



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 02:08 PM UTC

PDB ID : 7PHA / pdb_00007pha
EMDB ID : EMD-13411
Title : 70S ribosome with EF-Tu-tRNA and P-site tRNA in chloramphenicol-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-16
Resolution : 8.50 Å (reported)
Based on initial models : 4V5L, 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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

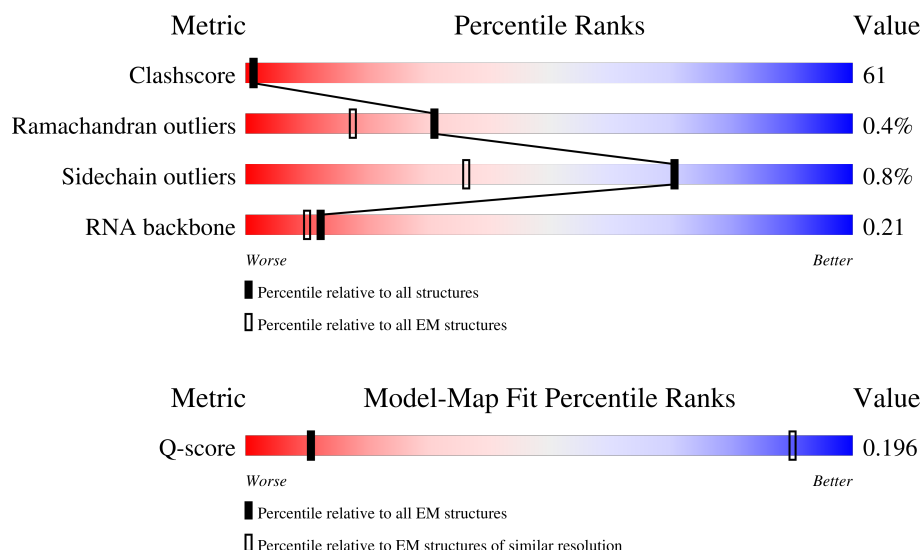
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.50 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	328 (8.00 - 9.00)

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	 27% 71%
2	1	59	 24% 76%
3	2	37	 24% 73%




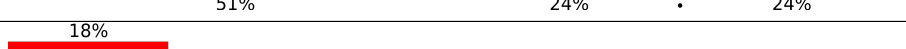
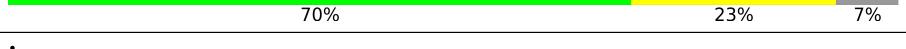
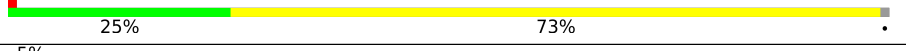

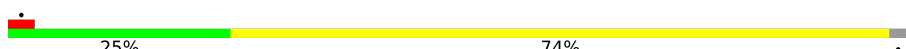
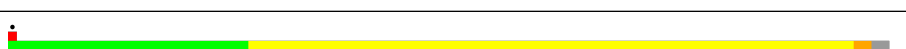
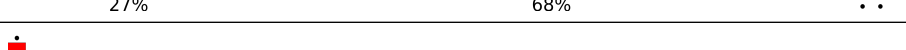
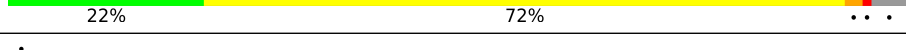
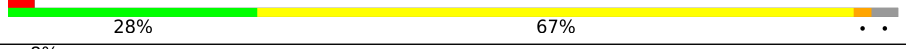

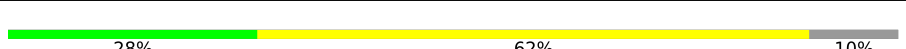
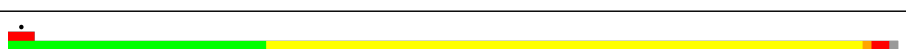
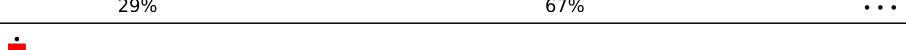



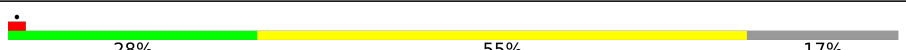
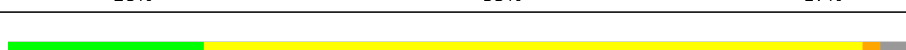
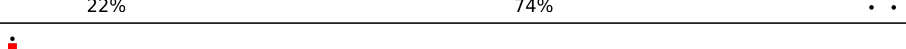



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Mol	Chain	Length	Quality of chain
4	9	394	
5	A	294	
6	B	273	
7	C	205	
8	D	219	
9	E	215	
10	F	155	
11	G	142	
12	H	132	
13	I	108	
14	J	121	
15	K	139	
16	L	124	
17	M	61	
18	N	86	
19	O	94	
20	P	85	
21	Q	104	
22	R	87	
23	S	87	
24	T	60	
25	a	287	
26	b	287	
27	c	212	
28	d	180	

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Mol	Chain	Length	Quality of chain
29	e	184	
30	f	149	
31	g	161	
32	h	137	
33	i	146	
34	j	122	
35	k	151	
36	l	139	
37	m	124	
38	n	116	
39	o	119	
40	p	127	
41	q	100	
42	r	159	
43	s	237	
44	t	111	
45	u	104	
46	v	65	
47	w	111	
48	x	97	
49	y	57	
50	z	53	
51	3	2907	
52	4	108	
53	5	1520	

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Mol	Chain	Length	Quality of chain
54	6	76	 54%42%
54	7	76	 33%64%

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 149139 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

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

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

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

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

- Molecule 4 is a protein called Elongation factor Tu.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 14 is a protein called 30S ribosomal protein S11.

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

- Molecule 15 is a protein called 30S ribosomal protein S12.

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

- Molecule 16 is a protein called 30S ribosomal protein S13.

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

- Molecule 17 is a protein called 30S ribosomal protein S14 type Z.

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

- Molecule 18 is a protein called 30S ribosomal protein S15.

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

- Molecule 19 is a protein called 30S ribosomal protein S16.

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

- Molecule 20 is a protein called 30S ribosomal protein S17.

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

- Molecule 21 is a protein called 30S ribosomal protein S18.

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

- Molecule 22 is a protein called 30S ribosomal protein S19.

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

- Molecule 23 is a protein called 30S ribosomal protein S20.

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

- Molecule 24 is a protein called 30S ribosomal protein S21.

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

- Molecule 25 is a protein called 50S ribosomal protein L2.

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

- Molecule 26 is a protein called 50S ribosomal protein L3.

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

- Molecule 27 is a protein called 50S ribosomal protein L4.

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

- Molecule 28 is a protein called 50S ribosomal protein L5.

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	123	Total	C	N	O	S	0	0
			936	599	160	174	3		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 42 is a protein called 50S ribosomal protein L22.

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

- Molecule 43 is a protein called 50S ribosomal protein L23.

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

- Molecule 44 is a protein called 50S ribosomal protein L24.

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

- Molecule 45 is a protein called 50S ribosomal protein L27.

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

- Molecule 46 is a protein called 50S ribosomal protein L28.

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

- Molecule 47 is a protein called 50S ribosomal protein L29.

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

- Molecule 48 is a protein called 50S ribosomal protein L31.

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

- Molecule 49 is a protein called 50S ribosomal protein L32.

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

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

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

- Molecule 51 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 52 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

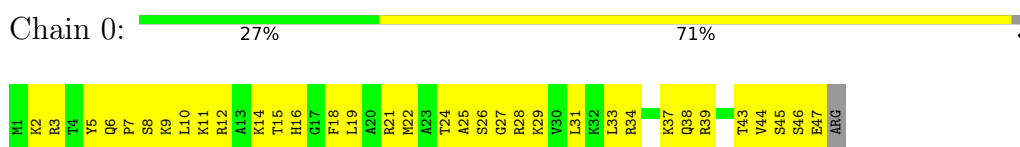
- Molecule 54 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	6	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
54	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

