



# wwPDB EM Validation Summary Report ⓘ

Oct 28, 2024 – 07:08 am GMT

PDB ID : 7PIQ  
EMDB ID : EMD-13447  
Title : 70S ribosome with A- and P-site tRNAs in pseudouridimycin-treated Mycoplasma pneumoniae cells  
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.  
Deposited on : 2021-08-23  
Resolution : 9.70 Å (reported)  
Based on initial models : 4V7C, 7OOC, 7OOD

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

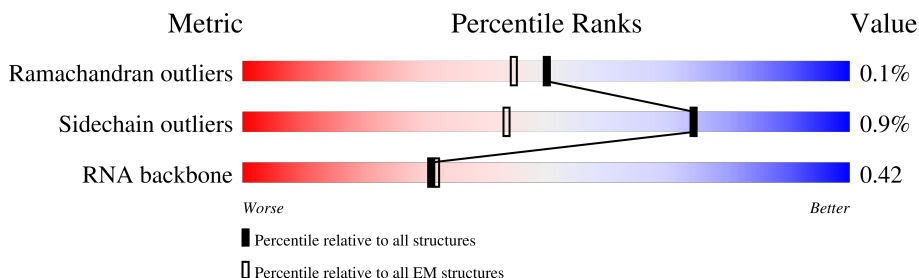
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 9.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	0	48	<div> <div>6%</div> <div>98%</div> <div>.</div> </div>
2	1	59	<div> <div>15%</div> <div>100%</div> </div>
3	2	37	<div> <div>22%</div> <div>97%</div> <div>.</div> </div>
4	A	294	<div> <div>33%</div> <div>81%</div> <div>18%</div> </div>
5	B	273	<div> <div>44%</div> <div>78%</div> <div>21%</div> </div>
6	C	205	<div> <div>37%</div> <div>99%</div> <div>.</div> </div>
7	D	219	<div> <div>27%</div> <div>69%</div> <div>30%</div> </div>
8	E	215	<div> <div>31%</div> <div>77%</div> <div>22%</div> </div>

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Mol	Chain	Length	Quality of chain
9	F	155	<div> <div>52%</div> <div>99%</div> <div>..</div> </div>
10	G	142	<div> <div>27%</div> <div>96%</div> <div>..</div> </div>
11	H	132	<div> <div>27%</div> <div>96%</div> <div>..</div> </div>
12	I	108	<div> <div>44%</div> <div>94%</div> <div>6%</div> </div>
13	J	121	<div> <div>36%</div> <div>93%</div> <div>6%</div> </div>
14	K	139	<div> <div>17%</div> <div>95%</div> <div>..</div> </div>
15	L	124	<div> <div>60%</div> <div>95%</div> <div>5%</div> </div>
16	M	61	<div> <div>20%</div> <div>98%</div> <div>.</div> </div>
17	N	86	<div> <div>16%</div> <div>97%</div> <div>.</div> </div>
18	O	94	<div> <div>12%</div> <div>84%</div> <div>15%</div> </div>
19	P	85	<div> <div>22%</div> <div>98%</div> <div>.</div> </div>
20	Q	104	<div> <div>15%</div> <div>62%</div> <div>38%</div> </div>
21	R	87	<div> <div>62%</div> <div>97%</div> <div>.</div> </div>
22	S	87	<div> <div>.</div> <div>85%</div> <div>11%</div> </div>
23	T	60	<div> <div>20%</div> <div>88%</div> <div>12%</div> </div>
24	a	287	<div> <div>16%</div> <div>99%</div> <div>..</div> </div>
25	b	287	<div> <div>17%</div> <div>79%</div> <div>20%</div> </div>
26	c	212	<div> <div>23%</div> <div>99%</div> <div>.</div> </div>
27	d	180	<div> <div>29%</div> <div>97%</div> <div>..</div> </div>
28	e	184	<div> <div>28%</div> <div>96%</div> <div>.</div> </div>
29	f	149	<div> <div>74%</div> <div>96%</div> <div>..</div> </div>
30	g	161	<div> <div>44%</div> <div>68%</div> <div>7%</div> <div>25%</div> </div>
31	h	137	<div> <div>71%</div> <div>93%</div> <div>7%</div> </div>
32	i	146	<div> <div>18%</div> <div>98%</div> <div>..</div> </div>
33	j	122	<div> <div>39%</div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
34	k	151	
35	l	139	
36	m	124	
37	n	116	
38	o	119	
39	p	127	
40	q	100	
41	r	159	
42	s	237	
43	t	111	
44	u	104	
45	v	65	
46	w	111	
47	x	97	
48	y	57	
49	z	53	
50	3	2907	
51	4	108	
52	5	1520	
53	6	76	
53	7	76	

## 2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 146057 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 30S ribosomal protein S2.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
30	g	121	Total	C	N	O	S	0
			910	580	158	169	3	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	p	112	Total	C	N	O	S	0	0
			934	594	186	152	2		

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

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

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

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

- 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		

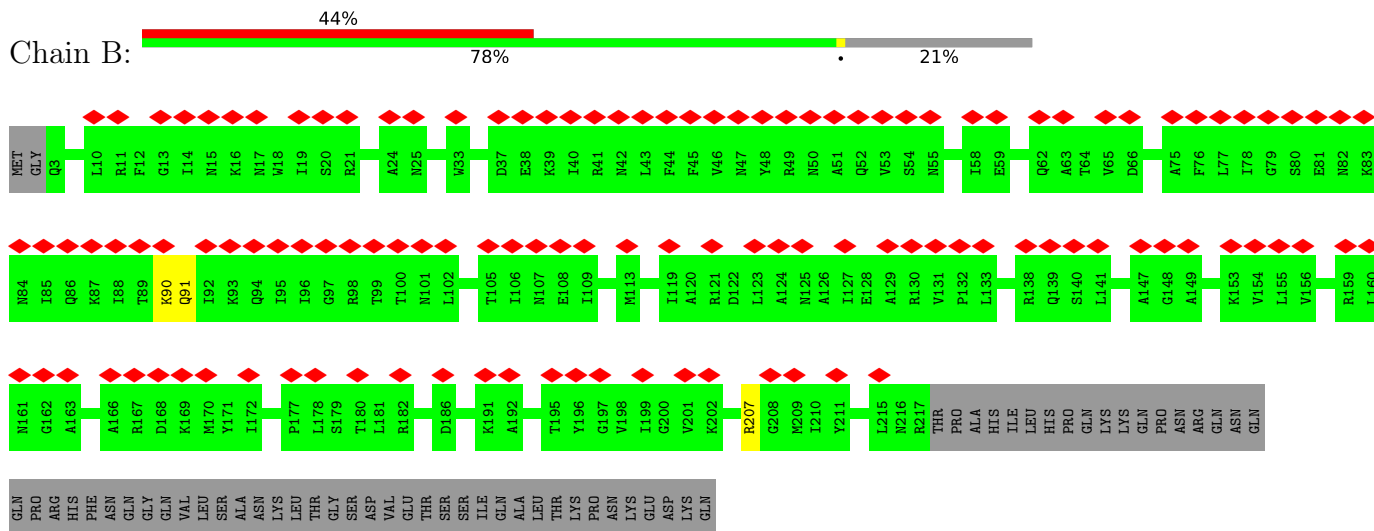
- Molecule 53 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	6	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
53	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

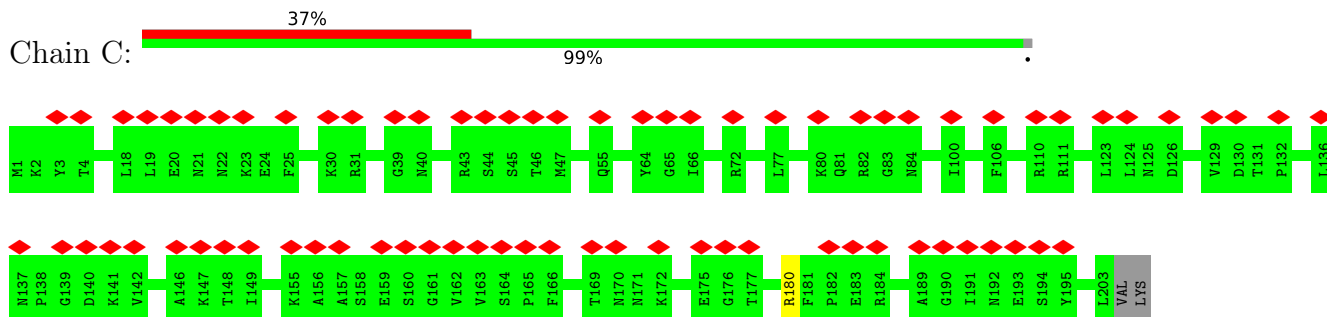


ASN  
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• Molecule 5: 30S ribosomal protein S3



