



# wwPDB EM Validation Summary Report

Nov 21, 2022 – 02:38 PM EST


PDB ID : 8EUI  
EMDB ID : EMD-24423  
Title : Ytm1 associated nascent 60S ribosome (-fkbp39) State 3  
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.  
Deposited on : 2022-10-18  
Resolution : 3.10 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](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>.

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

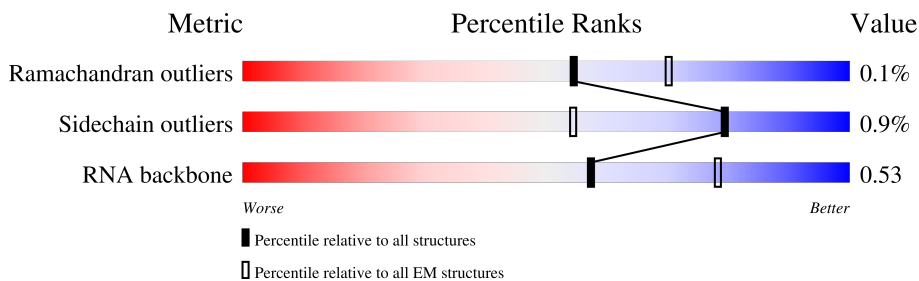
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 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 3.10 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.



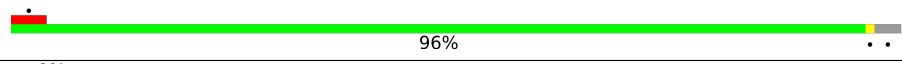
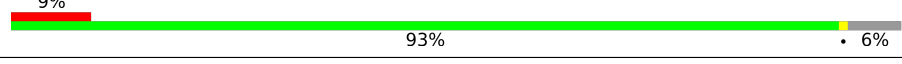
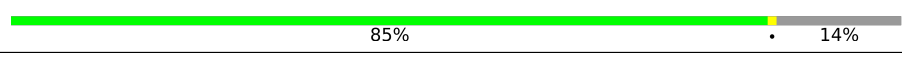
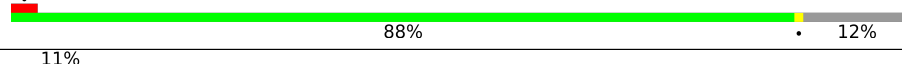
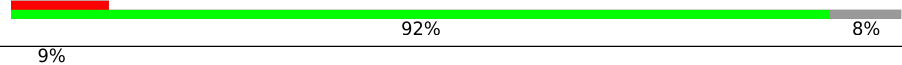

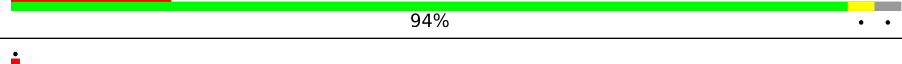
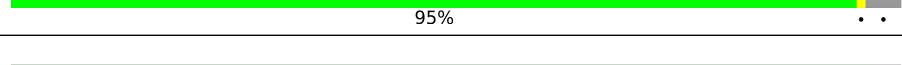
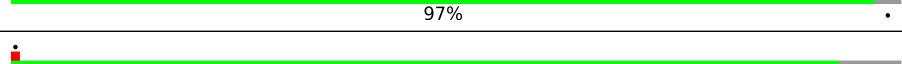
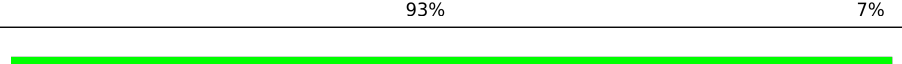
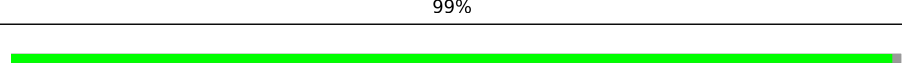
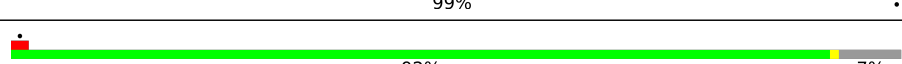
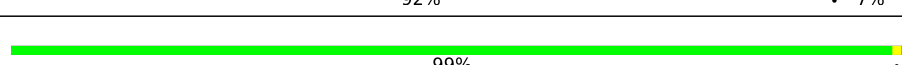
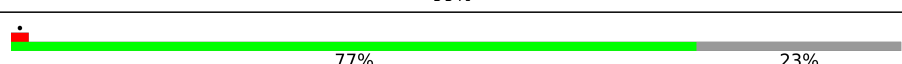
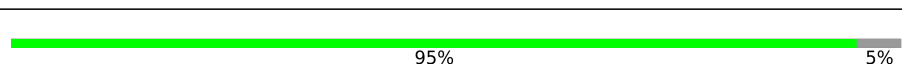
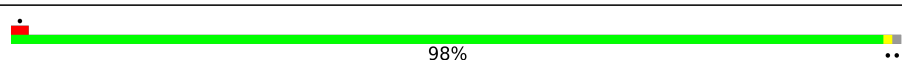
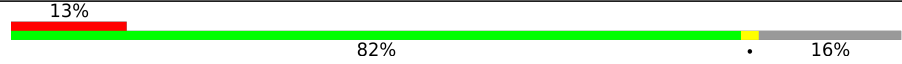
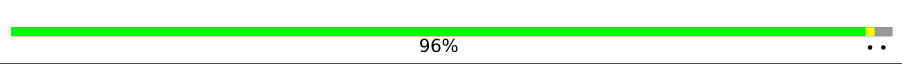

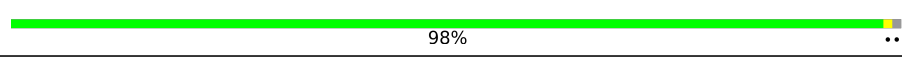
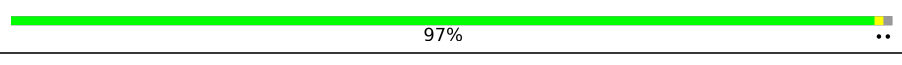
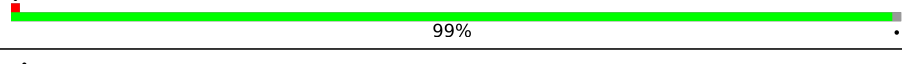
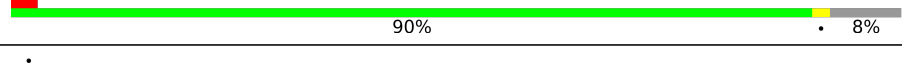


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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  $\leq 5\%$ . 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	1	3498	
2	2	165	
3	3	302	
4	8	51	
5	9	229	
6	A	253	
7	B	388	
8	C	363	


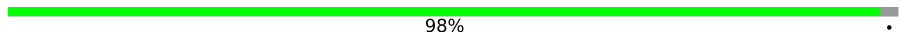

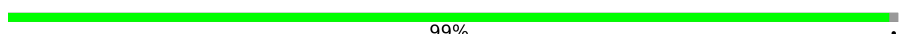
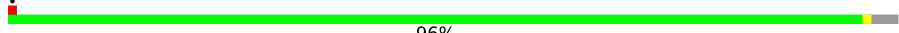







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Mol	Chain	Length	Quality of chain
9	D	294	 96%
10	E	195	 93%
11	F	250	 85%
12	G	259	 88%
13	H	190	 92%
14	I	221	 76%
15	J	174	 94%
16	K	94	 95%
17	L	208	 97%
18	M	134	 93%
19	N	201	 99%
20	O	197	 99%
21	P	187	 92%
22	Q	187	 99%
23	R	193	 77%
24	S	176	 95%
25	T	160	 98%
26	U	117	 82%
27	V	139	 96%
28	X	141	 82%
29	Y	126	 98%
30	Z	136	 97%
31	a	148	 99%
32	b	61	 90%
33	c	117	 80%

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Mol	Chain	Length	Quality of chain
34	d	113	 86% 14%
35	e	127	 91% 8%
36	f	108	 98%
37	g	112	 93% 5%
38	h	122	 99%
39	i	99	 96%
40	j	91	 91% 9%
41	k	74	 91% 5%
42	m	740	 14% 57% 43%
43	n	607	 17% 59% 41%
44	o	106	 92% 8%
45	p	440	 53% 65% 35%
46	u	192	 29% 69%

## 2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 122892 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 RNA (2863-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2855	61093	27299	11065	19874	2855	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1746	C	U	conflict	GB 157310483
1	2185	U	C	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (152-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	158	3354	1501	588	1107	158	0	0

