



wwPDB EM Validation Summary Report ⓘ

Oct 11, 2022 – 08:41 pm BST

PDB ID : 7PI9
EMDB ID : EMD-13433
Title : 70S ribosome with EF-Tu-tRNA and P-site tRNA in spectinomycin-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-19
Resolution : 6.30 Å (reported)
Based on initial models : 7OOC, 4V7C, 7OOD, 4V5L

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:

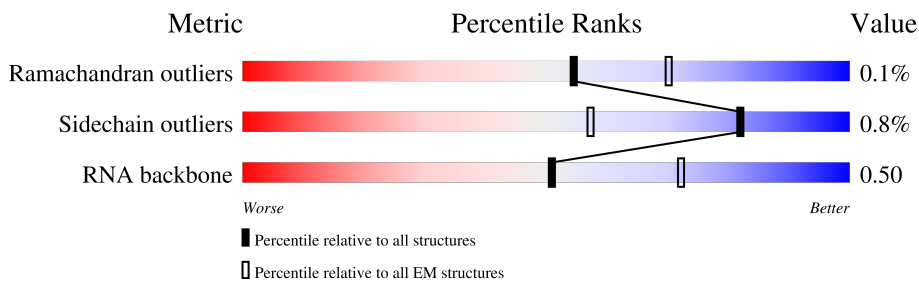
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 6.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	0	48	
2	1	59	
3	2	37	
4	9	394	
5	A	294	
6	B	273	
7	C	205	
8	D	219	

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Mol	Chain	Length	Quality of chain
9	E	215	21% 78% 22%
10	F	155	16% 99%
11	G	142	15% 99%
12	H	132	16% 96%
13	I	108	27% 93% 6%
14	J	121	17% 94% 6%
15	K	139	9% 95%
16	L	124	19% 94% 5%
17	M	61	18% 98%
18	N	86	10% 97%
19	O	94	12% 84% 15%
20	P	85	16% 98%
21	Q	104	9% 62% 38%
22	R	87	22% 94%
23	S	87	86% 11%
24	T	60	8% 88% 12%
25	a	287	8% 99%
26	b	287	7% 80% 20%
27	c	212	16% 99%
28	d	180	13% 97%
29	e	184	23% 95%
30	f	149	57% 95%
31	g	161	29% 71% 6% 22%
32	h	137	45% 93% 7%
33	i	146	5% 98%

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Mol	Chain	Length	Quality of chain
34	j	122	13% 100%
35	k	151	11% 97%
36	l	139	10% 97%
37	m	124	8% 94%
38	n	116	9% 97%
39	o	119	12% 97%
40	p	127	8% 90% 10%
41	q	100	16% 98%
42	r	159	5% 87% 13%
43	s	237	39% 61%
44	t	111	26% 99%
45	u	104	8% 82% 17%
46	v	65	12% 97%
47	w	111	12% 90% 10%
48	x	97	16% 45% 55%
49	y	57	9% 91% 7%
50	z	53	9% 92% 6%
51	3	2907	71% 27%
52	4	108	69% 29%
53	5	1520	74% 24%
54	6	76	21% 61% 38%
54	7	76	61% 38%

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 149163 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L34.

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

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

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

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

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

- Molecule 4 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	9	393	3021	1892	533	583	13	0	0

- Molecule 5 is a protein called 30S ribosomal protein S2.

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

- Molecule 6 is a protein called 30S ribosomal protein S3.

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

- Molecule 7 is a protein called 30S ribosomal protein S4.

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

- Molecule 8 is a protein called 30S ribosomal protein S5.

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

- Molecule 9 is a protein called 30S ribosomal protein S6.

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

- Molecule 10 is a protein called 30S ribosomal protein S7.

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

- Molecule 11 is a protein called 30S ribosomal protein S8.

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

- Molecule 12 is a protein called 30S ribosomal protein S9.

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

- Molecule 13 is a protein called 30S ribosomal protein S10.

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

- Molecule 14 is a protein called 30S ribosomal protein S11.

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

- Molecule 15 is a protein called 30S ribosomal protein S12.

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

- Molecule 16 is a protein called 30S ribosomal protein S13.

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

- Molecule 17 is a protein called 30S ribosomal protein S14 type Z.

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

- Molecule 18 is a protein called 30S ribosomal protein S15.

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

- Molecule 19 is a protein called 30S ribosomal protein S16.

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

- Molecule 20 is a protein called 30S ribosomal protein S17.

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

- Molecule 21 is a protein called 30S ribosomal protein S18.

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

- Molecule 22 is a protein called 30S ribosomal protein S19.

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

- Molecule 23 is a protein called 30S ribosomal protein S20.

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

- Molecule 24 is a protein called 30S ribosomal protein S21.

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

- Molecule 25 is a protein called 50S ribosomal protein L2.

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

- Molecule 26 is a protein called 50S ribosomal protein L3.

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

- Molecule 27 is a protein called 50S ribosomal protein L4.

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

- Molecule 28 is a protein called 50S ribosomal protein L5.

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

- Molecule 29 is a protein called 50S ribosomal protein L6.

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

- Molecule 30 is a protein called 50S ribosomal protein L9.

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

- Molecule 31 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	g	126	960	612	167	178	3	0	0

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

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

- Molecule 33 is a protein called 50S ribosomal protein L13.

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

- Molecule 34 is a protein called 50S ribosomal protein L14.

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

- Molecule 35 is a protein called 50S ribosomal protein L15.

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

- Molecule 36 is a protein called 50S ribosomal protein L16.

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

- Molecule 37 is a protein called 50S ribosomal protein L17.

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

- Molecule 38 is a protein called 50S ribosomal protein L18.

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

- Molecule 39 is a protein called 50S ribosomal protein L19.

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

- Molecule 40 is a protein called 50S ribosomal protein L20.

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

- Molecule 41 is a protein called 50S ribosomal protein L21.

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

- Molecule 42 is a protein called 50S ribosomal protein L22.

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

- Molecule 43 is a protein called 50S ribosomal protein L23.

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

- Molecule 44 is a protein called 50S ribosomal protein L24.

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

- Molecule 45 is a protein called 50S ribosomal protein L27.

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

- Molecule 46 is a protein called 50S ribosomal protein L28.

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

- Molecule 47 is a protein called 50S ribosomal protein L29.

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

- Molecule 48 is a protein called 50S ribosomal protein L31.

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

- Molecule 49 is a protein called 50S ribosomal protein L32.

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

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

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

- Molecule 51 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 52 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

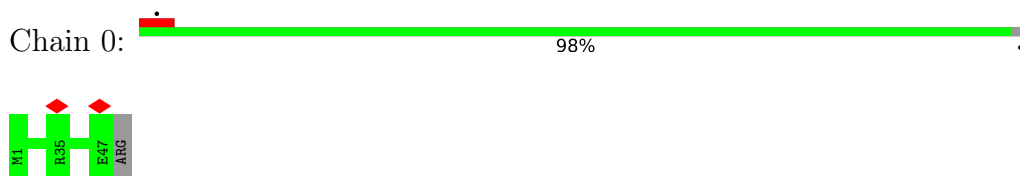
- Molecule 54 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	6	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
54	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

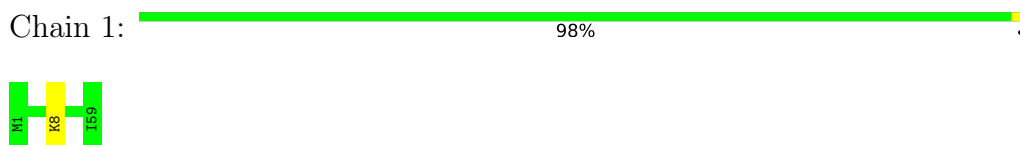
3 Residue-property plots [i](#)

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

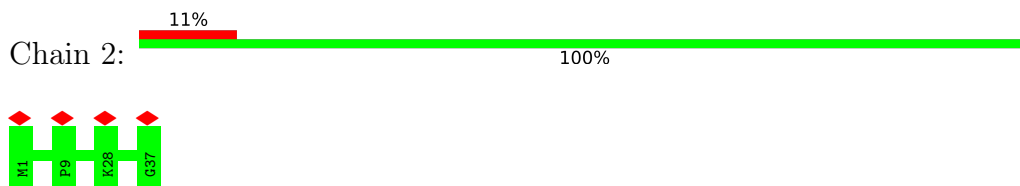
- Molecule 1: 50S ribosomal protein L34



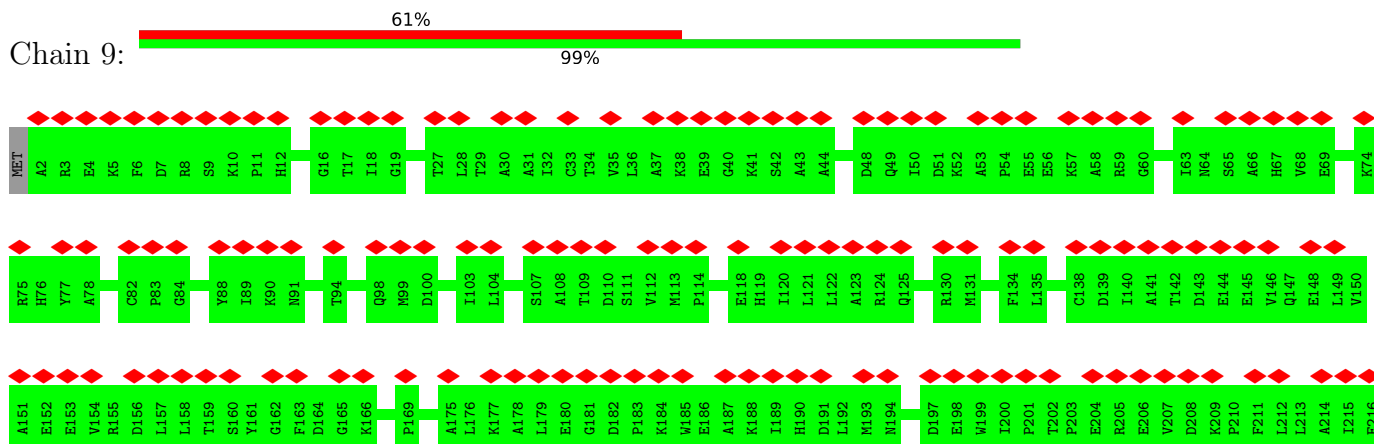
- Molecule 2: 50S ribosomal protein L35

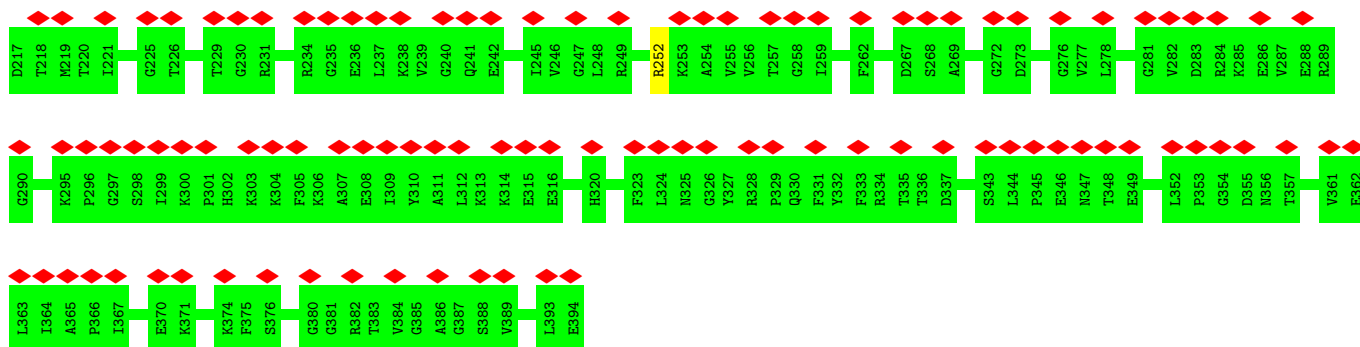


- Molecule 3: 50S ribosomal protein L36

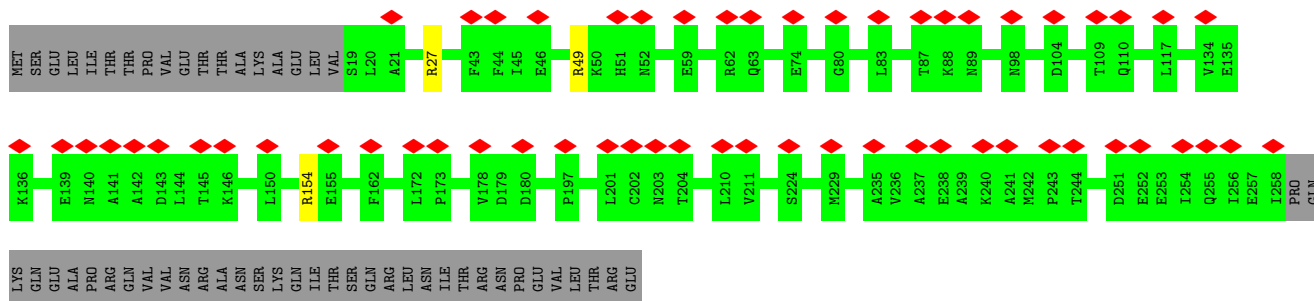
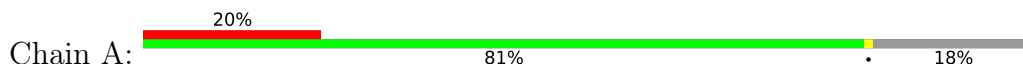


