



wwPDB EM Validation Summary Report ⓘ

Jul 3, 2025 – 11:11 AM EDT

PDB ID : 8V03 / pdb_00008v03
EMDB ID : EMD-42852
Title : E. coli 70S ribosome with unmodified P/E-tRNA^{Pro}(GGG) bound to slippery P-site CCC-C codon
Authors : Kimbrough, E.M.; Dunham, C.M.; Nguyen, H.A.
Deposited on : 2023-11-16
Resolution : 4.00 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
Mogul : 2022.3.0, CSD as543be (2022)
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

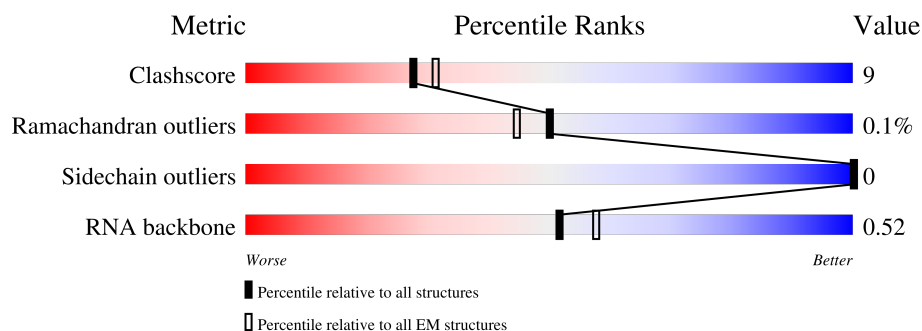
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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.













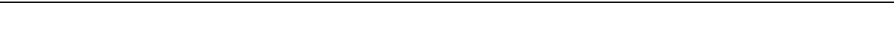

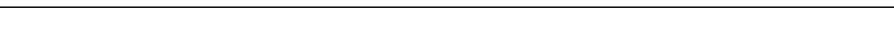
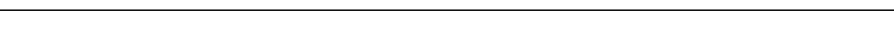











Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	53% 38% 9%
2	2	1540	55% 38% 7% .
3	3	120	55% 36% 9%
4	4	18	22% 78%
5	5	77	36% 39% 23% .
6	B	273	81% 18% .
7	C	209	85% 15%











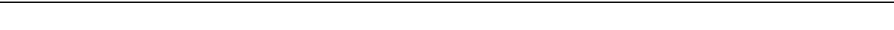

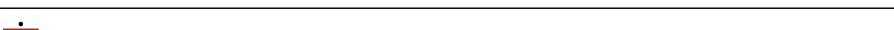
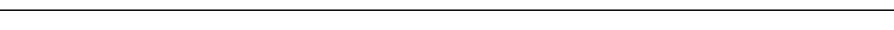
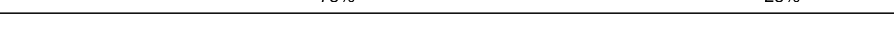






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Mol	Chain	Length	Quality of chain
8	D	201	
9	E	179	
10	F	177	
11	G	149	
12	J	142	
13	K	123	
14	L	144	
15	M	136	
16	N	127	
17	O	117	
18	P	115	
19	Q	118	
20	R	103	
21	S	110	
22	T	100	
23	U	104	
24	V	94	
25	W	84	
26	X	78	
27	Y	63	
28	Z	59	
29	b	57	
30	c	55	
31	d	46	
32	e	65	

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Mol	Chain	Length	Quality of chain
33	f	38	 76% 24%
34	g	241	 64% 26% 10%
35	h	206	 74% 26%
36	i	206	 69% 30%
37	j	167	 70% 23% 6%
38	k	135	 49% 25% 26%
39	l	179	 59% 25% 16%
40	m	130	 80% 19%
41	n	130	 53% 44% 3%
42	o	103	 72% 23% 5%
43	p	129	 72% 18% 10%
44	q	124	 77% 21% 2%
45	r	118	 71% 25% 4%
46	s	102	 75% 25% 1%
47	t	89	 79% 20% 1%
48	u	82	 79% 21%
49	v	84	 74% 21% 5%
50	w	75	 79% 8% 13%
51	x	92	 57% 29% 14%
52	y	87	 77% 21% 2%
53	z	71	 86% 6% 8%

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 144490 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	2900	Total	C	N	O	P	0	0
			62262	27774	11460	20128	2900		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1126835764
1	1847	G	A	conflict	GB 1126835764

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1531	Total	C	N	O	P	0	0
			32853	14652	6028	10642	1531		

- 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
			2572	1145	471	836	120		

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
			83	37	14	28	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	77	Total	C	N	O	P	0	0
			1648	733	297	541	77		

- Molecule 6 is a protein called 50S ribosomal protein L2.

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

- Molecule 7 is a protein called 50S ribosomal protein L3.

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

- Molecule 8 is a protein called 50S ribosomal protein L4.

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

- Molecule 9 is a protein called 50S ribosomal protein L5.

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

- Molecule 10 is a protein called 50S ribosomal protein L6.

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

- Molecule 11 is a protein called 50S ribosomal protein L9.

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

- Molecule 12 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 13 is a protein called 50S ribosomal protein L14.

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

- Molecule 14 is a protein called 50S ribosomal protein L15.

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

- Molecule 15 is a protein called 50S ribosomal protein L16.

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

- Molecule 16 is a protein called 50S ribosomal protein L17.

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

- Molecule 17 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 18 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 19 is a protein called 50S ribosomal protein L20.

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

- Molecule 20 is a protein called Large ribosomal subunit protein bL21.

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

- Molecule 21 is a protein called 50S ribosomal protein L22.

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

- Molecule 22 is a protein called 50S ribosomal protein L23.

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

- Molecule 23 is a protein called 50S ribosomal protein L24.

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

- Molecule 24 is a protein called Large ribosomal subunit protein bL25.

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

- Molecule 25 is a protein called Large ribosomal subunit protein bL27.

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

- Molecule 26 is a protein called 50S ribosomal protein L28.

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

- Molecule 27 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 28 is a protein called 50S ribosomal protein L30.

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

- Molecule 29 is a protein called 50S ribosomal protein L32.

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

- Molecule 30 is a protein called 50S ribosomal protein L33.

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

- Molecule 31 is a protein called 50S ribosomal protein L34.

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

- Molecule 32 is a protein called 50S ribosomal protein L35.

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

- Molecule 33 is a protein called 50S ribosomal protein L36.

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

- Molecule 34 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 35 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	206	Total	C	N	O	S	0	0
			1624	1028	305	288	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
			1141	709	218	208	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 Small ribosomal subunit protein uS8.

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 Small ribosomal subunit protein uS9.

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 Small ribosomal subunit protein uS10.

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 Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- 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 Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
s	36	ALA	-	insertion	UNP C3SR07

- Molecule 47 is a protein called Small ribosomal subunit protein uS15.

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 Small ribosomal subunit protein uS17.

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	0	0
			504	317	96	91		

- Molecule 51 is a protein called Small ribosomal subunit protein uS19.

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
			495	307	100	87	1		

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

Mol	Chain	Residues	Atoms		AltConf
54	1	196	Total	Mg	0
			196	196	
54	2	75	Total	Mg	0
			75	75	
54	3	1	Total	Mg	0
			1	1	
54	B	2	Total	Mg	0
			2	2	
54	D	2	Total	Mg	0
			2	2	
54	L	2	Total	Mg	0
			2	2	
54	Q	1	Total	Mg	0
			1	1	
54	b	1	Total	Mg	0
			1	1	
54	e	1	Total	Mg	0
			1	1	

- Molecule 55 is water.

Mol	Chain	Residues	Atoms		AltConf
55	1	479	Total	O	0
			479	479	
55	2	286	Total	O	0
			286	286	
55	3	10	Total	O	0
			10	10	
55	4	2	Total	O	0
			2	2	
55	5	1	Total	O	0
			1	1	
55	B	1	Total	O	0
			1	1	
55	C	1	Total	O	0
			1	1	
55	E	11	Total	O	0
			11	11	

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Mol	Chain	Residues	Atoms		AltConf
55	F	15	Total 15	O 15	0
55	G	10	Total 10	O 10	0
55	J	2	Total 2	O 2	0
55	K	1	Total 1	O 1	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	4	Total 4	O 4	0
55	P	2	Total 2	O 2	0
55	R	1	Total 1	O 1	0
55	T	5	Total 5	O 5	0
55	U	6	Total 6	O 6	0
55	V	4	Total 4	O 4	0
55	W	2	Total 2	O 2	0
55	X	1	Total 1	O 1	0
55	Y	1	Total 1	O 1	0
55	Z	1	Total 1	O 1	0
55	b	1	Total 1	O 1	0
55	c	1	Total 1	O 1	0
55	d	2	Total 2	O 2	0
55	e	1	Total 1	O 1	0

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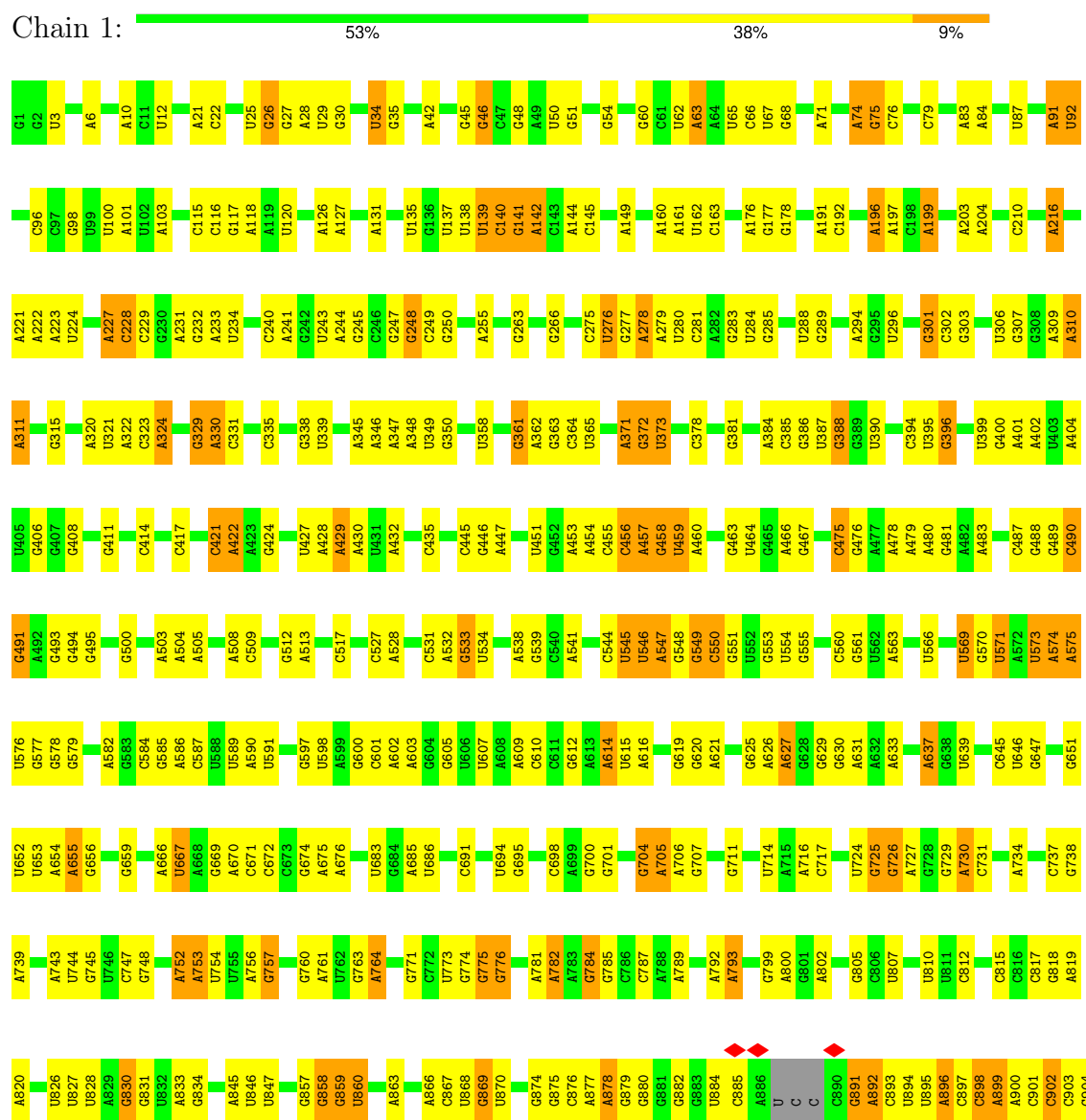
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Mol	Chain	Residues	Atoms		AltConf
55	f	1	Total 1	O 1	0
55	g	23	Total 23	O 23	0
55	h	13	Total 13	O 13	0
55	i	8	Total 8	O 8	0
55	j	8	Total 8	O 8	0
55	k	7	Total 7	O 7	0
55	l	13	Total 13	O 13	0
55	m	5	Total 5	O 5	0
55	n	9	Total 9	O 9	0
55	o	7	Total 7	O 7	0
55	p	6	Total 6	O 6	0
55	r	6	Total 6	O 6	0
55	s	5	Total 5	O 5	0
55	t	4	Total 4	O 4	0
55	v	4	Total 4	O 4	0
55	w	2	Total 2	O 2	0
55	x	8	Total 8	O 8	0
55	y	2	Total 2	O 2	0
55	z	5	Total 5	O 5	0

