wwPDB EM Validation Summary Report

Dec 10, 2022 – 08:44 am GMT

PDB ID	:	5ANC
EMDB ID	:	EMD-3147
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	:	4.20 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
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:

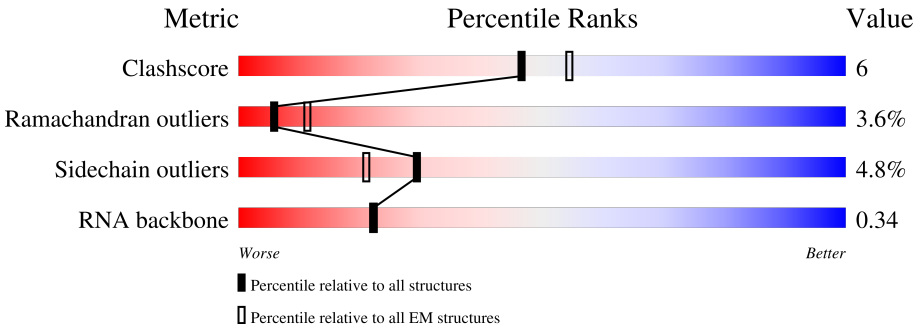
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance

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

The reported resolution of this entry is 4.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
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	70% 26%
2	B	188	5% 75% 24%
3	C	205	55% 95% 5%
4	D	166	41% 90% 10%
5	E	136	79% 18%
6	F	217	77% 20%
7	G	69	80% 19%

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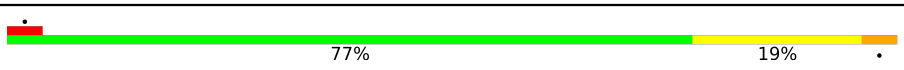
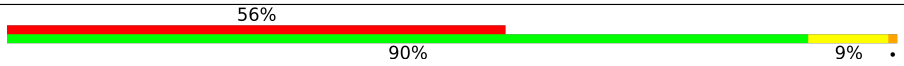
Mol	Chain	Length	Quality of chain
8	H	52	
9	J	250	
10	K	1120	
11	N	3741	

2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 46807 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
1	A	398	Total	C	N	O	S	0	0
			3176	2018	599	547	12		

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

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

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

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

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

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

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

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

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

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

- 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 RIBOSOME MATURATION PROTEIN SBDS.

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

- Molecule 10 is a protein called ELONGATION FACTOR TU GTP-BINDING DOMAIN-CONTAINING PROTEIN 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	1120	Total	C	N	O	S	0	0
			8800	5547	1518	1682	53		

- 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:

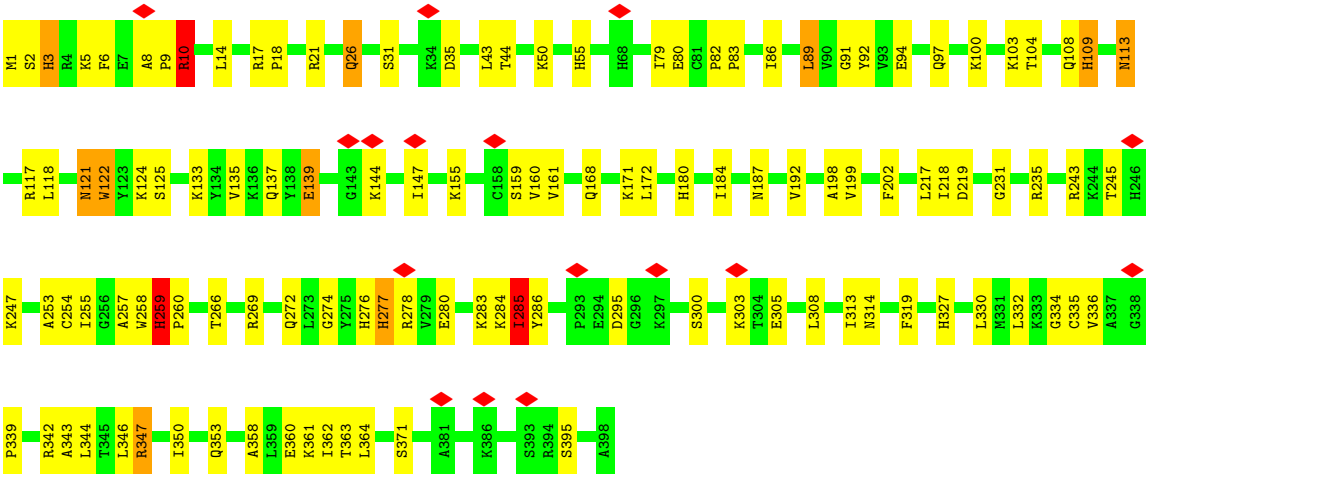
Chain	Residue	Modelled	Actual	Comment	Reference
N	3119	C	G	conflict	GB FR733594.

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.

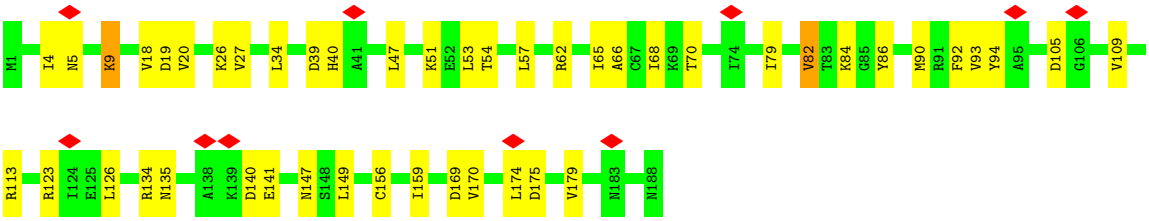
• Molecule 1: 60S RIBOSOMAL PROTEIN L3

Chain A:



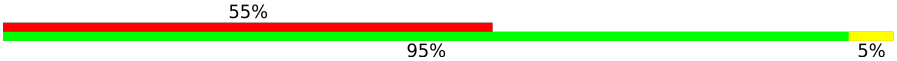
• Molecule 2: 60S RIBOSOMAL PROTEIN L9

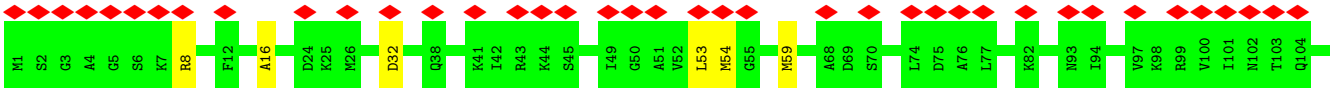
Chain B:

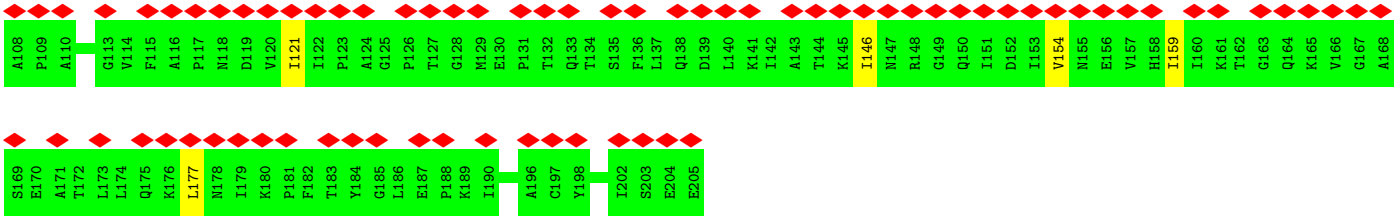


• Molecule 3: 60S ACIDIC RIBOSOMAL PROTEIN P0

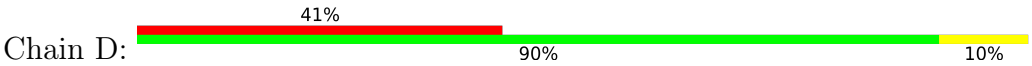
Chain C:

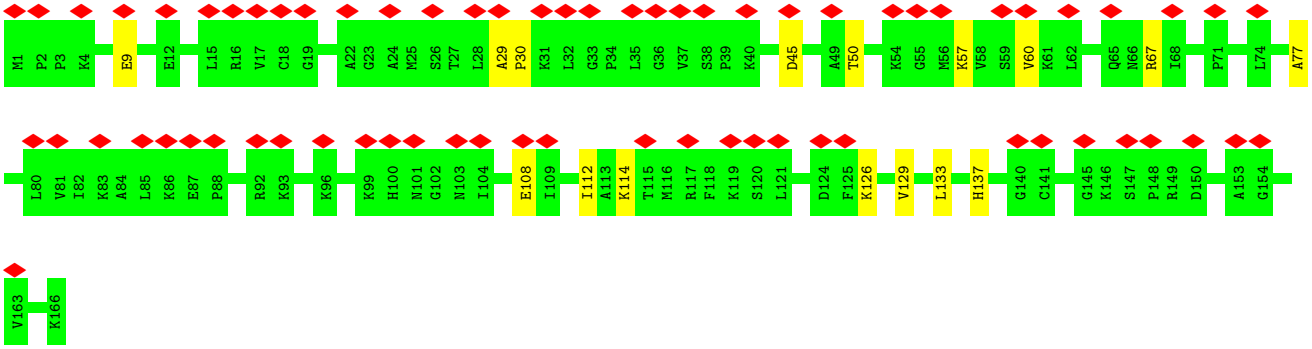




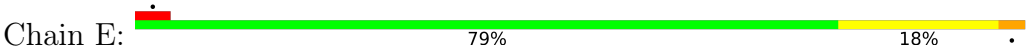


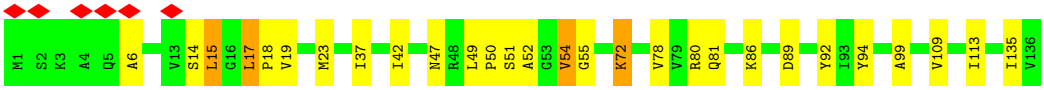
• Molecule 4: 60S RIBOSOMAL PROTEIN L12



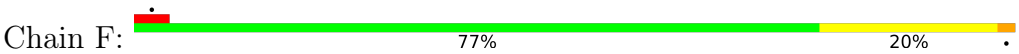


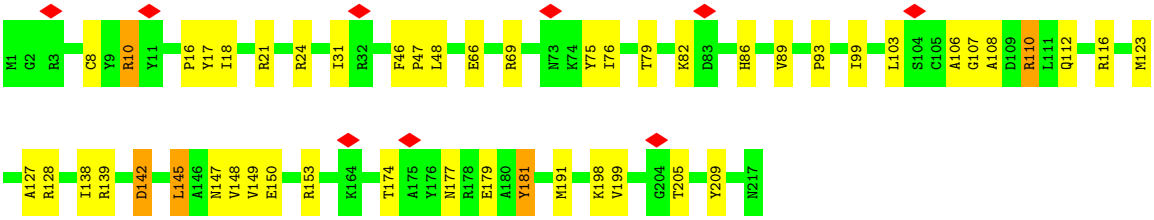
• Molecule 5: 60S RIBOSOMAL PROTEIN L23



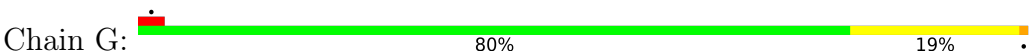


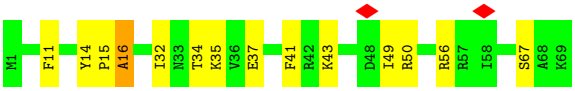
• Molecule 6: 60S RIBOSOMAL PROTEIN L10





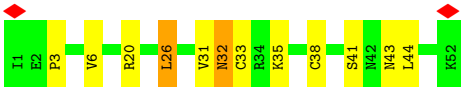
• Molecule 7: 60S RIBOSOMAL PROTEIN L24





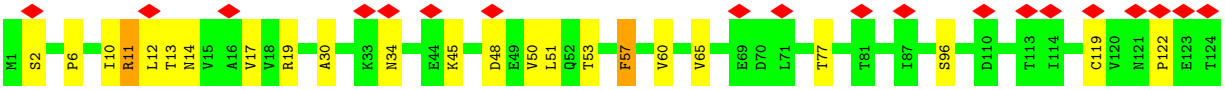
• Molecule 8: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

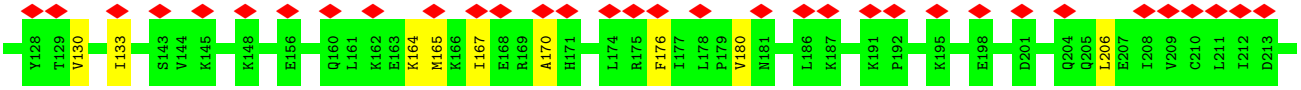
Chain H:

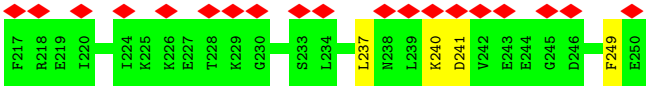


• Molecule 9: RIBOSOME MATURATION PROTEIN SBDS

Chain J:

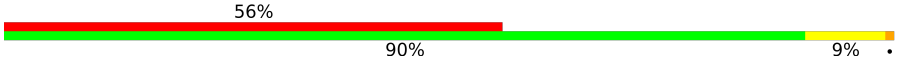


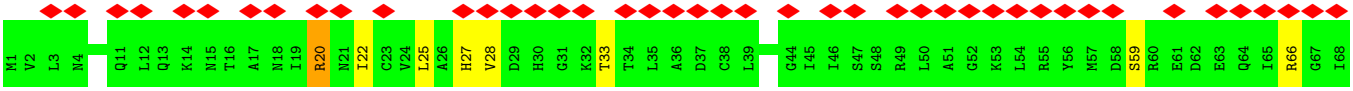


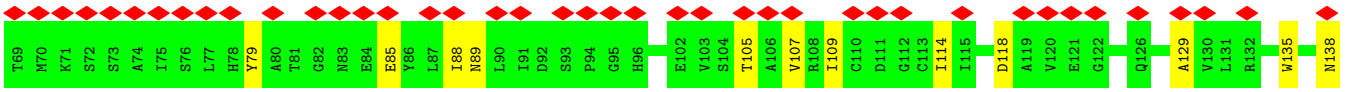


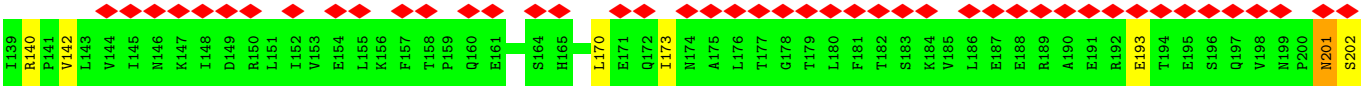
• Molecule 10: ELONGATION FACTOR TU GTP-BINDING DOMAIN-CONTAINING PROTEIN 1

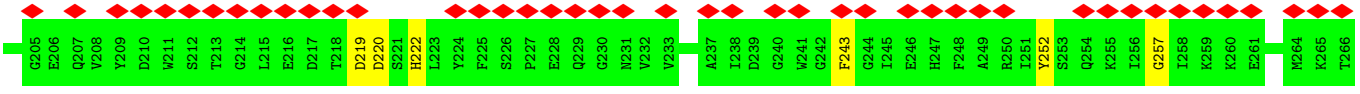
Chain K:

