



## wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 05:23 PM EST

PDB ID : 3JD5  
EMDB ID : EMD-5941  
Title : Cryo-EM structure of the small subunit of the mammalian mitochondrial ribosome  
Authors : Kaushal, P.S.; Sharma, M.R.; Booth, T.M.; Haque, E.M.; Tung, C.S.; Sanbonmatsu, K.Y.; Spremulli, L.L.; Agrawal, R.K.  
Deposited on : 2016-04-08  
Resolution : 7.00 Å (reported)  
Based on initial models : 3J9M, 5AJ3

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:

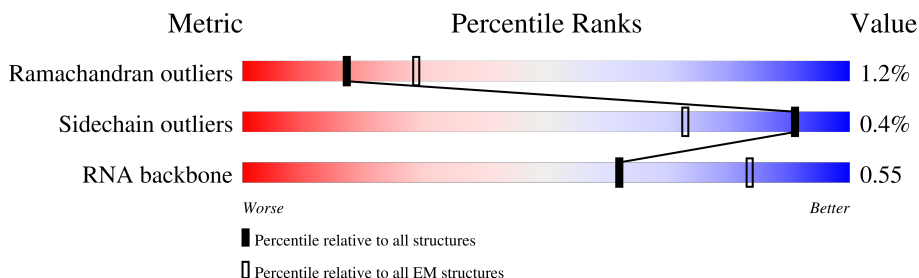
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP)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

# 1 Overall quality at a glance

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

The reported resolution of this entry is 7.00 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	955	
2	B	293	
3	C	167	
4	E	430	
5	F	124	
6	G	242	
7	I	396	
8	J	201	

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Mol	Chain	Length	Quality of chain
9	K	197	5% 69% 31%
10	L	139	15% 76% 22%
11	N	128	76% 21%
12	O	256	11% 67% 32%
13	P	135	10% 84% 14%
14	Q	130	13% 82% 16%
15	R	143	9% 67% 32%
16	U	87	10% 98% ..
17	a	359	12% 80% 19%
18	b	190	14% 69% 29%
19	c	173	21% 96% ..
20	d	205	7% 86% 14%
21	e	415	14% 81% 17%
22	f	189	7% 52% 48%
23	g	397	7% 84% 15%
24	h	386	26% 73%
25	i	106	6% 91% 8%
26	j	218	20% 95% ..
27	k	325	10% 83% 15%
28	m	118	44% 100%
29	n	199	5% 35% 64%
30	o	575	50% 78% 20%
31	p	258	7% 72% 28%
32	s	17	65% 94% 6%
32	z	17	6% 100%

## 2 Entry composition i

There are 32 unique types of molecules in this entry. The entry contains 64319 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 28S ribosomal RNA, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	952	20256	9090	3685	6529	952	0	0

- Molecule 2 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	217	1726	1102	319	298	7	0	0

- Molecule 3 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	132	1072	692	197	179	4	0	0

- Molecule 4 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	328	2613	1634	494	474	11	0	0

- Molecule 5 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	124	991	627	179	179	6	0	0

- Molecule 6 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	208	1720	1093	313	301	13	0	0

- Molecule 7 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	I	311	2541	1608	454	467	12	0	0

- Molecule 8 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	J	128	1049	676	180	190	3	0	0

- Molecule 9 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	K	136	1001	628	193	177	3	0	0

- Molecule 10 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	L	109	853	534	175	140	4	0	0

- Molecule 11 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	N	101	861	538	178	140	5	0	0

- Molecule 12 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	O	173	1421	904	258	250	9	0	0

- Molecule 13 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	P	116	916	580	180	151	5	0	0

- Molecule 14 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	109	Total	C	N	O	S	0	0
			857	555	153	145	4		

- Molecule 15 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	97	Total	C	N	O	S	0	0
			788	507	136	138	7		

- Molecule 16 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	U	86	Total	C	N	O	S	0	0
			737	457	148	124	8		

- Molecule 17 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	a	289	Total	C	N	O	S	0	0
			2356	1505	400	443	8		

- Molecule 18 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	b	135	Total	C	N	O	S	0	0
			1108	717	195	194	2		

- Molecule 19 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	c	168	Total	C	N	O	S	0	0
			1374	878	246	241	9		

- Molecule 20 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	d	176	Total	C	N	O	S	0	0
			1463	899	290	272	2		

- Molecule 21 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	e	344	Total	C	N	O	S	0	0
			2822	1804	476	529	13		

- Molecule 22 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	f	98	Total	C	N	O	S	0	0
			775	493	135	143	4		

- Molecule 23 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	g	338	Total	C	N	O	S	0	0
			2754	1774	482	488	10		

- Molecule 24 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	h	103	Total	C	N	O	S	0	0
			871	566	141	161	3		

- Molecule 25 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	i	98	Total	C	N	O	S	0	0
			818	519	153	143	3		

- Molecule 26 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	j	213	Total	C	N	O	S	0	0
			1792	1132	346	309	5		

- Molecule 27 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	k	275	Total	C	N	O	S	0	0
			2227	1418	377	421	11		

- Molecule 28 is a protein called Coiled-coil-helix-coiled-coil-helix domain containing 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	m	118	Total	C	N	O	S	0	0
			945	587	185	164	9		

- Molecule 29 is a protein called Aurora kinase A interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	n	72	Total	C	N	O	S	0	0
			642	409	142	89	2		

- Molecule 30 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	o	461	Total	C	N	O	S	0	0
			3273	2082	573	605	13		

- Molecule 31 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	p	187	Total	C	N	O	S	0	0
			1531	968	288	267	8		

- Molecule 32 is a protein called unknown.

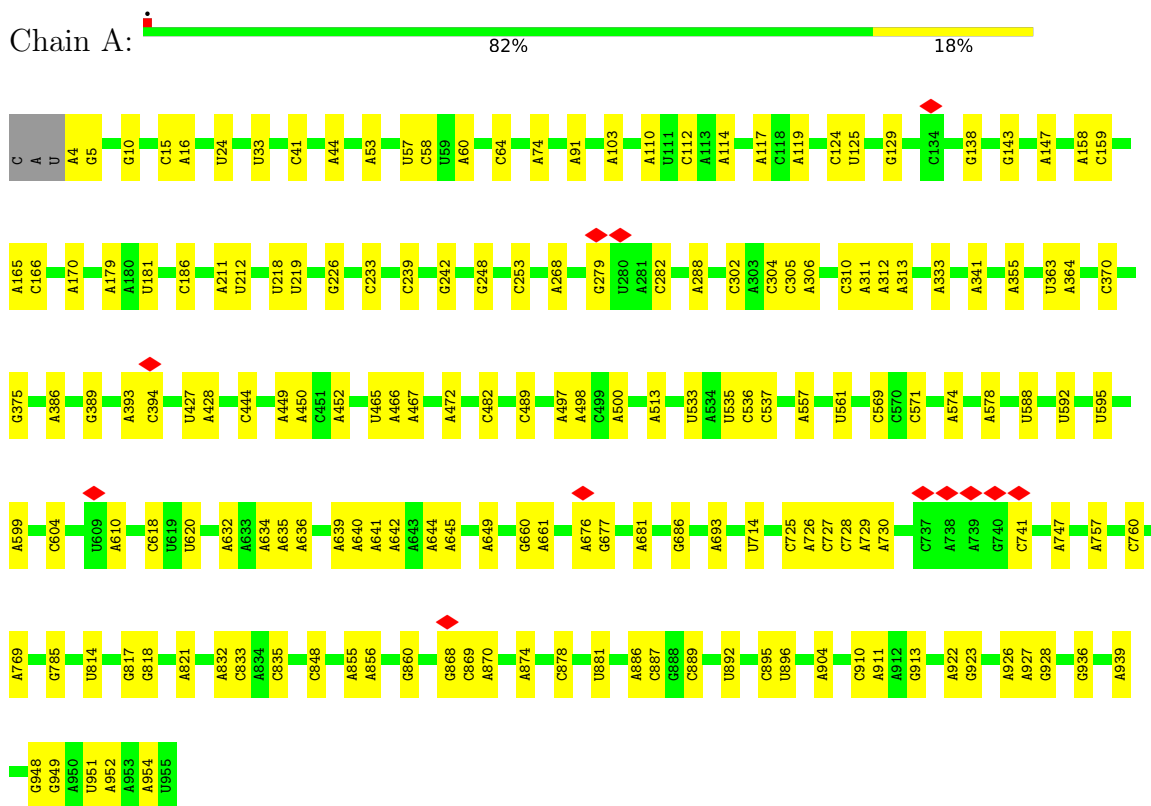
Mol	Chain	Residues	Atoms				AltConf	Trace
32	s	16	Total	C	N	O	0	0
			80	48	16	16		
32	z	17	Total	C	N	O	0	0
			86	51	17	18		



