



wwPDB EM Validation Summary Report ⓘ

Jul 3, 2025 – 10:58 AM EDT

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

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev118
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) : 2.44

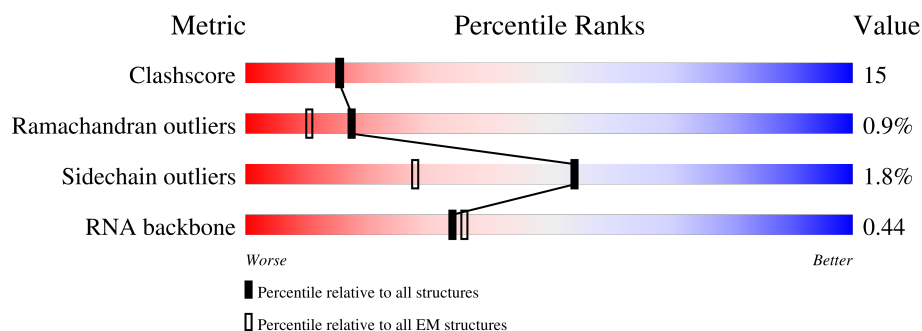
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.







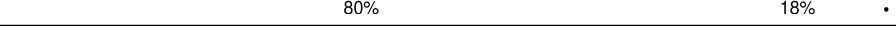
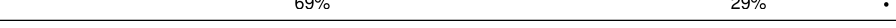

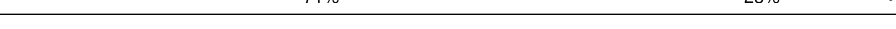
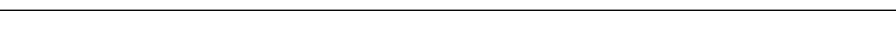
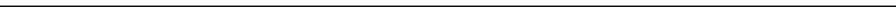















Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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 ≥ 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	
4	4	18	
5	5	77	
6	A	229	
7	B	273	






















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Mol	Chain	Length	Quality of chain
8	C	209	 76% 23% .
9	D	201	 73% 26% .
10	E	179	 61% 38% .
11	F	177	 70% 27% ..
12	G	149	 5% 80% 18% .
13	J	142	 69% 29% .
14	K	123	 61% 34% ..
15	L	144	 71% 28% ..
16	M	136	 72% 28% .
17	N	127	 64% 31% 6% .
18	O	117	 74% 25% .
19	P	115	 75% 22% ..
20	Q	118	 75% 22% ..
21	R	103	 75% 23% .
22	S	110	 79% 20% .
23	T	100	 67% 26% 7% .
24	U	104	 78% 20% .
25	V	94	 70% 29% .
26	W	84	 73% 17% 11% .
27	X	78	 63% 36% .
28	Y	63	 83% 16% .
29	Z	59	 68% 31% .
30	b	57	 74% 23% ..
31	c	55	 60% 31% 9% .
32	d	46	 74% 26% .

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

2 Entry composition [i](#)

There are 55 unique types of molecules in this entry. The entry contains 144496 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 23S ribosomal RNA.

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 4 is a RNA chain called mRNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 55 is water.

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

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

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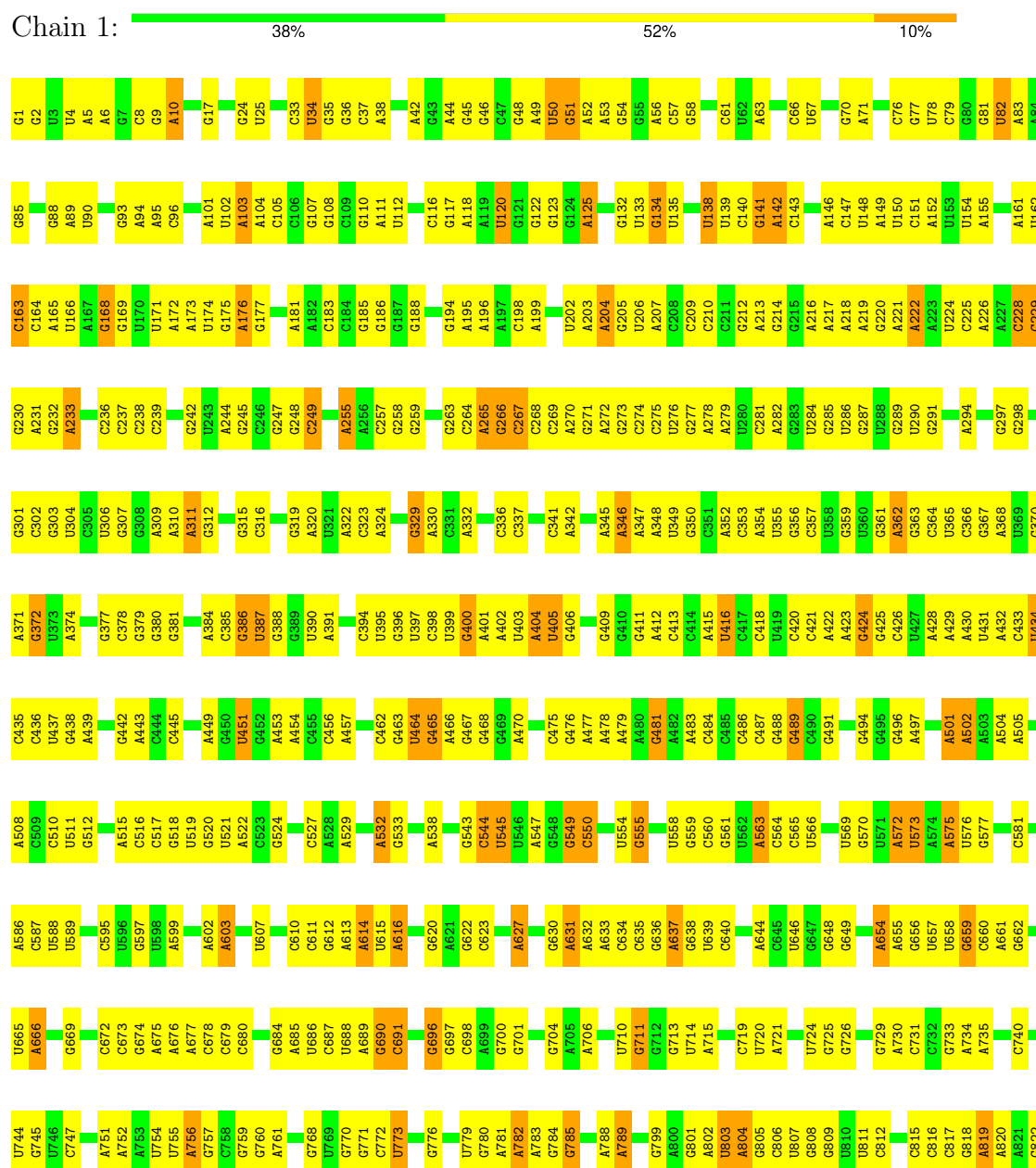
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Mol	Chain	Residues	Atoms		AltConf
55	w	4	Total	O	0
			4	4	
55	z	8	Total	O	0
			8	8	

