



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2022 – 04:03 am BST

PDB ID : 7PIP
EMDB ID : EMD-13446
Title : 70S ribosome with EF-Tu-tRNA and P-site tRNA in pseudouridimycin-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-23
Resolution : 9.30 Å (reported)
Based on initial models : 4V5L, 7OOC, 7OOD, 4V7C

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

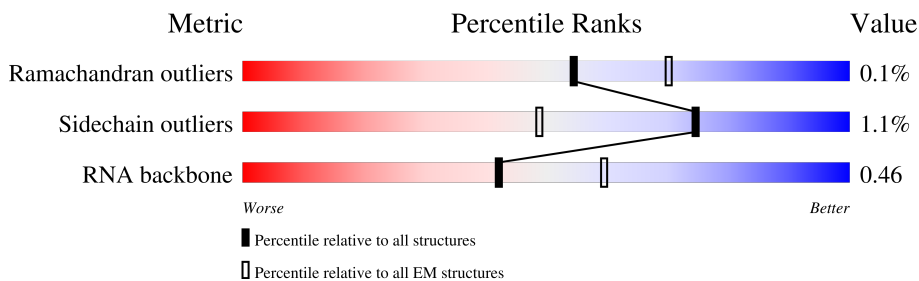
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 9.30 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	9	394	
5	A	294	
6	B	273	
7	C	205	
8	D	219	

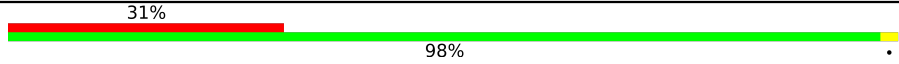
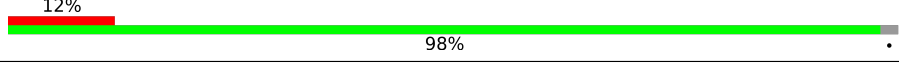
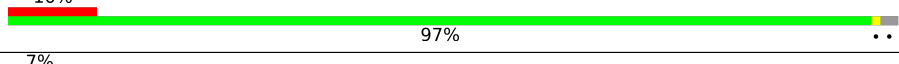
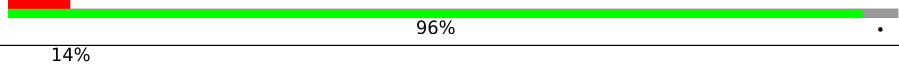
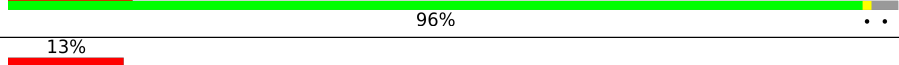
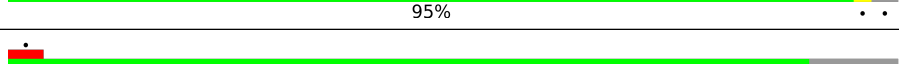
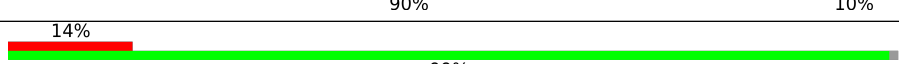
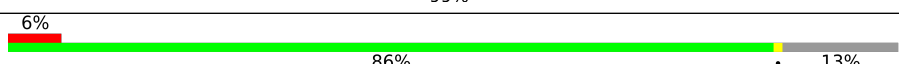

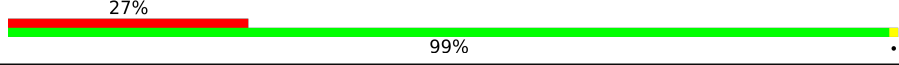

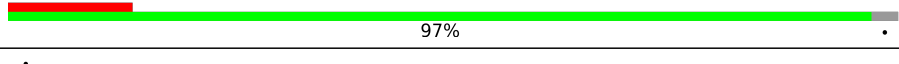
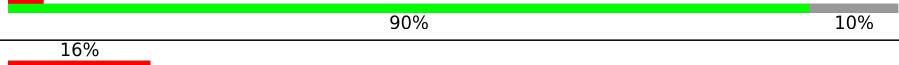

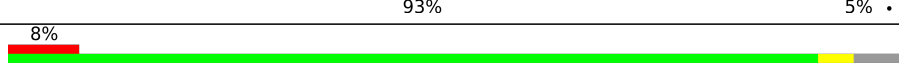
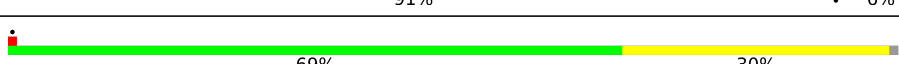






Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	E	215	21% 77% 22%
10	F	155	21% 99%
11	G	142	16% 95%
12	H	132	23% 96%
13	I	108	25% 91% 6%
14	J	121	20% 94% 6%
15	K	139	14% 94%
16	L	124	18% 91% 5%
17	M	61	30% 98%
18	N	86	12% 97%
19	O	94	85% 15%
20	P	85	16% 98%
21	Q	104	15% 62% 38%
22	R	87	29% 97%
23	S	87	87% 11%
24	T	60	10% 88% 12%
25	a	287	12% 99%
26	b	287	15% 79% 20%
27	c	212	17% 99%
28	d	180	26% 97%
29	e	184	23% 95%
30	f	149	68% 93%
31	g	161	30% 69% 6% 25%
32	h	137	35% 93% 7%
33	i	146	17% 99%

Continued on next page...

Continued from previous page...

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	

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 149091 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
			Total	C	N	O	S		
1	0	47	380	236	81	61	2	0	0

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

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

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

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

- Molecule 4 is a protein called Elongation factor Tu.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

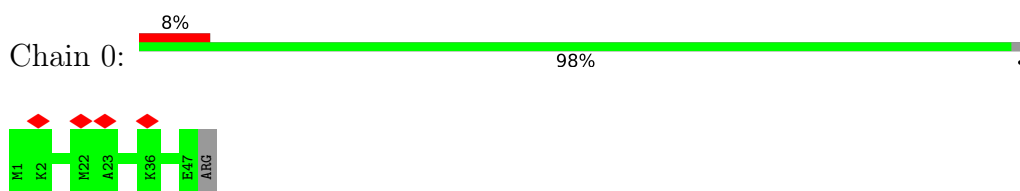
- Molecule 54 is a RNA chain called tRNA-Phe.

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

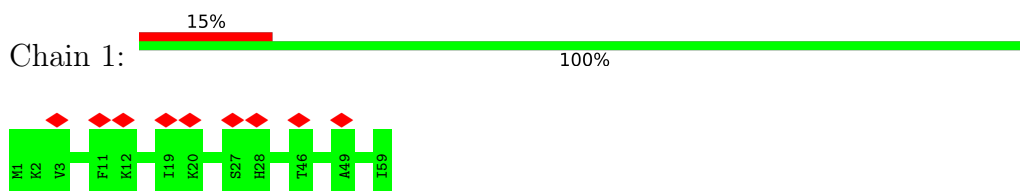
3 Residue-property plots [i](#)

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

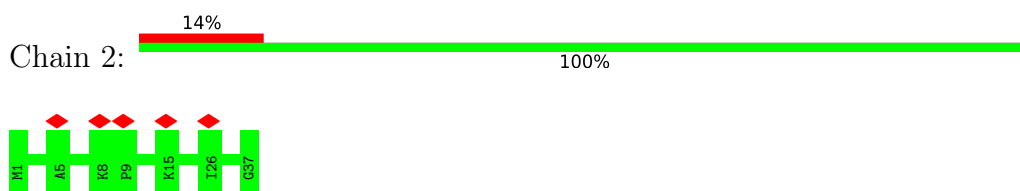
- Molecule 1: 50S ribosomal protein L34



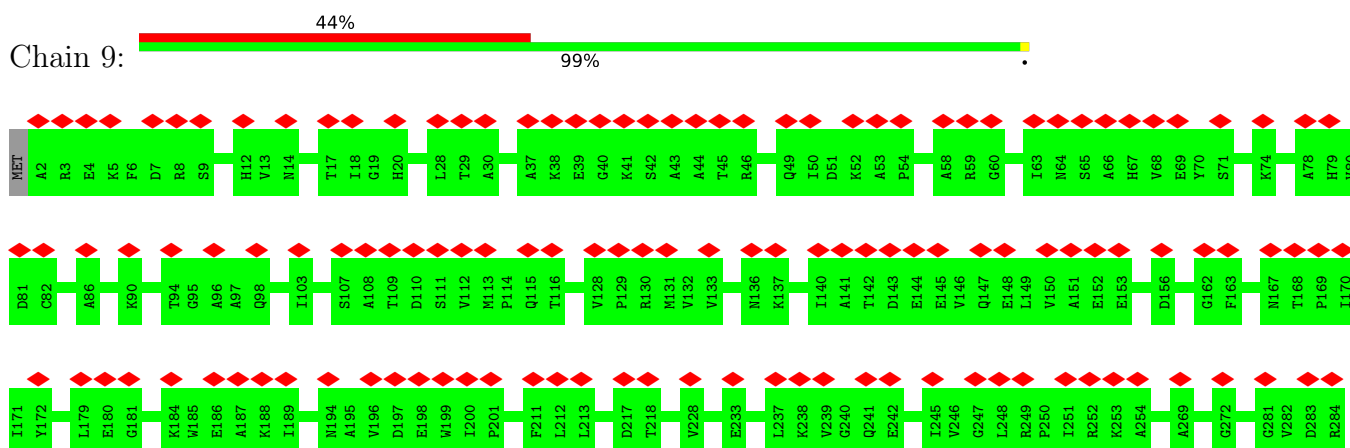
- Molecule 2: 50S ribosomal protein L35

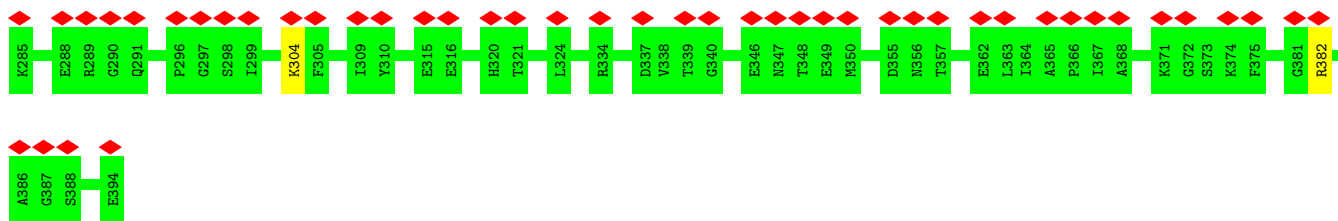


- Molecule 3: 50S ribosomal protein L36

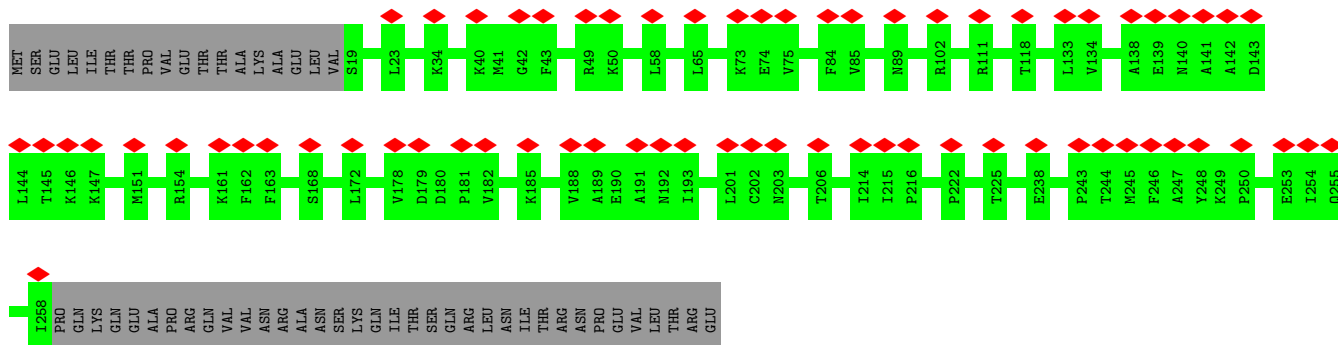
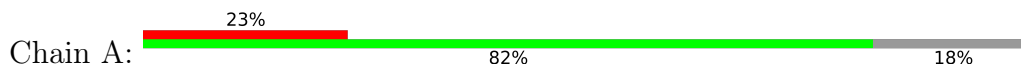


