



## wwPDB EM Validation Summary Report ⓘ

Oct 8, 2022 – 05:41 pm BST

PDB ID : 7PAN  
EMDB ID : EMD-13278  
Title : 70S ribosome with A/P- and P/E-site tRNAs in Mycoplasma pneumoniae cells  
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.  
Deposited on : 2021-07-30  
Resolution : 9.70 Å(reported)  
Based on initial models : 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

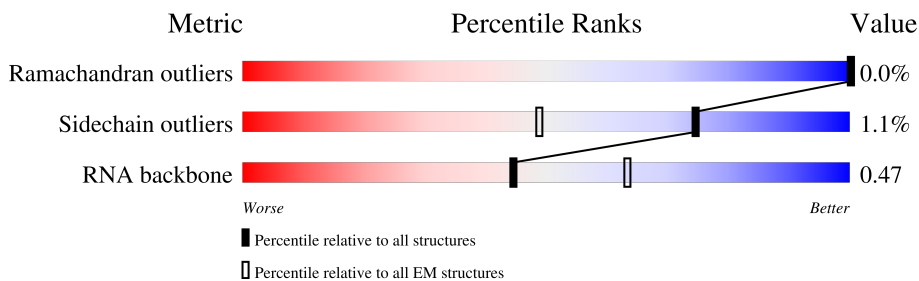
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 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 9.70 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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	48	
2	1	59	
3	2	37	
4	A	294	
5	B	273	
6	C	205	
7	D	219	
8	E	215	

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Mol	Chain	Length	Quality of chain
9	F	155	34% 99%
10	G	142	26% 99%
11	H	132	33% 95%
12	I	108	30% 92% 6%
13	J	121	31% 93% 6%
14	K	139	25% 95%
15	L	124	26% 95% 5%
16	M	61	28% 98%
17	N	86	14% 97%
18	O	94	15% 84% 15%
19	P	85	22% 98%
20	Q	104	10% 62% 38%
21	R	87	26% 95%
22	S	87	10% 89% 11%
23	T	60	12% 88% 12%
24	a	287	19% 98%
25	b	287	15% 79% 20%
26	c	212	18% 99%
27	d	180	32% 97%
28	e	184	36% 96%
29	f	149	72% 97%
30	g	161	39% 70% 8% 22%
31	h	137	67% 93% 7%
32	i	146	10% 98%
33	j	122	30% 100%

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Mol	Chain	Length	Quality of chain
34	k	151	14% 97% ..
35	l	139	21% 96% ..
36	m	124	16% 96% .
37	n	116	10% 97% .
38	o	119	29% 96% ..
39	p	127	8% 90% 10%
40	q	100	21% 98% ..
41	r	159	14% 87% . 13%
42	s	237	11% 38% 61%
43	t	111	25% 100%
44	u	104	10% 83% 17%
45	v	65	22% 95% ..
46	w	111	13% 88% . 10%
47	x	97	19% 45% 55%
48	y	57	21% 89% 7% ..
49	z	53	9% 89% 6% 6%
50	3	2907	. 69% 29% .
51	4	108	. 65% 32% .
52	5	1520	. 72% 26% .
53	7	76	7% 66% 34%
53	8	76	. 66% 34%

## 2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 146120 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 30S ribosomal protein S2.

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

- Molecule 5 is a protein called 30S ribosomal protein S3.

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

- Molecule 6 is a protein called 30S ribosomal protein S4.

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

- Molecule 7 is a protein called 30S ribosomal protein S5.

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

- Molecule 8 is a protein called 30S ribosomal protein S6.

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

- Molecule 9 is a protein called 30S ribosomal protein S7.

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

- Molecule 10 is a protein called 30S ribosomal protein S8.

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

- Molecule 11 is a protein called 30S ribosomal protein S9.

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

- Molecule 12 is a protein called 30S ribosomal protein S10.

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

- Molecule 13 is a protein called 30S ribosomal protein S11.

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

- Molecule 14 is a protein called 30S ribosomal protein S12.

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

- Molecule 15 is a protein called 30S ribosomal protein S13.

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

- Molecule 16 is a protein called 30S ribosomal protein S14 type Z.

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

- Molecule 17 is a protein called 30S ribosomal protein S15.

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

- Molecule 18 is a protein called 30S ribosomal protein S16.

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

- Molecule 19 is a protein called 30S ribosomal protein S17.

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

- Molecule 20 is a protein called 30S ribosomal protein S18.

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

- Molecule 21 is a protein called 30S ribosomal protein S19.

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

- Molecule 22 is a protein called 30S ribosomal protein S20.

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

- Molecule 23 is a protein called 30S ribosomal protein S21.

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

- Molecule 24 is a protein called 50S ribosomal protein L2.

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

- Molecule 25 is a protein called 50S ribosomal protein L3.

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

- Molecule 26 is a protein called 50S ribosomal protein L4.

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

- Molecule 27 is a protein called 50S ribosomal protein L5.

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

- Molecule 28 is a protein called 50S ribosomal protein L6.



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

- Molecule 29 is a protein called 50S ribosomal protein L9.

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

- Molecule 30 is a protein called 50S ribosomal protein L10.

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

- Molecule 31 is a protein called 50S ribosomal protein L11.

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

- Molecule 32 is a protein called 50S ribosomal protein L13.

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

- Molecule 33 is a protein called 50S ribosomal protein L14.

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

- Molecule 34 is a protein called 50S ribosomal protein L15.

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

- Molecule 35 is a protein called 50S ribosomal protein L16.

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

- Molecule 36 is a protein called 50S ribosomal protein L17.

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

- Molecule 37 is a protein called 50S ribosomal protein L18.

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

- Molecule 38 is a protein called 50S ribosomal protein L19.

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

- Molecule 39 is a protein called 50S ribosomal protein L20.

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

- Molecule 40 is a protein called 50S ribosomal protein L21.

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

- Molecule 41 is a protein called 50S ribosomal protein L22.

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

- Molecule 42 is a protein called 50S ribosomal protein L23.

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

- Molecule 43 is a protein called 50S ribosomal protein L24.

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

- Molecule 44 is a protein called 50S ribosomal protein L27.

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

- Molecule 45 is a protein called 50S ribosomal protein L28.

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

- Molecule 46 is a protein called 50S ribosomal protein L29.

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

- Molecule 47 is a protein called 50S ribosomal protein L31.

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

- Molecule 48 is a protein called 50S ribosomal protein L32.

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

- Molecule 49 is a protein called 50S ribosomal protein L33 1.

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

- Molecule 50 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 51 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

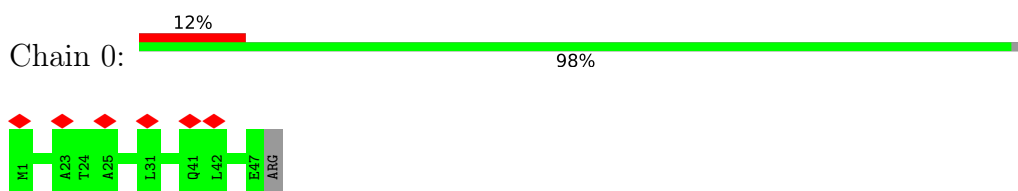
- Molecule 53 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
53	8	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