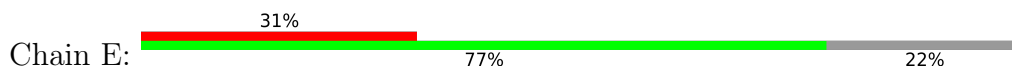
• Molecule 6: 30S ribosomal protein S4

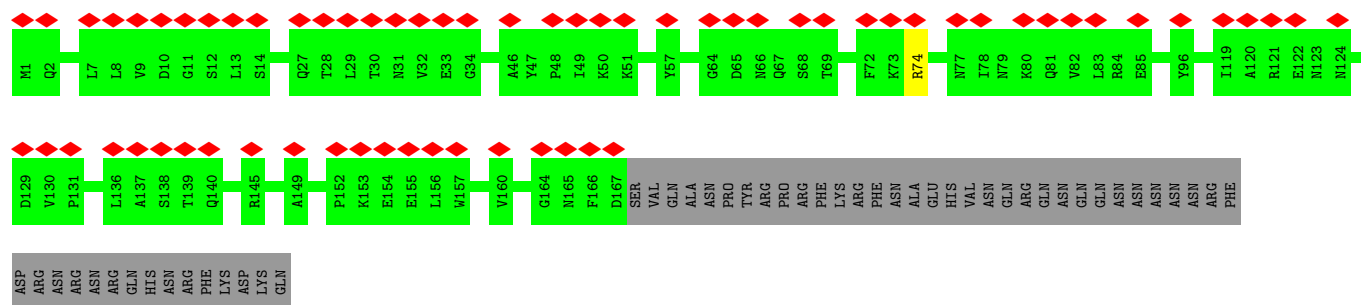


• Molecule 7: 30S ribosomal protein S5



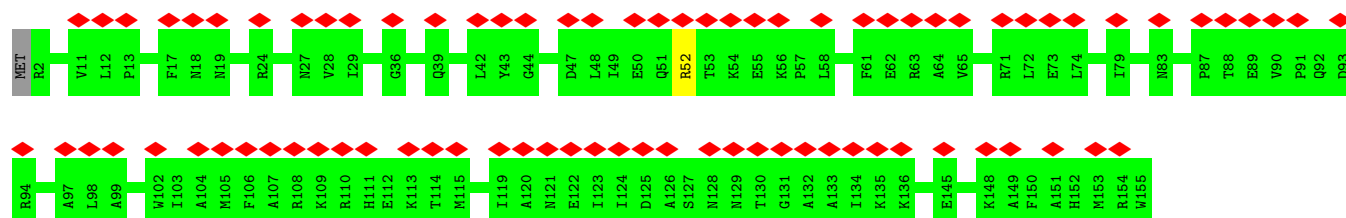
• Molecule 8: 30S ribosomal protein S6





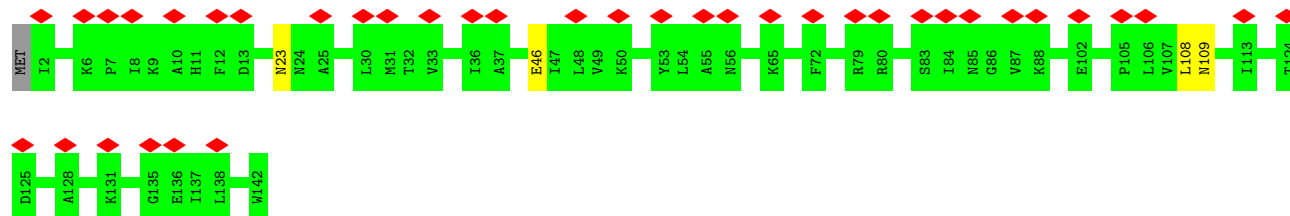
• Molecule 9: 30S ribosomal protein S7

Chain F: 52% 99%



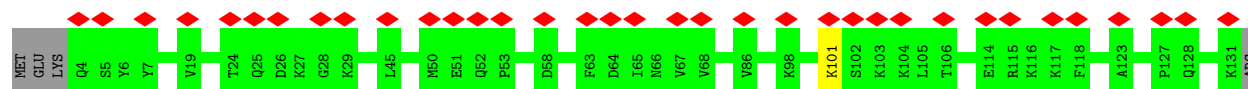
• Molecule 10: 30S ribosomal protein S8

Chain G: 27% 96%



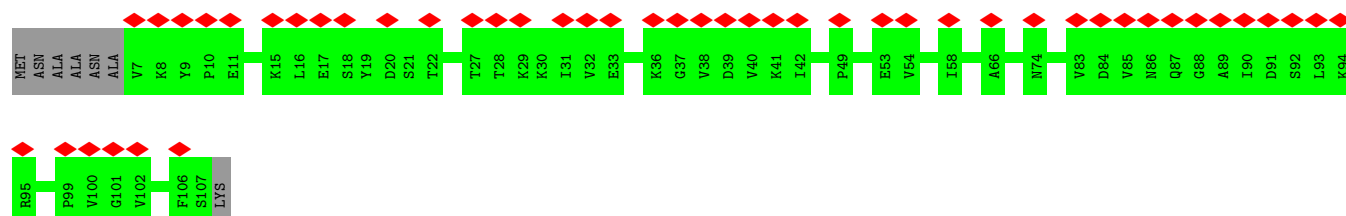
• Molecule 11: 30S ribosomal protein S9

Chain H: 27% 96%

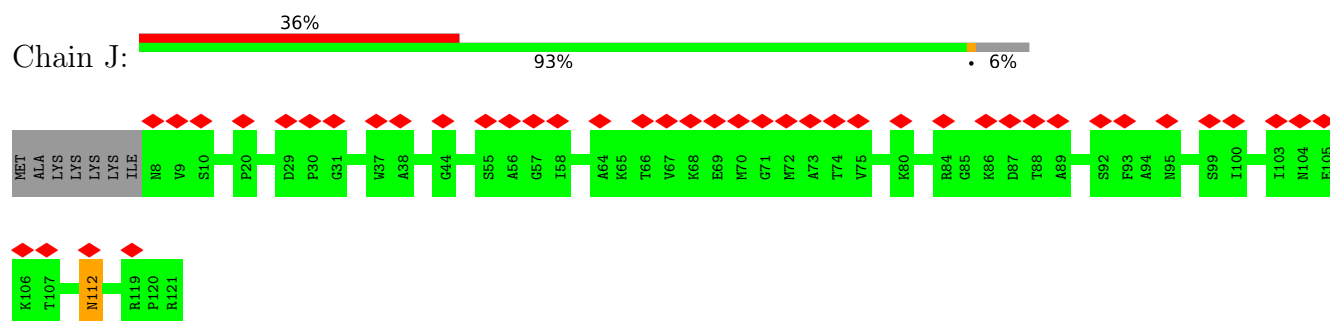


• Molecule 12: 30S ribosomal protein S10

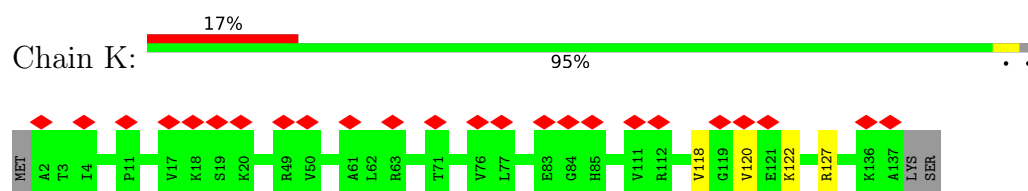
Chain I: 44% 94% 6%



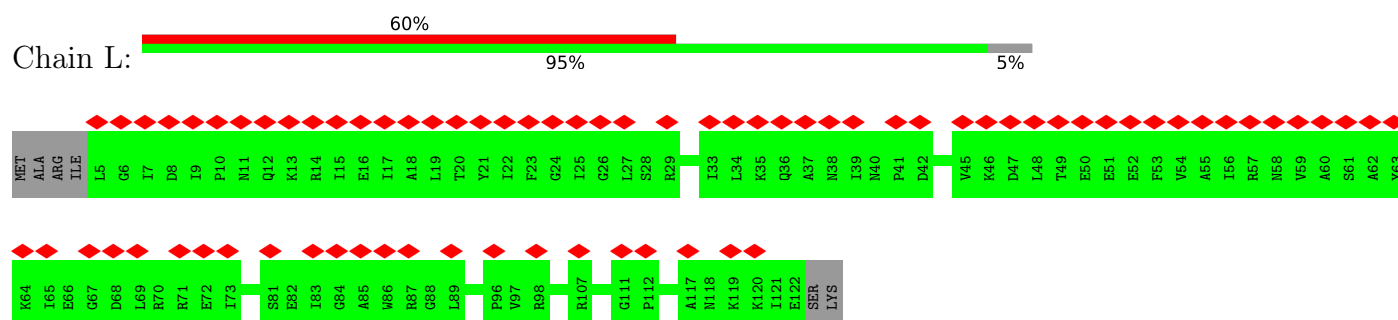
- Molecule 13: 30S ribosomal protein S11



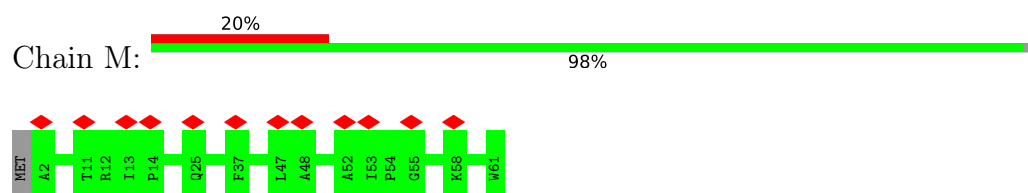
- Molecule 14: 30S ribosomal protein S12



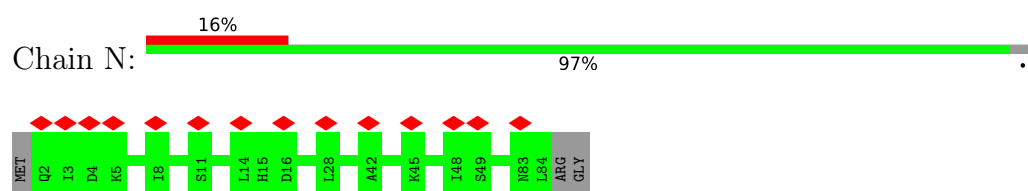
- Molecule 15: 30S ribosomal protein S13



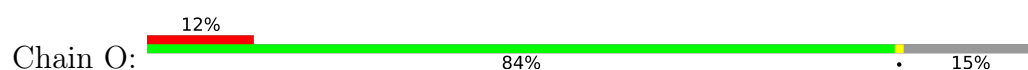
- Molecule 16: 30S ribosomal protein S14 type Z

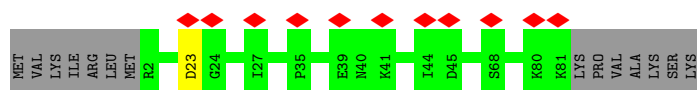


- Molecule 17: 30S ribosomal protein S15

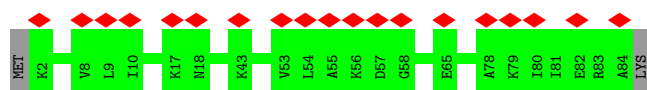


- Molecule 18: 30S ribosomal protein S16

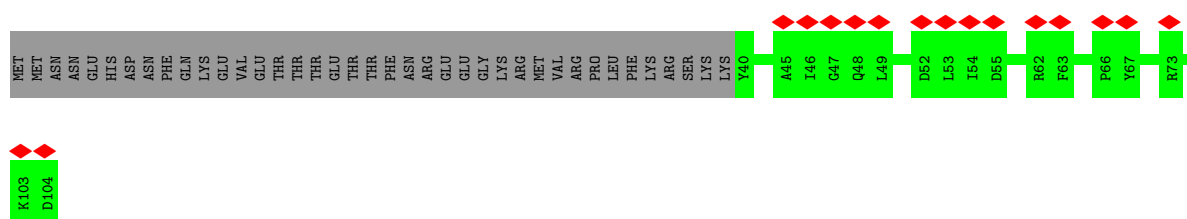




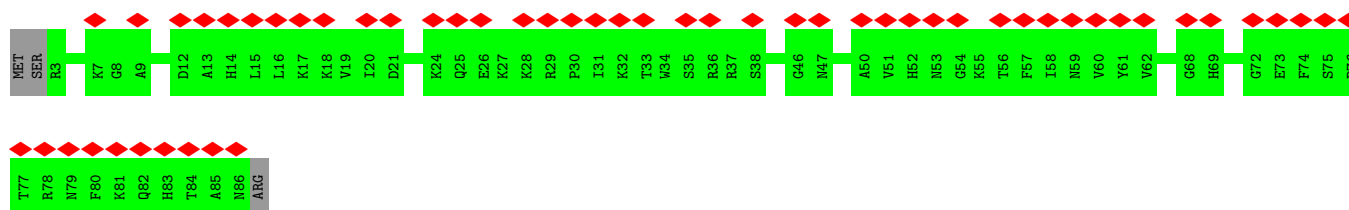
- Molecule 19: 30S ribosomal protein S17



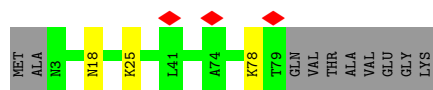
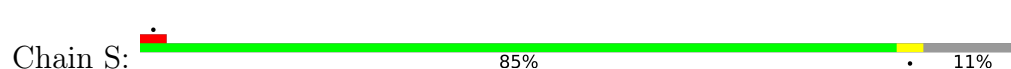
- Molecule 20: 30S ribosomal protein S18



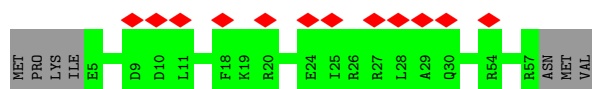
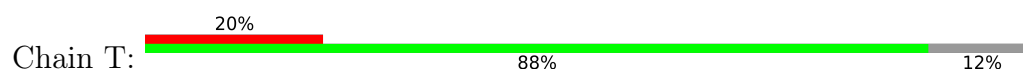
- Molecule 21: 30S ribosomal protein S19



- Molecule 22: 30S ribosomal protein S20

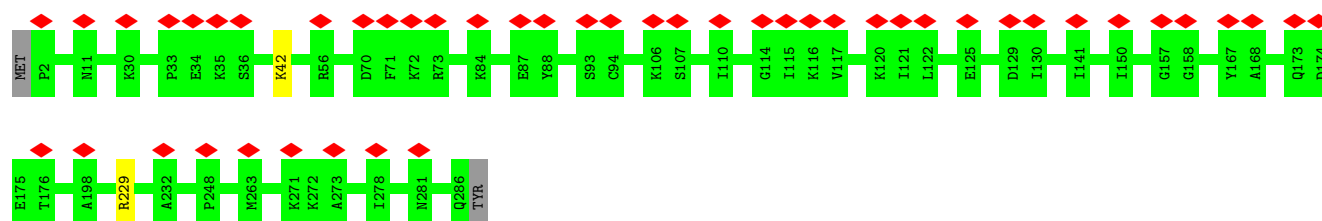


- Molecule 23: 30S ribosomal protein S21




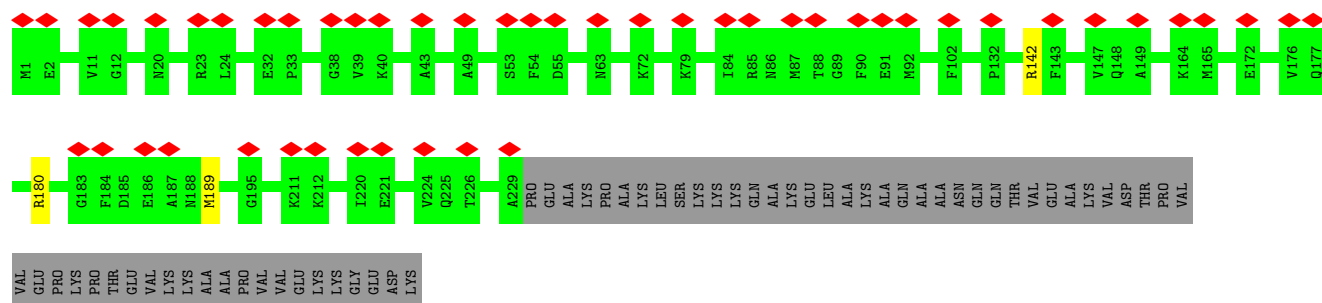
- Molecule 24: 50S ribosomal protein L2

Chain a: 



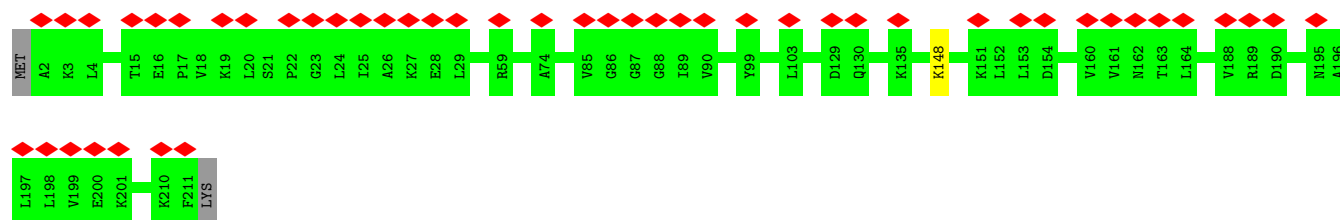
- Molecule 25: 50S ribosomal protein L3

Chain b: 



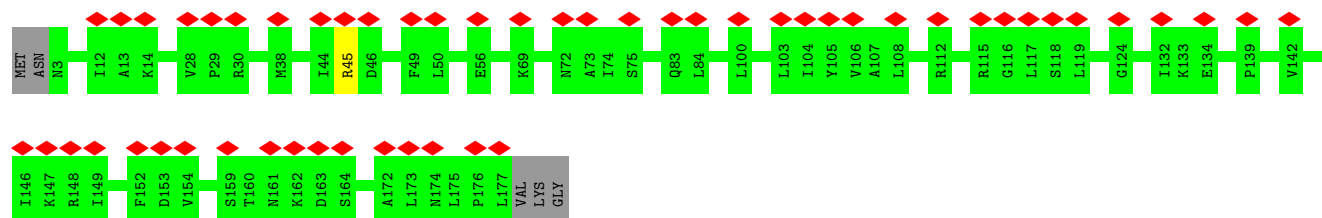
- Molecule 26: 50S ribosomal protein L4

Chain c: 



- Molecule 27: 50S ribosomal protein L5

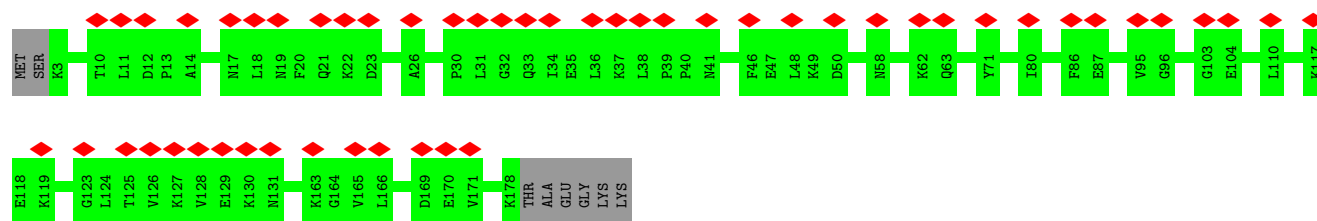
Chain d: 



