



## wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 05:36 AM UTC

PDB ID : 7OPE / pdb\_00007ope  
EMDB ID : EMD-13017  
Title : RqcH DR variant bound to 50S-peptidyl-tRNA-RqcP RQC complex (rigid body refinement)  
Authors : Crowe-McAuliffe, C.; Wilson, D.N.  
Deposited on : 2021-05-31  
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

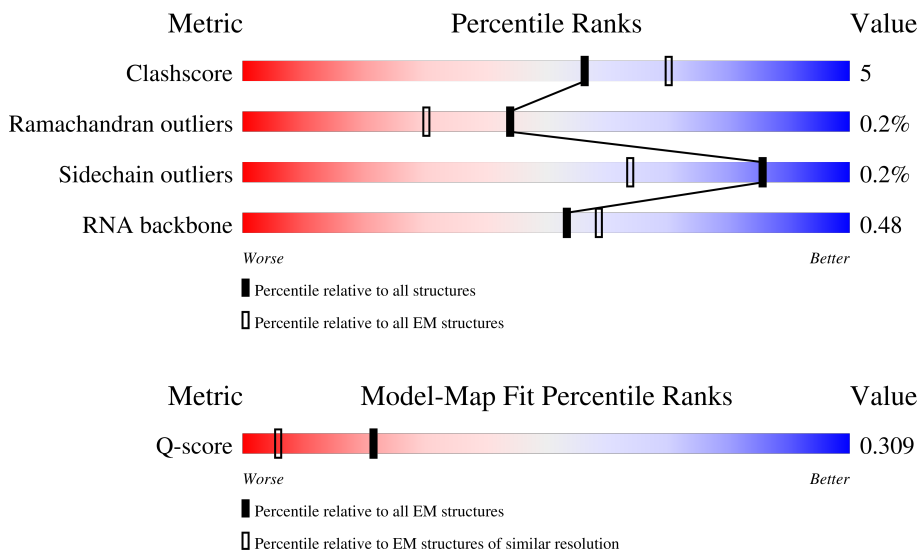
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.20 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.










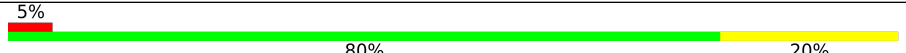
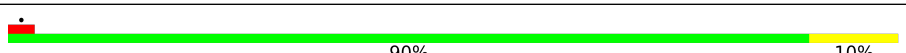
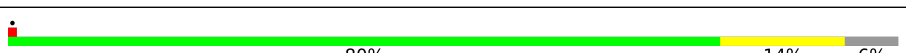
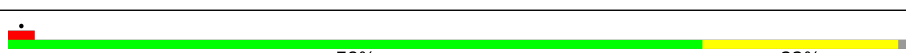
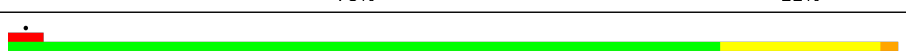

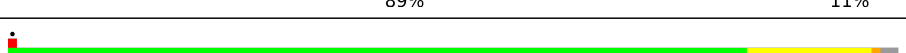
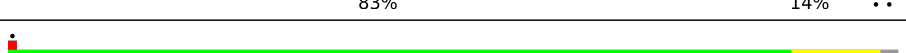

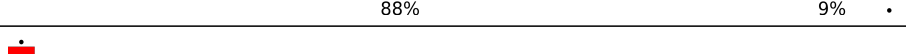
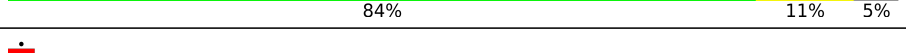
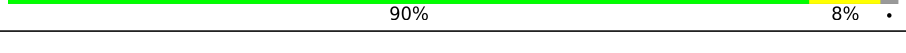




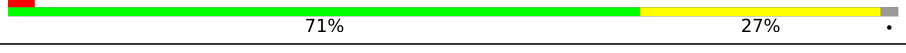
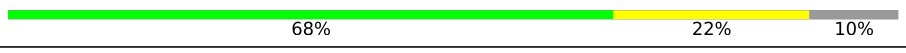
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 ( 2.70 - 3.70 )

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

Mol	Chain	Length	Quality of chain
1	A	2926	
2	B	119	
3	E	277	

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Mol	Chain	Length	Quality of chain
4	F	209	 85% 13%
5	G	207	 89% 10%
6	H	179	 8% 77% 20%
7	I	179	 84% 14%
8	K	141	 13% 82% 12% 6%
9	L	166	 10% 52% 16% 32%
10	N	145	 81% 17%
11	O	122	 5% 80% 20%
12	P	146	 90% 10%
13	Q	144	 80% 14% 6%
14	R	120	 78% 22%
15	S	120	 80% 18%
16	T	115	 10% 89% 11%
17	U	119	 83% 14%
18	V	102	 88% 10%
19	W	113	 88% 9%
20	X	95	 84% 11% 5%
21	Y	103	 90% 8%
22	2	76	 41% 38% 12% 8%
23	a	94	 72% 14% 14%
24	b	62	 19% 87% 6% 6%
25	c	66	 76% 23%
26	d	59	 71% 27%
27	f	59	 68% 22% 10%
28	g	49	 86% 12%

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Mol	Chain	Length	Quality of chain
29	h	44	<p>84% 16%</p>
30	i	66	<p>80% 17%</p>
31	j	37	<p>89% 11%</p>
32	1	86	<p>17% 92% 5%</p>
33	0	599	<p>50% 75% 12% 11%</p>

## 2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 93862 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 RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	2814	60436	26962	11170	19491	2813	0	0

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	112	2392	1068	435	778	111	0	0

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	E	272	2083	1296	408	373	6	0	0

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	F	206	1569	985	289	290	5	0	0

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	G	205	1561	980	289	290	2	0	0

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	H	176	1387	883	241	256	7	0	0

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	I	175	1342	835	248	257	2	0	0

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	K	132	974	612	172	184	6	0	0

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	L	113	886	559	152	174	1	0	0

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	N	142	1124	710	206	203	5	0	0

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	O	122	921	571	173	173	4	0	0

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	P	146	1082	671	207	202	2	0	0

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	Q	135	1076	690	205	176	5	0	0

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	R	119	Total	C	N	O	S	0	0
			954	583	186	181	4		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	120	Total	C	N	O	S	0	0
			913	564	176	172	1		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	115	Total	C	N	O	S	0	0
			945	600	185	159	1		

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	U	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	V	100	Total	C	N	O	0	0
			781	498	138	145		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	W	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	X	90	Total	C	N	O	S	0	0
			725	452	134	136	3		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Y	101	Total	C	N	O	S	0	0
			762	478	142	138	4		

- Molecule 22 is a RNA chain called tRNA-Ala-UGC.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	2	70	Total	C	N	O	P	0	0
			1496	666	271	489	70		

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	a	81	Total	C	N	O	0	0
			624	387	122	115		

- Molecule 24 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	b	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	c	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 26 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	d	58	Total	C	N	O	S	0	0
			456	281	89	85	1		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	f	53	Total	C	N	O	S	0	0
			418	258	84	69	7		

- Molecule 28 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	g	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	h	44	Total	C	N	O	S	0	0
			368	222	89	55	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	i	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	j	37	Total	C	N	O	S	0	0
			297	186	60	46	5		

- Molecule 32 is a protein called Uncharacterized protein YabO.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	1	83	Total	C	N	O	S	0	0
			659	410	121	126	2		

- Molecule 33 is a protein called Rqc2 homolog RqcH.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	0	532	Total	C	N	O	S	0	0
			3962	2504	705	743	10		

There are 29 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	97	ALA	ASP	conflict	UNP A0A6M4JI41
0	98	ALA	ARG	conflict	UNP A0A6M4JI41
0	571	GLY	-	expression tag	UNP A0A6M4JI41
0	572	SER	-	expression tag	UNP A0A6M4JI41
0	573	GLY	-	expression tag	UNP A0A6M4JI41
0	574	GLY	-	expression tag	UNP A0A6M4JI41

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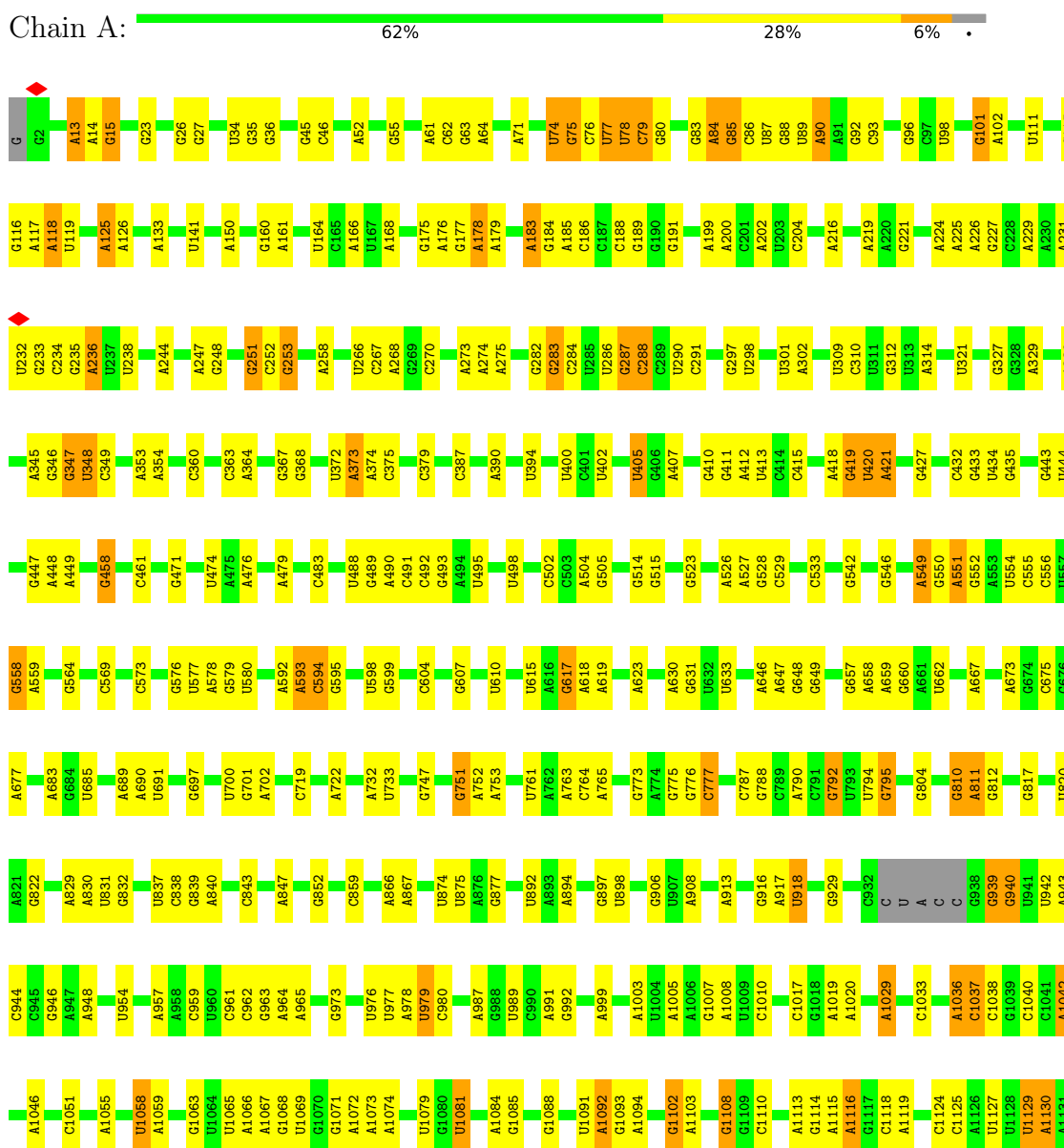
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Chain	Residue	Modelled	Actual	Comment	Reference
0	575	ASP	-	expression tag	UNP A0A6M4JI41
0	576	TYR	-	expression tag	UNP A0A6M4JI41
0	577	LYS	-	expression tag	UNP A0A6M4JI41
0	578	ASP	-	expression tag	UNP A0A6M4JI41
0	579	HIS	-	expression tag	UNP A0A6M4JI41
0	580	ASP	-	expression tag	UNP A0A6M4JI41
0	581	GLY	-	expression tag	UNP A0A6M4JI41
0	582	ASP	-	expression tag	UNP A0A6M4JI41
0	583	TYR	-	expression tag	UNP A0A6M4JI41
0	584	LYS	-	expression tag	UNP A0A6M4JI41
0	585	ASP	-	expression tag	UNP A0A6M4JI41
0	586	HIS	-	expression tag	UNP A0A6M4JI41
0	587	ASP	-	expression tag	UNP A0A6M4JI41
0	588	ILE	-	expression tag	UNP A0A6M4JI41
0	589	ASP	-	expression tag	UNP A0A6M4JI41
0	590	TYR	-	expression tag	UNP A0A6M4JI41
0	591	LYS	-	expression tag	UNP A0A6M4JI41
0	592	ASP	-	expression tag	UNP A0A6M4JI41
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0	594	ASP	-	expression tag	UNP A0A6M4JI41
0	595	ASP	-	expression tag	UNP A0A6M4JI41
0	596	LYS	-	expression tag	UNP A0A6M4JI41
0	597	GLY	-	expression tag	UNP A0A6M4JI41

