wwPDB EM Validation Summary Report ⓘ

Dec 10, 2022 – 08:36 am GMT

PDB ID	:	5AN9
EMDB ID	:	EMD-3145
Title	:	Mechanism of eIF6 release from the nascent 60S ribosomal subunit
Authors	:	Weis, F.; Giudice, E.; Churcher, M.; Jin, L.; Hilcenko, C.; Wong, C.C.; Traynor, D.; Kay, R.R.; Warren, A.J.
Deposited on	:	2015-09-06
Resolution	:	3.30 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

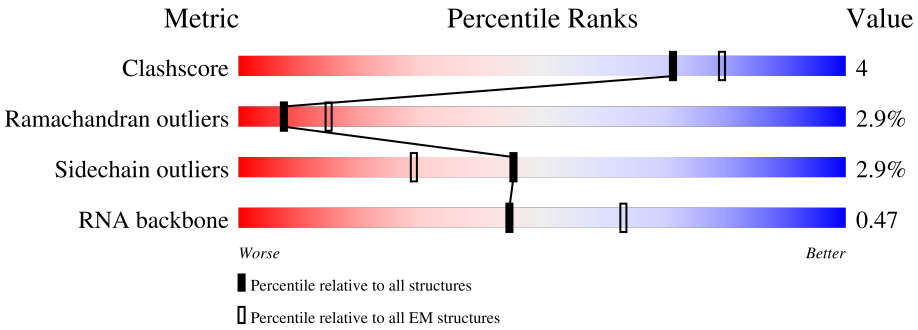
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	398	11% 82% 15% ·
2	B	188	10% 88% 12%
3	C	205	97% 97% ·
4	D	166	96% 96% · ·
5	E	136	8% 85% 15% ·
6	F	217	9% 86% 13%
7	G	69	17% 91% 9%

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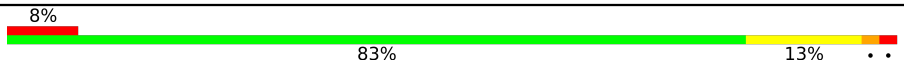
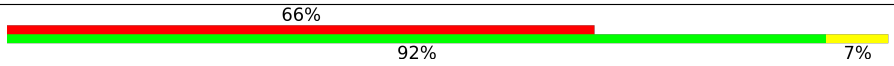
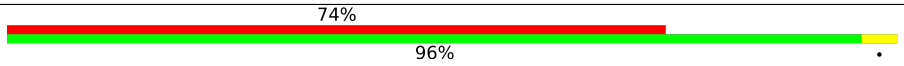
Mol	Chain	Length	Quality of chain
8	H	52	
9	I	224	
10	J	250	
11	N	3741	

2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 39693 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 60S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	398	3176	2018	599	547	12	0	0

- Molecule 2 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	188	1491	944	264	277	6	0	0

- Molecule 3 is a protein called 60S ACIDIC RIBOSOMAL PROTEIN P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	205	1571	998	271	294	8	0	0

- Molecule 4 is a protein called 60S RIBOSOMAL PROTEIN L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	166	1245	790	220	228	7	0	0

- Molecule 5 is a protein called 60S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	136	1017	640	188	181	8	0	0

- Molecule 6 is a protein called 60S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	217	1721	1079	332	297	13	0	0

- Molecule 7 is a protein called 60S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	69	Total	C	N	O	S	0	0
			586	378	105	99	4		

- Molecule 8 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	52	Total	C	N	O	S	0	0
			427	269	88	64	6		

- Molecule 9 is a protein called EUKARYOTIC TRANSLATION INITIATION FACTOR 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	224	Total	C	N	O	S	0	0
			1686	1048	290	338	10		

- Molecule 10 is a protein called RIBOSOME MATURATION PROTEIN SBDS.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	250	Total	C	N	O	S	0	0
			2015	1272	352	380	11		

- Molecule 11 is a RNA chain called 26S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	1162	Total	C	N	O	P	0	0
			24758	11082	4431	8087	1158		

There is a discrepancy between the modelled and reference sequences:

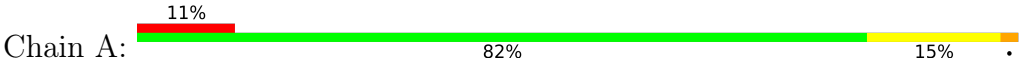
Chain	Residue	Modelled	Actual	Comment	Reference
N	3119	C	G	conflict	GB FR733594.

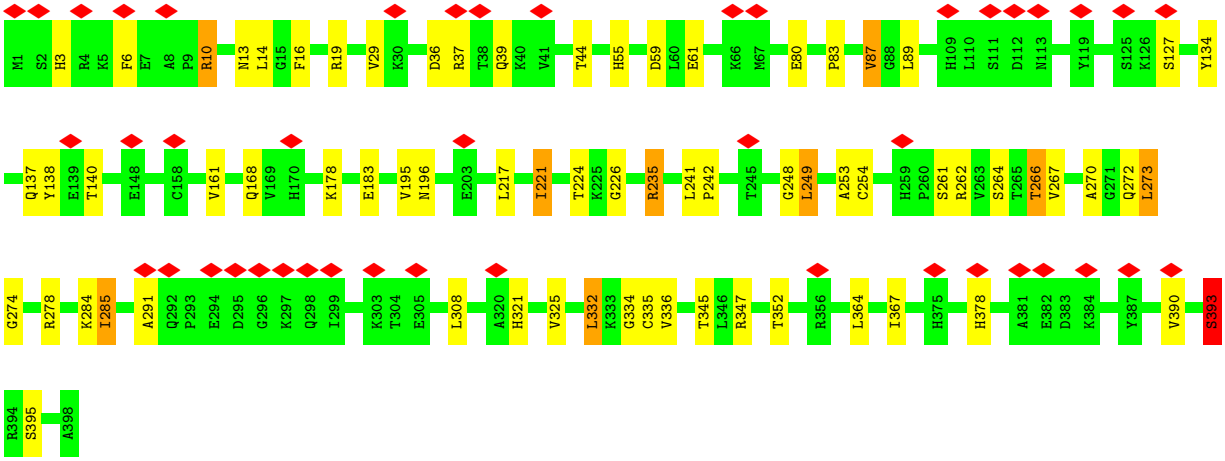
3 Residue-property plots (i)

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: 60S RIBOSOMAL PROTEIN L3

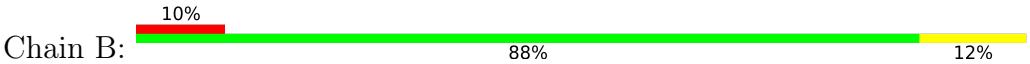
Chain A:

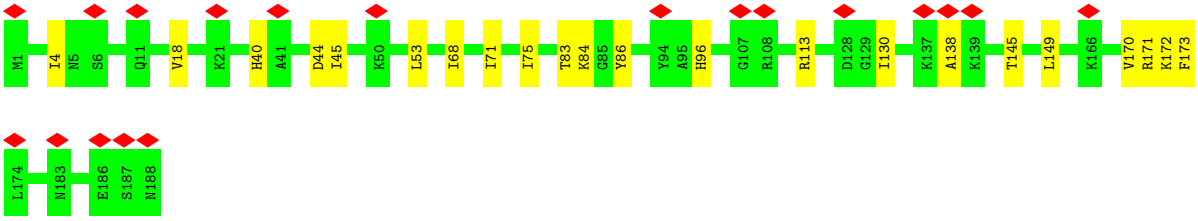




• Molecule 2: 60S RIBOSOMAL PROTEIN L9

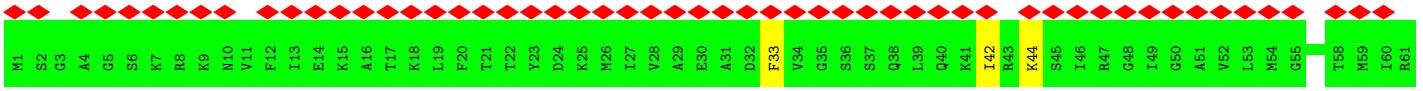
Chain B:

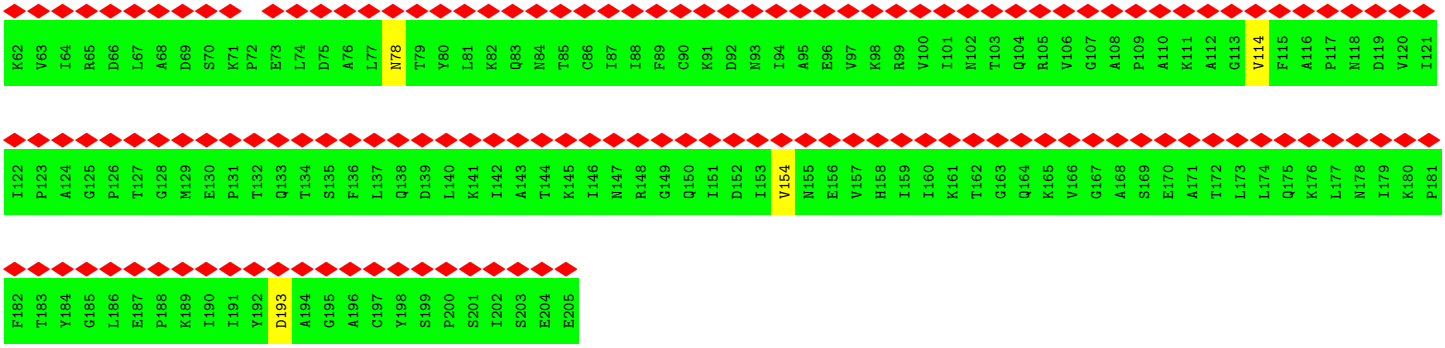




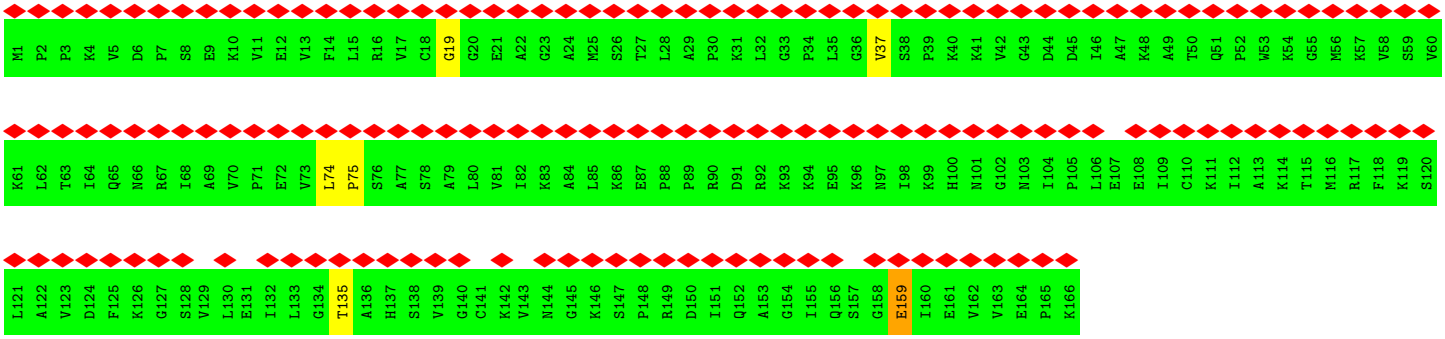
• Molecule 3: 60S ACIDIC RIBOSOMAL PROTEIN P0

Chain C:

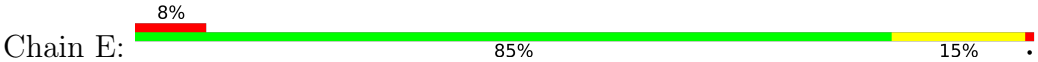


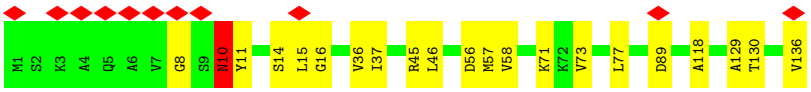


• Molecule 4: 60S RIBOSOMAL PROTEIN L12

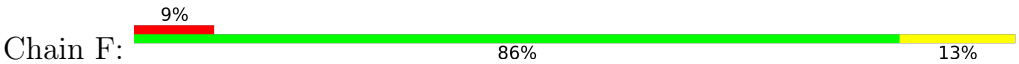


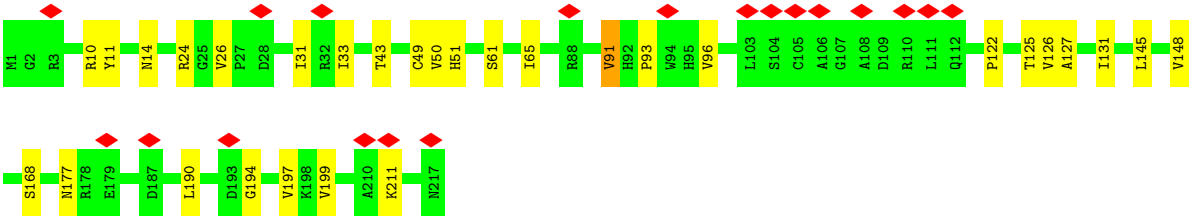
• Molecule 5: 60S RIBOSOMAL PROTEIN L23



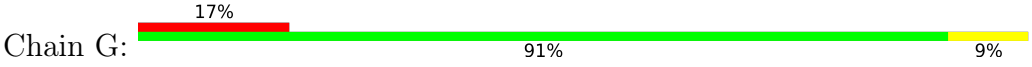


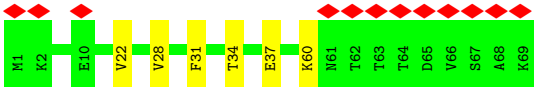
• Molecule 6: 60S RIBOSOMAL PROTEIN L10





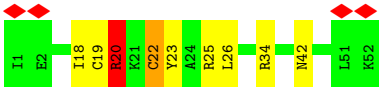
• Molecule 7: 60S RIBOSOMAL PROTEIN L24





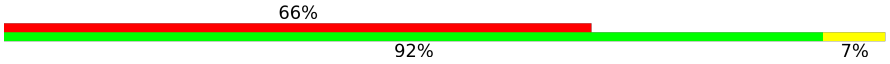
• Molecule 8: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

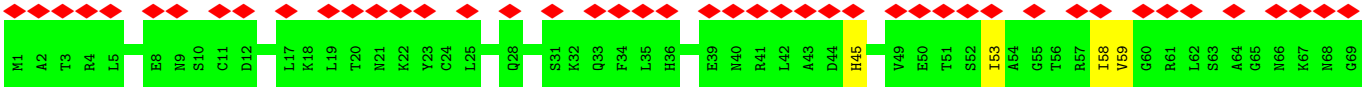
Chain H:

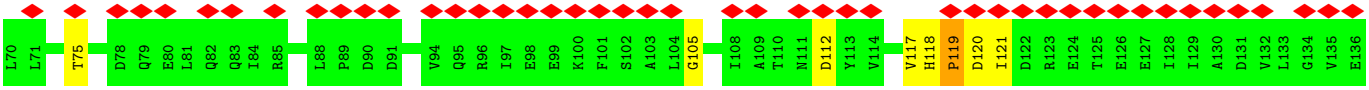


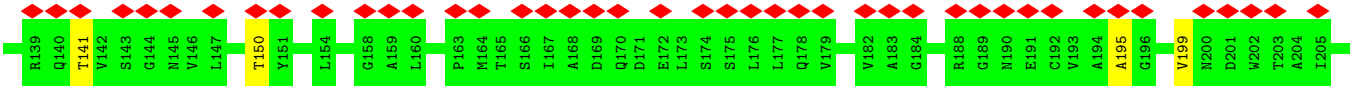
• Molecule 9: EUKARYOTIC TRANSLATION INITIATION FACTOR 6

