



wwPDB EM Validation Summary Report ⓘ

Sep 28, 2024 – 08:10 pm BST

PDB ID : 7PIC
EMDB ID : EMD-13436
Title : 70S ribosome with P/E-site tRNA in spectinomycin-treated *Mycoplasma pneumoniae* cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-19
Resolution : 9.10 Å (reported)
Based on initial models : 7OOC, 4V7C, 7OOD

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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

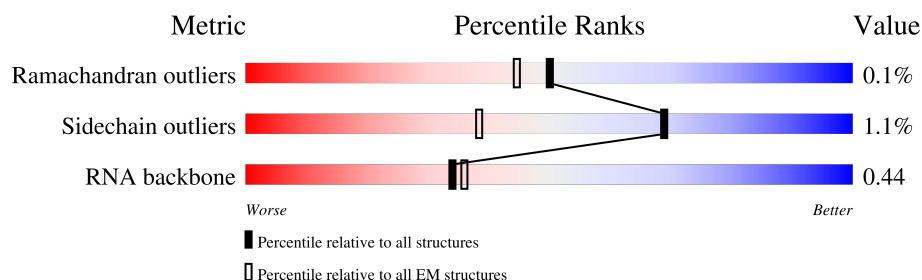
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.10 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	48	
2	1	59	
3	2	37	
4	A	294	
5	B	273	
6	C	205	
7	D	219	
8	E	215	

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Mol	Chain	Length	Quality of chain
9	F	155	15% 99% ..
10	G	142	13% 99% ..
11	H	132	13% 96% ..
12	I	108	17% 94% 6%
13	J	121	11% 93% 6%
14	K	139	10% 95% ...
15	L	124	23% 94% 5%
16	M	61	11% 97% ..
17	N	86	7% 97% .
18	O	94	7% 85% 15%
19	P	85	7% 94% ..
20	Q	104	62% 38%
21	R	87	13% 97% .
22	S	87	89% 11%
23	T	60	88% 12%
24	a	287	7% 99% .
25	b	287	11% 80% 20%
26	c	212	5% 99% .
27	d	180	16% 97% .
28	e	184	16% 96% .
29	f	149	45% 95% ..
30	g	161	16% 67% 9% 24%
31	h	137	42% 93% 7%
32	i	146	5% 98% ..
33	j	122	14% 99% .

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Mol	Chain	Length	Quality of chain
34	k	151	
35	l	139	
36	m	124	
37	n	116	
38	o	119	
39	p	127	
40	q	100	
41	r	159	
42	s	237	
43	t	111	
44	u	104	
45	v	65	
46	w	111	
47	x	97	
48	y	57	
49	z	53	
50	3	2907	
51	4	108	
52	5	1520	
53	8	76	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 144500 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 protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	240	Total	C	N	O	S	0	0
			1921	1226	334	352	9		

- Molecule 5 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	215	Total	C	N	O	S	0	0
			1698	1073	313	307	5		

- Molecule 6 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	203	Total	C	N	O	S	0	0
			1660	1051	314	290	5		

- Molecule 7 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	153	Total	C	N	O	S	0	0
			1173	742	226	202	3		

- Molecule 8 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	167	Total	C	N	O	S	0	0
			1362	857	240	263	2		

- Molecule 9 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	154	Total	C	N	O	S	0	0
			1246	785	239	216	6		

- Molecule 10 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	141	Total	C	N	O	S	0	0
			1110	723	193	192	2		

- Molecule 11 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	128	Total	C	N	O	S	0	0
			1028	655	191	181	1		

- Molecule 12 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	101	Total	C	N	O	S	0	0
			809	523	142	143	1		

- Molecule 13 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	114	Total	C	N	O	S	0	0
			829	514	153	156	6		

- Molecule 14 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	136	Total	C	N	O	S	0	0
			1076	680	213	181	2		

- Molecule 15 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	118	Total	C	N	O		0	0
			951	594	191	166			

- Molecule 16 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	60	Total	C	N	O	S	0	0
			474	302	96	72	4		

- Molecule 17 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	83	Total	C	N	O		0	0
			673	428	125	120			

- Molecule 18 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	80	Total	C	N	O	S	0	0
			646	414	119	111	2		

- Molecule 19 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	83	Total	C	N	O		0	0
			675	425	135	115			

- Molecule 20 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	65	Total	C	N	O	S	0	0
			535	342	103	86	4		

- Molecule 21 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	84	Total	C	N	O	S	0	0
			682	435	127	118	2		

- Molecule 22 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	77	Total	C	N	O	S	0	0
			629	383	135	111			

- Molecule 23 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	53	Total	C	N	O	S	0	0
			471	295	103	72	1		

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 26 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

- Molecule 28 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	e	176	Total	C	N	O		
			1396	899	247	250	0	0

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	f	145	Total	C	N	O	S	
			1182	763	206	210	3	0

- Molecule 30 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	g	123	Total	C	N	O	S	
			936	599	160	174	3	0

- Molecule 31 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	h	128	Total	C	N	O	S	
			959	616	160	177	6	0

- Molecule 32 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	i	144	Total	C	N	O	S	
			1164	737	213	209	5	0

- Molecule 33 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	j	122	Total	C	N	O	S	
			944	595	178	167	4	0

- Molecule 34 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	k	148	Total	C	N	O		
			1153	731	226	196	0	0

- Molecule 35 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

- Molecule 36 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	119	Total	C	N	O	S	0	0
			958	609	175	171	3		

- Molecule 37 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	n	112	Total	C	N	O	S	0	0
			889	557	175	155	2		

- Molecule 38 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	o	115	Total	C	N	O	S	0	0
			938	592	180	165	1		

- Molecule 39 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	p	114	Total	C	N	O	S	0	0
			947	603	188	154	2		

- Molecule 40 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	q	99	Total	C	N	O	S	0	0
			811	525	148	134	4		

- Molecule 41 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 42 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 43 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 45 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 46 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	w	100	Total	C	N	O	0	0
			818	517	153	148		

- Molecule 47 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

- Molecule 49 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 50 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 51 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

- Molecule 53 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	8	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

3 Residue-property plots [i](#)

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

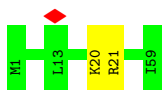
- Molecule 1: 50S ribosomal protein L34

Chain 0:  98%



- Molecule 2: 50S ribosomal protein L35

Chain 1:  97%




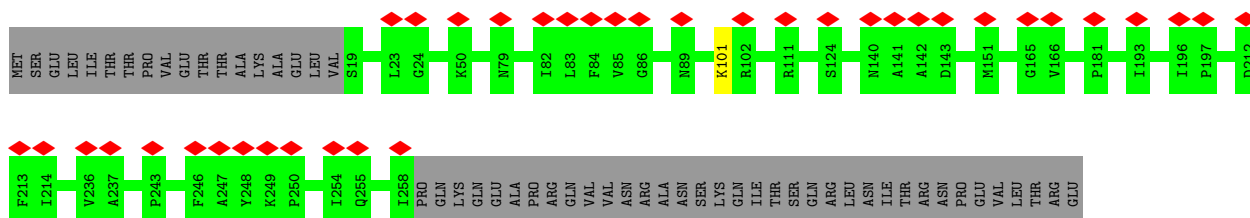
- Molecule 3: 50S ribosomal protein L36

Chain 2:  100%


There are no outlier residues recorded for this chain.

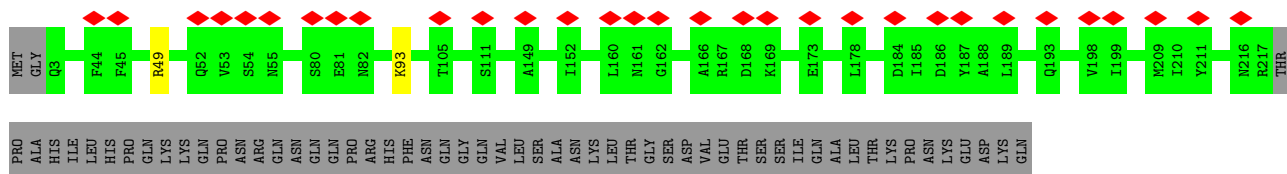
- Molecule 4: 30S ribosomal protein S2

Chain A:  13% 81% 18%

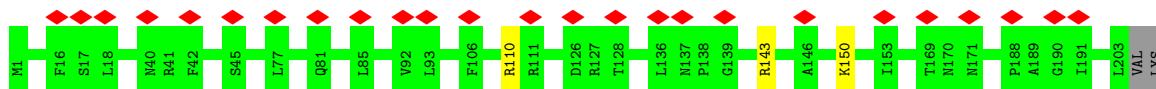


- Molecule 5: 30S ribosomal protein S3

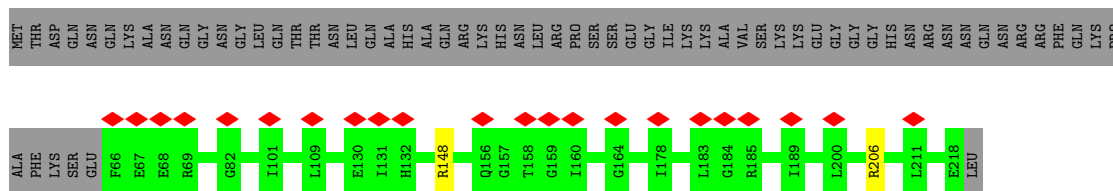
Chain B:  11% 78% 21%



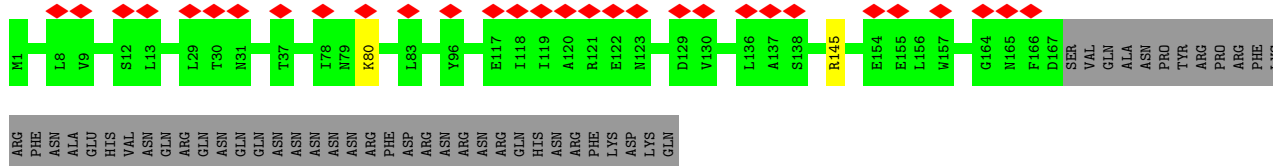
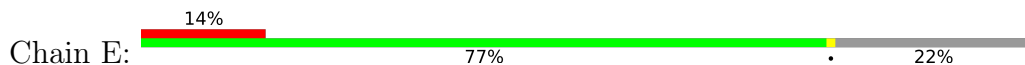
- Molecule 6: 30S ribosomal protein S4



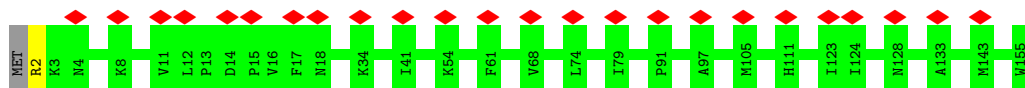
- Molecule 7: 30S ribosomal protein S5



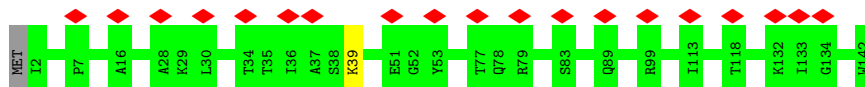
- Molecule 8: 30S ribosomal protein S6



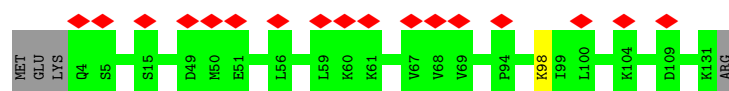
- Molecule 9: 30S ribosomal protein S7



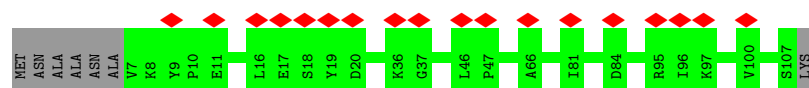
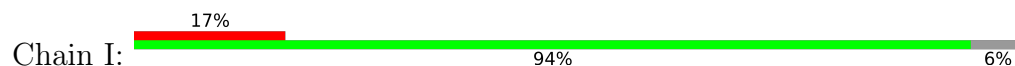
- Molecule 10: 30S ribosomal protein S8