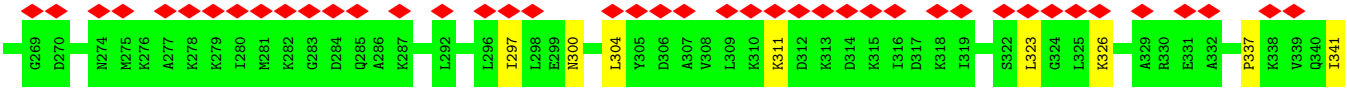


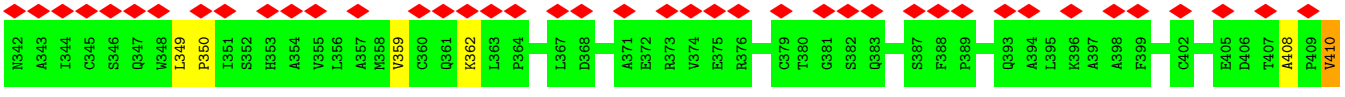


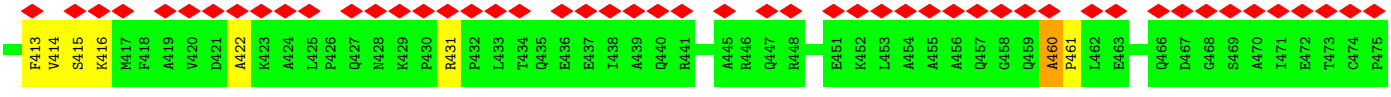


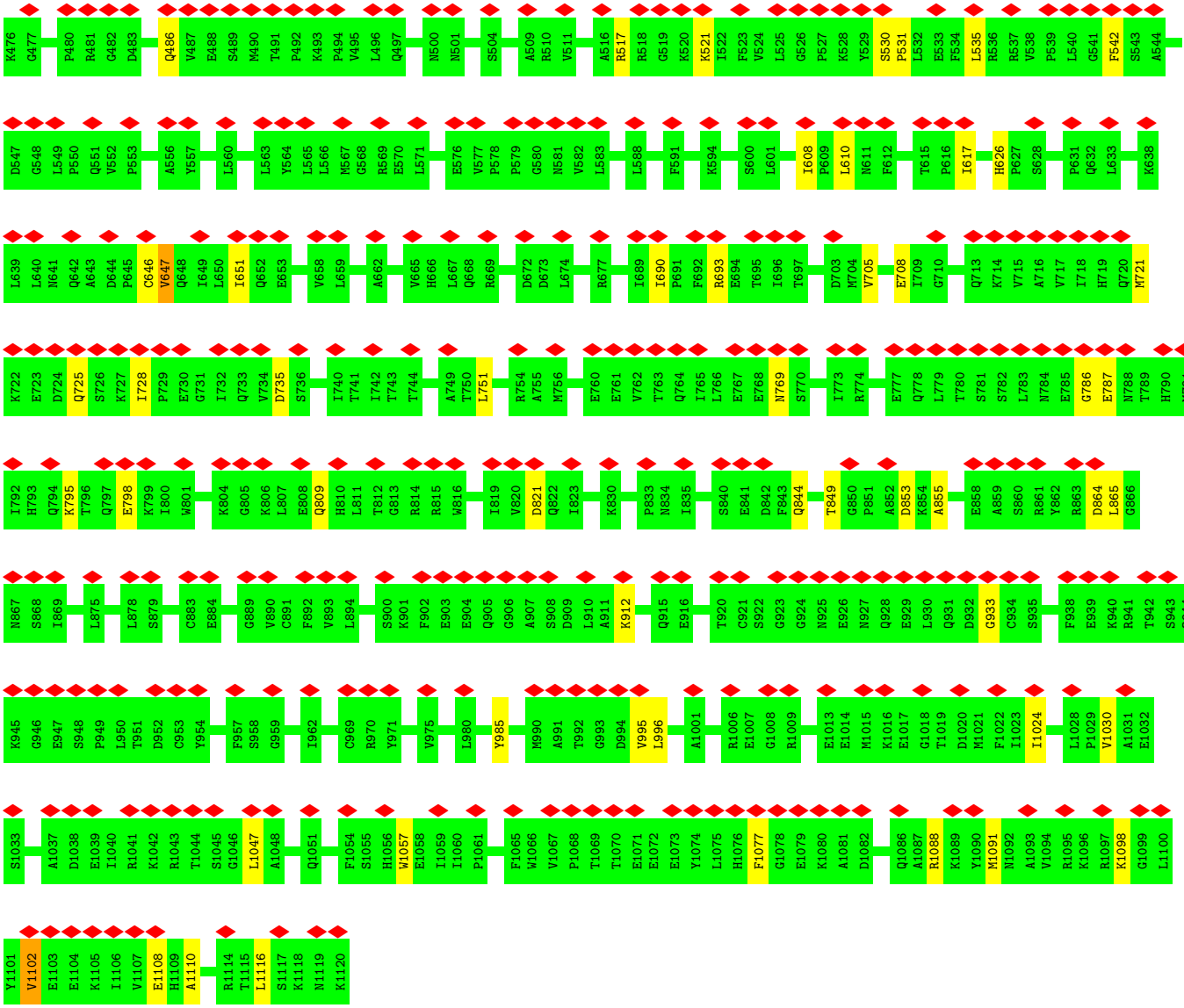






