



# wwPDB EM Validation Summary Report ⓘ

Oct 23, 2024 – 10:56 PM EDT

PDB ID : 6N8N  
EMDB ID : EMD-0373  
Title : Cryo-EM structure of Lsg1-engaged (LE) pre-60S ribosomal subunit  
Authors : Zhou, Y.; Musalgaonkar, S.; Johnson, A.W.; Taylor, D.W.  
Deposited on : 2018-11-29  
Resolution : 3.80 Å (reported)  
Based on initial model : 5T62

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.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

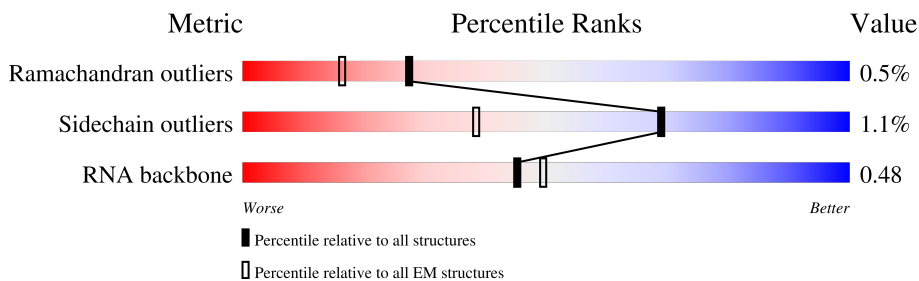
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.80 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	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	Y	364	
5	X	245	
6	W	640	
7	V	518	
8	D	254	

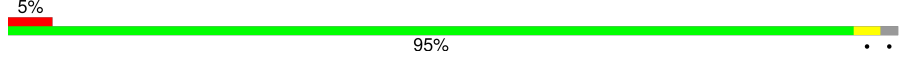
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Mol	Chain	Length	Quality of chain
9	E	387	98%
10	F	362	98%
11	G	297	93% 5%
12	H	176	88% 12%
13	I	244	87% 10%
14	J	256	87% 11%
15	K	191	97%
16	M	174	95%
17	N	199	95%
18	O	138	99%
19	Q	106	7% 96%
20	R	92	95%
21	S	217	21% 97%
22	a	204	99%
23	b	199	98%
24	c	184	7% 99%
25	d	186	99%
26	e	189	79% 20%
27	f	172	97%
28	g	160	96%
29	h	121	79% 20%
30	i	137	96%
31	j	155	39% 61%
32	k	142	85% 15%
33	l	127	97%

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Mol	Chain	Length	Quality of chain
34	m	136	 99%
35	n	149	 94%
36	o	59	 5% 95%
37	p	105	 90% 9%
38	q	113	 93% 5%
39	r	130	 95%
40	s	107	 98%
41	t	121	 86% 10%
42	u	120	 98%
43	v	100	 98%
44	w	88	 92% 5%
45	x	78	 99%
46	y	51	 96%
47	z	128	 7% 40% 60%
48	L	165	 74% 88% 11%

## 2 Entry composition [i](#)

There are 48 unique types of molecules in this entry. The entry contains 131813 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 *Saccharomyces cerevisiae* S288C 35S pre-ribosomal RNA (RDN37-1), miscRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	3203	68513	30603	12353	22354	3203	0	0

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

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

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

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

- Molecule 4 is a protein called Tyrosine-protein phosphatase YVH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	Y	128	991	625	179	179	8	0	0

- Molecule 5 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	X	234	1710	1063	294	346	7	0	0

- Molecule 6 is a protein called Large subunit GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	W	377	2972	1903	516	546	7	0	0

- Molecule 7 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	V	392	3034	1930	523	561	20	0	0

- Molecule 8 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	D	246	1874	1168	380	325	1	0	0

- Molecule 9 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	E	384	3059	1940	582	529	8	0	0

- Molecule 10 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 11 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	G	283	2280	1441	397	440	2	0	0

- Molecule 12 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	H	155	1217	785	220	211	1	0	0

- Molecule 13 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	I	220	1770	1143	322	304	1	0	0

- Molecule 14 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	J	227	1762	1128	315	316	3	0	0

- Molecule 15 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	K	188	1493	948	271	270	4	0	0

- Molecule 16 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	M	168	1344	841	251	248	4	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	N	193	1539	959	314	266	0	0

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

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

- Molecule 19 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	Q	102	819	514	166	134	5	0	0

- Molecule 20 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	R	88	673	416	135	116	6	0	0

- Molecule 21 is a protein called Ribosomal Protein uL1.

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

- Molecule 22 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 25 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 26 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	e	151	Total	C	N	O	0	0
			1219	757	258	204		

- Molecule 27 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	f	170	Total	C	N	O	S	0	0
			1432	922	265	242	3		

- Molecule 28 is a protein called 60S ribosomal protein L21-A.



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

- Molecule 29 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	h	97	766	496	126	144		0	0

- Molecule 30 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	i	132	981	617	184	173	7	0	0

- Molecule 31 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	j	61	509	328	100	80	1	0	0

- Molecule 32 is a protein called 60S ribosomal protein L25.

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

- Molecule 33 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	l	125	984	620	191	173		0	0

- Molecule 34 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 35 is a protein called 60S ribosomal protein L28.

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

- Molecule 36 is a protein called 60S ribosomal protein L29.

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

- Molecule 37 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	p	96	737	476	123	137	1	0	0

- Molecule 38 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	q	107	866	550	165	150	1	0	0

- Molecule 39 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	r	126	1012	641	204	166	1	0	0

- Molecule 40 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	s	106	850	540	165	144	1	0	0

- Molecule 41 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	t	109	861	533	175	149	4	0	0

- Molecule 42 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	v	98	Total	C	N	O	S	0	0
			753	471	150	130	2		

- Molecule 44 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	w	84	Total	C	N	O	S	0	0
			665	405	145	110	5		

- Molecule 45 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	x	77	Total	C	N	O	0	0
			608	388	114	106		

- Molecule 46 is a protein called 60S ribosomal protein L39.

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

- Molecule 47 is a protein called Ubiquitin-60S ribosomal protein L40.

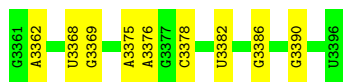
Mol	Chain	Residues	Atoms					AltConf	Trace
47	z	51	Total	C	N	O	S	0	0
			408	253	84	66	5		

- Molecule 48 is a protein called Ribosomal protein L12.

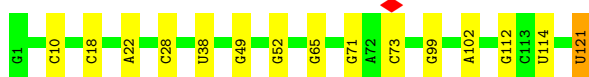
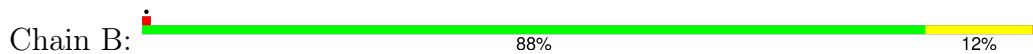
Mol	Chain	Residues	Atoms				AltConf	Trace
48	L	147	Total	C	N	O	0	0
			821	502	160	159		



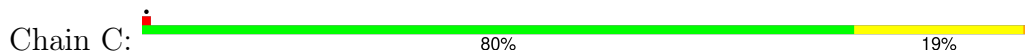




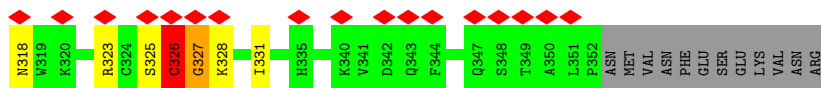
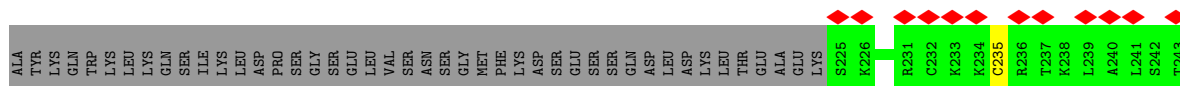
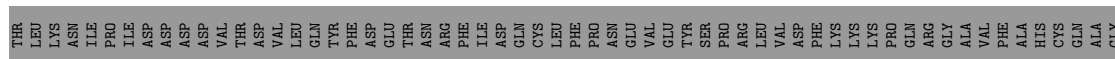
• Molecule 2: 5S rRNA