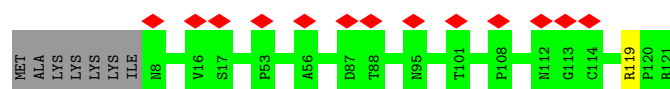
- Molecule 11: 30S ribosomal protein S9



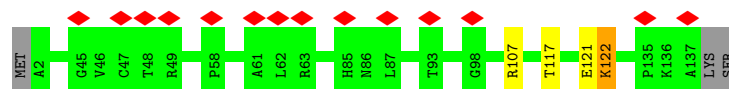
- Molecule 12: 30S ribosomal protein S10



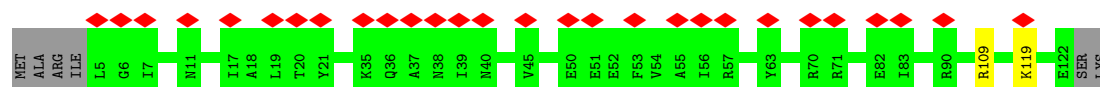
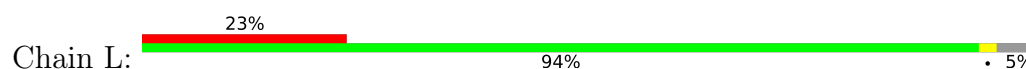
- Molecule 13: 30S ribosomal protein S11



- Molecule 14: 30S ribosomal protein S12



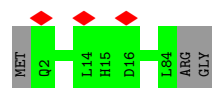
- Molecule 15: 30S ribosomal protein S13



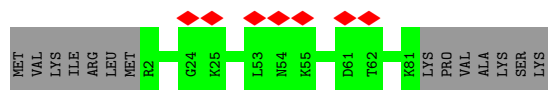
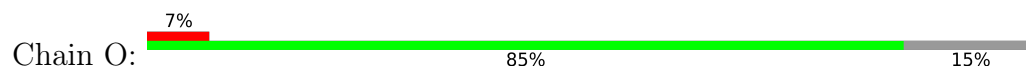
- Molecule 16: 30S ribosomal protein S14 type Z



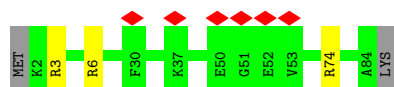
- Molecule 17: 30S ribosomal protein S15



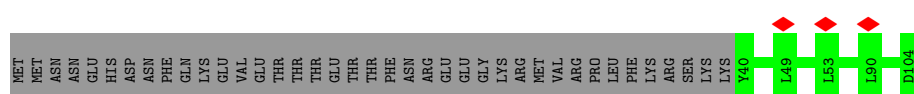
- Molecule 18: 30S ribosomal protein S16



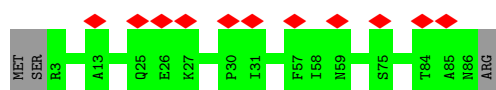
- Molecule 19: 30S ribosomal protein S17



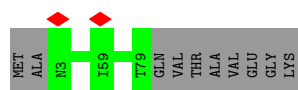
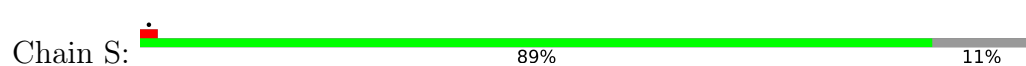
- Molecule 20: 30S ribosomal protein S18



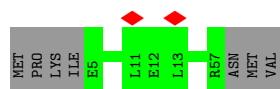
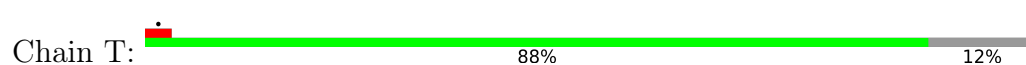
- Molecule 21: 30S ribosomal protein S19



- Molecule 22: 30S ribosomal protein S20

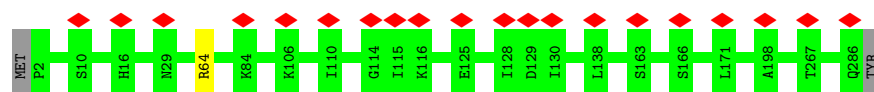


- Molecule 23: 30S ribosomal protein S21

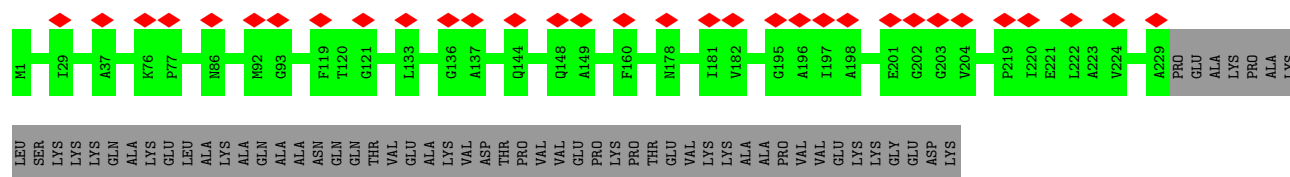
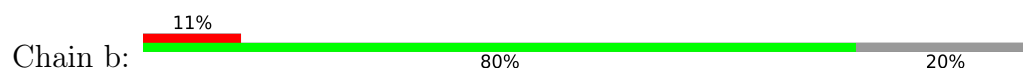


- Molecule 24: 50S ribosomal protein L2

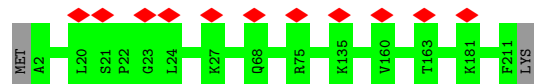




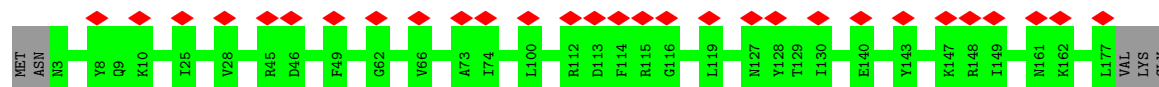
- Molecule 25: 50S ribosomal protein L3



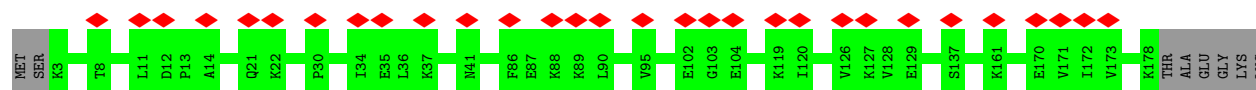
- Molecule 26: 50S ribosomal protein L4



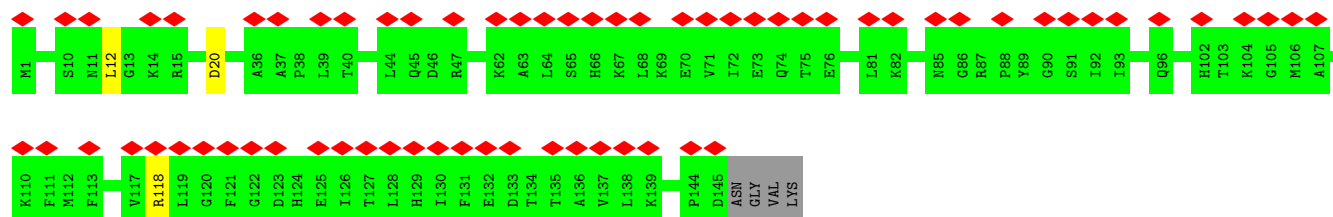
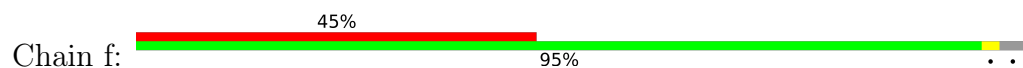
- Molecule 27: 50S ribosomal protein L5



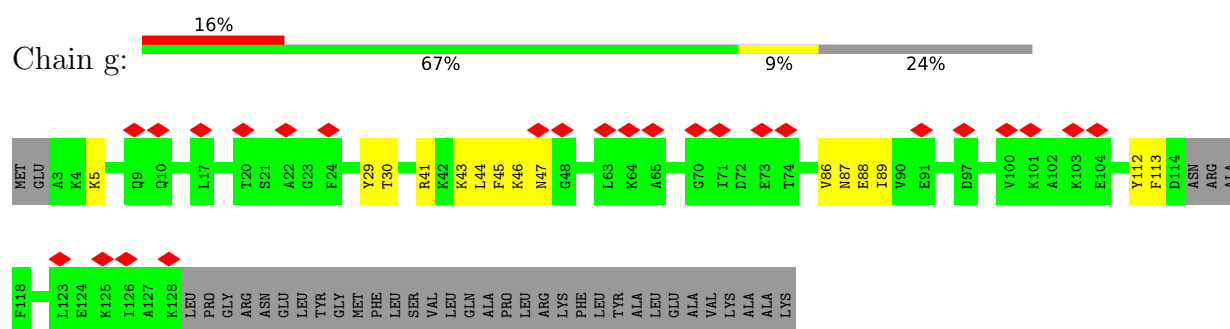
- Molecule 28: 50S ribosomal protein L6



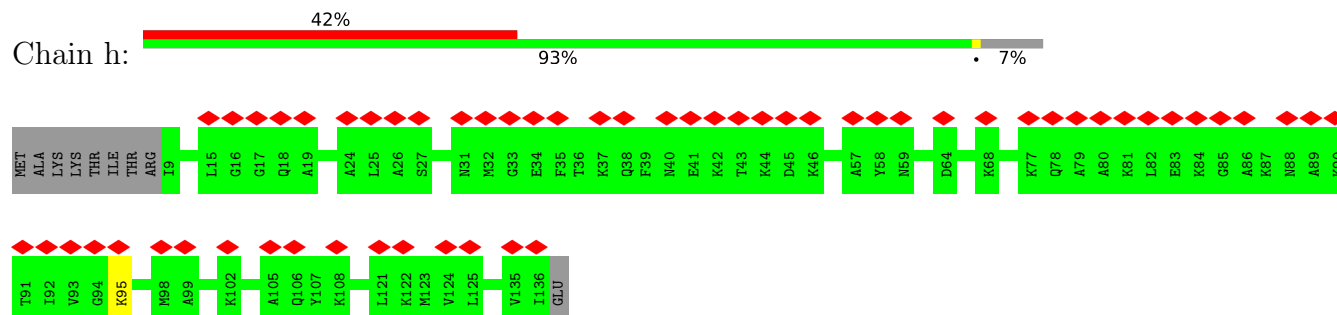
- Molecule 29: 50S ribosomal protein L9



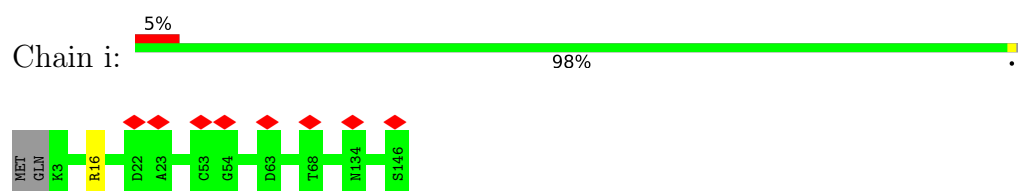
- Molecule 30: 50S ribosomal protein L10



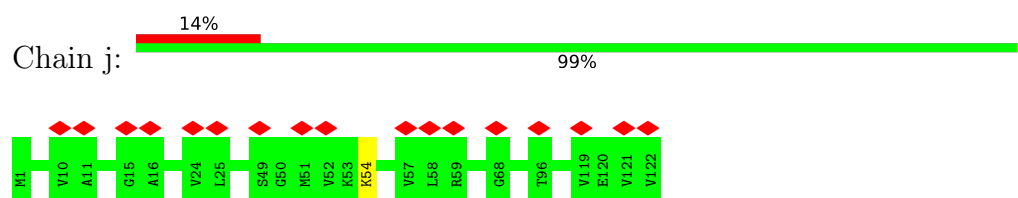
- Molecule 31: 50S ribosomal protein L11



