



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2026 – 01:20 pm BST

PDB ID : 7OII / pdb_00007oii
EMDB ID : EMD-12930
Title : CspA-70 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:

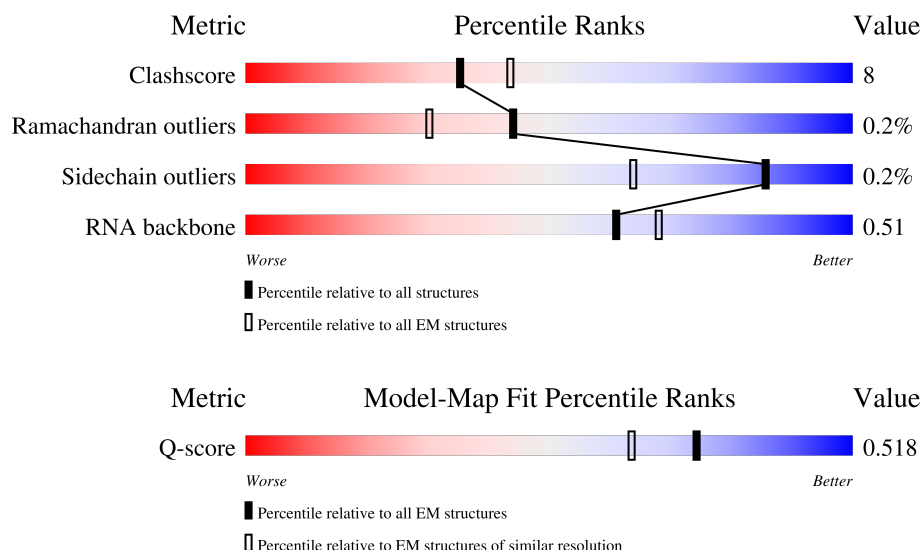
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal 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.



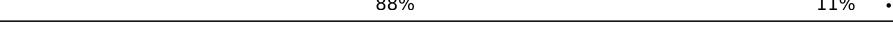
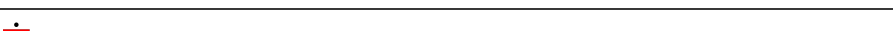
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	

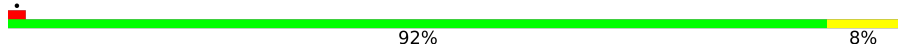
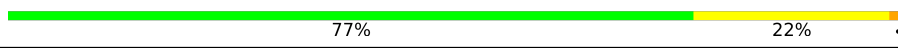
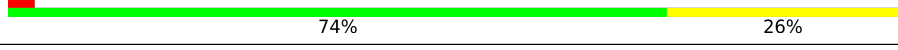
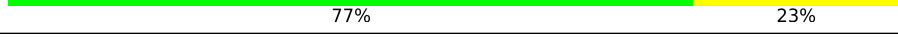
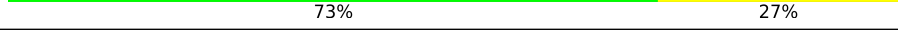
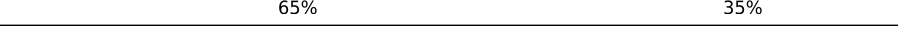
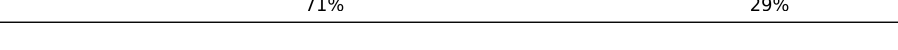
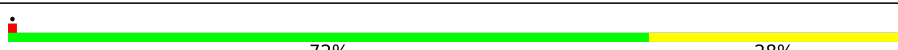
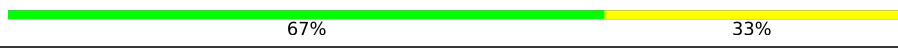
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Mol	Chain	Length	Quality of chain
4	C	271	
5	D	209	
6	E	201	
7	F	177	
8	G	175	
9	H	149	
10	I	142	
11	J	123	
12	K	144	
13	L	136	
14	M	119	
15	N	116	
16	O	114	
17	P	117	
18	Q	103	
19	R	110	
20	S	94	
21	T	103	
22	U	94	
23	V	84	
24	W	77	
25	X	62	
26	Y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

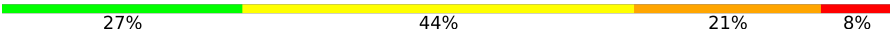
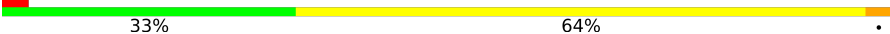
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Mol	Chain	Length	Quality of chain
29	b	52	
30	c	46	
31	d	64	
32	e	38	
33	f	225	
34	g	208	
35	h	205	
36	i	156	
37	j	104	
38	k	151	
39	l	129	
40	m	127	
41	n	99	
42	o	117	
43	p	123	
44	q	116	
45	r	100	
46	s	88	
47	t	82	
48	u	80	
49	v	66	
50	w	83	
51	x	86	
52	y	70	
53	4	6	

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Mol	Chain	Length	Quality of chain
54	z	85	
55	B	39	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
54	5MU	z	71	-	-	X	-

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 145171 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 50S ribosomal protein L24.

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

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
23	V	84	Total	C	N	O	S	0
			634	391	129	113	1	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	0
			625	388	129	106	2	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	0
			501	308	98	94	1	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	0
			448	281	87	78	2	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	0
			522	323	99	94	6	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 30S 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 DNA-binding protein family.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	B	39	Total	C	N	O	0	0
			250	159	43	48		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	8	ILE	VAL	conflict	UNP A0A1H2D2H5

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

Mol	Chain	Residues	Atoms		AltConf
56	1	282	Total 282	Mg 282	0
56	2	119	Total 119	Mg 119	0
56	3	8	Total 8	Mg 8	0
56	C	1	Total 1	Mg 1	0
56	D	1	Total 1	Mg 1	0
56	M	1	Total 1	Mg 1	0
56	P	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	4	1	Total 1	Mg 1	0
56	z	4	Total 4	Mg 4	0

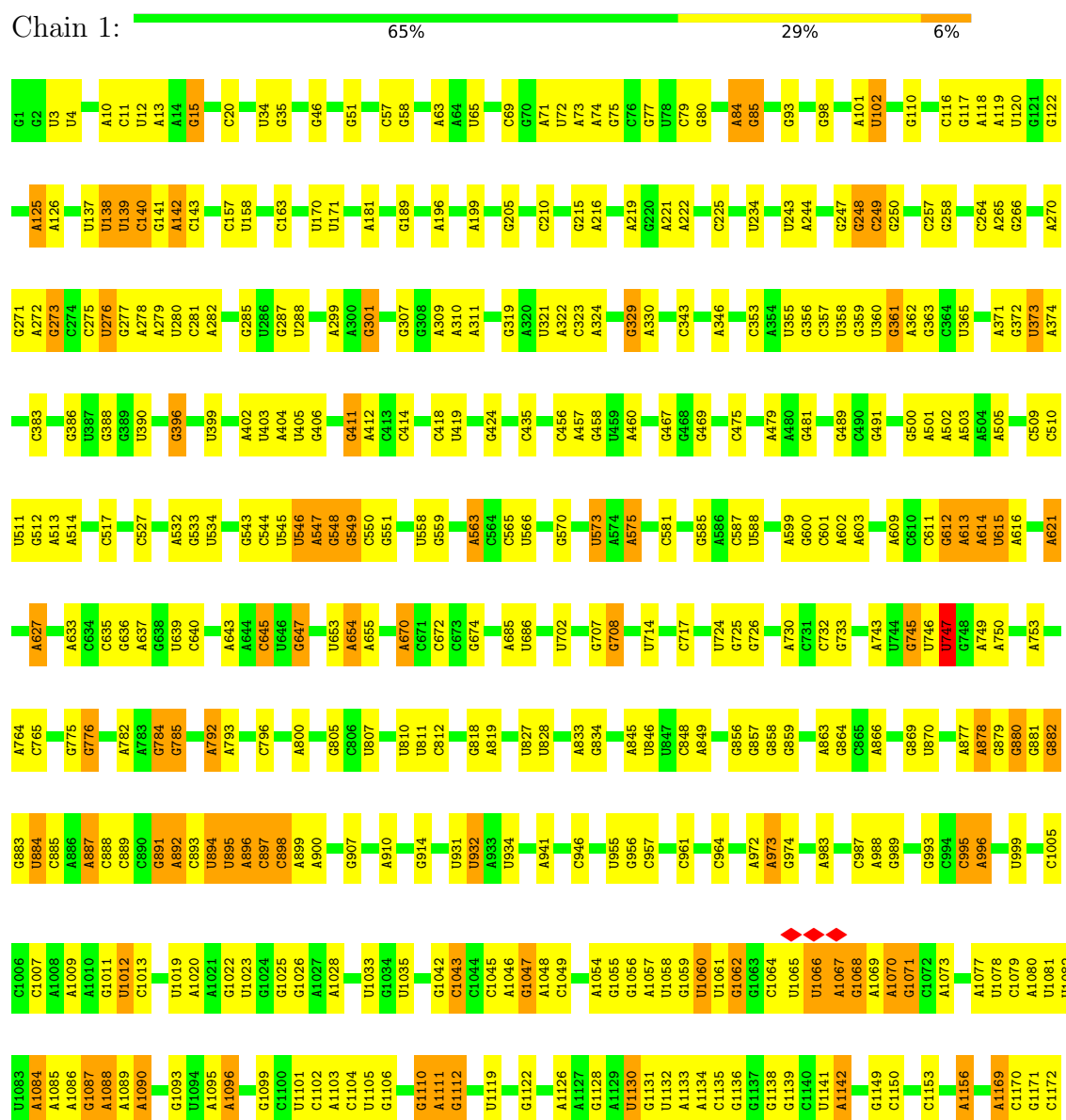
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