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	123	1042	657	199	180	6	0	0

- Molecule 4 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	8	50	437	273	98	65	1	0	0

- Molecule 5 is a RNA chain called RNA (118-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	9	118	2519	1124	452	825	118	0	0

- Molecule 6 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	A	245	1858	1158	374	321	5	0	0

- Molecule 7 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	B	377	3003	1901	567	525	10	0	0

- Molecule 8 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	C	359	2795	1765	536	491	3	0	0

- Molecule 9 is a protein called 60S ribosomal protein L5-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	D	284	2287	1447	406	430	4	0	0

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	E	183	1415	907	259	245	4	0	0

- Molecule 11 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	F	214	1745	1124	320	298	3	0	0

- Molecule 12 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	G	229	1804	1154	332	315	3	0	0

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	H	175	Total	C	N	O	0	0
			862	512	175	175		

- Molecule 14 is a protein called 60S ribosomal protein L10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	168	Total	C	N	O	S	0	0
			1354	858	251	240	5		

- Molecule 15 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	169	Total	C	N	O	S	0	0
			1359	860	255	239	5		

- Molecule 16 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	90	Total	C	N	O	S	0	0
			695	428	144	117	6		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	202	Total	C	N	O	S	0	0
			1612	1008	321	282	1		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	125	Total	C	N	O	S	0	0
			1007	644	191	168	4		

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	200	Total	C	N	O	S	0	0
			1676	1050	348	275	3		

- Molecule 20 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	O	196	1557	999	297	257	4	0	0

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	P	173	1369	865	264	237	3	0	0

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	Q	186	1487	934	300	252	1	0	0

- Molecule 23 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	R	149	1229	765	261	198	5	0	0

- Molecule 24 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	S	168	1408	909	263	231	5	0	0

- Molecule 25 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	T	159	1289	812	248	226	3	0	0

- Molecule 26 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
26	U	98	791	513	137	141	0	0

- Molecule 27 is a protein called 60S ribosomal protein L23-A.



Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	V	136	1015	638	189	180	8	0	0

- Molecule 28 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	X	117	939	599	173	166	1	0	0

- Molecule 29 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	Y	125	998	622	201	173	2	0	0

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	Z	134	1072	693	199	178	2	0	0

- Molecule 31 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	a	147	1169	740	235	192	2	0	0

- Molecule 32 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
32	b	56	471	284	107	80	0	0

- Molecule 33 is a protein called 60S ribosomal protein L30-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	c	95	712	453	124	131	4	0	0

- Molecule 34 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	97	Total	C	N	O	S	0	0
			810	512	159	136	3		

- Molecule 35 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	117	Total	C	N	O	S	0	0
			939	588	190	156	5		

- Molecule 36 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	106	Total	C	N	O	S	0	0
			839	534	162	140	3		

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	106	Total	C	N	O	S	0	0
			861	540	177	142	2		

- Molecule 38 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	h	121	Total	C	N	O	0	0
			999	629	194	176		

- Molecule 39 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	96	Total	C	N	O	S	0	0
			767	478	160	128	1		

- Molecule 40 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	83	Total	C	N	O	S	0	0
			657	402	141	107	7		

- Molecule 41 is a protein called 60S ribosomal protein L38-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	70	Total	C	N	O	S	0	0
			564	357	104	102	1		

- Molecule 42 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	425	Total	C	N	O	S	0	0
			3376	2168	592	605	11		

- Molecule 43 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	361	Total	C	N	O	S	0	0
			2966	1933	511	510	12		

- Molecule 44 is a protein called 60S ribosomal protein L42.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	98	Total	C	N	O	S	0	0
			796	502	159	130	5		

- Molecule 45 is a protein called Ribosome biogenesis protein ytm1.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	p	284	Total	C	N	O	0	0
			1401	833	284	284		

- Molecule 46 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	59	Total	C	N	O	S	0	0
			493	315	100	72	6		

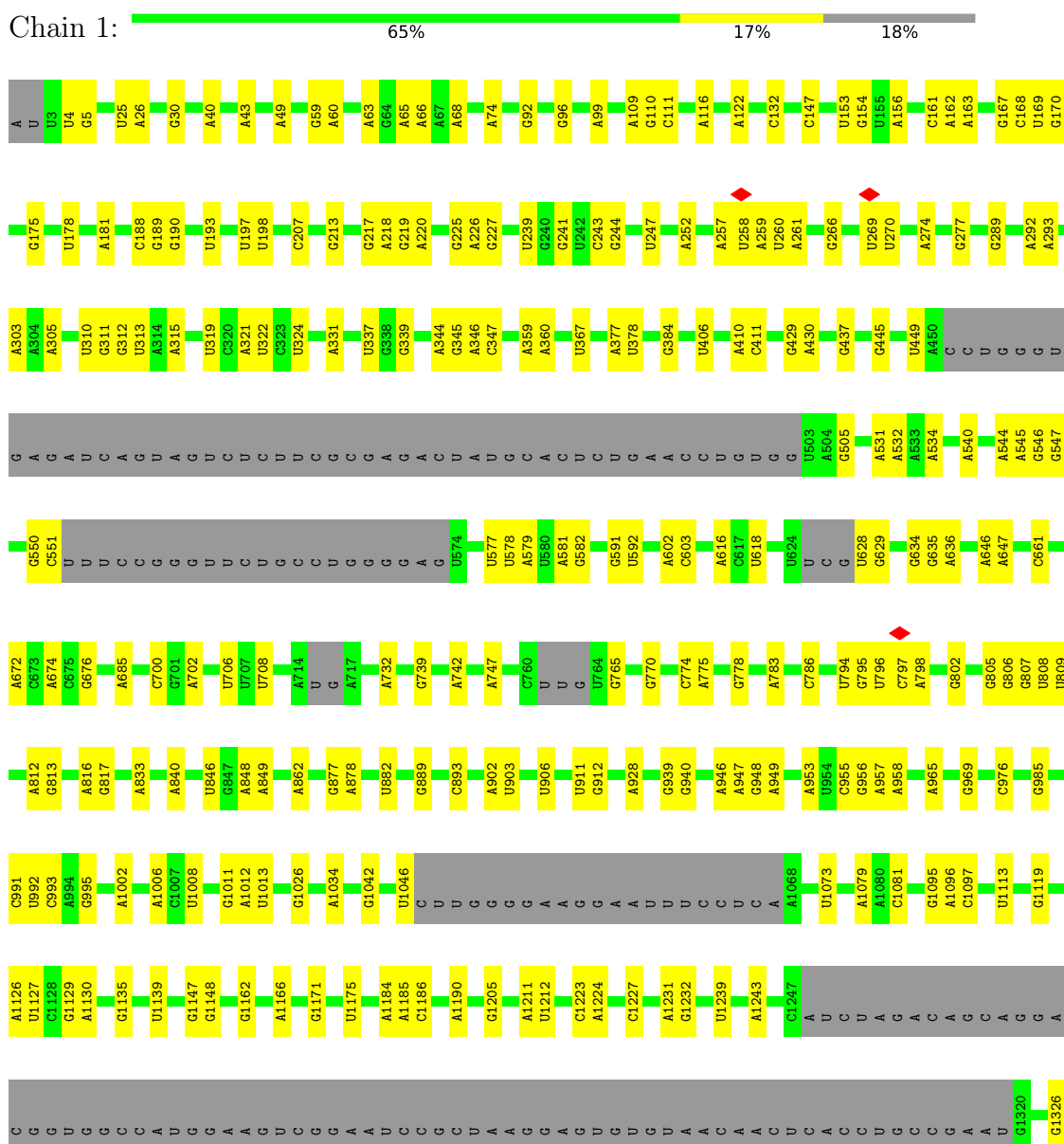
- Molecule 47 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
47	j	1	Total	Zn	0
			1	1	

### 3 Residue-property plots

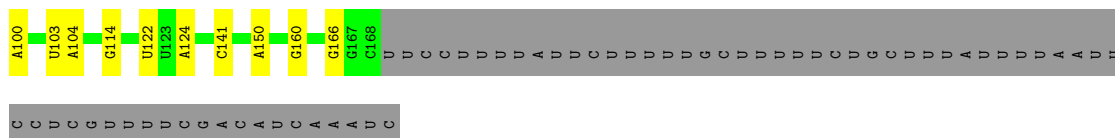
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: RNA (2863-MER)