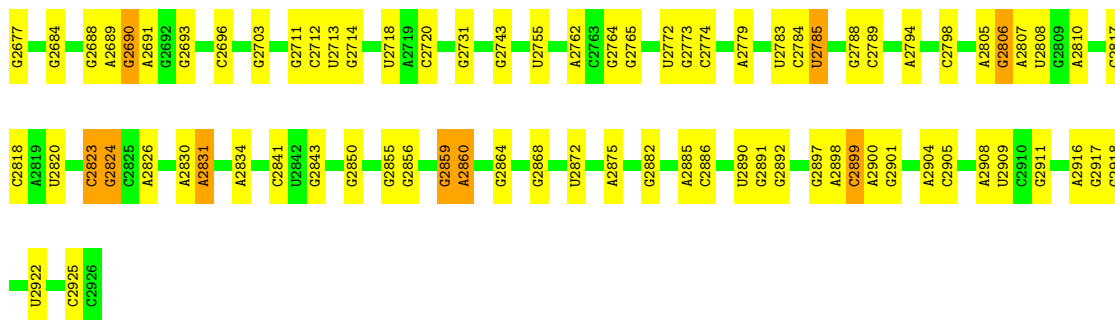
### 3 Residue-property plots i

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.

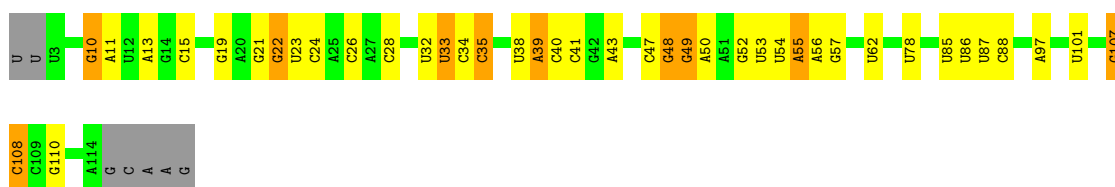
#### • Molecule 1: 23S rRNA



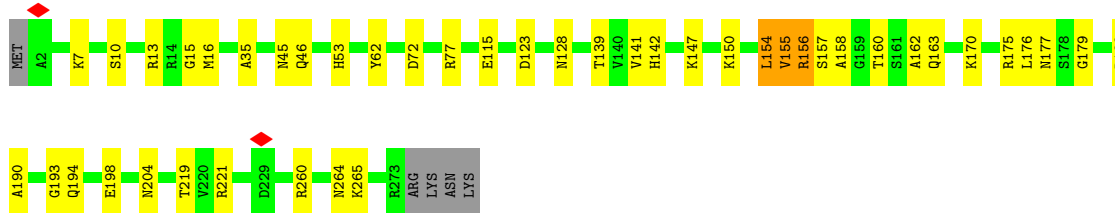
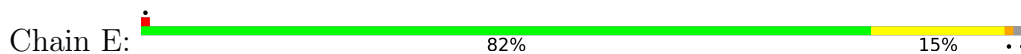
A2542	G2453	C2346	A2252	U2105	G1992	A1883	A1774	G1557	A1463	U1351	G1231	A1132
A2547	A2454	G2347	G2253	A2106	G1993	G1884	G1775	G1558	G1462	U1352	G1236	G1133
U2548	A2455	C2348	A2254	C2107	A1994	A1885	A1776	G1559	C1463	G1362	G1236	A1134
C2549	G2456	A2349	C2255	U2108	A1995	A1886	G1777	U1560	A1464	G1363	G1250	A1141
G2564	G2457	C2350	C2256	G2109	C1996	A1887	A1778	G1561	A1465	G1364	U1251	A1142
	U2458	U2351	G2267	U2121	A1999	A1888	G1779	U1565	U1466	C1365	U1252	U1143
	A2459	C2352	G2268	G2122	A2000	G1889	G1782	U1566	G1472	U1366	A1253	U1147
	U2460	U2353	U2274	A2123	G2001	C1892	C1783	U1567	A1473	G1367	A1253	C1148
	A2461	A2354	U2275	A2124	U1994	U1893	A1784	U1568	C1474	U1368	G1259	A1149
	G2464	C2356	G2278	U2125	G2009	U1894	G1785	A1569	G1475	C1369	A1260	C1150
	G2465	A2361	G2279	G2126	A2010	A1895	U1790	U1570	C1476	G1370	G1263	C1151
	A2468	A2362	U2127	U2128	U2011	G1898	U1791	G1571	G1481	C1372	G1264	G1152
	C2469	C2363	G2129	G2129	U2020	U1899	G1792	G1574	A1485	A1375	A1265	G1156
	U2470	U2364	G2130	U2021	G2021	G1904	G1793	A1575	A1488	G1376	A1266	A1157
	A2471	A2365	U2131	U2022	U2022	G1904	A1802	G1576	U1489	U1379	G1278	G1158
	G2472	C2366	A	C	C2025	G1935	C1803	G	A1490	U1380	G1278	G1159
	U2473	U2372	C	C	A2026	G1939	U1804	A	U1498	U1380	U1283	A1161
	A2474	U2373	A	A	A2027	U1940	C1811	A	A1499	C1384	A1284	C1162
	G2475	G2374	C	G	C2035	A	A1812	U	U1500	G1385	U1163	U1163
	C2476	C2375	C	C	C2035	A	A1813	U	U1501	C1388	C1164	C1164
	A2477	C2376	C	C	C2038	U	A1814	U	G1502	C1389	U1165	U1165
	G2484	C2379	C	U	G2038	U	A1820	A	A1506	C1390	G1171	G1171
	A2488	C2384	A	U	G2041	U	A1820	G	U1507	U1391	A1172	A1172
	G2605	U2385	U	A	U2048	U	G1828	U	C1508	U1392	A1173	A1173
	A2606	C2386	C	C	A1947	A	A1828	A	C1509	U1393	G1296	A1174
	C2607	U2386	C	C	A1948	A	A1829	A	C1509	G1403	G1304	A1175
	G2608	U2387	C	C	A1948	U	G1830	G1589	C1509	A1404	A1305	U1176
	A2498	A2390	C	C	G2050	U	A1831	A1582	A1516	A1406	G1306	G1177
	A2505	C2394	C	C	U2051	U	A1831	A1582	A1516	U1407	U1307	U1178
	G2506	U2394	C	U	C1953	C	A1831	U1595	G1525	A1417	G1311	A1179
	C2507	C2395	C	A	C1954	C	A1831	U1595	G1525	U1418	G1312	C1180
	U2508	U2396	C	C	C2054	U	A1831	G1600	C1527	A1418	A1312	C1181
	C2609	C2403	C	C	C2054	U	A1831	A1601	U1528	A1424	A1313	G1182
	A2631	G2404	C	U	A2060	U	A1831	U1602	G1529	A1425	A1314	G1185
	G2632	A2405	C	A	G2061	U	A1831	U1602	G1530	G1426	G1315	G1185
	U2633	A2406	C	G	A2062	U	A1831	A1608	G1531	A1427	G1315	G1185
	G2637	U2407	C	C	G2064	U	A1831	A1608	A1532	G1428	G1319	A1188
	U2638	G2412	A	A	C2072	U	A1831	A1614	A1533	G1431	G1322	A1189
	C2639	G2413	C	C	C2072	U	A1831	A1615	A1536	G1431	A1323	A1197
	U2642	U2414	C	U	A2078	U	A1831	G1616	A1536	A1434	G1324	C1198
	A2643	U2415	C	U	C2079	U	A1831	A1617	A1536	A1434	A1325	C1199
	U2644	U2416	C	U	A2080	U	A1831	C1625	A1540	U1435	A1325	G1200
	G2652	A2417	C	C	G2081	U	A1831	U1626	A1541	U1436	U1327	A1201
	C2652	G2420	C	C	C2081	U	A1831	A1627	A1542	A1442	G1333	A1202
	U2653	A2421	C	A	C2084	U	A1831	A1627	A1543	A1442	G1333	G1203
	G2659	U2425	C	A	G2085	U	A1831	A1631	A1544	A1442	G1333	C1204
	U2664	C2426	C	C	A2089	U	A1831	G1632	C1544	U1448	A1339	A1340
	U2665	U2427	C	C	G2090	U	A1831	G1633	C1544	C1449	A1340	G1209
	G2670	U2430	C	C	C2090	U	A1831	G1645	C1550	C1450	A1340	G1209
	C2674	U2431	C	C	G2098	U	A1831	G1645	C1551	U1451	A1341	G1209
	U2674	U2432	C	C	G2099	U	A1831	C1652	C1552	C1452	G1342	C1216
	G2674	C2442	C	C	A2100	U	A1831	A1653	U	A1453	C1343	U
	U2452	U2344	C	C	U2104	U	A1831	A1654	A1553	U1459	A1346	C
	U2452	U2345	C	C	U2104	U	A1831	A1655	A1556	U1460	A1346	G1220



