



wwPDB EM Validation Summary Report ⓘ

Oct 8, 2022 – 11:11 pm BST

PDB ID : 7PAL
EMDB ID : EMD-13276
Title : 70S ribosome with A- and P-site tRNAs in Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-07-30
Resolution : 4.70 Å(reported)
Based on initial models : 3J9W, 4V7C, 7OOD, 7OOC

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

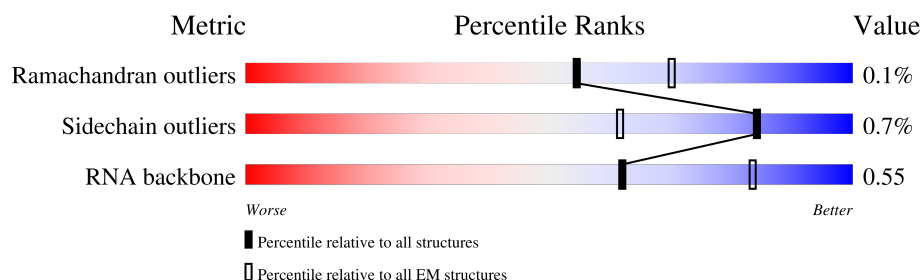
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

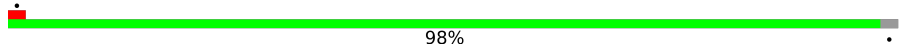
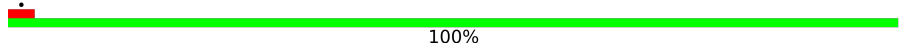
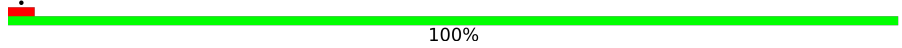


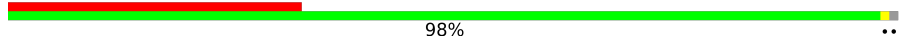

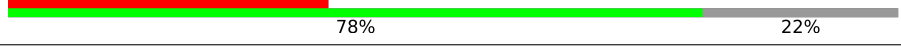
The reported resolution of this entry is 4.70 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	0	48	
2	1	59	
3	2	37	
4	A	294	
5	B	273	
6	C	205	
7	D	219	
8	E	215	

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Mol	Chain	Length	Quality of chain
9	F	155	43% 99%
10	G	142	25% 99%
11	H	132	36% 96%
12	I	108	34% 94%
13	J	121	24% 94%
14	K	139	15% 96%
15	L	124	49% 95%
16	M	61	13% 98%
17	N	86	23% 97%
18	O	94	26% 83%
19	P	85	32% 98%
20	Q	104	17% 62%
21	R	87	40% 95%
22	S	87	17% 85%
23	T	60	25% 88%
24	Z	6	83%
25	a	287	7% 99%
26	b	287	6% 80%
27	c	212	13% 99%
28	d	180	49% 96%
29	e	184	27% 95%
30	f	149	83% 96%
31	g	161	64% 70%
32	h	137	87% 93%
33	i	146	11% 98%

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Mol	Chain	Length	Quality of chain
34	j	122	
35	k	151	
36	l	139	
37	m	124	
38	n	116	
39	o	119	
40	p	127	
41	q	100	
42	r	159	
43	s	237	
44	t	111	
45	u	104	
46	v	65	
47	w	111	
48	x	97	
49	y	57	
50	z	53	
51	3	2907	
52	4	108	
53	5	1520	
54	6	76	
54	7	76	
55	Y	9	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 146334 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 nascent peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	5	Total	C	N	O	S	0	0
			31	20	5	6			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 55 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Y	9	Total	C	N	O	P	0	0
			183	84	29	62	8		

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.

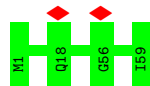
- Molecule 1: 50S ribosomal protein L34

Chain 0:  98%



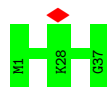
- Molecule 2: 50S ribosomal protein L35

Chain 1:  100%




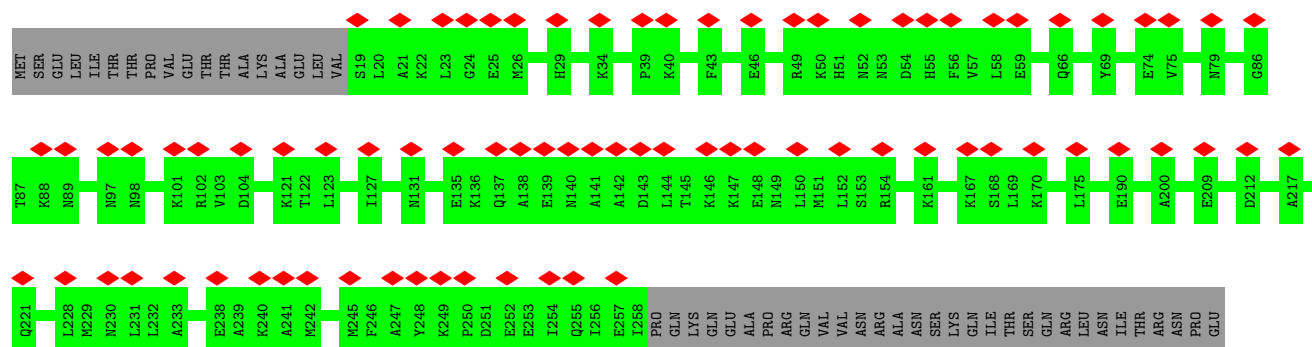
- Molecule 3: 50S ribosomal protein L36

Chain 2:  100%




- Molecule 4: 30S ribosomal protein S2

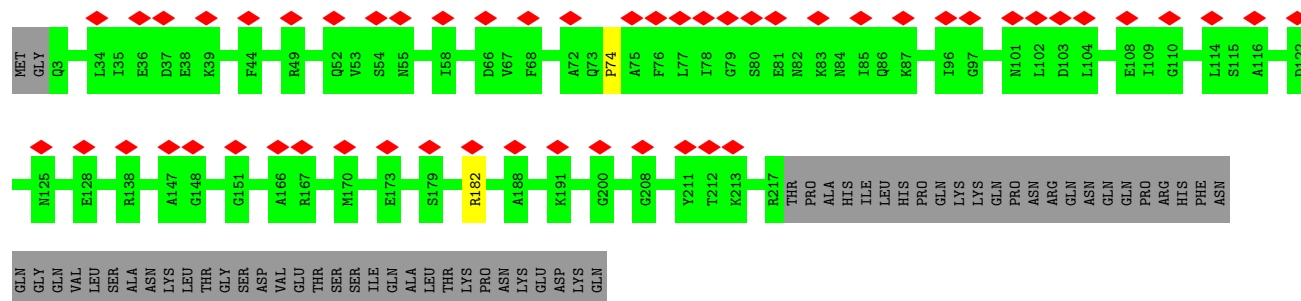
Chain A:  27% 82% 18%



VAL
LEU
THR
ARG
GLU

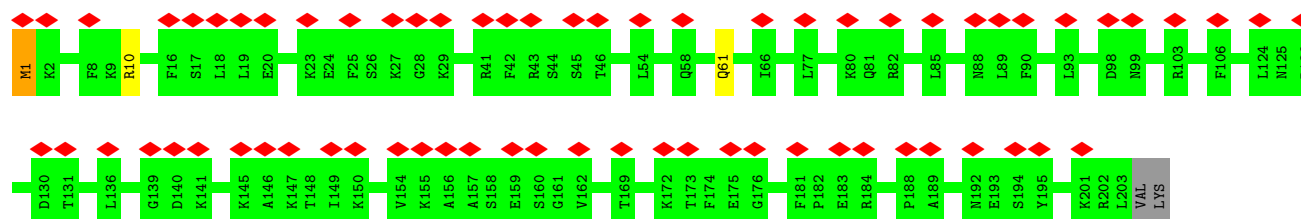
• Molecule 5: 30S ribosomal protein S3

Chain B: 



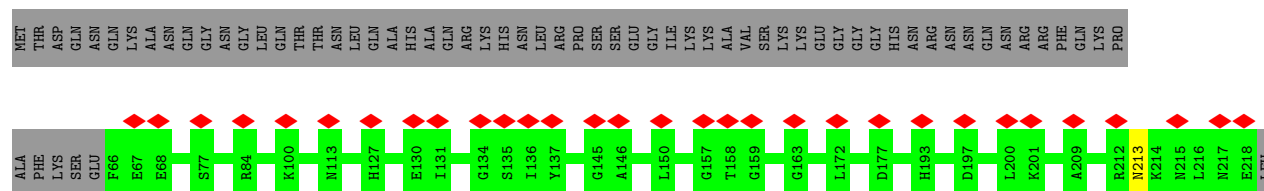
• Molecule 6: 30S ribosomal protein S4

Chain C: 




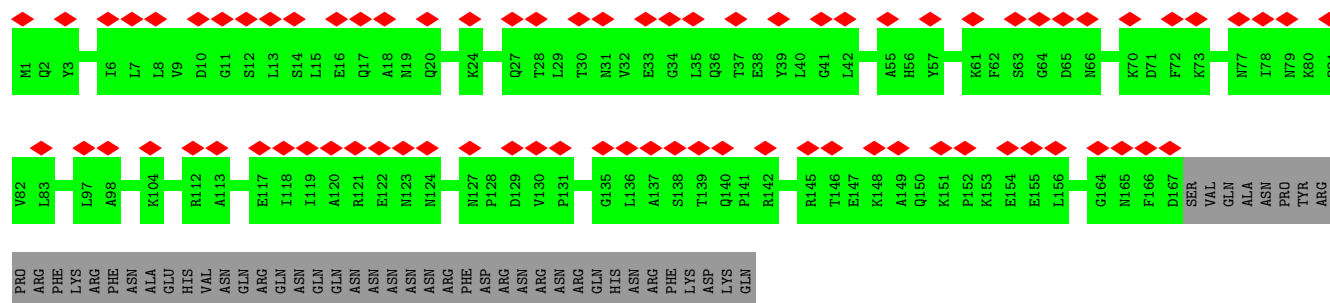
• Molecule 7: 30S ribosomal protein S5

Chain D: 

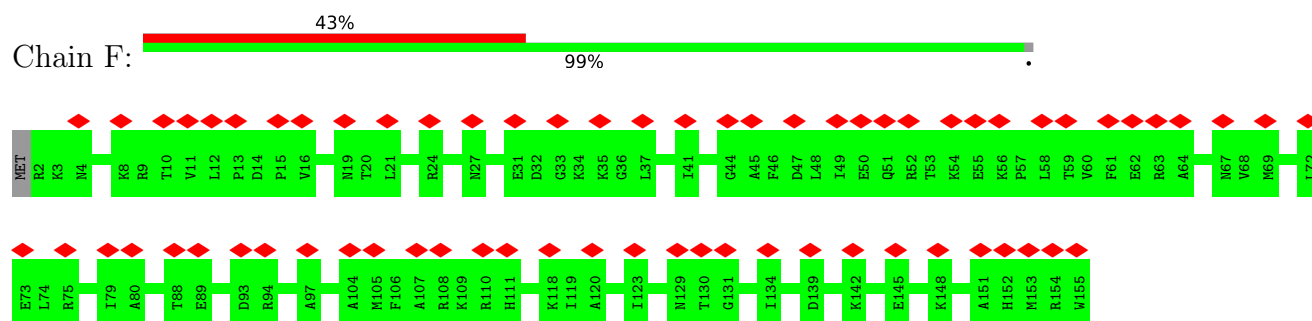


• Molecule 8: 30S ribosomal protein S6

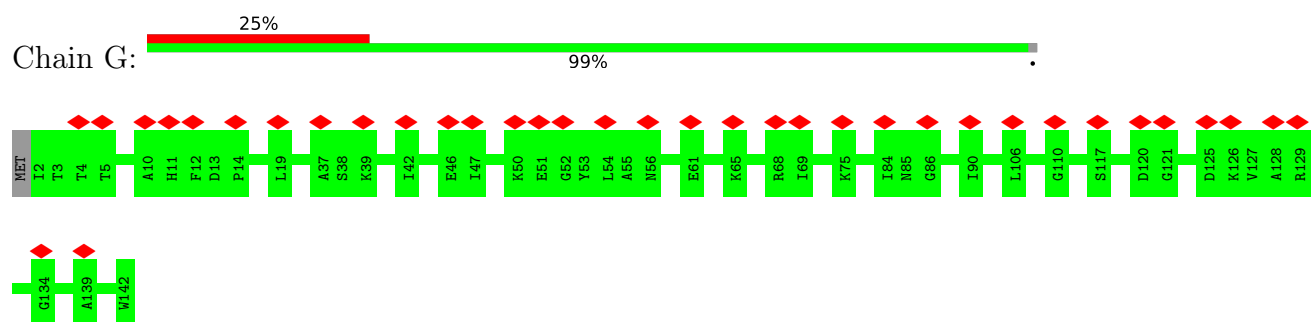
Chain E: 