Chain I:



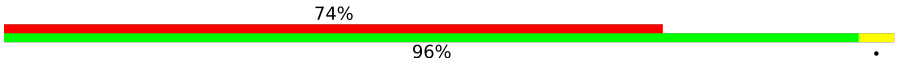


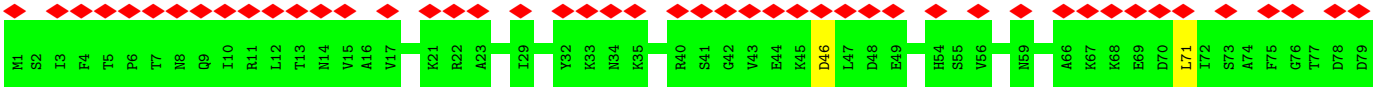


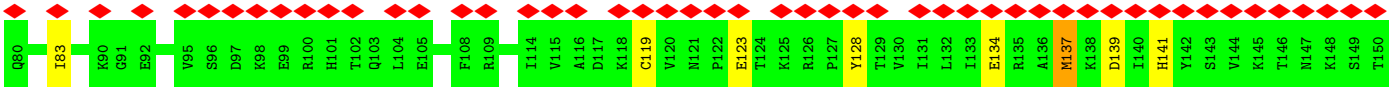


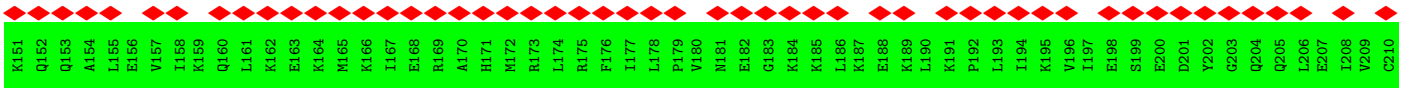
• Molecule 10: RIBOSOME MATURATION PROTEIN SBDS

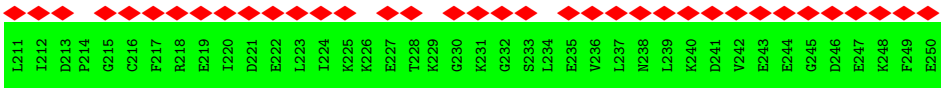
Chain J:





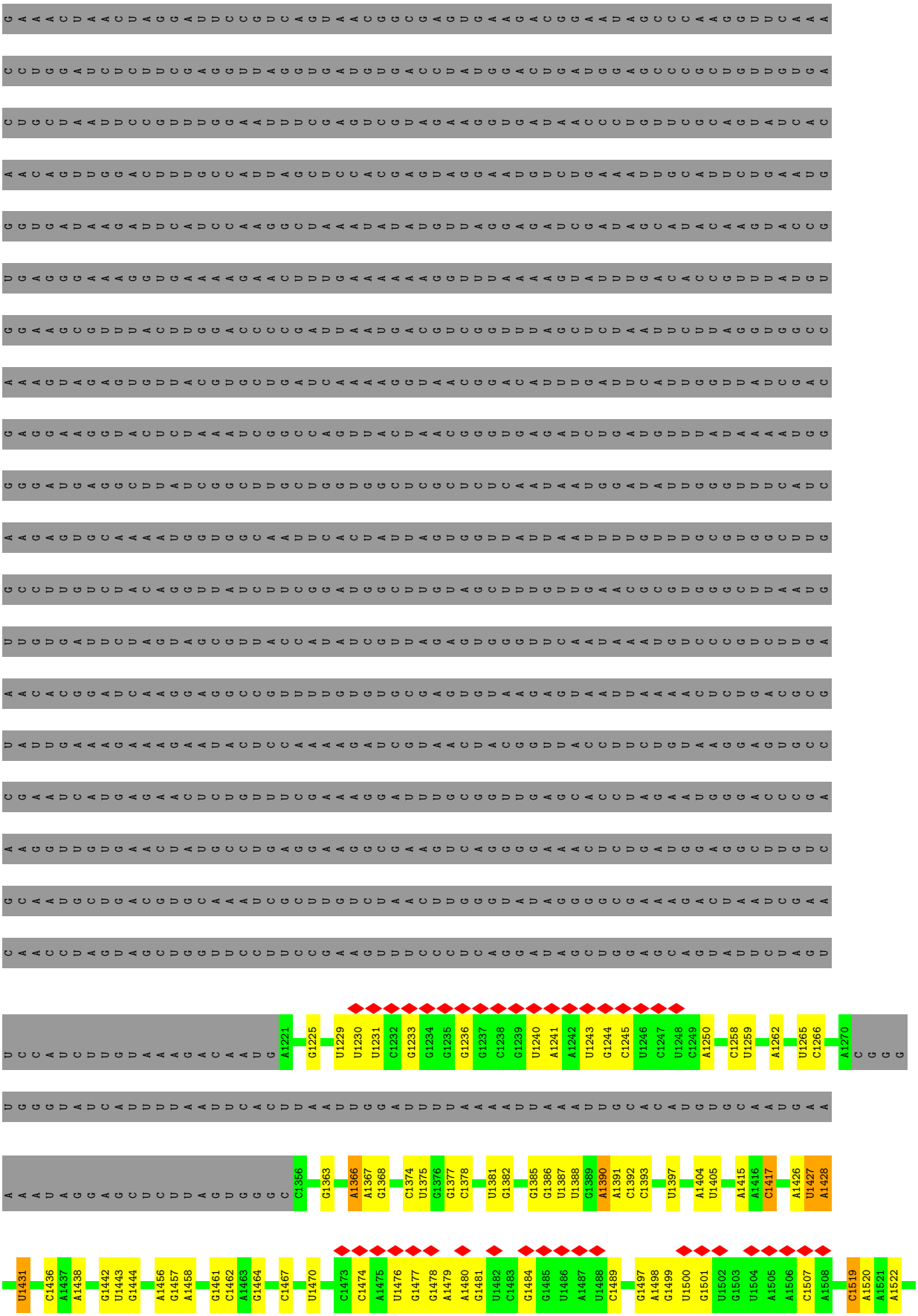


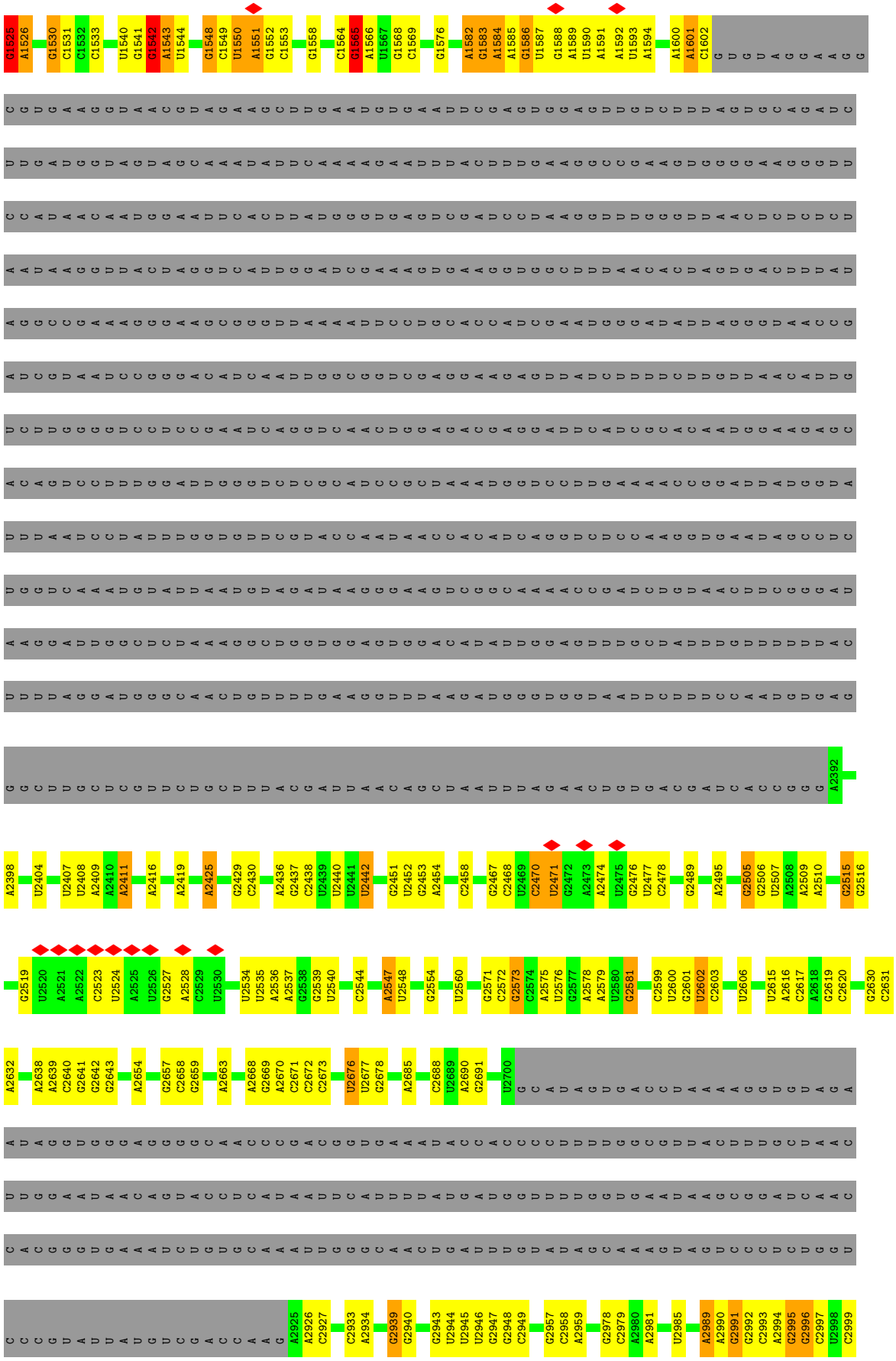


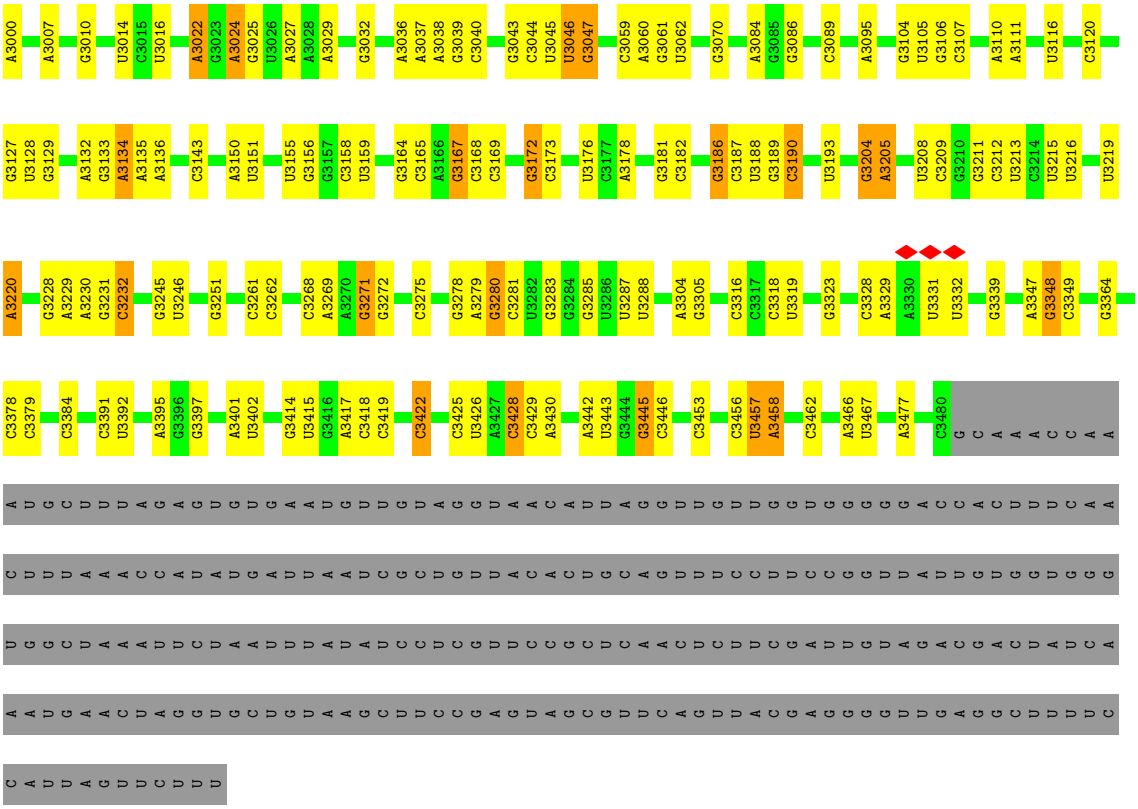


• Molecule 11: 26S RIBOSOMAL RNA

Chain N:


A1221 G1225 U1229 U1230 U1231 C1232 G1233 G1234 G1235 G1236 G1237 C1238 G1239 U1240 A1241 A1242 U1243 G1244 C1245 U1246 C1247 U1248 C1249 A1250 C1258 U1259 A1262 U1265 C1266 A1270
C1356 G1363 A1366 A1367 G1368 C1374 U1375 G1376 G1377 C1378 U1381 G1382 G1385 G1386 U1387 U1388 G1389 A1390 A1391 C1392 C1393 U1397 A1404 U1405 A1415 A1416 C1417 A1426 U1427 A1428
U1431 C1436 A1437 A1438 G1442 U1443 G1444 A1456 G1457 A1458 G1461 C1462 A1463 G1464 C1467 U1470 C1473 C1474 A1475 U1476 G1477 G1478 A1479 A1480 G1481 U1482 C1483 G1484 G1485 U1486 A1487 U1488 C1489 G1497 A1498 G1499 U1500 G1501 U1502 G1503 U1504 A1505 A1506 C1507 A1508 C1519 A1520 A1521 A1522


G1525 A1526 G1530 C1531 C1532 C1533 U1540 G1541 G1542 A1543 U1544 G1548 C1549 U1550 A1551 G1552 C1553 G1558 C1564 G1565 A1566 U1567 G1568 C1669 G1576 A1582 G1583 A1584 A1585 G1586 U1587 G1588 A1589 U1590 A1591 A1592 U1593 A1594 A1600 A1601 C1602
A2392
A2398 U2404 U2407 U2408 A2409 A2410 A2411 A2416 A2419 A2425 G2429 C2430 A2436 G2437 C2438 U2439 U2440 U2441 U2442 G2451 U2452 G2453 A2454 C2458 G2467 C2468 U2469 C2470 U2471 G2472 A2473 A2474 U2475 G2476 U2477 C2478 G2489 A2495 G2505 G2506 U2507 A2508 A2509 A2510 G2515 G2516
G2519 U2520 A2521 A2522 C2523 U2524 A2525 U2526 G2527 A2528 C2529 U2530 U2534 U2535 A2536 A2537 G2538 G2539 U2540 C2544 A2547 U2548 G2554 U2560 G2571 C2572 G2573 C2574 A2575 U2576 G2577 A2578 A2579 U2580 G2581 C2599 U2600 G2601 U2602 C2603 U2606 U2615 A2616 C2617 A2618 G2619 C2620 G2630 C2631
A2632 A2638 A2639 C2640 G2641 G2642 G2643 A2654 G2657 C2658 G2659 A2663 A2668 G2669 A2670 C2671 C2672 C2673 U2676 U2677 G2678 A2685 C2688 U2689 A2690 G2691 U2700
A2925 A2926 C2927 C2933 A2934 G2939 G2940 G2943 U2944 U2945 U2946 G2947 G2948 C2949 G2957 C2958 A2959 G2978 C2979 A2980 A2981 U2985 A2989 A2990 G2991 C2992 C2993 A2994 G2995 G2996 C2997 U2998 C2999



