wwPDB EM Validation Summary Report (i)

Oct 12, 2021 – 10:10 am BST

PDB ID	:	7OIB
EMDB ID	:	EMD-12924
Title	:	Cryo-EM structure of late human 39S mitoribosome assembly intermediates, state 3D
Authors	:	Cheng, J.; Berninghausen, O.; Beckmann, R.
Deposited on	:	2021-05-11
Resolution	:	3.30 Å(reported)

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 (i) symbol.

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

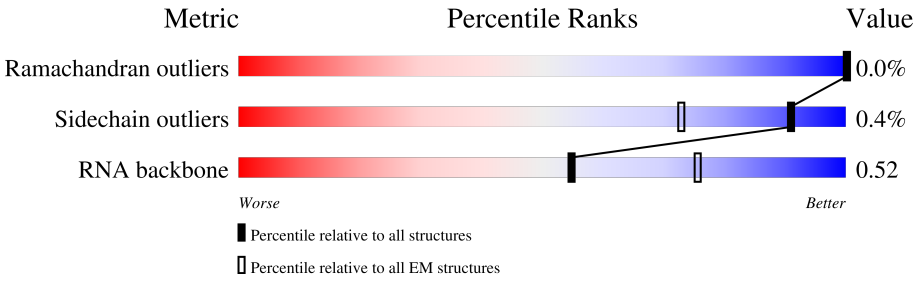
EMDB validation analysis	:	0.0.0.dev97
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 3.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=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 <=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	72% 28%
2	E	348	82% 18%
3	F	311	80% 20%
4	H	267	36% 64%
5	I	261	38% 59% 39%
6	J	192	69% 72% 27%
7	K	178	99%
8	L	145	79% 21%

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Mol	Chain	Length	Quality of chain
9	M	296	95%
10	N	251	80% 18%
11	O	175	86% 13%
12	P	180	77% 22%
13	Q	292	74% 26%
14	R	149	93% 6%
15	S	205	76% 24%
16	T	206	77% 23%
17	U	153	91% 9%
18	V	216	88% 11%
19	W	148	74% 26%
20	X	256	94% 5%
21	Y	250	70% 30%
22	Z	161	75% 25%
23	0	188	57% 43%
24	1	65	78% 20%
25	2	92	47% 53%
26	3	188	51% 49%
27	5	423	91% 9%
28	6	380	84% 15%
29	7	338	85% 15%
30	8	206	10% 46% 52%
31	9	137	85% 15%
32	a	142	58% 42%
33	b	215	69% 31%

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Mol	Chain	Length	Quality of chain
34	c	332	83% 17%
35	d	306	8% 68% 31%
36	e	279	29% 77% 22%
37	f	212	12% 54% 45%
38	g	166	78% 22%
39	h	158	63% 37%
40	i	128	76% 24%
41	j	123	69% 31%
42	k	112	21% 71% 29%
43	l	138	17% 83%
44	m	128	12% 34% 65%
45	o	102	77% 23%
46	p	206	62% 38%
47	q	222	54% 46%
48	r	196	74% 26%
49	s	439	84% 16%
50	A	1559	52% 17% 30%
51	B	69	57% 23% 19%

2 Entry composition (i)

There are 53 unique types of molecules in this entry. The entry contains 88360 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	220	Total	C	N	O	S	0	0
			1706	1059	339	299	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	285	Total	C	N	O	S	0	0
			2258	1457	384	406	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 L10, mitochondrial.

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

- Molecule 6 is a protein called 39S ribosomal protein L11, mitochondrial.

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

- Molecule 7 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 8 is a protein called 39S ribosomal protein L14, mitochondrial.

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

- Molecule 9 is a protein called 39S ribosomal protein L15, mitochondrial.

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

- Molecule 10 is a protein called 39S ribosomal protein L16, mitochondrial.

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

- Molecule 11 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 12 is a protein called 39S ribosomal protein L18, mitochondrial.

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

- Molecule 13 is a protein called 39S ribosomal protein L19, mitochondrial.

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

- Molecule 14 is a protein called 39S ribosomal protein L20, mitochondrial.

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

- Molecule 15 is a protein called 39S ribosomal protein L21, mitochondrial.

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

- Molecule 16 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	159	Total	C	N	O	S	0	0
			1305	835	239	224	7		

- Molecule 17 is a protein called 39S ribosomal protein L23, mitochondrial.

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

- Molecule 18 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	192	Total	C	N	O	S	0	0
			1575	1003	281	283	8		

- Molecule 19 is a protein called 39S ribosomal protein L27, mitochondrial.

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

- Molecule 20 is a protein called 39S ribosomal protein L28, mitochondrial.

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

- Molecule 21 is a protein called 39S ribosomal protein L47, mitochondrial.

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

- Molecule 22 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Z	120	Total	C	N	O	S	0	0
			978	626	183	166	3		

- Molecule 23 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	0	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 24 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	1	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

- Molecule 25 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	2	43	Total	C	N	O	S	0	0
			351	218	76	56	1		

- Molecule 26 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 27 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	5	387	Total	C	N	O	S	0	0
			3156	2039	548	558	11		

- Molecule 28 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	6	324	Total	C	N	O	S	0	0
			2640	1694	470	468	8		

- Molecule 29 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	7	287	Total	C	N	O	S	0	0
			2334	1495	397	425	17		

- Molecule 30 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	8	99	Total	C	N	O	S	0	0
			836	535	144	155	2		

- Molecule 31 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	9	117	Total	C	N	O	S	0	0
			947	614	163	168	2		

- Molecule 32 is a protein called 39S ribosomal protein L42, mitochondrial.

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

- Molecule 33 is a protein called 39S ribosomal protein L43, mitochondrial.

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

- Molecule 34 is a protein called 39S ribosomal protein L44, mitochondrial.

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

- Molecule 35 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	211	Total	C	N	O	S	0	0
			1741	1123	299	309	10		

- Molecule 36 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	217	Total	C	N	O	S	0	0
			1762	1124	310	323	5		

- Molecule 37 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	116	Total	C	N	O	S	0	0
			915	585	152	175	3		

- Molecule 38 is a protein called 39S ribosomal protein L49, mitochondrial.

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

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

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

- Molecule 40 is a protein called 39S ribosomal protein L51, mitochondrial.

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

- Molecule 41 is a protein called 39S ribosomal protein L52, mitochondrial.

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

- Molecule 42 is a protein called 39S ribosomal protein L53, mitochondrial.

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

- Molecule 43 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	l	23	Total	C	N	O	0	0
			221	137	52	32		

- Molecule 44 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	m	45	Total	C	N	O	S	0	0
			372	232	76	62	2		

- Molecule 45 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	79	Total	C	N	O	S	0	0
			665	420	130	112	3		

- Molecule 46 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

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

- Molecule 47 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	120	Total	C	N	O	S	0	0
			1011	633	194	179	5		

- Molecule 48 is a protein called 39S ribosomal protein S18a, mitochondrial.

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

- Molecule 49 is a protein called 39S ribosomal protein S30, mitochondrial.

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

- Molecule 50 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	A	1092	Total	C	N	O	P	0	0
			23184	10409	4202	7481	1092		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1437	U	UNK	conflict	GB 1025814679

- Molecule 51 is a RNA chain called mitochondrial Val tRNA.

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

- Molecule 52 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
52	W	1	Total	Mg	0
			1	1	
52	g	1	Total	Mg	0
			1	1	
52	A	47	Total	Mg	0
			47	47	

- Molecule 53 is ZINC ION (three-letter code: ZN) (formula: Zn).

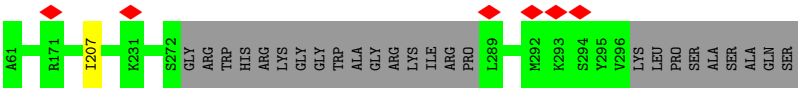
Mol	Chain	Residues	Atoms		AltConf
53	0	1	Total	Zn	0
			1	1	
53	r	1	Total	Zn	0
			1	1	

3 Residue-property plots (i)

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

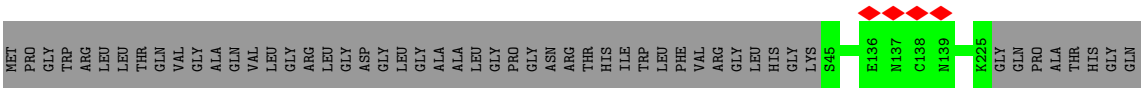
• Molecule 1: 39S ribosomal protein L2, mitochondrial

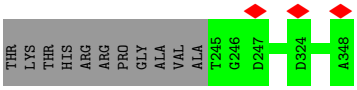
Chain D:



• Molecule 2: 39S ribosomal protein L3, mitochondrial

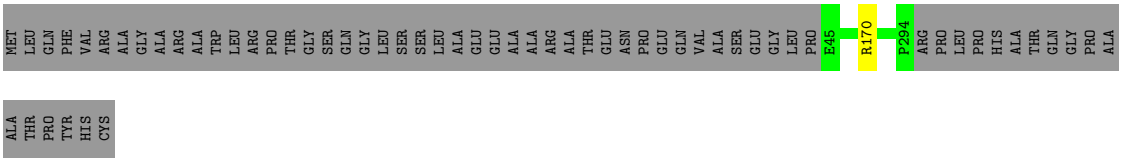
Chain E:





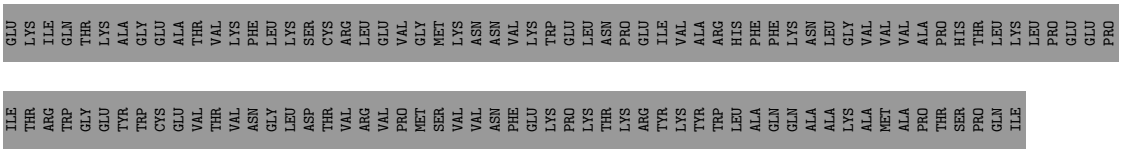
• Molecule 3: 39S ribosomal protein L4, mitochondrial

Chain F:



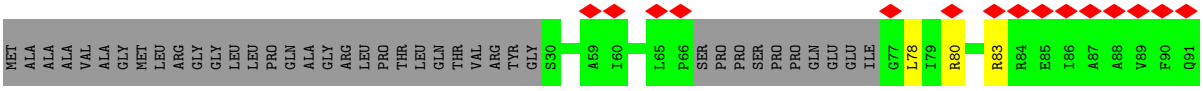
• Molecule 4: 39S ribosomal protein L9, mitochondrial

