



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:05 AM UTC

PDB ID : 7QH6 / pdb_00007qh6
EMDB ID : EMD-13965
Title : Cryo-EM structure of the human mtLSU assembly intermediate upon MRM2 depletion - class 1
Authors : Rebelo-Guiomar, P.; Pellegrino, S.; Dent, K.C.; Warren, A.J.; Minczuk, M.
Deposited on : 2021-12-10
Resolution : 3.08 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:

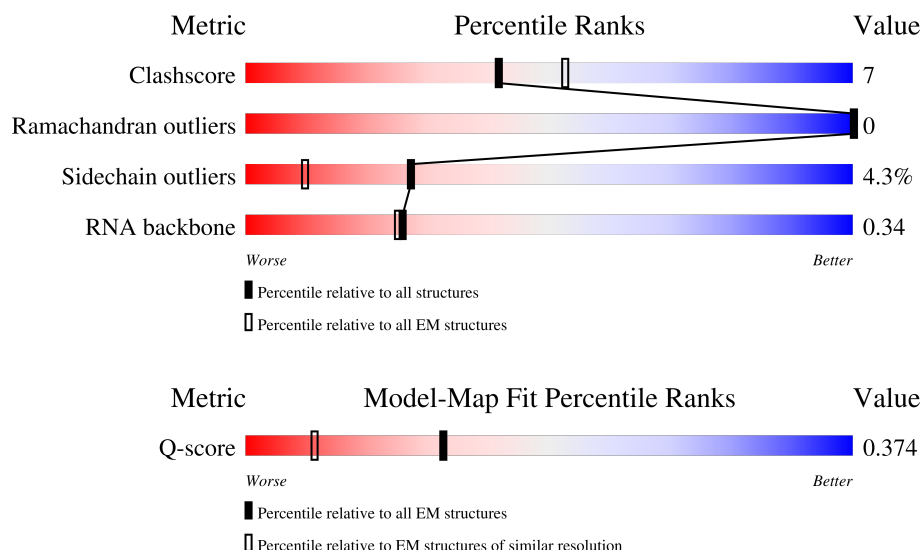
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.08 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.



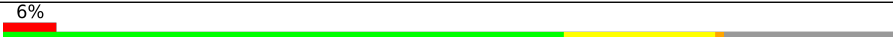
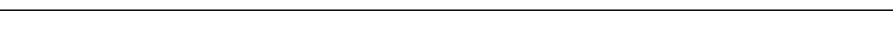
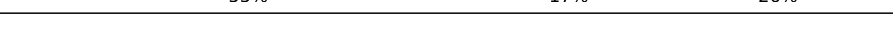
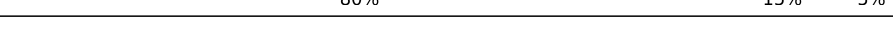
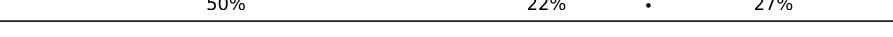
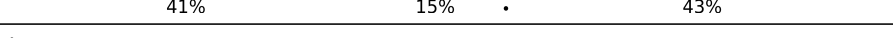
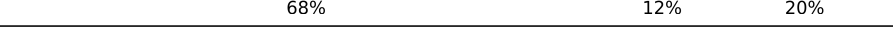
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14000 (2.58 - 3.58)

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	305	
2	E	348	
3	F	311	

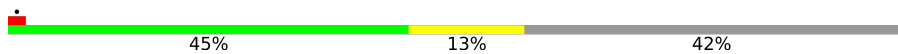
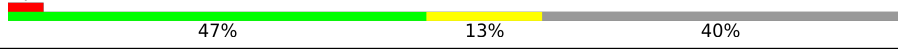
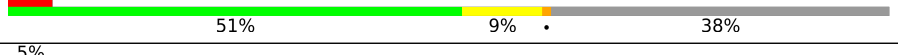
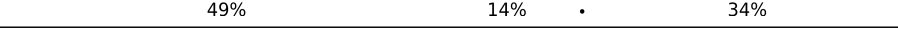
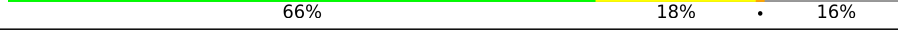
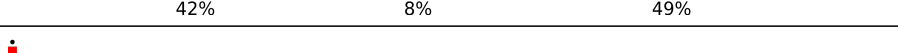
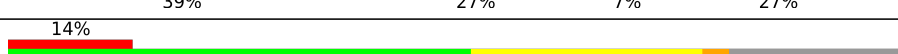
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Mol	Chain	Length	Quality of chain
4	H	267	
5	K	178	
6	L	145	
7	M	296	
8	N	251	
9	O	175	
10	P	180	
11	Q	292	
12	R	149	
13	S	205	
14	T	206	
15	U	153	
16	V	216	
17	W	148	
18	X	256	
19	Y	250	
20	Z	161	
21	0	188	
22	1	65	
23	2	92	
24	3	188	
25	5	423	
26	6	380	
27	7	338	
28	9	137	

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Mol	Chain	Length	Quality of chain
29	a	142	
30	b	215	
31	c	332	
32	d	306	
33	g	166	
34	h	158	
35	i	128	
36	j	123	
37	o	102	
38	p	206	
39	q	222	
40	r	196	
41	s	439	
42	u	234	
43	v	70	
44	w	156	
45	A	1559	
46	B	69	

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 83425 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	174	Total	C	N	O	S	0	0
			1349	834	268	240	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	284	Total	C	N	O	S	0	0
			2249	1451	382	405	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	0	0
			784	498	152	134		

- Molecule 5 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 6 is a protein called 39S ribosomal protein L14, mitochondrial.

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

- Molecule 7 is a protein called 39S ribosomal protein L15, mitochondrial.

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

- Molecule 8 is a protein called 39S ribosomal protein L16, mitochondrial.

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

- Molecule 9 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 10 is a protein called 39S ribosomal protein L18, mitochondrial.

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

- Molecule 11 is a protein called 39S ribosomal protein L19, mitochondrial.

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

- Molecule 12 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	R	140	Total	C	N	O	S	0	0
			1153	732	231	186	4		

- Molecule 13 is a protein called 39S ribosomal protein L21, mitochondrial.

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

- Molecule 14 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 15 is a protein called 39S ribosomal protein L23, mitochondrial.

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

- Molecule 16 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	V	163	Total	C	N	O	S	0	0
			1333	848	231	247	7		

- Molecule 17 is a protein called 39S ribosomal protein L27, mitochondrial.

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

- Molecule 18 is a protein called 39S ribosomal protein L28, mitochondrial.

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

- Molecule 19 is a protein called 39S ribosomal protein L47, mitochondrial.

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

- Molecule 20 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Z	117	Total	C	N	O	S	0	0
			955	610	179	163	3		

- Molecule 21 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	0	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 22 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

- Molecule 23 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2	45	Total	C	N	O	S	0	0
			367	227	81	58	1		

- Molecule 24 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 25 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	5	373	Total	C	N	O	S	0	0
			3037	1964	526	536	11		

- Molecule 26 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	6	324	Total	C	N	O	S	0	0
			2640	1694	470	468	8		

- Molecule 27 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	7	287	Total	C	N	O	S	0	0
			2334	1495	397	425	17		

- Molecule 28 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	9	117	Total	C	N	O	S	0	0
			947	614	163	168	2		

- Molecule 29 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	82	Total	C	N	O	S	0	0
			686	434	124	123	5		

- Molecule 30 is a protein called 39S ribosomal protein L43, mitochondrial.

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

- Molecule 31 is a protein called 39S ribosomal protein L44, mitochondrial.

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

- Molecule 32 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	185	Total	C	N	O	S	0	0
			1529	989	260	271	9		

- Molecule 33 is a protein called 39S ribosomal protein L49, mitochondrial.

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

- Molecule 34 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	100	Total	C	N	O	S	0	0
			827	524	146	155	2		

- Molecule 35 is a protein called 39S ribosomal protein L51, mitochondrial.

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

- Molecule 36 is a protein called 39S ribosomal protein L52, mitochondrial.

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

- Molecule 37 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	o	91	Total	C	N	O	S	0	0
			771	487	156	125	3		

- Molecule 38 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

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

- Molecule 39 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

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

- Molecule 40 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	r	130	Total	C	N	O	S	0	0
			1075	683	210	174	8		

- Molecule 41 is a protein called 39S ribosomal protein S30, mitochondrial.

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

- Molecule 42 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

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

- Molecule 43 is a protein called MIEF1 upstream open reading frame protein.

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

- Molecule 44 is a protein called Acyl carrier protein, mitochondrial.

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

- Molecule 45 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	A	1133	Total	C	N	O	P	0	0
			24063	10801	4361	7768	1133		

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 46 is a RNA chain called mitochondrial tRNAVal.

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

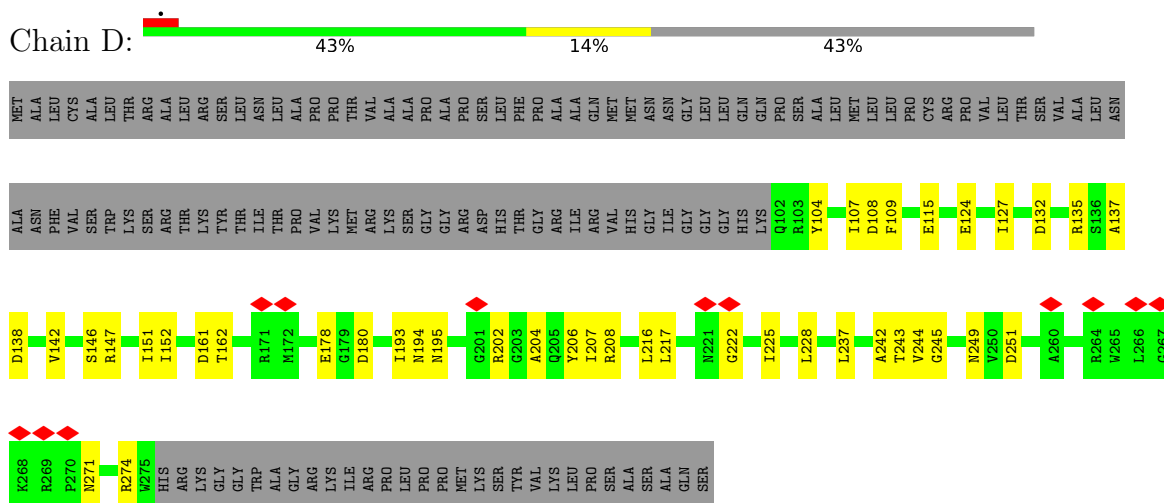
- Molecule 47 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
47	0	1	Total	Zn	0
			1	1	

