



## wwPDB EM Validation Summary Report ⓘ

Sep 28, 2024 – 06:21 pm BST

PDB ID : 7ZP8  
EMDB ID : EMD-14850  
Title : 70S E. coli ribosome with a stalled flamin domain 5 nascent chain  
Authors : Mitropoulou, A.; Plessa, E.; Wlodarski, T.; Ahn, M.; Chan, S.H.S.; Becker, T.A.; Beckmann, R.; Cabrita, L.D.; Christodoulou, J.  
Deposited on : 2022-04-26  
Resolution : 2.20 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](mailto: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

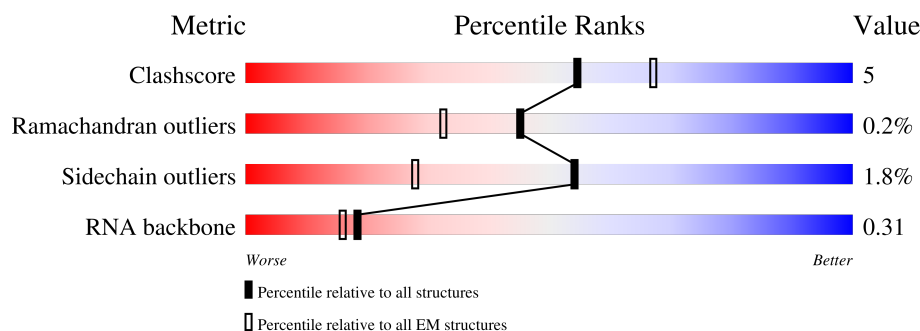
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.20 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.






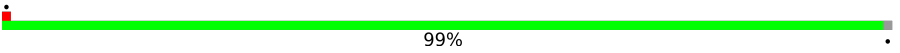
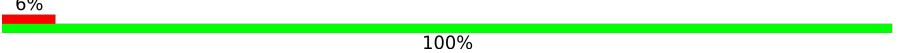
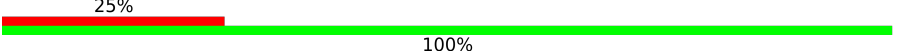
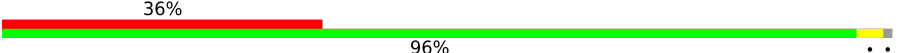
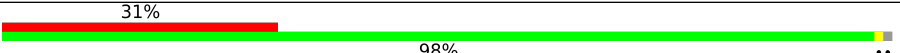

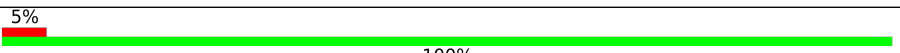
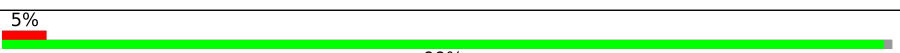
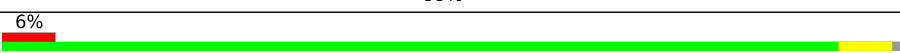
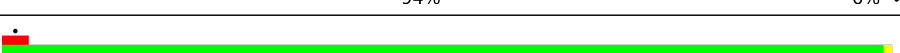
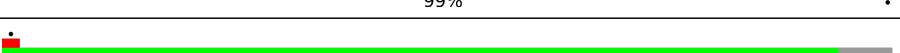
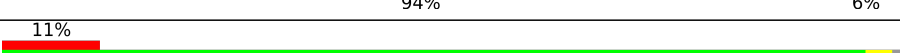
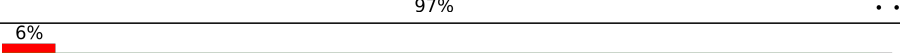
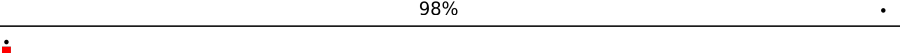
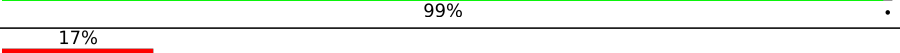
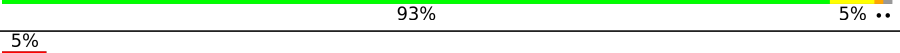
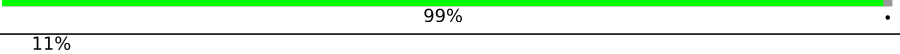

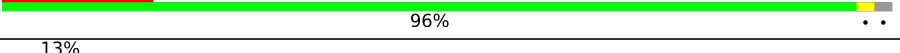
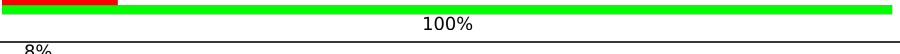
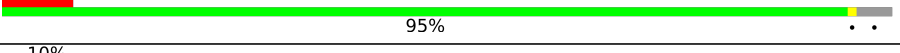
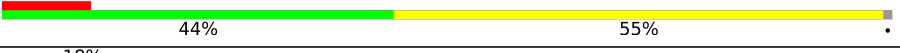
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	78	
2	1	63	
3	2	59	
4	3	57	
5	4	55	
6	6	46	
7	7	65	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	8	50	
9	a	120	
10	b	2904	
11	c	273	
12	d	209	
13	e	201	
14	f	179	
15	g	177	
16	h	149	
17	j	142	
18	k	123	
19	l	144	
20	m	136	
21	n	127	
22	o	117	
23	p	115	
24	q	118	
25	r	103	
26	s	110	
27	t	100	
28	u	104	
29	w	94	
30	y	85	
31	v	77	
32	z	148	

## 2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 90951 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 L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 2 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 3 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	57	Total	C	N	O	S	0	0
			439	276	86	75	2		

- Molecule 4 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	55	Total	C	N	O	S	0	0
			434	263	92	78	1		

- Molecule 5 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	4	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 6 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 7 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 8 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 9 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 10 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	b	2901	Total	C	N	O	P	0	0
			62281	27784	11464	20132	2901		

- Molecule 11 is a protein called 50S ribosomal protein L2.

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

- Molecule 12 is a protein called 50S ribosomal protein L3.

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

- Molecule 13 is a protein called 50S ribosomal protein L4.

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

- Molecule 14 is a protein called 50S ribosomal protein L5.

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

- Molecule 15 is a protein called 50S ribosomal protein L6.

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

- Molecule 16 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	h	39	Total	C	N	O	S	0	0
			287	184	51	51	1		

- Molecule 17 is a protein called 50S ribosomal protein L13.

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

- Molecule 18 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	k	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	l	143	Total	C	N	O	S	0	0
			1043	649	206	186	2		

- Molecule 20 is a protein called 50S ribosomal protein L16.

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

- Molecule 21 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	n	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 22 is a protein called 50S ribosomal protein L18.

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

- Molecule 23 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	p	113	Total	C	N	O	S	0	0
			908	570	177	160	1		

- Molecule 24 is a protein called 50S ribosomal protein L20.

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

- Molecule 25 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	r	102	Total	C	N	O	S	0	0
			810	513	152	143	2		

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	s	109	Total	C	N	O	S	0	0
			845	526	162	154	3		

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	t	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	u	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 29 is a protein called 50S ribosomal protein L25.

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

- Molecule 30 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	y	82	Total	C	N	O	S	0	0
			619	383	127	108	1		

- Molecule 31 is a RNA chain called Pro-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	v	76	Total	C	N	O	P	0	0
			1626	724	292	534	76		

- Molecule 32 is a protein called Gelation factor.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	z	33	Total	C	N	O	0	0
			277	186	44	47		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
z	20	MET	-	initiating methionine	UNP P13466
z	21	HIS	-	expression tag	UNP P13466
z	22	HIS	-	expression tag	UNP P13466
z	23	HIS	-	expression tag	UNP P13466
z	24	HIS	-	expression tag	UNP P13466
z	25	HIS	-	expression tag	UNP P13466
z	26	HIS	-	expression tag	UNP P13466
z	27	ALA	-	expression tag	UNP P13466
z	28	SER	-	expression tag	UNP P13466
z	149	GLU	-	expression tag	UNP P13466
z	150	LEU	-	expression tag	UNP P13466
z	151	PHE	-	expression tag	UNP P13466
z	152	SER	-	expression tag	UNP P13466

*Continued on next page...*



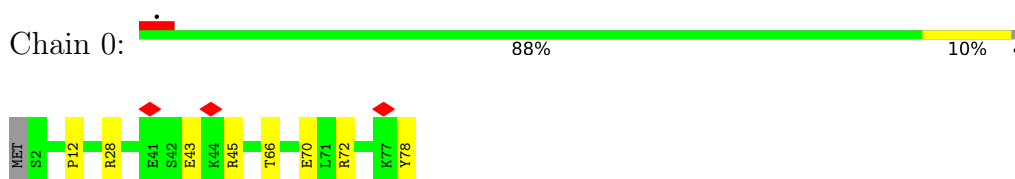
*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
z	153	THR	-	expression tag	UNP P13466
z	154	PRO	-	expression tag	UNP P13466
z	155	VAL	-	expression tag	UNP P13466
z	156	TRP	-	expression tag	UNP P13466
z	157	ILE	-	expression tag	UNP P13466
z	158	TRP	-	expression tag	UNP P13466
z	159	TRP	-	expression tag	UNP P13466
z	160	TRP	-	expression tag	UNP P13466
z	161	PRO	-	expression tag	UNP P13466
z	162	ARG	-	expression tag	UNP P13466
z	163	ILE	-	expression tag	UNP P13466
z	164	ARG	-	expression tag	UNP P13466
z	165	GLY	-	expression tag	UNP P13466
z	166	PRO	-	expression tag	UNP P13466
z	167	PRO	-	expression tag	UNP P13466

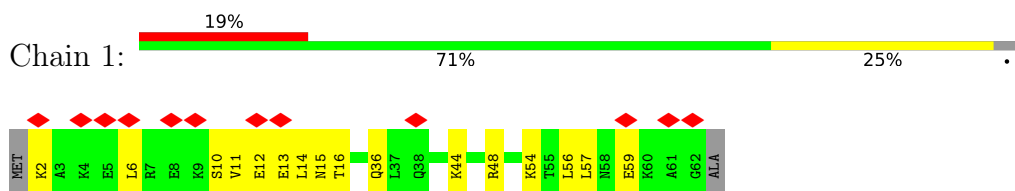
### 3 Residue-property plots [i](#)

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.

