



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 07:02 PM UTC

PDB ID : 8UUA / pdb_00008uua
EMDB ID : EMD-42577
Title : Cryo-EM structure of the *Listeria innocua* 50S ribosomal subunit in complex with HflXr (structure III)
Authors : Seely, S.M.; Basu, R.S.; Gagnon, M.G.
Deposited on : 2023-10-31
Resolution : 2.70 Å (reported)
Based on initial model : 7NHN

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:

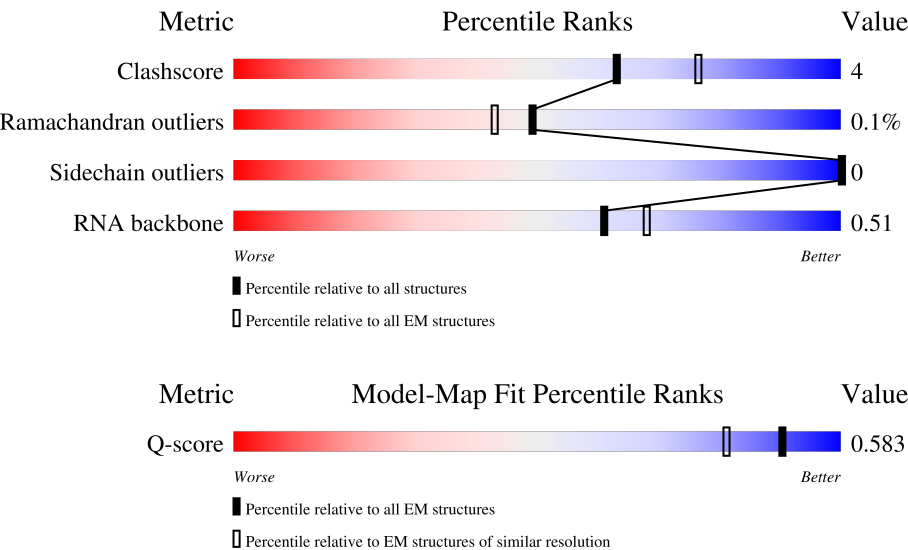
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.70 Å.

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



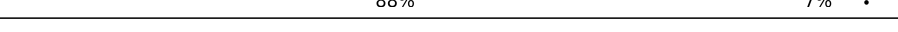
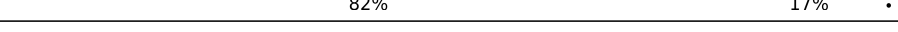
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10327 (2.20 - 3.20)

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 <=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	v	418	8% 73% 26%
2	A	2932	71% 24% ..
3	B	116	70% 28% ..

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Mol	Chain	Length	Quality of chain
4	C	277	
5	D	209	
6	E	207	
7	F	179	
8	G	178	
9	L	145	
10	M	122	
11	N	146	
12	O	144	
13	P	135	
14	Q	119	
15	R	114	
16	S	119	
17	T	102	
18	U	118	
19	V	94	
20	W	103	
21	Y	96	
22	Z	62	
23	1	63	
24	2	59	
25	3	81	
26	4	57	
27	5	49	
28	6	44	

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Mol	Chain	Length	Quality of chain
29	7	66	 89% 6% 5%
30	8	37	 84% 14% .

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 91008 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 GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	v	418	Total	C	N	O	S	0	0
			3294	2073	566	644	11		

- Molecule 2 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	2894	Total	C	N	O	P	0	0
			62168	27745	11501	20028	2894		

- Molecule 3 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	114	Total	C	N	O	P	0	0
			2428	1082	428	804	114		

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	273	Total	C	N	O	S	0	0
			2108	1307	415	379	7		

- Molecule 5 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	206	Total	C	N	O	S	0	0
			1583	995	291	293	4		

- Molecule 6 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	203	Total	C	N	O		0	0
			1539	974	285	280			

- Molecule 7 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	175	Total	C	N	O	S	0	0
			1171	730	207	229	5		

- Molecule 8 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	177	Total	C	N	O	S	0	0
			1355	851	251	252	1		

- Molecule 9 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	142	Total	C	N	O	S	0	0
			1117	709	201	204	3		

- Molecule 10 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	122	Total	C	N	O	S	0	0
			925	573	175	172	5		

- Molecule 11 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	N	144	Total	C	N	O	0	0
			1057	654	207	196		

- Molecule 12 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	133	Total	C	N	O	S	0	0
			1045	669	201	170	5		

- Molecule 13 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	122	Total	C	N	O	S	0	0
			957	601	187	168	1		

- Molecule 14 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	Q	118	Total	C	N	O	0	0
			913	563	176	174		

- Molecule 15 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	R	103	Total	C	N	O	S	0
			802	508	156	137	1	0

- Molecule 16 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	S	116	Total	C	N	O	S	0
			939	596	185	154	4	0

- Molecule 17 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	T	101	Total	C	N	O	S	0
			762	493	131	137	1	0

- Molecule 18 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	U	110	Total	C	N	O	0	0
			823	521	155	147		

- Molecule 19 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	V	90	Total	C	N	O	S	0
			720	457	123	138	2	0

- Molecule 20 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	W	102	Total	C	N	O	S	0
			719	459	135	122	3	0

- Molecule 21 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Y	76	Total	C	N	O	S	0	0
			571	350	111	109	1		

- Molecule 22 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Z	59	Total	C	N	O	S	0	0
			450	277	95	76	2		

- Molecule 23 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	1	59	Total	C	N	O	S	0	0
			483	296	94	92	1		

- Molecule 24 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	2	56	Total	C	N	O	S	0	0
			433	272	82	78	1		

- Molecule 25 is a protein called Large ribosomal subunit protein bL31B.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	3	59	Total	C	N	O	0	0
			292	174	59	59		

- Molecule 26 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	53	Total	C	N	O	S	0	0
			425	259	87	74	5		

- Molecule 27 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	5	47	Total	C	N	O	S	0	0
			390	238	78	71	3		

- Molecule 28 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	6	43	Total	C	N	O	S	0	0
			365	222	88	53	2		

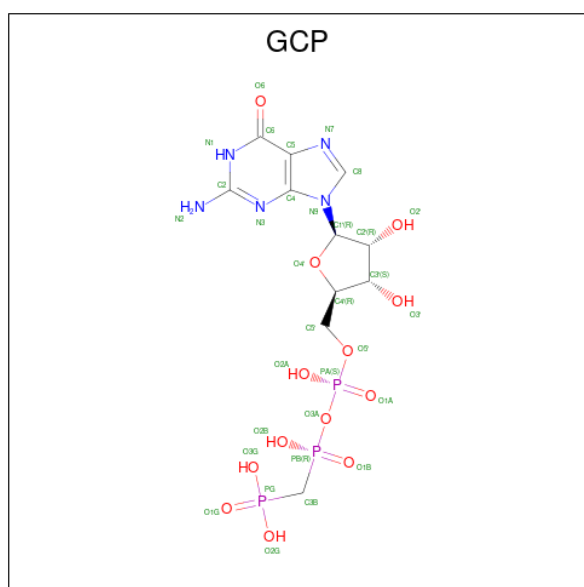
- Molecule 29 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	7	63	Total	C	N	O	S	0	0
			512	317	113	78	4		

- Molecule 30 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	8	36	Total	C	N	O	S	0	0
			292	183	59	44	6		

- Molecule 31 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
31	v	1	Total	C	N	O	P	0
			32	11	5	13	3	

- Molecule 32 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
32	A	192	Total	Mg	0
			192	192	

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Mol	Chain	Residues	Atoms		AltConf
32	C	2	Total 2	Mg 2	0
32	D	1	Total 1	Mg 1	0
32	M	1	Total 1	Mg 1	0
32	N	1	Total 1	Mg 1	0
32	V	1	Total 1	Mg 1	0
32	Z	1	Total 1	Mg 1	0
32	6	1	Total 1	Mg 1	0

- Molecule 33 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
33	O	1	Total 1	K 1	0

- Molecule 34 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
34	4	1	Total 1	Zn 1	0
34	5	1	Total 1	Zn 1	0
34	8	1	Total 1	Zn 1	0

- Molecule 35 is water.

Mol	Chain	Residues	Atoms		AltConf
35	A	130	Total 130	O 130	0
35	N	1	Total 1	O 1	0
35	P	1	Total 1	O 1	0
35	4	1	Total 1	O 1	0

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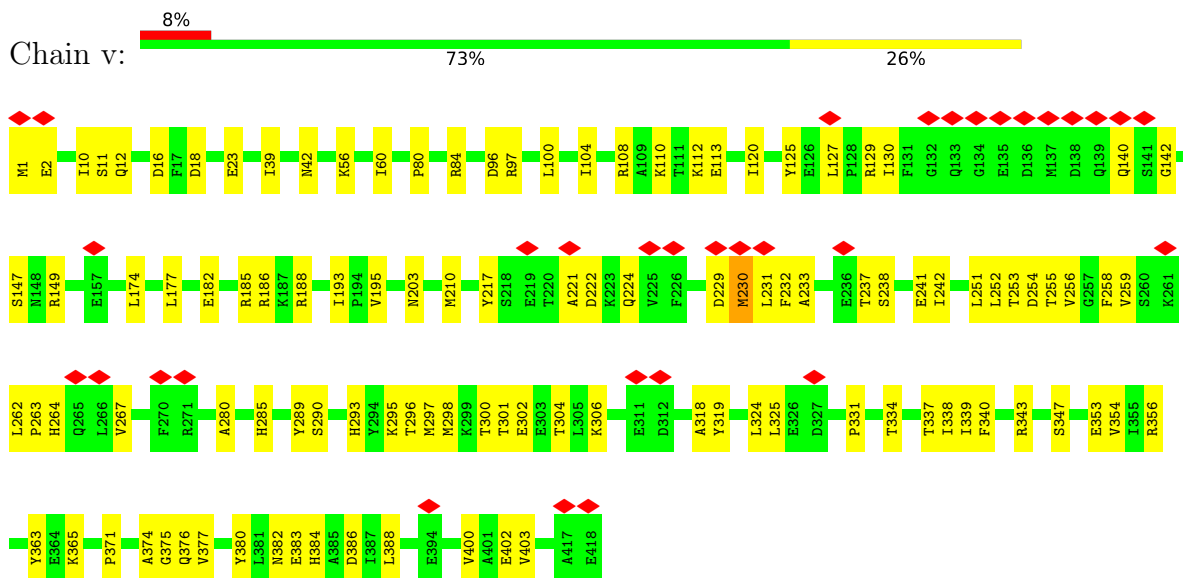
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Mol	Chain	Residues	Atoms		AltConf
35	8	1	Total	O	0
			1	1	

