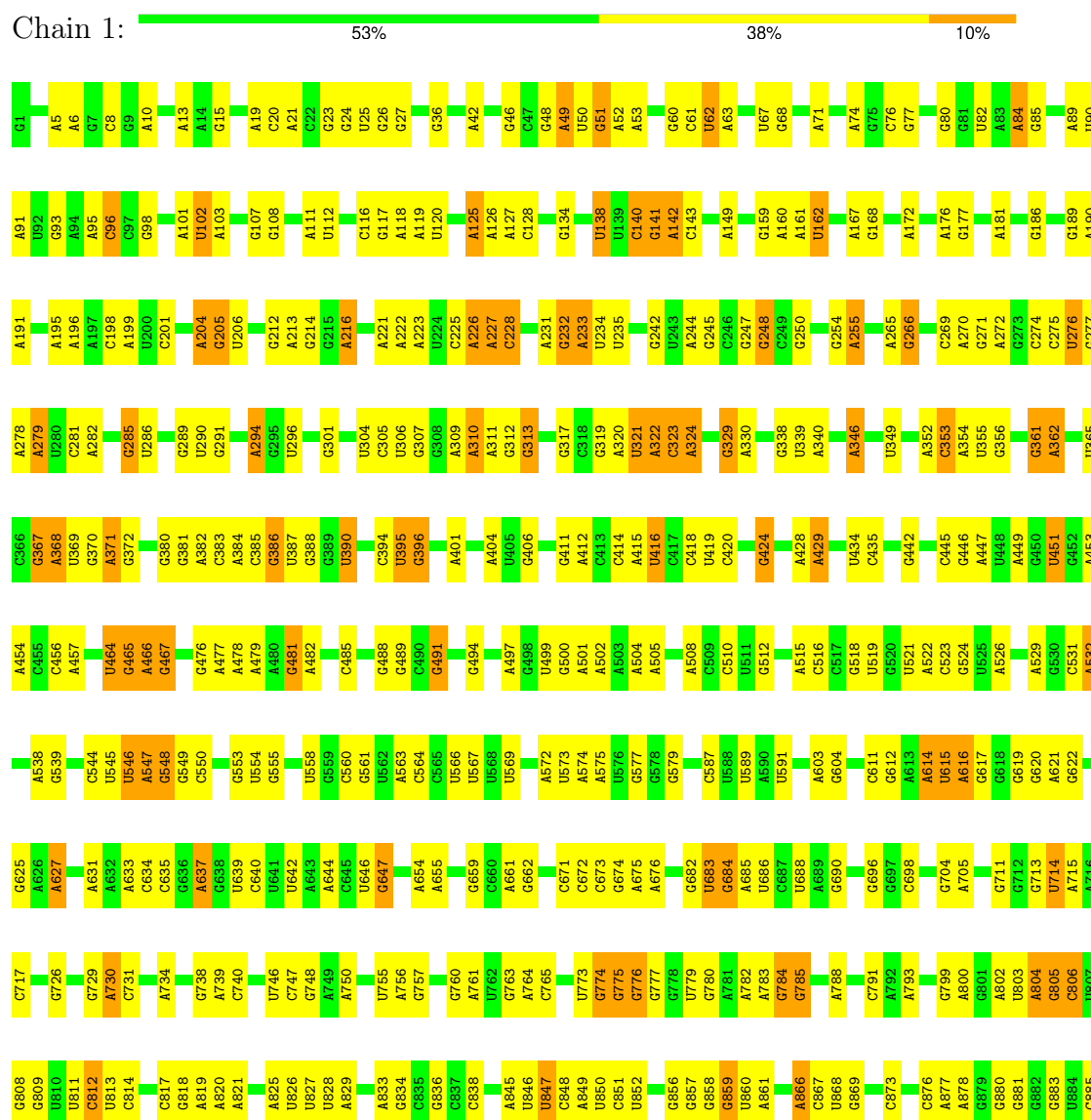
*Continued from previous page...*

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](#)

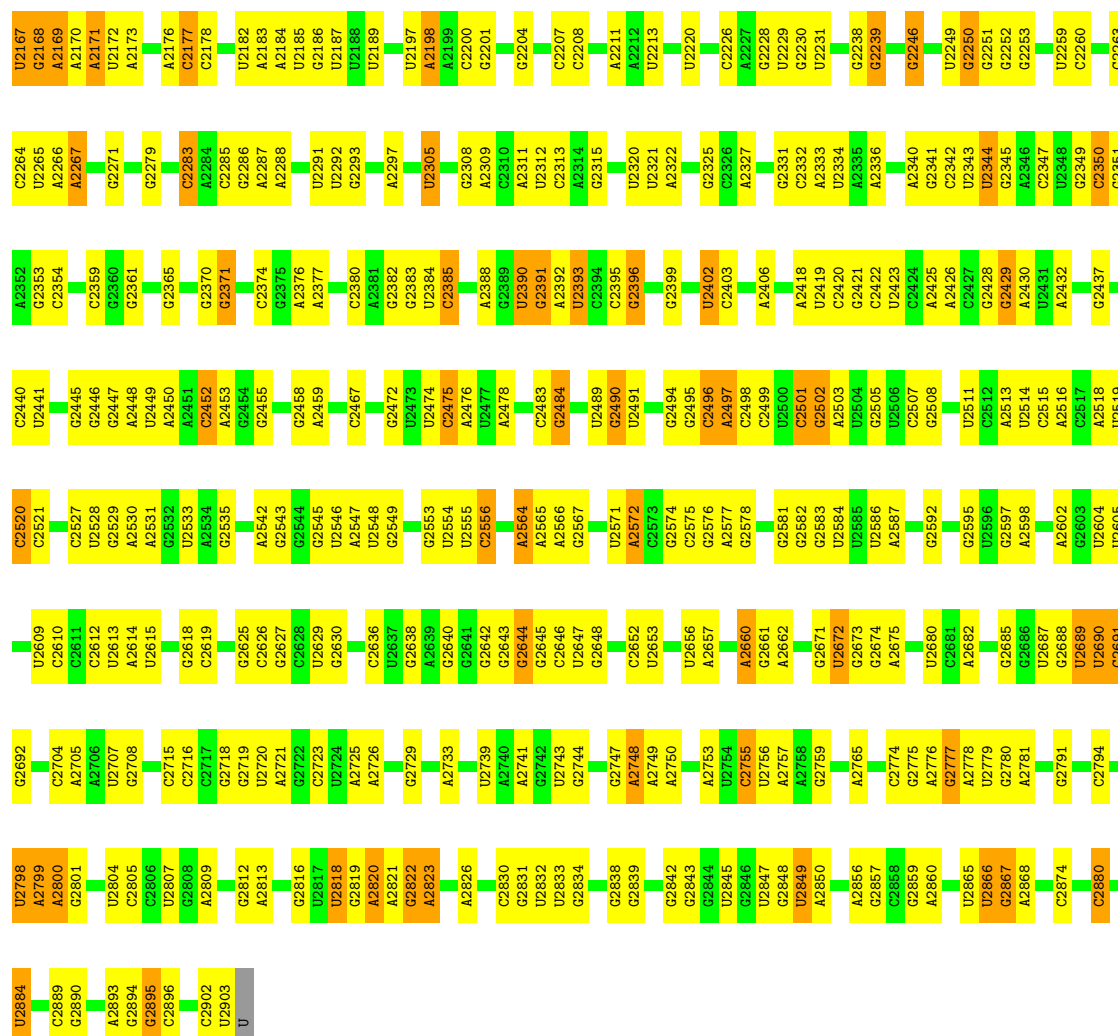
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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