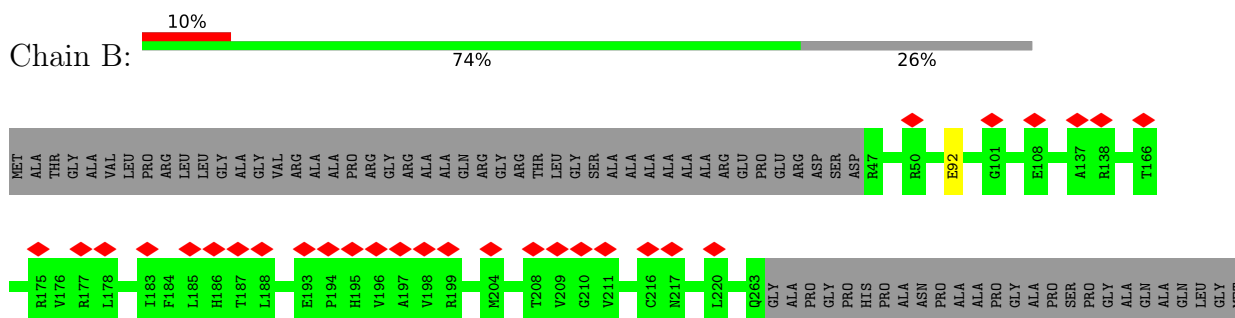
### 3 Residue-property plots [i](#)

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

- Molecule 1: 28S ribosomal RNA, mitochondrial

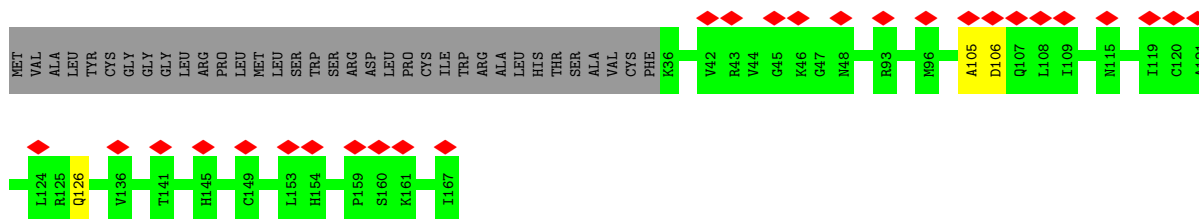
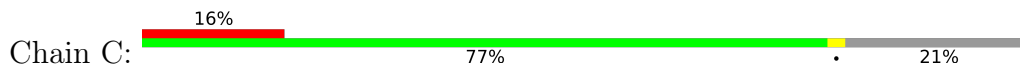


- Molecule 2: 28S ribosomal protein S2, mitochondrial

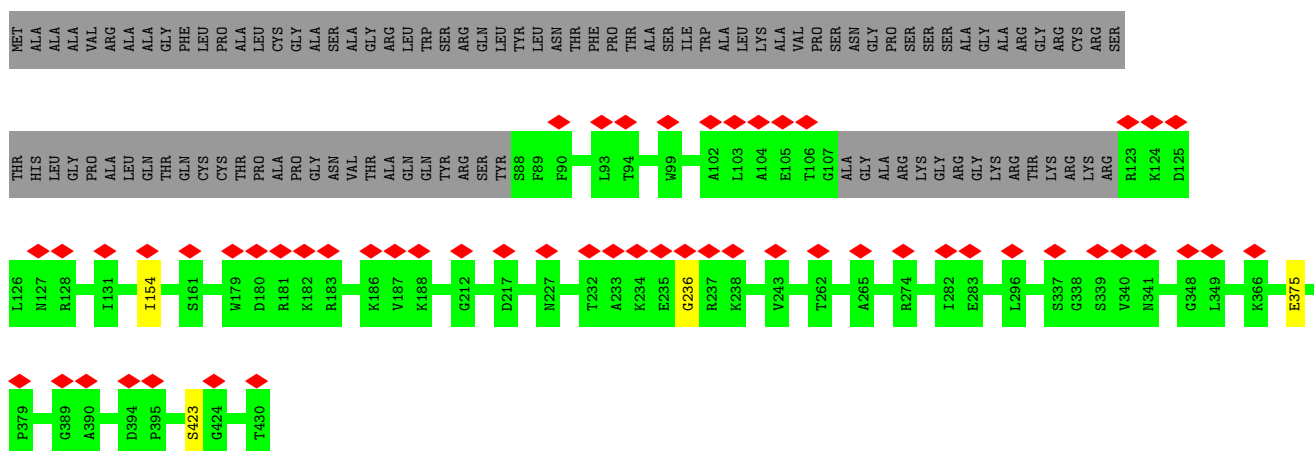
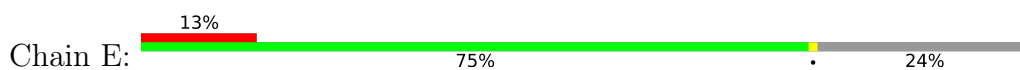


GLY  
HIS  
SER  
PRO

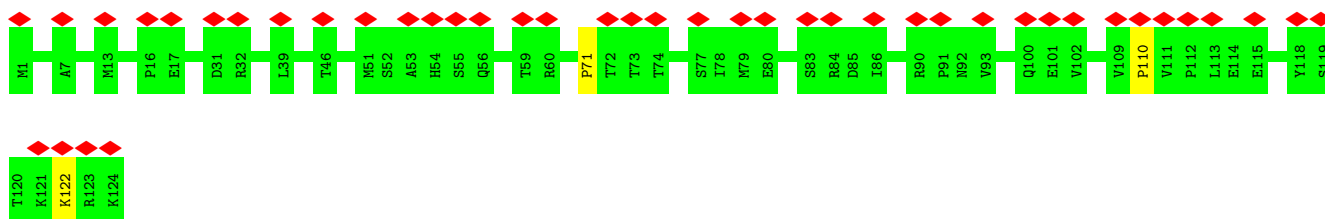
- Molecule 3: 28S ribosomal protein S24, mitochondrial



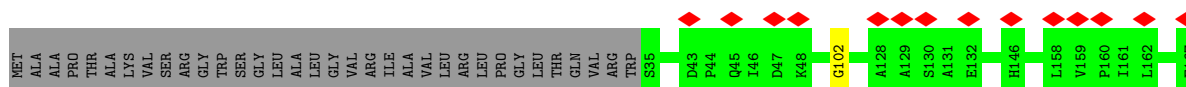
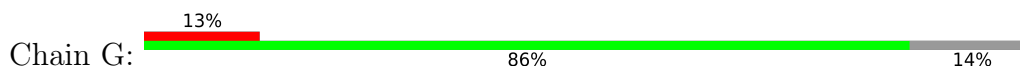
- Molecule 4: 28S ribosomal protein S5, mitochondrial



