



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:21 AM UTC

PDB ID : 7SSN / pdb_00007ssn
EMDB ID : EMD-25410
Title : Pre translocation 70S ribosome with A/P* and P/E tRNA (Structure II-B)
Authors : Carbone, C.E.; Korostelev, A.A.
Deposited on : 2021-11-11
Resolution : 3.20 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

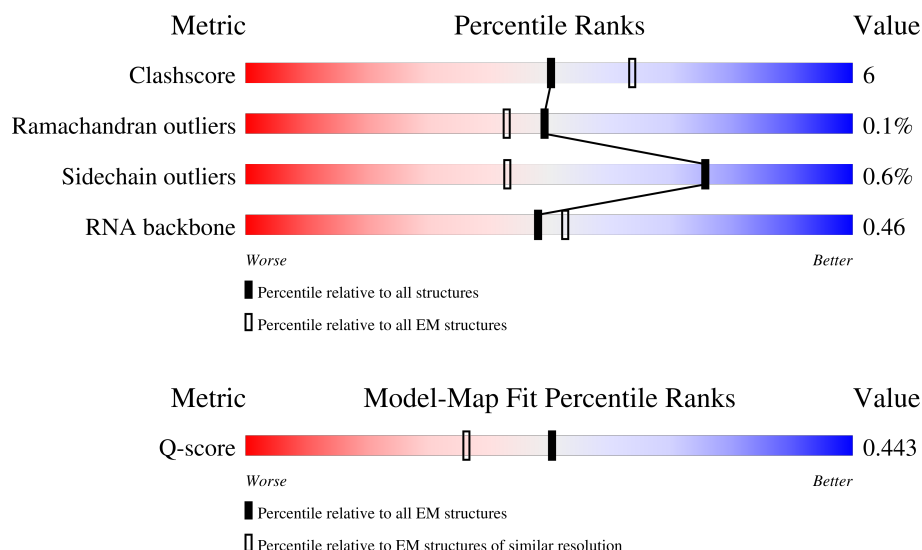
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



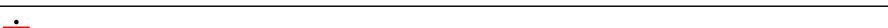
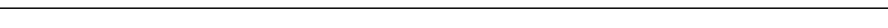
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	3	1539	
2	1	2903	
3	2	120	

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Mol	Chain	Length	Quality of chain
4	5	77	
5	b	271	
6	c	209	
7	d	201	
8	e	177	
9	f	176	
10	i	141	
11	j	142	
12	k	122	
13	l	143	
14	m	136	
15	n	120	
16	o	116	
17	p	114	
18	q	117	
19	r	103	
20	s	110	
21	t	93	
22	u	102	
23	v	94	
24	w	75	
25	x	77	
26	y	63	
27	z	58	
28	B	56	

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Mol	Chain	Length	Quality of chain
29	C	50	
30	D	46	
31	E	64	
32	F	38	
33	4	35	
34	6	77	
35	G	225	
36	H	206	
37	I	205	
38	J	157	
39	K	100	
40	L	151	
41	M	129	
42	N	127	
43	O	98	
44	P	116	
45	Q	123	
46	R	114	
47	S	100	
48	T	88	
49	U	82	
50	V	80	
51	W	65	
52	X	79	
53	Y	85	

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Mol	Chain	Length	Quality of chain
54	Z	65	 72%28%

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 145435 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 2 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

- Molecule 4 is a RNA chain called tRNA Pro.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		

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

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

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

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

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

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

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

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

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

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

- Molecule 10 is a protein called 50S ribosomal protein L11.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	u	102	Total	C	N	O		0	0
			780	492	146	142			

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

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

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

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

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

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

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

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

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

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

- Molecule 28 is a protein called 50S ribosomal protein L32.

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

- Molecule 29 is a protein called 50S ribosomal protein L33.

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

- Molecule 30 is a protein called 50S ribosomal protein L34.

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

- Molecule 31 is a protein called 50S ribosomal protein L35.

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

- Molecule 32 is a protein called 50S ribosomal protein L36.

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

- Molecule 33 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	4	19	Total	C	N	O	P	0	0
			413	186	85	124	18		

- Molecule 34 is a RNA chain called tRNA fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 35 is a protein called 30S ribosomal protein S2.

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

- Molecule 36 is a protein called 30S ribosomal protein S3.

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

- Molecule 37 is a protein called 30S ribosomal protein S4.

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

- Molecule 38 is a protein called 30S ribosomal protein S5.

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

- Molecule 39 is a protein called 30S ribosomal protein S6.

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

- Molecule 40 is a protein called 30S ribosomal protein S7.

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

- Molecule 41 is a protein called 30S ribosomal protein S8.

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

- Molecule 42 is a protein called 30S ribosomal protein S9.

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

- Molecule 43 is a protein called 30S ribosomal protein S10.

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

- Molecule 44 is a protein called 30S ribosomal protein S11.

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

- Molecule 45 is a protein called 30S ribosomal protein S12.

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

- Molecule 46 is a protein called 30S ribosomal protein S13.

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

- Molecule 47 is a protein called 30S ribosomal protein S14.

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

- Molecule 48 is a protein called 30S ribosomal protein S15.

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

- Molecule 49 is a protein called 30S ribosomal protein S16.

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

- Molecule 50 is a protein called 30S ribosomal protein S17.

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

- Molecule 51 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 52 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 53 is a protein called 30S ribosomal protein S20.

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

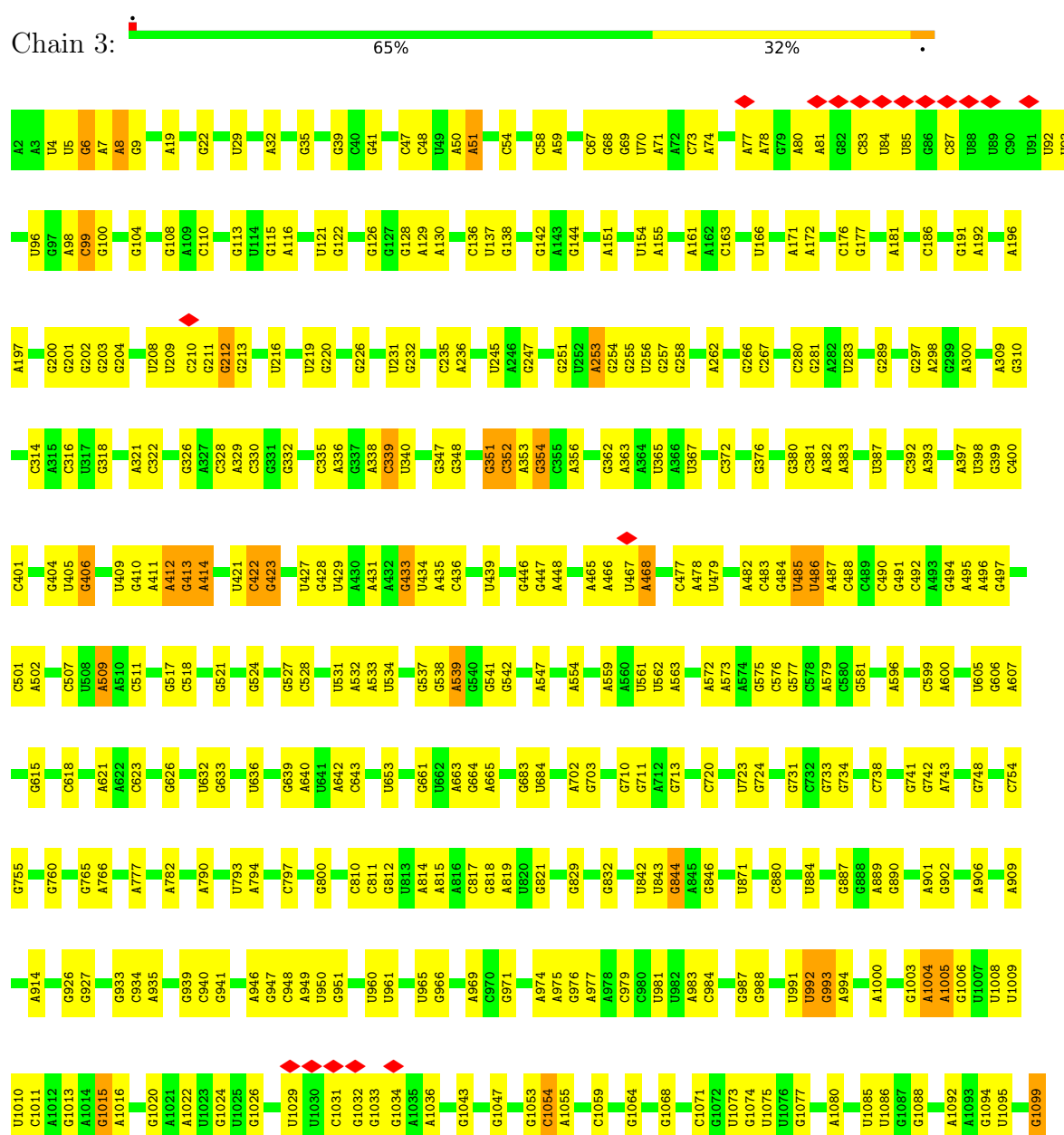
- Molecule 54 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

3 Residue-property plots

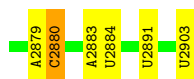
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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





C2752	U2613	G2490	U2384	G2250	G2150	A2071	U1955	A1808	G1674	G1514	A1365	U1249	G1112
U2756	U2614	U2491	C2385	U2257	G2152	C2072	U1956	A1809	G1682	A1515	A1366	G1250	U1113
A2757	U2615	U2492	G2391	G2276	C2153	A2077	A1960	G1811	U1688	A1522	G1367	A1253	G1114
A2758	C2620	C2498	C2394	G2279	U2155	C2078	U1963	G1816	G1695	G1524	G1368	U1254	G1115
A2764	G2621	U2500	C2395	C2283	G2156	A2087	G1964	G1817	G1898	A1528	U1379	A1255	C1118
A2765	G2629	G2502	G2396	C2285	G2157	A2088	U1965	U1816	G1895	A1532	A1383	G1256	U1119
A2778	U2641	A2503	U2402	C2287	A2158	G2092	A1966	G1819	A1698	A1533	A1386	A1265	G1120
G2780	G2642	U2504	G2403	A2288	G2159	C2093	C1967	U1820	G1699	A1534	A1387	G1271	G1124
C2788	C2646	G2505	U2404	A2287	G2162	A2094	U1971	G1826	G1703	A1535	U1394	A1272	A1126
G2791	U2647	U2514	A2405	A2288	C2165	A2095	G1972	U1827	G1715	A1536	A1403	A1273	A1127
G2791	G2648	A2516	A2406	A2288	U2166	C2096	G1972	G1828	U1716	A1537	A1403	A1274	G1128
G2793	C2651	G2517	A2407	A2288	U2167	A2097	G1980	A1829	G1733	G1538	A1427	U1275	U1129
C2794	A2654	A2518	G2409	C2300	G2168	U2099	U1981	C1833	G1738	U1542	G1416	G1278	U1130
A2799	C2658	U2522	A2412	U2306	U2172	C2104	U1982	G1842	G1743	G1543	A1419	U1294	U1131
A2800	A2665	U2533	A2418	A2309	A2173	G2107	U1991	C1843	G1750	G1544	A1420	A1133	A1133
G2801	A2665	A2534	U2423	A2310	C2174	A2108	G1992	G1857	G1756	U1558	C1428	G1296	A1134
G2808	G2669	G2535	U2424	A2311	G2175	U2109	U1993	G1867	A1764	U1559	A1437	A1300	A1135
A2809	G2673	A2547	A2425	A2312	G2177	G2110	C1997	C1868	A1755	G1560	U1438	A1301	A1142
G2811	G2674	U2554	A2426	C2313	C2178	U2111	U1999	G1869	U1757	C1585	C1447	C1305	A1151
U2817	A2682	C2559	G2428	A2314	U2182	G2112	C2000	A1871	U1758	A1570	G1448	C1311	A1165
U2818	C2683	A2560	A2430	U2321	U2192	A2114	G2002	U1880	C1764	A1583	G1449	C1314	C1172
G2819	C2683	A2560	A2435	A2322	A2198	U2118	G2010	G1884	A1756	U1584	C1461	U1325	U1173
A2820	G2688	A2564	U2438	A2325	A2199	A2119	A2020	G1884	A1757	C1585	C1462	U1326	U1174
A2823	U2689	A2565	A2439	C2326	U2203	G2120	C2021	A1901	U1758	A1587	A1469	U1329	G1179
U2833	U2690	C2567	A2440	A2327	G2204	U2121	U2022	G1905	C1764	G1588	G1471	C1330	U1180
U2845	G2709	A2572	U2441	A2328	C2208	G2123	G2024	G1906	C1766	A1586	G1475	G1331	U1181
G2846	C2714	G2574	G2445	U2334	A2211	A2126	G2029	G1907	U1779	U1594	G1478	G1341	G1182
U2847	C2715	C2574	G2446	A2335	A2212	G2125	A2030	G1906	A1784	A1603	G1482	C1345	G1186
G2848	C2716	C2579	G2447	A2336	U2213	U2130	A2031	G1929	A1785	A1618	A1490	C1351	A1205
C2855	U2720	U2584	A2448	G2345	U2219	U2131	A2032	G1929	G1788	U1647	G1491	U1352	G1206
U2847	A2722	U2586	A2461	C2350	U2220	G2133	A2033	G1930	A1791	U1648	A1494	A1353	C1211
G2857	A2726	A2587	A2469	C2354	G2221	A2135	U2039	G1930	G1797	G1649	A1496	G1355	G1212
C2855	U2728	C2594	A2476	C2354	G2222	G2138	C2043	A1936	C1800	U1657	A1503	A1358	G1223
G2857	A2732	G2595	U2477	G2357	G2223	U2139	G2049	A1937	A1801	G1680	A1509	G1360	G1236
A2860	A2733	A2598	G2481	G2357	U2229	G2140	C2055	A1938	G1807	G1667	G1510	C1363	A1247
U2861	U2743	A2602	A2482	G2361	G2230	A2141	G2056	U1939	A1791			G1364	G1248
G2864	G2744	G2603	C2483	C2362	U2231	A2143	A2060	U1940	G1797				
G2867	A2748	C2606	G2485	G2370	U2232	G2144	A2061	U1943	C1800				
A2868	A2749	G2607	C2486	A2381	U2234	C2145	A2062	U1944	A1801				
U2869	A2750	G2608	G2487	G2383	G2238	A2147	U2068	G1945	A1802				
A2873	G2751	U2609	U2489	G2383	G2239	U2149	A2070	G1954	G1807				



