



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2026 – 03:28 am BST

PDB ID : 7OIF / pdb_00007oif
EMDB ID : EMD-12928
Title : CspA-27 cotranslational folding intermediate 2
Authors : Agirrezabala, X.; Samatova, E.; Macher, M.; Liutkute, M.; Gil-Carton, D.;
Novacek, J.; Valle, M.; Rodnina, M.V.
Deposited on : 2021-05-11
Resolution : 3.00 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

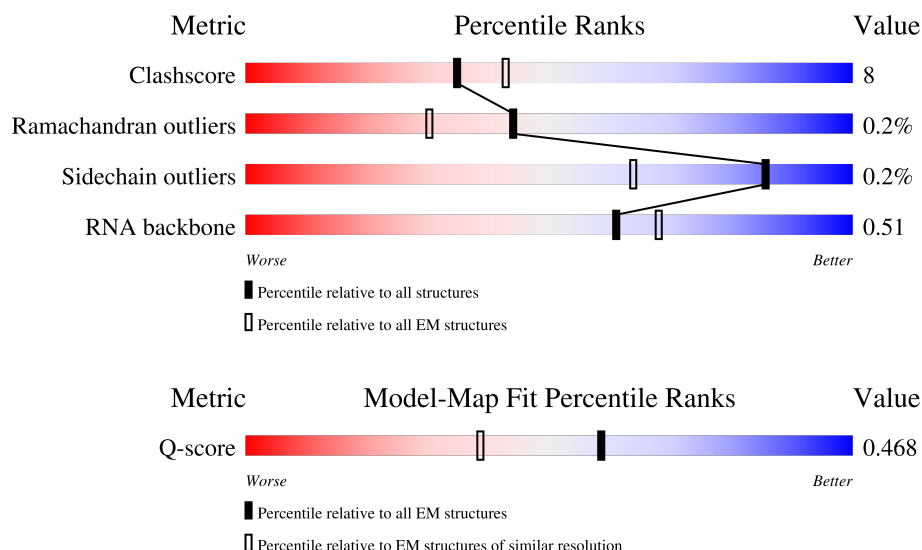
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

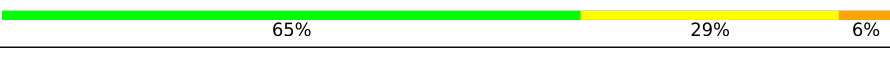
The reported resolution of this entry is 3.00 Å.

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)	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	14081 (2.50 - 3.50)

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	
2	2	1534	
3	3	120	

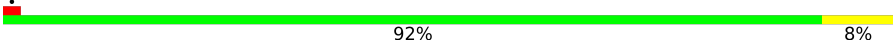
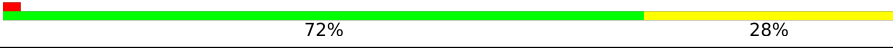
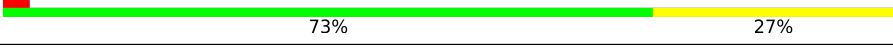
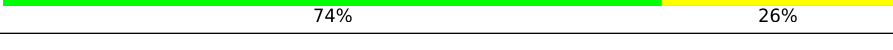
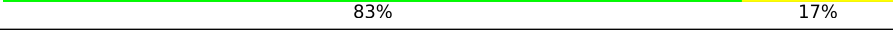
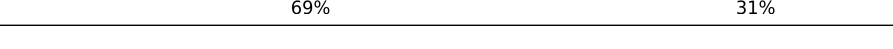
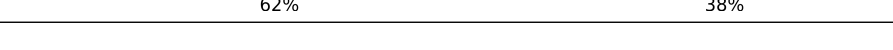
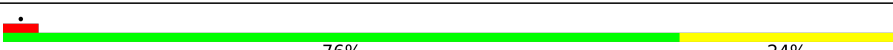
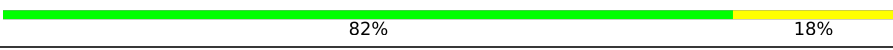
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Mol	Chain	Length	Quality of chain
4	4	6	 100%
5	C	271	 79% 21%
6	D	209	 84% 14% .
7	E	201	 84% 16%
8	F	177	 64% 36%
9	G	175	 78% 22%
10	H	149	 58% 56% 42% .
11	I	142	 85% 15%
12	J	123	 85% 15%
13	K	144	 79% 21%
14	L	136	 86% 14%
15	M	119	 82% 18%
16	N	116	 76% 24%
17	O	114	 83% 17%
18	P	117	 87% 13%
19	Q	103	 78% 20% ..
20	R	110	 74% 26%
21	S	94	 77% 22% .
22	T	103	 74% 26%
23	U	94	 79% 21%
24	V	80	 6% 80% 19% .
25	W	77	 83% 17%
26	X	62	 87% 13%
27	Y	58	 83% 17%
28	Z	66	 6% 58% 41% .

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Mol	Chain	Length	Quality of chain
29	a	56	
30	b	52	
31	c	46	
32	d	64	
33	e	38	
34	f	225	
35	g	208	
36	h	205	
37	i	156	
38	j	104	
39	k	151	
40	l	129	
41	m	127	
42	n	99	
43	o	117	
44	p	123	
45	q	116	
46	r	100	
47	s	88	
48	t	82	
49	u	80	
50	v	66	
51	w	83	
52	x	86	
53	y	70	

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Mol	Chain	Length	Quality of chain
54	z	88	25% 48% 22% 6%
55	B	27	19% 26% 59% 11% •

2 Entry composition [i](#)

There are 57 unique types of molecules in this entry. The entry contains 145152 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 RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	6	Total	C	N	O	P	0	0
			126	56	20	44	6		

- Molecule 5 is a protein called 50S ribosomal protein L2.

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

- Molecule 6 is a protein called 50S ribosomal protein L3.

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

- Molecule 7 is a protein called 50S ribosomal protein L4.

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

- Molecule 8 is a protein called 50S ribosomal protein L5.

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

- Molecule 9 is a protein called 50S ribosomal protein L6.

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

- Molecule 10 is a protein called 50S ribosomal protein L9.

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

- Molecule 11 is a protein called 50S ribosomal protein L13.

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

- Molecule 12 is a protein called 50S ribosomal protein L14.

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

- Molecule 13 is a protein called 50S ribosomal protein L15.

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

- Molecule 14 is a protein called 50S ribosomal protein L16.

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

- Molecule 15 is a protein called 50S ribosomal protein L17.

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

- Molecule 16 is a protein called 50S ribosomal protein L18.

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

- Molecule 17 is a protein called 50S ribosomal protein L19.

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

- Molecule 18 is a protein called 50S ribosomal protein L20.

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

- Molecule 19 is a protein called 50S ribosomal protein L21.

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

- Molecule 20 is a protein called 50S ribosomal protein L22.

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

- Molecule 21 is a protein called 50S ribosomal protein L23.

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

- Molecule 22 is a protein called 50S ribosomal protein L24.

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

- Molecule 23 is a protein called 50S ribosomal protein L25.

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

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	80	Total	C	N	O	S	0	0
			601	370	121	109	1		

- Molecule 25 is a protein called 50S ribosomal protein L28.

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

- Molecule 26 is a protein called 50S ribosomal protein L29.

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

- Molecule 27 is a protein called 50S ribosomal protein L30.

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

- Molecule 28 is a protein called 50S ribosomal protein L31.

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	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	d	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	e	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	f	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
54	z	88	Total	C	N	O	P	0	0
			1891	841	341	621	88		

- Molecule 55 is a protein called CspA transcriptional activator.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	B	27	Total	C	N	O	S	0	0
			205	132	32	39	2		

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

Mol	Chain	Residues	Atoms		AltConf
56	1	276	Total 276	Mg 276	0
56	2	119	Total 119	Mg 119	0
56	3	8	Total 8	Mg 8	0
56	4	1	Total 1	Mg 1	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	q	1	Total 1	Mg 1	0
56	r	1	Total 1	Mg 1	0
56	z	2	Total 2	Mg 2	0

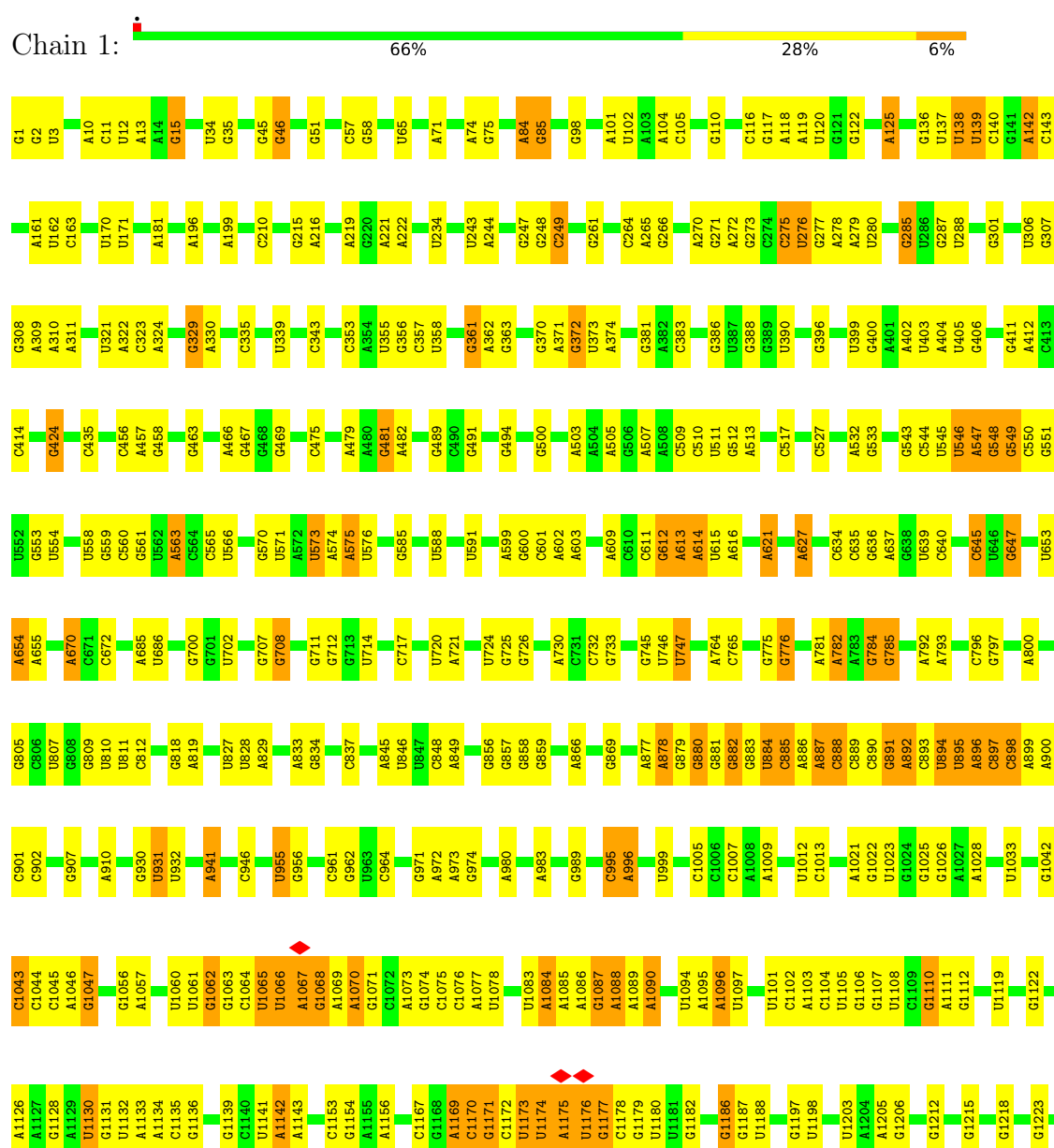
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

