



## wwPDB EM Validation Summary Report ⓘ

Nov 3, 2024 – 05:02 am GMT

PDB ID : 7PAH  
EMDB ID : EMD-13272  
Title : 70S ribosome with P- and E-site tRNAs in Mycoplasma pneumoniae cells  
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.  
Deposited on : 2021-07-30  
Resolution : 9.50 Å (reported)  
Based on initial models : 7OOD, 7OOC, 4V7C

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

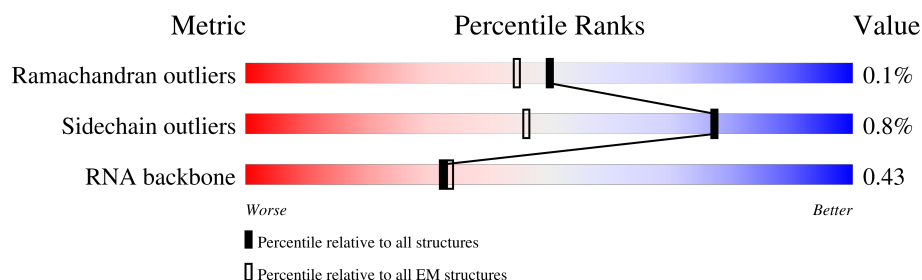
# 1 Overall quality at a glance

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	
2	1	59	
3	2	37	
4	A	294	
5	B	273	
6	C	205	
7	D	219	
8	E	215	

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Mol	Chain	Length	Quality of chain
9	F	155	
10	G	142	
11	H	132	
12	I	108	
13	J	121	
14	K	139	
15	L	124	
16	M	61	
17	N	86	
18	O	94	
19	P	85	
20	Q	104	
21	R	87	
22	S	87	
23	T	60	
24	a	287	
25	b	287	
26	c	212	
27	d	180	
28	e	184	
29	f	149	
30	g	161	
31	h	137	
32	i	146	
33	j	122	

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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	
53	8	76	

## 2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 146120 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
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		

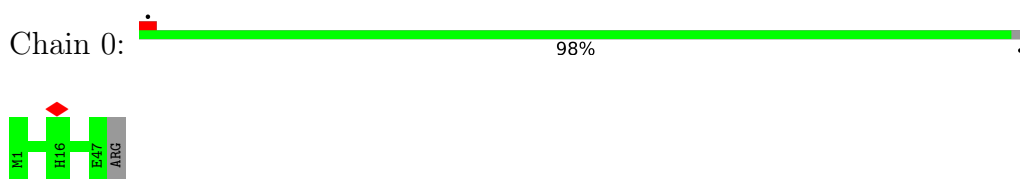
- Molecule 53 is a RNA chain called tRNA-Phe.

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

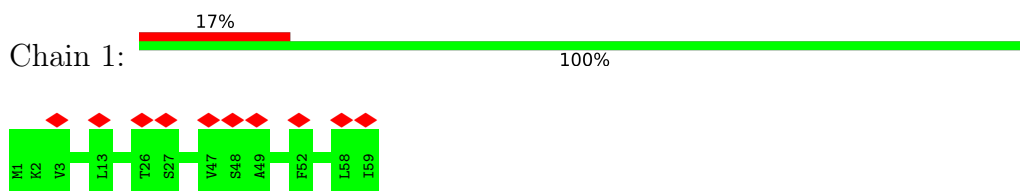
### 3 Residue-property plots

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

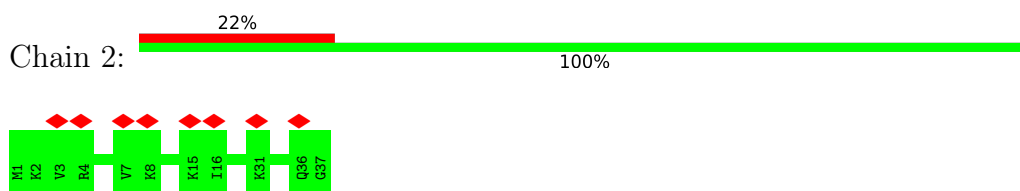
- Molecule 1: 50S ribosomal protein L34



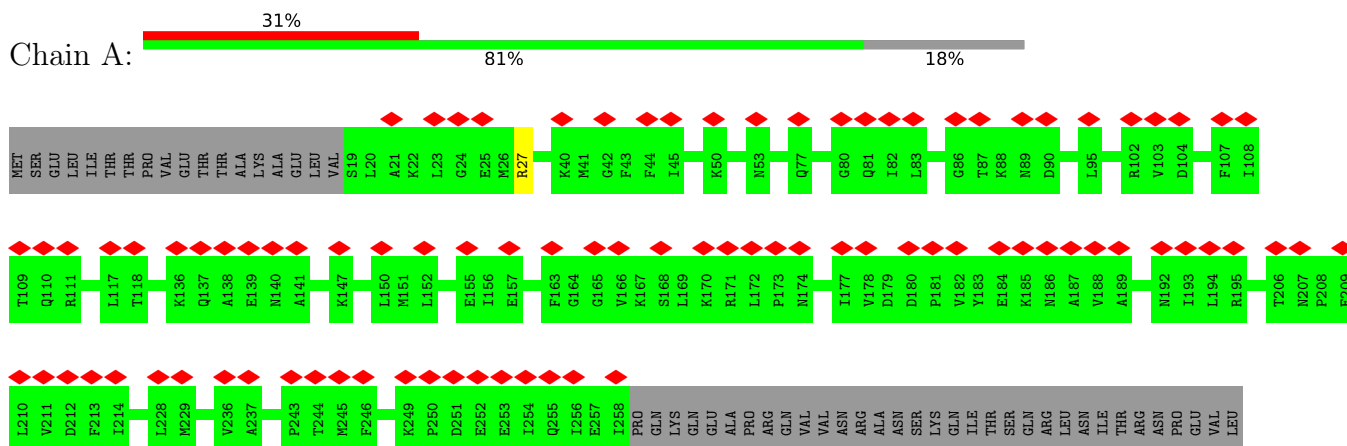
- Molecule 2: 50S ribosomal protein L35



- Molecule 3: 50S ribosomal protein L36




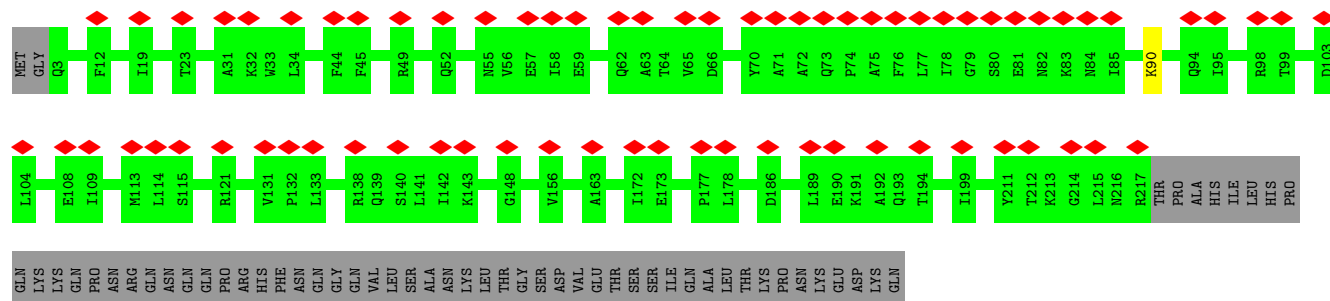
- Molecule 4: 30S ribosomal protein S2



THR  
ARG  
GLU

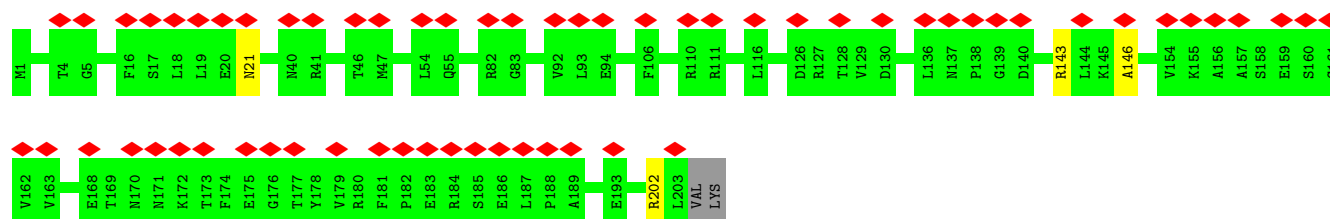
• Molecule 5: 30S ribosomal protein S3

Chain B: 



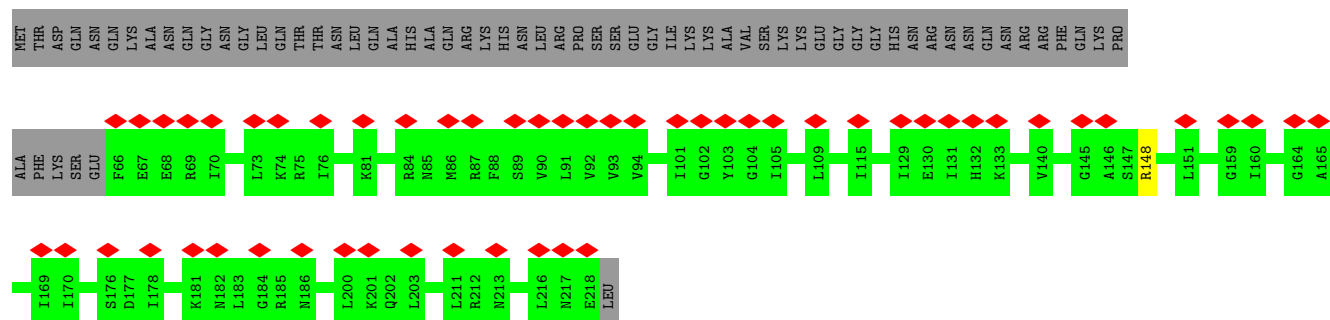
• Molecule 6: 30S ribosomal protein S4

Chain C: 




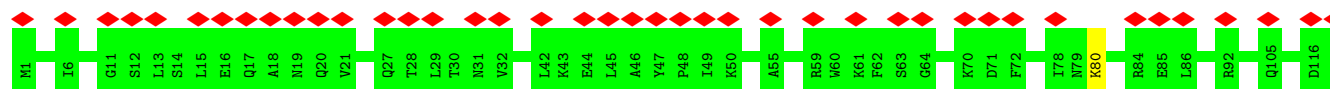
• Molecule 7: 30S ribosomal protein S5

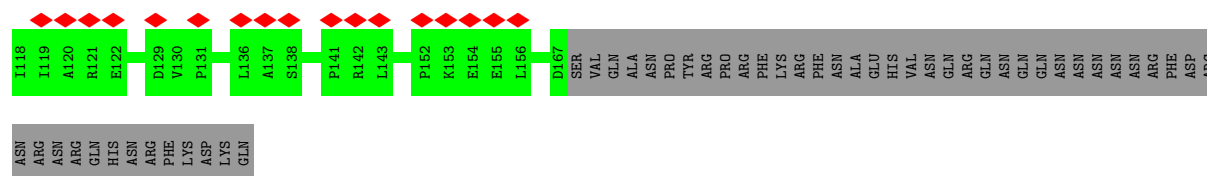
Chain D: 



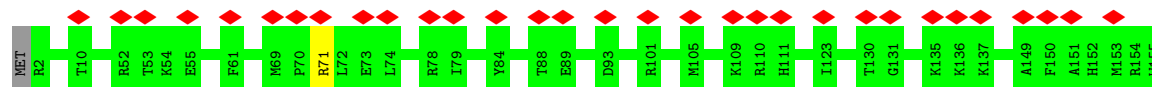
• Molecule 8: 30S ribosomal protein S6

Chain E: 

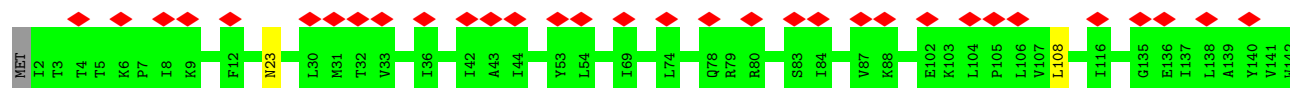




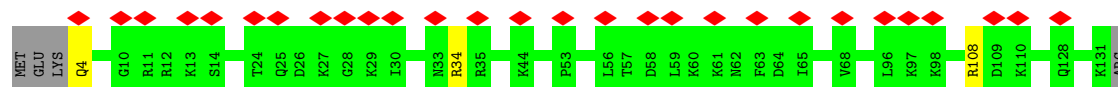
- Molecule 9: 30S ribosomal protein S7



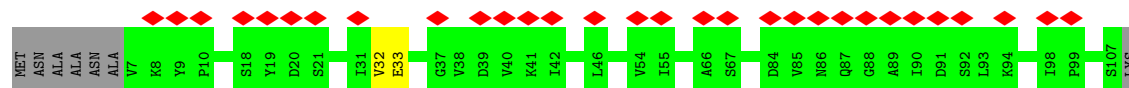
- Molecule 10: 30S ribosomal protein S8



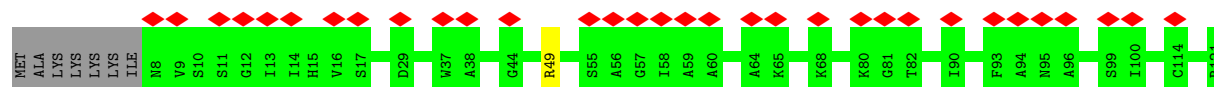
- Molecule 11: 30S ribosomal protein S9



- Molecule 12: 30S ribosomal protein S10

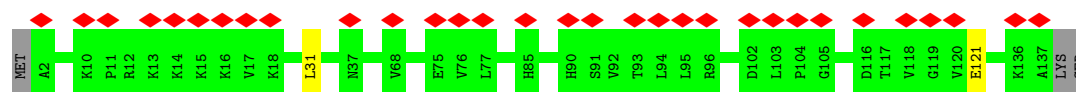


- Molecule 13: 30S ribosomal protein S11



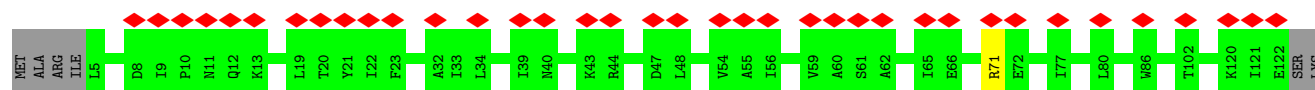
- Molecule 14: 30S ribosomal protein S12