- Molecule 5: 28S ribosomal protein S6, mitochondrial

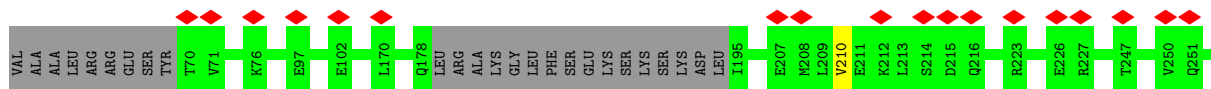
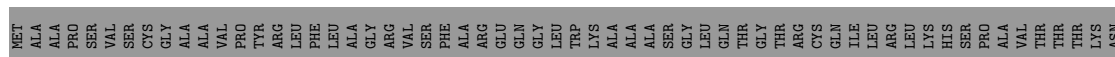
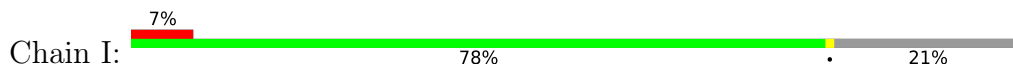


- Molecule 6: 28S ribosomal protein S7, mitochondrial

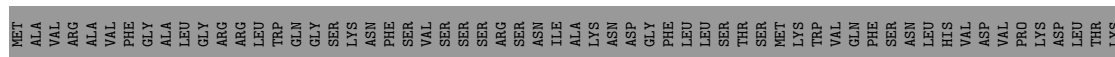




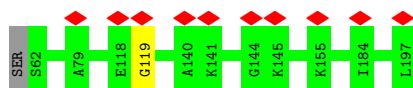
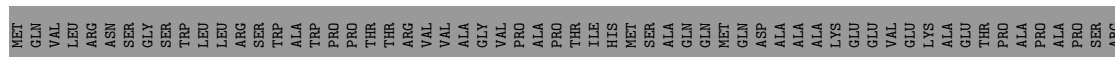
- Molecule 7: 28S ribosomal protein S9, mitochondrial



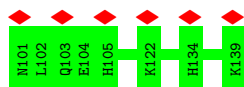
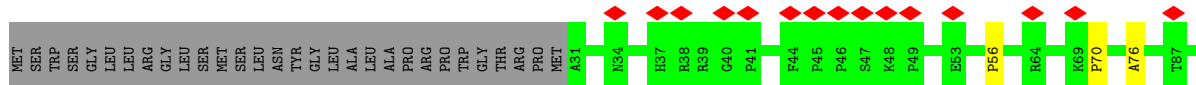
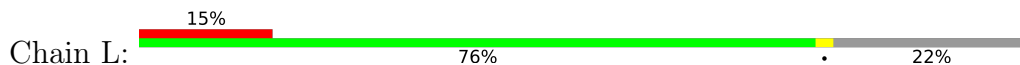
- Molecule 8: 28S ribosomal protein S10, mitochondrial



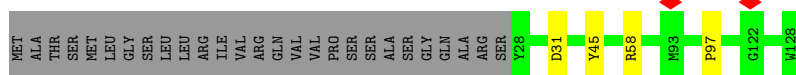
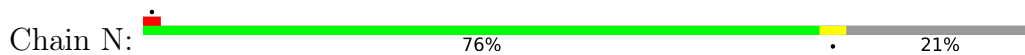
- Molecule 9: 28S ribosomal protein S11, mitochondrial



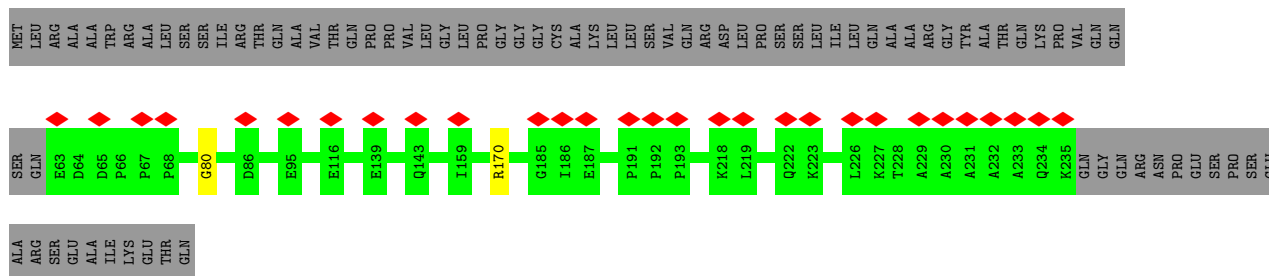
- Molecule 10: 28S ribosomal protein S12, mitochondrial



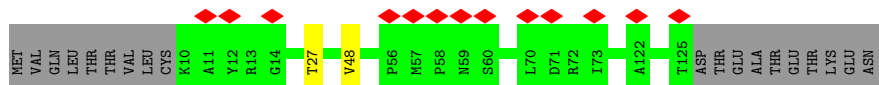
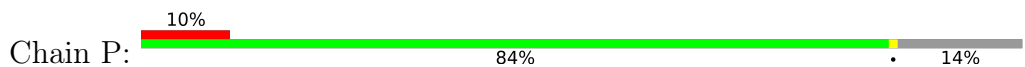
- Molecule 11: 28S ribosomal protein S14, mitochondrial



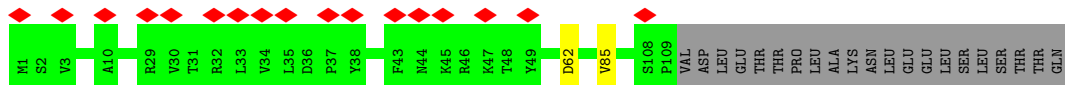
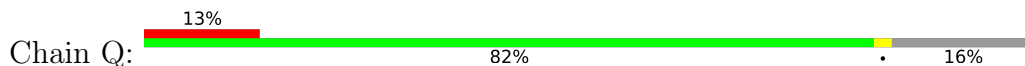
• Molecule 12: 28S ribosomal protein S15, mitochondrial



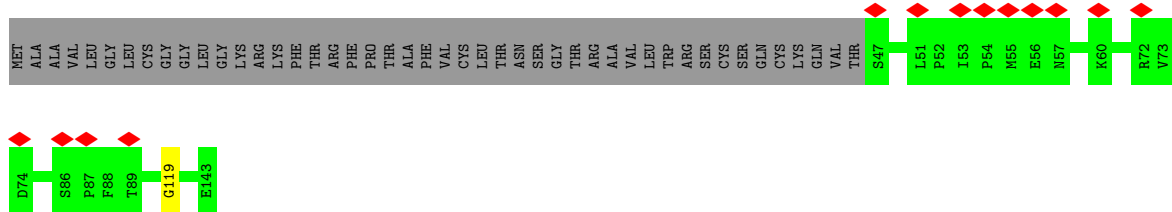
• Molecule 13: 28S ribosomal protein S16, mitochondrial



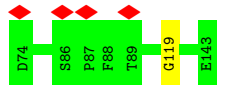
• Molecule 14: 28S ribosomal protein S17, mitochondrial

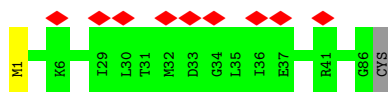


• Molecule 15: 28S ribosomal protein S18c, mitochondrial

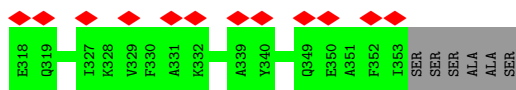
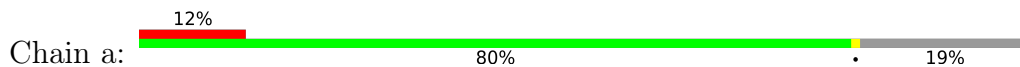