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	43063	Depositor
Resolution determination method	Not provided	
CTF correction method	EACH PARTICLE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	30	Depositor
Minimum defocus (nm)	2200	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	105263	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.554	Depositor
Minimum map value	-1.083	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.051	Depositor
Recommended contour level	0.14	Depositor
Map size (Å)	399.0, 399.0, 399.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	Depositor

5 Model quality

5.1 Standard geometry

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	0.45	0/3241	0.78	1/4339 (0.0%)
2	B	0.37	0/1510	0.68	0/2030
3	C	0.38	0/1592	0.57	0/2142
4	D	0.37	0/1265	0.58	0/1702
5	E	0.36	0/1032	0.69	0/1386
6	F	0.38	0/1752	0.70	0/2345
7	G	0.44	0/600	0.67	0/801
8	H	0.39	0/433	0.77	0/571
9	I	0.37	0/1706	0.62	0/2325
10	J	0.38	0/2038	0.64	0/2727
11	N	0.35	0/27702	0.74	7/43160 (0.0%)
All	All	0.36	0/42871	0.72	8/63528 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
5	E	0	1
9	I	0	1
All	All	0	4

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	N	2995	G	C2'-C3'-O3'	8.84	128.96	109.50
11	N	1582	A	C2'-C3'-O3'	7.68	126.41	109.50
11	N	1565	G	C4'-C3'-O3'	6.44	125.88	113.00
11	N	1519	C	C2'-C3'-O3'	6.32	123.81	113.70
11	N	2515	G	C2'-C3'-O3'	6.02	123.33	113.70

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	16	PHE	Peptide
1	A	393	SER	Peptide
5	E	10	ASN	Peptide
9	I	118	HIS	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	A	3176	0	3319	26	0
2	B	1491	0	1555	8	0
3	C	1571	0	1657	1	0
4	D	1245	0	1338	1	0
5	E	1017	0	1076	11	0
6	F	1721	0	1778	14	0
7	G	586	0	601	2	0
8	H	427	0	483	5	0
9	I	1686	0	1685	7	0
10	J	2015	0	2112	2	0
11	N	24758	0	12487	174	0
All	All	39693	0	28091	238	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 238 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:ILE:CD1	1:A:332:LEU:HD23	2.24	0.68
11:N:1415:A:N3	11:N:1564:C:O2'	2.26	0.67
6:F:96:VAL:HG12	6:F:125:THR:HG22	1.78	0.64
6:F:14:ASN:ND2	11:N:1363:G:OP2	2.29	0.64
5:E:36:VAL:HG13	5:E:58:VAL:HG13	1.79	0.63

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	A	396/398 (100%)	328 (83%)	50 (13%)	18 (4%)	2 15
2	B	186/188 (99%)	169 (91%)	14 (8%)	3 (2%)	9 36
3	C	203/205 (99%)	185 (91%)	15 (7%)	3 (2%)	10 38
4	D	164/166 (99%)	142 (87%)	17 (10%)	5 (3%)	4 24
5	E	134/136 (98%)	114 (85%)	13 (10%)	7 (5%)	2 13
6	F	215/217 (99%)	188 (87%)	21 (10%)	6 (3%)	5 25
7	G	67/69 (97%)	62 (92%)	4 (6%)	1 (2%)	10 38
8	H	50/52 (96%)	40 (80%)	8 (16%)	2 (4%)	3 18
9	I	222/224 (99%)	199 (90%)	17 (8%)	6 (3%)	5 26
10	J	248/250 (99%)	232 (94%)	13 (5%)	3 (1%)	13 42
All	All	1885/1905 (99%)	1659 (88%)	172 (9%)	54 (3%)	7 24

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	249	LEU
2	B	138	ALA
5	E	46	LEU
9	I	119	PRO
1	A	285	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	A	337/337 (100%)	317 (94%)	20 (6%)	19 49
2	B	168/168 (100%)	162 (96%)	6 (4%)	35 63
3	C	172/172 (100%)	169 (98%)	3 (2%)	60 78
4	D	139/139 (100%)	138 (99%)	1 (1%)	84 90
5	E	108/108 (100%)	104 (96%)	4 (4%)	34 63
6	F	180/180 (100%)	176 (98%)	4 (2%)	52 74
7	G	65/65 (100%)	64 (98%)	1 (2%)	65 81
8	H	48/48 (100%)	44 (92%)	4 (8%)	11 36
9	I	190/190 (100%)	189 (100%)	1 (0%)	88 93
10	J	228/228 (100%)	224 (98%)	4 (2%)	59 78
All	All	1635/1635 (100%)	1587 (97%)	48 (3%)	45 69

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	193	ASP
6	F	131	ILE
4	D	159	GLU
5	E	45	ARG
6	F	168	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	135	ASN
2	B	147	ASN
6	F	177	ASN
4	D	103	ASN
6	F	133	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	N	1158/3741 (30%)	216 (18%)	36 (3%)

5 of 216 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	N	1225	G
11	N	1229	U
11	N	1230	U
11	N	1231	U
11	N	1233	G

5 of 36 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	N	3231	G
11	N	3477	A
11	N	3283	G
11	N	3391	C
11	N	1582	A

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

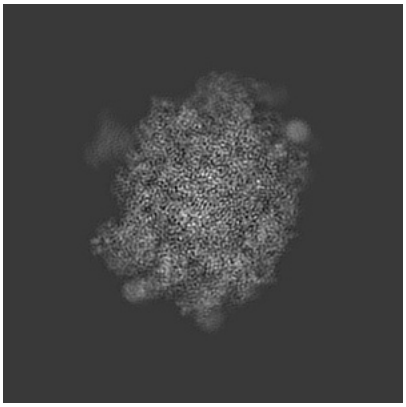
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-3145. These allow visual inspection of the internal detail of the map and identification of artifacts.

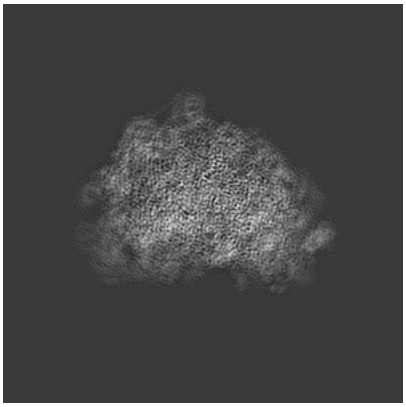
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

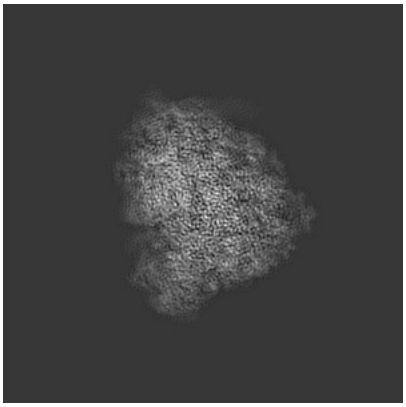
6.1.1 Primary map



X



Y

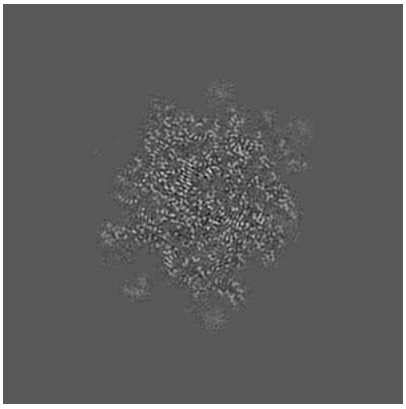


Z

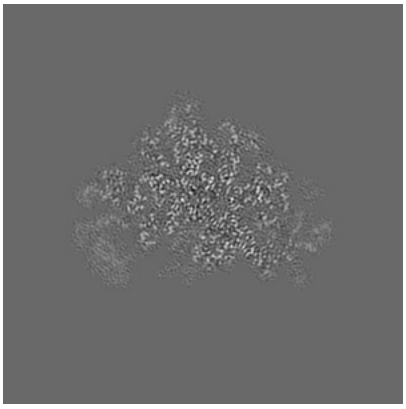
The images above show the map projected in three orthogonal directions.