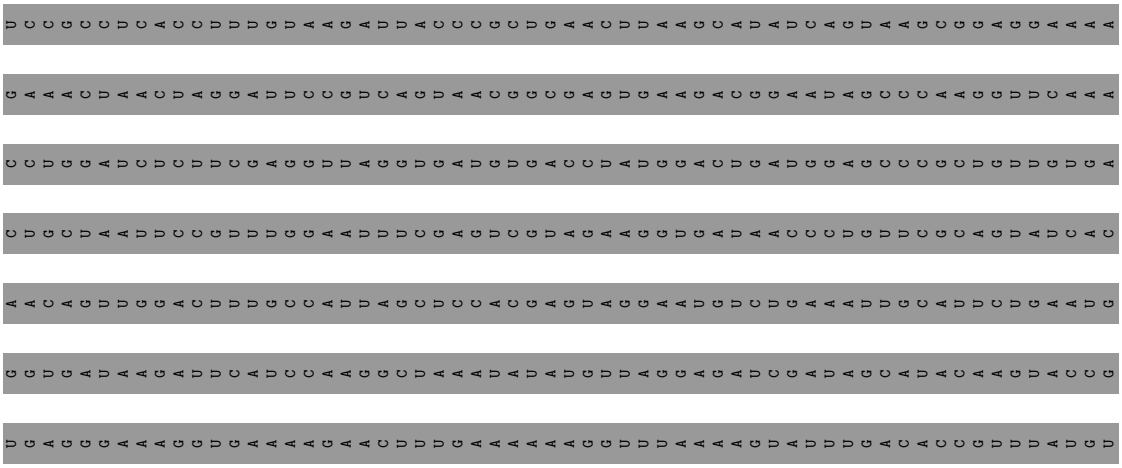


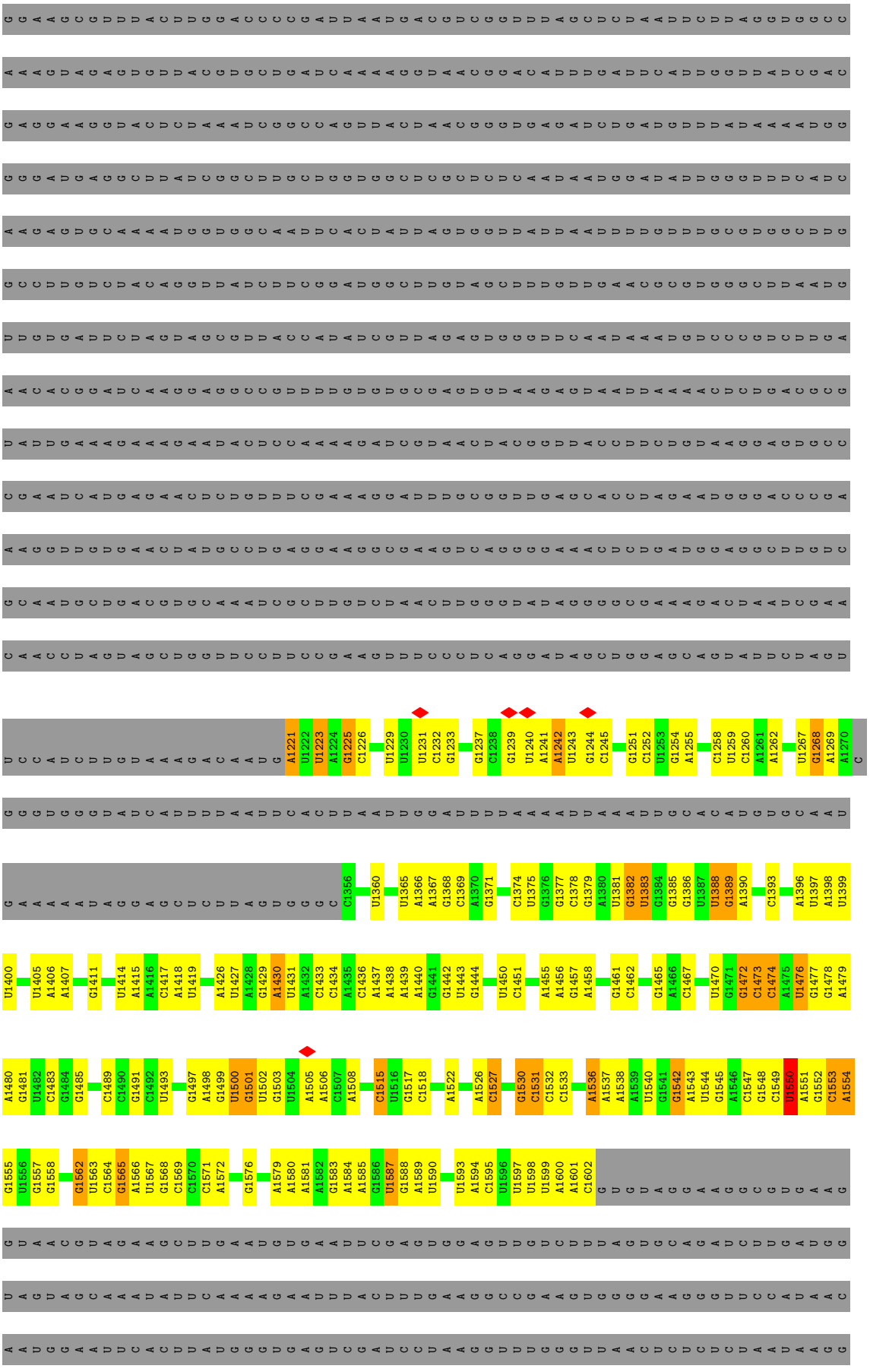


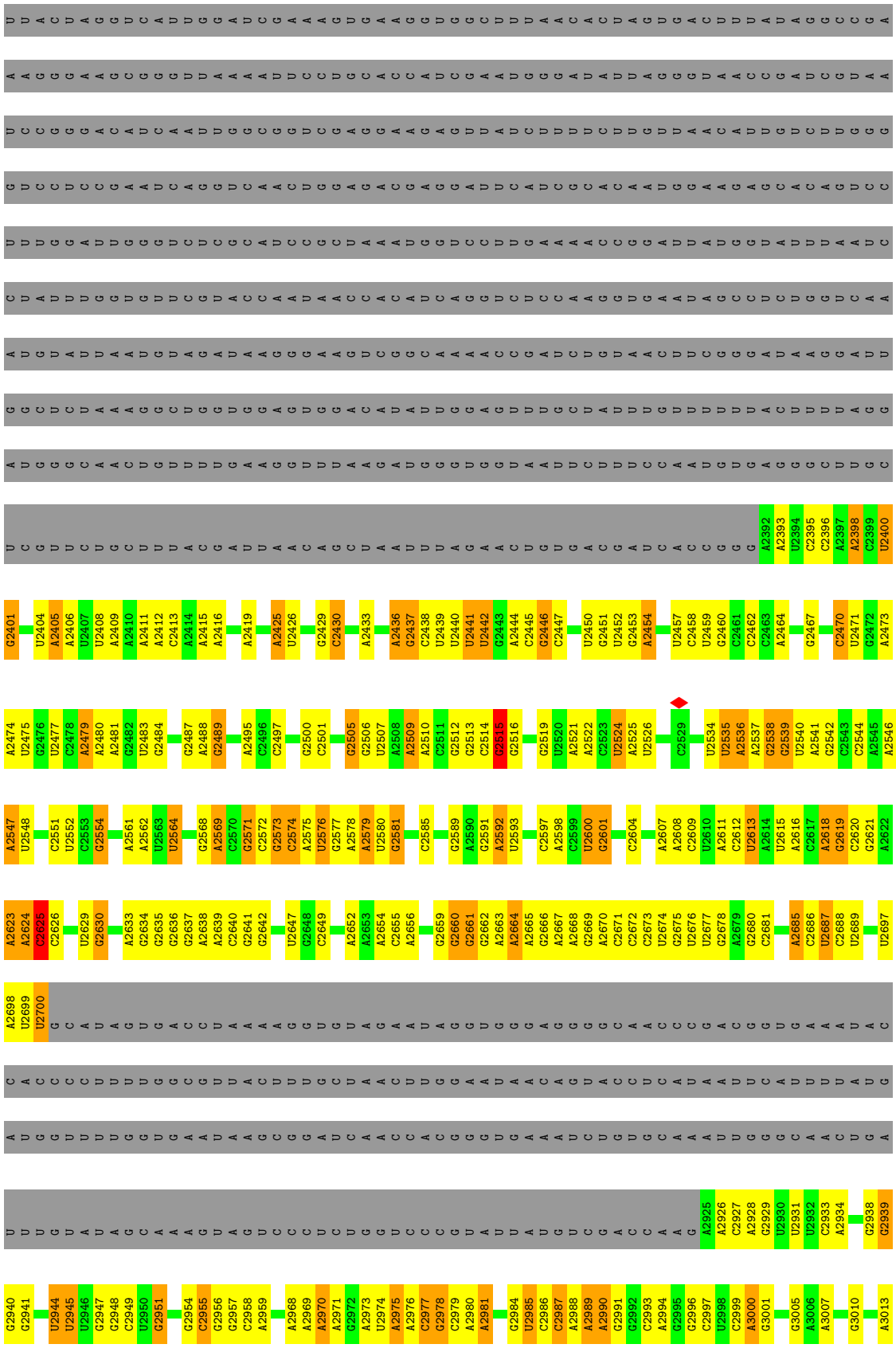


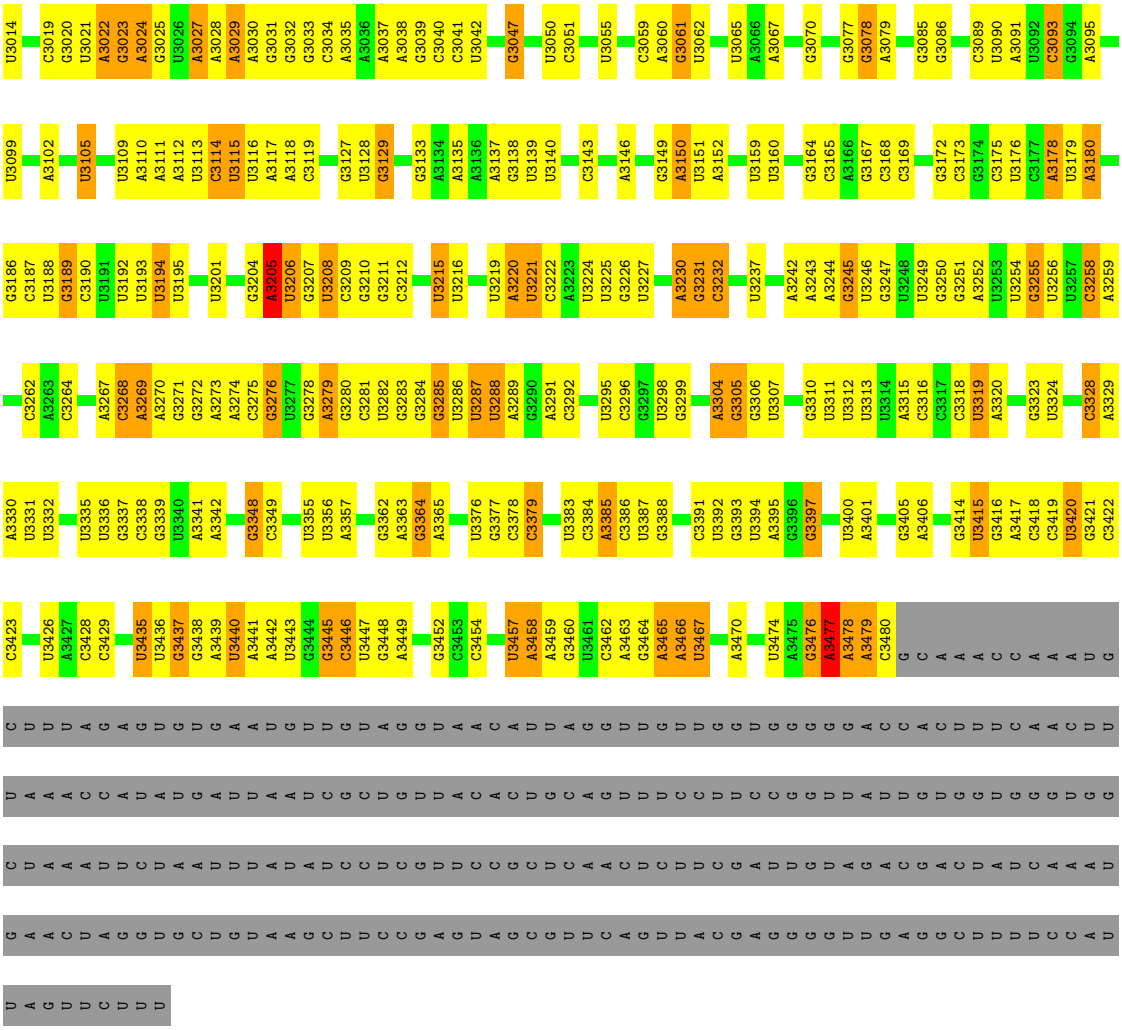
- Molecule 11: 26S RIBOSOMAL RNA

Chain N:





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U3099 A3102 U3105 U3109 A3110 A3111 A3112 U3113 C3114 U3115 U3116 A3117 A3118 C3119 G3127 U3128 G3129 G3133 A3134 A3135 A3136 A3137 G3138 U3139 U3140 C3143 A3146 G3149 A3150 U3151 A3152 U3159 U3160 G3164 C3165 A3166 G3167 C3168 C3169 G3172 C3173 G3174 C3175 U3176 C3177 A3178 U3179 A3180
G3186 C3187 U3188 G3189 C3190 U3191 U3192 U3193 U3194 U3195 U3201 G3204 A3205 U3206 G3207 U3208 C3209 G3210 G3211 C3212 U3215 U3216 U3219 A3220 U3221 C3222 A3223 U3224 U3225 G3226 U3227 A3230 G3231 C3232 U3237 A3242 A3243 A3244 G3245 U3246 G3247 U3248 U3249 G3250 G3251 A3252 U3253 U3254 G3255 U3256 U3257 C3258 A3259
C3262 A3263 C3264 A3267 C3268 A3269 A3270 G3271 G3272 A3273 A3274 C3275 G3276 U3277 G3278 A3279 G3280 C3281 U3282 G3283 G3284 G3285 U3286 U3287 U3288 A3289 G3290 A3291 C3292 U3295 C3296 G3297 U3298 G3299 A3304 G3305 G3306 U3307 G3310 U3311 U3312 U3313 U3314 A3315 C3316 C3317 C3318 U3319 A3320 G3323 U3324 C3328 A3329
A3330 U3331 U3332 U3335 U3336 G3337 C3338 G3339 U3340 A3341 A3342 G3348 C3349 U3355 U3356 A3357 G3362 A3363 G3364 A3365 U3376 G3377 C3378 C3379 U3383 C3384 A3385 C3386 U3387 G3388 C3391 U3392 G3393 U3394 A3395 G3396 G3397 U3400 A3401 G3405 A3406 G3414 U3415 G3416 A3417 C3418 C3419 U3420 G3421 C3422
C3423 U3426 A3427 C3428 C3429 U3435 U3436 G3437 G3438 A3439 U3440 A3441 A3442 U3443 G3444 G3445 C3446 U3447 G3448 A3449 G3452 C3453 C3454 U3457 A3458 A3459 G3460 U3461 C3462 A3463 G3464 A3465 A3466 U3467 A3470 U3474 A3475 G3476 A3477 A3478 A3479 C3480 G C A A C U A A C U A A C U

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	9794	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	0.676	Depositor
Minimum map value	-0.416	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.06	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	0.57	0/3241	0.86	1/4339 (0.0%)
2	B	0.42	0/1510	0.73	0/2030
3	C	0.39	0/1592	0.55	0/2142
4	D	0.40	0/1265	0.57	0/1702
5	E	0.48	0/1032	0.81	1/1386 (0.1%)
6	F	0.51	0/1752	0.79	1/2345 (0.0%)
7	G	0.53	0/600	0.79	0/801
8	H	0.46	0/433	0.84	0/571
9	J	0.45	0/2038	0.74	1/2727 (0.0%)
10	K	0.40	0/8969	0.63	0/12124
11	N	0.41	2/27702 (0.0%)	0.80	14/43160 (0.0%)
All	All	0.43	2/50134 (0.0%)	0.76	18/73327 (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	5
6	F	0	1
9	J	0	1
11	N	0	1
All	All	0	8

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	N	1550	U	O3'-P	5.07	1.67	1.61
11	N	2405	A	O3'-P	5.07	1.67	1.61

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	N	1221	A	C5'-C4'-O4'	7.66	118.29	109.10
11	N	2625	C	C2'-C3'-O3'	7.09	125.10	109.50
11	N	1221	A	C5'-C4'-C3'	6.37	126.19	116.00
11	N	2515	G	C2'-C3'-O3'	6.20	123.62	113.70
11	N	3421	G	C2'-C3'-O3'	6.18	123.59	113.70

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	GLN	Peptide
1	A	122	TRP	Peptide
1	A	277	HIS	Peptide
1	A	5	LYS	Peptide
1	A	9	PRO	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	56	0
2	B	1491	0	1555	19	0
3	C	1571	0	1657	1	0
4	D	1245	0	1338	4	0
5	E	1017	0	1076	14	0
6	F	1721	0	1778	22	0
7	G	586	0	601	5	0
8	H	427	0	483	6	0
9	J	2015	0	2112	15	0
10	K	8800	0	8840	27	0
11	N	24758	0	12487	382	0
All	All	46807	0	35246	522	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 522 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)
11:N:3224:U:N3	11:N:3466:A:C6	2.39	0.90
11:N:3224:U:C4	11:N:3466:A:N6	2.42	0.88
11:N:3224:U:N3	11:N:3466:A:N6	2.23	0.87
11:N:1598:U:H2'	11:N:1599:U:C6	2.13	0.84
1:A:79:ILE:HG21	1:A:344:LEU:HD12	1.63	0.81

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%)	313 (79%)	61 (15%)	22 (6%)	2	21
2	B	186/188 (99%)	159 (86%)	20 (11%)	7 (4%)	3	27
3	C	203/205 (99%)	168 (83%)	30 (15%)	5 (2%)	5	35
4	D	164/166 (99%)	131 (80%)	29 (18%)	4 (2%)	6	36
5	E	134/136 (98%)	113 (84%)	15 (11%)	6 (4%)	2	25
6	F	215/217 (99%)	171 (80%)	35 (16%)	9 (4%)	3	26
7	G	67/69 (97%)	52 (78%)	11 (16%)	4 (6%)	1	20
8	H	50/52 (96%)	41 (82%)	8 (16%)	1 (2%)	7	40
9	J	248/250 (99%)	214 (86%)	26 (10%)	8 (3%)	4	31
10	K	1118/1120 (100%)	939 (84%)	144 (13%)	35 (3%)	4	31
All	All	2781/2801 (99%)	2301 (83%)	379 (14%)	101 (4%)	6	28

5 of 101 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	44	THR
1	A	137	GLN
1	A	253	ALA

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Mol	Chain	Res	Type
1	A	259	HIS
1	A	395	SER

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%)	305 (90%)	32 (10%)	8 30
2	B	168/168 (100%)	157 (94%)	11 (6%)	17 44
3	C	172/172 (100%)	168 (98%)	4 (2%)	50 70
4	D	139/139 (100%)	134 (96%)	5 (4%)	35 60
5	E	108/108 (100%)	102 (94%)	6 (6%)	21 48
6	F	180/180 (100%)	167 (93%)	13 (7%)	14 41
7	G	65/65 (100%)	61 (94%)	4 (6%)	18 46
8	H	48/48 (100%)	44 (92%)	4 (8%)	11 37
9	J	228/228 (100%)	218 (96%)	10 (4%)	28 54
10	K	975/975 (100%)	948 (97%)	27 (3%)	43 65
All	All	2420/2420 (100%)	2304 (95%)	116 (5%)	29 52

5 of 116 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	94	TYR
10	K	787	GLU
7	G	11	PHE
10	K	751	LEU
10	K	410	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
9	J	52	GLN

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Mol	Chain	Res	Type
10	K	793	HIS
10	K	30	HIS
10	K	845	ASN
10	K	500	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	N	1159/3741 (30%)	362 (31%)	46 (3%)

5 of 362 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	N	1223	U
11	N	1225	G
11	N	1229	U
11	N	1231	U
11	N	1232	C

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	N	3070	G
11	N	3287	U
11	N	3115	U
11	N	3205	A
11	N	3316	C

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 (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

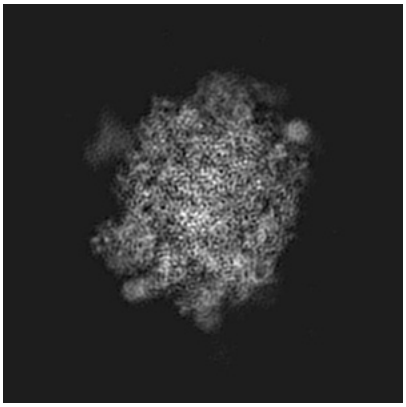
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-3147. These allow visual inspection of the internal detail of the map and identification of artifacts.

