



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:52 PM UTC

PDB ID : 7OF7 / pdb_00007of7
EMDB ID : EMD-12872
Title : Structure of a human mitochondrial ribosome large subunit assembly intermediate in complex with MTERF4-NSUN4 and GTPBP5 (dataset1).
Authors : Hillen, H.S.; Lavdovskaia, E.; Nadler, F.; Hanitsch, E.; Linden, A.; Bohnsack, K.E.; Urlaub, H.; Richter-Dennerlein, R.
Deposited on : 2021-05-04
Resolution : 2.50 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:

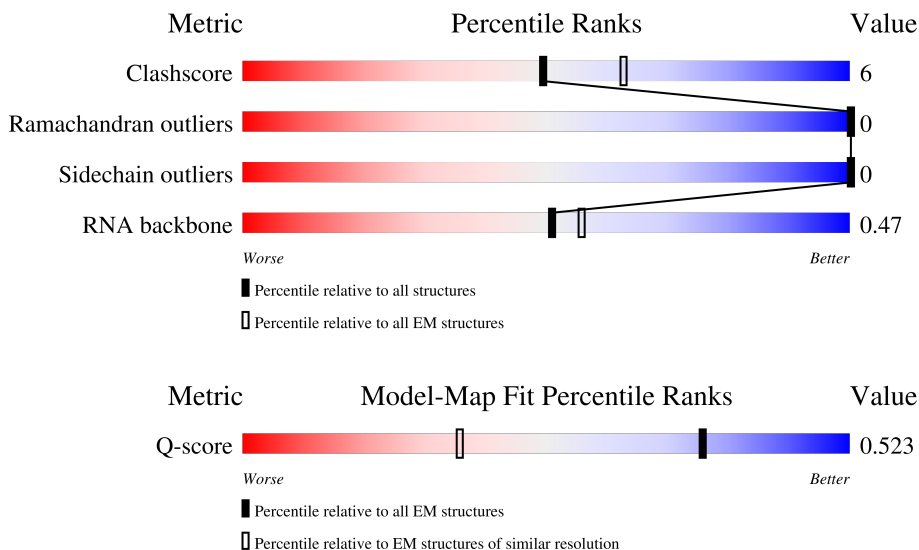
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.











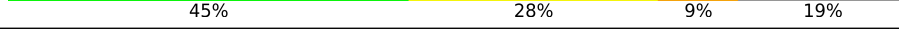

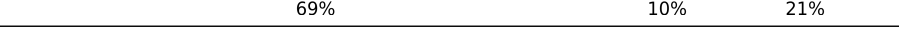
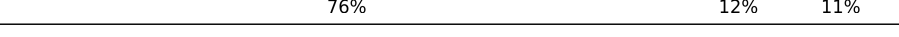

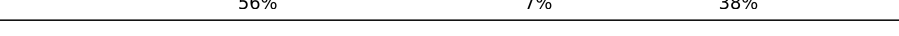

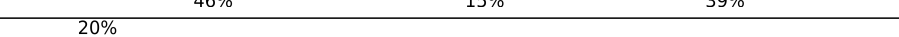
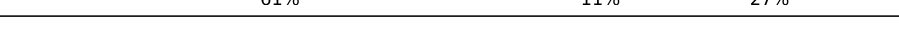

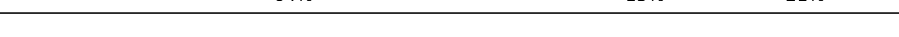






Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7115 (2.00 - 3.00)

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	0	108	 87% 13%
2	1	65	 72% 8% 20%
3	2	92	 40% 9% 51%

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Mol	Chain	Length	Quality of chain
4	3	188	
5	4	103	
6	5	423	
7	6	380	
8	7	338	
9	8	206	
10	9	137	
11	A	1559	
12	B	69	
13	C	384	
14	D	305	
15	E	348	
16	F	311	
17	G	381	
18	H	267	
19	I	261	
20	J	192	
21	K	178	
22	L	145	
23	M	296	
24	N	251	
25	O	175	
26	P	180	
27	Q	292	
28	R	149	





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Mol	Chain	Length	Quality of chain
29	S	205	67% 9% 24%
30	T	206	70% 11% 19%
31	U	153	9% 81% 10% 9%
32	V	216	20% 78%
33	W	148	58% 16% 26%
34	X	256	85% 10% 5%
35	Y	250	66% 30%
36	Z	161	65% 7% 29%
37	a	142	45% 5% 50%
38	b	215	56% 13% 31%
39	c	332	77% 6% 17%
40	d	306	13% 58% 8% 35%
41	e	279	59% 11% 29%
42	f	212	26% 39% 12% 49%
43	g	166	73% 22%
44	h	158	59% 7% 34%
45	i	128	69% 7% 24%
46	j	85	95% 5%
47	k	112	59% 12% 29%
48	m	128	17% 19% 78%
49	o	102	83% 8% 9%
50	p	206	54% 7% 38%
51	q	222	50% 7% 42%
52	r	196	67% 7% 26%
53	s	439	72% 12% 16%

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Mol	Chain	Length	Quality of chain
54	u	234	
55	v	70	
56	w	156	
57	x	406	

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 101032 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 L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	108	880	545	172	157	6	0	0

- Molecule 2 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	52	433	278	83	70	2	0	0

- Molecule 3 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	45	367	227	81	58	1	0	0

- Molecule 4 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	95	831	539	162	127	3	0	0

- Molecule 5 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	37	333	212	71	47	3	0	0

- Molecule 6 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	5	392	3199	2067	558	563	11	0	0

- Molecule 7 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	6	324	2723	1743	488	484	8	0	0

- Molecule 8 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	7	287	2334	1495	397	425	17	0	0

- Molecule 9 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	8	77	651	413	113	123	2	0	0

- Molecule 10 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	9	117	947	614	163	168	2	0	0

- Molecule 11 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
11	A	1376	29222	13113	5273	9460	1376	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3107	U	N	conflict	GB 1025814679

- Molecule 12 is a RNA chain called mitochondrial tRNAVal.

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

- Molecule 13 is a protein called 5-methylcytosine rRNA methyltransferase NSUN4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	C	338	2690	1715	470	489	16	1	0

- Molecule 14 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	D	240	1872	1165	378	320	9	0	0

- Molecule 15 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	E	308	2427	1559	423	434	11	0	0

- Molecule 16 is a protein called 39S ribosomal protein L4, mitochondrial.

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

- Molecule 17 is a protein called Transcription termination factor 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	G	238	1943	1243	336	352	12	0	0

- Molecule 18 is a protein called 39S ribosomal protein L9, mitochondrial.

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

- Molecule 19 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	I	158	1283	828	235	210	10	0	0

- Molecule 20 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	J	140	Total	C	N	O	S	0	0
			1061	680	192	187	2		

- Molecule 21 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 22 is a protein called 39S ribosomal protein L14, mitochondrial.

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

- Molecule 23 is a protein called 39S ribosomal protein L15, mitochondrial.

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

- Molecule 24 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	N	205	Total	C	N	O	S	0	0
			1654	1056	308	280	10		

- Molecule 25 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 26 is a protein called 39S ribosomal protein L18, mitochondrial.

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

- Molecule 27 is a protein called 39S ribosomal protein L19, mitochondrial.

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

- Molecule 28 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	R	116	Total	C	N	O	S	0	0
			971	616	200	151	4		

- Molecule 29 is a protein called 39S ribosomal protein L21, mitochondrial.

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

- Molecule 30 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	T	166	Total	C	N	O	S	0	0
			1368	875	254	232	7		

- Molecule 31 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	U	139	Total	C	N	O	S	0	0
			1154	734	220	197	3		

- Molecule 32 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	V	47	Total	C	N	O	S	0	0
			395	255	62	75	3		

- Molecule 33 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	W	109	Total	C	N	O	S	0	0
			859	552	162	142	3		

- Molecule 34 is a protein called 39S ribosomal protein L28, mitochondrial.

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

- Molecule 35 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Y	176	Total	C	N	O	S	0	0
			1517	970	291	252	4		

- Molecule 36 is a protein called 39S ribosomal protein L30, mitochondrial.

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

- Molecule 37 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	a	71	Total	C	N	O	S	0	0
			597	378	112	103	4		

- Molecule 38 is a protein called 39S ribosomal protein L43, mitochondrial.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	c	275	Total	C	N	O	S	0	0
			2217	1415	383	410	9		

- Molecule 40 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	d	199	Total	C	N	O	S	0	0
			1653	1075	276	293	9		

- Molecule 41 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	e	197	Total	C	N	O	S	0	0
			1599	1027	277	290	5		

- Molecule 42 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	f	108	Total	C	N	O	S	0	0
			857	549	140	165	3		

- Molecule 43 is a protein called 39S ribosomal protein L49, mitochondrial.

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

- Molecule 44 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	h	105	Total	C	N	O	S	0	0
			862	548	151	160	3		

- Molecule 45 is a protein called 39S ribosomal protein L51, mitochondrial.

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

- Molecule 46 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	j	85	Total	C	N	O	S	0	0
			684	423	133	126	2		

- Molecule 47 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	k	80	Total	C	N	O	S	0	0
			627	392	116	114	5		

- Molecule 48 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	m	28	Total	C	N	O	S	0	0
			234	151	44	37	2		

- Molecule 49 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	o	93	Total	C	N	O	S	0	0
			786	495	161	127	3		

- Molecule 50 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	p	127	Total	C	N	O	S	0	0
			1058	661	201	192	4		

- Molecule 51 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	q	128	Total	C	N	O	S	0	0
			1076	671	208	192	5		

- Molecule 52 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	r	146	Total	C	N	O	S	0	0
			1203	764	232	199	8		

- Molecule 53 is a protein called 39S ribosomal protein S30, mitochondrial.

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

- Molecule 54 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

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

- Molecule 55 is a protein called MIEF1 upstream open reading frame protein.

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

- Molecule 56 is a protein called Acyl carrier protein, mitochondrial.