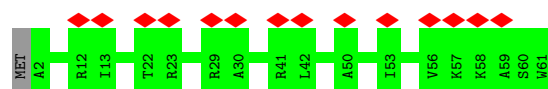
- Molecule 15: 30S ribosomal protein S13

Chain L: 94% 30% 5%



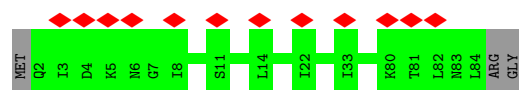
- Molecule 16: 30S ribosomal protein S14 type Z

Chain M: 98% 23%



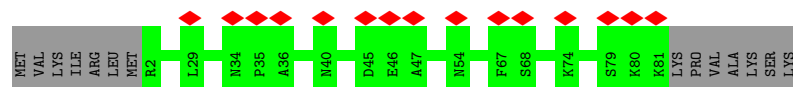
- Molecule 17: 30S ribosomal protein S15

Chain N: 97% 14%



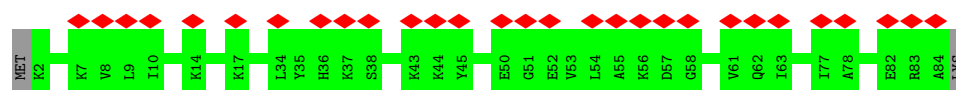
- Molecule 18: 30S ribosomal protein S16

Chain O: 85% 16% 15%



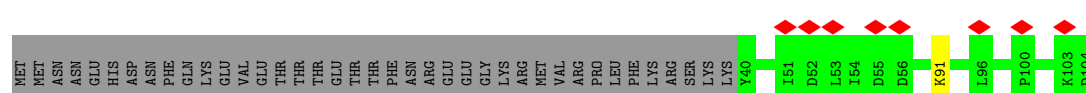
- Molecule 19: 30S ribosomal protein S17

Chain P: 98% 34%



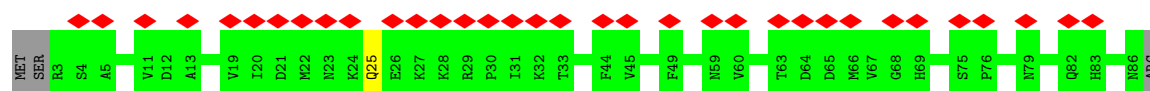
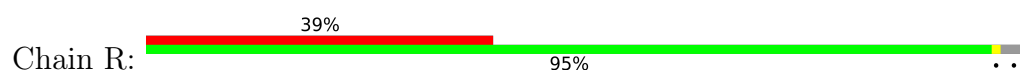
- Molecule 20: 30S ribosomal protein S18

Chain Q: 62% 8% 38%

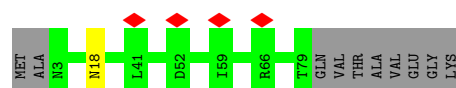
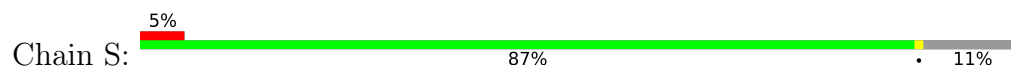


- Molecule 21: 30S ribosomal protein S19

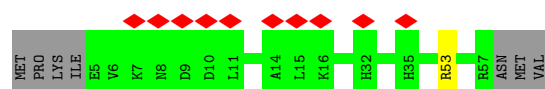
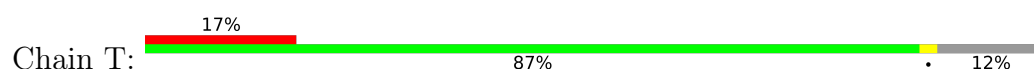




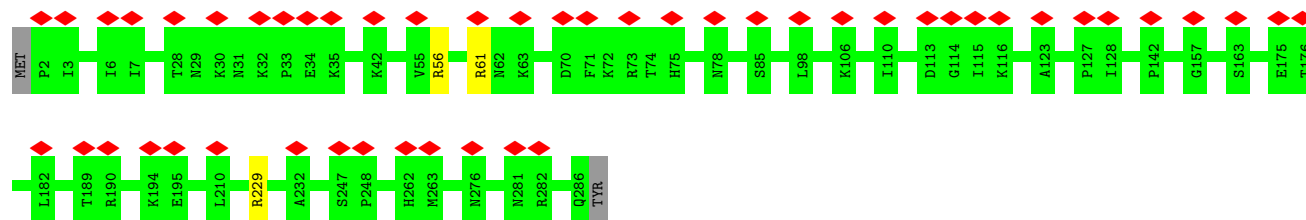
- Molecule 22: 30S ribosomal protein S20



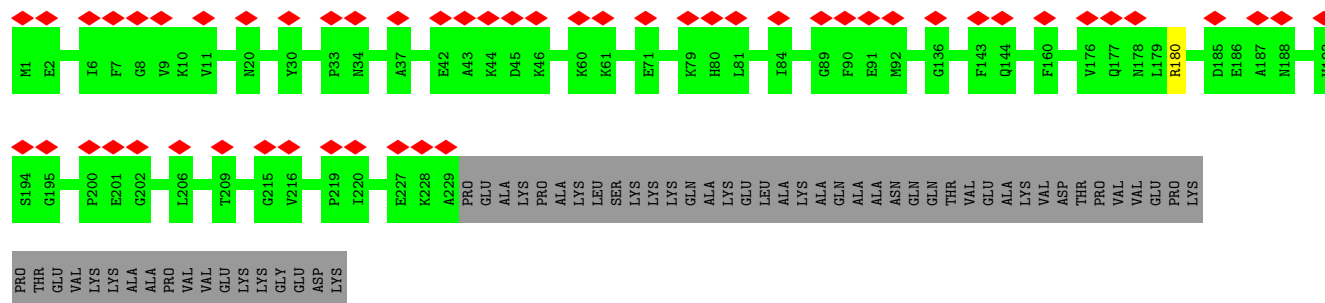
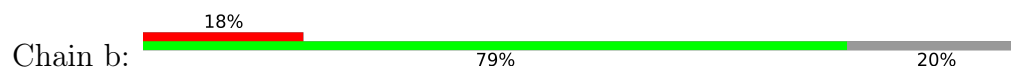
- Molecule 23: 30S ribosomal protein S21



- Molecule 24: 50S ribosomal protein L2

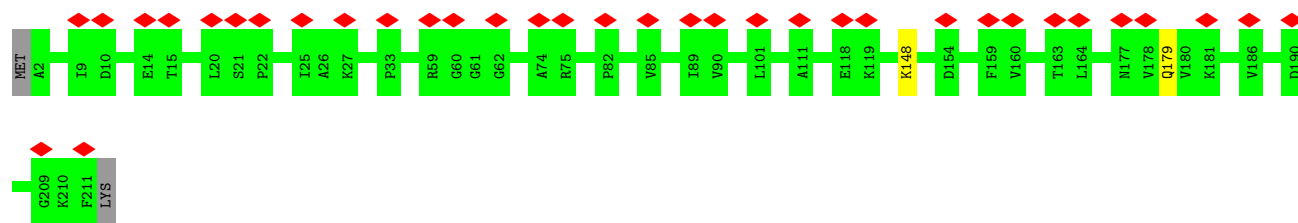


- Molecule 25: 50S ribosomal protein L3

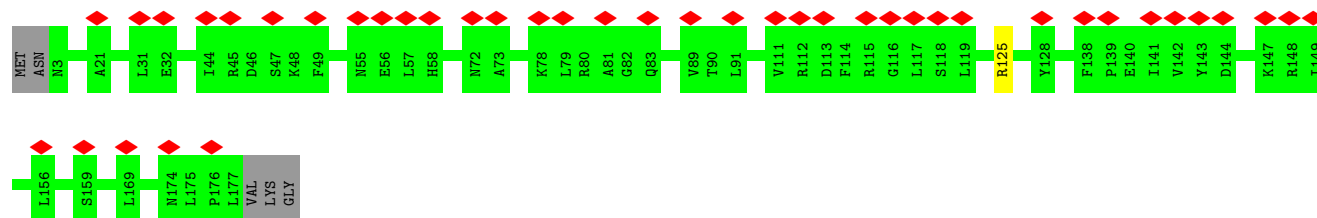


- Molecule 26: 50S ribosomal protein L4

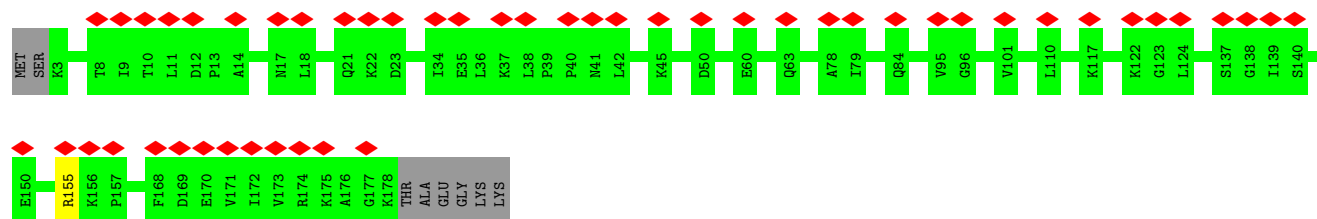




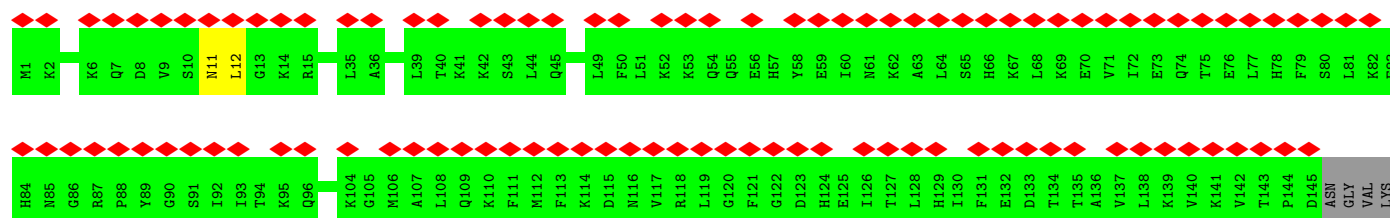
- Molecule 27: 50S ribosomal protein L5



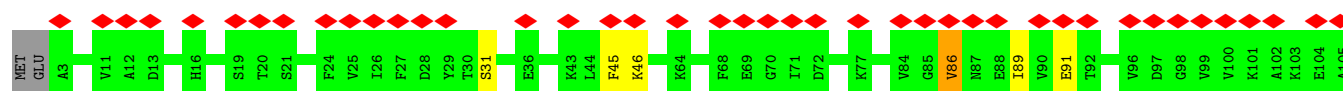
- Molecule 28: 50S ribosomal protein L6

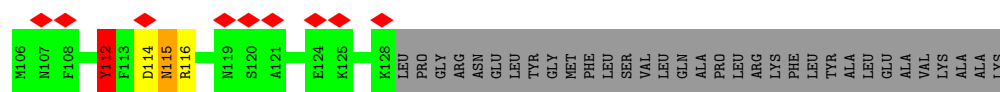


- Molecule 29: 50S ribosomal protein L9

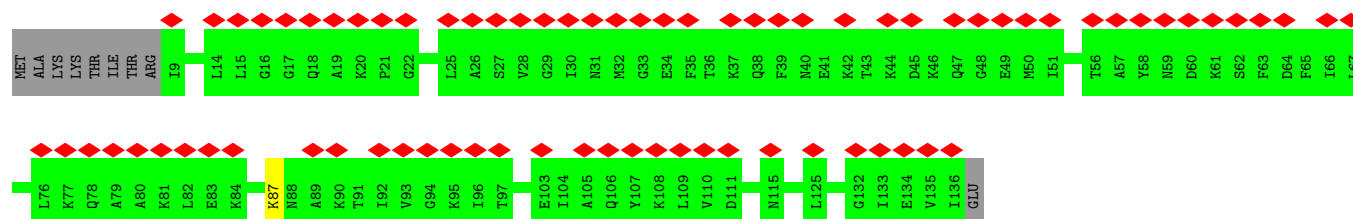
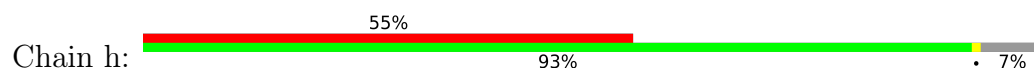