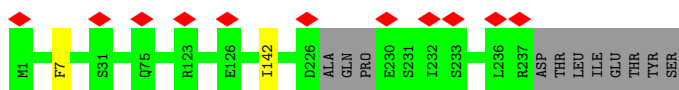
• Molecule 3: 5.8S rRNA



• Molecule 4: Tyrosine-protein phosphatase YVH1



• Molecule 5: Eukaryotic translation initiation factor 6

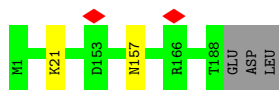


• Molecule 6: Large subunit GTPase 1

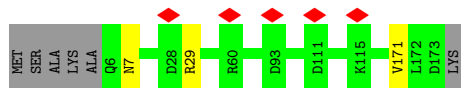




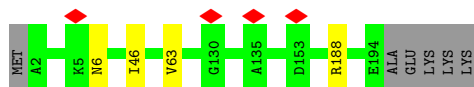




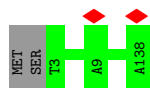
- Molecule 16: 60S ribosomal protein L11-A



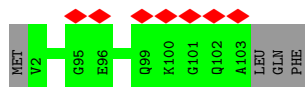
- Molecule 17: 60S ribosomal protein L13-A



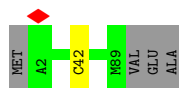
- Molecule 18: 60S ribosomal protein L14-A



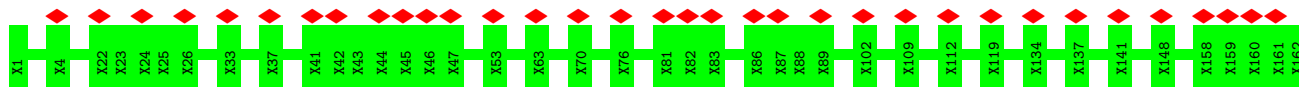
- Molecule 19: 60S ribosomal protein L42-A

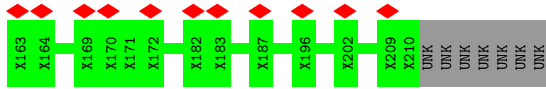


- Molecule 20: 60S ribosomal protein L43-A



- Molecule 21: Ribosomal Protein uL1





- Molecule 22: 60S ribosomal protein L15-A

Chain a: 99%



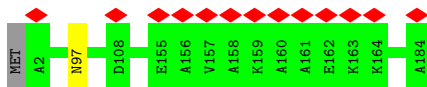
- Molecule 23: 60S ribosomal protein L16-A

Chain b: 98%



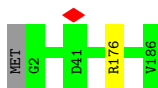
- Molecule 24: 60S ribosomal protein L17-A

Chain c: 99%



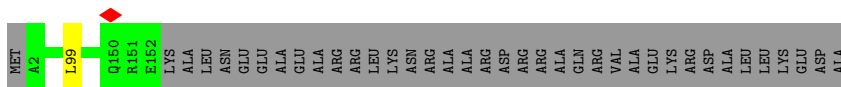
- Molecule 25: 60S ribosomal protein L18-A

Chain d: 99%



- Molecule 26: 60S ribosomal protein L19-A

Chain e: 79% 20%

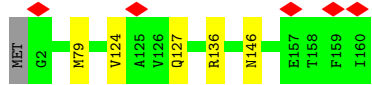


- Molecule 27: 60S ribosomal protein L20-A

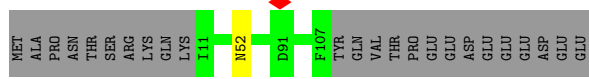
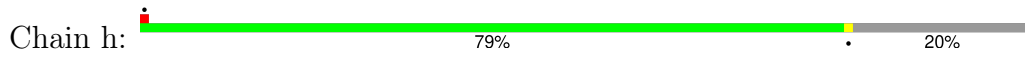
Chain f: 97%



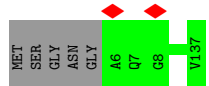
- Molecule 28: 60S ribosomal protein L21-A



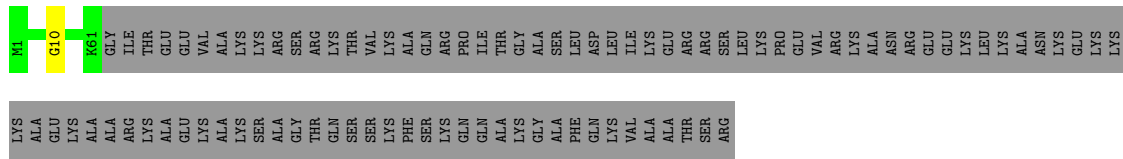
• Molecule 29: 60S ribosomal protein L22-A



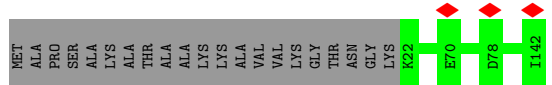
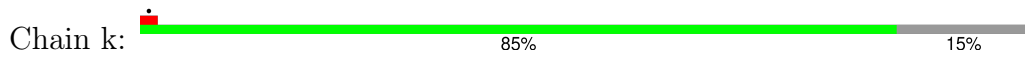
• Molecule 30: 60S ribosomal protein L23-A



• Molecule 31: 60S ribosomal protein L24-A



• Molecule 32: 60S ribosomal protein L25

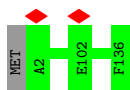


• Molecule 33: 60S ribosomal protein L26-A

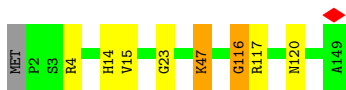


• Molecule 34: 60S ribosomal protein L27-A

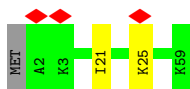
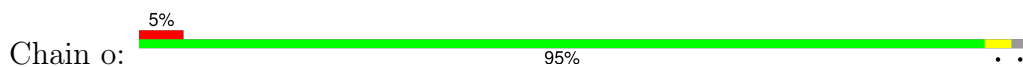




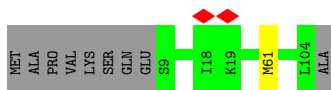
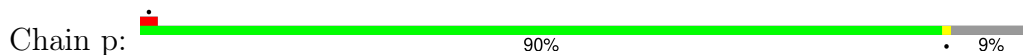
- Molecule 35: 60S ribosomal protein L28



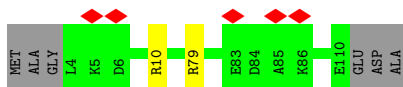
- Molecule 36: 60S ribosomal protein L29



- Molecule 37: 60S ribosomal protein L30



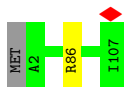
- Molecule 38: 60S ribosomal protein L31-A



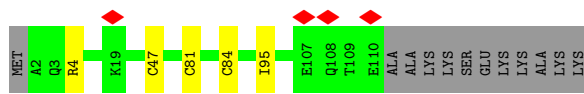
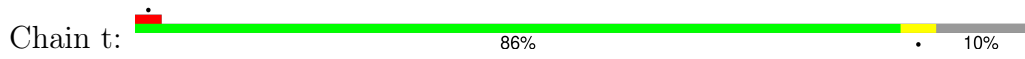
- Molecule 39: 60S ribosomal protein L32



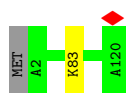
- Molecule 40: 60S ribosomal protein L33-A



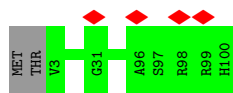
- Molecule 41: 60S ribosomal protein L34-A



- Molecule 42: 60S ribosomal protein L35-A



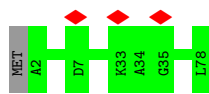
- Molecule 43: 60S ribosomal protein L36-A



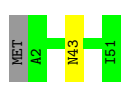
- Molecule 44: 60S ribosomal protein L37-A



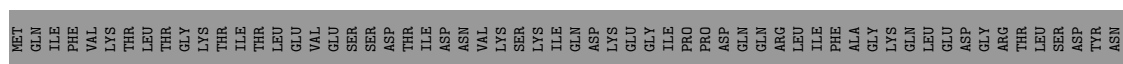
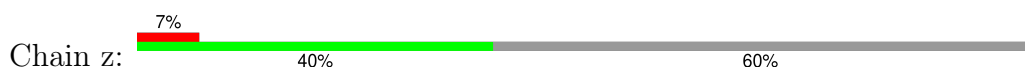
- Molecule 45: 60S ribosomal protein L38