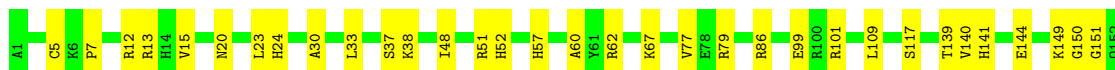
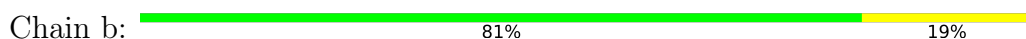
• Molecule 3: 5S rRNA



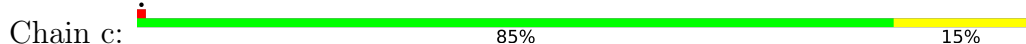
• Molecule 4: tRNA Pro



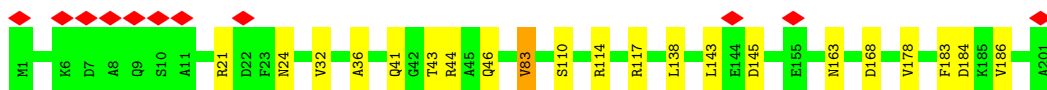
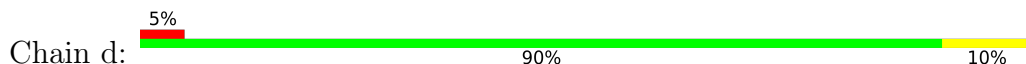
• Molecule 5: 50S ribosomal protein L2



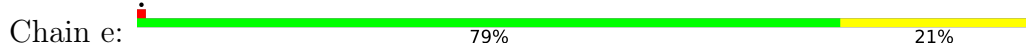
• Molecule 6: 50S ribosomal protein L3

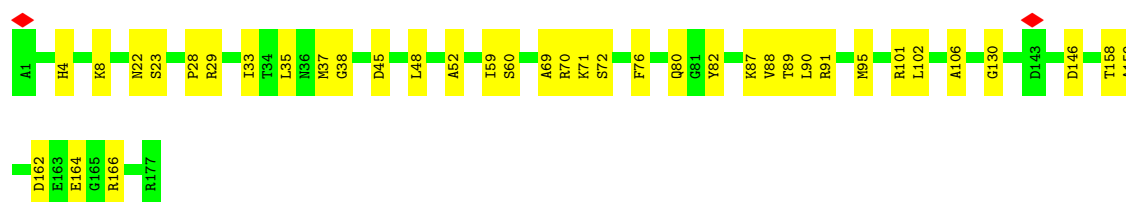


• Molecule 7: 50S ribosomal protein L4

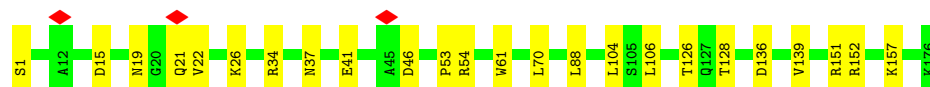
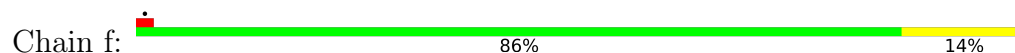


• Molecule 8: 50S ribosomal protein L5

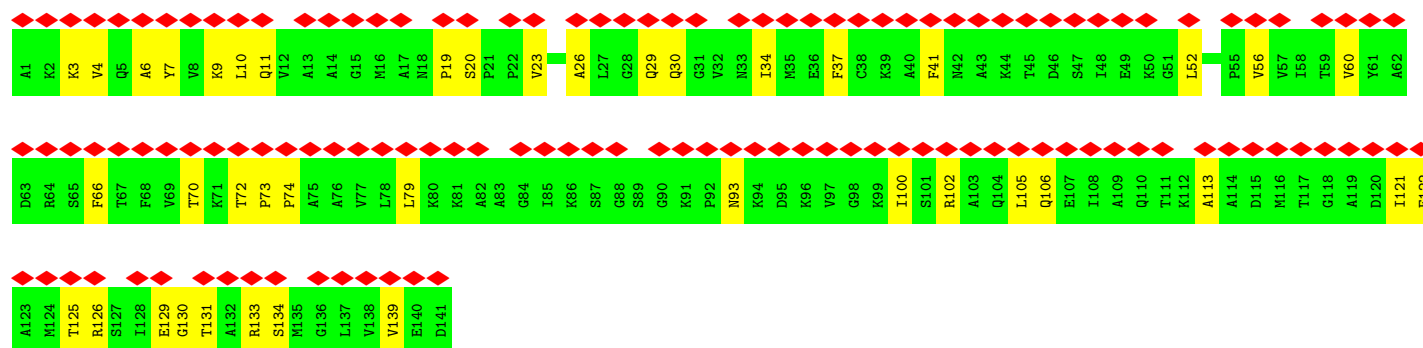
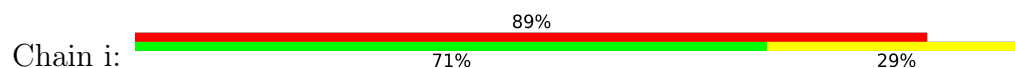




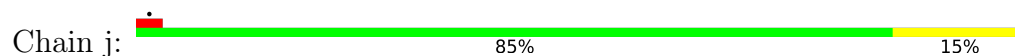
- Molecule 9: 50S ribosomal protein L6



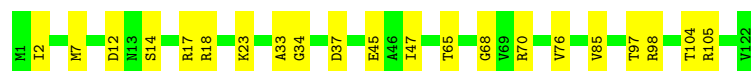
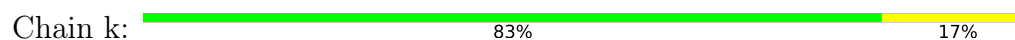
- Molecule 10: 50S ribosomal protein L11



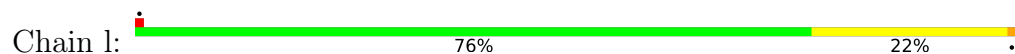
- Molecule 11: 50S ribosomal protein L13

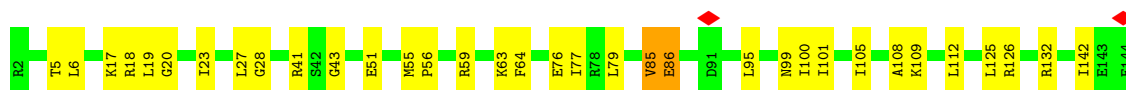


- Molecule 12: 50S ribosomal protein L14

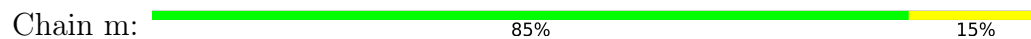


- Molecule 13: 50S ribosomal protein L15

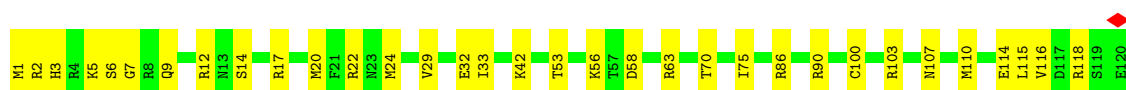




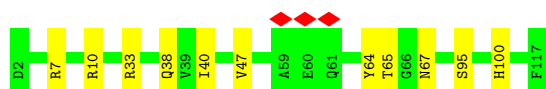
- Molecule 14: 50S ribosomal protein L16



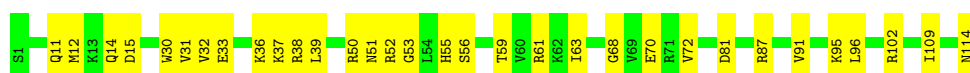
- Molecule 15: 50S ribosomal protein L17



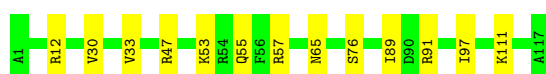
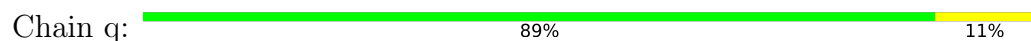
- Molecule 16: 50S ribosomal protein L18



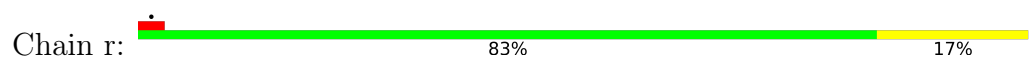
- Molecule 17: 50S ribosomal protein L19



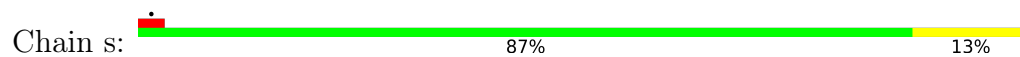
- Molecule 18: 50S ribosomal protein L20



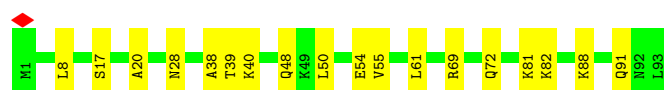
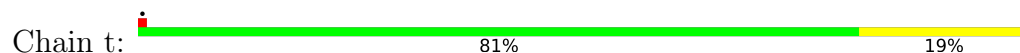
- Molecule 19: 50S ribosomal protein L21