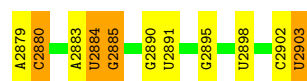
3 Residue-property plots

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

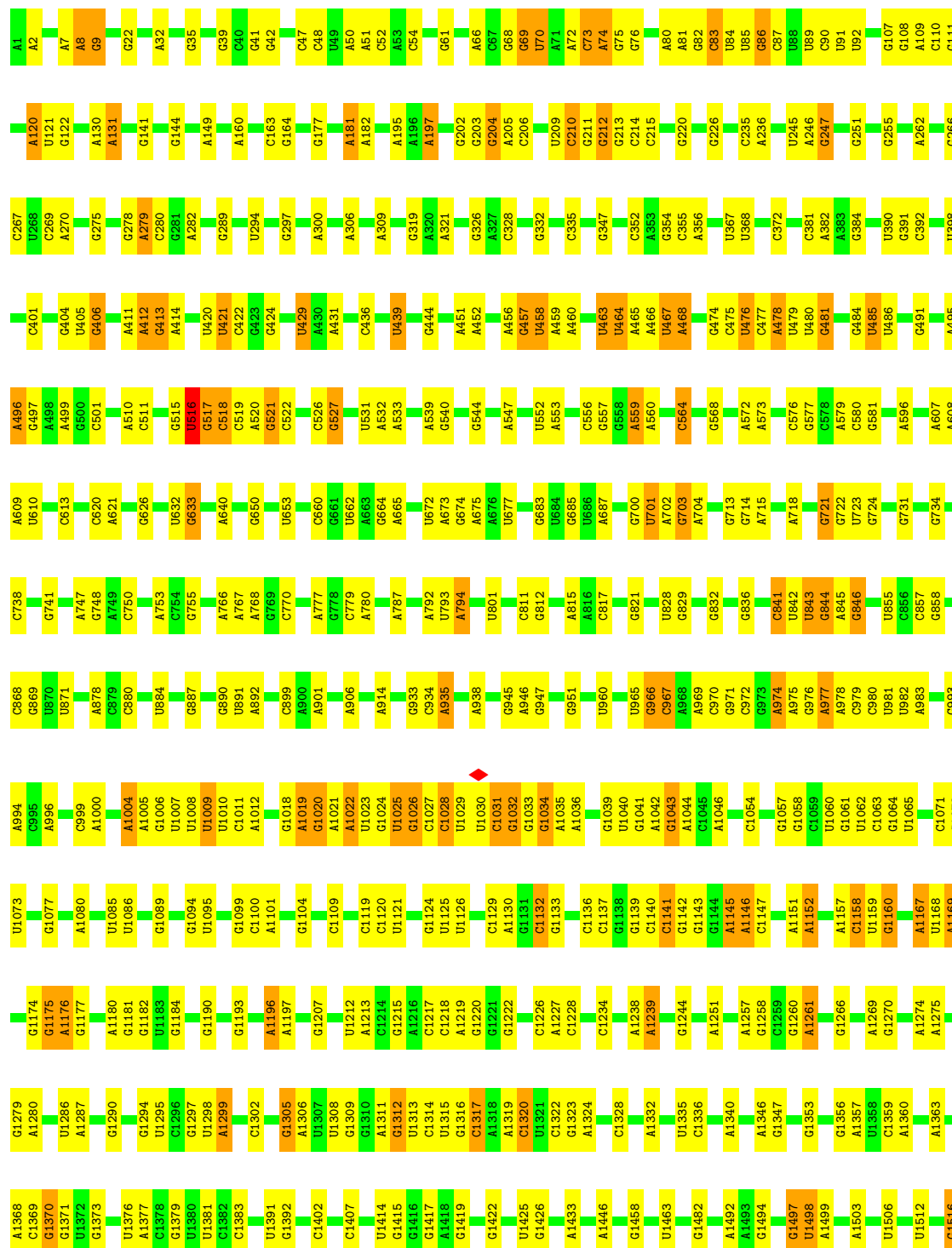


A2753	G2602	C2501	G2383	U2291	U2182	U2111	U1983	U1864	U1738	A1579	G1482	G1368	U1231
A2756	U2605	G2502	U2384	U2292	A2183	G2112	C1996	U1865	G1738	A1580	G1482	G1369	G1232
A2757	U2606	A2503	A2386	U2293	U2184	U2113	C1997	C1868	A1754	C1582	U1485	G1370	G1233
A2765	U2609	U2504	U2387	G2294	U2185	A2114	G2002	G1869	G1755	A1583	U1486	G1371	G1234
A2766	C2610	G2505	C2394	A2297	U2187	G2115	G2002	G1870	G1756	U1584	A1490	C1376	G1236
A2767	C2611	U2506	U2394	A2298	U2188	G2116	G2012	A1871	G1764	C1585	A1337	A1937	G1237
G2777	C2612	G2507	U2402	U2299	U2189	A2117	C2021	G1872	G1773	U1586	C1493	G1377	G1238
A2778	U2613	C2508	U2403	U2300	U2190	U2118	C2021	G1873	A1774	C1494	C1493	A1378	U1242
U2779	A2614	U2511	U2404	C2301	U2191	A2119	U2022	U1883	G1774	U1588	A1494	A1379	U1243
G2780	G2629	C2512	G2405	C2301	U2192	A2120	C2023	G1884	U1775	A1590	A1495	G1380	G1243
C2788	A2635	A2513	A2406	G2304	U2194	G2121	G2024	G1896	U1779	A1591	A1503	A1244	A1244
C2789	A2636	U2518	A2411	U2305	U2195	U2122	C2025	G1896	U1779	A1591	A1504	A1383	A1247
U2790	C2636	U2519	U2412	G2308	U2196	G2123	U2026	C1607	U1782	C1608	A1505	C1386	A1248
G2791	A2639	C2520	U2423	A2309	U2197	G2124	G2027	A1901	U1782	A1608	U1506	U1249	U1249
C2792	U2640	U2529	U2424	C2310	U2198	G2125	U2028	U1906	A1783	A1618	C1507	G1250	G1250
C2793	G2640	A2530	A2425	A2311	G2204	A2126	G2028	G1907	A1784	A1618	A1508	A1393	A1253
C2794	C2646	A2531	U2426	U2312	A2211	G2127	A2031	U1911	A1789	U1629	A1509	U1394	U1253
C2795	G2655	G2532	G2427	G2313	A2211	U2131	G2032	A1912	C1790	A1630	G1514	U1405	G1256
U2796	U2655	U2532	G2428	G2314	U2220	U2132	U2034	A1913	A1791	A1631	A1515	U1406	G1256
U2797	U2656	G2535	G2429	G2315	U2220	G2133	U2034	A1914	U1796	A1632	A1515	G1407	G1266
U2798	U2657	A2542	U2430	G2316	A2225	A2134	C2043	3TD1915	G1796	A1633	G1521	G1408	G1271
A2799	G2663	G2542	U2431	G2317	C2226	U2137	C2043	A1916	G1797	A1634	A1522	U1411	A1272
A2800	G2664	G2545	U2435	G2319	U2229	G2138	C2050	A1917	U1798	U1647	U1523	U1412	A1276
U2804	C2664	U2546	U2441	U2320	U2229	U2139	A2052	G1922	U1798	U1648	G1524	A1413	A1276
C2805	C2683	A2547	U2441	U2321	U2233	G2140	A2052	G1923	A1800	C1414	C1531	A1419	G1277
G2808	U2689	U2552	U2445	U2322	U2234	G2141	C2055	G1924	A1801	A1650	G1527	U1415	C1278
G2811	U2690	G2553	U2448	U2323	G2235	C2143	C2056	A1936	A1808	G1651	U1528	C1416	C1283
G2812	U2698	U2554	U2449	G2325	U2236	C2144	C2056	A1937	A1937	A1652	U1529	C1417	U1294
U2818	C2699	U2556	U2450	A2327	G2237	C2145	A2062	A1938	G1817	A1664	G1530	G1418	C1298
G2819	G2702	G2557	U2457	U2329	G2239	C2146	A2062	U1939	U1818	A1668	G1533	A1427	G1299
A2820	G2714	U2561	A2469	A2333	U2243	A2147	G2069	G1954	G1816	A1668	U1534	C1428	G1300
C2824	C2715	U2562	G2470	U2334	A2247	G2148	A2070	U1955	G1817	A1672	A1535	G1432	A1301
G2825	C2716	A2566	A2476	A2336	U2249	A2149	U2081	U1956	U1827	G1674	G1537	A1433	C1315
G2831	C2717	G2567	U2477	A2336	G2250	C2160	A2082	C1962	A1829	U1680	U1538	C1437	A1321
U2833	U2478	G2570	A2478	G2345	G2251	C2161	U2092	U1963	G1833	G1681	G1540	G1445	A1328
U2833	C2479	U2571	U2479	A2346	G2252	A2162	G2093	U1963	U1834	G1682	C1541	C1446	U1329
G2834	G2481	A2572	G2481	C2347	G2253	A2163	A2094	C1967	G1834	G1699	A1544	G1450	C1330
A2835	U2727	G2573	A2482	C2350	C2258	C2164	A2095	U1967	U1834	G1715	G1546	C1451	G1341
U2836	G2728	G2574	G2483	G2351	C2258	C2165	A2095	G1968	U1841	G1715	U1554	G1452	A1342
U2836	G2729	C2575	G2484	G2351	G2271	U2166	G2100	A1969	G1842	U1720	U1559	U1457	G1343
G2848	G2732	C2579	G2485	G2357	U2272	U2167	A2101	A1970	A1847	G1721	C1565	U1460	U1344
U2849	A2733	U2580	U2486	G2361	A2273	G2168	G2102	G1971	A1848	G1722	C1566	U1468	C1345
U2861	G2744	U2584	U2491	G2361	A2278	A2169	C2103	G1972	U1856	G1723	U1567	U1468	U1352
G2867	G2744	U2585	G2494	G2364	A2278	A2170	C2104	G1980	U1857	U1729	G1567	U1469	C1357
G2867	G2744	U2586	G2495	G2365	C2283	A2171	U2105	G1981	A1857	C1730	G1568	A1470	G1358
A2872	A2748	U2586	G2496	A2376	G2286	U2172	G2107	U1982	A1858	G1731	A1569	G1475	G1364
A2873	G2751	C2591	A2497	A2377	A2287	C2173	U2108	U1991	G1862	C1732	U1578	A1476	A1365
	G2752	G2592	C2498	A2377	A2288	C2174	G2110	G1992	G1863	G1733			
				C2178									
				C2179									
				U2180									
				U2181									



• Molecule 2: 16S rRNA

Chain 2: 65% 29% 6%





- Molecule 3: 5S rRNA

Chain 3: 77% 19%



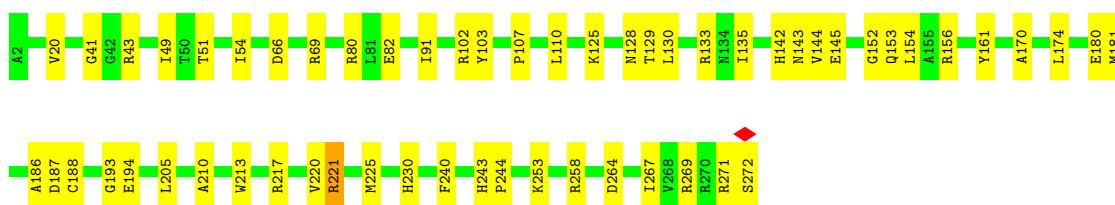
- Molecule 4: mRNA

Chain 4: 100%

There are no outlier residues recorded for this chain.

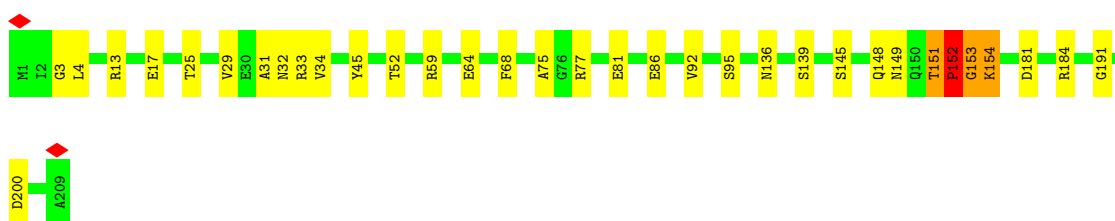
- Molecule 5: 50S ribosomal protein L2

Chain C: 79% 21%



- Molecule 6: 50S ribosomal protein L3

Chain D: 84% 14%



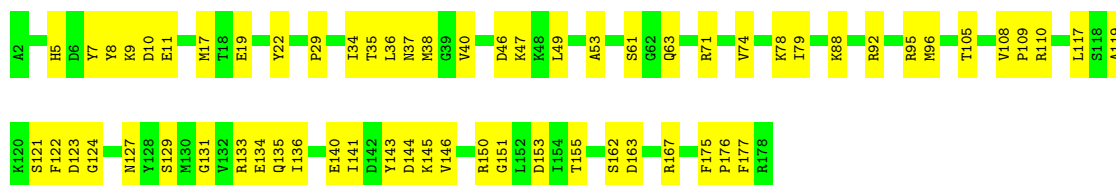
- Molecule 7: 50S ribosomal protein L4

Chain E: 84% 16%

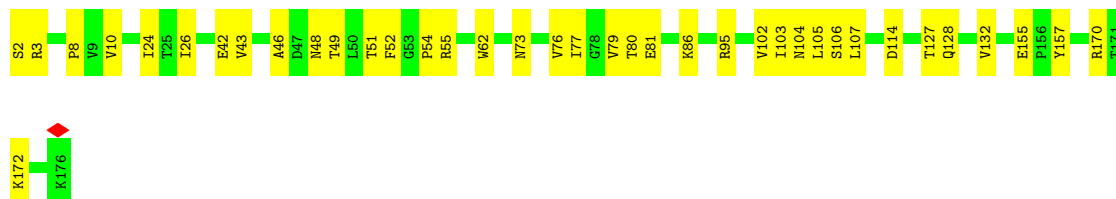
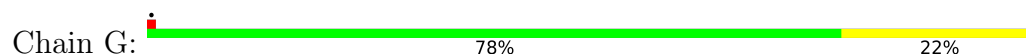


