



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 01:45 am BST

PDB ID : 5LZF
EMDB ID : EMD-4126
Title : Structure of the 70S ribosome with fMetSec-tRNA^{Sec} in the hybrid pre-translocation state (H)
Authors : Fischer, N.; Neumann, P.; Bock, L.V.; Maracci, C.; Wang, Z.; Paleskava, A.; Konevega, A.L.; Schroeder, G.F.; Grubmueller, H.; Ficner, R.; Rodnina, M.V.; Stark, H.
Deposited on : 2016-09-29
Resolution : 4.60 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

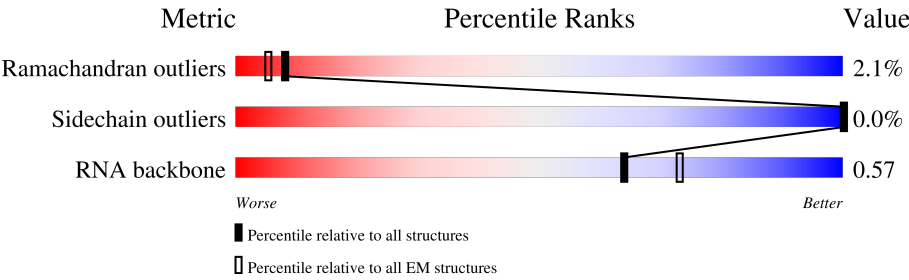
EMDB validation analysis : 0.0.1.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.60 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	a	1539	
2	b	218	
3	c	206	
4	d	205	
5	e	157	
6	f	100	
7	g	151	
8	h	129	

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Mol	Chain	Length	Quality of chain
9	i	127	20% 98% .
10	j	98	31% 96% ..
11	k	116	9% 97% .
12	l	123	11% 94% 5% .
13	m	114	25% 97% ..
14	n	100	21% 99% .
15	o	88	10% 95% 5%
16	p	82	21% 99% .
17	q	80	12% 99% .
18	r	65	12% 92% 8%
19	s	86	33% 94% 5% .
20	t	85	15% 100%
21	u	65	29% 92% 8%
22	v	77	5% 48% 27% 25%
23	x	48	48% 29% 38% 31% .
24	y	95	12% 53% 33% 15%
25	A	2903	. 69% 27% .
26	B	120	73% 26% .
27	C	271	7% 98% .
28	D	209	8% 98% .
29	E	201	11% 99% .
30	F	177	19% 97% .
31	G	176	9% 97% ..
32	I	141	86% 95% 5%
33	H	149	81% 97% .

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Mol	Chain	Length	Quality of chain
34	J	142	5% 99%
35	K	122	7% 97%
36	L	143	10% 97%
37	M	136	7% 97%
38	N	120	8% 99%
39	O	116	9% 100%
40	P	114	9% 99%
41	Q	117	• 100%
42	R	103	10% 99%
43	S	110	• 98%
44	T	93	9% 99%
45	U	102	9% 98%
46	V	94	6% 100%
47	W	75	8% 100%
48	X	77	6% 99%
49	Y	63	• 97%
50	Z	58	14% 100%
51	0	56	9% 100%
52	1	50	20% 98%
53	2	46	9% 96%
54	3	64	9% 98%
55	4	38	13% 97%
56	6	66	35% 94% 6%

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
1	G7M	a	527	X	-	-	-
25	G7M	A	2069	X	-	-	-

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 148005 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1539	Total	C	N	O	P	0	0
			33029	14738	6052	10700	1539		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	100	Total	C	N	O	S	0	0
			794	495	164	132	3		

- Molecule 15 is a protein called 30S ribosomal protein S15.

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

- Molecule 16 is a protein called 30S ribosomal protein S16.

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

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	r	65	Total	C	N	O	0	0
			505	317	96	92		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	86	Total	C	N	O	S	0	0
			687	438	131	116	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	65	Total	C	N	O	S	0	0
			496	307	100	88	1		

- Molecule 22 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	v	77	Total	C	N	O	P	S	0	0
			1643	733	297	535	77	1		

- Molecule 23 is a RNA chain called SECIS mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	x	48	Total	C	N	O	P	0	0
			1025	457	183	337	48		

- Molecule 24 is a RNA chain called fMetSec-tRNA^{Sec}.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	y	95	Total	C	N	O	P	0	0
			2031	907	357	672	95		

- Molecule 25 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A	2900	Total	C	N	O	P	0	0
			62275	27788	11459	20128	2900		

- Molecule 26 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B	120	Total	C	N	O	P	0	0
			2570	1144	468	838	120		

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	C	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 28 is a protein called 50S ribosomal protein L3.

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

- Molecule 29 is a protein called 50S ribosomal protein L4.

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

- Molecule 30 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	F	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 31 is a protein called 50S ribosomal protein L6.

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

- Molecule 32 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 33 is a protein called 50S ribosomal protein L9.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	K	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

- Molecule 38 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	N	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	T	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 45 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	U	102	Total	C	N	O	S	0	0
			780	492	146	142			

- Molecule 46 is a protein called 50S ribosomal protein L25.

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

- Molecule 47 is a protein called 50S ribosomal protein L27.

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

- Molecule 48 is a protein called 50S ribosomal protein L28.

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

- Molecule 49 is a protein called 50S ribosomal protein L29.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 52 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	1	50	Total	C	N	O	S	0	0
			410	263	75	72			

- Molecule 53 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 54 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 55 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 56 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	6	66	Total	C	N	O	S	0	0
			523	323	99	95	6		

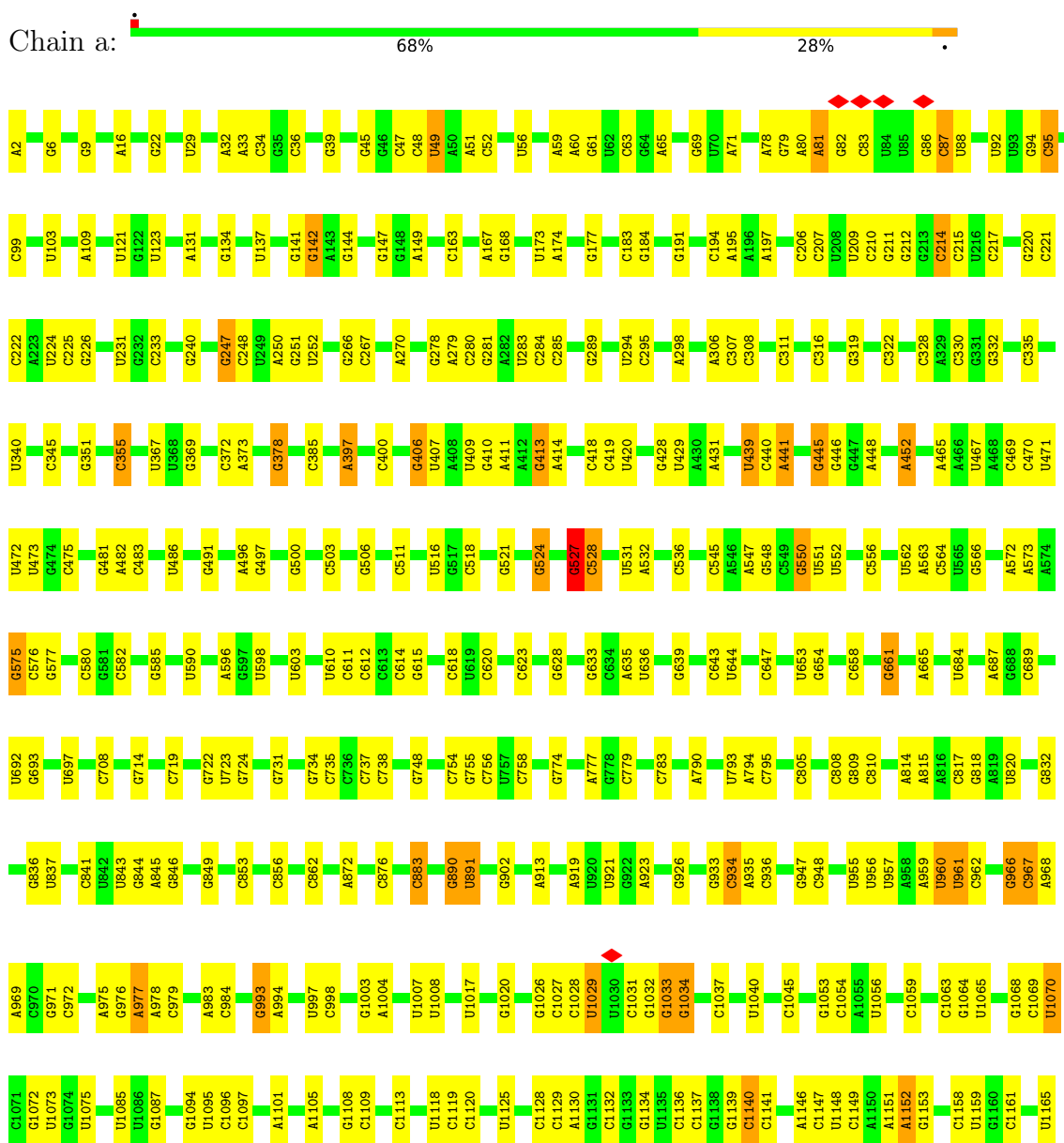
- Molecule 57 is ZINC ION (three-letter code: ZN) (formula: Zn).

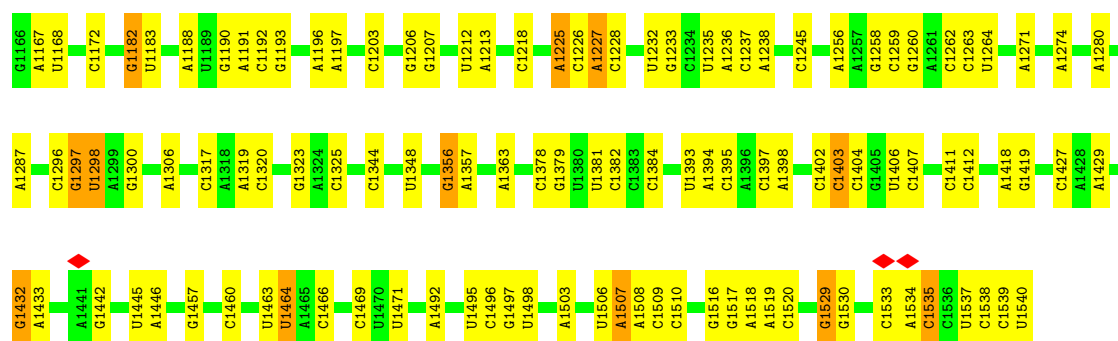
Mol	Chain	Residues	Atoms		AltConf
57	4	1	Total	Zn	0
			1	1	
57	6	1	Total	Zn	0
			1	1	

3 Residue-property plots

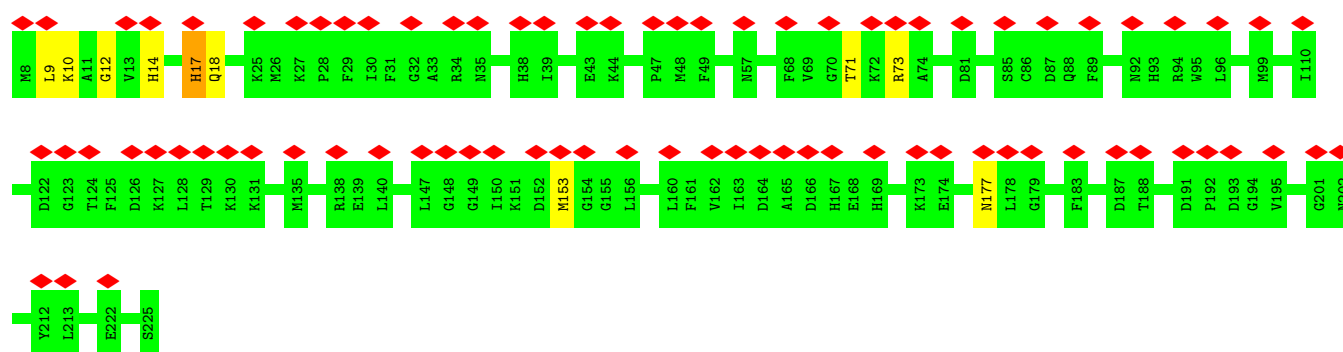
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S ribosomal RNA