- Molecule 30: 50S ribosomal protein L10

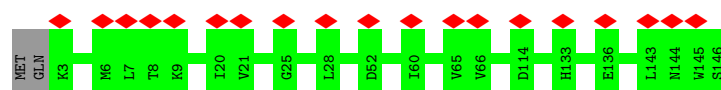




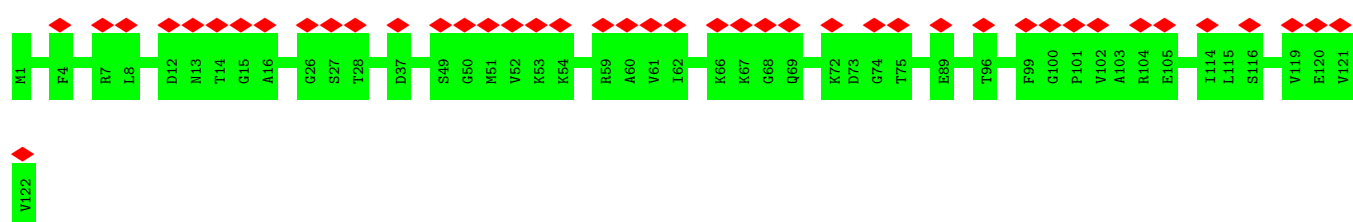
- Molecule 31: 50S ribosomal protein L11



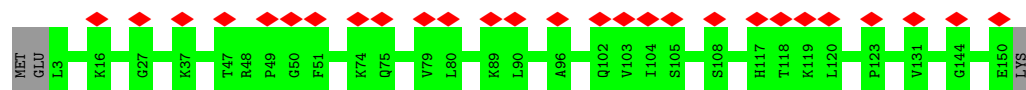
- Molecule 32: 50S ribosomal protein L13



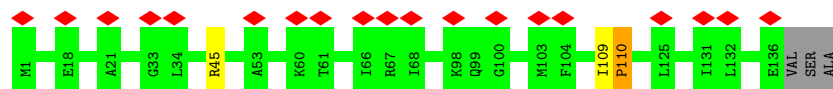
- Molecule 33: 50S ribosomal protein L14



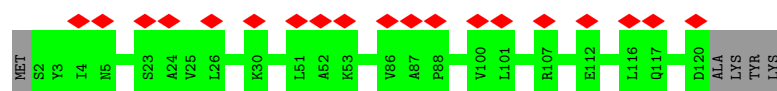
- Molecule 34: 50S ribosomal protein L15



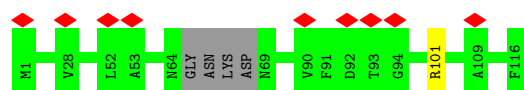
- Molecule 35: 50S ribosomal protein L16



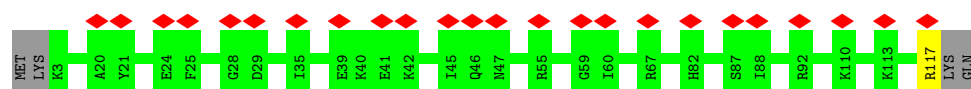
- Molecule 36: 50S ribosomal protein L17



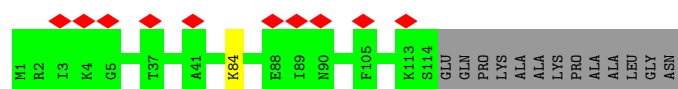
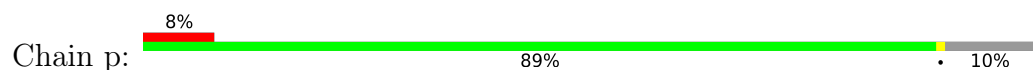
- Molecule 37: 50S ribosomal protein L18



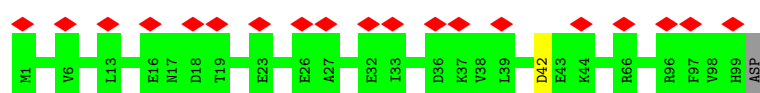
- Molecule 38: 50S ribosomal protein L19



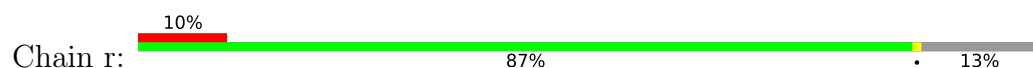
- Molecule 39: 50S ribosomal protein L20



- Molecule 40: 50S ribosomal protein L21

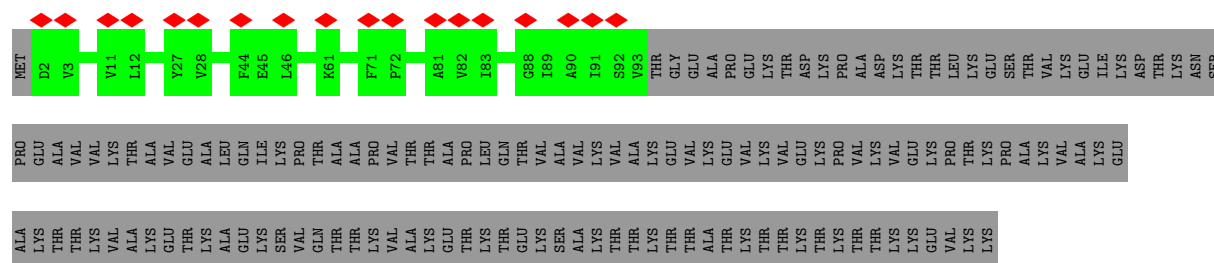


- Molecule 41: 50S ribosomal protein L22

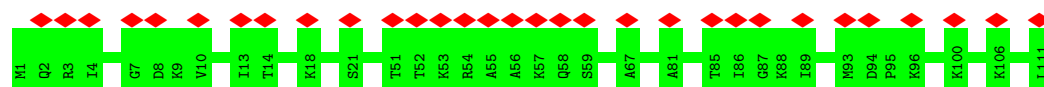


- Molecule 42: 50S ribosomal protein L23

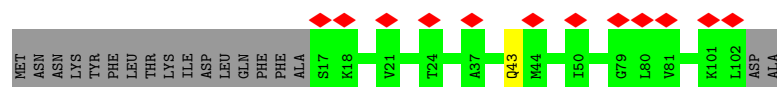
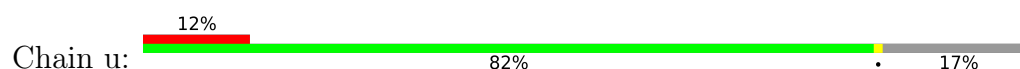




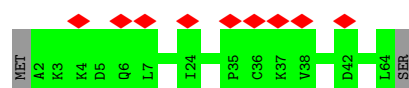
- Molecule 43: 50S ribosomal protein L24



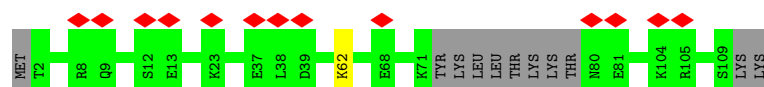
- Molecule 44: 50S ribosomal protein L27



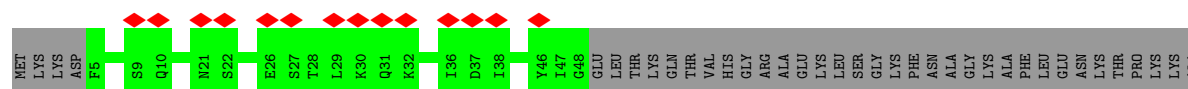
- Molecule 45: 50S ribosomal protein L28



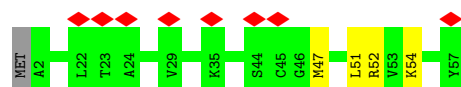
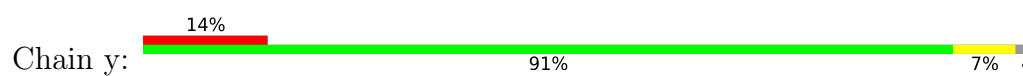
- Molecule 46: 50S ribosomal protein L29



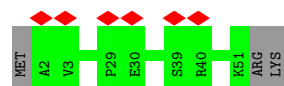
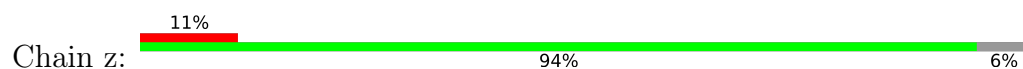
- Molecule 47: 50S ribosomal protein L31



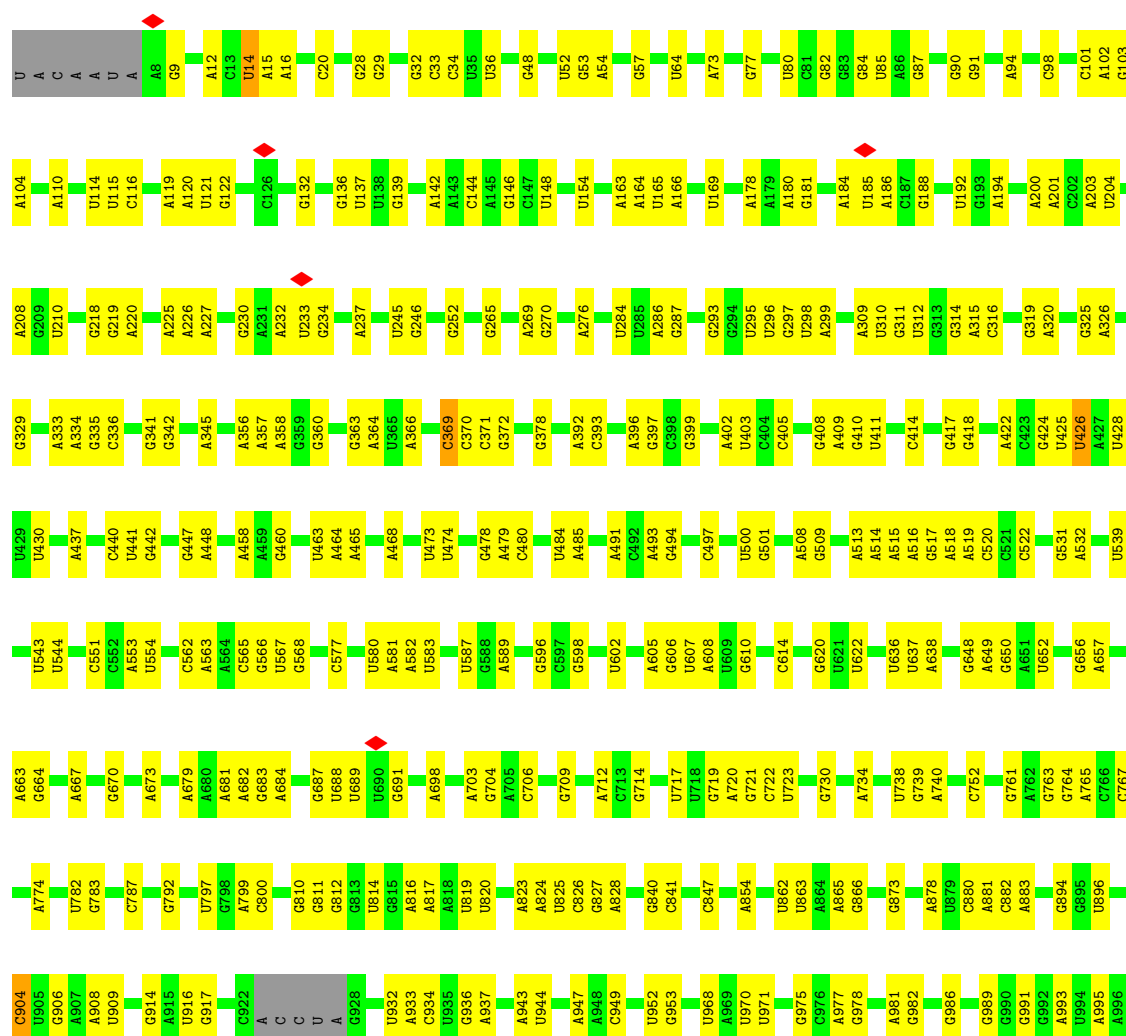
- Molecule 48: 50S ribosomal protein L32



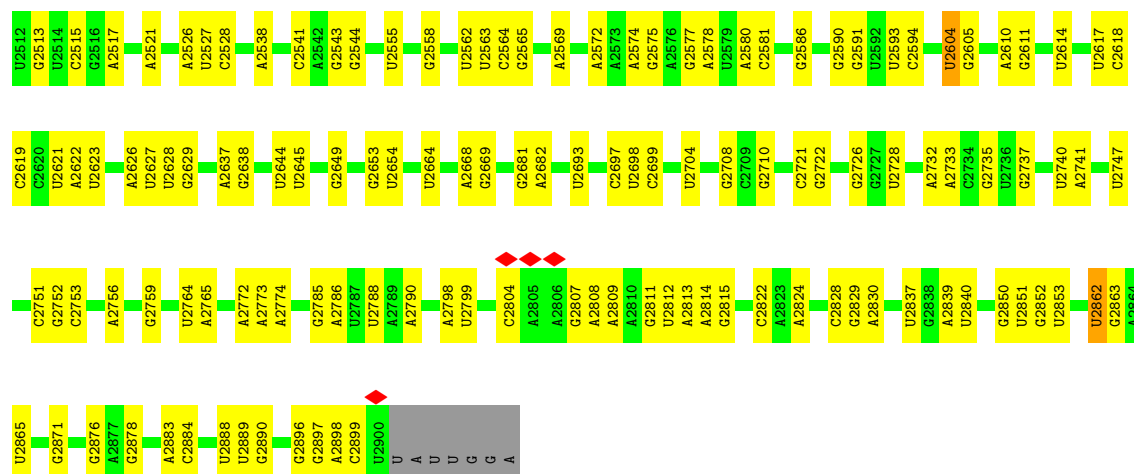
- Molecule 49: 50S ribosomal protein L33 1



