



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2026 – 01:47 pm BST

PDB ID : 7OT5 / pdb_00007ot5
EMDB ID : EMD-13055
Title : CspA-70 cotranslational folding intermediate 1
Authors : Agirrezabala, X.; Samatova, E.; Macher, M.; Liutkute, M.; Gil-Carton, D.;
Novacek, J.; Valle, M.; Rodnina, M.V.
Deposited on : 2021-06-09
Resolution : 2.90 Å(reported)
Based on initial model : 6ORE

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

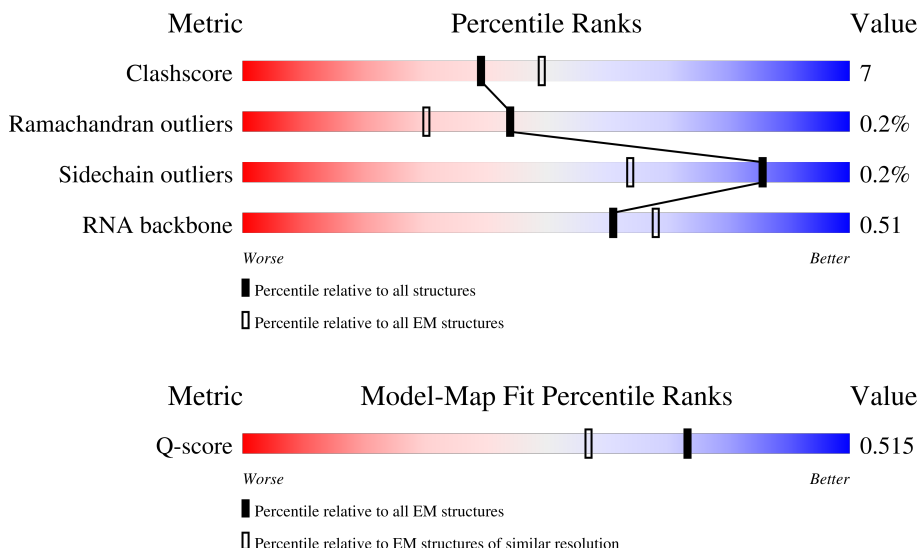
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	2903	 67% 27% 5%
2	2	1534	 67% 28% 5%
3	3	120	 75% 22% 3%

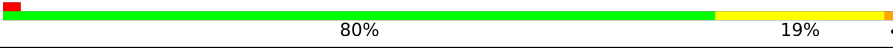
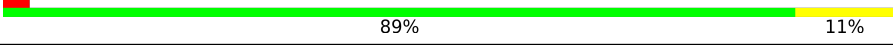
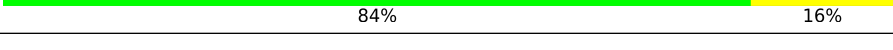
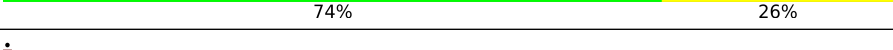
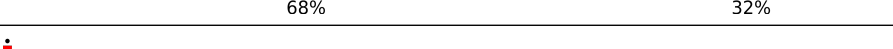
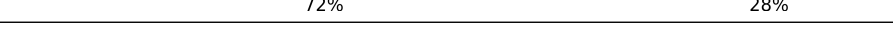
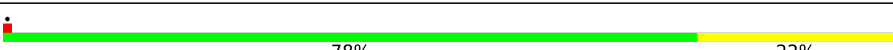
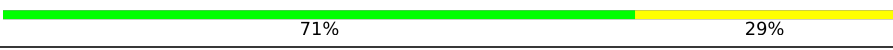
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Mol	Chain	Length	Quality of chain
4	C	271	
5	D	209	
6	E	201	
7	F	177	
8	G	175	
9	H	149	
10	I	142	
11	J	123	
12	K	144	
13	L	136	
14	M	119	
15	N	116	
16	O	114	
17	P	117	
18	Q	103	
19	R	110	
20	S	94	
21	T	103	
22	U	94	
23	V	81	
24	W	77	
25	X	62	
26	Y	58	
27	Z	66	
28	a	56	

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Mol	Chain	Length	Quality of chain
29	b	52	 90% 10%
30	c	46	 74% 26%
31	d	64	 80% 19%
32	e	38	 89% 11%
33	f	225	 65% 35%
34	g	208	 72% 28%
35	h	205	 84% 16%
36	i	156	 74% 26%
37	j	104	 68% 32%
38	k	151	 72% 28%
39	l	129	 80% 20%
40	m	127	 76% 24%
41	n	99	 62% 38%
42	o	117	 81% 19%
43	p	123	 76% 23%
44	q	116	 78% 22%
45	r	100	 75% 25%
46	s	88	 83% 16%
47	t	82	 83% 17%
48	u	80	 72% 28%
49	v	66	 89% 11%
50	w	83	 71% 29%
51	x	86	 74% 26%
52	y	70	 9% 69% 31%
53	4	6	 67% 17% 17%

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Mol	Chain	Length	Quality of chain
54	z	85	47% 22% 24% 7%
55	B	66	5% 30% 64% 5%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 145365 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2903	Total	C	N	O	P	0	0
			62336	27816	11470	20147	2903		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1534	Total	C	N	O	P	0	0
			32929	14693	6041	10661	1534		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a protein called 50S ribosomal protein L2.

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

- Molecule 5 is a protein called 50S ribosomal protein L3.

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

- Molecule 6 is a protein called 50S ribosomal protein L4.

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

- Molecule 7 is a protein called 50S ribosomal protein L5.

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

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 9 is a protein called 50S ribosomal protein L9.

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

- Molecule 10 is a protein called 50S ribosomal protein L13.

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

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 13 is a protein called 50S ribosomal protein L16.

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

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 15 is a protein called 50S ribosomal protein L18.

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

- Molecule 16 is a protein called 50S ribosomal protein L19.

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

- Molecule 17 is a protein called 50S ribosomal protein L20.

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

- Molecule 18 is a protein called 50S ribosomal protein L21.

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

- Molecule 19 is a protein called 50S ribosomal protein L22.

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

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 21 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	103	Total	C	N	O		
			788	498	148	142	0	0

- Molecule 22 is a protein called 50S ribosomal protein L25.

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

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	81	Total	C	N	O	S		
			610	376	123	110	1	0	0

- Molecule 24 is a protein called 50S ribosomal protein L28.

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

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	62	Total	C	N	O	S		
			501	308	98	94	1	0	0

- Molecule 26 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	58	Total	C	N	O	S		
			448	281	87	78	2	0	0

- Molecule 27 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	66	Total	C	N	O	S		
			522	323	99	94	6	0	0

- Molecule 28 is a protein called 50S ribosomal protein L32.

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

- Molecule 29 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	52	Total	C	N	O	S	0	0
			426	275	78	73			

- Molecule 30 is a protein called 50S ribosomal protein L34.

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

- Molecule 31 is a protein called 50S ribosomal protein L35.

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

- Molecule 32 is a protein called 50S ribosomal protein L36.

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

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 35 is a protein called 30S ribosomal protein S4.

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

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 38 is a protein called 30S ribosomal protein S7.

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

- Molecule 39 is a protein called 30S ribosomal protein S8.

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

- Molecule 40 is a protein called 30S ribosomal protein S9.

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

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	n	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 43 is a protein called 30S ribosomal protein S12.

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

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 45 is a protein called 30S ribosomal protein S14.

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

- Molecule 46 is a protein called 30S ribosomal protein S15.

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

- Molecule 47 is a protein called 30S ribosomal protein S16.

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

- Molecule 48 is a protein called 30S ribosomal protein S17.

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

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 50 is a protein called Ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 52 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	y	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	4	6	Total	C	N	O	P	0	0
			122	55	17	44	6		

- Molecule 54 is a RNA chain called tRNA-Leu.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	z	85	Total	C	N	O	P	0	0
			1830	822	328	595	85		

- Molecule 55 is a protein called Cold shock protein CspB.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	B	66	Total	C	N	O	S	0	0
			496	316	81	98	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	45	LYS	LEU	conflict	UNP A0A7U8W1U7
B	61	ALA	GLY	conflict	UNP A0A7U8W1U7

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	1	261	Total 261	Mg 261	0
56	2	113	Total 113	Mg 113	0
56	3	8	Total 8	Mg 8	0
56	C	1	Total 1	Mg 1	0
56	D	2	Total 2	Mg 2	0
56	P	1	Total 1	Mg 1	0
56	T	1	Total 1	Mg 1	0
56	a	2	Total 2	Mg 2	0
56	h	1	Total 1	Mg 1	0
56	m	1	Total 1	Mg 1	0
56	q	1	Total 1	Mg 1	0
56	z	2	Total 2	Mg 2	0

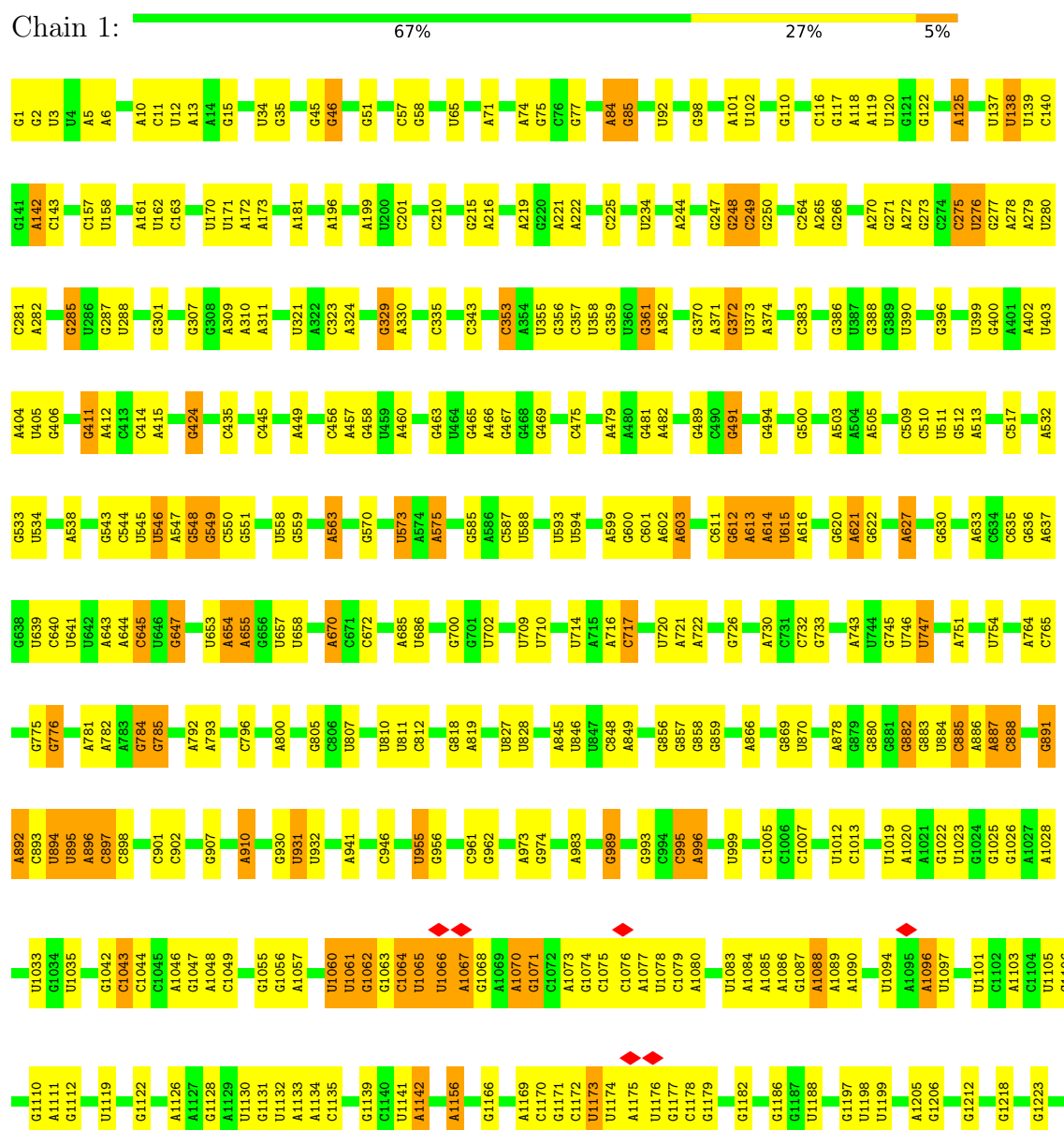
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	Z	1	Total 1	Zn 1	0
57	e	1	Total 1	Zn 1	0

