



## wwPDB EM Validation Summary Report ⓘ

Nov 2, 2022 – 01:04 AM EDT

PDB ID : 5T6R  
EMDB ID : EMD-8368  
Title : Nmd3 is a structural mimic of eIF5A, and activates the cpGTPase Lsg1 during 60S ribosome biogenesis: 60S-Nmd3 Complex  
Authors : Malyutin, A.G.; Musalgaonkar, S.; Patchett, S.; Frank, J.; Johnson, A.W.  
Deposited on : 2016-09-01  
Resolution : 4.50 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

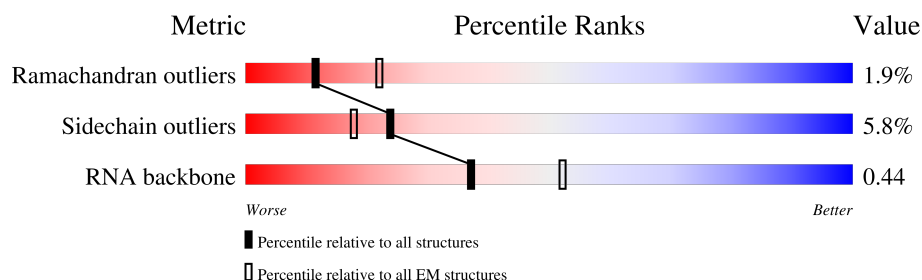
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.50 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	A	3396	
2	B	121	
3	C	158	
4	D	254	
5	E	387	
6	F	362	
7	G	297	
8	H	176	




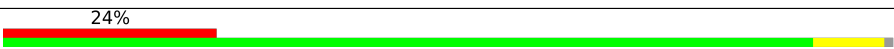
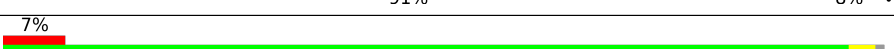
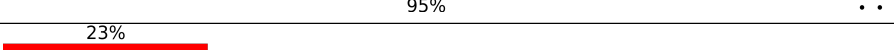
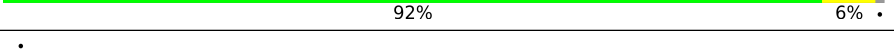
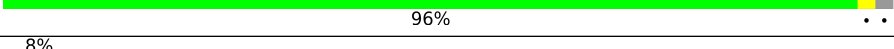


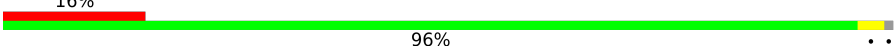

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Mol	Chain	Length	Quality of chain
9	I	244	
10	J	256	
11	K	191	
12	L	221	
13	M	174	
14	N	199	
15	O	138	
16	a	204	
17	b	199	
18	c	184	
19	d	186	
20	e	189	
21	f	172	
22	g	160	
23	h	121	
24	i	137	
25	j	155	
26	k	142	
27	l	127	
28	m	136	
29	n	149	
30	o	59	
31	p	105	
32	q	113	
33	r	130	

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Mol	Chain	Length	Quality of chain
34	s	107	
35	t	121	
36	u	120	
37	v	100	
38	w	88	
39	x	78	
40	y	51	
41	z	128	
42	Q	106	
43	R	92	
44	S	210	
45	V	917	

## 2 Entry composition

There are 48 unique types of molecules in this entry. The entry contains 126616 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 25S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3204	Total	C	N	O	P	0	0
			68535	30613	12358	22360	3204		

- Molecule 2 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 3 is a RNA chain called 5.8S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 12 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	211	Total	C	N	O	S	0	0
			1705	1083	322	294	6		

- Molecule 13 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 14 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 15 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	a	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	b	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 18 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	c	183	Total	C	N	O	0	0
			1420	882	281	257		

- Molecule 19 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	d	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 20 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	e	188	Total	C	N	O	0	0
			1521	935	326	260		

- Molecule 21 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	f	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 22 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	g	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 23 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	h	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	i	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 25 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	j	98	Total	C	N	O	S	0	0
			699	443	137	118	1		

- Molecule 26 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	k	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 27 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	l	126	Total	C	N	O	S	0	0
			993	625	192	176			

- Molecule 28 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	m	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 29 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	n	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	o	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	p	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 32 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	q	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	r	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 34 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	s	50	Total	C	N	O	0	0
			406	258	77	71		

- Molecule 35 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	t	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 36 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	u	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 37 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	v	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 38 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	w	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	x	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	y	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	z	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 42 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Q	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 43 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	R	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 44 is a protein called Ribosomal Protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	S	210	Total	C	N	O		0	0
			1050	630	210	210			

- Molecule 45 is a protein called Maltose binding protein, 60S ribosomal export protein Nmd3 fusion.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	V	251	Total	C	N	O	S	0	0
			1975	1263	333	372	7		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	-396	ILE	THR	conflict	UNP A0A0F8NYV9
V	-15	HIS	-	linker	UNP A0A0F8NYV9
V	-14	HIS	-	linker	UNP A0A0F8NYV9
V	-13	HIS	-	linker	UNP A0A0F8NYV9
V	-12	HIS	-	linker	UNP A0A0F8NYV9
V	-11	HIS	-	linker	UNP A0A0F8NYV9
V	-10	HIS	-	linker	UNP A0A0F8NYV9
V	-9	HIS	-	linker	UNP A0A0F8NYV9
V	-8	HIS	-	linker	UNP A0A0F8NYV9
V	-7	HIS	-	linker	UNP A0A0F8NYV9
V	-6	HIS	-	linker	UNP A0A0F8NYV9
V	-5	GLU	-	linker	UNP A0A0F8NYV9
V	-4	ASN	-	linker	UNP A0A0F8NYV9
V	-3	LEU	-	linker	UNP A0A0F8NYV9
V	-2	TYR	-	linker	UNP A0A0F8NYV9
V	-1	PHE	-	linker	UNP A0A0F8NYV9
V	0	GLN	-	linker	UNP A0A0F8NYV9
V	1	GLY	-	linker	UNP A0A0F8NYV9

- Molecule 46 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
46	A	84	Total 84	Mg 84	0
46	C	1	Total 1	Mg 1	0
46	i	1	Total 1	Mg 1	0

- Molecule 47 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
47	A	3	Total 3	K 3	0

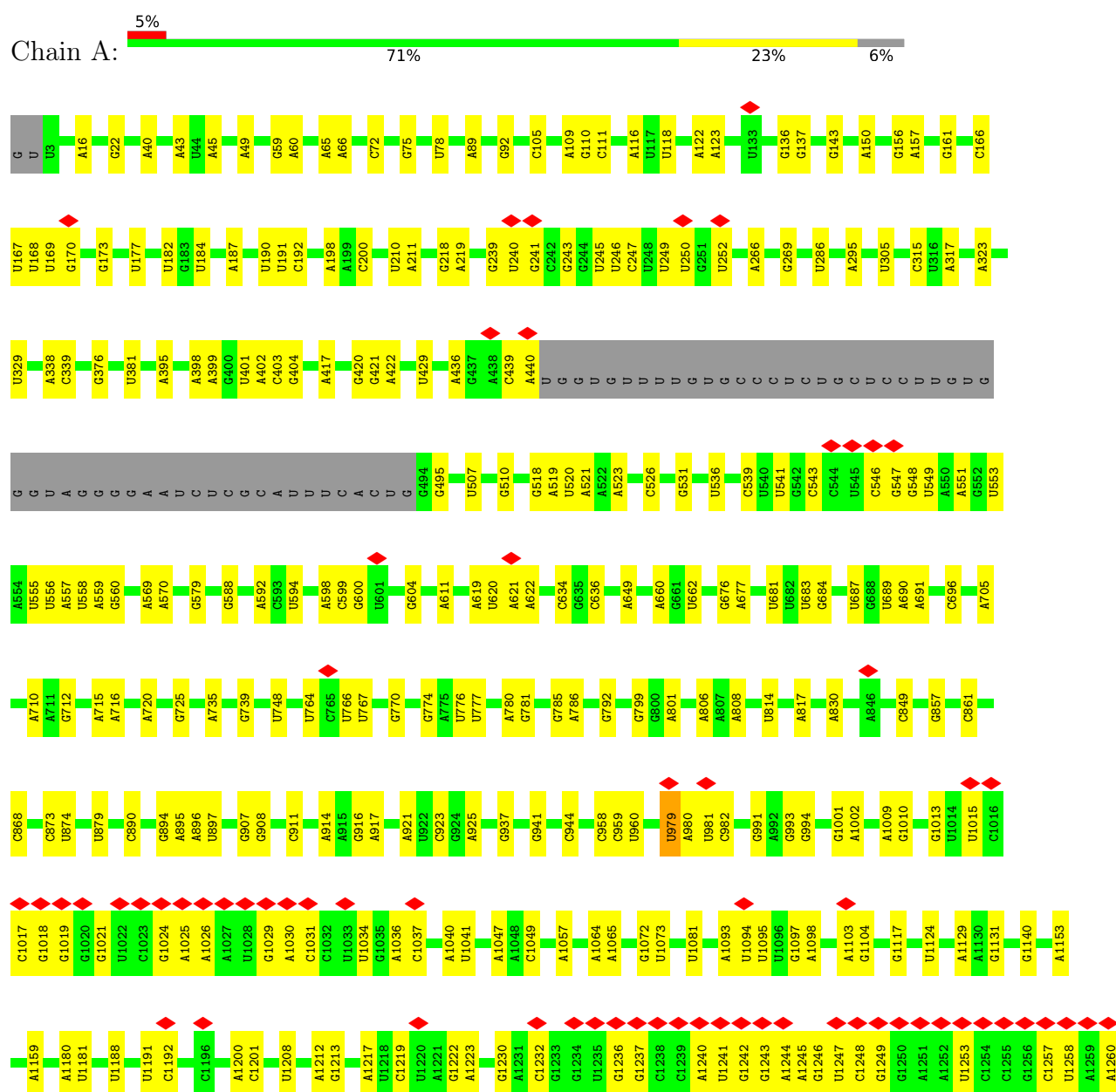
- Molecule 48 is water.

