



## wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:32 PM UTC

PDB ID : 6ND4 / pdb\_00006nd4  
EMDB ID : EMD-0441  
Title : Conformational switches control early maturation of the eukaryotic small ribosomal subunit  
Authors : Hunziker, M.; Barandun, J.; Klinge, S.  
Deposited on : 2018-12-13  
Resolution : 4.30 Å(reported)  
Based on initial model : 5WLC

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

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

EMDB validation analysis : 0.0.1.dev132  
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) : 2.49



Continued from previous page...

Mol	Chain	Length	Quality of chain
6	J	513	45% 90% 6%
7	K	183	28% 67% 33%
8	L	643	6% 70% 26%
9	M	1769	24% 76%
10	N	727	24% 86% 7% 7%
11	O	923	6% 83% 7% 10%
12	P	421	42% 82% 15%
13	Q	917	32% 86% 7% 6%
14	R	736	69% 91% 8%
15	S	594	77% 19%
16	T	939	81% 5% 14%
17	U	489	30% 77% 7% 17%
18	W	554	62% 7% 31%
19	Z	183	7% 86% 6% 8%
20	A	593	95%
21	D	214	12% 11% 88%
22	a	494	47% 73% 26%
23	b	503	41% 82% 16%
24	c	327	41% 57% 5% 38%
24	d	327	69% 67% 30%
25	e	126	88% 8%
25	f	126	96% 94%
26	g	573	68% 66% 32%
27	l	189	13% 13% 87%
28	x	24	50% 100%

## 2 Entry composition i

There are 28 unique types of molecules in this entry. The entry contains 63993 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 5'ETS rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	0	408	8594	3839	1488	2860	407	0	0

- Molecule 2 is a RNA chain called 18S rRNA 5' domain start.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	1	15	241	105	22	99	15	0	0

- Molecule 3 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	2	146	3106	1390	554	1016	146	0	0

- Molecule 4 is a protein called Utp17.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	H	834	4132	2464	834	834	0	0

- Molecule 5 is a protein called Utp8.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	I	487	2427	1453	487	487	0	0

- Molecule 6 is a protein called Utp15.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	J	493	2441	1455	493	493	0	0

- Molecule 7 is a protein called Utp9.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	K	123	612	366	123	123	0	0

- Molecule 8 is a protein called Utp5.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	L	473	2344	1398	473	473	0	0

- Molecule 9 is a protein called Utp10.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	M	431	2151	1289	431	431	0	0

- Molecule 10 is a protein called Utp4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	N	678	3355	1999	678	678	0	0

- Molecule 11 is a protein called Utp1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	O	832	4111	2447	832	832	0	0

- Molecule 12 is a protein called Utp6.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	P	359	1786	1068	359	359	0	0

- Molecule 13 is a protein called Utp12.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	Q	862	4262	2538	862	862	0	0

- Molecule 14 is a protein called Utp13.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	R	725	3604	2154	725	725	0	0

- Molecule 15 is a protein called Utp18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	S	481	2372	1410	481	481	0	0

- Molecule 16 is a protein called Utp21.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	T	812	4003	2379	812	812	0	0

- Molecule 17 is a protein called Sof1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	U	407	2014	1200	407	407	0	0

- Molecule 18 is a protein called Utp7.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	W	385	1895	1125	385	385	0	0

- Molecule 19 is a protein called Imp3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
19	Z	169	840	502	169	169	0	0

- Molecule 20 is a protein called Mpp10.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
20	A	31	155	93	31	31	0	0

- Molecule 21 is a protein called Bud21.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	D	25	Total	C	N	O	0	0
			124	74	25	25		

- Molecule 22 is a protein called Nop56.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	a	368	Total	C	N	O	0	0
			1822	1086	368	368		

- Molecule 23 is a protein called Nop58.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	b	425	Total	C	N	O	0	0
			2109	1259	425	425		

- Molecule 24 is a protein called Nop1.1.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	c	203	Total	C	N	O	0	0
			1000	594	203	203		
24	d	228	Total	C	N	O	0	0
			1122	666	228	228		

- Molecule 25 is a protein called Snu13.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	e	121	Total	C	N	O	0	0
			601	359	121	121		
25	f	121	Total	C	N	O	0	0
			601	359	121	121		

- Molecule 26 is a protein called Rrp9.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	g	391	Total	C	N	O	0	0
			1925	1143	391	391		

- Molecule 27 is a protein called Utp24.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	l	25	Total	C	N	O	0	0
			124	74	25	25		

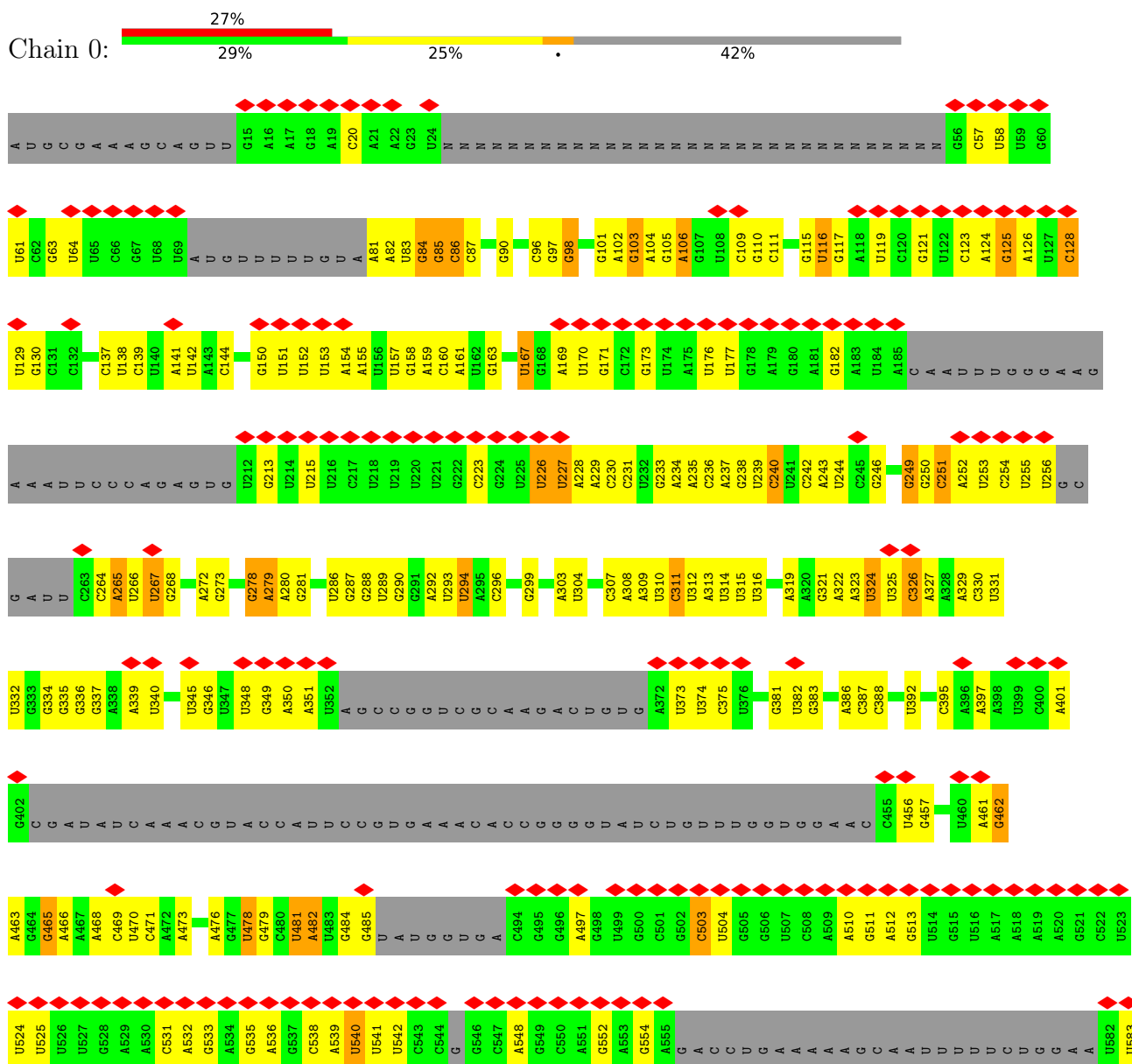
- Molecule 28 is a protein called Unidentified fragment.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
28	x	24	120	72	24	24	0	0