3 Residue-property plots

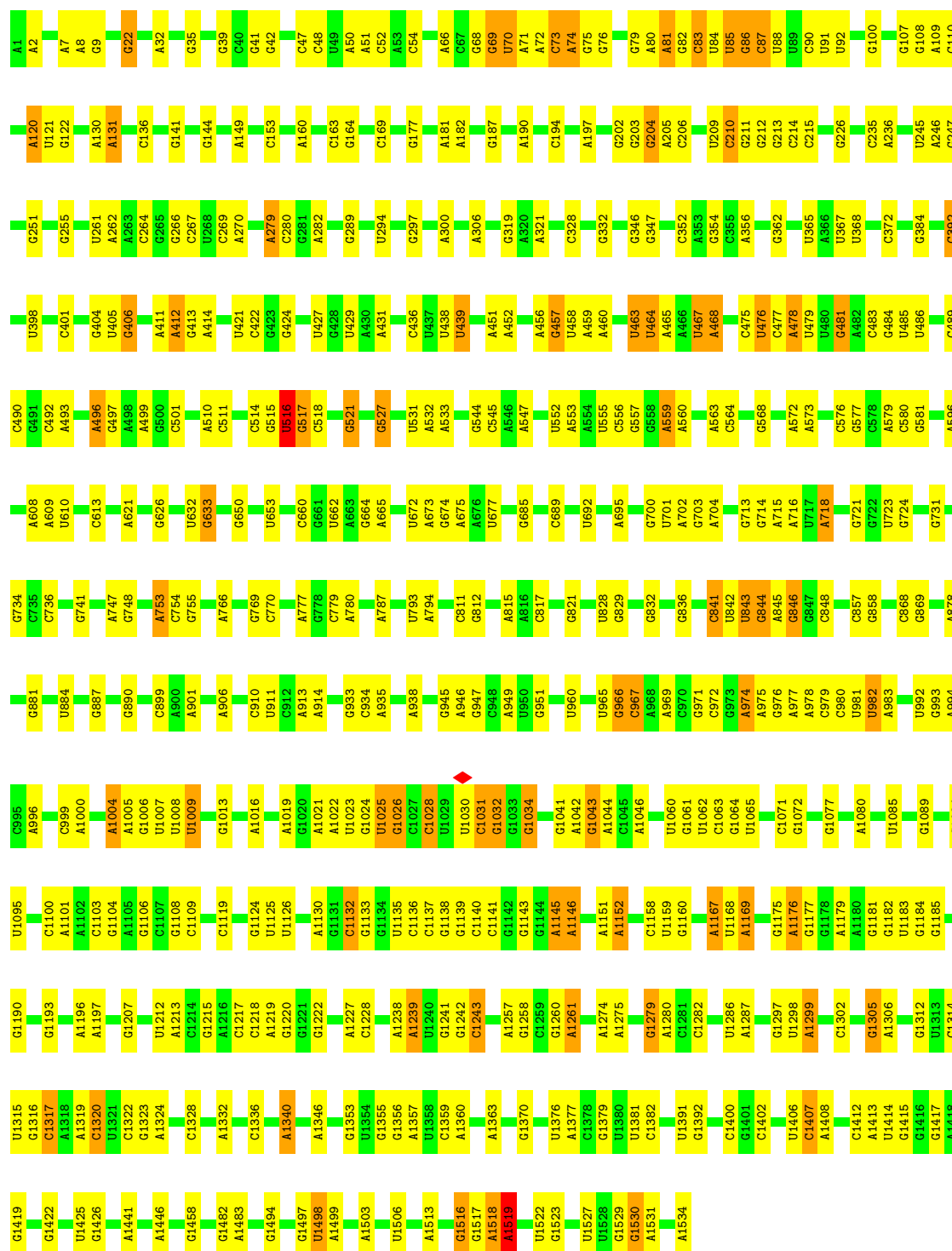
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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



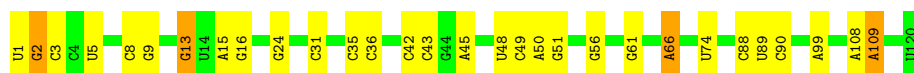
G2819	A1231	A1508	A1630	G1797	G1929	G2079	U2149	U2335	U2330	A2430	U2562	U2690	G2819
A2820	G1232	A1509	G1631	U1798	G1930	A2080	C2150	U2336	U2321	U2431	U2563	U2698	A2820
G2821	G1236	A1632	G1632	G1799	U1939	U2081	U2151	G2337	A2322	A2435	U2564	U2699	G2821
A2822	A1237	A1383	G1633	C1800	A1936	A2082	G2152	G2338	G2325	A2441	U2565	G2702	A2822
C2823	G1238	A1244	A1634	A1515	A1937	U2092	G2157	G2339	G2326	U2441	U2566	U2702	C2823
C2824	A1247	A1392	A1637	G1524	A1808	G2093	A2158	U2243	A2327	G2445	A2566	G2714	C2824
G2825	A1248	A1392	U1647	G1529	A1809	A2094	G2159	G2246	A2328	A2448	U2567	G2715	G2825
G2831	G1408	G1408	U1648	G1530	A1810	A2095	C2160	G2247	U2329	U2449	G2567	C2716	G2831
G2832	U1249	U1249	G1649	C1531	G1811	G2096	C2161	G2248	A2333	U2450	G2570	C2717	G2832
A2833	G1250	U1411	U1650	A1532	G1816	A2097	C2162	U2249	U2334	A2451	U2571	G2718	A2833
U2836	A1253	U1534	G1651	C1533	G1817	U2098	C2163	G2250	A2335	U2457	C2572	U2725	U2836
G2839	G1417	U1535	A1652	U1534	U1818	U2099	C2164	G2251	A2336	U2457	C2573	A2726	G2839
U2847	A1536	A1536	U1659	A1536	U1827	G2100	U2166	G2252	U2343	C2467	C2574	A2727	U2847
G2848	C1537	C1537	G1659	C1536	G1828	A2101	G2168	G2253	U2344	A2468	U2575	U2728	G2848
U2849	G1538	G1538	A1664	U1538	A1829	C2103	A2169	C2258	G2345	A2469	U2580	G2729	U2849
U2861	G1421	A1544	A1668	A1544	C1833	U2104	A2170	C2264	A2346	G2470	G2581	G2732	U2861
G2867	A1427	U1554	G1674	U1554	U1833	U2106	A2171	U2265	C2347	U2476	U2584	A2733	G2867
A2872	A1432	U1554	G1674	U1554	U1834	U2107	U2172	U2266	U2350	U2477	U2585	U2734	A2872
A2873	A1433	U1554	G1674	U1554	U1835	A2108	A2173	A2267	G2351	A2478	U2586	G2744	A2873
A2879	C1437	U1554	G1674	U1554	U1835	A2109	C2175	A2273	G2357	U2479	U2591	G2747	A2879
C2880	U1438	U1559	U1680	U1559	A1847	G2110	C2176	A2278	A2358	C2480	C2592	G2748	C2880
U2883	A1439	U1563	G1681	U1563	A1848	U2111	C2177	C2278	G2359	U2481	U2592	G2749	U2883
U2884	U1447	U1564	G1715	U1564	U1888	G2112	C2178	C2283	C2360	U2491	A2602	G2751	U2884
G2885	U1451	U1566	G1723	U1566	U1889	U2113	C2179	U2286	G2361	U2497	G2603	G2752	G2885
U2890	U1452	U1569	G1729	U1569	U1890	A2114	U2180	U2287	C2362	C2498	U2604	A2753	U2890
U2891	U1457	U1578	U1729	U1578	U1891	G2115	U2181	U2288	G2363	C2499	U2605	U2754	U2891
U2898	U1460	U1579	C1730	U1579	U1892	G2116	U2182	U2289	U2364	U2500	U2609	C2755	U2898
A2900	U1468	A1580	C1731	A1580	U1893	A2117	A2183	U2291	G2365	U2501	U2613	C2756	A2900
C2901	U1469	U1584	G1732	U1584	U1894	U2118	U2184	U2292	U2366	G2502	A2614	A2757	C2901
C2902	U1470	U1585	G1738	U1585	U1895	A2119	U2185	U2293	U2367	U2503	U2614	A2766	C2902
U2903	U1475	U1586	U1746	U1586	U1896	G2120	U2186	U2294	U2368	U2504	U2629	C2767	U2903
	U1476	U1587	U1747	U1587	U1897	U2121	U2187	U2297	A2376	U2506	U2635	G2777	U2898
	U1482	U1588	U1747	U1588	U1898	U2122	U2188	U2298	U2377	U2507	U2636	A2778	A2900
	U1483	U1589	U1754	U1589	U1899	G2123	U2189	U2299	G2383	C2508	U2637	G2779	A2901
	U1490	U1590	A1755	U1590	U1901	A2124	A2190	U2300	U2384	U2511	G2640	C2788	A2902
	U1493	U1591	G1756	U1591	G1906	A2125	A2191	U2301	U2385	U2512	U2646	C2789	C2903
	A1614	A1591	G1764	A1591	G1907	G2126	U2192	U2302	U2386	U2513	U2647	U2790	
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	A1621	C1606	U1773	C1606	G1907	U2128	U2194	U2304	U2388	U2515	U2649	A2792	
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	A1618	A1618	A1791	A1618	G1907	U2190	U2252	U2362	U2446	U2575			
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Chain 2:  67% 28% 5%



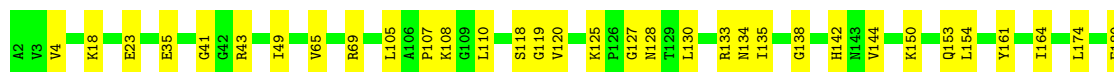
• Molecule 3: 5S rRNA

Chain 3:  75% 22%



- Molecule 4: 50S ribosomal protein L2

Chain C: 82% 18%



- Molecule 5: 50S ribosomal protein L3

Chain D: 86% 12%



- Molecule 6: 50S ribosomal protein L4

Chain E: 84% 16%



- Molecule 7: 50S ribosomal protein L5

Chain F: 70% 30%

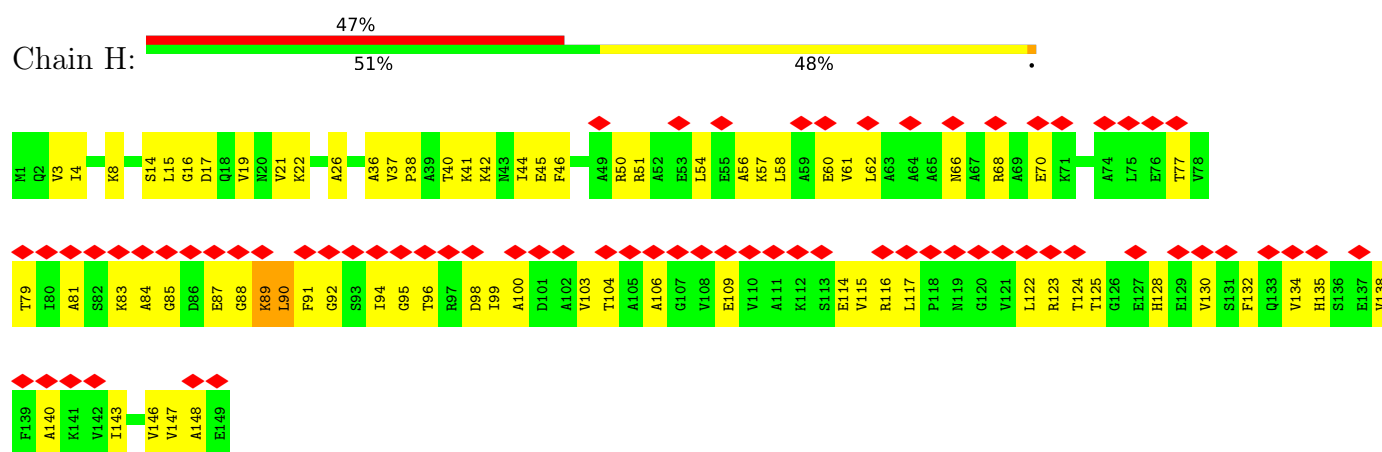


- Molecule 8: 50S ribosomal protein L6

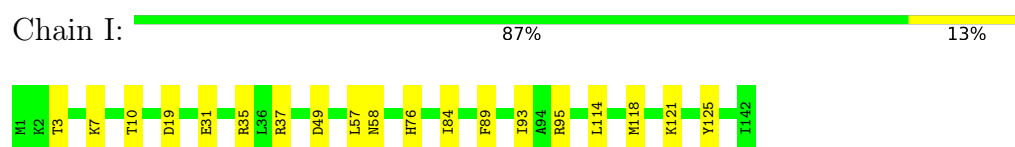
Chain G: 80% 19%



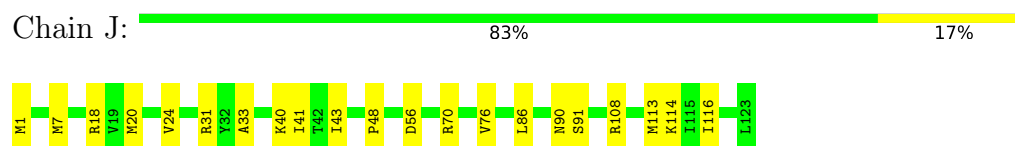
- Molecule 9: 50S ribosomal protein L9



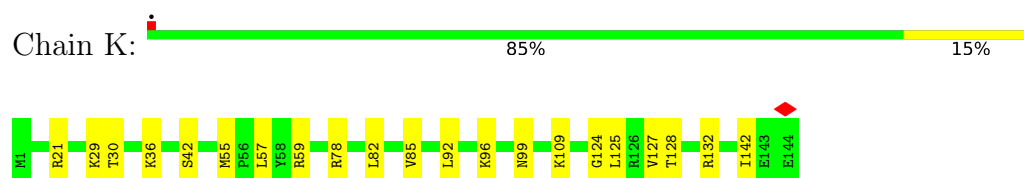
- Molecule 10: 50S ribosomal protein L13



