



wwPDB EM Validation Summary Report ⓘ

Nov 14, 2022 – 04:25 pm GMT

PDB ID : 7PIT
EMDB ID : EMD-13450
Title : 70S ribosome with EF-G, A/P- and P/E-site tRNAs in pseudouridimycin-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-23
Resolution : 5.70 Å (reported)
Based on initial models : 4V7D, 7OOC, 4V7C, 7OOD

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:

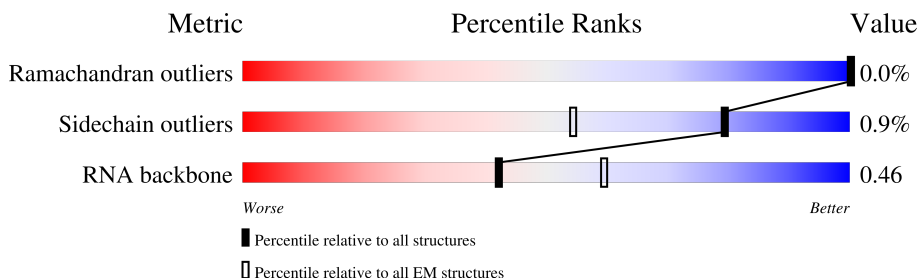
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 5.70 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.



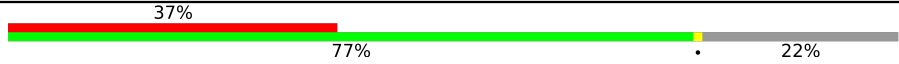
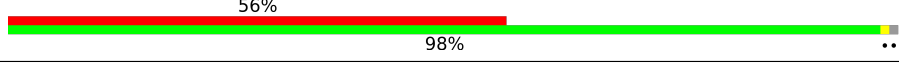
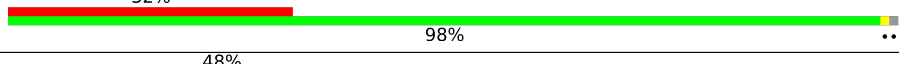
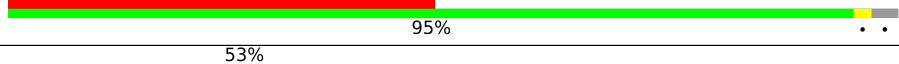
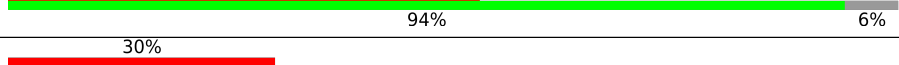
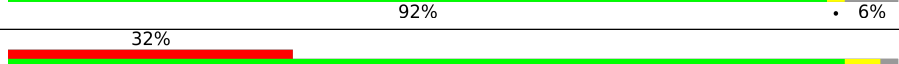
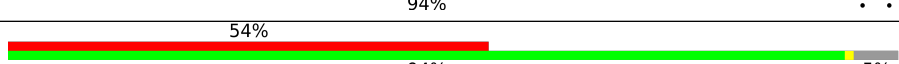
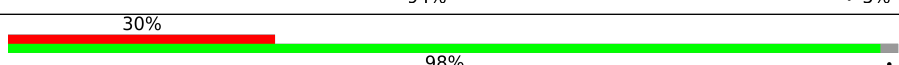
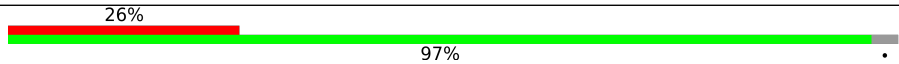

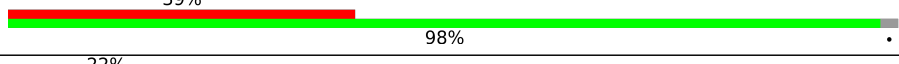
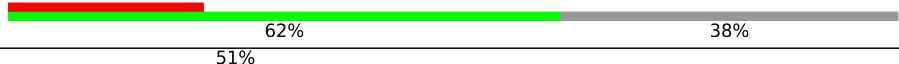
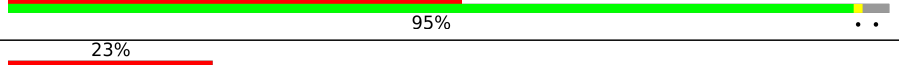
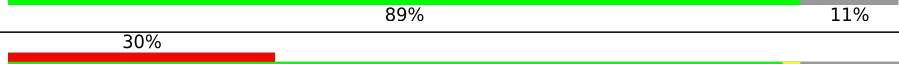

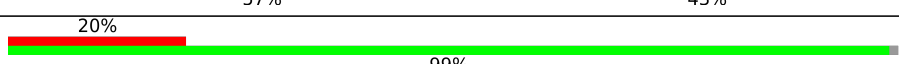

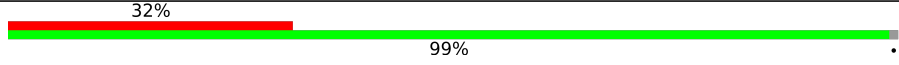
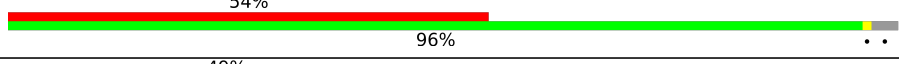
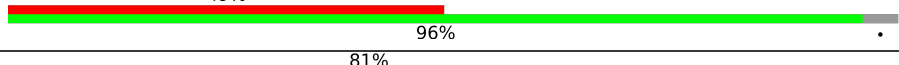
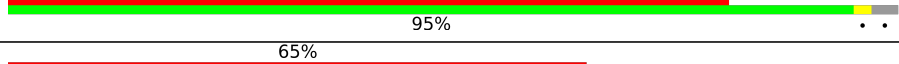

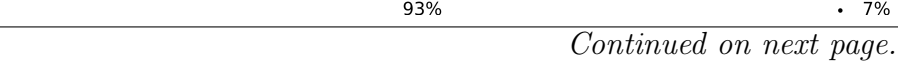


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	688	
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	W	122	
26	a	287	
27	b	287	
28	c	212	
29	d	180	
30	e	184	
31	f	149	
32	g	161	
33	h	137	

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Mol	Chain	Length	Quality of chain
34	i	146	25% 99%
35	j	122	42% 99%
36	k	151	23% 98%
37	l	139	29% 97%
38	m	124	13% 96%
39	n	116	38% 96%
40	o	119	39% 97%
41	p	127	18% 90% 10%
42	q	100	43% 98%
43	r	159	12% 87% 13%
44	s	237	9% 39% 61%
45	t	111	52% 99%
46	u	104	25% 83% 17%
47	v	65	29% 97%
48	w	111	21% 90% 10%
49	x	97	30% 44% 55%
50	y	57	21% 91% 7%
51	z	53	34% 94% 6%
52	3	2907	64% 35%
53	4	108	54% 43%
54	5	1520	67% 30%
55	7	76	59% 62% 38%
55	8	76	11% 62% 38%

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 151980 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 G.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	9	682	5326	3369	911	1021	25	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	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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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	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 L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	69	Total	C	N	O	S	0	0
			534	342	87	103	2		

- Molecule 26 is a protein called 50S ribosomal protein L2.

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

- Molecule 27 is a protein called 50S ribosomal protein L3.

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

- Molecule 28 is a protein called 50S ribosomal protein L4.

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

- Molecule 29 is a protein called 50S ribosomal protein L5.

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

- Molecule 30 is a protein called 50S ribosomal protein L6.

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

- Molecule 31 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	145	Total	C	N	O	S	0	0
			1160	746	204	207	3		

- Molecule 32 is a protein called 50S ribosomal protein L10.

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

- Molecule 33 is a protein called 50S ribosomal protein L11.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 46 is a protein called 50S ribosomal protein L27.

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

- Molecule 47 is a protein called 50S ribosomal protein L28.

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

- Molecule 48 is a protein called 50S ribosomal protein L29.

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

- Molecule 49 is a protein called 50S ribosomal protein L31.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L33 1.

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

- Molecule 52 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 53 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 54 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

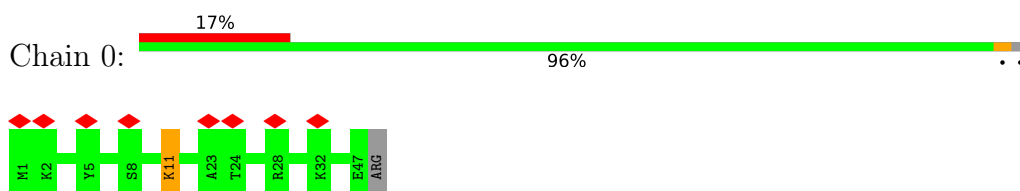
- Molecule 55 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
55	8	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

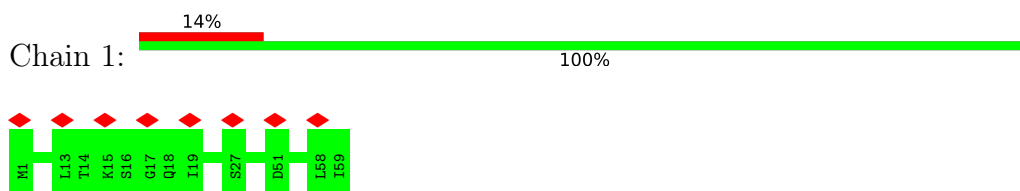
3 Residue-property plots [i](#)

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.