- Molecule 4: Elongation factor Tu

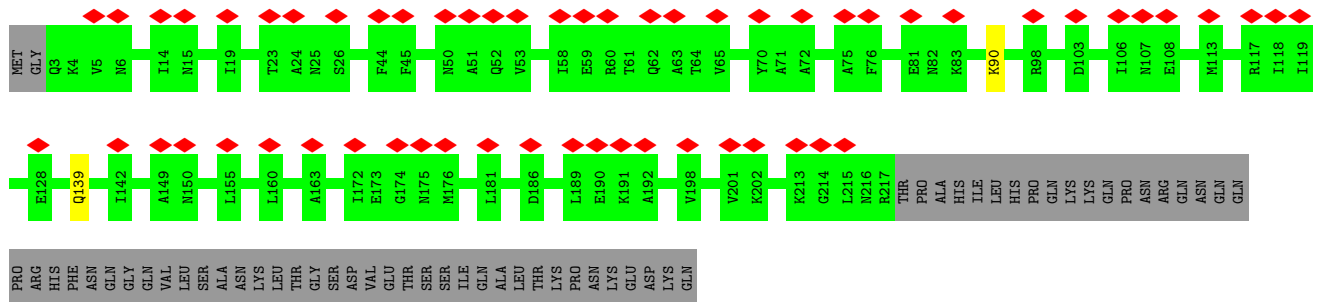
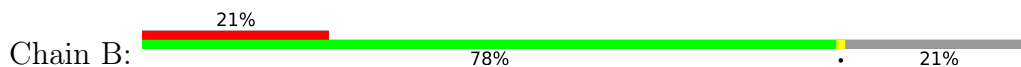




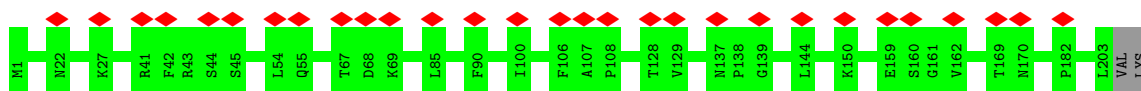
• Molecule 5: 30S ribosomal protein S2



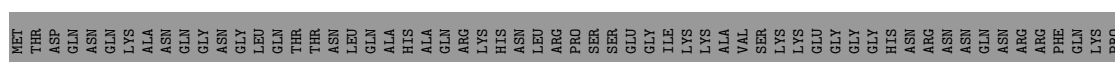
• Molecule 6: 30S ribosomal protein S3

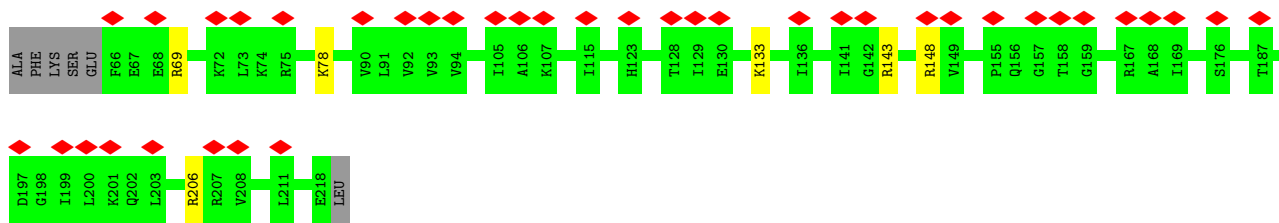


• Molecule 7: 30S ribosomal protein S4

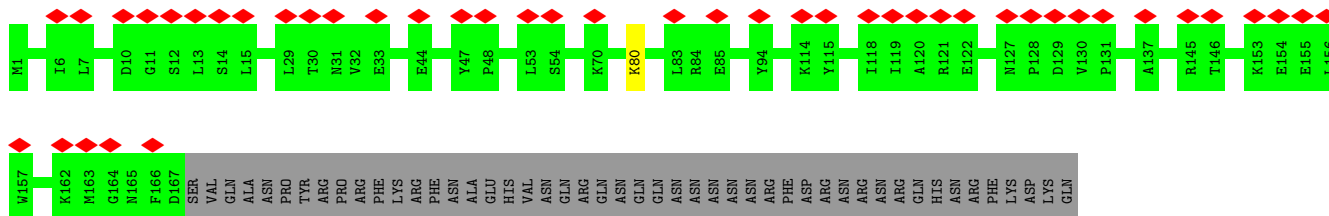
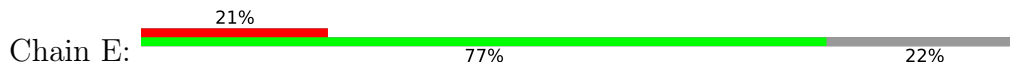


• Molecule 8: 30S ribosomal protein S5

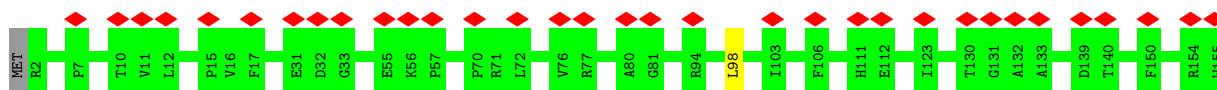




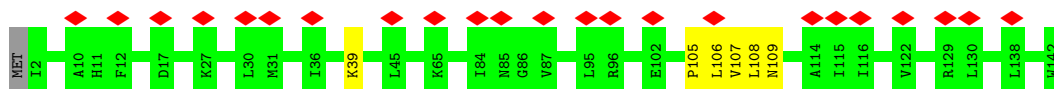
• Molecule 9: 30S ribosomal protein S6



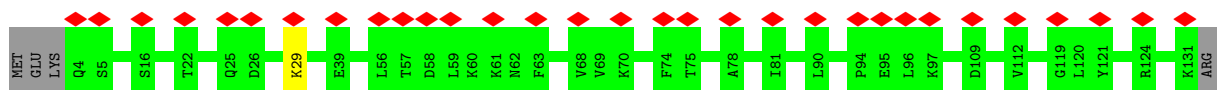
• Molecule 10: 30S ribosomal protein S7



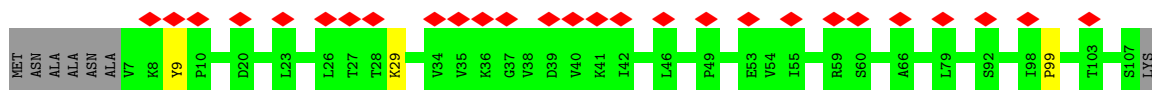
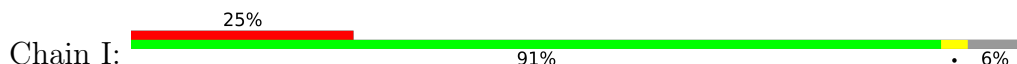
• Molecule 11: 30S ribosomal protein S8



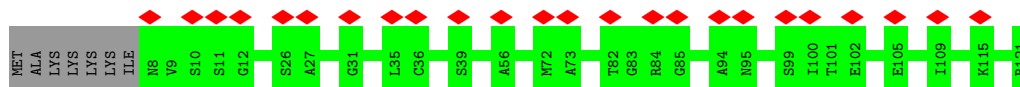
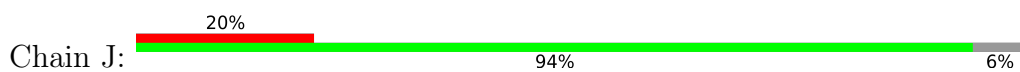
• Molecule 12: 30S ribosomal protein S9



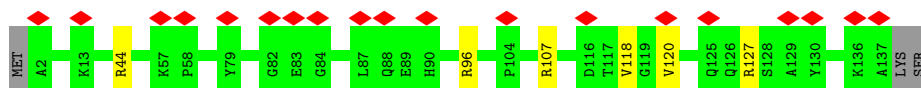
• Molecule 13: 30S ribosomal protein S10



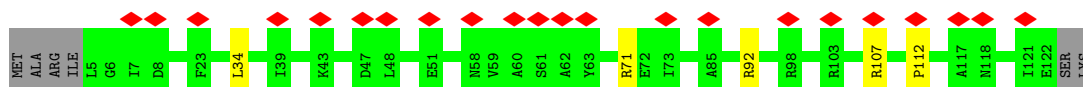
• Molecule 14: 30S ribosomal protein S11



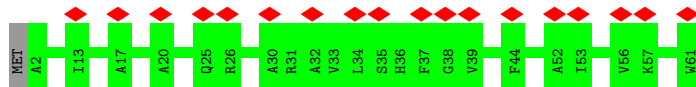
- Molecule 15: 30S ribosomal protein S12



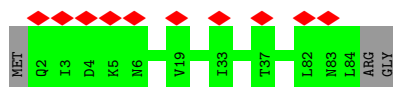
- Molecule 16: 30S ribosomal protein S13



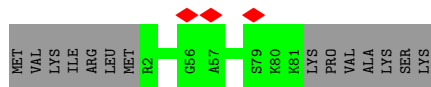
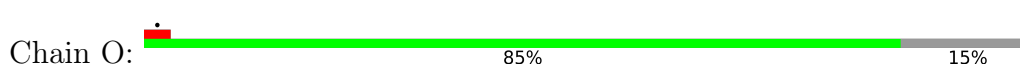
- Molecule 17: 30S ribosomal protein S14 type Z



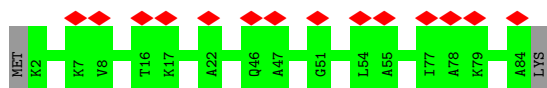
- Molecule 18: 30S ribosomal protein S15



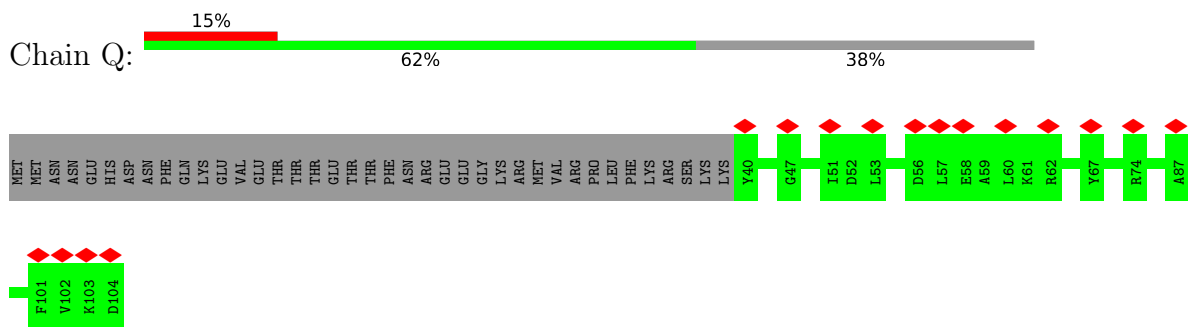
- Molecule 19: 30S ribosomal protein S16



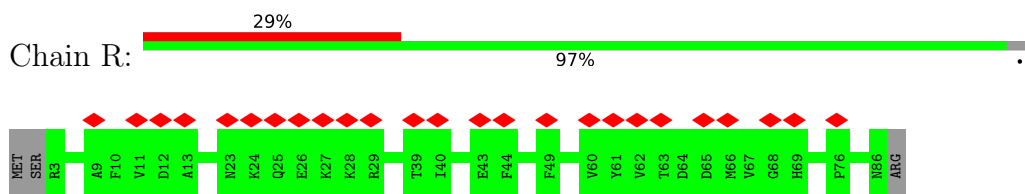
- Molecule 20: 30S ribosomal protein S17



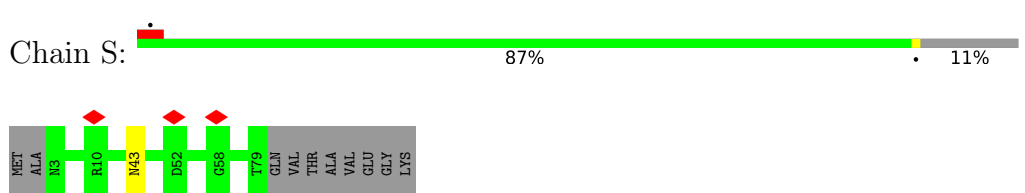
• Molecule 21: 30S ribosomal protein S18



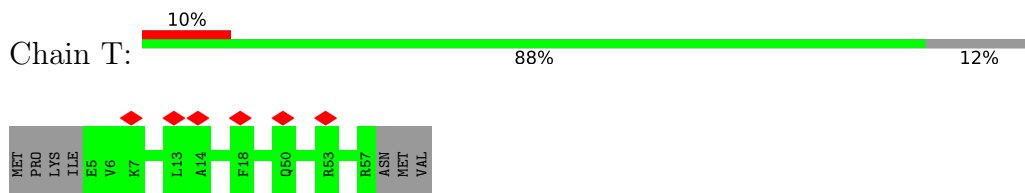
• Molecule 22: 30S ribosomal protein S19



