



## wwPDB EM Validation Summary Report ⓘ

Oct 28, 2024 – 08:52 am GMT

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 : 7OOD, 4V5L, 4V7C, 7OOC

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

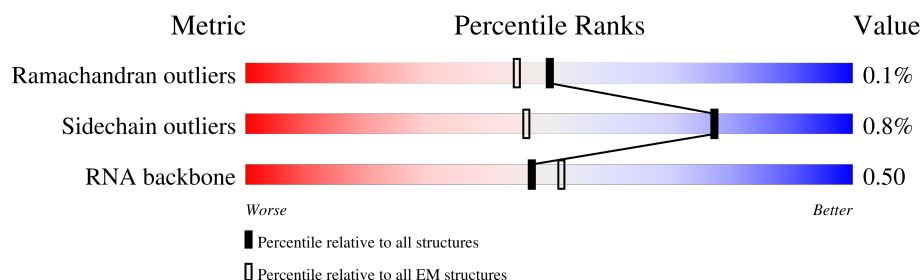
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

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

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

Mol	Chain	Length	Quality of chain
1	0	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	
10	F	155	
11	G	142	
12	H	132	
13	I	108	
14	J	121	
15	K	139	
16	L	124	
17	M	61	
18	N	86	
19	O	94	
20	P	85	
21	Q	104	
22	R	87	
23	S	87	
24	T	60	
25	a	287	
26	b	287	
27	c	212	
28	d	180	
29	e	184	
30	f	149	
31	g	161	
32	h	137	
33	i	146	

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Mol	Chain	Length	Quality of chain
34	j	122	
35	k	151	
36	l	139	
37	m	124	
38	n	116	
39	o	119	
40	p	127	
41	q	100	
42	r	159	
43	s	237	
44	t	111	
45	u	104	
46	v	65	
47	w	111	
48	x	97	
49	y	57	
50	z	53	
51	3	2907	
52	4	108	
53	5	1520	
54	6	76	
54	7	76	

## 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
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

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

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

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

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

- Molecule 4 is a protein called Elongation factor Tu.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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		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		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		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
28	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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	S	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		

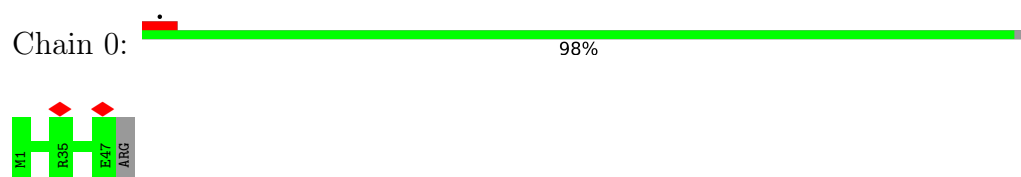
- Molecule 54 is a RNA chain called tRNA-Phe.

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		

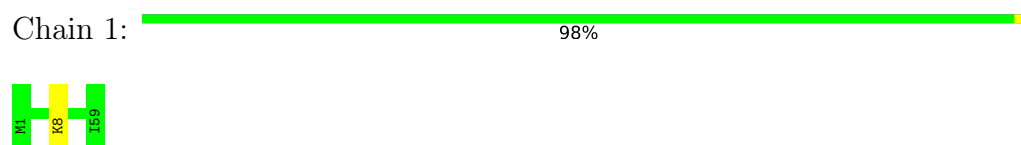
### 3 Residue-property plots [i](#)

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.

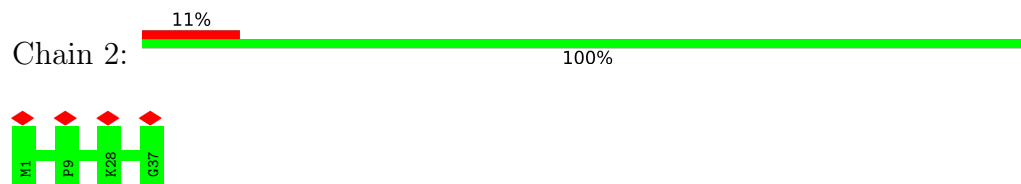
- Molecule 1: 50S ribosomal protein L34



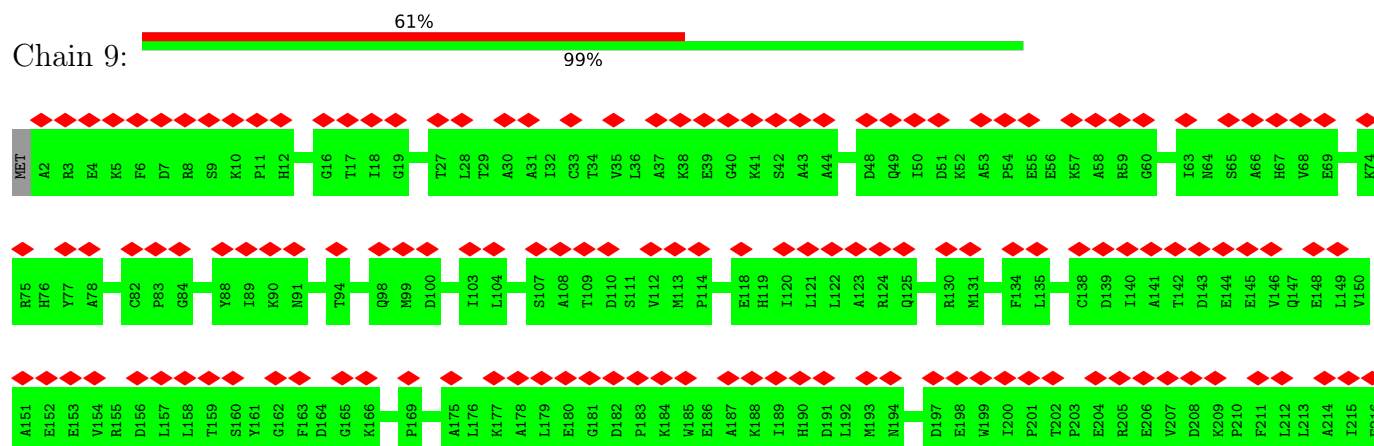
- Molecule 2: 50S ribosomal protein L35

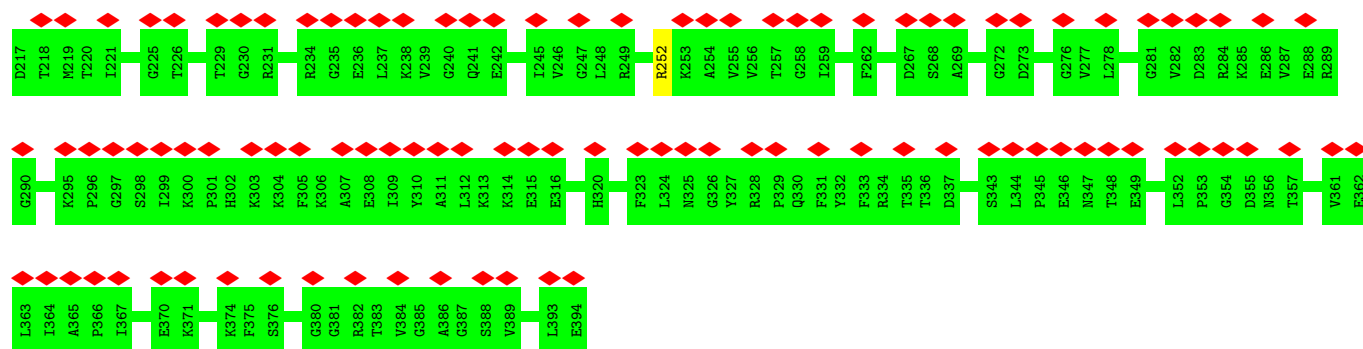


- Molecule 3: 50S ribosomal protein L36

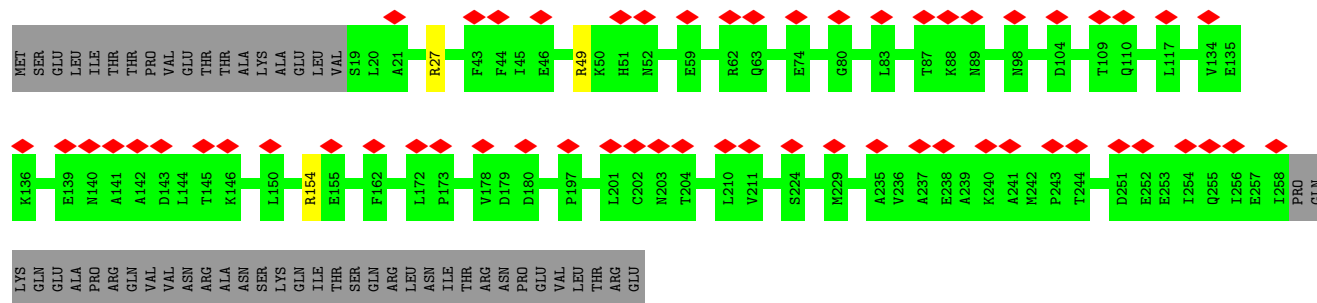
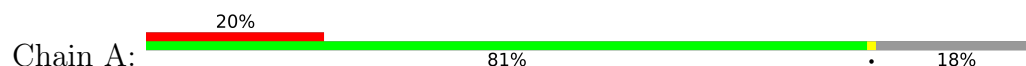


- Molecule 4: Elongation factor Tu

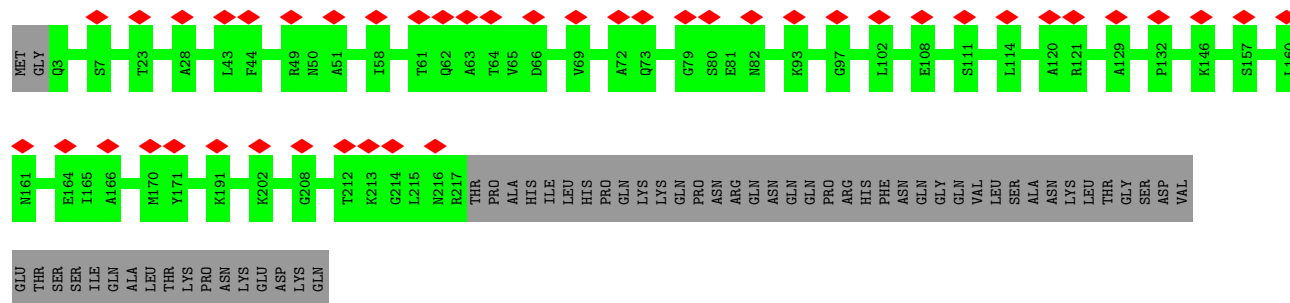
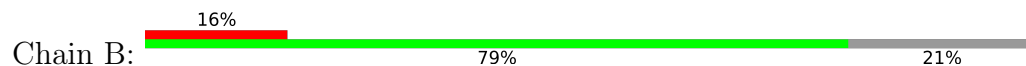