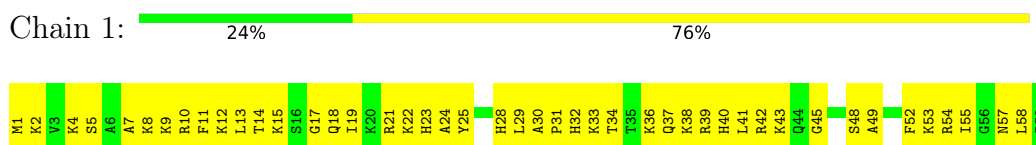
3 Residue-property plots

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

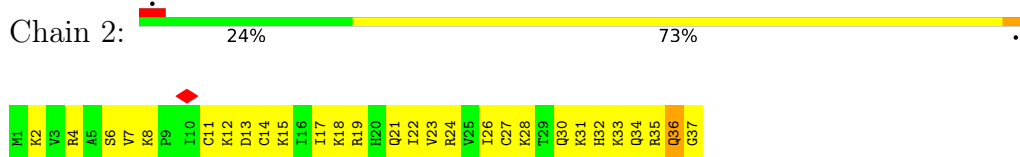
• Molecule 1: 50S ribosomal protein L34



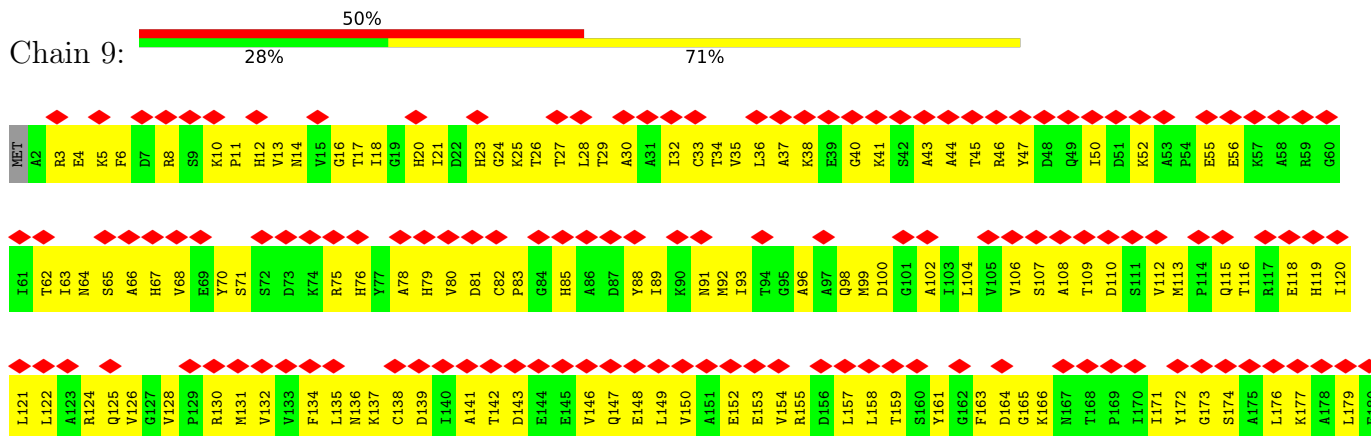
• Molecule 2: 50S ribosomal protein L35

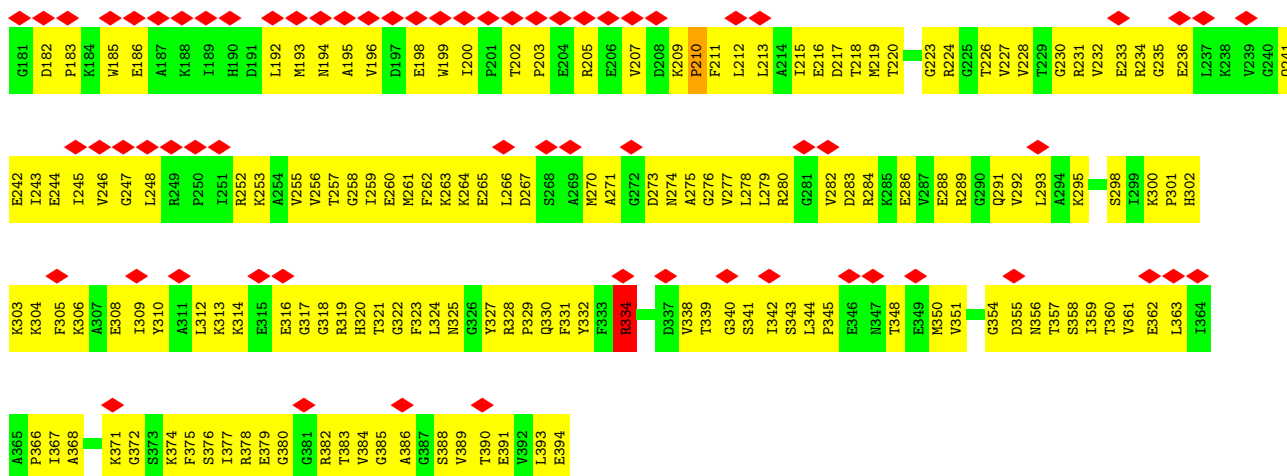


• Molecule 3: 50S ribosomal protein L36

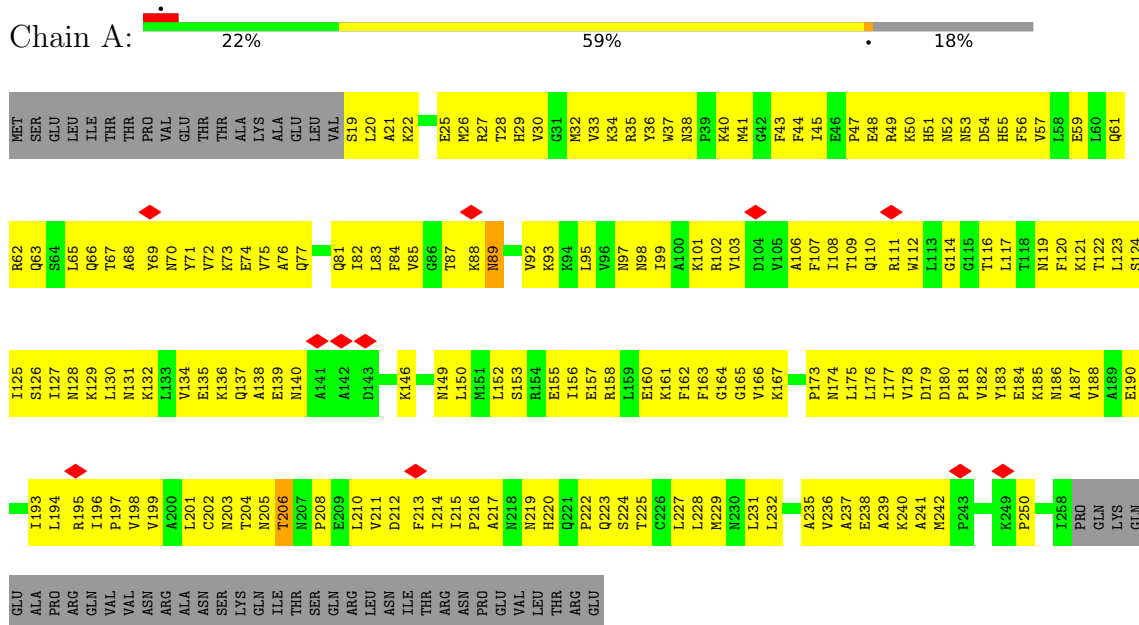


• Molecule 4: Elongation factor Tu

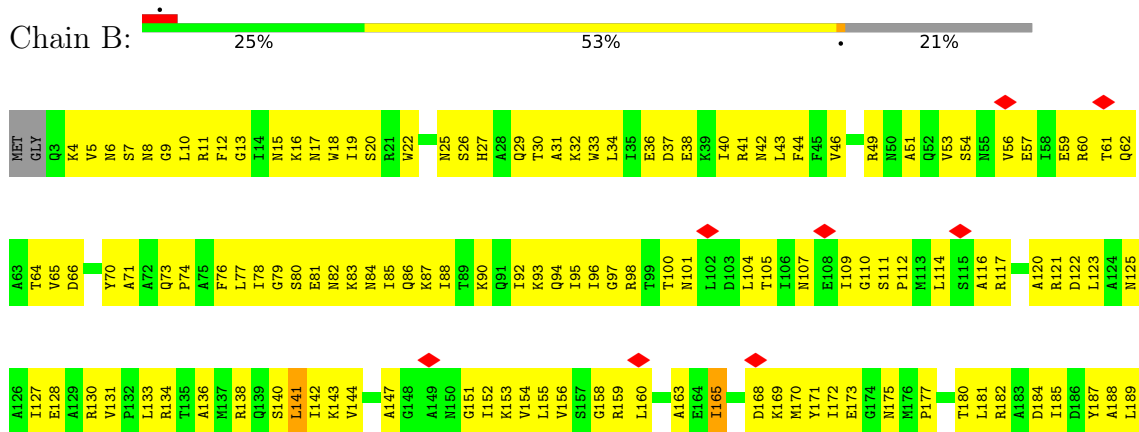


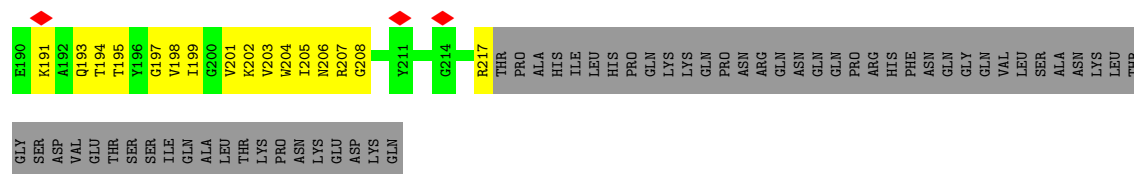


• Molecule 5: 30S ribosomal protein S2

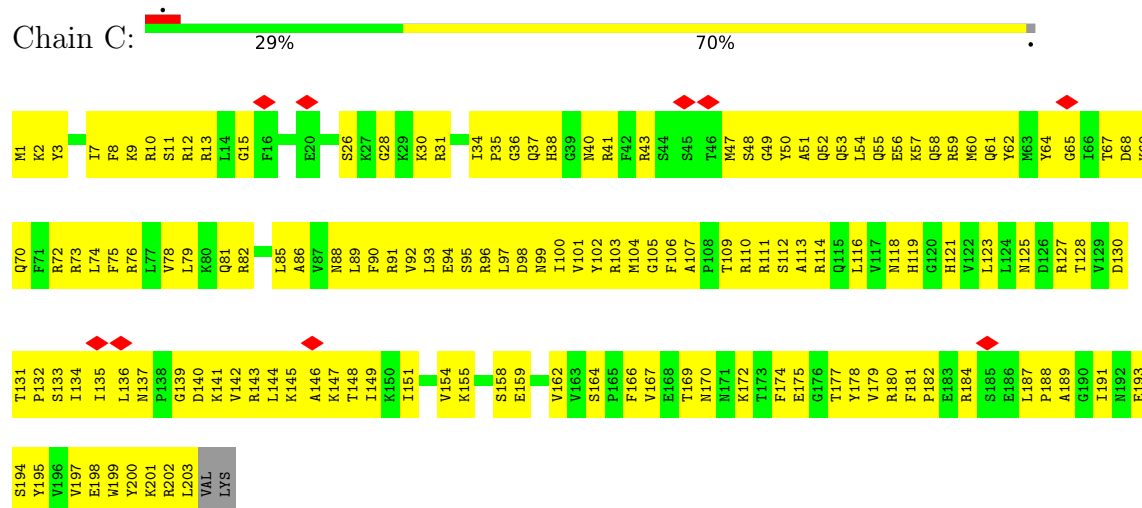


• Molecule 6: 30S ribosomal protein S3

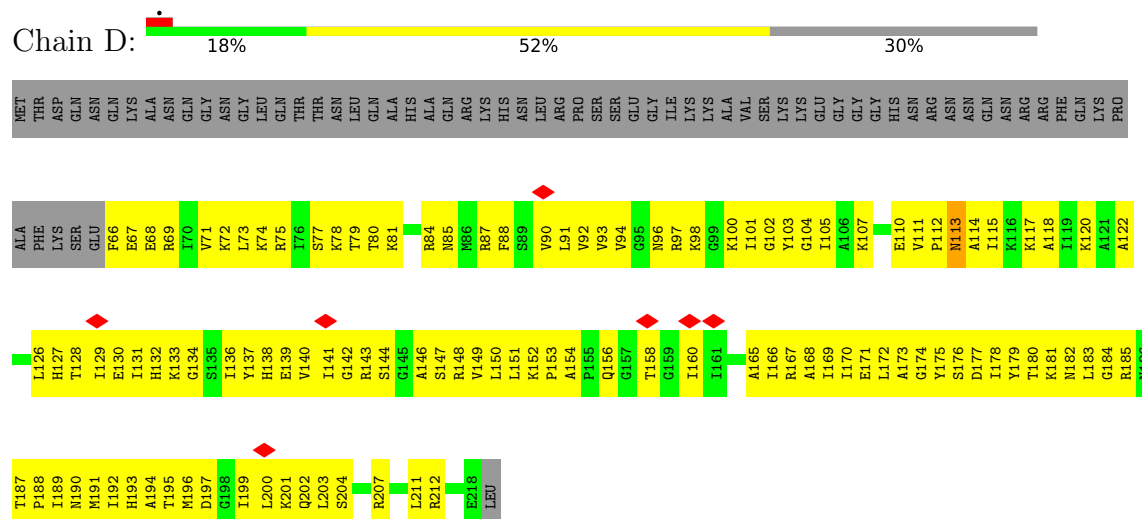




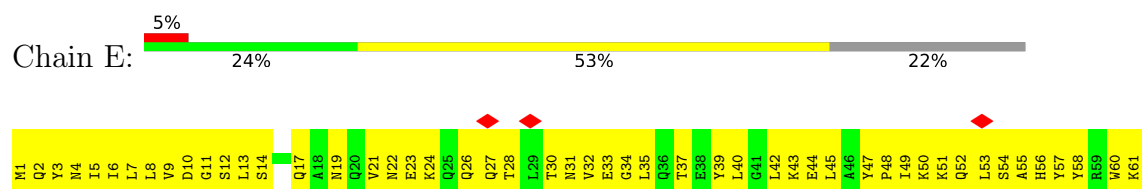
• Molecule 7: 30S ribosomal protein S4

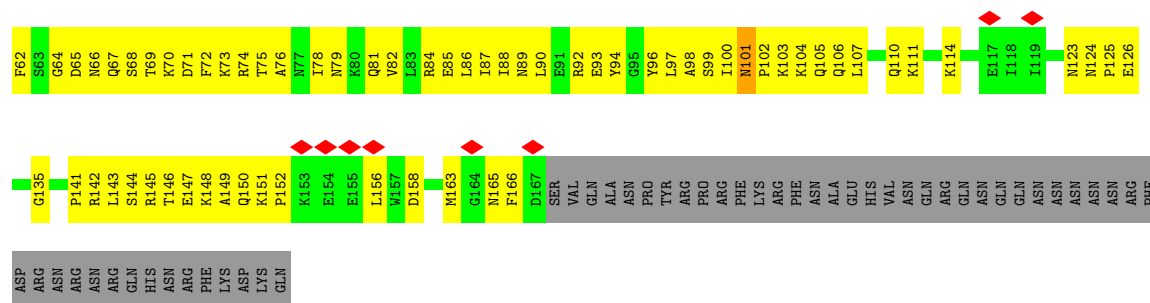


• Molecule 8: 30S ribosomal protein S5

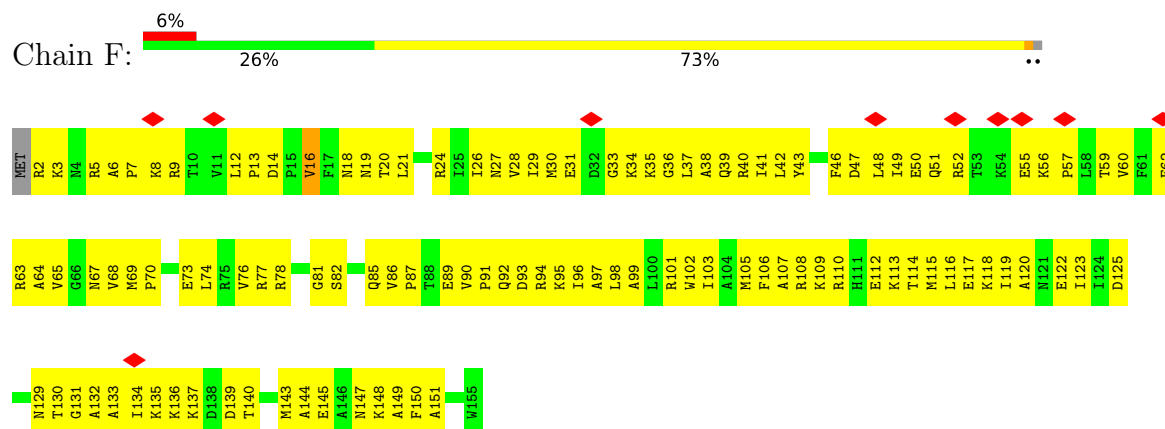


• Molecule 9: 30S ribosomal protein S6

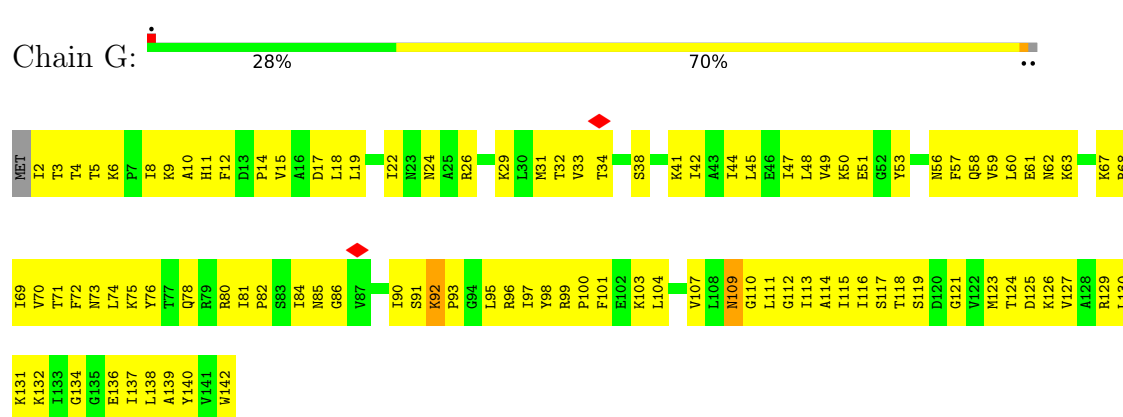




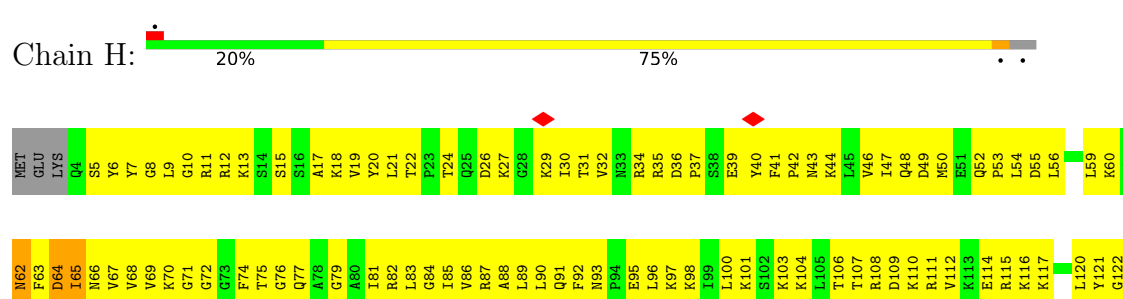
• Molecule 10: 30S ribosomal protein S7



• Molecule 11: 30S ribosomal protein S8



• Molecule 12: 30S ribosomal protein S9



A123
R124
A125
P127
Q128
T129
K131
ARG

• Molecule 13: 30S ribosomal protein S10

Chain I: 11% 30% 62% 6%

MET ASN ALA ALA ASN V7 K8 K73 Y9 P10 E11 L12 L13 L14 L15 L16 L17 L18 L19 L20 L21 L22 L23 L24 L25 T28 K29 K30 K31 L31 V32 E33 V34 V35 K41 K42 K43 G44 P45 L46 L47 L48 L49 T50 K51 K52 E53 V54 T55 T56 T57 T58 R59 S60 P61 H62 V63 D64 K65

A66 S67 E68 F69 Q70 F71 E72 K73 K74 R75 H76 K77 L78 L79 M80 I81 L82 V83 V84 V85 N86 I90 D91 L93 K94 R95 P99 V100 G101 V102 R105 F106 S107 LYS

• Molecule 14: 30S ribosomal protein S11

Chain J: 7% 32% 62% 6%

MET ALA LYS LYS LYS ILE N8 V9 S10 S11 G12 H15 V16 S17 C18 S19 P20 N21 N22 V25 S28 D29 G32 N33 V34 V37 A38 S39 S40 M43 C44 P45 K46 C47 S48 R49 K50 K51 T52 P53 Y54 S55 S56 S57 S58 A59 A60 D61 V63 A64 K65 T66

V67 K68 E69 M70 G71 G72 W75 V76 F78 F79 K80 G81 T82 G83 R84 C85 K86 D87 T88 A89 I90 R91 S92 F93 L98 S99 I100 E102 E103 N104 E105 K106 T107 I109 P108 P110 H111 N112 G113 C114 K115 P116 P117 K118 R119 P120 R121

• Molecule 15: 30S ribosomal protein S12

Chain K: 28% 69%

MET A2 T3 I4 A5 Q6 L7 K10 P11 R12 K16 V17 K18 S19 K20 L24 H25 Y26 N27 L28 N29 N30 L31 N32 K33 K34 N37 V38 Y39 S40 P41 L42 K43 R44 G45 V46 C47 T48 R49 V50 G51 T52 M53 T54 P55 K56 K57 P58 N59 S60 A61 L62 R63 K64 Y65 A66

K67 V68 R69 L70 W71 N72 E75 V76 L77 T78 T80 P81 G84 H85 N86 L87 Q88 E89 S91 V92 T93 L94 L95 R96 G97 G98 R99 V100 K101 D102 L103 P104 G105 V106 L107 Y108 H109 I110 V111 R112 G113 T114 L115 D116 T117 V118 G119 V120 E121 K122 R123 R124 Q125 Q126 R127 S128

A129 Y130 K133 K134 P135 K136 A137 LYS SER

• Molecule 16: 30S ribosomal protein S13

Chain L: 33% 62% 5%

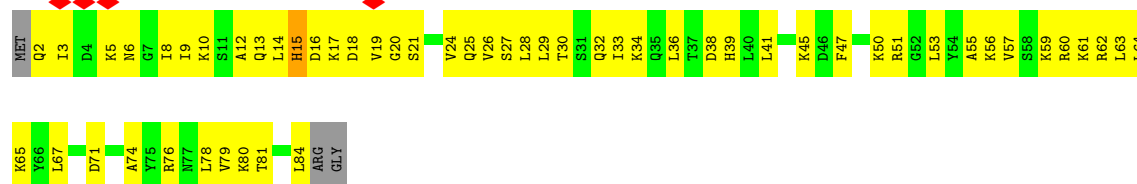
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G67 D68 L69 R70 R71 E72 I73 A74 L75 N76 H79 A85 W86 L89 R90 H91 R92 R93 R94 L95 P96 V97 R98 G99 Q100 R101 T102 R103 T104 N105 A106 R107 T108 T109 K110 G111 P112 R113 K114 T115 V116 K119 K120 I121 E122 SER LYS

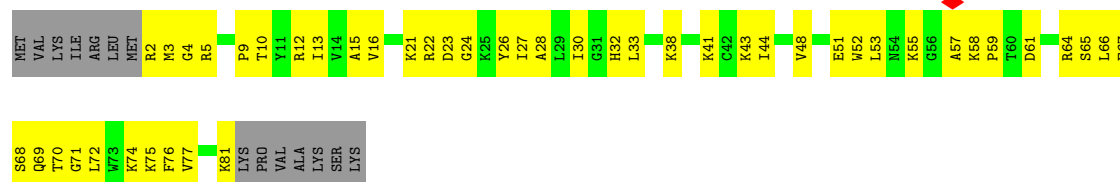
• Molecule 17: 30S ribosomal protein S14 type Z



• Molecule 18: 30S ribosomal protein S15



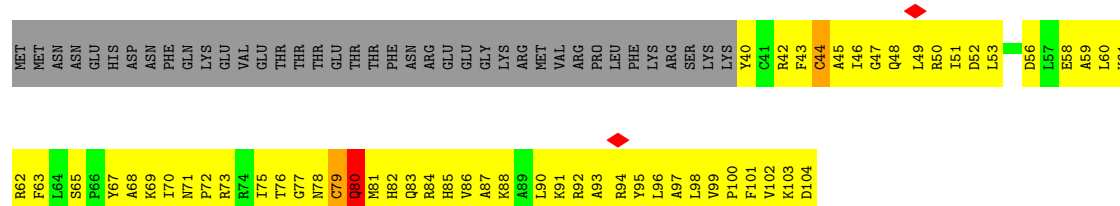
• Molecule 19: 30S ribosomal protein S16




• Molecule 20: 30S ribosomal protein S17

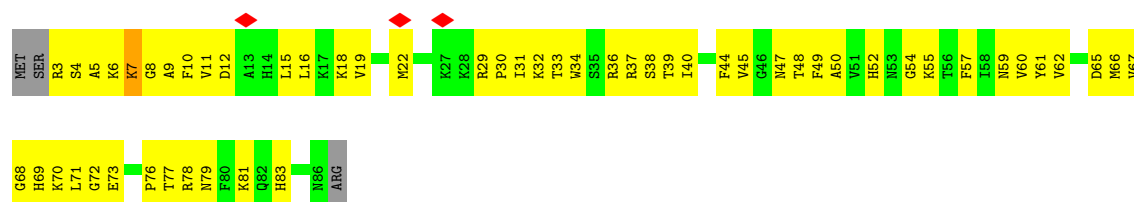


• Molecule 21: 30S ribosomal protein S18



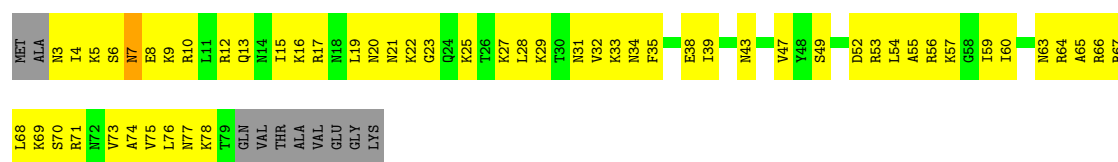
- Molecule 22: 30S ribosomal protein S19

Chain R:  33% 62%



- Molecule 23: 30S ribosomal protein S20

Chain S:  25% 62% 11%



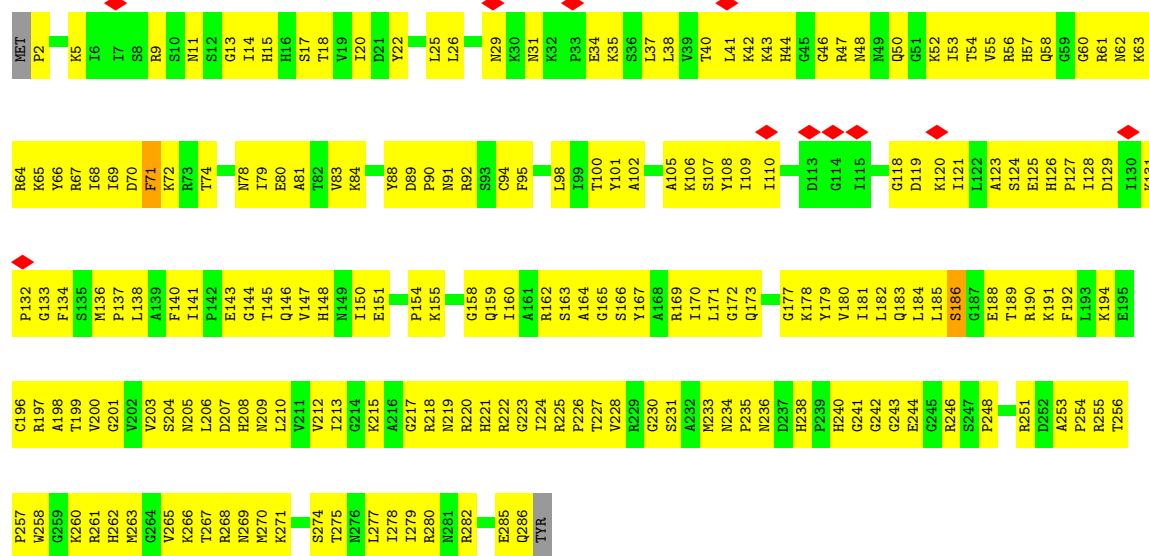
- Molecule 24: 30S ribosomal protein S21