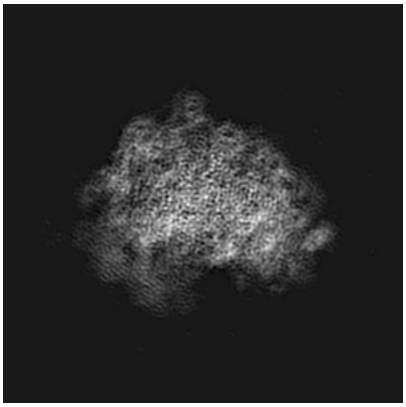
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

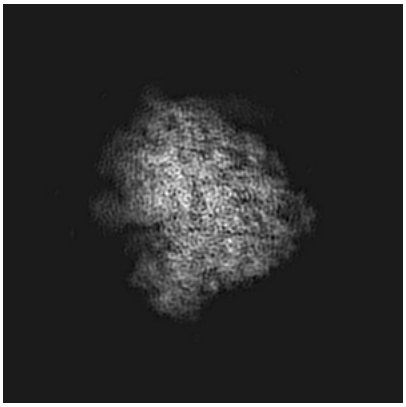
6.1.1 Primary map



X



Y

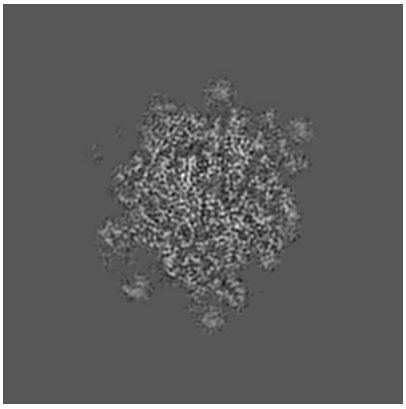


Z

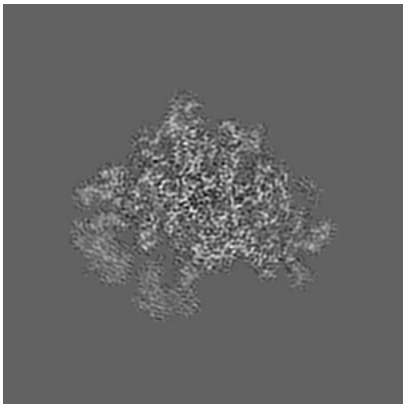
The images above show the map projected in three orthogonal directions.

6.2 Central slices

6.2.1 Primary map



X Index: 150



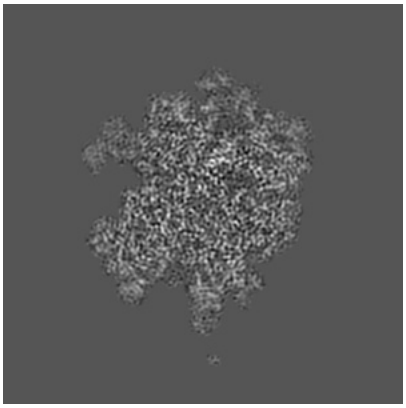
Y Index: 150

Z Index: 150

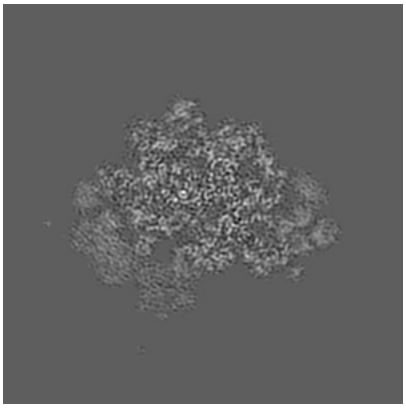
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

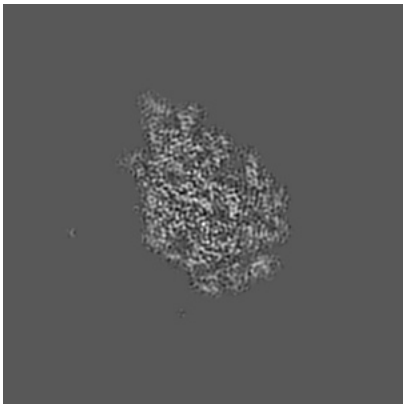
6.3.1 Primary map



X Index: 136



Y Index: 155



Z Index: 171

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 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

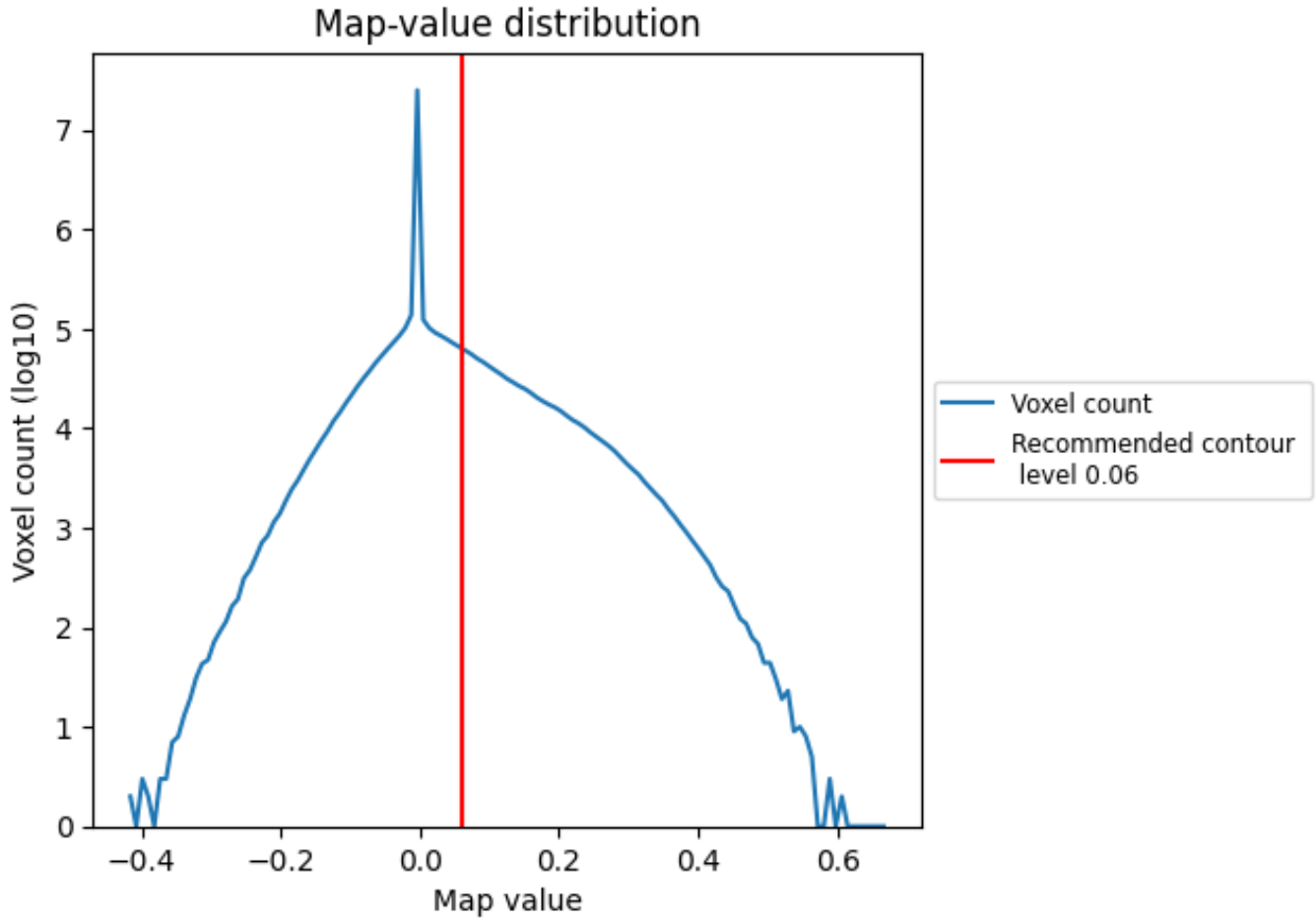
6.5 Mask visualisation (i)