### 3 Residue-property plots

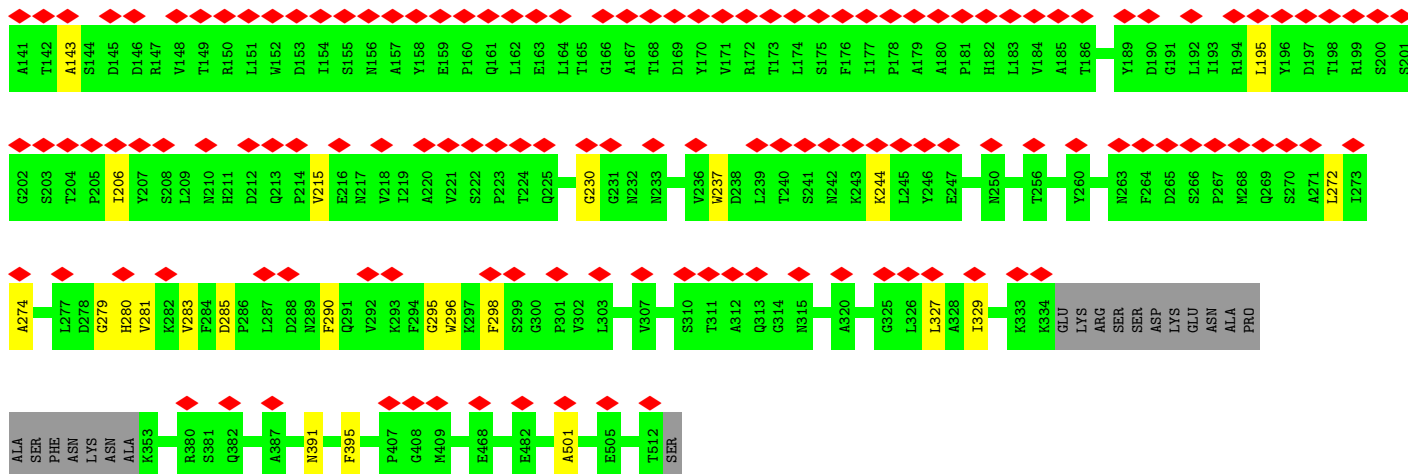
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