Chain H:



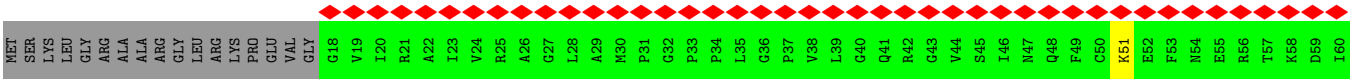
• Molecule 5: 39S ribosomal protein L10, mitochondrial

Chain I:



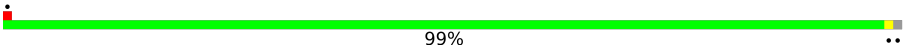
• Molecule 6: 39S ribosomal protein L11, mitochondrial

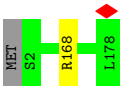
Chain J:



• Molecule 7: 39S ribosomal protein L13, mitochondrial

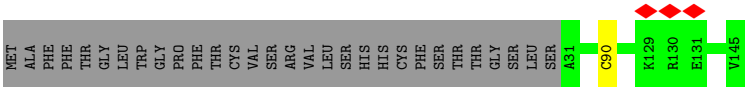
Chain K:





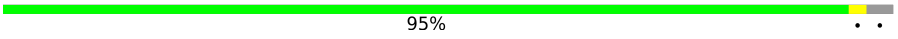
• Molecule 8: 39S ribosomal protein L14, mitochondrial

Chain L:



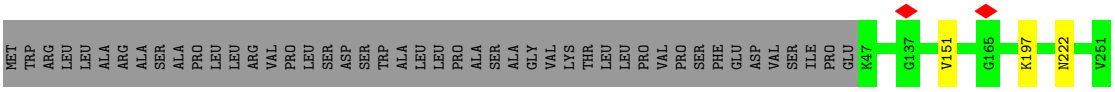
• Molecule 9: 39S ribosomal protein L15, mitochondrial

Chain M:



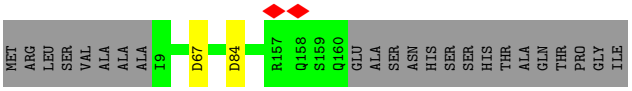
• Molecule 10: 39S ribosomal protein L16, mitochondrial

Chain N:



• Molecule 11: 39S ribosomal protein L17, mitochondrial

Chain O:

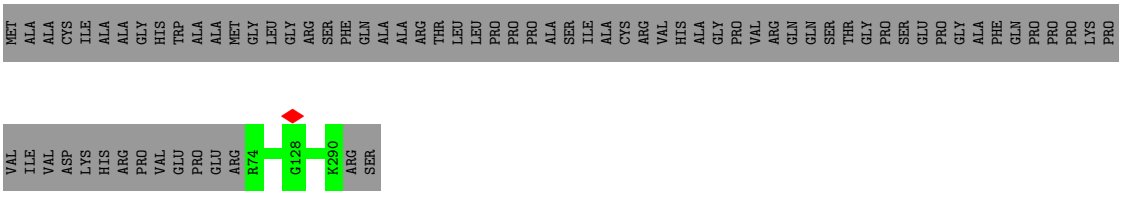


• Molecule 12: 39S ribosomal protein L18, mitochondrial

Chain P:

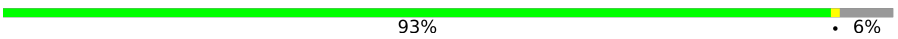
• Molecule 13: 39S ribosomal protein L19, mitochondrial

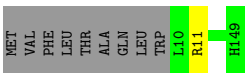
Chain Q:



• Molecule 14: 39S ribosomal protein L20, mitochondrial

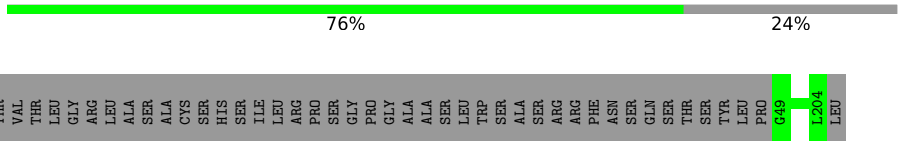
Chain R:





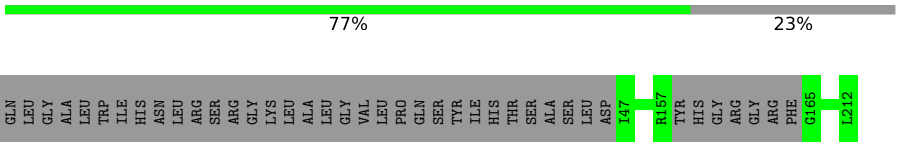
• Molecule 15: 39S ribosomal protein L21, mitochondrial

Chain S:



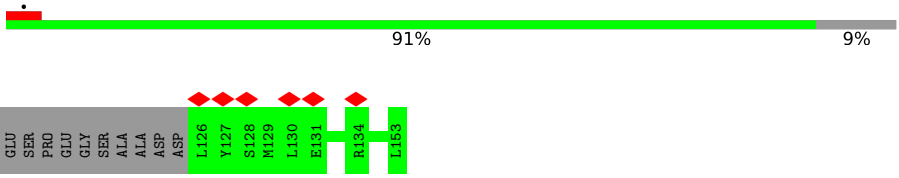
• Molecule 16: 39S ribosomal protein L22, mitochondrial

Chain T:



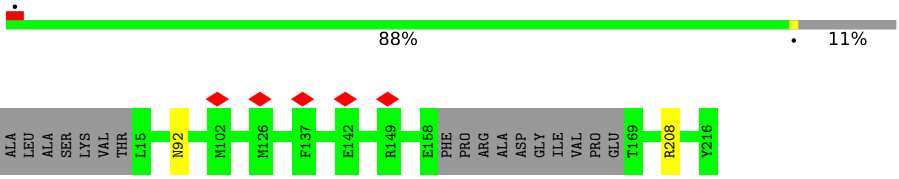
• Molecule 17: 39S ribosomal protein L23, mitochondrial

Chain U:



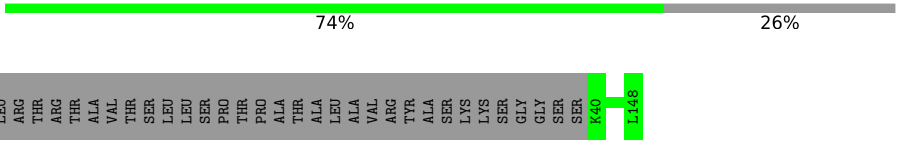
• Molecule 18: 39S ribosomal protein L24, mitochondrial

Chain V:



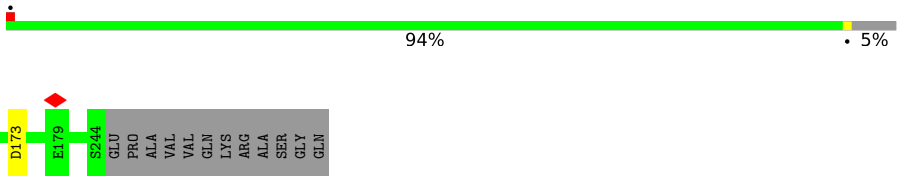
• Molecule 19: 39S ribosomal protein L27, mitochondrial

Chain W:



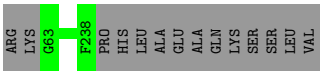
• Molecule 20: 39S ribosomal protein L28, mitochondrial

Chain X:



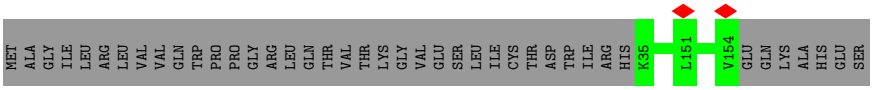
• Molecule 21: 39S ribosomal protein L47, mitochondrial

Chain Y:



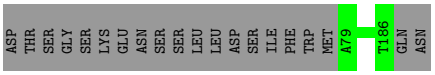
• Molecule 22: 39S ribosomal protein L30, mitochondrial

Chain Z:



• Molecule 23: 39S ribosomal protein L32, mitochondrial

Chain 0:

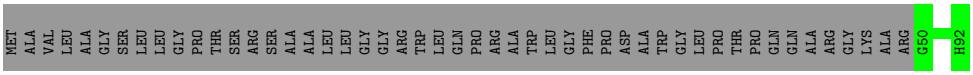


• Molecule 24: 39S ribosomal protein L33, mitochondrial

Chain 1:

• Molecule 25: 39S ribosomal protein L34, mitochondrial

Chain 2:

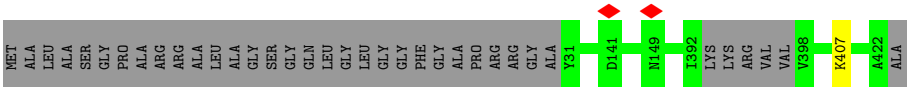


• Molecule 26: 39S ribosomal protein L35, mitochondrial

Chain 3:

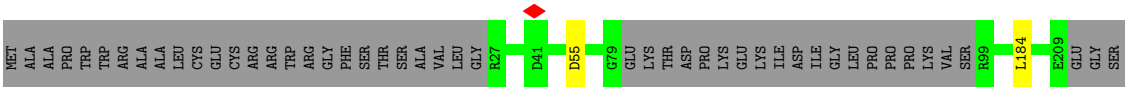
• Molecule 27: 39S ribosomal protein L37, mitochondrial

Chain 5:



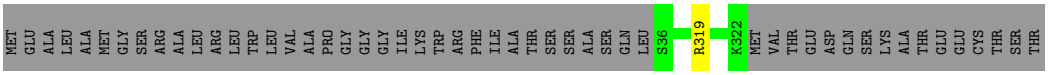
• Molecule 28: 39S ribosomal protein L38, mitochondrial

Chain 6:



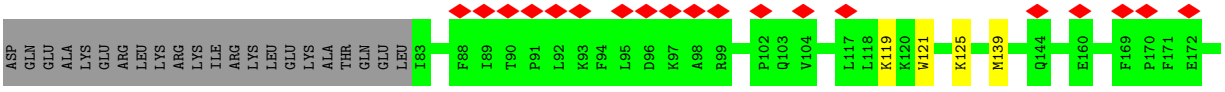
• Molecule 29: 39S ribosomal protein L39, mitochondrial

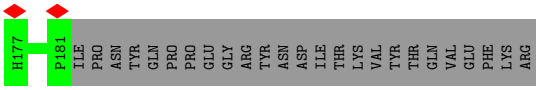
Chain 7:



• Molecule 30: 39S ribosomal protein L40, mitochondrial

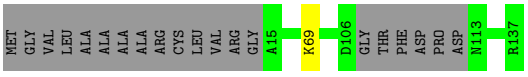
Chain 8:





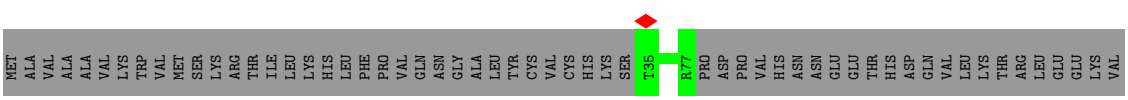
• Molecule 31: 39S ribosomal protein L41, mitochondrial

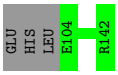
Chain 9:



• Molecule 32: 39S ribosomal protein L42, mitochondrial

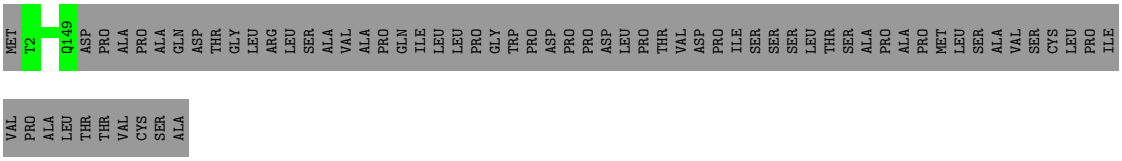
Chain a:





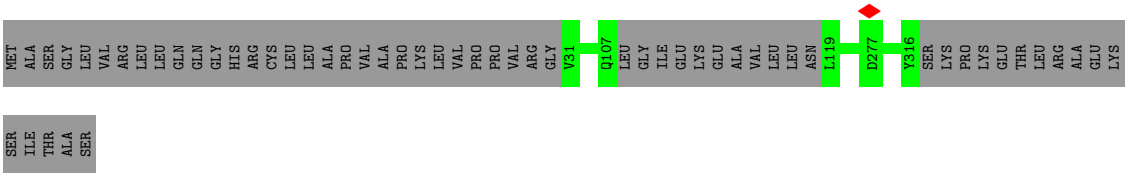
• Molecule 33: 39S ribosomal protein L43, mitochondrial

Chain b:



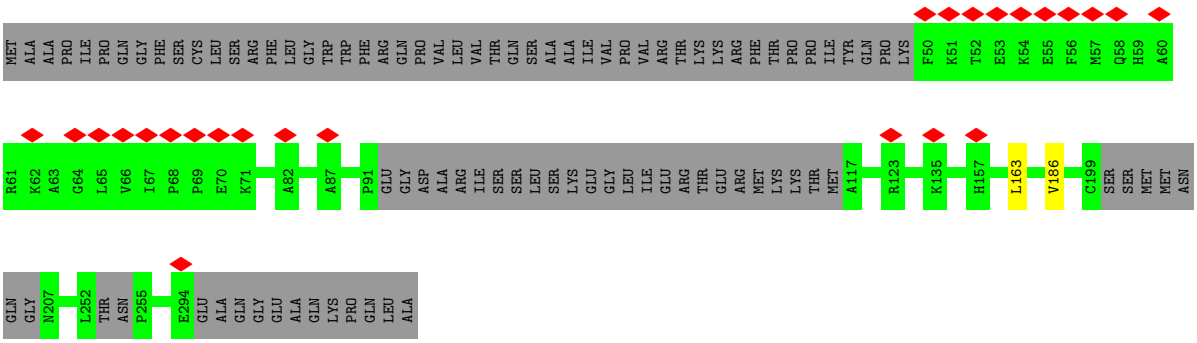
• Molecule 34: 39S ribosomal protein L44, mitochondrial

Chain c:



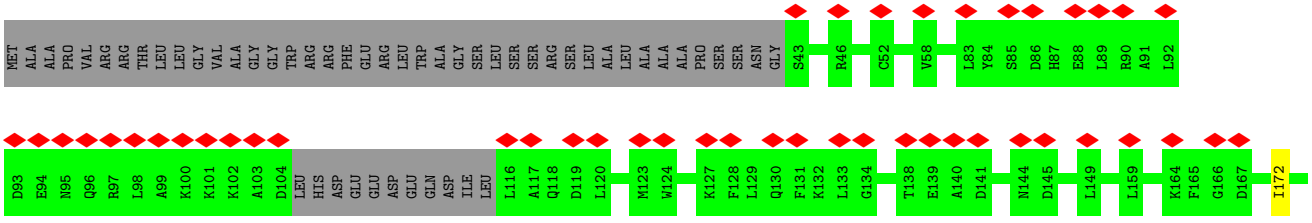
• Molecule 35: 39S ribosomal protein L45, mitochondrial

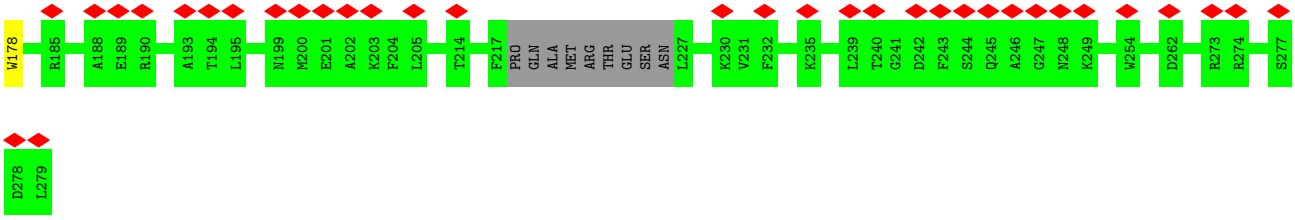
Chain d:



• Molecule 36: 39S ribosomal protein L46, mitochondrial

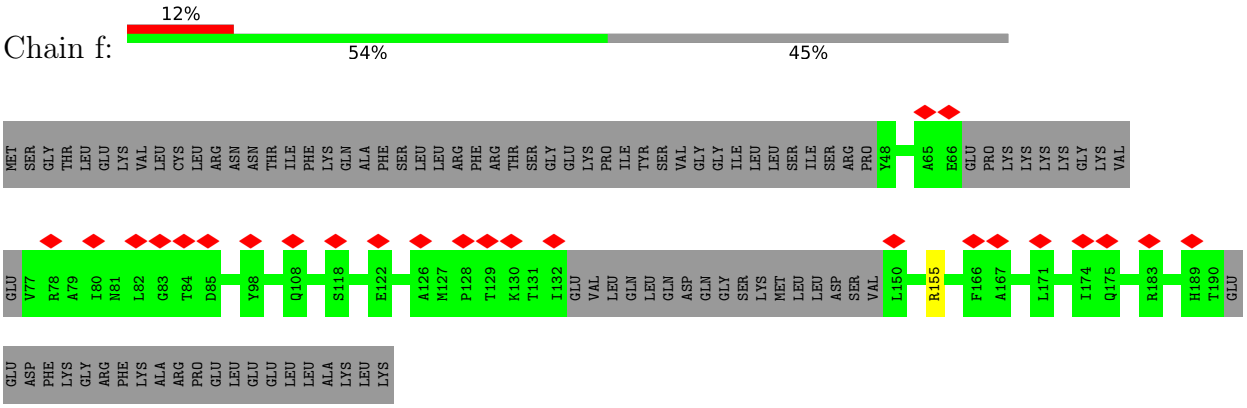
Chain e:





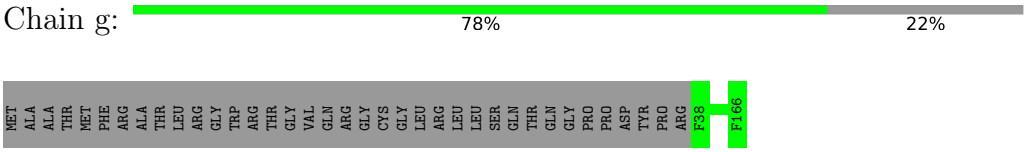
• Molecule 37: 39S ribosomal protein L48, mitochondrial

Chain f:



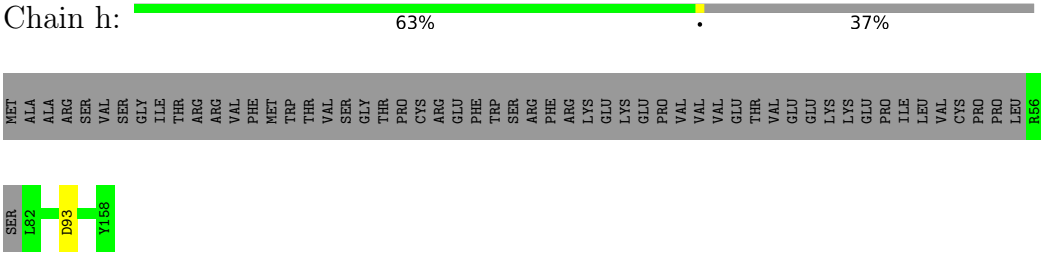
• Molecule 38: 39S ribosomal protein L49, mitochondrial

Chain g:



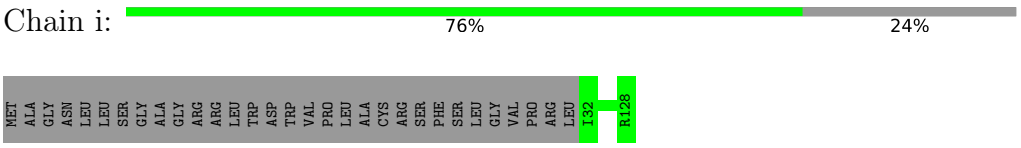
• Molecule 39: 39S ribosomal protein L50, mitochondrial

Chain h:



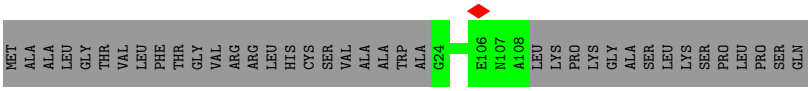
• Molecule 40: 39S ribosomal protein L51, mitochondrial

Chain i:



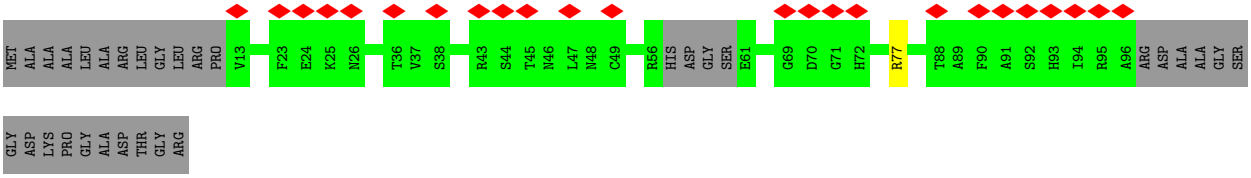
• Molecule 41: 39S ribosomal protein L52, mitochondrial

Chain j:



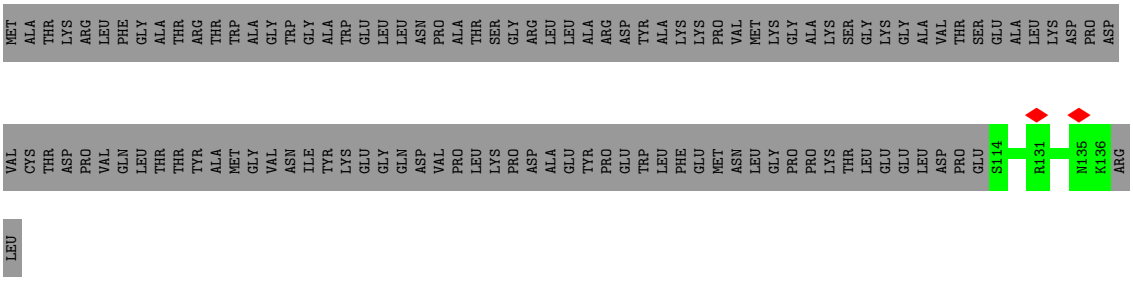
• Molecule 42: 39S ribosomal protein L53, mitochondrial

Chain k:



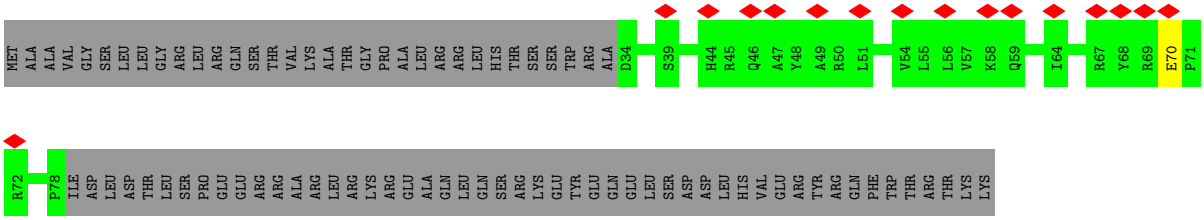
• Molecule 43: 39S ribosomal protein L54, mitochondrial

Chain l:



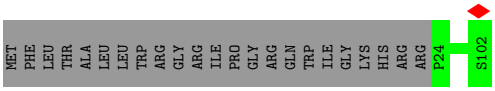
• Molecule 44: 39S ribosomal protein L55, mitochondrial

Chain m:



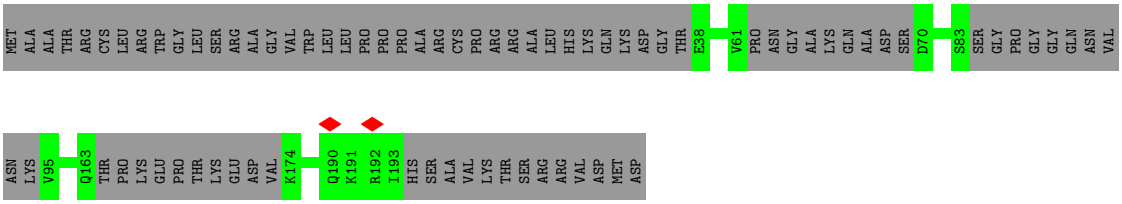
• Molecule 45: Ribosomal protein 63, mitochondrial

Chain o:



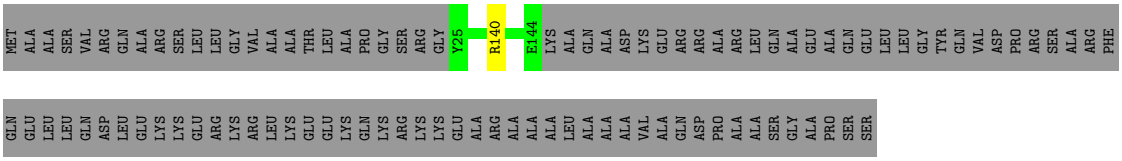
• Molecule 46: Peptidyl-tRNA hydrolase ICT1, mitochondrial

Chain p:



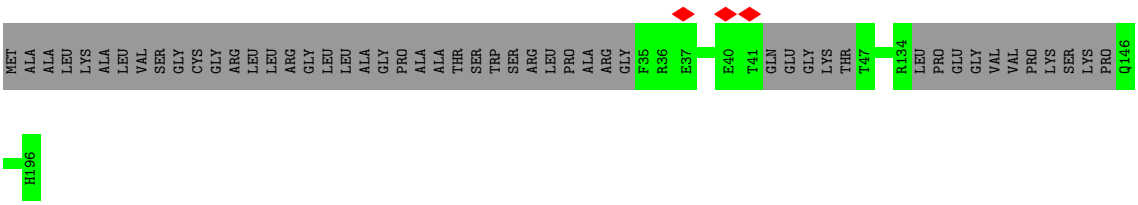
• Molecule 47: Growth arrest and DNA damage-inducible proteins-interacting protein 1

Chain q:



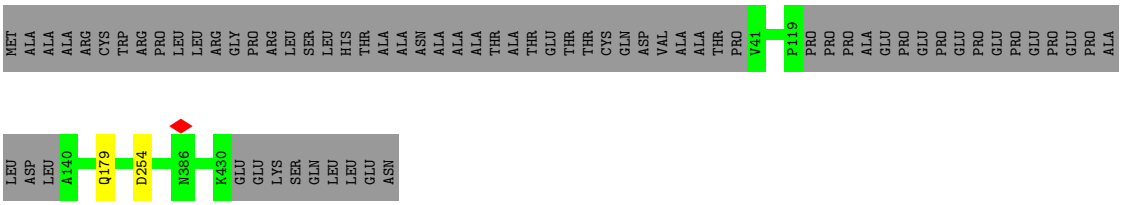
• Molecule 48: 39S ribosomal protein S18a, mitochondrial

Chain r:



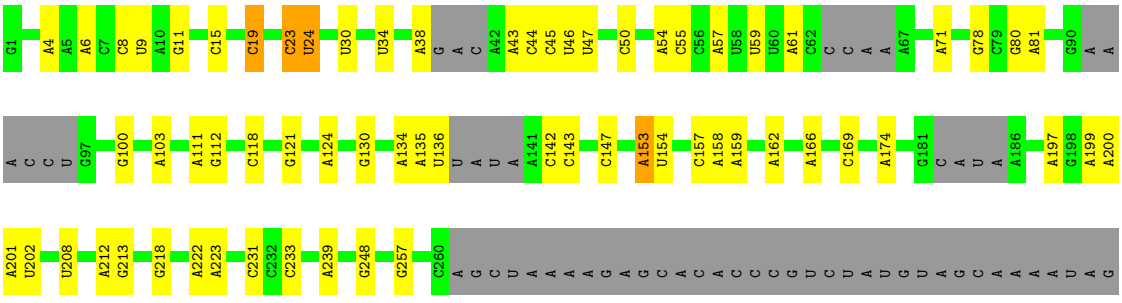
• Molecule 49: 39S ribosomal protein S30, mitochondrial

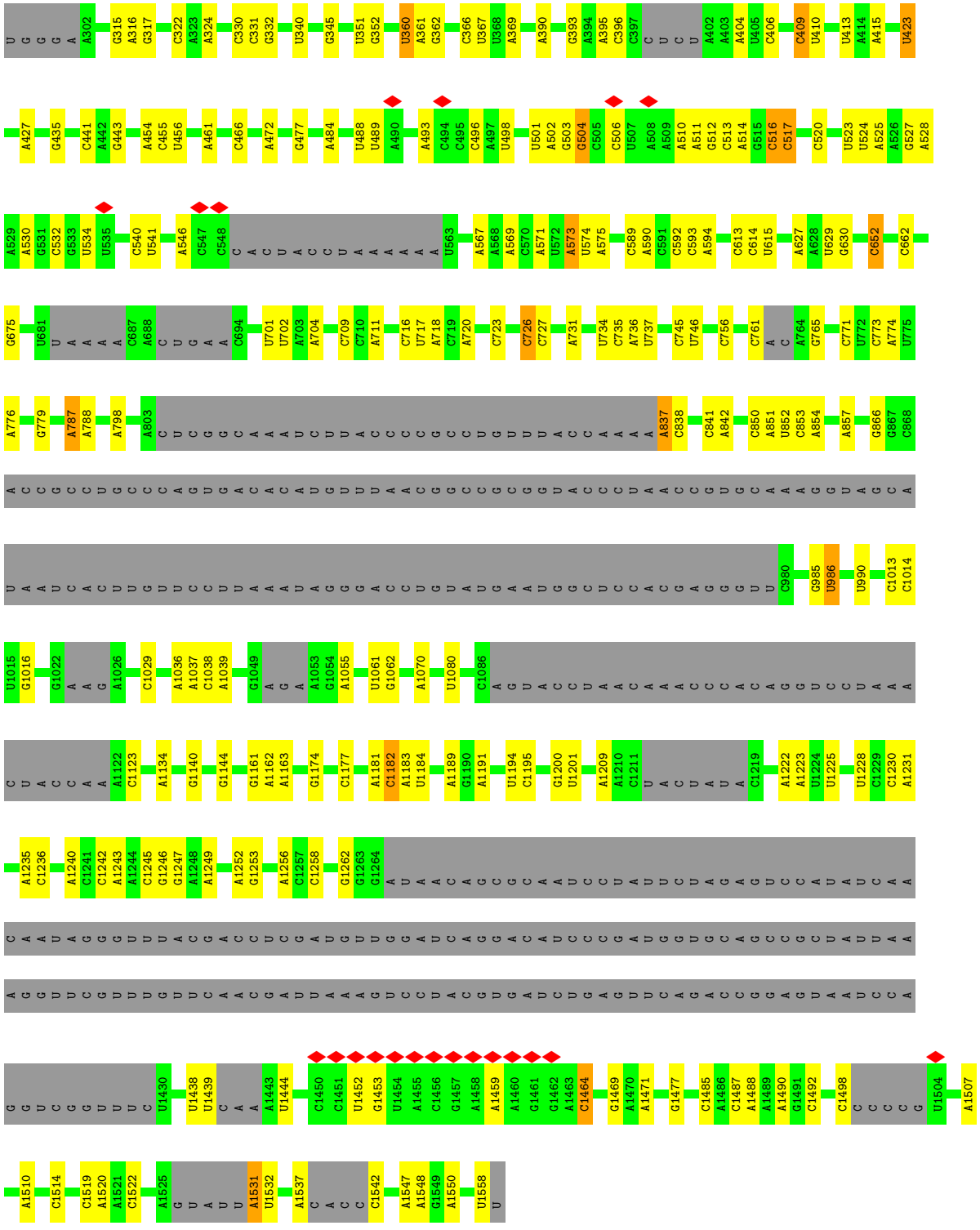
Chain s:



• Molecule 50: 16S rRNA

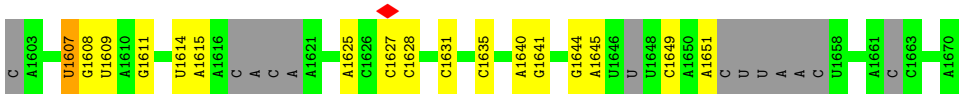
Chain A:





• Molecule 51: mitochondrial Val tRNA

Chain B:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	68090	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.869	Depositor
Minimum map value	-0.517	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	390.24, 390.24, 390.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	D	0.29	0/1736	0.65	0/2335
2	E	0.30	0/2322	0.58	0/3148
3	F	0.27	0/2071	0.61	0/2817
4	H	0.32	0/798	0.78	0/1073
5	I	0.30	0/1308	0.69	2/1761 (0.1%)
6	J	0.26	0/1077	0.56	0/1452
7	K	0.25	0/1495	0.57	0/2029
8	L	0.29	0/904	0.70	1/1218 (0.1%)
9	M	0.30	0/2359	0.67	3/3185 (0.1%)
10	N	0.30	1/1697 (0.1%)	0.59	0/2281
11	O	0.28	0/1269	0.70	2/1708 (0.1%)
12	P	0.30	0/1173	0.65	1/1588 (0.1%)
13	Q	0.31	0/1846	0.63	0/2487
14	R	0.27	0/1174	0.55	0/1572
15	S	0.26	0/1276	0.61	0/1729
16	T	0.27	0/1335	0.54	0/1796
17	U	0.27	0/1183	0.64	0/1600
18	V	0.26	0/1616	0.61	0/2189
19	W	0.26	0/881	0.57	0/1188
20	X	0.28	0/2090	0.60	1/2825 (0.0%)
21	Y	0.28	0/1552	0.61	0/2079
22	Z	0.24	0/1003	0.52	0/1354
23	0	0.27	0/895	0.57	0/1201
24	1	0.29	0/438	0.78	0/583
25	2	0.26	0/357	0.59	0/475
26	3	0.25	0/852	0.59	0/1136
27	5	0.27	0/3250	0.60	0/4429
28	6	0.28	0/2726	0.63	2/3715 (0.1%)
29	7	0.28	0/2391	0.60	0/3234
30	8	0.37	1/855 (0.1%)	0.68	1/1152 (0.1%)
31	9	0.30	0/972	0.57	0/1306
32	a	0.26	0/709	0.56	0/963

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	b	0.28	0/1202	0.63	0/1626
34	c	0.29	0/2264	0.56	0/3059
35	d	0.28	0/1790	0.60	1/2423 (0.0%)
36	e	0.27	0/1797	0.69	2/2422 (0.1%)
37	f	0.30	0/931	0.62	0/1259
38	g	0.28	0/1102	0.57	0/1503
39	h	0.27	0/847	0.59	1/1150 (0.1%)
40	i	0.26	0/849	0.66	0/1135
41	j	0.26	0/698	0.52	0/940
42	k	0.26	0/635	0.62	0/855
43	l	0.27	0/226	0.73	0/299
44	m	0.31	0/379	0.88	1/510 (0.2%)
45	o	0.26	0/682	0.59	0/916
46	p	0.30	0/1071	0.70	0/1433
47	q	0.28	0/1042	0.59	0/1413
48	r	0.26	0/1238	0.60	0/1676
49	s	0.27	0/3114	0.60	1/4225 (0.0%)
50	A	0.27	1/25926 (0.0%)	0.99	94/40305 (0.2%)
51	B	0.27	0/1328	1.01	7/2056 (0.3%)
All	All	0.28	3/92731 (0.0%)	0.76	120/130813 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
35	d	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	8	121	TRP	CB-CG	5.72	1.60	1.50
10	N	151	VAL	C-N	5.32	1.46	1.34
50	A	239	A	C6-N1	-5.05	1.32	1.35

The worst 5 of 120 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
50	A	340	U	C5-C4-O4	21.41	138.75	125.90
50	A	340	U	N3-C4-O4	-18.86	106.20	119.40
50	A	239	A	N1-C6-N6	-13.91	110.25	118.60

Continued on next page...

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
50	A	652	C	N1-C2-O2	9.22	124.44	118.90
50	A	118	C	N1-C2-O2	9.06	124.34	118.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
35	d	186	VAL	Peptide

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	D	216/305 (71%)	210 (97%)	5 (2%)	1 (0%)	29 61
2	E	281/348 (81%)	272 (97%)	9 (3%)	0	100 100
3	F	248/311 (80%)	240 (97%)	8 (3%)	0	100 100
4	H	93/267 (35%)	90 (97%)	3 (3%)	0	100 100
5	I	154/261 (59%)	143 (93%)	11 (7%)	0	100 100
6	J	138/192 (72%)	128 (93%)	10 (7%)	0	100 100
7	K	175/178 (98%)	170 (97%)	5 (3%)	0	100 100
8	L	113/145 (78%)	108 (96%)	5 (4%)	0	100 100
9	M	285/296 (96%)	276 (97%)	9 (3%)	0	100 100
10	N	203/251 (81%)	198 (98%)	5 (2%)	0	100 100
11	O	150/175 (86%)	146 (97%)	4 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	P	139/180 (77%)	130 (94%)	9 (6%)	0	100	100
13	Q	215/292 (74%)	207 (96%)	8 (4%)	0	100	100
14	R	138/149 (93%)	136 (99%)	2 (1%)	0	100	100
15	S	154/205 (75%)	149 (97%)	5 (3%)	0	100	100
16	T	155/206 (75%)	152 (98%)	3 (2%)	0	100	100
17	U	135/153 (88%)	127 (94%)	8 (6%)	0	100	100
18	V	188/216 (87%)	181 (96%)	7 (4%)	0	100	100
19	W	107/148 (72%)	105 (98%)	2 (2%)	0	100	100
20	X	241/256 (94%)	235 (98%)	6 (2%)	0	100	100
21	Y	174/250 (70%)	170 (98%)	4 (2%)	0	100	100
22	Z	118/161 (73%)	112 (95%)	6 (5%)	0	100	100
23	0	106/188 (56%)	103 (97%)	3 (3%)	0	100	100
24	1	50/65 (77%)	48 (96%)	2 (4%)	0	100	100
25	2	41/92 (45%)	40 (98%)	1 (2%)	0	100	100
26	3	93/188 (50%)	89 (96%)	4 (4%)	0	100	100
27	5	383/423 (90%)	367 (96%)	16 (4%)	0	100	100
28	6	316/380 (83%)	305 (96%)	11 (4%)	0	100	100
29	7	285/338 (84%)	270 (95%)	15 (5%)	0	100	100
30	8	97/206 (47%)	91 (94%)	6 (6%)	0	100	100
31	9	113/137 (82%)	109 (96%)	4 (4%)	0	100	100
32	a	78/142 (55%)	75 (96%)	3 (4%)	0	100	100
33	b	146/215 (68%)	136 (93%)	10 (7%)	0	100	100
34	c	271/332 (82%)	262 (97%)	9 (3%)	0	100	100
35	d	203/306 (66%)	196 (97%)	7 (3%)	0	100	100
36	e	211/279 (76%)	195 (92%)	16 (8%)	0	100	100
37	f	110/212 (52%)	103 (94%)	7 (6%)	0	100	100
38	g	127/166 (76%)	123 (97%)	4 (3%)	0	100	100
39	h	96/158 (61%)	92 (96%)	4 (4%)	0	100	100
40	i	95/128 (74%)	94 (99%)	1 (1%)	0	100	100
41	j	83/123 (68%)	83 (100%)	0	0	100	100
42	k	76/112 (68%)	72 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	l	21/138 (15%)	21 (100%)	0	0	100	100
44	m	43/128 (34%)	36 (84%)	7 (16%)	0	100	100
45	o	77/102 (76%)	75 (97%)	2 (3%)	0	100	100
46	p	119/206 (58%)	117 (98%)	2 (2%)	0	100	100
47	q	118/222 (53%)	118 (100%)	0	0	100	100
48	r	140/196 (71%)	135 (96%)	5 (4%)	0	100	100
49	s	366/439 (83%)	354 (97%)	12 (3%)	0	100	100
All	All	7684/10566 (73%)	7394 (96%)	289 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	207	ILE

