wwPDB EM Validation Summary Report (i)

Sep 16, 2026 – 08:27 PM EDT

PDB ID	:	9D89 / pdb_00009d89
EMDB ID	:	EMD-46632
Title	:	E. coli 50S ribosomal subunit in complex with PrAMP rumicidin-2 (focused refinement)
Authors	:	Pichkur, E.B.; Panteleev, P.V.; Konevega, A.L.
Deposited on	:	2024-08-19
Resolution	:	1.95 Å(reported)
Based on initial model	:	8B0X

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

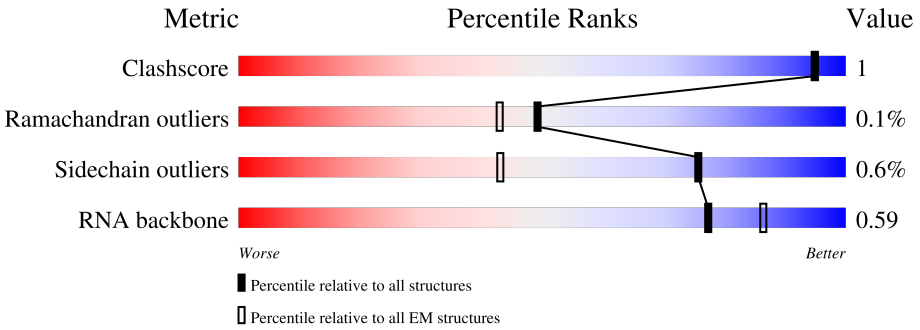
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

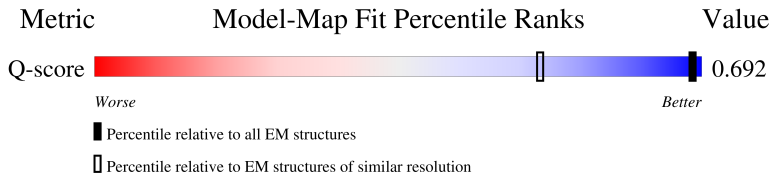
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.95 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	1316 (1.45 - 2.45)

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	0	55	93% 7%
2	1	46	98%
3	B	65	91% 8%

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Mol	Chain	Length	Quality of chain
4	C	38	92% 5%
5	D	2728	80% 18%
6	E	119	88% 10%
7	F	273	94% 5%
8	G	209	94% 6%
9	H	201	98%
10	I	144	97%
11	J	118	99%
12	K	93	98%
13	L	78	96%
14	M	56	93% 7%
15	f	177	17% 99%
16	g	176	6% 98%
17	h	38	11% 100%
18	i	142	94% 6%
19	j	123	96%
20	l	136	93% 6%
21	n	116	99%
22	o	114	99%
23	p	117	96%
24	q	103	99%
25	r	110	92% 6%
26	t	102	6% 94%
27	u	94	96%
28	w	77	94% 6%

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Mol	Chain	Length	Quality of chain
29	x	62	100%
30	y	58	95% 5%
31	T	16	94% 6%

2 Entry composition (i)

There are 35 unique types of molecules in this entry. The entry contains 90166 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	0	51	417	269	76	72	0	0

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	46	377	228	90	57	2	0	0

- Molecule 3 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	64	504	323	105	74	2	0	0

- Molecule 4 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	C	38	302	185	65	48	4	0	0

- Molecule 5 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	D	2728	58601	26147	10802	18924	2728	0	0

- Molecule 6 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	E	119	2549	1135	466	829	119	0	0

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	F	271	2082	1288	423	364	7	0	0

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	G	209	1566	980	288	294	4	0	0

- Molecule 9 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	H	201	1552	974	283	290	5	0	0

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	I	144	1053	654	207	190	2	0	0

- Molecule 11 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	J	118	945	585	194	161	5	0	0

- Molecule 12 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	K	93	738	466	139	131	2	0	0

- Molecule 13 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L	78	586	362	116	107	1	0	0

- Molecule 14 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	M	56	444	269	94	80	1	0	0

- Molecule 15 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	f	177	1410	899	249	256	6	0	0

- Molecule 16 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	g	176	1323	832	243	246	2	0	0

- Molecule 17 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	h	38	282	181	50	50	1	0	0

- Molecule 18 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	i	142	1129	714	212	199	4	0	0

- Molecule 19 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	j	123	946	593	181	166	6	0	0

- Molecule 20 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	l	136	1075	686	205	177	7	0	0

- Molecule 21 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
21	n	116	892	552	178	162	0	0

- Molecule 22 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	o	114	917	574	179	163	1	0	0

- Molecule 23 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
23	p	117	947	604	192	151	0	0

- Molecule 24 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	q	103	816	516	153	145	2	0	0

- Molecule 25 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	r	110	857	532	166	156	3	0	0

- Molecule 26 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
26	t	102	779	492	146	141	0	0

- Molecule 27 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	u	94	753	479	137	134	3	0	0

- Molecule 28 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	w	77	625	388	129	106	2	0	0

- Molecule 29 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	x	62	501	308	98	94	1	0	0

- Molecule 30 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	y	58	449	281	87	79	2	0	0

- Molecule 31 is a protein called Rumicidin-2 (12-27).

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
31	T	16	143	96	31	16	0	0

- Molecule 32 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
32	C	1	1	1	0

- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
33	D	198	198	198	0
33	E	3	3	3	0
33	F	1	1	1	0
33	G	1	1	1	0
33	M	1	1	1	0

- Molecule 34 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	AltConf
34	D	88	Total K 88 88	0
34	F	4	Total K 4 4	0
34	H	1	Total K 1 1	0

- Molecule 35 is water.

Mol	Chain	Residues	Atoms	AltConf
35	1	15	Total O 15 15	0
35	B	19	Total O 19 19	0
35	C	3	Total O 3 3	0
35	D	3780	Total O 3780 3780	0
35	E	48	Total O 48 48	0
35	F	79	Total O 79 79	0
35	G	38	Total O 38 38	0
35	H	36	Total O 36 36	0
35	I	38	Total O 38 38	0
35	J	22	Total O 22 22	0
35	K	12	Total O 12 12	0
35	L	14	Total O 14 14	0
35	M	25	Total O 25 25	0
35	h	1	Total O 1 1	0
35	i	22	Total O 22 22	0
35	j	12	Total O 12 12	0
35	l	26	Total O 26 26	0

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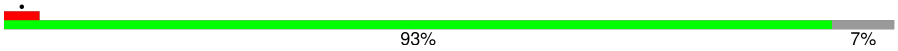
Mol	Chain	Residues	Atoms		AltConf
			Total	O	
35	o	13	13	13	0
			Total	O	
35	p	32	32	32	0
			Total	O	
35	q	19	19	19	0
			Total	O	
35	r	30	30	30	0
			Total	O	
35	t	6	6	6	0
			Total	O	
35	u	3	3	3	0
			Total	O	
35	w	9	9	9	0
			Total	O	
35	x	1	1	1	0
			Total	O	
35	y	5	5	5	0

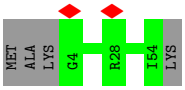
3 Residue-property plots (i)

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: 50S ribosomal protein L33

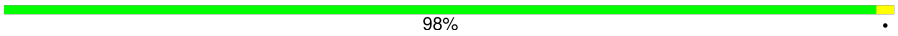
Chain 0:





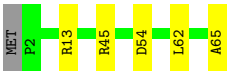
- Molecule 2: 50S ribosomal protein L34

Chain 1:



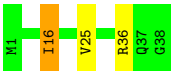
- Molecule 3: 50S ribosomal protein L35

Chain B:



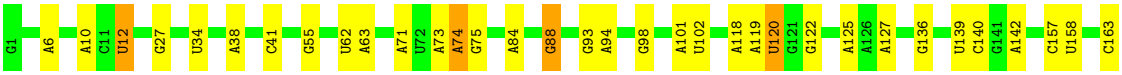
- Molecule 4: 50S ribosomal protein L36

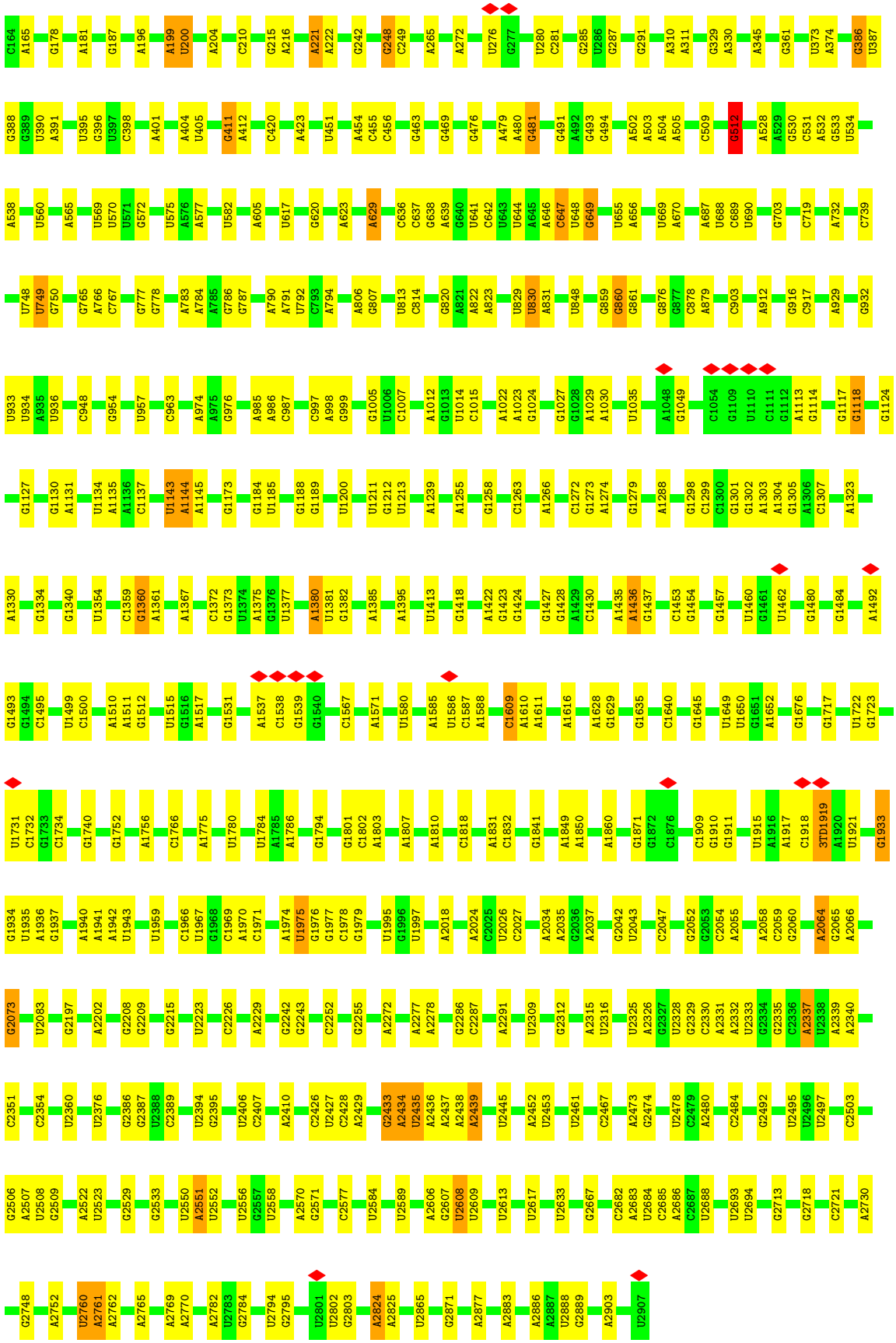
Chain C:



