



wwPDB EM Validation Summary Report ⓘ

Oct 28, 2024 – 02:46 am 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 : 7OOD, 4V7C, 7OOC, 4V7D

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:

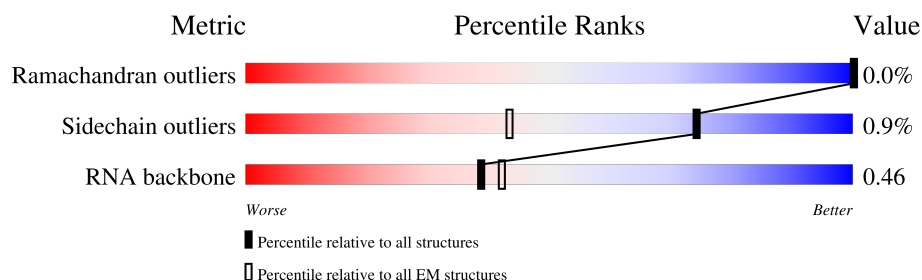
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 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 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	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 ≥ 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	
35	j	122	
36	k	151	
37	l	139	
38	m	124	
39	n	116	
40	o	119	
41	p	127	
42	q	100	
43	r	159	
44	s	237	
45	t	111	
46	u	104	
47	v	65	
48	w	111	
49	x	97	
50	y	57	
51	z	53	
52	3	2907	
53	4	108	
54	5	1520	
55	7	76	
55	8	76	

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
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 G.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	9	682	Total	C	N	O	S	0	0
			5326	3369	911	1021	25		

- 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 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
35	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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		

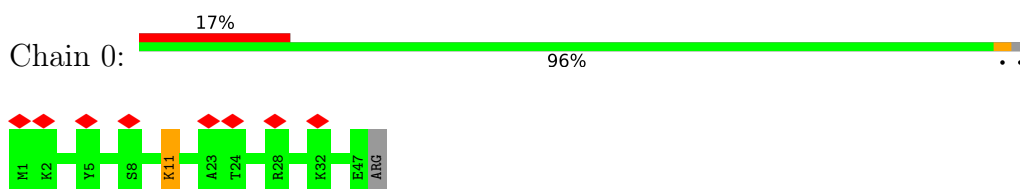
- Molecule 55 is a RNA chain called tRNA-Phe.

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		

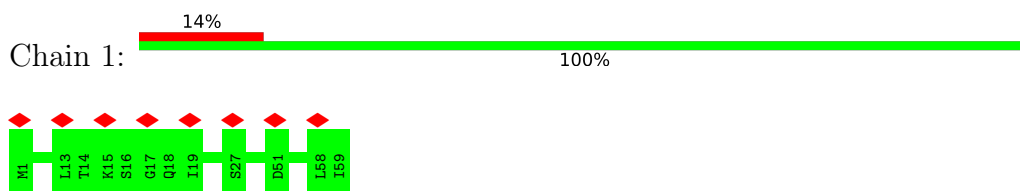
3 Residue-property plots [i](#)

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.

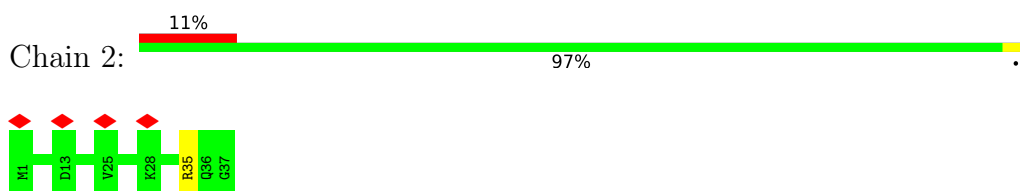
- Molecule 1: 50S ribosomal protein L34



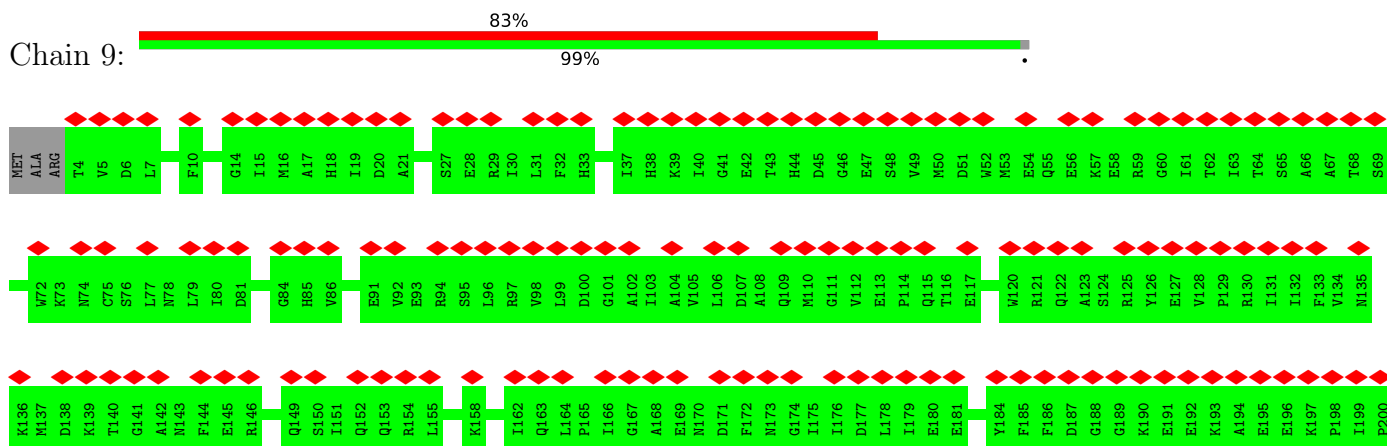
- Molecule 2: 50S ribosomal protein L35

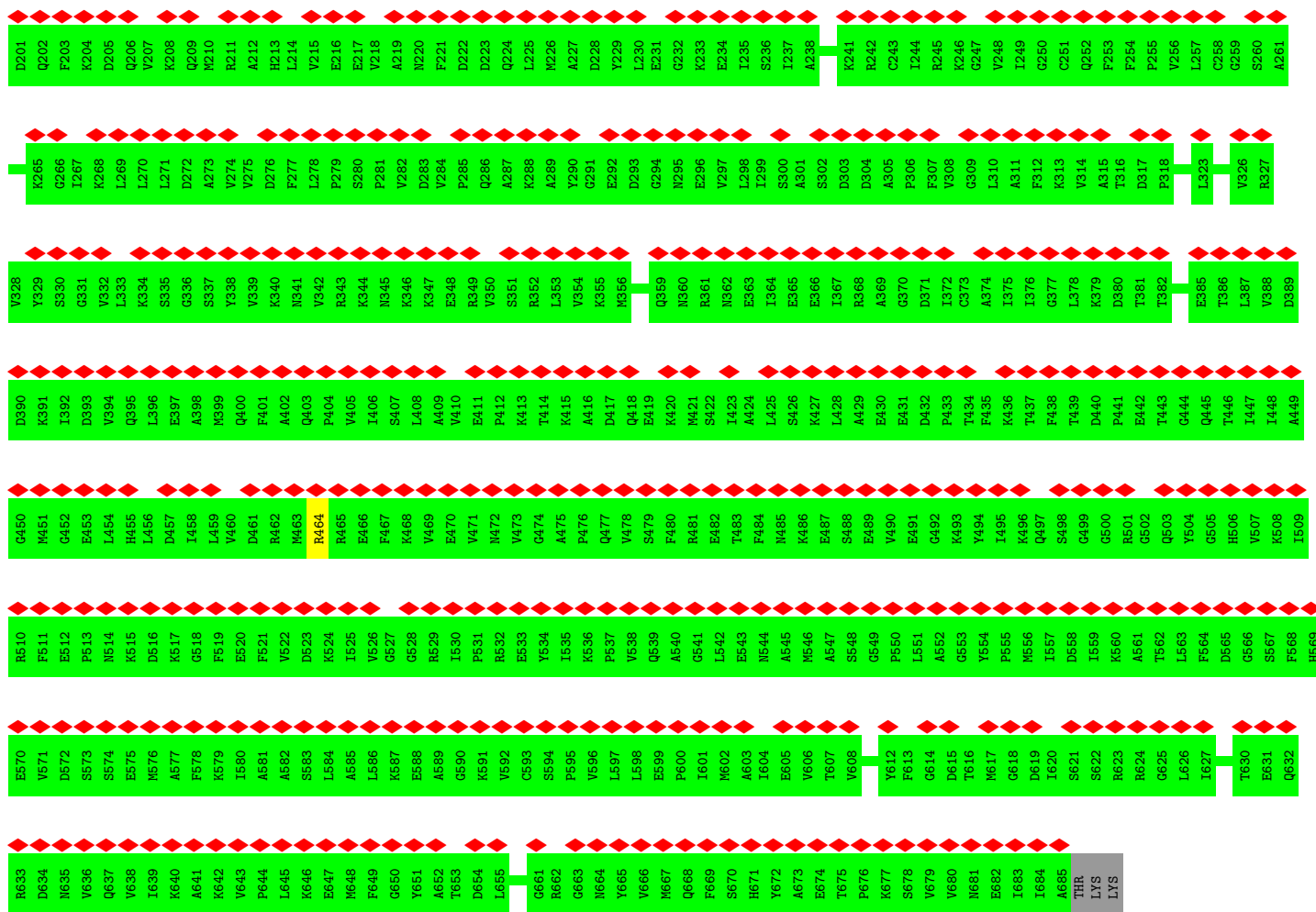


- Molecule 3: 50S ribosomal protein L36

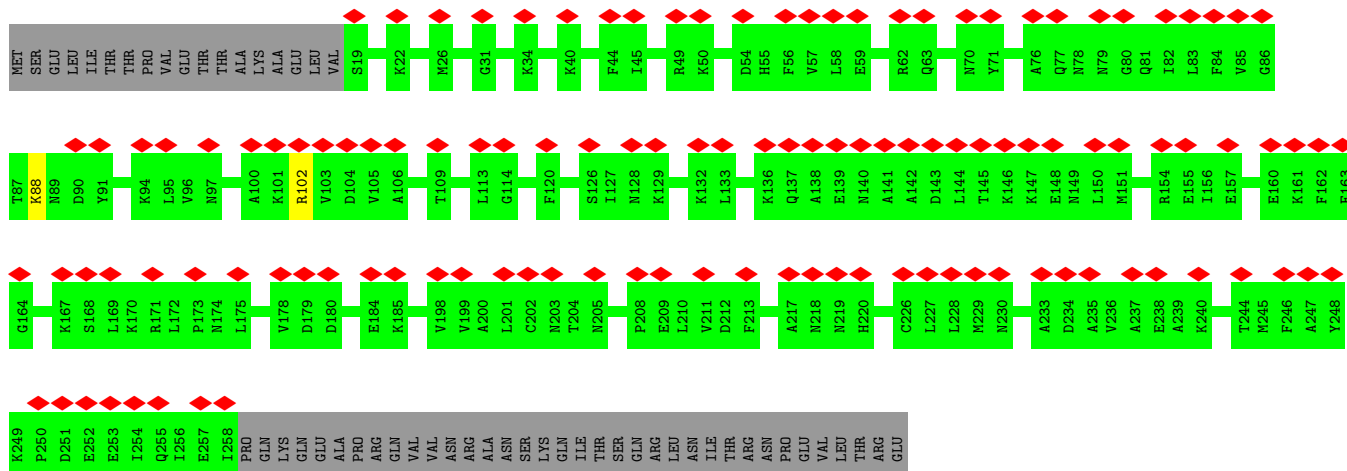
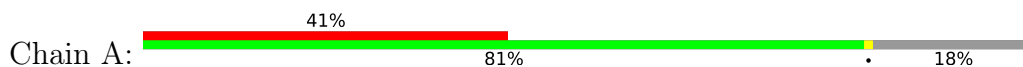