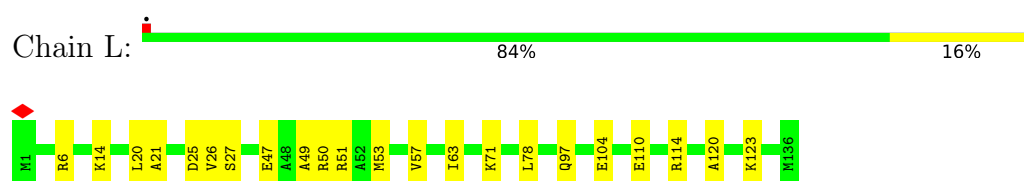
- Molecule 11: 50S ribosomal protein L14



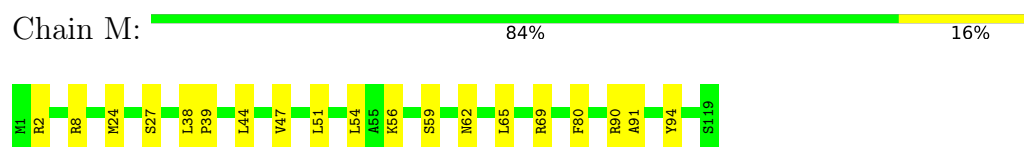
- Molecule 12: 50S ribosomal protein L15



- Molecule 13: 50S ribosomal protein L16



- Molecule 14: 50S ribosomal protein L17



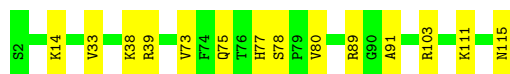
- Molecule 15: 50S ribosomal protein L18

Chain N:  77% 23%



- Molecule 16: 50S ribosomal protein L19

Chain O:  88% 12%



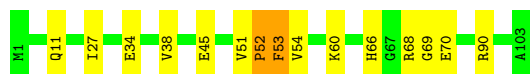
- Molecule 17: 50S ribosomal protein L20

Chain P:  90% 10%



- Molecule 18: 50S ribosomal protein L21

Chain Q:  85% 13% .



- Molecule 19: 50S ribosomal protein L22

Chain R:  72% 28%



- Molecule 20: 50S ribosomal protein L23

Chain S:  82% 18%



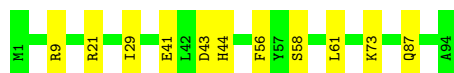
- Molecule 21: Ribosomal protein L24

Chain T:  71% 29%



- Molecule 22: 50S ribosomal protein L25

Chain U:  88% 12%



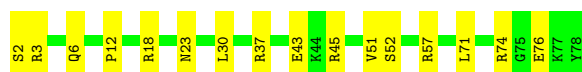
- Molecule 23: 50S ribosomal protein L27

Chain V:  5% 75% 25%



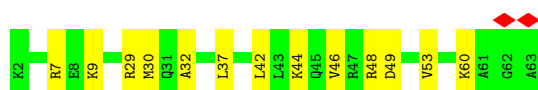
- Molecule 24: 50S ribosomal protein L28

Chain W:  79% 21%



- Molecule 25: 50S ribosomal protein L29

Chain X:  79% 21%



- Molecule 26: 50S ribosomal protein L30

Chain Y:  76% 24%



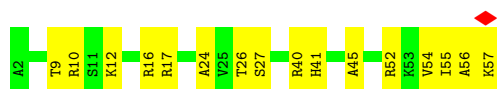
- Molecule 27: 50S ribosomal protein L31

Chain Z:  6% 67% 33%

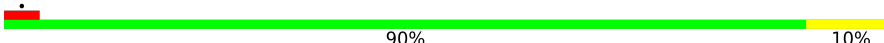


- Molecule 28: 50S ribosomal protein L32

Chain a:  71% 29%



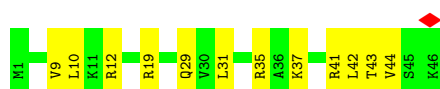
- Molecule 29: 50S ribosomal protein L33

Chain b:  90% 10%



- Molecule 30: 50S ribosomal protein L34

Chain c:  74% 26%



- Molecule 31: 50S ribosomal protein L35

Chain d:  80% 19%



- Molecule 32: 50S ribosomal protein L36

Chain e:  89% 11%



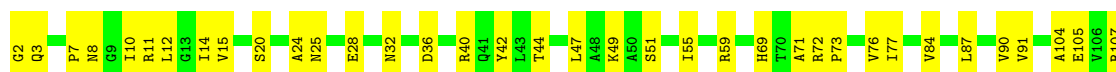
- Molecule 33: 30S ribosomal protein S2

Chain f:  65% 35%



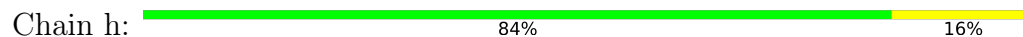
- Molecule 34: 30S ribosomal protein S3

Chain g:  72% 28%





- Molecule 35: 30S ribosomal protein S4



- Molecule 36: 30S ribosomal protein S5



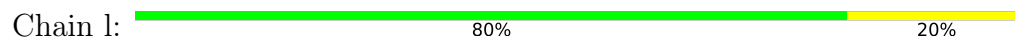
- Molecule 37: 30S ribosomal protein S6



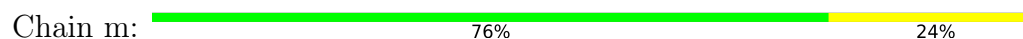
- Molecule 38: 30S ribosomal protein S7



- Molecule 39: 30S ribosomal protein S8

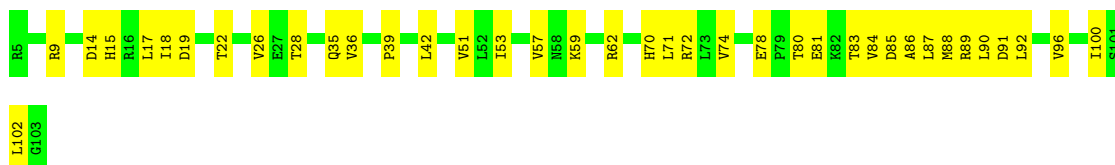


- Molecule 40: 30S ribosomal protein S9

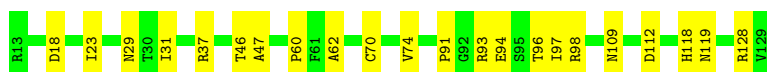
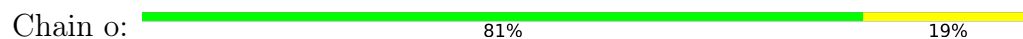




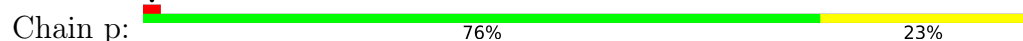
- Molecule 41: 30S ribosomal protein S10



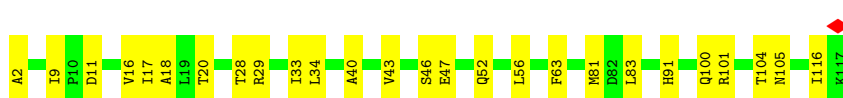
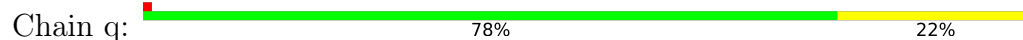
- Molecule 42: 30S ribosomal protein S11



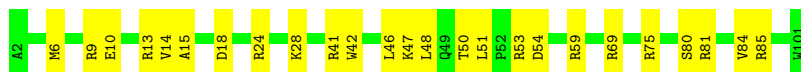
- Molecule 43: 30S ribosomal protein S12



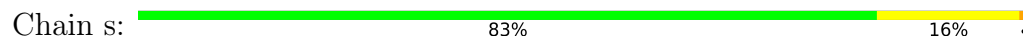
- Molecule 44: 30S ribosomal protein S13



- Molecule 45: 30S ribosomal protein S14

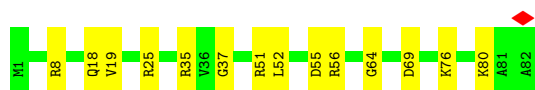


- Molecule 46: 30S ribosomal protein S15



- Molecule 47: 30S ribosomal protein S16

Chain t:  83% 17%



- Molecule 48: 30S ribosomal protein S17

Chain u:  72% 28%



- Molecule 49: 30S ribosomal protein S18

Chain v:  89% 11%



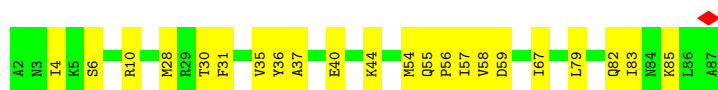
- Molecule 50: Ribosomal protein S19

Chain w:  71% 29%



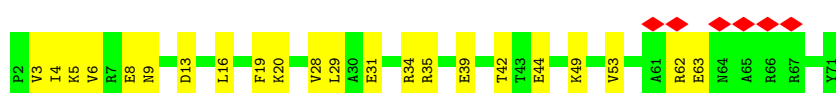
- Molecule 51: 30S ribosomal protein S20

Chain x:  74% 26%



- Molecule 52: 30S ribosomal protein S21

Chain y:  9% 69% 31%

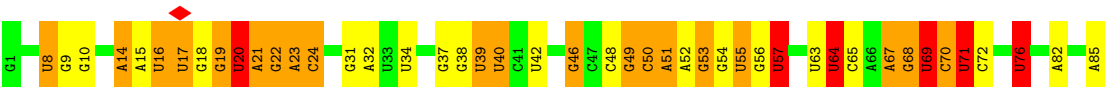


- Molecule 53: mRNA

Chain 4:  67% 17% 17%



● Molecule 54: tRNA-Leu



● Molecule 55: Cold shock protein CspB



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	26765	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.2	Depositor
Minimum defocus (nm)	-500	Depositor
Maximum defocus (nm)	-2200	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.176	Depositor
Minimum map value	-0.055	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	428.00003, 428.00003, 428.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 4OC, 2MG, OMG, 2MA, UR3, MA6, G7M, PSU, MG, 5MU, 0TD, OMC, OMU, ZN, 1MG, 3TD, 6MZ, 5MC

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	0.43	0/69286	0.46	2/108087 (0.0%)
2	2	0.39	0/36590	0.44	0/57074
3	3	0.37	0/2872	0.41	0/4478
4	C	0.57	0/2121	0.54	0/2852
5	D	0.56	0/1586	0.55	0/2134
6	E	0.51	0/1571	0.59	0/2113
7	F	0.44	0/1434	0.60	0/1926
8	G	0.37	0/1333	0.55	0/1805
9	H	0.32	0/1122	0.83	0/1515
10	I	0.55	0/1152	0.54	0/1551
11	J	0.53	0/955	0.53	0/1279
12	K	0.53	0/1062	0.59	0/1413
13	L	0.53	0/1093	0.56	0/1460
14	M	0.57	0/964	0.64	0/1289
15	N	0.48	0/902	0.62	0/1209
16	O	0.52	0/929	0.49	0/1242
17	P	0.62	0/960	0.65	0/1278
18	Q	0.53	0/829	0.62	0/1107
19	R	0.59	0/864	0.62	0/1156
20	S	0.50	0/752	0.52	0/1005
21	T	0.45	0/796	0.53	0/1062
22	U	0.49	0/766	0.57	0/1025
23	V	0.56	0/617	0.52	0/815
24	W	0.53	0/635	0.58	0/848
25	X	0.46	0/502	0.70	0/667
26	Y	0.52	0/452	0.56	0/605
27	Z	0.32	0/531	0.59	0/709
28	a	0.53	0/450	0.58	0/599
29	b	0.43	0/433	0.55	0/576
30	c	0.61	0/380	0.59	0/498
31	d	0.62	0/513	0.66	0/676