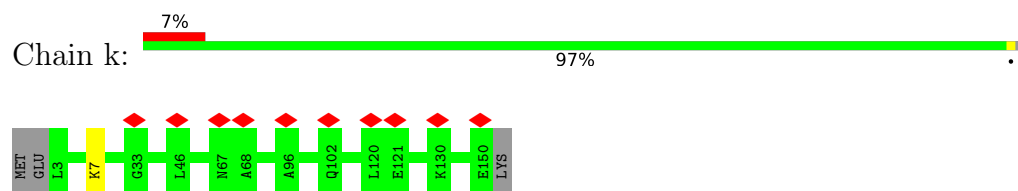
- Molecule 32: 50S ribosomal protein L13



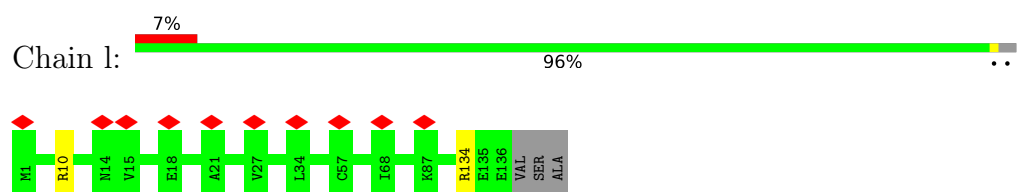
- Molecule 33: 50S ribosomal protein L14



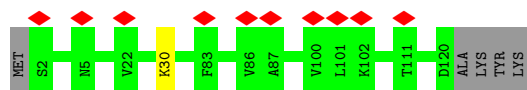
- Molecule 34: 50S ribosomal protein L15



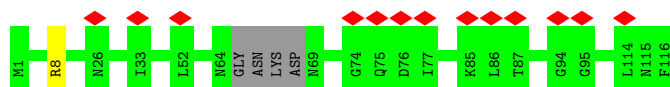
- Molecule 35: 50S ribosomal protein L16



- Molecule 36: 50S ribosomal protein L17



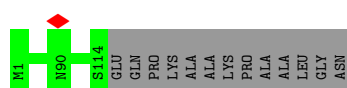
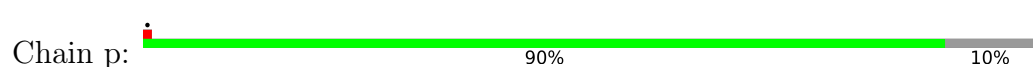
- Molecule 37: 50S ribosomal protein L18



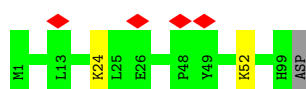
- Molecule 38: 50S ribosomal protein L19



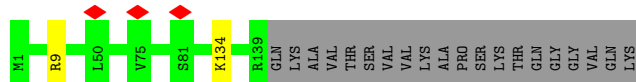
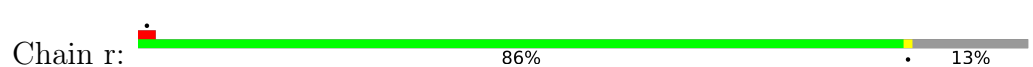
- Molecule 39: 50S ribosomal protein L20



- Molecule 40: 50S ribosomal protein L21

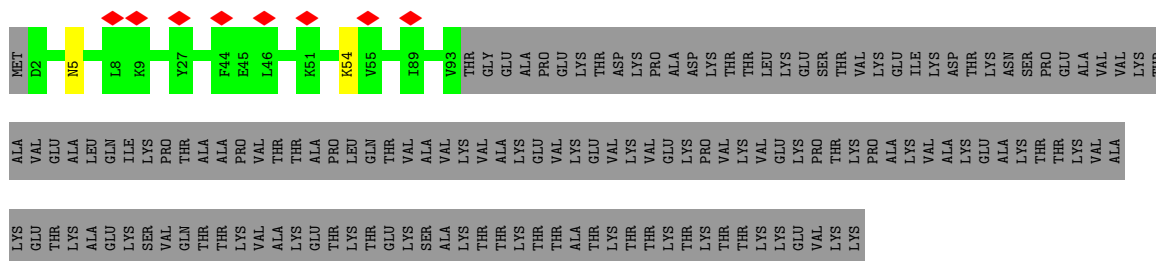


- Molecule 41: 50S ribosomal protein L22

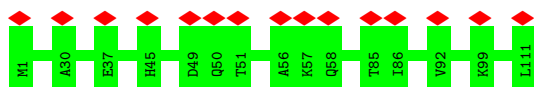


- Molecule 42: 50S ribosomal protein L23

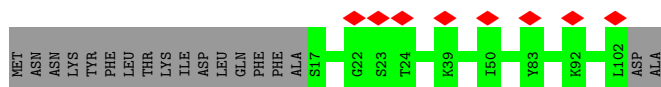
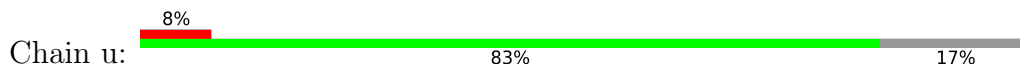




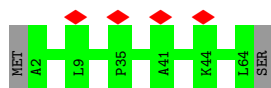
- Molecule 43: 50S ribosomal protein L24



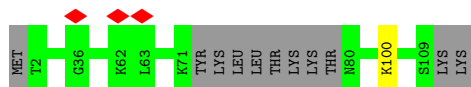
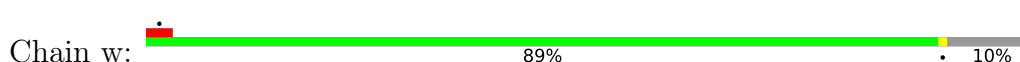
- Molecule 44: 50S ribosomal protein L27



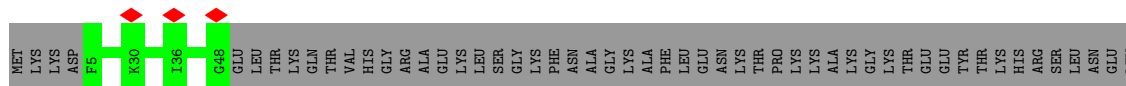
- Molecule 45: 50S ribosomal protein L28



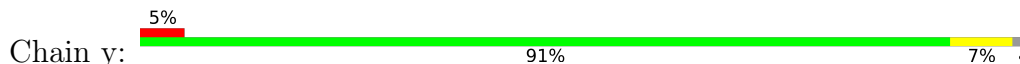
- Molecule 46: 50S ribosomal protein L29



- Molecule 47: 50S ribosomal protein L31



- Molecule 48: 50S ribosomal protein L32



U2799	G2646	G2543	A2438	G2312	U2195	G2076	C1972	U1827	G1706	G1594	G1491	U1354	G1253
U2800	A2647	A2540	A2442	U2313	G2196	U2083	A1976	A1828	U1707	C1599	G1492	C1355	G1257
U2801	G2653	G2550	A2443	U2314	U2197	A2084	A1977	C1708	C1709	A1600	A1493	G1356	U1260
C2804	G2656	G2551	U2449	G2315	U2200	C2085	U1978	G1835	A1710	A1603	A1502	U1360	U1264
A2805	A2662	U2555	G2453	U2327	U2202	G2091	G1982	G1842	A1715	U1612	G1507	U1368	G1265
A2806	G2663	G2561	A2456	A2330	U2203	U2020	U1983	A1855	A1716	U1618	G1508	U1369	G1266
A2807	U2664	U2562	U2457	U2331	A2206	A2109	A1984	G1856	U1727	A1619	U1509	A1370	A1267
A2808	G2669	U2563	A2458	U2332	G2207	U2110	U1989	U1873	U1728	U1627	A1510	U1372	U1268
A2809	G2669	G2564	A2458	U2333	U2208	U2111	U1989	A1873	G1729	U1627	A1515	C1373	A1274
A2810	G2681	G2565	G2472	U2334	U2208	U2111	C1987	A1873	C1730	U1627	A1515	C1373	A1274
G2811	G2681	C2566	G2472	A2335	G2211	A2112	U1998	G1876	G1733	C1632	C1518	U1380	U1279
U2812	C2689	C2567	A2477	U2342	U2212	U2113	U1999	C1877	G1733	C1633	A1519	U1380	U1279
A2813	G2689	U2570	C2483	A2343	U2219	U2118	U1999	A1878	G1733	A1534	U1522	A1283	A1284
G2815	U2693	A2574	A2484	A2344	A2220	U2116	U2000	A1879	G1741	U1534	U1522	A1283	A1284
C2822	C2697	G2575	U2487	C2350	A2231	G2122	C2003	U1890	U1748	G1640	U1529	G1408	U1285
A2823	U2698	A2578	C2488	U2351	G2232	A2123	G2006	A1891	A1749	G1641	U1541	U1425	G1286
A2825	G2710	G2581	U2487	U2352	A2233	A2124	U2007	A1891	A1752	A1644	U1541	U1425	G1286
A2826	C2711	G2582	G2492	G2353	C2234	G2122	A2008	A1907	G1763	G1645	U1541	U1425	G1286
A2827	C2712	U2583	G2493	A2354	C2234	A2123	A2009	A1908	U1764	G1646	U1541	U1425	G1286
A2830	A2713	G2584	G2494	C2355	G2238	U2125	A2010	A1908	G1765	U1546	U1546	U1425	G1286
U2831	G2714	A2585	G2496	A2362	U2244	A2126	G2011	A1908	U1766	A1431	U1546	U1425	G1286
G2835	C2721	G2586	U2497	U2365	G2246	A2126	A2012	G1913	G1767	A1431	U1546	U1425	G1286
U2836	G2722	U2586	U2499	U2366	G2247	A2126	A2012	G1914	U1768	A1431	U1546	U1425	G1286
G2837	C2734	G2590	U2500	G2370	G2247	A2126	A2012	G1914	U1768	A1431	U1546	U1425	G1286
U2838	G2737	U2593	U2501	G2373	U2251	A2137	G2028	A1926	U1771	A1431	U1546	U1425	G1286
A2839	G2741	C2594	G2502	G2379	G2254	U2138	A2030	A1926	G1772	A1431	U1546	U1425	G1286
U2853	A2741	A2595	G2503	G2379	G2254	U2138	A2037	A1931	A1780	A1663	U1557	U1444	U1298
A2854	U2747	U2604	C2504	A2382	G2259	G2140	A2038	C1931	A1780	A1669	A1558	U1445	A1314
U2862	G2752	G2605	C2506	U2391	C2282	A2145	A2040	A1934	U1784	U1670	A1559	G1446	A1315
A2863	A2756	A2610	U2508	U2392	A2276	U2149	C2041	A1935	U1785	U1679	A1559	G1446	A1315
U2865	G2760	G2611	G2510	C2393	G2277	C2150	G2046	G1936	U1786	U1679	A1559	G1446	A1315
G2871	U2766	U2618	U2511	G2397	G2278	U2153	U2047	G1937	U1787	U1679	A1559	G1446	A1315
A2872	U2766	C2619	U2512	G2397	G2279	U2153	G2050	A1943	U1788	U1680	A1559	G1446	A1315
G2876	U2766	G2620	U2514	C2410	U2280	A2154	G2056	A1944	U1789	G1681	A1559	G1446	A1315
A2881	U2771	A2622	U2516	C2411	A2281	A2157	A2056	A1945	U1790	G1682	A1559	G1446	A1315
U2882	A2772	G2629	A2517	A2415	A2281	A2157	A2056	U1947	U1791	G1683	A1559	G1446	A1315
A2883	A2773	C2632	A2521	G2418	U2281	U2163	G2059	U1950	A1794	U1687	A1559	G1446	A1315
C2884	U2774	C2633	A2526	C2428	A2294	G2164	G2062	A1951	A1798	U1692	A1559	G1446	A1315
U2888	A2786	U2636	U2527	U2431	A2295	U2166	G2063	G1952	A1798	U1692	A1559	G1446	A1315
G2890	U2787	A2637	U2527	C2432	A2296	G2169	A2066	G1956	U1815	A1698	A1559	G1446	A1315
A2895	U2787	G2638	C2631	A2433	U2289	A2170	A2067	A1961	U1816	A1699	A1559	G1446	A1315
G2896	A2789	U2644	G2537	A2434	U2290	A2171	A2068	U1962	U1820	G1700	A1559	G1446	A1315
G2897	A2790	U2644	G2538	C2435	C2302	A2179	A2069	U1963	G1821	G1701	A1559	G1446	A1315
A2898	U2791	U2645	A2539	G2437	C2305	U2180	C2070	U1970	G1822	A1702	A1559	G1446	A1315