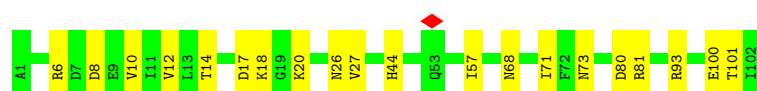
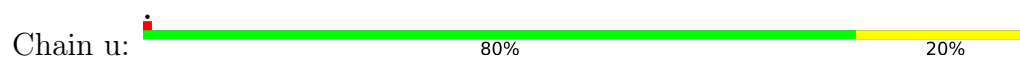
- Molecule 20: 50S ribosomal protein L22



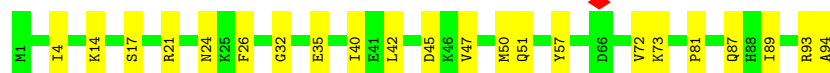
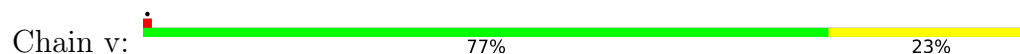
- Molecule 21: 50S ribosomal protein L23



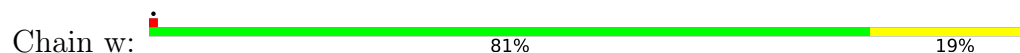
- Molecule 22: 50S ribosomal protein L24



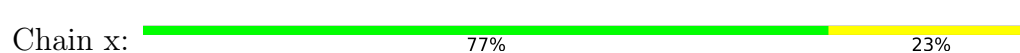
- Molecule 23: 50S ribosomal protein L25



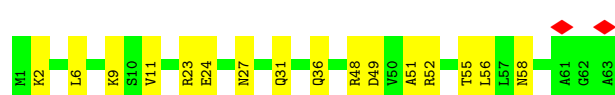
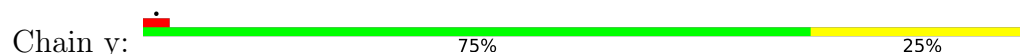
- Molecule 24: 50S ribosomal protein L27



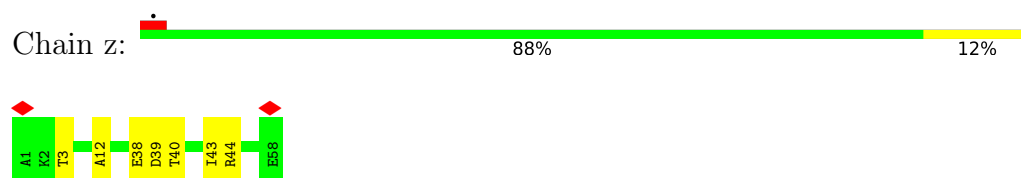
- Molecule 25: 50S ribosomal protein L28



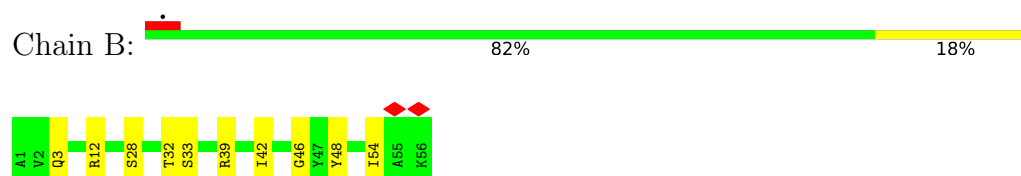
- Molecule 26: 50S ribosomal protein L29



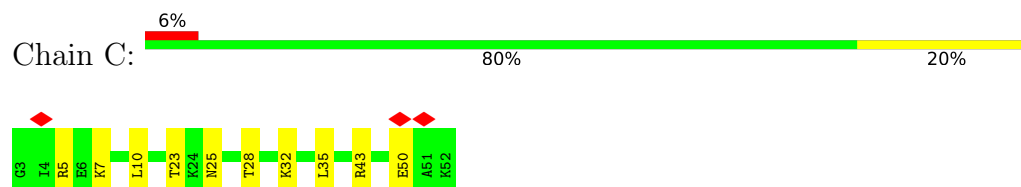
- Molecule 27: 50S ribosomal protein L30



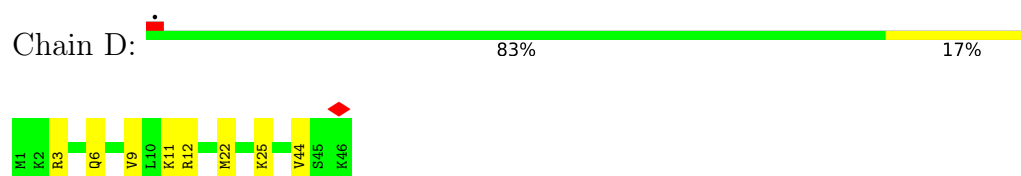
- Molecule 28: 50S ribosomal protein L32



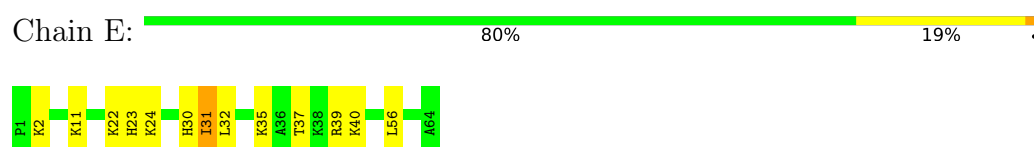
- Molecule 29: 50S ribosomal protein L33



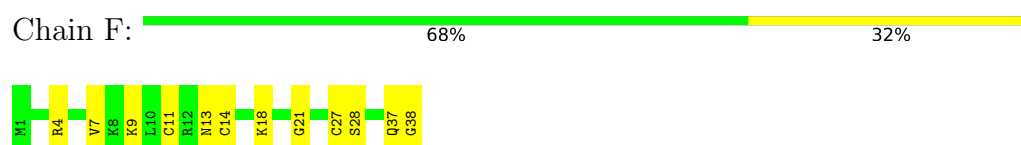
- Molecule 30: 50S ribosomal protein L34



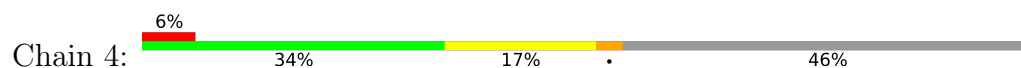
- Molecule 31: 50S ribosomal protein L35

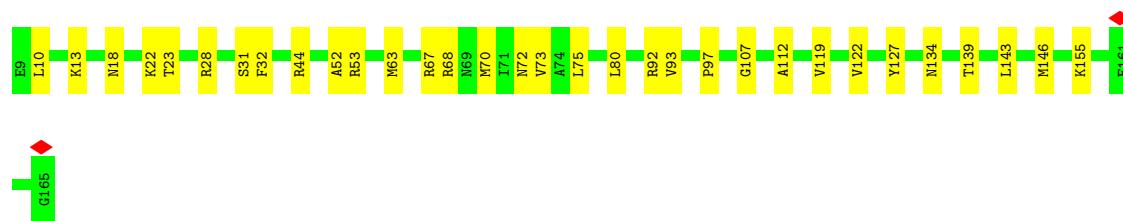


- Molecule 32: 50S ribosomal protein L36

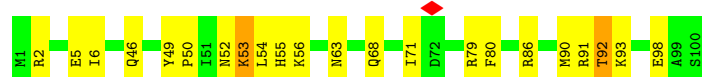
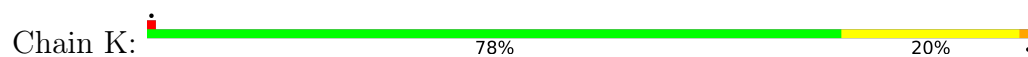


- Molecule 33: mRNA

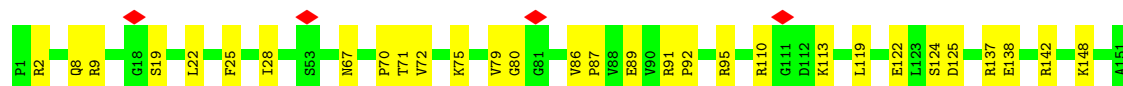
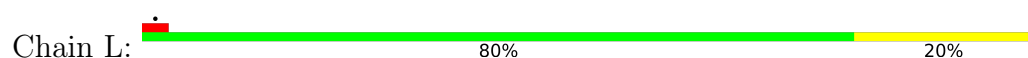




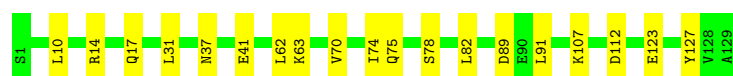
- Molecule 39: 30S ribosomal protein S6



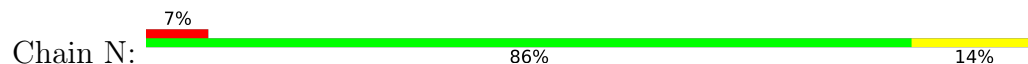
- Molecule 40: 30S ribosomal protein S7



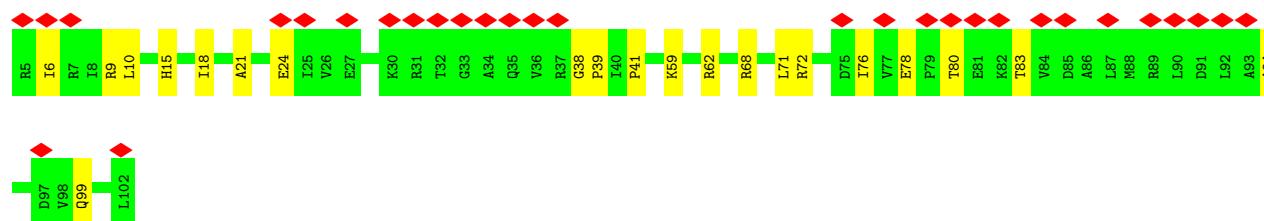
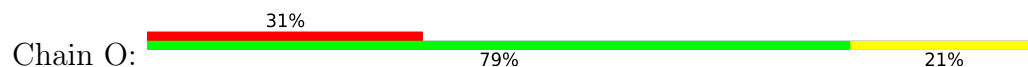
- Molecule 41: 30S ribosomal protein S8



- Molecule 42: 30S ribosomal protein S9



- Molecule 43: 30S ribosomal protein S10



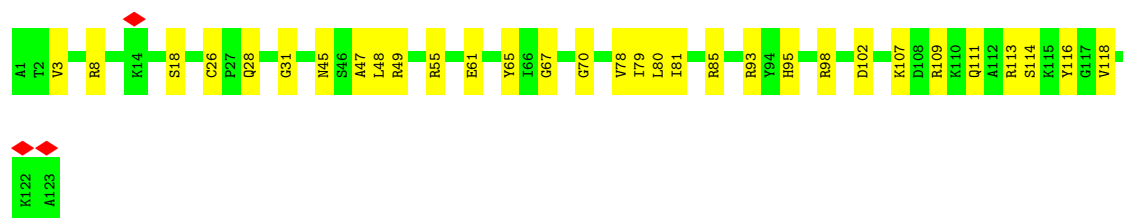
- Molecule 44: 30S ribosomal protein S11

Chain P:  78% 22%



- Molecule 45: 30S ribosomal protein S12

Chain Q:  75% 25%



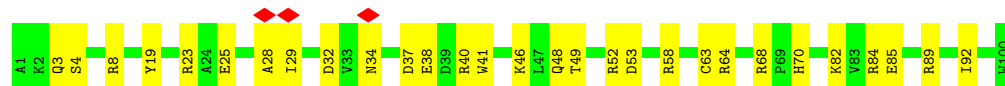
- Molecule 46: 30S ribosomal protein S13

Chain R:  81% 19%



- Molecule 47: 30S ribosomal protein S14

Chain S:  71% 29%



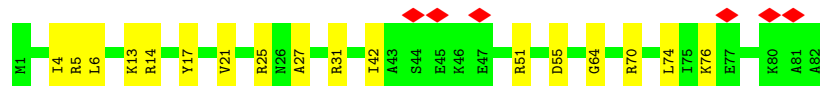
- Molecule 48: 30S ribosomal protein S15