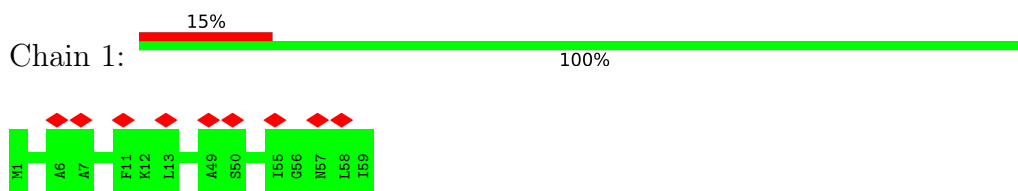
### 3 Residue-property plots

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

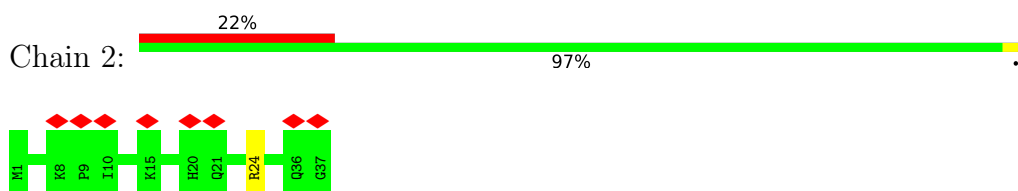
- Molecule 1: 50S ribosomal protein L34



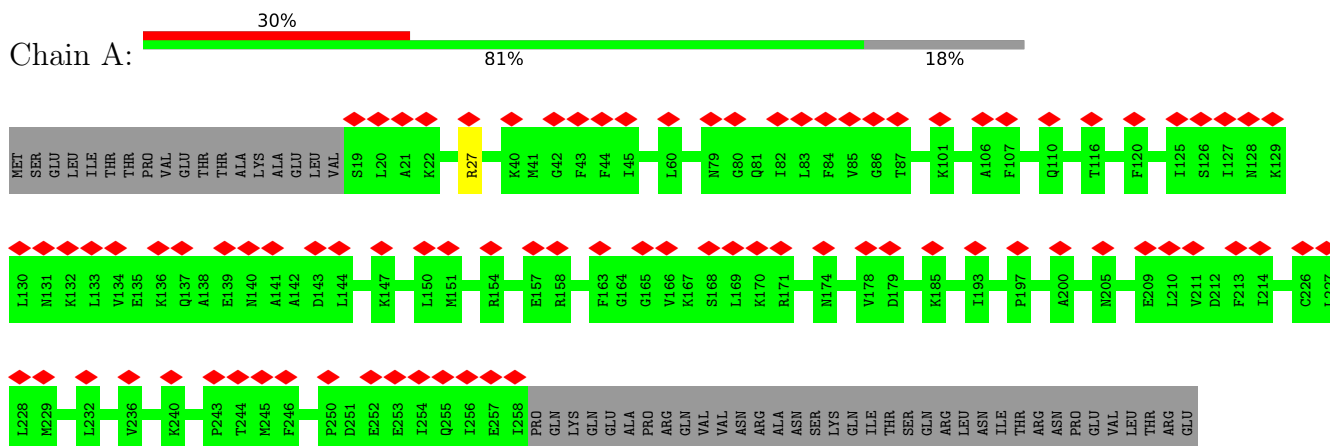
- Molecule 2: 50S ribosomal protein L35



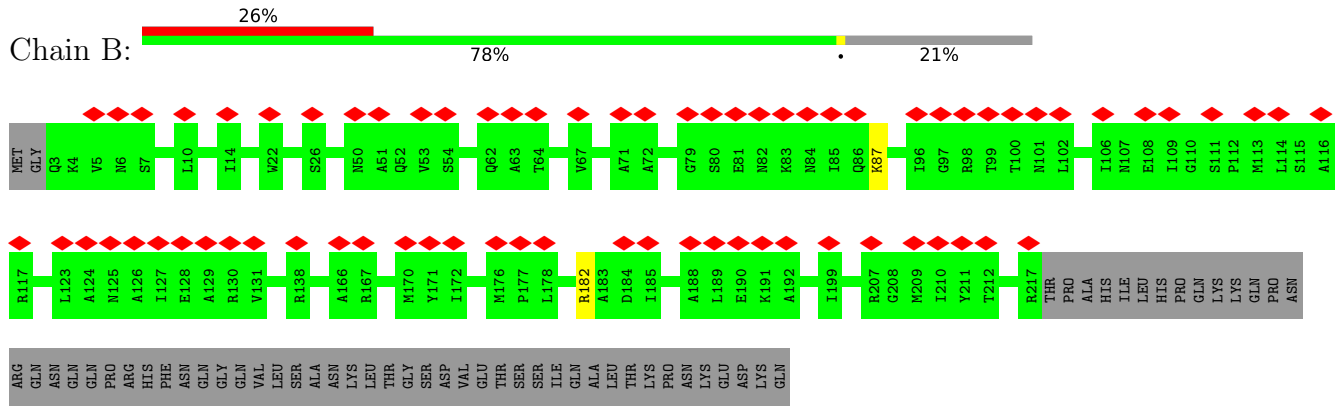
- Molecule 3: 50S ribosomal protein L36



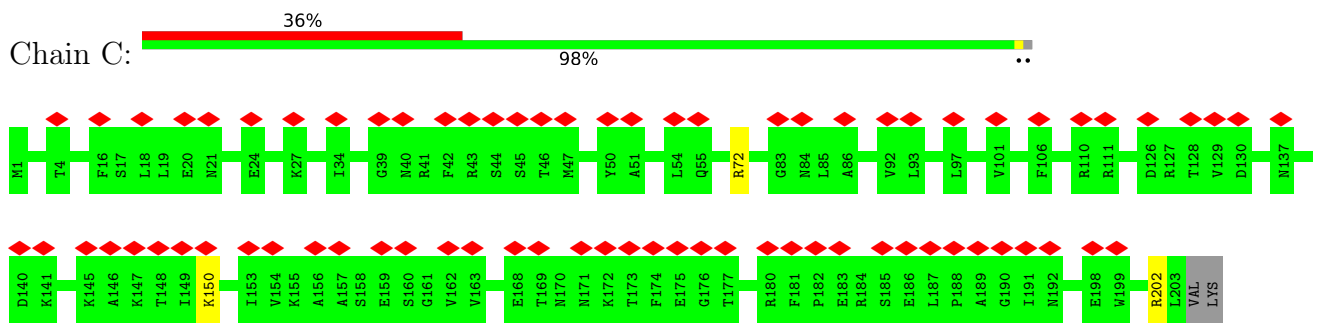
- Molecule 4: 30S ribosomal protein S2



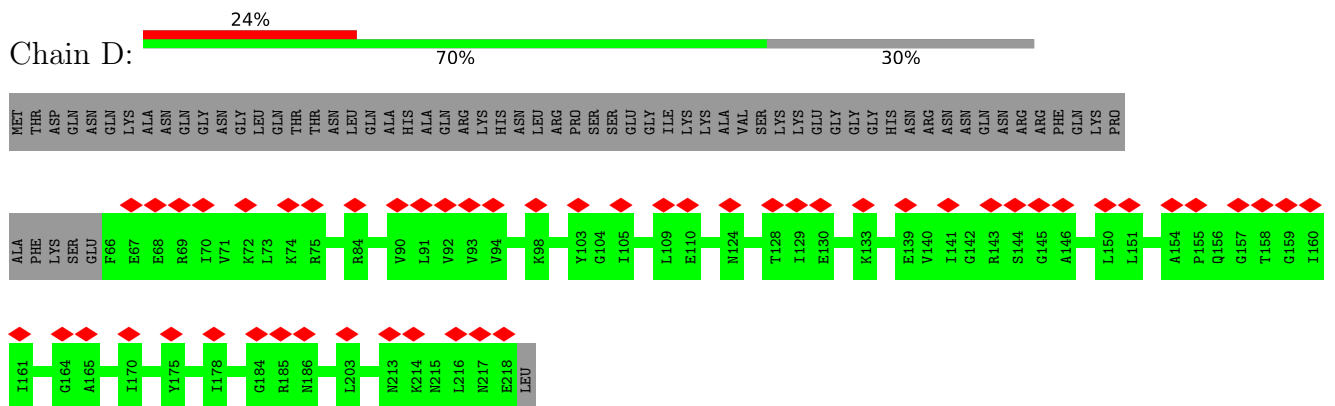
• Molecule 5: 30S ribosomal protein S3



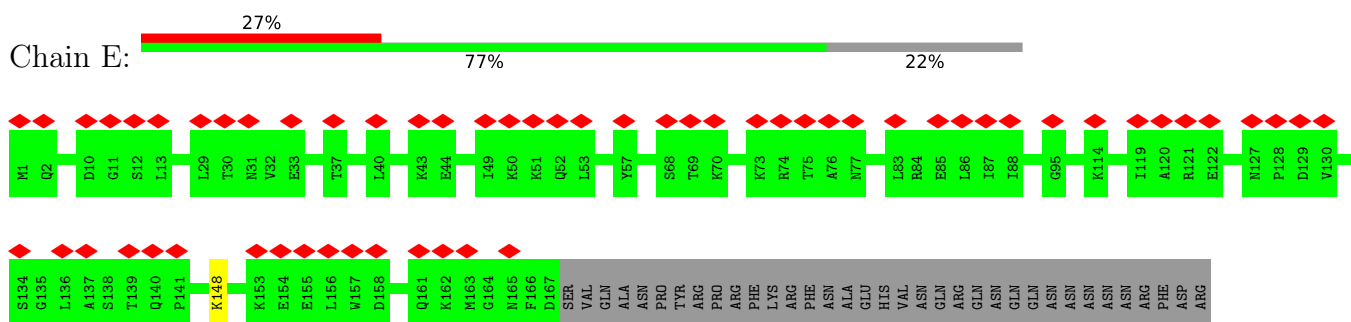
• Molecule 6: 30S ribosomal protein S4



• Molecule 7: 30S ribosomal protein S5

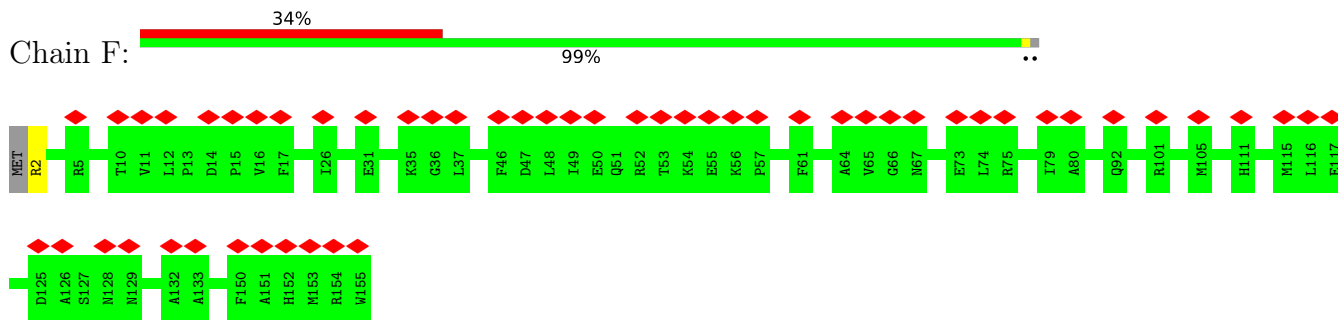


• Molecule 8: 30S ribosomal protein S6

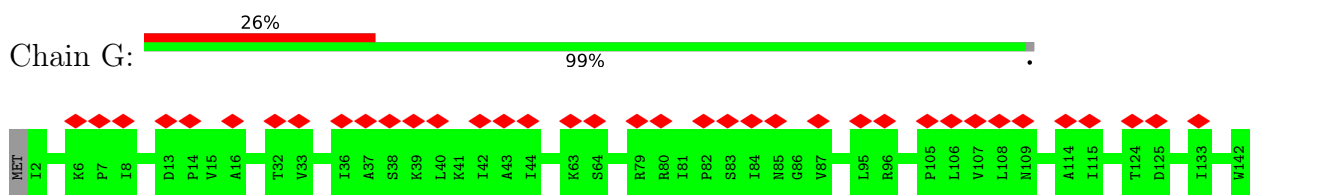


ASN  
ARG  
ASN  
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ASN  
ARG  
PHE  
LYS  
ASP  
LYS  
GLN

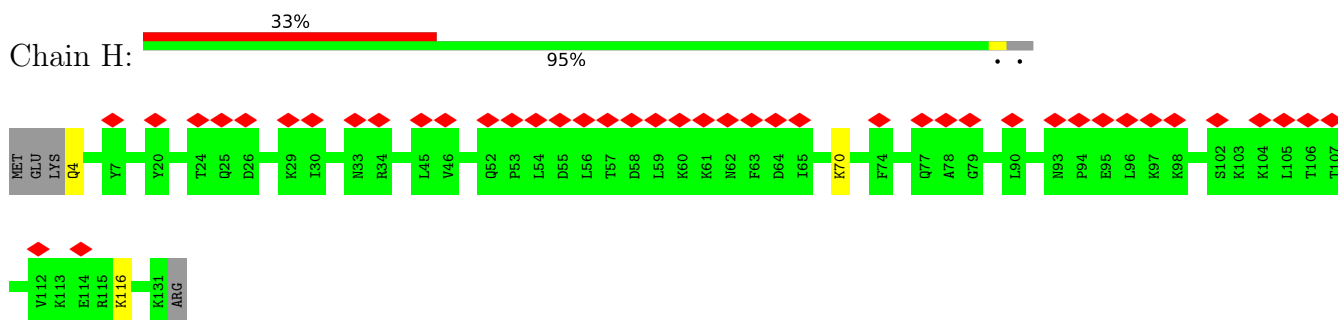
• Molecule 9: 30S ribosomal protein S7



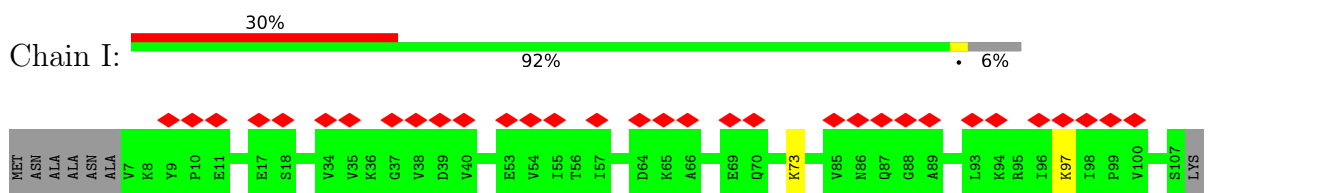
• Molecule 10: 30S ribosomal protein S8



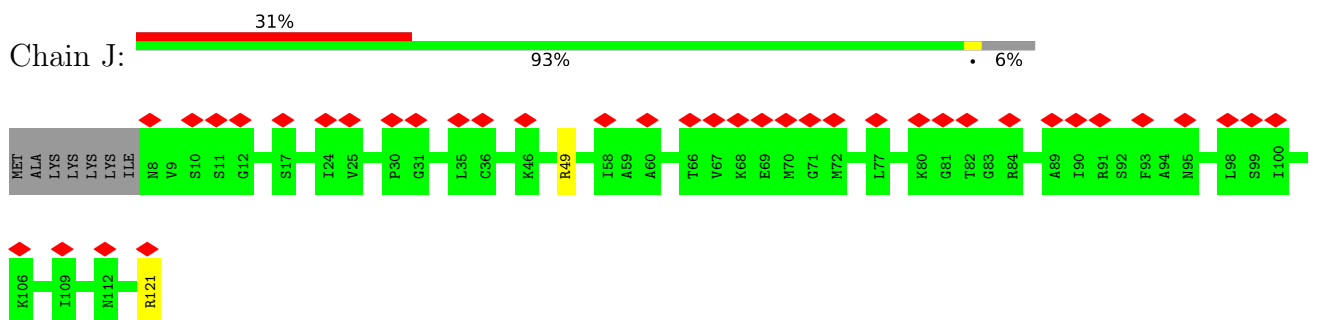
• Molecule 11: 30S ribosomal protein S9



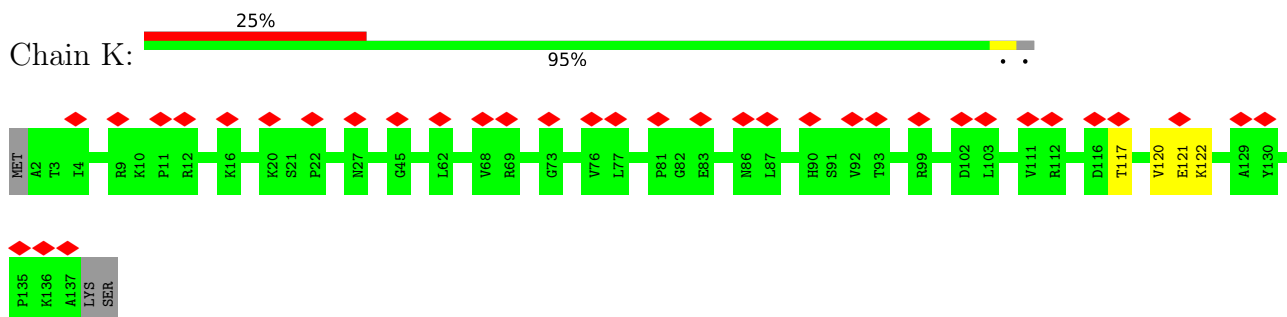
• Molecule 12: 30S ribosomal protein S10



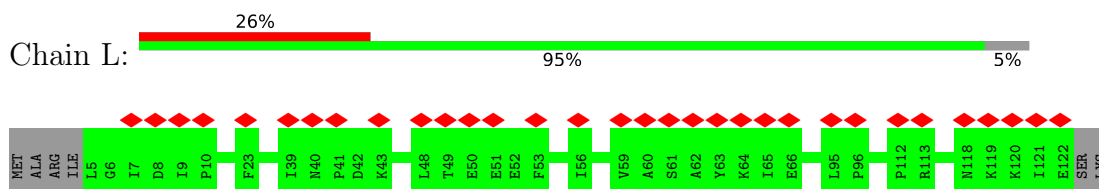
• Molecule 13: 30S ribosomal protein S11



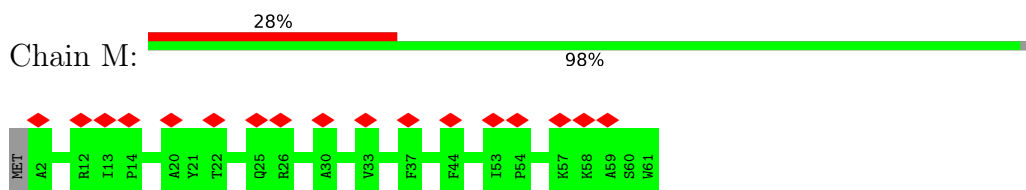
- Molecule 14: 30S ribosomal protein S12



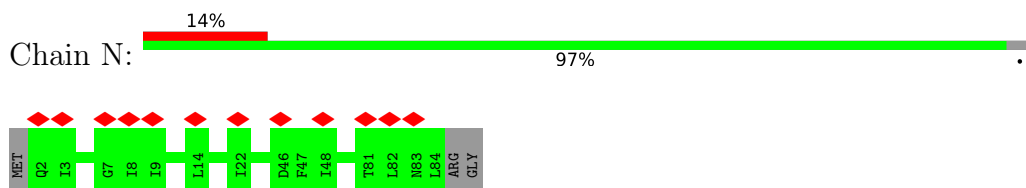
- Molecule 15: 30S ribosomal protein S13



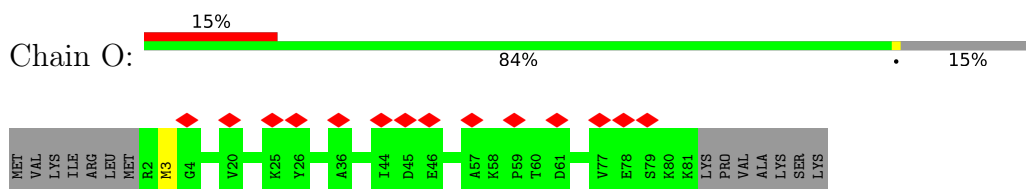
- Molecule 16: 30S ribosomal protein S14 type Z



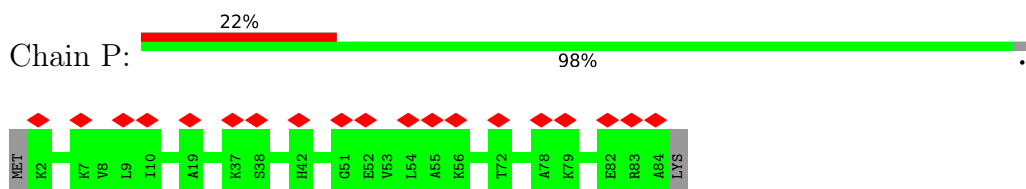
- Molecule 17: 30S ribosomal protein S15



- Molecule 18: 30S ribosomal protein S16

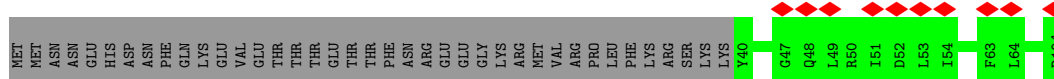


- Molecule 19: 30S ribosomal protein S17

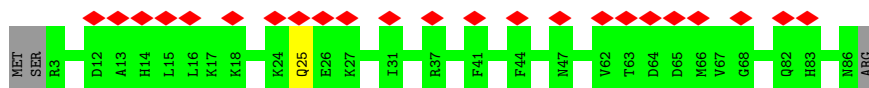


- Molecule 20: 30S ribosomal protein S18

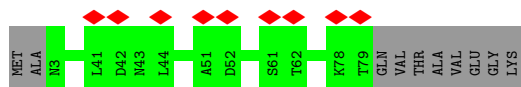
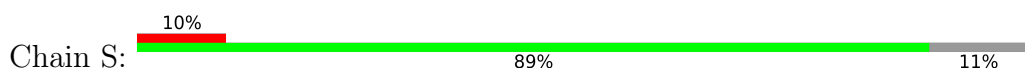