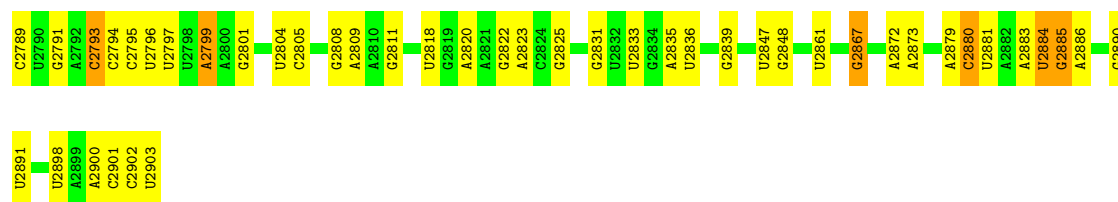
3 Residue-property plots

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

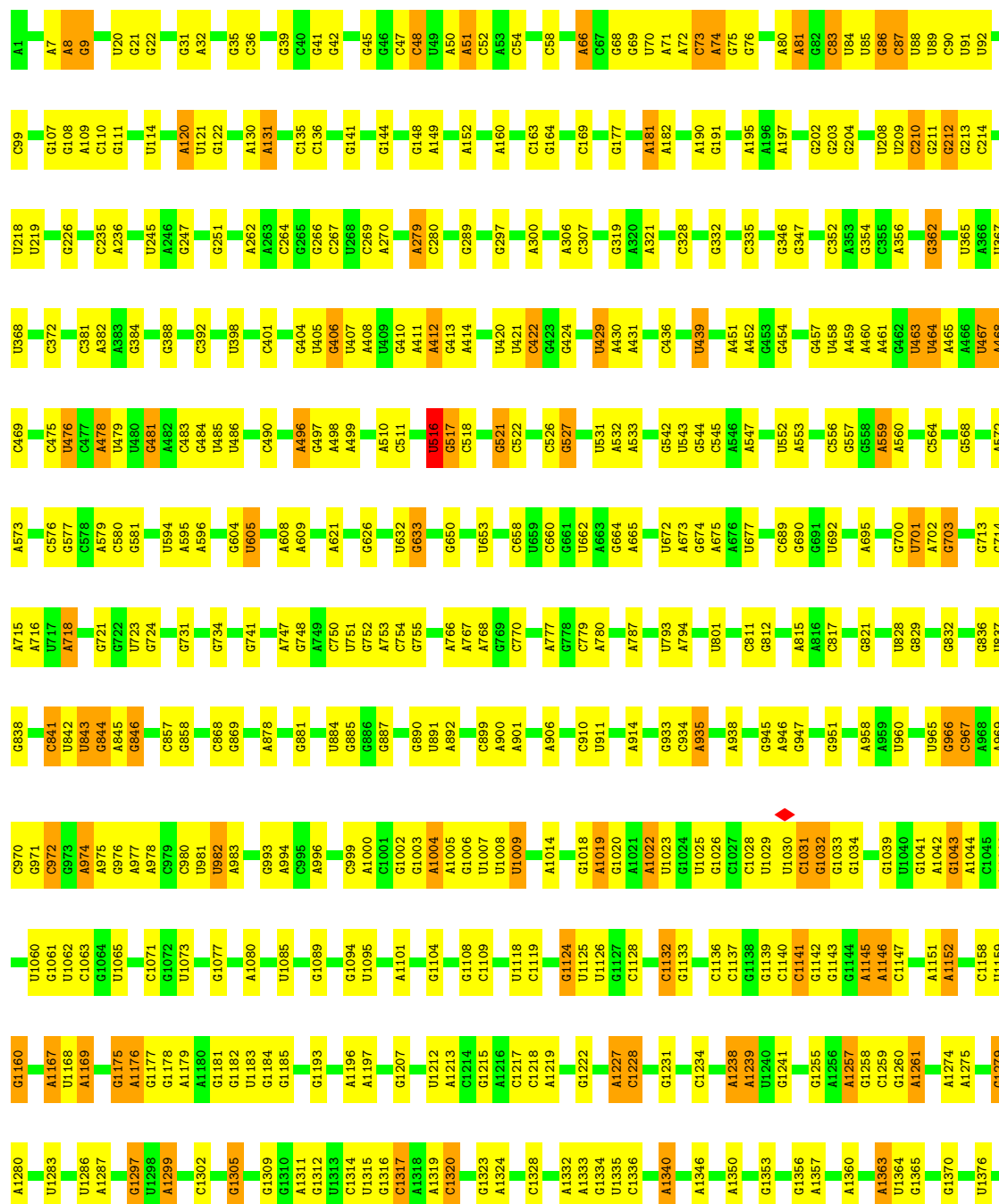


G2633	A2530	U2321	U2229	G2143	A2060	G1929	A1808	A1664	A1528	U1411	A1276	U1173
G2664	A2531	A2322	U2229	G2144	G2061	G1930	A1808	A1668	G1529	U1412	A1298	U1174
C2676	G2532	G2323	U2236	G2145	A2062	G1931	G1811	A1688	C1531	A1413	G1299	A1175
C2683	G2535	U2324	U2237	G2146	C2063	U1932	G1814	U1671	A1532	A1414	G1300	U1176
U2687	A2547	G2326	G2238	A2147	C2064	G1933	G1815	A1672	A1533	U1415	A1301	G1177
G2688	U2549	A2327	G2239	G2148	G2065	A1936	A1816	G1673	U1534	G1416	C1315	C1178
U2689	A2450	U2328	U2243	G2150	G2069	A1937	C1817	G1674	A1535	C1417	C1316	C1179
U2690	U2554	U2329	U2244	U2151	A2070	U1938	U1818	A1676	G1536	G1418	U1180	U1180
U2696	U2555	A2333	U2249	A2158	C2072	U1939	U1827	G1682	G1537	G1421	A1321	U1181
C2699	U2556	G2334	U2250	G2159	U2079	G1954	G1828	G1689	U1538	A1427	G1324	G1182
G2702	G2557	A2335	G2251	C2160	A2080	U1956	A1829	G1699	G1540	C1428	U1325	G1186
G2708	U2561	G2336	G2253	G2162	A2082	C1962	C1833	G1715	A1544	G1432	A1328	G1187
G2714	A2564	C2345	C2258	C2163	C2091	C1967	G1835	A1717	U1554	A1433	U1329	A1189
C2715	U2565	A2346	A2266	U2165	U2092	U1970	U1841	A1722	U1559	C1437	C1335	C1196
C2716	U2566	U2347	A2267	G2166	G2093	U1971	G1842	G1723	A1566	G1445	A1336	G1197
C2717	G2567	G2351	G2271	G2167	A2095	U1972	A1847	C1730	A1569	C1446	G1341	U1203
G2718	U2570	G2357	U2273	A2170	G2100	G1980	A1848	G1731	U1577	C1447	A1342	A1204
G2722	A2571	C2364	G2277	U2172	G2102	A1981	U1856	G1732	U1578	G1450	G1343	A1205
G2728	G2572	A2365	A2278	A2173	C2103	U1982	G1857	G1738	A1579	G1451	C1344	G1206
A2725	C2573	G2366	C2283	G2174	G2107	U1991	A1858	U1746	G1581	G1452	C1345	G1212
A2726	U2580	A2369	G2286	A2176	G2110	G1992	U1864	G1743	G1582	U1460	U1352	G1215
A2727	U2584	G2375	A2287	C2177	U2111	U1993	U1865	U1747	A1583	U1468	C1357	G1218
G2729	U2585	A2376	A2288	G2178	G2112	C1997	C1868	A1764	U1584	A1470	G1364	G1223
A2733	U2586	A2377	U2291	U2182	U2113	G2002	G1869	A1764	A1586	G1475	A1365	U1231
G2744	C2591	A2378	U2292	A2183	A2114	G2002	C1870	A1765	A1587	U1476	A1366	G1232
A2748	G2592	G2383	G2293	U2184	G2115	A2014	A1871	G1756	G1588	G1482	G1367	G1233
G2751	U2602	U2384	G2294	U2185	A2116	A2015	A1872	G1764	U1589	U1503	U1234	U1234
C2752	U2605	C2385	A2297	U2186	U2117	C2021	G1873	C1764	A1590	A1504	G1389	G1235
A2753	U2606	G2394	C2300	U2187	U2118	U2022	U1883	A1784	A1591	A1504	C1370	A1237
C2754	U2607	U2402	C2301	U2188	A2119	C2023	G1884	A1773	C1604	A1504	G1371	G1237
C2755	U2608	G2403	U2302	G2190	G2120	G2024	G1896	U1779	C1607	C1493	C1376	G1238
A2757	U2609	U2404	U2303	A2191	U2121	G2025	A1901	U1791	A1608	A1494	G1377	U1242
A2764	U2613	G2405	U2305	U2192	G2123	U2026	G1906	C1790	A1609	A1495	G1378	C1243
A2765	A2614	A2406	U2306	G2193	G2124	U2026	G1907	A1784	A1610	A1496	U1379	A1244
A2766	U2615	U2412	G2308	U2194	G2125	A2030	G1912	A1769	A1618	A1503	G1380	A1247
C2767	U2616	G2413	U2309	U2195	A2126	A2031	U1911	C1790	A1634	A1504	A1383	G1248
G2777	U2617	U2423	A2311	C2196	G2127	G2032	A1912	A1791	A1634	A1509	G1386	U1249
A2778	U2618	C2424	U2312	U2197	C2128	A2033	A1913	C1795	U1647	G1510	A1387	G1250
U2779	G2646	A2425	C2313	U2198	C2129	C2043	C1914	U1796	U1648	A1515	A1392	A1253
G2780	U2652	U2426	A2314	U2199	U2130	C2050	3TD1915	G1797	G1649	U1522	U1405	G1256
G2788	U2655	C2427	G2315	A2204	U2131	A2051	A1916	G1800	G1651	U1523	G1407	G1266
	U2656	U2428	A2317	A2211	U2132	A2052	U1917	A1801	A1652	G1524	G1408	A1271
	A2657	G2429	G2318	G2220	G2133	G2056	G1922	A1802	G1659	G1527	G1410	A1272
		A2430	U2320	G2226	A2134	G2056	U1923	A1803				
		U2431			U2139	G2141	C1924					
					A2142							



• Molecule 2: 16S rRNA

Chain 2: 66% 28% 6%

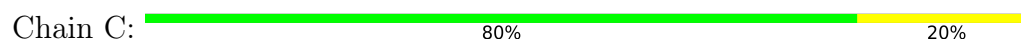




- Molecule 3: 5S rRNA



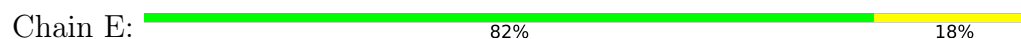
- Molecule 4: 50S ribosomal protein L2



- Molecule 5: 50S ribosomal protein L3



- Molecule 6: 50S ribosomal protein L4

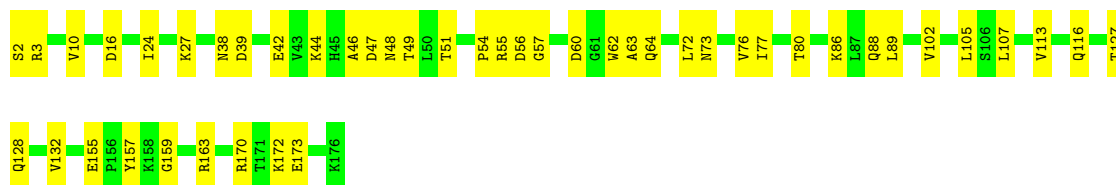


- Molecule 7: 50S ribosomal protein L5



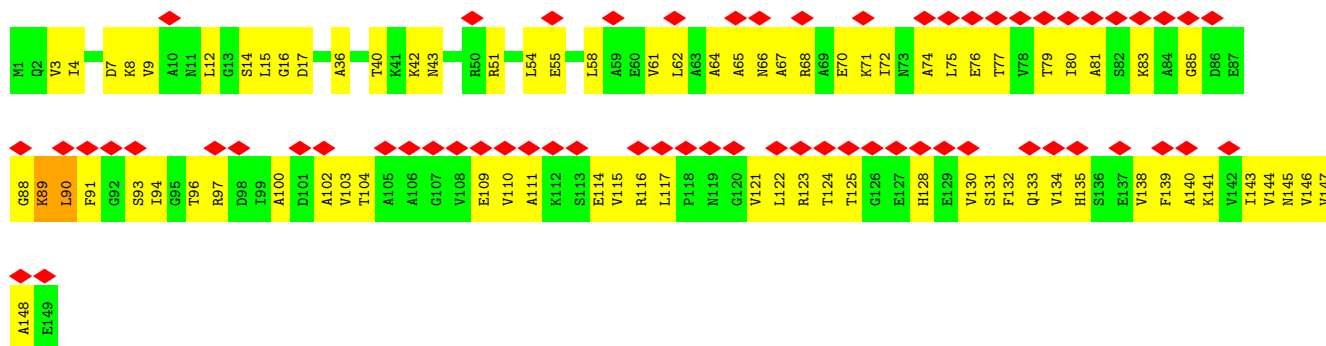
- Molecule 8: 50S ribosomal protein L6

Chain G:  74% 26%



• Molecule 9: 50S ribosomal protein L9

Chain H:  42% 48% 51%



• Molecule 10: 50S ribosomal protein L13

Chain I:  86% 14%



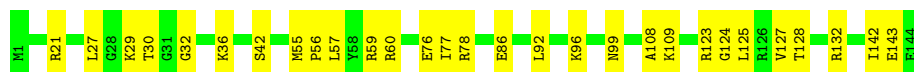
• Molecule 11: 50S ribosomal protein L14

Chain J:  84% 16%



• Molecule 12: 50S ribosomal protein L15

Chain K:  80% 20%



• Molecule 13: 50S ribosomal protein L16

Chain L:  84% 16%



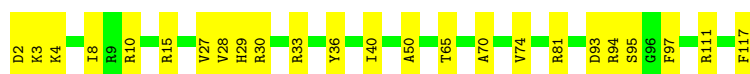
- Molecule 14: 50S ribosomal protein L17

Chain M: 82% 18%



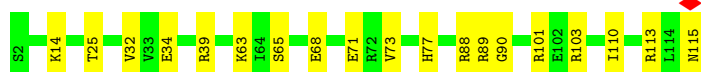
- Molecule 15: 50S ribosomal protein L18