Mol	Chain	Residues	Atoms		AltConf
48	A	10	Total 10	O 10	0
48	c	1	Total 1	O 1	0
48	e	1	Total 1	O 1	0

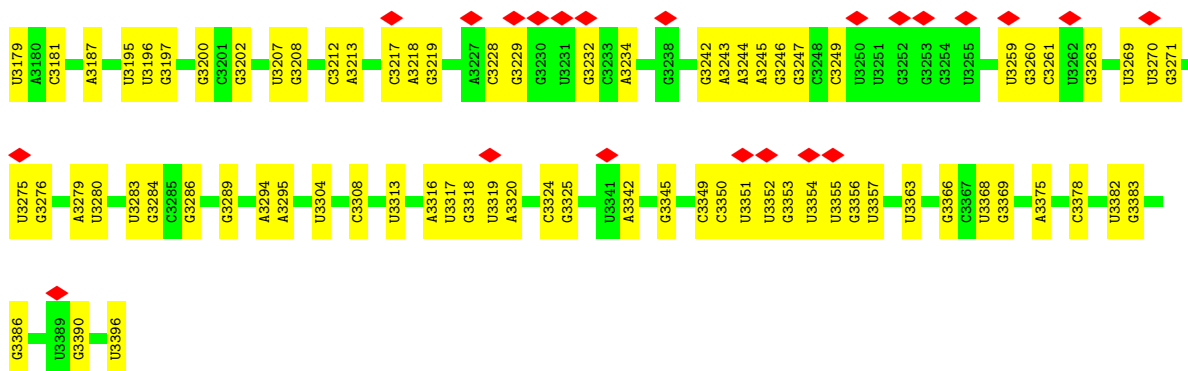
### 3 Residue-property plots

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.

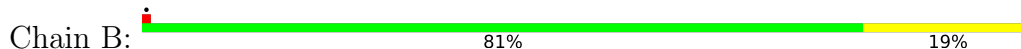
#### • Molecule 1: 25S Ribosomal RNA



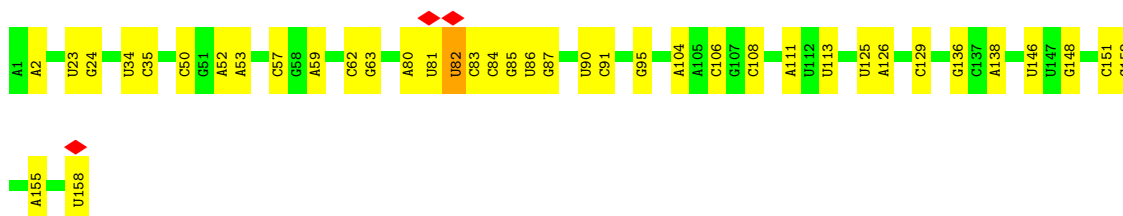




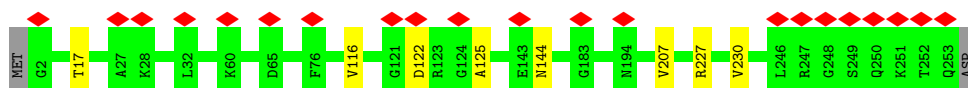
- Molecule 2: 5S Ribosomal RNA



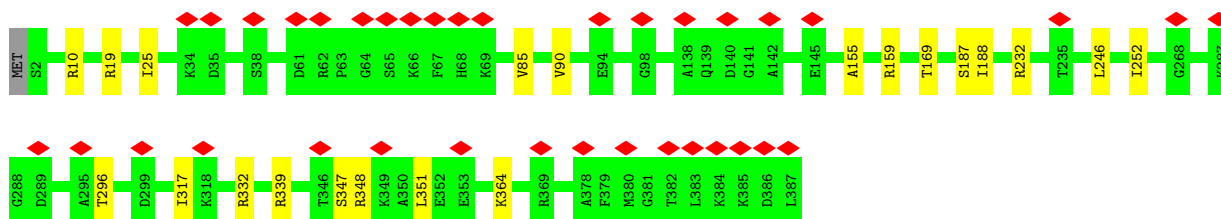
- Molecule 3: 5.8S Ribosomal RNA



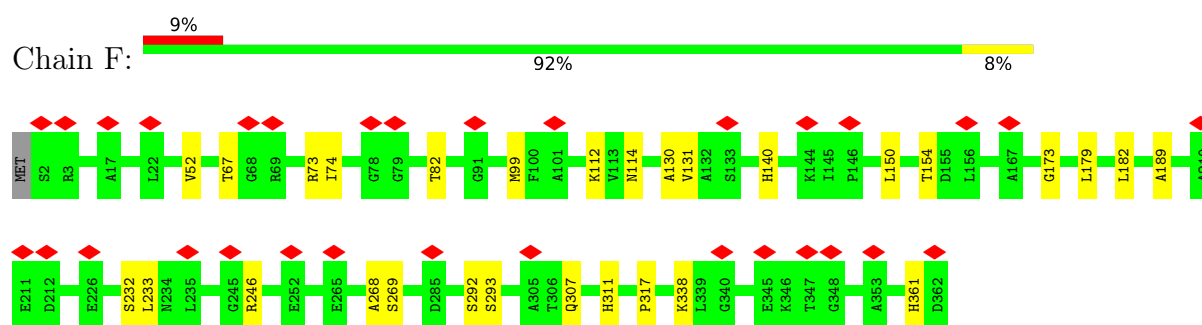
- Molecule 4: 60S ribosomal protein L2-A



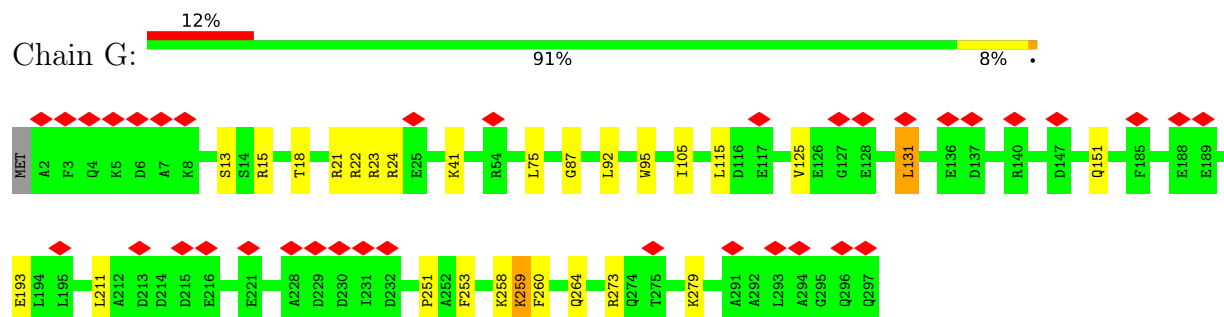
- Molecule 5: 60S ribosomal protein L3



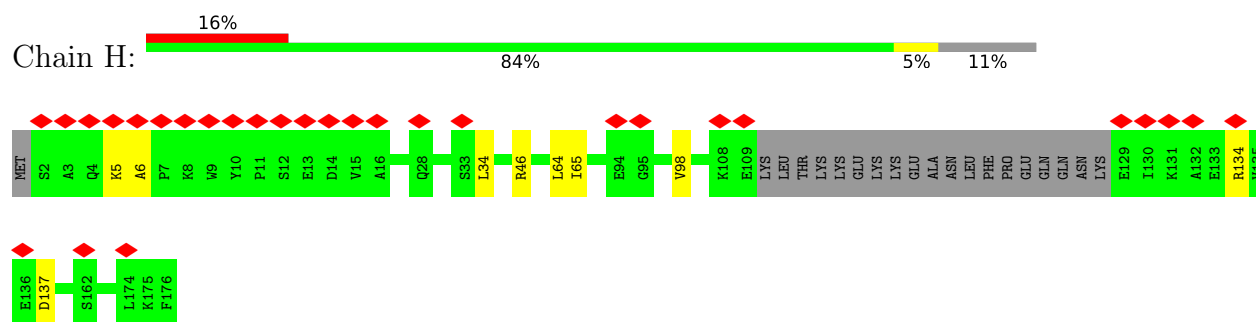
- Molecule 6: 60S ribosomal protein L4-A



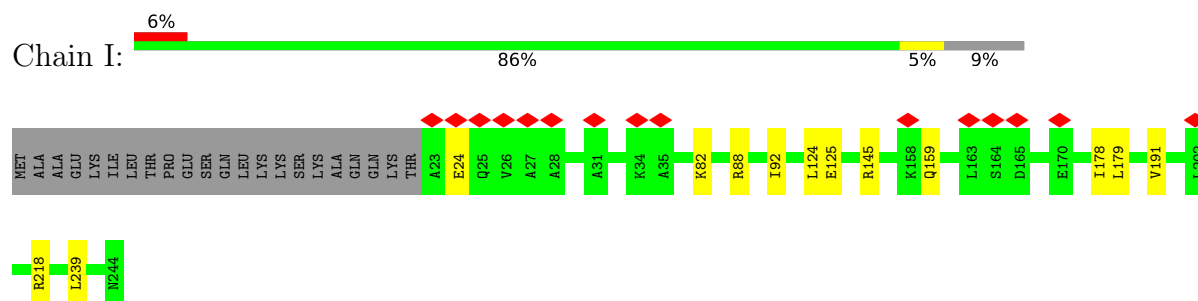
- Molecule 7: 60S ribosomal protein L5



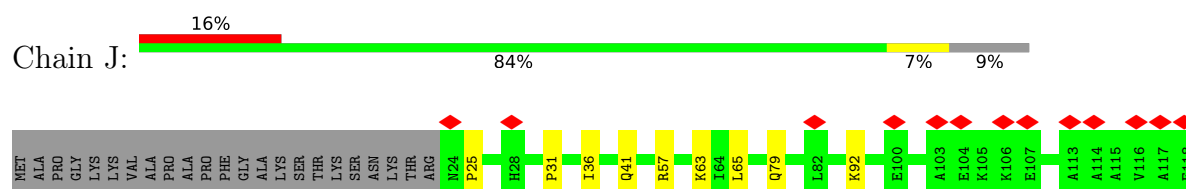
- Molecule 8: 60S ribosomal protein L6-A

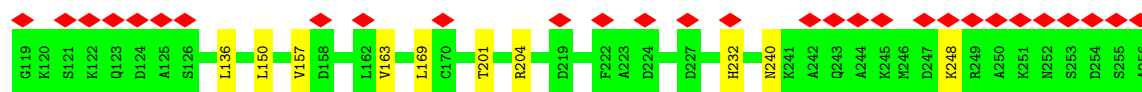


- Molecule 9: 60S ribosomal protein L7-A

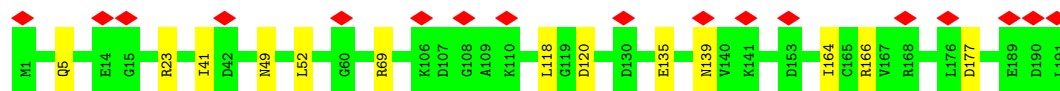


- Molecule 10: 60S ribosomal protein L8-A

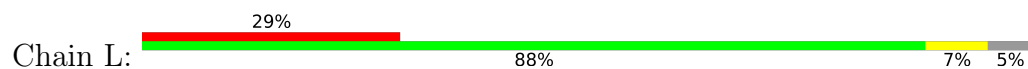




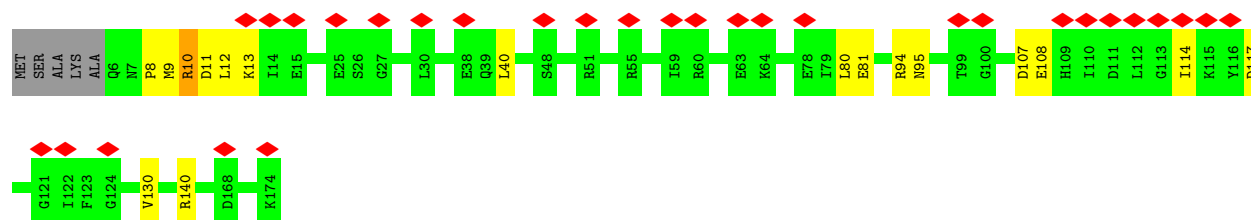
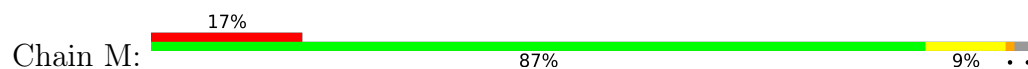
- Molecule 11: 60S ribosomal protein L9-A