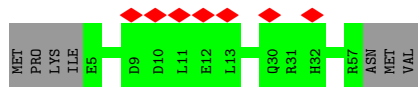
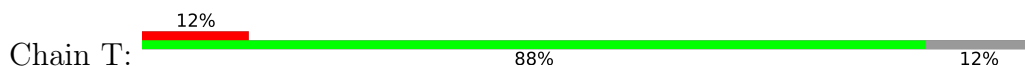
• Molecule 21: 30S ribosomal protein S19



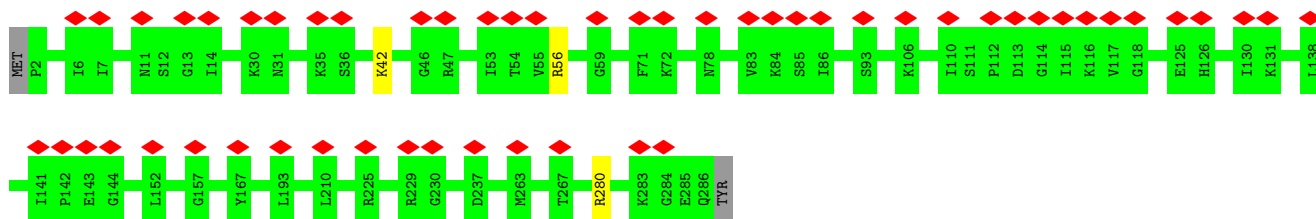
• Molecule 22: 30S ribosomal protein S20



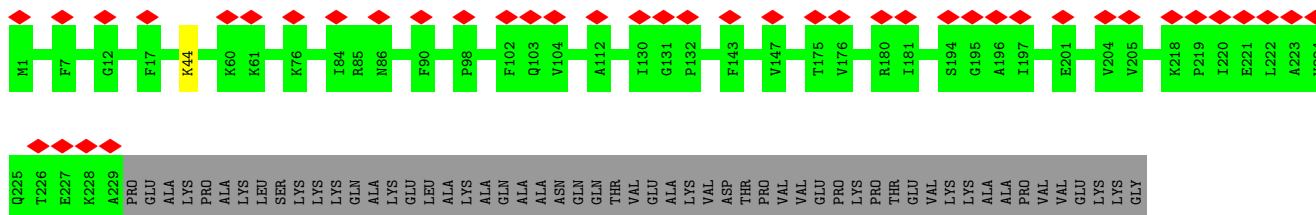
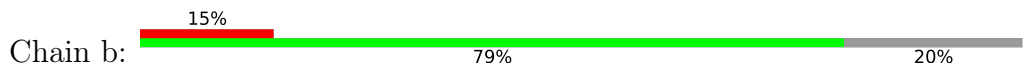
• Molecule 23: 30S ribosomal protein S21



• Molecule 24: 50S ribosomal protein L2

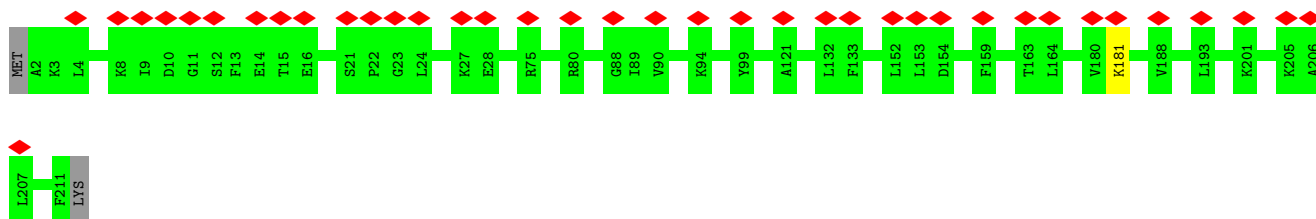


• Molecule 25: 50S ribosomal protein L3

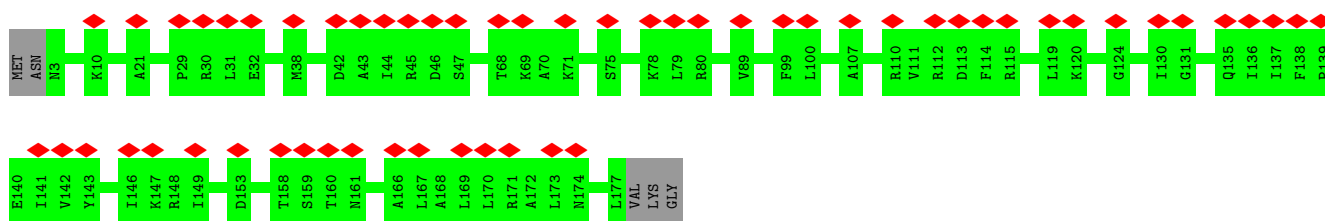


GLU  
ASP  
LYS

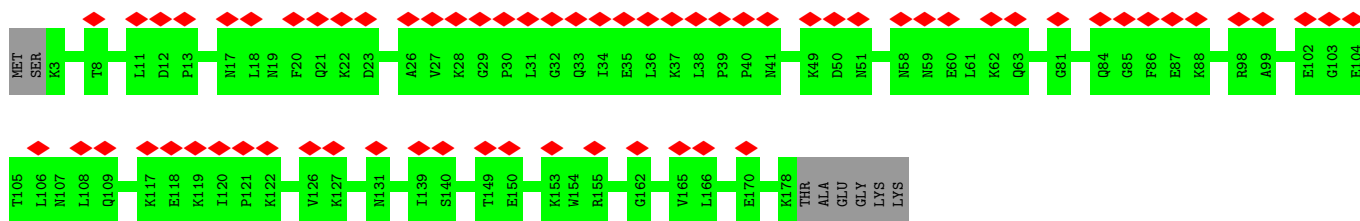
• Molecule 26: 50S ribosomal protein L4



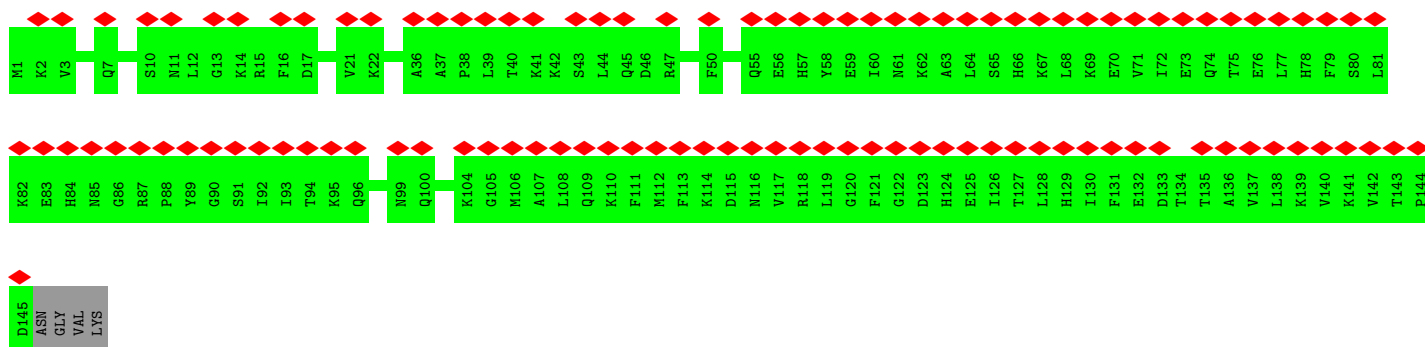
• Molecule 27: 50S ribosomal protein L5



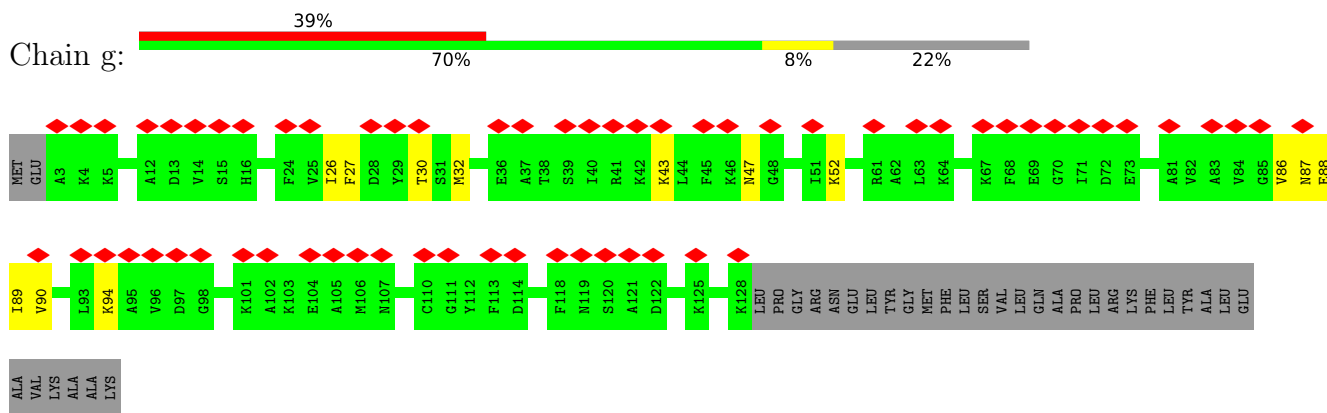
• Molecule 28: 50S ribosomal protein L6



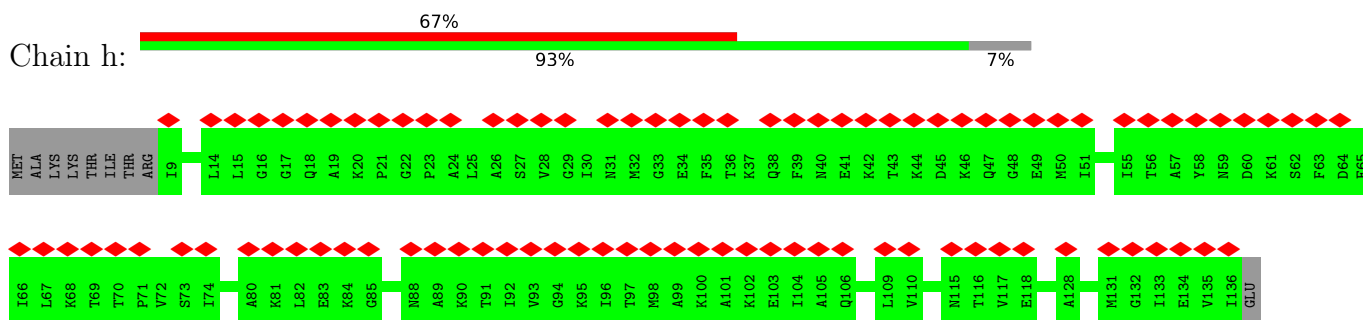
• Molecule 29: 50S ribosomal protein L9



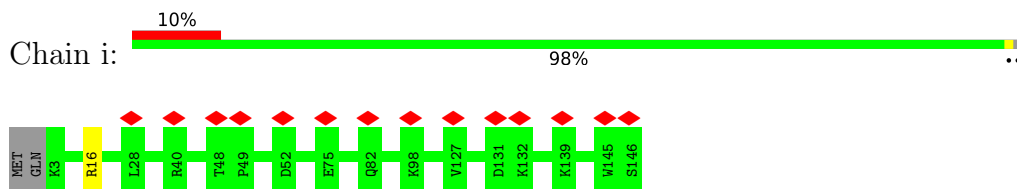
- Molecule 30: 50S ribosomal protein L10



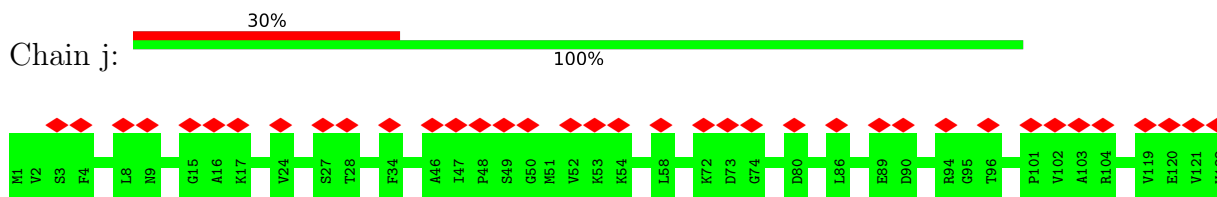
- Molecule 31: 50S ribosomal protein L11



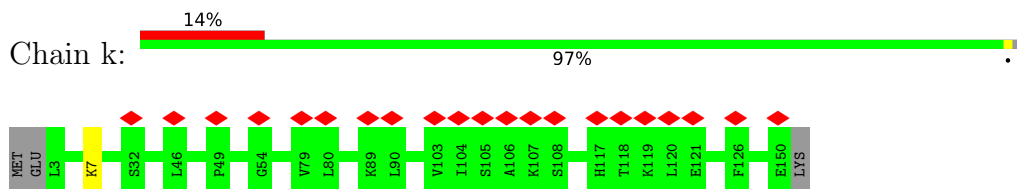
- Molecule 32: 50S ribosomal protein L13



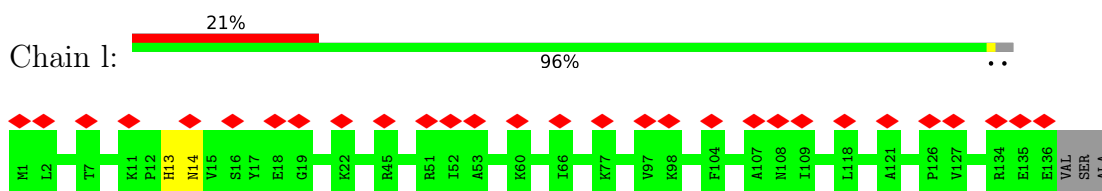
- Molecule 33: 50S ribosomal protein L14



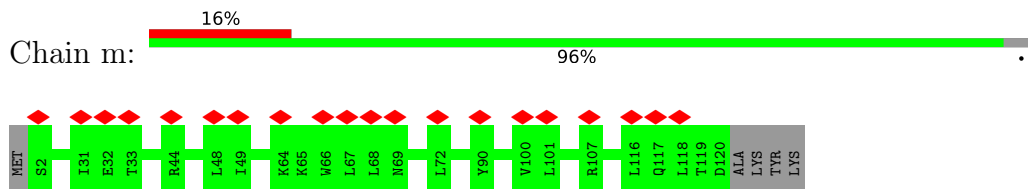
- Molecule 34: 50S ribosomal protein L15



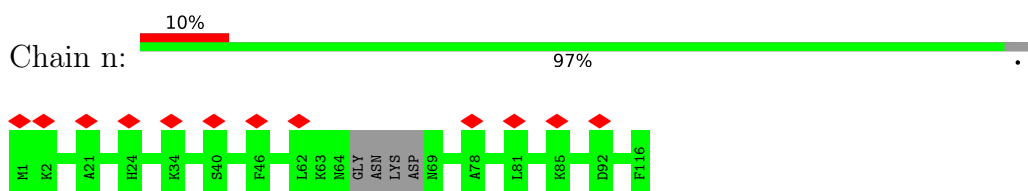
- Molecule 35: 50S ribosomal protein L16