• Molecule 16: 28S ribosomal protein S21, mitochondrial

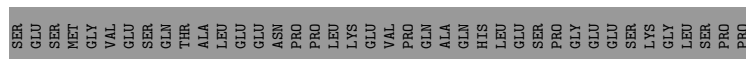
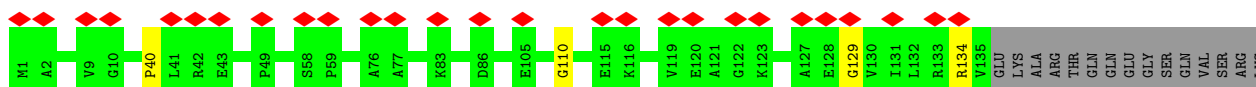




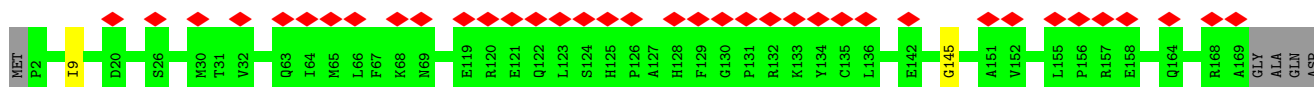
- Molecule 17: 28S ribosomal protein S22, mitochondrial



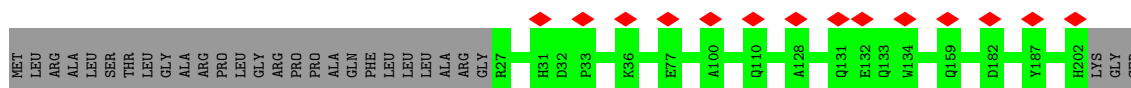
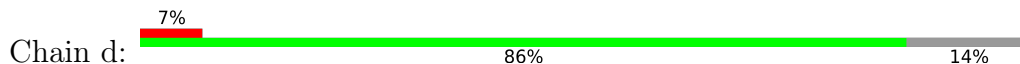
- Molecule 18: 28S ribosomal protein S23, mitochondrial



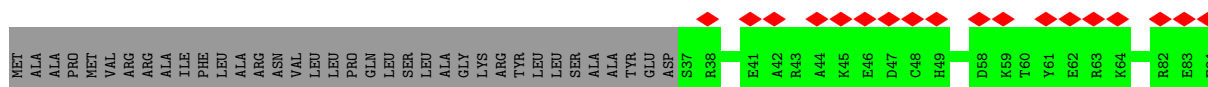
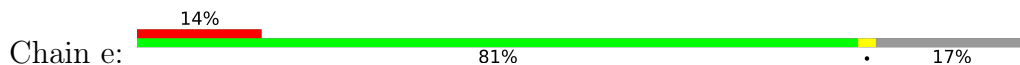
- Molecule 19: 28S ribosomal protein S25, mitochondrial



- Molecule 20: 28S ribosomal protein S26, mitochondrial



- Molecule 21: 28S ribosomal protein S27, mitochondrial











- Molecule 32: unknown



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	307556	Depositor
Resolution determination method	Not provided	
CTF correction method	CTFFIND3	Depositor
Microscope	JEOL 3200FS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	9.0	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	59717	Depositor
Image detector	GATAN ULTRASCAN 1000 (2k x 2k)	Depositor
Maximum map value	0.001	Depositor
Minimum map value	-0.000	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.00017	Depositor
Map size ( $\text{\AA}$ )	438.74997, 438.74997, 438.74997	wwPDB
Map dimensions	375, 375, 375	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.17, 1.17, 1.17	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	0.10	0/22681	0.65	0/35318
2	B	0.24	0/1766	0.38	0/2392
3	C	0.23	0/1100	0.39	0/1487
4	E	0.23	0/2664	0.38	0/3578
5	F	0.23	0/1009	0.41	0/1362
6	G	0.23	0/1760	0.37	0/2366
7	I	0.23	0/2598	0.38	0/3490
8	J	0.23	0/1071	0.39	0/1447
9	K	0.24	0/1021	0.43	0/1380
10	L	0.23	0/872	0.40	0/1171
11	N	0.21	0/878	0.36	0/1179
12	O	0.23	0/1443	0.34	0/1927
13	P	0.23	0/937	0.38	0/1262
14	Q	0.23	0/874	0.42	0/1183
15	R	0.23	0/805	0.38	0/1082
16	U	0.22	0/748	0.36	0/995
17	a	0.23	0/2403	0.37	0/3246
18	b	0.24	0/1135	0.37	0/1528
19	c	0.24	0/1406	0.40	0/1894
20	d	0.23	0/1489	0.34	0/2008
21	e	0.23	0/2881	0.38	0/3893
22	f	0.24	0/787	0.42	0/1059
23	g	0.23	0/2819	0.39	0/3814
24	h	0.24	0/899	0.35	0/1209
25	i	0.22	0/834	0.36	0/1112
26	j	0.22	0/1841	0.39	0/2493
27	k	0.22	0/2275	0.36	0/3075
28	m	0.23	0/961	0.39	0/1284
29	n	0.21	0/654	0.34	0/862
30	o	0.24	0/2605	0.36	0/3526
31	p	0.23	0/1583	0.37	0/2149
All	All	0.20	0/66799	0.50	0/94771

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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

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

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	215/293 (73%)	197 (92%)	17 (8%)	1 (0%)	29	69
3	C	130/167 (78%)	108 (83%)	19 (15%)	3 (2%)	6	34
4	E	326/430 (76%)	280 (86%)	43 (13%)	3 (1%)	17	57
5	F	122/124 (98%)	106 (87%)	14 (12%)	2 (2%)	9	44
6	G	206/242 (85%)	188 (91%)	17 (8%)	1 (0%)	29	69
7	I	309/396 (78%)	277 (90%)	31 (10%)	1 (0%)	41	77
8	J	126/201 (63%)	105 (83%)	19 (15%)	2 (2%)	9	44
9	K	134/197 (68%)	119 (89%)	14 (10%)	1 (1%)	22	63
10	L	107/139 (77%)	86 (80%)	18 (17%)	3 (3%)	5	30
11	N	99/128 (77%)	89 (90%)	9 (9%)	1 (1%)	15	54
12	O	171/256 (67%)	158 (92%)	12 (7%)	1 (1%)	25	66
13	P	114/135 (84%)	101 (89%)	11 (10%)	2 (2%)	8	40
14	Q	107/130 (82%)	92 (86%)	14 (13%)	1 (1%)	17	57
15	R	95/143 (66%)	85 (90%)	9 (10%)	1 (1%)	14	52
16	U	84/87 (97%)	80 (95%)	4 (5%)	0	100	100
17	a	287/359 (80%)	260 (91%)	27 (9%)	0	100	100
18	b	133/190 (70%)	120 (90%)	10 (8%)	3 (2%)	6	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	c	166/173 (96%)	148 (89%)	16 (10%)	2 (1%)	13	50
20	d	174/205 (85%)	166 (95%)	8 (5%)	0	100	100
21	e	340/415 (82%)	287 (84%)	46 (14%)	7 (2%)	7	36
22	f	96/189 (51%)	93 (97%)	3 (3%)	0	100	100
23	g	334/397 (84%)	302 (90%)	29 (9%)	3 (1%)	17	57
24	h	101/386 (26%)	90 (89%)	9 (9%)	2 (2%)	7	38
25	i	96/106 (91%)	89 (93%)	6 (6%)	1 (1%)	15	54
26	j	211/218 (97%)	173 (82%)	33 (16%)	5 (2%)	6	33
27	k	273/325 (84%)	243 (89%)	26 (10%)	4 (2%)	10	46
28	m	116/118 (98%)	94 (81%)	22 (19%)	0	100	100
29	n	70/199 (35%)	66 (94%)	2 (3%)	2 (3%)	4	29
30	o	306/575 (53%)	273 (89%)	24 (8%)	9 (3%)	4	29
31	p	185/258 (72%)	154 (83%)	29 (16%)	2 (1%)	14	52
All	All	5233/7181 (73%)	4629 (88%)	541 (10%)	63 (1%)	17	50

5 of 63 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	N	97	PRO
5	F	71	PRO
5	F	110	PRO
6	G	102	GLY
10	L	56	PRO