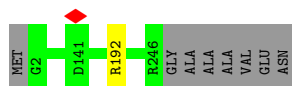




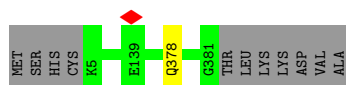




● Molecule 6: 60S ribosomal protein L2-A



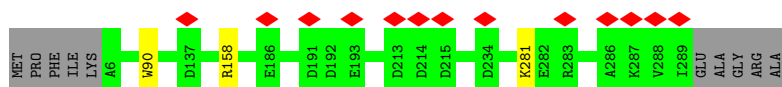
● Molecule 7: 60S ribosomal protein L3-A



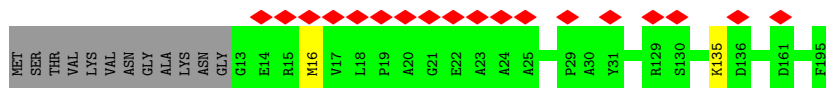
● Molecule 8: 60S ribosomal protein L4-B



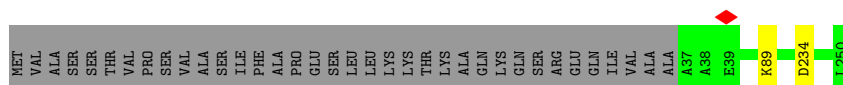
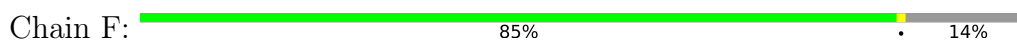
● Molecule 9: 60S ribosomal protein L5-A



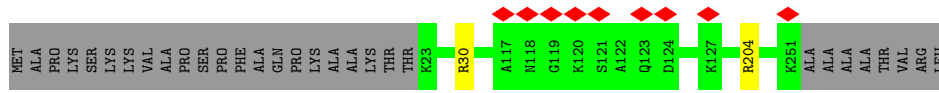
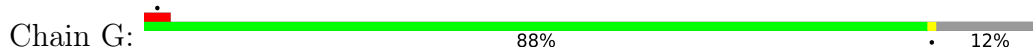
● Molecule 10: 60S ribosomal protein L6



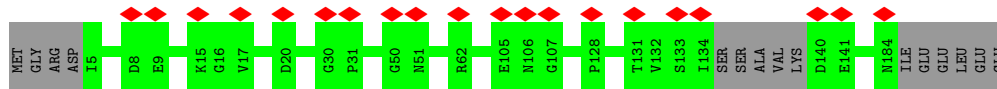
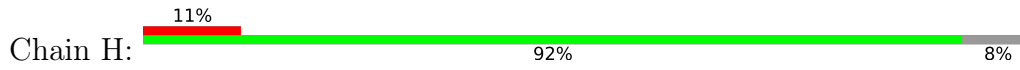
● Molecule 11: 60S ribosomal protein L7-B



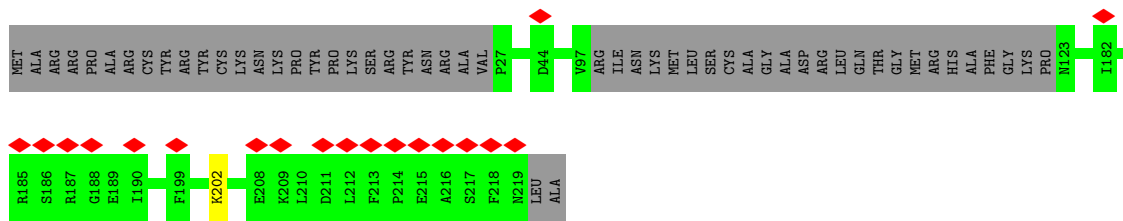
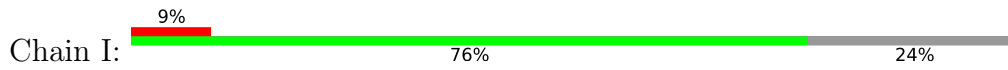
• Molecule 12: 60S ribosomal protein L8



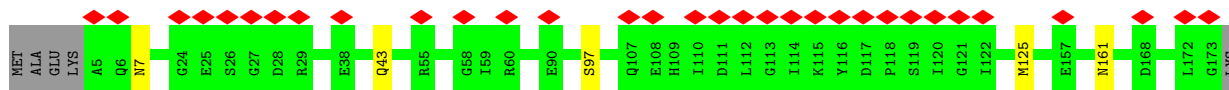
• Molecule 13: 60S ribosomal protein L9-A



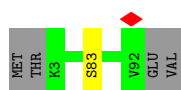
• Molecule 14: 60S ribosomal protein L10-A



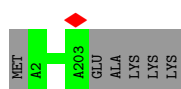
• Molecule 15: 60S ribosomal protein L11-A



• Molecule 16: 60S ribosomal protein L43-A



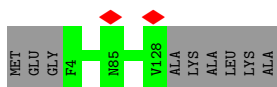
• Molecule 17: 60S ribosomal protein L13



• Molecule 18: 60S ribosomal protein L14

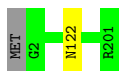


Chain M:  93% 7%



- Molecule 19: 60S ribosomal protein L15-A

Chain N:  99%



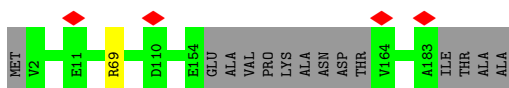
- Molecule 20: 60S ribosomal protein L16-B

Chain O:  99%



- Molecule 21: 60S ribosomal protein L17-A

Chain P:  92% 7%



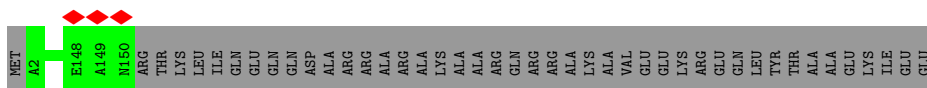
- Molecule 22: 60S ribosomal protein L18-A

Chain Q:  99%



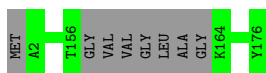
- Molecule 23: 60S ribosomal protein L19-A

Chain R:  77% 23%



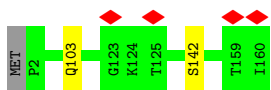
- Molecule 24: 60S ribosomal protein L20-A

Chain S:  95% 5%




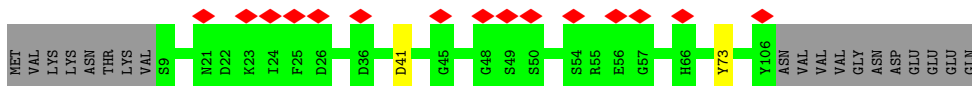
- Molecule 25: 60S ribosomal protein L21-A

Chain T:  98%



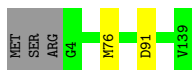
- Molecule 26: 60S ribosomal protein L22

Chain U:  13% 82% 16%




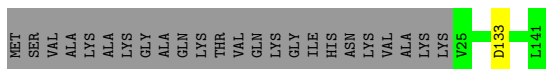
- Molecule 27: 60S ribosomal protein L23-A

Chain V:  96%



- Molecule 28: 60S ribosomal protein L25-A

Chain X:  82% 17%



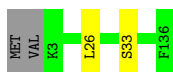
- Molecule 29: 60S ribosomal protein L26

Chain Y:  98%



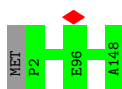
- Molecule 30: 60S ribosomal protein L27-A

Chain Z:  97%

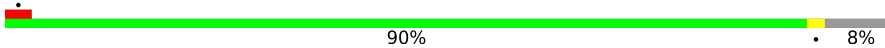


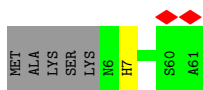
- Molecule 31: 60S ribosomal protein L28-A

Chain a:  99%




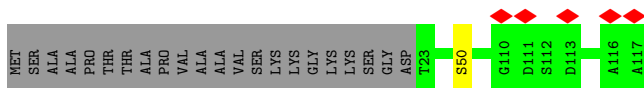
- Molecule 32: 60S ribosomal protein L29

Chain b:  90% 8%




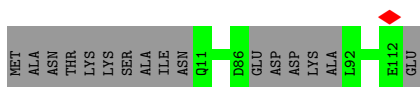
- Molecule 33: 60S ribosomal protein L30-2

Chain c:  80% 19%



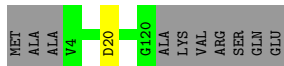
- Molecule 34: 60S ribosomal protein L31