- Molecule 4: Elongation factor G

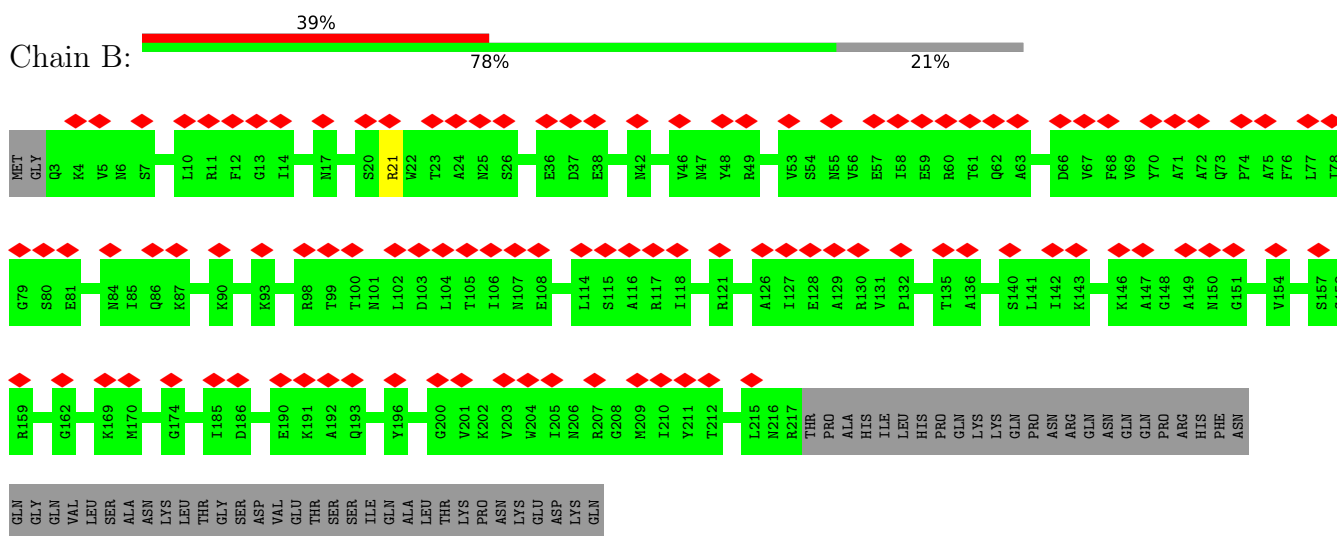




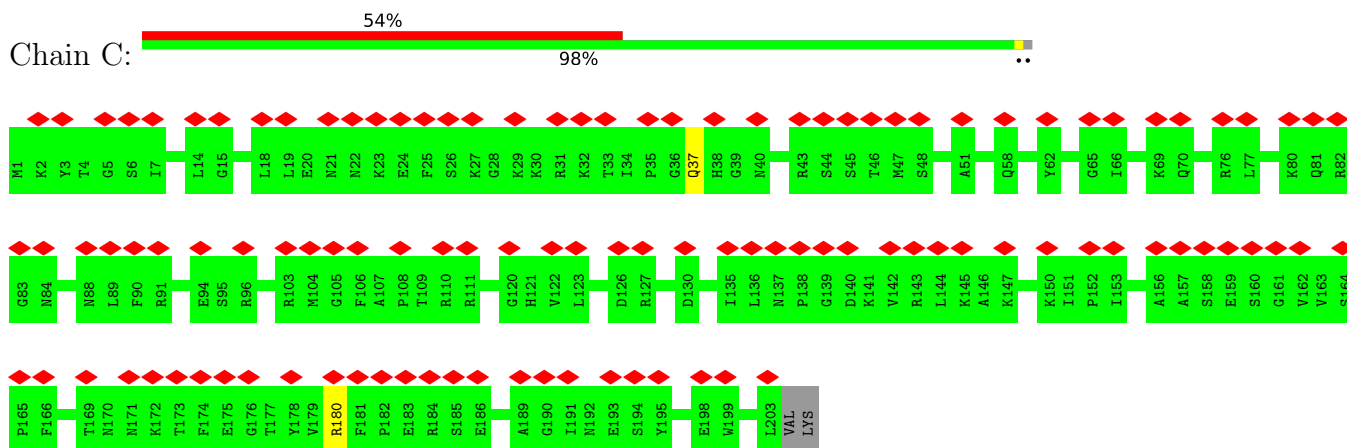
• Molecule 5: 30S ribosomal protein S2



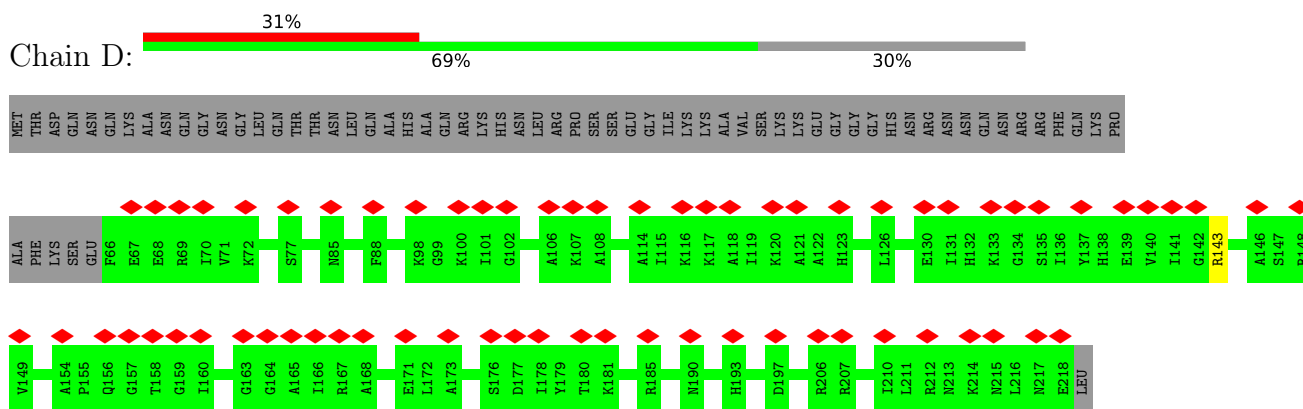
• Molecule 6: 30S ribosomal protein S3



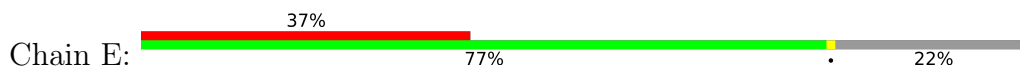
• Molecule 7: 30S ribosomal protein S4

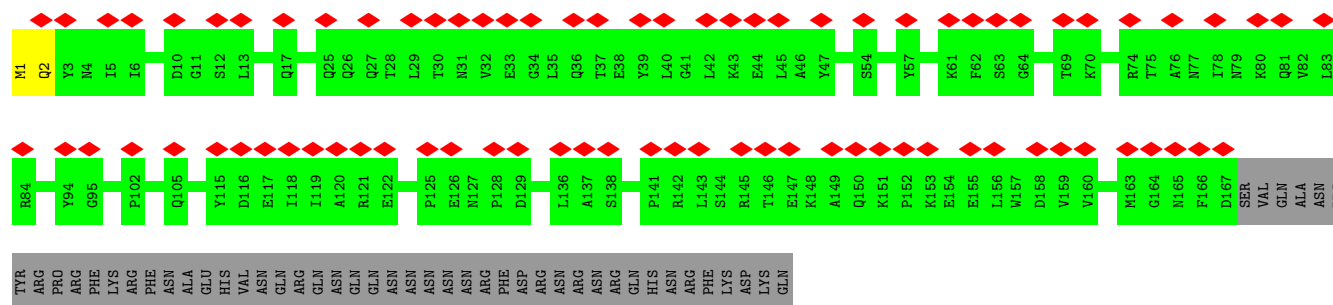


• Molecule 8: 30S ribosomal protein S5

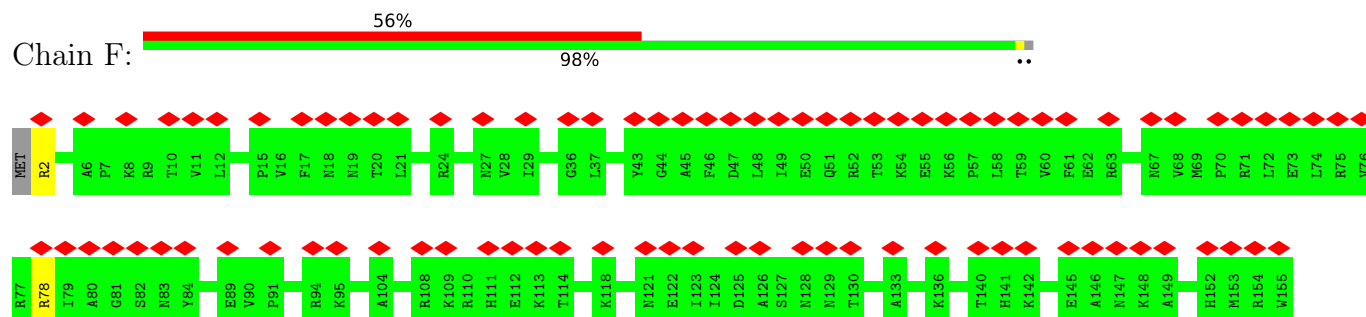


• Molecule 9: 30S ribosomal protein S6

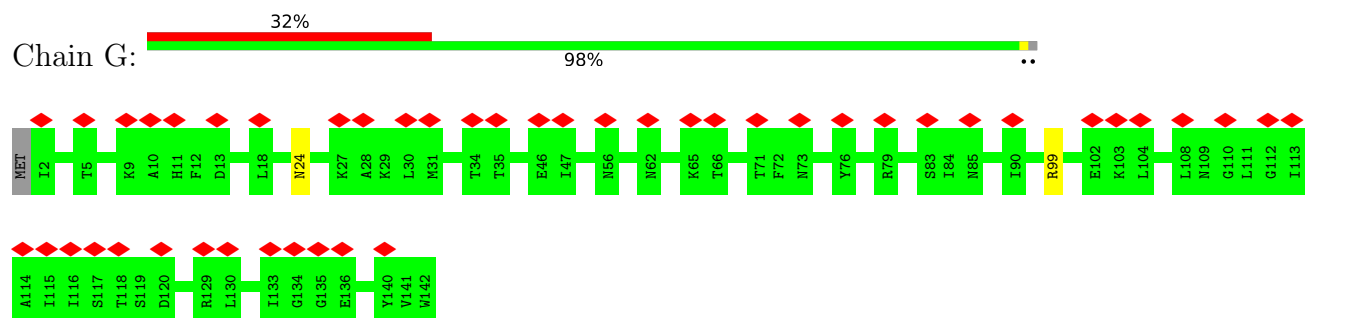




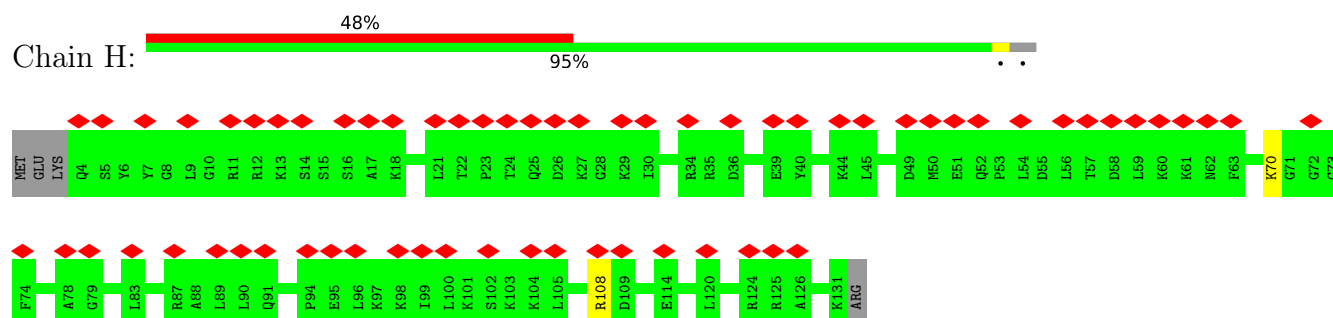
• Molecule 10: 30S ribosomal protein S7



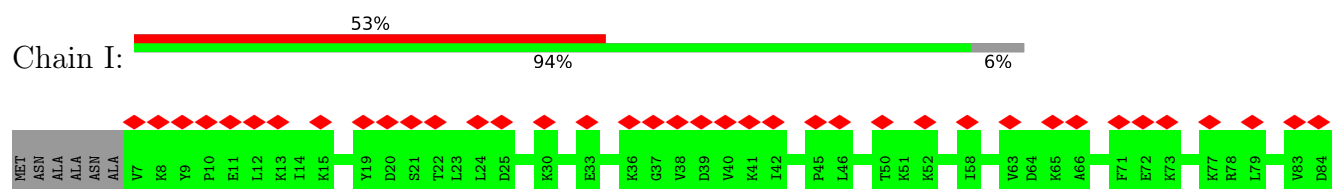
• Molecule 11: 30S ribosomal protein S8

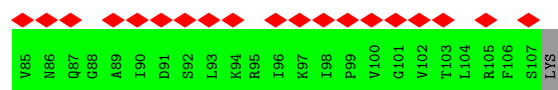


• Molecule 12: 30S ribosomal protein S9



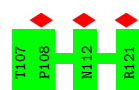
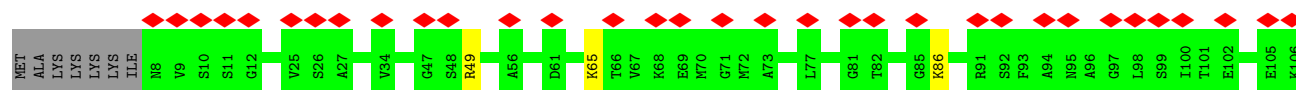
• Molecule 13: 30S ribosomal protein S10





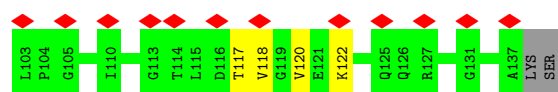
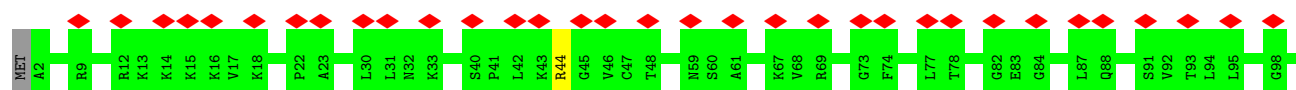
- Molecule 14: 30S ribosomal protein S11

Chain J: 30% 92% 6%



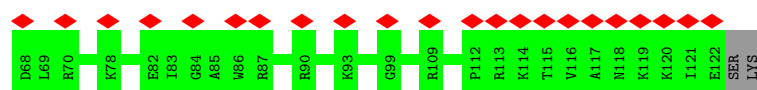
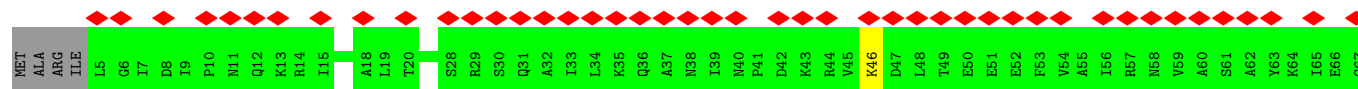
- Molecule 15: 30S ribosomal protein S12

Chain K: 32% 94% 0%



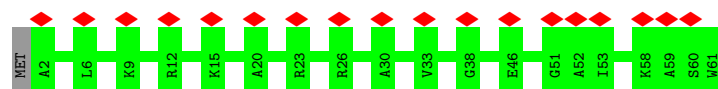
- Molecule 16: 30S ribosomal protein S13

Chain L: 54% 94% 5%



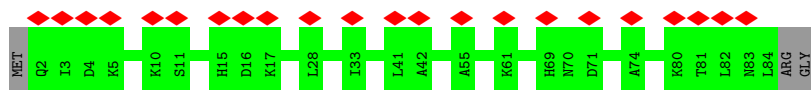
- Molecule 17: 30S ribosomal protein S14 type Z

Chain M: 30% 98% 0%

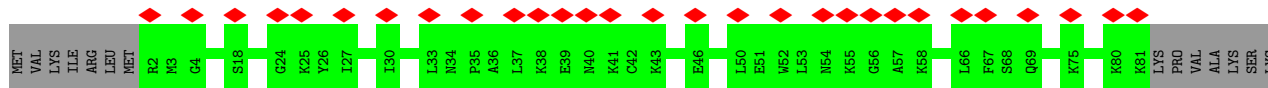
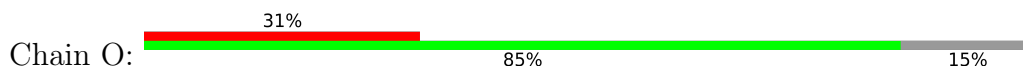


- Molecule 18: 30S ribosomal protein S15

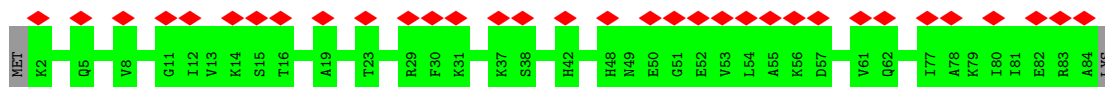
Chain N: 26% 97% 0%



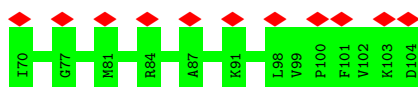
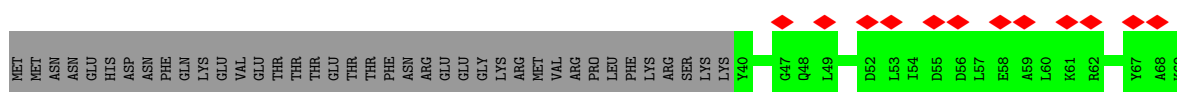
- Molecule 19: 30S ribosomal protein S16