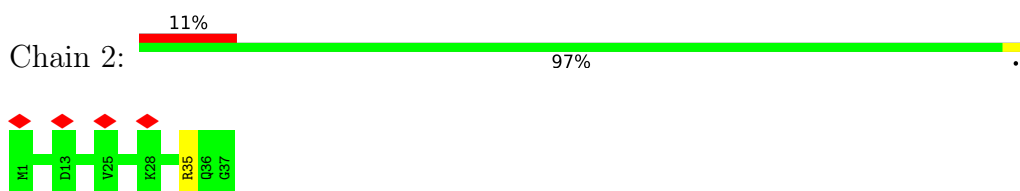
- Molecule 1: 50S ribosomal protein L34



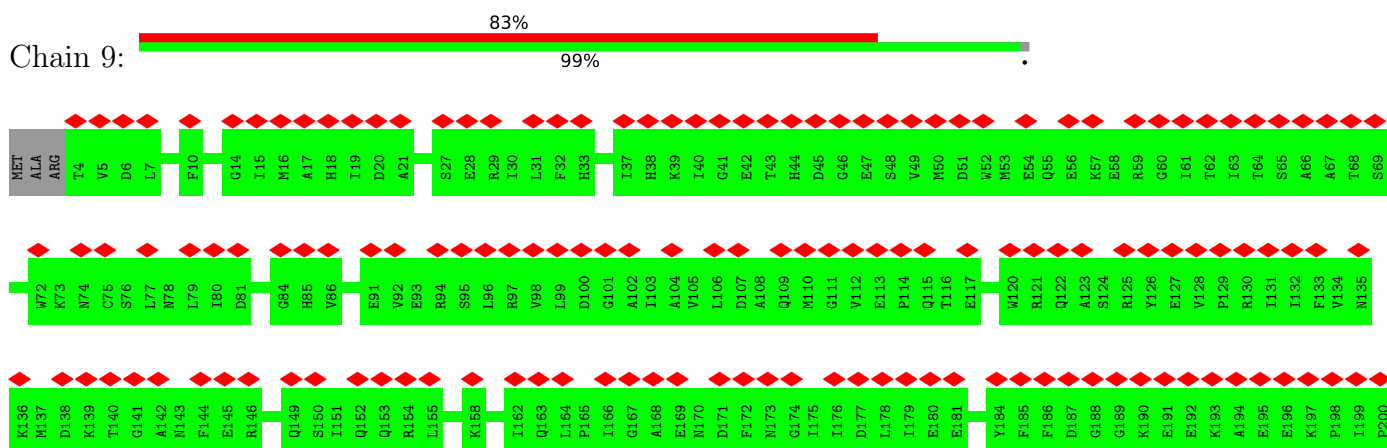
- Molecule 2: 50S ribosomal protein L35

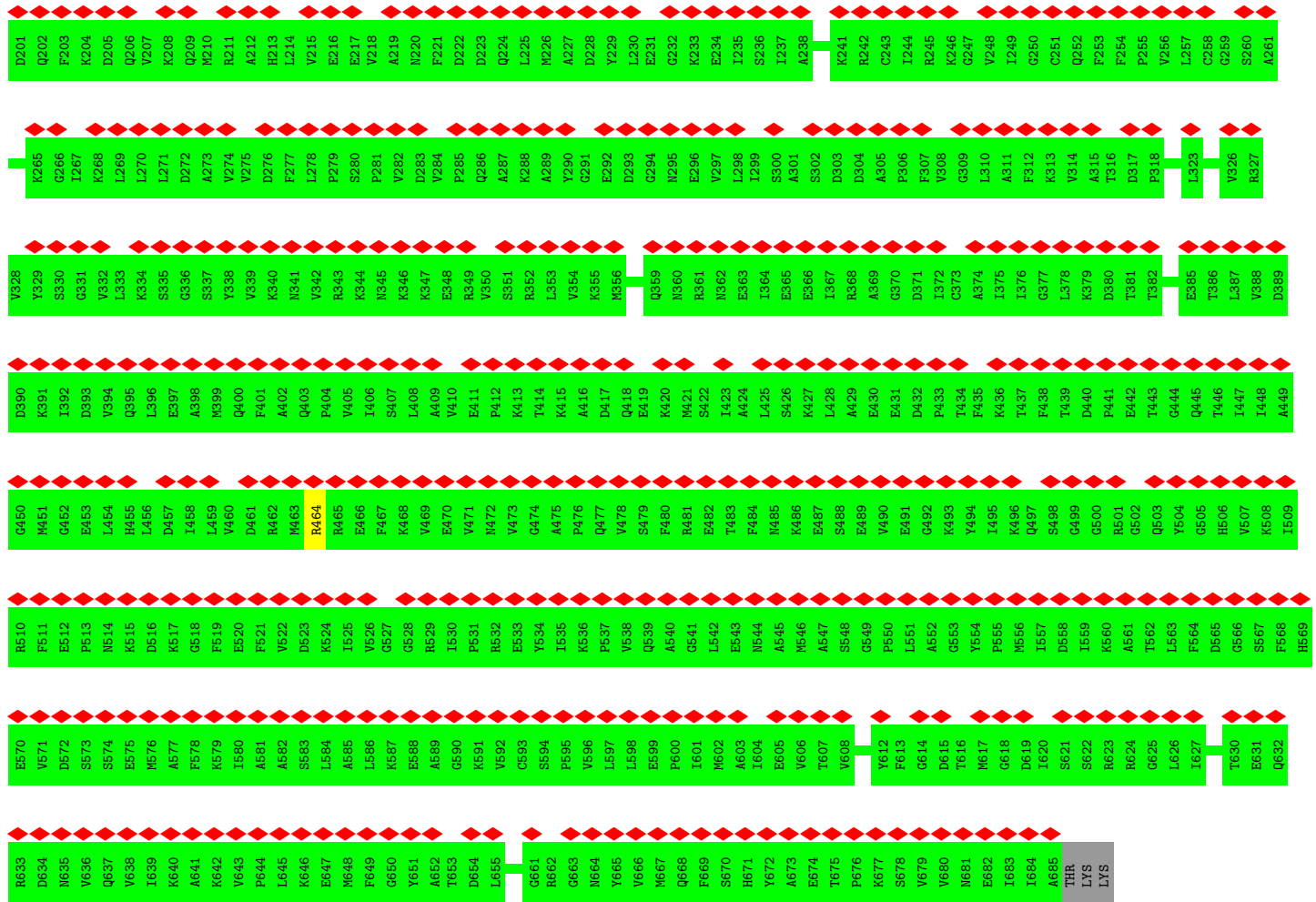


- Molecule 3: 50S ribosomal protein L36

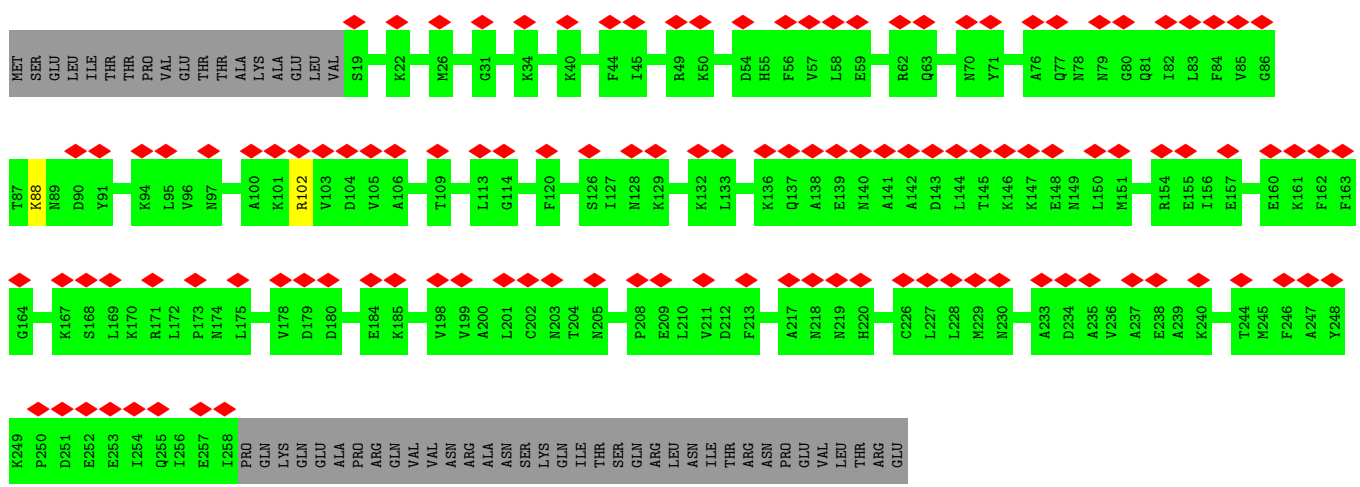
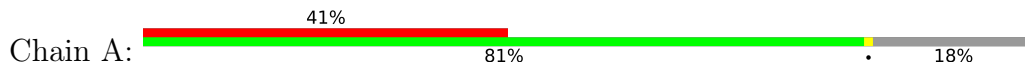


- Molecule 4: Elongation factor G

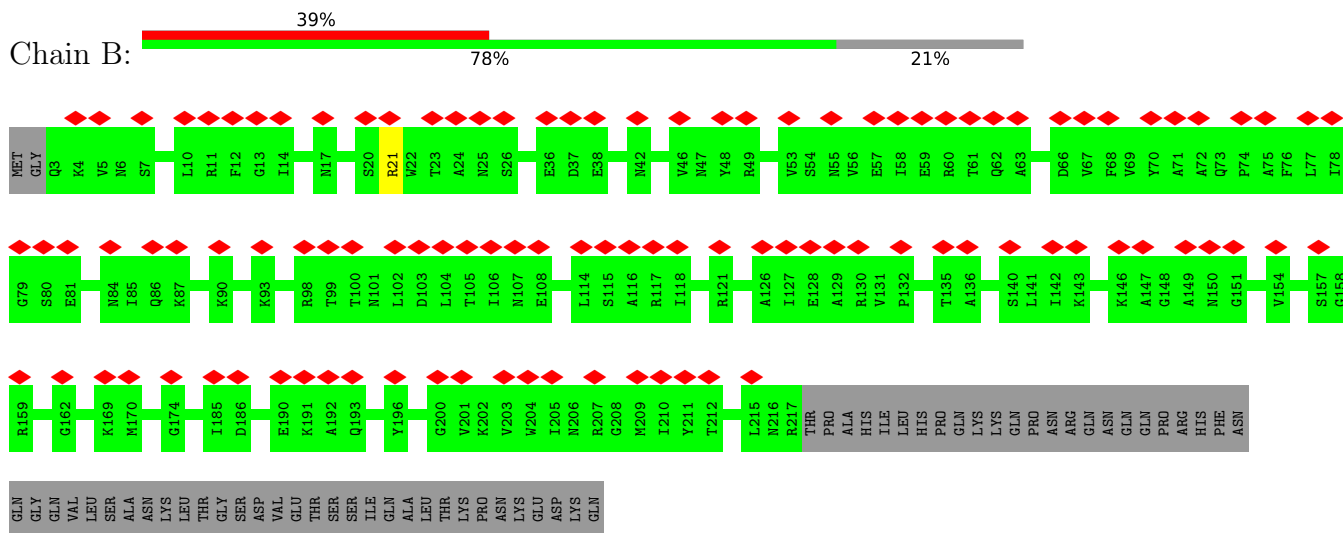




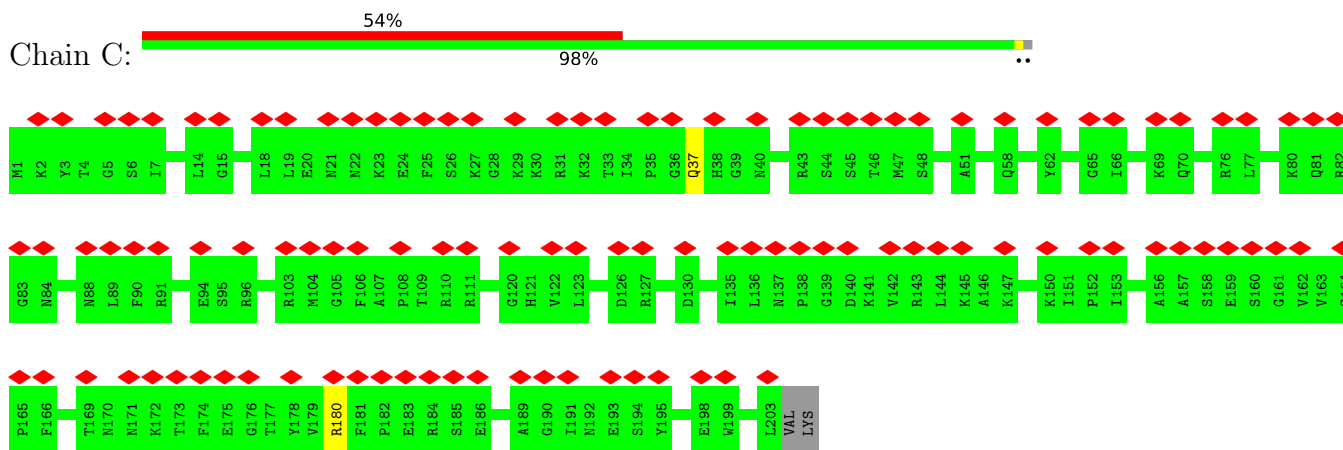
• Molecule 5: 30S ribosomal protein S2



• Molecule 6: 30S ribosomal protein S3



• Molecule 7: 30S ribosomal protein S4

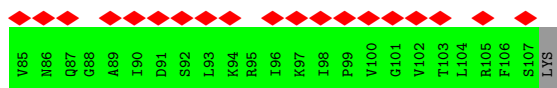


• Molecule 8: 30S ribosomal protein S5

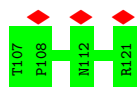
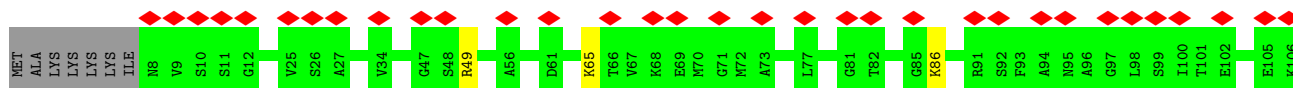
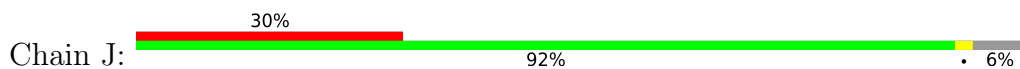


• Molecule 9: 30S ribosomal protein S6

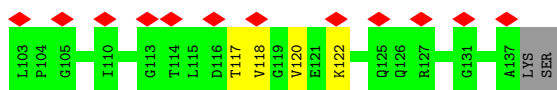
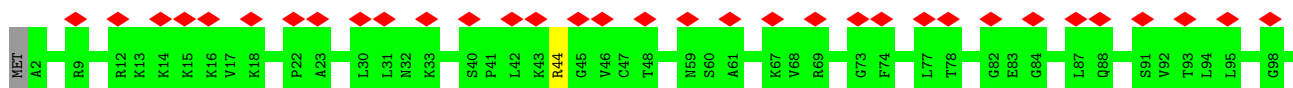




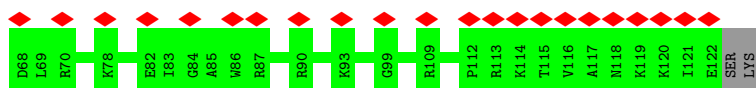
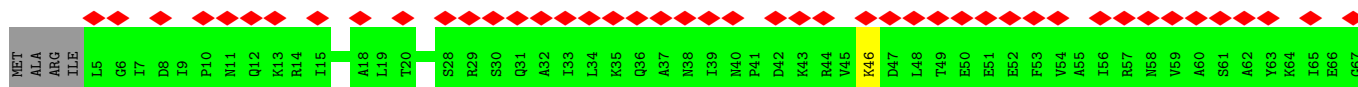
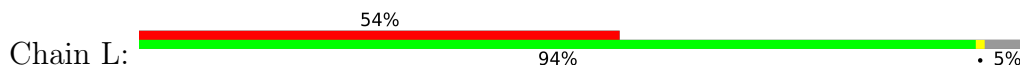
- Molecule 14: 30S ribosomal protein S11



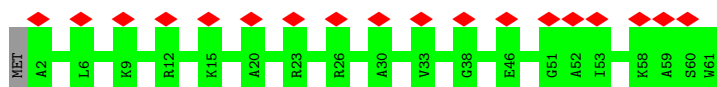
- Molecule 15: 30S ribosomal protein S12



- Molecule 16: 30S ribosomal protein S13

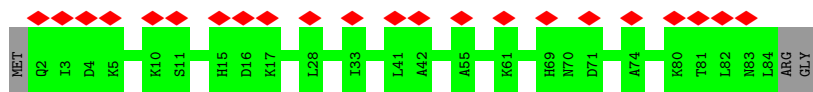


- Molecule 17: 30S ribosomal protein S14 type Z

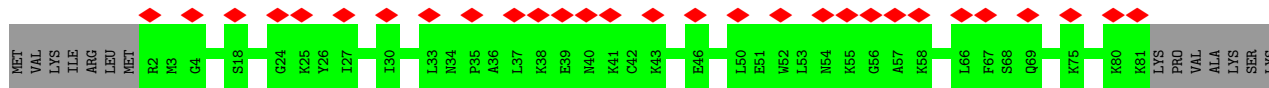
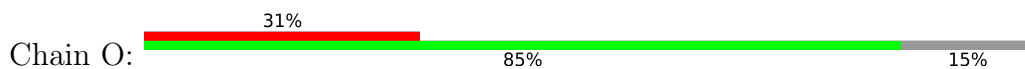


- Molecule 18: 30S ribosomal protein S15

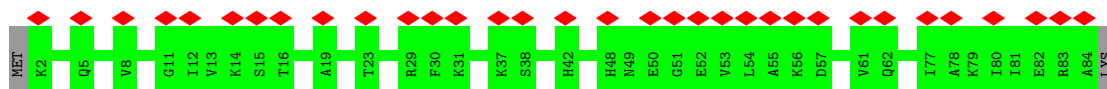
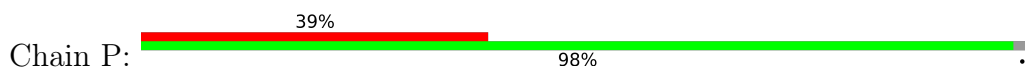




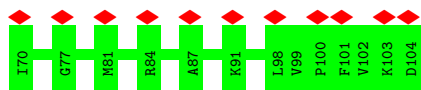
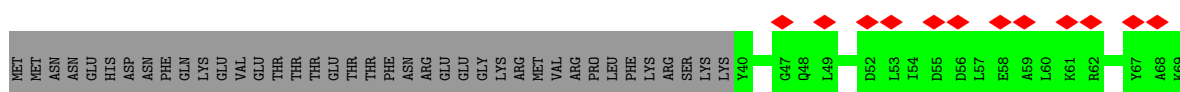
• Molecule 19: 30S ribosomal protein S16



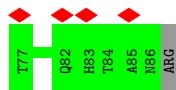
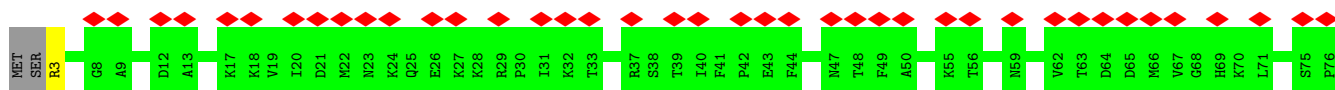
• Molecule 20: 30S ribosomal protein S17



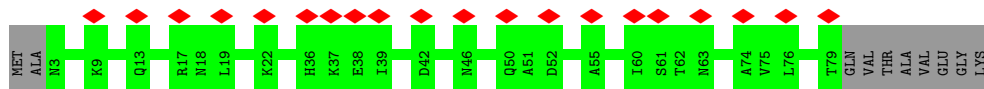
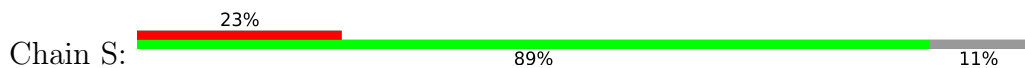
• Molecule 21: 30S ribosomal protein S18



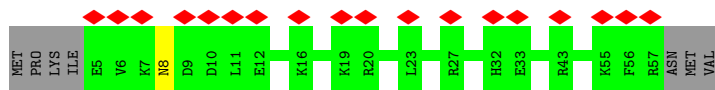
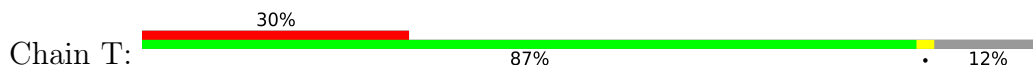
• Molecule 22: 30S ribosomal protein S19