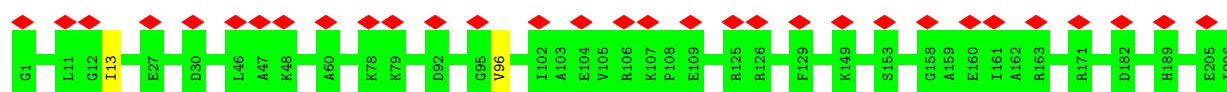




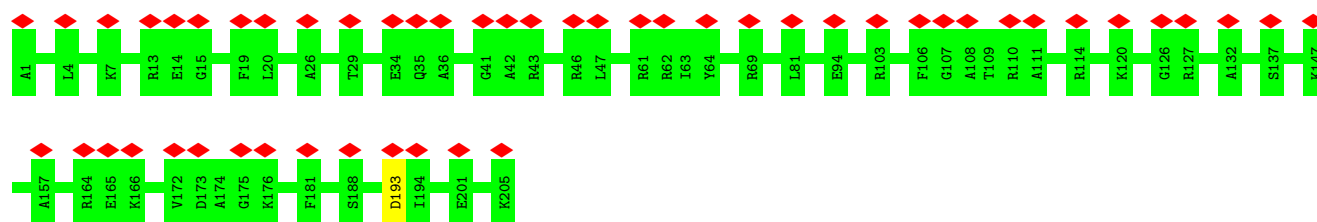
• Molecule 2: 30S ribosomal protein S2



• Molecule 3: 30S ribosomal protein S3

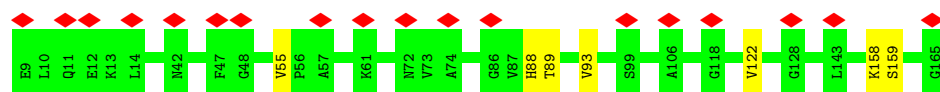


• Molecule 4: 30S ribosomal protein S4

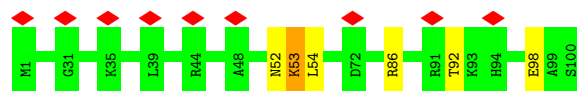
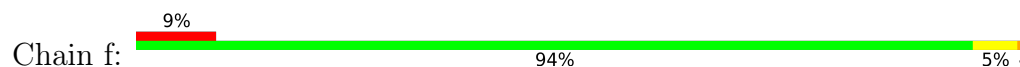


• Molecule 5: 30S ribosomal protein S5

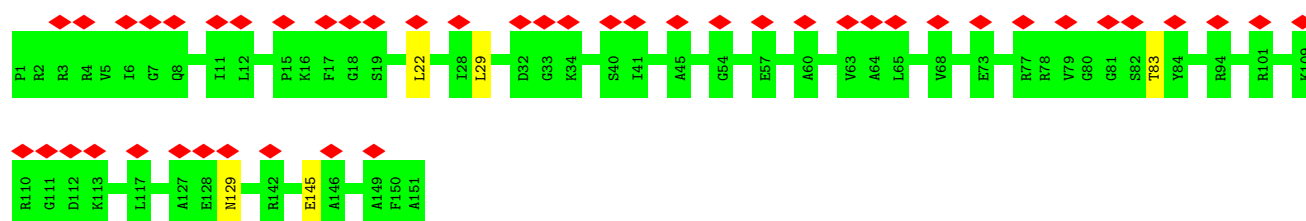




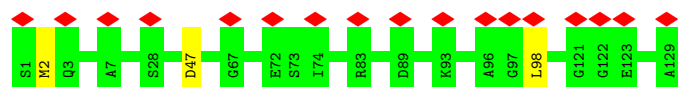
- Molecule 6: 30S ribosomal protein S6



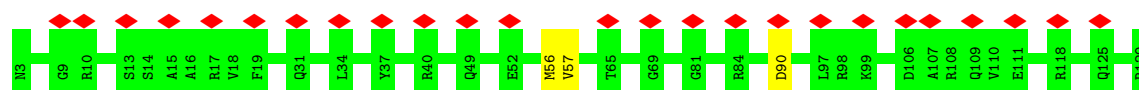
- Molecule 7: 30S ribosomal protein S7



- Molecule 8: 30S ribosomal protein S8



- Molecule 9: 30S ribosomal protein S9

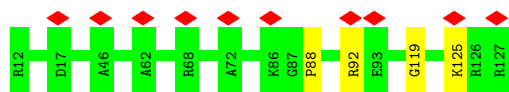


- Molecule 10: 30S ribosomal protein S10

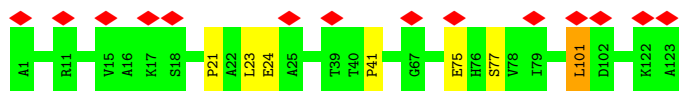


- Molecule 11: 30S ribosomal protein S11

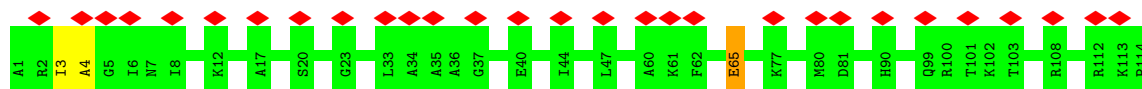




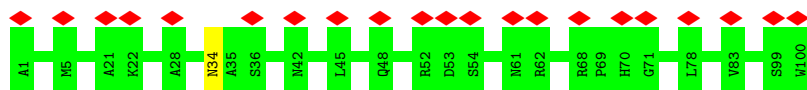
- Molecule 12: 30S ribosomal protein S12



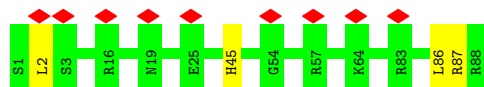
- Molecule 13: 30S ribosomal protein S13



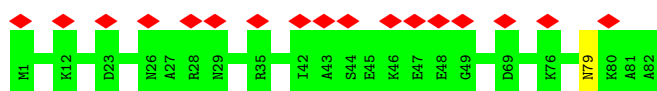
- Molecule 14: 30S ribosomal protein S14



- Molecule 15: 30S ribosomal protein S15



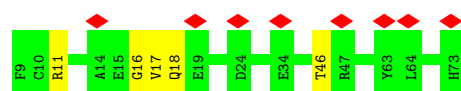
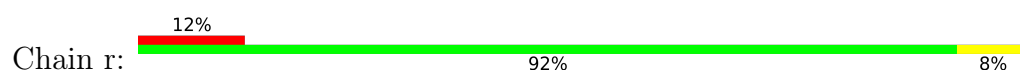
- Molecule 16: 30S ribosomal protein S16



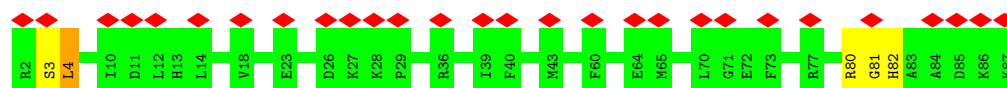
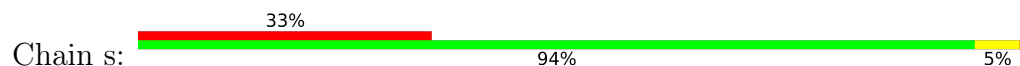
- Molecule 17: 30S ribosomal protein S17



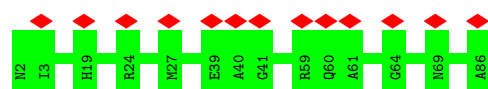
- Molecule 18: 30S ribosomal protein S18



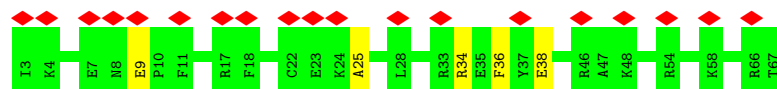
- Molecule 19: 30S ribosomal protein S19



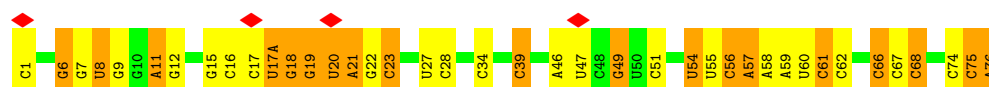
- Molecule 20: 30S ribosomal protein S20



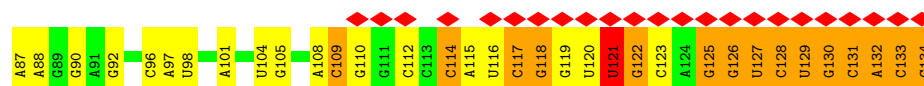
- Molecule 21: 30S ribosomal protein S21