C2104	U2026	A1937	U1827	G1733	C1644	C1531	C1428	G1333	G1235	A1134	U1060	A972	A886
U2105	G2027	A1938	G1828	G1734	G1645	C1532	G1432	G1341	G1236	C1135	U1061	A973	U887
U2106	A2030	A1939	A1829	A1735	C1646	A1532	G1433	A1342	A1247	G1136	G1062	G974	C388
G2107	A2031	U1940	C1830	G1736	U1647	C1533	A1434	A1343	A1248	G1137	C1063	A975	C389
A2108	G2032	C1941	G1831	G1738	U1648	A1534	G1435	G1344	U1249	C1140	C1064	G976	C390
U2109	A2033	C1942	G1835	A1739	G1649	C1535	G1436	C1345	G1250	U1141	U1065	A890	G891
G2110	U2034	U1943	C1836	G1739	A1650	C1536	G1437	G1346	C1251	U1142	U1066	A891	A892
U2111	G2035	U1944	G1837	G1743	A1651	G1537	U1438	A1347	G1252	A1143	A1067	A892	C993
G2112	C2036	C1838	G1838	G1743	A1652	C1538	U1438	C1348	A1253	A1147	A1068	A893	U894
U2113	U2037	U1955	G1839	G1753	A1653	C1541	G1441	A1353	U1254	C1153	A1070	A896	A896
A2114	G2038	A1956	G1840	A1754	A1654	U1542	U1442	A1354	A1255	G1154	G1071	C987	C987
G2115	U2039	C1958	G1842	G1755	C1656	G1543	C1447	A1354	G1256	A1155	C1072	A990	C988
U2116	C2043	U1963	C1843	G1756	C1656	A1544	C1447	C1357	A1265	G1162	G1075	G993	A900
G2117	A2044	G1964	U1758	A1759	G1666	G1555	C1451	G1360	G1266	G1162	G1075	C994	A900
U2118	C2045	C1965	A1844	A1759	G1666	G1555	C1452	G1360	U1267	G1162	G1075	C994	A900
G2119	G2046	A1966	A1847	A1762	G1667	C1558	A1453	A1367	U1267	G1162	G1075	C994	A900
U2120	U2047	G1967	A1848	G1763	A1668	U1559	C1454	A1367	A1268	G1168	U1078	C997	G907
G2121	G2048	G1968	A1849	G1764	A1669	G1560	G1455	G1368	C1270	A1169	A1079	G997	A910
C2122	C2049	U1969	A1854	C1764	C1670	U1561	G1456	G1368	A1271	C1170	A1080	C998	A911
G2123	G2050	A1970	G1857	U1769	U1671	U1562	G1456	G1368	A1272	G1171	U1081	U999	A912
A2124	A2051	U1971	A1858	U1773	G1672	U1563	C1461	G1374	U1273	C1172	U1082	C912	C912
G2125	C2052	G1972	A1858	A1773	G1673	C1564	C1461	A1378	U1273	U1174	U1083	A1000	U913
U2126	G2055	U1971	G1857	U1769	A1672	U1563	C1461	A1378	U1273	U1174	U1083	A1000	U913
A2127	C2056	G1972	A1858	A1773	G1674	C1564	C1461	A1378	U1273	U1174	U1083	A1000	U913
G2128	U2059	G1975	U1864	U1777	G1677	U1566	U1466	A1378	A1276	U1174	U1084	C1005	C914
U2131	A2060	U1982	G1869	U1776	A1677	A1566	U1467	A1383	U1281	A1175	A1085	C1006	C915
G2132	C2061	U1983	U1870	U1779	A1678	G1567	U1468	A1383	G1282	U1176	A1086	C1007	G916
A2133	U2062	U1991	G1873	U1780	G1681	U1569	A1470	A1384	U1282	G1177	A1087	A1008	A917
G2134	C2063	G1992	U1873	U1781	G1681	A1569	G1475	A1385	U1283	C1178	A1088	A1009	A918
U2137	U2064	U1995	G1878	U1782	G1687	U1577	G1475	C1386	A1284	U1181	A1089	A1010	U919
G2138	C2065	U1995	U1878	U1783	G1687	U1578	G1475	C1386	A1285	U1181	A1090	G1011	C922
U2139	A2066	C1996	G1888	U1784	G1687	U1579	G1482	U1394	A1286	G1182	U1094	C1013	U931
G2140	G2067	C1997	A1889	A1785	G1689	U1580	G1483	U1396	A1287	G1186	A1095	A932	U932
U2141	U2068	A1998	A1890	U1785	G1690	C1581	A1490	C1397	C1289	G1195	A1096	U933	U934
C2141	C2069	U1998	U1890	A1785	G1691	U1582	A1490	C1398	U1294	G1195	G1099	G1022	U934
A2142	U2070	G2001	G1897	A1789	A1700	A1583	A1496	C1399	U1294	G1195	G1099	G1022	A941
G2143	C2072	G2002	U1898	C1790	A1701	U1584	A1496	U1400	U1295	U1198	U1101	G1024	G942
U2144	U2073	A2003	U1898	A1791	G1702	C1585	U1497	G1401	G1296	U1199	C1102	G1025	C942
C2145	G2004	G2003	U1901	U1798	G1702	A1586	C1498	U1402	C1297	C1200	A1103	G1026	A945
G2146	U2075	A2005	A1901	U1798	G1702	C1586	C1498	U1402	C1297	C1200	A1103	G1026	A945
A2147	C2076	G2006	G1906	C1800	G1707	U1587	C1499	A1403	G1300	U1203	C1104	A1027	C946
G2148	U2077	U2006	G1906	G1799	G1707	U1587	C1499	A1403	G1300	U1203	C1104	A1027	C946
U2149	C2077	C2006	G1906	C1800	G1707	U1587	C1499	A1403	G1300	U1203	C1104	A1027	C946
G2150	U2078	U2006	G1907	A1801	U1712	A1598	G1501	U1404	A1301	A1204	G1106	A1028	A947
U2151	C2078	A2009	G1907	A1802	U1712	U1598	G1501	U1404	A1301	A1204	G1106	A1028	A947
C2151	U2079	G2010	U1912	A1802	U1714	U1602	A1504	G1407	A1302	A1205	U1107	U1033	G949
U2152	A2080	G2011	A1912	A1802	U1714	U1602	A1504	G1407	A1302	A1205	U1107	U1033	G949
G2153	U2081	U2011	A1913	A1808	G1715	C1606	A1505	A1505	A1304	G1211	A1099	A1039	G953
A2154	C2082	G2012	A1914	A1809	G1715	C1606	A1505	A1505	A1304	G1211	A1099	A1039	G953
G2155	G2083	A2013	U1915	A1810	U1720	C1607	A1506	U1506	A1301	A1204	G1106	A1040	G954
U2156	U2084	A2014	A1916	G1811	U1721	A1608	A1508	U1508	A1302	A1205	G1107	A1040	U955
C2156	A2090	A2015	U1916	G1811	G1721	U1608	A1508	U1508	A1302	A1205	G1107	A1040	G955
U2157	U2091	U2016	C1920	G1814	G1724	A1614	A1515	A1418	A1322	U1217	U1119	C1044	G956
G2158	C2091	U2017	A1915	A1815	U1725	A1614	A1515	A1418	A1322	U1217	U1119	C1044	G956
U2159	U2092	G2018	C1924	A1816	U1726	A1616	A1516	A1419	A1322	U1217	U1119	C1044	G956
C2160	A2094	A2019	G1924	G1817	C1727	A1617	A1516	A1419	A1322	U1217	U1119	C1044	G956
G2161	U2095	A2020	U1924	U1818	U1727	A1618	A1517	A1420	A1322	U1217	U1119	C1044	G956
C2162	A2096	U2022	A1927	U1819	C1728	A1619	A1518	A1421	A1322	U1217	U1119	C1044	G956
A2163	U2098	U2023	A1928	U1820	U1729	A1620	A1519	A1422	A1322	U1217	U1119	C1044	G956
G2164	C2023	G2024	U1929	U1821	U1730	A1621	A1520	A1423	A1322	U1217	U1119	C1044	G956
C2165	U2099	G2024	G1930	U1820	G1731	A1622	A1521	A1424	A1322	U1217	U1119	C1044	G956
U2166	G2100	C2025	U1931	A1821	C1732	A1623	A1522	A1425	A1322	U1217	U1119	C1044	G956





8%





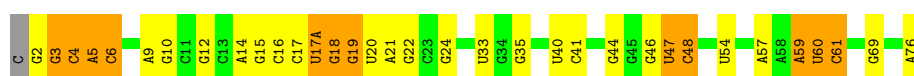
- Molecule 4: mRNA

Chain 4: 22% 78%



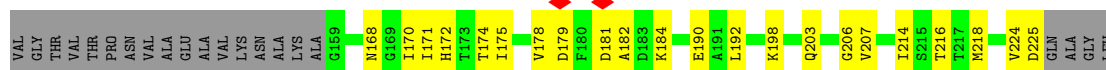
- Molecule 5: tRNA ProL(GGG)