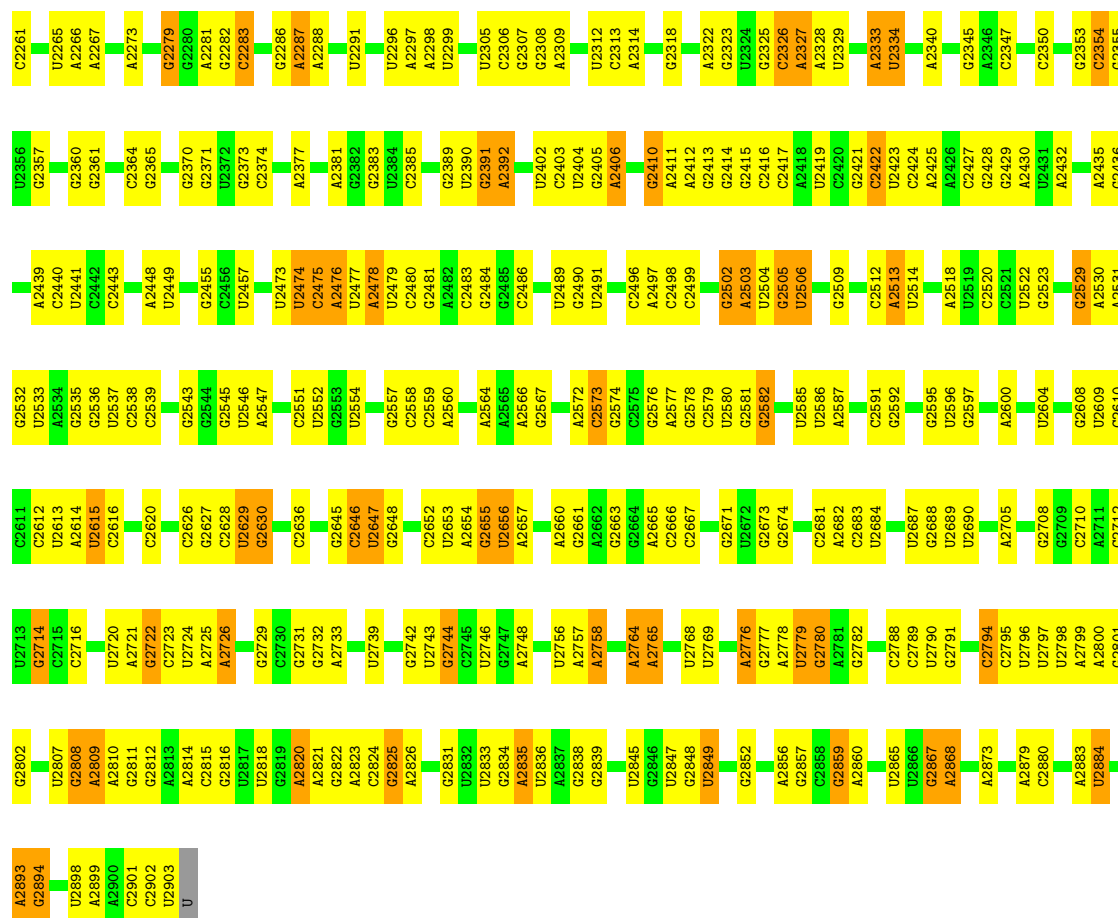
3 Residue-property plots [i](#)

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

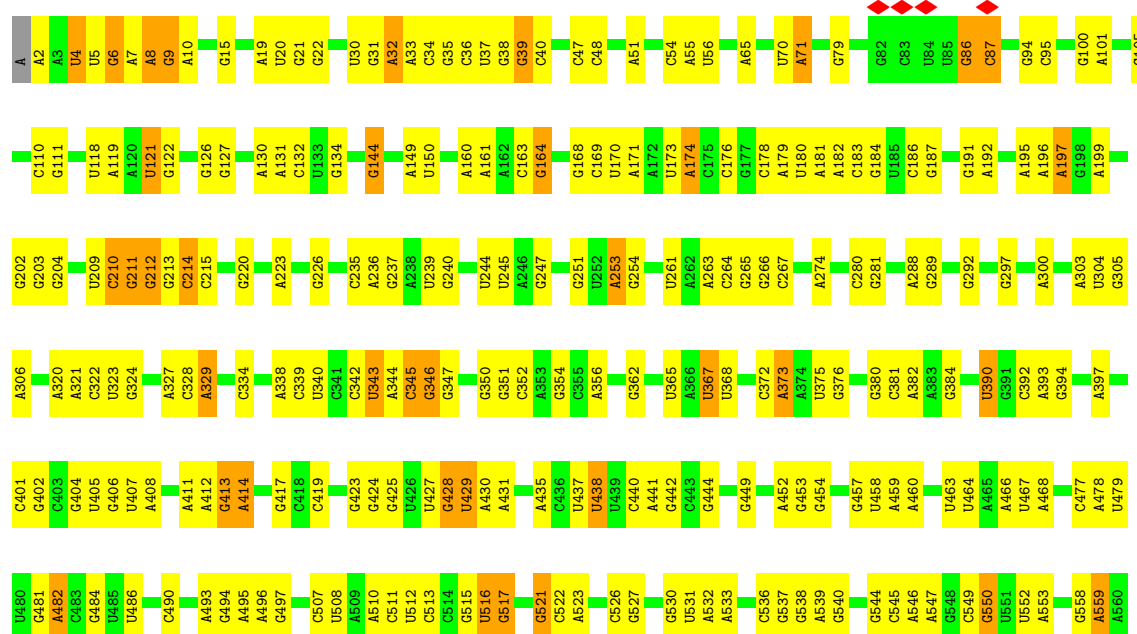


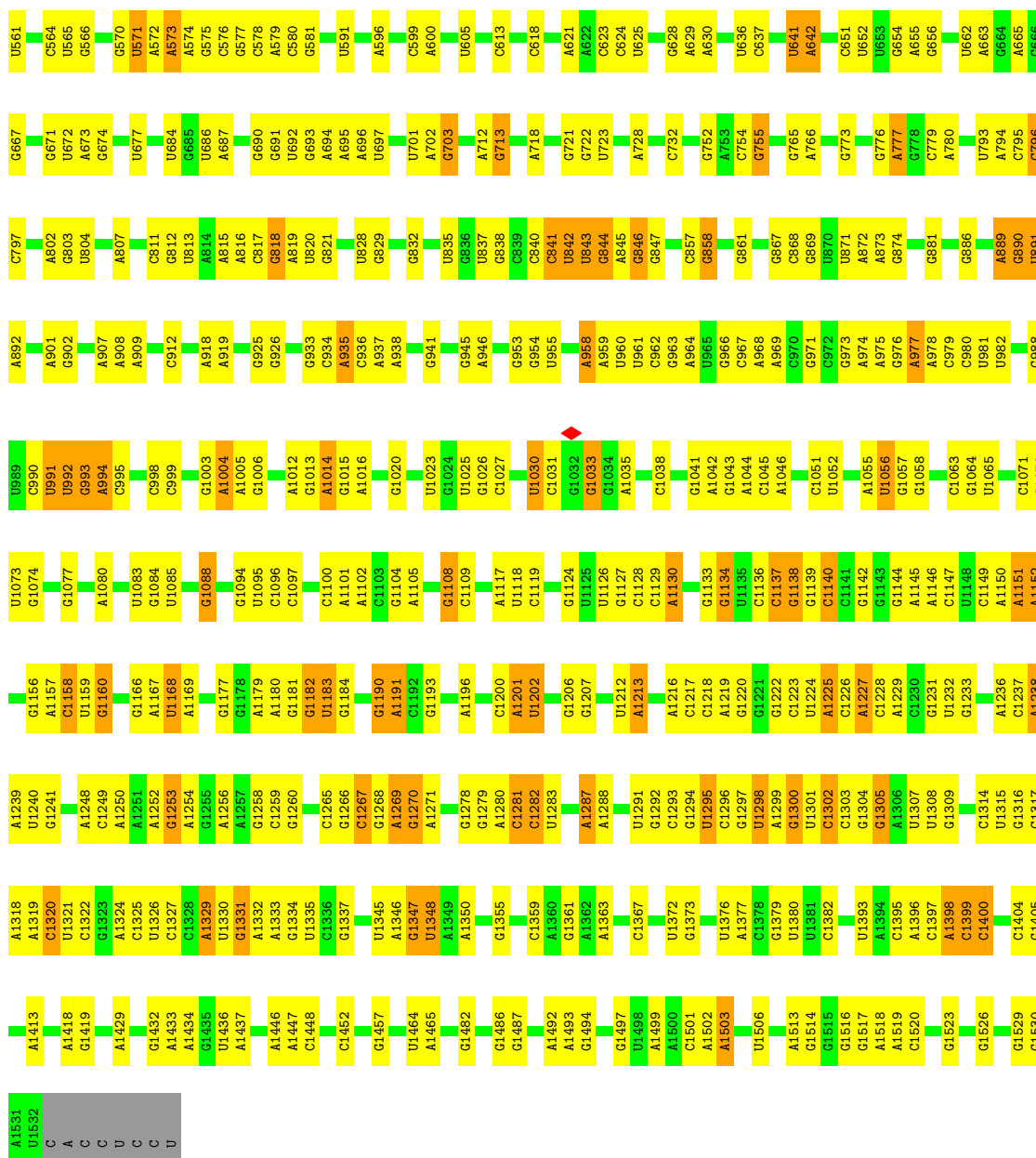
A2176	C2100	G1817	C1730	G1556	G1453	G1346	A1262	A1165	C1076	A996	G907
C2177	A2101	U1820	G1731	C1557	G1452	A1347	U1263	A1166	A1077	G997	G907
C2178	C2104	U1928	C1732	U1558	A1453	C1348	C1454	G1166	U1078	C998	A910
C2179	G1930	G1929	G1733	U1559	C1454	C1349	A1264	G1171	C1079	U999	A910
U2180	C2023	G1930	G1734	G1560	G1455	C1350	A1265	C1172	A1080	A1000	G914
U2181	G2024	U1931	A1735	C1561	G1456	C1351	G1271	C1173	U1081	C1007	G914
U2182	C2025	A1936	U1736	U1562	U1457	C1352	A1272	U1173	U1082	A1008	A918
U2183	U2026	U1927	G1737	U1563	U1458	A1353	A1272	U1174	U1083	A1009	A918
A2184	A2029	A1937	G1738	G1564	C1461	A1354	A1275	A1175	A1084	A1009	A928
A2185	G2030	A1938	G1739	U1565	U1468	G1358	A1275	A1176	A1085	A1010	A928
U2186	A2031	U1939	G1740	U1566	U1469	A1359	U1282	A1177	A1086	U1011	U929
U2187	A2032	C1941	A1744	U1567	A1468	A1359	U1283	U1012	G1087	U1012	G930
U2188	A2033	G1942	A1754	A1570	U1469	A1359	U1284	C1013	A1088	C1013	U931
G2190	A2034	U1943	A1755	A1571	A1469	A1359	U1285	U1109	A1089	U1019	U931
A2191	U2035	C1943	G1756	A1572	A1475	C1363	U1286	G1179	U1090	A1020	U932
G2192	G2036	U1943	A1757	A1573	U1476	G1364	A1286	U1180	A1090	A1021	U934
G2193	C2036	C1938	A1758	C1575	U1476	A1365	A1287	G1187	A1096	G1022	A941
A2194	U1951	C1938	U1758	U1576	U1481	G1377	A1288	U1188	U1097	U1023	G942
U2195	A1952	G1947	G1763	U1577	G1482	A1378	C1289	G1202	G1096	G1024	G946
U2196	A1953	A1943	C1764	U1578	U1490	U1379	C1290	U1203	U1101	G1025	G946
U2197	U1954	A1943	C1765	U1579	G1491	A1383	C1291	U1204	A1103	G1026	G953
U2198	U1955	G1857	U1769	C1582	G1491	A1384	G1292	A1204	C1104	A1027	G953
U2199	U1956	G1857	U1770	U1587	G1496	A1385	C1295	U1209	U1105	A1028	G956
U2200	G2049	C1957	U1771	U1588	U1497	A1386	C1298	G1211	G1031	G1031	A959
U2201	A2050	G1958	A1773	U1589	U1497	A1387	C1299	G1212	A1032	A1032	A960
U2202	A2051	G1959	C1774	C1585	U1498	A1387	A1301	G1215	G1110	U1033	C961
G2204	A2052	A1960	G1775	U1594	C1498	A1387	C1306	G1216	G1111	G1038	G962
C2207	C2055	C1961	U1779	U1595	A1504	A1392	C1306	U1217	A1112	A1039	U963
C2208	G2056	G1962	U1780	U1596	A1508	U1393	C1310	G1218	C1117	A1046	C964
C2209	G2057	A1871	U1781	U1597	A1509	U1394	G1311	U1224	C1118	G1047	G965
U2210	A2135	A1872	U1782	U1598	A1510	U1395	U1312	A1225	U1119	A1048	U967
A2211	G2136	G1875	A1783	U1602	A1515	U1396	U1313	A1226	G1049	C1049	C968
A2212	G2137	A1876	C1784	U1603	A1515	U1397	U1314	G1232	G1051	A1050	G969
U2213	G2138	G1879	C1785	C1605	U1520	U1400	U1315	G1233	C1052	G1052	U970
G2223	C2064	C1879	C1786	C1606	G1521	U1407	C1314	C1234	C1053	A1054	G971
G2224	G2065	G1884	C1787	C1607	A1522	G1407	C1315	U1234	A1126	A973	A973
A2225	C2066	A1885	A1791	C1611	U1523	G1416	C1320	G1235	G1123	G974	G974
C2226	G2067	U1886	A1792	C1612	G1524	C1417	A1321	G1236	G1124	A975	A975
G2230	U2068	U1887	U1793	C1613	A1525	G1418	A1322	A1237	G1125	G976	G976
G2231	G2069	G1888	G1794	C1614	G1526	G1419	C1323	G1238	U1130	G1059	A980
G2232	G2070	G1889	A1800	C1615	G1527	G1420	G1324	U1238	G1131	U1060	A981
G2233	G2071	A1900	C1800	C1616	G1528	G1421	U1325	U1242	U1132	U1061	A982
G2234	G2072	A1901	A1801	C1617	A1532	G1425	A1328	A1243	A1133	G1062	A983
A2239	C2073	G1905	A1802	C1618	C1533	G1426	U1329	A1244	G1134	C1063	A984
U2245	U2075	G1906	A1803	C1619	U1534	C1427	C1330	G1248	G1135	U1066	C985
C2248	U2076	G1907	A1804	C1620	A1535	C1428	G1333	U1249	G1136	C1067	C986
C2250	U2077	G1907	A1805	A1626	A1536	A1431	G1338	G1250	G1137	U1068	C987
G2251	A2080	C1997	C1806	A1627	C1537	G1432	G1339	C1251	U1141	G1069	A988
G2252	U2082	C1998	G1807	A1628	U1537	A1433	G1340	G1252	A1142	A1070	G989
G2253	U2083	C1999	U1713	A1629	G1537	A1433	U1340	A1253	A1143	A990	A990
C2254	A2082	C2002	U1714	A1630	C1538	G1437	G1341	U1254	C1153	C1072	G993
G2255	A2090	A2003	U1715	A1631	U1542	U1437	G1342	U1255	G1154	G1073	C994
G2256	U2091	A2003	U1716	A1632	G1543	U1438	A1342	G1256	A1155	A1074	C995
G2257	U2092	C2006	U1717	A1633	A1544	U1438	A1343	U1257	C1156	C1074	C995
U2258	G2093	A2170	G1724	A1634	A1544	U1438	A1344	U1258	C1157	C1075	C995
U2259	C2096	A2171	U1725	A1635	A1552	C1447	G1345	G1259	C1158	C1076	C995
C2260	G2096	A2172	C1726	A1636	A1555	G1450	C1345	G1260	C1159	C1077	C995
		A2013	U1729	A1640	G1555	G1450	C1345	G1261	C1160	C1078	C995