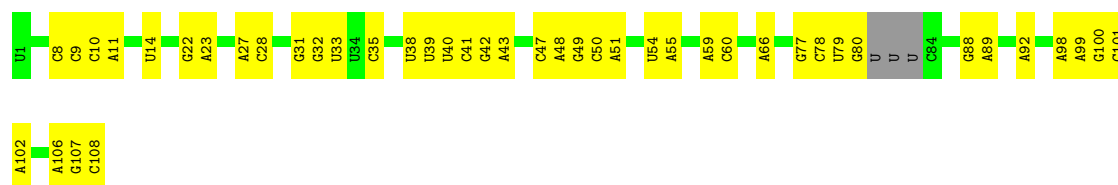
- Molecule 50: 23S ribosomal RNA



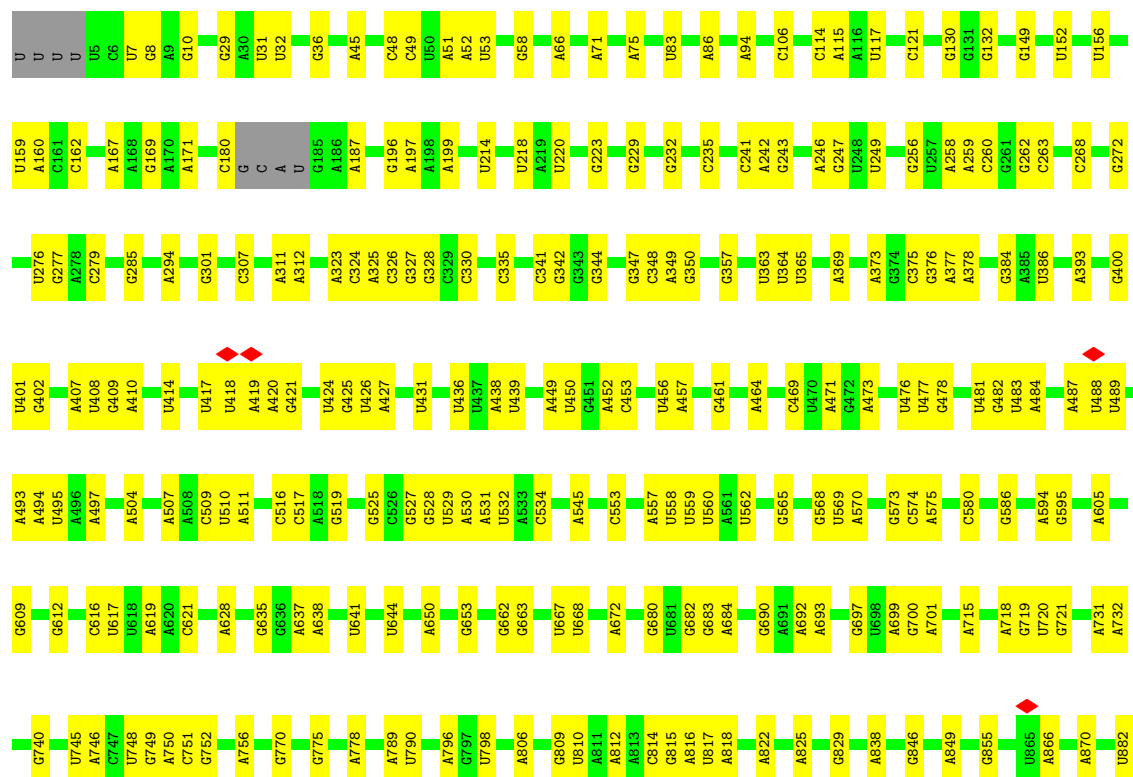
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U2414	U2414	G2312	U2193	U2099	U1998	G1876	A1762	U1617	G1528	A1406	G1301	A1208	C1107	
U2416	U2416	U2313	C2194	G2100	G1999	U1889	G1763	U1618	U1532	U1407	C1302	U1209	A1108	
C2417	C2417	G2316	U2195	G2106	G2004	A1892	G1765	G1635	U1533	U1418	U1303	A1210	G1109	
G2422	G2422	C2318	C2199	A2107	U2009	A1896	A1767	U1636	A1534	U1419	A1304	U1211	G1105	
U2431	U2431	A2317	U2200	C2108	G2010	A1896	G1768	A1637	G1540	A1421	A1315	C1212	U1113	
C2432	C2432	A2319	G2201	A2109	A2010	A1907	A1769	A1637	G1541	A1421	U1316	C1213	C1114	
A2433	A2433	U2202	G2201	U2110	G2011	A1907	A1770	G1640	G1542	A1422	C1317	U1214	G1115	
A2434	A2434	U2203	U2203	U2111	A2012	A1908	C1771	G1641	G1542	A1423	A1322	U1215	A1119	
A2435	A2435	C2204	U2205	A2112	C2013	G1909	G1772	G1642	U1543	U1424	A1323	U1216	A1016	
G2436	G2436	U2205	U2205	U2113	A2013	G1910	G1772	G1643	U1546	U1425	A1324	G1217	A1017	
A2437	A2437	A2206	A2206	U2114	A2020	G1910	G1777	A1644	G1547	C1426	C1325	G1231	G1123	
U2438	U2438	G2211	G2211	A2115	A2021	G1913	G1779	A1644	U1548	U1434	C1326	U1234	U1124	
A2439	A2439	G2212	U2212	U2116	A2022	G1913	A1780	A1648	U1549	A1435	A1327	U1235	G1020	
G2442	G2442	G2333	G2333	G2117	A2027	A1919	A1780	C1649	G1550	A1435	U1329	U1236	G1021	
A2443	A2443	U2334	U2219	A2123	G2027	A1920	G1783	A1650	U1551	U1448	U1330	G1236	A1026	
U2444	U2444	A2335	A2220	A2124	U2029	C1921	U1784	C1651	U1556	A1457	G1331	G1236	U1027	
C2445	C2445	U2221	U2221	U2125	A2030	A1934	A1789	U1678	U1566	A1455	A1335	G1242	A1032	
A2447	A2447	G2341	G2222	A2126	C2031	A1935	C1789	U1679	A1558	A1456	U1143	G1243	A1033	
C2448	C2448	A2342	C2222	G2127	G2032	G1937	U1790	G1681	U1559	U1467	U1144	G1253	U1035	
U2449	U2449	A2343	A2233	G2127	G2032	U1938	A1791	C1682	U	A1479	U1151	U1254	G1044	
G2452	G2452	A2344	U2228	A2130	A2037	C1948	A1809	G1687	G	A1480	U1151	G1255	A1045	
C2453	C2453	U2358	A2230	G2131	A2038	C1949	A1815	U1677	A	U1480	U1154	A1256	A1048	
A2456	A2456	G2353	A2231	A2132	G2039	C1949	A1816	U1678	C	U1481	U1154	G1257	U1049	
U2457	U2457	A2354	G2245	A2133	A2040	U1950	A1816	U1679	A	U1481	U1154	G1257	U1049	
A2458	A2458	C2355	G2246	A2144	C2041	A1951	U1820	U1679	A	U1482	U1157	G1257	U1049	
A2459	A2459	U2366	G2247	A2145	G2053	U1953	A1822	U1681	G1571	G1483	U1360	U1260	A1052	
C2460	C2460	G2365	C2247	C2144	G2053	U1953	A1822	U1682	A1577	U1486	U1361	G1262	A1052	
A2461	A2461	A2362	U2251	A2157	A2056	A1959	U1823	A1698	A1577	U1487	U1361	G1262	A1052	
U2469	U2469	U2366	G2258	C2158	C2057	U1962	A1826	A1698	U1581	U1487	U1368	G1265	A1055	
C2474	C2474	G2377	G2259	U2159	C2062	U1962	U1826	A1702	G1582	A1502	U1369	G1266	A1056	
A2484	A2484	U2380	G2266	U2160	G2063	G1966	A1828	A1703	U1583	A1502	A1370	G1267	G1057	
U2485	U2485	G2381	C2267	G2161	G2064	U1967	A1828	C1704	U1584	U1506	G1371	U1268	A1061	
C2486	C2486	A2386	G2267	G2164	A2067	C1968	G1831	U1705	A1585	G1507	C1373	A1277	U1068	
A2490	A2490	U2387	A2274	A2165	G2068	C1969	G1832	C1706	U1586	G1508	U1374	G1278	U1068	
G2492	G2492	C2391	A2275	U2166	A2069	C1970	G1836	U1707	U1587	C1511	G1375	U1279	G1075	
U2499	U2499	U2392	A2276	A2170	C2070	C1971	A1837	G1708	U1588	A1512	G1376	G1280	A1080	
C2504	C2504	C2393	A2277	A2171	C2071	U1973	U1837	U1713	A1589	A1513	A1377	A1281	A1081	
A2505	A2505	A2394	A2286	A2172	C2072	U1974	G1842	A1716	G1594	A1514	C1378	G1282	A1082	
G2507	G2507	U2395	U2291	G2173	U2075	A1977	A1855	A1716	A1600	A1515	A1387	G1283	A1083	
U2508	U2508	A2396	U2291	G2174	G2076	U1978	G1856	U1727	A1601	G1516	G1388	A1284	A1083	
C2509	C2509	G2397	U2291	U2175	G2079	G1979	A1864	U1748	G1602	G1517	C1390	G1286	U1095	
A2511	A2511	A2398	A2295	U2180	G2079	A1980	A1864	U1748	A1603	A1519	U1182	G1292	G1097	
C2510	C2510	G2402	A2296	A2181	U2083	C1986	U1871	A1751	U1612	A1520	A1393	A1292	U1096	
A2511	A2511	C2298	A2298	C2182	A2084	C1987	U1872	A1613	A1613	C1523	A1396	G1296	A1102	
				U2184									G1103	



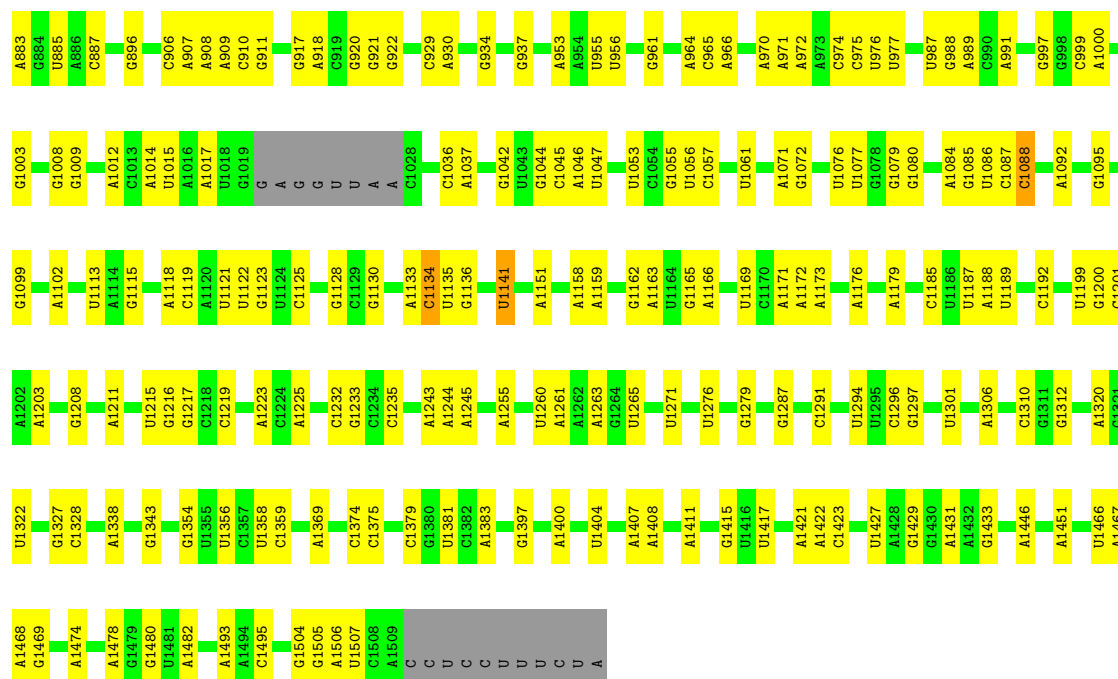
• Molecule 51: 5S ribosomal RNA



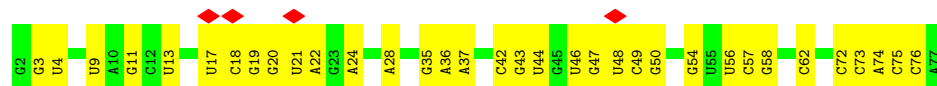
• Molecule 52: 16S ribosomal RNA



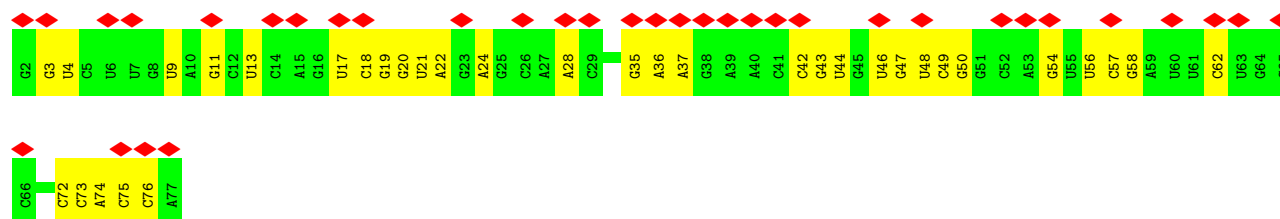




- Molecule 53: tRNA-Phe



- Molecule 53: tRNA-Phe



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	1803	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	1.376	Depositor
Minimum map value	-0.350	Depositor
Average map value	0.026	Depositor
Map value standard deviation	0.119	Depositor
Recommended contour level	0.47	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	Depositor