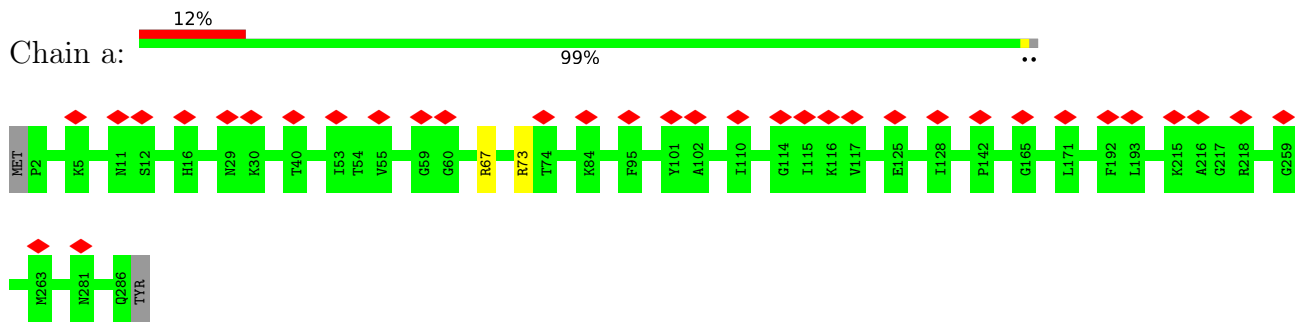
• Molecule 23: 30S ribosomal protein S20



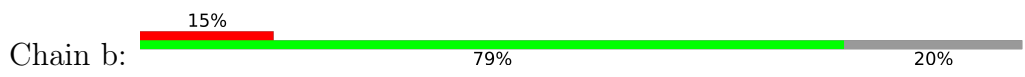
• Molecule 24: 30S ribosomal protein S21



• Molecule 25: 50S ribosomal protein L2

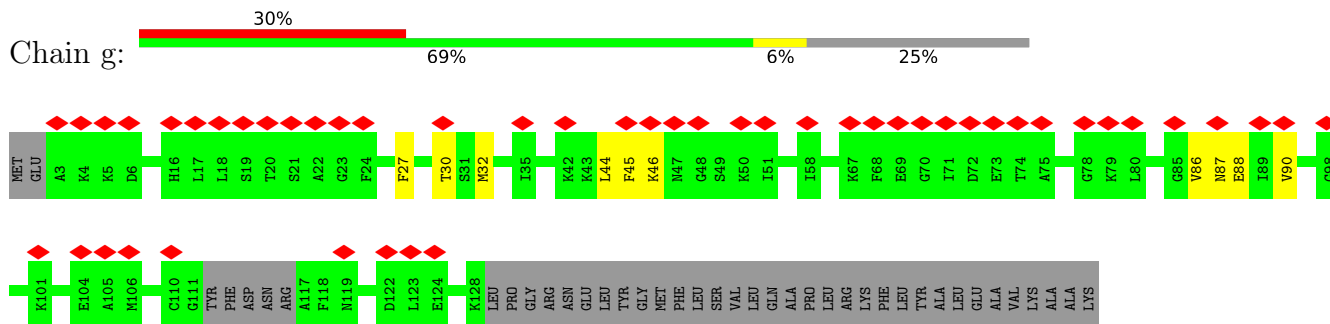


• Molecule 26: 50S ribosomal protein L3

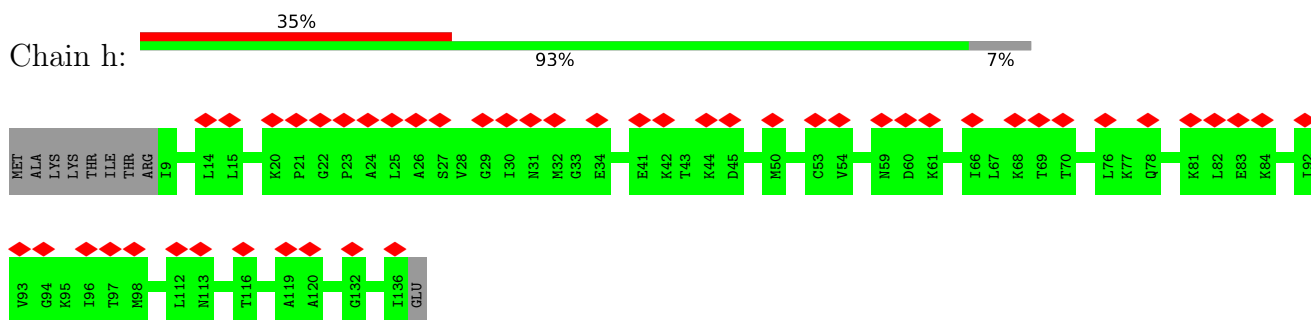


VAL
LYS

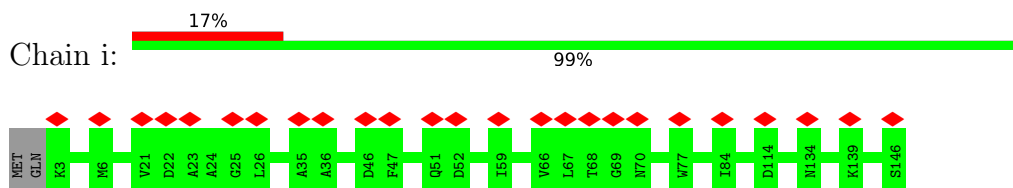
- Molecule 31: 50S ribosomal protein L10



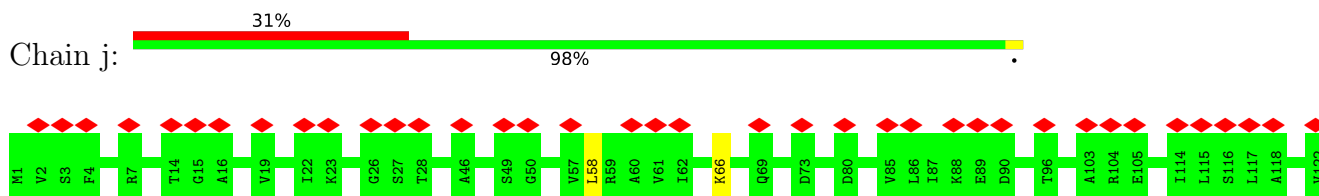
- Molecule 32: 50S ribosomal protein L11



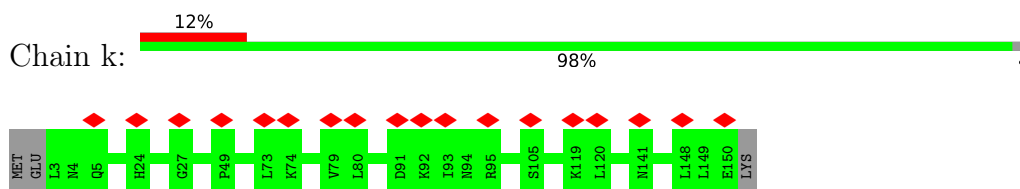
- Molecule 33: 50S ribosomal protein L13



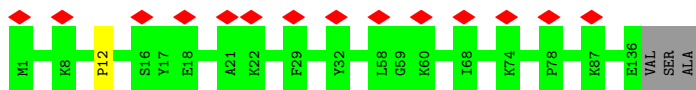
- Molecule 34: 50S ribosomal protein L14



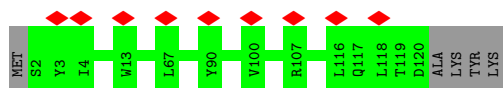
- Molecule 35: 50S ribosomal protein L15



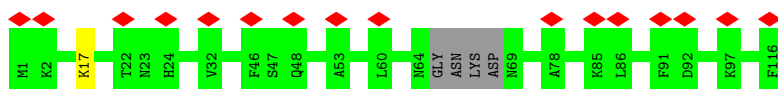
- Molecule 36: 50S ribosomal protein L16



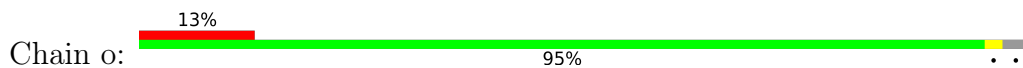
- Molecule 37: 50S ribosomal protein L17



- Molecule 38: 50S ribosomal protein L18



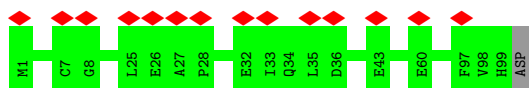
- Molecule 39: 50S ribosomal protein L19



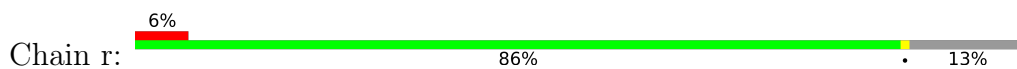
- Molecule 40: 50S ribosomal protein L20

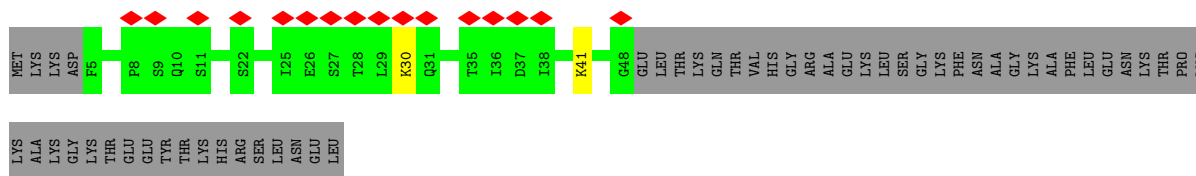


- Molecule 41: 50S ribosomal protein L21

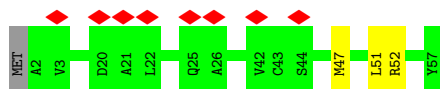
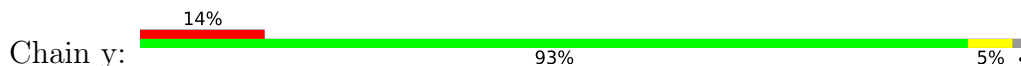


- Molecule 42: 50S ribosomal protein L22

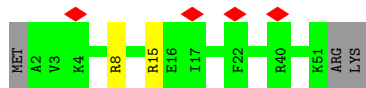




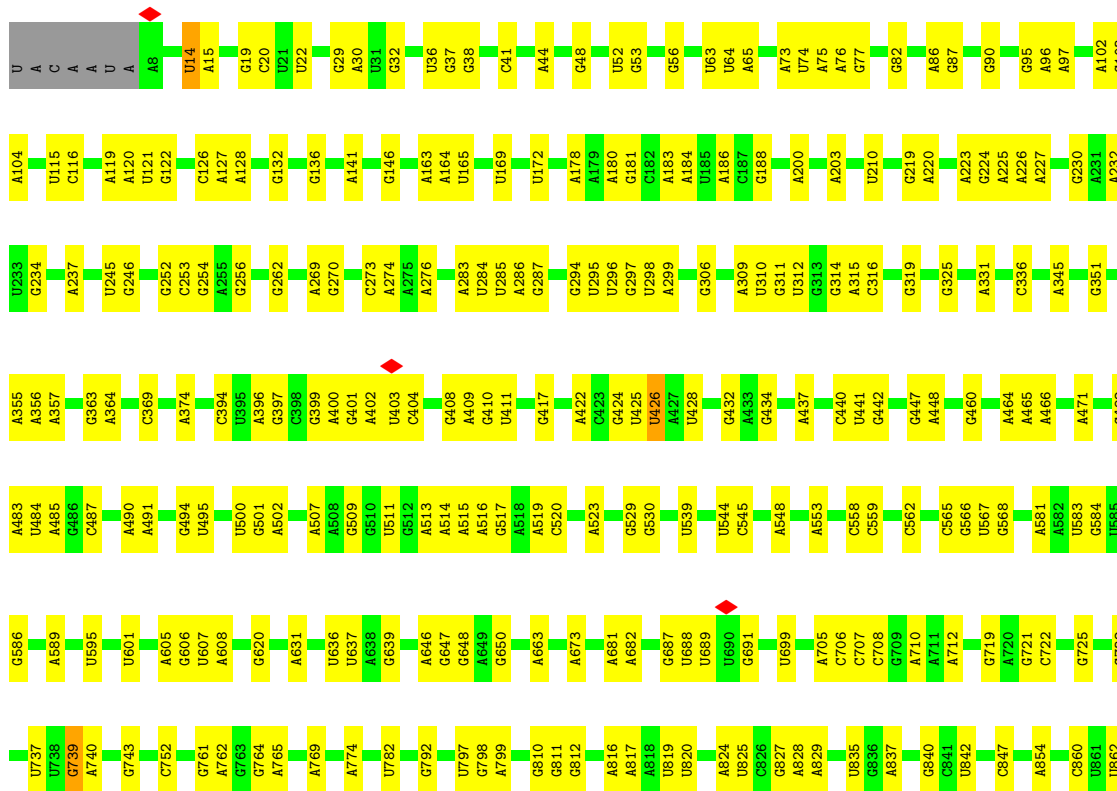
• Molecule 49: 50S ribosomal protein L32