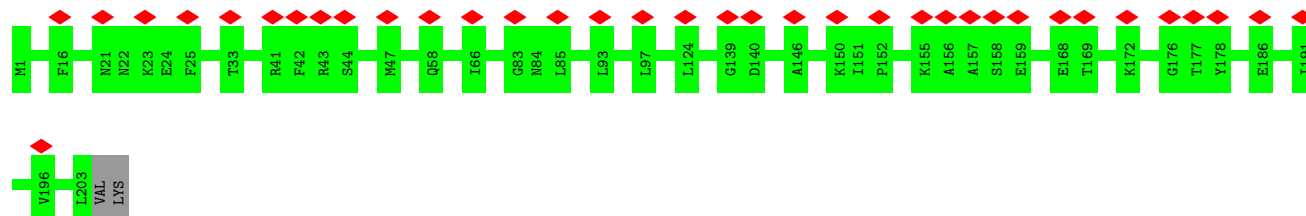
• Molecule 5: 30S ribosomal protein S2



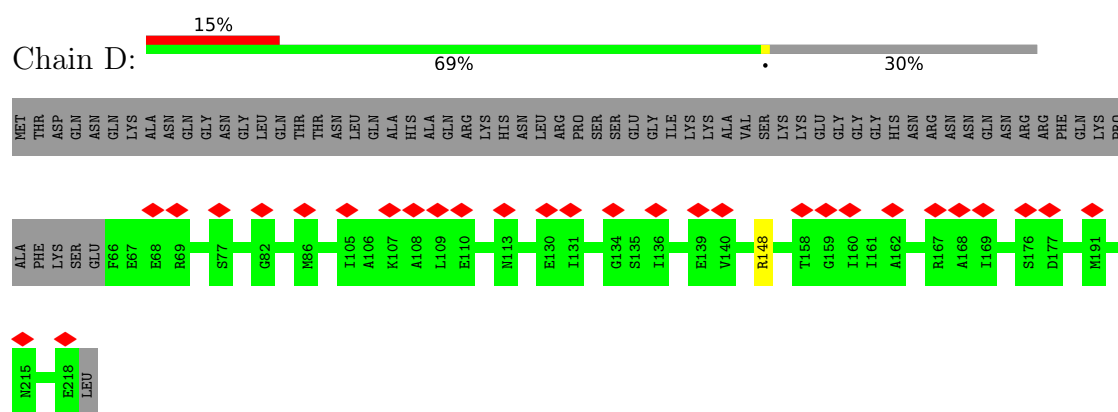
• Molecule 6: 30S ribosomal protein S3



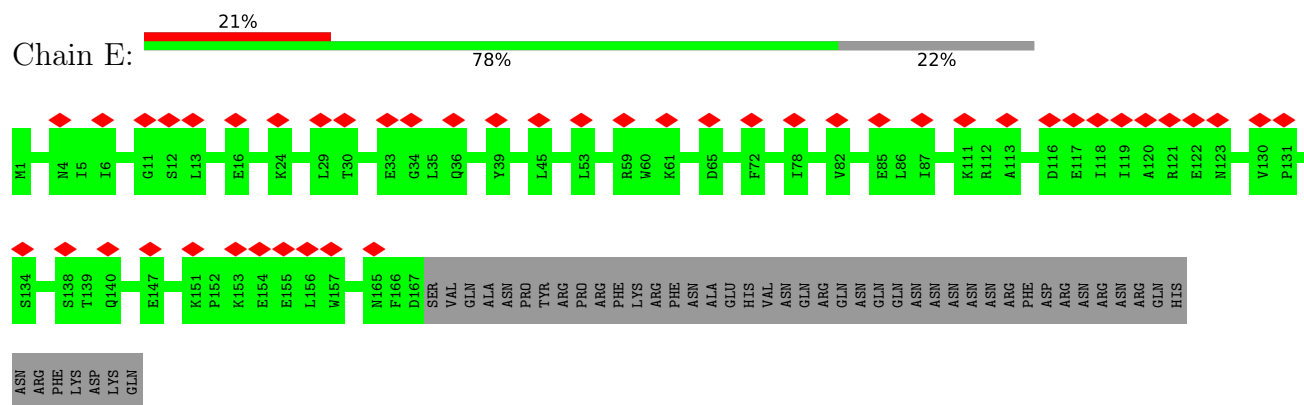
• Molecule 7: 30S ribosomal protein S4



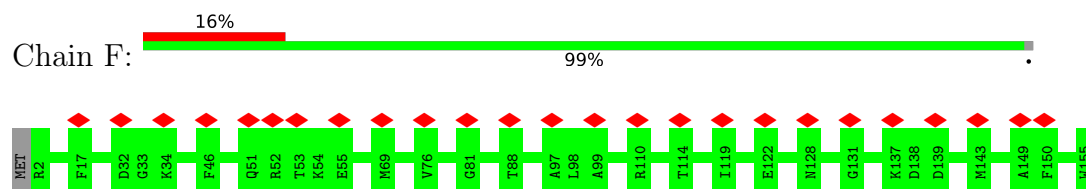
• Molecule 8: 30S ribosomal protein S5



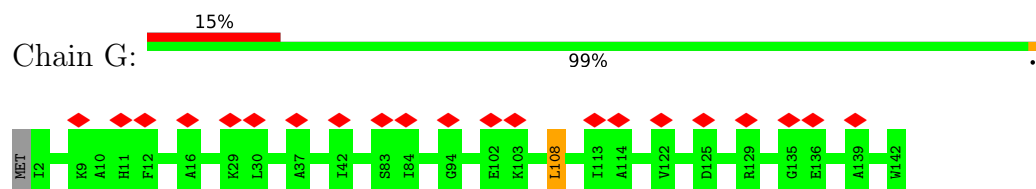
- Molecule 9: 30S ribosomal protein S6



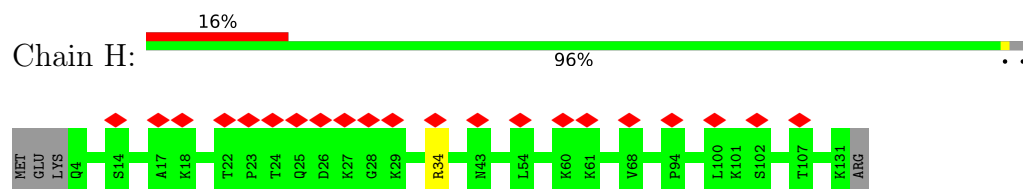
- Molecule 10: 30S ribosomal protein S7



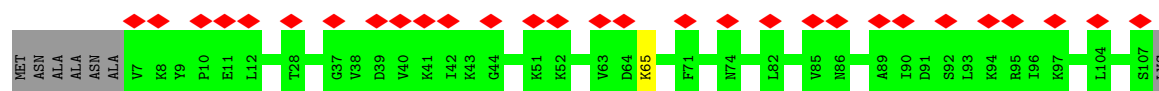
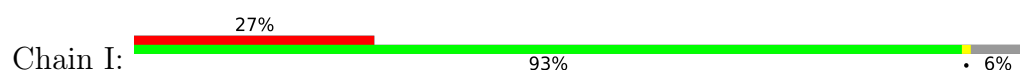
- Molecule 11: 30S ribosomal protein S8



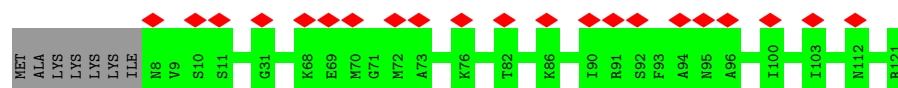
- Molecule 12: 30S ribosomal protein S9



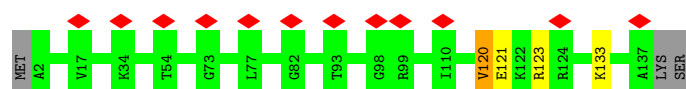
- Molecule 13: 30S ribosomal protein S10



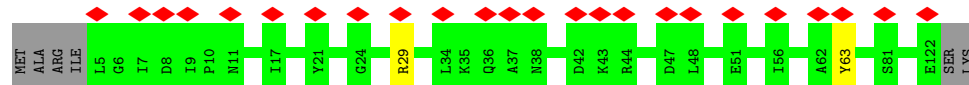
- Molecule 14: 30S ribosomal protein S11



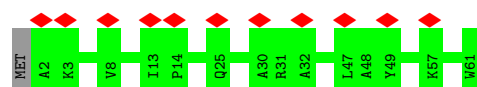
- Molecule 15: 30S ribosomal protein S12



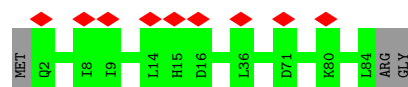
- Molecule 16: 30S ribosomal protein S13



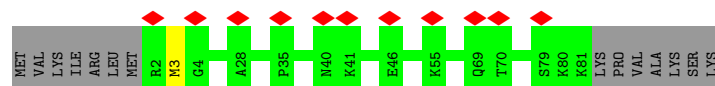
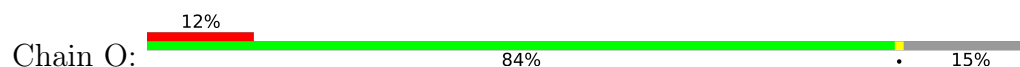
- Molecule 17: 30S ribosomal protein S14 type Z



- Molecule 18: 30S ribosomal protein S15

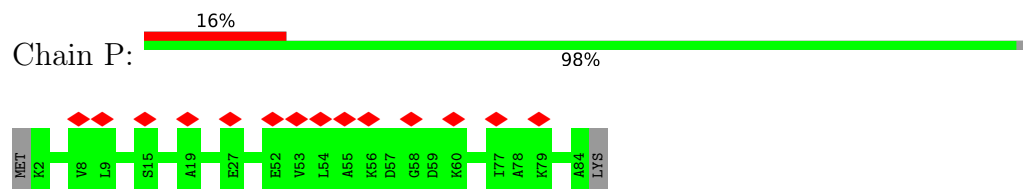


- Molecule 19: 30S ribosomal protein S16

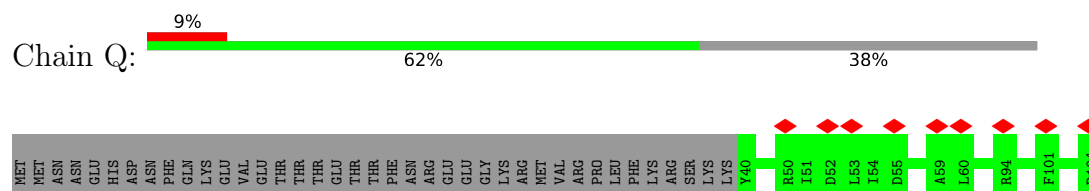




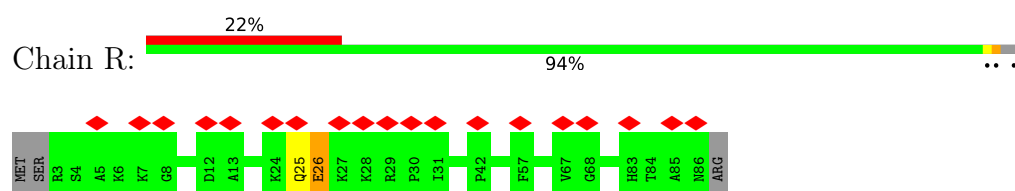
- Molecule 20: 30S ribosomal protein S17



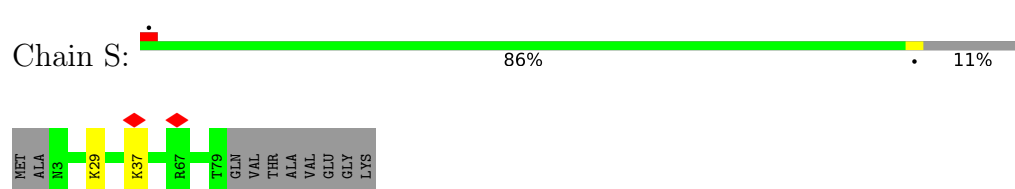
- Molecule 21: 30S ribosomal protein S18



