



wwPDB EM Validation Summary Report ⓘ

Oct 11, 2022 – 05:26 pm BST

PDB ID : 7PHC
EMDB ID : EMD-13413
Title : 70S ribosome with A*- and P/E-site tRNAs in chloramphenicol-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-16
Resolution : 9.90 Å (reported)
Based on initial models : 7OOC, 7OOD, 4V7C

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

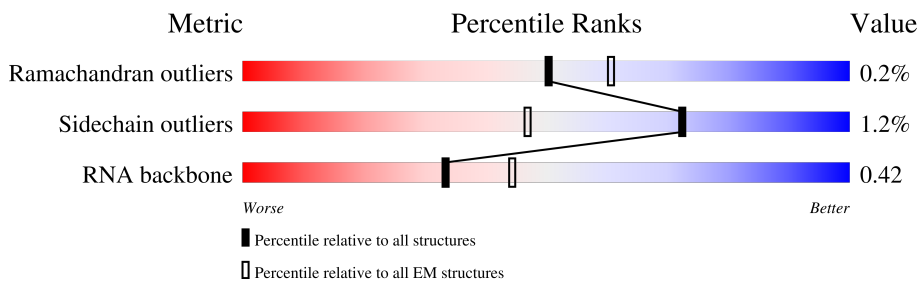
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 9.90 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	0	48	
2	1	59	
3	2	37	
4	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	44% 99%
10	G	142	19% 99%
11	H	132	38% 96%
12	I	108	19% 93% 6%
13	J	121	28% 93% 6%
14	K	139	16% 96%
15	L	124	35% 94% 5%
16	M	61	10% 97%
17	N	86	13% 94%
18	O	94	5% 84% 15%
19	P	85	16% 95%
20	Q	104	10% 62% 38%
21	R	87	14% 95%
22	S	87	1% 89% 11%
23	T	60	12% 88% 12%
24	a	287	9% 99%
25	b	287	5% 78% 20%
26	c	212	10% 99%
27	d	180	19% 97%
28	e	184	18% 96%
29	f	149	66% 95%
30	g	161	13% 68% 7% 22%
31	h	137	37% 93% 7%
32	i	146	10% 99%
33	j	122	15% 99%

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Mol	Chain	Length	Quality of chain
34	k	151	7% 97%
35	l	139	9% 97%
36	m	124	8% 96%
37	n	116	5% 97%
38	o	119	10% 97%
39	p	127	89% 10%
40	q	100	98%
41	r	159	5% 87% 13%
42	s	237	39% 61%
43	t	111	16% 100%
44	u	104	9% 83% 17%
45	v	65	6% 95%
46	w	111	11% 88% 10%
47	x	97	11% 45% 55%
48	y	57	12% 89% 7%
49	z	53	92% 6%
50	3	2907	65% 34%
51	4	108	61% 33%
52	5	1520	67% 31%
53	6	76	20% 62% 36%
53	8	76	38% 62% 36%

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 146142 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
14	K	136	Total	C	N	O	S	0	0
			1076	680	213	181	2		

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O		
28	e	176	1396	899	247	250	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- 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		

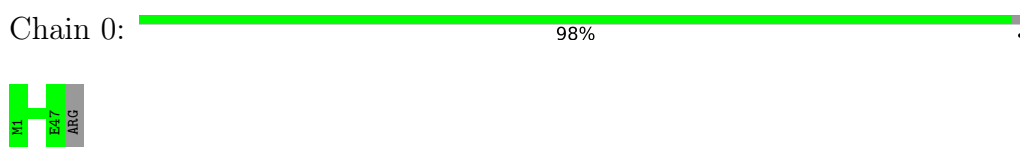
- Molecule 53 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	6	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		

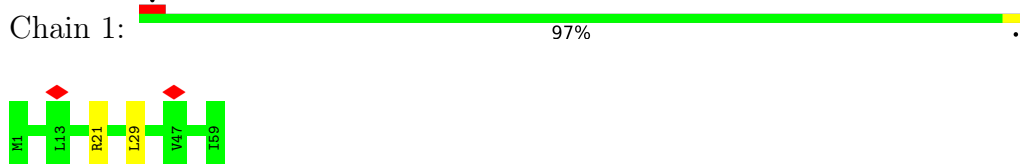
3 Residue-property plots [i](#)

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.