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	D	179/245 (73%)	179 (100%)	0	100	100
2	E	246/290 (85%)	246 (100%)	0	100	100
3	F	217/262 (83%)	216 (100%)	1 (0%)	88	93
4	H	86/228 (38%)	86 (100%)	0	100	100
5	I	145/232 (62%)	143 (99%)	2 (1%)	67	82
6	J	113/150 (75%)	112 (99%)	1 (1%)	78	87
7	K	155/156 (99%)	154 (99%)	1 (1%)	86	91
8	L	98/124 (79%)	98 (100%)	0	100	100
9	M	245/249 (98%)	241 (98%)	4 (2%)	62	79
10	N	172/211 (82%)	170 (99%)	2 (1%)	71	83
11	O	133/150 (89%)	133 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
12	P	123/155 (79%)	122 (99%)	1 (1%)	81 89
13	Q	199/256 (78%)	199 (100%)	0	100 100
14	R	118/126 (94%)	117 (99%)	1 (1%)	81 89
15	S	141/180 (78%)	141 (100%)	0	100 100
16	T	141/176 (80%)	141 (100%)	0	100 100
17	U	124/135 (92%)	124 (100%)	0	100 100
18	V	172/191 (90%)	170 (99%)	2 (1%)	71 83
19	W	89/119 (75%)	89 (100%)	0	100 100
20	X	219/229 (96%)	218 (100%)	1 (0%)	88 93
21	Y	159/223 (71%)	159 (100%)	0	100 100
22	Z	111/147 (76%)	111 (100%)	0	100 100
23	0	97/164 (59%)	97 (100%)	0	100 100
24	1	49/60 (82%)	48 (98%)	1 (2%)	55 76
25	2	38/72 (53%)	38 (100%)	0	100 100
26	3	88/166 (53%)	88 (100%)	0	100 100
27	5	348/368 (95%)	347 (100%)	1 (0%)	92 96
28	6	265/332 (80%)	263 (99%)	2 (1%)	81 89
29	7	263/303 (87%)	262 (100%)	1 (0%)	91 95
30	8	91/190 (48%)	89 (98%)	2 (2%)	52 74
31	9	99/112 (88%)	98 (99%)	1 (1%)	76 86
32	a	78/133 (59%)	78 (100%)	0	100 100
33	b	130/186 (70%)	130 (100%)	0	100 100
34	c	241/288 (84%)	241 (100%)	0	100 100
35	d	193/274 (70%)	193 (100%)	0	100 100
36	e	188/236 (80%)	188 (100%)	0	100 100
37	f	101/188 (54%)	100 (99%)	1 (1%)	76 86
38	g	119/148 (80%)	119 (100%)	0	100 100
39	h	95/148 (64%)	95 (100%)	0	100 100
40	i	86/110 (78%)	86 (100%)	0	100 100
41	j	68/97 (70%)	68 (100%)	0	100 100
42	k	71/90 (79%)	70 (99%)	1 (1%)	67 82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
43	l	23/116 (20%)	23 (100%)	0	100 100
44	m	40/113 (35%)	40 (100%)	0	100 100
45	o	68/87 (78%)	68 (100%)	0	100 100
46	p	117/181 (65%)	117 (100%)	0	100 100
47	q	104/178 (58%)	103 (99%)	1 (1%)	76 86
48	r	133/169 (79%)	133 (100%)	0	100 100
49	s	326/381 (86%)	325 (100%)	1 (0%)	92 96
All	All	6904/9124 (76%)	6876 (100%)	28 (0%)	91 95

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	V	208	ARG
49	s	179	GLN
27	5	407	LYS
37	f	155	ARG
24	1	38	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
42	k	15	GLN
49	s	179	GLN
49	s	427	ASN
49	s	240	GLN
17	U	16	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	A	1071/1559 (68%)	251 (23%)	11 (1%)
51	B	51/69 (73%)	15 (29%)	1 (1%)
All	All	1122/1628 (68%)	266 (23%)	12 (1%)

5 of 266 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	A	4	A
50	A	6	A
50	A	8	C
50	A	9	U
50	A	11	G

5 of 12 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	A	787	A
50	A	837	A
51	B	1607	U
50	A	1235	A
50	A	360	U

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 51 ligands modelled in this entry, 51 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

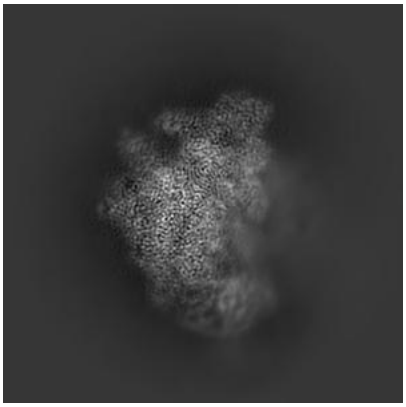
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-12924. These allow visual inspection of the internal detail of the map and identification of artifacts.

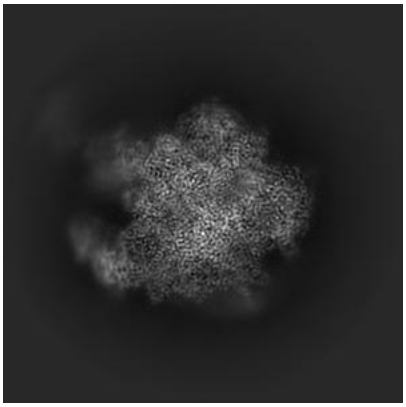
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

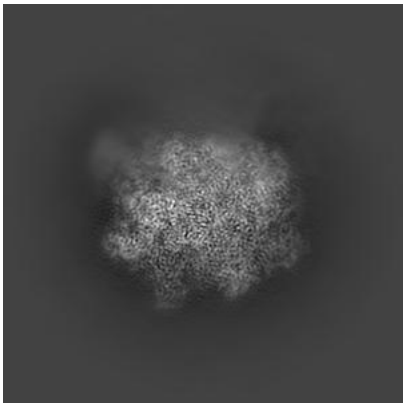
6.1.1 Primary map



X



Y



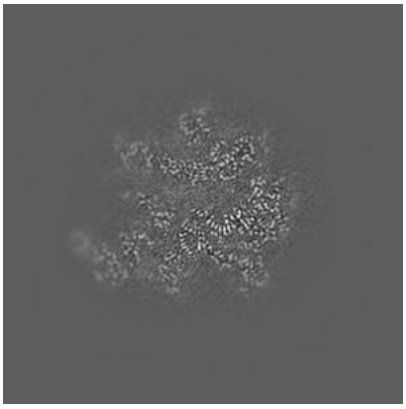
Z

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

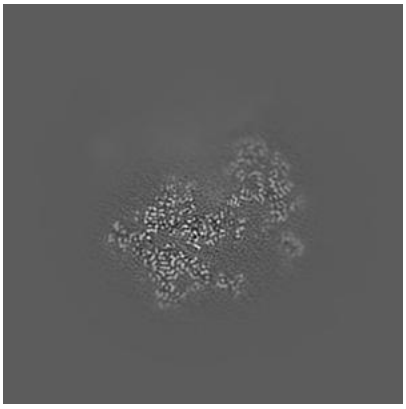
6.2 Central slices

6.2.1 Primary map

X Index: 180



Y Index: 180

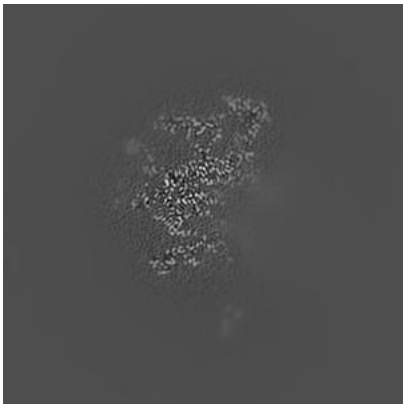


Z Index: 180

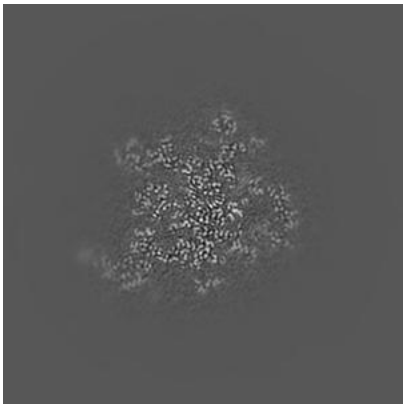
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

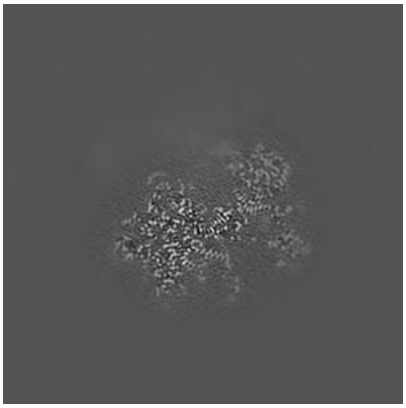
6.3.1 Primary map



X Index: 168



Y Index: 161

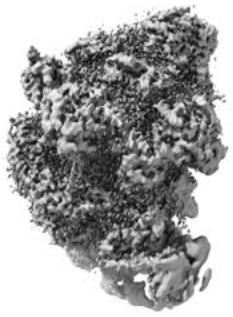


Z Index: 188

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

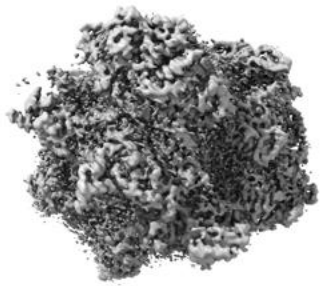
6.4 Orthogonal surface views (i)