Chain N: 79% 21%



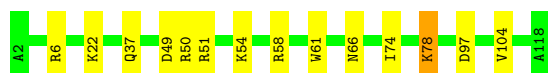
- Molecule 16: 50S ribosomal protein L19

Chain O: 83% 17%



- Molecule 17: 50S ribosomal protein L20

Chain P: 88% 11%



- Molecule 18: 50S ribosomal protein L21

Chain Q: 81% 17%



- Molecule 19: 50S ribosomal protein L22

Chain R: 76% 24%



- Molecule 20: 50S ribosomal protein L23

Chain S: 82% 18%



- Molecule 21: 50S ribosomal protein L24

Chain T: 75% 25%



- Molecule 22: 50S ribosomal protein L25

Chain U: 86% 14%



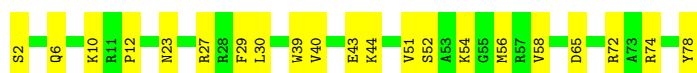
- Molecule 23: 50S ribosomal protein L27

Chain V: 5% 77% 21%



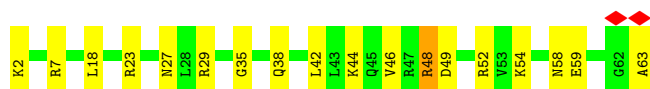
- Molecule 24: 50S ribosomal protein L28

Chain W: 73% 27%



- Molecule 25: 50S ribosomal protein L29

Chain X: 71% 27%

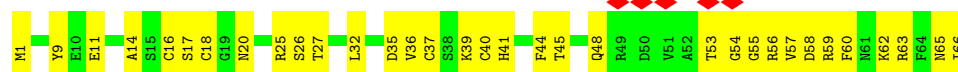


- Molecule 26: 50S ribosomal protein L30

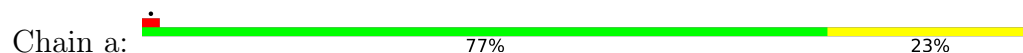
Chain Y: 84% 16%



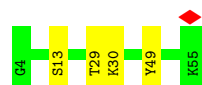
- Molecule 27: 50S ribosomal protein L31



- Molecule 28: 50S ribosomal protein L32



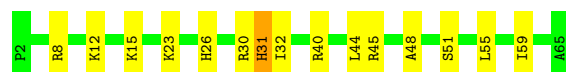
- Molecule 29: 50S ribosomal protein L33



- Molecule 30: 50S ribosomal protein L34



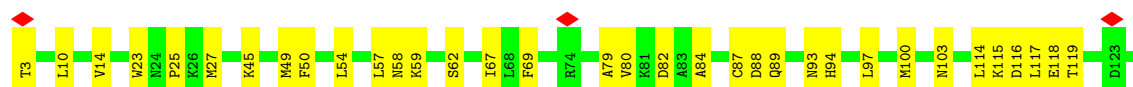
- Molecule 31: 50S ribosomal protein L35

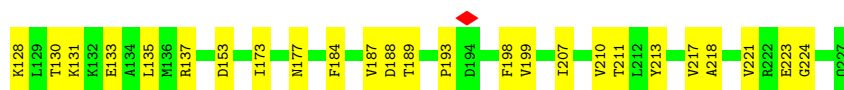


- Molecule 32: 50S ribosomal protein L36



- Molecule 33: 30S ribosomal protein S2

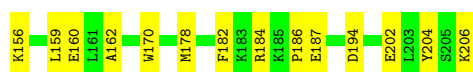
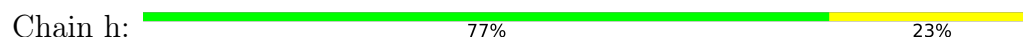




- Molecule 34: 30S ribosomal protein S3



- Molecule 35: 30S ribosomal protein S4



- Molecule 36: 30S ribosomal protein S5

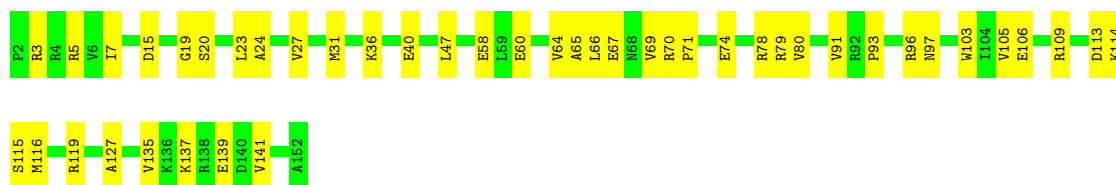


- Molecule 37: 30S ribosomal protein S6



- Molecule 38: 30S ribosomal protein S7





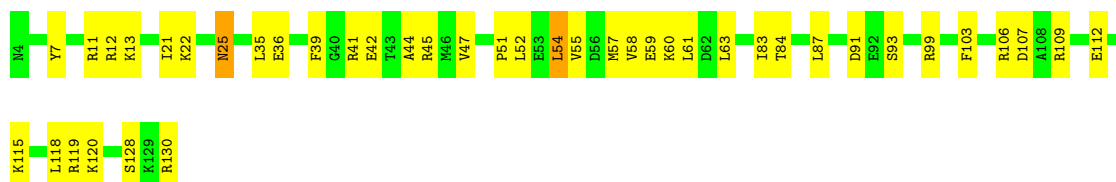
- Molecule 39: 30S ribosomal protein S8

Chain l: 84% 16%



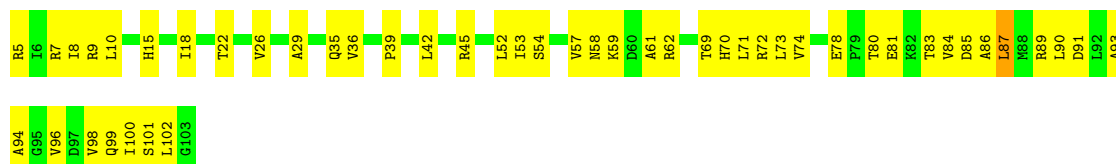
- Molecule 40: 30S ribosomal protein S9

Chain m: 67% 31% .



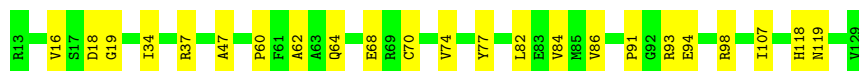
- Molecule 41: 30S ribosomal protein S10

Chain n: 52% 47% .



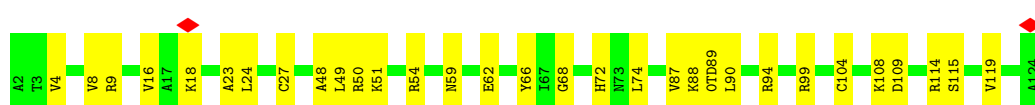
- Molecule 42: 30S ribosomal protein S11

Chain o: 80% 20%



- Molecule 43: 30S ribosomal protein S12

Chain p: 75% 25%



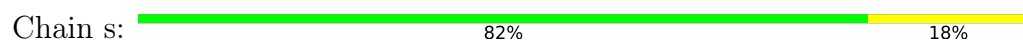
- Molecule 44: 30S ribosomal protein S13



- Molecule 45: 30S ribosomal protein S14



- Molecule 46: 30S ribosomal protein S15



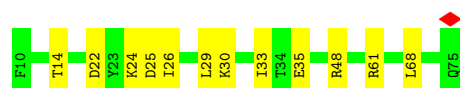
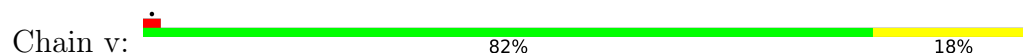
- Molecule 47: 30S ribosomal protein S16



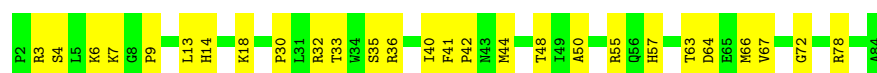
- Molecule 48: 30S ribosomal protein S17



- Molecule 49: 30S ribosomal protein S18

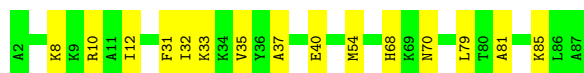


- Molecule 50: 30S ribosomal protein S19



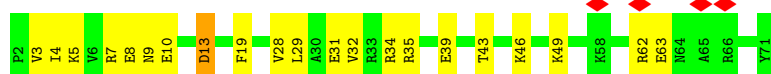
- Molecule 51: 30S ribosomal protein S20

Chain x:  83% 17%



- Molecule 52: 30S ribosomal protein S21

Chain y:  6% 70% 29%

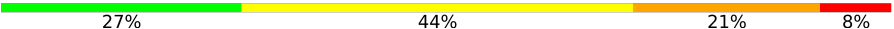


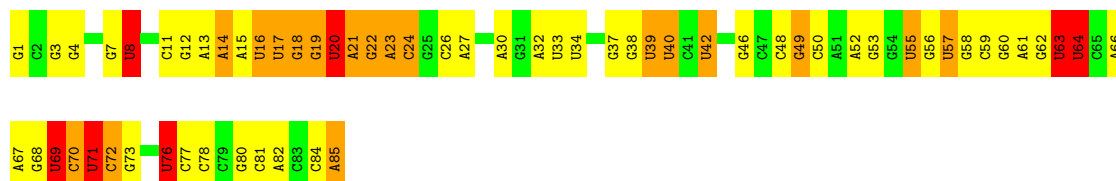
- Molecule 53: mRNA

Chain 4:  67% 17% 17%



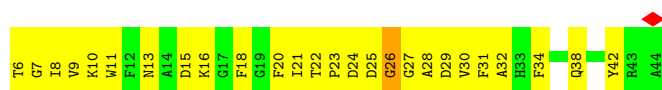
- Molecule 54: tRNA-Leu

Chain z:  27% 44% 21% 8%



- Molecule 55: Cold-shock DNA-binding protein family

Chain B:  33% 64%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	23782	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	0.157	Depositor
Minimum map value	-0.078	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.009	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: 0TD, 5MC, 1MG, OMU, MA6, 6MZ, OMC, UR3, 5MU, G7M, MG, 4OC, 2MA, PSU, 2MG, 3TD, ZN, OMG

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	0.75	0/69286	0.56	3/108087 (0.0%)
2	2	0.67	0/36590	0.51	0/57074
3	3	0.65	0/2872	0.49	0/4478
4	C	1.01	0/2121	0.68	0/2852
5	D	1.00	0/1586	0.70	1/2134 (0.0%)
6	E	0.92	0/1571	0.70	0/2113
7	F	0.72	0/1434	0.69	0/1926
8	G	0.65	0/1333	0.67	0/1805
9	H	0.48	0/1122	0.92	0/1515
10	I	0.96	0/1152	0.65	0/1551
11	J	0.95	0/955	0.69	0/1279
12	K	0.97	0/1062	0.73	0/1413
13	L	0.97	0/1093	0.68	0/1460
14	M	1.01	0/964	0.75	0/1289
15	N	0.84	0/902	0.70	0/1209
16	O	0.94	0/929	0.67	0/1242
17	P	1.11	0/960	0.80	0/1278
18	Q	0.90	0/829	0.68	0/1107
19	R	1.00	0/864	0.72	0/1156
20	S	0.89	0/752	0.64	0/1005
21	T	0.81	0/796	0.68	0/1062
22	U	0.83	0/766	0.68	0/1025
23	V	0.98	0/642	0.67	0/848
24	W	0.96	0/635	0.71	0/848
25	X	0.76	0/502	0.78	1/667 (0.1%)
26	Y	0.97	0/452	0.68	0/605
27	Z	0.56	0/531	0.76	0/709
28	a	0.97	0/450	0.69	0/599
29	b	0.75	0/433	0.63	0/576
30	c	1.04	0/380	0.78	0/498
31	d	1.06	0/513	0.79	0/676