Chain d:  86% 14%



- Molecule 35: 60S ribosomal protein L32-A

Chain e:  91% 8%



- Molecule 36: 60S ribosomal protein L33-B

Chain f:  98%



- Molecule 37: 60S ribosomal protein L34-A

Chain g:  93% 5%



- Molecule 38: 60S ribosomal protein L35

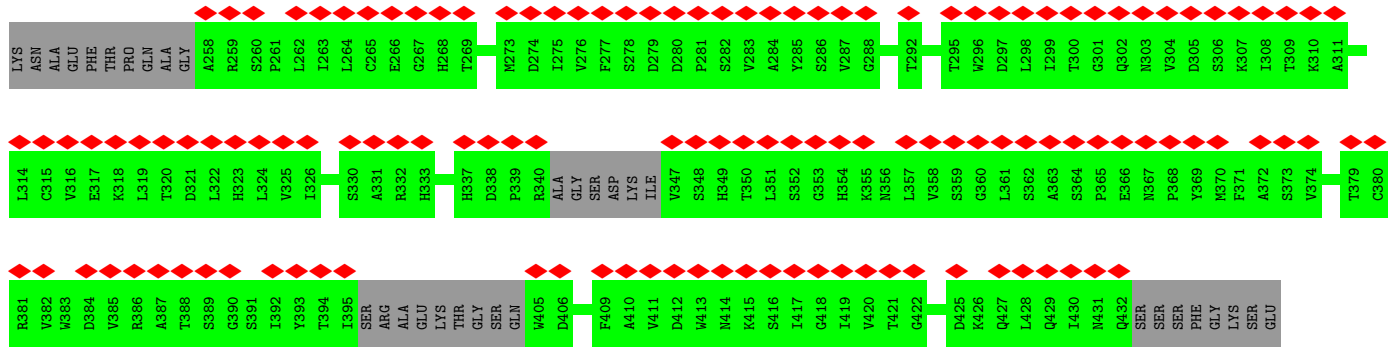
Chain h:  99%



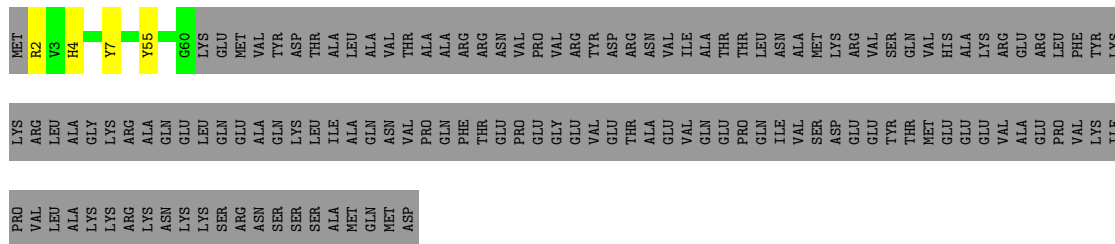
- Molecule 39: 60S ribosomal protein L36-B







• Molecule 46: Ribosome biogenesis protein rlp24



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	59000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	90	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.589	Depositor
Minimum map value	-0.293	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.05	Depositor
Map size ( $\text{\AA}$ )	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.06, 1.06, 1.06	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:  
ZN

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	1	0.42	0/68374	0.73	0/106528
2	2	0.45	0/3748	0.73	0/5835
3	3	0.35	0/1064	0.56	0/1431
4	8	0.30	0/448	0.58	0/597
5	9	0.26	0/2816	0.69	0/4388
6	A	0.31	0/1896	0.57	0/2556
7	B	0.29	0/3069	0.53	0/4130
8	C	0.30	0/2848	0.52	0/3842
9	D	0.26	0/2336	0.49	0/3142
10	E	0.28	0/1444	0.52	0/1948
11	F	0.30	0/1781	0.50	0/2389
12	G	0.29	0/1833	0.49	0/2467
13	H	0.24	0/860	0.43	0/1193
14	I	0.25	0/1379	0.49	0/1848
15	J	0.28	0/1382	0.53	0/1850
16	K	0.30	0/704	0.60	0/941
17	L	0.29	0/1644	0.53	0/2215
18	M	0.27	0/1024	0.52	0/1375
19	N	0.33	0/1717	0.56	0/2304
20	O	0.31	0/1588	0.50	0/2128
21	P	0.31	0/1393	0.52	0/1866
22	Q	0.30	0/1511	0.55	0/2019
23	R	0.28	0/1248	0.54	0/1661
24	S	0.28	0/1444	0.52	0/1939
25	T	0.32	0/1317	0.53	0/1772
26	U	0.29	0/805	0.49	0/1080
27	V	0.30	0/1031	0.53	0/1388
28	X	0.30	0/955	0.53	0/1285
29	Y	0.28	0/1008	0.58	0/1341
30	Z	0.29	0/1095	0.53	0/1467
31	a	0.31	0/1198	0.55	0/1608
32	b	0.30	0/479	0.57	0/634



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	c	0.27	0/721	0.47	0/969
34	d	0.29	0/824	0.54	0/1106
35	e	0.31	0/953	0.56	0/1271
36	f	0.31	0/859	0.53	0/1152
37	g	0.35	0/873	0.60	0/1170
38	h	0.29	0/1008	0.52	0/1340
39	i	0.27	0/774	0.56	0/1028
40	j	0.35	0/671	0.57	0/888
41	k	0.30	0/570	0.56	0/762
42	m	0.28	0/3471	0.50	0/4715
43	n	0.26	0/3037	0.47	0/4087
44	o	0.27	0/810	0.50	0/1074
45	p	0.24	0/1396	0.44	0/1935
46	u	0.50	0/509	0.63	0/678
All	All	0.37	0/131915	0.65	0/193342

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	3	121/302 (40%)	112 (93%)	7 (6%)	2 (2%)	9	36
4	8	48/51 (94%)	46 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	A	243/253 (96%)	234 (96%)	9 (4%)	0	100	100
7	B	375/388 (97%)	362 (96%)	13 (4%)	0	100	100
8	C	357/363 (98%)	338 (95%)	19 (5%)	0	100	100
9	D	282/294 (96%)	278 (99%)	4 (1%)	0	100	100
10	E	181/195 (93%)	167 (92%)	13 (7%)	1 (1%)	25	59
11	F	212/250 (85%)	206 (97%)	6 (3%)	0	100	100
12	G	227/259 (88%)	223 (98%)	4 (2%)	0	100	100
13	H	171/190 (90%)	167 (98%)	4 (2%)	0	100	100
14	I	164/221 (74%)	161 (98%)	3 (2%)	0	100	100
15	J	167/174 (96%)	163 (98%)	4 (2%)	0	100	100
16	K	88/94 (94%)	84 (96%)	4 (4%)	0	100	100
17	L	200/208 (96%)	190 (95%)	10 (5%)	0	100	100
18	M	123/134 (92%)	117 (95%)	6 (5%)	0	100	100
19	N	198/201 (98%)	188 (95%)	10 (5%)	0	100	100
20	O	194/197 (98%)	193 (100%)	1 (0%)	0	100	100
21	P	169/187 (90%)	162 (96%)	7 (4%)	0	100	100
22	Q	184/187 (98%)	173 (94%)	10 (5%)	1 (0%)	29	64
23	R	147/193 (76%)	146 (99%)	1 (1%)	0	100	100
24	S	164/176 (93%)	153 (93%)	11 (7%)	0	100	100
25	T	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
26	U	96/117 (82%)	90 (94%)	6 (6%)	0	100	100
27	V	134/139 (96%)	131 (98%)	3 (2%)	0	100	100
28	X	115/141 (82%)	114 (99%)	1 (1%)	0	100	100
29	Y	123/126 (98%)	119 (97%)	4 (3%)	0	100	100
30	Z	132/136 (97%)	125 (95%)	7 (5%)	0	100	100
31	a	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
32	b	54/61 (88%)	51 (94%)	2 (4%)	1 (2%)	8	33
33	c	93/117 (80%)	90 (97%)	3 (3%)	0	100	100
34	d	93/113 (82%)	92 (99%)	1 (1%)	0	100	100
35	e	115/127 (91%)	113 (98%)	2 (2%)	0	100	100
36	f	104/108 (96%)	99 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	g	104/112 (93%)	98 (94%)	6 (6%)	0	100	100
38	h	119/122 (98%)	118 (99%)	1 (1%)	0	100	100
39	i	94/99 (95%)	90 (96%)	4 (4%)	0	100	100
40	j	81/91 (89%)	78 (96%)	3 (4%)	0	100	100
41	k	68/74 (92%)	66 (97%)	2 (3%)	0	100	100
42	m	409/740 (55%)	386 (94%)	23 (6%)	0	100	100
43	n	351/607 (58%)	331 (94%)	20 (6%)	0	100	100
44	o	96/106 (91%)	93 (97%)	3 (3%)	0	100	100
45	p	274/440 (62%)	265 (97%)	9 (3%)	0	100	100
46	u	57/192 (30%)	55 (96%)	2 (4%)	0	100	100
All	All	7029/8593 (82%)	6760 (96%)	264 (4%)	5 (0%)	54	83

