



wwPDB EM Validation Summary Report ⓘ

Nov 3, 2024 – 10:13 pm GMT

PDB ID : 7QH7
EMDB ID : EMD-13967
Title : Cryo-EM structure of the human mtLSU assembly intermediate upon MRM2 depletion - class 4
Authors : Rebelo-Guiomar, P.; Pellegrino, S.; Dent, K.C.; Warren, A.J.; Minczuk, M.
Deposited on : 2021-12-10
Resolution : 2.89 Å(reported)
Based on initial model : 5OOL

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

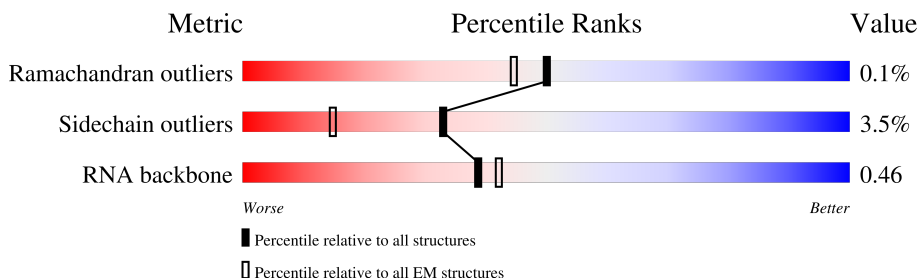
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.89 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.



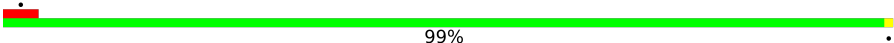
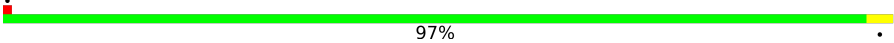
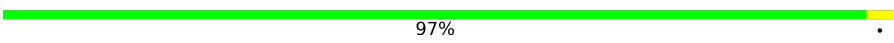
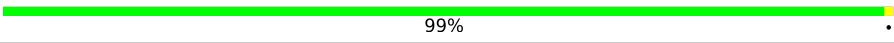
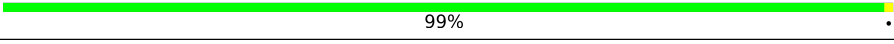
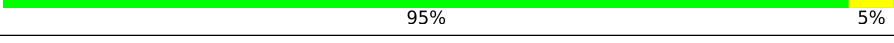
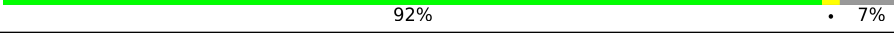
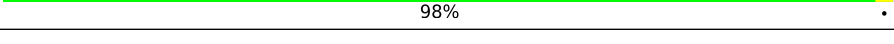
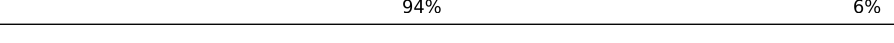
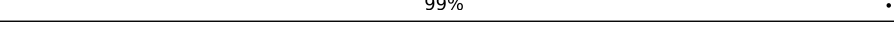
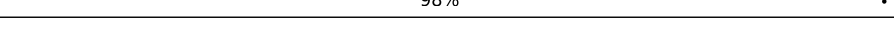
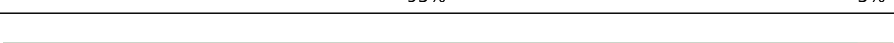



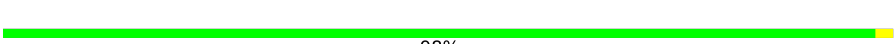


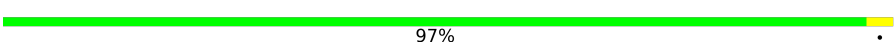

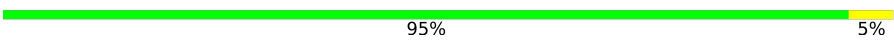
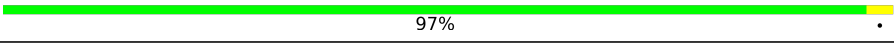
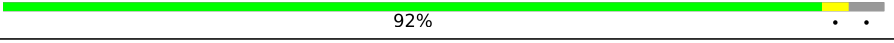


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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 ≥ 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	D	215	
2	E	304	
3	F	250	
4	H	95	
5	I	30	
6	K	177	
7	L	115	
8	M	287	




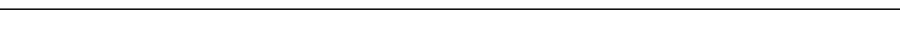
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	N	201	 99%
10	O	152	 97%
11	P	141	 97%
12	Q	217	 99%
13	R	139	 99%
14	S	156	 95% 5%
15	T	166	 92% 7%
16	U	125	 98%
17	V	48	 94% 6%
18	W	100	 99%
19	X	243	 98%
20	Y	175	 95% 5%
21	Z	115	 96%
22	0	108	 96%
23	1	49	 94% 6%
24	2	45	 98%
25	3	95	 98%
26	5	392	 96%
27	6	292	 96%
28	7	287	 97%
29	9	123	 91% 5%
30	a	80	 95% 5%
31	b	148	 97%
32	c	287	 92%
33	d	169	 90% 7%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	f	17	 94% 6%
35	g	129	 96% .
36	h	105	 90% 7% .
37	i	97	 99% .
38	j	86	 98% .
39	o	81	 96% .
40	p	125	 9% 99% .
41	q	101	 99% .
42	r	140	 89% . 8%
43	s	390	 91% . 5%
44	u	111	 95% 5%
45	v	69	 9% 99% .
46	w	79	 70% 100%
47	A	1256	 74% 26%
48	B	61	 18% 62% 30% 8%
49	4	37	 95% 5%

2 Entry composition [i](#)

There are 52 unique types of molecules in this entry. The entry contains 85397 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 protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	215	Total	C	N	O	S	0	0
			1671	1034	337	292	8		

- Molecule 2 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	304	Total	C	N	O	S	0	0
			2396	1539	416	430	11		

- Molecule 3 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	250	Total	C	N	O	S	0	0
			2013	1294	365	348	6		

- Molecule 4 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	95	Total	C	N	O	S	0	0
			784	498	152	134			

- Molecule 5 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	30	Total	C	N	O	S	0	0
			247	160	47	37	3		

- Molecule 6 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	177	Total	C	N	O	S	0	0
			1451	934	259	251	7		

- Molecule 7 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	115	Total	C	N	O	S	0	0
			889	559	171	154	5		

- Molecule 8 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	M	287	Total	C	N	O	S	0	0
			2305	1472	425	402	6		

- Molecule 9 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	N	201	Total	C	N	O	S	0	0
			1621	1033	302	276	10		

- Molecule 10 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	O	152	Total	C	N	O	S	0	0
			1245	784	239	215	7		

- Molecule 11 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	P	141	Total	C	N	O	S	0	0
			1148	719	221	203	5		

- Molecule 12 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Q	217	Total	C	N	O	S	0	0
			1805	1159	317	320	9		

- Molecule 13 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	R	139	Total	C	N	O	S	0	0
			1143	726	228	185	4		

- Molecule 14 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	S	156	Total	C	N	O	S	0	0
			1251	806	222	219	4		

- Molecule 15 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	155	Total	C	N	O	S	0	0
			1274	815	232	220	7		

- Molecule 16 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	U	125	Total	C	N	O	S	0	0
			1030	660	197	171	2		

- Molecule 17 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	V	48	Total	C	N	O	S	0	0
			402	259	63	77	3		

- Molecule 18 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	W	100	Total	C	N	O	S	0	0
			801	518	150	130	3		

- Molecule 19 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	X	243	Total	C	N	O	S	0	0
			2035	1317	351	362	5		

- Molecule 20 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Y	175	Total	C	N	O	S	0	0
			1506	961	290	251	4		

- Molecule 21 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Z	115	Total	C	N	O	S	0	0
			937	598	175	161	3		

- Molecule 22 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	0	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 23 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	1	49	Total	C	N	O	S	0	0
			408	263	77	66	2		

- Molecule 24 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	2	45	Total	C	N	O	S	0	0
			367	227	81	58	1		

- Molecule 25 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 26 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	5	392	Total	C	N	O	S	0	0
			3199	2067	558	563	11		

- Molecule 27 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	6	292	Total	C	N	O	S	0	0
			2460	1586	432	434	8		

- Molecule 28 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	7	287	Total	C	N	O	S	0	0
			2334	1495	397	425	17		

- Molecule 29 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	9	117	Total	C	N	O	S	0	0
			947	614	163	168	2		

- Molecule 30 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	80	Total	C	N	O	S	0	0
			672	425	124	118	5		

- Molecule 31 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	148	Total	C	N	O	S	0	0
			1178	733	229	213	3		

- Molecule 32 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	275	Total	C	N	O	S	0	0
			2214	1413	382	410	9		

- Molecule 33 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	157	Total	C	N	O	S	0	0
			1308	843	228	229	8		

- Molecule 34 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	f	17	Total	C	N	O	0	0
			142	95	26	21		

- Molecule 35 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	129	Total	C	N	O	S	0	0
			1067	690	185	190	2		