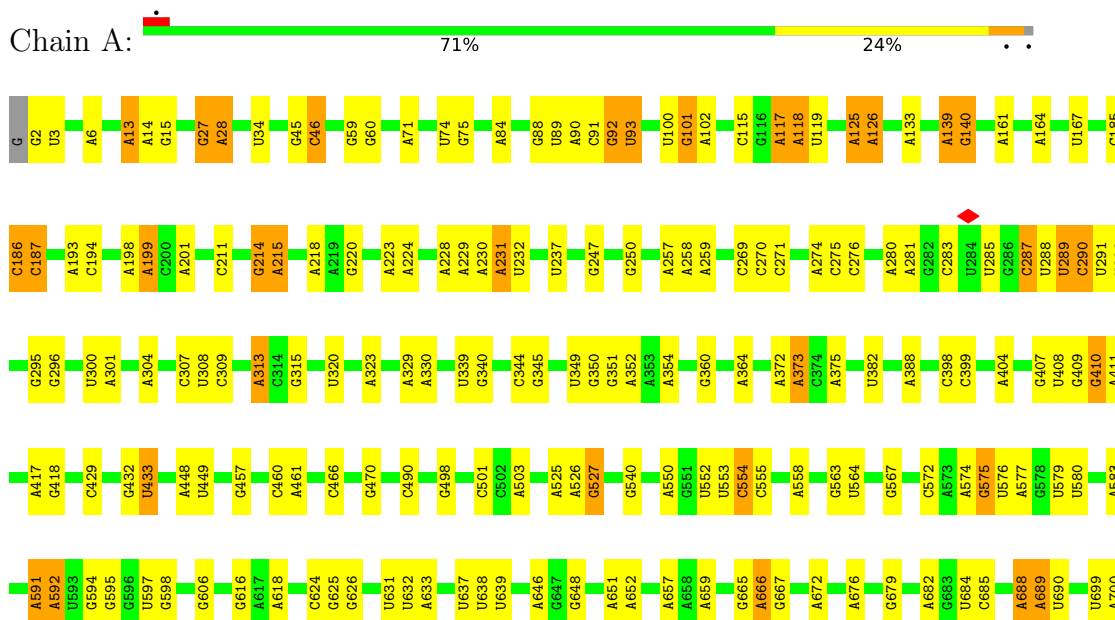
3 Residue-property plots

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

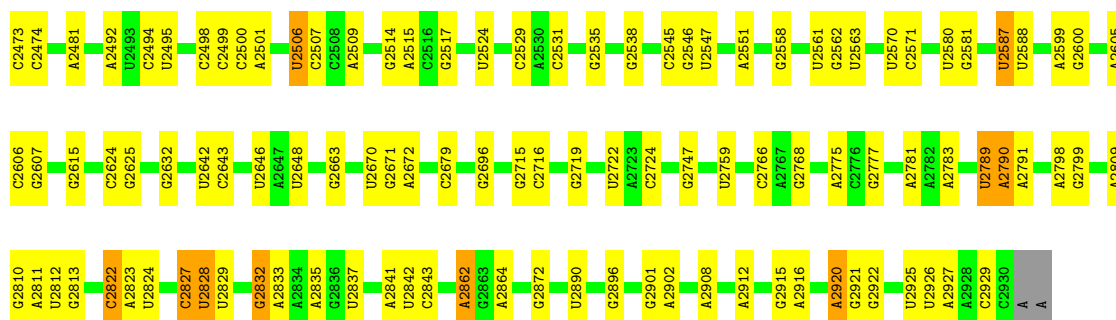
• Molecule 1: GTPase Hfx



• Molecule 2: 23S Ribosomal RNA



U2345 C2346 A2347 U2348 U2349	A2353 G2354 A2355	G2358 U2359 A2360 A2361 A2362 G2363 G2364 G2365 A2366 C2367	C2380 C2383 A2384 G2408 A2409 A2411 G2412 U2413	G2416 G2417 G2418	U2435 G2438 G2439 G2443 G2447	C2455 U2456 C2457 A2458	G2462 A2463 U2464	A2468 U2471 A2472	U2221 G2222	C2225 A2226 U2227	A2231 C2235 G2236 C2237	A2245 A2256 G2257 A2258 G2261 U2262 G2263	G2271 G2272	U2276 U2277	G2292 A2301 G2302 G2304 A2305 A2307	C2316 A2319 A2320 A2321	U2324 U2325 C2326 C2327 C2328 U2329	U2335 G2336 G2337 A2338	G2341 A2344	G2160 C2161 C2162 G2163 A2164 A2165 G2166 C2168 A2169	U2172 G2173 U2174 C2175 G2176 G2177 C2178 U2179 A2180 G2181 C2182 A2183 U2184 A2185 C2186 G2187 A2188 G2189 G2190 A2191 G2192 G2193 C2194 A2195 A2196 U2197	A2064 G2065 A2066 C2069 A2070 G2071 G2072 C2076 C2088 G2089	A2093 G2094 A2095 C2096 G2097 C2098 U2101 G2102 G2103 A2104 G2105 C2106 U2107 U2108 G2125 G2126 A2127	G2134 U2135 A2136 C2137 G2138 G2139 C2140 U2141 U2142 G2143 U2144 A2145 C2146 A2147 G2148 G2149 A2150 U2151 A2152 G2153 G2154 U2155	U2024 G2025 U2026 A2030 G2043 U2044 G2045 U2052 A2056 G2060	U1903 C1904 G1905 C1906 C1907 C1915 A1922 A1923 C1928 C1938 G1939	U1944 A1945 A1946 U1947 U1948 A1949 U1950 G1962 G1963	A1969 A1970 A1971 U1972 U1973 U1988 C1996 G1997	C2000 A2003 A2004 G2005 U2024 G2025 U2026 A2030 G2043 U2044 G2045 U2052 A2056 G2060	U1762 U1763 G1764 G1765 A1771 A1772 A1778 C1781 A1782 G1783 C1787 U1788 G1789 G1796 G1797 A1806 A1807 G1809 U1812 C1815 A1816 A1817 A1818 A1819 C1823 A1824 U1829 C1830 C1833 A1834 A1835 A1836 C1849 A1862 A1881 A1886 A1887 G1891 G1895 G1896 U1897 U1902	A A G U A C1593 G1594 G1595 A1596 C1611 G1612 A1618 A1619 G1620 A1621 U1630 A1634 A1635 G1636 A1637 G1638 U1642 C1656 A1657 A1658 A1659 C1660 A1681 G1682 A1683 A1684 U1685 A1695 G1696 G1697 G1698 A1699 G1700 A1701 U1708 U1712 G1716 G1723 C1724 A1749	G1497 A1502 A1508 A1509 C1517 C1518 A1519 G1528 U1529 G1530 U1531 G1532 A1533 G1534 A1535 A1536 G1537 U1538 A1539 C1542 A1543 A1544 A1545 U1546 C1547 G1548 G1549 C1550 U1551 U1552 C1553 U1554 U1555 G1558 A1559 A1560 U1569 G1570 U1571 G1572 A1573 U1574 G1575 A1579 A1580 G1581 G A A A U U	G1364 A1365 C1369 U1373 C1394 U1395 U1396 C1401 G1402 A1409 U1423 A1429 C1430 A1431 G1432 U1433 U1434 A1435 A1439 U1440 G1445 G1451 U1452 G1453 A1456 A1457 U1458 U1459 G1460 U1461 U1462 U1463 A1464 A1465 A1469 U1470 G1471 C1478 G1482 U1483 A1484 A1493 A1494	C1186 U1187 A1188 A1203 A1213 A1214 U1217 C U U C G G A1224 U1227 U1228 C1229 G1230 U1245 C1246 U1247 A1248 A1249 G1250 G1255 G1264 A1265 G1283 G1295 A1296 G1297 A1298 G1301 C1302 G1311 G1316 A1317 A1318 A1319 G1320 C1333 U1336 U1337 A1344 A1345	A1092 G1093 G1102 A1103 U1104 G1105 U1107 G1108 G1109 A1113 G1114 A1115 A1116 G1117 C1124 U1127 U1128 G1129 A1130 A1131 A1134 G1135 U1136 U1140 A1141 A1142 U1143 C1148 A1149 C1150 U1151 G1152 G1156 A1157 G1158 A1161 G1171 A1172 A1173 A1174 U1178 A1179 C1180 C1181 G1182 G1185	U950 C961 A964 C969 U973 A974 U979 A980 A987 G978 C979 G992 A993 C994 G1007 G1015 U1016 A1019 A1020 A1026 A1029 G1030 C1031 A1042 G1043 A1046 A1047 C1051 A1055 U1058 A1059 U1065 A1066 A1067 G1068 A1072 A1073 A1074 A1075 G1076 A1077 U1079	G851 C852 C858 U859 C860 A865 U873 U874 A875 G878 C879 G992 A993 C994 G1007 G1015 U1016 A1019 A1020 A1026 A1029 G1030 C1031 A1042 G1043 A1046 A1047 C1051 A1055 U1058 A1059 U1065 A1066 A1067 G1068 A1072 A1073 A1074 A1075 G1076 A1077 U1079	C851 C852 C858 U859 C860 A865 U873 U874 A875 G878 C879 G992 A993 C994 G1007 G1015 U1016 A1019 A1020 A1026 A1029 G1030 C1031 A1042 G1043 A1046 A1047 C1051 A1055 U1058 A1059 U1065 A1066 A1067 G1068 A1072 A1073 A1074 A1075 G1076 A1077 U1079	U703 A704 A714 G715 A716 G720 U732 G746 U749 G750 U759 U760 A761 U762 U763 A768 U776 C784 A789 C790 U791 U792 U793 G794 A798 A799 G809 A810 G811 G821 A825 A828 A829 U830 U831 C832 A835 U836 C837 G838 U842 U843
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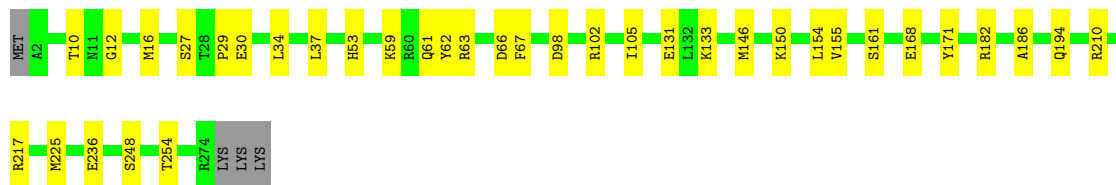
• Molecule 3: 5S Ribosomal RNA

Chain B: 70% 28% ..