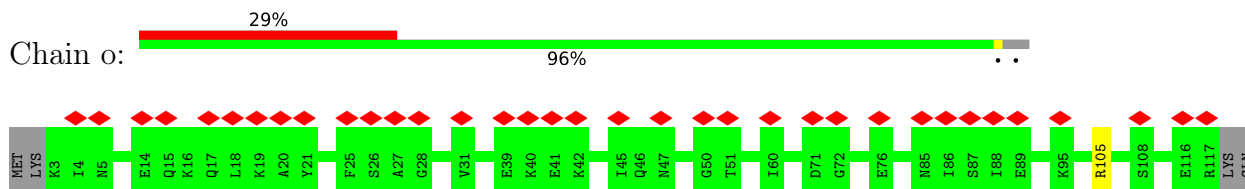
- Molecule 36: 50S ribosomal protein L17



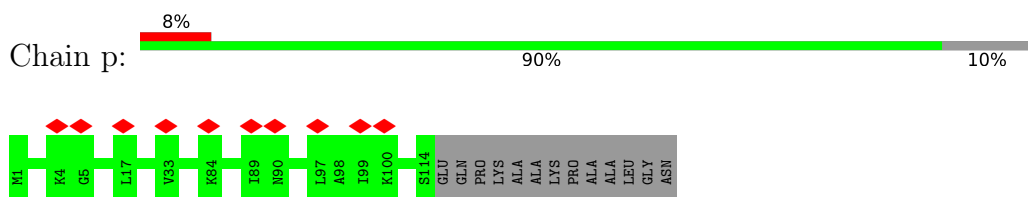
- Molecule 37: 50S ribosomal protein L18



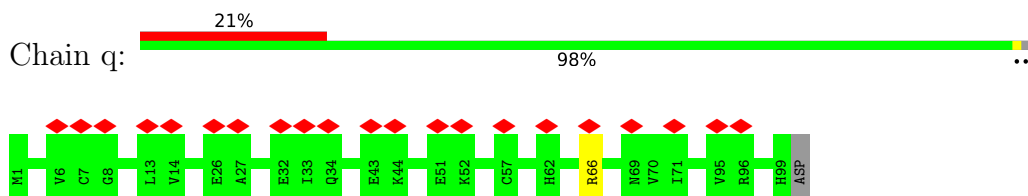
- Molecule 38: 50S ribosomal protein L19



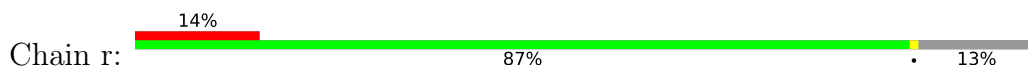
- Molecule 39: 50S ribosomal protein L20



- Molecule 40: 50S ribosomal protein L21

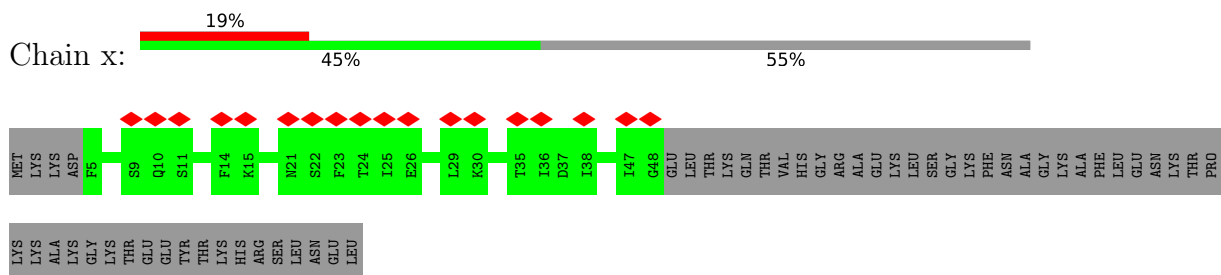


- Molecule 41: 50S ribosomal protein L22

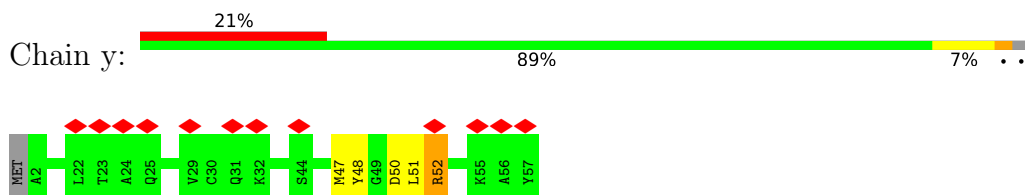




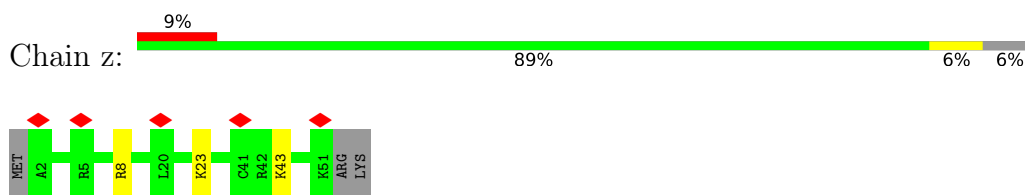
• Molecule 47: 50S ribosomal protein L31



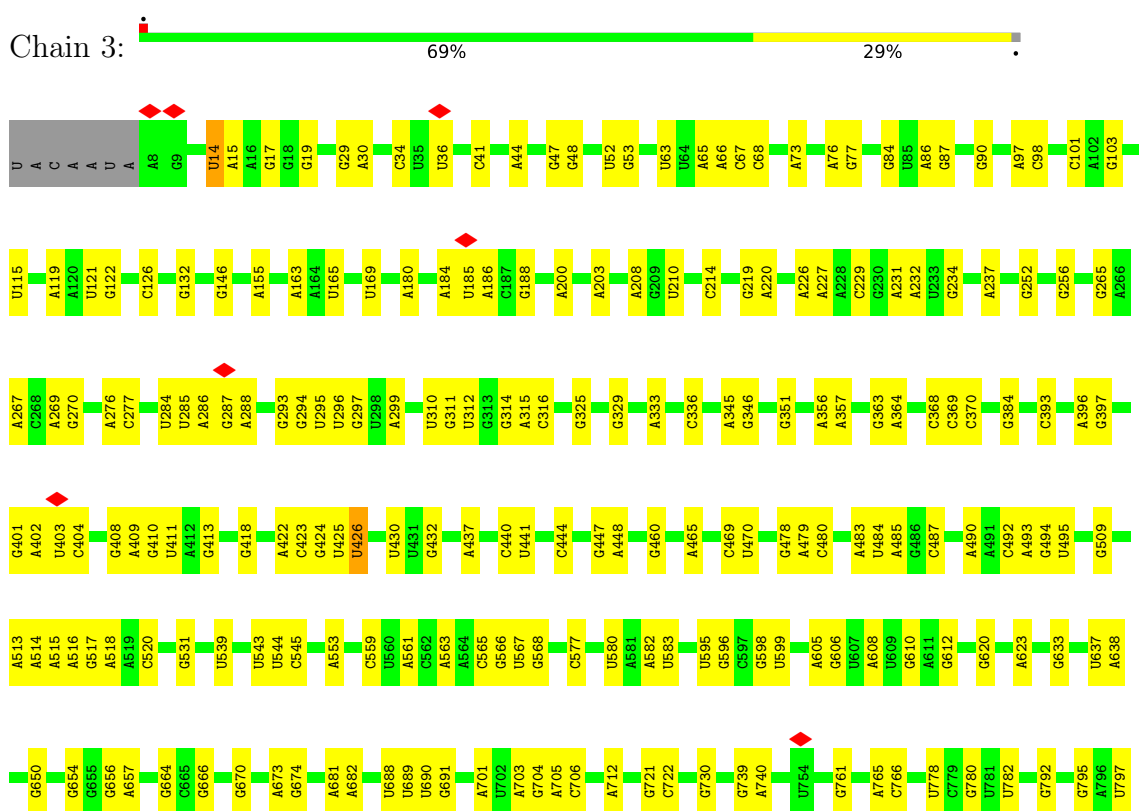
• Molecule 48: 50S ribosomal protein L32



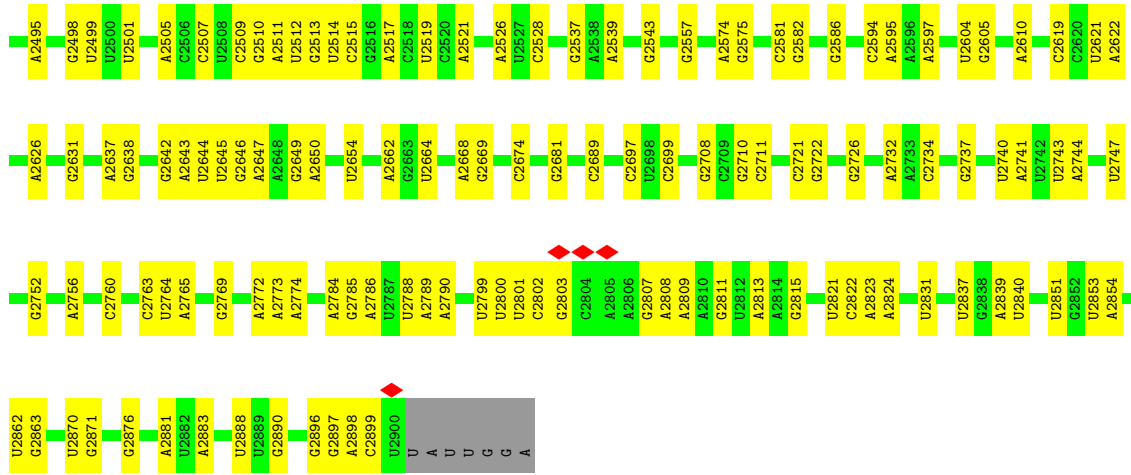
• Molecule 49: 50S ribosomal protein L33 1



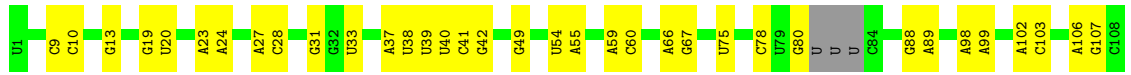
• Molecule 50: 23S ribosomal RNA



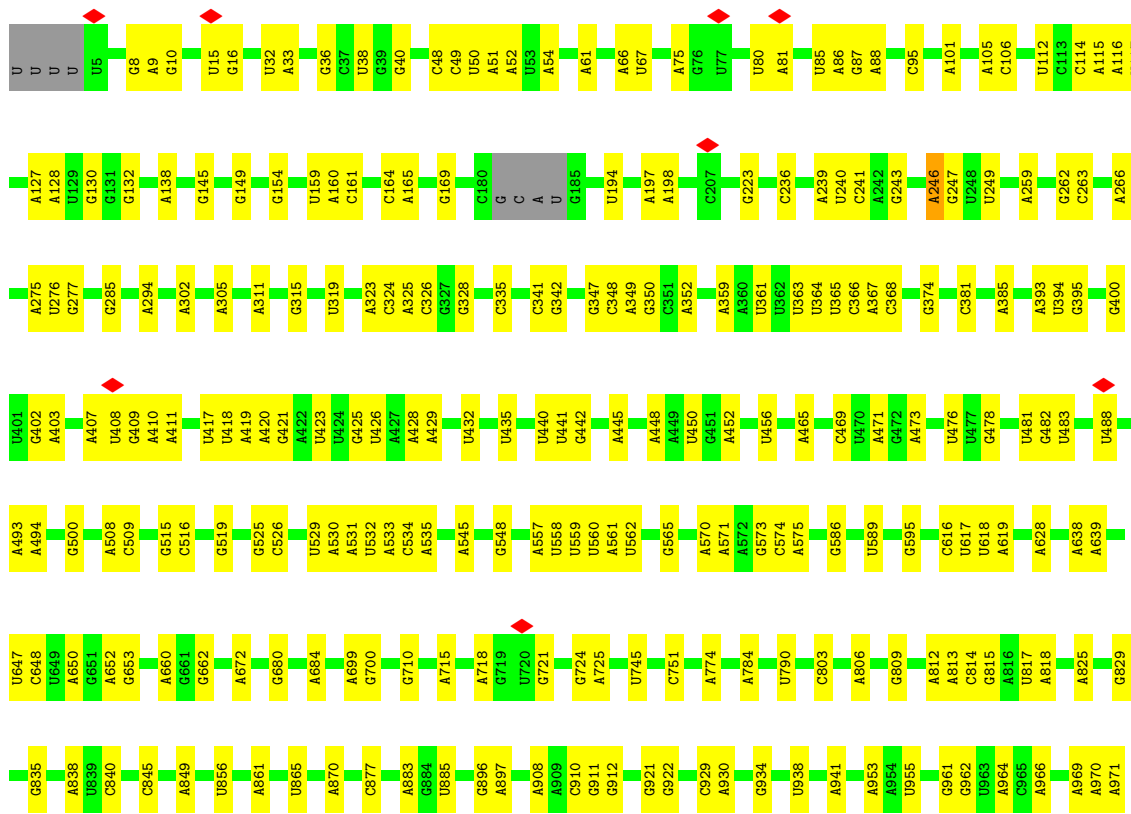
U2358	A2233	U2129	A2010	G1507	U1369	G1253	C1132	A1017	G914	G798
A2362	C2294	A2130	G2011	G1508	G1640	G1257	G1145	G1020	G917	A1799
A2366	A2235	A1891	A2020	A1513	U1372	C1258	A1146	A1027	G922	U808
U2380	G2246	G2135	G2028	A1520	C1378	A1259	G1147	U1027	A	G810
G2381	U2029	A1643	A1944	A1521	A1381	G1265	U1151	U1031	C	G811
G2391	A2037	A1648	A1762	A1522	A1388	G1266	U1154	A1032	U	G812
U2392	A2038	A1651	G1765	U1533	G1389	U1267	C1158	U1035	A	A816
G2393	G2040	A1652	A1767	A1534	G1389	U1268	U1165	A1048	G928	A817
A2396	C2041	U1655	G1768	A1535	A1393	A1271	G1166	U1049	G929	A818
G2397	G2046	A1660	A1770	A1542	G1402	A1277	U1167	A1048	C930	U819
C2410	U1922	A1669	A1791	U1546	A1406	G1278	A1168	A1052	U932	A823
C2411	A1923	G1668	A1792	G1547	U1407	U1279	A1169	C1053	A933	A824
U2414	A2055	A1669	U1784	A1548	G1408	G1280	C1170	U1054	C934	U825
A2415	G2058	A1675	U1790	U1549	A1412	G1282	U1176	A1055	U935	C826
G2422	G2062	G1676	A1791	U1550	A1413	A1283	A1177	A1056	G936	G827
G2423	G2063	U1679	A1792	A1558	A1420	G1286	A1186	G1057	A943	A828
C2424	A2067	A1680	A1804	U	U1422	A1282	U1186	U1068	A944	A837
U2431	G2068	G1681	U1805	G	U1422	A1282	A1186	G1068	A947	G840
C2432	A2069	C1682	G1806	A	A1423	U1293	A1191	G1089	A948	C841
A2433	C2070	A1688	C1807	A	U1424	G1294	U1192	A1072	C949	U842
G2436	C2071	A1688	C1808	G	U1425	A1295	A1195	U1095	U952	C847
G2437	U1950	A1689	A1809	U	C1426	G1296	A1195	A1081	U952	C847
A2438	G2076	C1690	A1810	G	U1431	U1297	A1202	A1082	U968	A854
U2439	G2087	A1694	A1816	A	A1431	A1298	G1203	A1083	A977	A855
A2440	U2089	G1695	U1821	C	A1435	G1301	A1204	A1092	A978	U862
A2441	G2100	A1699	G1822	A	C1436	C1302	A1204	A1092	G978	U863
A2442	A2100	A1702	A1823	G1570	U1444	U1303	A1208	U1096	A981	A864
A2443	G2106	A1703	U1823	G1571	U1445	U1304	A1210	U1096	G982	A865
U2449	A2107	C1704	A1826	U1579	U1448	A1308	U1211	G1098	U989	G866
G2453	C2108	A1704	U1827	G1580	U1448	A1314	C1212	C1099	G989	G871
G2454	U2110	G1708	A1828	A1585	A1455	A1314	G1215	U1100	G990	C872
G2455	U2111	C1709	A1828	U1586	C1456	C1317	U1215	U1101	U994	G873
U2457	U2112	A1717	G1831	U1587	A1457	A1322	G1217	A1102	A995	C880
A2458	A2113	G1718	A1836	A1589	G1463	A1322	G1218	G1103	A996	A881
A2459	C2114	G1719	C1837	A1592	U1466	A1328	U1219	A1104	C997	C882
C2460	A2115	C1720	A1842	U1593	U1467	U1329	U1229	A1105	U999	A887
A2477	U2116	U1727	G1842	G1594	U1467	U1341	U1234	G1106	U1000	A887
U2484	G2117	A1732	G1863	A1600	A1480	C1342	U1235	U1113	G1005	G894
U2485	A2118	A1732	A1863	A1603	U1481	C1349	U1240	C1114	U1006	G894
A2486	A2119	G1739	G1869	U1603	G1483	C1349	U1241	G1122	C1007	A899
U2487	A2123	U1740	U1872	U1612	U1486	U1354	G1242	A1123	A1008	U902
C2488	A2124	G1741	A1873	U1619	U1487	U1357	A1243	G1124	A1009	A903
G2492	A2126	G1747	G1876	U1619	U1487	U1357	A1250	G1125	G1010	C904
	G2127	U1748	C1877	A1493	A1493	U1360	G1252	G1126	A1011	A912
	U2009	U2009		U1494	U1494	U1361	C1252	A1130	A1012	U913
								A1131	A1016	