- Molecule 36 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	101	Total	C	N	O	S	0	0
			829	525	147	155	2		

- Molecule 37 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	97	Total	C	N	O	S	0	0
			827	532	165	126	4		

- Molecule 38 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	86	Total	C	N	O	S	0	0
			689	426	134	127	2		

- Molecule 39 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	o	81	Total	C	N	O	S	0	0
			687	432	138	114	3		

- Molecule 40 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	p	125	Total	C	N	O	S	0	0
			1045	653	199	189	4		

- Molecule 41 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	q	101	Total	C	N	O	S	0	0
			841	527	162	149	3		

- Molecule 42 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	129	Total	C	N	O	S	0	0
			1068	679	209	172	8		

- Molecule 43 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	370	Total	C	N	O	S	0	0
			3036	1946	542	534	14		

- Molecule 44 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	111	Total	C	N	O	S	0	0
			927	595	155	167	10		

- Molecule 45 is a protein called MIEF1 upstream open reading frame protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	v	69	Total	C	N	O		0	0
			588	372	116	100			

- Molecule 46 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	w	79	Total	C	N	O	S	0	0
			638	410	95	128	5		

- Molecule 47 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	A	1256	Total	C	N	O	P	0	0
			26670	11966	4809	8639	1256		

- Molecule 48 is a RNA chain called mitochondrial tRNA^{Val}.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	B	56	Total	C	N	O	P	0	0
			1191	534	214	387	56		

- Molecule 49 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	4	37	Total	C	N	O	S	0	0
			333	212	71	47	3		

- Molecule 50 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
50	E	1	Total	Mg	0
			1	1	
50	A	49	Total	Mg	0
			49	49	

- Molecule 51 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
51	0	1	Total	Zn	0
			1	1	
51	r	1	Total	Zn	0
			1	1	
51	4	1	Total	Zn	0
			1	1	

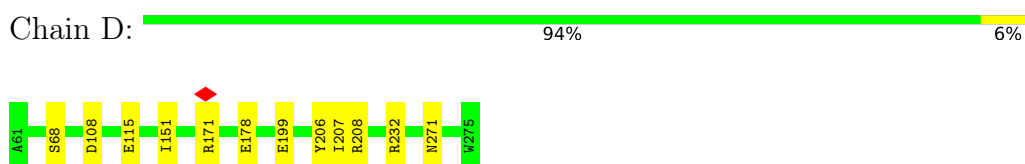
- Molecule 52 is water.

Mol	Chain	Residues	Atoms		AltConf
52	O	1	Total	O	0
			1	1	
52	T	1	Total	O	0
			1	1	
52	b	1	Total	O	0
			1	1	
52	i	1	Total	O	0
			1	1	
52	A	10	Total	O	0
			10	10	

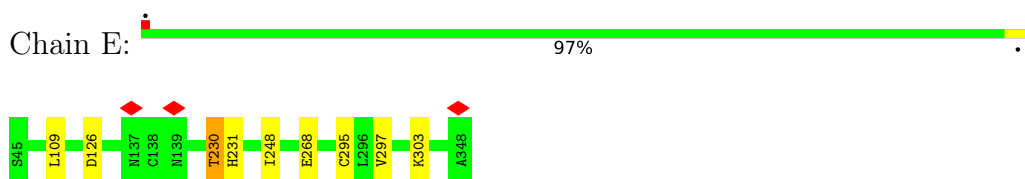
3 Residue-property plots [i](#)

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.

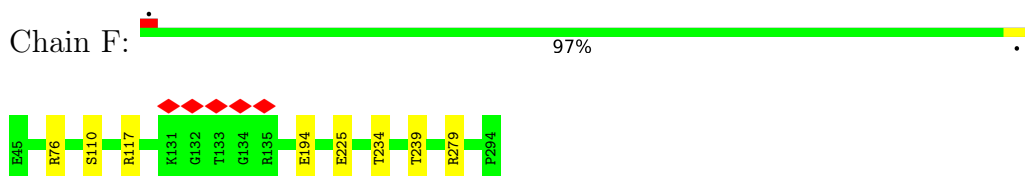
- Molecule 1: 39S ribosomal protein L2, mitochondrial



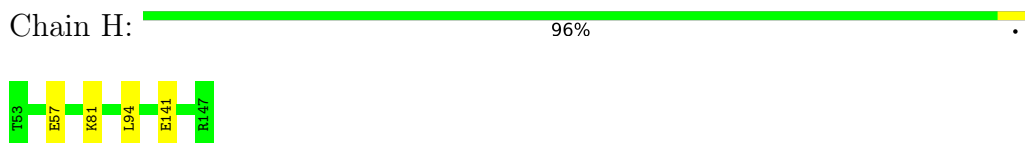
- Molecule 2: 39S ribosomal protein L3, mitochondrial



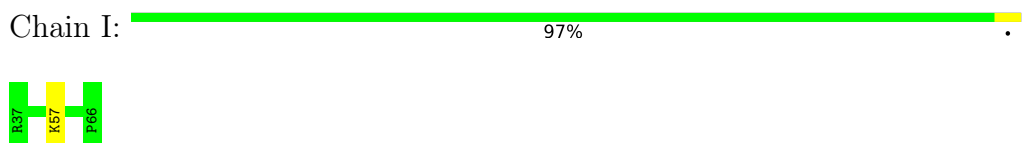
- Molecule 3: 39S ribosomal protein L4, mitochondrial



- Molecule 4: 39S ribosomal protein L9, mitochondrial



- Molecule 5: 39S ribosomal protein L10, mitochondrial



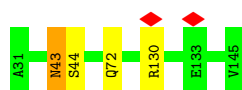
- Molecule 6: 39S ribosomal protein L13, mitochondrial

Chain K:  95% 5%



- Molecule 7: 39S ribosomal protein L14, mitochondrial

Chain L:  97% ..



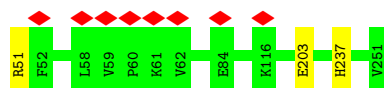
- Molecule 8: 39S ribosomal protein L15, mitochondrial

Chain M:  97% .



- Molecule 9: 39S ribosomal protein L16, mitochondrial

Chain N:  99% .



- Molecule 10: 39S ribosomal protein L17, mitochondrial

Chain O:  97% .



- Molecule 11: 39S ribosomal protein L18, mitochondrial

Chain P:  97% .



- Molecule 12: 39S ribosomal protein L19, mitochondrial

Chain Q:  99% .



- Molecule 13: 39S ribosomal protein L20, mitochondrial

Chain R:  99% .



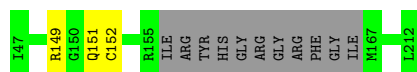
- Molecule 14: 39S ribosomal protein L21, mitochondrial

Chain S:  95% 5%



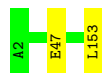
- Molecule 15: 39S ribosomal protein L22, mitochondrial

Chain T:  92% . 7%



- Molecule 16: 39S ribosomal protein L23, mitochondrial

Chain U:  98% .



- Molecule 17: 39S ribosomal protein L24, mitochondrial

Chain V:  94% 6%



- Molecule 18: 39S ribosomal protein L27, mitochondrial

Chain W:  99% .



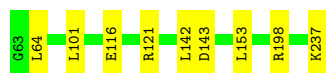
- Molecule 19: 39S ribosomal protein L28, mitochondrial

Chain X:  98% .



- Molecule 20: 39S ribosomal protein L47, mitochondrial

Chain Y:  95% 5%



- Molecule 21: 39S ribosomal protein L30, mitochondrial

Chain Z:  96% .



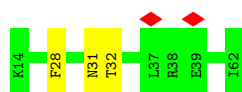
- Molecule 22: 39S ribosomal protein L32, mitochondrial

Chain 0:  96% .



- Molecule 23: 39S ribosomal protein L33, mitochondrial

Chain 1:  94% 6%



- Molecule 24: 39S ribosomal protein L34, mitochondrial

Chain 2:  98% .



- Molecule 25: 39S ribosomal protein L35, mitochondrial

Chain 3:  98% .



- Molecule 26: 39S ribosomal protein L37, mitochondrial

Chain 5:  96% .



- Molecule 27: 39S ribosomal protein L38, mitochondrial

- Chain 7:  97%

- Chain 9: 91% • 5%

A15 S19 S29 K39 T45 D106 GLY THR PHE ASP PRO ASP N113 R137

- Chain a: 95% 5%

- Chain b:  97%

- Chain c: 92% . .

V31	Y68	H69	Q106	GLN	LEU	GLY	TLE	GLU	GLY	LYS	GLU	ALA	VAL	LEU	LEU	ASN	L119	E164	C167	S181	Q193	F271	I281	E294	F307	S317
-----	-----	-----	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------

- Chain d: 90% 7%

A117
D127
F145
C151
L152
N153
C199
SER
SER
SER
MET
MET
MET
ASN
GLN
GLY
N207
K240
L252
THR
ASN
P255
K264
ILE
VAL
PRO
P268
P285

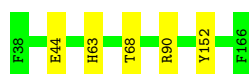
- WORLDWIDE
 **PDB**
PROTEIN DATA BANK

Chain f:  94% 6%



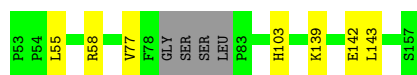
- Molecule 35: 39S ribosomal protein L49, mitochondrial

Chain g:  96% .



