wwPDB EM Validation Summary Report (i)

Oct 28, 2026 – 07:55 AM EDT

PDB ID	:	9YLQ / pdb_00009ylq
EMDB ID	:	EMD-73091
Title	:	Pseudomonas aeruginosa 50S ribosome (L1 stalk in 'mid' conformation)
Authors	:	Findlay, J.L.; Kanik, M.; Gauvin, C.C.; Williamson, K.S.; Franklin, M.J.; Lawrence, C.M.
Deposited on	:	2025-10-09
Resolution	:	2.25 Å(reported)
Based on initial model	:	7UNW

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 (i) 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 (i)) were used in the production of this report:

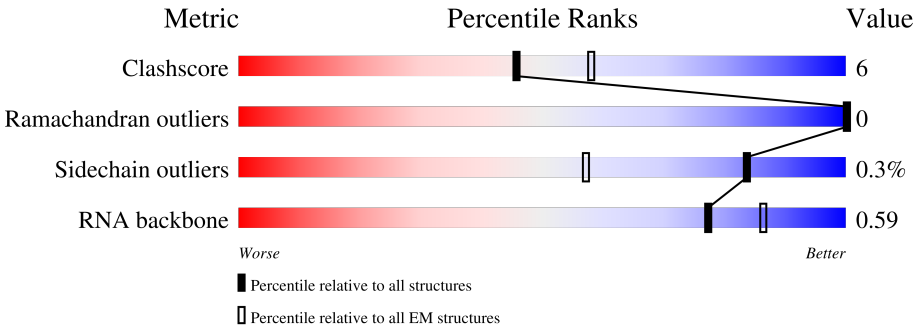
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

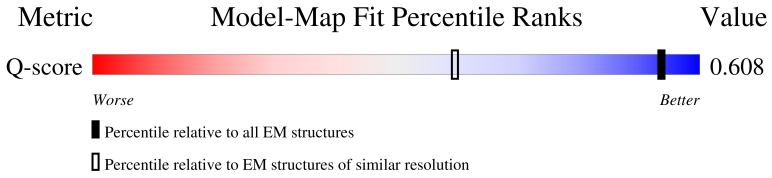
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.25 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	3458 (1.75 - 2.75)

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	A	2892	62% 33%
2	B	121	61% 31% 6%
3	C	231	17% 38% 19% 44%

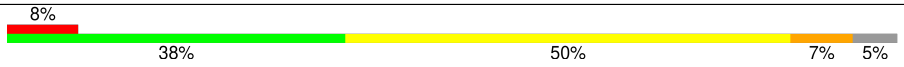
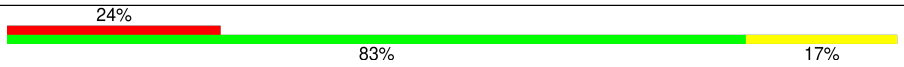
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Mol	Chain	Length	Quality of chain
4	D	273	82% 17%
5	E	211	87% 11%
6	F	200	85% 14%
7	G	179	75% 25%
8	H	177	83% 15%
9	I	148	26% 73% 5% 22%
10	L	142	88% 12%
11	M	122	86% 14%
12	N	144	88% 12%
13	O	137	74% 26%
14	P	129	80% 12% 8%
15	Q	116	87% 12%
16	R	116	6% 84% 14%
17	S	118	86% 14%
18	T	103	89% 11%
19	U	110	87% 13%
20	V	99	68% 27% 5%
21	W	104	86% 6% 9%
22	X	204	80% 13% 7%
23	Y	85	82% 8% 9%
24	Z	78	85% 14%
25	1	63	86% 11%
26	2	58	93%
27	4	60	75% 15% 10%
28	5	51	78% 22%

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Mol	Chain	Length	Quality of chain
29	6	44	
30	7	64	
31	8	38	
32	v	76	
33	J	166	
34	K	143	

2 Entry composition (i)

There are 37 unique types of molecules in this entry. The entry contains 98343 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	2837	60895	27173	11178	19708	2836	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	119	2535	1132	452	832	119	0	0

- Molecule 3 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	130	996	631	179	185	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	272	2072	1276	426	364	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	208	1564	968	298	293	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	200	1521	955	283	280	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	179	Total	C	N	O	S	0	0
			1435	914	256	260	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	174	Total	C	N	O	S	0	0
			1314	828	242	242	2		

- Molecule 9 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	115	Total	C	N	O	S	0	0
			858	539	152	166	1		

- Molecule 10 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	142	Total	C	N	O	S	0	0
			1130	718	206	202	4		

- Molecule 11 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 12 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	144	Total	C	N	O	S	0	0
			1066	654	215	194	3		

- Molecule 13 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	137	Total	C	N	O	S	0	0
			1085	689	211	181	4		

- Molecule 14 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	119	Total 952	C 595	N 191	O 161	S 5	0	0

- Molecule 15 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	115	Total 881	C 544	N 174	O 161	S 2	0	0

- Molecule 16 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	R	114	Total 901	C 567	N 171	O 162	S 1	0	0

- Molecule 17 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	S	117	Total 936	C 592	N 196	O 148	0	0

- Molecule 18 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	103	Total 822	C 521	N 156	O 143	S 2	0	0

- Molecule 19 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	110	Total 833	C 515	N 161	O 153	S 4	0	0

- Molecule 20 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	94	Total 739	C 472	N 134	O 132	S 1	0	0

- Molecule 21 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	95	Total	C	N	O	S	0	0
			738	466	142	129	1		

- Molecule 22 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	190	Total	C	N	O	S	0	0
			1445	915	262	265	3		

- Molecule 23 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	Y	77	Total	C	N	O	0	0
			581	367	112	102		

- Molecule 24 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	77	Total	C	N	O	S	0	0
			630	391	134	103	2		

- Molecule 25 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	1	61	Total	C	N	O	S	0	0
			490	301	96	91	2		

- Molecule 26 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	2	56	Total	C	N	O	S	0	0
			440	275	86	77	2		

- Molecule 27 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	4	54	Total	C	N	O	S	0	0
			431	258	91	81	1		

- Molecule 28 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	5	51	Total	C	N	O	S	0	0
			426	272	78	75	1		

- Molecule 29 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	6	44	Total	C	N	O	S	0	0
			365	222	87	54	2		

- Molecule 30 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	7	63	Total	C	N	O	S	0	0
			506	314	108	81	3		

- Molecule 31 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	8	38	Total	C	N	O	S	0	0
			307	186	69	48	4		

- Molecule 32 is a RNA chain called E-site tRNA-Ala.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	v	72	Total	C	N	O	P	0	0
			1540	686	277	505	72		

- Molecule 33 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	J	111	Total	C	N	O	S	0	0
			840	533	151	155	1		

- Molecule 34 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	K	143	Total	C	N	O	S	0	0
			1046	655	186	201	4		

- Molecule 35 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
35	A	196	Total Mg 196 196	0
35	B	3	Total Mg 3 3	0
35	D	1	Total Mg 1 1	0
35	E	1	Total Mg 1 1	0
35	4	1	Total Mg 1 1	0

- Molecule 36 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
36	8	1	Total Zn 1 1	0

- Molecule 37 is water.

Mol	Chain	Residues	Atoms	AltConf
37	A	4032	Total O 4032 4032	0
37	B	76	Total O 76 76	0
37	D	89	Total O 89 89	0
37	E	78	Total O 78 78	0
37	F	47	Total O 47 47	0
37	G	12	Total O 12 12	0
37	H	3	Total O 3 3	0
37	I	1	Total O 1 1	0
37	L	34	Total O 34 34	0
37	M	18	Total O 18 18	0
37	N	64	Total O 64 64	0
37	O	37	Total O 37 37	0

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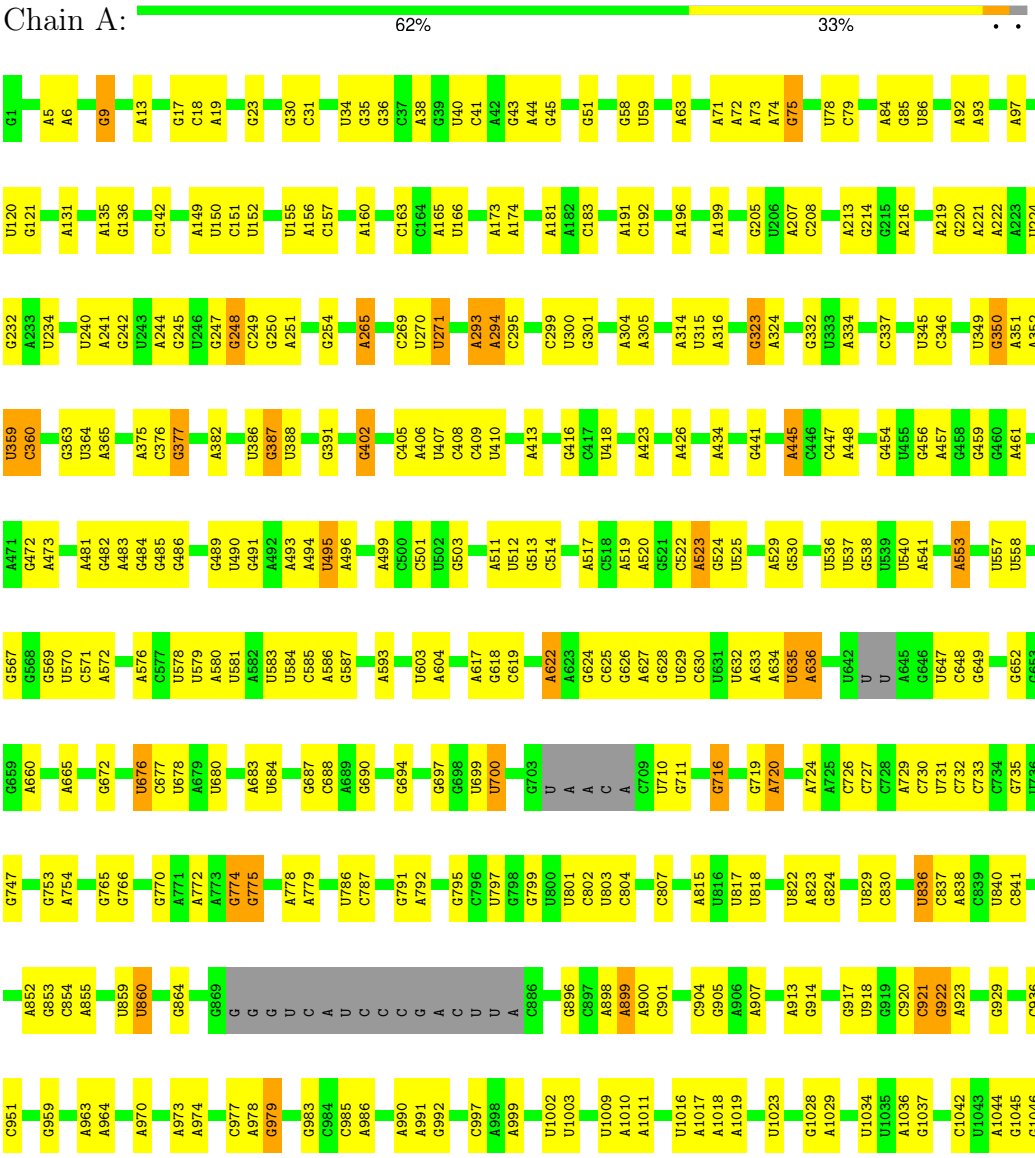
Mol	Chain	Residues	Atoms	AltConf
37	P	36	Total O 36 36	0
37	Q	6	Total O 6 6	0
37	R	25	Total O 25 25	0
37	S	44	Total O 44 44	0
37	T	32	Total O 32 32	0
37	U	40	Total O 40 40	0
37	V	26	Total O 26 26	0
37	W	11	Total O 11 11	0
37	X	22	Total O 22 22	0
37	Y	24	Total O 24 24	0
37	Z	20	Total O 20 20	0
37	1	3	Total O 3 3	0
37	2	16	Total O 16 16	0
37	4	32	Total O 32 32	0
37	5	1	Total O 1 1	0
37	6	23	Total O 23 23	0
37	7	22	Total O 22 22	0
37	8	8	Total O 8 8	0