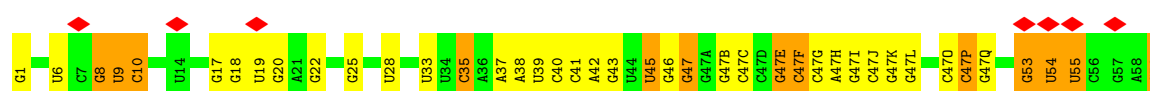
- Molecule 22: tRNA^{fMet}

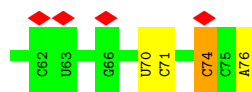


- Molecule 23: SECIS mRNA



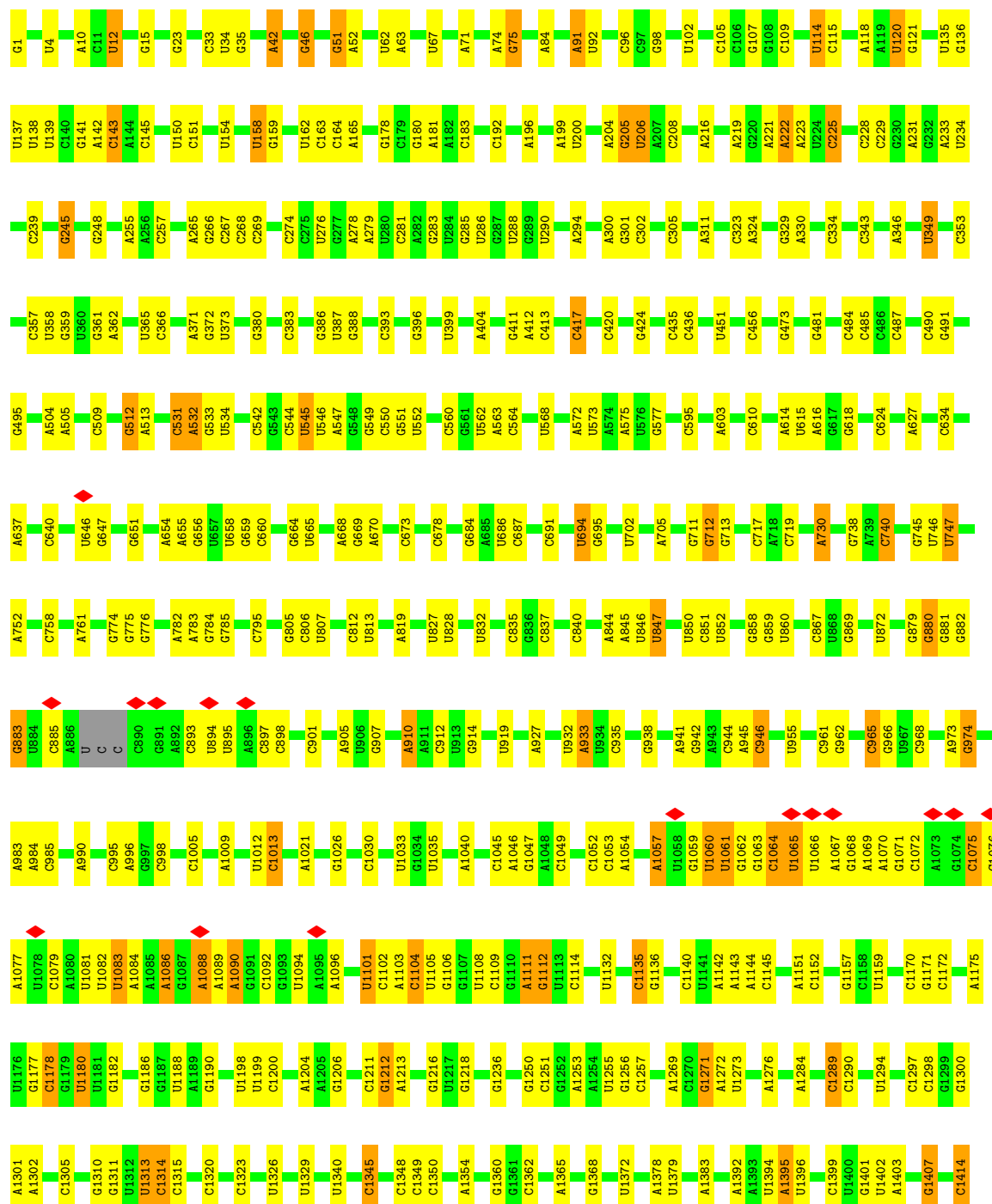
- Molecule 24: fMetSec-tRNA^{Sec}





• Molecule 25: 23S ribosomal RNA

Chain A: 69% 27%



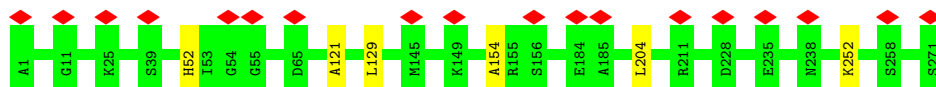
U2833	U2720	G2576	U2473	G2357	G2250	C2150	A2071	G1959	C1816	G1674	U1554	U1415
G2834	U2580	U2580	U2474	U2372	G2251	G2156	C2072	A1960	U1820	C1675	U1559	G1416
C2840	C2723	U2585	C2475	G2373	C2254	G2157	U2075	C1961	U1680	U1560	G1561	C1417
C2841	U2586	U2586	A2476	G2379	C2264	C2161	U2076	C1962	G1682	A1427	C1564	A1428
U2849	C2591	C2591	U2489	C2380	A2267	G2162	A2080	A1965	U1828	C1682	C1565	A1429
A2850	A2602	G2603	U2490	C2384	A2268	A2163	U2085	A1966	C1833	U1693	A1566	A1430
G2857	U2604	U2604	G2494	U2385	G2271	C2164	U2086	A1970	U1834	C1694	A1569	A1432
A2873	U2605	G2605	G2495	C2385	G2272	C2165	G2087	U1971	G1835	C1695	A1574	A1433
C2880	U2609	U2609	A2497	A2388	G2276	A2168	G2083	G1972	G1840	G1699	C1578	A1434
A2883	C2610	C2610	C2498	G2389	G2277	A2169	U2096	U1991	U1841	G1715	U1578	C1437
U2884	C2611	C2611	U2499	U2390	G2279	U2172	C2096	G1992	G1842	C1728	U1581	U1442
U2891	C2612	C2612	G2502	A2391	G2279	A2173	U2097	U1993	C1843	U1729	G1584	G1452
G2892	U2613	U2613	A2503	A2392	G2282	C2174	U2099	C1994	U1855	C1730	U1584	G1459
G2893	A2614	A2614	U2504	C2394	C2283	C2175	G2100	C1997	C1870	G1733	C1585	C1460
G2894	G2505	G2505	U2506	U2402	A2286	C2178	A2101	C2006	A1871	G1738	C1595	C1461
U2898	U2506	U2506	C2510	C2403	A2287	C2179	U2105	U2011	C1879	U1747	G1605	G1475
C2901	G2511	G2511	U2511	A2406	U2292	U2181	G2107	U2022	G1884	G1756	G1606	G1482
C2902	C2512	C2512	C2512	C2416	U2296	U2182	A2108	C2023	C1894	A1757	C1607	G1483
U2903	C2515	C2515	C2515	C2417	A2297	U2185	G2110	G2024	A1900	C1759	A1616	U1484
	A2634	A2634	A2518	C2420	U2298	U2188	C2111	C2025	A1901	C1760	A1618	U1485
	A2635	A2635	U2519	G2421	U2299	U2189	G2112	A2030	A1901	C1761	A1619	U1486
	C2636	C2636	U2520	C2422	U2305	G2190	G2116	A2031	G1906	A1762	G1619	U1487
	U2637	U2637	G2529	C2427	G2308	U2194	U2117	G2032	U1911	C1764	A1626	A1490
	A2776	A2776	G2535	G2428	A2309	U2195	U2118	U2034	A1912	C1769	G1627	C1493
	G2777	G2777	G2535	G2429	C2310	U2198	G2120	G2035	A1913	U1772	G1628	C1498
	G2782	G2782	G2543	A2430	U2312	A2199	U2122	G2043	C1914	A1773	U1636	C1499
	C2785	C2785	G2547	A2435	U2321	C2200	G2123	C2044	A1916	C1774	C1639	A1504
	C2793	C2793	U2547	A2439	G2325	G2204	G2125	G2049	G1924	A1784	G1644	A1505
	C2794	C2794	U2552	C2440	C2326	A2212	A2126	C2050	A1927	A1787	G1645	A1508
	U2795	U2795	U2553	U2441	A2327	U2213	G2127	A2051	A1928	A1791	C1646	A1509
	U2797	U2797	U2554	U2445	A2326	C2214	C2128	A2052	G1929	C1795	U1647	A1515
	U2798	U2798	U2555	G2445	U2329	G2223	U2130	C2055	G1930	C1796	U1648	U1523
	A2682	A2682	G2557	A2448	G2330	G2224	U2131	G2056	A1654	U1798	A1654	G1524
	C2683	C2683	C2558	U2449	G2331	G2225	U2132	A2060	A1655	G1799	C1656	C1531
	U2687	U2687	U2562	A2451	C2332	A2226	A2133	A2061	A1938	C1800	U1657	A1532
	U2689	U2689	U2563	G2452	A2333	C2226	A2135	A2062	U1939	A1801	C1533	C1533
	U2690	U2690	U2564	C2452	U2334	U2231	G2136	C2063	C1941	A1802	G1660	U1534
	G2816	G2816	A2566	U2457	A2335	G2238	G2141	C2066	U1955	A1803	G1666	C1536
	U2817	U2817	G2567	A2461	G2345	G2239	C2145	G2067	A1808	U1798	A1669	G1537
	U2818	U2818	U2568	C2462	A2346	U2243	C2146	U2068	A1809	G1799	C1537	U1539
	G2824	G2824	G2569	A2468	A2347	U2244	G2147	C2069	U1957	A1802	G1666	C1536
	A2820	A2820	G2570	A2469	C2347	U2245	G2148	C2069	C1957	A1803	A1669	G1537
	U2701	U2701	G2571	A2470	C2350	G2246	U2149	A2070	U1958	A1803	C1537	U1539
	G2702	G2702	G2572	C2470	C2354	G2246	U2149	A2070	U1958	A1803	C1537	U1539
	C2703	C2703	G2573									
	U2713	U2713	G2574									
	G2714	G2714	G2575									
	C2715	C2715	G2575									
	G2716	G2716										

• Molecule 26: 5S ribosomal RNA

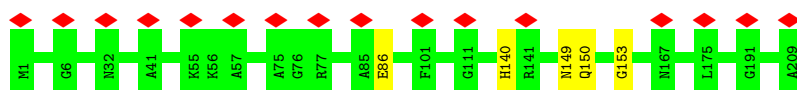
Chain B:  73% 26%



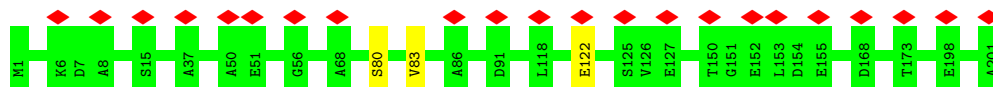
- Molecule 27: 50S ribosomal protein L2



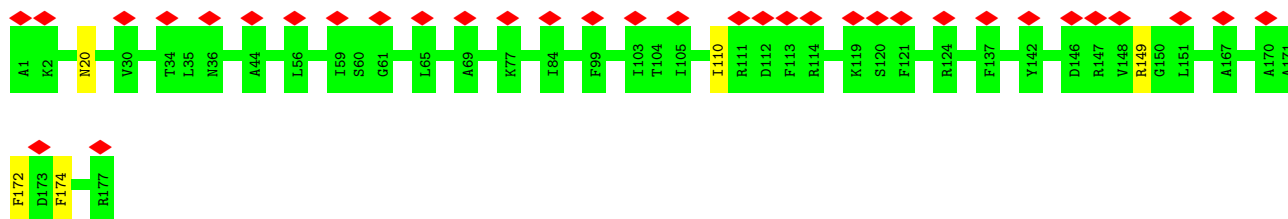
- Molecule 28: 50S ribosomal protein L3



- Molecule 29: 50S ribosomal protein L4



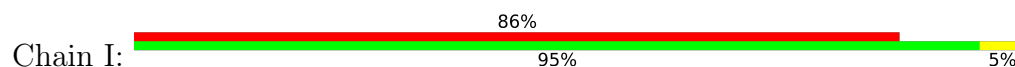
- Molecule 30: 50S ribosomal protein L5

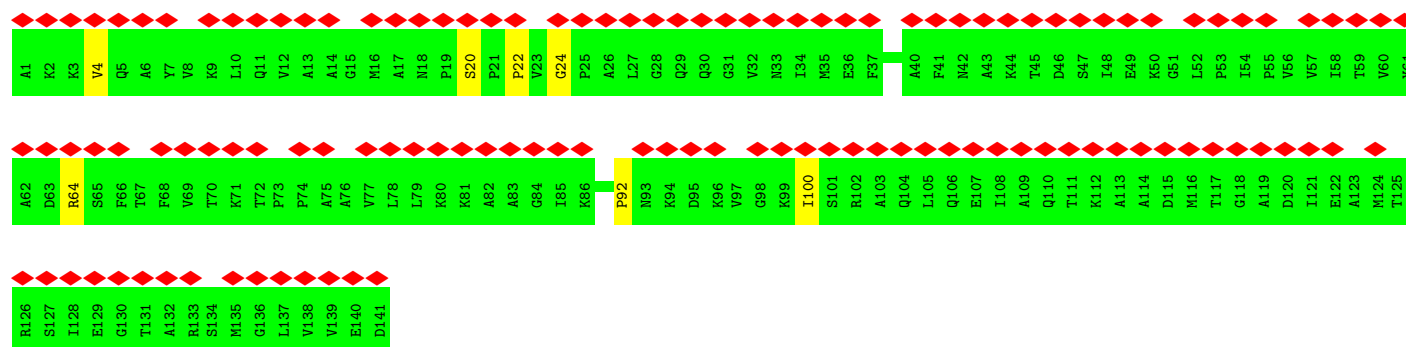


- Molecule 31: 50S ribosomal protein L6

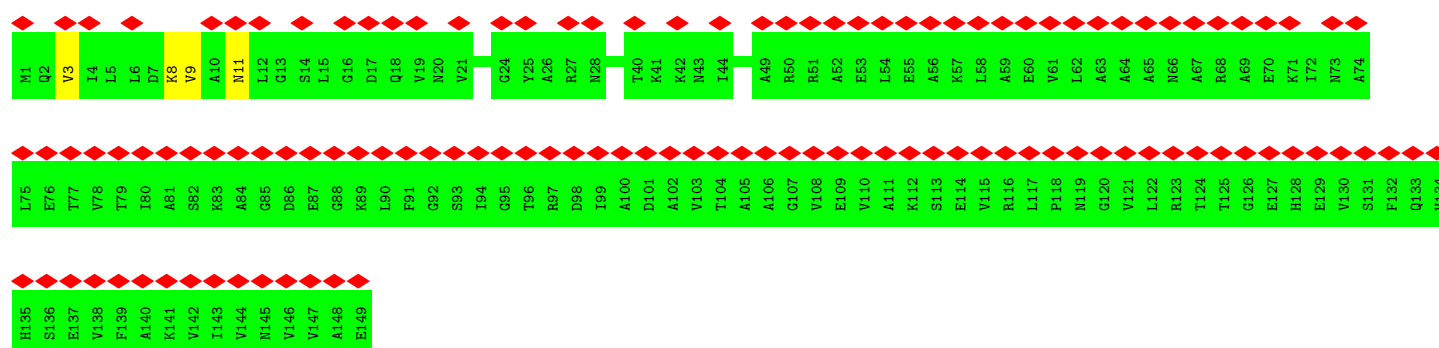
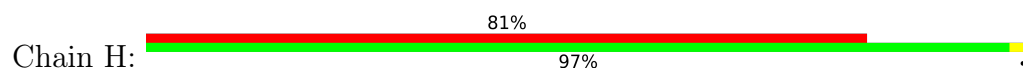


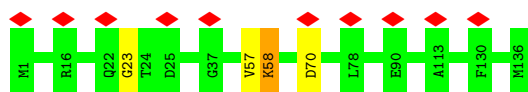
- Molecule 32: 50S ribosomal protein L11



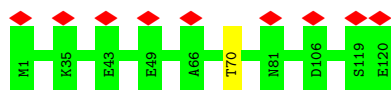


- Molecule 33: 50S ribosomal protein L9

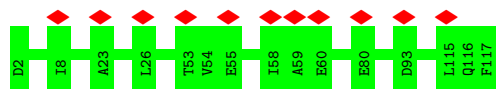




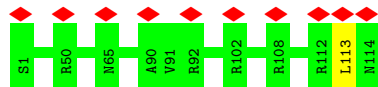
- Molecule 38: 50S ribosomal protein L17



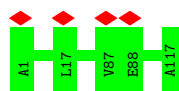
- Molecule 39: 50S ribosomal protein L18



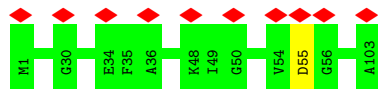
- Molecule 40: 50S ribosomal protein L19



- Molecule 41: 50S ribosomal protein L20



- Molecule 42: 50S ribosomal protein L21



- Molecule 43: 50S ribosomal protein L22



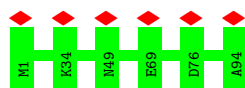
- Molecule 44: 50S ribosomal protein L23



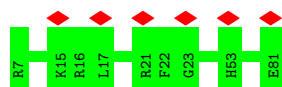
- Molecule 45: 50S ribosomal protein L24



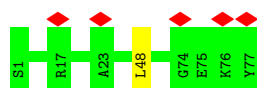
- Molecule 46: 50S ribosomal protein L25



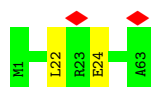
- Molecule 47: 50S ribosomal protein L27



- Molecule 48: 50S ribosomal protein L28

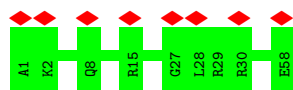


- Molecule 49: 50S ribosomal protein L29

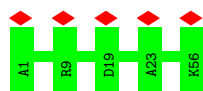


- Molecule 50: 50S ribosomal protein L30

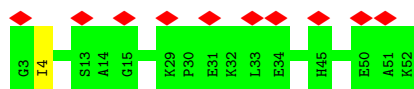




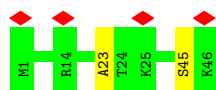
- Molecule 51: 50S ribosomal protein L32



- Molecule 52: 50S ribosomal protein L33



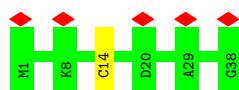
- Molecule 53: 50S ribosomal protein L34