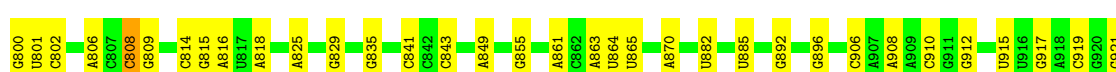
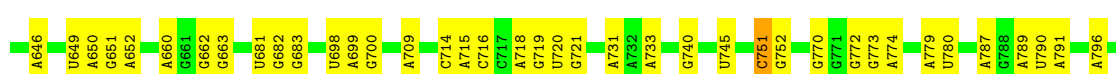
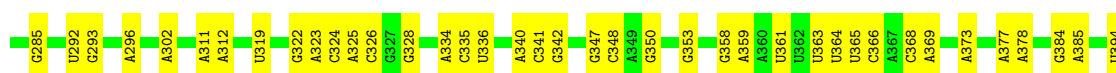
• Molecule 51: 5S ribosomal RNA

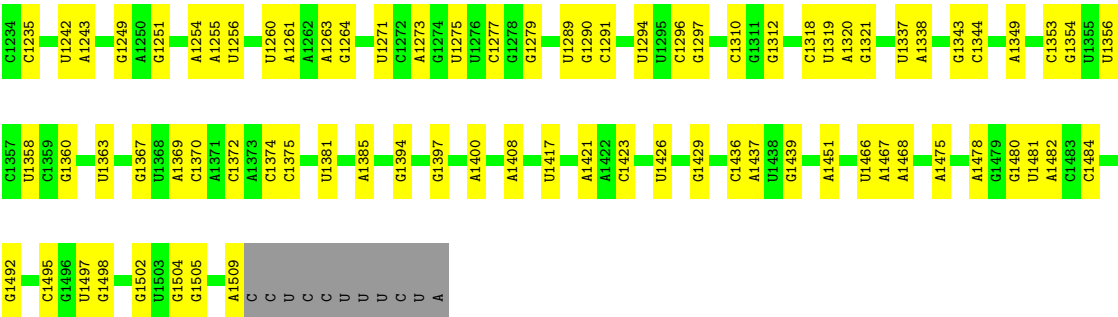
Chain 4: 58% 39%



• Molecule 52: 16S ribosomal RNA

Chain 5: 69% 29%





● Molecule 53: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	721	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.735	Depositor
Minimum map value	-0.678	Depositor
Average map value	0.024	Depositor
Map value standard deviation	0.122	Depositor
Recommended contour level	0.37	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0	0.23	0/383	0.38	0/504
2	1	0.24	0/484	0.43	0/637
3	2	0.22	0/306	0.46	0/401
4	A	0.24	0/1954	0.42	0/2642
5	B	0.24	0/1721	0.47	0/2323
6	C	0.24	0/1691	0.44	0/2267
7	D	0.24	0/1188	0.47	0/1593
8	E	0.25	0/1384	0.44	0/1867
9	F	0.23	0/1266	0.43	0/1700
10	G	0.24	0/1126	0.47	0/1517
11	H	0.24	0/1044	0.48	0/1395
12	I	0.23	0/820	0.49	0/1103
13	J	0.24	0/844	0.42	0/1136
14	K	0.28	0/1094	0.52	0/1468
15	L	0.23	0/962	0.44	0/1289
16	M	0.25	0/483	0.45	0/643
17	N	0.23	0/679	0.44	0/907
18	O	0.23	0/659	0.42	0/885
19	P	0.24	0/684	0.46	0/913
20	Q	0.24	0/545	0.44	0/730
21	R	0.24	0/698	0.45	0/936
22	S	0.23	0/631	0.38	0/838
23	T	0.23	0/475	0.41	0/621
24	a	0.23	0/2267	0.44	0/3044
25	b	0.26	0/1795	0.49	0/2412
26	c	0.25	0/1671	0.45	0/2246
27	d	0.24	0/1409	0.45	0/1894
28	e	0.25	0/1420	0.45	0/1912
29	f	0.25	0/1205	0.52	2/1616 (0.1%)
30	g	3.79	6/944 (0.6%)	0.62	0/1260
31	h	0.25	0/968	0.45	0/1298
32	i	0.23	0/1186	0.43	0/1592
33	j	0.24	0/953	0.46	0/1275
34	k	0.24	0/1170	0.46	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	l	0.24	0/1104	0.46	0/1481
36	m	0.24	0/973	0.46	0/1309
37	n	0.23	0/897	0.45	0/1198
38	o	0.24	0/948	0.45	0/1262
39	p	0.23	0/961	0.37	0/1278
40	q	0.23	0/828	0.48	0/1111
41	r	0.25	0/1077	0.46	0/1441
42	s	0.24	0/732	0.50	0/988
43	t	0.24	0/879	0.45	0/1165
44	u	0.24	0/665	0.48	0/884
45	v	0.23	0/519	0.45	0/695
46	w	0.22	0/826	0.43	0/1104
47	x	0.26	0/353	0.43	0/474
48	y	0.28	0/457	0.50	0/601
49	z	0.24	0/412	0.44	0/547
50	3	0.20	0/69073	0.80	50/107710 (0.0%)
51	4	0.19	0/2505	0.80	2/3902 (0.1%)
52	5	0.19	0/35768	0.80	38/55764 (0.1%)
53	8	0.18	0/1808	0.78	1/2817 (0.0%)
All	All	0.36	6/156894 (0.0%)	0.72	93/234154 (0.0%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	g	112	TYR	CD2-CE2	65.91	2.38	1.39
30	g	112	TYR	CD1-CE1	65.03	2.36	1.39
30	g	112	TYR	CE1-CZ	39.32	1.89	1.38
30	g	112	TYR	CE2-CZ	38.36	1.88	1.38
30	g	112	TYR	CG-CD2	31.20	1.79	1.39

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	5	808	C	C2-N1-C1'	9.02	128.73	118.80
52	5	264	C	N3-C2-O2	-8.70	115.81	121.90
50	3	2567	C	N3-C2-O2	-8.66	115.84	121.90
52	5	843	C	N3-C2-O2	-8.29	116.09	121.90
50	3	2428	C	N3-C2-O2	-8.06	116.26	121.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	43 (96%)	2 (4%)	0	100	100
2	1	57/59 (97%)	52 (91%)	5 (9%)	0	100	100
3	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
4	A	238/294 (81%)	225 (94%)	13 (6%)	0	100	100
5	B	213/273 (78%)	200 (94%)	13 (6%)	0	100	100
6	C	201/205 (98%)	188 (94%)	13 (6%)	0	100	100
7	D	151/219 (69%)	150 (99%)	1 (1%)	0	100	100
8	E	165/215 (77%)	148 (90%)	17 (10%)	0	100	100
9	F	152/155 (98%)	136 (90%)	16 (10%)	0	100	100
10	G	139/142 (98%)	126 (91%)	13 (9%)	0	100	100
11	H	126/132 (96%)	111 (88%)	15 (12%)	0	100	100
12	I	99/108 (92%)	90 (91%)	9 (9%)	0	100	100
13	J	112/121 (93%)	109 (97%)	3 (3%)	0	100	100
14	K	134/139 (96%)	124 (92%)	9 (7%)	1 (1%)	19	57
15	L	116/124 (94%)	102 (88%)	14 (12%)	0	100	100
16	M	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
17	N	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
18	O	78/94 (83%)	76 (97%)	2 (3%)	0	100	100
19	P	81/85 (95%)	79 (98%)	2 (2%)	0	100	100
20	Q	63/104 (61%)	55 (87%)	8 (13%)	0	100	100
21	R	82/87 (94%)	74 (90%)	8 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	S	75/87 (86%)	74 (99%)	1 (1%)	0	100	100
23	T	51/60 (85%)	50 (98%)	1 (2%)	0	100	100
24	a	283/287 (99%)	264 (93%)	19 (7%)	0	100	100
25	b	227/287 (79%)	208 (92%)	19 (8%)	0	100	100
26	c	208/212 (98%)	192 (92%)	16 (8%)	0	100	100
27	d	173/180 (96%)	159 (92%)	14 (8%)	0	100	100
28	e	174/184 (95%)	161 (92%)	13 (8%)	0	100	100
29	f	143/149 (96%)	130 (91%)	13 (9%)	0	100	100
30	g	119/161 (74%)	100 (84%)	16 (13%)	3 (2%)	4	26
31	h	126/137 (92%)	120 (95%)	6 (5%)	0	100	100
32	i	142/146 (97%)	133 (94%)	9 (6%)	0	100	100
33	j	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
34	k	146/151 (97%)	140 (96%)	6 (4%)	0	100	100
35	l	134/139 (96%)	127 (95%)	7 (5%)	0	100	100
36	m	117/124 (94%)	115 (98%)	2 (2%)	0	100	100
37	n	108/116 (93%)	102 (94%)	6 (6%)	0	100	100
38	o	113/119 (95%)	110 (97%)	3 (3%)	0	100	100
39	p	112/127 (88%)	110 (98%)	2 (2%)	0	100	100
40	q	97/100 (97%)	85 (88%)	12 (12%)	0	100	100
41	r	137/159 (86%)	128 (93%)	9 (7%)	0	100	100
42	s	90/237 (38%)	88 (98%)	2 (2%)	0	100	100
43	t	109/111 (98%)	101 (93%)	8 (7%)	0	100	100
44	u	84/104 (81%)	78 (93%)	6 (7%)	0	100	100
45	v	61/65 (94%)	56 (92%)	5 (8%)	0	100	100
46	w	96/111 (86%)	92 (96%)	4 (4%)	0	100	100
47	x	42/97 (43%)	42 (100%)	0	0	100	100
48	y	54/57 (95%)	50 (93%)	3 (6%)	1 (2%)	6	32
49	z	48/53 (91%)	45 (94%)	3 (6%)	0	100	100
All	All	5815/6670 (87%)	5430 (93%)	380 (6%)	5 (0%)	50	83

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	K	122	LYS
30	g	86	VAL
30	g	30	THR
48	y	51	LEU
30	g	88	GLU