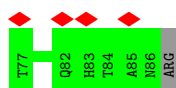
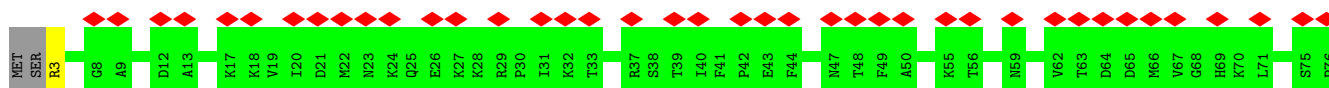
- Molecule 20: 30S ribosomal protein S17



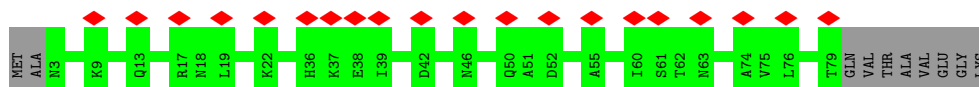
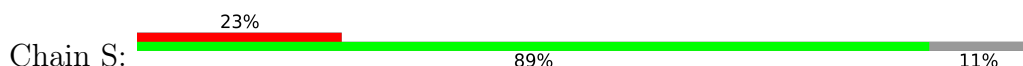
- Molecule 21: 30S ribosomal protein S18



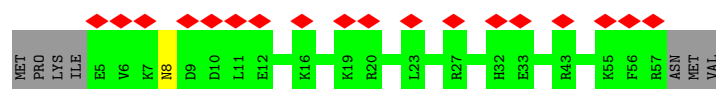
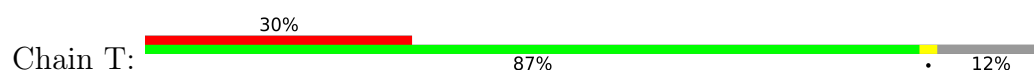
- Molecule 22: 30S ribosomal protein S19



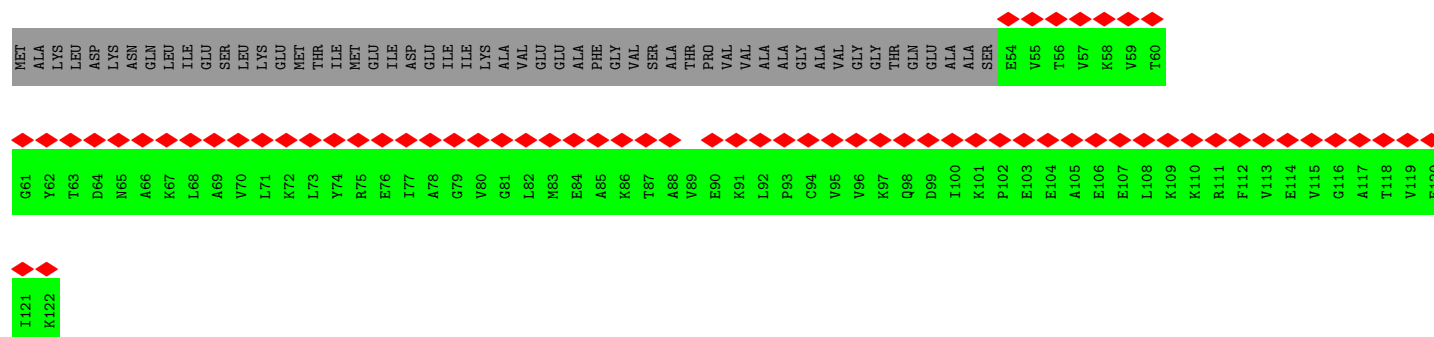
- Molecule 23: 30S ribosomal protein S20



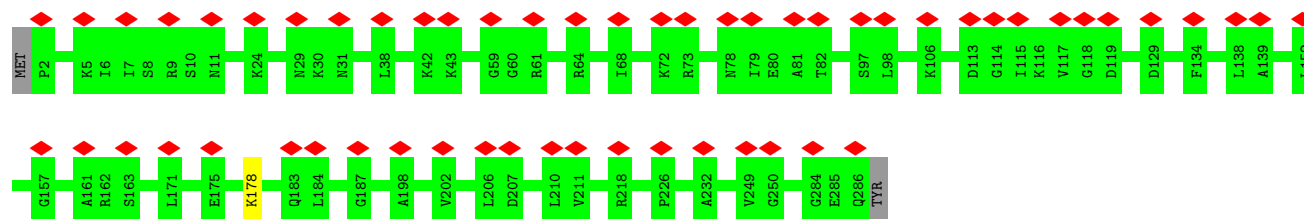
- Molecule 24: 30S ribosomal protein S21



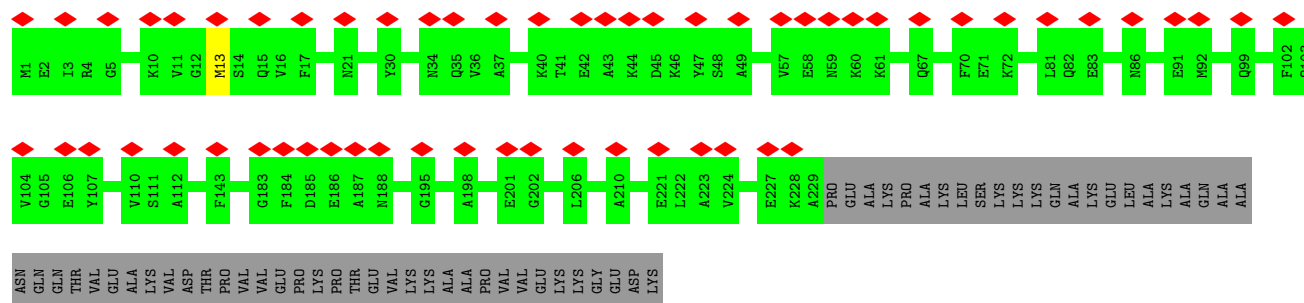
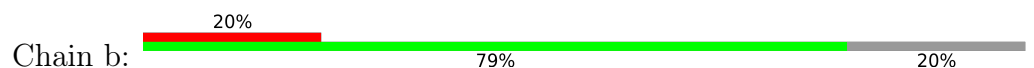
- Molecule 25: 50S ribosomal protein L7/L12



- Molecule 26: 50S ribosomal protein L2



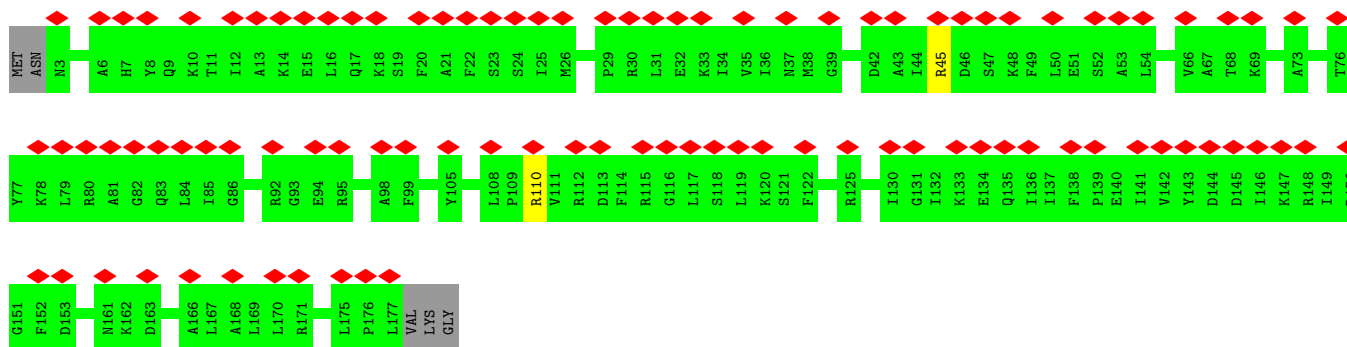
- Molecule 27: 50S ribosomal protein L3



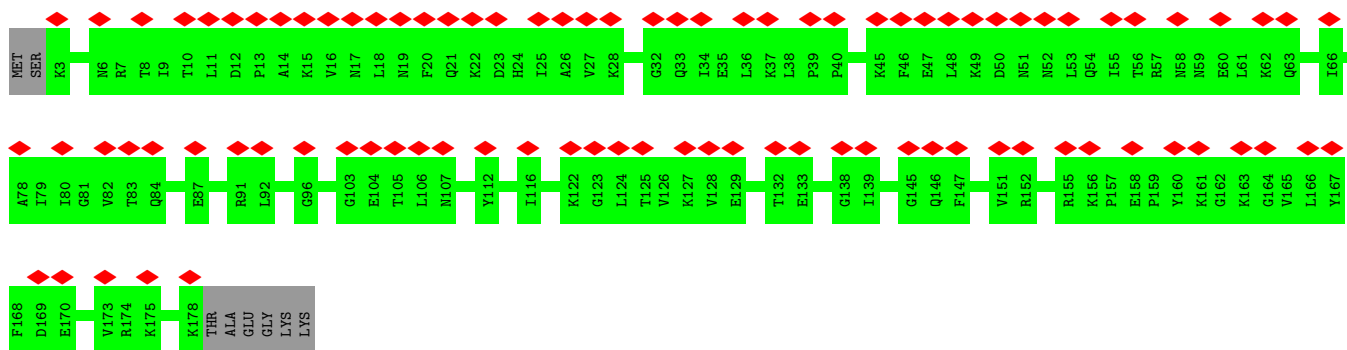
- Molecule 28: 50S ribosomal protein L4



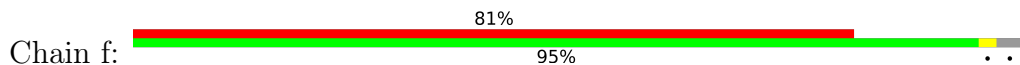
- Molecule 29: 50S ribosomal protein L5

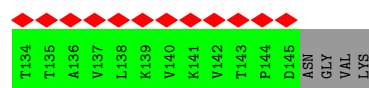


- Molecule 30: 50S ribosomal protein L6

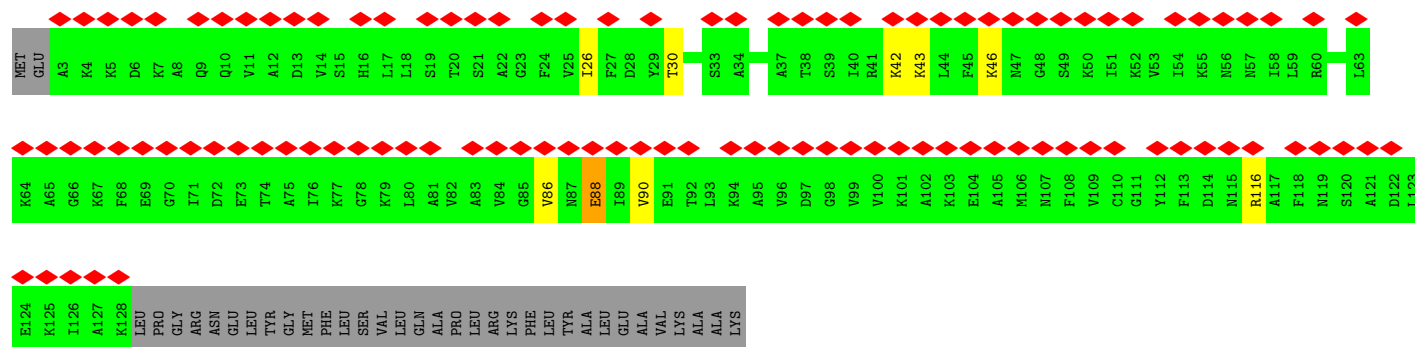
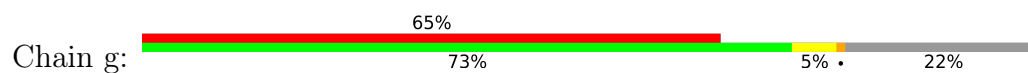


- Molecule 31: 50S ribosomal protein L9

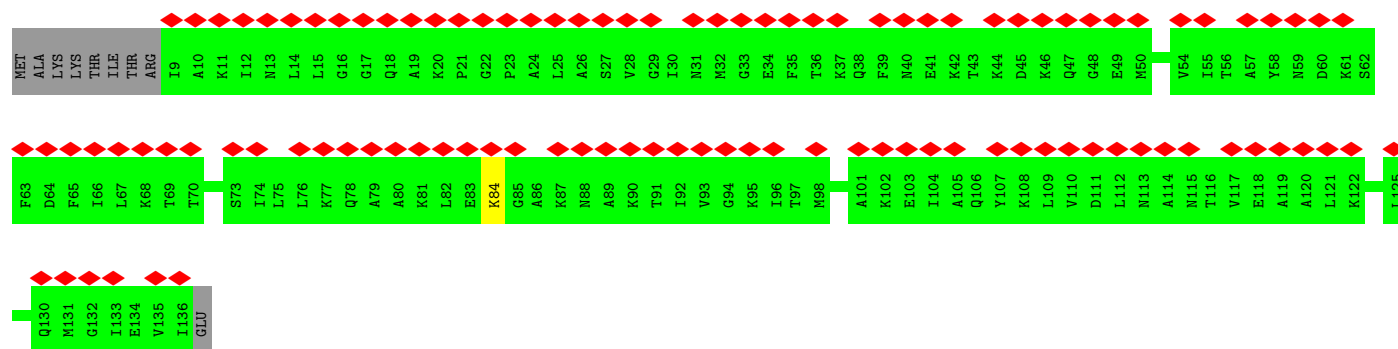
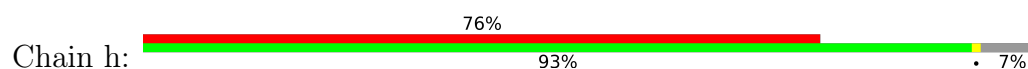




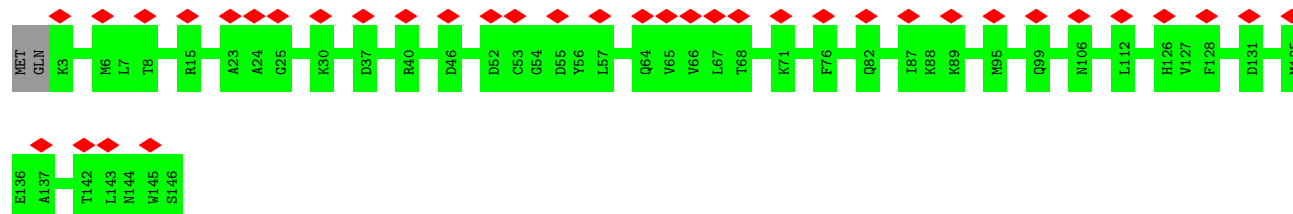
• Molecule 32: 50S ribosomal protein L10



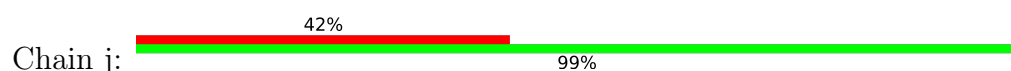
• Molecule 33: 50S ribosomal protein L11