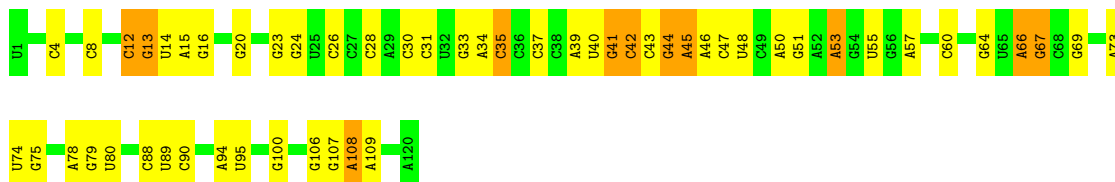
• Molecule 2: 16S ribosomal RNA

Chain 2: 55% 38% 7% .



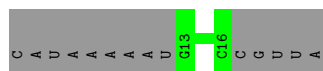


• Molecule 3: 5S ribosomal RNA



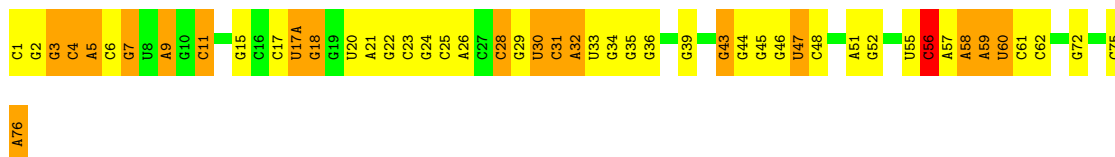
• Molecule 4: mRNA





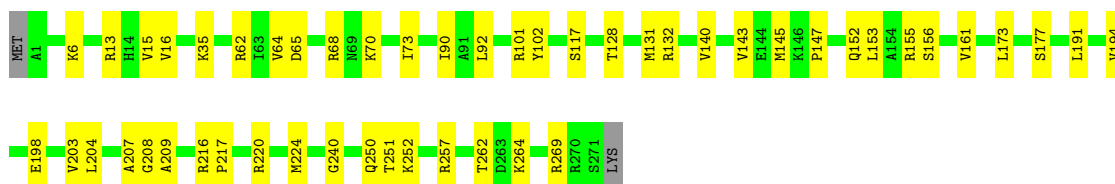
- Molecule 5: tRNA ProL (GGG)

Chain 5: 36% 39% 23%



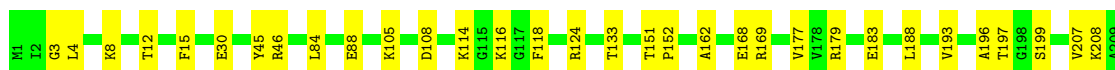
- Molecule 6: 50S ribosomal protein L2

Chain B: 81% 18%



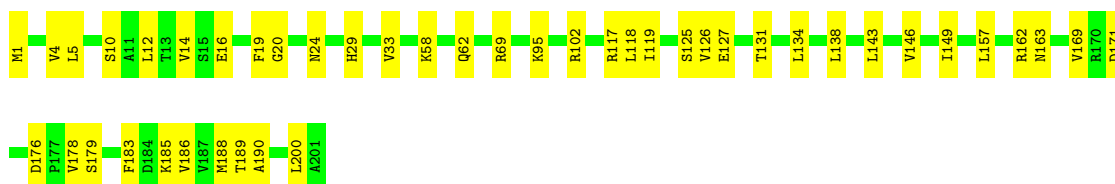
- Molecule 7: 50S ribosomal protein L3

Chain C: 85% 15%



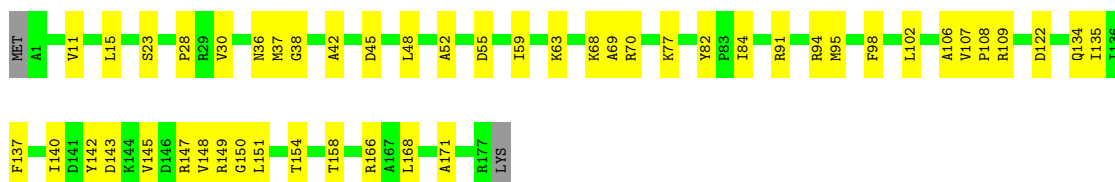
- Molecule 8: 50S ribosomal protein L4

Chain D: 78% 22%

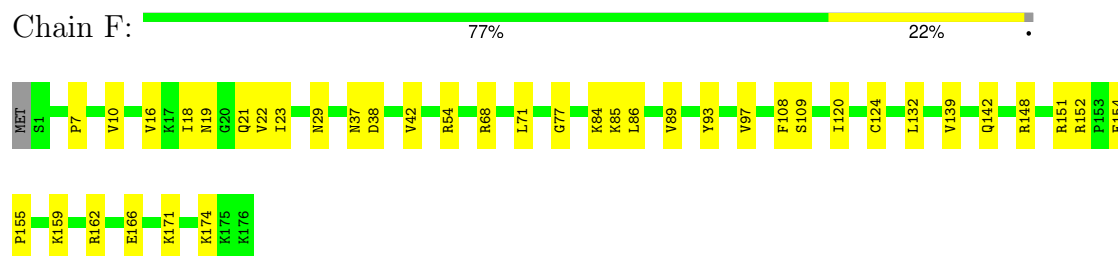


- Molecule 9: 50S ribosomal protein L5

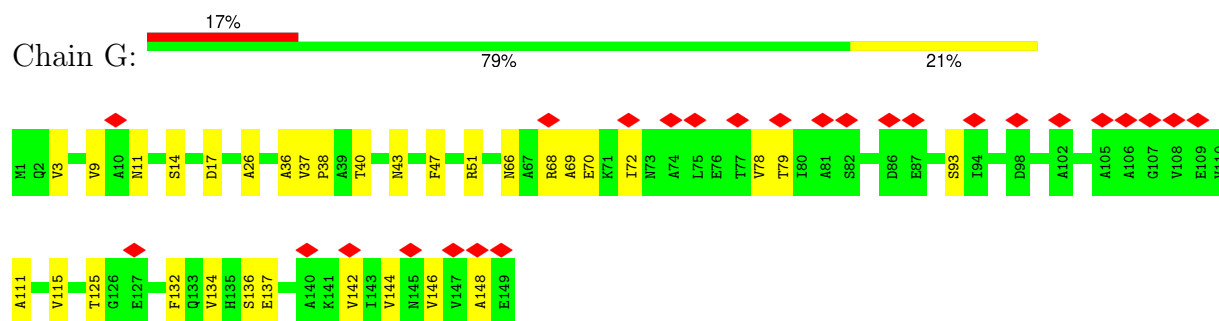
Chain E: 72% 27%



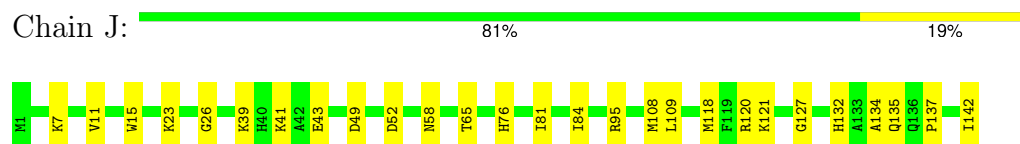
- Molecule 10: 50S ribosomal protein L6



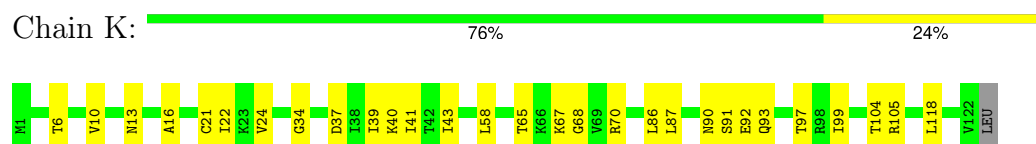
- Molecule 11: 50S ribosomal protein L9



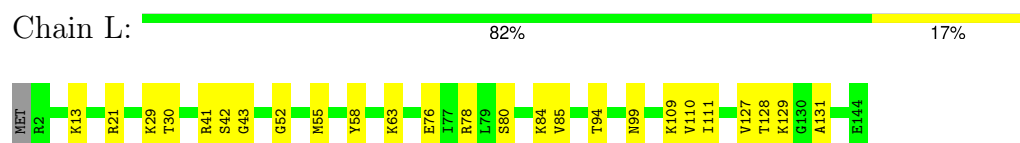
- Molecule 12: Large ribosomal subunit protein uL13



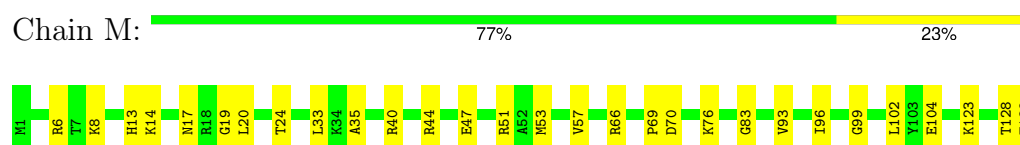
- Molecule 13: 50S ribosomal protein L14



- Molecule 14: 50S ribosomal protein L15



- Molecule 15: 50S ribosomal protein L16



- Molecule 16: 50S ribosomal protein L17

Chain N:  72% 23% 6%




- Molecule 17: Large ribosomal subunit protein uL18

Chain O:  76% 23% .




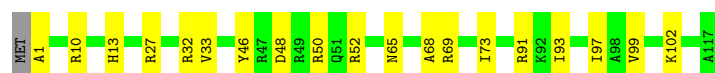
- Molecule 18: Large ribosomal subunit protein bL19

Chain P:  82% 17% .




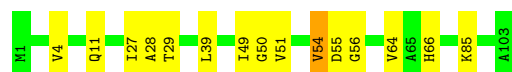
- Molecule 19: 50S ribosomal protein L20

Chain Q:  83% 16% .



- Molecule 20: Large ribosomal subunit protein bL21

Chain R:  85% 14% .




- Molecule 21: 50S ribosomal protein L22

Chain S:  73% 26% .




- Molecule 22: 50S ribosomal protein L23

Chain T:  82% 11% 7%




- Molecule 23: 50S ribosomal protein L24

Chain U:  76% 22%



- Molecule 24: Large ribosomal subunit protein bL25

Chain V:  79% 21%




- Molecule 25: Large ribosomal subunit protein bL27

Chain W:  74% 15% 11%




- Molecule 26: 50S ribosomal protein L28

Chain X:  85% 14%



- Molecule 27: Large ribosomal subunit protein uL29

Chain Y:  79% 21%




- Molecule 28: 50S ribosomal protein L30

Chain Z:  75% 24%




- Molecule 29: 50S ribosomal protein L32

Chain b:  88% 11%




- Molecule 30: 50S ribosomal protein L33

Chain c:  80% 11% 9%



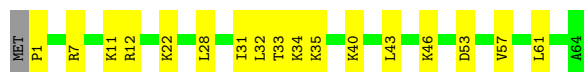
- Molecule 31: 50S ribosomal protein L34

Chain d:  78% 22%



- Molecule 32: 50S ribosomal protein L35

Chain e:  72% 26% .