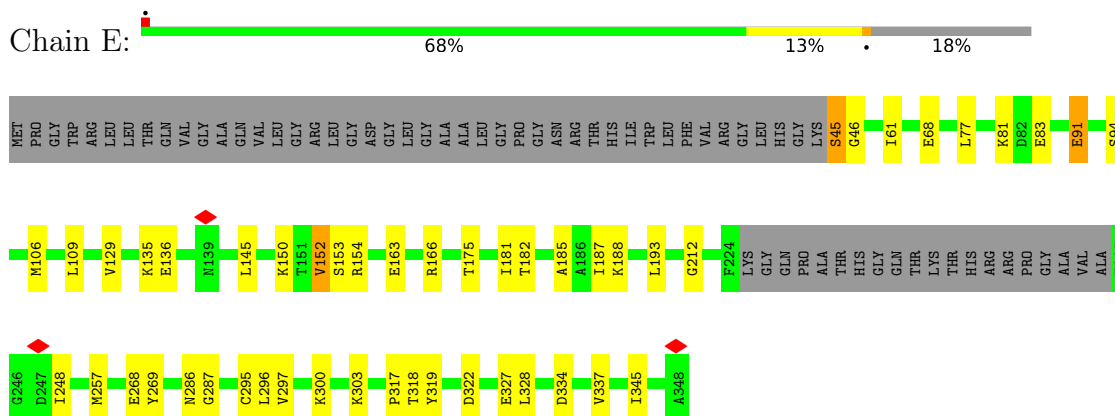
3 Residue-property plots

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

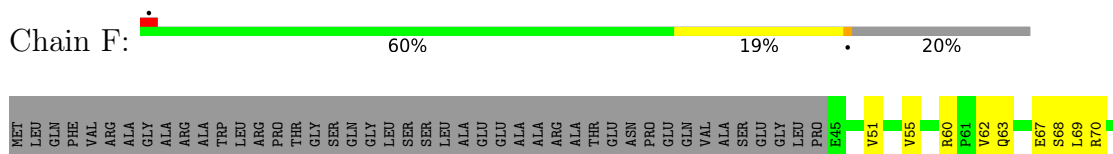
- Molecule 1: 39S ribosomal protein L2, mitochondrial

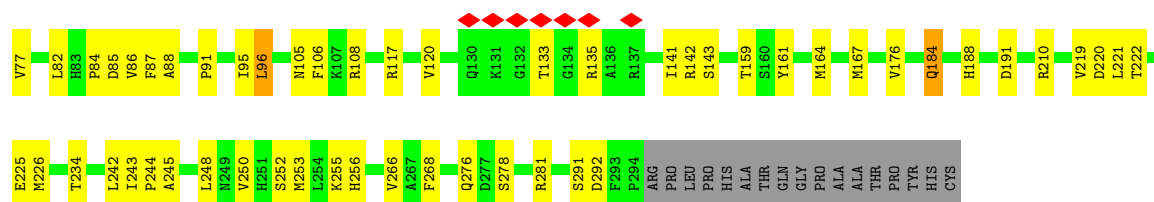


- Molecule 2: 39S ribosomal protein L3, mitochondrial

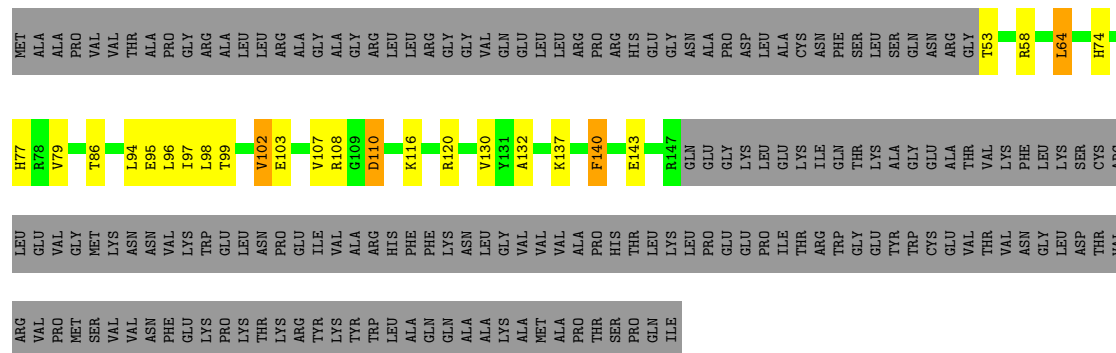


- Molecule 3: 39S ribosomal protein L4, mitochondrial

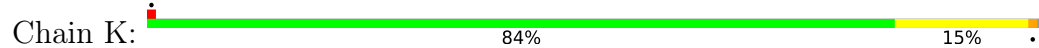




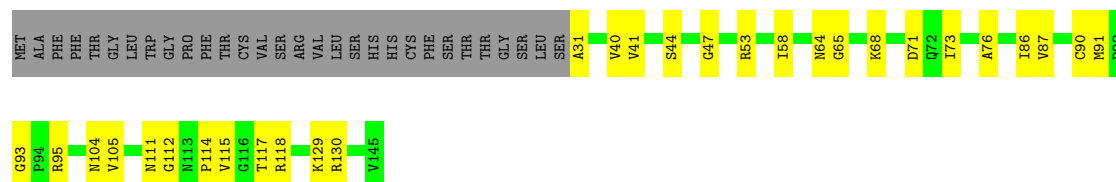
• Molecule 4: 39S ribosomal protein L9, mitochondrial



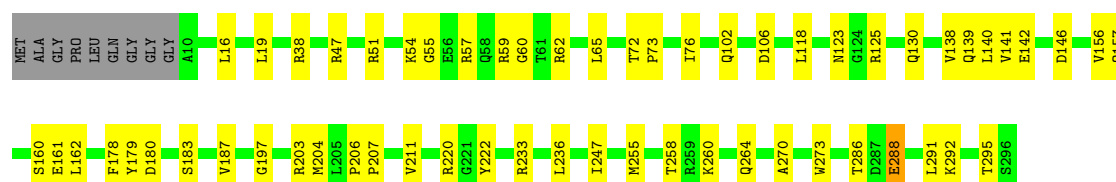
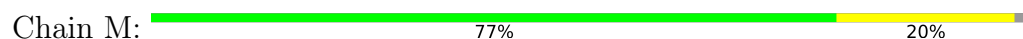
• Molecule 5: 39S ribosomal protein L13, mitochondrial



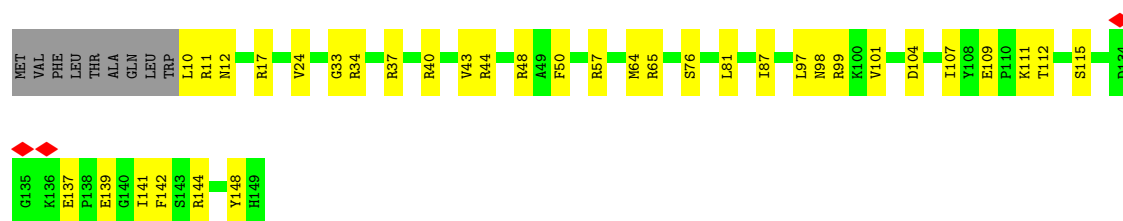
• Molecule 6: 39S ribosomal protein L14, mitochondrial



• Molecule 7: 39S ribosomal protein L15, mitochondrial

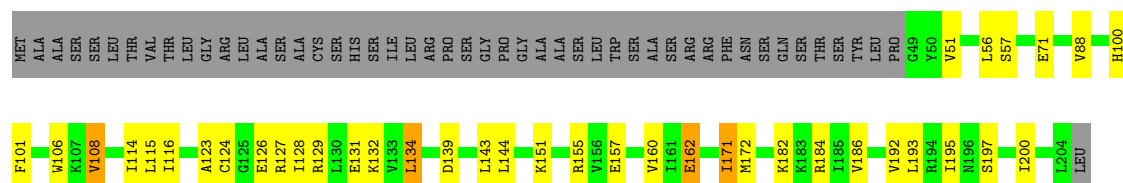


- Chain R: 70% 23% 6%



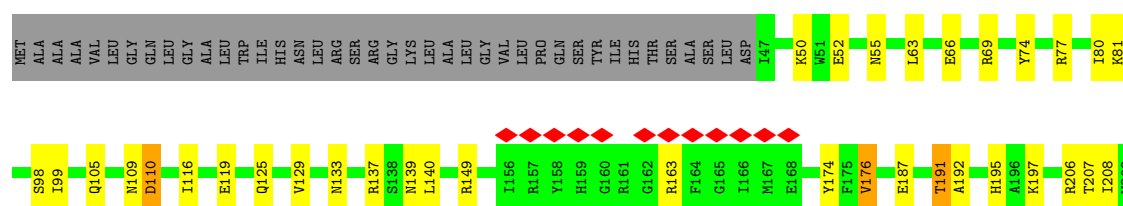
- Molecule 13: 39S ribosomal protein L21, mitochondrial

Chain S: 57% 17% 24%



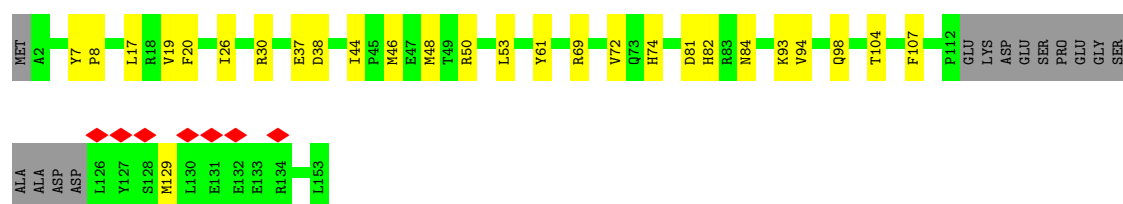
- Molecule 14: 39S ribosomal protein L22, mitochondrial

Chain T: 6% 63% 17% 19%



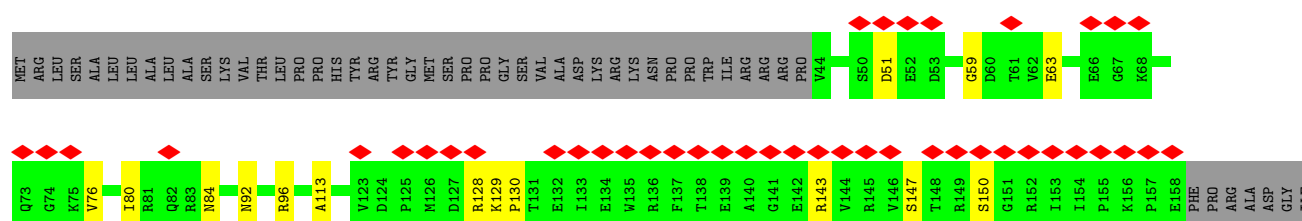
- Molecule 15: 39S ribosomal protein L23, mitochondrial

Chain U: 5% 73% 18% 9%



- Molecule 16: 39S ribosomal protein L24, mitochondrial

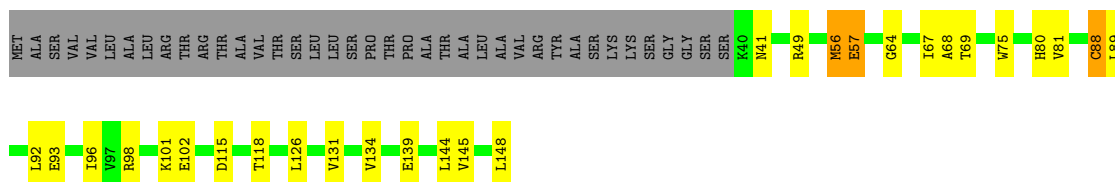
Chain V: 20% 63% 12% 25%





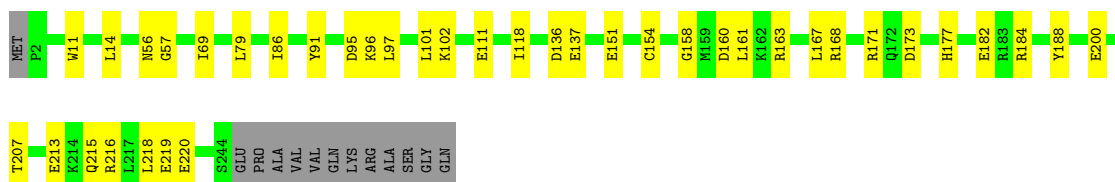
- Molecule 17: 39S ribosomal protein L27, mitochondrial