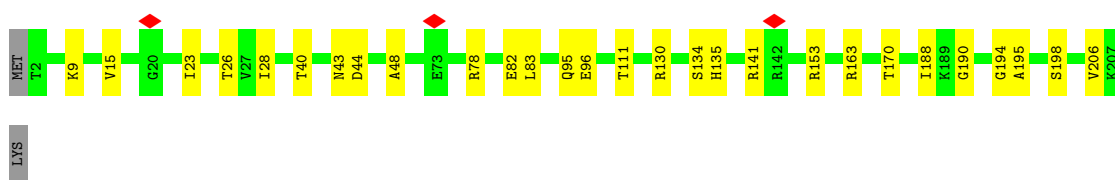
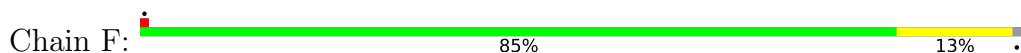
• Molecule 2: 5S rRNA



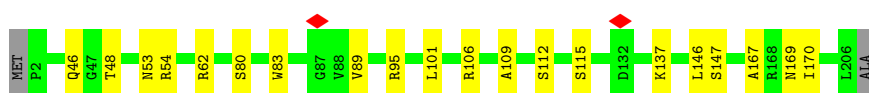
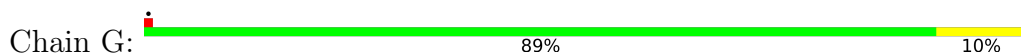
• Molecule 3: 50S ribosomal protein L2



• Molecule 4: 50S ribosomal protein L3

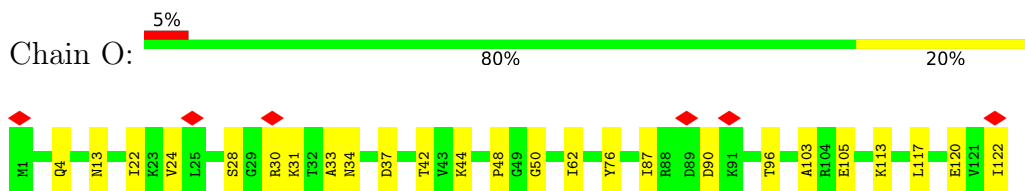


• Molecule 5: 50S ribosomal protein L4

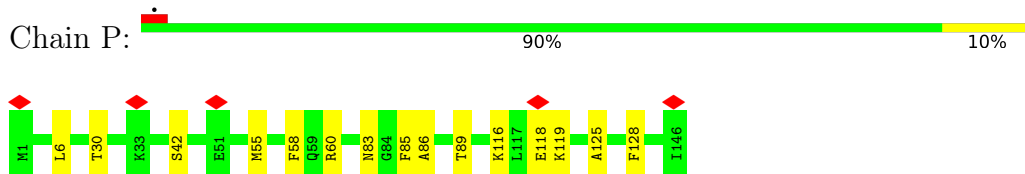


• Molecule 6: 50S ribosomal protein L5

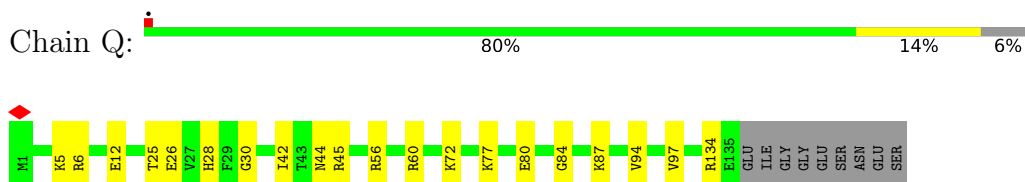




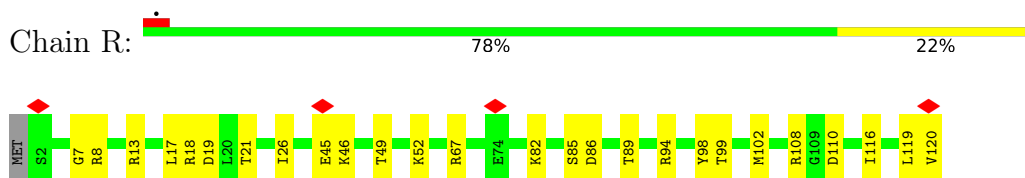
• Molecule 12: 50S ribosomal protein L15



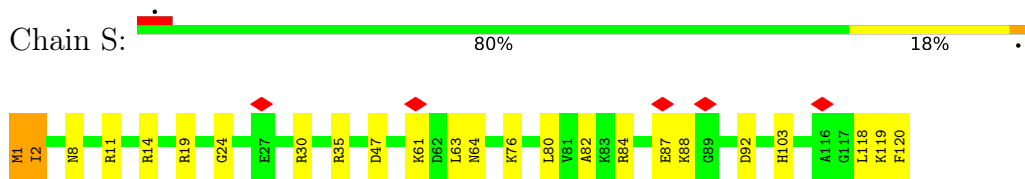
• Molecule 13: 50S ribosomal protein L16



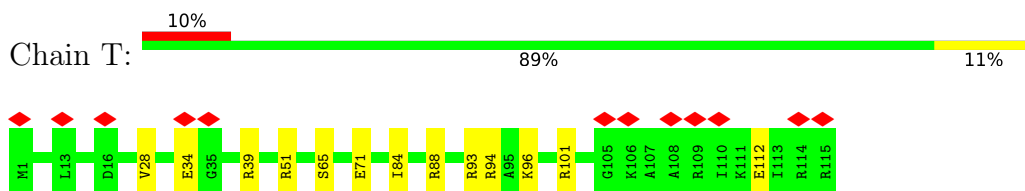
• Molecule 14: 50S ribosomal protein L17



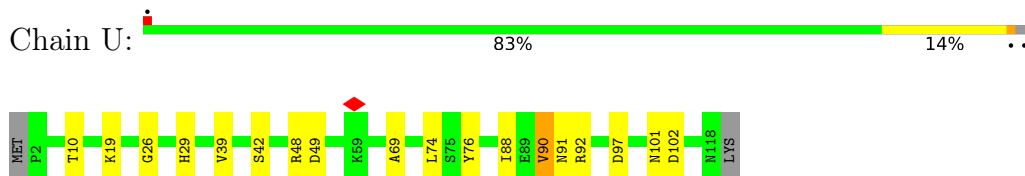
• Molecule 15: 50S ribosomal protein L18




• Molecule 16: 50S ribosomal protein L19



• Molecule 17: 50S ribosomal protein L20




- Molecule 18: 50S ribosomal protein L21

Chain V:  88% 10%




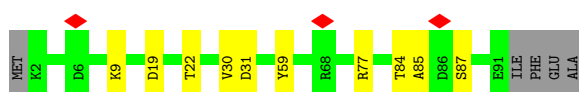
- Molecule 19: 50S ribosomal protein L22

Chain W:  88% 9%




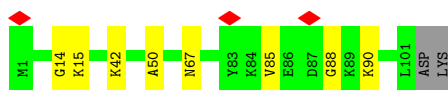
- Molecule 20: 50S ribosomal protein L23

Chain X:  84% 11% 5%



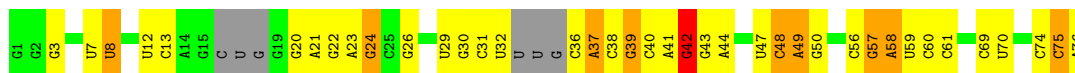
- Molecule 21: 50S ribosomal protein L24

Chain Y:  90% 8%



- Molecule 22: tRNA-Ala-UGC

Chain 2:  41% 38% 12% 8%




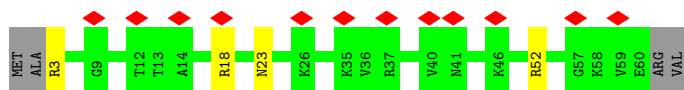
- Molecule 23: 50S ribosomal protein L27

Chain a:  72% 14% 14%




- Molecule 24: 50S ribosomal protein L28

Chain b:  19% 87% 6% 6%



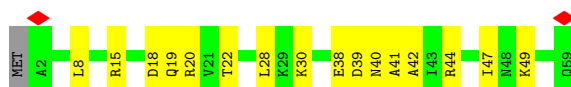
- Molecule 25: 50S ribosomal protein L29

Chain c:  76% 23%



- Molecule 26: 50S ribosomal protein L30

Chain d:  71% 27%




- Molecule 27: 50S ribosomal protein L32

Chain f:  68% 22% 10%




- Molecule 28: 50S ribosomal protein L33 1

Chain g:  86% 12%




- Molecule 29: 50S ribosomal protein L34

Chain h:  84% 16%




- Molecule 30: 50S ribosomal protein L35

Chain i:  80% 17%

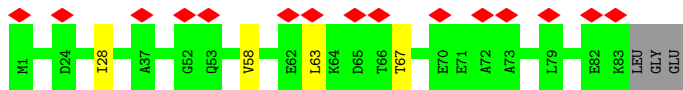
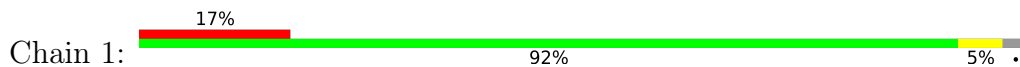


- Molecule 31: 50S ribosomal protein L36

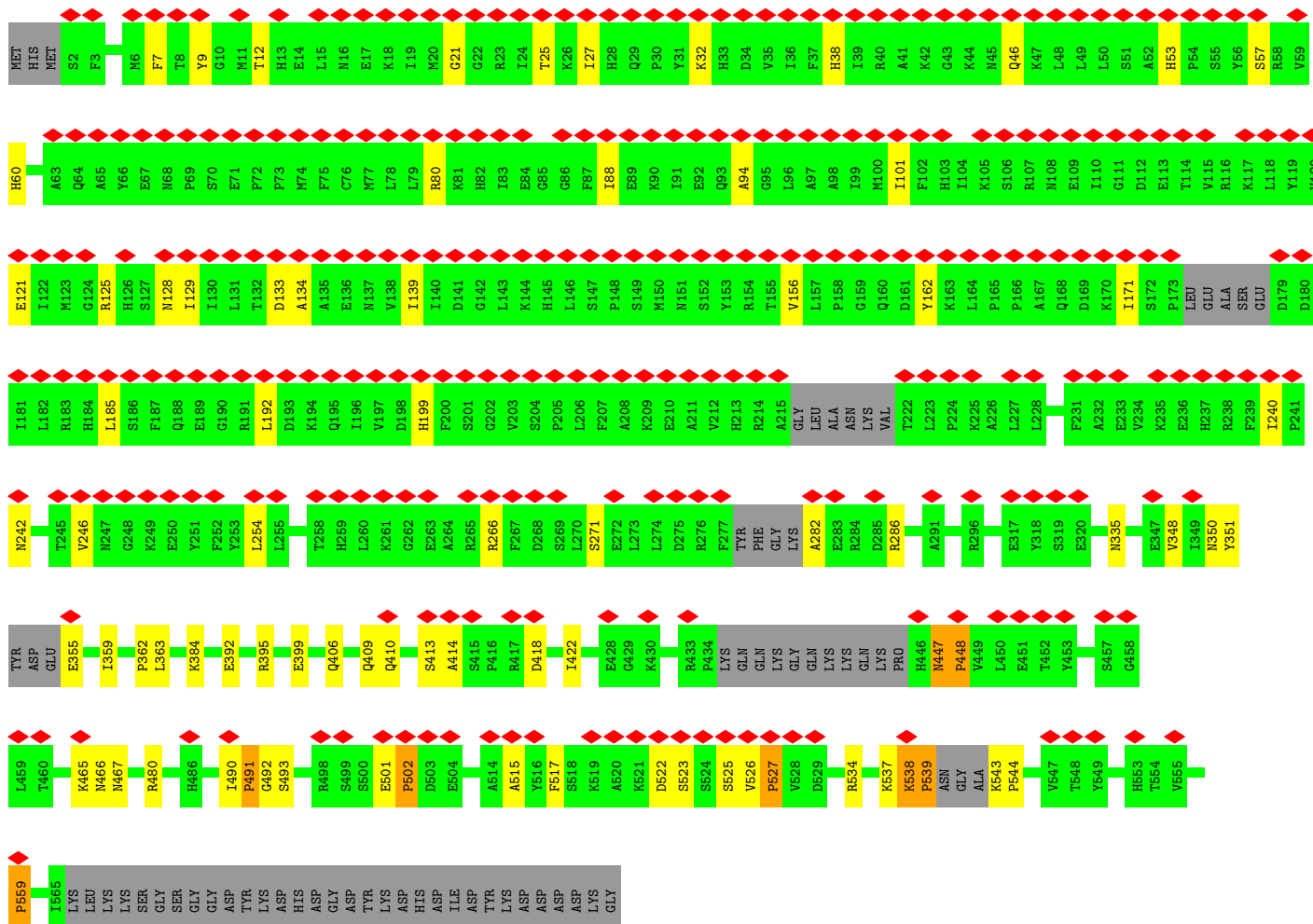
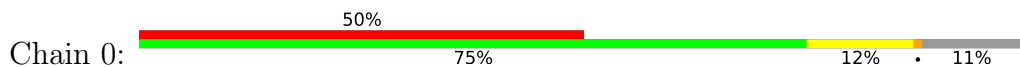
Chain j:  89% 11%