Chain T:  89% 10%



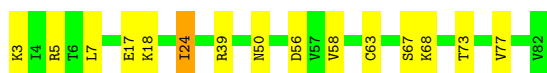
- Molecule 49: 30S ribosomal protein S16

Chain U:  7% 79% 21%



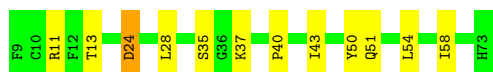
- Molecule 50: 30S ribosomal protein S17

Chain V:  81% 18%



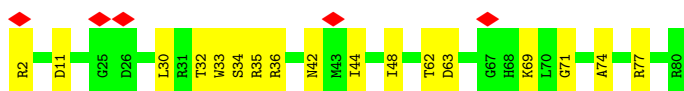
- Molecule 51: 30S ribosomal protein S18

Chain W: 82% 17%



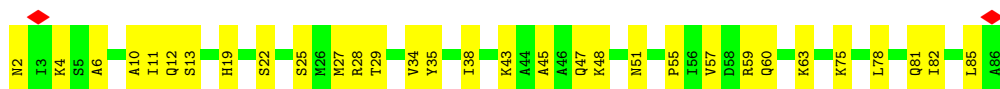
- Molecule 52: 30S ribosomal protein S19

Chain X: 6% 78% 22%



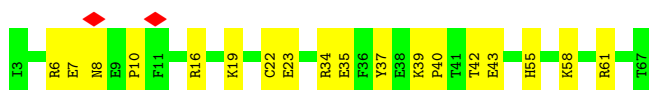
- Molecule 53: 30S ribosomal protein S20

Chain Y: 64% 36%



- Molecule 54: 30S ribosomal protein S21

Chain Z: 72% 28%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6895	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.2	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	18.747	Depositor
Minimum map value	-7.657	Depositor
Average map value	-0.022	Depositor
Map value standard deviation	1.168	Depositor
Recommended contour level	2.5	Depositor
Map size ($\text{\AA}$)	381.8, 381.8, 381.8	wwPDB
Map dimensions	460, 460, 460	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	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	3	0.34	0/36963	0.36	0/57662
2	1	0.42	0/69796	0.38	0/108888
3	2	0.34	0/2872	0.40	0/4479
4	5	0.28	0/1840	0.48	0/2868
5	b	0.42	0/2122	0.60	1/2852 (0.0%)
6	c	0.38	0/1586	0.53	0/2134
7	d	0.32	0/1571	0.58	2/2113 (0.1%)
8	e	0.28	0/1435	0.52	0/1926
9	f	0.26	0/1343	0.45	0/1816
10	i	0.29	0/1046	0.70	1/1410 (0.1%)
11	j	0.36	0/1152	0.48	0/1551
12	k	0.41	0/948	0.58	0/1268
13	l	0.38	0/1054	0.74	1/1403 (0.1%)
14	m	0.37	0/1093	0.51	0/1460
15	n	0.39	0/974	0.71	0/1301
16	o	0.27	0/902	0.48	0/1209
17	p	0.36	0/929	0.53	0/1242
18	q	0.39	0/960	0.50	0/1278
19	r	0.34	0/829	0.58	1/1107 (0.1%)
20	s	0.35	0/864	0.48	0/1156
21	t	0.30	0/745	0.51	0/994
22	u	0.27	0/788	0.55	0/1051
23	v	0.31	0/766	0.55	0/1025
24	w	0.35	0/582	0.54	0/769
25	x	0.39	0/635	0.59	0/848
26	y	0.26	0/510	0.51	0/677
27	z	0.34	0/453	0.64	0/605
28	B	0.35	0/450	0.54	0/599
29	C	0.26	0/417	0.46	0/554
30	D	0.42	0/380	0.57	0/498
31	E	0.40	0/513	0.60	0/676
32	F	0.39	0/303	0.47	0/397
33	4	0.56	0/465	0.49	0/725
34	6	0.32	0/1832	0.41	0/2855

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	G	0.27	0/1736	0.60	0/2338
36	H	0.26	0/1652	0.51	0/2225
37	I	0.27	0/1665	0.63	0/2227
38	J	0.33	0/1170	0.58	0/1573
39	K	0.31	0/836	0.79	4/1128 (0.4%)
40	L	0.25	0/1196	0.54	0/1602
41	M	0.31	0/989	0.49	0/1326
42	N	0.29	0/1034	0.69	1/1375 (0.1%)
43	O	0.27	0/797	0.62	0/1077
44	P	0.34	0/886	0.65	0/1195
45	Q	0.34	0/969	0.68	0/1300
46	R	0.26	0/893	0.62	0/1193
47	S	0.28	0/817	0.53	0/1088
48	T	0.33	0/722	0.54	0/964
49	U	0.26	0/659	0.52	0/884
50	V	0.28	0/658	0.55	0/881
51	W	0.34	0/545	0.57	0/731
52	X	0.25	0/653	0.57	0/877
53	Y	0.26	0/671	0.52	0/888
54	Z	0.34	0/551	1.04	2/728 (0.3%)
All	All	0.37	0/158217	0.44	13/236996 (0.0%)

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
14	m	0	1
15	n	0	1
31	E	0	1
37	I	0	1
39	K	0	3
42	N	0	1
44	P	0	1
54	Z	0	3
All	All	0	12

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	l	86	GLU	N-CA-C	-6.77	106.22	114.75
39	K	52	ASN	CA-C-N	6.49	133.94	121.54
39	K	52	ASN	C-N-CA	6.49	133.94	121.54
19	r	51	VAL	N-CA-C	-6.23	103.23	109.02
7	d	83	VAL	CA-C-N	6.11	133.21	121.54

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
31	E	30	HIS	Peptide
37	I	167	PRO	Peptide
39	K	53	LYS	Peptide
14	m	59	ARG	Peptide
15	n	116	VAL	Peptide

5.2 Too-close contacts [i](#)

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	3	33012	0	16618	223	0
2	1	62317	0	31346	303	0
3	2	2568	0	1303	12	0
4	5	1647	0	832	10	0
5	b	2083	0	2157	32	0
6	c	1565	0	1616	18	0
7	d	1552	0	1619	14	0
8	e	1411	0	1447	26	0
9	f	1323	0	1374	16	0
10	i	1032	0	1088	28	0
11	j	1129	0	1162	17	0
12	k	939	0	1012	13	0
13	l	1045	0	1117	23	0
14	m	1074	0	1157	13	0
15	n	961	0	1000	24	0
16	o	892	0	923	9	0
17	p	917	0	965	25	0
18	q	947	0	1022	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	r	816	0	839	13	0
20	s	857	0	922	8	0
21	t	739	0	807	13	0
22	u	780	0	834	12	0
23	v	753	0	780	14	0
24	w	575	0	592	9	0
25	x	625	0	655	14	0
26	y	509	0	543	9	0
27	z	449	0	491	3	0
28	B	444	0	461	7	0
29	C	410	0	440	8	0
30	D	377	0	418	5	0
31	E	504	0	574	10	0
32	F	302	0	341	8	0
33	4	413	0	209	5	0
34	6	1640	0	837	6	0
35	G	1705	0	1732	27	0
36	H	1625	0	1699	29	0
37	I	1643	0	1710	36	0
38	J	1157	0	1199	23	0
39	K	818	0	808	12	0
40	L	1182	0	1240	20	0
41	M	979	0	1034	15	0
42	N	1022	0	1070	11	0
43	O	787	0	828	17	0
44	P	870	0	878	18	0
45	Q	955	0	1019	24	0
46	R	884	0	944	15	0
47	S	805	0	847	21	0
48	T	714	0	737	7	0
49	U	649	0	666	14	0
50	V	649	0	691	11	0
51	W	536	0	552	7	0
52	X	638	0	665	14	0
53	Y	665	0	714	24	0
54	Z	545	0	579	10	0
All	All	145435	0	97113	1101	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 6.

The worst 5 of 1101 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)
2:1:136:G:H1	2:1:143:C:H42	1.33	0.75
18:q:57:ARG:HH12	18:q:91:ARG:HH21	1.33	0.74
1:3:664:G:H22	1:3:741:G:H1	1.40	0.69
1:3:1319:A:H5''	52:X:69:LYS:HE3	1.72	0.69
2:1:2305:U:H5''	8:e:130:GLY:HA3	1.75	0.68

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	b	269/271 (99%)	241 (90%)	28 (10%)	0	100	100
6	c	207/209 (99%)	196 (95%)	11 (5%)	0	100	100
7	d	199/201 (99%)	187 (94%)	12 (6%)	0	100	100
8	e	175/177 (99%)	163 (93%)	12 (7%)	0	100	100
9	f	174/176 (99%)	159 (91%)	15 (9%)	0	100	100
10	i	139/141 (99%)	116 (84%)	23 (16%)	0	100	100
11	j	140/142 (99%)	131 (94%)	9 (6%)	0	100	100
12	k	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
13	l	141/143 (99%)	120 (85%)	21 (15%)	0	100	100
14	m	134/136 (98%)	127 (95%)	7 (5%)	0	100	100
15	n	118/120 (98%)	100 (85%)	18 (15%)	0	100	100
16	o	114/116 (98%)	108 (95%)	6 (5%)	0	100	100
17	p	112/114 (98%)	106 (95%)	6 (5%)	0	100	100
18	q	115/117 (98%)	111 (96%)	4 (4%)	0	100	100
19	r	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
20	s	108/110 (98%)	103 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	t	91/93 (98%)	90 (99%)	1 (1%)	0	100	100
22	u	100/102 (98%)	86 (86%)	14 (14%)	0	100	100
23	v	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
24	w	73/75 (97%)	69 (94%)	4 (6%)	0	100	100
25	x	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
26	y	61/63 (97%)	59 (97%)	1 (2%)	1 (2%)	7	36
27	z	56/58 (97%)	49 (88%)	6 (11%)	1 (2%)	6	34
28	B	54/56 (96%)	49 (91%)	5 (9%)	0	100	100
29	C	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
30	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
31	E	62/64 (97%)	51 (82%)	10 (16%)	1 (2%)	7	36
32	F	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
35	G	216/225 (96%)	188 (87%)	28 (13%)	0	100	100
36	H	204/206 (99%)	190 (93%)	14 (7%)	0	100	100
37	I	203/205 (99%)	181 (89%)	22 (11%)	0	100	100
38	J	155/157 (99%)	136 (88%)	19 (12%)	0	100	100
39	K	98/100 (98%)	80 (82%)	17 (17%)	1 (1%)	12	45
40	L	149/151 (99%)	135 (91%)	14 (9%)	0	100	100
41	M	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
42	N	125/127 (98%)	102 (82%)	23 (18%)	0	100	100
43	O	96/98 (98%)	82 (85%)	14 (15%)	0	100	100
44	P	114/116 (98%)	97 (85%)	16 (14%)	1 (1%)	14	47
45	Q	121/123 (98%)	105 (87%)	16 (13%)	0	100	100
46	R	112/114 (98%)	100 (89%)	12 (11%)	0	100	100
47	S	98/100 (98%)	88 (90%)	10 (10%)	0	100	100
48	T	86/88 (98%)	78 (91%)	7 (8%)	1 (1%)	10	42
49	U	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
50	V	78/80 (98%)	67 (86%)	11 (14%)	0	100	100
51	W	63/65 (97%)	59 (94%)	4 (6%)	0	100	100
52	X	77/79 (98%)	71 (92%)	6 (8%)	0	100	100
53	Y	83/85 (98%)	80 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	Z	63/65 (97%)	46 (73%)	15 (24%)	2 (3%)	3	21
All	All	5506/5609 (98%)	4985 (90%)	513 (9%)	8 (0%)	49	79