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%

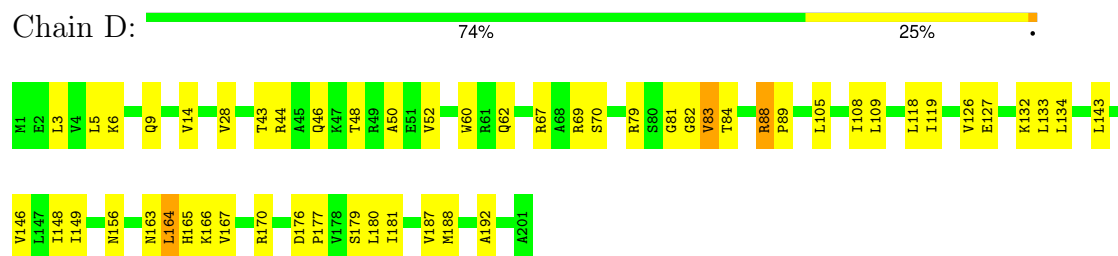


- Molecule 8: 50S ribosomal protein L3

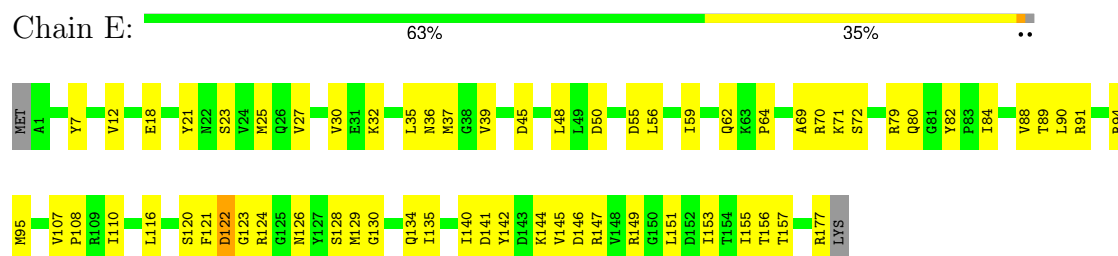
Chain C: 73% 26%



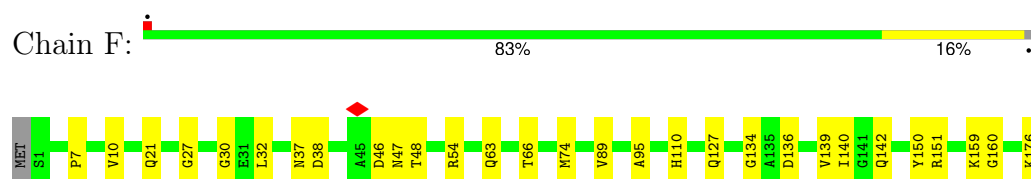
- Molecule 9: 50S ribosomal protein L4



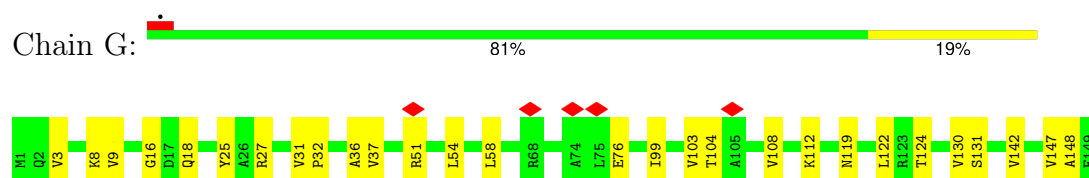
- Molecule 10: 50S ribosomal protein L5



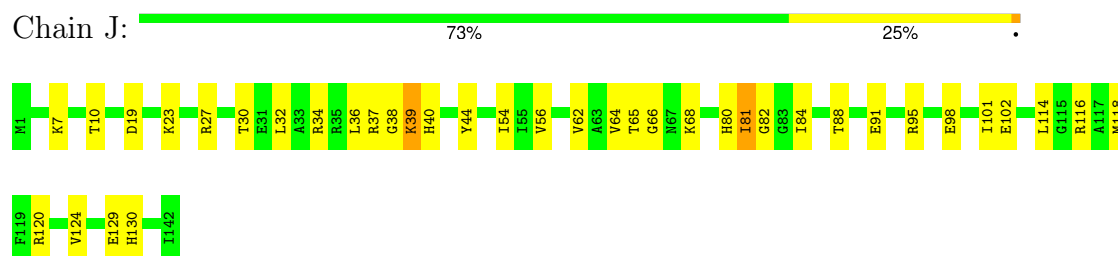
- Molecule 11: 50S ribosomal protein L6



- Molecule 12: 50S ribosomal protein L9

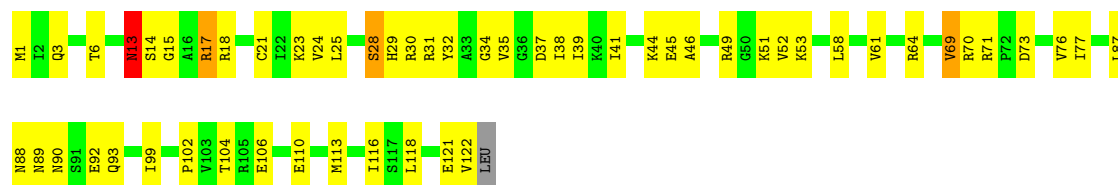


- Molecule 13: 50S ribosomal protein L13

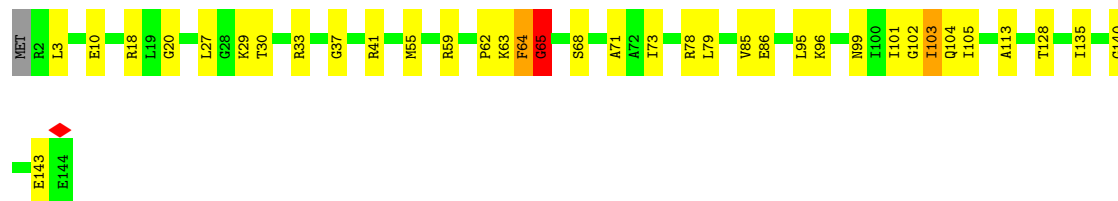


- Molecule 14: 50S ribosomal protein L14

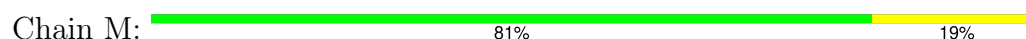




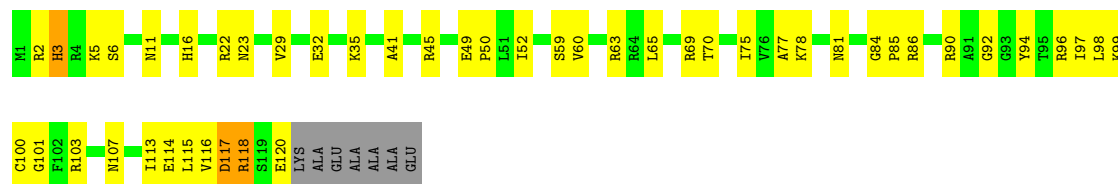
- Molecule 15: 50S ribosomal protein L15



- Molecule 16: 50S ribosomal protein L16



- Molecule 17: 50S ribosomal protein L17



- Molecule 18: 50S ribosomal protein L18

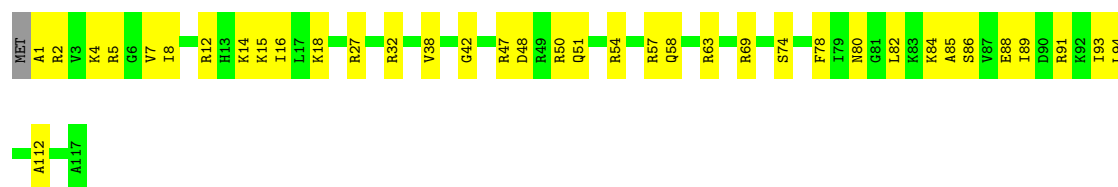


- Molecule 19: 50S ribosomal protein L19



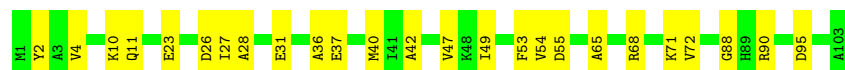
- Molecule 20: 50S ribosomal protein L20

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%



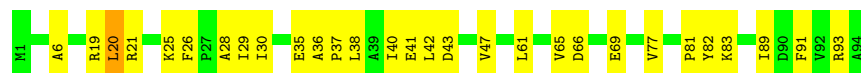
- Molecule 24: 50S ribosomal protein L24

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

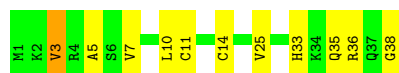
Chain e:  63% 34%



- Molecule 34: 50S ribosomal protein L36



Chain f:  71% 26% .




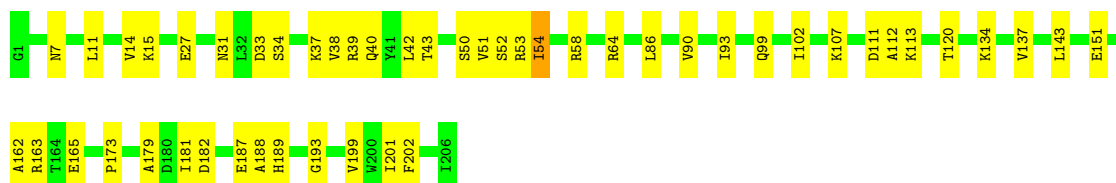
- Molecule 35: 30S ribosomal protein S2

Chain g:  62% 27% . 8%



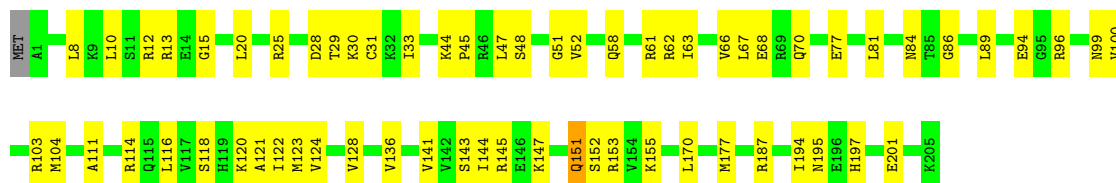
- Molecule 36: 30S ribosomal protein S3

Chain h:  76% 23%



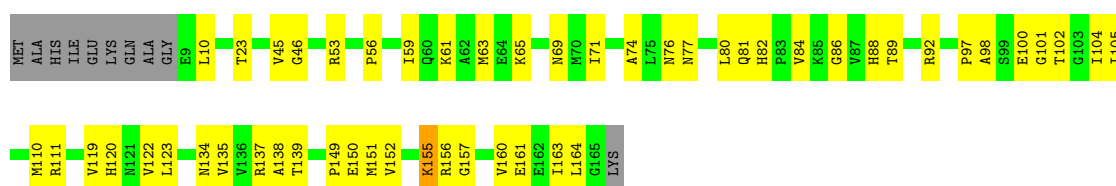
- Molecule 37: 30S ribosomal protein S4

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 ASP GLU ARG ARG ARG ASP ASP PHE ALA ASN THR ALA 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 P13 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 R118 L119 L123 S124 D125 K130 R137 E138 D139 R142 N147 A151 HIS TYR ARG TRP LEU LEU ARG SER PHE SER HIS GLN ALA 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

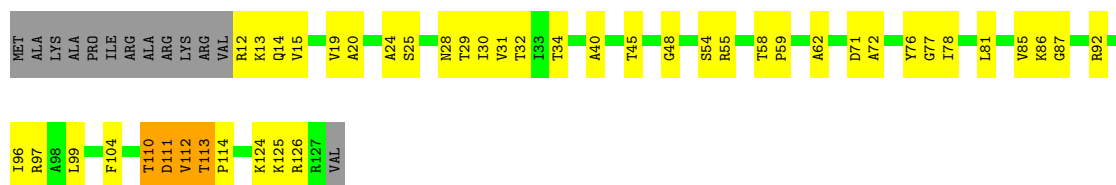
Chain o: 60% 32% 5%

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

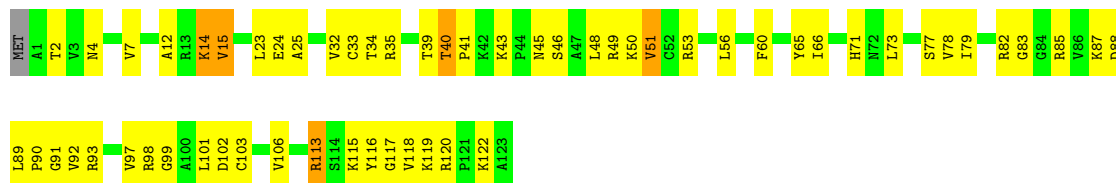
• Molecule 44: 30S ribosomal protein S11

Chain p: 56% 31% 10%



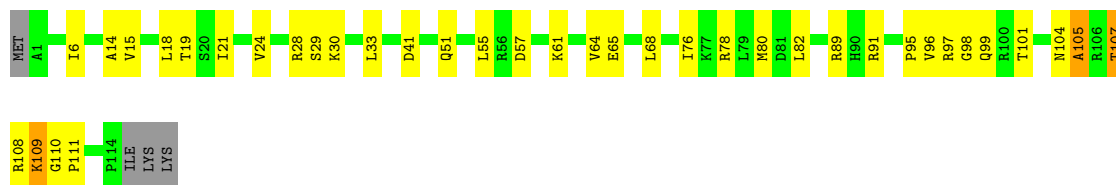
- Molecule 45: 30S ribosomal protein S12

Chain q: 52% 43% . .