• Molecule 50: 50S ribosomal protein L33 1



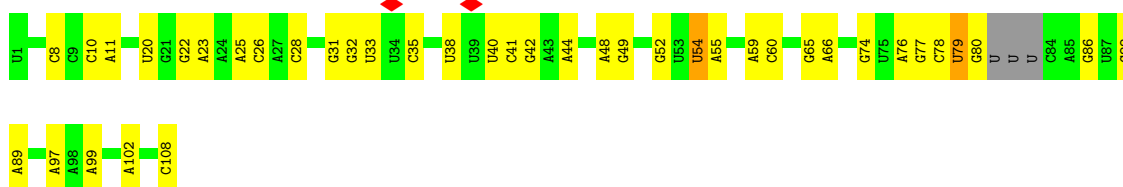
• Molecule 51: 23S ribosomal RNA



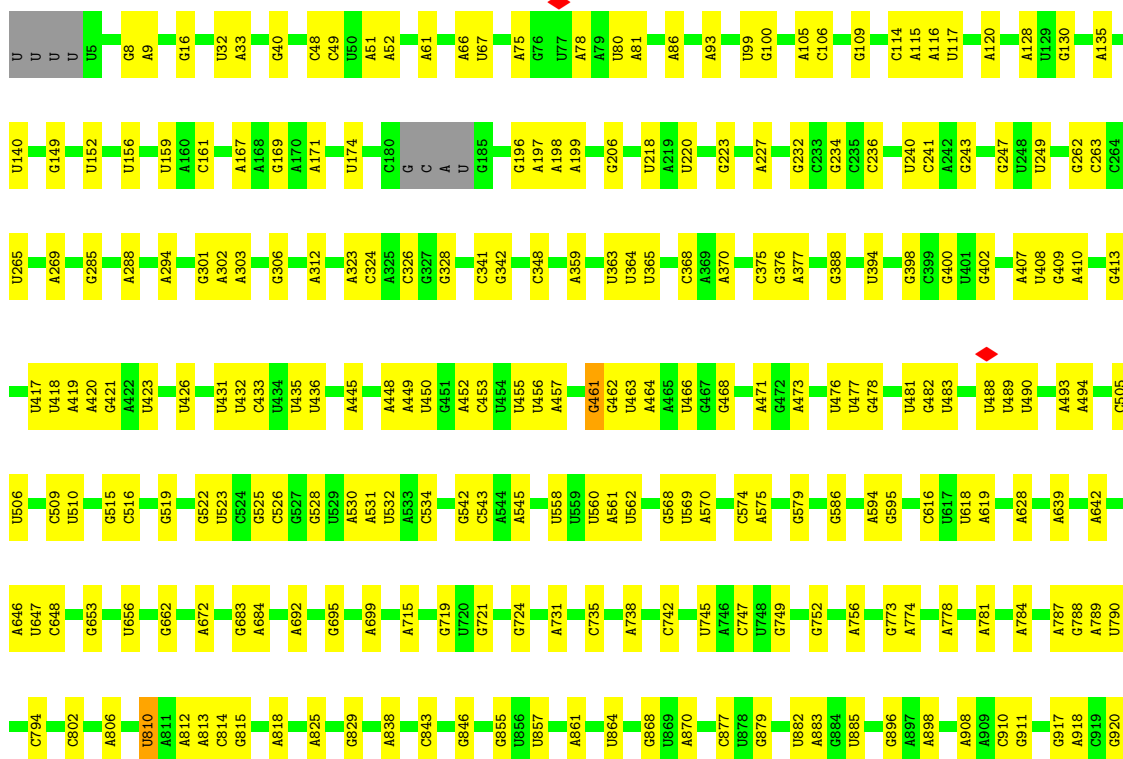
A2442	G2297	U2180	U2083	A1828	U1693	U1448	U1316	G1903	G1090	A977	U963
A2443	C2305	A2181	U1962	A1836	A1694	C1456	C1317	A1204	G1091	A977	A864
G2444	C2182	C2182	C1965	A1839	C1697	A1457	A1322	A1208	U1095	G982	A865
U2449	C2187	U2188	C1970	C1839	G1700	G1463	C1325	U1209	U1096	C984	C880
G2455	U2193	G2195	C1972	G1842	G1701	U1466	A1328	C1212	C1099	G989	A881
A2456	C2194	U2195	U1977	C1845	A1702	U1584	U1329	A1102	A1102	U994	C882
A2458	U2195	G2195	U1978	C1850	G1708	A1585	U1330	G1215	G1103	U984	A883
A2459	U2195	G2195	U1979	C1855	C1717	U1586	G1331	U1216	A1104	U997	A884
C2460	G2198	A2107	G1982	A1855	C1718	U1481	G1338	G1217	A1105	C998	U886
U2468	C2198	C2108	U1998	G1866	U1727	U1482	U1341	U1219	C1107	C1001	G895
C2475	U2200	U2110	C1999	G1871	A1728	U1486	G1353	A1225	A1108	A1002	U902
U2484	G2201	U2111	U2000	U1872	G1729	U1487	U1357	U1234	C1111	G1005	A903
U2485	U2202	A2112	C2003	A1873	G1733	U1497	U1360	U1235	G1115	U1006	C904
A2486	C2204	U2113	U2009	A1883	A1734	A1502	U1360	A1250	A1123	C1007	U905
U2487	U2205	C2114	G1736	C1886	G1736	A1506	U1369	G1251	G1124	A1009	G906
G2492	A2206	A2115	G1737	C1886	A1619	U1506	U1370	G1252	U1125	G1010	G914
A2495	G2211	U2117	G2011	U1890	A1630	G1508	A1374	A1256	A1130	A1016	G917
G2498	U2218	U2118	A2020	A1891	G1615	U1509	G1371	G1257	A1131	A1019	C921
U2499	A2220	A2124	G2027	A1892	G1616	A1510	U1374	G1265	C1132	A1026	C922
A2502	U2221	U2125	C2028	C1893	U1617	A1513	U1375	G1266	U1141	U1027	A
G2503	C2222	U2126	U2029	C1902	A1619	U1514	G1376	U1267	A1028	C1028	C
C2503	U2226	A2126	A2030	A1903	G1765	U1515	A1377	U1268	A1029	A1029	U
A2505	U2227	G2128	A2037	G1906	A1766	C1518	U1378	A1274	U1035	U1035	A
C2506	U2228	U2129	A2037	A1907	A1767	A1519	U1380	A1277	C1041	C1041	G928
C2507	A2231	A2130	G2039	G1913	A1769	A1632	U1387	U1278	U1151	U1151	G929
U2510	A2232	G2132	C2041	C1916	C1771	A1641	G1388	G1280	U1154	C1044	C930
G2513	G2246	A2134	C2042	A1920	C1772	A1643	A1393	A1281	U1165	A1045	G931
U2514	G2247	C2043	C2043	C1921	G1770	A1644	A1406	G1282	G1166	A1046	U932
A2521	G2258	C2044	C2045	A1923	A1780	C1645	U1407	A1283	U1167	A1047	A933
C2525	G2267	U2138	G2050	A1934	U1784	A1651	G1408	A1284	A1168	U1049	U935
U2527	A2274	C2139	A2055	A1938	A1788	A1652	A1412	U1285	A1169	A1052	G936
C2528	A2275	G2140	A2056	U1938	C1789	C1653	A1541	G1286	C1170	A1052	A937
A2538	A2276	U2152	C2062	A1943	A1792	A1661	U1546	A1292	G1171	A1055	A940
A2539	A2276	A2155	G2064	A1945	A1806	A1669	G1550	A1297	U1176	A1061	U944
U2431	U2280	G2155	U2067	A1945	C1807	A1681	U1559	A1298	A1177	A1062	A947
C2432	G2284	A2159	G2068	A1945	C1808	C1682	U	C1300	C1187	U1068	C949
A2433	G2285	G2068	A2069	A1950	A1809	G1683	G	C1301	G1188	G1075	U952
A2434	A2286	C2070	A1951	U1950	A1684	G1685	A	C1302	G1189	G1075	U953
C2435	U2162	C2071	C2071	A1951	A1685	U1686	G	U1303	A1190	A1080	G953
G2436	U2165	C2071	G2076	A1816	U1686	U1687	U	U1304	A1191	A1081	A964
U2437	U2166	A2170	A2077	A1817	G1687	A1688	A	G1305	U1192	A1082	U968
A2438	A2171	A2171	A2078	U1823	A1688	A1692	U	A1314	U1193	A1089	A969
U2439	A2172	G2173					C	A1315			U970

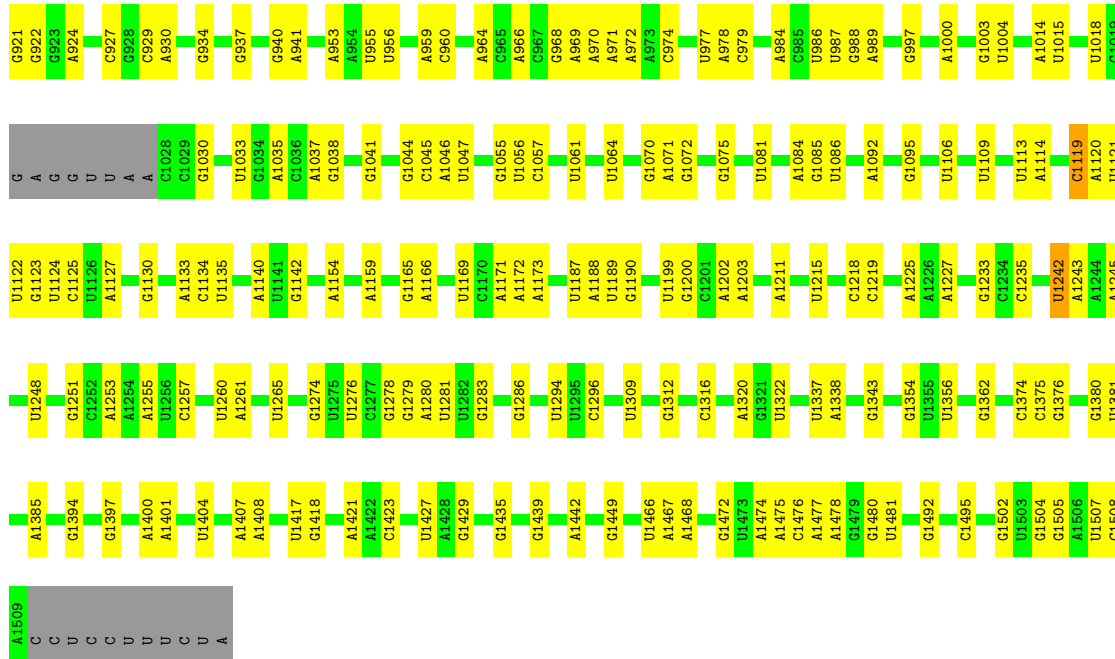


• Molecule 52: 5S ribosomal RNA

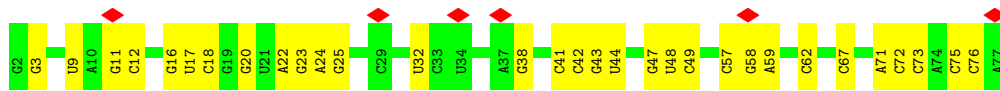


• Molecule 53: 16S ribosomal RNA

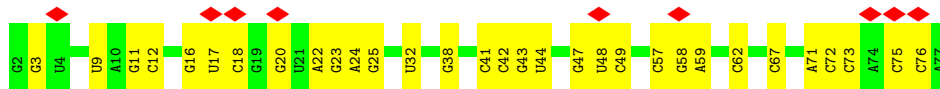




• Molecule 54: tRNA-Phe



• Molecule 54: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	1128	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	1.595	Depositor
Minimum map value	-0.633	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.113	Depositor
Recommended contour level	0.39	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 [i](#)

5.1 Standard geometry [i](#)

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	0.24	0/383	0.51	0/504
2	1	0.23	0/484	0.46	0/637
3	2	0.22	0/306	0.48	0/401
4	9	0.25	0/3071	0.49	0/4147
5	A	0.25	0/1954	0.48	0/2642
6	B	0.25	0/1721	0.50	0/2323
7	C	0.26	0/1691	0.47	0/2267
8	D	0.25	0/1188	0.52	0/1593
9	E	0.26	0/1384	0.51	0/1867
10	F	0.26	0/1266	0.51	1/1700 (0.1%)
11	G	0.28	0/1126	0.58	0/1517
12	H	0.25	0/1044	0.46	0/1395
13	I	0.31	0/820	0.65	2/1103 (0.2%)
14	J	0.26	0/844	0.49	0/1136
15	K	0.28	0/1094	0.56	0/1468
16	L	0.27	0/962	0.54	1/1289 (0.1%)
17	M	0.24	0/483	0.47	0/643
18	N	0.26	0/679	0.47	0/907
19	O	0.26	0/659	0.53	0/885
20	P	0.24	0/684	0.46	0/913
21	Q	0.25	0/545	0.52	0/730
22	R	0.25	0/698	0.54	0/936
23	S	0.23	0/631	0.37	0/838
24	T	0.29	0/475	0.60	0/621
25	a	0.23	0/2267	0.46	0/3044
26	b	0.29	0/1795	0.55	0/2412
27	c	0.25	0/1671	0.50	0/2246
28	d	0.28	0/1409	0.52	0/1894
29	e	0.28	0/1420	0.55	0/1912
30	f	0.26	0/1183	0.56	0/1587
31	g	0.36	0/916	0.57	0/1222
32	h	0.27	0/968	0.50	0/1298
33	i	0.25	0/1186	0.50	0/1592
34	j	0.24	0/953	0.54	1/1275 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	k	0.25	0/1170	0.49	0/1559
36	l	0.27	0/1104	0.52	0/1481
37	m	0.24	0/973	0.52	0/1309
38	n	0.26	0/897	0.49	0/1198
39	o	0.24	0/948	0.49	0/1262
40	p	0.24	0/961	0.44	0/1278
41	q	0.26	0/828	0.56	0/1111
42	r	0.24	0/1077	0.48	0/1441
43	s	0.26	0/732	0.51	0/988
44	t	0.25	0/879	0.52	0/1165
45	u	0.25	0/665	0.52	0/884
46	v	0.30	0/519	0.56	0/695
47	w	0.24	0/826	0.49	0/1104
48	x	0.38	0/353	0.51	0/474
49	y	0.31	0/457	0.52	0/601
50	z	0.25	0/412	0.53	0/547
51	3	0.21	0/69073	0.81	31/107710 (0.0%)
52	4	0.24	0/2505	0.87	4/3902 (0.1%)
53	5	0.20	0/35768	0.79	15/55764 (0.0%)
54	6	0.23	0/1808	0.88	0/2817
54	7	0.23	0/1808	0.88	0/2817
All	All	0.22	0/161723	0.74	55/241051 (0.0%)

There are no bond length outliers.