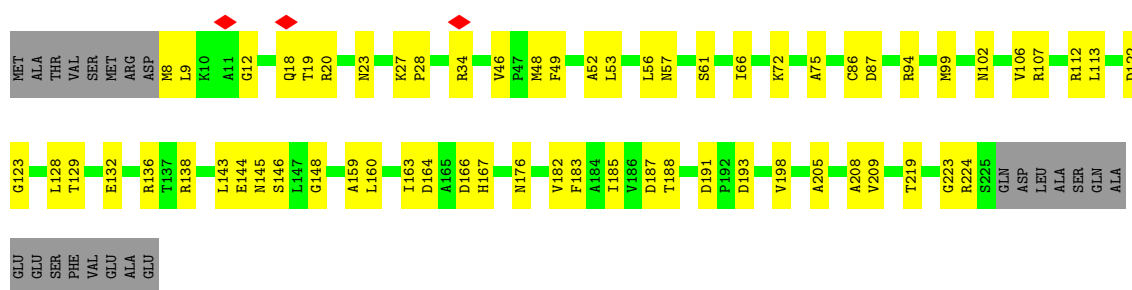
- Molecule 33: 50S ribosomal protein L36

Chain f:  76% 24%



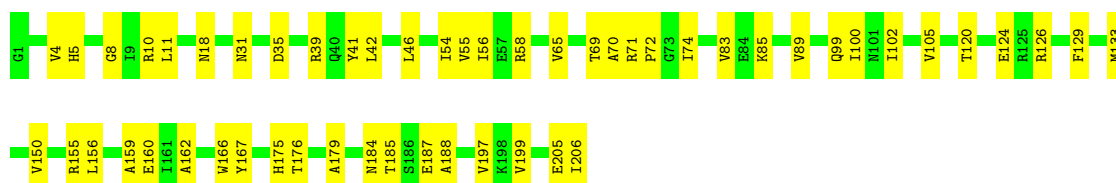
- Molecule 34: 30S ribosomal protein S2

Chain g:  64% 26% 10%

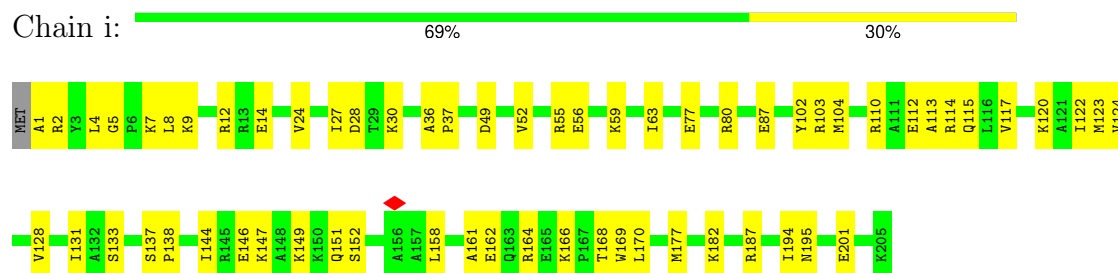


- Molecule 35: Small ribosomal subunit protein uS3

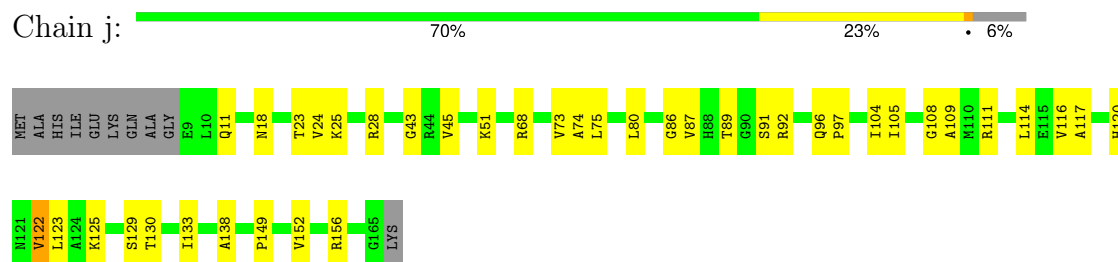
Chain h:  74% 26%



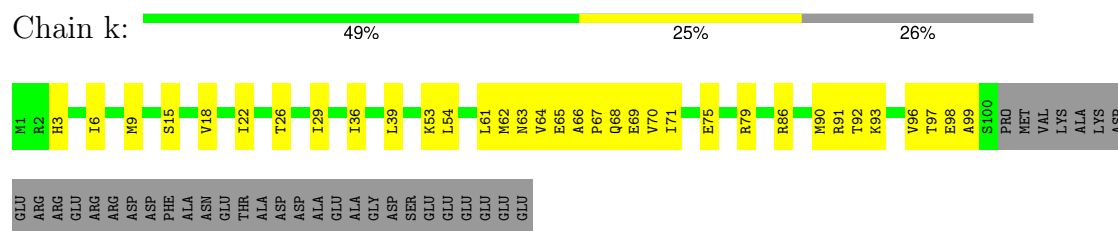
- Molecule 36: 30S ribosomal protein S4



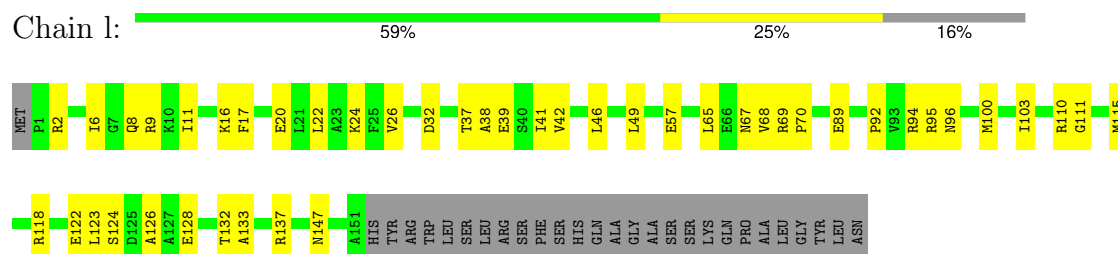
- Molecule 37: 30S ribosomal protein S5



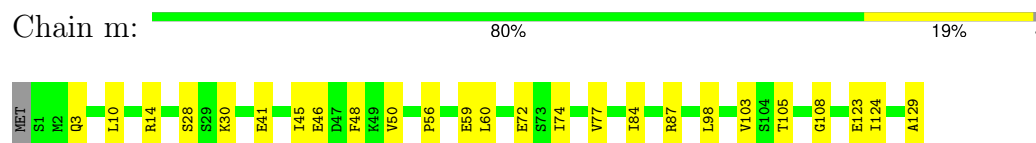
- Molecule 38: 30S ribosomal protein S6



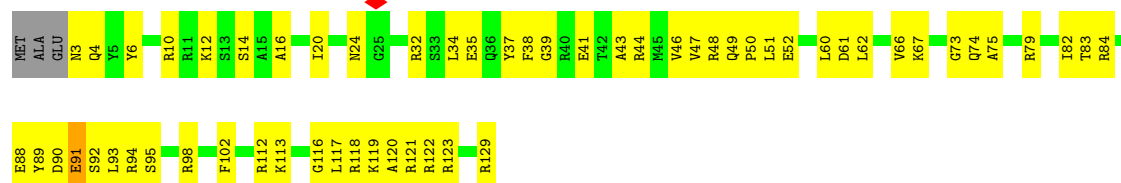
- Molecule 39: 30S ribosomal protein S7



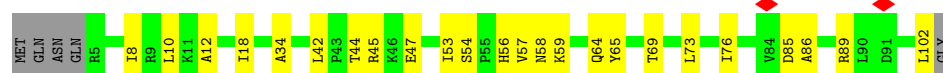
- Molecule 40: Small ribosomal subunit protein uS8



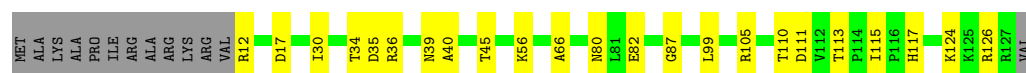
- Molecule 41: Small ribosomal subunit protein uS9



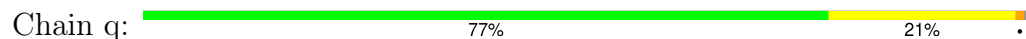
- Molecule 42: Small ribosomal subunit protein uS10



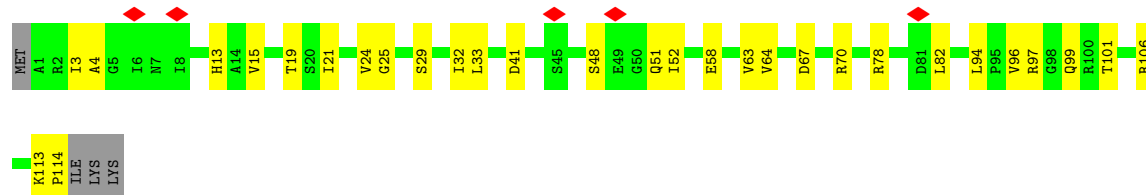
- Molecule 43: 30S ribosomal protein S11



- Molecule 44: Small ribosomal subunit protein uS12




- Molecule 45: 30S ribosomal protein S13

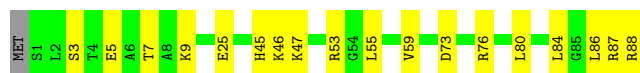


- Molecule 46: Small ribosomal subunit protein uS14




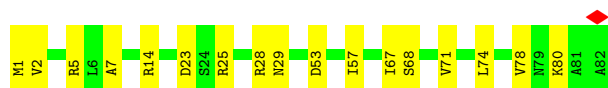
- Molecule 47: Small ribosomal subunit protein uS15

Chain t:  79% 20% .



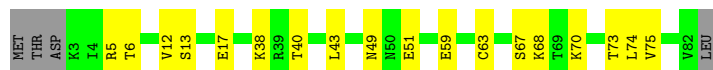
- Molecule 48: 30S ribosomal protein S16

Chain u:  79% 21%




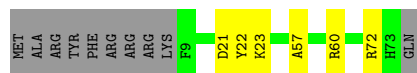
- Molecule 49: Small ribosomal subunit protein uS17

Chain v:  74% 21% 5%



- Molecule 50: 30S ribosomal protein S18

Chain w:  79% 8% 13%




- Molecule 51: Small ribosomal subunit protein uS19

Chain x:  57% 29% 14%




- Molecule 52: 30S ribosomal protein S20

Chain y:  77% 21%



- Molecule 53: 30S ribosomal protein S21

Chain z:  86% 6% 8%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38062	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)	600	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.158	Depositor
Minimum map value	-0.039	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.0289	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: 0TD, 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	0.12	0/69734	0.25	1/108788 (0.0%)
2	2	0.10	0/36787	0.24	0/57389
3	3	0.10	0/2876	0.23	0/4483
4	4	0.37	0/91	0.66	0/139
5	5	0.32	0/1841	0.60	2/2870 (0.1%)
6	B	0.18	0/2121	0.39	0/2852
7	C	0.16	0/1586	0.35	0/2134
8	D	0.16	0/1571	0.34	0/2113
9	E	0.18	0/1434	0.40	0/1926
10	F	0.17	0/1343	0.34	0/1816
11	G	0.15	0/1122	0.34	0/1515
12	J	0.15	0/1152	0.32	0/1551
13	K	0.17	0/947	0.36	0/1268
14	L	0.16	0/1054	0.41	0/1403
15	M	0.16	0/1093	0.36	0/1460
16	N	0.17	0/973	0.41	0/1301
17	O	0.15	0/902	0.33	0/1209
18	P	0.18	0/929	0.36	0/1242
19	Q	0.17	0/960	0.32	0/1278
20	R	0.17	0/829	0.38	0/1107
21	S	0.17	0/864	0.38	0/1156
22	T	0.16	0/744	0.32	0/994
23	U	0.15	0/787	0.35	0/1051
24	V	0.16	0/766	0.31	0/1025
25	W	0.16	0/582	0.35	0/769
26	X	0.16	0/635	0.31	0/848
27	Y	0.14	0/510	0.30	0/677
28	Z	0.17	0/453	0.38	0/605
29	b	0.17	0/450	0.36	0/599
30	c	0.14	0/416	0.32	0/554
31	d	0.18	0/380	0.38	0/498
32	e	0.16	0/513	0.38	0/676

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.19	0/303	0.37	0/397
34	g	0.15	0/1735	0.37	0/2338
35	h	0.17	0/1651	0.36	0/2225
36	i	0.15	0/1665	0.37	0/2227
37	j	0.17	0/1154	0.43	0/1554
38	k	0.17	0/835	0.42	0/1128
39	l	0.14	0/1195	0.34	0/1602
40	m	0.15	0/989	0.34	0/1326
41	n	0.17	0/1034	0.44	0/1375
42	o	0.17	0/796	0.37	0/1077
43	p	0.16	0/885	0.35	0/1195
44	q	0.16	0/960	0.36	0/1286
45	r	0.17	0/892	0.35	0/1193
46	s	0.16	0/811	0.37	0/1081
47	t	0.18	0/722	0.36	0/964
48	u	0.17	0/659	0.40	0/884
49	v	0.15	0/657	0.35	0/881
50	w	0.15	0/511	0.37	0/689
51	x	0.15	0/652	0.33	0/877
52	y	0.14	0/671	0.31	0/888
53	z	0.18	0/500	0.50	0/668
All	All	0.13	0/155722	0.29	3/233151 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
37	j	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	5	56	C	C2'-C3'-O3'	8.13	121.70	109.50
5	5	3	G	C4'-C3'-O3'	7.29	120.33	109.40
1	1	1119	U	C4'-C3'-O3'	-5.07	105.39	113.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
37	j	120	HIS	Peptide