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	3	13	HIS
3	3	11	VAL
22	Q	184	ALA
32	b	7	HIS
10	E	135	LYS

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

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	3	111/271 (41%)	109 (98%)	2 (2%)	59	82
4	8	46/47 (98%)	46 (100%)	0	100	100
6	A	188/192 (98%)	187 (100%)	1 (0%)	88	94
7	B	316/326 (97%)	315 (100%)	1 (0%)	92	96
8	C	296/297 (100%)	295 (100%)	1 (0%)	92	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	D	234/241 (97%)	231 (99%)	3 (1%)	69	87
10	E	146/155 (94%)	145 (99%)	1 (1%)	84	93
11	F	180/210 (86%)	178 (99%)	2 (1%)	73	89
12	G	191/212 (90%)	189 (99%)	2 (1%)	76	90
14	I	144/187 (77%)	143 (99%)	1 (1%)	84	93
15	J	142/146 (97%)	137 (96%)	5 (4%)	36	68
16	K	71/75 (95%)	70 (99%)	1 (1%)	67	86
17	L	162/167 (97%)	162 (100%)	0	100	100
18	M	108/113 (96%)	108 (100%)	0	100	100
19	N	175/176 (99%)	174 (99%)	1 (1%)	86	94
20	O	161/162 (99%)	161 (100%)	0	100	100
21	P	139/149 (93%)	138 (99%)	1 (1%)	84	93
22	Q	158/159 (99%)	158 (100%)	0	100	100
23	R	127/162 (78%)	127 (100%)	0	100	100
24	S	150/154 (97%)	150 (100%)	0	100	100
25	T	138/139 (99%)	136 (99%)	2 (1%)	67	86
26	U	85/103 (82%)	83 (98%)	2 (2%)	49	76
27	V	104/107 (97%)	102 (98%)	2 (2%)	57	81
28	X	104/122 (85%)	103 (99%)	1 (1%)	76	90
29	Y	110/111 (99%)	109 (99%)	1 (1%)	78	91
30	Z	113/115 (98%)	111 (98%)	2 (2%)	59	82
31	a	121/122 (99%)	121 (100%)	0	100	100
32	b	47/51 (92%)	47 (100%)	0	100	100
33	c	76/91 (84%)	75 (99%)	1 (1%)	69	87
34	d	89/102 (87%)	89 (100%)	0	100	100
35	e	100/107 (94%)	99 (99%)	1 (1%)	76	90
36	f	89/91 (98%)	89 (100%)	0	100	100
37	g	92/97 (95%)	90 (98%)	2 (2%)	52	78
38	h	106/107 (99%)	106 (100%)	0	100	100
39	i	82/84 (98%)	81 (99%)	1 (1%)	71	88
40	j	68/71 (96%)	68 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	k	63/66 (96%)	60 (95%)	3 (5%)	25	58
42	m	378/659 (57%)	374 (99%)	4 (1%)	73	89
43	n	319/532 (60%)	315 (99%)	4 (1%)	69	87
44	o	88/93 (95%)	88 (100%)	0	100	100
46	u	52/168 (31%)	48 (92%)	4 (8%)	13	41
All	All	5669/6739 (84%)	5617 (99%)	52 (1%)	79	91

5 of 52 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	X	133	ASP
37	g	97	GLU
46	u	4	HIS
29	Y	2	LYS
33	c	50	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
43	n	190	GLN
46	u	37	HIS
25	T	98	HIS
28	X	136	ASN
32	b	43	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2823/3498 (80%)	580 (20%)	10 (0%)
2	2	157/165 (95%)	33 (21%)	1 (0%)
5	9	117/229 (51%)	14 (11%)	0
All	All	3097/3892 (79%)	627 (20%)	11 (0%)

5 of 627 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	4	U
1	1	5	G

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Mol	Chain	Res	Type
1	1	25	U
1	1	26	A
1	1	30	G

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1640	A
1	1	2198	G
2	2	131	G
1	1	3441	G
1	1	948	G

#### 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 monosaccharides in this entry.

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

Of 1 ligands modelled in this entry, 1 is 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

There are no chain breaks in this entry.

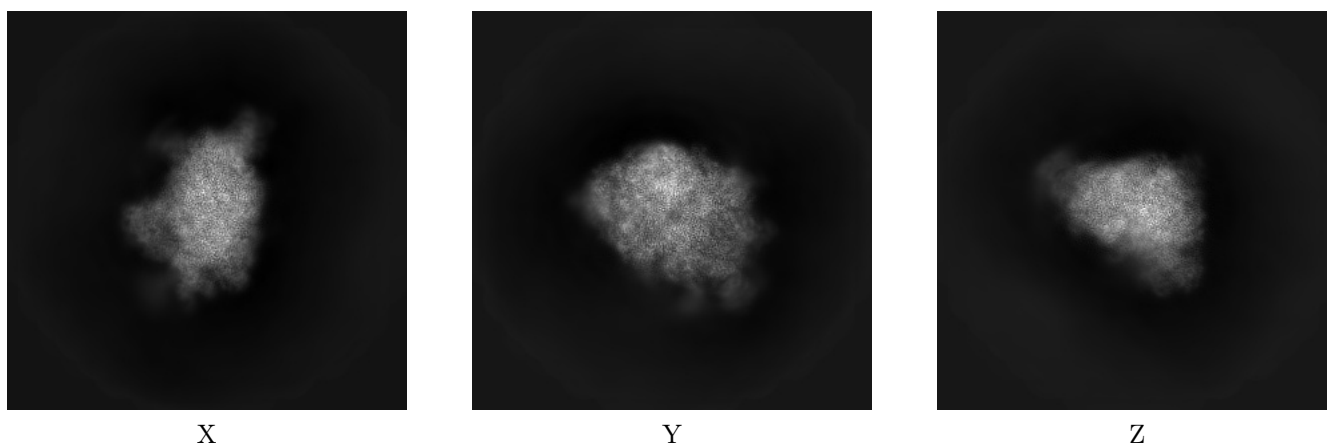
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24423. 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](#)

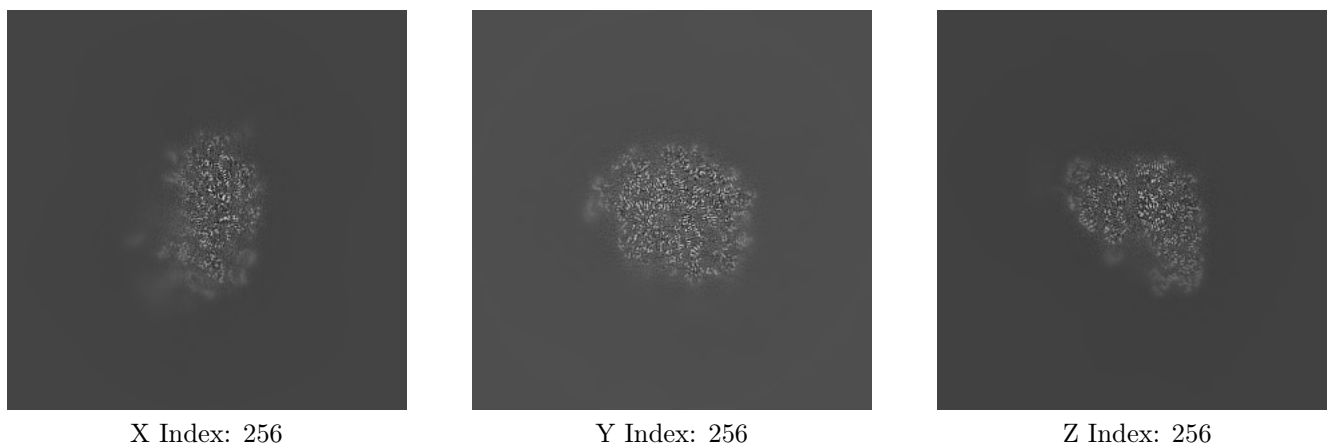
#### 6.1.1 Primary map



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

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

#### 6.2.1 Primary map

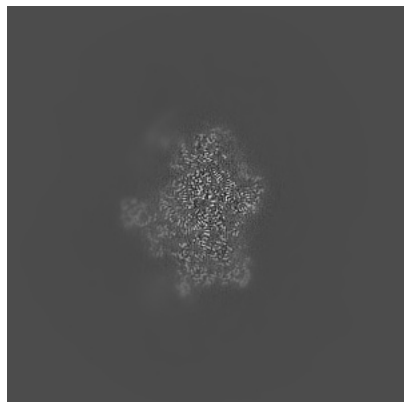




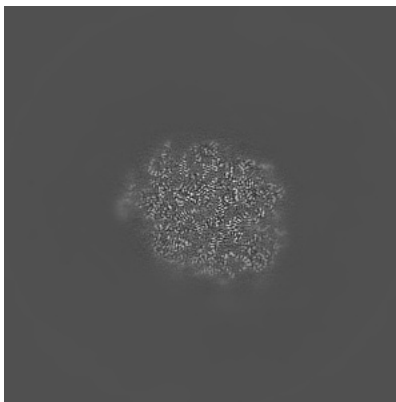
The images above show central slices of the map in three orthogonal directions.