6.4.1 Primary map



X

Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

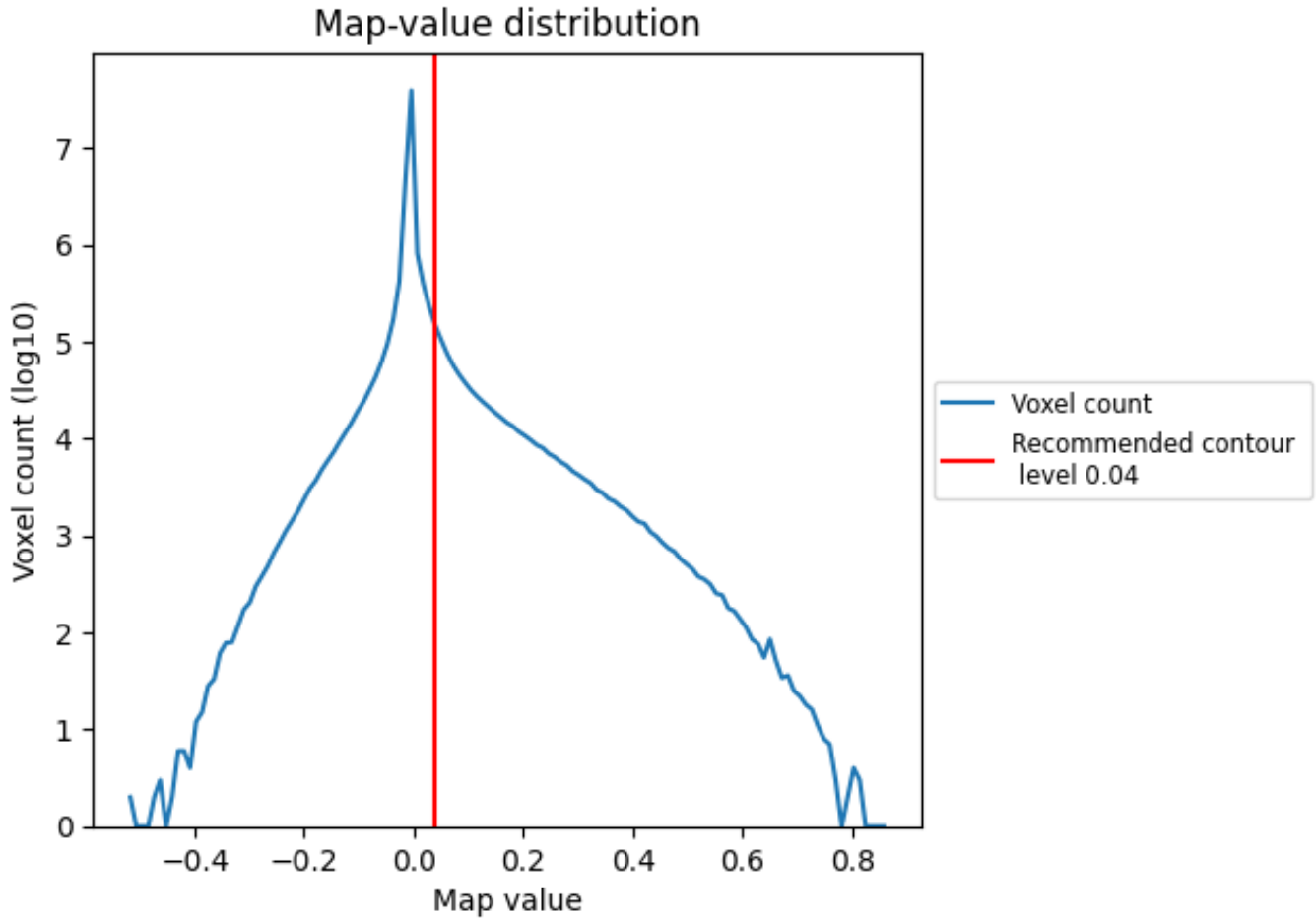
6.5 Mask visualisation (i)

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

7 Map analysis

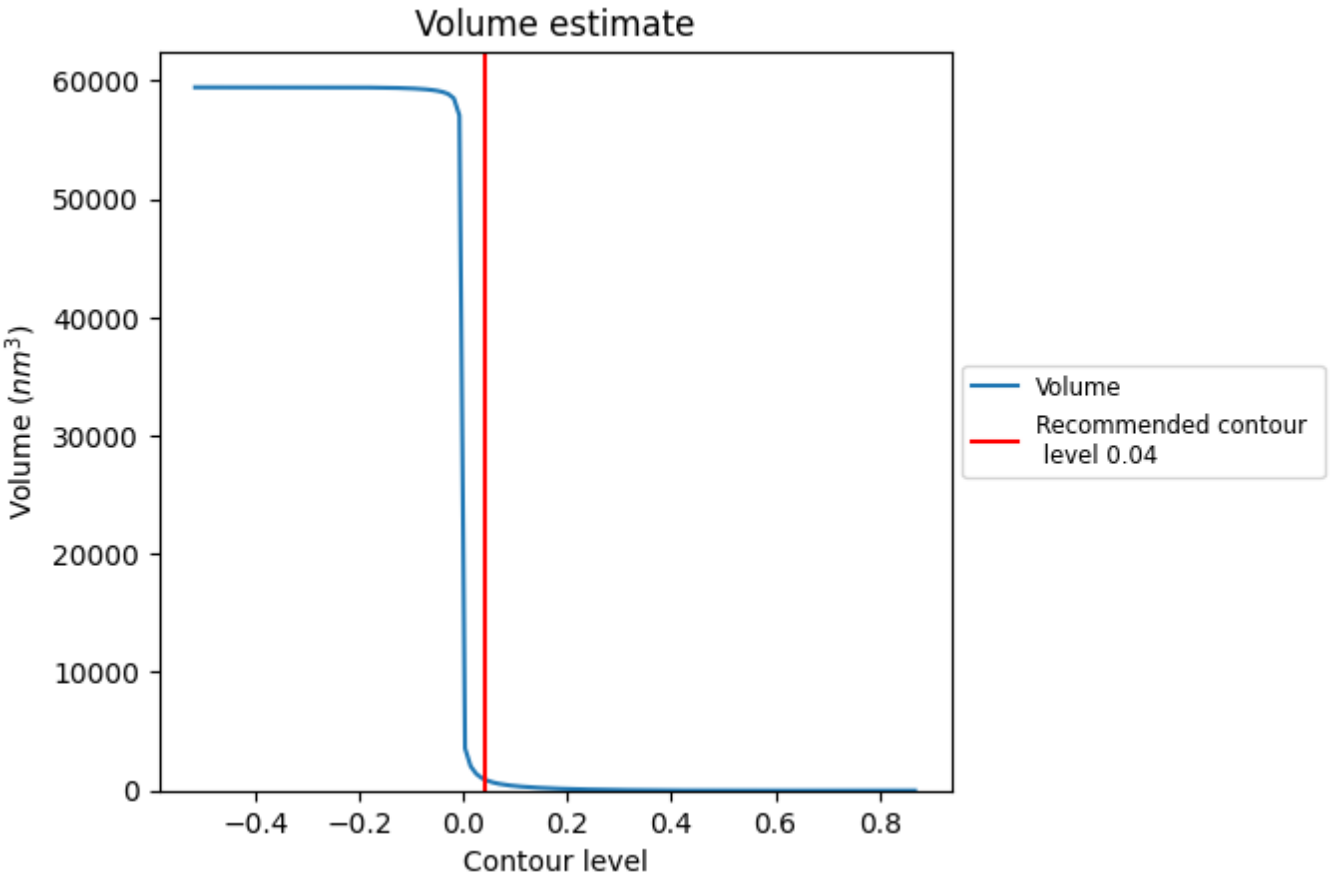
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

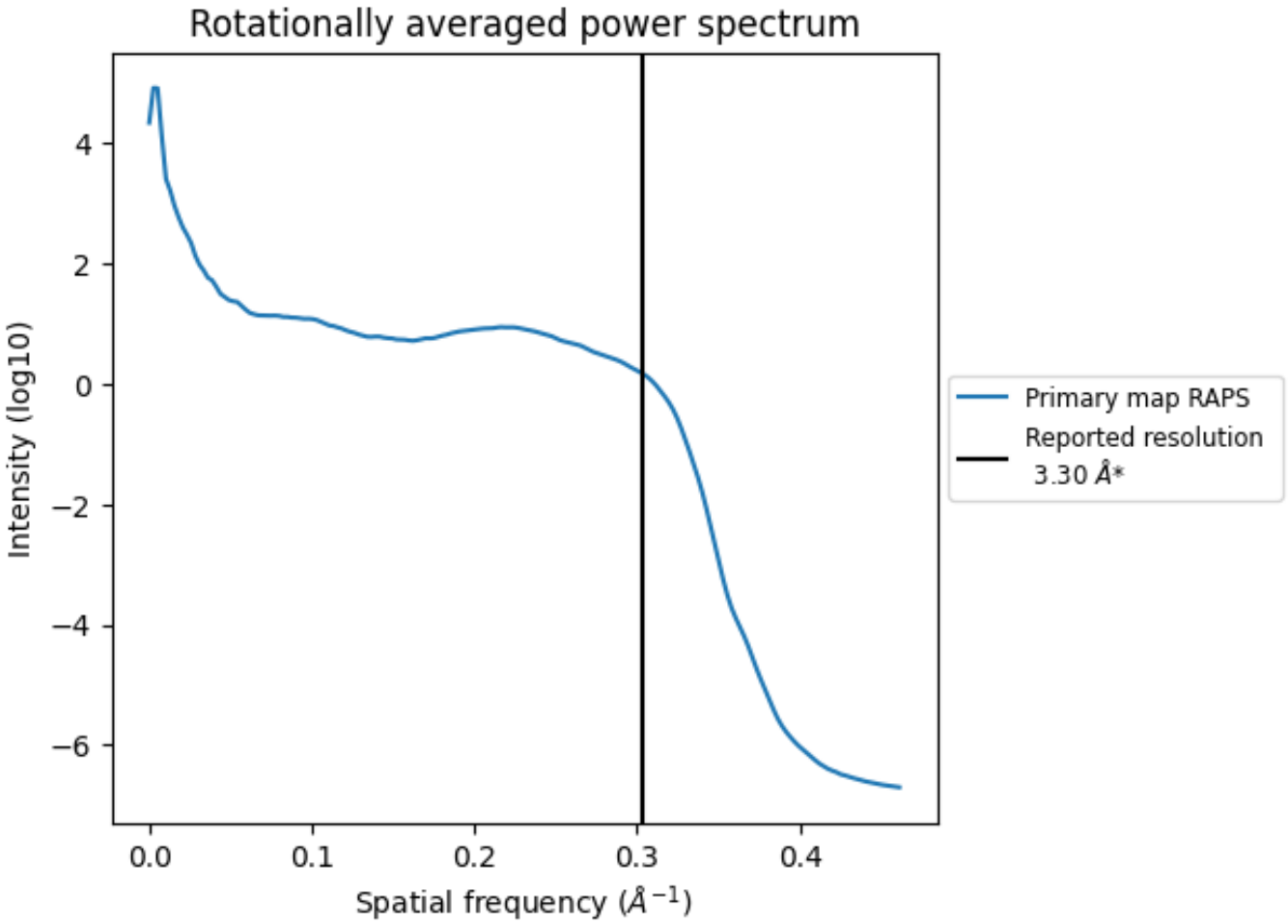
7.2 Volume estimate (i)