• Molecule 32: Uncharacterized protein YabO



• Molecule 33: Rqc2 homolog RqcH



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16700	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 ( $e^-/\text{\AA}^2$ )	34.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.033	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.007	Depositor
Map size ( $\text{\AA}$ )	344.4, 344.4, 344.4	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.82, 0.82, 0.82	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	A	0.56	4/67693 (0.0%)	0.50	20/105598 (0.0%)
2	B	0.51	0/2675	0.65	2/4170 (0.0%)
3	E	0.69	0/2120	0.55	0/2845
4	F	0.70	0/1591	0.54	0/2132
5	G	0.67	0/1580	0.53	0/2132
6	H	1.01	2/1406 (0.1%)	1.45	4/1888 (0.2%)
7	I	0.49	0/1360	0.48	0/1832
8	K	0.26	0/988	0.47	0/1336
9	L	0.26	0/892	0.49	0/1196
10	N	0.70	0/1147	0.50	0/1542
11	O	0.64	0/928	0.57	0/1245
12	P	0.64	0/1094	0.53	0/1457
13	Q	0.67	0/1099	0.53	0/1468
14	R	0.69	1/961 (0.1%)	0.58	0/1284
15	S	0.54	0/922	0.65	2/1236 (0.2%)
16	T	0.63	0/958	0.57	0/1279
17	U	0.74	0/952	0.58	0/1266
18	V	0.69	0/792	0.53	0/1063
19	W	0.68	0/851	0.55	0/1146
20	X	0.62	0/731	0.51	0/974
21	Y	0.58	0/772	0.60	2/1032 (0.2%)
22	2	0.54	0/1669	0.89	11/2596 (0.4%)
23	a	0.70	0/632	0.57	0/839
24	b	0.45	0/448	0.54	0/596
25	c	0.54	0/531	0.59	0/707
26	d	0.64	0/458	0.56	0/613
27	f	0.64	0/425	0.52	0/563
28	g	0.60	0/406	0.54	0/540
29	h	0.74	0/371	0.51	0/483
30	i	0.67	0/519	0.50	0/680
31	j	0.70	0/300	0.50	0/393
32	1	0.82	1/662 (0.2%)	1.30	0/882
33	0	0.37	1/4031 (0.0%)	0.67	16/5456 (0.3%)
All	All	0.58	9/101964 (0.0%)	0.56	57/152469 (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
1	A	0	15
2	B	0	4
3	E	0	1
6	H	0	1
8	K	0	1
13	Q	0	1
18	V	0	1
22	2	0	7
All	All	0	31

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1	58	VAL	C-N	9.52	1.46	1.33
1	A	1940	U	C1'-N1	7.12	1.59	1.48
6	H	170	LEU	C-O	-6.63	1.16	1.24
1	A	1220	G	P-OP2	6.26	1.61	1.49
1	A	1220	G	P-OP1	6.25	1.61	1.49

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	0	490	ILE	C-N-CD	-16.66	56.69	125.00
1	A	1939	G	O3'-P-O5'	-12.84	84.73	104.00
1	A	1947	A	C3'-C2'-O2'	-10.61	98.69	114.60
1	A	1947	A	C2'-C3'-O3'	10.30	124.95	109.50
22	2	48	C	OP1-P-O3'	-10.09	77.72	108.00

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1866	C	Sidechain
1	A	1952	U	Sidechain
1	A	1953	C	Sidechain
1	A	1955	U	Sidechain
1	A	1957	A	Sidechain

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	60436	0	30414	369	0
2	B	2392	0	1213	10	0
3	E	2083	0	2168	29	0
4	F	1569	0	1637	19	0
5	G	1561	0	1647	15	0
6	H	1387	0	1448	73	0
7	I	1342	0	1388	18	0
8	K	974	0	1011	14	0
9	L	886	0	920	17	0
10	N	1124	0	1162	18	0
11	O	921	0	977	21	0
12	P	1082	0	1132	11	0
13	Q	1076	0	1145	14	0
14	R	954	0	983	21	0
15	S	913	0	947	26	0
16	T	945	0	1020	9	0
17	U	940	0	1005	16	0
18	V	781	0	821	9	0
19	W	842	0	899	6	0
20	X	725	0	770	8	0
21	Y	762	0	821	6	0
22	2	1496	0	759	43	0
23	a	624	0	639	10	0
24	b	444	0	487	4	0
25	c	530	0	568	10	0
26	d	456	0	491	14	0
27	f	418	0	435	10	0
28	g	401	0	413	4	0
29	h	368	0	410	5	0
30	i	512	0	564	10	0
31	j	297	0	342	3	0
32	1	659	0	705	2	0
33	0	3962	0	3687	95	0
All	All	93862	0	63028	728	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 728 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2340:A:C2	6:H:79:LEU:HD11	1.55	1.39
1:A:2334:U:O4	6:H:151:GLY:HA3	1.38	1.22
33:0:537:LYS:C	33:0:539:PRO:HD2	1.65	1.21
1:A:2334:U:C4	6:H:151:GLY:HA3	1.76	1.19
6:H:125:ARG:HG3	15:S:1:MET:HB2	1.27	1.14

There are no symmetry-related clashes.

## 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	
3	E	270/277 (98%)	256 (95%)	12 (4%)	2 (1%)	18	52
4	F	204/209 (98%)	187 (92%)	17 (8%)	0	100	100
5	G	203/207 (98%)	184 (91%)	19 (9%)	0	100	100
6	H	174/179 (97%)	166 (95%)	8 (5%)	0	100	100
7	I	173/179 (97%)	153 (88%)	20 (12%)	0	100	100
8	K	130/141 (92%)	115 (88%)	15 (12%)	0	100	100
9	L	107/166 (64%)	106 (99%)	1 (1%)	0	100	100
10	N	140/145 (97%)	127 (91%)	13 (9%)	0	100	100
11	O	120/122 (98%)	105 (88%)	15 (12%)	0	100	100
12	P	144/146 (99%)	136 (94%)	8 (6%)	0	100	100
13	Q	133/144 (92%)	117 (88%)	16 (12%)	0	100	100
14	R	117/120 (98%)	106 (91%)	11 (9%)	0	100	100
15	S	118/120 (98%)	105 (89%)	12 (10%)	1 (1%)	16	50
16	T	113/115 (98%)	105 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	U	115/119 (97%)	106 (92%)	8 (7%)	1 (1%)	14	47
18	V	98/102 (96%)	80 (82%)	18 (18%)	0	100	100
19	W	107/113 (95%)	94 (88%)	13 (12%)	0	100	100
20	X	88/95 (93%)	83 (94%)	5 (6%)	0	100	100
21	Y	99/103 (96%)	84 (85%)	15 (15%)	0	100	100
23	a	79/94 (84%)	71 (90%)	8 (10%)	0	100	100
24	b	56/62 (90%)	50 (89%)	6 (11%)	0	100	100
25	c	63/66 (96%)	61 (97%)	2 (3%)	0	100	100
26	d	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
27	f	51/59 (86%)	47 (92%)	4 (8%)	0	100	100
28	g	46/49 (94%)	41 (89%)	5 (11%)	0	100	100
29	h	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
30	i	62/66 (94%)	59 (95%)	3 (5%)	0	100	100
31	j	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
32	1	81/86 (94%)	79 (98%)	2 (2%)	0	100	100
33	0	518/599 (86%)	476 (92%)	39 (8%)	3 (1%)	21	56
All	All	3742/4023 (93%)	3428 (92%)	307 (8%)	7 (0%)	44	73

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	E	156	ARG
15	S	2	ILE
33	0	491	PRO
3	E	155	VAL
33	0	447	ASN

### 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	
3	E	220/225 (98%)	220 (100%)	0	100	100
4	F	167/170 (98%)	167 (100%)	0	100	100
5	G	169/170 (99%)	169 (100%)	0	100	100
6	H	151/154 (98%)	146 (97%)	5 (3%)	33	65
7	I	148/151 (98%)	148 (100%)	0	100	100
8	K	102/110 (93%)	102 (100%)	0	100	100
9	L	98/138 (71%)	97 (99%)	1 (1%)	68	80
10	N	120/123 (98%)	120 (100%)	0	100	100
11	O	101/101 (100%)	101 (100%)	0	100	100
12	P	110/110 (100%)	110 (100%)	0	100	100
13	Q	109/116 (94%)	109 (100%)	0	100	100
14	R	99/100 (99%)	99 (100%)	0	100	100
15	S	93/93 (100%)	93 (100%)	0	100	100
16	T	100/100 (100%)	100 (100%)	0	100	100
17	U	96/98 (98%)	96 (100%)	0	100	100
18	V	83/84 (99%)	83 (100%)	0	100	100
19	W	90/93 (97%)	90 (100%)	0	100	100
20	X	81/85 (95%)	81 (100%)	0	100	100
21	Y	85/87 (98%)	85 (100%)	0	100	100
23	a	63/74 (85%)	63 (100%)	0	100	100
24	b	47/50 (94%)	47 (100%)	0	100	100
25	c	56/57 (98%)	56 (100%)	0	100	100
26	d	52/53 (98%)	52 (100%)	0	100	100
27	f	47/53 (89%)	47 (100%)	0	100	100
28	g	46/47 (98%)	46 (100%)	0	100	100
29	h	39/39 (100%)	39 (100%)	0	100	100
30	i	54/56 (96%)	54 (100%)	0	100	100
31	j	35/35 (100%)	35 (100%)	0	100	100
32	1	73/75 (97%)	72 (99%)	1 (1%)	59	77
33	0	374/527 (71%)	374 (100%)	0	100	100
All	All	3108/3374 (92%)	3101 (100%)	7 (0%)	85	89

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	H	150	ARG
6	H	165	GLU
32	1	63	LEU
9	L	14	GLU
6	H	120	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
21	Y	2	HIS
21	Y	53	GLN
33	0	326	GLN
25	c	16	GLN
33	0	259	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2808/2926 (95%)	667 (23%)	61 (2%)
2	B	111/119 (93%)	30 (27%)	3 (2%)
22	2	67/76 (88%)	15 (22%)	3 (4%)
All	All	2986/3121 (95%)	712 (23%)	67 (2%)

5 of 712 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	13	A
1	A	14	A
1	A	15	G
1	A	23	G
1	A	26	G

5 of 67 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2510	G
1	A	2805	A
22	2	58	A
1	A	1339	A
1	A	1313	A

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

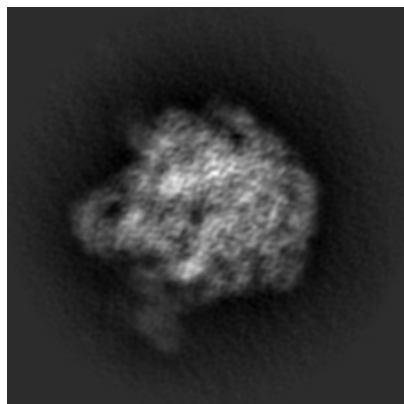
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13017. These allow visual inspection of the internal detail of the map and identification of artifacts.