- Molecule 54: 50S ribosomal protein L35



- Molecule 55: 50S ribosomal protein L36



- Molecule 56: 50S ribosomal protein L31



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19868	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY; Local CTF correction, after MSA based classification and averaging of local power spectra	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	2.225	Depositor
Minimum map value	-1.150	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.199	Depositor
Recommended contour level	0.4	Depositor
Map size (\AA)	315.52, 315.52, 315.52	wwPDB
Map dimensions	272, 272, 272	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.16, 1.16, 1.16	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 4OC, ZN, H2U, PSU, 4SU, G7M, UR3, 3TD, 5MU, 2MA, 6MZ, OMU, MA6, 2MG, OMC, 1MG, 5MC, OMG, 6IA

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	a	0.57	2/36701 (0.0%)	1.39	573/57246 (1.0%)
2	b	0.42	0/1736	0.70	0/2338
3	c	0.35	0/1652	0.59	0/2225
4	d	0.38	0/1665	0.61	0/2227
5	e	0.43	1/1170 (0.1%)	0.74	0/1573
6	f	0.40	0/836	0.75	1/1128 (0.1%)
7	g	0.34	0/1196	0.62	1/1602 (0.1%)
8	h	0.35	0/989	0.65	1/1326 (0.1%)
9	i	0.36	0/1034	0.68	0/1375
10	j	0.35	0/797	0.72	0/1077
11	k	0.37	0/886	0.69	0/1195
12	l	0.40	0/969	0.72	1/1300 (0.1%)
13	m	0.38	0/893	0.72	2/1193 (0.2%)
14	n	0.39	0/806	0.61	0/1074
15	o	0.34	0/722	0.59	1/964 (0.1%)
16	p	0.41	0/659	0.66	0/884
17	q	0.46	0/658	0.80	0/881
18	r	0.35	0/512	0.63	0/689
19	s	0.46	0/703	0.85	2/944 (0.2%)
20	t	0.40	0/671	0.59	0/888
21	u	0.53	1/501 (0.2%)	0.76	0/668
22	v	0.91	3/1746 (0.2%)	2.04	87/2721 (3.2%)
23	x	0.88	2/1145 (0.2%)	1.88	49/1781 (2.8%)
24	y	0.67	1/2168 (0.0%)	1.59	54/3375 (1.6%)
25	A	0.56	10/69173 (0.0%)	1.32	813/107908 (0.8%)
26	B	0.57	1/2873 (0.0%)	1.39	54/4478 (1.2%)
27	C	0.36	0/2122	0.68	1/2852 (0.0%)
28	D	0.38	0/1586	0.66	0/2134
29	E	0.38	0/1571	0.63	0/2113
30	F	0.42	0/1435	0.74	1/1926 (0.1%)
31	G	0.36	0/1343	0.62	1/1816 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	I	0.43	0/1046	0.74	1/1410 (0.1%)
33	H	0.36	0/1122	0.63	0/1515
34	J	0.39	0/1152	0.61	0/1551
35	K	0.40	0/948	0.66	0/1268
36	L	0.38	0/1054	0.68	0/1403
37	M	0.40	0/1093	0.68	1/1460 (0.1%)
38	N	0.38	0/974	0.64	0/1301
39	O	0.43	0/902	0.61	0/1209
40	P	0.36	0/929	0.66	1/1242 (0.1%)
41	Q	0.43	0/960	0.57	0/1278
42	R	0.36	0/829	0.70	0/1107
43	S	0.35	0/864	0.59	0/1156
44	T	0.36	0/745	0.64	0/994
45	U	0.39	0/788	0.70	0/1051
46	V	0.40	0/766	0.67	0/1025
47	W	0.35	0/582	0.57	0/769
48	X	0.34	0/635	0.60	1/848 (0.1%)
49	Y	0.38	0/510	0.64	0/677
50	Z	0.35	0/453	0.61	0/605
51	0	0.33	0/450	0.63	0/599
52	1	0.39	0/417	0.75	0/554
53	2	0.35	0/380	0.60	0/498
54	3	0.40	0/513	0.68	1/676 (0.1%)
55	4	0.52	0/303	0.91	1/397 (0.3%)
56	6	0.51	0/532	0.98	1/709 (0.1%)
All	All	0.53	21/159865 (0.0%)	1.23	1649/239203 (0.7%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	a	2	1
2	b	0	4
5	e	0	1
6	f	0	1
9	i	0	1
10	j	0	1
13	m	0	1
18	r	0	1
23	x	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
25	A	2	0
31	G	0	1
33	H	0	1
35	K	0	2
36	L	0	1
37	M	0	1
43	S	0	1
49	Y	0	1
All	All	4	20

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	v	61	C	N1-C6	-10.77	1.30	1.37
23	x	87	A	OP3-P	-10.64	1.48	1.61
26	B	1	U	OP3-P	-10.60	1.48	1.61
24	y	1	G	OP3-P	-10.59	1.48	1.61
25	A	1	G	OP3-P	-10.51	1.48	1.61

The worst 5 of 1649 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	v	61	C	C6-N1-C2	-17.40	113.34	120.30
22	v	61	C	N3-C4-C5	-15.90	115.54	121.90
24	y	35	C	C5-C6-N1	15.50	128.75	121.00
24	y	74	C	N1-C2-O2	14.94	127.87	118.90
1	a	419	C	C6-N1-C2	-14.23	114.61	120.30

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	a	527	G7M	C4',C3'
25	A	2069	G7M	C4',C3'

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	a	60	A	Sidechain
2	b	10	LYS	Peptide
2	b	12	GLY	Peptide
2	b	17	HIS	Peptide
2	b	73	ARG	Mainchain

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	
2	b	216/218 (99%)	189 (88%)	20 (9%)	7 (3%)	3	21
3	c	204/206 (99%)	197 (97%)	5 (2%)	2 (1%)	13	48
4	d	203/205 (99%)	188 (93%)	14 (7%)	1 (0%)	25	64
5	e	155/157 (99%)	134 (86%)	16 (10%)	5 (3%)	3	21
6	f	98/100 (98%)	86 (88%)	7 (7%)	5 (5%)	1	16
7	g	149/151 (99%)	131 (88%)	14 (9%)	4 (3%)	4	26
8	h	127/129 (98%)	116 (91%)	9 (7%)	2 (2%)	8	37
9	i	125/127 (98%)	105 (84%)	18 (14%)	2 (2%)	8	37
10	j	96/98 (98%)	85 (88%)	7 (7%)	4 (4%)	2	18
11	k	114/116 (98%)	99 (87%)	11 (10%)	4 (4%)	3	20
12	l	121/123 (98%)	103 (85%)	11 (9%)	7 (6%)	1	14
13	m	112/114 (98%)	101 (90%)	9 (8%)	2 (2%)	7	34
14	n	98/100 (98%)	88 (90%)	10 (10%)	0	100	100
15	o	86/88 (98%)	77 (90%)	6 (7%)	3 (4%)	3	20
16	p	80/82 (98%)	73 (91%)	6 (8%)	1 (1%)	10	42
17	q	78/80 (98%)	68 (87%)	9 (12%)	1 (1%)	10	42
18	r	63/65 (97%)	56 (89%)	3 (5%)	4 (6%)	1	14
19	s	84/86 (98%)	76 (90%)	4 (5%)	4 (5%)	2	17
20	t	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
21	u	63/65 (97%)	53 (84%)	6 (10%)	4 (6%)	1	14
27	C	269/271 (99%)	242 (90%)	22 (8%)	5 (2%)	6	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	D	207/209 (99%)	192 (93%)	10 (5%)	5 (2%)	5	28
29	E	199/201 (99%)	188 (94%)	8 (4%)	3 (2%)	8	39
30	F	175/177 (99%)	155 (89%)	16 (9%)	4 (2%)	5	29
31	G	174/176 (99%)	161 (92%)	9 (5%)	4 (2%)	5	29
32	I	139/141 (99%)	120 (86%)	13 (9%)	6 (4%)	2	18
33	H	147/149 (99%)	130 (88%)	14 (10%)	3 (2%)	6	32
34	J	140/142 (99%)	132 (94%)	6 (4%)	2 (1%)	9	40
35	K	120/122 (98%)	108 (90%)	9 (8%)	3 (2%)	4	27
36	L	141/143 (99%)	129 (92%)	8 (6%)	4 (3%)	4	24
37	M	134/136 (98%)	123 (92%)	8 (6%)	3 (2%)	5	29
38	N	118/120 (98%)	107 (91%)	10 (8%)	1 (1%)	16	54
39	O	114/116 (98%)	106 (93%)	8 (7%)	0	100	100
40	P	112/114 (98%)	103 (92%)	9 (8%)	0	100	100
41	Q	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
42	R	101/103 (98%)	91 (90%)	9 (9%)	1 (1%)	13	48
43	S	108/110 (98%)	101 (94%)	6 (6%)	1 (1%)	14	51
44	T	91/93 (98%)	83 (91%)	7 (8%)	1 (1%)	12	46
45	U	100/102 (98%)	90 (90%)	8 (8%)	2 (2%)	6	32
46	V	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
47	W	73/75 (97%)	69 (94%)	4 (6%)	0	100	100
48	X	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
49	Y	61/63 (97%)	58 (95%)	2 (3%)	1 (2%)	8	37
50	Z	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
51	0	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
52	1	48/50 (96%)	46 (96%)	1 (2%)	1 (2%)	5	30
53	2	44/46 (96%)	41 (93%)	1 (2%)	2 (4%)	2	17
54	3	62/64 (97%)	59 (95%)	2 (3%)	1 (2%)	8	37
55	4	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
56	6	64/66 (97%)	56 (88%)	5 (8%)	3 (5%)	2	17
All	All	5724/5824 (98%)	5199 (91%)	407 (7%)	118 (2%)	8	30

5 of 118 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	b	18	GLN
5	e	89	THR
5	e	93	VAL
6	f	53	LYS
6	f	54	LEU

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	
2	b	180/180 (100%)	180 (100%)	0	100	100
3	c	170/170 (100%)	170 (100%)	0	100	100
4	d	172/172 (100%)	172 (100%)	0	100	100
5	e	119/119 (100%)	119 (100%)	0	100	100
6	f	87/87 (100%)	87 (100%)	0	100	100
7	g	124/124 (100%)	124 (100%)	0	100	100
8	h	104/104 (100%)	104 (100%)	0	100	100
9	i	105/105 (100%)	105 (100%)	0	100	100
10	j	86/86 (100%)	86 (100%)	0	100	100
11	k	89/89 (100%)	89 (100%)	0	100	100
12	l	103/103 (100%)	103 (100%)	0	100	100
13	m	92/92 (100%)	92 (100%)	0	100	100
14	n	79/83 (95%)	78 (99%)	1 (1%)	65	77
15	o	76/76 (100%)	76 (100%)	0	100	100
16	p	65/65 (100%)	65 (100%)	0	100	100
17	q	74/74 (100%)	74 (100%)	0	100	100
18	r	48/56 (86%)	48 (100%)	0	100	100
19	s	74/74 (100%)	74 (100%)	0	100	100
20	t	65/65 (100%)	65 (100%)	0	100	100
21	u	44/55 (80%)	44 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	C	216/216 (100%)	216 (100%)	0	100	100
28	D	164/164 (100%)	164 (100%)	0	100	100
29	E	165/165 (100%)	165 (100%)	0	100	100
30	F	148/148 (100%)	148 (100%)	0	100	100
31	G	137/137 (100%)	137 (100%)	0	100	100
32	I	109/109 (100%)	109 (100%)	0	100	100
33	H	114/114 (100%)	114 (100%)	0	100	100
34	J	116/116 (100%)	116 (100%)	0	100	100
35	K	103/103 (100%)	103 (100%)	0	100	100
36	L	102/102 (100%)	102 (100%)	0	100	100
37	M	109/109 (100%)	109 (100%)	0	100	100
38	N	100/100 (100%)	100 (100%)	0	100	100
39	O	86/86 (100%)	86 (100%)	0	100	100
40	P	99/99 (100%)	99 (100%)	0	100	100
41	Q	89/89 (100%)	89 (100%)	0	100	100
42	R	84/84 (100%)	84 (100%)	0	100	100
43	S	93/93 (100%)	93 (100%)	0	100	100
44	T	80/80 (100%)	80 (100%)	0	100	100
45	U	83/83 (100%)	83 (100%)	0	100	100
46	V	78/78 (100%)	78 (100%)	0	100	100
47	W	57/57 (100%)	57 (100%)	0	100	100
48	X	67/67 (100%)	67 (100%)	0	100	100
49	Y	55/55 (100%)	55 (100%)	0	100	100
50	Z	48/48 (100%)	48 (100%)	0	100	100
51	0	47/47 (100%)	47 (100%)	0	100	100
52	1	45/45 (100%)	45 (100%)	0	100	100
53	2	38/38 (100%)	38 (100%)	0	100	100
54	3	51/51 (100%)	51 (100%)	0	100	100
55	4	34/34 (100%)	34 (100%)	0	100	100
56	6	59/59 (100%)	59 (100%)	0	100	100
All	All	4732/4755 (100%)	4731 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	n	34	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
46	V	87	GLN
55	4	35	GLN
56	6	41	HIS
55	4	37	GLN
10	j	58	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1535/1539 (99%)	238 (15%)	0
22	v	76/77 (98%)	28 (36%)	0
23	x	47/48 (97%)	30 (63%)	0
24	y	93/95 (97%)	31 (33%)	0
25	A	2894/2903 (99%)	569 (19%)	25 (0%)
26	B	119/120 (99%)	11 (9%)	1 (0%)
All	All	4764/4782 (99%)	907 (19%)	26 (0%)

5 of 907 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	6	G
1	a	9	G
1	a	22	G
1	a	32	A
1	a	39	G