- Molecule 5: 23S rRNA

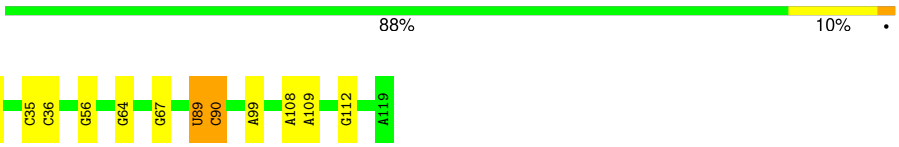
Chain D:




C164 A165 G178 A181 G187 A196 A199 U200 A204 C210 G215 A216 A221 A222 G242 G248 C249 A265 A272 U276 G277 U280 C281 G285 U286 G287 G291 A310 A311 G329 A330 A345 G361 U373 A374 G386 U387
G388 G389 U390 A391 U395 G396 U397 C398 A401 A404 U405 G411 A412 C420 A423 U451 A454 C455 C456 G463 G469 G476 A479 A480 G481 G491 A492 G493 G494 A502 A503 A504 A505 C509 G512 A528 A529 G530 C531 A532 G533 U534
A538 U560 A565 U569 U570 U571 G572 U575 A576 A577 U582 A605 U617 G620 A623 A629 C636 C637 G638 A639 G640 U641 C642 U643 U644 A645 A646 C647 U648 G649 U655 A656 U669 A670 A687 U688 C689 U690 G703 C719 A732 C739
U748 U749 G750 G765 A766 C767 G777 G778 A783 A784 A785 G786 G787 A790 A791 U792 C793 A794 A806 G807 U813 C814 G820 A821 A822 A823 U829 U830 A831 U848 G859 G860 G861 G876 G877 C878 A879 C903 A912 G916 C917 A929 G932
U933 U934 A935 U936 C948 G954 U957 C963 A974 A975 G976 A985 A986 C987 C997 A998 G999 G1005 U1006 C1007 A1012 G1013 U1014 C1015 A1022 A1023 G1024 G1027 G1028 A1029 A1030 U1035 A1048 G1049 C1054 G1109 U1110 C1111 G1112 A1113 G1114 G1117 G1118 G1124
G1127 G1130 A1131 U1134 A1135 A1136 C1137 U1143 A1144 A1145 G1173 G1184 U1185 G1188 G1189 U1200 U1211 G1212 U1213 A1239 A1255 G1258 C1263 A1266 C1272 G1273 A1274 G1279 A1288 G1298 C1299 C1300 G1301 G1302 A1303 A1304 G1305 A1306 C1307 A1323
A1330 G1334 G1340 U1354 C1359 G1360 A1361 A1367 C1372 G1373 U1374 A1375 G1376 U1377 A1380 U1381 G1382 A1385 A1395 U1413 G1418 A1422 G1423 G1424 G1427 G1428 A1429 C1430 A1435 A1436 G1437 C1453 G1454 G1457 U1460 G1461 U1462 G1480 G1484 A1492
G1493 G1494 C1495 U1499 C1500 A1510 A1511 G1512 U1515 G1516 A1517 G1531 A1537 C1538 G1539 G1540 C1567 A1571 U1580 A1585 U1586 C1587 A1588 C1609 A1610 A1611 A1616 A1628 G1629 G1635 C1640 G1645 U1649 U1650 G1651 A1652 G1676 G1717 U1722 G1723
U1731 C1732 G1733 C1734 G1740 G1752 A1756 C1766 A1775 U1780 U1784 A1785 A1786 G1794 G1801 C1802 A1803 A1807 A1810 C1818 A1831 C1832 G1841 A1849 A1850 A1860 G1871 G1872 C1876 C1909 G1910 G1911 U1915 A1916 A1917 C1918 3TD1919 A1920 U1921 G1933
G1934 U1935 A1936 G1937 A1940 A1941 A1942 U1943 U1959 C1966 U1967 G1968 C1969 A1970 C1971 A1974 U1975 G1976 G1977 C1978 G1979 U1995 G1996 U1997 A2018 A2024 C2025 U2026 C2027 A2034 A2035 G2036 A2037 G2042 U2043 C2047 G2052 G2053 C2054 A2055 A2058 C2059 G2060 A2064 G2065 A2066
G2073 U2083 G2197 A2202 G2208 G2209 G2215 U2223 C2226 A2229 G2242 G2243 C2252 G2255 A2272 A2277 A2278 G2286 C2287 A2291 U2309 G2312 A2315 U2316 U2325 A2326 G2327 U2328 G2329 C2330 A2331 A2332 U2333 G2334 G2335 C2336 A2337 U2338 A2339 A2340
C2351 C2354 U2360 U2376 G2386 G2387 U2388 C2389 U2394 G2395 U2406 C2407 A2410 C2426 U2427 C2428 A2429 G2433 A2434 U2435 A2436 A2437 A2438 A2439 U2445 A2452 U2453 U2461 C2467 A2473 G2474 U2478 C2479 A2480 C2484 G2492 U2495 U2496 U2497 C2503
G2506 A2507 U2508 G2509 A2522 U2523 G2529 G2533 U2550 A2551 U2552 U2556 G2557 U2558 A2570 G2571 C2577 U2584 U2589 A2606 G2607 U2608 U2609 U2613 U2617 U2633 G2667 C2682 A2683 U2684 C2685 A2686 C2687 U2688 U2693 U2694 G2713 G2718 C2721 A2730
G2748 A2752 U2760 A2761 A2762 A2765 A2769 A2770 A2782 U2783 G2784 U2794 G2795 U2801 U2802 G2803 A2824 A2825 U2865 G2871 A2877 A2883 A2886 A2887 U2888 G2889 A2903 U2907

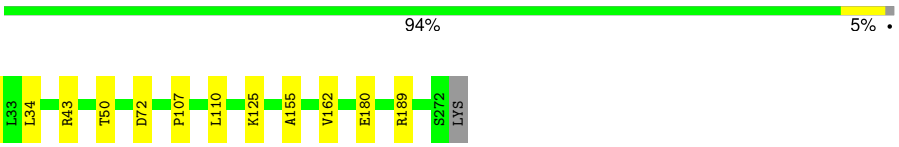
- Molecule 6: 5S rRNA

Chain E:



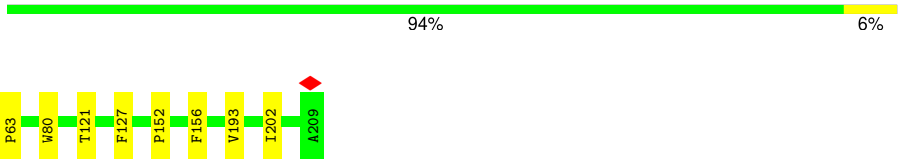
- Molecule 7: 50S ribosomal protein L2

Chain F:



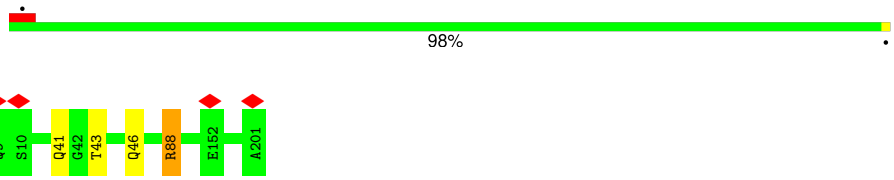
- Molecule 8: 50S ribosomal protein L3

Chain G:



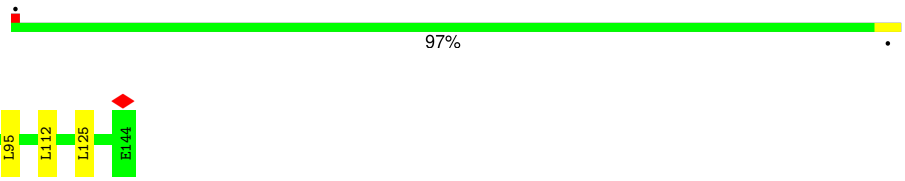
- Molecule 9: 50S ribosomal protein L4

Chain H:



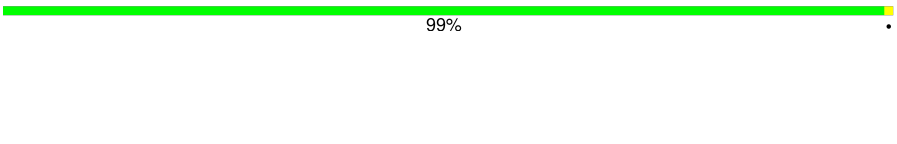
- Molecule 10: 50S ribosomal protein L15

Chain I:



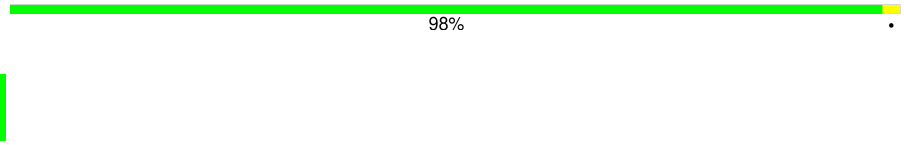
- Molecule 11: 50S ribosomal protein L17

Chain J:



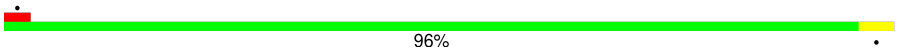
- Molecule 12: Large ribosomal subunit protein uL23

Chain K:



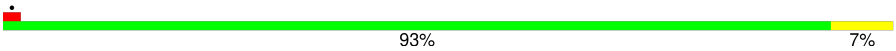
- Molecule 13: 50S ribosomal protein L27

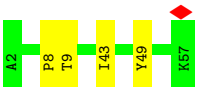
Chain L:



- Molecule 14: 50S ribosomal protein L32

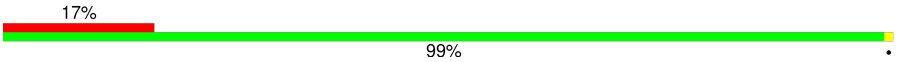
Chain M:

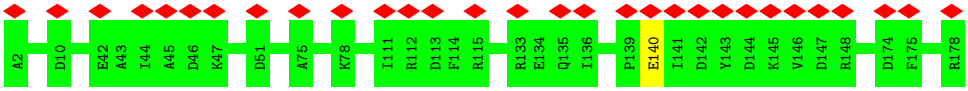




- Molecule 15: 50S ribosomal protein L5

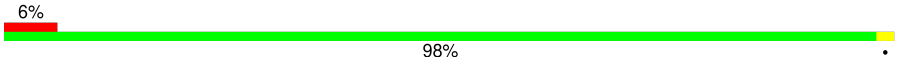
Chain f:

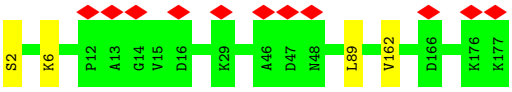




- Molecule 16: Large ribosomal subunit protein uL6

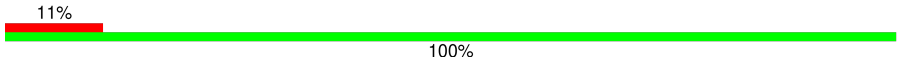
Chain g:

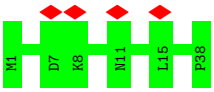




- Molecule 17: 50S ribosomal protein L9

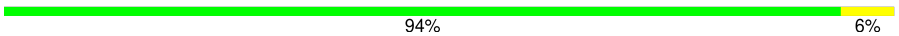
Chain h:





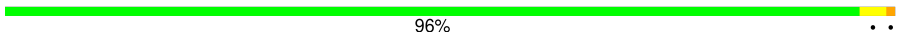
- Molecule 18: Large ribosomal subunit protein uL13

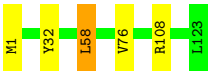
Chain i:



- Molecule 19: 50S ribosomal protein L14

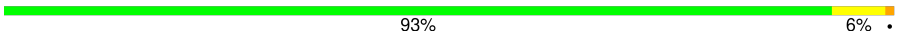
Chain j:

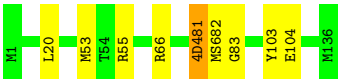




• Molecule 20: Large ribosomal subunit protein uL16

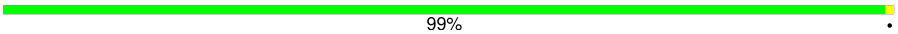
Chain l:





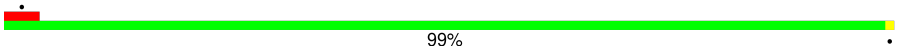
• Molecule 21: 50S ribosomal protein L18

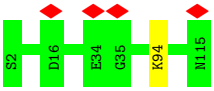
Chain n:



• Molecule 22: 50S ribosomal protein L19

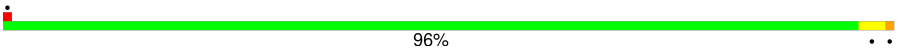
Chain o:

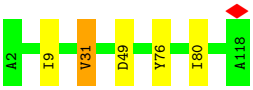




• Molecule 23: Large ribosomal subunit protein bL20

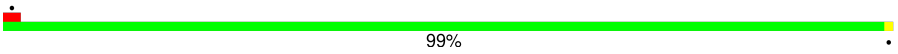
Chain p:

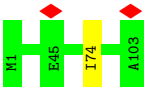




• Molecule 24: 50S ribosomal protein L21

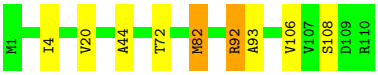
Chain q:



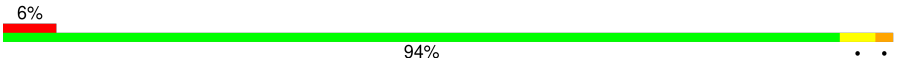


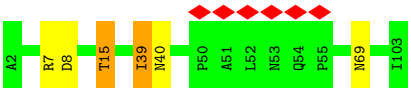
• Molecule 25: 50S ribosomal protein L22

Chain r:

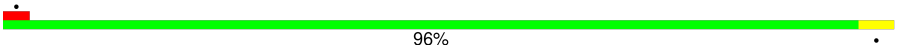


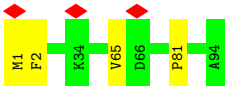
• Molecule 26: Large ribosomal subunit protein uL24

Chain t: 

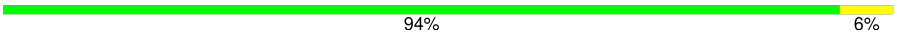


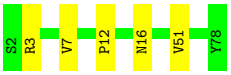
• Molecule 27: Large ribosomal subunit protein bL25

Chain u: 



• Molecule 28: 50S ribosomal protein L28

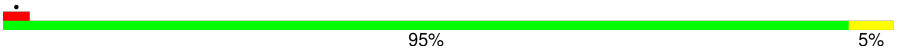
Chain w: 



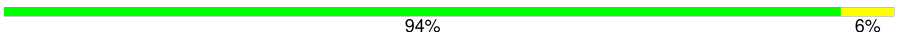
• Molecule 29: Large ribosomal subunit protein uL29

Chain x:

• Molecule 30: 50S ribosomal protein L30

Chain y: 

• Molecule 31: Rumicidin-2 (12-27)

Chain T: 

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	371000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	80	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	20000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	6.240	Depositor
Minimum map value	-0.674	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	0.274	Depositor
Recommended contour level	1.1	Depositor
Map size (Å)	441.856, 441.856, 441.856	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.863, 0.863, 0.863	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 1MG, MG, 2MG, 6MZ, 3TD, 4D4, 2MA, PSU, OMG, OMC, G7M, ZN, H2U, OMU, MEQ, 5MU, 5MC, MS6, K

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	0	0.45	0/424	0.78	0/565
2	1	0.52	0/380	0.84	0/498
3	B	0.51	0/513	0.89	1/676 (0.1%)
4	C	0.49	0/303	0.84	0/397
5	D	0.49	1/65057 (0.0%)	0.90	71/101481 (0.1%)
6	E	0.53	0/2850	0.81	1/4444 (0.0%)
7	F	0.50	0/2121	0.82	0/2852
8	G	0.47	0/1576	0.80	0/2119
9	H	0.46	0/1571	0.82	0/2113
10	I	0.48	0/1062	0.79	0/1413
11	J	0.49	0/958	0.87	0/1281
12	K	0.45	0/744	0.78	0/994
13	L	0.48	0/593	0.81	0/785
14	M	0.49	0/450	0.83	0/599
15	f	0.45	0/1434	0.82	0/1926
16	g	0.47	0/1343	0.82	0/1816
17	h	0.47	0/285	0.76	0/385
18	i	0.48	0/1152	0.81	0/1551
19	j	0.46	0/955	0.82	0/1279
20	l	0.47	0/1073	0.79	0/1433
21	n	0.45	0/902	0.83	0/1209
22	o	0.46	0/929	0.73	0/1242
23	p	0.49	0/960	0.85	1/1278 (0.1%)
24	q	0.45	0/829	0.76	0/1107
25	r	0.49	0/864	0.82	0/1156
26	t	0.46	0/787	0.75	0/1051
27	u	0.45	0/766	0.78	0/1025
28	w	0.46	0/635	0.79	0/848
29	x	0.41	0/502	0.84	0/667
30	y	0.47	0/453	0.81	0/605
31	T	0.65	0/154	0.92	0/213

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
All	All	0.48	1/92625 (0.0%)	0.87	74/139008 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	B	0	1
5	D	0	1
7	F	0	1
20	l	0	1
28	w	0	1
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	2073	G7M	O3'-P	5.01	1.61	1.56

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	D	2054	C	O3'-P-O5'	-10.26	88.60	104.00
5	D	204	A	O3'-P-O5'	-9.38	89.93	104.00
5	D	1975	U	O3'-P-O5'	-9.00	90.50	104.00
5	D	2226	C	O3'-P-O5'	-8.38	91.43	104.00
5	D	1640	C	O3'-P-O5'	-8.25	91.63	104.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	13	ARG	Sidechain
5	D	512	G	Sidechain
7	F	43	ARG	Sidechain
20	l	81	4D4	Mainchain
28	w	16	ASN	Peptide

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	0	417	0	451	0	0
2	1	377	0	418	1	0
3	B	504	0	572	2	0
4	C	302	0	340	1	0
5	D	58601	0	29472	110	0
6	E	2549	0	1291	1	0
7	F	2082	0	2153	7	0
8	G	1566	0	1618	5	0
9	H	1552	0	1619	2	0
10	I	1053	0	1129	3	0
11	J	945	0	989	1	0
12	K	738	0	807	1	0
13	L	586	0	596	2	0
14	M	444	0	458	3	0
15	f	1410	0	1444	0	0
16	g	1323	0	1371	2	0
17	h	282	0	302	0	0
18	i	1129	0	1162	5	0
19	j	946	0	1023	4	0
20	l	1075	0	1144	8	0
21	n	892	0	923	0	0
22	o	917	0	962	1	0
23	p	947	0	1019	4	0
24	q	816	0	839	1	0
25	r	857	0	922	6	0
26	t	779	0	830	3	0
27	u	753	0	780	2	0
28	w	625	0	652	2	0
29	x	501	0	531	0	0
30	y	449	0	488	2	0
31	T	143	0	145	0	0
32	C	1	0	0	0	0
33	D	198	0	0	0	0
33	E	3	0	0	0	0
33	F	1	0	0	0	0
33	G	1	0	0	0	0
33	M	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	D	88	0	0	0	0
34	F	4	0	0	0	0
34	H	1	0	0	0	0
35	1	15	0	0	0	0
35	B	19	0	0	0	0
35	C	3	0	0	0	0
35	D	3780	0	0	4	0
35	E	48	0	0	0	0
35	F	79	0	0	0	0
35	G	38	0	0	0	0
35	H	36	0	0	0	0
35	I	38	0	0	0	0
35	J	22	0	0	0	0
35	K	12	0	0	0	0
35	L	14	0	0	0	0
35	M	25	0	0	0	0
35	h	1	0	0	0	0
35	i	22	0	0	0	0
35	j	12	0	0	0	0
35	l	26	0	0	0	0
35	o	13	0	0	0	0
35	p	32	0	0	0	0
35	q	19	0	0	0	0
35	r	30	0	0	0	0
35	t	6	0	0	0	0
35	u	3	0	0	0	0
35	w	9	0	0	0	0
35	x	1	0	0	0	0
35	y	5	0	0	0	0
All	All	90166	0	56450	157	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 1.