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	I	99	PRO	CA-N-CD	-8.78	99.21	111.50
53	5	843	C	N3-C2-O2	-8.42	116.01	121.90
51	3	559	C	N3-C2-O2	-7.66	116.54	121.90
52	4	79	U	C2-N1-C1'	7.49	126.69	117.70
51	3	1916	C	N3-C2-O2	-7.18	116.87	121.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	43 (96%)	2 (4%)	0	100	100
2	1	57/59 (97%)	53 (93%)	4 (7%)	0	100	100
3	2	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
4	9	391/394 (99%)	360 (92%)	31 (8%)	0	100	100
5	A	238/294 (81%)	212 (89%)	26 (11%)	0	100	100
6	B	213/273 (78%)	200 (94%)	13 (6%)	0	100	100
7	C	201/205 (98%)	191 (95%)	10 (5%)	0	100	100
8	D	151/219 (69%)	143 (95%)	8 (5%)	0	100	100
9	E	165/215 (77%)	143 (87%)	22 (13%)	0	100	100
10	F	152/155 (98%)	137 (90%)	15 (10%)	0	100	100
11	G	139/142 (98%)	123 (88%)	15 (11%)	1 (1%)	22	63
12	H	126/132 (96%)	121 (96%)	5 (4%)	0	100	100
13	I	99/108 (92%)	84 (85%)	15 (15%)	0	100	100
14	J	112/121 (93%)	106 (95%)	6 (5%)	0	100	100
15	K	134/139 (96%)	117 (87%)	17 (13%)	0	100	100
16	L	116/124 (94%)	104 (90%)	11 (10%)	1 (1%)	17	57
17	M	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
18	N	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
19	O	78/94 (83%)	70 (90%)	8 (10%)	0	100	100
20	P	81/85 (95%)	79 (98%)	2 (2%)	0	100	100
21	Q	63/104 (61%)	54 (86%)	9 (14%)	0	100	100
22	R	82/87 (94%)	72 (88%)	10 (12%)	0	100	100
23	S	75/87 (86%)	75 (100%)	0	0	100	100
24	T	51/60 (85%)	49 (96%)	2 (4%)	0	100	100
25	a	283/287 (99%)	261 (92%)	22 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	b	227/287 (79%)	209 (92%)	18 (8%)	0	100	100
27	c	208/212 (98%)	196 (94%)	12 (6%)	0	100	100
28	d	173/180 (96%)	160 (92%)	13 (8%)	0	100	100
29	e	174/184 (95%)	165 (95%)	8 (5%)	1 (1%)	25	66
30	f	143/149 (96%)	128 (90%)	14 (10%)	1 (1%)	22	63
31	g	117/161 (73%)	107 (92%)	7 (6%)	3 (3%)	5	31
32	h	126/137 (92%)	115 (91%)	11 (9%)	0	100	100
33	i	142/146 (97%)	128 (90%)	14 (10%)	0	100	100
34	j	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
35	k	146/151 (97%)	137 (94%)	9 (6%)	0	100	100
36	l	134/139 (96%)	125 (93%)	8 (6%)	1 (1%)	22	63
37	m	117/124 (94%)	114 (97%)	3 (3%)	0	100	100
38	n	108/116 (93%)	98 (91%)	10 (9%)	0	100	100
39	o	113/119 (95%)	102 (90%)	11 (10%)	0	100	100
40	p	112/127 (88%)	109 (97%)	3 (3%)	0	100	100
41	q	97/100 (97%)	85 (88%)	12 (12%)	0	100	100
42	r	137/159 (86%)	124 (90%)	13 (10%)	0	100	100
43	s	90/237 (38%)	86 (96%)	4 (4%)	0	100	100
44	t	109/111 (98%)	101 (93%)	8 (7%)	0	100	100
45	u	84/104 (81%)	81 (96%)	3 (4%)	0	100	100
46	v	61/65 (94%)	61 (100%)	0	0	100	100
47	w	96/111 (86%)	91 (95%)	5 (5%)	0	100	100
48	x	42/97 (43%)	35 (83%)	7 (17%)	0	100	100
49	y	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
50	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	6204/7064 (88%)	5732 (92%)	464 (8%)	8 (0%)	54	86

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
31	g	88	GLU
29	e	169	ASP
31	g	32	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
31	g	30	THR
11	G	105	PRO

5.3.2 Protein sidechains [i](#)

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	9	324/325 (100%)	322 (99%)	2 (1%)	86	92
5	A	212/262 (81%)	212 (100%)	0	100	100
6	B	180/232 (78%)	178 (99%)	2 (1%)	73	84
7	C	181/183 (99%)	181 (100%)	0	100	100
8	D	123/178 (69%)	117 (95%)	6 (5%)	25	50
9	E	150/196 (76%)	149 (99%)	1 (1%)	84	90
10	F	131/132 (99%)	131 (100%)	0	100	100
11	G	123/124 (99%)	118 (96%)	5 (4%)	30	55
12	H	111/115 (96%)	110 (99%)	1 (1%)	78	87
13	I	95/99 (96%)	93 (98%)	2 (2%)	53	72
14	J	91/97 (94%)	91 (100%)	0	100	100
15	K	117/120 (98%)	111 (95%)	6 (5%)	24	48
16	L	100/105 (95%)	97 (97%)	3 (3%)	41	63
17	M	47/48 (98%)	47 (100%)	0	100	100
18	N	76/78 (97%)	76 (100%)	0	100	100
19	O	69/82 (84%)	69 (100%)	0	100	100
20	P	73/75 (97%)	73 (100%)	0	100	100
21	Q	56/94 (60%)	56 (100%)	0	100	100
22	R	74/77 (96%)	74 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	S	70/77 (91%)	69 (99%)	1 (1%)	67	80
24	T	49/56 (88%)	49 (100%)	0	100	100
25	a	241/243 (99%)	239 (99%)	2 (1%)	81	89
26	b	186/233 (80%)	185 (100%)	1 (0%)	88	93
27	c	182/184 (99%)	181 (100%)	1 (0%)	88	93
28	d	150/154 (97%)	150 (100%)	0	100	100
29	e	153/159 (96%)	153 (100%)	0	100	100
30	f	123/134 (92%)	118 (96%)	5 (4%)	30	55
31	g	96/129 (74%)	89 (93%)	7 (7%)	14	39
32	h	102/110 (93%)	102 (100%)	0	100	100
33	i	126/128 (98%)	126 (100%)	0	100	100
34	j	103/103 (100%)	102 (99%)	1 (1%)	76	86
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%)	105 (100%)	0	100	100
38	n	96/99 (97%)	95 (99%)	1 (1%)	76	86
39	o	101/105 (96%)	99 (98%)	2 (2%)	55	74
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%)	114 (98%)	2 (2%)	60	78
43	s	82/208 (39%)	81 (99%)	1 (1%)	71	83
44	t	96/96 (100%)	95 (99%)	1 (1%)	76	86
45	u	69/85 (81%)	68 (99%)	1 (1%)	67	80
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%)	39 (95%)	2 (5%)	25	50
49	y	48/49 (98%)	45 (94%)	3 (6%)	18	43
50	z	47/50 (94%)	45 (96%)	2 (4%)	29	53
All	All	5412/6076 (89%)	5351 (99%)	61 (1%)	74	84

5 of 61 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	S	43	ASN
48	x	41	LYS
30	f	47	ARG
48	x	30	LYS
50	z	8	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
42	r	38	ASN
44	t	17	ASN
20	P	5	GLN
18	N	35	GLN
47	w	64	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	3	2875/2907 (98%)	849 (29%)	29 (1%)
52	4	103/108 (95%)	38 (36%)	3 (2%)
53	5	1490/1520 (98%)	411 (27%)	7 (0%)
54	6	75/76 (98%)	30 (40%)	2 (2%)
54	7	75/76 (98%)	30 (40%)	2 (2%)
All	All	4618/4687 (98%)	1358 (29%)	43 (0%)

5 of 1358 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	3	14	U
51	3	15	A
51	3	20	C
51	3	22	U
51	3	29	G

5 of 43 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	3	2897	G
53	5	618	U
52	4	10	C
53	5	8	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	5	920	G

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.

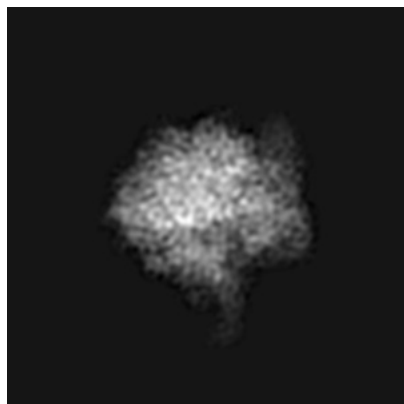
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13446. These allow visual inspection of the internal detail of the map and identification of artifacts.

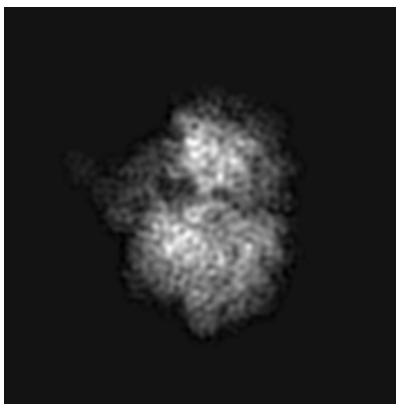
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

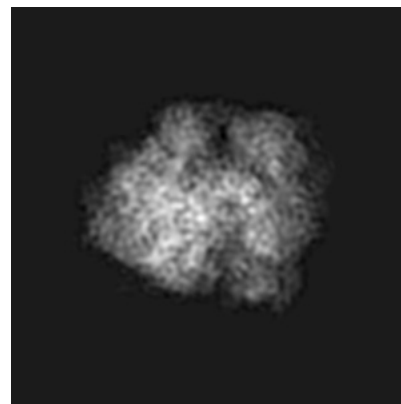
6.1.1 Primary map



X

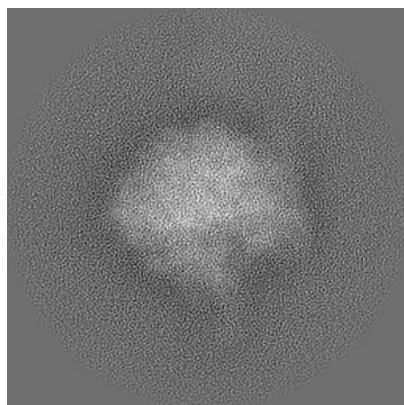


Y

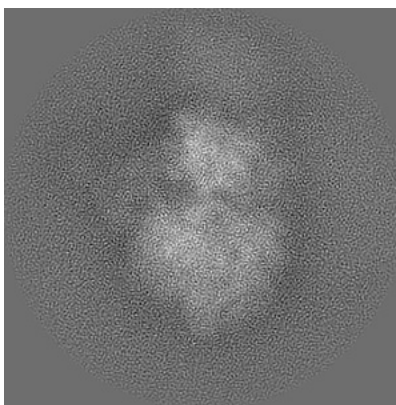


Z

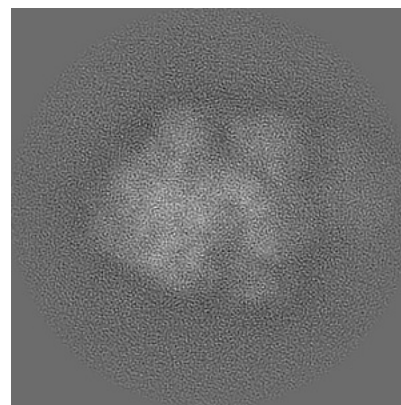
6.1.2 Raw map



X



Y

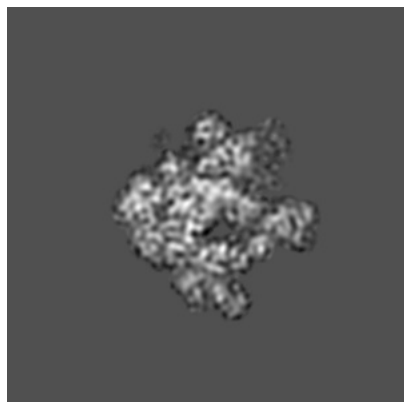


Z

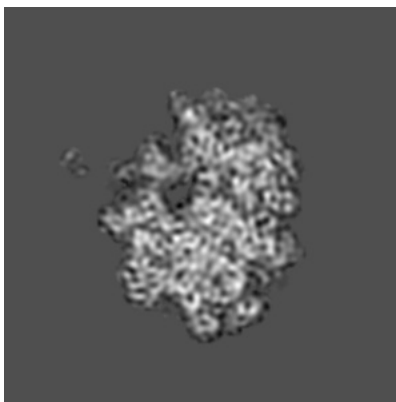
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