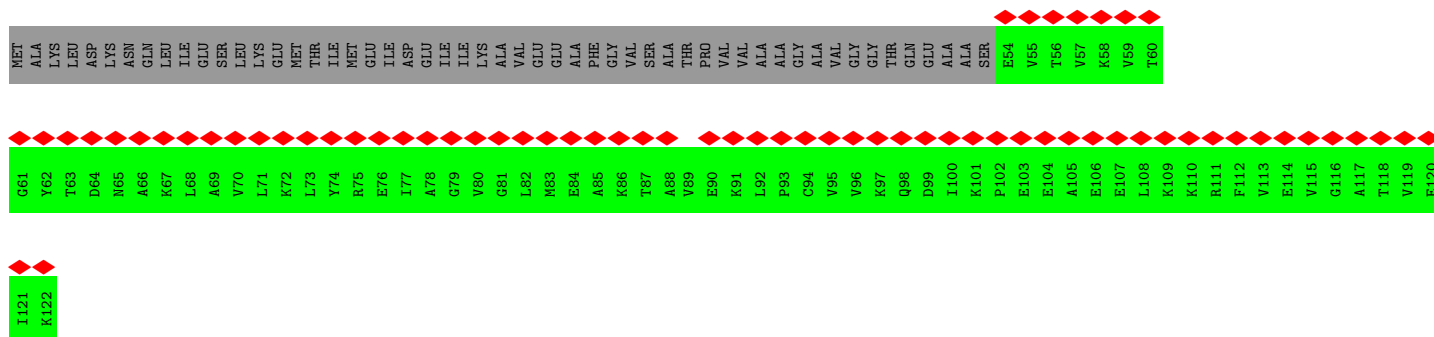
• Molecule 23: 30S ribosomal protein S20



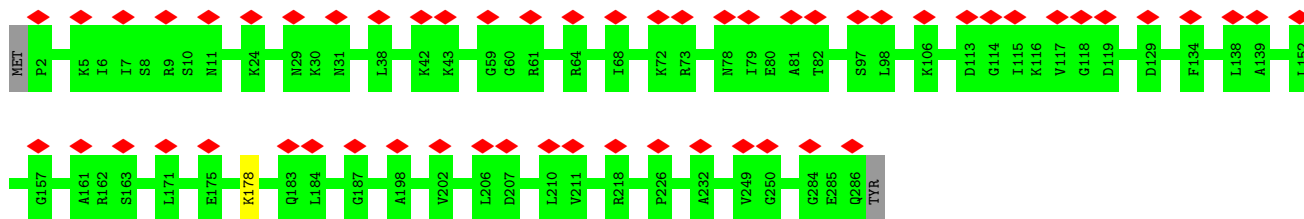
• Molecule 24: 30S ribosomal protein S21



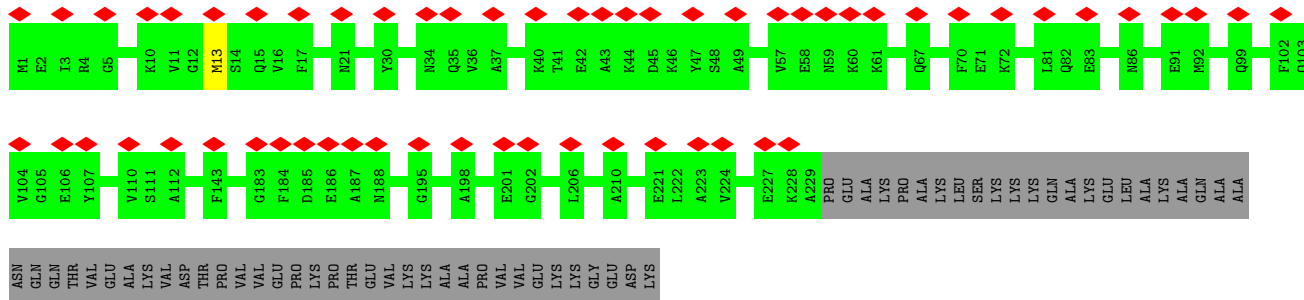
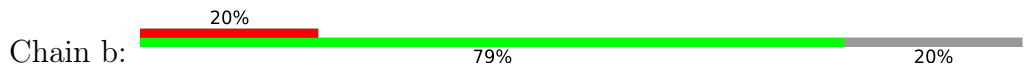
• Molecule 25: 50S ribosomal protein L7/L12



• Molecule 26: 50S ribosomal protein L2

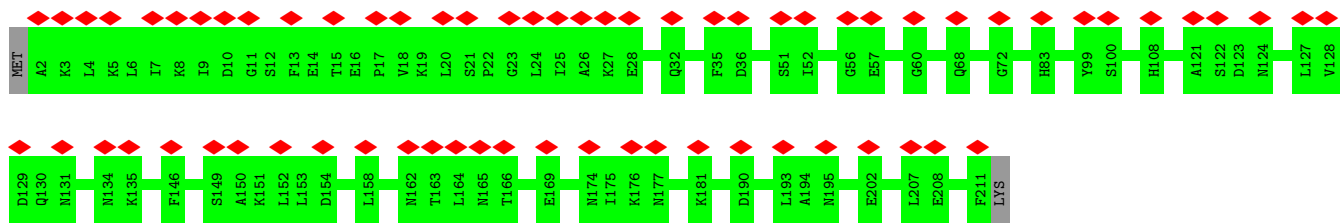


• Molecule 27: 50S ribosomal protein L3

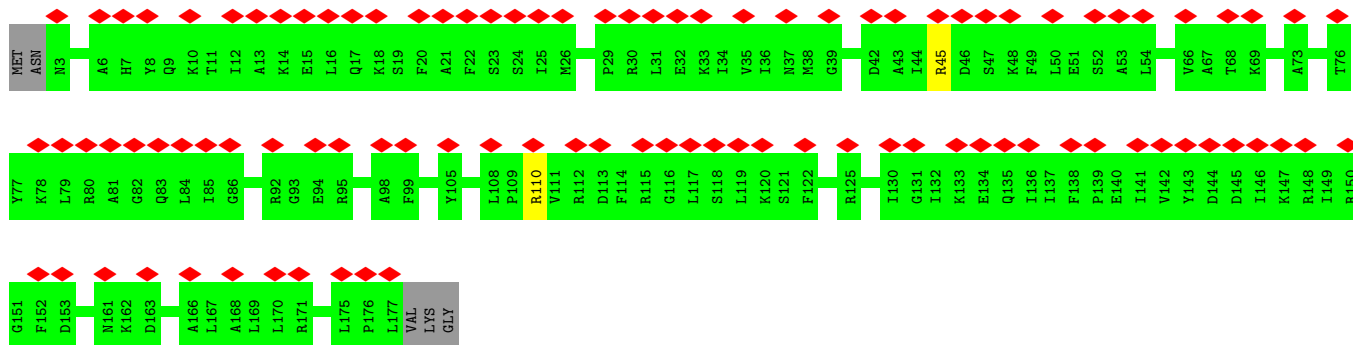


• Molecule 28: 50S ribosomal protein L4

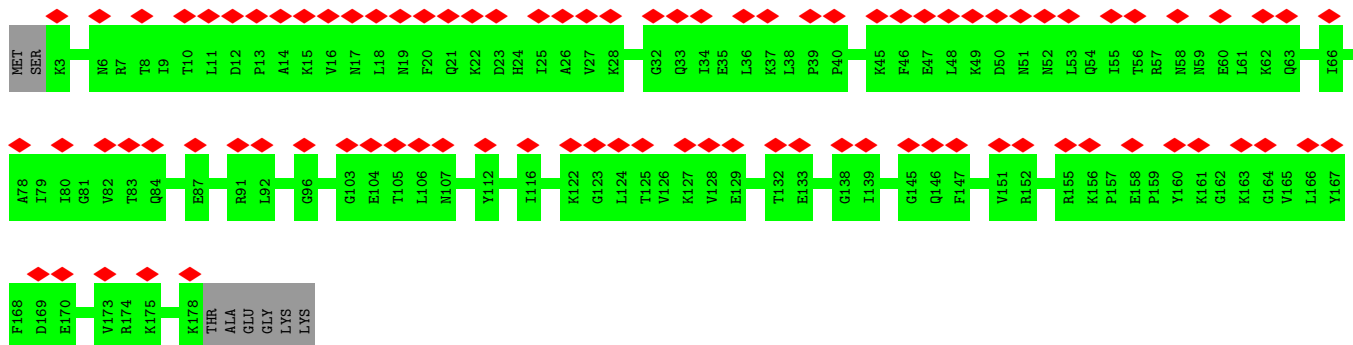




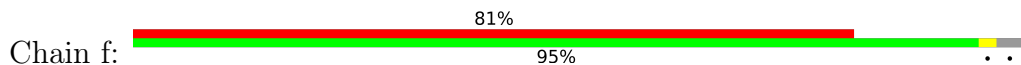
• Molecule 29: 50S ribosomal protein L5

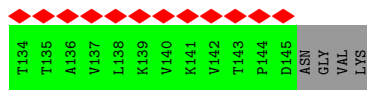


• Molecule 30: 50S ribosomal protein L6

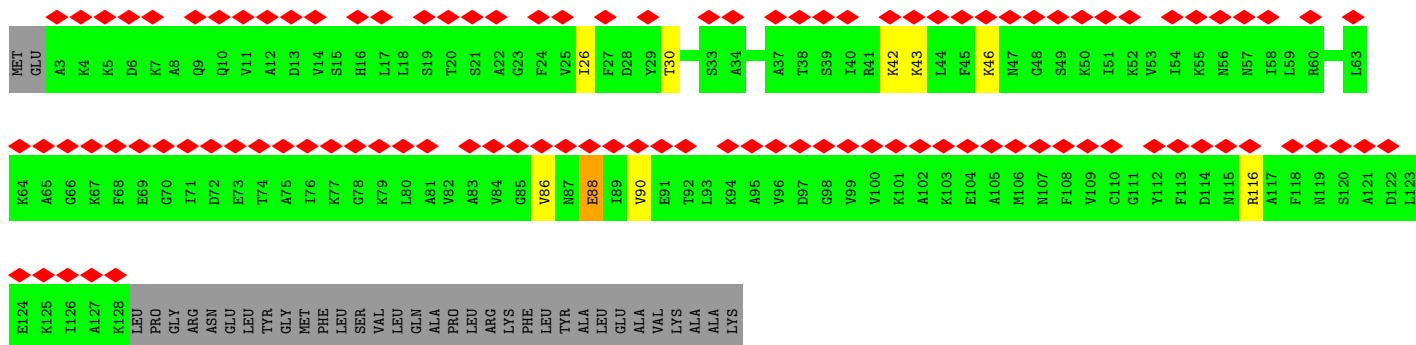


• Molecule 31: 50S ribosomal protein L9

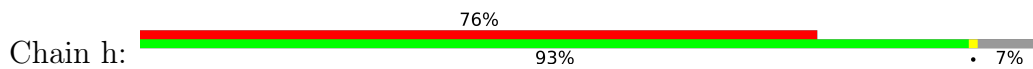




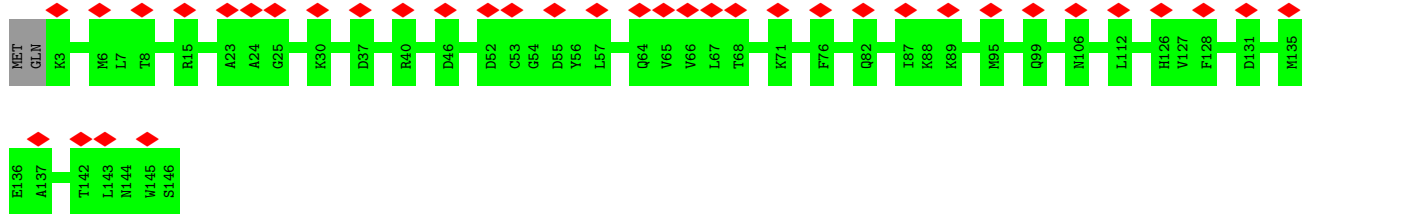
• Molecule 32: 50S ribosomal protein L10



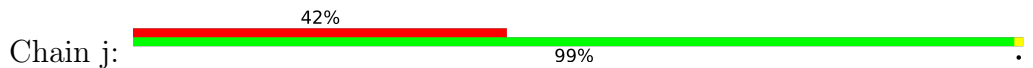
• Molecule 33: 50S ribosomal protein L11

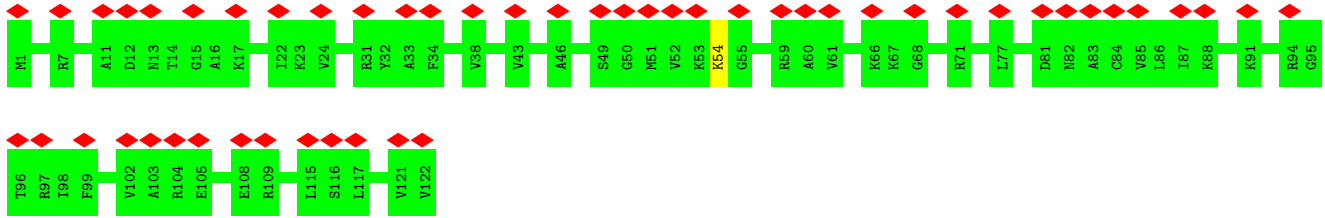


• Molecule 34: 50S ribosomal protein L13



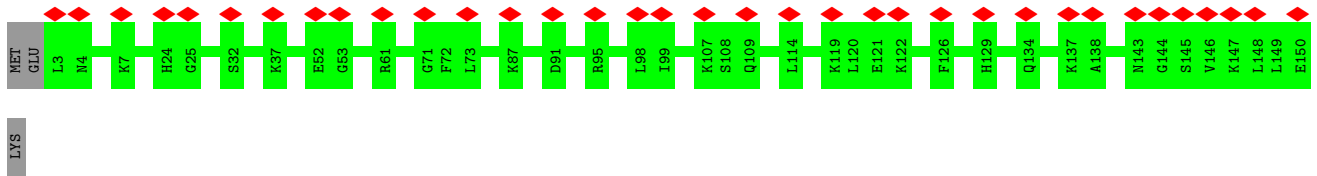
• Molecule 35: 50S ribosomal protein L14





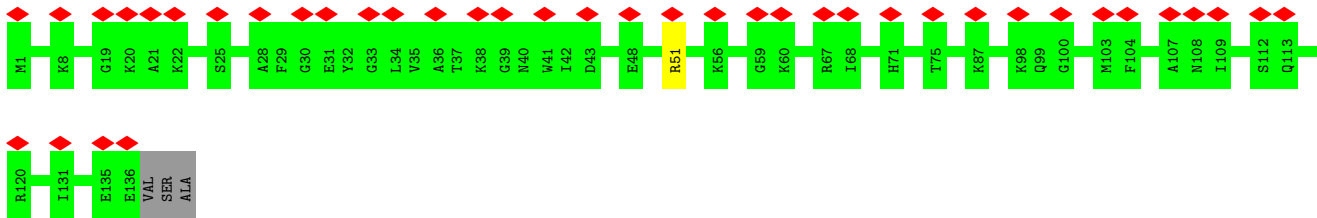
- Molecule 36: 50S ribosomal protein L15

Chain k: 23% 98%



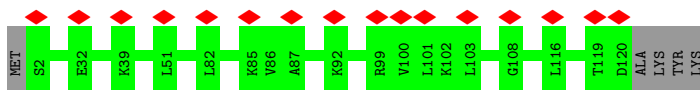
- Molecule 37: 50S ribosomal protein L16