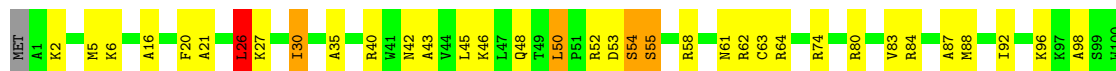
- Molecule 46: 30S ribosomal protein S13

Chain r: 64% 30% . .



- Molecule 47: 30S ribosomal protein S14

Chain s: 64% 30% . .



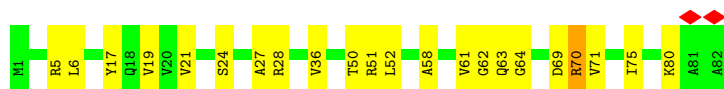
- Molecule 48: 30S ribosomal protein S15

Chain t: 69% 30% .



- Molecule 49: 30S ribosomal protein S16

Chain u: 73% 26% .



- Molecule 50: 30S ribosomal protein S17

MT	THR	ASP	K3	T4	R5		R10	V11	V12	S13	D14	K15	M16		T20	V21	V22	A23	T24	E25		V28	K29		F36		T41	K42	L43	H44	V45	H46	D47	E48	N49		C52	G53	I54		V57	V58	E59	L60		P65		T69	K70		R76	V77	V78		V82	F83
----	-----	-----	----	----	----	--	-----	-----	-----	-----	-----	-----	-----	--	-----	-----	-----	-----	-----	-----	--	-----	-----	--	-----	--	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	-----	-----	-----	--	-----	-----	-----	-----	--	-----	--	-----	-----	--	-----	-----	-----	--	-----	-----

- Chain w:  65% 21% 13%

[illegible]

- Chain x:  47% 39% 14%

LVS	MET
LVS	PRD
ALA	R2
LVS	S3
LVS	L4
LVS	I10
	D11
	L12
	H13
	L14
	V18
	E19
	K20
	A21
	V22
	D26
	K27
	K28
	P29
	L30
	R31
	T32
	W33
	S34
	R35
	T38
	L39
	F40
	P41
	N42
	W43
	L44
	G45
	L46
	L47
	L48
	W57
	F60
	W61
	T62
	D63
	K69
	L70
	R77
	T78
	T79
	R80
	GLY
	HIS
	ALA
	ALA
	ASP

- Chain γ:  64% 32% ..

MET
N2
A16
K7
K8
R9
A16
N20
A21
S22
K32
Y35
I38
N51
E52
M53
Q54
P55
I56
V57
Q60
I66
H67
K68
N69
K70
R73
H74
K75
T79
I82
K83
K84
L85
A86

## 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

*Continued on next page...*



*Continued from previous page...*

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

*Continued on next page...*

*Continued from previous page...*

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%)	12	43
8	C	207/209 (99%)	179 (86%)	26 (13%)	2 (1%)	13	44
9	D	199/201 (99%)	178 (89%)	20 (10%)	1 (0%)	25	57
10	E	175/179 (98%)	154 (88%)	20 (11%)	1 (1%)	22	54
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	39
14	K	120/123 (98%)	101 (84%)	17 (14%)	2 (2%)	7	36
15	L	141/144 (98%)	111 (79%)	27 (19%)	3 (2%)	5	33
16	M	134/136 (98%)	118 (88%)	16 (12%)	0	100	100
17	N	118/127 (93%)	97 (82%)	19 (16%)	2 (2%)	7	36
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

*Continued on next page...*

*Continued from previous page...*

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%)	12	43
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%)	8	37
34	f	36/38 (95%)	29 (81%)	7 (19%)	0	100	100
35	g	63/71 (89%)	48 (76%)	14 (22%)	1 (2%)	8	37
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	27
44	p	114/129 (88%)	101 (89%)	12 (10%)	1 (1%)	14	47
45	q	121/124 (98%)	92 (76%)	28 (23%)	1 (1%)	16	49
46	r	112/118 (95%)	99 (88%)	13 (12%)	0	100	100
47	s	98/101 (97%)	85 (87%)	12 (12%)	1 (1%)	13	44
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%)	10	40

*Continued on next page...*

*Continued from previous page...*

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%)	27	57

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%)	52	70
8	C	164/164 (100%)	160 (98%)	4 (2%)	44	63
9	D	165/165 (100%)	161 (98%)	4 (2%)	44	63
10	E	148/150 (99%)	147 (99%)	1 (1%)	81	88
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%)	56	73
14	K	103/104 (99%)	100 (97%)	3 (3%)	37	59
15	L	102/103 (99%)	101 (99%)	1 (1%)	73	82
16	M	109/109 (100%)	109 (100%)	0	100	100
17	N	100/103 (97%)	98 (98%)	2 (2%)	50	68
18	O	86/87 (99%)	82 (95%)	4 (5%)	22	48
19	P	99/100 (99%)	99 (100%)	0	100	100
20	Q	89/90 (99%)	88 (99%)	1 (1%)	70	80

*Continued on next page...*

*Continued from previous page...*

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%)	25	50
23	T	80/84 (95%)	78 (98%)	2 (2%)	42	62
24	U	83/85 (98%)	83 (100%)	0	100	100
25	V	78/78 (100%)	76 (97%)	2 (3%)	41	61
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%)	15	42
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%)	27	53
34	f	34/34 (100%)	34 (100%)	0	100	100
35	g	55/61 (90%)	53 (96%)	2 (4%)	30	55
36	h	170/170 (100%)	167 (98%)	3 (2%)	54	71
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%)	17	45
40	l	124/147 (84%)	122 (98%)	2 (2%)	58	74
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%)	45	64
44	p	89/99 (90%)	85 (96%)	4 (4%)	23	50
45	q	103/104 (99%)	96 (93%)	7 (7%)	13	40
46	r	92/96 (96%)	92 (100%)	0	100	100
47	s	83/84 (99%)	80 (96%)	3 (4%)	30	55
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

*Continued on next page...*

*Continued from previous page...*

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%)	60	75

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

*Continued on next page...*

*Continued from previous page...*

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.



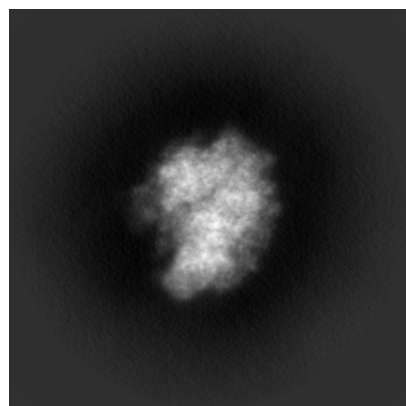
## 6 Map visualisation [i](#)

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.

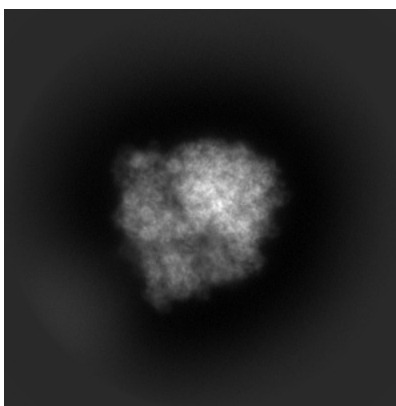
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