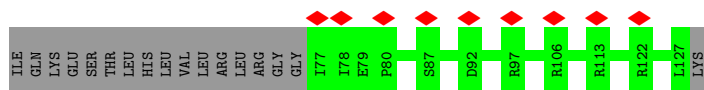


- Molecule 46: 60S ribosomal protein L39

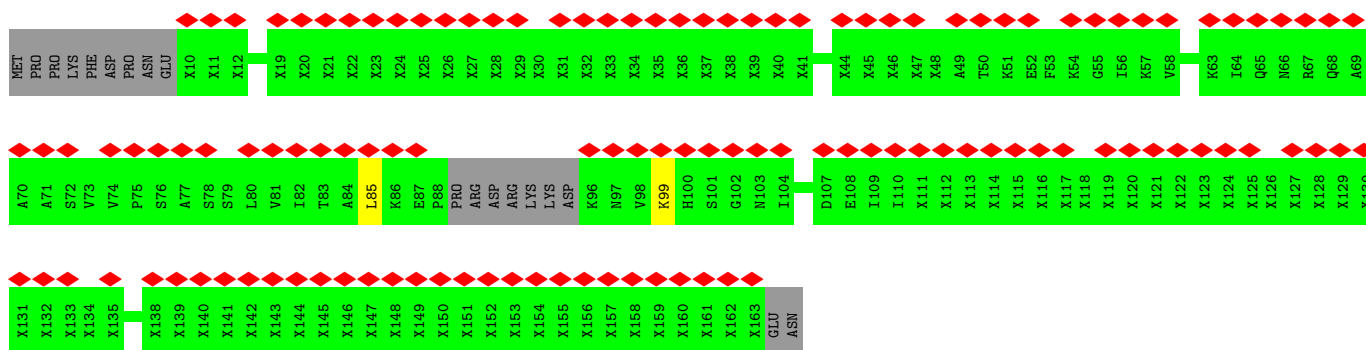
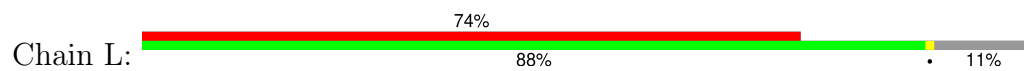


- Molecule 47: Ubiquitin-60S ribosomal protein L40





- Molecule 48: Ribosomal protein L12



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	54188	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.137	Depositor
Minimum map value	-0.091	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.022	Depositor
Map size ( $\text{\AA}$ )	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.1, 1.1, 1.1	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.66	1/76692 (0.0%)	0.94	131/119572 (0.1%)
2	B	0.57	0/2883	0.93	5/4491 (0.1%)
3	C	0.68	0/3746	0.92	5/5832 (0.1%)
4	Y	0.38	0/1016	0.91	4/1368 (0.3%)
5	X	0.31	0/1729	0.55	0/2355
6	W	0.34	0/3035	0.71	2/4119 (0.0%)
7	V	0.35	0/3093	0.66	2/4203 (0.0%)
8	D	0.39	0/1908	0.58	0/2564
9	E	0.41	0/3130	0.58	0/4206
10	F	0.37	0/2800	0.59	1/3790 (0.0%)
11	G	0.36	0/2329	0.58	2/3142 (0.1%)
12	H	0.34	0/1236	0.56	0/1661
13	I	0.37	0/1807	0.56	1/2432 (0.0%)
14	J	0.37	0/1794	0.58	0/2425
15	K	0.36	0/1514	0.57	0/2039
16	M	0.30	0/1365	0.61	0/1831
17	N	0.38	0/1564	0.59	0/2102
18	O	0.33	0/1068	0.50	0/1438
19	Q	0.37	0/831	0.57	0/1097
20	R	0.40	0/680	0.60	0/905
22	a	0.41	0/1757	0.54	0/2354
23	b	0.38	0/1585	0.51	0/2128
24	c	0.39	0/1443	0.58	0/1944
25	d	0.36	0/1465	0.57	0/1965
26	e	0.36	0/1236	0.56	1/1650 (0.1%)
27	f	0.38	0/1468	0.60	2/1973 (0.1%)
28	g	0.36	0/1300	0.55	0/1743
29	h	0.35	0/781	0.51	0/1058
30	i	0.39	0/996	0.55	0/1340
31	j	0.35	0/521	0.50	0/691
32	k	0.40	0/979	0.57	0/1321
33	l	0.34	0/995	0.56	1/1329 (0.1%)
34	m	0.39	0/1118	0.56	0/1497
35	n	0.38	0/1204	0.66	2/1612 (0.1%)



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
36	o	0.33	0/473	0.60	0/629
37	p	0.35	0/745	0.54	0/1001
38	q	0.39	0/880	0.57	0/1182
39	r	0.36	0/1033	0.56	0/1383
40	s	0.44	0/868	0.56	0/1168
41	t	0.43	1/871 (0.1%)	0.66	2/1164 (0.2%)
42	u	0.34	0/978	0.56	0/1301
43	v	0.33	0/759	0.56	0/1009
44	w	0.41	0/680	0.60	0/901
45	x	0.33	0/614	0.58	0/822
46	y	0.36	0/443	0.60	0/588
47	z	0.27	0/414	0.51	0/551
48	L	0.31	0/363	0.75	1/493 (0.2%)
All	All	0.56	2/140189 (0.0%)	0.83	162/206369 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	Y	0	3
5	X	0	2
6	W	0	17
7	V	0	4
9	E	0	1
10	F	0	2
11	G	0	2
13	I	0	3
14	J	0	2
15	K	0	1
16	M	0	2
17	N	0	1
27	f	0	1
35	n	0	3
36	o	0	2
42	u	0	1
All	All	0	47

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2259	A	C1'-N9	-5.70	1.38	1.46
41	t	81	CYS	CB-SG	5.03	1.90	1.82

The worst 5 of 162 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	t	81	CYS	CA-CB-SG	10.98	133.76	114.00
4	Y	331	ILE	CG1-CB-CG2	-10.01	89.38	111.40
1	A	2263	C	N1-C2-O2	8.71	124.13	118.90
2	B	121	U	N3-C2-O2	-8.67	116.13	122.20
1	A	2137	U	N1-C2-O2	8.64	128.85	122.80

There are no chirality outliers.

5 of 47 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	X	142	ILE	Peptide
5	X	7	PHE	Peptide
4	Y	325	SER	Peptide
4	Y	326	CYS	Peptide
4	Y	327	GLY	Peptide

## 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
4	Y	126/364 (35%)	99 (79%)	22 (18%)	5 (4%)	<b>2</b> <b>21</b>
5	X	230/245 (94%)	221 (96%)	9 (4%)	0	<b>100</b> <b>100</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	W	373/640 (58%)	313 (84%)	54 (14%)	6 (2%)	8	36
7	V	388/518 (75%)	323 (83%)	59 (15%)	6 (2%)	8	37
8	D	244/254 (96%)	225 (92%)	19 (8%)	0	100	100
9	E	382/387 (99%)	354 (93%)	26 (7%)	2 (0%)	25	58
10	F	359/362 (99%)	330 (92%)	26 (7%)	3 (1%)	16	49
11	G	281/297 (95%)	268 (95%)	12 (4%)	1 (0%)	30	63
12	H	151/176 (86%)	142 (94%)	9 (6%)	0	100	100
13	I	218/244 (89%)	207 (95%)	9 (4%)	2 (1%)	14	45
14	J	225/256 (88%)	217 (96%)	7 (3%)	1 (0%)	30	63
15	K	186/191 (97%)	176 (95%)	10 (5%)	0	100	100
16	M	166/174 (95%)	152 (92%)	14 (8%)	0	100	100
17	N	191/199 (96%)	172 (90%)	17 (9%)	2 (1%)	13	44
18	O	134/138 (97%)	129 (96%)	5 (4%)	0	100	100
19	Q	100/106 (94%)	94 (94%)	6 (6%)	0	100	100
20	R	86/92 (94%)	80 (93%)	6 (7%)	0	100	100
22	a	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
23	b	195/199 (98%)	191 (98%)	4 (2%)	0	100	100
24	c	181/184 (98%)	169 (93%)	12 (7%)	0	100	100
25	d	183/186 (98%)	175 (96%)	8 (4%)	0	100	100
26	e	149/189 (79%)	140 (94%)	9 (6%)	0	100	100
27	f	168/172 (98%)	155 (92%)	11 (6%)	2 (1%)	11	40
28	g	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
29	h	95/121 (78%)	91 (96%)	3 (3%)	1 (1%)	12	42
30	i	130/137 (95%)	129 (99%)	1 (1%)	0	100	100
31	j	59/155 (38%)	56 (95%)	2 (3%)	1 (2%)	7	34
32	k	119/142 (84%)	111 (93%)	8 (7%)	0	100	100
33	l	123/127 (97%)	121 (98%)	2 (2%)	0	100	100
34	m	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
35	n	146/149 (98%)	132 (90%)	11 (8%)	3 (2%)	5	32
36	o	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
37	p	94/105 (90%)	93 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	q	105/113 (93%)	98 (93%)	7 (7%)	0	100	100
39	r	124/130 (95%)	118 (95%)	6 (5%)	0	100	100
40	s	104/107 (97%)	96 (92%)	8 (8%)	0	100	100
41	t	107/121 (88%)	103 (96%)	4 (4%)	0	100	100
42	u	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
43	v	96/100 (96%)	90 (94%)	6 (6%)	0	100	100
44	w	82/88 (93%)	75 (92%)	7 (8%)	0	100	100
45	x	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
46	y	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
47	z	49/128 (38%)	46 (94%)	3 (6%)	0	100	100
48	L	53/165 (32%)	48 (91%)	5 (9%)	0	100	100
All	All	6989/8269 (84%)	6483 (93%)	471 (7%)	35 (0%)	27	58