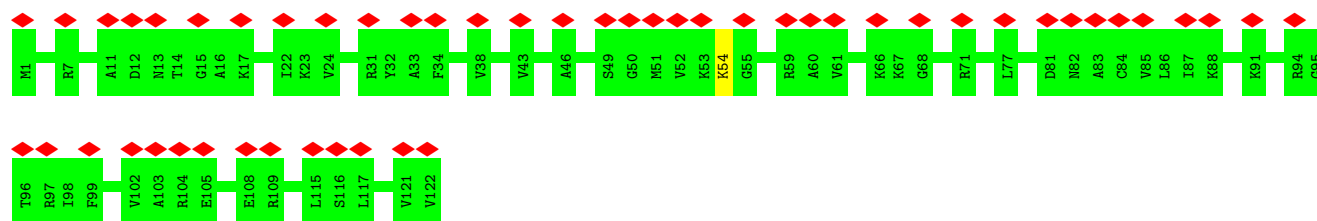


• Molecule 34: 50S ribosomal protein L13

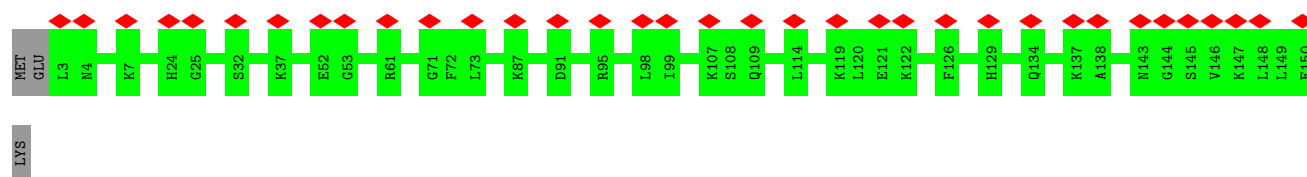


• Molecule 35: 50S ribosomal protein L14

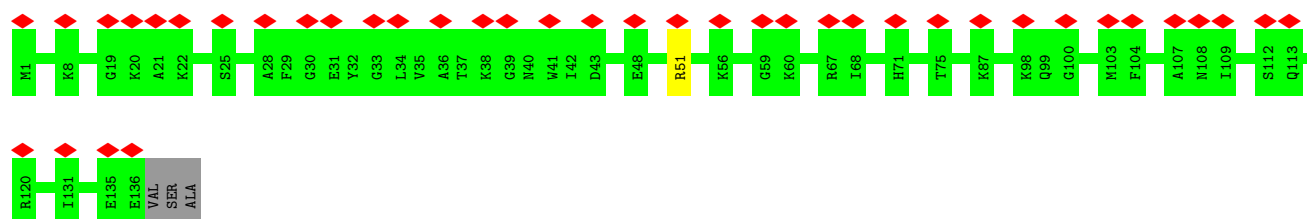




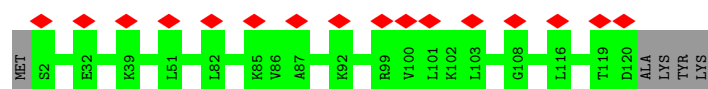
- Molecule 36: 50S ribosomal protein L15



- Molecule 37: 50S ribosomal protein L16



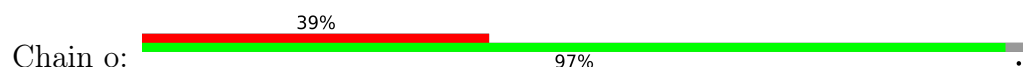
- Molecule 38: 50S ribosomal protein L17

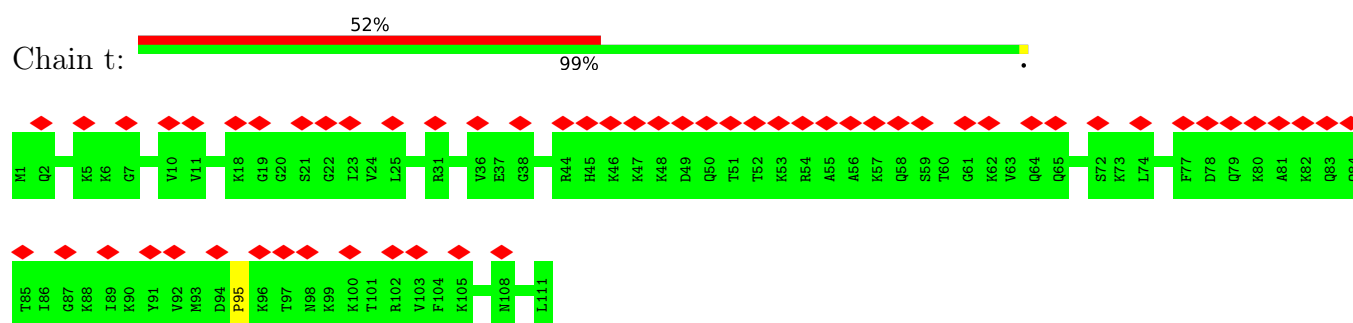


- Molecule 39: 50S ribosomal protein L18

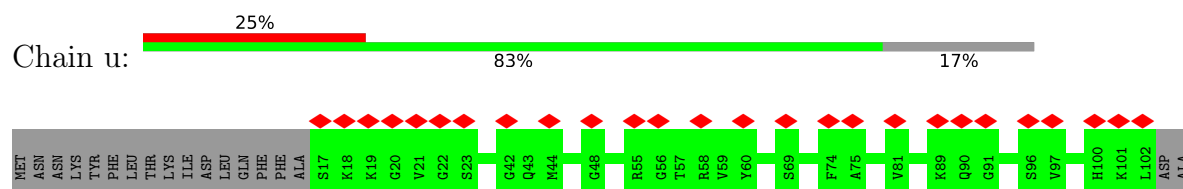


- Molecule 40: 50S ribosomal protein L19

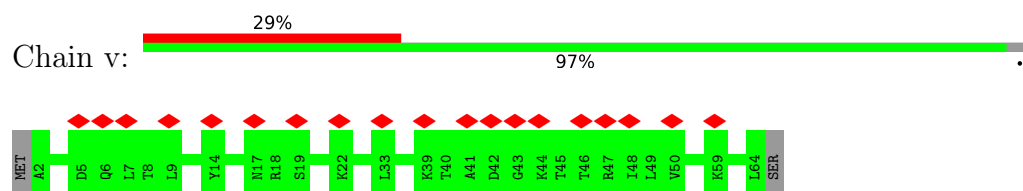




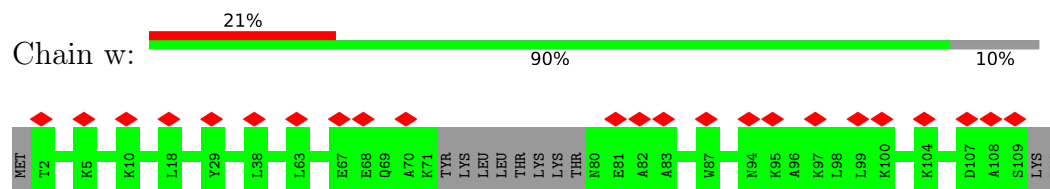
- Molecule 46: 50S ribosomal protein L27



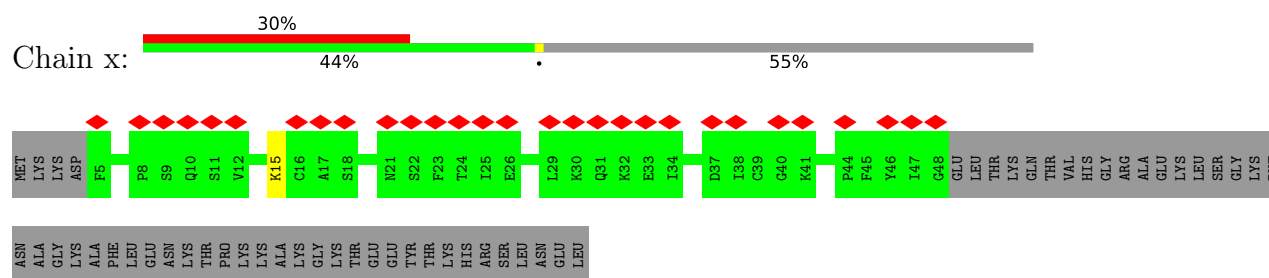
- Molecule 47: 50S ribosomal protein L28



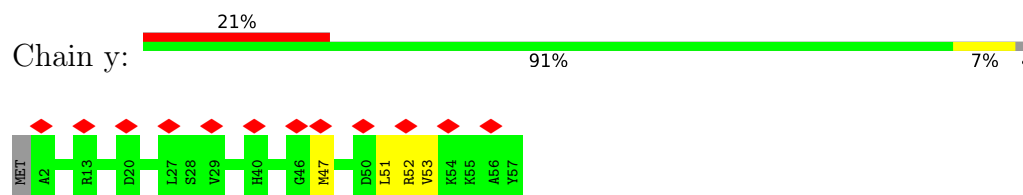
- Molecule 48: 50S ribosomal protein L29



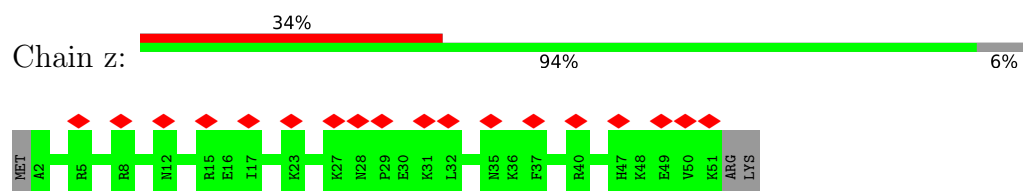
- Molecule 49: 50S ribosomal protein L31



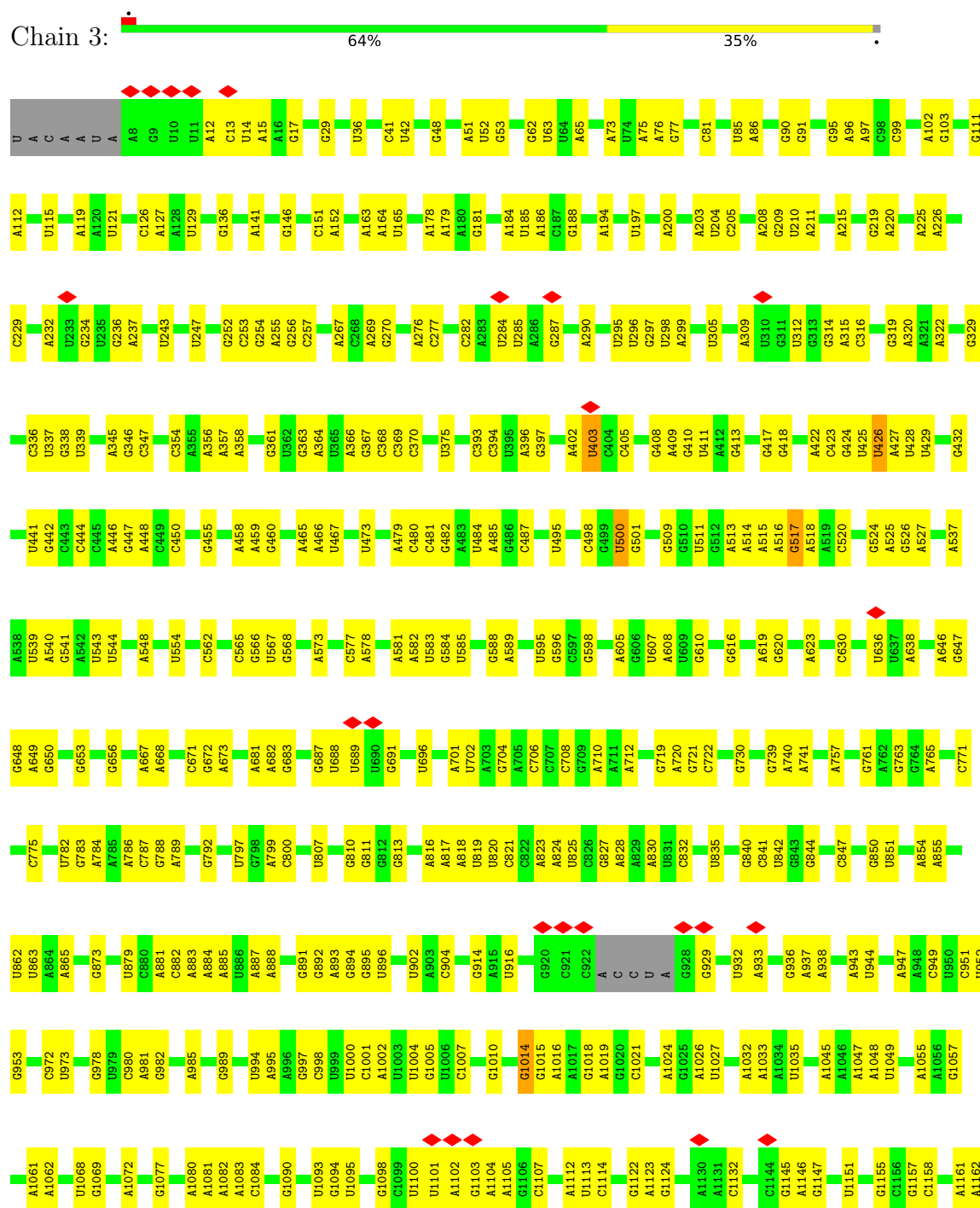
- Molecule 50: 50S ribosomal protein L32



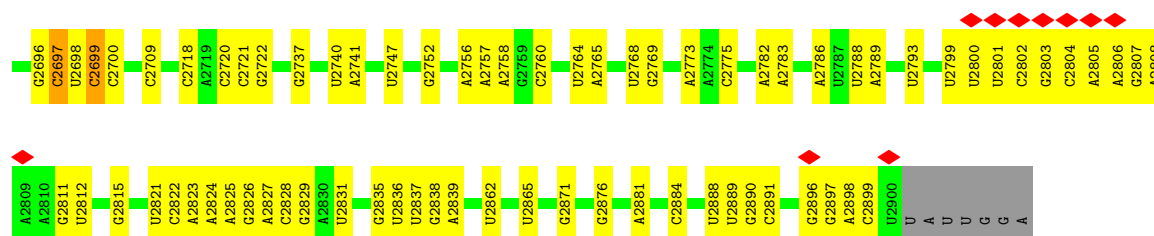
- Molecule 51: 50S ribosomal protein L33 1