- Molecule 36: 39S ribosomal protein L50, mitochondrial

Chain h:  90% 7% .



- Molecule 37: 39S ribosomal protein L51, mitochondrial

Chain i:  99% .



- Molecule 38: 39S ribosomal protein L52, mitochondrial

Chain j:  98% .



- Molecule 39: Ribosomal protein 63, mitochondrial

Chain o:  96% .



- Molecule 40: Peptidyl-tRNA hydrolase ICT1, mitochondrial

Chain p:  9% 99% .




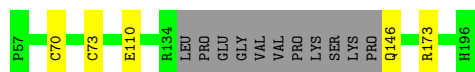
- Molecule 41: Growth arrest and DNA damage-inducible proteins-interacting protein 1

Chain q:  99%



- Molecule 42: 39S ribosomal protein S18a, mitochondrial

Chain r:  89% 8%



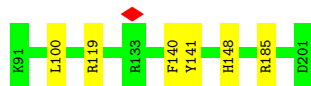
- Molecule 43: 39S ribosomal protein S30, mitochondrial

Chain s:  91% 5%



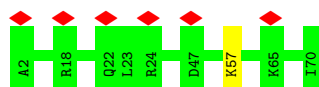
- Molecule 44: Mitochondrial assembly of ribosomal large subunit protein 1

Chain u:  95% 5%



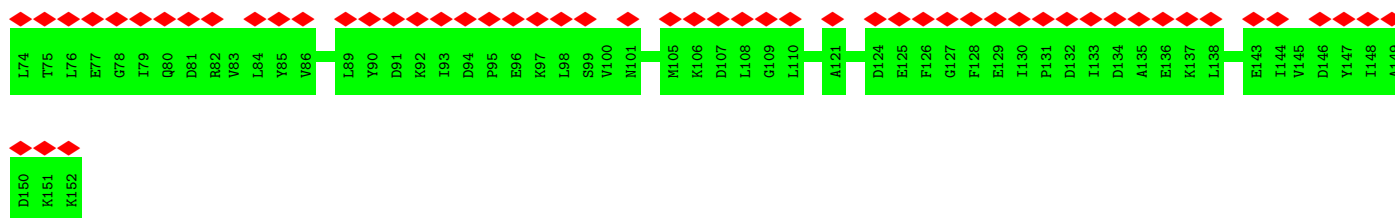
- Molecule 45: MIEF1 upstream open reading frame protein

Chain v:  9% 99%



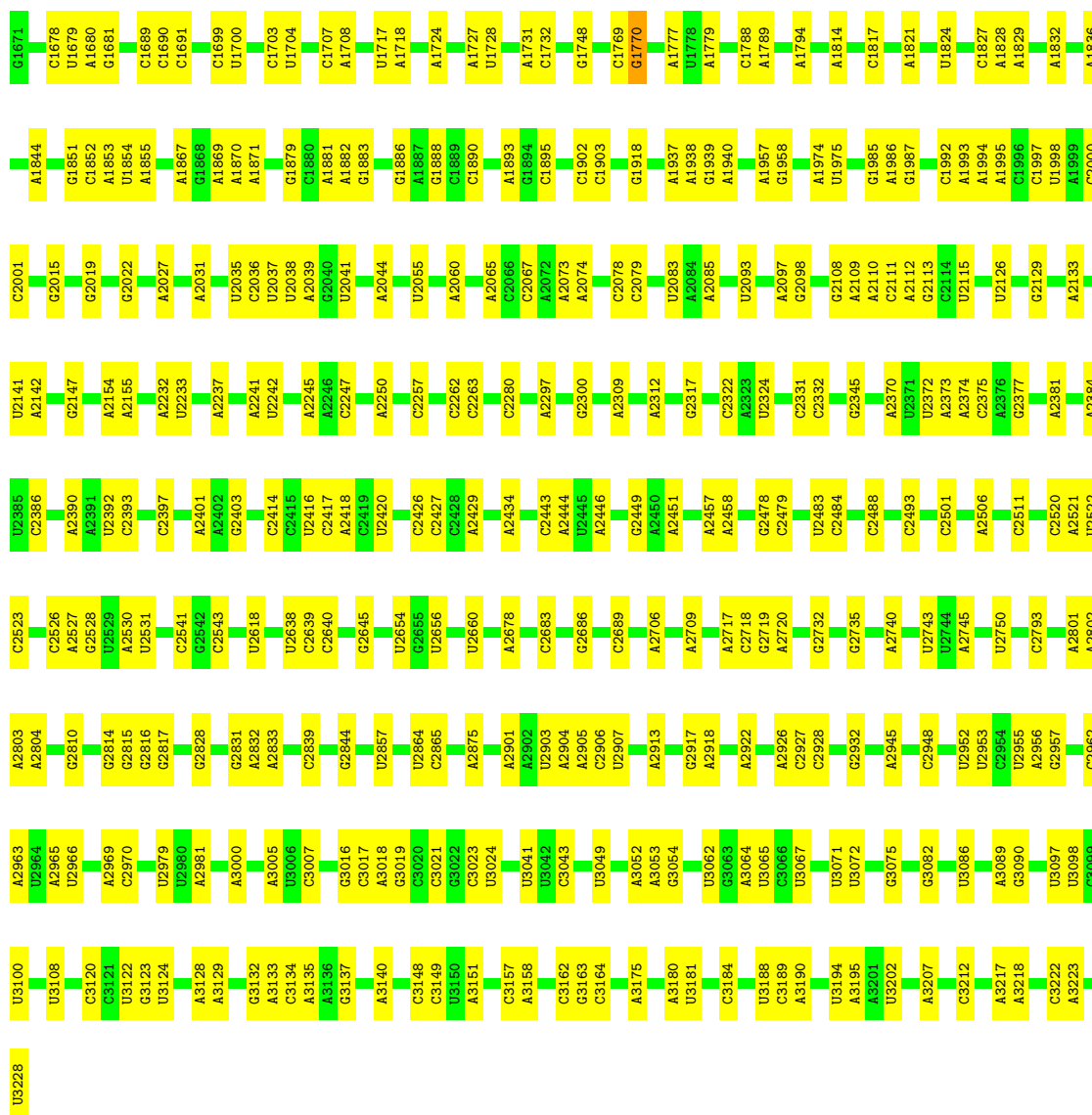
- Molecule 46: Acyl carrier protein, mitochondrial

Chain w:  70% 100%

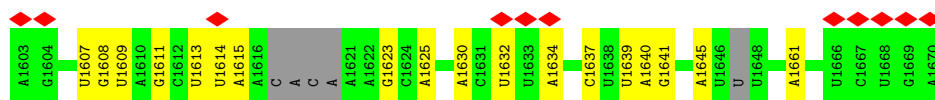


- Molecule 47: 16S ribosomal RNA

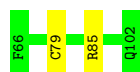
Chain A:  74% 26%



• Molecule 48: mitochondrial tRNAVal



• Molecule 49: 39S ribosomal protein L36, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	224933	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52.5	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.066	Depositor
Minimum map value	-0.017	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.01	Depositor
Map size (\AA)	381.59998, 381.59998, 381.59998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	D	0.37	0/1701	0.51	0/2288
2	E	0.44	0/2465	0.50	0/3344
3	F	0.49	0/2071	0.51	0/2817
4	H	0.38	0/798	0.51	0/1073
5	I	0.32	0/255	0.44	0/345
6	K	0.48	0/1495	0.46	0/2029
7	L	0.36	0/904	0.49	0/1218
8	M	0.46	0/2359	0.54	0/3185
9	N	0.29	0/1663	0.45	0/2236
10	O	0.46	0/1269	0.50	0/1708
11	P	0.30	0/1173	0.47	0/1588
12	Q	0.40	0/1846	0.47	0/2487
13	R	0.50	0/1163	0.49	0/1557
14	S	0.44	0/1276	0.52	0/1729
15	T	0.49	0/1304	0.48	0/1755
16	U	0.49	0/1058	0.51	0/1434
17	V	0.40	0/411	0.45	0/555
18	W	0.39	0/823	0.49	0/1113
19	X	0.40	0/2090	0.46	0/2825
20	Y	0.43	0/1540	0.47	0/2063
21	Z	0.37	0/960	0.49	0/1295
22	0	0.39	0/895	0.47	0/1201
23	1	0.25	0/413	0.46	0/550
24	2	0.57	0/373	0.55	0/496
25	3	0.53	0/852	0.49	0/1136
26	5	0.34	0/3294	0.48	0/4488
27	6	0.34	0/2546	0.46	0/3465
28	7	0.35	0/2391	0.48	0/3234
29	9	0.42	0/972	0.48	0/1306
30	a	0.44	0/694	0.51	0/941
31	b	0.45	0/1202	0.51	0/1626
32	c	0.39	0/2261	0.45	0/3055