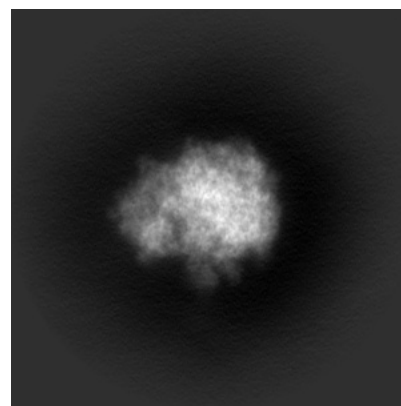
#### 6.1.1 Primary map



X

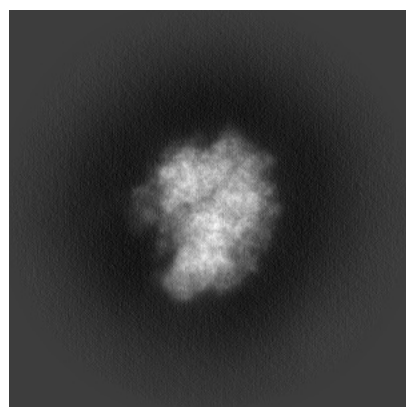


Y

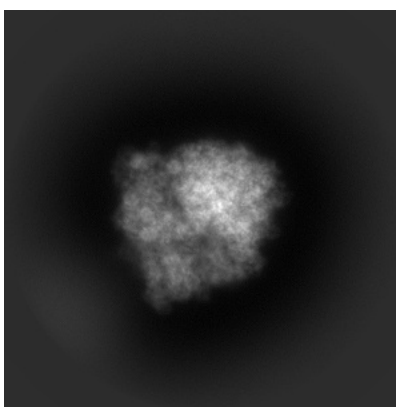


Z

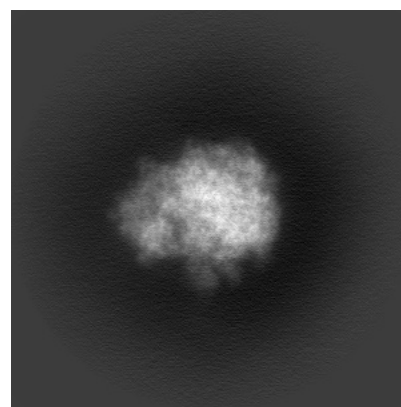
#### 6.1.2 Raw map



X



Y

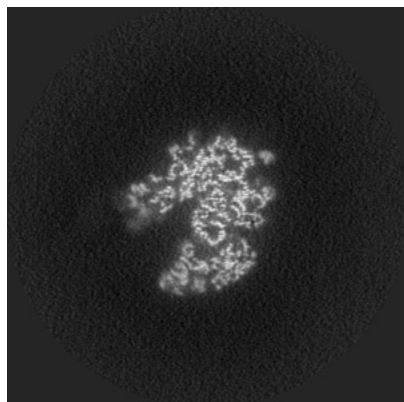


Z

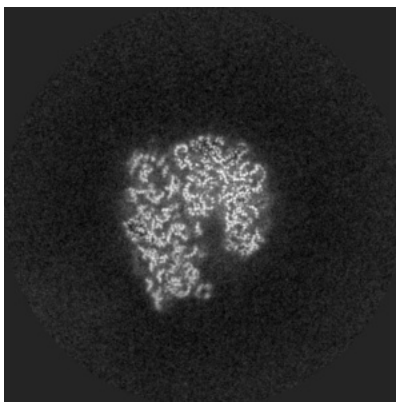
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

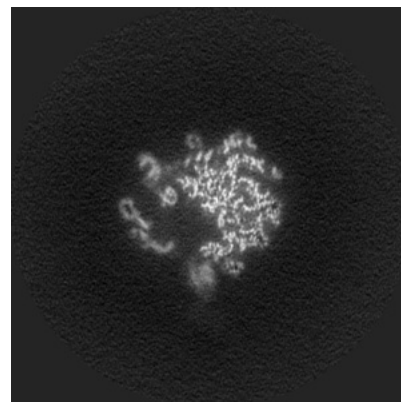
### 6.2.1 Primary map



X Index: 256

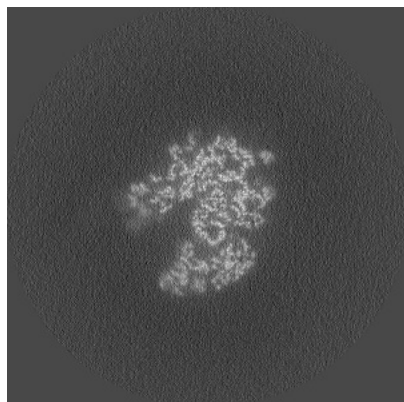


Y Index: 256

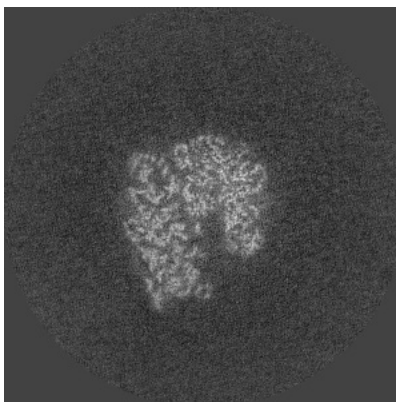


Z Index: 256

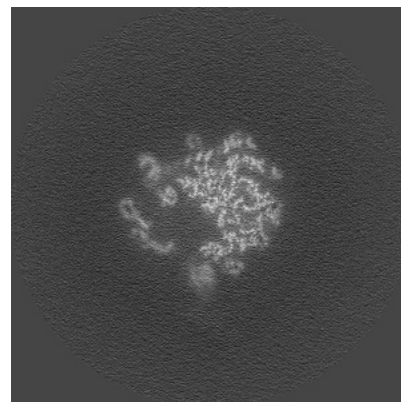
### 6.2.2 Raw map



X Index: 256



Y Index: 256

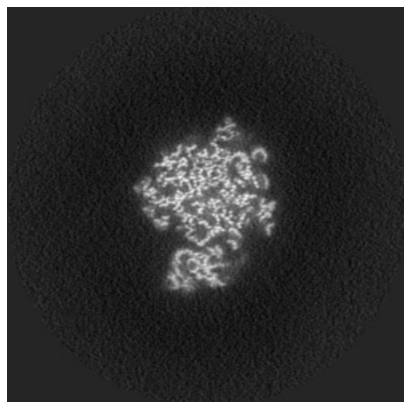


Z Index: 256

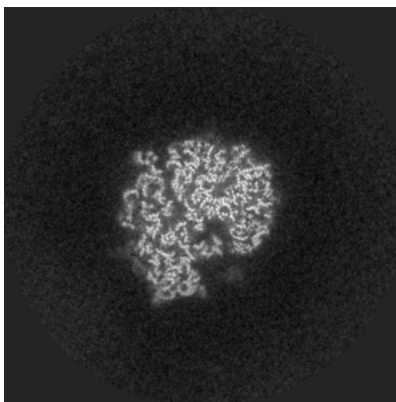
The images above show central slices of the map in three orthogonal directions.

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

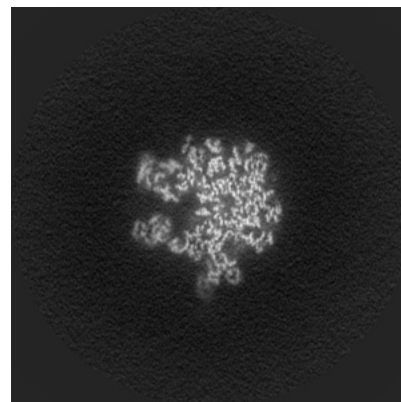
### 6.3.1 Primary map



X Index: 275

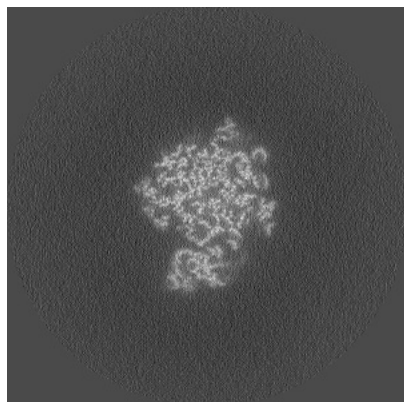


Y Index: 265

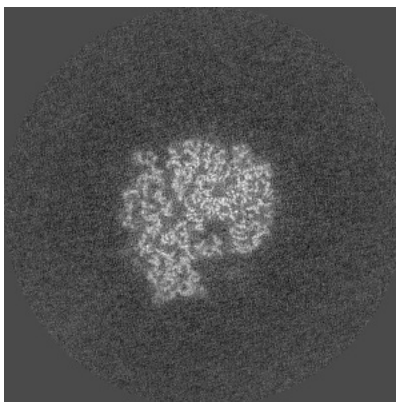


Z Index: 275

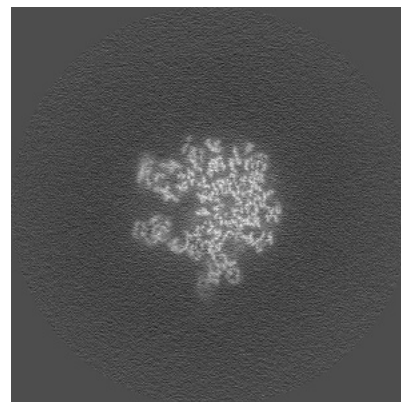
### 6.3.2 Raw map



X Index: 275



Y Index: 265

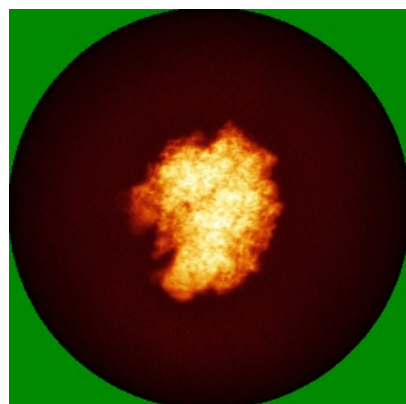


Z Index: 275

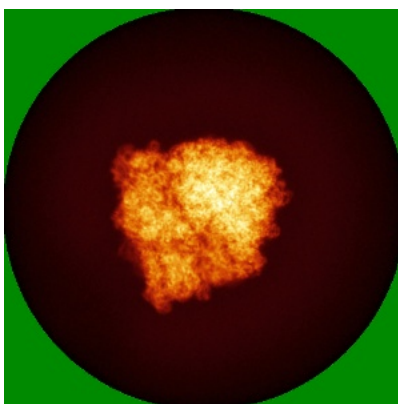
The images above show the largest variance slices of the map in three orthogonal directions.