- Molecule 4: Elongation factor Tu

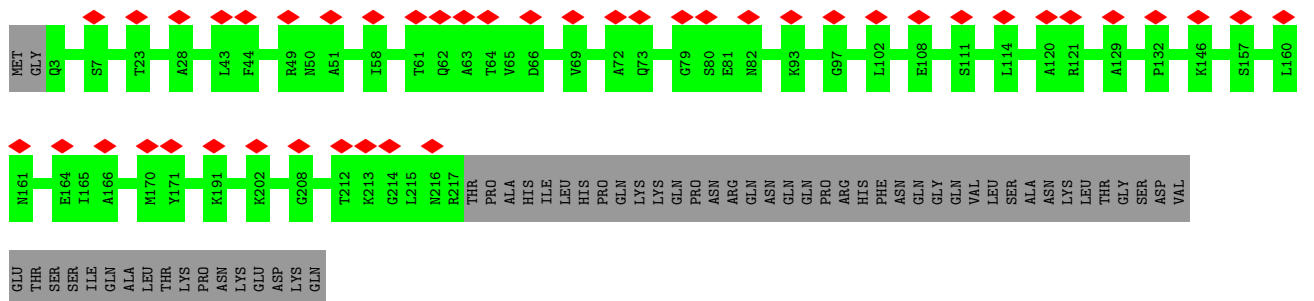
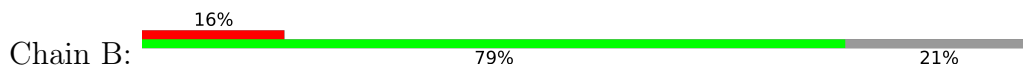




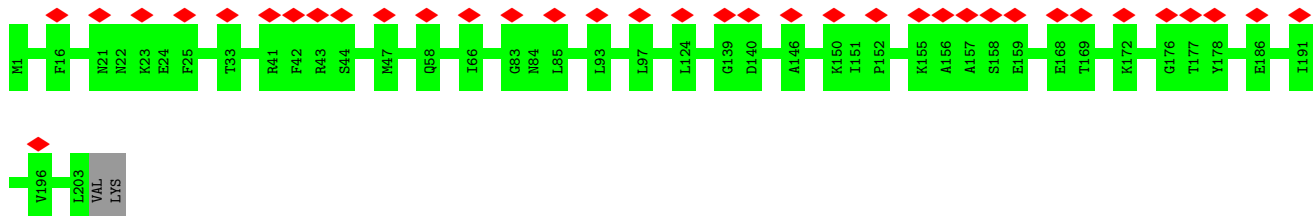
• Molecule 5: 30S ribosomal protein S2



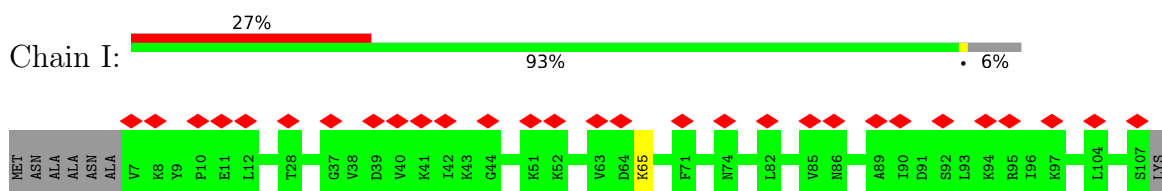
• Molecule 6: 30S ribosomal protein S3



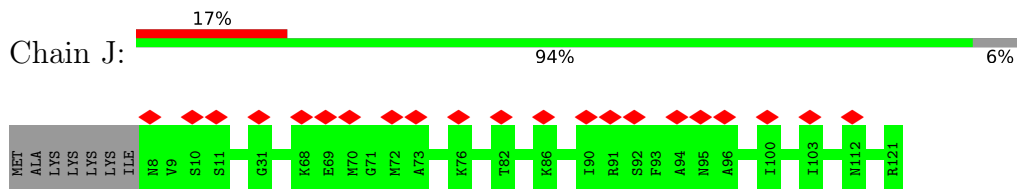
• Molecule 7: 30S ribosomal protein S4



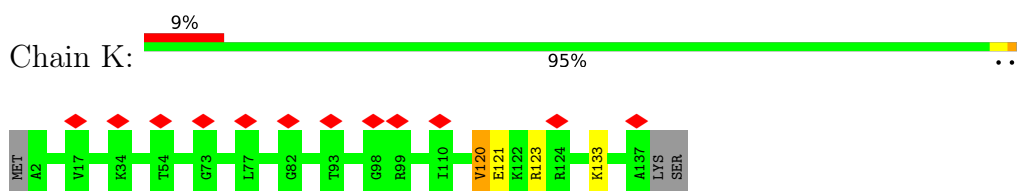
• Molecule 8: 30S ribosomal protein S5



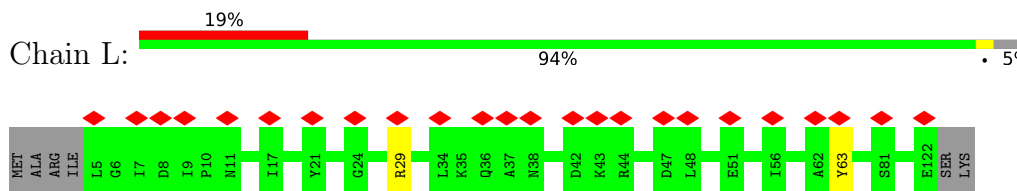
- Molecule 14: 30S ribosomal protein S11



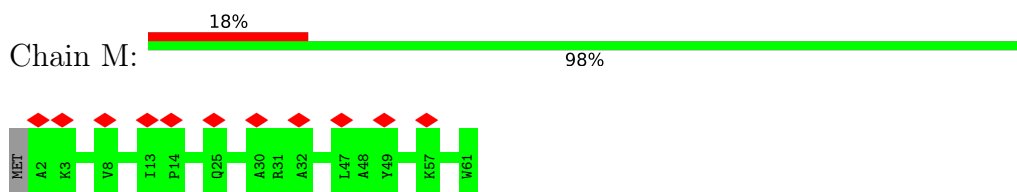
- Molecule 15: 30S ribosomal protein S12



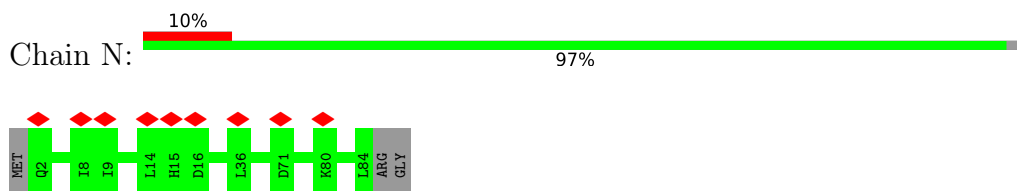
- Molecule 16: 30S ribosomal protein S13



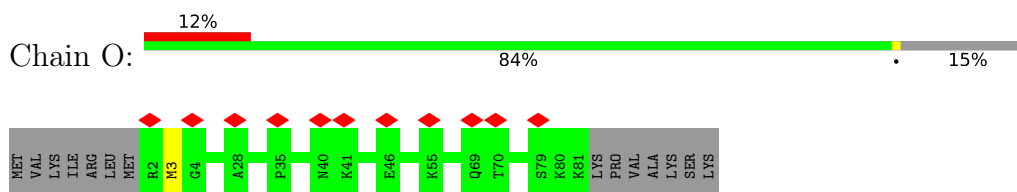
- Molecule 17: 30S ribosomal protein S14 type Z



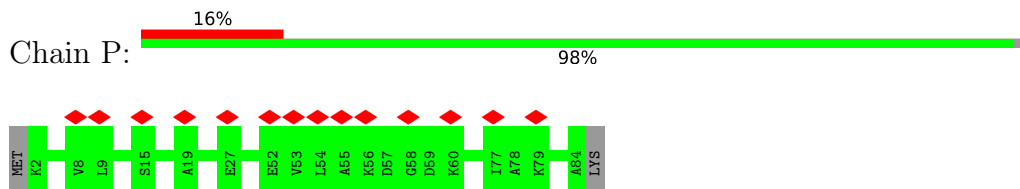
- Molecule 18: 30S ribosomal protein S15



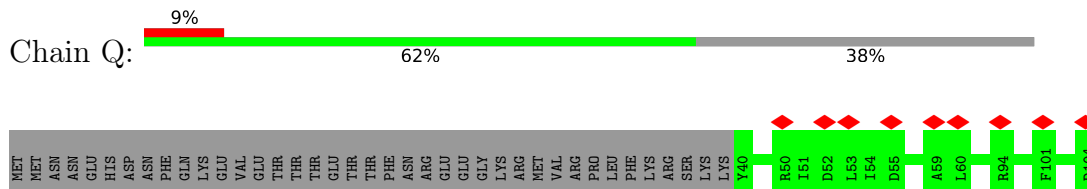
- Molecule 19: 30S ribosomal protein S16



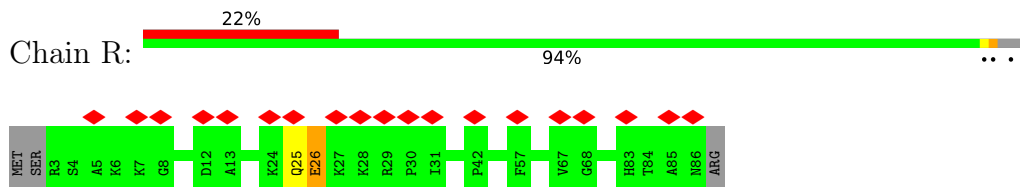
- Molecule 20: 30S ribosomal protein S17



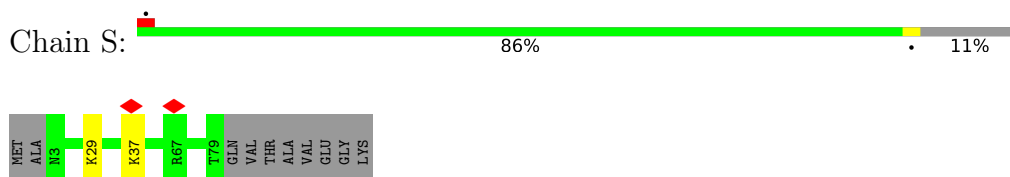
- Molecule 21: 30S ribosomal protein S18



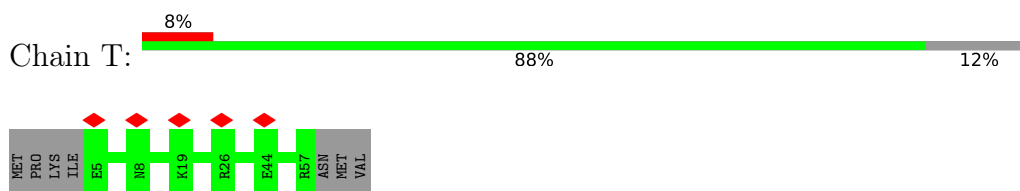
- Molecule 22: 30S ribosomal protein S19



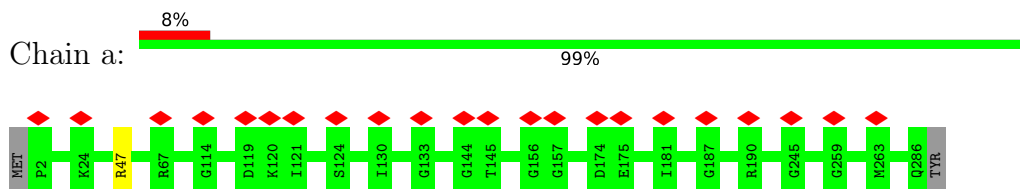
- Molecule 23: 30S ribosomal protein S20



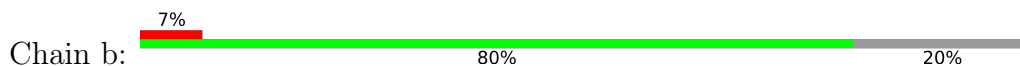
- Molecule 24: 30S ribosomal protein S21