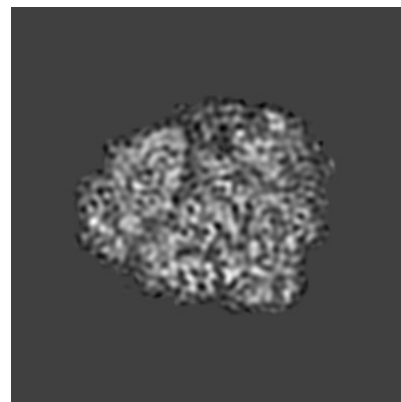
6.2.1 Primary map



X Index: 128

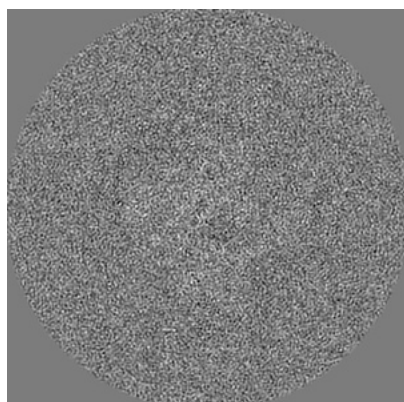


Y Index: 128

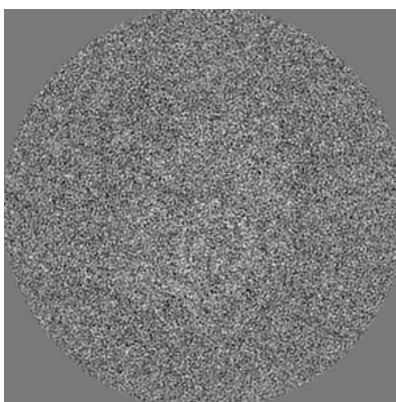


Z Index: 128

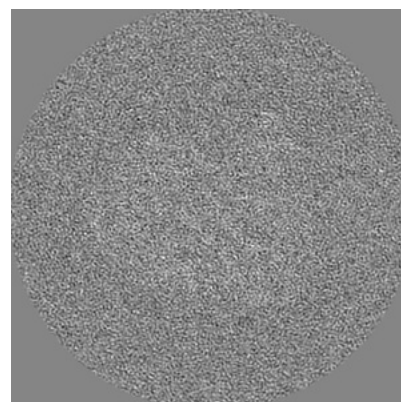
6.2.2 Raw map



X Index: 128



Y Index: 128

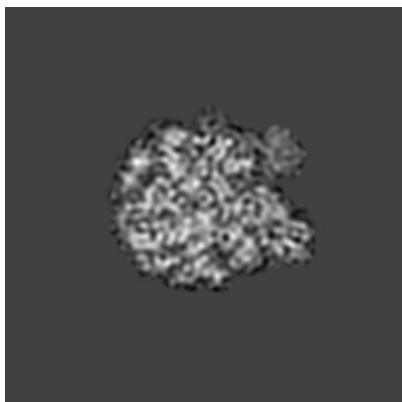


Z Index: 128

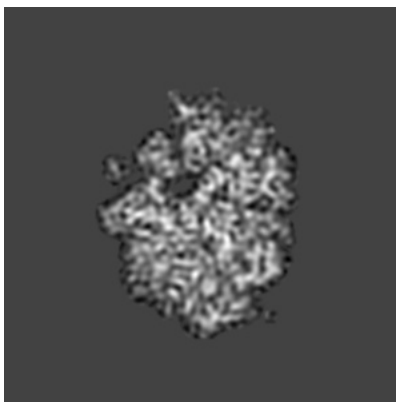
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

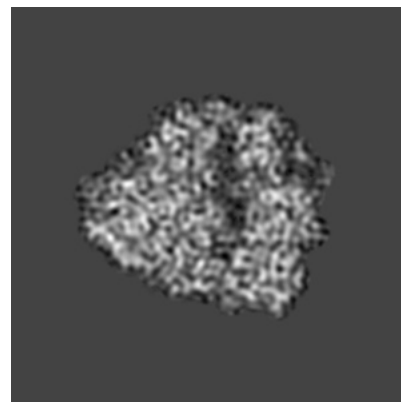
6.3.1 Primary map



X Index: 103

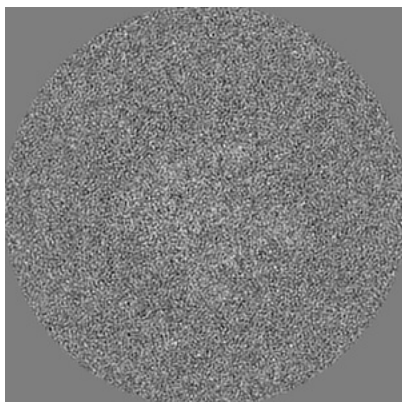


Y Index: 121

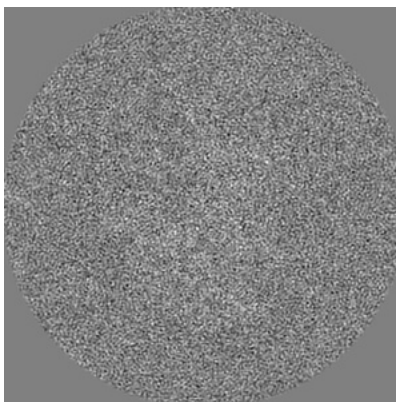


Z Index: 121

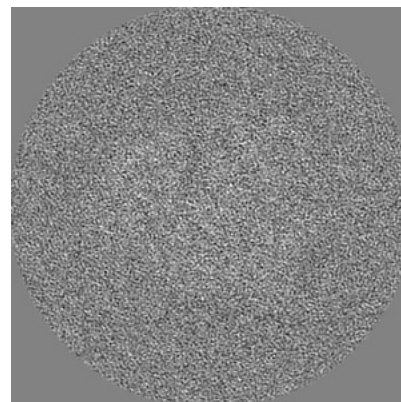
6.3.2 Raw map



X Index: 125



Y Index: 127

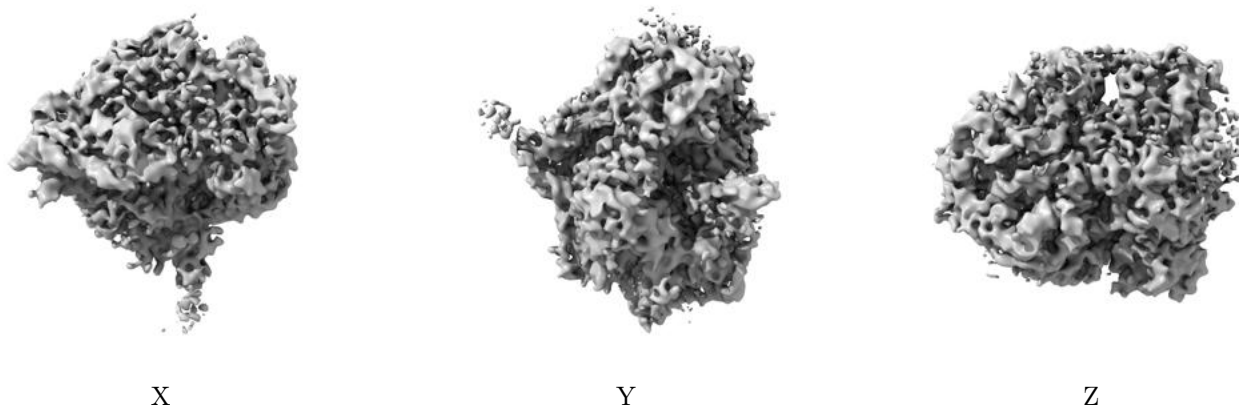


Z Index: 129

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

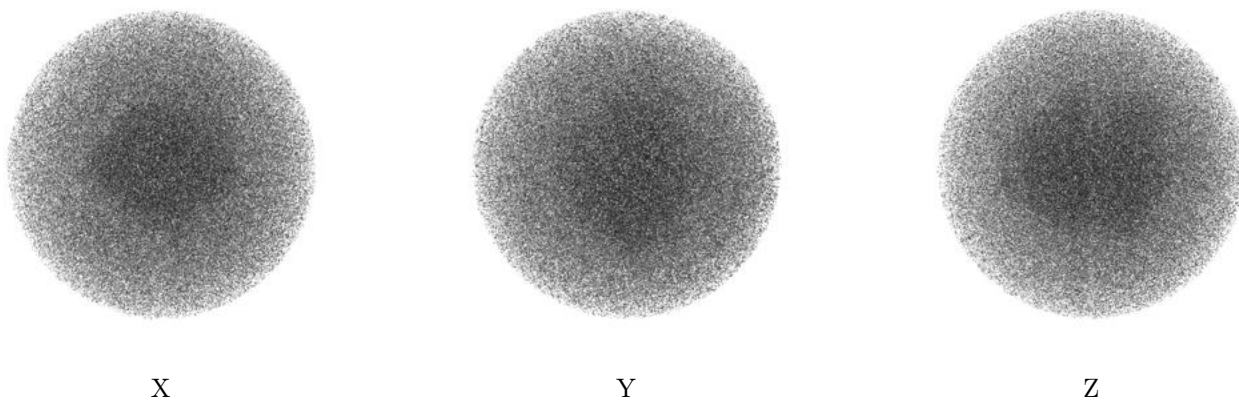
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.39. 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.

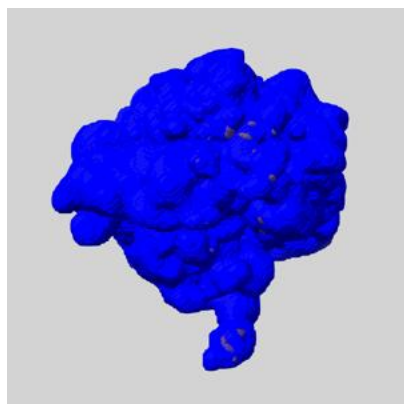
6.5 Mask visualisation [i](#)

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

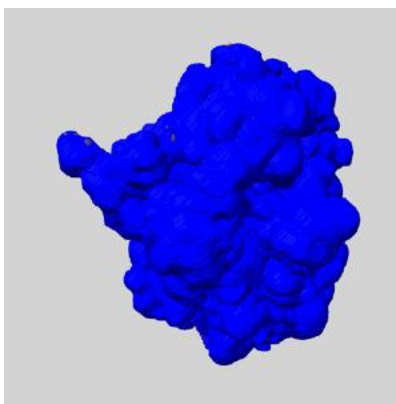
A mask typically either:

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

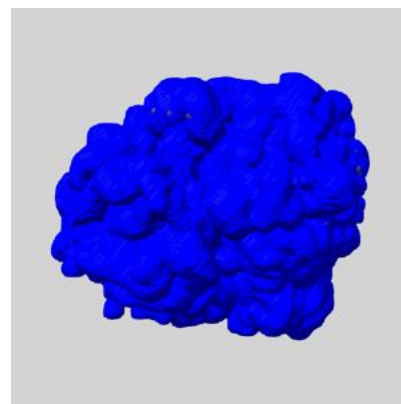
6.5.1 emd_13446_msk_1.map [i](#)