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

- Molecule 57 is a protein called Mitochondrial ribosome-associated GTPase 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	x	148	1073	659	205	204	5	0	0

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

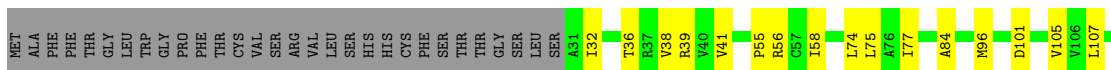
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
58	0	1	1	1	0
58	4	1	1	1	0
58	r	1	1	1	0

- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

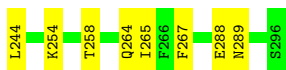
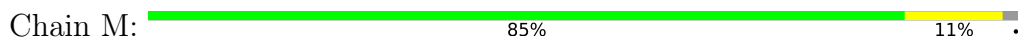
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
59	A	71	71	71	0
59	E	1	1	1	0
59	W	1	1	1	0
59	g	1	1	1	0



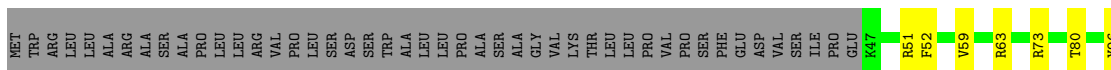
- Molecule 22: 39S ribosomal protein L14, mitochondrial



- Molecule 23: 39S ribosomal protein L15, mitochondrial



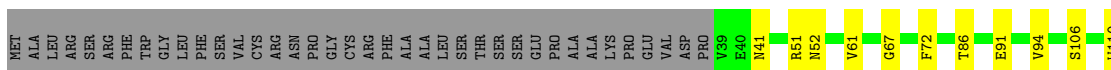
- Molecule 24: 39S ribosomal protein L16, mitochondrial



- Molecule 25: 39S ribosomal protein L17, mitochondrial

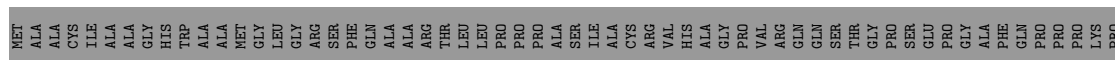


- Molecule 26: 39S ribosomal protein L18, mitochondrial





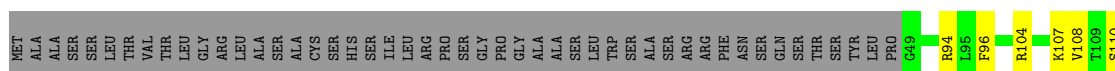
- Molecule 27: 39S ribosomal protein L19, mitochondrial



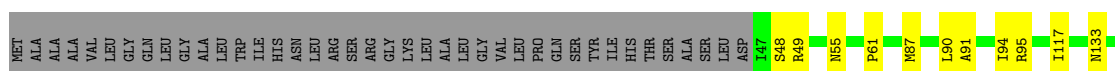
- Molecule 28: 39S ribosomal protein L20, mitochondrial



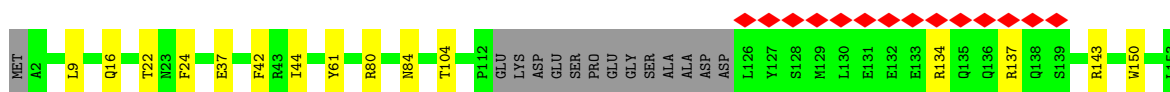
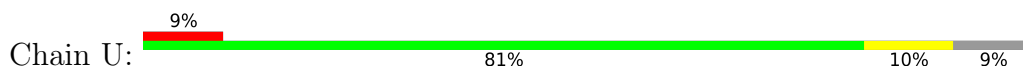
- Molecule 29: 39S ribosomal protein L21, mitochondrial



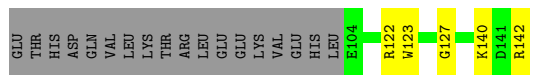
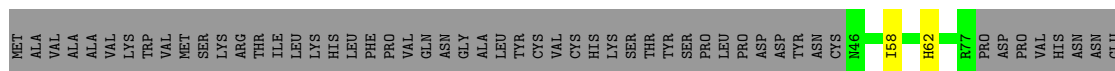
- Molecule 30: 39S ribosomal protein L22, mitochondrial



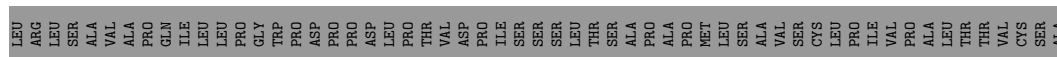
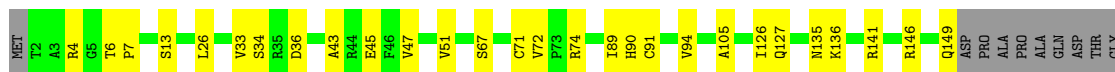
- Molecule 31: 39S ribosomal protein L23, mitochondrial



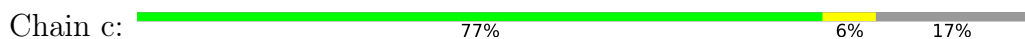
- Molecule 32: 39S ribosomal protein L24, mitochondrial



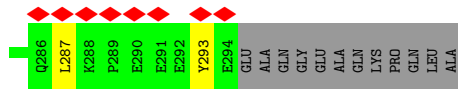
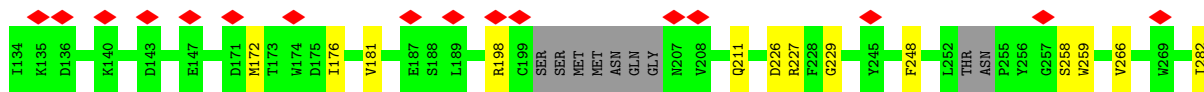
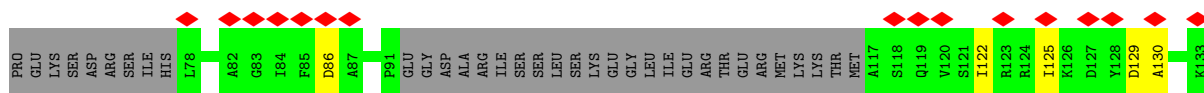
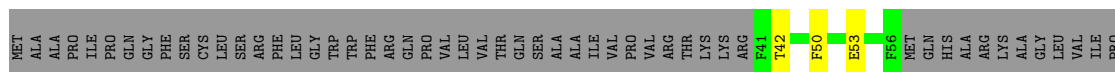
• Molecule 38: 39S ribosomal protein L43, mitochondrial



• Molecule 39: 39S ribosomal protein L44, mitochondrial

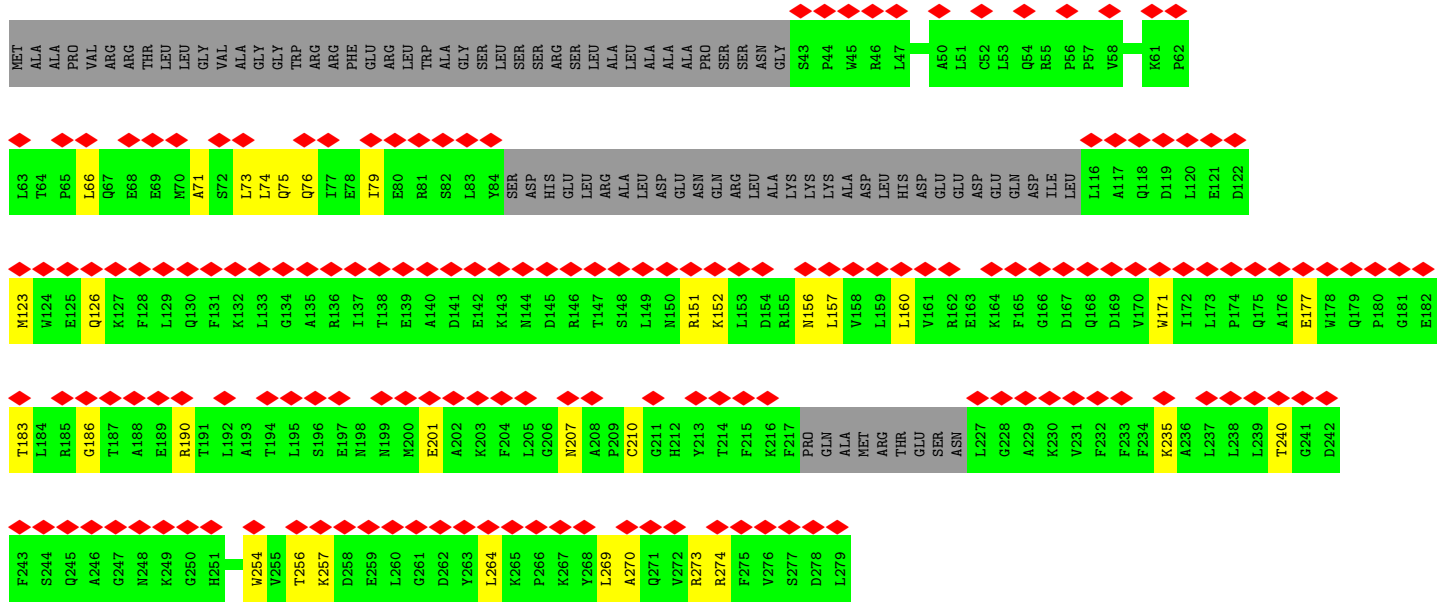


• Molecule 40: 39S ribosomal protein L45, mitochondrial

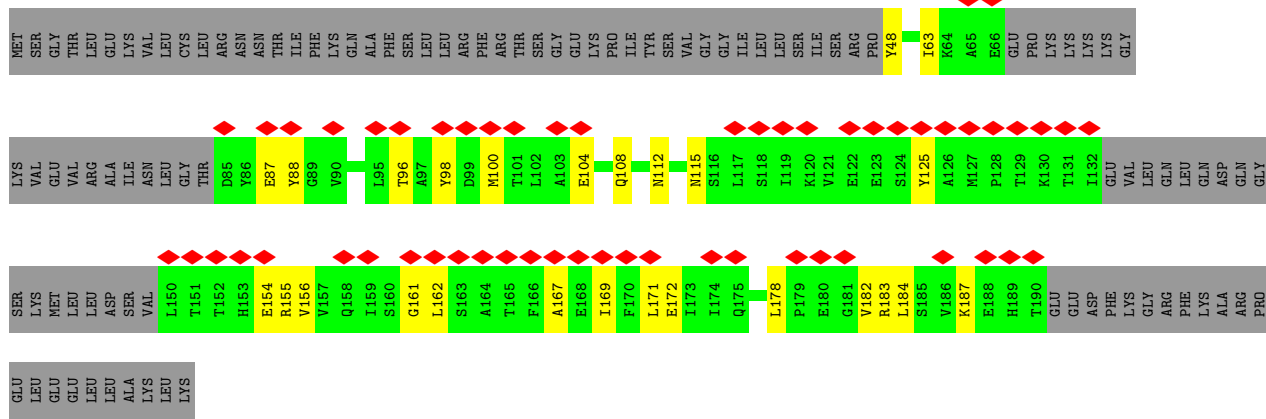
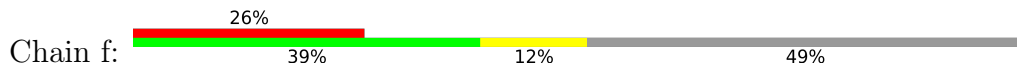


• Molecule 41: 39S ribosomal protein L46, mitochondrial

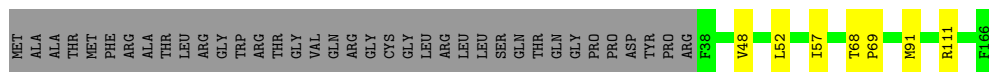




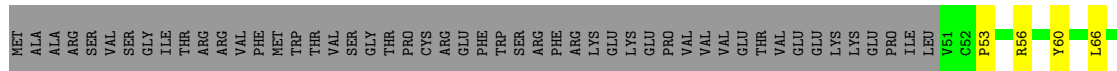
• Molecule 42: 39S ribosomal protein L48, mitochondrial