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.28	0/1344	0.47	0/1817
34	f	0.35	0/146	0.43	0/193
35	g	0.48	0/1102	0.51	0/1503
36	h	0.32	0/850	0.46	0/1154
37	i	0.54	0/849	0.49	0/1135
38	j	0.39	0/703	0.44	0/947
39	o	0.39	0/704	0.49	0/945
40	p	0.29	0/1058	0.47	0/1415
41	q	0.35	0/867	0.43	0/1176
42	r	0.41	0/1103	0.47	0/1493
43	s	0.44	0/3114	0.51	0/4225
44	u	0.30	0/949	0.46	0/1281
45	v	0.26	0/597	0.44	0/796
46	w	0.25	0/647	0.41	0/871
47	A	0.85	0/29818	0.86	11/46362 (0.0%)
48	B	0.19	0/1328	0.72	0/2056
49	4	0.39	0/341	0.51	0/451
All	All	0.59	0/90037	0.65	11/127962 (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
1	D	0	1
2	E	0	1
7	L	0	1
15	T	0	1
21	Z	0	1
All	All	0	5

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	A	3149	C	C6-N1-C2	-7.98	117.11	120.30
47	A	3148	C	N1-C2-O2	6.80	122.98	118.90
47	A	3163	G	N1-C2-N2	-5.81	110.97	116.20
47	A	2403	G	N3-C4-N9	5.74	129.44	126.00
47	A	3023	C	N3-C2-O2	-5.63	117.96	121.90

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	206	TYR	Peptide
2	E	230	THR	Peptide
7	L	43	ASN	Peptide
15	T	151	GLN	Peptide
21	Z	94	ALA	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	
1	D	213/215 (99%)	191 (90%)	21 (10%)	1 (0%)	25	56
2	E	302/304 (99%)	273 (90%)	27 (9%)	2 (1%)	19	49
3	F	248/250 (99%)	228 (92%)	20 (8%)	0	100	100
4	H	93/95 (98%)	83 (89%)	10 (11%)	0	100	100
5	I	28/30 (93%)	27 (96%)	1 (4%)	0	100	100
6	K	175/177 (99%)	162 (93%)	13 (7%)	0	100	100
7	L	113/115 (98%)	95 (84%)	17 (15%)	1 (1%)	14	43
8	M	285/287 (99%)	269 (94%)	16 (6%)	0	100	100
9	N	199/201 (99%)	187 (94%)	12 (6%)	0	100	100
10	O	150/152 (99%)	142 (95%)	8 (5%)	0	100	100
11	P	139/141 (99%)	129 (93%)	10 (7%)	0	100	100
12	Q	215/217 (99%)	192 (89%)	22 (10%)	1 (0%)	25	56
13	R	137/139 (99%)	133 (97%)	4 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	S	154/156 (99%)	141 (92%)	13 (8%)	0	100	100
15	T	151/166 (91%)	140 (93%)	11 (7%)	0	100	100
16	U	121/125 (97%)	115 (95%)	6 (5%)	0	100	100
17	V	46/48 (96%)	44 (96%)	2 (4%)	0	100	100
18	W	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
19	X	241/243 (99%)	230 (95%)	11 (5%)	0	100	100
20	Y	173/175 (99%)	164 (95%)	9 (5%)	0	100	100
21	Z	113/115 (98%)	101 (89%)	12 (11%)	0	100	100
22	0	106/108 (98%)	102 (96%)	4 (4%)	0	100	100
23	1	47/49 (96%)	45 (96%)	2 (4%)	0	100	100
24	2	43/45 (96%)	39 (91%)	4 (9%)	0	100	100
25	3	93/95 (98%)	87 (94%)	6 (6%)	0	100	100
26	5	390/392 (100%)	363 (93%)	27 (7%)	0	100	100
27	6	284/292 (97%)	253 (89%)	30 (11%)	1 (0%)	30	60
28	7	285/287 (99%)	262 (92%)	23 (8%)	0	100	100
29	9	113/123 (92%)	106 (94%)	7 (6%)	0	100	100
30	a	76/80 (95%)	64 (84%)	12 (16%)	0	100	100
31	b	146/148 (99%)	131 (90%)	15 (10%)	0	100	100
32	c	271/287 (94%)	255 (94%)	16 (6%)	0	100	100
33	d	149/169 (88%)	133 (89%)	16 (11%)	0	100	100
34	f	15/17 (88%)	13 (87%)	2 (13%)	0	100	100
35	g	127/129 (98%)	115 (91%)	12 (9%)	0	100	100
36	h	97/105 (92%)	89 (92%)	8 (8%)	0	100	100
37	i	95/97 (98%)	92 (97%)	3 (3%)	0	100	100
38	j	84/86 (98%)	81 (96%)	3 (4%)	0	100	100
39	o	79/81 (98%)	76 (96%)	3 (4%)	0	100	100
40	p	117/125 (94%)	110 (94%)	7 (6%)	0	100	100
41	q	99/101 (98%)	95 (96%)	4 (4%)	0	100	100
42	r	125/140 (89%)	111 (89%)	14 (11%)	0	100	100
43	s	366/390 (94%)	331 (90%)	35 (10%)	0	100	100
44	u	109/111 (98%)	100 (92%)	9 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	v	67/69 (97%)	60 (90%)	7 (10%)	0	100	100
46	w	77/79 (98%)	71 (92%)	6 (8%)	0	100	100
49	4	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
All	All	6889/7093 (97%)	6358 (92%)	525 (8%)	6 (0%)	50	77

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	230	THR
12	Q	226	PRO
27	6	325	ASP
2	E	231	HIS
7	L	130	ARG

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	
1	D	173/173 (100%)	163 (94%)	10 (6%)	17	46
2	E	259/259 (100%)	252 (97%)	7 (3%)	40	73
3	F	217/217 (100%)	209 (96%)	8 (4%)	29	64
4	H	86/86 (100%)	82 (95%)	4 (5%)	22	55
5	I	28/28 (100%)	27 (96%)	1 (4%)	30	65
6	K	155/155 (100%)	147 (95%)	8 (5%)	19	50
7	L	98/98 (100%)	95 (97%)	3 (3%)	35	70
8	M	245/245 (100%)	236 (96%)	9 (4%)	29	64
9	N	168/168 (100%)	165 (98%)	3 (2%)	54	82
10	O	133/133 (100%)	129 (97%)	4 (3%)	36	71
11	P	123/123 (100%)	119 (97%)	4 (3%)	33	68
12	Q	199/199 (100%)	197 (99%)	2 (1%)	73	91
13	R	117/117 (100%)	116 (99%)	1 (1%)	75	92

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	S	141/141 (100%)	133 (94%)	8 (6%)	17	47
15	T	138/146 (94%)	136 (99%)	2 (1%)	62	86
16	U	110/110 (100%)	108 (98%)	2 (2%)	54	82
17	V	44/44 (100%)	41 (93%)	3 (7%)	13	38
18	W	83/83 (100%)	82 (99%)	1 (1%)	67	89
19	X	219/219 (100%)	215 (98%)	4 (2%)	54	82
20	Y	158/158 (100%)	149 (94%)	9 (6%)	17	47
21	Z	106/106 (100%)	102 (96%)	4 (4%)	28	63
22	0	97/97 (100%)	93 (96%)	4 (4%)	26	60
23	1	46/46 (100%)	43 (94%)	3 (6%)	14	40
24	2	39/39 (100%)	38 (97%)	1 (3%)	41	74
25	3	88/88 (100%)	86 (98%)	2 (2%)	45	77
26	5	353/353 (100%)	339 (96%)	14 (4%)	27	61
27	6	259/259 (100%)	249 (96%)	10 (4%)	27	62
28	7	263/263 (100%)	255 (97%)	8 (3%)	36	71
29	9	99/104 (95%)	94 (95%)	5 (5%)	20	51
30	a	76/76 (100%)	72 (95%)	4 (5%)	19	49
31	b	130/130 (100%)	126 (97%)	4 (3%)	35	70
32	c	241/251 (96%)	231 (96%)	10 (4%)	26	60
33	d	146/157 (93%)	141 (97%)	5 (3%)	32	67
34	f	15/15 (100%)	14 (93%)	1 (7%)	13	39
35	g	119/119 (100%)	114 (96%)	5 (4%)	25	59
36	h	96/99 (97%)	89 (93%)	7 (7%)	11	34
37	i	86/86 (100%)	85 (99%)	1 (1%)	67	89
38	j	68/68 (100%)	66 (97%)	2 (3%)	37	72
39	o	70/70 (100%)	67 (96%)	3 (4%)	25	57
40	p	115/115 (100%)	114 (99%)	1 (1%)	75	92
41	q	86/86 (100%)	85 (99%)	1 (1%)	67	89
42	r	118/128 (92%)	113 (96%)	5 (4%)	25	59
43	s	326/344 (95%)	312 (96%)	14 (4%)	25	57
44	u	105/105 (100%)	99 (94%)	6 (6%)	17	47

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
45	v	59/59 (100%)	58 (98%)	1 (2%)	56 83
46	w	73/73 (100%)	73 (100%)	0	100 100
49	4	36/36 (100%)	34 (94%)	2 (6%)	17 47
All	All	6209/6274 (99%)	5993 (96%)	216 (4%)	33 66