The volume at the recommended contour level is 956 nm^3; this corresponds to an approximate mass of 863 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)

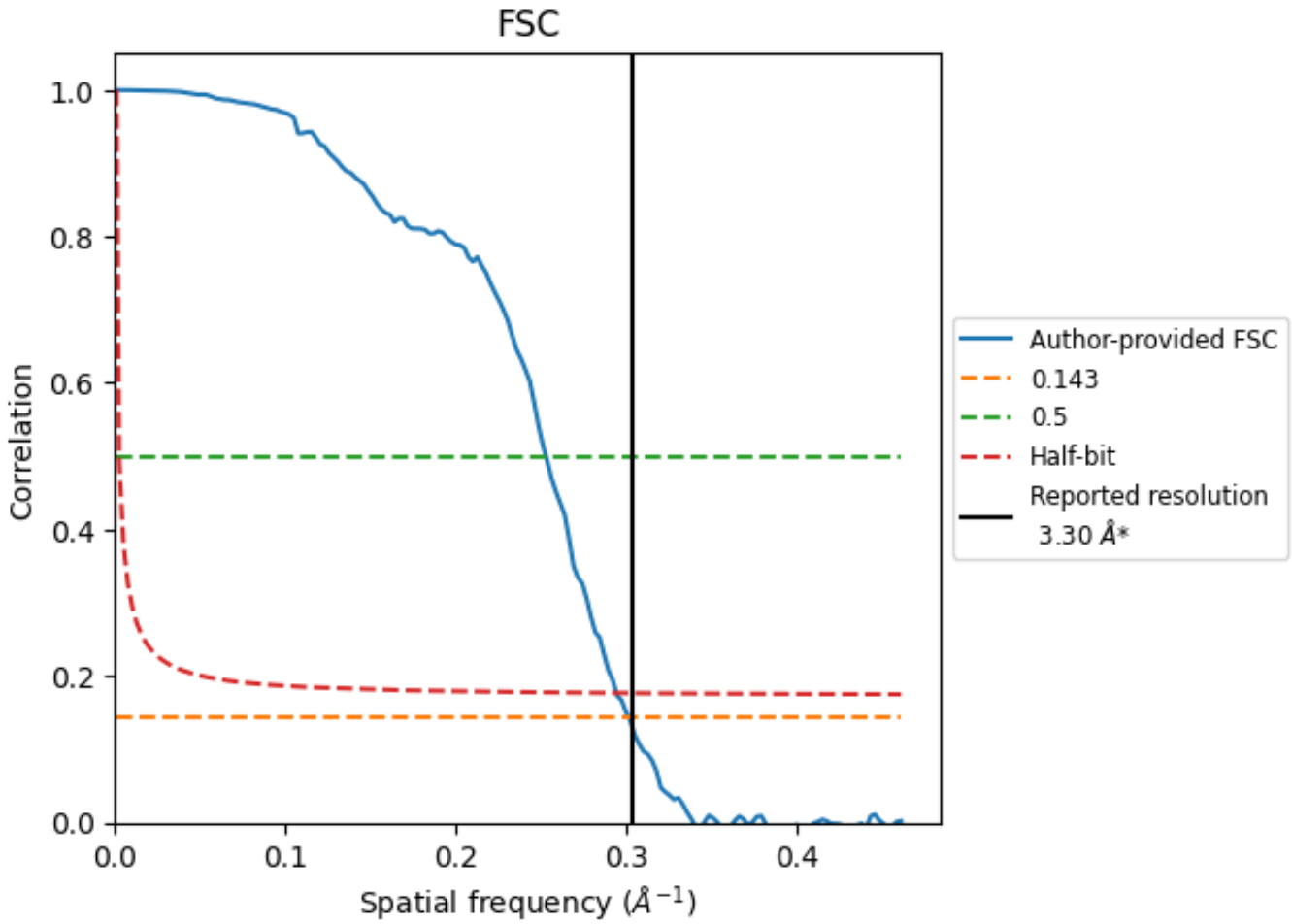


*Reported resolution corresponds to spatial frequency of 0.303 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.303 Å^{-1}

8.2 Resolution estimates (i)

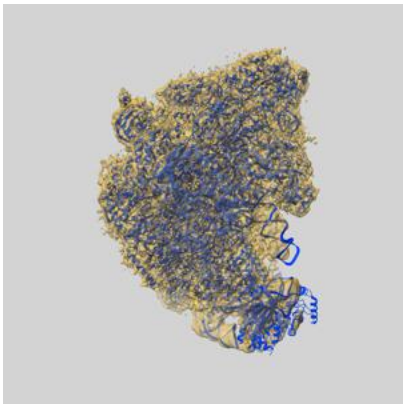
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.32	3.95	3.40
Unmasked-calculated*	-	-	-

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

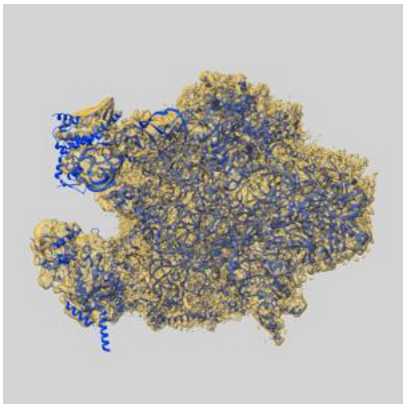
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-12924 and PDB model 7OIB. Per-residue inclusion information can be found in section 3 on page 13.

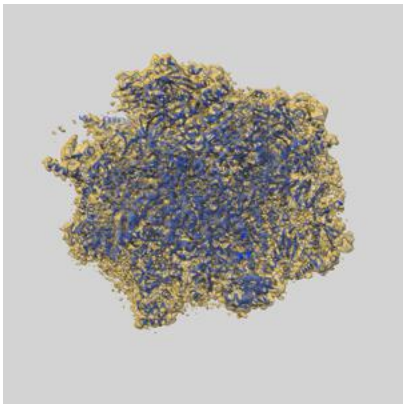
9.1 Map-model overlay



X



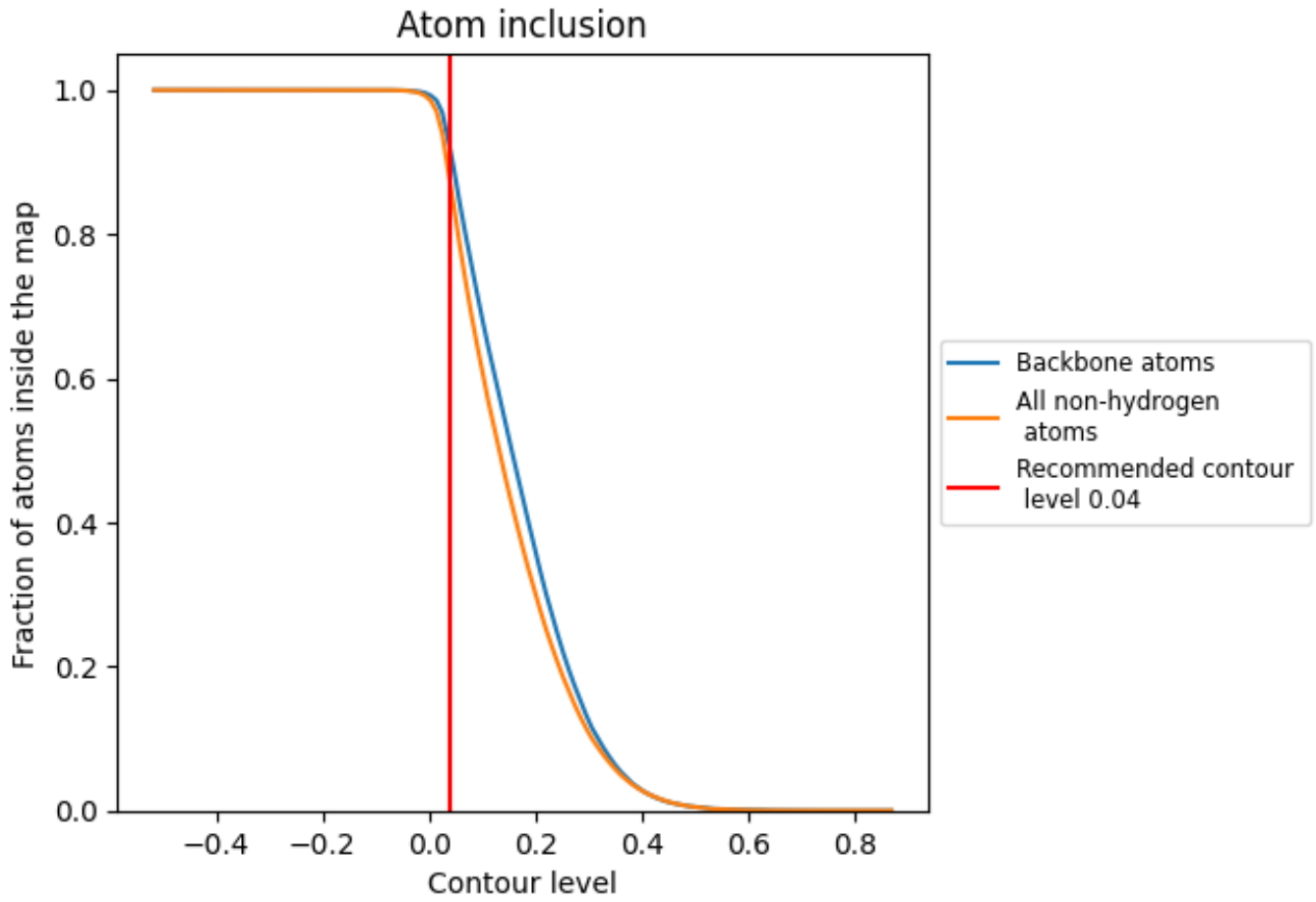
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04 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 Atom inclusion (i)



At the recommended contour level, 92% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.