• Molecule 43: 39S ribosomal protein L49, mitochondrial



• Molecule 44: 39S ribosomal protein L50, mitochondrial





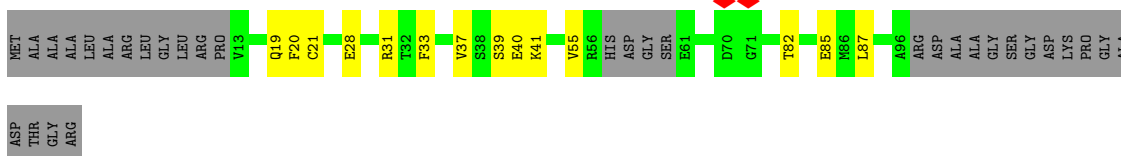
- Molecule 45: 39S ribosomal protein L51, mitochondrial



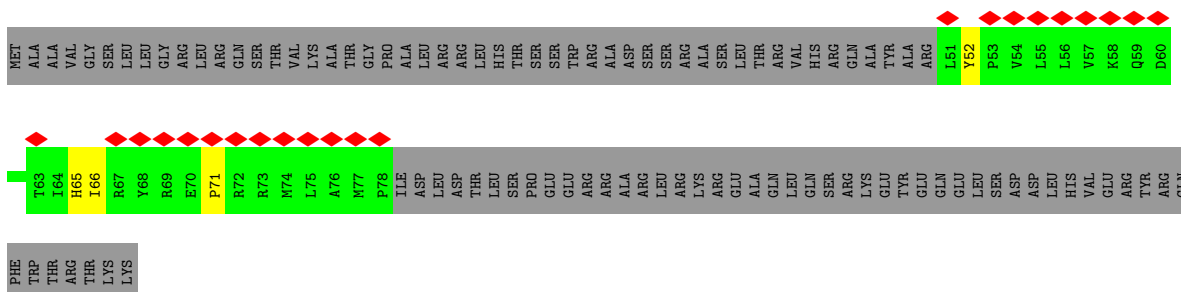
- Molecule 46: 39S ribosomal protein L52, mitochondrial



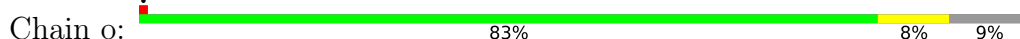
- Molecule 47: 39S ribosomal protein L53, mitochondrial



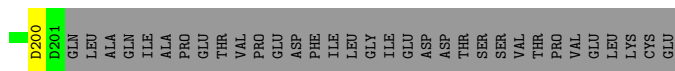
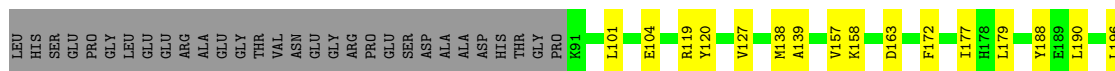
- Molecule 48: 39S ribosomal protein L55, mitochondrial



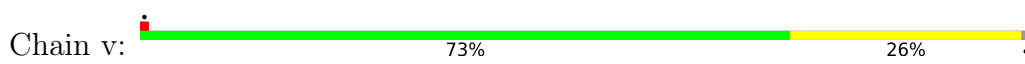
- Molecule 49: Ribosomal protein 63, mitochondrial



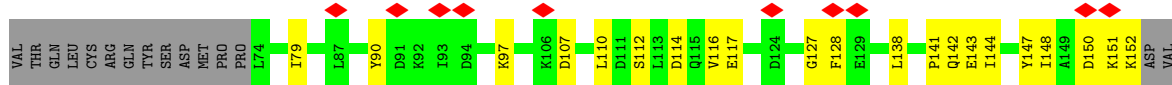
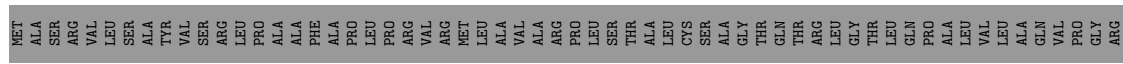
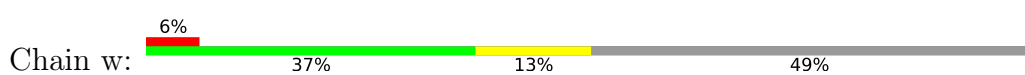
- Molecule 50: Peptidyl-tRNA hydrolase ICT1, mitochondrial



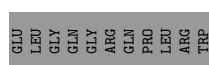
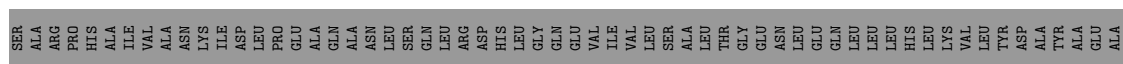
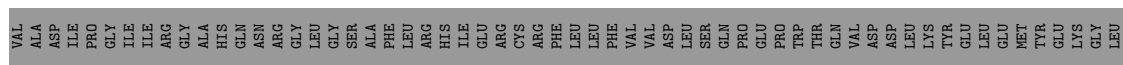
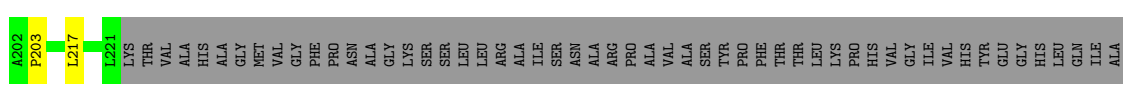
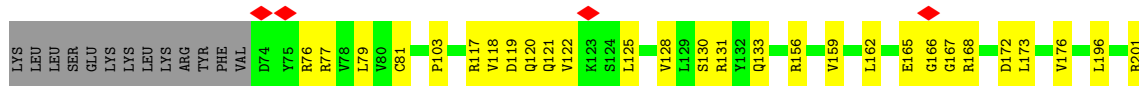
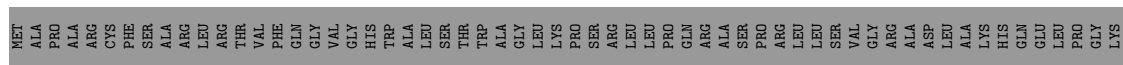
• Molecule 55: MIEF1 upstream open reading frame protein



• Molecule 56: Acyl carrier protein, mitochondrial



• Molecule 57: Mitochondrial ribosome-associated GTPase 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	98227	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 ($e^-/\text{\AA}^2$)	36	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.113	Depositor
Minimum map value	-0.035	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	367.49997, 367.49997, 367.49997	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	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, OMG, OMU

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	0	0.28	0/895	0.28	0/1201
2	1	0.11	0/438	0.26	0/583
3	2	0.38	0/373	0.35	0/496
4	3	0.34	0/852	0.31	0/1136
5	4	0.27	0/341	0.33	0/451
6	5	0.24	0/3294	0.33	0/4488
7	6	0.21	0/2809	0.32	0/3818
8	7	0.21	0/2391	0.32	0/3234
9	8	0.12	0/665	0.31	0/894
10	9	0.26	0/972	0.28	0/1306
11	A	0.38	0/32605	0.33	0/50720
12	B	0.12	0/1328	0.22	0/2056
13	C	0.15	0/2754	0.29	0/3734
14	D	0.29	0/1910	0.33	0/2569
15	E	0.32	0/2497	0.33	0/3386
16	F	0.33	0/2071	0.35	0/2817
17	G	0.17	0/1974	0.28	0/2652
18	H	0.23	0/798	0.29	0/1073
19	I	0.15	0/1308	0.30	0/1761
20	J	0.11	0/1077	0.26	0/1452
21	K	0.33	0/1495	0.31	0/2029
22	L	0.30	0/904	0.35	0/1218
23	M	0.31	0/2359	0.31	0/3185
24	N	0.24	0/1697	0.36	0/2281
25	O	0.32	0/1269	0.32	0/1708
26	P	0.23	0/1173	0.29	0/1588
27	Q	0.28	0/1846	0.31	0/2487
28	R	0.36	0/987	0.30	0/1320
29	S	0.33	0/1276	0.33	0/1729
30	T	0.33	0/1402	0.33	0/1886
31	U	0.28	0/1183	0.29	0/1600
32	V	0.22	0/404	0.24	0/545

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	W	0.33	0/881	0.30	0/1188
34	X	0.27	0/2090	0.28	0/2825
35	Y	0.29	0/1552	0.29	0/2079
36	Z	0.30	0/960	0.34	0/1295
37	a	0.29	0/616	0.28	0/833
38	b	0.31	0/1202	0.34	0/1626
39	c	0.27	0/2264	0.29	0/3059
40	d	0.13	0/1702	0.28	0/2307
41	e	0.10	0/1633	0.27	0/2204
42	f	0.15	0/873	0.32	0/1180
43	g	0.30	0/1102	0.33	0/1503
44	h	0.19	0/884	0.27	0/1203
45	i	0.37	0/849	0.32	0/1135
46	j	0.26	0/698	0.29	0/940
47	k	0.12	0/635	0.31	0/855
48	m	0.12	0/239	0.37	0/322
49	o	0.29	0/807	0.35	0/1083
50	p	0.18	0/1071	0.27	0/1433
51	q	0.19	0/1107	0.26	0/1498
52	r	0.25	0/1238	0.28	0/1676
53	s	0.31	0/3114	0.32	0/4225
54	u	0.20	0/949	0.32	0/1281
55	v	0.14	0/597	0.31	0/796
56	w	0.11	0/647	0.31	0/871
57	x	0.24	0/1091	0.38	0/1467
All	All	0.30	0/106148	0.31	0/150287

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](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	880	0	902	11	0
2	1	433	0	475	4	0
3	2	367	0	393	6	0
4	3	831	0	883	6	0
5	4	333	0	352	4	0
6	5	3199	0	3196	32	0
7	6	2723	0	2615	56	0
8	7	2334	0	2343	35	0
9	8	651	0	649	28	0
10	9	947	0	949	8	0
11	A	29222	0	14853	362	0
12	B	1191	0	607	14	0
13	C	2690	0	2677	26	0
14	D	1872	0	1932	23	0
15	E	2427	0	2436	28	0
16	F	2013	0	2044	27	0
17	G	1943	0	2030	19	0
18	H	784	0	832	9	0
19	I	1283	0	1369	34	0
20	J	1061	0	1141	20	0
21	K	1451	0	1448	16	0
22	L	889	0	941	22	0
23	M	2305	0	2378	24	0
24	N	1654	0	1681	32	0
25	O	1245	0	1283	15	0
26	P	1148	0	1148	17	0
27	Q	1805	0	1841	15	0
28	R	971	0	1045	15	0
29	S	1251	0	1322	20	0
30	T	1368	0	1410	19	0
31	U	1154	0	1154	11	0
32	V	395	0	392	2	0
33	W	859	0	888	24	0
34	X	2035	0	2054	20	0
35	Y	1517	0	1561	9	0
36	Z	937	0	983	9	0
37	a	597	0	584	6	0
38	b	1178	0	1180	20	0
39	c	2217	0	2220	13	0
40	d	1653	0	1632	15	0
41	e	1599	0	1604	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	f	857	0	852	22	0
43	g	1067	0	1056	7	0
44	h	862	0	845	8	0
45	i	827	0	857	10	0
46	j	684	0	673	3	0
47	k	627	0	636	12	0
48	m	234	0	250	3	0
49	o	786	0	791	8	0
50	p	1058	0	1083	9	0
51	q	1076	0	1049	13	0
52	r	1203	0	1219	11	0
53	s	3036	0	3022	36	0
54	u	927	0	921	15	0
55	v	588	0	604	17	0
56	w	638	0	637	15	0
57	x	1073	0	1045	23	0
58	0	1	0	0	0	0
58	4	1	0	0	0	0
58	r	1	0	0	0	0
59	A	71	0	0	0	0
59	E	1	0	0	0	0
59	W	1	0	0	0	0
59	g	1	0	0	0	0
All	All	101032	0	86967	1064	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 1064 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:3121:C:O2	11:A:3135:A:N6	1.97	0.97
10:9:28:ARG:NH1	11:A:2376:A:O2'	2.00	0.94
11:A:2182:G:O2'	11:A:2183:C:OP1	1.85	0.93
19:I:51:THR:OG1	24:N:250:ARG:NH2	2.00	0.93
11:A:2528:G:OP1	14:D:135:ARG:NH2	2.02	0.92