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	
1	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	49 (96%)	2 (4%)	27	48
3	2	35/35 (100%)	35 (100%)	0	100	100
4	A	212/262 (81%)	211 (100%)	1 (0%)	86	89
5	B	180/232 (78%)	178 (99%)	2 (1%)	70	80
6	C	181/183 (99%)	178 (98%)	3 (2%)	56	72
7	D	123/178 (69%)	121 (98%)	2 (2%)	58	73
8	E	150/196 (76%)	148 (99%)	2 (1%)	65	77
9	F	131/132 (99%)	130 (99%)	1 (1%)	79	85
10	G	123/124 (99%)	122 (99%)	1 (1%)	79	85
11	H	111/115 (96%)	110 (99%)	1 (1%)	75	83
12	I	95/99 (96%)	95 (100%)	0	100	100
13	J	91/97 (94%)	90 (99%)	1 (1%)	70	80
14	K	117/120 (98%)	113 (97%)	4 (3%)	32	51
15	L	100/105 (95%)	98 (98%)	2 (2%)	50	68
16	M	47/48 (98%)	46 (98%)	1 (2%)	48	66
17	N	76/78 (97%)	76 (100%)	0	100	100
18	O	69/82 (84%)	69 (100%)	0	100	100
19	P	73/75 (97%)	70 (96%)	3 (4%)	26	47
20	Q	56/94 (60%)	56 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	R	74/77 (96%)	74 (100%)	0	100	100
22	S	70/77 (91%)	70 (100%)	0	100	100
23	T	49/56 (88%)	49 (100%)	0	100	100
24	a	241/243 (99%)	240 (100%)	1 (0%)	89	91
25	b	186/233 (80%)	186 (100%)	0	100	100
26	c	182/184 (99%)	182 (100%)	0	100	100
27	d	150/154 (97%)	150 (100%)	0	100	100
28	e	153/159 (96%)	153 (100%)	0	100	100
29	f	131/134 (98%)	130 (99%)	1 (1%)	79	85
30	g	99/129 (77%)	88 (89%)	11 (11%)	5	17
31	h	102/110 (93%)	101 (99%)	1 (1%)	73	82
32	i	126/128 (98%)	125 (99%)	1 (1%)	79	85
33	j	103/103 (100%)	102 (99%)	1 (1%)	73	82
34	k	123/126 (98%)	122 (99%)	1 (1%)	79	85
35	l	113/115 (98%)	111 (98%)	2 (2%)	54	71
36	m	105/109 (96%)	104 (99%)	1 (1%)	73	82
37	n	96/99 (97%)	95 (99%)	1 (1%)	73	82
38	o	101/105 (96%)	101 (100%)	0	100	100
39	p	100/108 (93%)	100 (100%)	0	100	100
40	q	90/91 (99%)	88 (98%)	2 (2%)	47	65
41	r	116/132 (88%)	114 (98%)	2 (2%)	56	72
42	s	82/208 (39%)	80 (98%)	2 (2%)	44	62
43	t	96/96 (100%)	96 (100%)	0	100	100
44	u	69/85 (81%)	69 (100%)	0	100	100
45	v	58/60 (97%)	58 (100%)	0	100	100
46	w	87/98 (89%)	86 (99%)	1 (1%)	70	80
47	x	41/86 (48%)	41 (100%)	0	100	100
48	y	48/49 (98%)	45 (94%)	3 (6%)	15	36
49	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5099/5751 (89%)	5042 (99%)	57 (1%)	69	80

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	g	5	LYS
48	y	48	TYR
30	g	47	ASN
48	y	47	MET
41	r	9	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
29	f	61	ASN
40	q	62	HIS
36	m	59	ASN
42	s	19	ASN
11	H	77	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	910 (31%)	32 (1%)
51	4	103/108 (95%)	40 (38%)	3 (2%)
52	5	1490/1520 (98%)	432 (28%)	7 (0%)
53	8	75/76 (98%)	29 (38%)	1 (1%)
All	All	4543/4611 (98%)	1411 (31%)	43 (0%)

5 of 1411 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	13	C
50	3	14	U
50	3	15	A
50	3	27	U
50	3	29	G

5 of 43 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	3	2764	U
52	5	425	G
50	3	2800	U
51	4	10	C
52	5	533	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

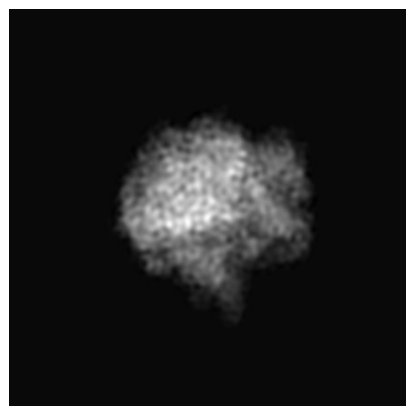
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13436. These allow visual inspection of the internal detail of the map and identification of artifacts.

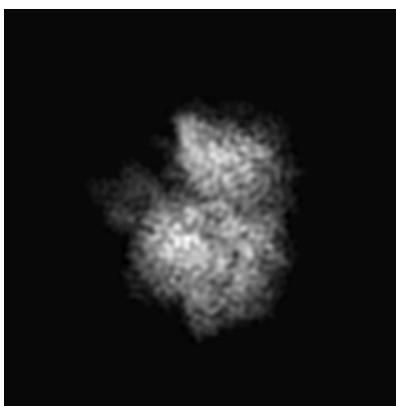
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

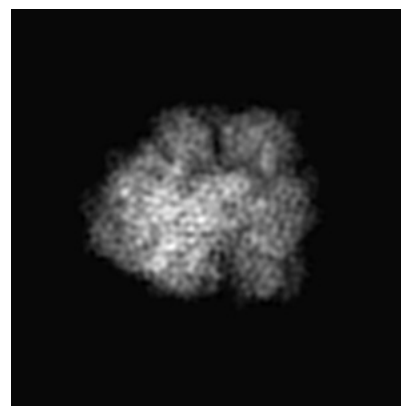
6.1.1 Primary map



X

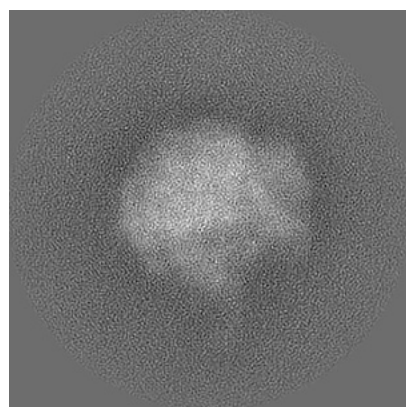


Y

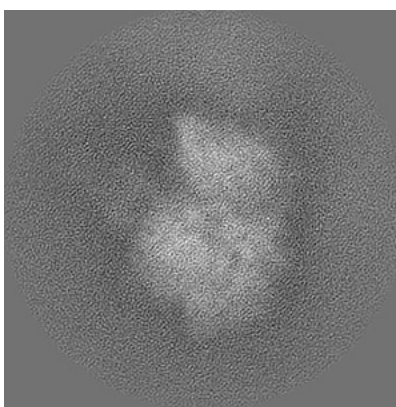


Z

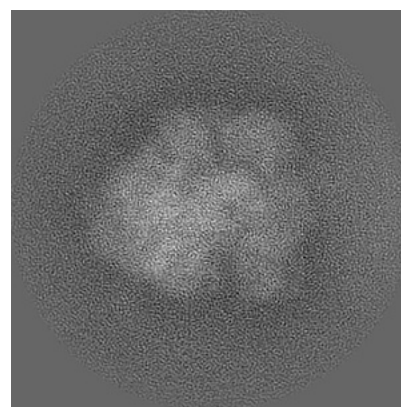
6.1.2 Raw map



X



Y

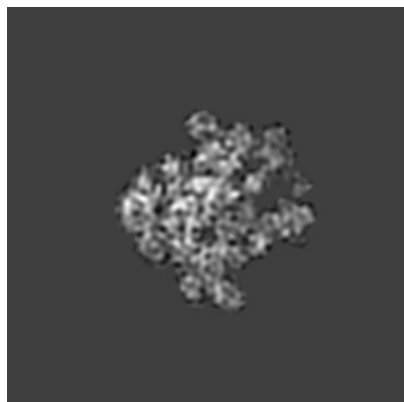


Z

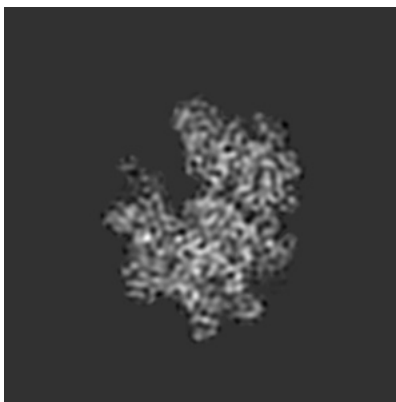
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

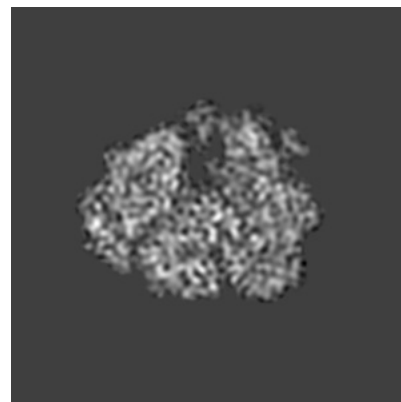
6.2.1 Primary map



X Index: 128

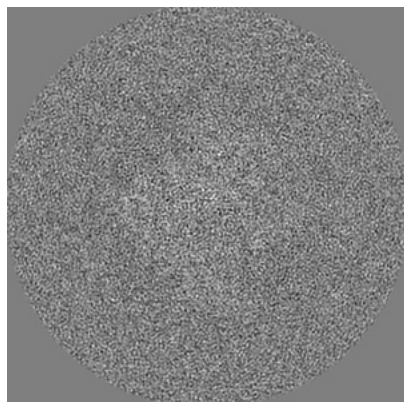


Y Index: 128

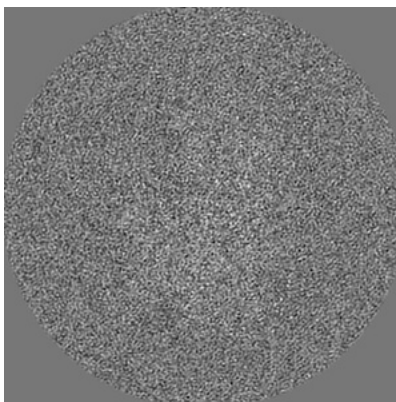


Z Index: 128

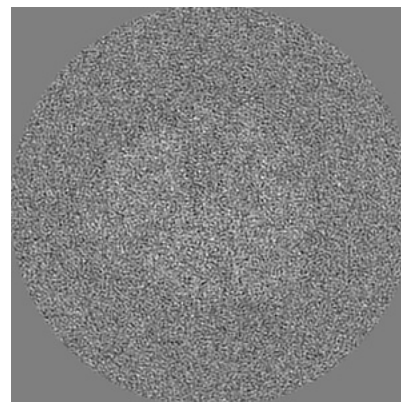
6.2.2 Raw map



X Index: 128



Y Index: 128

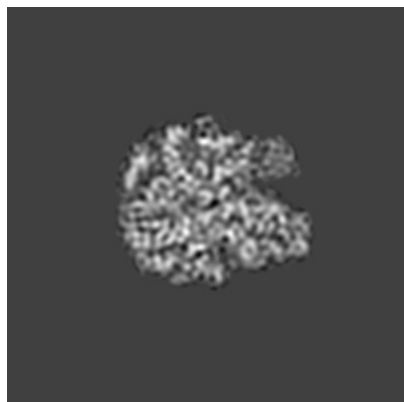


Z Index: 128

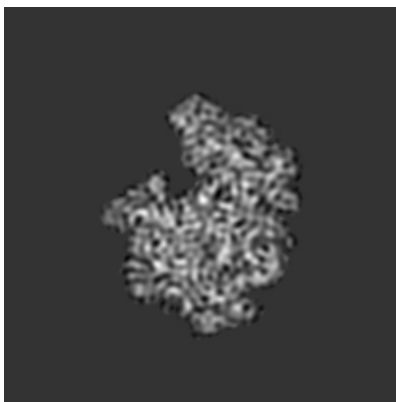
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