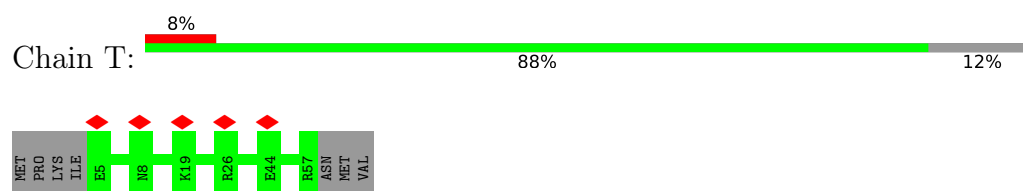
- Molecule 22: 30S ribosomal protein S19



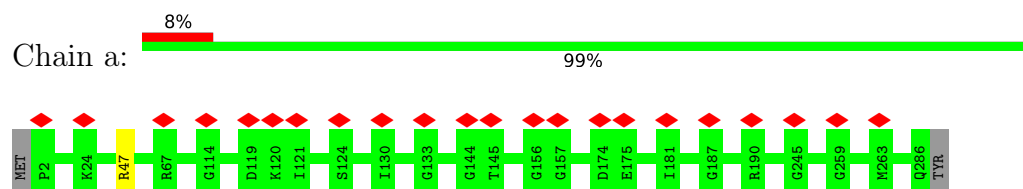
- Molecule 23: 30S ribosomal protein S20



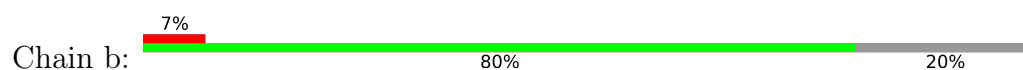
- Molecule 24: 30S ribosomal protein S21

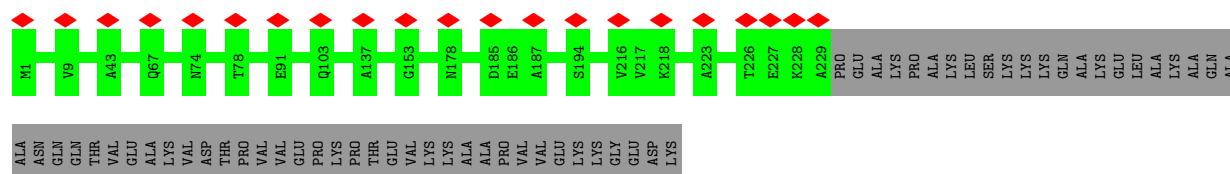


- Molecule 25: 50S ribosomal protein L2



- Molecule 26: 50S ribosomal protein L3

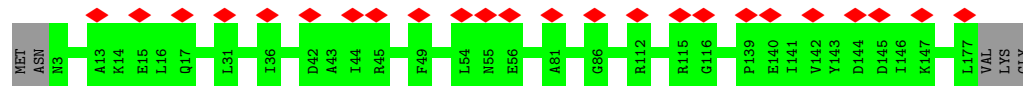




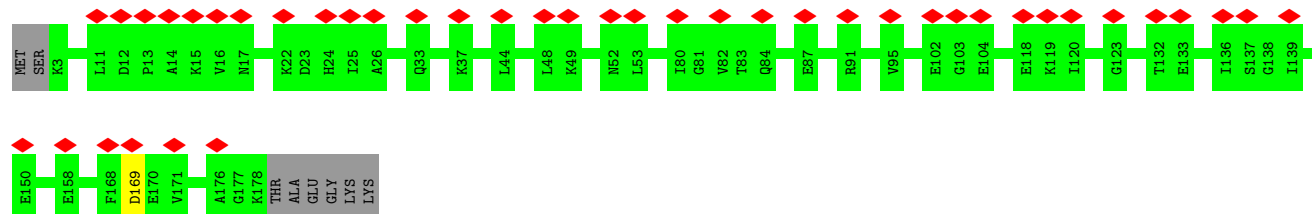
• Molecule 27: 50S ribosomal protein L4



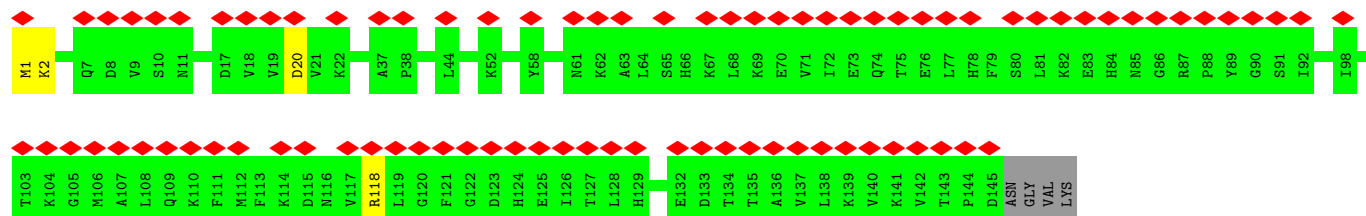
• Molecule 28: 50S ribosomal protein L5



• Molecule 29: 50S ribosomal protein L6

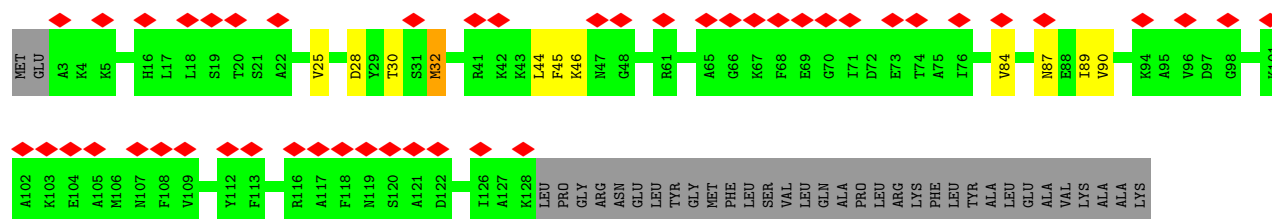


• Molecule 30: 50S ribosomal protein L9



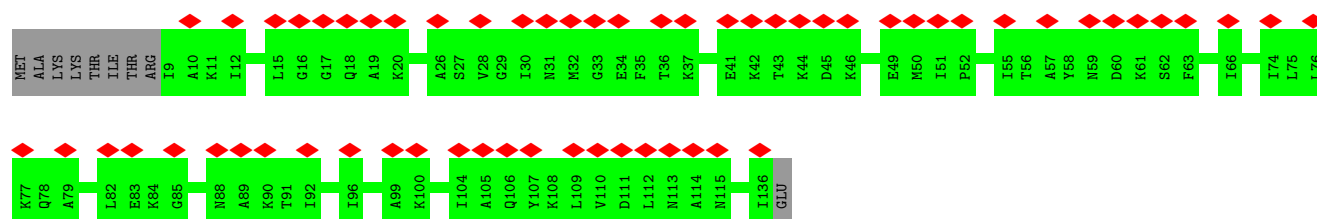
• Molecule 31: 50S ribosomal protein L10





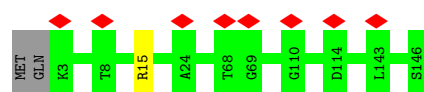
- Molecule 32: 50S ribosomal protein L11

Chain h: 45% 93% 7%



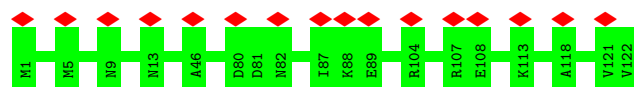
- Molecule 33: 50S ribosomal protein L13

Chain i: 5% 98% ..



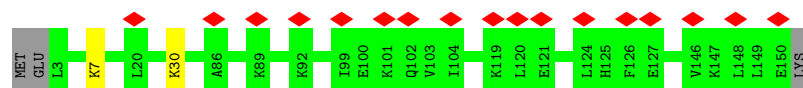
- Molecule 34: 50S ribosomal protein L14

Chain j: 13% 100%



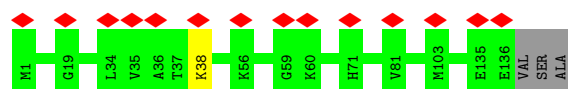
- Molecule 35: 50S ribosomal protein L15

Chain k: 11% 97% ..

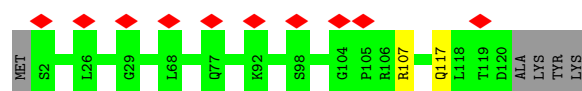


- Molecule 36: 50S ribosomal protein L16

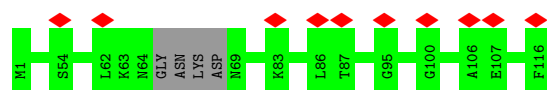
Chain l: 10% 97% ..



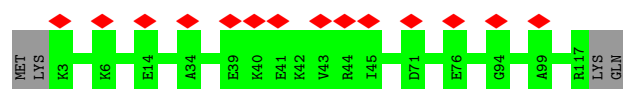
- Molecule 37: 50S ribosomal protein L17



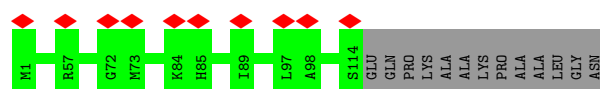
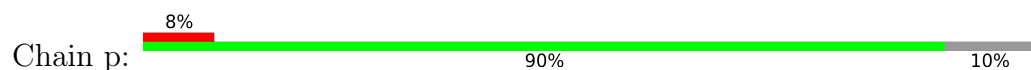
- Molecule 38: 50S ribosomal protein L18



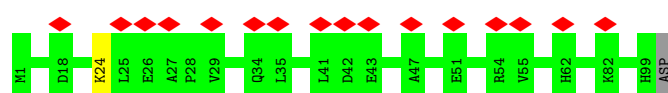
- Molecule 39: 50S ribosomal protein L19



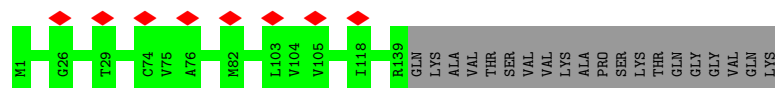
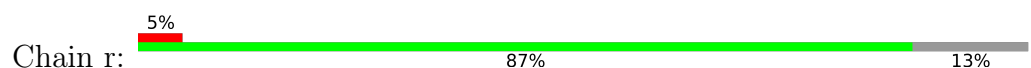
- Molecule 40: 50S ribosomal protein L20



- Molecule 41: 50S ribosomal protein L21



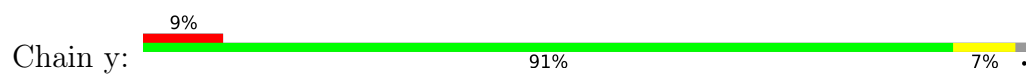
- Molecule 42: 50S ribosomal protein L22



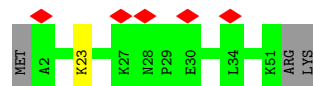
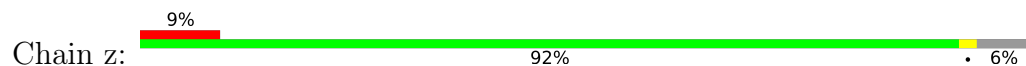
- Molecule 43: 50S ribosomal protein L23