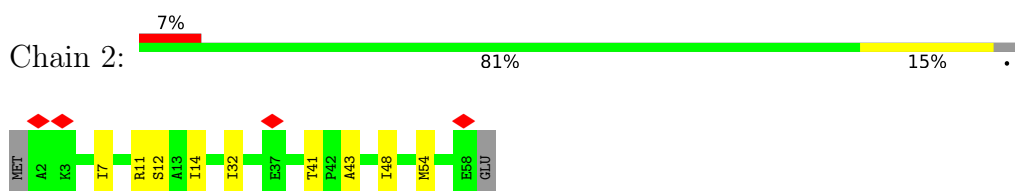
- Molecule 1: 50S ribosomal protein L28



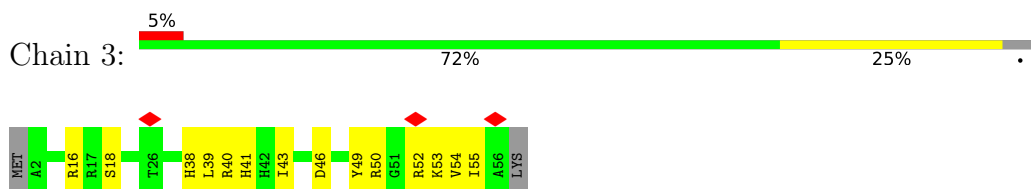
- Molecule 2: 50S ribosomal protein L29



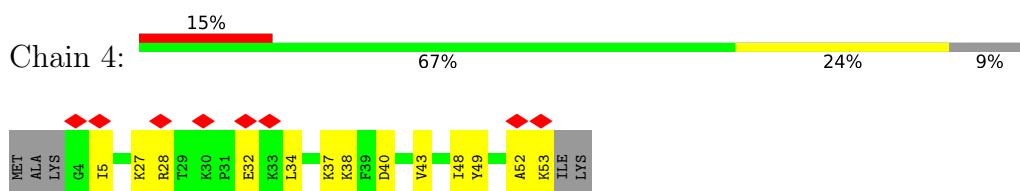
- Molecule 3: 50S ribosomal protein L30



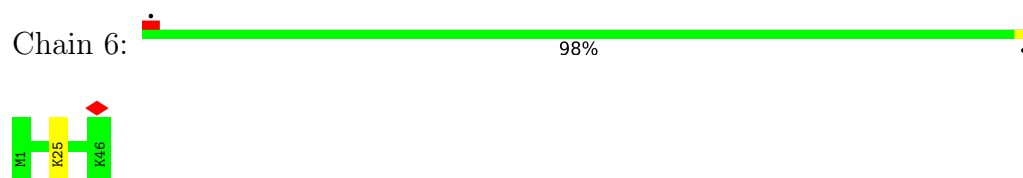
- Molecule 4: 50S ribosomal protein L32



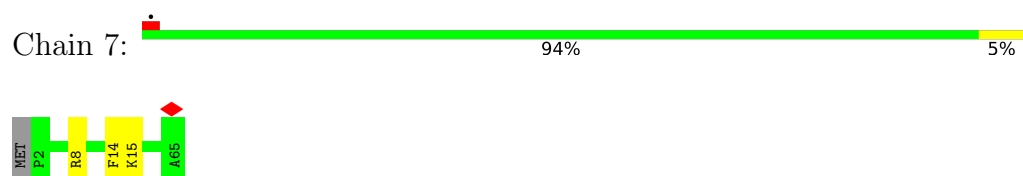
- Molecule 5: 50S ribosomal protein L33



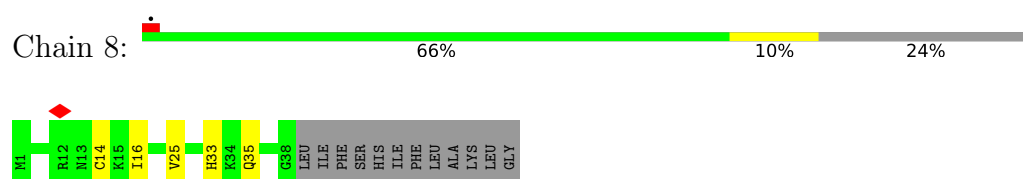
- Molecule 6: 50S ribosomal protein L34



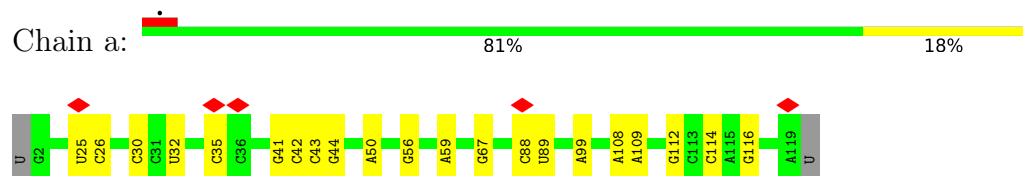
- Molecule 7: 50S ribosomal protein L35



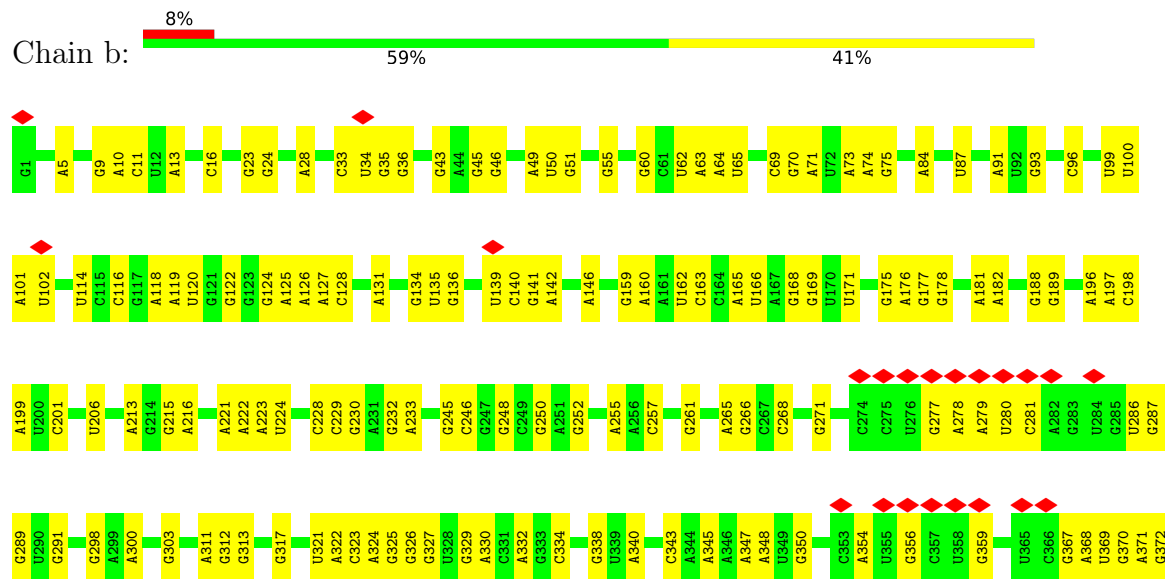
- Molecule 8: 50S ribosomal protein L36

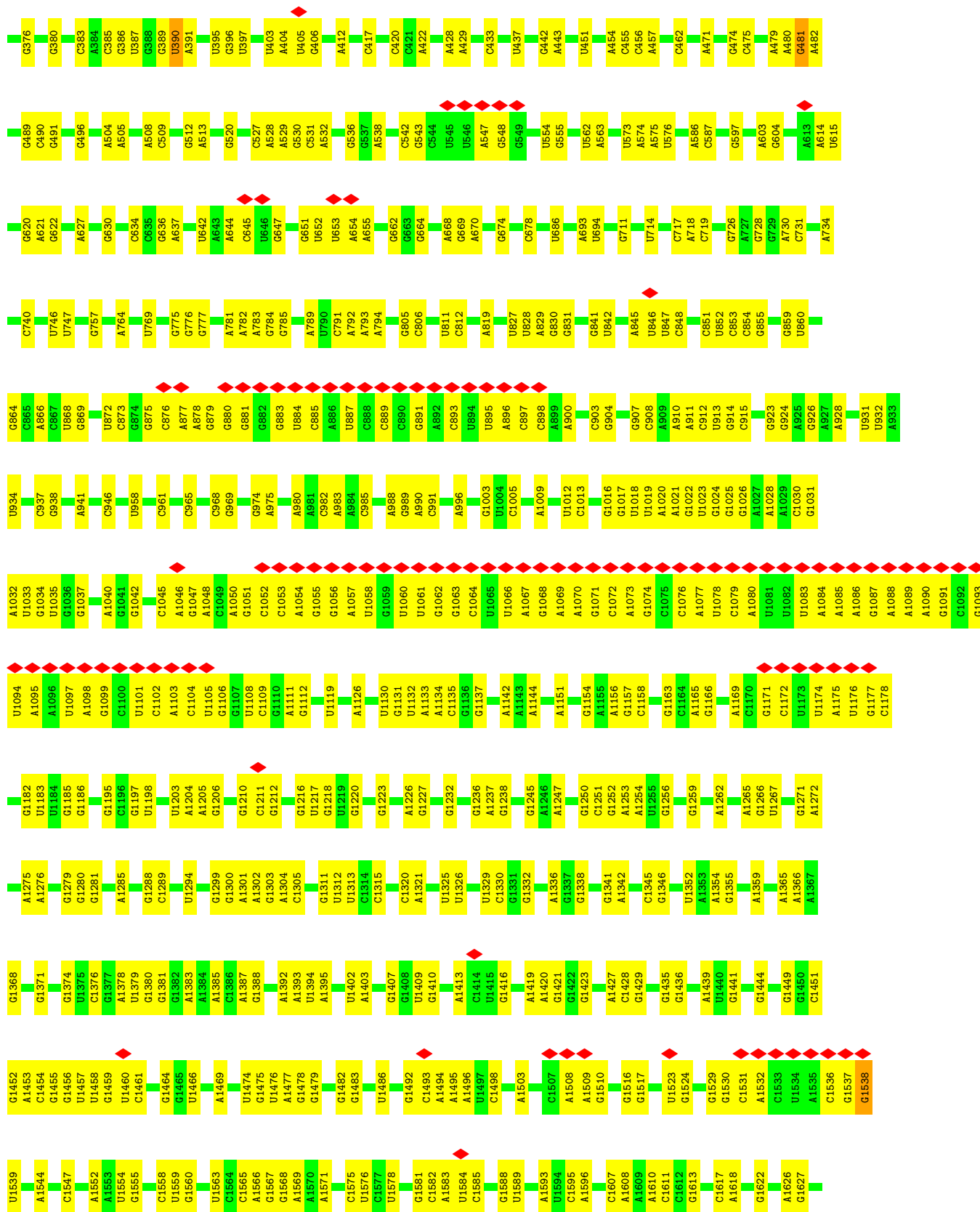


- Molecule 9: 5S rRNA

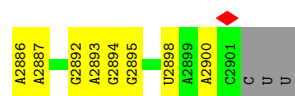


- Molecule 10: 23S rRNA



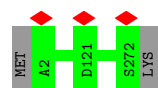


C2773	A2679	G2485	U2404	C2310	A2191	U2131	C2043	G1945	G1849	A1739	A1630
G2777	G2486	G2487	G2405	A2311	U2192	A2132	A2051	U1946	A1853	G1740	A1634
A2778	G2488	G2489	A2406	U2312	G2193	G2133	G2055	A1952	U1856	A1749	A1635
G2780	G2490	G2491	G2407	G2315	U2197	A2134	G2056	A1953	G1857	G1750	G1642
A2781	G2492	U2491	G2408	G2316	A2198	A2135	U2056	G1954	A1858	A1755	G1643
G2782	U2493	G2492	G2409	A2317	A2199	A2136	A2059	U1955	U1756	U1647	U1648
G2783	U2494	G2493	G2410	G2318	U2203	U2137	A2060	C1957	G1862	U1757	G1649
U2790	G2494	G2494	G2416	U2320	G2204	U2138	A2061	C1958	U1863	U1758	U1759
C2795	A2497	A2497	U2419	U2321	U2204	U2139	A2062	C1961	U1864	U1762	A1664
U2796	C2498	G2491	G2420	A2322	A2211	G2140	C2063	C1962	G1869	A1763	A1665
U2797	C2499	C2422	C2422	G2325	A2212	G2141	U2068	U1963	C1870	C1764	G1666
U2798	G2502	U2423	U2423	C2326	U2213	A2142	G2069	G1964	A1871	A1773	G1667
A2799	A2503	C2424	A2425	A2327	C2214	A2143	U2076	C1965	A1872	A1776	A1668
A2800	U2504	A2426	A2426	A2333	A2225	G2144	A2077	A1966	G1873	G1776	A1669
G2801	G2505	C2427	G2428	U2334	G2228	C2145	C2078	C1967	G1874	U1779	G1673
G2802	A2513	G2428	G2428	A2335	G2229	C2146	U2081	A1970	G1875	U1782	G1674
G2803	U2518	G2429	A2430	A2336	G2234	C2147	U2081	U1971	A1882	U1783	C1675
U2804	U2519	U2431	U2431	G2337	G2238	A2148	U2085	G1975	G1883	A1784	G1681
U2807	C2520	A2435	A2435	A2340	G2239	U2149	U2085	G1976	G1884	A1785	A1689
G2808	G2526	A2436	A2436	G2345	U2243	C2150	G2093	G1980	C1887	A1786	U1693
U2818	C2527	C2440	C2440	C2346	U2249	U2151	A2094	A1981	G1888	A1787	C1694
G2819	U2528	U2441	U2441	C2347	G2250	C2152	A2095	C1985	A1889	G1792	G1699
A2820	G2529	G2445	G2445	C2350	G2258	C2153	G2100	C1986	A1890	A1793	A1700
A2821	U2533	G2446	G2446	G2351	U2259	U2154	A2101	A1987	C1895	A1794	A1701
G2822	A2534	A2448	A2448	G2352	C2260	G2155	C2102	U1991	A1899	C1800	G1702
U2832	G2535	A2449	A2449	G2353	C2261	G2156	C2104	G1992	A1900	G1703	G1703