Chain l: 29% 97%



- Molecule 38: 50S ribosomal protein L17

Chain m: 13% 96%



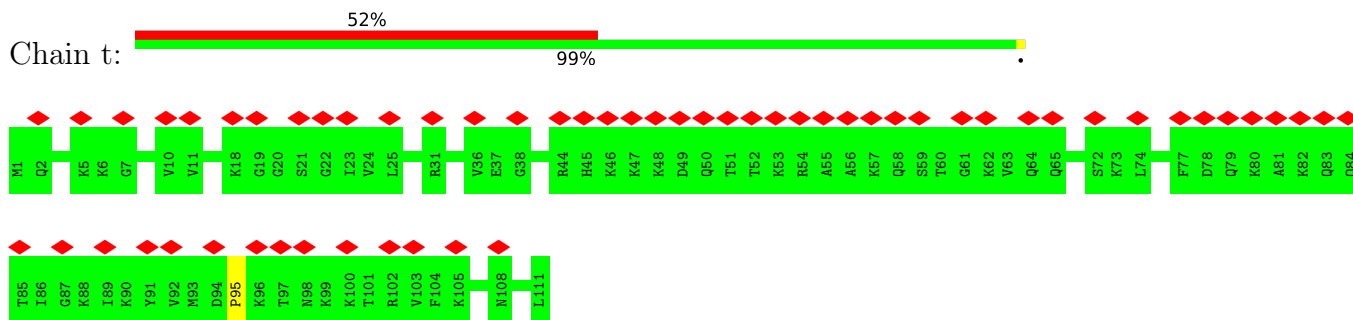
- Molecule 39: 50S ribosomal protein L18

Chain n: 38% 96%

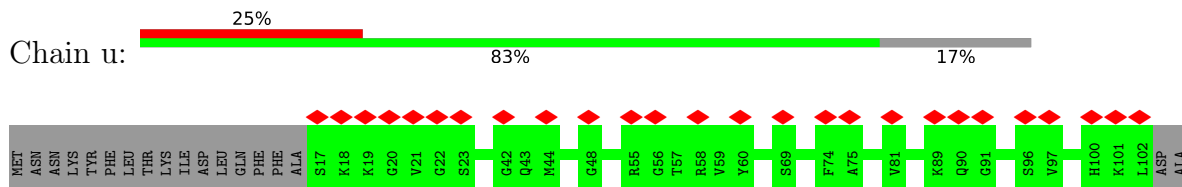


- Molecule 40: 50S ribosomal protein L19

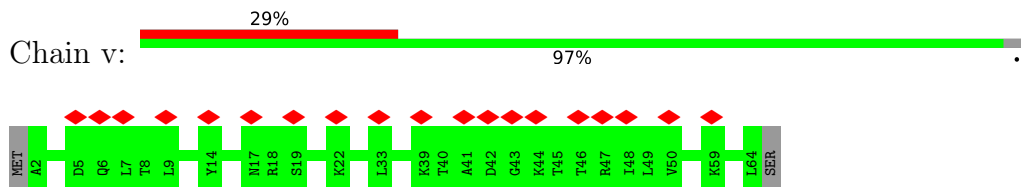
Chain o: 39% 97%



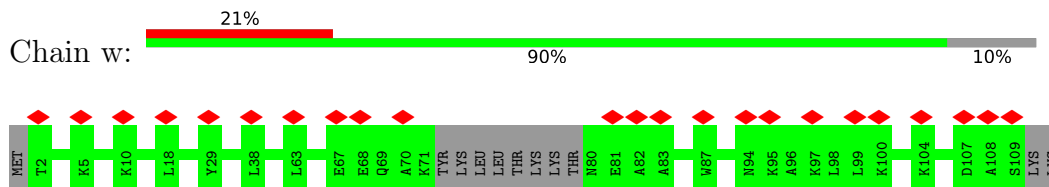
• Molecule 46: 50S ribosomal protein L27



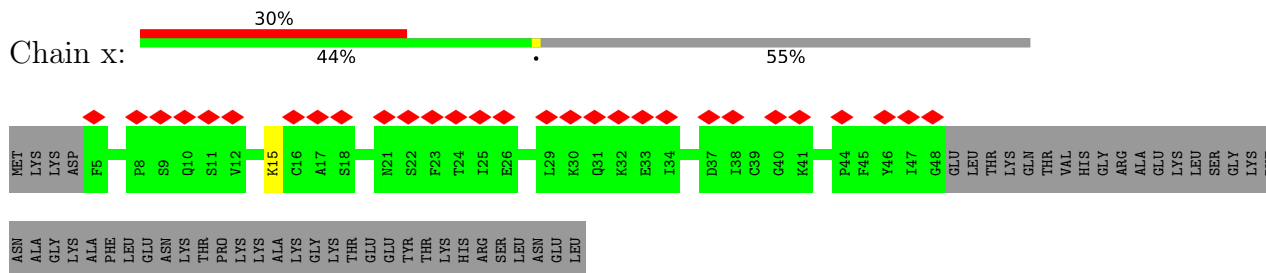
• Molecule 47: 50S ribosomal protein L28



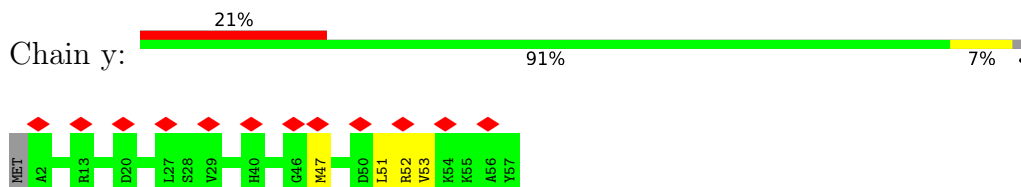
• Molecule 48: 50S ribosomal protein L29



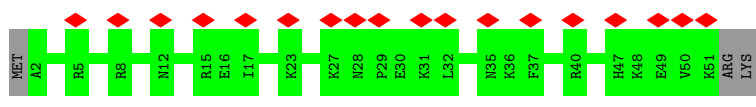
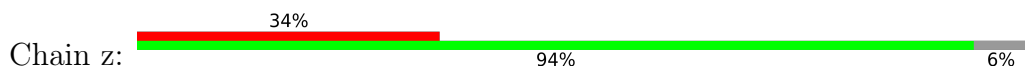
• Molecule 49: 50S ribosomal protein L31



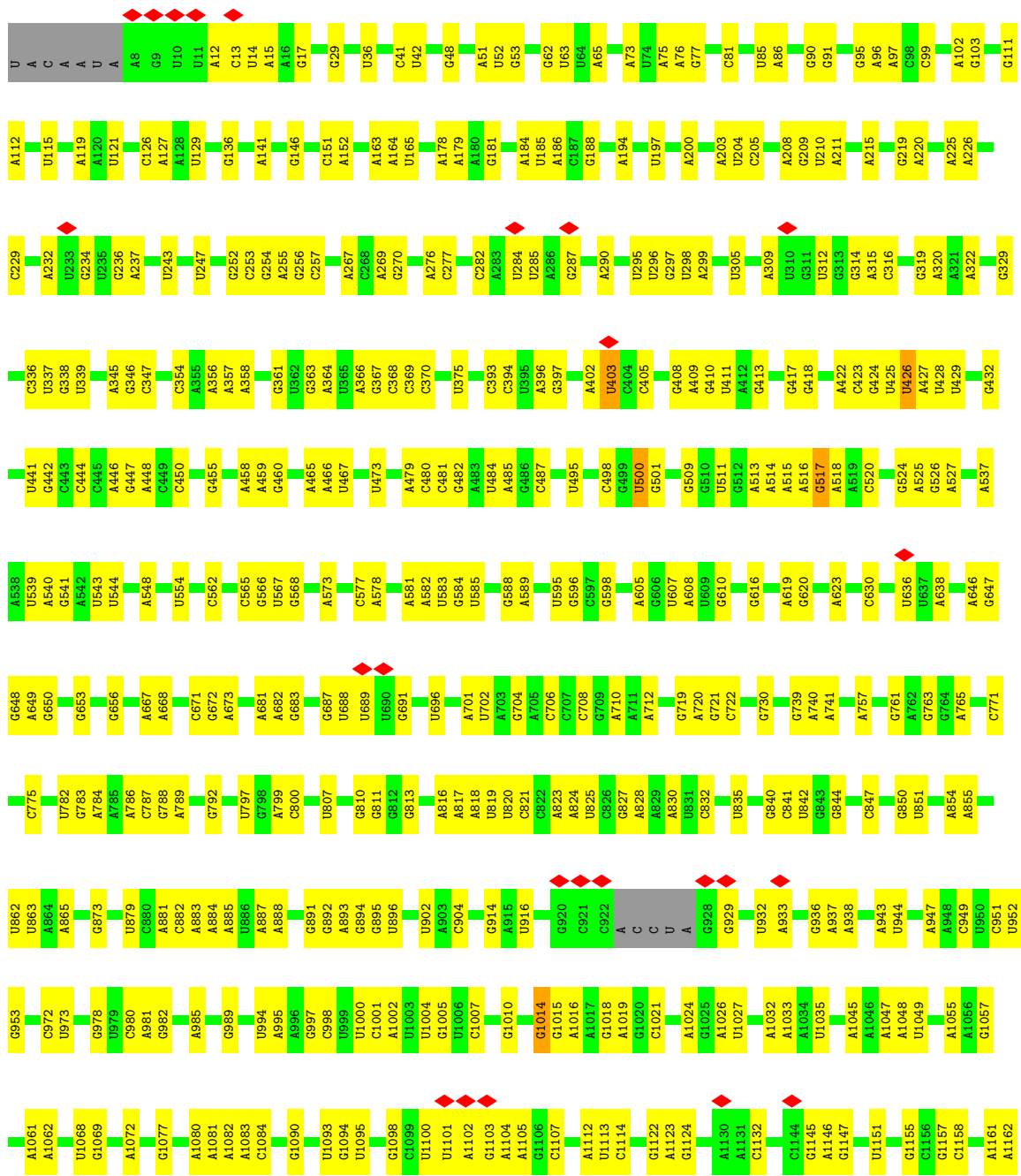
• Molecule 50: 50S ribosomal protein L32



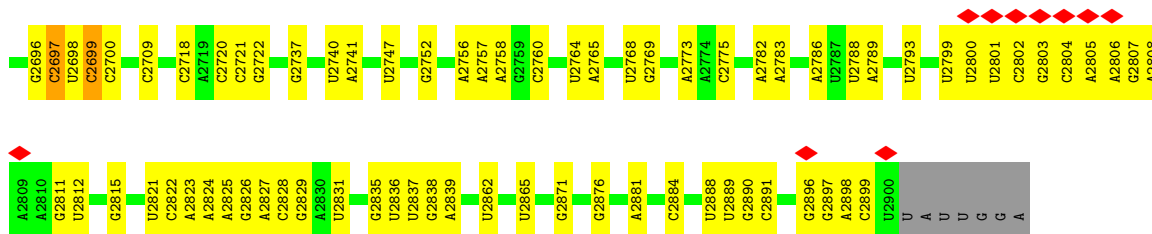
• Molecule 51: 50S ribosomal protein L33 1