- Molecule 28: 50S ribosomal protein L6

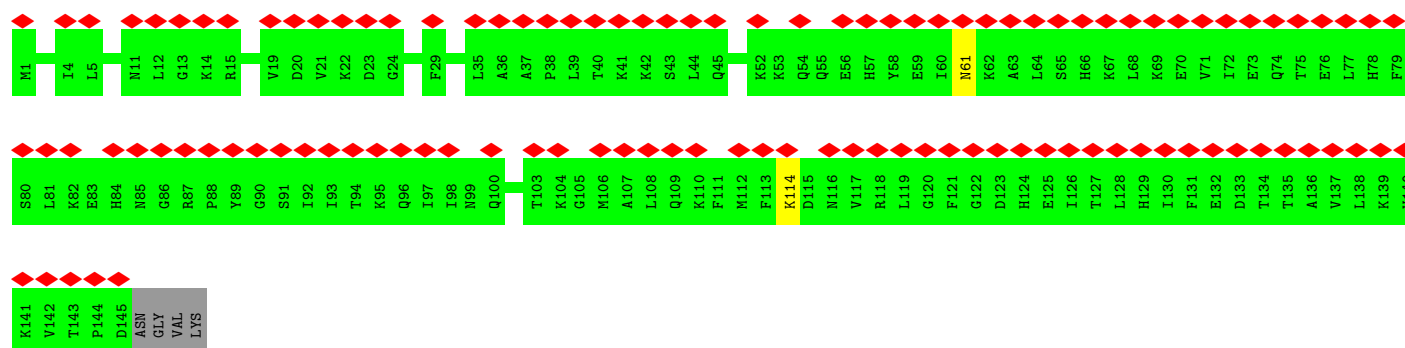
Chain e: 





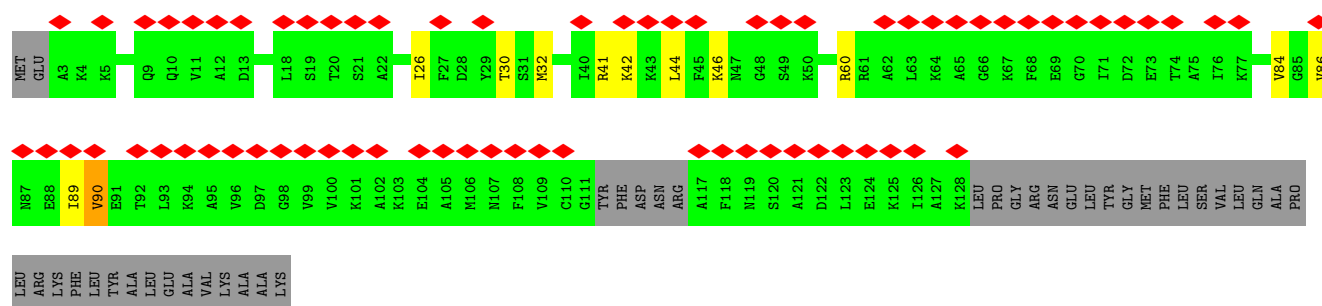
• Molecule 29: 50S ribosomal protein L9

Chain f: 74% 96%



• Molecule 30: 50S ribosomal protein L10

Chain g: 44% 68% 7% 25%



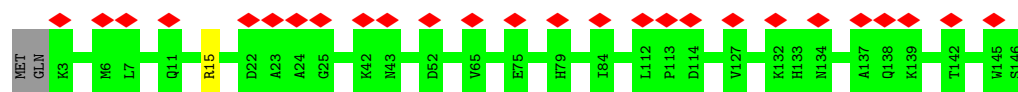
• Molecule 31: 50S ribosomal protein L11

Chain h: 71% 93% 7%

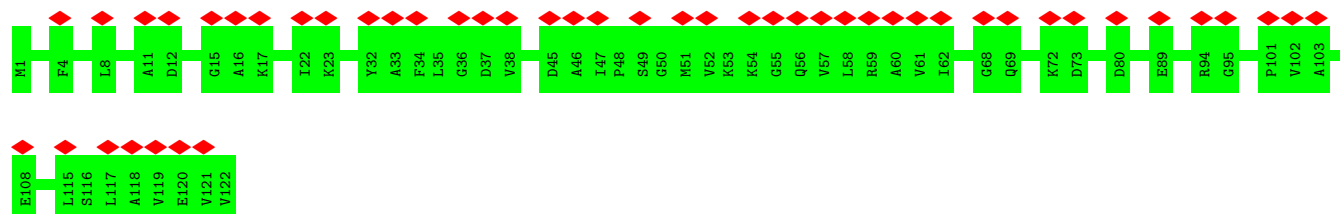
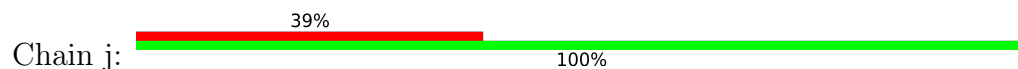


• Molecule 32: 50S ribosomal protein L13

Chain i: 18% 98%



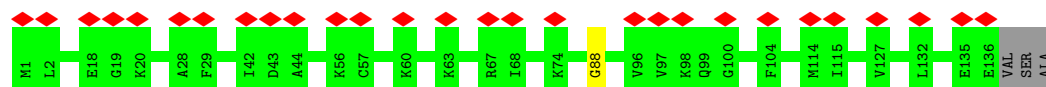
- Molecule 33: 50S ribosomal protein L14



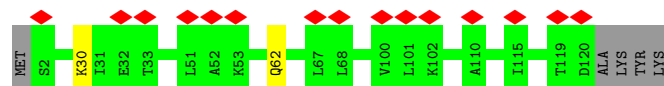
- Molecule 34: 50S ribosomal protein L15



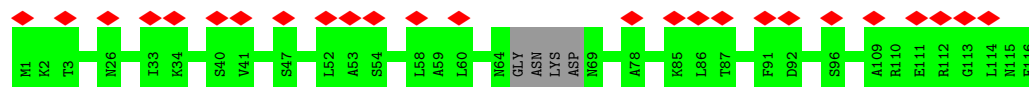
- Molecule 35: 50S ribosomal protein L16



- Molecule 36: 50S ribosomal protein L17

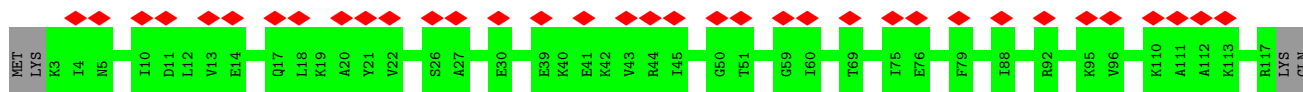


- Molecule 37: 50S ribosomal protein L18

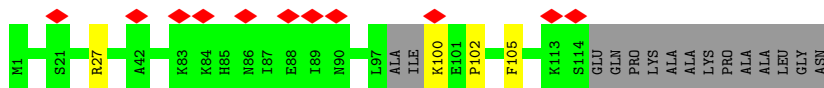
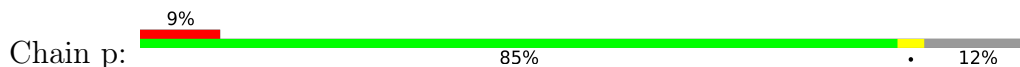


- Molecule 38: 50S ribosomal protein L19

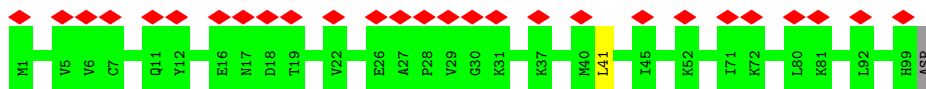




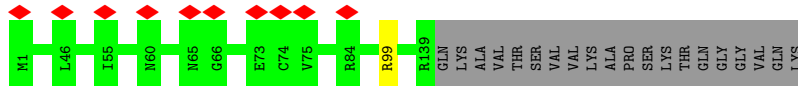
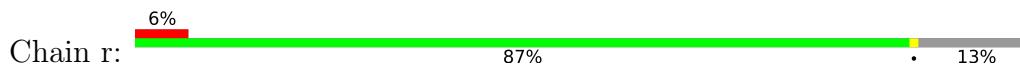
- Molecule 39: 50S ribosomal protein L20



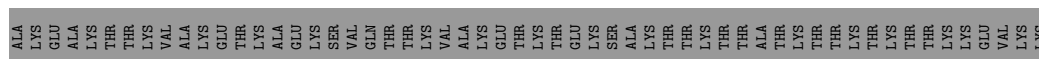
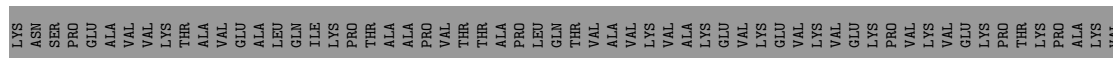
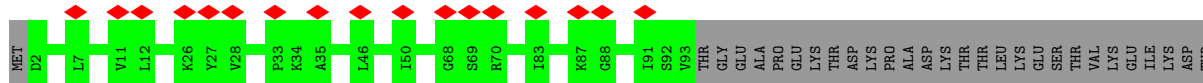
- Molecule 40: 50S ribosomal protein L21



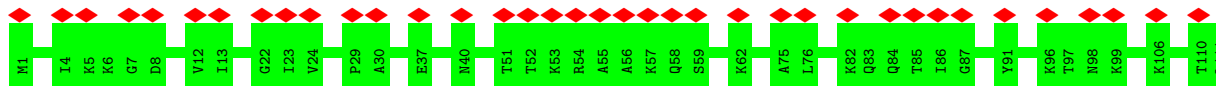
- Molecule 41: 50S ribosomal protein L22



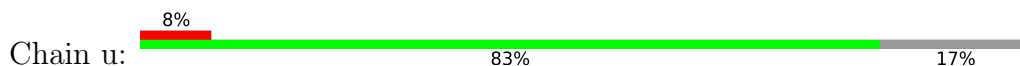
- Molecule 42: 50S ribosomal protein L23

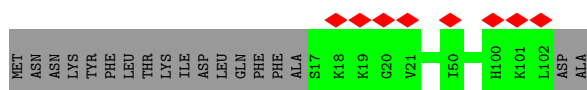


- Molecule 43: 50S ribosomal protein L24

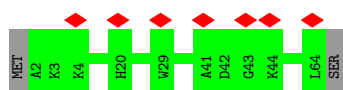


- Molecule 44: 50S ribosomal protein L27

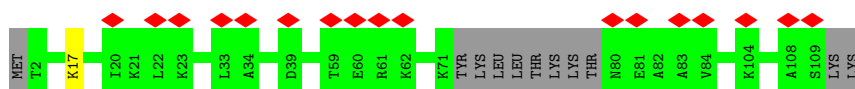
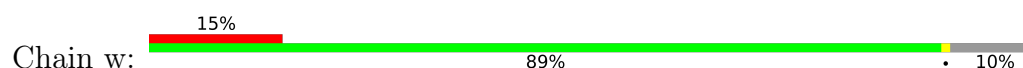




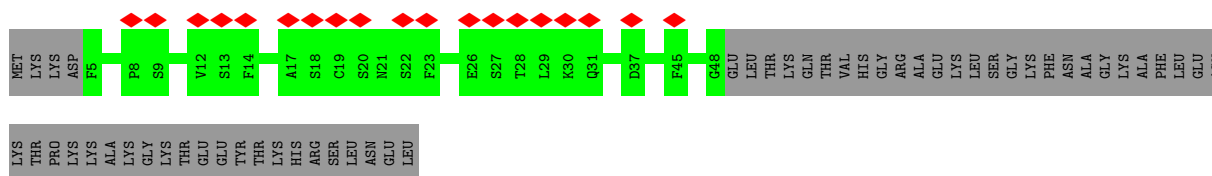
- Molecule 45: 50S ribosomal protein L28



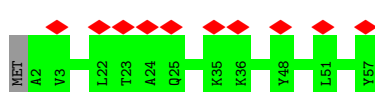
- Molecule 46: 50S ribosomal protein L29



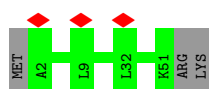
- Molecule 47: 50S ribosomal protein L31



- Molecule 48: 50S ribosomal protein L32



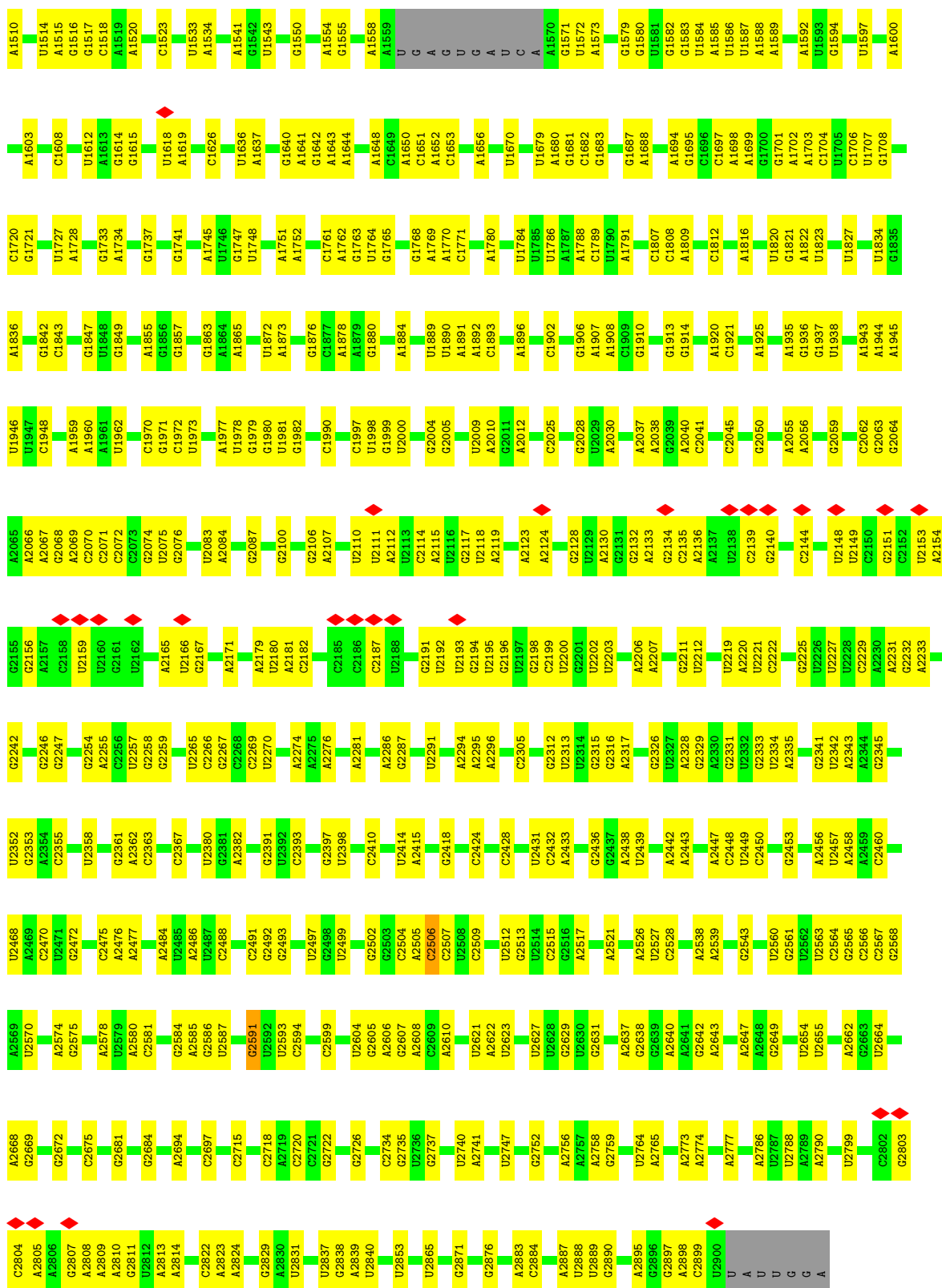
- Molecule 49: 50S ribosomal protein L33 1