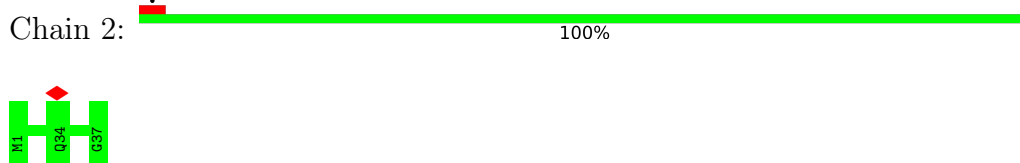
- Molecule 1: 50S ribosomal protein L34



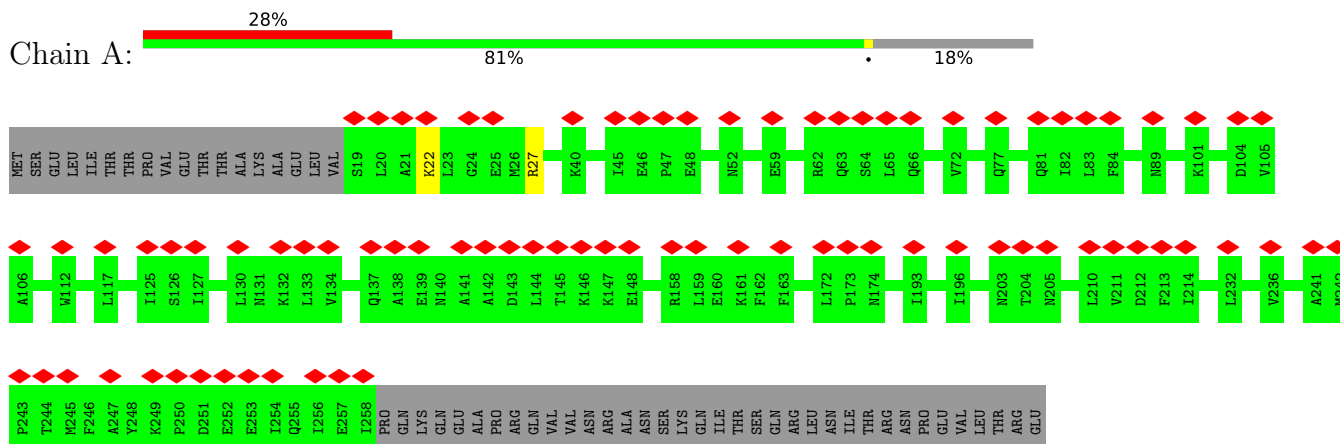
- Molecule 2: 50S ribosomal protein L35



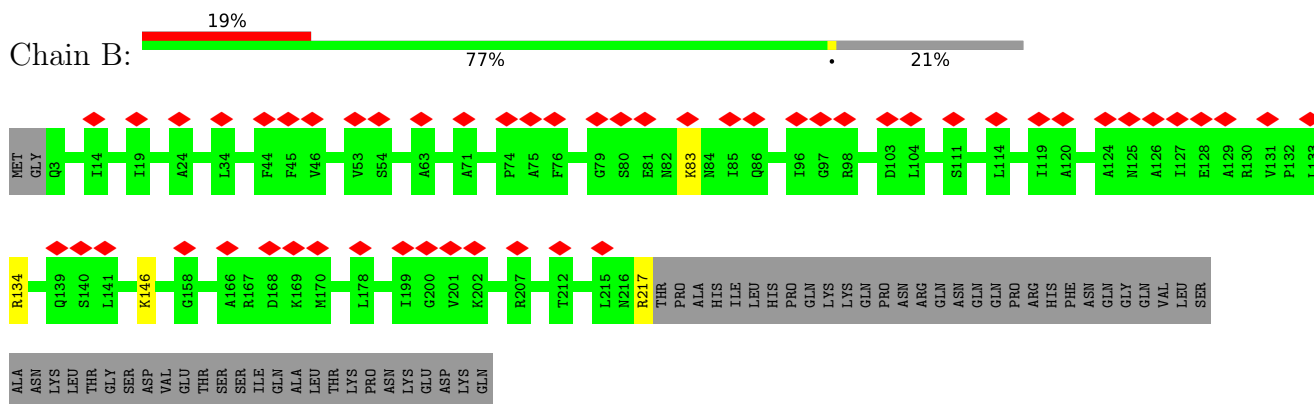
- Molecule 3: 50S ribosomal protein L36



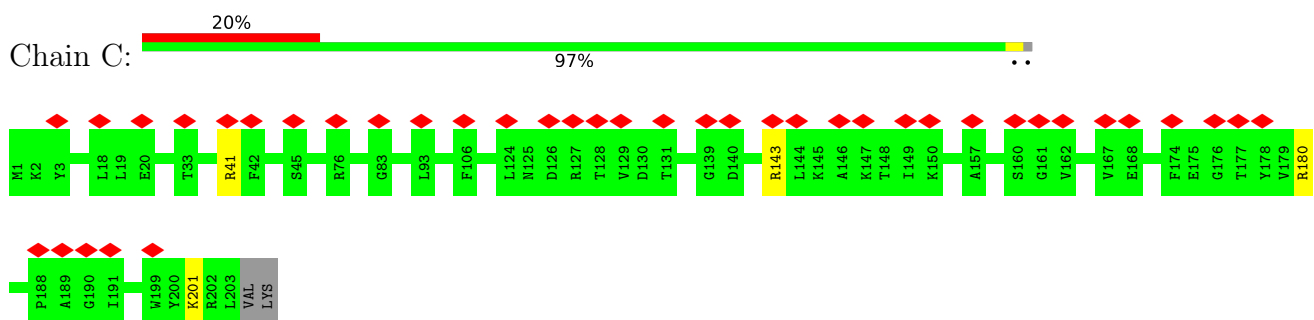
- Molecule 4: 30S ribosomal protein S2



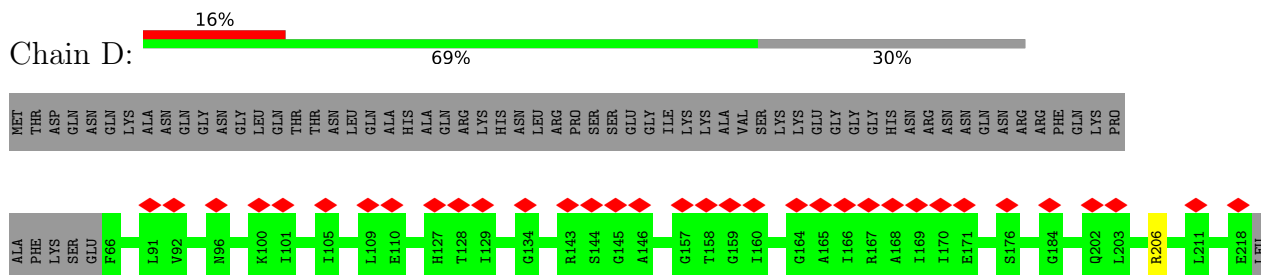
- Molecule 5: 30S ribosomal protein S3



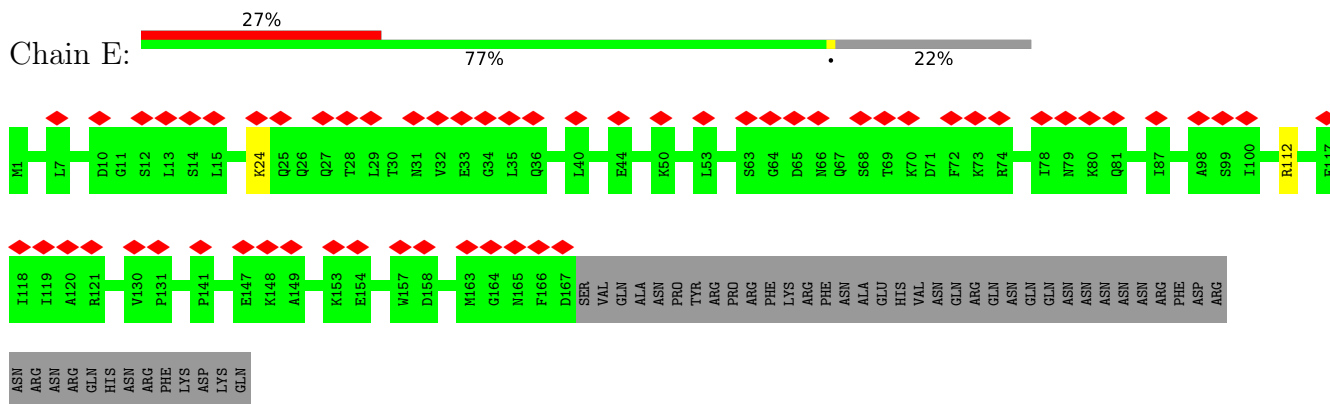
- Molecule 6: 30S ribosomal protein S4



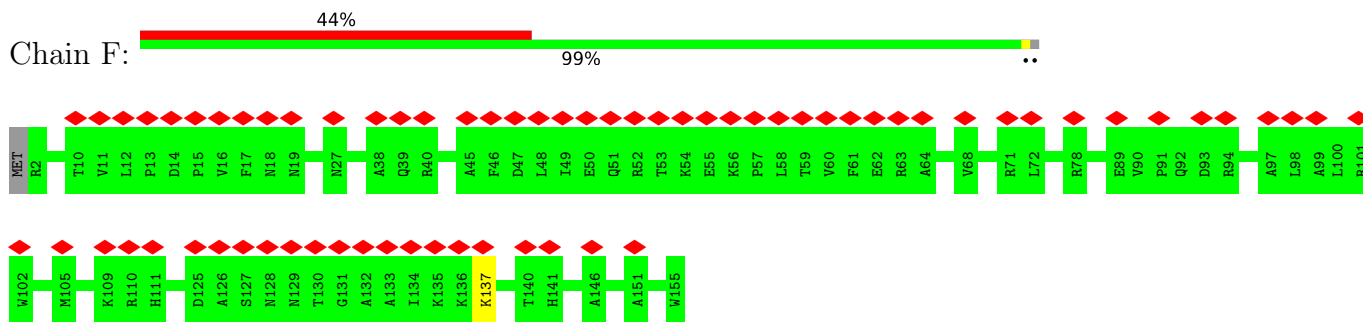
- Molecule 7: 30S ribosomal protein S5



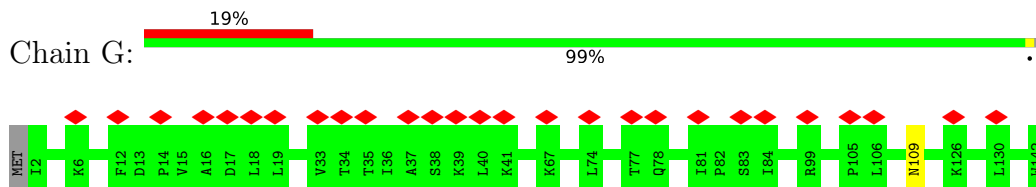
- Molecule 8: 30S ribosomal protein S6



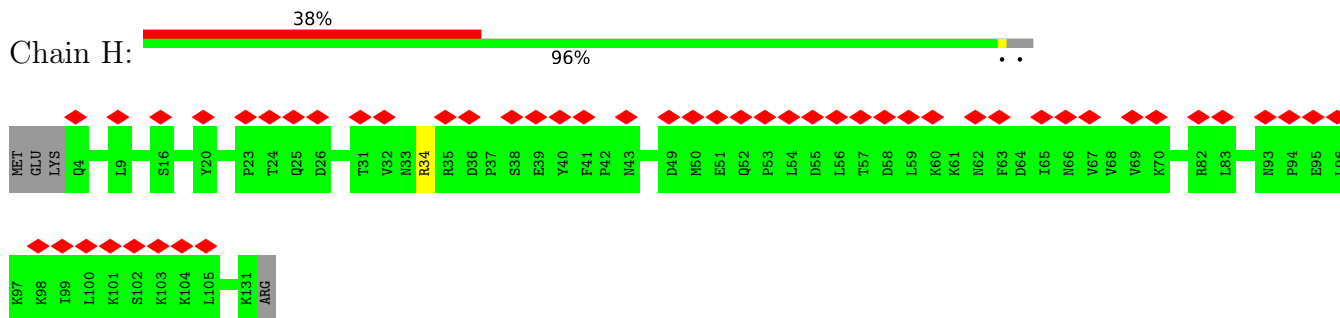
- Molecule 9: 30S ribosomal protein S7



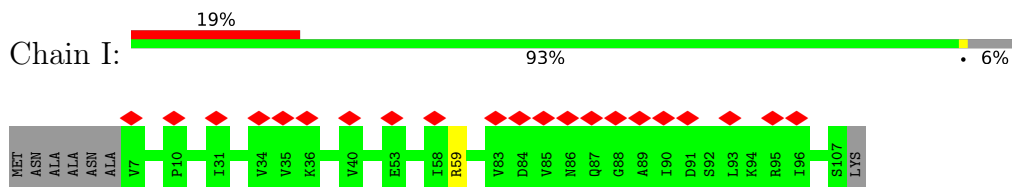
- Molecule 10: 30S ribosomal protein S8



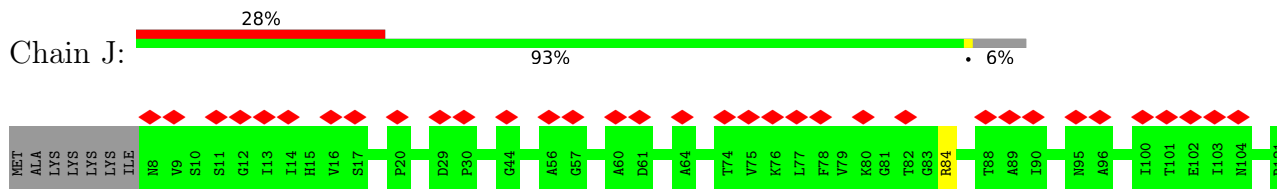
- Molecule 11: 30S ribosomal protein S9



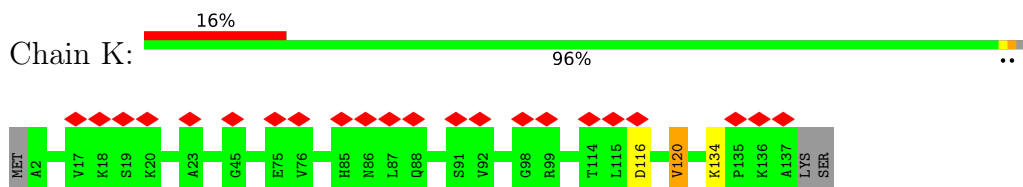
- Molecule 12: 30S ribosomal protein S10



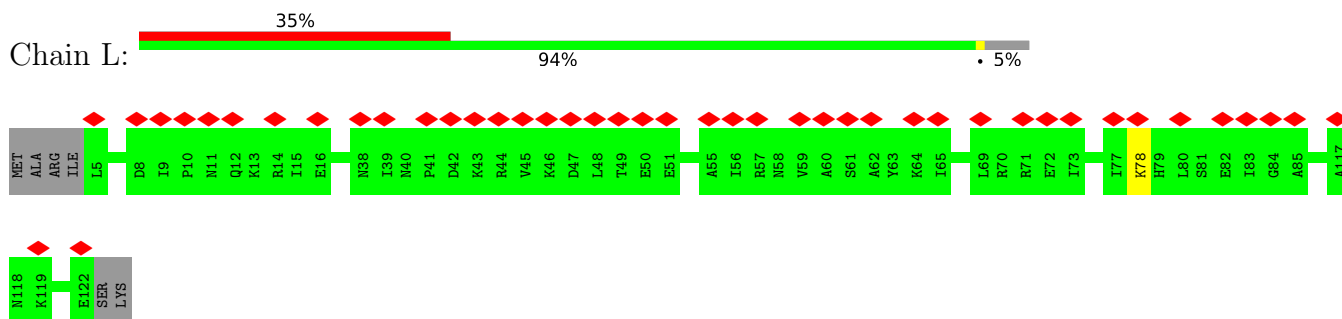
- Molecule 13: 30S ribosomal protein S11



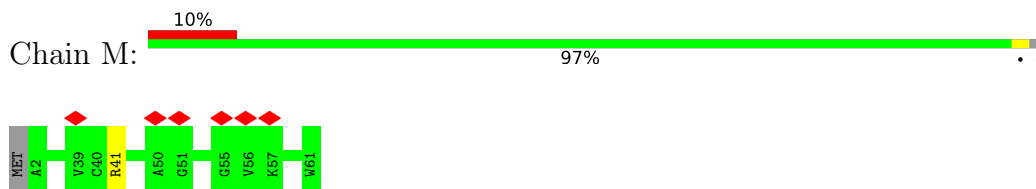
- Molecule 14: 30S ribosomal protein S12



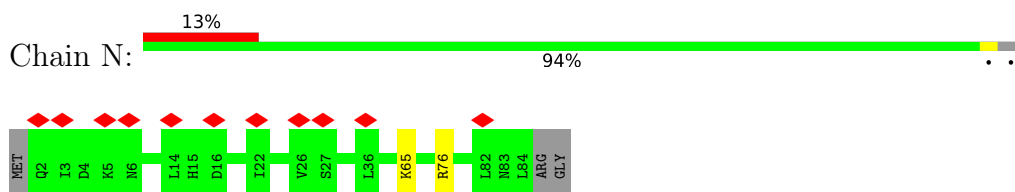
- Molecule 15: 30S ribosomal protein S13



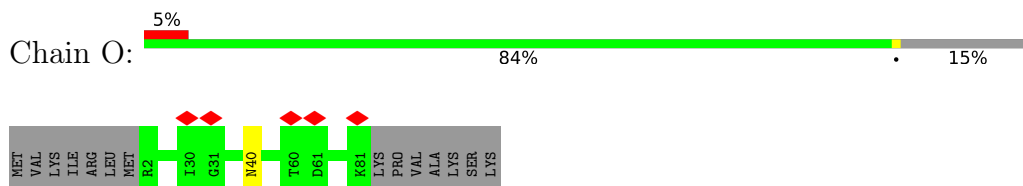
- Molecule 16: 30S ribosomal protein S14 type Z



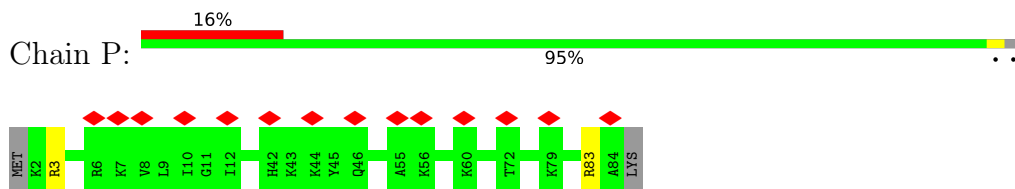
- Molecule 17: 30S ribosomal protein S15



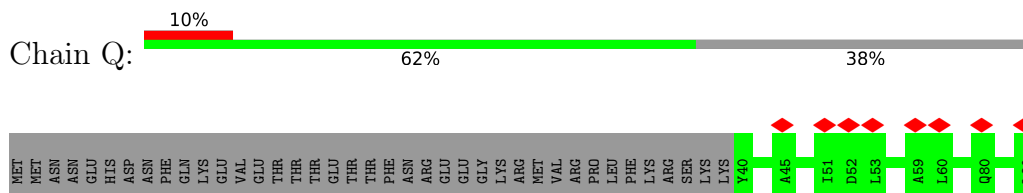
- Molecule 18: 30S ribosomal protein S16



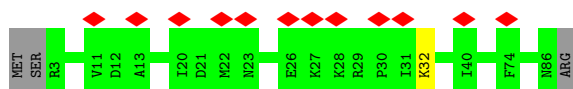
- Molecule 19: 30S ribosomal protein S17



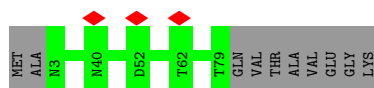
- Molecule 20: 30S ribosomal protein S18



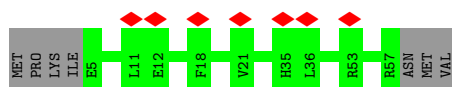
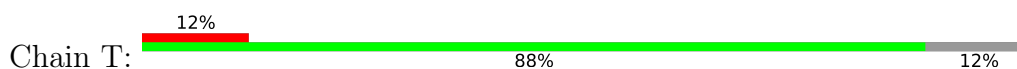
- Molecule 21: 30S ribosomal protein S19



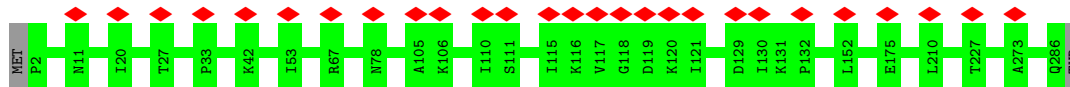
- Molecule 22: 30S ribosomal protein S20



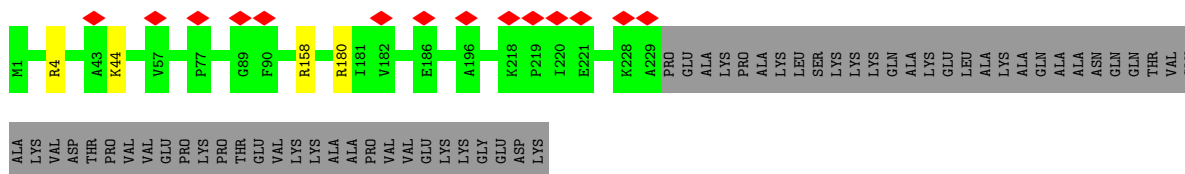
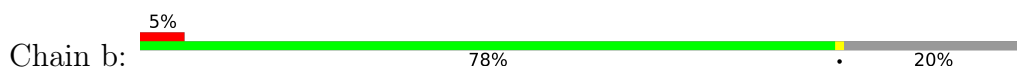
- Molecule 23: 30S ribosomal protein S21