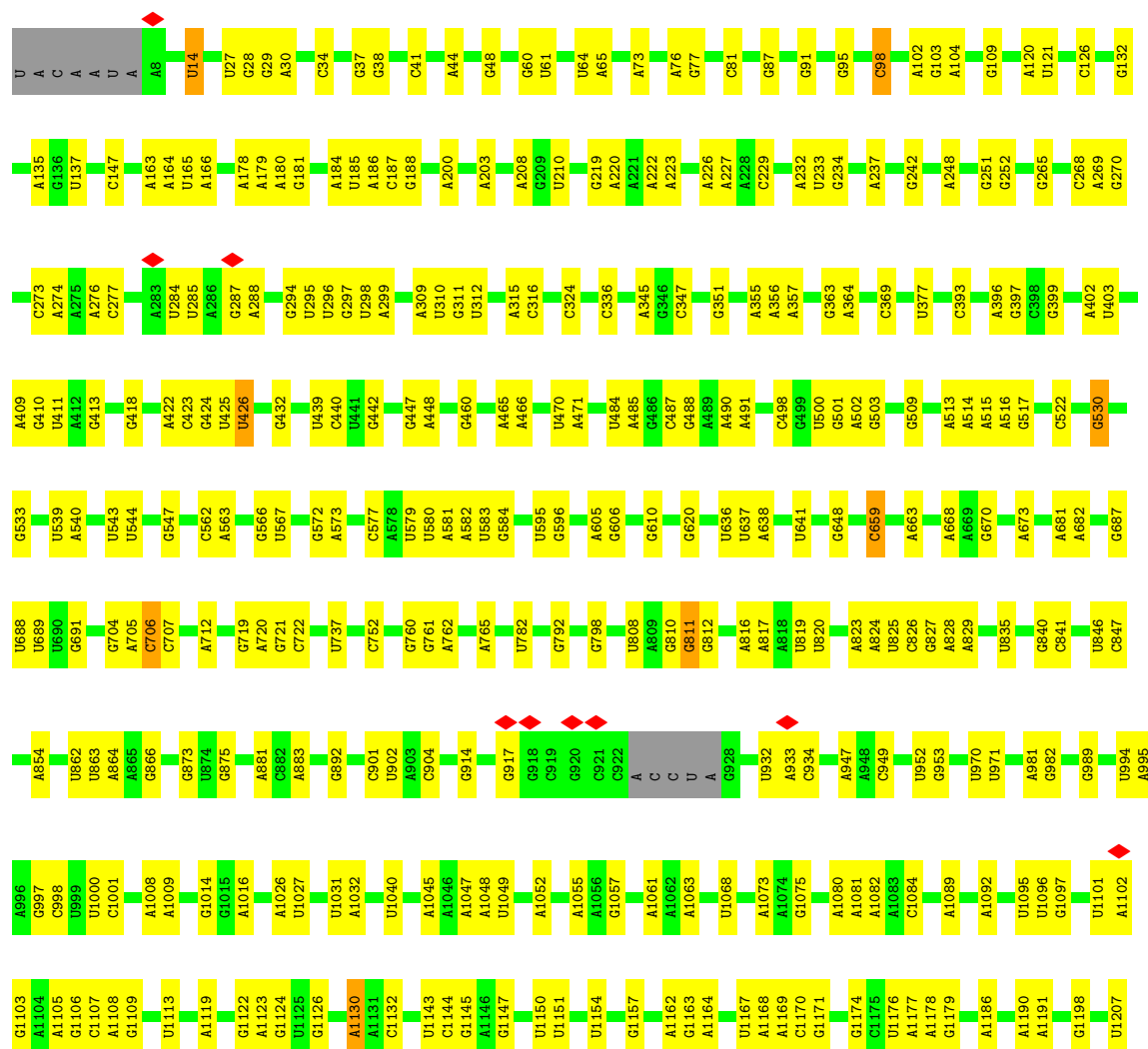
- 



- Molecule 50: 50S ribosomal protein L33 1



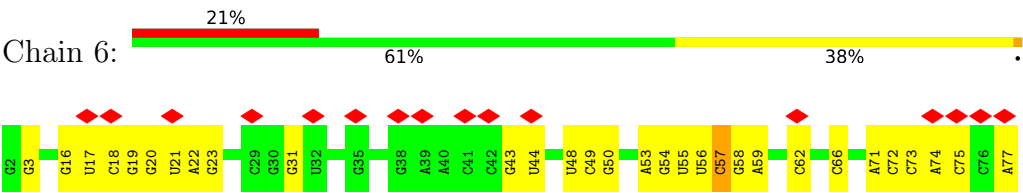
- Molecule 51: 23S ribosomal RNA



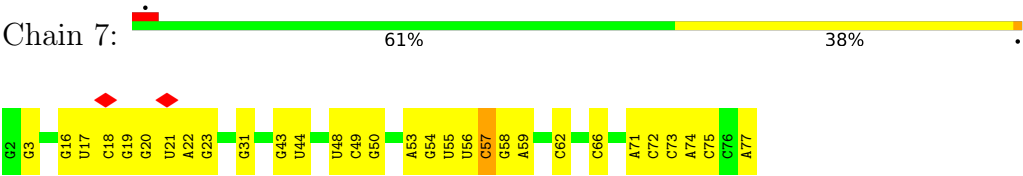
G2838	G2839	G2720	G2590	U2481	U2352	U2212	A2124	U1989	G1870	A1702	A1570	C1456	U1329	A1208
A2839	U2592	G2721	G2591	A2484	G2353	A2220	G2127	U1998	A1873	C1706	G1571	G1463	U1330	U1209
U2853	U2593	G2722	C2355	U2485	C2355	C2222	G2131	U2000	G1876	G1708	G1576	U1466	U1340	U1211
U2862	A2596	G2727	U2358	U2486	U2358	A2233	G2132	U2009	G1880	A1716	G1580	U1467	U1341	G2122
G2863	U2604	G2737	A2362	U2487	A2362	G2246	A2133	A2010	U1888	G1733	G1583	C1473	U1342	U1213
U2865	G2605	U2738	A2366	U2488	A2366	G2247	U2138	G2011	U1889	G1737	U1584	C1474	U1343	G1215
G2871	A2608	G2739	A2369	U2499	A2369	G2251	C2139	G2027	U1890	A1747	A1588	U1481	C1348	U1216
G2876	A2610	A2741	G2379	U2502	G2379	G2254	G2140	U2028	A1891	U1748	A1589	U1482	G1349	G1226
U2888	C2618	G2752	U2377	G2503	U2377	G2257	C2144	U2029	G1906	G1757	A1592	G1483	G1353	U1234
U2889	C2619	A2756	U2387	C2504	U2387	G2258	A2145	A2030	A1907	G1763	U1486	U1487	C1358	U1247
G2890	A2505	C2760	G2391	A2506	G2391	G2259	U2153	G2034	A1908	U1764	A1601	U1492	G1367	A1250
A2895	U2621	U2764	U2392	C2507	U2392	A2274	U2154	A2037	G1909	G1765	G1602	G1492	U1368	G1251
G2896	A2622	A2765	C2393	U2508	C2393	A2275	G2155	A2038	G1910	G1766	A1603	A1493	G1369	C1252
G2897	C2632	A2766	U2398	C2509	U2398	A2276	G2161	C2041	G1913	A1767	G1612	G1504	U1370	U1254
A2898	G2633	A2773	U2399	G2510	U2399	A2277	U2162	G2050	G1914	G1768	G1615	G1505	U1371	G1255
C2899	A2637	A2774	C2402	U2512	C2402	G2286	U2163	A2056	A1920	A1769	G1616	U1506	U1372	A1256
U2900	G2638	C2775	C2410	G2513	C2410	G2287	U2164	A2059	C1921	C1771	U1617	G1507	C1373	G1257
A	G2642	U2776	U2416	U2514	U2416	G2290	U2165	G2059	G1934	G1780	U1618	U1509	C1378	C1258
U	A2643	A2777	G2417	G2515	G2417	U2291	G2166	C2062	A1935	C1781	A1619	U1510	C1384	A1259
U	U2644	C2779	G2418	G2516	G2418	U2292	G2167	G2063	G1936	U1785	U1637	U1514	G1388	G1266
U	U2645	A2786	G2419	A2521	G2419	A2295	G2171	G2064	G1937	U1786	A1641	A1515	U1389	U1267
A	U2646	U2788	G2422	G2526	G2422	C2301	A2171	A2065	U1938	U1786	G1642	C1522	A1393	U1268
U2788	G2649	U2788	U2431	C2531	U2431	C2302	A2172	G2066	G1942	A1791	G1643	C1523	A1396	A1283
C2797	U2652	C2797	C2432	A2539	C2432	A2306	G2173	A2067	A1943	A1792	A1644	C1532	A1284	U1285
U2798	G2653	U2798	A2433	G2543	A2433	G2311	U2180	G2068	A1944	G1806	A1645	U1532	U1406	U1407
U2800	U2654	U2799	A2434	G2543	A2434	G2312	A2181	A2069	A1945	C1807	G1651	U1533	G1408	G1286
U2801	U2659	U2801	C2435	G2543	C2435	U2313	C2182	U2075	U1946	U1810	C1652	A1534	U1407	U1286
C2802	A2662	C2802	G2437	G2558	G2437	G2316	U2183	G2076	U1947	A1816	U1655	A1535	A1412	A1292
G2803	G2663	G2803	U2438	U2562	U2438	A2317	C2186	U2099	A1951	U1816	A1656	A1541	A1420	U1293
C2804	U2664	C2804	A2440	A2569	A2440	A2324	C2187	G2100	G1952	U1820	A1661	A1548	A1421	G1294
A2805	A2668	A2805	A2441	A2574	A2441	A2327	U2188	C2103	A1960	G1821	G1662	U1549	A1422	A1295
G2806	G2669	G2806	A2442	G2575	A2442	U2327	G2191	A2107	A1961	A1822	G1663	G1550	U1422	A1298
A2808	G2681	A2808	G2443	A2576	A2443	U2327	U2192	C2108	U1962	U1823	G1664	G1557	A1423	G1301
A2809	U2688	A2809	C2444	G2577	G2444	A2330	U2193	A2109	U1963	G1824	G1665	G1558	U1424	C1302
A2810	C2688	A2810	C2445	G2578	C2445	G2333	G2194	U2110	C1964	U1826	U1668	A1559	A1426	U1303
G2811	U2689	G2811	U2449	A2579	U2449	U2334	U2195	U2111	G1965	U1827	G	U	A1431	U1304
U2812	U2690	U2812	G2454	A2580	G2454	A2335	G2196	A2112	G1966	U1827	G	G	A1435	G1309
A2813	C2581	A2813	G2455	C2581	G2455	G2341	U2197	U2113	C1970	A1836	U1672	A1548	U1422	U1293
C2822	G2584	C2822	A2456	G2584	A2456	U2342	G2198	C2114	G1971	G1842	U1673	A1548	U1422	A1298
A2823	A2585	A2823	G2456	A2585	G2456	U2342	G2201	G2117	U1974	G1842	U1673	A1548	U1422	A1298
A2824	G2586	A2824	C2460	G2586	C2460	A2343	U2202	U2117	U1974	G1842	U1673	A1548	U1422	A1298
G2829	U2587	G2829	C2475	G2587	C2475	A2344	U2203	G2122	A1977	G1842	U1673	A1548	U1422	A1298
A2830	U2588	A2830	C2475	G2588	C2475	A2344	U2203	G2122	A1977	G1842	U1673	A1548	U1422	A1298
U2837	G2589	U2837	C2475	G2589	C2475	A2344	U2203	G2122	A1977	G1842	U1673	A1548	U1422	A1298

- 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 ⓘ

### 5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	0	0.23	0/383	0.43	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

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

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	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%)	19	57
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%)	19	57
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%)	3	21
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%)	50 83

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 ⓘ

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%)	50 68
3	2	35/35 (100%)	35 (100%)	0	100 100
4	9	324/325 (100%)	323 (100%)	1 (0%)	91 92
5	A	212/262 (81%)	209 (99%)	3 (1%)	62 75
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%)	58 73
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%)	79 85
12	H	111/115 (96%)	110 (99%)	1 (1%)	75 83
13	I	95/99 (96%)	94 (99%)	1 (1%)	70 80
14	J	91/97 (94%)	91 (100%)	0	100 100
15	K	117/120 (98%)	113 (97%)	4 (3%)	32 51
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%)	62	75
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%)	40	58
23	S	70/77 (91%)	68 (97%)	2 (3%)	37	56
24	T	49/56 (88%)	49 (100%)	0	100	100
25	a	241/243 (99%)	240 (100%)	1 (0%)	89	91
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%)	45	64
31	g	101/129 (78%)	93 (92%)	8 (8%)	10	29
32	h	102/110 (93%)	102 (100%)	0	100	100
33	i	126/128 (98%)	125 (99%)	1 (1%)	79	85
34	j	103/103 (100%)	103 (100%)	0	100	100
35	k	123/126 (98%)	121 (98%)	2 (2%)	58	73
36	l	113/115 (98%)	112 (99%)	1 (1%)	75	83
37	m	105/109 (96%)	103 (98%)	2 (2%)	52	69
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%)	70	80
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%)	73	82
45	u	69/85 (81%)	68 (99%)	1 (1%)	62	75
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%)	9	27
50	z	47/50 (94%)	46 (98%)	1 (2%)	48	66
All	All	5425/6076 (89%)	5380 (99%)	45 (1%)	77	85

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 ⓘ

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 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.