Chain T:  42% 47% 12%

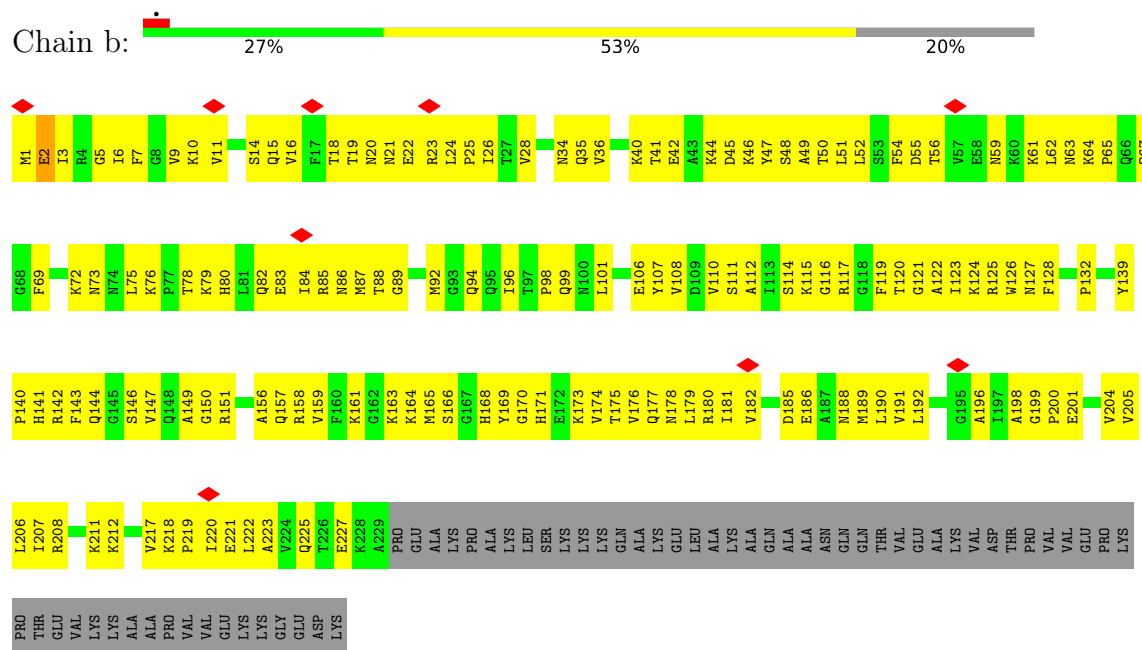


- Molecule 25: 50S ribosomal protein L2

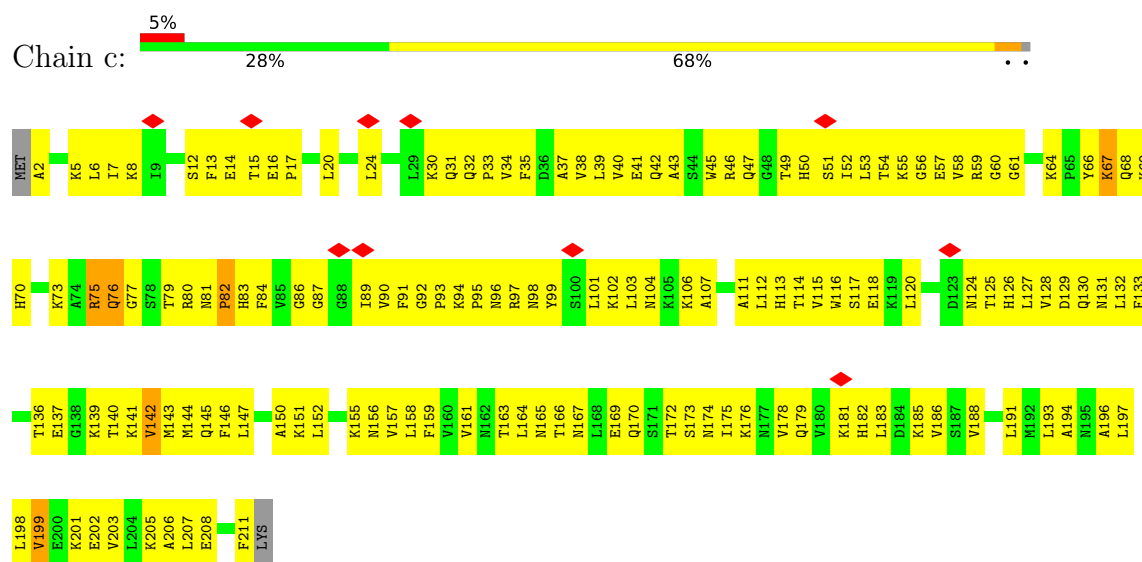
Chain a:  29% 70%



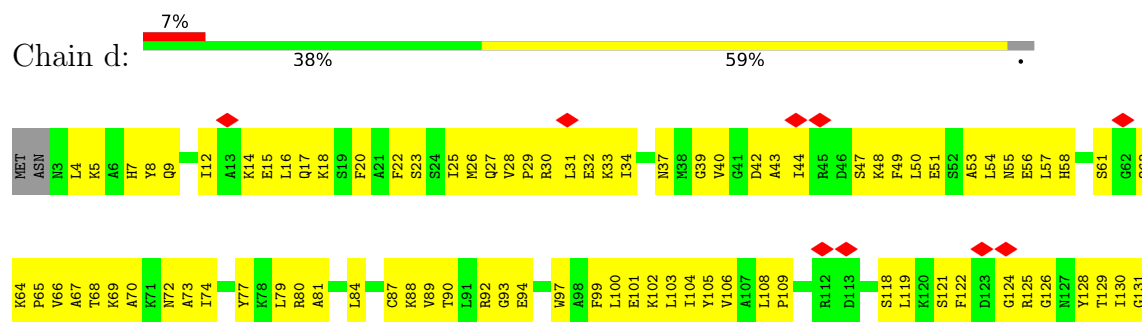
- Molecule 26: 50S ribosomal protein L3

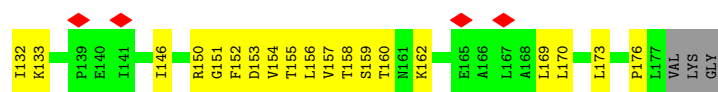


• Molecule 27: 50S ribosomal protein L4

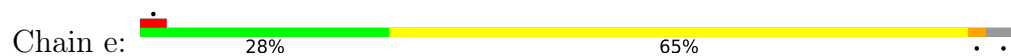


• Molecule 28: 50S ribosomal protein L5

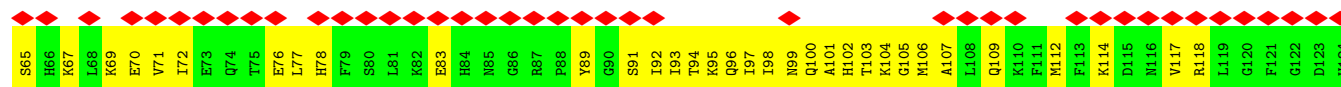




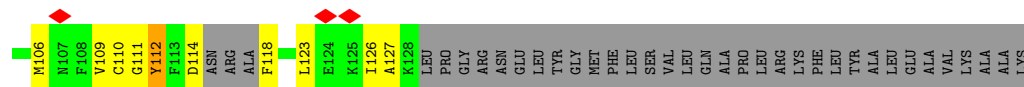
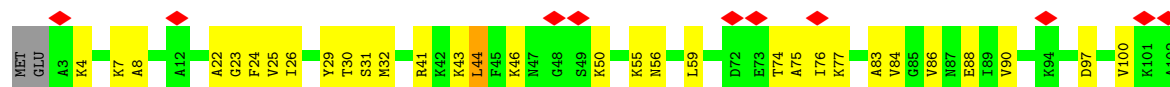
• Molecule 29: 50S ribosomal protein L6



• Molecule 30: 50S ribosomal protein L9

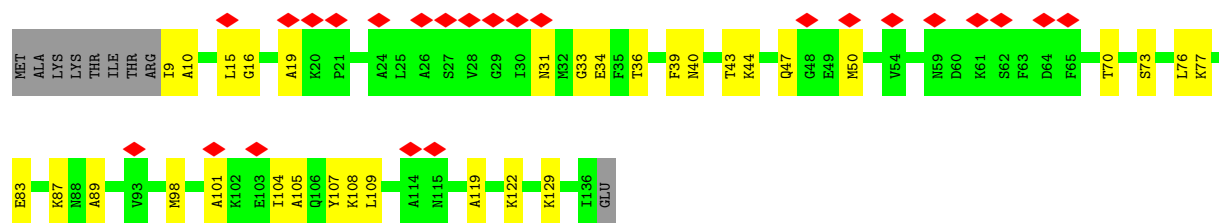


• Molecule 31: 50S ribosomal protein L10



• Molecule 32: 50S ribosomal protein L11





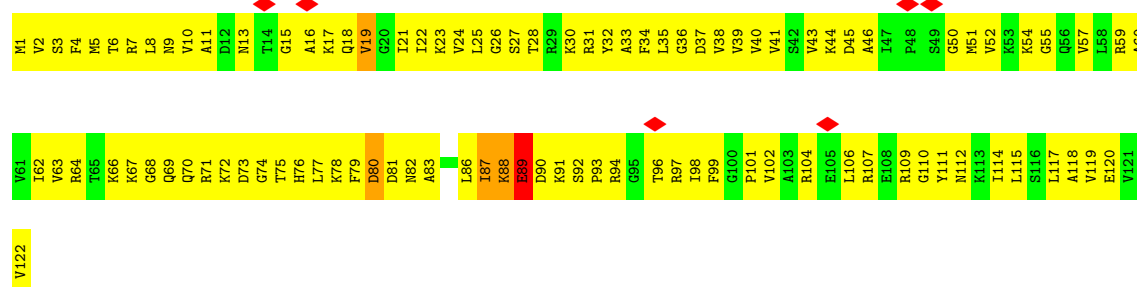
• Molecule 33: 50S ribosomal protein L13

Chain i: 25% 73%



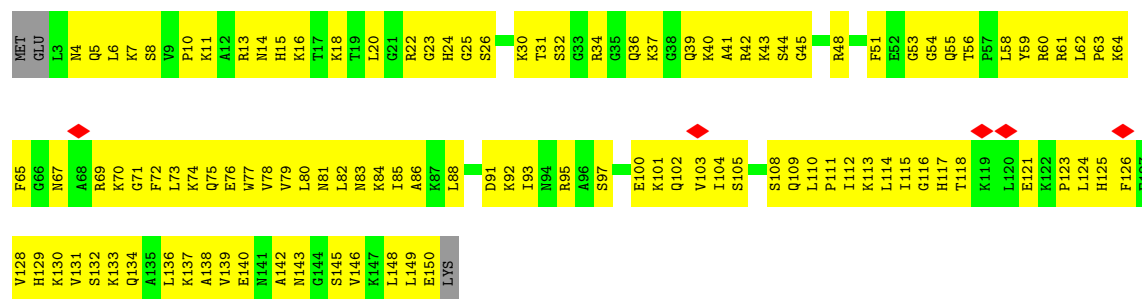
• Molecule 34: 50S ribosomal protein L14

Chain j: 5% 19% 77%




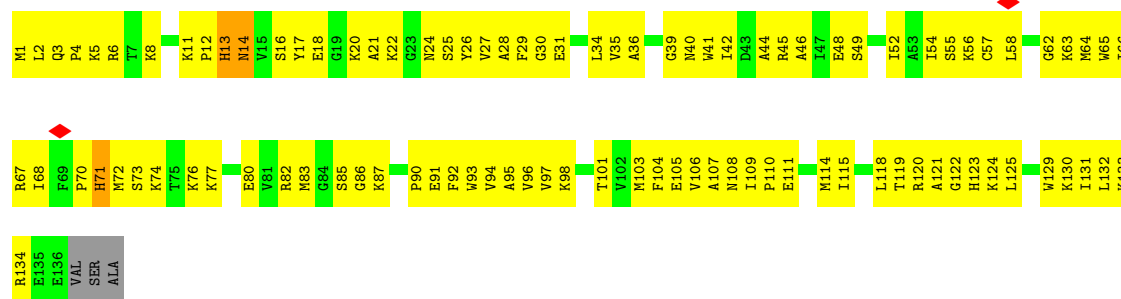
• Molecule 35: 50S ribosomal protein L15

Chain k: 25% 74%



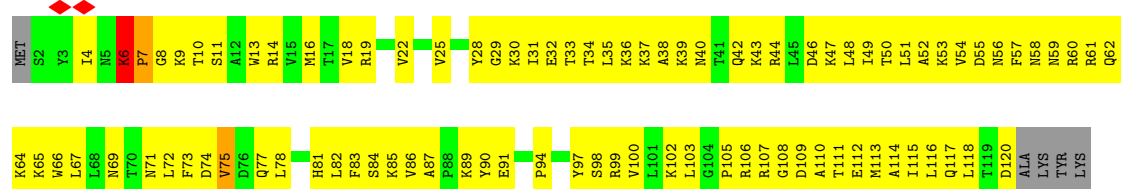
• Molecule 36: 50S ribosomal protein L16

Chain l: 



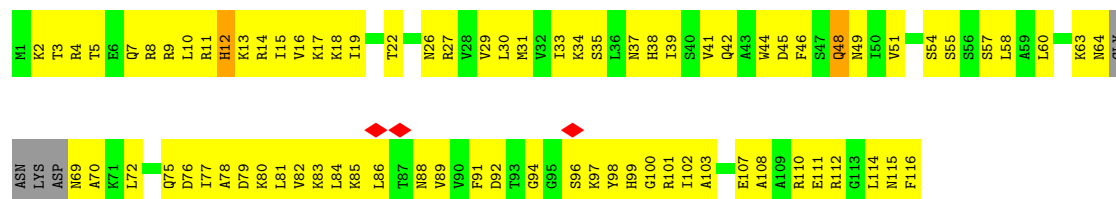
• Molecule 37: 50S ribosomal protein L17

Chain m: 



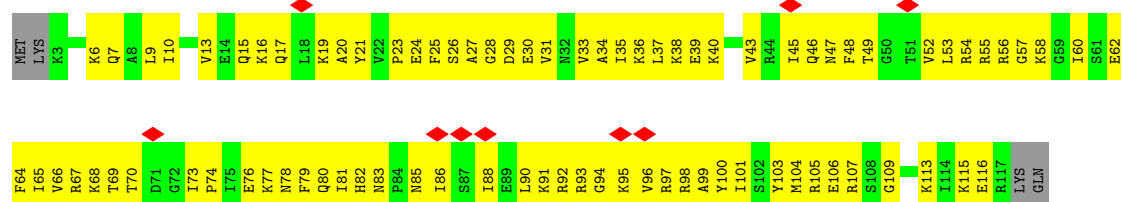
• Molecule 38: 50S ribosomal protein L18

Chain n: 



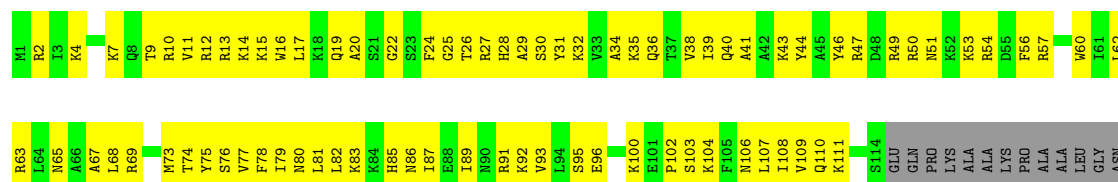
• Molecule 39: 50S ribosomal protein L19

Chain o: 



• Molecule 40: 50S ribosomal protein L20

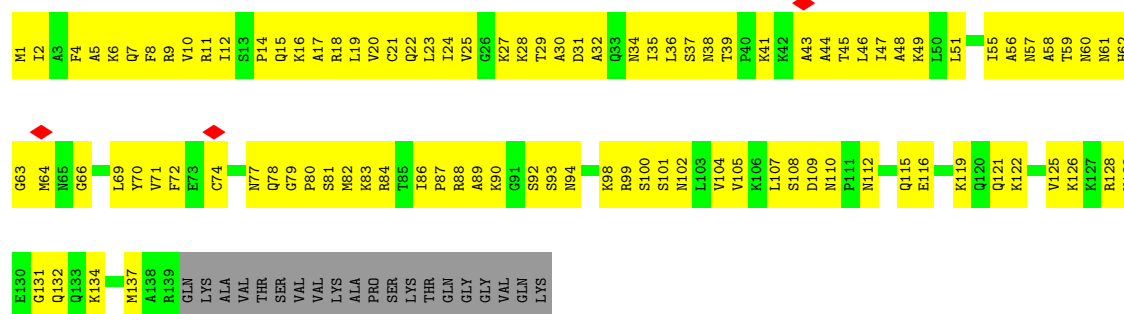
Chain p: 