## 5 Model quality ⓘ

### 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	0.22	0/383	0.39	0/504
2	1	0.24	0/484	0.48	0/637
3	2	0.23	0/306	0.48	0/401
4	A	0.26	0/1954	0.48	0/2642
5	B	0.24	0/1721	0.48	0/2323
6	C	0.25	0/1691	0.46	0/2267
7	D	0.25	0/1188	0.47	0/1593
8	E	0.24	0/1384	0.47	0/1867
9	F	0.24	0/1266	0.51	0/1700
10	G	0.27	0/1126	0.54	0/1517
11	H	0.27	0/1044	0.51	0/1395
12	I	0.30	0/820	0.61	2/1103 (0.2%)
13	J	0.25	0/844	0.45	0/1136
14	K	0.29	0/1094	0.59	1/1468 (0.1%)
15	L	0.23	0/962	0.44	0/1289
16	M	0.24	0/483	0.46	0/643
17	N	0.23	0/679	0.44	0/907
18	O	0.24	0/659	0.49	0/885
19	P	0.25	0/684	0.47	0/913
20	Q	0.28	0/545	0.56	1/730 (0.1%)
21	R	0.25	0/698	0.50	0/936
22	S	0.24	0/631	0.45	0/838
23	T	0.22	0/475	0.42	0/621
24	a	0.25	0/2267	0.49	0/3044
25	b	0.25	0/1795	0.48	0/2412
26	c	0.26	0/1671	0.50	0/2246
27	d	0.28	0/1409	0.52	0/1894
28	e	0.27	0/1420	0.51	1/1912 (0.1%)
29	f	0.29	0/1183	0.60	0/1587
30	g	0.88	6/969 (0.6%)	0.68	2/1295 (0.2%)
31	h	0.25	0/968	0.46	0/1298
32	i	0.24	0/1186	0.46	0/1592
33	j	0.25	0/953	0.49	0/1275
34	k	0.24	0/1170	0.48	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	l	0.24	0/1104	0.53	0/1481
36	m	0.24	0/973	0.47	0/1309
37	n	0.26	0/897	0.47	0/1198
38	o	0.24	0/948	0.45	0/1262
39	p	0.25	0/961	0.44	0/1278
40	q	0.29	0/828	0.58	2/1111 (0.2%)
41	r	0.41	0/1077	0.80	3/1441 (0.2%)
42	s	0.29	0/732	0.55	0/988
43	t	0.23	0/879	0.45	0/1165
44	u	0.25	0/665	0.49	0/884
45	v	0.23	0/519	0.46	0/695
46	w	0.23	0/826	0.45	0/1104
47	x	0.30	0/353	0.45	0/474
48	y	0.32	0/457	0.53	0/601
49	z	0.23	0/412	0.42	0/547
50	3	0.23	0/69073	0.85	50/107710 (0.0%)
51	4	0.21	0/2505	0.83	4/3902 (0.1%)
52	5	0.22	0/35768	0.83	26/55764 (0.0%)
53	7	0.22	0/1808	0.86	2/2817 (0.1%)
53	8	0.22	0/1808	0.86	2/2817 (0.1%)
All	All	0.25	6/158705 (0.0%)	0.77	96/236977 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	C	0	1
10	G	0	1
21	R	0	1
29	f	0	1
30	g	0	2
35	l	0	1
All	All	0	7

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	g	112	TYR	CG-CD1	14.84	1.58	1.39
30	g	112	TYR	CG-CD2	12.44	1.55	1.39
30	g	112	TYR	CE1-CZ	8.21	1.49	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	g	112	TYR	CE2-CZ	8.06	1.49	1.38
30	g	112	TYR	CD1-CE1	7.58	1.50	1.39

The worst 5 of 96 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	r	99	ARG	NE-CZ-NH2	15.80	128.20	120.30
41	r	99	ARG	NE-CZ-NH1	-14.49	113.05	120.30
50	3	370	C	N3-C2-O2	-10.41	114.61	121.90
50	3	371	C	N3-C2-O2	-9.04	115.57	121.90
52	5	268	C	N3-C2-O2	-8.88	115.69	121.90

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	C	21	ASN	Peptide
10	G	108	LEU	Peptide
21	R	25	GLN	Peptide
29	f	11	ASN	Peptide
30	g	112	TYR	Sidechain

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

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

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	44 (98%)	1 (2%)	0	100	100
2	1	57/59 (97%)	50 (88%)	7 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	2	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
4	A	238/294 (81%)	221 (93%)	17 (7%)	0	100	100
5	B	213/273 (78%)	201 (94%)	12 (6%)	0	100	100
6	C	201/205 (98%)	185 (92%)	15 (8%)	1 (0%)	25	64
7	D	151/219 (69%)	138 (91%)	13 (9%)	0	100	100
8	E	165/215 (77%)	147 (89%)	18 (11%)	0	100	100
9	F	152/155 (98%)	136 (90%)	16 (10%)	0	100	100
10	G	139/142 (98%)	123 (88%)	16 (12%)	0	100	100
11	H	126/132 (96%)	112 (89%)	14 (11%)	0	100	100
12	I	99/108 (92%)	93 (94%)	6 (6%)	0	100	100
13	J	112/121 (93%)	104 (93%)	8 (7%)	0	100	100
14	K	134/139 (96%)	111 (83%)	23 (17%)	0	100	100
15	L	116/124 (94%)	100 (86%)	16 (14%)	0	100	100
16	M	58/61 (95%)	52 (90%)	6 (10%)	0	100	100
17	N	81/86 (94%)	78 (96%)	3 (4%)	0	100	100
18	O	78/94 (83%)	70 (90%)	8 (10%)	0	100	100
19	P	81/85 (95%)	73 (90%)	8 (10%)	0	100	100
20	Q	63/104 (61%)	51 (81%)	12 (19%)	0	100	100
21	R	82/87 (94%)	70 (85%)	12 (15%)	0	100	100
22	S	75/87 (86%)	68 (91%)	7 (9%)	0	100	100
23	T	51/60 (85%)	51 (100%)	0	0	100	100
24	a	283/287 (99%)	259 (92%)	24 (8%)	0	100	100
25	b	227/287 (79%)	202 (89%)	25 (11%)	0	100	100
26	c	208/212 (98%)	195 (94%)	13 (6%)	0	100	100
27	d	173/180 (96%)	158 (91%)	15 (9%)	0	100	100
28	e	174/184 (95%)	164 (94%)	10 (6%)	0	100	100
29	f	143/149 (96%)	125 (87%)	17 (12%)	1 (1%)	19	57
30	g	124/161 (77%)	109 (88%)	12 (10%)	3 (2%)	5	27
31	h	126/137 (92%)	111 (88%)	15 (12%)	0	100	100
32	i	142/146 (97%)	131 (92%)	11 (8%)	0	100	100
33	j	120/122 (98%)	114 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	k	146/151 (97%)	134 (92%)	12 (8%)	0	100	100
35	l	134/139 (96%)	121 (90%)	11 (8%)	2 (2%)	8	40
36	m	117/124 (94%)	110 (94%)	7 (6%)	0	100	100
37	n	108/116 (93%)	99 (92%)	9 (8%)	0	100	100
38	o	113/119 (95%)	106 (94%)	7 (6%)	0	100	100
39	p	112/127 (88%)	109 (97%)	3 (3%)	0	100	100
40	q	97/100 (97%)	86 (89%)	11 (11%)	0	100	100
41	r	137/159 (86%)	127 (93%)	10 (7%)	0	100	100
42	s	90/237 (38%)	85 (94%)	5 (6%)	0	100	100
43	t	109/111 (98%)	101 (93%)	8 (7%)	0	100	100
44	u	84/104 (81%)	79 (94%)	5 (6%)	0	100	100
45	v	61/65 (94%)	59 (97%)	2 (3%)	0	100	100
46	w	96/111 (86%)	90 (94%)	6 (6%)	0	100	100
47	x	42/97 (43%)	41 (98%)	1 (2%)	0	100	100
48	y	54/57 (95%)	47 (87%)	7 (13%)	0	100	100
49	z	48/53 (91%)	46 (96%)	2 (4%)	0	100	100
All	All	5820/6670 (87%)	5320 (91%)	493 (8%)	7 (0%)	50	83

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	g	115	ASN
30	g	31	SER
30	g	86	VAL
6	C	146	ALA
29	f	12	LEU

### 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%)	35 (100%)	0	100	100
4	A	212/262 (81%)	211 (100%)	1 (0%)	86	89
5	B	180/232 (78%)	179 (99%)	1 (1%)	84	88
6	C	181/183 (99%)	179 (99%)	2 (1%)	70	80
7	D	123/178 (69%)	122 (99%)	1 (1%)	79	85
8	E	150/196 (76%)	149 (99%)	1 (1%)	81	87
9	F	131/132 (99%)	130 (99%)	1 (1%)	79	85
10	G	123/124 (99%)	122 (99%)	1 (1%)	79	85
11	H	111/115 (96%)	108 (97%)	3 (3%)	40	58
12	I	95/99 (96%)	95 (100%)	0	100	100
13	J	91/97 (94%)	90 (99%)	1 (1%)	70	80
14	K	117/120 (98%)	116 (99%)	1 (1%)	75	83
15	L	100/105 (95%)	99 (99%)	1 (1%)	73	82
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
22	S	70/77 (91%)	69 (99%)	1 (1%)	62	75
23	T	49/56 (88%)	48 (98%)	1 (2%)	50	68
24	a	241/243 (99%)	238 (99%)	3 (1%)	67	78
25	b	186/233 (80%)	185 (100%)	1 (0%)	86	89
26	c	182/184 (99%)	180 (99%)	2 (1%)	70	80
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%)	123 (100%)	0	100	100
30	g	101/129 (78%)	93 (92%)	8 (8%)	10	29
31	h	102/110 (93%)	101 (99%)	1 (1%)	73	82
32	i	126/128 (98%)	126 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	112 (99%)	1 (1%)	75	83
36	m	105/109 (96%)	105 (100%)	0	100	100
37	n	96/99 (97%)	95 (99%)	1 (1%)	73	82
38	o	101/105 (96%)	100 (99%)	1 (1%)	73	82
39	p	100/108 (93%)	99 (99%)	1 (1%)	73	82
40	q	90/91 (99%)	90 (100%)	0	100	100
41	r	116/132 (88%)	116 (100%)	0	100	100
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%)	68 (99%)	1 (1%)	62	75
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%)	44 (92%)	4 (8%)	9	27
49	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5093/5751 (89%)	5051 (99%)	42 (1%)	77	85

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	g	112	TYR
39	p	84	LYS
30	g	115	ASN
35	l	45	ARG
46	w	62	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
26	c	167	ASN
41	r	110	ASN
27	d	37	ASN
34	k	36	GLN

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Mol	Chain	Res	Type
49	z	24	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	964 (33%)	41 (1%)
51	4	103/108 (95%)	42 (40%)	3 (2%)
52	5	1490/1520 (98%)	427 (28%)	6 (0%)
53	7	75/76 (98%)	32 (42%)	2 (2%)
53	8	75/76 (98%)	32 (42%)	2 (2%)
All	All	4618/4687 (98%)	1497 (32%)	54 (1%)

5 of 1497 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	9	G
50	3	12	A
50	3	14	U
50	3	15	A
50	3	16	A

5 of 54 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	3	2164	G
50	3	2562	U
52	5	1158	A
50	3	2180	U
50	3	2395	U

## 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 ⓘ

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.

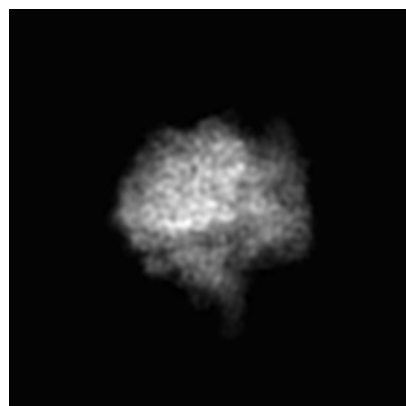
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13272. These allow visual inspection of the internal detail of the map and identification of artifacts.