The worst 5 of 157 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)
5:D:1305:G:N7	5:D:1609:C:N4	1.98	1.11
5:D:199:A:N7	5:D:2435:U:O2	2.11	0.83
5:D:12:U:H2'	5:D:12:U:O2	1.80	0.81
5:D:74:A:O2'	5:D:88:G:OP2	2.00	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:l:82:MS6:C	20:l:83:GLY:HA3	2.15	0.76

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	
1	0	49/55 (89%)	49 (100%)	0	0	100	100
2	1	44/46 (96%)	44 (100%)	0	0	100	100
3	B	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
4	C	36/38 (95%)	36 (100%)	0	0	100	100
7	F	269/273 (98%)	260 (97%)	9 (3%)	0	100	100
8	G	206/209 (99%)	200 (97%)	6 (3%)	0	100	100
9	H	199/201 (99%)	194 (98%)	5 (2%)	0	100	100
10	I	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
11	J	116/118 (98%)	110 (95%)	6 (5%)	0	100	100
12	K	91/93 (98%)	89 (98%)	2 (2%)	0	100	100
13	L	76/78 (97%)	74 (97%)	2 (3%)	0	100	100
14	M	54/56 (96%)	53 (98%)	1 (2%)	0	100	100
15	f	175/177 (99%)	165 (94%)	10 (6%)	0	100	100
16	g	174/176 (99%)	160 (92%)	14 (8%)	0	100	100
17	h	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
18	i	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
19	j	121/123 (98%)	116 (96%)	4 (3%)	1 (1%)	16	8
20	l	131/136 (96%)	128 (98%)	3 (2%)	0	100	100
21	n	114/116 (98%)	108 (95%)	5 (4%)	1 (1%)	14	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	o	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
23	p	115/117 (98%)	115 (100%)	0	0	100	100
24	q	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
25	r	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
26	t	100/102 (98%)	96 (96%)	3 (3%)	1 (1%)	12	5
27	u	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
28	w	75/77 (97%)	75 (100%)	0	0	100	100
29	x	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
30	y	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
31	T	14/16 (88%)	12 (86%)	2 (14%)	0	100	100
All	All	3068/3137 (98%)	2977 (97%)	88 (3%)	3 (0%)	49	41

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	j	108	ARG
21	n	88	LYS
26	t	39	ILE

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	46/49 (94%)	46 (100%)	0	100	100
2	1	38/38 (100%)	38 (100%)	0	100	100
3	B	51/52 (98%)	51 (100%)	0	100	100
4	C	34/34 (100%)	32 (94%)	2 (6%)	18	7
7	F	216/218 (99%)	215 (100%)	1 (0%)	81	82
8	G	163/163 (100%)	161 (99%)	2 (1%)	63	61
9	H	165/165 (100%)	164 (99%)	1 (1%)	78	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	I	103/103 (100%)	102 (99%)	1 (1%)	68	67
11	J	98/98 (100%)	98 (100%)	0	100	100
12	K	80/80 (100%)	80 (100%)	0	100	100
13	L	58/59 (98%)	58 (100%)	0	100	100
14	M	47/47 (100%)	47 (100%)	0	100	100
15	f	148/148 (100%)	147 (99%)	1 (1%)	76	76
16	g	137/137 (100%)	137 (100%)	0	100	100
17	h	30/30 (100%)	30 (100%)	0	100	100
18	i	116/116 (100%)	115 (99%)	1 (1%)	70	70
19	j	104/104 (100%)	103 (99%)	1 (1%)	68	67
20	l	107/107 (100%)	107 (100%)	0	100	100
21	n	86/86 (100%)	86 (100%)	0	100	100
22	o	99/99 (100%)	99 (100%)	0	100	100
23	p	89/89 (100%)	89 (100%)	0	100	100
24	q	84/84 (100%)	84 (100%)	0	100	100
25	r	93/93 (100%)	91 (98%)	2 (2%)	45	40
26	t	83/83 (100%)	82 (99%)	1 (1%)	63	61
27	u	78/78 (100%)	77 (99%)	1 (1%)	61	58
28	w	67/67 (100%)	67 (100%)	0	100	100
29	x	54/54 (100%)	54 (100%)	0	100	100
30	y	48/48 (100%)	48 (100%)	0	100	100
31	T	16/16 (100%)	15 (94%)	1 (6%)	16	6
All	All	2538/2545 (100%)	2523 (99%)	15 (1%)	76	79

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	f	140	GLU
27	u	65	VAL
18	i	96	ARG
31	T	21	LEU
25	r	92	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
18	i	138	GLN
24	q	6	GLN
29	x	58	ASN
21	n	29	HIS
26	t	46	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	D	2721/2728 (99%)	312 (11%)	47 (1%)
6	E	118/119 (99%)	14 (11%)	1 (0%)
All	All	2839/2847 (99%)	326 (11%)	48 (1%)

5 of 326 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	D	10	A
5	D	12	U
5	D	34	U
5	D	62	U
5	D	63	A

5 of 48 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	D	1585	A
5	D	2315	A
5	D	1628	A
5	D	1917	A
5	D	2406	U

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

27 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	$\#\|Z\| > 2$
5	G7M	D	2073	34,5	23,26,27	0.77	1 (4%)	34,39,42	0.62	1 (2%)
5	2MA	D	2507	34,33,5	22,25,26	0.95	1 (4%)	32,37,40	1.16	4 (12%)
5	6MZ	D	2034	5	22,25,26	0.47	0	29,36,39	0.68	0
5	5MU	D	1943	34,5	19,22,23	0.33	0	27,32,35	0.53	0
8	MEQ	G	150	8	8,9,10	0.49	0	5,10,12	0.65	0
5	PSU	D	2508	34,5	18,21,22	0.94	1 (5%)	21,30,33	0.93	0
5	PSU	D	1915	5	18,21,22	0.96	1 (5%)	21,30,33	0.62	0
5	PSU	D	2608	5	18,21,22	0.99	1 (5%)	21,30,33	0.87	1 (4%)
5	PSU	D	1921	5	18,21,22	0.97	1 (5%)	21,30,33	0.63	0
20	4D4	l	81	20	9,11,12	0.53	0	7,13,15	1.06	1 (14%)
5	5MU	D	749	5	19,22,23	0.28	0	27,32,35	0.51	0
5	PSU	D	957	5	18,21,22	0.91	1 (5%)	21,30,33	0.74	0
5	OMG	D	2255	34,5	23,26,27	0.32	0	32,38,41	0.38	0
5	PSU	D	2461	5	18,21,22	0.96	1 (5%)	21,30,33	0.71	0
5	3TD	D	1919	5	19,22,23	1.26	2 (10%)	23,32,35	0.76	0
5	6MZ	D	1620	5	22,25,26	0.35	0	29,36,39	0.62	0
5	1MG	D	747	5	23,26,27	0.68	0	33,39,42	0.56	0
5	PSU	D	2584	5	18,21,22	0.94	1 (5%)	21,30,33	0.81	0
5	H2U	D	2453	5	18,21,22	0.62	0	19,30,33	0.97	2 (10%)
5	PSU	D	748	33,5	18,21,22	0.97	1 (5%)	21,30,33	0.66	0
5	5MC	D	1966	34,5	19,22,23	0.64	1 (5%)	26,32,35	0.47	0
5	2MG	D	1837	5	23,26,27	0.36	0	33,38,41	0.44	0
20	MS6	l	82	-	5,7,8	0.74	0	2,7,9	0.11	0
5	2MG	D	2449	5	23,26,27	0.35	0	33,38,41	0.42	0
5	PSU	D	2609	5	18,21,22	0.96	1 (5%)	21,30,33	0.90	1 (4%)
5	OMC	D	2502	33,5	19,22,23	0.29	0	25,31,34	0.59	0
5	OMU	D	2556	5	19,22,23	0.26	0	25,31,34	0.58	1 (4%)

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
5	G7M	D	2073	34,5	-	1/7/25/26	0/3/3/3
5	2MA	D	2507	34,33,5	-	1/7/25/26	0/3/3/3
5	6MZ	D	2034	5	-	2/9/27/28	0/3/3/3
5	5MU	D	1943	34,5	-	0/7/25/26	0/2/2/2
8	MEQ	G	150	8	-	3/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PSU	D	2508	34,5	-	0/7/25/26	0/2/2/2
5	PSU	D	1915	5	-	0/7/25/26	0/2/2/2
5	PSU	D	2608	5	-	0/7/25/26	0/2/2/2
5	PSU	D	1921	5	-	0/7/25/26	0/2/2/2
20	4D4	l	81	20	-	1/11/12/14	-
5	5MU	D	749	5	-	0/7/25/26	0/2/2/2
5	PSU	D	957	5	-	0/7/25/26	0/2/2/2
5	OMG	D	2255	34,5	-	0/9/27/28	0/3/3/3
5	PSU	D	2461	5	-	0/7/25/26	0/2/2/2
5	3TD	D	1919	5	-	2/7/25/26	0/2/2/2
5	6MZ	D	1620	5	-	0/9/27/28	0/3/3/3
5	1MG	D	747	5	-	0/7/25/26	0/3/3/3
5	PSU	D	2584	5	-	0/7/25/26	0/2/2/2
5	H2U	D	2453	5	-	0/7/38/39	0/2/2/2
5	PSU	D	748	33,5	-	2/7/25/26	0/2/2/2
5	5MC	D	1966	34,5	-	0/7/25/26	0/2/2/2
5	2MG	D	1837	5	-	0/9/27/28	0/3/3/3
20	MS6	l	82	-	-	1/4/6/8	-
5	2MG	D	2449	5	-	0/9/27/28	0/3/3/3
5	PSU	D	2609	5	-	0/7/25/26	0/2/2/2
5	OMC	D	2502	33,5	-	0/9/27/28	0/2/2/2
5	OMU	D	2556	5	-	0/9/27/28	0/2/2/2

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	1919	3TD	C6-C5	3.89	1.39	1.35
5	D	1921	PSU	C6-C5	3.81	1.39	1.35
5	D	1915	PSU	C6-C5	3.81	1.39	1.35
5	D	2608	PSU	C6-C5	3.80	1.39	1.35
5	D	748	PSU	C6-C5	3.79	1.39	1.35

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	D	2507	2MA	CM2-C2-N1	3.46	122.31	117.13
5	D	2453	H2U	O2-C2-N1	-2.99	119.51	123.10
20	l	81	4D4	O-C-CA	-2.62	118.04	124.77
5	D	2507	2MA	C5-C4-N3	-2.60	124.44	127.18
5	D	2453	H2U	N3-C2-N1	2.57	119.23	116.65

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	1919	3TD	O4'-C4'-C5'-O5'
8	G	150	MEQ	NE2-CD-CG-CB
8	G	150	MEQ	OE1-CD-CG-CB
5	D	1919	3TD	C3'-C4'-C5'-O5'
5	D	2034	6MZ	O4'-C4'-C5'-O5'

There are no ring outliers.