#### • Molecule 1: 5'ETS rRNA

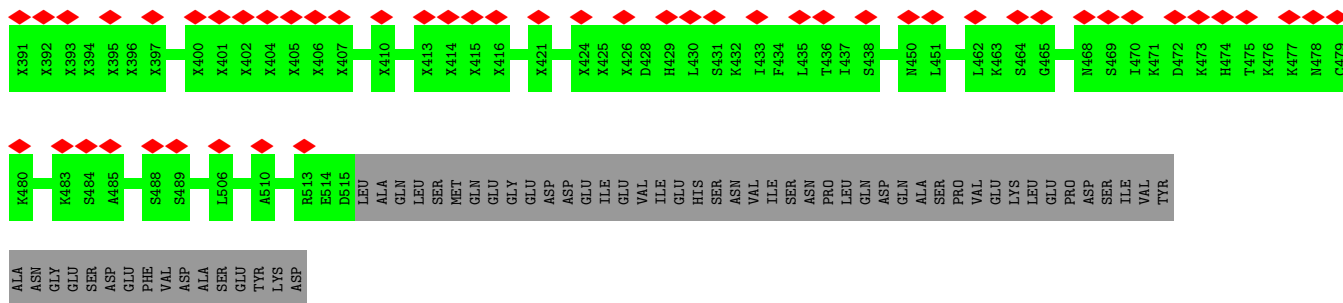




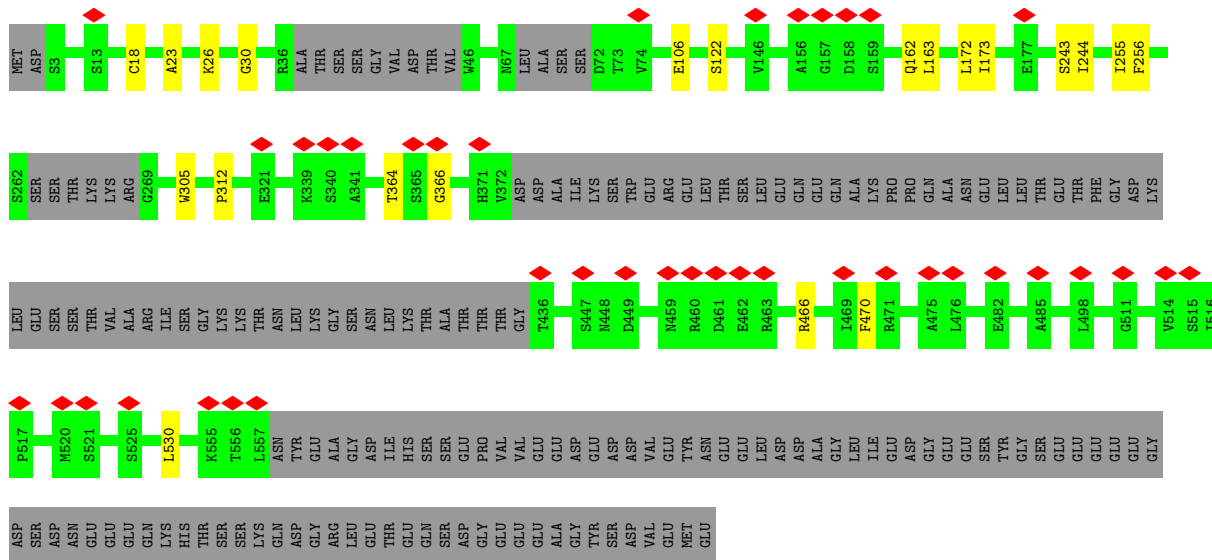




• Molecule 7: Utp9



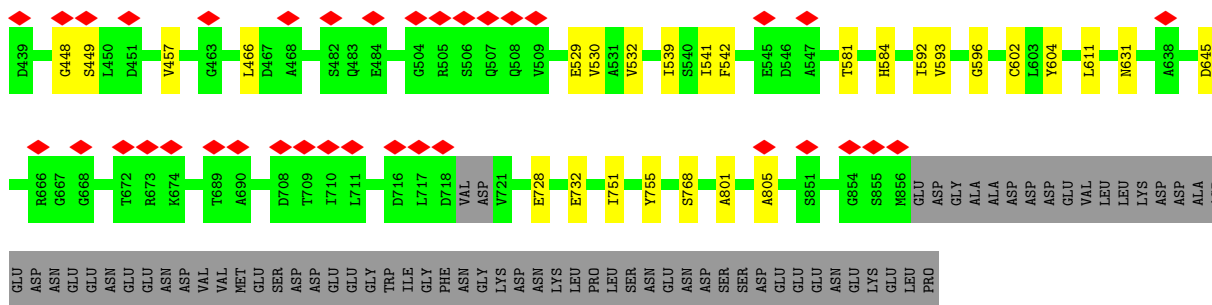
• Molecule 8: Utp5



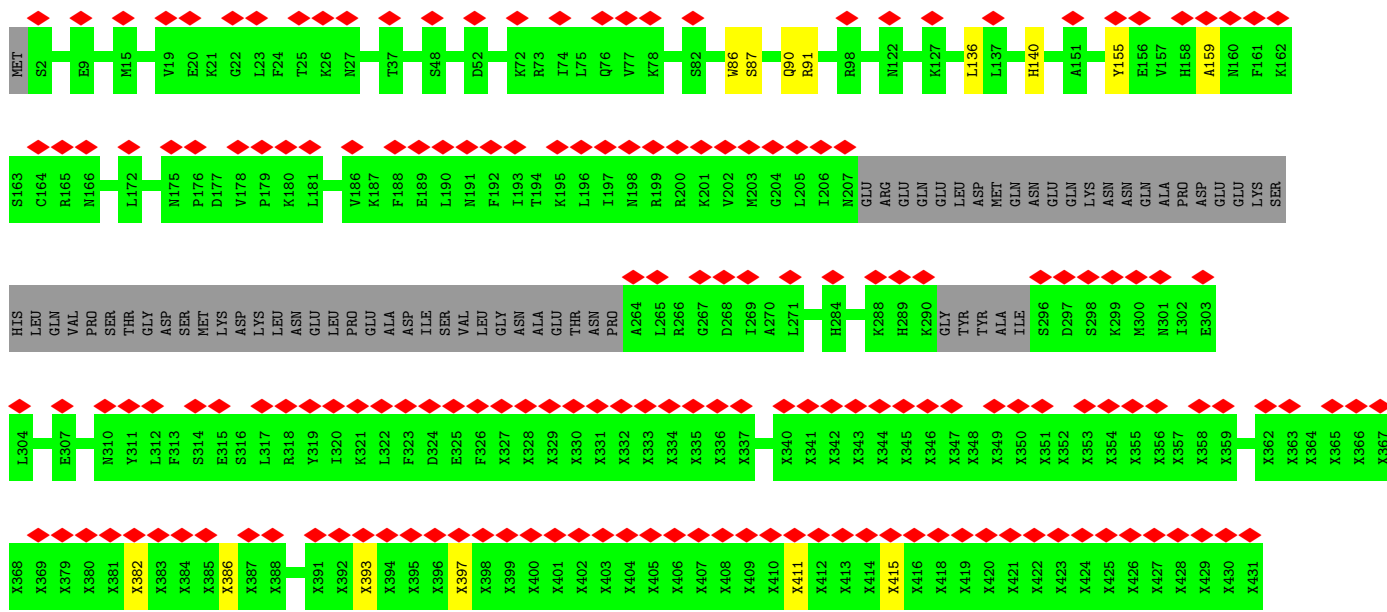
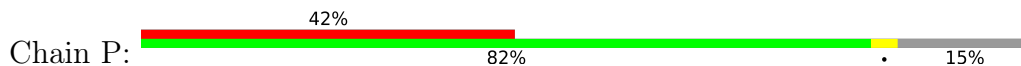
• Molecule 9: Utp10



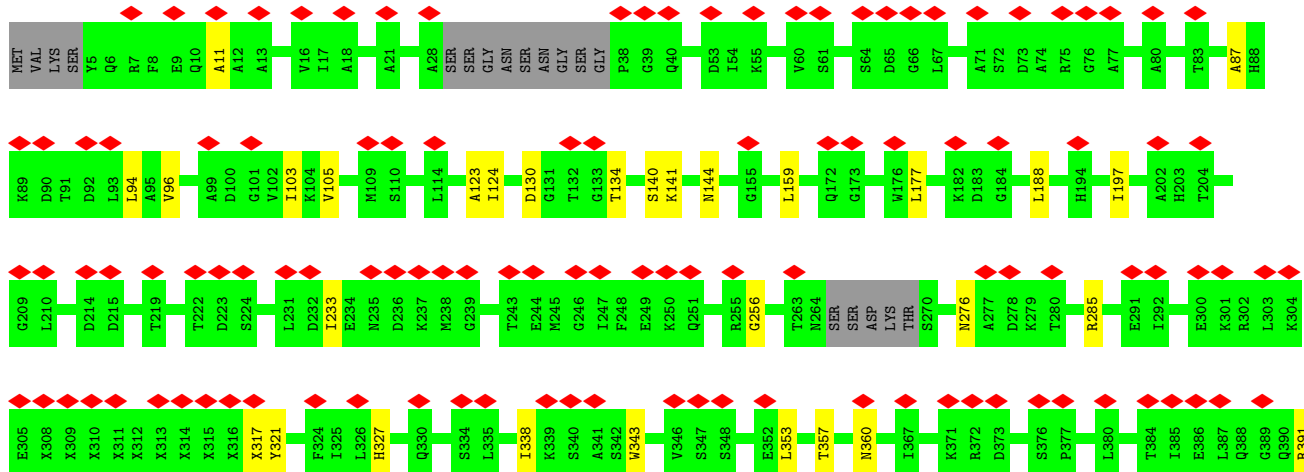
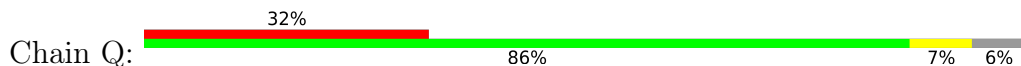




• Molecule 12: Utp6

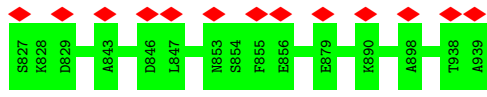
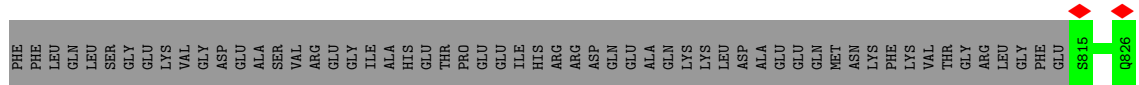


• Molecule 13: Utp12

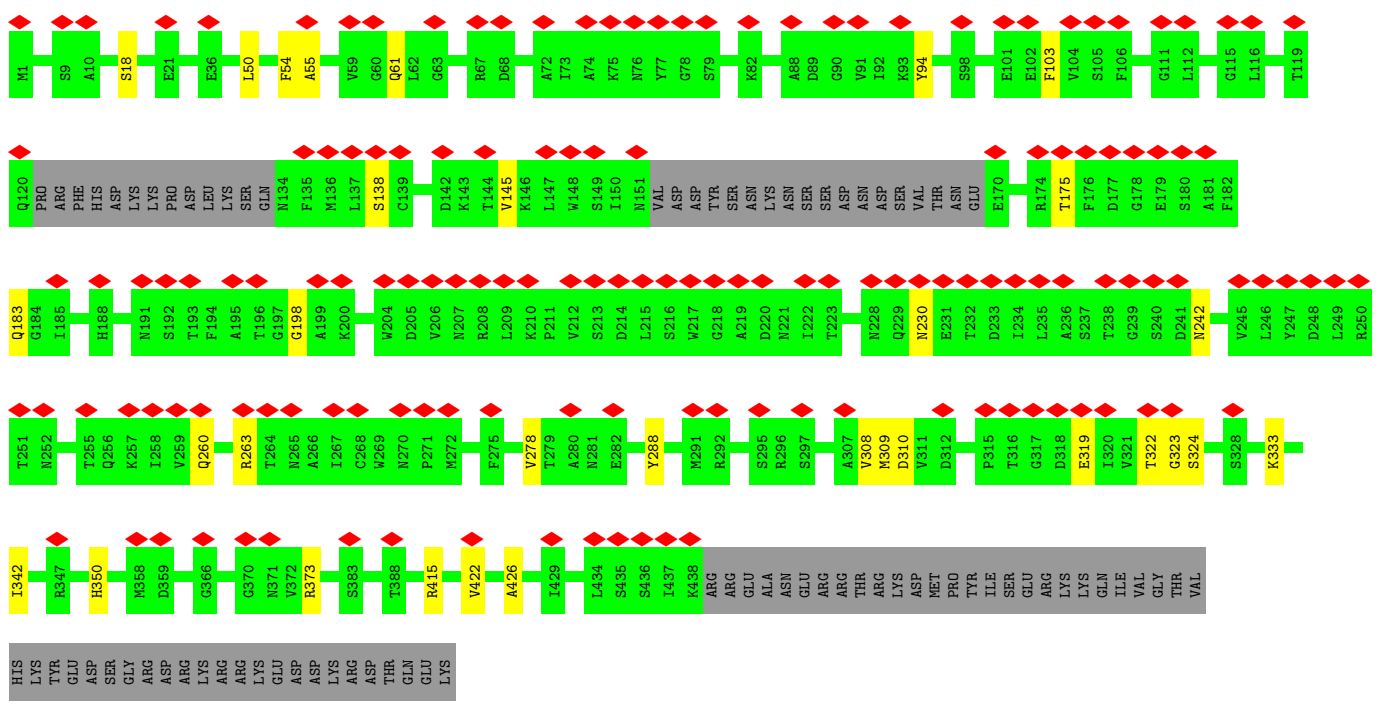
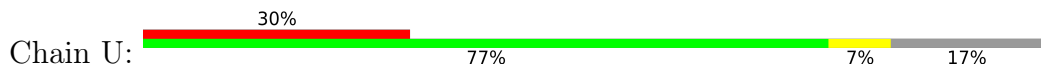