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

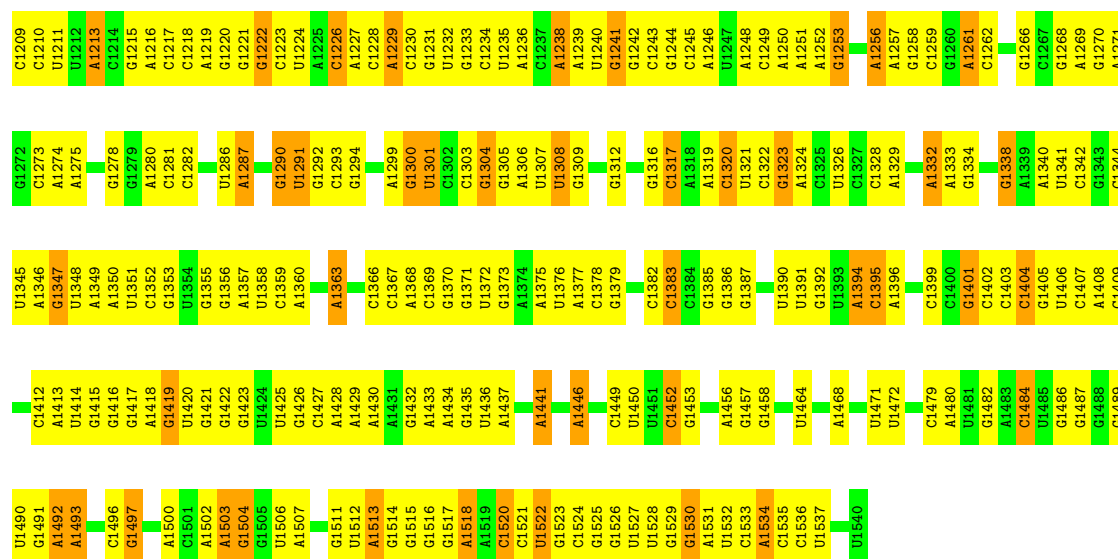
• Molecule 1: 23S ribosomal RNA



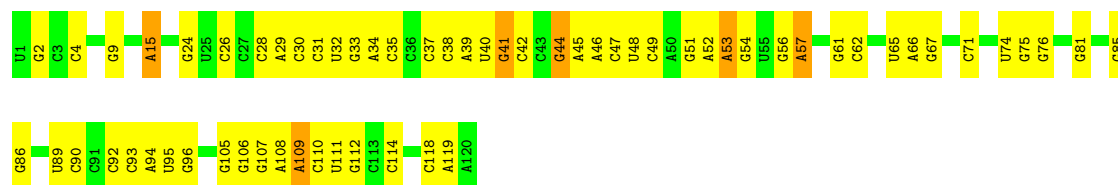
G1823	A1759	G1619	G1543	G1475	U1400	G1331	A1254	G1187	G1121	G1059	C982	U827
G1824	C1760	G1620	A1544	G1478	G1401	G1332	U1255	U1188	G1122	U1060	A983	U828
U1825	G1763	U1621	A1545	G1479	U1402	G1333	G1256	A1189	G1123	U1061	C915	A829
G1826	G1697	A1626	C1547	U1480	C1403	G1334	G1257	G1192	G1124	G1062	C989	A830
U1827	U1698	G1627	C1548	U1481	U1404	G1338	A1259	G1193	G1125	G1063	A990	G831
G1828	G1699	G1630	A1549	G1482	U1405	G1339	G1260	U1194	A1126	G1064	C993	A820
A1829	A1700	A1630	C1550	G1483	U1406	U1340	C1261	G1195	G1127	U1065	C994	G836
G1830	G1701	G1631	A1551	U1484	G1407	U1341	A1268	G1196	G1128	U1066	C995	A845
G1835	G1702	A1632	A1552	U1485	U1408	G1342	A1269	G1197	U1132	A1067	C996	U846
C1836	G1703	G1633	A1553	C1489	G1410	G1343	C1270	G1198	U1133	A1068	G997	A847
C1837	C1704	U1636	U1554	G1490	U1411	G1344	G1271	U1199	A1134	A1070	C998	C848
C1838	G1705	A1637	G1555	G1491	U1412	C1345	A1272	C1200	G1135	G1071	U999	U849
G1839	C1706	C1637	C1556	G1492	A1413	G1346	A1275	U1201	C1138	C1072	A1000	A827
U1840	G1707	C1638	C1557	U1493	C1414	A1347	A1276	U1202	G1139	A1073	A1001	U850
G1841	C1708	C1639	A1558	U1494	U1415	G1348	C1278	G1203	G1139	G1074	G1002	G855
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A1937	C2023	C2098	U2167	U2239	C2313	U2391	G2481	U2549	U2630	U2706	U2783	C2856	U37
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G1954	G2040	G2112	C2179	U2118	C2329	U2405	U2496	A2561	U2500	A2720	U2795	C2868	G49
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A1969	G2049	G2125	C2185	G2125	C2335	U2411	U2502	U2567	G2506	A2726	U2801	C2874	A61
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G1972	G2056	G2128	C2188	G2128	C2338	U2414	U2505	U2570	G2509	A2729	U2804	C2877	A66
G1973	G2056	C2129	C2189	G2129	C2339	U2415	U2506	U2571	G2510	U2730	U2805	C2878	U70
C1974	A2060	U2130	C2204	U2131	C2340	U2416	U2507	U2572	G2511	A2731	U2806	C2879	A71
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G1153	U1085	A1016	G954	C881	G799	G723	G654	C580	C518	A451	C388	C314	A247	A162	G86
G1154	U1086	U1017	U955	C882	G800	G724	A655	C581	C519	A452	A389	A315	G248	G163	C87
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A1156	U1088	A1021	U957	C884	U801	A729	U657	A583	G521	G454	A393	G324	U251	G165	U89
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A1158	U1090	U1023	A959	C885	A808	G731	U659	C585	A523	A456	A397	C328	G254	A176	G94
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G1160	U1092	U1025	U961	C887	C810	G733	G661	U590	C525	U458	U399	A459	U256	C176	
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C1163	A1095	C1028	U964	A892	U813	C736	G664	U593	C528	A462	U333	U332	G259	A181	C99
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U1168	C1100	G1034	C970	A900	G818	C745	A673	A600	A534	U407	A408	A338	C265	C186	G104
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C1172	A1105	A1038	A974	U904		A749	U677	A608	A539		A411	C345	C269	A190	G108
U1173	G1106	C1038	A975	U905	U828	C750	U678	A609	G540	U476	A412	C346	A270	C191	A109
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U1175	G1108	A1042	A977	A907	G833	G752	C680		G542	A478	A414	G348	C272	C193	G111
C1176	C1109	G1043	C978	A908	U834	A753	A681	C613	U543	U479	A415	A349	U273	C194	G112
G1177	A1110	A1044	C979		U835	C754	C682	G614	G544	U480	G416	G350	A274	A195	G113
U1178	C1111	C1045	C980	A913	G836	G755	G683	G615	C545	G481	G417	G351	G275		U114
A1179	A1112	A1046	U981	A914	U837	G756	U684	G616	A546		C418	C352	G276	A199	G115
C1180	C1113	U1047	U982	A915	G838	U757	G685	G617	A547	G484	C419	A353	C277		
G1181	U1114	G1048	C983	U916	U839	U758	U686	C618	G548	U485	U420	G354	G278	G203	A120
U1182	C1115		C984	A917	U842	A759	A687	U619	C549	U486	C422	C355	A279	G204	U121
C1183	U1116	G1053	C985	A918	U843	G760	G688	C620		A487	G423		C280	A205	G122
G1184	U1117	C1054	U986	A919	G844		C689	A621	U552	C488	G424	G358	G281	U209	U123
U1185	C1118	A1055	C987		A845	G763	G690	A622	A553	C489	G425	G359	A282	C210	C124
G1186	C1119	U1056	G988	G922	G846	G764	G691	C623	A554	C490	U426	G360	U283	U125	U126
U1187	C1120	G1057	U989	G927	U849	A766	U692	C624	U555	G491	U427	A363	G285	G127	G126
A1188	U1121	G1058		G928	U850	U767	G693	U625	C556	C492	U428	A364	C213	C214	G128
U1189	U1122	C1059		G929	G851	A768	G693	U626	C557	A493	U429	U365	G214		
G1190	U1123	U1060	G993	C930			A696	G627	U558	G494	U430	U365	C289	A129	A130
U1191	G1124	G1061	A994	C931	U855	G771	A702	A630	A559	A495	A430	A366	C290	U219	
C1192	U1125	U1062	C995	C931	U856		G703	C631	A560	A496	A431	U367	G291	G220	A131
U1193	U1126	C1063	A996	C932	C856		A704	U632	U561	G497	A432	U368	G292	U224	G142
U1194	G1127	G1064	U997	G933	C857	G778	G705	U633	U562		G433	G369	G293	C225	A143
C1195	C1128	U1065	C998	C934	G858	G779	A706	C634	A563	C501	A435		U294	G226	
A1196		C1066	C999	A935	G859	A780	U707		C564	A502	A436	C372	G297	G226	
A1197	U1135	A1067	A1000	C936		A781	U708	C637	U565	C503	U437	A373	G298	U229	G147
	C1136	G1068	C1001	A937	A864	A782	C708	U638	G566	C504	U438	A374	A298	G230	A148
C1200	C1137	C1069	G1002	A938	A865	A783	U709	U639	G567	G505	U439	U375	G299	G231	A149
A1201	G1138	U1070	U1003	G939		G784	G710		G568	G506	U440	G376	A300	U150	
U1202	G1139		A1004	C940	C868	A784	G711	U641	C569	C507	C440	G377	A301	G232	A151
C1203	U1073	U1074	A1005		G869		A712	A642	G570	U508	A441	G378	G302	A152	A152
A1204	C1141	G1074	G1006	G945	U870	U788	G713	C643	U571	A509	G442	C379	A303	C235	C153
U1205	G1142	U1075	U1007	A946	U871	U789	G714	U644	A572	A510	C443	G380	G307	A236	U154
G1206	G1143	U1076	U1008	C947	A872	A790	A715	G645	A573	C511	G444	C381	C307	G237	A155
G1207	G1144	G1077	U1009	G948	A873	G791	A716	G646	A574	U512	G445	A382	C308	C156	
C1208	A1145	U1078	A949	A949	G874	A792		C647	G575	C513	G446	A383	A309	G240	U157



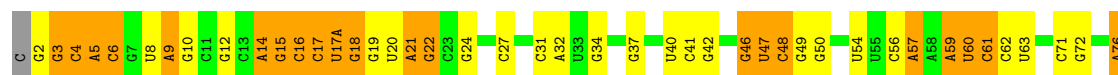
• Molecule 3: 5S ribosomal RNA



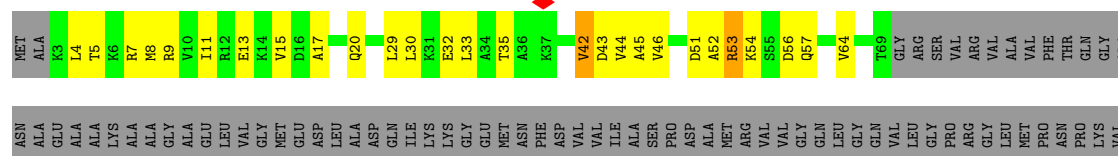
• Molecule 4: mRNA



• Molecule 5: tRNA ProL(GGG)



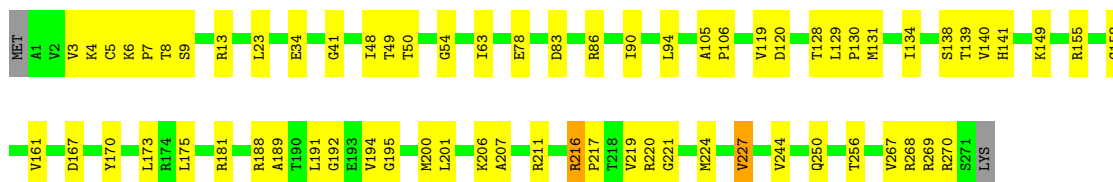
• Molecule 6: 50S ribosomal protein L1





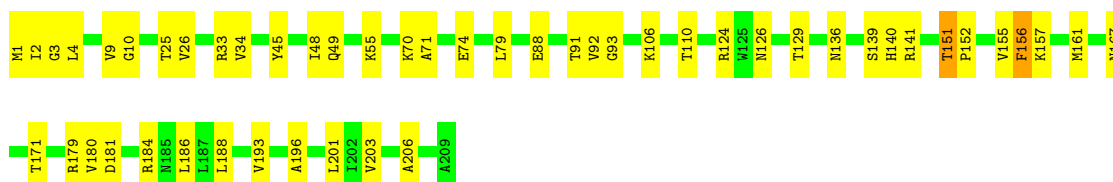
• Molecule 7: 50S ribosomal protein L2

Chain B: 74% 24% ..



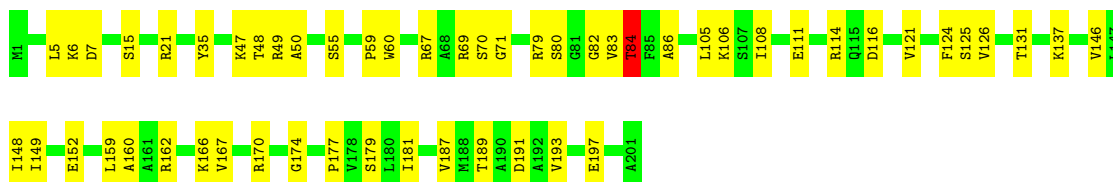
• Molecule 8: 50S ribosomal protein L3

Chain C: 76% 23% .



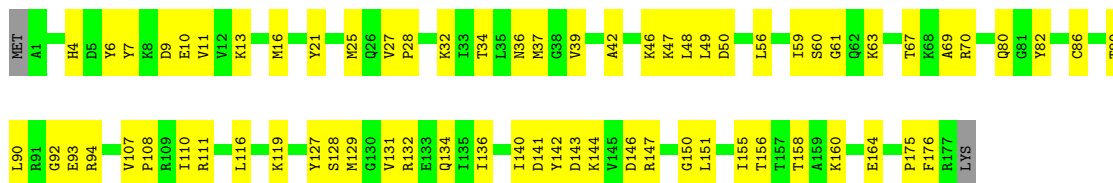
• Molecule 9: 50S ribosomal protein L4

Chain D: 73% 26%



• Molecule 10: 50S ribosomal protein L5

Chain E: 61% 38% .