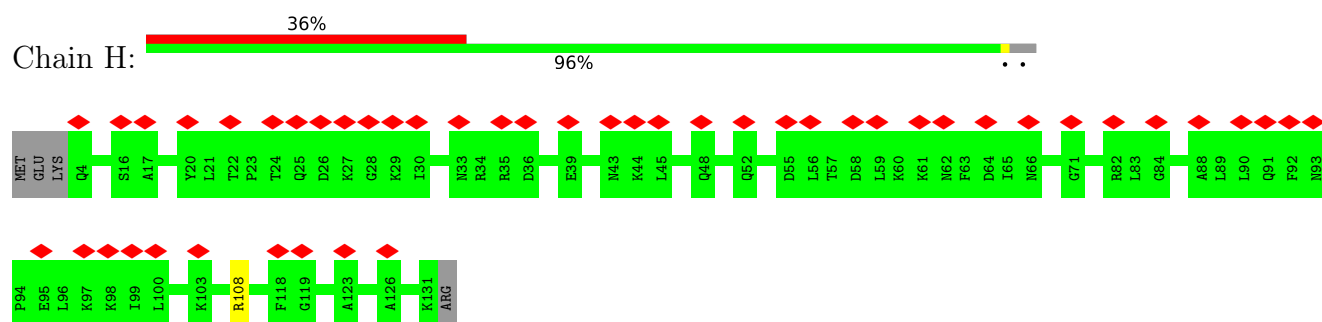
- Molecule 9: 30S ribosomal protein S7



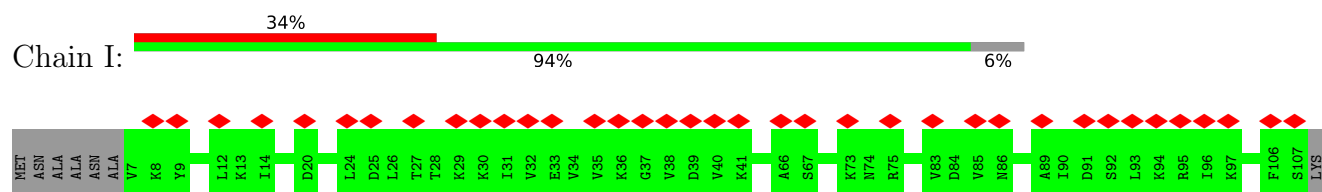
- Molecule 10: 30S ribosomal protein S8



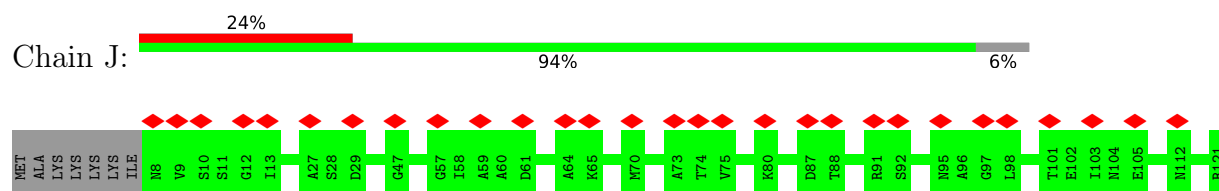
- Molecule 11: 30S ribosomal protein S9



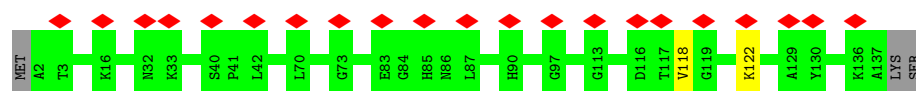
- Molecule 12: 30S ribosomal protein S10



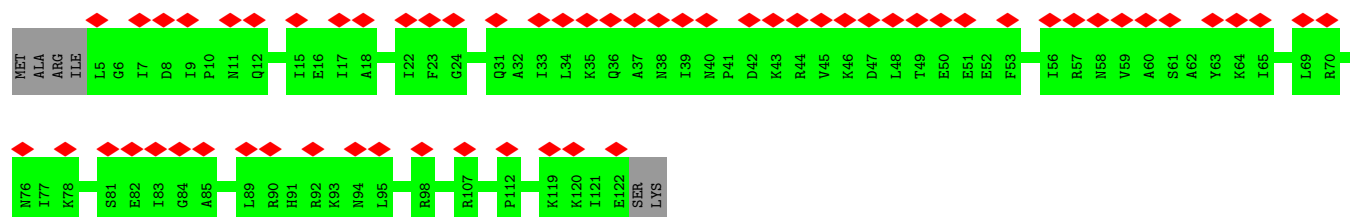
- Molecule 13: 30S ribosomal protein S11



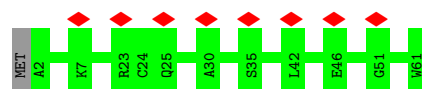
- Molecule 14: 30S ribosomal protein S12



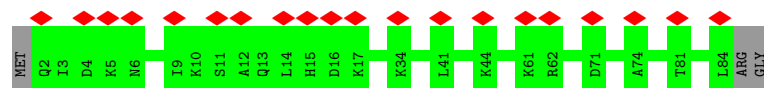
- Molecule 15: 30S ribosomal protein S13



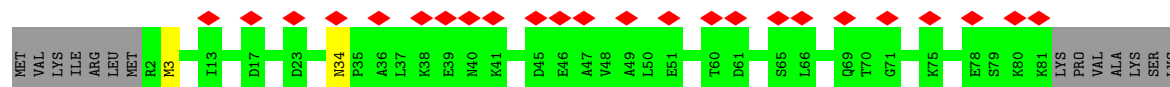
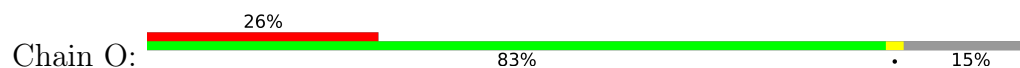
- Molecule 16: 30S ribosomal protein S14 type Z



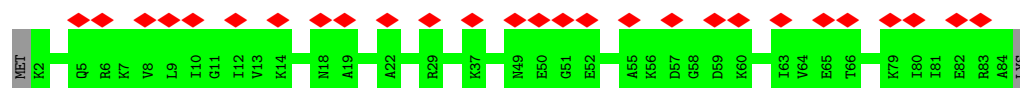
- Molecule 17: 30S ribosomal protein S15



- Molecule 18: 30S ribosomal protein S16

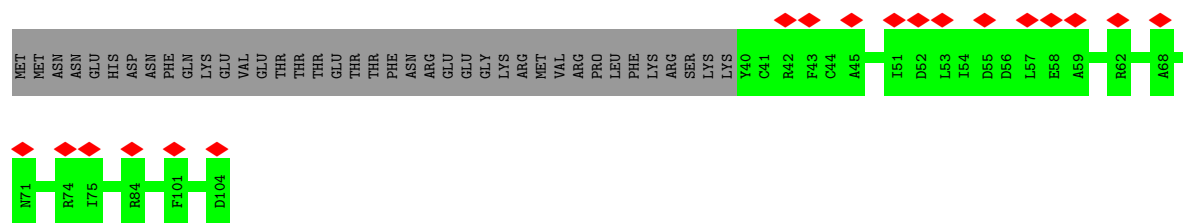


- Molecule 19: 30S ribosomal protein S17

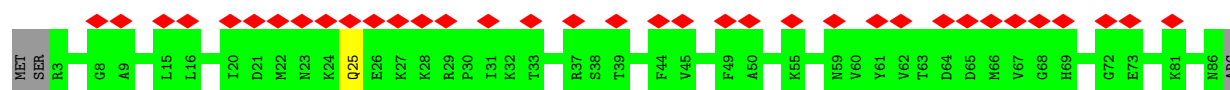
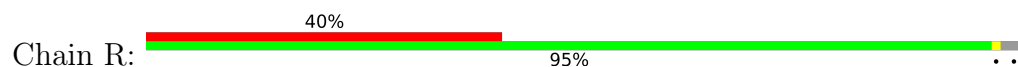


- Molecule 20: 30S ribosomal protein S18

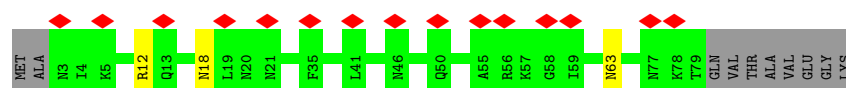
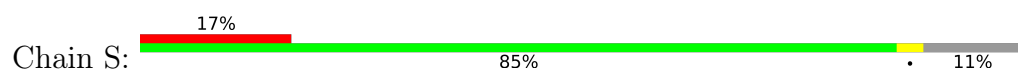




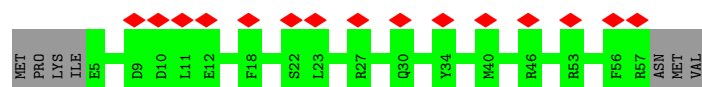
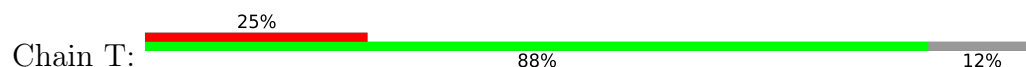
- Molecule 21: 30S ribosomal protein S19



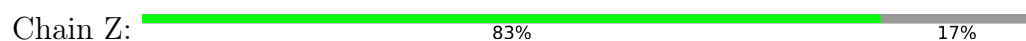
- Molecule 22: 30S ribosomal protein S20



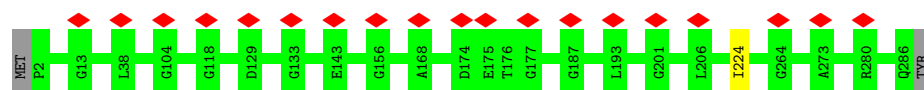
- Molecule 23: 30S ribosomal protein S21