X



Y

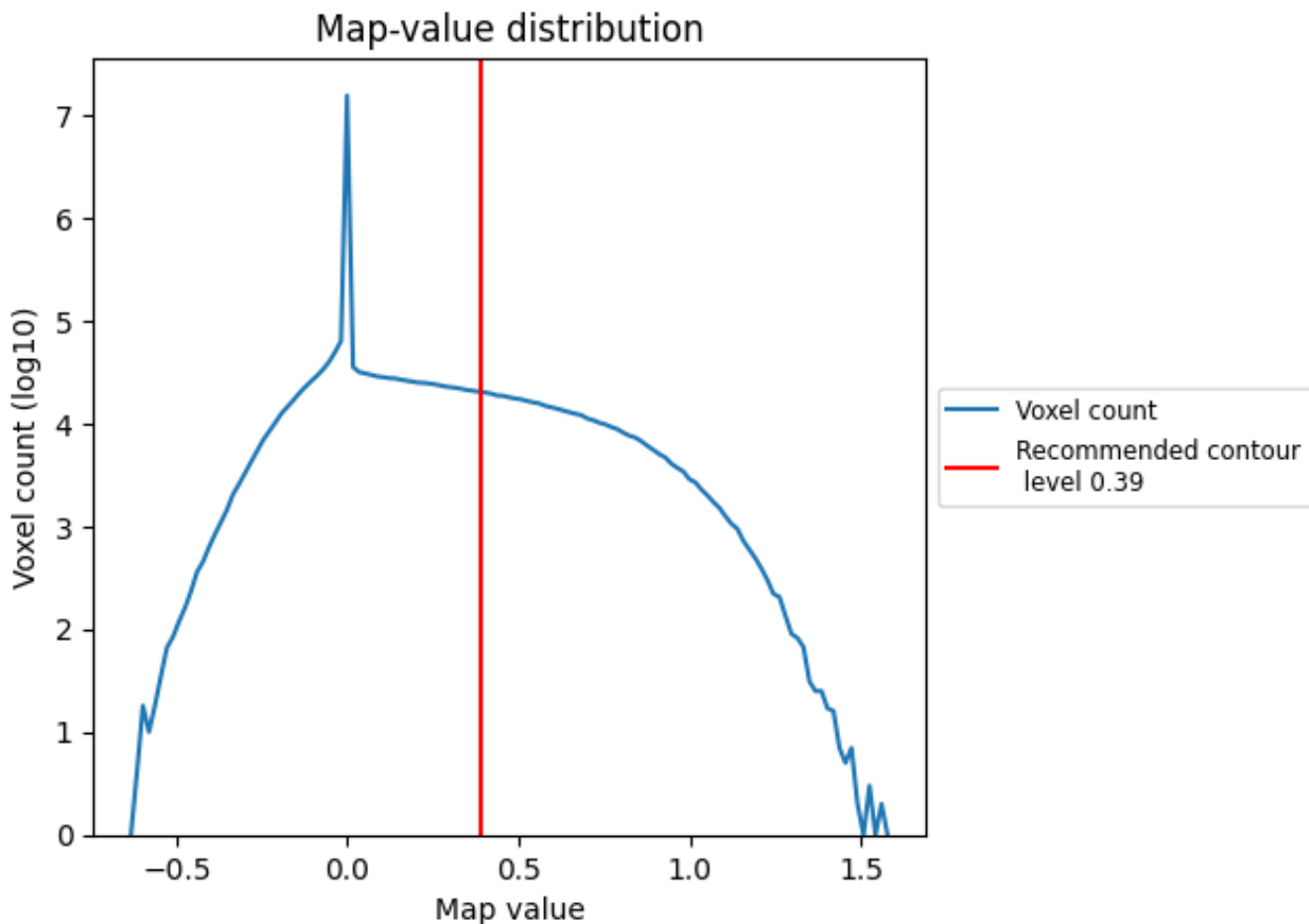


Z

7 Map analysis [i](#)

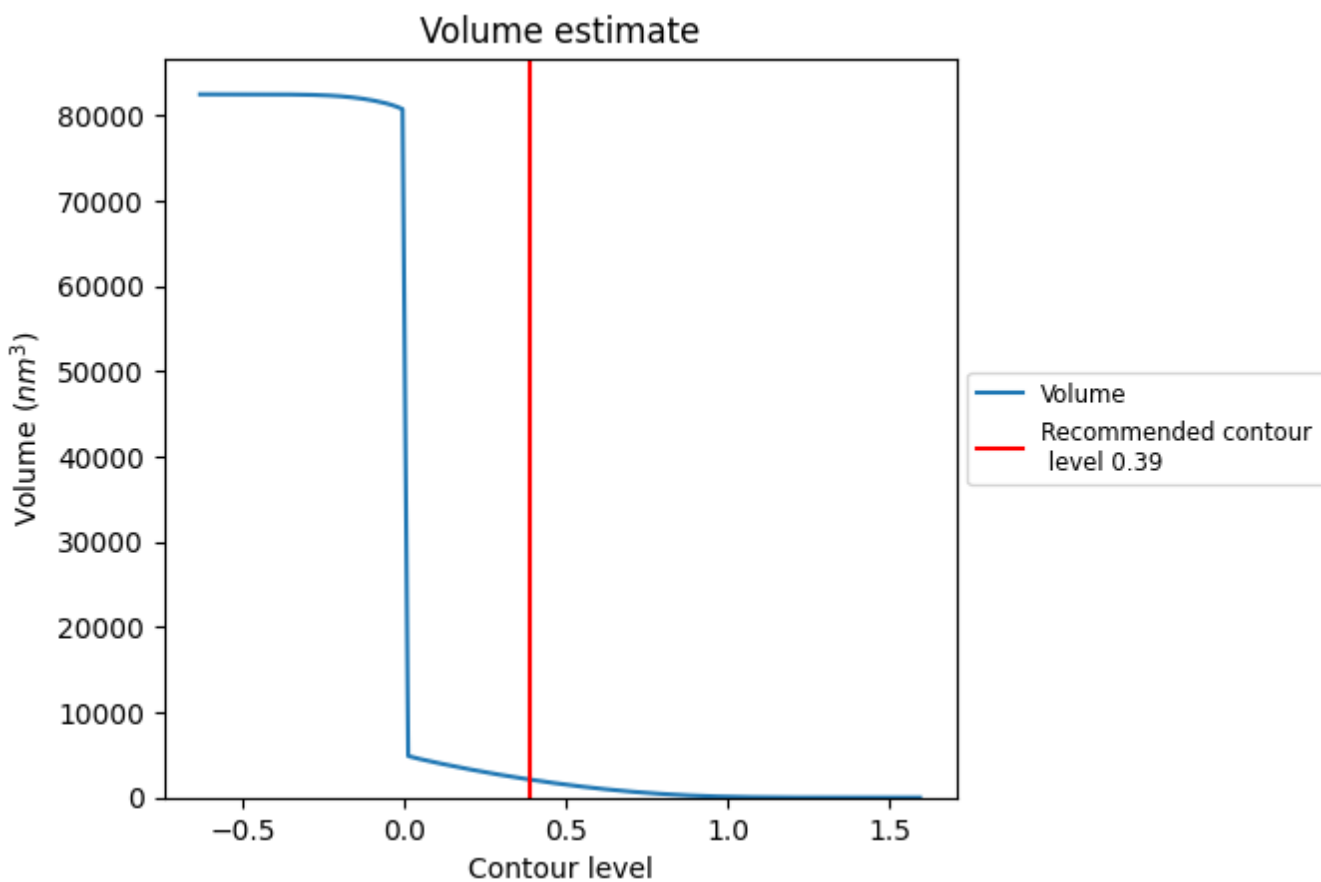
This section contains the results of statistical analysis of the map.

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.

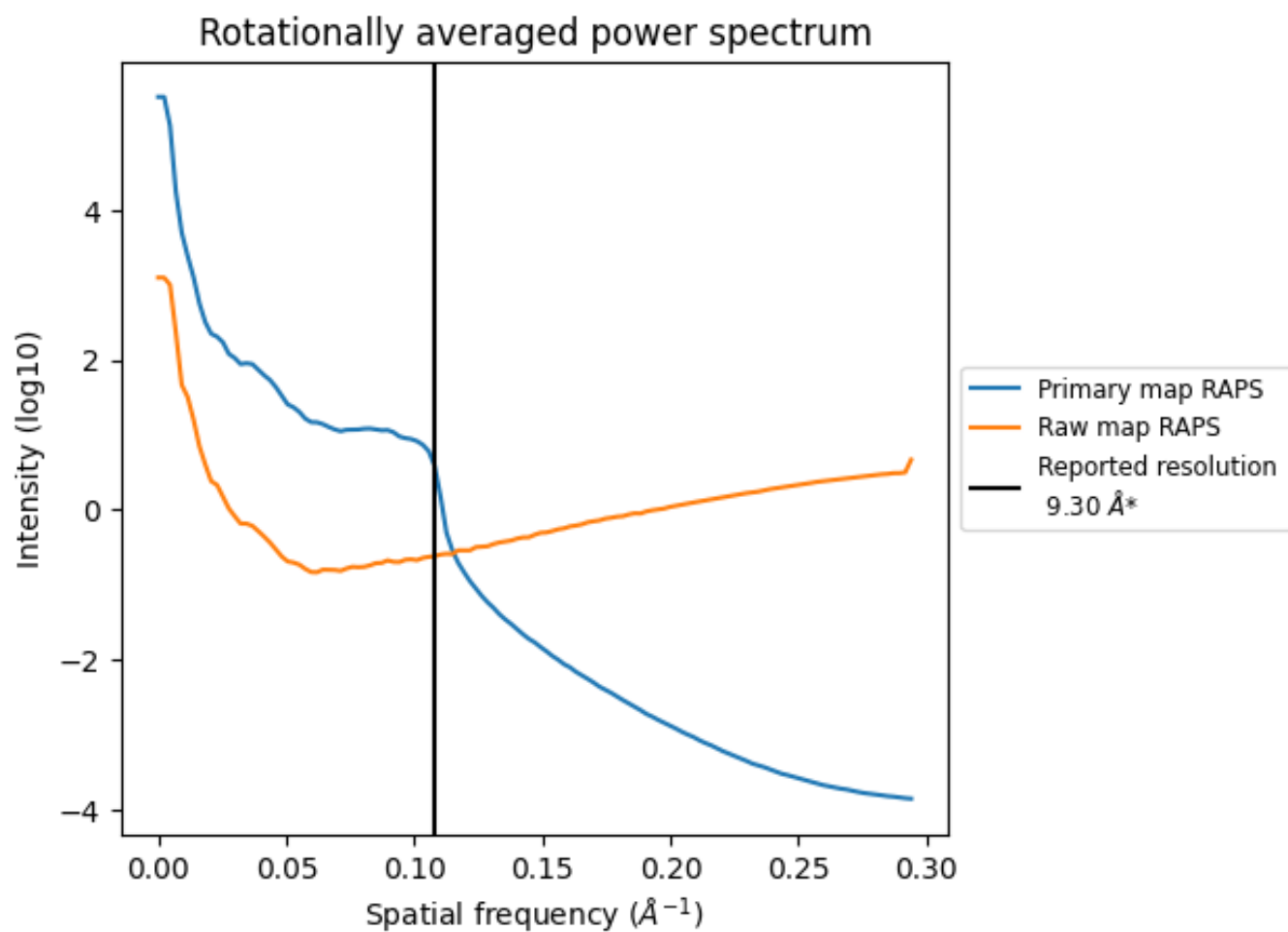
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2100 nm³; this corresponds to an approximate mass of 1897 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 [i](#)

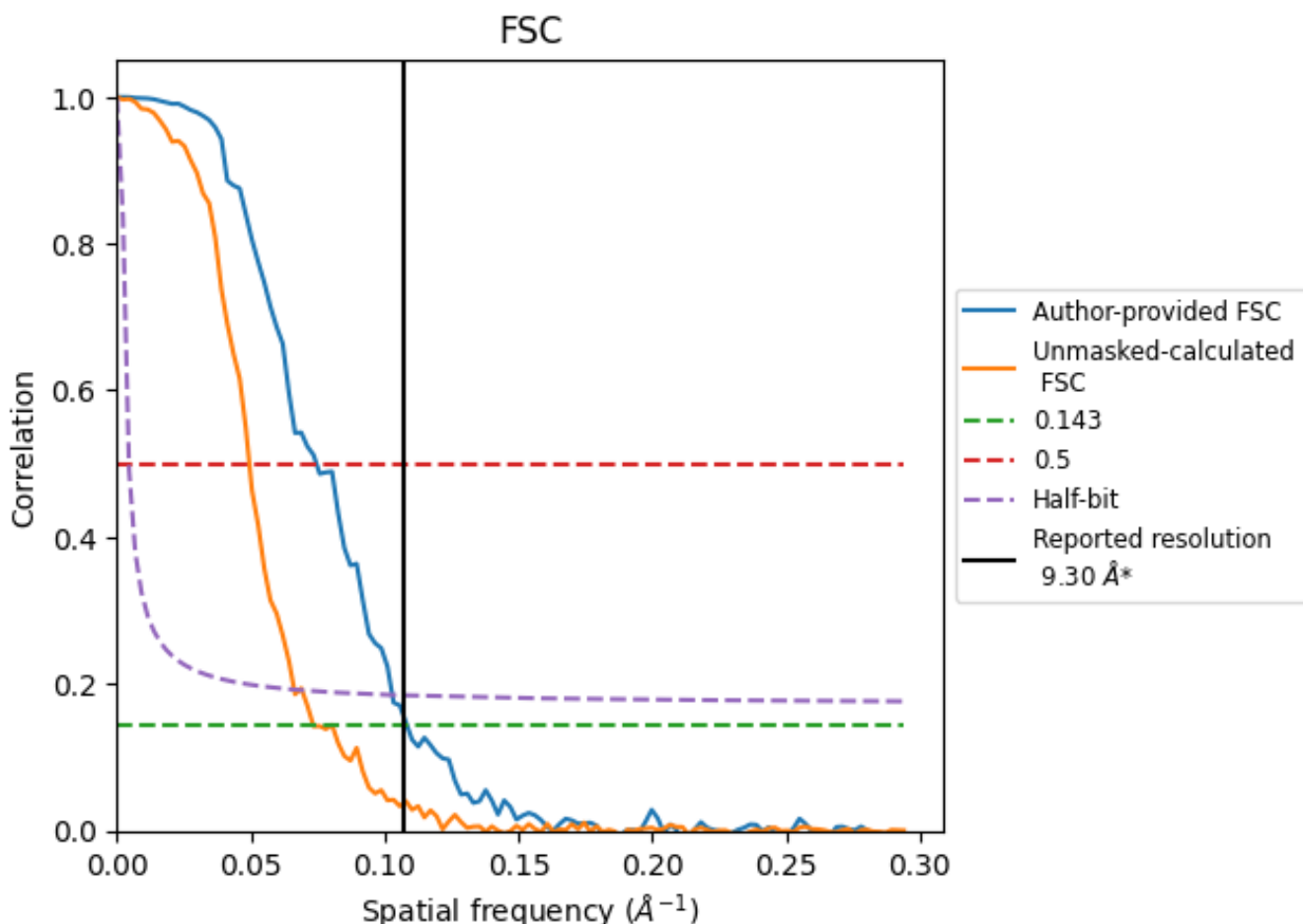


*Reported resolution corresponds to spatial frequency of 0.108 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.108 Å⁻¹