6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	2034	6MZ	3	0
5	D	1943	5MU	1	0
5	D	2608	PSU	1	0
5	D	749	5MU	1	0
5	D	2255	OMG	1	0
20	l	82	MS6	4	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 298 ligands modelled in this entry, 298 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
5	D	6
20	l	1

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	880:A	O3'	901:A	P	17.61
1	D	544:G	O3'	551:C	P	17.04
1	D	1054:C	O3'	1109:G	P	17.03
1	D	2102:U	O3'	2195:A	P	16.99
1	D	1174:C	O3'	1179:G	P	15.94

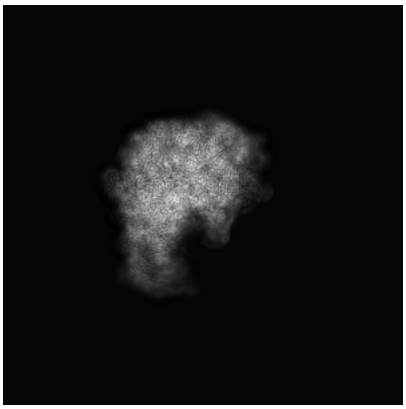
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-46632. These allow visual inspection of the internal detail of the map and identification of artifacts.

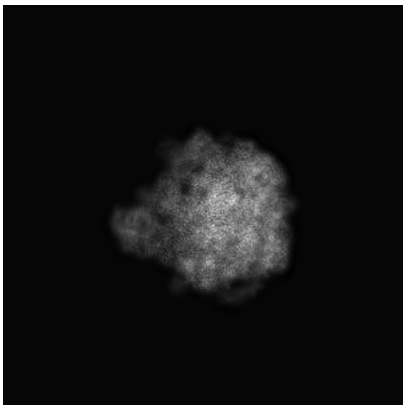
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

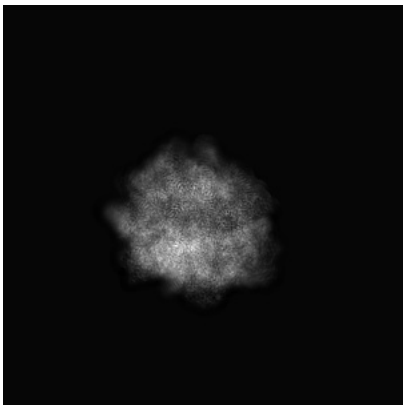
6.1.1 Primary map



X

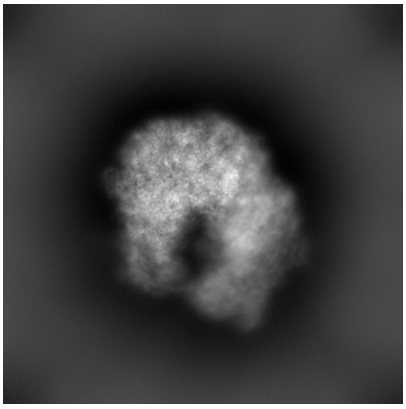


Y

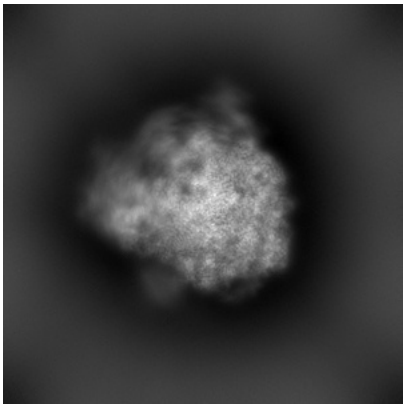


Z

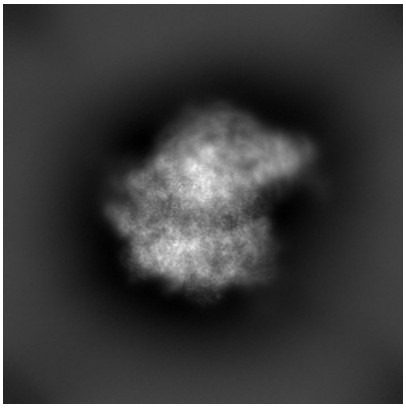
6.1.2 Raw map



X



Y

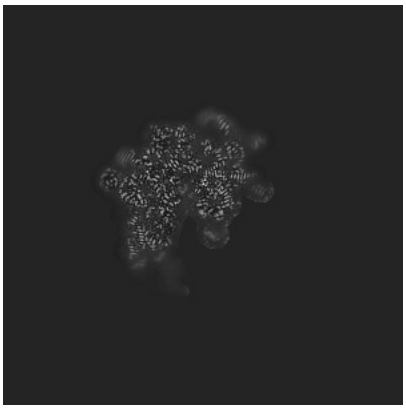


Z

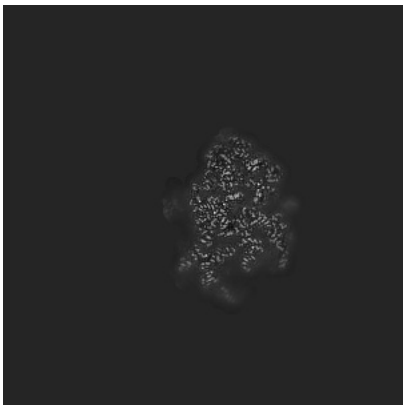
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

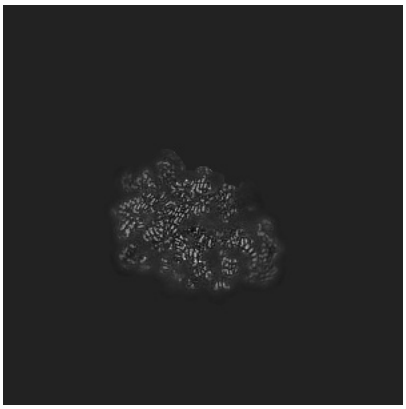
6.2.1 Primary map



X Index: 256

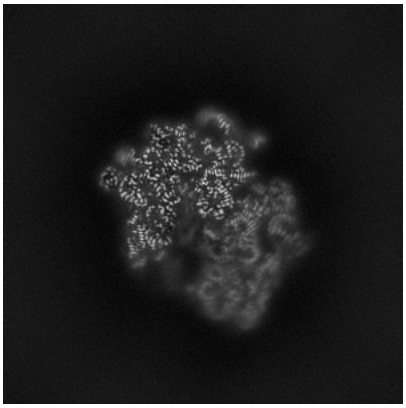


Y Index: 256

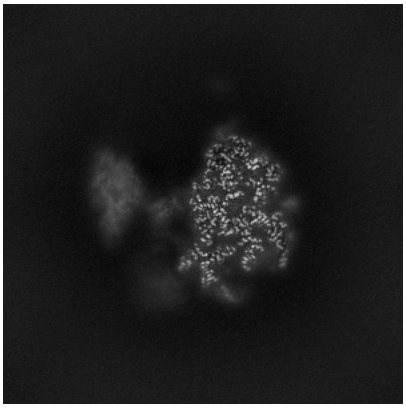


Z Index: 256

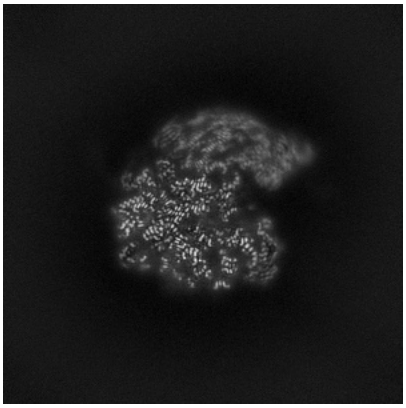
6.2.2 Raw map



X Index: 256



Y Index: 256



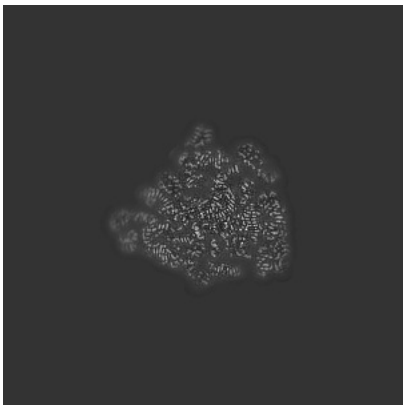
Z Index: 256

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

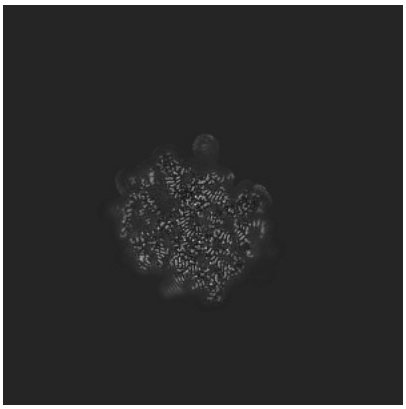
6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 225