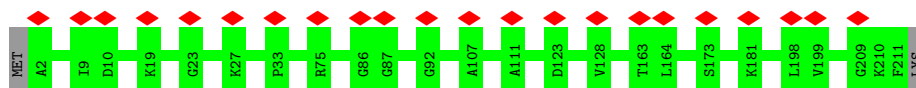
- Molecule 24: 50S ribosomal protein L2



- Molecule 25: 50S ribosomal protein L3

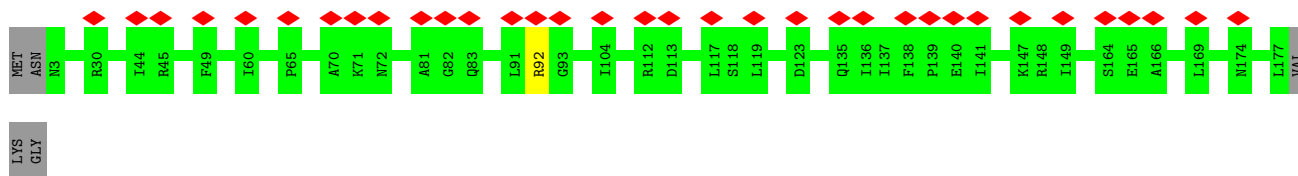


- Molecule 26: 50S ribosomal protein L4

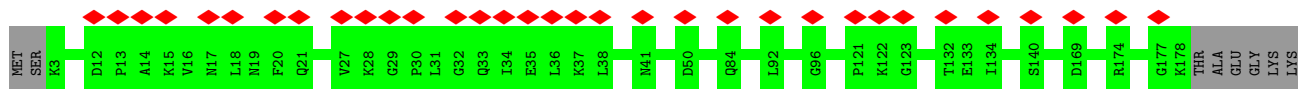


- Molecule 27: 50S ribosomal protein L5

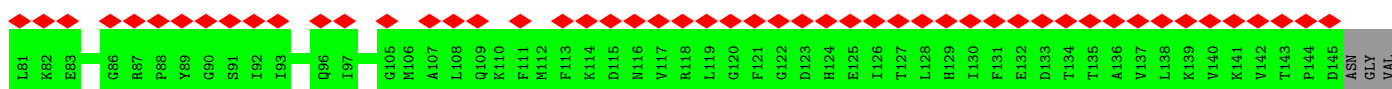
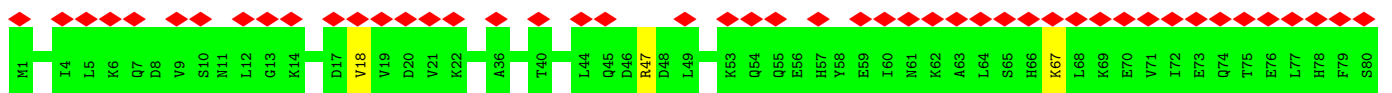
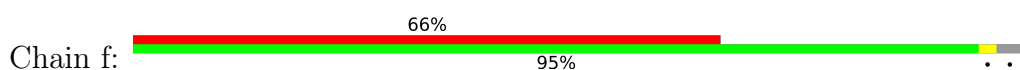




• Molecule 28: 50S ribosomal protein L6

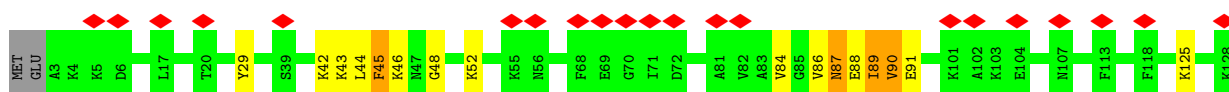


• Molecule 29: 50S ribosomal protein L9



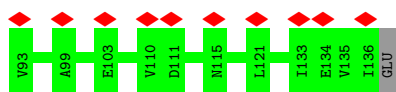
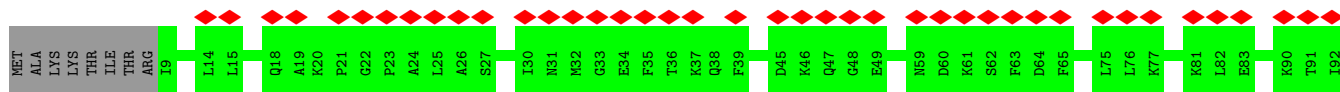
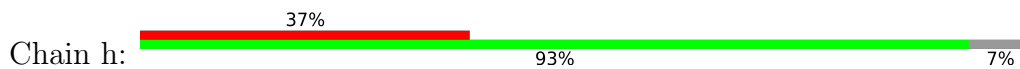
LYS

• Molecule 30: 50S ribosomal protein L10

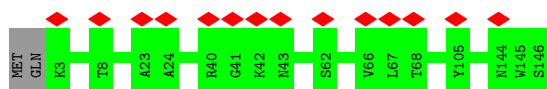


LEU PRO GLY ARG ASN GLU LEU TYR GLY MET PHE LEU SER VAL LEU GLN ALA PRO LEU ARG LYS PHE TYR LEU LEU ALA VAL ALA LYS

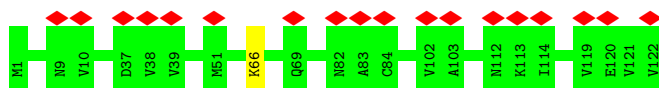
• Molecule 31: 50S ribosomal protein L11



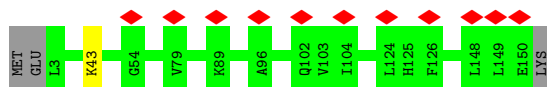
• Molecule 32: 50S ribosomal protein L13



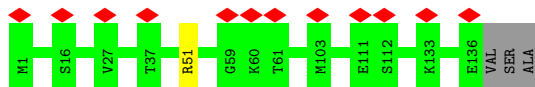
- Molecule 33: 50S ribosomal protein L14



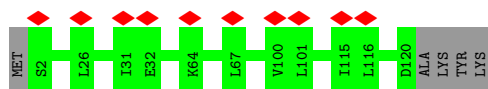
- Molecule 34: 50S ribosomal protein L15



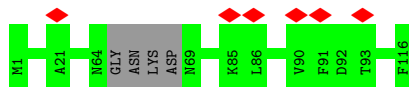
- Molecule 35: 50S ribosomal protein L16



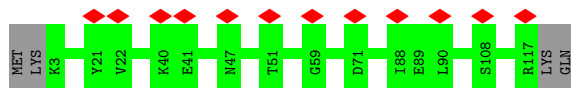
- Molecule 36: 50S ribosomal protein L17



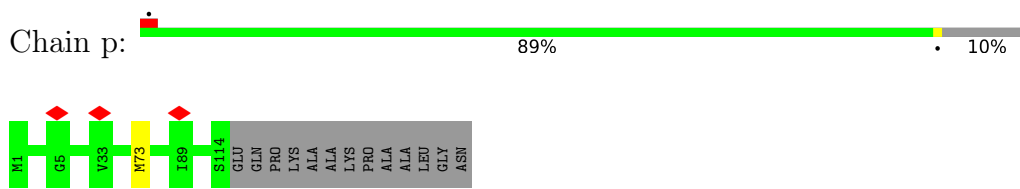
- Molecule 37: 50S ribosomal protein L18



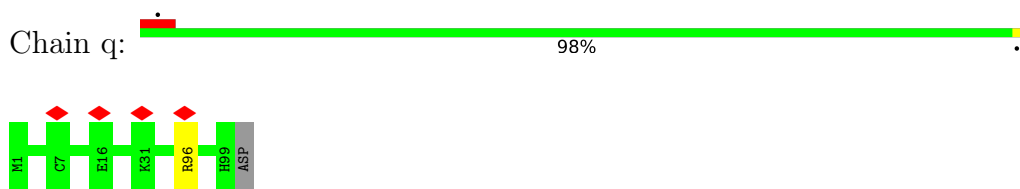
- Molecule 38: 50S ribosomal protein L19



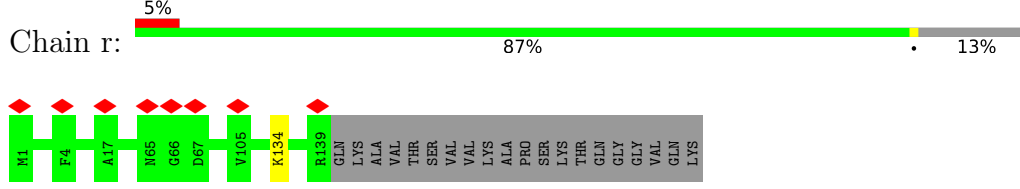
• Molecule 39: 50S ribosomal protein L20



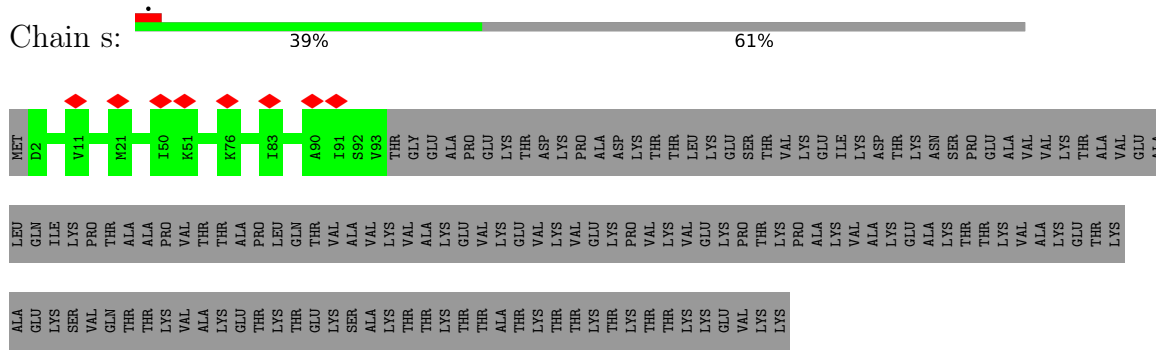
• Molecule 40: 50S ribosomal protein L21



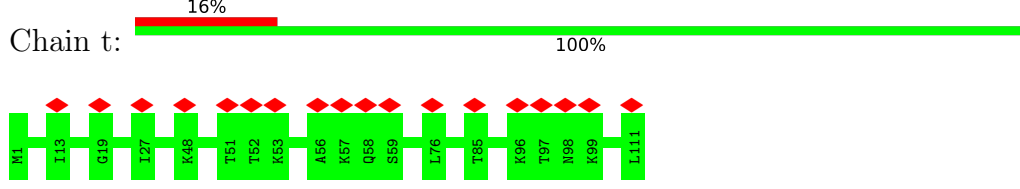
• Molecule 41: 50S ribosomal protein L22



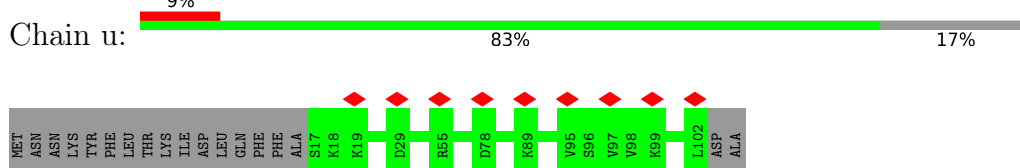
• Molecule 42: 50S ribosomal protein L23



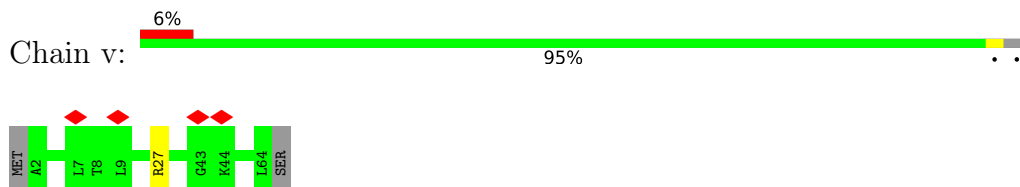
• Molecule 43: 50S ribosomal protein L24



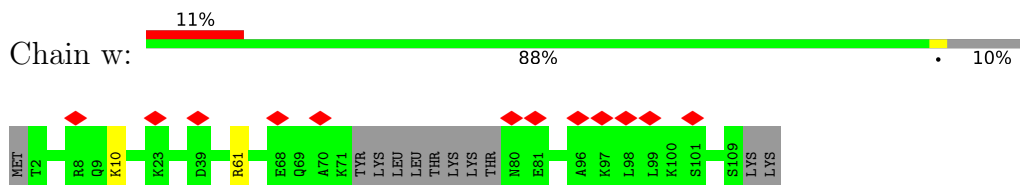
• Molecule 44: 50S ribosomal protein L27



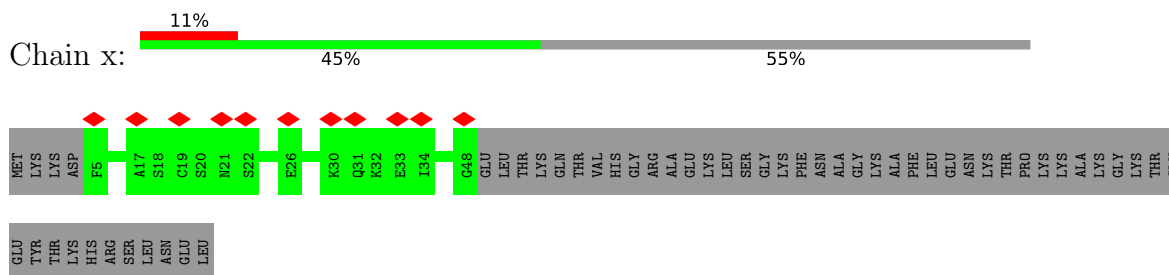
- Molecule 45: 50S ribosomal protein L28



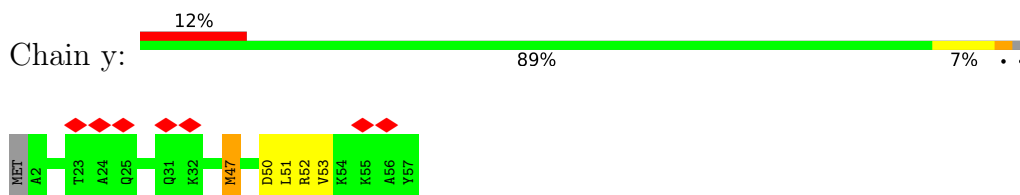
- Molecule 46: 50S ribosomal protein L29



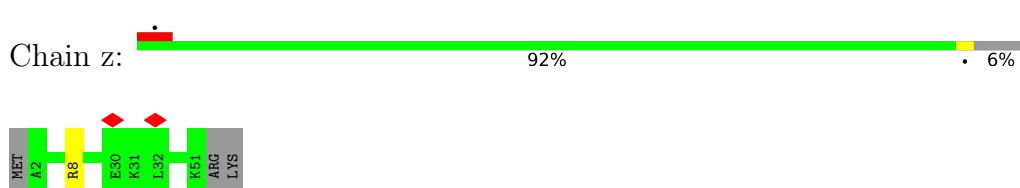
- Molecule 47: 50S ribosomal protein L31