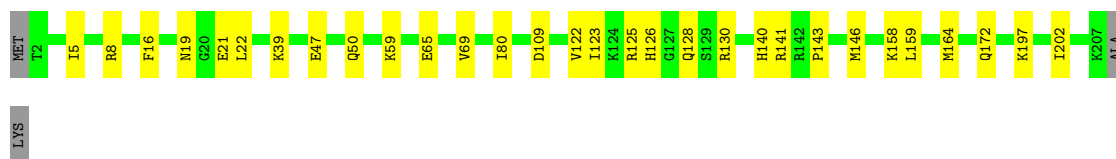
• Molecule 4: Large ribosomal subunit protein uL2

Chain C: 86% 13% .



• Molecule 5: Large ribosomal subunit protein uL3

Chain D: 84% 14% .



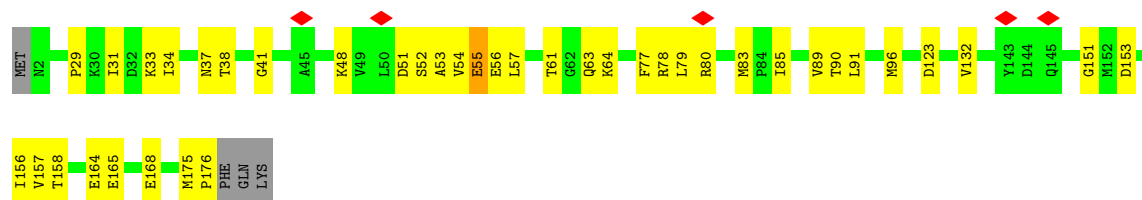
• Molecule 6: Large ribosomal subunit protein uL4

Chain E: 89% 9% .

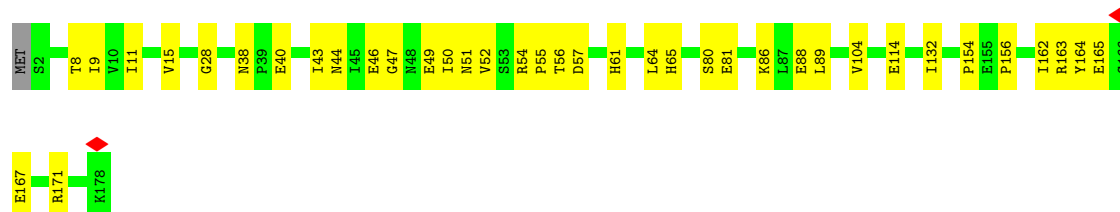
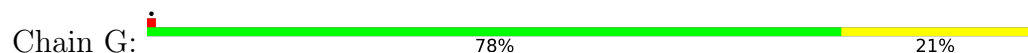


• Molecule 7: Large ribosomal subunit protein uL5

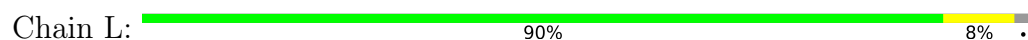
Chain F: 75% 22% ..



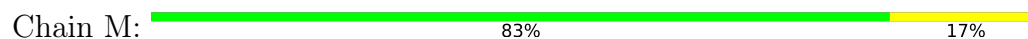
- Molecule 8: Large ribosomal subunit protein uL6



- Molecule 9: Large ribosomal subunit protein uL13



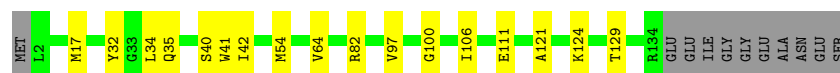
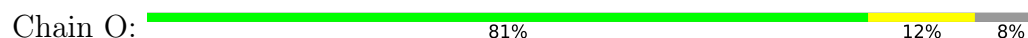
- Molecule 10: Large ribosomal subunit protein uL14



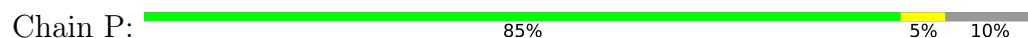
- Molecule 11: Large ribosomal subunit protein uL15

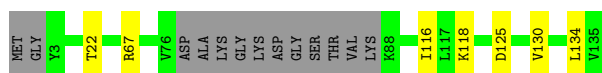


- Molecule 12: Large ribosomal subunit protein uL16

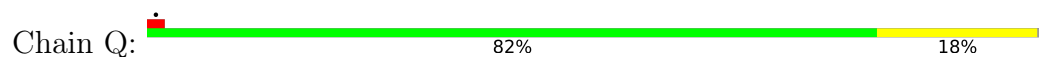


- Molecule 13: Large ribosomal subunit protein bL17

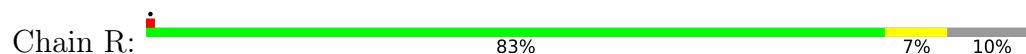




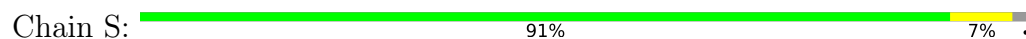
- Molecule 14: Large ribosomal subunit protein uL18



- Molecule 15: Large ribosomal subunit protein bL19



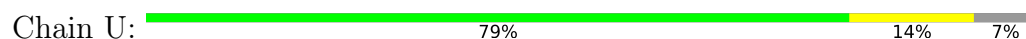
- Molecule 16: Large ribosomal subunit protein bL20



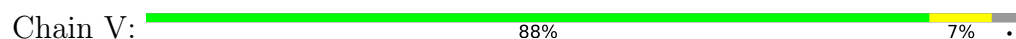
- Molecule 17: Large ribosomal subunit protein bL21



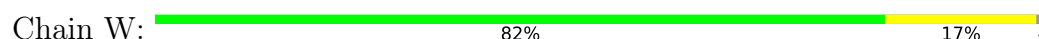
- Molecule 18: Large ribosomal subunit protein uL22



- Molecule 19: Large ribosomal subunit protein uL23

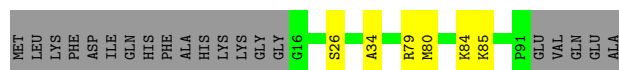


- Molecule 20: Large ribosomal subunit protein uL24





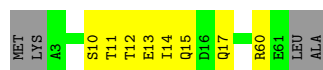
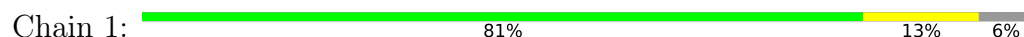
- Molecule 21: Large ribosomal subunit protein bL27



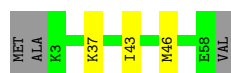
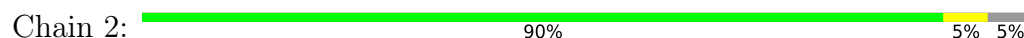
- Molecule 22: Large ribosomal subunit protein bL28



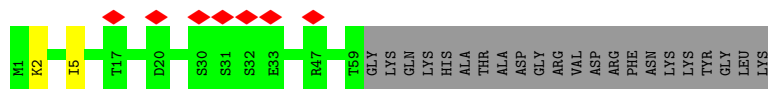
- Molecule 23: Large ribosomal subunit protein uL29



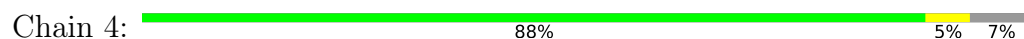
- Molecule 24: Large ribosomal subunit protein uL30



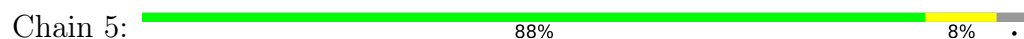
- Molecule 25: Large ribosomal subunit protein bL31B



- Molecule 26: Large ribosomal subunit protein bL32



- Molecule 27: Large ribosomal subunit protein bL33





- Molecule 28: Large ribosomal subunit protein bL34

Chain 6: 82% 16% .



- Molecule 29: Large ribosomal subunit protein bL35

Chain 7: 89% 6% 5%



- Molecule 30: Large ribosomal subunit protein bL36

Chain 8: 84% 14% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	332513	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.0	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.373	Depositor
Minimum map value	-0.712	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.084	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	435.2, 435.2, 435.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG, K, GCP

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	v	0.18	0/3336	0.37	0/4499
2	A	0.38	0/69651	0.38	0/108655
3	B	0.22	0/2711	0.26	0/4224
4	C	0.34	0/2144	0.44	0/2875
5	D	0.34	0/1605	0.46	0/2156
6	E	0.31	0/1559	0.48	0/2104
7	F	0.19	0/1180	0.48	2/1606 (0.1%)
8	G	0.21	0/1377	0.36	0/1857
9	L	0.33	0/1140	0.41	0/1532
10	M	0.31	0/932	0.41	0/1248
11	N	0.30	0/1068	0.36	0/1427
12	O	0.33	0/1067	0.41	0/1428
13	P	0.32	0/968	0.43	0/1297
14	Q	0.20	0/922	0.33	0/1231
15	R	0.32	0/814	0.37	0/1097
16	S	0.34	0/952	0.41	0/1266
17	T	0.32	0/775	0.41	0/1045
18	U	0.33	0/833	0.47	0/1127
19	V	0.30	0/728	0.38	0/977
20	W	0.25	0/727	0.39	0/976
21	Y	0.33	0/578	0.44	0/770
22	Z	0.36	0/455	0.48	0/604
23	1	0.26	0/484	0.40	0/646
24	2	0.31	0/436	0.40	0/585
25	3	0.10	0/291	0.31	0/404
26	4	0.31	0/433	0.41	0/577
27	5	0.25	0/394	0.31	0/529
28	6	0.36	0/368	0.46	0/479
29	7	0.34	0/519	0.48	0/675
30	8	0.32	0/295	0.35	0/387
All	All	0.35	0/98742	0.38	2/148283 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	F	55	GLU	CA-C-N	-5.06	112.62	120.31
7	F	55	GLU	C-N-CA	-5.06	112.62	120.31