5 of 216 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	5	176	TYR
29	9	113	ASN
43	s	221	HIS
26	5	361	THR
27	6	374	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	E	128	HIS
13	R	36	ASN
32	c	69	HIS
42	r	79	HIS
43	s	382	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
47	A	1230/1256 (97%)	323 (26%)	10 (0%)
48	B	51/61 (83%)	17 (33%)	1 (1%)
All	All	1281/1317 (97%)	340 (26%)	11 (0%)

5 of 340 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
47	A	1678	C
47	A	1679	U
47	A	1680	A
47	A	1681	G
47	A	1689	C

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
47	A	2638	U
47	A	2718	C
48	B	1614	U
47	A	2905	A
47	A	2417	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 53 ligands modelled in this entry, 53 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
47	A	25
27	6	3

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
40	p	3
48	B	2
16	U	1
30	a	1

The worst 5 of 35 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2545:U	O3'	2611:C	P	40.96
1	6	79:GLY	C	131:PRO	N	39.19
1	U	112:PRO	C	140:SER	N	37.93
1	A	2880:A	O3'	2896:G	P	32.37
1	A	2982:C	O3'	2994:U	P	30.68

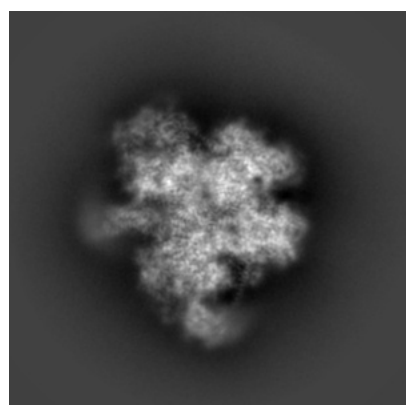
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13967. These allow visual inspection of the internal detail of the map and identification of artifacts.

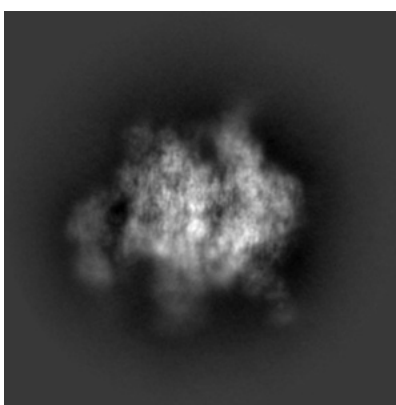
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

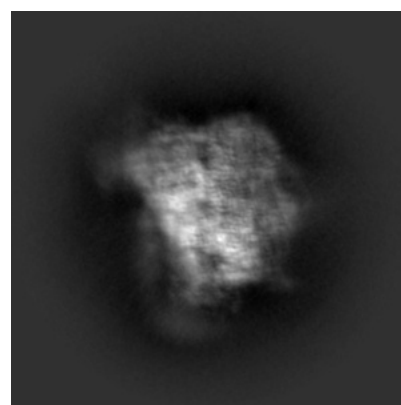
6.1.1 Primary map



X



Y

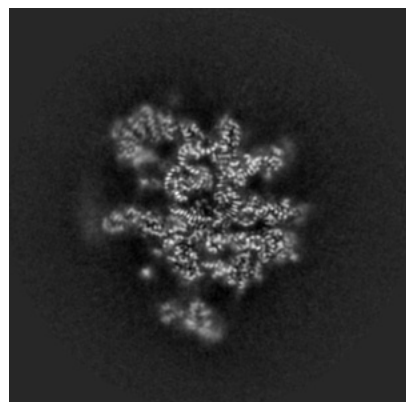


Z

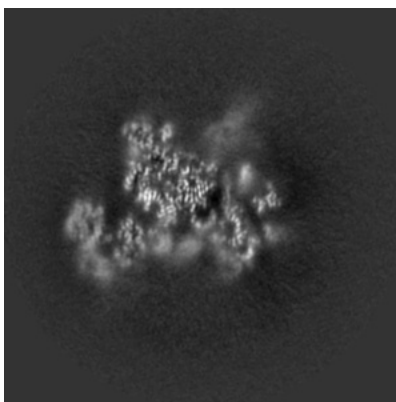
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

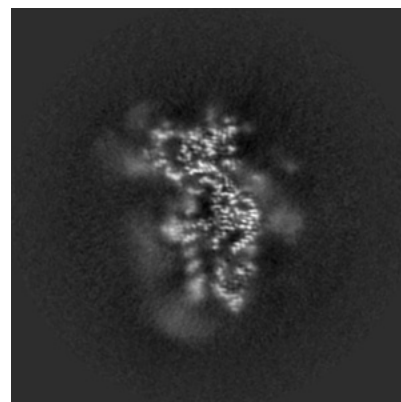
6.2.1 Primary map



X Index: 180



Y Index: 180

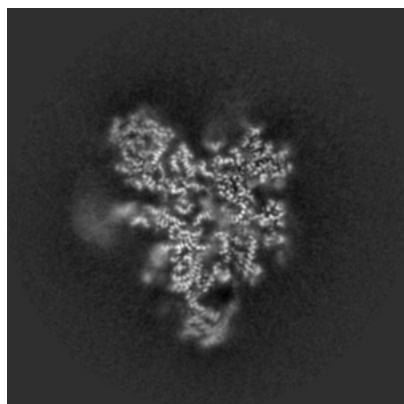


Z Index: 180

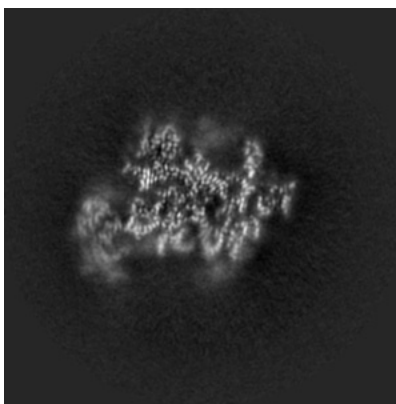
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

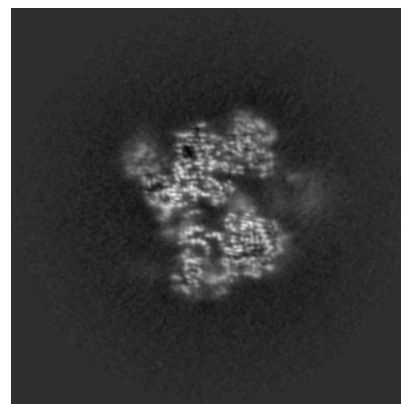
6.3.1 Primary map



X Index: 164



Y Index: 164

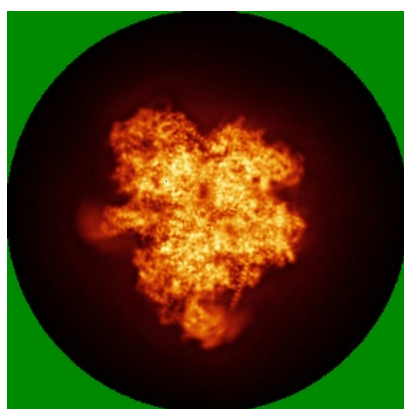


Z Index: 221

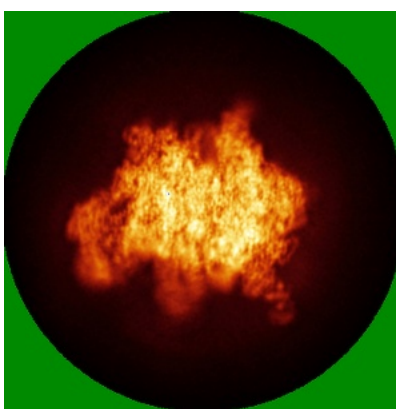
The images above show the largest variance slices of the map in three orthogonal directions.

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

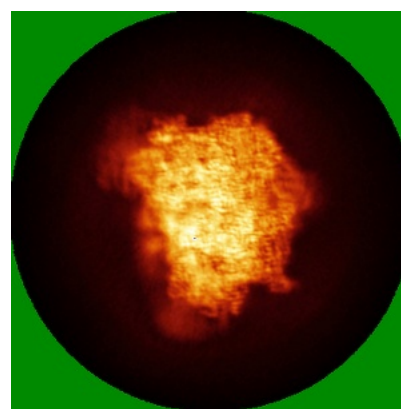
6.4.1 Primary map



X



Y

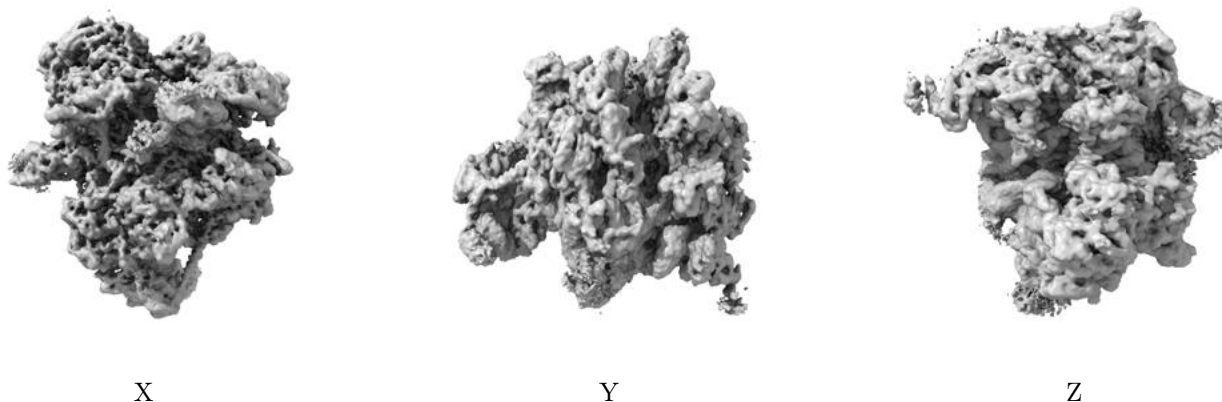


Z

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 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