### 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	
2	B	186/230 (81%)	186 (100%)	0	100	100
3	C	113/142 (80%)	113 (100%)	0	100	100
4	E	273/346 (79%)	272 (100%)	1 (0%)	91	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	F	109/109 (100%)	108 (99%)	1 (1%)	78	87
6	G	183/208 (88%)	183 (100%)	0	100	100
7	I	267/333 (80%)	266 (100%)	1 (0%)	91	94
8	J	118/182 (65%)	116 (98%)	2 (2%)	60	78
9	K	102/151 (68%)	102 (100%)	0	100	100
10	L	94/118 (80%)	94 (100%)	0	100	100
11	N	91/113 (80%)	88 (97%)	3 (3%)	38	61
12	O	159/226 (70%)	158 (99%)	1 (1%)	86	92
13	P	95/113 (84%)	95 (100%)	0	100	100
14	Q	95/115 (83%)	94 (99%)	1 (1%)	73	84
15	R	89/126 (71%)	89 (100%)	0	100	100
16	U	77/78 (99%)	76 (99%)	1 (1%)	69	81
17	a	255/307 (83%)	253 (99%)	2 (1%)	81	89
18	b	115/163 (71%)	114 (99%)	1 (1%)	78	87
19	c	152/155 (98%)	152 (100%)	0	100	100
20	d	147/168 (88%)	147 (100%)	0	100	100
21	e	307/362 (85%)	307 (100%)	0	100	100
22	f	85/160 (53%)	85 (100%)	0	100	100
23	g	301/352 (86%)	301 (100%)	0	100	100
24	h	94/341 (28%)	93 (99%)	1 (1%)	73	84
25	i	88/94 (94%)	87 (99%)	1 (1%)	73	84
26	j	190/193 (98%)	190 (100%)	0	100	100
27	k	252/292 (86%)	252 (100%)	0	100	100
28	m	102/102 (100%)	102 (100%)	0	100	100
29	n	66/173 (38%)	66 (100%)	0	100	100
30	o	277/369 (75%)	276 (100%)	1 (0%)	91	94
31	p	166/226 (74%)	166 (100%)	0	100	100
All	All	4648/6047 (77%)	4631 (100%)	17 (0%)	91	94

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	h	339	ARG

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Mol	Chain	Res	Type
30	o	61	LYS
11	N	58	ARG
12	O	170	ARG
14	Q	62	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 67 such sidechains are listed below:

Mol	Chain	Res	Type
27	k	270	GLN
29	n	178	GLN
31	p	207	GLN
11	N	60	ASN
10	L	106	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	952/955 (99%)	170 (17%)	3 (0%)

5 of 170 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	5	G
1	A	10	G
1	A	16	A
1	A	24	U
1	A	33	U

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	4	A
1	A	15	C
1	A	363	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](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
30	o	13
21	e	1
23	g	1

The worst 5 of 15 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	o	383:TYR	C	386:UNK	N	27.66
1	o	399:UNK	C	417:MET	N	21.54
1	o	143:GLU	C	145:UNK	N	20.88
1	e	291:THR	C	292:ALA	N	20.27
1	g	69:ILE	C	70:SER	N	20.27



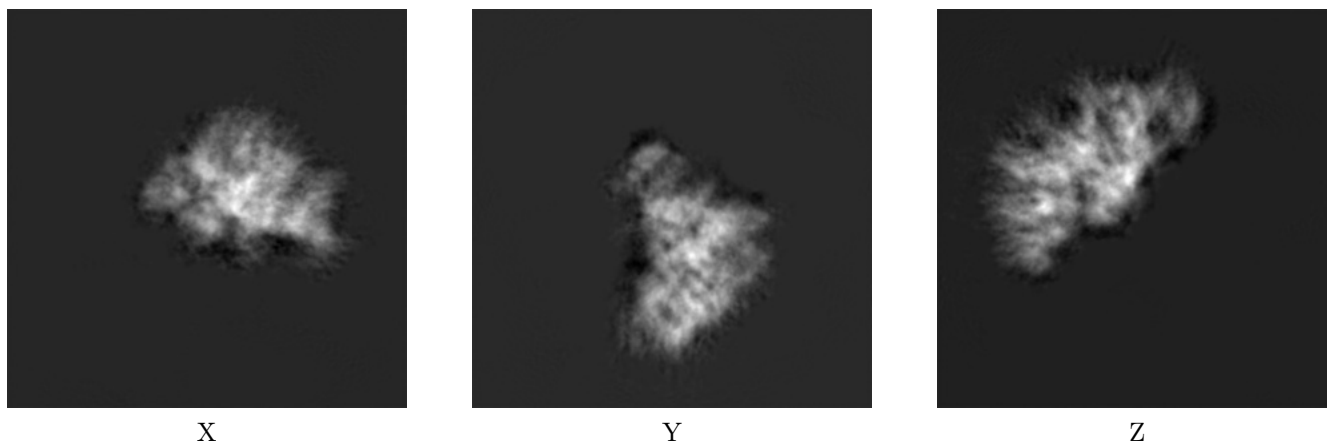
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5941. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

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

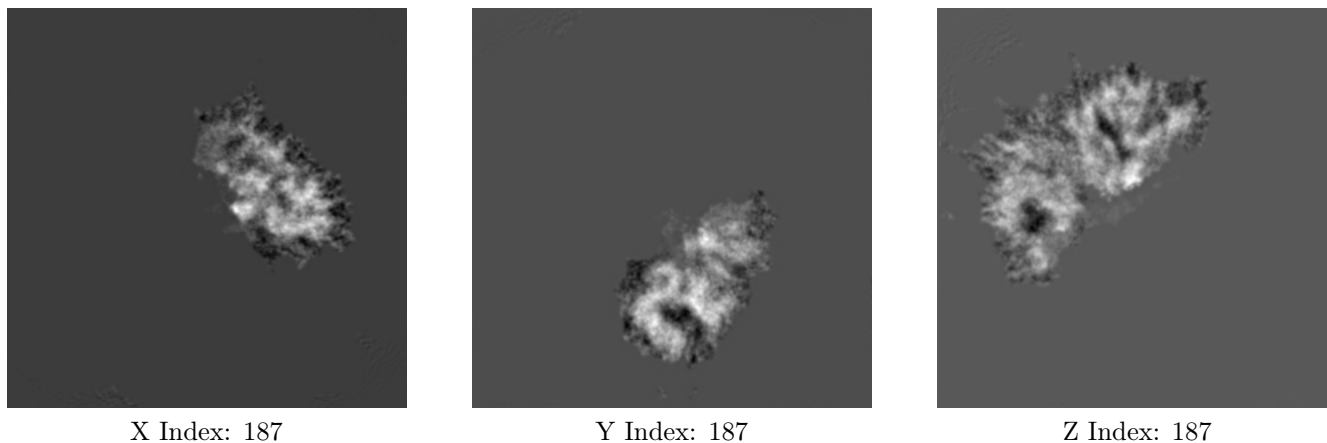
#### 6.1.1 Primary map



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

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

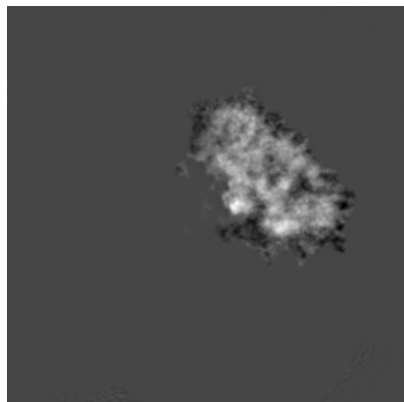
#### 6.2.1 Primary map



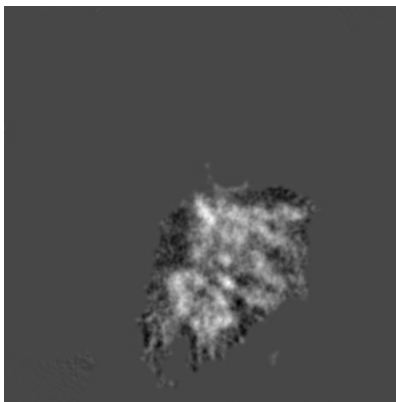
The images above show central slices of the map in three orthogonal directions.