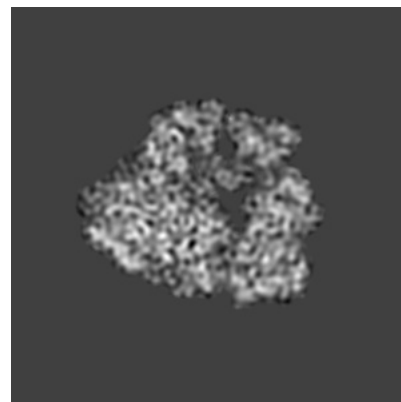
6.3.1 Primary map



X Index: 104

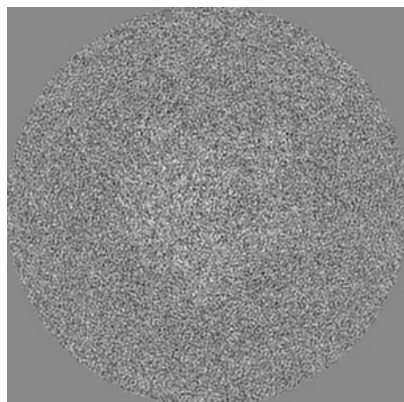


Y Index: 121

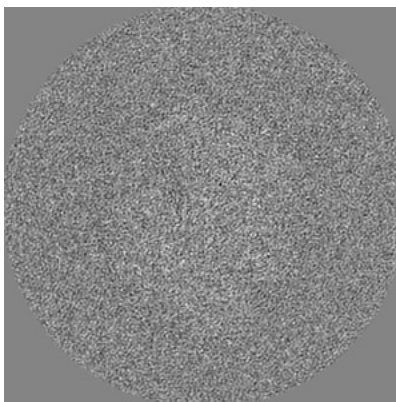


Z Index: 120

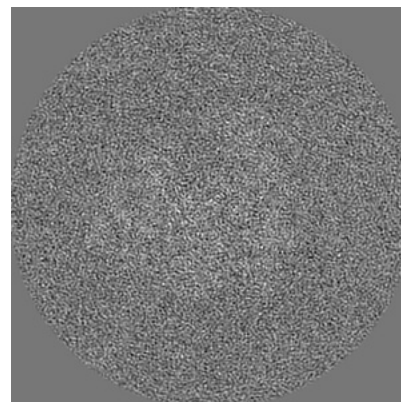
6.3.2 Raw map



X Index: 119



Y Index: 123

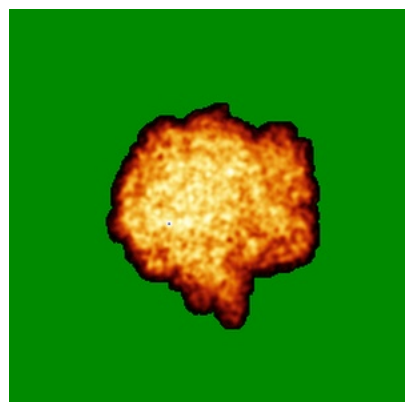


Z Index: 135

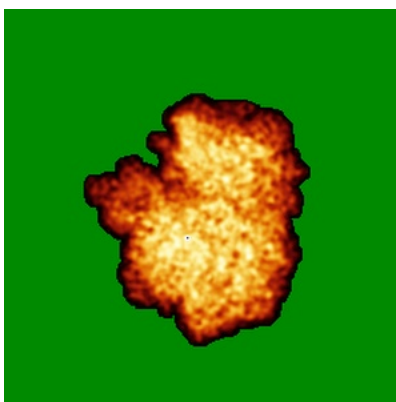
The images above show the largest variance slices of the map in three orthogonal directions.

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

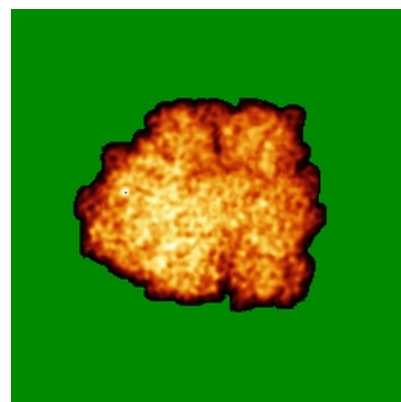
6.4.1 Primary map



X

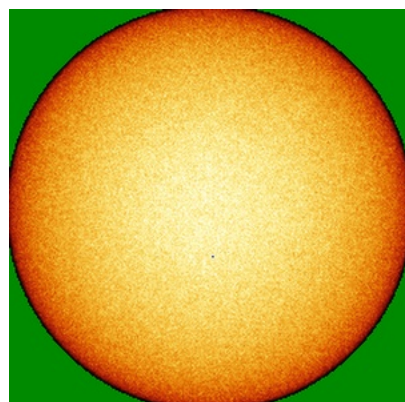


Y

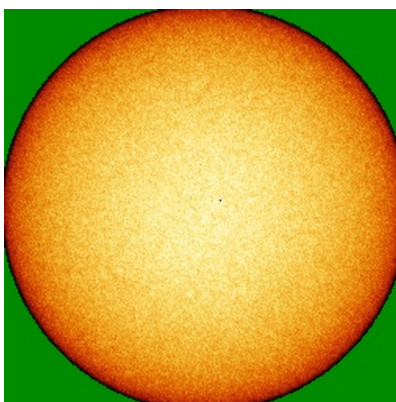


Z

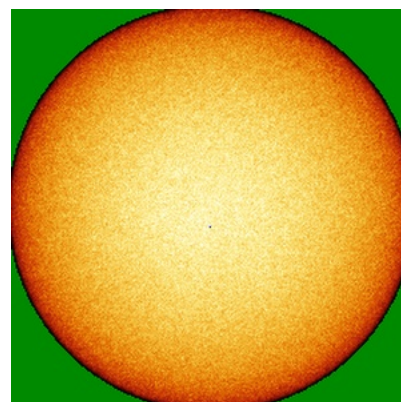
6.4.2 Raw map



X



Y



Z

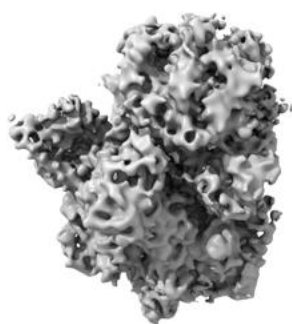
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

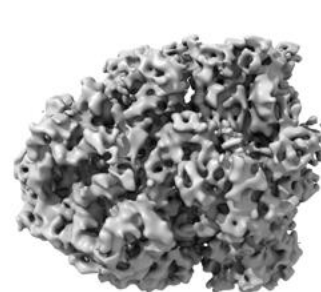
6.5.1 Primary map



X



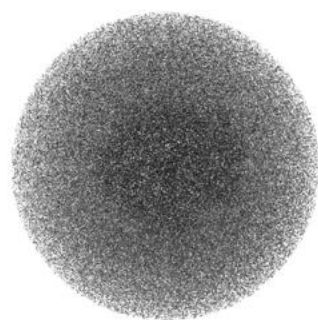
Y



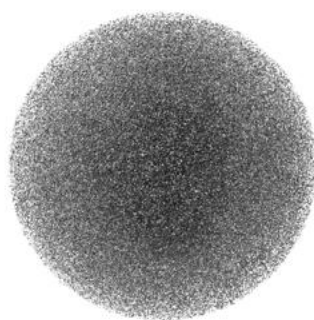
Z

The images above show the 3D surface view of the map at the recommended contour level 0.37. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

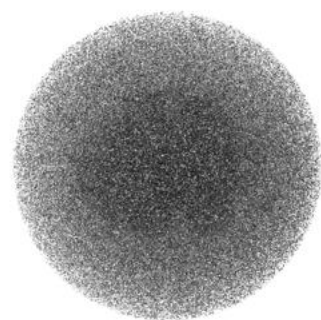
6.5.2 Raw map



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.

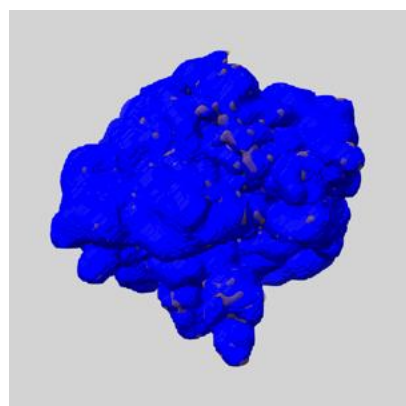
6.6 Mask visualisation [i](#)

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

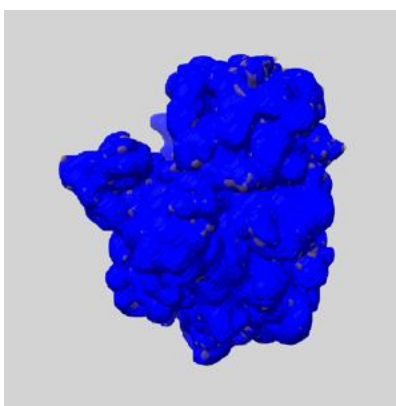
A mask typically either:

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

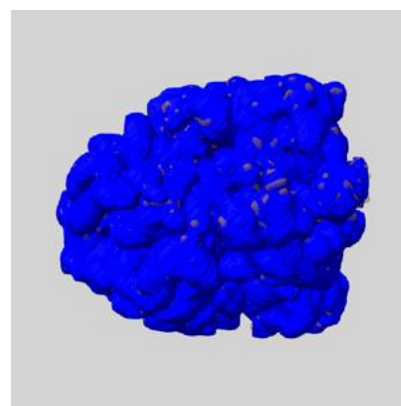
6.6.1 emd_13436_msk_1.map [i](#)