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	z	12	ALA
39	K	54	LEU
48	T	46	LYS
54	Z	8	ASN
26	y	24	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	b	216/216 (100%)	214 (99%)	2 (1%)	70	81
6	c	164/164 (100%)	161 (98%)	3 (2%)	51	74
7	d	165/165 (100%)	164 (99%)	1 (1%)	78	84
8	e	148/148 (100%)	147 (99%)	1 (1%)	76	83
9	f	137/137 (100%)	137 (100%)	0	100	100
10	i	109/109 (100%)	109 (100%)	0	100	100
11	j	116/116 (100%)	115 (99%)	1 (1%)	70	81
12	k	103/103 (100%)	102 (99%)	1 (1%)	68	80
13	l	102/102 (100%)	99 (97%)	3 (3%)	37	67
14	m	109/109 (100%)	109 (100%)	0	100	100
15	n	100/100 (100%)	100 (100%)	0	100	100
16	o	86/86 (100%)	86 (100%)	0	100	100
17	p	99/99 (100%)	99 (100%)	0	100	100
18	q	89/89 (100%)	89 (100%)	0	100	100
19	r	84/84 (100%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	s	93/93 (100%)	92 (99%)	1 (1%)	65	79
21	t	80/80 (100%)	80 (100%)	0	100	100
22	u	83/83 (100%)	82 (99%)	1 (1%)	63	79
23	v	78/78 (100%)	78 (100%)	0	100	100
24	w	57/57 (100%)	57 (100%)	0	100	100
25	x	67/67 (100%)	67 (100%)	0	100	100
26	y	55/55 (100%)	55 (100%)	0	100	100
27	z	48/48 (100%)	48 (100%)	0	100	100
28	B	47/47 (100%)	47 (100%)	0	100	100
29	C	45/45 (100%)	45 (100%)	0	100	100
30	D	38/38 (100%)	37 (97%)	1 (3%)	40	69
31	E	51/51 (100%)	51 (100%)	0	100	100
32	F	34/34 (100%)	34 (100%)	0	100	100
35	G	180/186 (97%)	180 (100%)	0	100	100
36	H	170/170 (100%)	170 (100%)	0	100	100
37	I	172/172 (100%)	171 (99%)	1 (1%)	78	84
38	J	119/119 (100%)	117 (98%)	2 (2%)	53	75
39	K	87/87 (100%)	87 (100%)	0	100	100
40	L	124/124 (100%)	124 (100%)	0	100	100
41	M	104/104 (100%)	104 (100%)	0	100	100
42	N	105/105 (100%)	104 (99%)	1 (1%)	68	80
43	O	86/86 (100%)	85 (99%)	1 (1%)	63	79
44	P	89/89 (100%)	86 (97%)	3 (3%)	32	64
45	Q	103/103 (100%)	103 (100%)	0	100	100
46	R	92/92 (100%)	90 (98%)	2 (2%)	45	71
47	S	83/83 (100%)	83 (100%)	0	100	100
48	T	76/76 (100%)	75 (99%)	1 (1%)	61	78
49	U	65/65 (100%)	65 (100%)	0	100	100
50	V	74/74 (100%)	73 (99%)	1 (1%)	59	77
51	W	56/56 (100%)	55 (98%)	1 (2%)	51	74
52	X	70/70 (100%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	Y	65/65 (100%)	65 (100%)	0	100	100
54	Z	55/55 (100%)	55 (100%)	0	100	100
All	All	4578/4584 (100%)	4550 (99%)	28 (1%)	76	84

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	D	44	VAL
51	W	24	ASP
38	J	122	VAL
46	R	64	VAL
38	J	119	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 81 such sidechains are listed below:

Mol	Chain	Res	Type
37	I	73	ASN
43	O	58	ASN
37	I	135	GLN
40	L	27	ASN
49	U	26	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	1538/1539 (99%)	290 (18%)	2 (0%)
2	1	2902/2903 (99%)	563 (19%)	9 (0%)
3	2	119/120 (99%)	23 (19%)	1 (0%)
33	4	18/35 (51%)	3 (16%)	0
34	6	76/77 (98%)	23 (30%)	0
4	5	76/77 (98%)	30 (39%)	2 (2%)
All	All	4729/4751 (99%)	932 (19%)	14 (0%)

5 of 932 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	4	U
1	3	5	U
1	3	6	G

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Mol	Chain	Res	Type
1	3	7	A
1	3	8	A

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	1	1070	A
2	1	1106	G
4	5	43	U
3	2	88	C
4	5	41	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

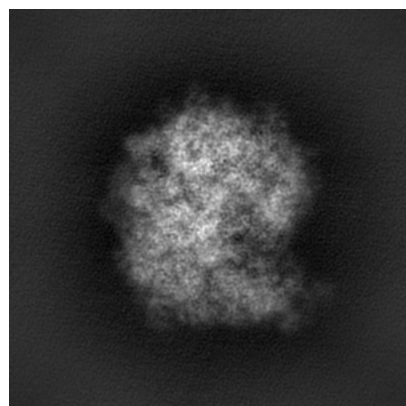
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25410. These allow visual inspection of the internal detail of the map and identification of artifacts.

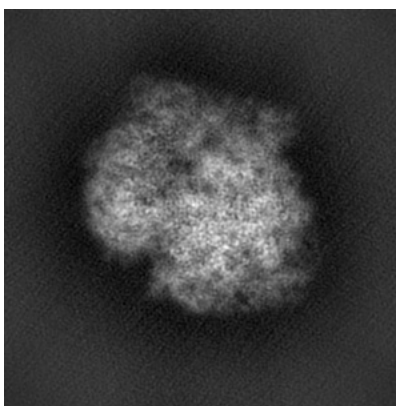
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

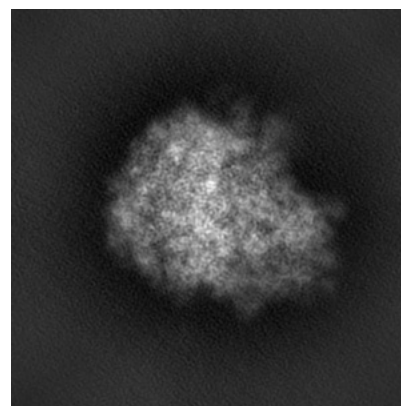
6.1.1 Primary map



X

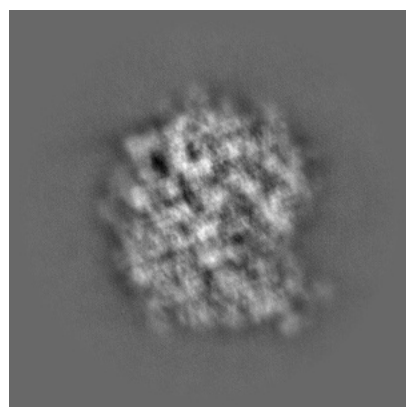


Y

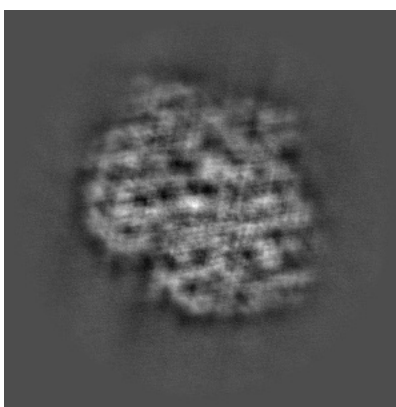


Z

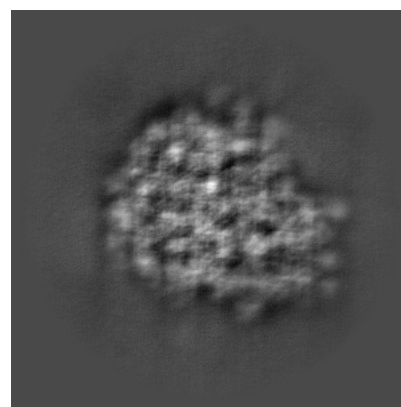
6.1.2 Raw map



X



Y

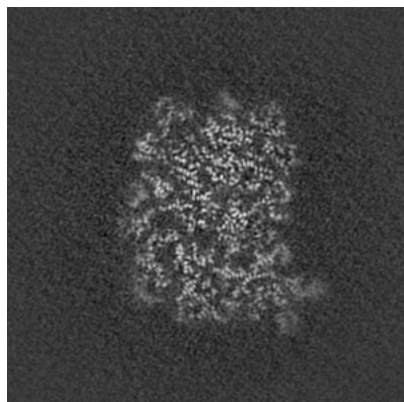


Z

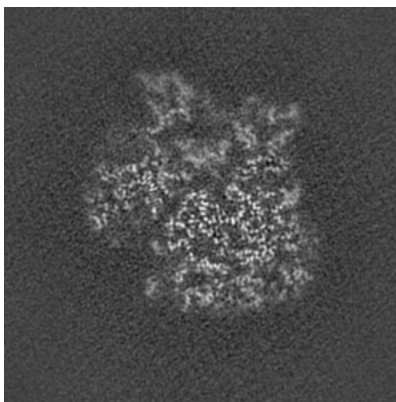
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

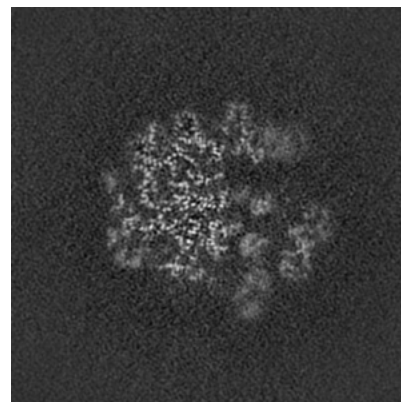
6.2.1 Primary map



X Index: 230

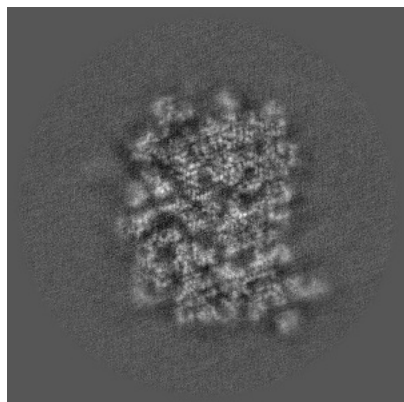


Y Index: 230

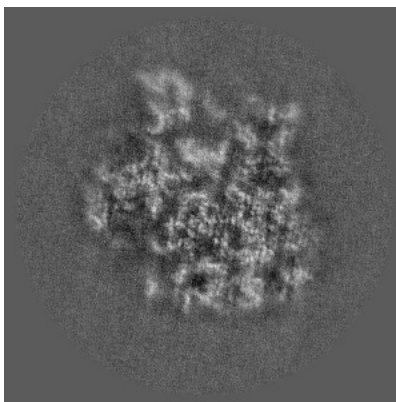


Z Index: 230

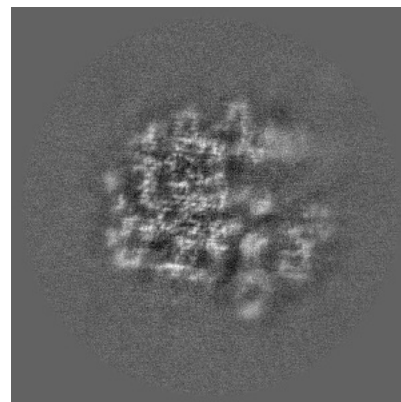
6.2.2 Raw map



X Index: 230



Y Index: 230

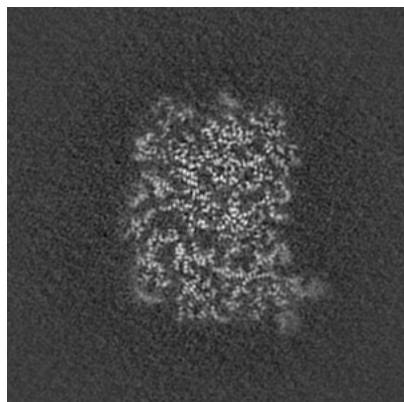


Z Index: 230

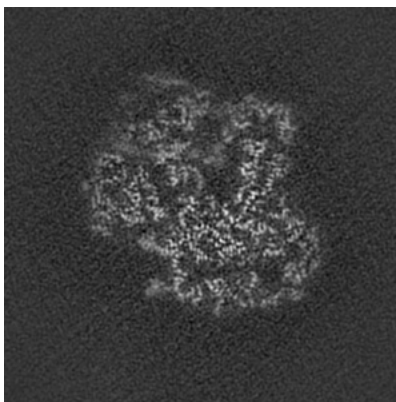
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