- Molecule 8: 50S ribosomal protein L5

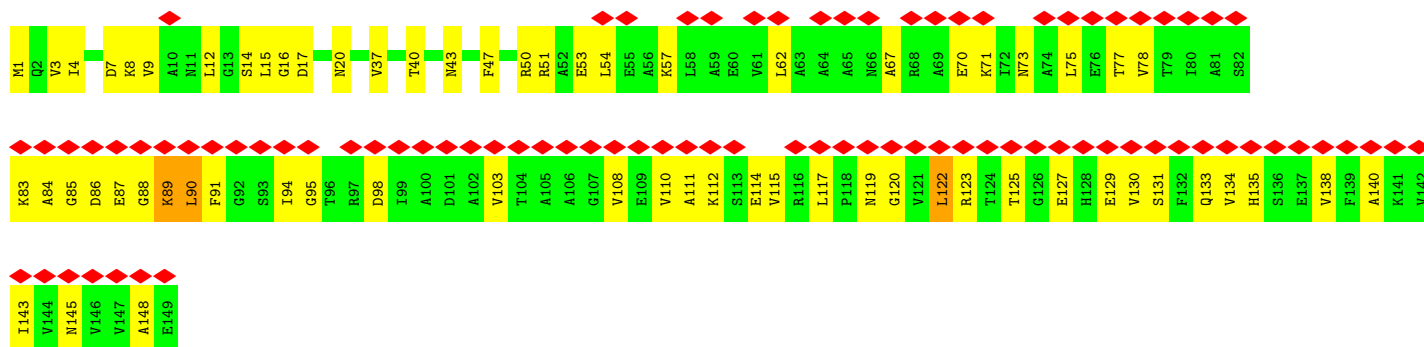
Chain F: 64% 36%



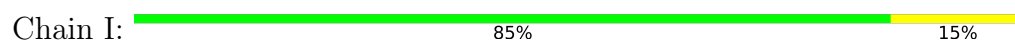
- Molecule 9: 50S ribosomal protein L6



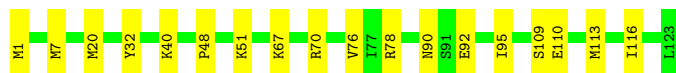
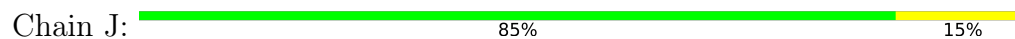
- Molecule 10: 50S ribosomal protein L9



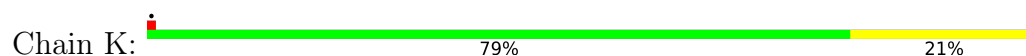
- Molecule 11: 50S ribosomal protein L13



- Molecule 12: 50S ribosomal protein L14

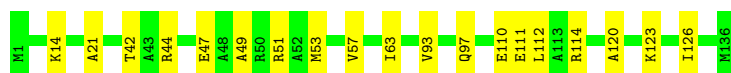
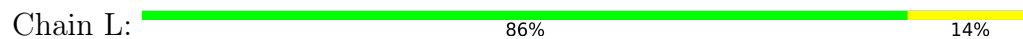


- Molecule 13: 50S ribosomal protein L15

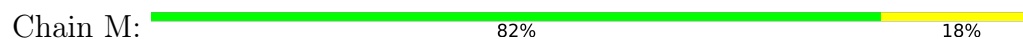




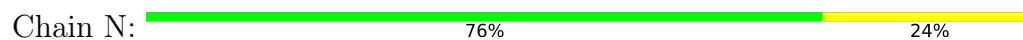
- Molecule 14: 50S ribosomal protein L16



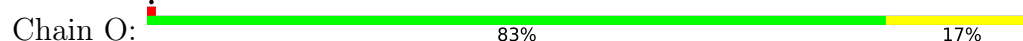
- Molecule 15: 50S ribosomal protein L17



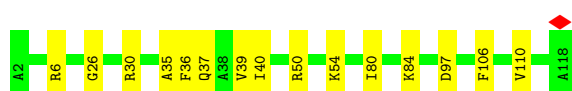
- Molecule 16: 50S ribosomal protein L18



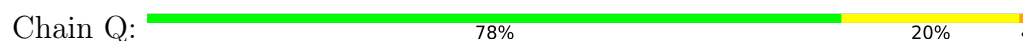
- Molecule 17: 50S ribosomal protein L19



- Molecule 18: 50S ribosomal protein L20



- Molecule 19: 50S ribosomal protein L21



- Molecule 20: 50S ribosomal protein L22





- Molecule 21: 50S ribosomal protein L23

Chain S: 77% 22%



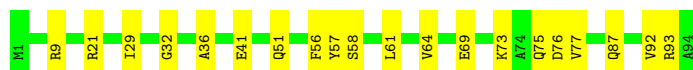
- Molecule 22: 50S ribosomal protein L24

Chain T: 74% 26%



- Molecule 23: 50S ribosomal protein L25

Chain U: 79% 21%



- Molecule 24: 50S ribosomal protein L27

Chain V: 6% 80% 19%



- Molecule 25: 50S ribosomal protein L28

Chain W: 83% 17%



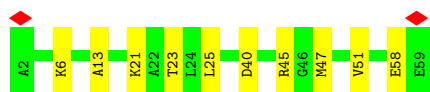
- Molecule 26: 50S ribosomal protein L29

Chain X: 87% 13%



- Molecule 27: 50S ribosomal protein L30

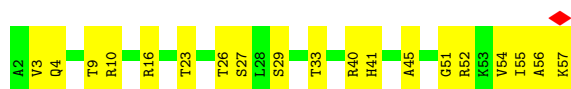
Chain Y: 83% 17%



- Molecule 28: 50S ribosomal protein L31



- Molecule 29: 50S ribosomal protein L32



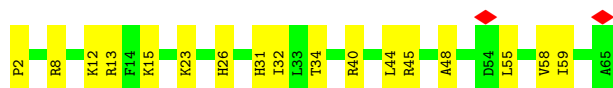
- Molecule 30: 50S ribosomal protein L33



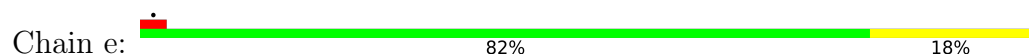
- Molecule 31: 50S ribosomal protein L34



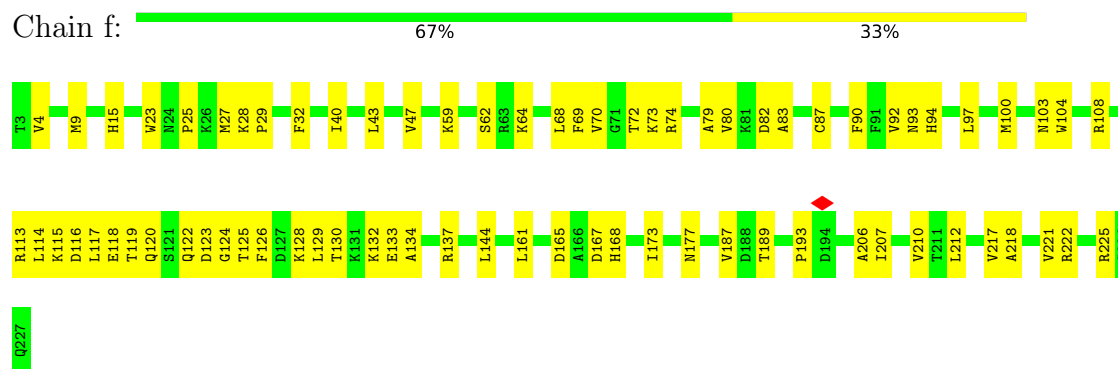
- Molecule 32: 50S ribosomal protein L35



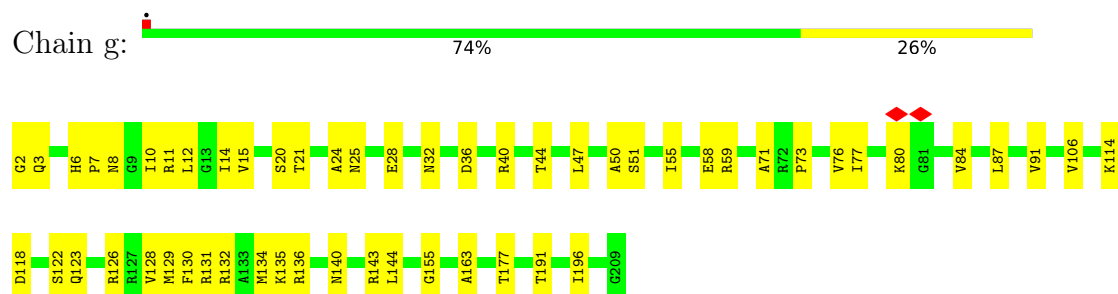
- Molecule 33: 50S ribosomal protein L36



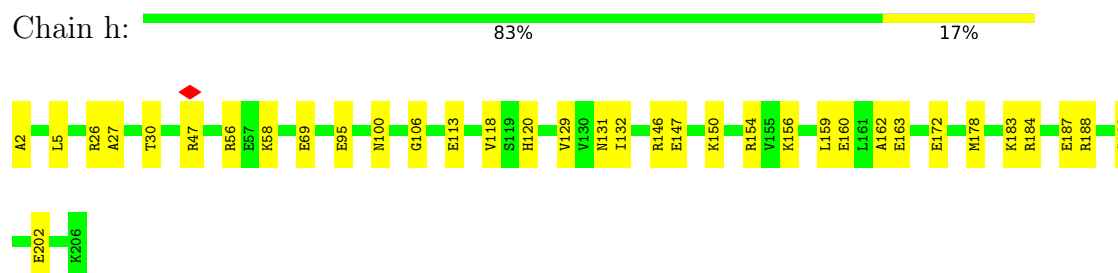
- Molecule 34: 30S ribosomal protein S2



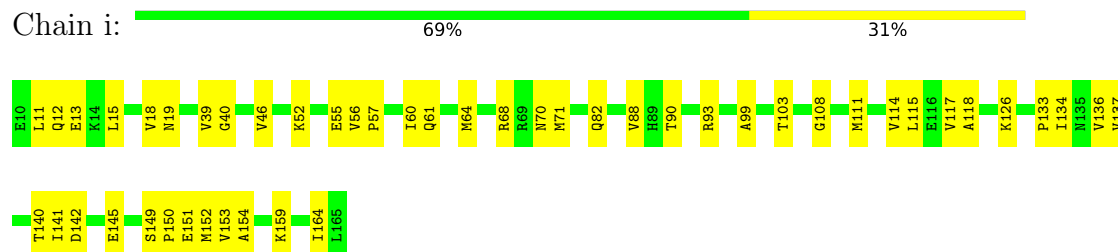
- Molecule 35: 30S ribosomal protein S3



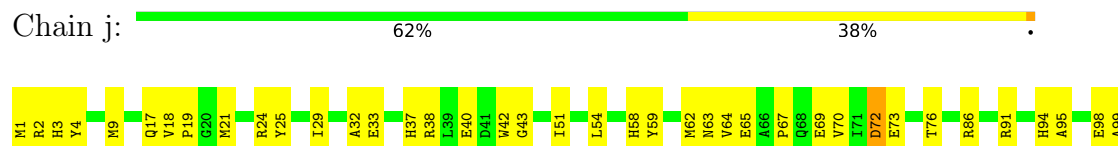
- Molecule 36: 30S ribosomal protein S4



- Molecule 37: 30S ribosomal protein S5



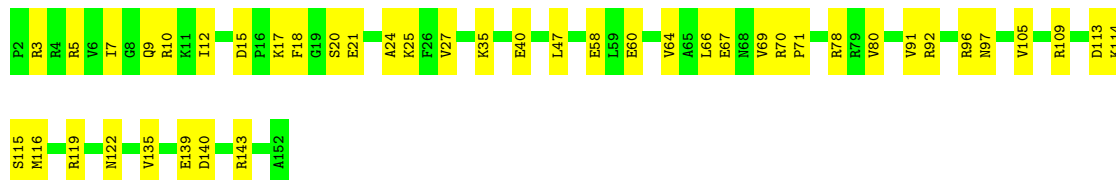
- Molecule 38: 30S ribosomal protein S6





- Molecule 39: 30S ribosomal protein S7

Chain k: 72% 28%



- Molecule 40: 30S ribosomal protein S8

Chain l: 78% 22%



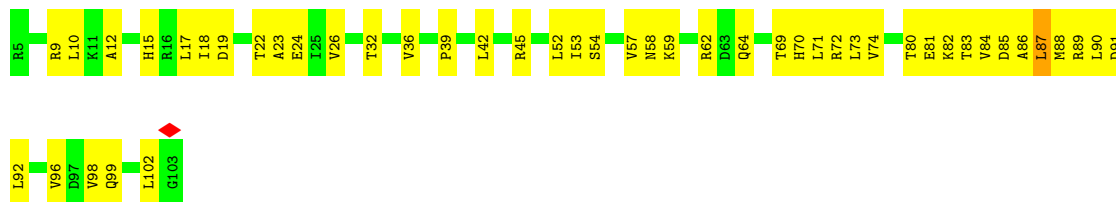
- Molecule 41: 30S ribosomal protein S9

Chain m: 68% 32%



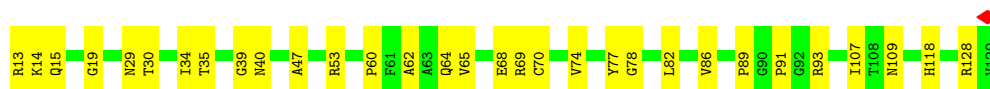
- Molecule 42: 30S ribosomal protein S10