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	62262	0	31313	905	0
2	2	32853	0	16530	477	0
3	3	2572	0	1302	41	0
4	4	83	0	45	0	0
5	5	1648	0	834	36	0
6	B	2082	0	2157	42	0
7	C	1565	0	1616	25	0
8	D	1552	0	1619	38	0
9	E	1410	0	1447	48	0
10	F	1323	0	1374	27	0
11	G	1111	0	1148	21	0
12	J	1129	0	1162	21	0
13	K	938	0	1012	23	0
14	L	1045	0	1117	25	0
15	M	1074	0	1157	24	0
16	N	960	0	1000	24	0
17	O	892	0	923	21	0
18	P	917	0	965	15	0
19	Q	947	0	1022	21	0
20	R	816	0	839	12	0
21	S	857	0	922	20	0
22	T	738	0	807	8	0
23	U	779	0	834	16	0
24	V	753	0	780	14	0
25	W	575	0	592	11	0
26	X	625	0	655	12	0
27	Y	509	0	543	10	0
28	Z	449	0	491	10	0
29	b	444	0	461	5	0
30	c	409	0	440	4	0
31	d	377	0	418	7	0
32	e	504	0	574	17	0
33	f	302	0	343	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	g	1704	0	1732	47	0
35	h	1624	0	1699	44	0
36	i	1643	0	1710	51	0
37	j	1141	0	1170	34	0
38	k	817	0	808	29	0
39	l	1181	0	1240	38	0
40	m	979	0	1034	22	0
41	n	1022	0	1070	55	0
42	o	786	0	828	21	0
43	p	869	0	878	22	0
44	q	957	0	1017	24	0
45	r	883	0	944	20	0
46	s	799	0	841	23	0
47	t	714	0	737	13	0
48	u	649	0	666	14	0
49	v	648	0	691	17	0
50	w	504	0	502	6	0
51	x	637	0	665	26	0
52	y	665	0	714	16	0
53	z	495	0	486	3	0
54	1	196	0	0	0	0
54	2	75	0	0	0	0
54	3	1	0	0	0	0
54	B	2	0	0	0	0
54	D	2	0	0	0	0
54	L	2	0	0	0	0
54	Q	1	0	0	0	0
54	b	1	0	0	0	0
54	e	1	0	0	0	0
55	1	479	0	0	55	0
55	2	286	0	0	37	0
55	3	10	0	0	0	0
55	4	2	0	0	0	0
55	5	1	0	0	0	0
55	B	1	0	0	0	0
55	C	1	0	0	0	0
55	E	11	0	0	4	0
55	F	15	0	0	0	0
55	G	10	0	0	0	0
55	J	2	0	0	1	0
55	K	1	0	0	0	0
55	L	2	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	M	2	0	0	0	0
55	N	1	0	0	0	0
55	O	4	0	0	1	0
55	P	2	0	0	0	0
55	R	1	0	0	0	0
55	T	5	0	0	1	0
55	U	6	0	0	2	0
55	V	4	0	0	3	0
55	W	2	0	0	1	0
55	X	1	0	0	1	0
55	Y	1	0	0	1	0
55	Z	1	0	0	0	0
55	b	1	0	0	0	0
55	c	1	0	0	0	0
55	d	2	0	0	0	0
55	e	1	0	0	0	0
55	f	1	0	0	1	0
55	g	23	0	0	7	0
55	h	13	0	0	3	0
55	i	8	0	0	2	0
55	j	8	0	0	3	0
55	k	7	0	0	1	0
55	l	13	0	0	4	0
55	m	5	0	0	1	0
55	n	9	0	0	4	0
55	o	7	0	0	1	0
55	p	6	0	0	1	0
55	r	6	0	0	0	0
55	s	5	0	0	1	0
55	t	4	0	0	1	0
55	v	4	0	0	1	0
55	w	2	0	0	0	0
55	x	8	0	0	3	0
55	y	2	0	0	1	0
55	z	5	0	0	0	0
All	All	144490	0	95874	2177	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 9.

The worst 5 of 2177 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)
39:l:26:VAL:HG22	39:l:42:VAL:HG21	1.49	0.94
1:1:1322:A:N1	1:1:1333:G:O2'	2.00	0.94
1:1:2258:C:O2'	1:1:2427:C:OP2	1.86	0.92
1:1:2014:A:O2'	1:1:2015:A:O4'	1.88	0.90
1:1:2645:G:OP2	1:1:2645:G:N2	2.03	0.90

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	B	269/273 (98%)	246 (91%)	23 (9%)	0	100	100
7	C	207/209 (99%)	187 (90%)	20 (10%)	0	100	100
8	D	199/201 (99%)	184 (92%)	15 (8%)	0	100	100
9	E	175/179 (98%)	154 (88%)	21 (12%)	0	100	100
10	F	174/177 (98%)	166 (95%)	8 (5%)	0	100	100
11	G	147/149 (99%)	132 (90%)	15 (10%)	0	100	100
12	J	140/142 (99%)	131 (94%)	9 (6%)	0	100	100
13	K	120/123 (98%)	109 (91%)	11 (9%)	0	100	100
14	L	141/144 (98%)	113 (80%)	28 (20%)	0	100	100
15	M	134/136 (98%)	125 (93%)	9 (7%)	0	100	100
16	N	118/127 (93%)	108 (92%)	10 (8%)	0	100	100
17	O	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
18	P	112/115 (97%)	107 (96%)	5 (4%)	0	100	100
19	Q	115/118 (98%)	112 (97%)	3 (3%)	0	100	100
20	R	101/103 (98%)	92 (91%)	8 (8%)	1 (1%)	13	47
21	S	108/110 (98%)	99 (92%)	8 (7%)	1 (1%)	14	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	T	91/100 (91%)	85 (93%)	6 (7%)	0	100	100
23	U	100/104 (96%)	91 (91%)	9 (9%)	0	100	100
24	V	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
25	W	73/84 (87%)	68 (93%)	5 (7%)	0	100	100
26	X	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
27	Y	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
28	Z	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
29	b	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
30	c	48/55 (87%)	44 (92%)	4 (8%)	0	100	100
31	d	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
32	e	62/65 (95%)	56 (90%)	6 (10%)	0	100	100
33	f	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
34	g	216/241 (90%)	199 (92%)	17 (8%)	0	100	100
35	h	204/206 (99%)	198 (97%)	6 (3%)	0	100	100
36	i	203/206 (98%)	182 (90%)	21 (10%)	0	100	100
37	j	155/167 (93%)	135 (87%)	19 (12%)	1 (1%)	22	58
38	k	98/135 (73%)	83 (85%)	15 (15%)	0	100	100
39	l	149/179 (83%)	138 (93%)	11 (7%)	0	100	100
40	m	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
41	n	125/130 (96%)	102 (82%)	22 (18%)	1 (1%)	16	53
42	o	96/103 (93%)	80 (83%)	15 (16%)	1 (1%)	13	47
43	p	114/129 (88%)	100 (88%)	14 (12%)	0	100	100
44	q	120/124 (97%)	108 (90%)	12 (10%)	0	100	100
45	r	112/118 (95%)	99 (88%)	13 (12%)	0	100	100
46	s	99/102 (97%)	85 (86%)	14 (14%)	0	100	100
47	t	86/89 (97%)	80 (93%)	5 (6%)	1 (1%)	11	43
48	u	80/82 (98%)	72 (90%)	8 (10%)	0	100	100
49	v	78/84 (93%)	68 (87%)	10 (13%)	0	100	100
50	w	63/75 (84%)	54 (86%)	9 (14%)	0	100	100
51	x	77/92 (84%)	72 (94%)	5 (6%)	0	100	100
52	y	83/87 (95%)	80 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	z	63/71 (89%)	48 (76%)	15 (24%)	0	100	100
All	All	5514/5816 (95%)	5017 (91%)	491 (9%)	6 (0%)	50	81

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
47	t	46	LYS
37	j	122	VAL
41	n	91	GLU
42	o	34	ALA
21	S	64	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	B	216/218 (99%)	216 (100%)	0	100	100
7	C	164/164 (100%)	164 (100%)	0	100	100
8	D	165/165 (100%)	165 (100%)	0	100	100
9	E	148/150 (99%)	148 (100%)	0	100	100
10	F	137/138 (99%)	137 (100%)	0	100	100
11	G	114/114 (100%)	114 (100%)	0	100	100
12	J	116/116 (100%)	116 (100%)	0	100	100
13	K	103/104 (99%)	103 (100%)	0	100	100
14	L	102/103 (99%)	102 (100%)	0	100	100
15	M	109/109 (100%)	109 (100%)	0	100	100
16	N	100/103 (97%)	100 (100%)	0	100	100
17	O	86/87 (99%)	86 (100%)	0	100	100
18	P	99/100 (99%)	99 (100%)	0	100	100
19	Q	89/90 (99%)	89 (100%)	0	100	100
20	R	84/84 (100%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	S	93/93 (100%)	93 (100%)	0	100	100
22	T	80/84 (95%)	80 (100%)	0	100	100
23	U	83/85 (98%)	83 (100%)	0	100	100
24	V	78/78 (100%)	78 (100%)	0	100	100
25	W	57/62 (92%)	57 (100%)	0	100	100
26	X	67/68 (98%)	67 (100%)	0	100	100
27	Y	55/55 (100%)	55 (100%)	0	100	100
28	Z	48/49 (98%)	48 (100%)	0	100	100
29	b	47/48 (98%)	47 (100%)	0	100	100
30	c	45/49 (92%)	45 (100%)	0	100	100
31	d	38/38 (100%)	38 (100%)	0	100	100
32	e	51/52 (98%)	51 (100%)	0	100	100
33	f	34/34 (100%)	34 (100%)	0	100	100
34	g	180/199 (90%)	180 (100%)	0	100	100
35	h	170/170 (100%)	170 (100%)	0	100	100
36	i	172/173 (99%)	172 (100%)	0	100	100
37	j	114/126 (90%)	114 (100%)	0	100	100
38	k	87/116 (75%)	87 (100%)	0	100	100
39	l	124/147 (84%)	124 (100%)	0	100	100
40	m	104/105 (99%)	104 (100%)	0	100	100
41	n	105/107 (98%)	105 (100%)	0	100	100
42	o	86/90 (96%)	86 (100%)	0	100	100
43	p	89/99 (90%)	89 (100%)	0	100	100
44	q	102/103 (99%)	102 (100%)	0	100	100
45	r	92/96 (96%)	92 (100%)	0	100	100
46	s	79/84 (94%)	79 (100%)	0	100	100
47	t	76/77 (99%)	76 (100%)	0	100	100
48	u	65/65 (100%)	65 (100%)	0	100	100
49	v	74/78 (95%)	74 (100%)	0	100	100
50	w	48/65 (74%)	48 (100%)	0	100	100
51	x	70/79 (89%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	y	65/66 (98%)	65 (100%)	0	100	100
53	z	44/61 (72%)	44 (100%)	0	100	100
All	All	4554/4746 (96%)	4554 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
42	o	58	ASN
44	q	77	HIS
51	x	51	HIS
22	T	92	ASN
21	S	9	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2898/2904 (99%)	547 (18%)	58 (2%)
2	2	1530/1540 (99%)	233 (15%)	14 (0%)
3	3	119/120 (99%)	17 (14%)	4 (3%)
4	4	3/18 (16%)	0	0
5	5	76/77 (98%)	31 (40%)	5 (6%)
All	All	4626/4659 (99%)	828 (17%)	81 (1%)

5 of 828 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	12	U
1	1	26	G
1	1	34	U
1	1	35	G

5 of 81 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2893	A
2	2	1432	G
2	2	86	G

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Mol	Chain	Res	Type
2	2	1182	G
3	3	108	A

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
44	0TD	q	89	44	8,9,10	1.54	1 (12%)	6,11,13	1.14	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
44	0TD	q	89	44	-	3/7/12/14	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	q	89	0TD	CB-CA	-2.14	1.54	1.54

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
44	q	89	0TD	CG-CB-SB-CSB
44	q	89	0TD	SB-CB-CG-OD1
44	q	89	0TD	SB-CB-CG-OD2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
44	q	89	0TD	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 281 ligands modelled in this entry, 281 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.

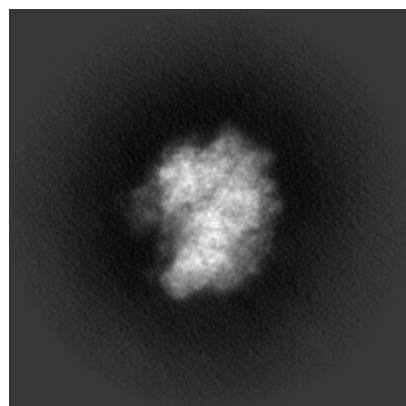
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42852. These allow visual inspection of the internal detail of the map and identification of artifacts.