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

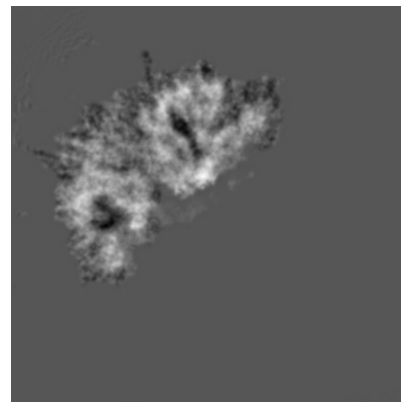
### 6.3.1 Primary map



X Index: 180



Y Index: 217



Z Index: 189

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

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

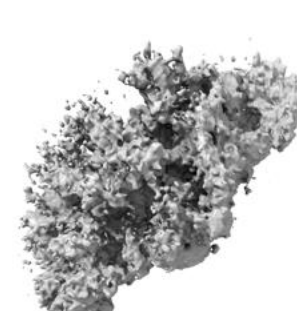
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.00017. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

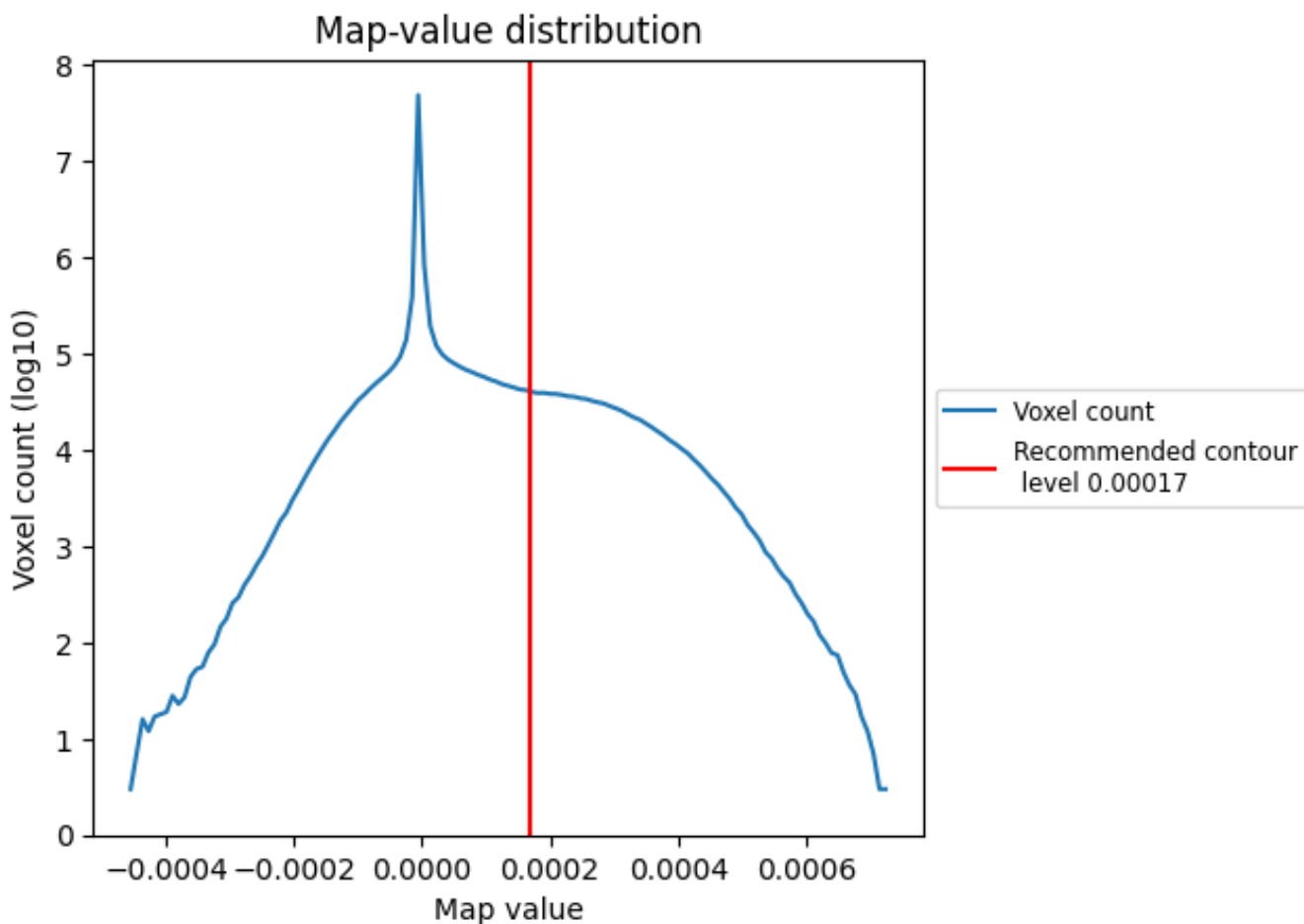
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

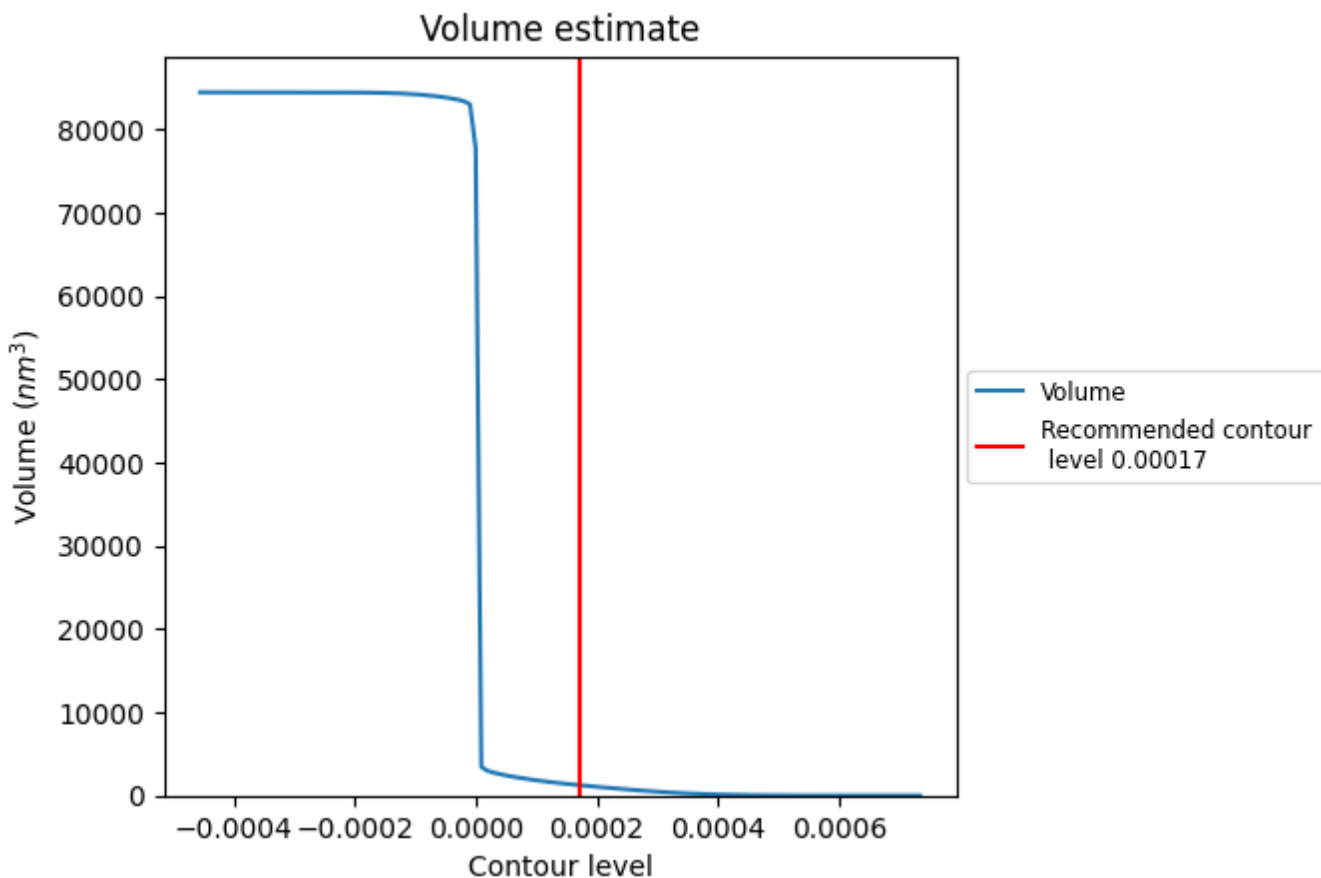
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

