



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 02:13 AM UTC

PDB ID : 7OID / pdb_00007oid
EMDB ID : EMD-12926
Title : Cryo-EM structure of late human 39S mitoribosome assembly intermediates, state 5A
Authors : Cheng, J.; Berninghausen, O.; Beckmann, R.
Deposited on : 2021-05-11
Resolution : 3.70 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 ⓘ symbol.

The types of validation reports are described at

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

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

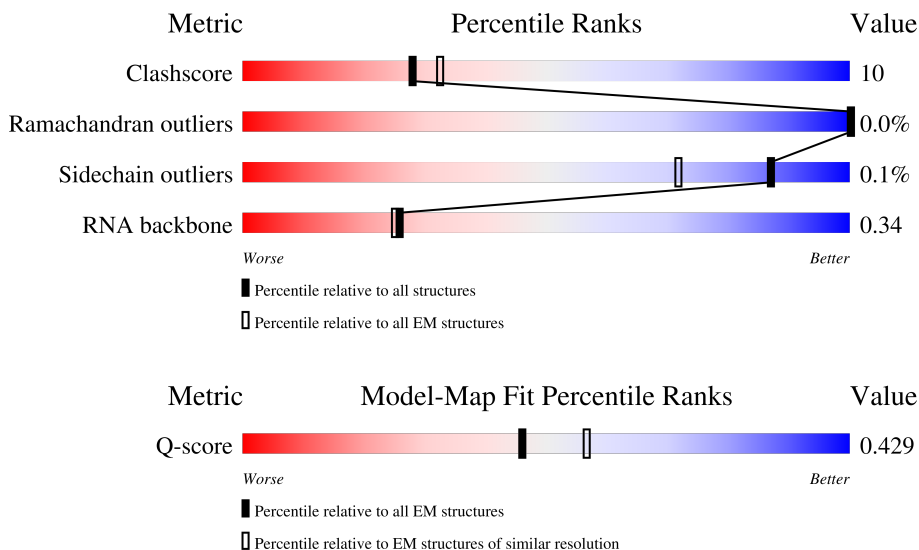
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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


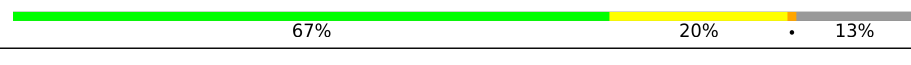
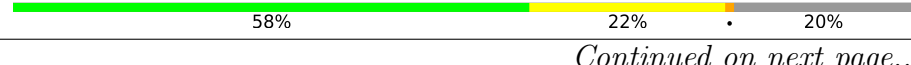
The reported resolution of this entry is 3.70 Å.

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.




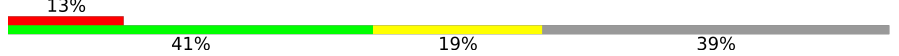










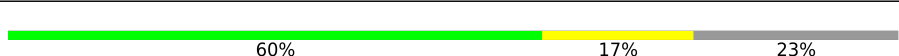
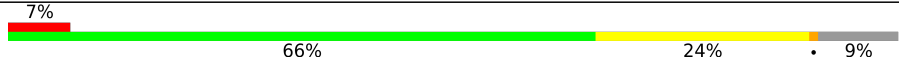
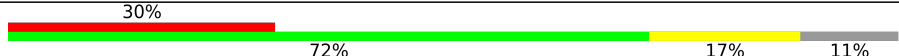

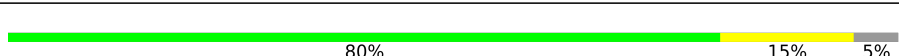
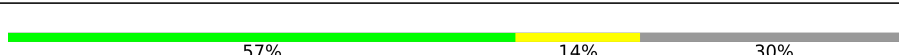
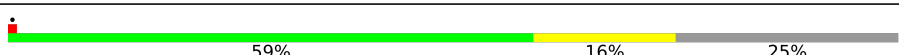
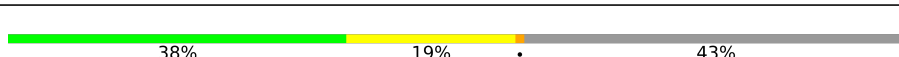
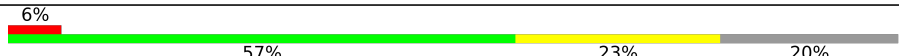



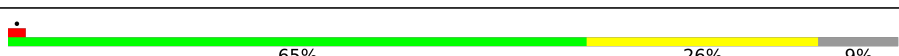
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	



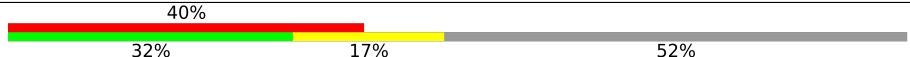


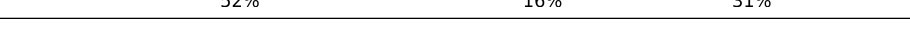
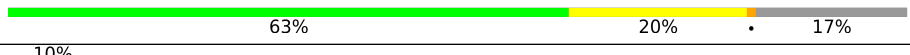
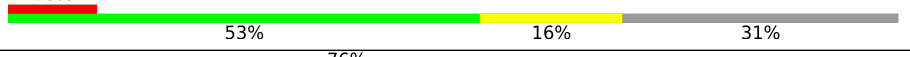

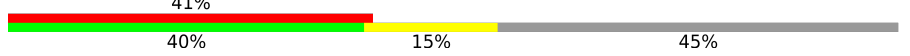

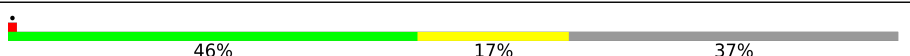

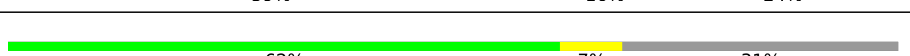
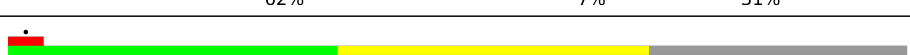
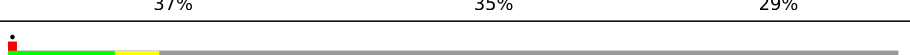



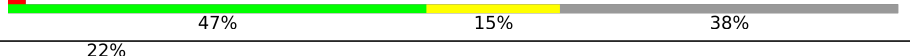
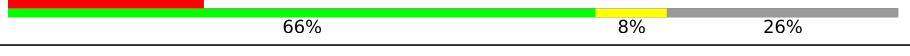




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Mol	Chain	Length	Quality of chain
4	H	267	
5	I	261	
6	J	192	
7	K	178	
8	L	145	
9	M	296	
10	N	251	
11	O	175	
12	P	180	
13	Q	292	
14	R	149	
15	S	205	
16	T	206	
17	U	153	
18	V	216	
19	W	148	
20	X	256	
21	Y	250	
22	Z	161	
23	0	188	
24	1	65	
25	2	92	
26	3	188	
27	4	103	
28	5	423	


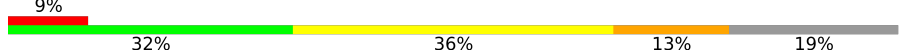
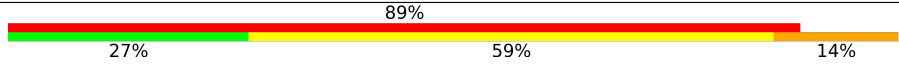
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Mol	Chain	Length	Quality of chain
29	6	380	
30	7	338	
31	8	206	
32	9	137	
33	a	142	
34	b	215	
35	c	332	
36	d	306	
37	e	279	
38	f	212	
39	g	166	
40	h	158	
41	i	128	
42	j	123	
43	k	112	
44	l	138	
45	m	128	
46	o	102	
47	p	206	
48	q	222	
49	r	196	
50	s	439	
51	u	234	
52	v	70	
53	w	156	

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Mol	Chain	Length	Quality of chain
54	A	1559	
55	B	69	
56	z	73	

2 Entry composition [i](#)

There are 59 unique types of molecules in this entry. The entry contains 101125 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
			Total	C	N	O	S		
1	D	236	Total	C	N	O	S	0	0
			1842	1145	373	315	9		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 27 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	4	36	322	203	70	46	3	0	0

- Molecule 28 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	5	387	3156	2039	548	558	11	0	0

- Molecule 29 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	6	324	2640	1694	470	468	8	0	0

- Molecule 30 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	7	287	2334	1495	397	425	17	0	0

- Molecule 31 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	8	99	836	535	144	155	2	0	0

- Molecule 32 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	9	117	947	614	163	168	2	0	0

- Molecule 33 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	a	73	611	385	115	106	5	0	0

- Molecule 34 is a protein called 39S ribosomal protein L43, mitochondrial.

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

- Molecule 35 is a protein called 39S ribosomal protein L44, mitochondrial.

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

- Molecule 36 is a protein called 39S ribosomal protein L45, mitochondrial.

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

- Molecule 37 is a protein called 39S ribosomal protein L46, mitochondrial.

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

- Molecule 38 is a protein called 39S ribosomal protein L48, mitochondrial.

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

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

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

- Molecule 40 is a protein called 39S ribosomal protein L50, mitochondrial.

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

- Molecule 41 is a protein called 39S ribosomal protein L51, mitochondrial.

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

- Molecule 42 is a protein called 39S ribosomal protein L52, mitochondrial.

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

- Molecule 43 is a protein called 39S ribosomal protein L53, mitochondrial.

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

- Molecule 44 is a protein called 39S ribosomal protein L54, mitochondrial.

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

- Molecule 45 is a protein called 39S ribosomal protein L55, mitochondrial.

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

- Molecule 46 is a protein called Ribosomal protein 63, mitochondrial.

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

- Molecule 47 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

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

- Molecule 48 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	q	164	1379	858	267	249	5	0	0

- Molecule 49 is a protein called 39S ribosomal protein S18a, mitochondrial.