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	e	0.53	0/303	0.48	0/397
33	f	0.41	0/1791	0.71	1/2413 (0.0%)
34	g	0.45	0/1663	0.59	0/2241
35	h	0.46	0/1665	0.60	0/2227
36	i	0.51	0/1165	0.62	0/1568
37	j	0.42	0/867	0.64	0/1171
38	k	0.43	0/1195	0.64	0/1602
39	l	0.49	0/989	0.55	0/1326
40	m	0.45	0/1034	0.66	1/1375 (0.1%)
41	n	0.42	0/800	0.71	0/1082
42	o	0.43	0/893	0.61	0/1205
43	p	0.48	0/960	0.57	0/1286
44	q	0.44	0/909	0.63	0/1215
45	r	0.46	0/817	0.61	0/1088
46	s	0.46	0/722	0.60	0/964
47	t	0.48	0/659	0.58	0/884
48	u	0.42	0/657	0.51	0/881
49	v	0.47	0/553	0.58	0/743
50	w	0.40	0/680	0.52	0/915
51	x	0.50	0/675	0.70	0/895
52	y	0.40	0/597	0.66	0/792
53	4	0.47	0/134	0.88	0/205
54	z	0.38	0/1768	0.49	1/2759 (0.0%)
55	B	0.46	0/507	0.80	1/682 (0.1%)
All	All	0.44	0/156455	0.50	6/233969 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	z	67	A	C1'-C2'-O2'	-6.85	101.53	111.80
1	1	2171	A	C1'-C2'-O2'	-6.10	102.66	111.80
1	1	2133	G	N9-C1'-C2'	5.54	122.31	114.00
40	m	54	LEU	N-CA-C	-5.30	105.15	111.03
55	B	53	PHE	CB-CA-C	5.14	118.15	110.08

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	62336	0	31363	512	0
2	2	32929	0	16582	254	0
3	3	2569	0	1299	14	0
4	C	2082	0	2154	34	0
5	D	1565	0	1616	26	0
6	E	1552	0	1619	23	0
7	F	1410	0	1444	51	0
8	G	1313	0	1358	21	0
9	H	1111	0	1148	66	0
10	I	1129	0	1162	13	0
11	J	946	0	1023	16	0
12	K	1053	0	1129	17	0
13	L	1074	0	1157	16	0
14	M	951	0	994	14	0
15	N	892	0	923	22	0
16	O	917	0	962	10	0
17	P	947	0	1019	13	0
18	Q	816	0	839	13	0
19	R	857	0	922	34	0
20	S	746	0	811	13	0
21	T	788	0	844	23	0
22	U	753	0	780	6	0
23	V	610	0	628	15	0
24	W	625	0	652	12	0
25	X	501	0	531	8	0
26	Y	448	0	488	12	0
27	Z	522	0	520	18	0
28	a	444	0	458	13	0
29	b	426	0	464	3	0
30	c	377	0	418	10	0
31	d	504	0	572	13	0
32	e	302	0	340	4	0
33	f	1760	0	1787	76	0
34	g	1636	0	1710	42	0
35	h	1643	0	1706	24	0
36	i	1152	0	1196	34	0
37	j	848	0	846	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	k	1181	0	1238	33	0
39	l	979	0	1031	22	0
40	m	1022	0	1070	22	0
41	n	790	0	831	27	0
42	o	877	0	887	17	0
43	p	957	0	1017	20	0
44	q	900	0	965	27	0
45	r	805	0	844	26	0
46	s	714	0	734	16	0
47	t	649	0	666	10	0
48	u	648	0	691	16	0
49	v	544	0	560	6	0
50	w	663	0	688	23	0
51	x	669	0	719	15	0
52	y	589	0	629	17	0
53	4	122	0	64	2	0
54	z	1830	0	942	47	0
55	B	496	0	475	77	0
56	1	261	0	0	0	0
56	2	113	0	0	0	0
56	3	8	0	0	0	0
56	C	1	0	0	0	0
56	D	2	0	0	0	0
56	P	1	0	0	0	0
56	T	1	0	0	0	0
56	a	2	0	0	0	0
56	h	1	0	0	0	0
56	m	1	0	0	0	0
56	q	1	0	0	0	0
56	z	2	0	0	0	0
57	Z	1	0	0	0	0
57	e	1	0	0	0	0
All	All	145365	0	97515	1674	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 7.

The worst 5 of 1674 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)
1:1:1335:C:HO2'	55:B:5:MET:N	1.31	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:151:THR:HG23	5:D:152:PRO:HD3	1.31	1.08
19:R:69:LEU:HD22	19:R:107:VAL:HG22	1.40	1.01
1:1:621:A:H5'	1:1:621:A:H8	1.27	0.99
2:2:1028:C:C2	2:2:1034:G:N2	2.30	0.99

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	
4	C	269/271 (99%)	257 (96%)	12 (4%)	0	100	100
5	D	207/209 (99%)	201 (97%)	3 (1%)	3 (1%)	9	30
6	E	199/201 (99%)	197 (99%)	2 (1%)	0	100	100
7	F	175/177 (99%)	165 (94%)	9 (5%)	1 (1%)	21	51
8	G	173/175 (99%)	162 (94%)	11 (6%)	0	100	100
9	H	147/149 (99%)	136 (92%)	9 (6%)	2 (1%)	9	30
10	I	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
11	J	121/123 (98%)	119 (98%)	2 (2%)	0	100	100
12	K	142/144 (99%)	139 (98%)	3 (2%)	0	100	100
13	L	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
14	M	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
15	N	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
16	O	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
17	P	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
18	Q	101/103 (98%)	94 (93%)	5 (5%)	2 (2%)	6	22
19	R	108/110 (98%)	107 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	S	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
21	T	101/103 (98%)	93 (92%)	8 (8%)	0	100	100
22	U	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
23	V	79/81 (98%)	72 (91%)	6 (8%)	1 (1%)	9	32
24	W	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
25	X	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
26	Y	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
27	Z	64/66 (97%)	60 (94%)	4 (6%)	0	100	100
28	a	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
29	b	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
30	c	44/46 (96%)	44 (100%)	0	0	100	100
31	d	62/64 (97%)	58 (94%)	4 (6%)	0	100	100
32	e	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
33	f	223/225 (99%)	212 (95%)	11 (5%)	0	100	100
34	g	206/208 (99%)	197 (96%)	9 (4%)	0	100	100
35	h	203/205 (99%)	199 (98%)	4 (2%)	0	100	100
36	i	154/156 (99%)	144 (94%)	10 (6%)	0	100	100
37	j	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
38	k	149/151 (99%)	145 (97%)	4 (3%)	0	100	100
39	l	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
40	m	125/127 (98%)	118 (94%)	7 (6%)	0	100	100
41	n	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
42	o	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
43	p	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
44	q	114/116 (98%)	110 (96%)	4 (4%)	0	100	100
45	r	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
46	s	86/88 (98%)	84 (98%)	2 (2%)	0	100	100
47	t	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
48	u	78/80 (98%)	75 (96%)	3 (4%)	0	100	100
49	v	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
50	w	81/83 (98%)	80 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	x	84/86 (98%)	84 (100%)	0	0	100	100
52	y	68/70 (97%)	67 (98%)	1 (2%)	0	100	100
55	B	64/66 (97%)	46 (72%)	17 (27%)	1 (2%)	7	27
All	All	5677/5778 (98%)	5462 (96%)	205 (4%)	10 (0%)	44	72

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	D	152	PRO
5	D	153	GLY
5	D	154	LYS
9	H	90	LEU
18	Q	52	PRO

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	
4	C	216/216 (100%)	216 (100%)	0	100	100
5	D	164/164 (100%)	163 (99%)	1 (1%)	78	93
6	E	165/165 (100%)	165 (100%)	0	100	100
7	F	148/148 (100%)	148 (100%)	0	100	100
8	G	136/136 (100%)	135 (99%)	1 (1%)	76	92
9	H	114/114 (100%)	113 (99%)	1 (1%)	70	90
10	I	116/116 (100%)	116 (100%)	0	100	100
11	J	104/104 (100%)	104 (100%)	0	100	100
12	K	103/103 (100%)	103 (100%)	0	100	100
13	L	109/109 (100%)	109 (100%)	0	100	100
14	M	99/99 (100%)	99 (100%)	0	100	100
15	N	86/86 (100%)	86 (100%)	0	100	100
16	O	99/99 (100%)	99 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	P	89/89 (100%)	89 (100%)	0	100	100
18	Q	84/84 (100%)	84 (100%)	0	100	100
19	R	93/93 (100%)	93 (100%)	0	100	100
20	S	81/81 (100%)	81 (100%)	0	100	100
21	T	84/84 (100%)	84 (100%)	0	100	100
22	U	78/78 (100%)	78 (100%)	0	100	100
23	V	60/60 (100%)	60 (100%)	0	100	100
24	W	67/67 (100%)	67 (100%)	0	100	100
25	X	54/54 (100%)	54 (100%)	0	100	100
26	Y	48/48 (100%)	48 (100%)	0	100	100
27	Z	59/59 (100%)	59 (100%)	0	100	100
28	a	47/47 (100%)	47 (100%)	0	100	100
29	b	47/47 (100%)	47 (100%)	0	100	100
30	c	38/38 (100%)	38 (100%)	0	100	100
31	d	51/51 (100%)	50 (98%)	1 (2%)	48	78
32	e	34/34 (100%)	34 (100%)	0	100	100
33	f	187/187 (100%)	187 (100%)	0	100	100
34	g	171/171 (100%)	171 (100%)	0	100	100
35	h	172/172 (100%)	172 (100%)	0	100	100
36	i	119/119 (100%)	119 (100%)	0	100	100
37	j	91/91 (100%)	91 (100%)	0	100	100
38	k	124/124 (100%)	124 (100%)	0	100	100
39	l	104/104 (100%)	104 (100%)	0	100	100
40	m	105/105 (100%)	105 (100%)	0	100	100
41	n	86/86 (100%)	86 (100%)	0	100	100
42	o	90/90 (100%)	90 (100%)	0	100	100
43	p	102/102 (100%)	102 (100%)	0	100	100
44	q	94/94 (100%)	94 (100%)	0	100	100
45	r	83/83 (100%)	83 (100%)	0	100	100
46	s	76/76 (100%)	75 (99%)	1 (1%)	61	86
47	t	65/65 (100%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	u	74/74 (100%)	74 (100%)	0	100	100
49	v	57/57 (100%)	57 (100%)	0	100	100
50	w	72/72 (100%)	72 (100%)	0	100	100
51	x	65/65 (100%)	64 (98%)	1 (2%)	57	84
52	y	60/60 (100%)	60 (100%)	0	100	100
55	B	52/52 (100%)	47 (90%)	5 (10%)	8	26
All	All	4722/4722 (100%)	4711 (100%)	11 (0%)	85	96

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
55	B	52	SER
55	B	53	PHE
55	B	56	GLU
55	B	54	THR
46	s	89	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
14	M	73	ASN
51	x	52	ASN
24	W	36	HIS
51	x	82	GLN
40	m	110	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2903 (99%)	498 (17%)	14 (0%)
2	2	1532/1534 (99%)	254 (16%)	3 (0%)
3	3	119/120 (99%)	16 (13%)	0
53	4	5/6 (83%)	0	1 (20%)
54	z	84/85 (98%)	31 (36%)	0
All	All	4642/4648 (99%)	799 (17%)	18 (0%)

5 of 799 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	15	G
1	1	34	U
1	1	35	G
1	1	46	G

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	516	PSU
53	4	3	U
2	2	1145	A
1	1	1379	U
1	1	2756	U