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	v	3294	0	3305	75	0
2	A	62168	0	31257	344	0
3	B	2428	0	1229	15	0
4	C	2108	0	2184	26	0
5	D	1583	0	1646	21	0
6	E	1539	0	1624	16	0
7	F	1171	0	1041	32	0
8	G	1355	0	1403	24	0
9	L	1117	0	1145	8	0
10	M	925	0	982	13	0
11	N	1057	0	1073	10	0
12	O	1045	0	1103	10	0
13	P	957	0	993	5	0
14	Q	913	0	939	12	0
15	R	802	0	836	7	0
16	S	939	0	1011	9	0
17	T	762	0	779	5	0
18	U	823	0	861	13	0
19	V	720	0	743	4	0
20	W	719	0	744	11	0
21	Y	571	0	570	5	0
22	Z	450	0	476	7	0
23	1	483	0	500	4	0
24	2	433	0	479	3	0
25	3	292	0	119	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	4	425	0	423	2	0
27	5	390	0	395	5	0
28	6	365	0	417	6	0
29	7	512	0	562	3	0
30	8	292	0	334	5	0
31	v	32	0	14	3	0
32	6	1	0	0	0	0
32	A	192	0	0	0	0
32	C	2	0	0	0	0
32	D	1	0	0	0	0
32	M	1	0	0	0	0
32	N	1	0	0	0	0
32	V	1	0	0	0	0
32	Z	1	0	0	0	0
33	O	1	0	0	0	0
34	4	1	0	0	0	0
34	5	1	0	0	0	0
34	8	1	0	0	0	0
35	4	1	0	0	0	0
35	8	1	0	0	0	0
35	A	130	0	0	0	0
35	N	1	0	0	0	0
35	P	1	0	0	0	0
All	All	91008	0	59187	623	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 4.

The worst 5 of 623 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)
2:A:2141:U:H3	2:A:2214:G:H1	1.10	0.96
20:W:9:VAL:HG13	20:W:68:VAL:HG13	1.50	0.93
2:A:2263:G:H1'	22:Z:32:ASN:HB3	1.50	0.91
1:v:108:ARG:HH12	1:v:231:LEU:HB3	1.36	0.89
2:A:2173:G:H1	2:A:2184:U:H3	0.89	0.88

There are no symmetry-related clashes.

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	v	416/418 (100%)	393 (94%)	22 (5%)	1 (0%)	43	68
4	C	271/277 (98%)	259 (96%)	11 (4%)	1 (0%)	30	54
5	D	204/209 (98%)	197 (97%)	7 (3%)	0	100	100
6	E	201/207 (97%)	192 (96%)	9 (4%)	0	100	100
7	F	173/179 (97%)	159 (92%)	14 (8%)	0	100	100
8	G	175/178 (98%)	169 (97%)	6 (3%)	0	100	100
9	L	140/145 (97%)	139 (99%)	1 (1%)	0	100	100
10	M	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
11	N	142/146 (97%)	134 (94%)	8 (6%)	0	100	100
12	O	131/144 (91%)	131 (100%)	0	0	100	100
13	P	118/135 (87%)	114 (97%)	4 (3%)	0	100	100
14	Q	116/119 (98%)	110 (95%)	6 (5%)	0	100	100
15	R	101/114 (89%)	99 (98%)	2 (2%)	0	100	100
16	S	114/119 (96%)	110 (96%)	4 (4%)	0	100	100
17	T	99/102 (97%)	97 (98%)	2 (2%)	0	100	100
18	U	108/118 (92%)	107 (99%)	1 (1%)	0	100	100
19	V	88/94 (94%)	86 (98%)	2 (2%)	0	100	100
20	W	100/103 (97%)	96 (96%)	4 (4%)	0	100	100
21	Y	74/96 (77%)	68 (92%)	6 (8%)	0	100	100
22	Z	57/62 (92%)	50 (88%)	7 (12%)	0	100	100
23	1	57/63 (90%)	53 (93%)	4 (7%)	0	100	100
24	2	54/59 (92%)	52 (96%)	2 (4%)	0	100	100
25	3	57/81 (70%)	51 (90%)	6 (10%)	0	100	100
26	4	51/57 (90%)	48 (94%)	3 (6%)	0	100	100
27	5	45/49 (92%)	45 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	6	41/44 (93%)	41 (100%)	0	0	100	100
29	7	61/66 (92%)	56 (92%)	5 (8%)	0	100	100
30	8	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
All	All	3348/3543 (94%)	3202 (96%)	144 (4%)	2 (0%)	49	73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	v	230	MET
4	C	155	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	v	353/365 (97%)	353 (100%)	0	100	100
4	C	221/225 (98%)	221 (100%)	0	100	100
5	D	169/171 (99%)	169 (100%)	0	100	100
6	E	165/174 (95%)	165 (100%)	0	100	100
7	F	97/155 (63%)	97 (100%)	0	100	100
8	G	145/147 (99%)	145 (100%)	0	100	100
9	L	119/121 (98%)	119 (100%)	0	100	100
10	M	101/101 (100%)	101 (100%)	0	100	100
11	N	104/115 (90%)	104 (100%)	0	100	100
12	O	103/113 (91%)	103 (100%)	0	100	100
13	P	95/111 (86%)	95 (100%)	0	100	100
14	Q	96/97 (99%)	96 (100%)	0	100	100
15	R	84/99 (85%)	84 (100%)	0	100	100
16	S	95/97 (98%)	95 (100%)	0	100	100
17	T	75/82 (92%)	75 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	U	83/97 (86%)	83 (100%)	0	100	100
19	V	78/84 (93%)	78 (100%)	0	100	100
20	W	69/88 (78%)	69 (100%)	0	100	100
21	Y	58/76 (76%)	58 (100%)	0	100	100
22	Z	46/53 (87%)	46 (100%)	0	100	100
23	1	51/55 (93%)	51 (100%)	0	100	100
24	2	50/52 (96%)	50 (100%)	0	100	100
26	4	47/50 (94%)	47 (100%)	0	100	100
27	5	44/48 (92%)	44 (100%)	0	100	100
28	6	39/39 (100%)	39 (100%)	0	100	100
29	7	53/56 (95%)	53 (100%)	0	100	100
30	8	35/35 (100%)	35 (100%)	0	100	100
All	All	2675/2906 (92%)	2675 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
15	R	41	GLN
17	T	101	ASN
30	8	36	GLN
15	R	66	ASN
17	T	11	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	A	2890/2932 (98%)	465 (16%)	23 (0%)
3	B	113/116 (97%)	14 (12%)	0
All	All	3003/3048 (98%)	479 (15%)	23 (0%)

5 of 479 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	A	13	A

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Mol	Chain	Res	Type
2	A	14	A
2	A	28	A
2	A	34	U
2	A	46	C

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A	1569	U
2	A	2438	G
2	A	1886	A
2	A	2463	A
2	A	809	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 205 ligands modelled in this entry, 204 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
31	GCP	v	501	-	32,34,34	1.41	6 (18%)	49,54,54	1.80	8 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
31	GCP	v	501	-	-	4/19/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	v	501	GCP	C5-C4	3.07	1.47	1.38
31	v	501	GCP	PG-O3G	2.78	1.61	1.55
31	v	501	GCP	PG-O2G	2.63	1.60	1.55
31	v	501	GCP	C6-N1	-2.59	1.34	1.38
31	v	501	GCP	C5-N7	-2.23	1.34	1.39

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	v	501	GCP	C5-C4-N3	-6.18	118.56	128.39
31	v	501	GCP	C2-N3-C4	4.93	120.79	112.30
31	v	501	GCP	N9-C4-N3	4.81	135.58	125.95
31	v	501	GCP	PB-O3A-PA	-3.34	121.47	132.37
31	v	501	GCP	C6-C5-N7	3.02	135.78	130.29

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
31	v	501	GCP	C5'-O5'-PA-O1A
31	v	501	GCP	C5'-O5'-PA-O3A
31	v	501	GCP	PB-C3B-PG-O1G
31	v	501	GCP	O4'-C4'-C5'-O5'

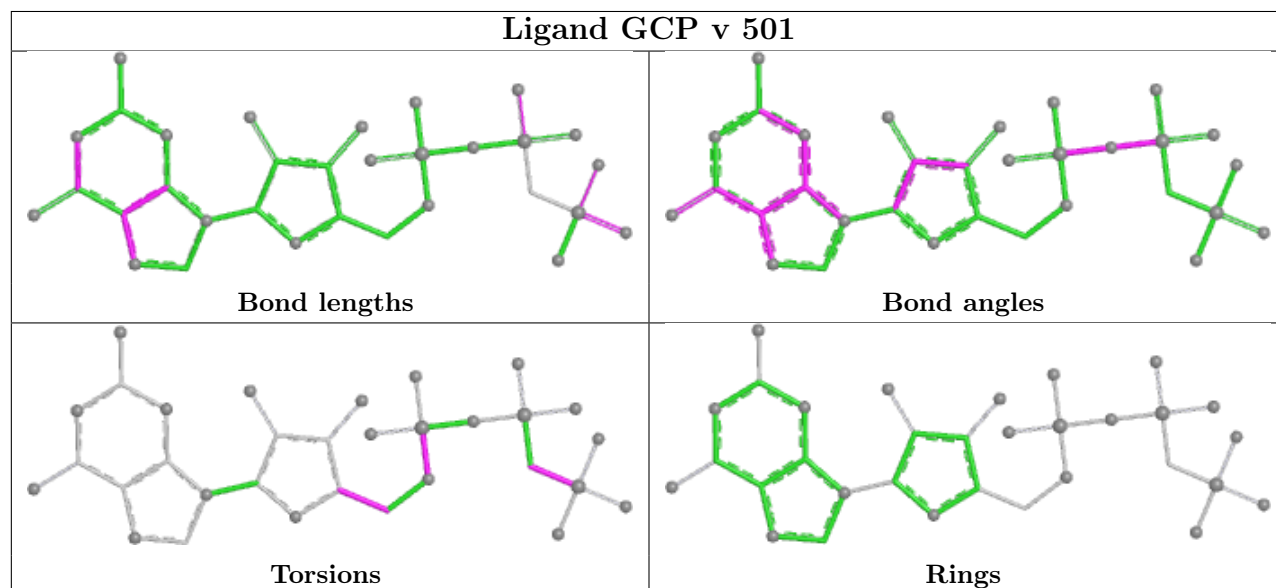
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
31	v	501	GCP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

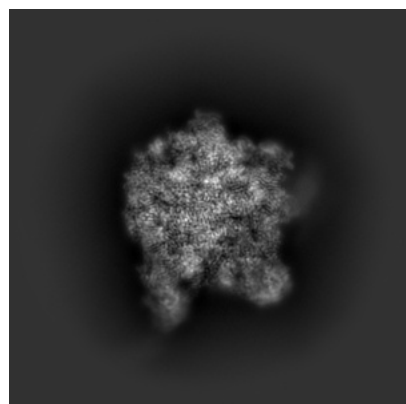
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42577. These allow visual inspection of the internal detail of the map and identification of artifacts.