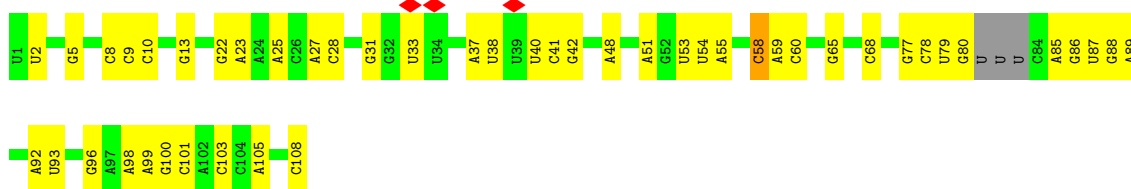
• Molecule 52: 23S ribosomal RNA



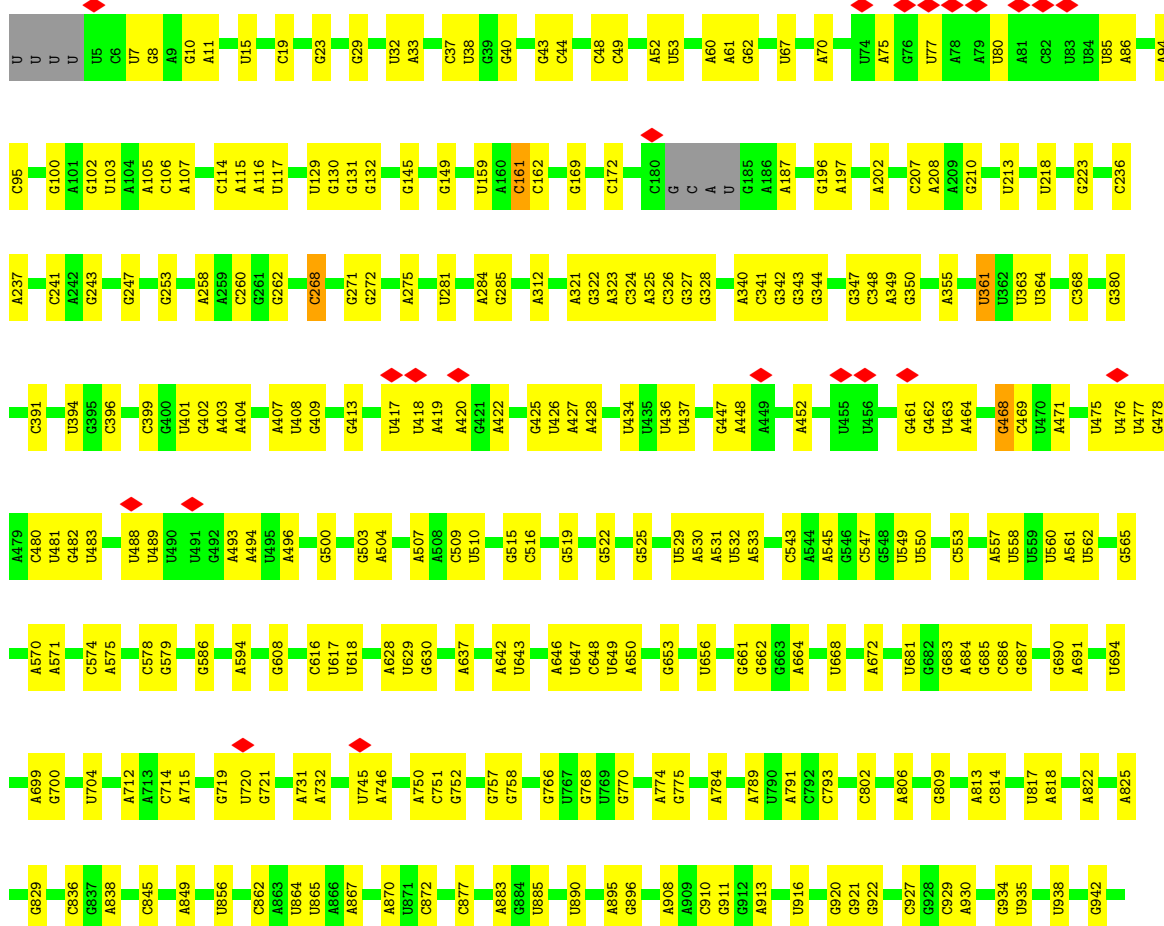
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A2572	U2468	U2351	A2230	U2148	G2059	A1945	C1813	A1694	A1585	U1501	U1360	G1263	A1164
A2573	G2355	C2355	A2231	G2151	C2062	A1951	C1814	G1695	U1586	A1502	U1361	G1265	U1165
A2574	U2368	G2368	G2232	G2152	G2063	A1959	U1816	A1698	U1587	U1508	U1369	G1266	U1166
G2575	A2376	A2389	A2233	A2153	G2064	A1962	A1817	G1700	A1588	G1508	U1370	U1260	U1167
A2580	G2476	G2389	A2235	U2154	A2065	U1982	G1818	G1701	A1589	U1509	G1371	G1267	U1168
C2581	A2477	A2389	G2242	A2155	A2066	C1969	G1819	A1702	A1592	U1510	U1374	A1267	C1170
G2586	G2478	G2360	G2243	C2070	G2068	C1970	U1820	A1703	U1593	A1513	G1375	U1268	G1171
G2590	A2477	A2362	G2244	C2071	A2069	C1971	U1821	C1704	G1594	U1514	U1376	A1274	U1176
G2590	G2483	U2385	G2245	U2159	C2070	G1971	U1822	U1705	U1597	U1515	A1381	C1274	A1177
U2604	A2484	U2385	G2247	U2160	C2071	U1972	U1824	U1706	A1603	U1516	G1383	A1276	A1178
G2605	U2485	U2380	U2251	U2161	U1974	U1974	U1825	U1707	A1517	G1517	G1277	A1277	U1179
A2606	A2486	U2387	U2252	A2165	G2076	A1977	A1826	A1708	U1610	G1518	A1278	A1186	A1186
G2607	U2490	C2388	U2253	U2166	U2083	A1978	U1827	A1715	C1611	A1519	A1281	A1190	A1190
G2611	C2491	A2389	G2254	G2169	A2084	U1978	G1832	A1716	U1612	U1522	G1282	A1191	U1191
G2612	G2492	G2391	A2274	G2173	C2085	C1987	A1836	G1721	G1615	U1528	C1404	A1283	U1192
U2617	A2495	U2392	A2275	G2174	U2089	C1990	C1837	G1729	U1618	C1531	A1406	G1286	G1197
C2618	U2497	C2393	A2276	U2175	G2100	C1999	G1842	C1730	A1619	A1532	G1408	C1287	G1197
C2619	U2498	G2397	A2280	U2179	A2101	U1998	C1845	G1737	U1623	U1533	G1409	C1288	A1201
G2620	U2500	U2399	A2286	A2179	G2106	G1999	A1865	U1743	G1628	A1534	A1410	U1293	A1202
U2621	C2504	G2399	G2287	U2180	G2106	U2000	A1891	U1748	U1641	A1536	C1411	A1298	A1203
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C2634	C2507	C2411	U2291	A2184	U2111	A2010	C1877	U1748	A1644	G1542	U1424	G1301	U1209
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G2642	C2305	U2189	U2189	U2189	A2115	U2018	A1891	A1766	C1649	U1544	C1427	U1304	U1214
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U2644	U2313	U2199	U2199	G2117	U2117	C2025	A1904	A1766	A1650	U1549	A1431	A1308	G1215
A2647	G2316	G2199	U2199	G2117	U2117	C2025	U1905	A1766	C1651	U1549	A1431	A1308	G1215
G2649	G2316	U2199	U2199	G2117	U2117	C2025	G1906	A1766	A1652	U1549	A1431	A1308	G1215
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A2662	G2322	G2201	G2201	A2126	A2124	G2032	A1907	A1766	A1656	U1549	A1431	A1308	G1215
U2664	U2327	U2202	U2202	G2127	A2127	U2035	G1913	A1780	G1663	U1559	A1456	A1322	G1226
A2668	A2328	U2205	U2205	G2127	A2127	A2037	A1919	U1784	C1672	U1559	A1456	A1322	G1226
G2669	G2329	A2206	A2206	G2130	A2130	A2037	A1919	U1784	C1672	U1559	A1456	A1322	G1226
G2681	A2330	G2210	G2210	G2131	A2131	A2037	A1919	U1784	C1672	U1559	A1456	A1322	G1226
A2685	G2333	G2211	G2211	G2132	A2132	G2039	A1920	U1786	C1676	U1559	A1456	A1322	G1226
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A2687	A2335	G2212	G2212	G2134	A2134	A2040	C1921	A1788	U1679	U1559	A1456	A1322	G1226
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C2689	G2341	U2219	U2219	A2136	A2136	A2042	C1927	A1788	U1679	U1559	A1456	A1322	G1226
U2690	U2342	A2221	A2221	A2137	A2137	C2043	C1927	A1788	U1679	U1559	A1456	A1322	G1226
	A2343	U2221	U2221	A2137	A2137	C2043	C1927	A1788	U1679	U1559	A1456	A1322	G1226
	A2344	C2223	C2223	A2138	A2138	C2044	C1931	A1791	U1681	U1559	A1456	A1322	G1226
		A2224	A2224	C2139	C2139	C2050	C1931	A1791	U1681	U1559	A1456	A1322	G1226
		G2225	G2225	G2140	G2140	A2055	G1836	U1805	G1685	U1572	U1487	G1352	A1249
		U2226	U2226	A2141	A2141	C2057	G1937	U1807	G1685	U1572	U1487	G1352	A1250

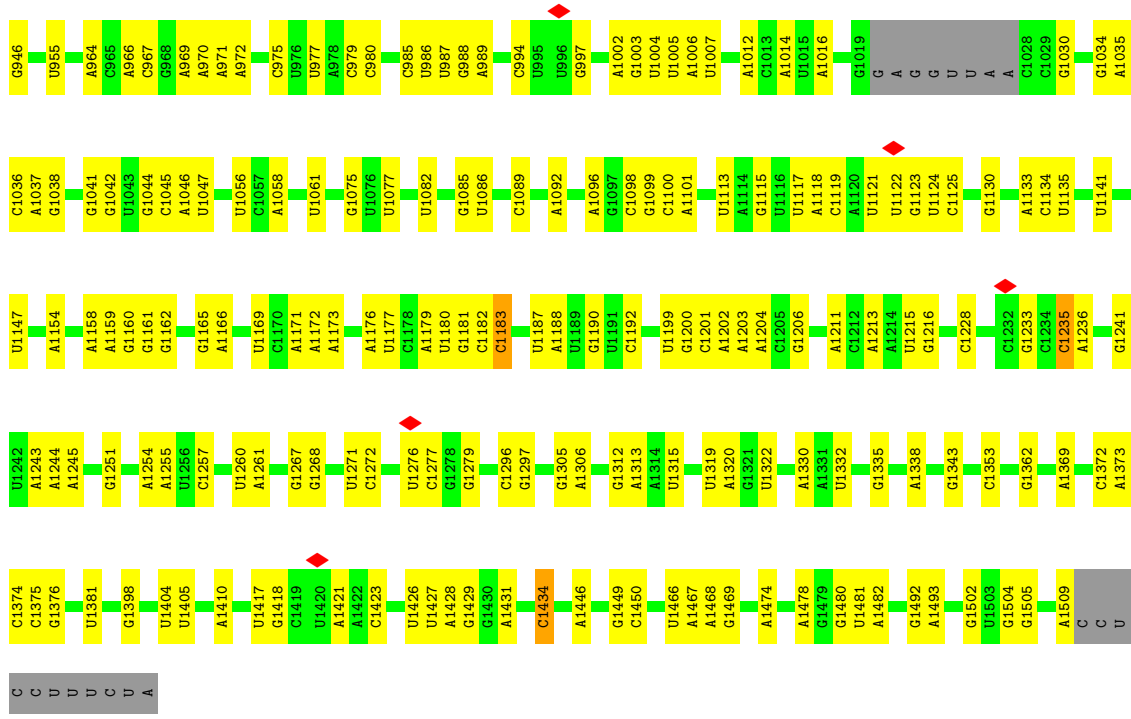


• Molecule 53: 5S ribosomal RNA

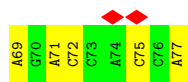
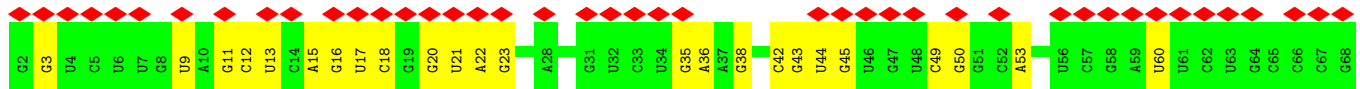


• Molecule 54: 16S ribosomal RNA

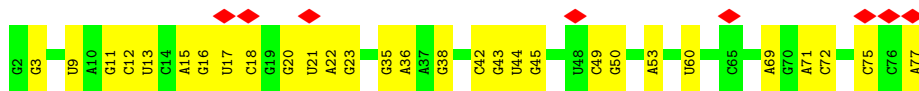




• Molecule 55: tRNA-Phe



• Molecule 55: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	8730	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 K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.874	Depositor
Minimum map value	-0.889	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.121	Depositor
Recommended contour level	0.54	Depositor
Map size (\AA)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	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	0.27	0/383	0.58	1/504 (0.2%)
2	1	0.26	0/484	0.54	0/637
3	2	0.24	0/306	0.53	0/401
4	9	0.26	0/5419	0.50	0/7307
5	A	0.29	0/1954	0.56	0/2642
6	B	0.25	0/1721	0.48	0/2323
7	C	0.26	0/1691	0.49	0/2267
8	D	0.24	0/1188	0.48	0/1593
9	E	0.28	0/1384	0.51	0/1867
10	F	0.28	0/1266	0.48	0/1700
11	G	0.26	0/1126	0.56	0/1517
12	H	0.25	0/1044	0.47	0/1395
13	I	0.26	0/820	0.55	0/1103
14	J	0.25	0/844	0.49	0/1136
15	K	0.29	0/1094	0.53	0/1468
16	L	0.25	0/962	0.51	0/1289
17	M	0.27	0/483	0.53	0/643
18	N	0.27	0/679	0.56	0/907
19	O	0.28	0/659	0.51	0/885
20	P	0.23	0/684	0.47	0/913
21	Q	0.26	0/545	0.50	0/730
22	R	0.27	0/698	0.51	0/936
23	S	0.24	0/631	0.44	0/838
24	T	0.28	0/475	0.50	0/621
25	W	0.24	0/538	0.44	0/722
26	a	0.25	0/2267	0.50	0/3044
27	b	0.27	0/1795	0.52	0/2412
28	c	0.25	0/1671	0.50	0/2246
29	d	0.24	0/1409	0.49	0/1894
30	e	0.26	0/1420	0.50	0/1912
31	f	0.26	0/1183	0.56	1/1587 (0.1%)
32	g	0.39	0/969	0.64	0/1295
33	h	0.26	0/968	0.49	0/1298
34	i	0.25	0/1186	0.51	0/1592

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	j	0.28	0/953	0.55	0/1275
36	k	0.25	0/1170	0.49	0/1559
37	l	0.25	0/1104	0.52	0/1481
38	m	0.25	0/973	0.49	0/1309
39	n	0.27	0/897	0.56	0/1198
40	o	0.26	0/948	0.53	0/1262
41	p	0.25	0/961	0.50	0/1278
42	q	0.37	0/828	0.61	0/1111
43	r	0.25	0/1077	0.55	0/1441
44	s	0.25	0/732	0.51	0/988
45	t	0.25	0/879	0.50	0/1165
46	u	0.25	0/665	0.50	0/884
47	v	0.24	0/519	0.53	0/695
48	w	0.32	0/826	0.52	0/1104
49	x	0.27	0/353	0.48	0/474
50	y	0.30	0/457	0.60	0/601
51	z	0.23	0/412	0.46	0/547
52	3	0.21	0/69073	0.82	56/107710 (0.1%)
53	4	0.19	0/2505	0.81	5/3902 (0.1%)
54	5	0.21	0/35768	0.80	25/55764 (0.0%)
55	7	0.20	0/1808	0.81	0/2817
55	8	0.21	0/1808	0.80	0/2817
All	All	0.23	0/164662	0.74	88/245006 (0.0%)

There are no bond length outliers.

The worst 5 of 88 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	3	1320	C	N3-C2-O2	-8.79	115.75	121.90
52	3	394	C	N3-C2-O2	-8.57	115.90	121.90
52	3	1987	C	N3-C2-O2	-8.44	115.99	121.90
54	5	161	C	N3-C2-O2	-8.02	116.29	121.90
52	3	2474	C	C6-N1-C2	-8.01	117.09	120.30

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

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%)	33 (94%)	2 (6%)	0	100	100
4	9	680/688 (99%)	625 (92%)	55 (8%)	0	100	100
5	A	238/294 (81%)	216 (91%)	22 (9%)	0	100	100
6	B	213/273 (78%)	191 (90%)	22 (10%)	0	100	100
7	C	201/205 (98%)	188 (94%)	13 (6%)	0	100	100
8	D	151/219 (69%)	145 (96%)	6 (4%)	0	100	100
9	E	165/215 (77%)	150 (91%)	15 (9%)	0	100	100
10	F	152/155 (98%)	144 (95%)	8 (5%)	0	100	100
11	G	139/142 (98%)	119 (86%)	20 (14%)	0	100	100
12	H	126/132 (96%)	109 (86%)	17 (14%)	0	100	100
13	I	99/108 (92%)	90 (91%)	9 (9%)	0	100	100
14	J	112/121 (93%)	109 (97%)	3 (3%)	0	100	100
15	K	134/139 (96%)	114 (85%)	20 (15%)	0	100	100
16	L	116/124 (94%)	99 (85%)	17 (15%)	0	100	100
17	M	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
18	N	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
19	O	78/94 (83%)	73 (94%)	5 (6%)	0	100	100
20	P	81/85 (95%)	76 (94%)	5 (6%)	0	100	100
21	Q	63/104 (61%)	58 (92%)	5 (8%)	0	100	100
22	R	82/87 (94%)	76 (93%)	6 (7%)	0	100	100
23	S	75/87 (86%)	74 (99%)	1 (1%)	0	100	100
24	T	51/60 (85%)	50 (98%)	1 (2%)	0	100	100
25	W	67/122 (55%)	63 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	a	283/287 (99%)	252 (89%)	31 (11%)	0	100	100
27	b	227/287 (79%)	210 (92%)	17 (8%)	0	100	100
28	c	208/212 (98%)	193 (93%)	15 (7%)	0	100	100
29	d	173/180 (96%)	152 (88%)	21 (12%)	0	100	100
30	e	174/184 (95%)	162 (93%)	12 (7%)	0	100	100
31	f	143/149 (96%)	131 (92%)	12 (8%)	0	100	100
32	g	124/161 (77%)	111 (90%)	12 (10%)	1 (1%)	19	60
33	h	126/137 (92%)	113 (90%)	13 (10%)	0	100	100
34	i	142/146 (97%)	132 (93%)	10 (7%)	0	100	100
35	j	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
36	k	146/151 (97%)	135 (92%)	11 (8%)	0	100	100
37	l	134/139 (96%)	127 (95%)	7 (5%)	0	100	100
38	m	117/124 (94%)	115 (98%)	2 (2%)	0	100	100
39	n	108/116 (93%)	98 (91%)	10 (9%)	0	100	100
40	o	113/119 (95%)	103 (91%)	10 (9%)	0	100	100
41	p	112/127 (88%)	106 (95%)	6 (5%)	0	100	100
42	q	97/100 (97%)	86 (89%)	11 (11%)	0	100	100
43	r	137/159 (86%)	126 (92%)	11 (8%)	0	100	100
44	s	90/237 (38%)	87 (97%)	3 (3%)	0	100	100
45	t	109/111 (98%)	93 (85%)	15 (14%)	1 (1%)	17	56
46	u	84/104 (81%)	78 (93%)	6 (7%)	0	100	100
47	v	61/65 (94%)	56 (92%)	5 (8%)	0	100	100
48	w	96/111 (86%)	91 (95%)	5 (5%)	0	100	100
49	x	42/97 (43%)	38 (90%)	4 (10%)	0	100	100
50	y	54/57 (95%)	51 (94%)	2 (4%)	1 (2%)	8	38
51	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	6567/7480 (88%)	6043 (92%)	521 (8%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	g	88	GLU
50	y	53	VAL

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Mol	Chain	Res	Type
45	t	95	PRO