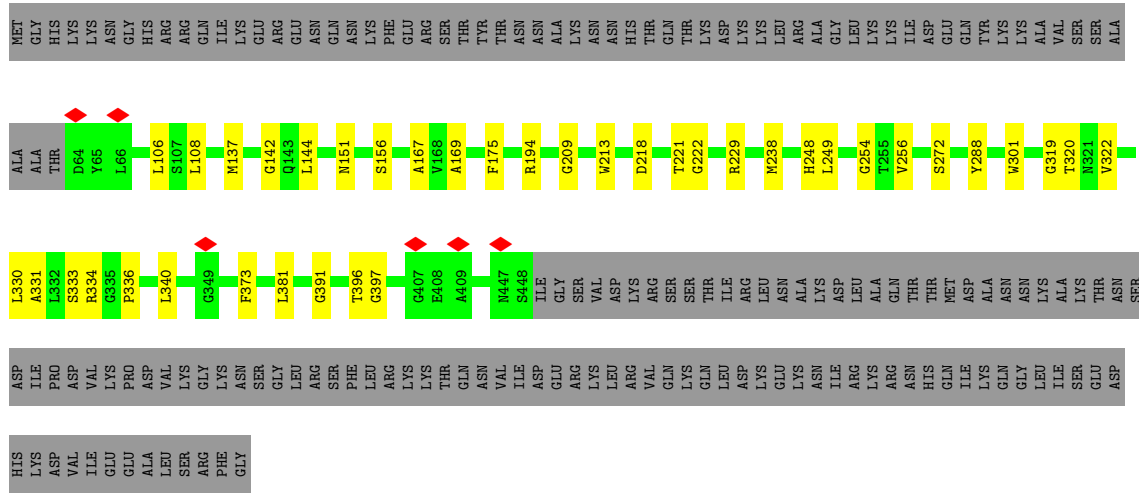




• Molecule 17: Sof1



• Molecule 18: Utp7

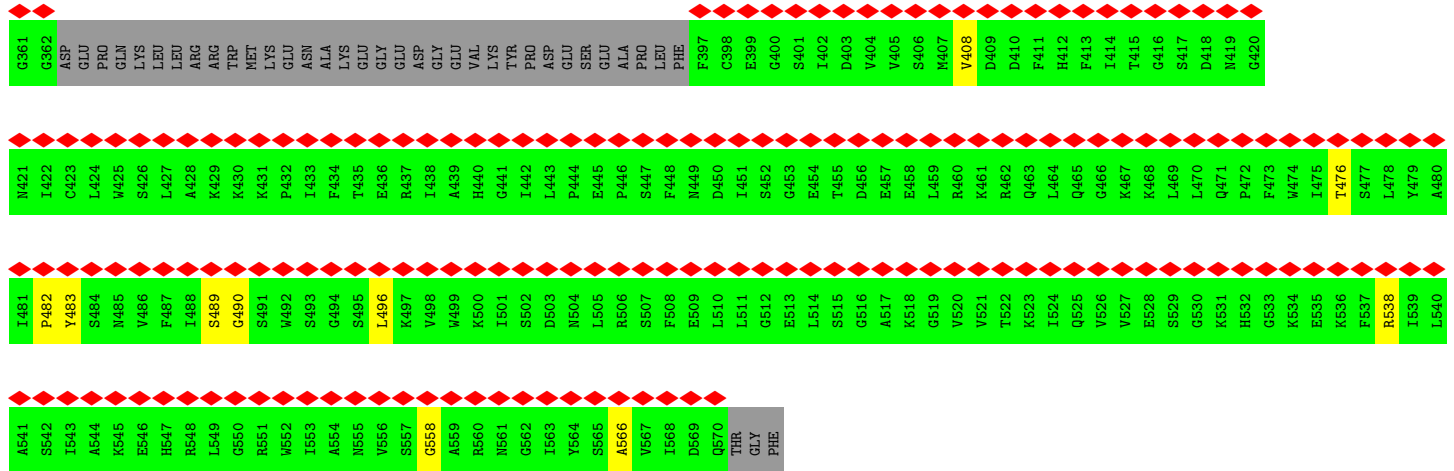




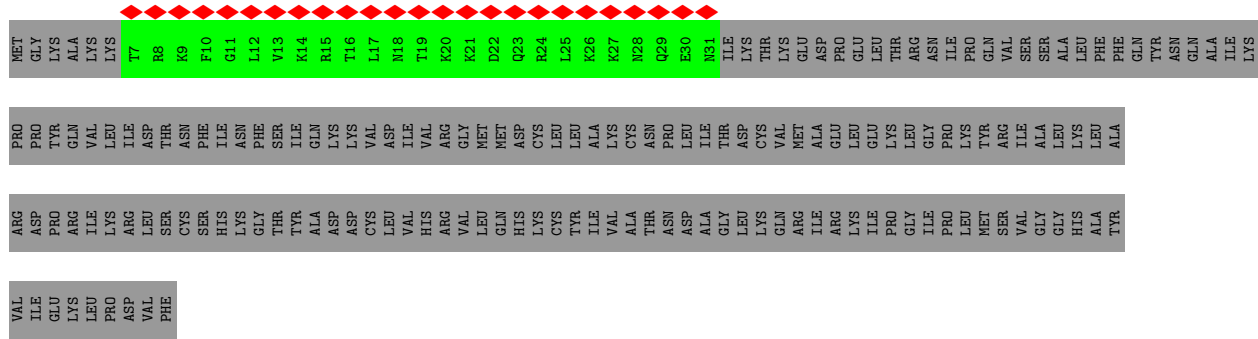




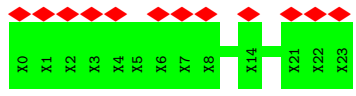




• Molecule 27: Utp24



• Molecule 28: Unidentified fragment



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	52629	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	31.25	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.091	Depositor
Minimum map value	-0.049	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0203	Depositor
Map size ( $\text{\AA}$ )	576.0, 576.0, 576.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.6, 1.6, 1.6	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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	0.30	0/9470	0.50	2/14733 (0.0%)
2	1	0.31	0/160	0.55	0/246
3	2	1.91	12/3467 (0.3%)	0.54	4/5383 (0.1%)
4	H	0.35	0/4057	0.73	5/5649 (0.1%)
5	I	0.25	0/659	0.66	0/916
6	J	0.29	0/2439	0.69	1/3397 (0.0%)
7	K	0.26	0/436	0.61	0/607
8	L	0.38	0/2339	0.71	0/3254
9	M	0.38	0/2150	0.66	2/3006 (0.1%)
10	N	0.33	0/3280	0.71	0/4563
11	O	0.39	0/4108	0.74	0/5717
12	P	0.28	0/1308	0.63	0/1821
13	Q	0.31	0/4081	0.77	5/5675 (0.1%)
14	R	0.32	0/785	0.64	0/1094
15	S	0.44	0/2368	0.71	0/3289
16	T	0.41	1/4000 (0.0%)	0.73	1/5561 (0.0%)
17	U	0.31	0/2011	0.73	0/2798
18	W	0.43	0/1894	0.71	0/2632
19	Z	0.42	1/839 (0.1%)	0.74	1/1170 (0.1%)
20	A	0.35	0/154	0.87	1/214 (0.5%)
21	D	0.22	0/123	0.65	0/170
22	a	0.28	0/1688	0.65	0/2346
23	b	0.32	0/1487	0.71	0/2069
24	c	0.27	0/998	0.64	0/1385
24	d	0.30	0/1120	0.64	0/1554
25	e	0.35	0/600	0.71	0/836
25	f	0.29	0/600	0.67	0/836
26	g	0.29	0/1922	0.66	0/2668
27	l	0.23	0/123	0.56	0/170
All	All	0.57	14/58666 (0.0%)	0.67	22/83759 (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
4	H	0	4
5	I	0	1
10	N	0	1
11	O	0	2
13	Q	0	2
16	T	0	1
17	U	0	3
20	A	0	1
25	e	0	1
All	All	0	16

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	2	248	G	C2-N3	49.68	2.32	1.32
3	2	248	G	N3-C4	48.78	2.33	1.35
3	2	248	G	N1-C2	40.23	2.18	1.37
3	2	248	G	C6-N1	40.20	2.19	1.39
3	2	248	G	C5-C6	37.12	2.16	1.42

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	524	U	OP1-P-O3'	-8.68	81.97	108.00
4	H	28	VAL	N-CA-C	-8.25	105.87	113.71
4	H	769	ASN	CA-C-N	7.05	135.13	121.18
4	H	769	ASN	C-N-CA	7.05	135.13	121.18
13	Q	785	PRO	N-CA-CB	7.03	110.63	103.25