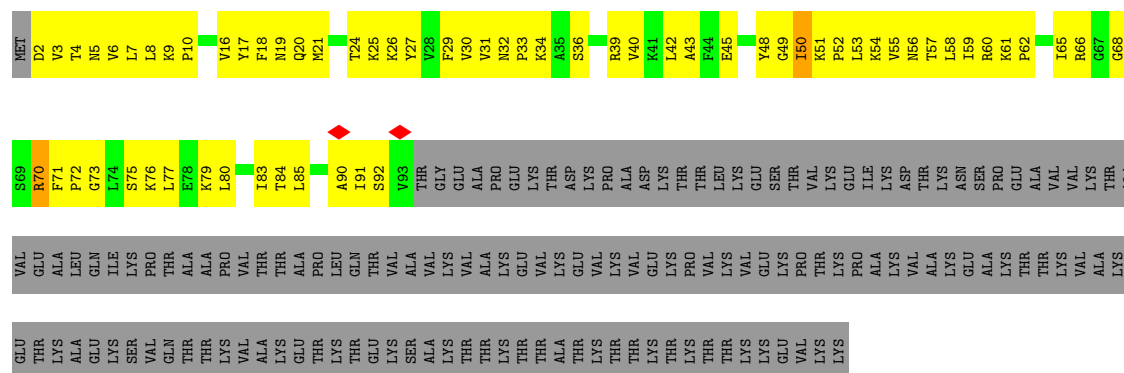
• Molecule 41: 50S ribosomal protein L21



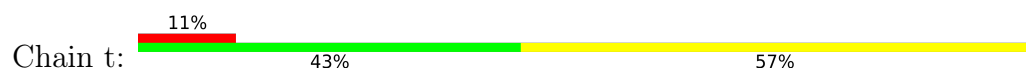
• Molecule 42: 50S ribosomal protein L22

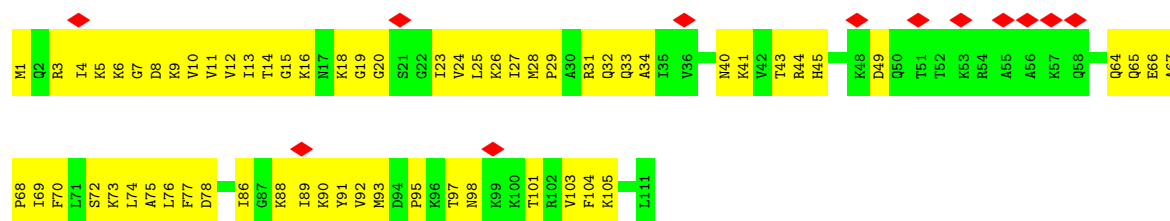


• Molecule 43: 50S ribosomal protein L23

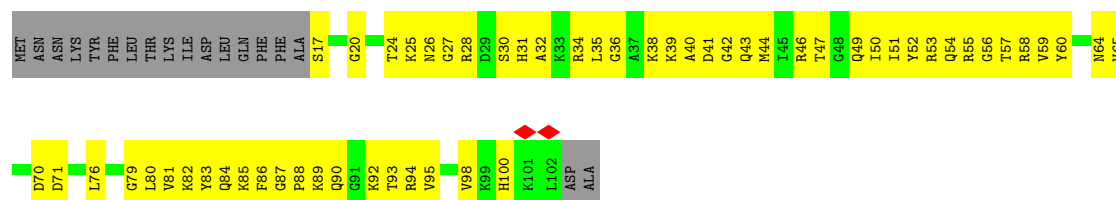


• Molecule 44: 50S ribosomal protein L24





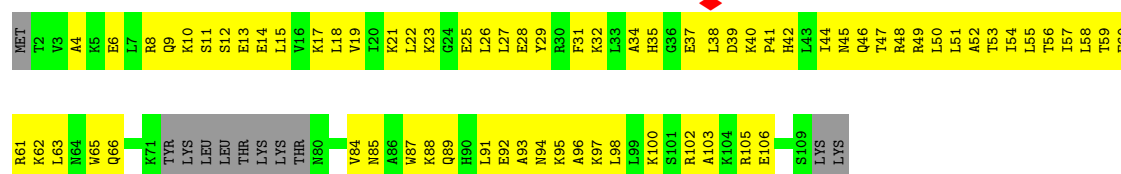
• Molecule 45: 50S ribosomal protein L27



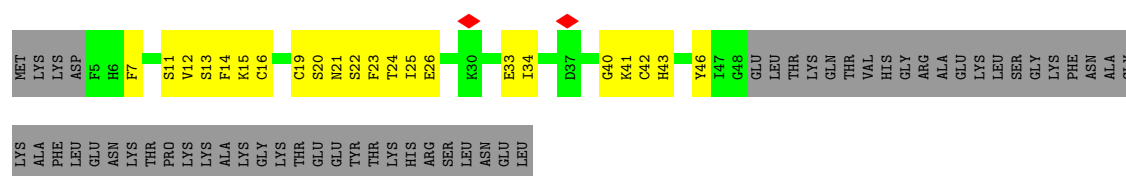
• Molecule 46: 50S ribosomal protein L28



• Molecule 47: 50S ribosomal protein L29

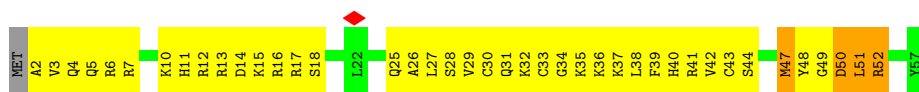


• Molecule 48: 50S ribosomal protein L31



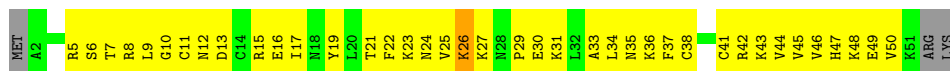
• Molecule 49: 50S ribosomal protein L32





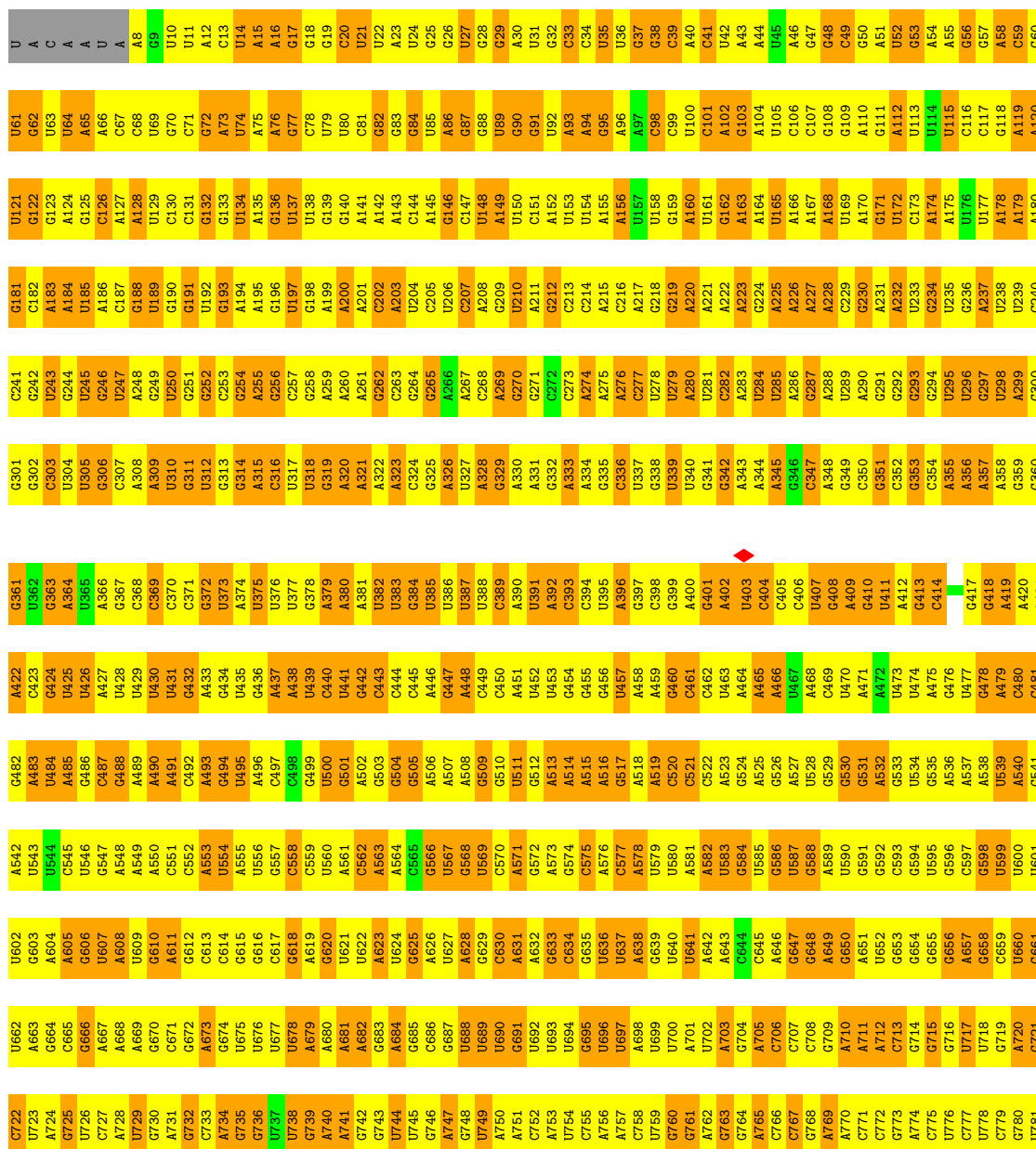
- Molecule 50: 50S ribosomal protein L33 1

Chain z: 21% 72% 6%



- Molecule 51: 23S ribosomal RNA

Chain 3: 52% 44%



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A1745	G1685	G1625	G1505	U1445	A1324	U1264	A1204	C1144	C1084	A1024	A964	A903	G843	G783
U1746	A1686	C1626	U1506	G1446	C1325	G1265	U1205	G1145	A1085	G1025	U965	C904	G844	G784
G1747	G1687	U1627	U1507	A1447	C1326	G1266	U1206	A1146	A1086	A1026	U966	U905	U845	A785
A1748	A1688	G1628	G1508	U1448	C1327	U1267	U1207	G1147	C1087	U1027	U967	G906	U846	A786
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A1750	C1690	A1630	A1510	G1450	U1329	C1269	U1209	G1149	A1089	A1029	A969	A908	U848	G788
A1751	A1691	A1631	C1511	U1451	U1330	C1270	U1210	U1150	U1090	U1030	U970	U911	G849	A789
A1752	A1692	C1632	A1512	A1452	G1331	A1271	A1211	U1151	G1091	U1031	U971	U911	G850	U790
U1753	G1693	C1633	A1513	A1453	U1331	U1272	C1212	U1152	A1092	A1032	C972	A912	U851	A791
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G1755	G1695	G1635	A1515	A1455	A1335	A1274	U1214	U1154	G1094	A1034	C974	G914	G853	G793
A1756	C1696	U1636	G1516	A1456	A1336	C1275	G1215	G1155	U1095	U1035	G975	A915	A854	G794
G1757	A1697	A1637	G1517	A1457	G1337	A1276	U1216	C1156	U1096	A1036	C976	U916	A855	G795
A1758	A1698	A1638	C1518	A1458	U1338	A1277	G1217	G1157	U1097	A1037	A977	G917	A856	A796
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U1767	U1707	U1647	U1527	U1467	A1347	G1286	G1226	G1166	G1106	A1046	G986	U	A865	G805
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A1769	C1709	C1649	U1529	A1469	U1349	C1288	G1228	A1168	A1108	A1048	G988	G928	G867	U807
U1770	A1710	A1650	G1530	C1470	A1350	G1289	U1229	A1169	G1109	U1049	G989	G929	U868	U808
C1771	A1711	C1651	U1531	A1471	G1351	G1290	U1230	C1170	C1110	A1050	G990	C930	U869	A809
G1772	A1712	A1592	A1532	C1472	G1352	C1291	G1231	G1171	C1111	U1051	G991	G931	A870	G810
A1773	G1713	C1653	U1533	C1473	A1353	A1413	U1232	G1172	A1112	A1052	G992	U932	A871	G811
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G1778	A1718	U1658	U1538	A1478	C1358	U1297	A1237	A1177	U1117	G1057	G997	A937	A876	A816
U1779	C1719	C1659	U1539	A1479	U1359	A1298	A1238	A1178	U1118	U1058	C998	A938	G877	A817
A1780	G1720	A1660	G1540	A1480	U1360	A1299	G1239	G1179	U1119	G1059	U999	U939	A878	A818
C1781	A1721	A1661	A1541	U1481	U1361	C1300	U1240	U1180	A1120	G1060	U1000	A940	U879	U819
U1782	U1722	G1662	U1482	U1482	C1362	G1301	U1241	A1181	A1121	A1061	C1001	C941	C880	U820
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A1800	U1740	A1680	A1500	U1440	U1380	C1319	A1259	A1199	C1139	U1079	A1019	C959	A898	U838
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C1802	C1742	A1682	A	A1502	A1382	C1321	U1261	A1201	U1141	A1081	C1021	U961	G900	G840
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U2527	C2528	C2529	U2530	C2531	C2532	A2533	C2534	C2535	U2536	C2537	A2538	A2539	C2540	C2541	U2542	C2543	C2544	U2545	U2546	C2547	C2548	C2549	A2550	C2551	C2552	C2553	U2554	U2555	C2556	C2557	C2558	U2559	U2560	U2561	U2562	U2563	C2564	C2565	C2566	C2567	C2568	C2569	U2570	U2571	C2572	C2573	C2574	C2575	C2576	C2577	C2578	C2579	U2580	C2581	C2582	C2583	C2584	C2585	C2586		
G2407	G2408	G2409	G2410	G2411	G2412	G2413	G2414	G2415	G2416	G2417	G2418	G2419	G2420	G2421	G2422	G2423	G2424	G2425	G2426	U2427	G2428	G2429	G2430	U2431	G2432	G2433	G2434	G2435	G2436	G2437	G2438	G2439	U2440	U2441	U2442	G2443	G2444	G2445	G2446	U2447	G2448	U2449	U2450	G2451	G2452	G2453	G2454	U2455	U2456	U2457	U2458	U2459	U2460	U2461	U2462	U2463	U2464	U2465	U2466		
G2347	U2348	G2349	G2350	U2351	U2352	G2353	A2354	C2355	U2356	U2357	U2358	U2359	A2360	G2361	A2362	G2363	A2364	G2365	A2366	G2367	A2368	G2369	G2370	U2371	C2372	G2373	A2374	C2375	A2376	C2377	G2378	G2379	U2380	G2381	A2382	G2383	A2384	A2385	A2386	U2387	G2388	A2389	G2390	U2391	U2392	C2393	A2394	U2395	A2396	C2397	U2398	U2399	A2400	U2401	C2402	C2403	G2404	G2405	U2406		
G2287	G2288	G2289	G2290	U2291	G2292	G2293	C2294	A2295	U2296	G2297	U2298	U2299	A2300	C2301	G2302	U2303	U2304	G2305	A2306	G2307	U2308	A2309	G2310	U2311	G2312	U2313	U2314	G2315	G2316	G2317	A2318	U2319	U2320	G2321	G2322	U2323	A2324	U2325	G2326	U2327	A2328	U2329	A2330	G2331	U2332	U2333	A2334	U2335	A2336	U2337	U2338	U2339	U2340	U2341	U2342	A2343	A2344	G2345	G2346		
U2227	U2228	C2229	A2230	U2231	G2232	G2233	C2234	A2235	U2236	U2237	U2238	U2239	U2240	A2241	G2242	G2243	U2244	G2245	G2246	G2247	C2248	A2249	G2250	U2251	U2252	U2253	G2254	U2255	A2256	G2257	U2258	U2259	G2260	G2261	G2262	G2263	G2264	U2265	U2266	G2267	C2268	G2269	U2270	C2271	U2272	U2273	A2274	A2275	A2276	A2277	G2278	G2279	U2280	U2281	A2282	C2283	G2284	G2285	A2286		
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G2105	G2106	A2107	C2108	U2109	U2110	U2111	A2112	U2113	C2114	U2115	U2116	U2117	U2118	A2119	G2120	A2121	G2122	A2123	A2124	U2125	A2126	G2127	U2128	U2129	A2130	U2131	G2132	U2133	C2134	U2135	U2136	U2137	U2138	U2139	G2140	A2141	U2142	U2143	U2144	A2145	U2146	U2147	U2148	U2149	C2150	U2151	C2152	U2153	A2154	G2155	U2156	A2157	C2158	U2159	U2160	U2161	U2162	U2163	G2164	C2165	U2166
C2045	G2046	C1986	U2047	U2048	U2049	G2050	G2051	C2052	C2053	C2054	A2055	U2056	C2057	U2058	G2059	A2060	C2061	G2062	G2063	G2064	A2065	A2066	U2067	G2068	A2069	U2070	C2071	C2072	C2073	G2074	U2075	G2076	A2077	U2078	C2079	C2080	U2081	U2082	U2083	A2084	C2085	A2086	U2087	U2088	A2089	U2090	C2091	U2092	U2093	A2094	U2095	U2096	U2097	U2098	U2099	A2100	A2101	U2102	C2103	A2104	
A1925	A1926	C1927	U1928	U1929	U1930	C1931	C1932	U1933	A1934	A1935	U1936	G1937	U1938	A1939	U1940	C1941	G1942	A1943	A1944	A1945	U1946	U1947	C1948	U1949	U1950	A1951	G1952	A1953	C1954	G1955	G1956	G1957	U1958	A1959	A1960	A1961	U1962	U1963	U1964	C1965	U1966	U1967	C1968	C1969	U1970	G1971	C1972	U1973	U1974	G1975	U1976	A1977	U1978	U1979	A1980	U1981	G1982	A1983	A1984		
A1864	A1865	G1866	C1867	A1868	G1869	G1870	U1871	U1872	A1873	G1874	C1875	A1876	C1877	A1878	G1879	U1880	G1881	G1882	A1883	A1884	G1885	C1886	U1887	U1888	U1889	U1890	A1891	A1892	C1893	U1894	G1895	A1896	A1897	G1898	C1899	A1900	A1901	C1902	A1903	G1904	U1905	G1906	A1907	U1908	C1909	G1910	G1911	C1912	G1913	G1914	C1915	U1916	G1917	U1918	U1919	A1920	C1921	U1922	A1923	U1924	
A1804	U1805	C1806	C1807	C1808	A1809	A1810	A1811	A1812	C1813	G1814	A1815	C1816	A1817	G1818	G1819	U1820	U1821	G1822	U1823	G1824	U1825	A1826	U1827	U1828	U1829	G1830	G1831	G1832	G1833	U1834	G1835	A1836	C1837	A1838	C1839	C1840	U1841	G1842	C1843	C1844	C1845	A1846	G1847	U1848	C1849	C1850	U1851	G1852	G1853	A1854	U1855	G1856	U1857	U1858	U1859	A1860	A1861	A1862	G1863		
G2709	G2710	G2711	G2712	G2713	G2714	G2715	G2716	G2717	G2718	G2719	G2720	G2721	G2722	G2723	G2724	G2725	G2726	G2727	G2728	G2729	G2730	G2731	G2732	G2733	G2734	G2735	G2736	G2737	G2738	G2739	G2740	G2741	G2742	G2743	G2744	G2745	G2746	G2747	G2748	G2749	G2750	G2751	G2752	G2753	G2754	G2755	G2756	G2757	G2758	G2759	G2760	G2761	G2762	G2763	G2764	G2765	G2766	G2767	G2768		

U2889	U2890	U2891	U2892	U2893	U2894	U2895	U2896	U2897	U2898	U2899	U2900	U	A	U	U	U	G	G	A
G2829	A2830	U2831	G2832	A2833	C2834	G2835	U2836	U2837	G2838	A2839	U2840	A2841	G2842	G2843	U2844	U2845	A2846	C2847	U2848
U2769	U2770	G2771	A2772	C2773	A2774	C2775	U2776	A2777	U2778	C2779	U2780	C2781	A2782	U2783	A2784	U2785	A2786	U2787	U2788
U2889	G2890	C2891	U2892	G2893	C2894	A2895	U2896	G2897	A2898	C2899	U2900	U	A	U	U	G	G	A	

• Molecule 52: 5S ribosomal RNA

Chain 4: . 40% 56% .