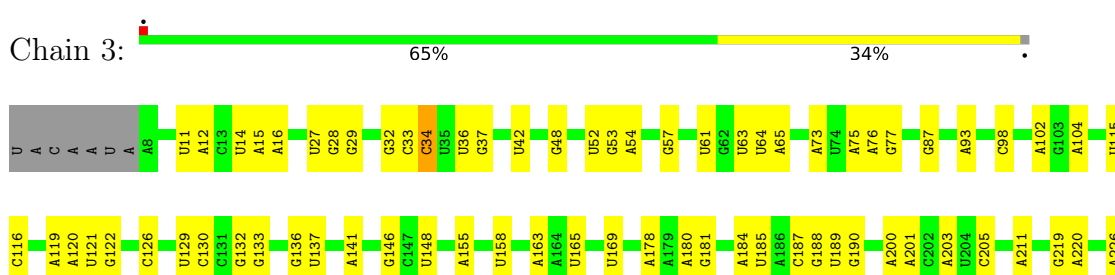
- Molecule 48: 50S ribosomal protein L32



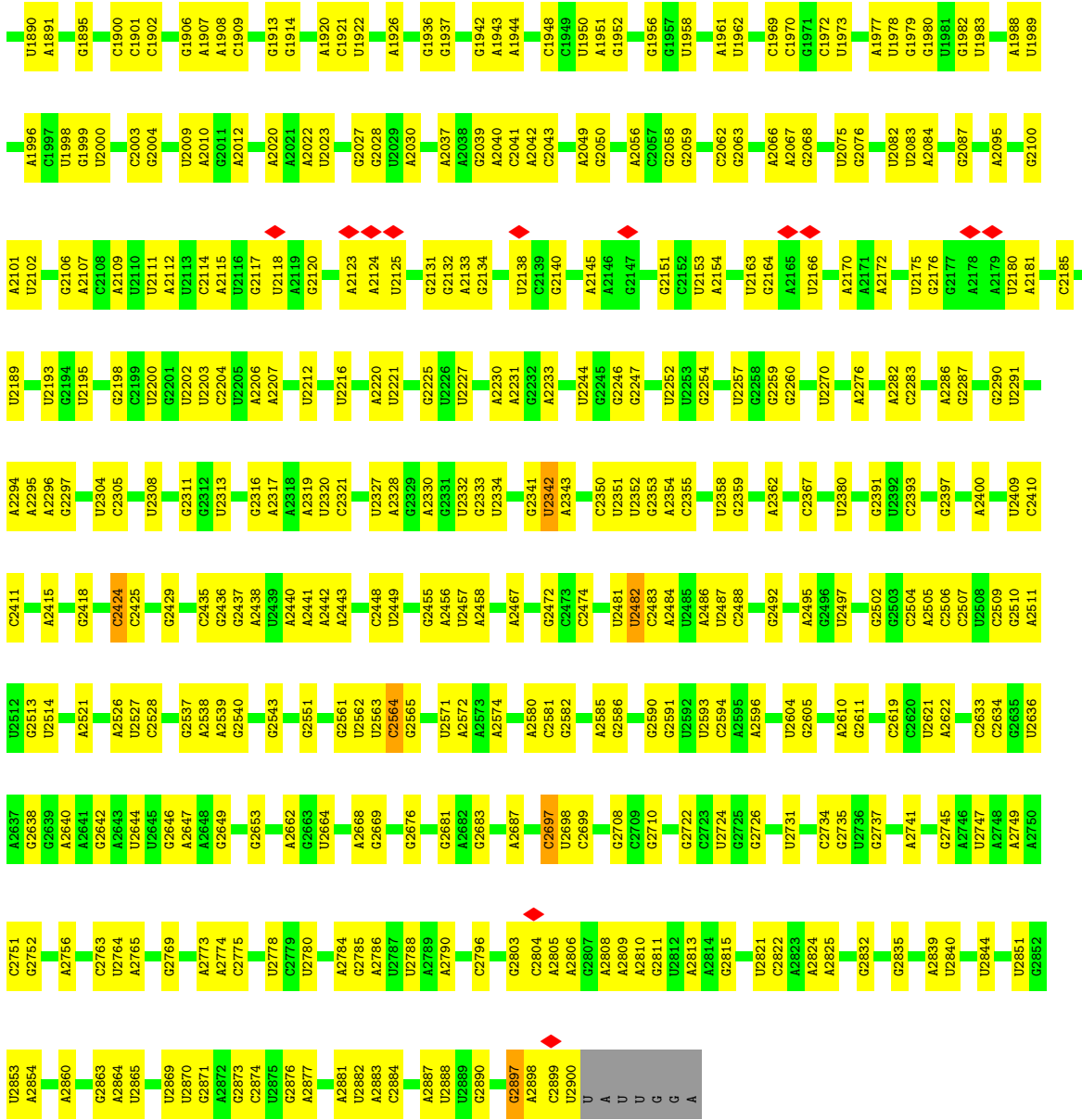
- Molecule 49: 50S ribosomal protein L33 1



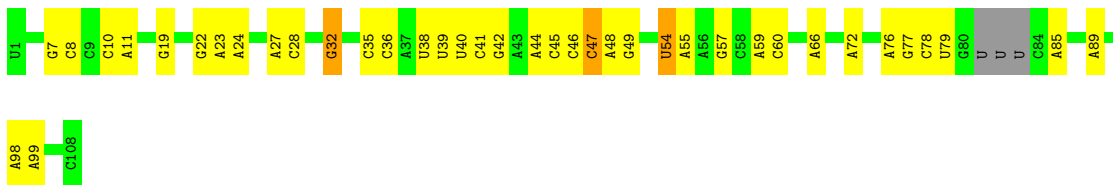
- Molecule 50: 23S ribosomal RNA



C229	C230	A231	A232	U233	A237	G246	G249	G251	C253	G256	C258	A259	G270	A276	C277	U278	U284	U285	A286	G287	A288	U289	G293	G294	U295	U296	G297	U298	A299	G306	A309	U310	G311	U312	G313	G314	A315	G319	A320										
G325	G329	A333	C336	U339	A345	A346	A347	C347	A355	A356	A357	A358	G363	A364	U365	A366	C369	C370	C371	G372	U373	A374	U375	A379	U383	G384	U385	A392	C393	C394	U395	A396	G397	G401	A402	U403	C404	G408	A409	G410	U411	A412	G418	A422					
C423	G424	U425	U426	A427	U428	G432	A433	G434	A437	A438	U439	C440	U441	G442	G447	A448	U457	A458	A459	G460	A468	A471	A479	C480	C481	G482	A483	U484	C487	A491	C492	A493	G494	U495	U500	G501	A506	G509	G510	U511	A514	A515	A516	G517	A518	A519			
C520	G531	A538	U539	A540	U544	C545	A553	C559	C562	A563	A564	C565	U566	G568	A582	U583	U585	C586	U587	A589	U590	G591	U595	U596	C597	G598	U599	U600	G601	U607	A608	G615	C634	G635	U636	U637	G650	A657	G658	C659	U660	G661							
U662	A663	A669	A673	U676	A679	A680	A681	G683	U688	U689	U690	C696	A697	U694	U700	A701	A703	C706	C707	U708	G709	A710	U711	A712	G719	A720	G721	C722	U723	A724	A734	U737	A740	C752	G650	G760	G761	A762	G763	G764	A765	U776	U782						
C787	G792	C800	G810	G811	G812	A816	A817	A818	U819	U820	U825	C826	A827	A828	U835	G836	A837	G840	C841	U842	C847	U851	A854	A855	U862	U863	A864	A865	G871	U874	A881	C882	A883	A884	U885	U886	A888	G889	U890	G891	A893	A894	A895	A896	G897				
G894	G895	U902	A903	C904	U906	G906	U916	A917	G917	G920	C921	C922	A	C	C	U	A	U932	A933	G936	U944	A947	U948	C949	U952	G953	U966	U967	U968	A969	U970	U971	G975	C976	A977	G978	A981	G982	A985	G989	A993	U994	A995	A996	G997				
C998	A1008	G1010	A1011	G1012	A1016	G1018	A1019	G1020	C1021	C1022	C1023	A1024	G1025	A1026	U1027	C1028	A1029	A1032	A1044	A1045	A1046	U1047	A1048	U1049	A1050	U1051	A1052	A1055	A1056	G1057	A1061	U1068	G1069	A1074	G1075	U1076	G1077	A1081	A1082	A1083	C1087	A1088	A1089	U1095	U1096	G1097			
G1098	G1103	A1104	A1105	C1107	A1108	C1111	A1112	U1113	U1114	U1115	U1116	U1117	U1118	A1119	A1120	U1121	A1123	U1125	G1126	U1129	A1130	A1131	C1132	A1133	U1134	U1135	U1136	U1137	U1138	G1145	U1146	U1147	U1148	U1151	U1154	A1162	G1166	U1167	A1168	A1169	C1170	G1171	C1175	U1176	A1177	A1178	U1179	A1186	C1187
A1191	A1201	U1206	U1207	A1208	U1209	A1210	G1215	G1221	U1230	A1233	U1234	A1243	C1247	A1250	G1251	C1252	A1256	G1257	C1258	U1260	G1266	A1267	U1268	C1269	A1274	A1277	U1279	A1281	A1282	A1283	A1284	U1285	G1286	A1292	U1293	G1294	A1295	U1296	U1297	A1298									
A1299	C1300	C1301	C1302	U1303	U1304	A1308	A1314	A1315	U1316	C1317	U1318	C1319	A1322	A1323	U1329	U1330	G1338	U1339	U1340	U1341	C1342	G1345	C1349	U1357	U1360	G1366	G1367	A1370	U1371	U1372	C1373	A1381	G1388	A1393	A1406	U1407	A1420	U1421	U1422	A1423	U1424	U1425	C1426						
A1431	U1434	A1437	G1438	C1444	U1445	U1448	A1455	A1456	A1457	G1463	U1466	U1487	A1480	U1481	U1482	G1483	U1487	A1493	U1494	A1495	G1506	U1507	G1508	U1509	A1510	C1518	A1519	C1523	C1524	G1525	G1530	U1533	A1534	A1541	G1544	U1545	A1546	U1549	A1550	G1550									
G1557	A1559	U	C	A	U	U	A	A1570	G1571	A1578	G1579	U1580	U1581	G1582	U1583	A1584	U1585	U1586	U1587	A1588	U1589	A1592	U1593	G1594	C1599	A1600	A1601	U1612	G1615	U1618	A1619	C1622	G1635	U1636	A1637	G1642	A1643	C1645	A1648	C1649	A1650	C1651							
A1652	A1656	A1660	G1663	A1666	G1676	U1679	A1680	C1681	G1682	G1683	A1688	U1691	A1692	C1697	A1703	C1704	U1705	C1706	U1707	G1708	A1711	U1712	U1713	U1714	A1715	A1716	C1720	U1727	A1728	G1729	C1730	G1733	A1734	A1735	G1736	G1741	C1742	U1745	U1746	G1747	U1748	A1754	A1759	G1763					
G1760	C1761	A1762	G1763	U1764	G1765	A1766	A1767	G1768	A1769	A1770	C1771	G1774	A1780	U1786	A1787	C1789	U1790	A1791	A1792	A1793	A1794	A1798	C1807	G1808	A1809	U1820	G1821	A1822	U1823	G1824	A1836	C1837	G1842	C1843	A1846	G1847	A1855	A1865	A1873	G1874	C1875	G1876	A1877	A1878	A1879				