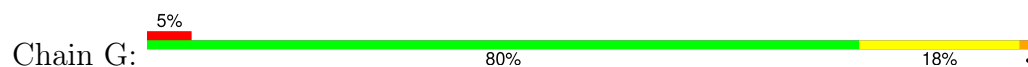
• Molecule 11: 50S ribosomal protein L6

Chain F: 70% 27% ..

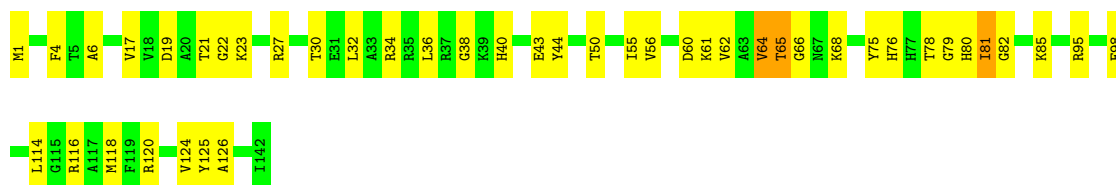




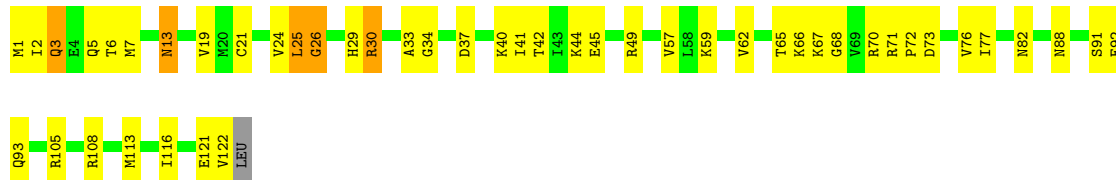
- Molecule 12: 50S ribosomal protein L9



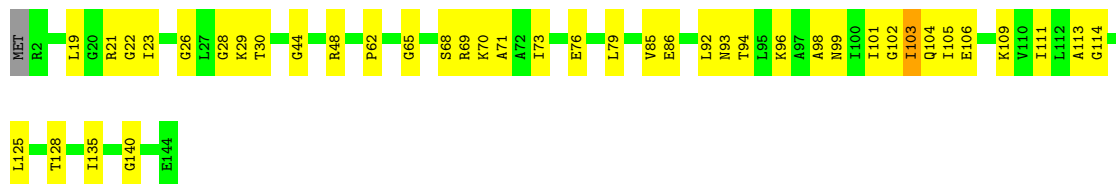
- Molecule 13: 50S ribosomal protein L13



- Molecule 14: 50S ribosomal protein L14



- Molecule 15: 50S ribosomal protein L15

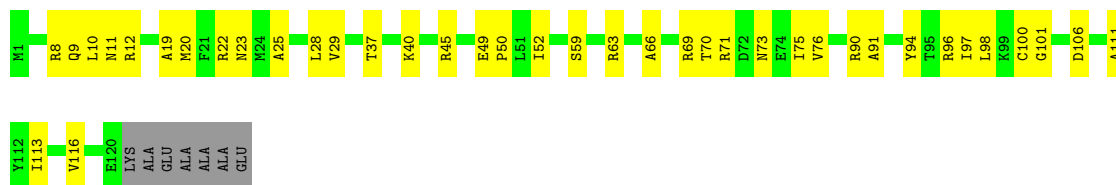


- Molecule 16: 50S ribosomal protein L16



- Molecule 17: 50S ribosomal protein L17

Chain N:  64% 31% 6%



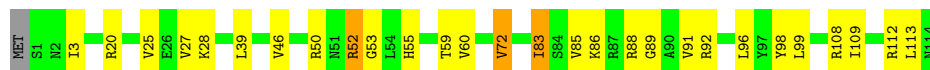
- Molecule 18: 50S ribosomal protein L18

Chain O:  74% 25%



- Molecule 19: 50S ribosomal protein L19

Chain P:  75% 22%



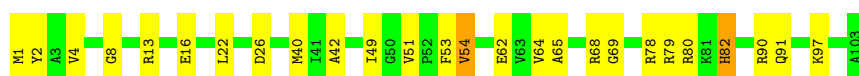
- Molecule 20: 50S ribosomal protein L20

Chain Q:  75% 22%




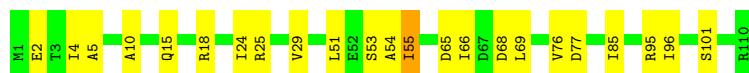
- Molecule 21: 50S ribosomal protein L21

Chain R:  75% 23%



- Molecule 22: 50S ribosomal protein L22

Chain S:  79% 20%




- Molecule 23: 50S ribosomal protein L23

Chain T:  67% 26% 7%



- Molecule 24: 50S ribosomal protein L24

Chain U:  78% 20%



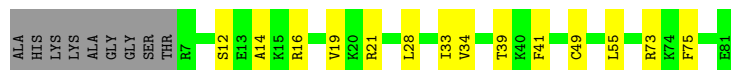
- Molecule 25: 50S ribosomal protein L25

Chain V:  70% 29%



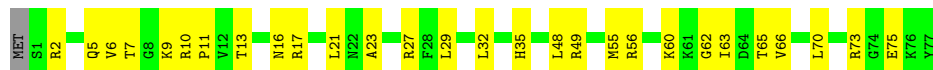
- Molecule 26: 50S ribosomal protein L27

Chain W:  73% 17% 11%




- Molecule 27: 50S ribosomal protein L28

Chain X:  63% 36%



- Molecule 28: 50S ribosomal protein L29

Chain Y:  83% 16%



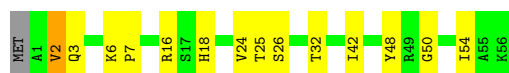
- Molecule 29: 50S ribosomal protein L30