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
32	e	0.97	0/303	0.68	0/397
33	f	0.63	0/1791	0.74	0/2413
34	g	0.77	0/1663	0.68	0/2241
35	h	0.76	0/1665	0.69	0/2227
36	i	0.88	0/1165	0.75	0/1568
37	j	0.70	0/867	0.73	0/1171
38	k	0.70	0/1195	0.74	0/1602
39	l	0.89	0/989	0.69	0/1326
40	m	0.78	0/1034	0.78	1/1375 (0.1%)
41	n	0.73	0/800	0.94	2/1082 (0.2%)
42	o	0.76	0/893	0.68	0/1205
43	p	0.84	0/960	0.70	0/1286
44	q	0.73	0/909	0.74	0/1215
45	r	0.81	0/817	0.72	0/1088
46	s	0.83	0/722	0.69	0/964
47	t	0.84	0/659	0.67	0/884
48	u	0.75	0/657	0.67	0/881
49	v	0.81	0/553	0.69	0/743
50	w	0.66	0/680	0.66	0/915
51	x	0.83	0/675	0.77	0/895
52	y	0.65	0/597	0.72	0/792
53	4	0.79	0/134	0.87	1/205 (0.5%)
54	z	0.66	0/1768	0.57	0/2759
55	B	0.60	0/255	0.80	1/347 (0.3%)
All	All	0.76	0/156228	0.59	10/233667 (0.0%)

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	n	54	SER	CA-C-N	8.52	128.50	119.05
41	n	54	SER	C-N-CA	8.52	128.50	119.05
1	1	708	G	O3'-P-O5'	-7.33	93.01	104.00
5	D	152	PRO	CA-N-CD	-5.79	103.89	112.00
25	X	48	ARG	CA-CB-CG	5.66	125.42	114.10

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	31349	578	0
2	2	32929	0	16586	284	0
3	3	2569	0	1299	15	0
4	C	2082	0	2154	35	0
5	D	1565	0	1616	26	0
6	E	1552	0	1619	30	0
7	F	1410	0	1444	46	0
8	G	1313	0	1358	28	0
9	H	1111	0	1148	83	0
10	I	1129	0	1162	17	0
11	J	946	0	1023	15	0
12	K	1053	0	1129	26	0
13	L	1074	0	1157	16	0
14	M	951	0	994	20	0
15	N	892	0	923	19	0
16	O	917	0	962	18	0
17	P	947	0	1019	13	0
18	Q	816	0	839	21	0
19	R	857	0	922	19	0
20	S	746	0	811	14	0
21	T	788	0	844	20	0
22	U	753	0	780	7	0
23	V	634	0	653	13	0
24	W	625	0	652	13	0
25	X	501	0	531	18	0
26	Y	448	0	488	5	0
27	Z	522	0	521	27	0
28	a	444	0	458	13	0
29	b	426	0	464	2	0
30	c	377	0	418	11	0
31	d	504	0	572	13	0
32	e	302	0	340	7	0
33	f	1760	0	1787	44	0
34	g	1636	0	1710	50	0
35	h	1643	0	1706	39	0
36	i	1152	0	1196	30	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	31	0
39	l	979	0	1031	20	0
40	m	1022	0	1070	31	0
41	n	790	0	831	43	0
42	o	877	0	887	14	0
43	p	957	0	1017	28	0
44	q	900	0	965	32	0
45	r	805	0	844	27	0
46	s	714	0	734	17	0
47	t	649	0	666	15	0
48	u	648	0	691	14	0
49	v	544	0	560	8	0
50	w	663	0	688	26	0
51	x	669	0	719	9	0
52	y	589	0	629	14	0
53	4	122	0	64	1	0
54	z	1830	0	939	64	0
55	B	250	0	199	58	0
56	1	282	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	1	0	0	0	0
56	M	1	0	0	0	0
56	P	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	z	4	0	0	0	0
57	Z	1	0	0	0	0
57	e	1	0	0	0	0
All	All	145171	0	97252	1843	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 1843 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:6:THR:N	1.36	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:151:THR:HG23	5:D:152:PRO:HD3	1.25	1.17
54:z:21:A:N7	54:z:56:G:N2	2.07	1.02
1:l:2483:C:N3	13:L:123:LYS:NZ	2.09	1.01
40:m:57:MET:HE2	40:m:61:LEU:HD11	1.48	0.95

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%)	256 (95%)	13 (5%)	0	100	100
5	D	207/209 (99%)	201 (97%)	3 (1%)	3 (1%)	9	36
6	E	199/201 (99%)	197 (99%)	2 (1%)	0	100	100
7	F	175/177 (99%)	164 (94%)	10 (6%)	1 (1%)	21	56
8	G	173/175 (99%)	162 (94%)	11 (6%)	0	100	100
9	H	147/149 (99%)	135 (92%)	10 (7%)	2 (1%)	9	36
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%)	138 (97%)	4 (3%)	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%)	109 (97%)	3 (3%)	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	28
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%)	91 (99%)	1 (1%)	0	100	100
21	T	101/103 (98%)	93 (92%)	8 (8%)	0	100	100
22	U	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
23	V	82/84 (98%)	73 (89%)	7 (8%)	2 (2%)	4	24
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%)	59 (92%)	5 (8%)	0	100	100
28	a	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
29	b	50/52 (96%)	50 (100%)	0	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%)	211 (95%)	12 (5%)	0	100	100
34	g	206/208 (99%)	197 (96%)	9 (4%)	0	100	100
35	h	203/205 (99%)	200 (98%)	3 (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%)	117 (94%)	8 (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%)	109 (96%)	5 (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%)	64 (100%)	0	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%)	66 (97%)	2 (3%)	0	100	100
55	B	37/39 (95%)	29 (78%)	8 (22%)	0	100	100
All	All	5653/5754 (98%)	5440 (96%)	203 (4%)	10 (0%)	44	76

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
23	V	5	LYS

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	88
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%)	136 (100%)	0	100	100
9	H	114/114 (100%)	113 (99%)	1 (1%)	70	85
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%)	88 (99%)	1 (1%)	65	83
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%)	83 (99%)	1 (1%)	63	82
22	U	78/78 (100%)	78 (100%)	0	100	100
23	V	62/62 (100%)	62 (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%)	49 (96%)	2 (4%)	28	62
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%)	169 (99%)	2 (1%)	63	82
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%)	104 (99%)	1 (1%)	68	84
41	n	86/86 (100%)	85 (99%)	1 (1%)	63	82
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%)	76 (100%)	0	100	100
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%)	65 (100%)	0	100	100
52	y	60/60 (100%)	59 (98%)	1 (2%)	53	78
55	B	16/28 (57%)	16 (100%)	0	100	100
All	All	4688/4700 (100%)	4677 (100%)	11 (0%)	85	92

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

Mol	Chain	Res	Type
34	g	165	THR
40	m	25	ASN
52	y	13	ASP
41	n	87	LEU
31	d	31	HIS

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

Mol	Chain	Res	Type
44	q	8	ASN
46	s	50	HIS
51	x	20	HIS
14	M	31	HIS
13	L	60	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2903 (99%)	496 (17%)	10 (0%)
2	2	1532/1534 (99%)	256 (16%)	5 (0%)
3	3	119/120 (99%)	16 (13%)	0
53	4	5/6 (83%)	1 (20%)	0
54	z	84/85 (98%)	27 (32%)	0
All	All	4642/4648 (99%)	796 (17%)	15 (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 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1475	G
2	2	1109	C
1	1	2189	U
2	2	1145	A
2	2	86	G

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	$\# Z > 2$
54	5MU	z	42	54,2	19,22,23	4.34	7 (36%)	28,32,35	3.84	11 (39%)
54	5MU	z	69	54	19,22,23	6.60	6 (31%)	28,32,35	28.78	14 (50%)
43	0TD	p	89	43	7,9,10	1.49	1 (14%)	6,11,13	1.92	2 (33%)
1	OMU	1	2552	1	19,22,23	2.74	6 (31%)	26,31,34	1.67	6 (23%)
2	4OC	2	1402	2	20,23,24	2.69	8 (40%)	26,32,35	1.08	1 (3%)
54	5MU	z	39	54	19,22,23	1.44	5 (26%)	28,32,35	2.17	9 (32%)
1	PSU	1	1917	1	18,21,22	1.01	1 (5%)	22,30,33	2.13	5 (22%)
2	5MC	2	1407	2	18,22,23	3.12	7 (38%)	26,32,35	0.90	1 (3%)
54	5MU	z	40	54	19,22,23	1.38	5 (26%)	28,32,35	2.27	11 (39%)
2	5MC	2	967	2	18,22,23	3.27	7 (38%)	26,32,35	1.12	2 (7%)
1	PSU	1	2457	1	18,21,22	1.18	2 (11%)	22,30,33	2.20	5 (22%)
54	5MU	z	20	54,56	19,22,23	4.78	7 (36%)	28,32,35	3.73	9 (32%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MU	1	747	1	19,22,23	4.50	7 (36%)	28,32,35	3.78	9 (32%)
1	1MG	1	745	1	22,26,27	2.72	7 (31%)	33,39,42	2.29	8 (24%)
1	6MZ	1	1618	1	22,25,26	2.52	6 (27%)	30,36,39	3.29	12 (40%)
54	5MU	z	8	54	19,22,23	4.51	7 (36%)	28,32,35	3.93	9 (32%)
1	6MZ	1	2030	1	22,25,26	2.52	6 (27%)	30,36,39	3.33	12 (40%)
1	2MA	1	2503	56,1	22,25,26	3.43	10 (45%)	33,37,40	2.18	9 (27%)
1	2MG	1	1835	1	23,26,27	2.54	8 (34%)	32,38,41	2.09	8 (25%)
1	3TD	1	1915	1	18,22,23	4.04	7 (38%)	22,32,35	1.54	3 (13%)
1	PSU	1	1911	1	18,21,22	0.90	0	22,30,33	1.87	3 (13%)
1	PSU	1	2580	56,1	18,21,22	1.14	1 (5%)	22,30,33	2.23	6 (27%)
1	5MU	1	1939	56,1	19,22,23	4.39	7 (36%)	28,32,35	3.71	10 (35%)
1	5MC	1	1962	1	18,22,23	3.04	7 (38%)	26,32,35	1.26	5 (19%)
1	G7M	1	2069	1	23,26,27	2.68	9 (39%)	35,39,42	2.31	12 (34%)
2	2MG	2	1207	2	23,26,27	2.59	8 (34%)	32,38,41	2.04	9 (28%)
54	5MU	z	63	54	19,22,23	1.45	6 (31%)	28,32,35	2.45	13 (46%)
54	5MU	z	57	54	19,22,23	4.54	7 (36%)	28,32,35	3.71	9 (32%)
2	MA6	2	1518	2	23,26,27	1.63	6 (26%)	34,38,41	3.25	11 (32%)
2	2MG	2	1516	2	23,26,27	2.58	8 (34%)	32,38,41	2.09	10 (31%)
1	OMC	1	2498	56,1	19,22,23	2.51	6 (31%)	26,31,34	0.96	0
1	PSU	1	955	1	18,21,22	1.08	1 (5%)	22,30,33	1.99	5 (22%)
1	2MG	1	2445	1	23,26,27	2.56	8 (34%)	32,38,41	1.87	9 (28%)
1	PSU	1	2605	1	18,21,22	1.05	1 (5%)	22,30,33	1.92	4 (18%)
1	PSU	1	2504	1	18,21,22	0.98	1 (5%)	22,30,33	1.85	4 (18%)
2	2MG	2	966	2	23,26,27	2.77	7 (30%)	32,38,41	2.10	8 (25%)
54	5MU	z	71	54	19,22,23	1.34	5 (26%)	28,32,35	2.21	9 (32%)
2	UR3	2	1498	2	19,22,23	2.41	6 (31%)	26,32,35	1.04	2 (7%)
2	MA6	2	1519	2	23,26,27	1.65	6 (26%)	34,38,41	3.36	11 (32%)
54	5MU	z	64	54	19,22,23	1.44	6 (31%)	28,32,35	2.32	7 (25%)
2	PSU	2	516	56,2	18,21,22	0.97	1 (5%)	22,30,33	1.88	3 (13%)
54	5MU	z	55	54	19,22,23	4.68	7 (36%)	28,32,35	3.48	9 (32%)
2	G7M	2	527	2	23,26,27	2.72	9 (39%)	35,39,42	2.22	11 (31%)
1	OMG	1	2251	54,1	23,26,27	2.07	6 (26%)	33,38,41	1.70	8 (24%)
54	5MU	z	76	54	19,22,23	1.43	6 (31%)	28,32,35	2.14	9 (32%)
1	PSU	1	746	56,1	18,21,22	1.04	2 (11%)	22,30,33	1.74	3 (13%)