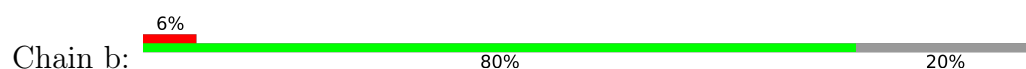
- Molecule 24: nascent peptide

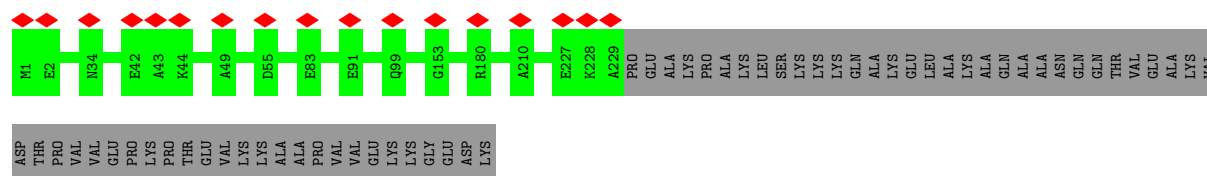


- Molecule 25: 50S ribosomal protein L2



- Molecule 26: 50S ribosomal protein L3

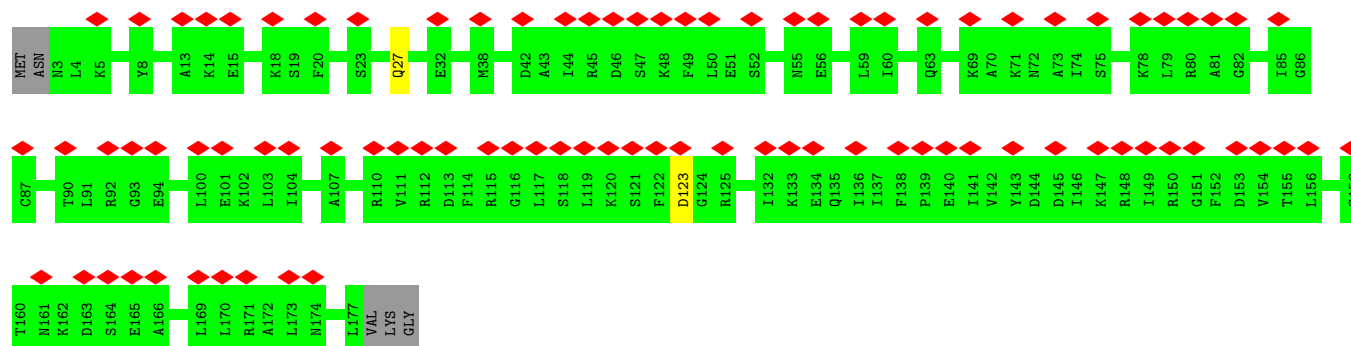




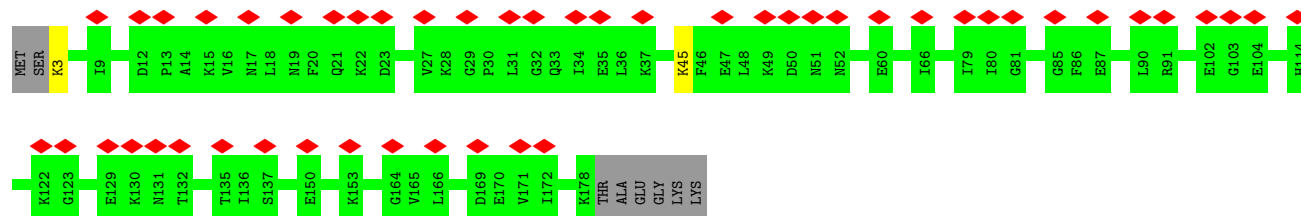
• Molecule 27: 50S ribosomal protein L4



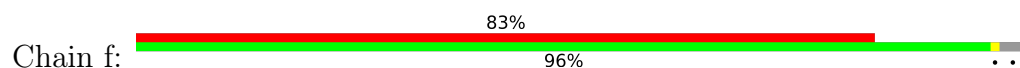
• Molecule 28: 50S ribosomal protein L5

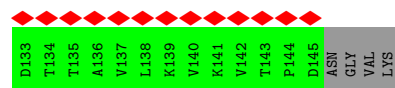


• Molecule 29: 50S ribosomal protein L6

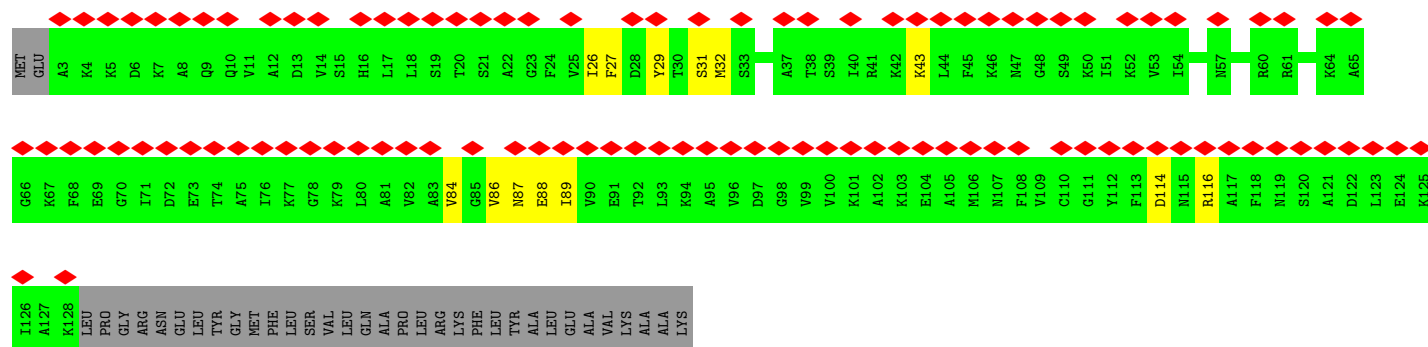


• Molecule 30: 50S ribosomal protein L9

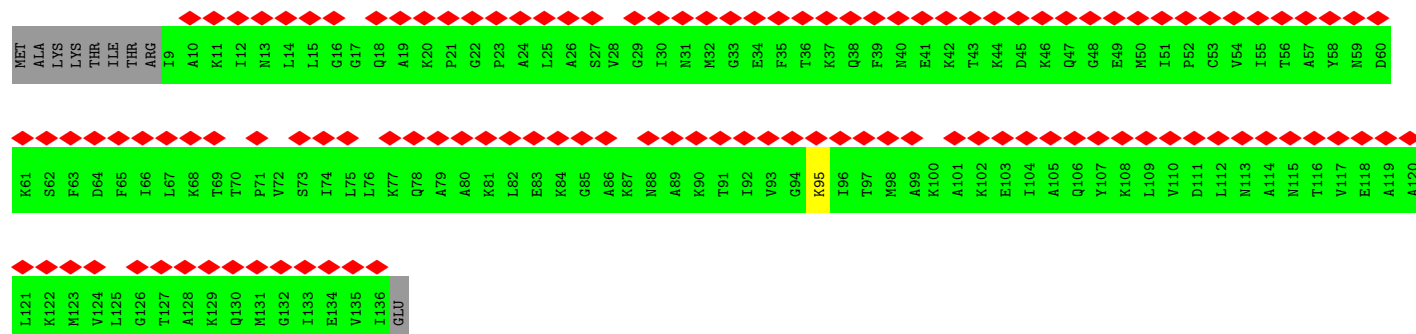
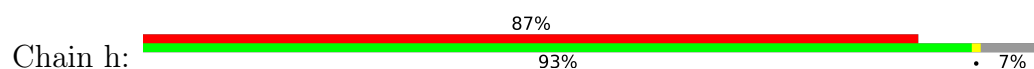




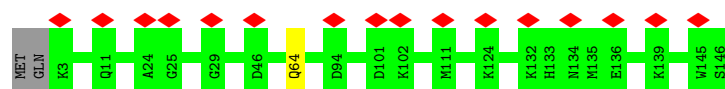
• Molecule 31: 50S ribosomal protein L10



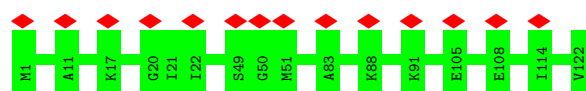
• Molecule 32: 50S ribosomal protein L11



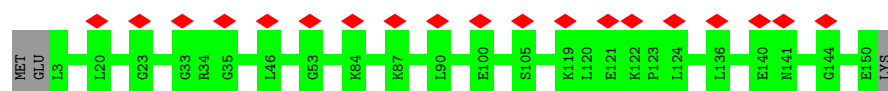
• Molecule 33: 50S ribosomal protein L13



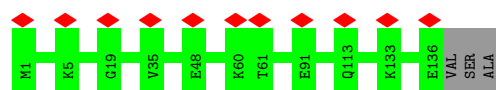
• Molecule 34: 50S ribosomal protein L14



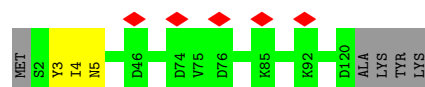
• Molecule 35: 50S ribosomal protein L15



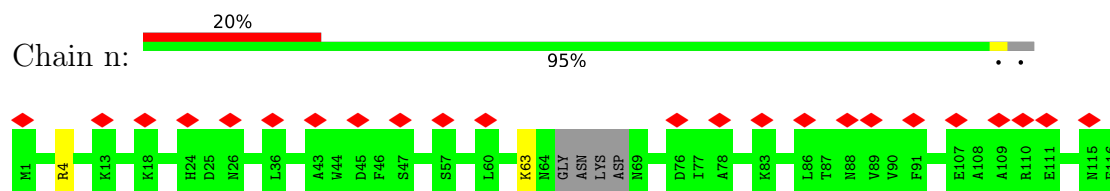
- Molecule 36: 50S ribosomal protein L16



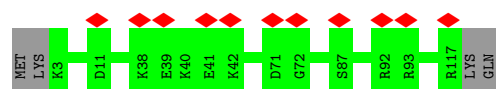
- Molecule 37: 50S ribosomal protein L17



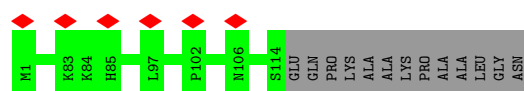
- Molecule 38: 50S ribosomal protein L18



- Molecule 39: 50S ribosomal protein L19

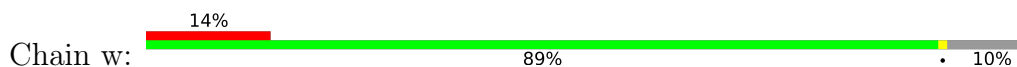


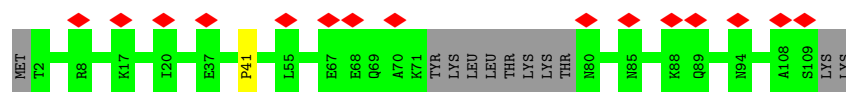
- Molecule 40: 50S ribosomal protein L20



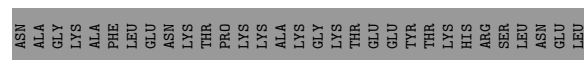
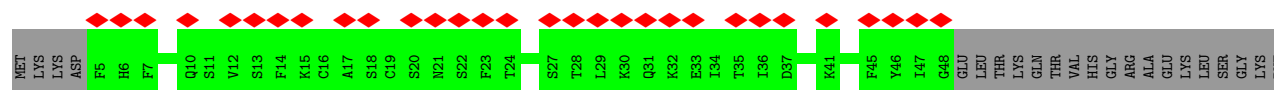
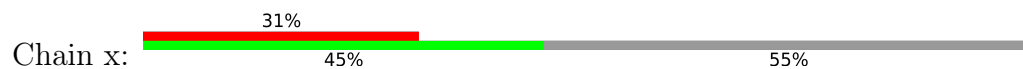
- Molecule 41: 50S ribosomal protein L21



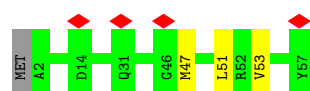




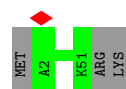
- Molecule 48: 50S ribosomal protein L31



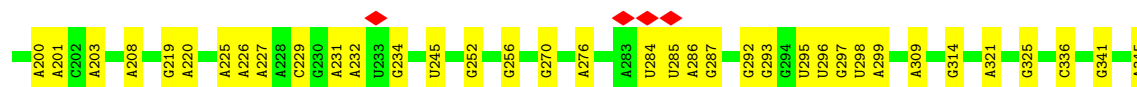
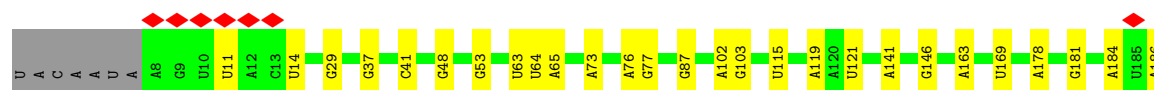
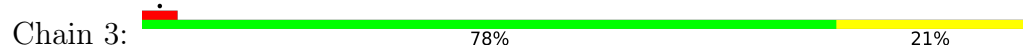
- Molecule 49: 50S ribosomal protein L32