Chain Z:  68% 31%



- Molecule 30: 50S ribosomal protein L32

Chain b:  74% 23%



- Molecule 31: 50S ribosomal protein L33

Chain c:  60% 31% 9%



- Molecule 32: 50S ribosomal protein L34

Chain d:  74% 26%



- Molecule 33: 50S ribosomal protein L35

Chain e:  57% 37% 5%




- Molecule 34: 50S ribosomal protein L36

Chain f:  71% 29%



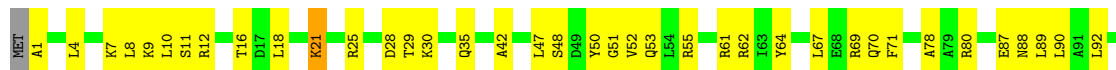
- Molecule 35: 30S ribosomal protein S3

Chain h:  80% 19%



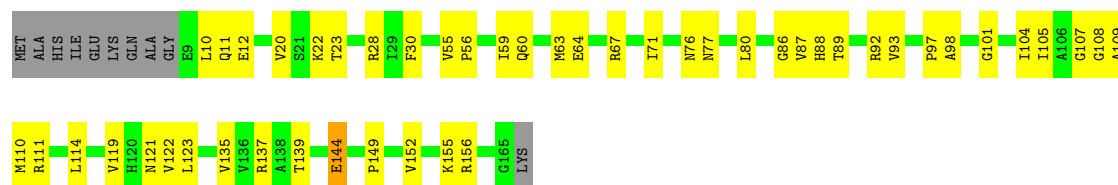
- Molecule 36: 30S ribosomal protein S4

Chain i:  68% 31%



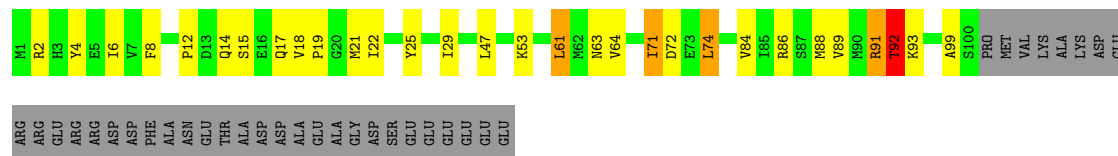
- Molecule 37: 30S ribosomal protein S5

Chain j:  65% 28% 6%



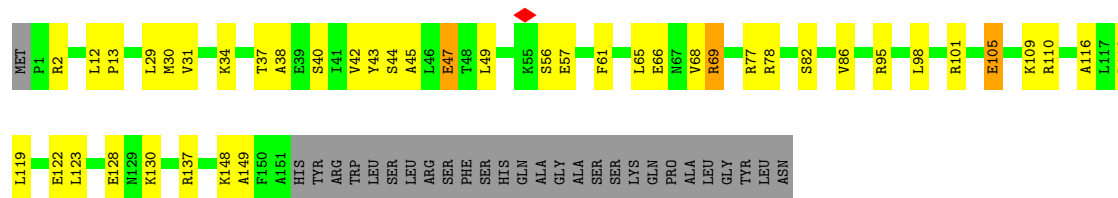
- Molecule 38: 30S ribosomal protein S6

Chain k: 52% 19% 26%



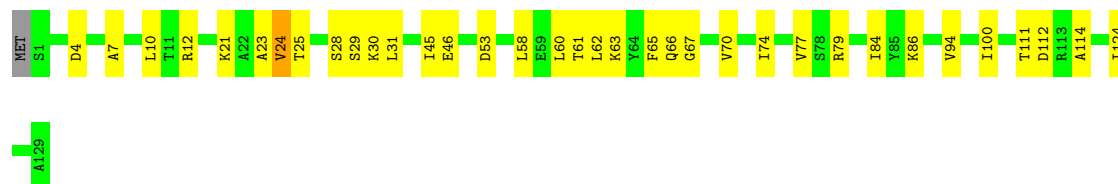
- Molecule 39: 30S ribosomal protein S7

Chain l: 60% 22% 16%



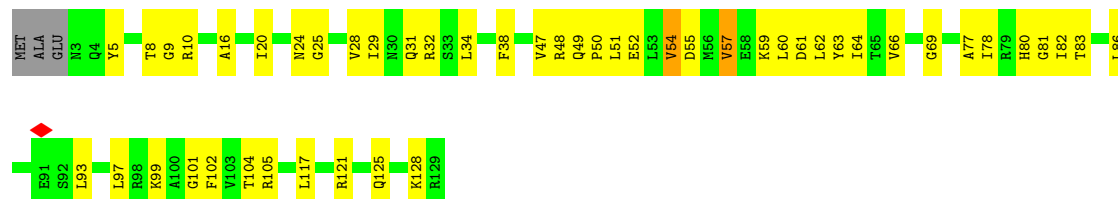
- Molecule 40: 30S ribosomal protein S8

Chain m: 72% 26%



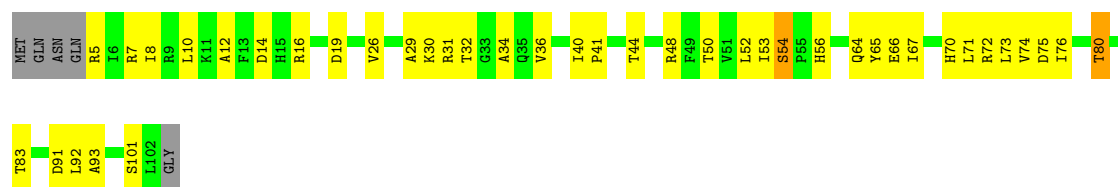
- Molecule 41: 30S ribosomal protein S9

Chain n: 60% 36%



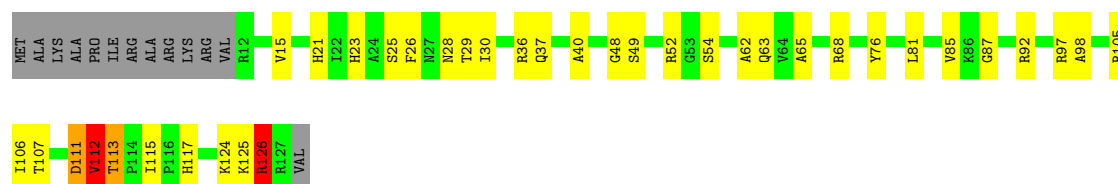
- Molecule 42: 30S ribosomal protein S10

Chain o: 



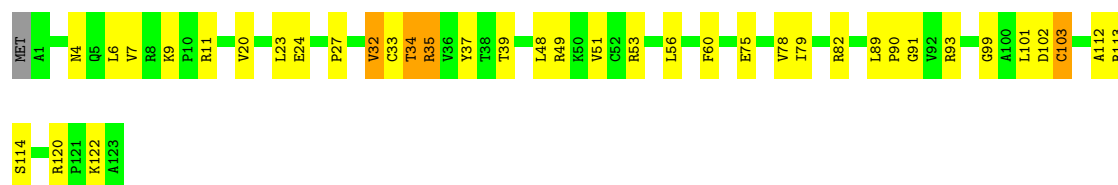
- Molecule 43: 30S ribosomal protein S11

Chain p: 



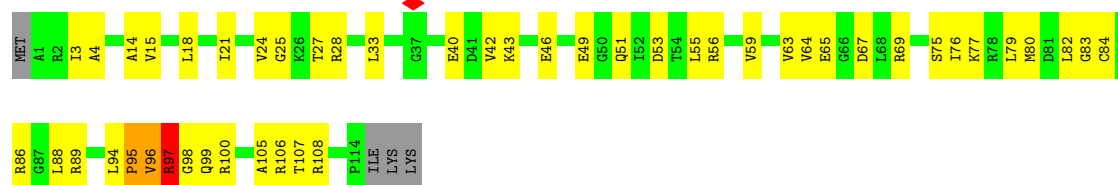
- Molecule 44: 30S ribosomal protein S12

Chain q: 



- Molecule 45: 30S ribosomal protein S13

Chain r: 



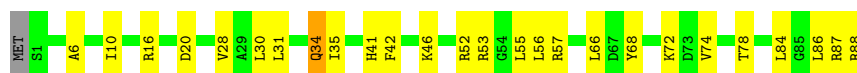
- Molecule 46: 30S ribosomal protein S14

Chain s: 

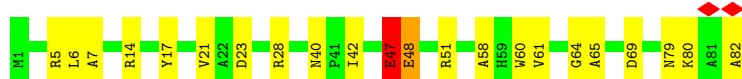


- Molecule 47: 30S ribosomal protein S15

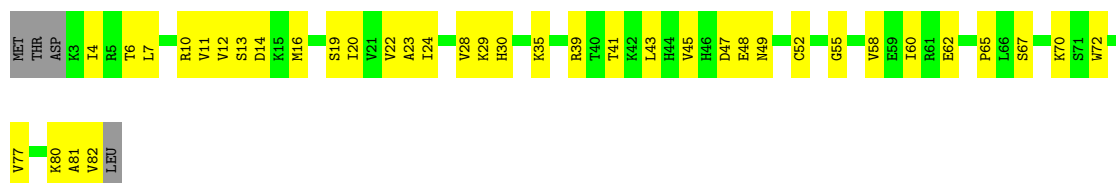
Chain t: 



- Molecule 48: 30S ribosomal protein S16



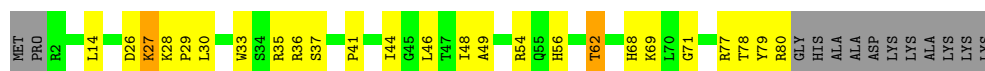
- Molecule 49: 30S ribosomal protein S17



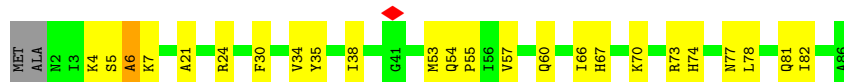
- Molecule 50: 30S ribosomal protein S18



- Molecule 51: 30S ribosomal protein S19



- Molecule 52: 30S ribosomal protein S20



- Molecule 53: 30S ribosomal protein S21



4 Experimental information

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

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

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

There are no bond length outliers.

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

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

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

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

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

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

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

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

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

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

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	A	130/229 (57%)	118 (91%)	11 (8%)	1 (1%)	16	51
7	B	269/273 (98%)	235 (87%)	33 (12%)	1 (0%)	30	64
8	C	207/209 (99%)	178 (86%)	28 (14%)	1 (0%)	25	60
9	D	199/201 (99%)	175 (88%)	23 (12%)	1 (0%)	25	60
10	E	175/179 (98%)	153 (87%)	22 (13%)	0	100	100
11	F	174/177 (98%)	156 (90%)	17 (10%)	1 (1%)	22	57
12	G	147/149 (99%)	138 (94%)	8 (5%)	1 (1%)	19	54
13	J	140/142 (99%)	124 (89%)	14 (10%)	2 (1%)	9	40
14	K	120/123 (98%)	96 (80%)	19 (16%)	5 (4%)	2	17
15	L	141/144 (98%)	112 (79%)	25 (18%)	4 (3%)	4	25
16	M	134/136 (98%)	116 (87%)	17 (13%)	1 (1%)	19	54
17	N	118/127 (93%)	96 (81%)	21 (18%)	1 (1%)	16	51
18	O	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
19	P	112/115 (97%)	99 (88%)	13 (12%)	0	100	100
20	Q	115/118 (98%)	110 (96%)	5 (4%)	0	100	100
21	R	101/103 (98%)	90 (89%)	11 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	S	108/110 (98%)	102 (94%)	6 (6%)	0	100	100
23	T	91/100 (91%)	83 (91%)	8 (9%)	0	100	100
24	U	100/104 (96%)	92 (92%)	7 (7%)	1 (1%)	13	47
25	V	92/94 (98%)	83 (90%)	8 (9%)	1 (1%)	12	44
26	W	73/84 (87%)	64 (88%)	9 (12%)	0	100	100
27	X	75/78 (96%)	68 (91%)	7 (9%)	0	100	100
28	Y	61/63 (97%)	59 (97%)	1 (2%)	1 (2%)	8	37
29	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
30	b	54/57 (95%)	46 (85%)	8 (15%)	0	100	100
31	c	48/55 (87%)	46 (96%)	2 (4%)	0	100	100
32	d	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
33	e	62/65 (95%)	54 (87%)	4 (6%)	4 (6%)	1	8
34	f	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	25
35	h	204/206 (99%)	191 (94%)	13 (6%)	0	100	100
36	i	203/206 (98%)	183 (90%)	19 (9%)	1 (0%)	25	60
37	j	155/167 (93%)	134 (86%)	21 (14%)	0	100	100
38	k	98/135 (73%)	89 (91%)	7 (7%)	2 (2%)	6	32
39	l	149/179 (83%)	141 (95%)	8 (5%)	0	100	100
40	m	127/130 (98%)	115 (91%)	11 (9%)	1 (1%)	16	51
41	n	125/130 (96%)	110 (88%)	14 (11%)	1 (1%)	16	51
42	o	96/103 (93%)	82 (85%)	13 (14%)	1 (1%)	13	47
43	p	114/129 (88%)	105 (92%)	8 (7%)	1 (1%)	14	49
44	q	121/124 (98%)	96 (79%)	23 (19%)	2 (2%)	7	36
45	r	112/118 (95%)	97 (87%)	13 (12%)	2 (2%)	7	35
46	s	98/101 (97%)	87 (89%)	10 (10%)	1 (1%)	13	47
47	t	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
48	u	80/82 (98%)	69 (86%)	9 (11%)	2 (2%)	4	28
49	v	78/84 (93%)	61 (78%)	17 (22%)	0	100	100
50	w	63/75 (84%)	59 (94%)	3 (5%)	1 (2%)	8	37
51	x	77/92 (84%)	66 (86%)	10 (13%)	1 (1%)	10	41
52	y	83/87 (95%)	79 (95%)	3 (4%)	1 (1%)	11	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	z	63/71 (89%)	49 (78%)	11 (18%)	3 (5%)	2	14
All	All	5428/5803 (94%)	4818 (89%)	563 (10%)	47 (1%)	17	49