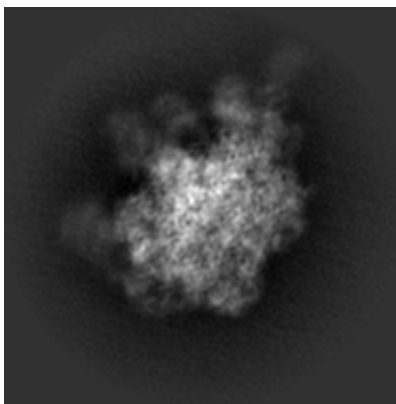
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

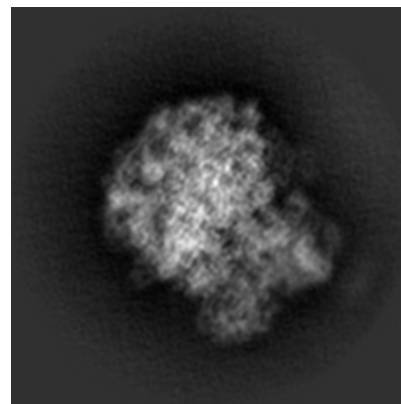
#### 6.1.1 Primary map



X

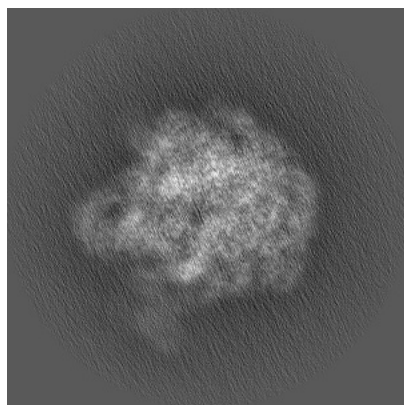


Y

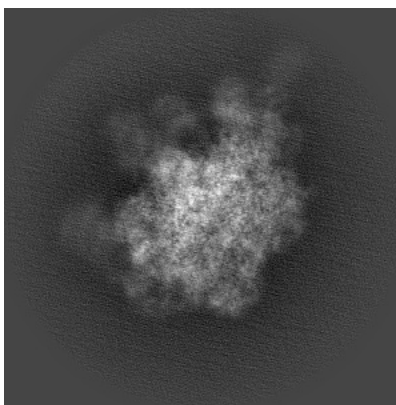


Z

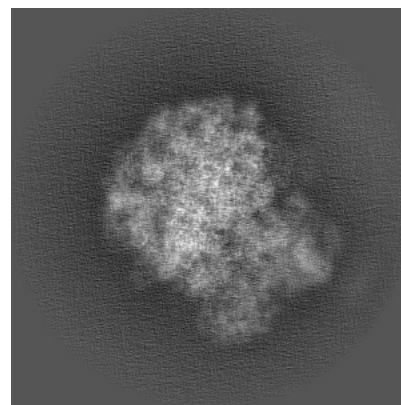
#### 6.1.2 Raw map



X



Y

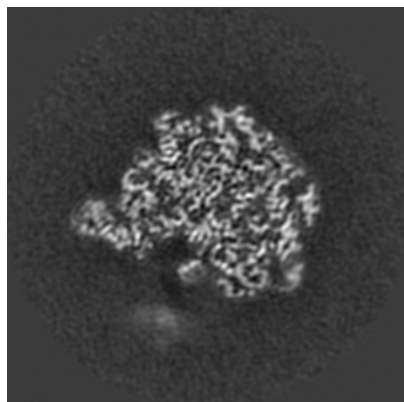


Z

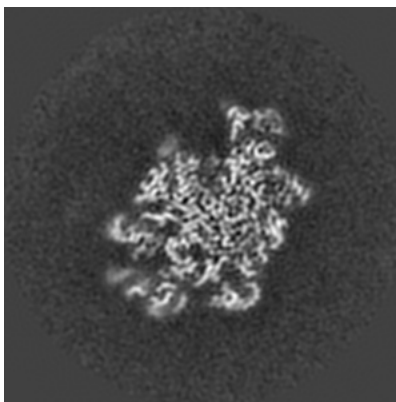
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

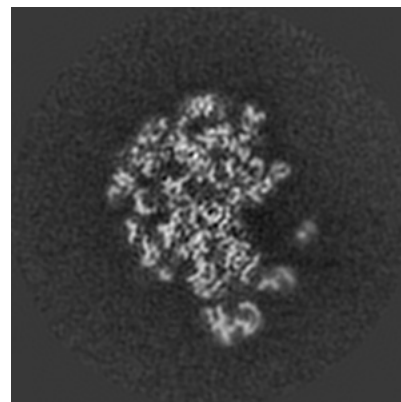
### 6.2.1 Primary map



X Index: 210

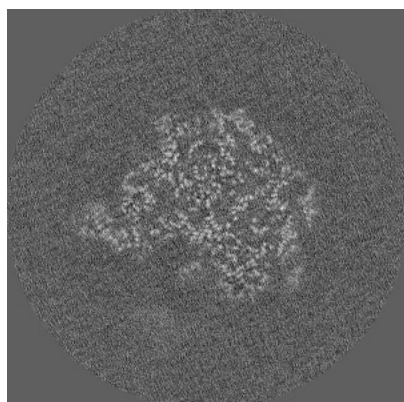


Y Index: 210

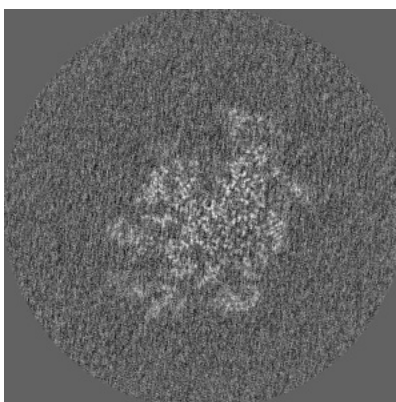


Z Index: 210

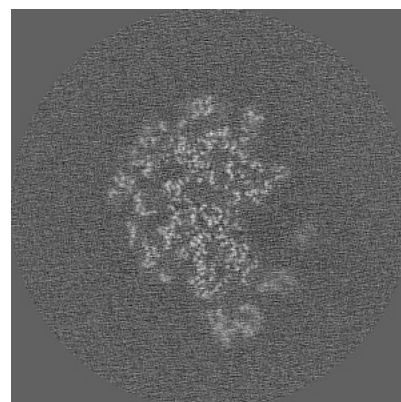
### 6.2.2 Raw map



X Index: 210



Y Index: 210

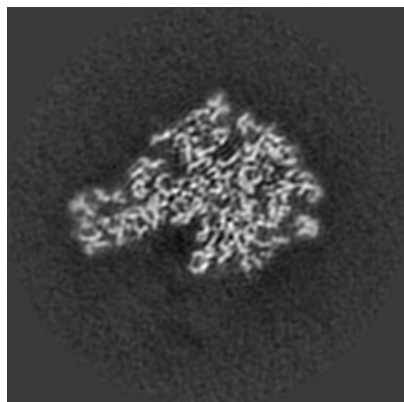


Z Index: 210

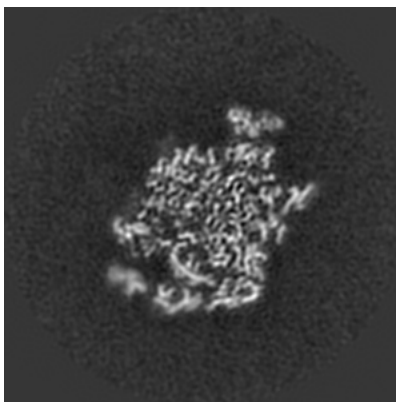
The images above show central slices of the map in three orthogonal directions.

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

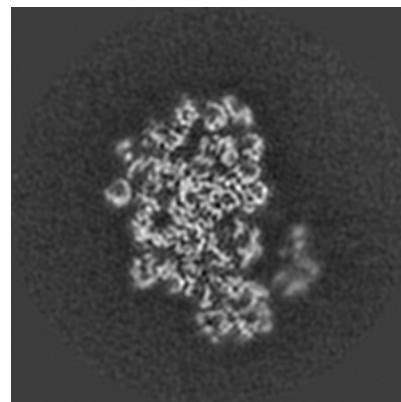
### 6.3.1 Primary map



X Index: 227

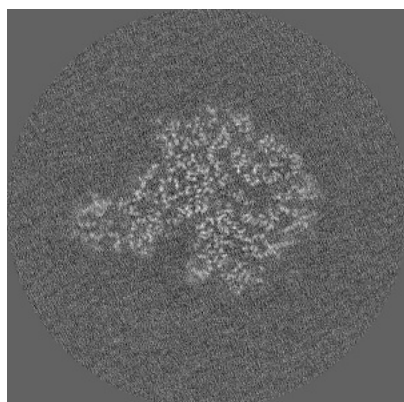


Y Index: 217

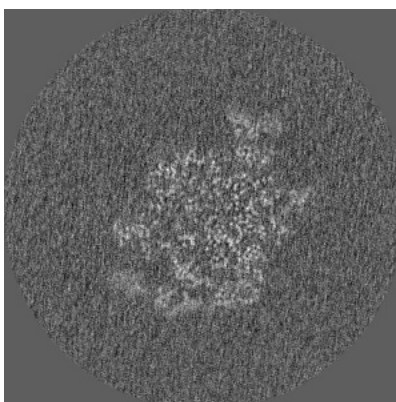


Z Index: 191

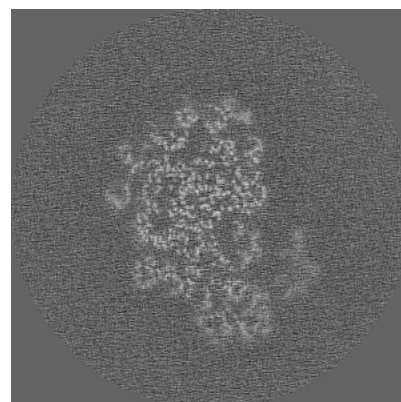
### 6.3.2 Raw map



X Index: 219



Y Index: 216

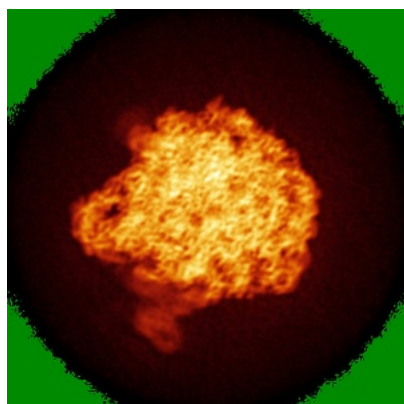


Z Index: 190

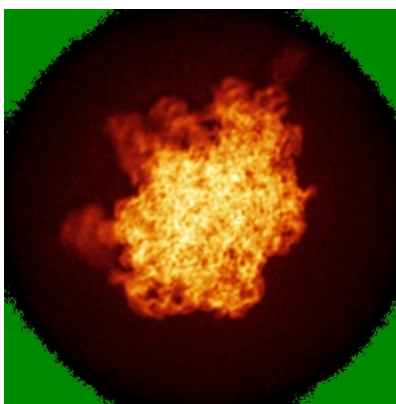
The images above show the largest variance slices of the map in three orthogonal directions.