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
54	5MU	z	42	54,2	-	0/7/25/26	0/2/2/2
54	5MU	z	69	54	-	2/7/25/26	1/2/2/2
43	0TD	p	89	43	-	3/7/12/14	-
1	OMU	1	2552	1	-	0/9/27/28	0/2/2/2
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
54	5MU	z	39	54	-	4/7/25/26	0/2/2/2
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
54	5MU	z	40	54	-	2/7/25/26	0/2/2/2
2	5MC	2	967	2	-	2/7/25/26	0/2/2/2
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
54	5MU	z	20	54,56	-	4/7/25/26	0/2/2/2
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
1	6MZ	1	1618	1	-	3/9/27/28	0/3/3/3
54	5MU	z	8	54	-	2/7/25/26	0/2/2/2
1	6MZ	1	2030	1	-	2/9/27/28	0/3/3/3
1	2MA	1	2503	56,1	-	2/7/25/26	0/3/3/3
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
1	3TD	1	1915	1	-	3/7/25/26	0/2/2/2
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2580	56,1	-	0/7/25/26	0/2/2/2
1	5MU	1	1939	56,1	-	0/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
1	G7M	1	2069	1	-	1/7/25/26	0/3/3/3
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
54	5MU	z	63	54	-	2/7/25/26	0/2/2/2
54	5MU	z	57	54	-	2/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	3/11/29/30	0/3/3/3
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
1	OMC	1	2498	56,1	-	0/9/27/28	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	2/9/27/28	0/3/3/3
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	2MG	2	966	2	-	0/9/27/28	0/3/3/3
54	5MU	z	71	54	-	3/7/25/26	0/2/2/2
2	UR3	2	1498	2	-	1/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	5/11/29/30	0/3/3/3
54	5MU	z	64	54	-	2/7/25/26	0/2/2/2
2	PSU	2	516	56,2	-	2/7/25/26	0/2/2/2
54	5MU	z	55	54	-	0/7/25/26	0/2/2/2
2	G7M	2	527	2	-	3/7/25/26	0/3/3/3
1	OMG	1	2251	54,1	-	0/9/27/28	0/3/3/3
54	5MU	z	76	54	-	2/7/25/26	0/2/2/2
1	PSU	1	746	56,1	-	1/7/25/26	0/2/2/2

The worst 5 of 257 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	z	69	5MU	C6-C5	23.78	1.73	1.34
1	1	1915	3TD	C6-C5	11.71	1.49	1.35
54	z	57	5MU	C2-N1	11.02	1.56	1.38
54	z	20	5MU	C2-N1	10.76	1.55	1.38
1	1	2503	2MA	C4-N3	10.57	1.47	1.34

The worst 5 of 336 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	z	69	5MU	C6-C5-C4	-115.15	21.76	118.03
54	z	69	5MU	C5-C4-N3	-87.09	40.98	115.31
54	z	69	5MU	C6-N1-C2	-29.10	91.84	121.30
54	z	69	5MU	O4-C4-C5	-25.79	95.01	124.90
54	z	69	5MU	N3-C2-N1	-18.31	90.58	114.89

There are no chirality outliers.

5 of 64 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'

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
54	z	69	5MU	C2-C4-C5-C6-N1-N3

27 monomers are involved in 52 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	z	42	5MU	1	0
54	z	69	5MU	2	0
1	1	2552	OMU	1	0
2	2	1402	4OC	1	0
54	z	39	5MU	2	0
54	z	40	5MU	1	0
1	1	2457	PSU	1	0
54	z	20	5MU	4	0
1	1	747	5MU	4	0
1	1	745	1MG	1	0
54	z	8	5MU	3	0
1	1	2030	6MZ	2	0
1	1	2503	2MA	1	0
1	1	1915	3TD	2	0
1	1	2580	PSU	1	0
1	1	1962	5MC	1	0
54	z	63	5MU	2	0
2	2	1518	MA6	4	0
2	2	1516	2MG	1	0
1	1	2498	OMC	3	0
1	1	2445	2MG	2	0
54	z	71	5MU	7	0
2	2	1519	MA6	5	0
54	z	64	5MU	1	0
2	2	516	PSU	1	0
54	z	55	5MU	2	0
54	z	76	5MU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 424 ligands modelled in this entry, 424 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.

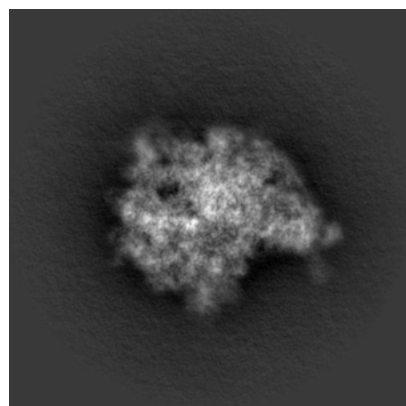
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12930. These allow visual inspection of the internal detail of the map and identification of artifacts.

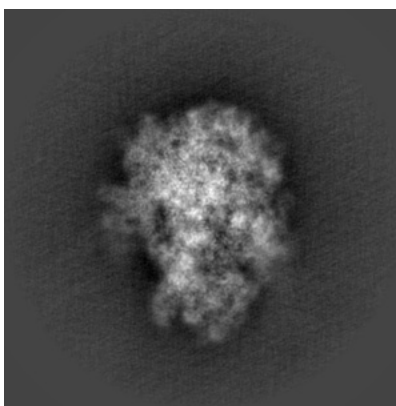
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

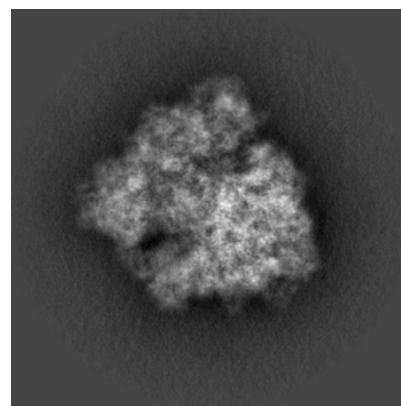
6.1.1 Primary map



X

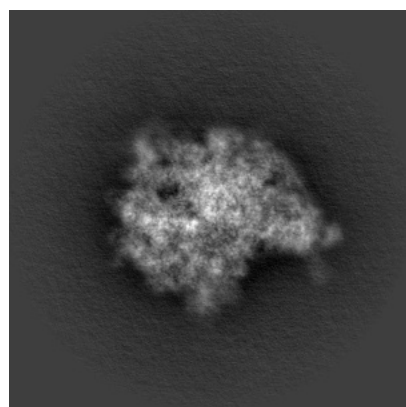


Y

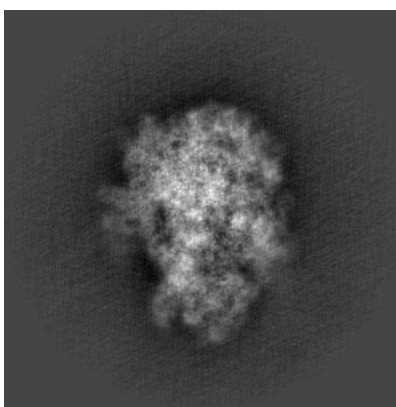


Z

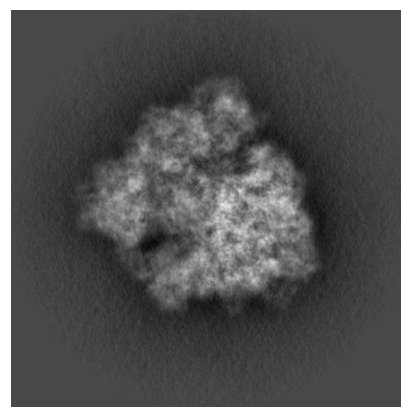
6.1.2 Raw map



X



Y

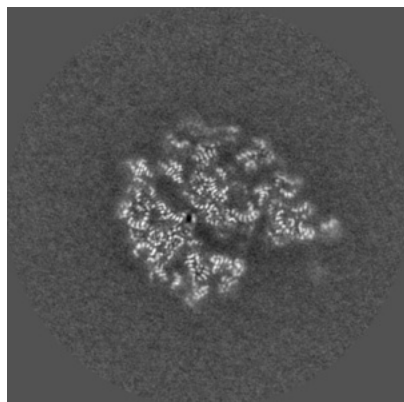


Z

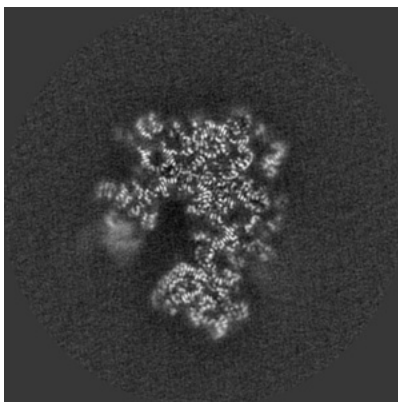
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

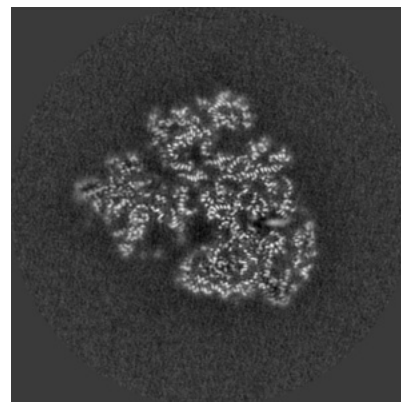
6.2.1 Primary map



X Index: 200

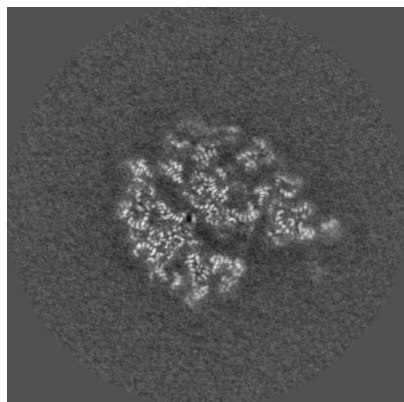


Y Index: 200

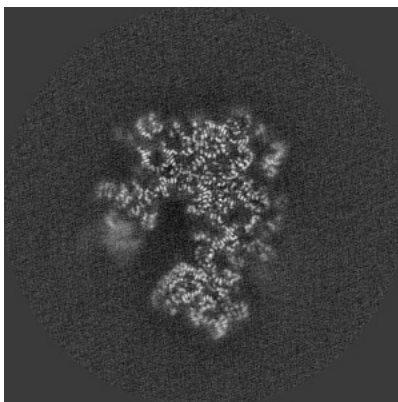


Z Index: 200

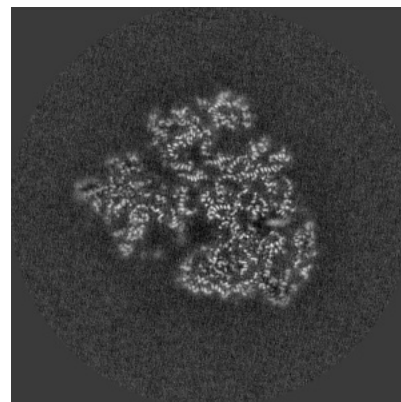
6.2.2 Raw map



X Index: 200



Y Index: 200

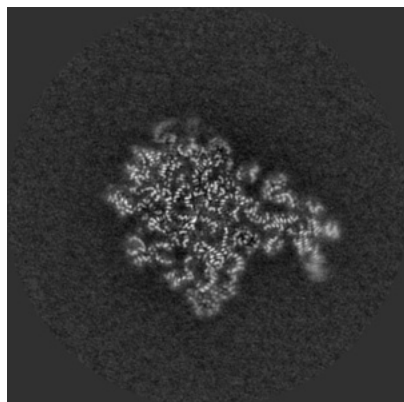


Z Index: 200

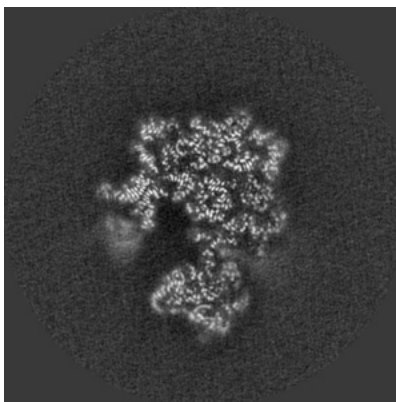
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