3 Residue-property plots (i)

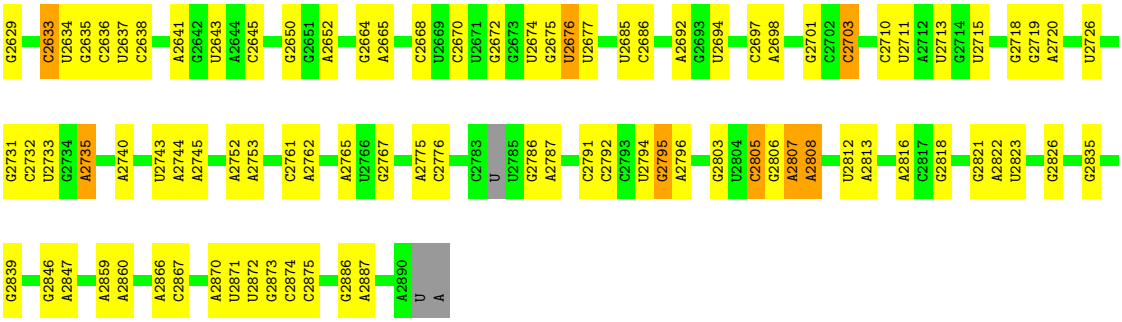
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

Chain A:



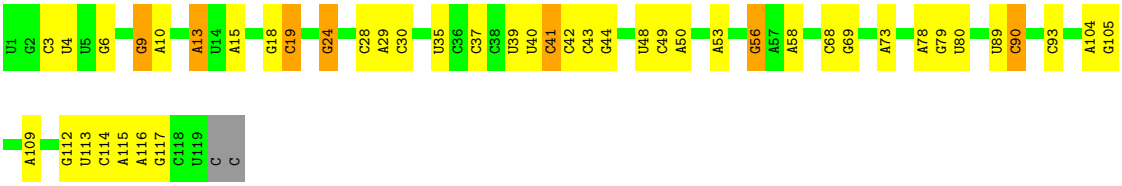
G1053 C1054
G1058 A1059
A1060 G1061
C1062
A1063 G1064 C1065 C1066 A1067
C1068 C1069 C1070 U1071 U1072 U1073 A1074
G1077 A1078
U1084 A1085 A1086 U1087
G1097 U1098 C1099 G1100 A1101 G1102
G1115 A1116
U1120 G1121 U1122 A1123 A1124 C1125 G1126
U1131 C1132 A1133
A1140 C1141
C1144
G1157 U1158
G1162 U A A
G1166 U1167 G1168 A1169
G1180
U1185 U1186 C1187
G1193
A1211 G1212 A1213 A1214
G1223
G1235 U1236 G1237 C1238 G1239 A1240 A1241 U1242 G1243
U1250 G1251 A1252 G1253
A1256 C1257 G1258 A1259
A1273
C1276 A1277
A1281
C1284 C1285 G1286 A1287 A1288 A1289
G1298 U1299
U1300 C1301 C1302 U1303 G1304
C1307 A1308 A1309 C1310
U1316
C1320 G1321
G1325
U1328
U1339 A1340 A1341
G1344 G1345
G1348 C1349 U1350 G1351 A1352 A1353
C1357 G1358 U1359
A1365 U1366
A1372 C1373 A1374
A1379 A1380 U1381 A1382 U1383
U1392 U1393 C1394 U1395
G1403 C1404 G1405 A1406
U1407 G1408
G1413 A1414 C1415
G1416 G1417 A1418 G1419 A1420 A1421 G1422 G1423 C1424 U1425 A1426
C1433 U1434 U1435 G1436 G1437 C1438 G1439
U1447
A1450 A1451 G1452 U1453
A1456 A1457
C1459 U1460 G1461
G1469
U1480
A1483 U1484 C1485
U1492 U1493 C1494 A1495 A1496
A1515
G1519 U C U U
U U A G A U
G1530 A1531 C1532 G1533 A1534 A1535 G1536
U1553 C1554 C1555 A1556
A1559 A1560 A1561
U1568
C1572 U1573 U C1575
A1587 A1588
C1594
C1597 A1598 A1599 A1600
A1608
G1616
G1621 A1622 G1623 A1624
A1627
G1635 C1636 U1637 U1638
A1644
G1649
G1656 G1657 A1658
G1664
U1670 G1671 G1672 C1673 A1674
A1680 C1681
G1687 A1688 G1689
G1692
U1708 G1709 A1710
U1717
C1722 G1723 U1724
G1732
G1736
G1740 A1741 A1742 G1743
C1747
G1751
U1756 G1757
A1760 C1761
U1766
A1770 A1771 A1772 A1773
C1777 A1778 G1779
C1780 A1781 C1782 U1783 C1784 U1785
G1786 C1787 A1788 A1789 A1790
A1795 A1796 A1797
C1803
A1808
G1813 U1814 G1815 A1816 C1817
U1821 G1822
G1833 A1834 A1835
U1838 U1839 A1840 A1841 U1842 U1843 G1844 A1845
G1850 U1851
G1860 C1861
U1867 C1868
A1872
A1876 A1877
C1889
C1892 G1893
G1894 C C G U A
G1909 U1910 C1911
G1916 G1917 U1918
A1923 A1924 A1925
C1929 U1930
U1933 C1934
U1942
C1945
U1950 G1951 C1952 A1953 C1954 G1955 A1956 A1957 U1958 G1959
G1976 C1977 U1978 G1979 U1980
C1986 C1987 C1988 G1989 A1990 G1991
G1997 U1998 G1999 A2000 A2001 A2002
A2006 A2007 A2008 U2009 C2010 G2011 C2012 U2013
A2017 A2018 G2019 A2020
A2024 G2025 U2026
U2030
U2038
C2042 G2043
A2047 G2048 A2049 C2050 C2051 C2052 C2053
G2056 A2057 A2058 C2059 C2060 U2061 U2062
U2066 G2067
U2073 U2074 G2075
U2079 G2080
G2087
A2088 G2089 C2090 C2091 U2092 G2093 C2094 U2095 U2096 G2097 U2098 G2099
G2102 C2103 A2104
C2110 G2111 G2112 A2113 G2114
U2117
G2120 A2121 A2122
C2128 A2129 C2130 G2131
U2137 C2138 G2139 C2140 G2141 U2142 G2143 G2144 A2145 G2146 C2147 G2148 A2149
C2152 U2153 U2154 G2155
A2156 A2157 A2158
U2159 A2160 C2161 C2162 A2163
C2164 C2165 C2166 U2167 G2168 G2169 C2170 A2171 U2172 C2173 C2174 U2175 U2176 G2177
U2182 C2183 U2184 A2185 A2186
G2191
C2195
A2198 A2199 U2200 C2201
A2209
A2212 C2213 A2214 G2215 U2216
U2220 G2221
G2225 G2226 C2227 A2228 G2229 U2230 U2231 U2232 G2233 A2234
G2237 G2238
C2245
A2255
G2258
U2259 A2260 A2261
G2266
G2269 U2270 A2271 C2272 G2273 A2274 A2275
U2278 G2279
U2283
A2287 C2288 C2289
U2292 C2293 G2294 G2295
A2298 U2299 C2300 G2301
C2304 G2305 C2306 A2307 G2308 A2309
A2312 U2313 A2314 A2315 A2316 G2317
A2321 A2322 A2323
G2326 C2327
G2332 A2333 C2334 U2335 G2336 C2337
G2338 A2341
C2346 A2347 C2348
C2351 G2352 A2353
A2356
U2359 A2360 C2361 G2362 A2363 A2364 A2365
G2370 U2371 C2372 U2373
G2376 U2377 G2378 A2379
U2388 U C2390 U2391 G2392 U2393 A2394
G2397 A2398
U2406
A2412 A2413 C2414 G2415 G2416 A2417 U2418 A2419
A2422
U2428 C2429 C2430 G2431
G2432
A2435
C2439 A2440
C2449 C2450
C2454 A2455 A2456
U2460 U2461 C2462 A2463 U2464
G2471 G2472 C2473 G2474 G2475
G2481 G2482 C2483
C2486 U2487 C2488 G2489 A2490 U2491 G2492 U2493
U2498 C2499 A2500 U2501 C2502 A2503 C2504 A2505
G2516 A2517 A2518 G2519
G2522 G2523 U2524 C2525 C2526
G2531
A2534 U2535
U2539
G2544 C2545
A2551 A2552 A2553 G2554 U2555
A2559
C2563 A2564 G2565 C2566
G2569 G2570
C2578 G2579
G2582
A2585
C2588 A2589
U2592 C2593 C2594 G2595 U2596
U2600 A2601 U2602 C2603 U2604 G2605
U2616 U2617 G2618 A2619 G2620
U2623 U2624 G2625 A2626 G2627 A2628



• Molecule 2: 5S rRNA

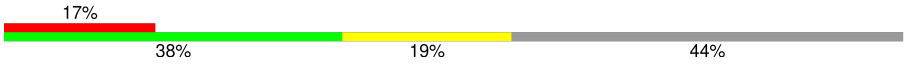
Chain B:

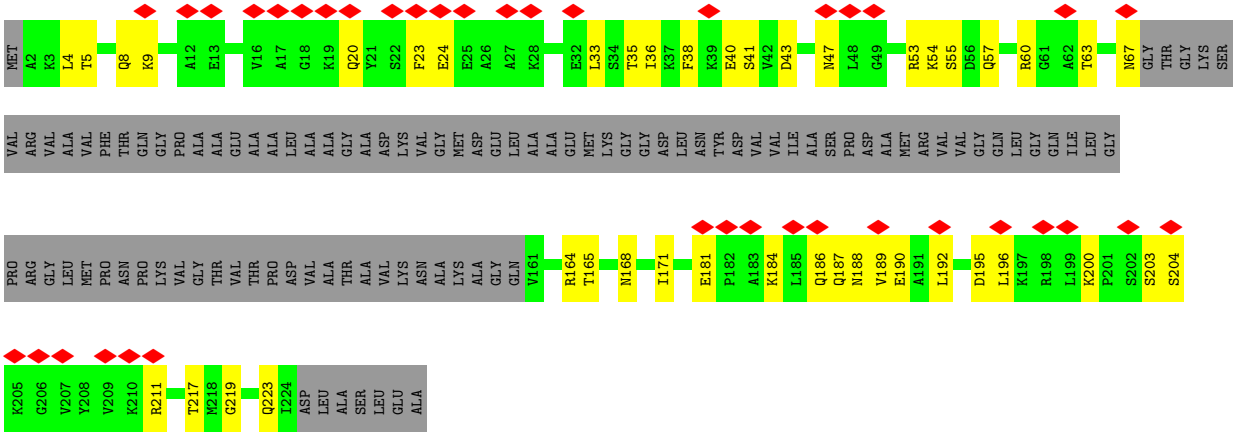




• Molecule 3: Large ribosomal subunit protein uL1

Chain C:

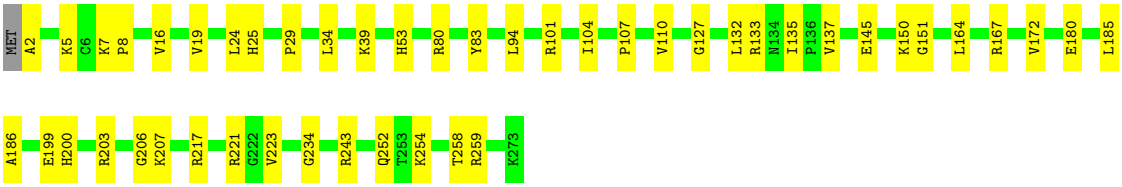




• Molecule 4: Large ribosomal subunit protein uL2

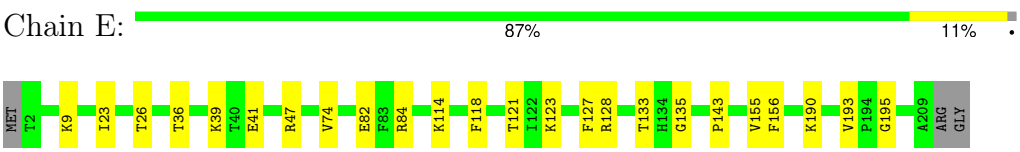
Chain D:





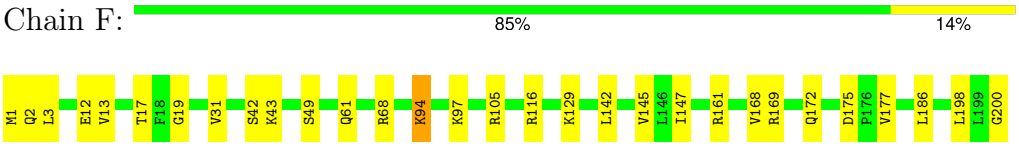
• Molecule 5: Large ribosomal subunit protein uL3

Chain E:



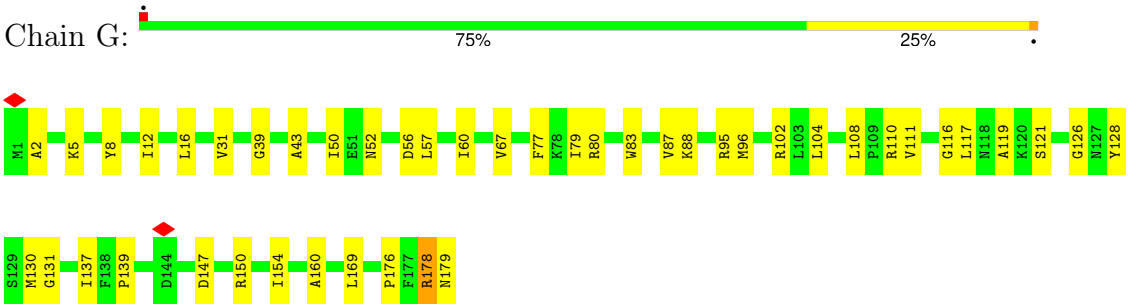
• Molecule 6: Large ribosomal subunit protein uL4

Chain F:



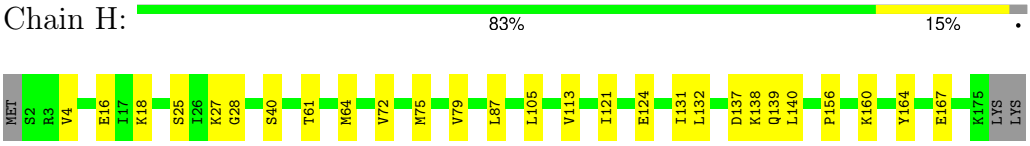
• Molecule 7: Large ribosomal subunit protein uL5

Chain G:



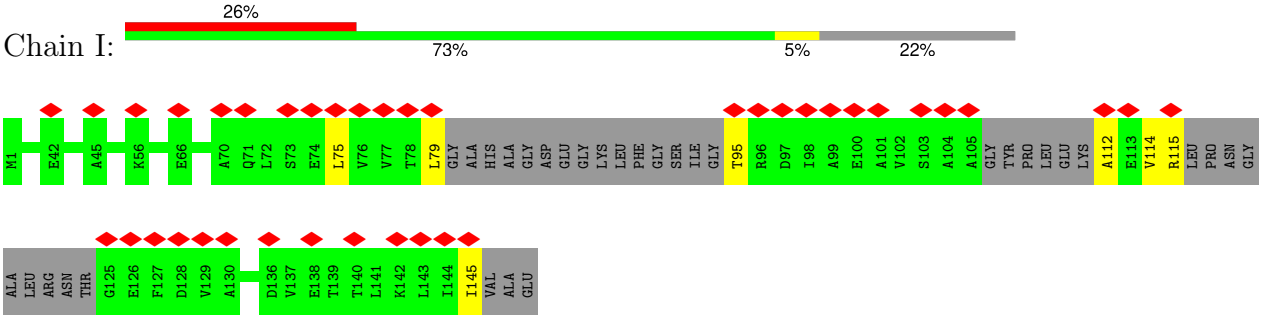
• Molecule 8: Large ribosomal subunit protein uL6

Chain H:



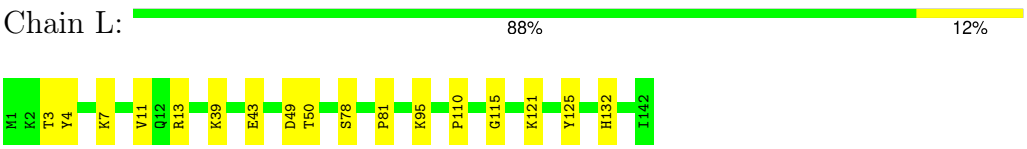
• Molecule 9: Large ribosomal subunit protein bL9

Chain I:



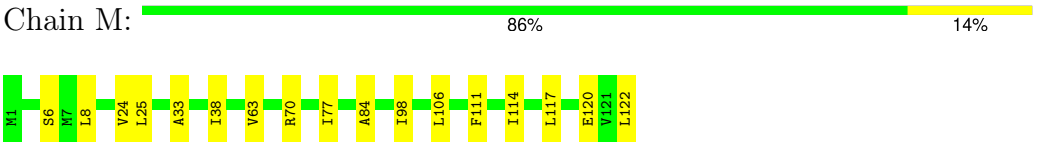
• Molecule 10: Large ribosomal subunit protein uL13

Chain L:



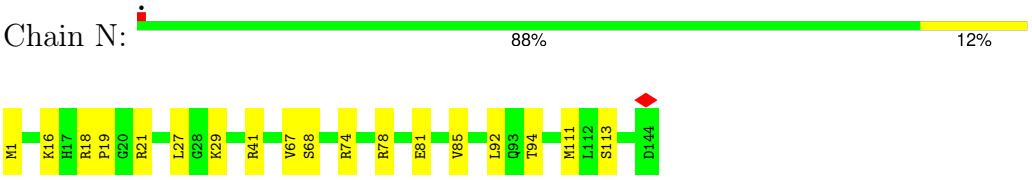
• Molecule 11: Large ribosomal subunit protein uL14

Chain M:



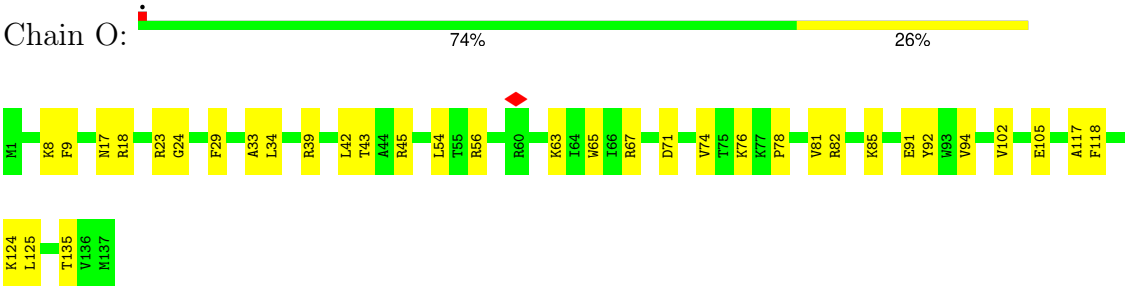
• Molecule 12: Large ribosomal subunit protein uL15

Chain N:



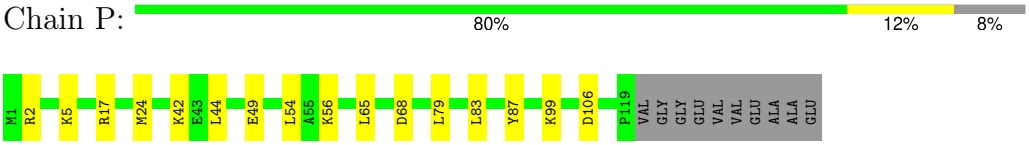
• Molecule 13: Large ribosomal subunit protein uL16

Chain O:



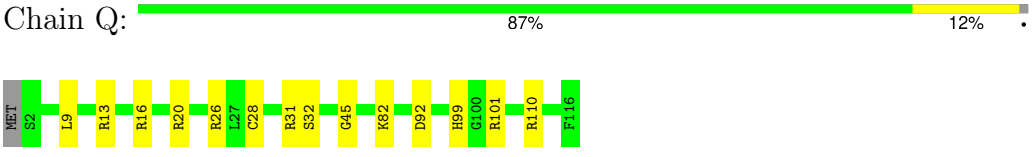
• Molecule 14: Large ribosomal subunit protein bL17

Chain P:



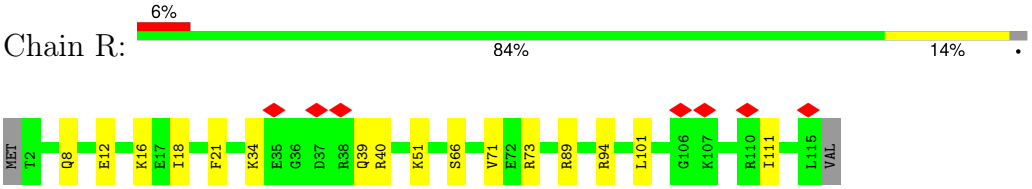
• Molecule 15: Large ribosomal subunit protein uL18

Chain Q:



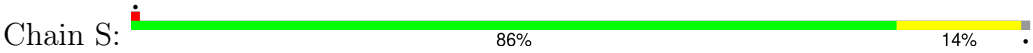
• Molecule 16: Large ribosomal subunit protein bL19

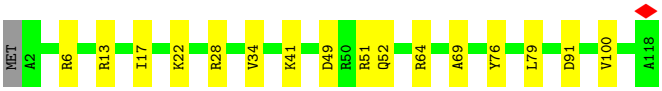
Chain R:



• Molecule 17: Large ribosomal subunit protein bL20

Chain S:





• Molecule 18: Large ribosomal subunit protein bL21

Chain T:

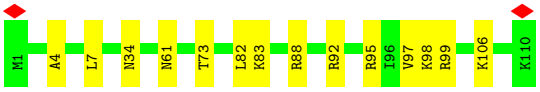




• Molecule 19: Large ribosomal subunit protein uL22

Chain U:

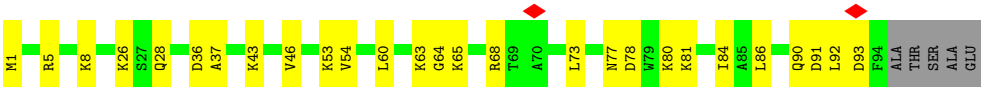




• Molecule 20: Large ribosomal subunit protein uL23

Chain V:

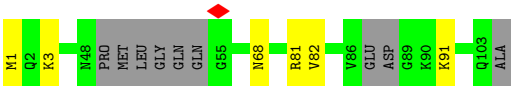




• Molecule 21: Large ribosomal subunit protein uL24

Chain W:

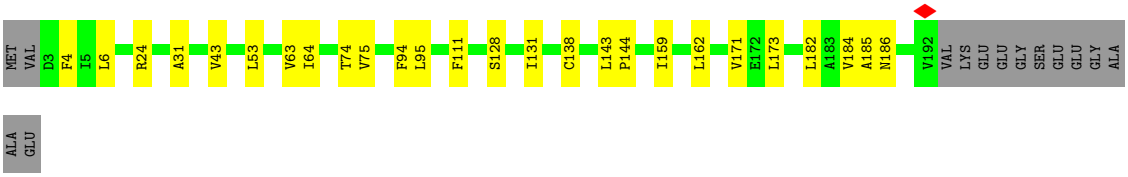




• Molecule 22: Large ribosomal subunit protein bL25

Chain X:





• Molecule 23: Large ribosomal subunit protein bL27

Chain Y:





• Molecule 24: Large ribosomal subunit protein bL28

Chain Z:





• Molecule 25: Large ribosomal subunit protein uL29

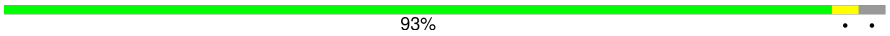
Chain 1:





• Molecule 26: Large ribosomal subunit protein uL30

Chain 2:

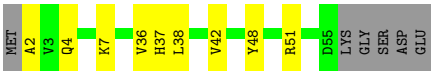




• Molecule 27: Large ribosomal subunit protein bL32

Chain 4:

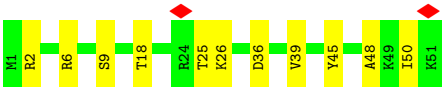




• Molecule 28: Large ribosomal subunit protein bL33

Chain 5:

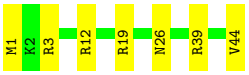




• Molecule 29: Large ribosomal subunit protein bL34

Chain 6:

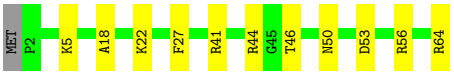




• Molecule 30: Large ribosomal subunit protein bL35

Chain 7:

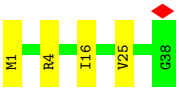




• Molecule 31: Large ribosomal subunit protein bL36A

Chain 8:

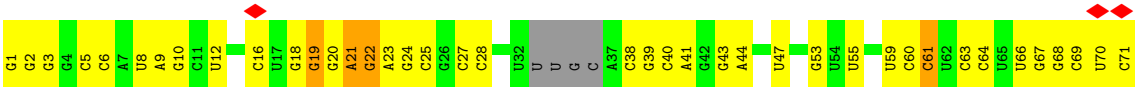


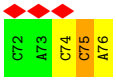


• Molecule 32: E-site tRNA-Ala

Chain v:



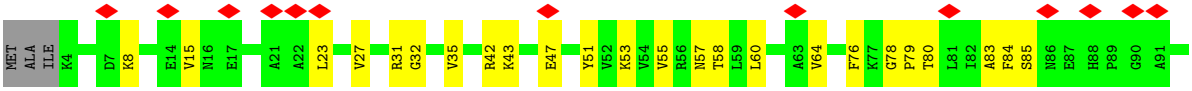


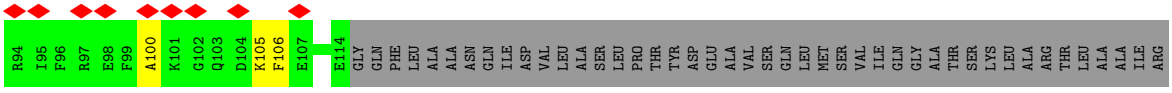


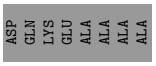
• Molecule 33: Large ribosomal subunit protein uL10

Chain J:





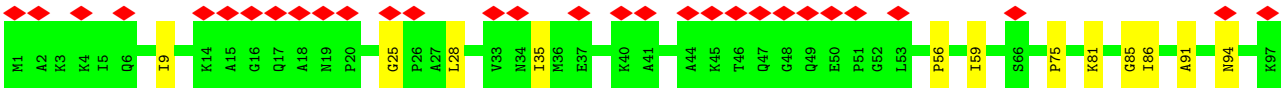


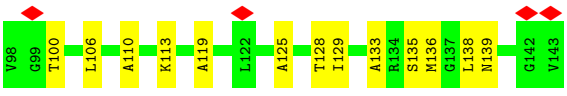


• Molecule 34: Large ribosomal subunit protein uL11

Chain K:







4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	642285	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	54.3	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	36000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	81.289	Depositor
Minimum map value	-47.287	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.057	Depositor
Recommended contour level	3	Depositor
Map size (Å)	468.408, 468.408, 468.408	wwPDB
Map dimensions	696, 696, 696	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.673, 0.673, 0.673	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OMU, 7MG, OMG, 5MC, ZN, 1MG, OMC, PSU, 5MU, 2MG, MG, 2MA, 6MZ

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	0.28	0/67882	0.74	17/105870 (0.0%)
2	B	0.31	0/2833	0.67	1/4413 (0.0%)
3	C	0.14	0/1006	0.32	0/1351
4	D	0.15	0/2108	0.27	0/2831
5	E	0.20	0/1587	0.34	0/2138
6	F	0.17	0/1541	0.28	0/2075
7	G	0.25	0/1456	0.37	0/1953
8	H	0.09	0/1332	0.22	0/1794
9	I	0.11	0/861	0.24	0/1159
10	L	0.24	0/1156	0.38	0/1559
11	M	0.11	0/947	0.27	0/1268
12	N	0.11	0/1078	0.28	0/1436
13	O	0.12	0/1105	0.26	0/1476
14	P	0.19	0/968	0.31	0/1294
15	Q	0.18	0/888	0.29	0/1183
16	R	0.16	0/910	0.34	0/1218
17	S	0.14	0/946	0.30	0/1257
18	T	0.09	0/835	0.23	0/1117
19	U	0.09	0/837	0.23	0/1114
20	V	0.08	0/749	0.22	0/1002
21	W	0.09	0/743	0.24	0/988
22	X	0.09	0/1468	0.21	0/1987
23	Y	0.09	0/589	0.24	0/782
24	Z	0.16	0/641	0.23	0/854
25	1	0.17	0/491	0.31	0/654
26	2	0.08	0/444	0.23	0/597
27	4	0.31	0/437	0.55	0/583
28	5	0.09	0/433	0.24	0/576
29	6	0.16	0/368	0.36	0/482
30	7	0.16	0/511	0.27	0/668
31	8	0.08	0/308	0.22	0/404
32	v	0.22	0/1674	0.63	0/2605

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	J	0.48	0/850	0.63	0/1142
34	K	0.33	0/1061	0.42	0/1435
All	All	0.26	0/101043	0.65	18/151265 (0.0%)

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1911	C	C2-N1-C1'	-7.12	110.97	118.80
1	A	1097	G	N3-C4-N9	-6.80	121.92	126.00
1	A	9	G	O4'-C1'-N9	6.40	113.32	108.20
1	A	503	G	O4'-C1'-N9	6.11	113.09	108.20
1	A	1071	U	N3-C2-O2	-6.06	117.96	122.20

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	A	60895	0	30644	601	0
2	B	2535	0	1283	30	0
3	C	996	0	1065	34	0
4	D	2072	0	2152	38	0
5	E	1564	0	1575	19	0
6	F	1521	0	1581	26	0
7	G	1435	0	1504	30	0
8	H	1314	0	1373	17	0
9	I	858	0	890	4	0
10	L	1130	0	1160	15	0
11	M	938	0	1012	12	0
12	N	1066	0	1112	14	0
13	O	1085	0	1157	25	0
14	P	952	0	996	12	0
15	Q	881	0	920	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	R	901	0	958	10	0
17	S	936	0	1025	16	0
18	T	822	0	858	7	0
19	U	833	0	897	10	0
20	V	739	0	788	18	0
21	W	738	0	806	5	0
22	X	1445	0	1486	18	0
23	Y	581	0	603	6	0
24	Z	630	0	653	8	0
25	1	490	0	520	5	0
26	2	440	0	469	2	0
27	4	431	0	424	7	0
28	5	426	0	457	8	0
29	6	365	0	409	6	0
30	7	506	0	569	10	0
31	8	307	0	342	3	0
32	v	1540	0	783	29	0
33	J	840	0	867	21	0
34	K	1046	0	1089	23	0
35	4	1	0	0	0	0
35	A	196	0	0	0	0
35	B	3	0	0	0	0
35	D	1	0	0	0	0
35	E	1	0	0	0	0
36	8	1	0	0	0	0
37	1	3	0	0	0	0
37	2	16	0	0	0	0
37	4	32	0	0	1	0
37	5	1	0	0	0	0
37	6	23	0	0	1	0
37	7	22	0	0	0	0
37	8	8	0	0	0	0
37	A	4032	0	0	29	0
37	B	76	0	0	2	0
37	D	89	0	0	1	0
37	E	78	0	0	0	0
37	F	47	0	0	3	0
37	G	12	0	0	0	0
37	H	3	0	0	0	0
37	I	1	0	0	0	0
37	L	34	0	0	0	0
37	M	18	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	N	64	0	0	0	0
37	O	37	0	0	2	0
37	P	36	0	0	0	0
37	Q	6	0	0	1	0
37	R	25	0	0	0	0
37	S	44	0	0	1	0
37	T	32	0	0	0	0
37	U	40	0	0	1	0
37	V	26	0	0	0	0
37	W	11	0	0	0	0
37	X	22	0	0	2	0
37	Y	24	0	0	0	0
37	Z	20	0	0	0	0
All	All	98343	0	62427	932	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 6.

The worst 5 of 932 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)
33:J:43:LYS:HG2	33:J:47:GLU:OE1	1.80	0.82
3:C:47:ASN:HD22	3:C:211:ARG:HB3	1.46	0.80
7:G:119:ALA:HB3	7:G:179:ASN:HB2	1.64	0.80
1:A:558:U:H1'	1:A:2017:6MZ:H9C1	1.68	0.76
32:v:40:C:H2'	32:v:41:A:H8	1.52	0.75

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	C	126/231 (54%)	121 (96%)	5 (4%)	0	100	100
4	D	270/273 (99%)	266 (98%)	4 (2%)	0	100	100
5	E	206/211 (98%)	201 (98%)	5 (2%)	0	100	100
6	F	198/200 (99%)	198 (100%)	0	0	100	100
7	G	177/179 (99%)	174 (98%)	3 (2%)	0	100	100
8	H	172/177 (97%)	172 (100%)	0	0	100	100
9	I	107/148 (72%)	103 (96%)	4 (4%)	0	100	100
10	L	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
11	M	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
12	N	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
13	O	135/137 (98%)	134 (99%)	1 (1%)	0	100	100
14	P	117/129 (91%)	115 (98%)	2 (2%)	0	100	100
15	Q	113/116 (97%)	111 (98%)	2 (2%)	0	100	100
16	R	112/116 (97%)	108 (96%)	4 (4%)	0	100	100
17	S	115/118 (98%)	115 (100%)	0	0	100	100
18	T	101/103 (98%)	101 (100%)	0	0	100	100
19	U	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
20	V	92/99 (93%)	91 (99%)	1 (1%)	0	100	100
21	W	89/104 (86%)	87 (98%)	2 (2%)	0	100	100
22	X	188/204 (92%)	185 (98%)	3 (2%)	0	100	100
23	Y	75/85 (88%)	74 (99%)	1 (1%)	0	100	100
24	Z	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
25	1	59/63 (94%)	59 (100%)	0	0	100	100
26	2	54/58 (93%)	53 (98%)	1 (2%)	0	100	100
27	4	52/60 (87%)	51 (98%)	1 (2%)	0	100	100
28	5	49/51 (96%)	49 (100%)	0	0	100	100
29	6	42/44 (96%)	42 (100%)	0	0	100	100
30	7	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
31	8	36/38 (95%)	36 (100%)	0	0	100	100
33	J	109/166 (66%)	105 (96%)	4 (4%)	0	100	100
34	K	141/143 (99%)	135 (96%)	6 (4%)	0	100	100
All	All	3581/3913 (92%)	3521 (98%)	60 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	C	110/180 (61%)	110 (100%)	0	100	100
4	D	212/213 (100%)	212 (100%)	0	100	100
5	E	160/162 (99%)	160 (100%)	0	100	100
6	F	157/158 (99%)	156 (99%)	1 (1%)	78	84
7	G	153/153 (100%)	151 (99%)	2 (1%)	61	72
8	H	137/141 (97%)	137 (100%)	0	100	100
9	I	85/107 (79%)	84 (99%)	1 (1%)	63	74
10	L	119/119 (100%)	119 (100%)	0	100	100
11	M	102/102 (100%)	102 (100%)	0	100	100
12	N	106/106 (100%)	105 (99%)	1 (1%)	70	79
13	O	110/110 (100%)	110 (100%)	0	100	100
14	P	98/104 (94%)	98 (100%)	0	100	100
15	Q	86/87 (99%)	86 (100%)	0	100	100
16	R	96/98 (98%)	95 (99%)	1 (1%)	68	77
17	S	87/88 (99%)	86 (99%)	1 (1%)	65	75
18	T	86/86 (100%)	86 (100%)	0	100	100
19	U	87/87 (100%)	87 (100%)	0	100	100
20	V	79/82 (96%)	79 (100%)	0	100	100
21	W	81/88 (92%)	81 (100%)	0	100	100
22	X	154/164 (94%)	154 (100%)	0	100	100
23	Y	57/61 (93%)	57 (100%)	0	100	100
24	Z	66/67 (98%)	66 (100%)	0	100	100
25	1	54/55 (98%)	53 (98%)	1 (2%)	50	61
26	2	48/49 (98%)	48 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
27	4	47/52 (90%)	46 (98%)	1 (2%)	47 58
28	5	47/47 (100%)	47 (100%)	0	100 100
29	6	37/37 (100%)	37 (100%)	0	100 100
30	7	54/55 (98%)	54 (100%)	0	100 100
31	8	34/34 (100%)	34 (100%)	0	100 100
33	J	82/122 (67%)	81 (99%)	1 (1%)	63 74
34	K	110/110 (100%)	110 (100%)	0	100 100
All	All	2941/3124 (94%)	2931 (100%)	10 (0%)	84 90