Chain n: 53% 46%



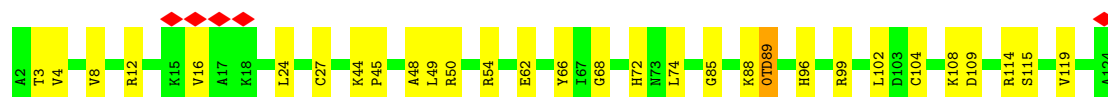
- Molecule 43: 30S ribosomal protein S11

Chain o: 74% 26%



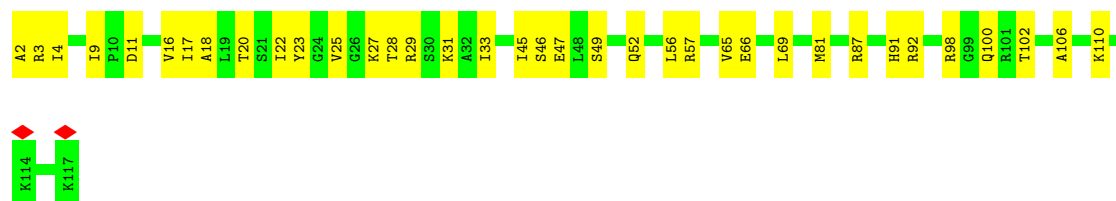
- Molecule 44: 30S ribosomal protein S12

Chain p:  76% 24%



- Molecule 45: 30S ribosomal protein S13

Chain q:  69% 31%



- Molecule 46: 30S ribosomal protein S14

Chain r:  77% 23%



- Molecule 47: 30S ribosomal protein S15

Chain s:  83% 17%



- Molecule 48: 30S ribosomal protein S16

Chain t:  85% 15%



- Molecule 49: 30S ribosomal protein S17

Chain u:  66% 34%

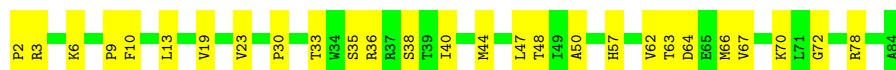


- Molecule 50: 30S ribosomal protein S18

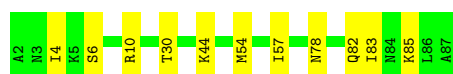
Chain v:  82% 18%



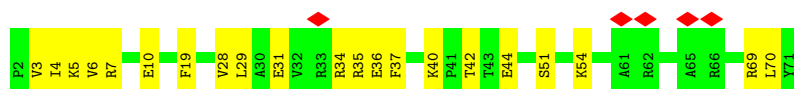
- Molecule 51: 30S ribosomal protein S19



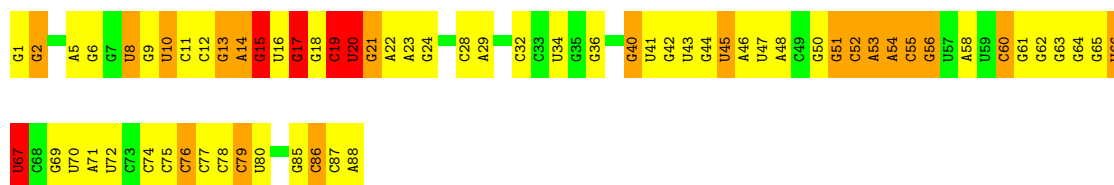
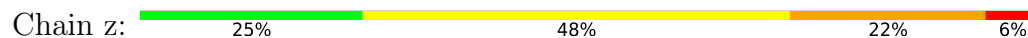
- Molecule 52: 30S ribosomal protein S20



- Molecule 53: 30S ribosomal protein S21



- Molecule 54: tRNA-Ser



- Molecule 55: CspA transcriptional activator



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	44182	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	0.119	Depositor
Minimum map value	-0.042	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: 2MG, 2MA, UR3, 1MG, 5MU, 0TD, PSU, OMG, 5MC, G7M, 6MZ, MA6, MG, OMU, 4OC, FME, 3TD, ZN, OMC

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	0.83	0/69286	0.56	7/108087 (0.0%)
2	2	0.73	0/36590	0.52	0/57074
3	3	0.72	0/2872	0.50	0/4478
4	4	0.65	0/139	0.48	0/214
5	C	1.12	1/2121 (0.0%)	0.72	0/2852
6	D	1.11	0/1586	0.71	1/2134 (0.0%)
7	E	1.02	0/1571	0.70	0/2113
8	F	0.78	0/1434	0.70	0/1926
9	G	0.71	0/1333	0.65	0/1805
10	H	0.53	0/1122	0.91	0/1515
11	I	1.09	0/1152	0.68	0/1551
12	J	1.06	0/955	0.69	0/1279
13	K	1.10	0/1062	0.73	0/1413
14	L	1.05	0/1093	0.67	0/1460
15	M	1.14	0/964	0.76	0/1289
16	N	0.91	0/902	0.74	0/1209
17	O	1.04	0/929	0.66	0/1242
18	P	1.19	0/960	0.78	0/1278
19	Q	1.00	0/829	0.71	2/1107 (0.2%)
20	R	1.11	0/864	0.71	0/1156
21	S	0.98	0/752	0.65	0/1005
22	T	0.83	0/796	0.63	0/1062
23	U	0.93	0/766	0.70	0/1025
24	V	1.06	0/608	0.66	0/804
25	W	1.04	0/635	0.70	0/848
26	X	0.88	0/502	0.74	0/667
27	Y	1.08	0/452	0.67	0/605
28	Z	0.67	1/531 (0.2%)	0.80	2/709 (0.3%)
29	a	1.06	0/450	0.68	0/599
30	b	0.87	0/433	0.62	0/576
31	c	1.20	0/380	0.76	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	d	1.16	0/513	0.77	0/676
33	e	1.08	0/303	0.66	0/397
34	f	0.68	0/1791	0.73	0/2413
35	g	0.85	0/1663	0.71	0/2241
36	h	0.84	0/1665	0.69	0/2227
37	i	0.97	0/1165	0.76	0/1568
38	j	0.76	0/867	0.75	0/1171
39	k	0.74	0/1195	0.72	0/1602
40	l	0.95	0/989	0.69	0/1326
41	m	0.83	0/1034	0.79	0/1375
42	n	0.75	0/800	0.75	0/1082
43	o	0.83	0/893	0.69	0/1205
44	p	0.95	0/960	0.72	0/1286
45	q	0.82	0/909	0.75	0/1215
46	r	0.89	0/817	0.72	0/1088
47	s	0.90	0/722	0.71	0/964
48	t	0.93	0/659	0.69	0/884
49	u	0.80	0/657	0.64	0/881
50	v	0.87	0/553	0.72	0/743
51	w	0.75	0/680	0.69	0/915
52	x	0.90	0/675	0.78	0/895
53	y	0.69	0/597	0.71	0/792
54	z	0.66	2/2062 (0.1%)	0.65	7/3208 (0.2%)
55	B	0.64	0/200	1.15	2/267 (0.7%)
All	All	0.84	4/156438 (0.0%)	0.60	21/234001 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	z	20	U	C5-C6	6.33	1.46	1.34
54	z	20	U	C2-N3	5.39	1.48	1.37
28	Z	6	HIS	C-N	5.37	1.40	1.33
5	C	221	ARG	CB-CG	-5.07	1.37	1.52

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	z	67	U	O5'-P-OP1	-9.70	78.89	108.00
1	1	2512	C	C5'-C4'-C3'	7.62	127.43	116.00
54	z	19	C	OP2-P-O3'	-7.56	85.32	108.00
28	Z	6	HIS	CA-C-N	7.15	127.08	120.21
28	Z	6	HIS	C-N-CA	7.15	127.08	120.21

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	31365	573	0
2	2	32929	0	16586	320	0
3	3	2569	0	1301	17	0
4	4	126	0	65	0	0
5	C	2082	0	2154	39	0
6	D	1565	0	1616	30	0
7	E	1552	0	1619	27	0
8	F	1410	0	1444	57	0
9	G	1313	0	1358	23	0
10	H	1111	0	1148	60	0
11	I	1129	0	1162	16	0
12	J	946	0	1023	17	0
13	K	1053	0	1129	25	0
14	L	1074	0	1157	13	0
15	M	951	0	994	19	0
16	N	892	0	923	19	0
17	O	917	0	962	14	0
18	P	947	0	1019	10	0
19	Q	816	0	839	23	0
20	R	857	0	922	20	0
21	S	746	0	811	16	0
22	T	788	0	843	20	0
23	U	753	0	780	13	0
24	V	601	0	615	13	0
25	W	625	0	652	11	0
26	X	501	0	531	5	0
27	Y	448	0	488	6	0
28	Z	522	0	520	25	0
29	a	444	0	458	13	0
30	b	426	0	464	3	0
31	c	377	0	418	11	0
32	d	504	0	572	13	0
33	e	302	0	340	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	f	1760	0	1787	64	0
35	g	1636	0	1710	40	0
36	h	1643	0	1707	31	0
37	i	1152	0	1196	36	0
38	j	848	0	846	37	0
39	k	1181	0	1238	38	0
40	l	979	0	1031	23	0
41	m	1022	0	1070	33	0
42	n	790	0	831	37	0
43	o	877	0	887	24	0
44	p	957	0	1017	24	0
45	q	900	0	965	31	0
46	r	805	0	844	25	0
47	s	714	0	734	12	0
48	t	649	0	666	8	0
49	u	648	0	691	20	0
50	v	544	0	560	9	0
51	w	663	0	688	23	0
52	x	669	0	719	8	0
53	y	589	0	629	18	0
54	z	1891	0	955	63	0
55	B	205	0	195	27	0
56	1	276	0	0	0	0
56	2	119	0	0	0	0
56	3	8	0	0	0	0
56	4	1	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	q	1	0	0	0	0
56	r	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	145152	0	97244	1854	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 8.

The worst 5 of 1854 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)
6:D:151:THR:HG23	6:D:152:PRO:HD3	1.27	1.15
55:B:2:SER:HA	55:B:5:MET:HB3	1.41	1.03
1:1:1068:G:N2	1:1:1095:A:N3	2.10	0.99
42:n:57:VAL:O	42:n:58:ASN:ND2	1.98	0.97
55:B:2:SER:HA	55:B:5:MET:CB	1.96	0.94

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	
5	C	269/271 (99%)	256 (95%)	13 (5%)	0	100	100
6	D	207/209 (99%)	200 (97%)	4 (2%)	3 (1%)	9	36
7	E	199/201 (99%)	197 (99%)	2 (1%)	0	100	100
8	F	175/177 (99%)	163 (93%)	11 (6%)	1 (1%)	21	56
9	G	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
10	H	147/149 (99%)	137 (93%)	8 (5%)	2 (1%)	9	36
11	I	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
12	J	121/123 (98%)	119 (98%)	2 (2%)	0	100	100
13	K	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
14	L	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
15	M	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
16	N	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
17	O	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
18	P	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
19	Q	101/103 (98%)	93 (92%)	6 (6%)	2 (2%)	6	28
20	R	108/110 (98%)	106 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	S	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
22	T	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
23	U	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
24	V	78/80 (98%)	72 (92%)	6 (8%)	0	100	100
25	W	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
26	X	60/62 (97%)	60 (100%)	0	0	100	100
27	Y	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
28	Z	64/66 (97%)	60 (94%)	4 (6%)	0	100	100
29	a	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
30	b	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
31	c	44/46 (96%)	44 (100%)	0	0	100	100
32	d	62/64 (97%)	58 (94%)	4 (6%)	0	100	100
33	e	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
34	f	223/225 (99%)	209 (94%)	14 (6%)	0	100	100
35	g	206/208 (99%)	195 (95%)	11 (5%)	0	100	100
36	h	203/205 (99%)	200 (98%)	3 (2%)	0	100	100
37	i	154/156 (99%)	144 (94%)	10 (6%)	0	100	100
38	j	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
39	k	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
40	l	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
41	m	125/127 (98%)	118 (94%)	7 (6%)	0	100	100
42	n	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
43	o	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
44	p	120/123 (98%)	113 (94%)	7 (6%)	0	100	100
45	q	114/116 (98%)	108 (95%)	6 (5%)	0	100	100
46	r	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
47	s	86/88 (98%)	84 (98%)	2 (2%)	0	100	100
48	t	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
49	u	78/80 (98%)	75 (96%)	3 (4%)	0	100	100
50	v	64/66 (97%)	64 (100%)	0	0	100	100
51	w	81/83 (98%)	79 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	x	84/86 (98%)	84 (100%)	0	0	100	100
53	y	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
55	B	25/27 (93%)	19 (76%)	5 (20%)	1 (4%)	2	14
All	All	5637/5738 (98%)	5420 (96%)	208 (4%)	9 (0%)	44	76

