



## wwPDB EM Validation Summary Report ⓘ

Oct 28, 2024 – 10:53 pm GMT

PDB ID : 7PIO  
EMDB ID : EMD-13445  
Title : 70S ribosome with P-site tRNA in pseudouridimycin-treated *Mycoplasma pneumoniae* cells  
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.  
Deposited on : 2021-08-23  
Resolution : 9.50 Å (reported)  
Based on initial models : 7OOD, 4V7C, 7OOC

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

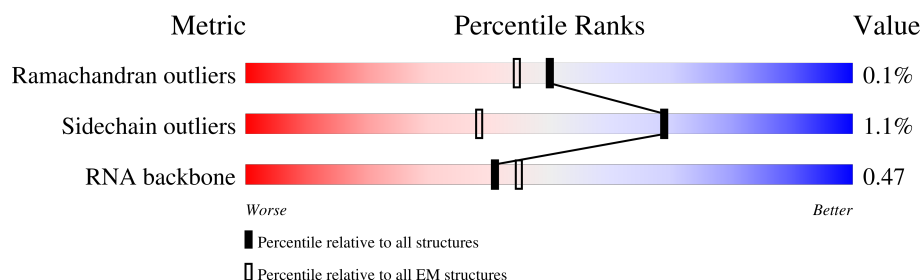
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 9.50 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)
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>8%</div> <div>96%</div> </div>
2	1	59	<div> <div>24%</div> <div>100%</div> </div>
3	2	37	<div> <div>19%</div> <div>97%</div> </div>
4	A	294	<div> <div>30%</div> <div>81%</div> <div>18%</div> </div>
5	B	273	<div> <div>31%</div> <div>78%</div> <div>21%</div> </div>
6	C	205	<div> <div>30%</div> <div>99%</div> </div>
7	D	219	<div> <div>21%</div> <div>68%</div> <div>30%</div> </div>
8	E	215	<div> <div>28%</div> <div>77%</div> <div>22%</div> </div>

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Mol	Chain	Length	Quality of chain
9	F	155	25% 99% ..
10	G	142	29% 98% ..
11	H	132	33% 96% ..
12	I	108	39% 92% 6%
13	J	121	26% 92% .. 6%
14	K	139	27% 97% ..
15	L	124	30% 95% 5%
16	M	61	33% 98% .
17	N	86	21% 95% ..
18	O	94	17% 85% 15%
19	P	85	27% 98% .
20	Q	104	26% 62% 38%
21	R	87	33% 97% .
22	S	87	8% 89% 11%
23	T	60	22% 87% . 12%
24	a	287	13% 99% .
25	b	287	17% 80% 20%
26	c	212	21% 99% .
27	d	180	22% 97% ..
28	e	184	30% 94% ..
29	f	149	77% 97% ..
30	g	161	40% 75% . 22%
31	h	137	68% 93% 7%
32	i	146	14% 97% ..
33	j	122	25% 99% .

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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	7	76	

## 2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 144502 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	126	Total	C	N	O	S	0
			960	612	167	178	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	114	Total	C	N	O	S	0	0
			947	603	188	154	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		

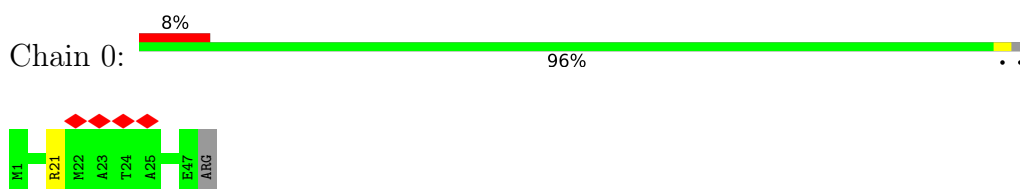
- Molecule 53 is a RNA chain called tRNA-Phe.

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

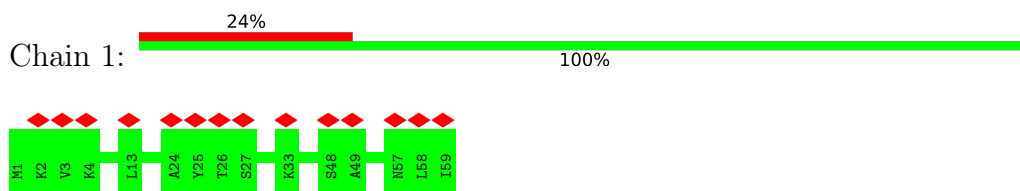
### 3 Residue-property plots [i](#)