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

- Molecule 50 is a protein called 39S ribosomal protein S30, mitochondrial.

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

- Molecule 51 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

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

- Molecule 52 is a protein called MIEF1 upstream open reading frame protein.

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

- Molecule 53 is a protein called Acyl carrier protein, mitochondrial.

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

- Molecule 54 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
54	A	1472	31265	14027	5646	10120	1472	0	0

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 55 is a RNA chain called mitochondrial Val tRNA.

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

- Molecule 56 is a RNA chain called mitochondrial tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
56	z	73	1547	696	280	499	72	0	0

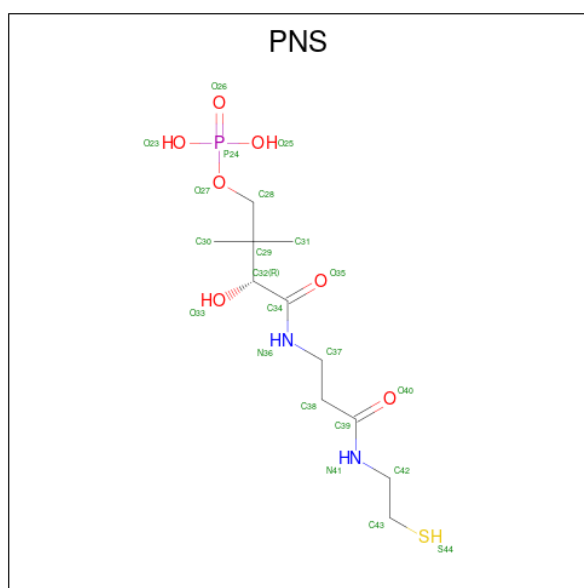
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	I	1	Total	Zn	0
			1	1	
57	0	1	Total	Zn	0
			1	1	

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
58	g	1	Total	Mg	0
			1	1	
58	A	1	Total	Mg	0
			1	1	

- Molecule 59 is 4'-PHOSPHOPANTETHEINE (CCD ID: PNS) (formula: C₁₁H₂₃N₂O₇PS).

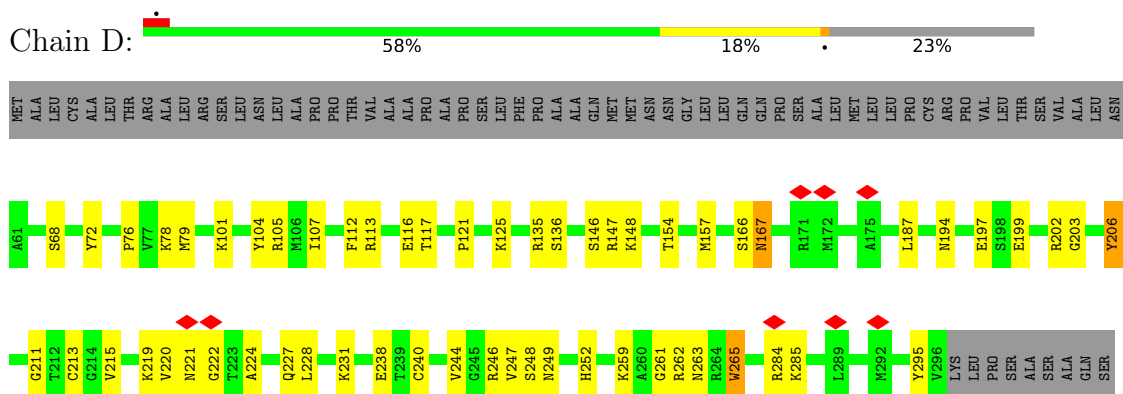


Mol	Chain	Residues	Atoms					AltConf	
			Total	C	N	O	P		S
59	v	1	21	11	2	6	1	1	0

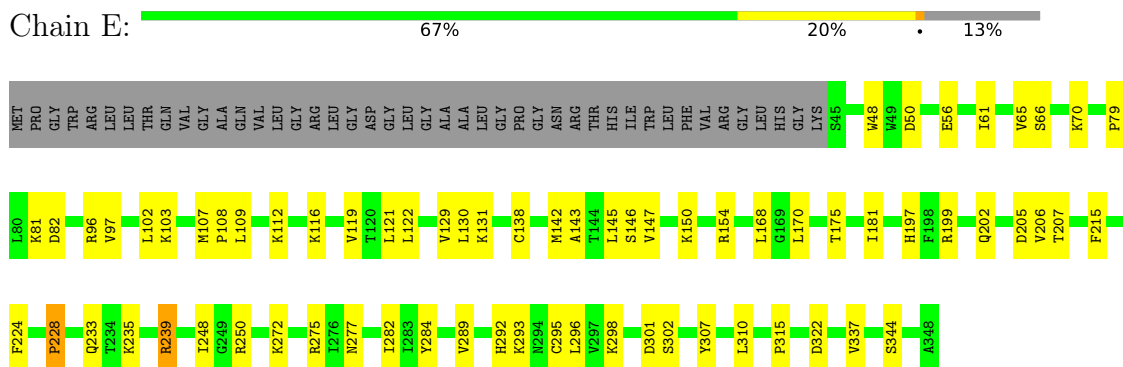
3 Residue-property plots

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.

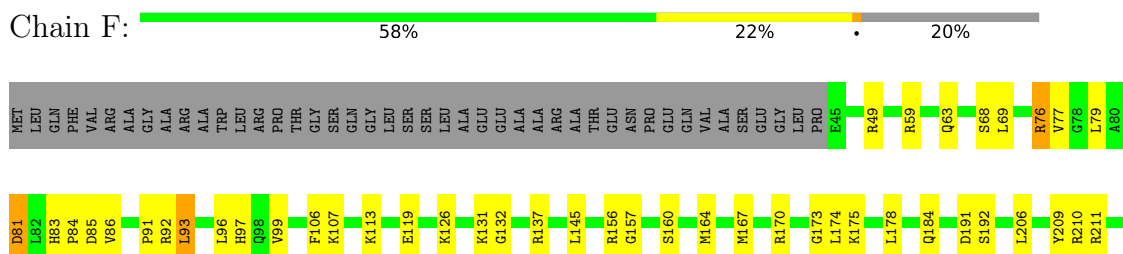
- Molecule 1: 39S ribosomal protein L2, mitochondrial




- Molecule 2: 39S ribosomal protein L3, mitochondrial

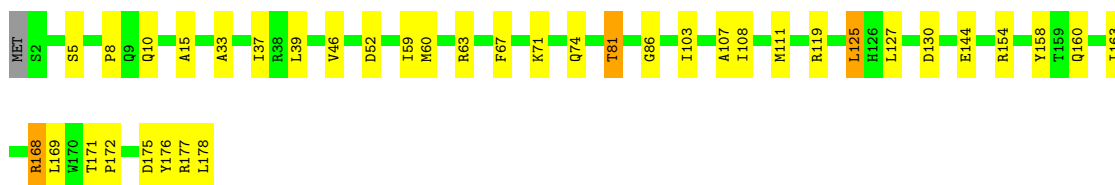


- Molecule 3: 39S ribosomal protein L4, mitochondrial



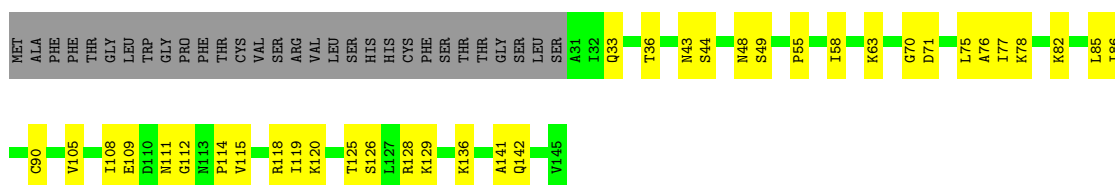
- Molecule 7: 39S ribosomal protein L13, mitochondrial

Chain K:  78% 20% ..



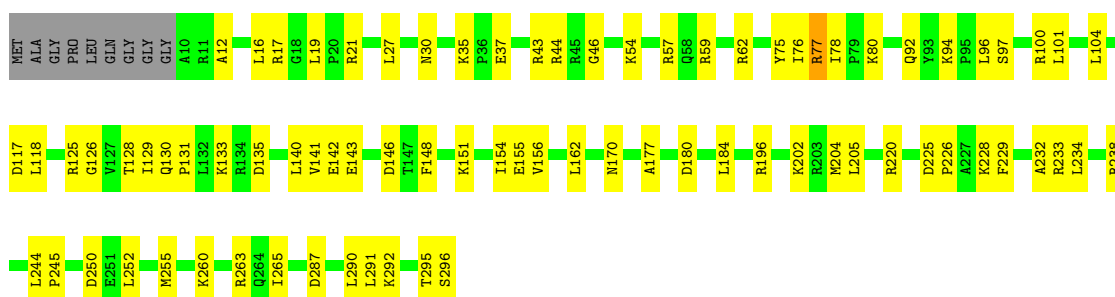
- Molecule 8: 39S ribosomal protein L14, mitochondrial

Chain L:  54% 25% 21%



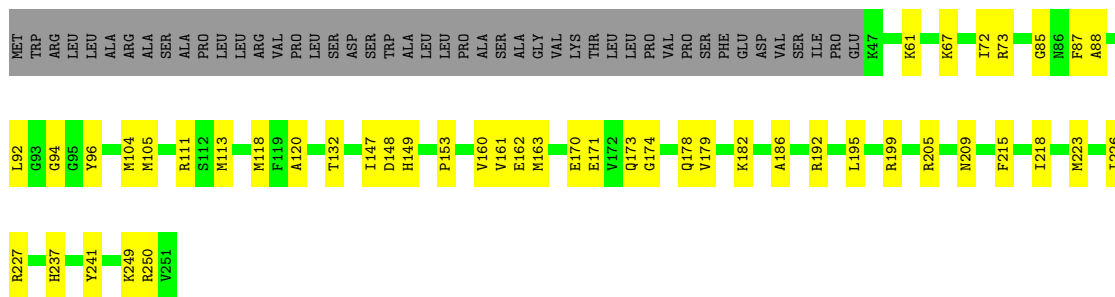
- Molecule 9: 39S ribosomal protein L15, mitochondrial

Chain M:  70% 27% .