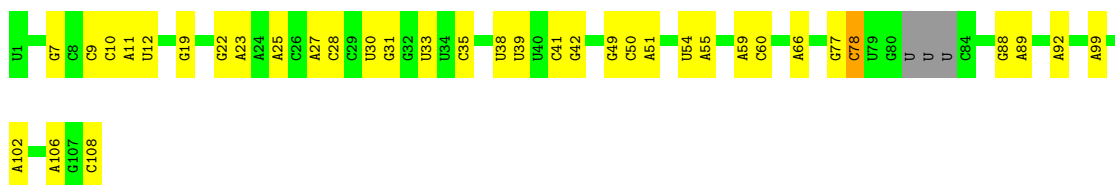


- Molecule 50: 23S ribosomal RNA



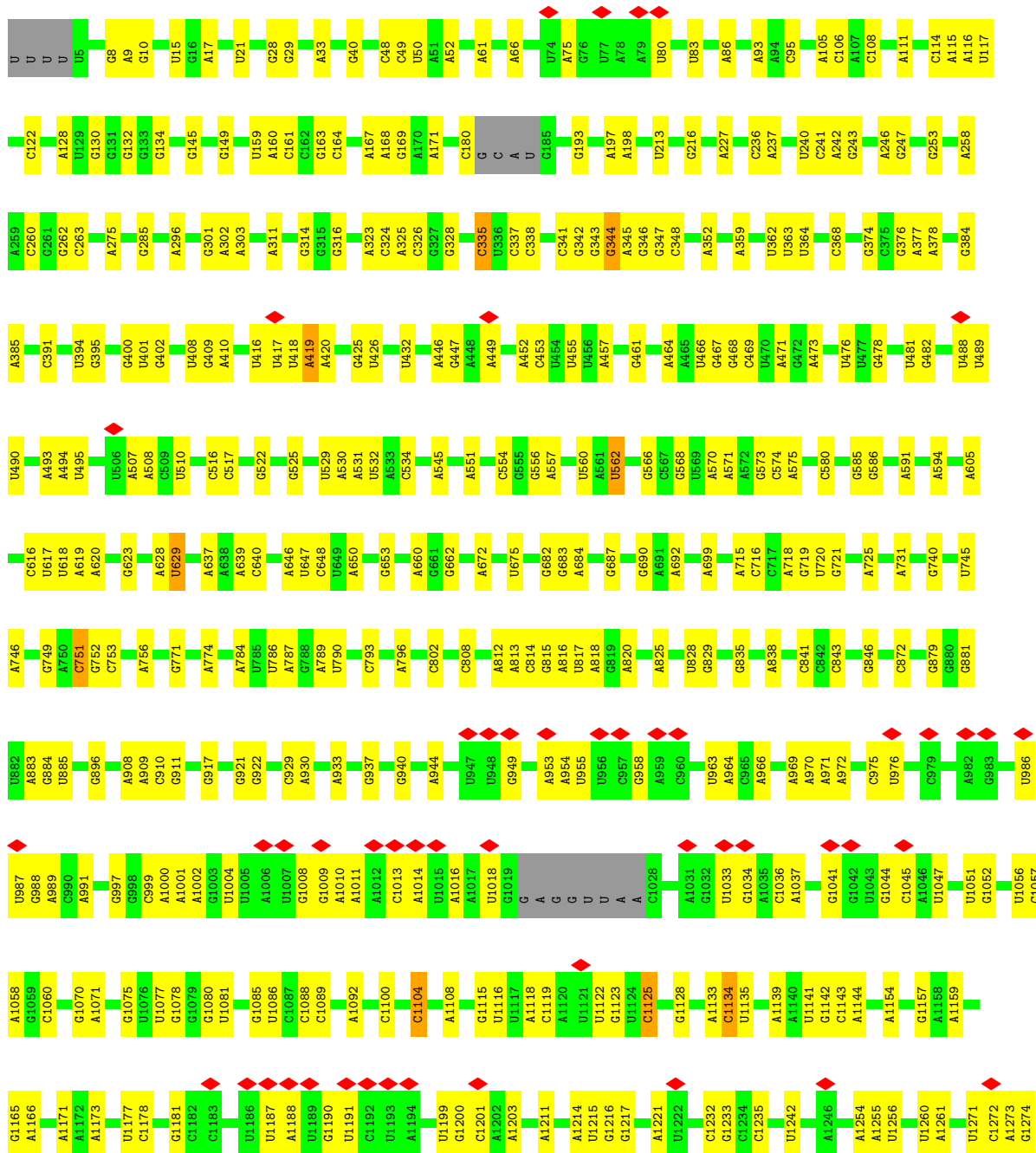
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A102	G103	U115	C116	A119	A120	U121	G122	A127	C128	U129	G132	G136	G139	G140	A141	C144	A145	G146	A163	A164	U165	A166	U169	C173	A178	A179	A180	A286	G287	A291	U296	G297	U298	A299	G306	A309	U310	G209	G311	A211	A217	G218	G219	A220					
A225	A226	A227	A228	A231	A232	U233	G234	U235	A236	G237	U238	G242	U245	G246	U247	G252	A364	C253	G254	A255	G256	A261	G265	A269	G270	A276	A283	U284	U285	A286	G291	U296	G297	U298	A299	G306	A309	U310	G209	G311	A211	A217	G218	G219	A220				
G319	C324	G329	A330	A331	G335	U339	A345	G353	C354	A355	A356	A357	G363	A364	U365	U377	A381	C393	A396	G397	C398	G399	A400	A401	A402	U403	C404	G408	A409	G410	U411	G417	A421	A422	C423	G424	U425	A426	U427	U428	U431	A432	A433	G434					
A437	U441	C442	C443	C444	G447	A448	U457	A458	A459	G460	A465	U470	A471	G478	A479	G482	A483	U484	C487	G488	A491	U495	U500	G501	A502	G503	A508	G509	G510	U511	G512	A513	A514	A515	A516	G517	G520	A523	U528	G531	U539								
A540	U543	A548	A553	C562	A563	A564	C565	G566	U567	G568	C575	A576	C577	A578	U580	A581	A582	U583	A589	U590	U595	G596	C597	G598	A605	G606	U607	A608	U609	A611	G612	A619	G620	C634	G635	U636	U637	A638	G648	A649	G650	G653	G656						
G661	U662	A663	G666	A673	G674	U675	A681	A682	U688	U689	G691	U692	U696	A705	C706	A711	G719	A720	G721	C722	G725	U737	U738	G739	A740	G761	G764	A765	C766	G767	A769	C777	U781	U782	G783	A784	A785	A786	G792	C793	G794	G795							
A796	U797	G798	A799	G803	A806	G810	G811	G812	A816	A817	A818	U819	U820	C821	A824	U825	C826	G827	A828	A829	A830	U831	U835	G836	A837	G840	U842	U845	U846	C847	A854	A858	U862	A864	A865	C868	A881	C882	A883	A884	A885	G892							
U896	C901	U902	A903	C904	U905	G906	G914	G918	C922	A	C	U	A	G928	G929	C930	G931	U932	A933	C934	U935	G936	U944	A947	A948	U950	C951	U952	G953	U962	U968	U973	A977	A981	G982	G986	G989	A993	U994	A995	A996	G997							
C998	C1001	A1008	A1009	A1016	A1017	A1018	A1019	G1020	C1021	C1022	C1023	A1024	G1025	A1026	U1027	A1032	A1033	G1034	U1035	C1042	C1043	C1044	A1045	A1046	U1047	A1048	U1049	A1052	C1053	U1054	A1055	A1056	G1057	A1061	U1068	G1069	G1075	A1080	A1081	A1082	A1083	C1084	U1095	U1096	G1097	G1098	C1099	U1100	
U1101	A1102	G1103	A1104	A1105	A1106	C1107	A1108	U1113	C1114	G1115	A1119	G1122	A1123	G1124	U1125	G1126	A1130	A1131	C1132	C1144	G1145	A1146	G1147	U1148	G1149	U1150	U1151	U1154	G1157	C1158	C1159	A1162	G1163	A1164	U1165	G1166	U1167	A1168	A1169	C1170	G1171	U1176	A1177	A1186	A1191	U1192	U1193		
U1196	A1201	A1202	G1203	A1204	U1207	U1208	A1209	A1210	G1215	U1216	G1217	G1218	U1219	G1224	A1225	G1226	U1234	U1235	G1236	A1242	A1243	C1247	A1248	A1249	A1250	G1251	G1252	G1253	U1254	G1255	A1256	G1257	G1266	A1267	U1268	C1269	U1279	G1280	A1281	G1282	A1283	U1284	U1285	G1286	C1287	A1292	A1295	G1296	
U1297	A1298	C1299	G1300	G1301	C1302	U1303	A1314	C1317	U1318	C1319	C1320	C1321	A1324	C1325	C1326	G1327	U1328	U1329	U1330	G1331	U1334	A1335	G1338	U1339	U1340	U1341	C1342	C1343	C1348	G1349	G1353	U1357	C1358	G1359	U1360	U1361	U1369	A1370	G1371	U1372	C1373	U1374	G1375	U1376	A1377	C1378	G1379	U1380	G1388
G1389	C1390	A1393	A1396	G1397	U1407	G1408	C1411	A1412	A1413	A1421	U1422	A1423	U1424	U1428	A1431	A1435	C1436	C1444	U1445	G1446	A1447	U1448	A1455	C1456	A1457	A1461	A1462	G1463	U1466	U1467	A1479	A1480	U1481	U1482	G1483	G1484	U1487	A1500	U1501	A1502	G1507	G1508	U1509						