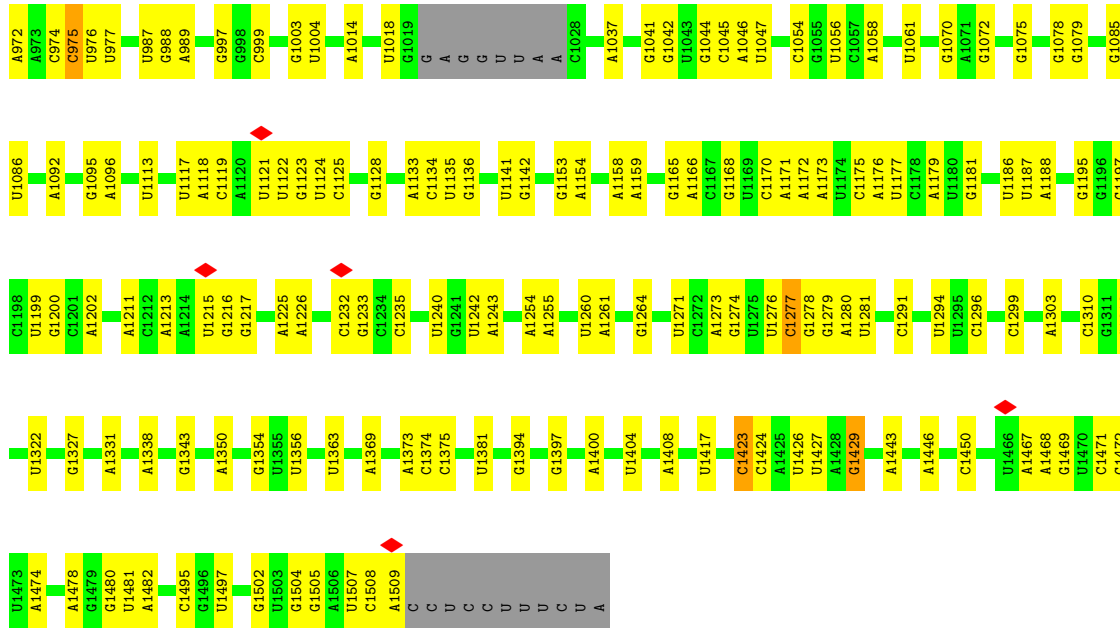
• Molecule 51: 5S ribosomal RNA



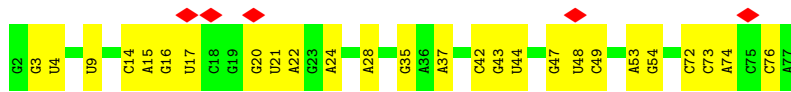
• Molecule 52: 16S ribosomal RNA



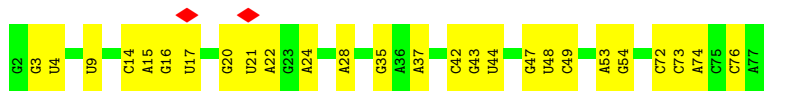




• Molecule 53: tRNA-Phe



• Molecule 53: tRNA-Phe



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	1449	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	1.387	Depositor
Minimum map value	-0.395	Depositor
Average map value	0.026	Depositor
Map value standard deviation	0.118	Depositor
Recommended contour level	0.47	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	0	0.24	0/383	0.41	0/504
2	1	0.23	0/484	0.44	0/637
3	2	0.22	0/306	0.48	0/401
4	A	0.26	0/1954	0.46	0/2642
5	B	0.24	0/1721	0.48	0/2323
6	C	0.25	0/1691	0.45	0/2267
7	D	0.24	0/1188	0.47	0/1593
8	E	0.24	0/1384	0.46	0/1867
9	F	0.25	0/1266	0.44	0/1700
10	G	0.25	0/1126	0.48	0/1517
11	H	0.25	0/1044	0.46	0/1395
12	I	0.25	0/820	0.48	0/1103
13	J	0.26	0/844	0.45	0/1136
14	K	0.29	0/1094	0.52	0/1468
15	L	0.24	0/962	0.45	0/1289
16	M	0.27	0/483	0.45	0/643
17	N	0.23	0/679	0.41	0/907
18	O	0.25	0/659	0.45	0/885
19	P	0.25	0/684	0.46	0/913
20	Q	0.25	0/545	0.43	0/730
21	R	0.25	0/698	0.49	0/936
22	S	0.23	0/631	0.42	0/838
23	T	0.22	0/475	0.40	0/621
24	a	0.24	0/2267	0.47	0/3044
25	b	0.26	0/1795	0.48	0/2412
26	c	0.25	0/1671	0.44	0/2246
27	d	0.25	0/1409	0.43	0/1894
28	e	0.25	0/1420	0.47	0/1912
29	f	0.26	0/1183	0.49	0/1587
30	g	0.36	0/969	0.56	0/1295
31	h	0.26	0/968	0.45	0/1298
32	i	0.24	0/1186	0.45	0/1592
33	j	0.25	0/953	0.48	0/1275
34	k	0.25	0/1170	0.47	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	l	0.25	0/1104	0.44	0/1481
36	m	0.25	0/973	0.45	0/1309
37	n	0.24	0/897	0.44	0/1198
38	o	0.25	0/948	0.48	0/1262
39	p	0.25	0/961	0.42	0/1278
40	q	0.26	0/828	0.49	0/1111
41	r	0.25	0/1077	0.44	0/1441
42	s	0.25	0/732	0.50	0/988
43	t	0.25	0/879	0.48	0/1165
44	u	0.26	0/665	0.49	0/884
45	v	0.25	0/519	0.50	0/695
46	w	0.23	0/826	0.44	0/1104
47	x	0.25	0/353	0.45	0/474
48	y	0.30	0/457	0.53	0/601
49	z	0.25	0/412	0.47	0/547
50	3	0.22	0/69073	0.82	39/107710 (0.0%)
51	4	0.19	0/2505	0.78	2/3902 (0.1%)
52	5	0.21	0/35768	0.80	21/55764 (0.0%)
53	7	0.22	0/1808	0.84	0/2817
53	8	0.22	0/1808	0.83	0/2817
All	All	0.23	0/158705	0.74	62/236977 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
21	R	0	1
35	l	0	1
41	r	0	1
42	s	0	1
All	All	0	4

There are no bond length outliers.

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	3	2187	C	N1-C2-O2	9.15	124.39	118.90
50	3	2187	C	N3-C2-O2	-8.63	115.86	121.90
50	3	559	C	N3-C2-O2	-8.19	116.17	121.90
50	3	1718	C	N3-C2-O2	-8.00	116.30	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	3	545	C	N1-C2-O2	7.85	123.61	118.90

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	R	25	GLN	Peptide
35	l	13	HIS	Peptide
41	r	9	ARG	Peptide
42	s	65	ILE	Peptide

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	44 (98%)	1 (2%)	0	100	100
2	1	57/59 (97%)	52 (91%)	5 (9%)	0	100	100
3	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
4	A	238/294 (81%)	213 (90%)	25 (10%)	0	100	100
5	B	213/273 (78%)	197 (92%)	16 (8%)	0	100	100
6	C	201/205 (98%)	189 (94%)	12 (6%)	0	100	100
7	D	151/219 (69%)	145 (96%)	6 (4%)	0	100	100
8	E	165/215 (77%)	143 (87%)	22 (13%)	0	100	100
9	F	152/155 (98%)	140 (92%)	12 (8%)	0	100	100
10	G	139/142 (98%)	123 (88%)	16 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	H	126/132 (96%)	113 (90%)	13 (10%)	0	100	100
12	I	99/108 (92%)	94 (95%)	5 (5%)	0	100	100
13	J	112/121 (93%)	102 (91%)	10 (9%)	0	100	100
14	K	134/139 (96%)	121 (90%)	13 (10%)	0	100	100
15	L	116/124 (94%)	103 (89%)	13 (11%)	0	100	100
16	M	58/61 (95%)	49 (84%)	9 (16%)	0	100	100
17	N	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
18	O	78/94 (83%)	72 (92%)	6 (8%)	0	100	100
19	P	81/85 (95%)	78 (96%)	3 (4%)	0	100	100
20	Q	63/104 (61%)	53 (84%)	10 (16%)	0	100	100
21	R	82/87 (94%)	67 (82%)	15 (18%)	0	100	100
22	S	75/87 (86%)	75 (100%)	0	0	100	100
23	T	51/60 (85%)	50 (98%)	1 (2%)	0	100	100
24	a	283/287 (99%)	247 (87%)	36 (13%)	0	100	100
25	b	227/287 (79%)	207 (91%)	20 (9%)	0	100	100
26	c	208/212 (98%)	202 (97%)	6 (3%)	0	100	100
27	d	173/180 (96%)	168 (97%)	5 (3%)	0	100	100
28	e	174/184 (95%)	163 (94%)	11 (6%)	0	100	100
29	f	143/149 (96%)	131 (92%)	12 (8%)	0	100	100
30	g	124/161 (77%)	113 (91%)	11 (9%)	0	100	100
31	h	126/137 (92%)	117 (93%)	9 (7%)	0	100	100
32	i	142/146 (97%)	134 (94%)	8 (6%)	0	100	100
33	j	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
34	k	146/151 (97%)	133 (91%)	13 (9%)	0	100	100
35	l	134/139 (96%)	131 (98%)	2 (2%)	1 (1%)	22	63
36	m	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
37	n	108/116 (93%)	101 (94%)	7 (6%)	0	100	100
38	o	113/119 (95%)	101 (89%)	12 (11%)	0	100	100
39	p	112/127 (88%)	107 (96%)	5 (4%)	0	100	100
40	q	97/100 (97%)	87 (90%)	10 (10%)	0	100	100
41	r	137/159 (86%)	130 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	s	90/237 (38%)	84 (93%)	6 (7%)	0	100	100
43	t	109/111 (98%)	98 (90%)	11 (10%)	0	100	100
44	u	84/104 (81%)	80 (95%)	4 (5%)	0	100	100
45	v	61/65 (94%)	56 (92%)	5 (8%)	0	100	100
46	w	96/111 (86%)	93 (97%)	3 (3%)	0	100	100
47	x	42/97 (43%)	37 (88%)	5 (12%)	0	100	100
48	y	54/57 (95%)	49 (91%)	4 (7%)	1 (2%)	8	38
49	z	48/53 (91%)	46 (96%)	2 (4%)	0	100	100
All	All	5820/6670 (87%)	5378 (92%)	440 (8%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
48	y	52	ARG
35	l	14	ASN