- Molecule 50: 50S ribosomal protein L33 1



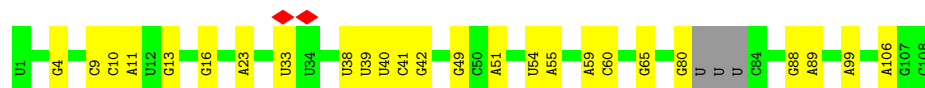
- Molecule 51: 23S ribosomal RNA



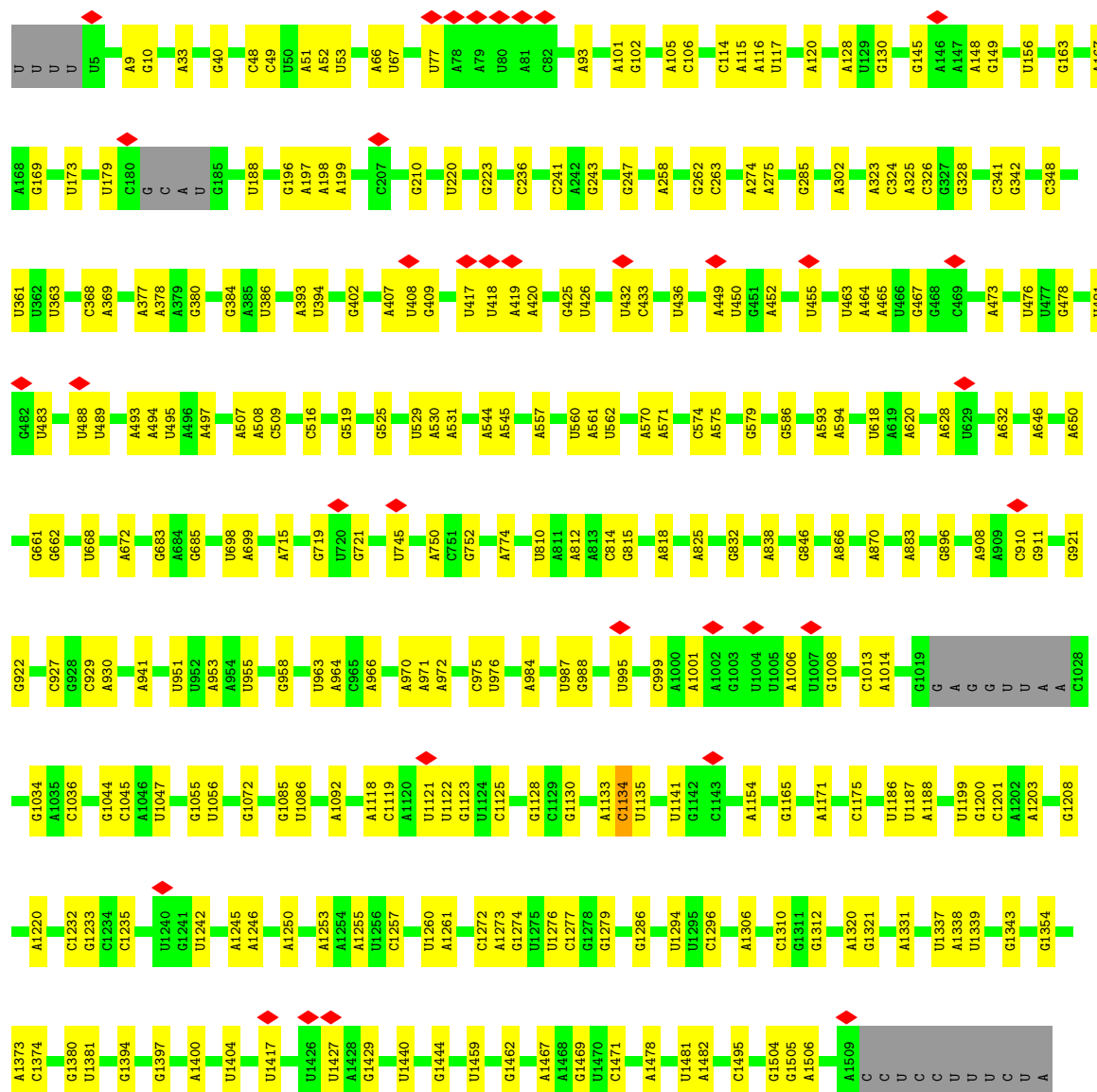
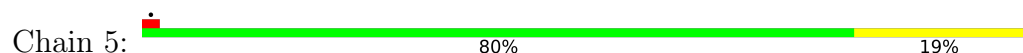
A3668	A2343	A2511	A2344	A2181	A1959	A1751	G1580	C1444	A1298	G1166	U1049	U896
G2669	A2344	U2512	C2182	C2182	A1962	A1752	U1581	U1445	G1301	U1167	G1057	C901
G2676	G2353	U2513	U2183	U2183	U1962	U1764	G1582	A1446	G1301	U1446	G1057	U902
A2687	A2354	A2184	A2184	A2184	U1977	G1765	G1583	U1453	U1301	A1168	U1058	A903
U2690	C2355	U2125	C2185	C2185	U1978	A1766	U1584	U1456	U1304	C1170	G1059	C904
C2691	U2356	A2126	C2186	C2186	U1979	A1769	U1585	C1456	A1312	G1173	U1060	U905
G2540	A2366	G2127	C2187	C2187	U1998	A1770	U1586	U1466	A1328	U1176	G906	G906
C2697	G2369	U2128	U2188	U2188	A1999	A1771	U1587	U1467	C1317	A1177	U1068	G914
C2721	G2391	U2129	U2189	U2189	U2000	A1780	U1588	U1480	A1329	U1186	G1069	G917
G2722	U2392	A2130	G2190	G2190	A2009	A1788	A1589	A1481	U1330	A1204	A1080	C921
G2737	C2393	G2131	U2191	U2191	A2010	A1788	U1592	U1482	C1333	A1081	A1081	C922
A2741	G2399	A2133	U2192	U2192	C2013	A1791	U1612	G1483	U1337	A1208	A1082	A
A2750	G2194	C2135	U2193	U2193	A2030	C1807	U1618	U1487	G1337	U1209	U1093	C
C2751	U2195	A2136	U2195	U2195	A2038	C1808	A1619	U1494	U1338	U1210	U1094	U
G2752	G2198	A2137	U2198	U2198	G2039	A1809	C1622	U1502	U1340	U1211	U1095	A
A2756	A2206	U2138	A2206	A2206	A2040	U1820	G1640	A1502	C1342	G1215	U1096	G928
C2760	A2207	C2139	A2207	A2207	C2041	A1641	A1641	G1507	C1349	U1216	G1097	U932
U2764	U2219	G2140	U2219	U2219	C2043	G1642	G1642	G1508	U1360	U1217	G1098	A933
A2765	U2221	U2142	U2221	U2221	G2050	U1644	A1644	U1509	U1361	G1218	U1099	U944
G2769	A2233	G2143	U2233	U2233	G2053	A1828	C1651	A1510	U1369	U1219	U1101	A947
A2786	G2246	A2145	U2246	U2246	C2057	A1836	A1652	U1513	U1375	U1234	A1102	A948
U2787	G2247	A2146	U2247	U2247	G2058	G1842	A1681	U1514	G1376	U1235	A1103	C949
A2789	A2276	U2147	U2276	U2276	G2059	C1845	C1682	A1515	C1378	G1242	A1105	U952
G2798	A2286	U2148	U2286	U2286	C2062	A1846	G1683	C1518	C1379	A1250	A1106	G953
U2799	U2291	U2149	U2291	U2291	G2063	A1946	A1688	C1523	U1380	G1251	C1107	A981
U2800	U2294	C2150	U2294	U2294	A2067	A1873	A1694	U1533	A1381	G1255	A1108	G982
C2801	A2295	G2151	U2295	U2295	G2068	A1891	C1697	A1534	A1382	G1257	C1114	A996
G2803	C2305	U2153	U2305	U2305	A2069	A1896	U1707	A1535	A1393	G1265	G1115	G997
C2804	G2312	A2154	U2312	U2312	G2076	A1903	G1708	A1541	A1396	G1266	A1123	A1008
A2805	U2313	G2155	U2313	U2313	A2084	G1906	U1714	U1557	A1406	U1267	A1124	A1009
G2806	G2316	A2157	U2316	U2316	U2099	U1715	A1715	A1558	U1407	U1268	G1125	G1010
A2807	A2317	C2158	U2317	U2317	G2100	A1716	A1716	A1559	G1408	C1269	U1126	A1016
A2808	U2318	U2159	U2318	U2318	G2106	G1913	U1723	U	C1414	A1277	U1129	A1019
A2810	A2319	U2160	U2319	U2319	U2111	A1914	A1728	G	A1423	G1278	A1130	A1024
G2811	U2327	G2161	U2327	U2327	A2112	A1920	A1728	A	U1424	A1281	A1131	G1025
U2812	A2330	U2162	U2330	U2330	U2113	G1936	A1735	G	U1425	G1282	C1132	A1026
A2813	G2333	C2163	U2333	U2333	C2114	G1937	A1735	U	C1426	A1283	U1137	A1032
A2823	U2334	G2165	U2334	U2334	A2115	U1938	A1735	A	A1431	U1285	C1139	A1033
A2824	A2335	A2166	U2335	U2335	U2116	A1944	A1735	C	U1434	G1287	G1147	G1039
U2837	U2340	C2167	U2340	U2340	G2117	G1952	G1747	A	A1437	A1295	U1151	A1045
U2853	G2341	G2169	U2341	U2341	U2118	A2119	U1748	G1570		G1296	U1151	A1048
	U2342	A2170	A2170	A2170	A2120	G2120				U1297	U1164	
		A2171	A2171	A2171							G1160	
		A2172	A2172	A2172								
		G2173	G2173	G2173								
		U2174	U2174	U2174								
		U2175	U2175	U2175								
		G2176	G2176	G2176								
		G2177	G2177	G2177								
		A2178	A2178	A2178								
		A2179	A2179	A2179								
		U2180	U2180	U2180								



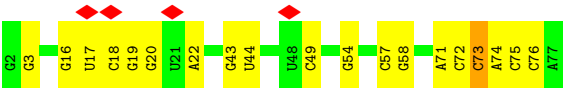
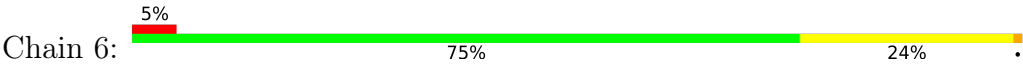
• Molecule 52: 5S ribosomal RNA



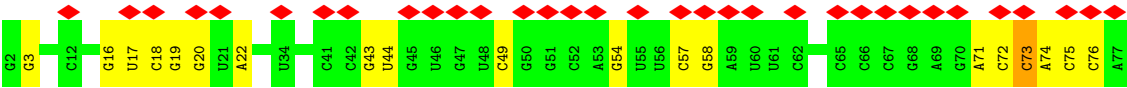
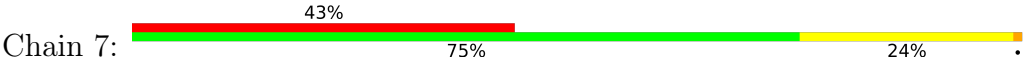
• Molecule 53: 16S ribosomal RNA



• Molecule 54: tRNA-Phe



• Molecule 54: tRNA-Phe



• Molecule 55: mRNA



There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	32086	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	2.977	Depositor
Minimum map value	-1.334	Depositor
Average map value	0.025	Depositor
Map value standard deviation	0.150	Depositor
Recommended contour level	0.65	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	0.23	0/383	0.46	0/504
2	1	0.23	0/484	0.48	0/637
3	2	0.23	0/306	0.47	0/401
4	A	0.26	0/1954	0.47	0/2642
5	B	0.26	0/1721	0.52	1/2323 (0.0%)
6	C	0.27	0/1691	0.47	1/2267 (0.0%)
7	D	0.24	0/1188	0.50	0/1593
8	E	0.25	0/1384	0.46	0/1867
9	F	0.27	0/1266	0.49	0/1700
10	G	0.25	0/1126	0.50	0/1517
11	H	0.25	0/1044	0.49	0/1395
12	I	0.25	0/820	0.53	0/1103
13	J	0.25	0/844	0.46	0/1136
14	K	0.27	0/1094	0.54	0/1468
15	L	0.26	0/962	0.49	0/1289
16	M	0.25	0/483	0.43	0/643
17	N	0.23	0/679	0.44	0/907
18	O	0.24	0/659	0.44	0/885
19	P	0.24	0/684	0.46	0/913
20	Q	0.25	0/545	0.46	0/730
21	R	0.27	0/698	0.48	0/936
22	S	0.24	0/631	0.46	0/838
23	T	0.26	0/475	0.43	0/621
24	Z	0.23	0/30	0.69	0/41
25	a	0.24	0/2267	0.47	1/3044 (0.0%)
26	b	0.26	0/1795	0.50	0/2412
27	c	0.25	0/1671	0.48	1/2246 (0.0%)
28	d	0.25	0/1409	0.50	1/1894 (0.1%)
29	e	0.26	0/1420	0.51	0/1912
30	f	0.24	0/1183	0.43	0/1587
31	g	0.35	0/969	0.57	0/1295
32	h	0.25	0/968	0.48	0/1298
33	i	0.28	0/1186	0.51	0/1592
34	j	0.26	0/953	0.48	0/1275

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	k	0.25	0/1170	0.50	0/1559
36	l	0.25	0/1104	0.48	0/1481
37	m	0.29	0/973	0.53	0/1309
38	n	0.25	0/897	0.49	0/1198
39	o	0.24	0/948	0.50	0/1262
40	p	0.27	0/961	0.49	0/1278
41	q	0.26	0/828	0.55	2/1111 (0.2%)
42	r	0.25	0/1077	0.46	0/1441
43	s	0.26	0/732	0.50	0/988
44	t	0.26	0/879	0.51	0/1165
45	u	0.25	0/665	0.48	0/884
46	v	0.23	0/519	0.46	0/695
47	w	0.26	0/826	0.48	1/1104 (0.1%)
48	x	0.26	0/353	0.47	0/474
49	y	0.30	0/457	0.56	0/601
50	z	0.24	0/412	0.51	0/547
51	3	0.19	0/69073	0.77	16/107710 (0.0%)
52	4	0.18	0/2505	0.74	0/3902
53	5	0.18	0/35768	0.75	8/55764 (0.0%)
54	6	0.20	0/1808	0.82	1/2817 (0.0%)
54	7	0.20	0/1808	0.82	1/2817 (0.0%)
55	Y	0.15	0/203	0.69	0/313
All	All	0.21	0/158938	0.70	34/237331 (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
21	R	0	1
31	g	0	1
37	m	0	1
All	All	0	4

There are no bond length outliers.