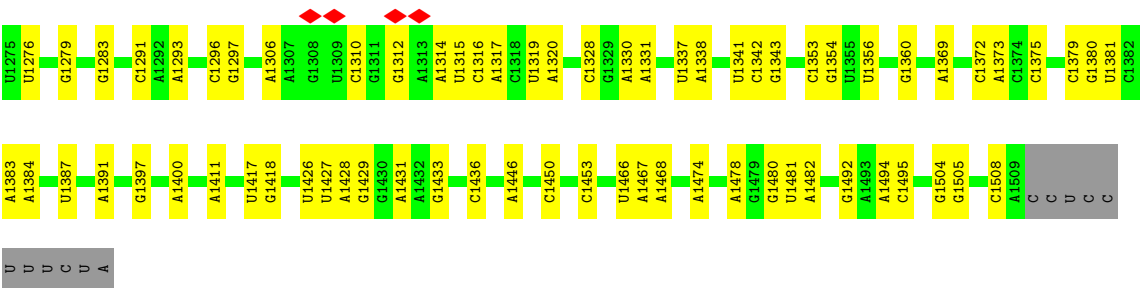




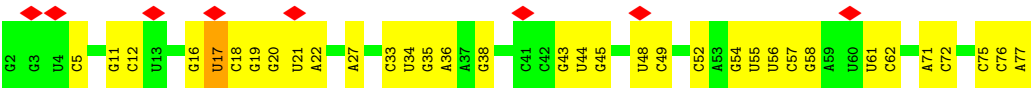
• Molecule 52: 16S ribosomal RNA

Chain 5: 69% 29%

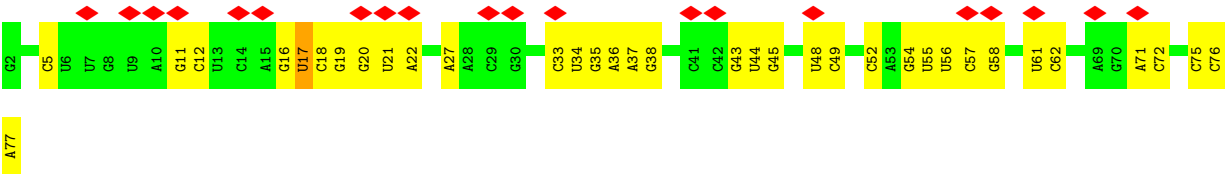




• Molecule 53: tRNA-Phe



• 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	1534	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	1.401	Depositor
Minimum map value	-0.507	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.105	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	0.25	0/383	0.49	0/504
2	1	0.23	0/484	0.49	0/637
3	2	0.30	0/306	0.60	0/401
4	A	0.25	0/1954	0.50	0/2642
5	B	0.25	0/1721	0.54	1/2323 (0.0%)
6	C	0.28	0/1691	0.49	0/2267
7	D	0.27	0/1188	0.52	0/1593
8	E	0.29	0/1384	0.57	2/1867 (0.1%)
9	F	0.24	0/1266	0.54	0/1700
10	G	0.29	0/1126	0.54	1/1517 (0.1%)
11	H	0.25	0/1044	0.49	0/1395
12	I	0.25	0/820	0.50	0/1103
13	J	0.28	0/844	0.53	1/1136 (0.1%)
14	K	0.29	0/1094	0.53	0/1468
15	L	0.23	0/962	0.48	0/1289
16	M	0.25	0/483	0.43	0/643
17	N	0.24	0/679	0.43	0/907
18	O	0.25	0/659	0.51	1/885 (0.1%)
19	P	0.27	0/684	0.52	0/913
20	Q	0.24	0/545	0.44	0/730
21	R	0.27	0/698	0.53	0/936
22	S	0.23	0/631	0.42	0/838
23	T	0.26	0/475	0.58	0/621
24	a	0.25	0/2267	0.47	0/3044
25	b	0.29	0/1795	0.59	1/2412 (0.0%)
26	c	0.24	0/1671	0.49	0/2246
27	d	0.28	0/1409	0.52	0/1894
28	e	0.26	0/1420	0.54	0/1912
29	f	0.27	0/1183	0.55	0/1587
30	g	0.37	0/916	0.56	0/1222
31	h	0.25	0/968	0.47	0/1298
32	i	0.26	0/1186	0.45	0/1592
33	j	0.28	0/953	0.53	0/1275
34	k	0.27	0/1170	0.48	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	l	0.26	0/1104	0.52	1/1481 (0.1%)
36	m	0.27	0/973	0.51	0/1309
37	n	0.24	0/897	0.50	0/1198
38	o	0.24	0/948	0.49	0/1262
39	p	3.10	6/947 (0.6%)	0.61	2/1257 (0.2%)
40	q	0.24	0/828	0.52	1/1111 (0.1%)
41	r	0.27	0/1077	0.49	0/1441
42	s	0.25	0/732	0.49	0/988
43	t	0.25	0/879	0.49	0/1165
44	u	0.30	0/665	0.54	0/884
45	v	0.23	0/519	0.47	0/695
46	w	0.29	0/826	0.53	0/1104
47	x	0.24	0/353	0.44	0/474
48	y	0.32	0/457	0.53	0/601
49	z	0.23	0/412	0.45	0/547
50	3	0.24	0/69073	0.85	55/107710 (0.1%)
51	4	0.22	0/2505	0.84	1/3902 (0.0%)
52	5	0.22	0/35768	0.83	29/55764 (0.1%)
53	6	0.24	0/1808	0.92	4/2817 (0.1%)
53	7	0.24	0/1808	0.92	4/2817 (0.1%)
All	All	0.34	6/158638 (0.0%)	0.77	104/236883 (0.0%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	p	105	PHE	CE1-CZ	44.56	2.22	1.37
39	p	105	PHE	CE2-CZ	44.52	2.21	1.37
39	p	105	PHE	CD2-CE2	42.45	2.24	1.39
39	p	105	PHE	CD1-CE1	42.10	2.23	1.39
39	p	105	PHE	CG-CD2	27.69	1.80	1.38

The worst 5 of 104 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	l	88	GLY	C-N-CA	9.22	144.74	121.70
50	3	1023	C	N3-C2-O2	-9.14	115.50	121.90
52	5	843	C	N3-C2-O2	-8.36	116.05	121.90
52	5	1453	C	N3-C2-O2	-8.30	116.09	121.90
50	3	892	G	C4-C5-N7	-8.11	107.56	110.80

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	43 (96%)	2 (4%)	0	100	100
2	1	57/59 (97%)	52 (91%)	5 (9%)	0	100	100
3	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
4	A	238/294 (81%)	221 (93%)	17 (7%)	0	100	100
5	B	213/273 (78%)	200 (94%)	13 (6%)	0	100	100
6	C	201/205 (98%)	188 (94%)	13 (6%)	0	100	100
7	D	151/219 (69%)	139 (92%)	12 (8%)	0	100	100
8	E	165/215 (77%)	141 (86%)	24 (14%)	0	100	100
9	F	152/155 (98%)	130 (86%)	22 (14%)	0	100	100
10	G	139/142 (98%)	124 (89%)	14 (10%)	1 (1%)	19	57
11	H	126/132 (96%)	115 (91%)	11 (9%)	0	100	100
12	I	99/108 (92%)	87 (88%)	12 (12%)	0	100	100
13	J	112/121 (93%)	107 (96%)	4 (4%)	1 (1%)	14	52
14	K	134/139 (96%)	116 (87%)	18 (13%)	0	100	100
15	L	116/124 (94%)	109 (94%)	7 (6%)	0	100	100
16	M	58/61 (95%)	57 (98%)	1 (2%)	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%)	72 (89%)	9 (11%)	0	100	100
20	Q	63/104 (61%)	58 (92%)	5 (8%)	0	100	100
21	R	82/87 (94%)	74 (90%)	8 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	S	75/87 (86%)	75 (100%)	0	0	100	100
23	T	51/60 (85%)	49 (96%)	2 (4%)	0	100	100
24	a	283/287 (99%)	261 (92%)	22 (8%)	0	100	100
25	b	227/287 (79%)	204 (90%)	23 (10%)	0	100	100
26	c	208/212 (98%)	199 (96%)	9 (4%)	0	100	100
27	d	173/180 (96%)	155 (90%)	18 (10%)	0	100	100
28	e	174/184 (95%)	164 (94%)	10 (6%)	0	100	100
29	f	143/149 (96%)	130 (91%)	13 (9%)	0	100	100
30	g	117/161 (73%)	108 (92%)	8 (7%)	1 (1%)	14	52
31	h	126/137 (92%)	114 (90%)	12 (10%)	0	100	100
32	i	142/146 (97%)	132 (93%)	10 (7%)	0	100	100
33	j	120/122 (98%)	111 (92%)	9 (8%)	0	100	100
34	k	146/151 (97%)	135 (92%)	11 (8%)	0	100	100
35	l	134/139 (96%)	125 (93%)	9 (7%)	0	100	100
36	m	117/124 (94%)	108 (92%)	9 (8%)	0	100	100
37	n	108/116 (93%)	96 (89%)	12 (11%)	0	100	100
38	o	113/119 (95%)	98 (87%)	15 (13%)	0	100	100
39	p	108/127 (85%)	100 (93%)	7 (6%)	1 (1%)	14	52
40	q	97/100 (97%)	82 (84%)	15 (16%)	0	100	100
41	r	137/159 (86%)	127 (93%)	10 (7%)	0	100	100
42	s	90/237 (38%)	81 (90%)	9 (10%)	0	100	100
43	t	109/111 (98%)	100 (92%)	9 (8%)	0	100	100
44	u	84/104 (81%)	77 (92%)	7 (8%)	0	100	100
45	v	61/65 (94%)	60 (98%)	1 (2%)	0	100	100
46	w	96/111 (86%)	90 (94%)	6 (6%)	0	100	100
47	x	42/97 (43%)	37 (88%)	5 (12%)	0	100	100
48	y	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
49	z	48/53 (91%)	46 (96%)	2 (4%)	0	100	100
All	All	5809/6670 (87%)	5335 (92%)	470 (8%)	4 (0%)	50	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	g	90	VAL
39	p	102	PRO
10	G	109	ASN
13	J	112	ASN

### 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	56
4	A	212/262 (81%)	211 (100%)	1 (0%)	86	89
5	B	180/232 (78%)	178 (99%)	2 (1%)	70	80
6	C	181/183 (99%)	180 (99%)	1 (1%)	84	88
7	D	123/178 (69%)	122 (99%)	1 (1%)	79	85
8	E	150/196 (76%)	150 (100%)	0	100	100
9	F	131/132 (99%)	130 (99%)	1 (1%)	79	85
10	G	123/124 (99%)	121 (98%)	2 (2%)	58	73
11	H	111/115 (96%)	110 (99%)	1 (1%)	75	83
12	I	95/99 (96%)	95 (100%)	0	100	100
13	J	91/97 (94%)	91 (100%)	0	100	100
14	K	117/120 (98%)	113 (97%)	4 (3%)	32	51
15	L	100/105 (95%)	100 (100%)	0	100	100
16	M	47/48 (98%)	47 (100%)	0	100	100
17	N	76/78 (97%)	76 (100%)	0	100	100
18	O	69/82 (84%)	69 (100%)	0	100	100
19	P	73/75 (97%)	73 (100%)	0	100	100
20	Q	56/94 (60%)	56 (100%)	0	100	100
21	R	74/77 (96%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	S	70/77 (91%)	67 (96%)	3 (4%)	25	46
23	T	49/56 (88%)	49 (100%)	0	100	100
24	a	241/243 (99%)	239 (99%)	2 (1%)	79	85
25	b	186/233 (80%)	184 (99%)	2 (1%)	70	80
26	c	182/184 (99%)	181 (100%)	1 (0%)	86	89
27	d	150/154 (97%)	149 (99%)	1 (1%)	81	87
28	e	153/159 (96%)	153 (100%)	0	100	100
29	f	123/134 (92%)	121 (98%)	2 (2%)	58	73
30	g	96/129 (74%)	84 (88%)	12 (12%)	3	15
31	h	102/110 (93%)	102 (100%)	0	100	100
32	i	126/128 (98%)	125 (99%)	1 (1%)	79	85
33	j	103/103 (100%)	103 (100%)	0	100	100
34	k	123/126 (98%)	123 (100%)	0	100	100
35	l	113/115 (98%)	113 (100%)	0	100	100
36	m	105/109 (96%)	103 (98%)	2 (2%)	52	69
37	n	96/99 (97%)	96 (100%)	0	100	100
38	o	101/105 (96%)	101 (100%)	0	100	100
39	p	99/108 (92%)	97 (98%)	2 (2%)	50	68
40	q	90/91 (99%)	90 (100%)	0	100	100
41	r	116/132 (88%)	115 (99%)	1 (1%)	75	83
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%)	58 (100%)	0	100	100
46	w	87/98 (89%)	86 (99%)	1 (1%)	70	80
47	x	41/86 (48%)	41 (100%)	0	100	100
48	y	48/49 (98%)	48 (100%)	0	100	100
49	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5087/5751 (88%)	5043 (99%)	44 (1%)	74	83

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

Mol	Chain	Res	Type
30	g	41	ARG
30	g	89	ILE
30	g	42	LYS
30	g	60	ARG
32	i	15	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
37	n	42	GLN
41	r	57	ASN
48	y	40	HIS
19	P	62	GLN
19	P	25	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	975 (33%)	34 (1%)
51	4	103/108 (95%)	35 (33%)	3 (2%)
52	5	1490/1520 (98%)	440 (29%)	12 (0%)
53	6	75/76 (98%)	31 (41%)	6 (8%)
53	7	75/76 (98%)	32 (42%)	6 (8%)
All	All	4618/4687 (98%)	1513 (32%)	61 (1%)

5 of 1513 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	12	A
50	3	14	U
50	3	15	A
50	3	16	A
50	3	17	G

5 of 61 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	3	2506	C
53	7	16	G
51	4	54	U
53	6	76	C

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Mol	Chain	Res	Type
53	7	71	A

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

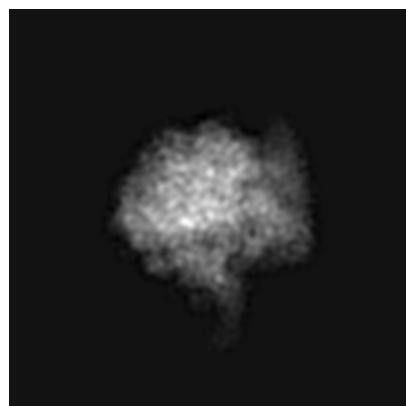
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13447. These allow visual inspection of the internal detail of the map and identification of artifacts.

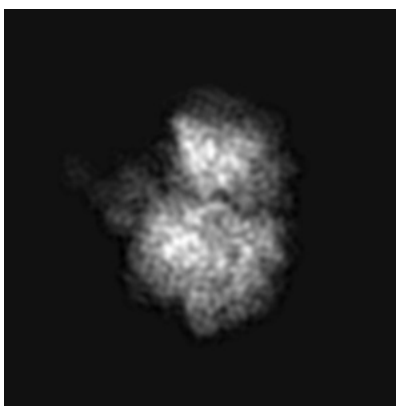
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

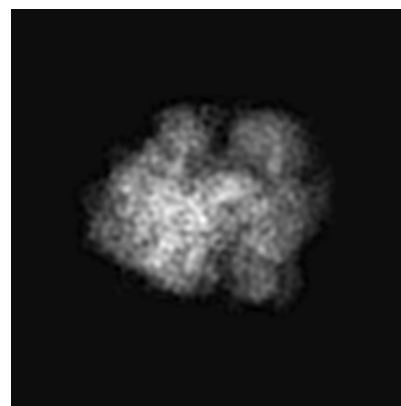
#### 6.1.1 Primary map



X

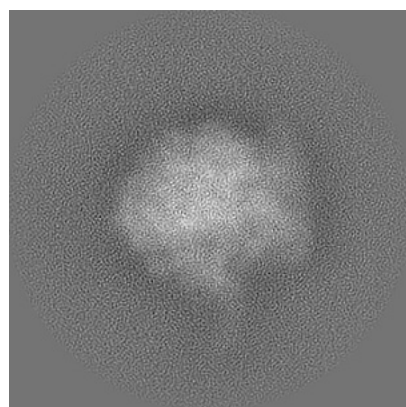


Y

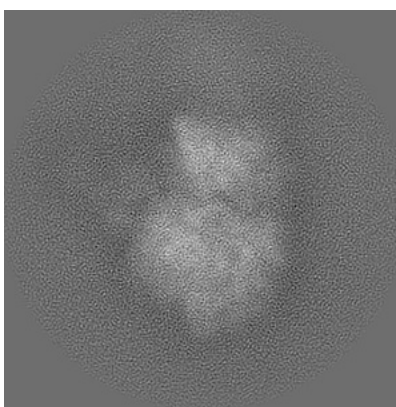


Z

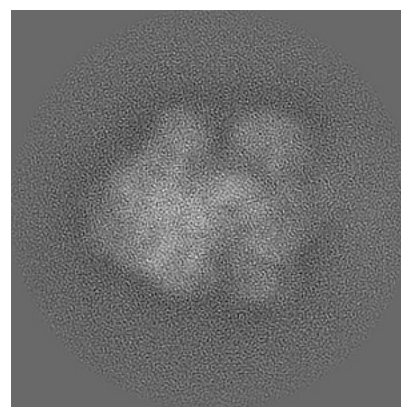
#### 6.1.2 Raw map



X



Y

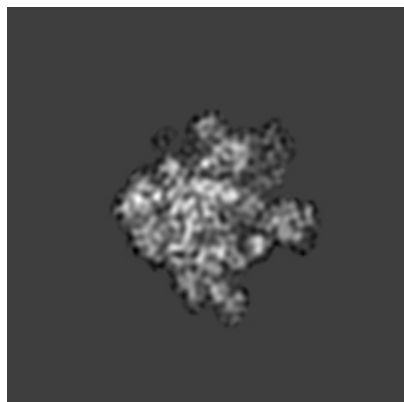


Z

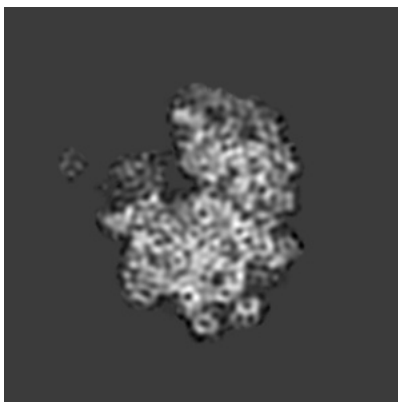
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