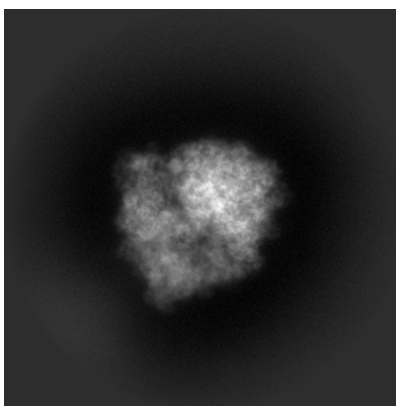
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

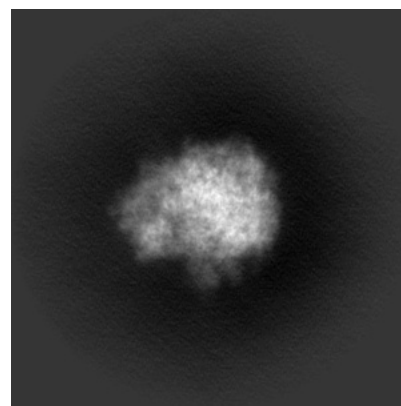
6.1.1 Primary map



X

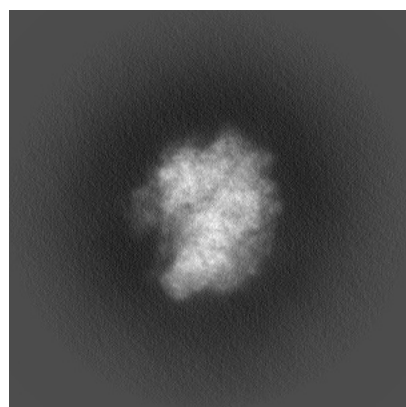


Y

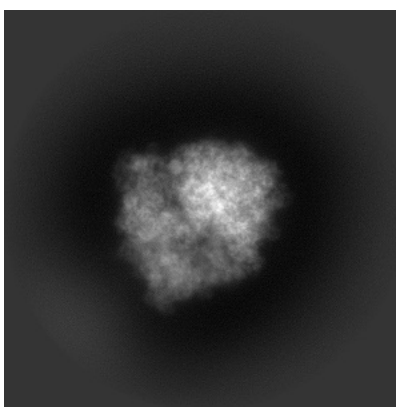


Z

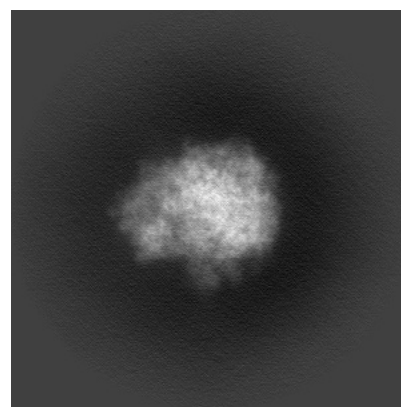
6.1.2 Raw map



X



Y

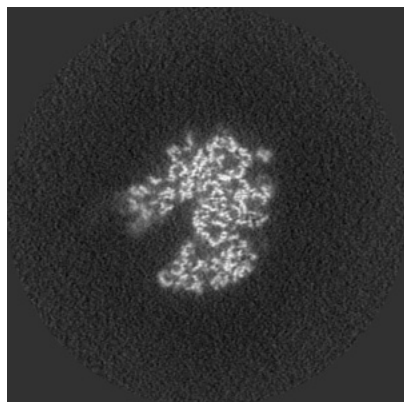


Z

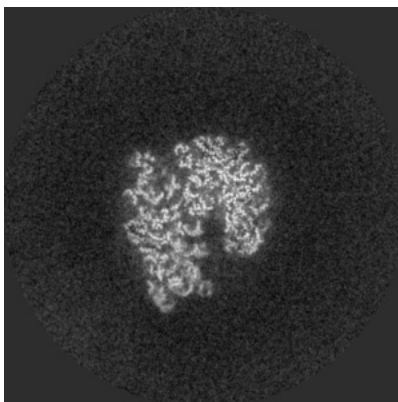
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

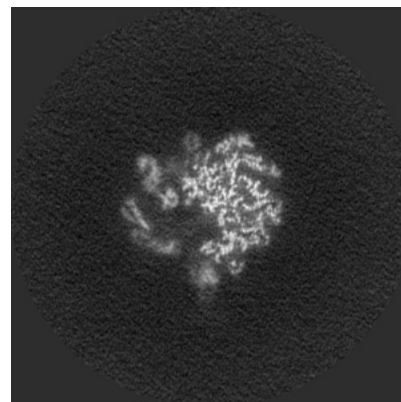
6.2.1 Primary map



X Index: 256

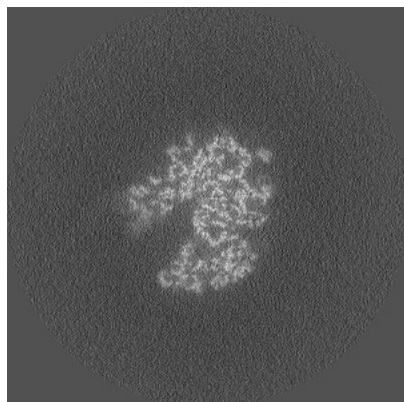


Y Index: 256

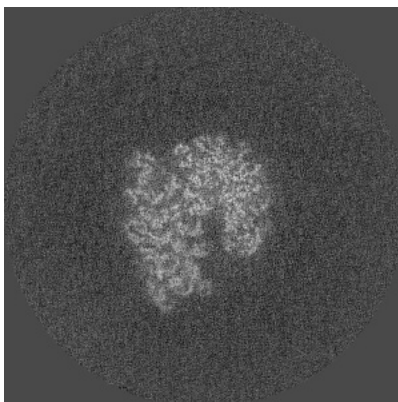


Z Index: 256

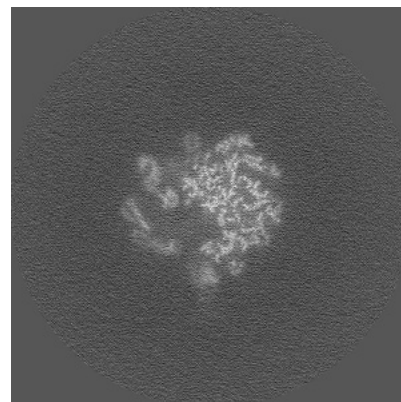
6.2.2 Raw map



X Index: 256



Y Index: 256

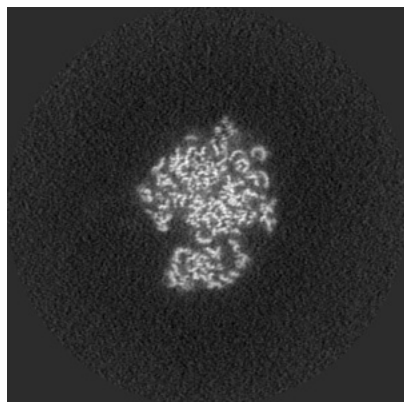


Z Index: 256

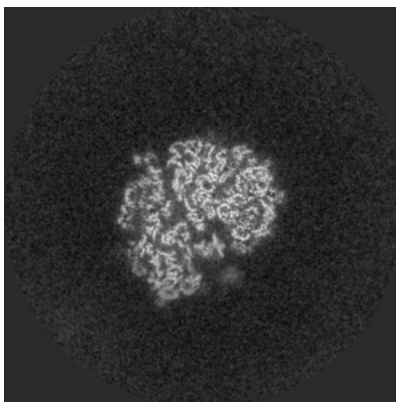
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

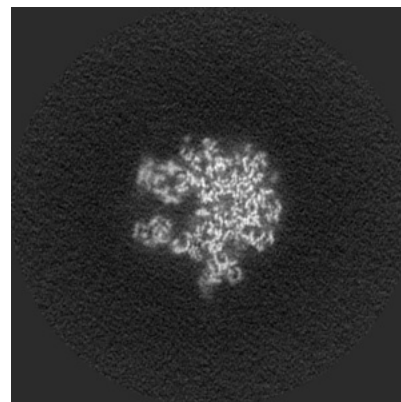
6.3.1 Primary map



X Index: 271

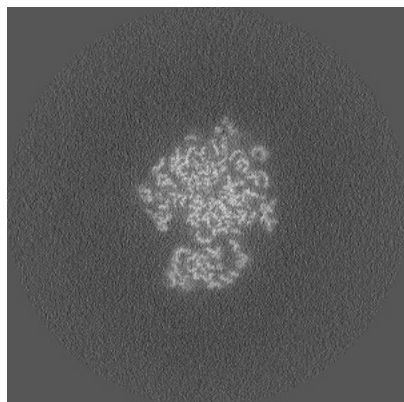


Y Index: 267

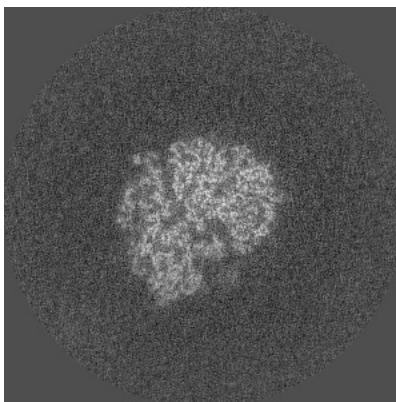


Z Index: 274

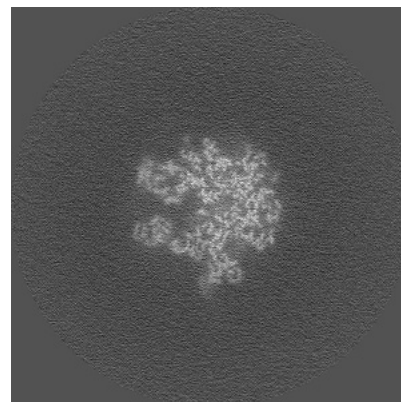
6.3.2 Raw map



X Index: 271



Y Index: 266

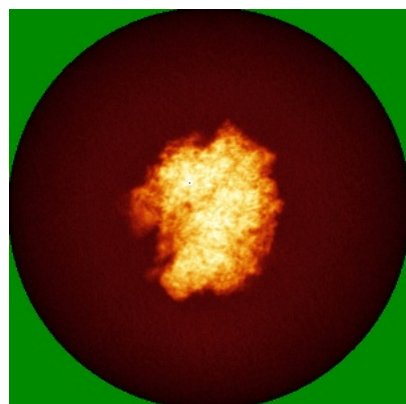


Z Index: 273

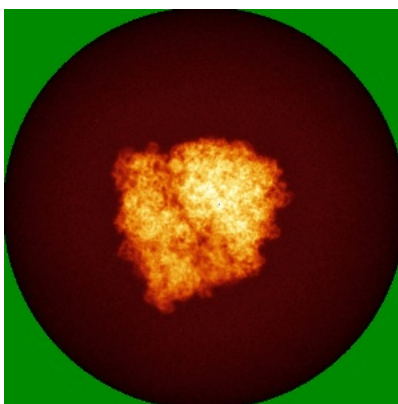
The images above show the largest variance slices of the map in three orthogonal directions.

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

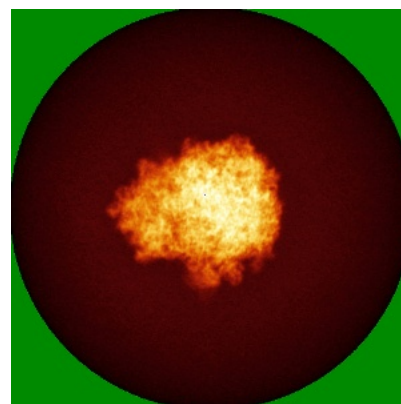
6.4.1 Primary map



X

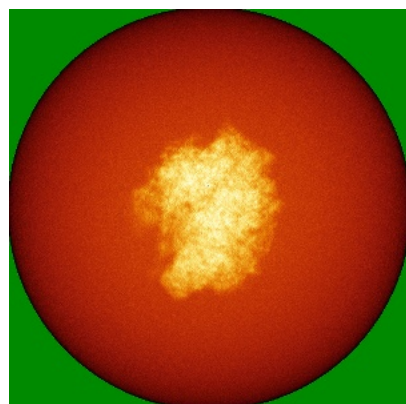


Y

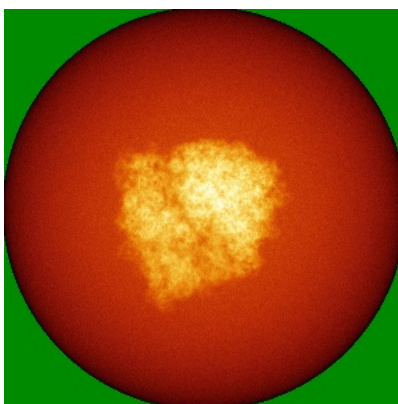


Z

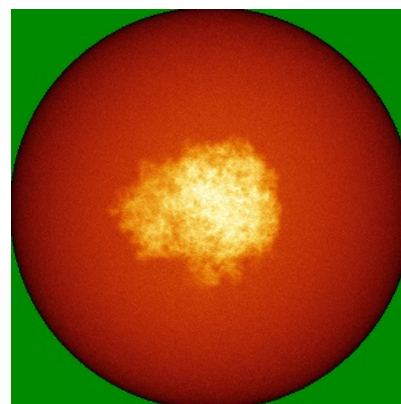
6.4.2 Raw map



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



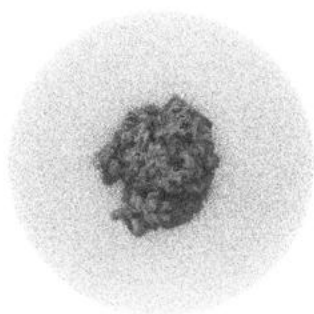
Y



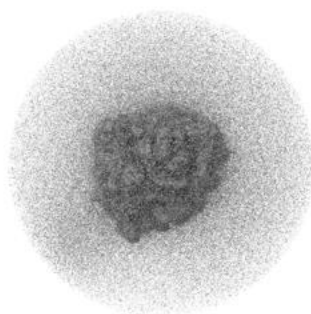
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0289. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

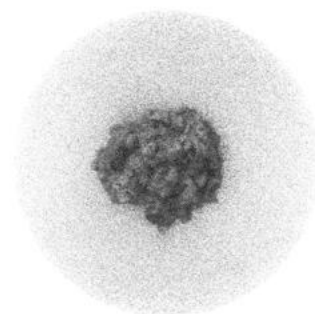
6.5.2 Raw map



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.