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

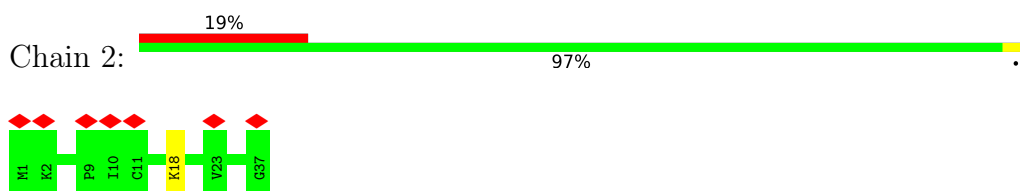
- Molecule 1: 50S ribosomal protein L34



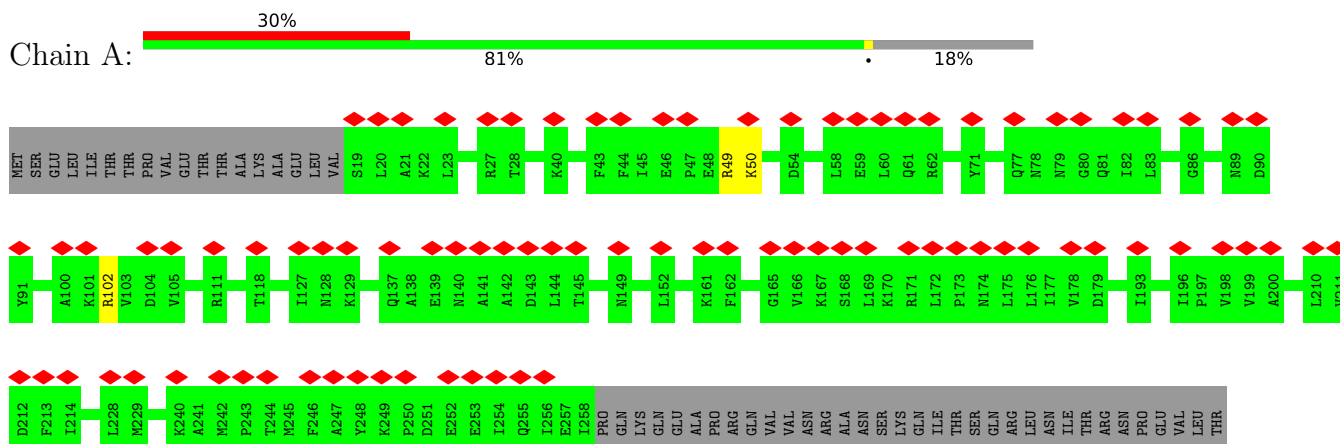
- Molecule 2: 50S ribosomal protein L35



- Molecule 3: 50S ribosomal protein L36

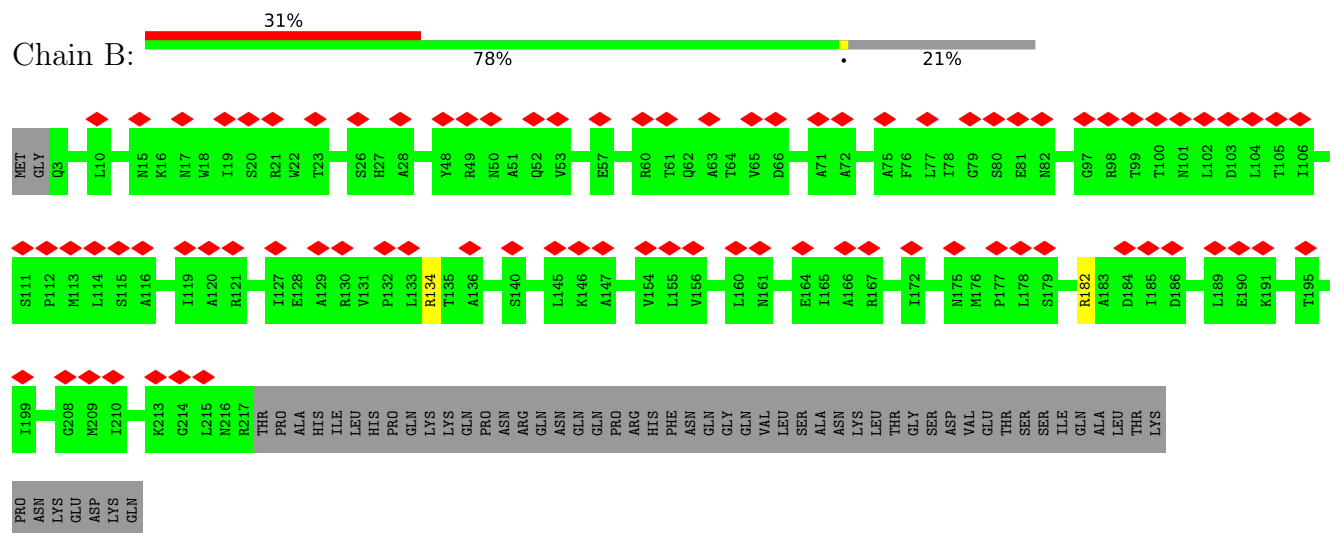


- Molecule 4: 30S ribosomal protein S2

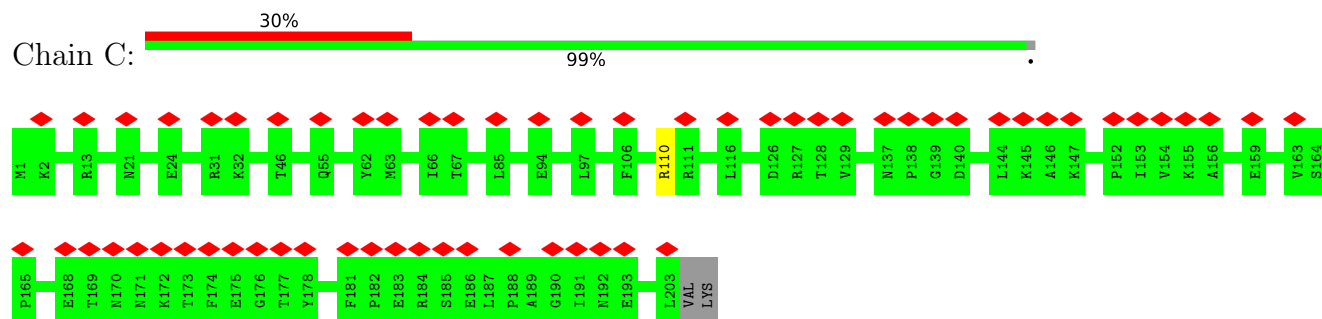


ARG  
GLU

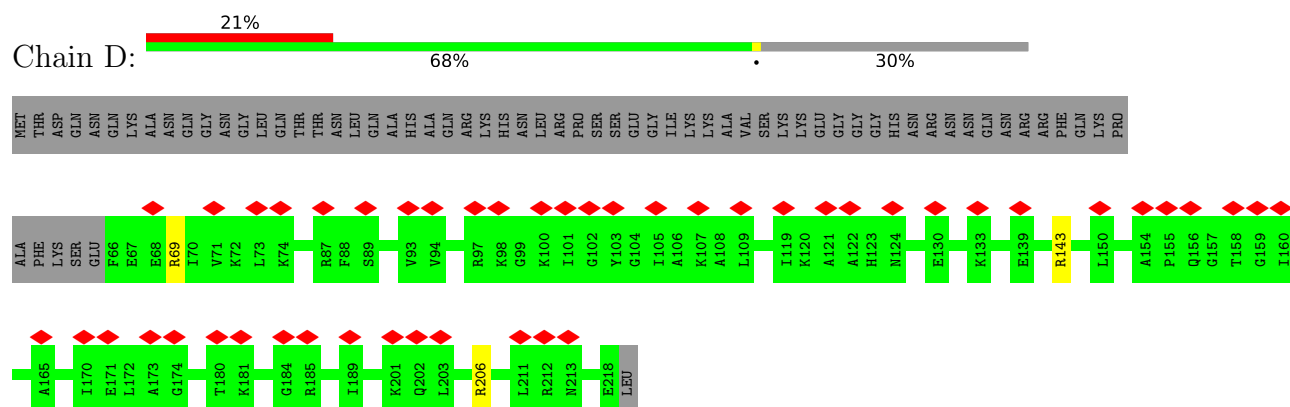
• Molecule 5: 30S ribosomal protein S3



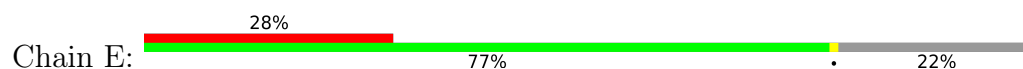
• Molecule 6: 30S ribosomal protein S4

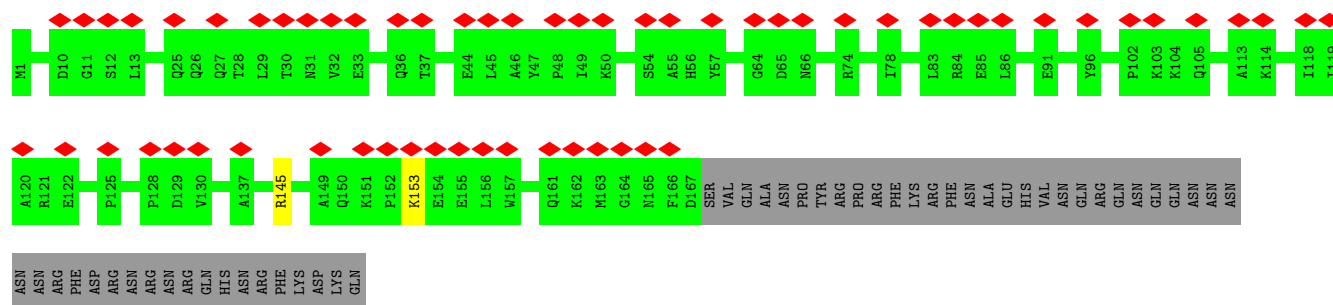


• Molecule 7: 30S ribosomal protein S5

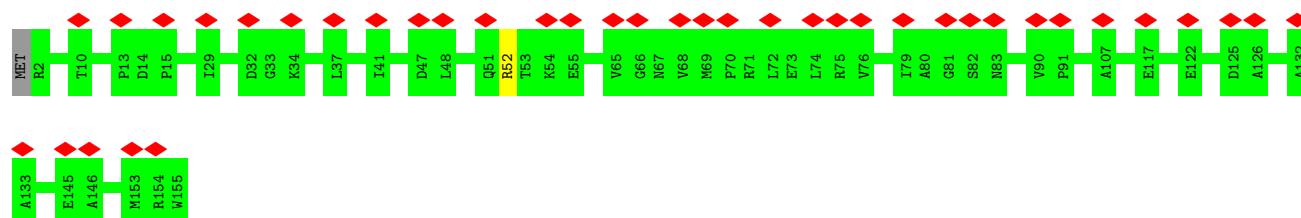


• Molecule 8: 30S ribosomal protein S6

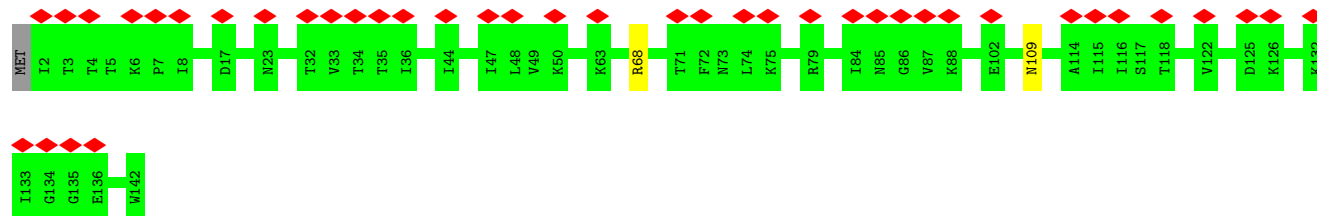




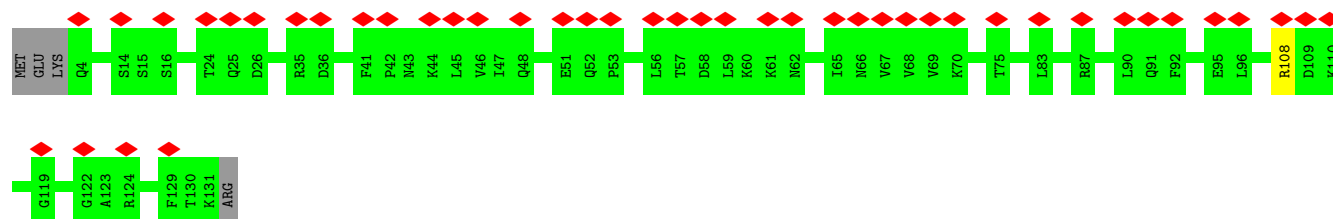
- Molecule 9: 30S ribosomal protein S7



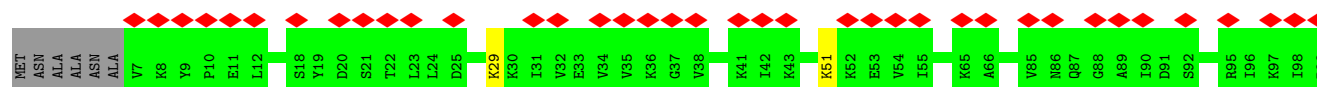
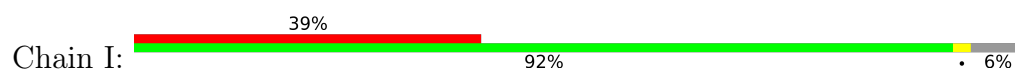
- Molecule 10: 30S ribosomal protein S8

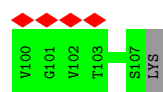


- Molecule 11: 30S ribosomal protein S9

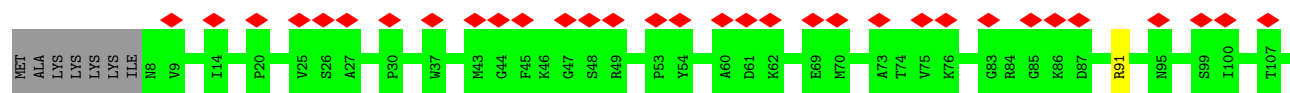
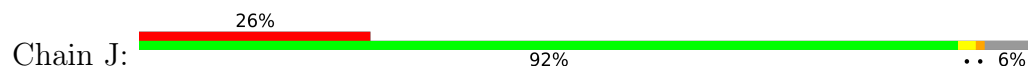


- Molecule 12: 30S ribosomal protein S10

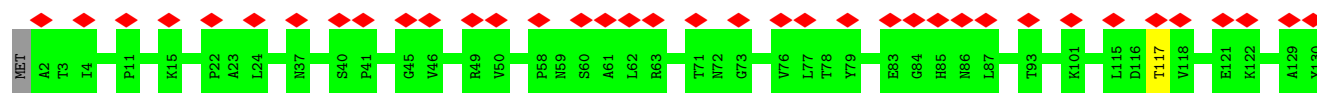




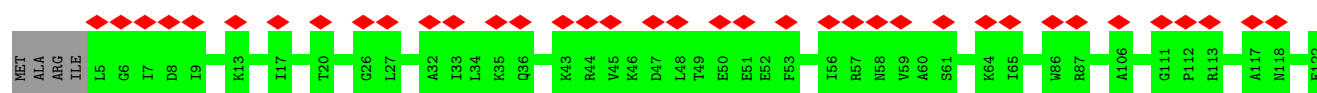
- Molecule 13: 30S ribosomal protein S11



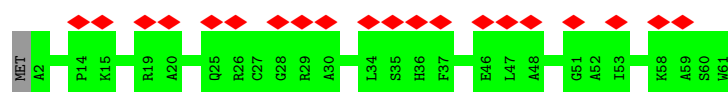
- Molecule 14: 30S ribosomal protein S12



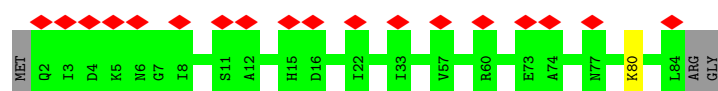
- Molecule 15: 30S ribosomal protein S13



- Molecule 16: 30S ribosomal protein S14 type Z

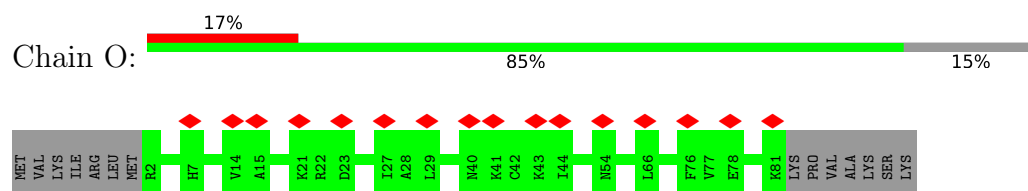


- Molecule 17: 30S ribosomal protein S15

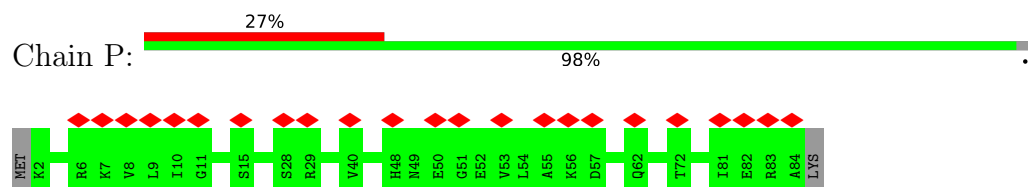




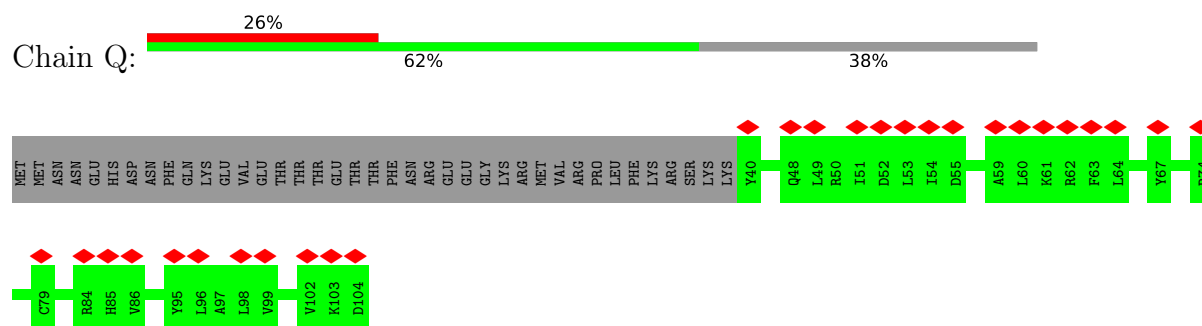
- Molecule 18: 30S ribosomal protein S16



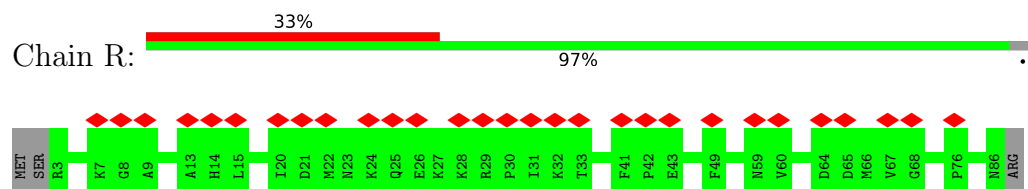
- Molecule 19: 30S ribosomal protein S17



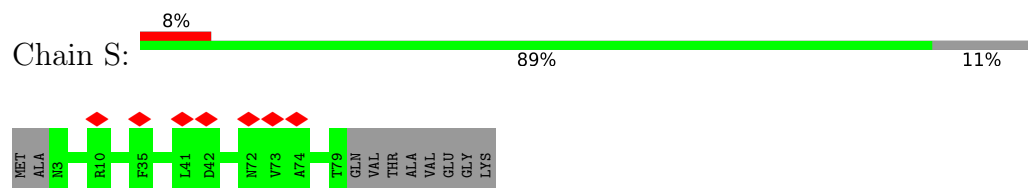
- Molecule 20: 30S ribosomal protein S18



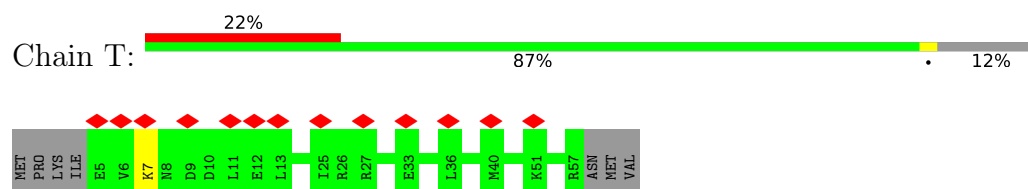
- Molecule 21: 30S ribosomal protein S19



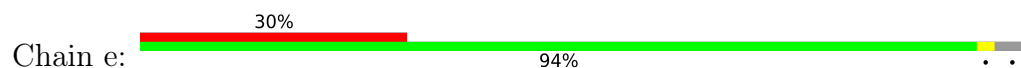
- Molecule 22: 30S ribosomal protein S20