- Molecule 10: 39S ribosomal protein L16, mitochondrial

Chain N:  63% 19% 18%

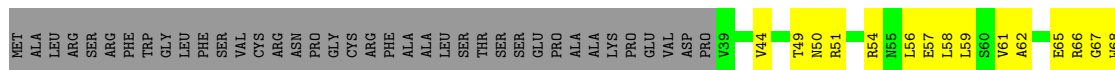


- Molecule 11: 39S ribosomal protein L17, mitochondrial

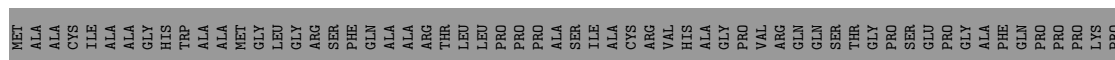
Chain O:  64% 23% 13%



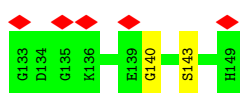
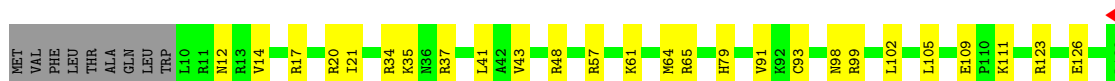
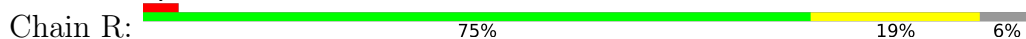
• Molecule 12: 39S ribosomal protein L18, mitochondrial



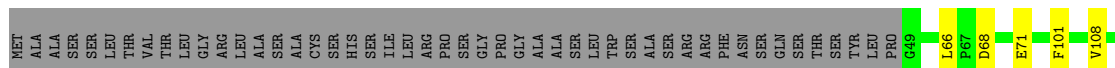
• Molecule 13: 39S ribosomal protein L19, mitochondrial



• Molecule 14: 39S ribosomal protein L20, mitochondrial

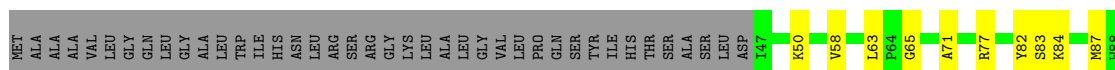


• Molecule 15: 39S ribosomal protein L21, mitochondrial





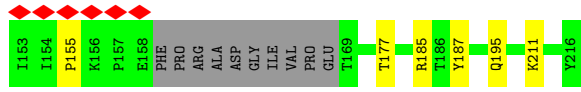
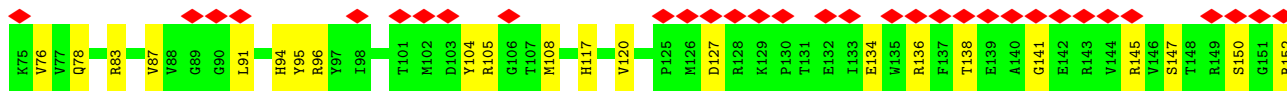
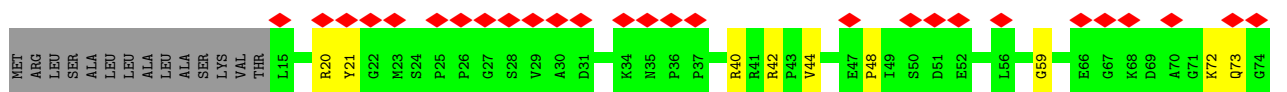
- Molecule 16: 39S ribosomal protein L22, mitochondrial



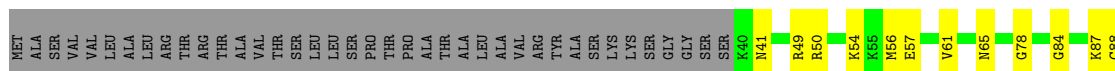
- Molecule 17: 39S ribosomal protein L23, mitochondrial



- Molecule 18: 39S ribosomal protein L24, mitochondrial



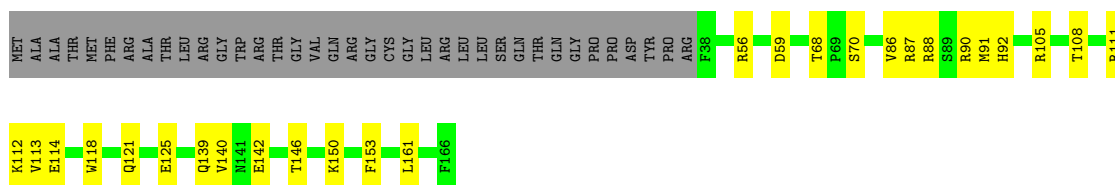
- Molecule 19: 39S ribosomal protein L27, mitochondrial



- Molecule 20: 39S ribosomal protein L28, mitochondrial

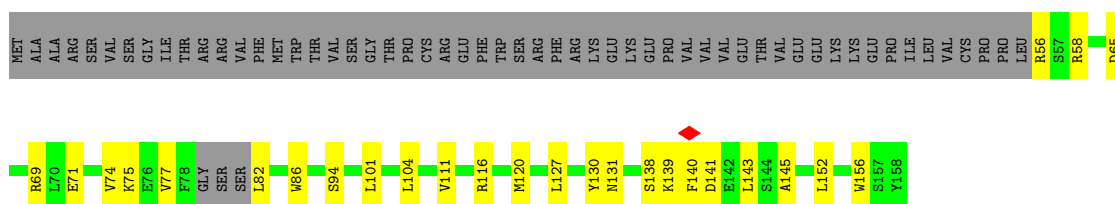
- Molecule 39: 39S ribosomal protein L49, mitochondrial

Chain g:  62% 16% 22%



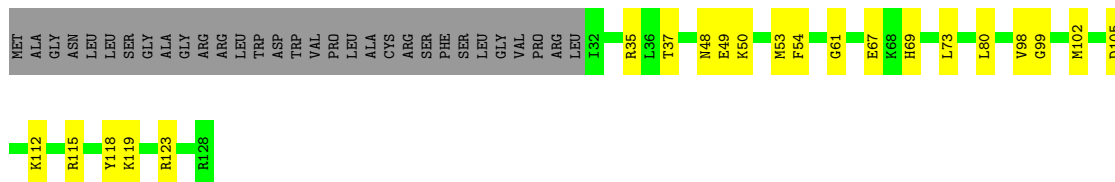
- Molecule 40: 39S ribosomal protein L50, mitochondrial

Chain h:  46% 17% 37%



- Molecule 41: 39S ribosomal protein L51, mitochondrial

Chain i:  59% 16% 24%




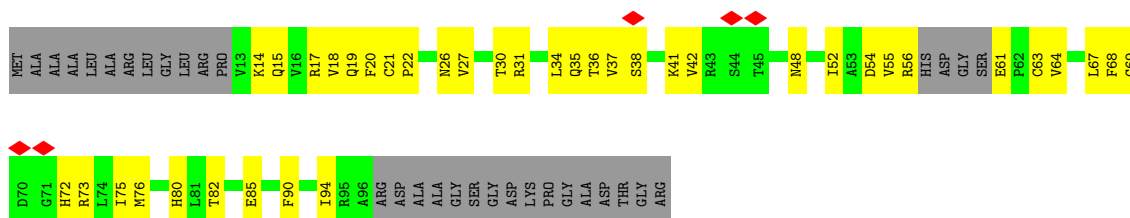
- Molecule 42: 39S ribosomal protein L52, mitochondrial