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	106/108 (98%)	105 (99%)	1 (1%)	0	100	100
2	1	50/65 (77%)	49 (98%)	1 (2%)	0	100	100
3	2	43/92 (47%)	42 (98%)	1 (2%)	0	100	100
4	3	93/188 (50%)	90 (97%)	3 (3%)	0	100	100
5	4	35/103 (34%)	34 (97%)	1 (3%)	0	100	100
6	5	390/423 (92%)	376 (96%)	14 (4%)	0	100	100
7	6	316/380 (83%)	303 (96%)	13 (4%)	0	100	100
8	7	285/338 (84%)	268 (94%)	17 (6%)	0	100	100
9	8	75/206 (36%)	72 (96%)	3 (4%)	0	100	100
10	9	113/137 (82%)	112 (99%)	1 (1%)	0	100	100
13	C	335/384 (87%)	317 (95%)	18 (5%)	0	100	100
14	D	238/305 (78%)	232 (98%)	6 (2%)	0	100	100
15	E	306/348 (88%)	296 (97%)	10 (3%)	0	100	100
16	F	248/311 (80%)	242 (98%)	6 (2%)	0	100	100
17	G	236/381 (62%)	225 (95%)	11 (5%)	0	100	100
18	H	93/267 (35%)	88 (95%)	5 (5%)	0	100	100
19	I	154/261 (59%)	146 (95%)	8 (5%)	0	100	100
20	J	138/192 (72%)	126 (91%)	12 (9%)	0	100	100
21	K	175/178 (98%)	171 (98%)	4 (2%)	0	100	100
22	L	113/145 (78%)	109 (96%)	4 (4%)	0	100	100
23	M	285/296 (96%)	282 (99%)	3 (1%)	0	100	100
24	N	203/251 (81%)	191 (94%)	12 (6%)	0	100	100
25	O	150/175 (86%)	147 (98%)	3 (2%)	0	100	100
26	P	139/180 (77%)	134 (96%)	5 (4%)	0	100	100
27	Q	215/292 (74%)	212 (99%)	3 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	R	114/149 (76%)	113 (99%)	1 (1%)	0	100	100
29	S	154/205 (75%)	151 (98%)	3 (2%)	0	100	100
30	T	164/206 (80%)	161 (98%)	3 (2%)	0	100	100
31	U	135/153 (88%)	133 (98%)	2 (2%)	0	100	100
32	V	45/216 (21%)	45 (100%)	0	0	100	100
33	W	107/148 (72%)	105 (98%)	2 (2%)	0	100	100
34	X	241/256 (94%)	236 (98%)	5 (2%)	0	100	100
35	Y	174/250 (70%)	170 (98%)	4 (2%)	0	100	100
36	Z	113/161 (70%)	110 (97%)	3 (3%)	0	100	100
37	a	67/142 (47%)	67 (100%)	0	0	100	100
38	b	146/215 (68%)	141 (97%)	5 (3%)	0	100	100
39	c	271/332 (82%)	267 (98%)	4 (2%)	0	100	100
40	d	189/306 (62%)	183 (97%)	6 (3%)	0	100	100
41	e	191/279 (68%)	179 (94%)	12 (6%)	0	100	100
42	f	102/212 (48%)	94 (92%)	8 (8%)	0	100	100
43	g	127/166 (76%)	120 (94%)	7 (6%)	0	100	100
44	h	101/158 (64%)	99 (98%)	2 (2%)	0	100	100
45	i	95/128 (74%)	94 (99%)	1 (1%)	0	100	100
46	j	83/85 (98%)	83 (100%)	0	0	100	100
47	k	76/112 (68%)	70 (92%)	6 (8%)	0	100	100
48	m	26/128 (20%)	20 (77%)	6 (23%)	0	100	100
49	o	91/102 (89%)	89 (98%)	2 (2%)	0	100	100
50	p	119/206 (58%)	116 (98%)	3 (2%)	0	100	100
51	q	126/222 (57%)	126 (100%)	0	0	100	100
52	r	140/196 (71%)	133 (95%)	7 (5%)	0	100	100
53	s	366/439 (83%)	358 (98%)	8 (2%)	0	100	100
54	u	109/234 (47%)	100 (92%)	9 (8%)	0	100	100
55	v	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
56	w	77/156 (49%)	73 (95%)	4 (5%)	0	100	100
57	x	146/406 (36%)	138 (94%)	8 (6%)	0	100	100
All	All	8496/12044 (70%)	8208 (97%)	288 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	0	97/97 (100%)	97 (100%)	0	100	100
2	1	49/60 (82%)	49 (100%)	0	100	100
3	2	39/72 (54%)	39 (100%)	0	100	100
4	3	88/166 (53%)	88 (100%)	0	100	100
5	4	36/89 (40%)	36 (100%)	0	100	100
6	5	353/368 (96%)	353 (100%)	0	100	100
7	6	286/332 (86%)	286 (100%)	0	100	100
8	7	263/303 (87%)	263 (100%)	0	100	100
9	8	70/190 (37%)	70 (100%)	0	100	100
10	9	99/112 (88%)	99 (100%)	0	100	100
13	C	293/328 (89%)	293 (100%)	0	100	100
14	D	194/245 (79%)	194 (100%)	0	100	100
15	E	262/290 (90%)	262 (100%)	0	100	100
16	F	217/262 (83%)	217 (100%)	0	100	100
17	G	221/350 (63%)	221 (100%)	0	100	100
18	H	86/228 (38%)	86 (100%)	0	100	100
19	I	145/232 (62%)	145 (100%)	0	100	100
20	J	113/150 (75%)	113 (100%)	0	100	100
21	K	155/156 (99%)	155 (100%)	0	100	100
22	L	98/124 (79%)	98 (100%)	0	100	100
23	M	245/249 (98%)	245 (100%)	0	100	100
24	N	172/211 (82%)	172 (100%)	0	100	100
25	O	133/150 (89%)	133 (100%)	0	100	100
26	P	123/155 (79%)	123 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	Q	199/256 (78%)	199 (100%)	0	100	100
28	R	101/126 (80%)	101 (100%)	0	100	100
29	S	141/180 (78%)	141 (100%)	0	100	100
30	T	146/176 (83%)	146 (100%)	0	100	100
31	U	124/135 (92%)	124 (100%)	0	100	100
32	V	43/191 (22%)	43 (100%)	0	100	100
33	W	89/119 (75%)	89 (100%)	0	100	100
34	X	219/229 (96%)	219 (100%)	0	100	100
35	Y	159/223 (71%)	159 (100%)	0	100	100
36	Z	106/147 (72%)	106 (100%)	0	100	100
37	a	67/133 (50%)	67 (100%)	0	100	100
38	b	130/186 (70%)	130 (100%)	0	100	100
39	c	241/288 (84%)	241 (100%)	0	100	100
40	d	184/274 (67%)	184 (100%)	0	100	100
41	e	171/236 (72%)	171 (100%)	0	100	100
42	f	95/188 (50%)	95 (100%)	0	100	100
43	g	119/148 (80%)	119 (100%)	0	100	100
44	h	100/148 (68%)	100 (100%)	0	100	100
45	i	86/110 (78%)	86 (100%)	0	100	100
46	j	68/68 (100%)	68 (100%)	0	100	100
47	k	71/90 (79%)	71 (100%)	0	100	100
48	m	26/113 (23%)	26 (100%)	0	100	100
49	o	79/87 (91%)	79 (100%)	0	100	100
50	p	117/181 (65%)	117 (100%)	0	100	100
51	q	110/178 (62%)	110 (100%)	0	100	100
52	r	133/169 (79%)	133 (100%)	0	100	100
53	s	326/381 (86%)	326 (100%)	0	100	100
54	u	105/200 (52%)	105 (100%)	0	100	100
55	v	59/60 (98%)	59 (100%)	0	100	100
56	w	73/136 (54%)	73 (100%)	0	100	100
57	x	109/320 (34%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	7633/10395 (73%)	7633 (100%)	0	100 100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
38	b	129	GLN
46	j	99	GLN
39	c	69	HIS
43	g	92	HIS
50	p	104	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	1359/1559 (87%)	294 (21%)	21 (1%)
12	B	51/69 (73%)	16 (31%)	1 (1%)
All	All	1410/1628 (86%)	310 (21%)	22 (1%)

5 of 310 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	1672	C
11	A	1676	A
11	A	1677	C
11	A	1679	U
11	A	1680	A

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	A	2695	G
11	A	2905	A
11	A	2837	A
11	A	3092	U
11	A	2182	G

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

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	OMG	A	3040	11	23,26,27	1.26	4 (17%)	32,38,41	2.05	7 (21%)
11	OMG	A	2815	11	23,26,27	1.18	2 (8%)	32,38,41	2.12	7 (21%)
11	OMU	A	3039	11	19,22,23	1.33	3 (15%)	25,31,34	2.08	5 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	OMG	A	3040	11	-	0/9/27/28	0/3/3/3
11	OMG	A	2815	11	-	2/9/27/28	0/3/3/3
11	OMU	A	3039	11	-	0/9/27/28	0/2/2/2

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	3039	OMU	C4-N3	-3.18	1.33	1.38
11	A	2815	OMG	C5-C4	2.92	1.46	1.38
11	A	3040	OMG	C6-N1	-2.76	1.33	1.38
11	A	3039	OMU	C2-N3	-2.76	1.33	1.38
11	A	3040	OMG	C5-C4	2.74	1.46	1.38

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	3040	OMG	C5-C4-N3	-6.02	118.81	128.39
11	A	2815	OMG	C5-C4-N3	-5.79	119.17	128.39
11	A	3040	OMG	C2-N3-C4	5.08	121.05	112.30
11	A	2815	OMG	C2-N3-C4	5.04	120.98	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	3039	OMU	C4-N3-C2	-4.88	120.55	126.61

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	A	2815	OMG	O4'-C4'-C5'-O5'
11	A	2815	OMG	C3'-C4'-C5'-O5'

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	A	3040	OMG	4	0
11	A	2815	OMG	2	0
11	A	3039	OMU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 77 ligands modelled in this entry, 77 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

There are no chain breaks in this entry.