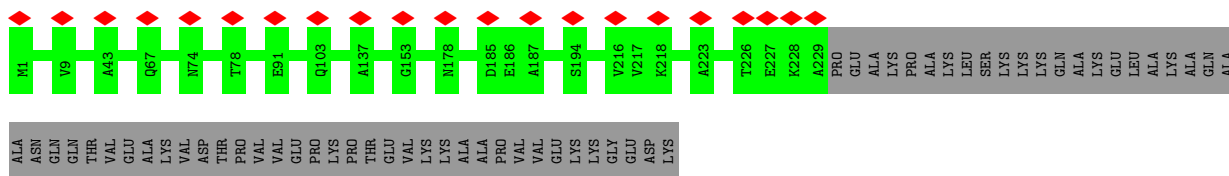


- Molecule 25: 50S ribosomal protein L2

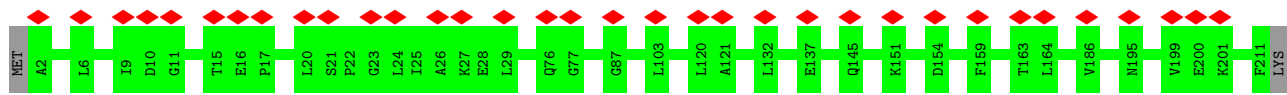


- Molecule 26: 50S ribosomal protein L3

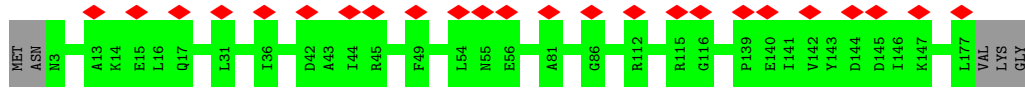




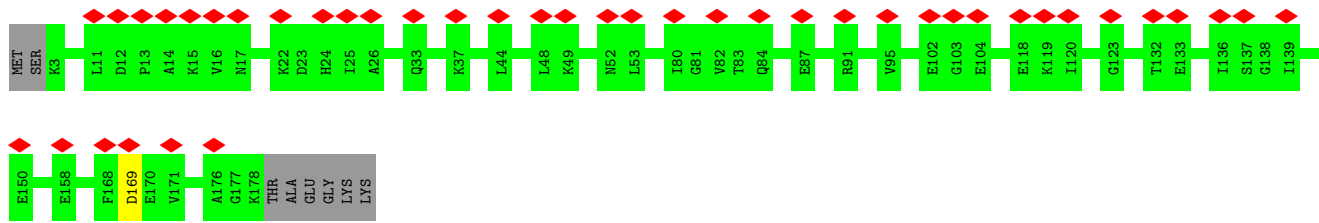
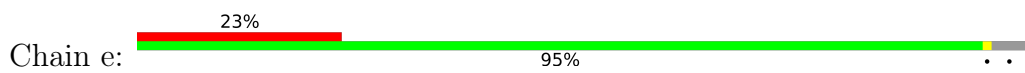
• Molecule 27: 50S ribosomal protein L4



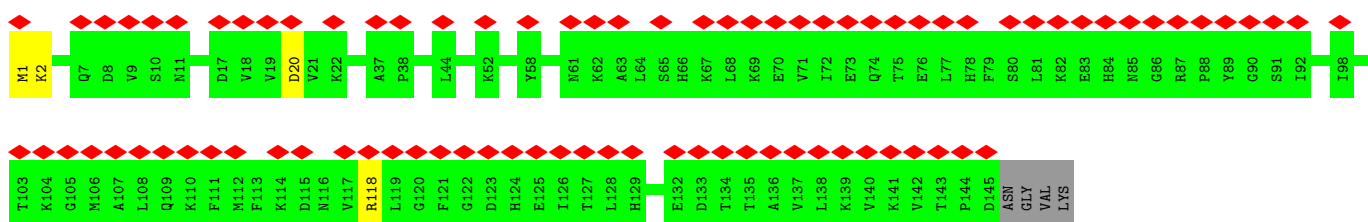
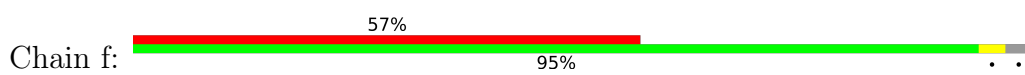
• Molecule 28: 50S ribosomal protein L5



• Molecule 29: 50S ribosomal protein L6

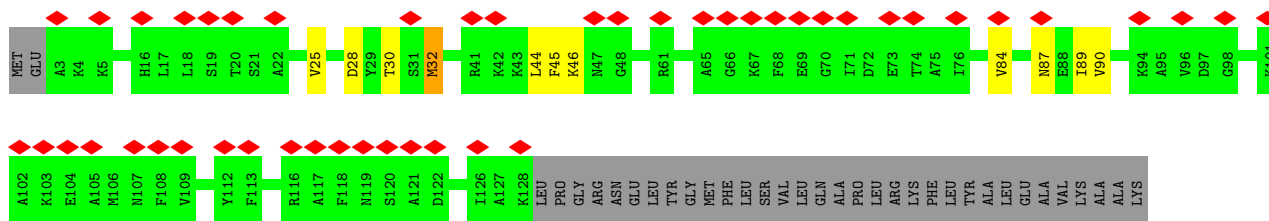


• Molecule 30: 50S ribosomal protein L9

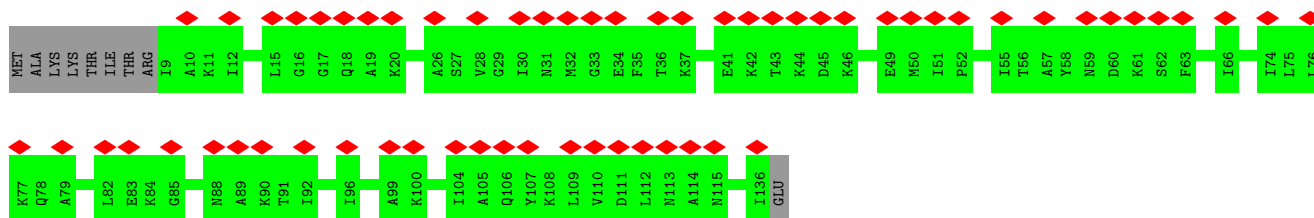
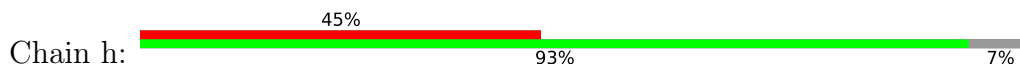


• Molecule 31: 50S ribosomal protein L10

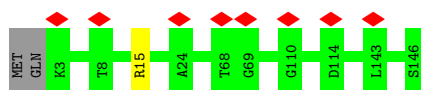




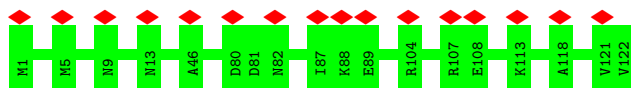
- Molecule 32: 50S ribosomal protein L11



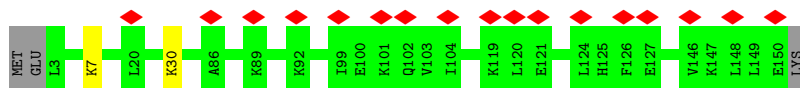
- Molecule 33: 50S ribosomal protein L13



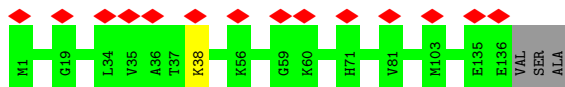
- Molecule 34: 50S ribosomal protein L14



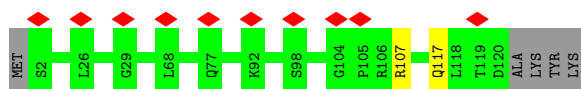
- Molecule 35: 50S ribosomal protein L15



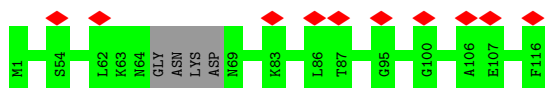
- Molecule 36: 50S ribosomal protein L16



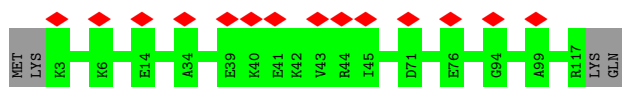
- Molecule 37: 50S ribosomal protein L17



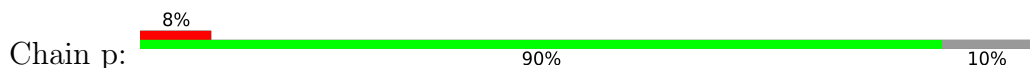
- Molecule 38: 50S ribosomal protein L18



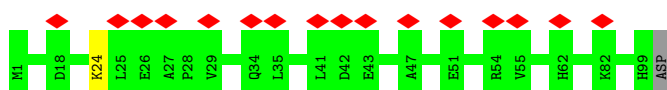
- Molecule 39: 50S ribosomal protein L19



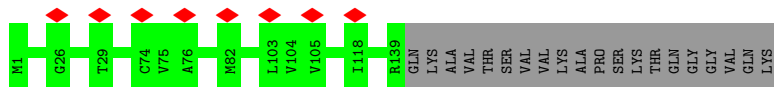
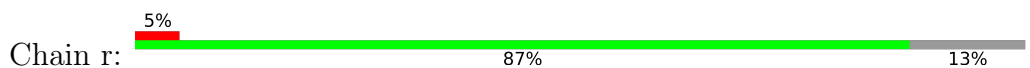
- Molecule 40: 50S ribosomal protein L20



- Molecule 41: 50S ribosomal protein L21

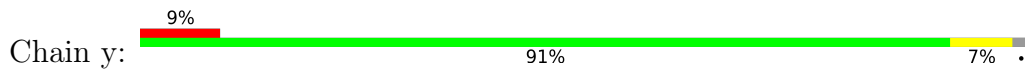


- Molecule 42: 50S ribosomal protein L22

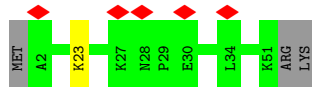
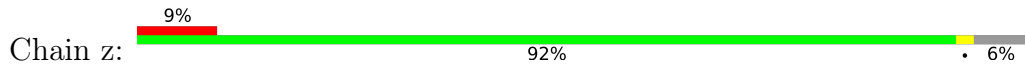