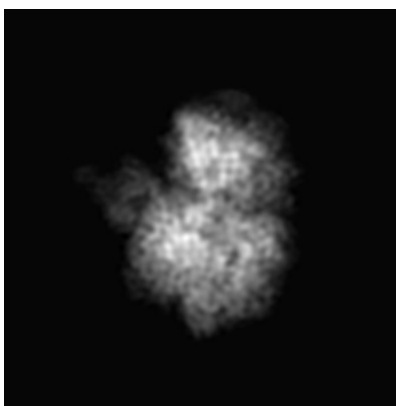
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

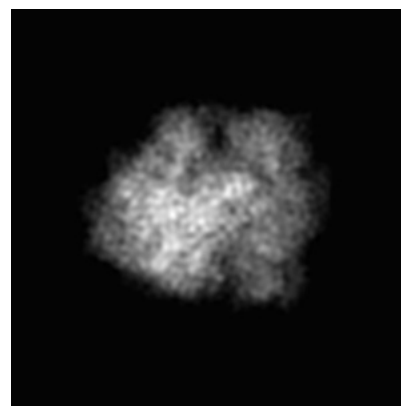
#### 6.1.1 Primary map



X

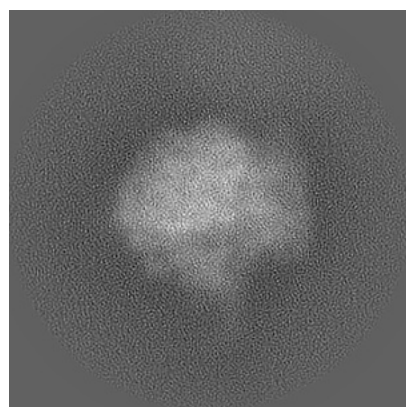


Y

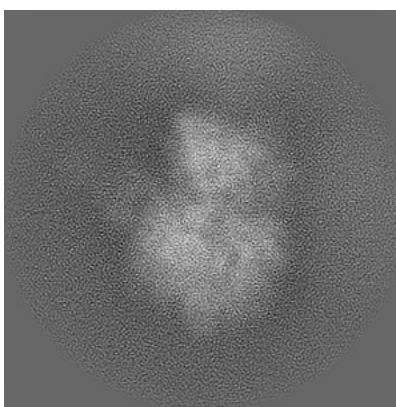


Z

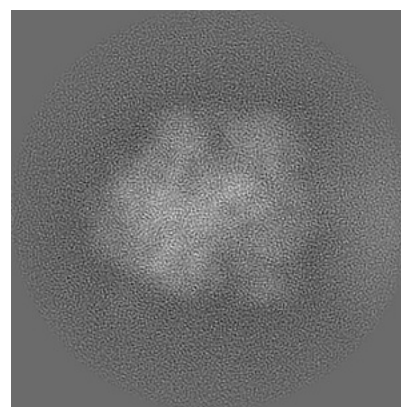
#### 6.1.2 Raw map



X



Y

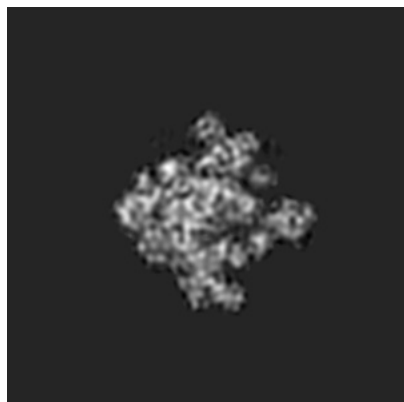


Z

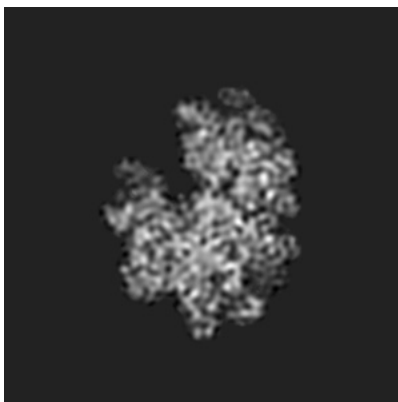
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

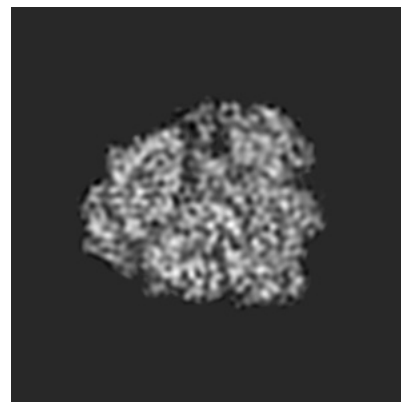
### 6.2.1 Primary map



X Index: 128

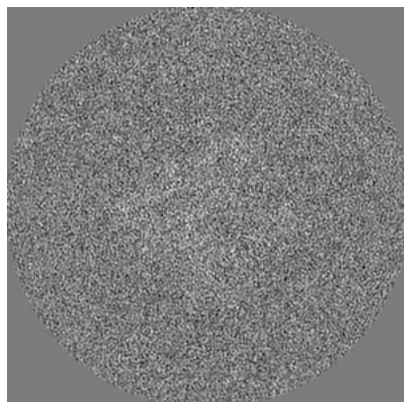


Y Index: 128

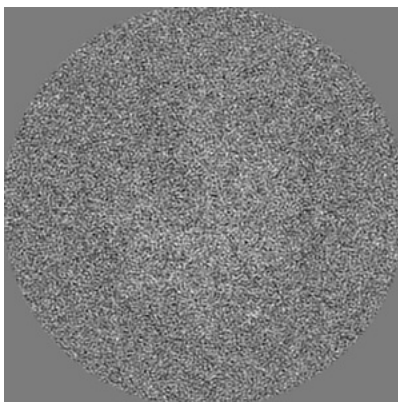


Z Index: 128

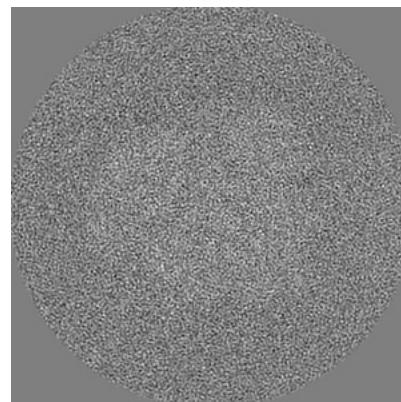
### 6.2.2 Raw map



X Index: 128



Y Index: 128



Z Index: 128

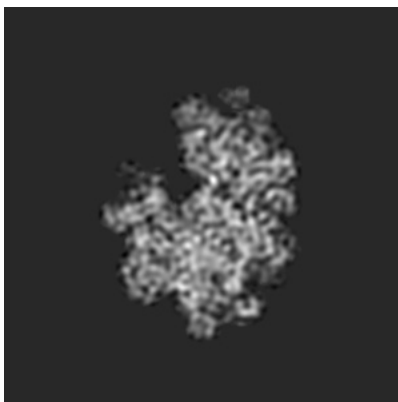
The images above show central slices of the map in three orthogonal directions.

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

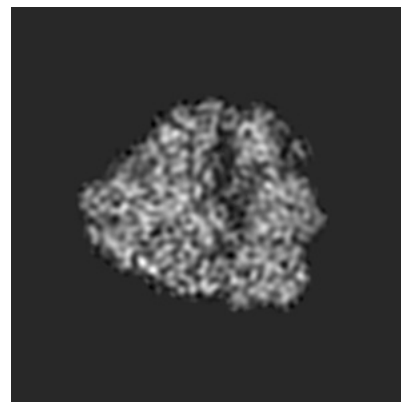
### 6.3.1 Primary map



X Index: 104

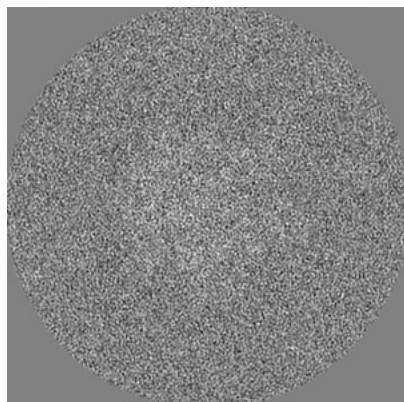


Y Index: 126

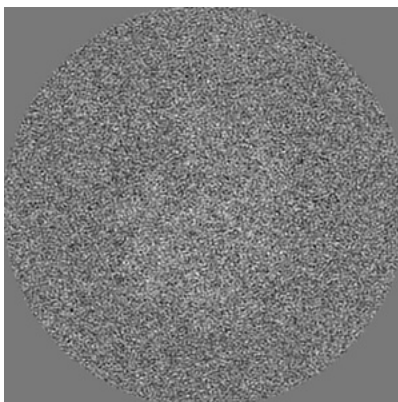


Z Index: 122

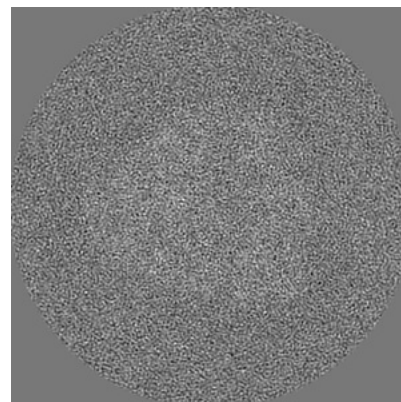
### 6.3.2 Raw map



X Index: 121



Y Index: 123



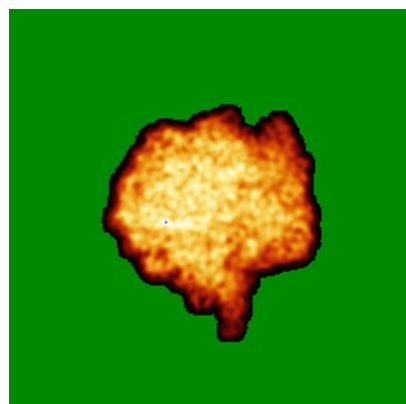
Z Index: 123

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

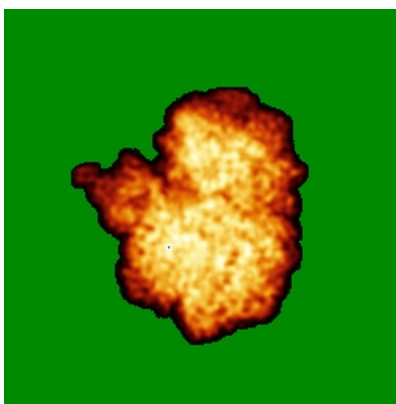


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

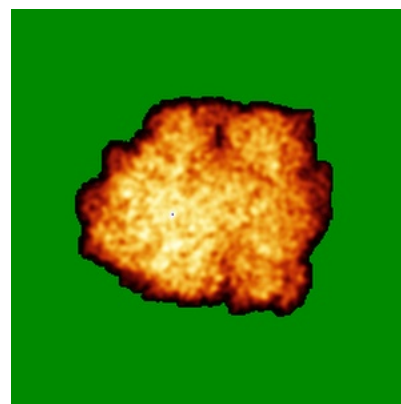
### 6.4.1 Primary map



X

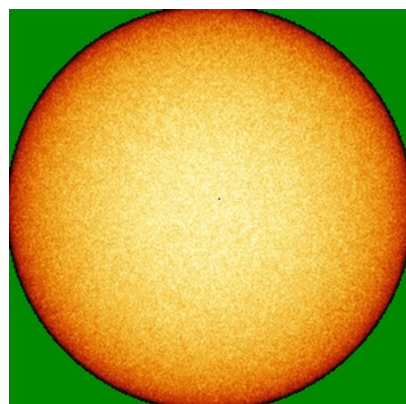


Y

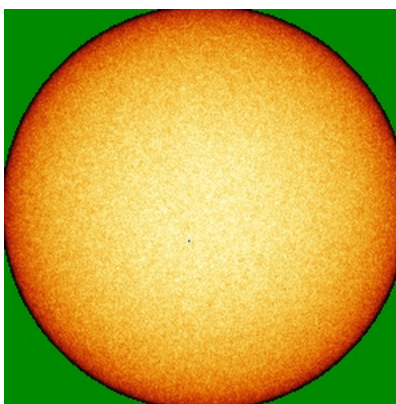


Z

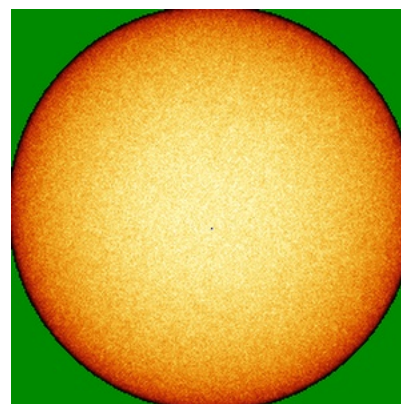
### 6.4.2 Raw map



X



Y



Z

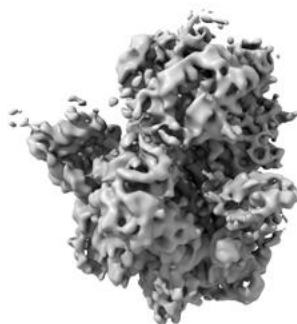
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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

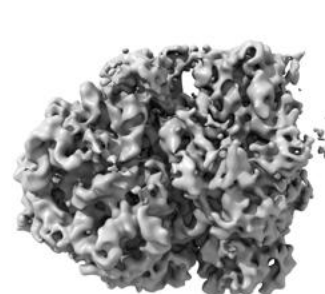
### 6.5.1 Primary map



X



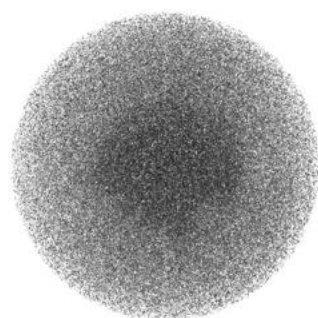
Y



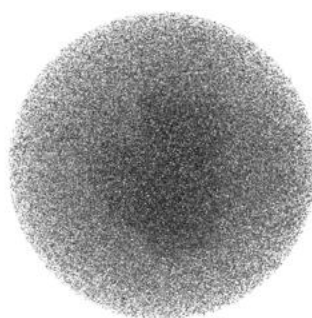
Z

The images above show the 3D surface view of the map at the recommended contour level 0.47. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