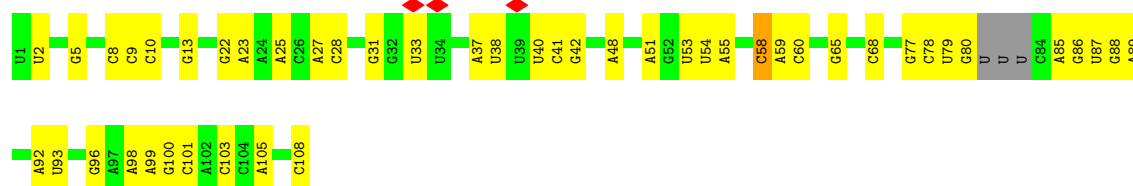
- Molecule 52: 23S ribosomal RNA



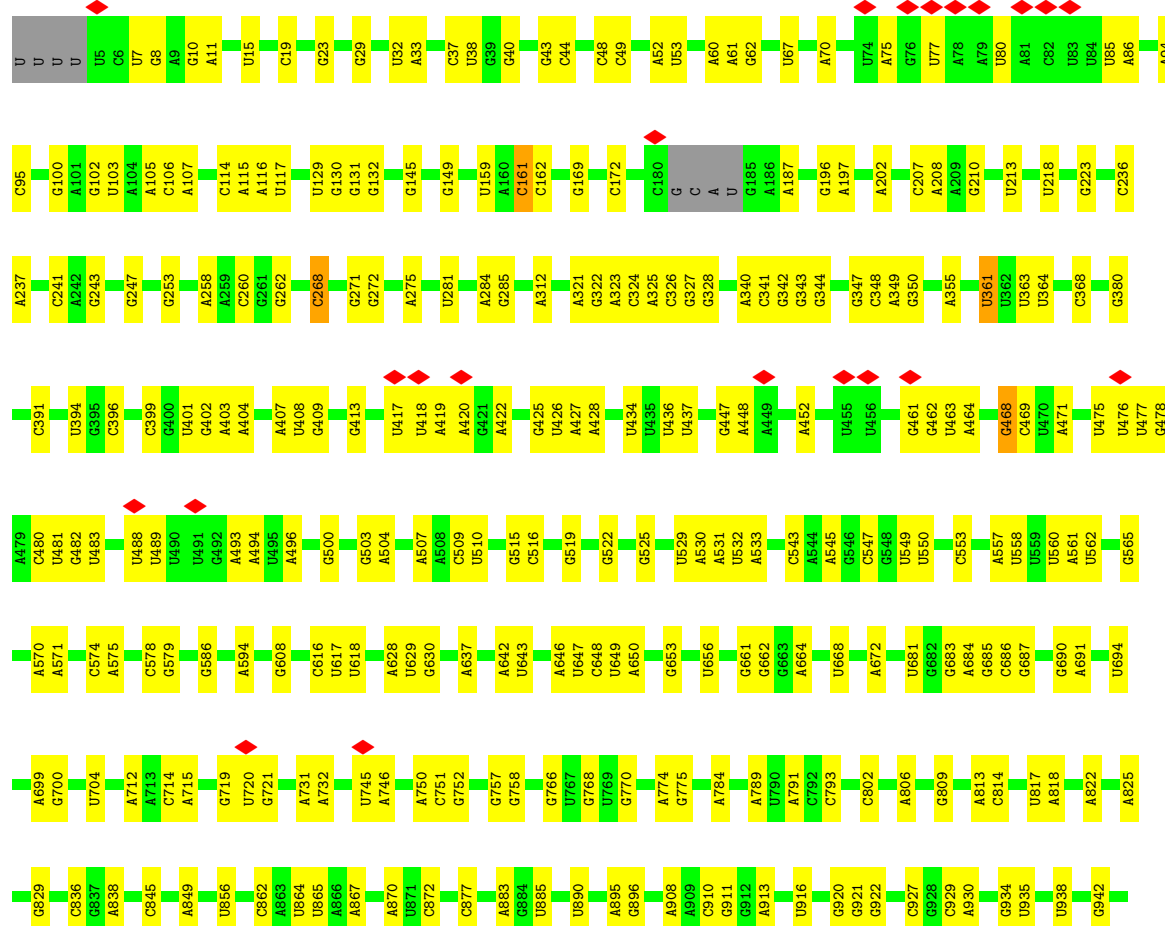
G2561	G2464	G2345	G2229	G2144	G2058	A1944	C1812	U1693	U1584	C1359	G1252	G1163
A2572	U2468	U2351	A2230	U2148	G2059	A1945	C1813	A1694	A1585	U1360	G1253	A1164
A2573	G2231	G2355	G2232	G2151	C2062	A1951	U1814	G1695	U1586	U1361	G1257	U1165
A2574	G2233	G2355	G2234	G2152	C2063	A1959	U1815	A1698	U1587	U1369	U1260	U1166
A2580	A2235	U2358	G2235	G2153	G2064	U1962	U1816	G1700	A1589	U1370	U1266	U1167
C2581	G2236	A2360	A2066	U2154	A2065	U1962	U1817	G1701	G1507	G1371	G1267	U1168
G2586	G2242	G2361	G2067	G2155	A2066	C1969	U1818	A1702	U1508	U1374	U1268	U1169
G2586	G2243	A2362	G2068	G2156	G2070	C1970	U1819	A1703	U1509	G1375	G1277	C1170
G2590	G2245	G2365	G2069	U2158	C2071	G1971	U1820	C1704	U1510	U1376	U1274	C1171
G2604	G2247	U2385	G2075	U2159	U1974	U1973	U1821	G1705	A1513	U1377	A1274	U1176
G2605	U2251	U2380	G2076	U2160	U1977	U1978	U1822	U1706	U1514	U1381	A1275	U1177
G2607	U2252	U2387	U2083	A2165	A1978	U1978	U1823	A1715	U1515	U1382	A1276	A1178
G2611	U2253	G2388	A2084	U2166	G1979	G1979	U1824	A1716	A1516	U1383	A1277	G1179
G2612	G2254	U2389	C2085	G2169	C1987	U1987	U1825	U1717	G1517	C1390	A1278	A1186
U2617	A2275	U2392	A2089	G2173	U1988	U1988	U1826	A1718	A1518	A1393	A1281	A1190
C2618	A2276	G2393	G2100	G2174	G1999	G1999	U1827	A1719	A1519	U1404	A1282	A1191
C2619	G2276	U2399	A2101	U2175	U2000	U2000	G1832	U1721	U1522	G1405	A1283	A1192
C2620	A2277	U2399	G2106	G2176	C2003	C2004	A1836	G1729	G1528	U1406	G1286	U1193
U2621	A2278	U2399	G2107	G2177	G2004	G2004	C1837	C1730	C1531	U1407	G1287	G1197
G2631	U2280	U2399	G2108	U2178	U2009	U2010	G1842	U1737	U1532	G1408	G1288	A1201
C2634	U2291	U2399	A2109	C2182	U2110	U2110	A1845	U1743	U1533	A1410	U1293	A1202
A2637	A2294	U2414	U2111	A2184	U2111	U2111	U1889	G1747	U1534	U1422	A1299	U1207
G2638	A2295	U2414	U2112	G2187	U2112	U2112	U1890	U1748	A1540	A1423	G1301	A1208
G2642	C2305	C2424	U2113	U2188	U2113	U2113	A1891	G1753	A1541	U1424	G1302	U1209
A2643	G2312	C2430	U2114	U2189	U2114	U2114	A1892	U1764	A1542	U1425	U1303	A1210
U2644	U2313	U2431	U2115	U2190	U2115	U2115	U1904	G1765	A1543	G1426	U1304	U1213
A2647	G2316	A2434	U2116	U2191	U2116	U2116	U1905	A1766	A1544	C1427	A1308	U1214
G2649	A2319	G2435	U2117	U2192	U2117	U2117	G1906	A1769	U1548	A1431	A1312	G1215
U2654	G2320	G2436	U2118	U2193	U2118	U2118	A1903	U1770	U1549	C1444	G1313	U1216
A2662	G2321	G2437	U2119	G2194	U2119	U2119	G1904	C1771	G1557	U1445	U1217	G1217
G2664	G2322	U2439	U2200	U2195	U2120	U2120	U1906	G1772	A1558	U1448	G1319	U1218
U2668	U2327	G2444	U2201	U2196	U2121	U2121	A1907	U1779	A1559	G1449	C1320	U1219
G2668	A2328	C2445	U2202	U2197	U2122	U2122	G1913	A1780	U	C1456	C1321	G1221
G2669	G2329	U2446	U2203	U2198	A2123	A2123	A1919	U1784	G	U	A1322	G1226
G2681	A2330	A2447	U2204	U2199	A2124	A2124	A1920	U1785	A	G	A1328	G1227
A2685	G2333	G2448	G2210	U2205	U2125	U2125	A1921	A1786	U	U	U1329	U1229
C2686	U2334	U2449	G2211	A2206	U2126	U2126	C1921	A1787	G	U	G1333	U1234
A2687	U2335	U2450	U2212	A2207	U2127	U2127	U1922	A1788	A	U	U1339	U1235
C2688	A2336	G2455	U2213	U2208	G2130	G2130	C1927	U1789	C	U	U1340	G1236
C2689	G2341	A2456	U2214	U2209	U2131	U2131	G1931	U1805	A	A	U1341	U1240
U2690	U2342	A2457	A2220	A2210	A2136	A2136	G1936	G1806	A	U	G1342	U1241
	U2343	A2458	U2221	U2211	A2137	A2137	G1937	C1807	G1570	A1485	A1242	G1242
	A2344	C2460	U2222	U2212	U2138	U2138	A1943	C1808	G1571	U1486	A1243	U1249
			U2223	U2213	G2139	G2139		C1809	U1572	U1487	G1351	A1250
			G2225	U2224	G2140	G2140		A1809	U1581	A1497	G1352	A1251
			U2226	U2225	A2141	A2141			G1583			

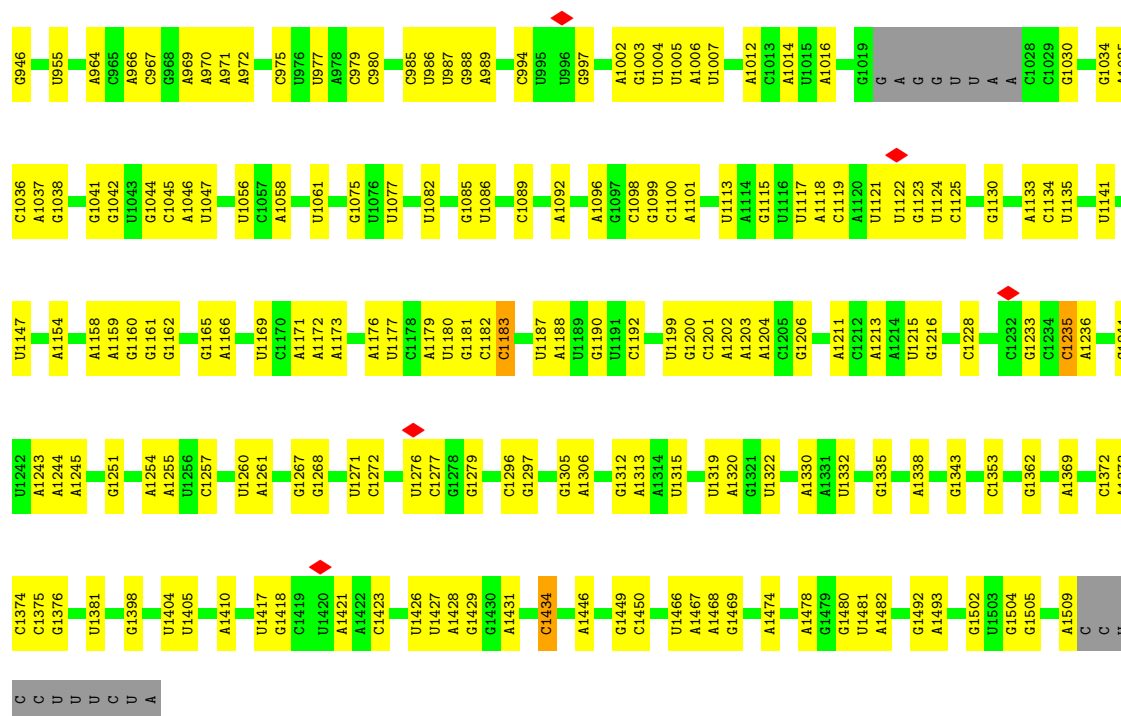


• Molecule 53: 5S ribosomal RNA



• 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 (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	0.27	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

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%)	16	54
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%)	14	51
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%)	6	32
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 ⓘ

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%)	42	61
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	34 (97%)	1 (3%)	37	56
4	9	579/584 (99%)	578 (100%)	1 (0%)	92	94
5	A	212/262 (81%)	210 (99%)	2 (1%)	75	83
6	B	180/232 (78%)	179 (99%)	1 (1%)	84	88
7	C	181/183 (99%)	179 (99%)	2 (1%)	70	79
8	D	123/178 (69%)	122 (99%)	1 (1%)	79	84
9	E	150/196 (76%)	148 (99%)	2 (1%)	65	76
10	F	131/132 (99%)	129 (98%)	2 (2%)	60	75
11	G	123/124 (99%)	121 (98%)	2 (2%)	58	73
12	H	111/115 (96%)	109 (98%)	2 (2%)	54	71
13	I	95/99 (96%)	95 (100%)	0	100	100
14	J	91/97 (94%)	88 (97%)	3 (3%)	33	52
15	K	117/120 (98%)	112 (96%)	5 (4%)	25	46
16	L	100/105 (95%)	99 (99%)	1 (1%)	73	81
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%)	62	75
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%)	50	67
25	W	58/98 (59%)	58 (100%)	0	100	100
26	a	241/243 (99%)	240 (100%)	1 (0%)	89	90
27	b	186/233 (80%)	185 (100%)	1 (0%)	86	89
28	c	182/184 (99%)	182 (100%)	0	100	100
29	d	150/154 (97%)	148 (99%)	2 (1%)	65	76
30	e	153/159 (96%)	153 (100%)	0	100	100
31	f	123/134 (92%)	121 (98%)	2 (2%)	58	73
32	g	101/129 (78%)	92 (91%)	9 (9%)	8	25
33	h	102/110 (93%)	101 (99%)	1 (1%)	73	81
34	i	126/128 (98%)	126 (100%)	0	100	100
35	j	103/103 (100%)	102 (99%)	1 (1%)	73	81
36	k	123/126 (98%)	123 (100%)	0	100	100
37	l	113/115 (98%)	112 (99%)	1 (1%)	75	83
38	m	105/109 (96%)	105 (100%)	0	100	100
39	n	96/99 (97%)	95 (99%)	1 (1%)	73	81
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%)	70	79
43	r	116/132 (88%)	115 (99%)	1 (1%)	75	83
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%)	44	62
50	y	48/49 (98%)	45 (94%)	3 (6%)	15	36
51	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5730/6433 (89%)	5677 (99%)	53 (1%)	74	83

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 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.