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	H	105	HIS	Peptide
4	H	180	ASP	Peptide
4	H	453	HIS	Peptide
4	H	477	VAL	Peptide
5	I	576	ARG	Peptide

## 5.2 Too-close contacts

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	8594	0	4350	61	0
2	1	241	0	139	1	0
3	2	3106	0	1577	36	0
4	H	4132	0	1739	21	0
5	I	2427	0	680	17	0
6	J	2441	0	1083	17	0
7	K	612	0	220	0	0
8	L	2344	0	1023	12	0
9	M	2151	0	944	6	0
10	N	3355	0	1431	28	0
11	O	4111	0	1853	34	0
12	P	1786	0	649	7	0
13	Q	4262	0	1858	33	0
14	R	3604	0	979	30	0
15	S	2372	0	1043	13	0
16	T	4003	0	1790	28	0
17	U	2014	0	890	17	0
18	W	1895	0	853	22	0
19	Z	840	0	354	6	0
20	A	155	0	70	3	0
21	D	124	0	51	1	0
22	a	1822	0	810	3	0
23	b	2109	0	871	7	0
24	c	1000	0	453	8	0
24	d	1122	0	514	4	0
25	e	601	0	289	5	0
25	f	601	0	289	1	0
26	g	1925	0	863	8	0
27	l	124	0	50	0	0
28	x	120	0	26	0	0
All	All	63993	0	27741	403	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 5.

The worst 5 of 403 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)
3:2:323:G:C6	3:2:323:G:C5	1.74	1.65
3:2:323:G:C4	3:2:323:G:N3	1.69	1.61
3:2:323:G:C2	3:2:323:G:N1	1.72	1.55
3:2:323:G:C6	3:2:323:G:N1	1.75	1.52
3:2:248:G:C5	3:2:248:G:C4	2.05	1.36

There are no symmetry-related clashes.

### 5.3 Torsion angles [i](#)

#### 5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

#### 5.3.2 Protein sidechains [i](#)

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

#### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	389/700 (55%)	143 (36%)	6 (1%)
2	1	6/15 (40%)	1 (16%)	0
3	2	139/146 (95%)	60 (43%)	1 (0%)
All	All	534/861 (62%)	204 (38%)	7 (1%)

5 of 204 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	20	C
1	0	61	U
1	0	63	G
1	0	64	U
1	0	82	A

5 of 7 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	313	A

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	0	314	U
3	2	327	G
1	0	325	U
1	0	311	C

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

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

#### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

#### 5.6 Ligand geometry [i](#)

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
14	R	14
5	I	9
3	2	6
13	Q	4
22	a	3
4	H	2
10	N	2
12	P	2
7	K	2
23	b	2
1	0	1

The worst 5 of 47 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	788:THR	C	818:UNK	N	46.57
1	I	358:UNK	C	457:UNK	N	42.14
1	N	689:UNK	C	731:HIS	N	41.05
1	R	615:UNK	C	649:GLU	N	29.13
1	R	323:UNK	C	329:UNK	N	28.33

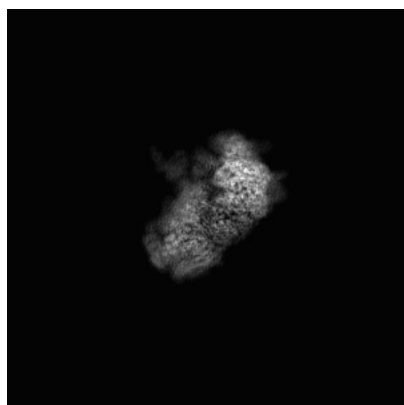
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0441. These allow visual inspection of the internal detail of the map and identification of artifacts.

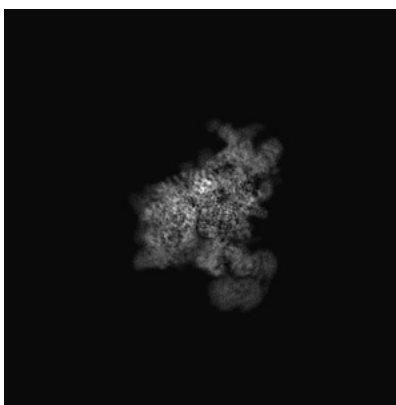
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

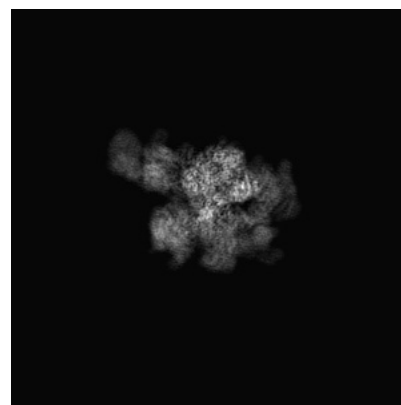
#### 6.1.1 Primary map



X



Y



Z

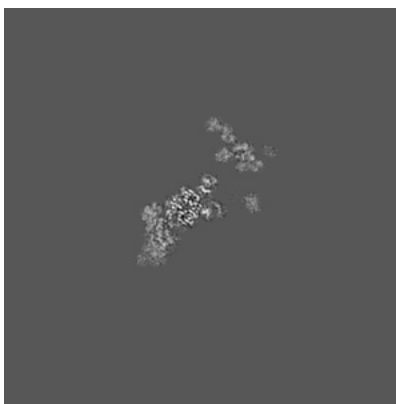
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

#### 6.2.1 Primary map



X Index: 180



Y Index: 180

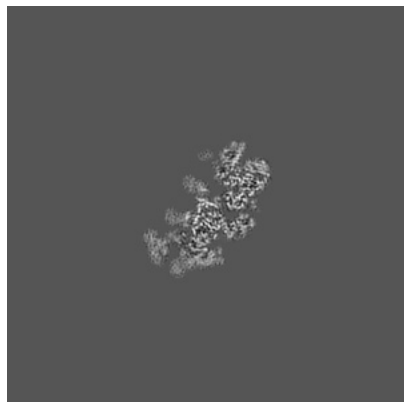


Z Index: 180

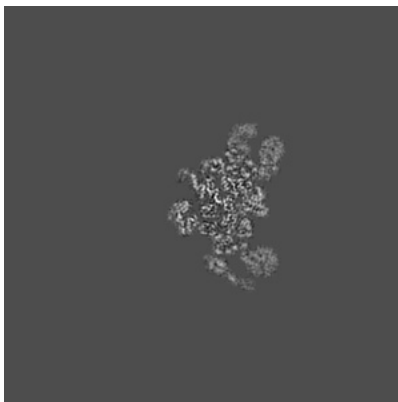
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

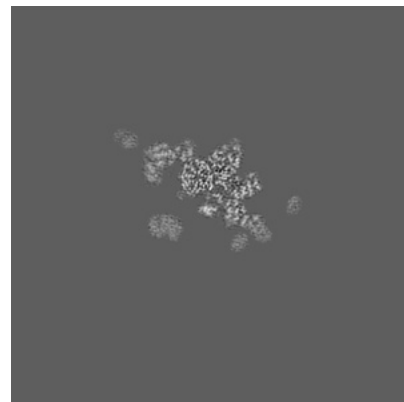
### 6.3.1 Primary map



X Index: 177



Y Index: 204

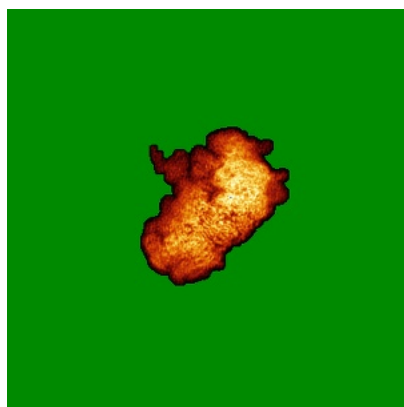


Z Index: 185

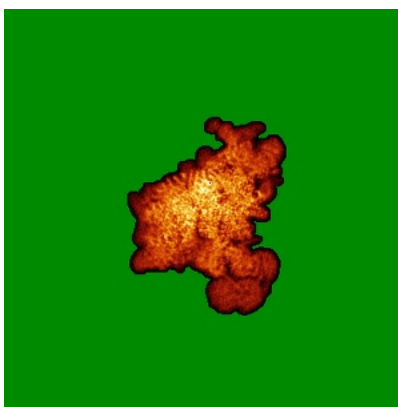
The images above show the largest variance slices of the map in three orthogonal directions.