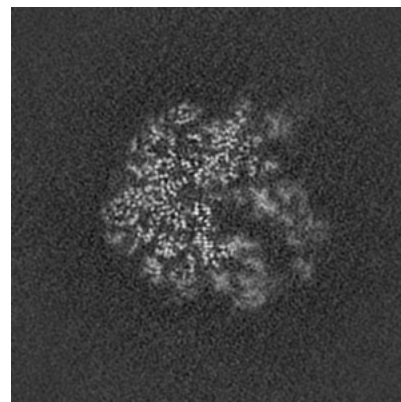
6.3.1 Primary map



X Index: 229

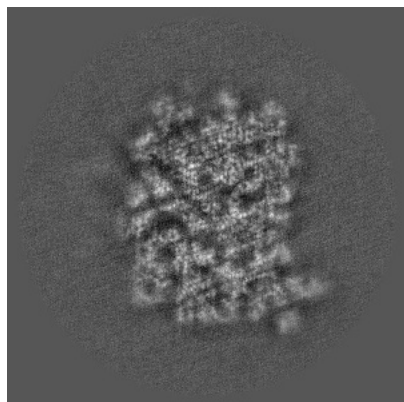


Y Index: 221

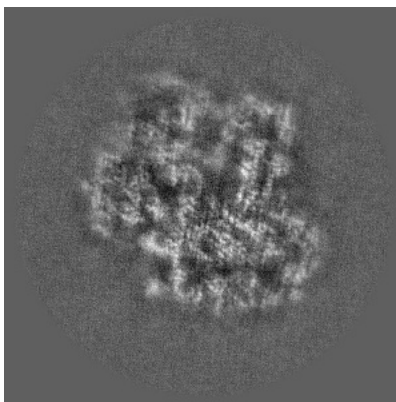


Z Index: 251

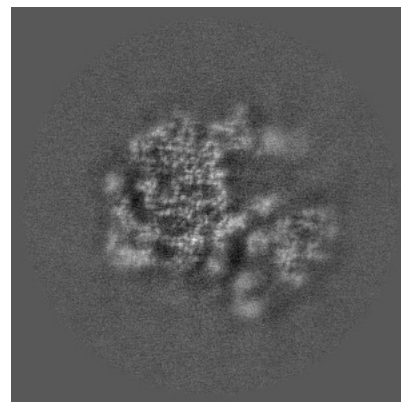
6.3.2 Raw map



X Index: 229



Y Index: 221

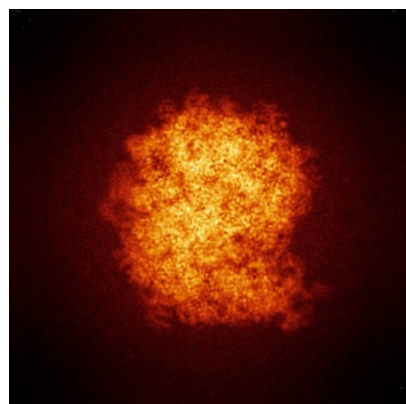


Z Index: 223

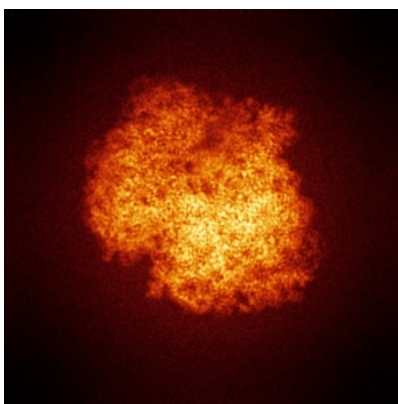
The images above show the largest variance slices of the map in three orthogonal directions.

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

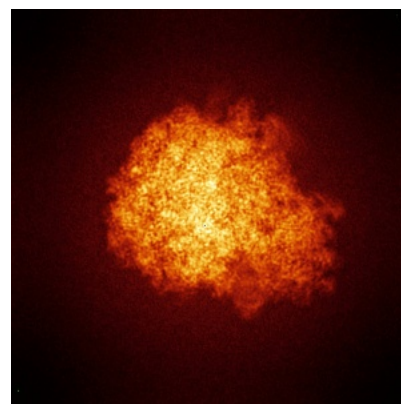
6.4.1 Primary map



X

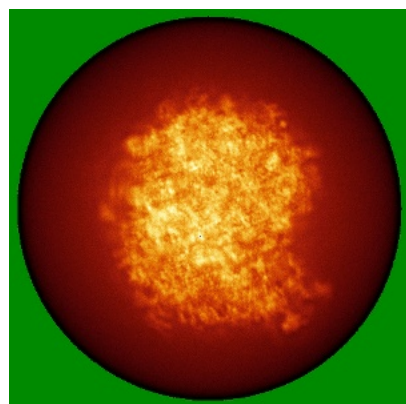


Y

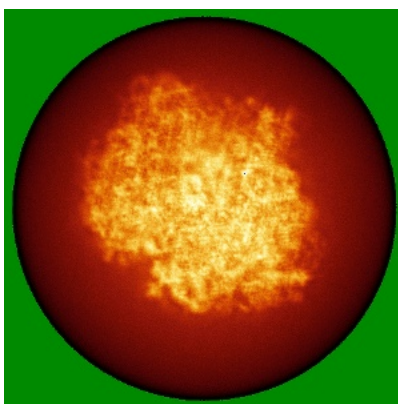


Z

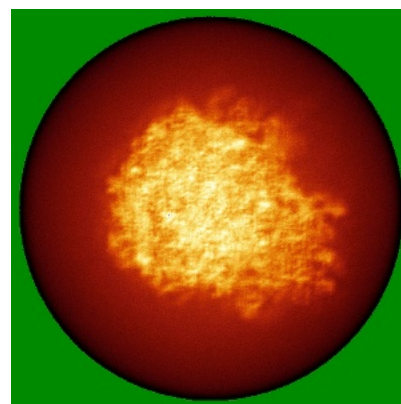
6.4.2 Raw map



X



Y

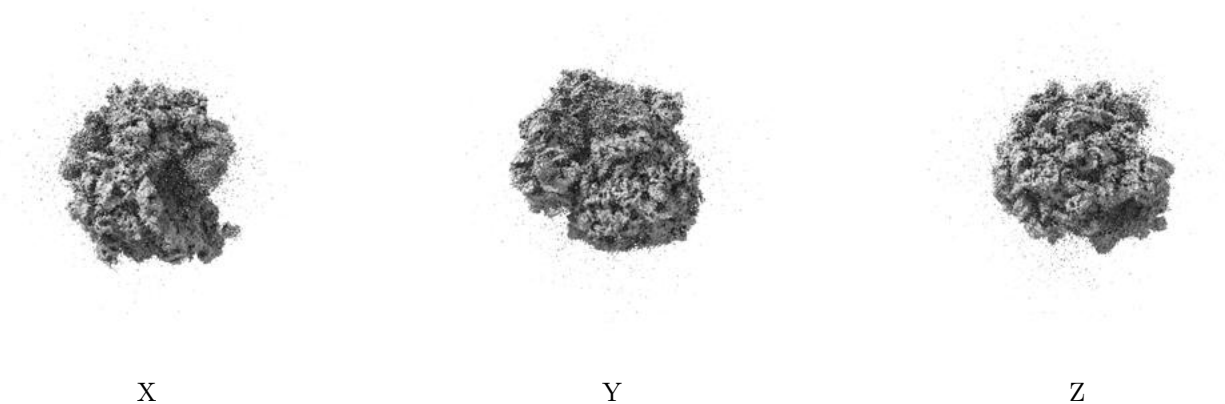


Z

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.

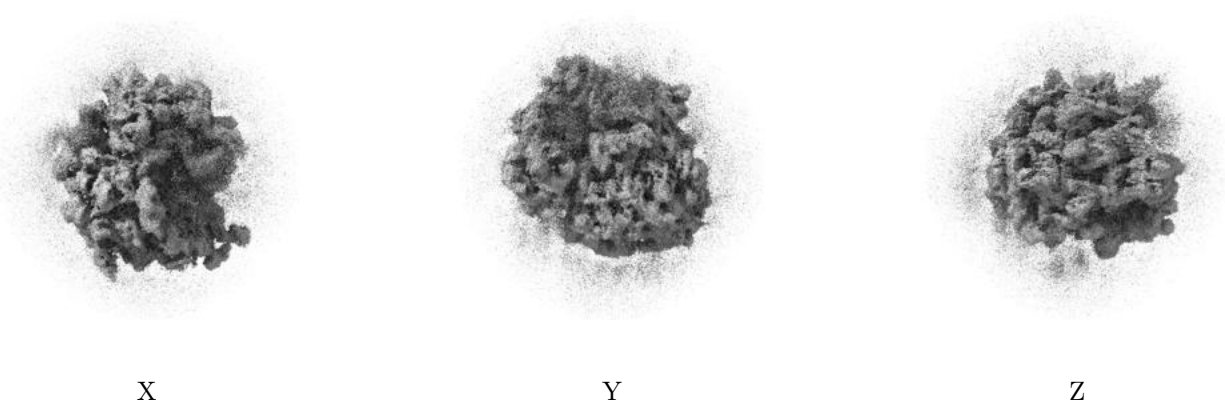
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. 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.

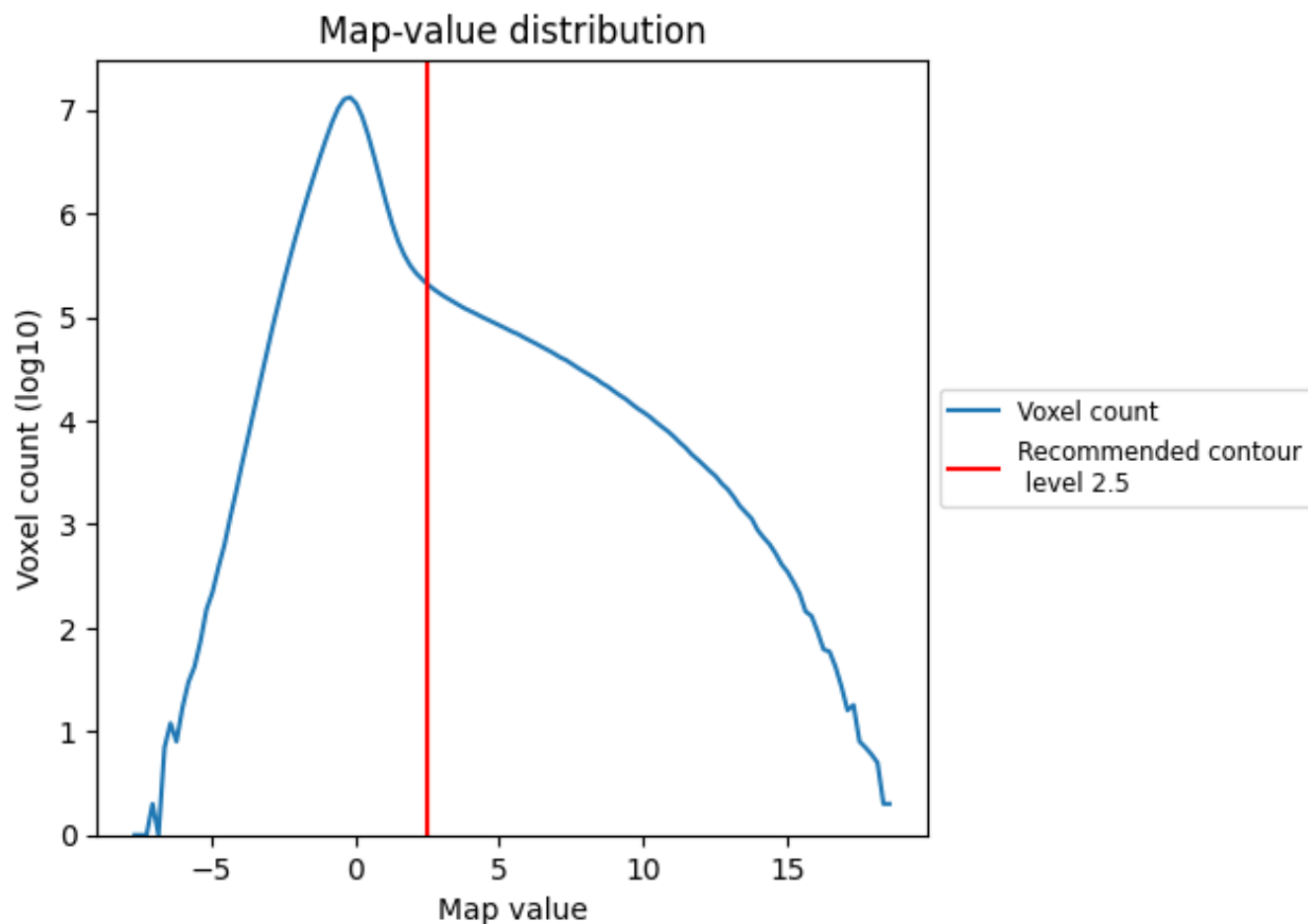
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