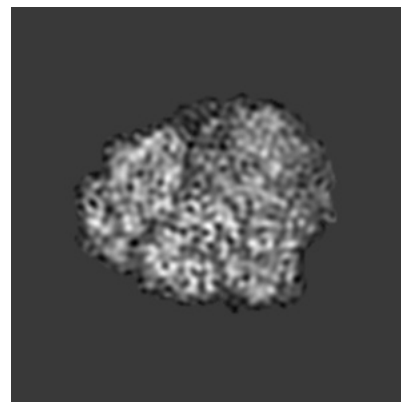
### 6.2.1 Primary map



X Index: 128

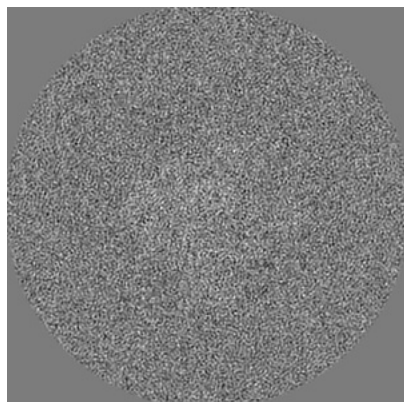


Y Index: 128

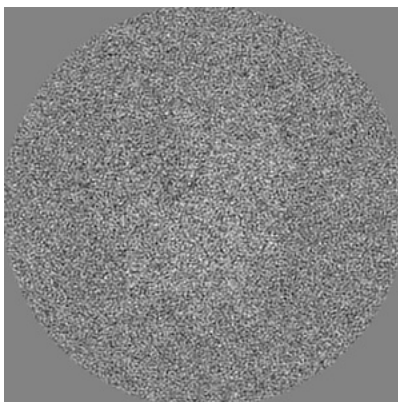


Z Index: 128

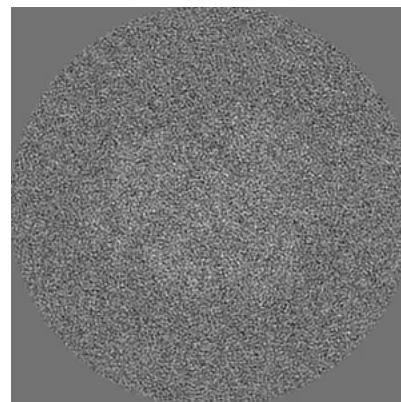
### 6.2.2 Raw map



X Index: 128



Y Index: 128

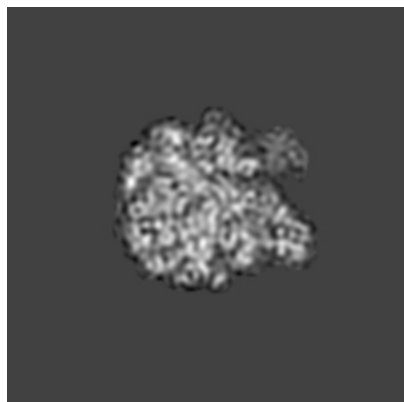


Z Index: 128

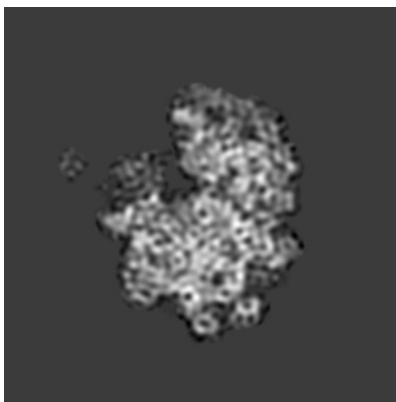
The images above show central slices of the map in three orthogonal directions.

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

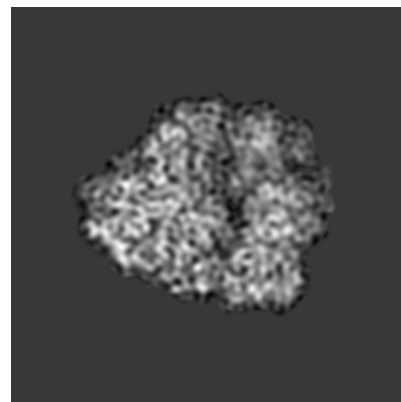
### 6.3.1 Primary map



X Index: 101

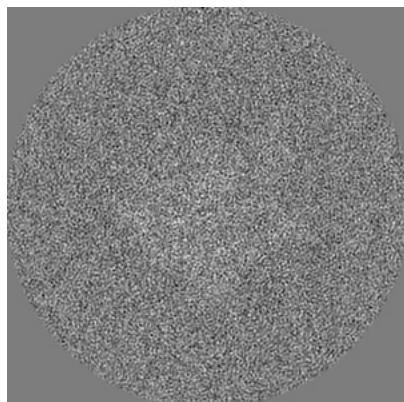


Y Index: 128

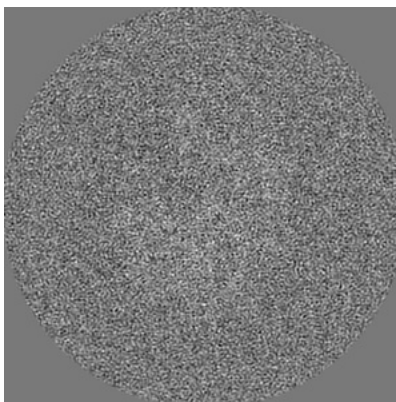


Z Index: 121

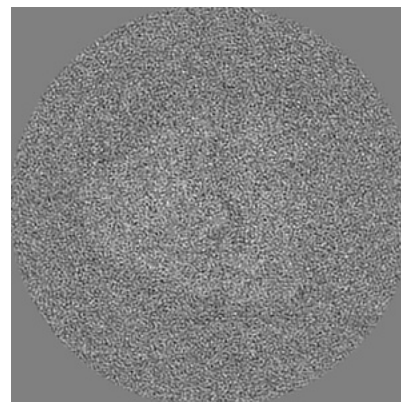
### 6.3.2 Raw map



X Index: 121



Y Index: 130

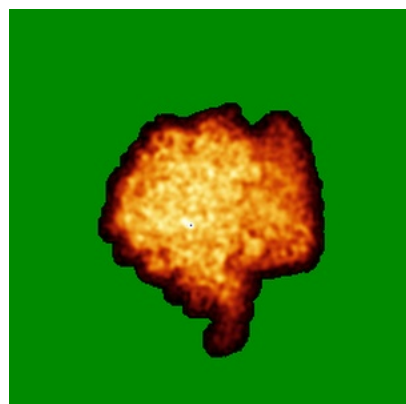


Z Index: 123

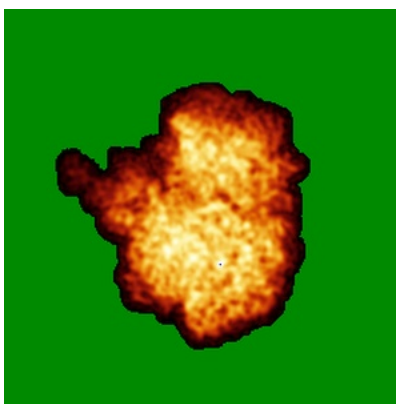
The images above show the largest variance slices of the map in three orthogonal directions.

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

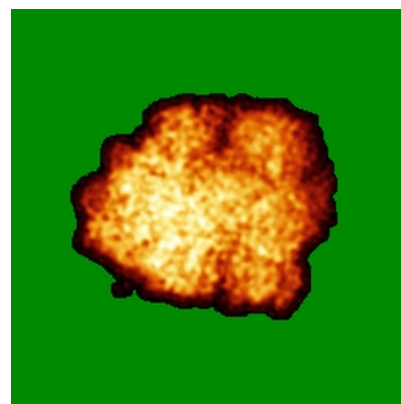
### 6.4.1 Primary map



X

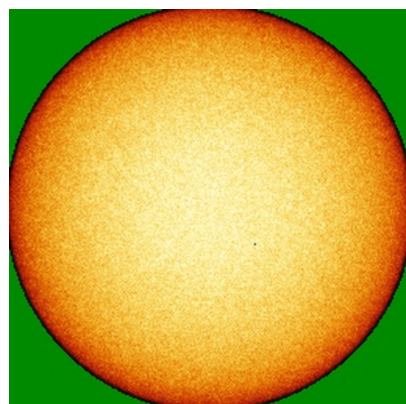


Y

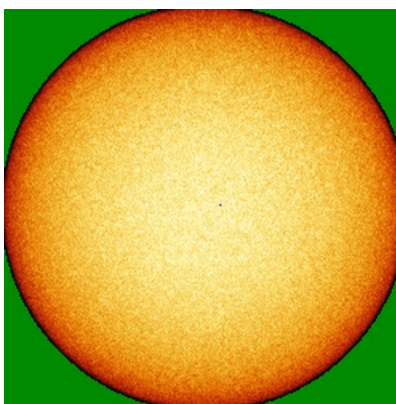


Z

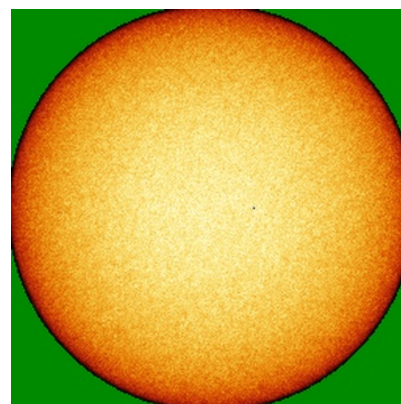
### 6.4.2 Raw map



X



Y

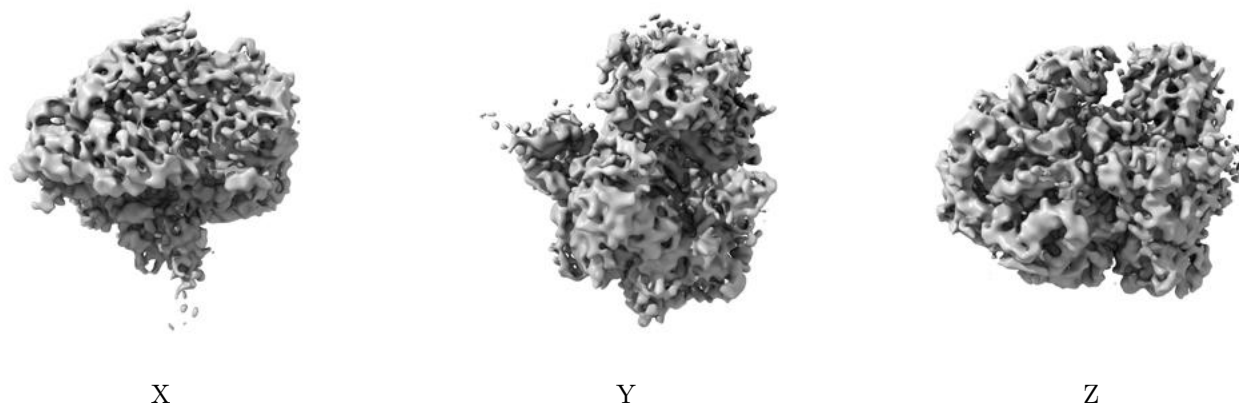


Z

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

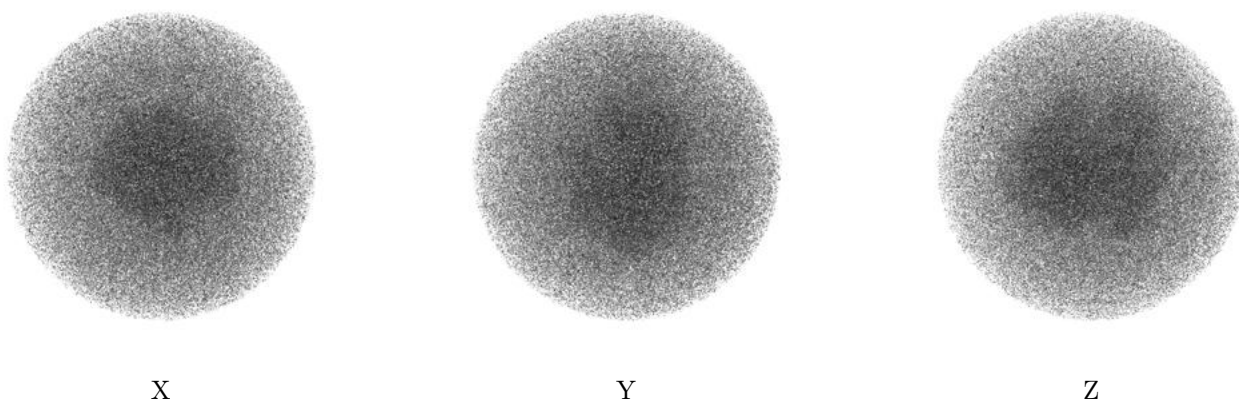
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. 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



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.