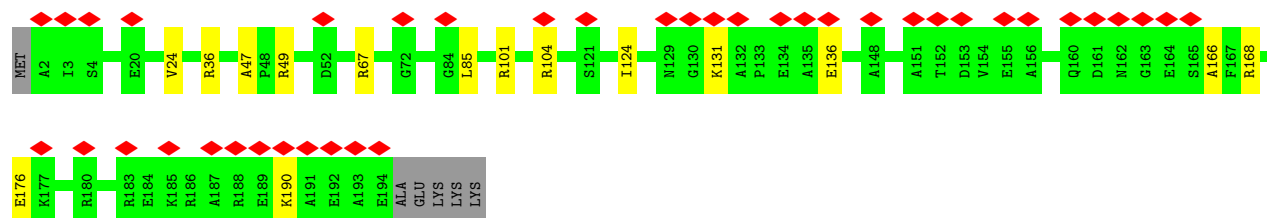
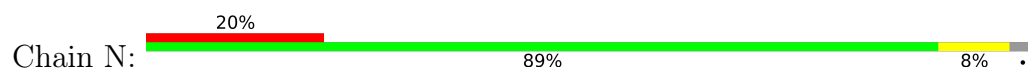
- Molecule 12: 60S ribosomal protein L10



- Molecule 13: 60S ribosomal protein L11-A

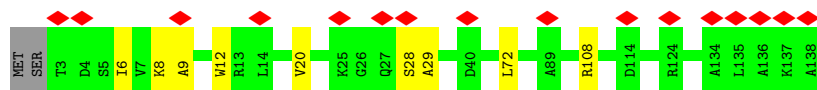


- Molecule 14: 60S ribosomal protein L13-A



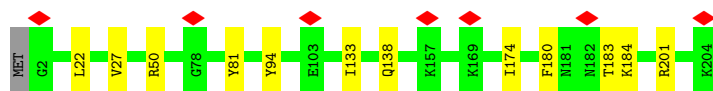
- Molecule 15: 60S ribosomal protein L14-A





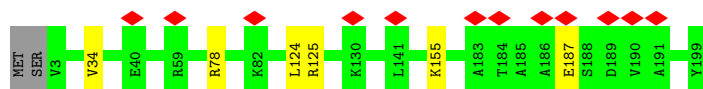
- Molecule 16: 60S ribosomal protein L15-A

Chain a: 94% 6%



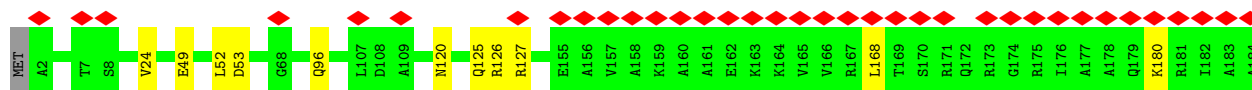
- Molecule 17: 60S ribosomal protein L16-A

Chain b: 96% 6%



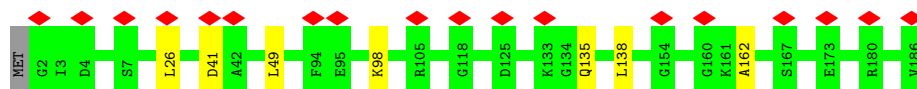
- Molecule 18: 60S ribosomal protein L17-A

Chain c: 93% 20% 6%



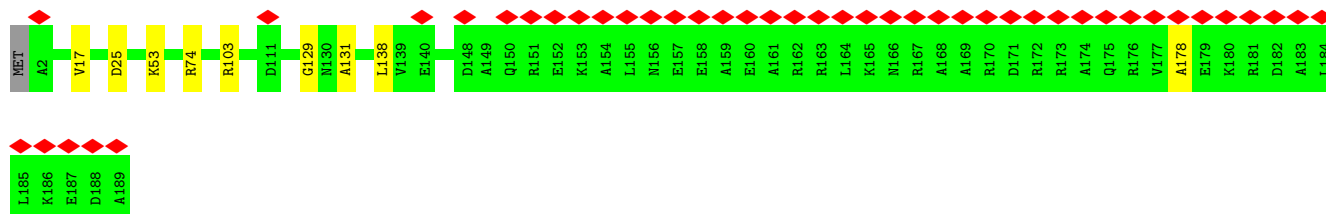
- Molecule 19: 60S ribosomal protein L18-A

Chain d: 96% 10%



- Molecule 20: 60S ribosomal protein L19-A

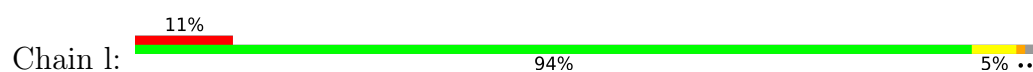
Chain e: 95% 23% 5%



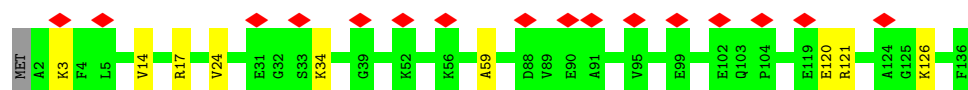
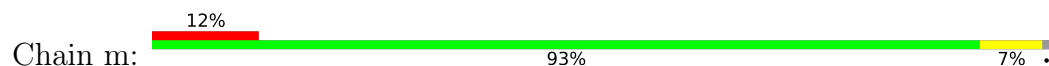
- Molecule 21: 60S ribosomal protein L20-A

Chain f: 95% 5%

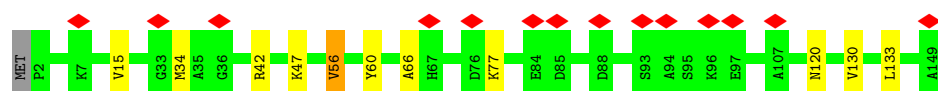




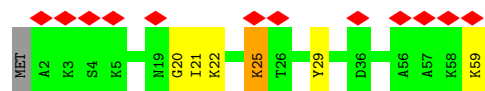
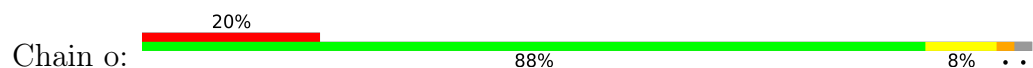
- Molecule 28: 60S ribosomal protein L27-A



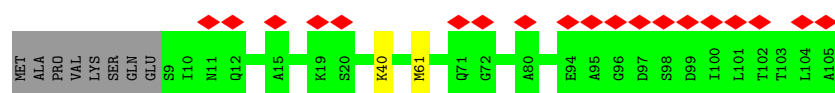
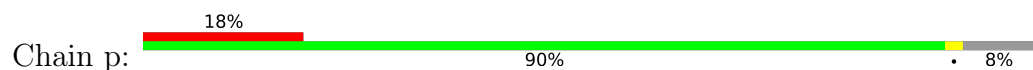
- Molecule 29: 60S ribosomal protein L28



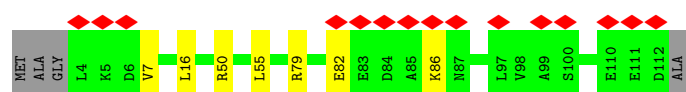
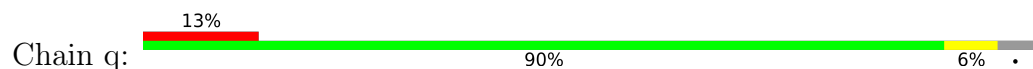
- Molecule 30: 60S ribosomal protein L29



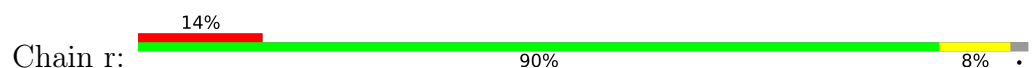
- Molecule 31: 60S ribosomal protein L30



- Molecule 32: 60S ribosomal protein L31-A

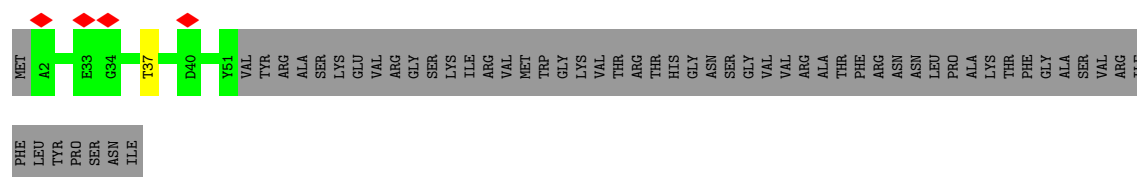


- Molecule 33: 60S ribosomal protein L32

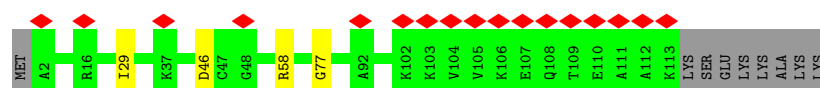
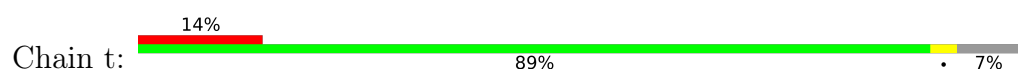




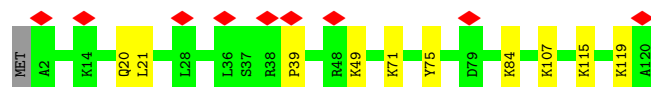
- Molecule 34: 60S ribosomal protein L33-A



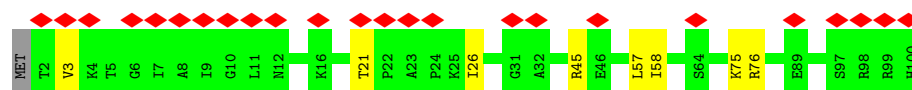
- Molecule 35: 60S ribosomal protein L34-A