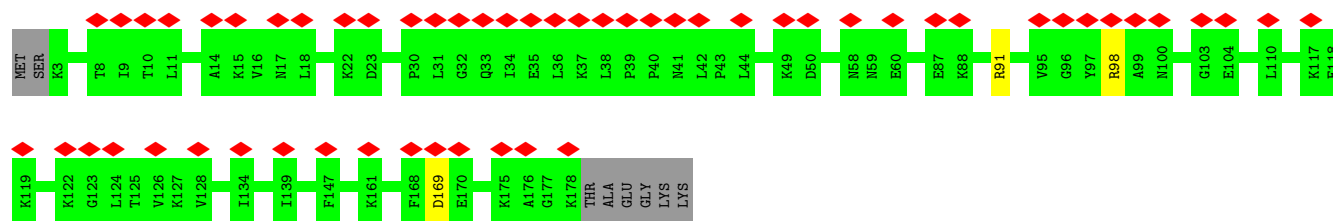


- Molecule 23: 30S ribosomal protein S21



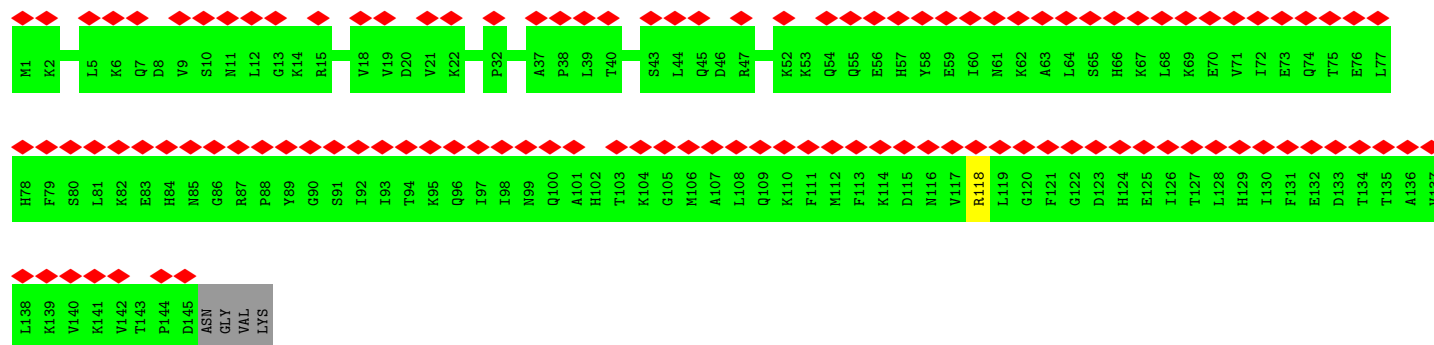
- Molecule 24: 50S ribosomal protein L2





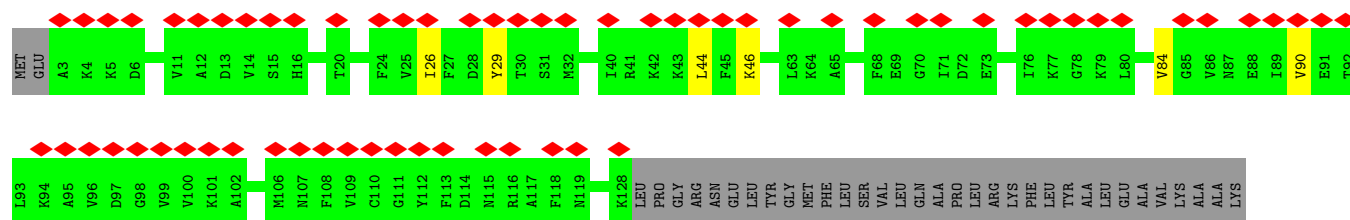
• Molecule 29: 50S ribosomal protein L9

Chain f: 77% 97%



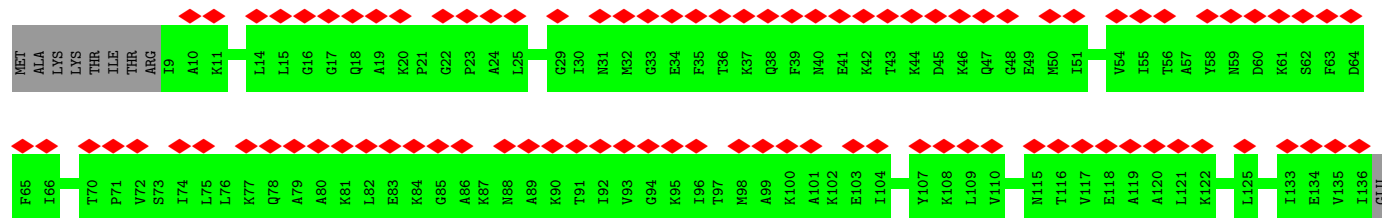
• Molecule 30: 50S ribosomal protein L10

Chain g: 40% 75% 22%



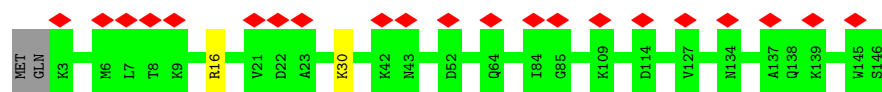
• Molecule 31: 50S ribosomal protein L11

Chain h: 68% 93% 7%

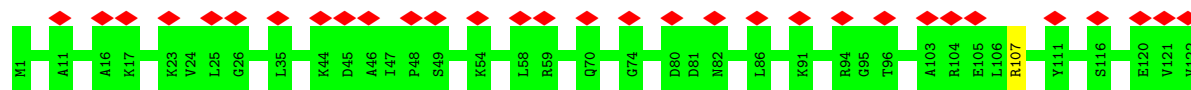


• Molecule 32: 50S ribosomal protein L13

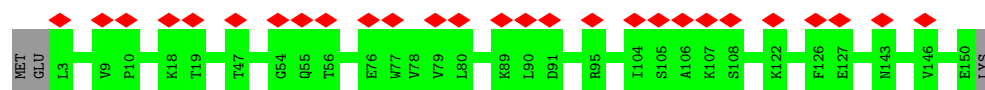
Chain i: 14% 97%



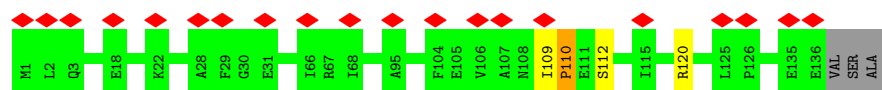
- Molecule 33: 50S ribosomal protein L14



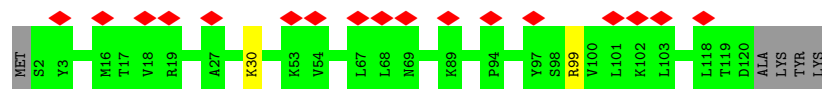
- Molecule 34: 50S ribosomal protein L15



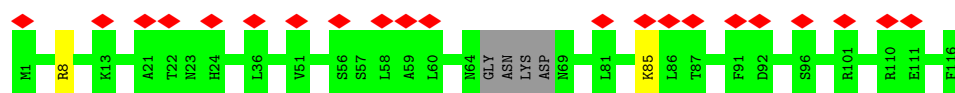
- Molecule 35: 50S ribosomal protein L16



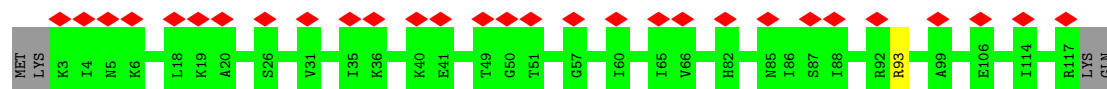
- Molecule 36: 50S ribosomal protein L17



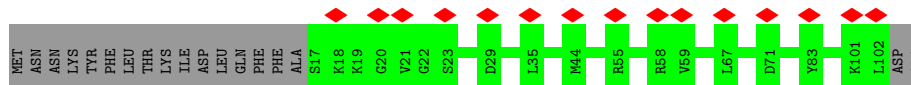
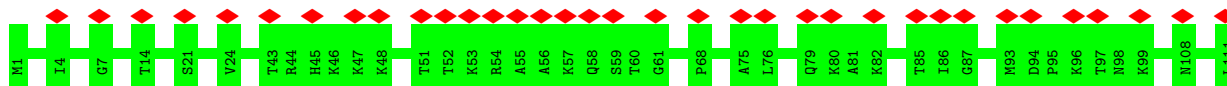
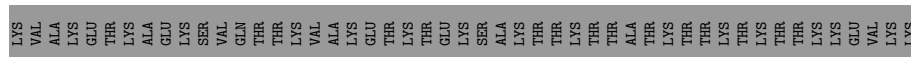
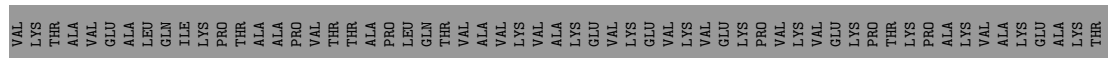
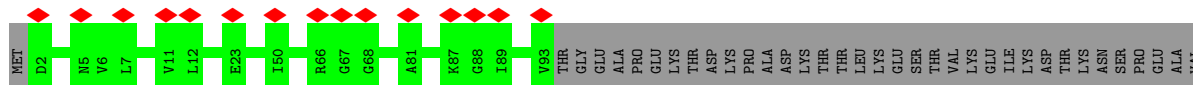
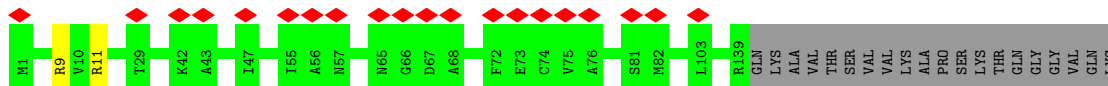
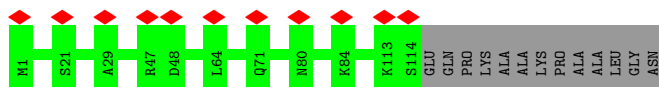
- Molecule 37: 50S ribosomal protein L18



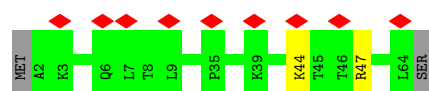
- Molecule 38: 50S ribosomal protein L19



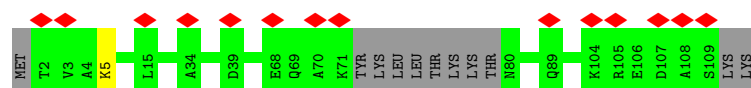
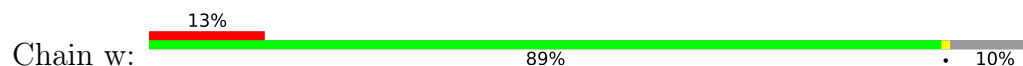
- Molecule 39: 50S ribosomal protein L20



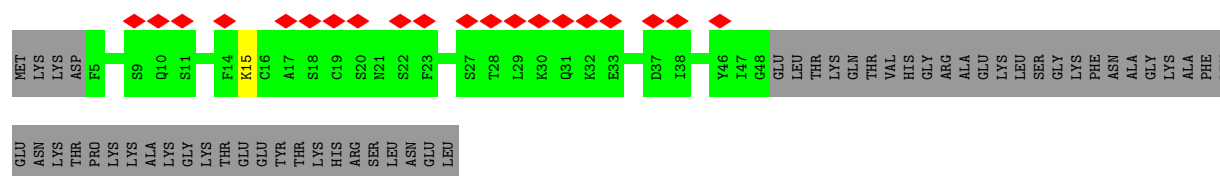
- 



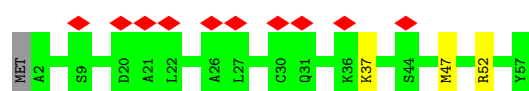
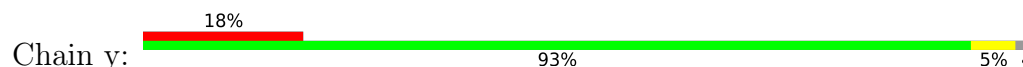
- Molecule 46: 50S ribosomal protein L29



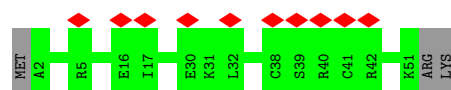
- Molecule 47: 50S ribosomal protein L31



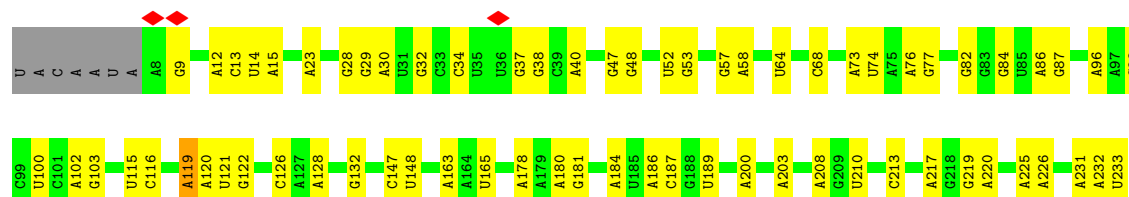
- Molecule 48: 50S ribosomal protein L32



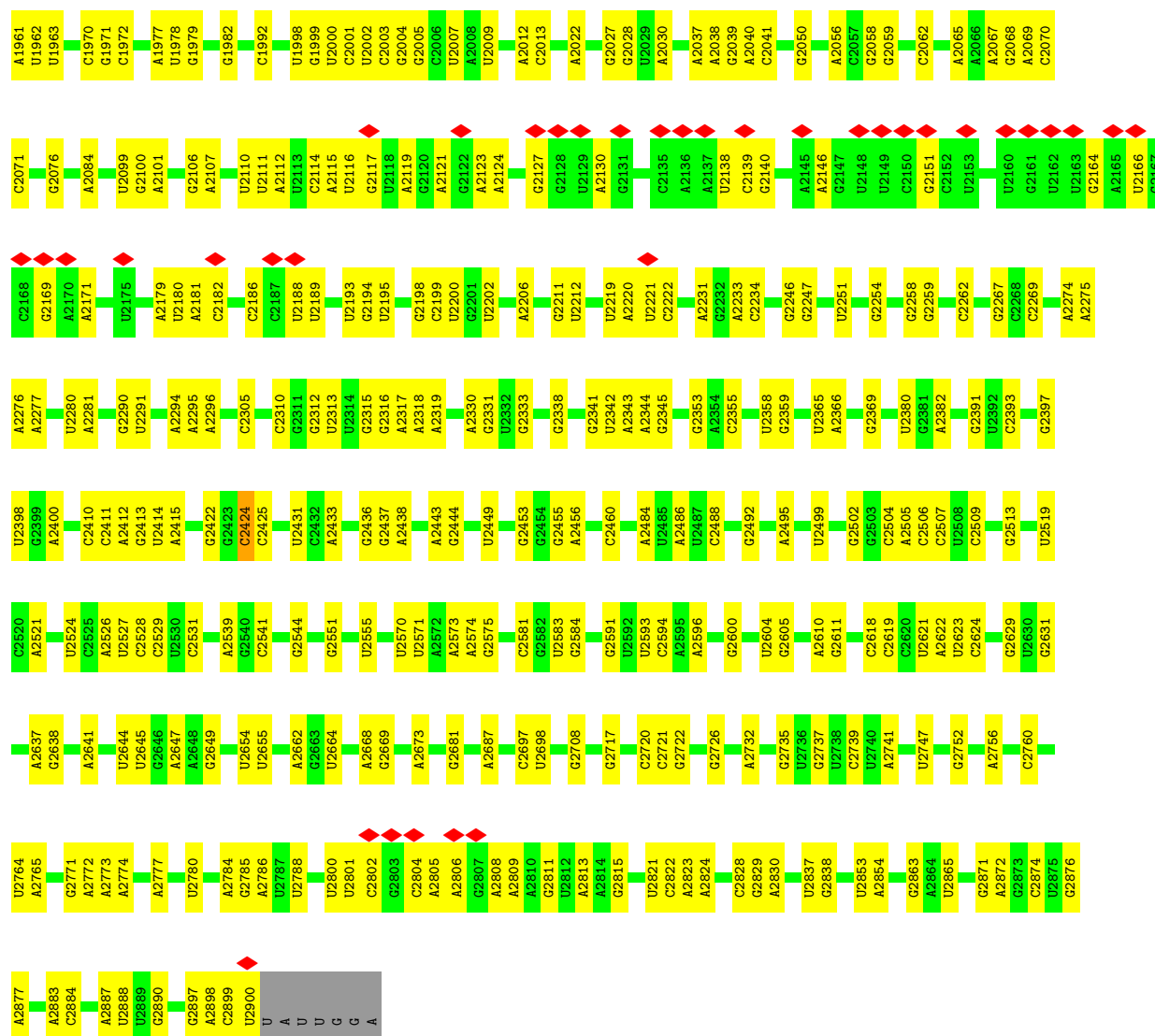
- Molecule 49: 50S ribosomal protein L33 1