U2833	G2536	G2454	G2454	C2355	C2266	G2157	U2105	C1996	G1906	C1706	G1707
G2834	U2537	G2455	G2455	C2361	A2266	A2158	U2106	C1997	A1805	A1713	U1714
A2835	G2543	U2457	U2457	C2364	A2267	G2159	G2107	A1998	A1913	U1715	U1716
U2836	U2546	G2458	G2458	C2367	A2268	C2161	C2108	C1999	C1914	G1816	G1721
A2837	G2547	A2459	A2459	C2368	A2273	G2162	U2109	G2002	U1917	G1817	G1725
G2843	C2550	G2464	G2464	C2369	A2278	A2163	G2110	A2020	G1921	G1818	G1726
G2848	U2554	A2468	A2468	U2379	G2282	C2164	U2111	C2021	G1922	A1821	A1727
U2849	G2555	G2469	G2469	G2383	C2283	C2165	G2112	U2022	U1923	G1823	C1728
G2859	C2556	A2471	A2471	U2384	G2286	U2166	U2113	C2023	C1924	U1827	U1729
A2860	U2560	G2472	G2472	C2385	U2287	G2167	A2114	G2024	C1925	G1828	U1730
U2861	A2561	U2473	U2473	G2386	A2288	G2168	G2115	U1926	U1927	A1829	G1731
G2864	U2562	U2474	U2474	U2389	G2295	A2169	G2116	A1928	G1929	C1833	C1732
U2865	U2563	C2475	C2475	U2390	U2296	A2170	A2117	A2030	G1930	C1836	G1734
U2866	A2564	U2476	U2476	G2391	A2297	A2171	U2118	A2031	U1931	U1848	G1735
G2867	A2565	G2477	G2477	G2396	A2298	U2172	A2119	G2032	A1937	U1833	U1736
U2871	U2566	U2478	U2478	U2397	G2299	A2173	G2120	U2034	A1938	U1836	U1737
A2879	G2567	C2480	C2480	U2398	U2305	C2174	G2121	C2035	U1939	U1848	G1738
A2883	A2572	G2481	G2481	G2399	C2306	C2175	U2122	C2036	U1940	U1848	G1738
U2884	C2573	A2482	A2482	U2402	G2307	A2176	G2123	U2039	U1944	U1848	G1738
G2885	G2574	G2484	G2484	C2403	G2308	C2177	G2124	U2039	U1944	U1848	G1738



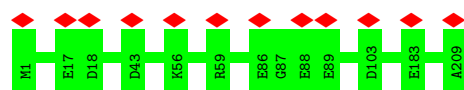
- Molecule 11: 50S ribosomal protein L2

Chain c: 99%



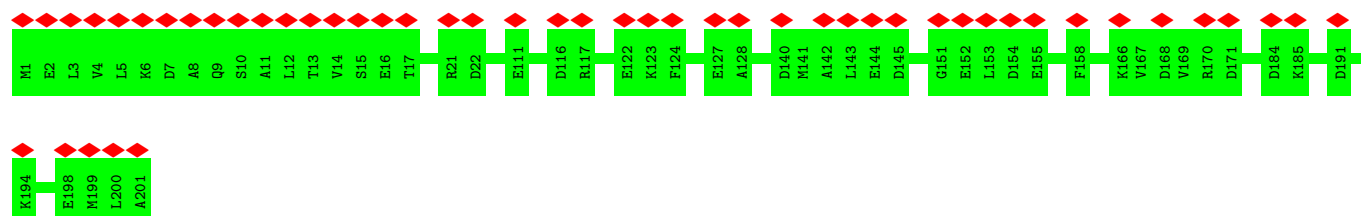
- Molecule 12: 50S ribosomal protein L3

Chain d: 6% 100%



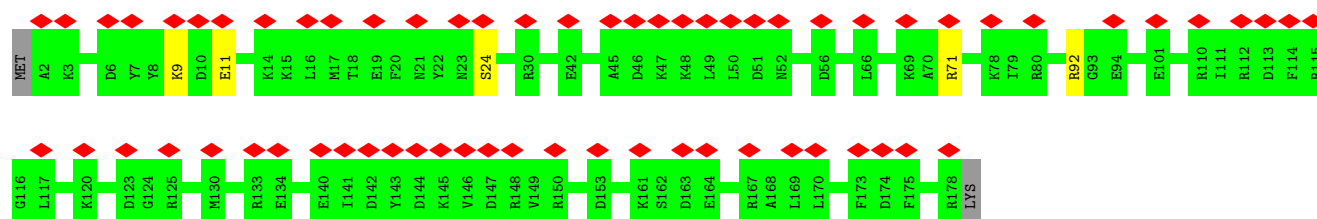
- Molecule 13: 50S ribosomal protein L4

Chain e: 25% 100%



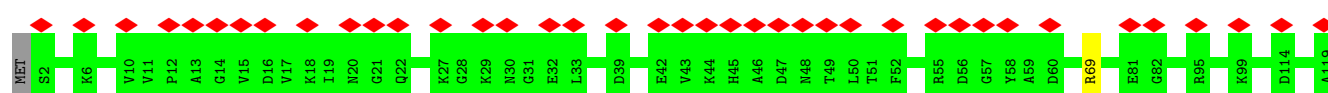
- Molecule 14: 50S ribosomal protein L5

Chain f: 36% 96%



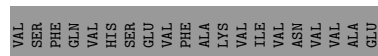
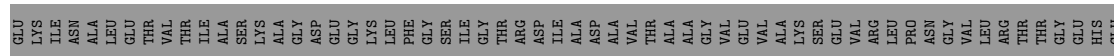
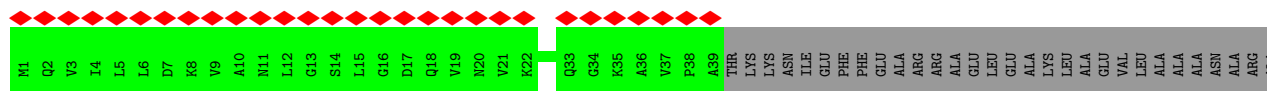
- Molecule 15: 50S ribosomal protein L6

Chain g: 31% 98%

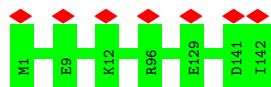




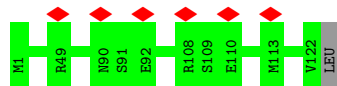
- Molecule 16: 50S ribosomal protein L9



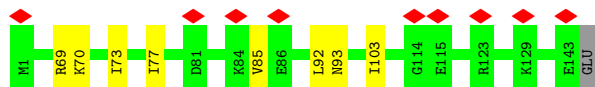
- Molecule 17: 50S ribosomal protein L13



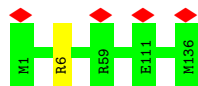
- Molecule 18: 50S ribosomal protein L14



- Molecule 19: 50S ribosomal protein L15

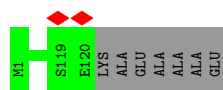


- Molecule 20: 50S ribosomal protein L16

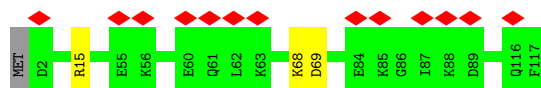


- Molecule 21: 50S ribosomal protein L17

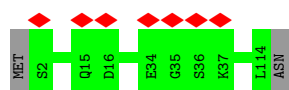




- Molecule 22: 50S ribosomal protein L18



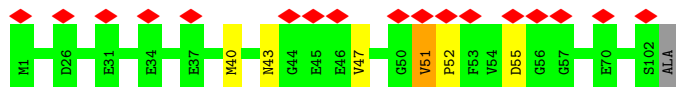
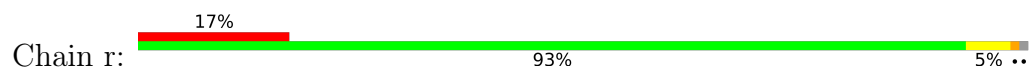
- Molecule 23: 50S ribosomal protein L19