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	34 (97%)	1 (3%)	42	64
4	A	212/262 (81%)	211 (100%)	1 (0%)	88	93
5	B	180/232 (78%)	178 (99%)	2 (1%)	73	84
6	C	181/183 (99%)	178 (98%)	3 (2%)	60	78
7	D	123/178 (69%)	123 (100%)	0	100	100
8	E	150/196 (76%)	149 (99%)	1 (1%)	84	90
9	F	131/132 (99%)	130 (99%)	1 (1%)	81	89
10	G	123/124 (99%)	123 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	H	111/115 (96%)	108 (97%)	3 (3%)	44	65
12	I	95/99 (96%)	93 (98%)	2 (2%)	53	72
13	J	91/97 (94%)	89 (98%)	2 (2%)	52	71
14	K	117/120 (98%)	113 (97%)	4 (3%)	37	60
15	L	100/105 (95%)	100 (100%)	0	100	100
16	M	47/48 (98%)	47 (100%)	0	100	100
17	N	76/78 (97%)	76 (100%)	0	100	100
18	O	69/82 (84%)	68 (99%)	1 (1%)	67	80
19	P	73/75 (97%)	73 (100%)	0	100	100
20	Q	56/94 (60%)	56 (100%)	0	100	100
21	R	74/77 (96%)	74 (100%)	0	100	100
22	S	70/77 (91%)	70 (100%)	0	100	100
23	T	49/56 (88%)	49 (100%)	0	100	100
24	a	241/243 (99%)	238 (99%)	3 (1%)	71	83
25	b	186/233 (80%)	185 (100%)	1 (0%)	88	93
26	c	182/184 (99%)	181 (100%)	1 (0%)	88	93
27	d	150/154 (97%)	150 (100%)	0	100	100
28	e	153/159 (96%)	153 (100%)	0	100	100
29	f	123/134 (92%)	123 (100%)	0	100	100
30	g	101/129 (78%)	88 (87%)	13 (13%)	4	18
31	h	102/110 (93%)	102 (100%)	0	100	100
32	i	126/128 (98%)	125 (99%)	1 (1%)	81	89
33	j	103/103 (100%)	103 (100%)	0	100	100
34	k	123/126 (98%)	122 (99%)	1 (1%)	81	89
35	l	113/115 (98%)	113 (100%)	0	100	100
36	m	105/109 (96%)	105 (100%)	0	100	100
37	n	96/99 (97%)	96 (100%)	0	100	100
38	o	101/105 (96%)	100 (99%)	1 (1%)	76	86
39	p	100/108 (93%)	100 (100%)	0	100	100
40	q	90/91 (99%)	89 (99%)	1 (1%)	73	84
41	r	116/132 (88%)	116 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	s	82/208 (39%)	82 (100%)	0	100	100
43	t	96/96 (100%)	96 (100%)	0	100	100
44	u	69/85 (81%)	69 (100%)	0	100	100
45	v	58/60 (97%)	57 (98%)	1 (2%)	60	78
46	w	87/98 (89%)	85 (98%)	2 (2%)	50	70
47	x	41/86 (48%)	41 (100%)	0	100	100
48	y	48/49 (98%)	43 (90%)	5 (10%)	7	24
49	z	47/50 (94%)	44 (94%)	3 (6%)	17	42
All	All	5093/5751 (89%)	5039 (99%)	54 (1%)	74	84

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	g	30	THR
30	g	88	GLU
48	y	51	LEU
30	g	32	MET
30	g	52	LYS

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

Mol	Chain	Res	Type
36	m	21	GLN
41	r	57	ASN
46	w	66	GLN
41	r	61	ASN
41	r	7	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	829 (28%)	31 (1%)
51	4	103/108 (95%)	33 (32%)	2 (1%)
52	5	1490/1520 (98%)	393 (26%)	6 (0%)
53	7	75/76 (98%)	25 (33%)	1 (1%)
53	8	75/76 (98%)	25 (33%)	1 (1%)
All	All	4618/4687 (98%)	1305 (28%)	41 (0%)

5 of 1305 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	14	U
50	3	15	A
50	3	17	G
50	3	29	G
50	3	30	A

5 of 41 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	3	2823	A
52	5	425	G
50	3	2862	U
51	4	59	A
52	5	1133	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.

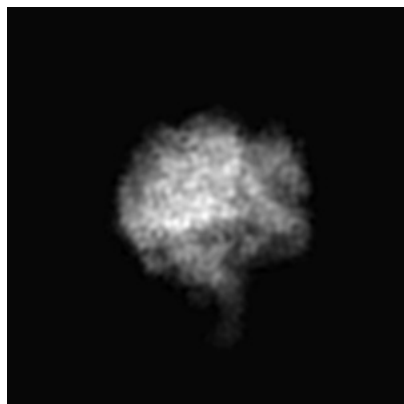
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13278. These allow visual inspection of the internal detail of the map and identification of artifacts.

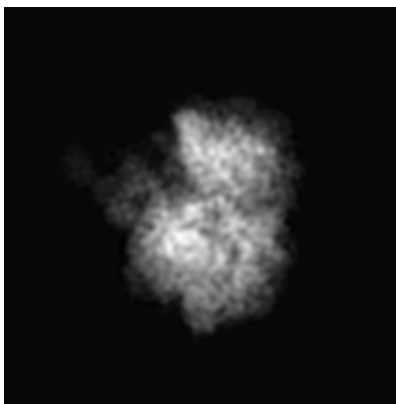
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

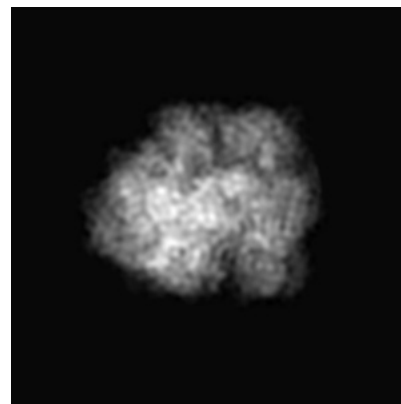
#### 6.1.1 Primary map



X

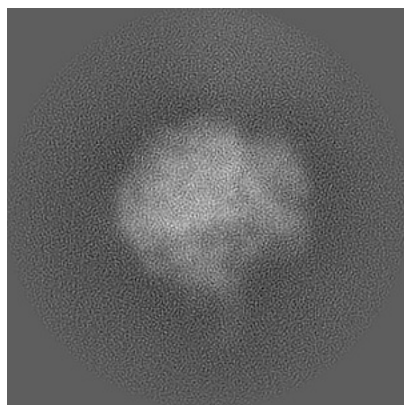


Y

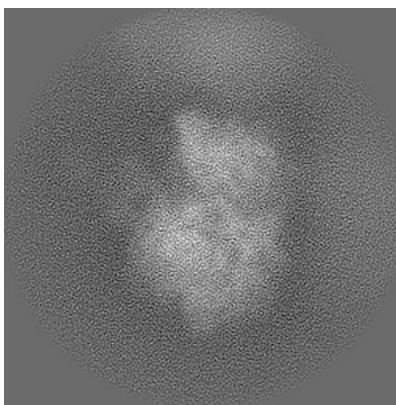


Z

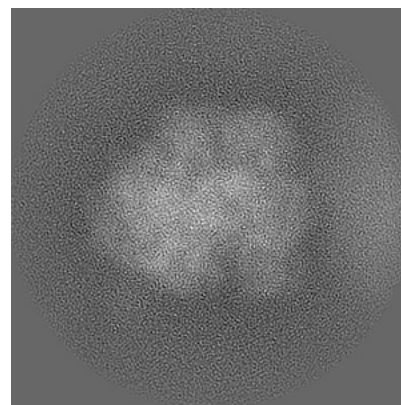
#### 6.1.2 Raw map



X



Y

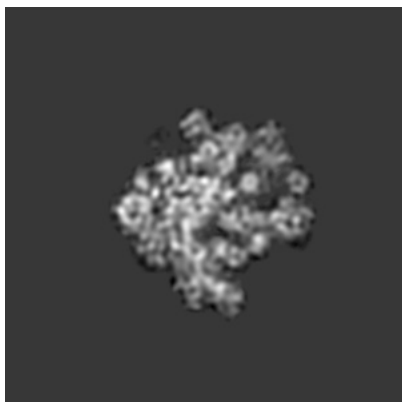


Z

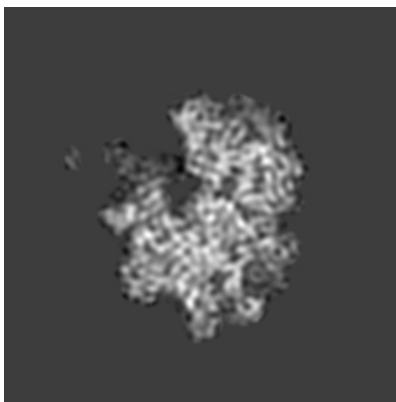
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

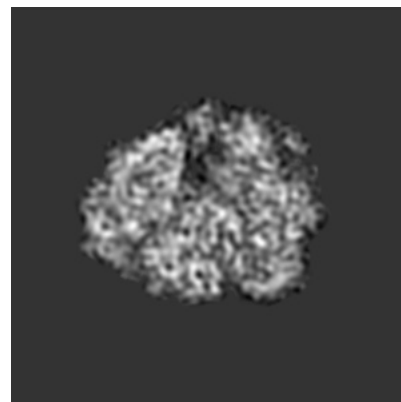
### 6.2.1 Primary map



X Index: 128

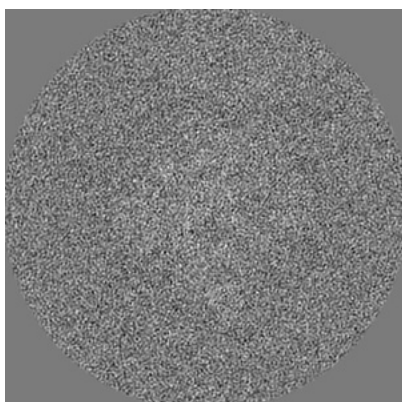


Y Index: 128

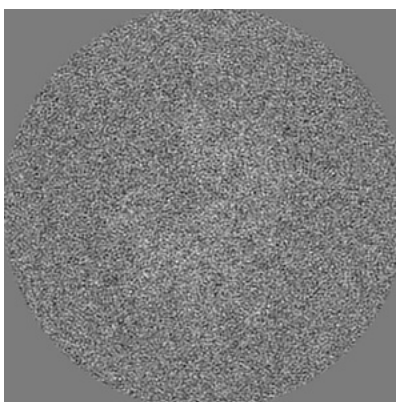


Z Index: 128

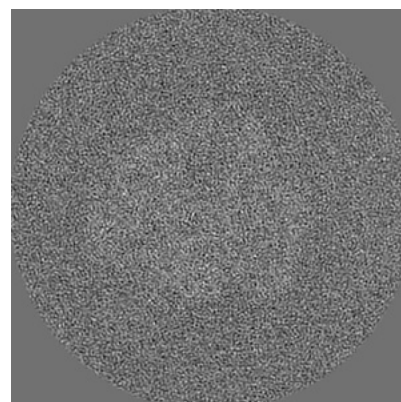
### 6.2.2 Raw map



X Index: 128



Y Index: 128

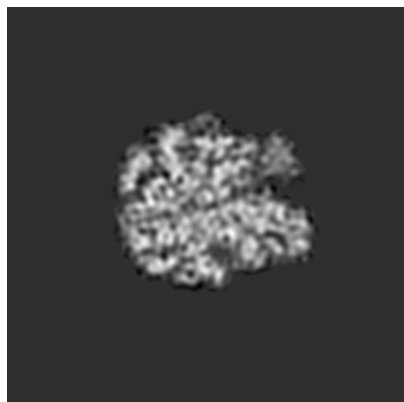


Z Index: 128

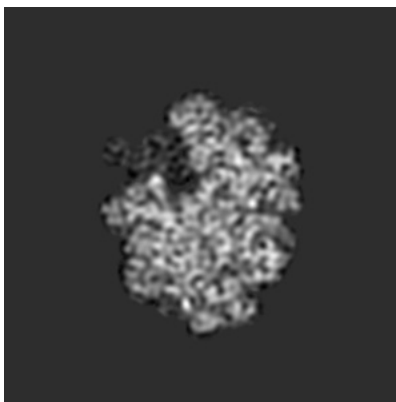
The images above show central slices of the map in three orthogonal directions.

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

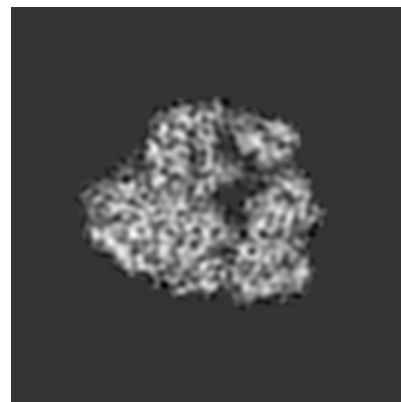
### 6.3.1 Primary map



X Index: 105

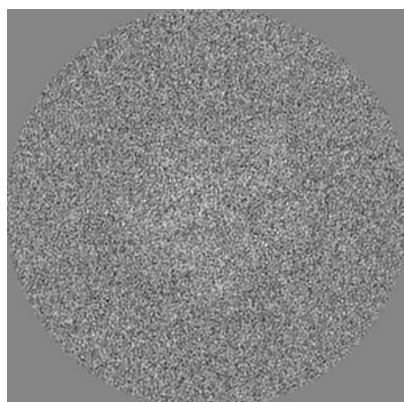


Y Index: 121

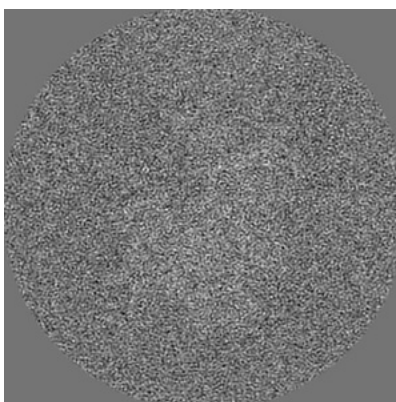


Z Index: 120

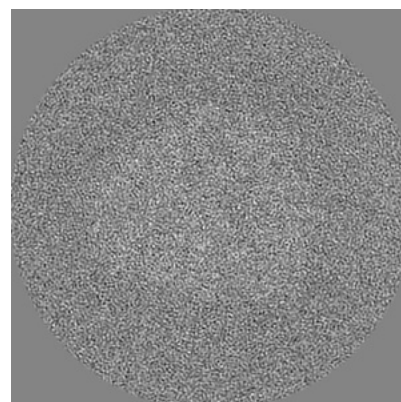
### 6.3.2 Raw map



X Index: 121



Y Index: 129



Z Index: 125

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

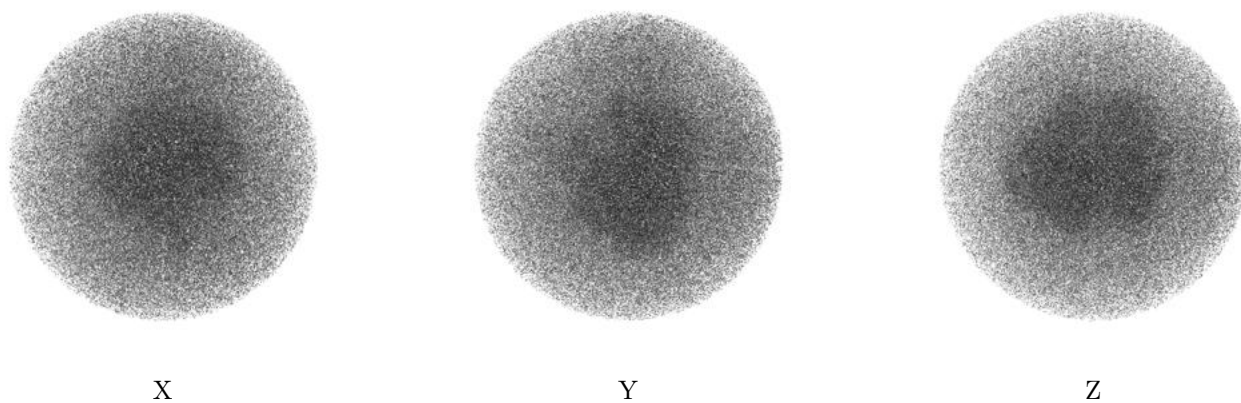
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.47. 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.