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

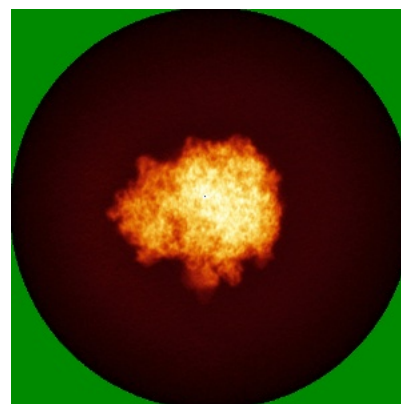
### 6.4.1 Primary map



X

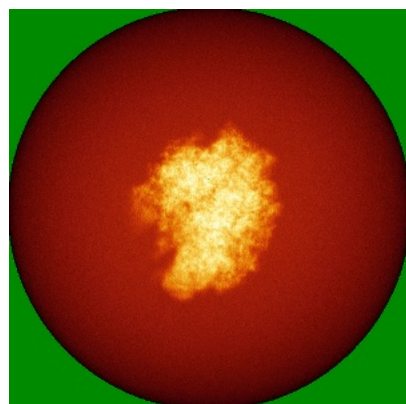


Y

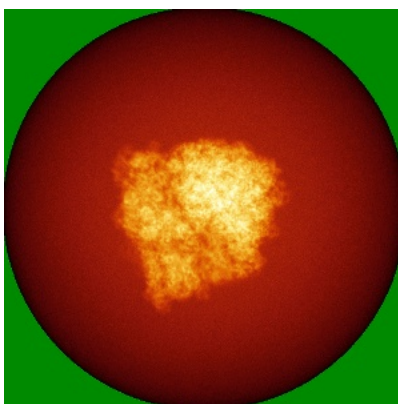


Z

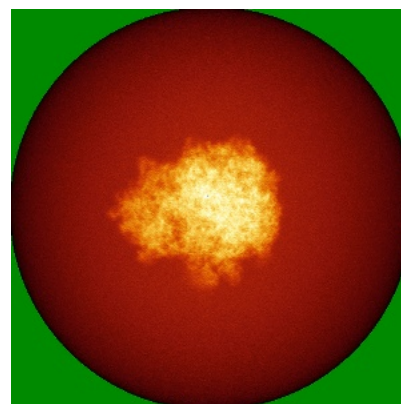
### 6.4.2 Raw map



X



Y



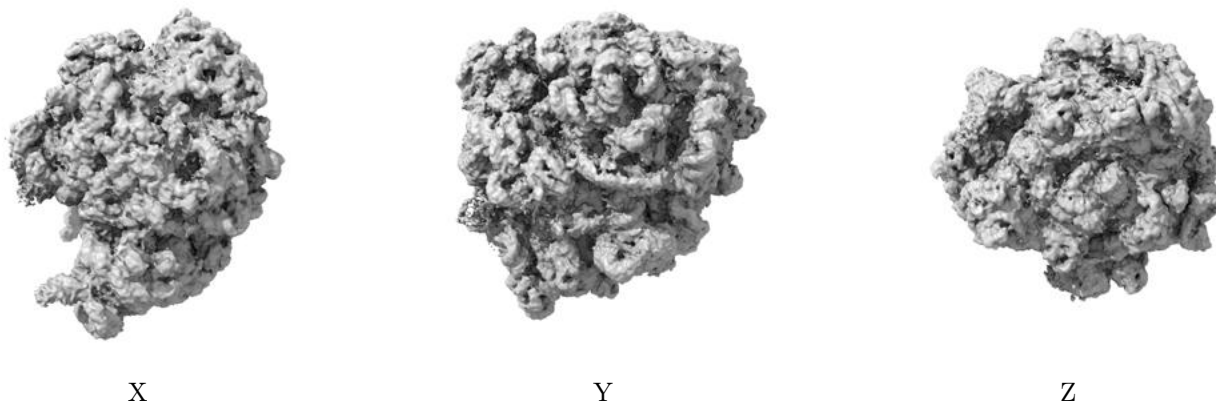
Z

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.



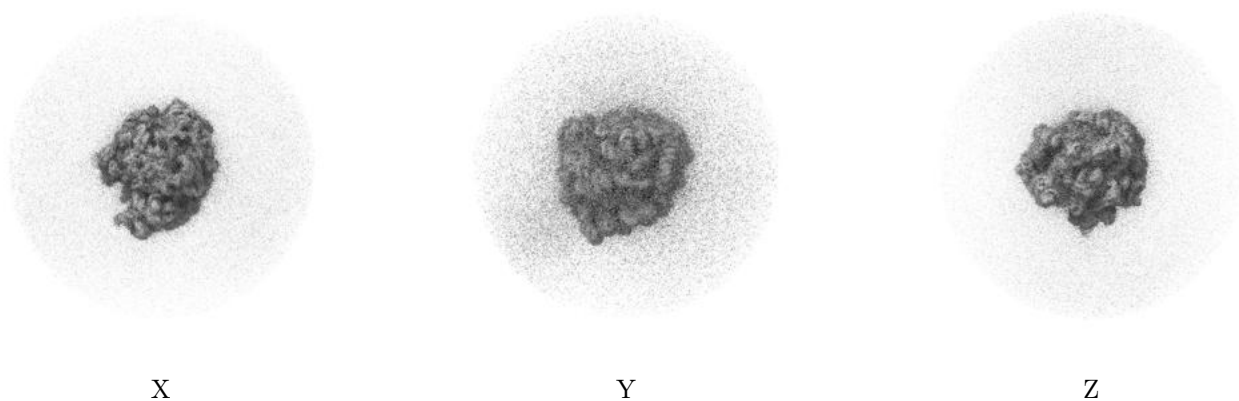
## 6.5 Orthogonal surface views [i](#)

### 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.

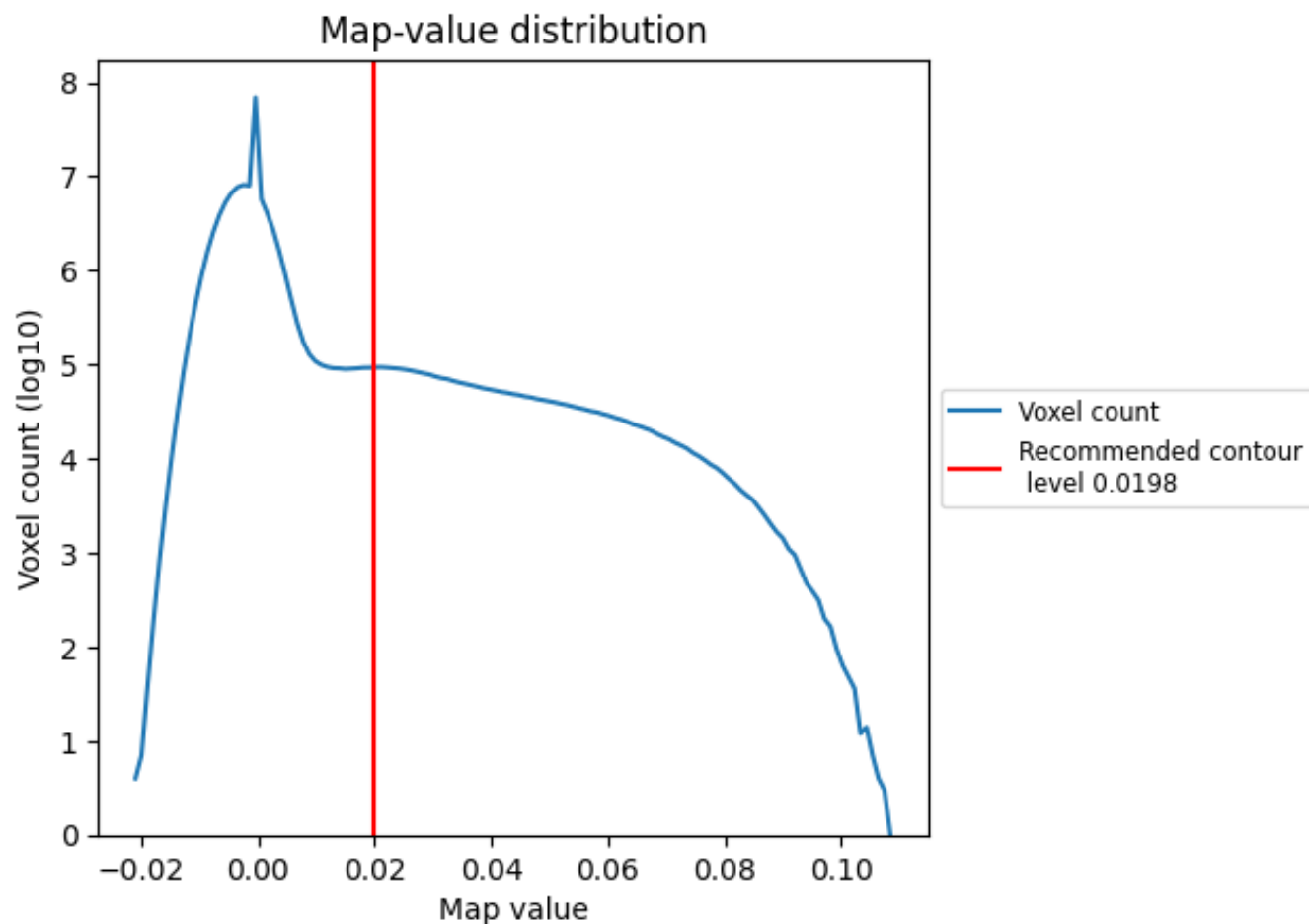
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