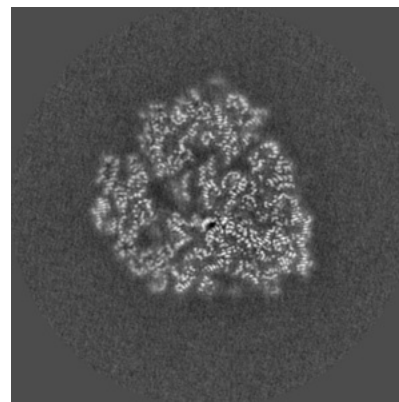
6.3.1 Primary map



X Index: 215

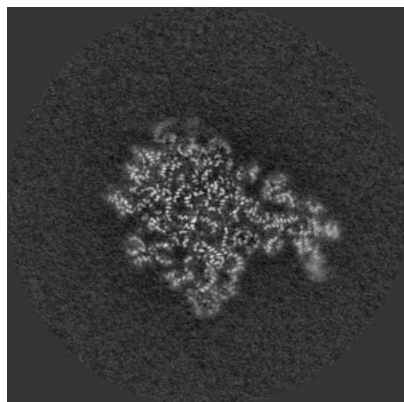


Y Index: 205

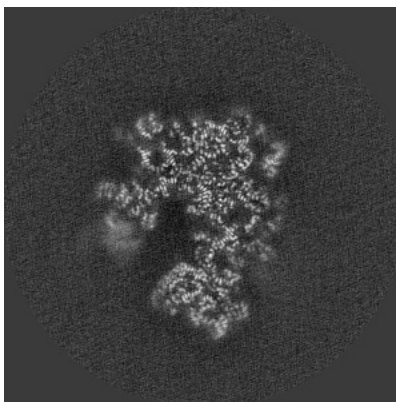


Z Index: 188

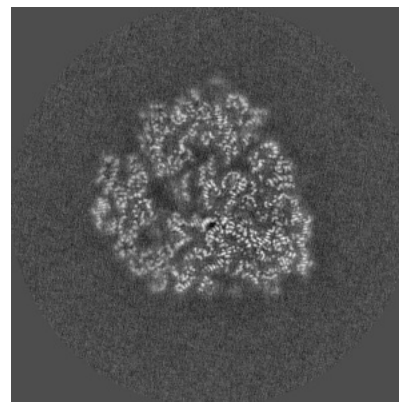
6.3.2 Raw map



X Index: 215



Y Index: 200

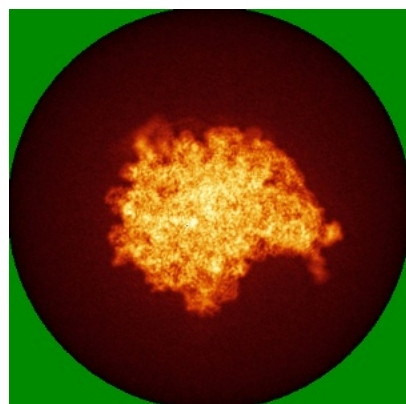


Z Index: 188

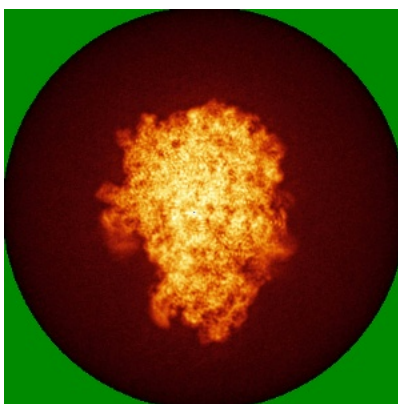
The images above show the largest variance slices of the map in three orthogonal directions.

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

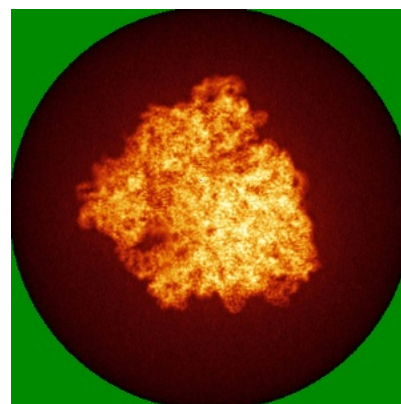
6.4.1 Primary map



X

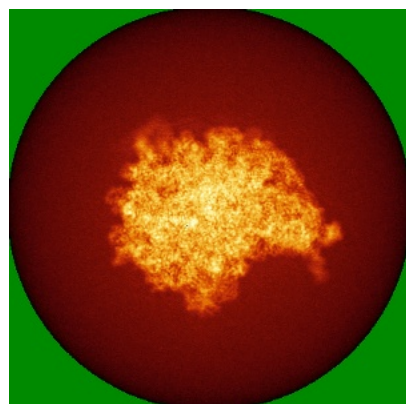


Y

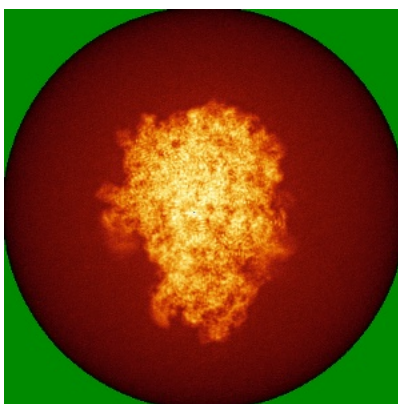


Z

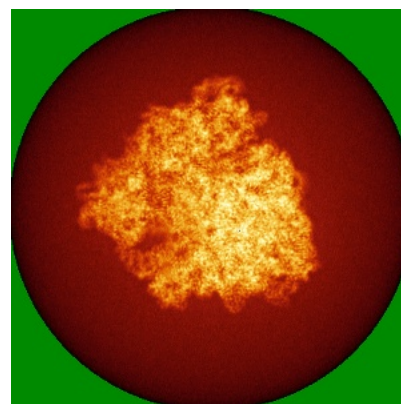
6.4.2 Raw map



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



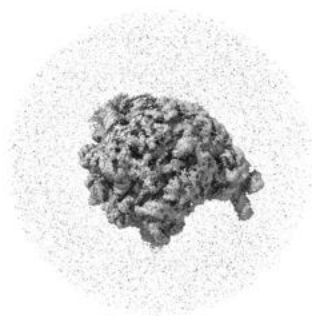
Y



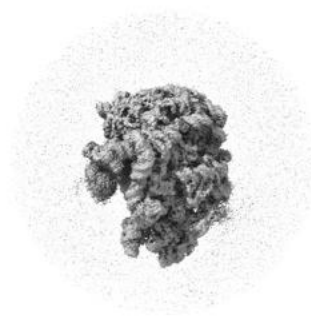
Z

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.

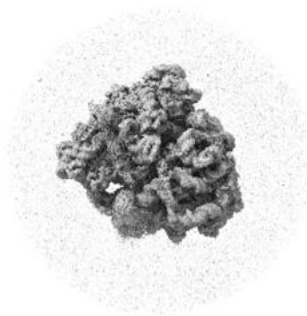
6.5.2 Raw map



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.

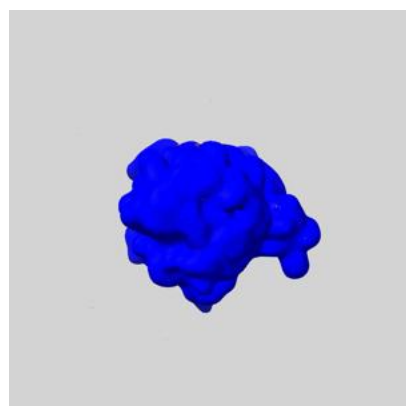
6.6 Mask visualisation [i](#)

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

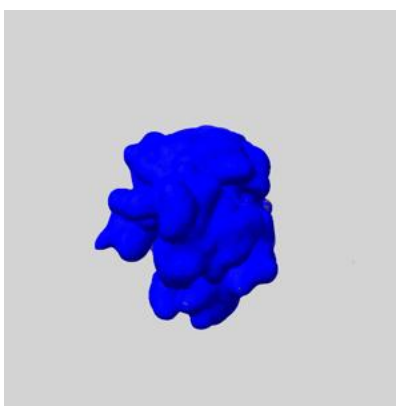
A mask typically either:

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

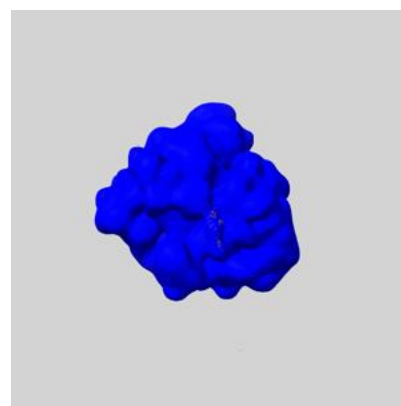
6.6.1 emd_12930_msk_1.map [i](#)