Chain j:  62% 7% 31%

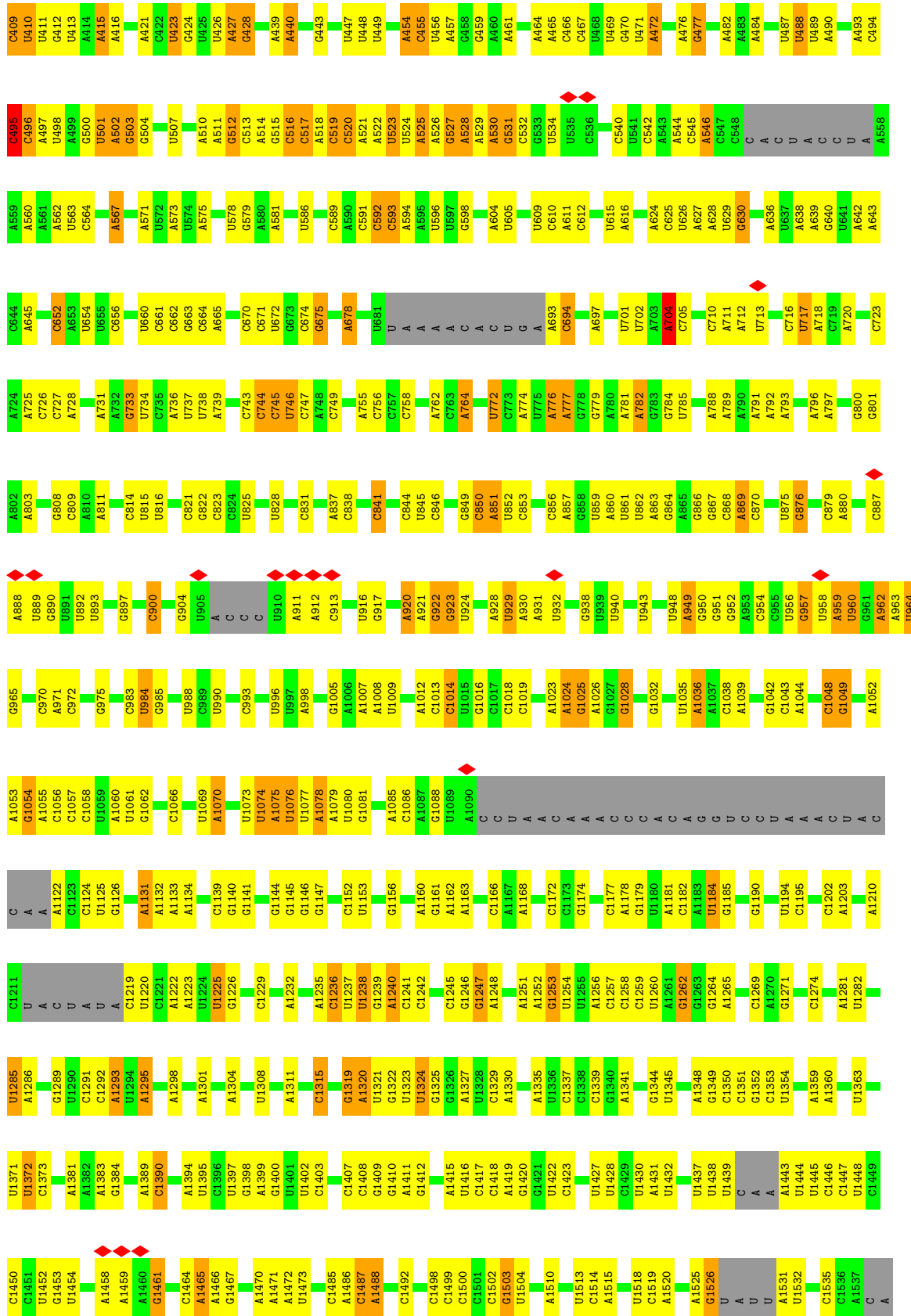


- Molecule 43: 39S ribosomal protein L53, mitochondrial

Chain k:  37% 35% 29%

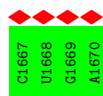
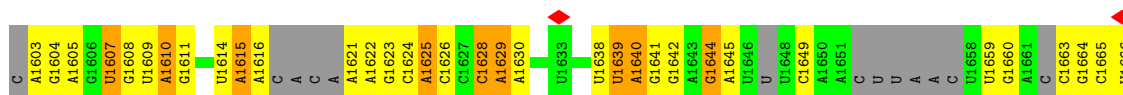


- Molecule 44: 39S ribosomal protein L54, mitochondrial

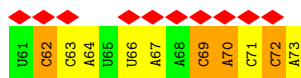
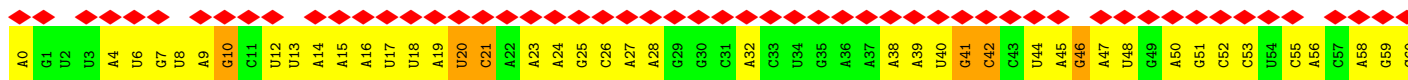
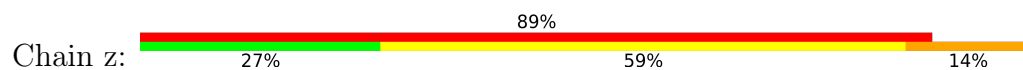




- Molecule 55: mitochondrial Val tRNA



- Molecule 56: mitochondrial tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	22042	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 ($e^-/\text{\AA}^2$)	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	0.973	Depositor
Minimum map value	-0.548	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.04	Depositor
Map size (\AA)	390.24, 390.24, 390.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	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: PNS, ZN, MG

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	0.39	0/1879	0.80	2/2527 (0.1%)
2	E	0.71	0/2465	0.90	4/3344 (0.1%)
3	F	0.80	0/2071	0.85	4/2817 (0.1%)
4	H	0.57	1/798 (0.1%)	0.97	7/1073 (0.7%)
5	I	0.44	0/1308	0.82	1/1761 (0.1%)
6	J	0.24	0/1077	0.57	0/1452
7	K	0.79	0/1495	0.84	1/2029 (0.0%)
8	L	0.65	0/904	0.86	3/1218 (0.2%)
9	M	0.81	0/2359	0.87	2/3185 (0.1%)
10	N	0.61	0/1697	0.81	1/2281 (0.0%)
11	O	0.69	0/1269	0.84	0/1708
12	P	0.47	0/1173	0.76	0/1588
13	Q	0.57	0/1846	0.83	0/2487
14	R	0.90	1/1174 (0.1%)	0.90	0/1572
15	S	0.84	1/1276 (0.1%)	0.91	0/1729
16	T	0.72	0/1335	0.80	0/1796
17	U	0.63	1/1183 (0.1%)	0.89	1/1600 (0.1%)
18	V	0.29	0/1616	0.64	0/2189
19	W	0.74	0/881	0.80	3/1188 (0.3%)
20	X	0.54	1/2090 (0.0%)	0.72	2/2825 (0.1%)
21	Y	0.58	0/1552	0.79	1/2079 (0.0%)
22	Z	0.72	0/1003	0.78	0/1354
23	0	0.68	0/895	0.86	2/1201 (0.2%)
24	1	0.26	0/438	0.74	0/583
25	2	0.90	0/357	0.80	0/475
26	3	0.91	0/852	0.92	0/1136
27	4	0.53	0/329	0.63	0/435
28	5	0.34	0/3250	0.66	4/4429 (0.1%)
29	6	0.52	1/2726 (0.0%)	0.75	1/3715 (0.0%)
30	7	0.43	0/2391	0.65	0/3234
31	8	0.26	0/855	0.69	0/1152
32	9	0.56	1/972 (0.1%)	0.79	0/1306

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	a	0.61	0/630	0.86	1/852 (0.1%)
34	b	0.74	0/1202	0.87	1/1626 (0.1%)
35	c	0.52	0/2264	0.73	0/3059
36	d	0.29	0/1790	0.66	0/2423
37	e	0.19	0/1797	0.53	0/2422
38	f	0.31	0/931	0.56	0/1259
39	g	0.70	0/1102	0.79	0/1503
40	h	0.42	0/847	0.71	0/1150
41	i	0.92	0/849	0.91	1/1135 (0.1%)
42	j	0.56	0/698	0.66	0/940
43	k	0.28	0/635	0.76	0/855
44	l	0.24	0/226	0.64	0/299
45	m	0.23	0/379	0.63	0/510
46	o	0.76	0/807	0.94	0/1083
47	p	0.37	0/1071	0.67	0/1433
48	q	0.39	0/1413	0.66	1/1906 (0.1%)
49	r	0.63	0/1238	0.84	3/1676 (0.2%)
50	s	0.53	0/3114	0.73	4/4225 (0.1%)
51	u	0.37	0/949	0.81	0/1281
52	v	0.30	0/597	0.75	0/796
53	w	0.24	0/647	0.71	0/871
54	A	0.73	0/34974	0.64	4/54421 (0.0%)
55	B	0.19	0/1328	0.37	0/2056
56	z	0.16	0/1729	0.36	0/2685
All	All	0.63	7/106733 (0.0%)	0.72	54/151934 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1
2	E	0	2
3	F	0	1
5	I	0	1
7	K	0	2
9	M	0	1
13	Q	0	2
15	S	0	1
17	U	0	1
20	X	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
23	0	0	1
29	6	0	1
35	c	0	1
49	r	0	1
50	s	0	1
All	All	0	18

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	X	52	ILE	C-N	-7.95	1.22	1.33
29	6	155	TYR	CA-C	-7.66	1.42	1.52
17	U	43	ARG	CA-CB	-6.54	1.43	1.53
4	H	75	ARG	CA-C	-5.85	1.44	1.52
32	9	70	LEU	C-N	-5.57	1.25	1.32

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	76	ARG	CG-CD-NE	-7.22	96.13	112.00
4	H	66	GLY	N-CA-C	7.07	119.43	110.38
41	i	98	VAL	N-CA-C	-6.98	105.53	112.17
28	5	85	PRO	CA-N-CD	-6.88	102.36	112.00
4	H	142	GLU	N-CA-CB	6.83	120.81	110.30

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	206	TYR	Peptide
2	E	228	PRO	Peptide
2	E	315	PRO	Peptide
3	F	81	ASP	Peptide
5	I	101	ASN	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	1842	0	1896	46	0
2	E	2396	0	2402	48	0
3	F	2013	0	2044	61	0
4	H	784	0	832	23	0
5	I	1283	0	1369	43	0
6	J	1061	0	1141	27	0
7	K	1451	0	1448	30	0
8	L	889	0	941	26	0
9	M	2305	0	2378	69	0
10	N	1654	0	1681	33	0
11	O	1245	0	1283	29	0
12	P	1148	0	1148	40	0
13	Q	1805	0	1841	36	0
14	R	1153	0	1214	28	0
15	S	1251	0	1322	45	0
16	T	1305	0	1352	30	0
17	U	1154	0	1154	37	0
18	V	1575	0	1583	30	0
19	W	859	0	888	24	0
20	X	2035	0	2054	32	0
21	Y	1517	0	1561	29	0
22	Z	978	0	1030	20	0
23	0	880	0	902	31	0
24	1	433	0	475	11	0
25	2	351	0	375	8	0
26	3	831	0	883	24	0
27	4	322	0	346	4	0
28	5	3156	0	3138	81	0
29	6	2640	0	2464	81	0
30	7	2334	0	2343	34	0
31	8	836	0	844	33	0
32	9	947	0	949	21	0
33	a	611	0	595	16	0
34	b	1178	0	1180	34	0
35	c	2217	0	2220	51	0
36	d	1741	0	1727	38	0
37	e	1762	0	1767	44	0
38	f	915	0	917	23	0
39	g	1067	0	1056	21	0
40	h	827	0	806	22	0
41	i	827	0	857	17	0
42	j	684	0	673	9	0
43	k	627	0	636	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	l	221	0	227	8	0
45	m	372	0	387	10	0
46	o	786	0	791	20	0
47	p	1058	0	1083	20	0
48	q	1379	0	1359	13	0
49	r	1203	0	1219	35	0
50	s	3036	0	3022	83	0
51	u	927	0	921	31	0
52	v	588	0	604	16	0
53	w	638	0	636	22	0
54	A	31265	0	15878	430	0
55	B	1191	0	607	32	0
56	z	1547	0	790	37	0
57	0	1	0	0	0	0
57	I	1	0	0	0	0
58	A	1	0	0	0	0
58	g	1	0	0	0	0
59	v	21	0	21	3	0
All	All	101125	0	85260	1747	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 10.