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	D	152	PRO
6	D	153	GLY
6	D	154	LYS
10	H	90	LEU
19	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	
5	C	216/216 (100%)	216 (100%)	0	100	100
6	D	164/164 (100%)	163 (99%)	1 (1%)	78	88
7	E	165/165 (100%)	165 (100%)	0	100	100
8	F	148/148 (100%)	148 (100%)	0	100	100
9	G	136/136 (100%)	136 (100%)	0	100	100
10	H	114/114 (100%)	113 (99%)	1 (1%)	70	85
11	I	116/116 (100%)	116 (100%)	0	100	100
12	J	104/104 (100%)	104 (100%)	0	100	100
13	K	103/103 (100%)	103 (100%)	0	100	100
14	L	109/109 (100%)	109 (100%)	0	100	100
15	M	99/99 (100%)	99 (100%)	0	100	100
16	N	86/86 (100%)	86 (100%)	0	100	100
17	O	99/99 (100%)	99 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	P	89/89 (100%)	89 (100%)	0	100	100
19	Q	84/84 (100%)	84 (100%)	0	100	100
20	R	93/93 (100%)	93 (100%)	0	100	100
21	S	81/81 (100%)	80 (99%)	1 (1%)	63	82
22	T	84/84 (100%)	84 (100%)	0	100	100
23	U	78/78 (100%)	78 (100%)	0	100	100
24	V	59/59 (100%)	58 (98%)	1 (2%)	53	78
25	W	67/67 (100%)	67 (100%)	0	100	100
26	X	54/54 (100%)	54 (100%)	0	100	100
27	Y	48/48 (100%)	48 (100%)	0	100	100
28	Z	59/59 (100%)	59 (100%)	0	100	100
29	a	47/47 (100%)	47 (100%)	0	100	100
30	b	47/47 (100%)	47 (100%)	0	100	100
31	c	38/38 (100%)	38 (100%)	0	100	100
32	d	51/51 (100%)	50 (98%)	1 (2%)	48	76
33	e	34/34 (100%)	34 (100%)	0	100	100
34	f	187/187 (100%)	187 (100%)	0	100	100
35	g	171/171 (100%)	171 (100%)	0	100	100
36	h	172/172 (100%)	172 (100%)	0	100	100
37	i	119/119 (100%)	119 (100%)	0	100	100
38	j	91/91 (100%)	90 (99%)	1 (1%)	65	83
39	k	124/124 (100%)	124 (100%)	0	100	100
40	l	104/104 (100%)	104 (100%)	0	100	100
41	m	105/105 (100%)	105 (100%)	0	100	100
42	n	86/86 (100%)	85 (99%)	1 (1%)	63	82
43	o	90/90 (100%)	90 (100%)	0	100	100
44	p	102/102 (100%)	102 (100%)	0	100	100
45	q	94/94 (100%)	94 (100%)	0	100	100
46	r	83/83 (100%)	83 (100%)	0	100	100
47	s	76/76 (100%)	76 (100%)	0	100	100
48	t	65/65 (100%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	u	74/74 (100%)	74 (100%)	0	100	100
50	v	57/57 (100%)	57 (100%)	0	100	100
51	w	72/72 (100%)	72 (100%)	0	100	100
52	x	65/65 (100%)	64 (98%)	1 (2%)	57	80
53	y	60/60 (100%)	60 (100%)	0	100	100
55	B	20/20 (100%)	18 (90%)	2 (10%)	7	29
All	All	4689/4689 (100%)	4679 (100%)	10 (0%)	85	92

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
52	x	57	ILE
55	B	9	VAL
55	B	12	PHE
24	V	10	THR
32	d	31	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
52	x	20	HIS
52	x	61	GLN
18	P	71	GLN
16	N	116	GLN
52	x	82	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2903 (99%)	500 (17%)	14 (0%)
2	2	1532/1534 (99%)	250 (16%)	4 (0%)
3	3	119/120 (99%)	15 (12%)	0
4	4	5/6 (83%)	0	0
54	z	87/88 (98%)	31 (35%)	0
All	All	4645/4651 (99%)	796 (17%)	18 (0%)

5 of 796 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
2	2	1145	A
2	2	1109	C
1	1	2116	G
1	1	2756	U

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

37 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$
2	PSU	2	516	2,56	18,21,22	1.04	1 (5%)	22,30,33	1.90	4 (18%)
2	MA6	2	1519	2	23,26,27	1.70	6 (26%)	34,38,41	3.16	11 (32%)
1	PSU	1	2457	1	18,21,22	1.20	2 (11%)	22,30,33	2.12	5 (22%)
1	PSU	1	955	1,56	18,21,22	1.11	1 (5%)	22,30,33	2.08	4 (18%)
54	5MU	z	66	54	19,22,23	4.51	7 (36%)	28,32,35	3.82	11 (39%)
1	6MZ	1	2030	1	22,25,26	2.58	6 (27%)	30,36,39	3.29	12 (40%)
2	UR3	2	1498	2,56	19,22,23	2.39	6 (31%)	26,32,35	0.99	2 (7%)
2	MA6	2	1518	2	23,26,27	1.70	6 (26%)	34,38,41	3.36	11 (32%)
2	G7M	2	527	2	23,26,27	2.81	9 (39%)	35,39,42	2.24	11 (31%)
1	PSU	1	2605	1	18,21,22	1.08	1 (5%)	22,30,33	2.00	4 (18%)
2	2MG	2	1516	2	23,26,27	2.55	8 (34%)	32,38,41	2.10	10 (31%)
1	OMC	1	2498	1,56	19,22,23	2.46	6 (31%)	26,31,34	1.00	2 (7%)

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	3.87	6 (33%)	22,32,35	1.41	2 (9%)
1	2MG	1	2445	1	23,26,27	2.50	7 (30%)	32,38,41	1.91	9 (28%)
44	0TD	p	89	44	7,9,10	1.38	0	6,11,13	1.93	2 (33%)
2	2MG	2	966	2	23,26,27	2.65	8 (34%)	32,38,41	2.01	7 (21%)
1	PSU	1	1917	1	18,21,22	1.03	1 (5%)	22,30,33	2.03	5 (22%)
1	PSU	1	746	1,56	18,21,22	1.03	1 (5%)	22,30,33	1.76	3 (13%)
1	5MC	1	1962	1	18,22,23	3.07	7 (38%)	26,32,35	1.10	3 (11%)
2	5MC	2	1407	2	18,22,23	3.03	7 (38%)	26,32,35	0.91	1 (3%)
1	PSU	1	2580	1,56	18,21,22	1.14	2 (11%)	22,30,33	1.82	5 (22%)
1	5MU	1	1939	1,56	19,22,23	4.17	7 (36%)	28,32,35	3.76	9 (32%)
1	PSU	1	1911	1	18,21,22	1.01	1 (5%)	22,30,33	1.95	5 (22%)
1	6MZ	1	1618	1	22,25,26	2.47	7 (31%)	30,36,39	3.31	11 (36%)
1	OMU	1	2552	1	19,22,23	2.64	6 (31%)	26,31,34	1.78	6 (23%)
2	5MC	2	967	2	18,22,23	3.23	7 (38%)	26,32,35	1.01	2 (7%)
55	FME	B	1	55	8,9,10	0.50	0	7,9,11	1.12	1 (14%)
2	2MG	2	1207	2	23,26,27	2.58	8 (34%)	32,38,41	1.94	10 (31%)
1	OMG	1	2251	1,54	23,26,27	2.13	6 (26%)	33,38,41	1.66	8 (24%)
54	OMG	z	17	54	27,27,27	3.41	9 (33%)	40,41,41	6.54	15 (37%)
1	G7M	1	2069	1	23,26,27	2.73	8 (34%)	35,39,42	2.19	12 (34%)
2	4OC	2	1402	2	20,23,24	2.68	8 (40%)	26,32,35	1.09	1 (3%)
1	5MU	1	747	1	19,22,23	4.42	7 (36%)	28,32,35	3.78	10 (35%)
1	2MA	1	2503	1,56	22,25,26	3.47	10 (45%)	33,37,40	2.23	9 (27%)
1	PSU	1	2504	1	18,21,22	1.08	1 (5%)	22,30,33	1.93	5 (22%)
1	2MG	1	1835	1	23,26,27	2.52	9 (39%)	32,38,41	1.99	8 (25%)
1	1MG	1	745	1	22,26,27	2.77	7 (31%)	33,39,42	2.15	7 (21%)

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
2	PSU	2	516	2,56	-	2/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	2/11/29/30	0/3/3/3
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	PSU	1	955	1,56	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
54	5MU	z	66	54	-	2/7/25/26	0/2/2/2
1	6MZ	1	2030	1	-	4/9/27/28	0/3/3/3
2	UR3	2	1498	2,56	-	0/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
2	G7M	2	527	2	-	3/7/25/26	0/3/3/3
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
1	OMC	1	2498	1,56	-	0/9/27/28	0/2/2/2
1	3TD	1	1915	1	-	2/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	2/9/27/28	0/3/3/3
44	0TD	p	89	44	-	2/7/12/14	-
2	2MG	2	966	2	-	2/9/27/28	0/3/3/3
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	PSU	1	746	1,56	-	1/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	PSU	1	2580	1,56	-	0/7/25/26	0/2/2/2
1	5MU	1	1939	1,56	-	0/7/25/26	0/2/2/2
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
1	6MZ	1	1618	1	-	4/9/27/28	0/3/3/3
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
55	FME	B	1	55	-	4/7/9/11	-
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
1	OMG	1	2251	1,54	-	0/9/27/28	0/3/3/3
54	OMG	z	17	54	-	3/12/28/28	0/3/3/3
1	G7M	1	2069	1	-	1/7/25/26	0/3/3/3
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
1	2MA	1	2503	1,56	-	2/7/25/26	0/3/3/3
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3

The worst 5 of 199 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	11.21	1.48	1.35
54	z	66	5MU	C2-N1	10.77	1.55	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2503	2MA	C4-N3	10.67	1.47	1.34
1	1	747	5MU	C2-N1	10.18	1.54	1.38
54	z	17	OMG	O6-C6	-10.11	1.04	1.23

The worst 5 of 243 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	z	17	OMG	O6-C6-N1	-29.76	63.06	120.12
54	z	17	OMG	O6-C6-C5	-23.83	63.37	126.60
2	2	1518	MA6	N1-C6-N6	-14.31	101.43	117.08
2	2	1519	MA6	N1-C6-N6	-13.10	102.76	117.08
54	z	66	5MU	C5-C4-N3	12.53	126.01	115.31

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
2	2	527	G7M	C3'-C4'-C5'-O5'
2	2	967	5MC	O4'-C4'-C5'-O5'
2	2	967	5MC	C3'-C4'-C5'-O5'

There are no ring outliers.

18 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	516	PSU	2	0
2	2	1519	MA6	1	0
1	1	2457	PSU	1	0
1	1	955	PSU	1	0
54	z	66	5MU	5	0
1	1	2030	6MZ	3	0
2	2	1498	UR3	1	0
2	2	1518	MA6	1	0
2	2	1516	2MG	1	0
1	1	2498	OMC	1	0
1	1	1915	3TD	2	0
1	1	2445	2MG	1	0
44	p	89	0TD	2	0
1	1	2580	PSU	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	2552	OMU	1	0
55	B	1	FME	4	0
54	z	17	OMG	5	0
1	1	1835	2MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 418 ligands modelled in this entry, 418 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.

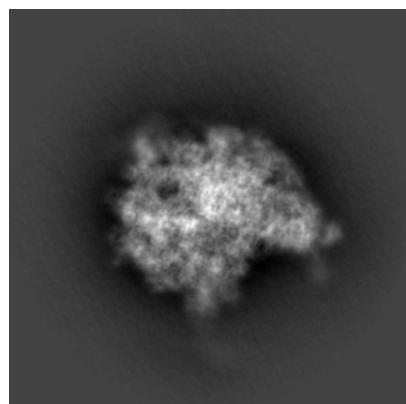
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12928. These allow visual inspection of the internal detail of the map and identification of artifacts.