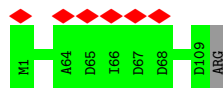
- Molecule 24: 50S ribosomal protein L20



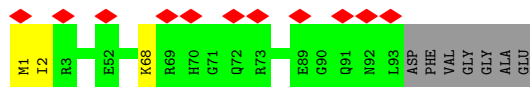
- Molecule 25: 50S ribosomal protein L21



- Molecule 26: 50S ribosomal protein L22

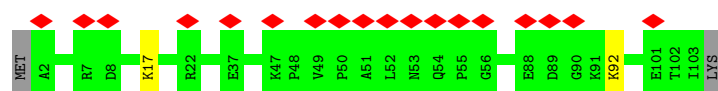


- Molecule 27: 50S ribosomal protein L23

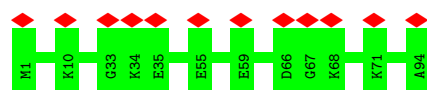


- Molecule 28: 50S ribosomal protein L24





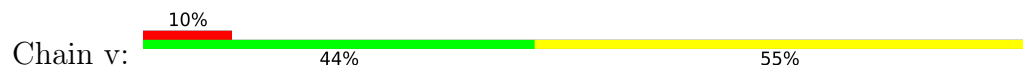
- Molecule 29: 50S ribosomal protein L25



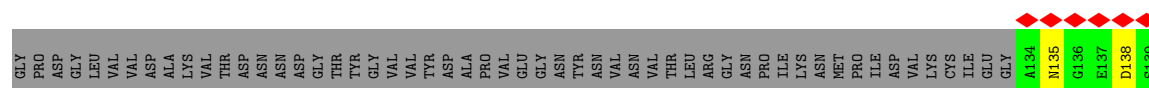
- Molecule 30: 50S ribosomal protein L27



- Molecule 31: Pro-tRNA



- Molecule 32: Gelation factor



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	614463	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	14.45	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.099	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.02965	Depositor
Map size (Å)	411.648, 411.648, 411.648	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.072, 1.072, 1.072	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	0.42	0/635	0.52	0/848
2	1	0.34	0/496	0.51	0/660
3	2	0.37	0/443	0.50	0/593
4	3	0.46	0/440	0.61	0/588
5	4	0.47	0/416	0.60	0/554
6	6	0.38	0/380	0.49	0/498
7	7	0.43	0/513	0.52	0/676
8	8	0.42	0/302	0.50	0/397
9	a	0.74	0/2828	0.79	0/4410
10	b	0.49	0/69757	0.78	7/108827 (0.0%)
11	c	0.43	0/2121	0.54	0/2852
12	d	0.43	0/1586	0.53	0/2134
13	e	0.39	0/1571	0.49	0/2113
14	f	0.39	0/1434	0.57	0/1926
15	g	0.38	0/1343	0.53	0/1816
16	h	0.34	0/290	0.64	0/392
17	j	0.44	0/1152	0.52	0/1551
18	k	0.44	0/947	0.53	0/1268
19	l	0.50	0/1052	0.59	0/1401
20	m	0.41	0/1093	0.55	0/1460
21	n	0.42	0/973	0.51	0/1301
22	o	0.42	0/902	0.56	0/1209
23	p	0.44	0/920	0.49	0/1231
24	q	0.49	0/960	0.48	0/1278
25	r	0.49	0/823	0.57	0/1100
26	s	0.40	0/852	0.50	0/1142
27	t	0.40	0/744	0.50	0/994
28	u	0.42	0/787	0.57	0/1051
29	w	0.39	0/766	0.50	0/1025
30	y	0.44	0/627	0.57	0/829
31	v	0.52	0/1817	0.82	1/2832 (0.0%)
32	z	0.65	0/291	0.70	0/400
All	All	0.48	0/99261	0.73	8/149356 (0.0%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b	2864	G	C2'-C3'-O3'	7.82	126.69	109.50
10	b	1595	C	C2'-C3'-O3'	7.31	125.58	109.50
10	b	1626	A	C2'-C3'-O3'	6.64	124.33	113.70
10	b	9	G	C2'-C3'-O3'	6.20	123.63	113.70
10	b	481	G	C1'-O4'-C4'	-6.18	104.96	109.90

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	625	0	652	4	0
2	1	495	0	526	12	0
3	2	439	0	482	5	0
4	3	434	0	445	8	0
5	4	409	0	440	8	0
6	6	377	0	418	0	0
7	7	504	0	572	2	0
8	8	301	0	341	3	0
9	a	2529	0	1281	0	0
10	b	62281	0	31323	0	0
11	c	2082	0	2154	0	0
12	d	1565	0	1616	0	0
13	e	1552	0	1619	0	0
14	f	1410	0	1444	0	0
15	g	1323	0	1371	0	0
16	h	287	0	307	0	0
17	j	1129	0	1162	0	0
18	k	938	0	1012	0	0
19	l	1043	0	1123	0	0
20	m	1074	0	1157	0	0
21	n	960	0	1000	0	0
22	o	892	0	923	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	p	908	0	956	0	0
24	q	947	0	1019	0	0
25	r	810	0	834	0	0
26	s	845	0	909	0	0
27	t	738	0	807	0	0
28	u	779	0	831	0	0
29	w	753	0	780	0	0
30	y	619	0	642	0	0
31	v	1626	0	821	0	0
32	z	277	0	250	0	0
All	All	90951	0	59217	42	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 42 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:54:VAL:HG23	4:3:55:ILE:HG12	1.70	0.73
4:3:40:ARG:HG3	4:3:41:HIS:ND1	2.08	0.68
2:1:2:LYS:HE3	2:1:6:LEU:HD11	1.79	0.64
2:1:11:VAL:O	2:1:15:ASN:ND2	2.30	0.64
2:1:36:GLN:N	2:1:36:GLN:OE1	2.33	0.62

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
2	1	59/63 (94%)	56 (95%)	3 (5%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	2	55/59 (93%)	53 (96%)	2 (4%)	0	100	100
4	3	53/57 (93%)	49 (92%)	4 (8%)	0	100	100
5	4	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
6	6	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
7	7	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
8	8	36/50 (72%)	35 (97%)	1 (3%)	0	100	100
11	c	269/273 (98%)	258 (96%)	11 (4%)	0	100	100
12	d	207/209 (99%)	197 (95%)	10 (5%)	0	100	100
13	e	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
14	f	175/179 (98%)	164 (94%)	10 (6%)	1 (1%)	22	23
15	g	174/177 (98%)	159 (91%)	15 (9%)	0	100	100
16	h	37/149 (25%)	32 (86%)	5 (14%)	0	100	100
17	j	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
18	k	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
19	l	141/144 (98%)	132 (94%)	9 (6%)	0	100	100
20	m	134/136 (98%)	133 (99%)	1 (1%)	0	100	100
21	n	118/127 (93%)	111 (94%)	7 (6%)	0	100	100
22	o	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
23	p	111/115 (96%)	110 (99%)	1 (1%)	0	100	100
24	q	115/118 (98%)	115 (100%)	0	0	100	100
25	r	100/103 (97%)	93 (93%)	5 (5%)	2 (2%)	6	4
26	s	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
27	t	91/100 (91%)	87 (96%)	4 (4%)	0	100	100
28	u	100/104 (96%)	83 (83%)	17 (17%)	0	100	100
29	w	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
30	y	80/85 (94%)	76 (95%)	3 (4%)	1 (1%)	10	8
32	z	31/148 (21%)	23 (74%)	6 (19%)	2 (6%)	1	0
All	All	3087/3427 (90%)	2937 (95%)	144 (5%)	6 (0%)	45	52

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	r	52	PRO

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
32	z	148	VAL
25	r	51	VAL
30	y	44	LYS
14	f	71	ARG

### 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	67/68 (98%)	67 (100%)	0	100	100
2	1	54/55 (98%)	54 (100%)	0	100	100
3	2	47/49 (96%)	47 (100%)	0	100	100
4	3	46/48 (96%)	44 (96%)	2 (4%)	25	32
5	4	45/49 (92%)	45 (100%)	0	100	100
6	6	38/38 (100%)	37 (97%)	1 (3%)	41	54
7	7	51/52 (98%)	51 (100%)	0	100	100
8	8	34/44 (77%)	34 (100%)	0	100	100
11	c	216/218 (99%)	216 (100%)	0	100	100
12	d	164/164 (100%)	164 (100%)	0	100	100
13	e	165/165 (100%)	165 (100%)	0	100	100
14	f	148/150 (99%)	144 (97%)	4 (3%)	40	53
15	g	137/138 (99%)	135 (98%)	2 (2%)	60	75
16	h	30/114 (26%)	30 (100%)	0	100	100
17	j	116/116 (100%)	116 (100%)	0	100	100
18	k	103/104 (99%)	103 (100%)	0	100	100
19	l	102/103 (99%)	94 (92%)	8 (8%)	10	11
20	m	109/109 (100%)	108 (99%)	1 (1%)	75	86
21	n	100/103 (97%)	100 (100%)	0	100	100
22	o	86/87 (99%)	83 (96%)	3 (4%)	31	41

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	p	98/100 (98%)	98 (100%)	0	100	100
24	q	89/90 (99%)	89 (100%)	0	100	100
25	r	84/84 (100%)	79 (94%)	5 (6%)	16	19
26	s	92/93 (99%)	92 (100%)	0	100	100
27	t	80/84 (95%)	77 (96%)	3 (4%)	28	37
28	u	83/85 (98%)	81 (98%)	2 (2%)	44	57
29	w	78/78 (100%)	78 (100%)	0	100	100
30	y	61/63 (97%)	61 (100%)	0	100	100
32	z	29/121 (24%)	14 (48%)	15 (52%)	0	0
All	All	2552/2772 (92%)	2506 (98%)	46 (2%)	54	69

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	t	68	LYS
32	z	145	THR
28	u	17	LYS
32	z	138	ASP
32	z	148	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
20	m	45	GLN
22	o	67	ASN
28	u	69	ASN
23	p	12	GLN
25	r	11	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	b	2900/2904 (99%)	1194 (41%)	0
31	v	75/77 (97%)	41 (54%)	0
9	a	117/120 (97%)	21 (17%)	0
All	All	3092/3101 (99%)	1256 (40%)	0



5 of 1256 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	a	25	U
9	a	26	C
9	a	30	C
9	a	32	U
9	a	35	C

There are no RNA pucker outliers to report.