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

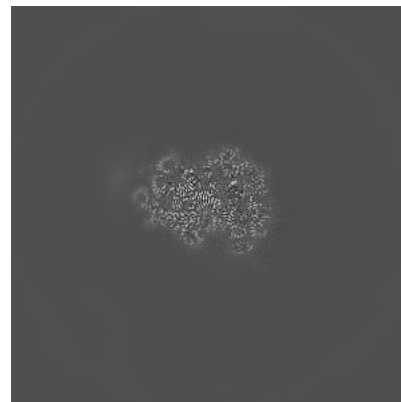
### 6.3.1 Primary map



X Index: 282



Y Index: 262



Z Index: 276

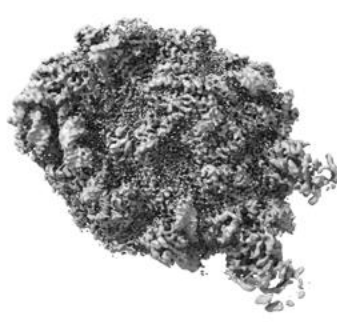
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

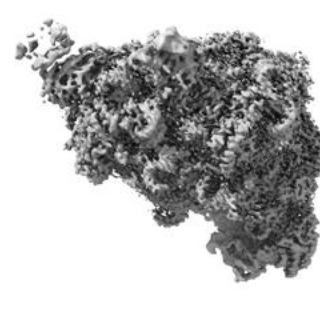
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

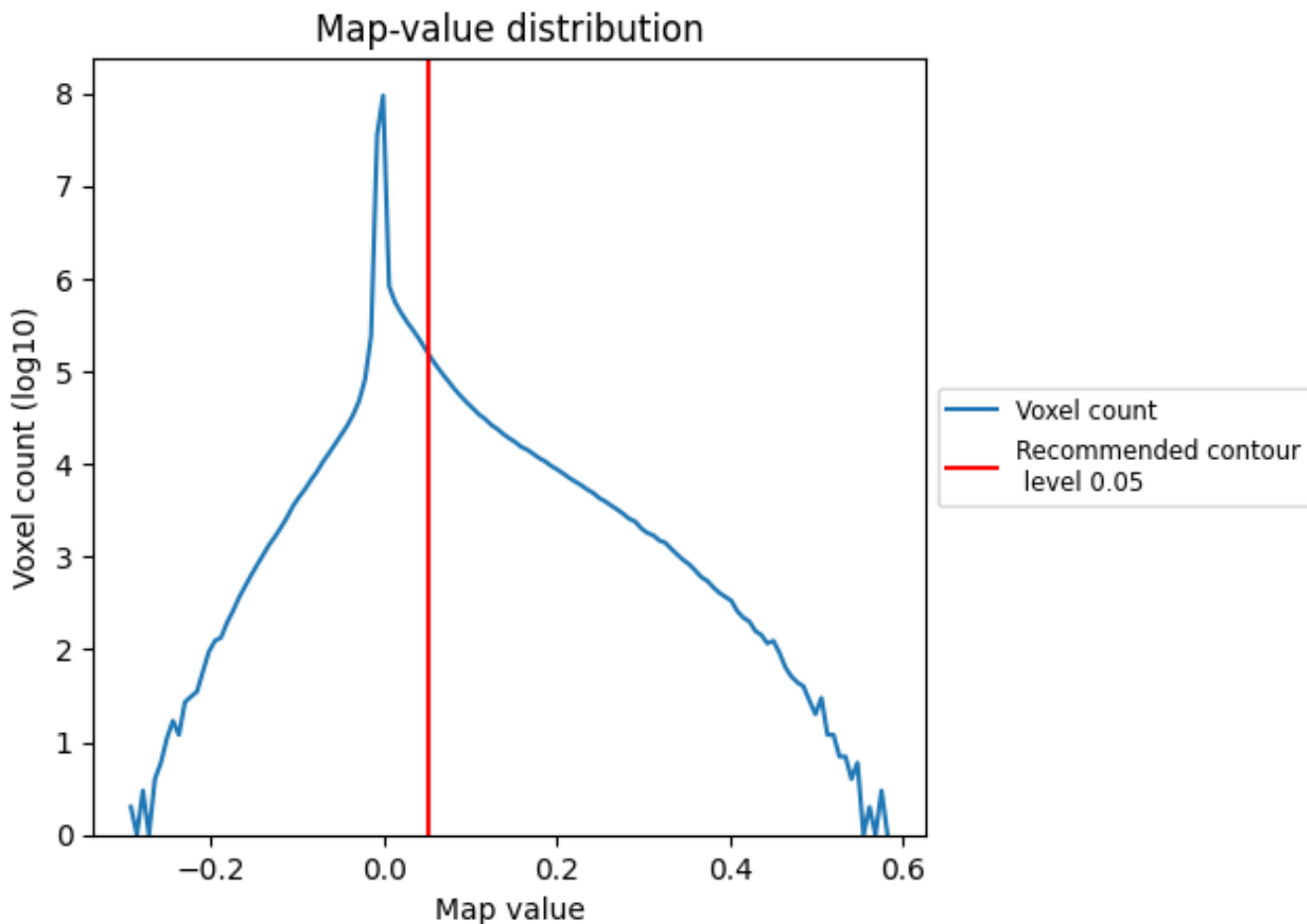
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

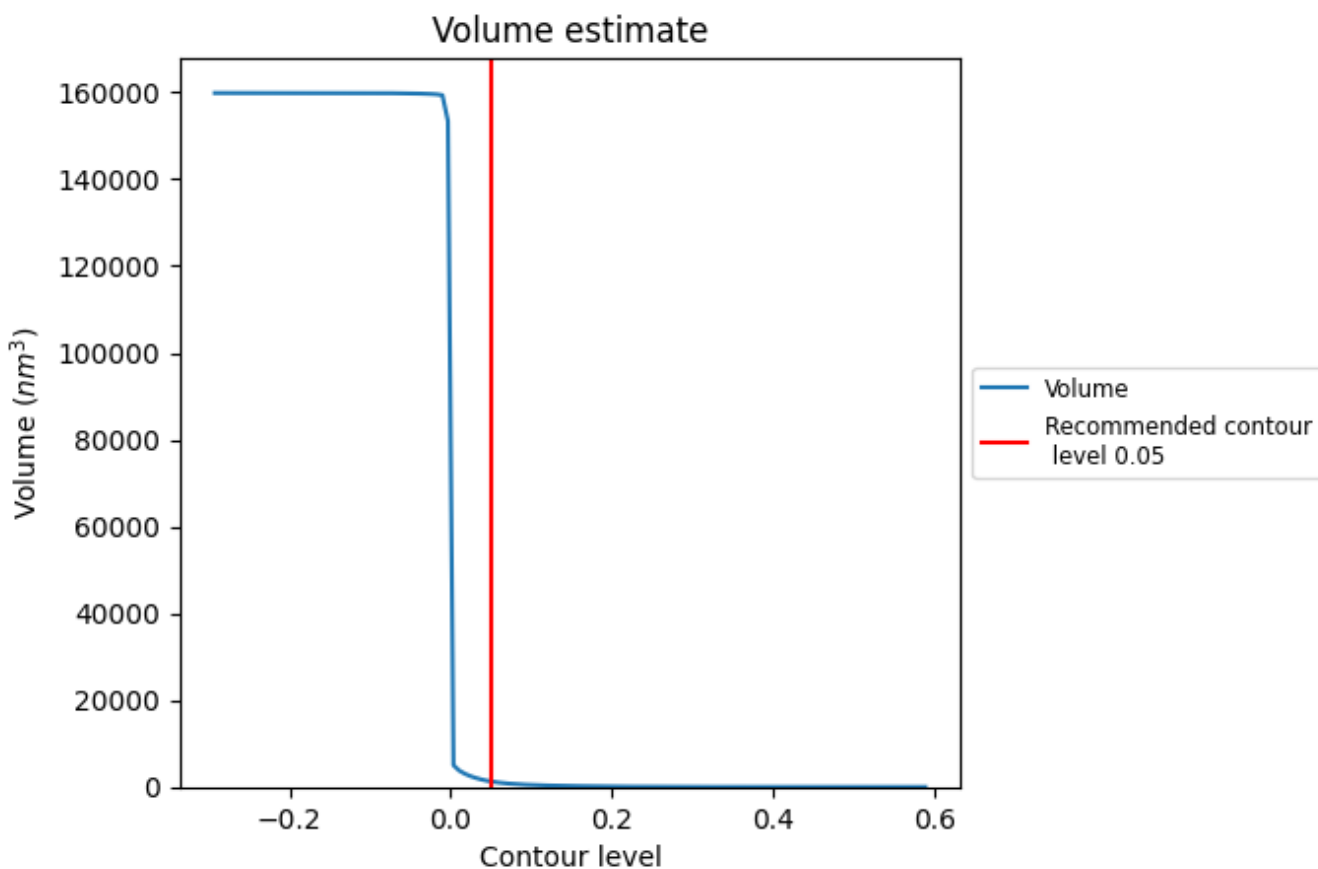
This section contains the results of statistical analysis of the map.