X



Y

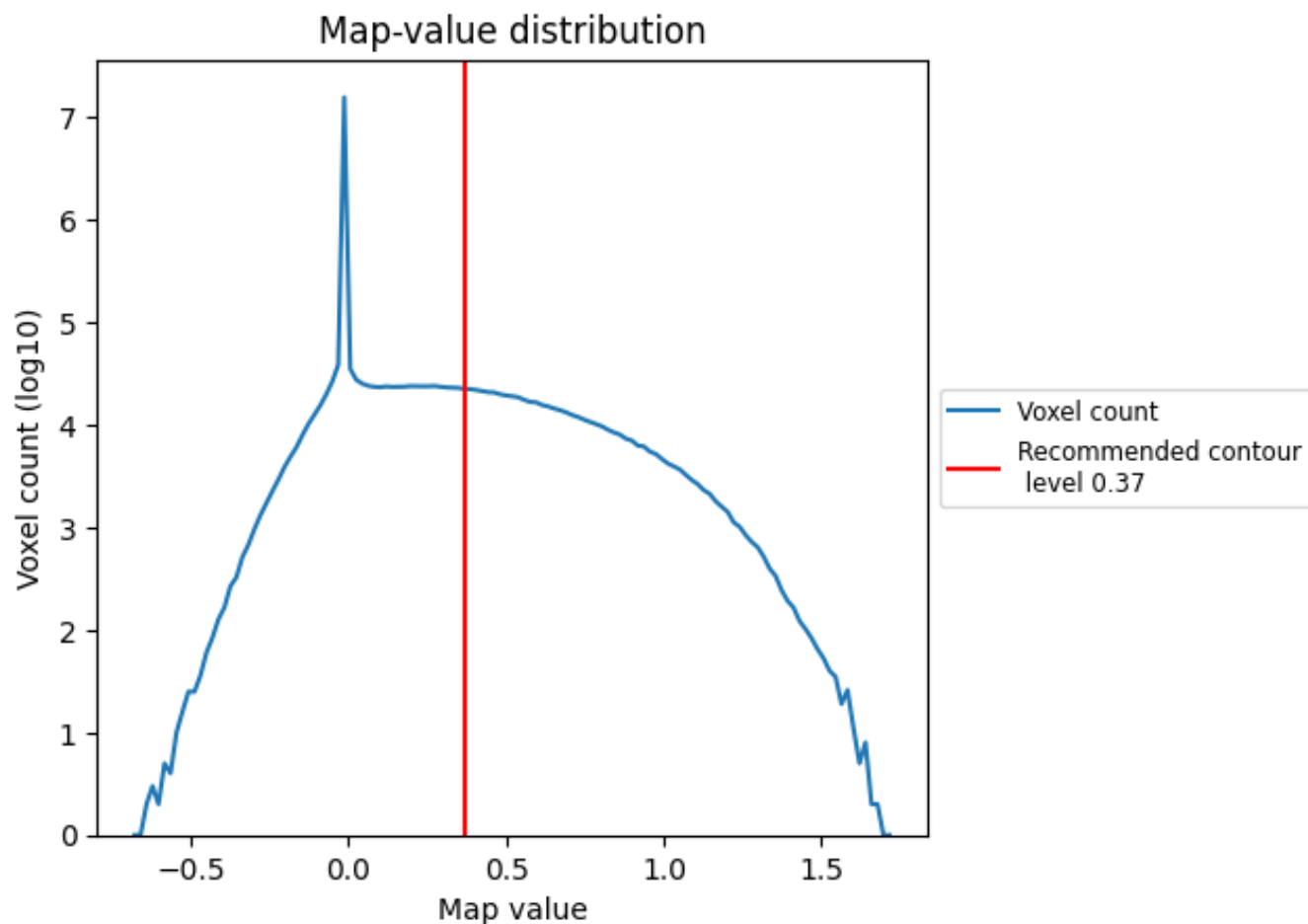


Z

7 Map analysis [i](#)

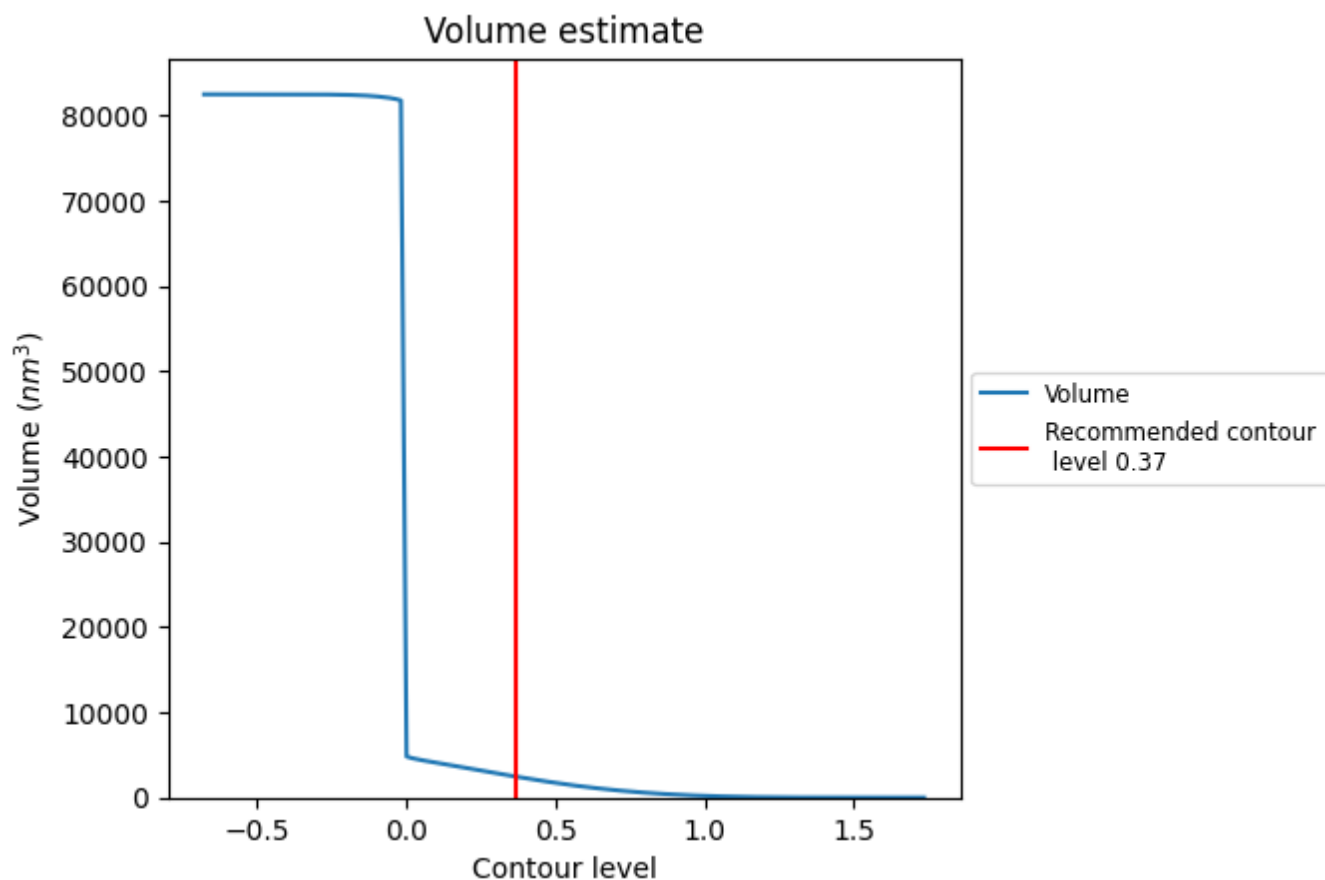
This section contains the results of statistical analysis of the map.

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.

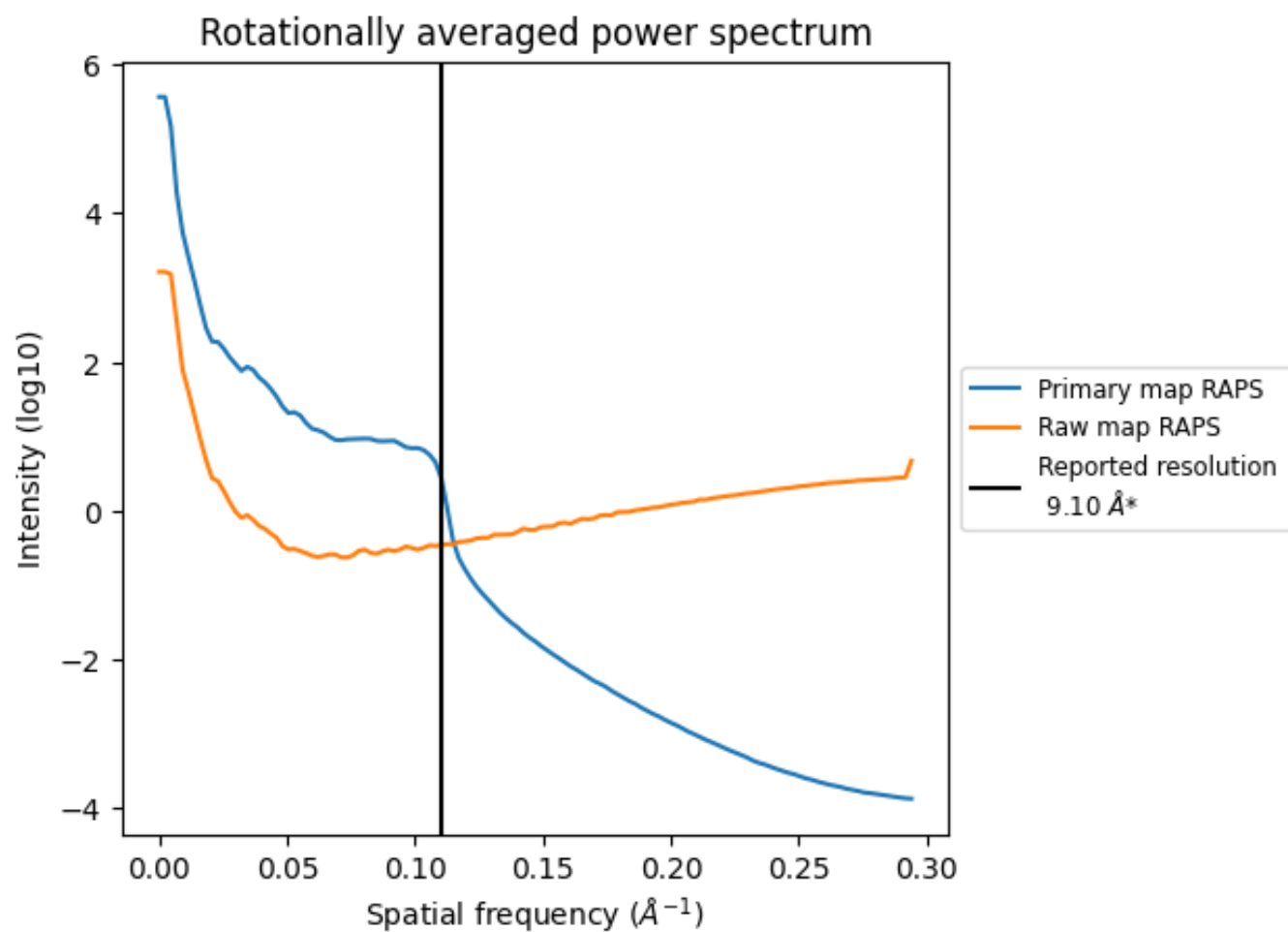
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2444 nm³; this corresponds to an approximate mass of 2208 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 ⓘ

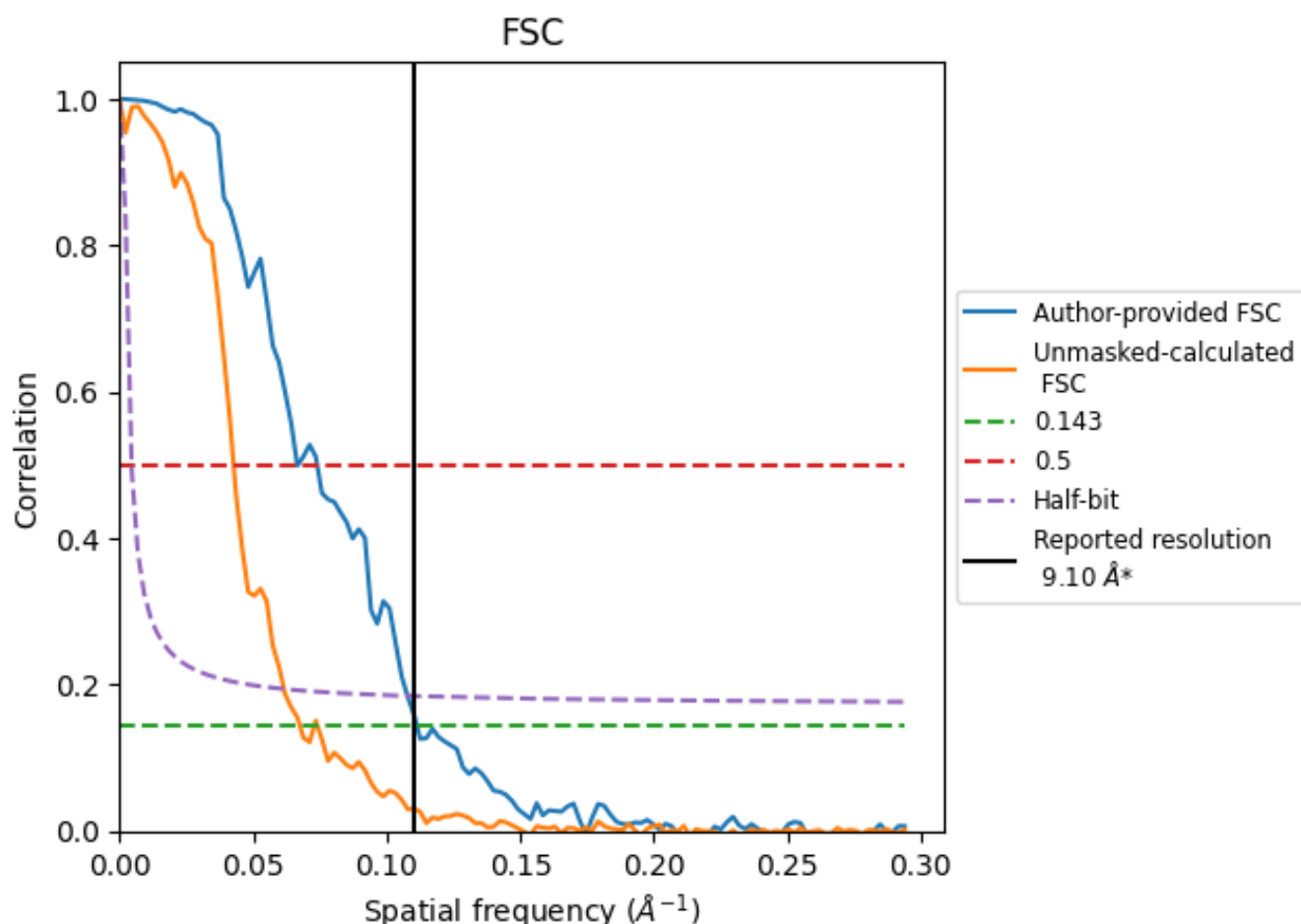


*Reported resolution corresponds to spatial frequency of 0.110 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.110 Å⁻¹