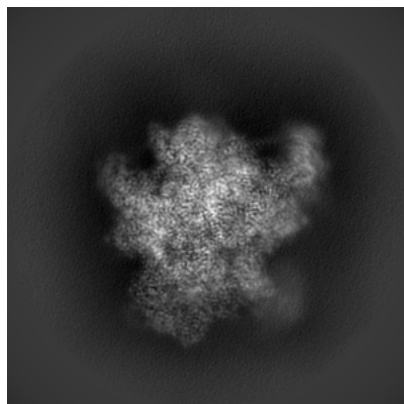
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12872. These allow visual inspection of the internal detail of the map and identification of artifacts.

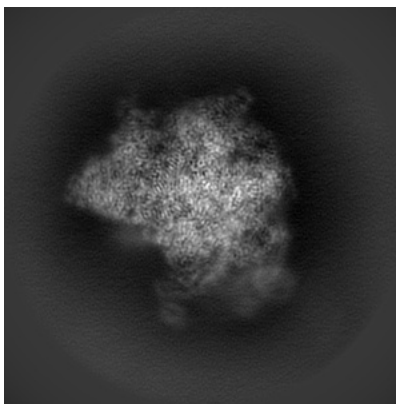
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

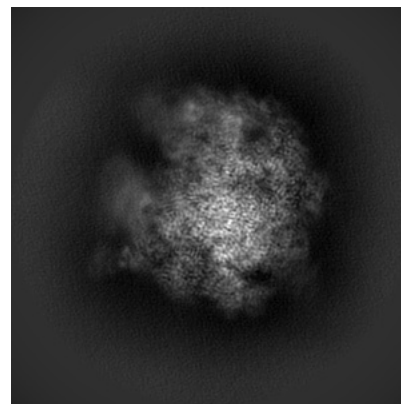
6.1.1 Primary map



X

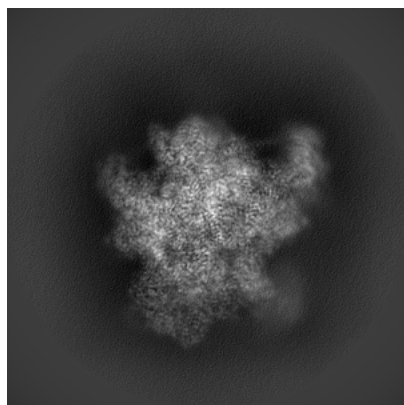


Y

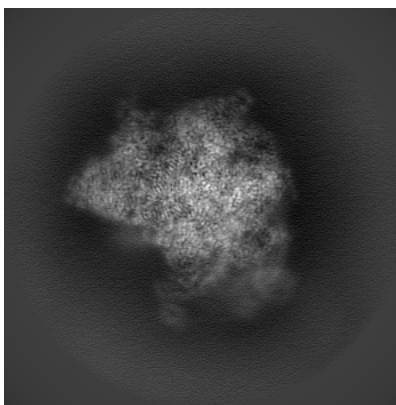


Z

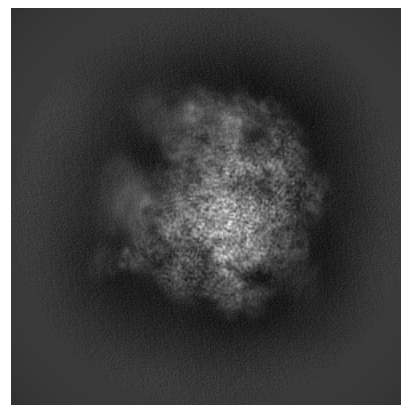
6.1.2 Raw map



X



Y

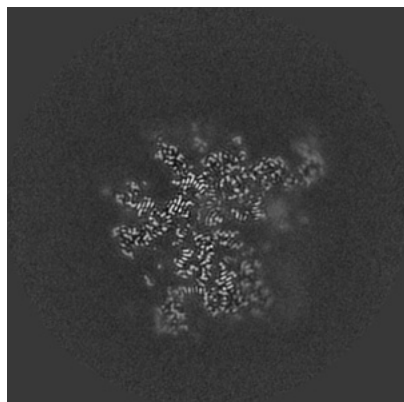


Z

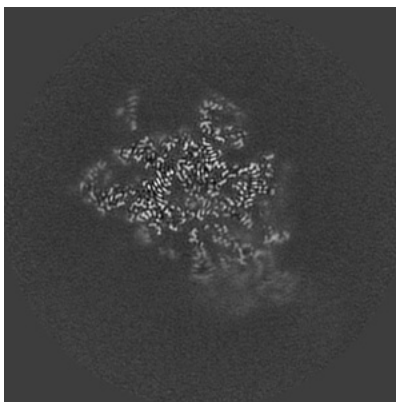
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

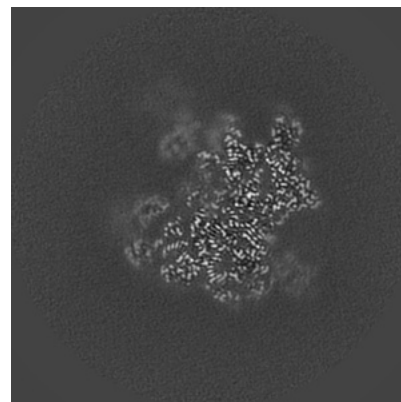
6.2.1 Primary map



X Index: 175

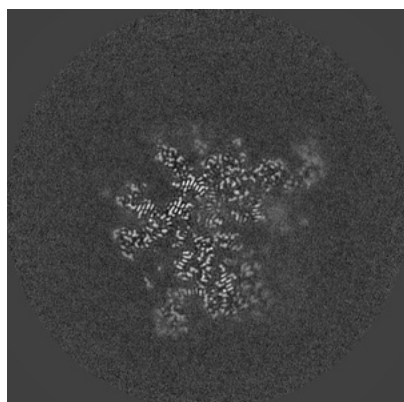


Y Index: 175

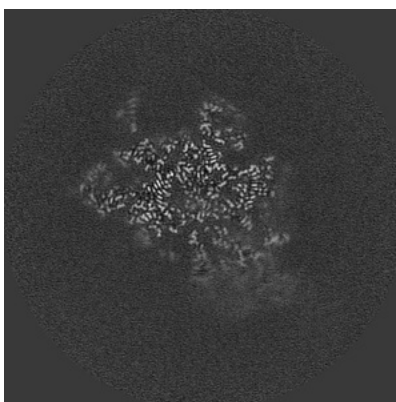


Z Index: 175

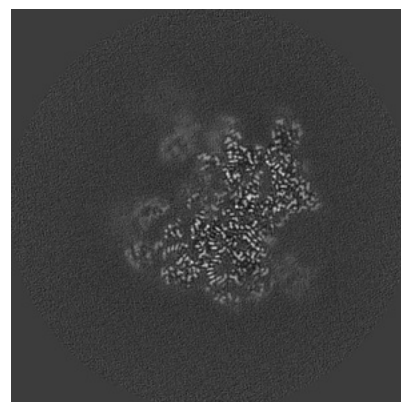
6.2.2 Raw map



X Index: 175



Y Index: 175

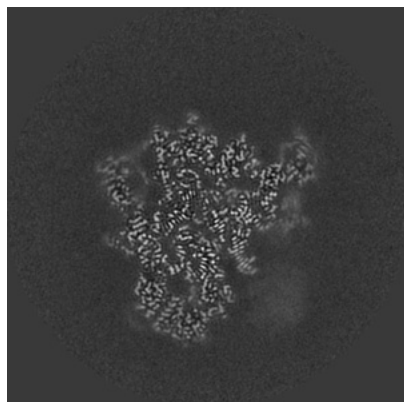


Z Index: 175

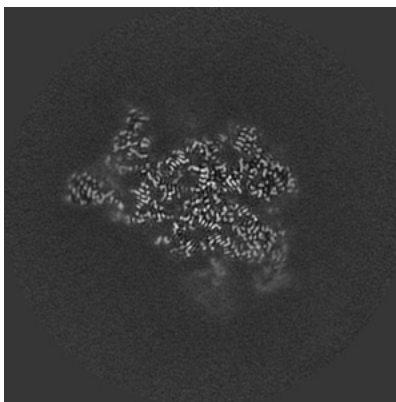
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

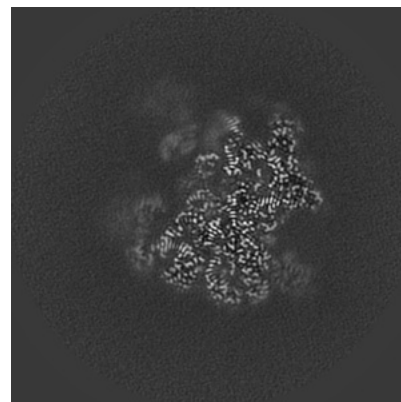
6.3.1 Primary map



X Index: 188

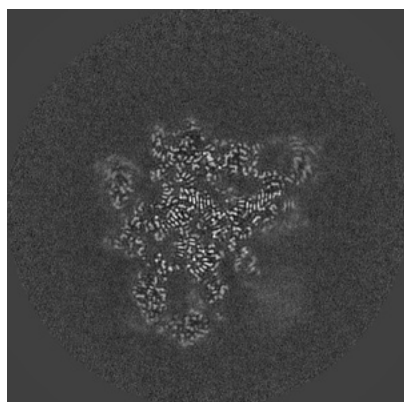


Y Index: 159

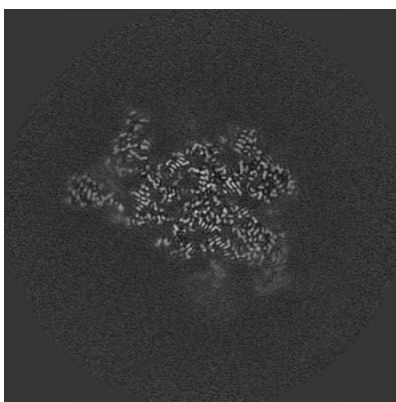


Z Index: 178

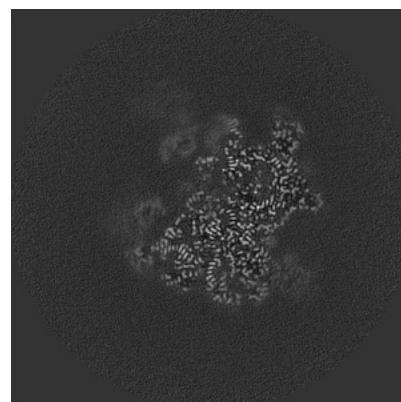
6.3.2 Raw map



X Index: 192



Y Index: 159

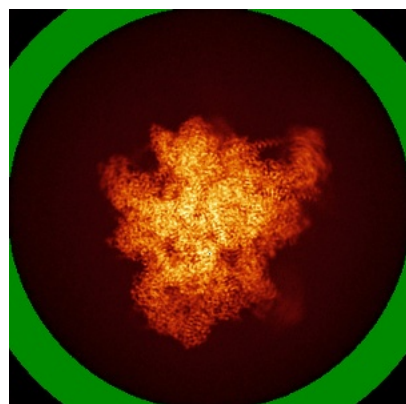


Z Index: 177

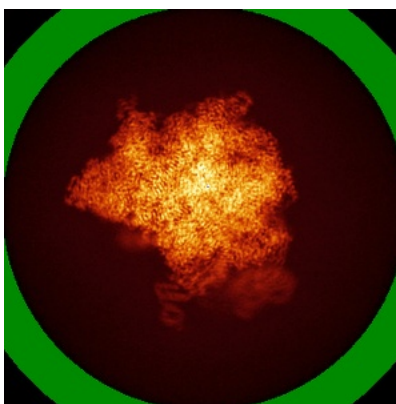
The images above show the largest variance slices of the map in three orthogonal directions.