### 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.

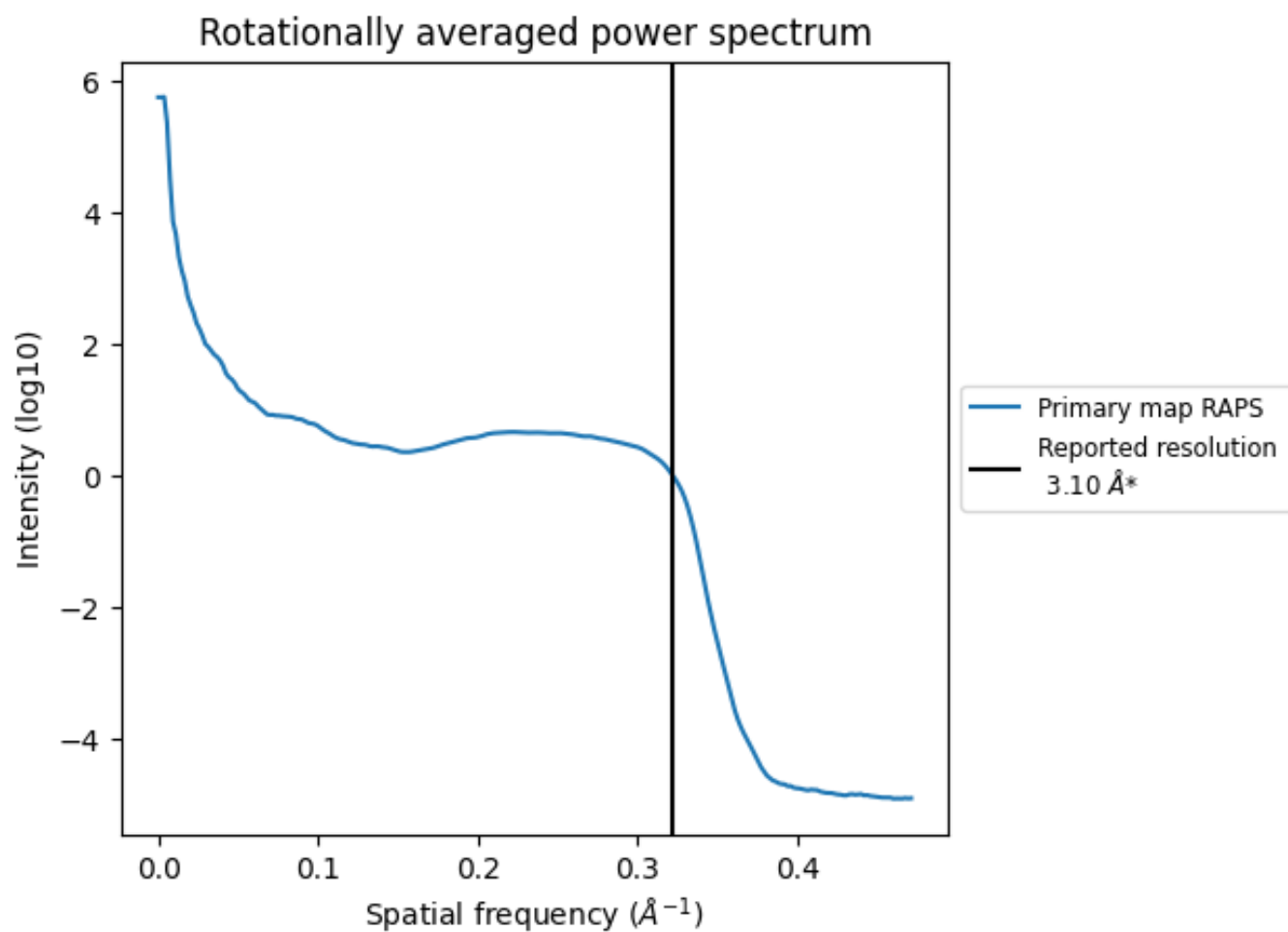
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1266  $\text{nm}^3$ ; this corresponds to an approximate mass of 1144 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 0.323 Å<sup>-1</sup>

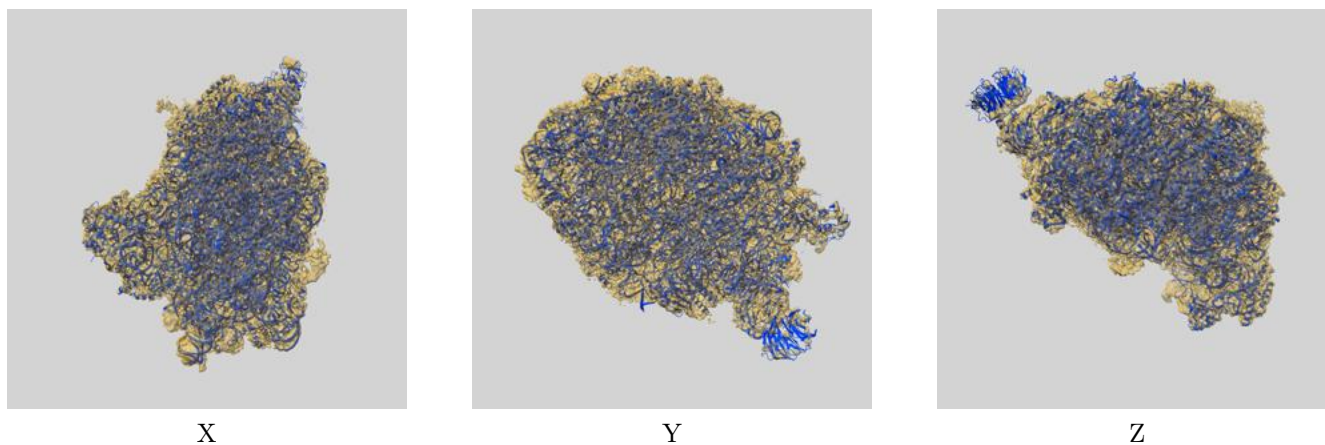
## 8 Fourier-Shell correlation

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

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

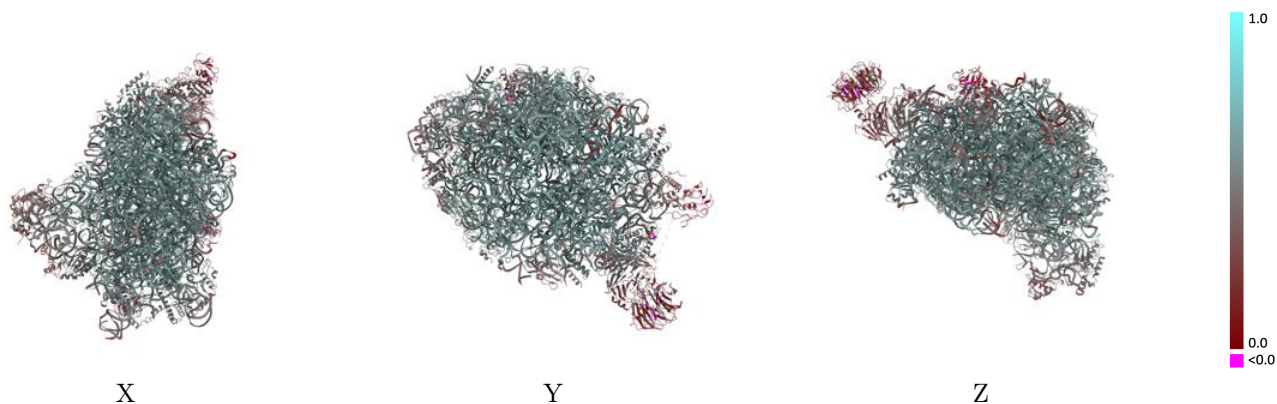
This section contains information regarding the fit between EMDB map EMD-24423 and PDB model 8EUI. Per-residue inclusion information can be found in section 3 on page 12.