- Molecule 43: 50S ribosomal protein L23

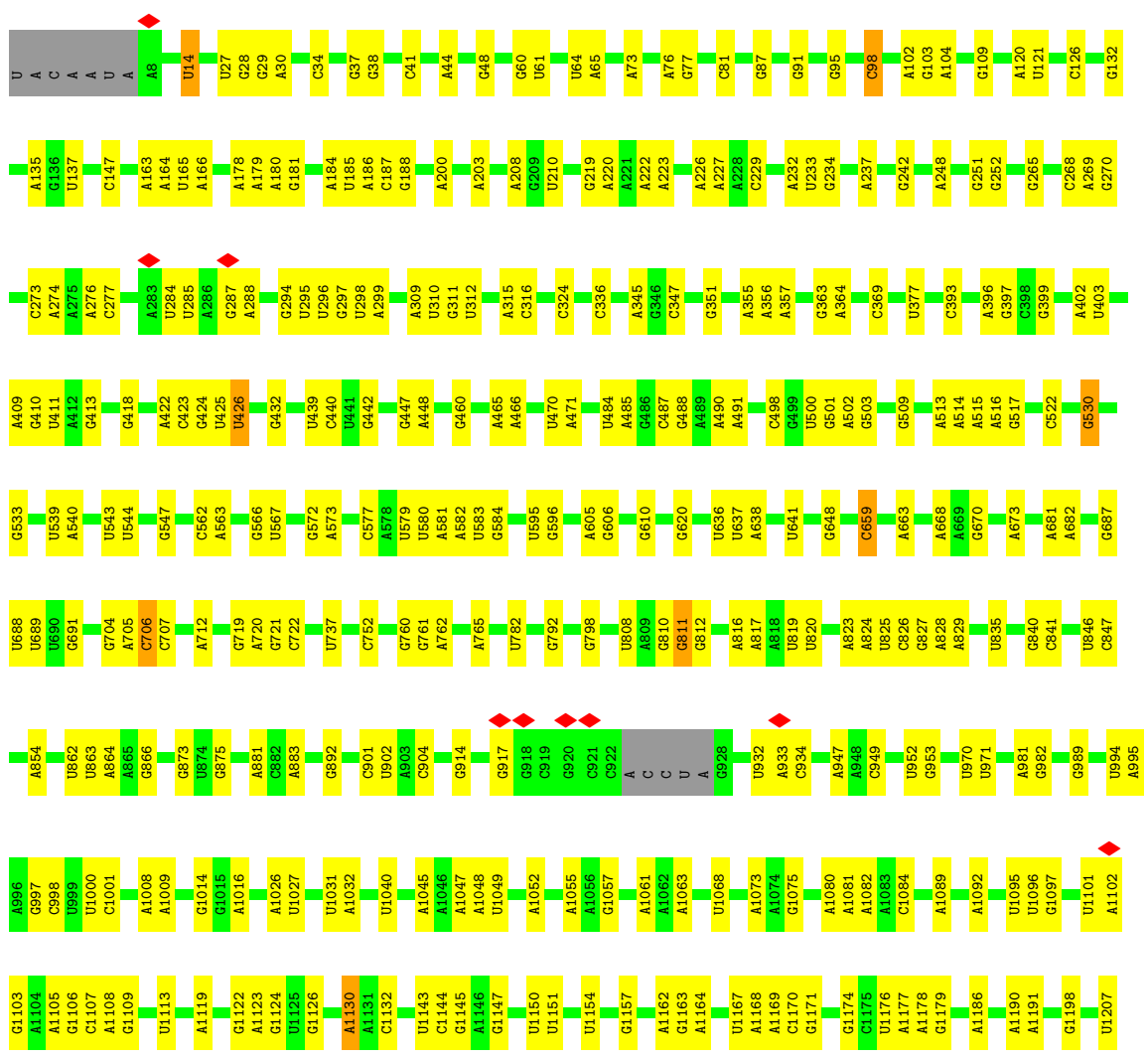




• Molecule 50: 50S ribosomal protein L33 1

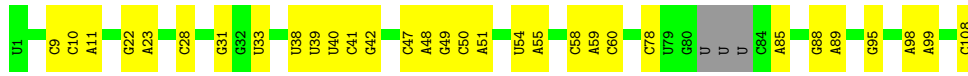


• Molecule 51: 23S ribosomal RNA

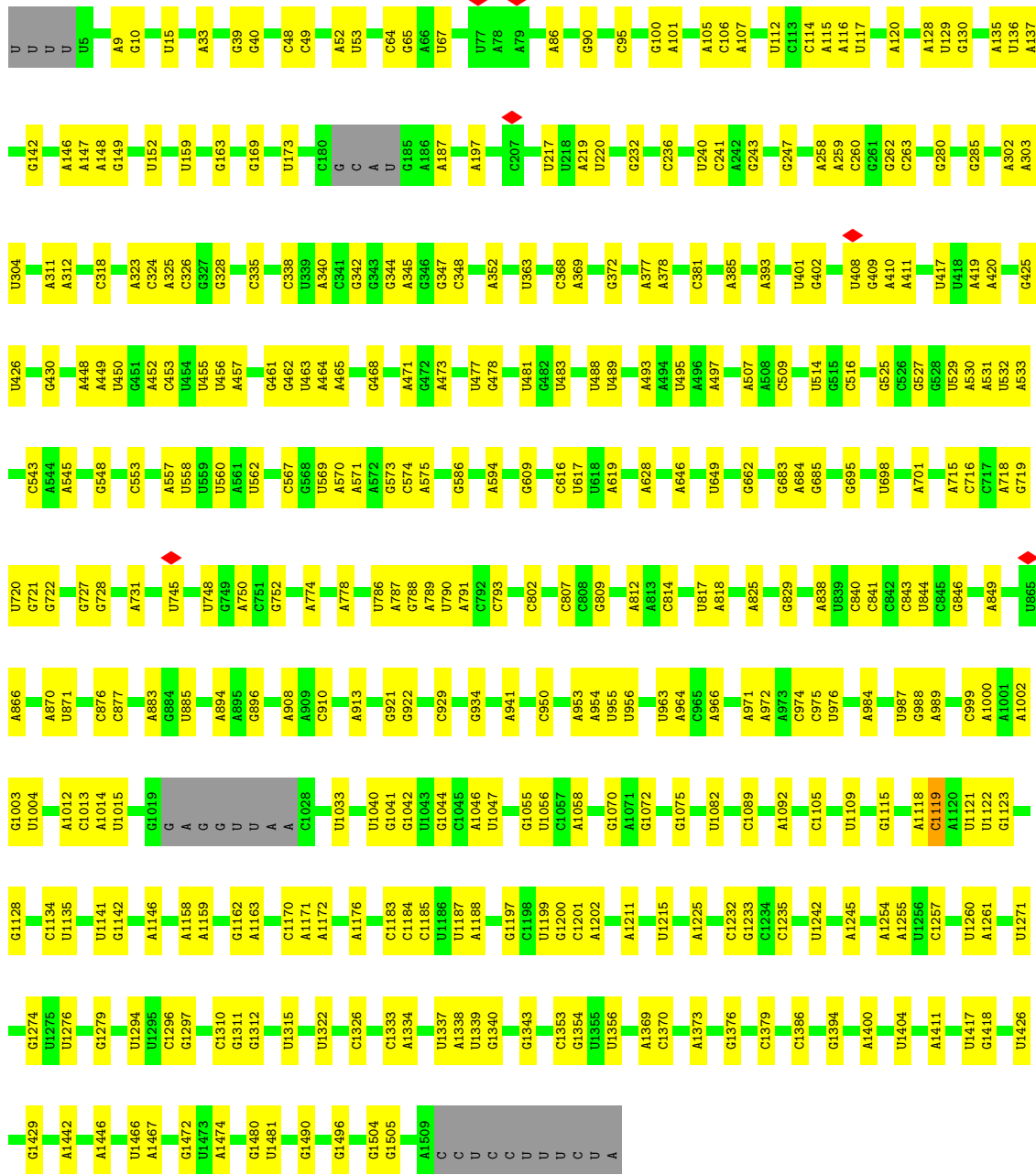


G2838	G2839	U2853	U2853	U2862	G2863	U2864	U2865	G2871	G2876	U2888	U2889	G2890	G2897	G2898	U2900	U	A	U	U	U	G	G	A	U2837																						
C2720	G2721	G2722	G2727	G2737	U2738	C2739	U2740	A2741	G2752	A2756	C2760	U2764	A2765	A2773	A2774	C2775	U2776	A2777	U2778	C2779	A2786	U2788	C2797	A2798	U2799	U2800	U2801	C2802	A2662	G2663	U2664	A2668	G2669	G2681	C2688	U2689	C2697	U2698	U2704	A2713	G2714					
U2481	U2484	U2485	U2486	U2487	U2488	G2492	G2498	U2499	G2502	G2503	C2504	U2505	A2506	C2507	U2508	C2509	G2510	A2511	U2512	G2513	U2514	G2515	G2642	U2643	U2644	U2645	G2649	U2662	G2663	U2664	A2668	G2669	G2681	C2688	U2689	C2697	U2698	U2704	A2713	G2714						
U2352	G2353	A2354	C2355	U2358	A2362	A2366	G2369	G2379	U2387	G2391	U2392	C2393	U2398	C2399	C2402	C2410	U2416	U2417	G2418	G2422	U2431	A2432	A2433	A2434	C2435	G2436	G2437	A2438	U2439	A2440	A2441	A2442	A2443	G2444	C2445	U2449	G2454	G2455	A2456	C2460	C2475					
U2212	A2220	U2221	C2222	A2233	G2246	G2247	U2251	G2254	U2257	G2258	G2259	A2274	A2275	A2276	G2286	G2287	G2290	U2291	A2294	A2295	C2301	C2302	A2306	G2311	G2312	U2313	G2316	A2317	A2324	U2327	U2327	U2327	A2330	G2333	U2334	A2335	G2341	U2342	A2343	A2344	U2351					
U1989	U1998	U1999	U2000	U2009	A2010	G2011	G2027	U2028	U2029	A2030	G2034	A2037	A2038	C2041	G2050	A2056	G2059	C2062	A2067	G2068	A2069	G2069	G2069	G2069	G2069	U2075	G2076	U2099	G2100	C2103	A2107	C2108	A2109	U2110	U2111	A2112	U2113	C2114	G2117	U2122	A2123					
G1870	A1873	G1876	G1880	U1888	U1889	U1890	A1891	G1906	A1907	A1908	C1909	G1910	G1913	G1914	A1920	C1921	C1927	A1934	A1935	G1936	U1937	U1938	G1942	A1943	A1944	A1945	U1946	A1951	G1952	A1960	A1961	U1962	U1963	C1964	C1965	G1966	C1970	G1971	U1974	A1977	U1978	G1979				
A1702	C1706	U1707	G1708	A1716	G1733	G1737	G1747	U1748	G1757	G1763	U1764	G1765	A1766	G1767	G1768	A1769	A1770	C1771	G1772	C1780	A1781	U1785	U1786	A1791	A1792	G1806	C1807	A1810	A1816	U1820	G1821	U1822	U1823	G1824	U1825	U1826	U1827	A1836	G1842	C1850	A1865					
A1570	G1571	G1576	G1580	G1583	U1584	A1585	A1588	A1589	A1592	A1600	A1601	G1602	A1603	U1612	G1615	G1616	U1617	U1618	A1619	A1637	G1640	G1642	A1643	A1644	C1645	C1651	A1652	U1655	A1656	A1661	G1662	G1663	A1664	G1665	G1668	U1672	U1673	G1681	C1682	A1694						
U1329	U1330	U1340	U1341	C1342	C1343	C1348	C1349	G1353	G1358	U1361	G1367	U1368	U1369	U1370	G1371	G1372	C1373	C1378	C1384	G1388	G1389	A1393	A1396	A1406	U1407	G1408	A1412	A1420	A1421	U1422	A1423	U1424	G1425	C1426	A1431	A1435	C1444	U1445	U1448	A1455						
C1456	G1463	U1466	U1467	C1473	C1474	A1480	U1481	U1482	G1483	U1486	U1487	G1492	A1493	G1504	G1505	U1506	G1508	U1509	A1510	A1513	U1514	A1515	U1522	C1523	A1532	U1533	A1534	A1535	A1541	A1548	U1549	G1550	G1557	A1558	U1559	U	G	A	A	G	U	G	A	U	C	A
A1208	U1209	A1210	U1211	C1212	U1213	G1215	U1216	G1226	U1234	C1247	A1250	G1251	C1252	G1253	U1254	G1255	A1256	G1257	C1258	U1260	U1261	G1262	G1266	U1267	A1283	A1284	U1285	G1286	A1292	U1293	G1294	A1295	A1298	G1301	C1302	U1303	U1304	G1309	C1321	U1322	A1323	G1326	U1327	A1328		

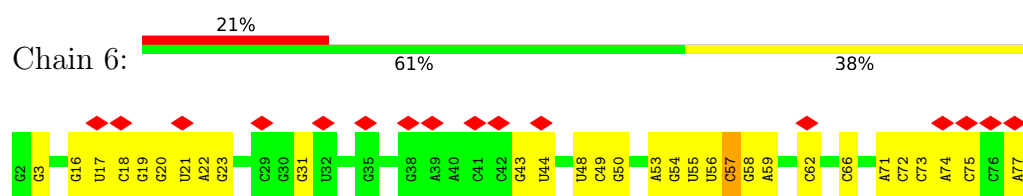
• Molecule 52: 5S ribosomal RNA



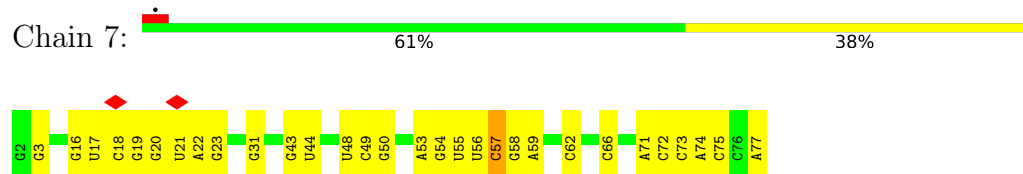
• Molecule 53: 16S ribosomal RNA



• Molecule 54: tRNA-Phe



• Molecule 54: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	2239	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.410	Depositor
Minimum map value	-1.114	Depositor
Average map value	0.026	Depositor
Map value standard deviation	0.144	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	Depositor

5 Model quality i

5.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.23	0/383	0.43	0/504
2	1	0.23	0/484	0.44	0/637
3	2	0.23	0/306	0.45	0/401
4	9	0.24	0/3071	0.47	0/4147
5	A	0.25	0/1954	0.45	0/2642
6	B	0.24	0/1721	0.48	0/2323
7	C	0.25	0/1691	0.44	0/2267
8	D	0.25	0/1188	0.46	0/1593
9	E	0.24	0/1384	0.46	0/1867
10	F	0.23	0/1266	0.44	0/1700
11	G	0.26	0/1126	0.47	0/1517
12	H	0.24	0/1044	0.44	0/1395
13	I	0.23	0/820	0.47	0/1103
14	J	0.25	0/844	0.42	0/1136
15	K	0.28	0/1094	0.52	0/1468
16	L	3.69	8/962 (0.8%)	1.01	6/1289 (0.5%)
17	M	0.24	0/483	0.44	0/643
18	N	0.22	0/679	0.42	0/907
19	O	0.23	0/659	0.43	0/885
20	P	0.24	0/684	0.47	0/913
21	Q	0.23	0/545	0.44	0/730
22	R	0.26	0/698	0.53	1/936 (0.1%)
23	S	0.23	0/631	0.42	0/838
24	T	0.22	0/475	0.40	0/621
25	a	0.23	0/2267	0.44	0/3044
26	b	0.25	0/1795	0.48	0/2412
27	c	0.24	0/1671	0.46	0/2246
28	d	0.24	0/1409	0.45	0/1894
29	e	0.25	0/1420	0.48	1/1912 (0.1%)
30	f	0.25	0/1205	0.49	1/1616 (0.1%)
31	g	0.34	0/969	0.58	0/1295
32	h	0.26	0/968	0.46	0/1298
33	i	0.24	0/1186	0.43	0/1592
34	j	0.24	0/953	0.45	0/1275