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	1	7	ARG
27	4	51	ARG
33	J	60	LEU
9	I	75	LEU
12	N	92	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
16	R	53	ASN
20	V	61	ASN
17	S	44	GLN
18	T	69	HIS
20	V	90	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2827/2892 (97%)	313 (11%)	6 (0%)
2	B	118/121 (97%)	17 (14%)	0
32	v	70/76 (92%)	15 (21%)	0
All	All	3015/3089 (97%)	345 (11%)	6 (0%)

5 of 345 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	G
1	A	34	U
1	A	45	G
1	A	51	G
1	A	63	A

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1046	G
1	A	1307	C
1	A	2743	U
1	A	635	U
1	A	221	A

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

14 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\#\|Z\|>2$
1	2MG	A	1822	1	23,26,27	0.43	0	33,38,41	0.47	0
32	5MU	v	54	32	19,22,23	0.35	0	27,32,35	0.63	0
1	6MZ	A	1608	1	22,25,26	2.39	4 (18%)	29,36,39	2.33	9 (31%)
1	2MA	A	2490	1,35	22,25,26	1.70	5 (22%)	32,37,40	3.65	12 (37%)
1	6MZ	A	2017	1	22,25,26	2.34	5 (22%)	29,36,39	2.50	11 (37%)
1	7MG	A	2056	1	23,26,27	1.13	1 (4%)	27,39,42	0.86	1 (3%)
32	PSU	v	55	32	18,21,22	1.11	1 (5%)	21,30,33	1.93	4 (19%)
1	1MG	A	735	1	23,26,27	3.16	8 (34%)	33,39,42	1.84	9 (27%)
1	OMC	A	2485	1,35	19,22,23	0.48	0	25,31,34	0.64	0
1	2MG	A	2432	1	23,26,27	0.49	0	33,38,41	0.49	0
1	OMG	A	2238	1	23,26,27	0.44	0	32,38,41	0.45	0
1	5MC	A	1949	1	19,22,23	0.54	0	26,32,35	0.63	0
1	5MU	A	1926	1	19,22,23	0.42	0	27,32,35	0.58	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	OMU	A	2539	1	19,22,23	3.10	8 (42%)	25,31,34	1.82	4 (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
1	2MG	A	1822	1	-	2/9/27/28	0/3/3/3
32	5MU	v	54	32	-	0/7/25/26	0/2/2/2
1	6MZ	A	1608	1	-	0/9/27/28	0/3/3/3
1	2MA	A	2490	1,35	-	1/7/25/26	0/3/3/3
1	6MZ	A	2017	1	-	2/9/27/28	0/3/3/3
1	7MG	A	2056	1	-	1/7/37/38	0/3/3/3
32	PSU	v	55	32	-	0/7/25/26	0/2/2/2
1	1MG	A	735	1	-	0/7/25/26	0/3/3/3
1	OMC	A	2485	1,35	-	0/9/27/28	0/2/2/2
1	2MG	A	2432	1	-	2/9/27/28	0/3/3/3
1	OMG	A	2238	1	-	1/9/27/28	0/3/3/3
1	5MC	A	1949	1	-	0/7/25/26	0/2/2/2
1	5MU	A	1926	1	-	0/7/25/26	0/2/2/2
1	OMU	A	2539	1	-	0/9/27/28	0/2/2/2

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1608	6MZ	C6-N6	9.73	1.45	1.34
1	A	735	1MG	C2-N3	9.65	1.48	1.33
1	A	2017	6MZ	C6-N6	9.35	1.44	1.34
1	A	2539	OMU	C2-N1	8.09	1.51	1.38
1	A	735	1MG	C4-N3	6.95	1.50	1.34

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	2490	2MA	N6-C6-N1	-9.23	104.58	117.03
1	A	2490	2MA	CM2-C2-N3	9.13	130.79	117.13
1	A	2490	2MA	C5-C4-N3	-8.59	118.13	127.18
1	A	2017	6MZ	C9-N6-C6	-6.95	116.40	122.85
1	A	2490	2MA	N3-C4-N9	6.36	135.06	126.99

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	2238	OMG	C1'-C2'-O2'-CM2
1	A	1822	2MG	C3'-C4'-C5'-O5'
1	A	2432	2MG	C3'-C4'-C5'-O5'
1	A	1822	2MG	O4'-C4'-C5'-O5'
1	A	2017	6MZ	O4'-C4'-C5'-O5'

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1822	2MG	1	0
1	A	2017	6MZ	2	0
1	A	2432	2MG	1	0
1	A	2238	OMG	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 203 ligands modelled in this entry, 203 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

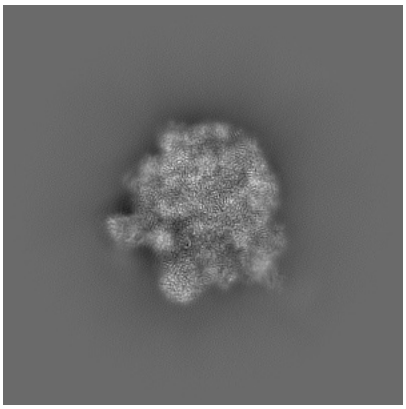
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-73091. These allow visual inspection of the internal detail of the map and identification of artifacts.

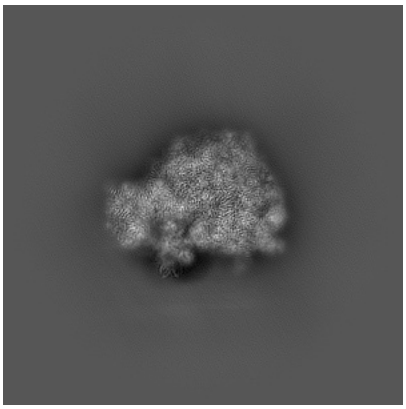
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

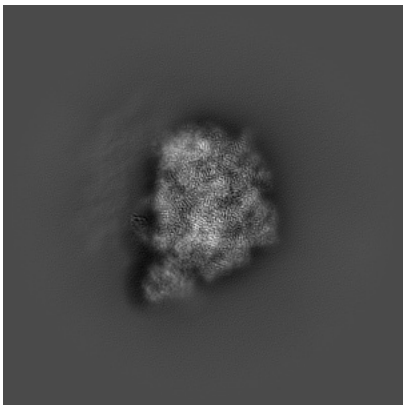
6.1.1 Primary map



X

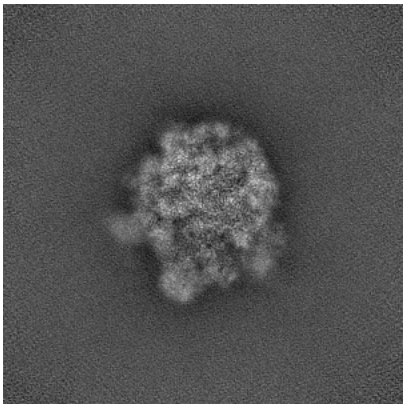


Y

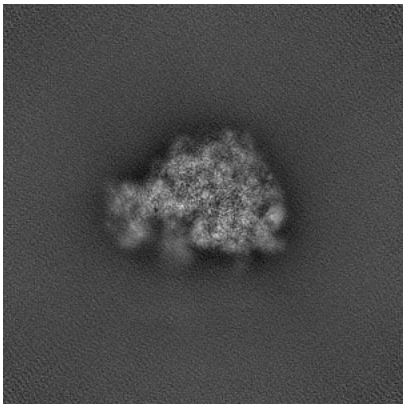


Z

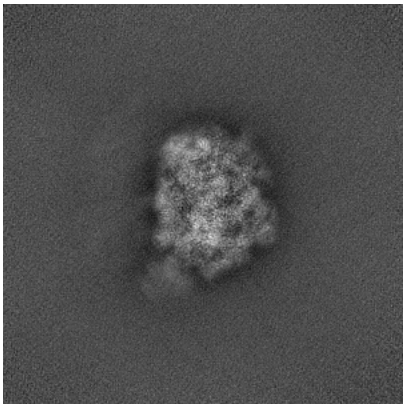
6.1.2 Raw map



X



Y

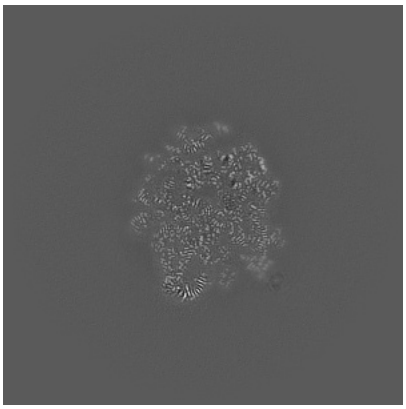


Z

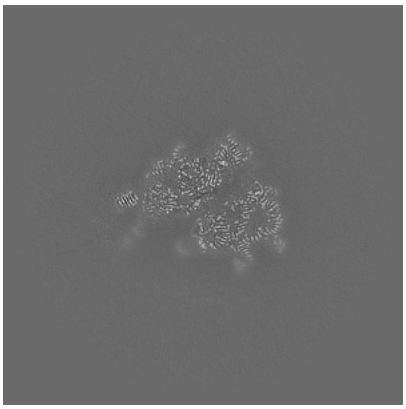
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

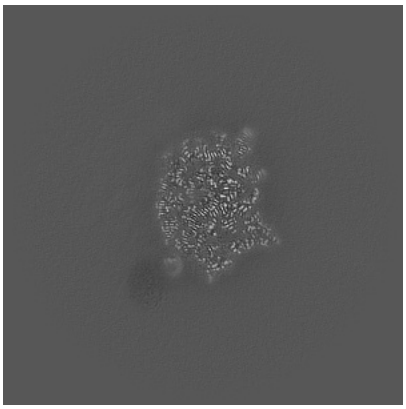
6.2.1 Primary map



X Index: 348

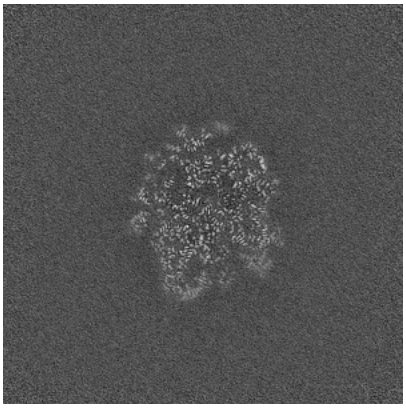


Y Index: 348

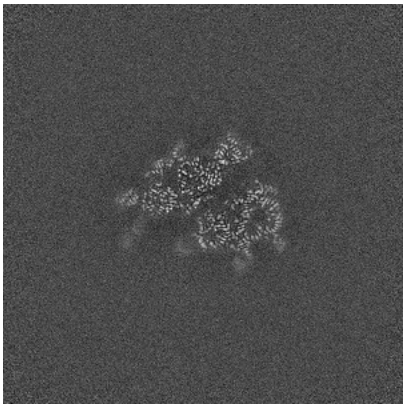


Z Index: 348

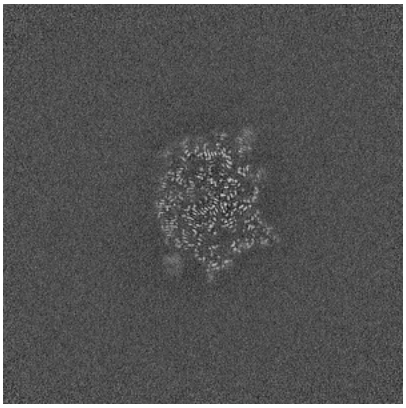
6.2.2 Raw map



X Index: 348



Y Index: 348

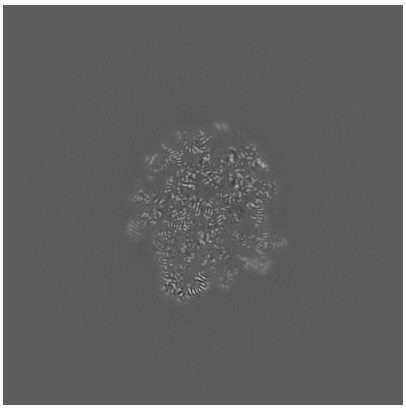


Z Index: 348

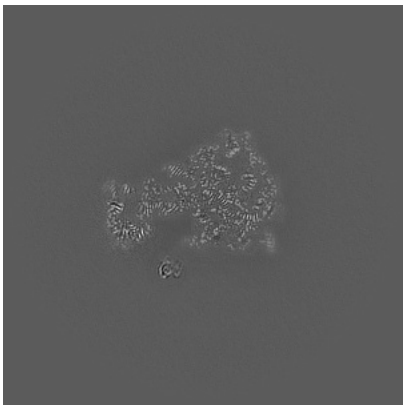
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