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	V	95	VAL
10	F	339	LEU
11	G	259	LYS
13	I	178	ILE
4	Y	326	CYS

### 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	
4	Y	110/323 (34%)	107 (97%)	3 (3%)	40	60
5	X	186/211 (88%)	186 (100%)	0	100	100
6	W	316/555 (57%)	309 (98%)	7 (2%)	47	64
7	V	332/467 (71%)	327 (98%)	5 (2%)	60	74
8	D	189/196 (96%)	188 (100%)	1 (0%)	86	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	E	317/323 (98%)	314 (99%)	3 (1%)	75	82
10	F	288/289 (100%)	285 (99%)	3 (1%)	73	80
11	G	236/245 (96%)	232 (98%)	4 (2%)	56	72
12	H	131/153 (86%)	131 (100%)	0	100	100
13	I	185/205 (90%)	183 (99%)	2 (1%)	70	79
14	J	182/208 (88%)	181 (100%)	1 (0%)	86	90
15	K	168/171 (98%)	167 (99%)	1 (1%)	84	88
16	M	146/150 (97%)	145 (99%)	1 (1%)	81	86
17	N	153/159 (96%)	152 (99%)	1 (1%)	81	86
18	O	107/109 (98%)	107 (100%)	0	100	100
19	Q	87/91 (96%)	87 (100%)	0	100	100
20	R	69/72 (96%)	68 (99%)	1 (1%)	62	75
22	a	175/176 (99%)	173 (99%)	2 (1%)	70	79
23	b	160/162 (99%)	158 (99%)	2 (1%)	65	76
24	c	140/146 (96%)	139 (99%)	1 (1%)	81	86
25	d	150/151 (99%)	149 (99%)	1 (1%)	81	86
26	e	125/154 (81%)	125 (100%)	0	100	100
27	f	155/156 (99%)	153 (99%)	2 (1%)	65	76
28	g	136/137 (99%)	131 (96%)	5 (4%)	29	53
29	h	84/107 (78%)	84 (100%)	0	100	100
30	i	102/105 (97%)	102 (100%)	0	100	100
31	j	54/129 (42%)	54 (100%)	0	100	100
32	k	104/118 (88%)	104 (100%)	0	100	100
33	l	108/110 (98%)	107 (99%)	1 (1%)	75	82
34	m	115/116 (99%)	115 (100%)	0	100	100
35	n	118/119 (99%)	116 (98%)	2 (2%)	56	72
36	o	46/47 (98%)	46 (100%)	0	100	100
37	p	81/88 (92%)	80 (99%)	1 (1%)	67	77
38	q	92/97 (95%)	90 (98%)	2 (2%)	47	64
39	r	108/111 (97%)	105 (97%)	3 (3%)	38	59
40	s	90/91 (99%)	89 (99%)	1 (1%)	70	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	t	94/103 (91%)	91 (97%)	3 (3%)	34	56
42	u	104/105 (99%)	104 (100%)	0	100	100
43	v	78/82 (95%)	78 (100%)	0	100	100
44	w	69/71 (97%)	66 (96%)	3 (4%)	25	49
45	x	67/69 (97%)	67 (100%)	0	100	100
46	y	45/46 (98%)	44 (98%)	1 (2%)	47	64
47	z	46/116 (40%)	46 (100%)	0	100	100
48	L	31/65 (48%)	30 (97%)	1 (3%)	34	56
All	All	5879/6904 (85%)	5815 (99%)	64 (1%)	69	79

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	t	47	CYS
44	w	22	CYS
11	G	85	ARG
11	G	24	ARG
44	w	25	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
17	N	25	HIS
24	c	97	ASN
17	N	137	GLN
22	a	37	HIS
28	g	146	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3200/3396 (94%)	705 (22%)	37 (1%)
2	B	120/121 (99%)	15 (12%)	0
3	C	157/158 (99%)	31 (19%)	2 (1%)
All	All	3477/3675 (94%)	751 (21%)	39 (1%)

5 of 751 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	17	G
1	A	18	G
1	A	22	G
1	A	26	A
1	A	40	A

5 of 39 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2513	U
1	A	3228	C
1	A	2537	U
1	A	3078	U
3	C	82	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 oligosaccharides in this entry.

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

There are no ligands in this entry.

#### 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

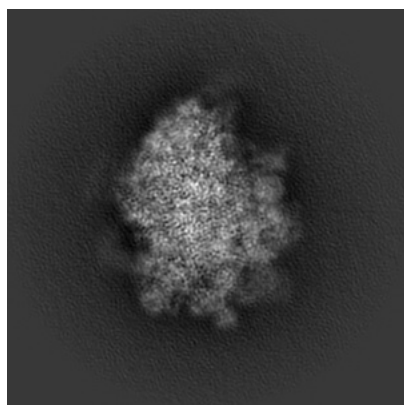
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0373. These allow visual inspection of the internal detail of the map and identification of artifacts.

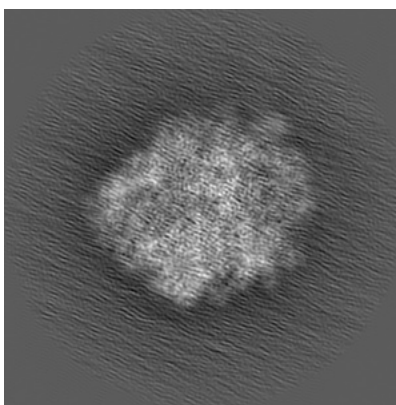
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

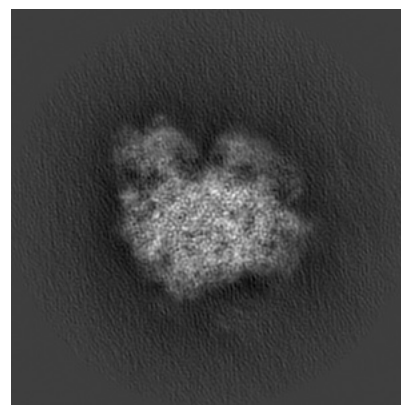
#### 6.1.1 Primary map



X



Y

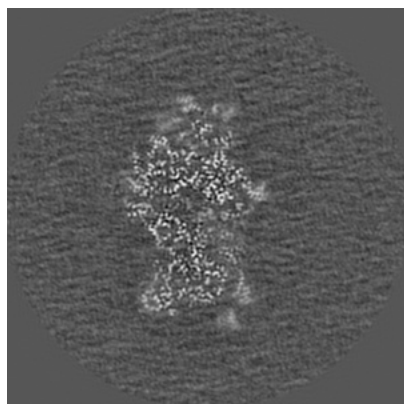


Z

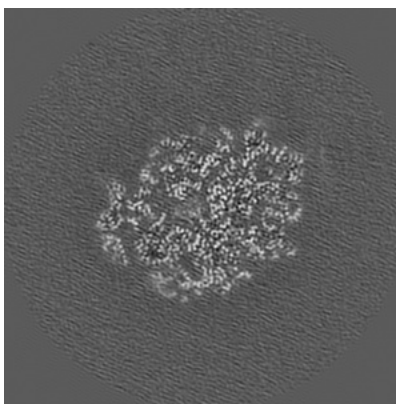
The images above show the map projected in three orthogonal directions.