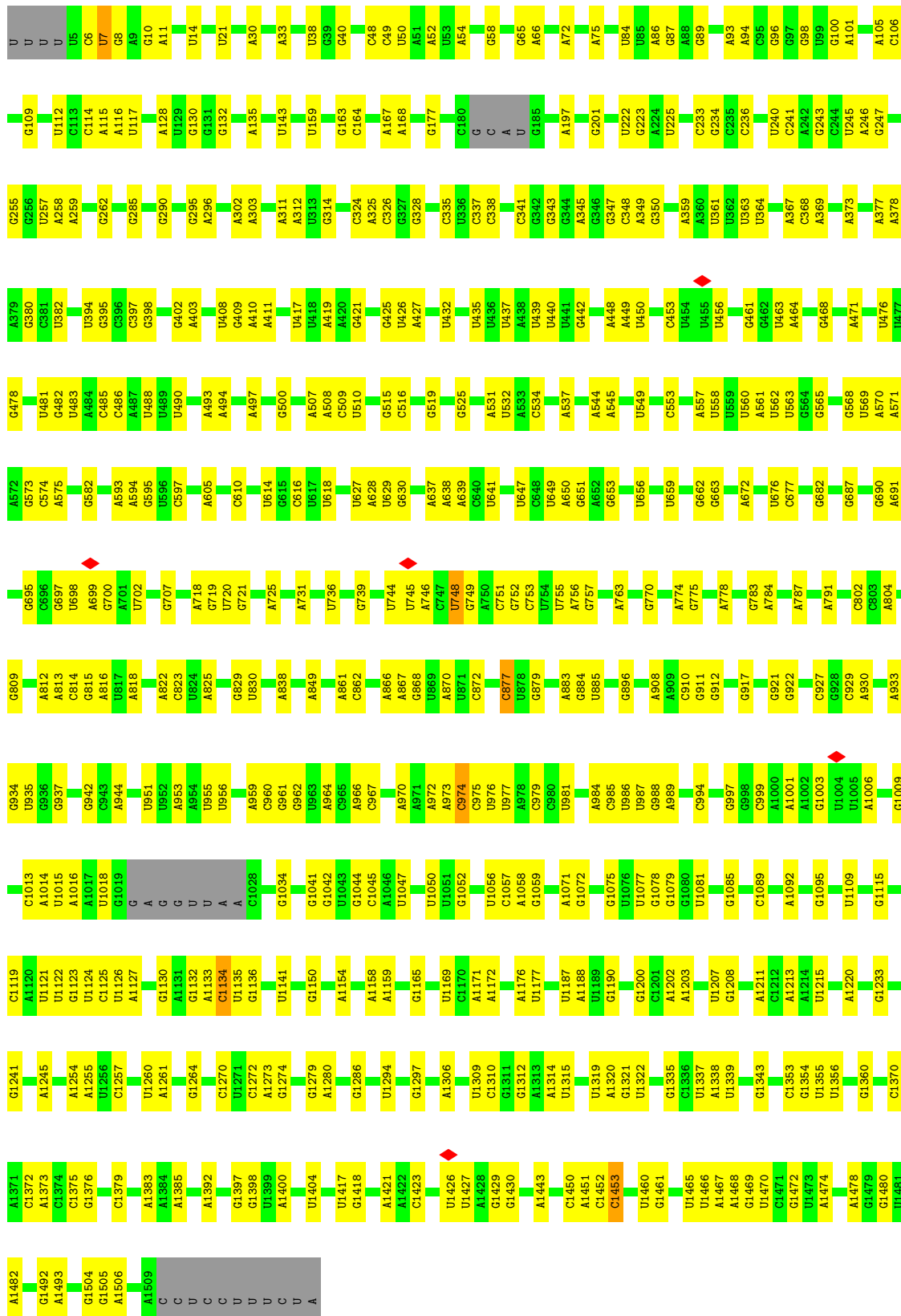


- Molecule 51: 5S ribosomal RNA



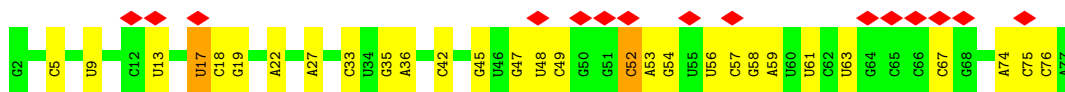
- Molecule 52: 16S ribosomal RNA



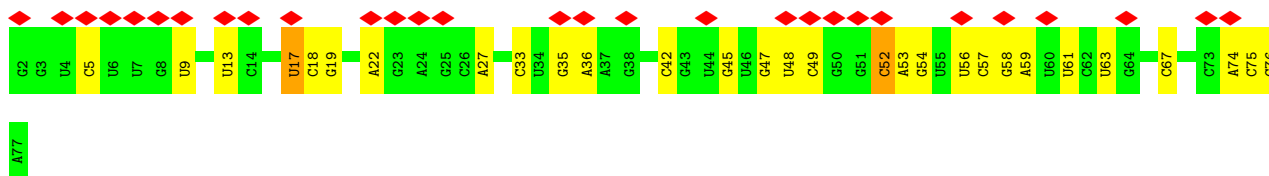


- Molecule 53: tRNA-Phe





• 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	1082	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	1.435	Depositor
Minimum map value	-0.515	Depositor
Average map value	0.024	Depositor
Map value standard deviation	0.115	Depositor
Recommended contour level	0.39	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	0.25	0/484	0.51	1/637 (0.2%)
3	2	0.23	0/306	0.45	0/401
4	A	0.26	0/1954	0.45	0/2642
5	B	0.25	0/1721	0.47	0/2323
6	C	0.24	0/1691	0.45	0/2267
7	D	0.24	0/1188	0.46	0/1593
8	E	0.28	0/1384	0.51	0/1867
9	F	0.28	0/1266	0.49	0/1700
10	G	0.26	0/1126	0.51	0/1517
11	H	0.26	0/1044	0.52	0/1395
12	I	0.25	0/820	0.50	0/1103
13	J	0.25	0/844	0.45	0/1136
14	K	0.29	0/1094	0.54	0/1468
15	L	0.24	0/962	0.48	0/1289
16	M	0.25	0/483	0.45	0/643
17	N	0.24	0/679	0.43	0/907
18	O	0.24	0/659	0.46	0/885
19	P	0.25	0/684	0.49	0/913
20	Q	0.25	0/545	0.46	0/730
21	R	0.24	0/698	0.45	0/936
22	S	0.23	0/631	0.41	0/838
23	T	0.23	0/475	0.47	0/621
24	a	0.24	0/2267	0.47	0/3044
25	b	0.25	0/1795	0.47	0/2412
26	c	0.25	0/1671	0.47	0/2246
27	d	0.25	0/1409	0.47	0/1894
28	e	0.25	0/1420	0.49	0/1912
29	f	0.25	0/1205	0.51	0/1616
30	g	0.34	0/969	0.57	0/1295
31	h	0.25	0/968	0.50	0/1298
32	i	0.24	0/1186	0.45	0/1592
33	j	0.24	0/953	0.46	0/1275
34	k	0.25	0/1170	0.48	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	l	0.24	0/1104	0.45	0/1481
36	m	0.24	0/973	0.46	0/1309
37	n	0.23	0/897	0.45	0/1198
38	o	0.24	0/948	0.46	0/1262
39	p	0.24	0/961	0.42	0/1278
40	q	0.24	0/828	0.46	0/1111
41	r	0.24	0/1077	0.47	0/1441
42	s	0.24	0/732	0.45	0/988
43	t	0.25	0/879	0.45	0/1165
44	u	0.25	0/665	0.45	0/884
45	v	0.24	0/519	0.52	0/695
46	w	0.24	0/826	0.46	0/1104
47	x	0.25	0/353	0.44	0/474
48	y	0.30	0/457	0.53	0/601
49	z	0.24	0/412	0.42	0/547
50	3	0.22	0/69073	0.83	60/107710 (0.1%)
51	4	0.24	0/2505	0.90	10/3902 (0.3%)
52	5	0.22	0/35768	0.83	20/55764 (0.0%)
53	6	0.27	0/1808	0.94	7/2817 (0.2%)
53	8	0.27	0/1808	0.94	7/2817 (0.2%)
All	All	0.23	0/158727	0.76	105/237006 (0.0%)

There are no bond length outliers.

The worst 5 of 105 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	3	1023	C	N3-C2-O2	-10.05	114.87	121.90
52	5	1453	C	N3-C2-O2	-9.44	115.29	121.90
51	4	47	C	N3-C2-O2	-8.69	115.82	121.90
50	3	559	C	N3-C2-O2	-8.66	115.84	121.90
50	3	1900	C	N3-C2-O2	-8.56	115.90	121.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	44 (98%)	1 (2%)	0	100	100
2	1	57/59 (97%)	50 (88%)	7 (12%)	0	100	100
3	2	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
4	A	238/294 (81%)	221 (93%)	17 (7%)	0	100	100
5	B	213/273 (78%)	197 (92%)	16 (8%)	0	100	100
6	C	201/205 (98%)	185 (92%)	16 (8%)	0	100	100
7	D	151/219 (69%)	140 (93%)	11 (7%)	0	100	100
8	E	165/215 (77%)	149 (90%)	16 (10%)	0	100	100
9	F	152/155 (98%)	139 (91%)	13 (9%)	0	100	100
10	G	139/142 (98%)	122 (88%)	16 (12%)	1 (1%)	22	63
11	H	126/132 (96%)	111 (88%)	15 (12%)	0	100	100
12	I	99/108 (92%)	92 (93%)	7 (7%)	0	100	100
13	J	112/121 (93%)	106 (95%)	6 (5%)	0	100	100
14	K	134/139 (96%)	121 (90%)	11 (8%)	2 (2%)	10	46
15	L	116/124 (94%)	104 (90%)	12 (10%)	0	100	100
16	M	58/61 (95%)	54 (93%)	4 (7%)	0	100	100
17	N	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
18	O	78/94 (83%)	75 (96%)	3 (4%)	0	100	100
19	P	81/85 (95%)	76 (94%)	5 (6%)	0	100	100
20	Q	63/104 (61%)	59 (94%)	4 (6%)	0	100	100
21	R	82/87 (94%)	69 (84%)	13 (16%)	0	100	100
22	S	75/87 (86%)	75 (100%)	0	0	100	100
23	T	51/60 (85%)	48 (94%)	3 (6%)	0	100	100
24	a	283/287 (99%)	258 (91%)	25 (9%)	0	100	100
25	b	227/287 (79%)	204 (90%)	23 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	c	208/212 (98%)	193 (93%)	15 (7%)	0	100	100
27	d	173/180 (96%)	164 (95%)	9 (5%)	0	100	100
28	e	174/184 (95%)	160 (92%)	14 (8%)	0	100	100
29	f	143/149 (96%)	133 (93%)	9 (6%)	1 (1%)	22	63
30	g	124/161 (77%)	101 (82%)	17 (14%)	6 (5%)	2	21
31	h	126/137 (92%)	116 (92%)	10 (8%)	0	100	100
32	i	142/146 (97%)	129 (91%)	13 (9%)	0	100	100
33	j	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
34	k	146/151 (97%)	137 (94%)	9 (6%)	0	100	100
35	l	134/139 (96%)	127 (95%)	7 (5%)	0	100	100
36	m	117/124 (94%)	104 (89%)	13 (11%)	0	100	100
37	n	108/116 (93%)	101 (94%)	7 (6%)	0	100	100
38	o	113/119 (95%)	106 (94%)	7 (6%)	0	100	100
39	p	112/127 (88%)	109 (97%)	3 (3%)	0	100	100
40	q	97/100 (97%)	87 (90%)	10 (10%)	0	100	100
41	r	137/159 (86%)	128 (93%)	9 (7%)	0	100	100
42	s	90/237 (38%)	84 (93%)	6 (7%)	0	100	100
43	t	109/111 (98%)	101 (93%)	8 (7%)	0	100	100
44	u	84/104 (81%)	78 (93%)	6 (7%)	0	100	100
45	v	61/65 (94%)	56 (92%)	5 (8%)	0	100	100
46	w	96/111 (86%)	95 (99%)	1 (1%)	0	100	100
47	x	42/97 (43%)	36 (86%)	6 (14%)	0	100	100
48	y	54/57 (95%)	46 (85%)	6 (11%)	2 (4%)	3	24
49	z	48/53 (91%)	46 (96%)	2 (4%)	0	100	100
All	All	5820/6670 (87%)	5363 (92%)	445 (8%)	12 (0%)	50	81

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	G	109	ASN
29	f	18	VAL
30	g	45	PHE
30	g	48	GLY
30	g	87	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%)	50 (98%)	1 (2%)	55	74
3	2	35/35 (100%)	35 (100%)	0	100	100
4	A	212/262 (81%)	210 (99%)	2 (1%)	78	87
5	B	180/232 (78%)	176 (98%)	4 (2%)	52	71
6	C	181/183 (99%)	177 (98%)	4 (2%)	52	71
7	D	123/178 (69%)	122 (99%)	1 (1%)	81	89
8	E	150/196 (76%)	148 (99%)	2 (1%)	69	81
9	F	131/132 (99%)	130 (99%)	1 (1%)	81	89
10	G	123/124 (99%)	123 (100%)	0	100	100
11	H	111/115 (96%)	110 (99%)	1 (1%)	78	87
12	I	95/99 (96%)	94 (99%)	1 (1%)	73	84
13	J	91/97 (94%)	90 (99%)	1 (1%)	73	84
14	K	117/120 (98%)	115 (98%)	2 (2%)	60	78
15	L	100/105 (95%)	99 (99%)	1 (1%)	76	86
16	M	47/48 (98%)	46 (98%)	1 (2%)	53	72
17	N	76/78 (97%)	74 (97%)	2 (3%)	46	66
18	O	69/82 (84%)	68 (99%)	1 (1%)	67	80
19	P	73/75 (97%)	71 (97%)	2 (3%)	44	65
20	Q	56/94 (60%)	56 (100%)	0	100	100
21	R	74/77 (96%)	73 (99%)	1 (1%)	67	80
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%)	241 (100%)	0	100	100
25	b	186/233 (80%)	182 (98%)	4 (2%)	52	71
26	c	182/184 (99%)	182 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	d	150/154 (97%)	149 (99%)	1 (1%)	84	90
28	e	153/159 (96%)	153 (100%)	0	100	100
29	f	131/134 (98%)	129 (98%)	2 (2%)	65	80
30	g	101/129 (78%)	87 (86%)	14 (14%)	3	17
31	h	102/110 (93%)	102 (100%)	0	100	100
32	i	126/128 (98%)	126 (100%)	0	100	100
33	j	103/103 (100%)	102 (99%)	1 (1%)	76	86
34	k	123/126 (98%)	122 (99%)	1 (1%)	81	89
35	l	113/115 (98%)	112 (99%)	1 (1%)	78	87
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%)	101 (100%)	0	100	100
39	p	100/108 (93%)	99 (99%)	1 (1%)	76	86
40	q	90/91 (99%)	89 (99%)	1 (1%)	73	84
41	r	116/132 (88%)	115 (99%)	1 (1%)	78	87
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%)	44 (92%)	4 (8%)	11	34
49	z	47/50 (94%)	46 (98%)	1 (2%)	53	72
All	All	5101/5751 (89%)	5038 (99%)	63 (1%)	72	83

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	b	4	ARG
45	v	27	ARG
30	g	29	TYR
41	r	134	LYS
48	y	50	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
25	b	35	GLN
43	t	2	GLN
27	d	63	GLN
37	n	24	HIS
26	c	134	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	961 (33%)	37 (1%)
51	4	103/108 (95%)	36 (34%)	3 (2%)
52	5	1490/1520 (98%)	463 (31%)	9 (0%)
53	6	75/76 (98%)	28 (37%)	3 (4%)
53	8	75/76 (98%)	28 (37%)	3 (4%)
All	All	4618/4687 (98%)	1516 (32%)	55 (1%)

5 of 1516 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	11	U
50	3	12	A
50	3	14	U
50	3	15	A
50	3	16	A

5 of 55 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	3	2486	A
50	3	2882	U
53	8	74	A
53	6	18	C
50	3	2504	C

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

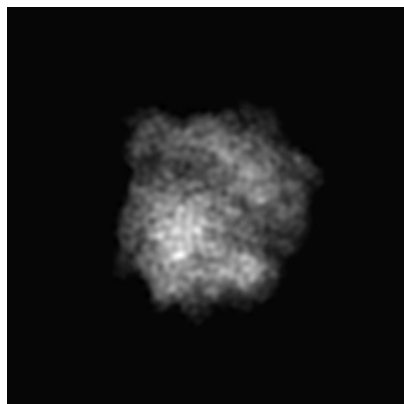
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13413. These allow visual inspection of the internal detail of the map and identification of artifacts.