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

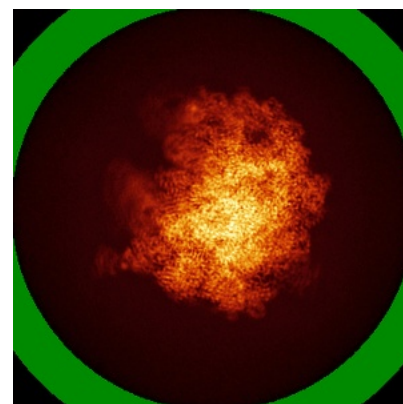
6.4.1 Primary map



X

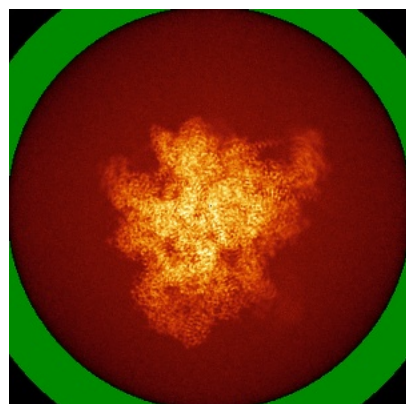


Y

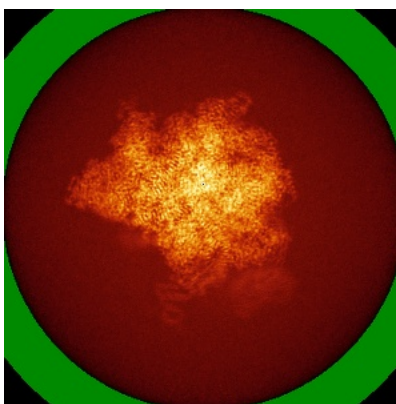


Z

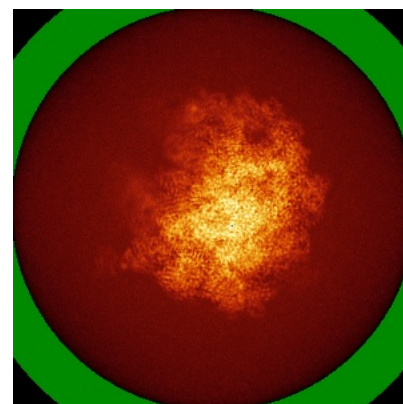
6.4.2 Raw map



X



Y

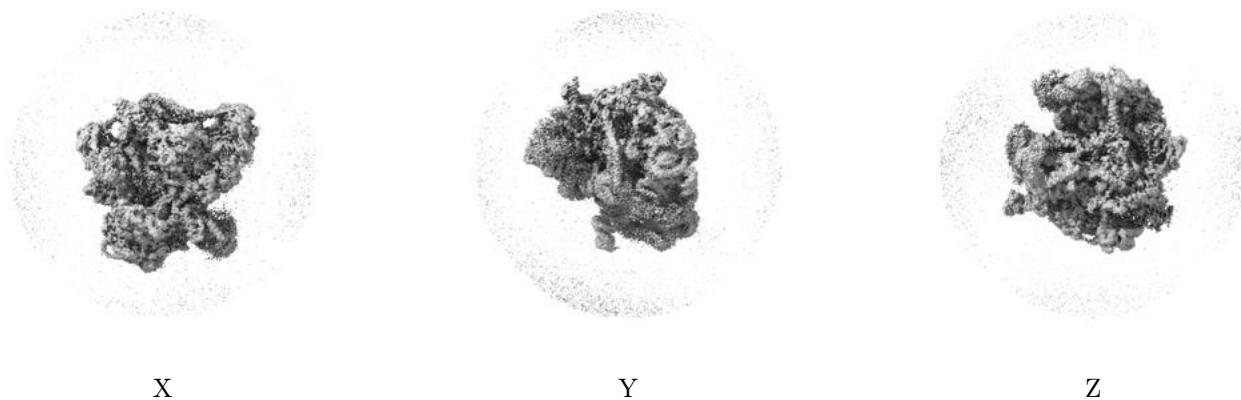


Z

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

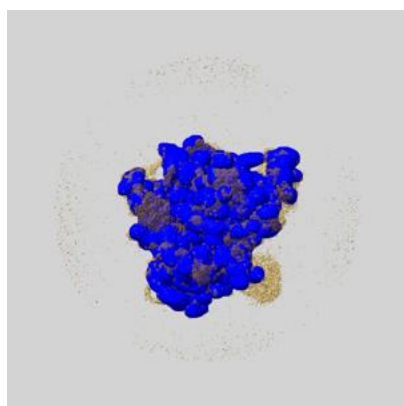
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

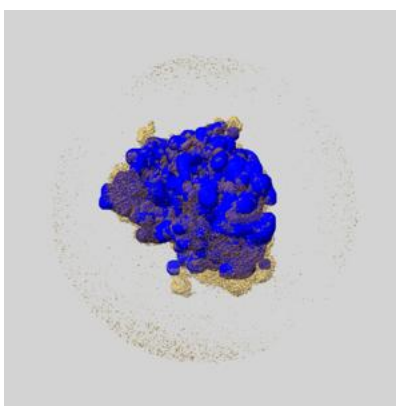
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

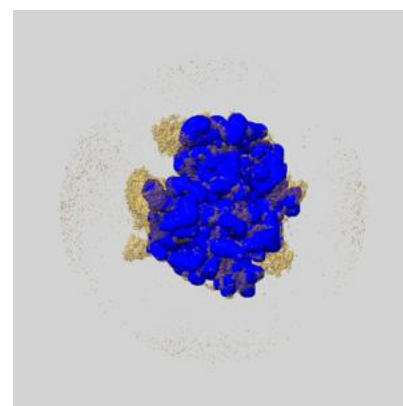
6.6.1 emd_12872_msk_1.map [i](#)