5 of 26 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	A	2061	G
25	A	2168	G
25	A	2610	C
25	A	2162	G
25	A	2194	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

43 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$
25	6MZ	A	1618	25	18,25,26	0.97	1 (5%)	16,36,39	2.11	4 (25%)
25	PSU	A	746	25	18,21,22	1.36	2 (11%)	22,30,33	1.84	4 (18%)
25	OMC	A	2498	25	19,22,23	0.90	0	26,31,34	1.22	4 (15%)
1	MA6	a	1519	1	18,26,27	1.02	2 (11%)	19,38,41	1.81	4 (21%)
1	PSU	a	516	1	18,21,22	1.38	3 (16%)	22,30,33	1.94	4 (18%)
1	MA6	a	1518	1	18,26,27	0.91	1 (5%)	19,38,41	1.92	6 (31%)
24	H2U	y	19	24	18,21,22	0.97	2 (11%)	21,30,33	1.20	2 (9%)
24	6IA	y	37	24	22,29,30	0.79	1 (4%)	22,41,44	1.72	4 (18%)
25	6MZ	A	2030	25	18,25,26	0.93	1 (5%)	16,36,39	2.65	4 (25%)
1	2MG	a	1207	1	18,26,27	0.92	1 (5%)	16,38,41	1.09	2 (12%)
1	4OC	a	1402	1	20,23,24	0.78	1 (5%)	26,32,35	1.14	2 (7%)
25	5MU	A	747	25	19,22,23	1.35	4 (21%)	28,32,35	1.99	7 (25%)
22	PSU	v	55	22	18,21,22	1.56	3 (16%)	22,30,33	2.08	5 (22%)
25	1MG	A	745	25	18,26,27	0.86	1 (5%)	19,39,42	1.04	2 (10%)
25	G7M	A	2069	25	20,26,27	1.56	3 (15%)	17,39,42	1.56	3 (17%)
25	3TD	A	1915	25	18,22,23	4.08	7 (38%)	22,32,35	1.76	3 (13%)
1	5MC	a	967	1	18,22,23	0.93	2 (11%)	26,32,35	1.27	3 (11%)
22	4SU	v	8	22	18,21,22	1.71	4 (22%)	26,30,33	2.71	7 (26%)
24	PSU	y	55	24	18,21,22	1.49	3 (16%)	22,30,33	1.67	3 (13%)
1	UR3	a	1498	1	19,22,23	1.06	2 (10%)	26,32,35	1.73	4 (15%)
25	PSU	A	1917	25	18,21,22	1.53	3 (16%)	22,30,33	1.94	3 (13%)
1	5MC	a	1407	1	18,22,23	1.02	2 (11%)	26,32,35	1.32	3 (11%)
25	5MC	A	1962	25	18,22,23	0.92	2 (11%)	26,32,35	1.05	2 (7%)
25	H2U	A	2449	25	18,21,22	1.08	3 (16%)	21,30,33	1.66	3 (14%)
22	H2U	v	20	22	18,21,22	0.95	2 (11%)	21,30,33	1.33	3 (14%)
25	PSU	A	2604	25	18,21,22	1.49	3 (16%)	22,30,33	1.92	3 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	2MA	A	2503	25	17,25,26	1.00	1 (5%)	17,37,40	0.96	2 (11%)
24	5MU	y	54	24	19,22,23	1.34	4 (21%)	28,32,35	2.08	7 (25%)
25	OMU	A	2552	25	19,22,23	1.23	3 (15%)	26,31,34	1.95	8 (30%)
1	G7M	a	527	1	20,26,27	1.59	3 (15%)	17,39,42	1.69	4 (23%)
1	2MG	a	966	1	18,26,27	0.94	1 (5%)	16,38,41	1.23	3 (18%)
25	PSU	A	2504	25	18,21,22	1.42	4 (22%)	22,30,33	1.89	4 (18%)
25	5MU	A	1939	25	19,22,23	1.38	5 (26%)	28,32,35	2.27	6 (21%)
25	2MG	A	1835	25	18,26,27	0.99	1 (5%)	16,38,41	1.31	2 (12%)
1	2MG	a	1516	1	18,26,27	0.87	1 (5%)	16,38,41	1.12	2 (12%)
25	PSU	A	955	25	18,21,22	1.41	2 (11%)	22,30,33	2.03	3 (13%)
25	PSU	A	2580	25	18,21,22	1.35	2 (11%)	22,30,33	1.88	4 (18%)
25	PSU	A	2605	25	18,21,22	1.32	2 (11%)	22,30,33	1.90	3 (13%)
25	PSU	A	1911	25	18,21,22	1.40	3 (16%)	22,30,33	2.06	4 (18%)
25	OMG	A	2251	25,24	18,26,27	1.01	1 (5%)	19,38,41	0.98	2 (10%)
25	2MG	A	2445	25	18,26,27	0.93	1 (5%)	16,38,41	1.17	3 (18%)
22	5MU	v	54	22	19,22,23	1.51	3 (15%)	28,32,35	2.10	9 (32%)
25	PSU	A	2457	25	18,21,22	1.41	2 (11%)	22,30,33	1.92	4 (18%)

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
25	6MZ	A	1618	25	-	2/5/27/28	0/3/3/3
25	PSU	A	746	25	-	1/7/25/26	0/2/2/2
25	OMC	A	2498	25	-	0/9/27/28	0/2/2/2
1	MA6	a	1519	1	-	2/7/29/30	0/3/3/3
1	PSU	a	516	1	-	0/7/25/26	0/2/2/2
1	MA6	a	1518	1	-	2/7/29/30	0/3/3/3
24	H2U	y	19	24	-	4/7/38/39	0/2/2/2
24	6IA	y	37	24	-	4/9/31/32	0/3/3/3
25	6MZ	A	2030	25	-	2/5/27/28	0/3/3/3
1	2MG	a	1207	1	-	0/5/27/28	0/3/3/3
1	4OC	a	1402	1	-	2/9/29/30	0/2/2/2
25	5MU	A	747	25	-	2/7/25/26	0/2/2/2
22	PSU	v	55	22	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	G7M	A	2069	25	2/2/5/5	2/3/25/26	0/3/3/3
25	1MG	A	745	25	-	0/3/25/26	0/3/3/3
25	3TD	A	1915	25	-	5/7/25/26	0/2/2/2
1	5MC	a	967	1	-	0/7/25/26	0/2/2/2
22	4SU	v	8	22	-	1/7/25/26	0/2/2/2
24	PSU	y	55	24	-	1/7/25/26	0/2/2/2
1	UR3	a	1498	1	-	2/7/25/26	0/2/2/2
25	PSU	A	1917	25	-	0/7/25/26	0/2/2/2
1	5MC	a	1407	1	-	0/7/25/26	0/2/2/2
25	5MC	A	1962	25	-	4/7/25/26	0/2/2/2
25	H2U	A	2449	25	-	0/7/38/39	0/2/2/2
22	H2U	v	20	22	-	5/7/38/39	0/2/2/2
25	PSU	A	2604	25	-	0/7/25/26	0/2/2/2
25	2MA	A	2503	25	-	2/3/25/26	0/3/3/3
24	5MU	y	54	24	-	2/7/25/26	0/2/2/2
25	OMU	A	2552	25	-	2/9/27/28	0/2/2/2
1	G7M	a	527	1	2/2/5/5	3/3/25/26	0/3/3/3
1	2MG	a	966	1	-	0/5/27/28	0/3/3/3
25	PSU	A	2504	25	-	0/7/25/26	0/2/2/2
25	5MU	A	1939	25	-	0/7/25/26	0/2/2/2
25	2MG	A	1835	25	-	1/5/27/28	0/3/3/3
1	2MG	a	1516	1	-	0/5/27/28	0/3/3/3
25	PSU	A	955	25	-	0/7/25/26	0/2/2/2
25	PSU	A	2580	25	-	0/7/25/26	0/2/2/2
25	PSU	A	2605	25	-	0/7/25/26	0/2/2/2
25	PSU	A	1911	25	-	0/7/25/26	0/2/2/2
25	OMG	A	2251	25,24	-	1/5/27/28	0/3/3/3
25	2MG	A	2445	25	-	2/5/27/28	0/3/3/3
22	5MU	v	54	22	-	3/7/25/26	0/2/2/2
25	PSU	A	2457	25	-	0/7/25/26	0/2/2/2

The worst 5 of 98 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	1915	3TD	C6-C5	11.87	1.49	1.35
25	A	1915	3TD	C2-N1	9.20	1.49	1.37
25	A	1915	3TD	C6-N1	5.79	1.45	1.36
1	a	527	G7M	C5-C4	4.59	1.48	1.39
22	v	8	4SU	C4-S4	-4.57	1.59	1.68

The worst 5 of 164 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	v	8	4SU	C5-C4-S4	-7.22	115.16	124.47
22	v	8	4SU	C4-N3-C2	-6.97	120.57	127.34
25	A	955	PSU	N1-C2-N3	6.62	122.63	115.13
25	A	2030	6MZ	C9-N6-C6	-6.62	117.17	122.87
25	A	2030	6MZ	C2-N1-C6	6.49	122.15	116.59

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	a	527	G7M	C4'
1	a	527	G7M	C3'
25	A	2069	G7M	C4'
25	A	2069	G7M	C3'

5 of 59 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	a	1518	MA6	C5-C6-N6-C9
1	a	1519	MA6	C5-C6-N6-C10
22	v	20	H2U	O4'-C1'-N1-C2
22	v	20	H2U	O4'-C1'-N1-C6
22	v	54	5MU	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

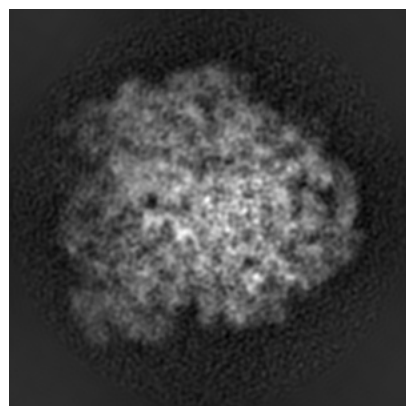
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4126. These allow visual inspection of the internal detail of the map and identification of artifacts.

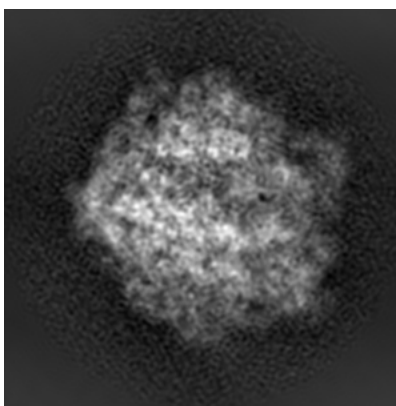
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

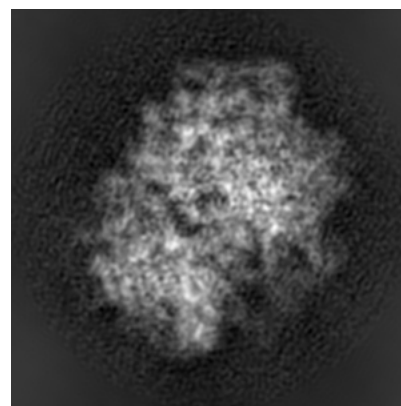
6.1.1 Primary map



X

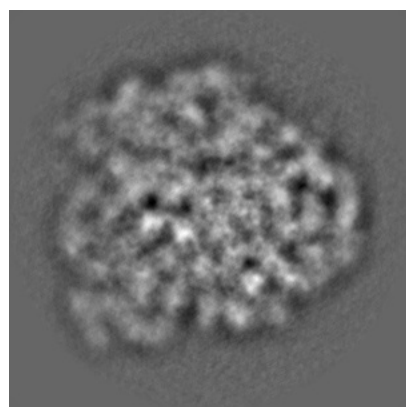


Y

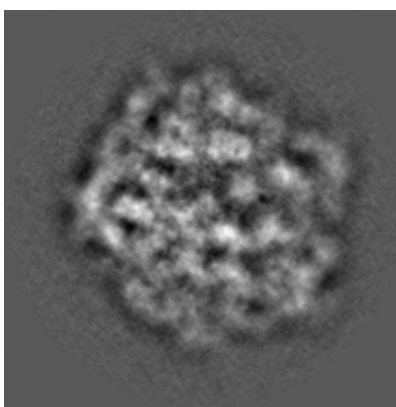


Z

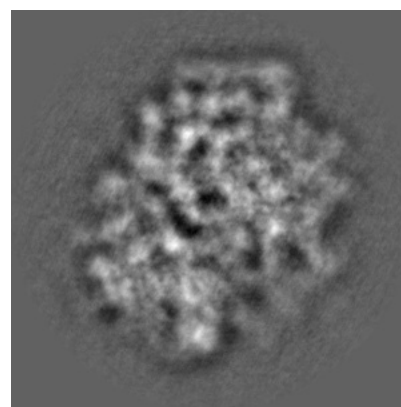
6.1.2 Raw map



X



Y

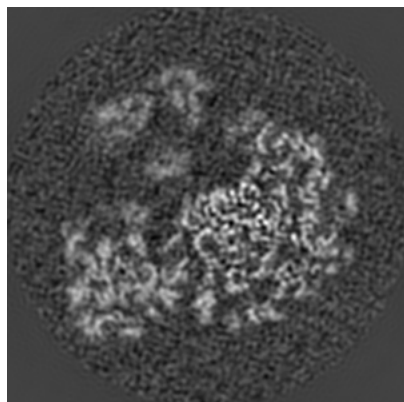


Z

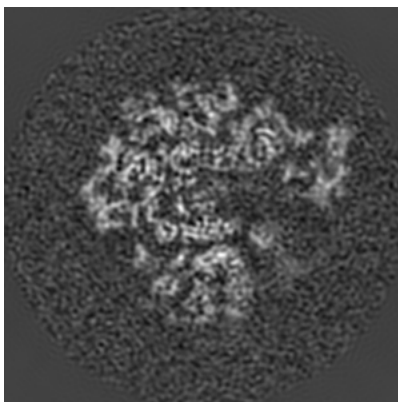
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