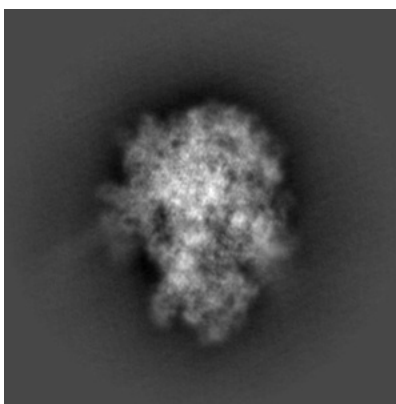
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

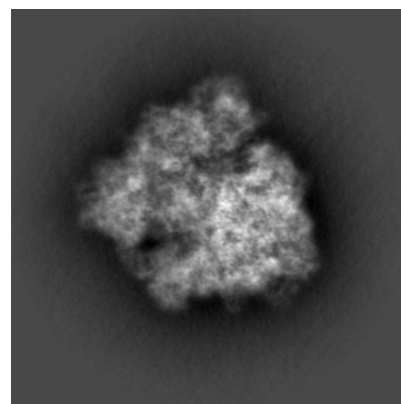
6.1.1 Primary map



X

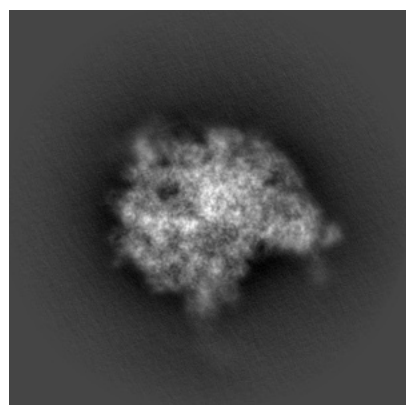


Y

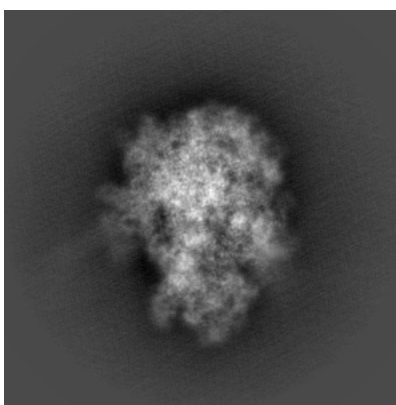


Z

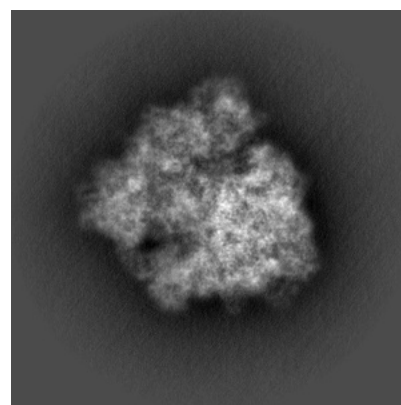
6.1.2 Raw map



X



Y

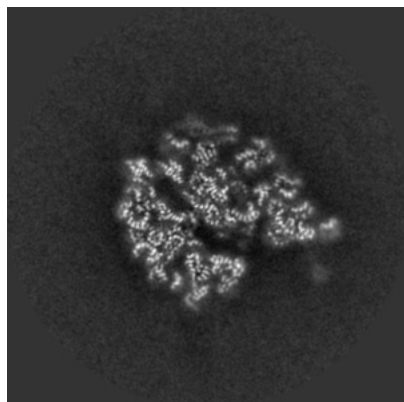


Z

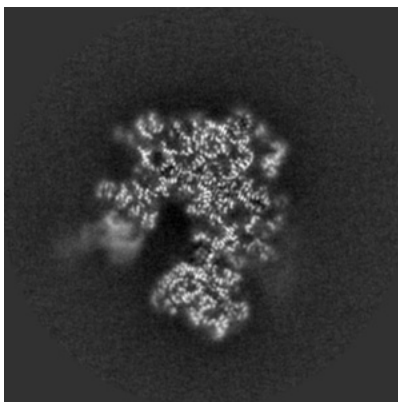
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

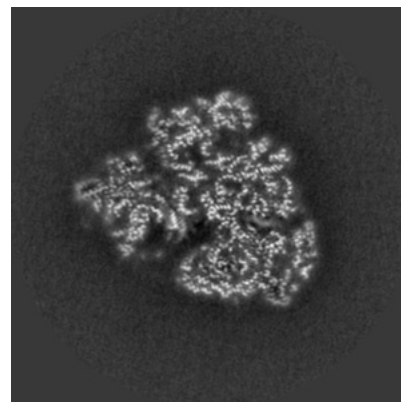
6.2.1 Primary map



X Index: 200

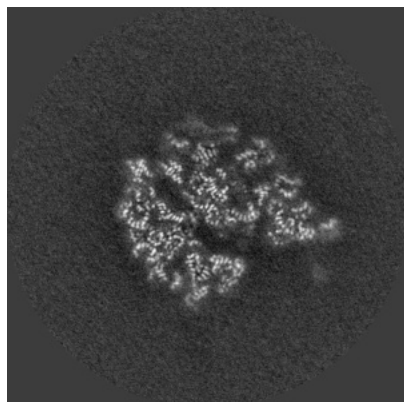


Y Index: 200

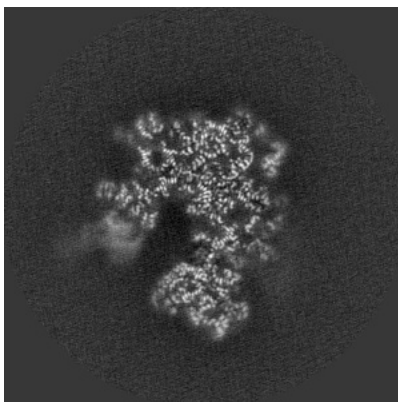


Z Index: 200

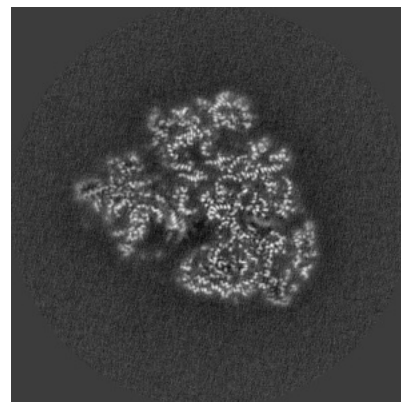
6.2.2 Raw map



X Index: 200



Y Index: 200

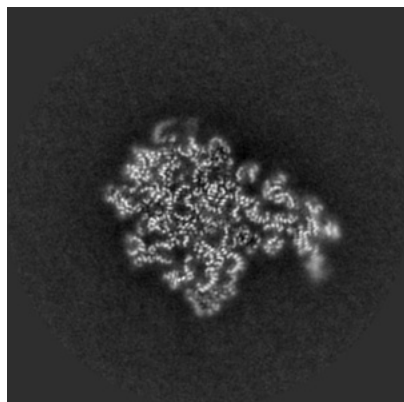


Z Index: 200

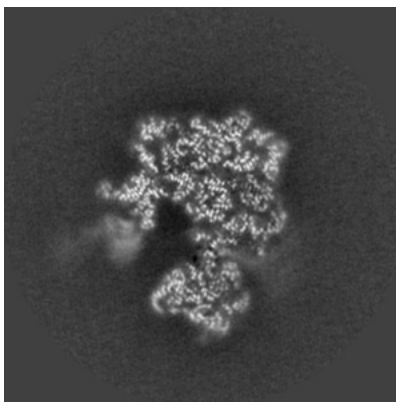
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

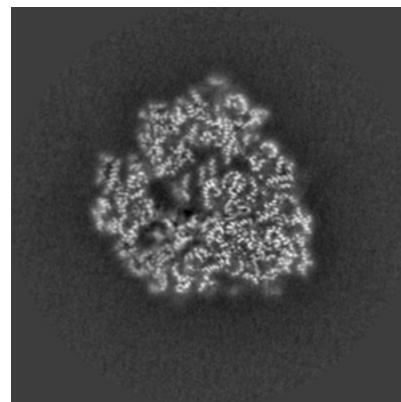
6.3.1 Primary map



X Index: 216

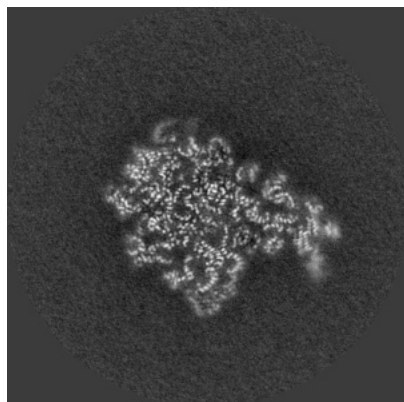


Y Index: 205

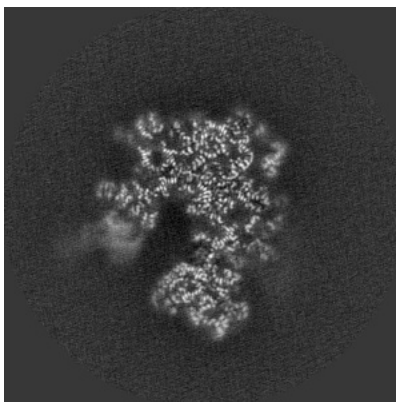


Z Index: 187

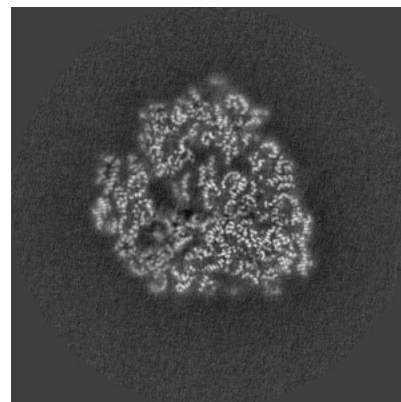
6.3.2 Raw map



X Index: 216



Y Index: 200

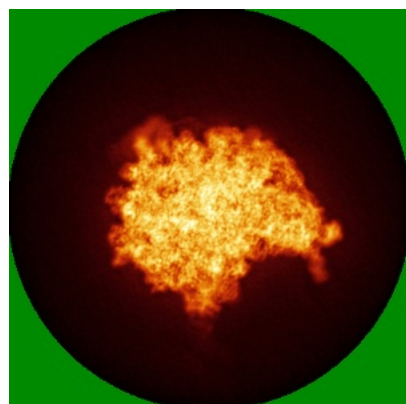


Z Index: 188

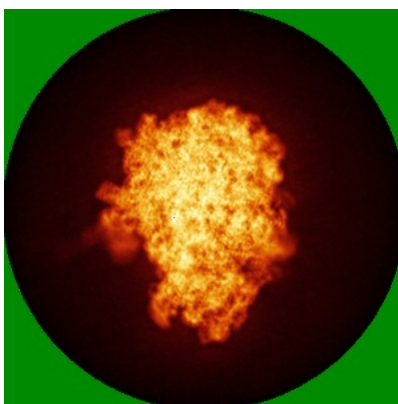
The images above show the largest variance slices of the map in three orthogonal directions.

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

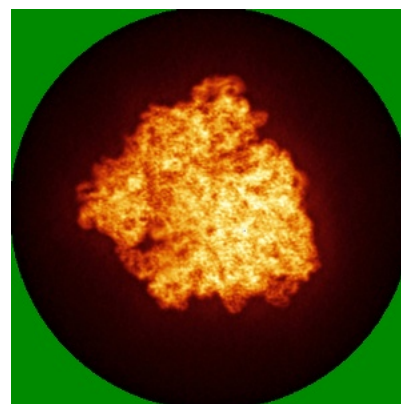
6.4.1 Primary map



X

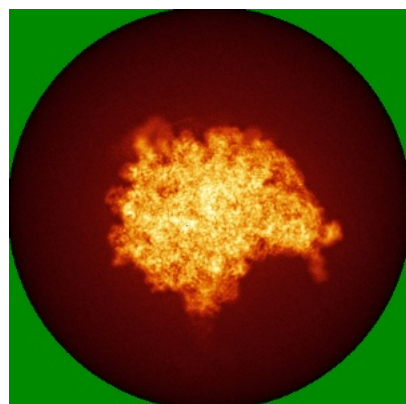


Y

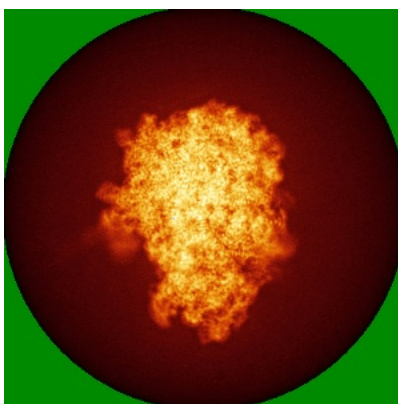


Z

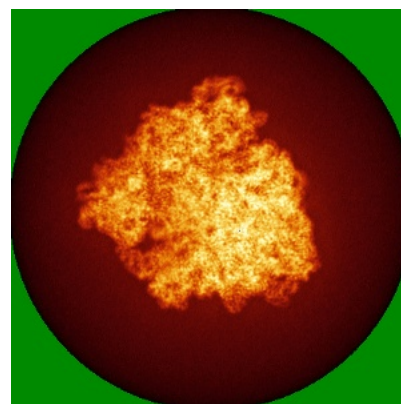
6.4.2 Raw map



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.