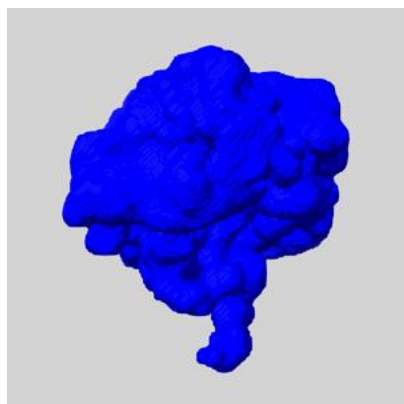
## 6.5 Mask visualisation [i](#)

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

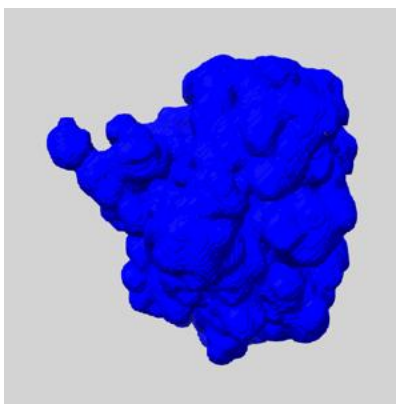
A mask typically either:

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

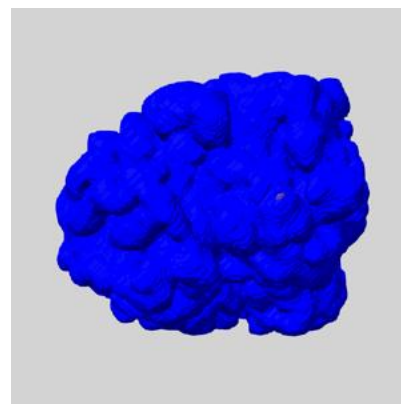
### 6.5.1 emd\_13278\_msk\_1.map [i](#)



X



Y

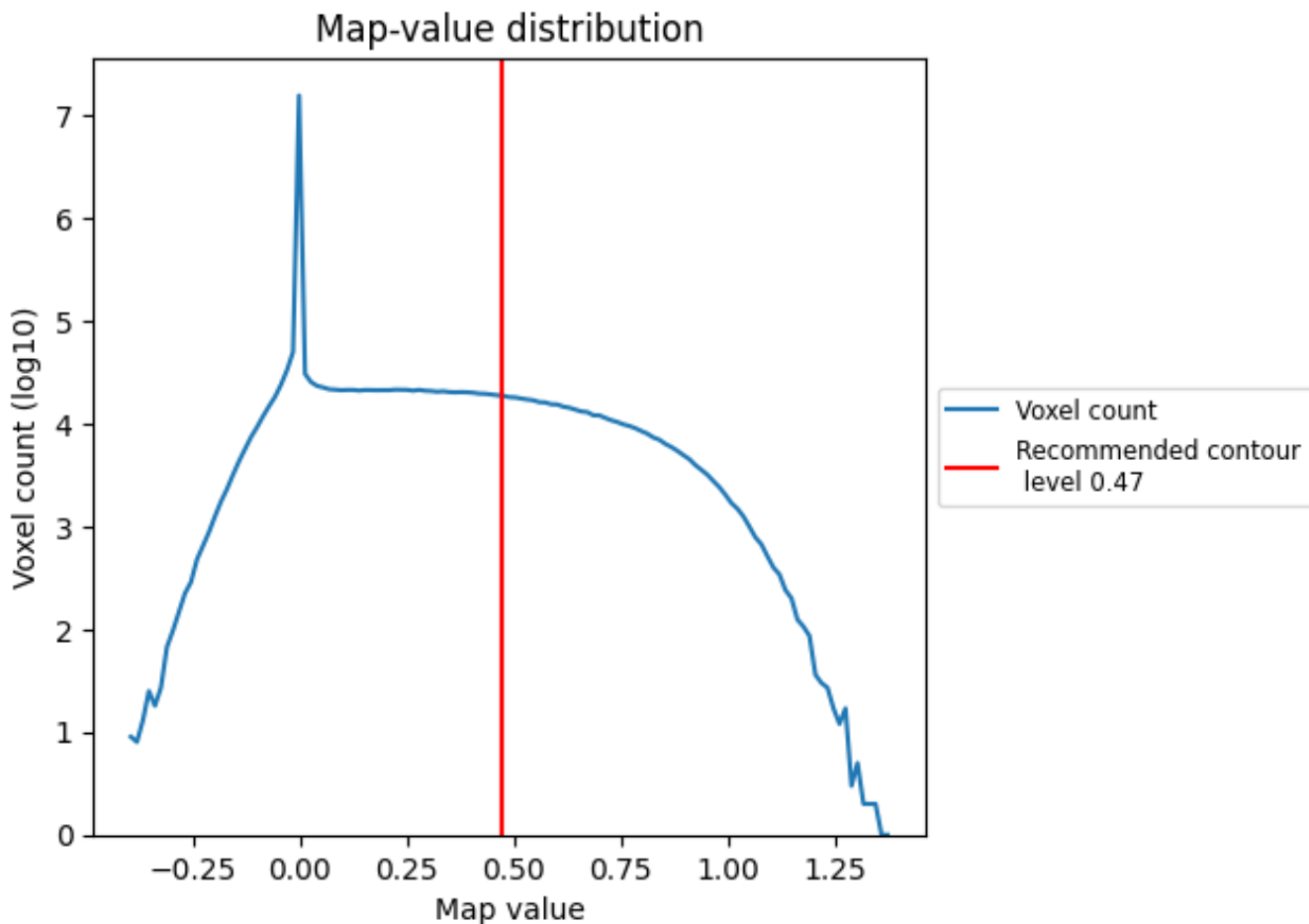


Z

## 7 Map analysis [i](#)

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

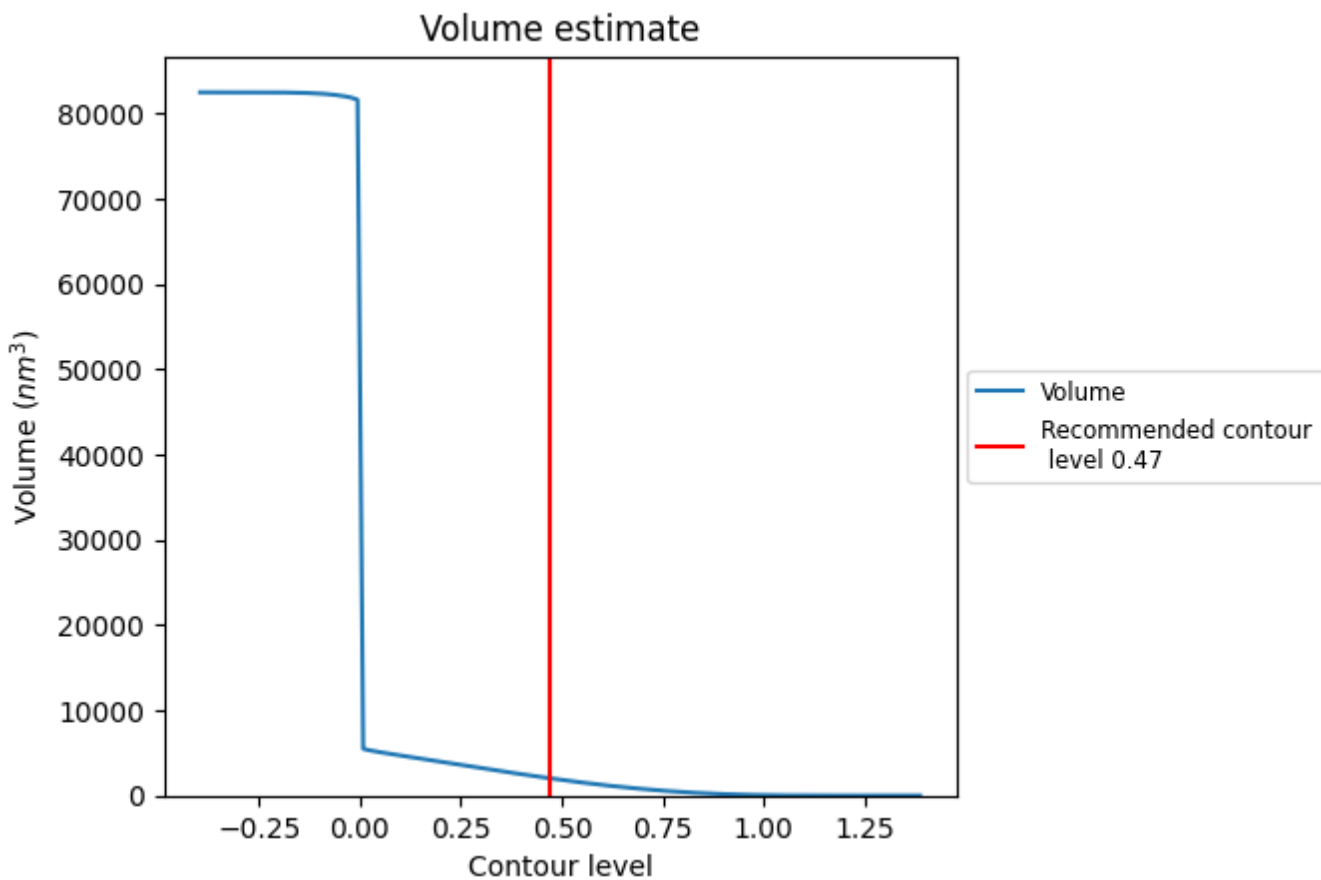
### 7.1 Map-value distribution [i](#)



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.



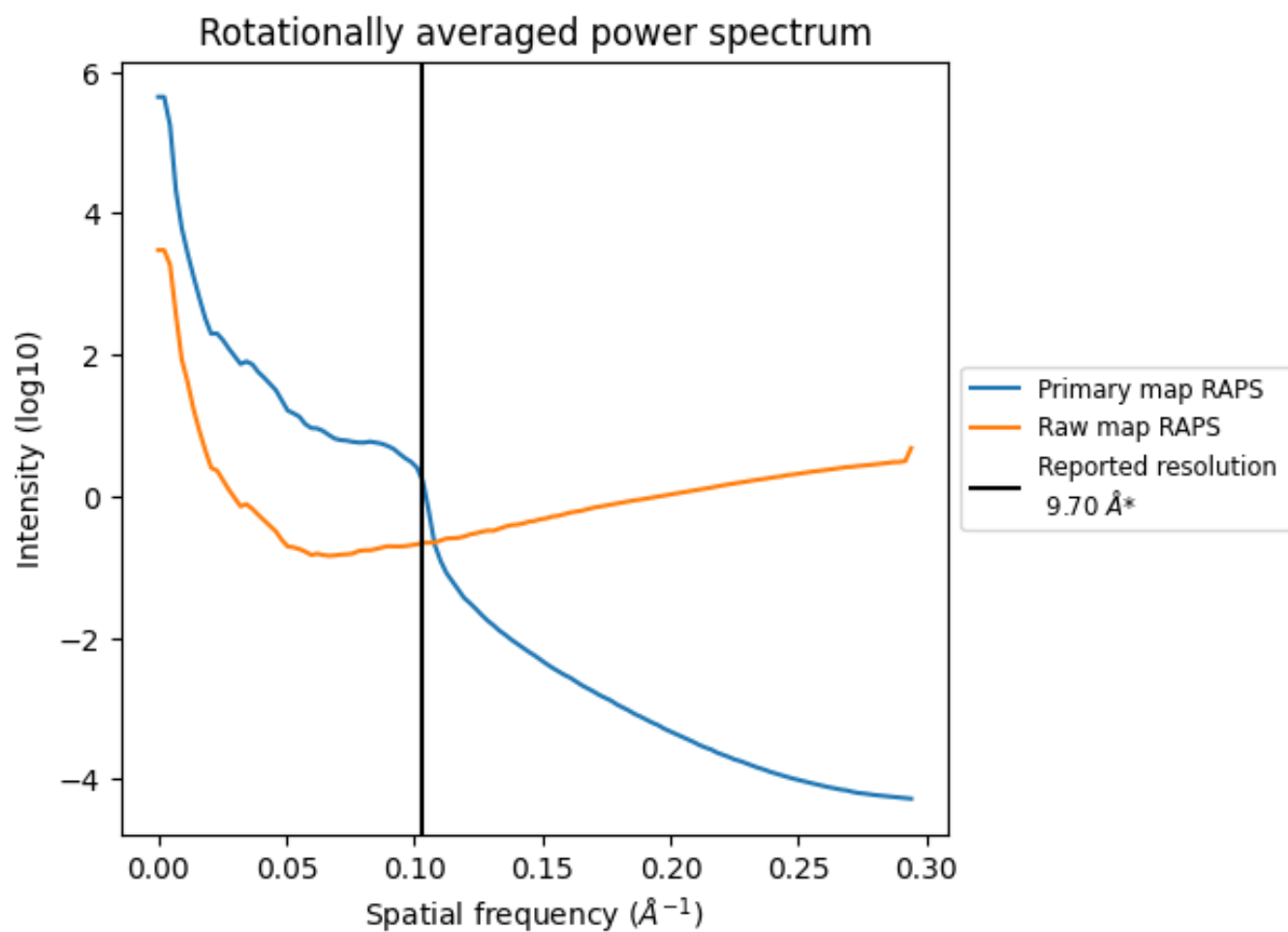
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2033 nm<sup>3</sup>; this corresponds to an approximate mass of 1837 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](#)