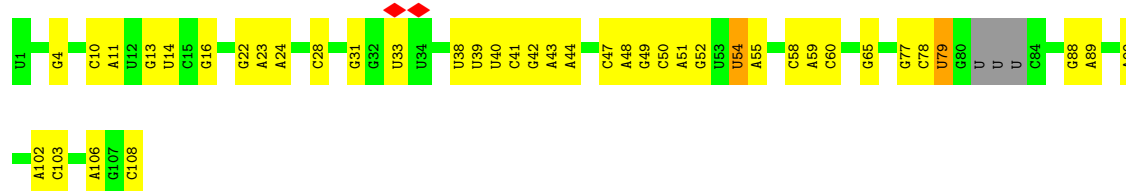
- Molecule 50: 23S ribosomal RNA



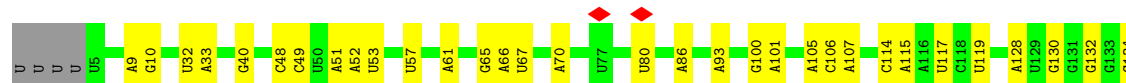
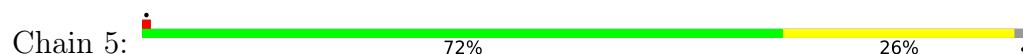
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A237	G482	G596	A720	U862	G982	U1095	A1208	A1323	U1586	A1698	U1820
U245	A483	U599	G721	U863	G987	U1096	U1209	A1324	U1587	A1699	G1821
G246	U484	A805	C722	G873	G990	G1103	U1210	U1328	U1481	G1708	A1822
U247	A485	G606	A734	U987	G994	A1104	U1211	U1329	U1482	G1709	U1823
G252	U835	U607	U737	A881	U994	G1105	U1212	G1338	G1483	U1713	A1836
C265	C393	A608	U738	C882	U995	A1106	U1213	U1339	U1486	U1714	A1715
A269	A396	U609	G739	A883	A996	A1107	U1214	U1340	U1487	A1716	G1842
G270	G398	G610	U744	A884	G997	C1111	U1215	U1341	U1494	G1717	C1843
C273	C399	A492	U752	A885	G998	A1112	G1217	C1342	A1502	U1718	A1846
A276	U403	G494	C752	G994	G1005	U1113	U1234	U1343	U1602	G1719	U1846
A283	G408	C613	G761	U902	U1006	A1119	U1235	U1353	U1612	C1720	C1850
U285	A409	C614	A762	A903	C1007	A1120	G1236	U1354	G1507	U1727	C1850
A286	U411	G615	G763	A904	A1008	A1121	A1243	U1357	G1508	G1733	A1855
G287	A422	G616	A765	U905	A1009	G1122	G1242	U1360	A1515	G1741	G1856
A288	C423	G620	A772	G906	A1010	A1123	A1243	U1368	C1518	G1747	G1863
G293	U425	G625	C775	A907	A1011	U1125	C1247	U1370	A1519	U1748	G1866
C294	U426	U500	C775	A908	G1015	A1130	A1248	A1371	C1523	A1751	U1871
U295	U430	G501	C787	U911	A1019	A1131	A1249	U1380	U1533	C1761	U1872
U296	U431	A502	G788	G914	G1020	C1132	A1250	U1383	A1534	A1762	A1873
G297	U432	A507	A789	A915	C1021	U1140	G1251	A1393	C1536	G1763	G1876
U298	U433	G509	G810	U916	A1026	G1147	G1252	G1405	A1541	U1764	C1877
A299	G434	G510	U819	C919	U1027	U1148	U1266	A1406	G1542	A1766	U1889
A309	U437	G511	U825	C922	A1032	G1149	U1267	U1407	U1546	G1767	A1890
U310	A437	G512	U826	A	A1033	U1150	U1268	G1408	U1549	G1768	A1891
G314	U441	G513	A817	C	A1034	U1151	U1268	U1420	G1550	A1770	A1892
A315	G442	G514	U818	U	U1035	U1154	U1277	A1421	G1553	C1771	A1896
G319	C443	G515	U819	G928	C1041	U1162	G1278	U1422	A1559	G1778	C1899
G325	C444	G516	U820	A	A1045	A1165	U1279	U1424	U	A1780	G1906
G329	C445	G517	A828	G928	A1046	G1166	G1280	A1431	G	U1783	A1907
C336	G456	G518	U829	U932	A1047	U1167	A1281	A1435	A	U1784	A1908
A345	A466	G519	U835	A933	A1048	A1168	A1282	U1440	U	U1785	G1913
G351	C461	G520	U836	U934	A1052	A1169	A1283	U1444	G	U1786	A1920
A356	C462	G521	A837	U935	A1055	C1170	U1285	G1445	U	A1787	C1921
G363	G467	G522	U840	G936	A1056	G1174	G1286	A1447	C	C1789	U1934
A364	A468	G523	C841	A942	A1061	U1175	A1292	U1448	A	U1791	A1937
U365	A471	G524	U842	A943	A1080	U1176	G1301	C1456	U1570	A1792	U1938
A366	A472	G525	C847	U944	A1081	A1177	U1302	U1464	G1571	A1793	A1945
G369	U473	G526	U851	U945	A1082	U1178	U1303	U1465	A	C1794	G1952
	U474	G527		U946	A1089	G1179	A1314	U1466	U1577	U1807	U1953
	A475	G528		U947	U1093	A1186	C1319	U1467		C1808	
		G529		A948		A1187				A1809	
		G530		C949		A1188				A1810	
		G531		U952		U1191					
		G532		G953		U1192					
		G533		U954		U1193					
		G534		U955		U1194					
		G535		U956		A1195					
		G536		U957							
		G537		U958							
		G538		U959							
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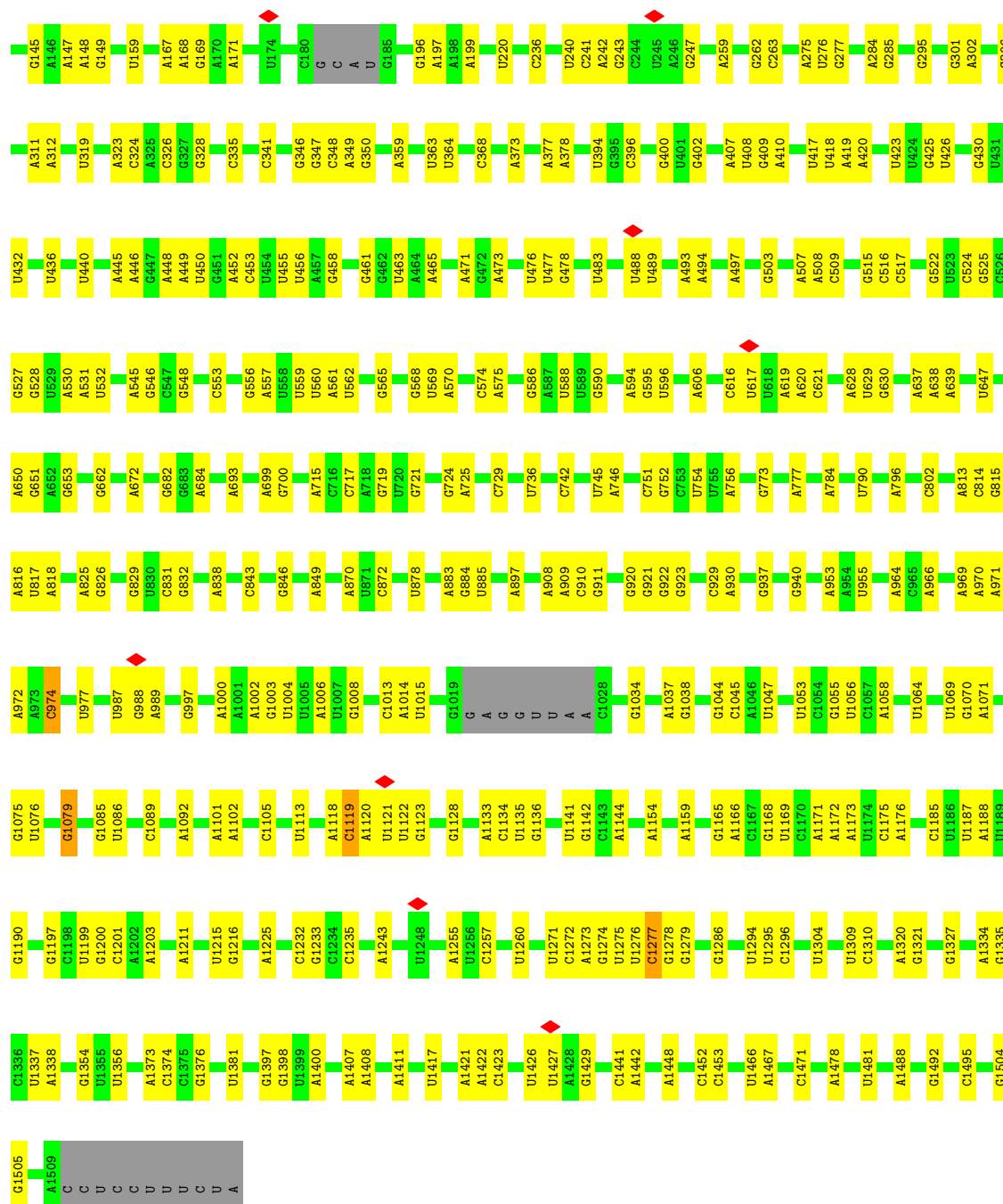
• Molecule 51: 5S ribosomal RNA



• Molecule 52: 16S ribosomal RNA

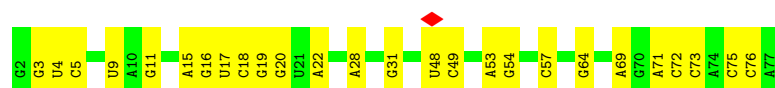






• Molecule 53: tRNA-Phe

Chain 7: 66% 34%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	1457	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	1.466	Depositor
Minimum map value	-0.600	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.108	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	0.27	0/383	0.56	0/504
2	1	0.27	0/484	0.49	0/637
3	2	0.22	0/306	0.46	0/401
4	A	0.26	0/1954	0.51	0/2642
5	B	0.25	0/1721	0.49	0/2323
6	C	0.25	0/1691	0.44	0/2267
7	D	0.26	0/1188	0.51	0/1593
8	E	0.24	0/1384	0.47	0/1867
9	F	0.28	0/1266	0.58	0/1700
10	G	0.26	0/1126	0.50	0/1517
11	H	0.24	0/1044	0.49	0/1395
12	I	0.24	0/820	0.52	0/1103
13	J	0.30	0/844	0.60	1/1136 (0.1%)
14	K	0.29	0/1094	0.53	0/1468
15	L	0.27	0/962	0.51	0/1289
16	M	0.25	0/483	0.45	0/643
17	N	0.23	0/679	0.45	0/907
18	O	0.25	0/659	0.52	0/885
19	P	0.23	0/684	0.46	0/913
20	Q	0.23	0/545	0.48	0/730
21	R	0.25	0/698	0.47	0/936
22	S	0.22	0/631	0.39	0/838
23	T	0.24	0/475	0.47	0/621
24	a	0.24	0/2267	0.48	0/3044
25	b	0.25	0/1795	0.50	0/2412
26	c	0.25	0/1671	0.48	0/2246
27	d	0.27	0/1409	0.51	0/1894
28	e	0.26	0/1420	0.52	0/1912
29	f	0.24	0/1183	0.49	0/1587
30	g	0.35	0/969	0.53	0/1295
31	h	0.25	0/968	0.50	0/1298
32	i	0.25	0/1186	0.46	0/1592
33	j	0.24	0/953	0.50	0/1275
34	k	0.24	0/1170	0.46	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	l	0.30	0/1104	0.54	1/1481 (0.1%)
36	m	0.24	0/973	0.46	0/1309
37	n	0.26	0/897	0.47	0/1198
38	o	0.24	0/948	0.49	0/1262
39	p	0.24	0/961	0.44	0/1278
40	q	0.24	0/828	0.51	0/1111
41	r	0.25	0/1077	0.46	0/1441
42	s	0.24	0/732	0.47	0/988
43	t	0.26	0/879	0.52	0/1165
44	u	0.25	0/665	0.49	0/884
45	v	0.24	0/519	0.53	0/695
46	w	0.24	0/826	0.44	0/1104
47	x	0.26	0/353	0.43	0/474
48	y	0.31	0/457	0.53	0/601
49	z	0.22	0/412	0.44	0/547
50	3	0.20	0/69073	0.80	40/107710 (0.0%)
51	4	0.20	0/2505	0.80	2/3902 (0.1%)
52	5	0.19	0/35768	0.79	22/55764 (0.0%)
53	7	0.19	0/1808	0.83	2/2817 (0.1%)
All	All	0.22	0/156897	0.73	68/234160 (0.0%)

There are no bond length outliers.