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	3	567	U	C2-N1-C1'	7.90	127.18	117.70
53	5	361	U	C2-N1-C1'	7.84	127.11	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	w	41	PRO	CA-N-CD	-7.65	100.79	111.50
51	3	567	U	N1-C2-O2	7.30	127.91	122.80
51	3	1507	G	O4'-C1'-N9	6.77	113.62	108.20

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	C	1	MET	Peptide
21	R	25	GLN	Peptide
31	g	114	ASP	Peptide
37	m	3	TYR	Peptide

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%)	43 (96%)	2 (4%)	0	100	100
2	1	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
3	2	35/37 (95%)	35 (100%)	0	0	100	100
4	A	238/294 (81%)	214 (90%)	24 (10%)	0	100	100
5	B	213/273 (78%)	196 (92%)	17 (8%)	0	100	100
6	C	201/205 (98%)	187 (93%)	14 (7%)	0	100	100
7	D	151/219 (69%)	145 (96%)	6 (4%)	0	100	100
8	E	165/215 (77%)	144 (87%)	21 (13%)	0	100	100
9	F	152/155 (98%)	143 (94%)	9 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	G	139/142 (98%)	126 (91%)	13 (9%)	0	100	100
11	H	126/132 (96%)	111 (88%)	15 (12%)	0	100	100
12	I	99/108 (92%)	89 (90%)	10 (10%)	0	100	100
13	J	112/121 (93%)	110 (98%)	2 (2%)	0	100	100
14	K	134/139 (96%)	119 (89%)	15 (11%)	0	100	100
15	L	116/124 (94%)	104 (90%)	12 (10%)	0	100	100
16	M	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
17	N	81/86 (94%)	78 (96%)	3 (4%)	0	100	100
18	O	78/94 (83%)	72 (92%)	6 (8%)	0	100	100
19	P	81/85 (95%)	75 (93%)	6 (7%)	0	100	100
20	Q	63/104 (61%)	55 (87%)	8 (13%)	0	100	100
21	R	82/87 (94%)	70 (85%)	12 (15%)	0	100	100
22	S	75/87 (86%)	73 (97%)	2 (3%)	0	100	100
23	T	51/60 (85%)	49 (96%)	2 (4%)	0	100	100
24	Z	3/6 (50%)	2 (67%)	1 (33%)	0	100	100
25	a	283/287 (99%)	264 (93%)	19 (7%)	0	100	100
26	b	227/287 (79%)	216 (95%)	11 (5%)	0	100	100
27	c	208/212 (98%)	198 (95%)	10 (5%)	0	100	100
28	d	173/180 (96%)	157 (91%)	16 (9%)	0	100	100
29	e	174/184 (95%)	161 (92%)	13 (8%)	0	100	100
30	f	143/149 (96%)	131 (92%)	12 (8%)	0	100	100
31	g	124/161 (77%)	112 (90%)	11 (9%)	1 (1%)	19	60
32	h	126/137 (92%)	121 (96%)	5 (4%)	0	100	100
33	i	142/146 (97%)	135 (95%)	7 (5%)	0	100	100
34	j	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
35	k	146/151 (97%)	134 (92%)	12 (8%)	0	100	100
36	l	134/139 (96%)	130 (97%)	4 (3%)	0	100	100
37	m	117/124 (94%)	109 (93%)	7 (6%)	1 (1%)	17	56
38	n	108/116 (93%)	100 (93%)	8 (7%)	0	100	100
39	o	113/119 (95%)	104 (92%)	9 (8%)	0	100	100
40	p	112/127 (88%)	107 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	q	97/100 (97%)	90 (93%)	7 (7%)	0	100	100
42	r	137/159 (86%)	127 (93%)	10 (7%)	0	100	100
43	s	90/237 (38%)	84 (93%)	6 (7%)	0	100	100
44	t	109/111 (98%)	104 (95%)	5 (5%)	0	100	100
45	u	84/104 (81%)	80 (95%)	4 (5%)	0	100	100
46	v	61/65 (94%)	57 (93%)	4 (7%)	0	100	100
47	w	96/111 (86%)	92 (96%)	4 (4%)	0	100	100
48	x	42/97 (43%)	34 (81%)	8 (19%)	0	100	100
49	y	54/57 (95%)	49 (91%)	4 (7%)	1 (2%)	8	40
50	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	5823/6676 (87%)	5407 (93%)	413 (7%)	3 (0%)	54	85

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
37	m	4	ILE
49	y	53	VAL
31	g	87	ASN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	A	212/262 (81%)	212 (100%)	0	100	100
5	B	180/232 (78%)	179 (99%)	1 (1%)	86	92
6	C	181/183 (99%)	179 (99%)	2 (1%)	73	85
7	D	123/178 (69%)	122 (99%)	1 (1%)	81	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	E	150/196 (76%)	150 (100%)	0	100	100
9	F	131/132 (99%)	131 (100%)	0	100	100
10	G	123/124 (99%)	123 (100%)	0	100	100
11	H	111/115 (96%)	110 (99%)	1 (1%)	78	88
12	I	95/99 (96%)	95 (100%)	0	100	100
13	J	91/97 (94%)	91 (100%)	0	100	100
14	K	117/120 (98%)	115 (98%)	2 (2%)	60	78
15	L	100/105 (95%)	100 (100%)	0	100	100
16	M	47/48 (98%)	47 (100%)	0	100	100
17	N	76/78 (97%)	76 (100%)	0	100	100
18	O	69/82 (84%)	67 (97%)	2 (3%)	42	64
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%)	67 (96%)	3 (4%)	29	54
23	T	49/56 (88%)	49 (100%)	0	100	100
24	Z	3/3 (100%)	3 (100%)	0	100	100
25	a	241/243 (99%)	241 (100%)	0	100	100
26	b	186/233 (80%)	186 (100%)	0	100	100
27	c	182/184 (99%)	182 (100%)	0	100	100
28	d	150/154 (97%)	149 (99%)	1 (1%)	84	90
29	e	153/159 (96%)	151 (99%)	2 (1%)	69	82
30	f	123/134 (92%)	121 (98%)	2 (2%)	62	79
31	g	101/129 (78%)	90 (89%)	11 (11%)	6	25
32	h	102/110 (93%)	101 (99%)	1 (1%)	76	86
33	i	126/128 (98%)	125 (99%)	1 (1%)	81	89
34	j	103/103 (100%)	103 (100%)	0	100	100
35	k	123/126 (98%)	123 (100%)	0	100	100
36	l	113/115 (98%)	113 (100%)	0	100	100
37	m	105/109 (96%)	104 (99%)	1 (1%)	76	86
38	n	96/99 (97%)	94 (98%)	2 (2%)	53	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	o	101/105 (96%)	101 (100%)	0	100	100
40	p	100/108 (93%)	100 (100%)	0	100	100
41	q	90/91 (99%)	90 (100%)	0	100	100
42	r	116/132 (88%)	116 (100%)	0	100	100
43	s	82/208 (39%)	82 (100%)	0	100	100
44	t	96/96 (100%)	96 (100%)	0	100	100
45	u	69/85 (81%)	69 (100%)	0	100	100
46	v	58/60 (97%)	58 (100%)	0	100	100
47	w	87/98 (89%)	87 (100%)	0	100	100
48	x	41/86 (48%)	41 (100%)	0	100	100
49	y	48/49 (98%)	46 (96%)	2 (4%)	30	55
50	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5096/5754 (89%)	5061 (99%)	35 (1%)	84	90

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	h	95	LYS
33	i	64	GLN
38	n	63	LYS
28	d	27	GLN
22	S	63	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
35	k	36	GLN
40	p	36	GLN
42	r	38	ASN
41	q	87	GLN
36	l	99	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	3	2875/2907 (98%)	587 (20%)	25 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	4	103/108 (95%)	24 (23%)	2 (1%)
53	5	1490/1520 (98%)	279 (18%)	5 (0%)
54	6	75/76 (98%)	18 (24%)	1 (1%)
54	7	75/76 (98%)	18 (24%)	1 (1%)
55	Y	8/9 (88%)	0	0
All	All	4626/4696 (98%)	926 (20%)	34 (0%)

5 of 926 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	3	11	U
51	3	29	G
51	3	37	G
51	3	41	C
51	3	48	G

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	5	419	A
53	5	1186	U
54	6	16	G
51	3	1507	G
51	3	1297	U

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

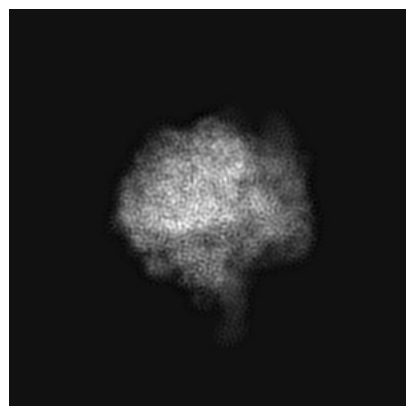
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13276. These allow visual inspection of the internal detail of the map and identification of artifacts.

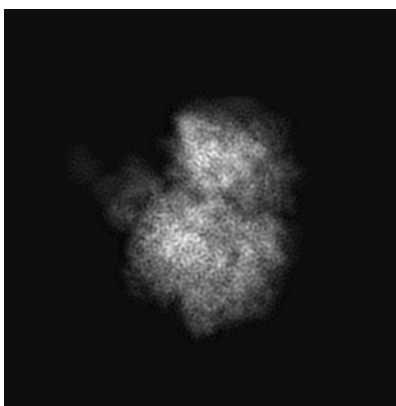
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

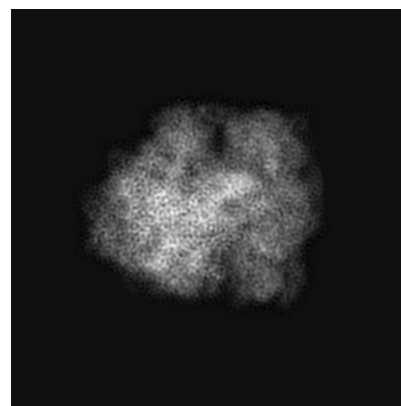
6.1.1 Primary map



X

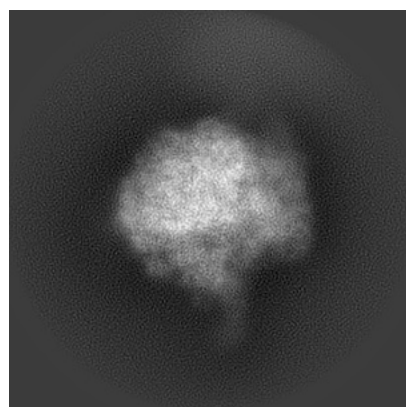


Y

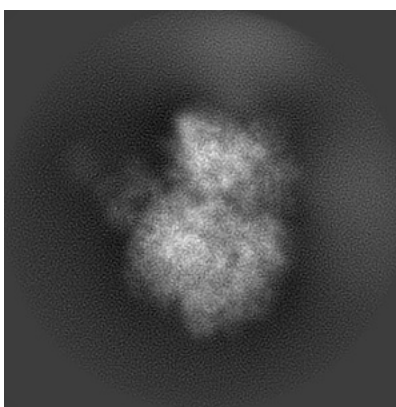


Z

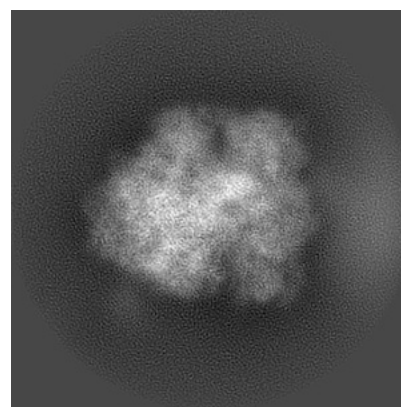
6.1.2 Raw map



X



Y

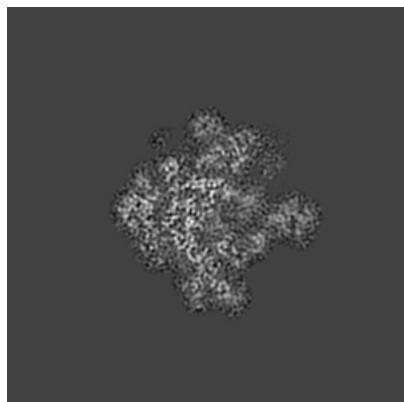


Z

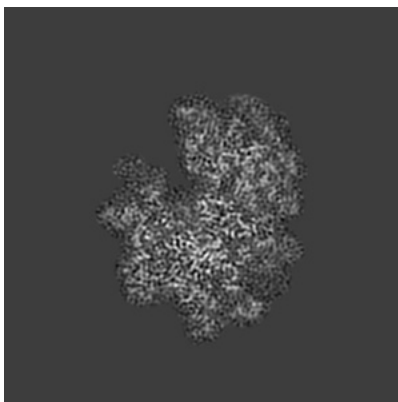
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