X



Y

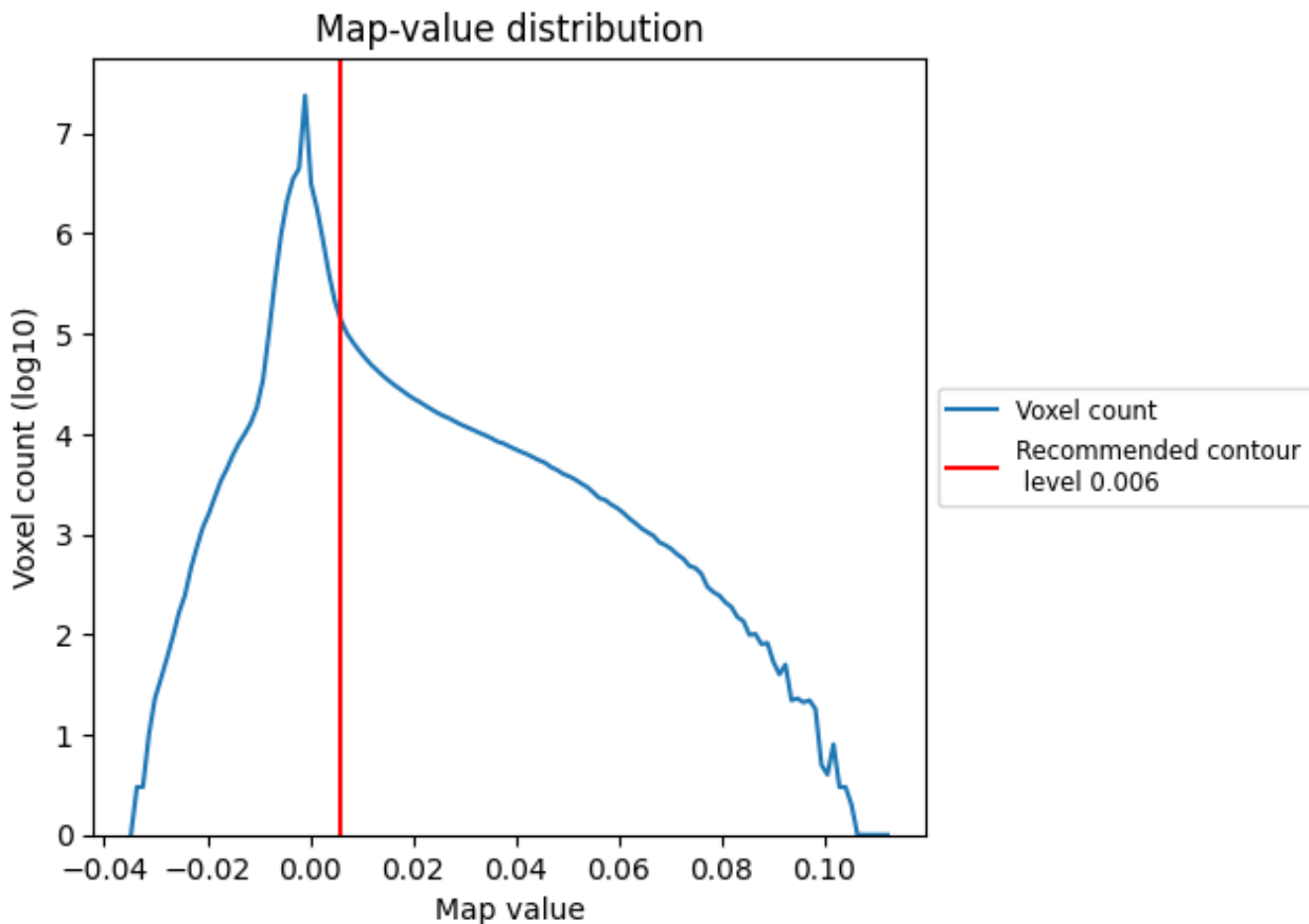


Z

7 Map analysis [i](#)

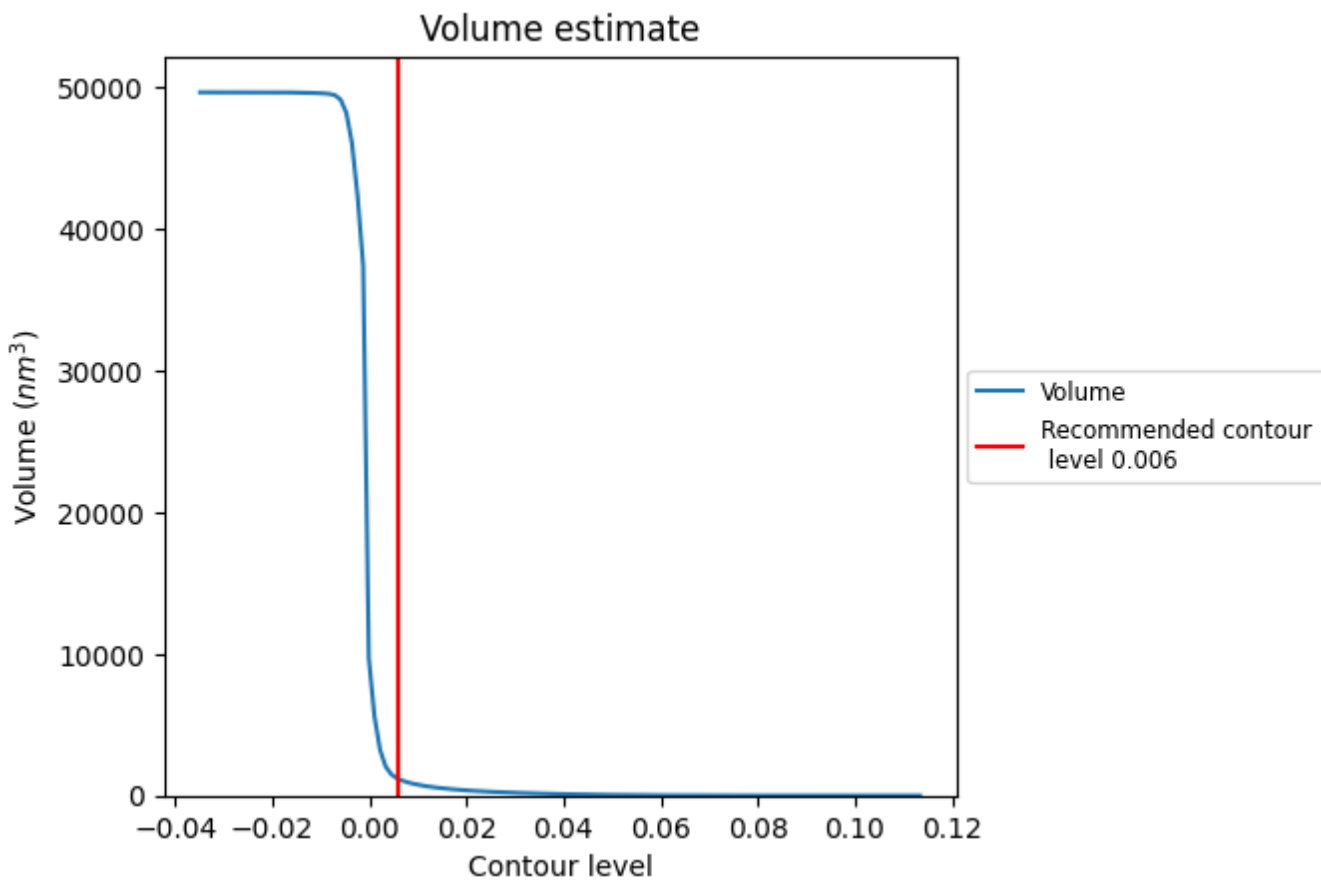
This section contains the results of statistical analysis of the map.

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.

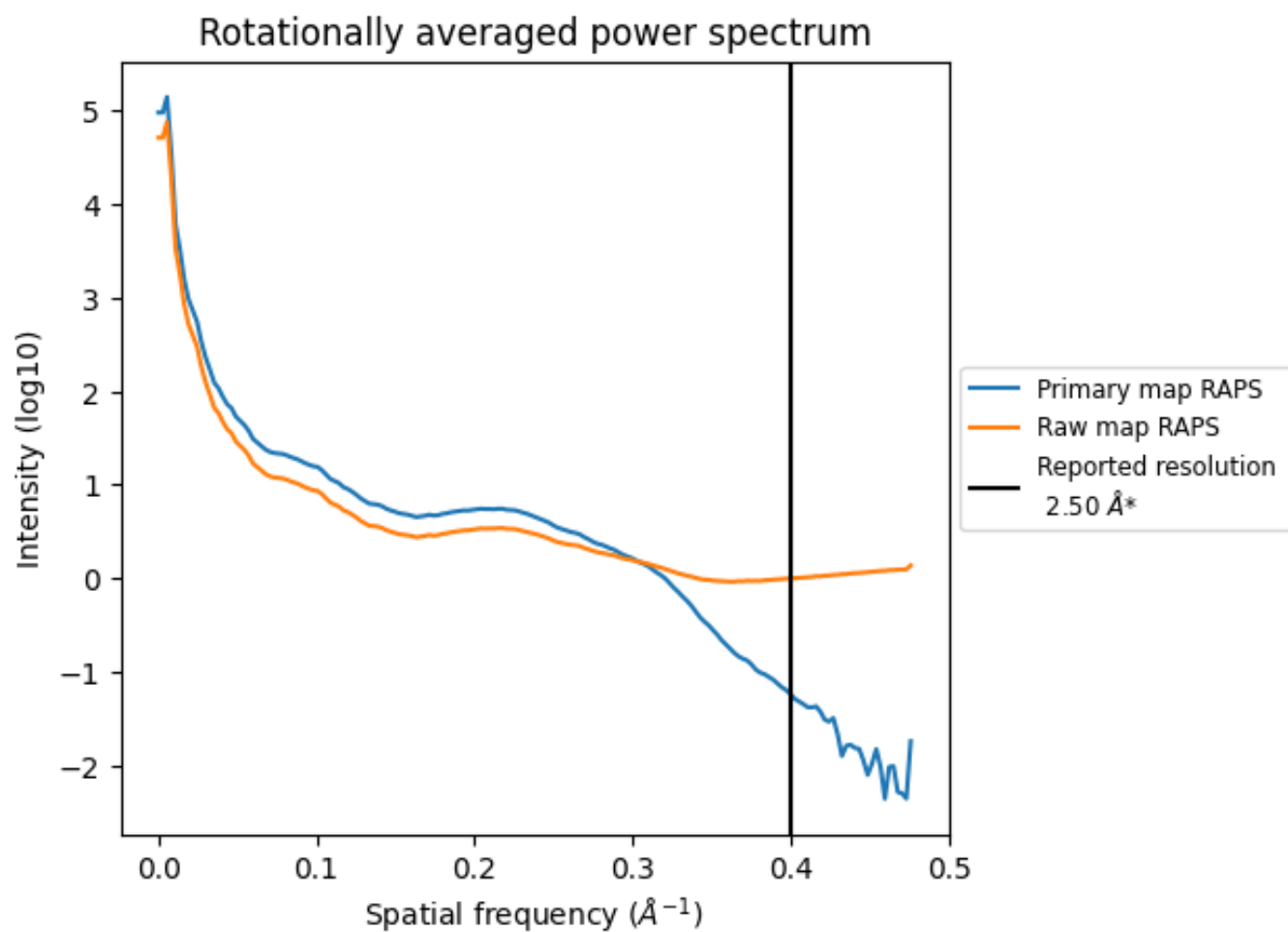
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1175 nm³; this corresponds to an approximate mass of 1062 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](#)

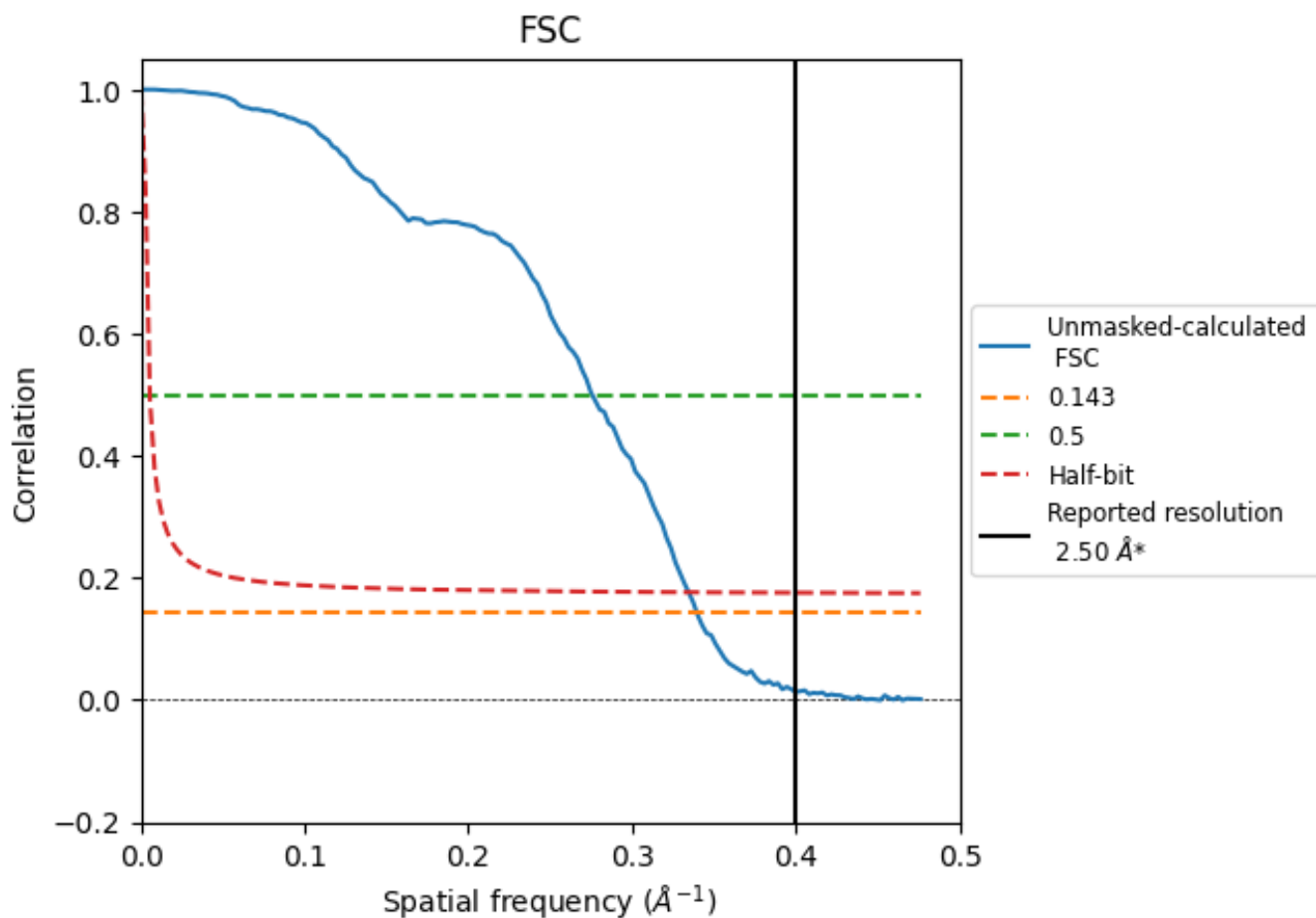


*Reported resolution corresponds to spatial frequency of 0.400 Å⁻¹

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 0.400 Å⁻¹

8.2 Resolution estimates [i](#)

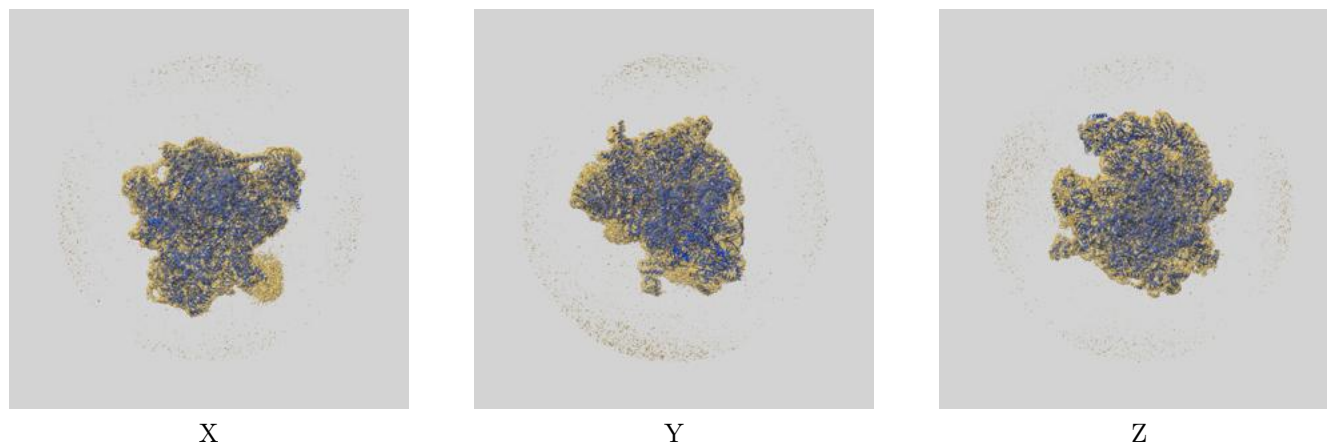
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.94	3.63	2.99