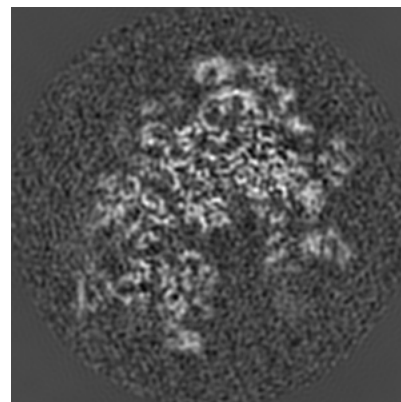
6.2.1 Primary map



X Index: 136

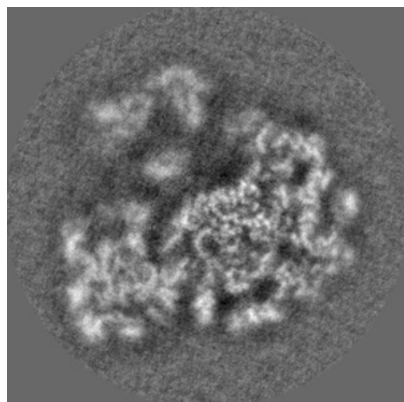


Y Index: 136

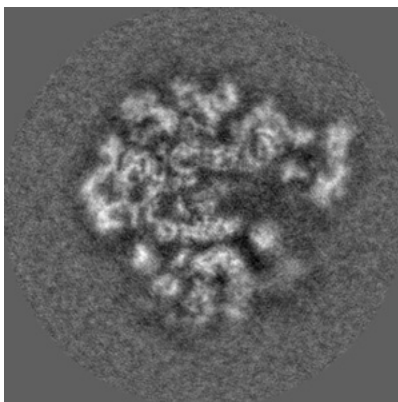


Z Index: 136

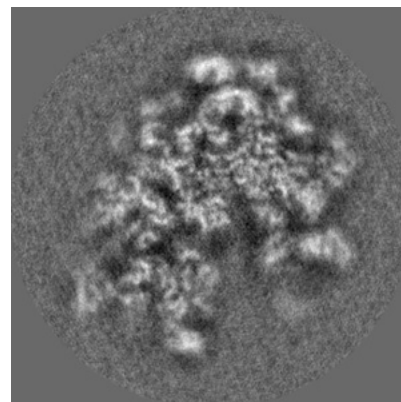
6.2.2 Raw map



X Index: 136



Y Index: 136

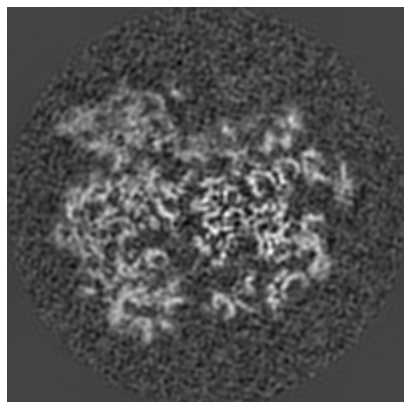


Z Index: 136

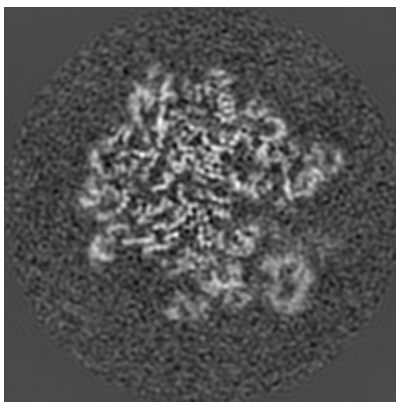
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

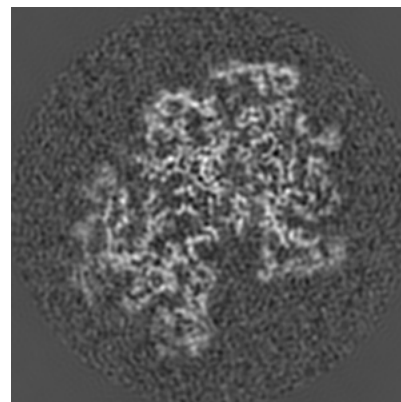
6.3.1 Primary map



X Index: 119

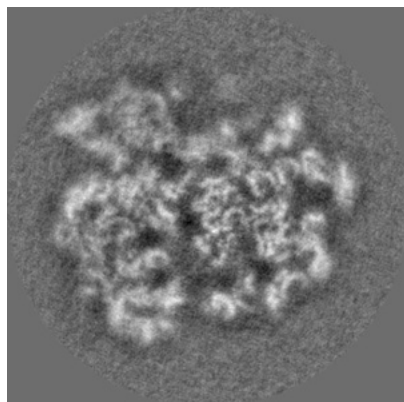


Y Index: 156

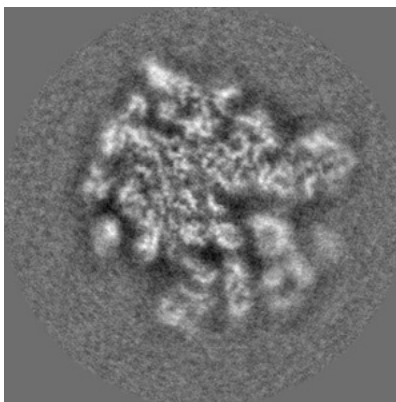


Z Index: 127

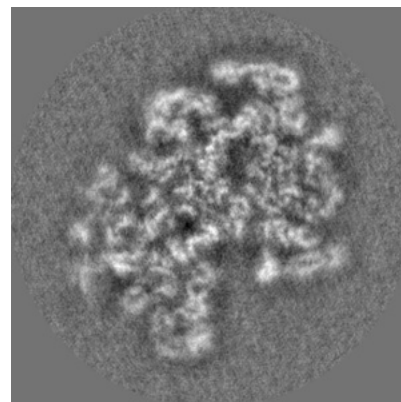
6.3.2 Raw map



X Index: 119



Y Index: 147

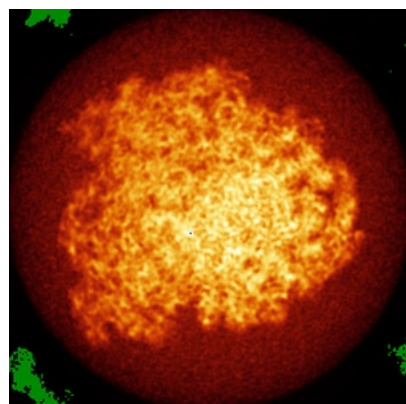


Z Index: 125

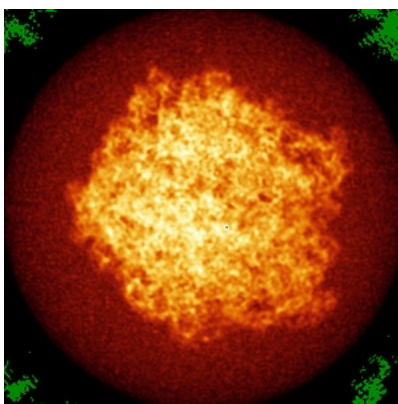
The images above show the largest variance slices of the map in three orthogonal directions.

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

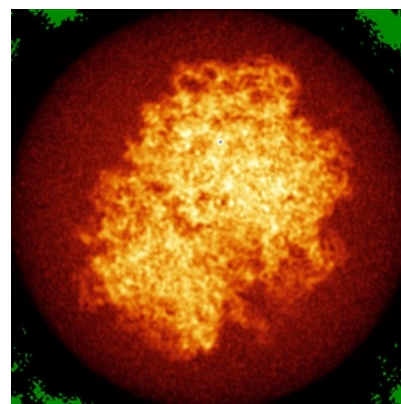
6.4.1 Primary map



X

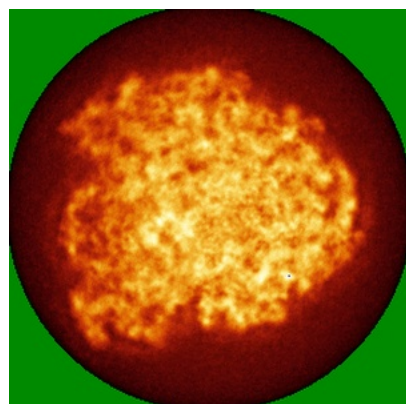


Y

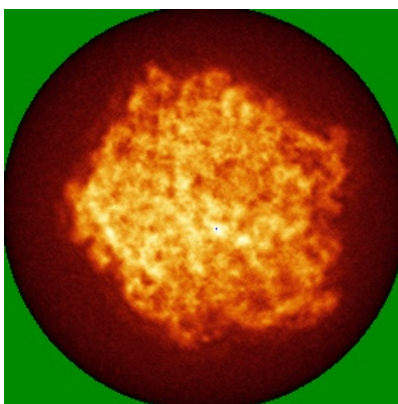


Z

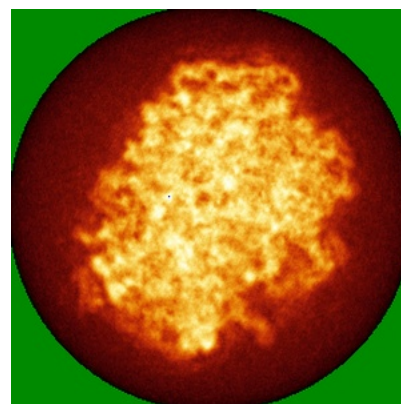
6.4.2 Raw map



X



Y

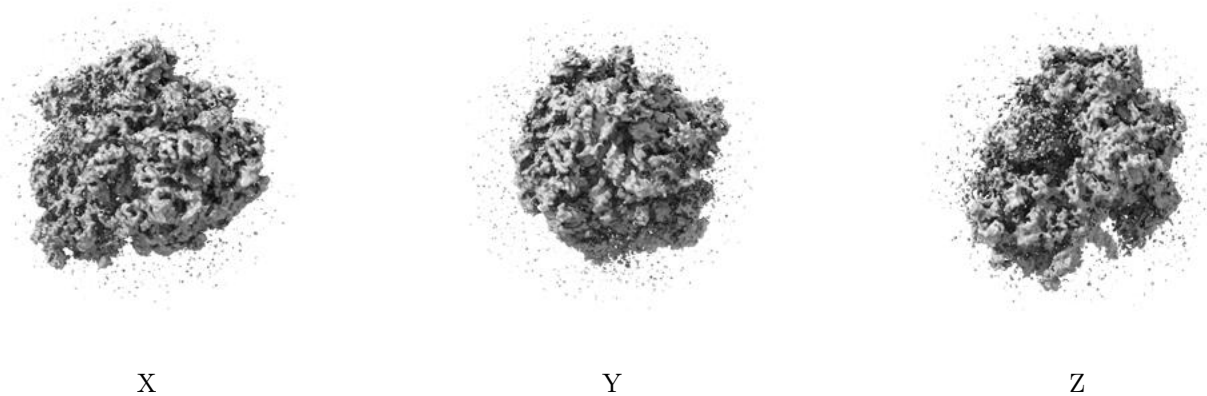


Z

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.