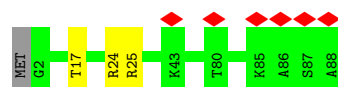
- Molecule 36: 60S ribosomal protein L35-A



- Molecule 37: 60S ribosomal protein L36-A

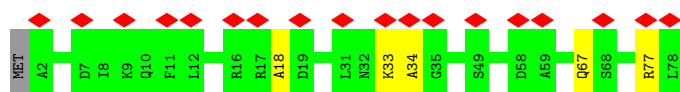


- Molecule 38: 60S ribosomal protein L37-A



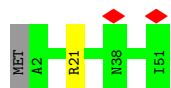
- Molecule 39: 60S ribosomal protein L38





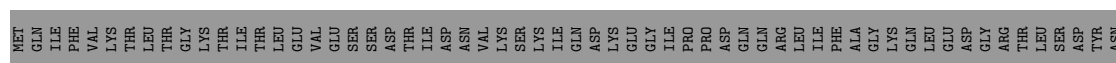
- Molecule 40: 60S ribosomal protein L39

Chain y: 96%



- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain z: 8%  
37% 59%



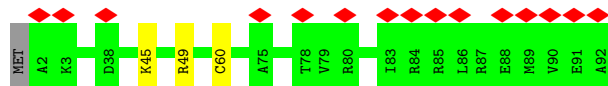
- Molecule 42: 60S ribosomal protein L42-A

Chain Q: 22%  
88% 11%



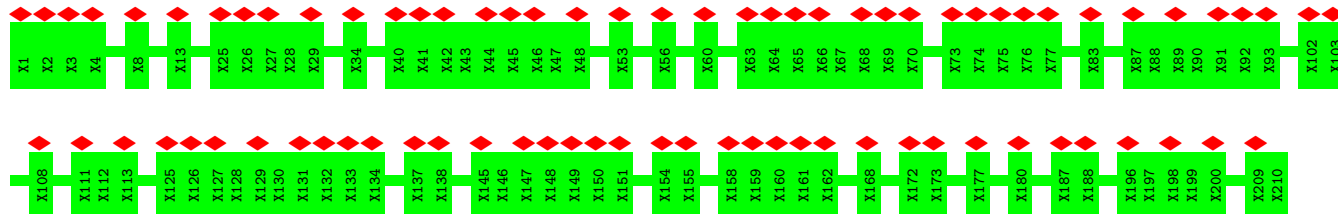
- Molecule 43: 60S ribosomal protein L43-A

Chain R: 16%  
96%



- Molecule 44: Ribosomal Protein uL1

Chain S: 37%  
100%



- Molecule 45: Maltose binding protein, 60S ribosomal export protein Nmd3 fusion



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	65650	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.094	Depositor
Minimum map value	-0.053	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0165	Depositor
Map size (Å)	403.2, 403.2, 403.2	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.26, 1.26, 1.26	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	0.24	1/76717 (0.0%)	0.69	8/119611 (0.0%)
2	B	0.24	0/2883	0.67	0/4491
3	C	0.23	0/3746	0.68	1/5832 (0.0%)
4	D	0.35	0/1948	0.63	0/2617
5	E	0.36	0/3146	0.62	0/4228
6	F	0.37	0/2800	0.58	0/3790
7	G	0.38	0/2425	0.60	1/3271 (0.0%)
8	H	0.37	0/1260	0.56	0/1694
9	I	0.38	0/1821	0.57	0/2451
10	J	0.37	0/1836	0.54	0/2481
11	K	0.36	0/1539	0.57	0/2073
12	L	0.38	0/1741	0.61	0/2335
13	M	0.38	0/1374	0.64	0/1842
14	N	0.39	0/1568	0.65	0/2106
15	O	0.36	0/1068	0.59	0/1438
16	a	0.38	0/1757	0.68	0/2354
17	b	0.37	0/1585	0.55	0/2128
18	c	0.36	0/1443	0.62	0/1944
19	d	0.37	0/1465	0.65	0/1965
20	e	0.36	0/1538	0.62	0/2050
21	f	0.36	0/1481	0.59	0/1990
22	g	0.36	0/1300	0.58	0/1743
23	h	0.39	0/812	0.51	0/1099
24	i	0.36	0/1018	0.59	0/1369
25	j	0.38	0/712	0.58	0/958
26	k	0.35	0/979	0.55	0/1321
27	l	0.36	0/1004	0.60	0/1341
28	m	0.37	0/1118	0.54	0/1497
29	n	0.35	0/1204	0.62	0/1612
30	o	0.37	0/473	0.61	0/629
31	p	0.36	0/751	0.50	0/1008
32	q	0.35	0/890	0.60	0/1196

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	r	0.36	0/1041	0.60	0/1394
34	s	0.36	0/414	0.58	0/556
35	t	0.35	0/890	0.63	0/1189
36	u	0.37	0/978	0.60	0/1301
37	v	0.40	0/778	0.60	0/1034
38	w	0.39	0/696	0.66	0/923
39	x	0.35	0/618	0.56	0/826
40	y	0.39	0/443	0.64	0/588
41	z	0.38	0/423	0.61	0/562
42	Q	0.37	0/860	0.60	0/1136
43	R	0.37	0/701	0.65	0/934
45	V	0.39	0/2015	0.75	3/2738 (0.1%)
All	All	0.30	1/135259 (0.0%)	0.66	13/199645 (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
30	o	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2595	A	C5-C6	5.44	1.46	1.41

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	V	386	GLY	C-N-CA	14.40	157.70	121.70
45	V	386	GLY	O-C-N	-13.14	101.67	122.70
45	V	386	GLY	CA-C-N	9.55	138.20	117.20
1	A	2249	G	C2'-C3'-O3'	7.62	126.26	109.50
1	A	1307	G	C2'-C3'-O3'	7.11	125.14	109.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
30	o	20	GLY	Peptide

## 5.2 Too-close contacts ⓘ

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

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	
4	D	250/254 (98%)	228 (91%)	20 (8%)	2 (1%)	19	60
5	E	384/387 (99%)	343 (89%)	34 (9%)	7 (2%)	8	42
6	F	359/362 (99%)	311 (87%)	32 (9%)	16 (4%)	2	24
7	G	294/297 (99%)	267 (91%)	19 (6%)	8 (3%)	5	34
8	H	152/176 (86%)	137 (90%)	12 (8%)	3 (2%)	7	40
9	I	220/244 (90%)	203 (92%)	14 (6%)	3 (1%)	11	47
10	J	231/256 (90%)	202 (87%)	24 (10%)	5 (2%)	6	38
11	K	189/191 (99%)	173 (92%)	16 (8%)	0	100	100
12	L	207/221 (94%)	187 (90%)	17 (8%)	3 (1%)	11	47
13	M	167/174 (96%)	145 (87%)	15 (9%)	7 (4%)	3	25
14	N	191/199 (96%)	170 (89%)	19 (10%)	2 (1%)	15	54
15	O	134/138 (97%)	125 (93%)	5 (4%)	4 (3%)	4	31
16	a	201/204 (98%)	189 (94%)	9 (4%)	3 (2%)	10	46
17	b	195/199 (98%)	187 (96%)	7 (4%)	1 (0%)	29	68
18	c	181/184 (98%)	161 (89%)	20 (11%)	0	100	100
19	d	183/186 (98%)	169 (92%)	11 (6%)	3 (2%)	9	45
20	e	186/189 (98%)	175 (94%)	7 (4%)	4 (2%)	6	38
21	f	170/172 (99%)	158 (93%)	10 (6%)	2 (1%)	13	50
22	g	157/160 (98%)	142 (90%)	12 (8%)	3 (2%)	8	41
23	h	98/121 (81%)	84 (86%)	13 (13%)	1 (1%)	15	54
24	i	134/137 (98%)	126 (94%)	7 (5%)	1 (1%)	22	62

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	j	96/155 (62%)	83 (86%)	10 (10%)	3 (3%)	4	31
26	k	119/142 (84%)	111 (93%)	7 (6%)	1 (1%)	19	60
27	l	124/127 (98%)	115 (93%)	7 (6%)	2 (2%)	9	45
28	m	133/136 (98%)	113 (85%)	18 (14%)	2 (2%)	10	46
29	n	146/149 (98%)	125 (86%)	16 (11%)	5 (3%)	3	29
30	o	56/59 (95%)	48 (86%)	5 (9%)	3 (5%)	2	22
31	p	95/105 (90%)	89 (94%)	6 (6%)	0	100	100
32	q	107/113 (95%)	98 (92%)	7 (6%)	2 (2%)	8	41
33	r	125/130 (96%)	115 (92%)	8 (6%)	2 (2%)	9	45
34	s	48/107 (45%)	46 (96%)	2 (4%)	0	100	100
35	t	110/121 (91%)	105 (96%)	3 (3%)	2 (2%)	8	42
36	u	117/120 (98%)	108 (92%)	6 (5%)	3 (3%)	5	35
37	v	97/100 (97%)	88 (91%)	7 (7%)	2 (2%)	7	39
38	w	85/88 (97%)	76 (89%)	9 (11%)	0	100	100
39	x	75/78 (96%)	68 (91%)	4 (5%)	3 (4%)	3	26
40	y	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
41	z	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	7	40
42	Q	103/106 (97%)	88 (85%)	11 (11%)	4 (4%)	3	26
43	R	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
45	V	249/917 (27%)	222 (89%)	20 (8%)	7 (3%)	5	33
All	All	6355/7475 (85%)	5756 (91%)	479 (8%)	120 (2%)	11	41

5 of 120 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	292	SER
9	I	178	ILE
10	J	31	PRO
10	J	157	VAL
14	N	47	ALA