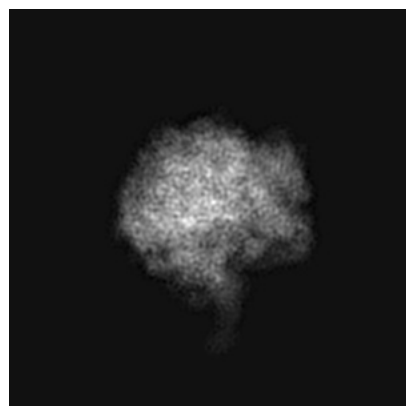
6 Map visualisation [i](#)

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

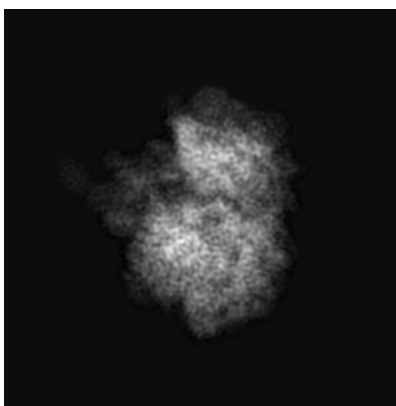
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

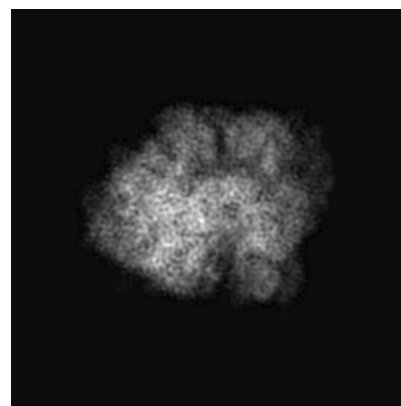
6.1.1 Primary map



X

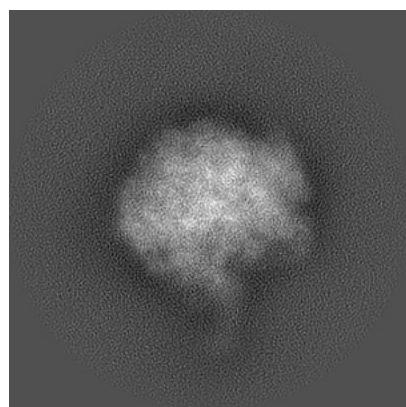


Y

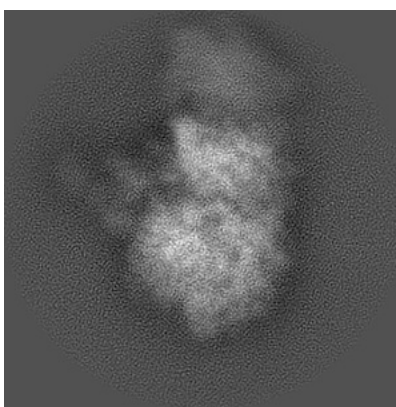


Z

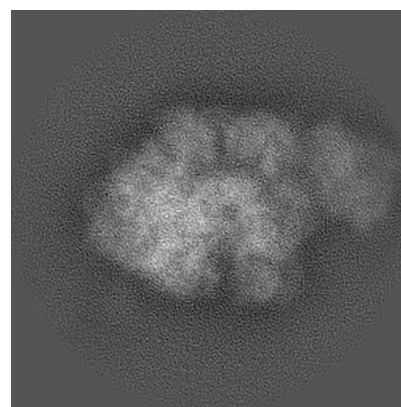
6.1.2 Raw map



X



Y

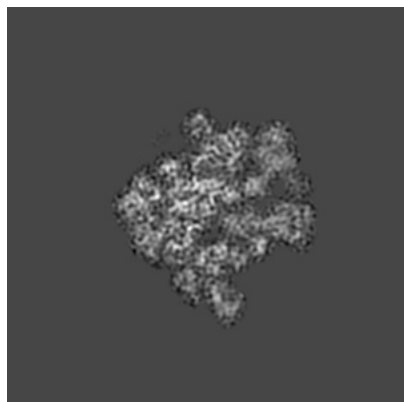


Z

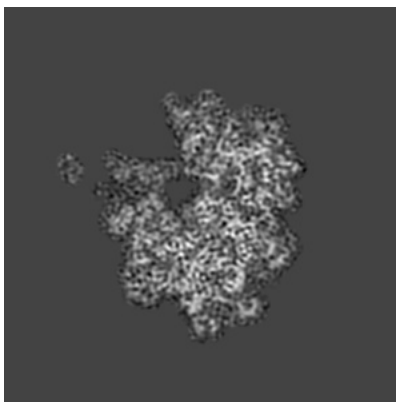
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

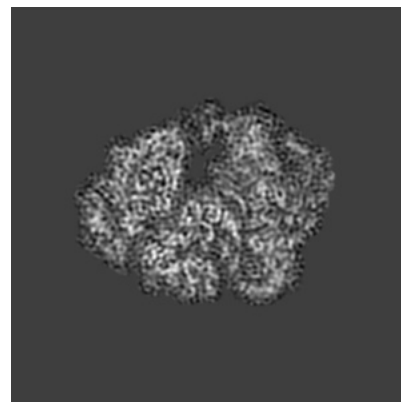
6.2.1 Primary map



X Index: 128

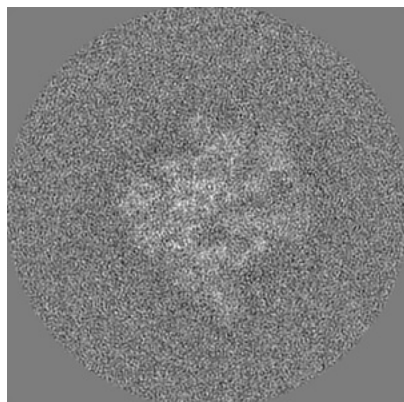


Y Index: 128

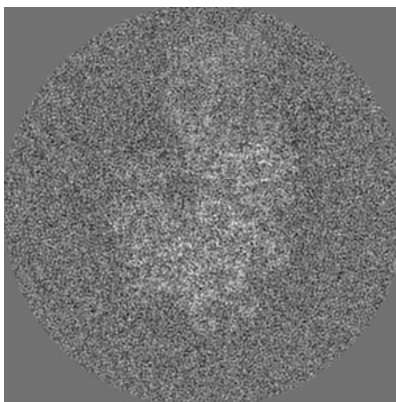


Z Index: 128

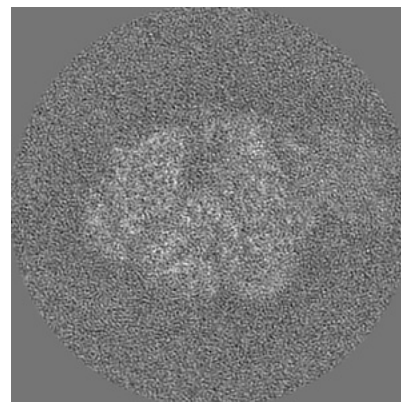
6.2.2 Raw map



X Index: 128



Y Index: 128

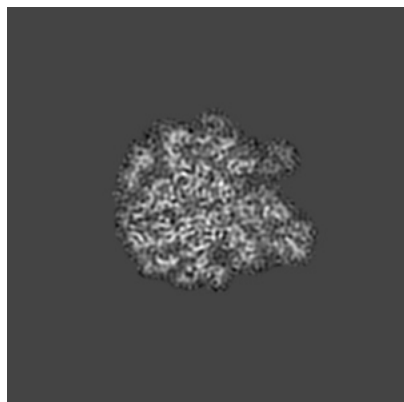


Z Index: 128

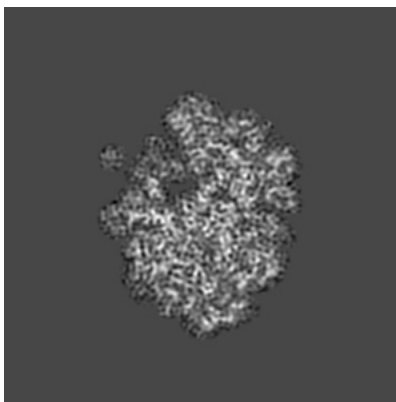
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

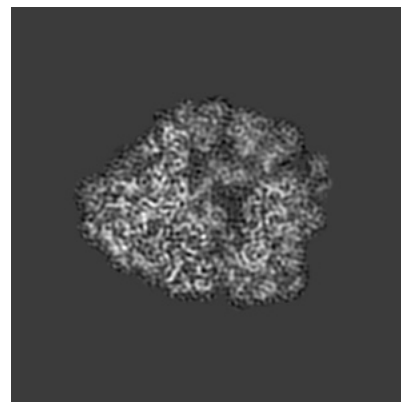
6.3.1 Primary map



X Index: 103

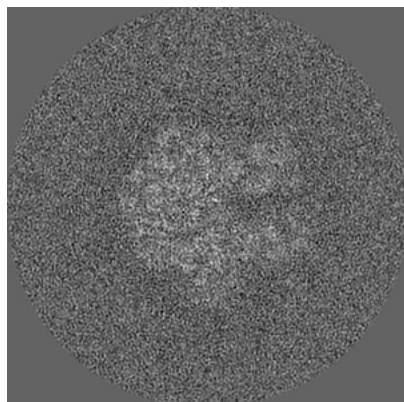


Y Index: 120

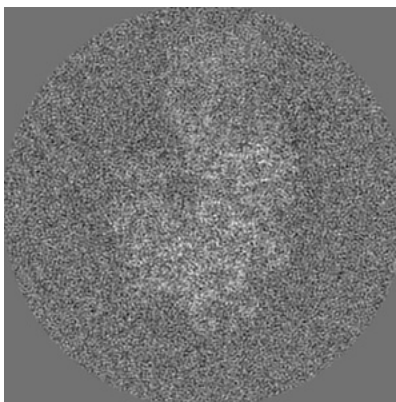


Z Index: 122

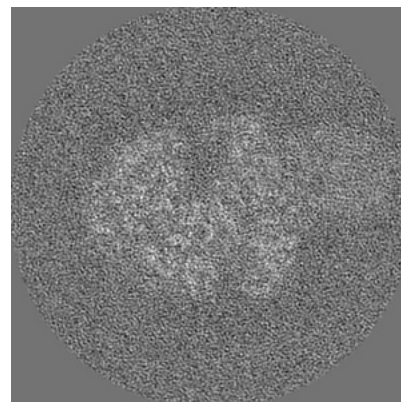
6.3.2 Raw map



X Index: 117



Y Index: 128

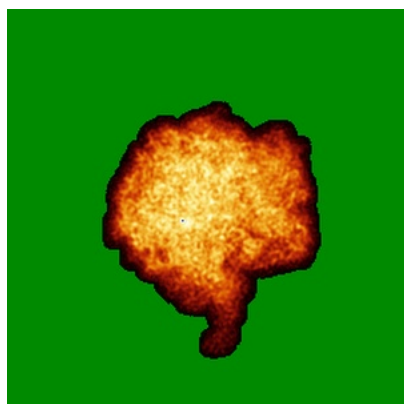


Z Index: 129

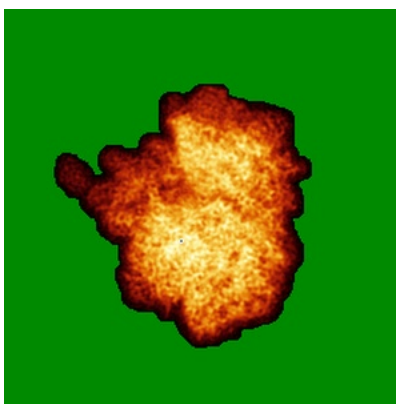
The images above show the largest variance slices of the map in three orthogonal directions.

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

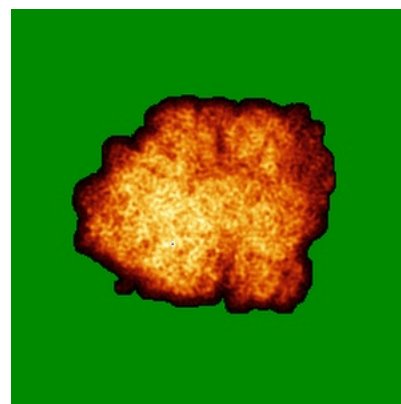
6.4.1 Primary map



X

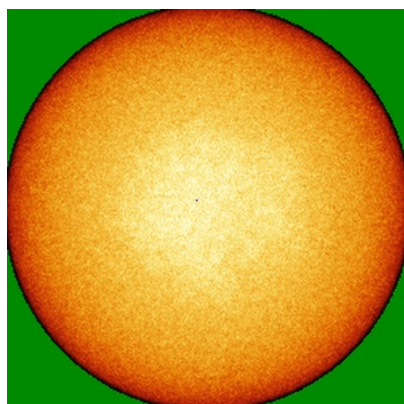


Y

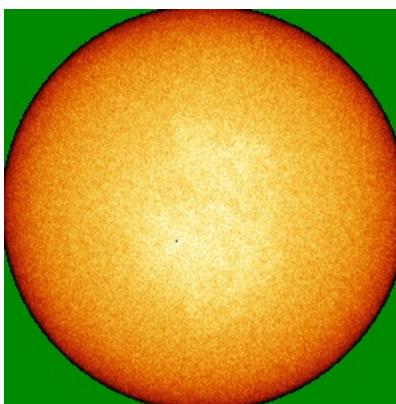


Z

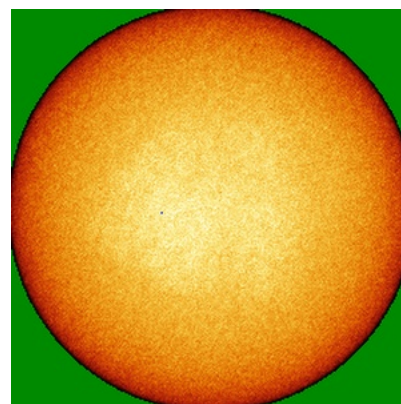
6.4.2 Raw map



X



Y

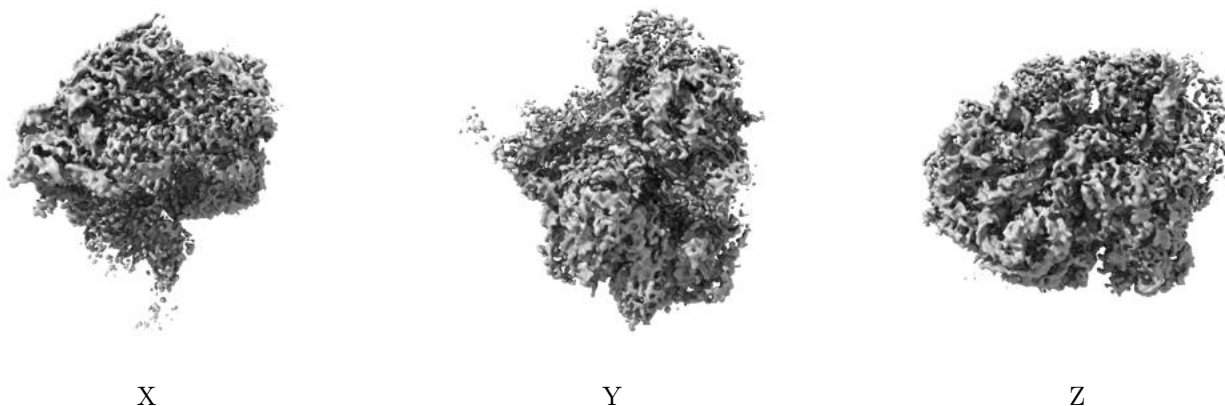


Z

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

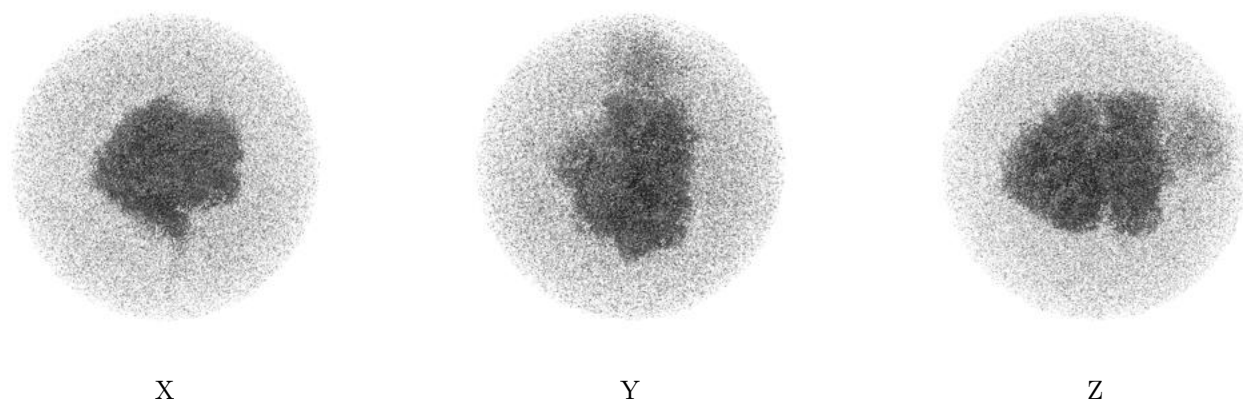
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.54. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