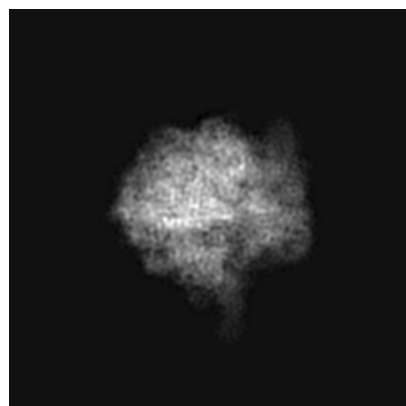
## 6 Map visualisation [i](#)

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

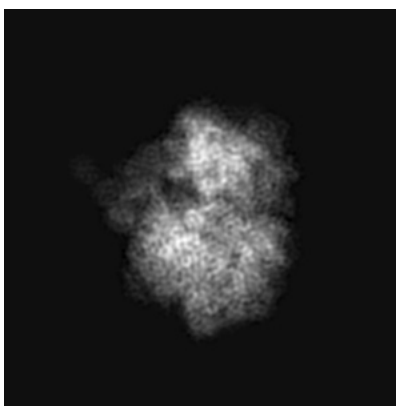
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

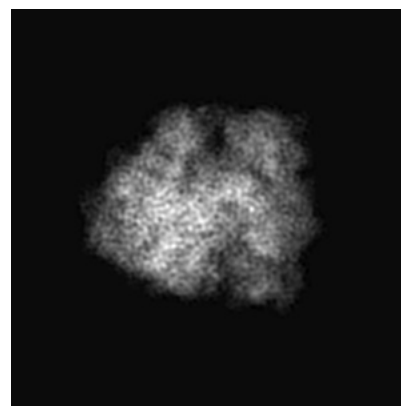
#### 6.1.1 Primary map



X

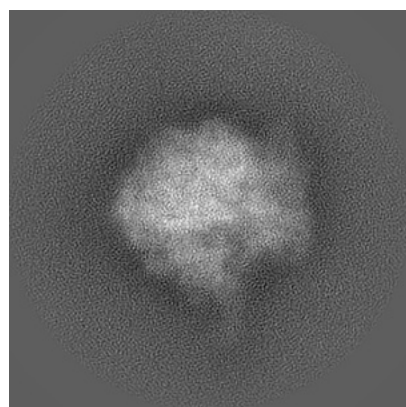


Y

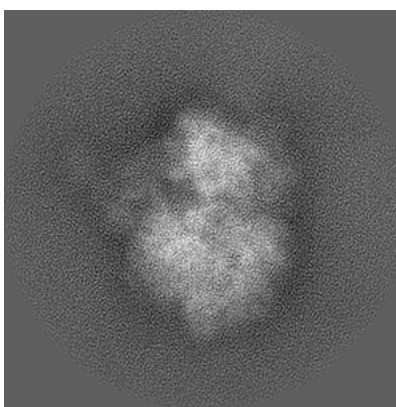


Z

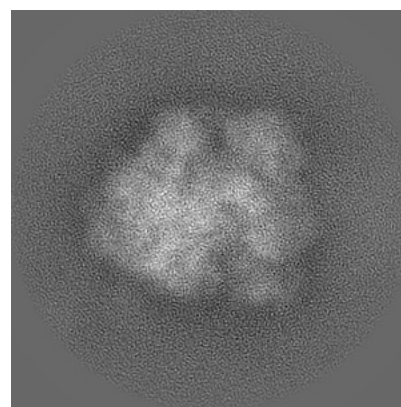
#### 6.1.2 Raw map



X



Y

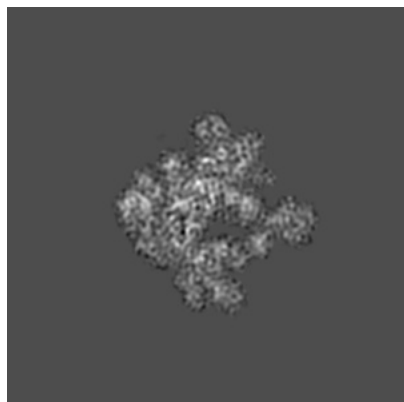


Z

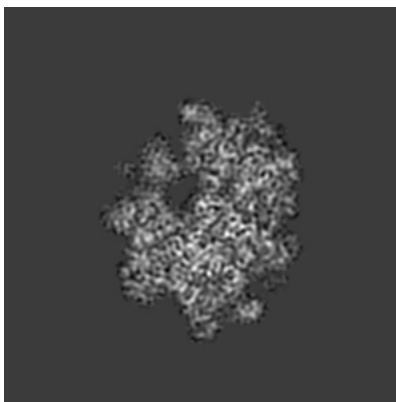
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

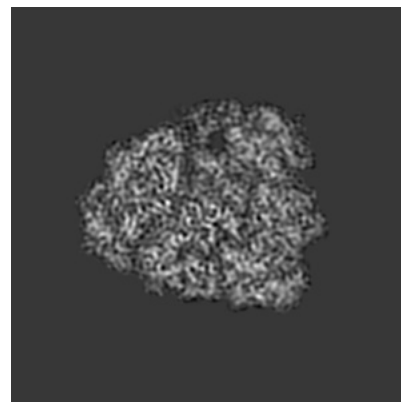
### 6.2.1 Primary map



X Index: 128

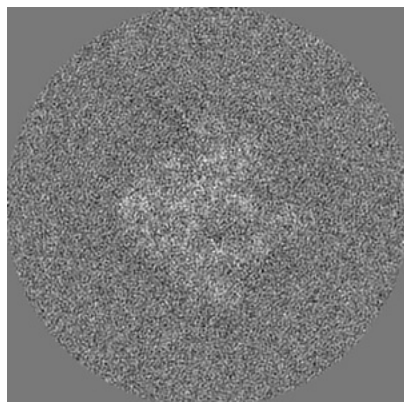


Y Index: 128

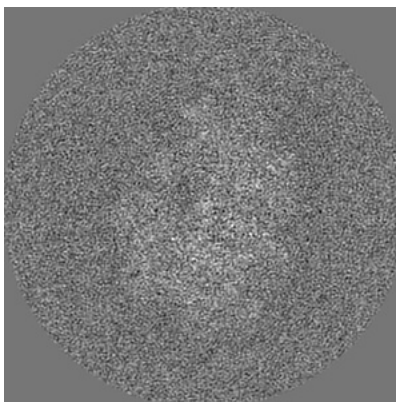


Z Index: 128

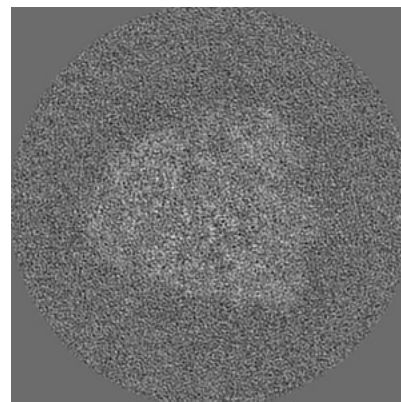
### 6.2.2 Raw map



X Index: 128



Y Index: 128

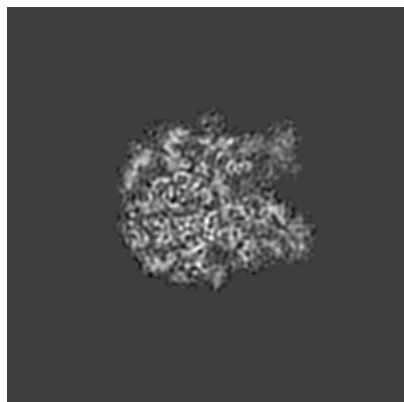


Z Index: 128

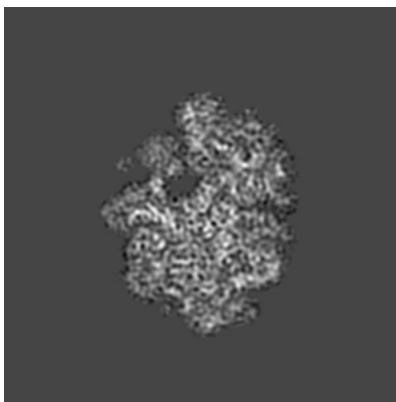
The images above show central slices of the map in three orthogonal directions.