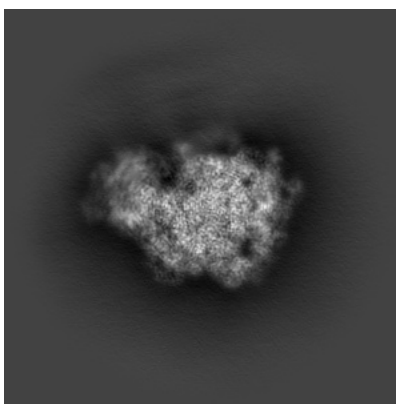
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

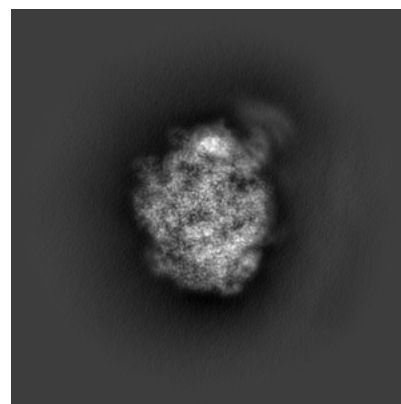
6.1.1 Primary map



X

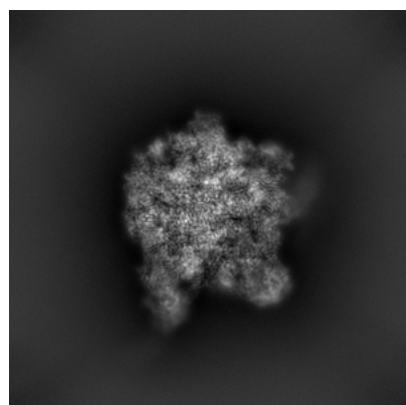


Y

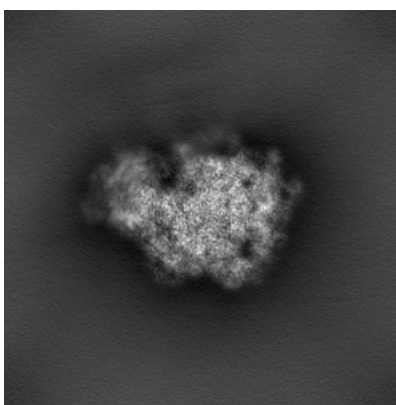


Z

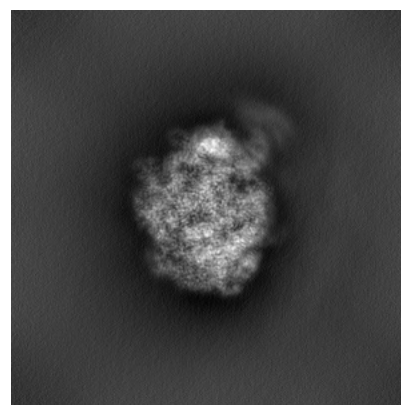
6.1.2 Raw map



X



Y

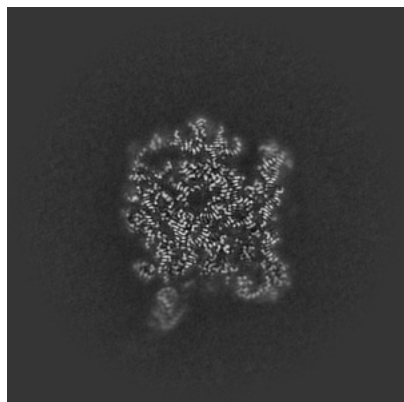


Z

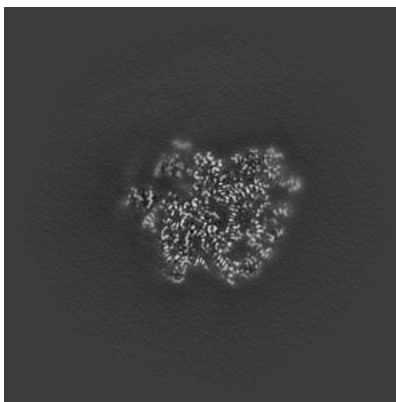
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

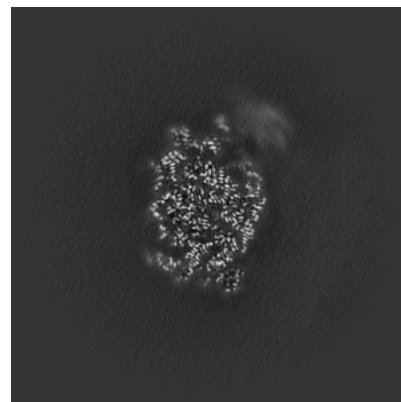
6.2.1 Primary map



X Index: 256

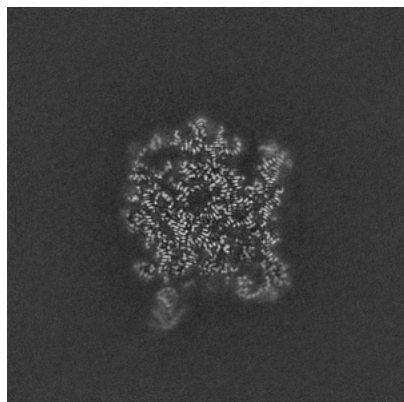


Y Index: 256

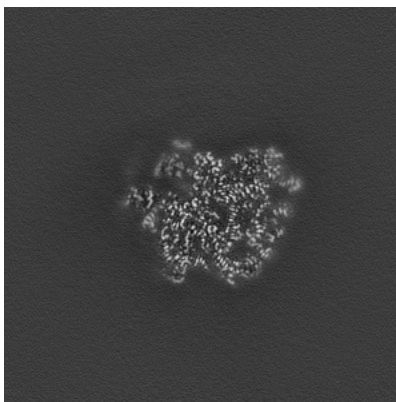


Z Index: 256

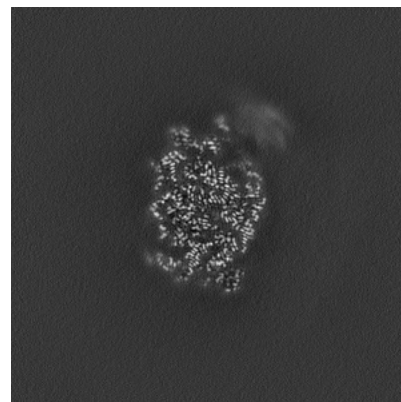
6.2.2 Raw map



X Index: 256



Y Index: 256

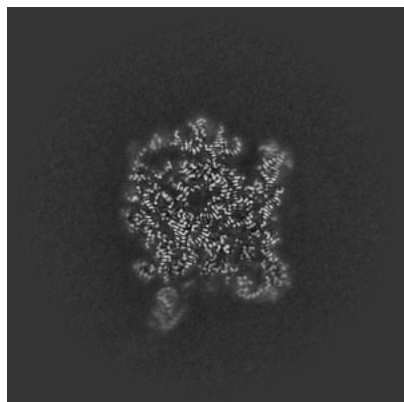


Z Index: 256

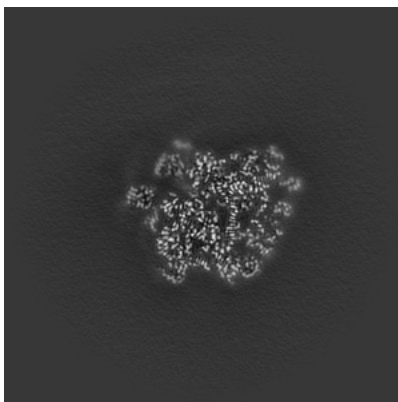
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

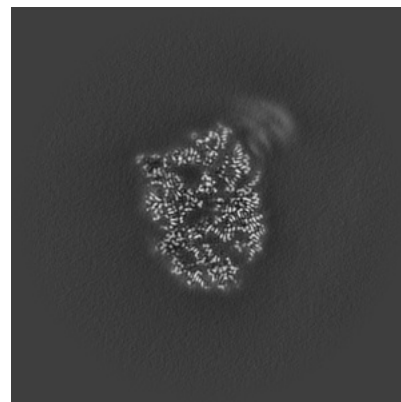
6.3.1 Primary map



X Index: 256

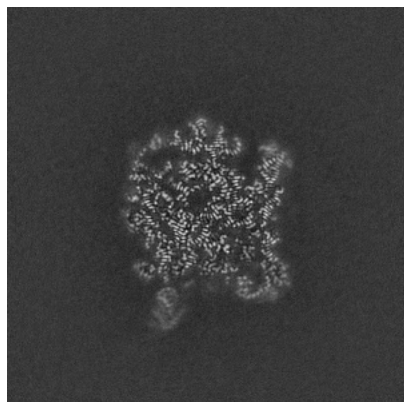


Y Index: 254

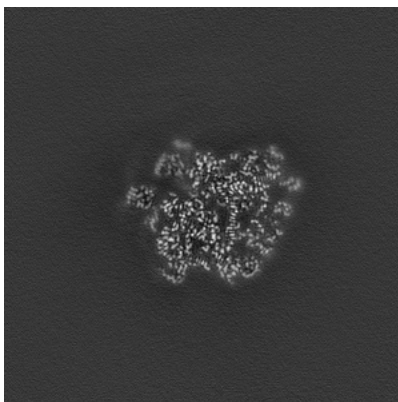


Z Index: 274

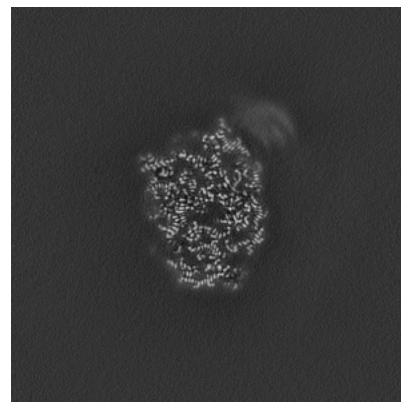
6.3.2 Raw map



X Index: 256



Y Index: 254

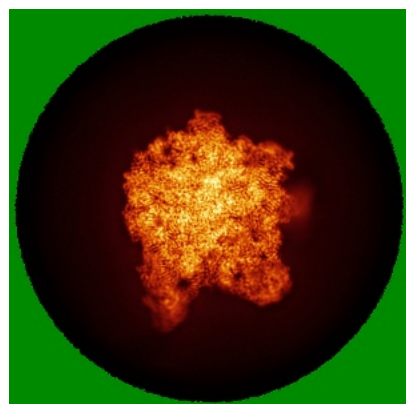


Z Index: 267

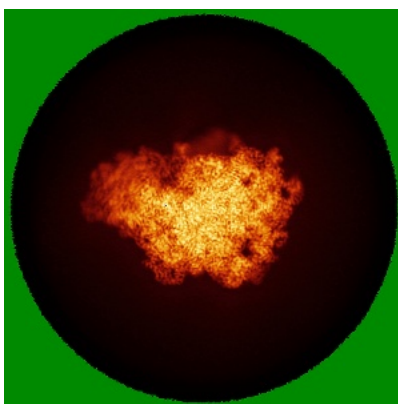
The images above show the largest variance slices of the map in three orthogonal directions.