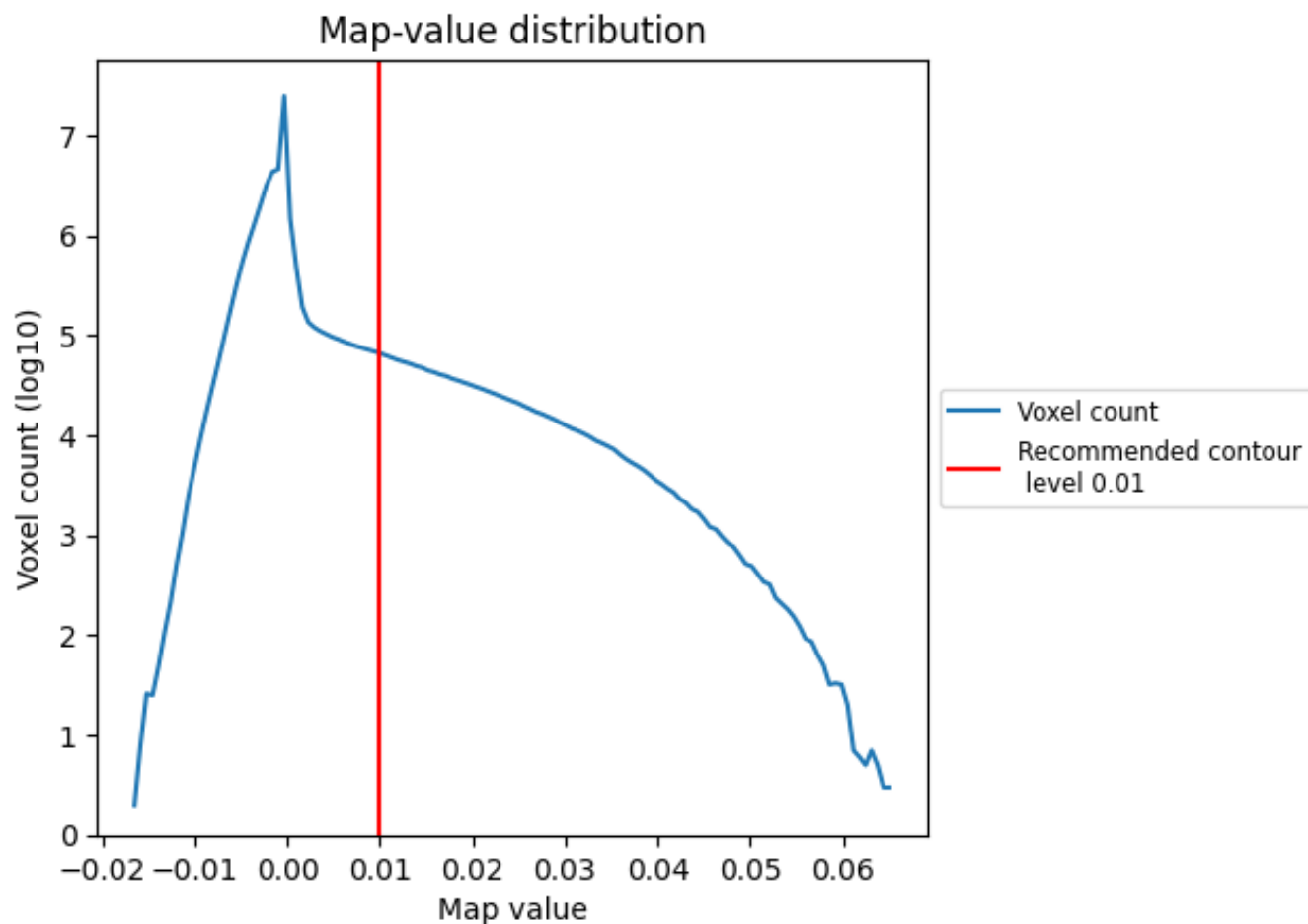
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

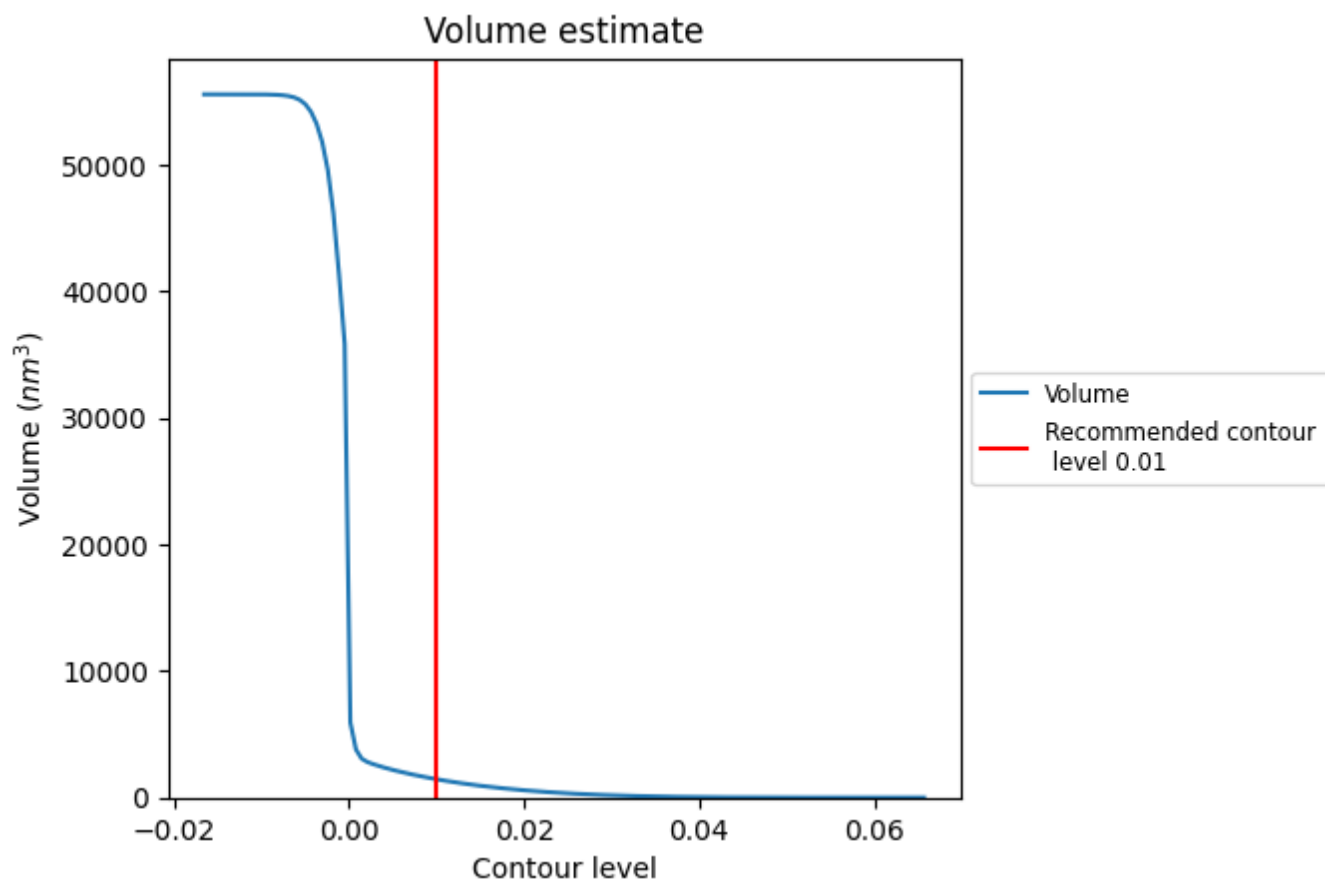
This section contains the results of statistical analysis of the map.

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.