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	5	751	C	C2-N1-C1'	9.21	128.93	118.80
52	5	1453	C	N3-C2-O2	-9.13	115.51	121.90
52	5	974	C	N1-C2-O2	9.02	124.31	118.90
52	5	974	C	C2-N1-C1'	8.51	128.16	118.80
50	3	462	C	N3-C2-O2	-8.44	115.99	121.90

There are no chirality outliers.

There are no planarity outliers.

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

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

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	42 (93%)	3 (7%)	0	100	100
2	1	57/59 (97%)	49 (86%)	8 (14%)	0	100	100
3	2	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
4	A	238/294 (81%)	209 (88%)	29 (12%)	0	100	100
5	B	213/273 (78%)	201 (94%)	12 (6%)	0	100	100
6	C	201/205 (98%)	193 (96%)	8 (4%)	0	100	100
7	D	151/219 (69%)	143 (95%)	8 (5%)	0	100	100
8	E	165/215 (77%)	148 (90%)	17 (10%)	0	100	100
9	F	152/155 (98%)	138 (91%)	14 (9%)	0	100	100
10	G	139/142 (98%)	128 (92%)	11 (8%)	0	100	100
11	H	126/132 (96%)	120 (95%)	6 (5%)	0	100	100
12	I	99/108 (92%)	91 (92%)	8 (8%)	0	100	100
13	J	112/121 (93%)	106 (95%)	5 (4%)	1 (1%)	14	52
14	K	134/139 (96%)	116 (87%)	18 (13%)	0	100	100
15	L	116/124 (94%)	107 (92%)	9 (8%)	0	100	100
16	M	58/61 (95%)	58 (100%)	0	0	100	100
17	N	81/86 (94%)	79 (98%)	2 (2%)	0	100	100
18	O	78/94 (83%)	70 (90%)	8 (10%)	0	100	100
19	P	81/85 (95%)	78 (96%)	3 (4%)	0	100	100
20	Q	63/104 (61%)	56 (89%)	7 (11%)	0	100	100
21	R	82/87 (94%)	70 (85%)	12 (15%)	0	100	100
22	S	75/87 (86%)	74 (99%)	1 (1%)	0	100	100
23	T	51/60 (85%)	48 (94%)	3 (6%)	0	100	100
24	a	283/287 (99%)	263 (93%)	20 (7%)	0	100	100
25	b	227/287 (79%)	213 (94%)	14 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	c	208/212 (98%)	192 (92%)	16 (8%)	0	100	100
27	d	173/180 (96%)	158 (91%)	15 (9%)	0	100	100
28	e	174/184 (95%)	159 (91%)	14 (8%)	1 (1%)	22	60
29	f	143/149 (96%)	128 (90%)	15 (10%)	0	100	100
30	g	124/161 (77%)	111 (90%)	13 (10%)	0	100	100
31	h	126/137 (92%)	107 (85%)	19 (15%)	0	100	100
32	i	142/146 (97%)	133 (94%)	9 (6%)	0	100	100
33	j	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
34	k	146/151 (97%)	136 (93%)	10 (7%)	0	100	100
35	l	134/139 (96%)	125 (93%)	6 (4%)	3 (2%)	5	29
36	m	117/124 (94%)	108 (92%)	9 (8%)	0	100	100
37	n	108/116 (93%)	101 (94%)	7 (6%)	0	100	100
38	o	113/119 (95%)	109 (96%)	4 (4%)	0	100	100
39	p	112/127 (88%)	110 (98%)	2 (2%)	0	100	100
40	q	97/100 (97%)	87 (90%)	10 (10%)	0	100	100
41	r	137/159 (86%)	130 (95%)	7 (5%)	0	100	100
42	s	90/237 (38%)	85 (94%)	5 (6%)	0	100	100
43	t	109/111 (98%)	103 (94%)	6 (6%)	0	100	100
44	u	84/104 (81%)	80 (95%)	4 (5%)	0	100	100
45	v	61/65 (94%)	57 (93%)	4 (7%)	0	100	100
46	w	96/111 (86%)	87 (91%)	9 (9%)	0	100	100
47	x	42/97 (43%)	36 (86%)	6 (14%)	0	100	100
48	y	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
49	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	5820/6670 (87%)	5390 (93%)	425 (7%)	5 (0%)	50	83

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
35	l	109	ILE
35	l	112	SER
28	e	169	ASP
35	l	110	PRO
13	J	113	GLY

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	40/41 (98%)	39 (98%)	1 (2%)	42	61
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	34 (97%)	1 (3%)	37	56
4	A	212/262 (81%)	209 (99%)	3 (1%)	62	75
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%)	120 (98%)	3 (2%)	44	62
8	E	150/196 (76%)	148 (99%)	2 (1%)	65	77
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%)	93 (98%)	2 (2%)	48	66
13	J	91/97 (94%)	89 (98%)	2 (2%)	47	65
14	K	117/120 (98%)	116 (99%)	1 (1%)	75	83
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%)	75 (99%)	1 (1%)	65	77
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
22	S	70/77 (91%)	70 (100%)	0	100	100
23	T	49/56 (88%)	48 (98%)	1 (2%)	50	68
24	a	241/243 (99%)	240 (100%)	1 (0%)	89	91
25	b	186/233 (80%)	186 (100%)	0	100	100
26	c	182/184 (99%)	181 (100%)	1 (0%)	86	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	d	150/154 (97%)	149 (99%)	1 (1%)	81	87
28	e	153/159 (96%)	151 (99%)	2 (1%)	65	77
29	f	123/134 (92%)	122 (99%)	1 (1%)	79	85
30	g	101/129 (78%)	95 (94%)	6 (6%)	16	37
31	h	102/110 (93%)	102 (100%)	0	100	100
32	i	126/128 (98%)	124 (98%)	2 (2%)	58	73
33	j	103/103 (100%)	102 (99%)	1 (1%)	73	82
34	k	123/126 (98%)	123 (100%)	0	100	100
35	l	113/115 (98%)	112 (99%)	1 (1%)	75	83
36	m	105/109 (96%)	103 (98%)	2 (2%)	52	69
37	n	96/99 (97%)	94 (98%)	2 (2%)	48	66
38	o	101/105 (96%)	100 (99%)	1 (1%)	73	82
39	p	100/108 (93%)	100 (100%)	0	100	100
40	q	90/91 (99%)	90 (100%)	0	100	100
41	r	116/132 (88%)	114 (98%)	2 (2%)	56	72
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%)	56 (97%)	2 (3%)	32	51
46	w	87/98 (89%)	86 (99%)	1 (1%)	70	80
47	x	41/86 (48%)	40 (98%)	1 (2%)	44	62
48	y	48/49 (98%)	45 (94%)	3 (6%)	15	36
49	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5093/5751 (89%)	5039 (99%)	54 (1%)	69	80

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

Mol	Chain	Res	Type
28	e	98	ARG
30	g	90	VAL
46	w	5	LYS
29	f	118	ARG
30	g	44	LEU



Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
26	c	167	ASN
35	l	3	GLN
41	r	22	GLN
29	f	78	HIS
36	m	5	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	849 (29%)	38 (1%)
51	4	103/108 (95%)	39 (37%)	5 (4%)
52	5	1490/1520 (98%)	385 (25%)	2 (0%)
53	7	75/76 (98%)	24 (32%)	1 (1%)
All	All	4543/4611 (98%)	1297 (28%)	46 (1%)

5 of 1297 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	9	G
50	3	12	A
50	3	13	C
50	3	14	U
50	3	15	A

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	3	2220	A
50	3	2808	A
50	3	2504	C
50	3	2668	A
50	3	2897	G

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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.

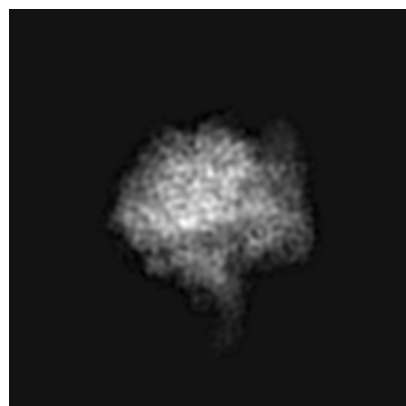
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13445. These allow visual inspection of the internal detail of the map and identification of artifacts.

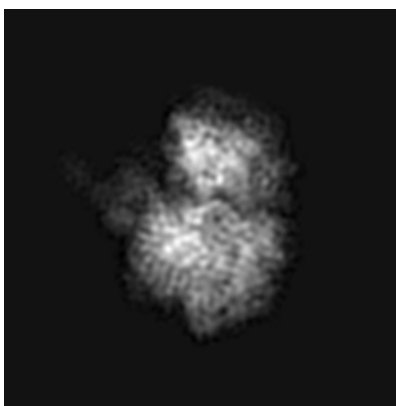
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

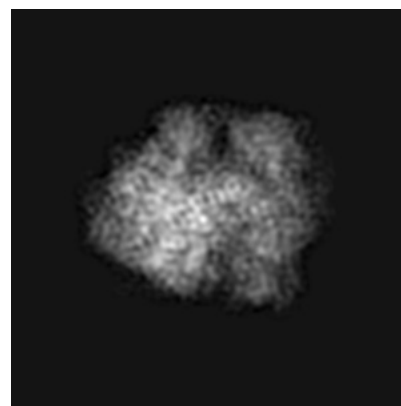
#### 6.1.1 Primary map



X

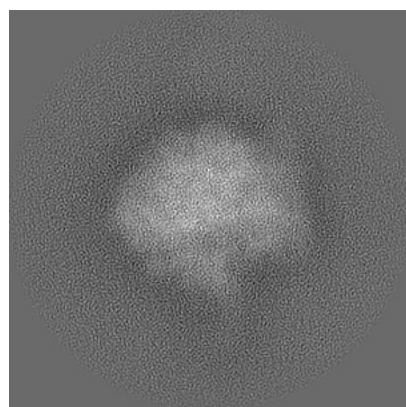


Y

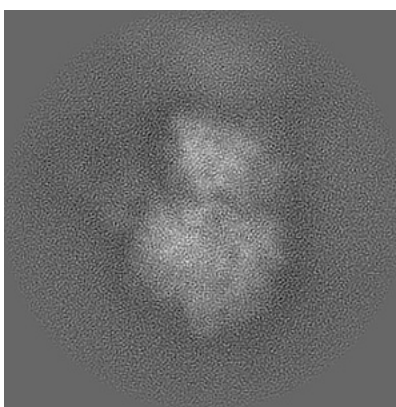


Z

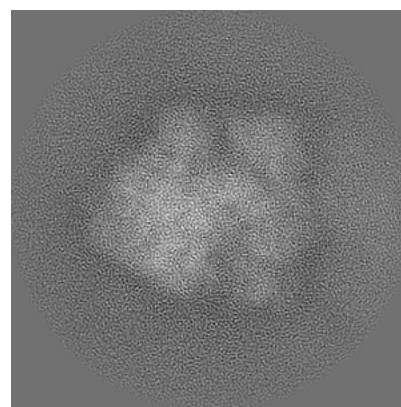
#### 6.1.2 Raw map



X



Y

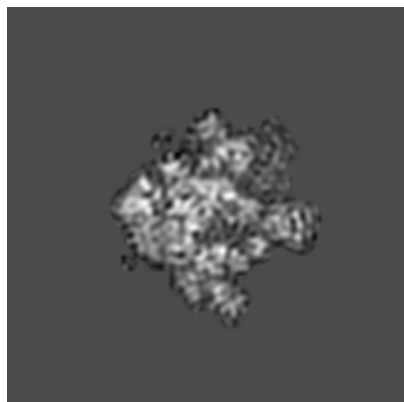


Z

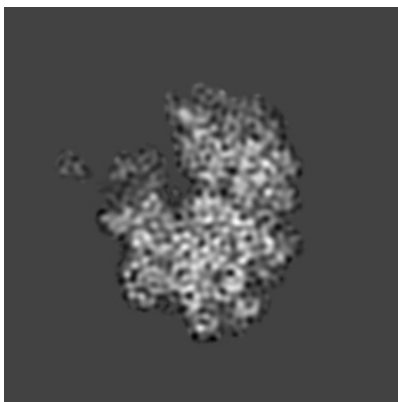
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