The worst 5 of 1747 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)
54:A:360:U:O4	54:A:454:A:C6	1.84	1.29
54:A:390:A:N6	54:A:409:C:C4	2.15	1.14
54:A:390:A:C6	54:A:409:C:N4	2.16	1.13
50:s:367:PHE:O	50:s:398:SER:HA	1.49	1.10
54:A:1446:C:H42	54:A:1470:A:N6	1.53	1.06

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	
						30	60
1	D	234/305 (77%)	204 (87%)	29 (12%)	1 (0%)	30	60
2	E	302/348 (87%)	266 (88%)	36 (12%)	0	100	100
3	F	248/311 (80%)	229 (92%)	19 (8%)	0	100	100
4	H	93/267 (35%)	86 (92%)	7 (8%)	0	100	100
5	I	154/261 (59%)	143 (93%)	11 (7%)	0	100	100
6	J	138/192 (72%)	126 (91%)	12 (9%)	0	100	100
7	K	175/178 (98%)	164 (94%)	11 (6%)	0	100	100
8	L	113/145 (78%)	103 (91%)	10 (9%)	0	100	100
9	M	285/296 (96%)	271 (95%)	14 (5%)	0	100	100
10	N	203/251 (81%)	194 (96%)	9 (4%)	0	100	100
11	O	150/175 (86%)	138 (92%)	12 (8%)	0	100	100
12	P	139/180 (77%)	133 (96%)	6 (4%)	0	100	100
13	Q	215/292 (74%)	201 (94%)	14 (6%)	0	100	100
14	R	138/149 (93%)	136 (99%)	2 (1%)	0	100	100
15	S	154/205 (75%)	134 (87%)	20 (13%)	0	100	100
16	T	155/206 (75%)	150 (97%)	5 (3%)	0	100	100
17	U	135/153 (88%)	116 (86%)	19 (14%)	0	100	100
18	V	188/216 (87%)	178 (95%)	10 (5%)	0	100	100
19	W	107/148 (72%)	98 (92%)	9 (8%)	0	100	100
20	X	241/256 (94%)	229 (95%)	12 (5%)	0	100	100
21	Y	174/250 (70%)	168 (97%)	6 (3%)	0	100	100
22	Z	118/161 (73%)	111 (94%)	7 (6%)	0	100	100
23	0	106/188 (56%)	103 (97%)	3 (3%)	0	100	100
24	1	50/65 (77%)	46 (92%)	4 (8%)	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	4	34/103 (33%)	33 (97%)	1 (3%)	0	100	100
28	5	383/423 (90%)	354 (92%)	29 (8%)	0	100	100
29	6	316/380 (83%)	298 (94%)	18 (6%)	0	100	100
30	7	285/338 (84%)	264 (93%)	21 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	8	97/206 (47%)	87 (90%)	10 (10%)	0	100	100
32	9	113/137 (82%)	102 (90%)	11 (10%)	0	100	100
33	a	69/142 (49%)	64 (93%)	5 (7%)	0	100	100
34	b	146/215 (68%)	127 (87%)	19 (13%)	0	100	100
35	c	271/332 (82%)	262 (97%)	9 (3%)	0	100	100
36	d	203/306 (66%)	193 (95%)	10 (5%)	0	100	100
37	e	211/279 (76%)	193 (92%)	18 (8%)	0	100	100
38	f	110/212 (52%)	100 (91%)	10 (9%)	0	100	100
39	g	127/166 (76%)	120 (94%)	7 (6%)	0	100	100
40	h	96/158 (61%)	93 (97%)	3 (3%)	0	100	100
41	i	95/128 (74%)	88 (93%)	7 (7%)	0	100	100
42	j	83/123 (68%)	81 (98%)	2 (2%)	0	100	100
43	k	76/112 (68%)	72 (95%)	4 (5%)	0	100	100
44	l	21/138 (15%)	21 (100%)	0	0	100	100
45	m	43/128 (34%)	37 (86%)	6 (14%)	0	100	100
46	o	91/102 (89%)	85 (93%)	5 (6%)	1 (1%)	11	42
47	p	119/206 (58%)	114 (96%)	5 (4%)	0	100	100
48	q	162/222 (73%)	155 (96%)	7 (4%)	0	100	100
49	r	140/196 (71%)	129 (92%)	11 (8%)	0	100	100
50	s	366/439 (83%)	343 (94%)	23 (6%)	0	100	100
51	u	109/234 (47%)	103 (94%)	6 (6%)	0	100	100
52	v	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
53	w	77/156 (49%)	70 (91%)	7 (9%)	0	100	100
All	All	8059/11129 (72%)	7508 (93%)	549 (7%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
46	o	13	PRO
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	190/245 (78%)	190 (100%)	0	100	100
2	E	259/290 (89%)	259 (100%)	0	100	100
3	F	217/262 (83%)	217 (100%)	0	100	100
4	H	86/228 (38%)	86 (100%)	0	100	100
5	I	145/232 (62%)	145 (100%)	0	100	100
6	J	113/150 (75%)	113 (100%)	0	100	100
7	K	155/156 (99%)	155 (100%)	0	100	100
8	L	98/124 (79%)	98 (100%)	0	100	100
9	M	245/249 (98%)	244 (100%)	1 (0%)	84	81
10	N	172/211 (82%)	172 (100%)	0	100	100
11	O	133/150 (89%)	133 (100%)	0	100	100
12	P	123/155 (79%)	123 (100%)	0	100	100
13	Q	199/256 (78%)	198 (100%)	1 (0%)	81	80
14	R	118/126 (94%)	118 (100%)	0	100	100
15	S	141/180 (78%)	140 (99%)	1 (1%)	76	77
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%)	172 (100%)	0	100	100
19	W	89/119 (75%)	89 (100%)	0	100	100
20	X	219/229 (96%)	219 (100%)	0	100	100
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%)	49 (100%)	0	100	100
25	2	38/72 (53%)	38 (100%)	0	100	100
26	3	88/166 (53%)	88 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	4	35/89 (39%)	35 (100%)	0	100	100
28	5	348/368 (95%)	348 (100%)	0	100	100
29	6	265/332 (80%)	265 (100%)	0	100	100
30	7	263/303 (87%)	263 (100%)	0	100	100
31	8	91/190 (48%)	91 (100%)	0	100	100
32	9	99/112 (88%)	99 (100%)	0	100	100
33	a	69/133 (52%)	68 (99%)	1 (1%)	59	70
34	b	130/186 (70%)	130 (100%)	0	100	100
35	c	241/288 (84%)	240 (100%)	1 (0%)	84	81
36	d	193/274 (70%)	193 (100%)	0	100	100
37	e	188/236 (80%)	188 (100%)	0	100	100
38	f	101/188 (54%)	101 (100%)	0	100	100
39	g	119/148 (80%)	119 (100%)	0	100	100
40	h	95/148 (64%)	95 (100%)	0	100	100
41	i	86/110 (78%)	86 (100%)	0	100	100
42	j	68/97 (70%)	68 (100%)	0	100	100
43	k	71/90 (79%)	71 (100%)	0	100	100
44	l	23/116 (20%)	23 (100%)	0	100	100
45	m	40/113 (35%)	40 (100%)	0	100	100
46	o	79/87 (91%)	79 (100%)	0	100	100
47	p	117/181 (65%)	117 (100%)	0	100	100
48	q	141/178 (79%)	141 (100%)	0	100	100
49	r	133/169 (79%)	133 (100%)	0	100	100
50	s	326/381 (86%)	326 (100%)	0	100	100
51	u	105/200 (52%)	105 (100%)	0	100	100
52	v	59/60 (98%)	59 (100%)	0	100	100
53	w	73/136 (54%)	73 (100%)	0	100	100
All	All	7239/9609 (75%)	7234 (100%)	5 (0%)	87	88

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	M	30	ASN

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Mol	Chain	Res	Type
13	Q	139	GLN
15	S	118	ASN
33	a	137	ASN
35	c	134	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 73 such sidechains are listed below:

Mol	Chain	Res	Type
42	j	26	GLN
53	w	101	ASN
42	j	99	GLN
48	q	120	HIS
15	S	140	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
54	A	1460/1559 (93%)	448 (30%)	26 (1%)
55	B	51/69 (73%)	16 (31%)	1 (1%)
56	z	70/73 (95%)	36 (51%)	0
All	All	1581/1701 (92%)	500 (31%)	27 (1%)

5 of 500 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
54	A	8	C
54	A	9	U
54	A	11	G
54	A	19	C
54	A	22	A

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	A	860	A
54	A	958	U
54	A	1443	A
54	A	889	U
54	A	983	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 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
59	PNS	v	101	-	14,20,21	2.15	4 (28%)	18,26,29	1.47	3 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	PNS	v	101	-	-	12/24/26/27	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	v	101	PNS	C39-N41	5.04	1.45	1.33
59	v	101	PNS	C34-N36	4.82	1.44	1.33
59	v	101	PNS	O40-C39	-2.49	1.18	1.23
59	v	101	PNS	O35-C34	-2.33	1.18	1.23

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	v	101	PNS	C37-C38-C39	-3.47	106.61	112.39
59	v	101	PNS	C38-C37-N36	-2.26	107.19	112.00
59	v	101	PNS	C31-C29-C32	2.11	112.36	108.77