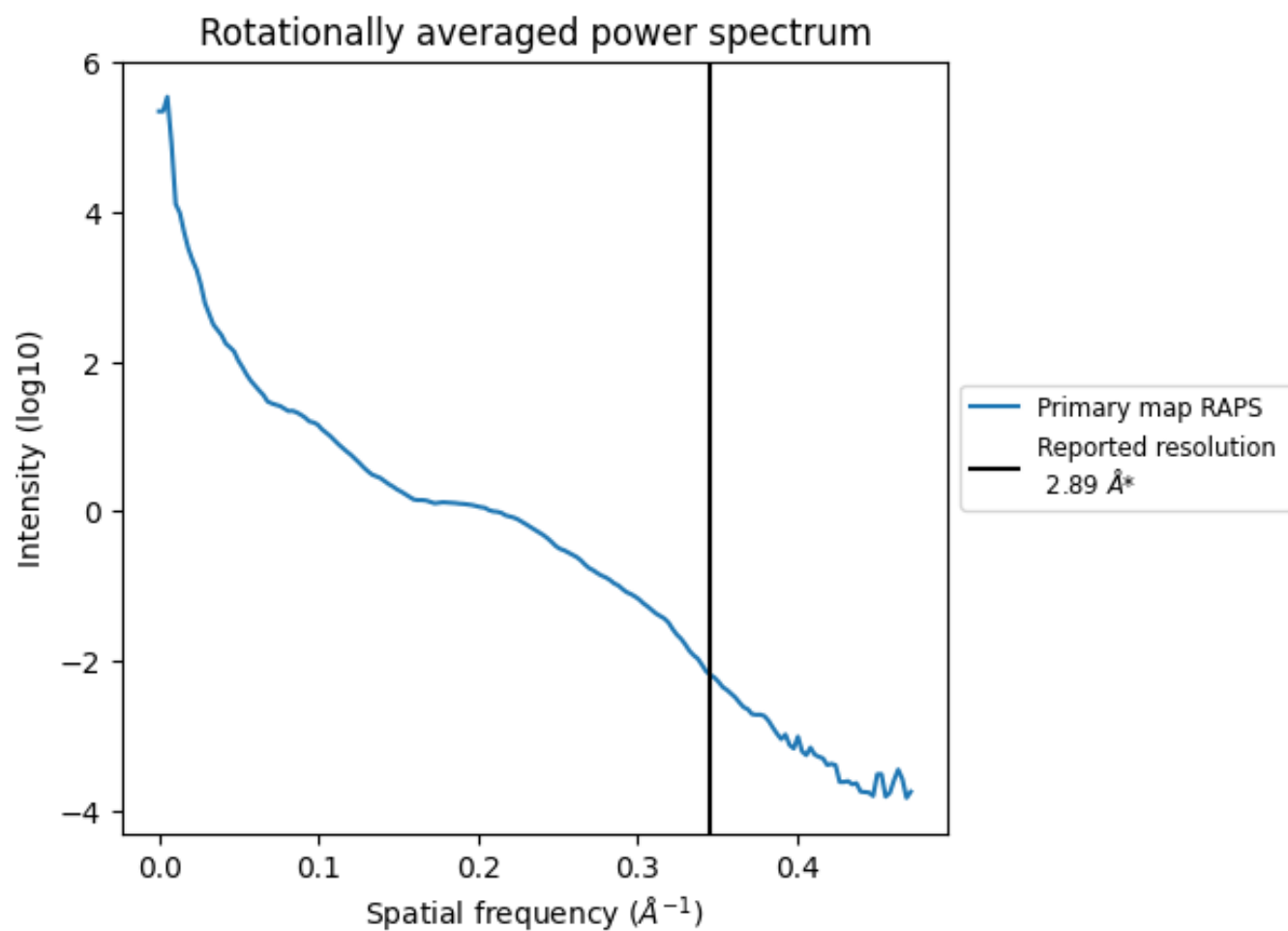
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1452 nm^3 ; this corresponds to an approximate mass of 1312 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 ⓘ

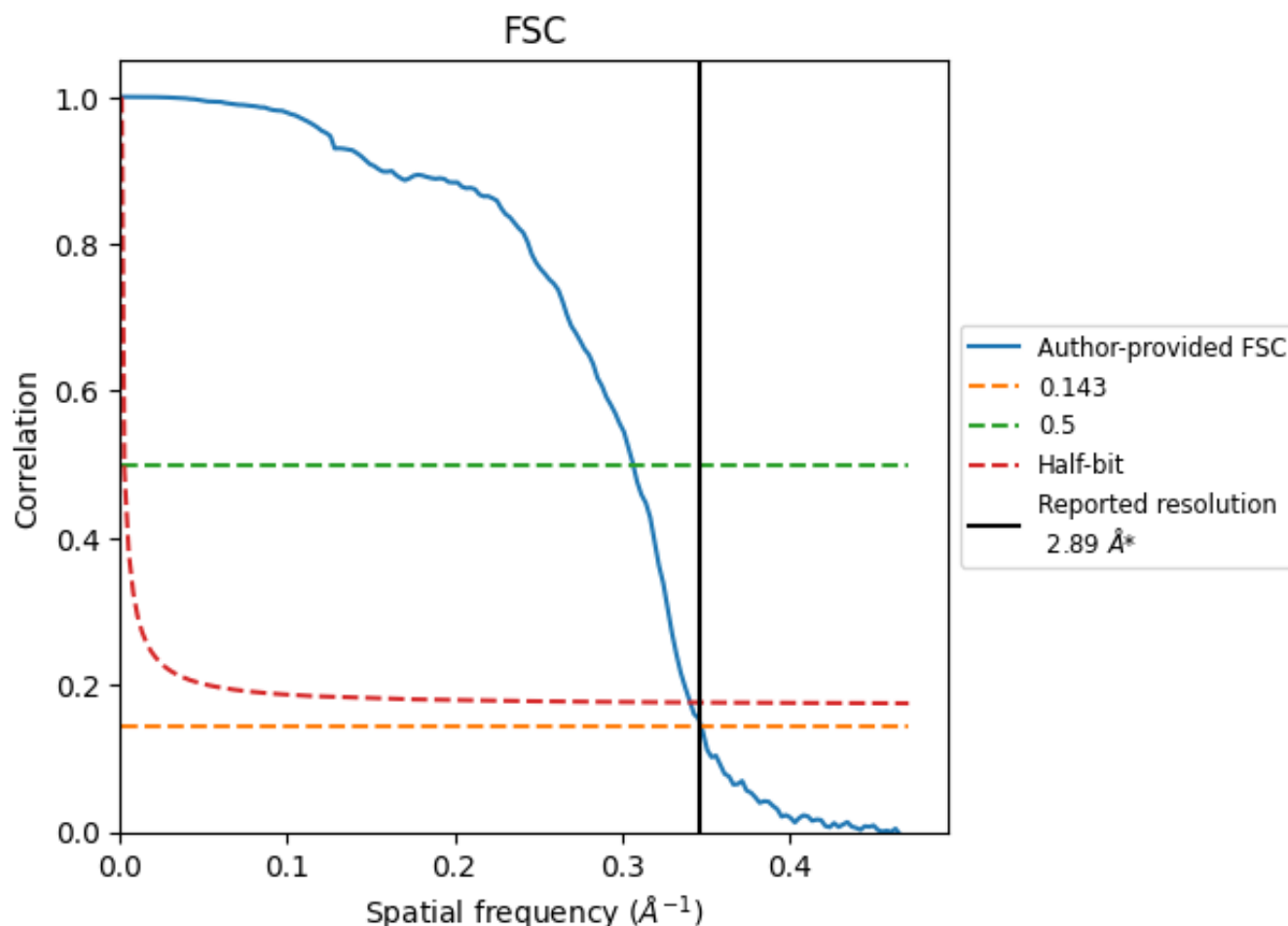


*Reported resolution corresponds to spatial frequency of 0.346 Å⁻¹

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 0.346 Å⁻¹

8.2 Resolution estimates [i](#)

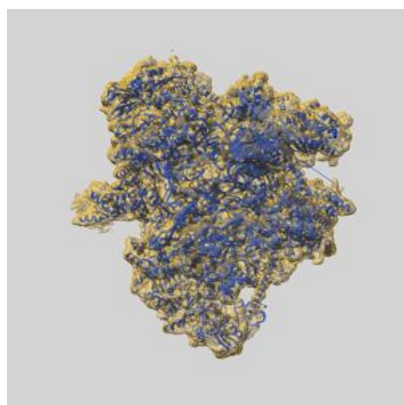
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.89	-	-
Author-provided FSC curve	2.88	3.26	2.93
Unmasked-calculated*	-	-	-

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

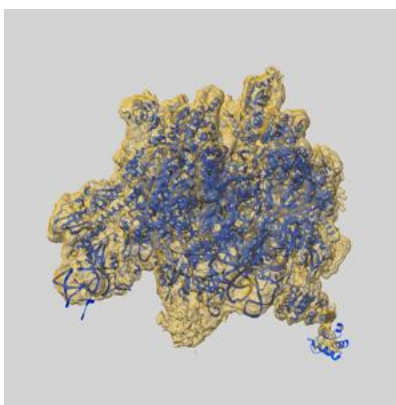
9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-13967 and PDB model 7QH7. Per-residue inclusion information can be found in section 3 on page 13.