U1	U2	U3	G4	G5	A6	G6	C7	C8	C9	C10	A11	G12	G13	C15	G16	U18	G19	U20	G21
G62	U63	G64	G65	A66	G67	C68	C69	G70	A71	G72	U73	G74	U75	U76	U77	U78	U79	U80	U
U1	U2	U3	G4	G5	A6	G6	C7	C8	C9	C10	A11	G12	G13	C15	G16	U18	G19	U20	G21
G62	U63	G64	G65	A66	G67	C68	C69	G70	A71	G72	U73	G74	U75	U76	U77	U78	U79	U80	U

• Molecule 53: 16S ribosomal RNA

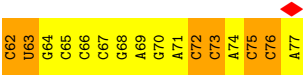
Chain 5: . 57% 38% .

U	U	U	U	U5	C6	U7	G8	A9	G10	A11	G12	U13	U14	U15	U16	U17	U18	C19	C20
A61	G62	U63	C64	A65	A66	U67	C68	A69	G70	A71	G72	U73	U74	A75	G76	U77	A78	A79	U80
C121	C122	U123	C124	A125	A126	U127	C128	A129	G130	A131	G132	U133	U134	A135	G136	U137	A138	C139	U140
G	C	A	U	G185	A186	U187	C188	A189	G190	A191	G192	U193	U194	A195	G196	U197	A198	C199	U200
C241	A242	G243	C244	U245	A246	U247	C248	A249	G250	A251	U252	G253	U254	A255	G256	U257	A258	C259	U260
G301	A302	U303	U304	A305	G306	C307	C308	A309	G310	A311	U312	U313	G314	A315	G316	U317	A318	C319	U320
U361	U362	U363	U364	U365	C366	U367	C368	A369	G370	U371	G372	A373	G374	A375	G376	U377	A378	C379	U380
G421	A422	U423	U424	G425	U426	A427	C428	A429	G430	U431	U432	C433	U434	A435	U436	U437	A438	C439	U440
U481	G482	U483	A484	C485	G486	A487	U488	A489	U490	A491	G492	C493	U494	A495	U496	A497	U498	C499	U500
C541	G542	C543	A544	C545	G546	C547	G548	U549	U550	A551	U552	C553	U554	A555	U556	A557	U558	C559	U560
U561	G562	U563	G564	C565	U566	C567	G568	U569	U570	A571	U572	C573	U574	A575	U576	C577	U578	C579	U580
U581	G582	U583	C584	G585	U586	C587	G588	U589	U590	A591	U592	C593	U594	A595	U596	C597	U598	C599	U600

U1503	A1443	A1383	A1323	A1263	A1203	C1143	A1083	G	U963	A903	C843	A781	G721	G661	U601
G1504	G1444	A1384	A1324	G1264	A1204	A1144	A1084	U	A964	C904	U844	G782	G722	G662	G602
G1505	A1445	A1385	U1325	U1265	G1205	A1145	G1085	U	C965	U905	C845	G783	G723	G663	U603
A1506	A1446	C1386	C1326	U1266	G1206	A1146	U1086	A	A966	C906	C846	G784	G724	G664	U604
U1507	U1447	U1387	G1327	G1267	U1207	U1147	C1087	A	C967	A907	C847	U785	A725	G665	A605
C1508	A1448	A1388	G1328	G1268	U1208	U1148	U1088	G1028	G968	A908	U848	U786	A726	U666	A606
A1509	G1449	U1389	G1329	U1269	C1209	G1149	G1089	C1029	A969	A909	A849	A787	G727	U667	A607
C	C1450	A1390	A1330	C1270	U1210	G1150	G1090	G1029	A970	C910	C850	G788	G728	U668	G608
C	A1451	A1391	A1331	U1271	A1211	A1151	C1091	A1031	A971	G911	U851	A789	C729	U669	G609
U	C1452	C1392	C1332	C1272	C1212	G1152	A1092	G1032	A972	G912	C852	U790	G730	G670	C610
C	A1453	A1393	C1333	A1273	A1213	G1153	A1093	U1033	A973	A913	A853	A791	A731	G671	A611
C	G1454	G1394	A1334	G1274	A1214	A1154	G1094	G1034	C974	A914	A854	C792	A732	A672	G612
C	G1455	G1395	G1335	U1275	G1215	A1155	G1095	A1035	C975	A915	G855	C793	A733	A673	C613
U	U1456	U1396	C1336	U1276	G1216	G1156	A1096	C1036	U976	U916	U856	C794	A734	U674	U614
C	G1457	G1397	U1337	C1277	G1217	G1157	G1097	A1037	U977	G917	U857	U795	C735	U675	G615
U	A1458	A1398	A1338	G1278	C1218	A1158	G1098	G1038	A858	A918	A796	U796	U736	U676	C616
C	U1459	U1399	U1339	G1279	A1219	A1159	G1099	G1039	C979	C919	A859	G797	U737	C677	U617
U	U1460	A1400	G1340	A1280	G1220	G1160	U1100	U1040	C980	G920	C860	U798	A738	A678	U618
A	G1461	U1401	U1341	U1281	A1221	G1161	A1101	G1041	U981	G921	A861	A799	G739	U679	A619
	G1462	U1402	G1342	U1282	U1222	G1162	A1102	G1042	A982	G922	C862	C800	G740	G680	A620
	A1463	A1403	G1343	G1283	A1223	A1163	C1103	U1043	G983	G923	A863	C801	C741	U681	C621
	G1464	U1404	C1344	A1284	C1224	U1164	C1104	G1044	A984	A924	U864	C802	C742	G682	A622
	U1465	U1405	G1345	G1285	A1225	G1165	C1105	G1045	C985	C925	U865	C803	A743	G683	G623
	U1466	G1406	G1346	G1286	A1226	A1166	U1106	A1046	U986	C926	A866	C804	G744	U684	U624
	A1467	U1407	U1347	G1287	A1227	G1167	U1107	U1047	U987	C927	A867	C807	U745	G685	U625
	A1468	A1408	G1348	C1288	C1228	G1168	A1108	G1048	C988	G928	C868	C808	A746	C886	G626
	G1469	A1409	U1349	U1289	A1229	U1169	U1109	U1049	A989	C929	U869	C809	C747	G687	U627
	U1470	A1410	A1350	G1290	G1230	C1170	C1110	U1050	C990	A930	A870	U810	U748	G688	A628
	C1471	A1411	U1351	C1291	G1231	A1171	G1111	U1051	A991	C931	U871	A811	G749	U689	U629
	G1472	C1412	A1352	A1292	C1232	A1172	U1112	G1052	U992	A932	C872	A812	A750	G690	G630
	U1473	G1413	C1353	A1293	G1233	A1173	U1113	U1053	C993	A933	U873	A813	C751	C631	C631
	A1474	U1414	G1354	U1294	C1234	U1174	A1114	C1054	C994	G934	C874	C814	C752	A632	A632
	A1475	G1415	U1355	U1295	C1235	C1175	G1115	G1055	U995	U935	C875	G815	C753	U633	U633
	G1476	U1416	U1356	C1296	A1236	A1176	U1116	U1056	U996	G936	C876	U817	U754	A634	A634
	A1477	U1417	C1357	G1297	G1237	U1177	U1117	C1057	G997	G937	C877	U818	U755	G635	G635
	A1478	G1418	U1358	U1298	C1238	C1178	A1118	A1058	C998	U938	U878	A818	A756	C636	G636
	G1479	C1419	C1359	C1299	U1239	A1179	G1119	G1059	C999	G939	G879	G819	G757	G637	A637
	G1480	U1420	G1360	C1300	U1240	U1180	A1120	G1060	A1000	G940	C880	A820	G758	U638	A638
	U1481	A1421	G1361	U1301	G1241	G1181	U1121	U1061	A1001	A941	C881	U821	C759	A639	A639
	A1482	A1422	G1362	C1302	U1242	C1182	U1122	C1062	A1002	G942	U882	A822	U760	C640	C640
	C1483	C1423	U1363	A1303	C1243	C1183	G1123	G1063	G1003	C943	A883	C823	U761	U641	U641
	C1484	C1424	C1364	U1304	A1244	C1184	U1124	U1064	U1004	A944	C884	U824	G762	A701	A701
	C1485	A1425	U1365	G1305	A1245	G1185	C1125	G1065	U1005	U945	U885	A825	A763	U703	U643
	C1486	U1426	U1366	A1306	A1246	U1186	U1126	U1066	A1006	G946	A886	C826	A764	U704	U644
	U1487	U1427	G1367	A1307	G1247	U1187	A1127	C1067	U1007	U947	C887	C827	A765	A645	A645
	A1488	A1428	A1368	G1308	U1248	A1188	G1128	U1068	G1008	U948	A888	U828	G766	U646	A646
	C1489	G1429	U1369	U1309	G1249	U1189	C1129	U1069	G1009	G949	U889	G829	U767	U647	U647
	G1490	G1430	C1370	G1310	A1250	G1190	G1130	G1070	C950	C950	U890	U830	G768	C648	C648
	A1491	A1431	A1371	G1311	G1251	U1191	A1131	U1071	U951	U951	C891	C831	U769	U649	U649
	G1492	A1432	C1372	G1312	C1252	C1192	G1132	G1072	A1012	U952	G892	G832	G770	G710	A650
	A1493	G1433	A1373	A1313	A1253	U1193	A1133	A1073	C1013	A953	C893	G833	G771	G711	G651
	A1494	C1434	C1374	A1314	A1254	A1194	C1134	U1074	A1014	A954	A894	A712	G772	A712	A652
	C1495	G1435	G1375	U1315	A1255	G1195	U1135	G1075	U955	U955	A895	G835	G773	A713	G653
	G1496	C1436	G1376	C1316	U1256	G1196	U1136	U1076	A1016	U956	G896	C836	A774	C714	U654
	U1497	A1437	C1377	A1317	C1257	G1197	U1137	U1077	C957	C957	A897	A837	G775	A715	G655
	G1498	U1438	C1378	C1318	U1258	C1198	G1138	G1078	U1018	G958	A898	A838	C776	C716	U656
	G1499	G1439	C1379	U1319	G1259	U1199	A1139	G1079	G1019	A959	U899	U839	A777	C717	G657
	G1500	U1440	G1380	A1320	U1260	G1201	U1140	U1080	A	C960	G900	C840	A778	A718	U658
	U1501	U1441	U1381	A1321	A1261	C1202	U1141	U1081	G	A	A901	C841	A779	G719	U659
	G1502	A1442	C1382	U1322	A1262	A1202	G1142	U1082	G	G962	A902	C842	U780	U720	A660

● Molecule 54: tRNA-Phe





• Molecule 54: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	1786	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	1.572	Depositor
Minimum map value	-0.560	Depositor
Average map value	0.024	Depositor
Map value standard deviation	0.126	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.29	0/383	0.66	0/504
2	1	0.29	0/484	0.71	0/637
3	2	0.38	0/306	0.65	0/401
4	9	0.27	0/3071	0.62	0/4147
5	A	0.30	0/1954	0.66	5/2642 (0.2%)
6	B	0.30	0/1721	0.64	0/2323
7	C	0.28	0/1691	0.62	0/2267
8	D	0.28	0/1188	0.63	0/1593
9	E	0.38	0/1384	0.79	2/1867 (0.1%)
10	F	0.28	0/1266	0.67	1/1700 (0.1%)
11	G	0.34	0/1126	0.76	3/1517 (0.2%)
12	H	0.33	0/1044	0.74	1/1395 (0.1%)
13	I	0.31	0/820	0.74	1/1103 (0.1%)
14	J	0.28	0/844	0.65	1/1136 (0.1%)
15	K	0.34	0/1094	0.72	0/1468
16	L	0.25	0/962	0.57	0/1289
17	M	0.30	0/483	0.71	1/643 (0.2%)
18	N	0.30	0/679	0.58	0/907
19	O	0.24	0/659	0.60	0/885
20	P	0.33	0/684	0.66	2/913 (0.2%)
21	Q	0.41	0/545	0.90	2/730 (0.3%)
22	R	0.27	0/698	0.66	1/936 (0.1%)
23	S	0.34	0/631	0.69	1/838 (0.1%)
24	T	0.28	0/475	0.60	0/621
25	a	0.29	0/2267	0.69	1/3044 (0.0%)
26	b	0.30	0/1795	0.69	1/2412 (0.0%)
27	c	0.33	0/1671	0.75	3/2246 (0.1%)
28	d	0.30	0/1409	0.68	0/1894
29	e	0.35	0/1420	0.75	4/1912 (0.2%)
30	f	0.27	0/1205	0.66	0/1616
31	g	1.95	6/944 (0.6%)	0.84	3/1260 (0.2%)
32	h	0.25	0/968	0.55	0/1298
33	i	0.30	0/1186	0.62	0/1592
34	j	0.31	0/953	0.73	0/1275

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	k	0.31	0/1170	0.70	1/1559 (0.1%)
36	l	0.33	0/1104	0.67	1/1481 (0.1%)
37	m	0.32	0/973	0.65	1/1309 (0.1%)
38	n	0.30	0/897	0.67	1/1198 (0.1%)
39	o	0.30	0/948	0.71	1/1262 (0.1%)
40	p	0.32	0/961	0.64	1/1278 (0.1%)
41	q	0.31	0/828	0.75	2/1111 (0.2%)
42	r	0.29	0/1077	0.66	0/1441
43	s	0.28	0/732	0.77	3/988 (0.3%)
44	t	0.27	0/879	0.68	0/1165
45	u	0.28	0/665	0.67	0/884
46	v	0.30	0/519	0.73	1/695 (0.1%)
47	w	0.26	0/826	0.52	0/1104
48	x	0.24	0/353	0.67	1/474 (0.2%)
49	y	0.38	0/457	0.74	1/601 (0.2%)
50	z	0.28	0/412	0.74	1/547 (0.2%)
51	3	0.29	0/69073	0.47	0/107710
52	4	0.29	0/2505	0.48	0/3902
53	5	0.28	0/35768	0.46	0/55764
54	6	0.26	0/1808	0.52	0/2817
54	7	0.27	0/1808	0.52	0/2817
All	All	0.33	6/161773 (0.0%)	0.54	48/241118 (0.0%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	g	112	TYR	CD2-CE2	31.31	2.32	1.38
31	g	112	TYR	CD1-CE1	30.87	2.31	1.38
31	g	112	TYR	CE1-CZ	20.99	1.88	1.38
31	g	112	TYR	CE2-CZ	20.70	1.88	1.38
31	g	112	TYR	CG-CD2	17.36	1.75	1.39

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	36	TYR	N-CA-C	-10.23	96.45	110.68
21	Q	44	CYS	N-CA-C	-9.69	100.72	112.54
9	E	123	ASN	CA-C-N	-9.52	107.87	121.20
9	E	123	ASN	C-N-CA	-9.52	107.87	121.20
10	F	16	VAL	N-CA-C	-8.19	105.93	113.71

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	380	0	429	55	0
2	1	477	0	530	66	0
3	2	304	0	350	43	0
4	9	3021	0	3050	332	0
5	A	1921	0	1973	189	0
6	B	1698	0	1768	166	0
7	C	1660	0	1719	195	0
8	D	1173	0	1267	153	0
9	E	1362	0	1377	166	0
10	F	1246	0	1308	132	0
11	G	1110	0	1226	128	0
12	H	1028	0	1094	143	0
13	I	809	0	894	94	0
14	J	829	0	855	93	0
15	K	1076	0	1170	145	0
16	L	951	0	1014	87	0
17	M	474	0	509	74	0
18	N	673	0	730	58	0
19	O	646	0	677	53	0
20	P	675	0	728	78	0
21	Q	535	0	562	74	0
22	R	682	0	691	91	0
23	S	629	0	681	78	0
24	T	471	0	522	38	0
25	a	2225	0	2301	271	0
26	b	1762	0	1808	230	0
27	c	1644	0	1731	192	0
28	d	1388	0	1469	116	0
29	e	1396	0	1481	132	0
30	f	1182	0	1227	162	0
31	g	936	0	989	27	0
32	h	959	0	1039	24	0
33	i	1164	0	1192	134	0
34	j	944	0	1019	129	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	k	1153	0	1256	162	0
36	l	1079	0	1134	132	0
37	m	958	0	1011	114	0
38	n	889	0	952	113	0
39	o	938	0	1008	124	0
40	p	947	0	1028	117	0
41	q	811	0	858	91	0
42	r	1068	0	1150	125	0
43	s	720	0	803	84	0
44	t	872	0	972	74	0
45	u	657	0	695	89	0
46	v	513	0	560	73	0
47	w	818	0	870	85	0
48	x	344	0	333	19	0
49	y	452	0	472	80	0
50	z	408	0	440	50	0
51	3	61664	0	30951	6388	0
52	4	2239	0	1137	256	0
53	5	31943	0	16058	3265	0
54	6	1618	0	821	143	0
54	7	1618	0	821	155	0
All	All	149139	0	102710	14408	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 61.