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

7 Map analysis

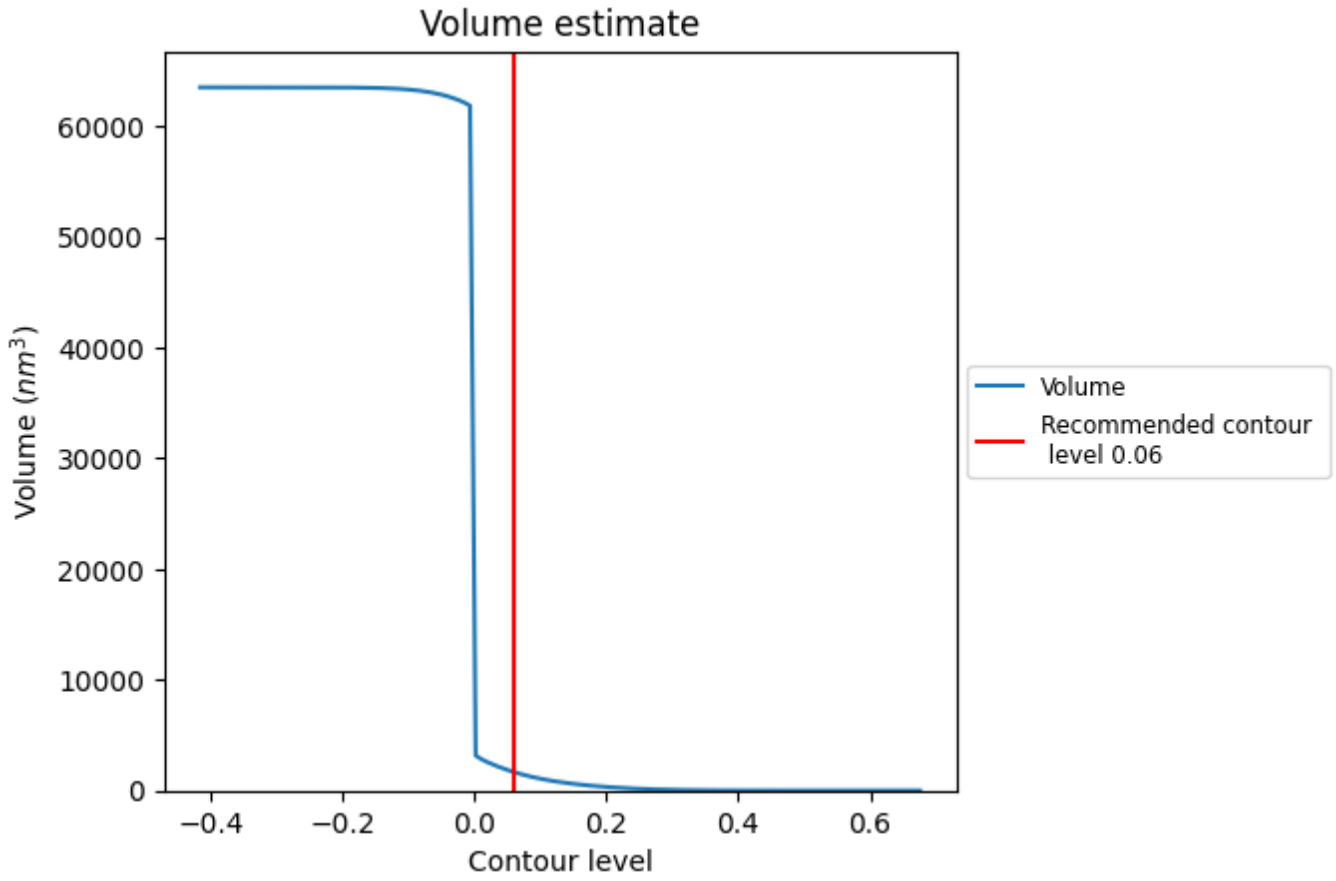
This section contains the results of statistical analysis of the map.

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.

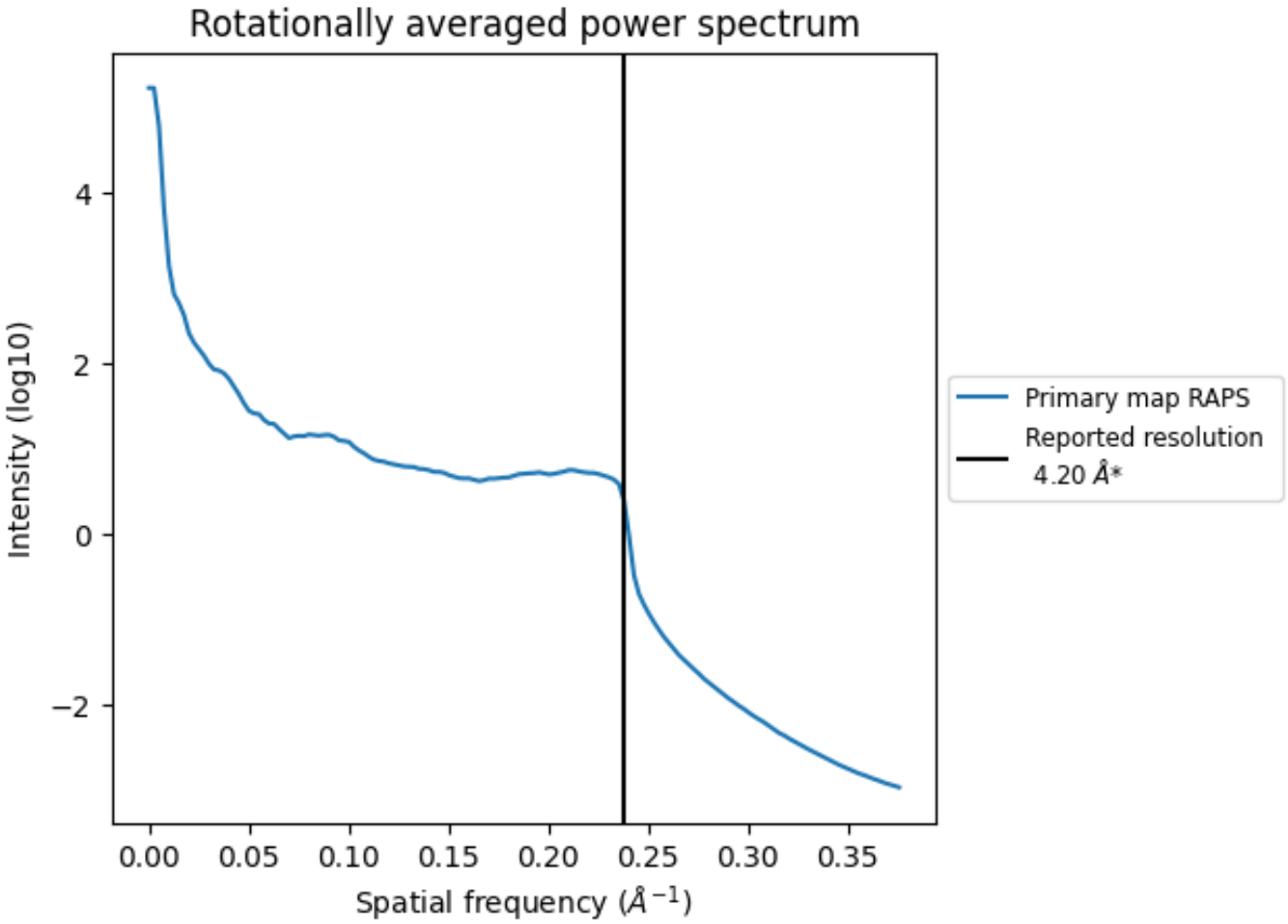
7.2 Volume estimate (i)



The volume at the recommended contour level is 1667 nm^3; this corresponds to an approximate mass of 1506 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 0.238 Å^{-1}

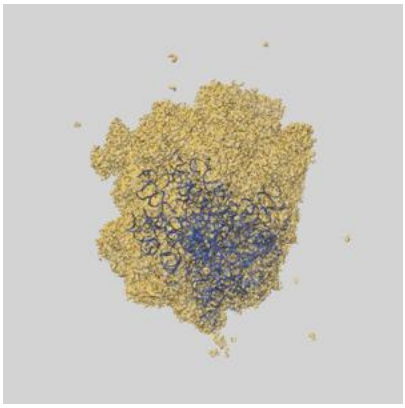
8 Fourier-Shell correlation (i)

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

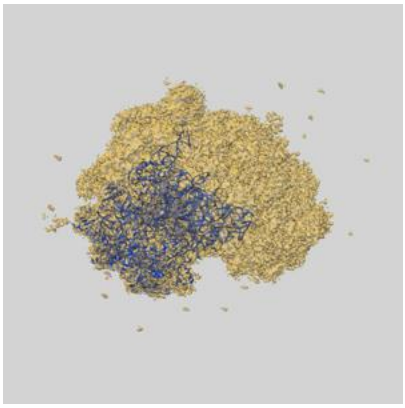
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-3147 and PDB model 5ANC. Per-residue inclusion information can be found in section 3 on page 6.