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%)	39 (98%)	1 (2%)	47	68
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	34 (97%)	1 (3%)	42	64
4	9	579/584 (99%)	578 (100%)	1 (0%)	93	96
5	A	212/262 (81%)	210 (99%)	2 (1%)	78	87
6	B	180/232 (78%)	179 (99%)	1 (1%)	86	92
7	C	181/183 (99%)	179 (99%)	2 (1%)	73	84
8	D	123/178 (69%)	122 (99%)	1 (1%)	81	89
9	E	150/196 (76%)	148 (99%)	2 (1%)	69	82
10	F	131/132 (99%)	129 (98%)	2 (2%)	65	80
11	G	123/124 (99%)	121 (98%)	2 (2%)	62	79
12	H	111/115 (96%)	109 (98%)	2 (2%)	59	77
13	I	95/99 (96%)	95 (100%)	0	100	100
14	J	91/97 (94%)	88 (97%)	3 (3%)	38	61
15	K	117/120 (98%)	112 (96%)	5 (4%)	29	53
16	L	100/105 (95%)	99 (99%)	1 (1%)	76	86
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%)	69 (100%)	0	100	100
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%)	73 (99%)	1 (1%)	67	80
23	S	70/77 (91%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	T	49/56 (88%)	48 (98%)	1 (2%)	55	74
25	W	58/98 (59%)	58 (100%)	0	100	100
26	a	241/243 (99%)	240 (100%)	1 (0%)	91	94
27	b	186/233 (80%)	185 (100%)	1 (0%)	88	93
28	c	182/184 (99%)	182 (100%)	0	100	100
29	d	150/154 (97%)	148 (99%)	2 (1%)	69	82
30	e	153/159 (96%)	153 (100%)	0	100	100
31	f	123/134 (92%)	121 (98%)	2 (2%)	62	79
32	g	101/129 (78%)	92 (91%)	9 (9%)	9	30
33	h	102/110 (93%)	101 (99%)	1 (1%)	76	86
34	i	126/128 (98%)	126 (100%)	0	100	100
35	j	103/103 (100%)	102 (99%)	1 (1%)	76	86
36	k	123/126 (98%)	123 (100%)	0	100	100
37	l	113/115 (98%)	112 (99%)	1 (1%)	78	87
38	m	105/109 (96%)	105 (100%)	0	100	100
39	n	96/99 (97%)	95 (99%)	1 (1%)	76	86
40	o	101/105 (96%)	101 (100%)	0	100	100
41	p	100/108 (93%)	100 (100%)	0	100	100
42	q	90/91 (99%)	89 (99%)	1 (1%)	73	84
43	r	116/132 (88%)	115 (99%)	1 (1%)	78	87
44	s	82/208 (39%)	82 (100%)	0	100	100
45	t	96/96 (100%)	96 (100%)	0	100	100
46	u	69/85 (81%)	69 (100%)	0	100	100
47	v	58/60 (97%)	58 (100%)	0	100	100
48	w	87/98 (89%)	87 (100%)	0	100	100
49	x	41/86 (48%)	40 (98%)	1 (2%)	49	69
50	y	48/49 (98%)	45 (94%)	3 (6%)	18	43
51	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5730/6433 (89%)	5677 (99%)	53 (1%)	79	87

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	a	178	LYS
32	g	30	THR
49	x	15	LYS
27	b	13	MET
31	f	114	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
28	c	68	GLN
36	k	67	ASN
28	c	76	GLN
29	d	58	HIS
38	m	117	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	2875/2907 (98%)	980 (34%)	39 (1%)
53	4	103/108 (95%)	44 (42%)	3 (2%)
54	5	1490/1520 (98%)	454 (30%)	12 (0%)
55	7	75/76 (98%)	29 (38%)	1 (1%)
55	8	75/76 (98%)	29 (38%)	1 (1%)
All	All	4618/4687 (98%)	1536 (33%)	56 (1%)

5 of 1536 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	12	A
52	3	13	C
52	3	14	U
52	3	15	A
52	3	17	G

5 of 56 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	2333	G
55	8	16	G
52	3	2764	U
55	7	16	G

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Mol	Chain	Res	Type
54	5	1037	A

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

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

5.5 Carbohydrates [i](#)

There are no 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.

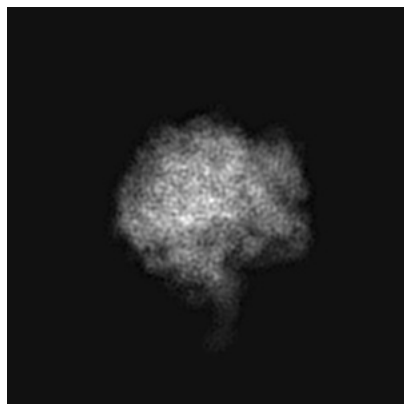
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13450. These allow visual inspection of the internal detail of the map and identification of artifacts.

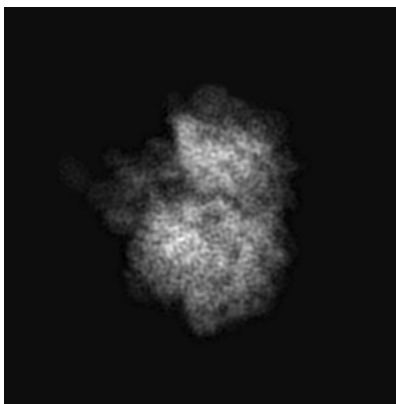
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

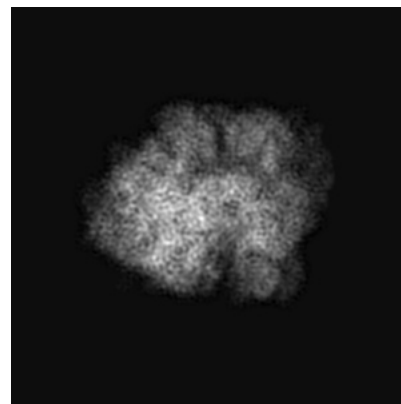
6.1.1 Primary map



X

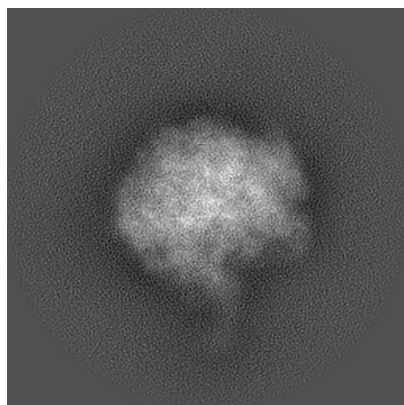


Y

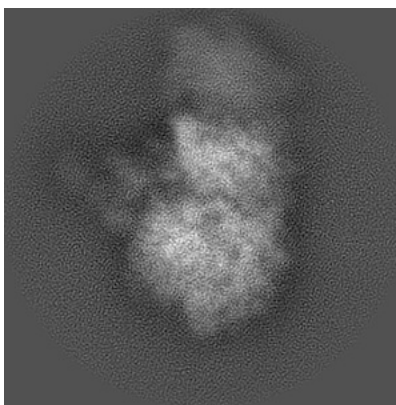


Z

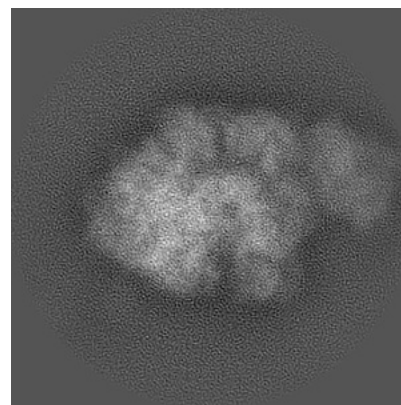
6.1.2 Raw map



X



Y

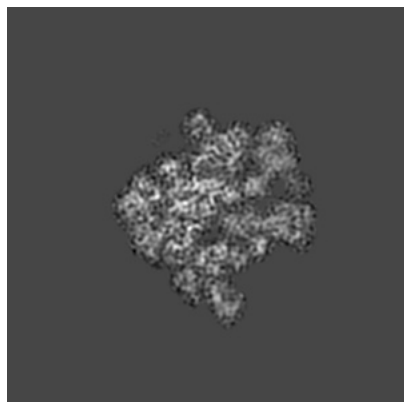


Z

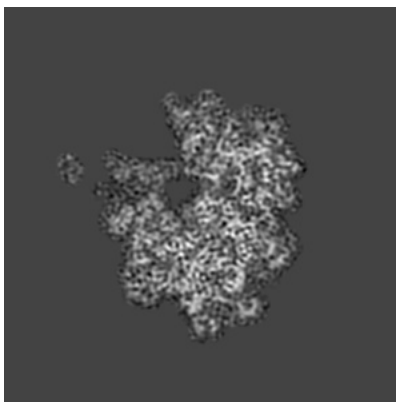
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

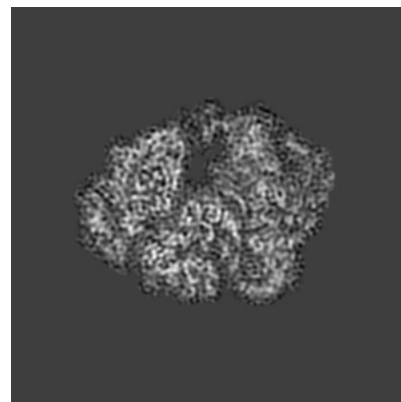
6.2.1 Primary map



X Index: 128

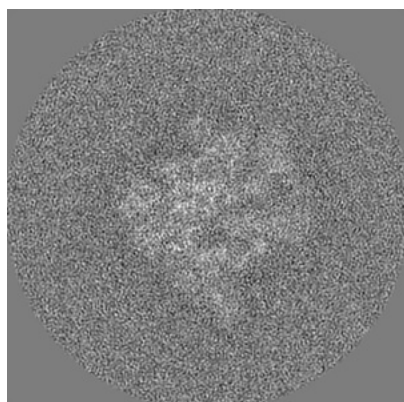


Y Index: 128

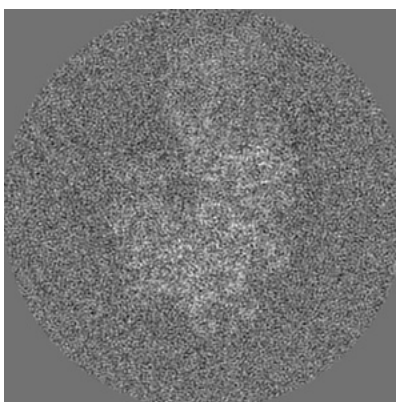


Z Index: 128

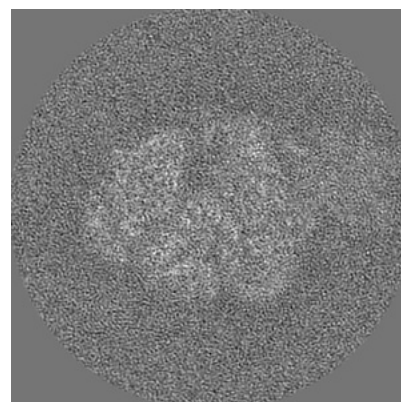
6.2.2 Raw map



X Index: 128



Y Index: 128

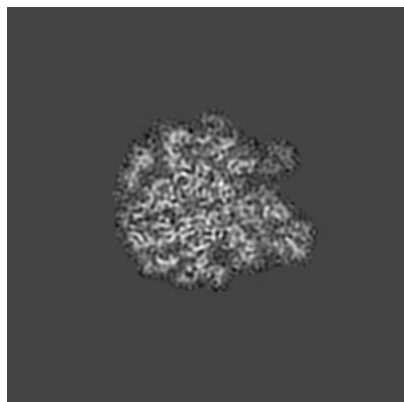


Z Index: 128

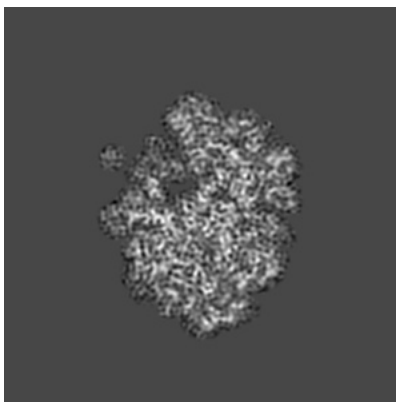
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

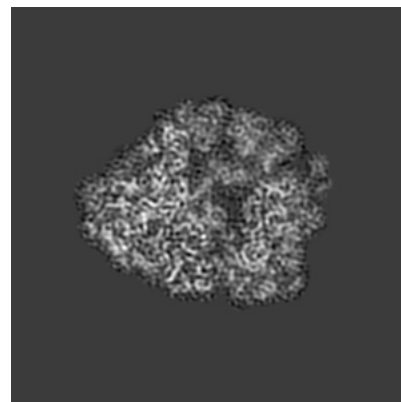
6.3.1 Primary map



X Index: 103

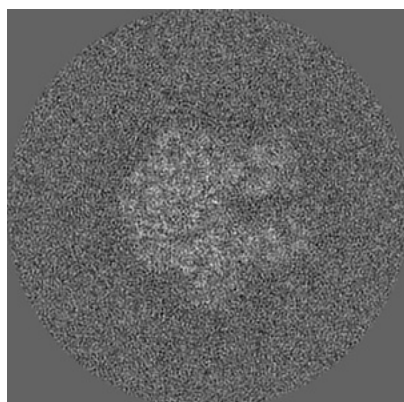


Y Index: 120

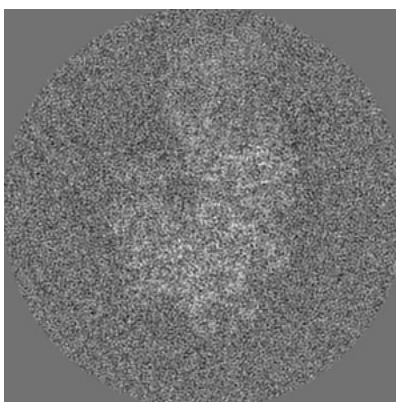


Z Index: 122

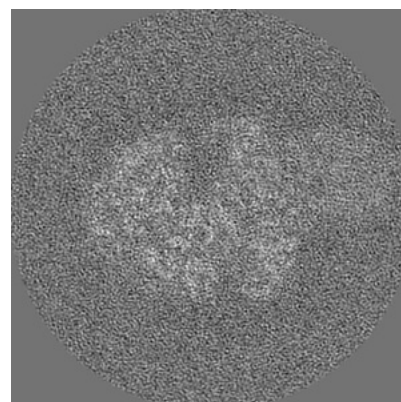
6.3.2 Raw map



X Index: 117



Y Index: 128

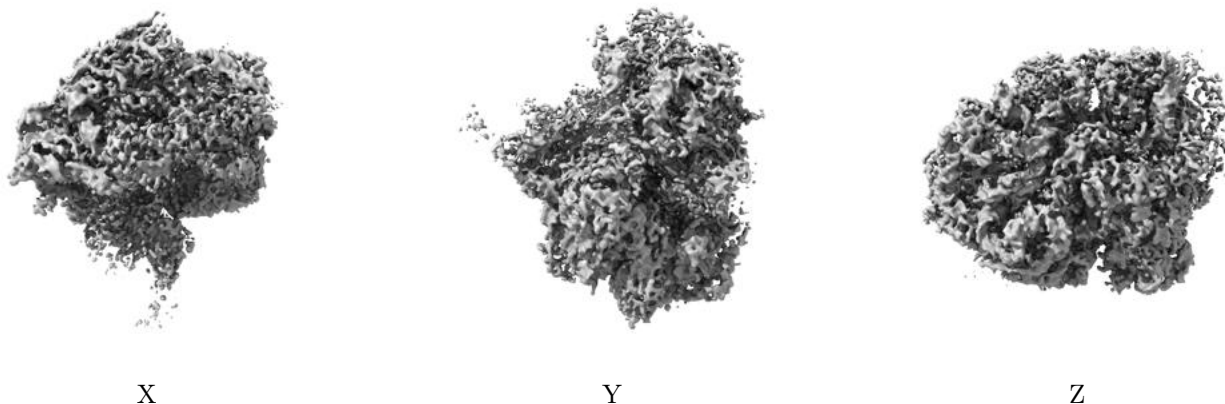


Z Index: 129

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

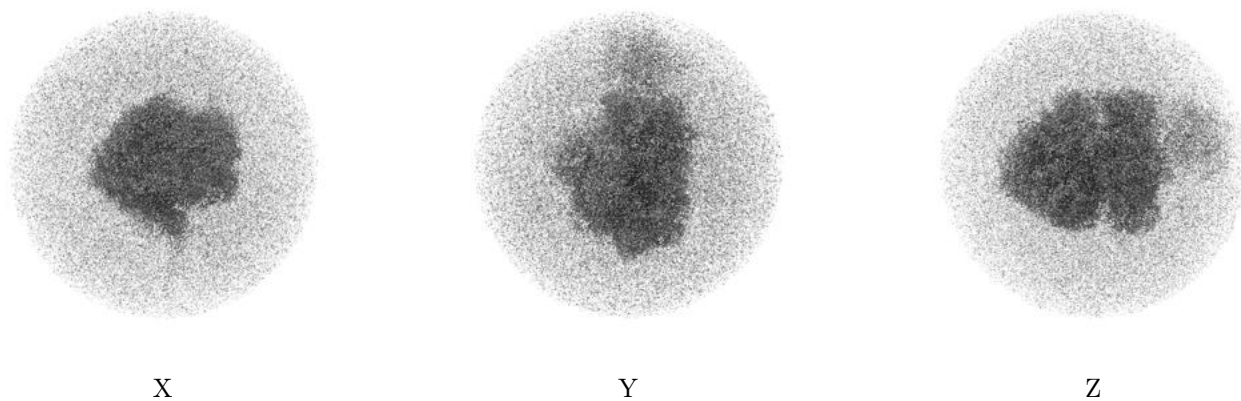
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.54. 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.