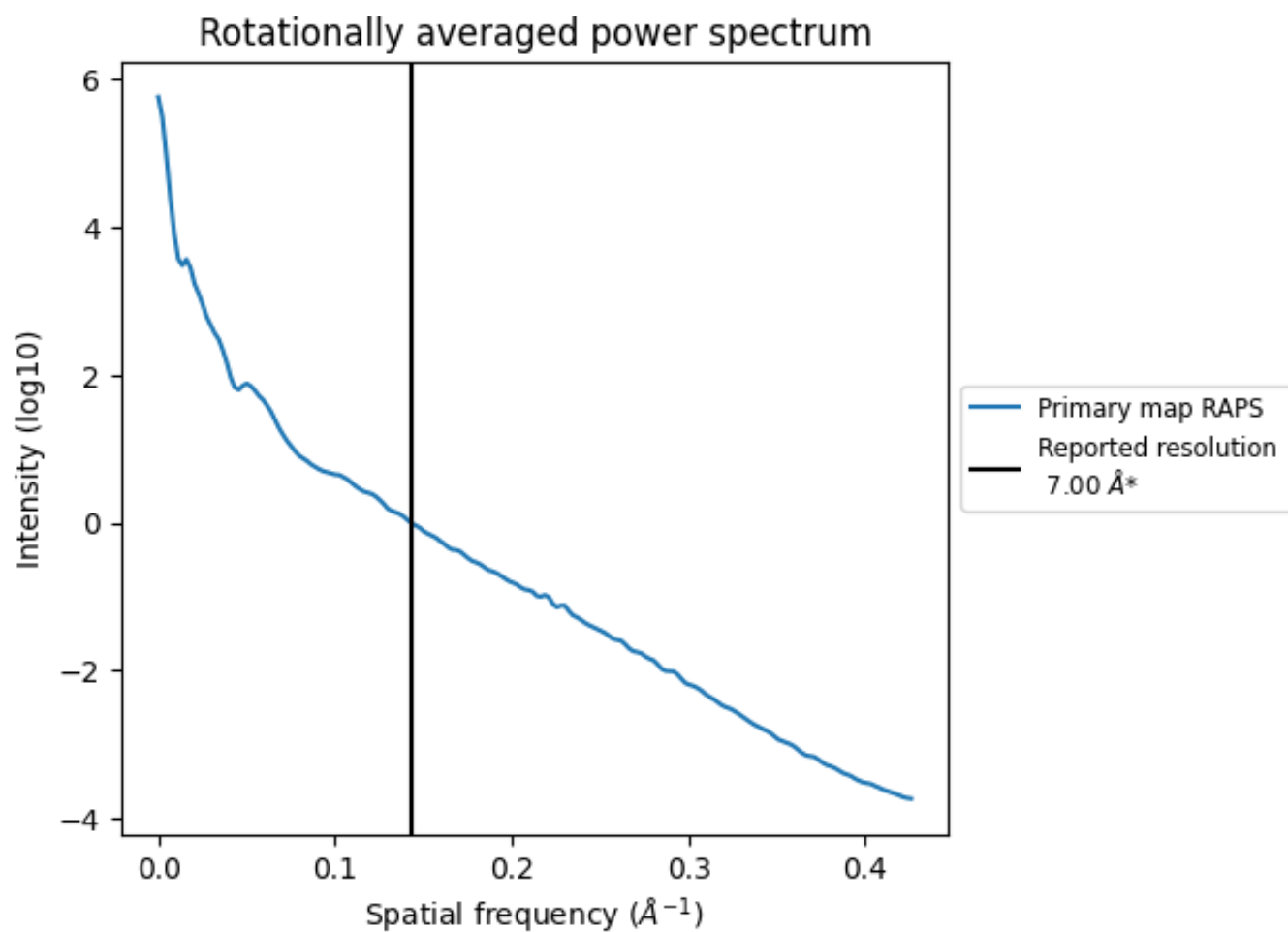
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1255 nm<sup>3</sup>; this corresponds to an approximate mass of 1134 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 0.143 Å<sup>-1</sup>

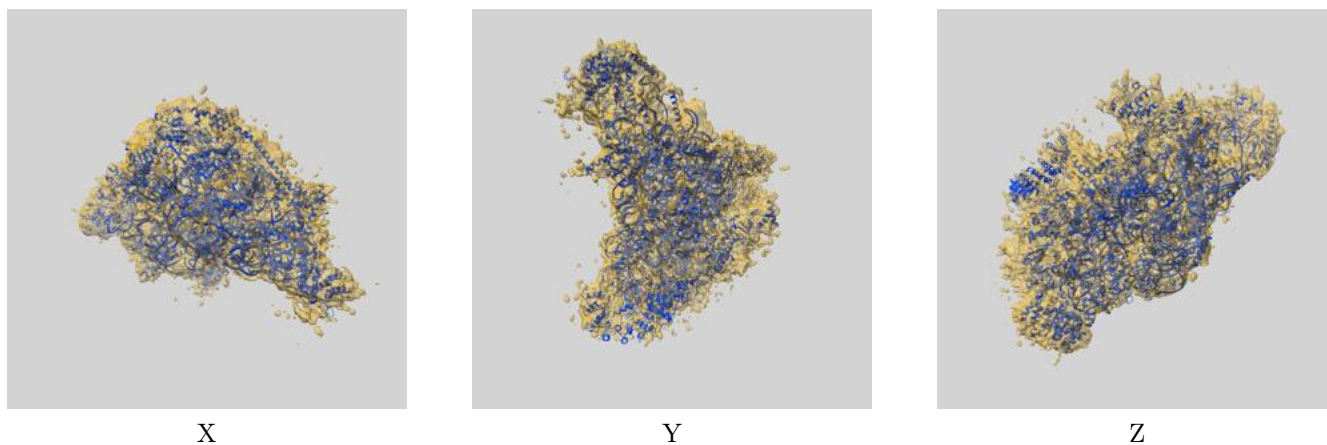
## 8 Fourier-Shell correlation

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

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

This section contains information regarding the fit between EMDB map EMD-5941 and PDB model 3JD5. Per-residue inclusion information can be found in section 3 on page 9.