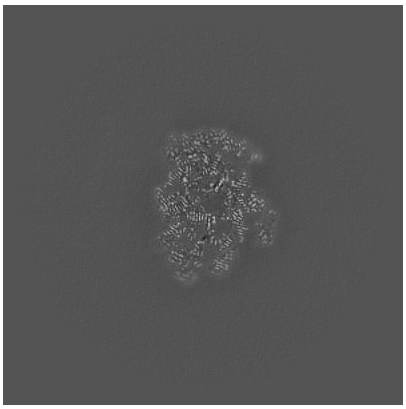
6.3.1 Primary map



X Index: 353

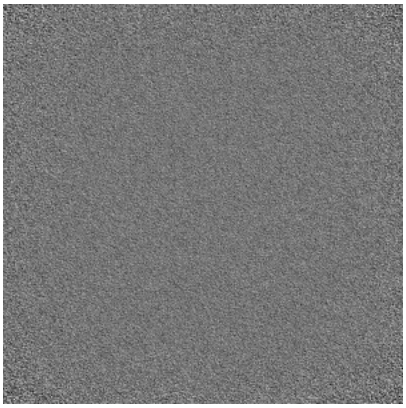


Y Index: 319

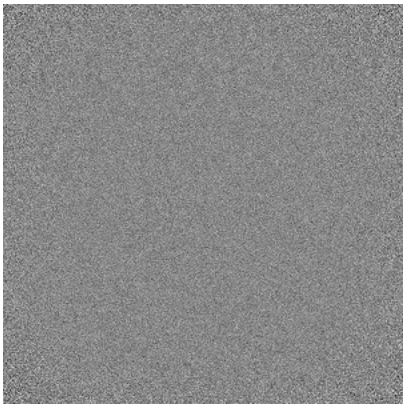


Z Index: 380

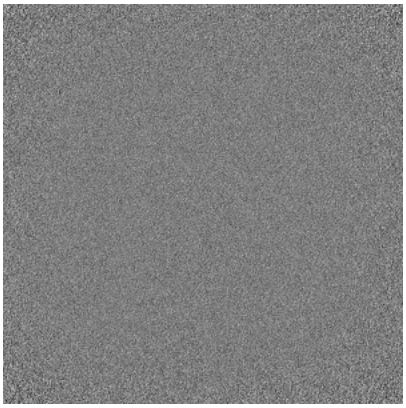
6.3.2 Raw map



X Index: 0



Y Index: 0

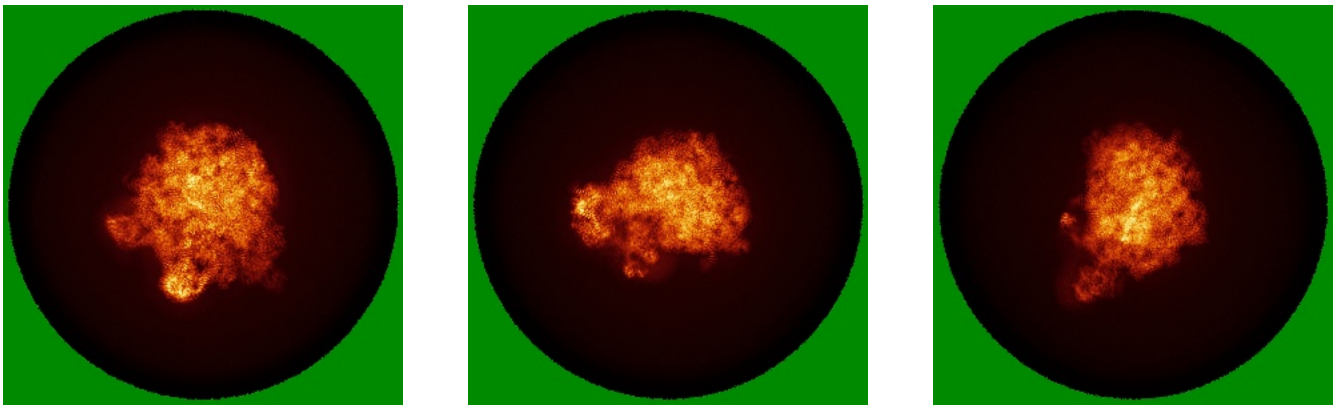


Z Index: 0

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

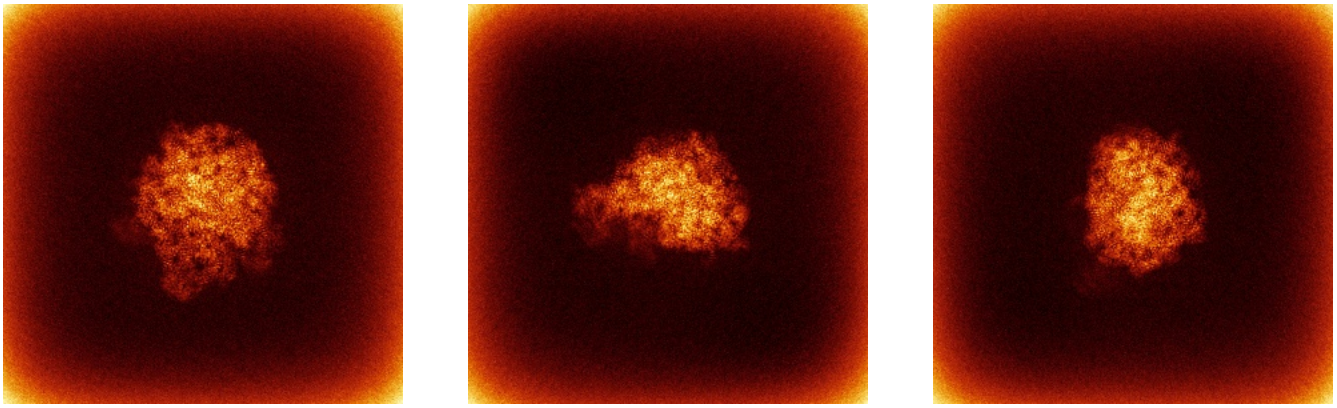
6.4 Orthogonal standard-deviation projections (False-color) (i)

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)

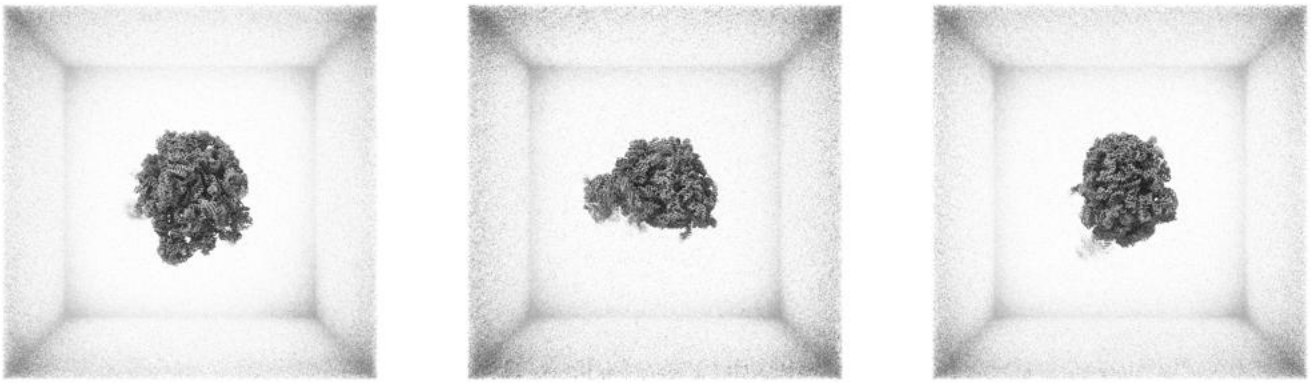
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 3.0. 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.

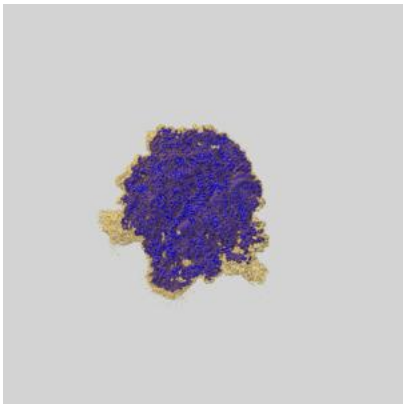
6.6 Mask visualisation (i)

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

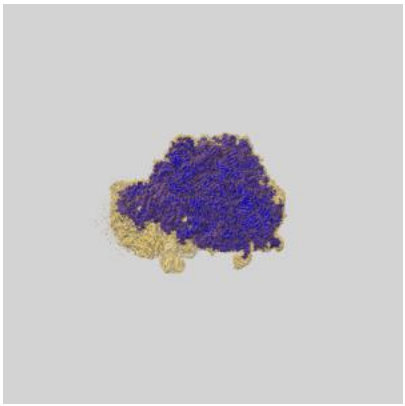
A mask typically either:

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

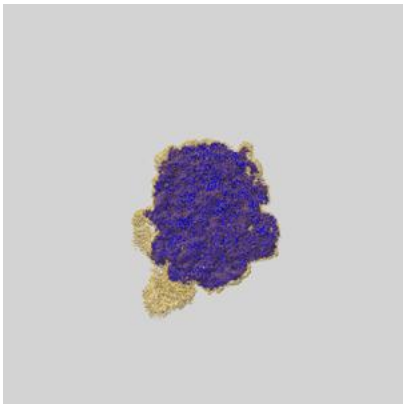
6.6.1 emd_73091_msk_1.map (i)