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	k	0.24	0/1170	0.46	0/1559
36	l	0.25	0/1104	0.46	0/1481
37	m	0.24	0/973	0.46	0/1309
38	n	0.23	0/897	0.44	0/1198
39	o	0.24	0/948	0.44	0/1262
40	p	0.23	0/961	0.40	0/1278
41	q	0.25	0/828	0.48	0/1111
42	r	0.24	0/1077	0.43	0/1441
43	s	0.25	0/732	0.48	0/988
44	t	0.23	0/879	0.43	0/1165
45	u	0.24	0/665	0.45	0/884
46	v	0.22	0/519	0.48	0/695
47	w	0.23	0/826	0.40	0/1104
48	x	0.25	0/353	0.44	0/474
49	y	0.28	0/457	0.52	0/601
50	z	0.23	0/412	0.43	0/547
51	3	0.58	8/69073 (0.0%)	0.81	60/107710 (0.1%)
52	4	0.17	0/2505	0.74	0/3902
53	5	0.19	0/35768	0.78	28/55764 (0.1%)
54	6	0.59	2/1808 (0.1%)	0.93	7/2817 (0.2%)
54	7	0.60	2/1808 (0.1%)	0.93	7/2817 (0.2%)
All	All	0.51	20/161798 (0.0%)	0.73	111/241153 (0.0%)

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	3	1130	A	N3-C4	80.97	1.83	1.34
51	3	1130	A	C6-N1	66.55	1.82	1.35
16	L	63	TYR	CD1-CE1	63.20	2.34	1.39
16	L	63	TYR	CD2-CE2	58.27	2.26	1.39
51	3	1130	A	C5-C4	51.22	1.74	1.38

The worst 5 of 111 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	3	1130	A	N1-C2-N3	-28.25	115.17	129.30
51	3	1130	A	C2-N3-C4	22.99	122.09	110.60
16	L	29	ARG	CD-NE-CZ	21.55	153.77	123.60
16	L	29	ARG	NE-CZ-NH2	20.36	130.48	120.30
51	3	1130	A	C4-C5-N7	-17.15	102.12	110.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

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	45/48 (94%)	44 (98%)	1 (2%)	0	100	100
2	1	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
3	2	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
4	9	391/394 (99%)	366 (94%)	25 (6%)	0	100	100
5	A	238/294 (81%)	223 (94%)	15 (6%)	0	100	100
6	B	213/273 (78%)	202 (95%)	11 (5%)	0	100	100
7	C	201/205 (98%)	193 (96%)	8 (4%)	0	100	100
8	D	151/219 (69%)	146 (97%)	5 (3%)	0	100	100
9	E	165/215 (77%)	149 (90%)	16 (10%)	0	100	100
10	F	152/155 (98%)	147 (97%)	5 (3%)	0	100	100
11	G	139/142 (98%)	128 (92%)	10 (7%)	1 (1%)	22	63
12	H	126/132 (96%)	115 (91%)	11 (9%)	0	100	100
13	I	99/108 (92%)	84 (85%)	15 (15%)	0	100	100
14	J	112/121 (93%)	109 (97%)	3 (3%)	0	100	100
15	K	134/139 (96%)	114 (85%)	19 (14%)	1 (1%)	22	63
16	L	116/124 (94%)	106 (91%)	10 (9%)	0	100	100
17	M	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
18	N	81/86 (94%)	79 (98%)	2 (2%)	0	100	100
19	O	78/94 (83%)	72 (92%)	6 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	P	81/85 (95%)	78 (96%)	3 (4%)	0	100	100
21	Q	63/104 (61%)	57 (90%)	6 (10%)	0	100	100
22	R	82/87 (94%)	72 (88%)	10 (12%)	0	100	100
23	S	75/87 (86%)	73 (97%)	2 (3%)	0	100	100
24	T	51/60 (85%)	48 (94%)	3 (6%)	0	100	100
25	a	283/287 (99%)	264 (93%)	19 (7%)	0	100	100
26	b	227/287 (79%)	214 (94%)	13 (6%)	0	100	100
27	c	208/212 (98%)	197 (95%)	11 (5%)	0	100	100
28	d	173/180 (96%)	161 (93%)	12 (7%)	0	100	100
29	e	174/184 (95%)	165 (95%)	9 (5%)	0	100	100
30	f	143/149 (96%)	131 (92%)	12 (8%)	0	100	100
31	g	124/161 (77%)	109 (88%)	11 (9%)	4 (3%)	4	26
32	h	126/137 (92%)	117 (93%)	9 (7%)	0	100	100
33	i	142/146 (97%)	132 (93%)	10 (7%)	0	100	100
34	j	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
35	k	146/151 (97%)	137 (94%)	9 (6%)	0	100	100
36	l	134/139 (96%)	125 (93%)	9 (7%)	0	100	100
37	m	117/124 (94%)	108 (92%)	9 (8%)	0	100	100
38	n	108/116 (93%)	101 (94%)	7 (6%)	0	100	100
39	o	113/119 (95%)	107 (95%)	6 (5%)	0	100	100
40	p	112/127 (88%)	109 (97%)	3 (3%)	0	100	100
41	q	97/100 (97%)	83 (86%)	14 (14%)	0	100	100
42	r	137/159 (86%)	130 (95%)	7 (5%)	0	100	100
43	s	90/237 (38%)	82 (91%)	8 (9%)	0	100	100
44	t	109/111 (98%)	104 (95%)	5 (5%)	0	100	100
45	u	84/104 (81%)	81 (96%)	3 (4%)	0	100	100
46	v	61/65 (94%)	58 (95%)	3 (5%)	0	100	100
47	w	96/111 (86%)	91 (95%)	5 (5%)	0	100	100
48	x	42/97 (43%)	39 (93%)	3 (7%)	0	100	100
49	y	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
50	z	48/53 (91%)	45 (94%)	3 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	6211/7064 (88%)	5803 (93%)	402 (6%)	6 (0%)	54 85

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	K	120	VAL
11	G	108	LEU
31	g	28	ASP
31	g	87	ASN
31	g	32	MET

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	0	40/41 (98%)	40 (100%)	0	100 100
2	1	51/51 (100%)	50 (98%)	1 (2%)	55 74
3	2	35/35 (100%)	35 (100%)	0	100 100
4	9	324/325 (100%)	323 (100%)	1 (0%)	92 95
5	A	212/262 (81%)	209 (99%)	3 (1%)	67 80
6	B	180/232 (78%)	180 (100%)	0	100 100
7	C	181/183 (99%)	181 (100%)	0	100 100
8	D	123/178 (69%)	121 (98%)	2 (2%)	62 79
9	E	150/196 (76%)	150 (100%)	0	100 100
10	F	131/132 (99%)	131 (100%)	0	100 100
11	G	123/124 (99%)	122 (99%)	1 (1%)	81 89
12	H	111/115 (96%)	110 (99%)	1 (1%)	78 87
13	I	95/99 (96%)	94 (99%)	1 (1%)	73 84
14	J	91/97 (94%)	91 (100%)	0	100 100
15	K	117/120 (98%)	113 (97%)	4 (3%)	37 60
16	L	100/105 (95%)	100 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	M	47/48 (98%)	47 (100%)	0	100	100
18	N	76/78 (97%)	76 (100%)	0	100	100
19	O	69/82 (84%)	68 (99%)	1 (1%)	67	80
20	P	73/75 (97%)	73 (100%)	0	100	100
21	Q	56/94 (60%)	56 (100%)	0	100	100
22	R	74/77 (96%)	72 (97%)	2 (3%)	44	65
23	S	70/77 (91%)	68 (97%)	2 (3%)	42	64
24	T	49/56 (88%)	49 (100%)	0	100	100
25	a	241/243 (99%)	240 (100%)	1 (0%)	91	94
26	b	186/233 (80%)	186 (100%)	0	100	100
27	c	182/184 (99%)	182 (100%)	0	100	100
28	d	150/154 (97%)	150 (100%)	0	100	100
29	e	153/159 (96%)	153 (100%)	0	100	100
30	f	131/134 (98%)	128 (98%)	3 (2%)	50	70
31	g	101/129 (78%)	93 (92%)	8 (8%)	12	36
32	h	102/110 (93%)	102 (100%)	0	100	100
33	i	126/128 (98%)	125 (99%)	1 (1%)	81	89
34	j	103/103 (100%)	103 (100%)	0	100	100
35	k	123/126 (98%)	121 (98%)	2 (2%)	62	79
36	l	113/115 (98%)	112 (99%)	1 (1%)	78	87
37	m	105/109 (96%)	103 (98%)	2 (2%)	57	75
38	n	96/99 (97%)	96 (100%)	0	100	100
39	o	101/105 (96%)	101 (100%)	0	100	100
40	p	100/108 (93%)	100 (100%)	0	100	100
41	q	90/91 (99%)	89 (99%)	1 (1%)	73	84
42	r	116/132 (88%)	116 (100%)	0	100	100
43	s	82/208 (39%)	82 (100%)	0	100	100
44	t	96/96 (100%)	95 (99%)	1 (1%)	76	86
45	u	69/85 (81%)	68 (99%)	1 (1%)	67	80
46	v	58/60 (97%)	58 (100%)	0	100	100
47	w	87/98 (89%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	x	41/86 (48%)	41 (100%)	0	100	100
49	y	48/49 (98%)	44 (92%)	4 (8%)	11	34
50	z	47/50 (94%)	46 (98%)	1 (2%)	53	72
All	All	5425/6076 (89%)	5380 (99%)	45 (1%)	82	89

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	g	84	VAL
37	m	107	ARG
31	g	89	ILE
35	k	7	LYS
41	q	24	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
26	b	144	GLN
28	d	127	ASN
38	n	7	GLN
29	e	58	ASN
28	d	27	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	3	2875/2907 (98%)	779 (27%)	32 (1%)
52	4	103/108 (95%)	29 (28%)	4 (3%)
53	5	1490/1520 (98%)	341 (22%)	7 (0%)
54	6	75/76 (98%)	28 (37%)	5 (6%)
54	7	75/76 (98%)	28 (37%)	5 (6%)
All	All	4618/4687 (98%)	1205 (26%)	53 (1%)

5 of 1205 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	3	14	U
51	3	27	U
51	3	28	G

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Mol	Chain	Res	Type
51	3	29	G
51	3	30	A

5 of 53 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	3	2604	U
52	4	59	A
54	7	18	C
51	3	2668	A
52	4	10	C

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 monosaccharides 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.

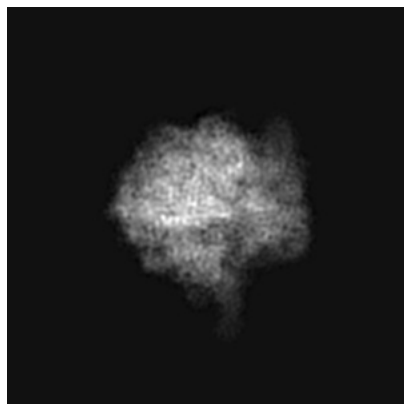
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13433. These allow visual inspection of the internal detail of the map and identification of artifacts.