### 5.3.2 Protein sidechains ⓘ

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	
4	D	193/196 (98%)	187 (97%)	6 (3%)	40	63
5	E	318/323 (98%)	304 (96%)	14 (4%)	28	54
6	F	288/289 (100%)	275 (96%)	13 (4%)	27	54
7	G	244/245 (100%)	224 (92%)	20 (8%)	11	37
8	H	134/153 (88%)	128 (96%)	6 (4%)	27	54
9	I	186/205 (91%)	176 (95%)	10 (5%)	22	49
10	J	187/208 (90%)	173 (92%)	14 (8%)	13	40
11	K	171/171 (100%)	158 (92%)	13 (8%)	13	40
12	L	177/187 (95%)	164 (93%)	13 (7%)	14	41
13	M	147/150 (98%)	136 (92%)	11 (8%)	13	40
14	N	154/159 (97%)	141 (92%)	13 (8%)	11	36
15	O	107/109 (98%)	102 (95%)	5 (5%)	26	52
16	a	175/176 (99%)	166 (95%)	9 (5%)	24	50
17	b	160/162 (99%)	155 (97%)	5 (3%)	40	63
18	c	140/146 (96%)	129 (92%)	11 (8%)	12	38
19	d	150/151 (99%)	146 (97%)	4 (3%)	44	66
20	e	153/154 (99%)	148 (97%)	5 (3%)	38	61
21	f	156/156 (100%)	149 (96%)	7 (4%)	27	54
22	g	136/137 (99%)	125 (92%)	11 (8%)	11	37
23	h	87/107 (81%)	85 (98%)	2 (2%)	50	70
24	i	104/105 (99%)	98 (94%)	6 (6%)	20	47
25	j	57/129 (44%)	57 (100%)	0	100	100
26	k	104/118 (88%)	96 (92%)	8 (8%)	13	39
27	l	109/110 (99%)	103 (94%)	6 (6%)	21	49
28	m	115/116 (99%)	108 (94%)	7 (6%)	18	46
29	n	118/119 (99%)	111 (94%)	7 (6%)	19	47
30	o	46/47 (98%)	43 (94%)	3 (6%)	17	44
31	p	81/88 (92%)	79 (98%)	2 (2%)	47	68
32	q	92/97 (95%)	87 (95%)	5 (5%)	22	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	r	109/111 (98%)	101 (93%)	8 (7%)	14	41
34	s	43/91 (47%)	42 (98%)	1 (2%)	50	70
35	t	95/103 (92%)	93 (98%)	2 (2%)	53	72
36	u	104/105 (99%)	97 (93%)	7 (7%)	16	43
37	v	81/82 (99%)	75 (93%)	6 (7%)	13	40
38	w	70/71 (99%)	67 (96%)	3 (4%)	29	55
39	x	68/69 (99%)	66 (97%)	2 (3%)	42	64
40	y	45/46 (98%)	44 (98%)	1 (2%)	52	71
41	z	47/116 (40%)	43 (92%)	4 (8%)	10	36
42	Q	90/91 (99%)	82 (91%)	8 (9%)	9	33
43	R	71/72 (99%)	68 (96%)	3 (4%)	30	55
45	V	224/791 (28%)	193 (86%)	31 (14%)	3	19
All	All	5336/6261 (85%)	5024 (94%)	312 (6%)	24	47

5 of 312 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	q	16	LEU
45	V	177	LEU
33	r	33	ARG
38	w	17	THR
45	V	356	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
42	Q	82	GLN
45	V	231	GLN
45	V	388	ASN
45	V	163	GLN
16	a	87	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3201/3396 (94%)	770 (24%)	77 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	120/121 (99%)	22 (18%)	2 (1%)
3	C	157/158 (99%)	38 (24%)	3 (1%)
All	All	3478/3675 (94%)	830 (23%)	82 (2%)

5 of 830 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	16	A
1	A	22	G
1	A	40	A
1	A	43	A
1	A	45	A

5 of 82 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2585	G
1	A	3242	G
1	A	2754	G
1	A	3056	U
1	A	3351	U

## 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 89 ligands modelled in this entry, 89 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

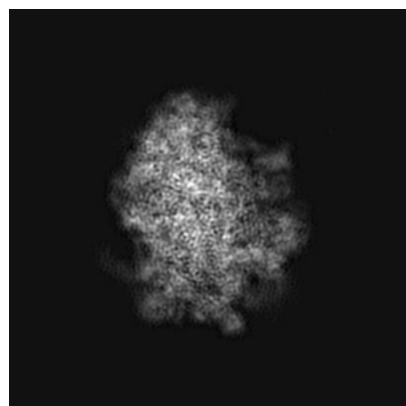
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8368. These allow visual inspection of the internal detail of the map and identification of artifacts.

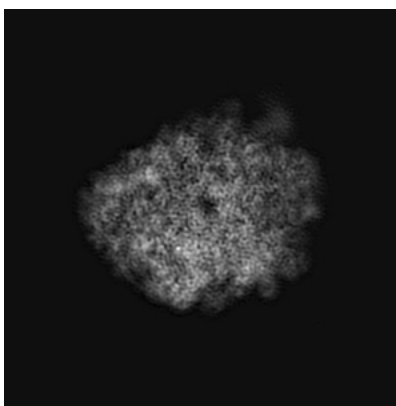
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

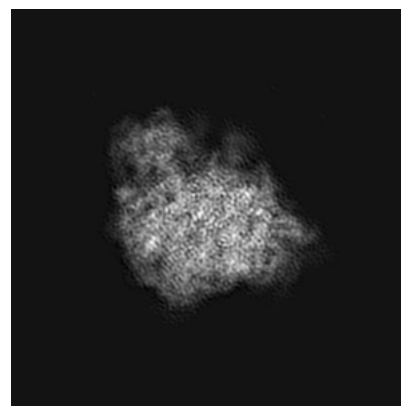
#### 6.1.1 Primary map



X

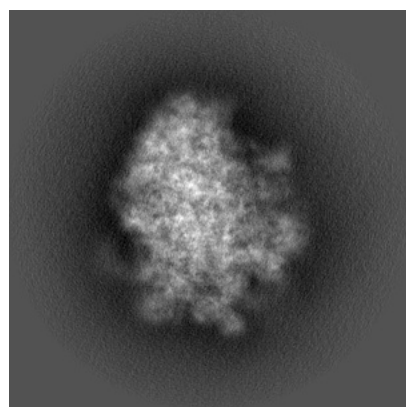


Y

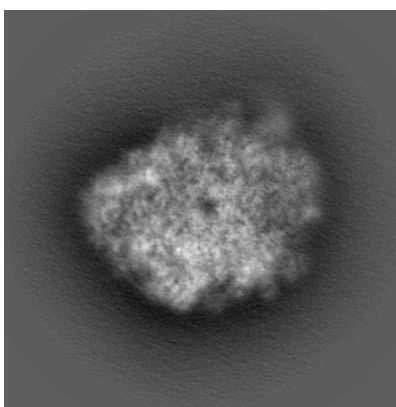


Z

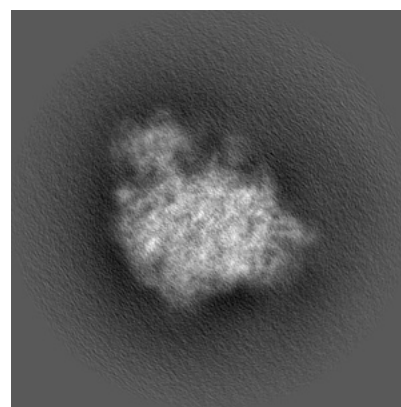
#### 6.1.2 Raw map



X



Y

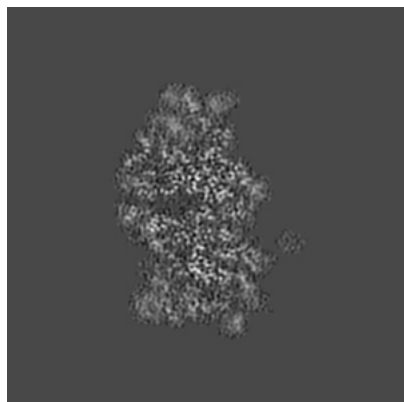


Z

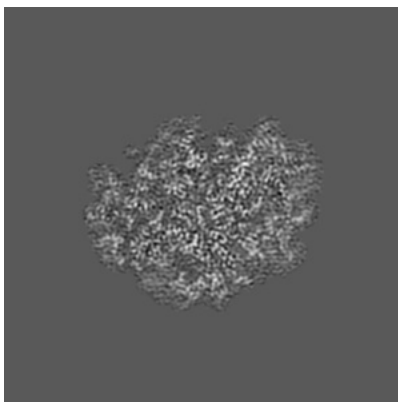
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

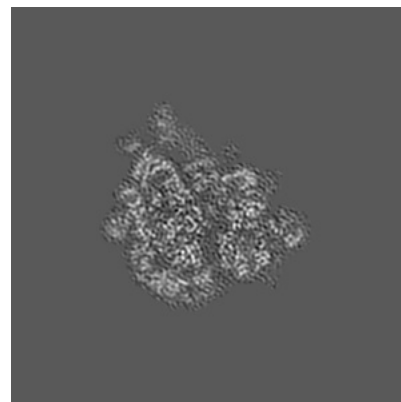
### 6.2.1 Primary map



X Index: 160

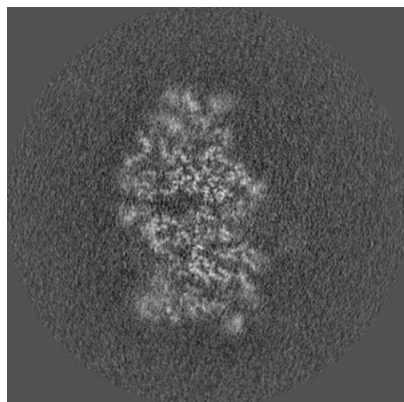


Y Index: 160

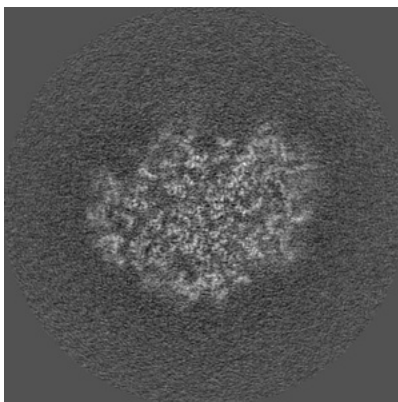


Z Index: 160

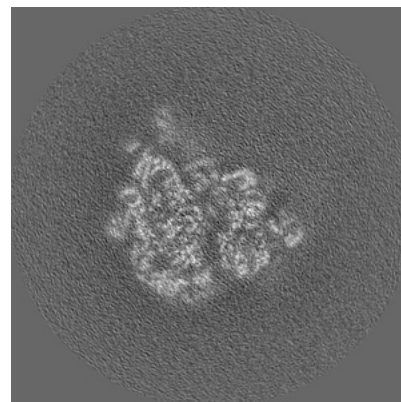
### 6.2.2 Raw map



X Index: 160



Y Index: 160

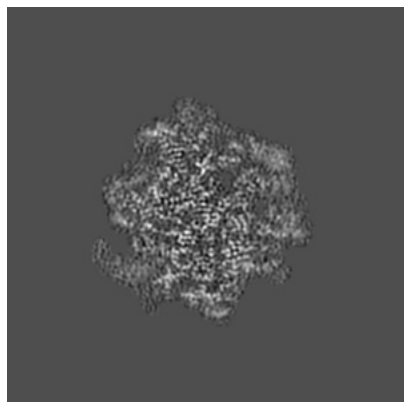


Z Index: 160

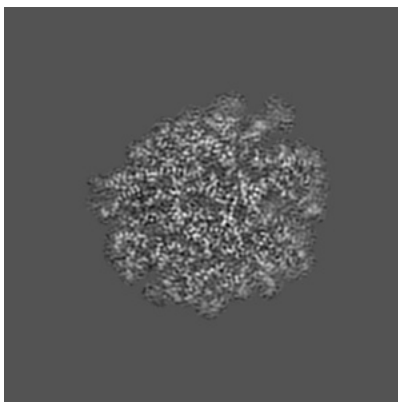
The images above show central slices of the map in three orthogonal directions.