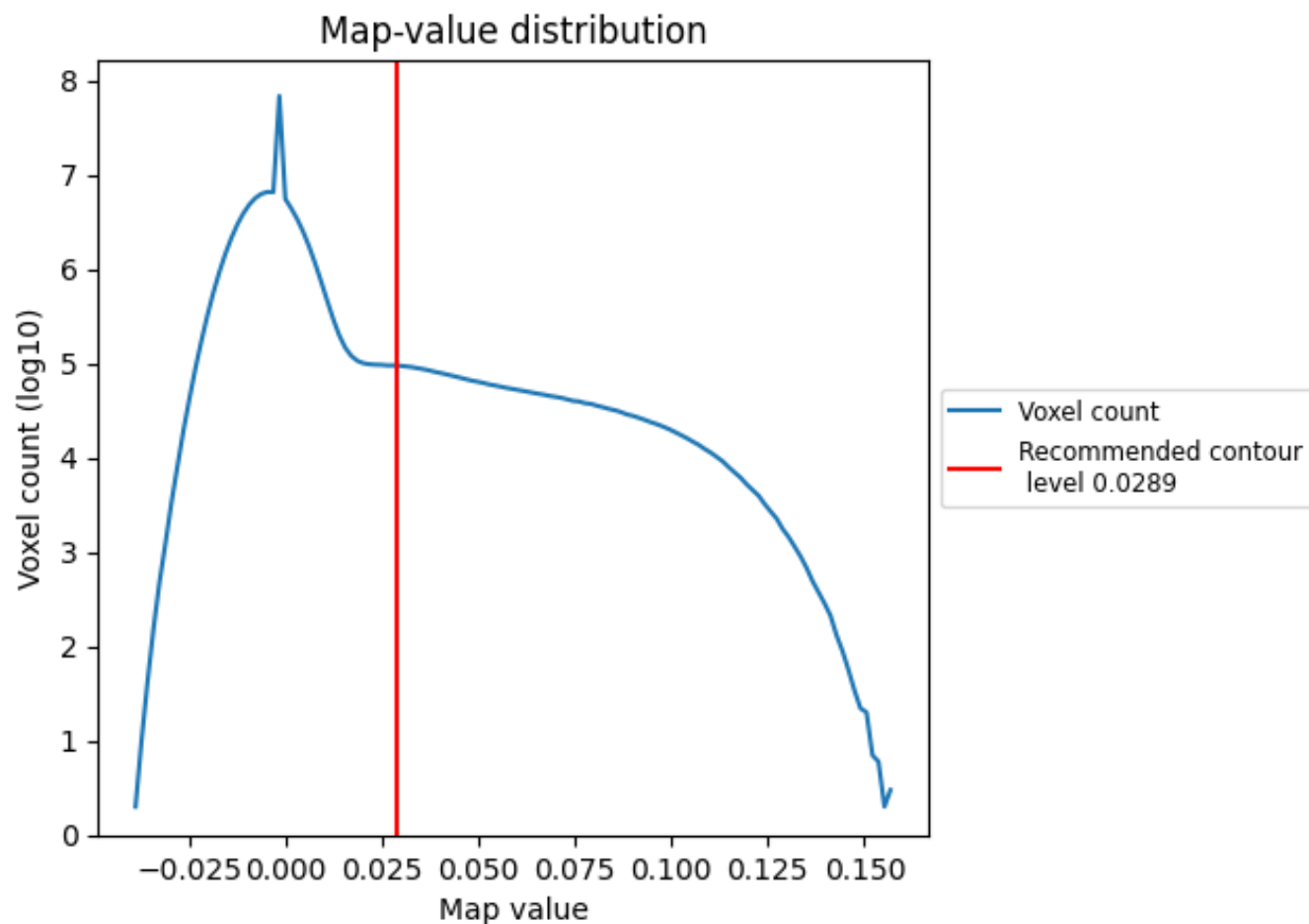
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

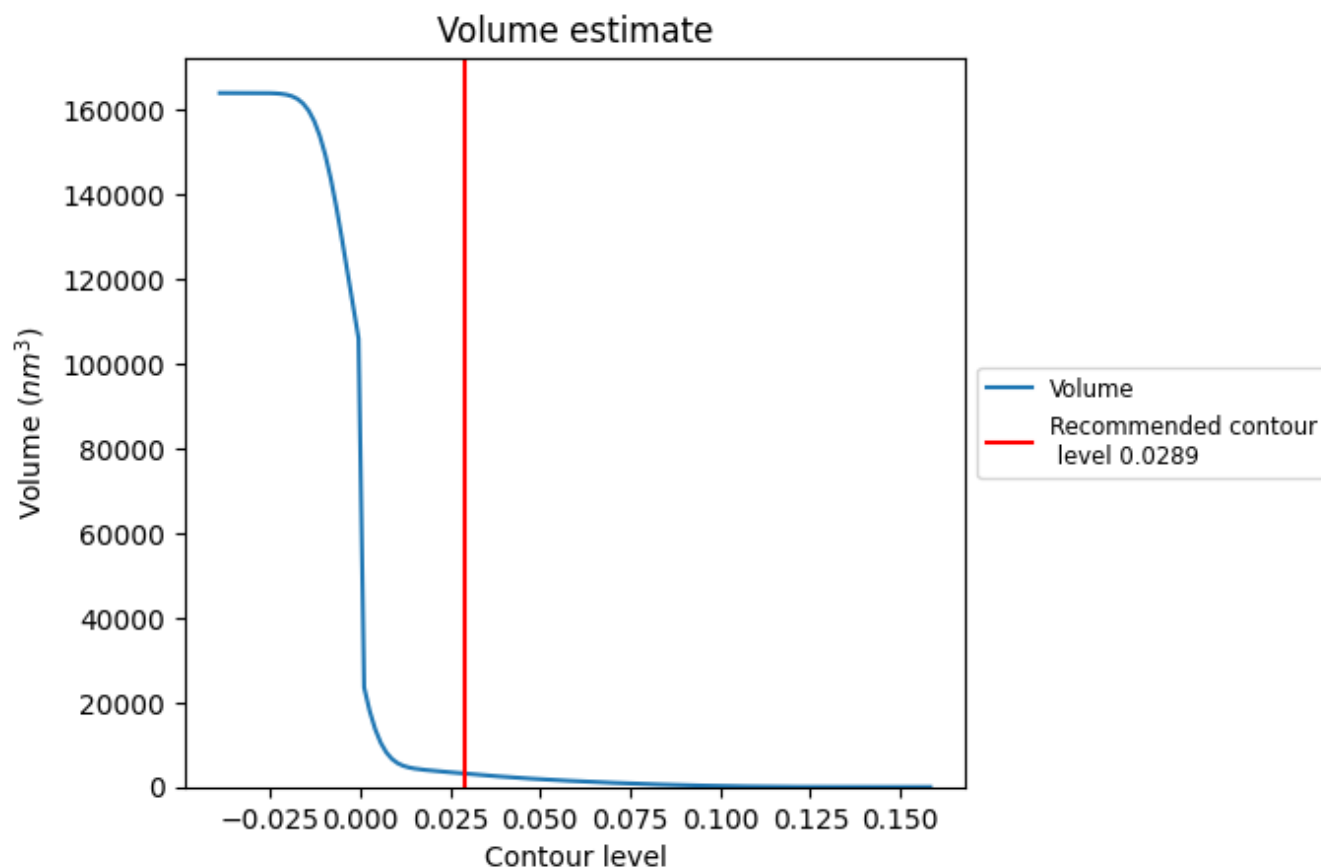
This section contains the results of statistical analysis of the map.

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.

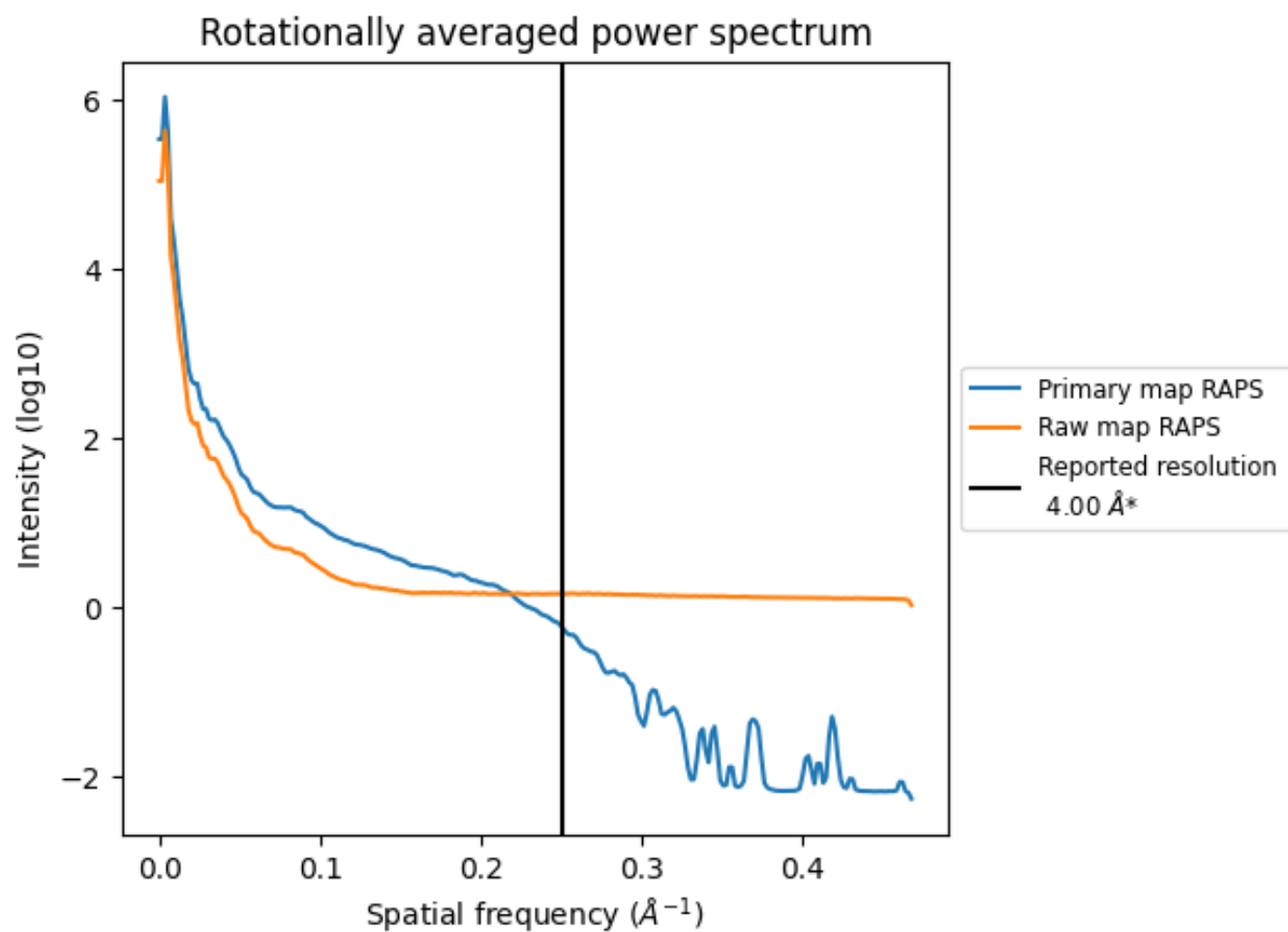
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3177 nm³; this corresponds to an approximate mass of 2870 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 ⓘ