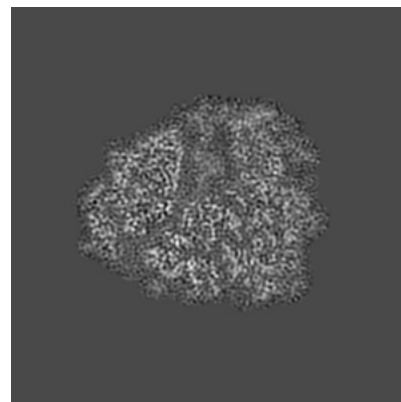
6.2.1 Primary map



X Index: 128

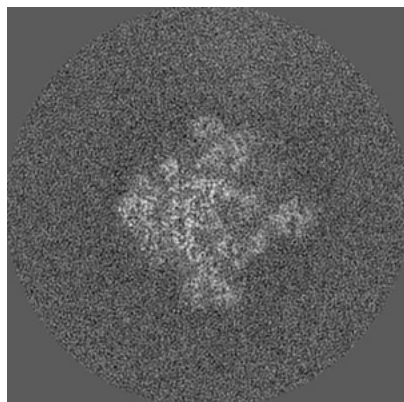


Y Index: 128

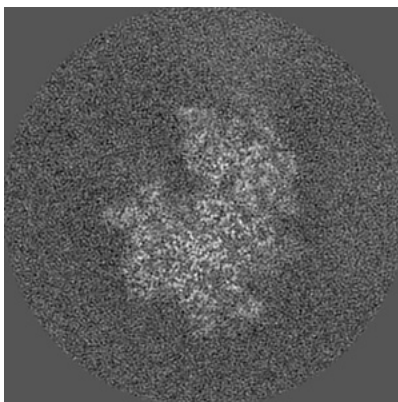


Z Index: 128

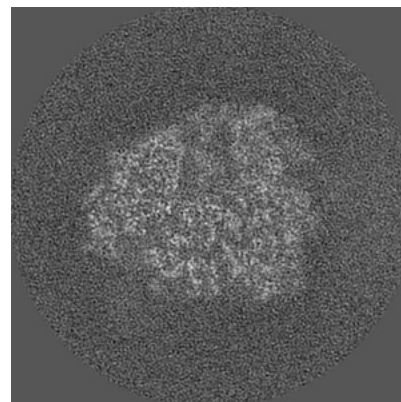
6.2.2 Raw map



X Index: 128



Y Index: 128

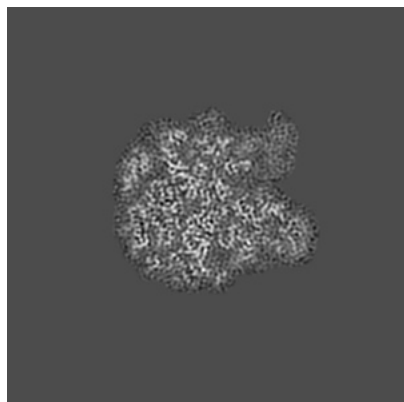


Z Index: 128

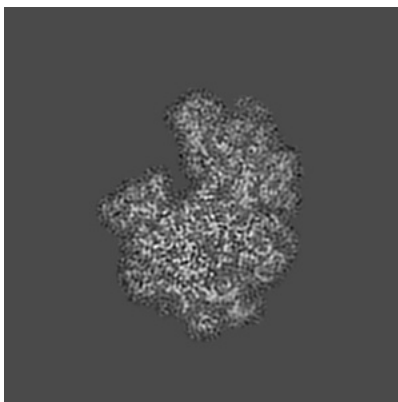
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

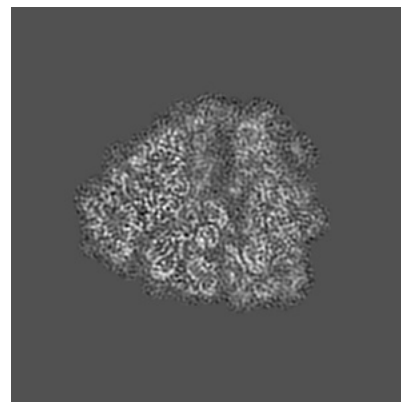
6.3.1 Primary map



X Index: 103

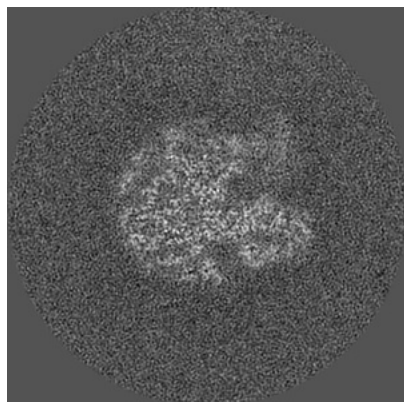


Y Index: 122

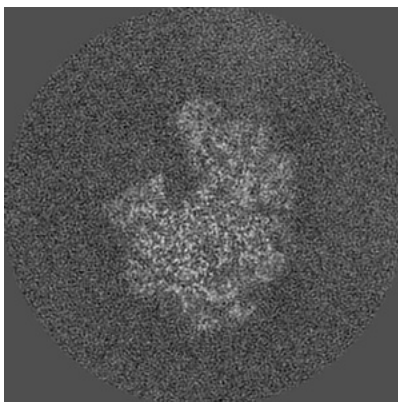


Z Index: 125

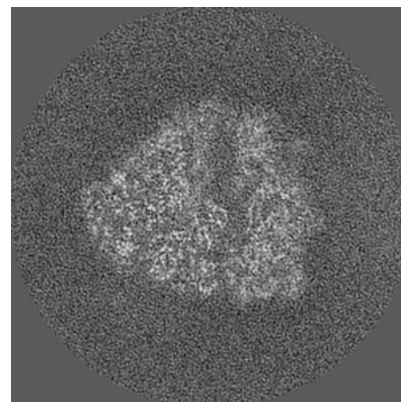
6.3.2 Raw map



X Index: 108



Y Index: 122

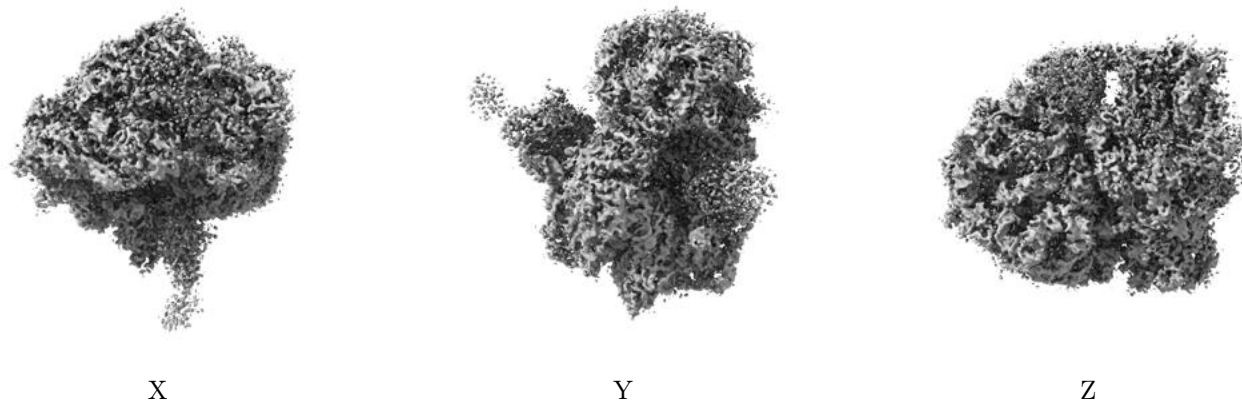


Z Index: 124

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

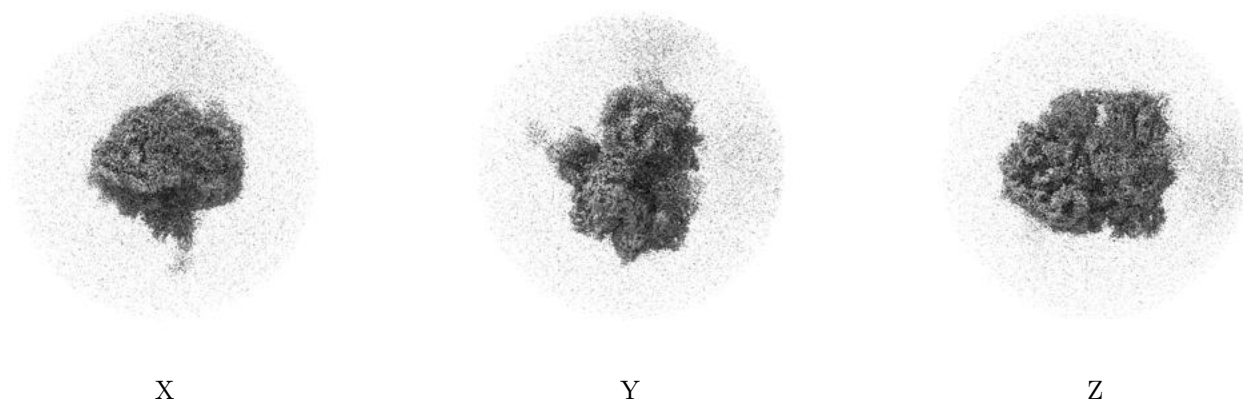
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.65. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



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

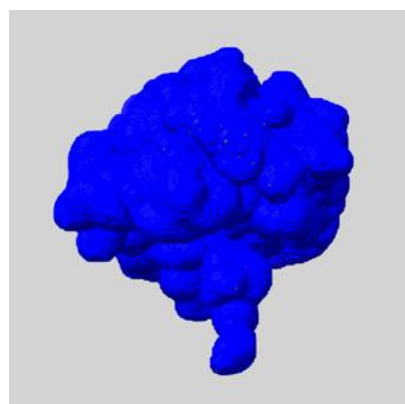
6.5 Mask visualisation [i](#)

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

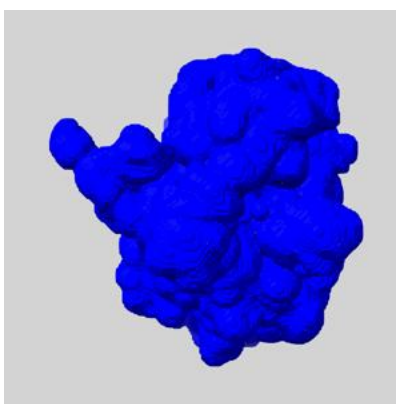
A mask typically either:

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

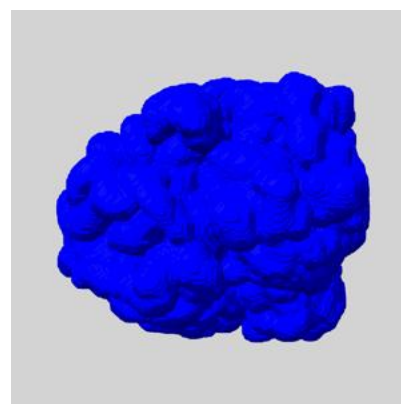
6.5.1 emd_13276_msk_1.map [i](#)