5 of 47 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	A	110/177 (62%)	108 (98%)	2 (2%)	54	77
7	B	216/218 (99%)	214 (99%)	2 (1%)	75	89
8	C	164/164 (100%)	161 (98%)	3 (2%)	54	77
9	D	165/165 (100%)	159 (96%)	6 (4%)	30	62
10	E	148/150 (99%)	148 (100%)	0	100	100
11	F	137/138 (99%)	133 (97%)	4 (3%)	37	67
12	G	114/114 (100%)	110 (96%)	4 (4%)	31	63
13	J	116/116 (100%)	112 (97%)	4 (3%)	32	63
14	K	103/104 (99%)	97 (94%)	6 (6%)	17	49
15	L	102/103 (99%)	102 (100%)	0	100	100
16	M	109/109 (100%)	109 (100%)	0	100	100
17	N	100/103 (97%)	100 (100%)	0	100	100
18	O	86/87 (99%)	85 (99%)	1 (1%)	67	85
19	P	99/100 (99%)	96 (97%)	3 (3%)	36	66
20	Q	89/90 (99%)	87 (98%)	2 (2%)	47	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	R	84/84 (100%)	81 (96%)	3 (4%)	30	62
22	S	93/93 (100%)	89 (96%)	4 (4%)	25	57
23	T	80/84 (95%)	80 (100%)	0	100	100
24	U	83/85 (98%)	82 (99%)	1 (1%)	67	85
25	V	78/78 (100%)	78 (100%)	0	100	100
26	W	57/62 (92%)	56 (98%)	1 (2%)	54	77
27	X	67/68 (98%)	67 (100%)	0	100	100
28	Y	55/55 (100%)	54 (98%)	1 (2%)	54	77
29	Z	48/49 (98%)	47 (98%)	1 (2%)	48	74
30	b	47/48 (98%)	46 (98%)	1 (2%)	48	74
31	c	45/49 (92%)	44 (98%)	1 (2%)	47	73
32	d	38/38 (100%)	38 (100%)	0	100	100
33	e	51/52 (98%)	50 (98%)	1 (2%)	50	75
34	f	34/34 (100%)	34 (100%)	0	100	100
35	h	170/170 (100%)	169 (99%)	1 (1%)	84	92
36	i	172/173 (99%)	170 (99%)	2 (1%)	67	85
37	j	119/126 (94%)	118 (99%)	1 (1%)	79	90
38	k	87/116 (75%)	82 (94%)	5 (6%)	17	50
39	l	124/147 (84%)	121 (98%)	3 (2%)	44	71
40	m	104/105 (99%)	103 (99%)	1 (1%)	73	87
41	n	105/107 (98%)	104 (99%)	1 (1%)	73	87
42	o	86/90 (96%)	85 (99%)	1 (1%)	67	85
43	p	89/99 (90%)	86 (97%)	3 (3%)	32	63
44	q	103/104 (99%)	102 (99%)	1 (1%)	73	87
45	r	92/96 (96%)	90 (98%)	2 (2%)	47	73
46	s	83/84 (99%)	83 (100%)	0	100	100
47	t	76/77 (99%)	75 (99%)	1 (1%)	65	83
48	u	65/65 (100%)	63 (97%)	2 (3%)	35	66
49	v	74/78 (95%)	74 (100%)	0	100	100
50	w	56/65 (86%)	56 (100%)	0	100	100
51	x	70/79 (89%)	69 (99%)	1 (1%)	62	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	y	65/66 (98%)	63 (97%)	2 (3%)	35	66
53	z	55/61 (90%)	54 (98%)	1 (2%)	54	77
All	All	4513/4725 (96%)	4434 (98%)	79 (2%)	54	77

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

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

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

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

5.3.3 RNA ⓘ

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

5 of 943 RNA backbone outliers are listed below:

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

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Mol	Chain	Res	Type
1	1	46	G

5 of 20 RNA pucker outliers are listed below:

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

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

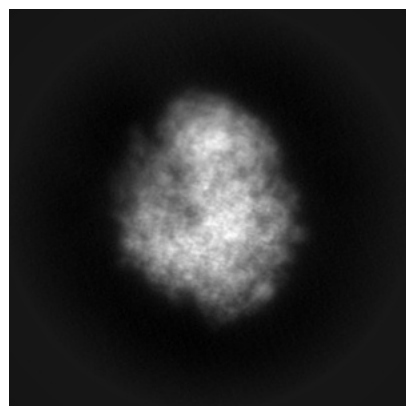
6 Map visualisation [i](#)

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

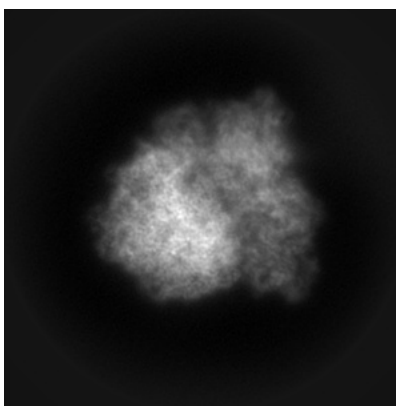
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

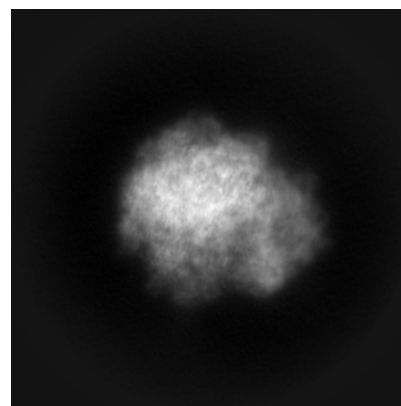
6.1.1 Primary map



X

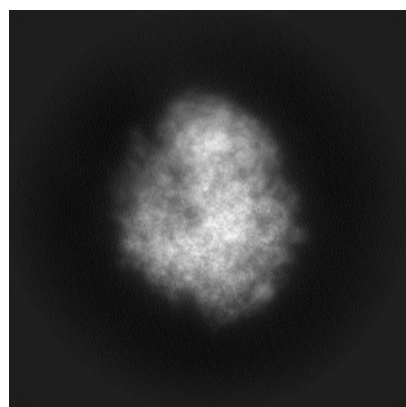


Y

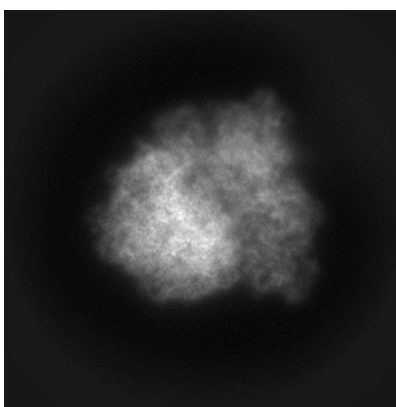


Z

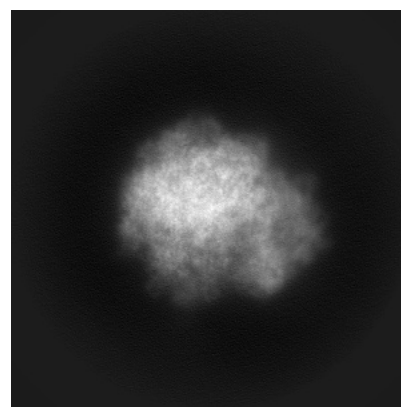
6.1.2 Raw map



X



Y

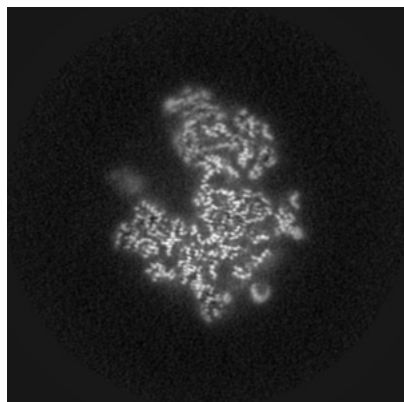


Z

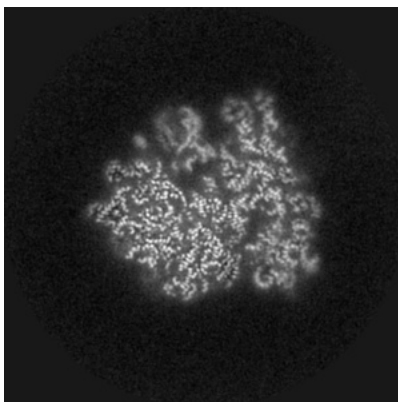
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

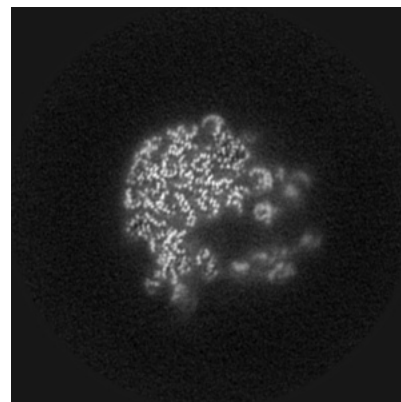
6.2.1 Primary map



X Index: 200

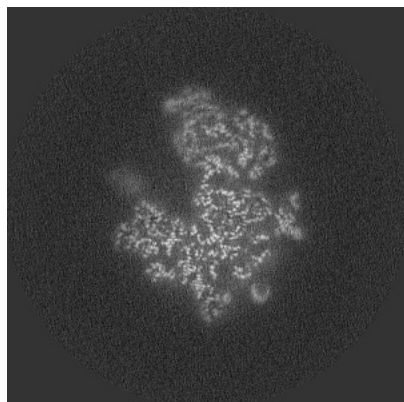


Y Index: 200

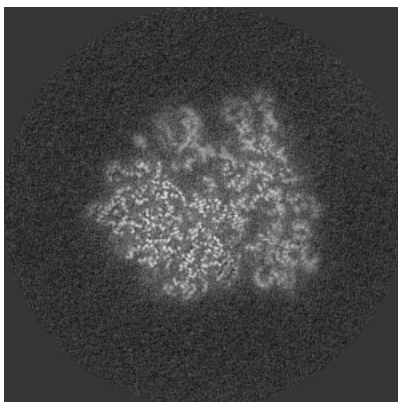


Z Index: 200

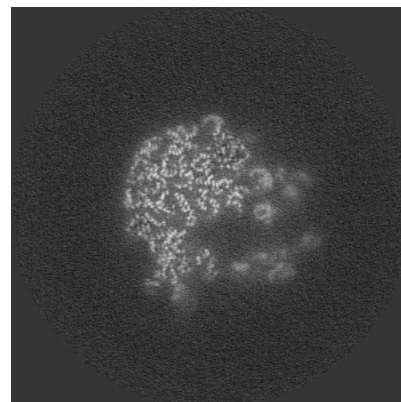
6.2.2 Raw map



X Index: 200



Y Index: 200

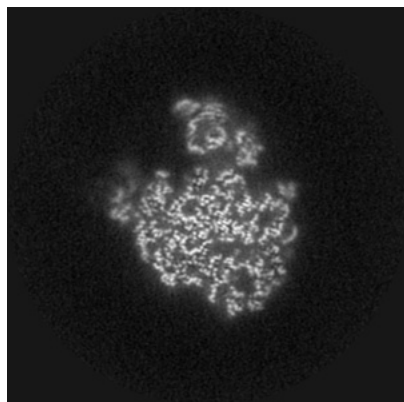


Z Index: 200

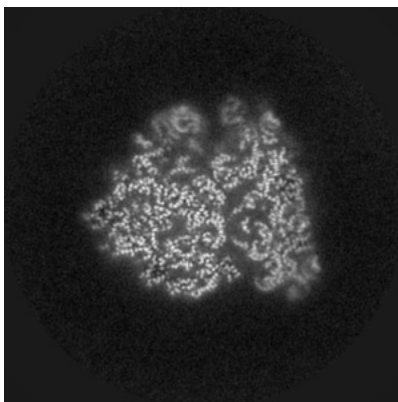
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