## 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.

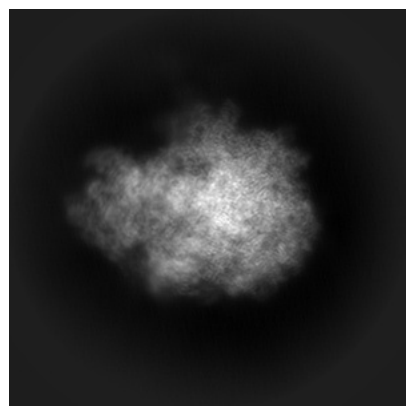
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14850. These allow visual inspection of the internal detail of the map and identification of artifacts.

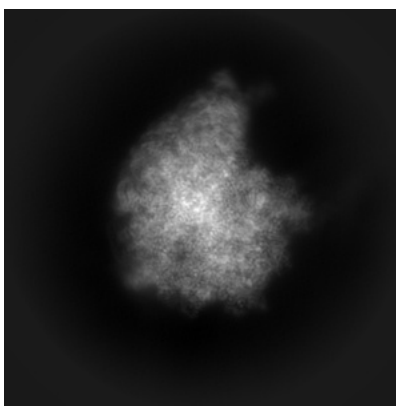
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

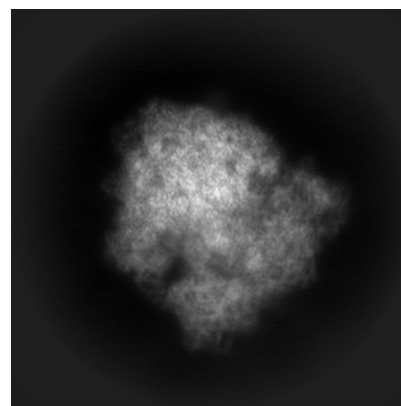
#### 6.1.1 Primary map



X

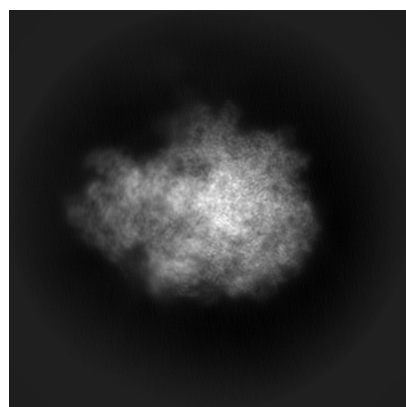


Y

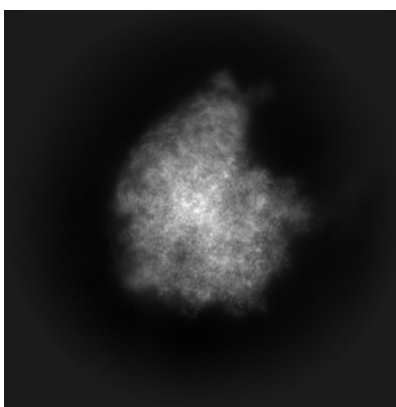


Z

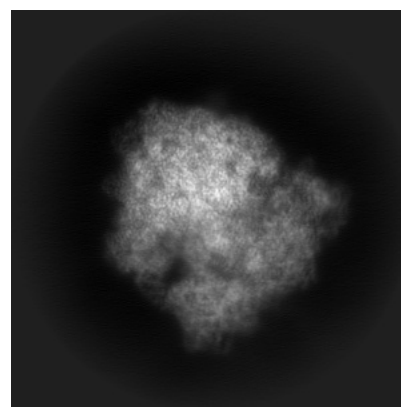
#### 6.1.2 Raw map



X



Y

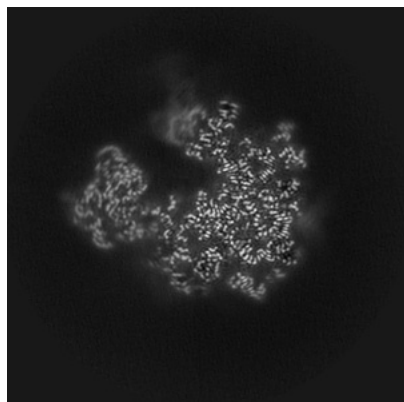


Z

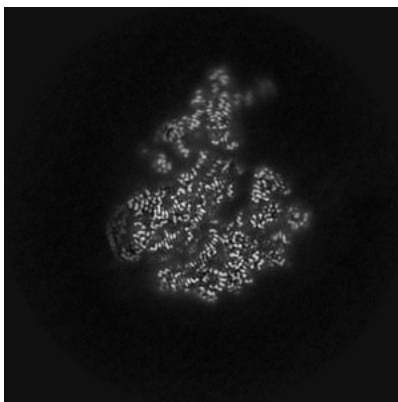
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

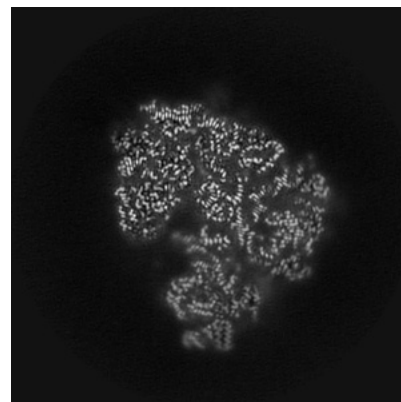
### 6.2.1 Primary map



X Index: 192

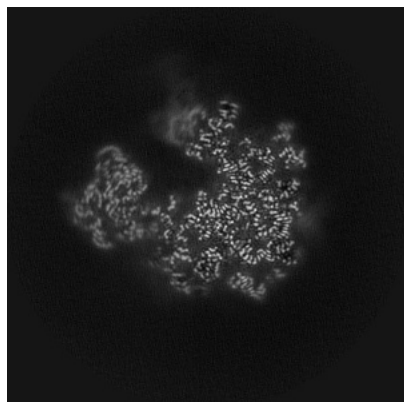


Y Index: 192

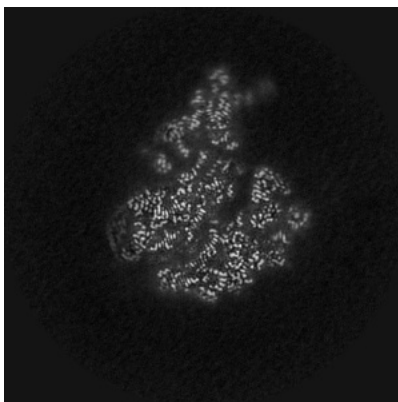


Z Index: 192

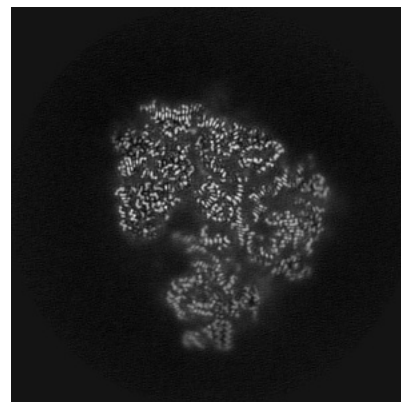
### 6.2.2 Raw map



X Index: 192



Y Index: 192

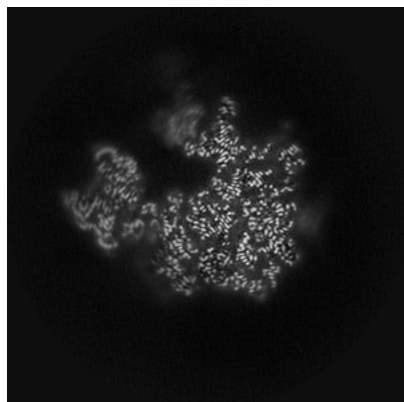


Z Index: 192

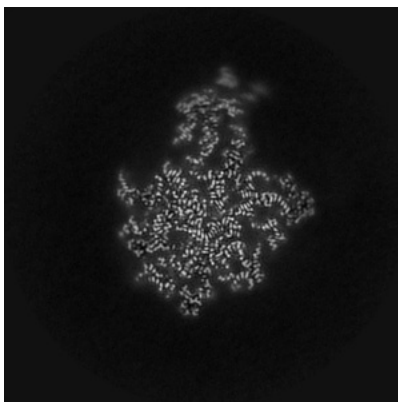
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

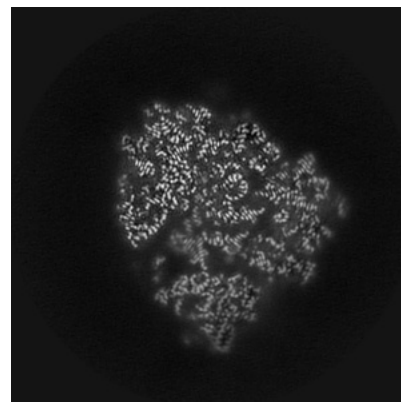
### 6.3.1 Primary map



X Index: 197

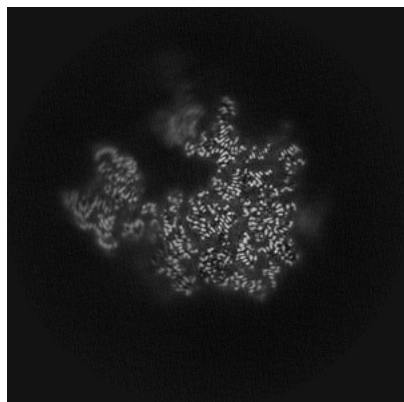


Y Index: 211

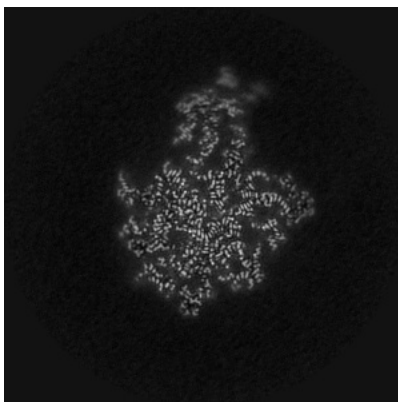


Z Index: 198

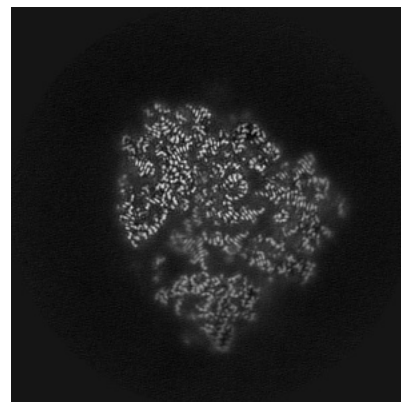
### 6.3.2 Raw map



X Index: 197



Y Index: 211

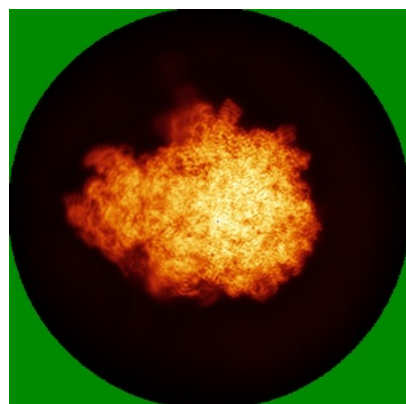


Z Index: 198

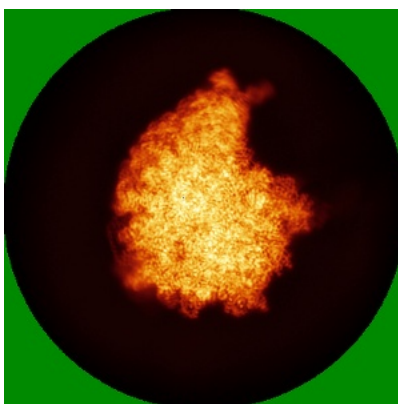
The images above show the largest variance slices of the map in three orthogonal directions.