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

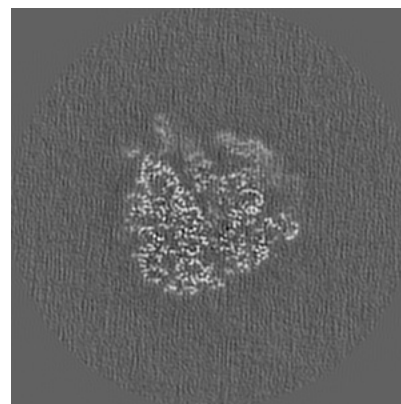
#### 6.2.1 Primary map



X Index: 192



Y Index: 192



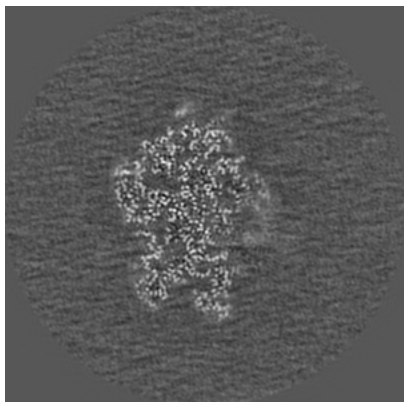
Z Index: 192



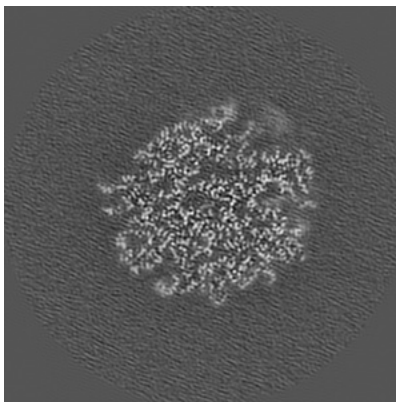
The images above show central slices of the map in three orthogonal directions.

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

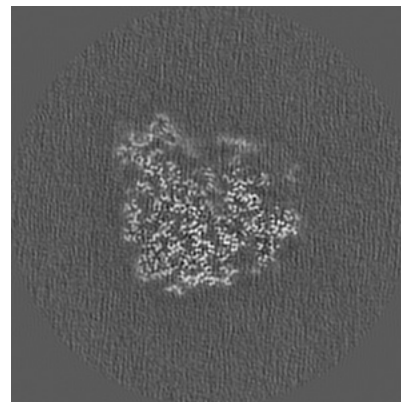
### 6.3.1 Primary map



X Index: 173



Y Index: 173

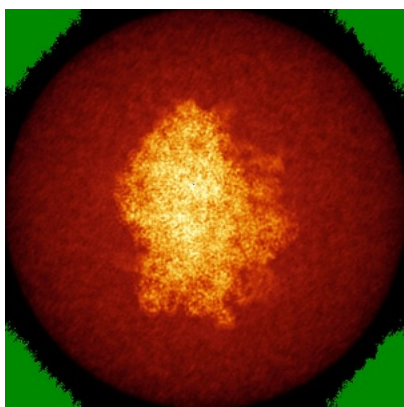


Z Index: 185

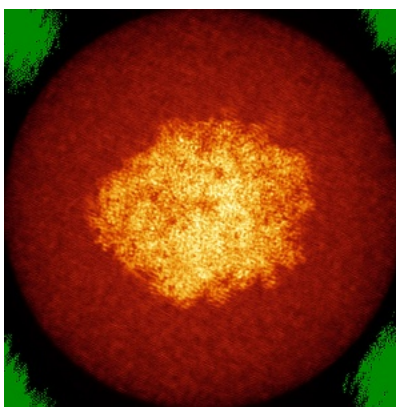
The images above show the largest variance slices of the map in three orthogonal directions.

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

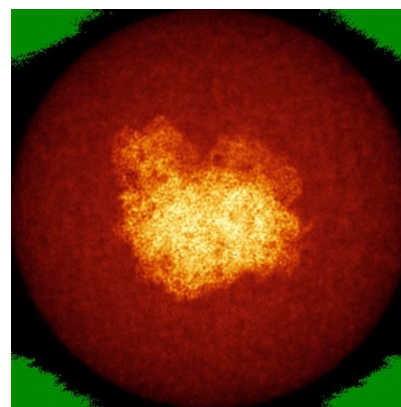
### 6.4.1 Primary map



X



Y

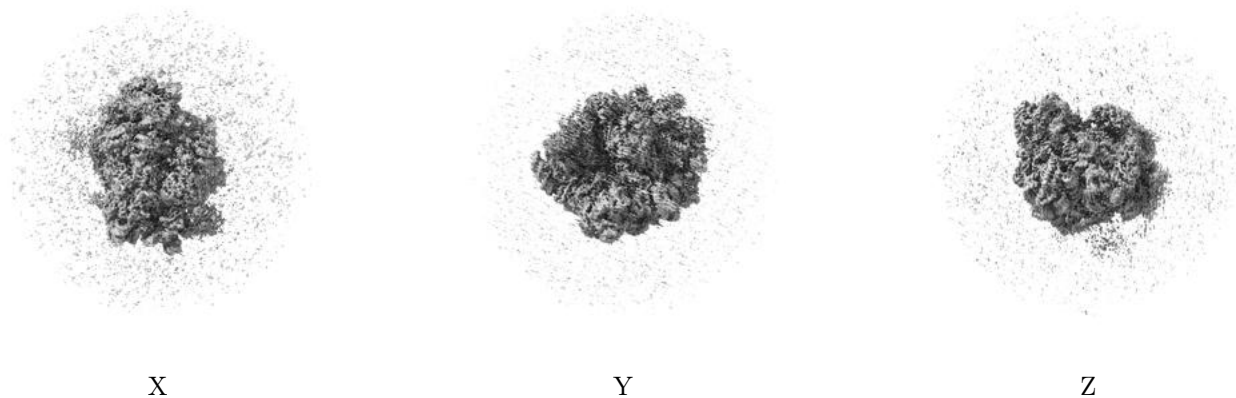


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.022. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

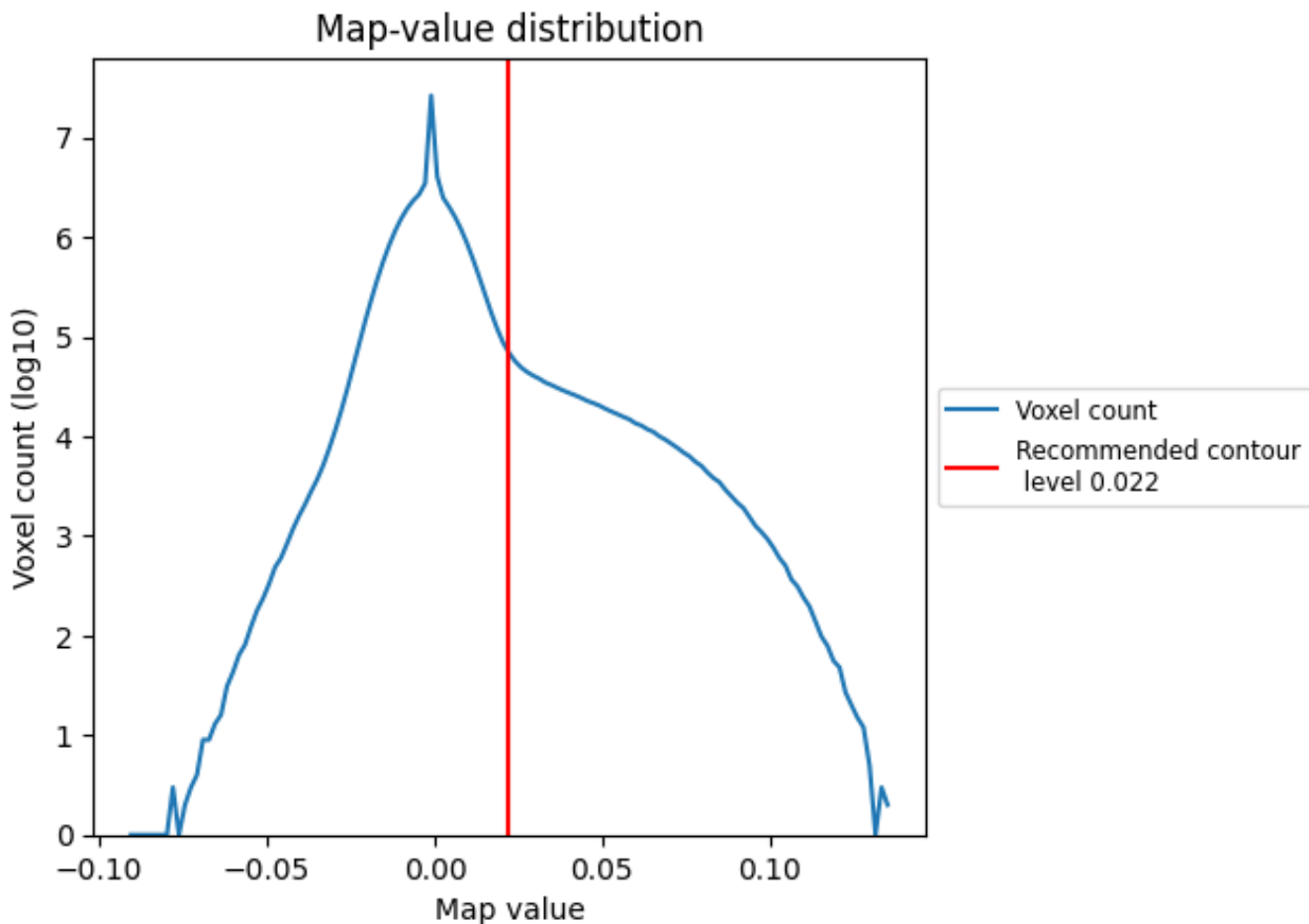
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