The worst 5 of 14408 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:5:LEU:HD11	30:f:34:LYS:CG	1.34	1.56
30:f:5:LEU:HD12	30:f:34:LYS:CB	1.35	1.56
30:f:5:LEU:CD1	30:f:34:LYS:HB3	1.33	1.53
53:5:778:A:N6	53:5:798:U:C2	1.79	1.50
30:f:5:LEU:CD1	30:f:34:LYS:CB	1.93	1.40

There are no symmetry-related clashes.

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%)	44 (77%)	13 (23%)	0	100	100
3	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
4	9	391/394 (99%)	347 (89%)	42 (11%)	2 (0%)	24	63
5	A	238/294 (81%)	202 (85%)	35 (15%)	1 (0%)	30	67
6	B	213/273 (78%)	182 (85%)	31 (15%)	0	100	100
7	C	201/205 (98%)	170 (85%)	30 (15%)	1 (0%)	24	63
8	D	151/219 (69%)	132 (87%)	19 (13%)	0	100	100
9	E	165/215 (77%)	126 (76%)	39 (24%)	0	100	100
10	F	152/155 (98%)	126 (83%)	25 (16%)	1 (1%)	18	56
11	G	139/142 (98%)	113 (81%)	25 (18%)	1 (1%)	18	56
12	H	126/132 (96%)	110 (87%)	15 (12%)	1 (1%)	16	54
13	I	99/108 (92%)	84 (85%)	15 (15%)	0	100	100
14	J	112/121 (93%)	100 (89%)	12 (11%)	0	100	100
15	K	134/139 (96%)	107 (80%)	26 (19%)	1 (1%)	18	56
16	L	116/124 (94%)	102 (88%)	14 (12%)	0	100	100
17	M	58/61 (95%)	49 (84%)	9 (16%)	0	100	100
18	N	81/86 (94%)	76 (94%)	5 (6%)	0	100	100
19	O	78/94 (83%)	67 (86%)	11 (14%)	0	100	100
20	P	81/85 (95%)	71 (88%)	10 (12%)	0	100	100
21	Q	63/104 (61%)	45 (71%)	16 (25%)	2 (3%)	3	21
22	R	82/87 (94%)	62 (76%)	19 (23%)	1 (1%)	10	44
23	S	75/87 (86%)	68 (91%)	7 (9%)	0	100	100
24	T	51/60 (85%)	47 (92%)	4 (8%)	0	100	100
25	a	283/287 (99%)	231 (82%)	52 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	b	227/287 (79%)	196 (86%)	31 (14%)	0	100	100
27	c	208/212 (98%)	182 (88%)	24 (12%)	2 (1%)	12	49
28	d	173/180 (96%)	141 (82%)	32 (18%)	0	100	100
29	e	174/184 (95%)	156 (90%)	17 (10%)	1 (1%)	21	59
30	f	143/149 (96%)	120 (84%)	21 (15%)	2 (1%)	9	40
31	g	119/161 (74%)	102 (86%)	16 (13%)	1 (1%)	16	54
32	h	126/137 (92%)	114 (90%)	12 (10%)	0	100	100
33	i	142/146 (97%)	119 (84%)	23 (16%)	0	100	100
34	j	120/122 (98%)	107 (89%)	12 (10%)	1 (1%)	16	54
35	k	146/151 (97%)	124 (85%)	22 (15%)	0	100	100
36	l	134/139 (96%)	111 (83%)	22 (16%)	1 (1%)	18	56
37	m	117/124 (94%)	103 (88%)	13 (11%)	1 (1%)	14	51
38	n	108/116 (93%)	88 (82%)	20 (18%)	0	100	100
39	o	113/119 (95%)	100 (88%)	13 (12%)	0	100	100
40	p	112/127 (88%)	98 (88%)	14 (12%)	0	100	100
41	q	97/100 (97%)	76 (78%)	19 (20%)	2 (2%)	5	30
42	r	137/159 (86%)	116 (85%)	21 (15%)	0	100	100
43	s	90/237 (38%)	74 (82%)	16 (18%)	0	100	100
44	t	109/111 (98%)	94 (86%)	15 (14%)	0	100	100
45	u	84/104 (81%)	72 (86%)	12 (14%)	0	100	100
46	v	61/65 (94%)	52 (85%)	9 (15%)	0	100	100
47	w	96/111 (86%)	79 (82%)	17 (18%)	0	100	100
48	x	42/97 (43%)	37 (88%)	5 (12%)	0	100	100
49	y	54/57 (95%)	46 (85%)	8 (15%)	0	100	100
50	z	48/53 (91%)	40 (83%)	8 (17%)	0	100	100
All	All	6206/7064 (88%)	5285 (85%)	899 (14%)	22 (0%)	31	67

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	G	109	ASN
12	H	62	ASN
21	Q	79	CYS

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Mol	Chain	Res	Type
21	Q	80	GLN
27	c	76	GLN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	34 (97%)	1 (3%)	37	58
4	9	324/325 (100%)	323 (100%)	1 (0%)	86	86
5	A	212/262 (81%)	212 (100%)	0	100	100
6	B	180/232 (78%)	178 (99%)	2 (1%)	65	76
7	C	181/183 (99%)	181 (100%)	0	100	100
8	D	123/178 (69%)	122 (99%)	1 (1%)	73	80
9	E	150/196 (76%)	149 (99%)	1 (1%)	76	81
10	F	131/132 (99%)	131 (100%)	0	100	100
11	G	123/124 (99%)	123 (100%)	0	100	100
12	H	111/115 (96%)	109 (98%)	2 (2%)	51	68
13	I	95/99 (96%)	94 (99%)	1 (1%)	65	76
14	J	91/97 (94%)	91 (100%)	0	100	100
15	K	117/120 (98%)	116 (99%)	1 (1%)	70	79
16	L	100/105 (95%)	99 (99%)	1 (1%)	68	78
17	M	47/48 (98%)	47 (100%)	0	100	100
18	N	76/78 (97%)	75 (99%)	1 (1%)	61	74
19	O	69/82 (84%)	69 (100%)	0	100	100
20	P	73/75 (97%)	73 (100%)	0	100	100
21	Q	56/94 (60%)	55 (98%)	1 (2%)	51	68
22	R	74/77 (96%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	S	70/77 (91%)	70 (100%)	0	100	100
24	T	49/56 (88%)	49 (100%)	0	100	100
25	a	241/243 (99%)	240 (100%)	1 (0%)	84	84
26	b	186/233 (80%)	186 (100%)	0	100	100
27	c	182/184 (99%)	176 (97%)	6 (3%)	33	55
28	d	150/154 (97%)	150 (100%)	0	100	100
29	e	153/159 (96%)	151 (99%)	2 (1%)	61	74
30	f	131/134 (98%)	131 (100%)	0	100	100
31	g	99/129 (77%)	94 (95%)	5 (5%)	21	42
32	h	102/110 (93%)	102 (100%)	0	100	100
33	i	126/128 (98%)	126 (100%)	0	100	100
34	j	103/103 (100%)	98 (95%)	5 (5%)	22	43
35	k	123/126 (98%)	123 (100%)	0	100	100
36	l	113/115 (98%)	111 (98%)	2 (2%)	51	68
37	m	105/109 (96%)	102 (97%)	3 (3%)	37	58
38	n	96/99 (97%)	95 (99%)	1 (1%)	68	78
39	o	101/105 (96%)	101 (100%)	0	100	100
40	p	100/108 (93%)	100 (100%)	0	100	100
41	q	90/91 (99%)	88 (98%)	2 (2%)	45	64
42	r	116/132 (88%)	116 (100%)	0	100	100
43	s	82/208 (39%)	82 (100%)	0	100	100
44	t	96/96 (100%)	96 (100%)	0	100	100
45	u	69/85 (81%)	69 (100%)	0	100	100
46	v	58/60 (97%)	58 (100%)	0	100	100
47	w	87/98 (89%)	87 (100%)	0	100	100
48	x	41/86 (48%)	41 (100%)	0	100	100
49	y	48/49 (98%)	44 (92%)	4 (8%)	10	30
50	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5423/6076 (89%)	5379 (99%)	44 (1%)	70	80

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	j	80	ASP
37	m	6	LYS
34	j	87	ILE
36	l	13	HIS
38	n	12	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 148 such sidechains are listed below:

Mol	Chain	Res	Type
35	k	143	ASN
47	w	45	ASN
36	l	123	HIS
41	q	73	HIS
11	G	109	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	3	2875/2907 (98%)	1332 (46%)	45 (1%)
52	4	103/108 (95%)	62 (60%)	4 (3%)
53	5	1490/1520 (98%)	615 (41%)	14 (0%)
54	6	75/76 (98%)	32 (42%)	2 (2%)
54	7	75/76 (98%)	48 (64%)	5 (6%)
All	All	4618/4687 (98%)	2089 (45%)	70 (1%)

5 of 2089 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	3	14	U
51	3	15	A
51	3	16	A
51	3	17	G
51	3	20	C

5 of 70 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	5	928	G
53	5	1133	A
54	7	4	U
51	3	1507	G

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Mol	Chain	Res	Type
51	3	1481	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

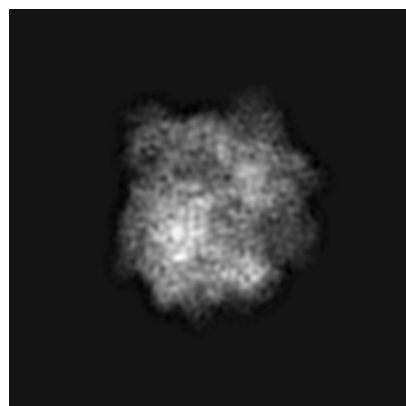
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13411. These allow visual inspection of the internal detail of the map and identification of artifacts.

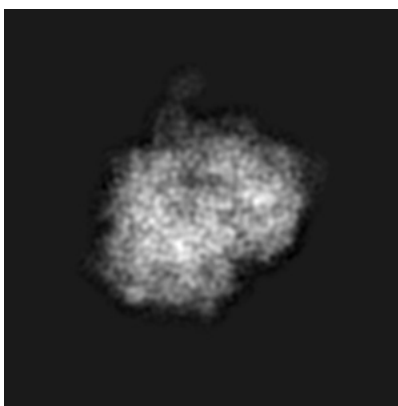
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

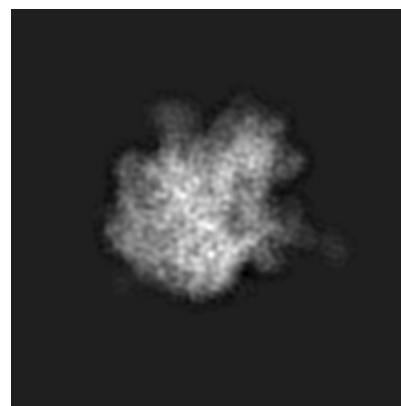
6.1.1 Primary map



X

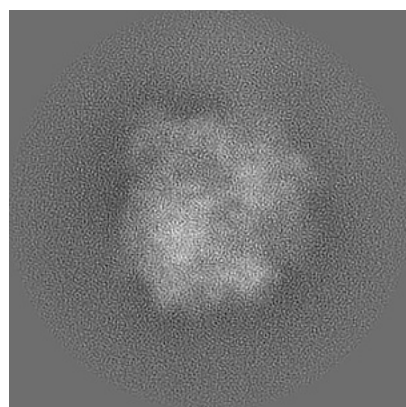


Y

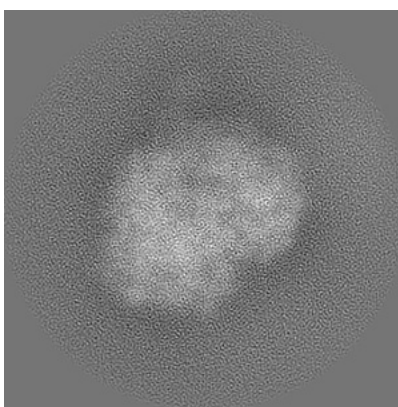


Z

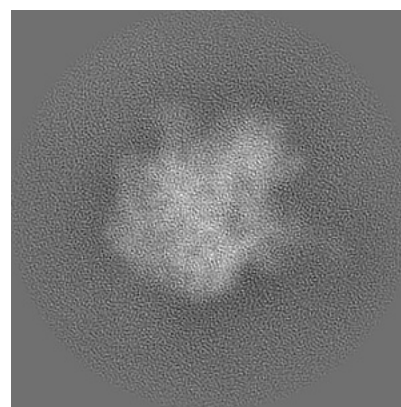
6.1.2 Raw map



X



Y

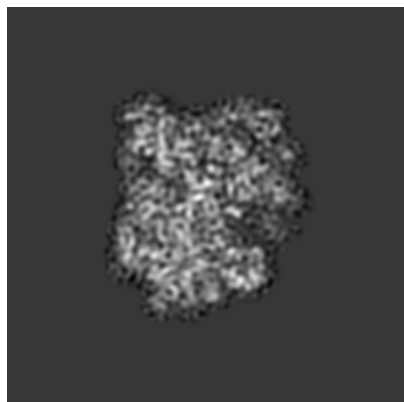


Z

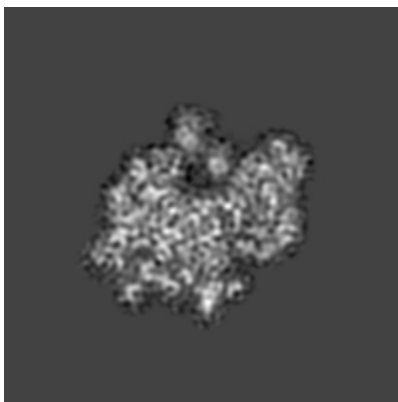
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

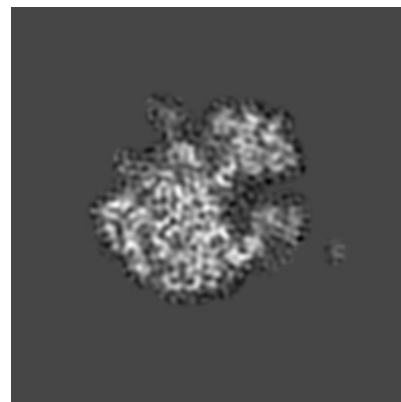
6.2.1 Primary map



X Index: 128

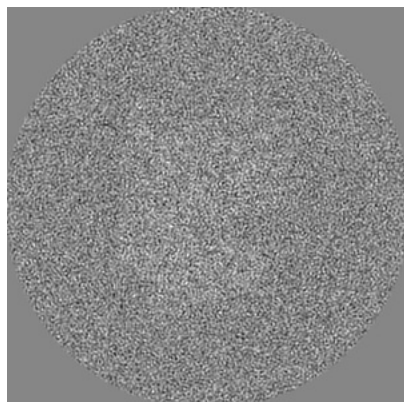


Y Index: 128

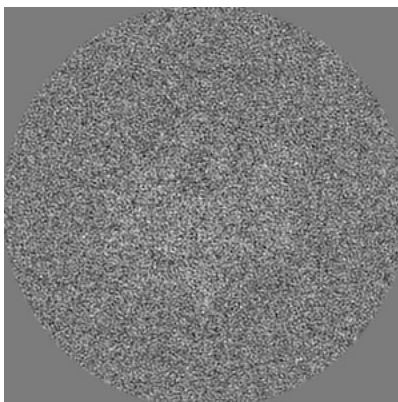


Z Index: 128

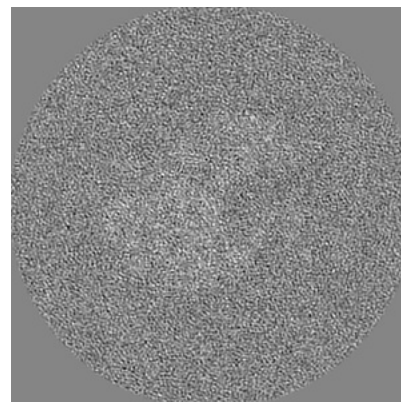
6.2.2 Raw map



X Index: 128



Y Index: 128

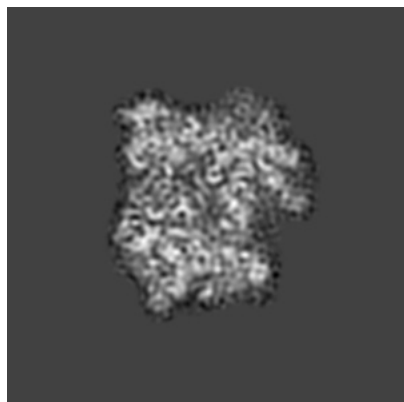


Z Index: 128

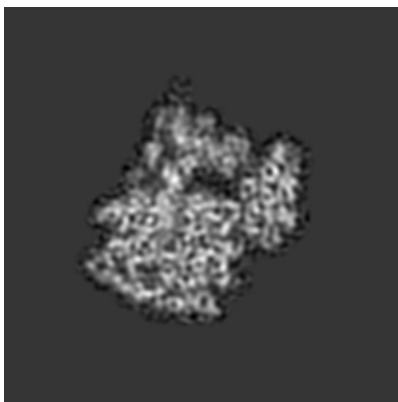
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