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.94 differs from the reported value 2.5 by more than 10 %

9 Map-model fit [i](#)

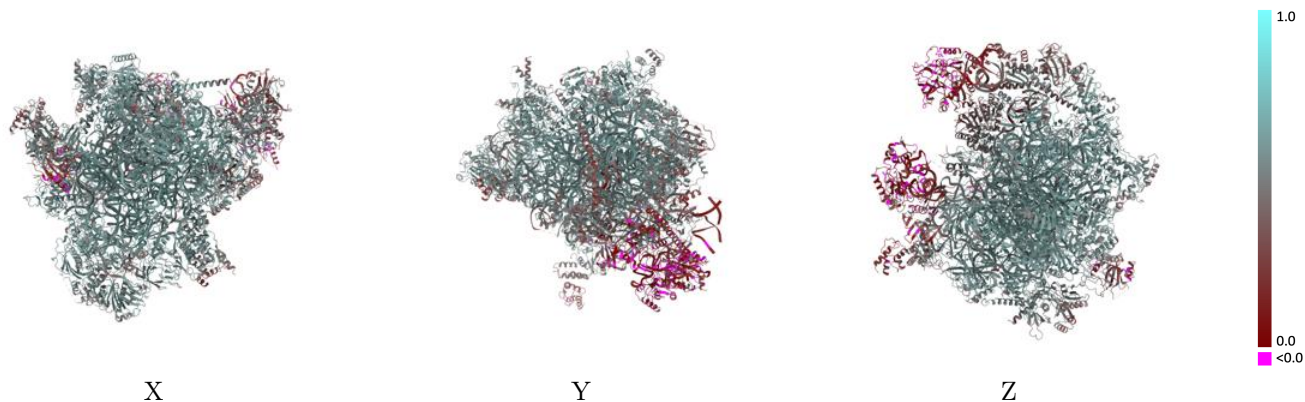
This section contains information regarding the fit between EMDB map EMD-12872 and PDB model 7OF7. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



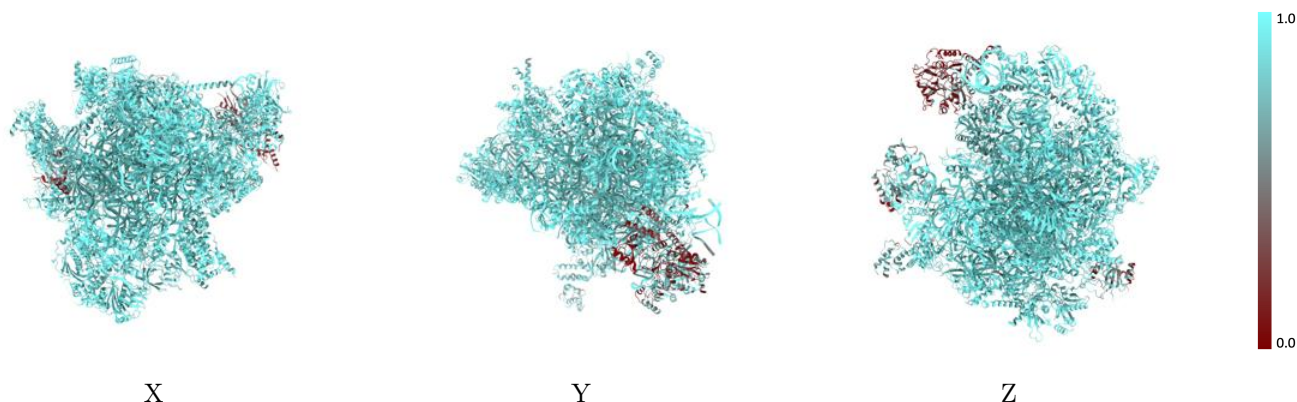
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



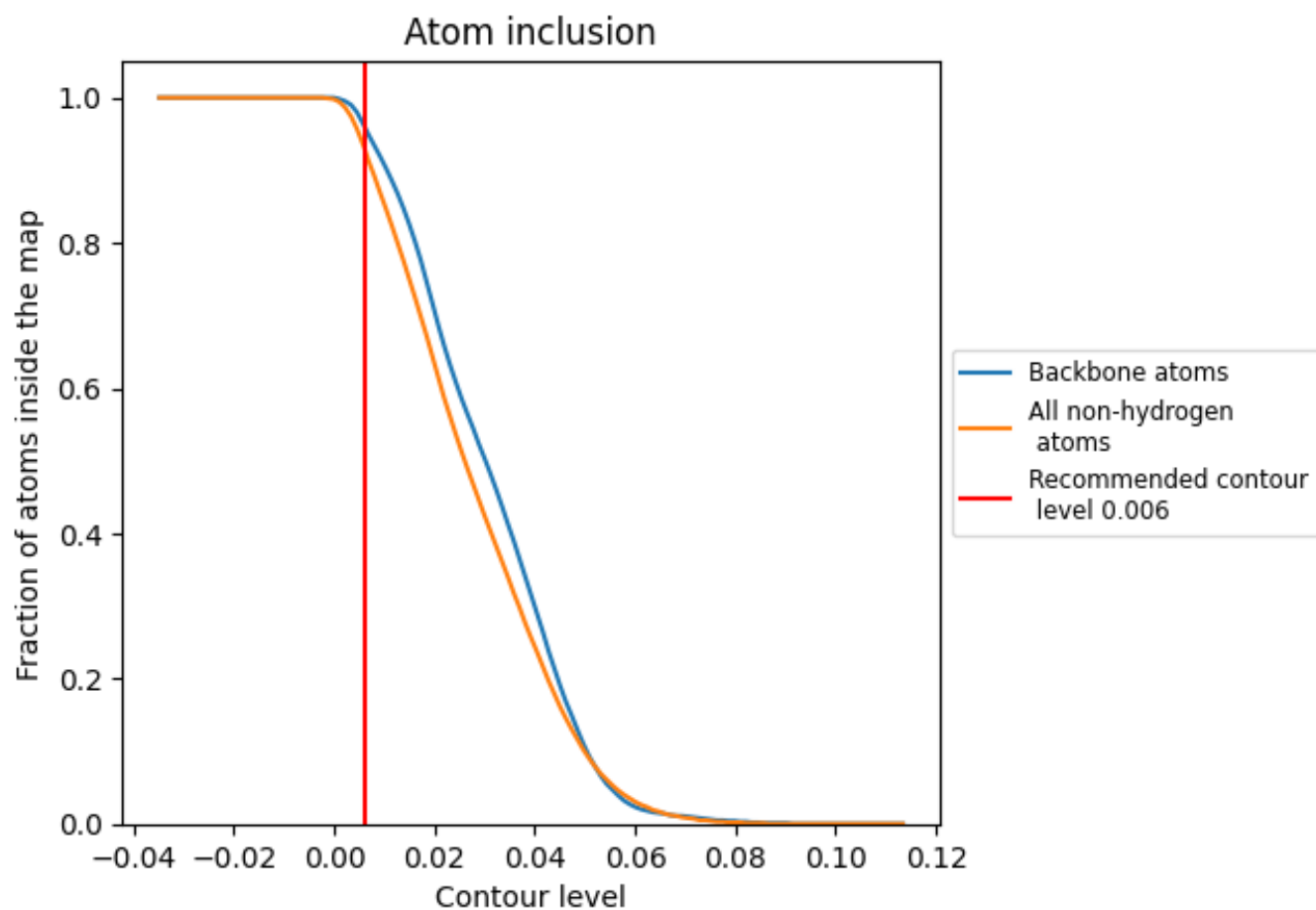
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.006).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 93% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9310	 0.5230
0	 0.9640	 0.5670
1	 0.8860	 0.3710
2	 1.0000	 0.6420
3	 0.9840	 0.6260
4	 0.9750	 0.5650
5	 0.9590	 0.5370
6	 0.9460	 0.4560
7	 0.9360	 0.4950
8	 0.3370	 0.1560
9	 0.9510	 0.5530
A	 0.9950	 0.5800
B	 0.9350	 0.2930
C	 0.9100	 0.4110
D	 0.9610	 0.5800
E	 0.9720	 0.5880
F	 0.9840	 0.6080
G	 0.9000	 0.4410
H	 0.9260	 0.5320
I	 0.8200	 0.2460
J	 0.5860	 0.0940
K	 0.9840	 0.6050
L	 0.9690	 0.5830
M	 0.9740	 0.5980
N	 0.9480	 0.5390
O	 0.9800	 0.5950
P	 0.9670	 0.5120
Q	 0.9610	 0.5710
R	 0.9870	 0.6170
S	 0.9690	 0.5900
T	 0.9740	 0.6050
U	 0.8710	 0.5420
V	 0.9560	 0.5360
W	 0.9790	 0.5970
X	 0.9570	 0.5700



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Chain	Atom inclusion	Q-score
Y	 0.9630	 0.5840
Z	 0.9660	 0.5910
a	 0.9690	 0.5940
b	 0.9800	 0.5990
c	 0.9590	 0.5590
d	 0.6550	 0.3280
e	 0.1900	 0.0940
f	 0.4250	 0.2540
g	 0.9830	 0.5930
h	 0.9300	 0.4890
i	 0.9870	 0.6300
j	 0.9620	 0.5720
k	 0.8780	 0.2730
m	 0.2140	 0.1370
o	 0.9730	 0.6040
p	 0.9240	 0.4990
q	 0.8860	 0.4520
r	 0.9700	 0.5440
s	 0.9680	 0.5800
u	 0.9450	 0.4580
v	 0.8790	 0.3490
w	 0.6790	 0.1820
x	 0.8820	 0.3910