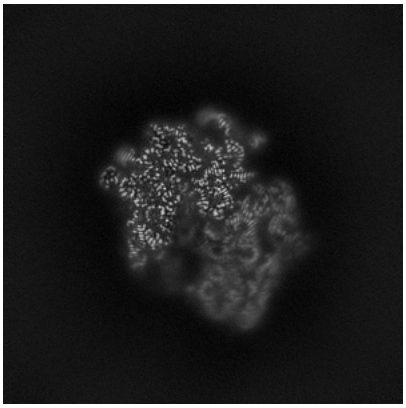


Y Index: 199

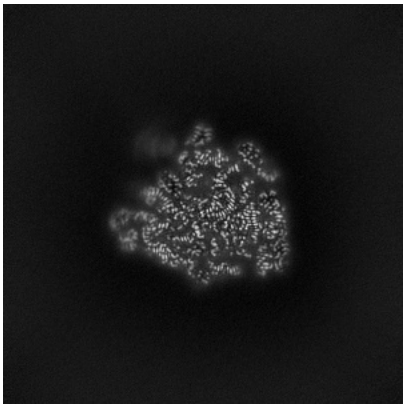


Z Index: 270

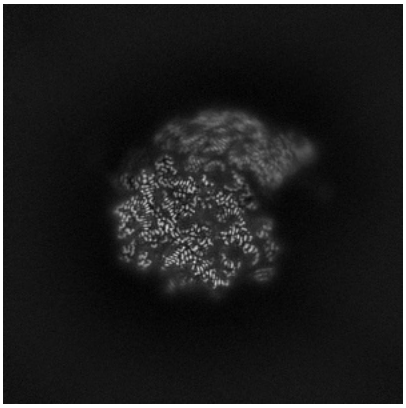
6.3.2 Raw map



X Index: 255



Y Index: 199

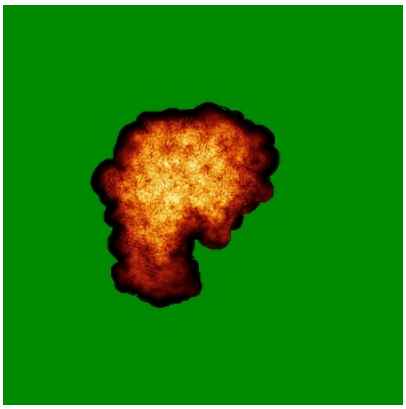


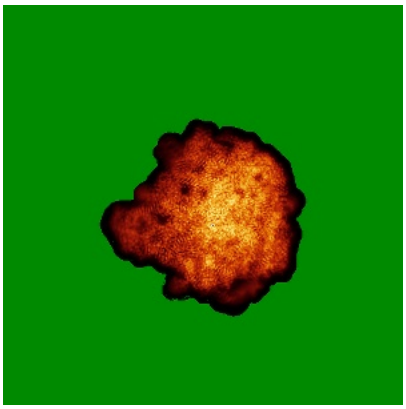
Z Index: 261

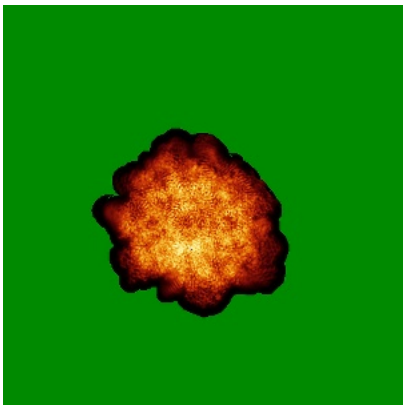
The images above show the largest variance slices of the map in three orthogonal directions.

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

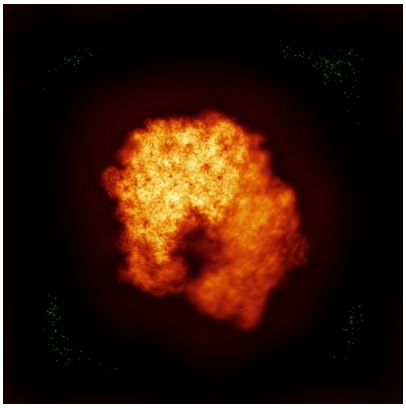
6.4.1 Primary map

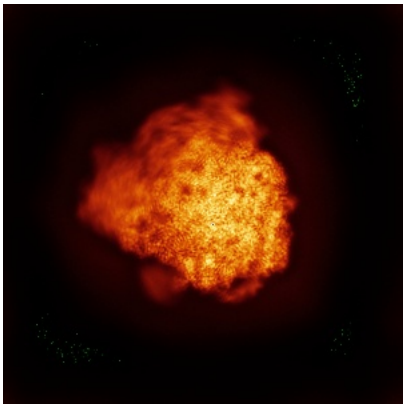

X

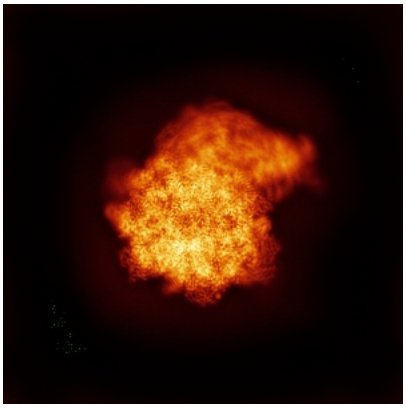

Y


Z

6.4.2 Raw map


X

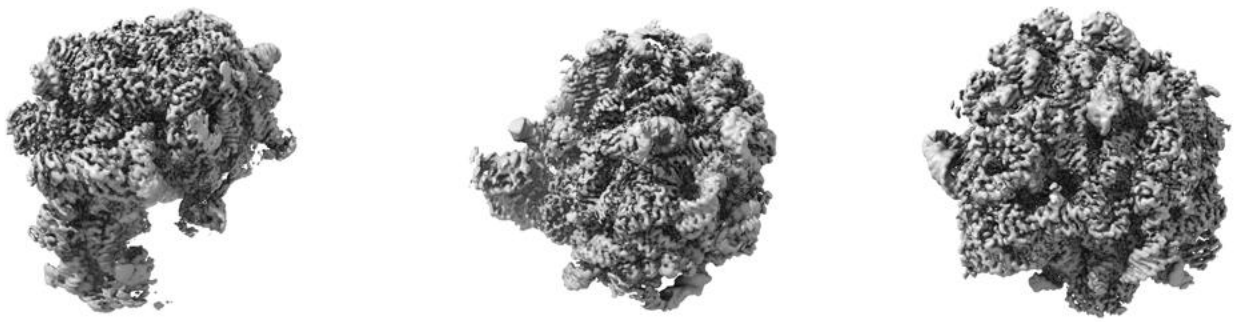

Y


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 1.1. 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.

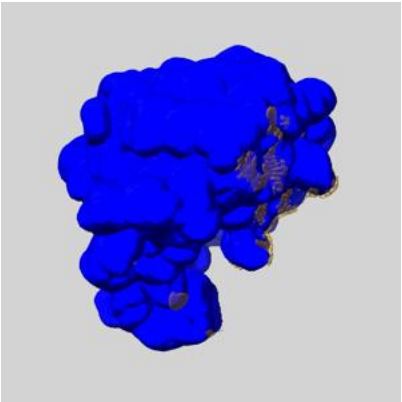
6.6 Mask visualisation (i)

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

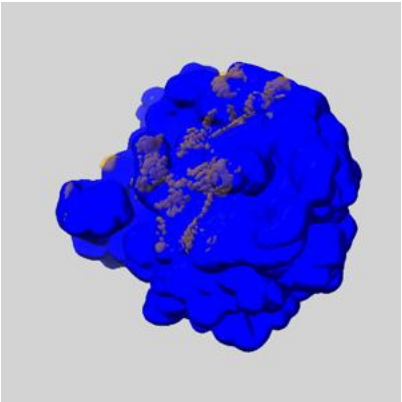
A mask typically either:

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

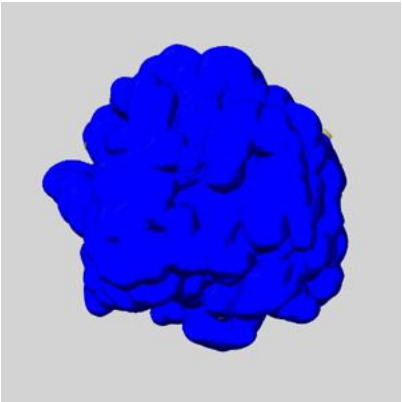
6.6.1 emd_46632_msk_1.map (i)