8.2 Resolution estimates [i](#)

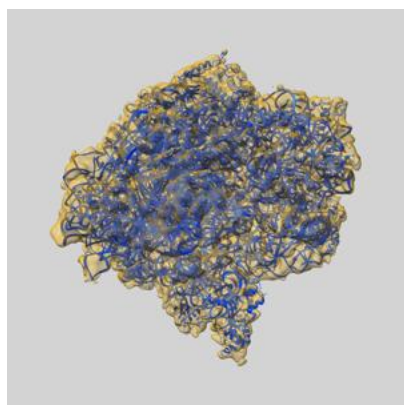
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.10	-	-
Author-provided FSC curve	8.98	15.02	9.28
Unmasked-calculated*	14.79	23.36	16.23

*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 14.79 differs from the reported value 9.1 by more than 10 %

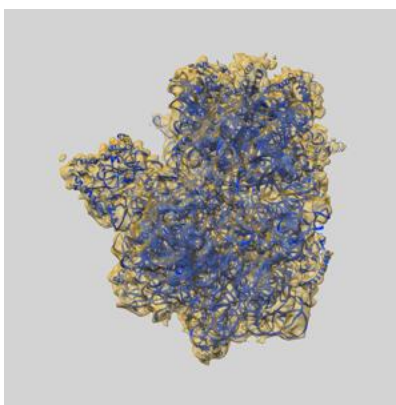
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13436 and PDB model 7PIC. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

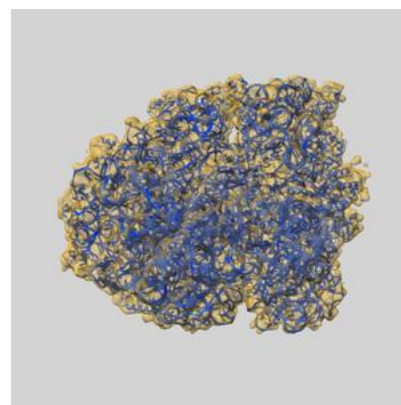
9.1 Map-model overlay [i](#)



X



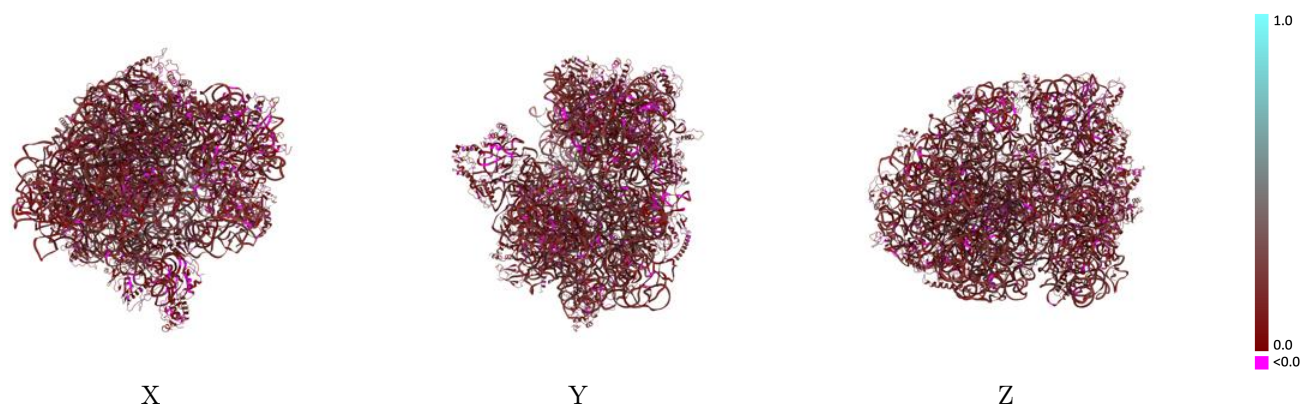
Y



Z

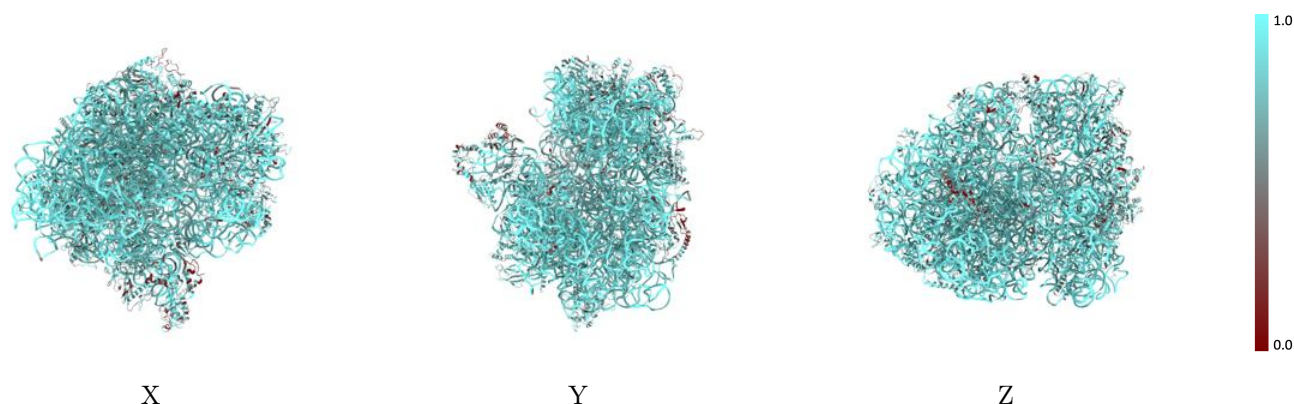
The images above show the 3D surface view of the map at the recommended contour level 0.37 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



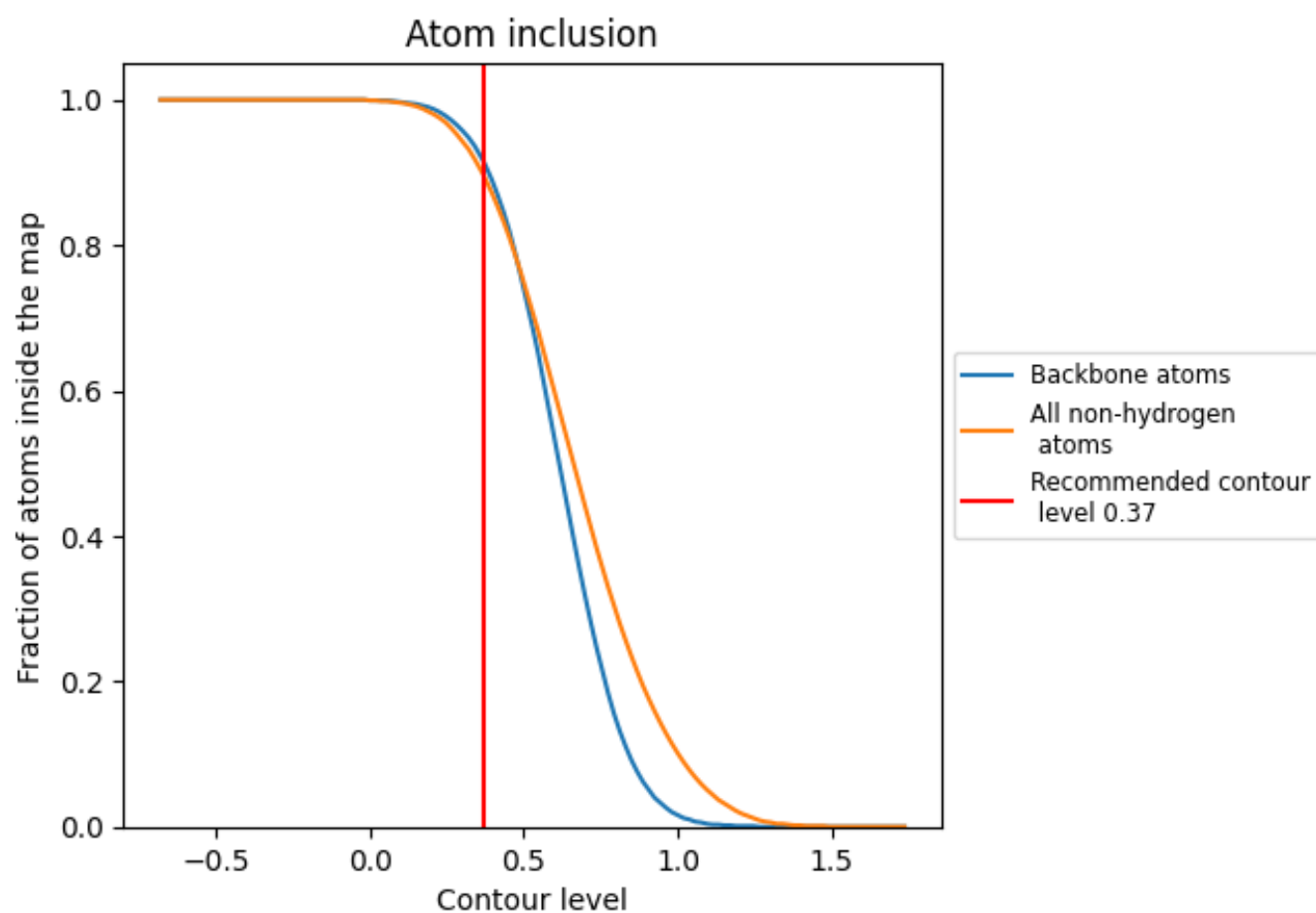
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.37).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% 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 (0.37) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8960	 0.1540
0	 0.8880	 0.1410
1	 0.8800	 0.1460
2	 0.8620	 0.1380
3	 0.9620	 0.1630
4	 0.9590	 0.1660
5	 0.9590	 0.1600
8	 0.9260	 0.1540
A	 0.7230	 0.1560
B	 0.7190	 0.1470
C	 0.7550	 0.1380
D	 0.7200	 0.1320
E	 0.6550	 0.1600
F	 0.7170	 0.1250
G	 0.7080	 0.1340
H	 0.7510	 0.1090
I	 0.6920	 0.1070
J	 0.8100	 0.1200
K	 0.7800	 0.1290
L	 0.6590	 0.1230
M	 0.7320	 0.0930
N	 0.8080	 0.1760
O	 0.8160	 0.1390
P	 0.8310	 0.1370
Q	 0.7890	 0.1510
R	 0.7490	 0.1180
S	 0.8540	 0.1650
T	 0.7950	 0.1630
a	 0.8220	 0.1250
b	 0.7790	 0.1260
c	 0.8150	 0.1580
d	 0.6960	 0.1340
e	 0.7040	 0.1430
f	 0.4630	 0.1430
g	 0.6560	 0.1110



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Chain	Atom inclusion	Q-score
h	 0.4990	 0.1010
i	 0.8260	 0.1460
j	 0.7000	 0.1400
k	 0.8450	 0.1380
l	 0.8180	 0.1290
m	 0.8130	 0.1330
n	 0.7770	 0.1330
o	 0.7940	 0.1460
p	 0.8670	 0.1470
q	 0.8160	 0.1510
r	 0.8630	 0.1420
s	 0.7870	 0.1480
t	 0.7310	 0.1420
u	 0.8310	 0.1130
v	 0.8550	 0.1390
w	 0.8370	 0.1880
x	 0.7430	 0.1860
y	 0.7970	 0.1160
z	 0.8590	 0.1700