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

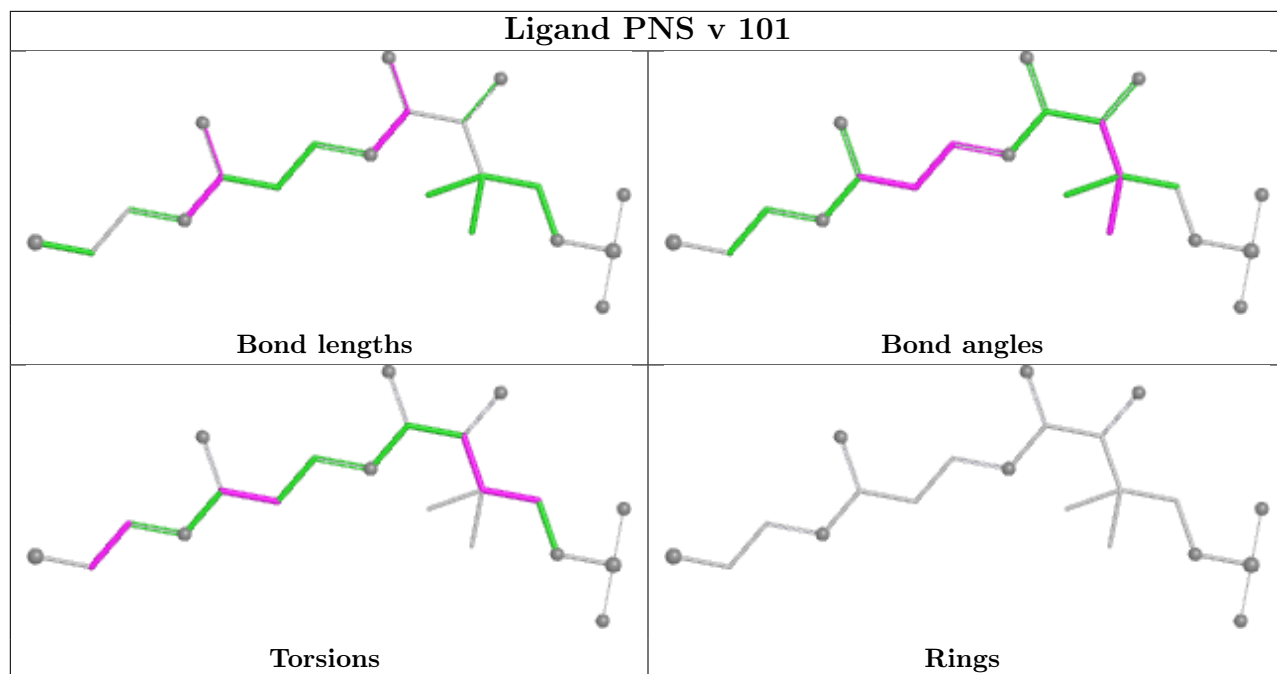
Mol	Chain	Res	Type	Atoms
59	v	101	PNS	O27-C28-C29-C30
59	v	101	PNS	O27-C28-C29-C31
59	v	101	PNS	O27-C28-C29-C32
59	v	101	PNS	C28-C29-C32-O33
59	v	101	PNS	C28-C29-C32-C34

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	v	101	PNS	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
56	z	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	z	4:A	O3'	6:U	P	9.11

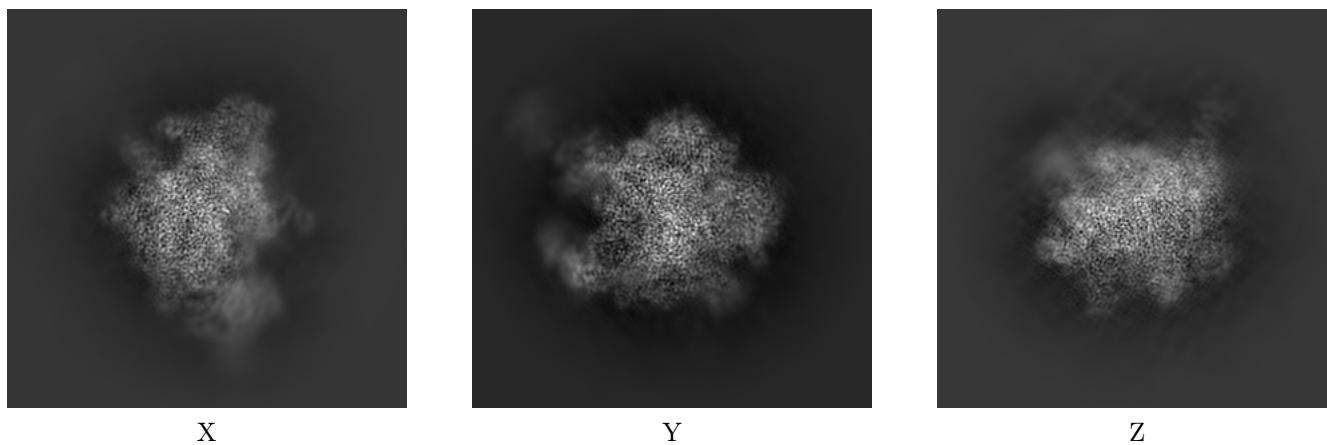
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12926. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

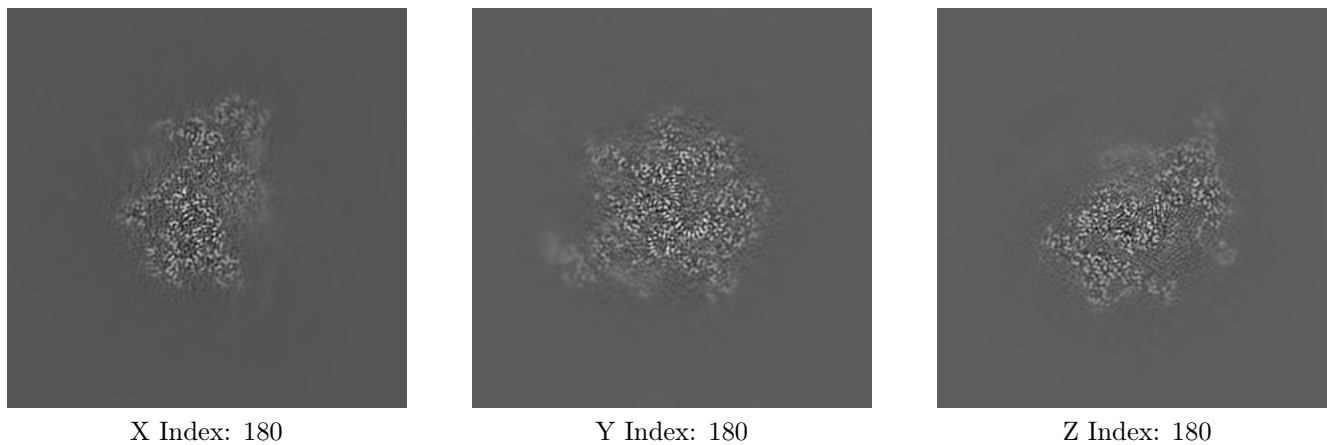
6.1.1 Primary map



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

6.2 Central slices [i](#)

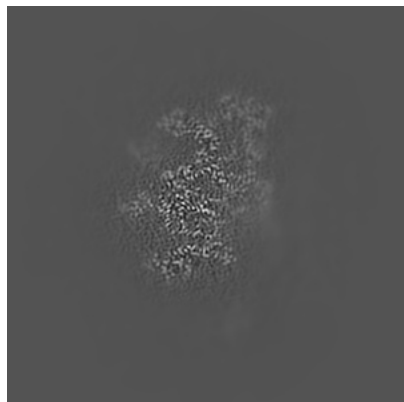
6.2.1 Primary map



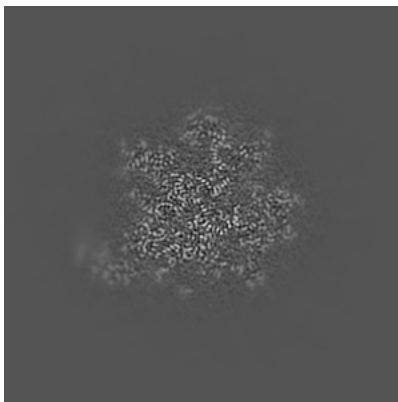
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

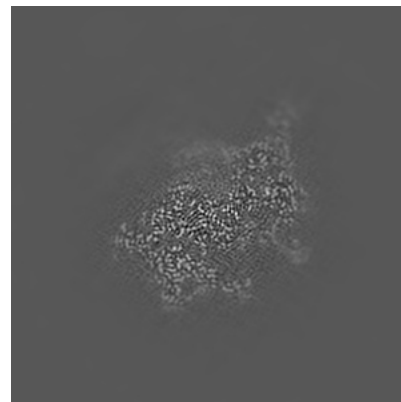
6.3.1 Primary map



X Index: 172



Y Index: 173

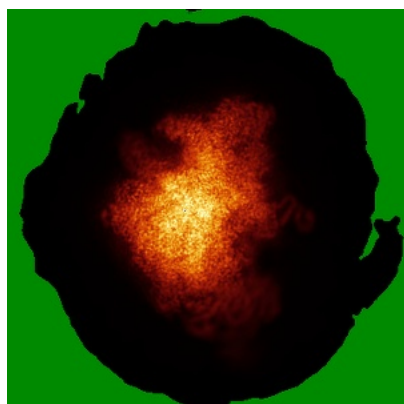


Z Index: 179

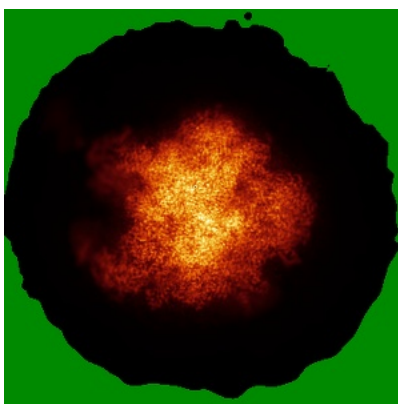
The images above show the largest variance slices of the map in three orthogonal directions.