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

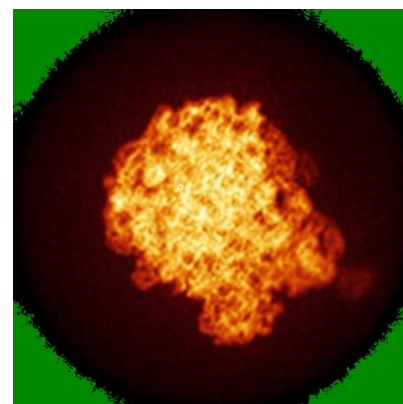
### 6.4.1 Primary map



X

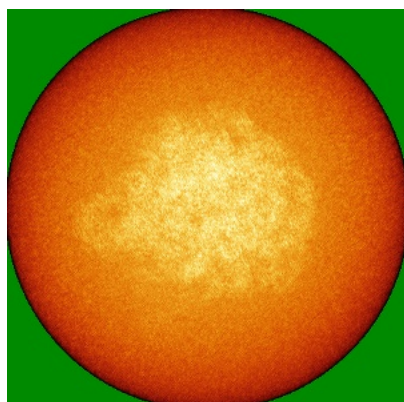


Y

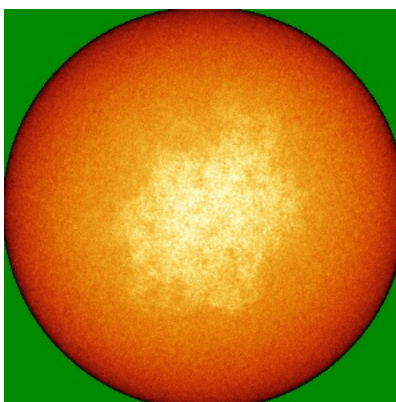


Z

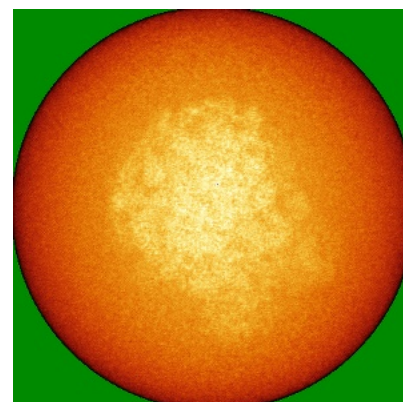
### 6.4.2 Raw map



X



Y

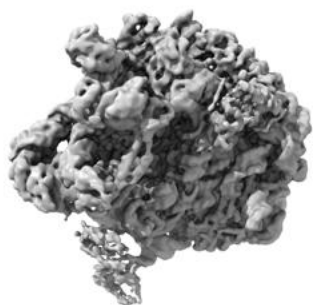


Z

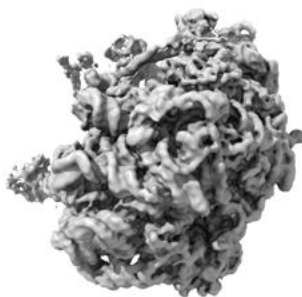
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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

### 6.5.1 Primary map



X



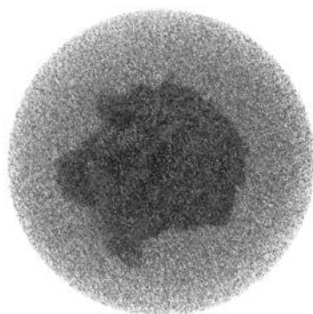
Y



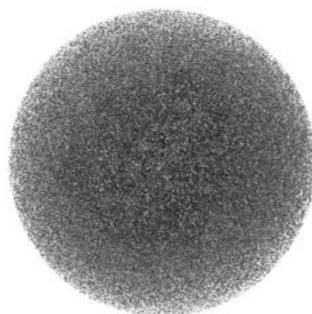
Z

The images above show the 3D surface view of the map at the recommended contour level 0.007. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

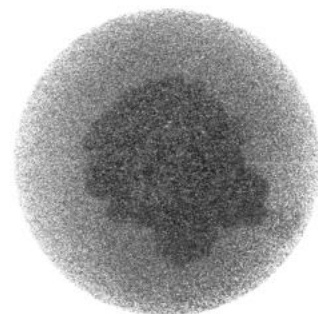
### 6.5.2 Raw map



X



Y



Z

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

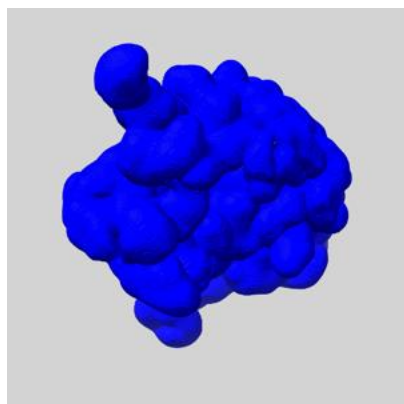
## 6.6 Mask visualisation [i](#)

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

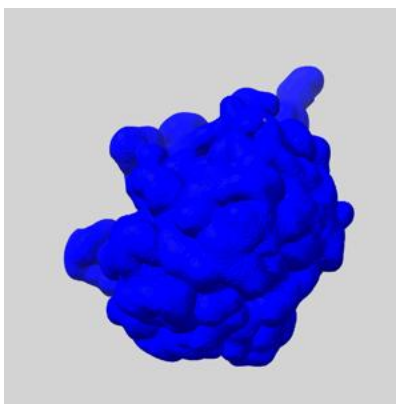
A mask typically either:

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

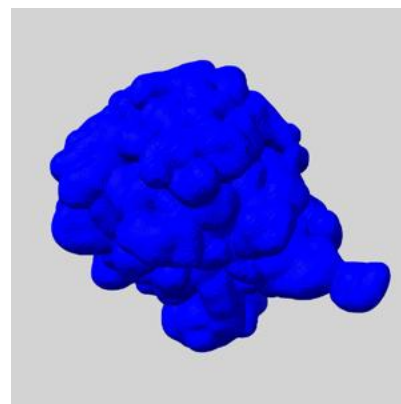
### 6.6.1 emd\_13017\_msk\_1.map [i](#)