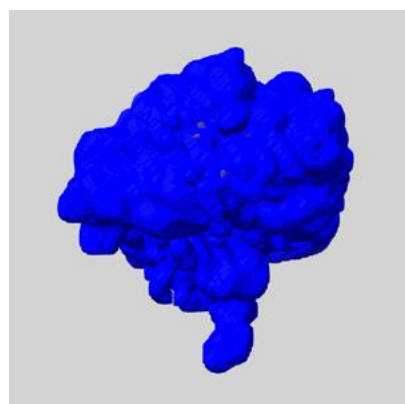
## 6.6 Mask visualisation [i](#)

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

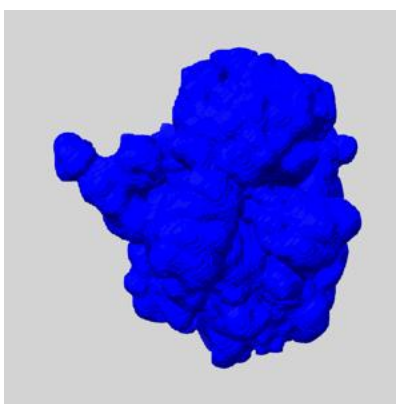
A mask typically either:

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

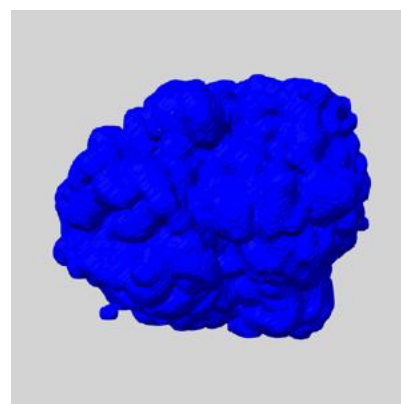
### 6.6.1 emd\_13447\_msk\_1.map [i](#)



X



Y

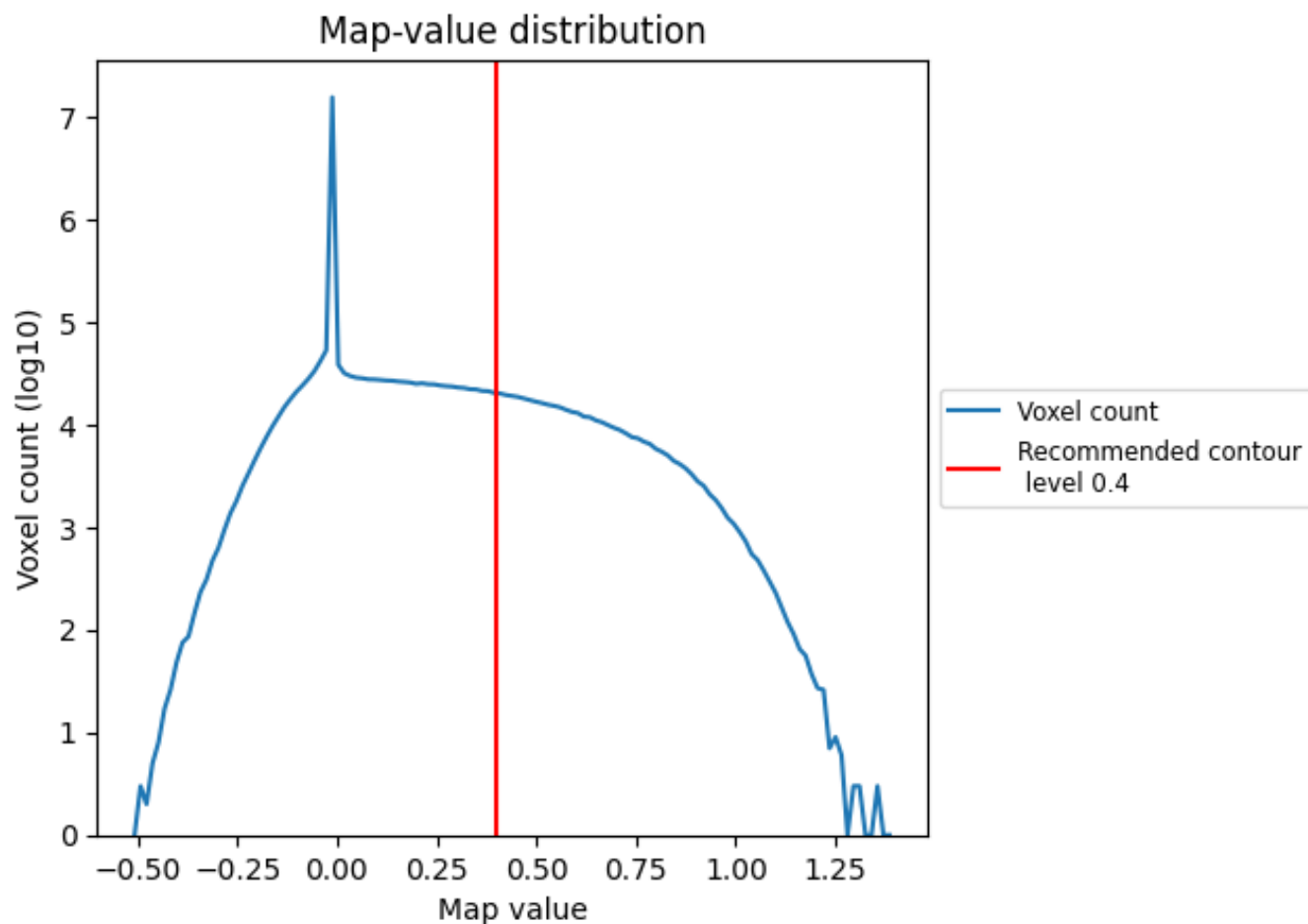


Z

## 7 Map analysis [i](#)

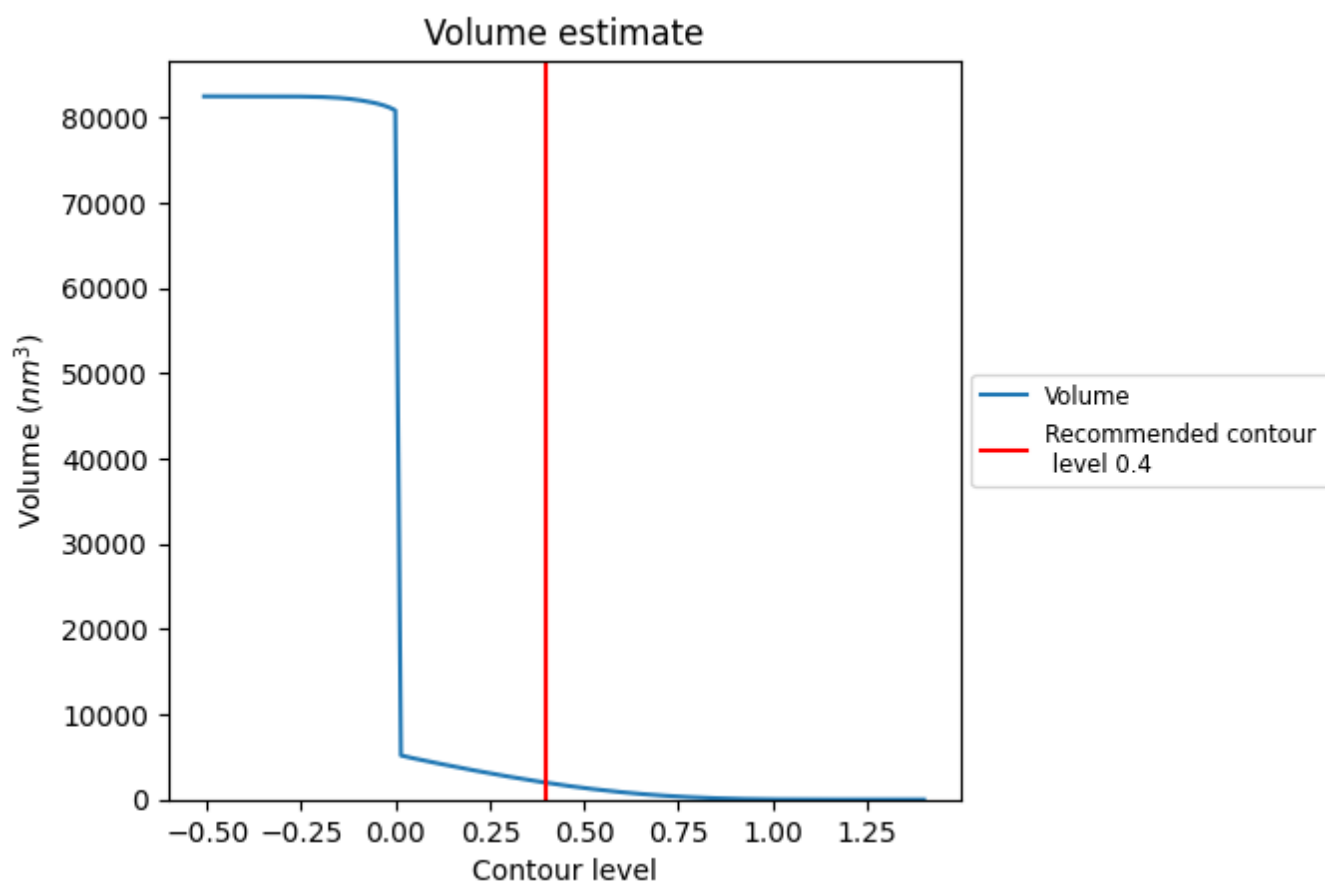
This section contains the results of statistical analysis of the map.

### 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.

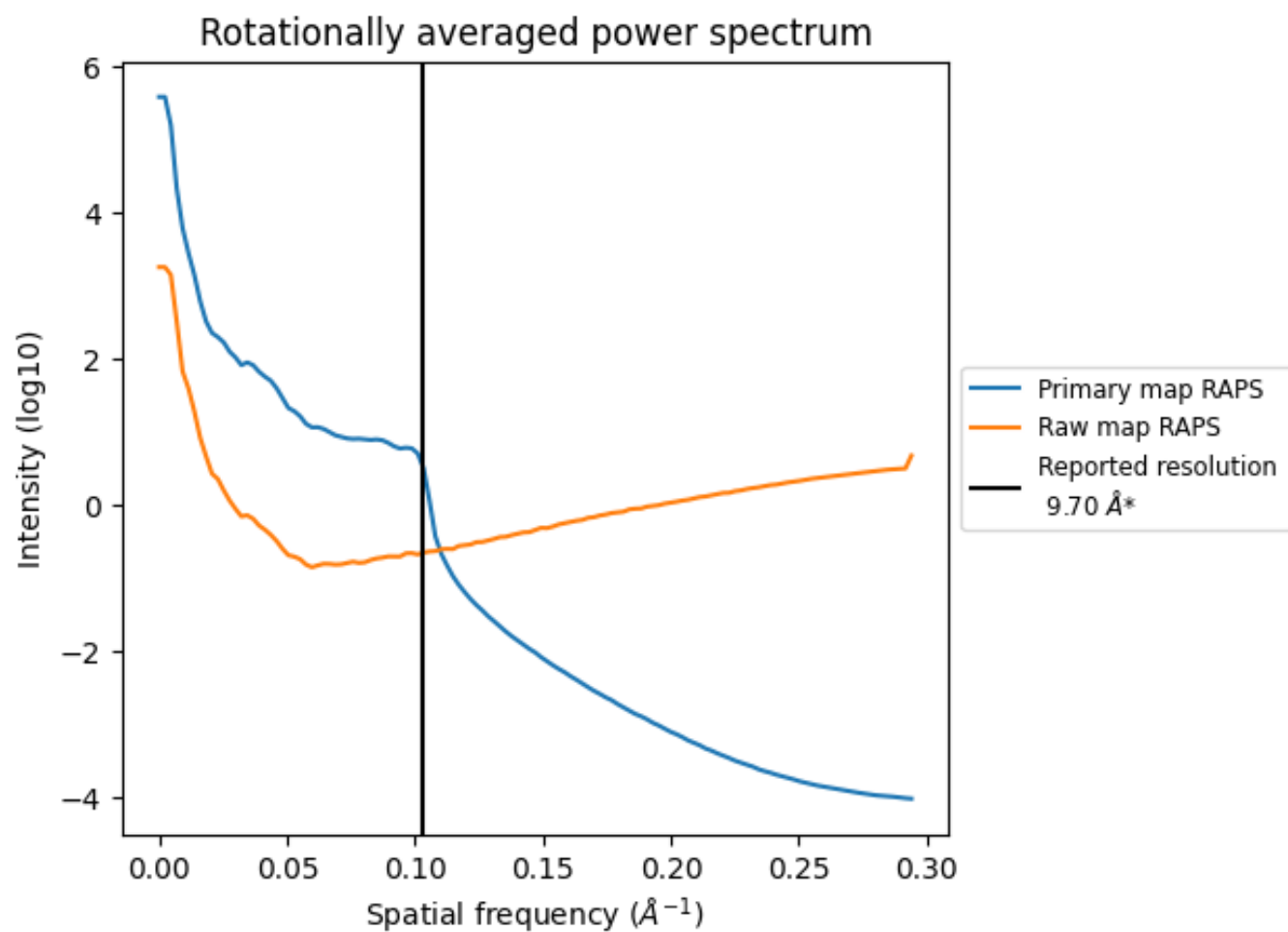
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1975 nm<sup>3</sup>; this corresponds to an approximate mass of 1784 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 ⓘ