X



Y

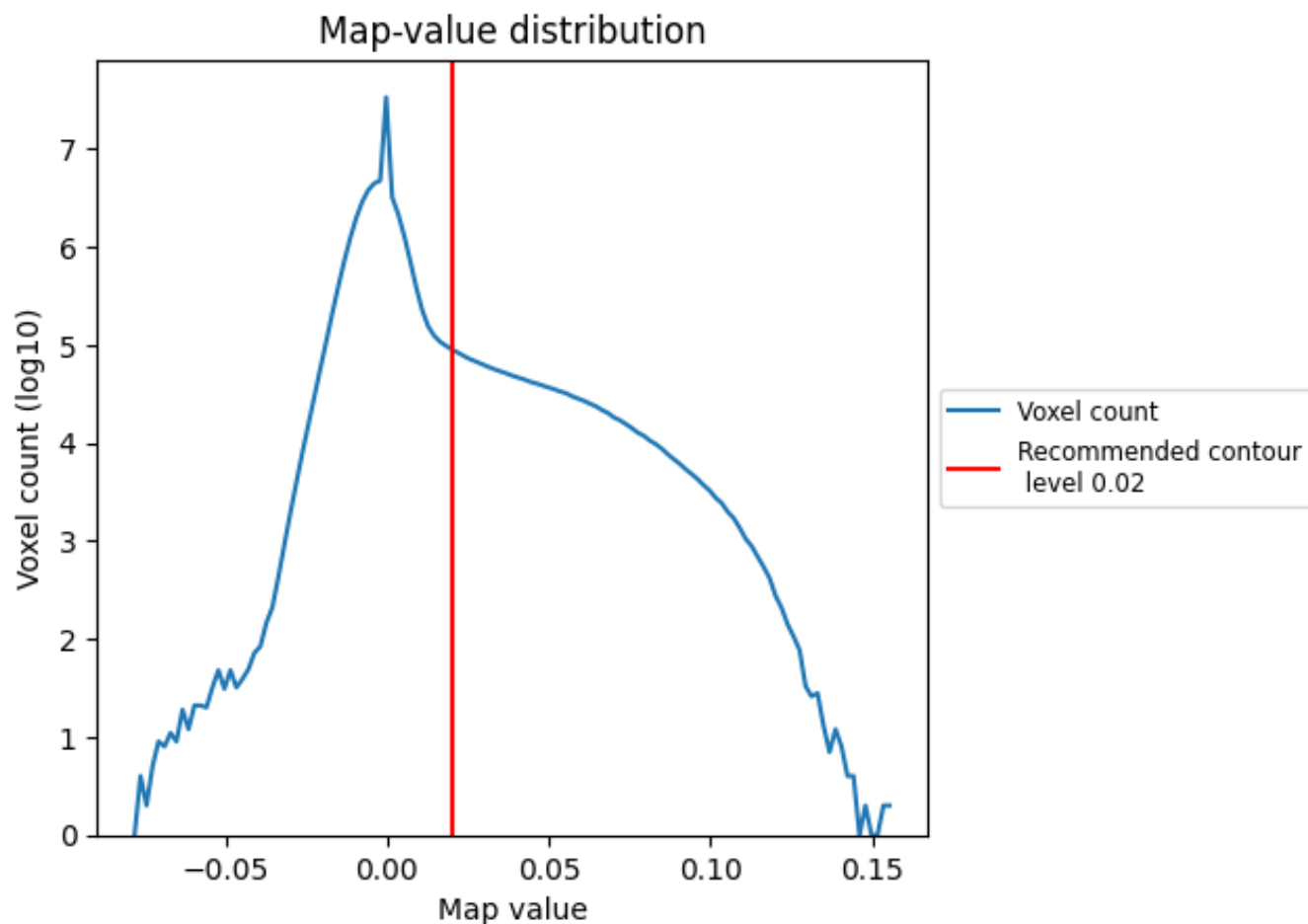


Z

7 Map analysis [i](#)

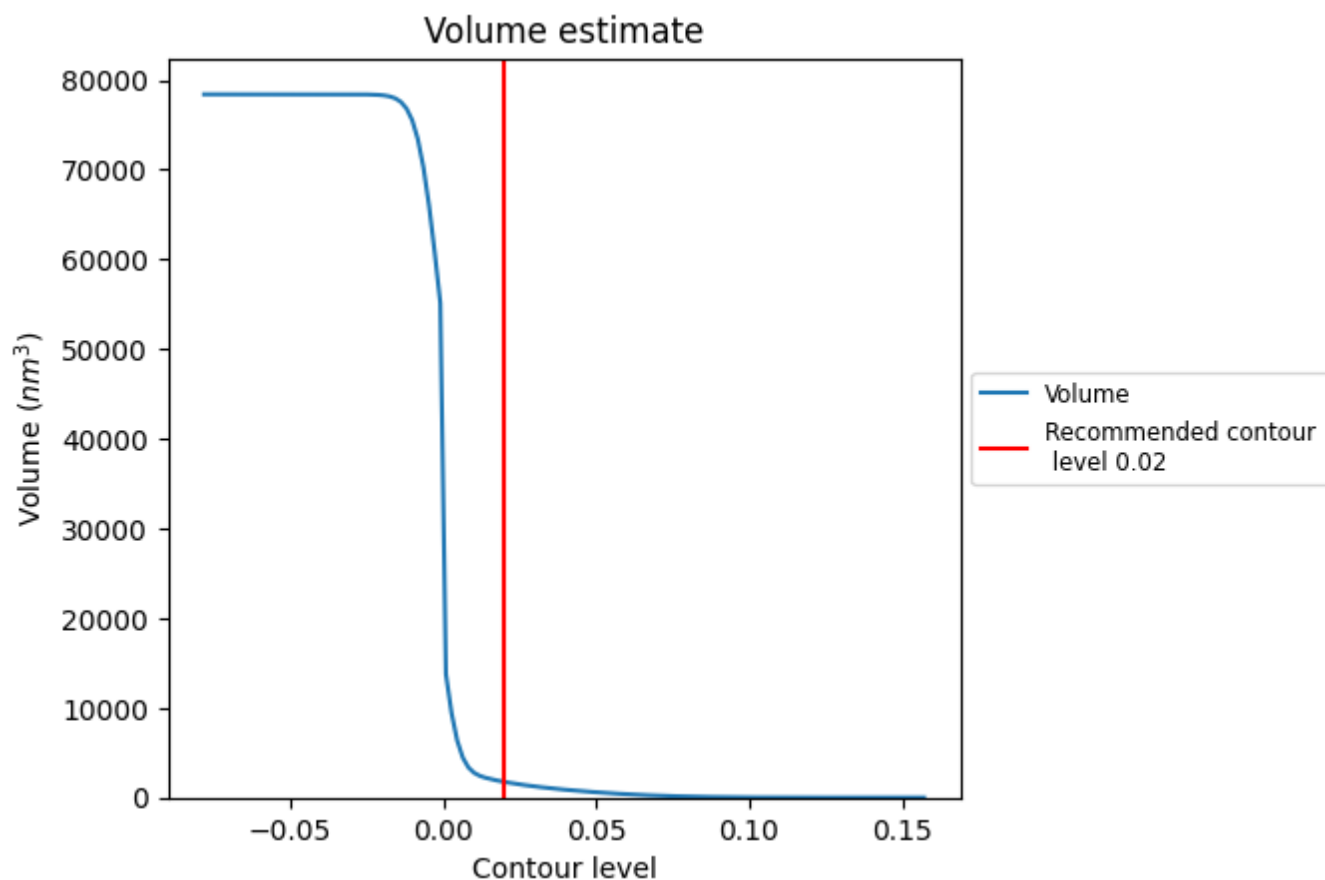
This section contains the results of statistical analysis of the map.

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.

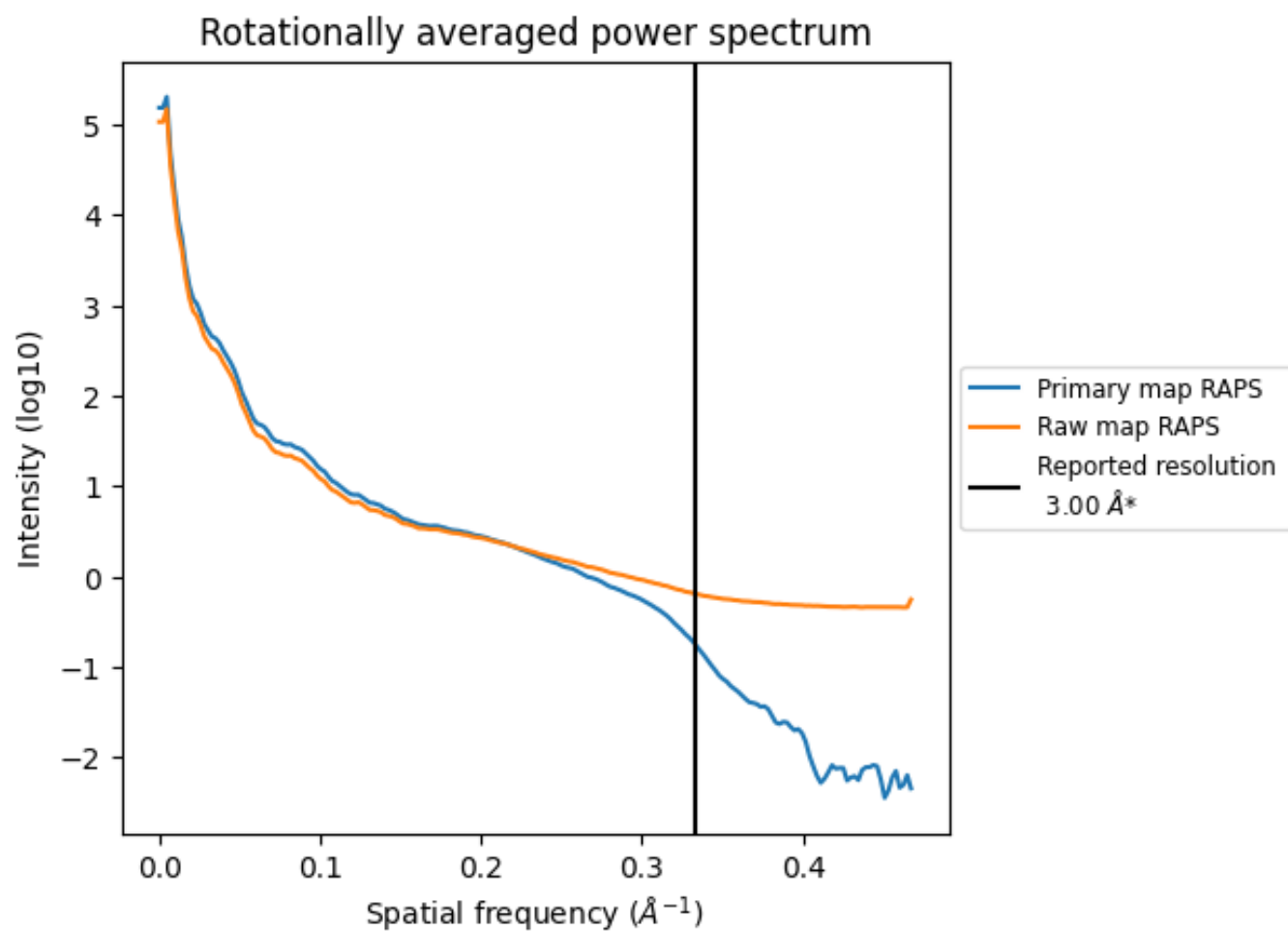
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1748 nm³; this corresponds to an approximate mass of 1579 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 ⓘ

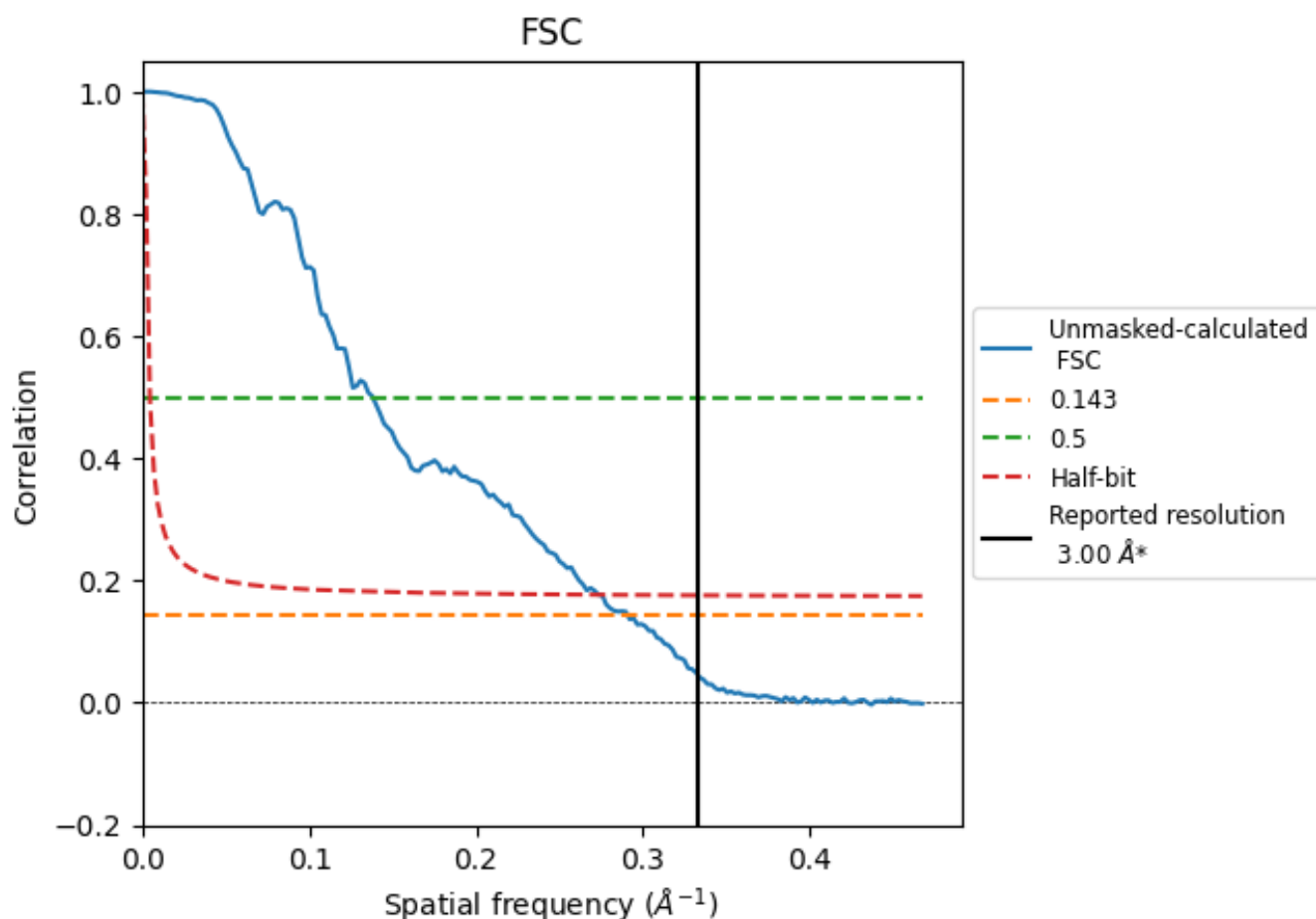


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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](#)