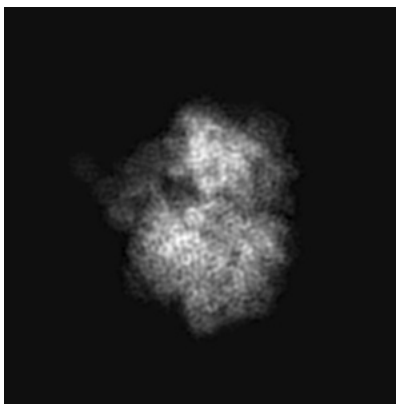
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

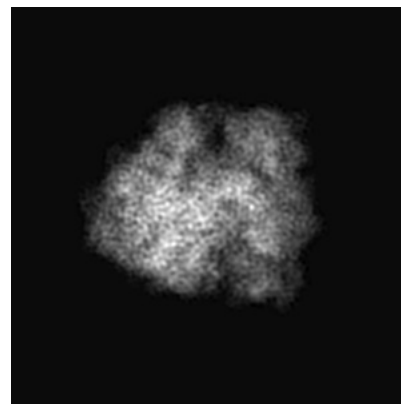
6.1.1 Primary map



X

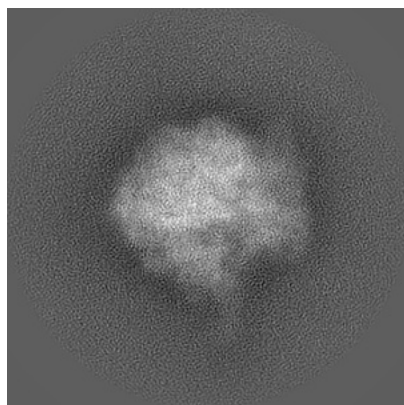


Y

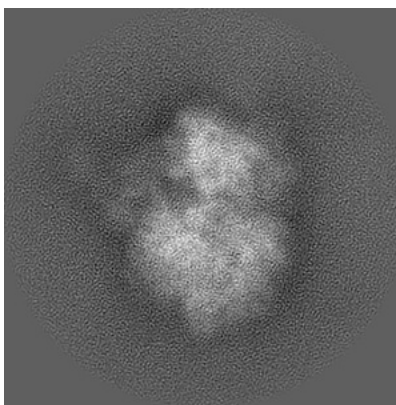


Z

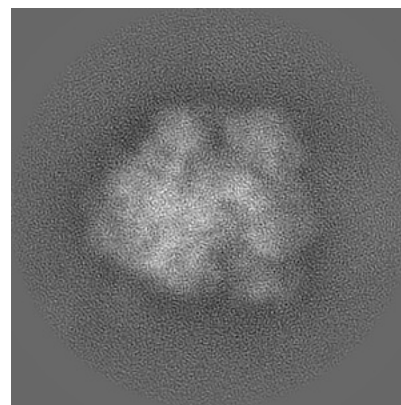
6.1.2 Raw map



X



Y

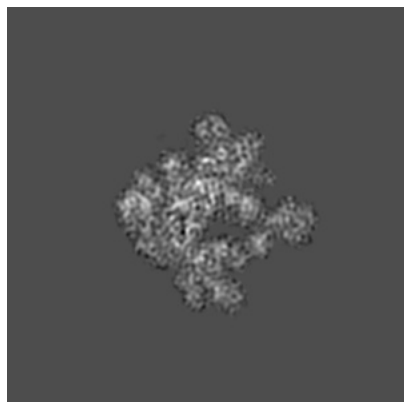


Z

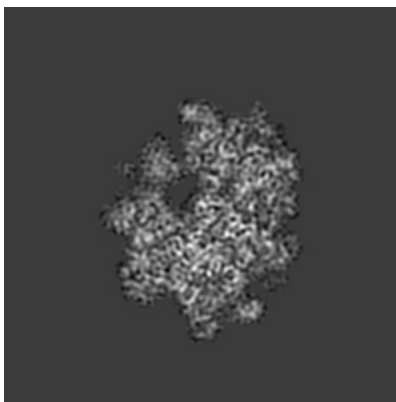
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

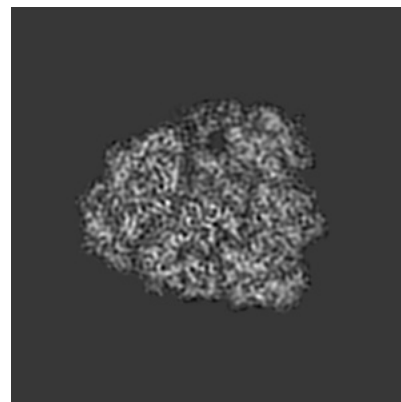
6.2.1 Primary map



X Index: 128

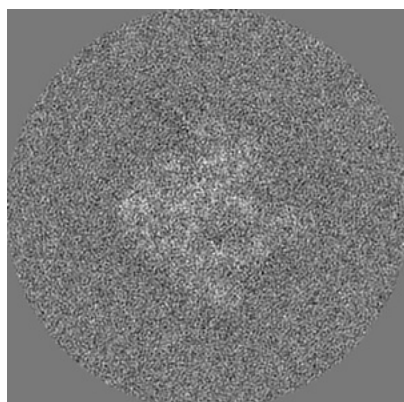


Y Index: 128

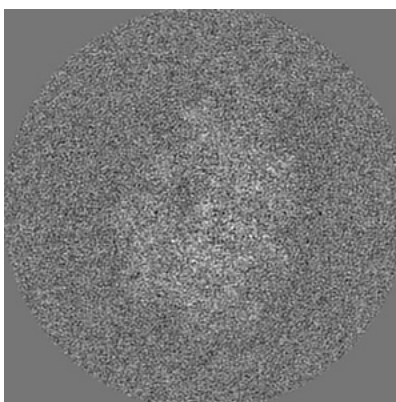


Z Index: 128

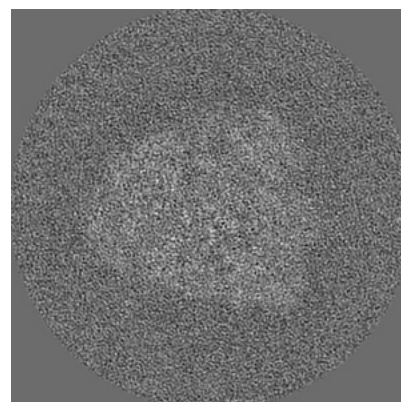
6.2.2 Raw map



X Index: 128



Y Index: 128

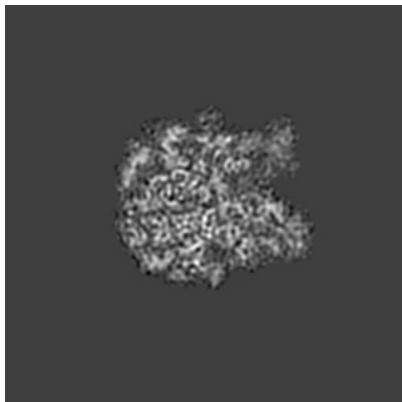


Z Index: 128

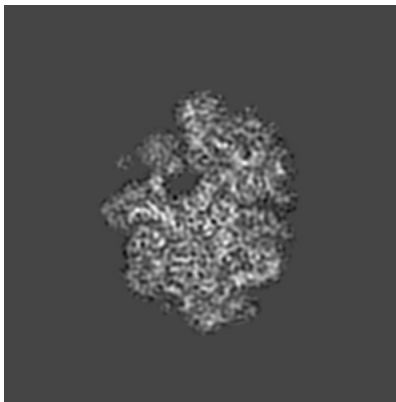
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

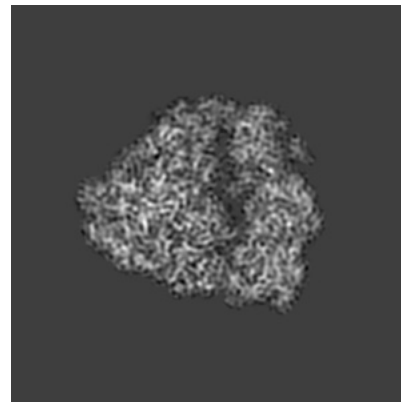
6.3.1 Primary map



X Index: 103

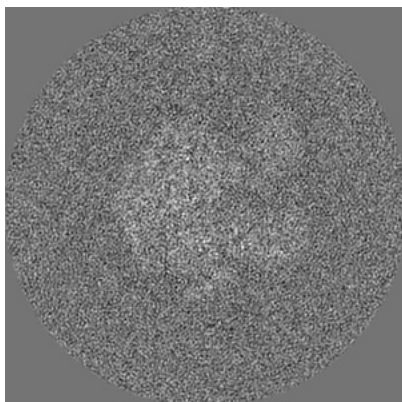


Y Index: 120

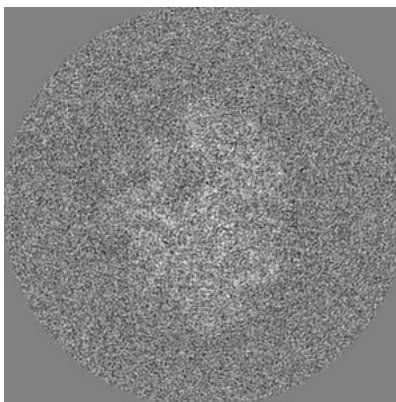


Z Index: 122

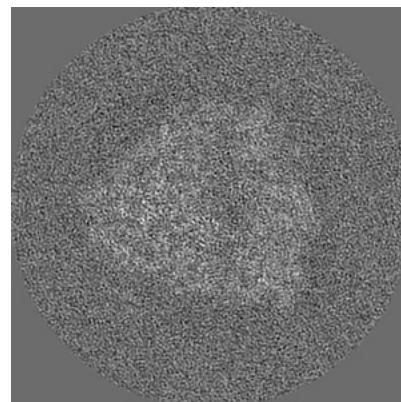
6.3.2 Raw map



X Index: 114



Y Index: 120



Z Index: 122

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

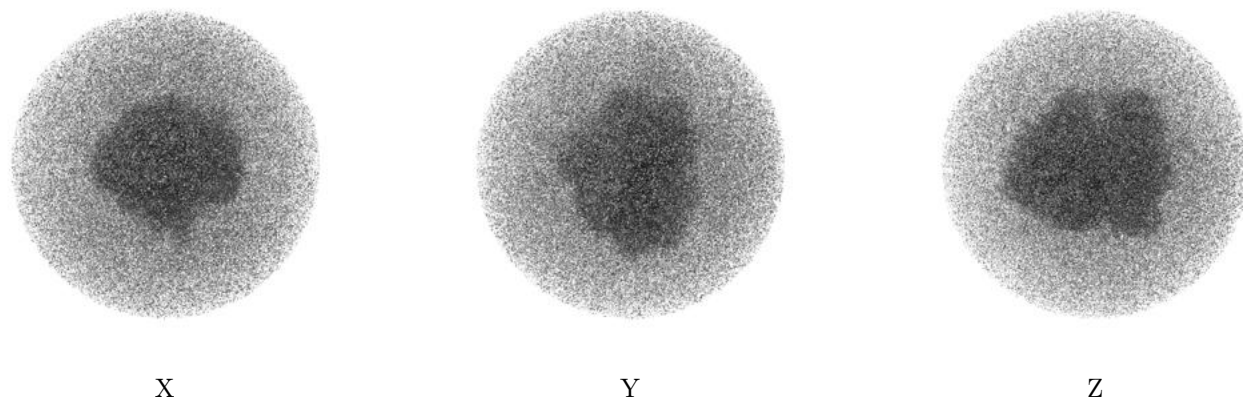
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

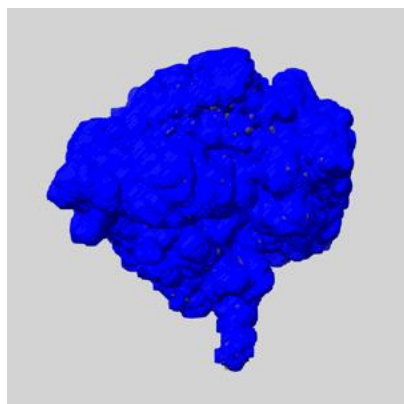
6.5 Mask visualisation [i](#)

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

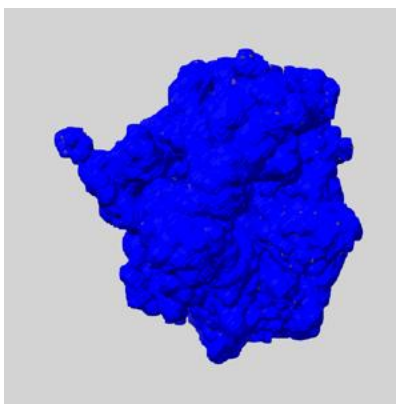
A mask typically either:

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

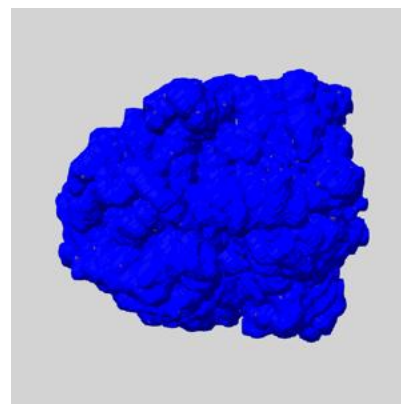
6.5.1 emd_13433_msk_1.map [i](#)