Chain W: 55% 17% 26%



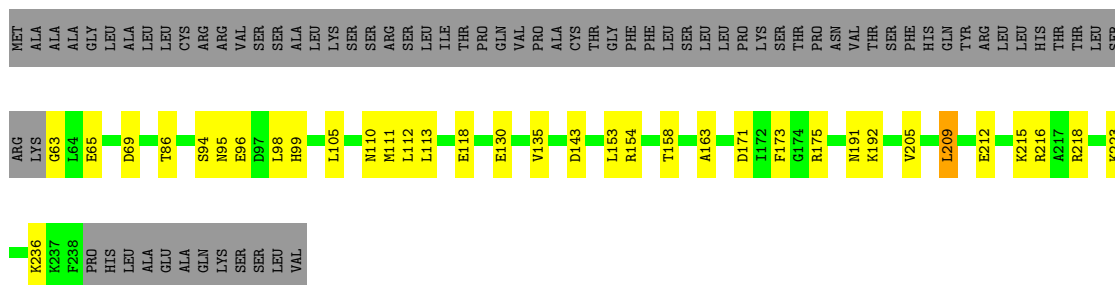
- Molecule 18: 39S ribosomal protein L28, mitochondrial

Chain X: 80% 15% 5%



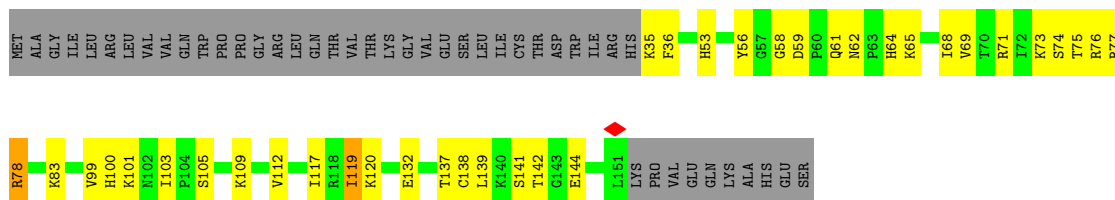
- Molecule 19: 39S ribosomal protein L47, mitochondrial

Chain Y: 56% 14% 30%



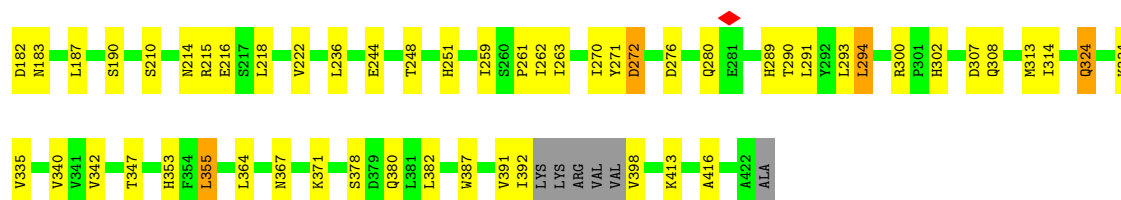
- Molecule 20: 39S ribosomal protein L30, mitochondrial

Chain Z: 50% 22% 27%

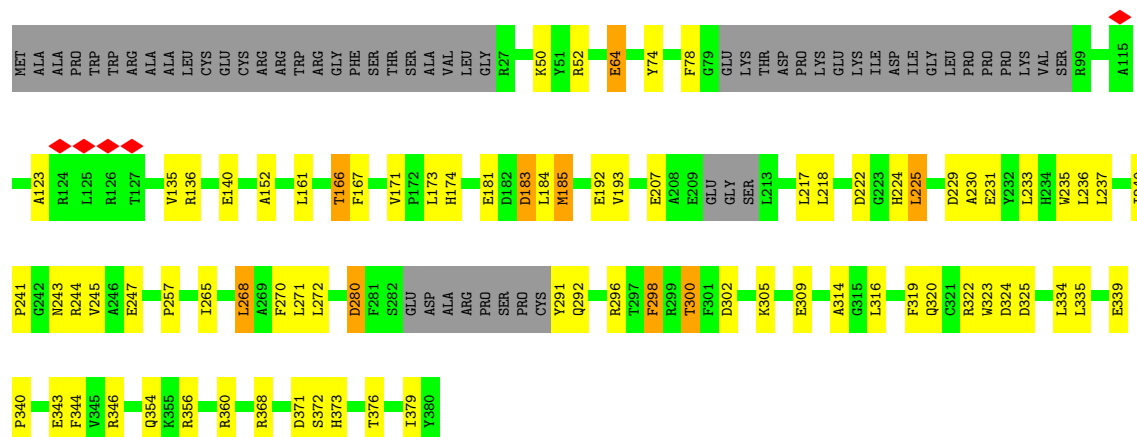


- Molecule 21: 39S ribosomal protein L32, mitochondrial

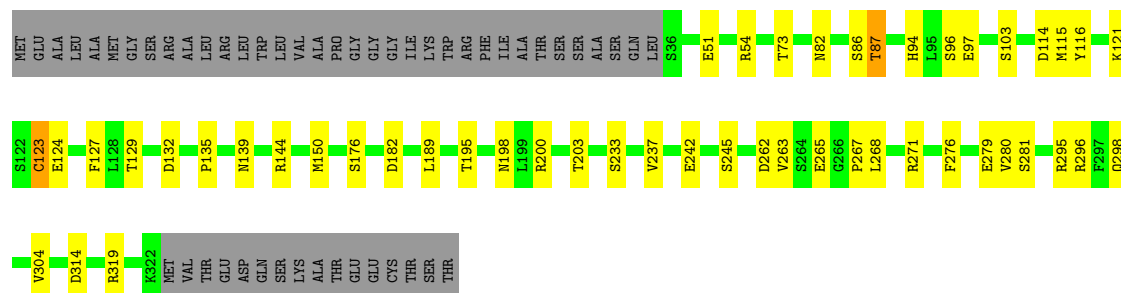
Chain 0: 41% 15% 43%



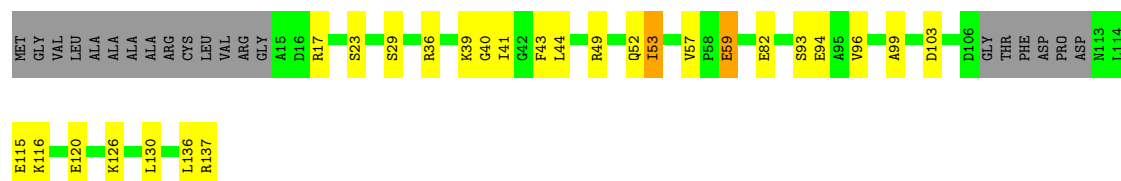
- Molecule 26: 39S ribosomal protein L38, mitochondrial



- Molecule 27: 39S ribosomal protein L39, mitochondrial

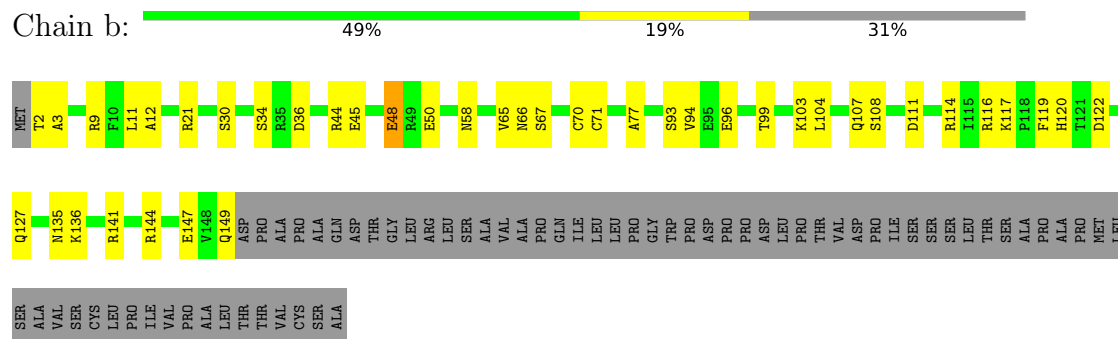


- Molecule 28: 39S ribosomal protein L41, mitochondrial

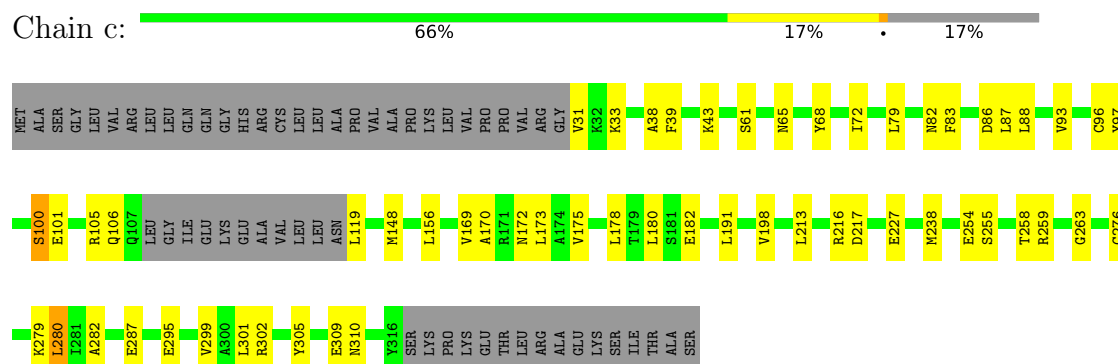


- Molecule 29: 39S ribosomal protein L42, mitochondrial

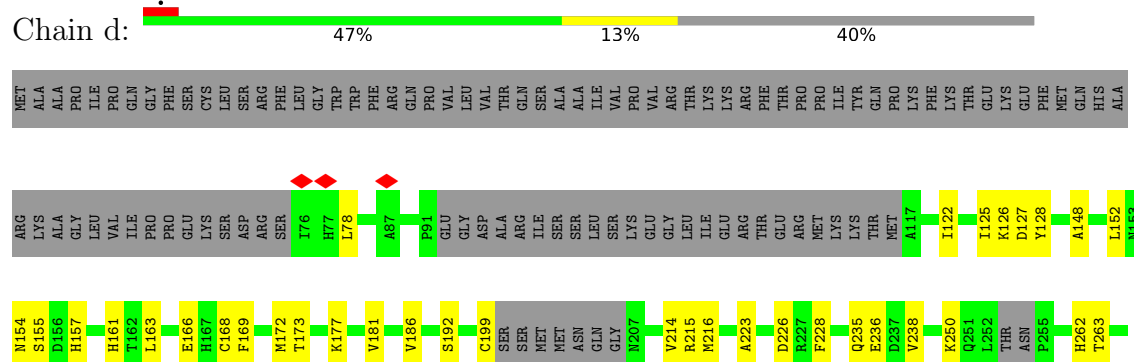
- Molecule 30: 39S ribosomal protein L43, mitochondrial