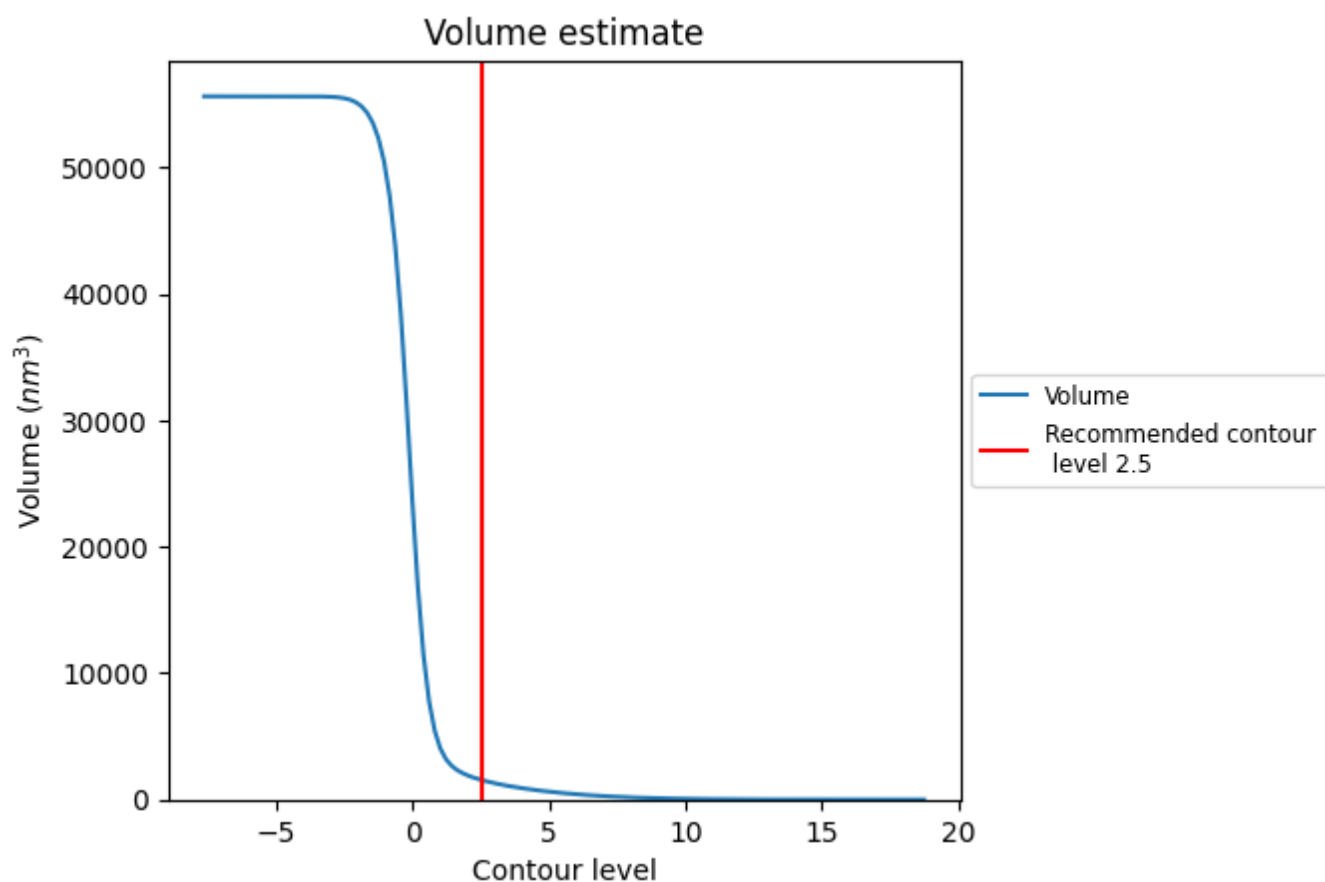
This section contains the results of statistical analysis of the map.

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.

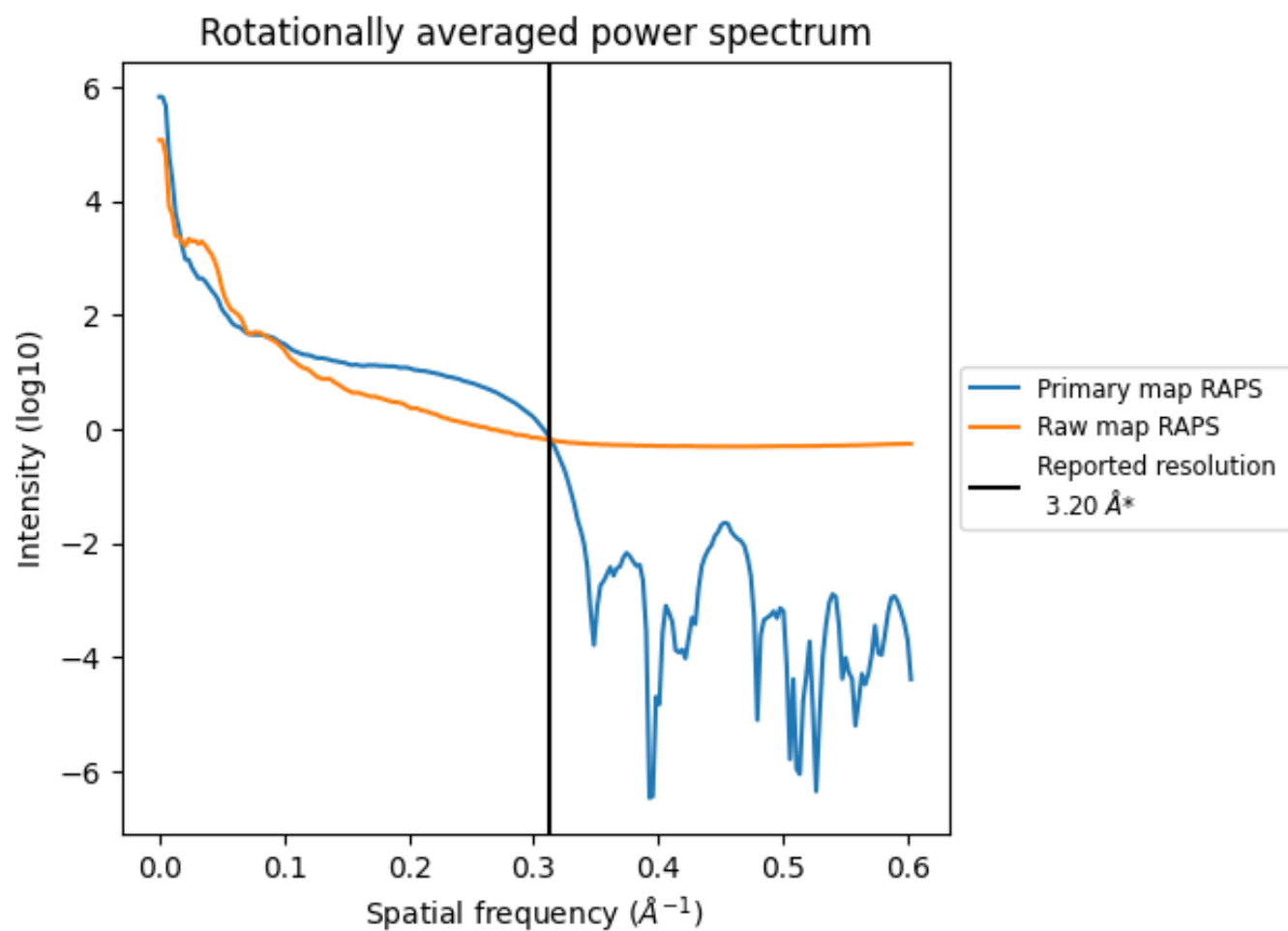
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1561 nm³; this corresponds to an approximate mass of 1410 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 ⓘ