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

46 non-standard protein/DNA/RNA residues are 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	$\# Z > 2$
1	3TD	1	1915	1	18,22,23	4.07	7 (38%)	22,32,35	1.58	2 (9%)
1	PSU	1	1917	1	18,21,22	1.06	1 (5%)	22,30,33	1.88	5 (22%)
1	5MU	1	747	1	19,22,23	4.63	7 (36%)	28,32,35	3.73	10 (35%)
2	4OC	2	1402	2	20,23,24	2.93	8 (40%)	26,32,35	0.94	0
54	5MU	z	76	54	19,22,23	1.45	5 (26%)	28,32,35	2.21	7 (25%)
54	5MU	z	64	54	19,22,23	1.44	6 (31%)	28,32,35	2.38	10 (35%)
1	2MA	1	2503	1,56	22,25,26	3.68	9 (40%)	33,37,40	2.40	9 (27%)
1	5MU	1	1939	1,56	19,22,23	4.61	7 (36%)	28,32,35	3.72	9 (32%)
2	5MC	2	1407	2	18,22,23	3.34	7 (38%)	26,32,35	0.85	1 (3%)
1	OMU	1	2552	1	19,22,23	2.87	8 (42%)	26,31,34	1.64	5 (19%)
2	5MC	2	967	2	18,22,23	3.44	7 (38%)	26,32,35	1.03	2 (7%)
43	0TD	p	89	43	7,9,10	1.51	1 (14%)	6,11,13	1.91	2 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	1	2504	1	18,21,22	0.98	2 (11%)	22,30,33	1.82	4 (18%)
1	OMC	1	2498	1,56	19,22,23	2.73	7 (36%)	26,31,34	0.86	0
54	5MU	z	63	54	19,22,23	1.46	6 (31%)	28,32,35	2.18	8 (28%)
54	5MU	z	39	54	19,22,23	1.44	6 (31%)	28,32,35	2.20	9 (32%)
1	OMG	1	2251	1,54	23,26,27	2.17	7 (30%)	33,38,41	1.71	8 (24%)
54	5MU	z	8	54	19,22,23	4.71	7 (36%)	28,32,35	3.68	10 (35%)
54	5MU	z	69	54	19,22,23	1.41	6 (31%)	28,32,35	1.92	7 (25%)
2	UR3	2	1498	56,2	19,22,23	2.63	6 (31%)	26,32,35	1.07	2 (7%)
1	PSU	1	2605	1	18,21,22	0.98	2 (11%)	22,30,33	1.96	5 (22%)
2	2MG	2	1516	2	23,26,27	2.68	9 (39%)	32,38,41	2.08	10 (31%)
54	5MU	z	71	54	19,22,23	1.44	6 (31%)	28,32,35	2.15	8 (28%)
54	5MU	z	55	54	19,22,23	4.79	7 (36%)	28,32,35	3.58	9 (32%)
1	PSU	1	955	1,56	18,21,22	0.99	2 (11%)	22,30,33	1.93	5 (22%)
1	2MG	1	1835	1	23,26,27	2.68	8 (34%)	32,38,41	2.10	8 (25%)
1	G7M	1	2069	1	23,26,27	2.56	9 (39%)	35,39,42	2.21	11 (31%)
2	MA6	2	1519	2	23,26,27	1.47	4 (17%)	34,38,41	3.28	11 (32%)
54	5MU	z	20	56,54	19,22,23	4.94	7 (36%)	28,32,35	3.63	10 (35%)
54	5MU	z	42	2,54	19,22,23	4.58	7 (36%)	28,32,35	3.73	10 (35%)
1	2MG	1	2445	1	23,26,27	2.62	8 (34%)	32,38,41	2.00	9 (28%)
1	1MG	1	745	1	22,26,27	2.86	7 (31%)	33,39,42	2.16	7 (21%)
54	5MU	z	40	54	19,22,23	1.39	5 (26%)	28,32,35	2.29	12 (42%)
2	2MG	2	966	2	23,26,27	2.79	7 (30%)	32,38,41	2.11	7 (21%)
1	PSU	1	2580	1,56	18,21,22	1.01	1 (5%)	22,30,33	1.95	6 (27%)
2	PSU	2	516	56,2	18,21,22	0.98	1 (5%)	22,30,33	1.85	4 (18%)
54	5MU	z	57	54	19,22,23	4.71	7 (36%)	28,32,35	3.64	10 (35%)
1	6MZ	1	2030	1	22,25,26	2.52	6 (27%)	30,36,39	3.29	12 (40%)
1	6MZ	1	1618	1	22,25,26	2.37	5 (22%)	30,36,39	3.29	11 (36%)
1	PSU	1	1911	1	18,21,22	0.98	1 (5%)	22,30,33	1.87	5 (22%)
2	2MG	2	1207	2	23,26,27	2.68	9 (39%)	32,38,41	2.08	10 (31%)
1	5MC	1	1962	1	18,22,23	3.29	7 (38%)	26,32,35	1.13	3 (11%)
2	MA6	2	1518	2	23,26,27	1.45	4 (17%)	34,38,41	3.15	11 (32%)
1	PSU	1	746	1,56	18,21,22	1.02	1 (5%)	22,30,33	1.77	4 (18%)
2	G7M	2	527	2	23,26,27	2.65	8 (34%)	35,39,42	2.26	10 (28%)
1	PSU	1	2457	1	18,21,22	1.02	1 (5%)	22,30,33	1.98	5 (22%)

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
1	3TD	1	1915	1	-	3/7/25/26	0/2/2/2
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
54	5MU	z	76	54	-	0/7/25/26	0/2/2/2
54	5MU	z	64	54	-	4/7/25/26	0/2/2/2
1	2MA	1	2503	1,56	-	2/7/25/26	0/3/3/3
1	5MU	1	1939	1,56	-	0/7/25/26	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	0/9/27/28	0/2/2/2
2	5MC	2	967	2	-	2/7/25/26	0/2/2/2
43	0TD	p	89	43	-	2/7/12/14	-
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
1	OMC	1	2498	1,56	-	0/9/27/28	0/2/2/2
54	5MU	z	63	54	-	0/7/25/26	0/2/2/2
54	5MU	z	39	54	-	3/7/25/26	0/2/2/2
1	OMG	1	2251	1,54	-	0/9/27/28	0/3/3/3
54	5MU	z	8	54	-	2/7/25/26	0/2/2/2
54	5MU	z	69	54	-	5/7/25/26	0/2/2/2
2	UR3	2	1498	56,2	-	0/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
54	5MU	z	71	54	-	3/7/25/26	0/2/2/2
54	5MU	z	55	54	-	0/7/25/26	0/2/2/2
1	PSU	1	955	1,56	-	0/7/25/26	0/2/2/2
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
1	G7M	1	2069	1	-	1/7/25/26	0/3/3/3
2	MA6	2	1519	2	-	2/11/29/30	0/3/3/3
54	5MU	z	20	56,54	-	2/7/25/26	0/2/2/2
54	5MU	z	42	2,54	-	0/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	2/9/27/28	0/3/3/3
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
54	5MU	z	40	54	-	2/7/25/26	0/2/2/2
2	2MG	2	966	2	-	0/9/27/28	0/3/3/3
1	PSU	1	2580	1,56	-	0/7/25/26	0/2/2/2

Continued on next page...

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PSU	2	516	56,2	-	2/7/25/26	0/2/2/2
54	5MU	z	57	54	-	0/7/25/26	0/2/2/2
1	6MZ	1	2030	1	-	2/9/27/28	0/3/3/3
1	6MZ	1	1618	1	-	2/9/27/28	0/3/3/3
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
1	PSU	1	746	1,56	-	1/7/25/26	0/2/2/2
2	G7M	2	527	2	-	3/7/25/26	0/3/3/3
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2

The worst 5 of 259 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	11.83	1.49	1.35
1	1	2503	2MA	C4-N3	11.34	1.48	1.34
54	z	20	5MU	C2-N1	11.28	1.56	1.38
54	z	57	5MU	C2-N1	11.11	1.56	1.38
54	z	55	5MU	C2-N1	11.07	1.56	1.38

The worst 5 of 323 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1519	MA6	N1-C6-N6	-13.02	102.84	117.08
54	z	8	5MU	C5-C4-N3	12.58	126.05	115.31
2	2	1518	MA6	N1-C6-N6	-12.51	103.40	117.08
54	z	20	5MU	C5-C4-N3	12.49	125.97	115.31
1	1	747	5MU	C5-C4-N3	12.27	125.78	115.31

There are no chirality outliers.

5 of 51 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	1618	6MZ	O4'-C4'-C5'-O5'
1	1	1618	6MZ	C3'-C4'-C5'-O5'
1	1	1915	3TD	C2'-C1'-C5-C4
1	1	1915	3TD	O4'-C1'-C5-C4
1	1	1915	3TD	O4'-C1'-C5-C6

There are no ring outliers.

28 monomers are involved in 42 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	1915	3TD	2	0
54	z	76	5MU	1	0
54	z	64	5MU	1	0
1	1	2503	2MA	1	0
1	1	1939	5MU	1	0
2	2	1407	5MC	1	0
1	1	2552	OMU	1	0
43	p	89	0TD	1	0
1	1	2504	PSU	1	0
1	1	2498	OMC	1	0
54	z	39	5MU	2	0
54	z	69	5MU	6	0
2	2	1498	UR3	1	0
2	2	1516	2MG	1	0
54	z	71	5MU	4	0
54	z	55	5MU	1	0
1	1	955	PSU	1	0
2	2	1519	MA6	2	0
54	z	20	5MU	4	0
1	1	2445	2MG	1	0
54	z	40	5MU	1	0
1	1	2580	PSU	1	0
2	2	516	PSU	2	0
54	z	57	5MU	1	0
1	1	2030	6MZ	2	0
1	1	1618	6MZ	1	0
1	1	1962	5MC	2	0
2	2	1518	MA6	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 396 ligands modelled in this entry, 396 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.

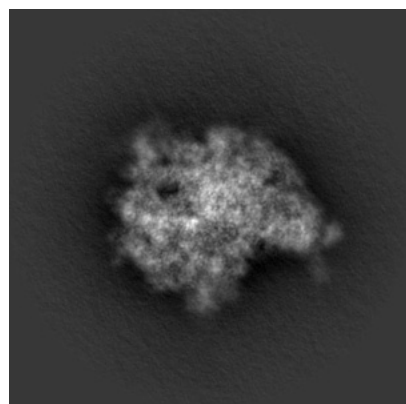
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13055. These allow visual inspection of the internal detail of the map and identification of artifacts.

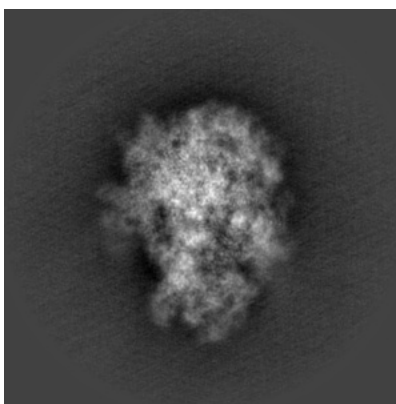
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

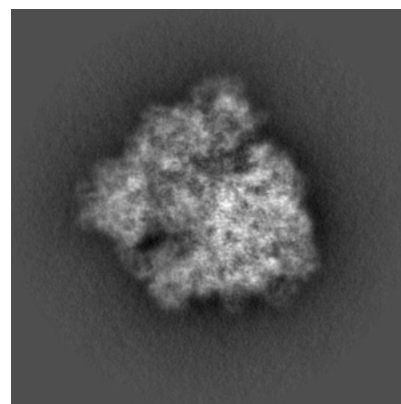
6.1.1 Primary map



X

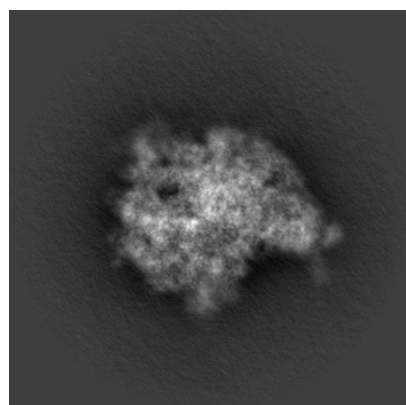


Y

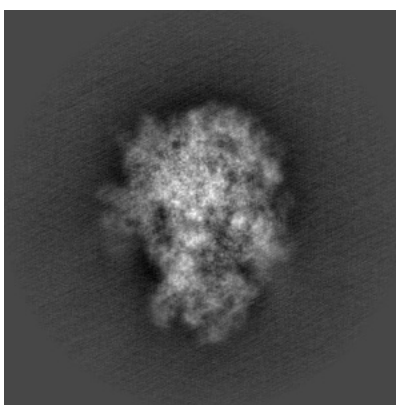


Z

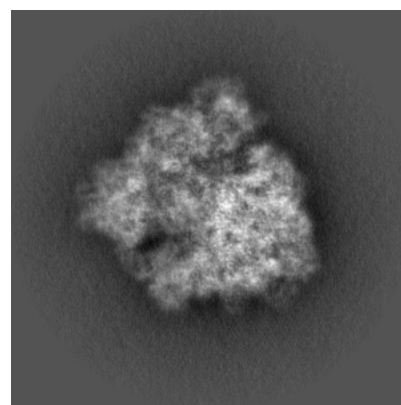
6.1.2 Raw map



X



Y

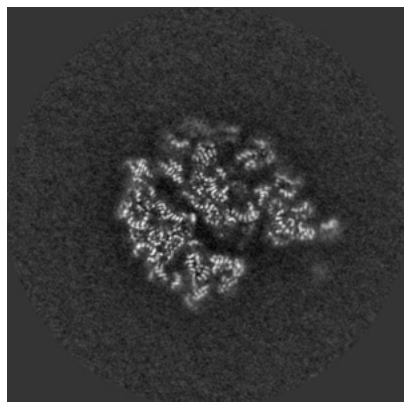


Z

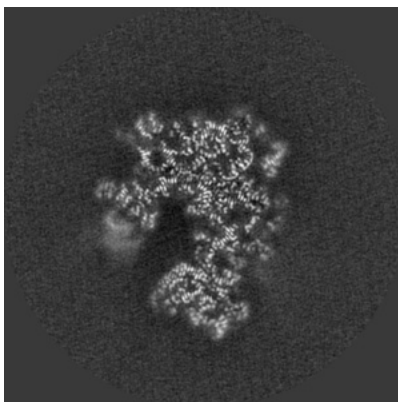
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