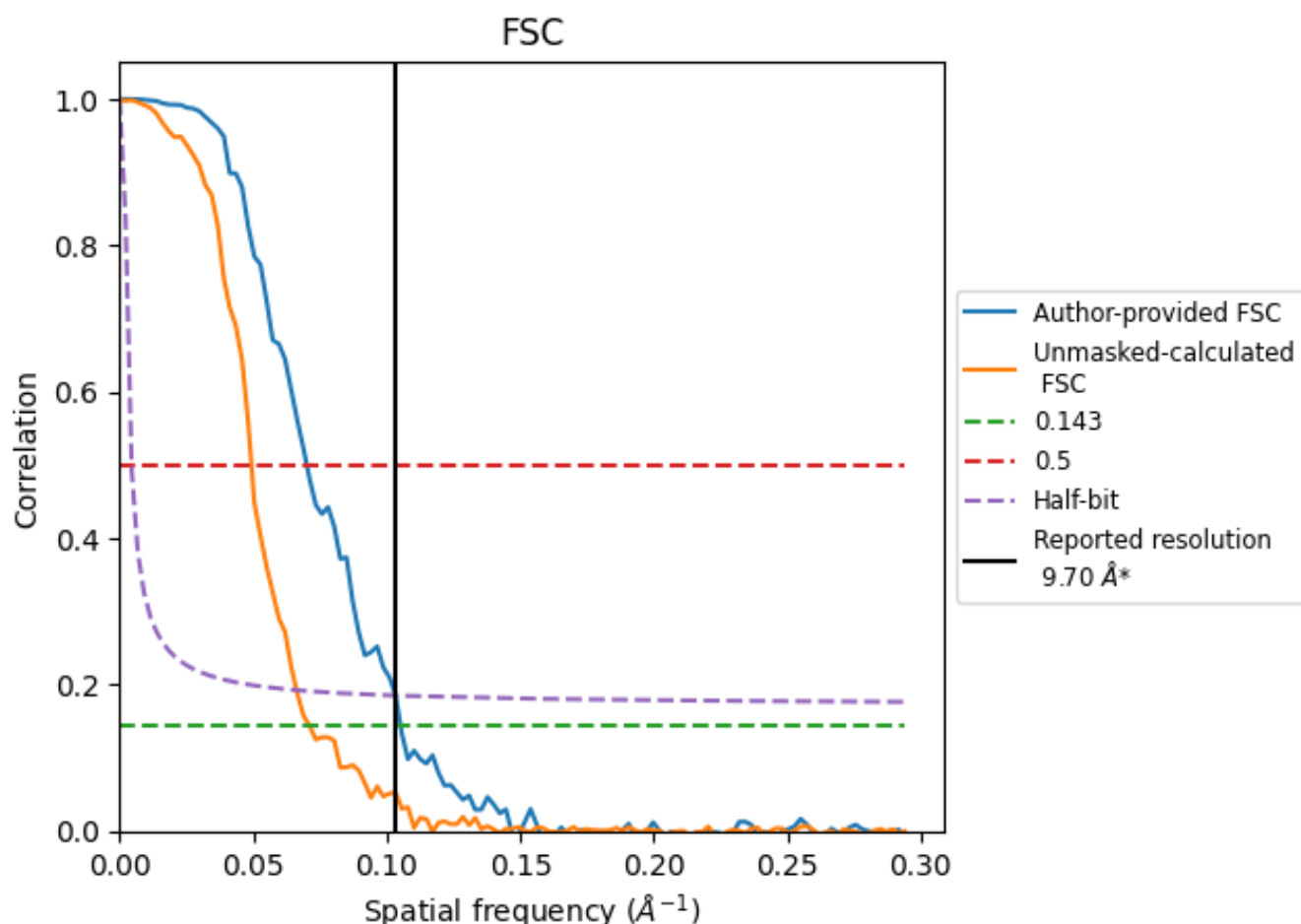


\*Reported resolution corresponds to spatial frequency of 0.103  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



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

## 8.2 Resolution estimates [i](#)

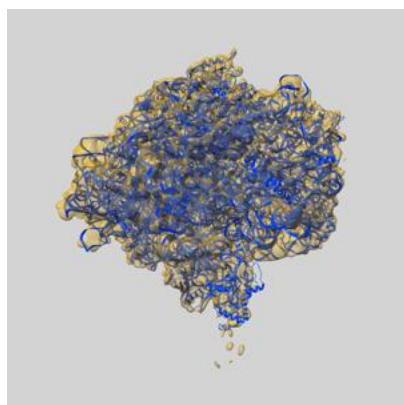
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.70	-	-
Author-provided FSC curve	9.51	14.27	9.67
Unmasked-calculated*	14.04	20.24	15.08

\*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 14.04 differs from the reported value 9.7 by more than 10 %

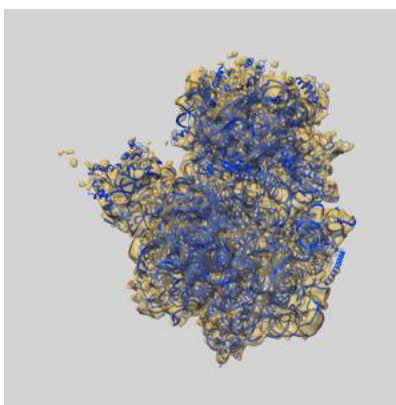
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13447 and PDB model 7PIQ. Per-residue inclusion information can be found in section [3](#) on page [13](#).

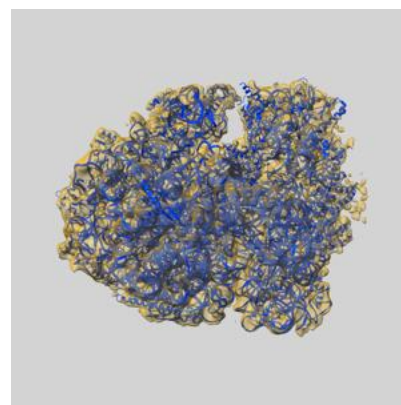
### 9.1 Map-model overlay [i](#)



X



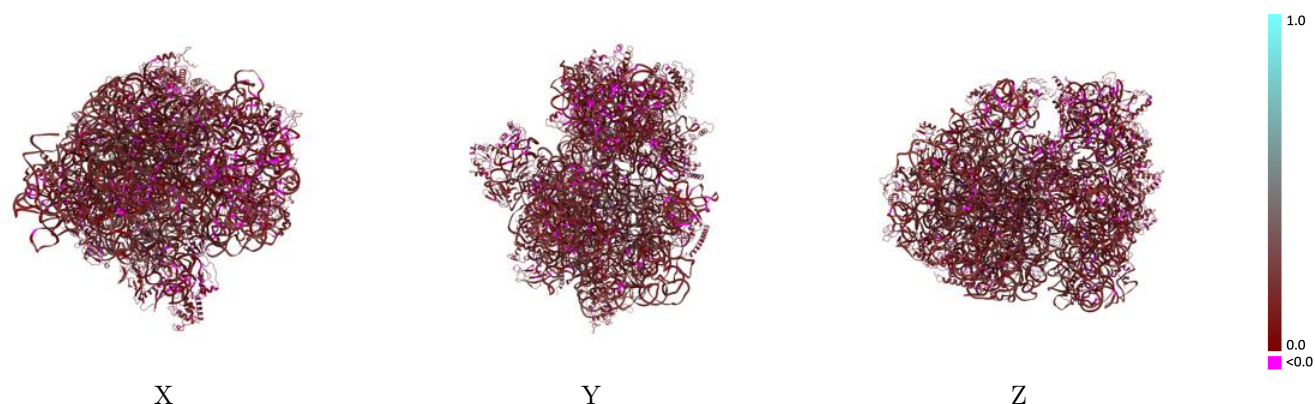
Y



Z

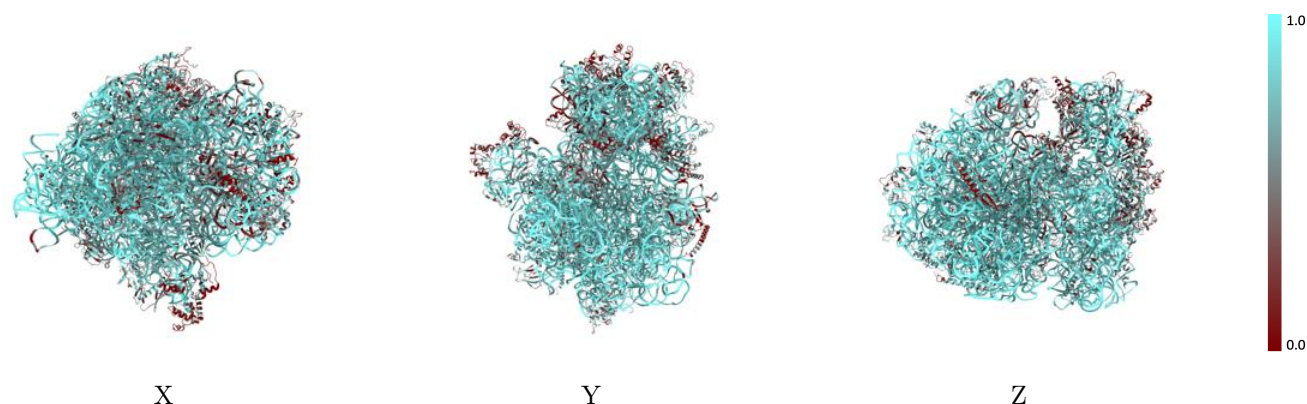
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



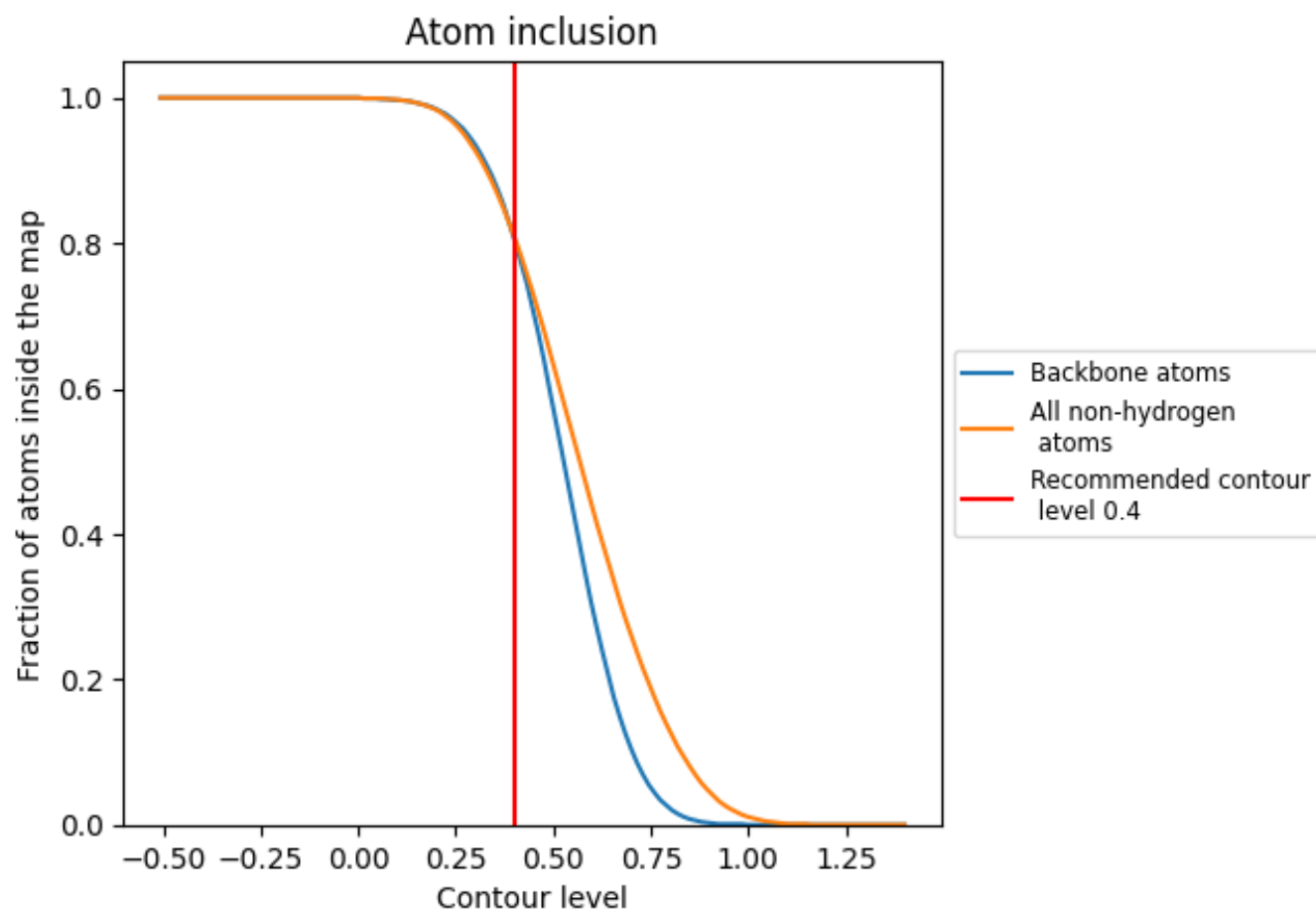
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 81% of all backbone atoms, 81% 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	 0.8090	 0.1480
0	 0.7810	 0.1420
1	 0.7320	 0.1210
2	 0.7160	 0.0980
3	 0.9400	 0.1620
4	 0.9430	 0.1680
5	 0.8970	 0.1510
6	 0.7050	 0.1480
7	 0.5640	 0.0990
A	 0.4780	 0.1600
B	 0.3780	 0.1200
C	 0.5500	 0.1090
D	 0.5000	 0.1210
E	 0.4690	 0.1550
F	 0.3960	 0.1110
G	 0.6030	 0.1150
H	 0.5990	 0.0970
I	 0.4670	 0.1130
J	 0.5350	 0.1120
K	 0.6720	 0.1080
L	 0.3390	 0.1190
M	 0.6610	 0.0600
N	 0.6770	 0.1470
O	 0.7230	 0.1400
P	 0.6270	 0.1240
Q	 0.6510	 0.1280
R	 0.3160	 0.0610
S	 0.7690	 0.1500
T	 0.6000	 0.1780
a	 0.7070	 0.1120
b	 0.6070	 0.1140
c	 0.6410	 0.1390
d	 0.5650	 0.1250
e	 0.5680	 0.1410
f	 0.2250	 0.1420



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Chain	Atom inclusion	Q-score
g	 0.3650	 0.1190
h	 0.2300	 0.0950
i	 0.7070	 0.1370
j	 0.5080	 0.1200
k	 0.7110	 0.1360
l	 0.6810	 0.1260
m	 0.7320	 0.1240
n	 0.6640	 0.1370
o	 0.5680	 0.1440
p	 0.7450	 0.1280
q	 0.6080	 0.1260
r	 0.7730	 0.1540
s	 0.6540	 0.1430
t	 0.5520	 0.1100
u	 0.7470	 0.1130
v	 0.7290	 0.1120
w	 0.6580	 0.1800
x	 0.4780	 0.1610
y	 0.6960	 0.0940
z	 0.7980	 0.1460