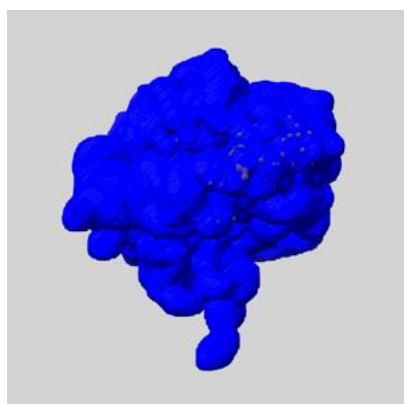
6.5 Mask visualisation [i](#)

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

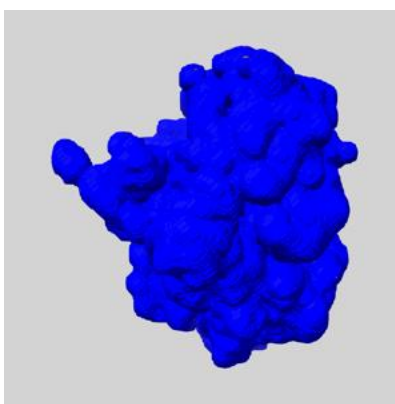
A mask typically either:

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

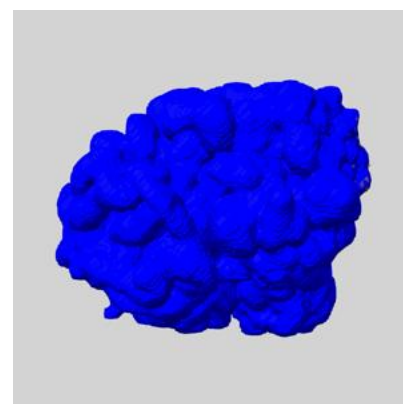
6.5.1 emd_13450_msk_1.map [i](#)



X



Y

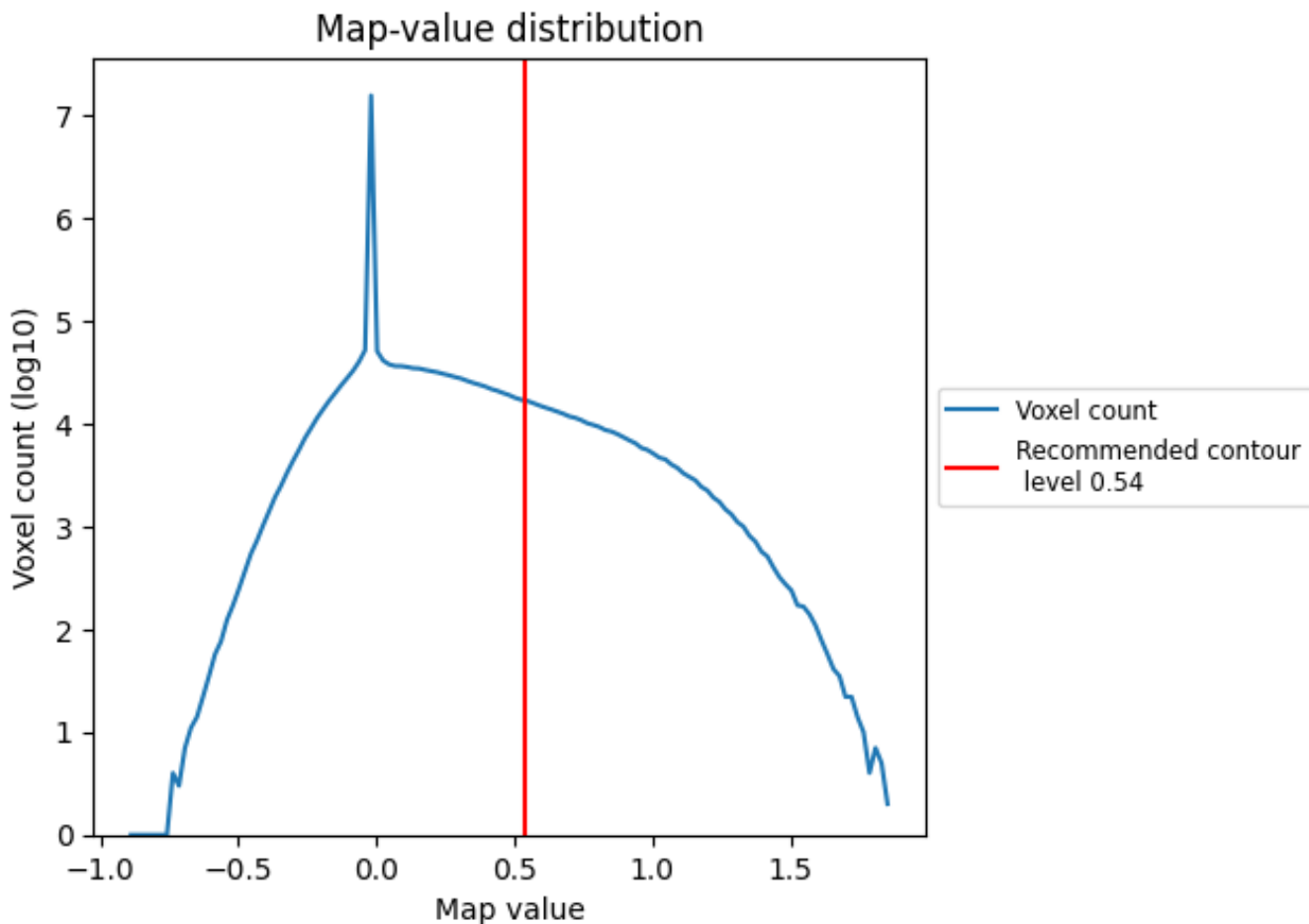


Z

7 Map analysis [i](#)

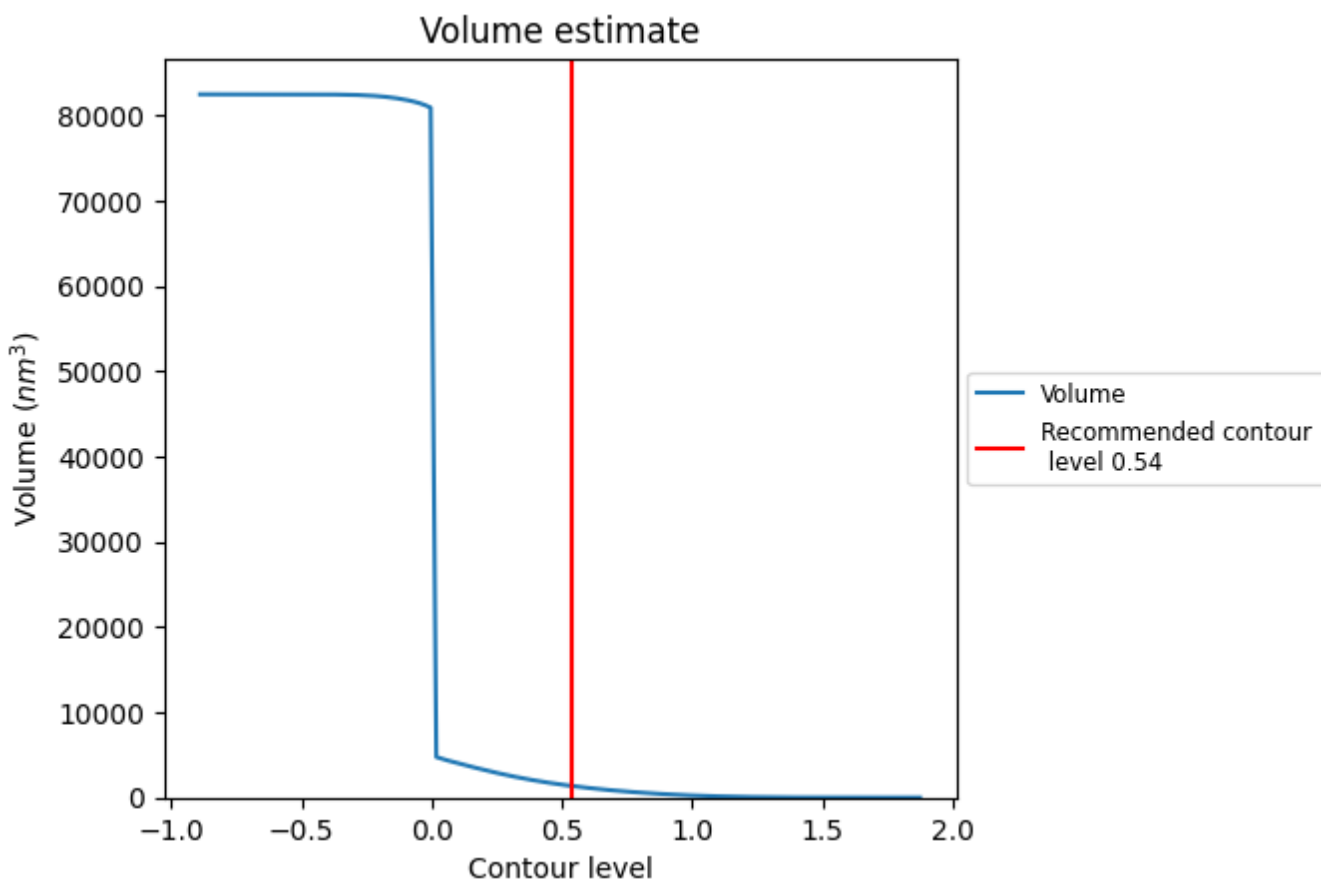
This section contains the results of statistical analysis of the map.

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.

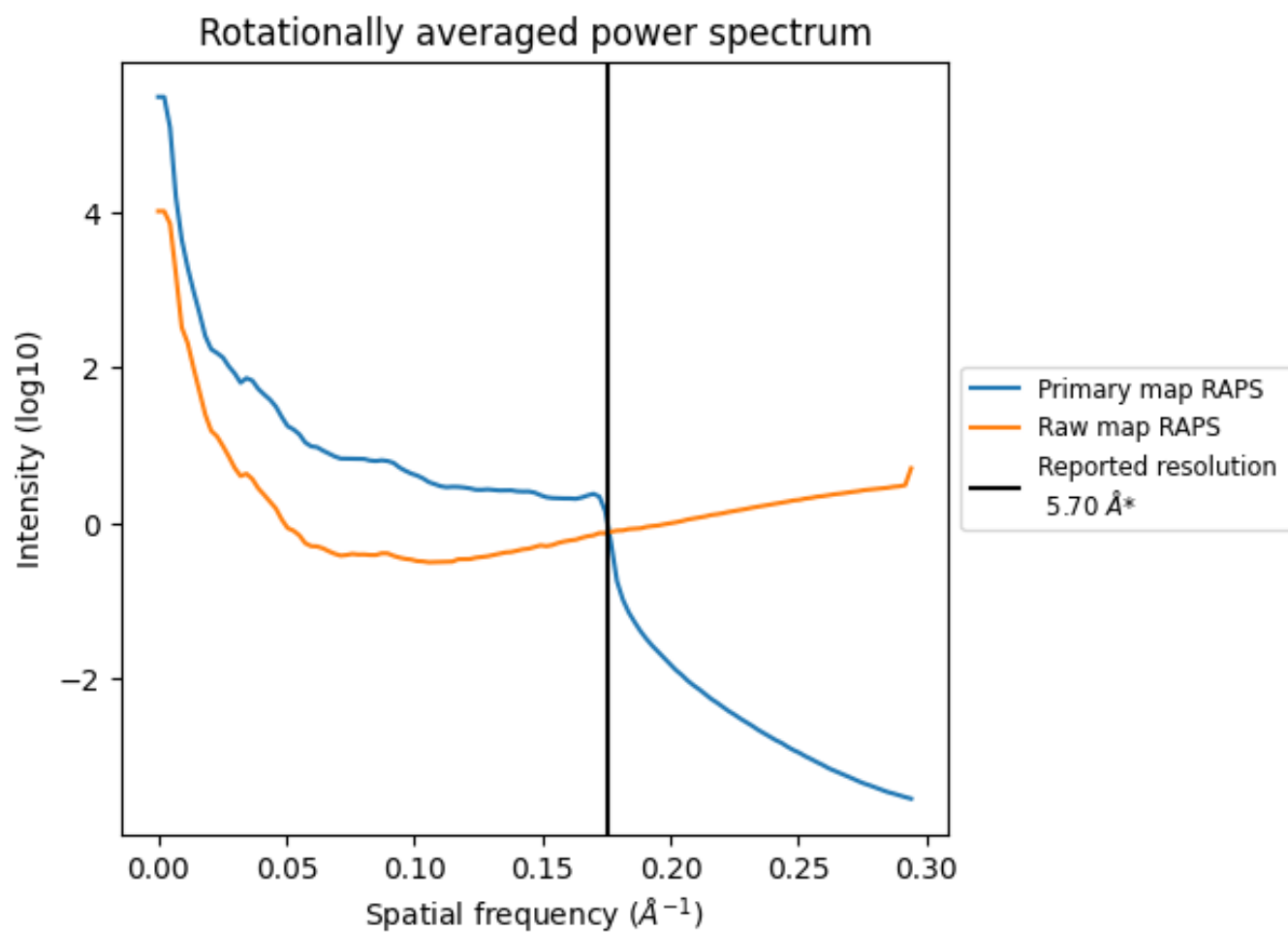
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1353 nm³; this corresponds to an approximate mass of 1222 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