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

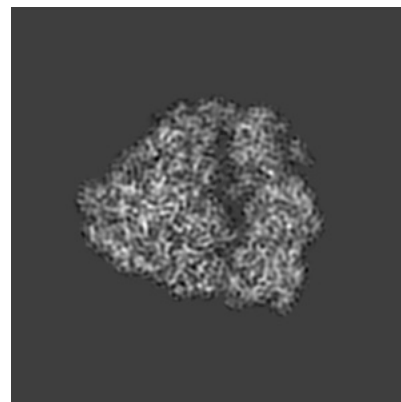
### 6.3.1 Primary map



X Index: 103

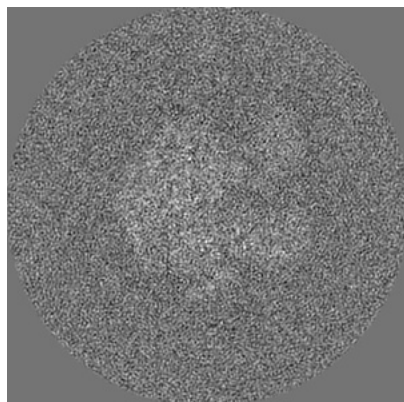


Y Index: 120

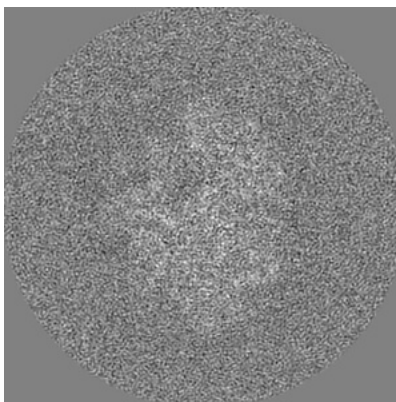


Z Index: 122

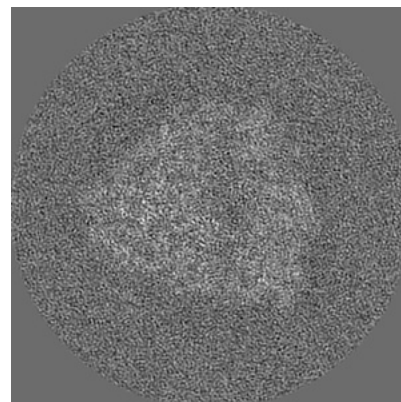
### 6.3.2 Raw map



X Index: 114



Y Index: 120



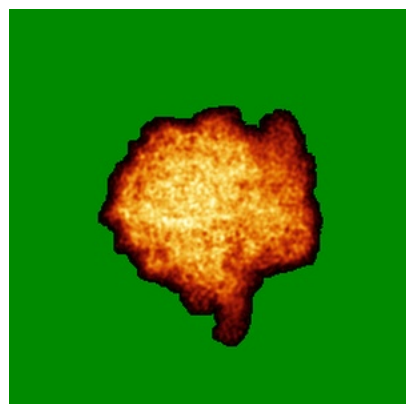
Z Index: 122

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

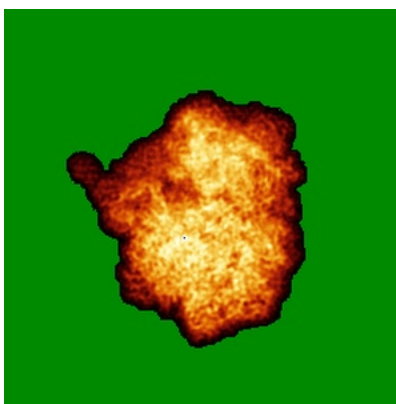


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

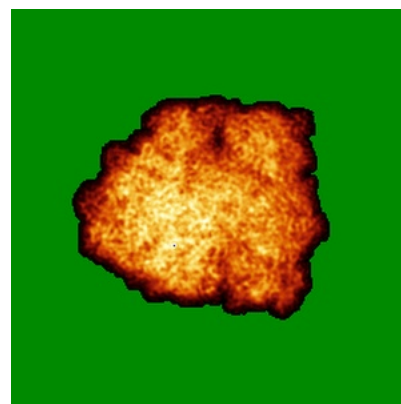
### 6.4.1 Primary map



X

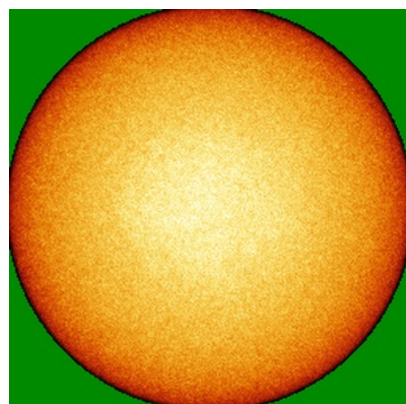


Y

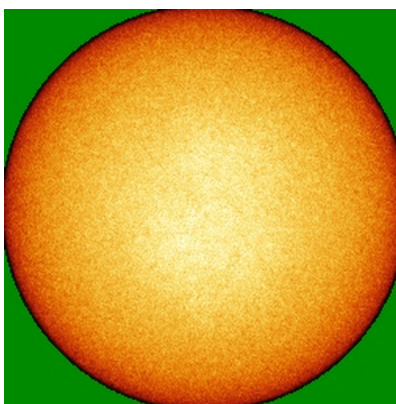


Z

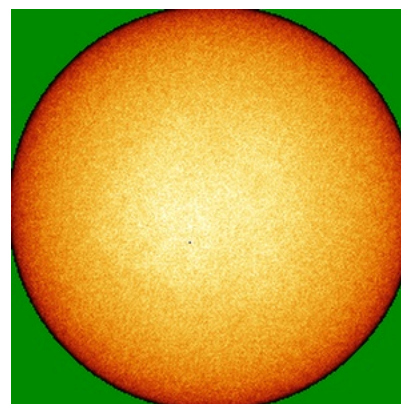
### 6.4.2 Raw map



X



Y



Z

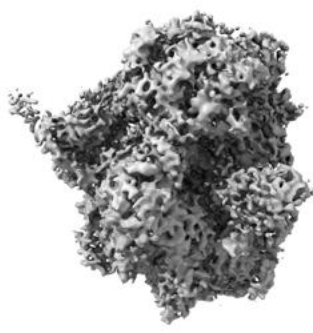
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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

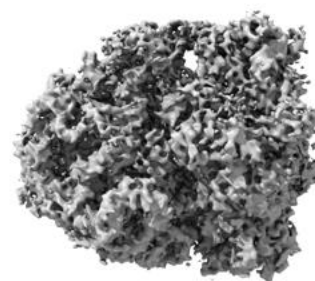
### 6.5.1 Primary map



X



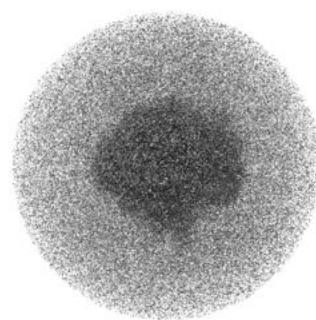
Y



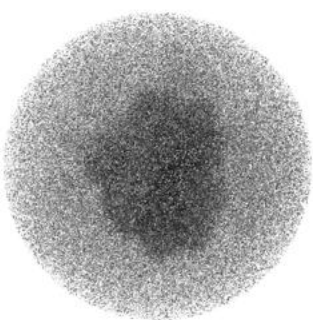
Z

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

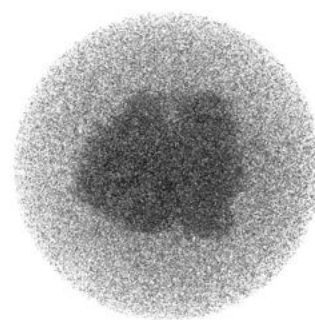
### 6.5.2 Raw map



X



Y



Z

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

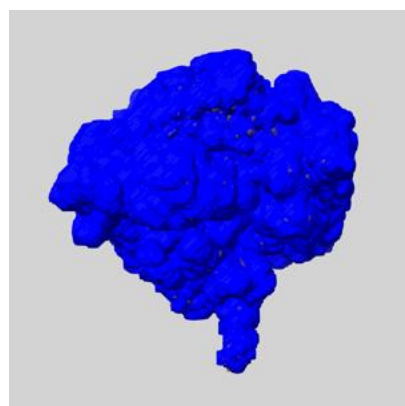
## 6.6 Mask visualisation [i](#)

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

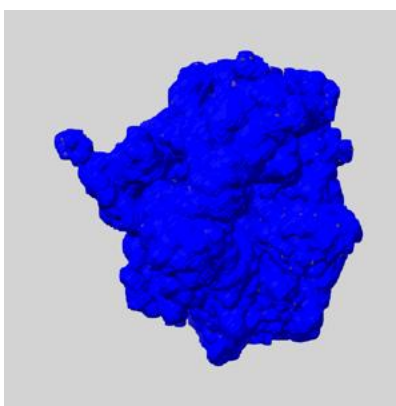
A mask typically either:

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

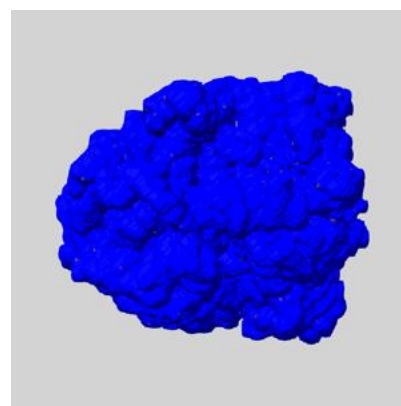
### 6.6.1 emd\_13433\_msk\_1.map [i](#)