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

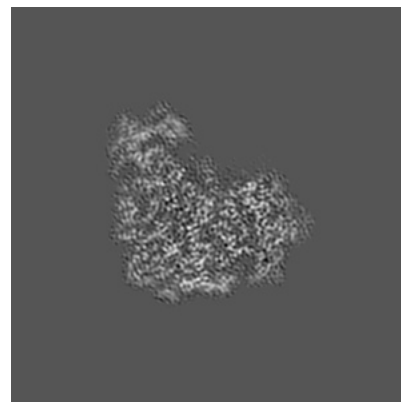
### 6.3.1 Primary map



X Index: 129

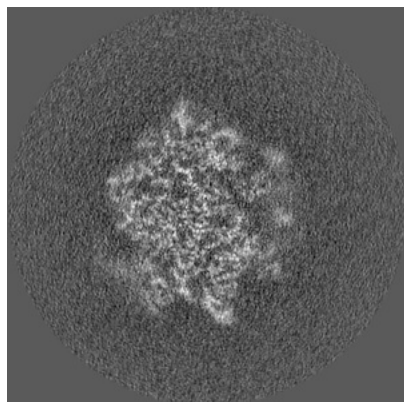


Y Index: 142

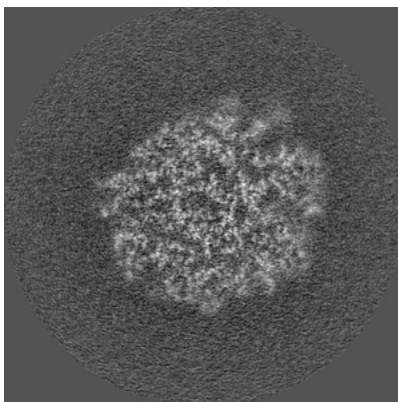


Z Index: 151

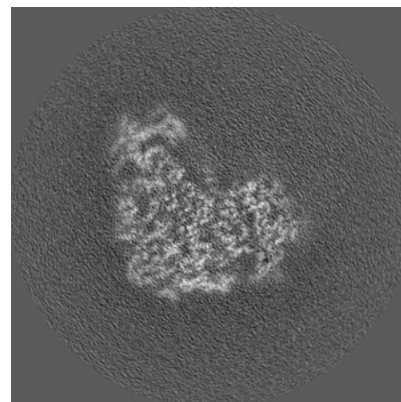
### 6.3.2 Raw map



X Index: 135



Y Index: 142

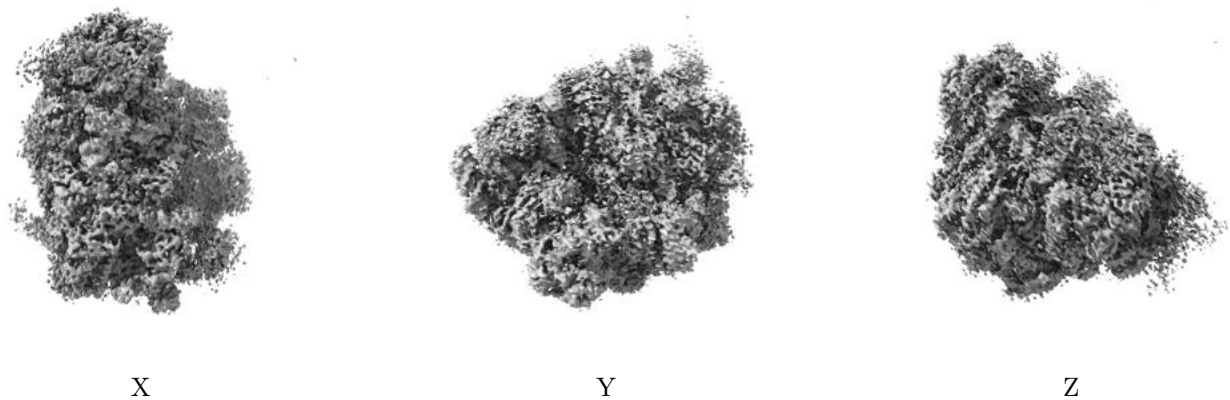


Z Index: 151

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

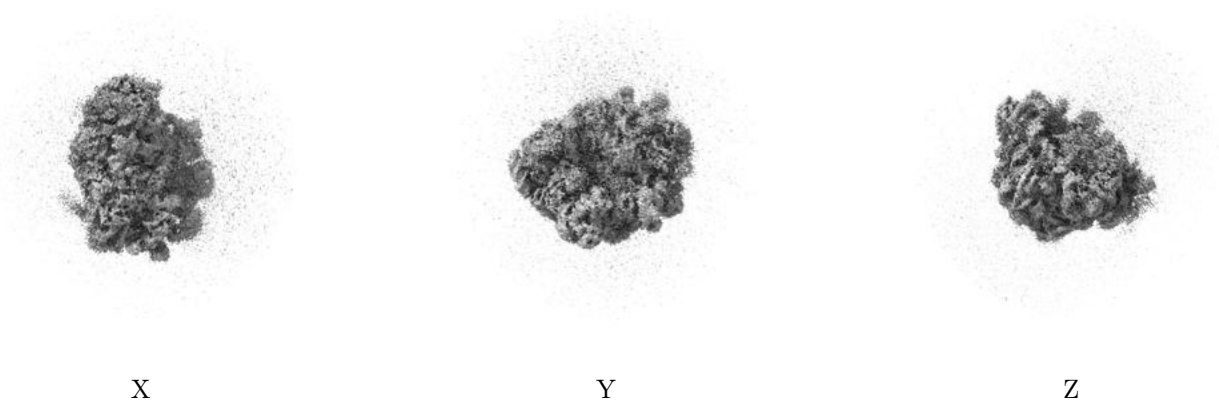
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0165. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

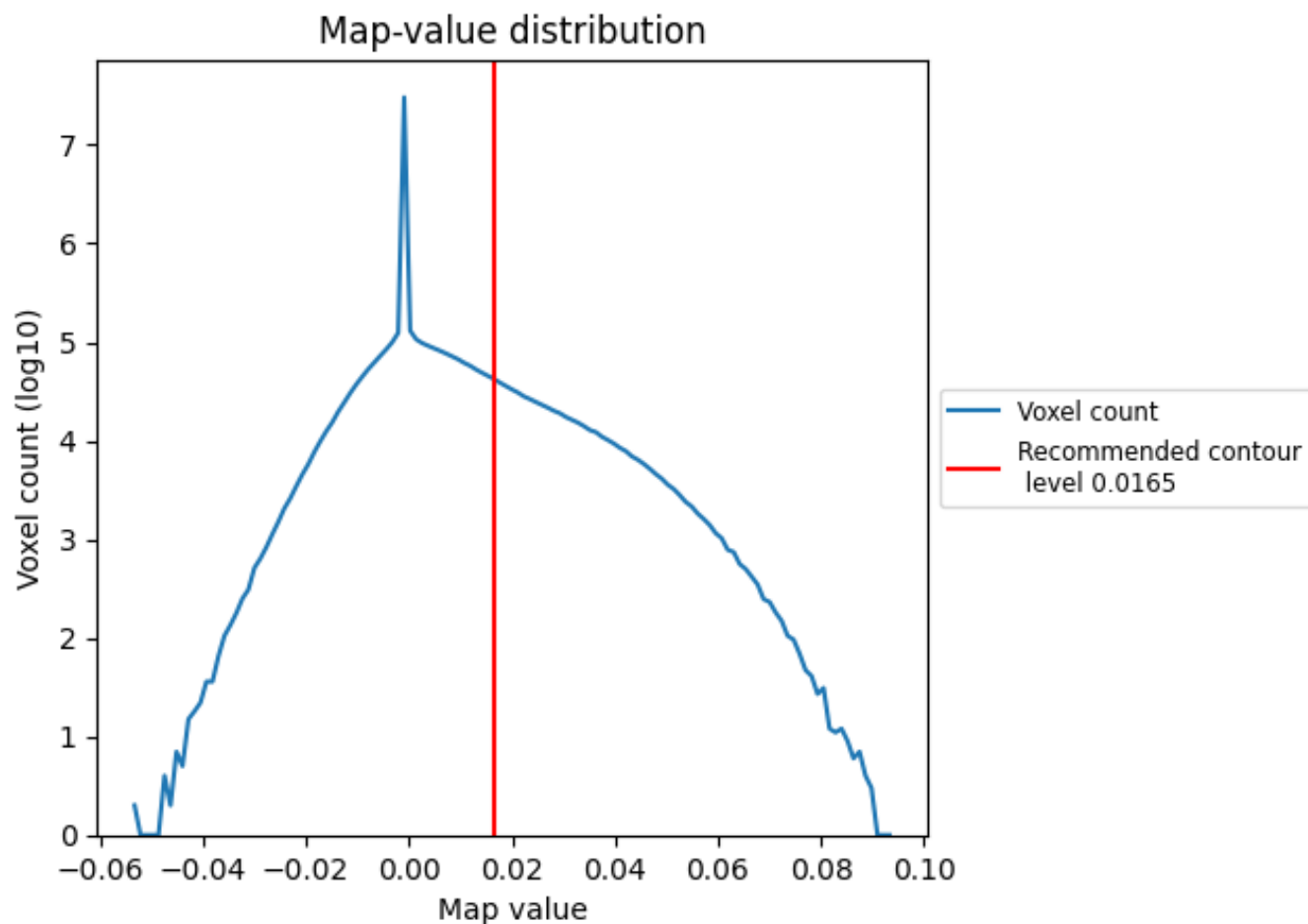
## 6.5 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