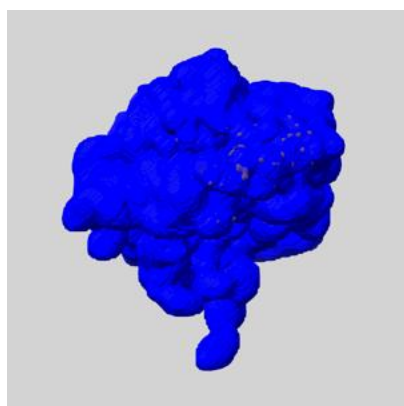
6.6 Mask visualisation [i](#)

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

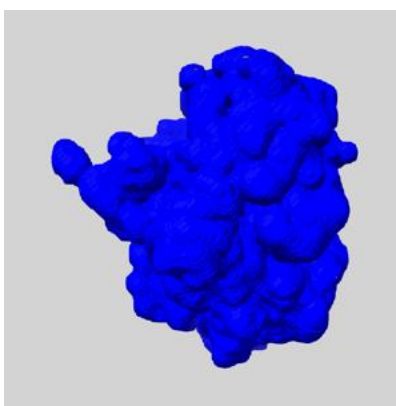
A mask typically either:

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

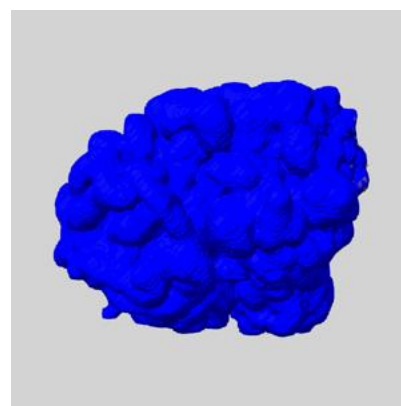
6.6.1 emd_13450_msk_1.map [i](#)



X



Y

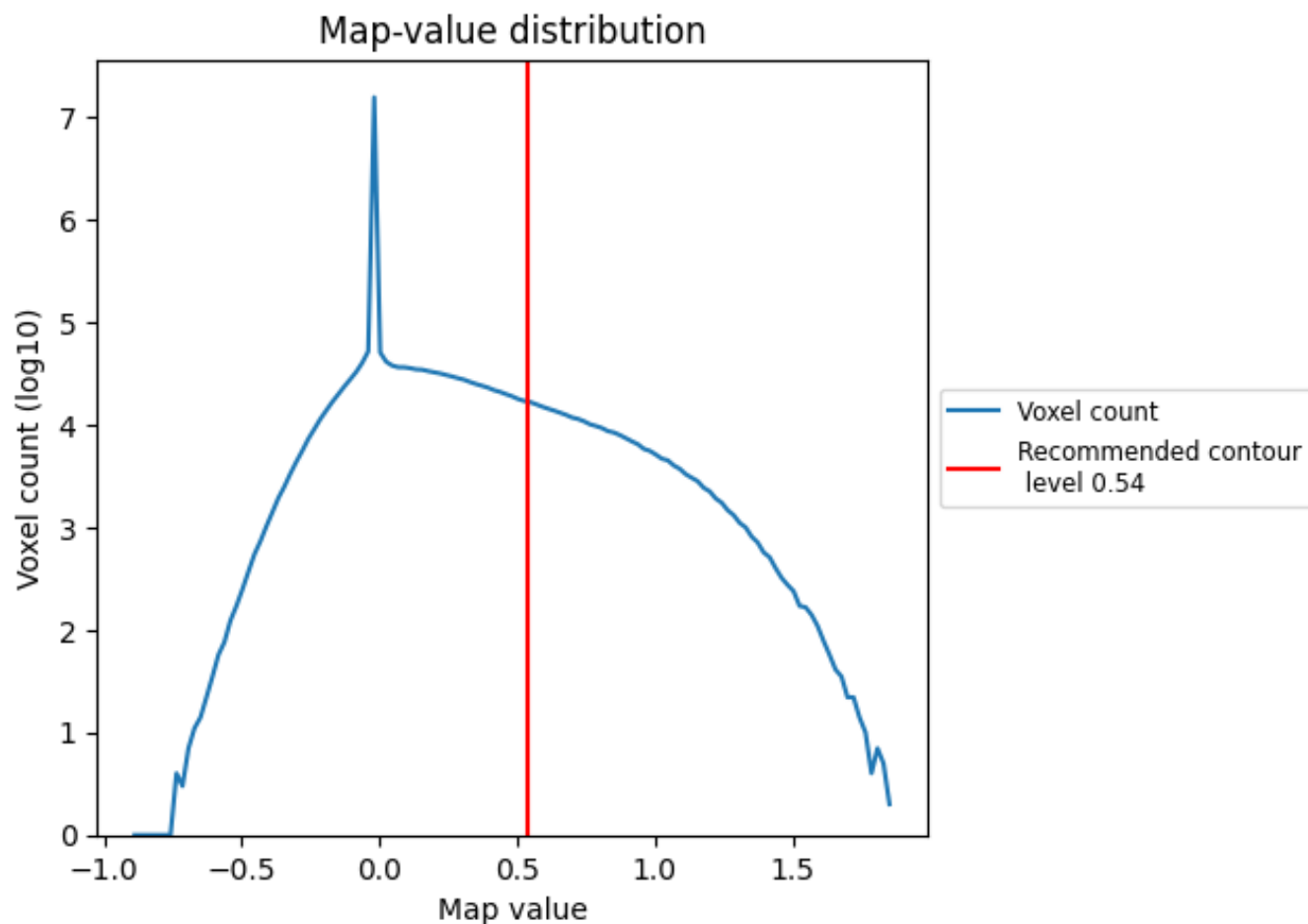


Z

7 Map analysis [i](#)

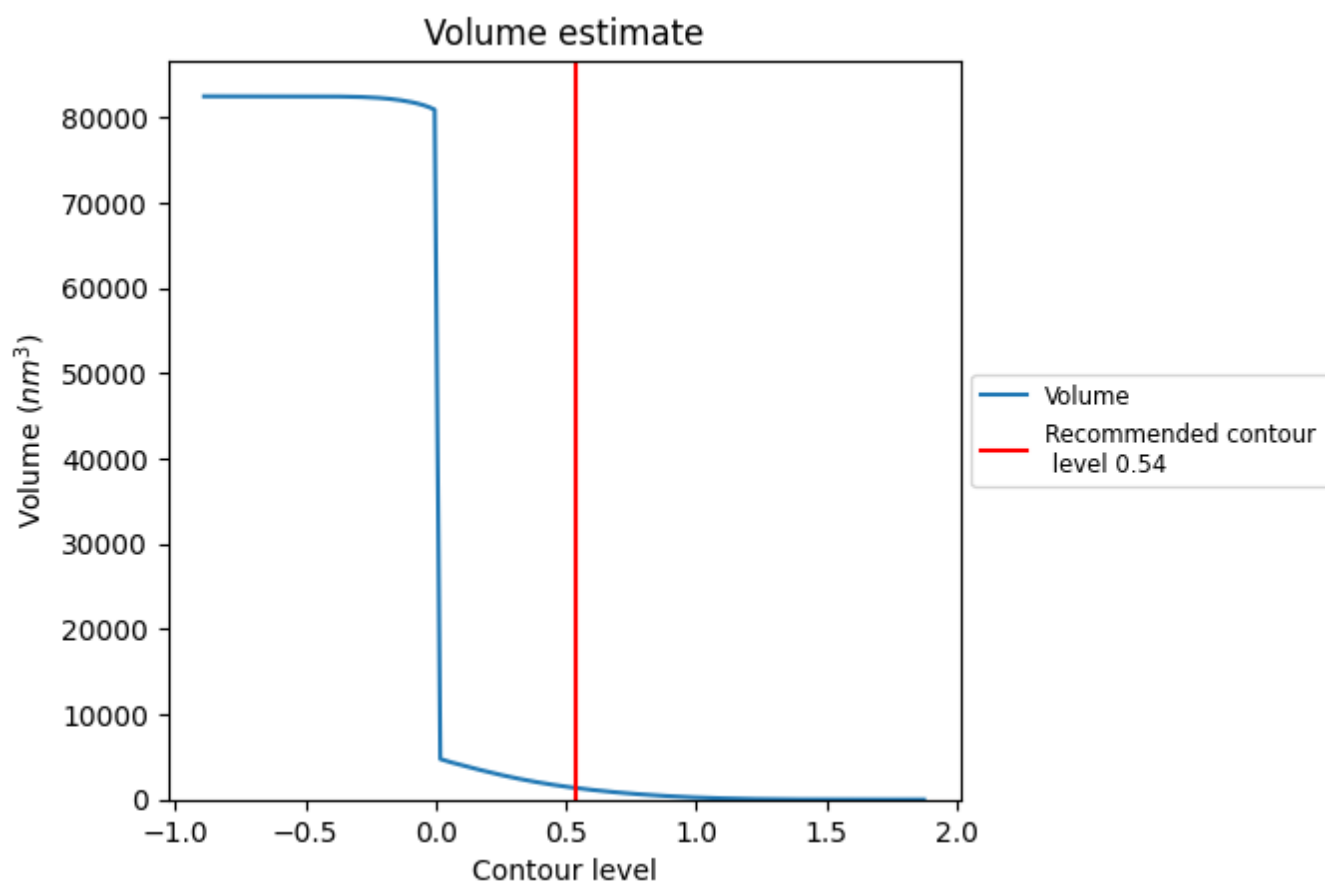
This section contains the results of statistical analysis of the map.

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.

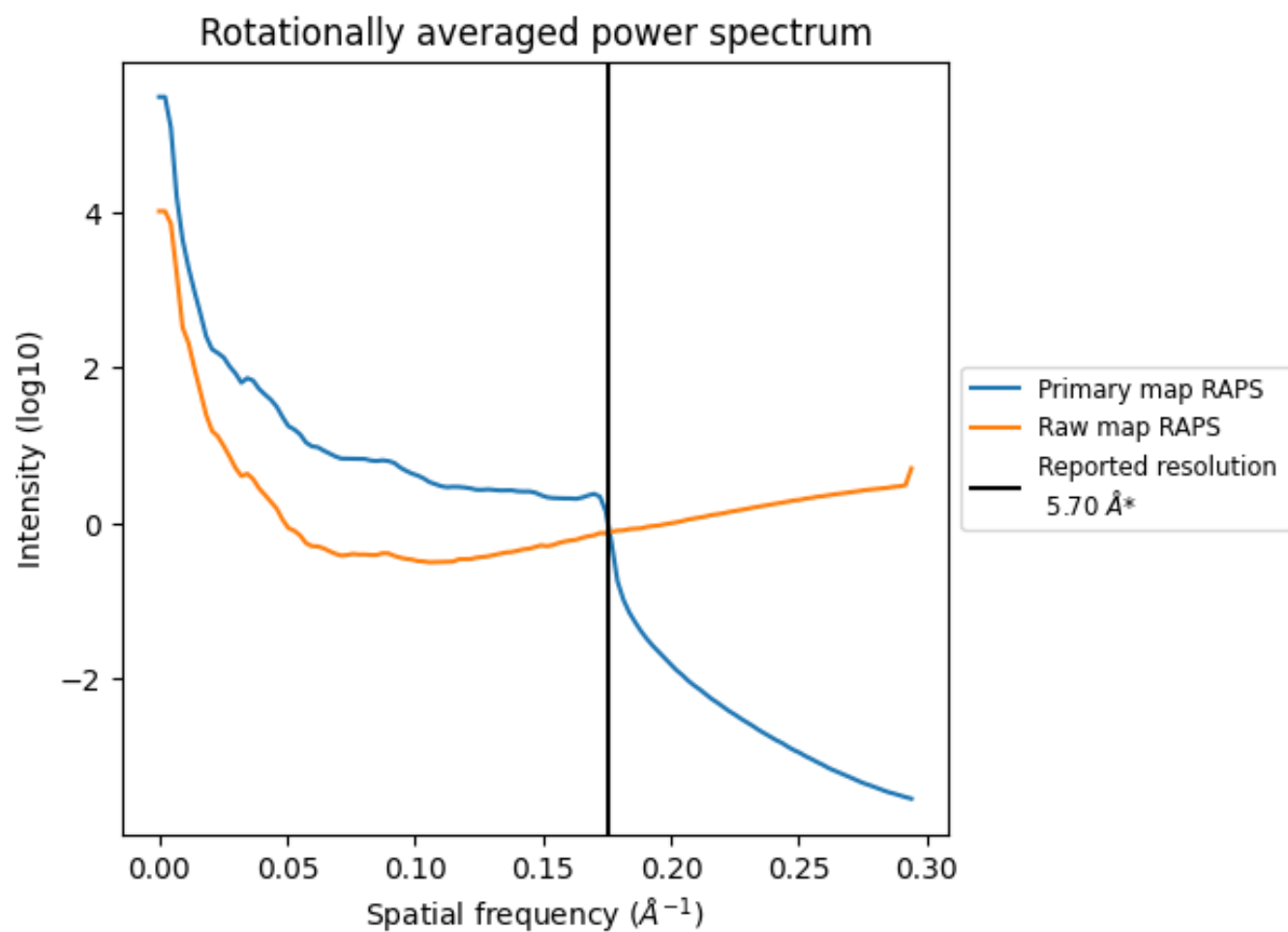
7.2 Volume estimate [i](#)