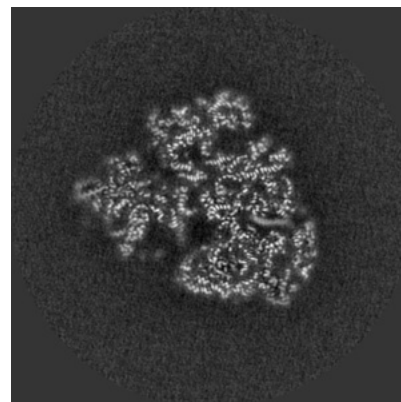
6.2.1 Primary map



X Index: 200

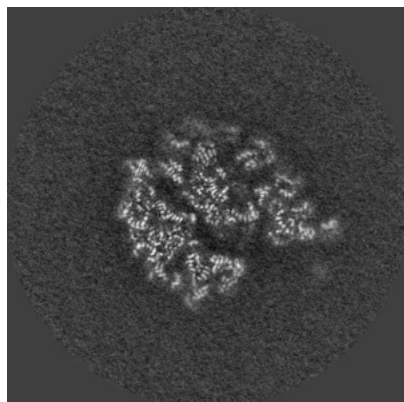


Y Index: 200

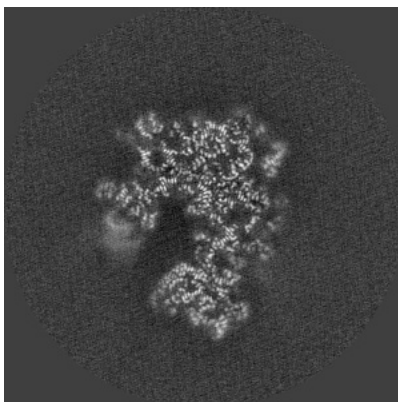


Z Index: 200

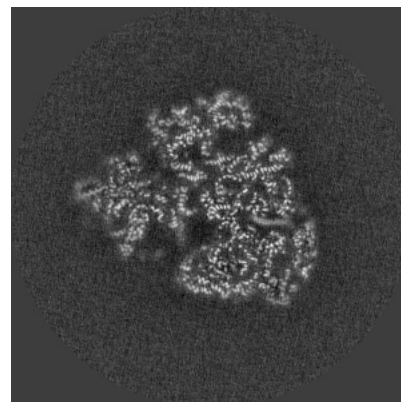
6.2.2 Raw map



X Index: 200



Y Index: 200

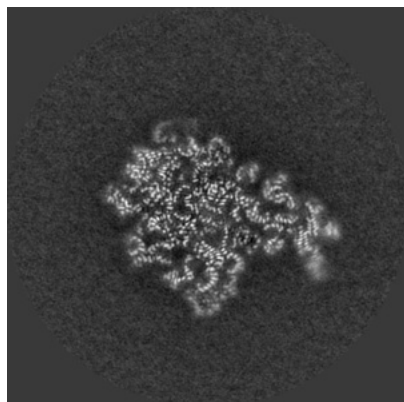


Z Index: 200

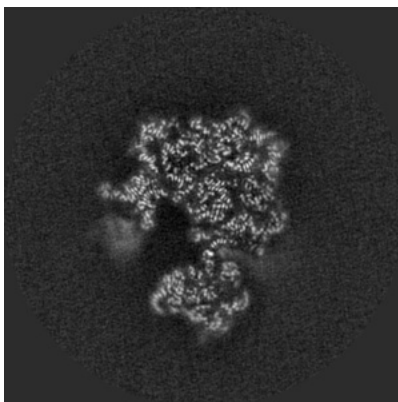
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

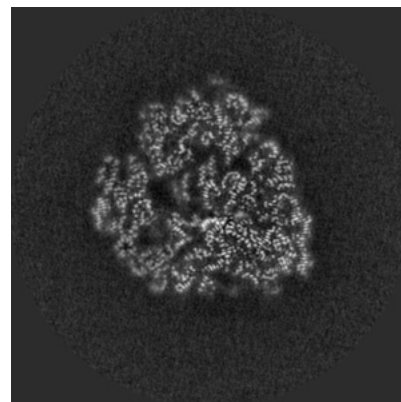
6.3.1 Primary map



X Index: 216

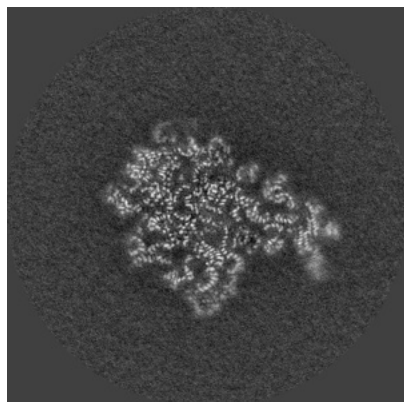


Y Index: 206

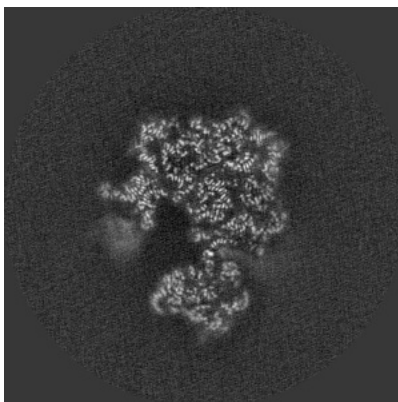


Z Index: 188

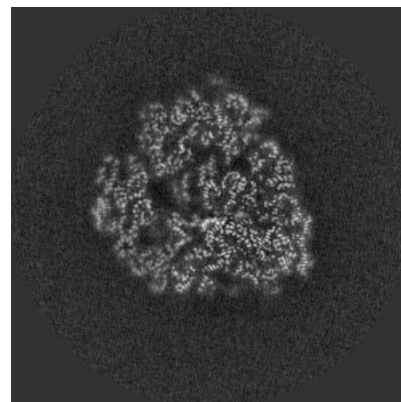
6.3.2 Raw map



X Index: 216



Y Index: 206

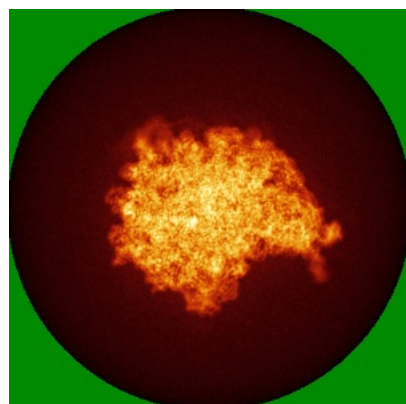


Z Index: 188

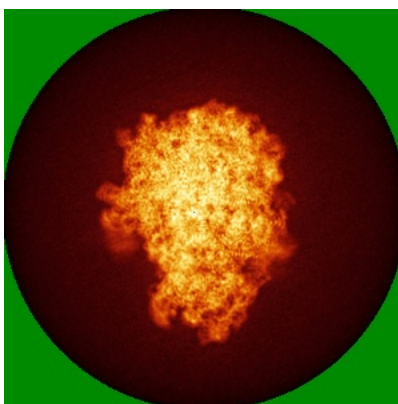
The images above show the largest variance slices of the map in three orthogonal directions.

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

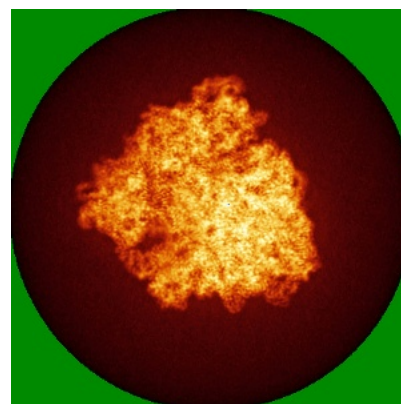
6.4.1 Primary map



X

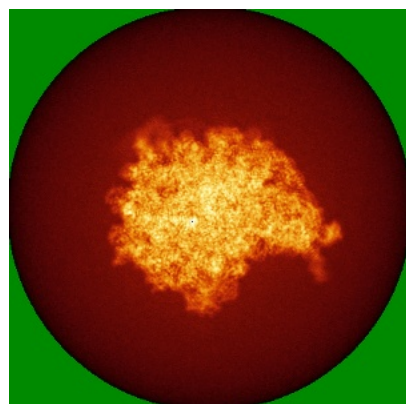


Y

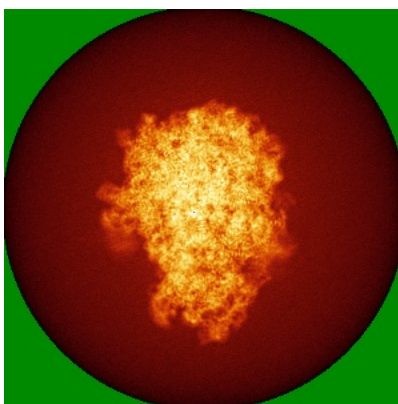


Z

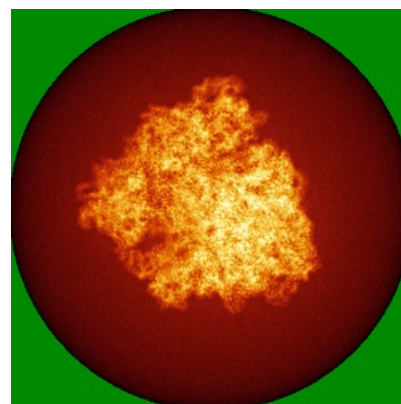
6.4.2 Raw map



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



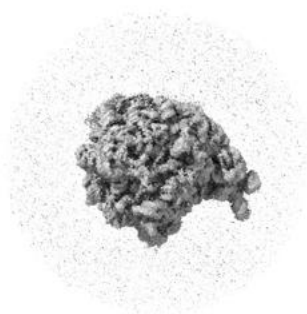
Y



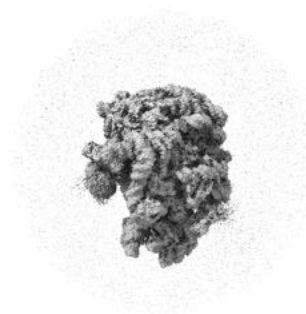
Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

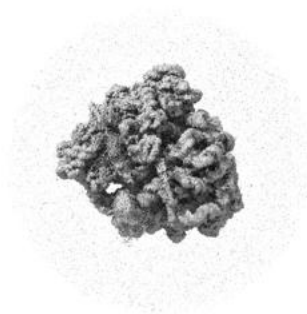
6.5.2 Raw map



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.

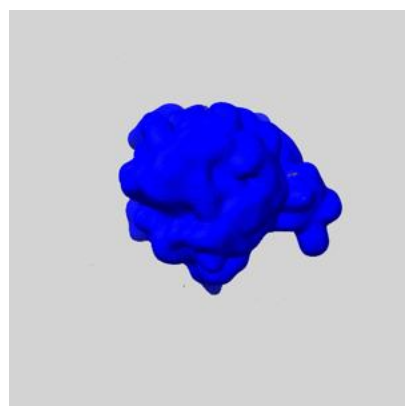
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

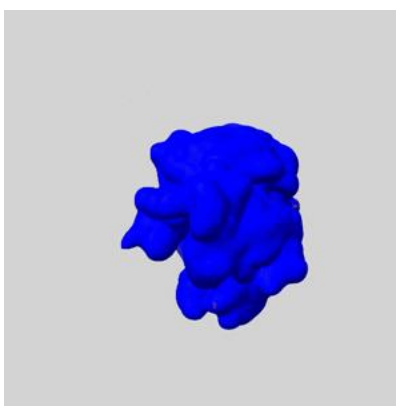
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

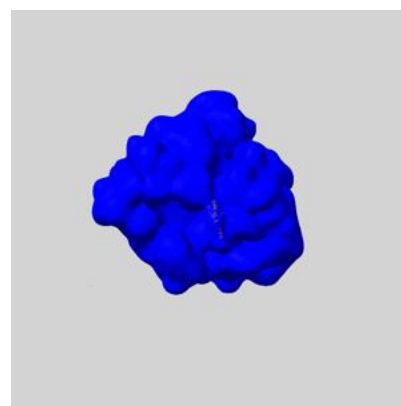
6.6.1 emd_13055_msk_1.map [i](#)