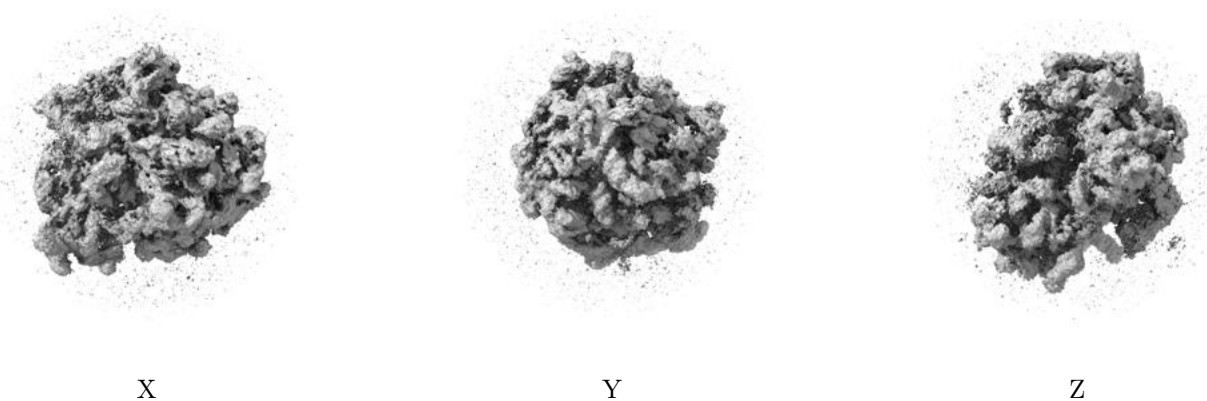
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. 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



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

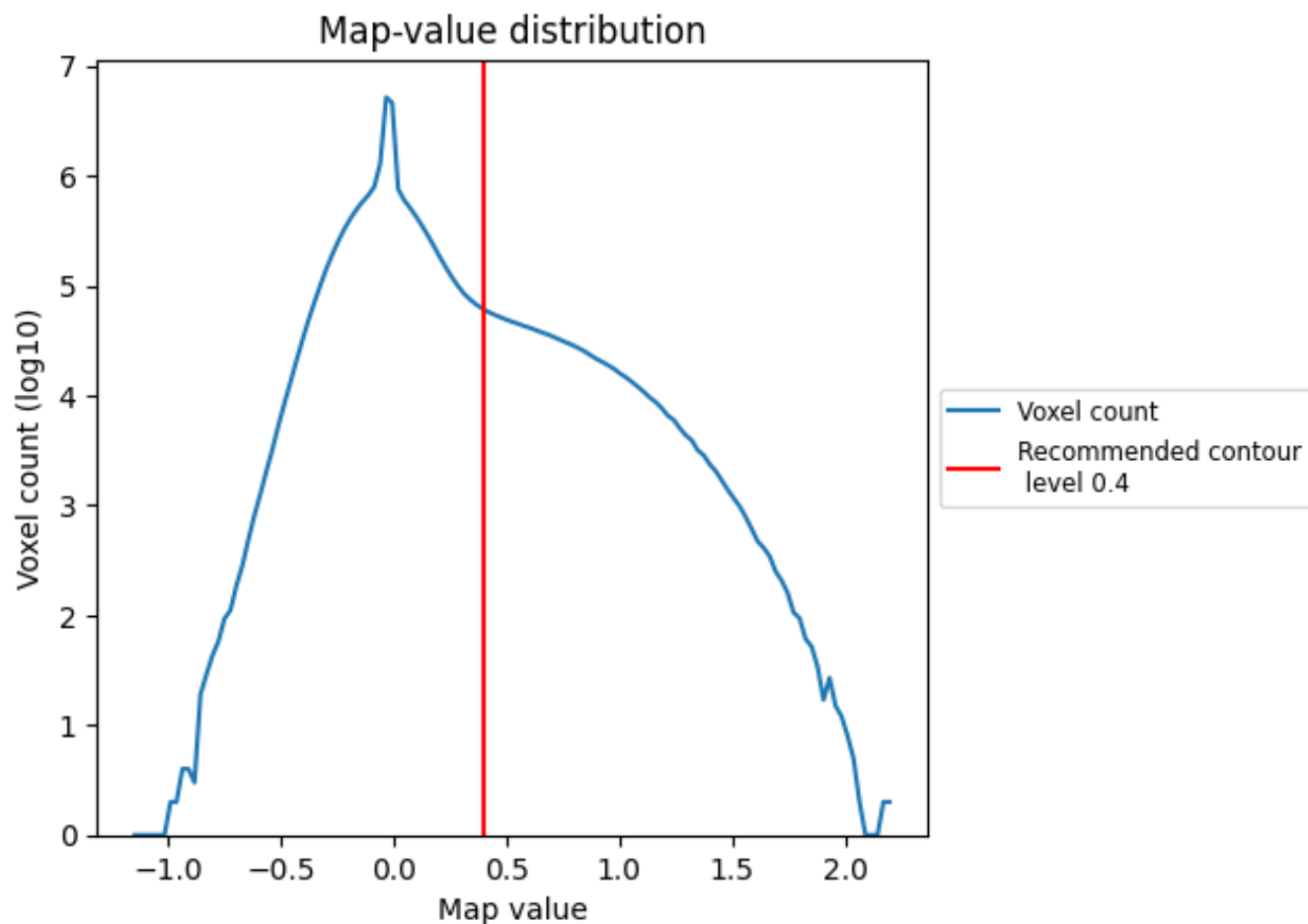
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

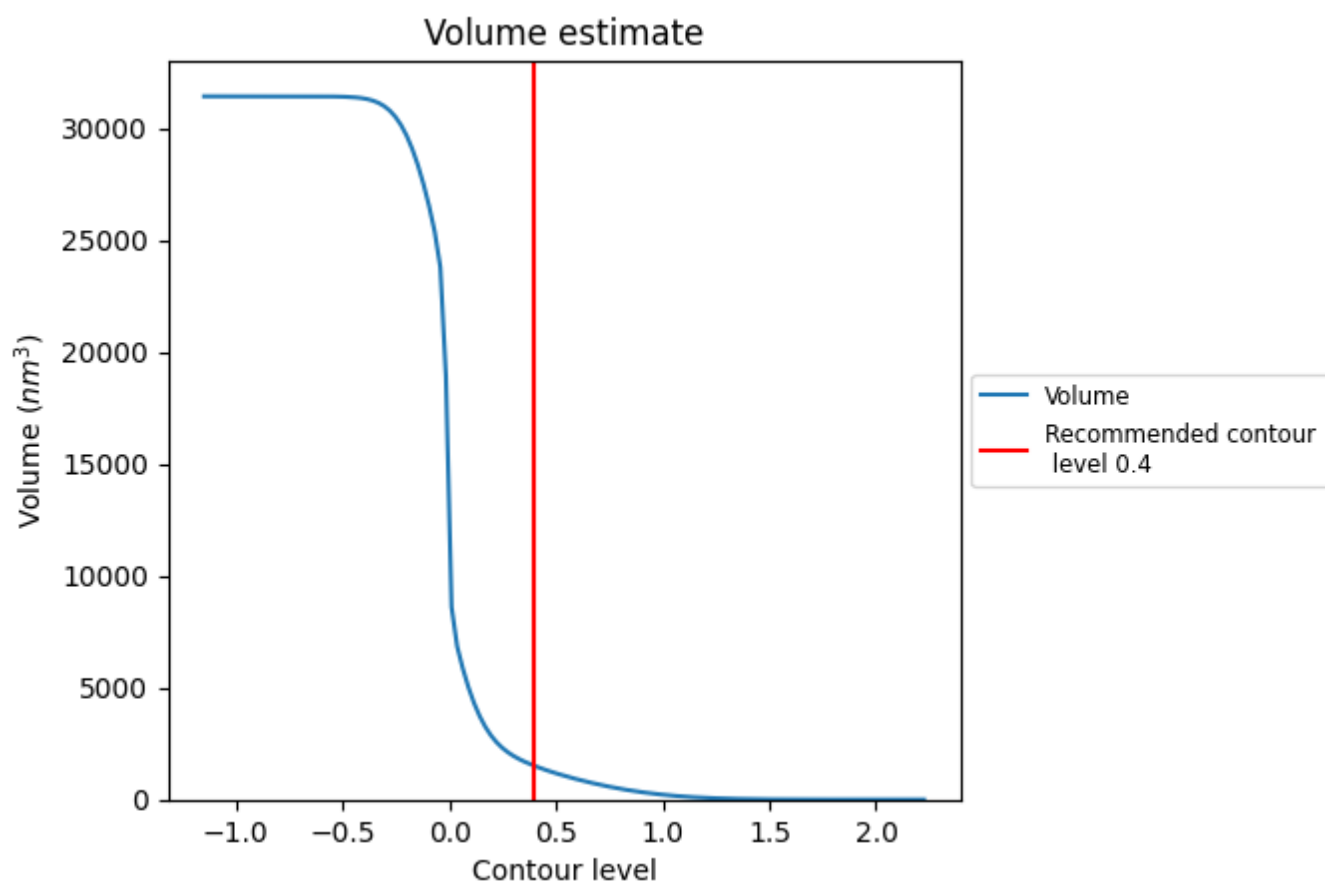
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

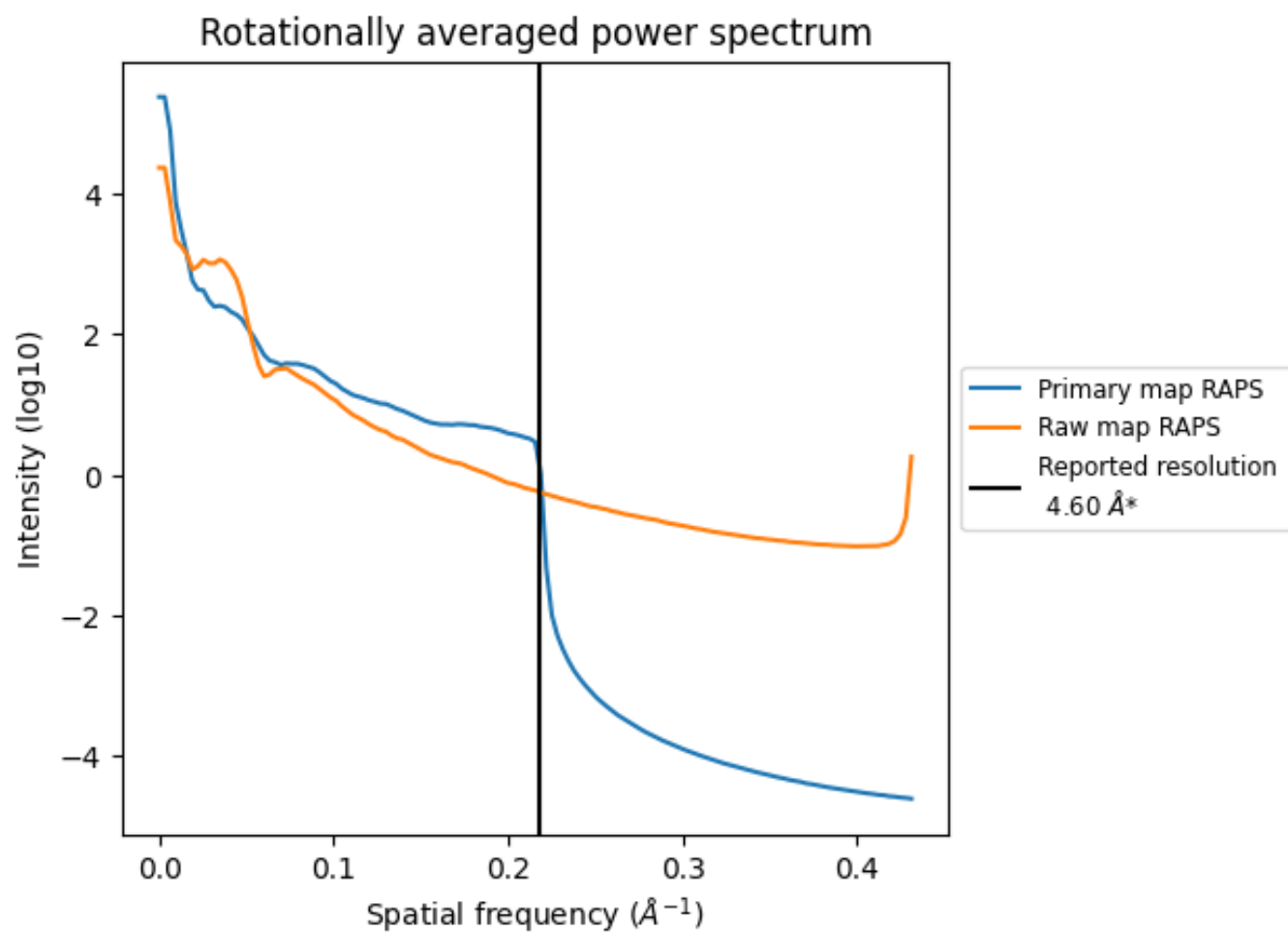
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1502 nm³; this corresponds to an approximate mass of 1357 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 ⓘ