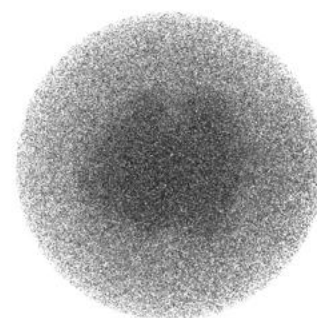
### 6.5.2 Raw map



X



Y



Z

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



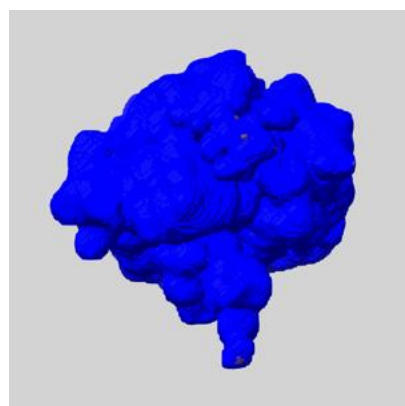
## 6.6 Mask visualisation [i](#)

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

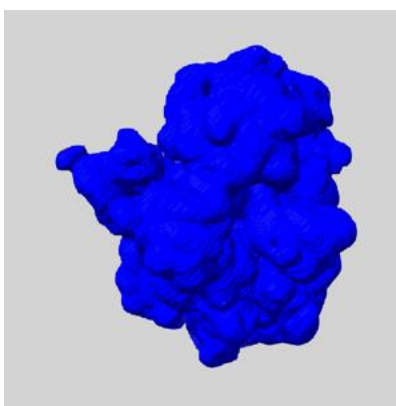
A mask typically either:

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

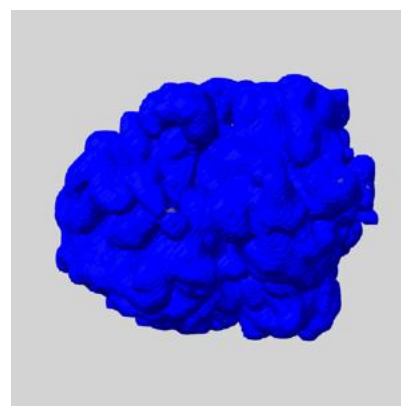
### 6.6.1 emd\_13272\_msk\_1.map [i](#)



X



Y

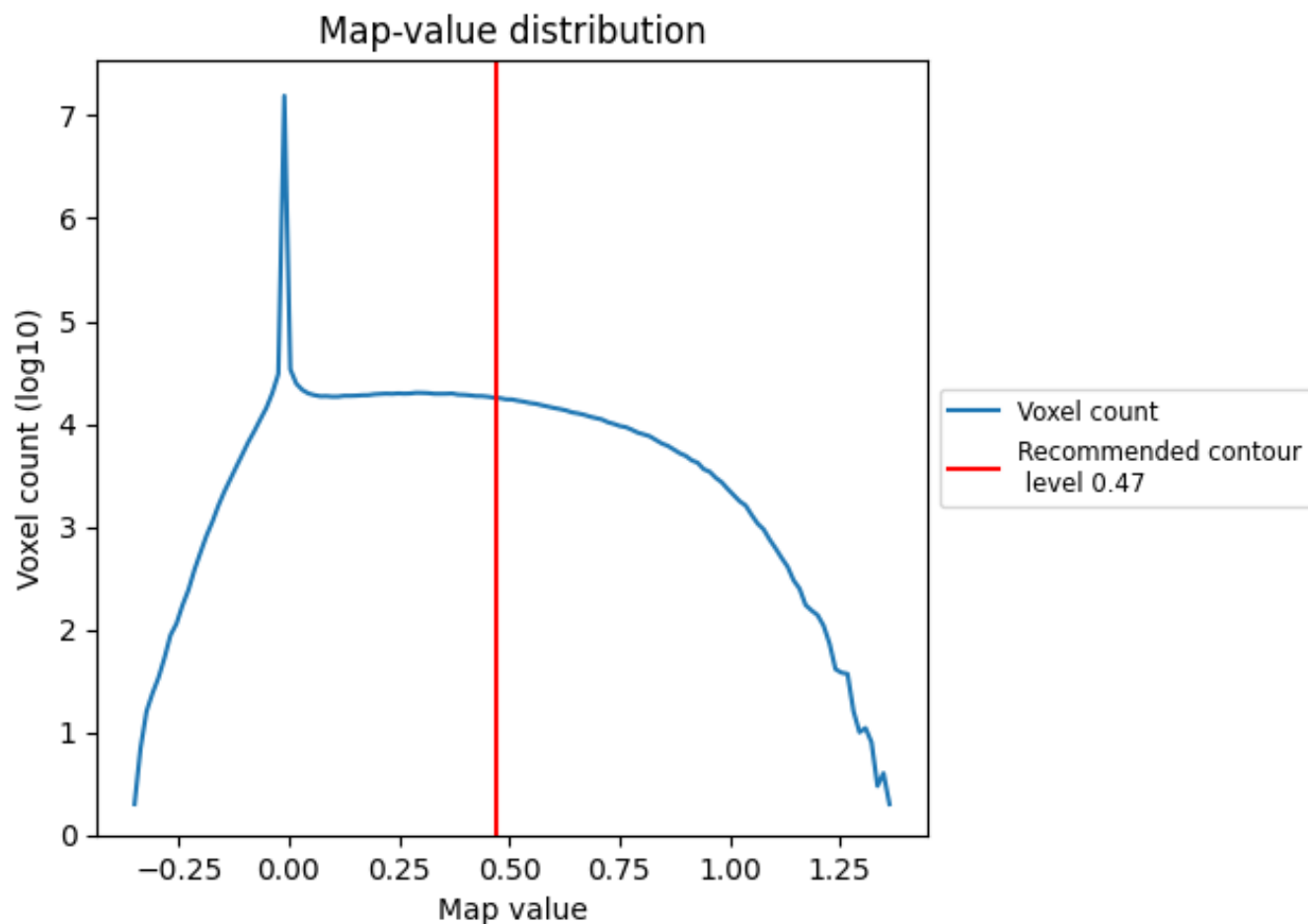


Z

## 7 Map analysis [i](#)

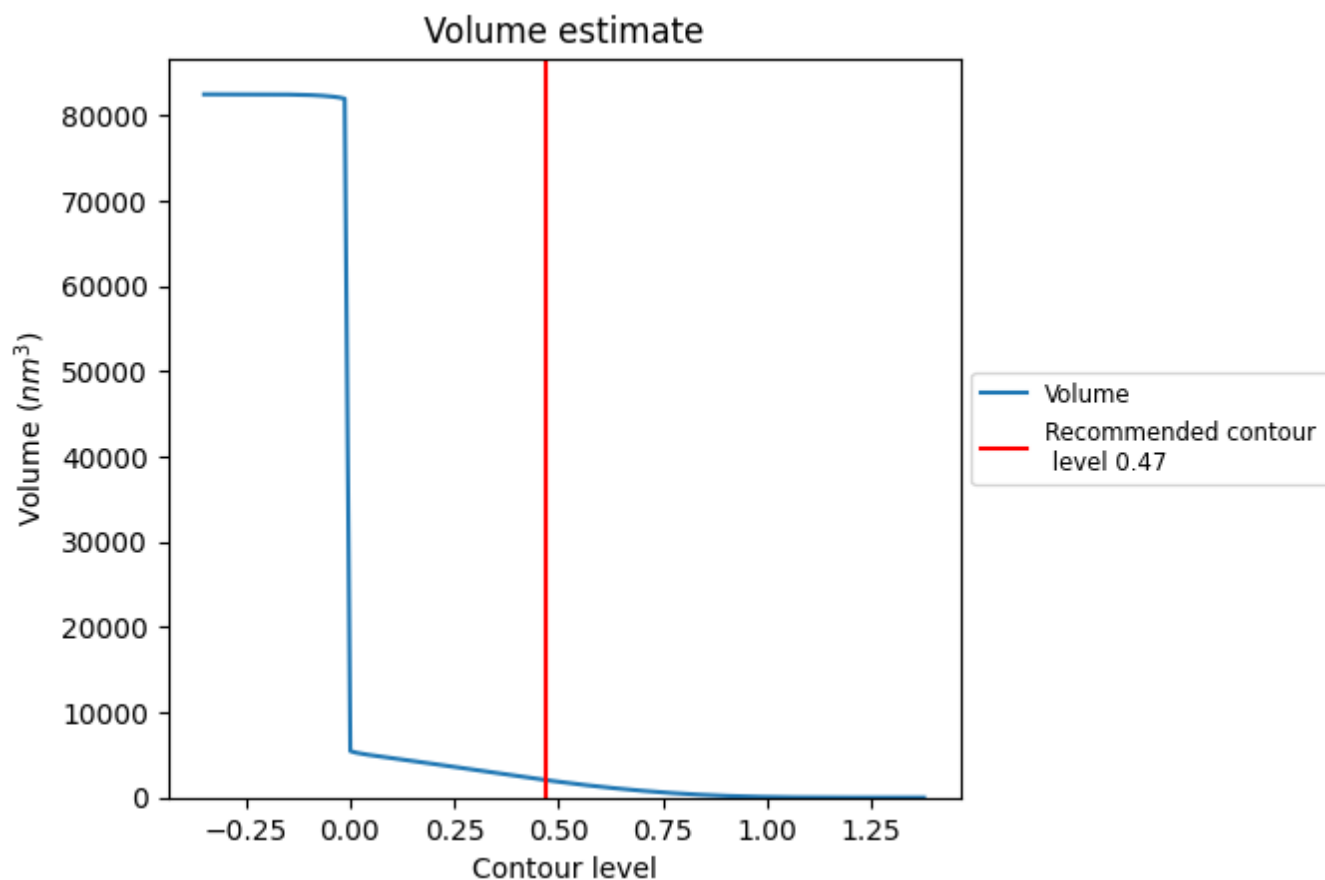
This section contains the results of statistical analysis of the map.

### 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.

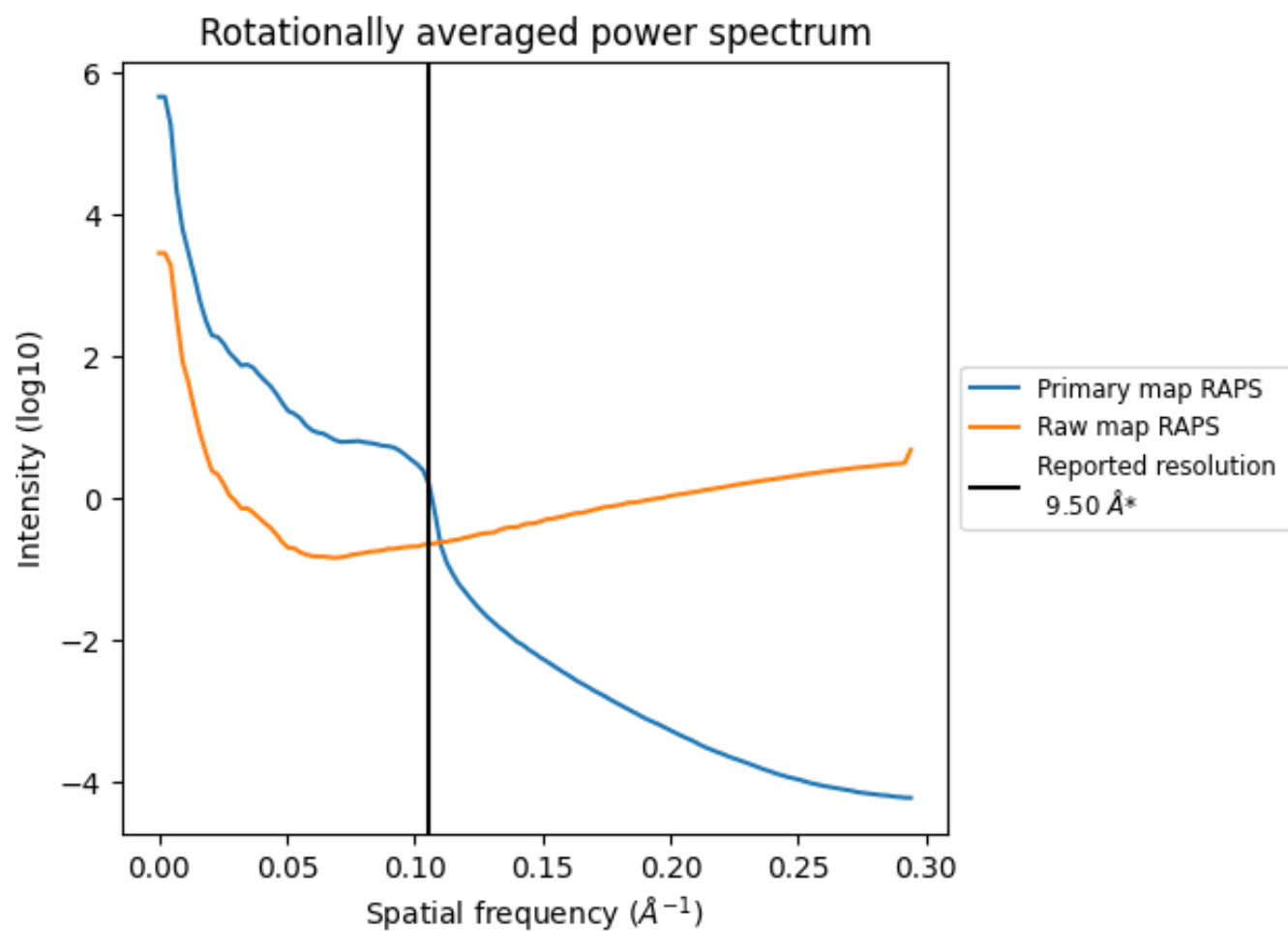
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2047 nm<sup>3</sup>; this corresponds to an approximate mass of 1849 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 ⓘ