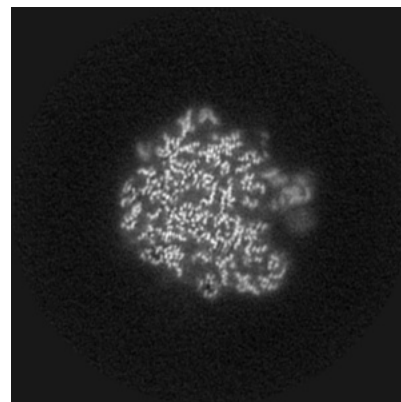
6.3.1 Primary map



X Index: 169

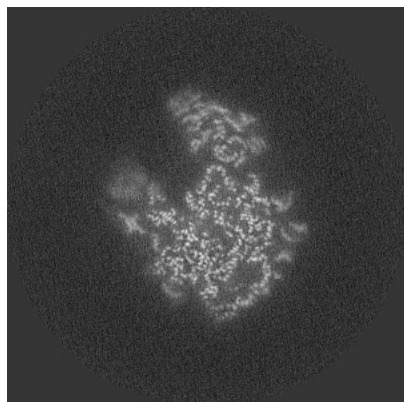


Y Index: 208

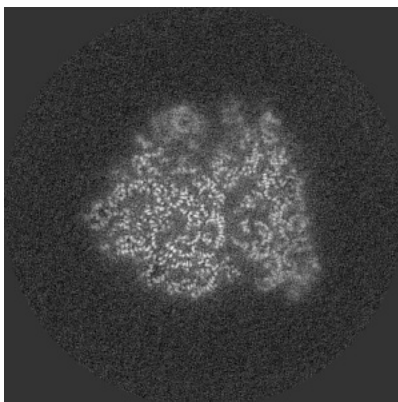


Z Index: 170

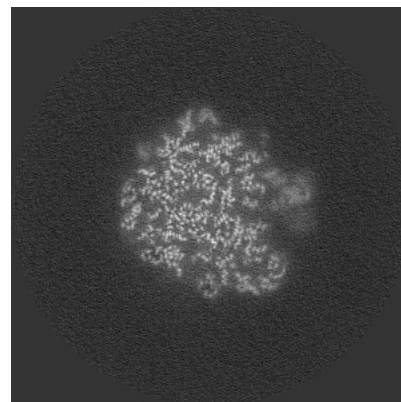
6.3.2 Raw map



X Index: 182



Y Index: 209

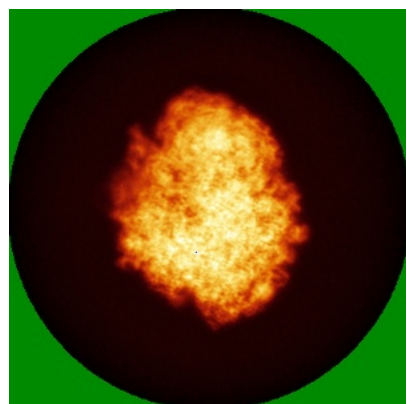


Z Index: 170

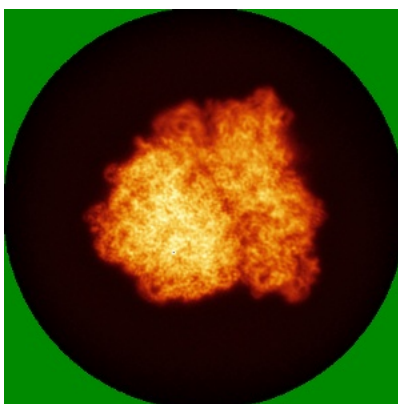
The images above show the largest variance slices of the map in three orthogonal directions.

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

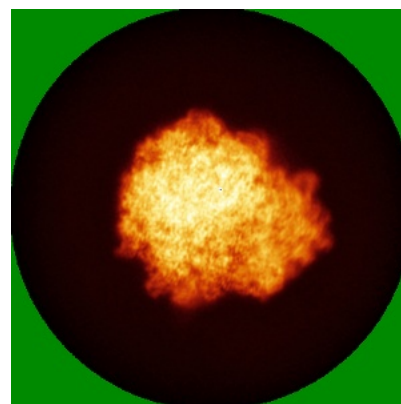
6.4.1 Primary map



X

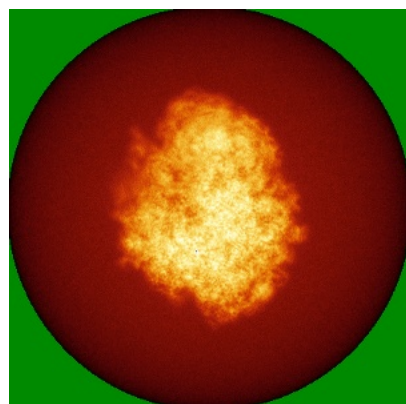


Y

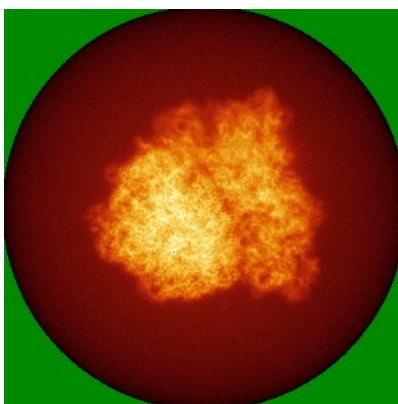


Z

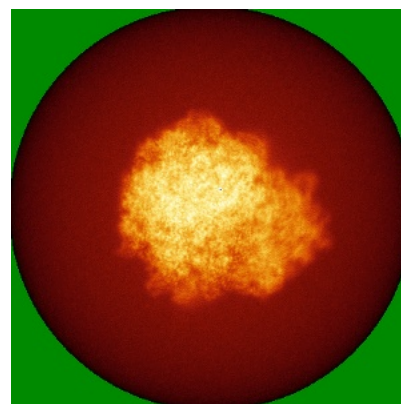
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



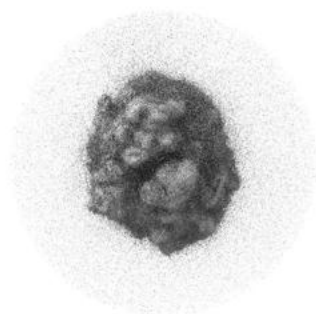
Y



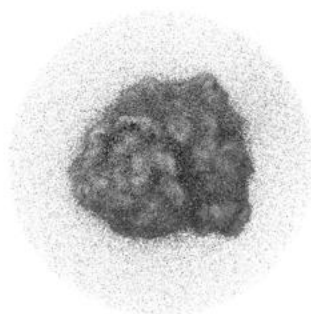
Z

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

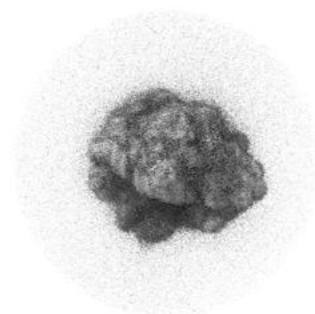
6.5.2 Raw map



X



Y



Z

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

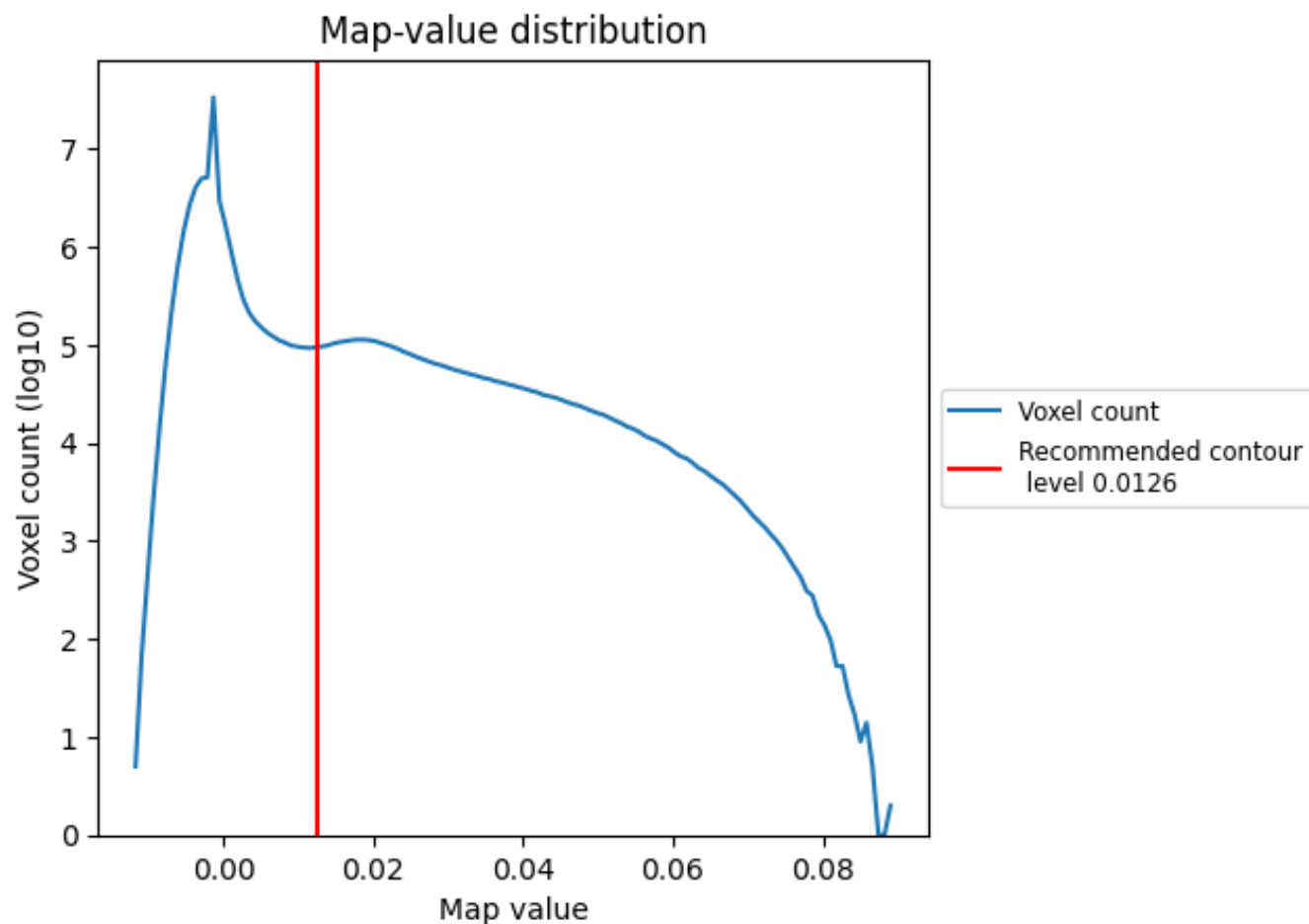
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