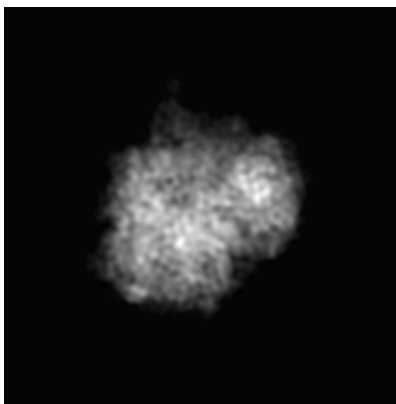
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

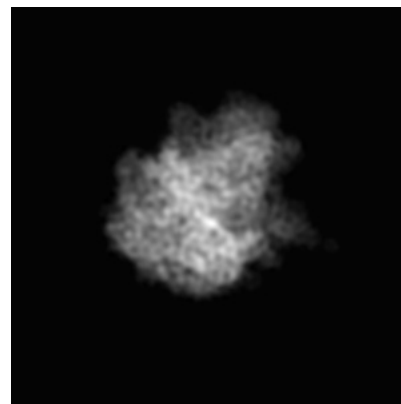
6.1.1 Primary map



X

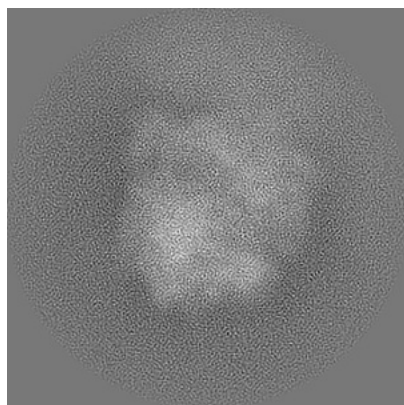


Y

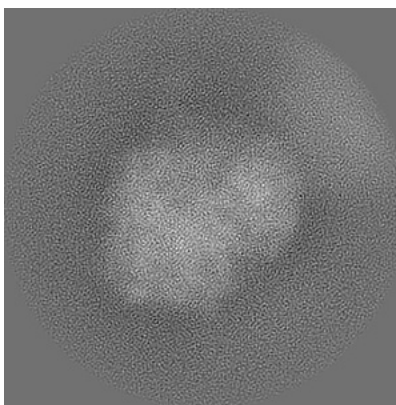


Z

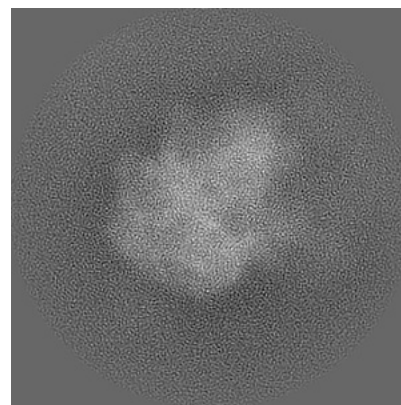
6.1.2 Raw map



X



Y

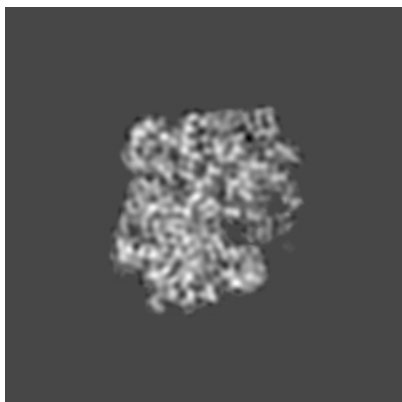


Z

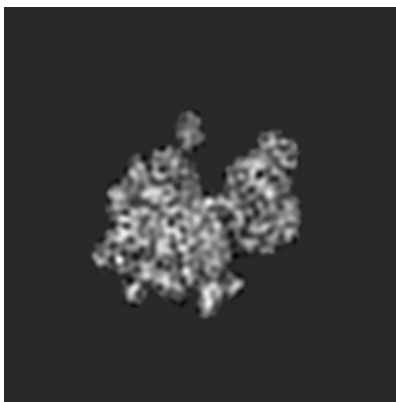
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

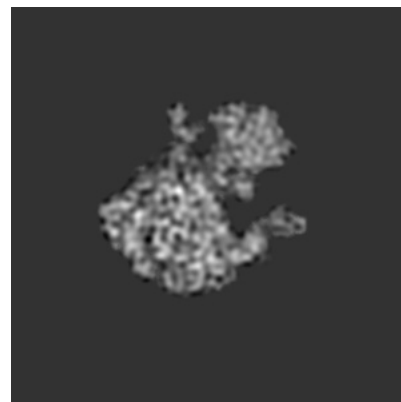
6.2.1 Primary map



X Index: 128

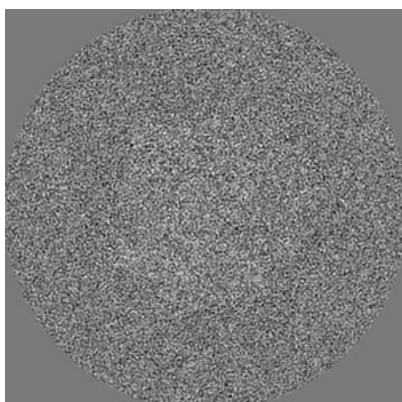


Y Index: 128

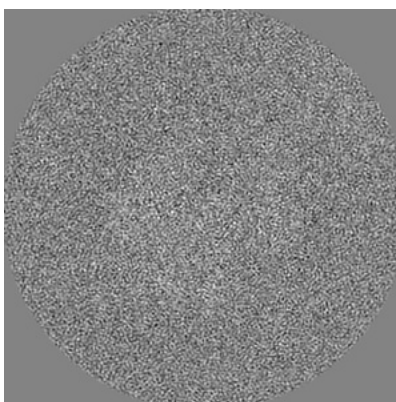


Z Index: 128

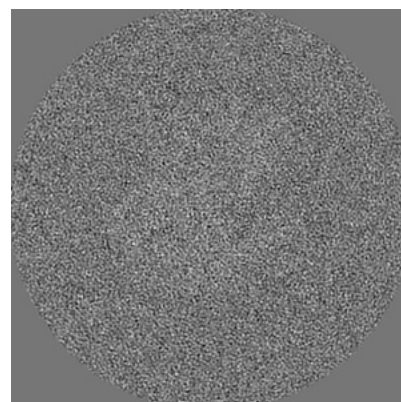
6.2.2 Raw map



X Index: 128



Y Index: 128

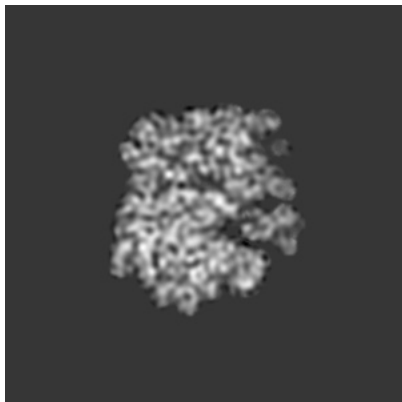


Z Index: 128

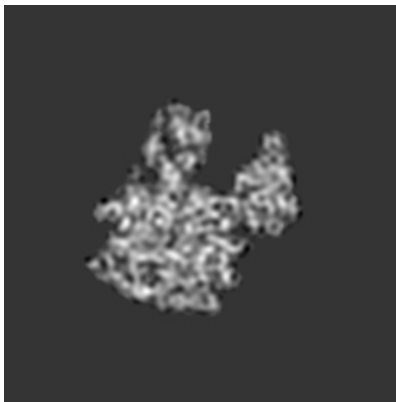
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

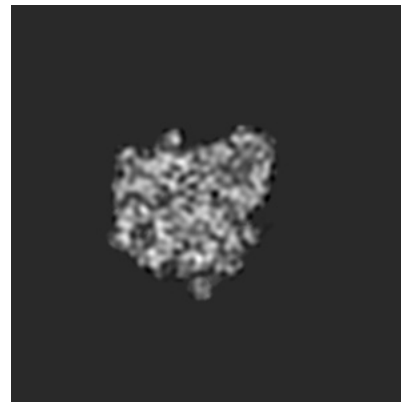
6.3.1 Primary map



X Index: 122

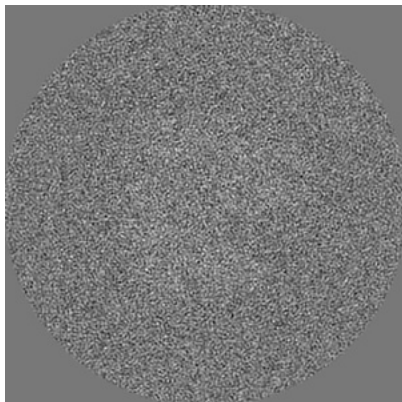


Y Index: 117

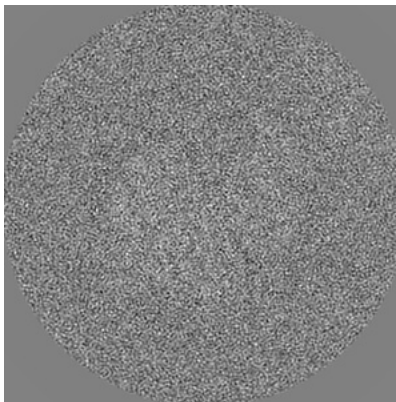


Z Index: 86

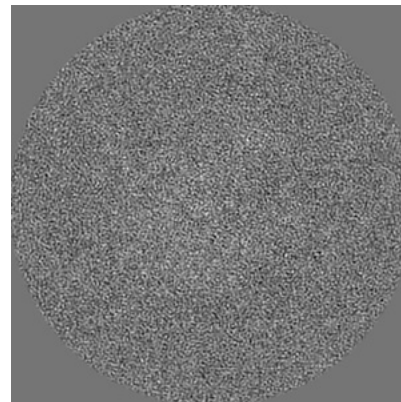
6.3.2 Raw map



X Index: 135



Y Index: 130

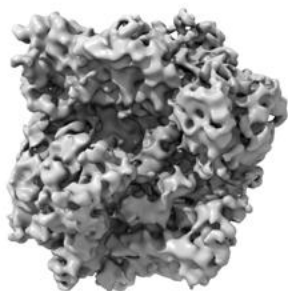


Z Index: 123

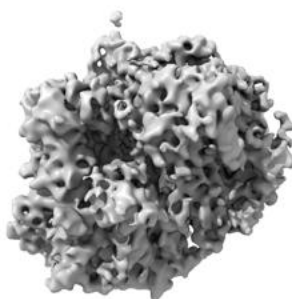
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

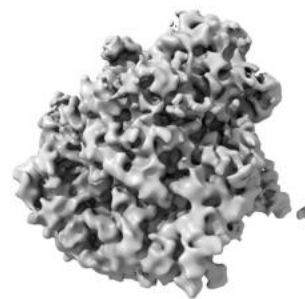
6.4.1 Primary map



X



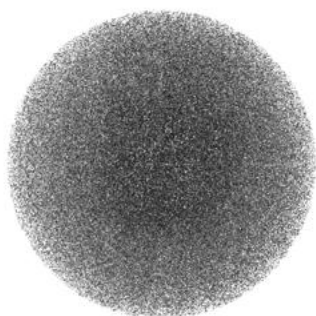
Y



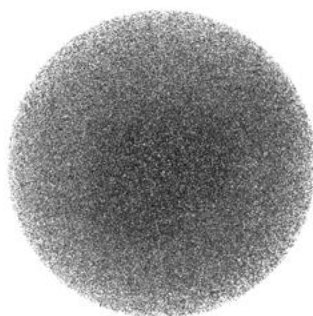
Z

The images above show the 3D surface view of the map at the recommended contour level 0.39. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

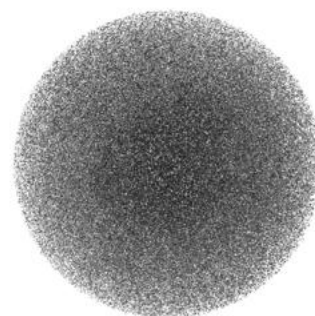
6.4.2 Raw map



X



Y



Z

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

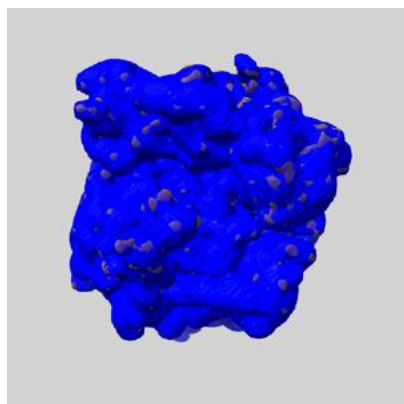
6.5 Mask visualisation [i](#)

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

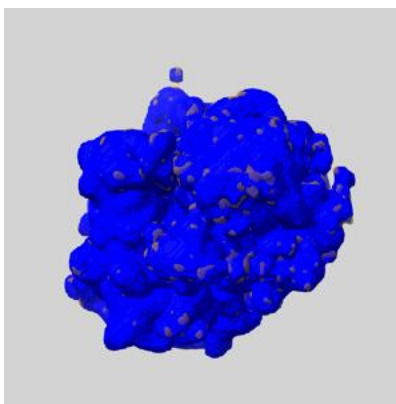
A mask typically either:

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

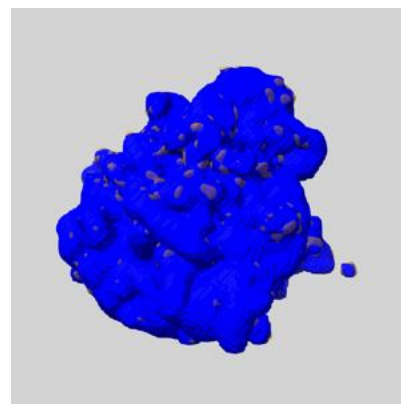
6.5.1 emd_13413_msk_1.map [i](#)



X



Y

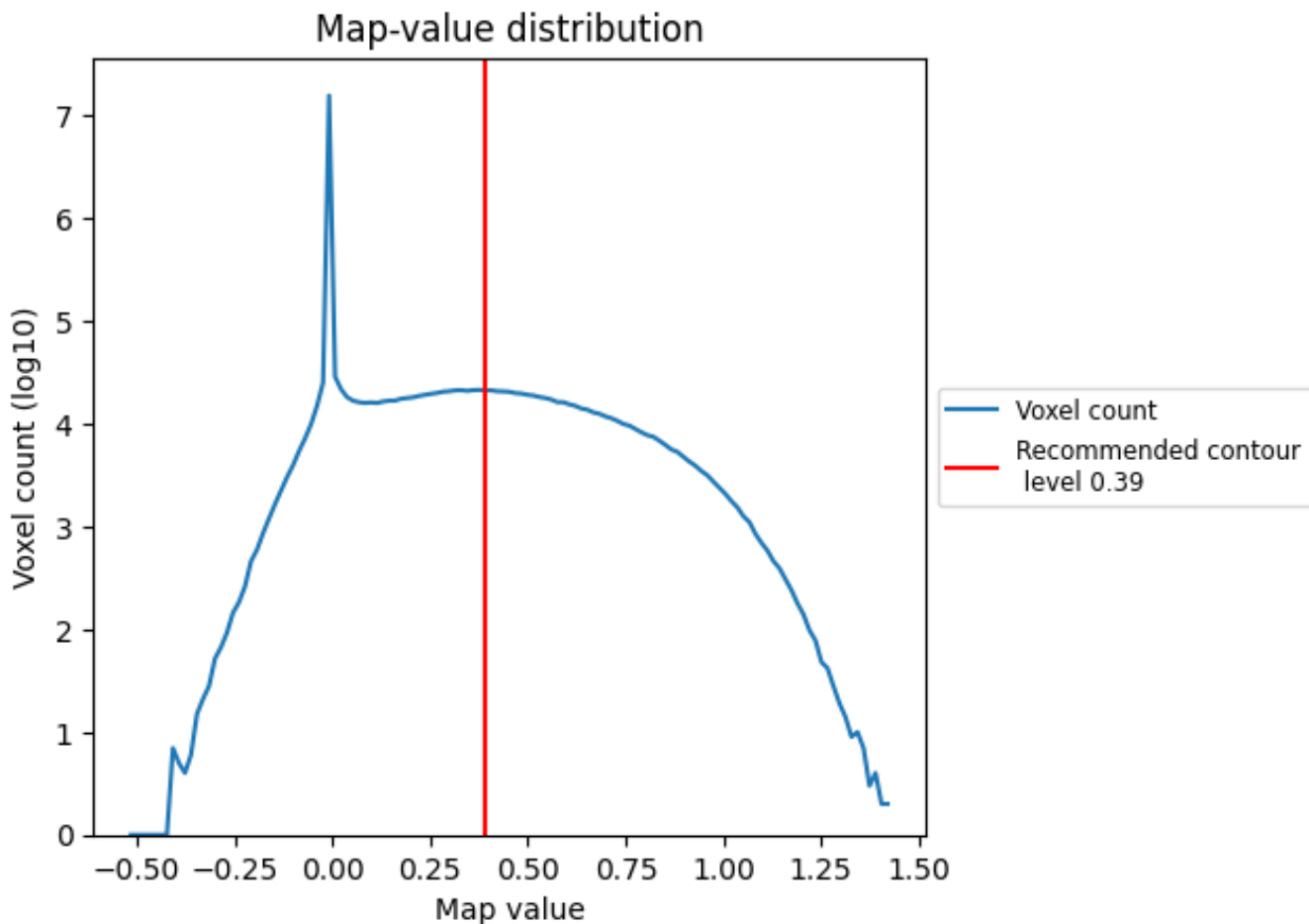


Z

7 Map analysis [i](#)

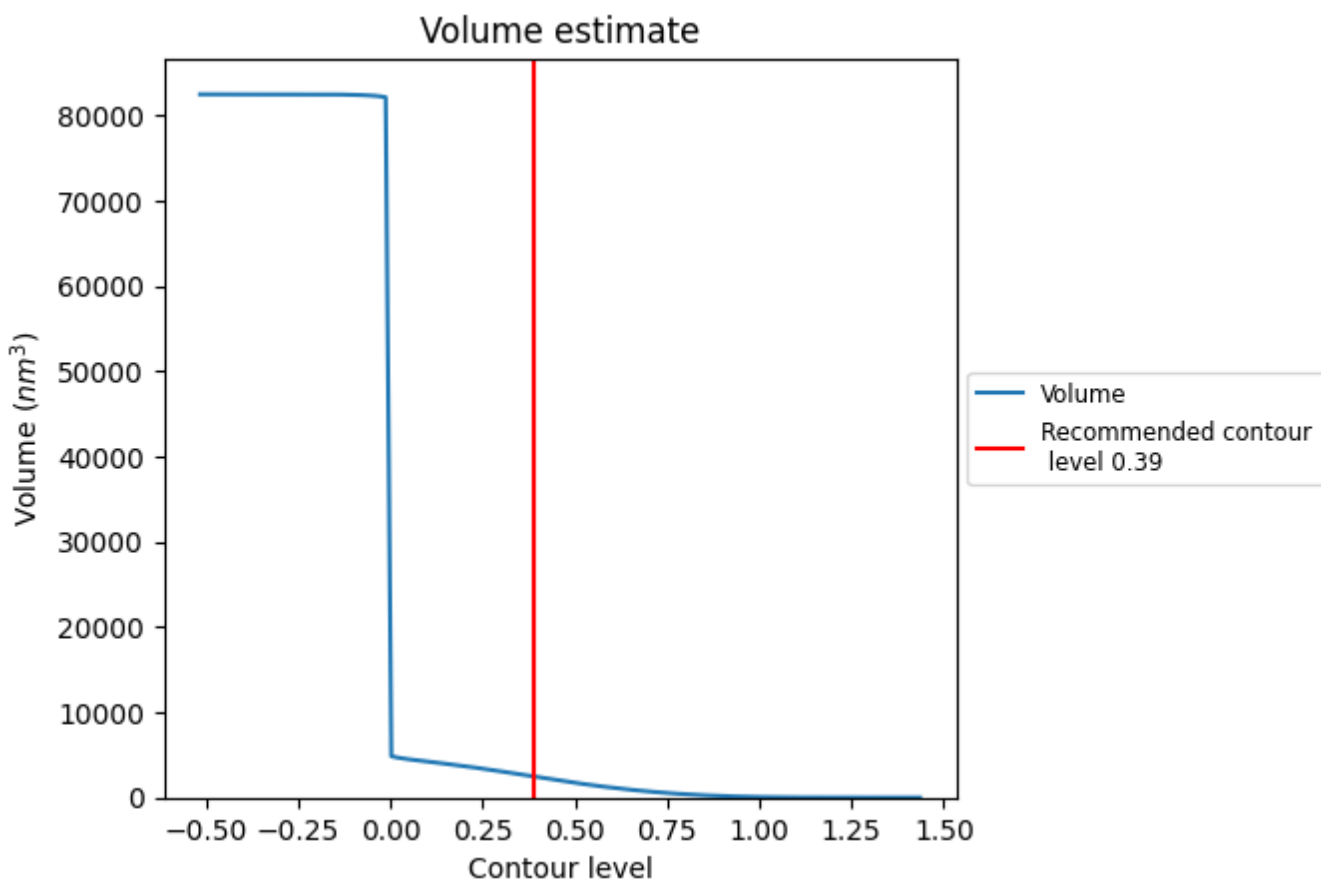
This section contains the results of statistical analysis of the map.

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.

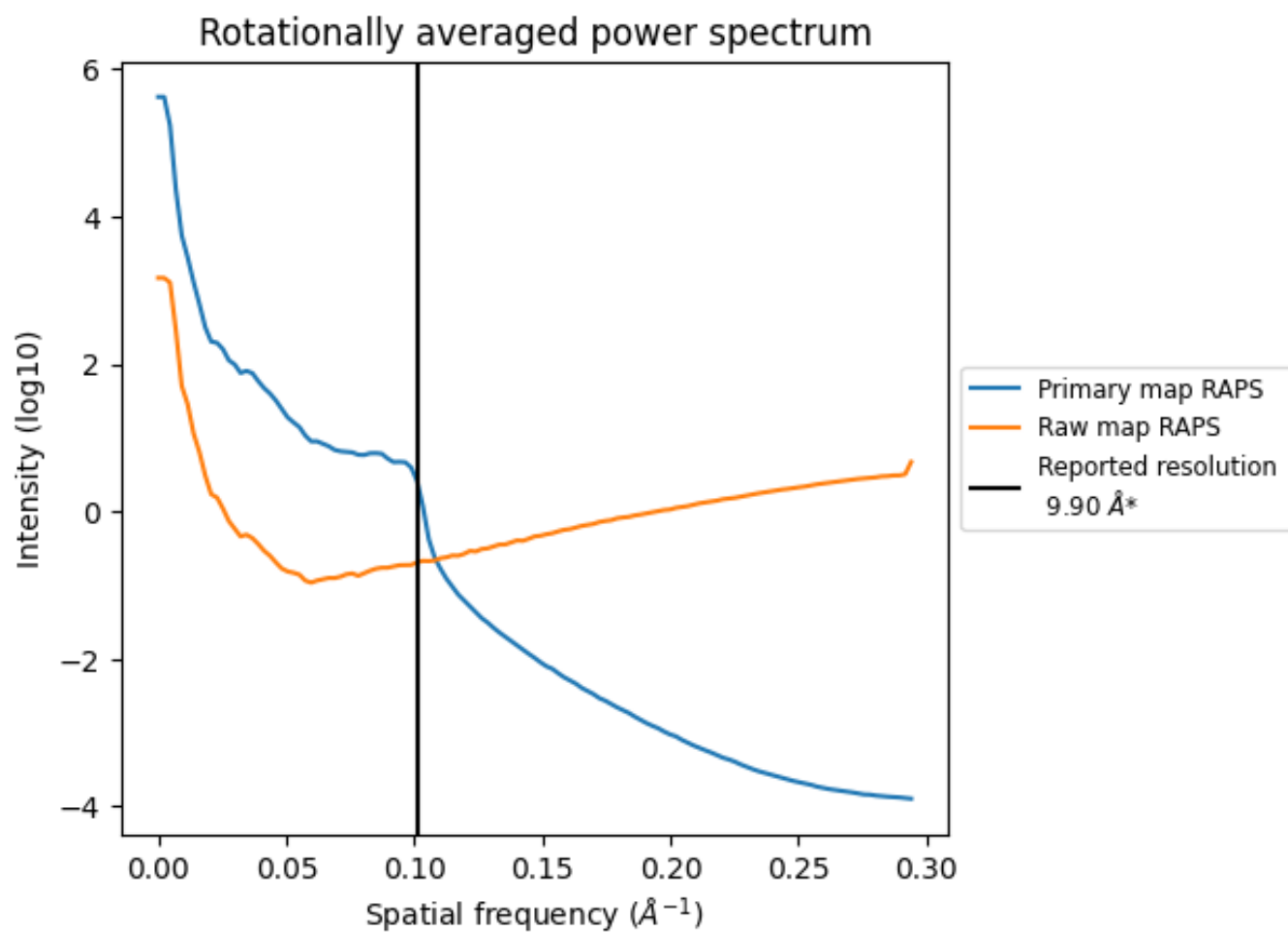
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2460 nm³; this corresponds to an approximate mass of 2222 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