- Molecule 31: 39S ribosomal protein L44, mitochondrial

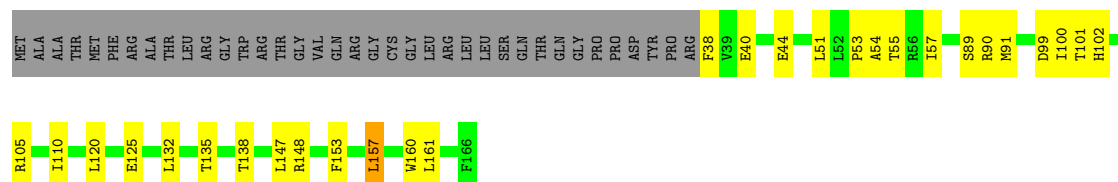


- Molecule 32: 39S ribosomal protein L45, mitochondrial

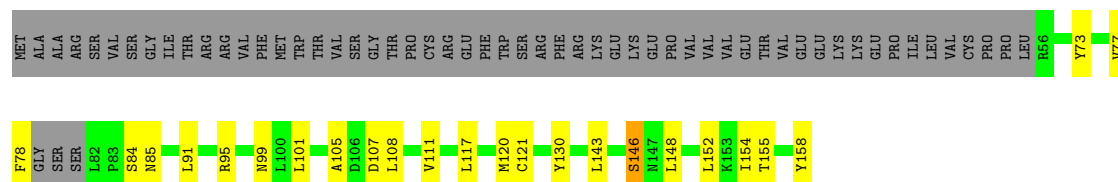




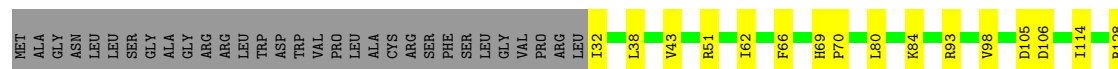
- Molecule 33: 39S ribosomal protein L49, mitochondrial



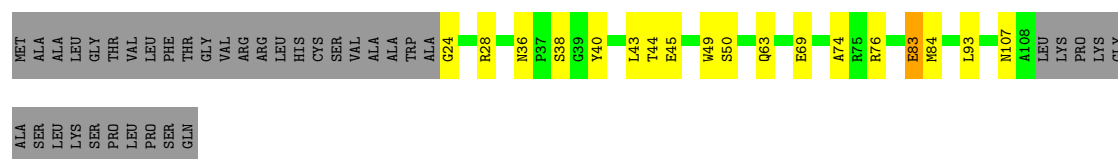
- Molecule 34: 39S ribosomal protein L50, mitochondrial

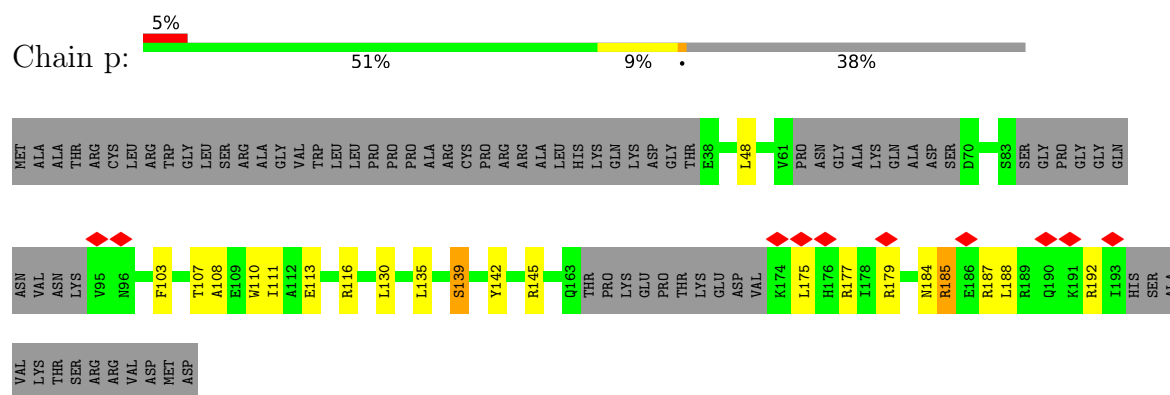


- Molecule 35: 39S ribosomal protein L51, mitochondrial

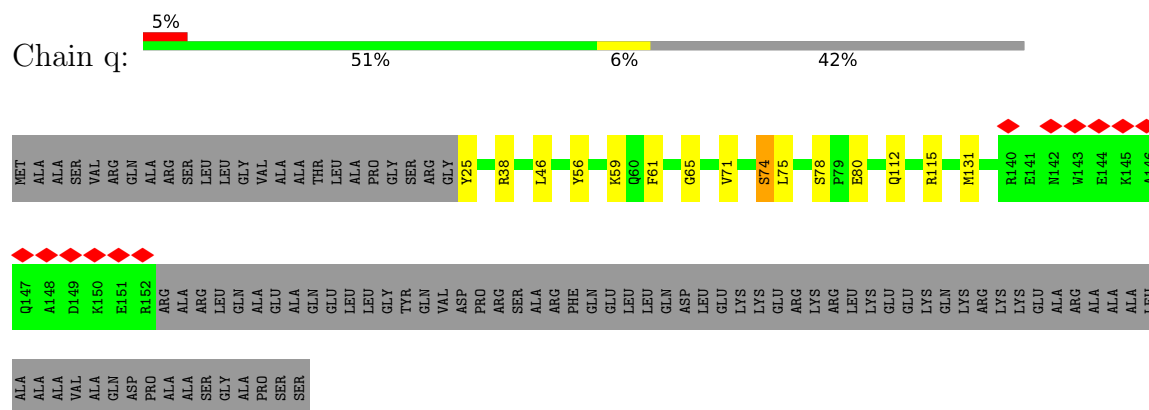


- Molecule 36: 39S ribosomal protein L52, mitochondrial

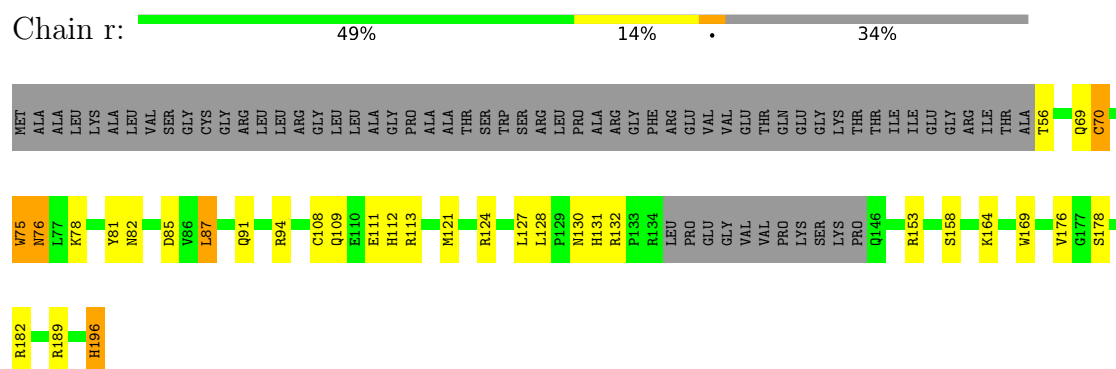




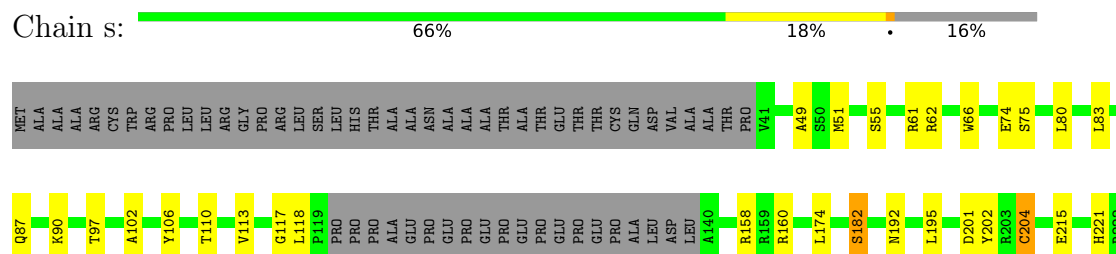
- Molecule 39: Growth arrest and DNA damage-inducible proteins-interacting protein 1



- Molecule 40: 39S ribosomal protein S18a, mitochondrial



- Molecule 41: 39S ribosomal protein S30, mitochondrial





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	119341	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	0.060	Depositor
Minimum map value	-0.020	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	381.59998, 381.59998, 381.59998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:
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	0.19	0/1371	0.41	0/1848
2	E	0.25	0/2313	0.43	0/3137
3	F	0.35	0/2071	0.47	0/2817
4	H	0.26	0/798	0.47	0/1073
5	K	0.31	0/1495	0.44	0/2029
6	L	0.20	0/904	0.47	0/1218
7	M	0.31	0/2359	0.50	0/3185
8	N	0.22	0/1697	0.42	0/2281
9	O	0.29	0/1269	0.47	0/1708
10	P	0.23	0/1173	0.47	0/1588
11	Q	0.22	0/1846	0.47	0/2487
12	R	0.35	0/1174	0.51	0/1572
13	S	0.32	0/1276	0.52	0/1729
14	T	0.30	0/1402	0.49	0/1886
15	U	0.27	0/1183	0.46	0/1600
16	V	0.17	0/1362	0.34	0/1842
17	W	0.31	0/881	0.50	0/1188
18	X	0.26	0/2090	0.45	0/2825
19	Y	0.30	0/1552	0.45	0/2079
20	Z	0.29	0/979	0.47	0/1321
21	0	0.27	0/895	0.46	0/1201
22	1	0.20	0/438	0.46	0/583
23	2	0.40	0/373	0.60	0/496
24	3	0.38	0/852	0.48	0/1136
25	5	0.20	0/3126	0.42	0/4259
26	6	0.25	0/2726	0.45	0/3715
27	7	0.22	0/2391	0.42	0/3234
28	9	0.27	0/972	0.46	0/1306
29	a	0.29	0/709	0.53	0/963
30	b	0.32	0/1202	0.50	0/1626
31	c	0.26	0/2264	0.42	0/3059
32	d	0.17	0/1573	0.39	0/2134

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.33	0/1102	0.52	0/1503
34	h	0.23	0/847	0.43	0/1150
35	i	0.38	0/849	0.50	0/1135
36	j	0.27	0/698	0.54	0/940
37	o	0.30	0/792	0.46	0/1064
38	p	0.20	0/1071	0.37	0/1433
39	q	0.24	0/1107	0.41	0/1498
40	r	0.24	0/1110	0.45	0/1504
41	s	0.25	0/3114	0.46	0/4225
42	u	0.16	0/949	0.33	0/1281
43	v	0.17	0/597	0.40	0/796
44	w	0.16	0/647	0.37	0/871
45	A	0.30	0/26912	0.39	0/41848
46	B	0.11	0/1328	0.25	0/2056
All	All	0.27	0/87839	0.43	0/124429

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
13	S	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	S	101	PHE	Peptide

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.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1349	0	1378	28	0
2	E	2249	0	2251	32	0
3	F	2013	0	2044	44	0
4	H	784	0	832	18	0
5	K	1451	0	1448	27	0
6	L	889	0	941	15	0
7	M	2305	0	2378	39	0
8	N	1654	0	1681	17	0
9	O	1245	0	1283	33	0
10	P	1148	0	1148	25	0
11	Q	1805	0	1841	32	0
12	R	1153	0	1214	30	0
13	S	1251	0	1322	28	0
14	T	1368	0	1410	24	0
15	U	1154	0	1154	21	0
16	V	1333	0	1337	15	0
17	W	859	0	888	21	0
18	X	2035	0	2054	20	0
19	Y	1517	0	1561	24	0
20	Z	955	0	1001	27	0
21	0	880	0	902	19	0
22	1	433	0	475	8	0
23	2	367	0	393	11	0
24	3	831	0	883	16	0
25	5	3037	0	3026	63	0
26	6	2640	0	2464	56	0
27	7	2334	0	2343	30	0
28	9	947	0	949	18	0
29	a	686	0	658	12	0
30	b	1178	0	1180	32	0
31	c	2217	0	2220	39	0
32	d	1529	0	1510	29	0
33	g	1067	0	1056	19	0
34	h	827	0	806	13	0
35	i	827	0	857	16	0
36	j	684	0	673	16	0
37	o	771	0	775	16	0
38	p	1058	0	1083	13	0
39	q	1076	0	1049	9	0
40	r	1075	0	1090	24	0
41	s	3036	0	3022	51	0
42	u	927	0	921	18	0
43	v	588	0	604	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	w	638	0	637	7	0
45	A	24063	0	12238	221	0
46	B	1191	0	607	6	0
47	0	1	0	0	0	0
All	All	83425	0	71587	1029	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 7.