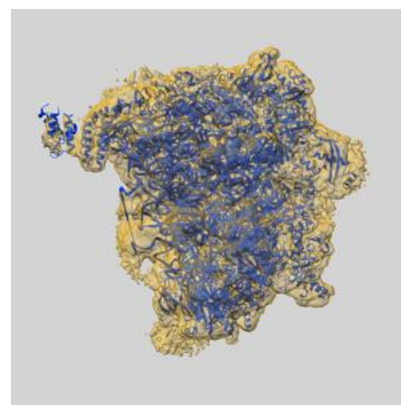
9.1 Map-model overlay ⓘ



X



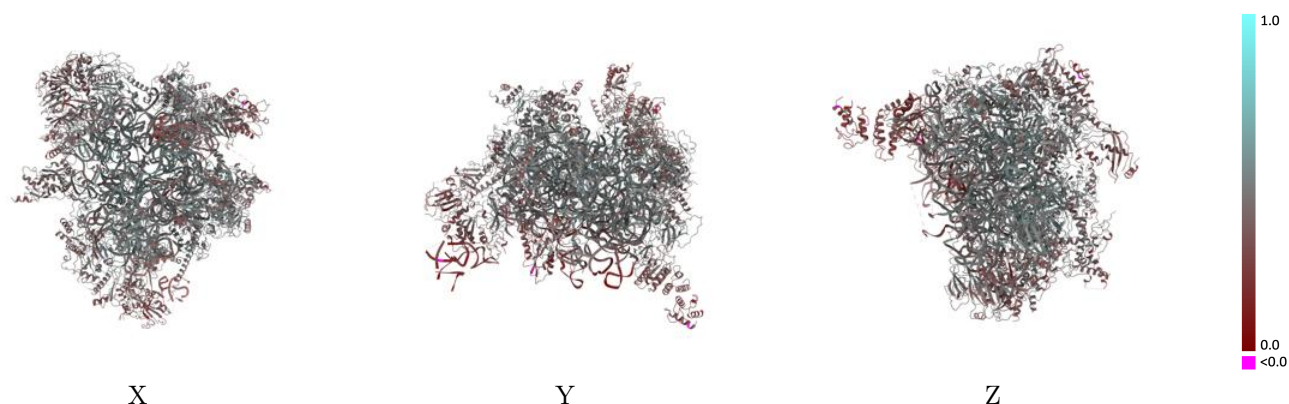
Y



Z

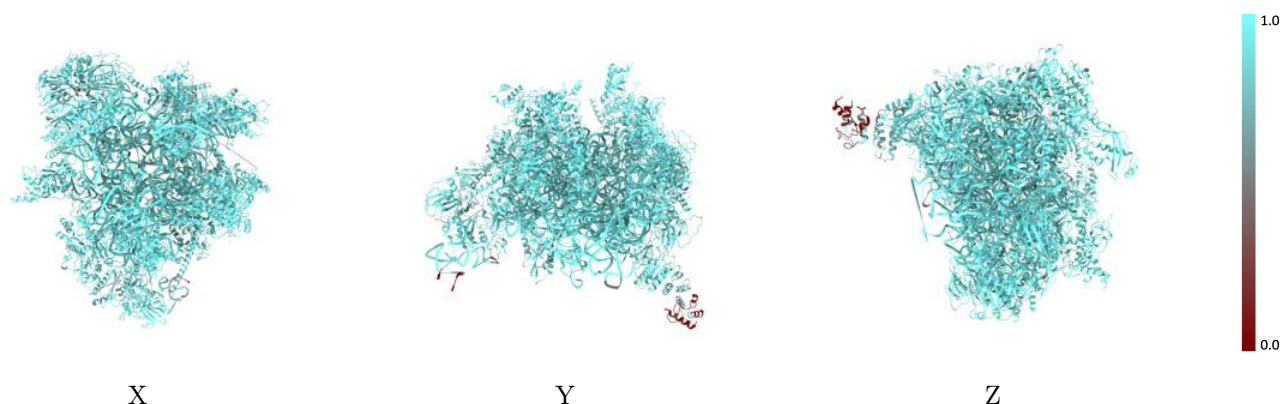
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



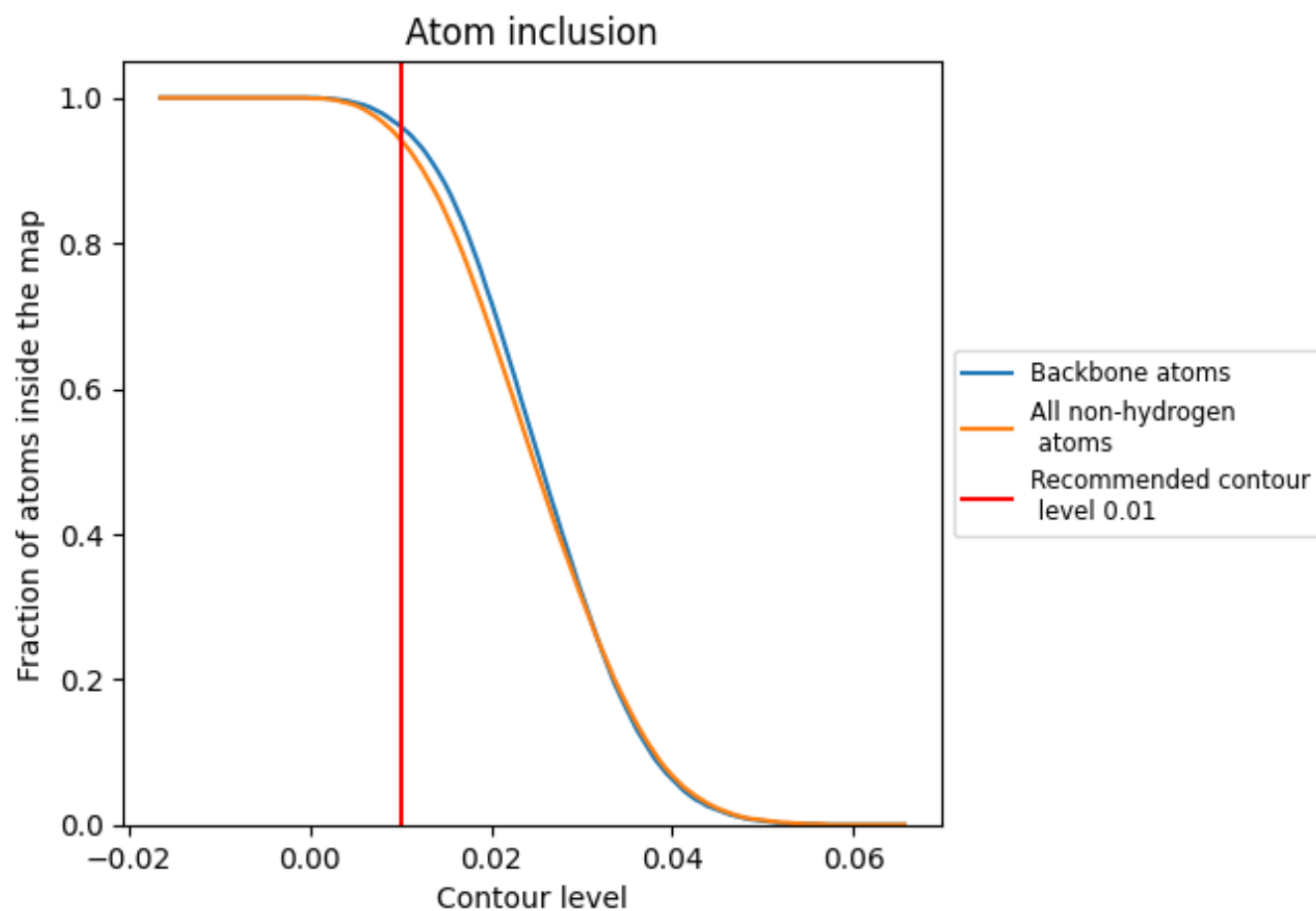
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 94% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9420	 0.4410
0	 0.9410	 0.4630
1	 0.9020	 0.1990
2	 0.9720	 0.5350
3	 0.9660	 0.5030
4	 0.8710	 0.4360
5	 0.9220	 0.4080
6	 0.9420	 0.3680
7	 0.9410	 0.3960
9	 0.9470	 0.4510
A	 0.9910	 0.4620
B	 0.7760	 0.2050
D	 0.9490	 0.4560
E	 0.9500	 0.4730
F	 0.9420	 0.4960
H	 0.9210	 0.4220
I	 0.9460	 0.3800
K	 0.9600	 0.4840
L	 0.9260	 0.4540
M	 0.9400	 0.4800
N	 0.8940	 0.3230
O	 0.9590	 0.4800
P	 0.9570	 0.3590
Q	 0.9220	 0.4550
R	 0.9340	 0.4890
S	 0.9440	 0.4830
T	 0.9330	 0.4900
U	 0.9720	 0.4880
V	 0.9520	 0.4270
W	 0.9490	 0.4400
X	 0.9300	 0.4420
Y	 0.9550	 0.4580
Z	 0.9270	 0.4720
a	 0.9340	 0.4790
b	 0.9590	 0.4940



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
c	 0.9530	 0.4440
d	 0.9790	 0.3490
f	 0.9290	 0.3930
g	 0.9610	 0.4780
h	 0.9580	 0.4170
i	 0.9550	 0.5160
j	 0.8990	 0.4510
o	 0.9200	 0.4500
p	 0.7690	 0.3750
q	 0.9180	 0.3970
r	 0.9630	 0.4520
s	 0.9370	 0.4570
u	 0.9010	 0.3510
v	 0.7070	 0.3000
w	 0.2320	 0.2320