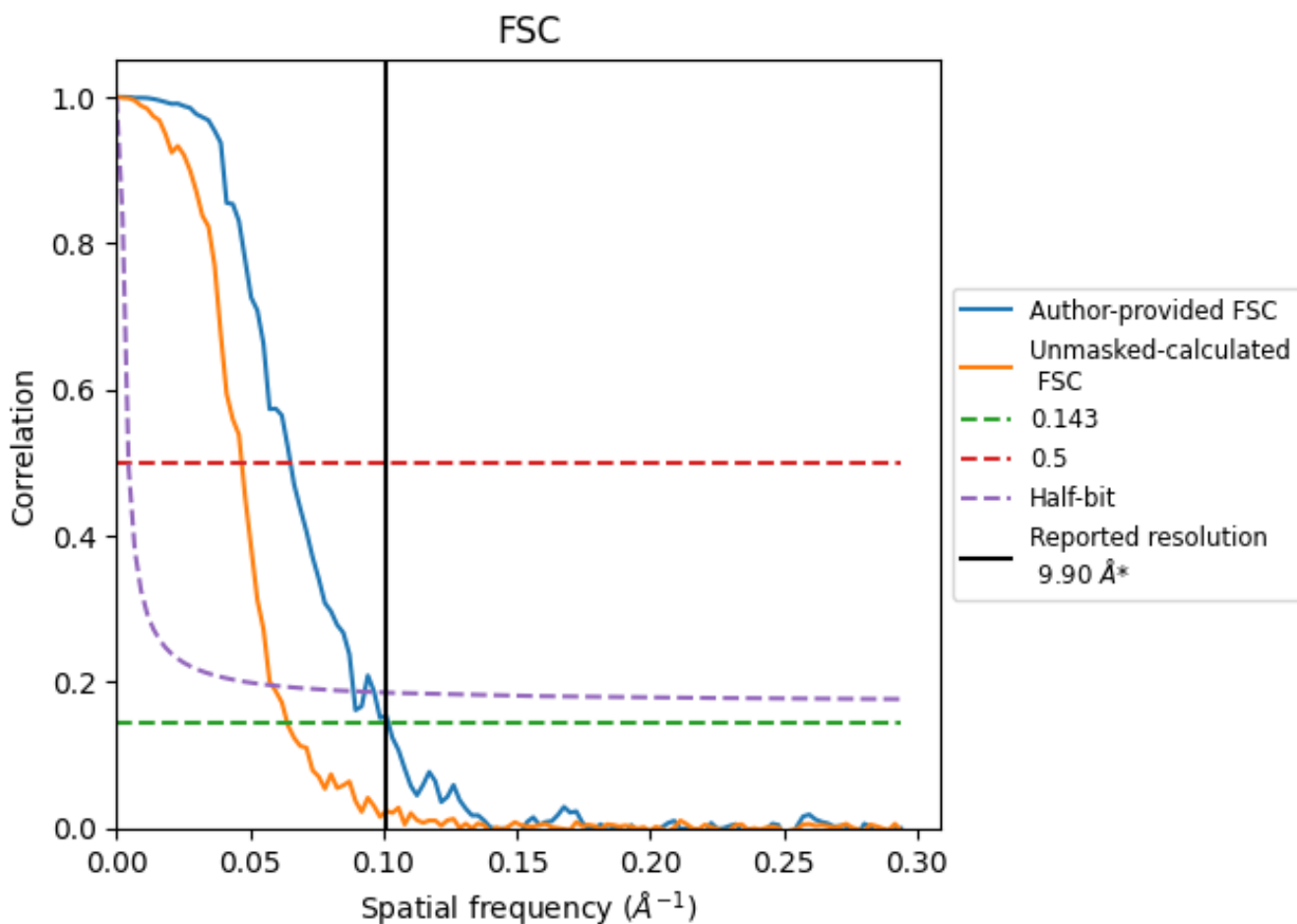


*Reported resolution corresponds to spatial frequency of 0.101 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.101 Å⁻¹

8.2 Resolution estimates [i](#)

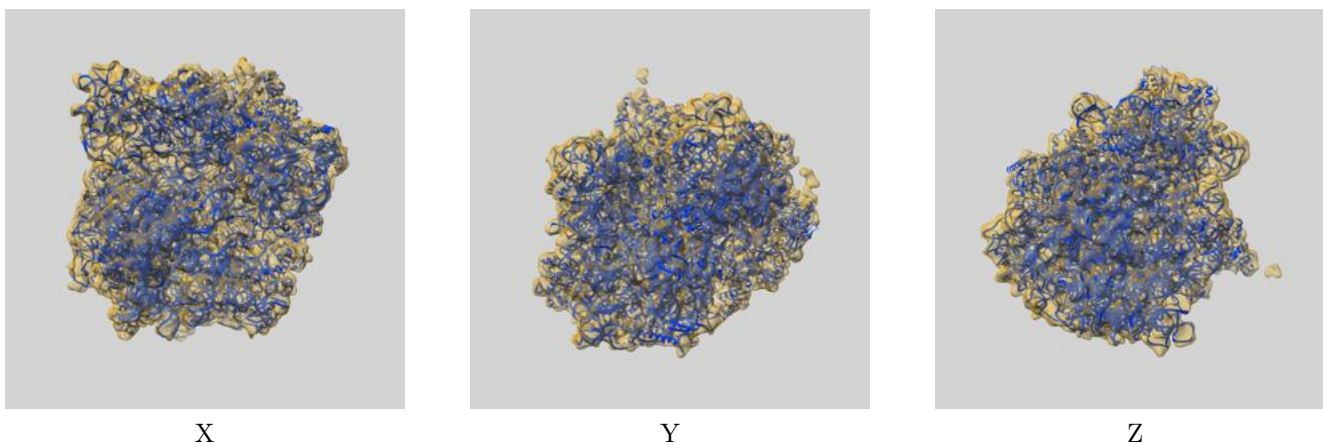
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.90	-	-
Author-provided FSC curve	9.81	15.34	11.26
Unmasked-calculated*	15.60	21.28	17.12

*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 15.60 differs from the reported value 9.9 by more than 10 %

9 Map-model fit [i](#)

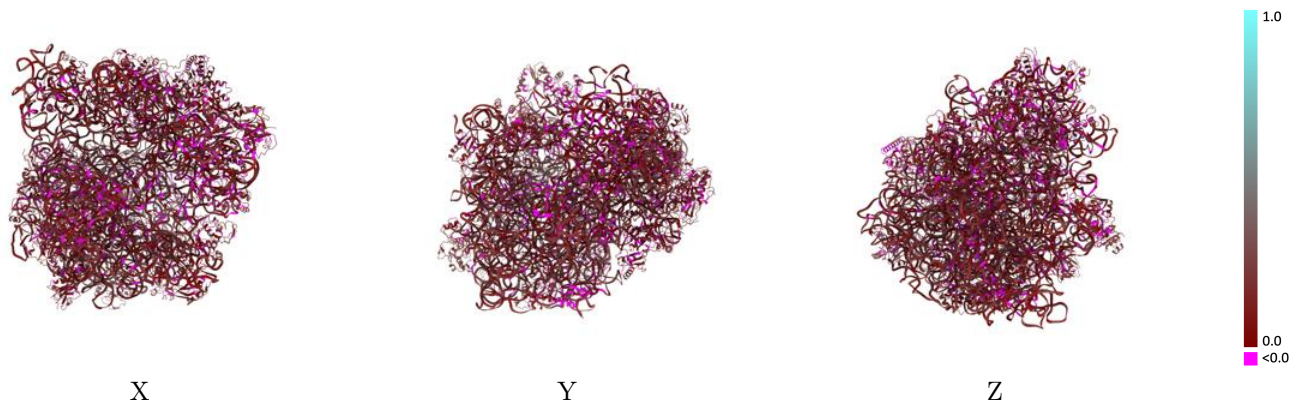
This section contains information regarding the fit between EMDB map EMD-13413 and PDB model 7PHC. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



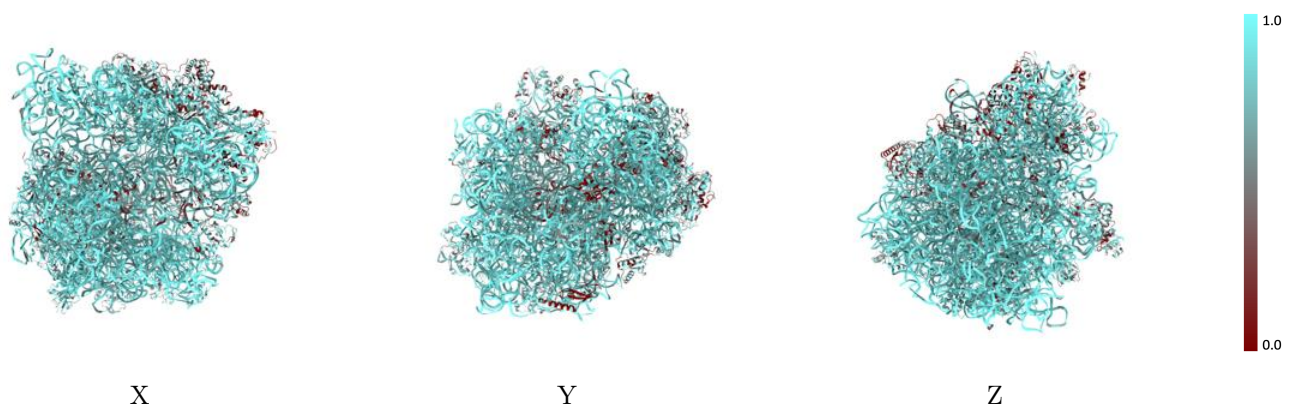
The images above show the 3D surface view of the map at the recommended contour level 0.39 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



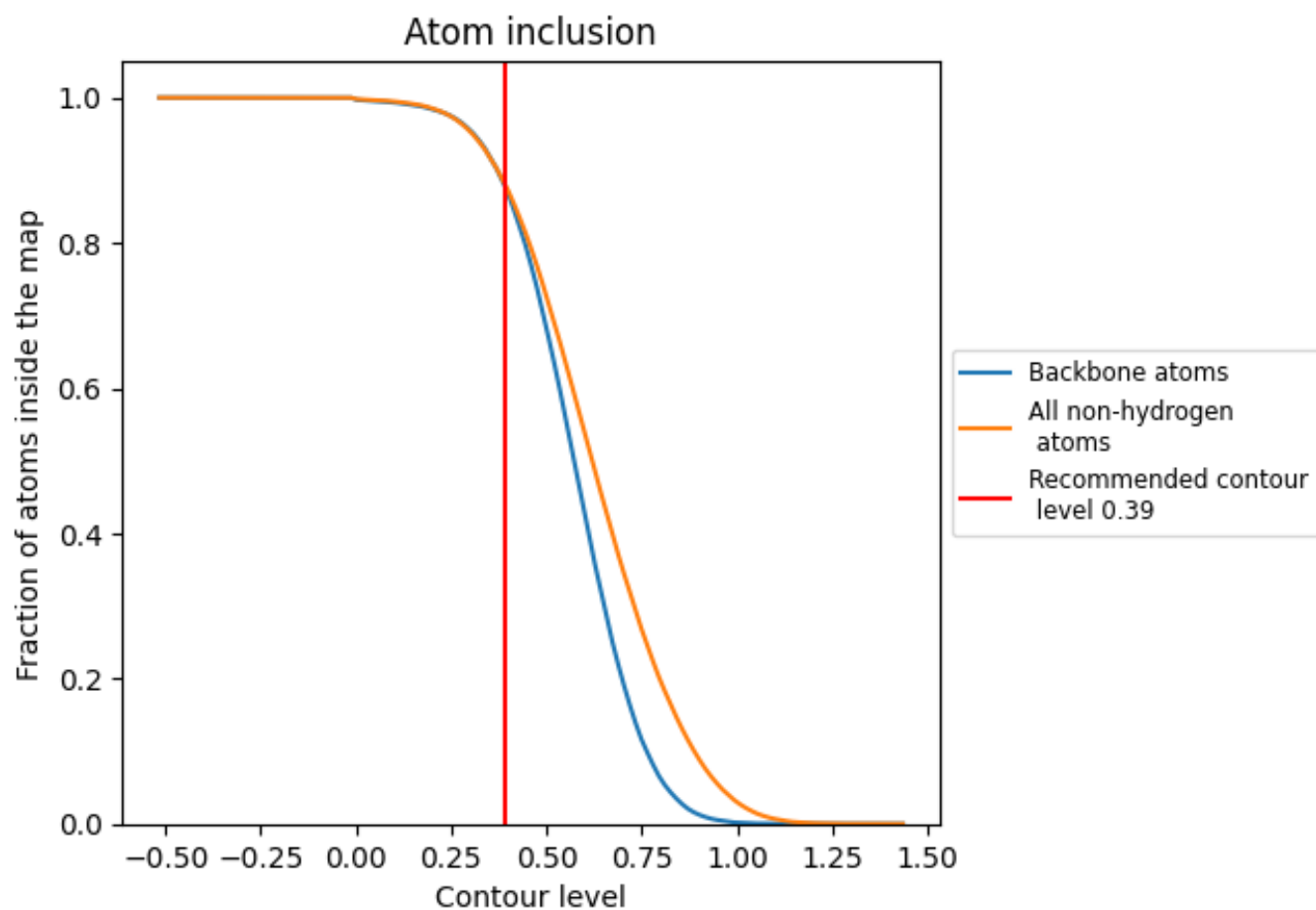
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.39).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 88% 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 (0.39) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8822	 0.1330
0	 0.9014	 0.1350
1	 0.9227	 0.1310
2	 0.8851	 0.0940
3	 0.9676	 0.1480
4	 0.9656	 0.1500
5	 0.9562	 0.1370
6	 0.7305	 0.1220
8	 0.5884	 0.0750
A	 0.5737	 0.1190
B	 0.6667	 0.1130
C	 0.6901	 0.1140
D	 0.6638	 0.1050
E	 0.5584	 0.1040
F	 0.4934	 0.0910
G	 0.6893	 0.0990
H	 0.5554	 0.0850
I	 0.7182	 0.1080
J	 0.6193	 0.0780
K	 0.7529	 0.1120
L	 0.6078	 0.1050
M	 0.8505	 0.0770
N	 0.7311	 0.1330
O	 0.8633	 0.1360
P	 0.7473	 0.1080
Q	 0.7519	 0.0870
R	 0.7687	 0.0640
S	 0.8689	 0.1130
T	 0.7522	 0.1530
a	 0.8224	 0.0980
b	 0.8214	 0.1120
c	 0.7850	 0.1290
d	 0.6915	 0.1130
e	 0.7151	 0.1330
f	 0.3091	 0.0510



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Chain	Atom inclusion	Q-score
g	 0.6842	 0.1230
h	 0.5089	 0.0900
i	 0.8142	 0.1210
j	 0.7261	 0.1210
k	 0.8261	 0.1080
l	 0.8294	 0.1180
m	 0.8408	 0.1040
n	 0.8304	 0.1230
o	 0.8145	 0.1380
p	 0.9016	 0.1160
q	 0.8135	 0.1250
r	 0.8637	 0.1280
s	 0.8350	 0.1210
t	 0.7364	 0.1320
u	 0.7891	 0.0840
v	 0.8626	 0.1170
w	 0.7740	 0.1510
x	 0.6822	 0.1470
y	 0.8502	 0.1270
z	 0.8967	 0.1210