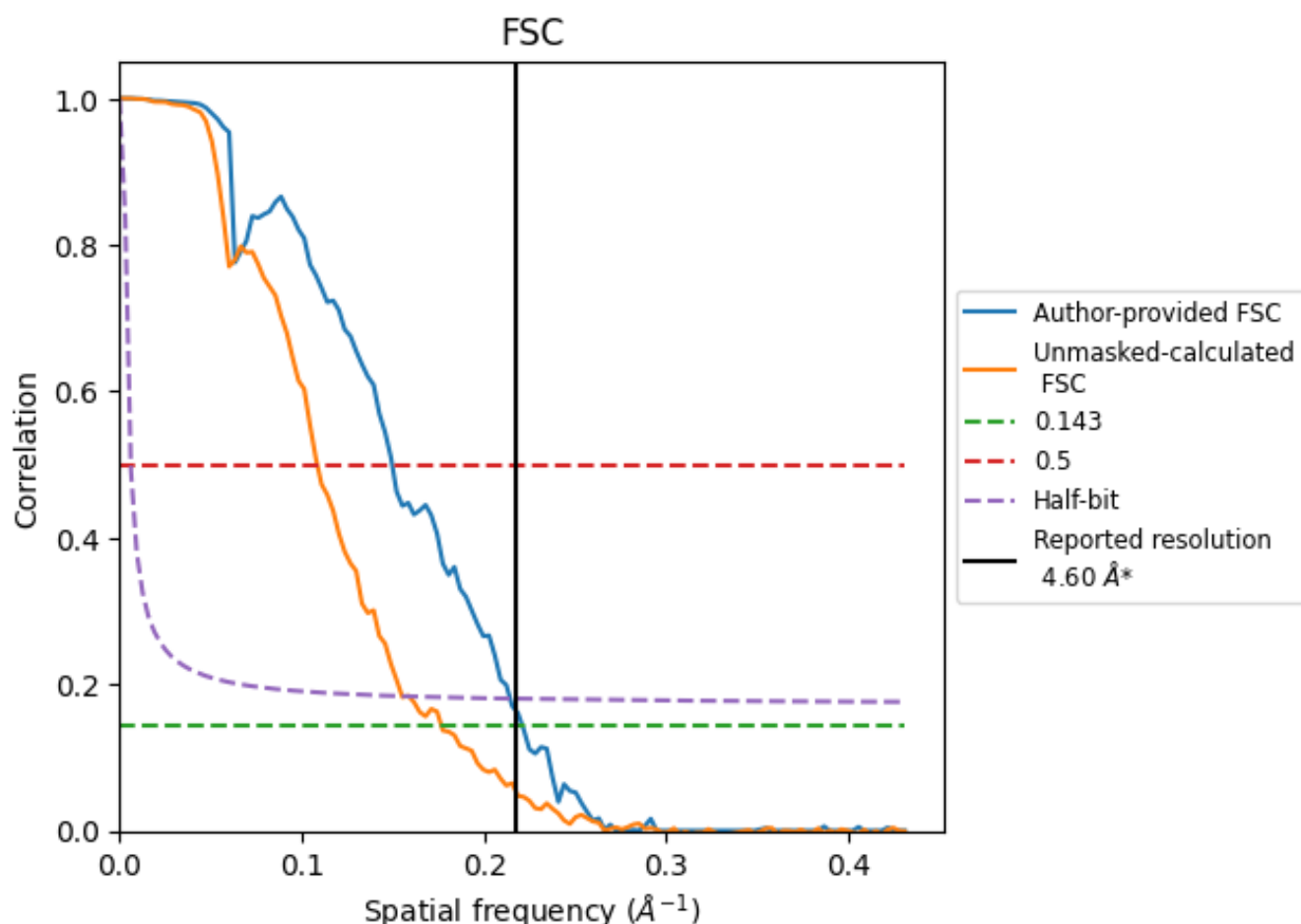


*Reported resolution corresponds to spatial frequency of 0.217 \AA^{-1}

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 0.217 Å⁻¹

8.2 Resolution estimates [i](#)

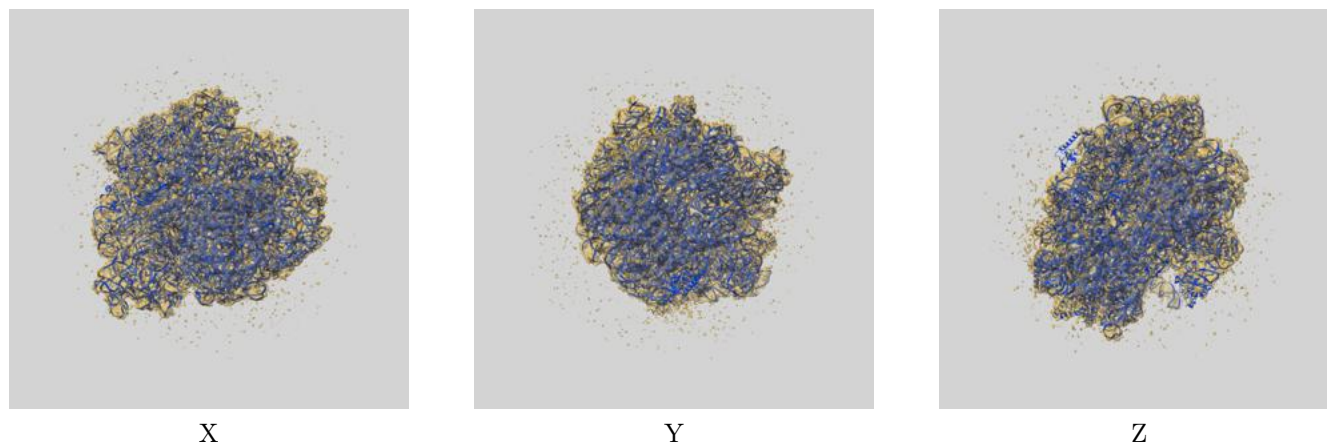
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.52	6.68	4.66
Unmasked-calculated*	5.66	9.22	6.45

*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 5.66 differs from the reported value 4.6 by more than 10 %

9 Map-model fit [i](#)

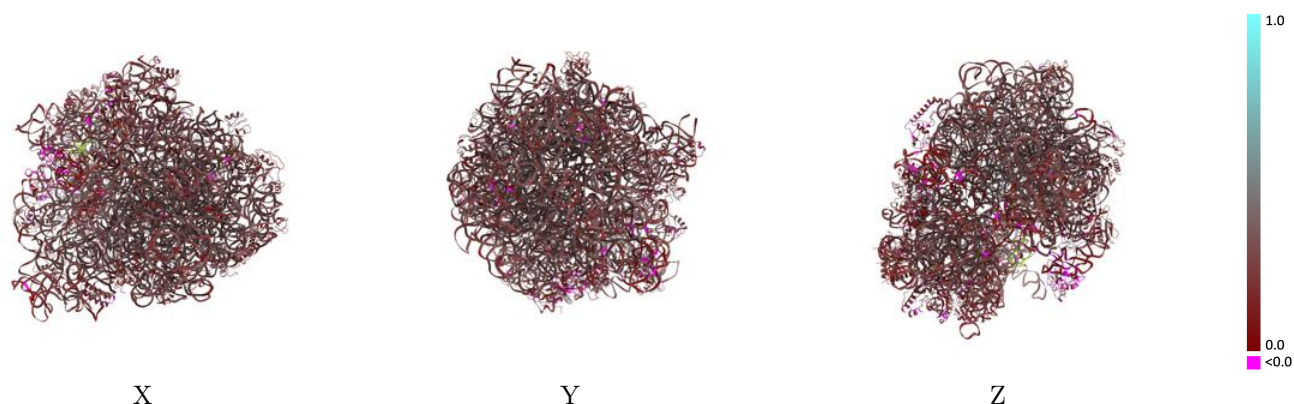
This section contains information regarding the fit between EMDB map EMD-4126 and PDB model 5LZF. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



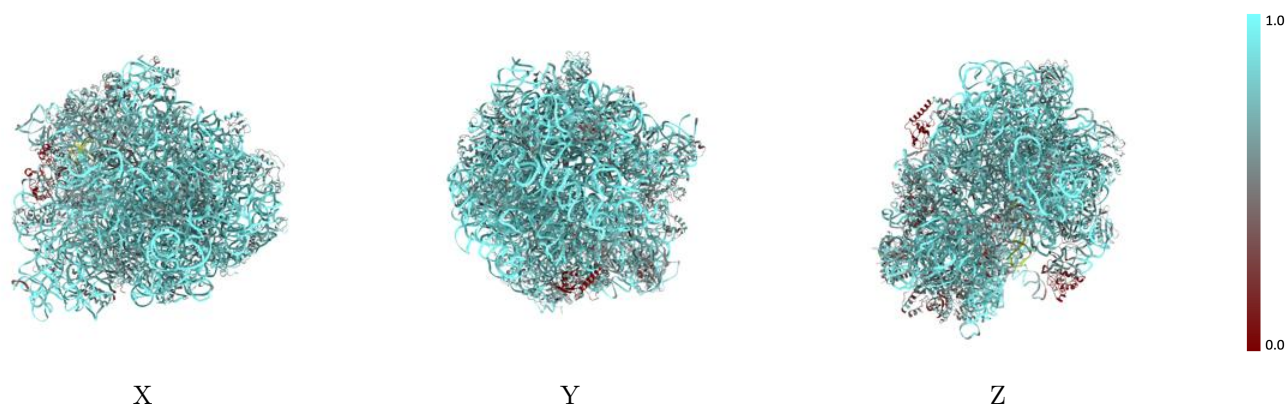
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



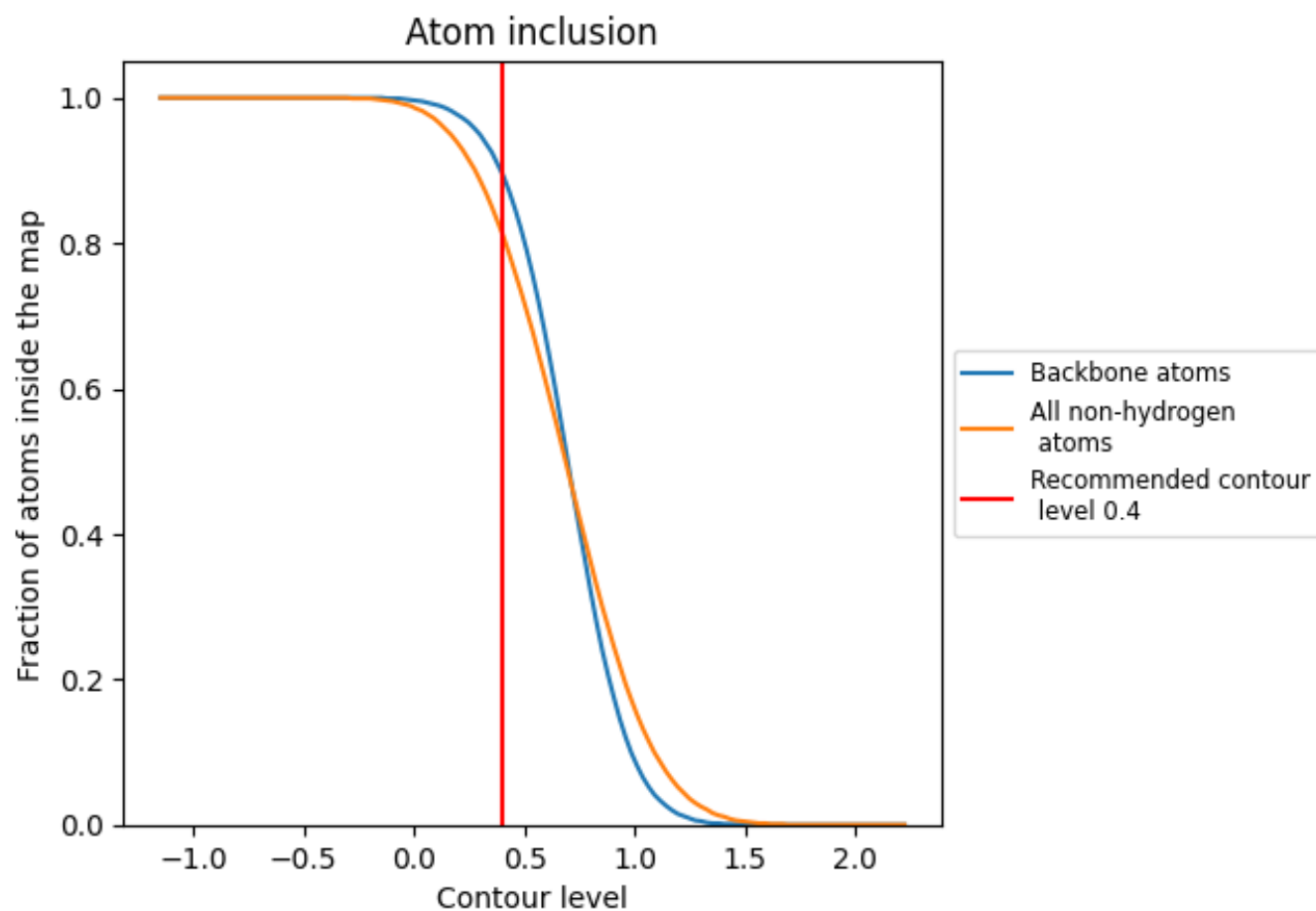
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 81% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8140	 0.2790
0	 0.6780	 0.2920
1	 0.5950	 0.2450
2	 0.7040	 0.2960
3	 0.6880	 0.3060
4	 0.6280	 0.2790
6	 0.5420	 0.1820
A	 0.9190	 0.3090
B	 0.9110	 0.2760
C	 0.6820	 0.2990
D	 0.6660	 0.2750
E	 0.6590	 0.2700
F	 0.5930	 0.1870
G	 0.6670	 0.2310
H	 0.1660	 0.1300
I	 0.1460	 0.0750
J	 0.7110	 0.2780
K	 0.6540	 0.2850
L	 0.6590	 0.2850
M	 0.6690	 0.2790
N	 0.6880	 0.2700
O	 0.6570	 0.2200
P	 0.6360	 0.2530
Q	 0.6980	 0.2640
R	 0.6930	 0.2750
S	 0.6720	 0.2890
T	 0.6470	 0.2670
U	 0.6680	 0.2600
V	 0.6540	 0.2340
W	 0.6400	 0.2670
X	 0.6870	 0.2770
Y	 0.6640	 0.2000
Z	 0.6640	 0.2640
a	 0.9060	 0.2870
b	 0.4750	 0.2000



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Chain	Atom inclusion	Q-score
c	 0.6190	 0.2400
d	 0.5550	 0.2030
e	 0.6440	 0.2550
f	 0.6560	 0.2440
g	 0.5300	 0.2020
h	 0.6610	 0.2500
i	 0.5680	 0.2120
j	 0.5290	 0.2150
k	 0.6860	 0.2640
l	 0.6540	 0.2750
m	 0.5740	 0.1910
n	 0.6040	 0.2220
o	 0.6770	 0.2330
p	 0.6090	 0.2380
q	 0.6540	 0.2510
r	 0.6440	 0.2290
s	 0.5190	 0.1910
t	 0.6120	 0.1890
u	 0.5770	 0.1960
v	 0.8130	 0.2110
x	 0.4830	 0.1870
y	 0.5790	 0.1740