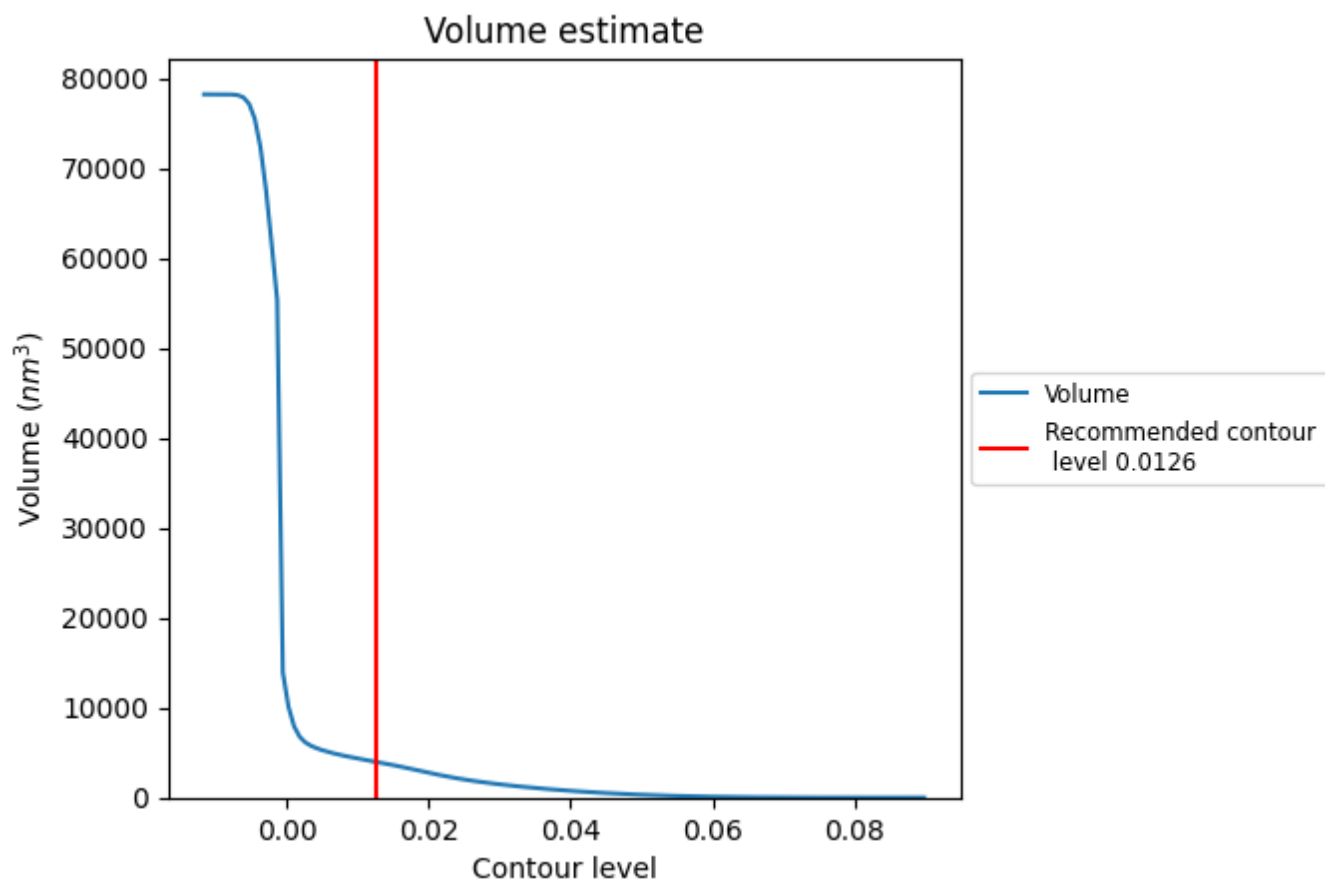
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

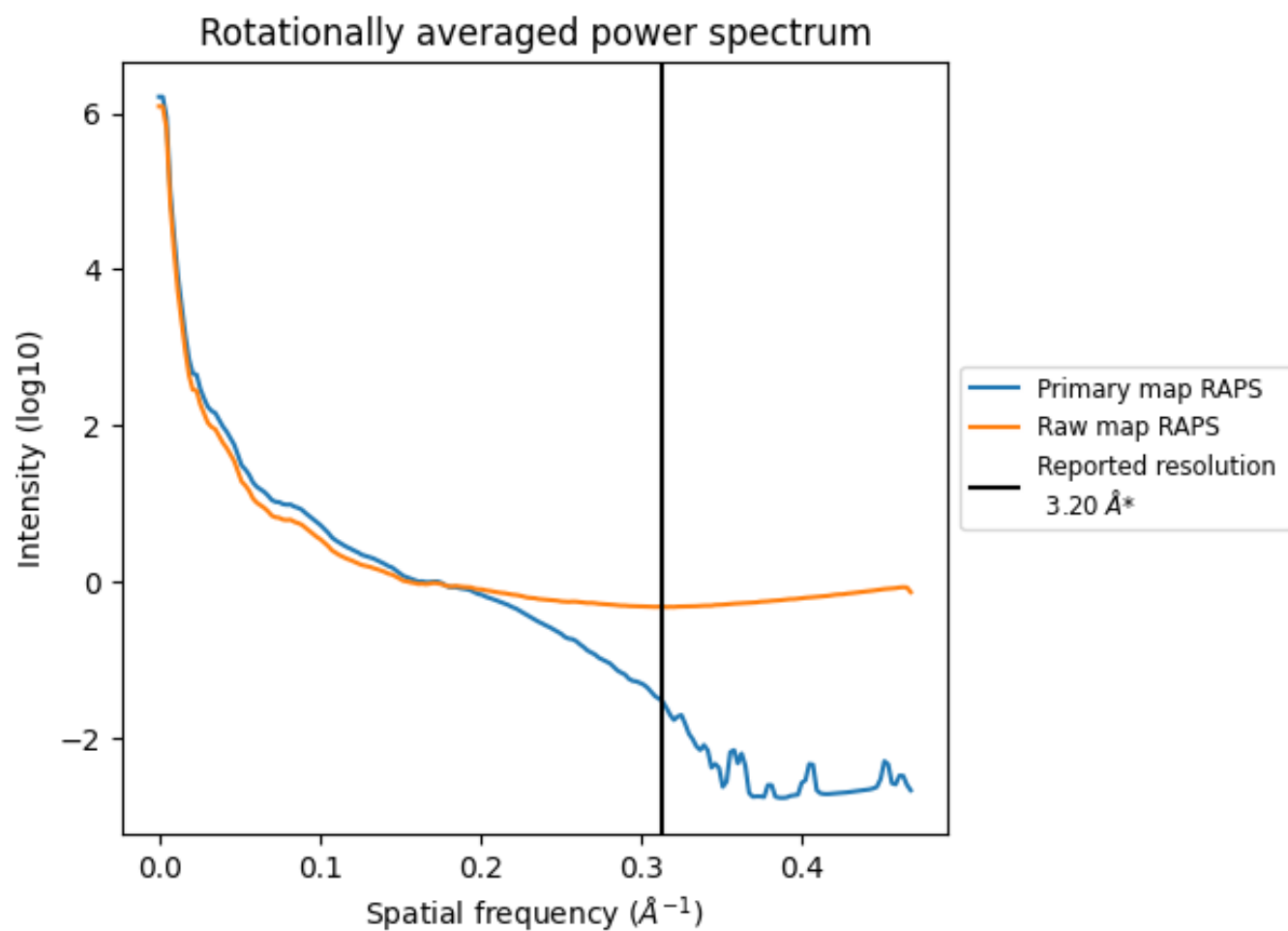
7.2 Volume estimate [i](#)