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

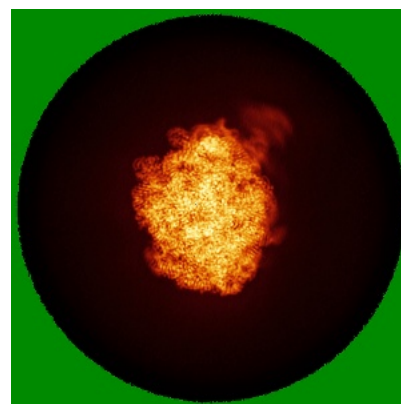
6.4.1 Primary map



X

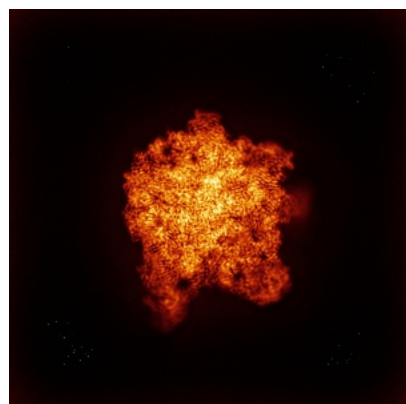


Y

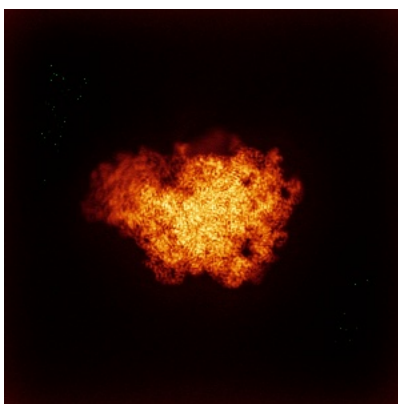


Z

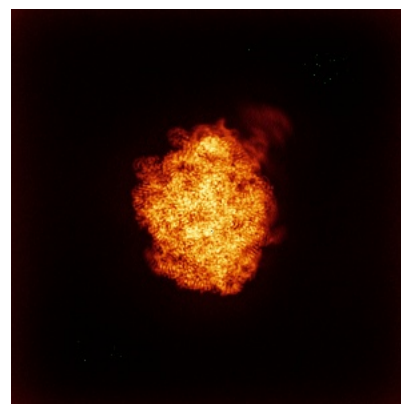
6.4.2 Raw map



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 0.3. 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.

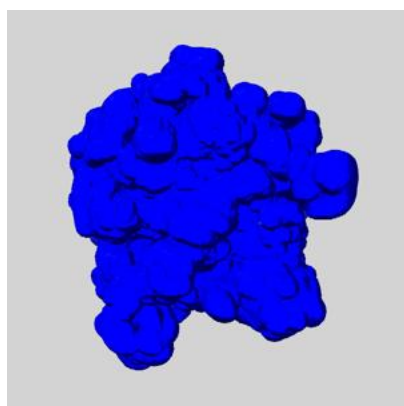
6.6 Mask visualisation [i](#)

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

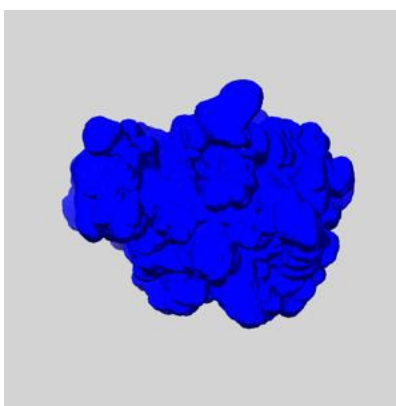
A mask typically either:

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

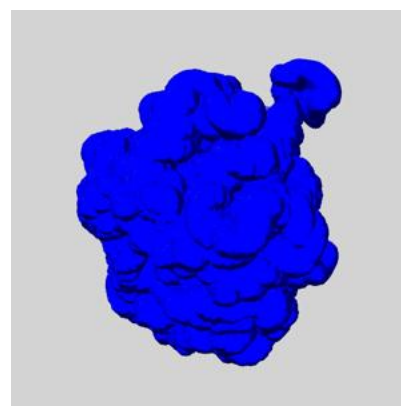
6.6.1 emd_42577_msk_1.map [i](#)