X



Y

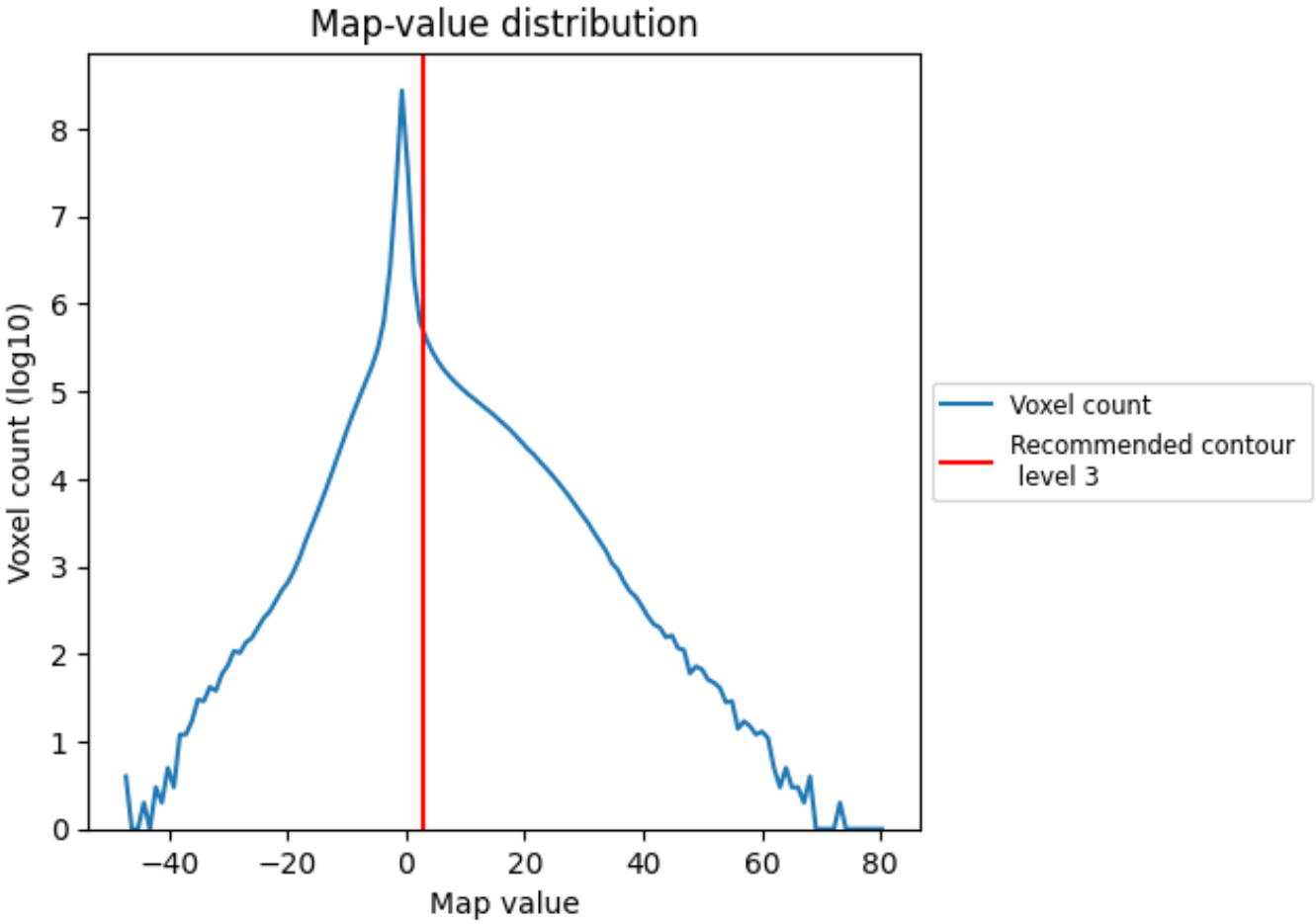


Z

7 Map analysis

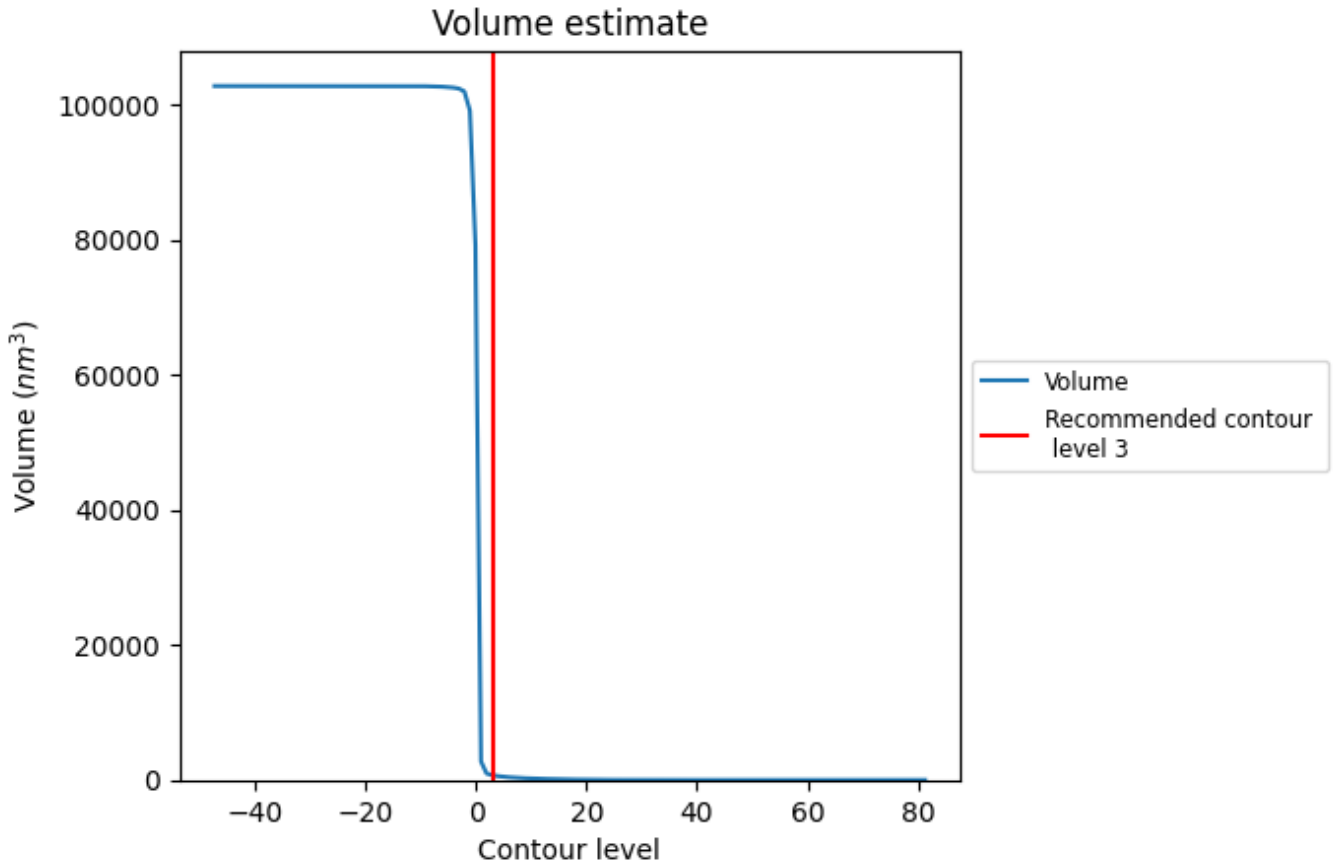
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

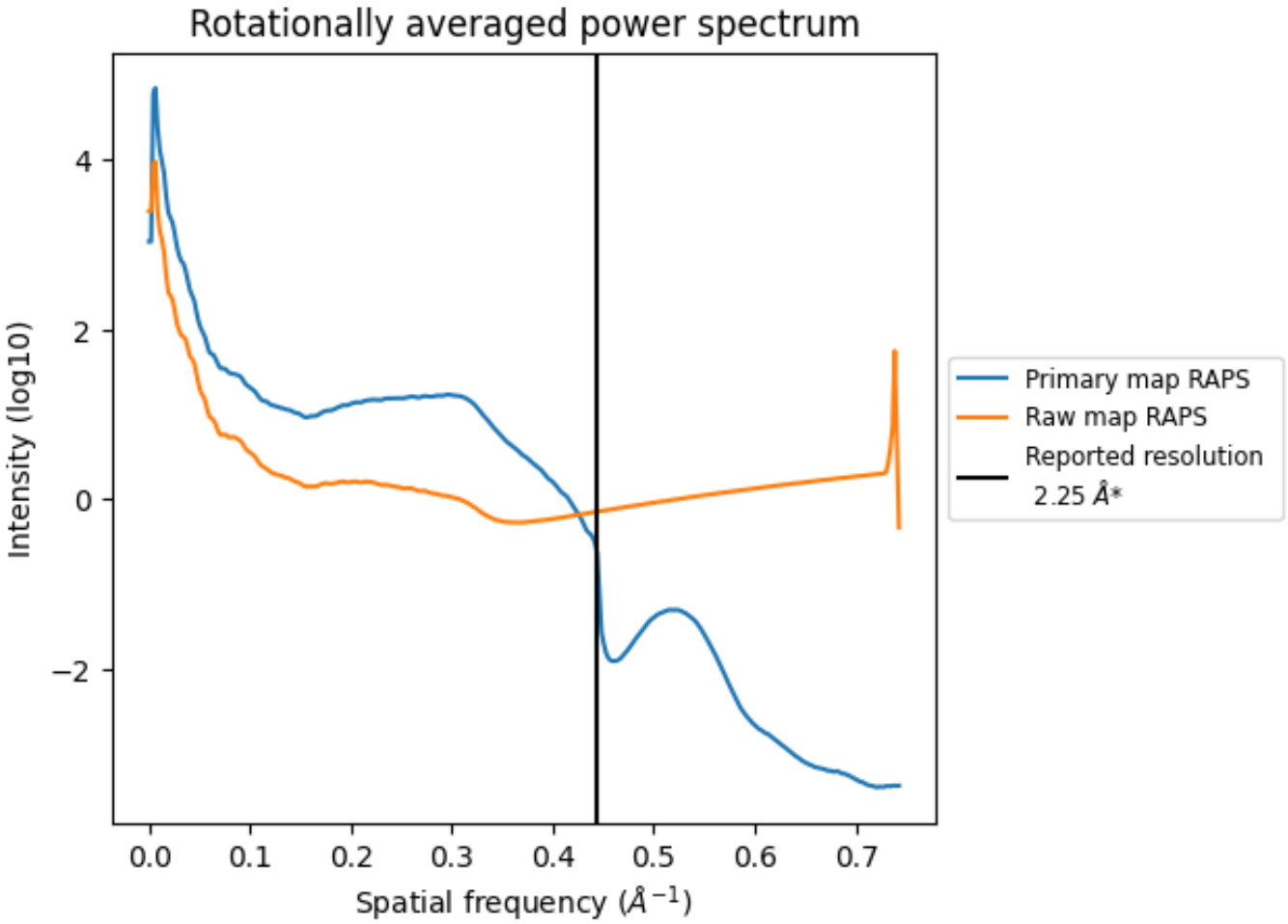
7.2 Volume estimate (i)



The volume at the recommended contour level is 712 nm^3; this corresponds to an approximate mass of 643 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)