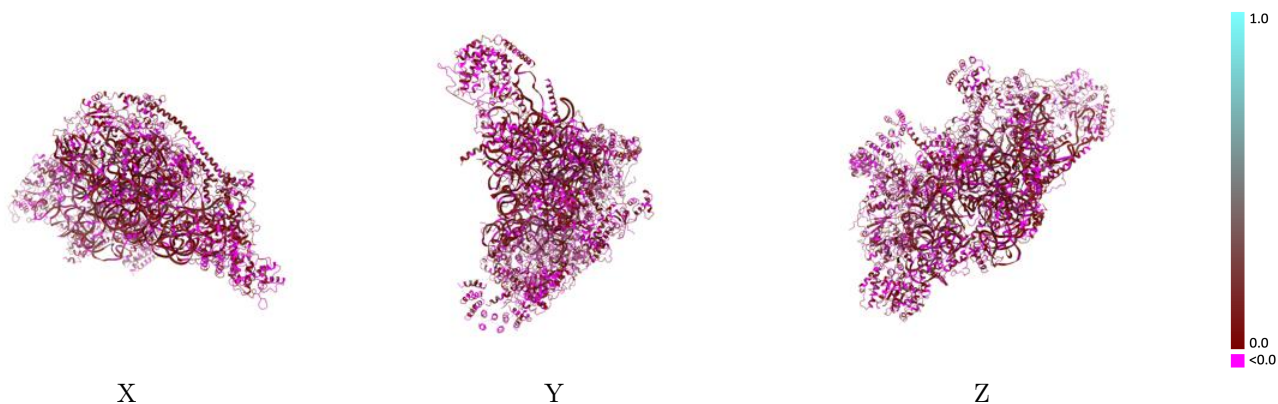
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.00017 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.

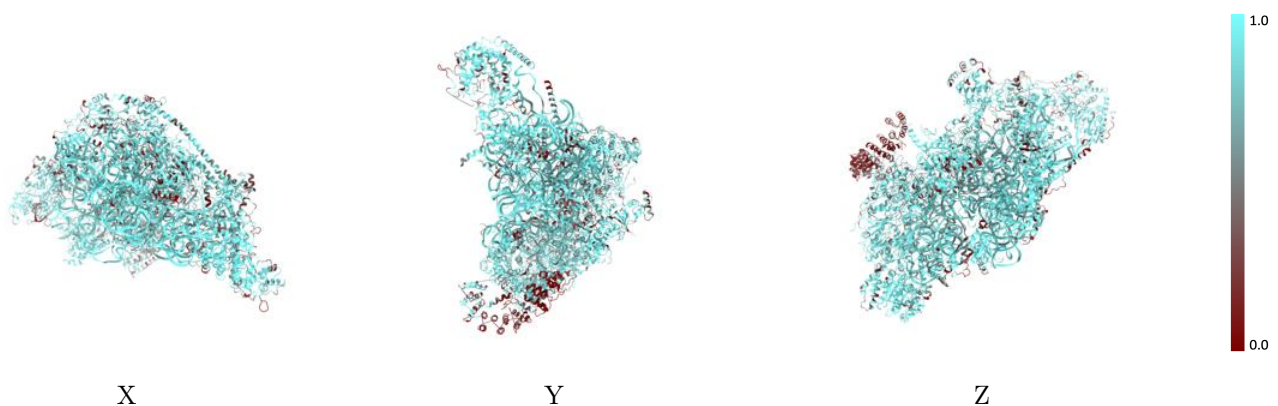


## 9.2 Q-score mapped to coordinate model [i](#)



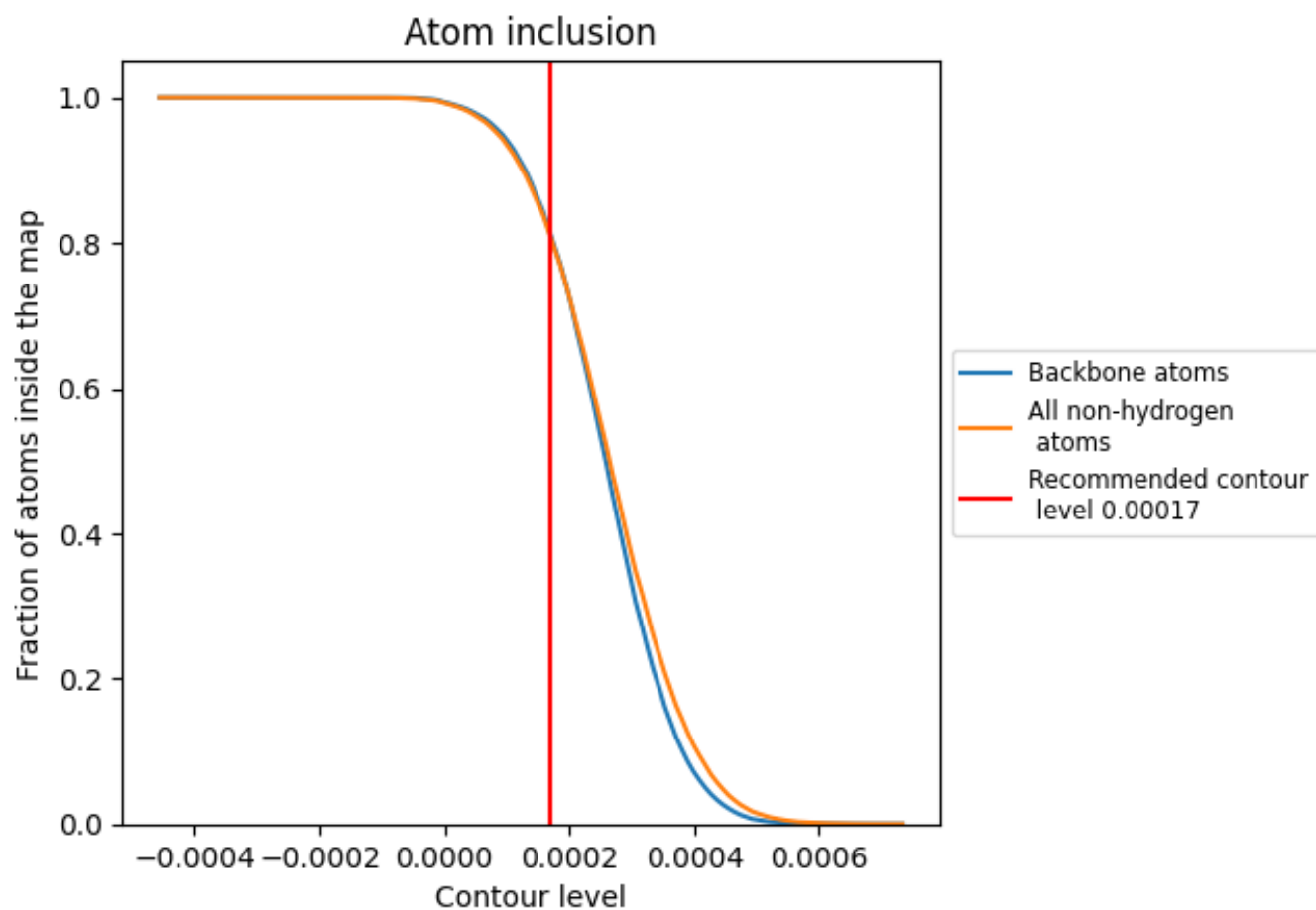
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00017).





































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 81% 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 (0.00017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8094	 0.0610
A	 0.9205	 0.0840
B	 0.8051	 0.0380
C	 0.7098	 0.0260
E	 0.7686	 0.0560
F	 0.5768	 0.0460
G	 0.7703	 0.0350
I	 0.8412	 0.0720
J	 0.8655	 0.0430
K	 0.8663	 0.0610
L	 0.7193	 0.0480
N	 0.9449	 0.0530
O	 0.7677	 0.0560
P	 0.8018	 0.0220
Q	 0.7595	 0.0430
R	 0.8104	 0.0690
U	 0.8317	 0.0960
a	 0.7999	 0.0620
b	 0.7123	 0.0460
c	 0.6945	 0.0530
d	 0.8530	 0.0880
e	 0.7707	 0.0360
f	 0.7918	 0.0330
g	 0.8741	 0.0490
h	 0.8873	 0.0910
i	 0.8962	 0.0640
j	 0.7222	 0.0540
k	 0.8166	 0.0410
m	 0.5197	 0.0330
n	 0.8010	 0.0430
o	 0.3517	 0.0210
p	 0.8458	 0.0590
s	 0.3000	 0.0650
z	 0.9535	 0.0690