X



Y

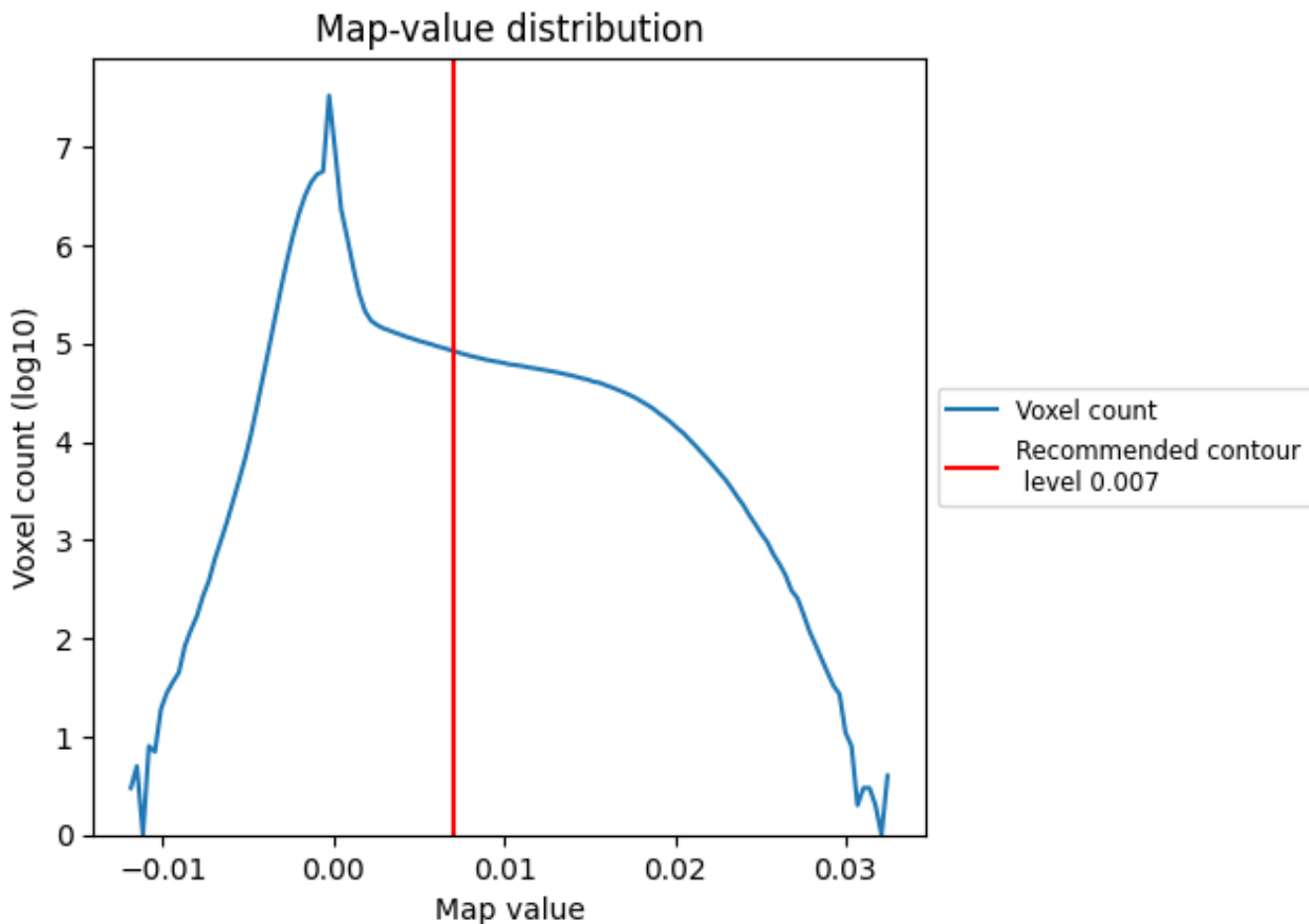


Z

## 7 Map analysis [i](#)

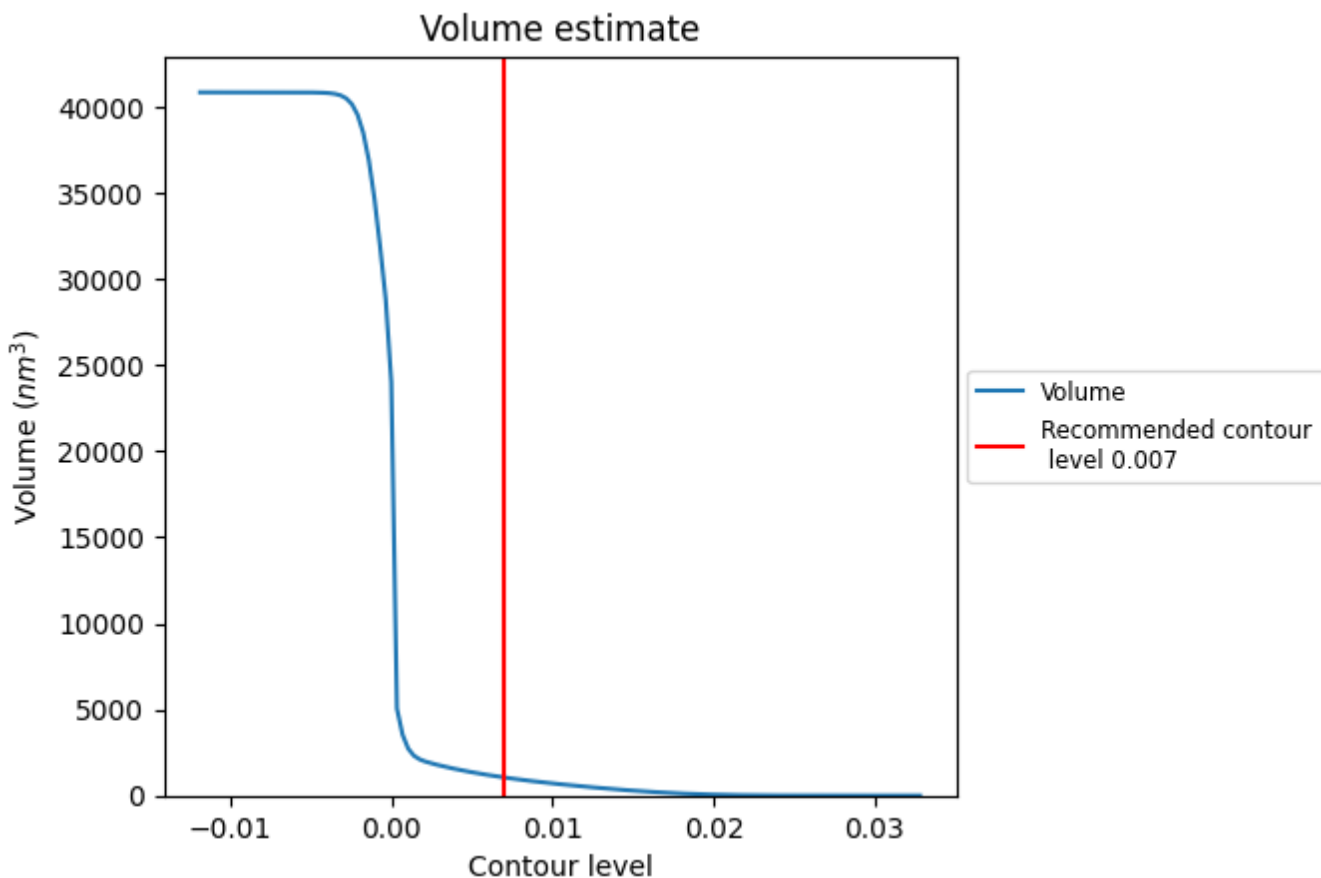
This section contains the results of statistical analysis of the map.

### 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.

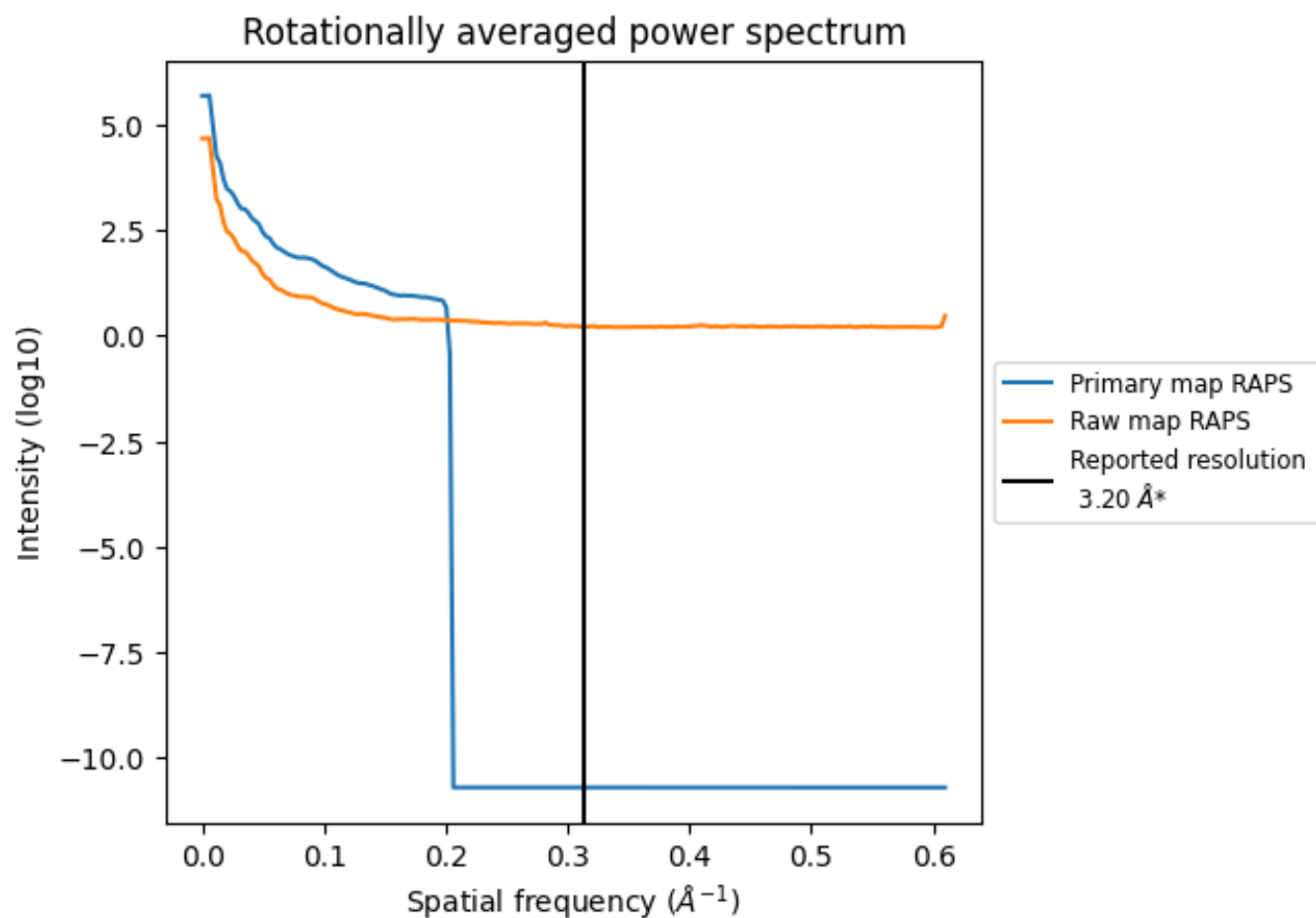
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1052 nm<sup>3</sup>; this corresponds to an approximate mass of 950 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](#)