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

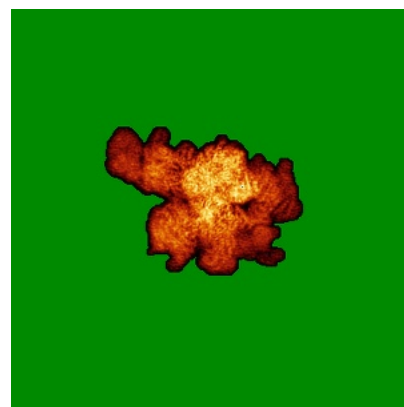
### 6.4.1 Primary map



X



Y



Z

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

This section was not generated.

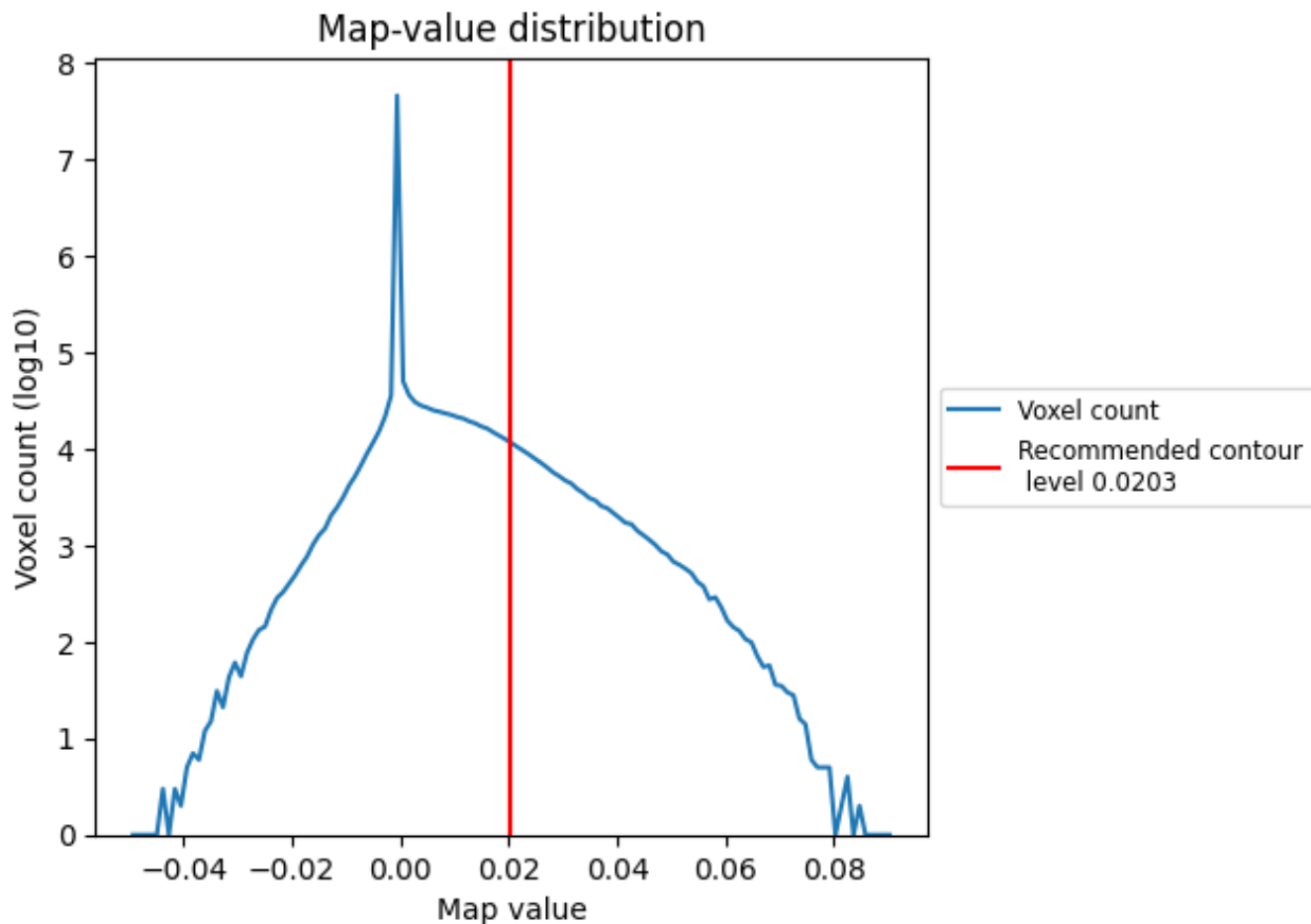
## 6.6 Mask visualisation

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

## 7 Map analysis [i](#)

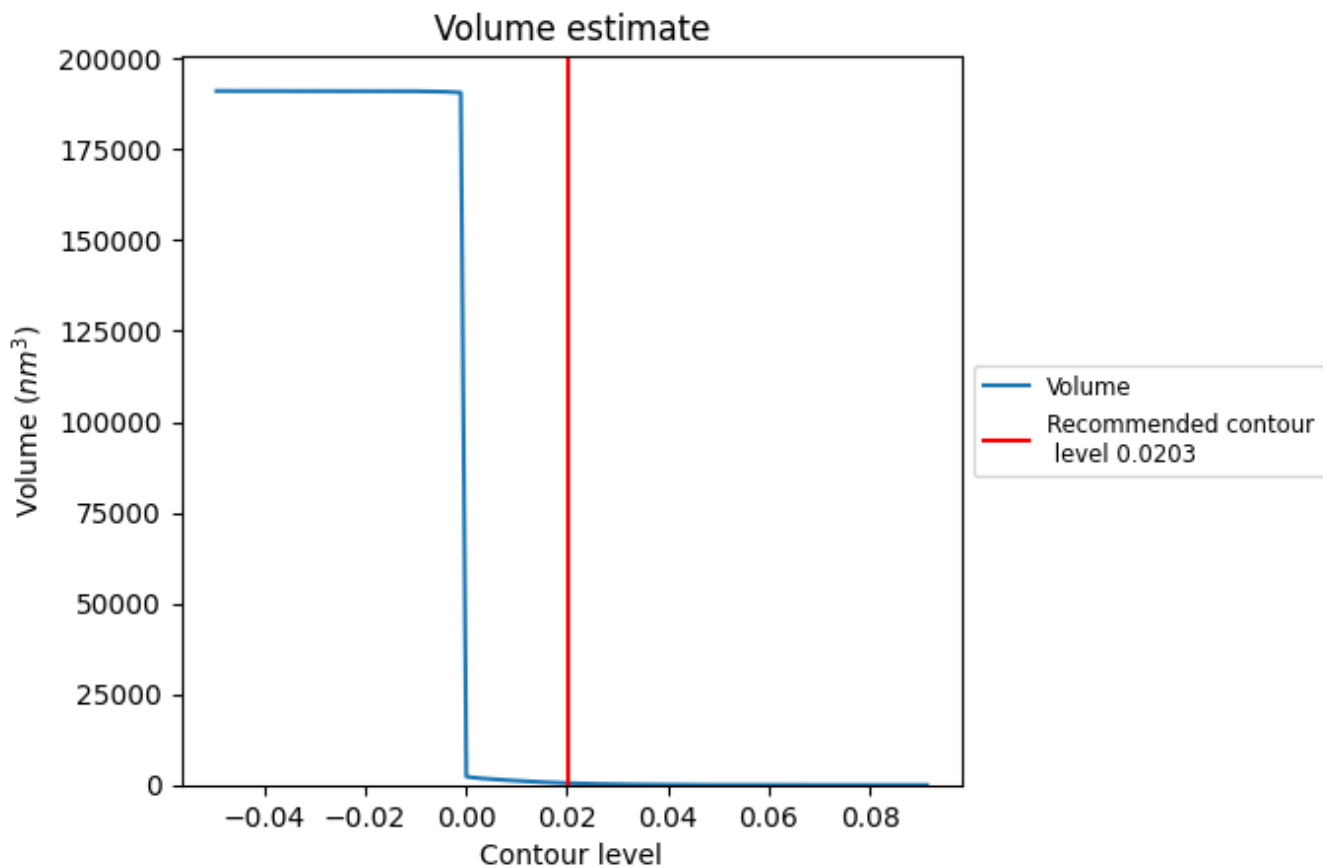
This section contains the results of statistical analysis of the map.