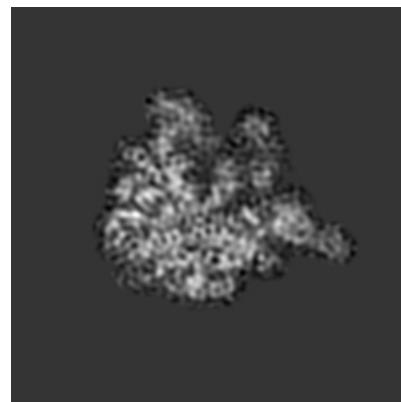
6.3.1 Primary map



X Index: 134

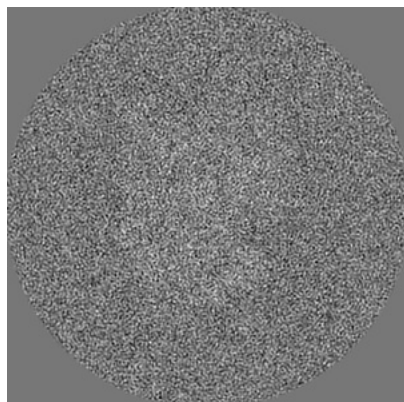


Y Index: 117

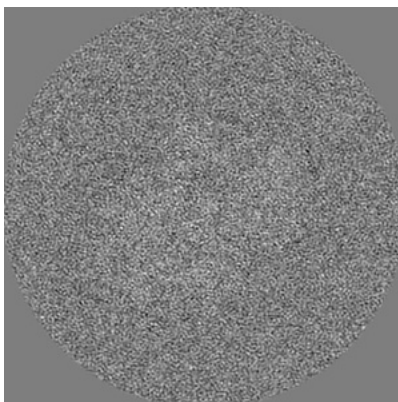


Z Index: 113

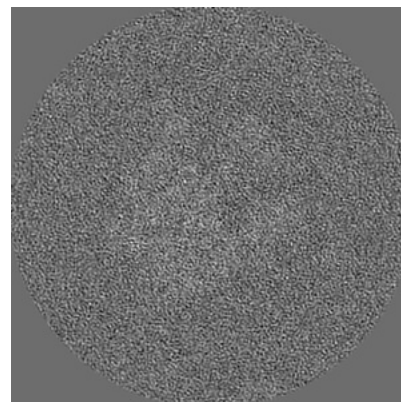
6.3.2 Raw map



X Index: 130



Y Index: 120

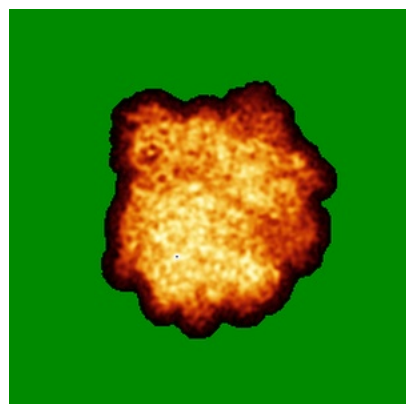


Z Index: 120

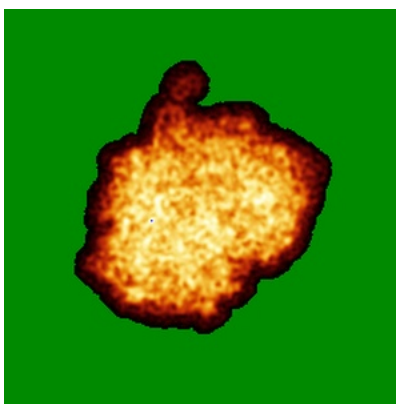
The images above show the largest variance slices of the map in three orthogonal directions.

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

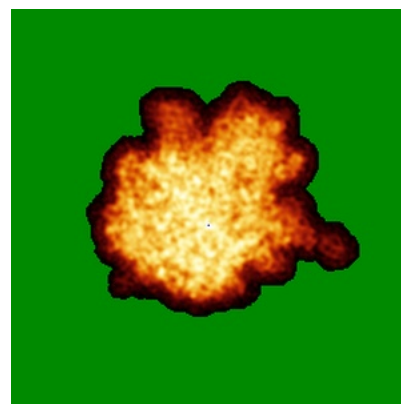
6.4.1 Primary map



X

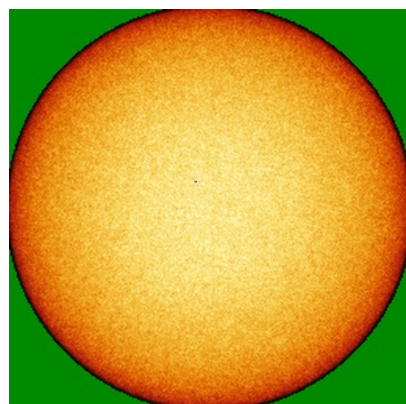


Y

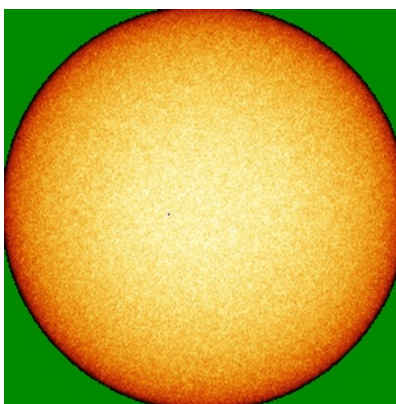


Z

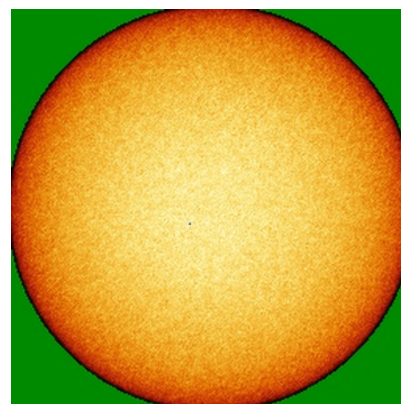
6.4.2 Raw map



X



Y

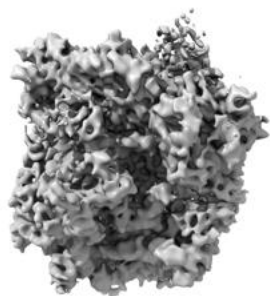


Z

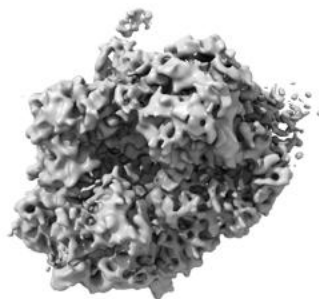
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

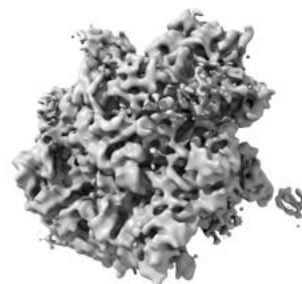
6.5.1 Primary map



X



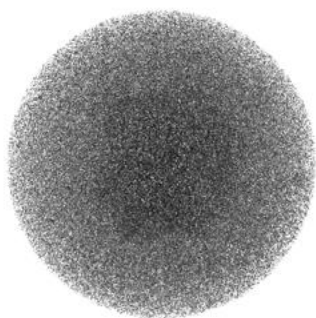
Y



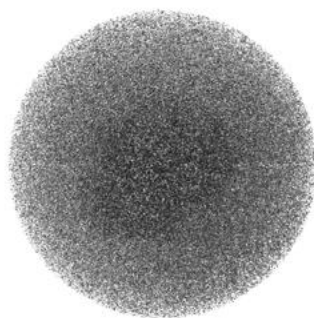
Z

The images above show the 3D surface view of the map at the recommended contour level 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

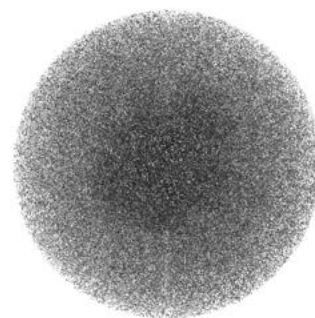
6.5.2 Raw map



X



Y



Z

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

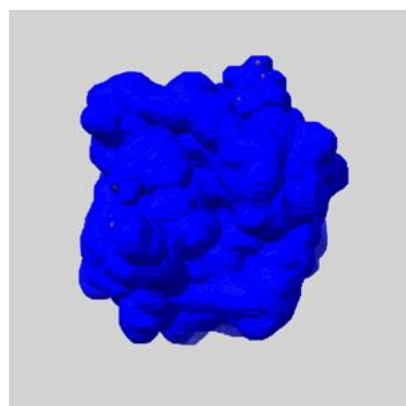
6.6 Mask visualisation [i](#)

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

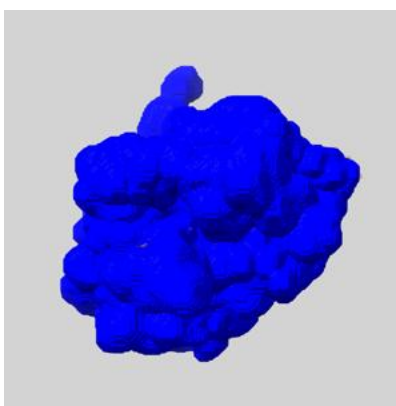
A mask typically either:

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

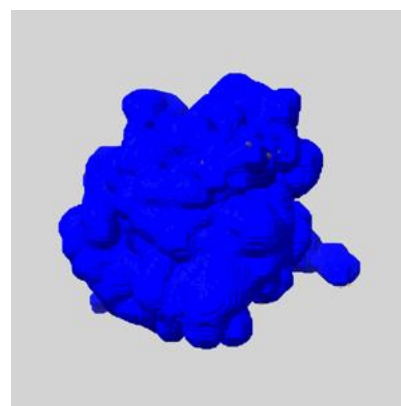
6.6.1 emd_13411_msk_1.map [i](#)



X



Y

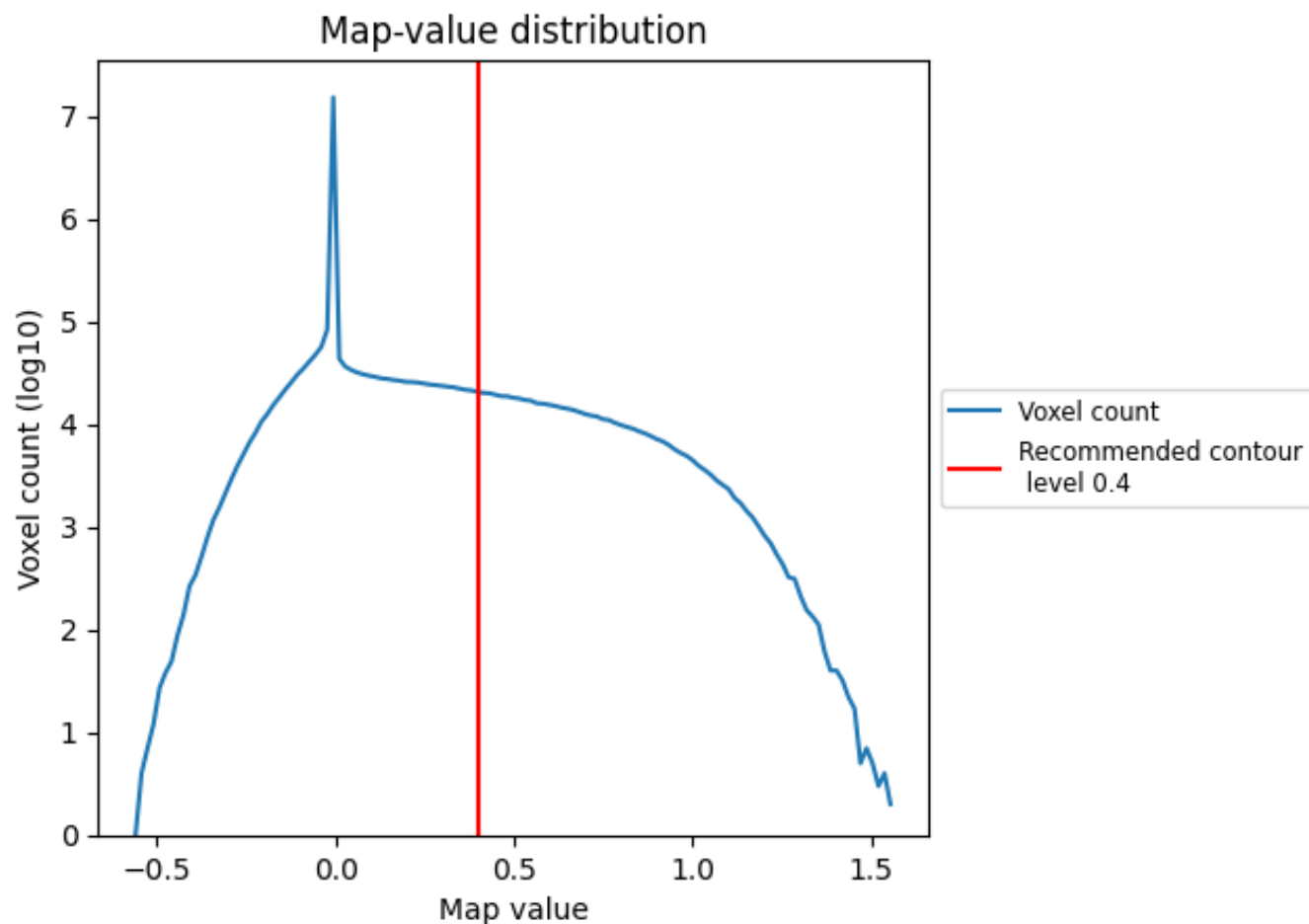


Z

7 Map analysis [i](#)

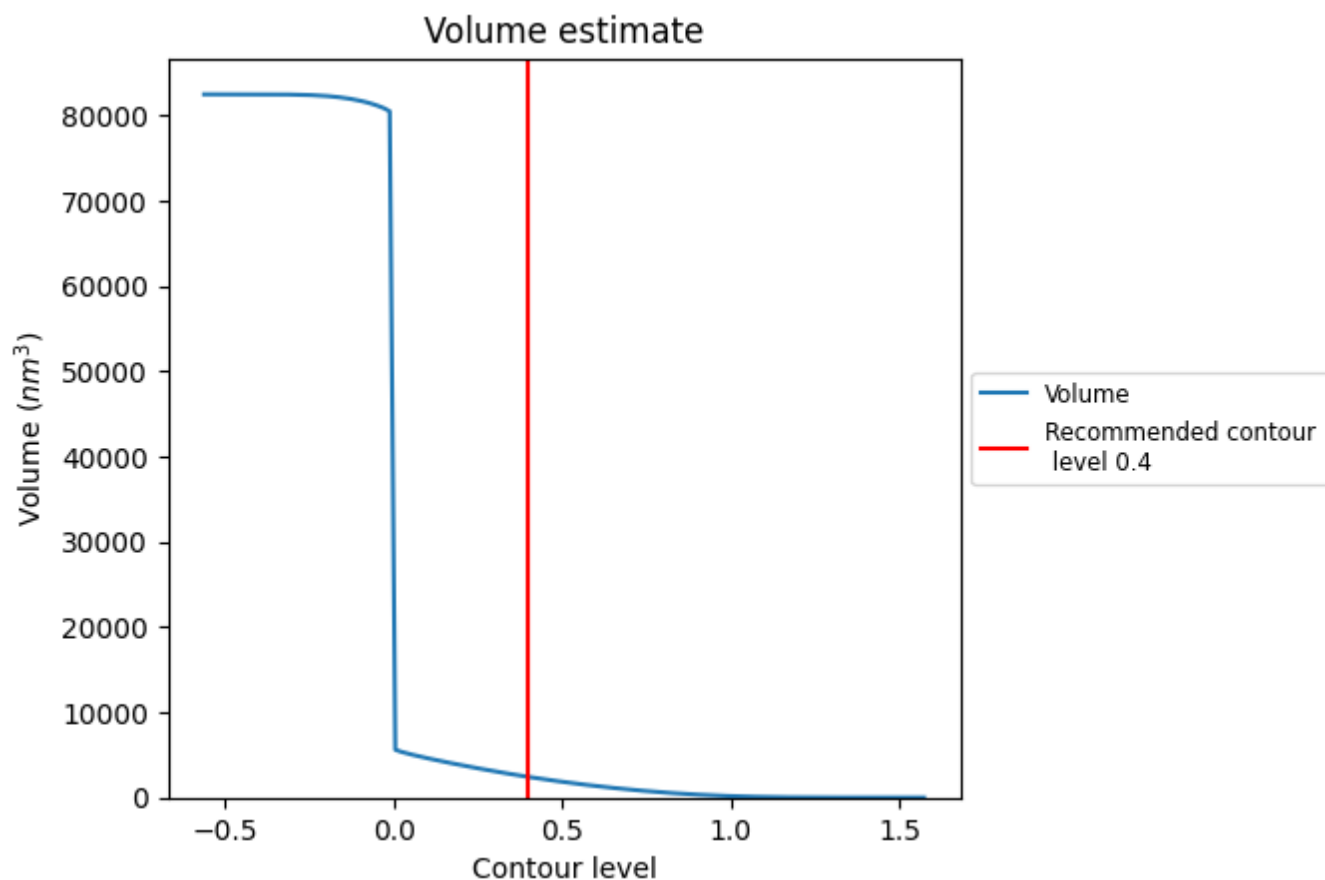
This section contains the results of statistical analysis of the map.

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.