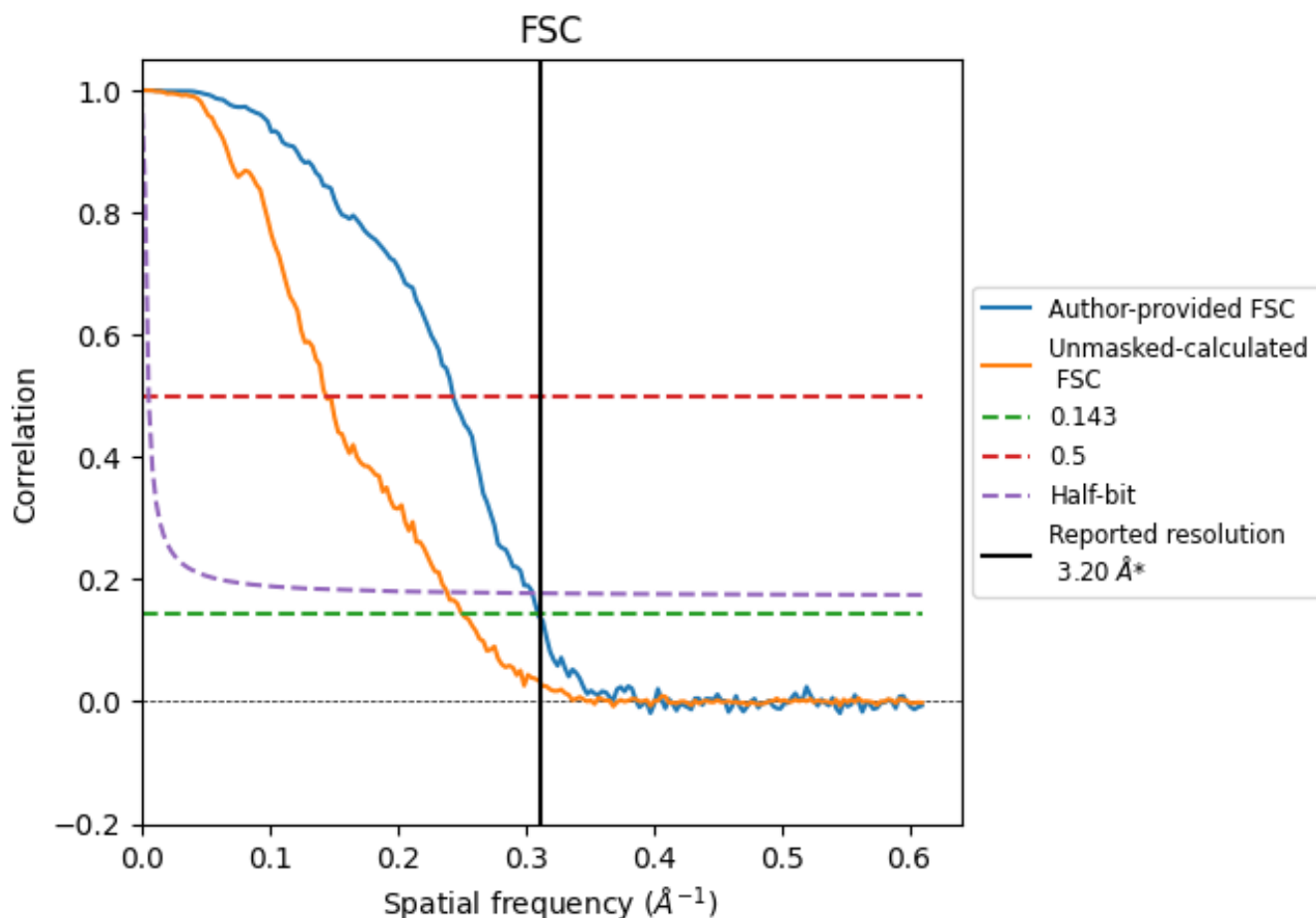


\*Reported resolution corresponds to spatial frequency of 0.312 Å<sup>-1</sup>

## 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 0.312 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

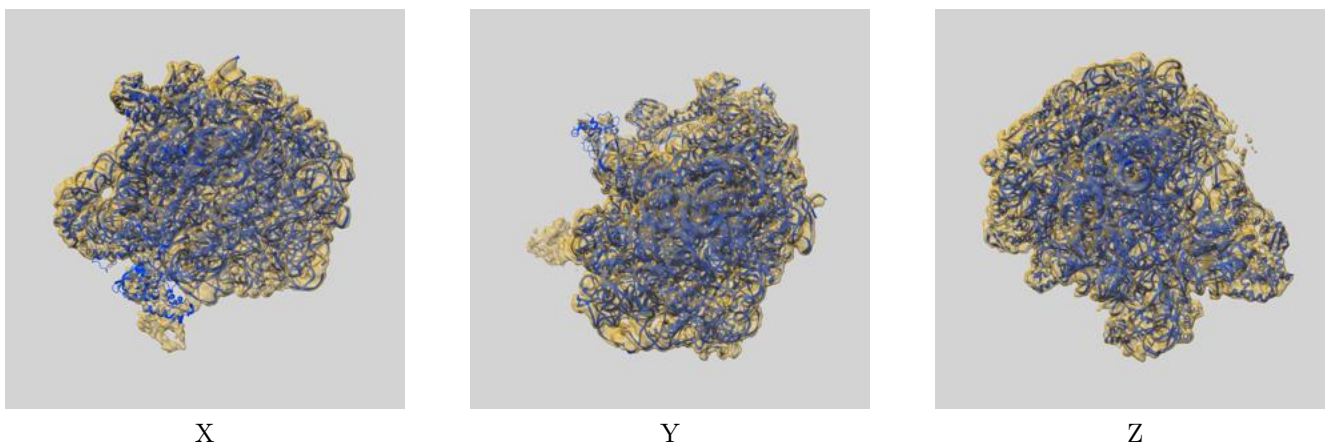
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.23	4.11	3.27
Unmasked-calculated*	3.99	6.93	4.19

\*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 3.99 differs from the reported value 3.2 by more than 10 %

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

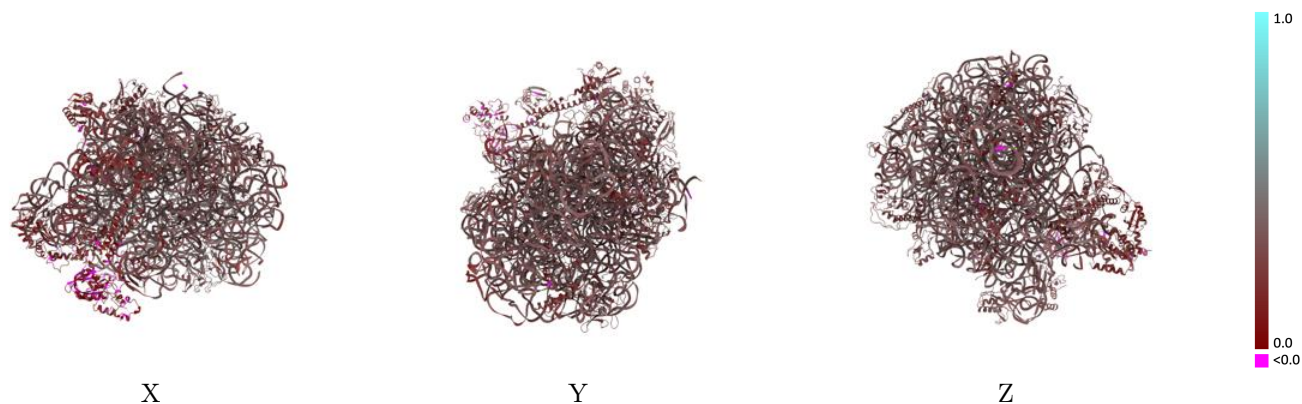
This section contains information regarding the fit between EMDB map EMD-13017 and PDB model 7OPE. Per-residue inclusion information can be found in section 3 on page 11.

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



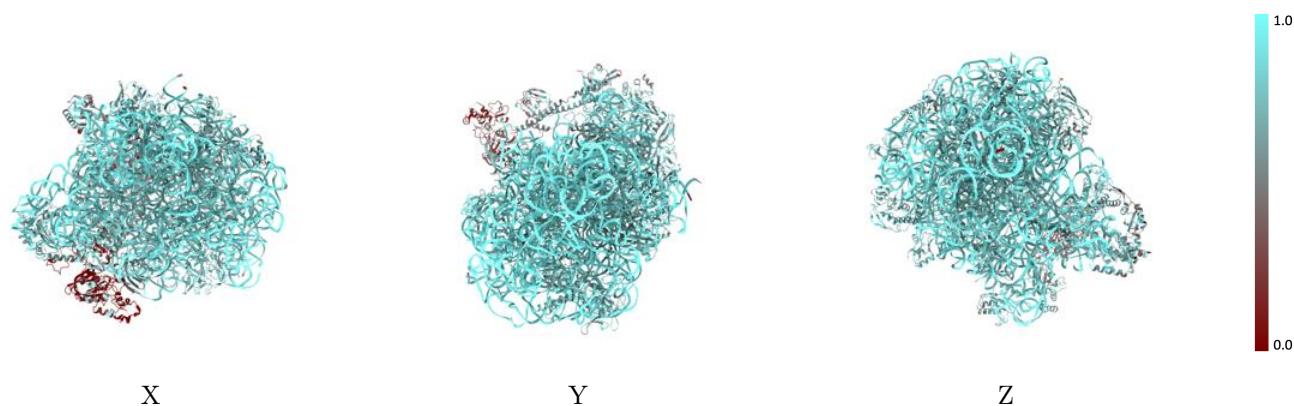
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



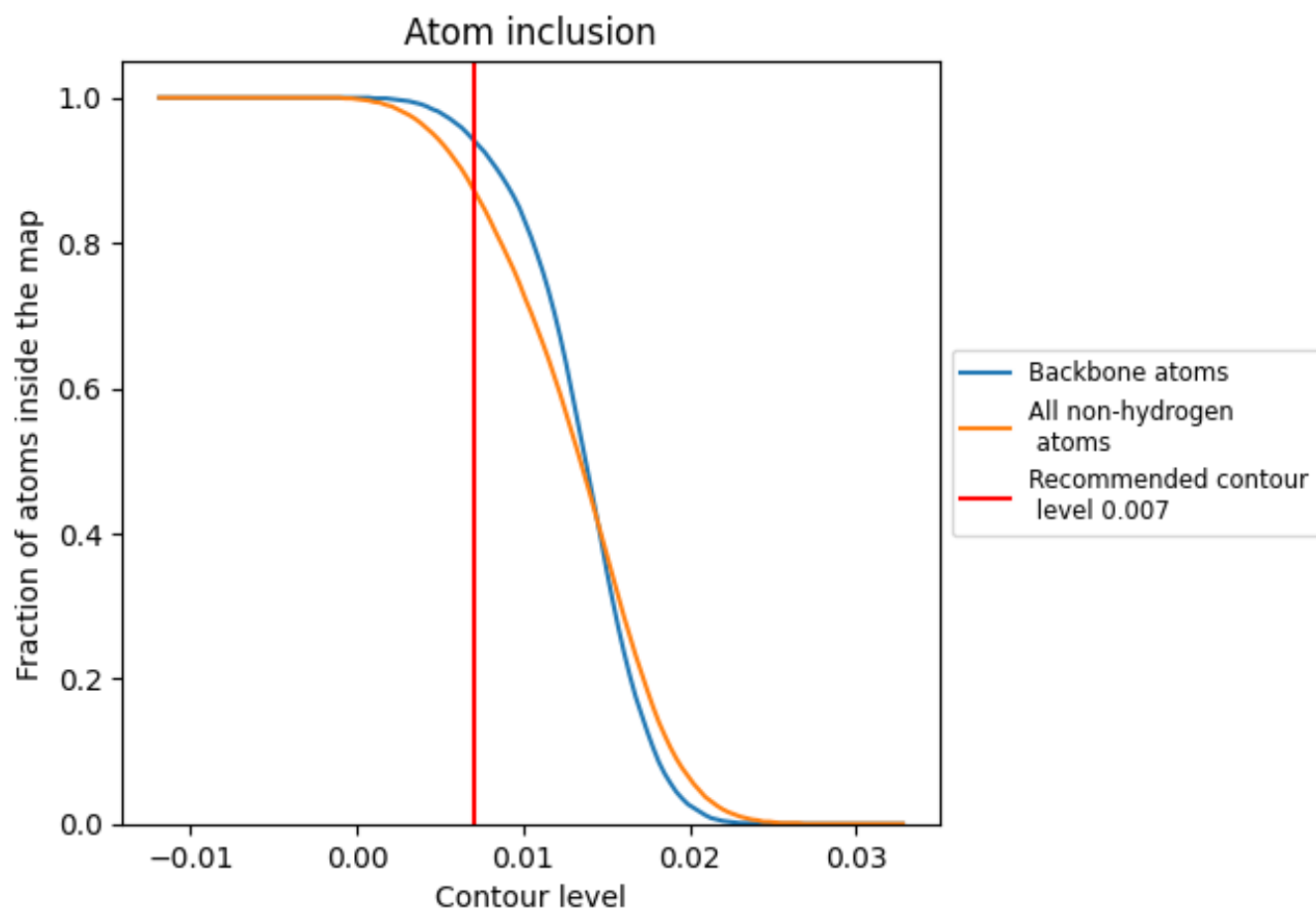
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).





































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 87% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8740	 0.3090
0	 0.3380	 0.1470
1	 0.5730	 0.2490
2	 0.9180	 0.3030
A	 0.9630	 0.3310
B	 0.9770	 0.3290
E	 0.7650	 0.2990
F	 0.7350	 0.2990
G	 0.7550	 0.2890
H	 0.6420	 0.2020
I	 0.7560	 0.2910
K	 0.6790	 0.1940
L	 0.6440	 0.2150
N	 0.7420	 0.2950
O	 0.7020	 0.2860
P	 0.7450	 0.2870
Q	 0.7620	 0.3130
R	 0.7240	 0.2620
S	 0.7470	 0.2640
T	 0.6880	 0.2960
U	 0.7630	 0.2580
V	 0.7900	 0.3270
W	 0.7630	 0.3020
X	 0.7440	 0.3020
Y	 0.7590	 0.3050
a	 0.7530	 0.2880
b	 0.5440	 0.2640
c	 0.7410	 0.2410
d	 0.7470	 0.2760
f	 0.7800	 0.3020
g	 0.7910	 0.2860
h	 0.7510	 0.2770
i	 0.7460	 0.3070
j	 0.7530	 0.2990