X



Y

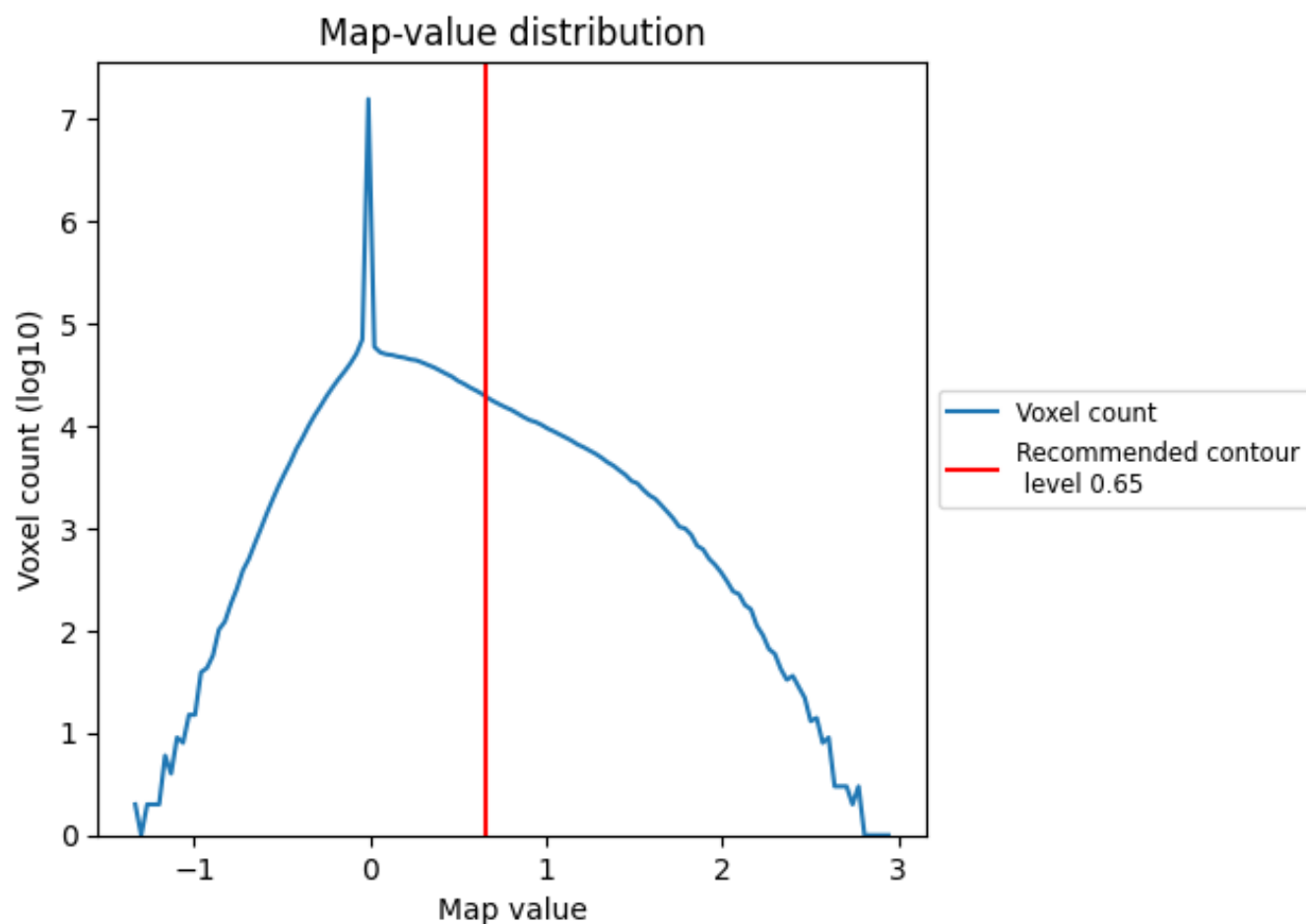


Z

7 Map analysis [i](#)

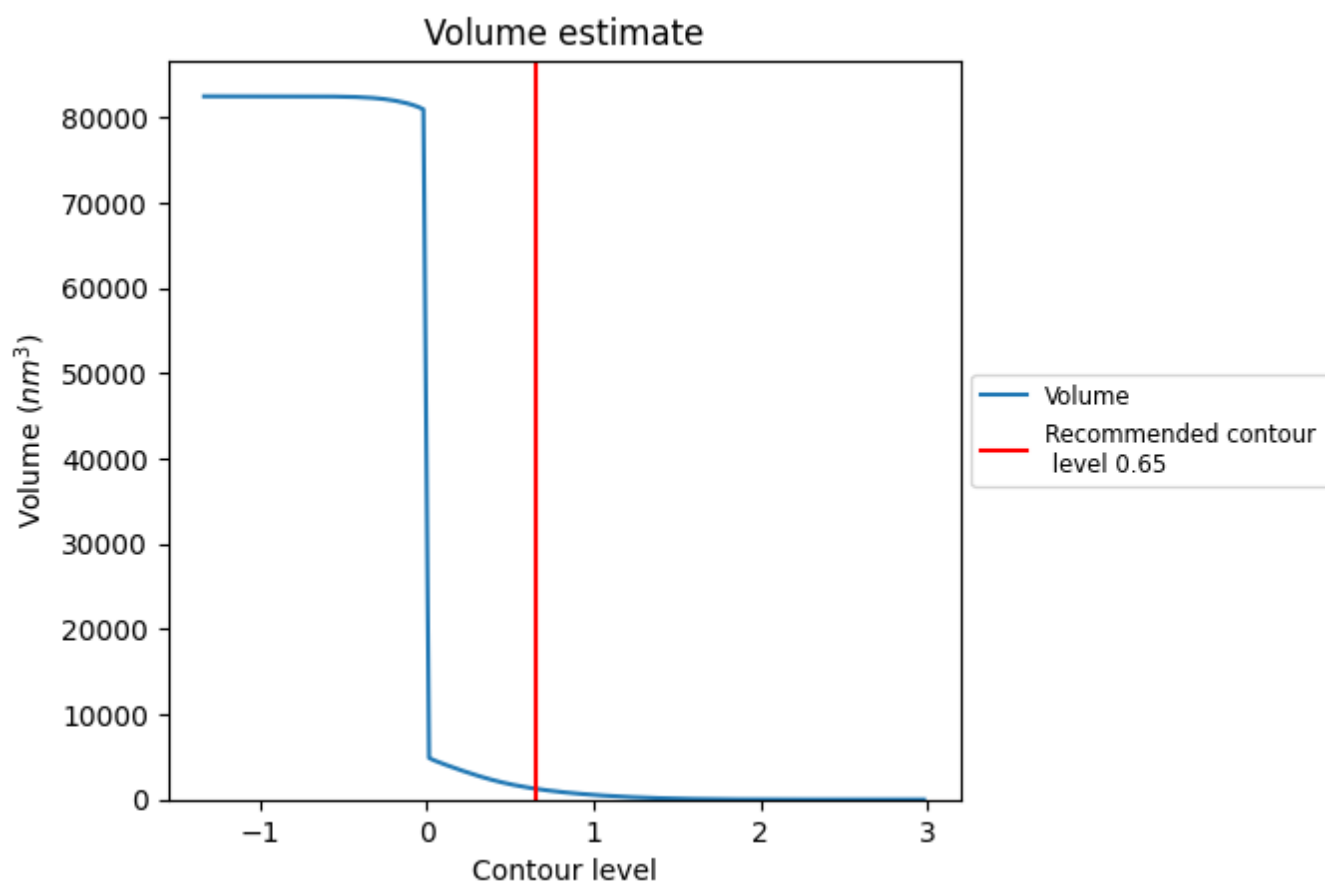
This section contains the results of statistical analysis of the map.

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.

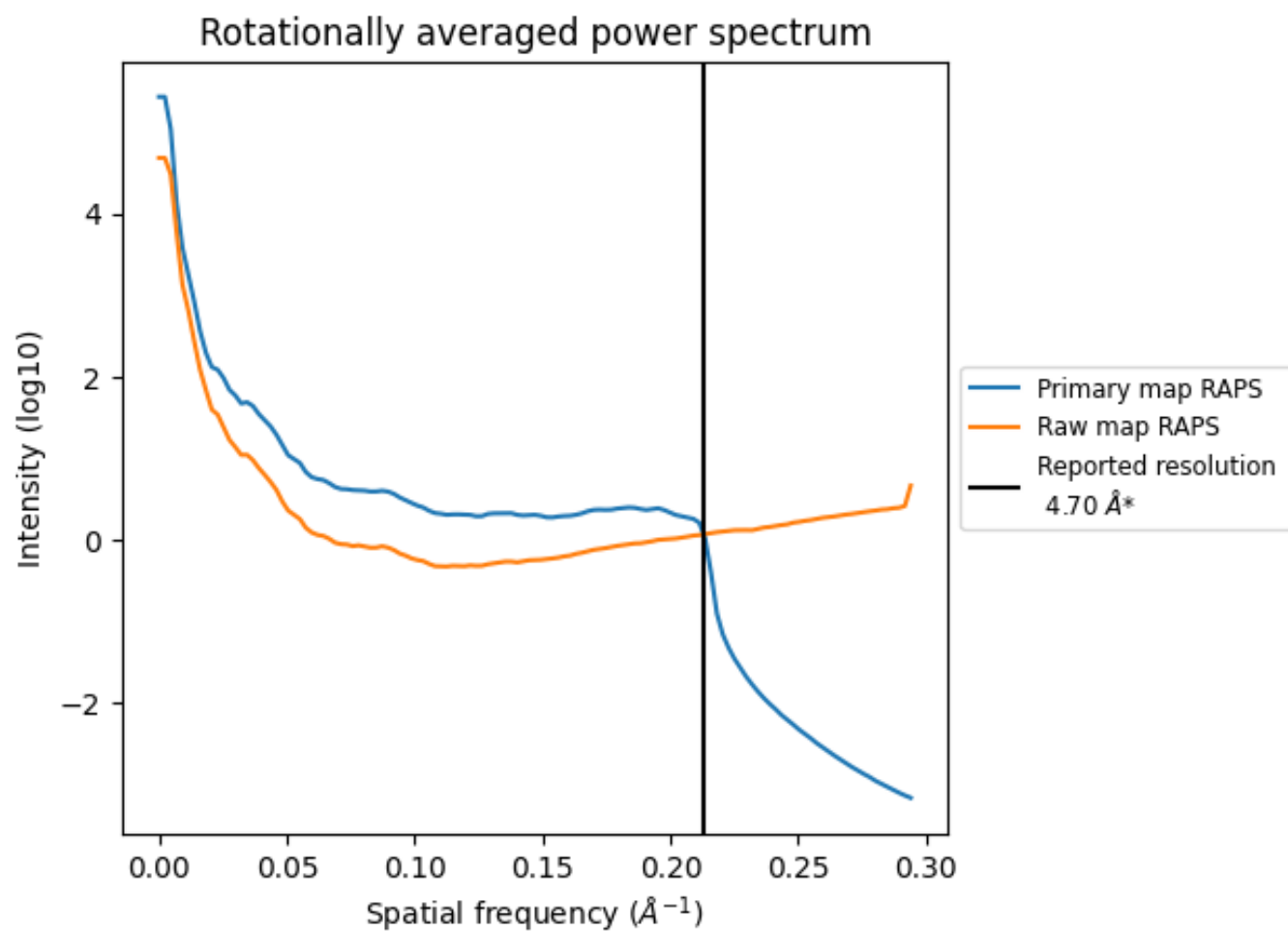
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1271 nm³; this corresponds to an approximate mass of 1148 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 ⓘ