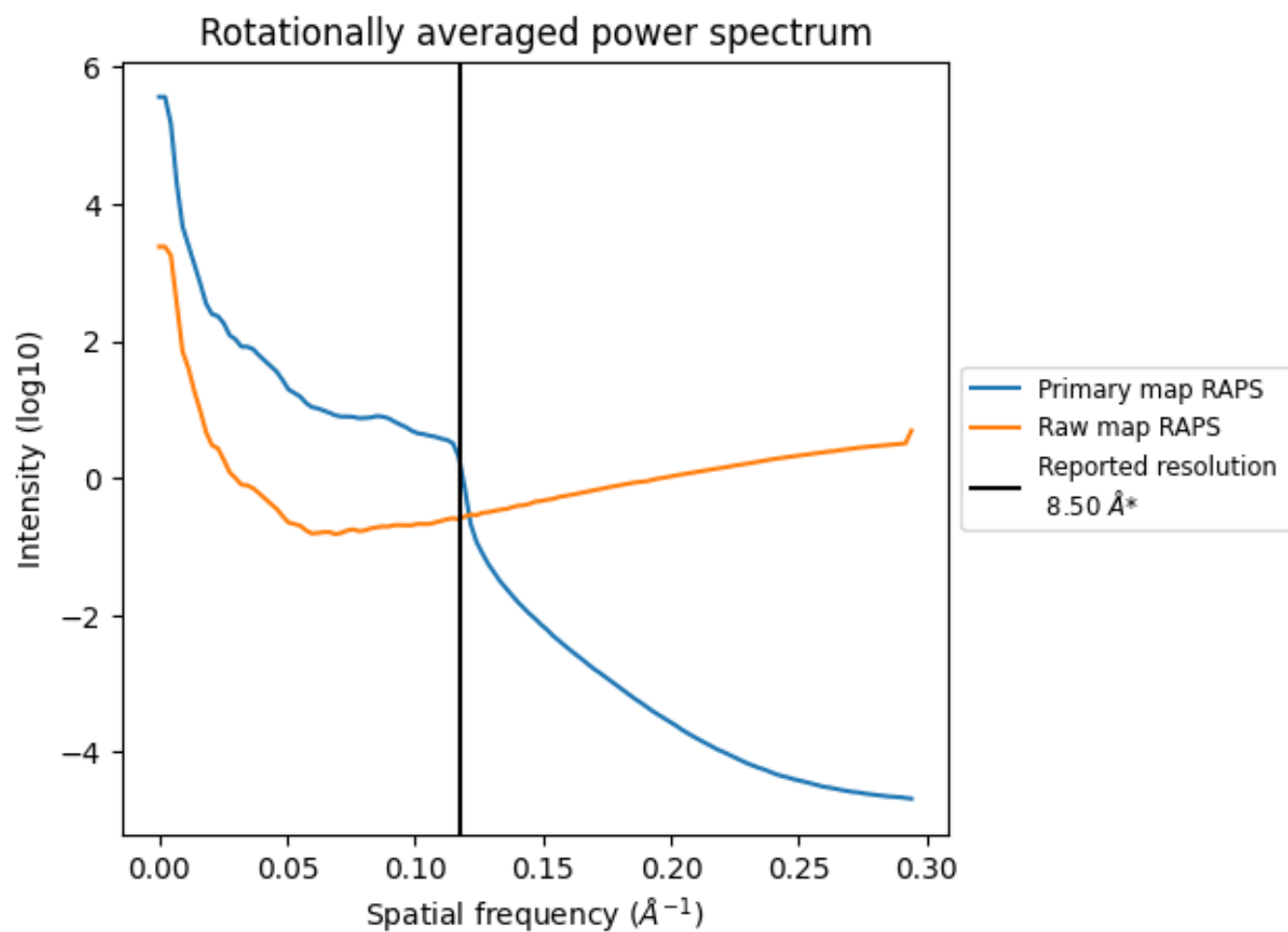
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2426 nm^3 ; this corresponds to an approximate mass of 2192 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

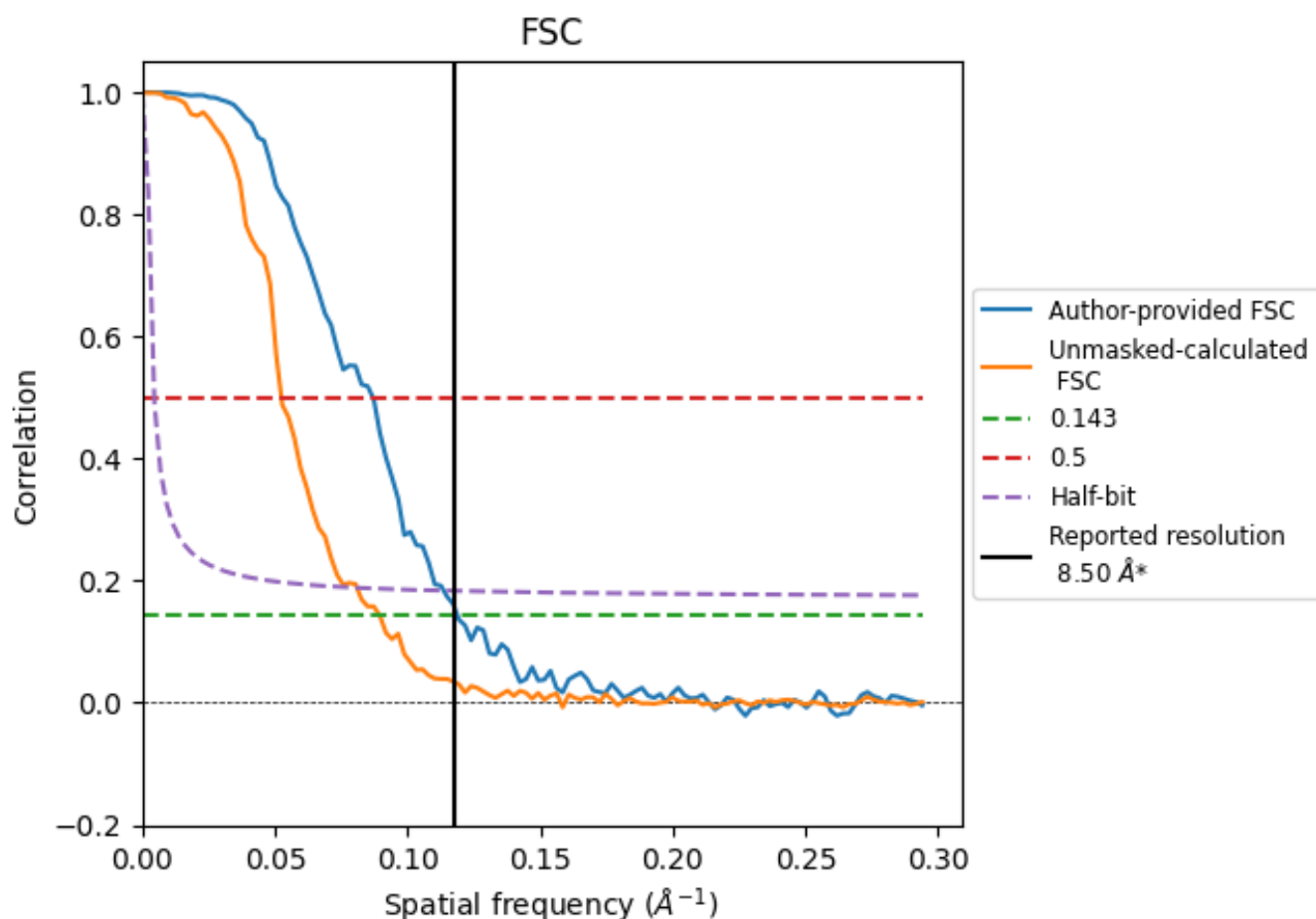


*Reported resolution corresponds to spatial frequency of 0.118 Å⁻¹

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 0.118 Å⁻¹

8.2 Resolution estimates [i](#)

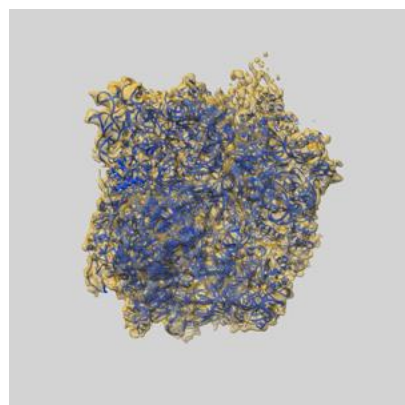
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.50	-	-
Author-provided FSC curve	8.42	11.49	8.80
Unmasked-calculated*	11.17	19.05	12.36

*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 11.17 differs from the reported value 8.5 by more than 10 %

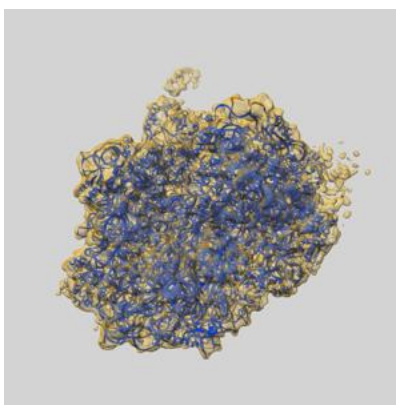
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13411 and PDB model 7PHA. Per-residue inclusion information can be found in section [3](#) on page [14](#).

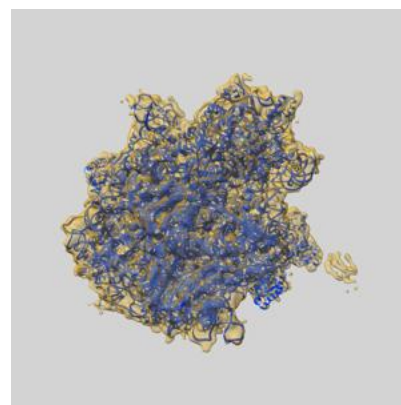
9.1 Map-model overlay [i](#)



X



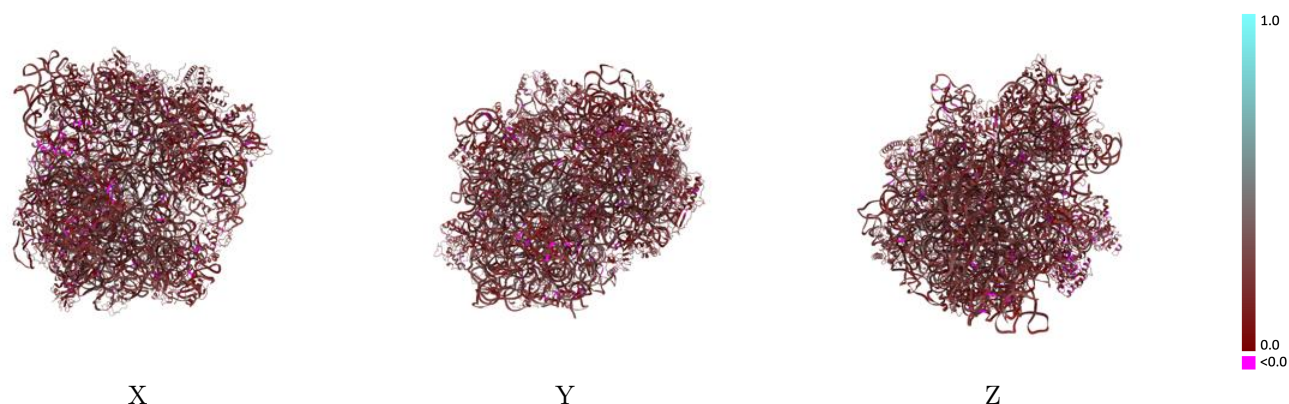
Y



Z

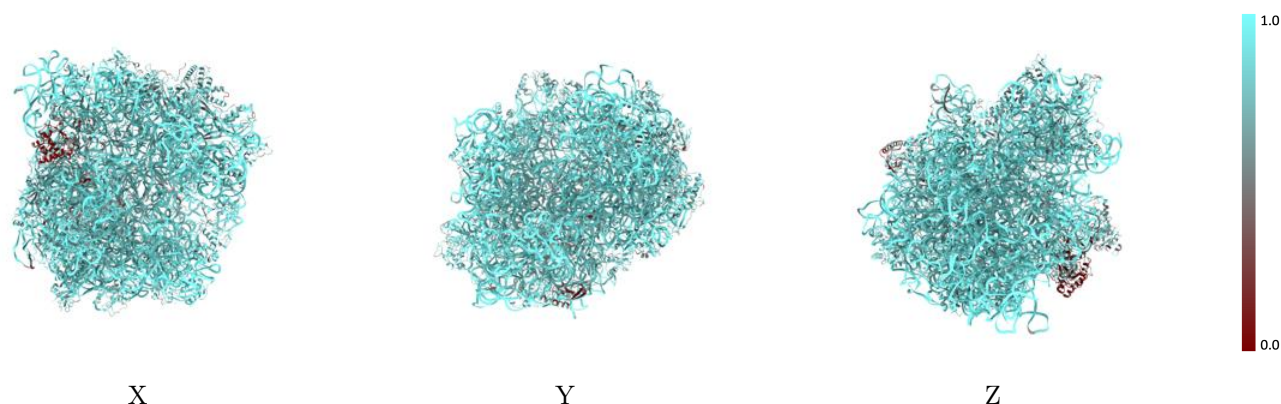
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



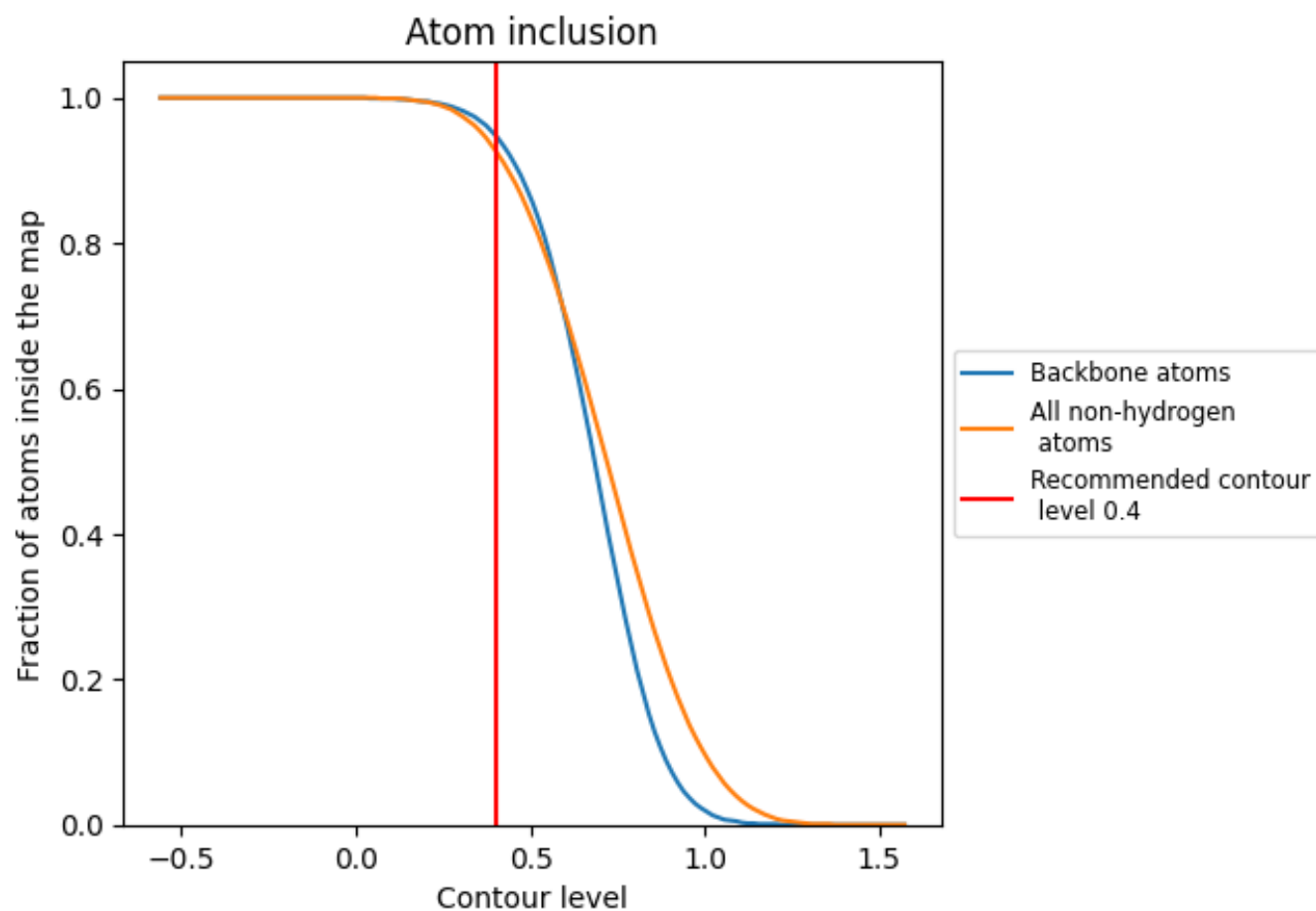
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9270	 0.1960
0	 0.9200	 0.1720
1	 0.9030	 0.1840
2	 0.8550	 0.1370
3	 0.9860	 0.2050
4	 0.9920	 0.2070
5	 0.9890	 0.2070
6	 0.9250	 0.1850
7	 0.9820	 0.1980
9	 0.4360	 0.1500
A	 0.7930	 0.1990
B	 0.8220	 0.1960
C	 0.8350	 0.1790
D	 0.8090	 0.1730
E	 0.7780	 0.2010
F	 0.7950	 0.1730
G	 0.8190	 0.1700
H	 0.8700	 0.1730
I	 0.7800	 0.1650
J	 0.8320	 0.1610
K	 0.8750	 0.1840
L	 0.8480	 0.1860
M	 0.8920	 0.1450
N	 0.8140	 0.1920
O	 0.9050	 0.1770
P	 0.8540	 0.1810
Q	 0.8860	 0.1890
R	 0.8840	 0.1650
S	 0.9080	 0.1900
T	 0.8880	 0.2210
a	 0.8800	 0.1690
b	 0.8540	 0.1650
c	 0.8520	 0.1840
d	 0.8260	 0.1760
e	 0.8230	 0.1930



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Chain	Atom inclusion	Q-score
f	 0.4380	 0.1740
g	 0.7380	 0.1570
h	 0.6830	 0.1800
i	 0.9030	 0.1820
j	 0.8210	 0.1850
k	 0.8760	 0.1700
l	 0.8730	 0.1700
m	 0.8570	 0.1760
n	 0.8820	 0.1820
o	 0.7980	 0.1830
p	 0.9070	 0.1740
q	 0.8410	 0.1860
r	 0.9070	 0.1850
s	 0.8520	 0.1960
t	 0.7680	 0.1820
u	 0.8950	 0.1700
v	 0.9090	 0.1650
w	 0.8760	 0.2150
x	 0.8600	 0.2100
y	 0.9010	 0.1730
z	 0.9240	 0.1940