### 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.

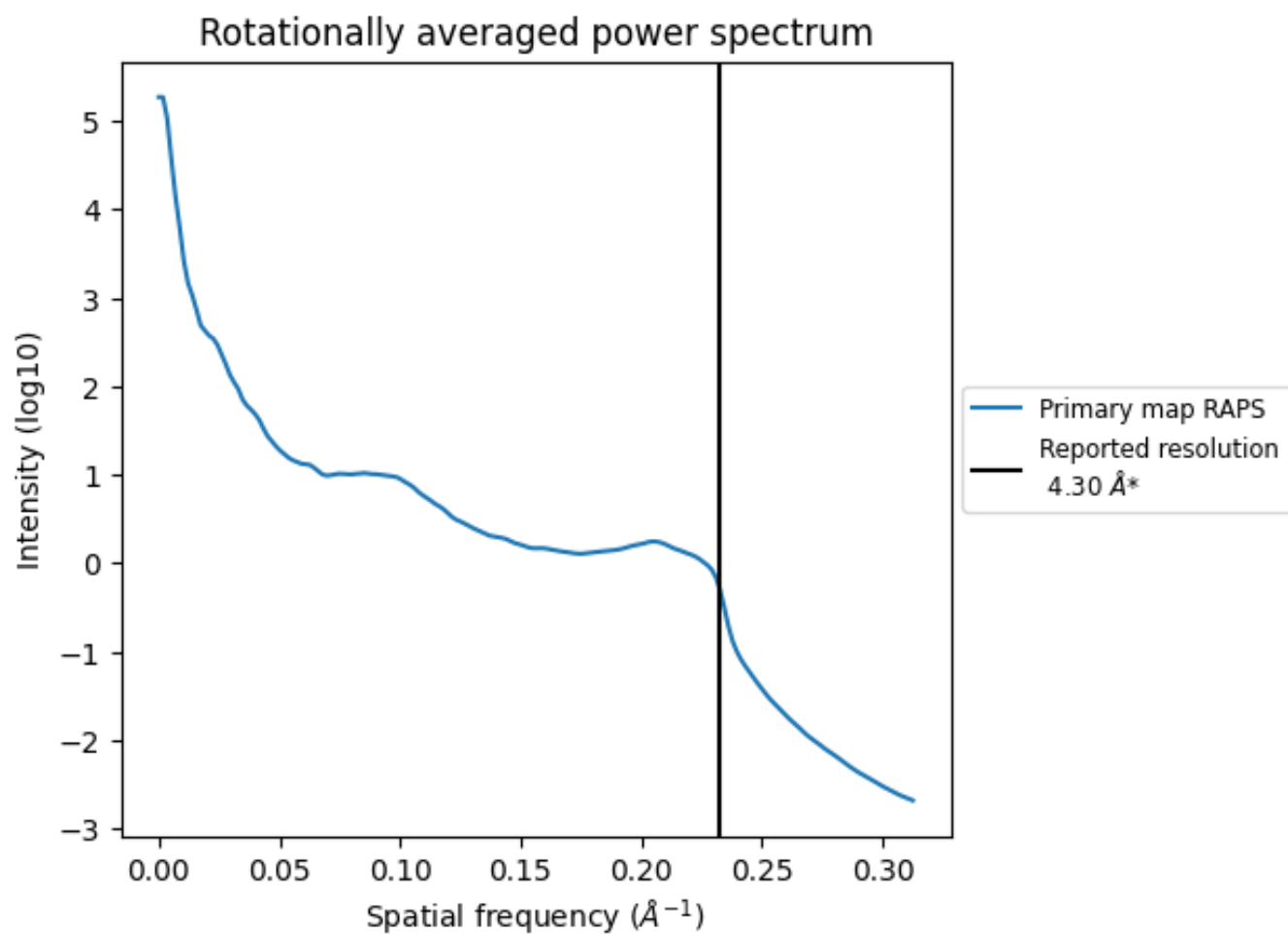
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 494 nm<sup>3</sup>; this corresponds to an approximate mass of 446 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](#)

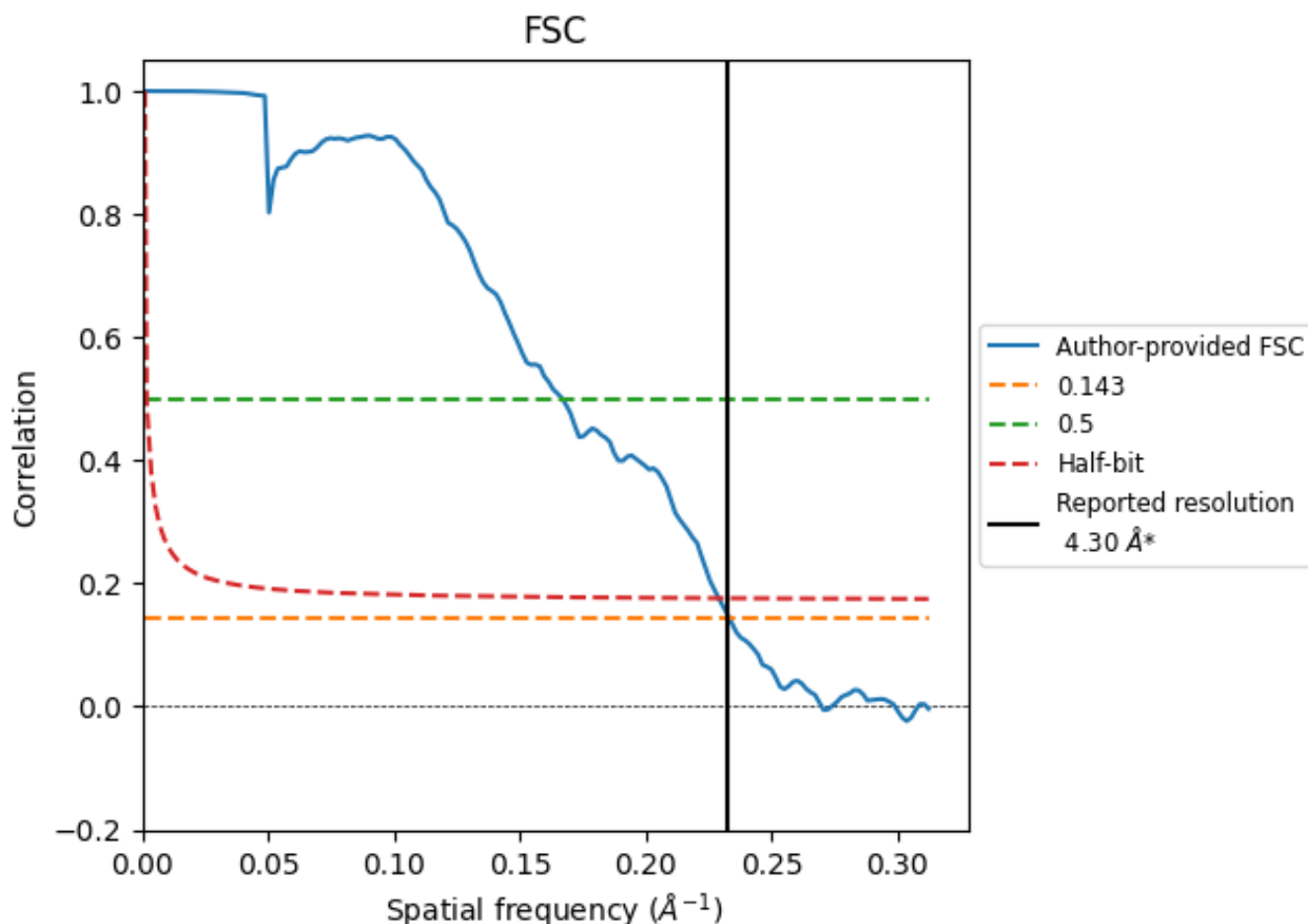


\*Reported resolution corresponds to spatial frequency of 0.233 Å<sup>-1</sup>

## 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 0.233 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.28	6.00	4.37
Unmasked-calculated*	-	-	-