X



Y

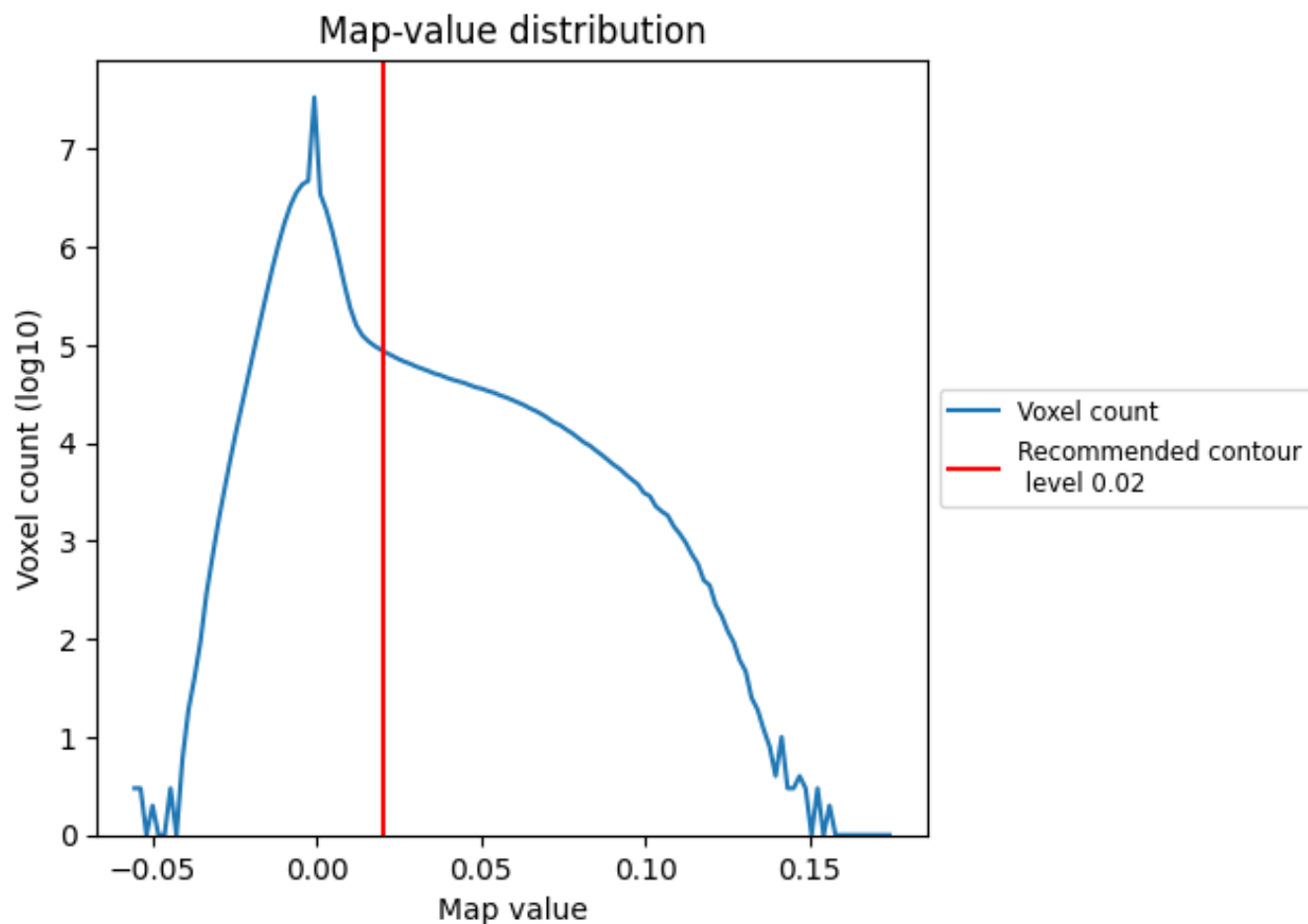


Z

7 Map analysis [i](#)

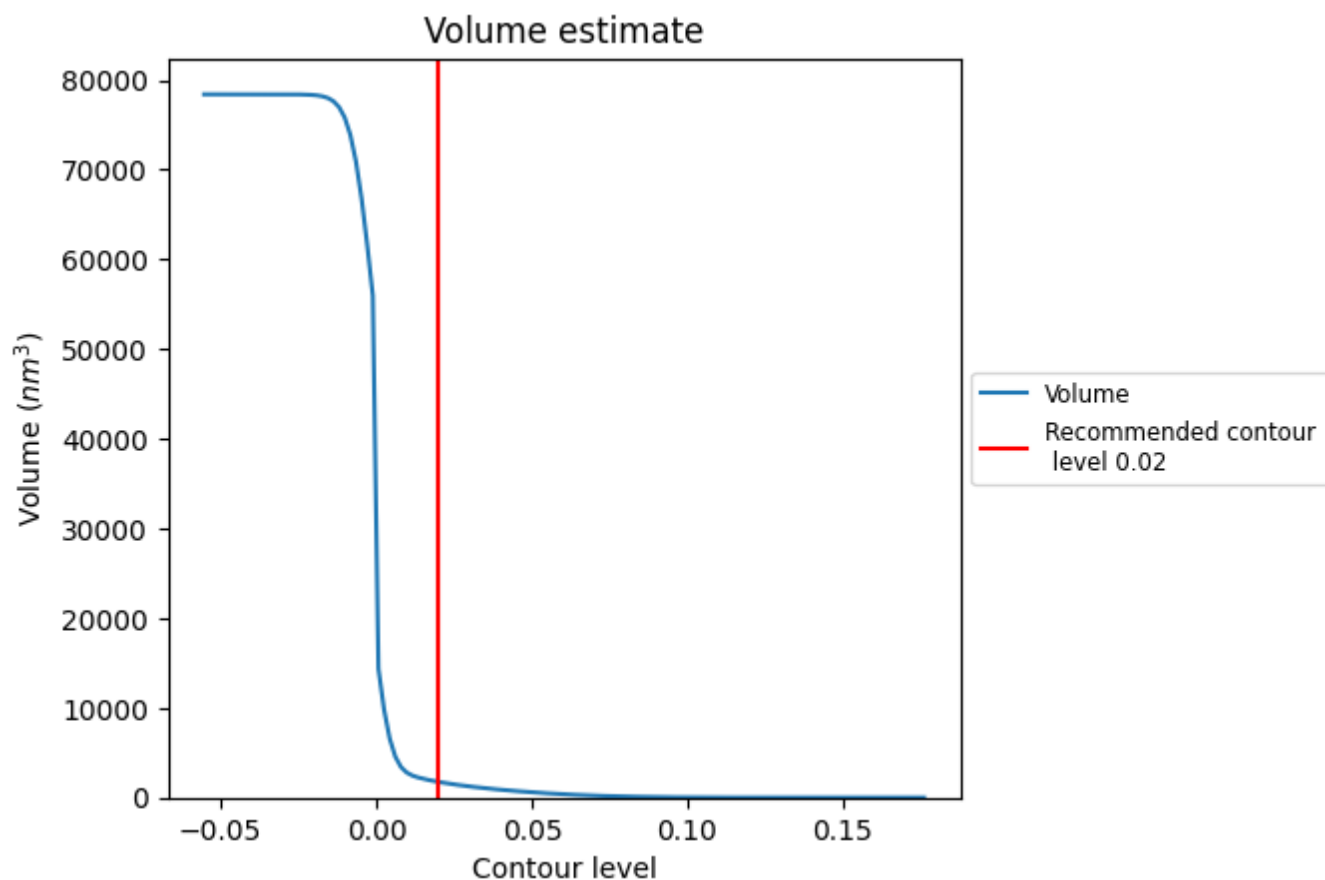
This section contains the results of statistical analysis of the map.

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.

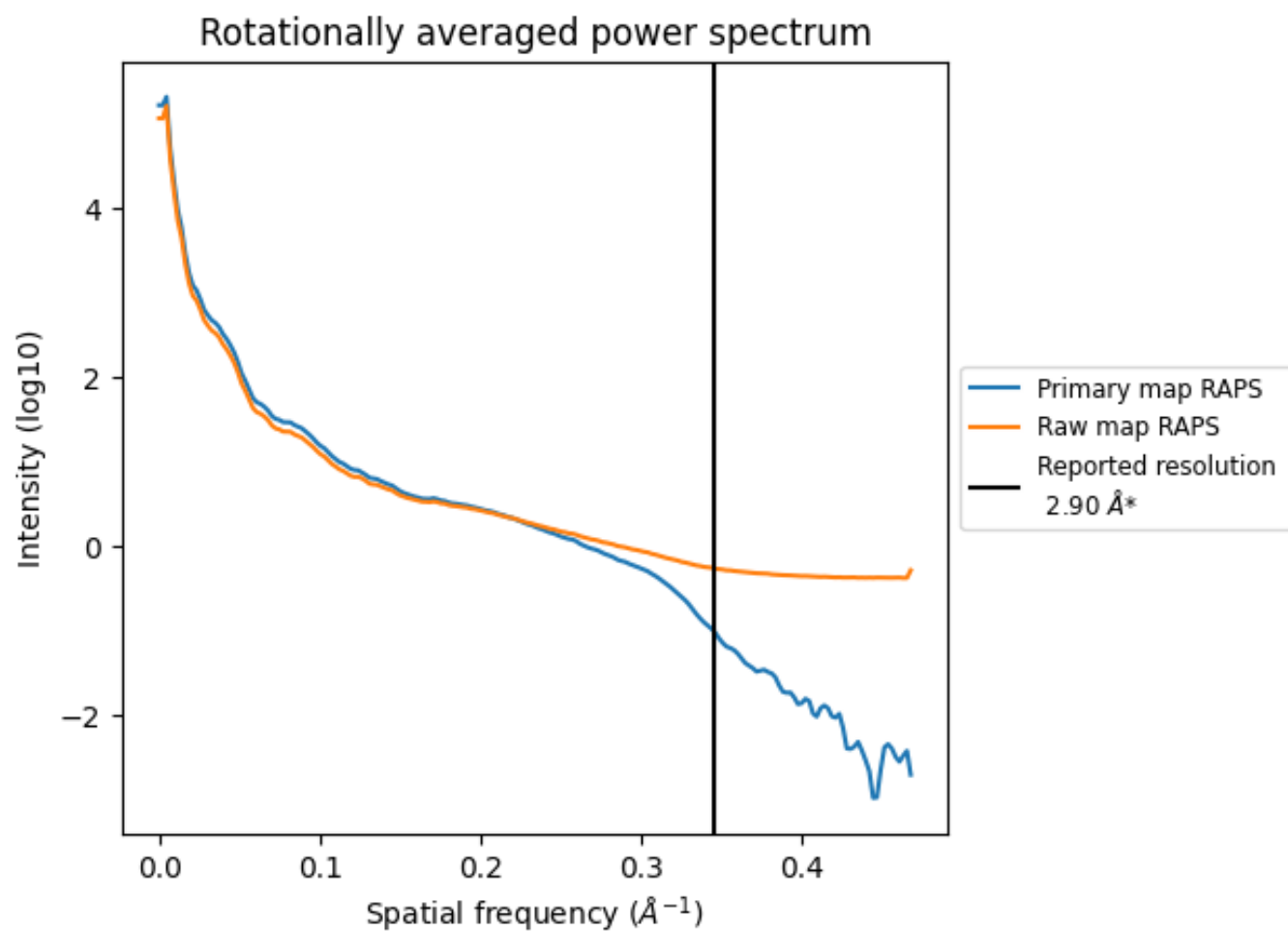
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1746 nm³; this corresponds to an approximate mass of 1577 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 ⓘ

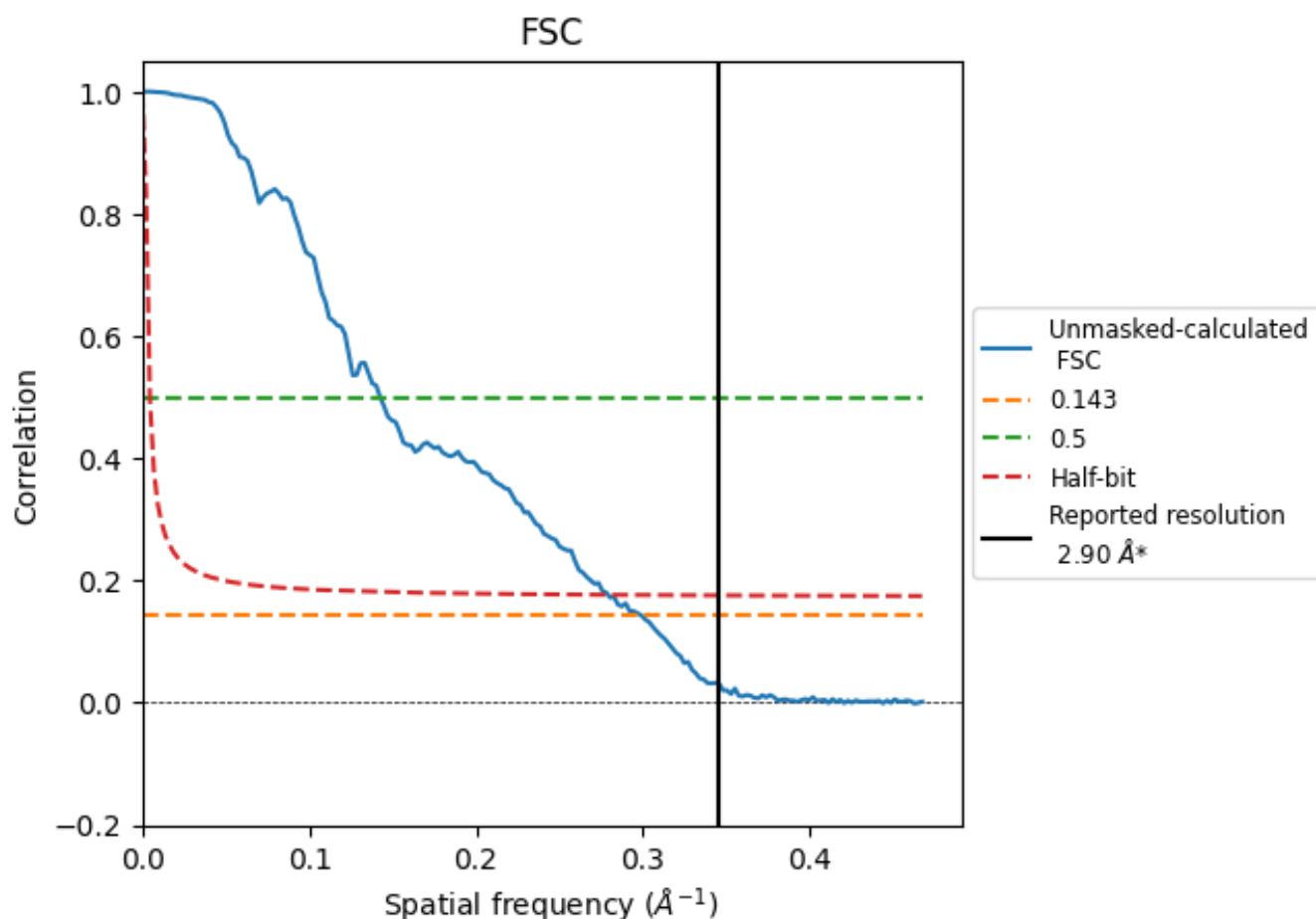


*Reported resolution corresponds to spatial frequency of $0.345 \text{ \AA}^{-1}$