X



Y



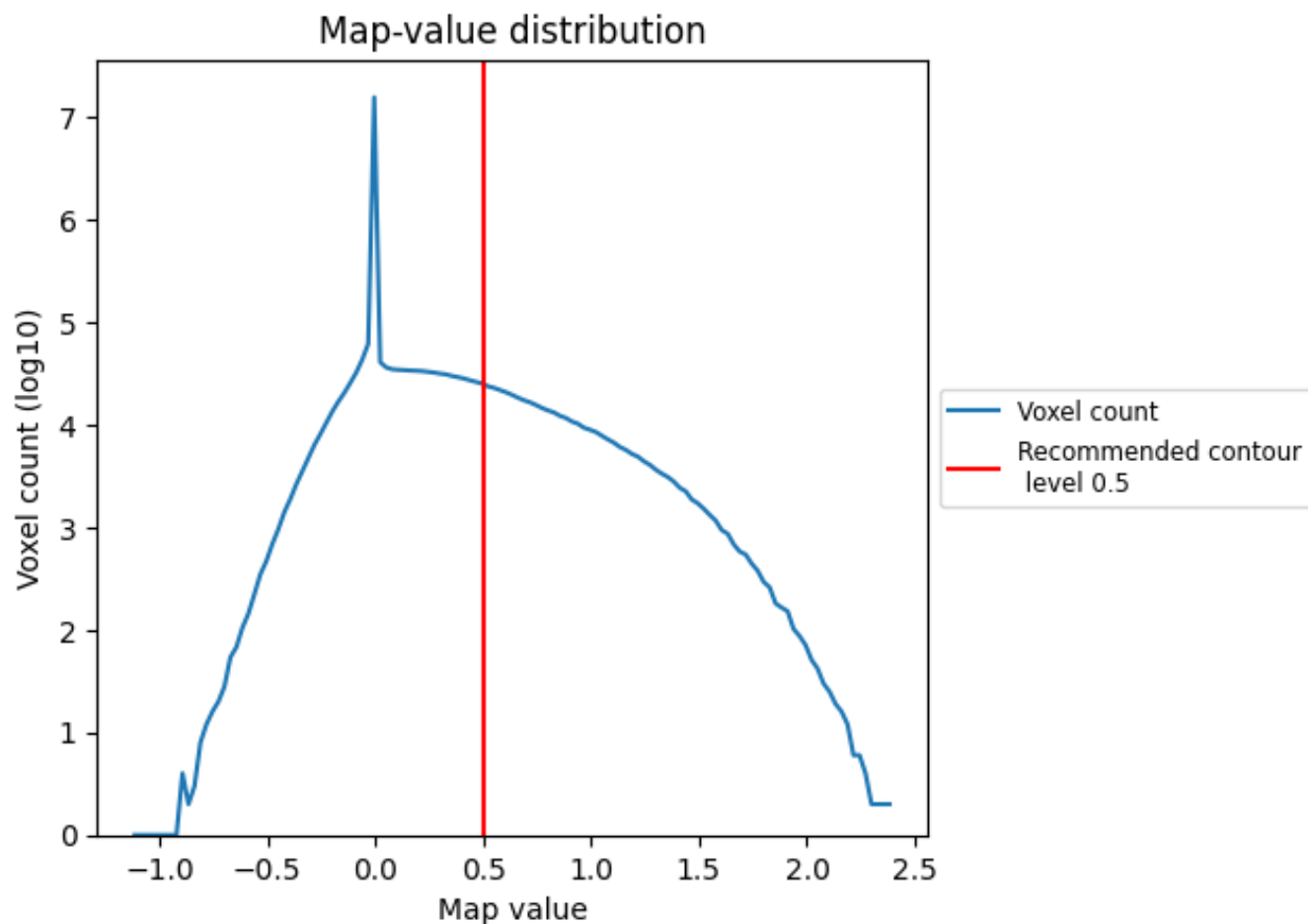
Z



## 7 Map analysis [i](#)

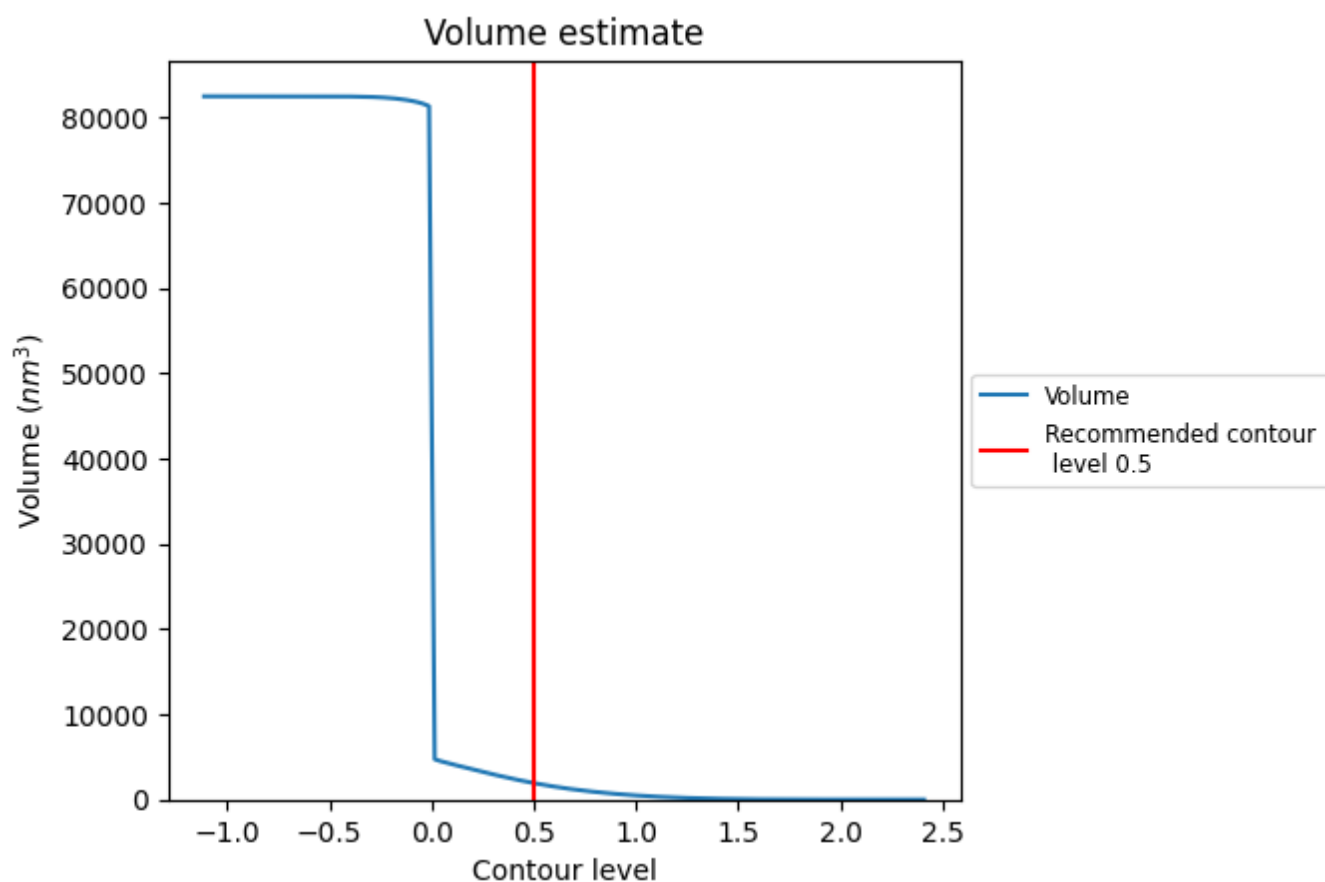
This section contains the results of statistical analysis of the map.

### 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.

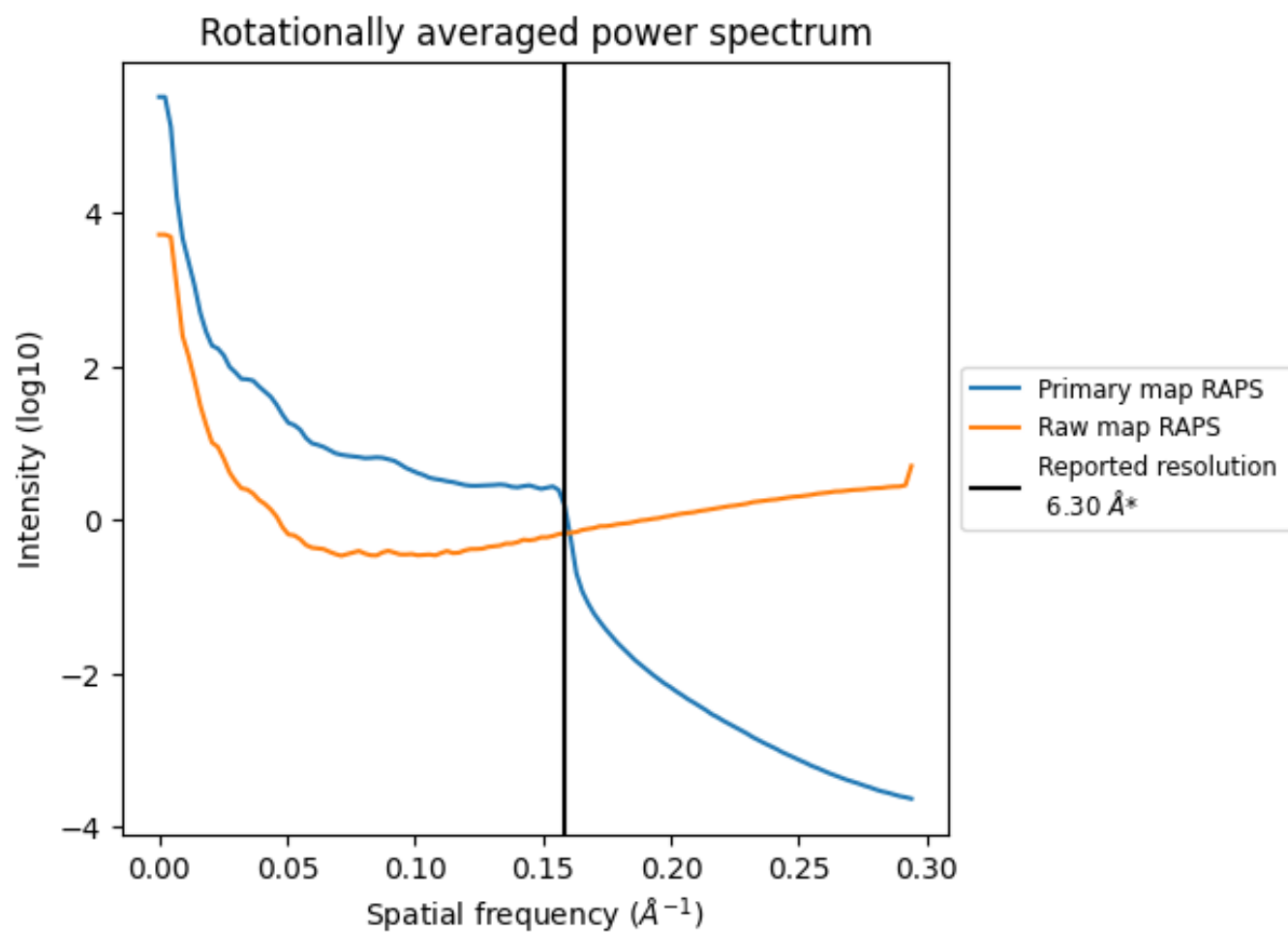
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1935 nm<sup>3</sup>; 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 ⓘ

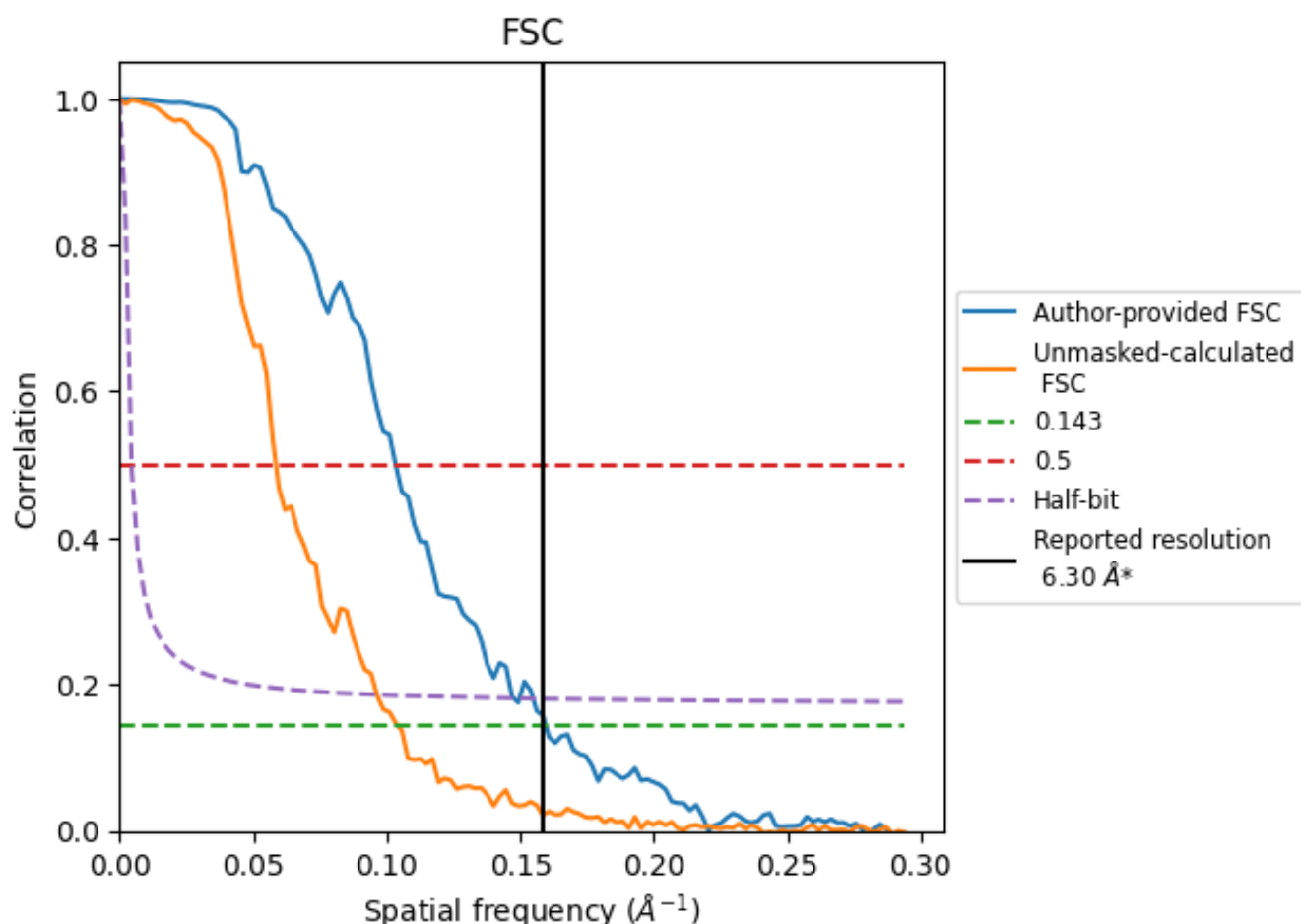


\*Reported resolution corresponds to spatial frequency of 0.159  $\text{\AA}^{-1}$