X



Y

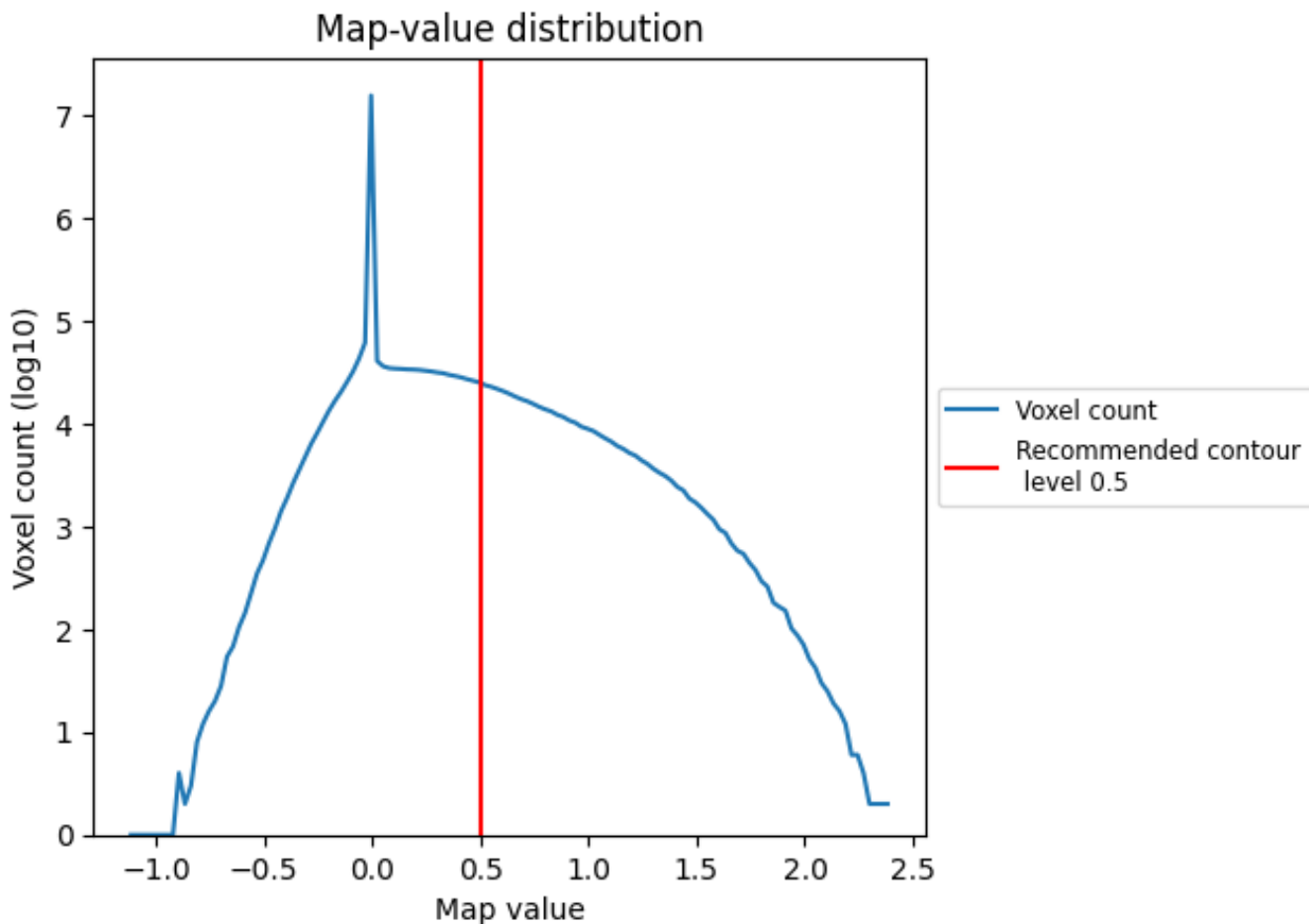


Z

7 Map analysis [i](#)

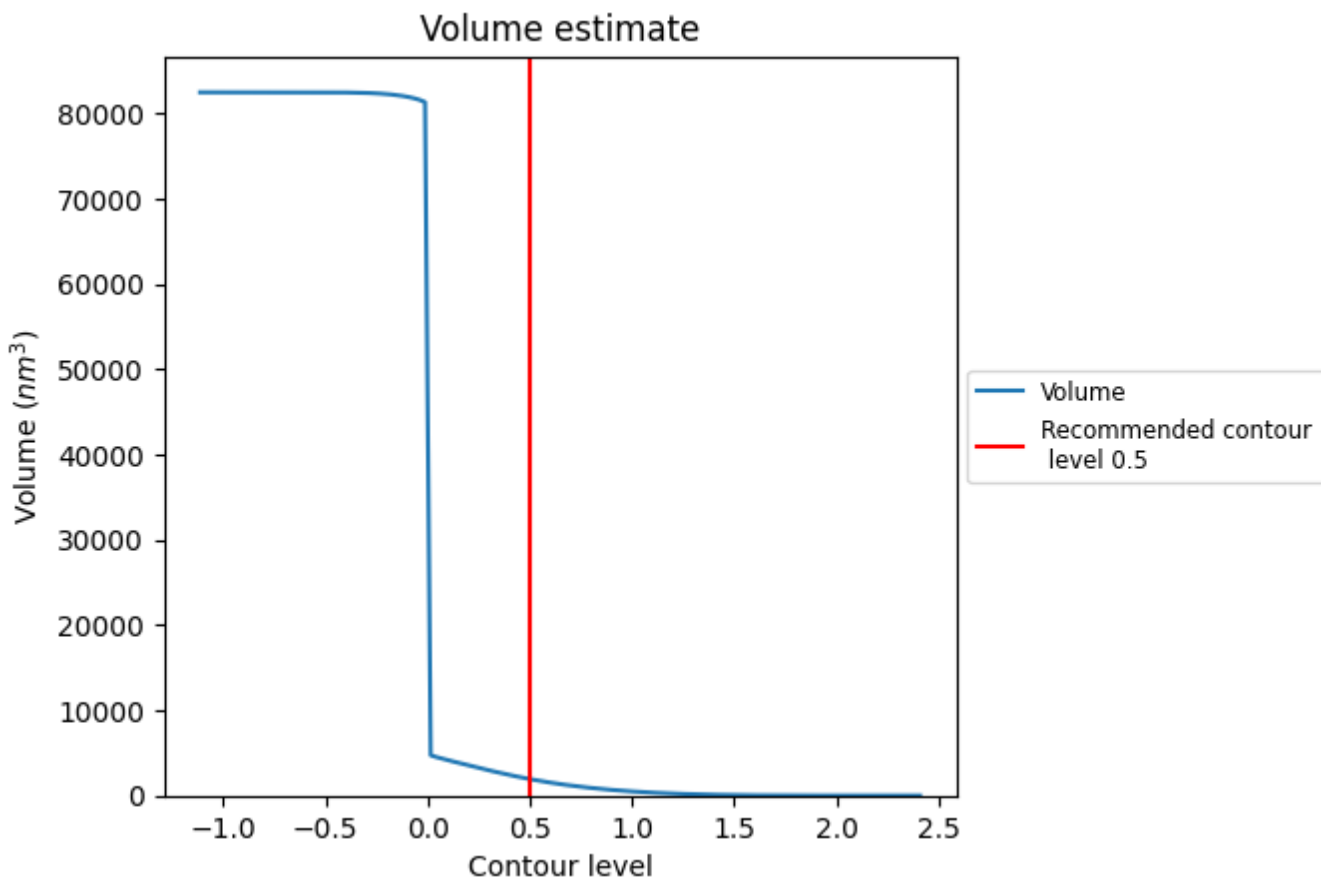
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

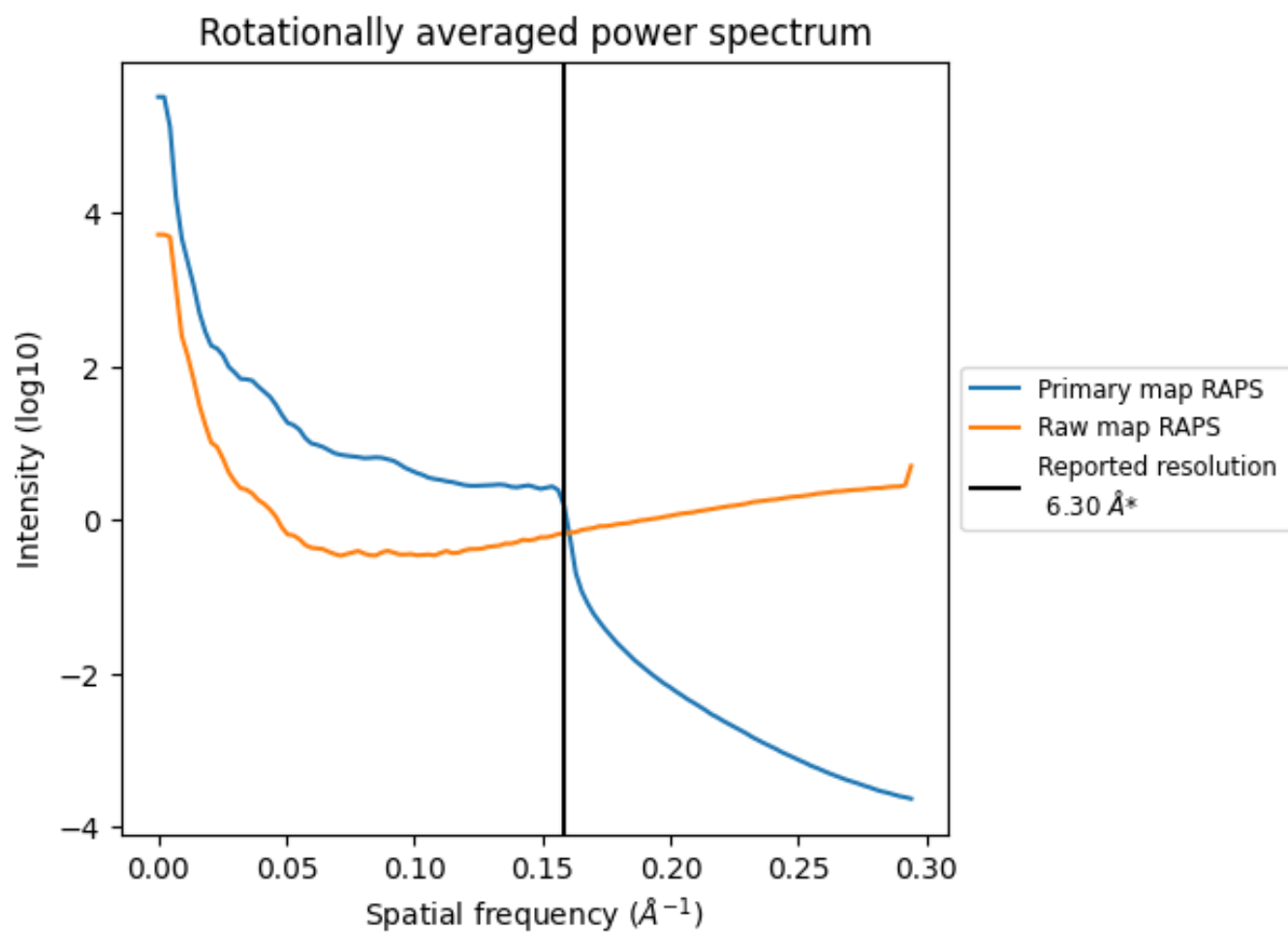
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1935 nm³; this corresponds to an approximate mass of 1748 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 [i](#)