X



Y

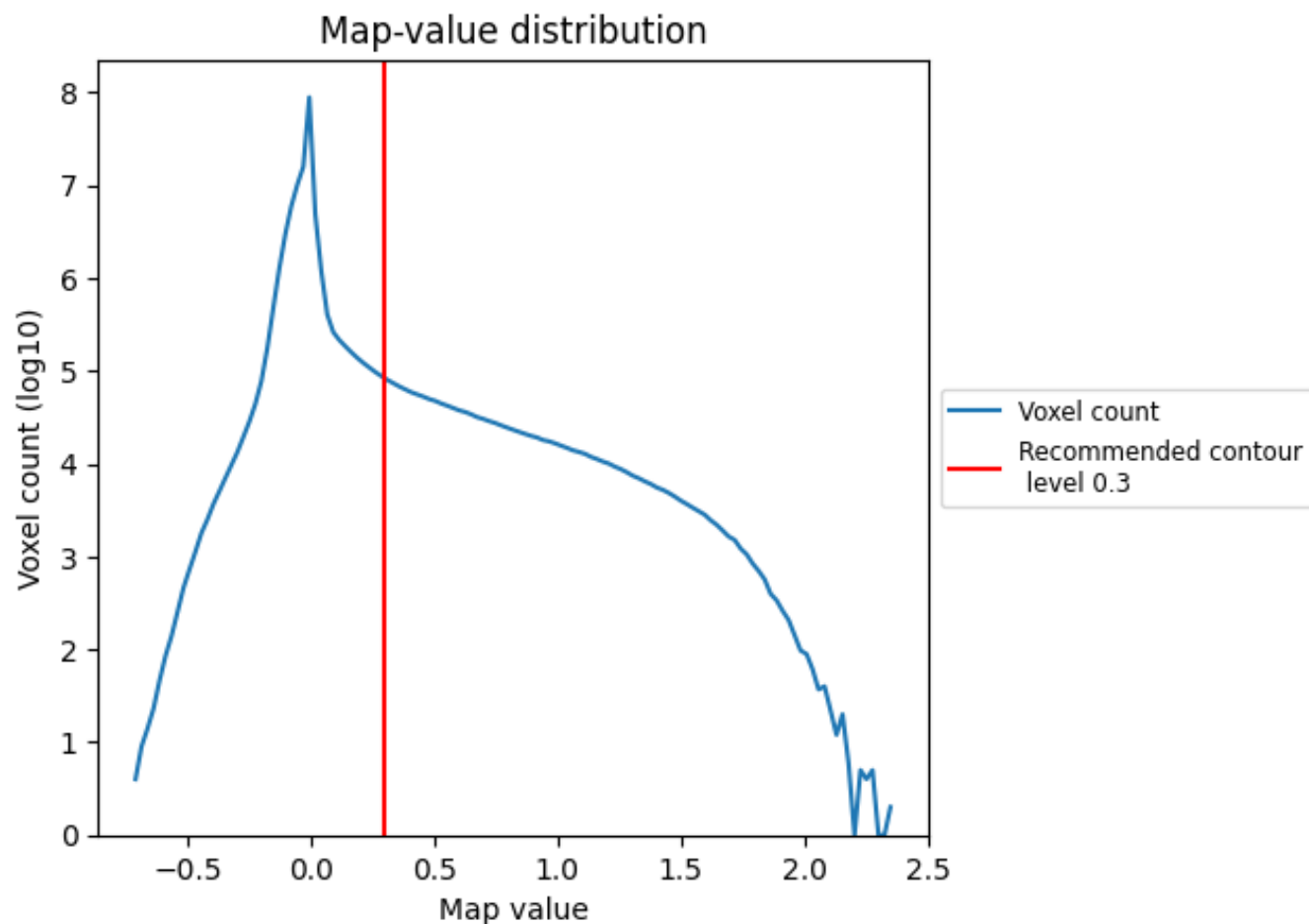


Z

7 Map analysis [i](#)

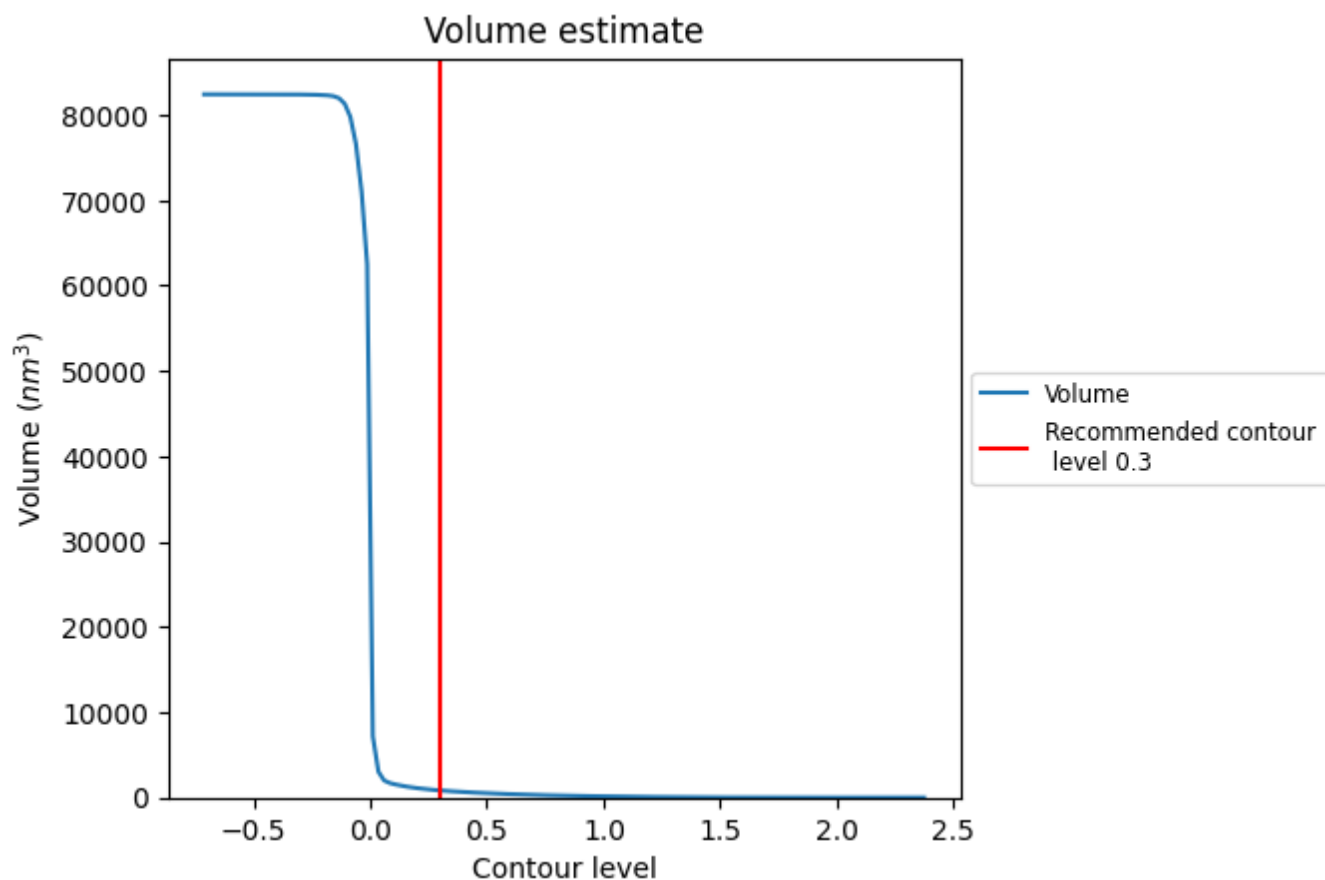
This section contains the results of statistical analysis of the map.

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.

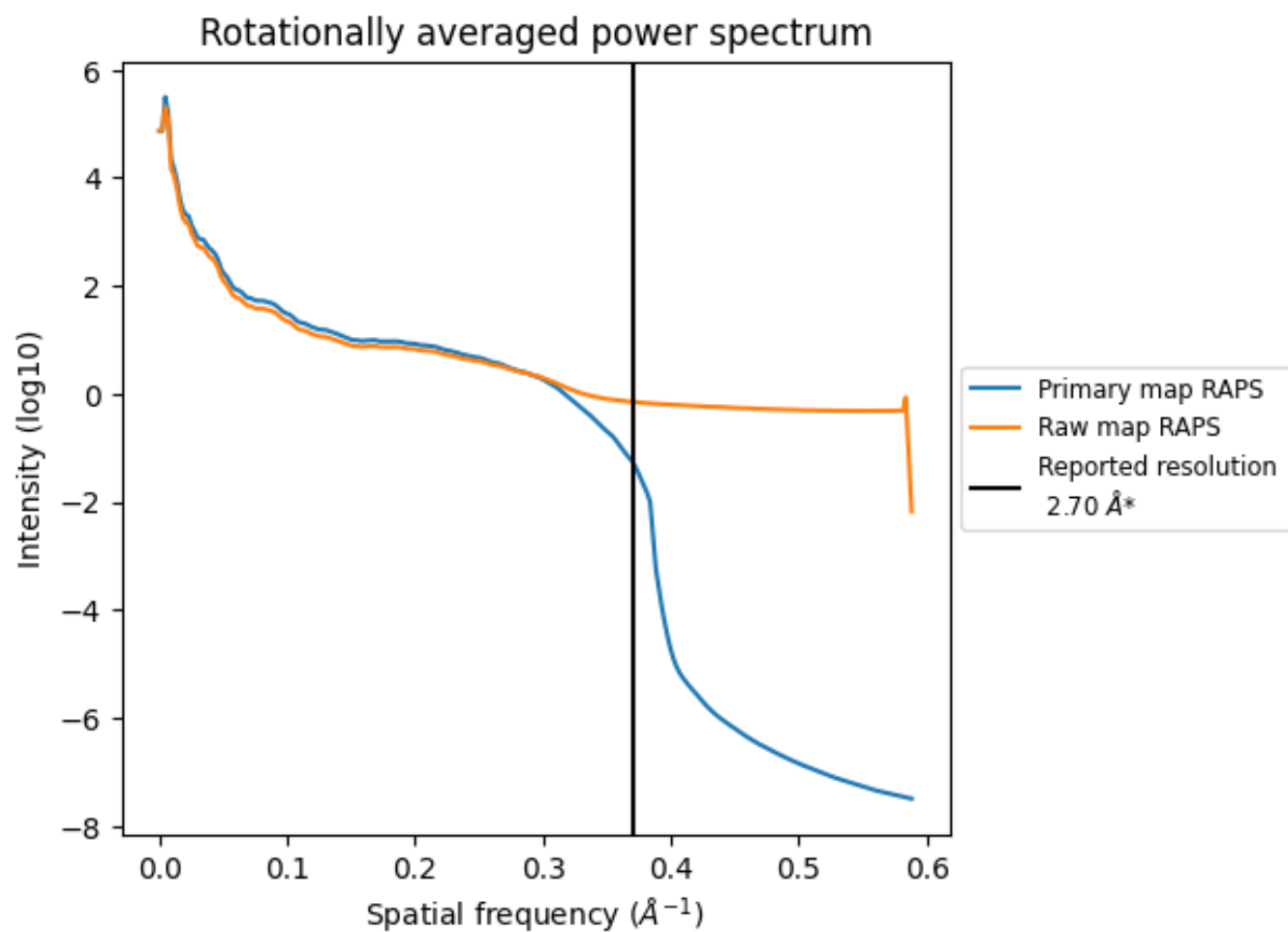
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 834 nm³; this corresponds to an approximate mass of 753 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

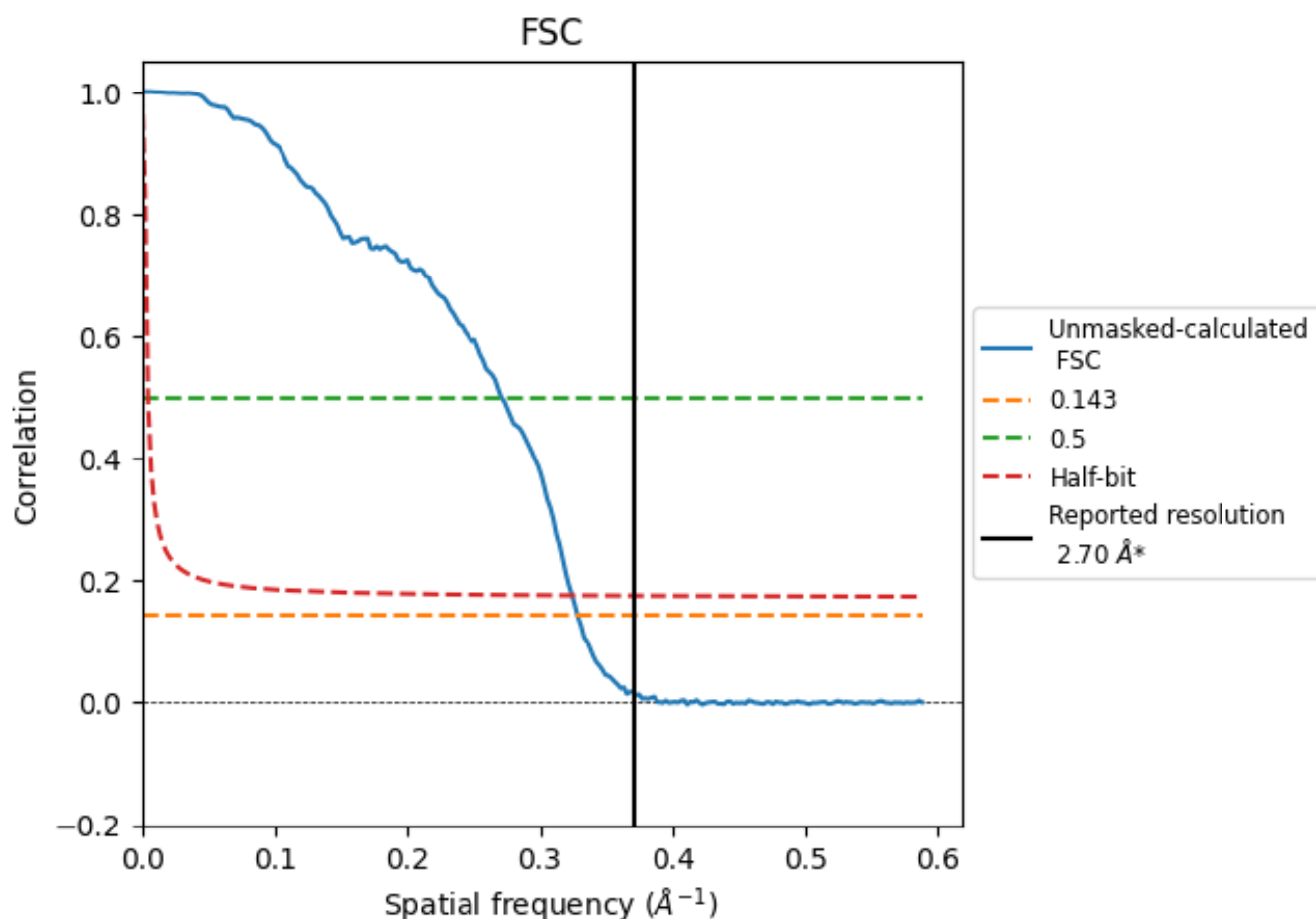


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

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 0.370 Å⁻¹

8.2 Resolution estimates [i](#)

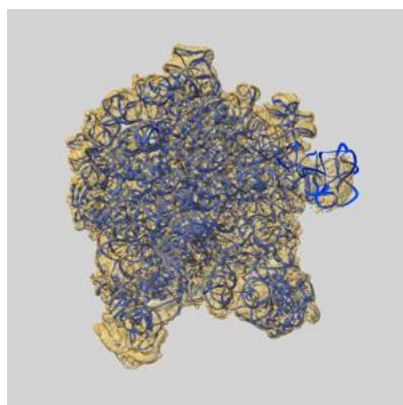
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.05	3.69	3.08

*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 3.05 differs from the reported value 2.7 by more than 10 %

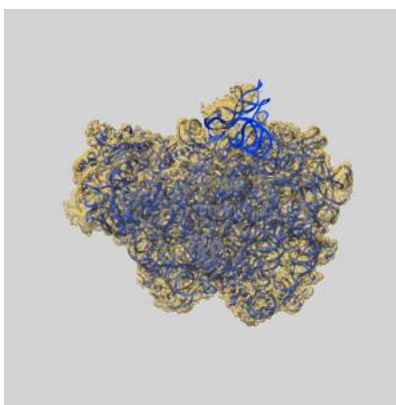
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-42577 and PDB model 8UUA. Per-residue inclusion information can be found in section [3](#) on page [12](#).