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

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.159 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

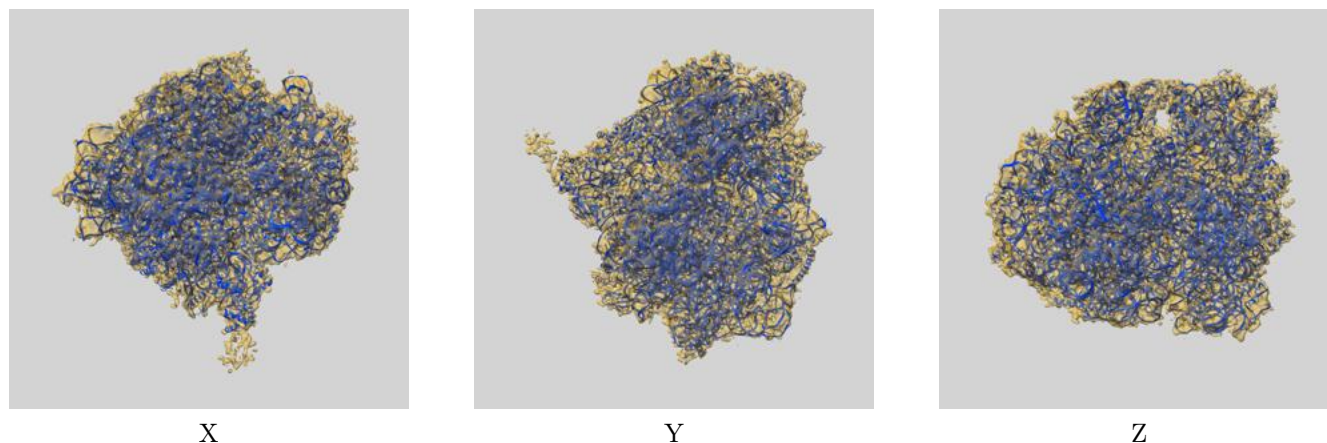
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.30	-	-
Author-provided FSC curve	6.27	9.67	6.77
Unmasked-calculated*	9.59	17.06	10.37

\*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](#)

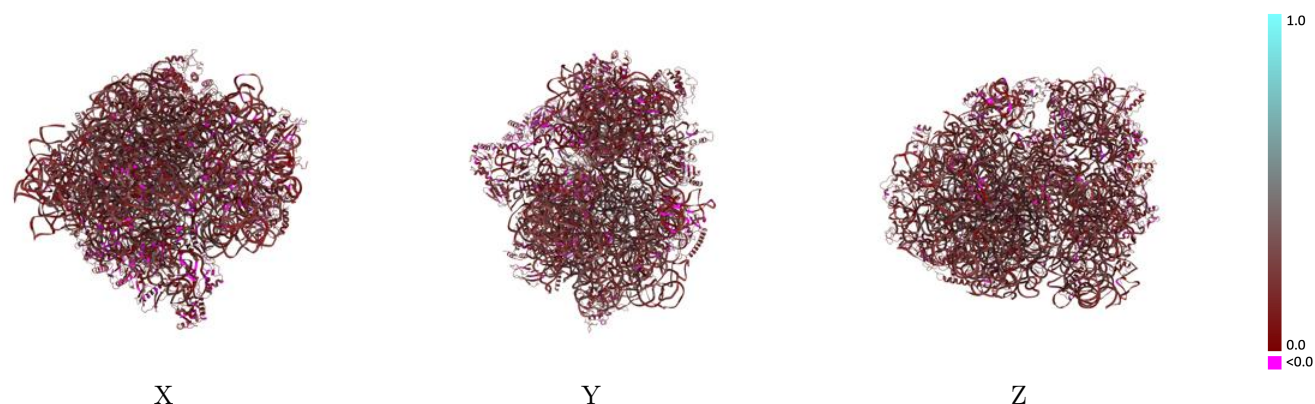
This section contains information regarding the fit between EMDB map EMD-13433 and PDB model 7PI9. Per-residue inclusion information can be found in section 3 on page 13.

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



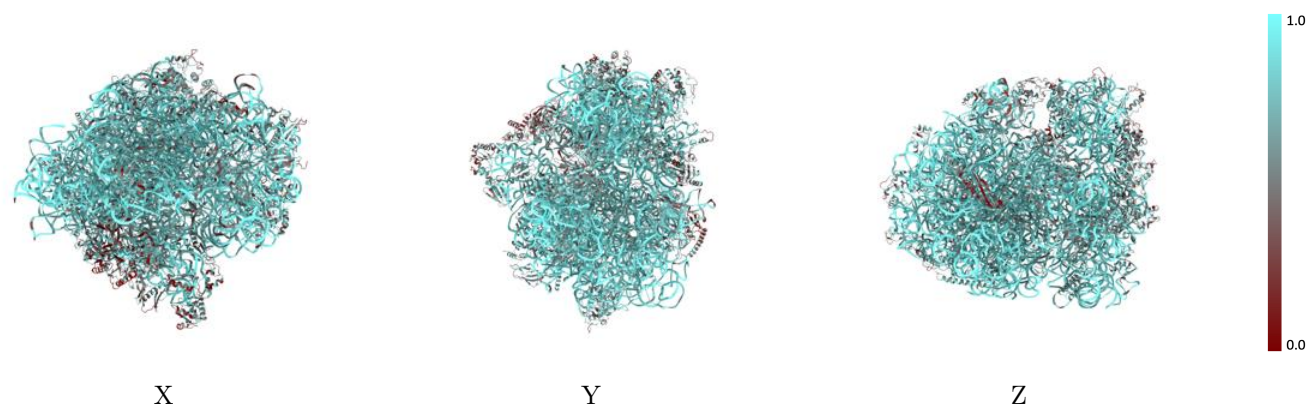
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



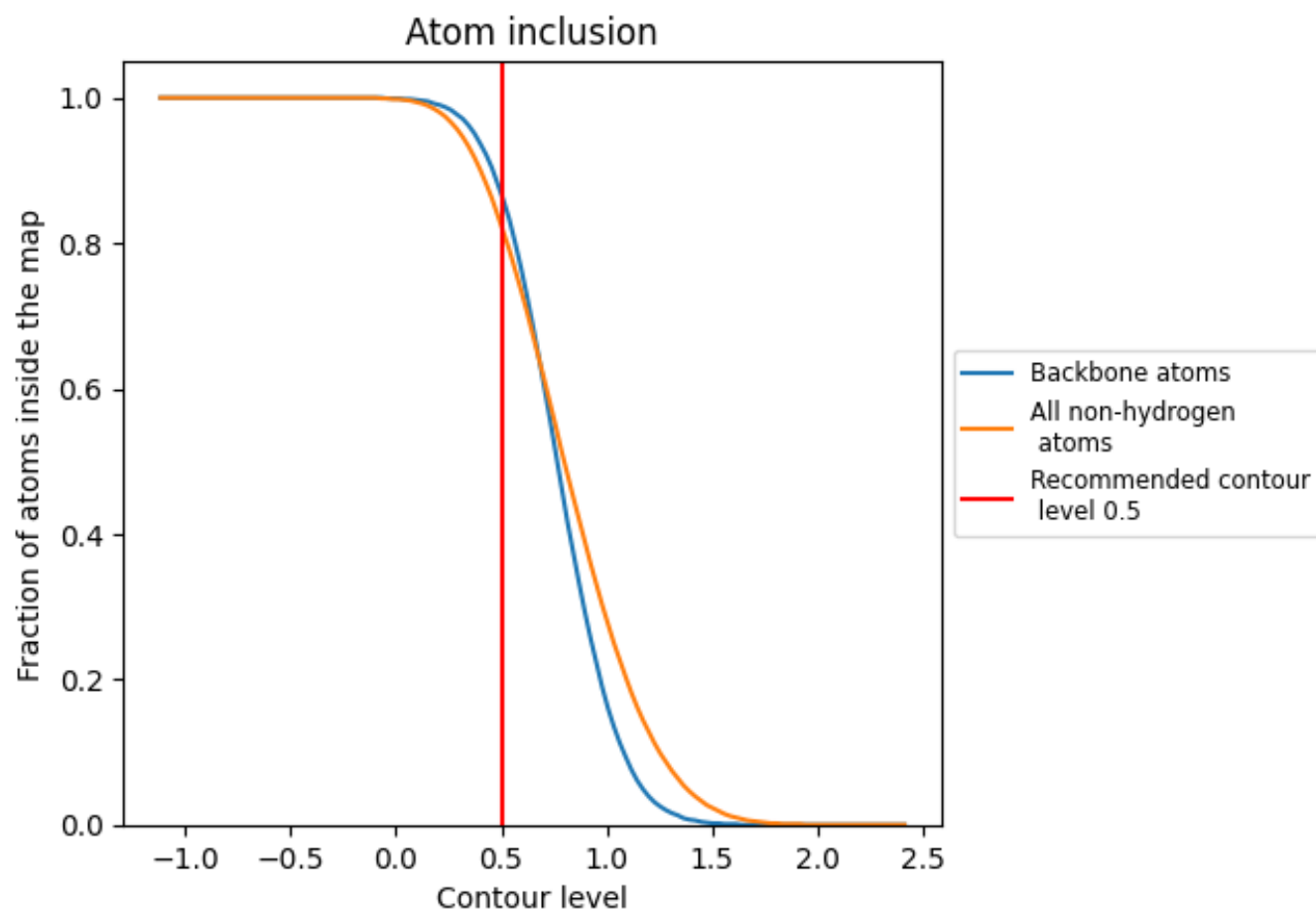
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.8240	 0.2080
0	 0.7430	 0.1890
1	 0.7790	 0.2090
2	 0.7230	 0.2040
3	 0.9270	 0.2200
4	 0.9300	 0.2240
5	 0.9270	 0.2140
6	 0.5980	 0.0730
7	 0.8510	 0.1790
9	 0.3290	 0.1580
A	 0.5830	 0.1990
B	 0.6140	 0.1880
C	 0.6450	 0.1760
D	 0.6100	 0.1960
E	 0.5580	 0.2050
F	 0.6340	 0.1920
G	 0.6460	 0.1960
H	 0.6640	 0.1920
I	 0.5580	 0.1630
J	 0.6250	 0.1930
K	 0.6890	 0.1950
L	 0.6260	 0.1870
M	 0.6900	 0.1760
N	 0.6510	 0.2100
O	 0.7010	 0.1840
P	 0.6420	 0.2130
Q	 0.6720	 0.2110
R	 0.6390	 0.1570
S	 0.7230	 0.1790
T	 0.6740	 0.2060
a	 0.7280	 0.2080
b	 0.6880	 0.2020
c	 0.6670	 0.2000
d	 0.6470	 0.1920
e	 0.5760	 0.2020



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Chain	Atom inclusion	Q-score
f	 0.3440	 0.1760
g	 0.4950	 0.1680
h	 0.4340	 0.1800
i	 0.7390	 0.2140
j	 0.6590	 0.2150
k	 0.7080	 0.2230
l	 0.7280	 0.2160
m	 0.7210	 0.1910
n	 0.7090	 0.1950
o	 0.6640	 0.2180
p	 0.7060	 0.1790
q	 0.6810	 0.2150
r	 0.7420	 0.1890
s	 0.7380	 0.2160
t	 0.5900	 0.2030
u	 0.7470	 0.2150
v	 0.7150	 0.2090
w	 0.6800	 0.2080
x	 0.5390	 0.1930
y	 0.7510	 0.2000
z	 0.7050	 0.2020