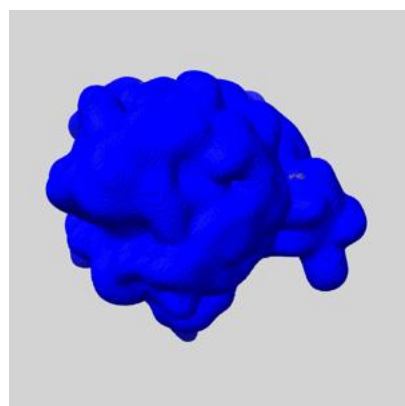
6.6 Mask visualisation [i](#)

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

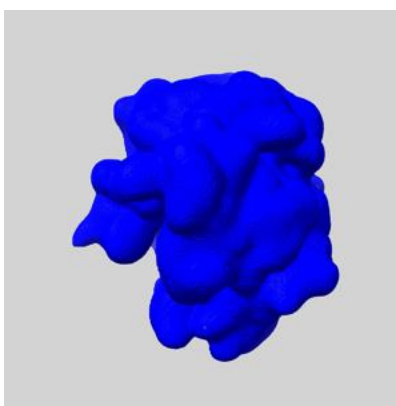
A mask typically either:

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

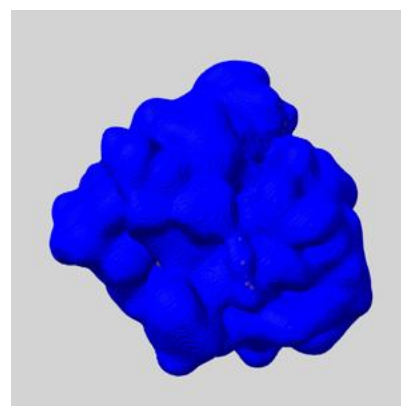
6.6.1 emd_12928_msk_1.map [i](#)



X



Y

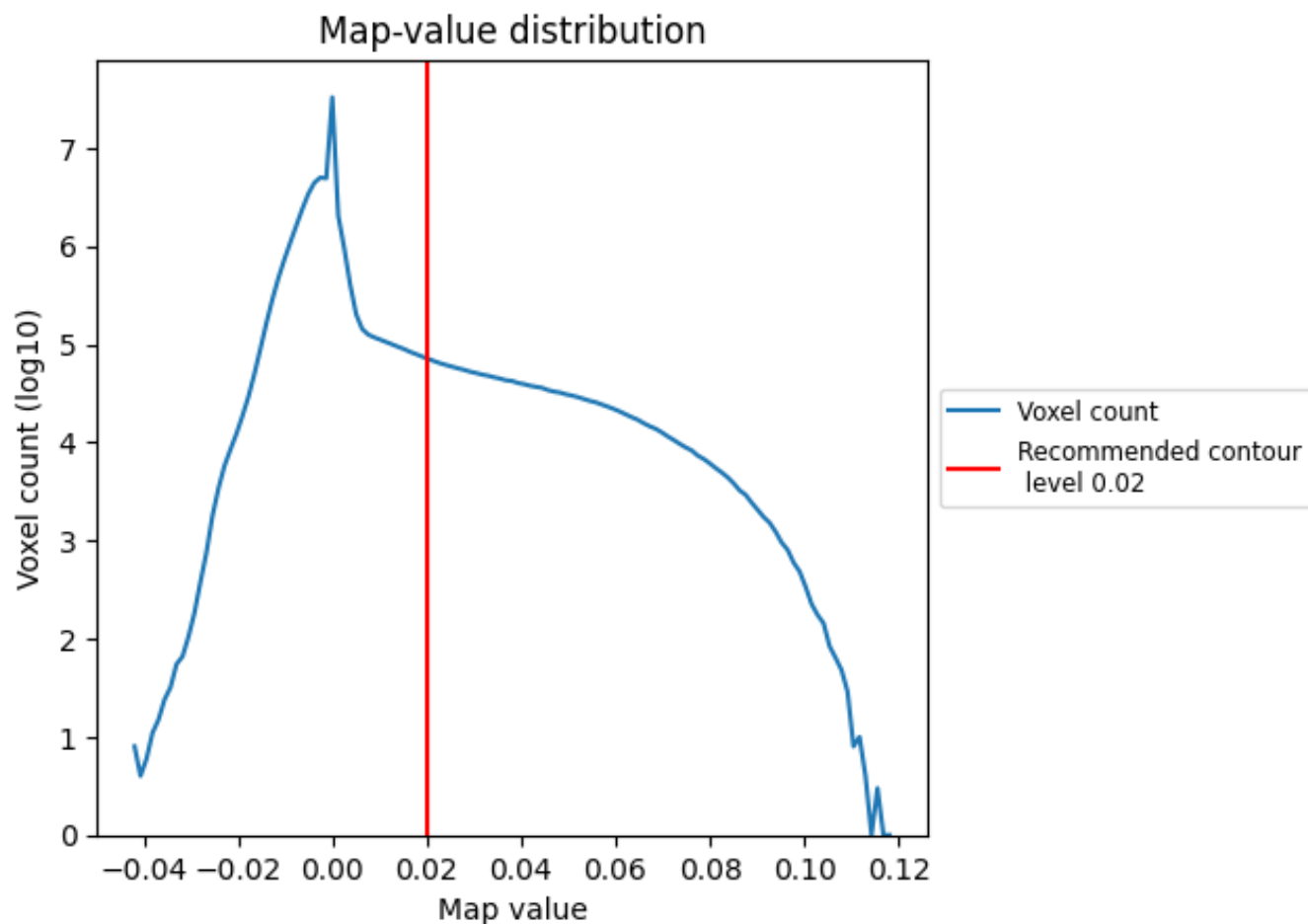


Z

7 Map analysis [i](#)

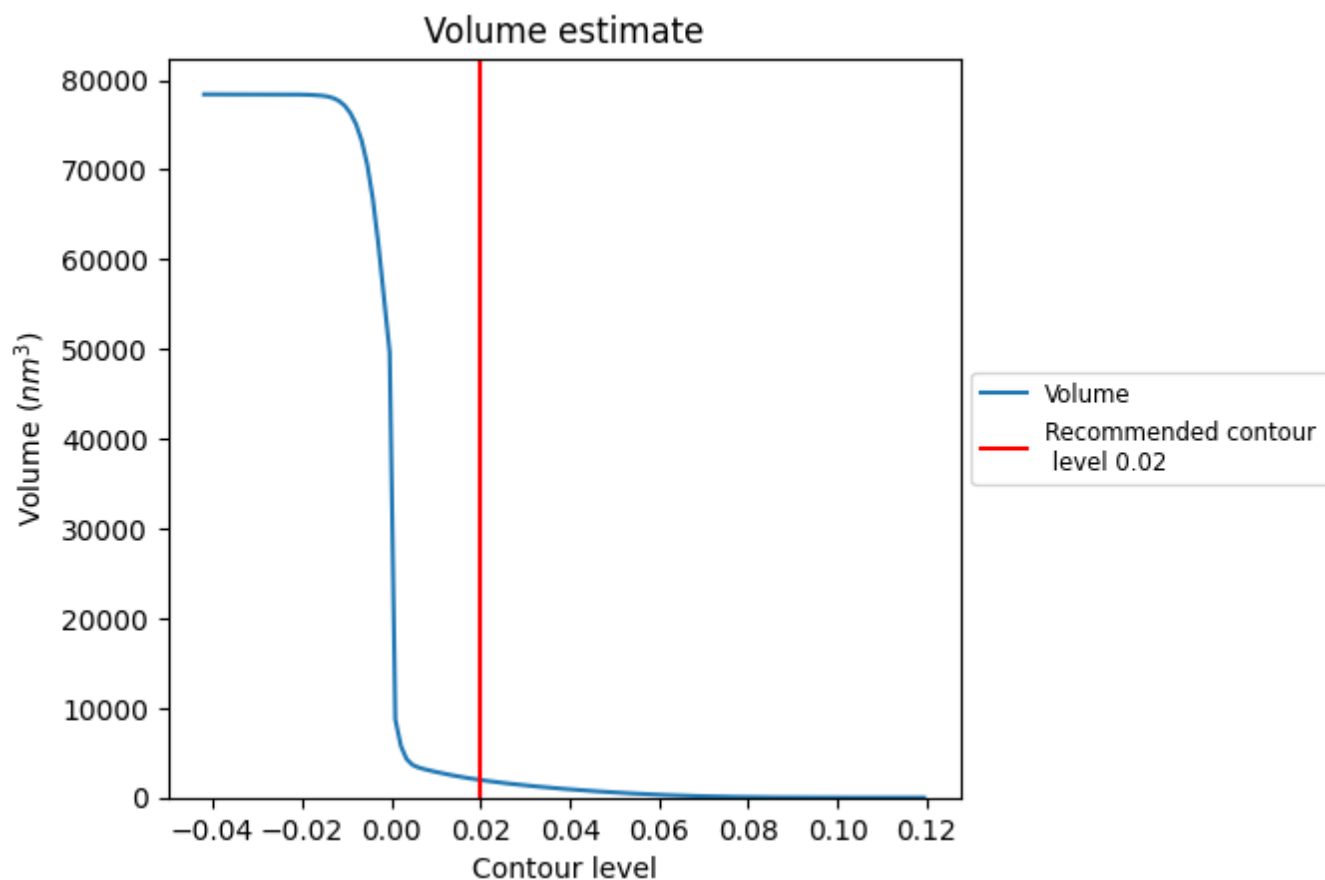
This section contains the results of statistical analysis of the map.

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.

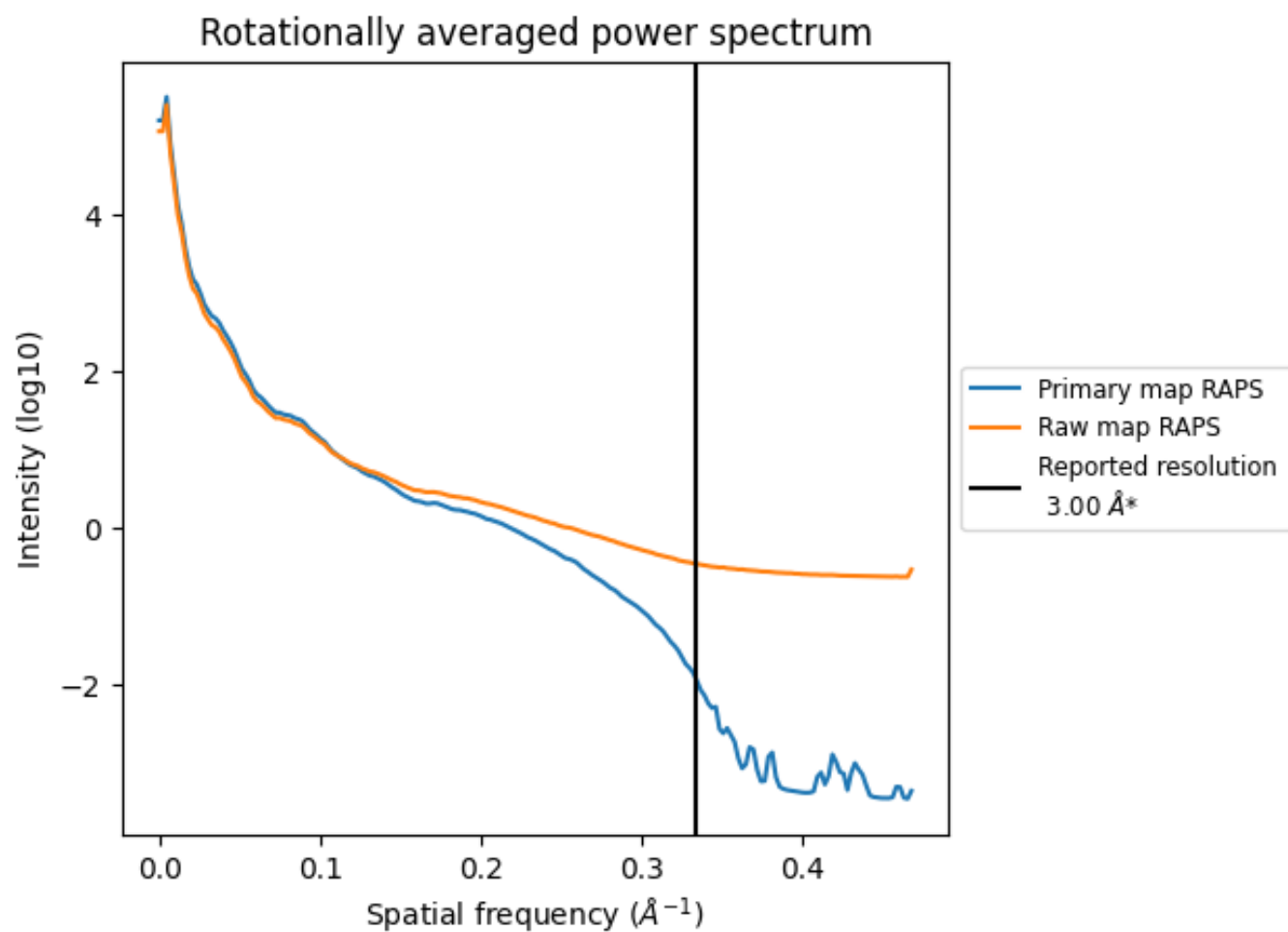
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1958 nm^3 ; this corresponds to an approximate mass of 1769 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 ⓘ