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

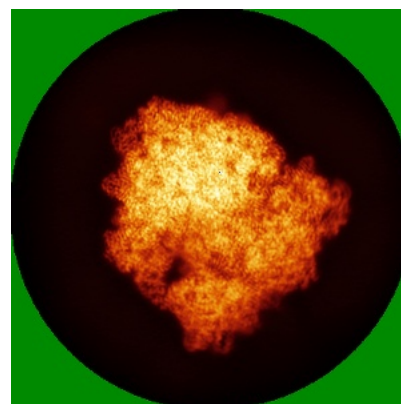
### 6.4.1 Primary map



X



Y

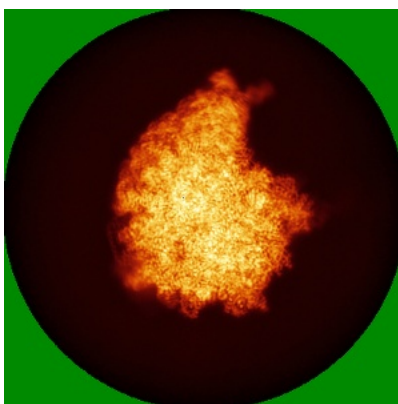


Z

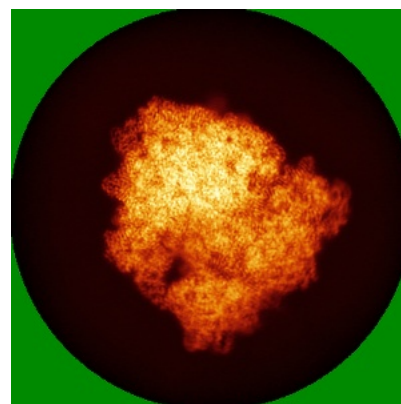
### 6.4.2 Raw map



X



Y

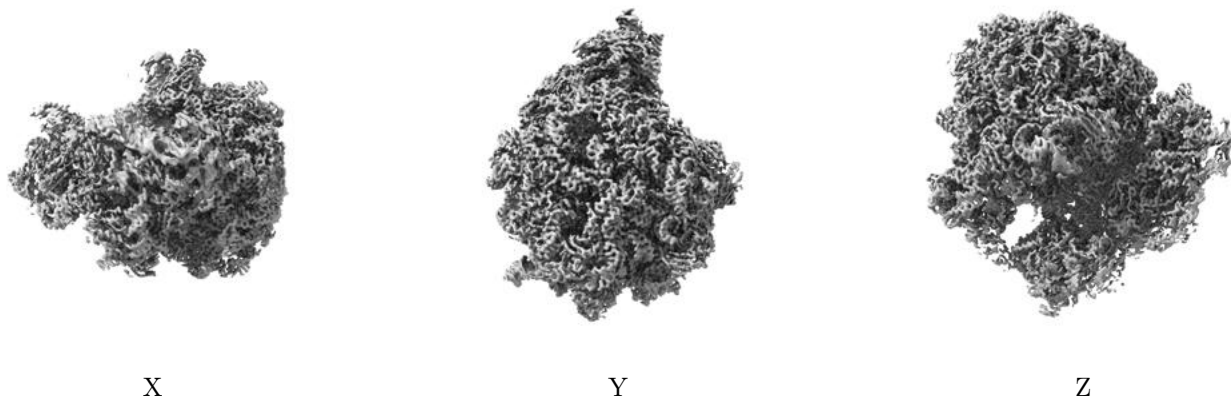


Z

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.

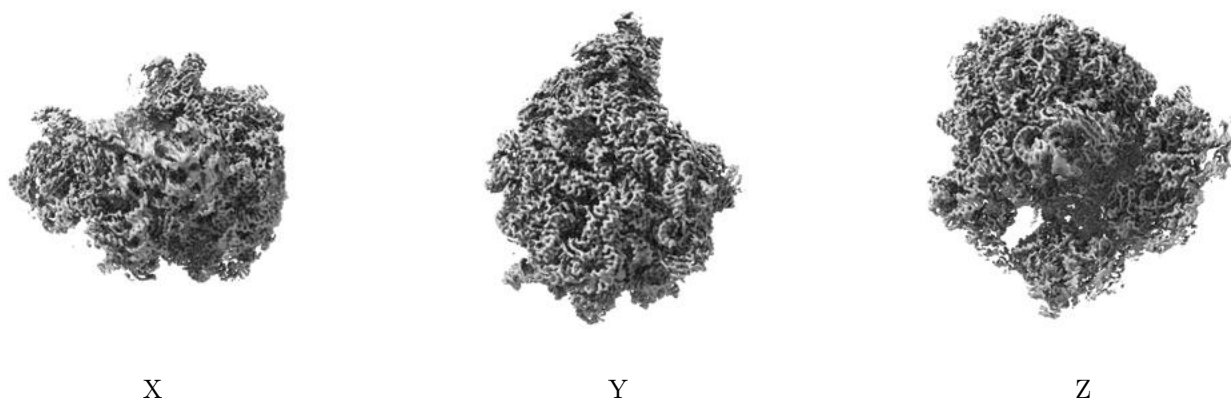
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02965. 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](#)

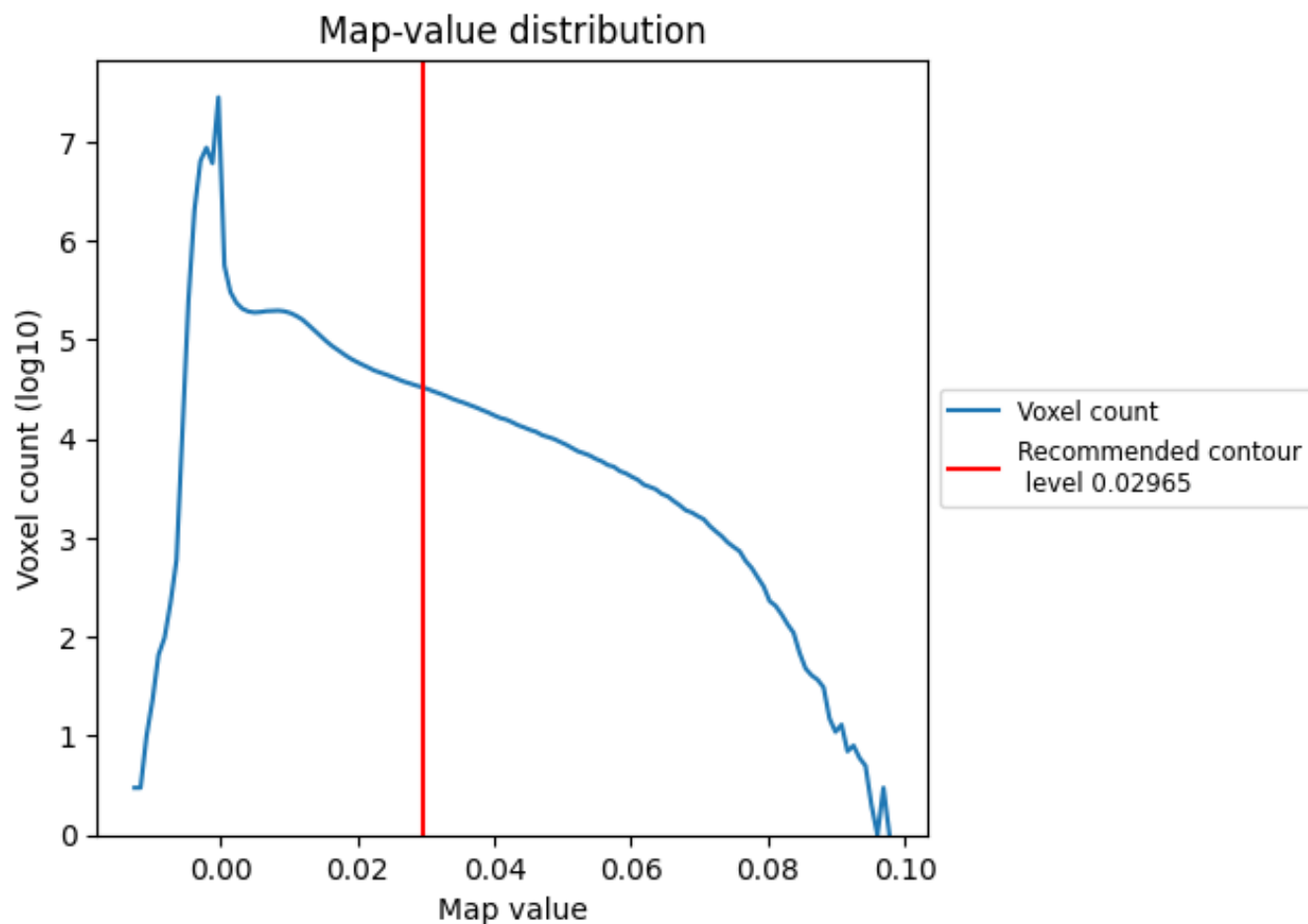
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