The worst 5 of 1029 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)
3:F:234:THR:O	39:q:25:TYR:N	2.10	0.84
18:X:96:LYS:O	45:A:1728:U:O2'	1.95	0.83
9:O:41:ARG:NH2	21:0:134:THR:OG1	2.11	0.83
27:7:135:PRO:O	27:7:139:ASN:ND2	2.11	0.83
9:O:37:VAL:HG21	9:O:80:LEU:HD22	1.62	0.82

There are no symmetry-related clashes.

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	172/305 (56%)	158 (92%)	14 (8%)	0	100	100
2	E	280/348 (80%)	262 (94%)	18 (6%)	0	100	100
3	F	248/311 (80%)	230 (93%)	18 (7%)	0	100	100
4	H	93/267 (35%)	86 (92%)	7 (8%)	0	100	100
5	K	175/178 (98%)	161 (92%)	14 (8%)	0	100	100
6	L	113/145 (78%)	105 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	M	285/296 (96%)	265 (93%)	20 (7%)	0	100	100
8	N	203/251 (81%)	189 (93%)	14 (7%)	0	100	100
9	O	150/175 (86%)	142 (95%)	8 (5%)	0	100	100
10	P	139/180 (77%)	132 (95%)	7 (5%)	0	100	100
11	Q	215/292 (74%)	198 (92%)	17 (8%)	0	100	100
12	R	138/149 (93%)	128 (93%)	10 (7%)	0	100	100
13	S	154/205 (75%)	144 (94%)	10 (6%)	0	100	100
14	T	164/206 (80%)	152 (93%)	12 (7%)	0	100	100
15	U	135/153 (88%)	128 (95%)	7 (5%)	0	100	100
16	V	159/216 (74%)	150 (94%)	9 (6%)	0	100	100
17	W	107/148 (72%)	100 (94%)	7 (6%)	0	100	100
18	X	241/256 (94%)	229 (95%)	12 (5%)	0	100	100
19	Y	174/250 (70%)	165 (95%)	9 (5%)	0	100	100
20	Z	115/161 (71%)	107 (93%)	8 (7%)	0	100	100
21	0	106/188 (56%)	102 (96%)	4 (4%)	0	100	100
22	1	50/65 (77%)	45 (90%)	5 (10%)	0	100	100
23	2	43/92 (47%)	36 (84%)	7 (16%)	0	100	100
24	3	93/188 (50%)	89 (96%)	4 (4%)	0	100	100
25	5	369/423 (87%)	342 (93%)	27 (7%)	0	100	100
26	6	316/380 (83%)	290 (92%)	26 (8%)	0	100	100
27	7	285/338 (84%)	262 (92%)	23 (8%)	0	100	100
28	9	113/137 (82%)	107 (95%)	6 (5%)	0	100	100
29	a	78/142 (55%)	72 (92%)	6 (8%)	0	100	100
30	b	146/215 (68%)	132 (90%)	14 (10%)	0	100	100
31	c	271/332 (82%)	258 (95%)	13 (5%)	0	100	100
32	d	177/306 (58%)	166 (94%)	11 (6%)	0	100	100
33	g	127/166 (76%)	120 (94%)	7 (6%)	0	100	100
34	h	96/158 (61%)	90 (94%)	6 (6%)	0	100	100
35	i	95/128 (74%)	85 (90%)	10 (10%)	0	100	100
36	j	83/123 (68%)	79 (95%)	4 (5%)	0	100	100
37	o	89/102 (87%)	81 (91%)	8 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	p	119/206 (58%)	112 (94%)	7 (6%)	0	100	100
39	q	126/222 (57%)	119 (94%)	7 (6%)	0	100	100
40	r	126/196 (64%)	118 (94%)	8 (6%)	0	100	100
41	s	366/439 (83%)	340 (93%)	26 (7%)	0	100	100
42	u	109/234 (47%)	98 (90%)	11 (10%)	0	100	100
43	v	67/70 (96%)	62 (92%)	5 (8%)	0	100	100
44	w	77/156 (49%)	67 (87%)	10 (13%)	0	100	100
All	All	6987/9498 (74%)	6503 (93%)	484 (7%)	0	100	100

There are no Ramachandran outliers to report.

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	140/245 (57%)	139 (99%)	1 (1%)	76	80
2	E	245/290 (84%)	236 (96%)	9 (4%)	30	58
3	F	217/262 (83%)	205 (94%)	12 (6%)	19	47
4	H	86/228 (38%)	79 (92%)	7 (8%)	11	34
5	K	155/156 (99%)	152 (98%)	3 (2%)	50	70
6	L	98/124 (79%)	94 (96%)	4 (4%)	27	56
7	M	245/249 (98%)	238 (97%)	7 (3%)	37	63
8	N	172/211 (82%)	167 (97%)	5 (3%)	37	63
9	O	133/150 (89%)	125 (94%)	8 (6%)	17	45
10	P	123/155 (79%)	116 (94%)	7 (6%)	18	46
11	Q	199/256 (78%)	195 (98%)	4 (2%)	48	69
12	R	118/126 (94%)	116 (98%)	2 (2%)	53	71
13	S	141/180 (78%)	131 (93%)	10 (7%)	13	39
14	T	146/176 (83%)	135 (92%)	11 (8%)	12	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	U	124/135 (92%)	120 (97%)	4 (3%)	34	61
16	V	146/191 (76%)	143 (98%)	3 (2%)	47	68
17	W	89/119 (75%)	83 (93%)	6 (7%)	15	41
18	X	219/229 (96%)	207 (94%)	12 (6%)	19	47
19	Y	159/223 (71%)	152 (96%)	7 (4%)	25	54
20	Z	108/147 (74%)	99 (92%)	9 (8%)	10	33
21	0	97/164 (59%)	89 (92%)	8 (8%)	10	34
22	1	49/60 (82%)	49 (100%)	0	100	100
23	2	39/72 (54%)	36 (92%)	3 (8%)	12	36
24	3	88/166 (53%)	83 (94%)	5 (6%)	18	46
25	5	335/368 (91%)	323 (96%)	12 (4%)	31	58
26	6	265/332 (80%)	245 (92%)	20 (8%)	12	37
27	7	263/303 (87%)	258 (98%)	5 (2%)	50	70
28	9	99/112 (88%)	93 (94%)	6 (6%)	17	44
29	a	78/133 (59%)	72 (92%)	6 (8%)	12	36
30	b	130/186 (70%)	123 (95%)	7 (5%)	20	48
31	c	241/288 (84%)	230 (95%)	11 (5%)	24	53
32	d	170/274 (62%)	168 (99%)	2 (1%)	63	75
33	g	119/148 (80%)	114 (96%)	5 (4%)	26	55
34	h	95/148 (64%)	91 (96%)	4 (4%)	26	55
35	i	86/110 (78%)	82 (95%)	4 (5%)	23	52
36	j	68/97 (70%)	66 (97%)	2 (3%)	37	63
37	o	78/87 (90%)	73 (94%)	5 (6%)	16	42
38	p	117/181 (65%)	109 (93%)	8 (7%)	14	40
39	q	110/178 (62%)	108 (98%)	2 (2%)	51	70
40	r	119/169 (70%)	113 (95%)	6 (5%)	22	50
41	s	326/381 (86%)	313 (96%)	13 (4%)	28	56
42	u	105/200 (52%)	103 (98%)	2 (2%)	50	70
43	v	59/60 (98%)	58 (98%)	1 (2%)	53	71
44	w	73/136 (54%)	72 (99%)	1 (1%)	59	73
All	All	6272/8205 (76%)	6003 (96%)	269 (4%)	27	55

5 of 269 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	o	28	SER
38	p	130	LEU
41	s	243	ILE
17	W	56	MET
16	V	194	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
38	p	184	ASN
40	r	76	ASN
41	s	300	HIS
19	Y	89	GLN
18	X	241	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	A	1113/1559 (71%)	358 (32%)	15 (1%)
46	B	51/69 (73%)	13 (25%)	0
All	All	1164/1628 (71%)	371 (31%)	15 (1%)

5 of 371 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	A	1679	U
45	A	1680	A
45	A	1681	G
45	A	1685	C
45	A	1689	C

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
45	A	2653	C
45	A	3130	A
45	A	2905	A
45	A	3168	C
45	A	3117	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 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

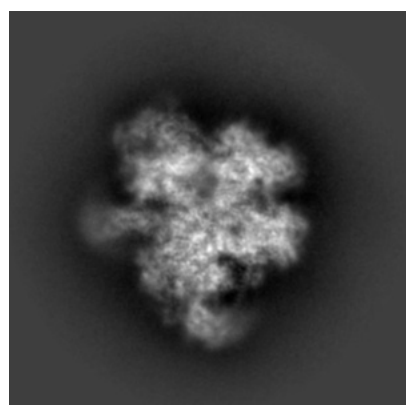
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13965. These allow visual inspection of the internal detail of the map and identification of artifacts.