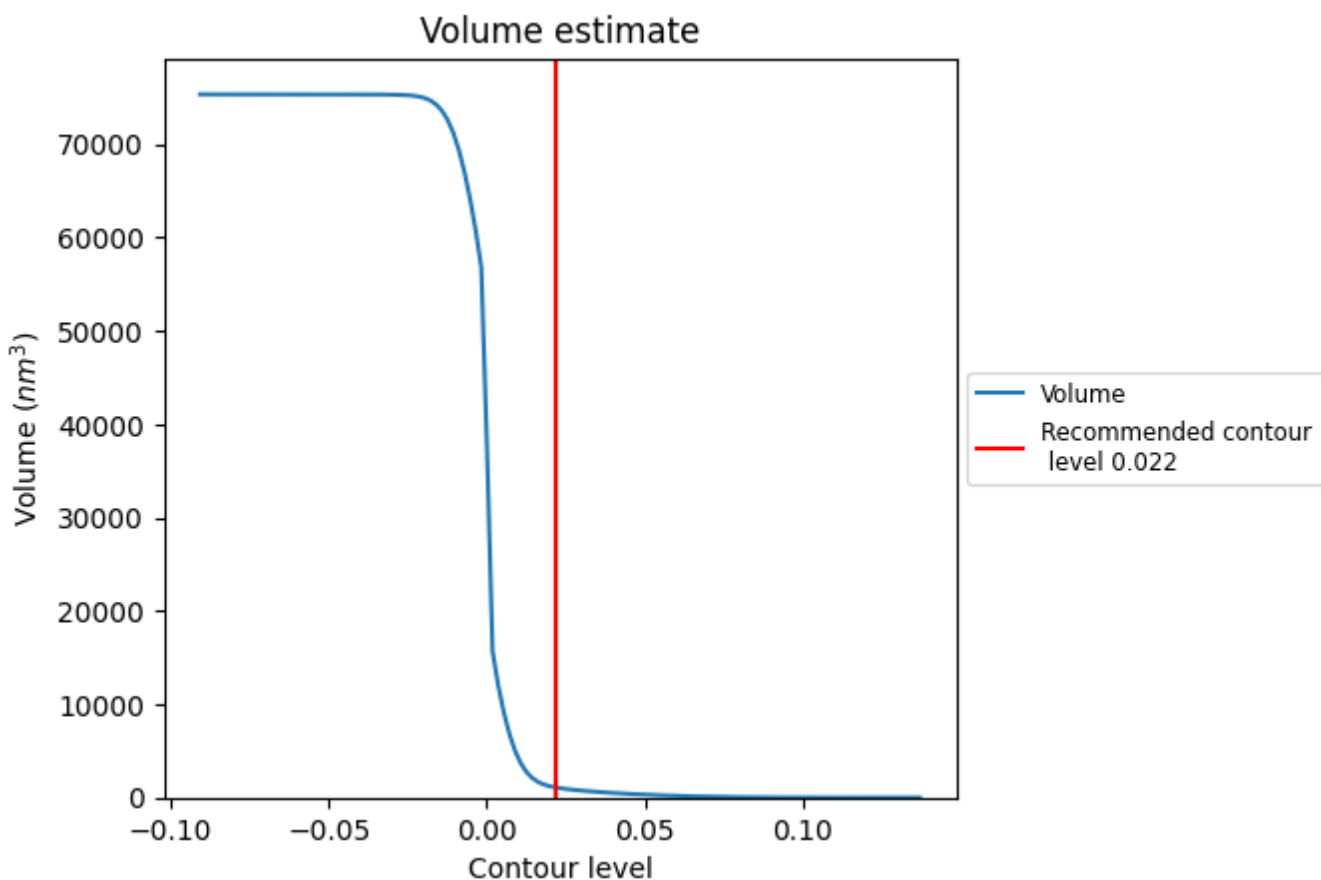
This section contains the results of statistical analysis of the map.

### 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.

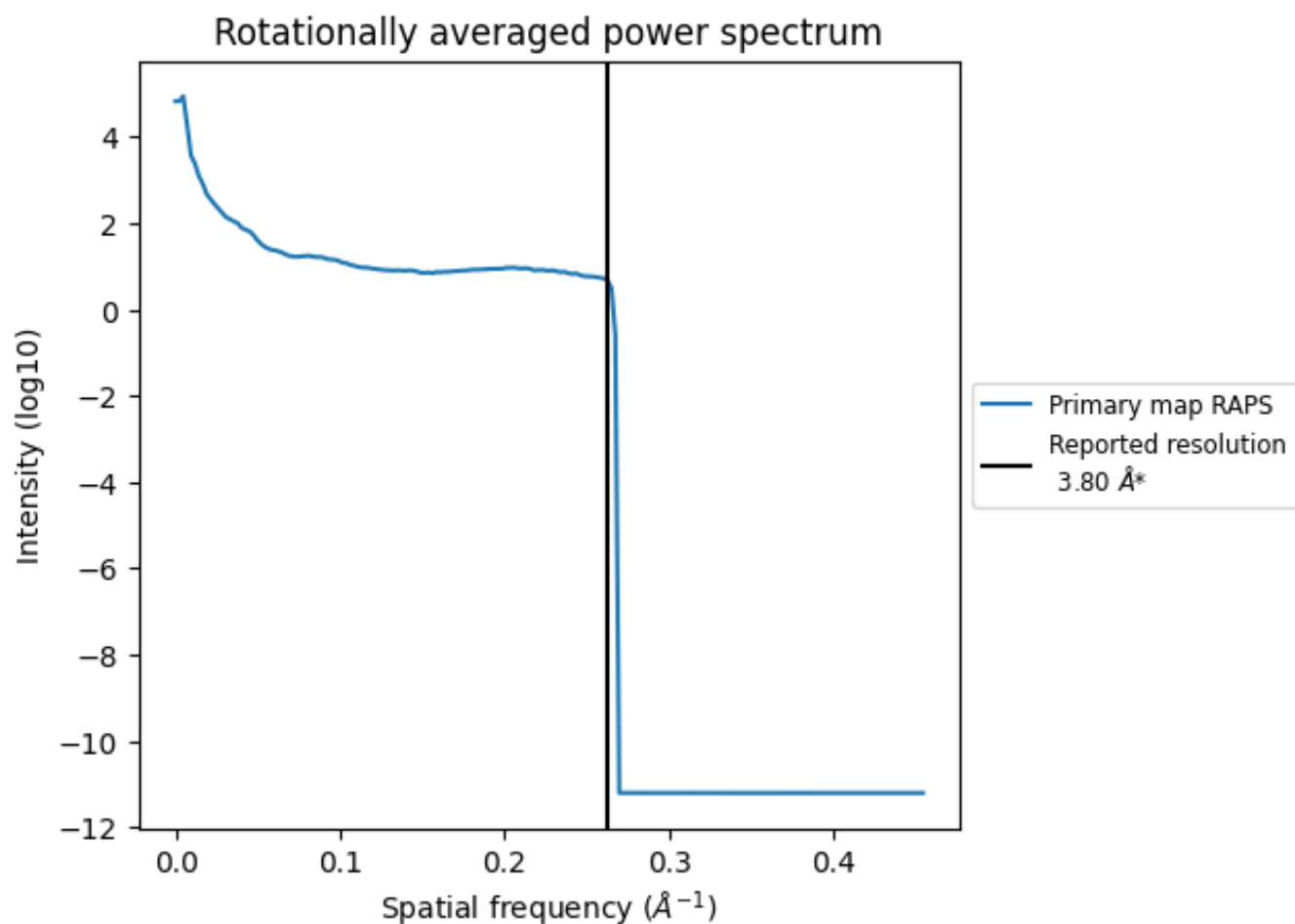
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1068  $\text{nm}^3$ ; this corresponds to an approximate mass of 965 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 [\(i\)](#)