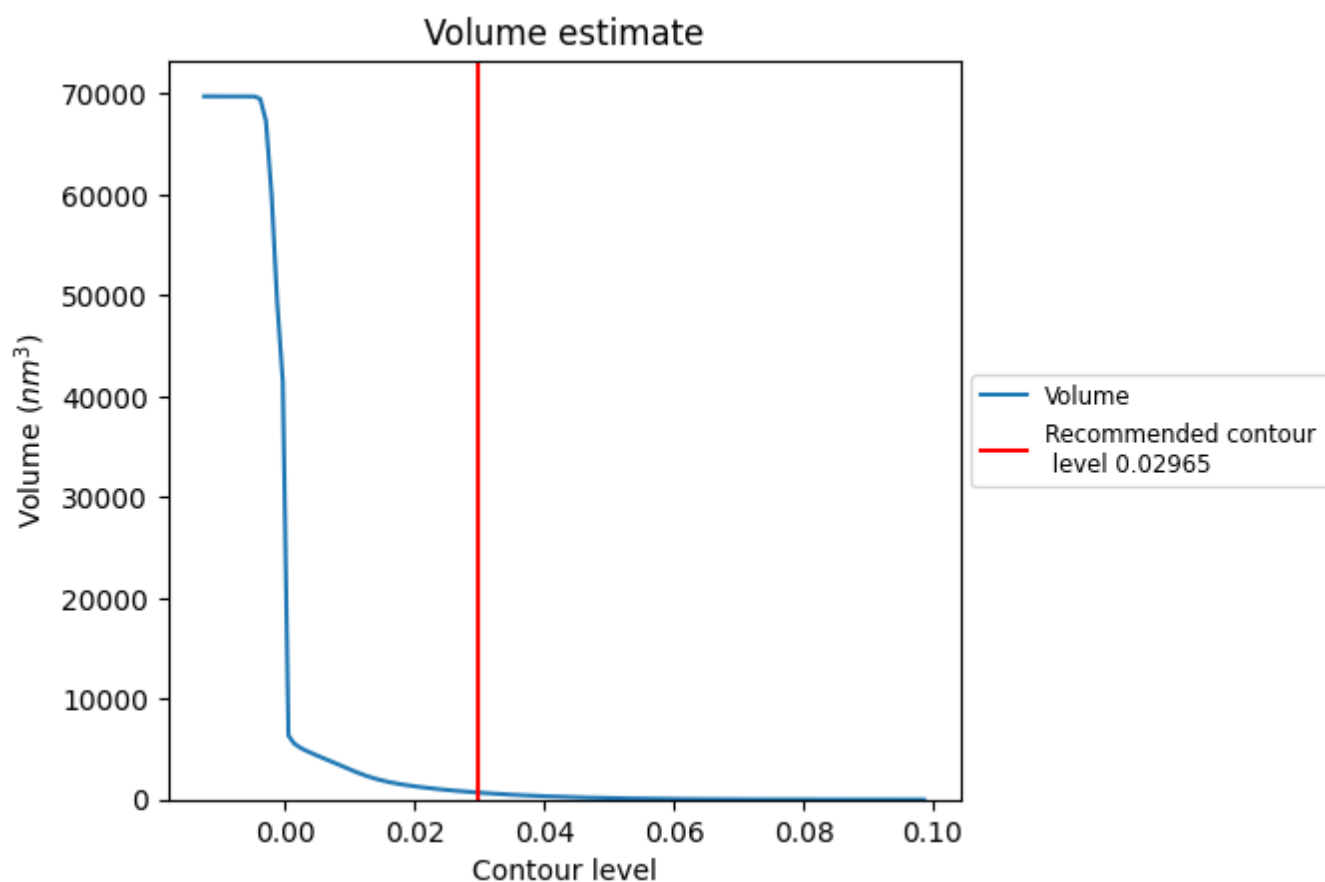
This section contains the results of statistical analysis of the map.

### 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](#)

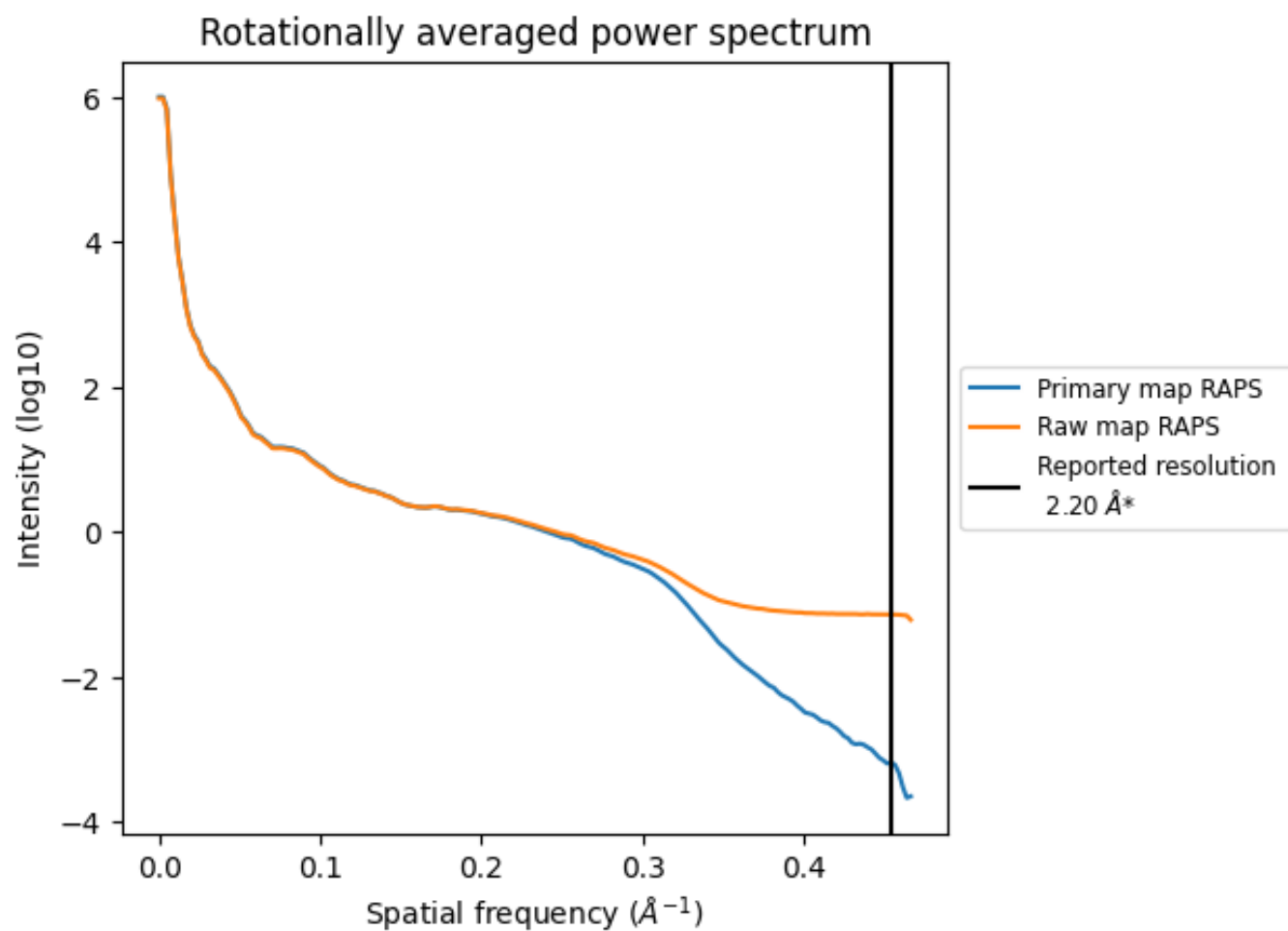


The volume at the recommended contour level is 698  $\text{nm}^3$ ; this corresponds to an approximate mass of 631 kDa.

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 ⓘ

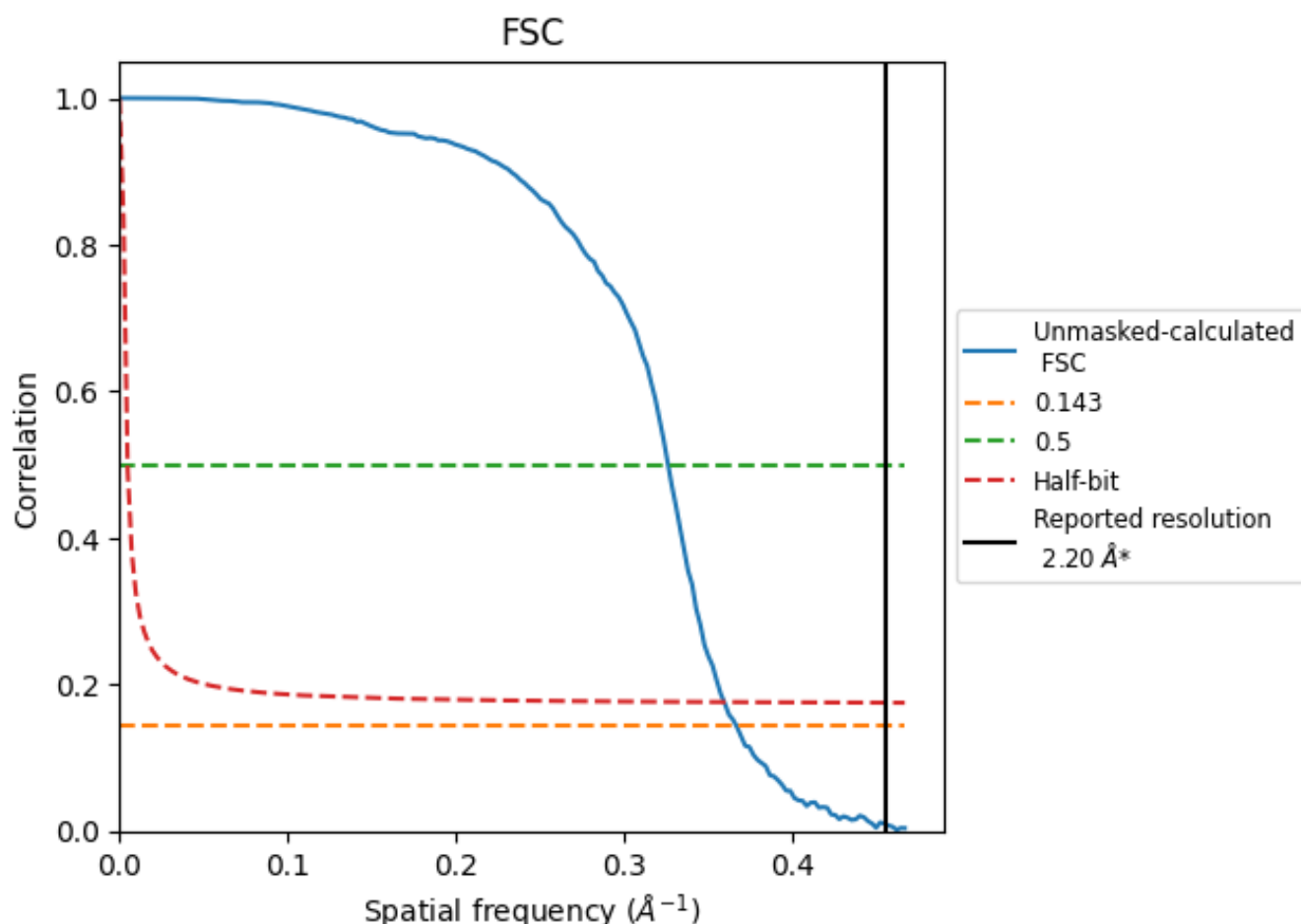


\*Reported resolution corresponds to spatial frequency of 0.455  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.455 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