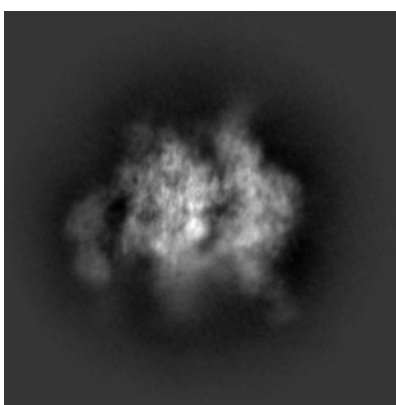
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

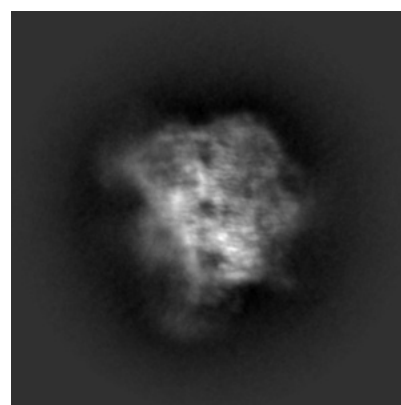
6.1.1 Primary map



X



Y

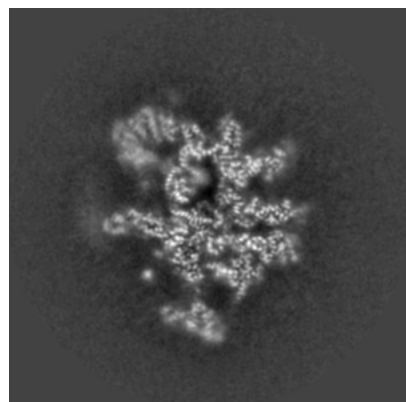


Z

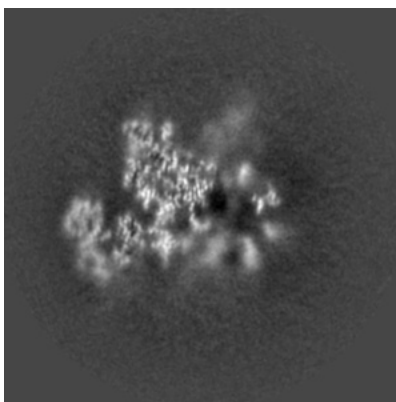
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

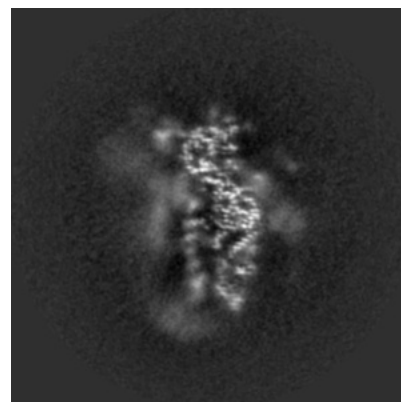
6.2.1 Primary map



X Index: 180



Y Index: 180

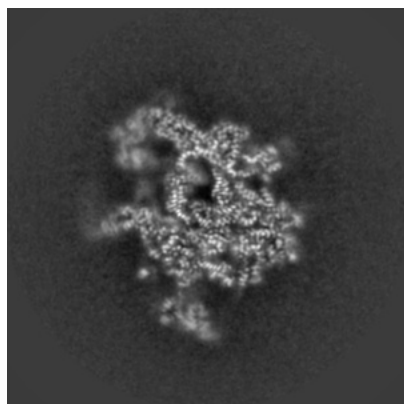


Z Index: 180

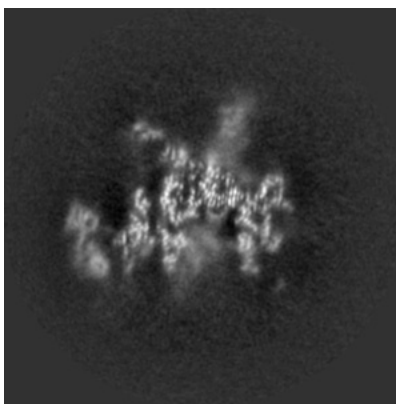
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

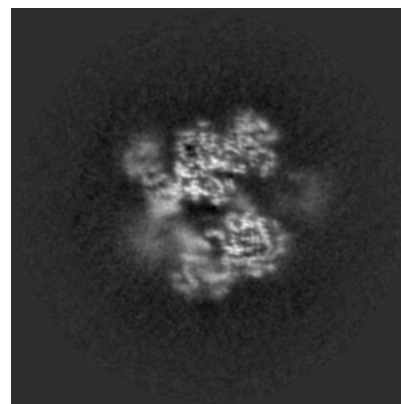
6.3.1 Primary map



X Index: 186



Y Index: 191

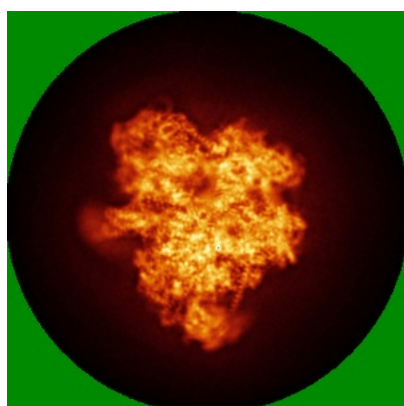


Z Index: 221

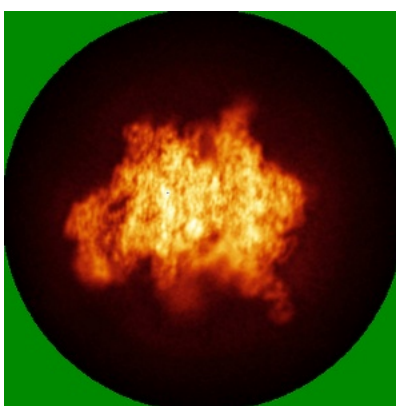
The images above show the largest variance slices of the map in three orthogonal directions.

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

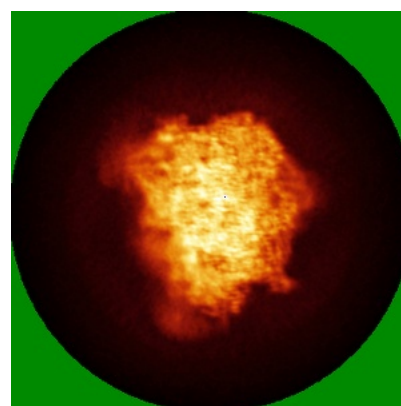
6.4.1 Primary map



X



Y

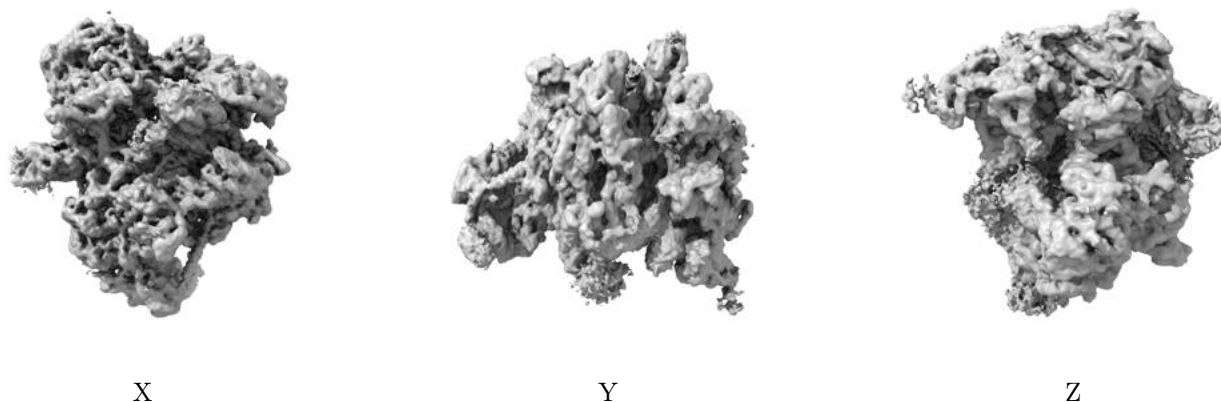


Z

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.

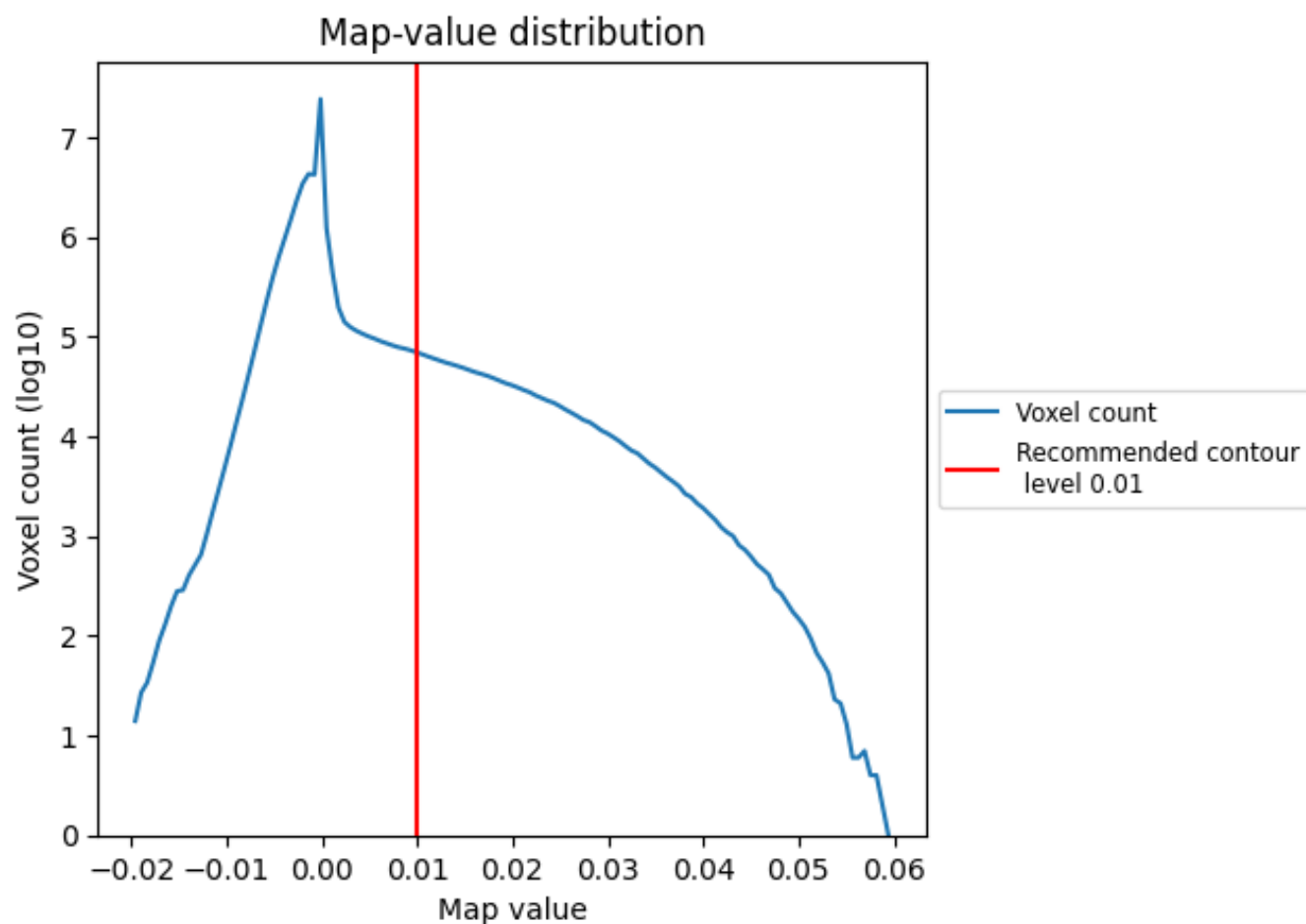
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