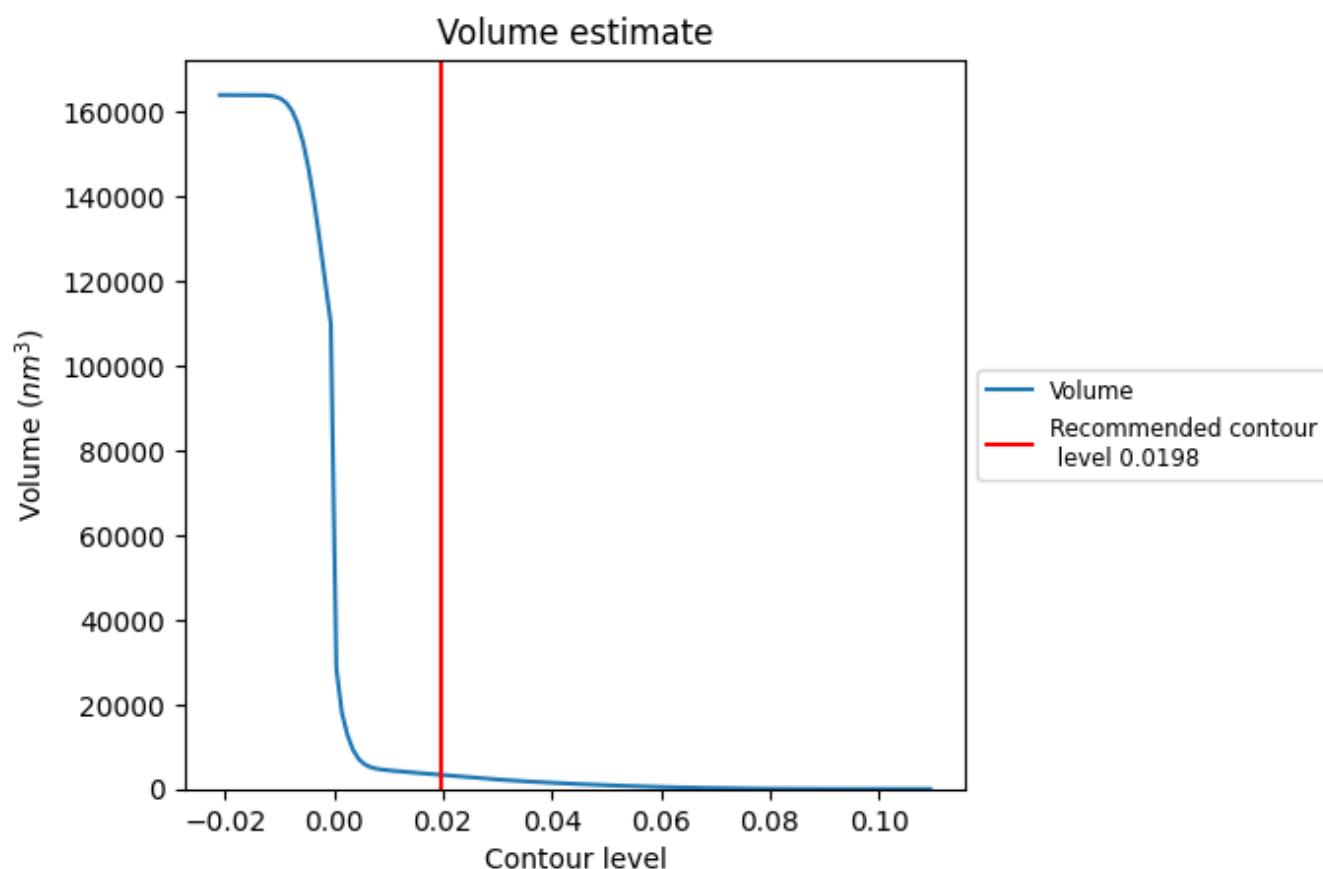
This section contains the results of statistical analysis of the map.

### 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.

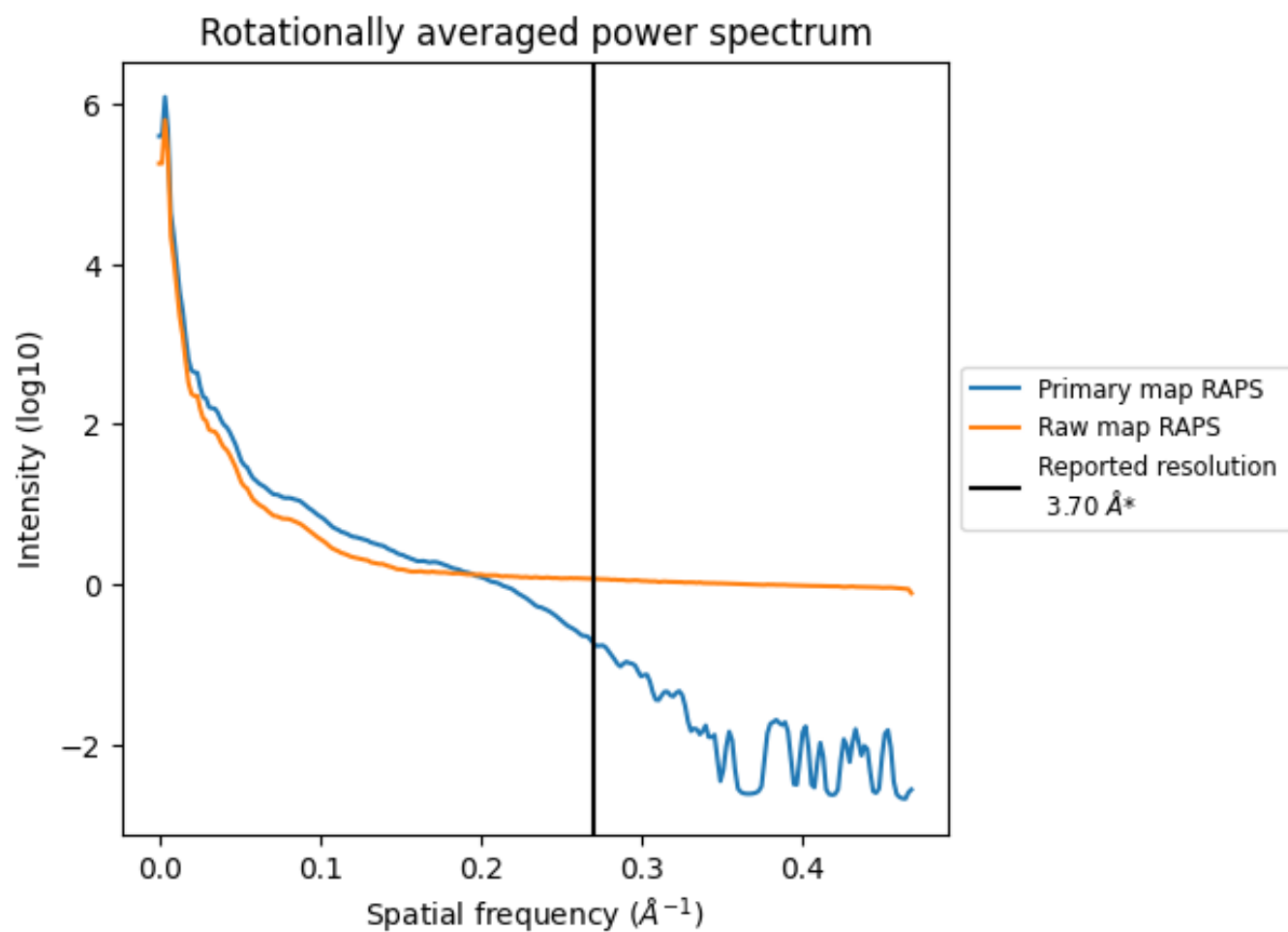
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3313 nm<sup>3</sup>; 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 ⓘ



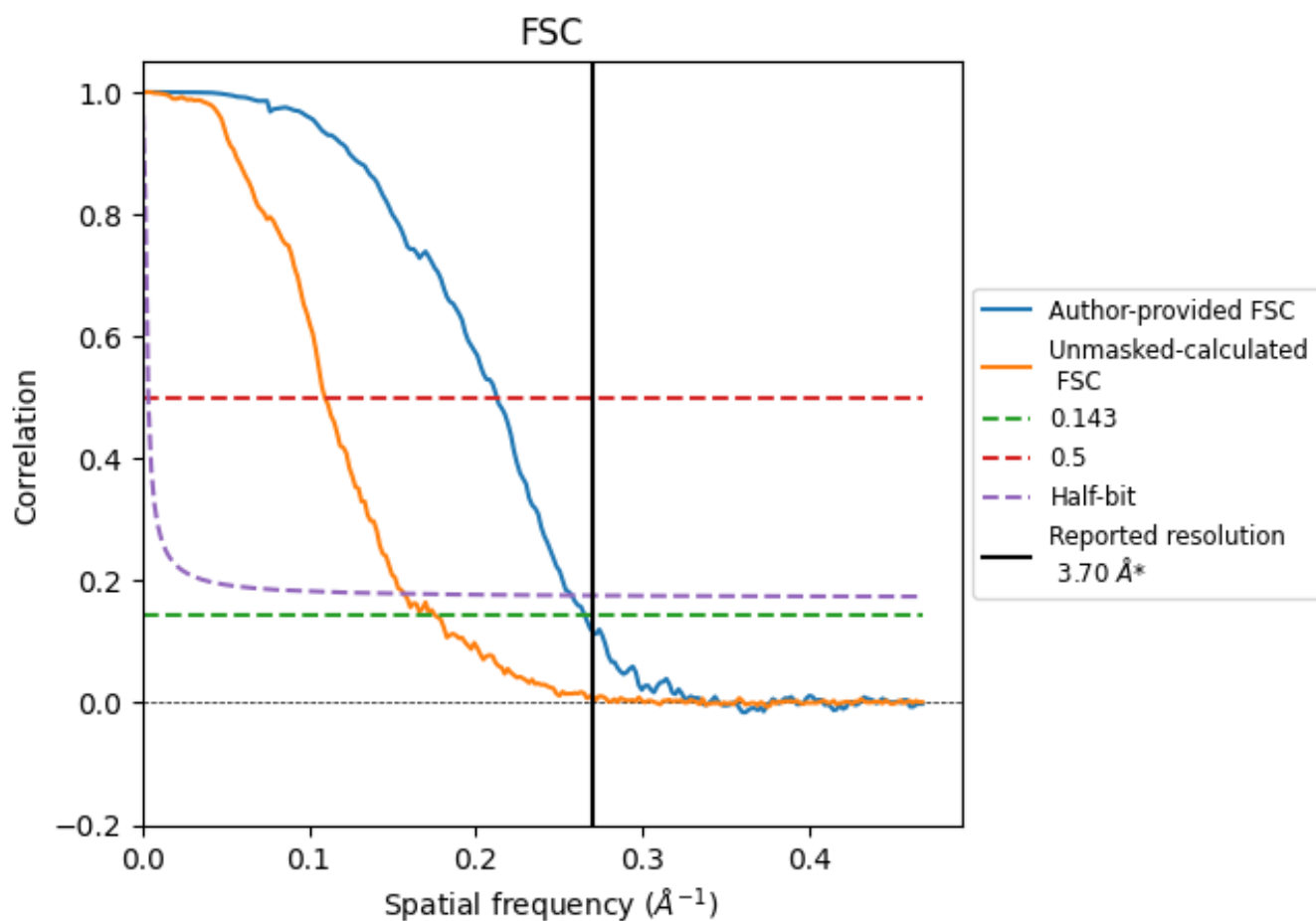
\*Reported resolution corresponds to spatial frequency of 0.270 Å<sup>-1</sup>