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

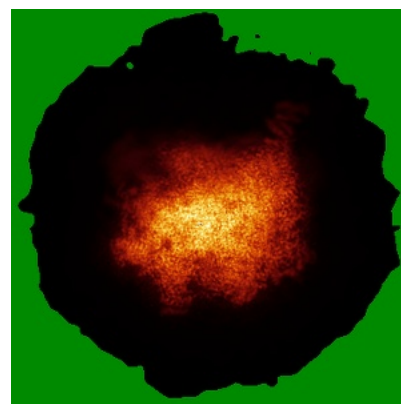
6.4.1 Primary map



X



Y

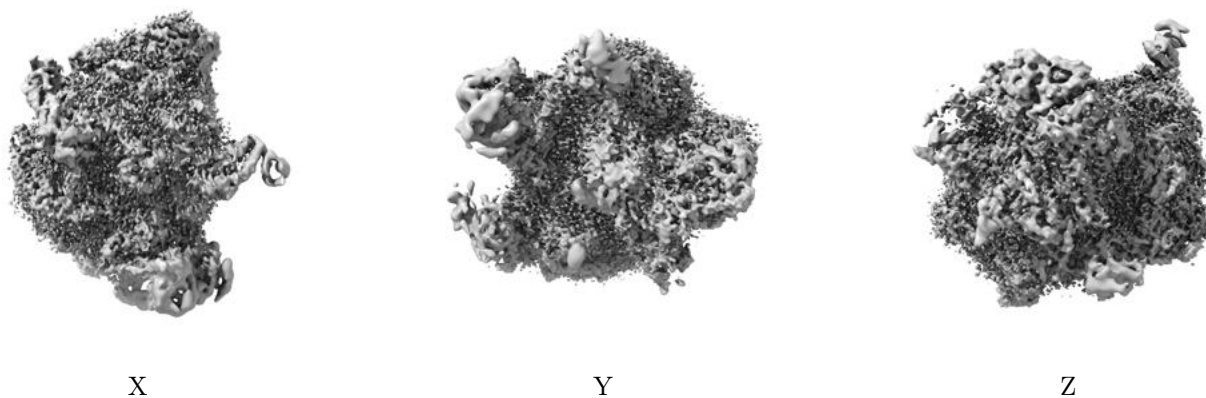


Z

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

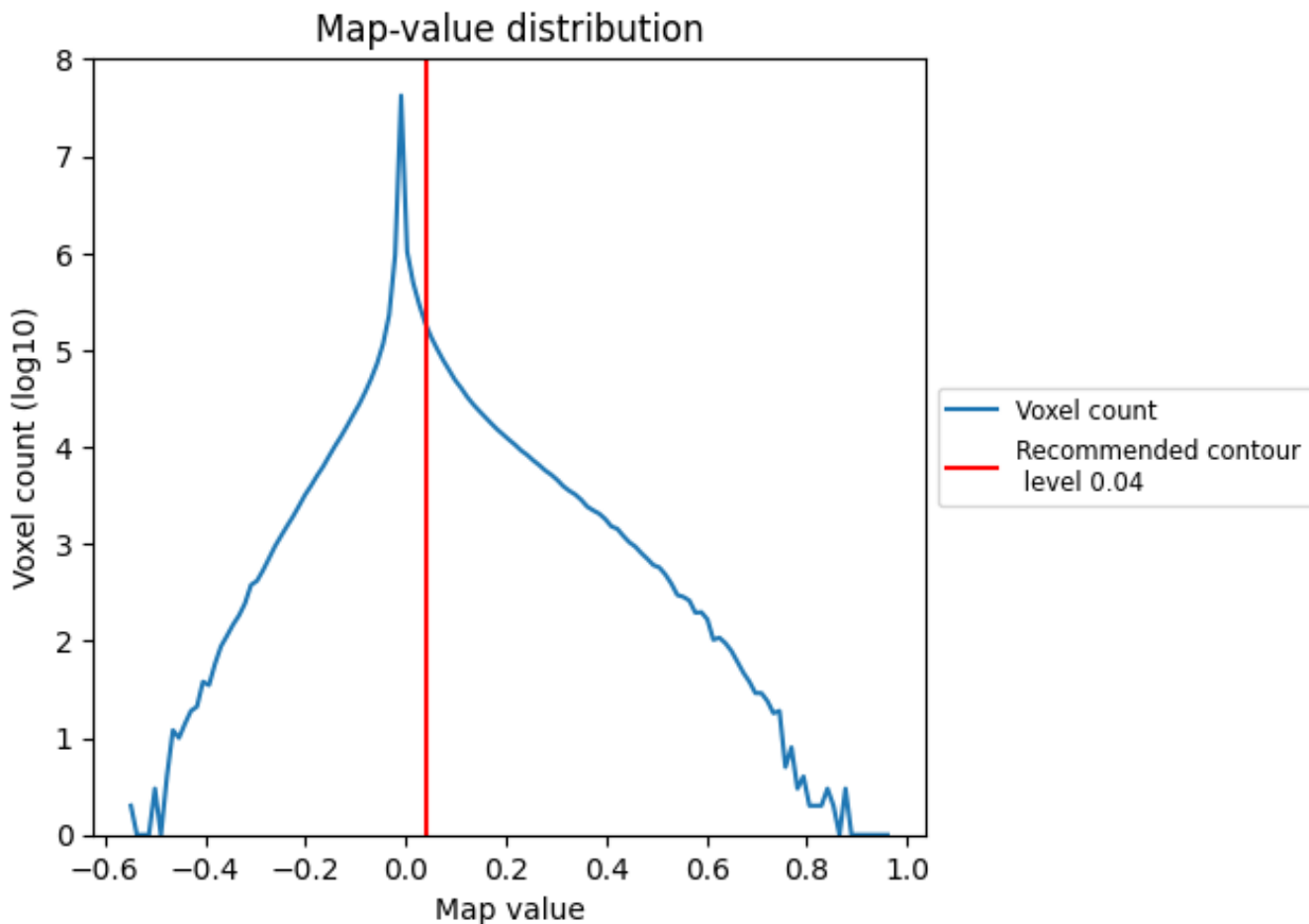
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

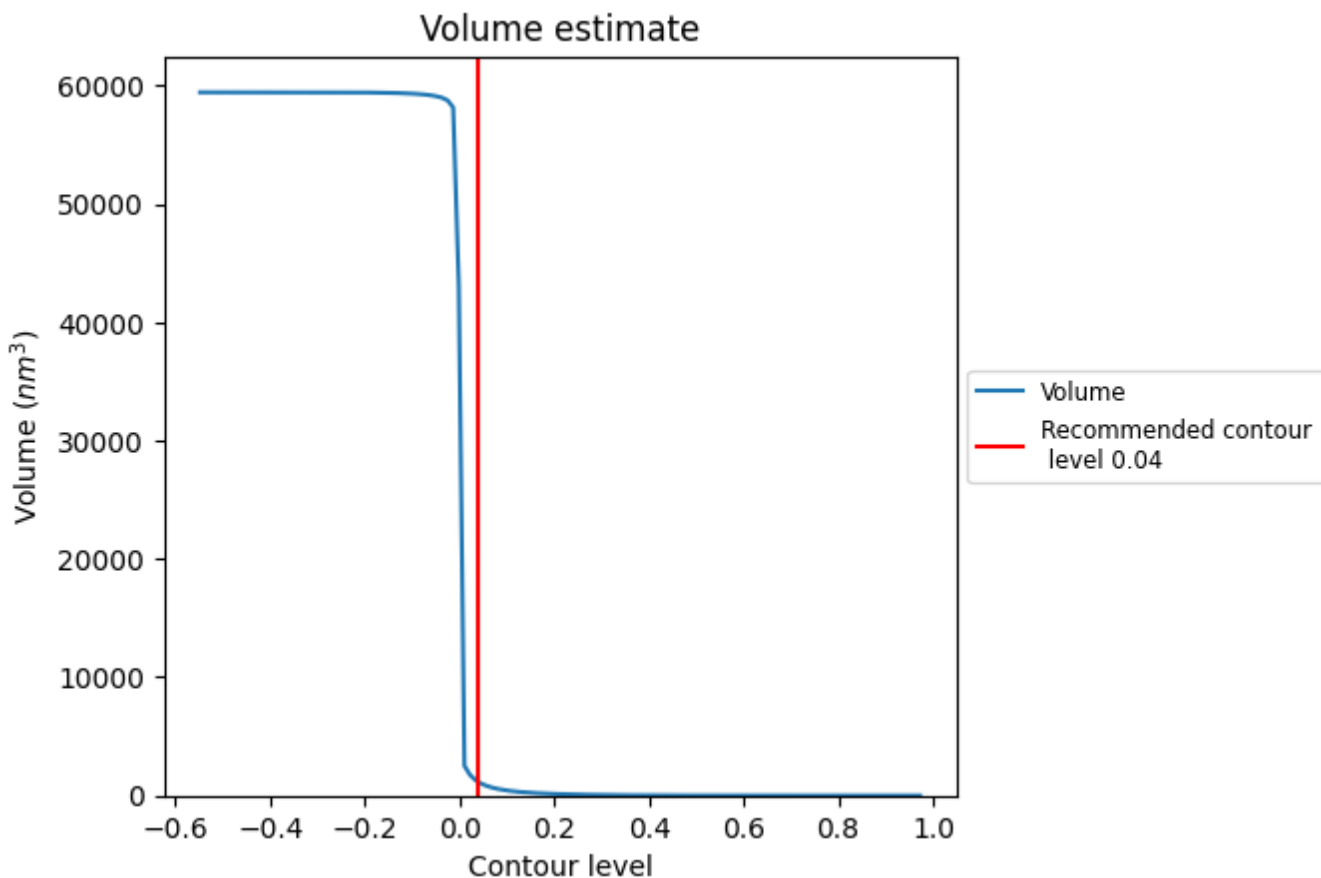
This section contains the results of statistical analysis of the map.