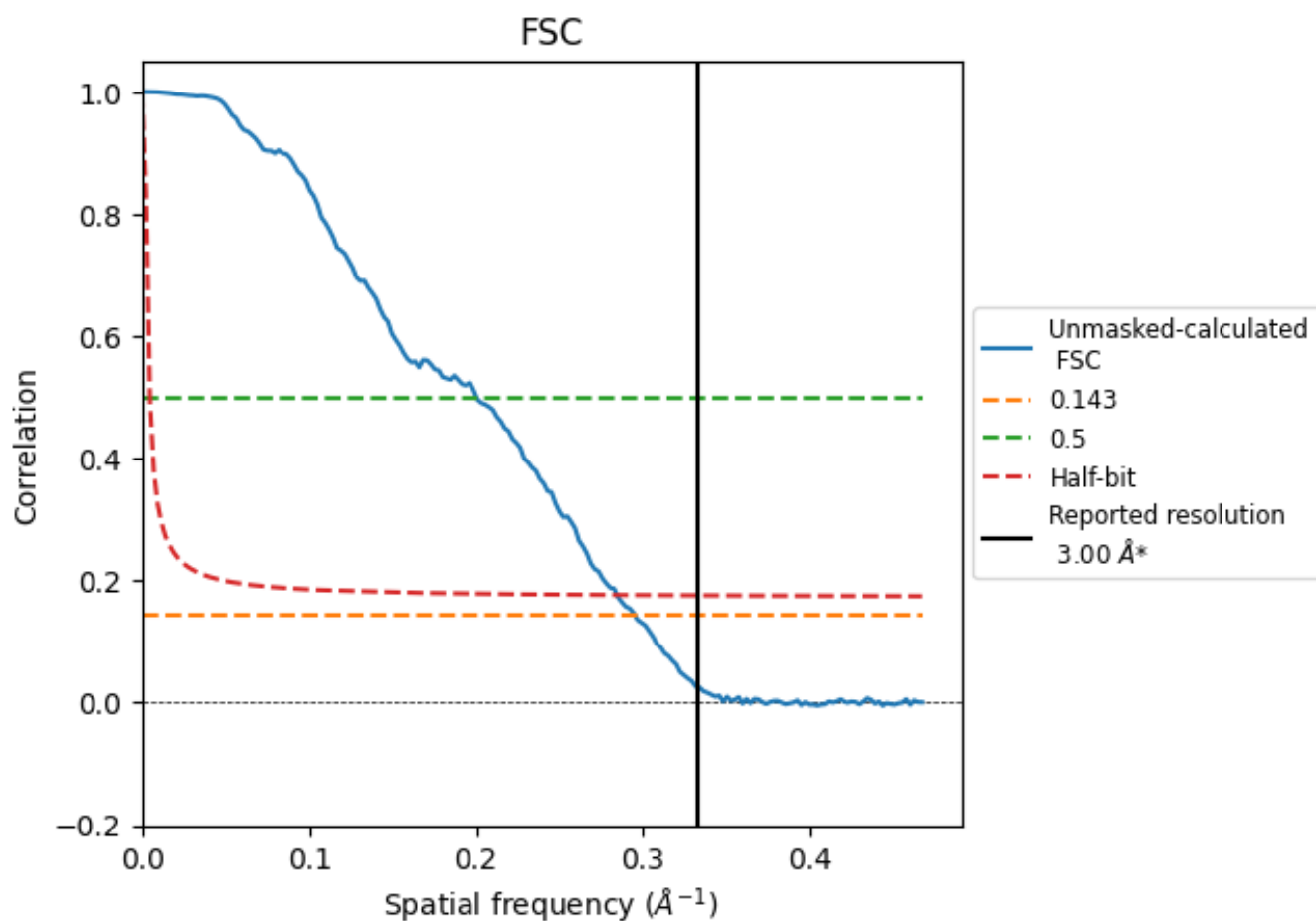


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

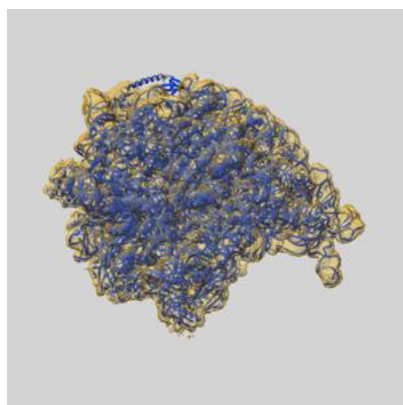
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.39	4.99	3.52

*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 3.39 differs from the reported value 3.0 by more than 10 %

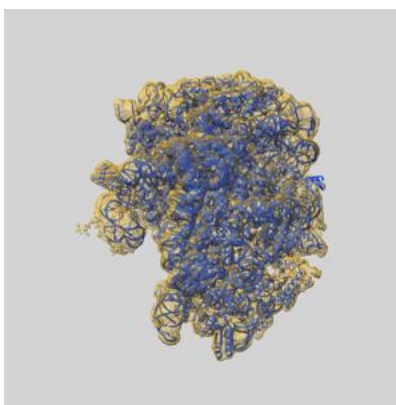
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12928 and PDB model 7OIF. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

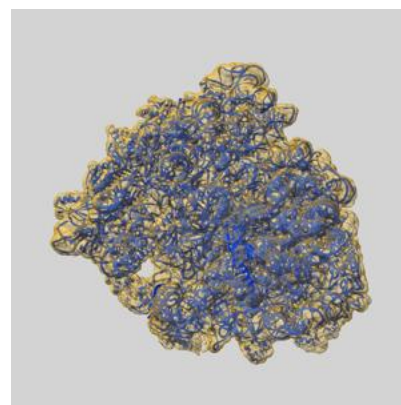
9.1 Map-model overlay [i](#)



X



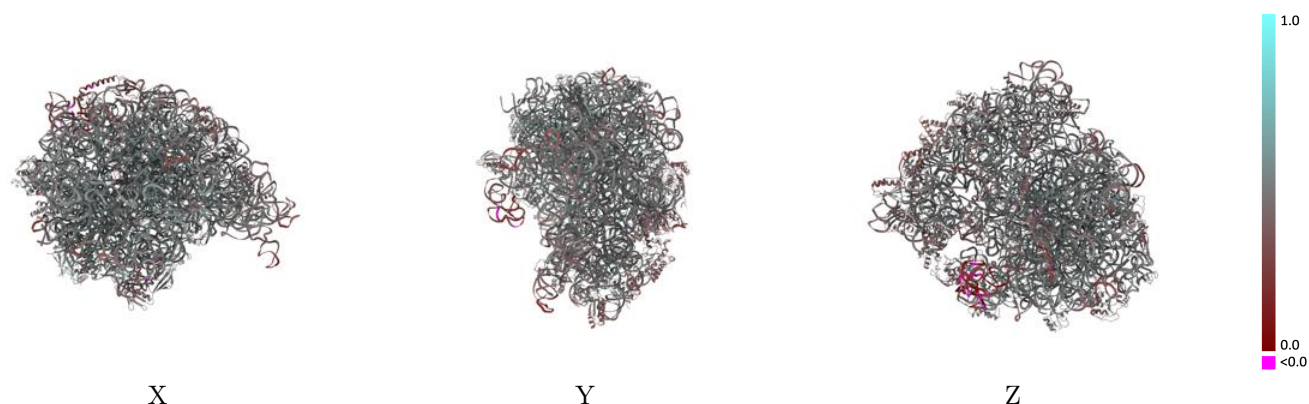
Y



Z

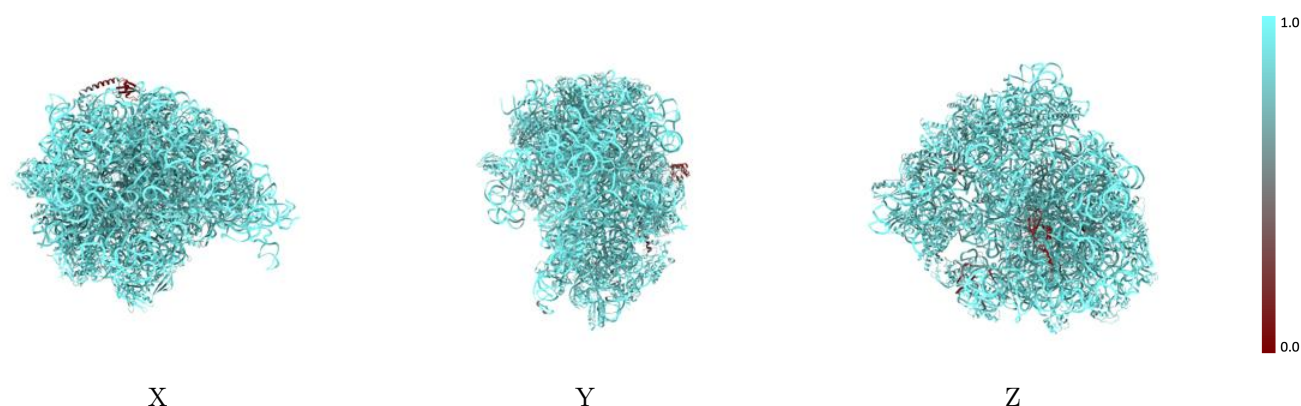
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



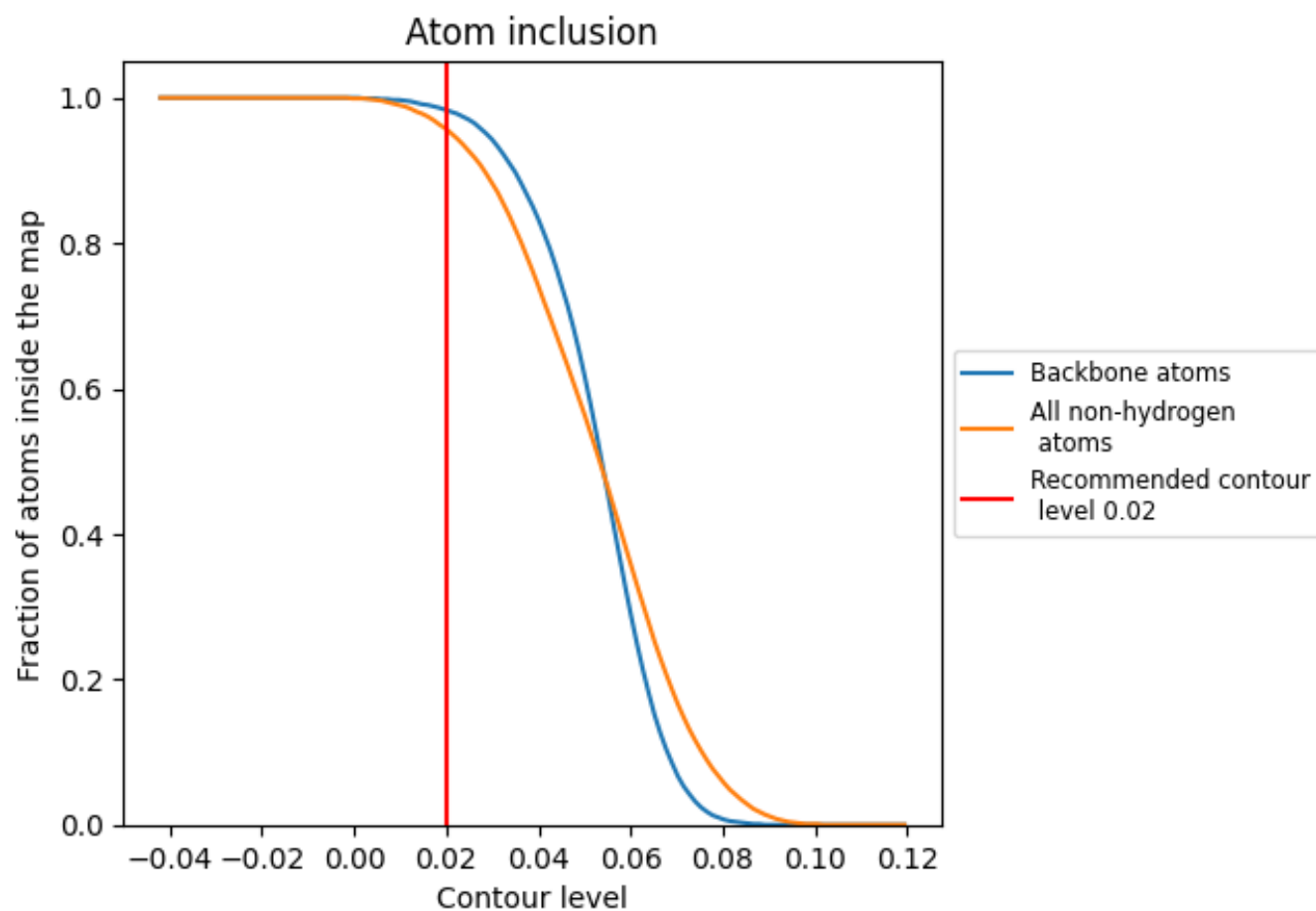
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.9570	 0.4680
1	 0.9860	 0.4780
2	 0.9950	 0.4720
3	 0.9970	 0.4700
4	 0.9610	 0.4570
B	 0.6130	 0.3050
C	 0.9030	 0.5150
D	 0.9140	 0.5060
E	 0.9070	 0.4720
F	 0.8940	 0.4250
G	 0.9250	 0.4350
H	 0.3850	 0.3300
I	 0.9120	 0.4930
J	 0.8570	 0.4940
K	 0.9190	 0.4880
L	 0.8940	 0.4910
M	 0.9400	 0.4950
N	 0.9370	 0.4470
O	 0.8740	 0.4830
P	 0.9350	 0.4840
Q	 0.9130	 0.4970
R	 0.8680	 0.4890
S	 0.8920	 0.4620
T	 0.9050	 0.4590
U	 0.8980	 0.4610
V	 0.8750	 0.5030
W	 0.9030	 0.4810
X	 0.8770	 0.4050
Y	 0.8940	 0.4750
Z	 0.8830	 0.3910
a	 0.8860	 0.4900
b	 0.8350	 0.4750
c	 0.9070	 0.5070
d	 0.9100	 0.5260
e	 0.9250	 0.5010



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Chain	Atom inclusion	Q-score
f	 0.8640	 0.3940
g	 0.8920	 0.4370
h	 0.8970	 0.4320
i	 0.9080	 0.4670
j	 0.8890	 0.4330
k	 0.8830	 0.4020
l	 0.8870	 0.4600
m	 0.9130	 0.4280
n	 0.8540	 0.4100
o	 0.9040	 0.4500
p	 0.8480	 0.4820
q	 0.9090	 0.4260
r	 0.9170	 0.4490
s	 0.9060	 0.4410
t	 0.9440	 0.4620
u	 0.8810	 0.4470
v	 0.9040	 0.4400
w	 0.9160	 0.4380
x	 0.9280	 0.4340
y	 0.7140	 0.3730
z	 0.9760	 0.4220