X



Y

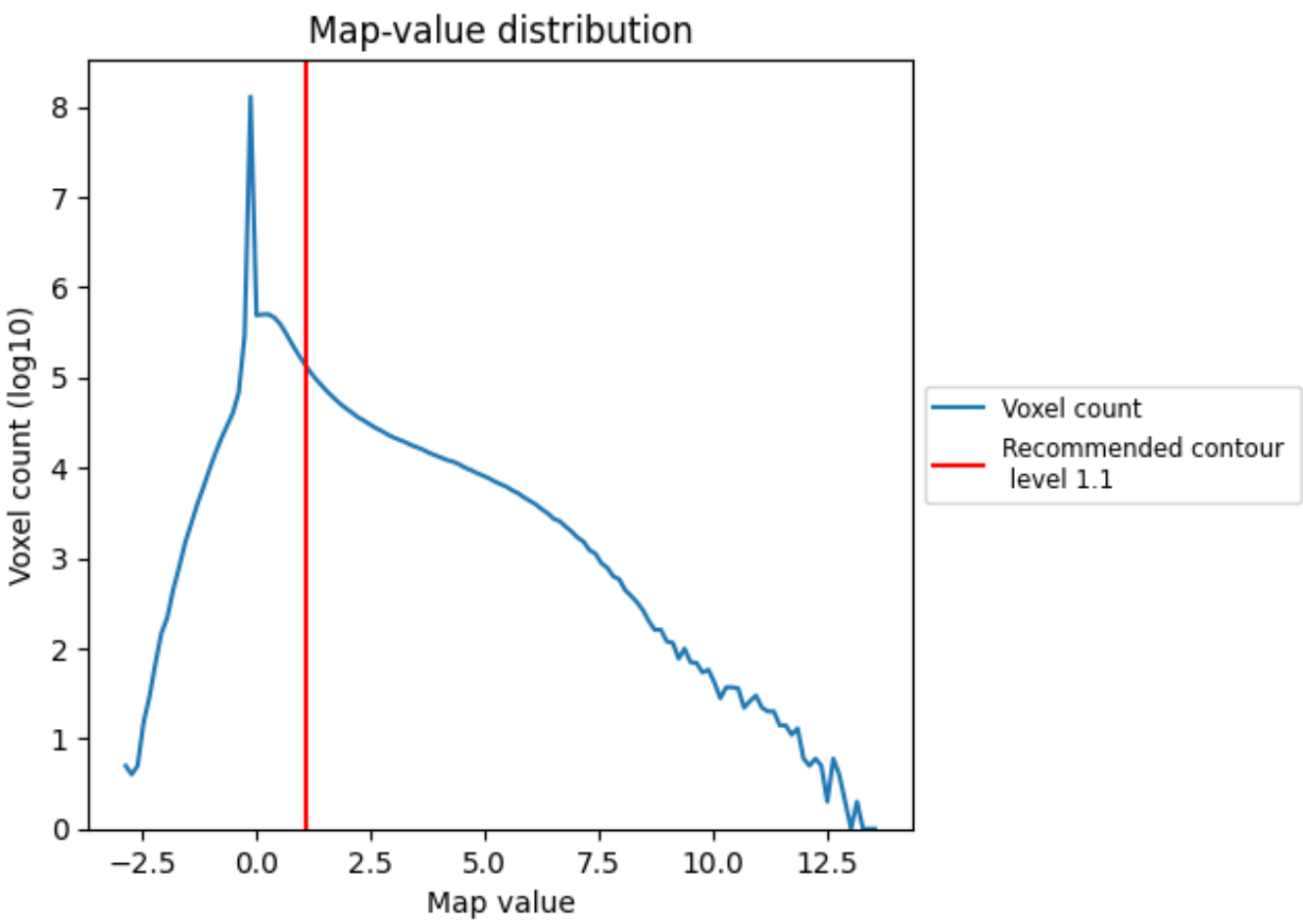


Z

7 Map analysis (i)

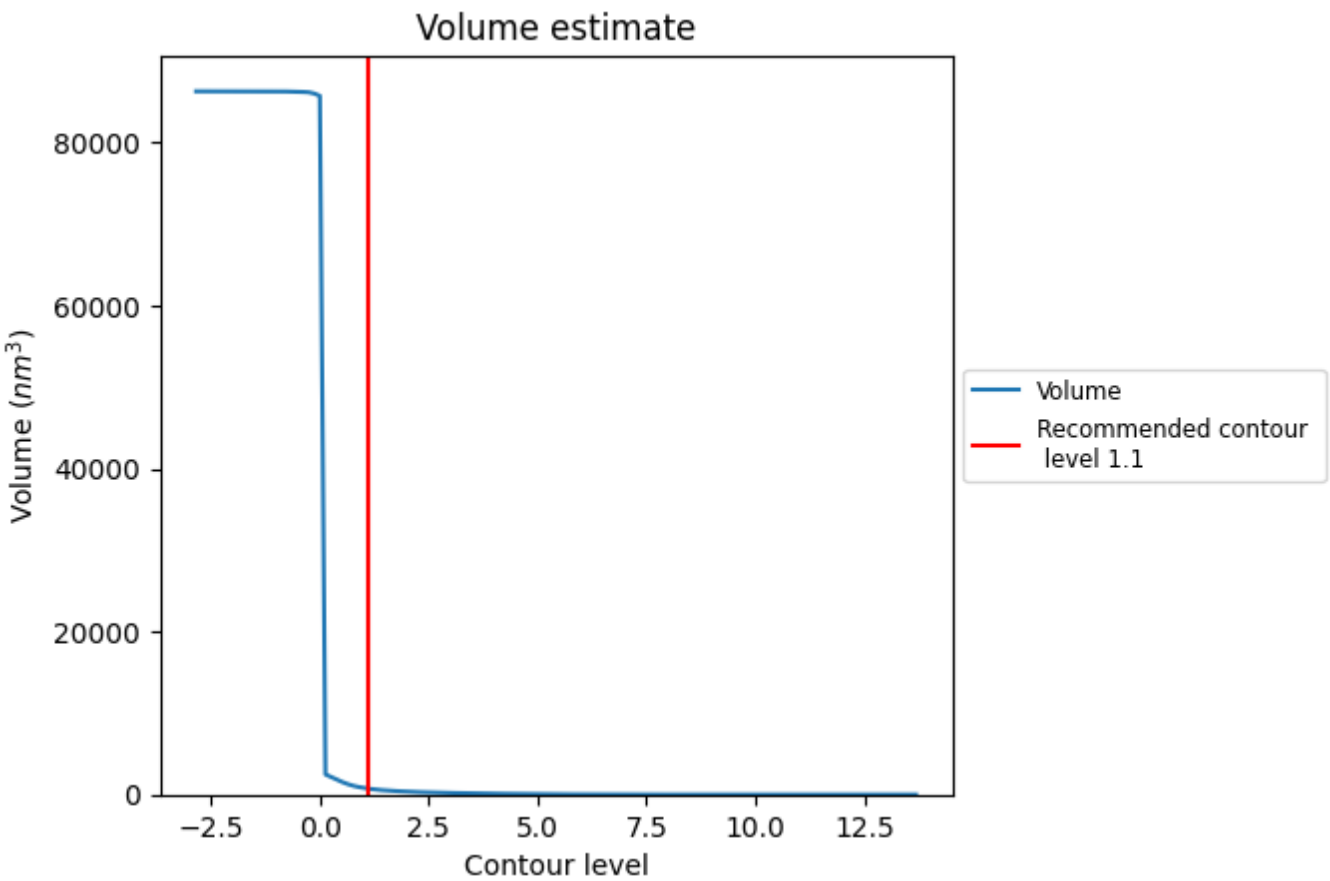
This section contains the results of statistical analysis of the map.

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.

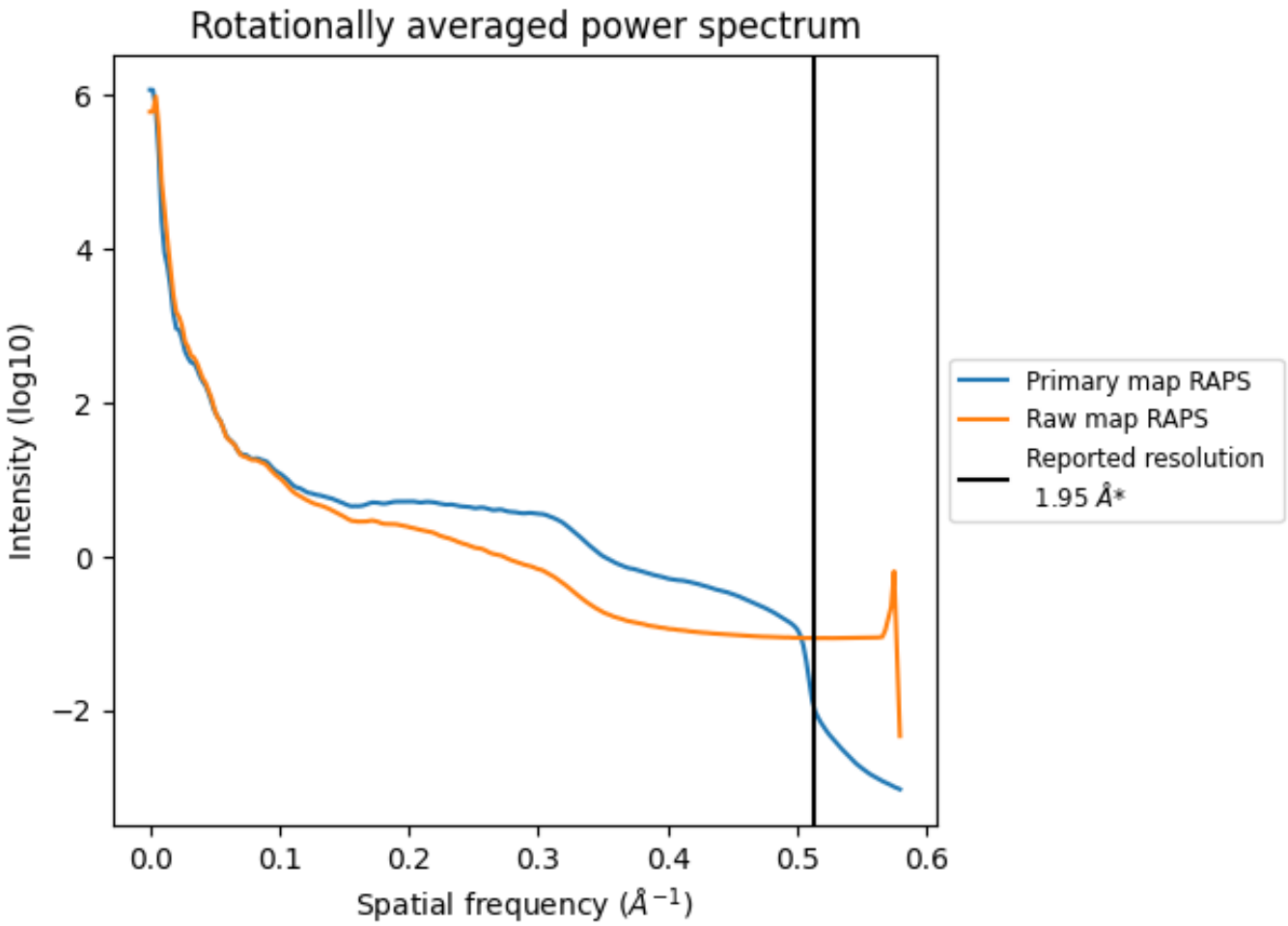
7.2 Volume estimate (i)



The volume at the recommended contour level is 734 nm^3; this corresponds to an approximate mass of 663 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)

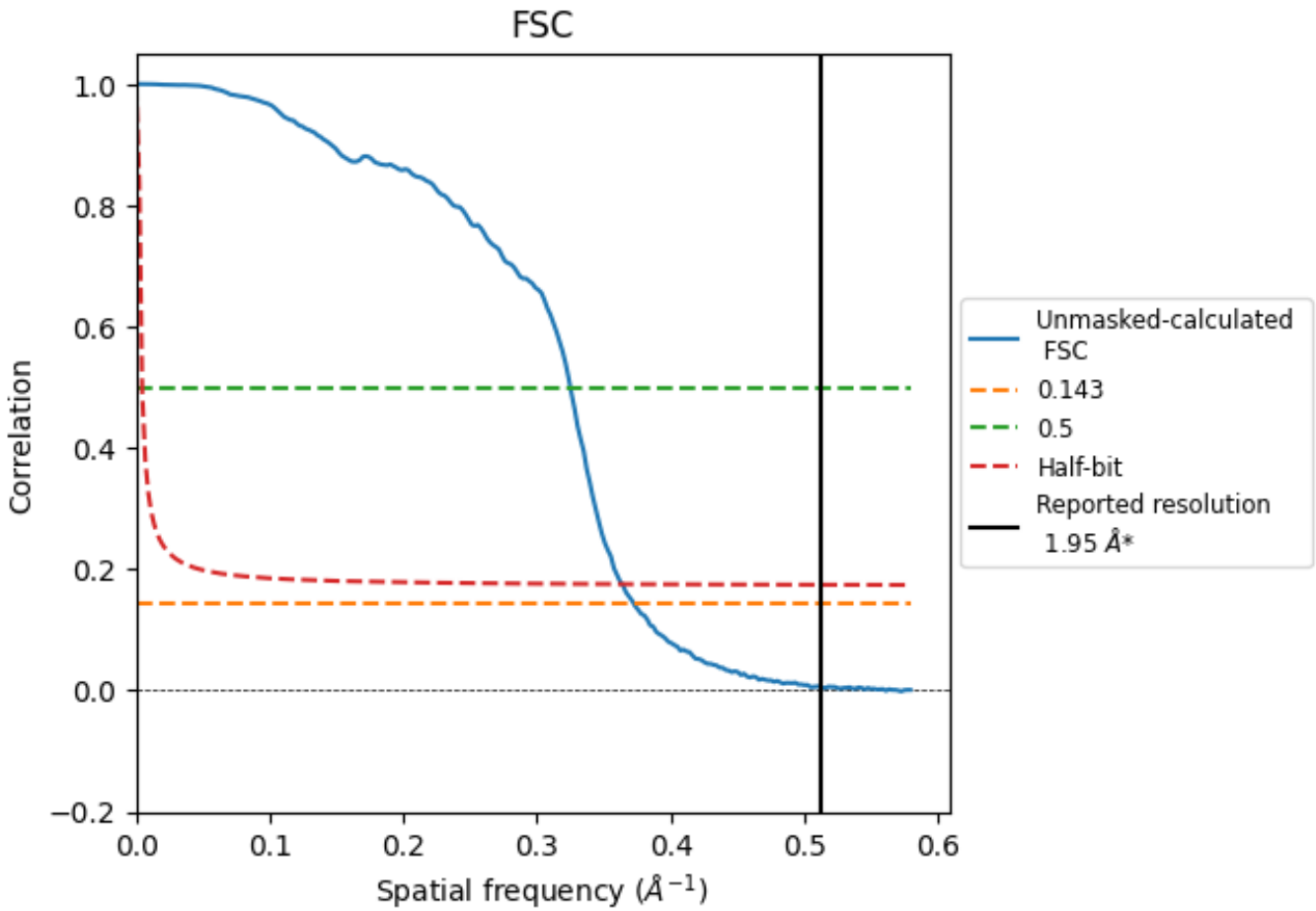


*Reported resolution corresponds to spatial frequency of 0.513 Å^{-1}

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 0.513 Å^{-1}

8.2 Resolution estimates (i)

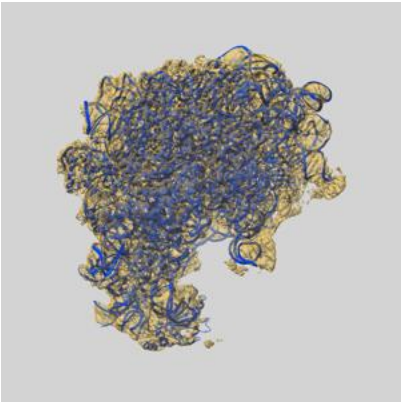
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	1.95	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.69	3.08	2.75