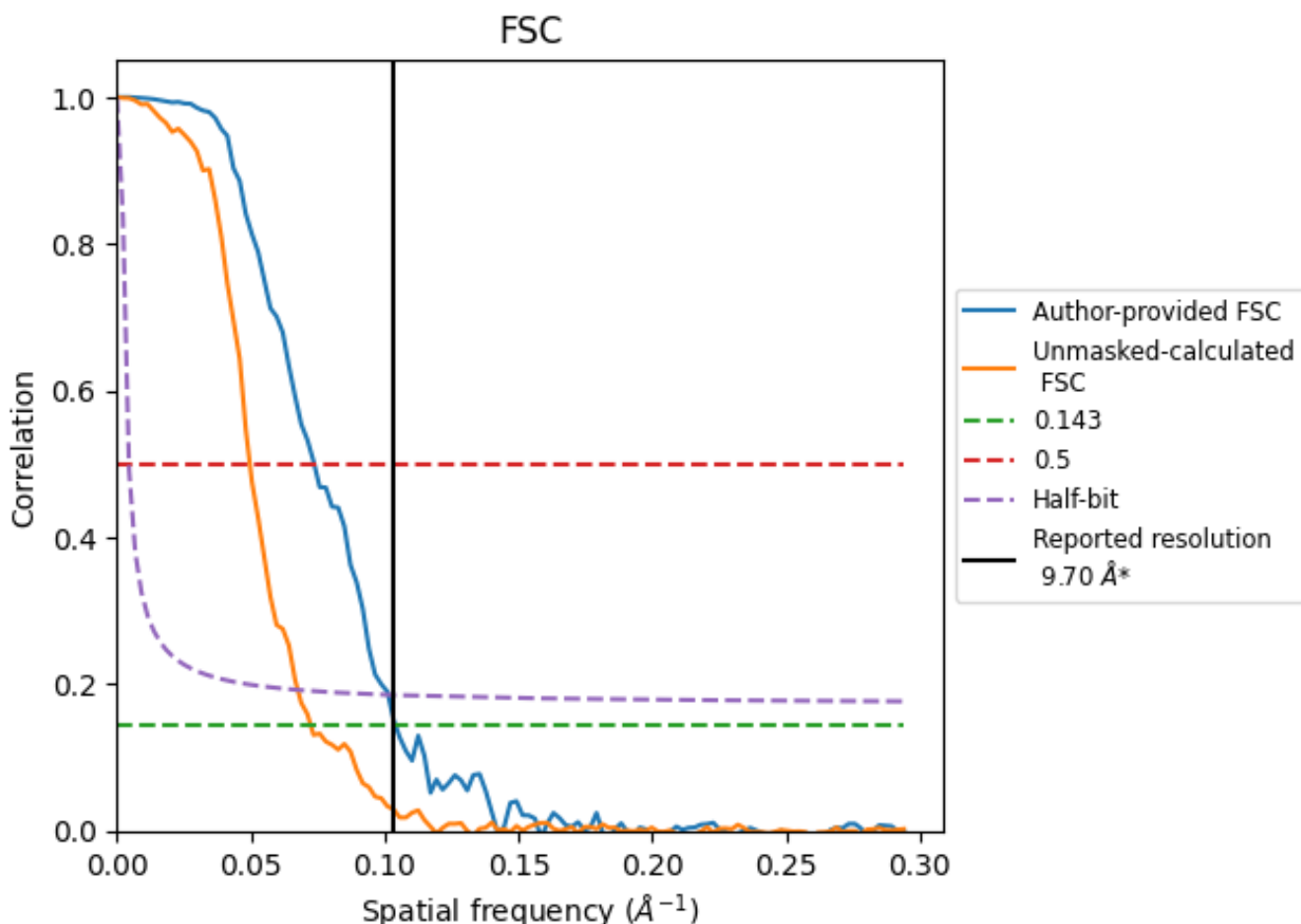


\*Reported resolution corresponds to spatial frequency of 0.103 Å<sup>-1</sup>

## 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 0.103 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

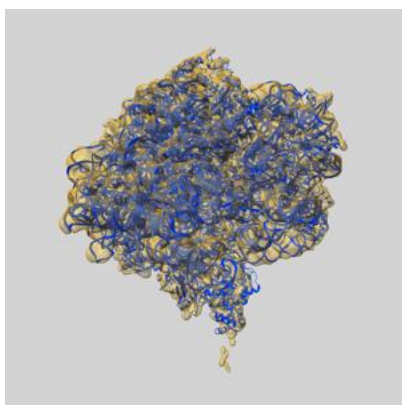
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.70	-	-
Author-provided FSC curve	9.61	13.57	9.87
Unmasked-calculated*	13.79	20.12	14.79

\*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 13.79 differs from the reported value 9.7 by more than 10 %

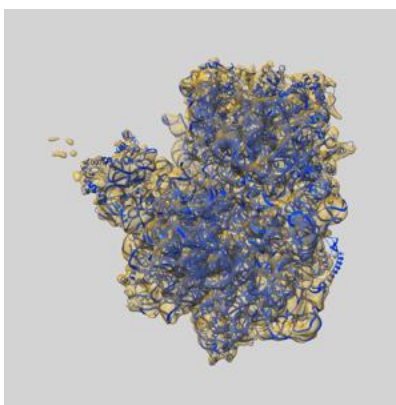
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13278 and PDB model 7PAN. Per-residue inclusion information can be found in section 3 on page 13.

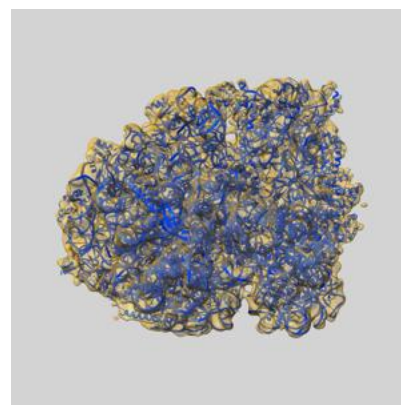
### 9.1 Map-model overlay [i](#)



X



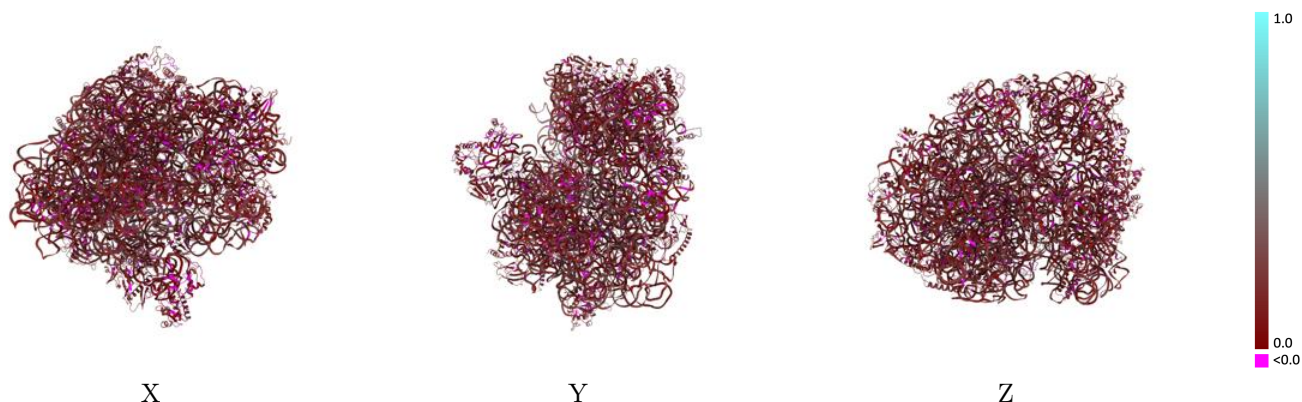
Y



Z

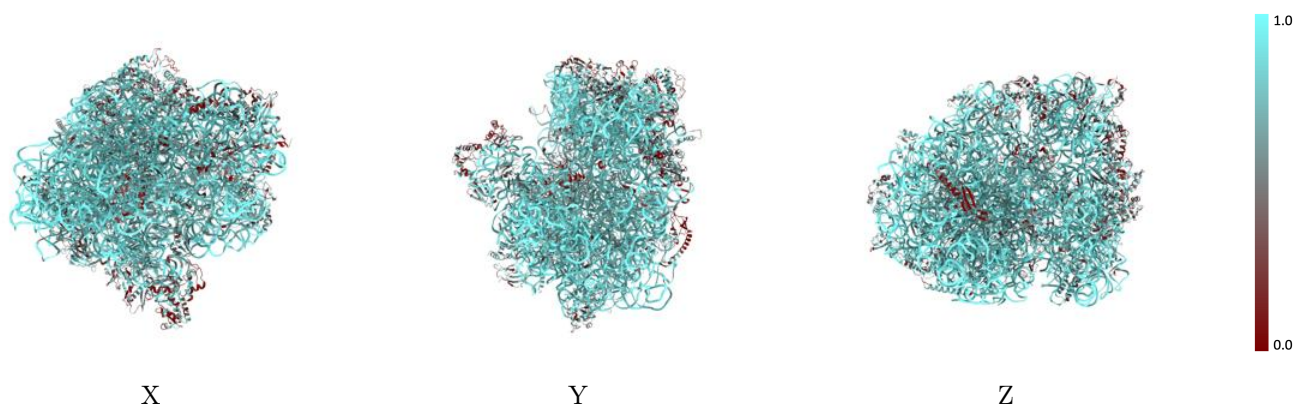
The images above show the 3D surface view of the map at the recommended contour level 0.47 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



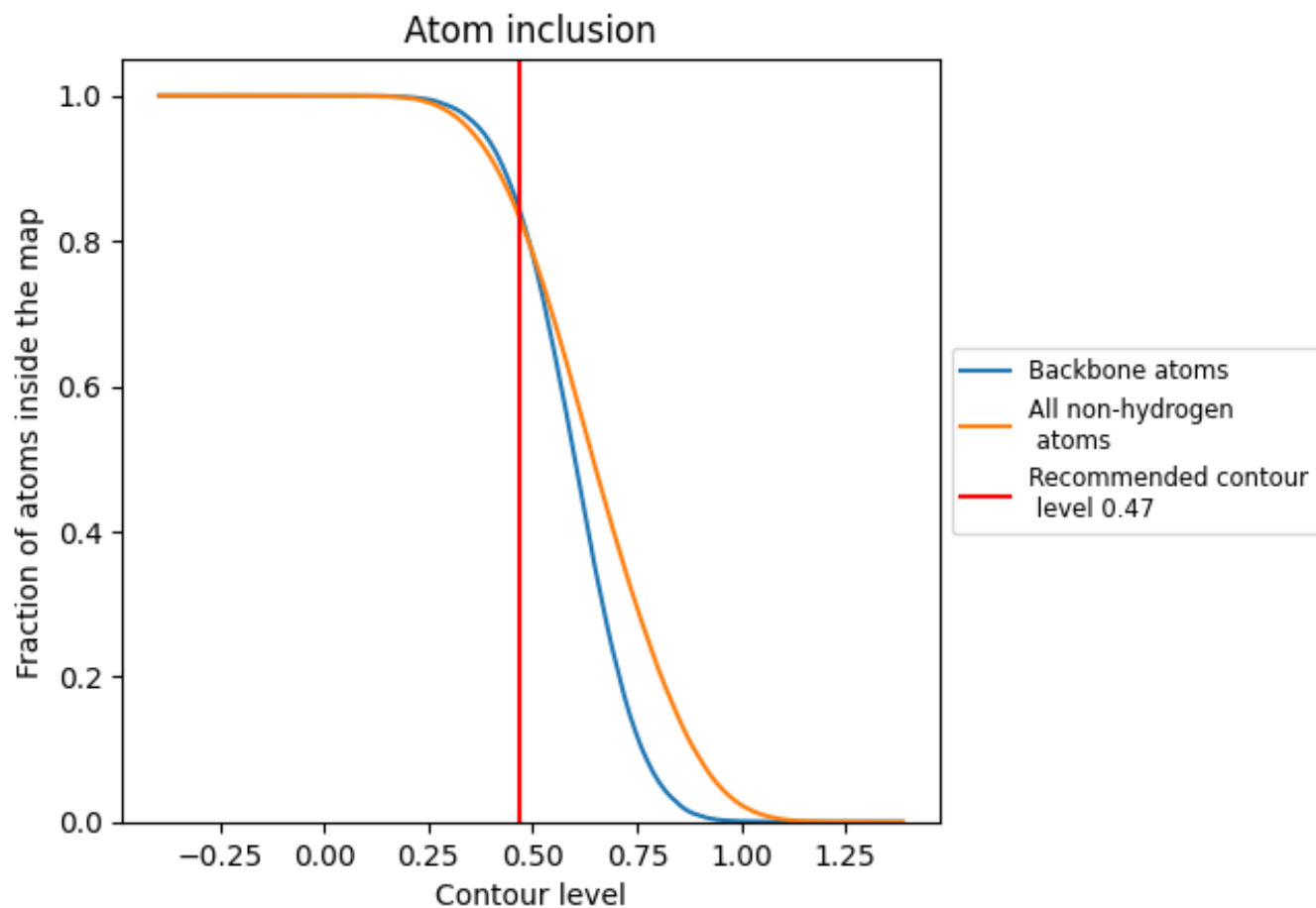
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.47).







































































## 9.4 Atom inclusion [i](#)

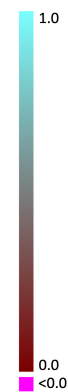


At the recommended contour level, 84% of all backbone atoms, 83% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.47) and Q-score for the entire model and for each chain.









































Chain	Atom inclusion	Q-score
All	 0.8294	 0.1470
0	 0.7534	 0.1220
1	 0.7060	 0.1230
2	 0.6453	 0.0820
3	 0.9401	 0.1570
4	 0.9437	 0.1640
5	 0.9355	 0.1570
7	 0.7491	 0.1370
8	 0.8826	 0.1570
A	 0.5061	 0.1420
B	 0.5405	 0.1360
C	 0.5638	 0.1210
D	 0.5659	 0.1190
E	 0.5187	 0.1510
F	 0.5091	 0.1280
G	 0.6040	 0.1200
H	 0.5604	 0.1100
I	 0.5384	 0.1290
J	 0.5924	 0.1180
K	 0.6303	 0.1150
L	 0.5991	 0.1220
M	 0.6374	 0.0800
N	 0.6601	 0.1710
O	 0.6693	 0.1390
P	 0.6712	 0.1360
Q	 0.6667	 0.1260
R	 0.6284	 0.0970
S	 0.7115	 0.1280
T	 0.6496	 0.1670
a	 0.6753	 0.0960
b	 0.6578	 0.1160
c	 0.6794	 0.1350
d	 0.5596	 0.1310
e	 0.5196	 0.1290
f	 0.2315	 0.1430



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Chain	Atom inclusion	Q-score
g	 0.4316	 0.1160
h	 0.2508	 0.0830
i	 0.7379	 0.1360
j	 0.5924	 0.1140
k	 0.7105	 0.1120
l	 0.6758	 0.1180
m	 0.6838	 0.1210
n	 0.7105	 0.1370
o	 0.5719	 0.1390
p	 0.7574	 0.1250
q	 0.6471	 0.1450
r	 0.6759	 0.1330
s	 0.6164	 0.1360
t	 0.5923	 0.1150
u	 0.7531	 0.1110
v	 0.6788	 0.1040
w	 0.7041	 0.1740
x	 0.5044	 0.1390
y	 0.7005	 0.1110
z	 0.7506	 0.1370