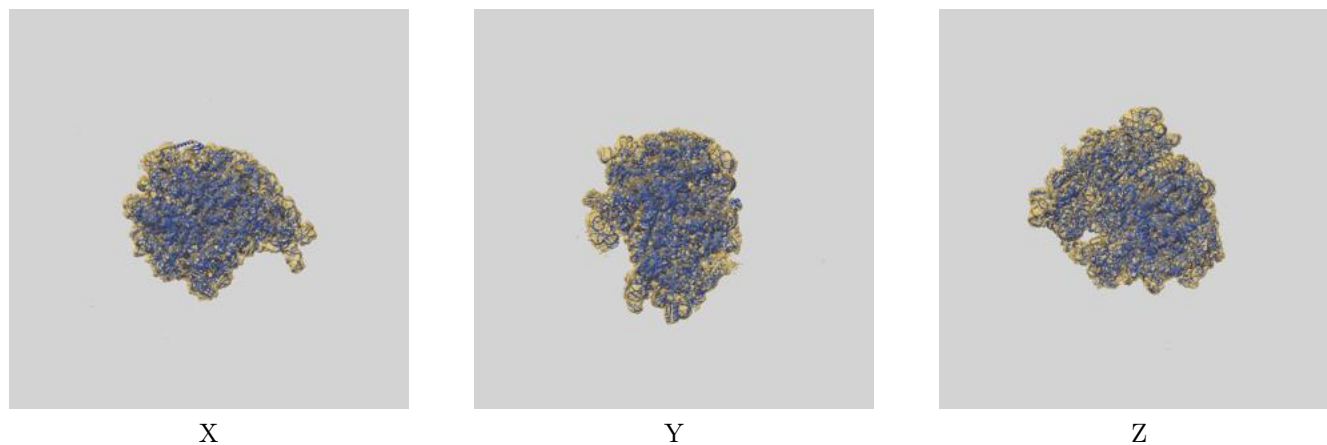
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.44	7.24	3.66

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

9 Map-model fit [i](#)

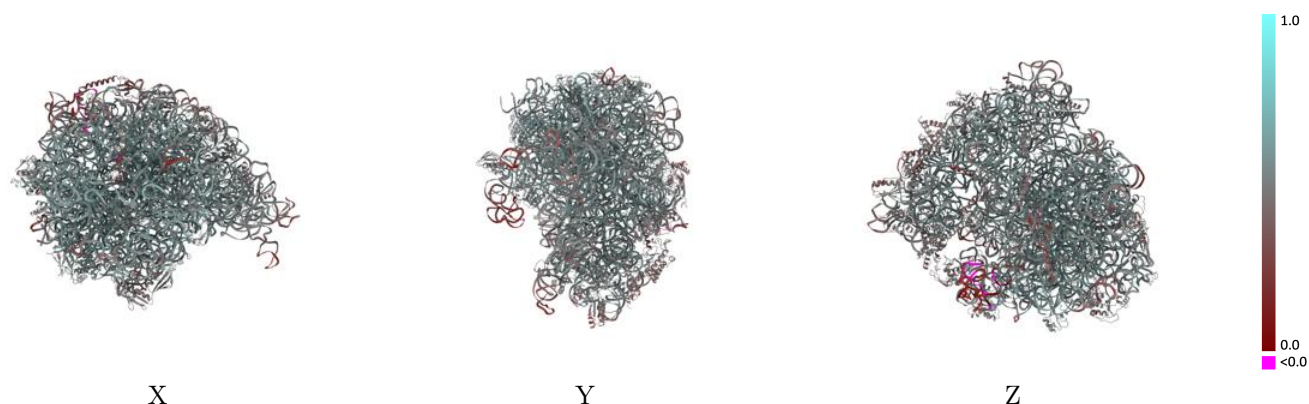
This section contains information regarding the fit between EMDB map EMD-12930 and PDB model 7OII. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



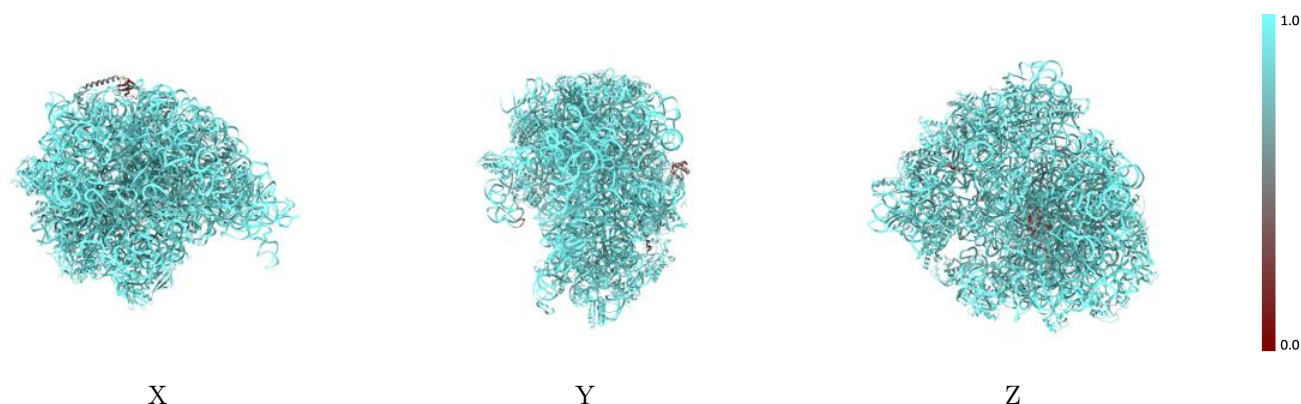
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



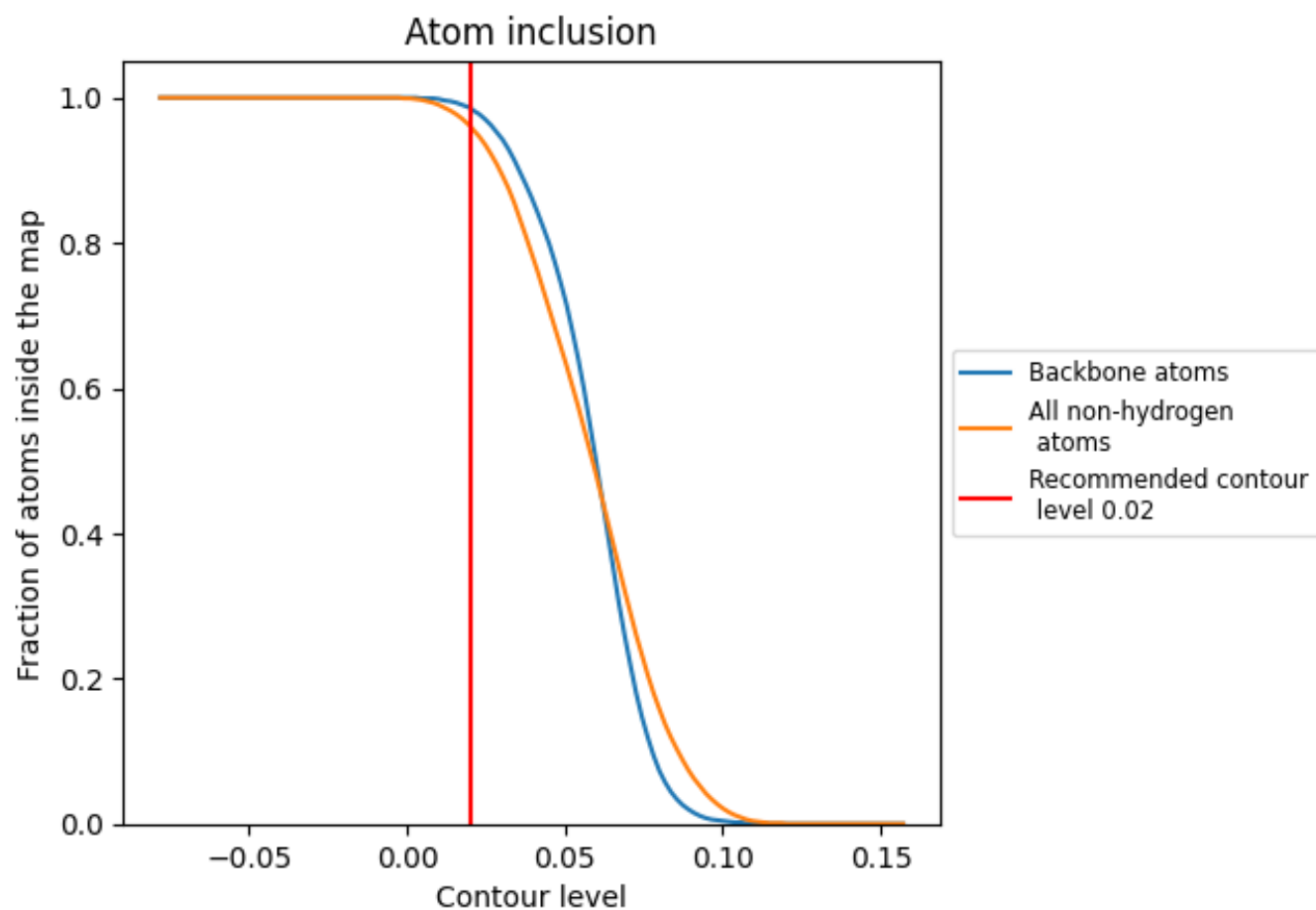
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 99% 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	 0.9610	 0.5180
1	 0.9870	 0.5310
2	 0.9940	 0.5240
3	 0.9950	 0.5230
4	 0.9840	 0.5110
B	 0.9160	 0.2230
C	 0.9160	 0.5640
D	 0.9320	 0.5490
E	 0.9220	 0.5170
F	 0.9020	 0.4600
G	 0.9150	 0.4660
H	 0.4990	 0.3620
I	 0.9300	 0.5430
J	 0.8830	 0.5450
K	 0.9420	 0.5390
L	 0.9150	 0.5400
M	 0.9560	 0.5530
N	 0.9370	 0.4960
O	 0.9010	 0.5410
P	 0.9440	 0.5450
Q	 0.9310	 0.5270
R	 0.8840	 0.5280
S	 0.9000	 0.5140
T	 0.9240	 0.5050
U	 0.9050	 0.5040
V	 0.8720	 0.5510
W	 0.9150	 0.5350
X	 0.8770	 0.4450
Y	 0.9080	 0.5260
Z	 0.8790	 0.4050
a	 0.9070	 0.5390
b	 0.8610	 0.5080
c	 0.9040	 0.5590
d	 0.9270	 0.5700
e	 0.9040	 0.5410



Continued on next page...

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Chain	Atom inclusion	Q-score
f	 0.8570	 0.4310
g	 0.9040	 0.4830
h	 0.9090	 0.4790
i	 0.9120	 0.5130
j	 0.9020	 0.4670
k	 0.8720	 0.4510
l	 0.9050	 0.5130
m	 0.9130	 0.4740
n	 0.8690	 0.4370
o	 0.9120	 0.4920
p	 0.8750	 0.5200
q	 0.9150	 0.4650
r	 0.9200	 0.4970
s	 0.9220	 0.4880
t	 0.9360	 0.5040
u	 0.8880	 0.4900
v	 0.8910	 0.4900
w	 0.9300	 0.4760
x	 0.9160	 0.4820
y	 0.7460	 0.3980
z	 0.9630	 0.4710