*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 2.69 differs from the reported value 1.95 by more than 10 %

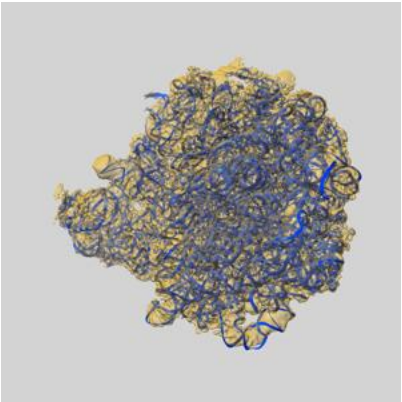
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-46632 and PDB model 9D89. Per-residue inclusion information can be found in section 3 on page 12.

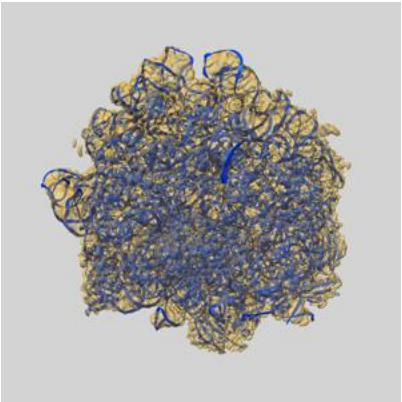
9.1 Map-model overlay (i)



X



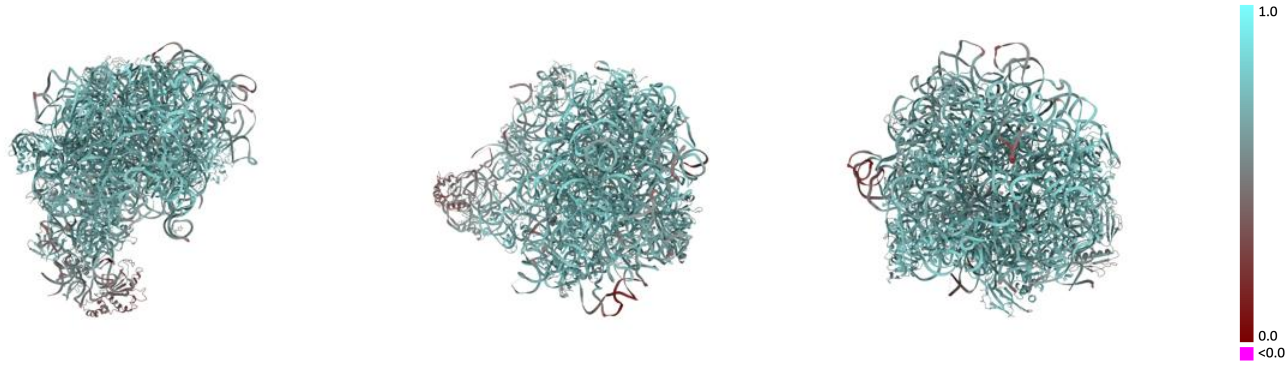
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.1 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.

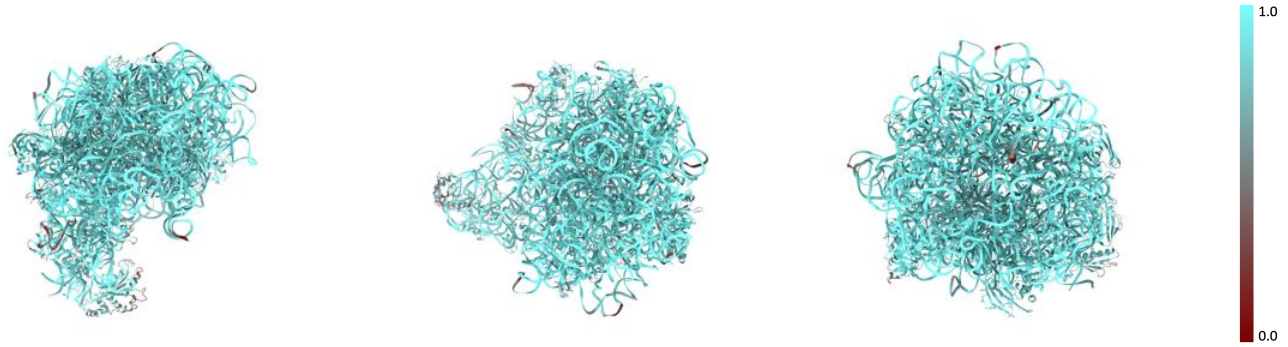
9.2 Q-score mapped to coordinate model (i)



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.

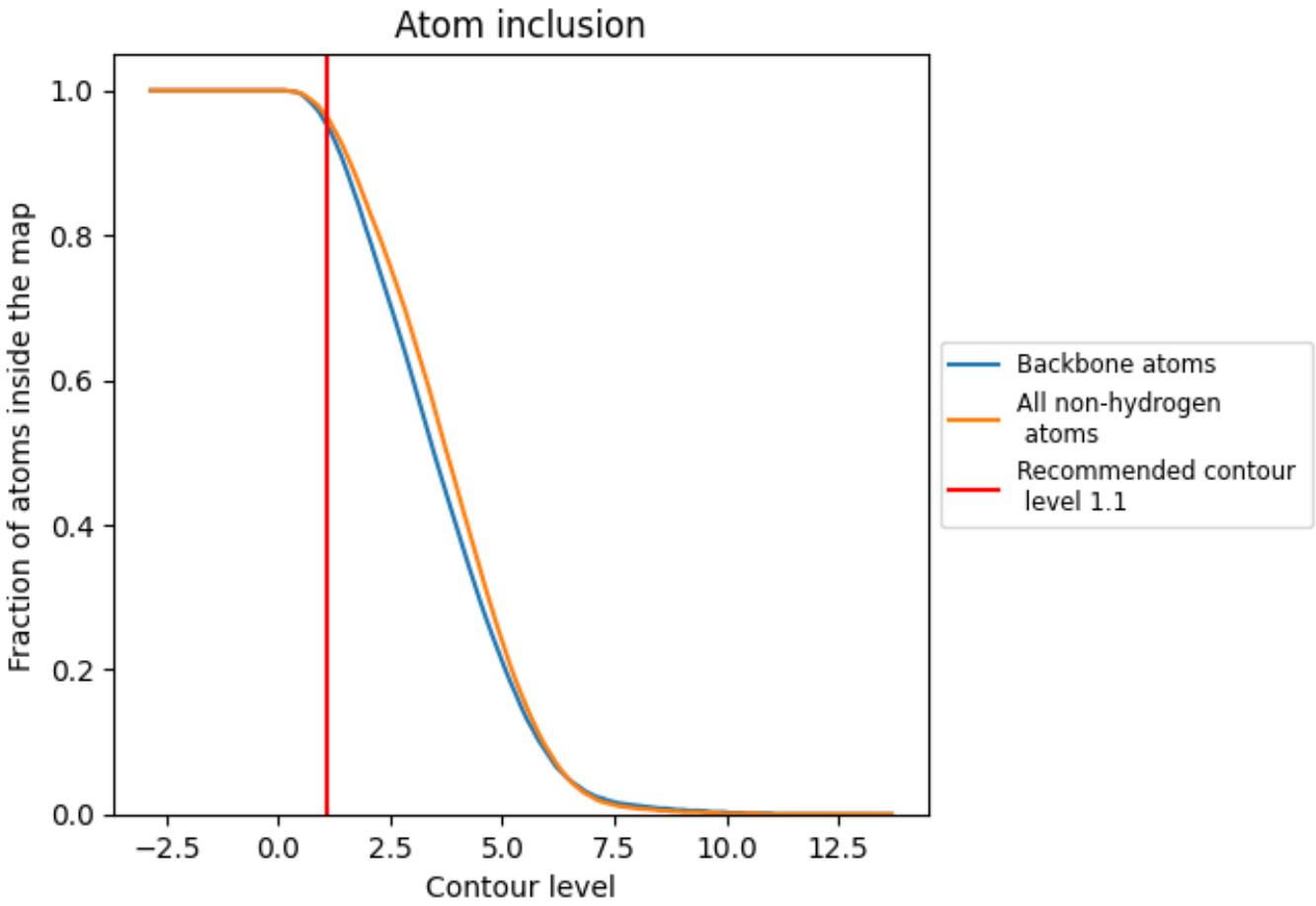
9.3 Atom inclusion mapped to coordinate model (i)



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 (1.1).

9.4 Atom inclusion (i)



At the recommended contour level, 95% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (1.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9620	0.6920
0	0.8700	0.6750
1	0.9830	0.7710
B	0.9800	0.7500
C	0.9490	0.6780
D	0.9820	0.7030
E	0.9720	0.5670
F	0.9700	0.7390
G	0.9550	0.7310
H	0.9060	0.6970
I	0.9500	0.7180
J	0.9870	0.7540
K	0.9320	0.6860
L	0.9340	0.7110
M	0.9300	0.7110
T	0.9480	0.6340
f	0.6500	0.3860
g	0.8100	0.5610
h	0.7600	0.6050
i	0.9590	0.7320
j	0.9510	0.7200
l	0.9520	0.7160
n	0.8880	0.5800
o	0.9050	0.6980
p	0.9810	0.7630
q	0.9250	0.6980
r	0.9460	0.7250
t	0.8890	0.6570
u	0.8650	0.6340
w	0.9430	0.7000
x	0.8920	0.6470
y	0.9180	0.7170