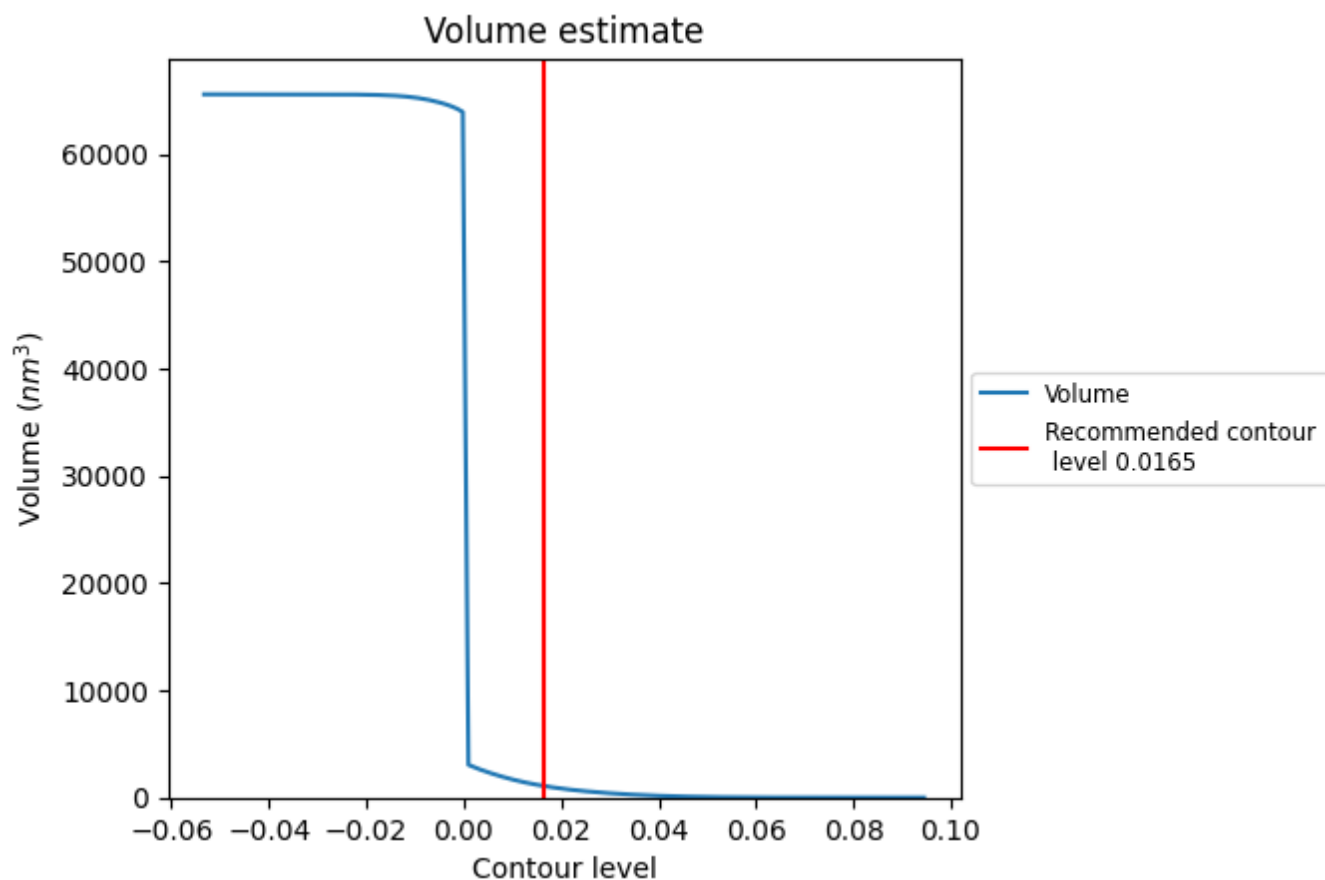
This section contains the results of statistical analysis of the map.

### 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.

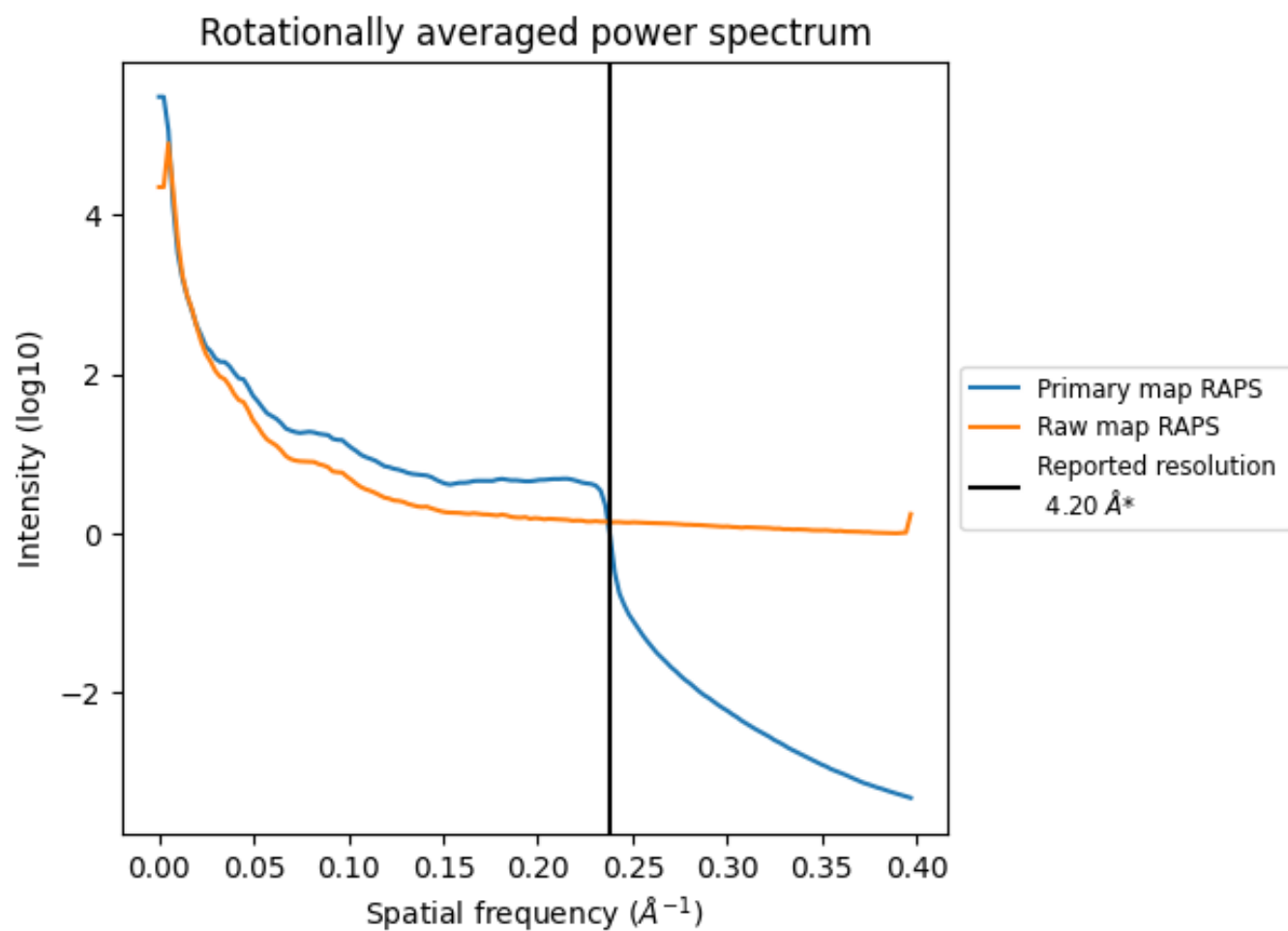
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1077 nm<sup>3</sup>; this corresponds to an approximate mass of 972 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 ⓘ

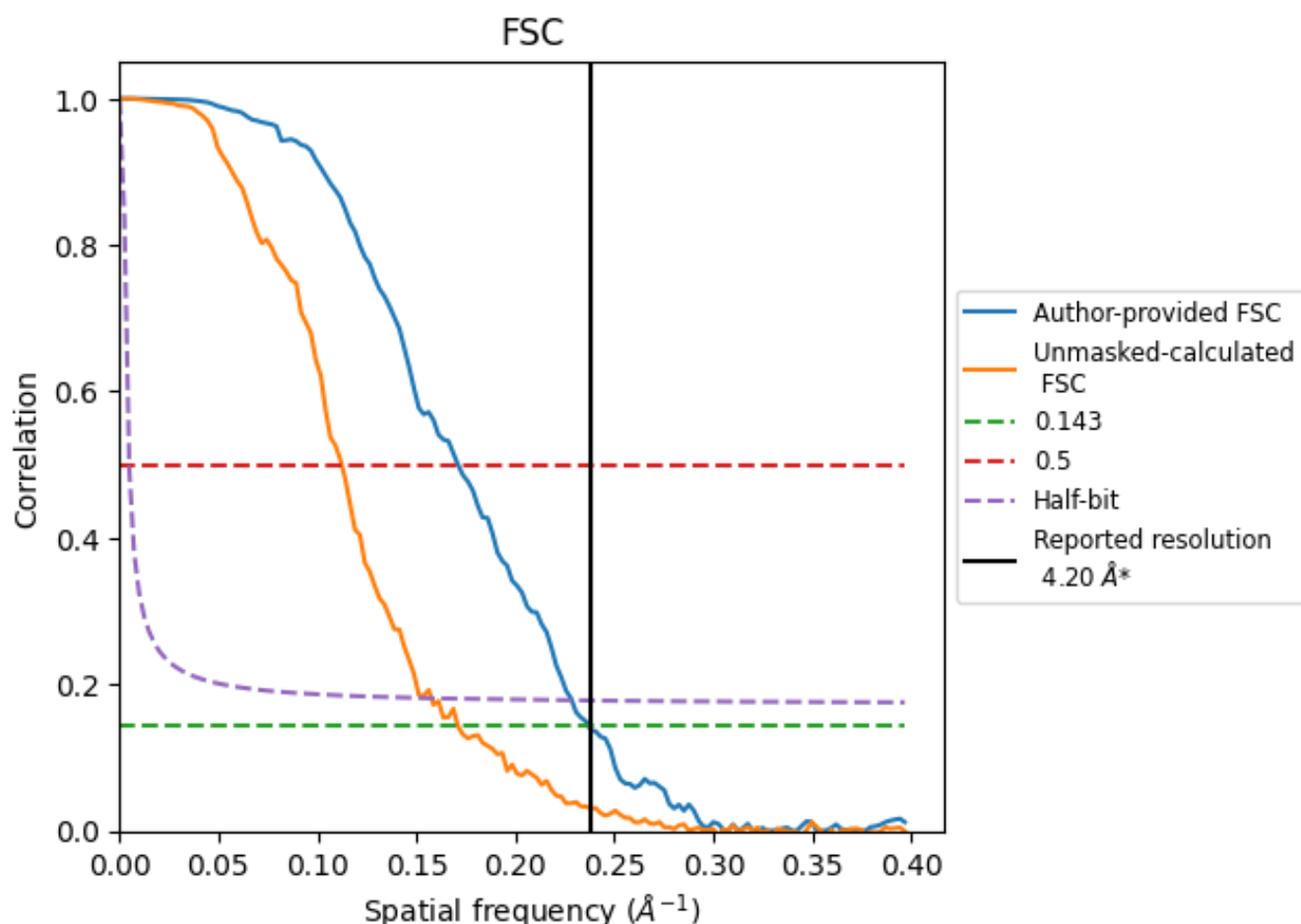


\*Reported resolution corresponds to spatial frequency of  $0.238 \text{ \AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.238  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