6.2 Central slices

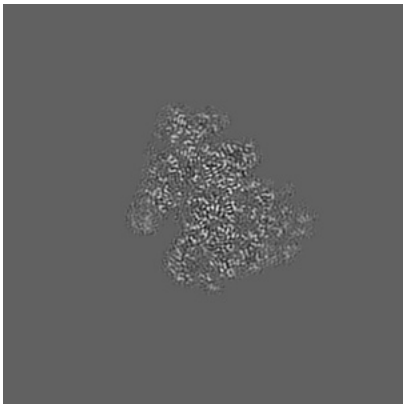
6.2.1 Primary map



X Index: 150



Y Index: 150

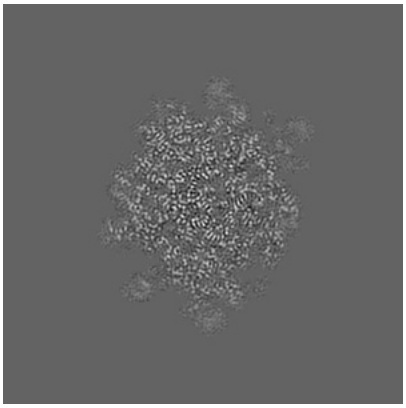


Z Index: 150

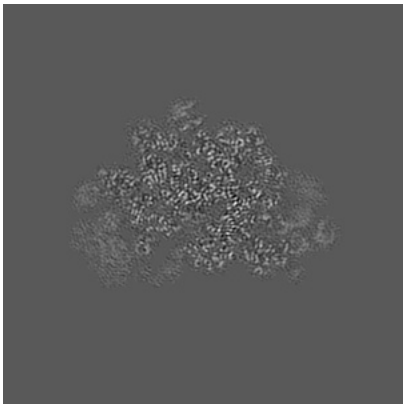
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 153



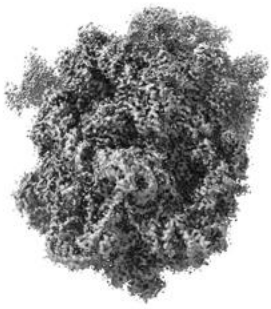
Y Index: 155

Z Index: 161

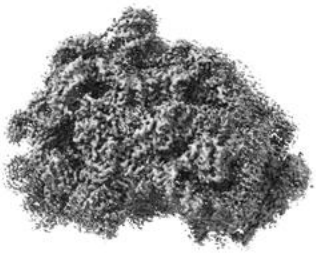
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map



X



Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.14. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

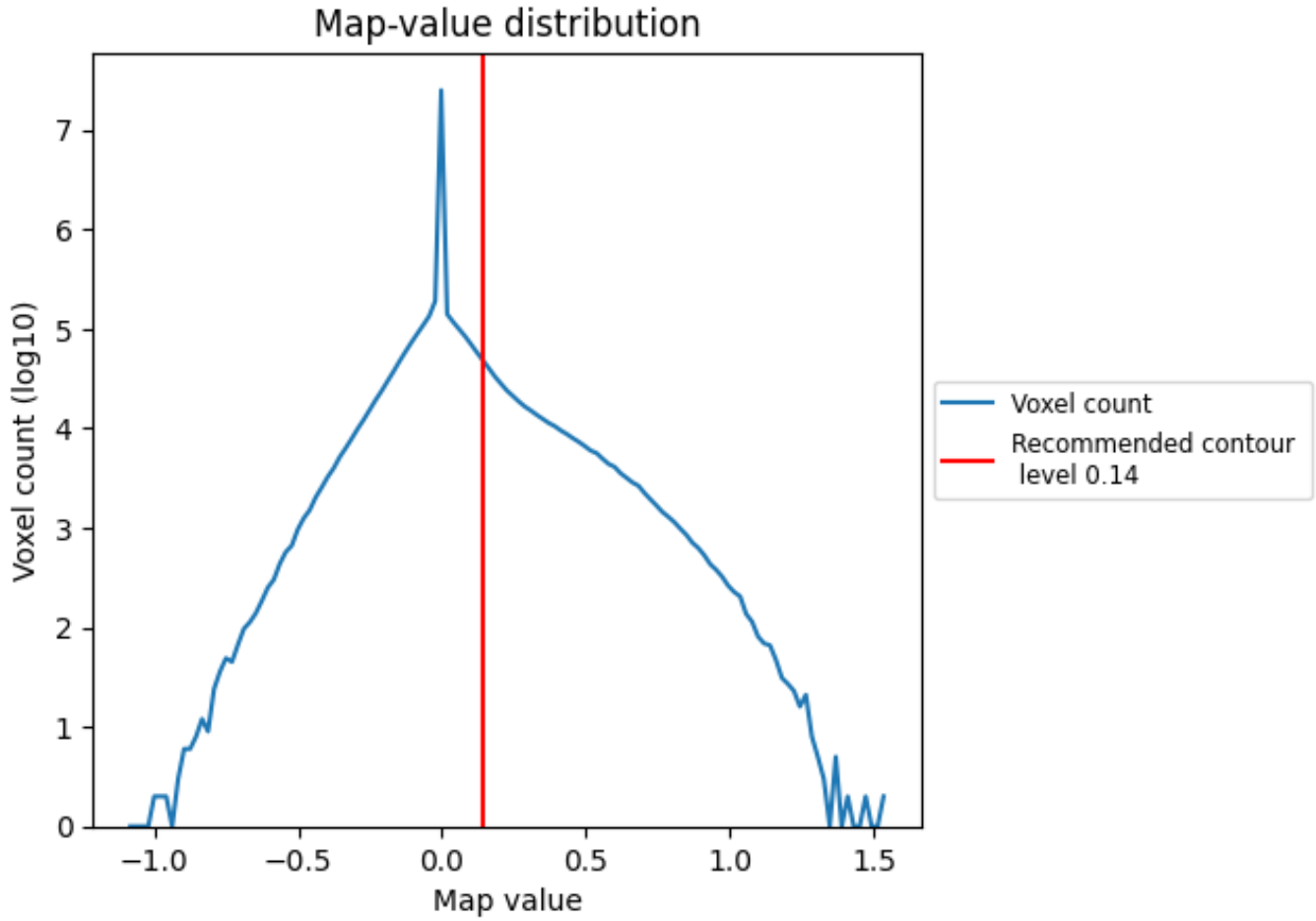
6.5 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