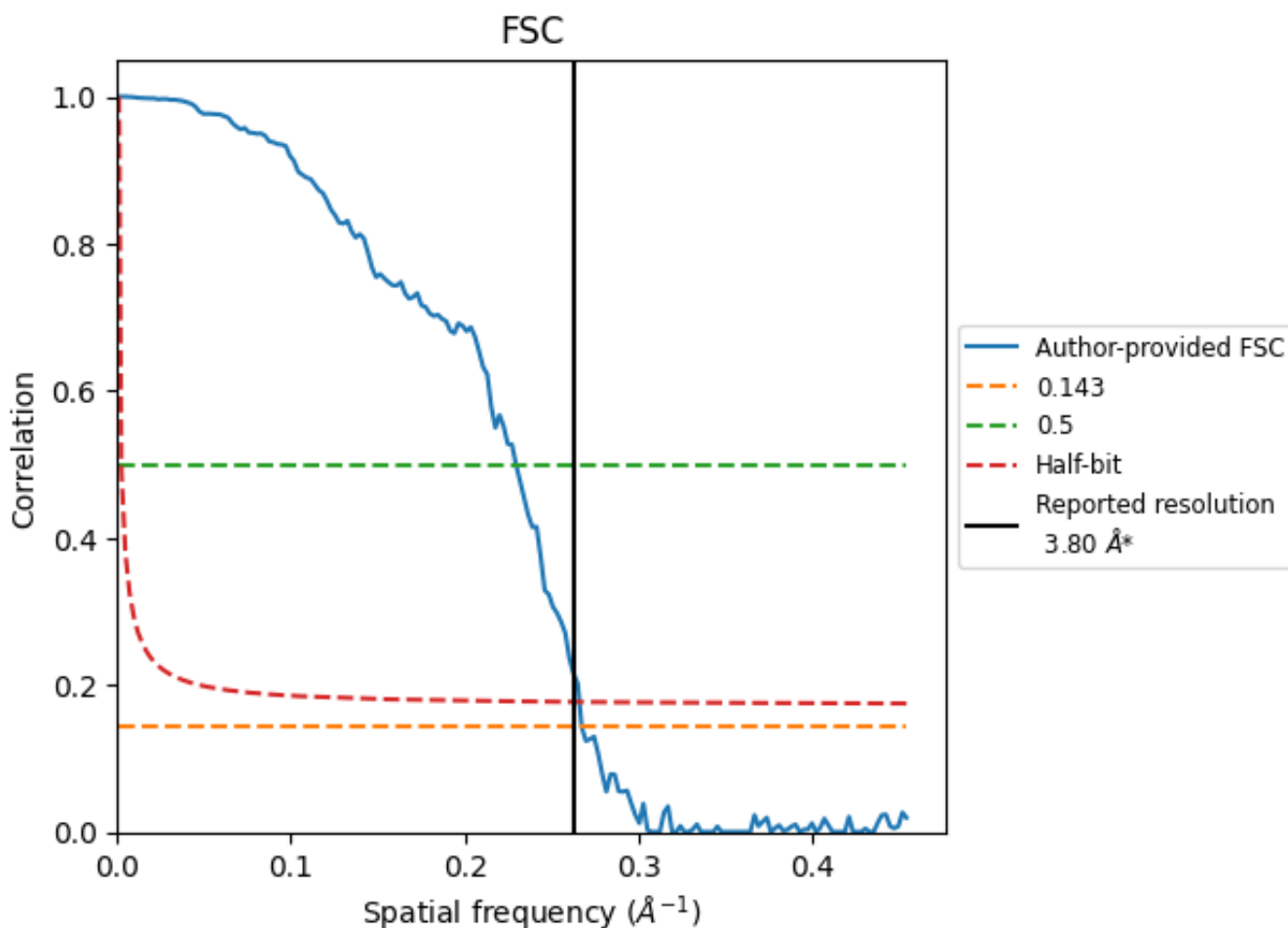


\*Reported resolution corresponds to spatial frequency of 0.263 Å<sup>-1</sup>

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

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.263 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

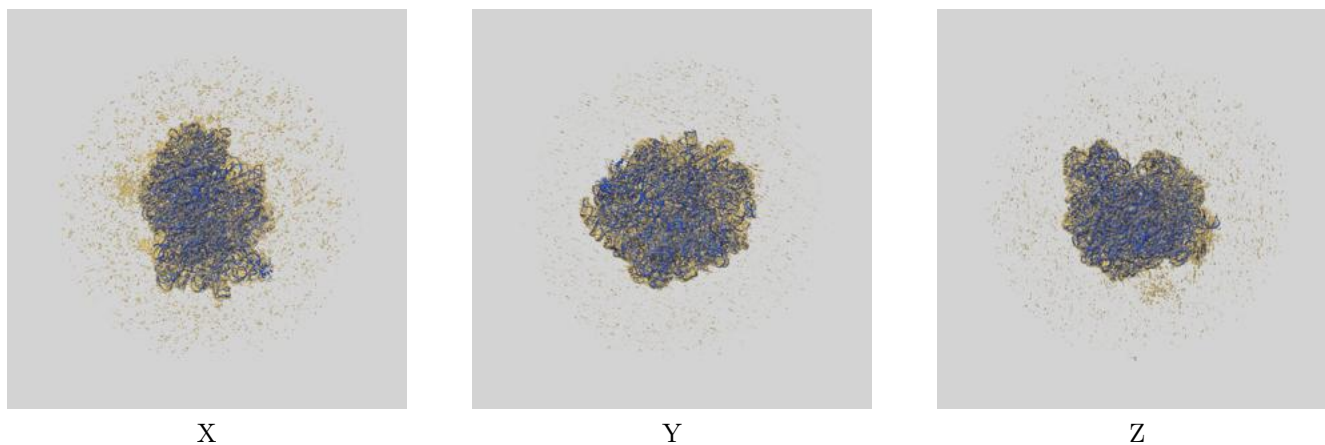
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.74	4.35	3.76
Unmasked-calculated*	-	-	-

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

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

This section contains information regarding the fit between EMDB map EMD-0373 and PDB model 6N8N. Per-residue inclusion information can be found in section 3 on page 12.