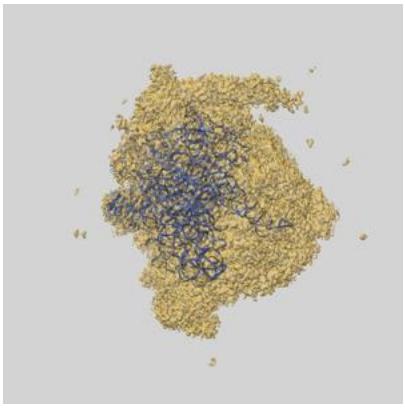
9.1 Map-model overlay



X



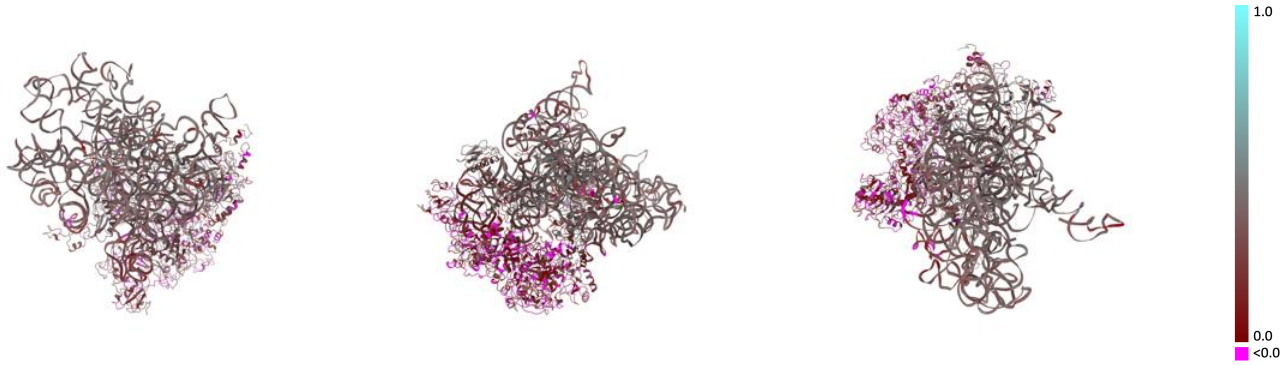
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06 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.

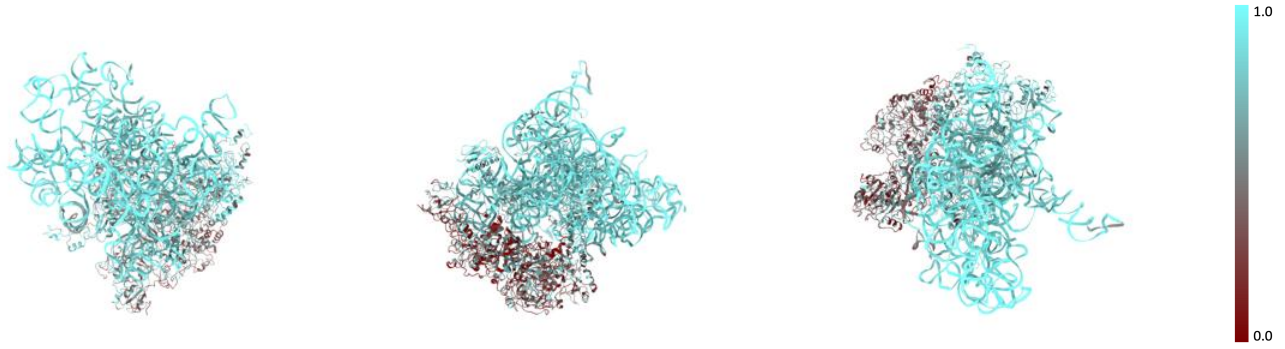
9.2 Q-score mapped to coordinate model (i)



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.

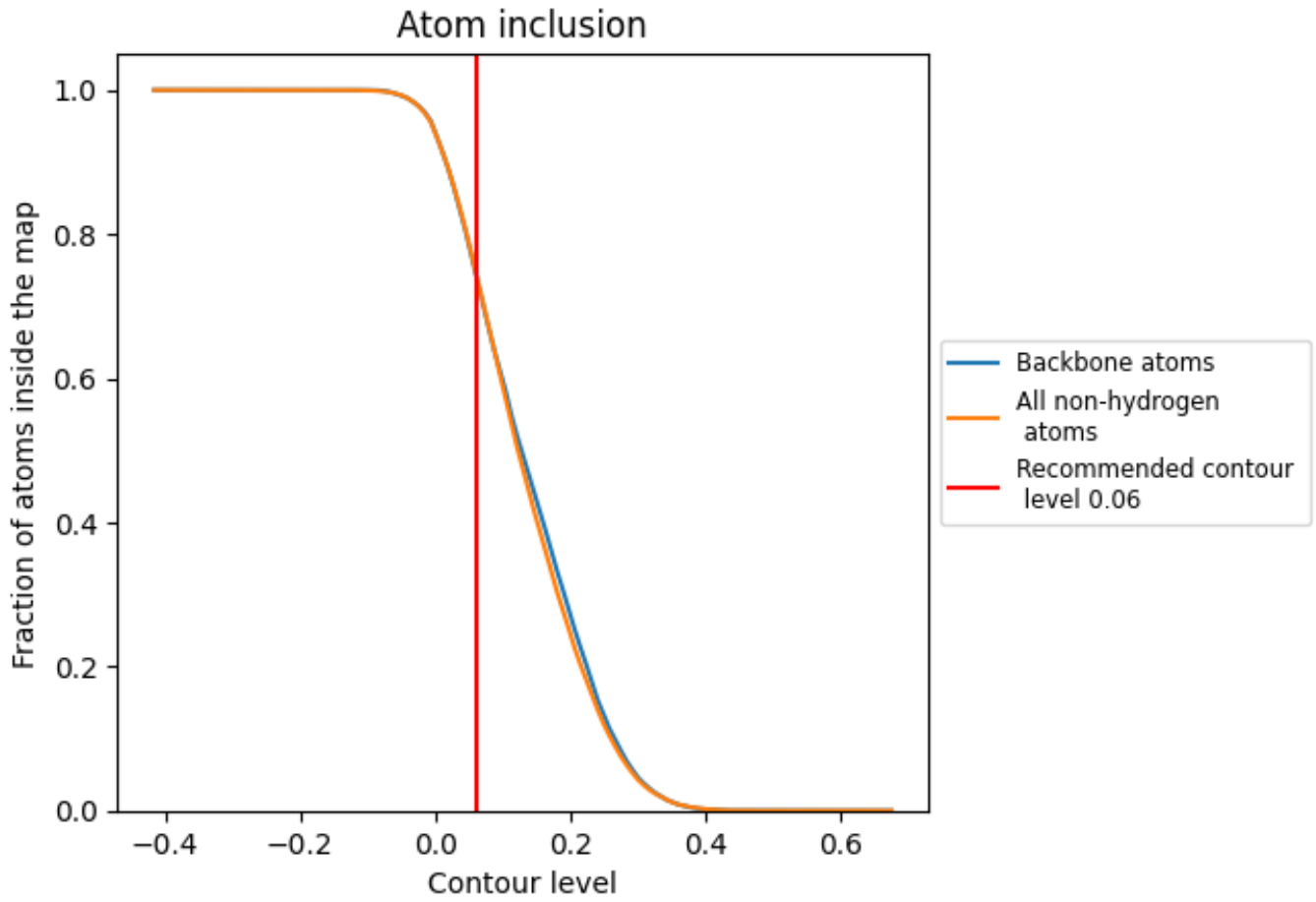
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.06).

9.4 Atom inclusion (i)



At the recommended contour level, 74% of all backbone atoms, 75% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7475	0.2870
A	0.8236	0.3410
B	0.7874	0.3300
C	0.3742	0.1340
D	0.4773	0.1360
E	0.8245	0.3670
F	0.8037	0.3540
G	0.8060	0.2920
H	0.8378	0.3570
J	0.5685	0.2110
K	0.3674	0.1140
N	0.9100	0.3540