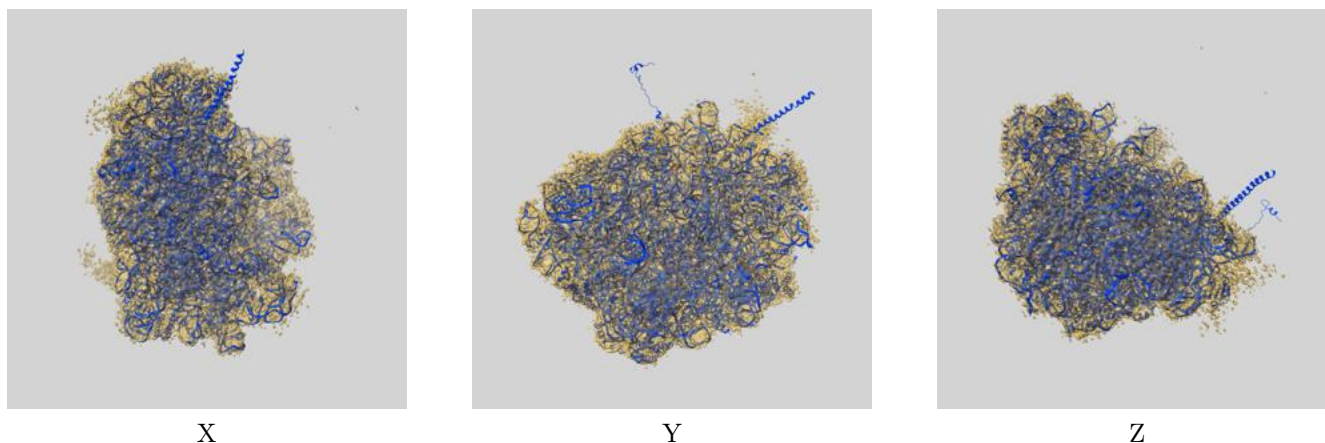
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.22	5.85	4.38
Unmasked-calculated*	5.85	8.91	6.35

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.85 differs from the reported value 4.2 by more than 10 %

## 9 Map-model fit ⓘ

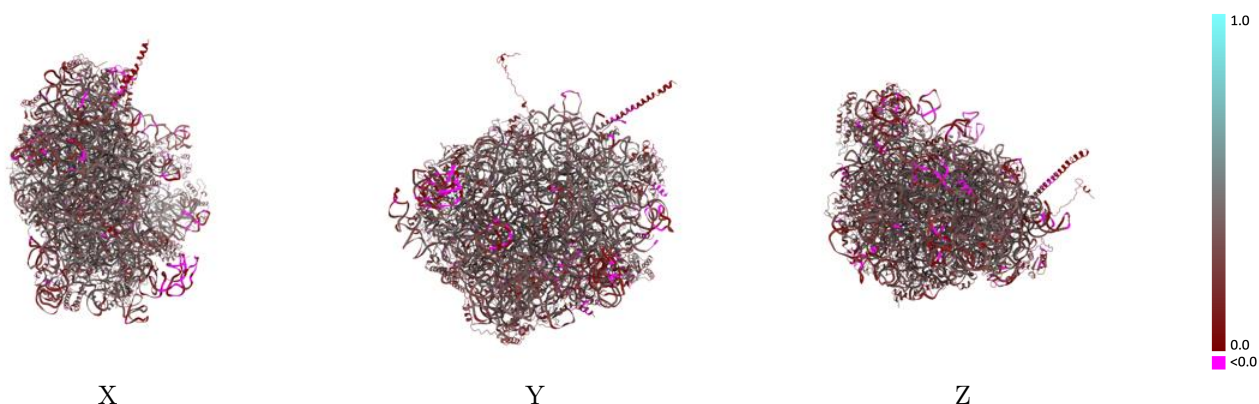
This section contains information regarding the fit between EMDB map EMD-8368 and PDB model 5T6R. Per-residue inclusion information can be found in section 3 on page 13.

### 9.1 Map-model overlay ⓘ



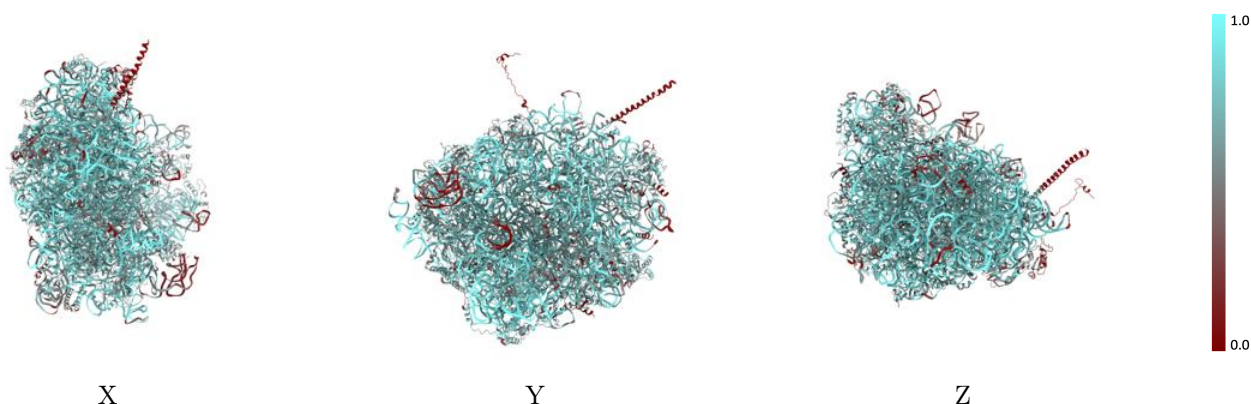
The images above show the 3D surface view of the map at the recommended contour level 0.0165 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



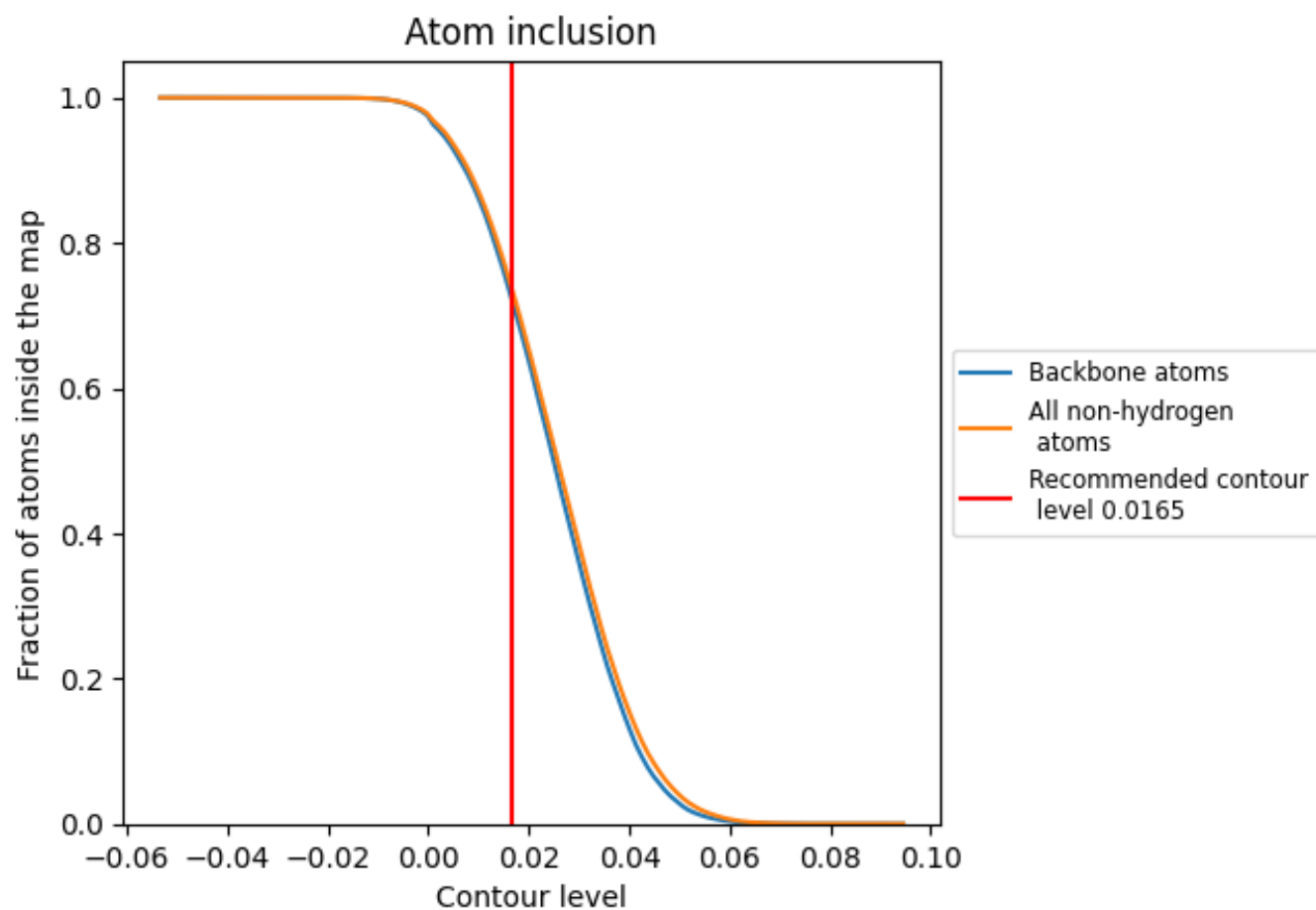
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0165).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 74% 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 (0.0165) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7400	 0.3250
A	 0.8232	 0.3290
B	 0.9054	 0.3530
C	 0.8664	 0.3520
D	 0.6726	 0.3640
E	 0.6783	 0.3520
F	 0.6638	 0.3480
G	 0.6510	 0.2870
H	 0.5779	 0.2710
I	 0.6751	 0.3430
J	 0.6258	 0.2860
K	 0.6671	 0.3190
L	 0.5254	 0.2980
M	 0.6183	 0.2730
N	 0.6059	 0.2880
O	 0.6472	 0.3090
Q	 0.5713	 0.2890
R	 0.6428	 0.3190
S	 0.5695	 0.2070
V	 0.5159	 0.2850
a	 0.7031	 0.3720
b	 0.6909	 0.3650
c	 0.6061	 0.3270
d	 0.6530	 0.3480
e	 0.5579	 0.2800
f	 0.6755	 0.3700
g	 0.6573	 0.3530
h	 0.3299	 0.2210
i	 0.5765	 0.2660
j	 0.4436	 0.2280
k	 0.6507	 0.3440
l	 0.6335	 0.3140
m	 0.6405	 0.3020
n	 0.6760	 0.3590
o	 0.5819	 0.3170



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Chain	Atom inclusion	Q-score
p	 0.5841	 0.2710
q	 0.6600	 0.3520
r	 0.6318	 0.3520
s	 0.6777	 0.3860
t	 0.6216	 0.3170
u	 0.6458	 0.3010
v	 0.5450	 0.2580
w	 0.7038	 0.3700
x	 0.5326	 0.2600
y	 0.6337	 0.3470
z	 0.5955	 0.3140