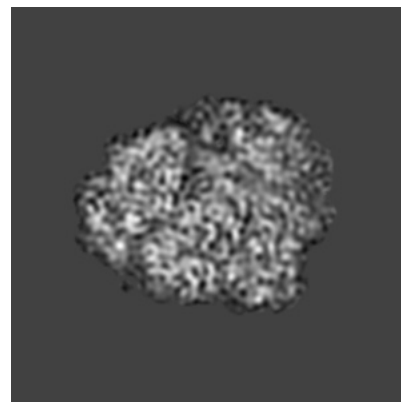
### 6.2.1 Primary map



X Index: 128

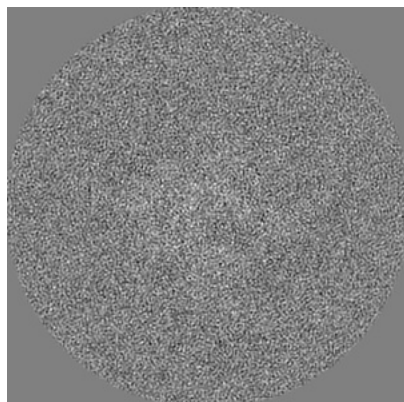


Y Index: 128

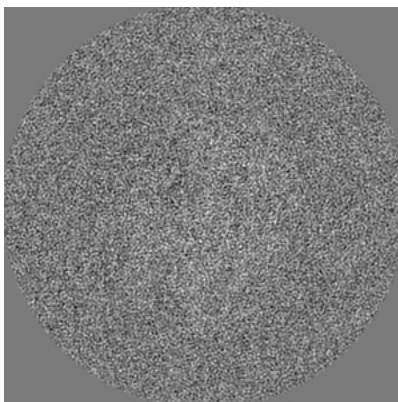


Z Index: 128

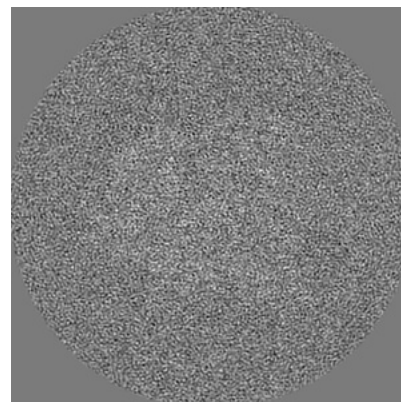
### 6.2.2 Raw map



X Index: 128



Y Index: 128

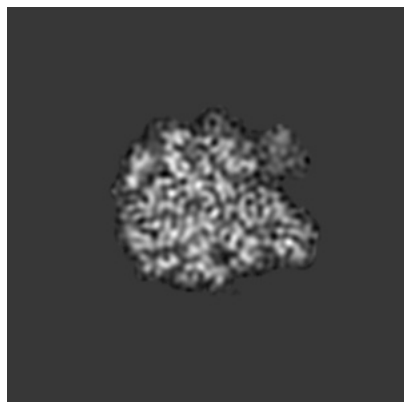


Z Index: 128

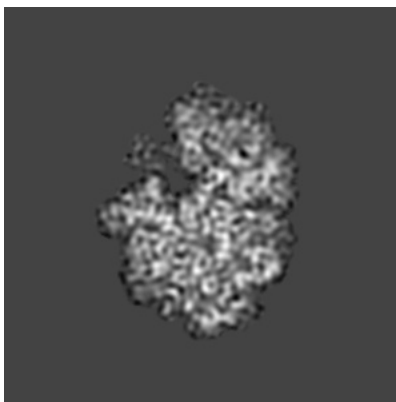
The images above show central slices of the map in three orthogonal directions.

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

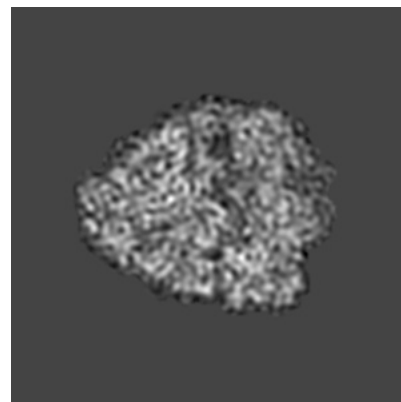
### 6.3.1 Primary map



X Index: 103

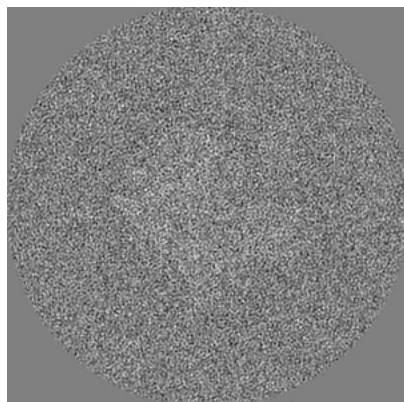


Y Index: 121

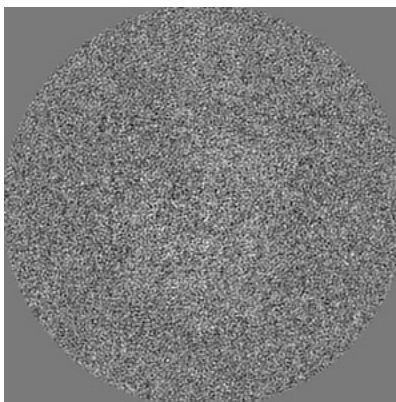


Z Index: 124

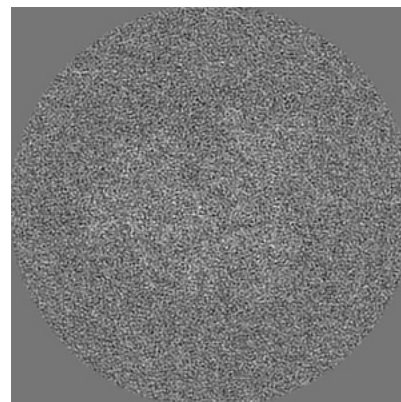
### 6.3.2 Raw map



X Index: 118



Y Index: 126



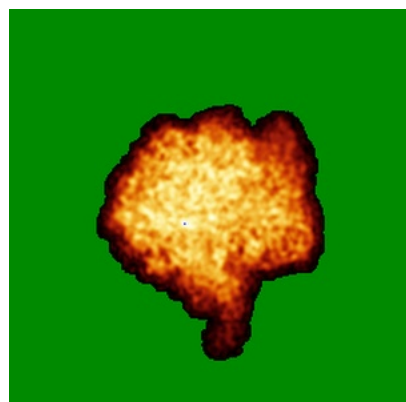
Z Index: 132

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

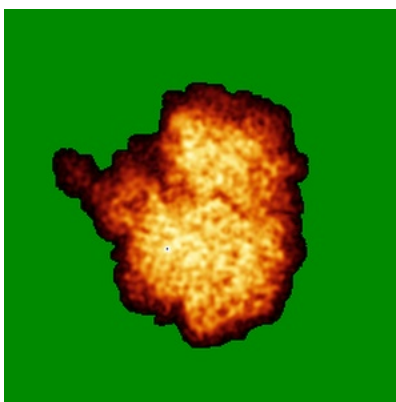


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

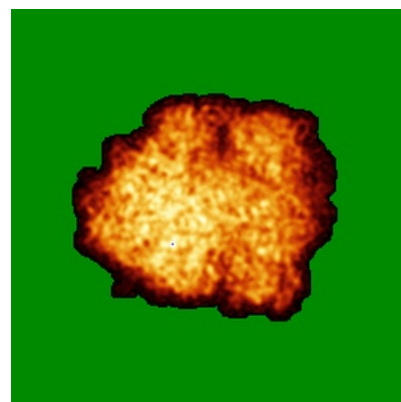
### 6.4.1 Primary map



X

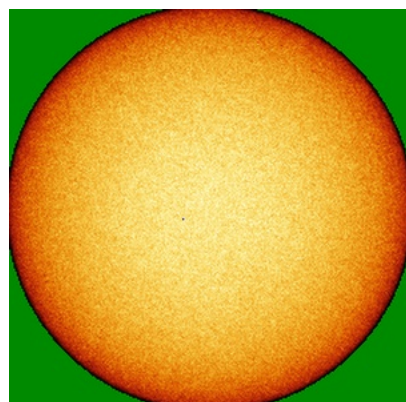


Y

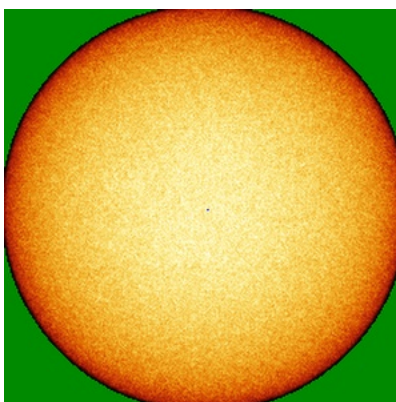


Z

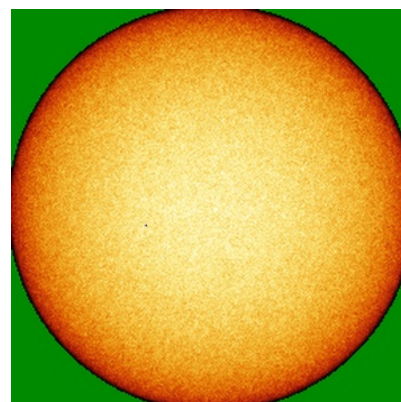
### 6.4.2 Raw map



X



Y

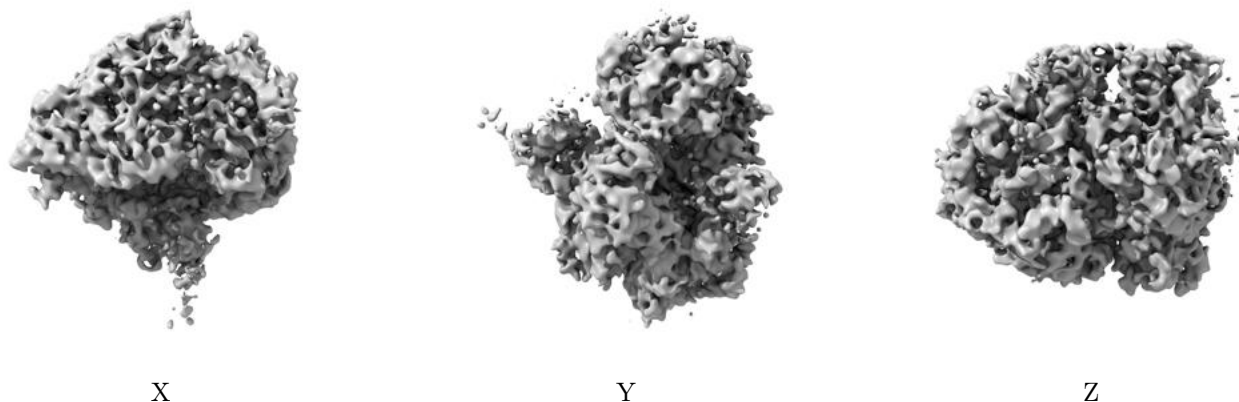


Z

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.

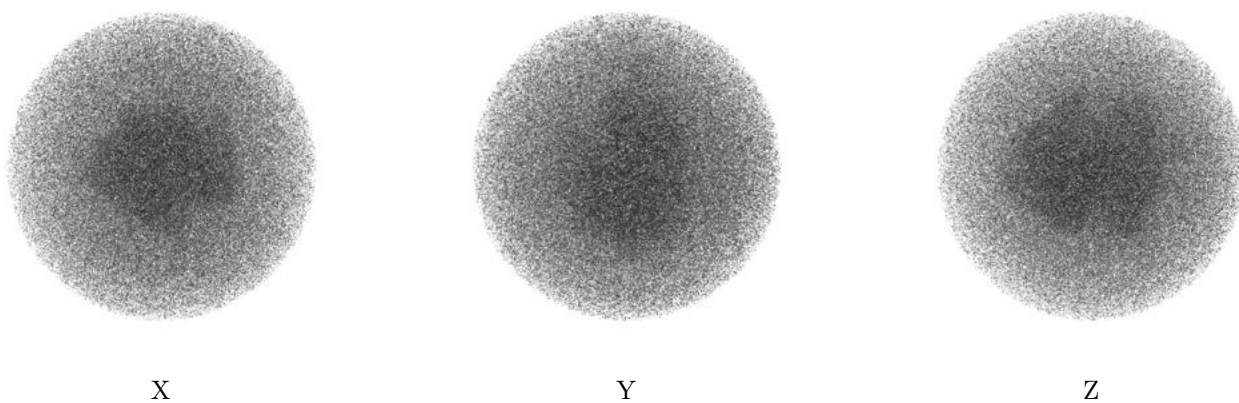
## 6.5 Orthogonal surface views [i](#)

### 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.

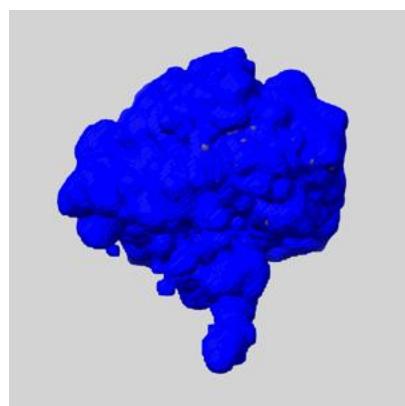
## 6.6 Mask visualisation [i](#)

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

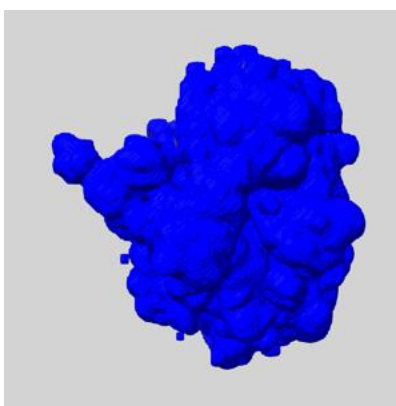
A mask typically either:

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

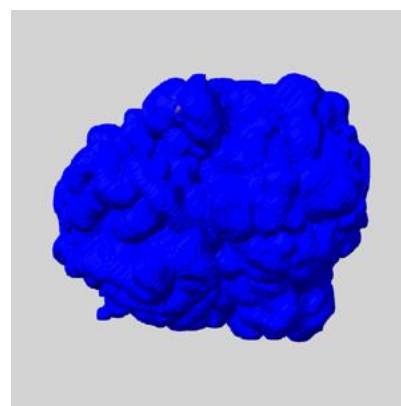
### 6.6.1 emd\_13445\_msk\_1.map [i](#)



X



Y



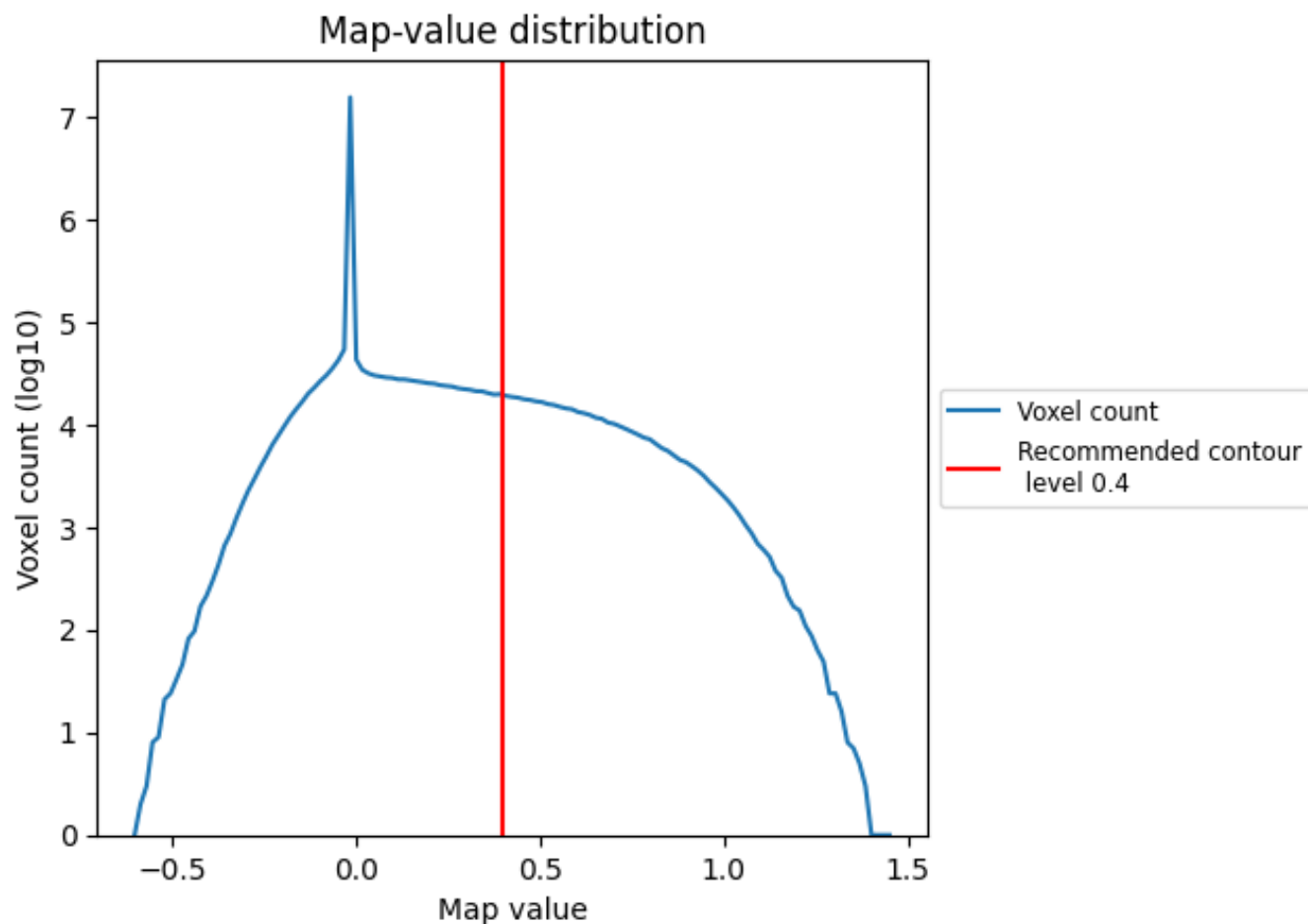
Z



## 7 Map analysis [i](#)

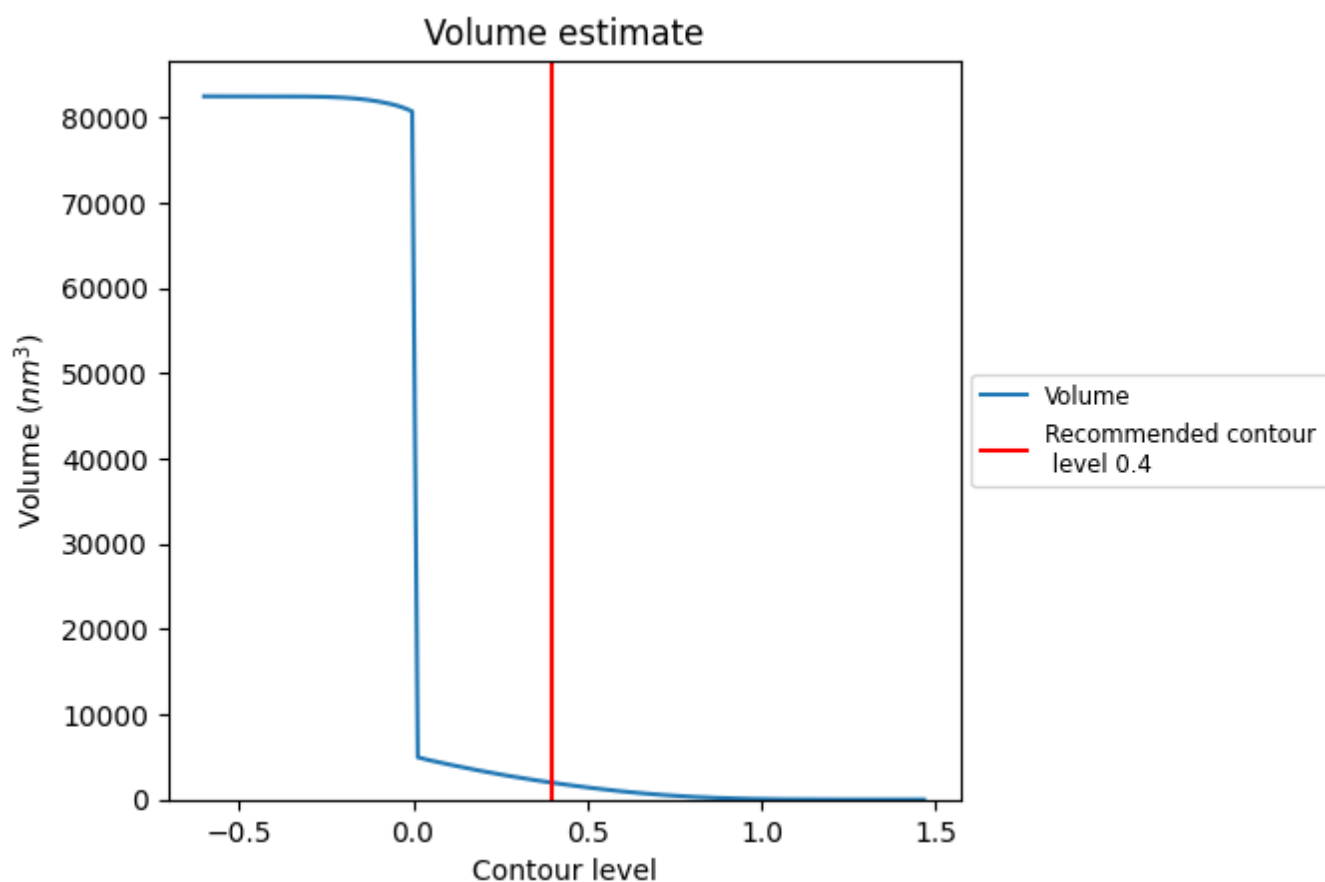
This section contains the results of statistical analysis of the map.

### 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.

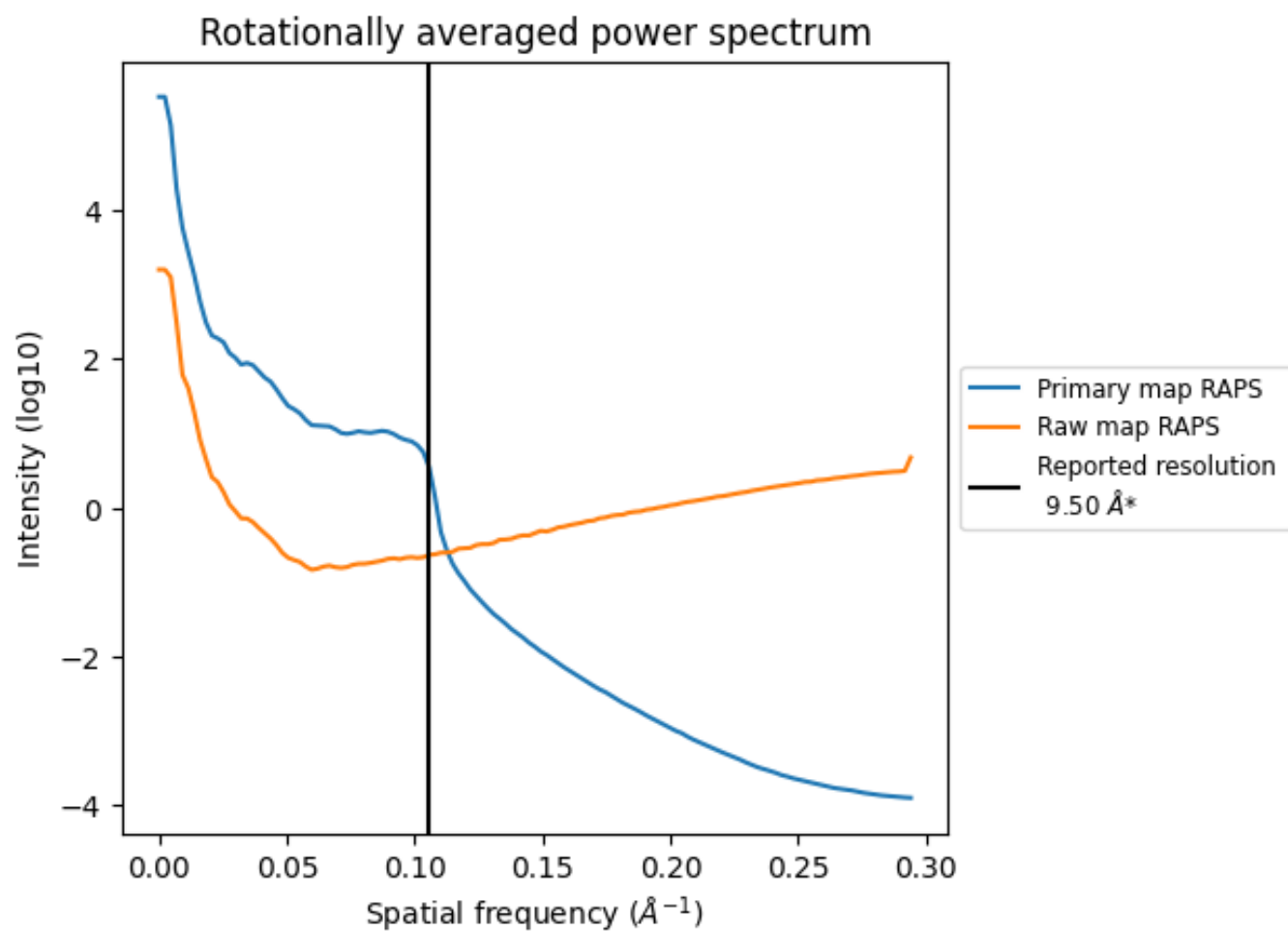
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1971 nm<sup>3</sup>; this corresponds to an approximate mass of 1780 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 ⓘ