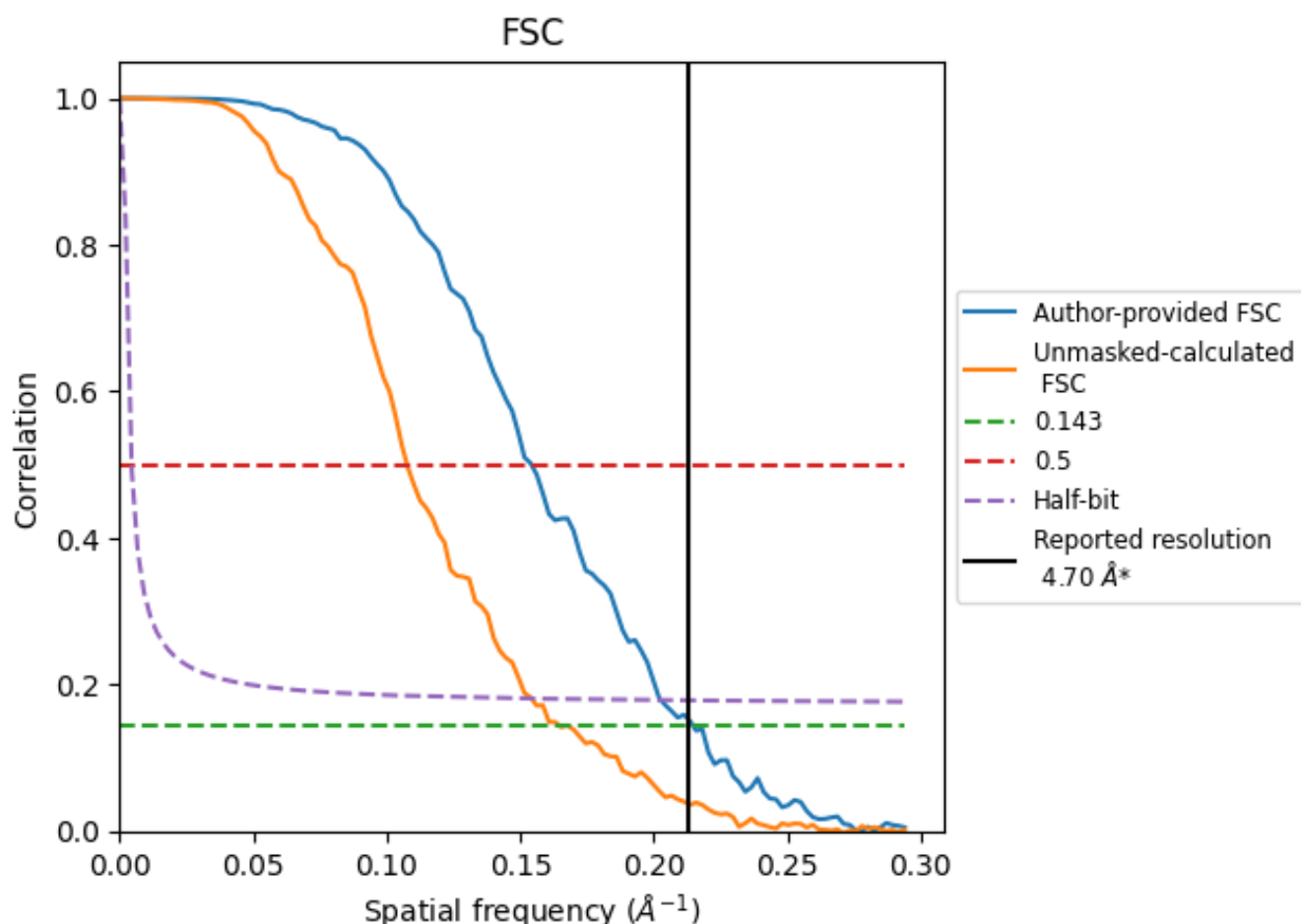


*Reported resolution corresponds to spatial frequency of 0.213 \AA^{-1}

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 0.213 Å⁻¹

8.2 Resolution estimates [i](#)

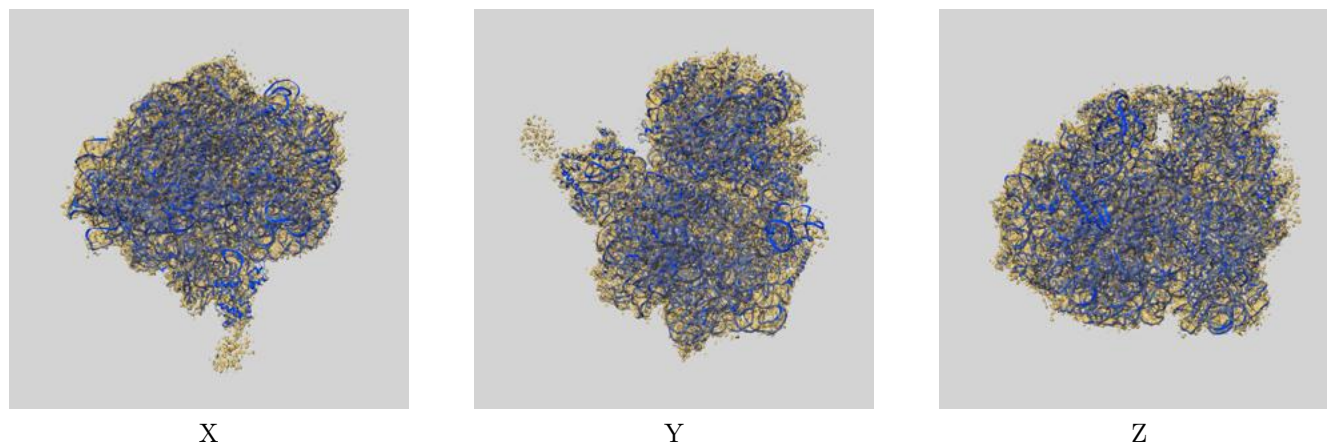
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	4.66	6.49	4.93
Unmasked-calculated*	6.06	9.29	6.48

*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 6.06 differs from the reported value 4.7 by more than 10 %

9 Map-model fit [i](#)

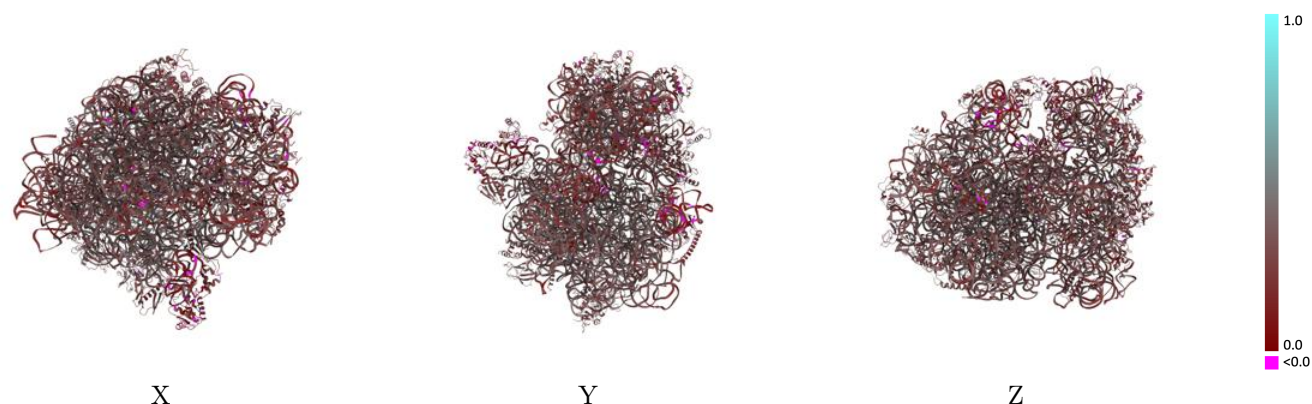
This section contains information regarding the fit between EMDB map EMD-13276 and PDB model 7PAL. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



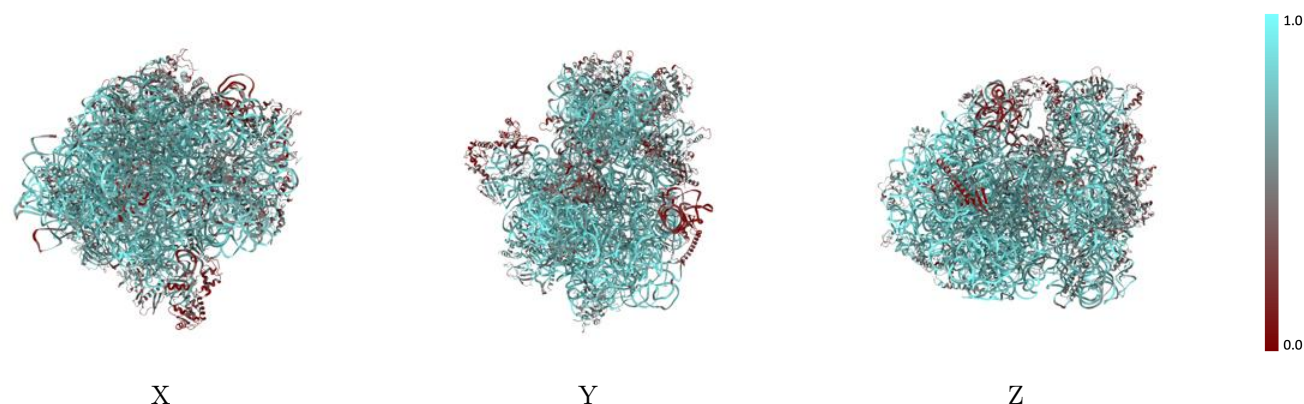
The images above show the 3D surface view of the map at the recommended contour level 0.65 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



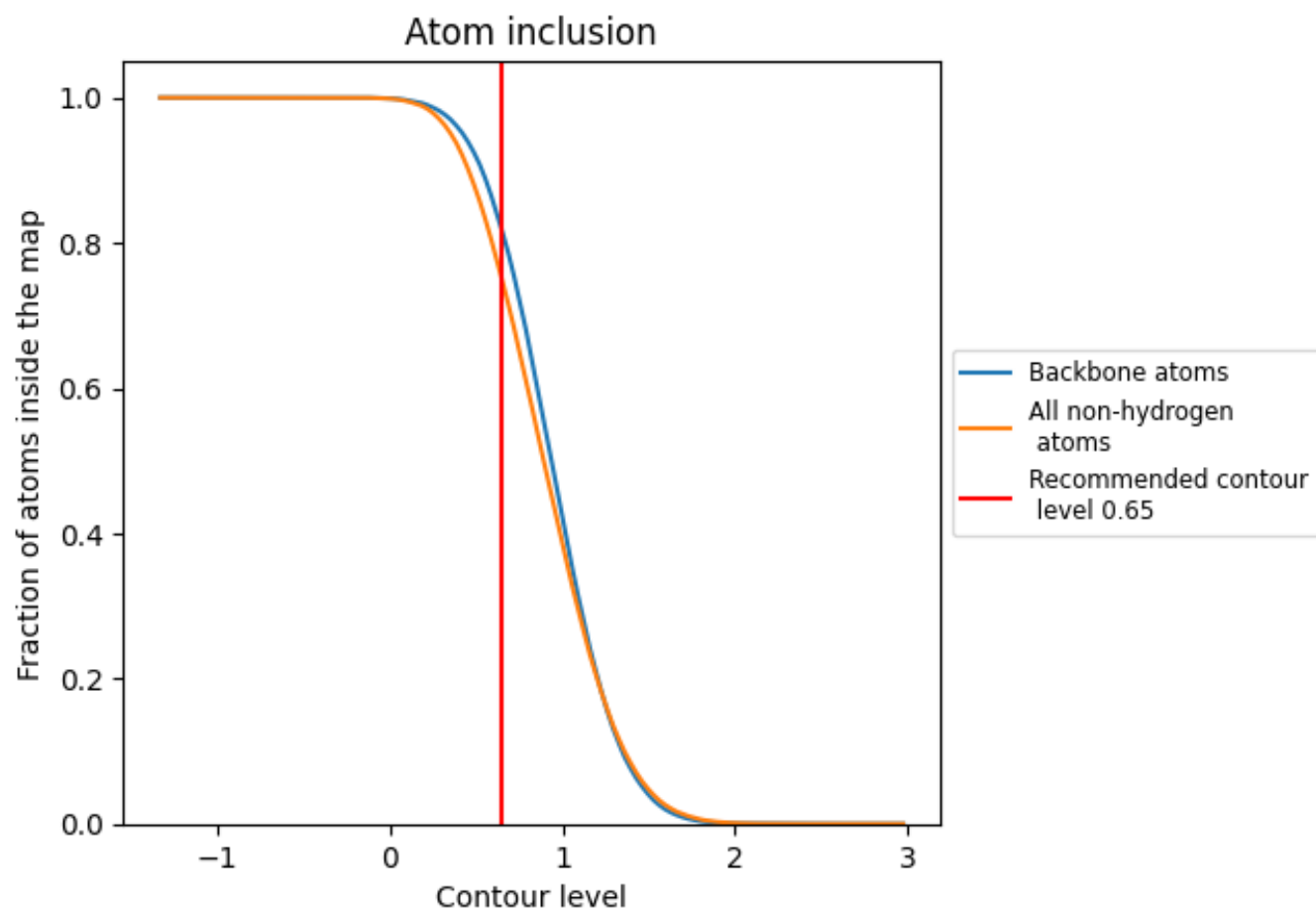
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.65).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 75% 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 (0.65) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7486	 0.3240
0	 0.7808	 0.3900
1	 0.7210	 0.3840
2	 0.7568	 0.3980
3	 0.8498	 0.3360
4	 0.8490	 0.3230
5	 0.8349	 0.3140
6	 0.7460	 0.2760
7	 0.4734	 0.1370
A	 0.4844	 0.2990
B	 0.5326	 0.3190
C	 0.5171	 0.2990
D	 0.5852	 0.3400
E	 0.4356	 0.3010
F	 0.4248	 0.2600
G	 0.5518	 0.3180
H	 0.4805	 0.2820
I	 0.5031	 0.3110
J	 0.5496	 0.3210
K	 0.6312	 0.3660
L	 0.3932	 0.2640
M	 0.6264	 0.3170
N	 0.5257	 0.2950
O	 0.5803	 0.3300
P	 0.5449	 0.3290
Q	 0.5426	 0.3020
R	 0.4552	 0.2820
S	 0.5820	 0.2880
T	 0.5223	 0.3260
Y	 0.8743	 0.3590
Z	 0.6774	 0.3370
a	 0.6937	 0.3750
b	 0.6780	 0.3660
c	 0.6308	 0.3570
d	 0.4227	 0.2450



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Chain	Atom inclusion	Q-score
e	 0.5342	 0.3210
f	 0.1871	 0.2380
g	 0.2463	 0.1980
h	 0.1327	 0.2190
i	 0.6582	 0.3570
j	 0.6511	 0.3830
k	 0.6726	 0.3660
l	 0.6872	 0.3700
m	 0.6859	 0.3480
n	 0.5963	 0.3230
o	 0.6443	 0.3610
p	 0.6940	 0.3200
q	 0.6521	 0.3790
r	 0.7226	 0.3710
s	 0.6601	 0.3730
t	 0.5122	 0.3540
u	 0.6781	 0.3620
v	 0.6828	 0.3710
w	 0.5868	 0.3380
x	 0.3411	 0.2780
y	 0.6751	 0.3620
z	 0.7078	 0.3670