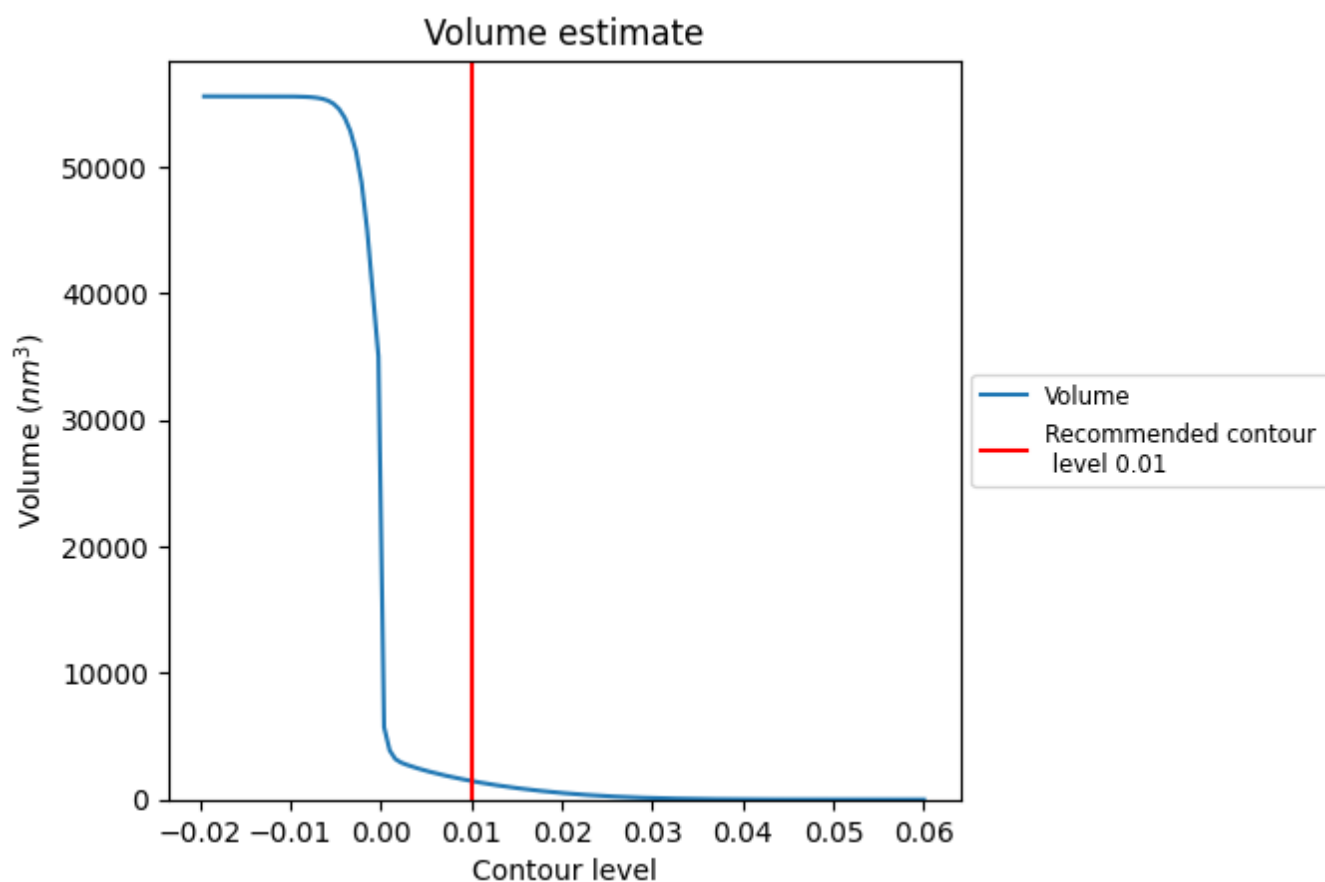
This section contains the results of statistical analysis of the map.

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.

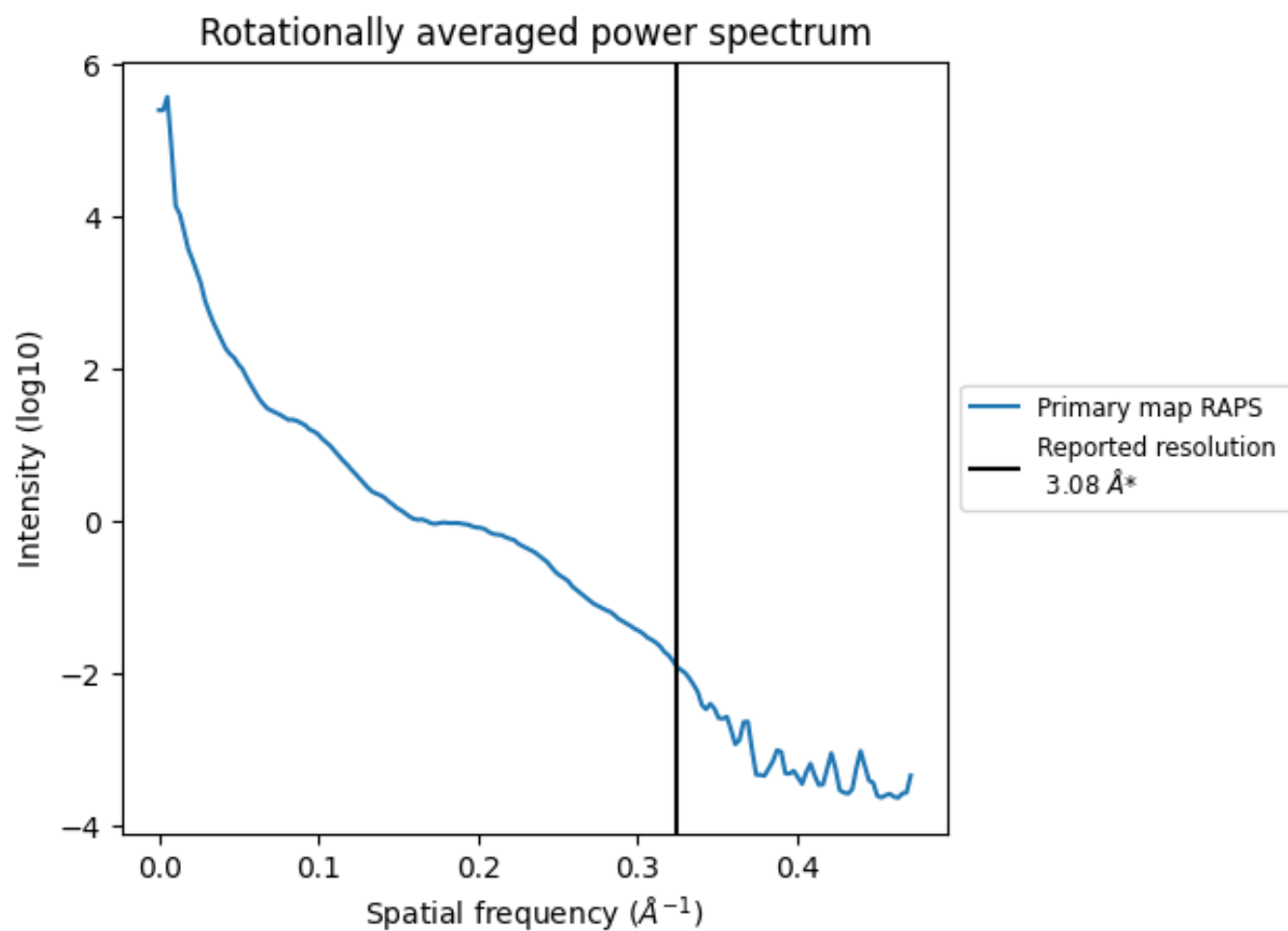
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1470 nm^3 ; this corresponds to an approximate mass of 1328 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 ⓘ

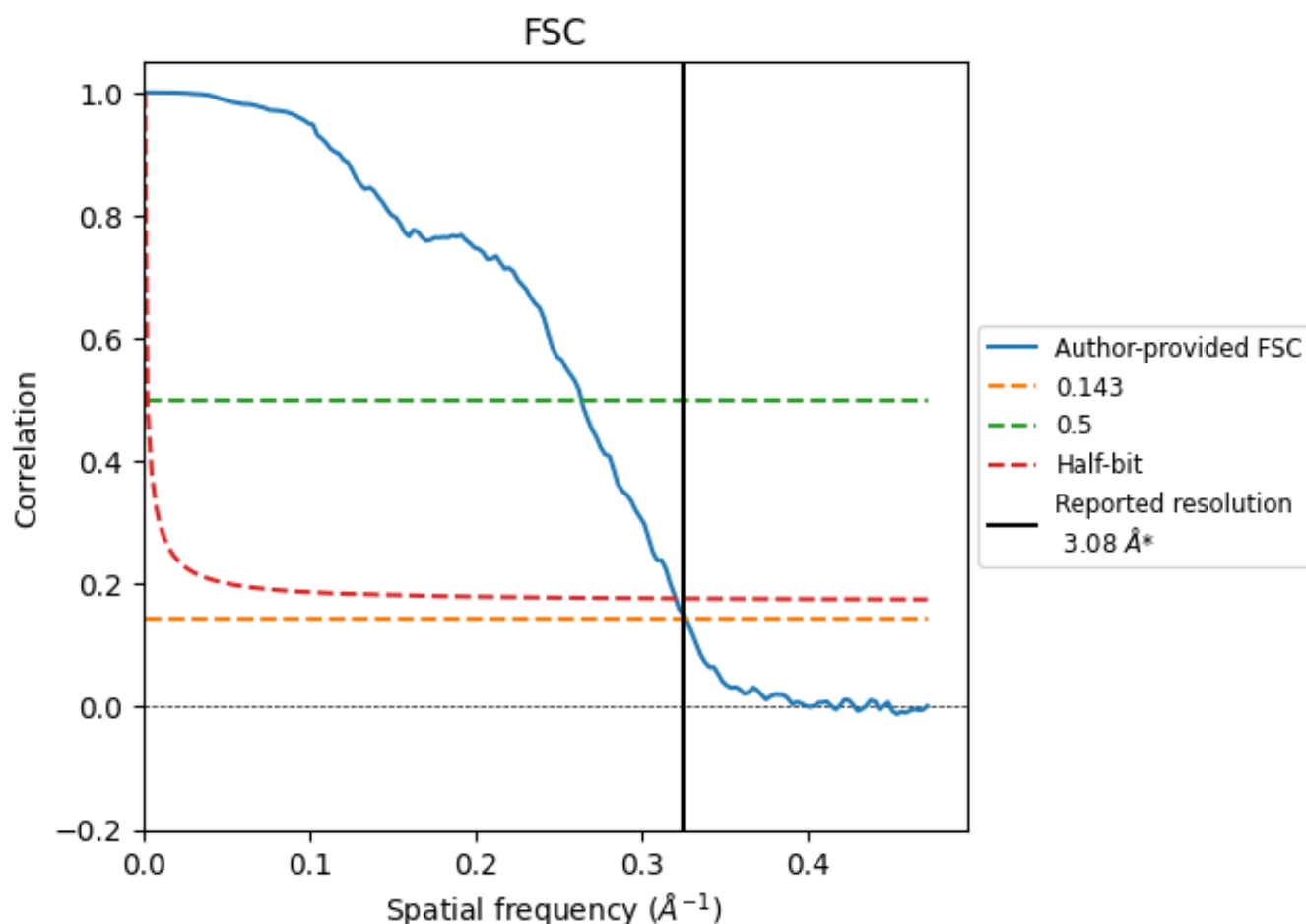


*Reported resolution corresponds to spatial frequency of 0.325 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.325 Å⁻¹