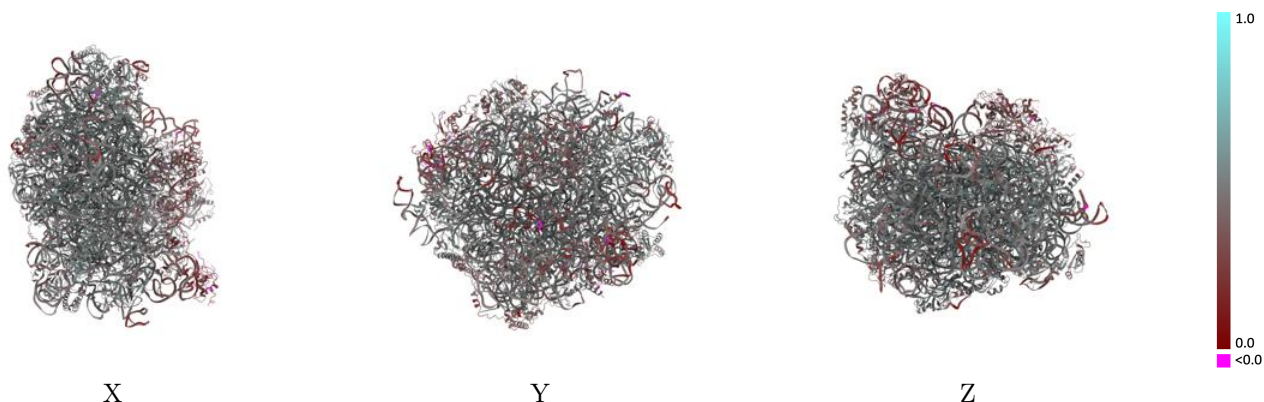
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.022 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.

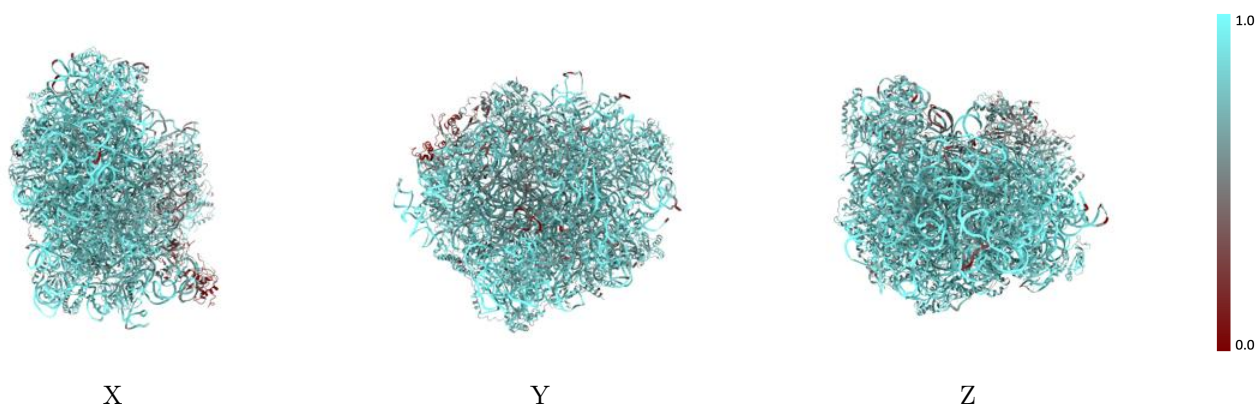


## 9.2 Q-score mapped to coordinate model [i](#)



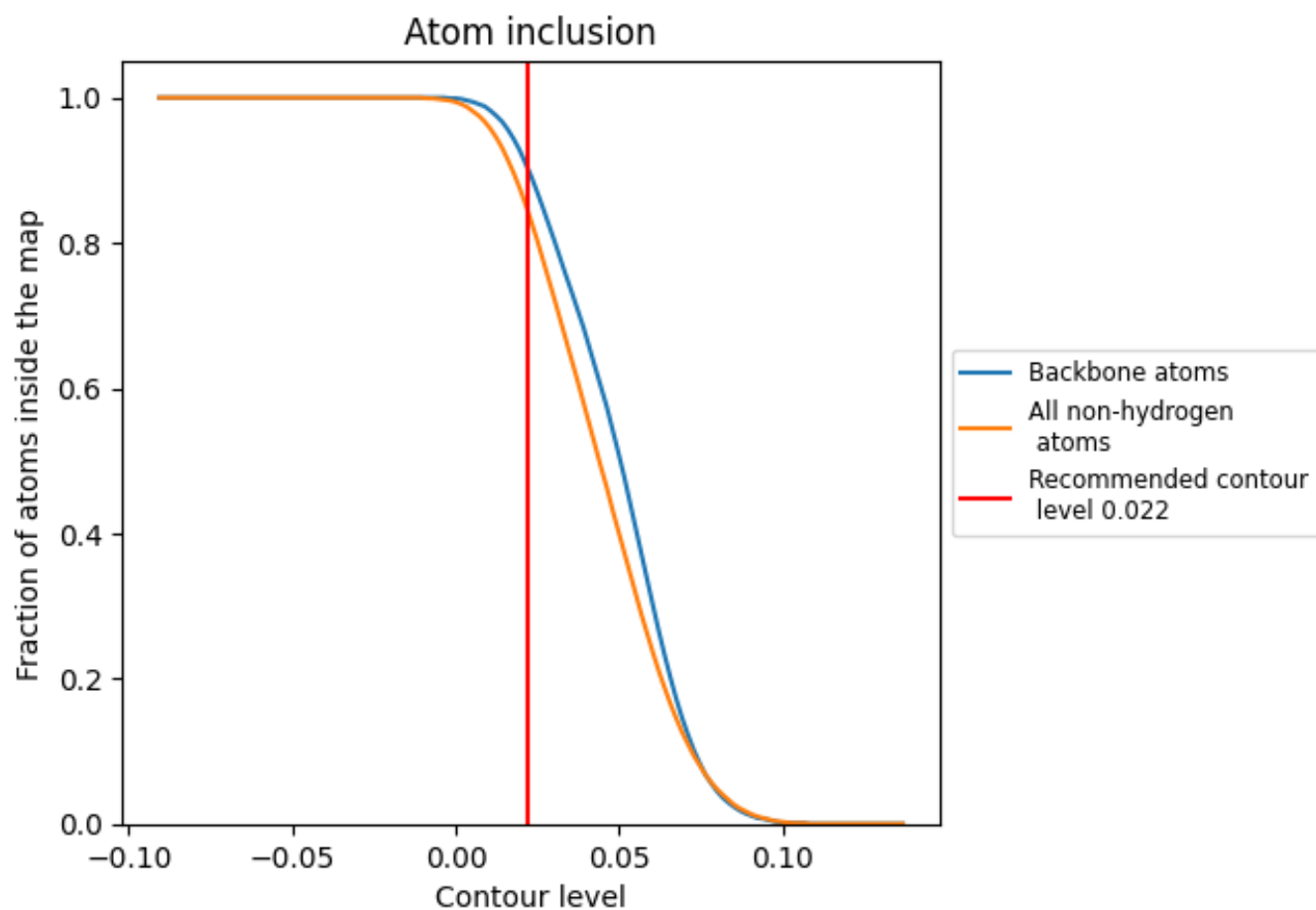
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.022).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 85% 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 (0.022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8460	 0.4570
A	 0.9100	 0.4590
B	 0.9520	 0.4610
C	 0.9400	 0.4730
D	 0.8240	 0.5080
E	 0.8270	 0.4900
F	 0.7950	 0.4810
G	 0.7750	 0.4170
H	 0.7870	 0.4620
I	 0.8080	 0.4740
J	 0.8030	 0.4600
K	 0.7870	 0.4730
L	 0.2100	 0.2090
M	 0.7240	 0.3840
N	 0.7880	 0.4620
O	 0.8050	 0.4690
Q	 0.7450	 0.4820
R	 0.8130	 0.4930
S	 0.7010	 0.3340
V	 0.6160	 0.4010
W	 0.6460	 0.3470
X	 0.7030	 0.4330
Y	 0.3890	 0.3310
a	 0.8250	 0.5050
b	 0.8180	 0.4940
c	 0.7800	 0.4820
d	 0.7960	 0.4860
e	 0.8310	 0.4900
f	 0.8100	 0.4800
g	 0.7680	 0.4780
h	 0.7930	 0.4390
i	 0.7580	 0.4890
j	 0.7850	 0.4810
k	 0.7940	 0.4690
l	 0.7970	 0.4860



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Chain	Atom inclusion	Q-score
m	 0.8220	 0.4730
n	 0.8160	 0.4950
o	 0.7260	 0.4380
p	 0.7770	 0.4580
q	 0.7680	 0.4640
r	 0.7890	 0.4950
s	 0.8320	 0.5030
t	 0.7850	 0.4910
u	 0.8080	 0.4660
v	 0.7640	 0.4510
w	 0.8700	 0.5130
x	 0.7480	 0.4440
y	 0.7930	 0.5030
z	 0.5560	 0.4530