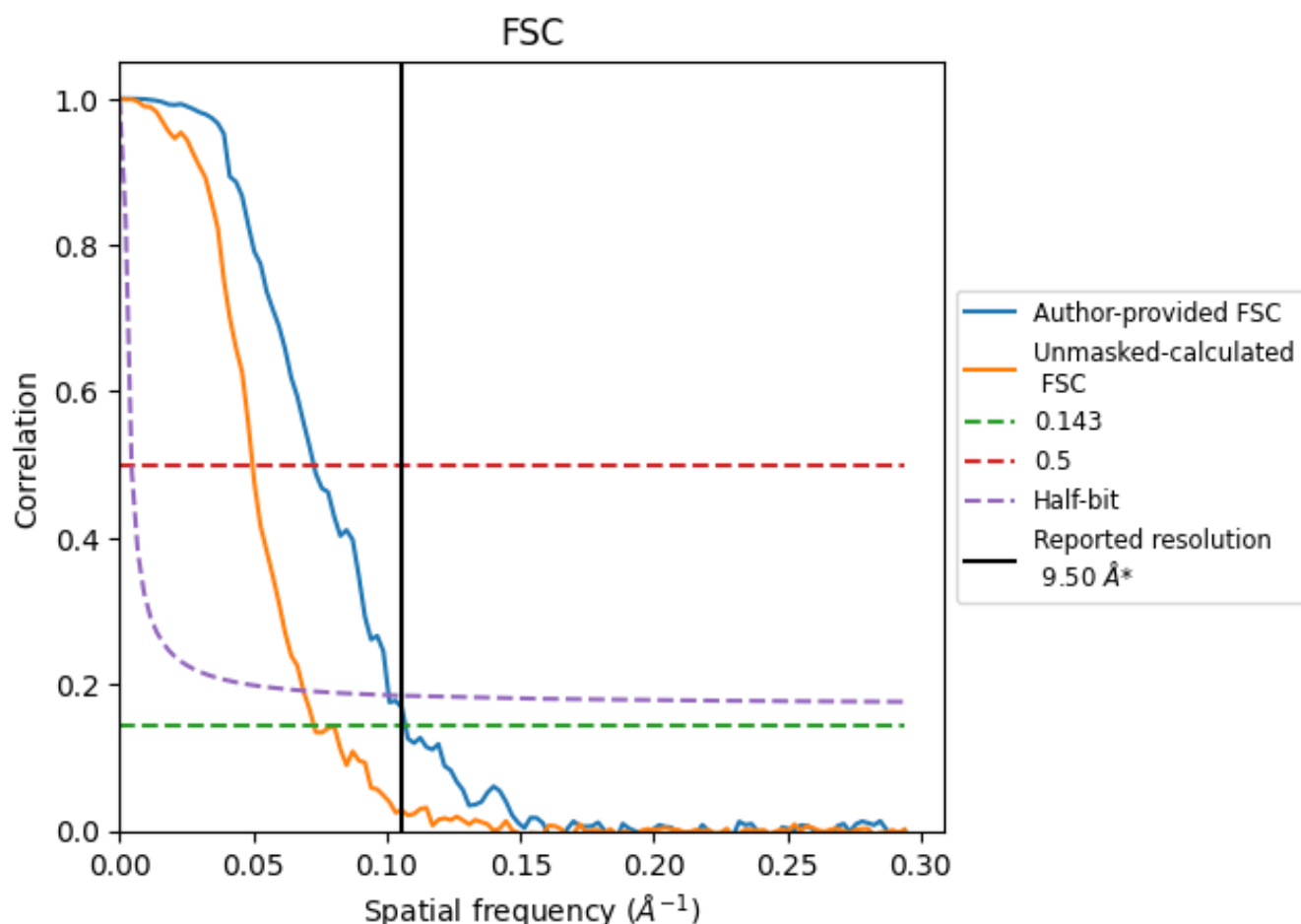


\*Reported resolution corresponds to spatial frequency of 0.105  $\text{\AA}^{-1}$

## 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 0.105 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

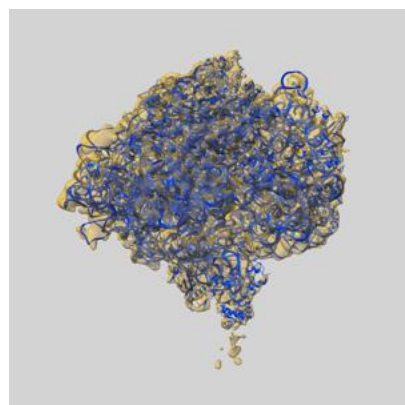
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.50	-	-
Author-provided FSC curve	9.35	13.76	9.92
Unmasked-calculated*	13.72	20.08	14.51

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 13.72 differs from the reported value 9.5 by more than 10 %

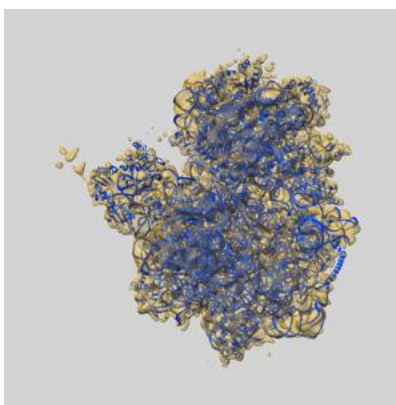
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13445 and PDB model 7PIO. Per-residue inclusion information can be found in section [3](#) on page [13](#).

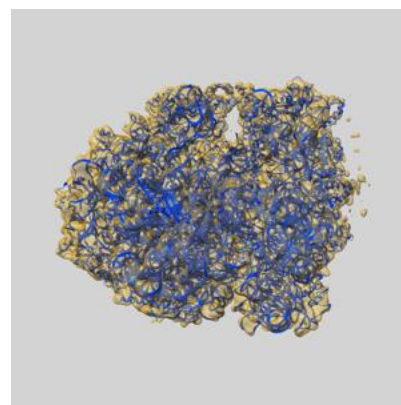
### 9.1 Map-model overlay [i](#)



X



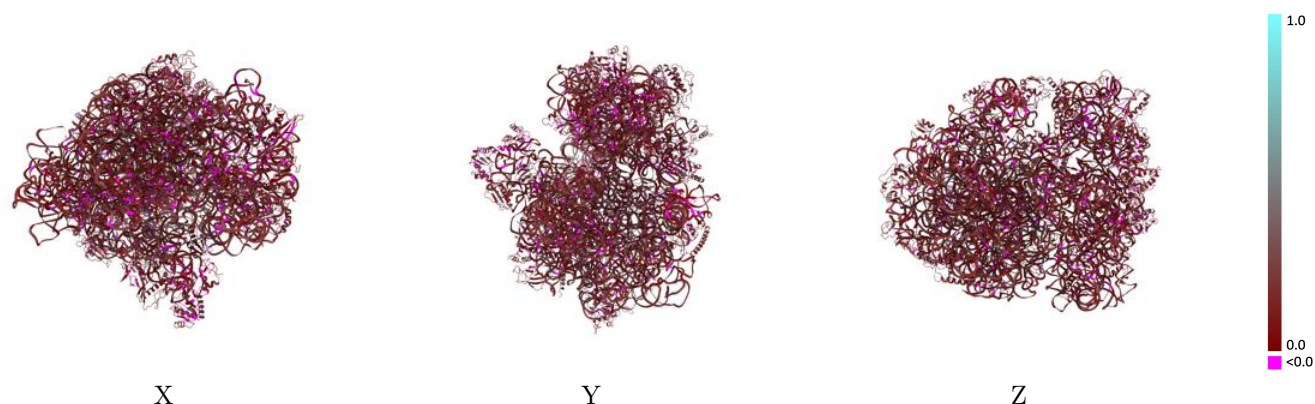
Y



Z

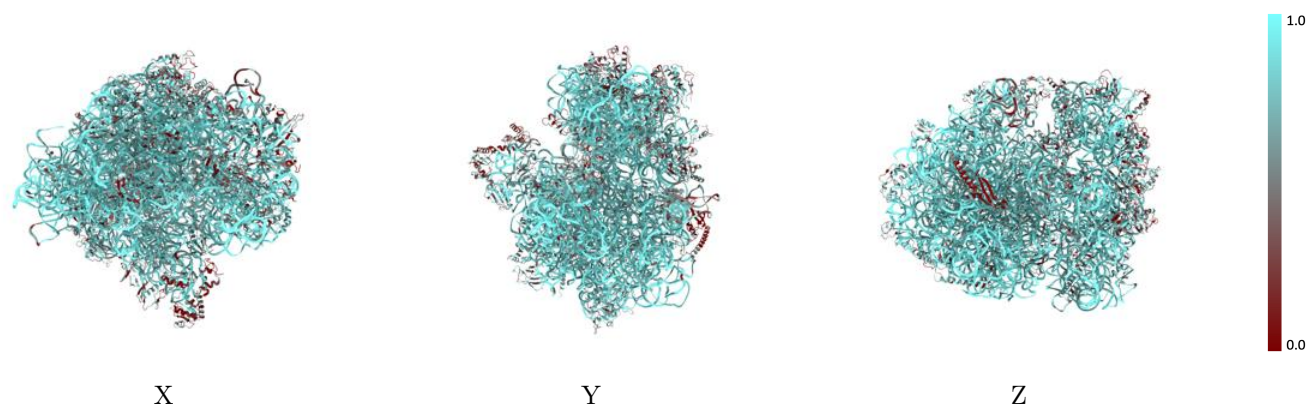
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



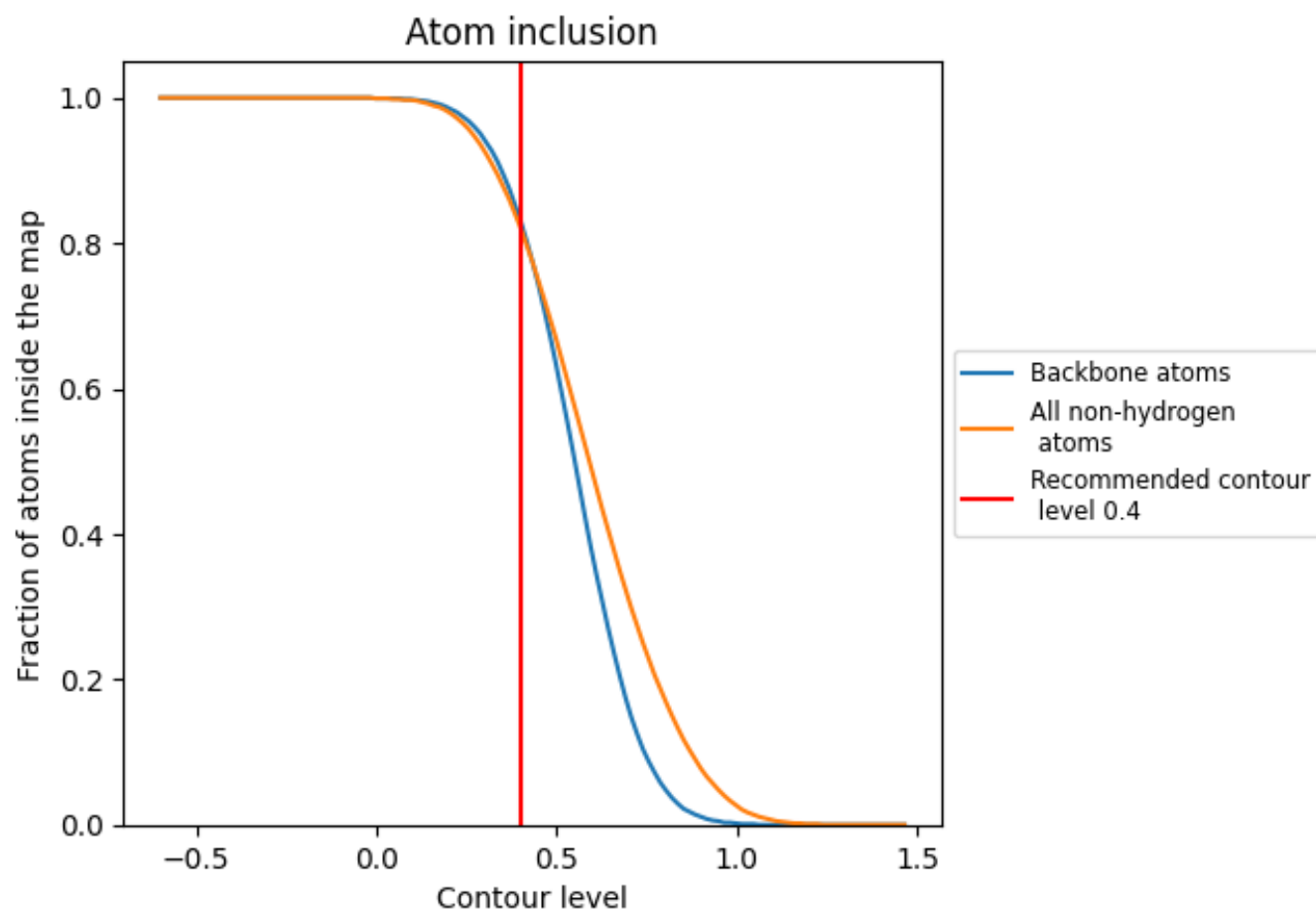
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 83% of all backbone atoms, 82% 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	 0.8210	 0.1550
0	 0.8110	 0.1480
1	 0.6460	 0.1130
2	 0.7130	 0.0970
3	 0.9270	 0.1650
4	 0.9400	 0.1820
5	 0.9180	 0.1580
7	 0.8690	 0.1760
A	 0.5250	 0.1680
B	 0.5240	 0.1400
C	 0.5790	 0.1290
D	 0.5810	 0.1360
E	 0.5080	 0.1630
F	 0.5840	 0.1510
G	 0.5950	 0.1360
H	 0.5540	 0.1010
I	 0.5110	 0.1320
J	 0.6080	 0.1210
K	 0.6270	 0.1240
L	 0.5730	 0.1380
M	 0.5800	 0.1120
N	 0.6570	 0.1710
O	 0.6710	 0.1300
P	 0.6150	 0.1090
Q	 0.5370	 0.1180
R	 0.5600	 0.0880
S	 0.7380	 0.1530
T	 0.6270	 0.1720
a	 0.7150	 0.1300
b	 0.6730	 0.1190
c	 0.6720	 0.1530
d	 0.6350	 0.1390
e	 0.5590	 0.1500
f	 0.1940	 0.1330
g	 0.3970	 0.1230



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Chain	Atom inclusion	Q-score
h	 0.2460	 0.0890
i	 0.6920	 0.1400
j	 0.5840	 0.1360
k	 0.6880	 0.1340
l	 0.7170	 0.1360
m	 0.6960	 0.1250
n	 0.6590	 0.1500
o	 0.6100	 0.1440
p	 0.7430	 0.1310
q	 0.6610	 0.1490
r	 0.6940	 0.1440
s	 0.7040	 0.1670
t	 0.5730	 0.1510
u	 0.6770	 0.1060
v	 0.6710	 0.1310
w	 0.6890	 0.1830
x	 0.4930	 0.1750
y	 0.6940	 0.1110
z	 0.6930	 0.1410