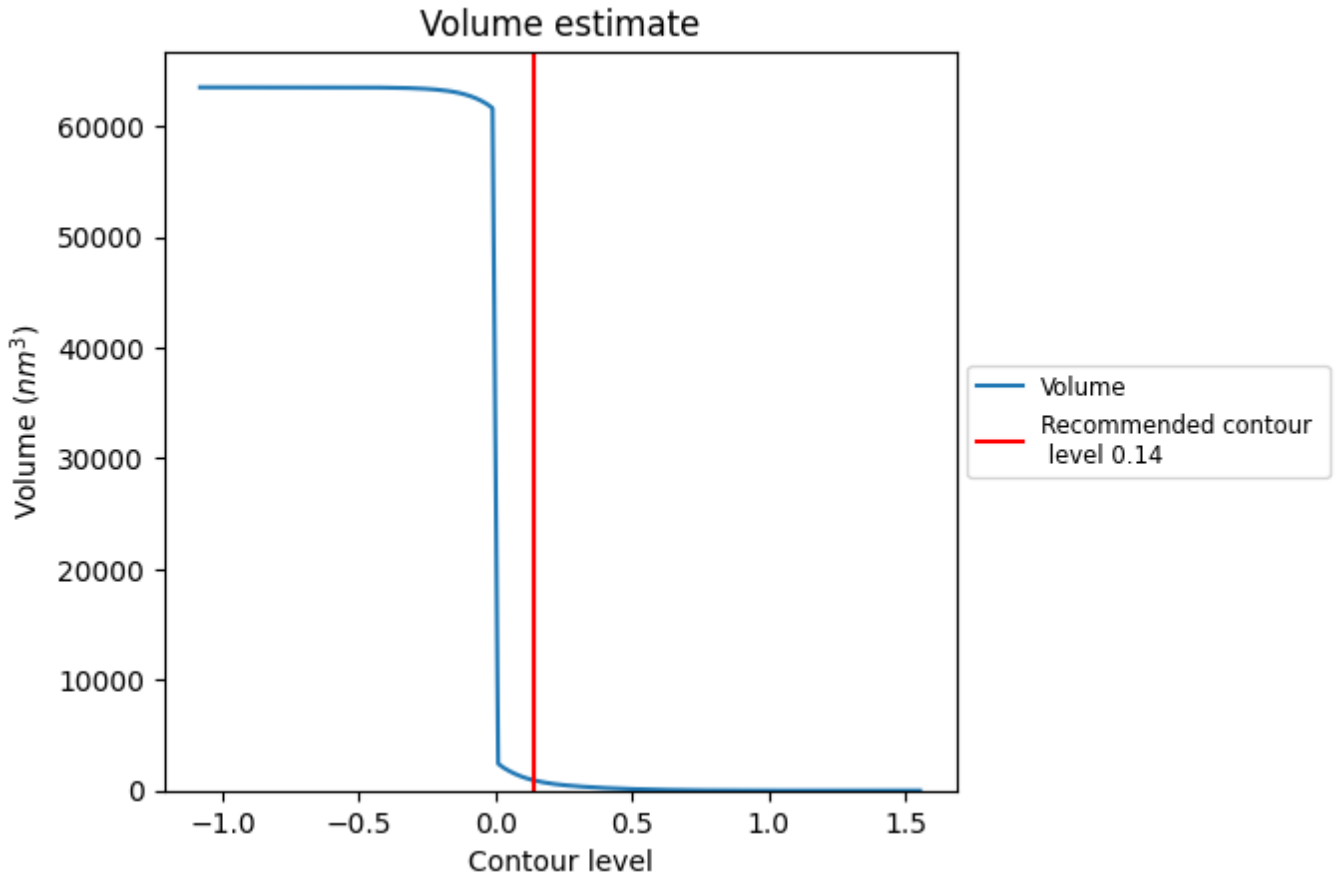
This section contains the results of statistical analysis of the map.

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.

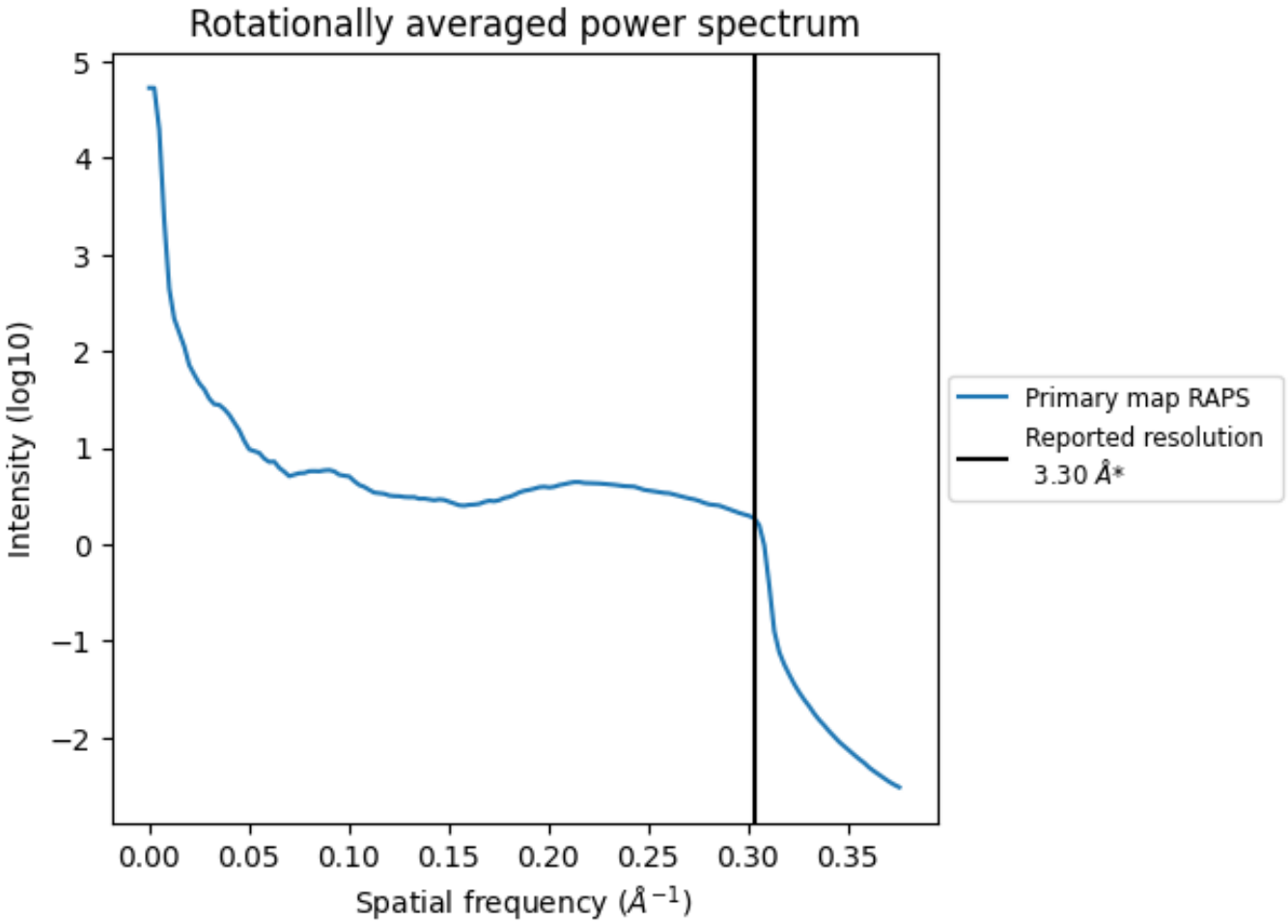
7.2 Volume estimate (i)



The volume at the recommended contour level is 926 nm^3; this corresponds to an approximate mass of 837 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 0.303 Å^{-1}

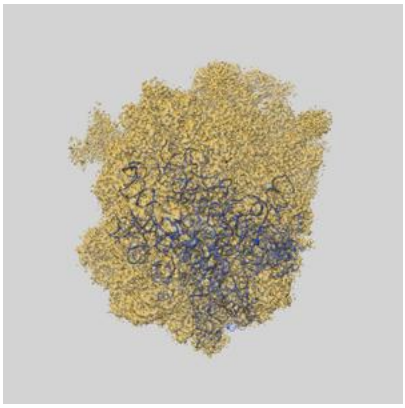
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

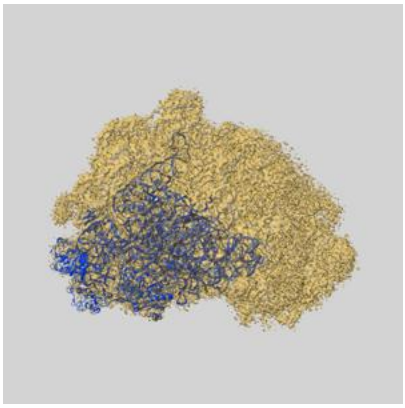
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-3145 and PDB model 5AN9. Per-residue inclusion information can be found in section 3 on page 6.