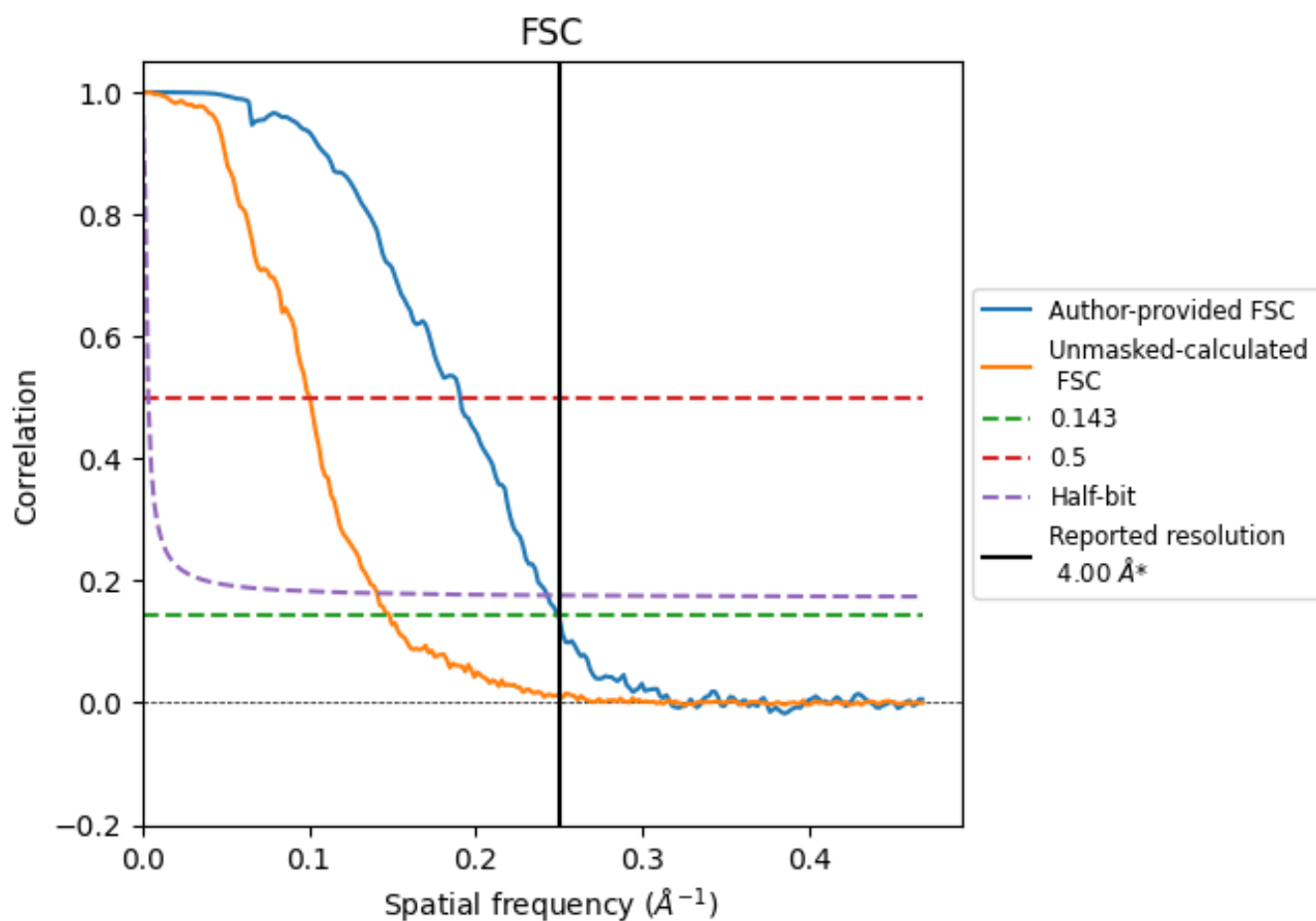


*Reported resolution corresponds to spatial frequency of 0.250 \AA^{-1}

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

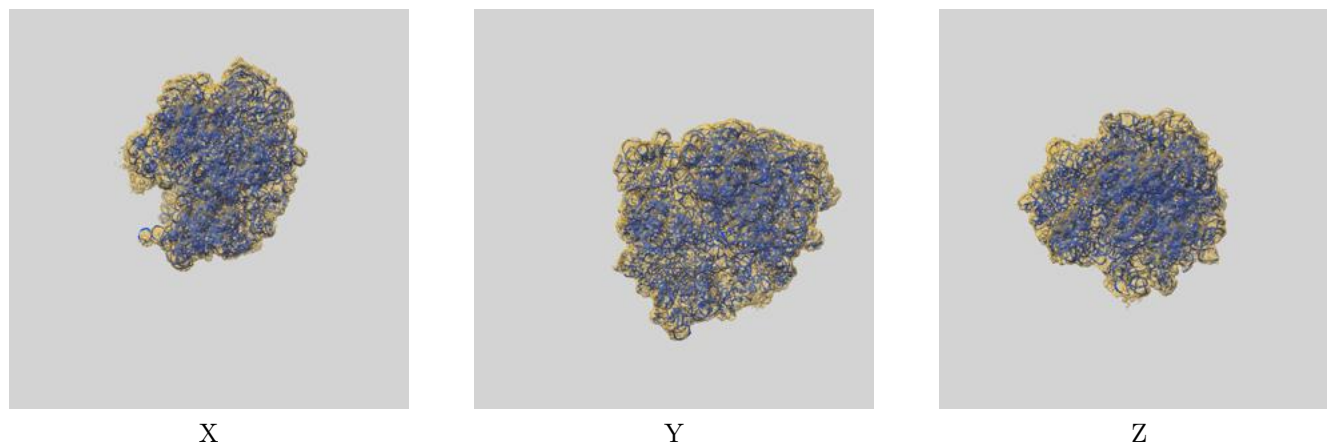
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	4.01	5.24	4.12
Unmasked-calculated*	6.75	9.95	7.10

*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 6.75 differs from the reported value 4.0 by more than 10 %

9 Map-model fit [i](#)

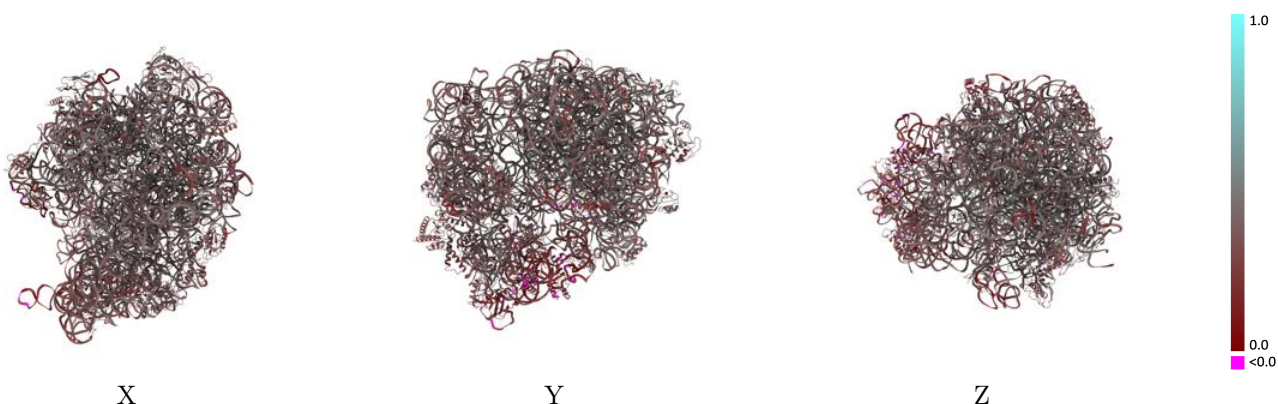
This section contains information regarding the fit between EMDB map EMD-42852 and PDB model 8V03. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



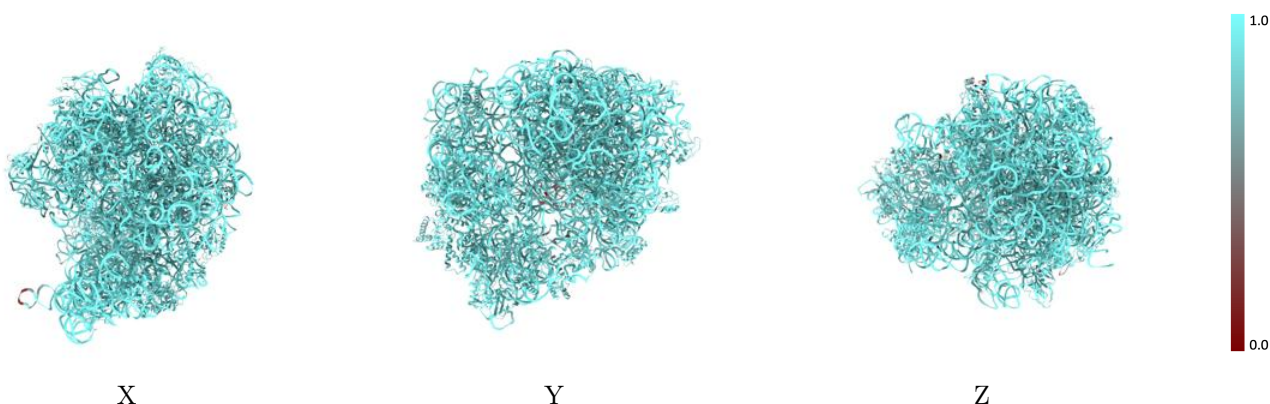
The images above show the 3D surface view of the map at the recommended contour level 0.0289 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



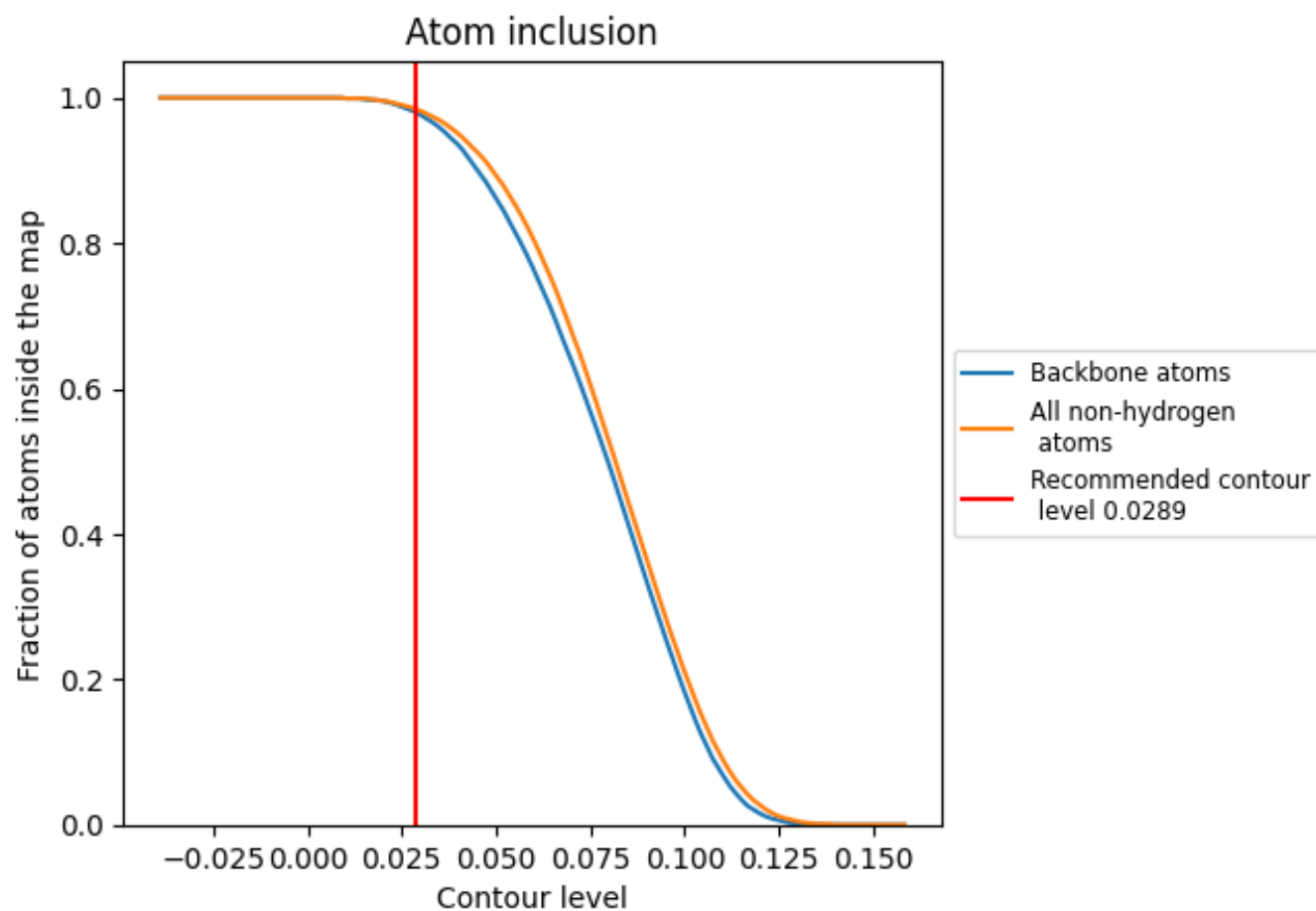
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0289).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.0289) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9840	 0.3570
1	 0.9950	 0.3800
2	 0.9920	 0.3390
3	 0.9980	 0.3640
4	 1.0000	 0.3340
5	 0.9990	 0.3320
B	 0.9990	 0.4220
C	 0.9830	 0.4060
D	 0.9670	 0.3840
E	 0.9580	 0.2610
F	 0.9430	 0.3390
G	 0.6990	 0.2460
J	 0.9900	 0.3830
K	 0.9900	 0.4080
L	 0.9690	 0.3940
M	 0.9950	 0.3990
N	 0.9980	 0.3910
O	 0.9640	 0.3510
P	 0.9790	 0.3850
Q	 0.9870	 0.3610
R	 0.9590	 0.4000
S	 0.9830	 0.3830
T	 0.9790	 0.3840
U	 0.9820	 0.3700
V	 0.9550	 0.3560
W	 0.9960	 0.4070
X	 0.9820	 0.3750
Y	 0.9440	 0.3040
Z	 0.9680	 0.3950
b	 0.9930	 0.3910
c	 0.9800	 0.3940
d	 1.0000	 0.4050
e	 1.0000	 0.4010
f	 0.9970	 0.3840
g	 0.8600	 0.2800



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Chain	Atom inclusion	Q-score
h	 0.9690	 0.2970
i	 0.9760	 0.2620
j	 0.9920	 0.3660
k	 0.9330	 0.3190
l	 0.9440	 0.1630
m	 0.9620	 0.3710
n	 0.9400	 0.2020
o	 0.9380	 0.2790
p	 0.9860	 0.3710
q	 0.9860	 0.3580
r	 0.9150	 0.1870
s	 0.9870	 0.2780
t	 0.9840	 0.3400
u	 0.9860	 0.3540
v	 0.9730	 0.3450
w	 0.9900	 0.3310
x	 0.9470	 0.1700
y	 0.9880	 0.2890
z	 0.9600	 0.2670