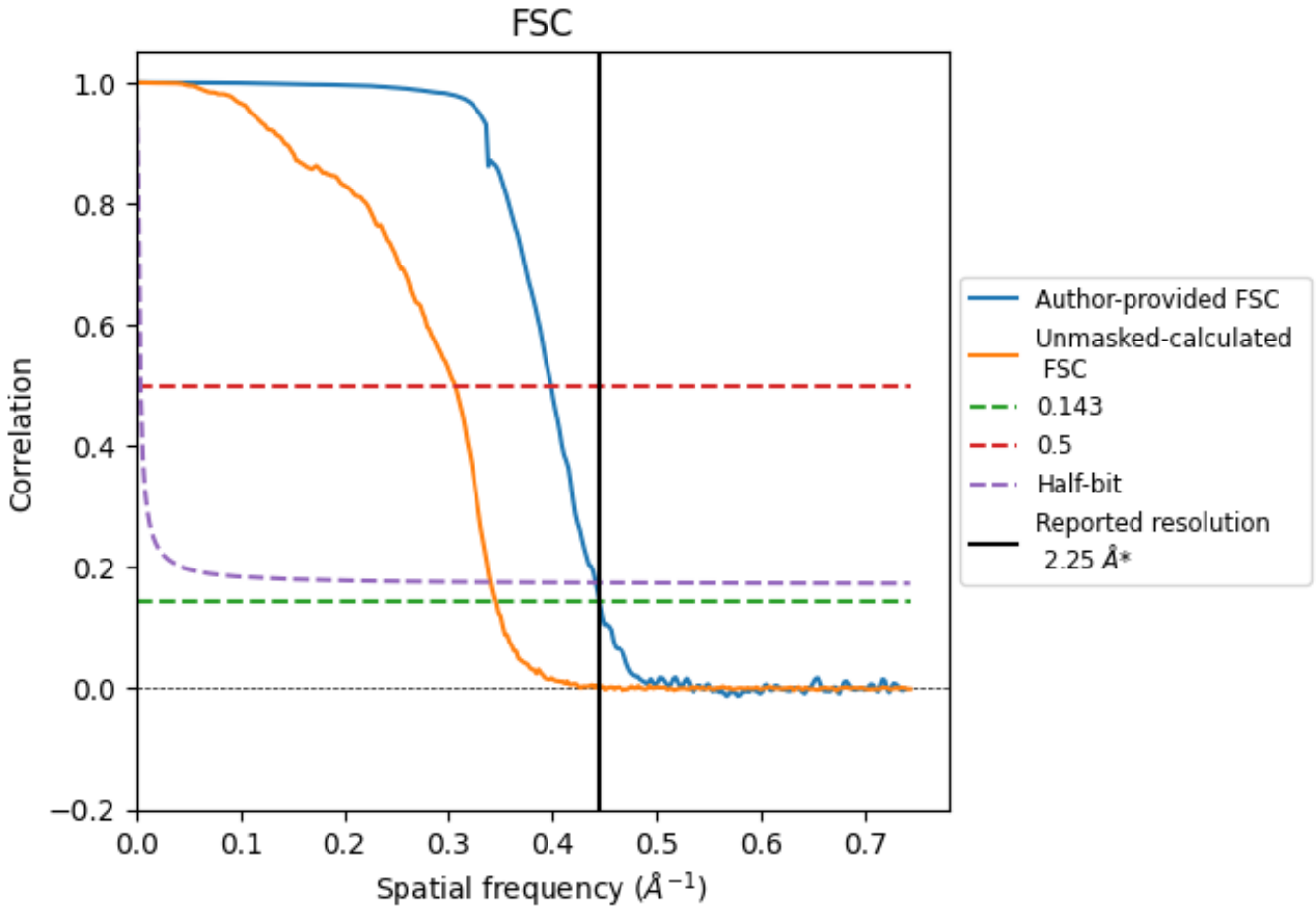


*Reported resolution corresponds to spatial frequency of 0.444 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.444 Å^{-1}

8.2 Resolution estimates (i)

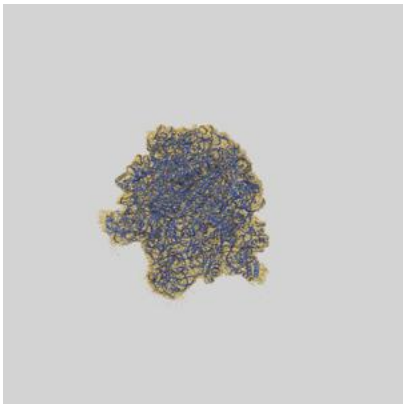
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.25	-	-
Author-provided FSC curve	2.25	2.51	2.27
Unmasked-calculated*	2.89	3.27	2.94

*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 2.89 differs from the reported value 2.25 by more than 10 %

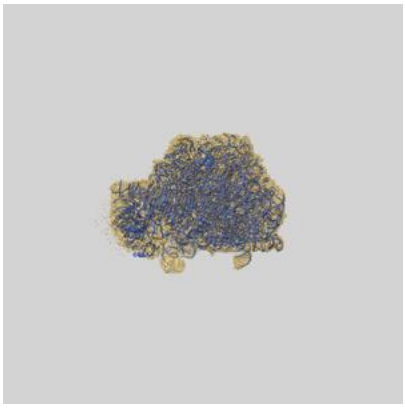
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-73091 and PDB model 9YLQ. Per-residue inclusion information can be found in section 3 on page 12.

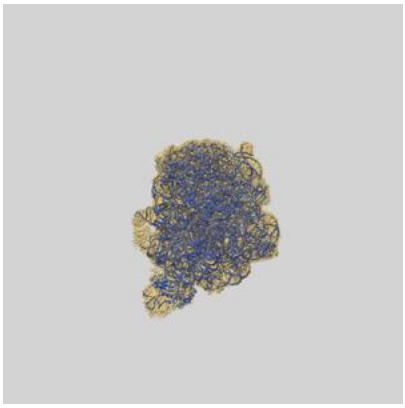
9.1 Map-model overlay



X



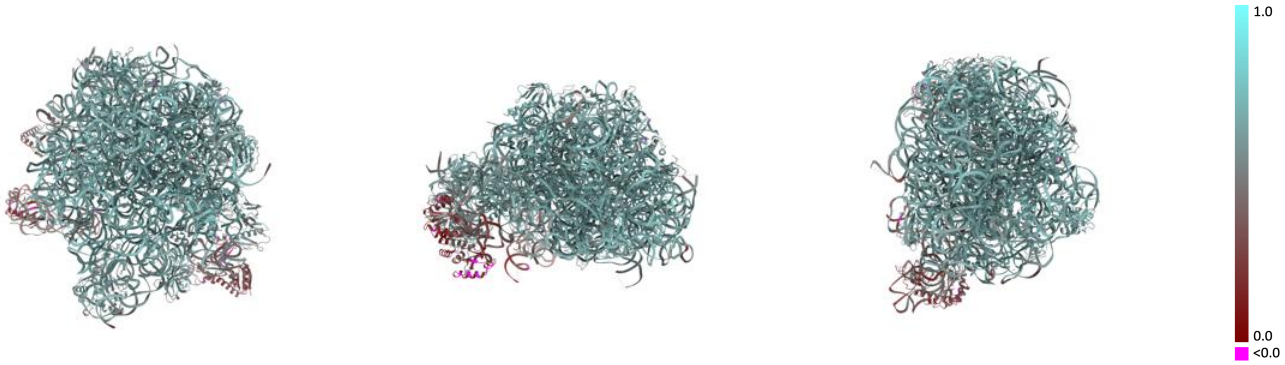
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.0 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.

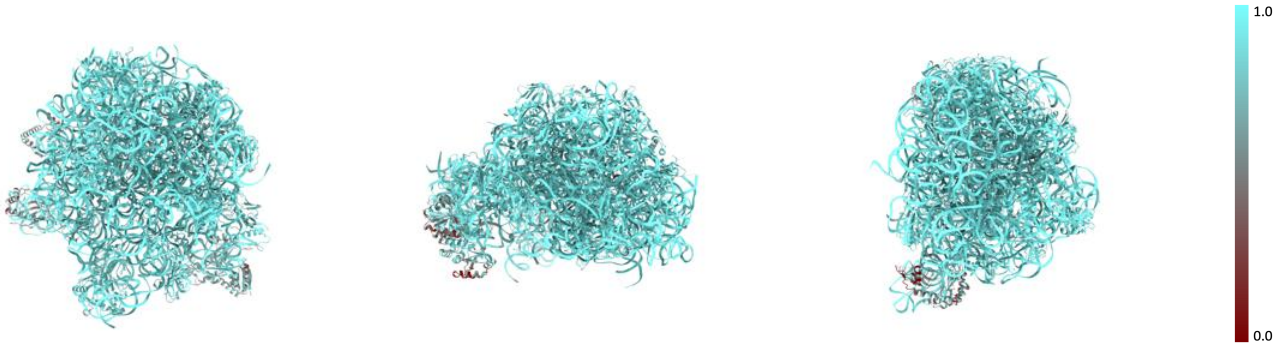
9.2 Q-score mapped to coordinate model



X Y Z

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

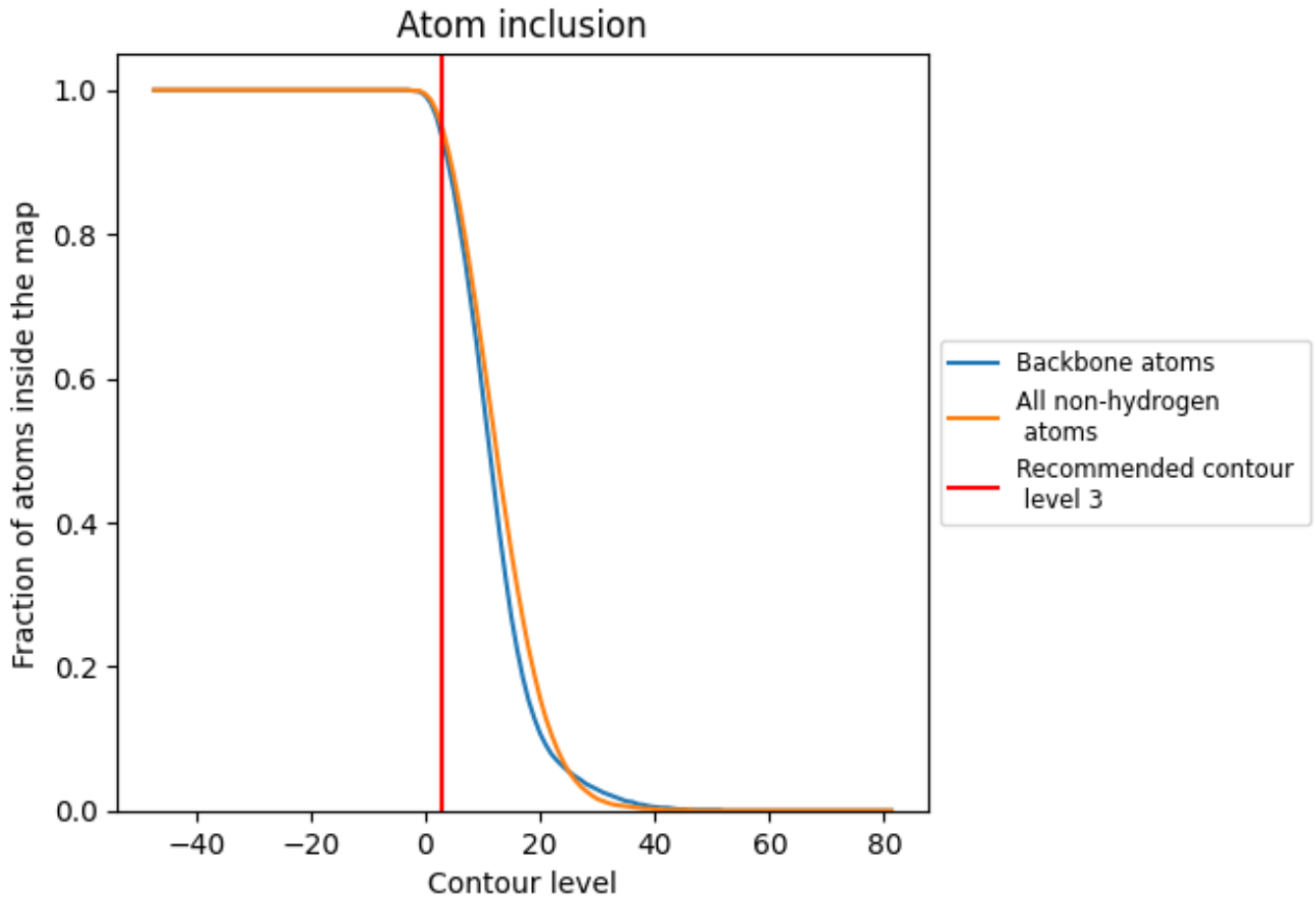
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (3).

9.4 Atom inclusion (i)



At the recommended contour level, 93% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9460	0.6080
1	0.9170	0.6020
2	0.9530	0.6460
4	0.9330	0.6200
5	0.8390	0.5760
6	0.9450	0.6690
7	0.9610	0.6660
8	0.9490	0.6450
A	0.9780	0.6330
B	0.9780	0.6050
C	0.5880	0.2460
D	0.9570	0.6600
E	0.9500	0.6510
F	0.9480	0.6400
G	0.8940	0.5280
H	0.8950	0.5500
I	0.5440	0.3930
J	0.5870	0.2350
K	0.5980	0.1920
L	0.9450	0.6470
M	0.9070	0.6140
N	0.9470	0.6500
O	0.9250	0.6430
P	0.9670	0.6580
Q	0.9400	0.6040
R	0.8900	0.6040
S	0.9660	0.6630
T	0.9320	0.6240
U	0.9150	0.6390
V	0.9090	0.6040
W	0.9090	0.5780
X	0.8860	0.5720
Y	0.9290	0.6490
Z	0.9340	0.6430
v	0.8240	0.2600