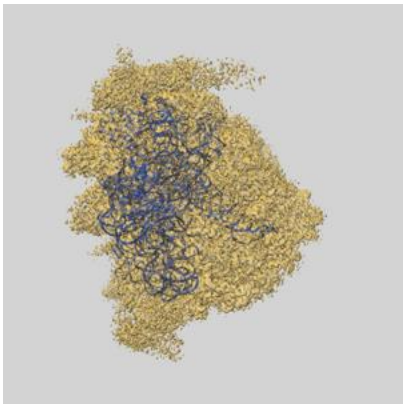
9.1 Map-model overlay



X



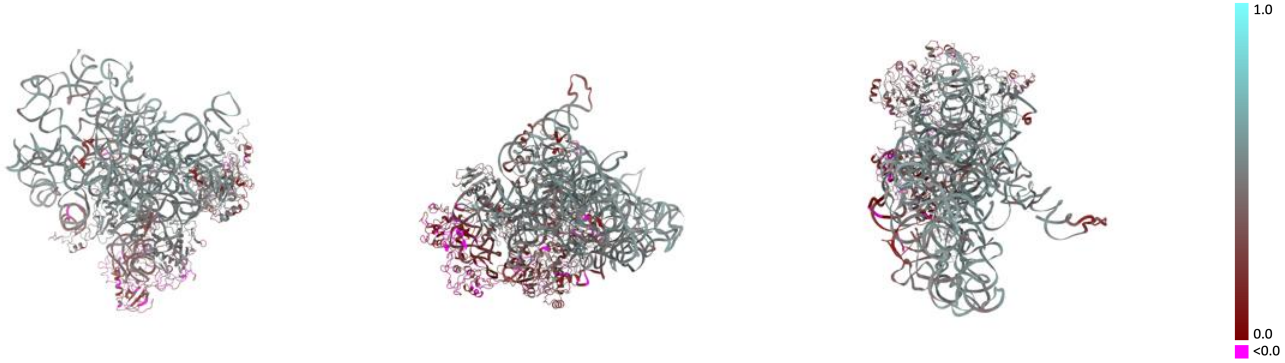
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.14 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.

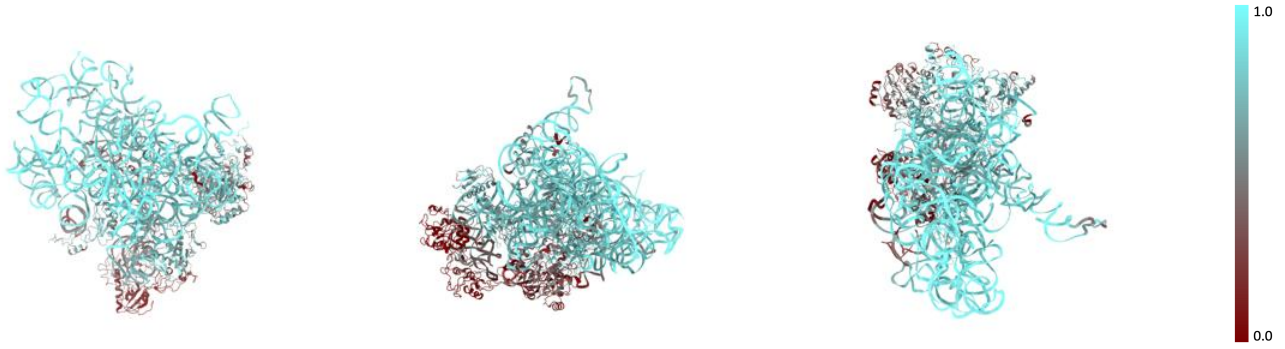
9.2 Q-score mapped to coordinate model (i)



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.

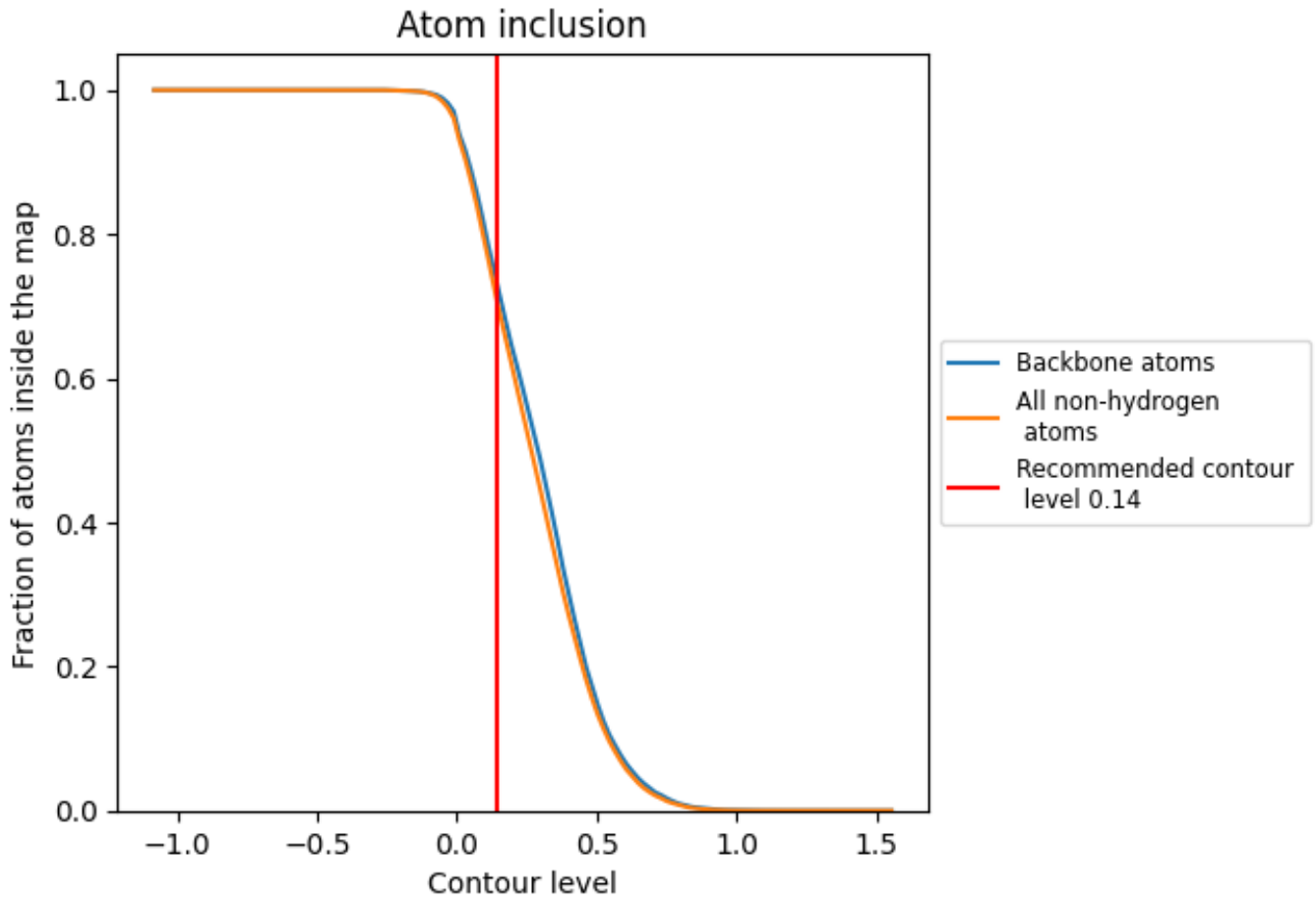
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.14).

9.4 Atom inclusion (i)



At the recommended contour level, 74% of all backbone atoms, 71% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.14) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7128	0.4230
A	0.7032	0.4140
B	0.6619	0.4100
C	0.0742	0.1170
D	0.0909	0.1010
E	0.7392	0.4670
F	0.6843	0.4240
G	0.6261	0.3910
H	0.7167	0.4310
I	0.3289	0.2950
J	0.2843	0.2180
N	0.8508	0.4840