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 ⓘ

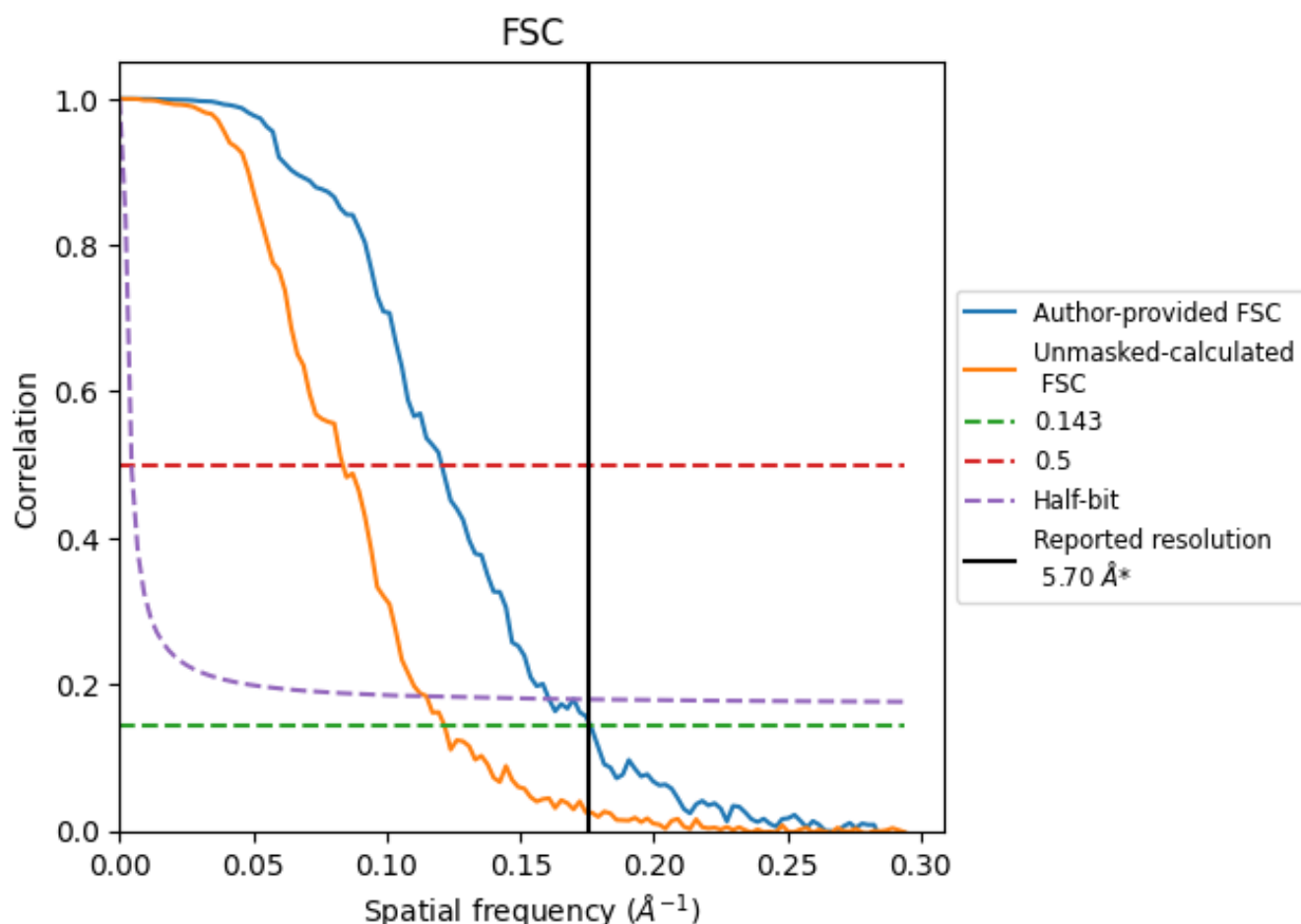


*Reported resolution corresponds to spatial frequency of 0.175 \AA^{-1}

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 0.175 \AA^{-1}

8.2 Resolution estimates [i](#)

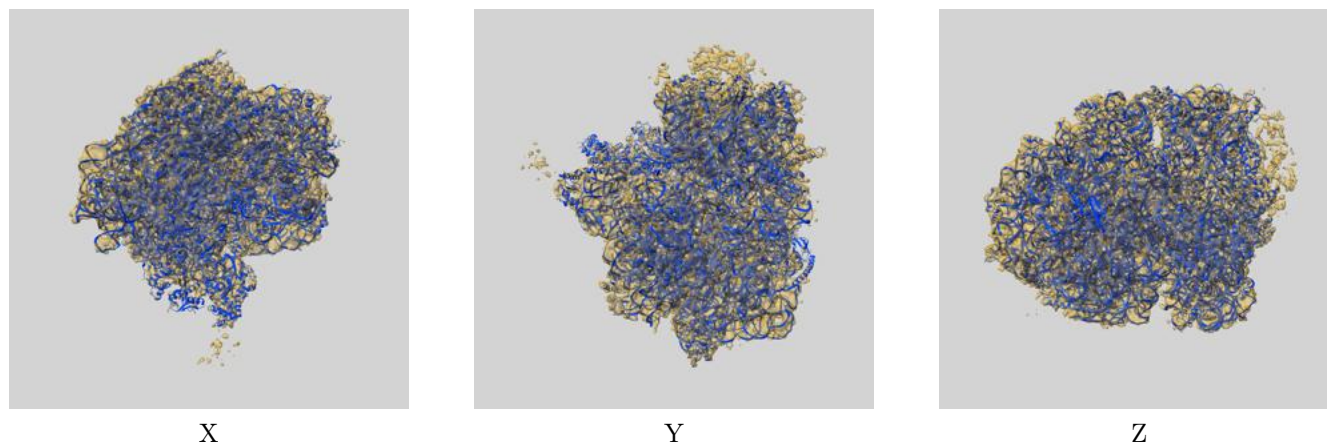
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.70	-	-
Author-provided FSC curve	5.67	8.29	6.22
Unmasked-calculated*	8.21	11.96	8.70

*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](#)

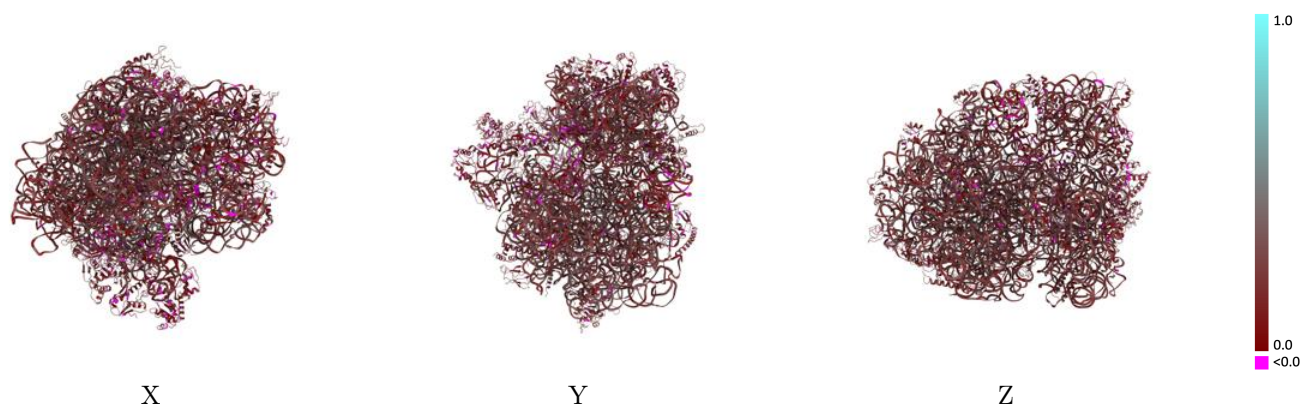
This section contains information regarding the fit between EMDB map EMD-13450 and PDB model 7PIT. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



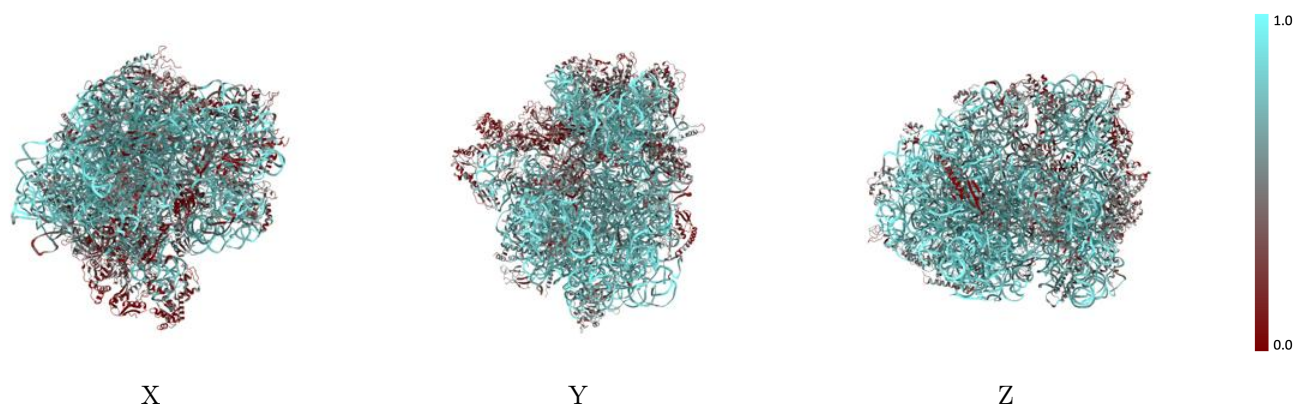
The images above show the 3D surface view of the map at the recommended contour level 0.54 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



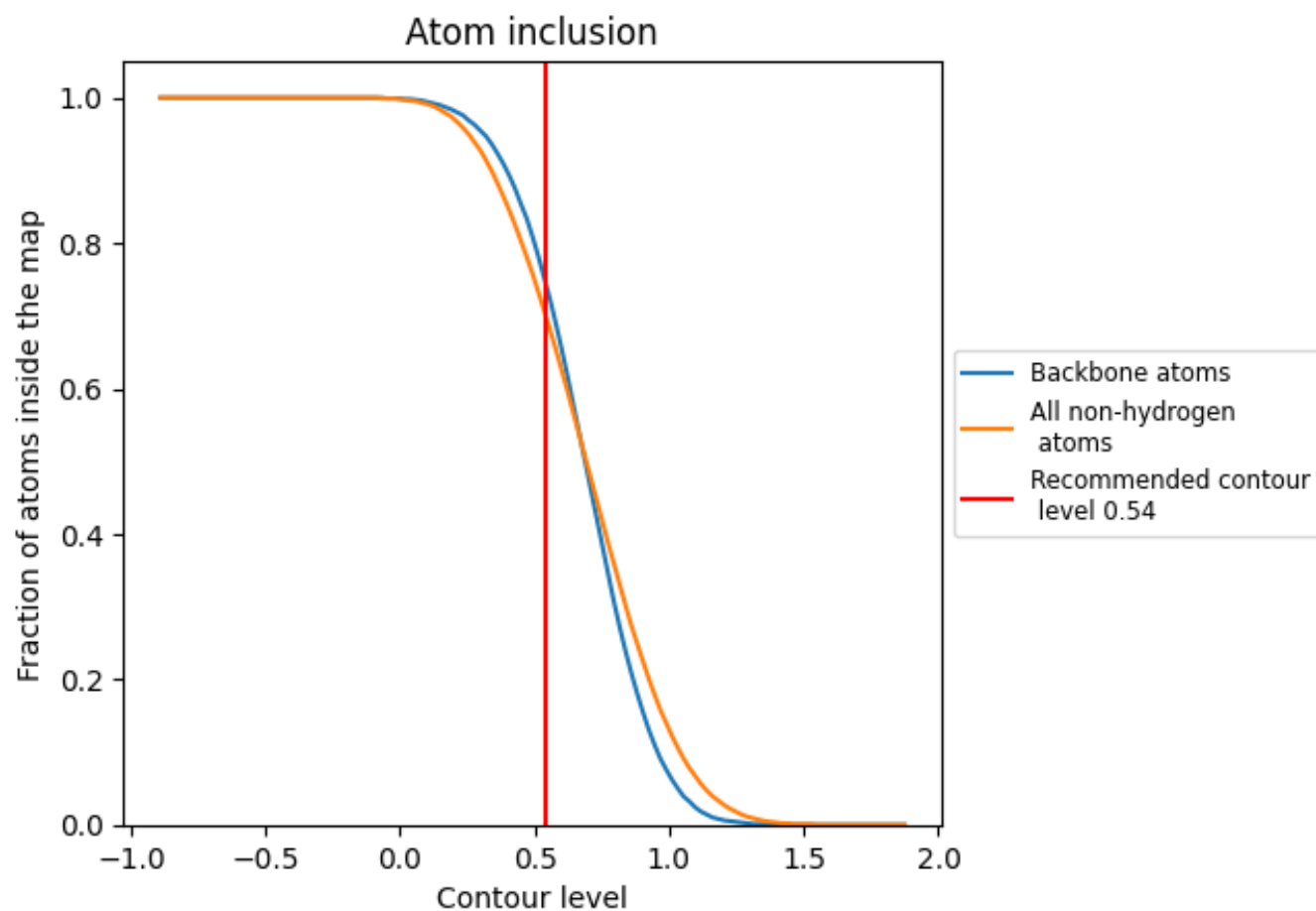
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.7020	 0.2390
0	 0.5840	 0.2160
1	 0.5790	 0.2550
2	 0.6150	 0.2680
3	 0.8660	 0.2590
4	 0.8190	 0.2440
5	 0.8430	 0.2460
7	 0.3630	 0.0970
8	 0.7080	 0.1860
9	 0.1670	 0.1860
A	 0.3910	 0.2110
B	 0.4040	 0.2280
C	 0.3900	 0.2050
D	 0.4480	 0.2400
E	 0.4000	 0.2200
F	 0.3490	 0.2140
G	 0.4850	 0.2060
H	 0.4220	 0.2270
I	 0.3250	 0.2020
J	 0.5140	 0.2250
K	 0.5110	 0.2340
L	 0.3660	 0.2190
M	 0.4920	 0.2180
N	 0.5060	 0.2230
O	 0.5200	 0.2320
P	 0.4930	 0.2400
Q	 0.5150	 0.2480
R	 0.4000	 0.1700
S	 0.5340	 0.1980
T	 0.4980	 0.2310
W	 0.0450	 0.1760
a	 0.5930	 0.2410
b	 0.5340	 0.2320
c	 0.5200	 0.2460
d	 0.3910	 0.2060



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Chain	Atom inclusion	Q-score
e	 0.3800	 0.2150
f	 0.1520	 0.1850
g	 0.1850	 0.1540
h	 0.1750	 0.1750
i	 0.5520	 0.2300
j	 0.4660	 0.2410
k	 0.5450	 0.2570
l	 0.5400	 0.2300
m	 0.5980	 0.2290
n	 0.5040	 0.2230
o	 0.4600	 0.2310
p	 0.5400	 0.1950
q	 0.4880	 0.2340
r	 0.6060	 0.2290
s	 0.5440	 0.2580
t	 0.3810	 0.2270
u	 0.5230	 0.2250
v	 0.4990	 0.2050
w	 0.5260	 0.2260
x	 0.2940	 0.2420
y	 0.6180	 0.2560
z	 0.5060	 0.2420