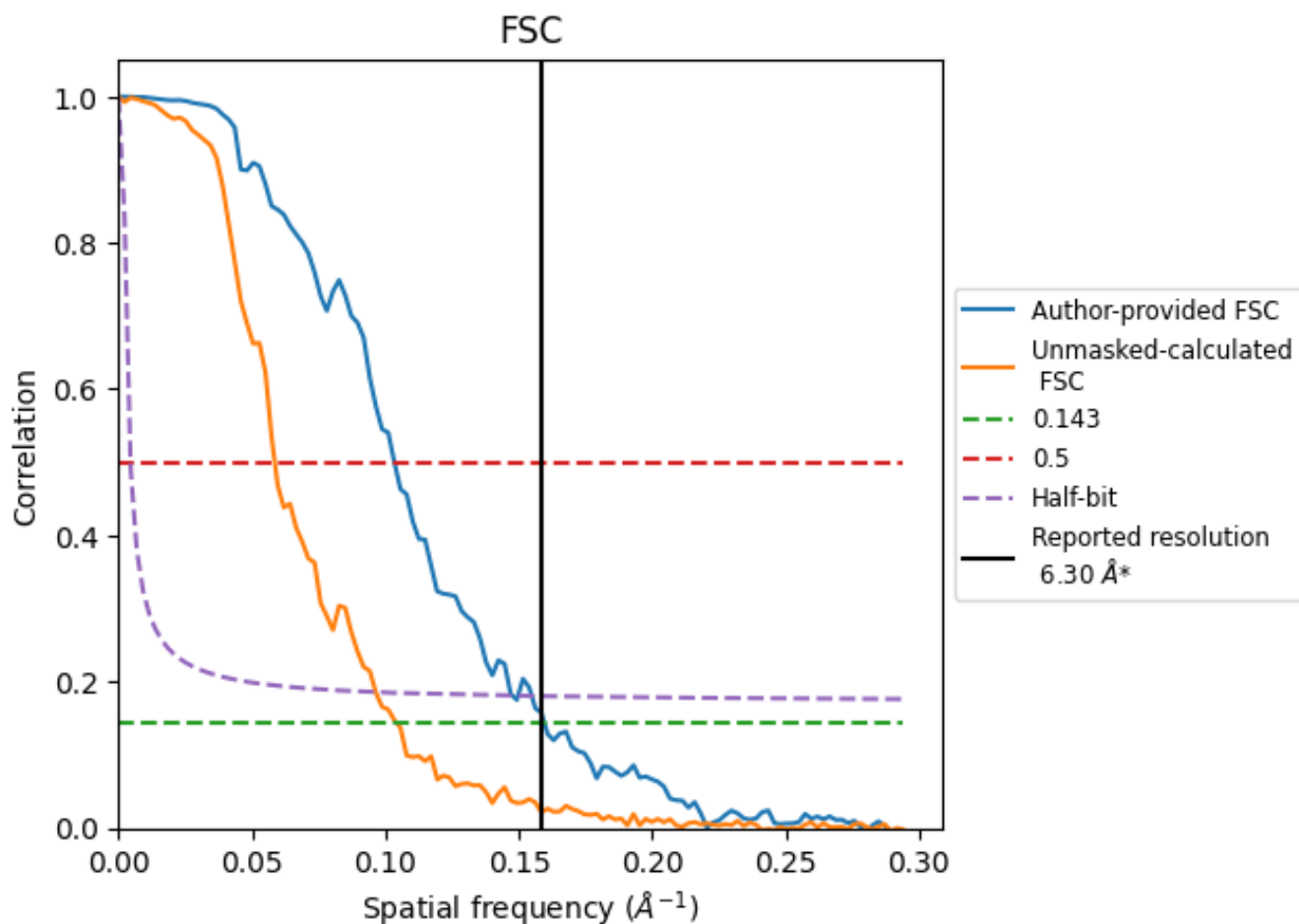


*Reported resolution corresponds to spatial frequency of 0.159 \AA^{-1}

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 0.159 Å⁻¹

8.2 Resolution estimates

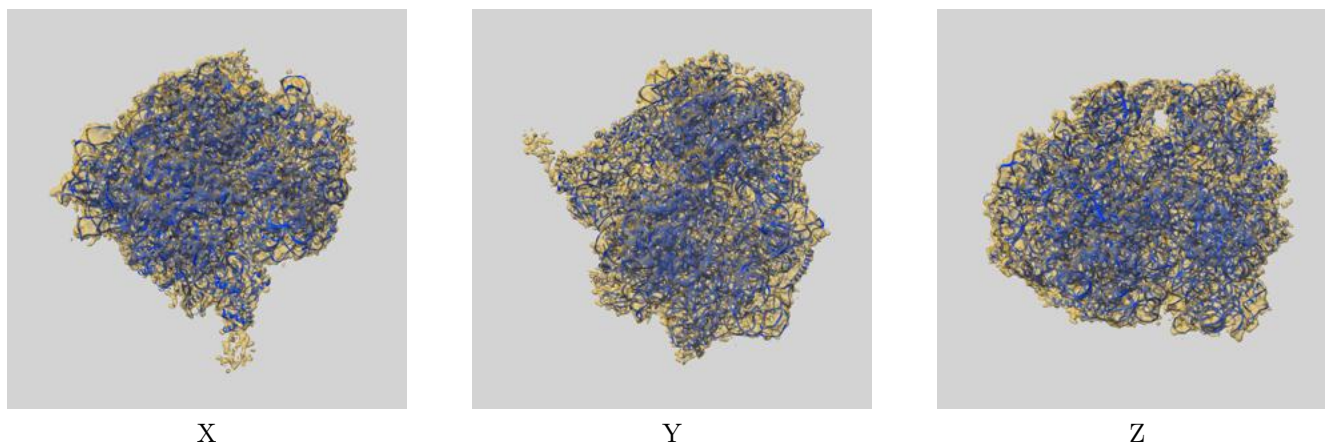
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.30	-	-
Author-provided FSC curve	6.27	9.67	6.77
Unmasked-calculated*	9.59	17.06	10.37

*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 9.59 differs from the reported value 6.3 by more than 10 %

9 Map-model fit [i](#)

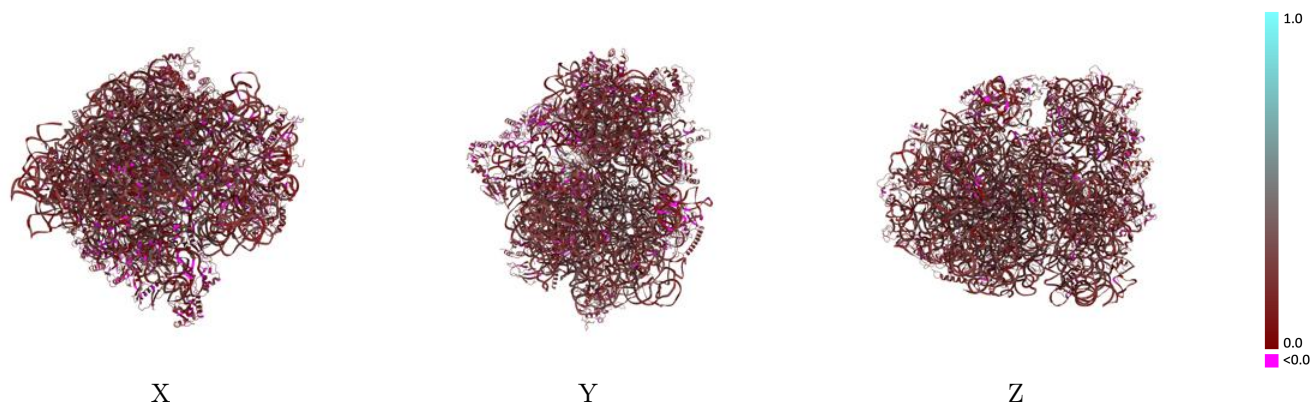
This section contains information regarding the fit between EMDB map EMD-13433 and PDB model 7PI9. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



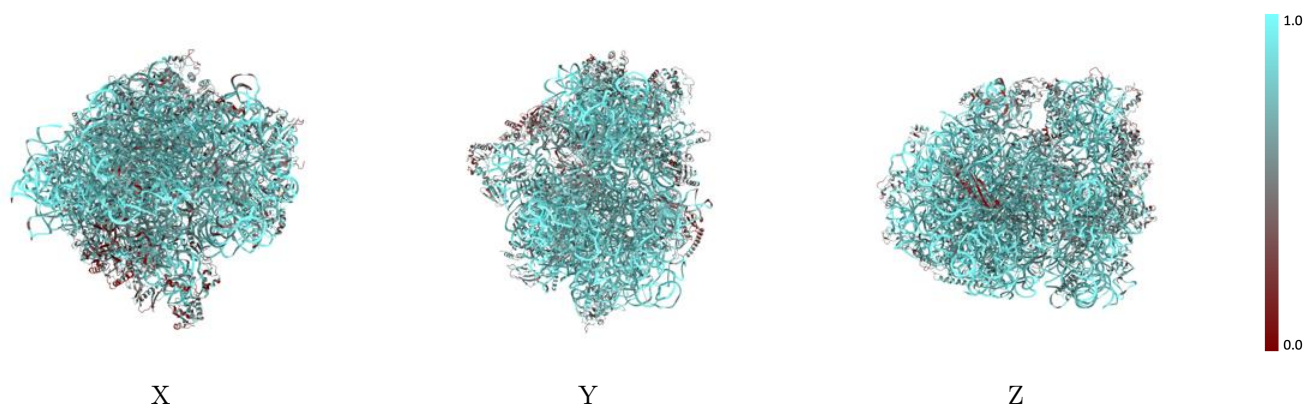
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



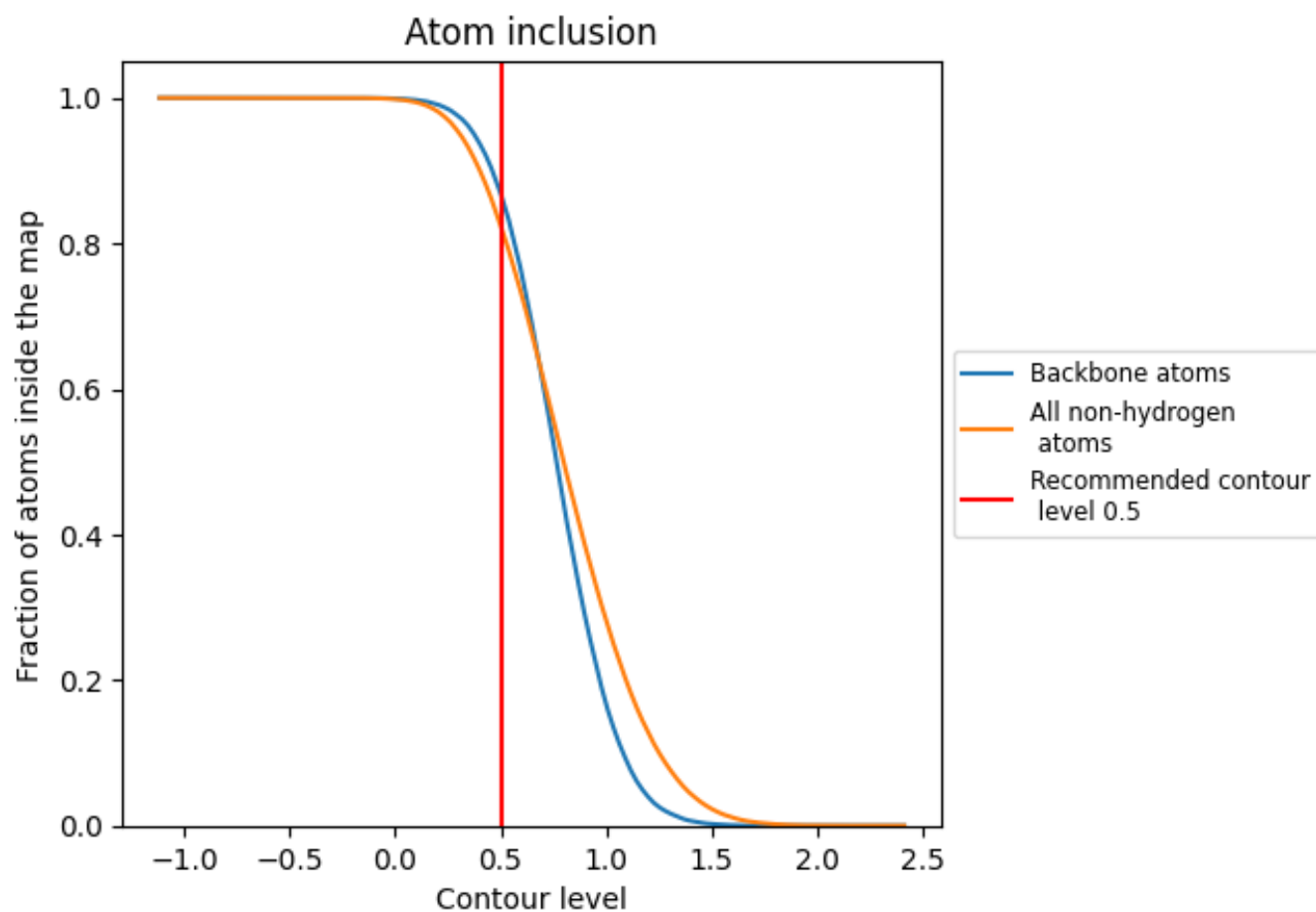
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 82% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8243	 0.2080
0	 0.7425	 0.1890
1	 0.7790	 0.2090
2	 0.7230	 0.2040
3	 0.9274	 0.2200
4	 0.9303	 0.2240
5	 0.9272	 0.2140
6	 0.5977	 0.0730
7	 0.8511	 0.1790
9	 0.3293	 0.1580
A	 0.5827	 0.1990
B	 0.6135	 0.1880
C	 0.6453	 0.1760
D	 0.6096	 0.1960
E	 0.5576	 0.2050
F	 0.6339	 0.1920
G	 0.6462	 0.1960
H	 0.6643	 0.1920
I	 0.5585	 0.1630
J	 0.6255	 0.1930
K	 0.6887	 0.1950
L	 0.6264	 0.1870
M	 0.6901	 0.1760
N	 0.6511	 0.2100
O	 0.7011	 0.1840
P	 0.6423	 0.2130
Q	 0.6725	 0.2110
R	 0.6388	 0.1570
S	 0.7230	 0.1790
T	 0.6741	 0.2060
a	 0.7279	 0.2080
b	 0.6884	 0.2020
c	 0.6671	 0.2000
d	 0.6473	 0.1920
e	 0.5756	 0.2020



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Chain	Atom inclusion	Q-score
f	 0.3442	 0.1760
g	 0.4947	 0.1680
h	 0.4336	 0.1800
i	 0.7388	 0.2140
j	 0.6587	 0.2150
k	 0.7079	 0.2230
l	 0.7280	 0.2160
m	 0.7212	 0.1910
n	 0.7093	 0.1950
o	 0.6641	 0.2180
p	 0.7060	 0.1790
q	 0.6809	 0.2150
r	 0.7417	 0.1890
s	 0.7377	 0.2160
t	 0.5900	 0.2030
u	 0.7469	 0.2150
v	 0.7152	 0.2090
w	 0.6804	 0.2080
x	 0.5394	 0.1930
y	 0.7512	 0.2000
z	 0.7053	 0.2020