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

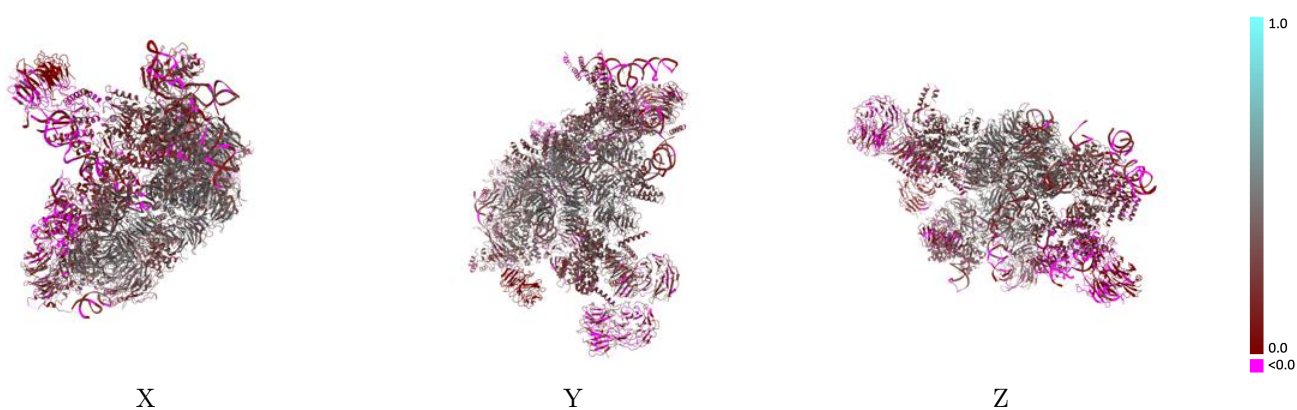
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0441 and PDB model 6ND4. Per-residue inclusion information can be found in section 3 on page 9.

### 9.1 Map-model overlay [i](#)

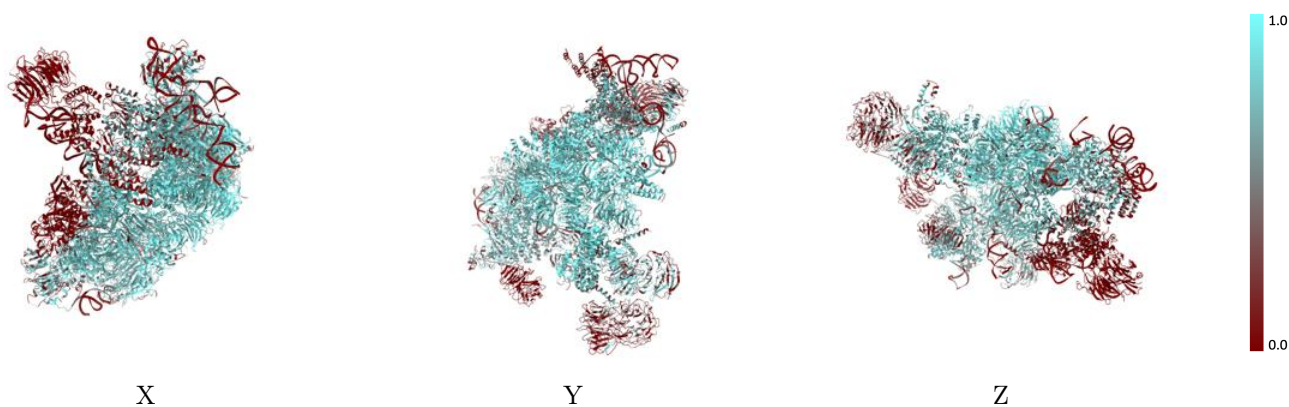
This section was not generated.

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



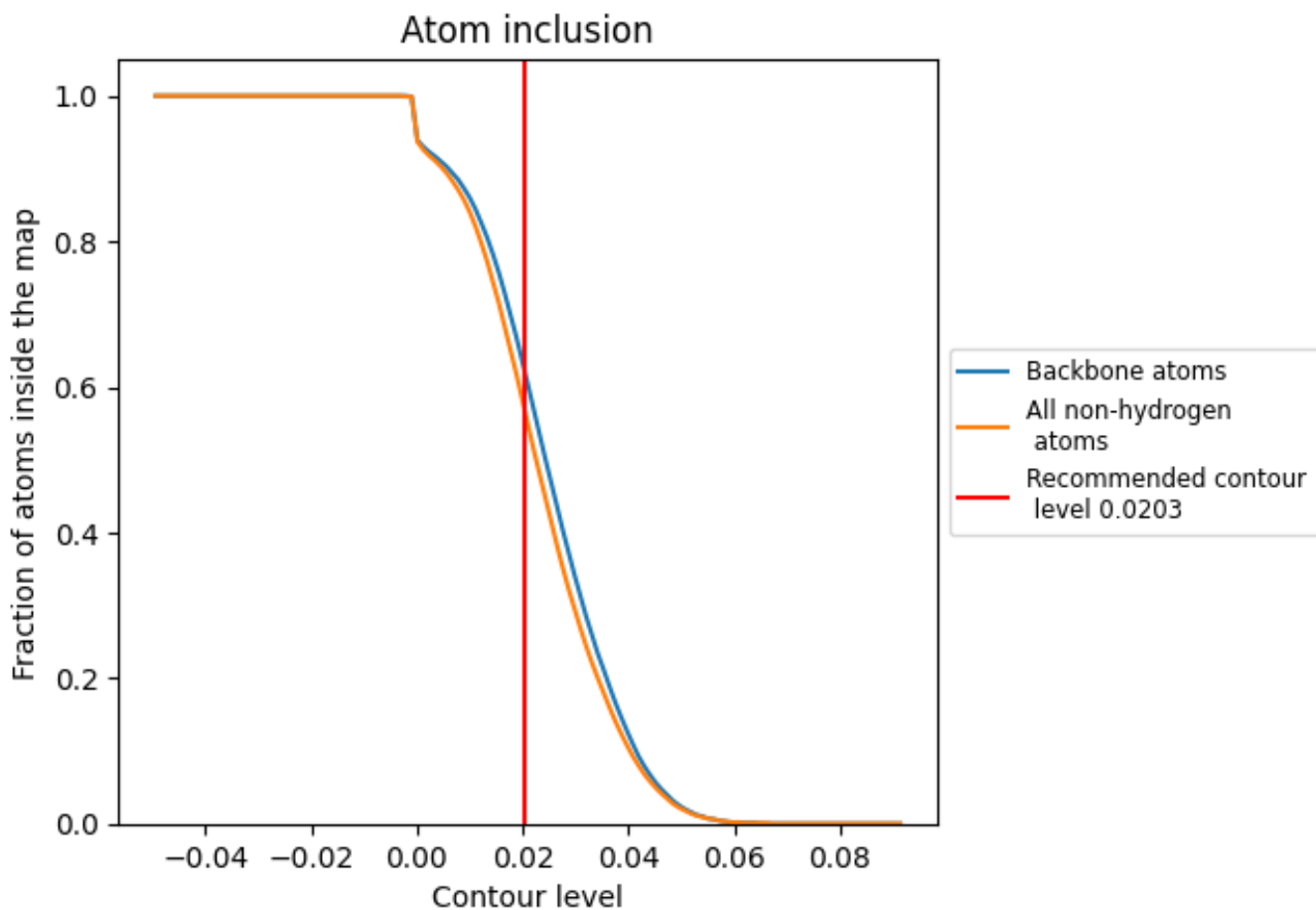
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

### 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0203).































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 57% 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 (0.0203) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5690	 0.2600
0	 0.4770	 0.2040
1	 0.1870	 0.1290
2	 0.4090	 0.1860
A	 0.7420	 0.3040
D	 0.0080	 0.0810
H	 0.7410	 0.3340
I	 0.2550	 0.1020
J	 0.5060	 0.2290
K	 0.5150	 0.2280
L	 0.8250	 0.3740
M	 0.8840	 0.3690
N	 0.6750	 0.2950
O	 0.8360	 0.3920
P	 0.4800	 0.2180
Q	 0.5960	 0.2540
R	 0.3120	 0.1230
S	 0.8760	 0.4280
T	 0.8710	 0.4070
U	 0.5780	 0.2680
W	 0.8720	 0.4170
Z	 0.7940	 0.3540
a	 0.3540	 0.2140
b	 0.4590	 0.2040
c	 0.3240	 0.2090
d	 0.0300	 0.0830
e	 0.8400	 0.3590
f	 0.0280	 0.0610
g	 0.0050	 -0.0060
l	 0.0000	 0.1690
x	 0.5170	 0.2560