8.2 Resolution estimates

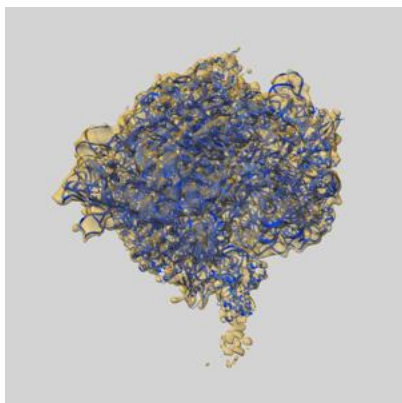
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.30	-	-
Author-provided FSC curve	9.23	13.40	9.72
Unmasked-calculated*	13.62	20.16	15.08

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 13.62 differs from the reported value 9.3 by more than 10 %

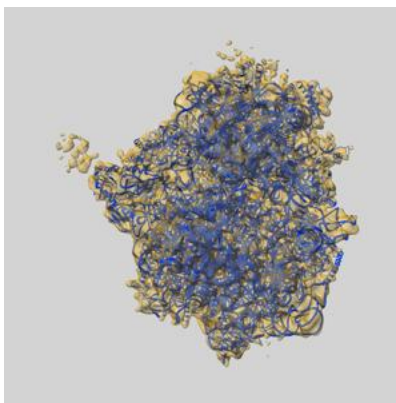
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13446 and PDB model 7PIP. Per-residue inclusion information can be found in section 3 on page 13.

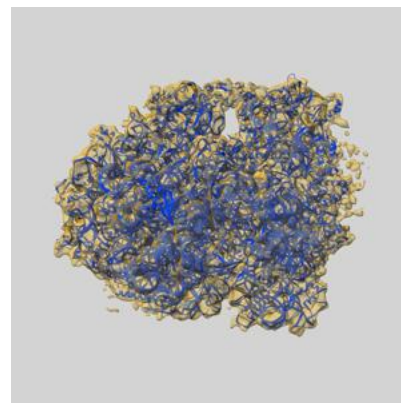
9.1 Map-model overlay [i](#)



X



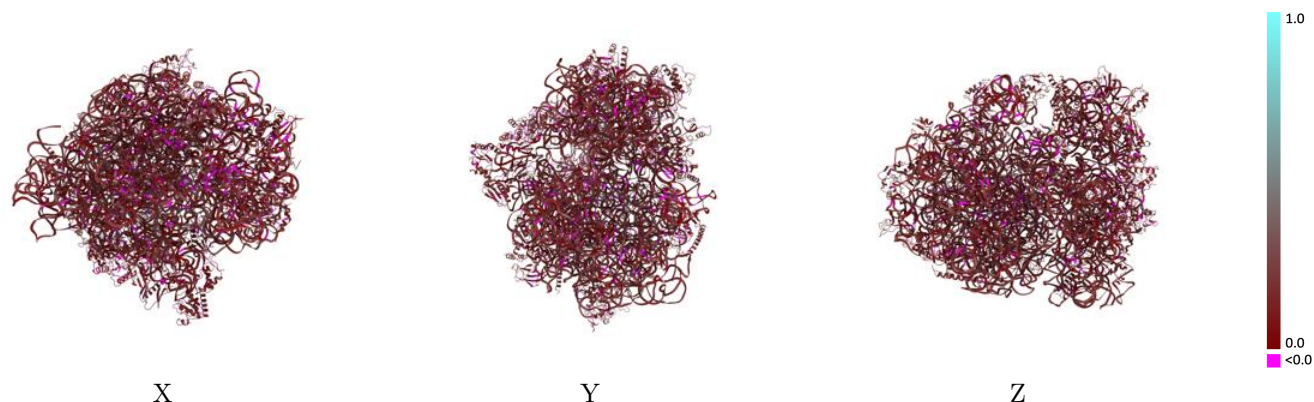
Y



Z

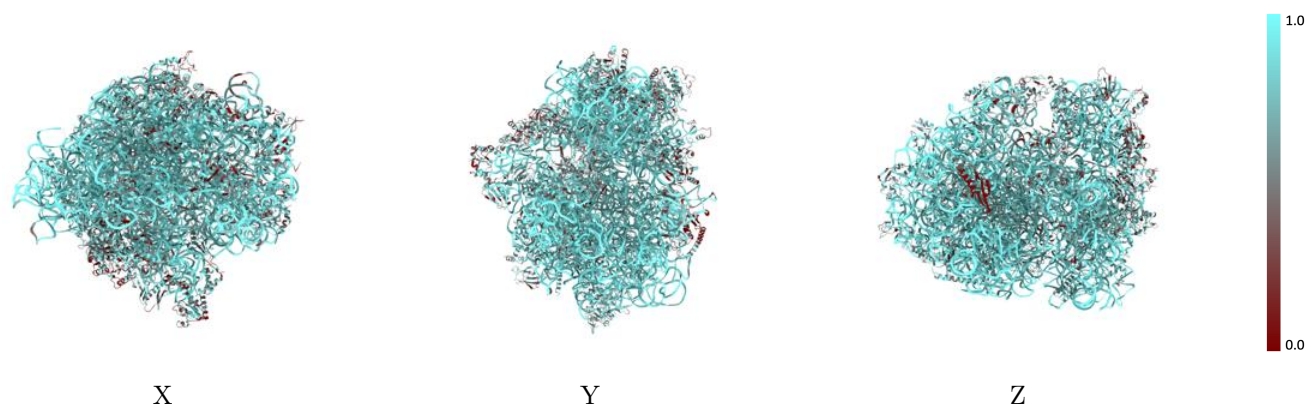
The images above show the 3D surface view of the map at the recommended contour level 0.39 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



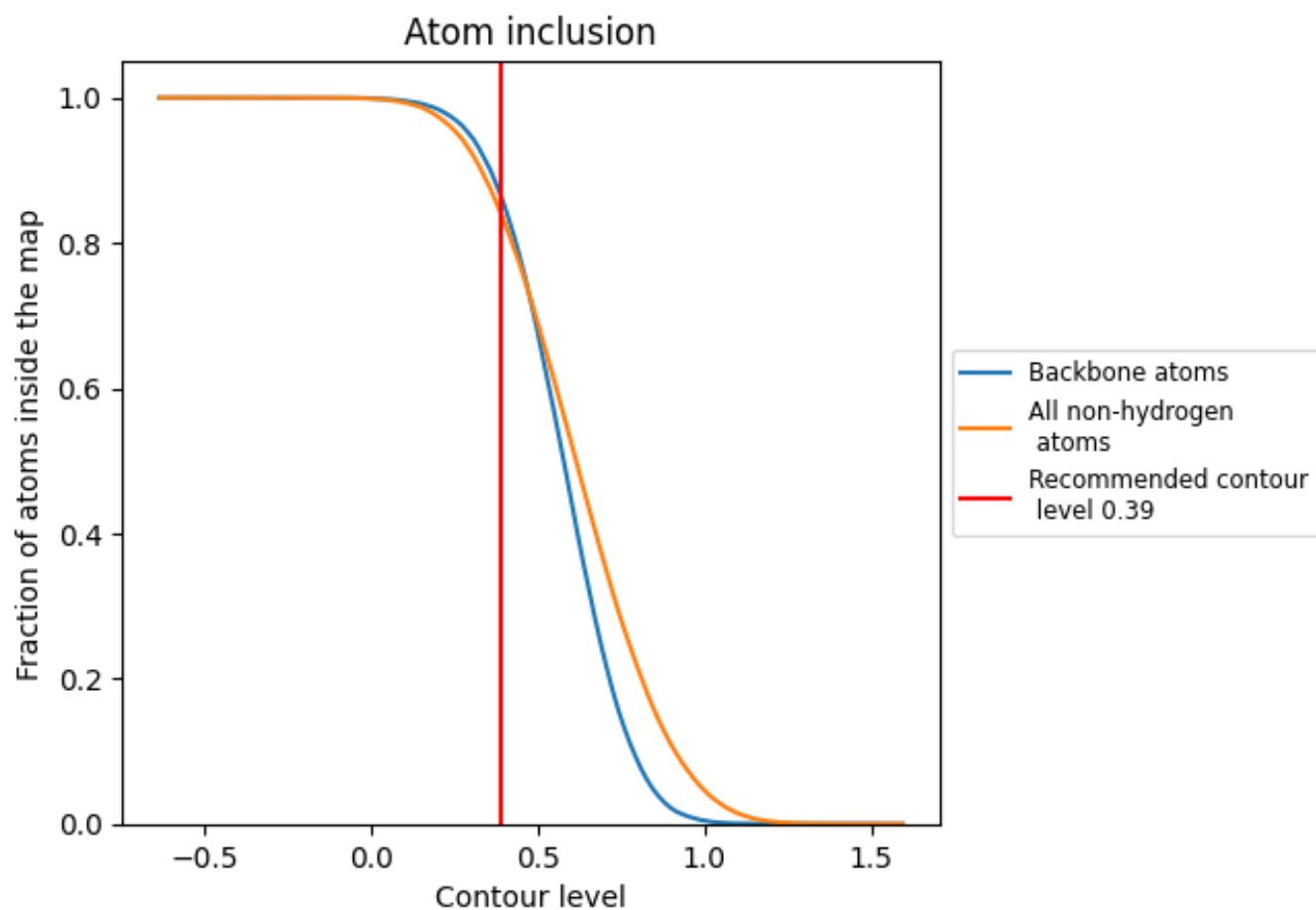
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.39).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% 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 (0.39) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8418	 0.1590
0	 0.7945	 0.1400
1	 0.7618	 0.1410
2	 0.7466	 0.1130
3	 0.9413	 0.1680
4	 0.9415	 0.1790
5	 0.9439	 0.1710
6	 0.7849	 0.1530
7	 0.7497	 0.1100
9	 0.4821	 0.1290
A	 0.5774	 0.1580
B	 0.5900	 0.1450
C	 0.6758	 0.1420
D	 0.6323	 0.1390
E	 0.6040	 0.1620
F	 0.6306	 0.1450
G	 0.6581	 0.1360
H	 0.6264	 0.1110
I	 0.6075	 0.1400
J	 0.6401	 0.1270
K	 0.7011	 0.1410
L	 0.6569	 0.1480
M	 0.6242	 0.1050
N	 0.7024	 0.1720
O	 0.8188	 0.1670
P	 0.7306	 0.1640
Q	 0.6202	 0.1360
R	 0.6179	 0.0970
S	 0.7787	 0.1640
T	 0.7188	 0.1880
a	 0.7315	 0.1280
b	 0.6843	 0.1320
c	 0.6904	 0.1490
d	 0.6193	 0.1470
e	 0.6301	 0.1530



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
f	 0.2463	 0.1380
g	 0.5150	 0.1540
h	 0.5225	 0.1410
i	 0.7029	 0.1310
j	 0.5902	 0.1290
k	 0.7414	 0.1430
l	 0.7280	 0.1410
m	 0.7415	 0.1370
n	 0.6770	 0.1450
o	 0.6817	 0.1550
p	 0.7716	 0.1390
q	 0.6846	 0.1400
r	 0.7960	 0.1710
s	 0.6700	 0.1370
t	 0.6272	 0.1510
u	 0.7641	 0.1170
v	 0.7515	 0.1520
w	 0.7553	 0.1870
x	 0.5394	 0.1620
y	 0.7465	 0.1270
z	 0.7935	 0.1300