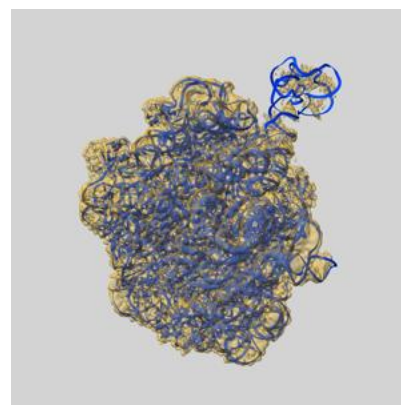
9.1 Map-model overlay [i](#)



X



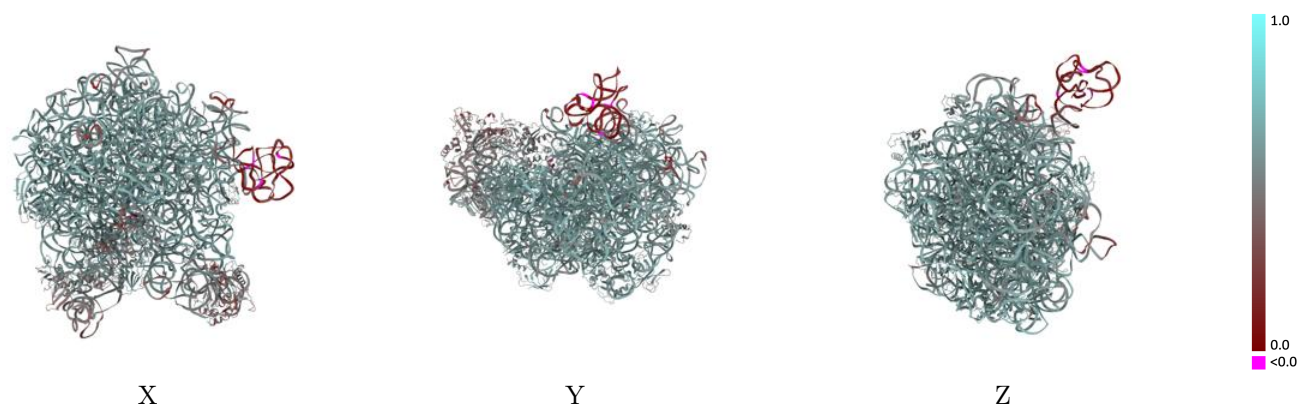
Y



Z

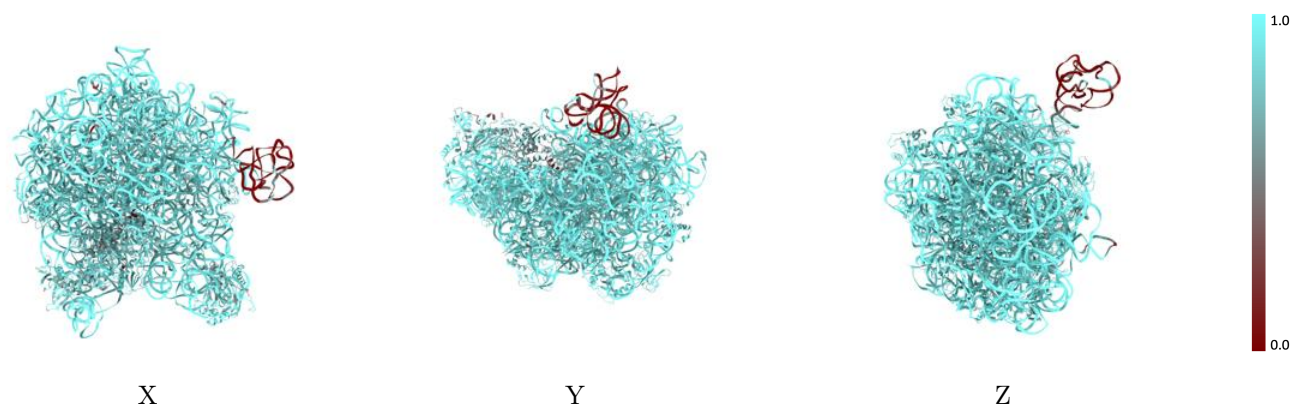
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



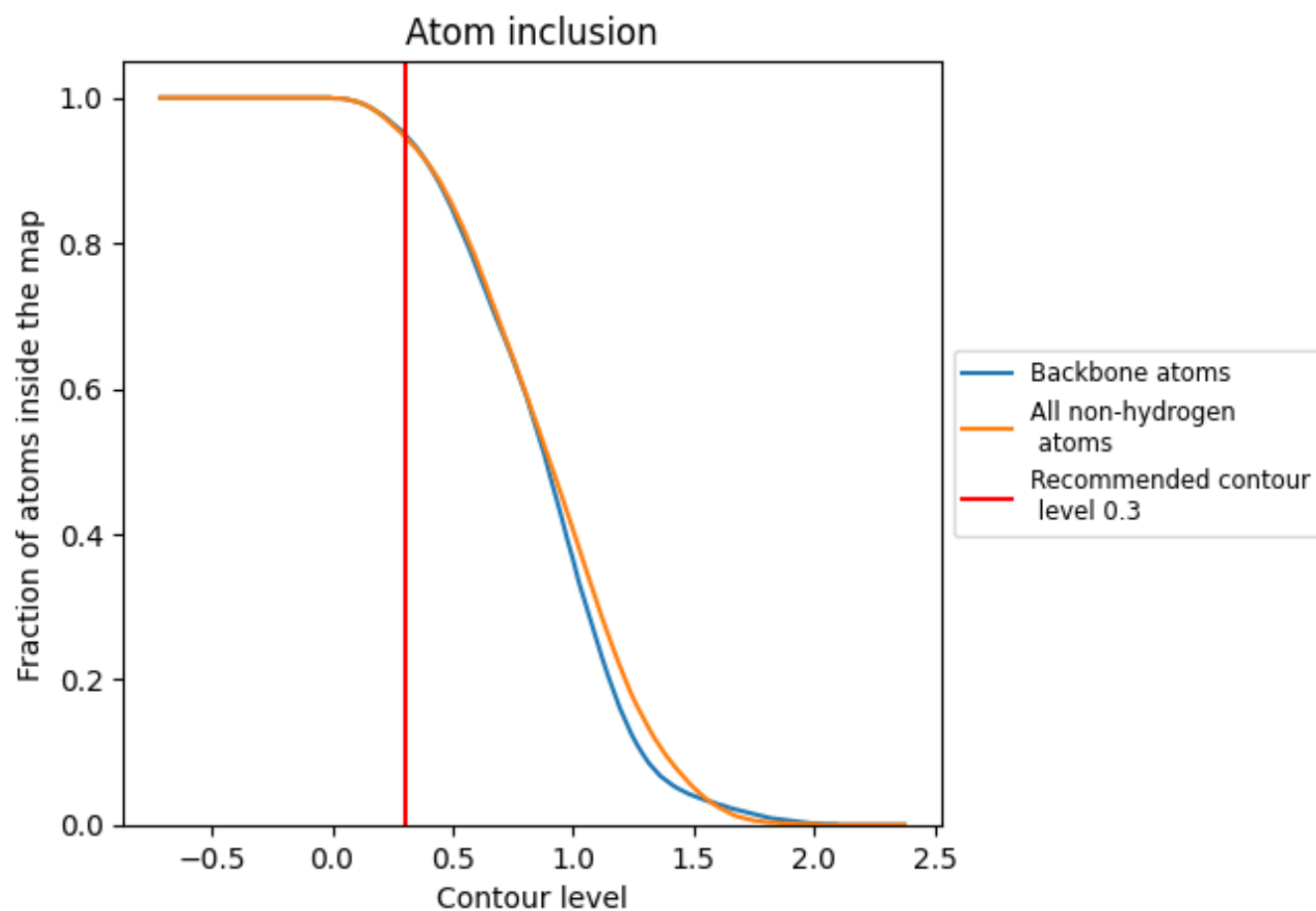
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 95% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9470	 0.5830
1	 0.9380	 0.5630
2	 0.9320	 0.6020
3	 0.7840	 0.3990
4	 0.9390	 0.6110
5	 0.9310	 0.6080
6	 0.9680	 0.6350
7	 0.9660	 0.6350
8	 0.9300	 0.6190
A	 0.9650	 0.5890
B	 0.9860	 0.5260
C	 0.9490	 0.6170
D	 0.9510	 0.6140
E	 0.9340	 0.5940
F	 0.8210	 0.4180
G	 0.8590	 0.5170
L	 0.9580	 0.6140
M	 0.9180	 0.6040
N	 0.9270	 0.5920
O	 0.9360	 0.6040
P	 0.9490	 0.6120
Q	 0.8790	 0.5060
R	 0.9420	 0.6050
S	 0.9710	 0.6160
T	 0.9640	 0.6120
U	 0.9450	 0.6120
V	 0.9390	 0.5960
W	 0.9380	 0.5710
Y	 0.9550	 0.6240
Z	 0.9360	 0.5990
v	 0.7170	 0.4820