## 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](#)

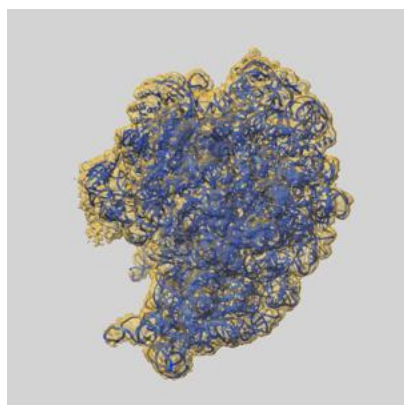
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.77	4.70	3.88
Unmasked-calculated*	5.69	9.13	6.37

\*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 %

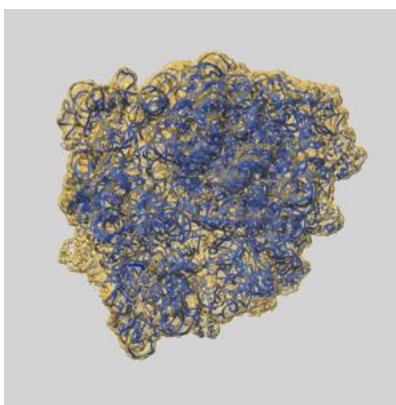
## 9 Map-model fit [i](#)

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.

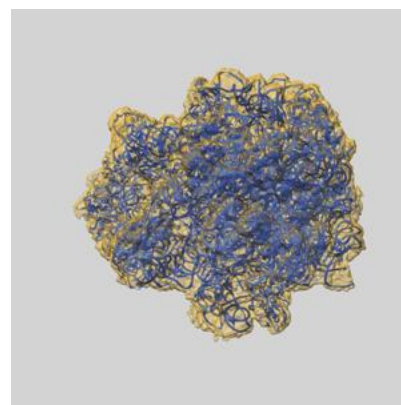
### 9.1 Map-model overlay [i](#)



X



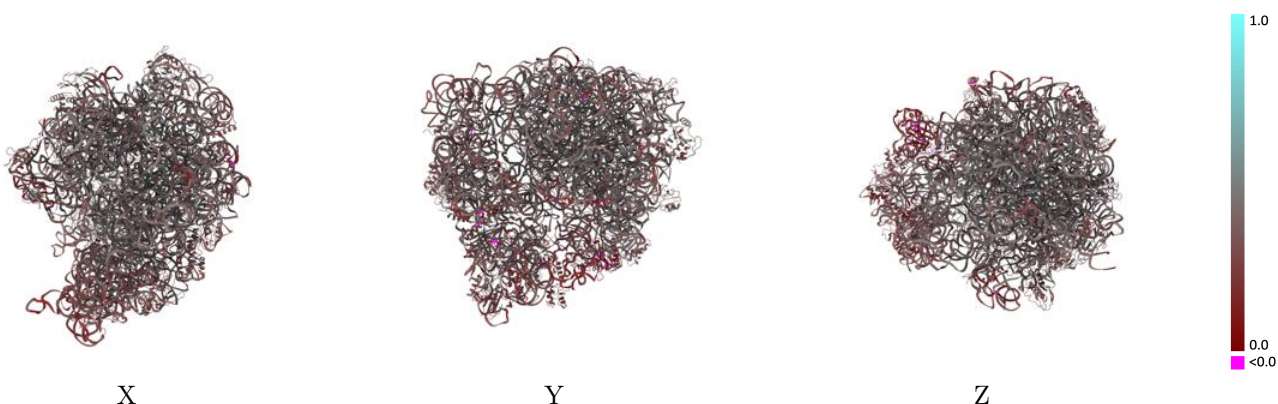
Y



Z

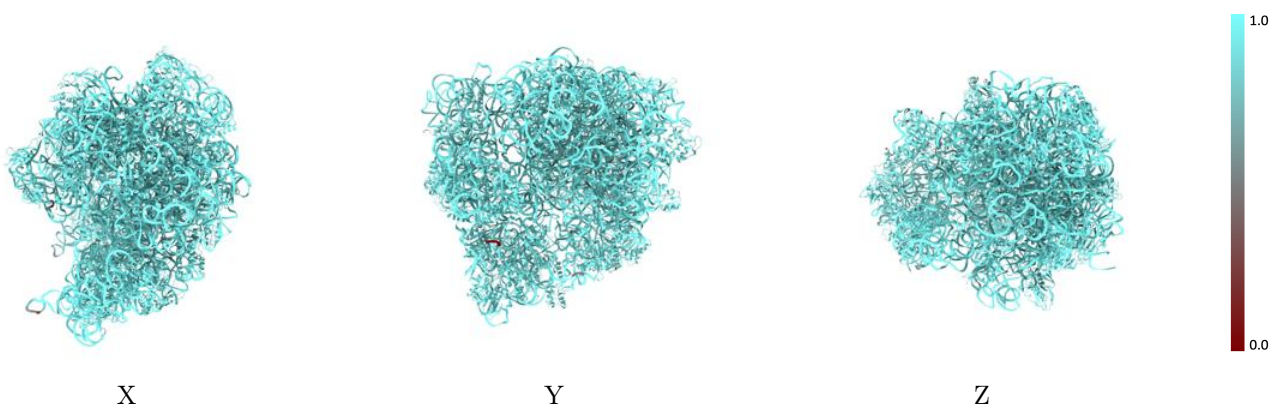
The images above show the 3D surface view of the map at the recommended contour level 0.0198 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



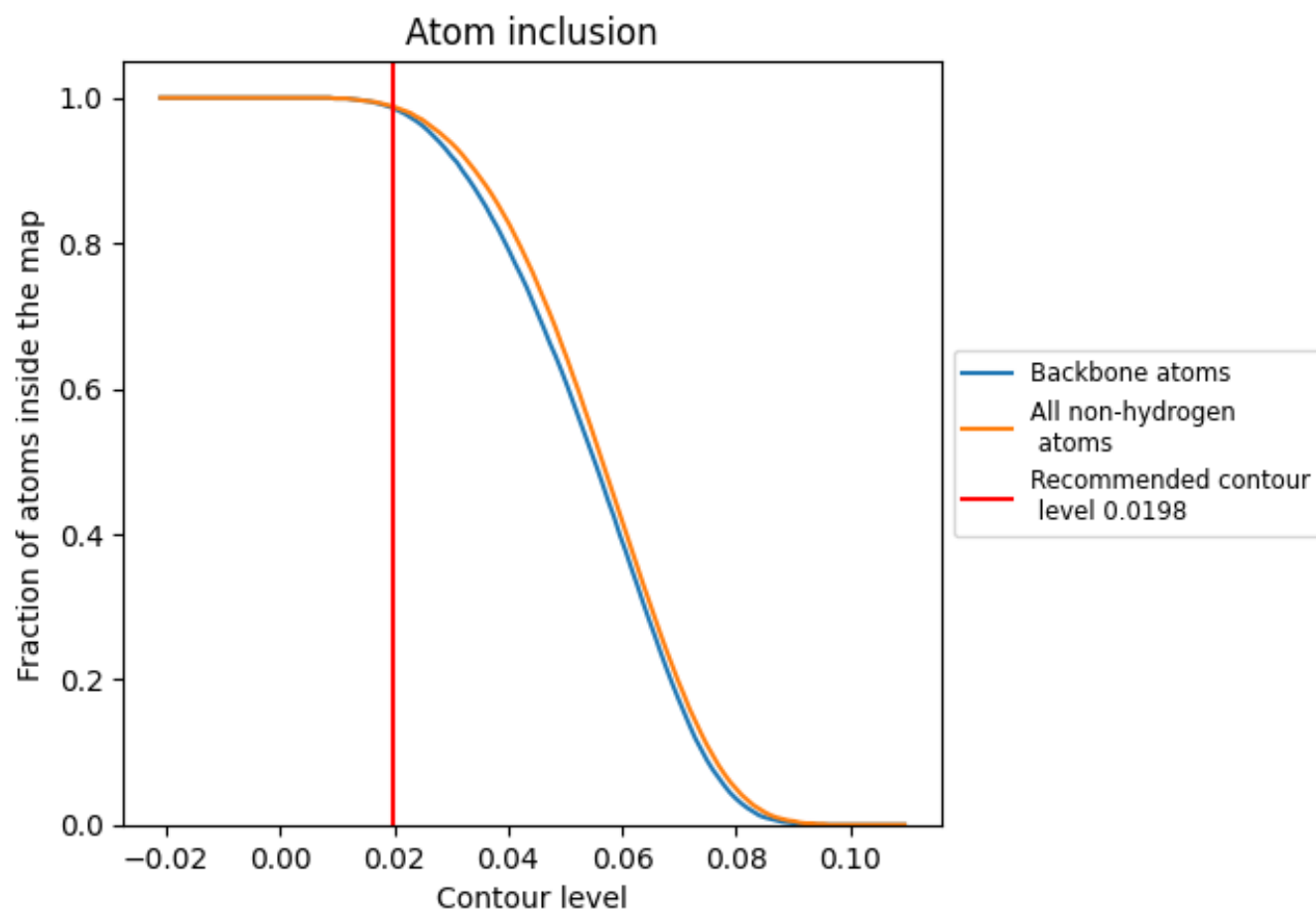
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



*Continued on next page...*

*Continued from previous page...*

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