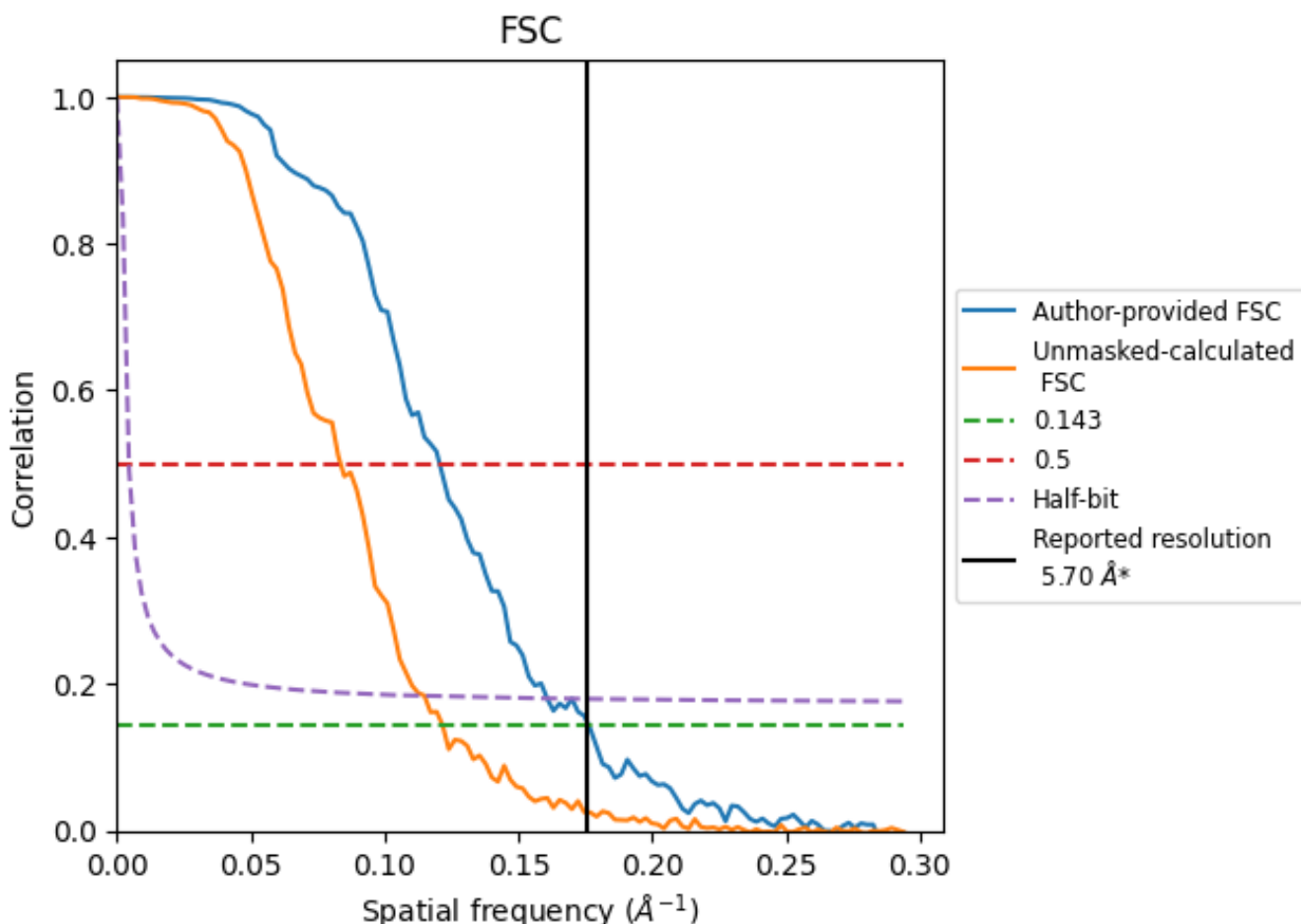


*Reported resolution corresponds to spatial frequency of 0.175 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.175 Å⁻¹

8.2 Resolution estimates [i](#)

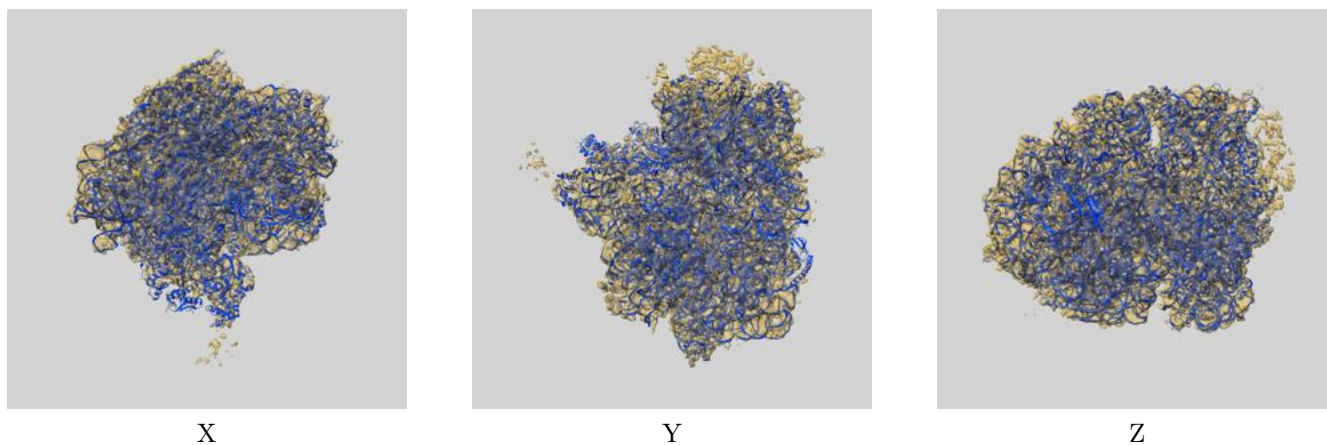
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.70	-	-
Author-provided FSC curve	5.67	8.29	6.22
Unmasked-calculated*	8.21	11.96	8.70

*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 8.21 differs from the reported value 5.7 by more than 10 %

9 Map-model fit [i](#)

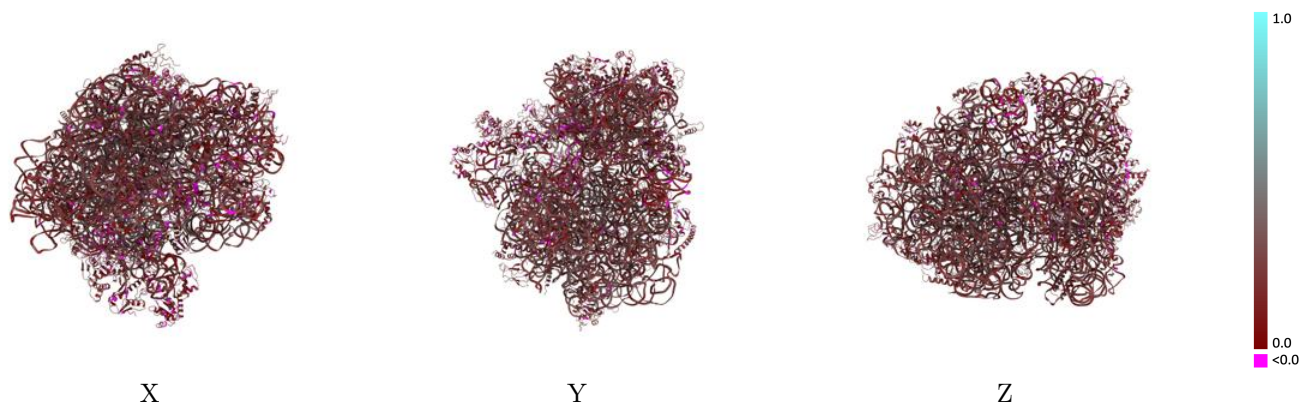
This section contains information regarding the fit between EMDB map EMD-13450 and PDB model 7PIT. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



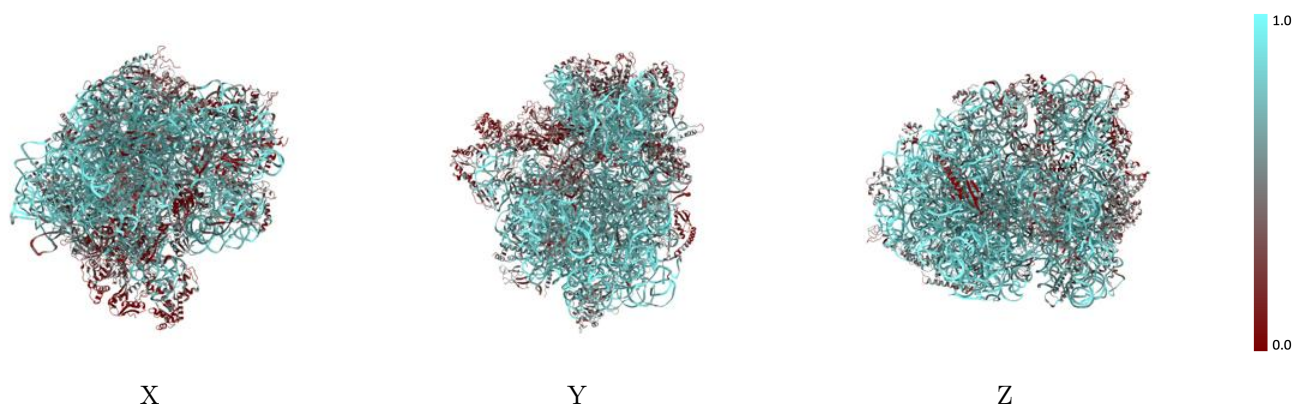
The images above show the 3D surface view of the map at the recommended contour level 0.54 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



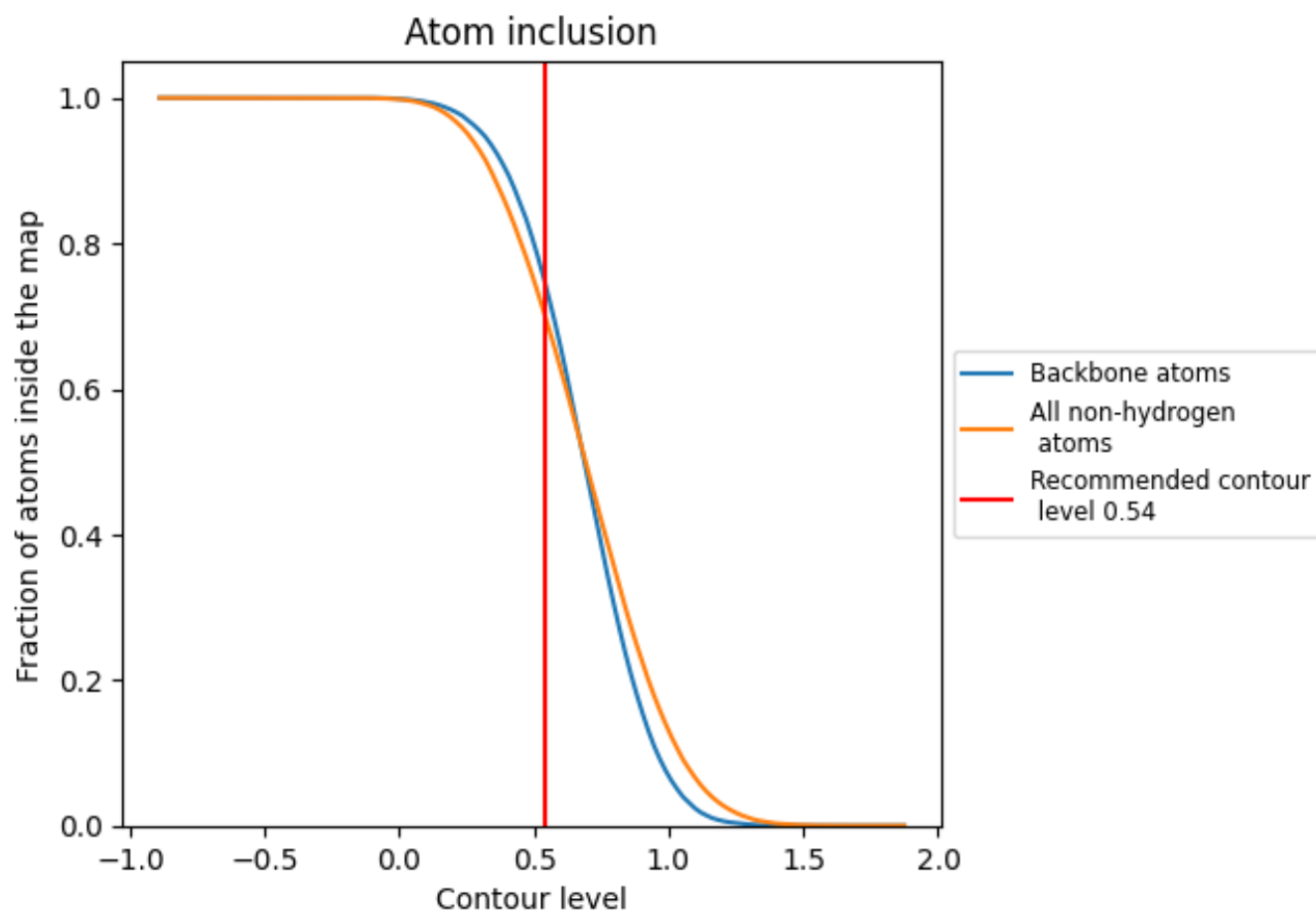
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.54).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 70% 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 (0.54) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7018	 0.2390
0	 0.5836	 0.2160
1	 0.5794	 0.2550
2	 0.6149	 0.2690
3	 0.8664	 0.2590
4	 0.8191	 0.2440
5	 0.8426	 0.2460
7	 0.3628	 0.0970
8	 0.7083	 0.1860
9	 0.1671	 0.1860
A	 0.3909	 0.2110
B	 0.4040	 0.2280
C	 0.3902	 0.2050
D	 0.4480	 0.2400
E	 0.4004	 0.2200
F	 0.3488	 0.2140
G	 0.4849	 0.2060
H	 0.4216	 0.2270
I	 0.3245	 0.2020
J	 0.5141	 0.2250
K	 0.5115	 0.2340
L	 0.3660	 0.2190
M	 0.4923	 0.2180
N	 0.5060	 0.2230
O	 0.5199	 0.2320
P	 0.4932	 0.2400
Q	 0.5155	 0.2480
R	 0.4000	 0.1700
S	 0.5344	 0.1980
T	 0.4978	 0.2310
W	 0.0455	 0.1760
a	 0.5927	 0.2410
b	 0.5340	 0.2320
c	 0.5197	 0.2460
d	 0.3910	 0.2060



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Chain	Atom inclusion	Q-score
e	 0.3801	 0.2150
f	 0.1523	 0.1850
g	 0.1853	 0.1540
h	 0.1755	 0.1750
i	 0.5521	 0.2300
j	 0.4663	 0.2410
k	 0.5455	 0.2570
l	 0.5403	 0.2300
m	 0.5983	 0.2290
n	 0.5040	 0.2230
o	 0.4599	 0.2310
p	 0.5399	 0.1950
q	 0.4881	 0.2340
r	 0.6063	 0.2290
s	 0.5444	 0.2580
t	 0.3810	 0.2260
u	 0.5234	 0.2250
v	 0.4990	 0.2050
w	 0.5256	 0.2260
x	 0.2945	 0.2420
y	 0.6175	 0.2560
z	 0.5063	 0.2420