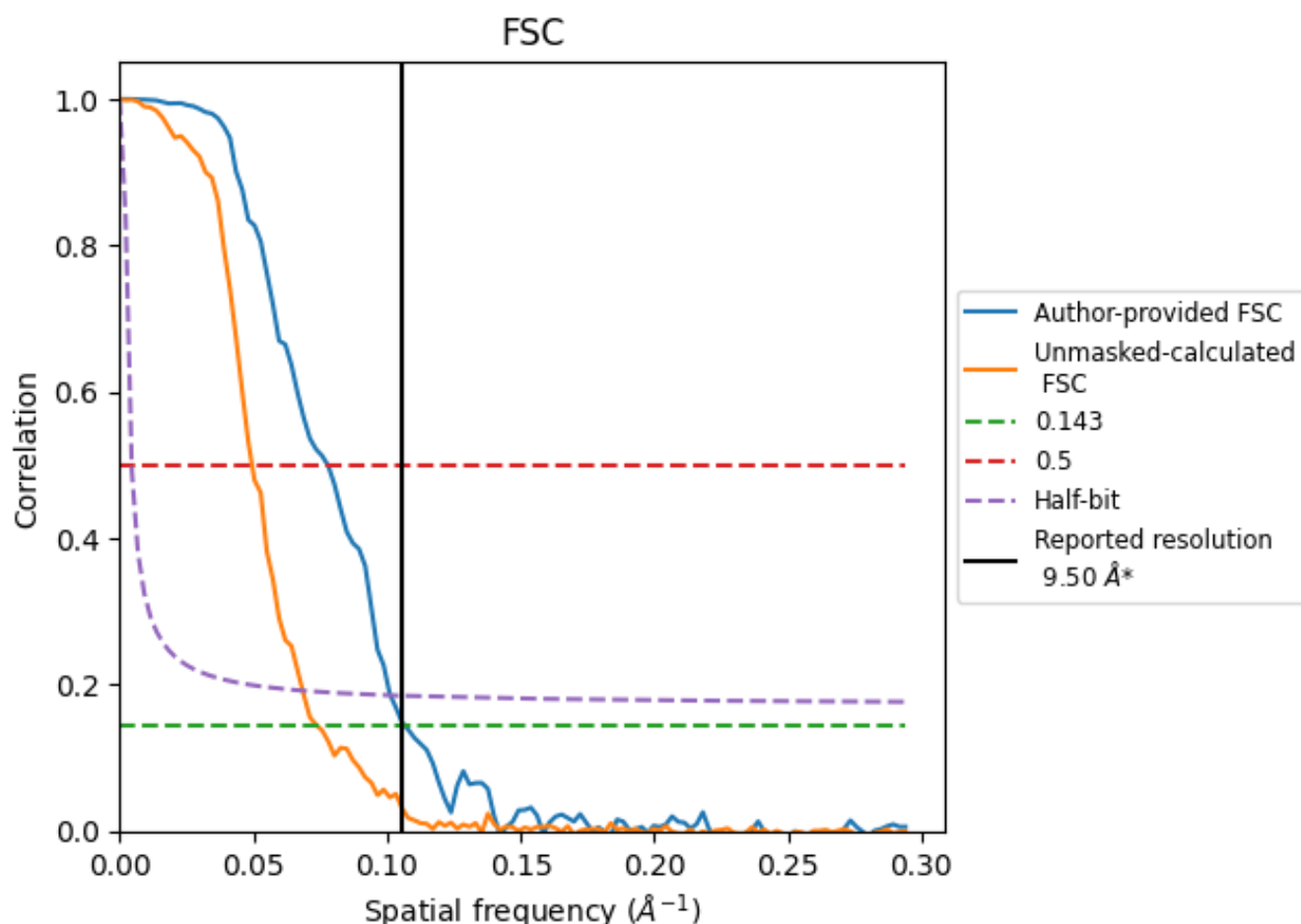


\*Reported resolution corresponds to spatial frequency of 0.105  $\text{\AA}^{-1}$

## 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  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

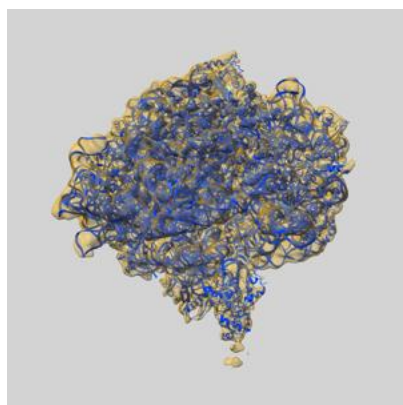
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.50	-	-
Author-provided FSC curve	9.36	12.85	9.87
Unmasked-calculated*	13.51	20.16	14.60

\*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 13.51 differs from the reported value 9.5 by more than 10 %

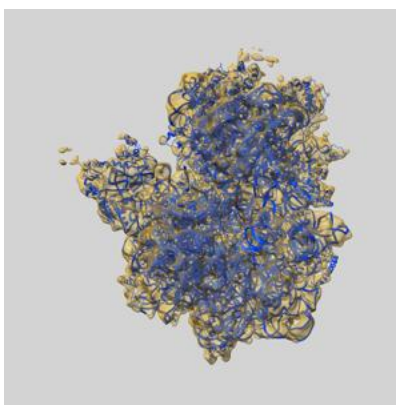
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13272 and PDB model 7PAH. Per-residue inclusion information can be found in section [3](#) on page [13](#).

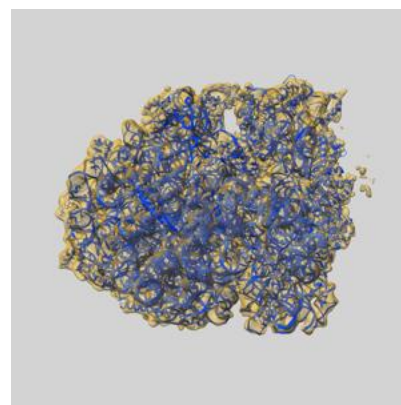
### 9.1 Map-model overlay [i](#)



X



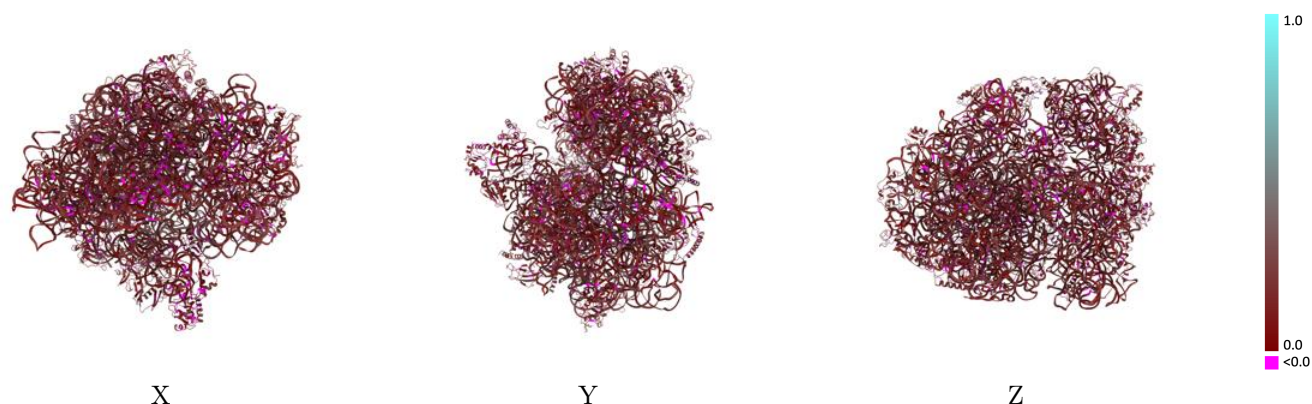
Y



Z

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

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



The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

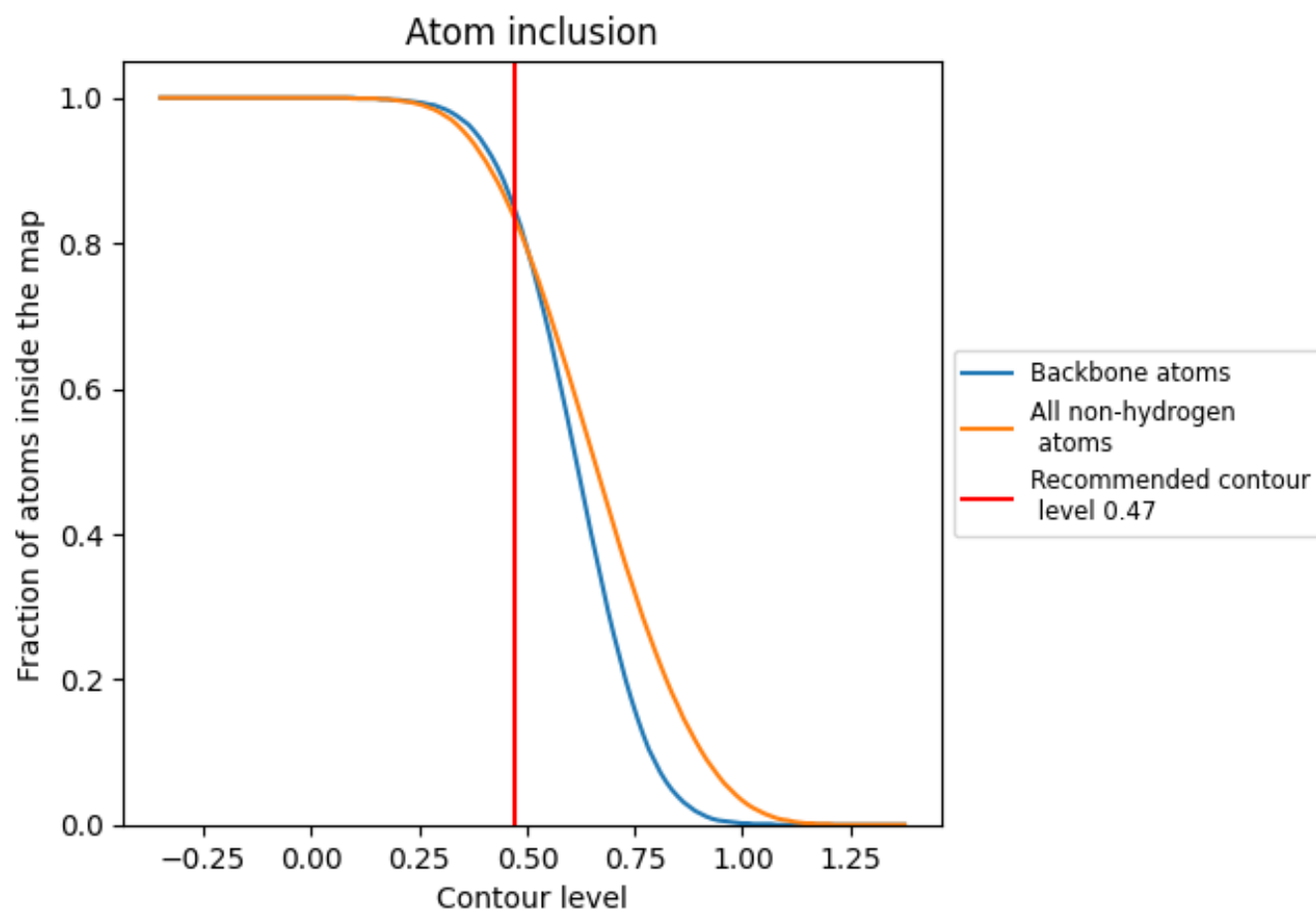
## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.47).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ









































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

Chain	Atom inclusion	Q-score
All	 0.8370	 0.1540
0	 0.8000	 0.1280
1	 0.6820	 0.0980
2	 0.6930	 0.0720
3	 0.9490	 0.1660
4	 0.9580	 0.1780
5	 0.9400	 0.1620
7	 0.8490	 0.1580
8	 0.4730	 0.0800
A	 0.5210	 0.1520
B	 0.5520	 0.1430
C	 0.6010	 0.1330
D	 0.5270	 0.1270
E	 0.5290	 0.1530
F	 0.6000	 0.1340
G	 0.6130	 0.1350
H	 0.6380	 0.1320
I	 0.5760	 0.1330
J	 0.6050	 0.1220
K	 0.6500	 0.1080
L	 0.5860	 0.1350
M	 0.6550	 0.0800
N	 0.6830	 0.1560
O	 0.7380	 0.1420
P	 0.5980	 0.1100
Q	 0.6880	 0.1390
R	 0.5120	 0.0960
S	 0.7560	 0.1590
T	 0.6790	 0.1810
a	 0.7020	 0.1170
b	 0.6570	 0.1230
c	 0.6790	 0.1340
d	 0.6300	 0.1310
e	 0.5650	 0.1610
f	 0.2570	 0.1390



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Chain	Atom inclusion	Q-score
g	 0.4640	 0.1110
h	 0.3630	 0.1130
i	 0.7270	 0.1430
j	 0.5720	 0.1330
k	 0.6870	 0.1260
l	 0.7210	 0.1290
m	 0.6680	 0.1350
n	 0.7650	 0.1530
o	 0.6110	 0.1440
p	 0.7700	 0.1230
q	 0.6570	 0.1280
r	 0.7510	 0.1450
s	 0.6330	 0.1510
t	 0.5740	 0.1380
u	 0.7500	 0.1070
v	 0.7430	 0.1300
w	 0.6950	 0.1770
x	 0.5450	 0.1410
y	 0.7170	 0.1110
z	 0.7480	 0.1230