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 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

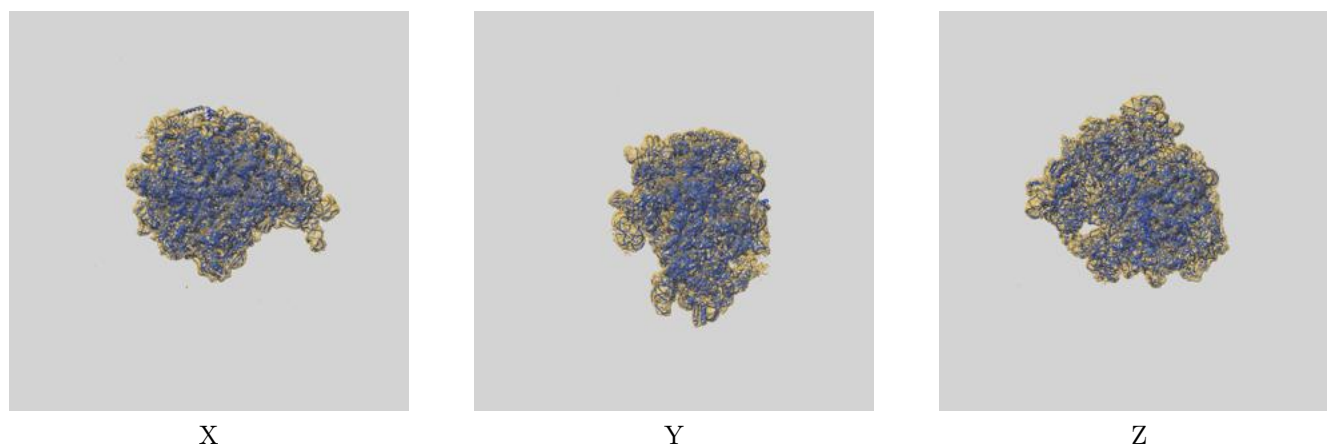
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.34	7.01	3.58

*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 3.34 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

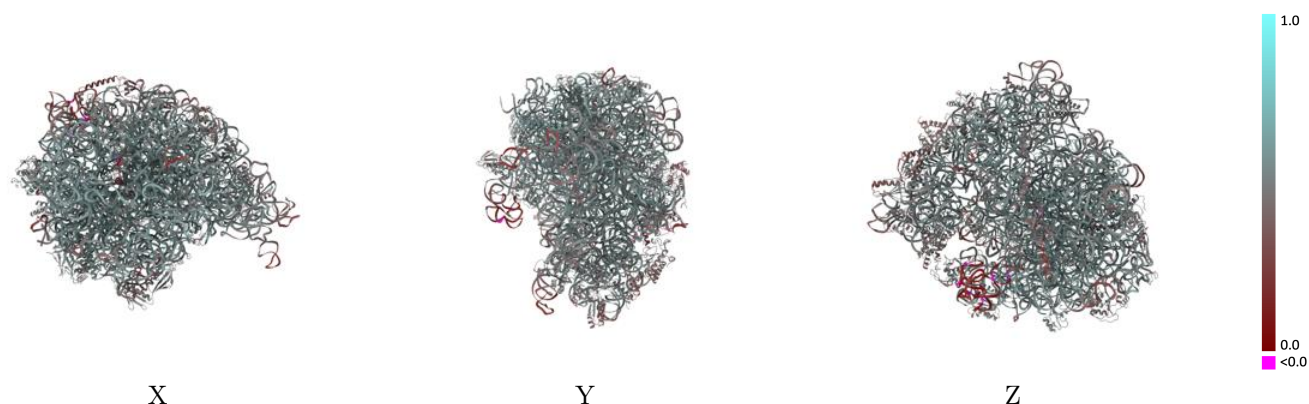
This section contains information regarding the fit between EMDB map EMD-13055 and PDB model 7OT5. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



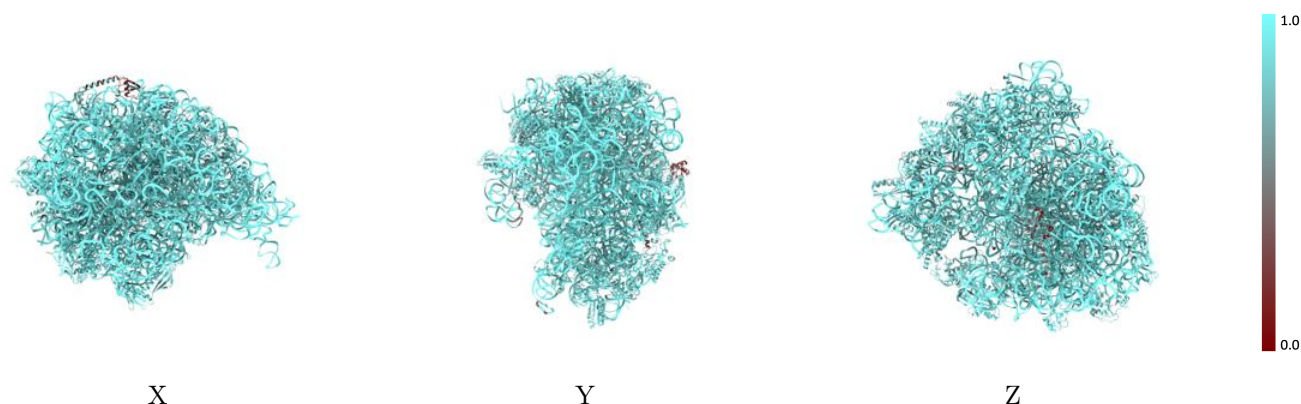
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



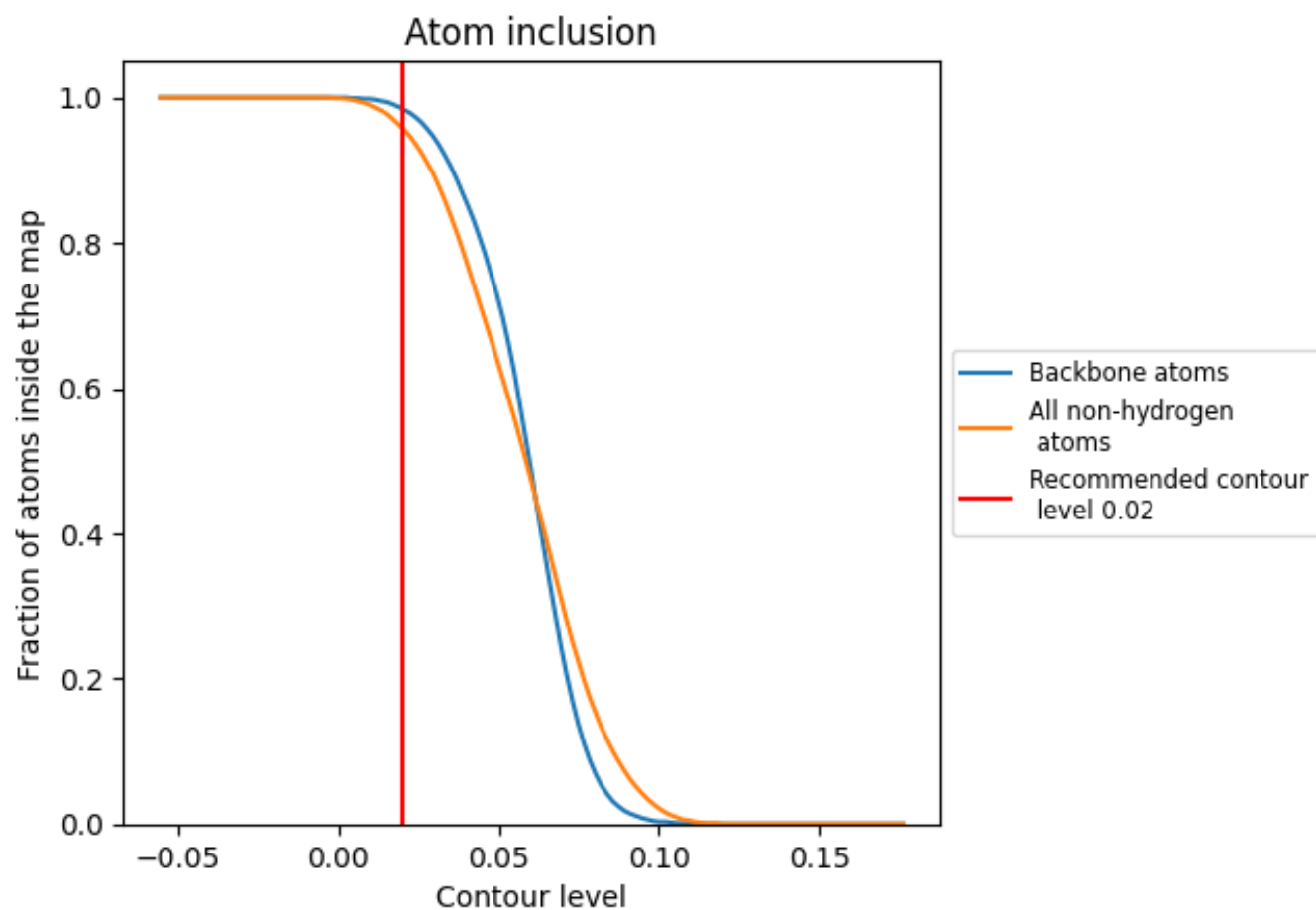
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9580	 0.5150
1	 0.9880	 0.5290
2	 0.9940	 0.5210
3	 0.9970	 0.5180
4	 1.0000	 0.5110
B	 0.7870	 0.2210
C	 0.9090	 0.5600
D	 0.9260	 0.5480
E	 0.9180	 0.5130
F	 0.8940	 0.4580
G	 0.9210	 0.4640
H	 0.4720	 0.3550
I	 0.9140	 0.5370
J	 0.8720	 0.5360
K	 0.9160	 0.5330
L	 0.8930	 0.5340
M	 0.9430	 0.5470
N	 0.9320	 0.4880
O	 0.9030	 0.5330
P	 0.9350	 0.5340
Q	 0.9270	 0.5290
R	 0.8890	 0.5230
S	 0.8750	 0.5100
T	 0.9160	 0.5060
U	 0.9130	 0.5130
V	 0.8840	 0.5480
W	 0.9080	 0.5320
X	 0.8790	 0.4560
Y	 0.9010	 0.5240
Z	 0.8710	 0.4060
a	 0.8880	 0.5340
b	 0.8470	 0.5070
c	 0.8930	 0.5690
d	 0.9230	 0.5690
e	 0.9040	 0.5310



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Chain	Atom inclusion	Q-score
f	 0.8460	 0.4240
g	 0.8930	 0.4770
h	 0.9060	 0.4780
i	 0.9050	 0.5160
j	 0.9030	 0.4690
k	 0.8620	 0.4420
l	 0.9010	 0.5080
m	 0.9110	 0.4710
n	 0.8540	 0.4370
o	 0.9050	 0.4830
p	 0.8700	 0.5220
q	 0.9060	 0.4610
r	 0.9160	 0.4880
s	 0.9040	 0.4780
t	 0.9220	 0.4930
u	 0.8720	 0.4880
v	 0.9010	 0.4870
w	 0.9290	 0.4750
x	 0.9050	 0.4740
y	 0.7370	 0.4060
z	 0.9560	 0.4630