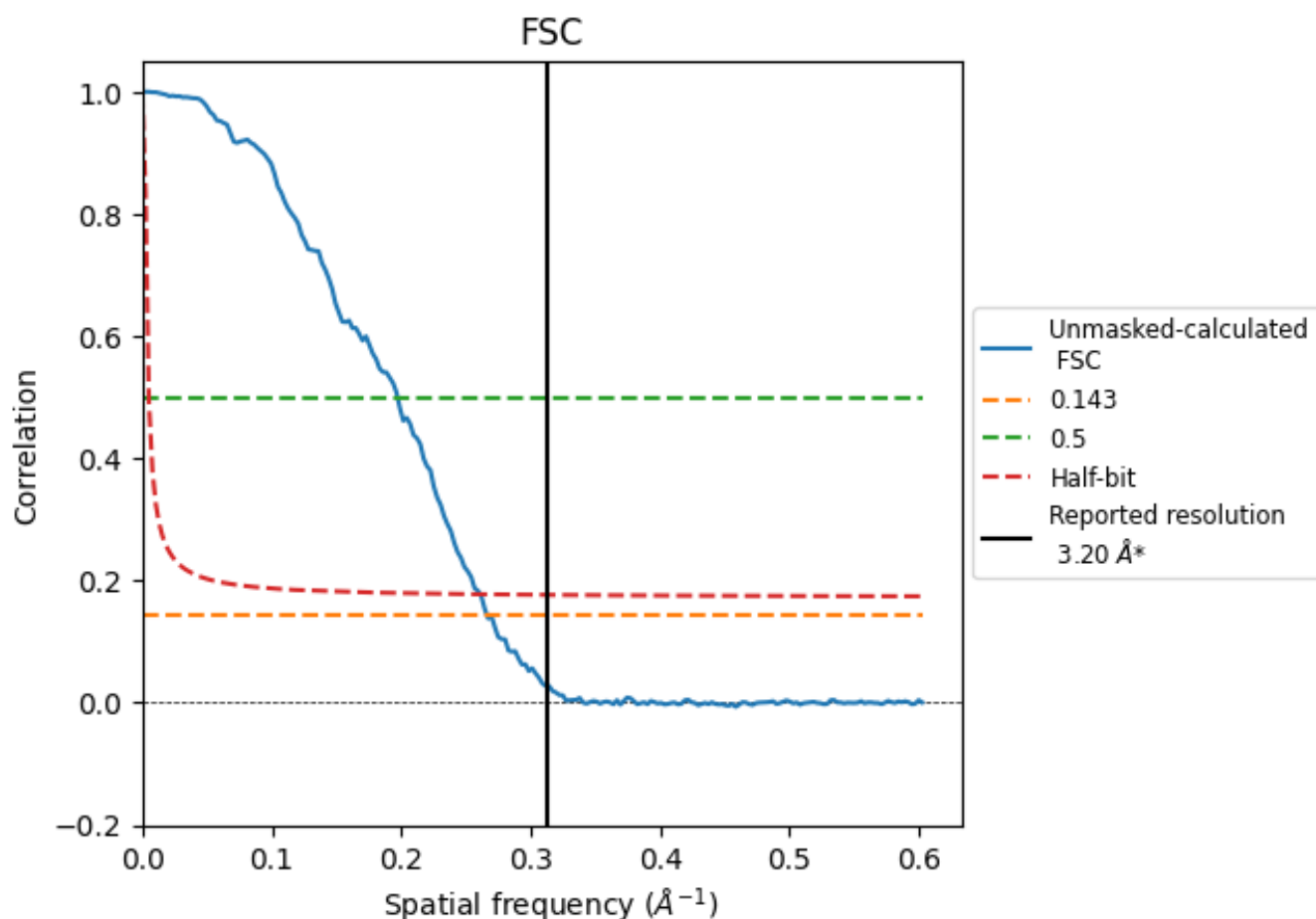


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

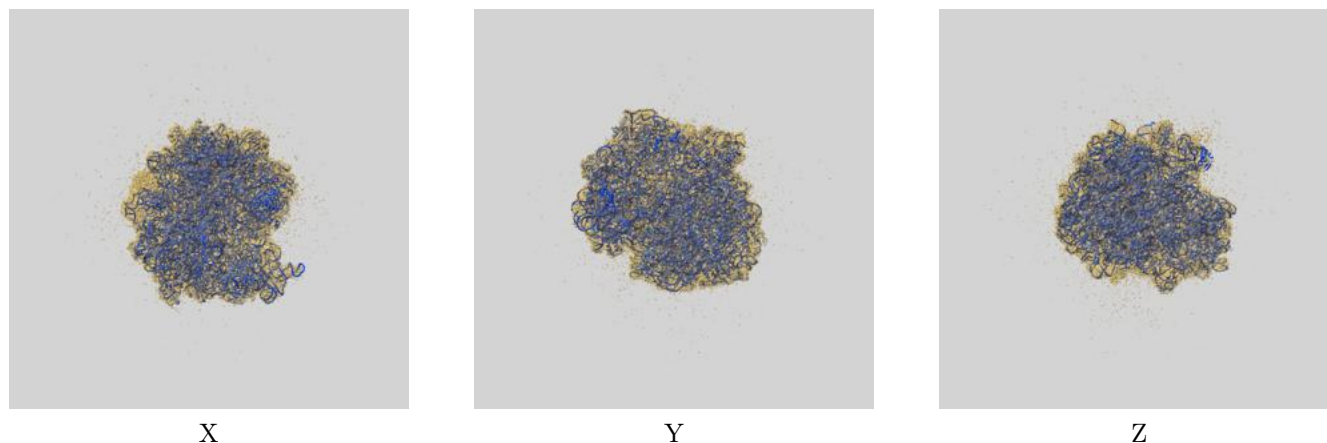
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.76	5.07	3.83

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.76 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

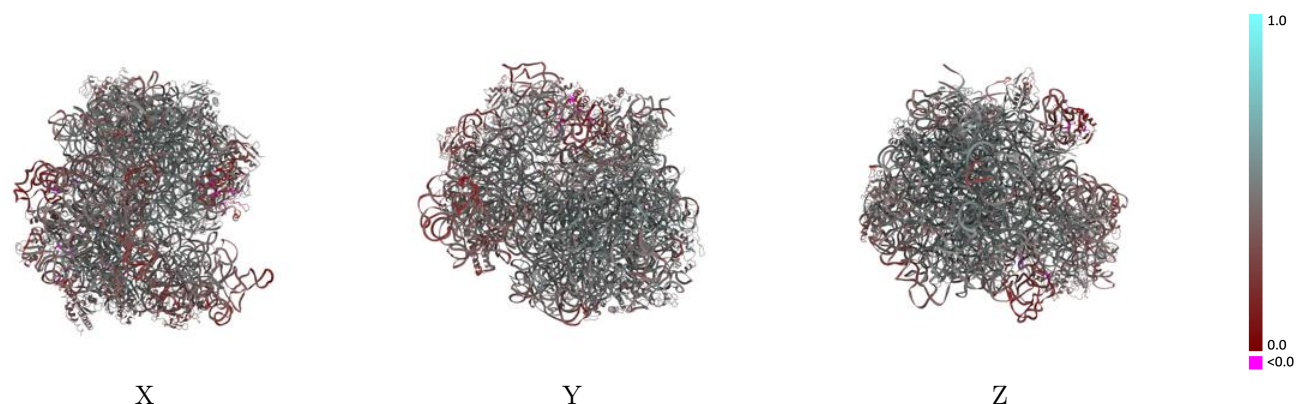
This section contains information regarding the fit between EMDB map EMD-25410 and PDB model 7SSN. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



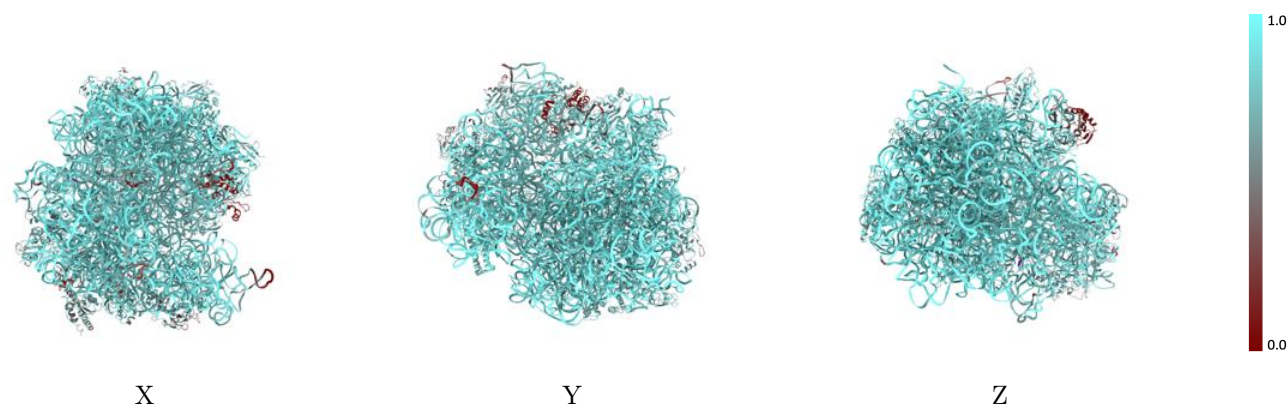
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



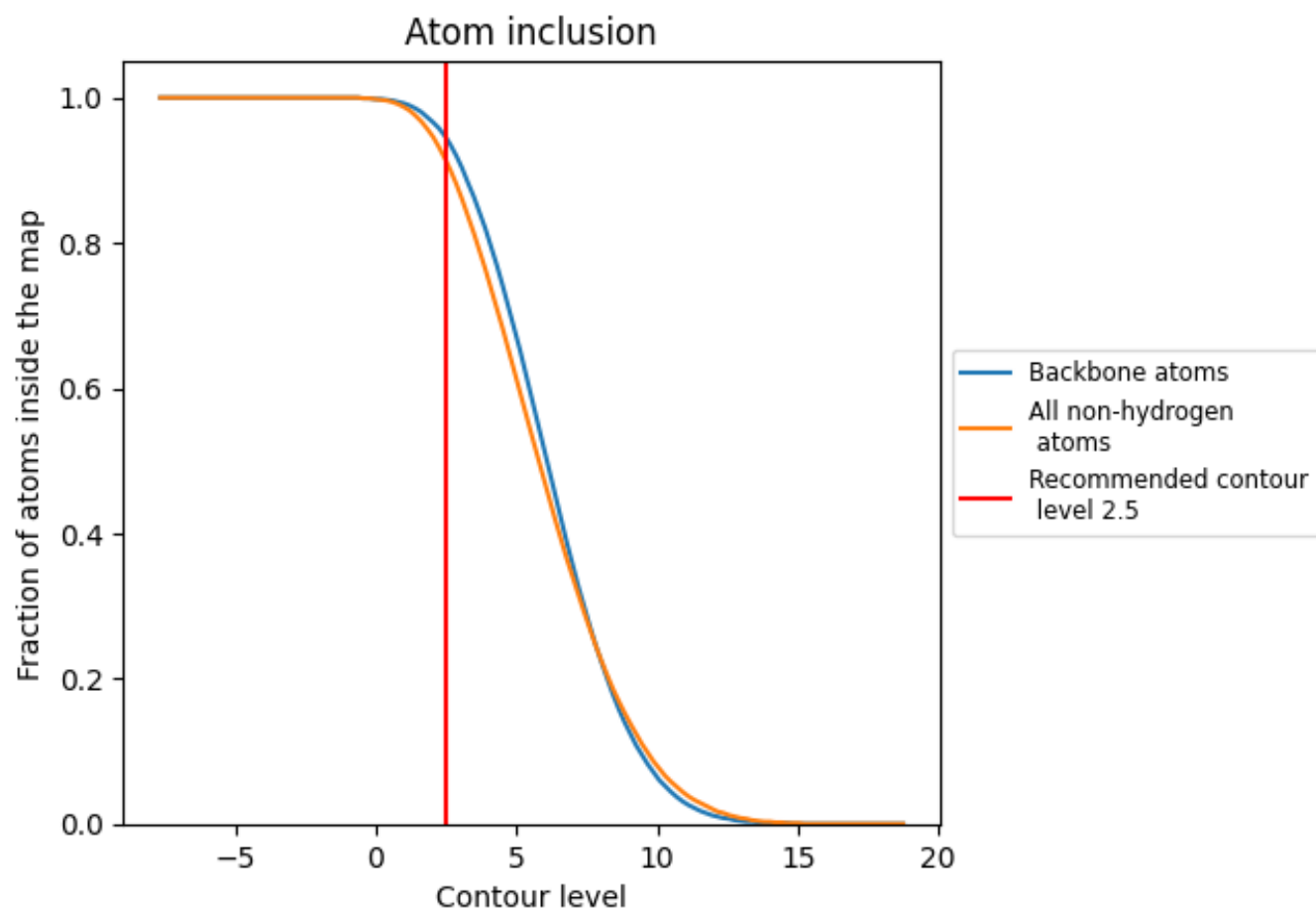
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 91% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9130	 0.4430
1	 0.9670	 0.4630
2	 0.9510	 0.4350
3	 0.9390	 0.4290
4	 0.7720	 0.2680
5	 0.9670	 0.3650
6	 0.9690	 0.3960
B	 0.8900	 0.4860
C	 0.8030	 0.4450
D	 0.9520	 0.5030
E	 0.9270	 0.5100
F	 0.9010	 0.4980
G	 0.6470	 0.3880
H	 0.7840	 0.4310
I	 0.6800	 0.3500
J	 0.8330	 0.4440
K	 0.8220	 0.3840
L	 0.7500	 0.3870
M	 0.8170	 0.4490
N	 0.7390	 0.4080
O	 0.5620	 0.3640
P	 0.8880	 0.4500
Q	 0.8680	 0.4450
R	 0.7990	 0.4000
S	 0.8010	 0.4310
T	 0.8750	 0.4130
U	 0.7930	 0.4190
V	 0.8580	 0.4210
W	 0.8640	 0.4230
X	 0.8100	 0.4110
Y	 0.7850	 0.3680
Z	 0.7380	 0.3480
b	 0.9420	 0.4940
c	 0.8890	 0.4900
d	 0.7830	 0.4530



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Chain	Atom inclusion	Q-score
e	 0.8300	 0.3990
f	 0.8370	 0.4220
i	 0.1660	 0.1980
j	 0.8750	 0.4820
k	 0.8750	 0.4650
l	 0.8740	 0.4740
m	 0.9000	 0.4910
n	 0.8960	 0.4780
o	 0.8330	 0.4270
p	 0.8750	 0.4660
q	 0.9060	 0.5000
r	 0.8520	 0.4890
s	 0.8680	 0.4810
t	 0.8550	 0.4330
u	 0.7690	 0.4320
v	 0.8420	 0.4490
w	 0.9070	 0.4940
x	 0.8980	 0.4760
y	 0.7790	 0.4030
z	 0.8630	 0.4850