8.2 Resolution estimates [i](#)

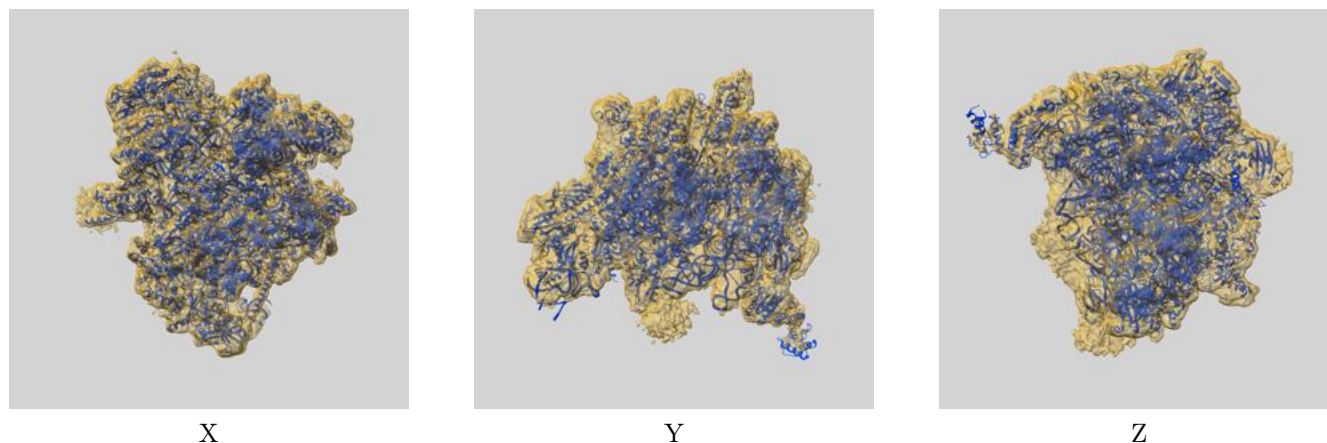
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.08	-	-
Author-provided FSC curve	3.06	3.79	3.12
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

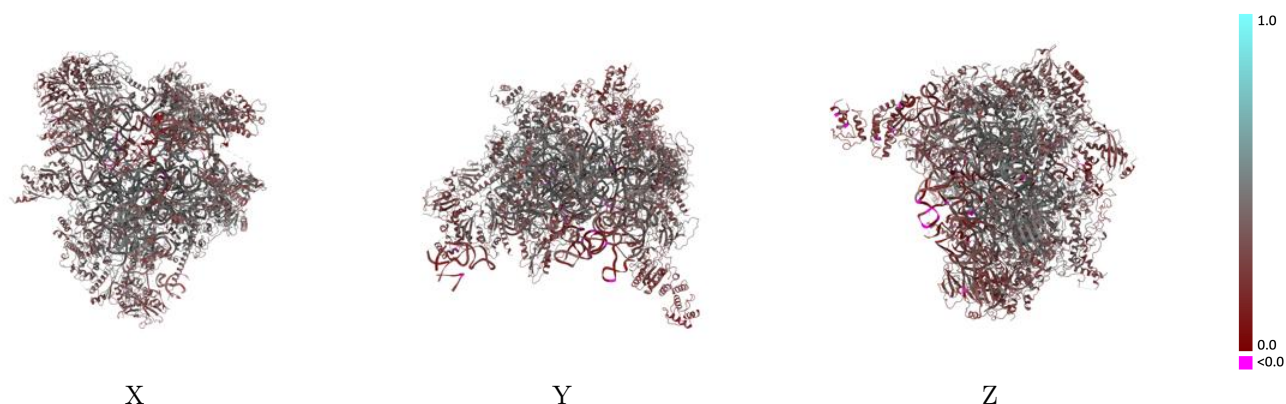
This section contains information regarding the fit between EMDB map EMD-13965 and PDB model 7QH6. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



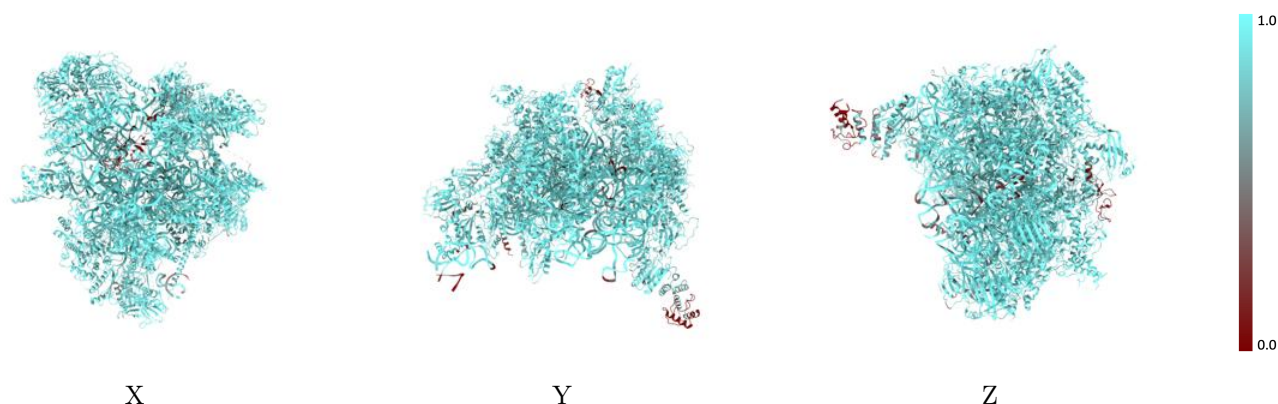
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



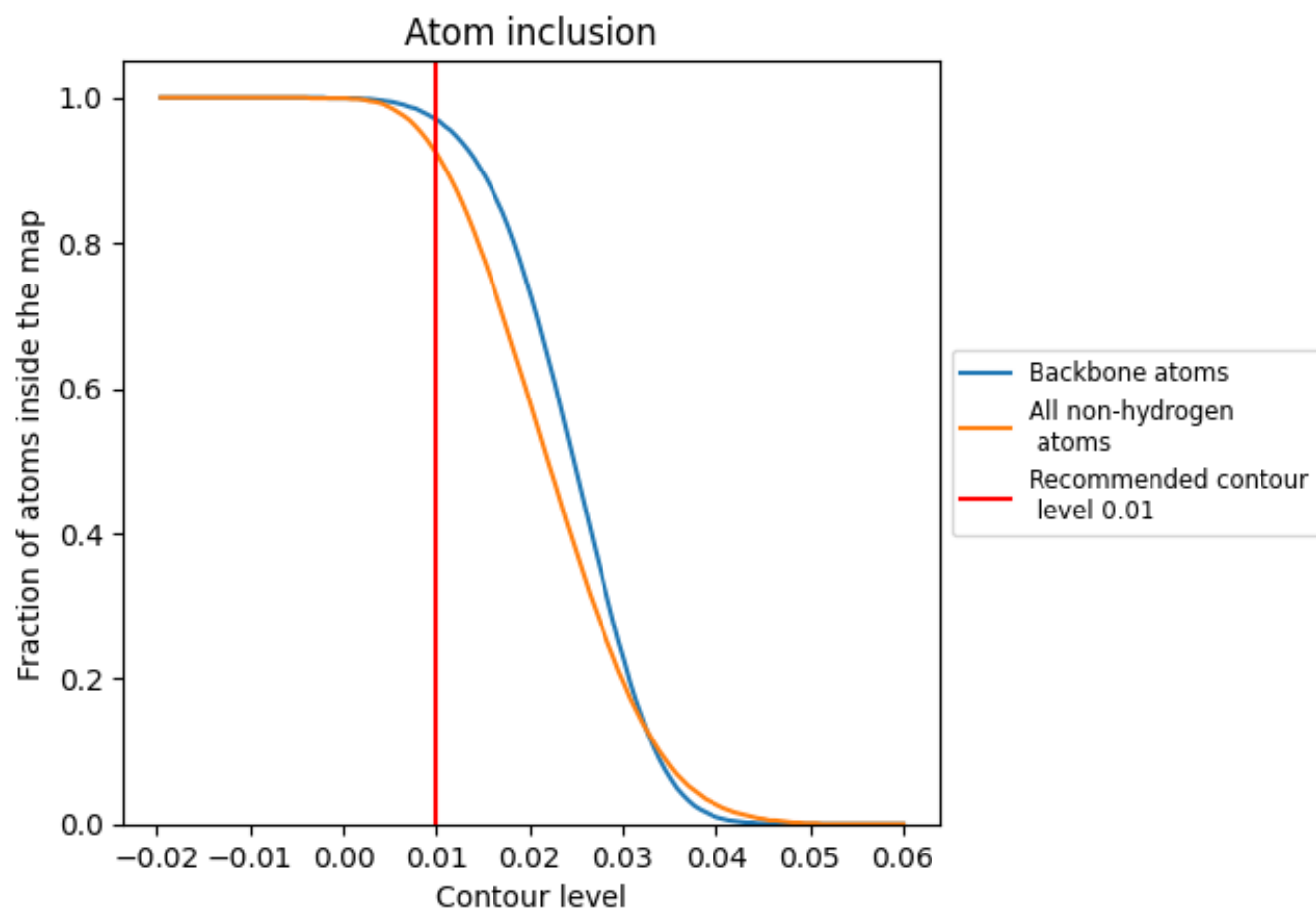
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 97% of all backbone atoms, 92% 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	 0.9240	 0.3740
0	 0.9370	 0.3980
1	 0.9290	 0.2150
2	 0.9430	 0.4390
3	 0.9370	 0.4640
5	 0.9170	 0.3150
6	 0.9370	 0.3440
7	 0.9400	 0.3480
9	 0.9450	 0.3830
A	 0.9680	 0.3810
B	 0.7940	 0.2040
D	 0.8890	 0.2740
E	 0.9460	 0.3950
F	 0.9210	 0.4450
H	 0.9160	 0.3710
K	 0.9420	 0.4230
L	 0.9270	 0.3380
M	 0.9310	 0.4290
N	 0.9270	 0.3690
O	 0.9440	 0.4180
P	 0.9450	 0.3540
Q	 0.8990	 0.3710
R	 0.9070	 0.4310
S	 0.9340	 0.4330
T	 0.8600	 0.3980
U	 0.8950	 0.3940
V	 0.6720	 0.2610
W	 0.9540	 0.4380
X	 0.9210	 0.3890
Y	 0.9560	 0.3990
Z	 0.9050	 0.4340
a	 0.9100	 0.4070
b	 0.9720	 0.4450
c	 0.9480	 0.3890
d	 0.8900	 0.2920



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Chain	Atom inclusion	Q-score
g	 0.9650	 0.4300
h	 0.9430	 0.3700
i	 0.9590	 0.4550
j	 0.9110	 0.4070
o	 0.9120	 0.3760
p	 0.8080	 0.3460
q	 0.8080	 0.3250
r	 0.9610	 0.3730
s	 0.9360	 0.3940
u	 0.9150	 0.2750
v	 0.6880	 0.2350
w	 0.1750	 0.1840