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

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

7.3 Rotationally averaged power spectrum ⓘ

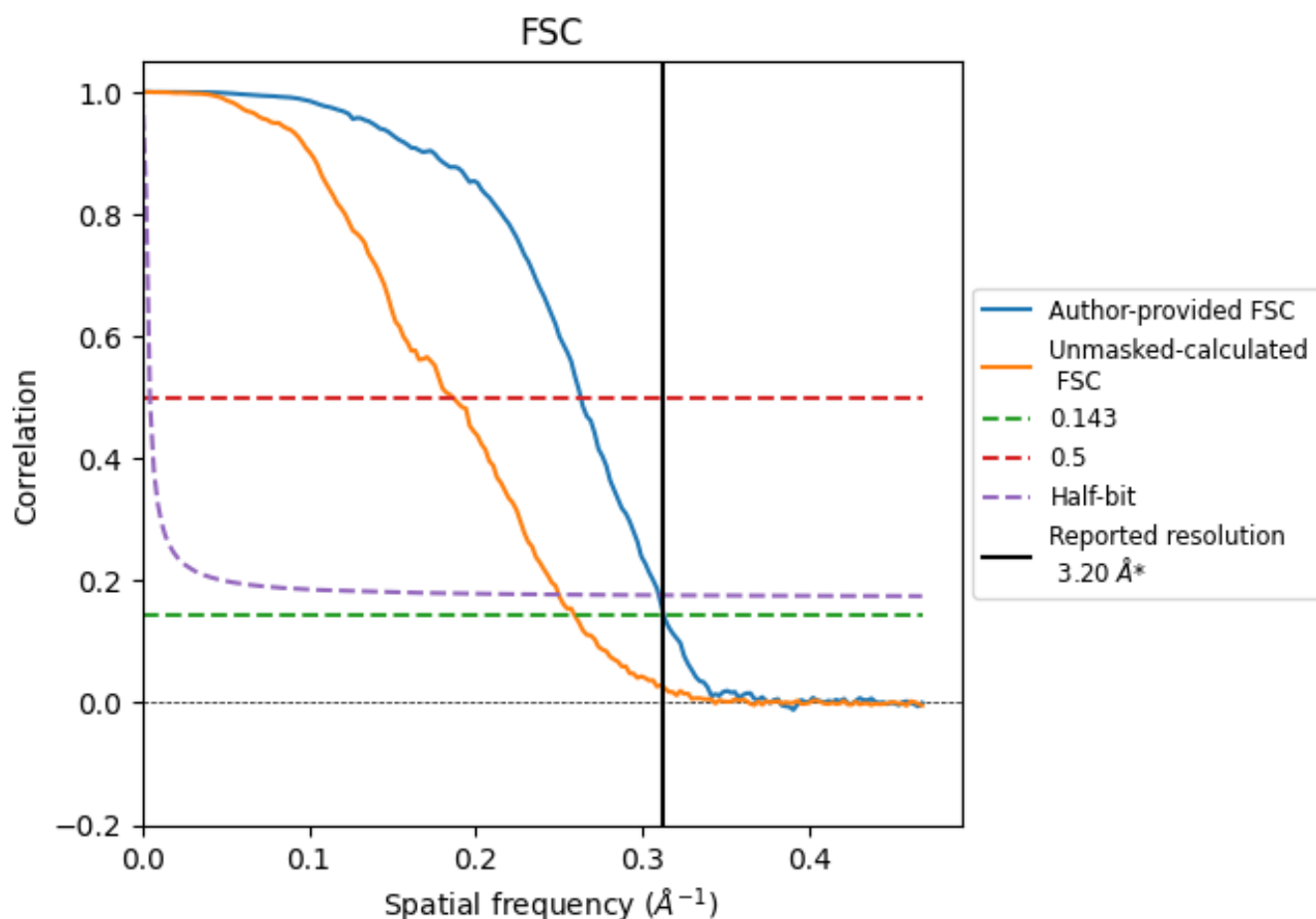


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

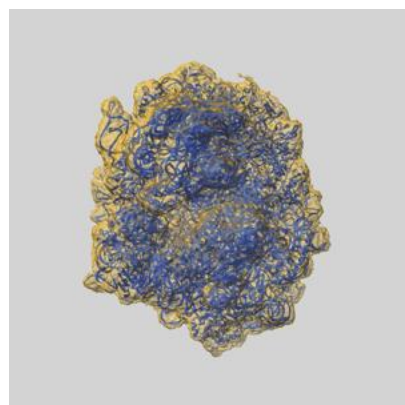
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.20	3.80	3.23
Unmasked-calculated*	3.86	5.37	4.00

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

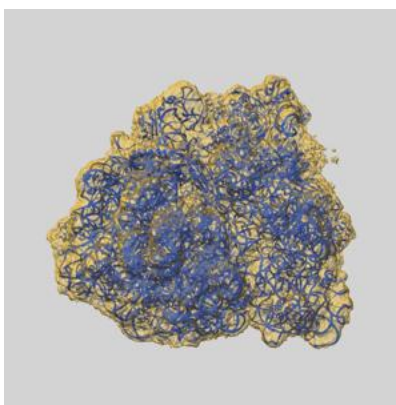
9 Map-model fit [i](#)

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

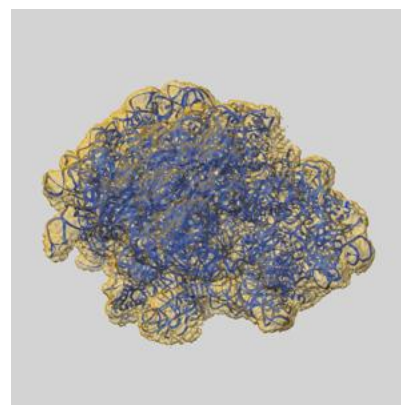
9.1 Map-model overlay [i](#)



X



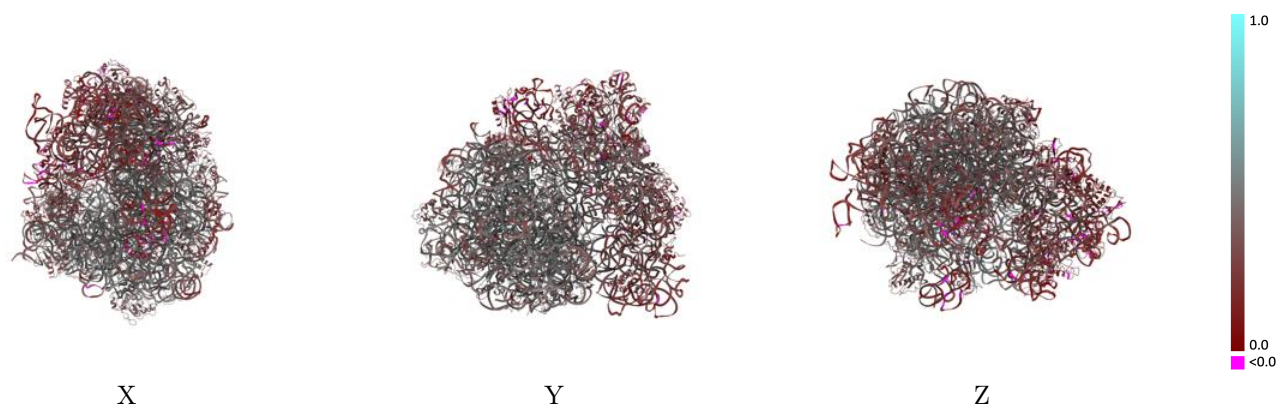
Y



Z

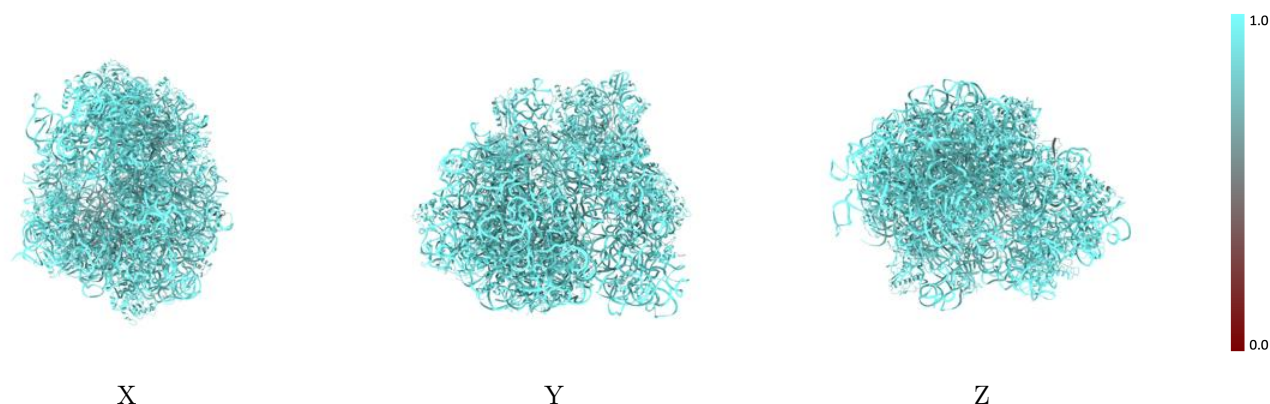
The images above show the 3D surface view of the map at the recommended contour level 0.0126 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



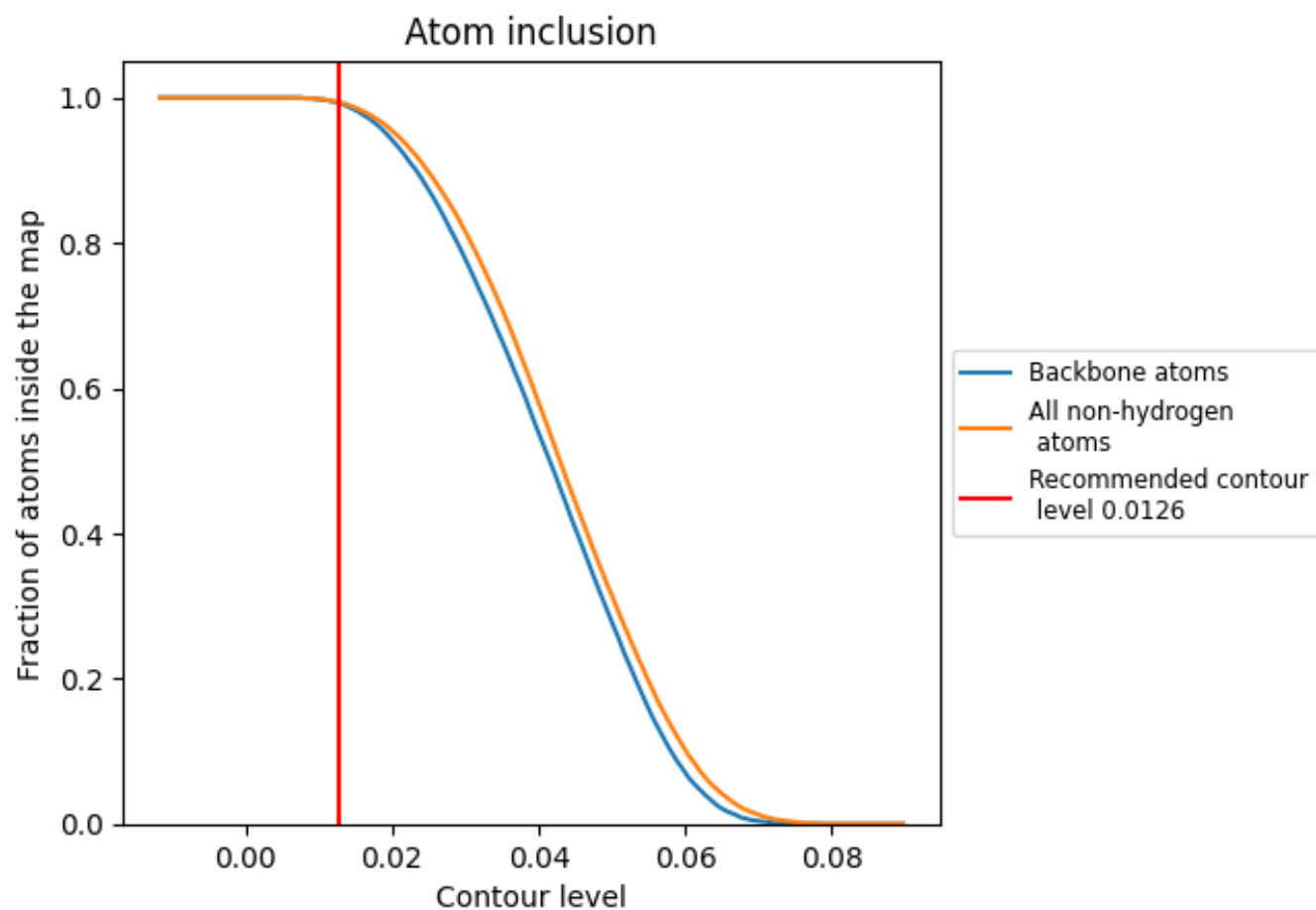
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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 (0.0126).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ







































The table lists the average atom inclusion at the recommended contour level (0.0126) and Q-score for the entire model and for each chain.

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



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