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



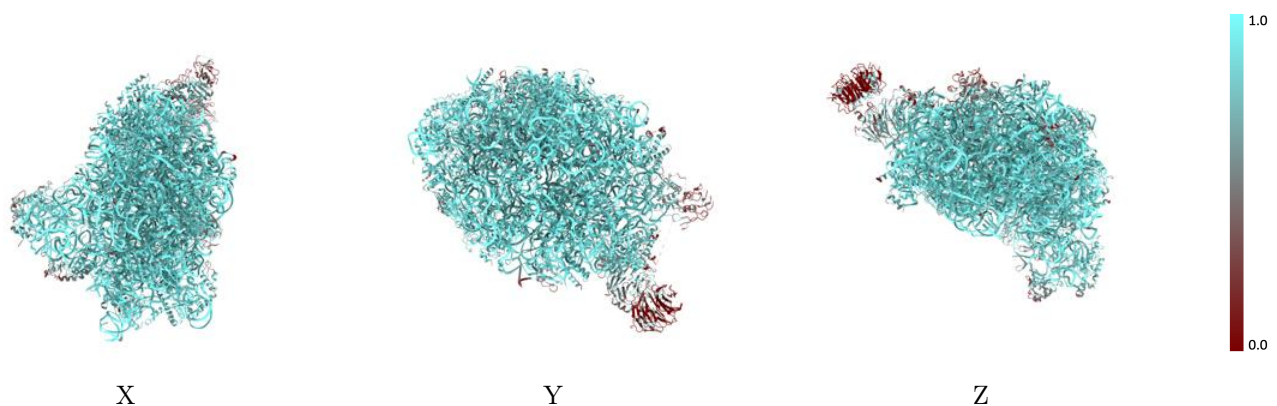
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



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.

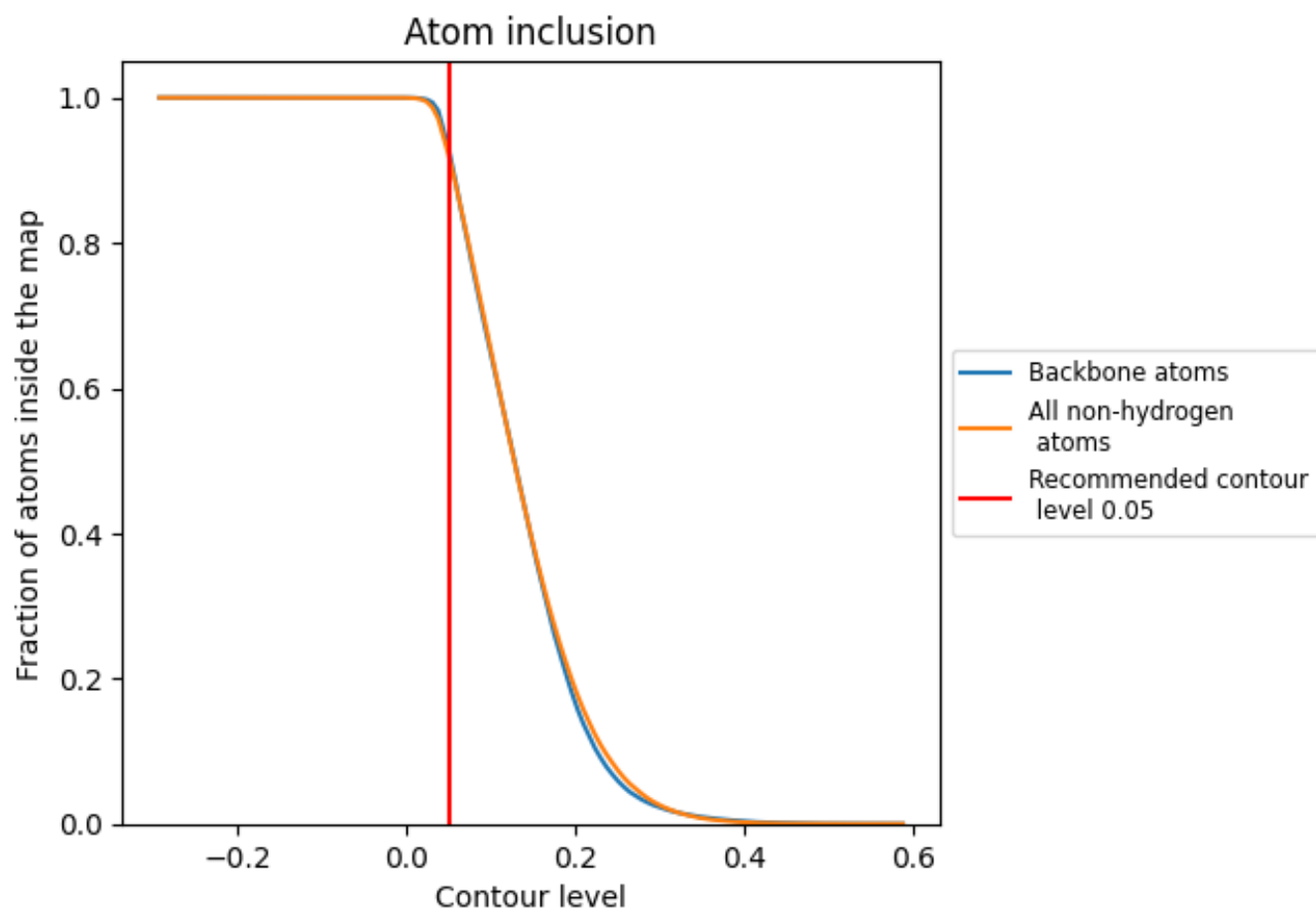
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.05).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 92% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9220	 0.5360
1	 0.9815	 0.5650
2	 0.9642	 0.5680
3	 0.7532	 0.4160
8	 0.9760	 0.5880
9	 0.9798	 0.4840
A	 0.9561	 0.5800
B	 0.9422	 0.5610
C	 0.9486	 0.5700
D	 0.8234	 0.4530
E	 0.7971	 0.4580
F	 0.9295	 0.5540
G	 0.8889	 0.5290
H	 0.8051	 0.3970
I	 0.7110	 0.4400
J	 0.6424	 0.3590
K	 0.9535	 0.5710
L	 0.9255	 0.5650
M	 0.9222	 0.4980
N	 0.9844	 0.6080
O	 0.9492	 0.5530
P	 0.9189	 0.5520
Q	 0.9596	 0.5710
R	 0.9423	 0.5570
S	 0.9126	 0.5180
T	 0.9273	 0.5490
U	 0.7056	 0.4050
V	 0.9484	 0.5560
X	 0.9553	 0.5750
Y	 0.9293	 0.5520
Z	 0.9110	 0.5250
a	 0.9514	 0.5850
b	 0.9161	 0.5410
c	 0.8398	 0.4990
d	 0.9462	 0.5760



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Chain	Atom inclusion	Q-score
e	 0.9724	 0.5910
f	 0.9644	 0.5720
g	 0.9504	 0.5840
h	 0.9379	 0.5660
i	 0.9293	 0.5410
j	 0.9889	 0.6120
k	 0.8236	 0.4730
m	 0.5993	 0.3460
n	 0.6156	 0.3550
o	 0.8943	 0.5390
p	 0.1827	 0.2420
u	 0.9116	 0.4920