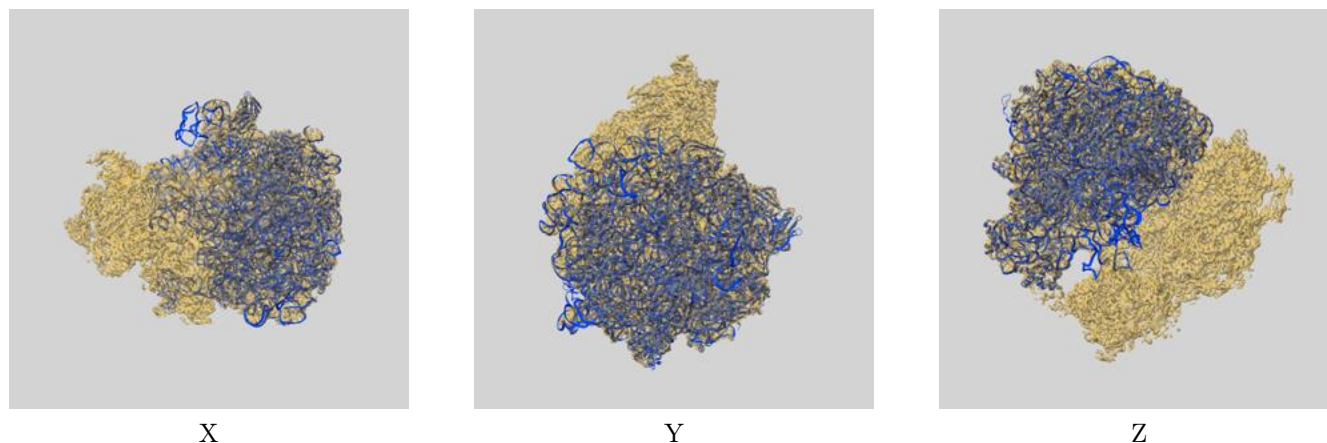
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.73	3.07	2.78

\*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 2.73 differs from the reported value 2.2 by more than 10 %

## 9 Map-model fit [i](#)

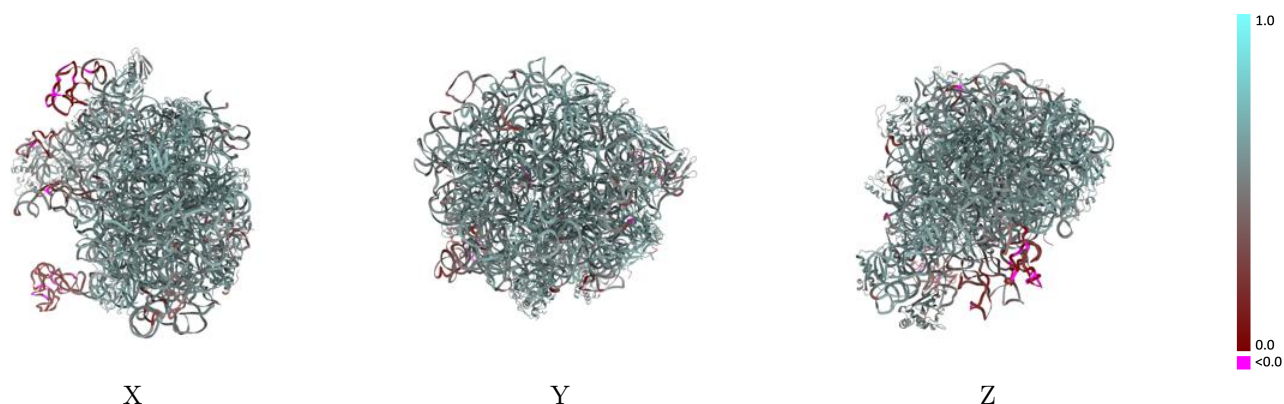
This section contains information regarding the fit between EMDB map EMD-14850 and PDB model 7ZP8. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

### 9.1 Map-model overlay [i](#)



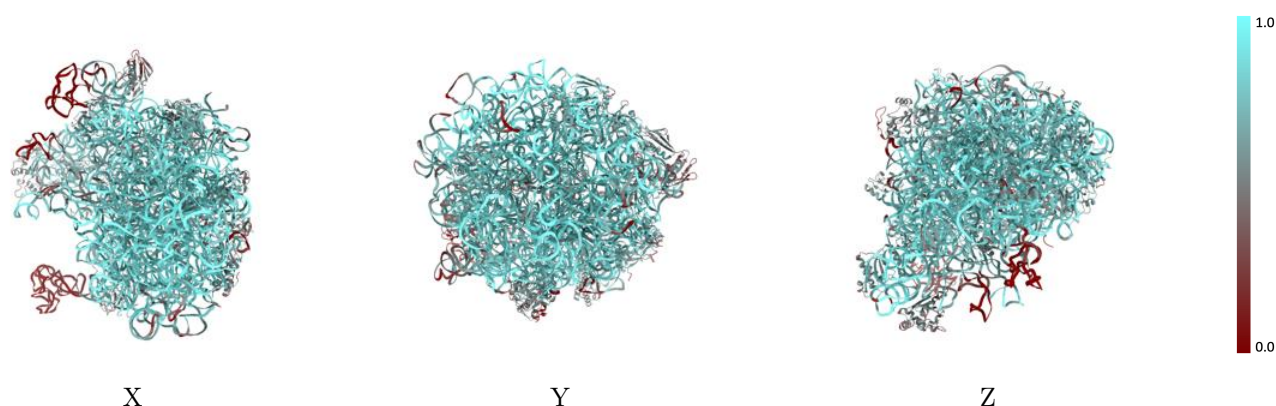
The images above show the 3D surface view of the map at the recommended contour level 0.02965 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



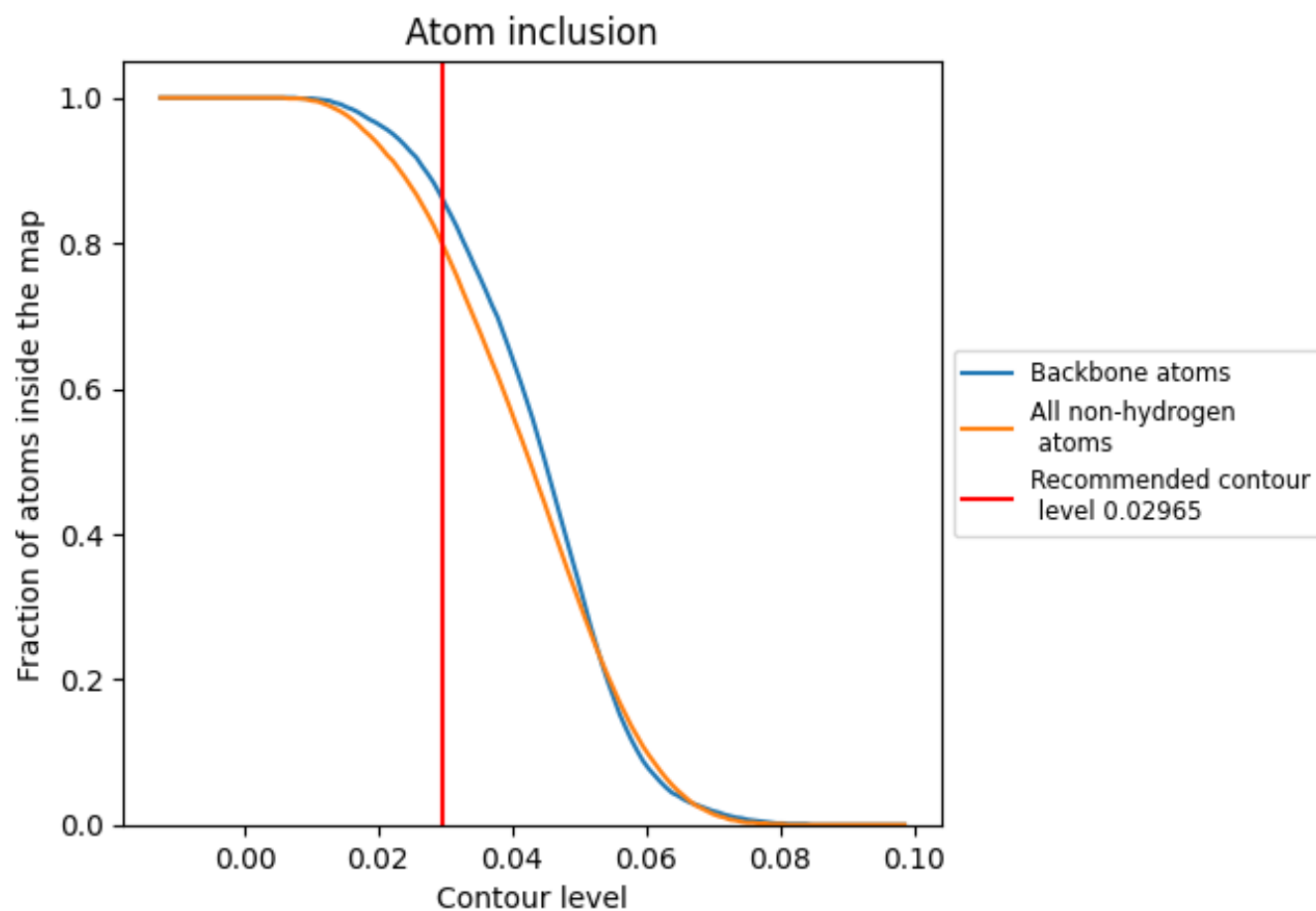
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02965).



































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 80% 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 (0.02965) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7970	 0.5450
0	 0.8050	 0.6060
1	 0.5900	 0.5440
2	 0.7490	 0.5970
3	 0.7490	 0.5780
4	 0.6230	 0.5630
6	 0.9150	 0.6310
7	 0.8660	 0.6240
8	 0.7770	 0.6060
a	 0.8650	 0.5650
b	 0.8380	 0.5330
c	 0.8400	 0.6180
d	 0.7650	 0.6110
e	 0.6060	 0.5800
f	 0.4740	 0.5080
g	 0.4990	 0.5400
h	 0.1970	 0.4970
j	 0.7710	 0.5980
k	 0.7360	 0.6060
l	 0.7310	 0.5870
m	 0.7730	 0.6040
n	 0.8080	 0.6130
o	 0.6360	 0.5540
p	 0.7530	 0.6060
q	 0.8090	 0.6100
r	 0.6570	 0.5740
s	 0.7590	 0.6060
t	 0.6510	 0.5780
u	 0.5500	 0.5500
v	 0.6440	 0.4040
w	 0.6580	 0.5880
y	 0.7550	 0.5950
z	 0.1780	 0.3270