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.

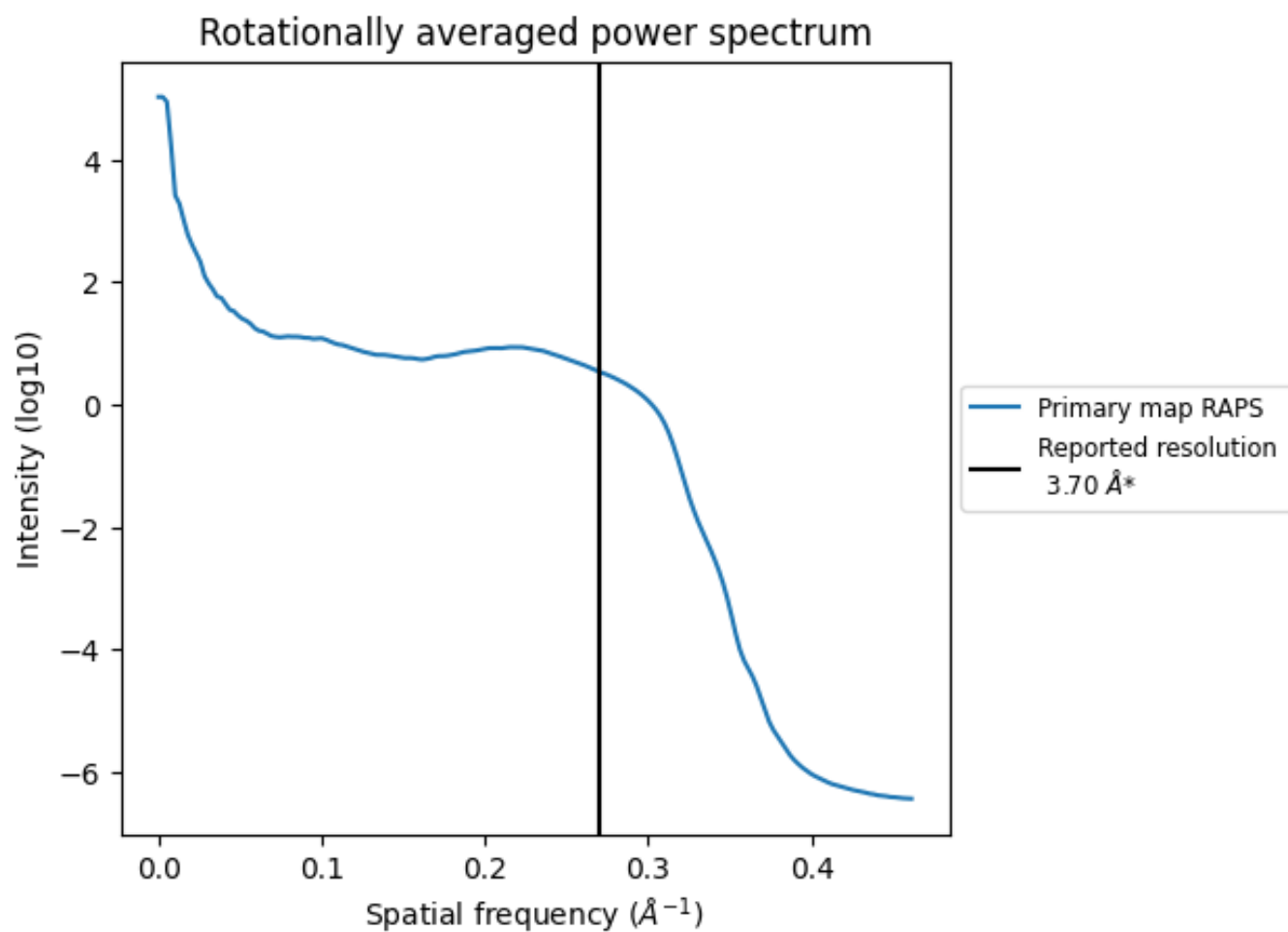
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1150 nm^3 ; this corresponds to an approximate mass of 1038 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](#)

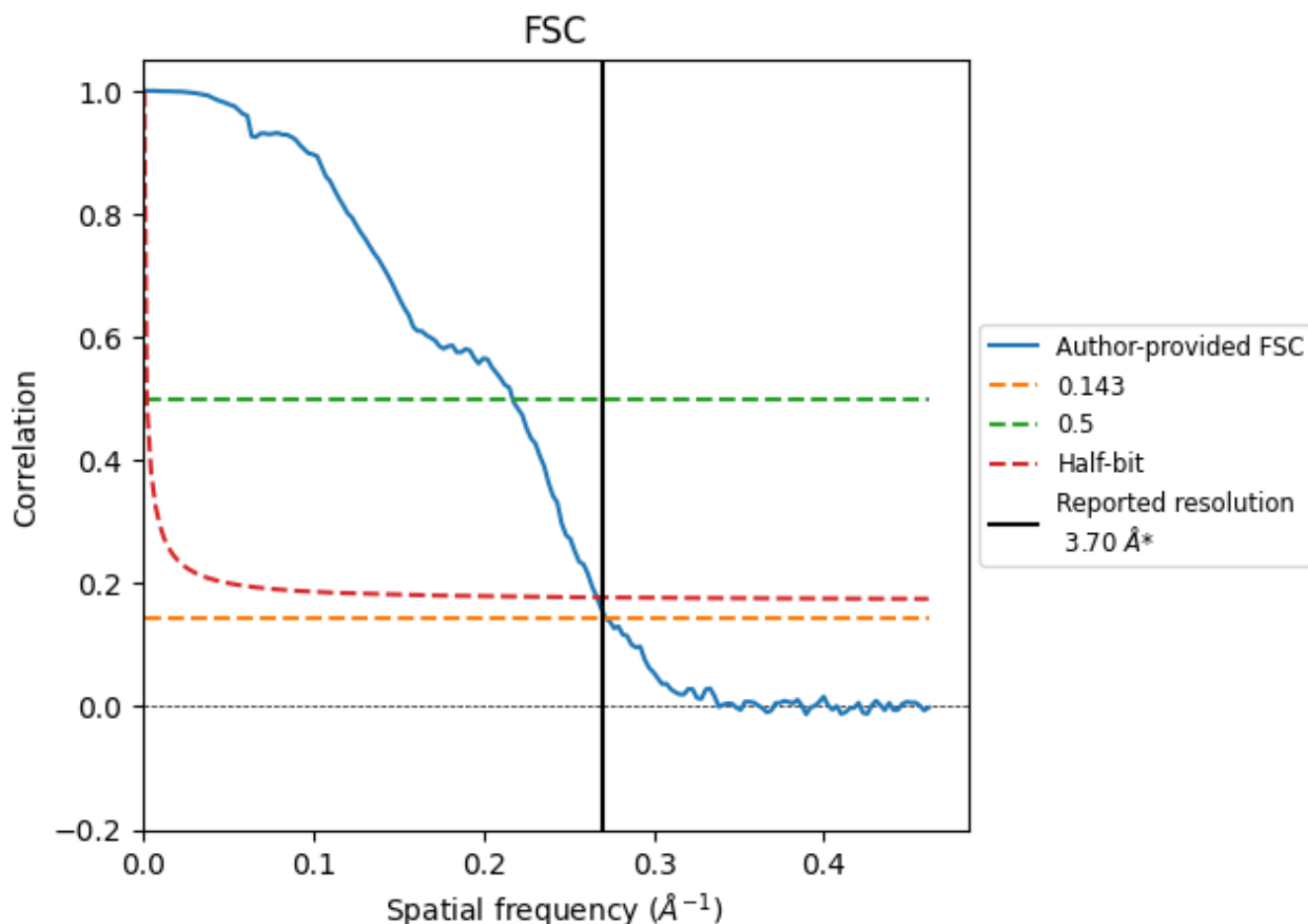


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.270 \AA^{-1}

8.2 Resolution estimates [i](#)

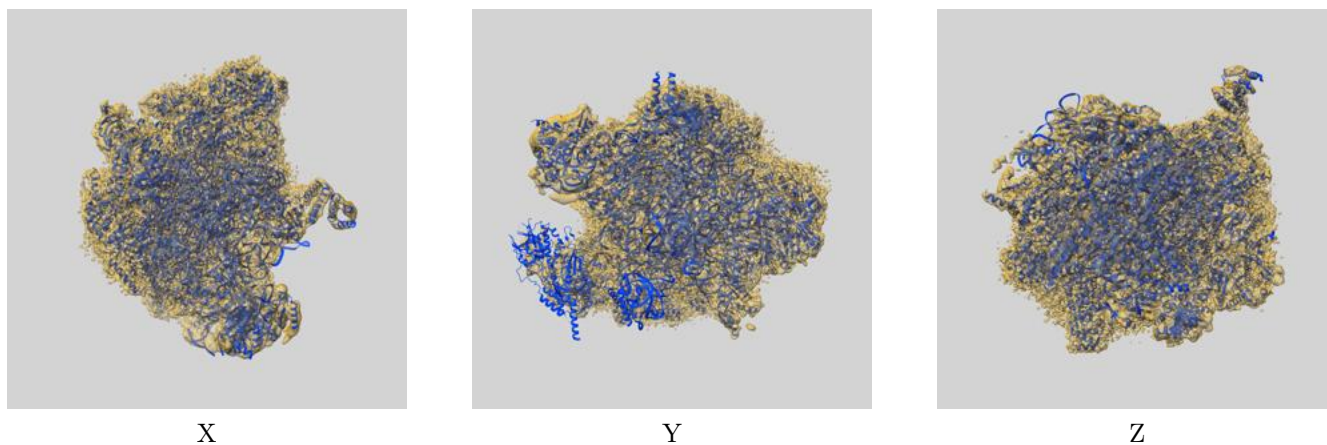
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.68	4.60	3.75
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

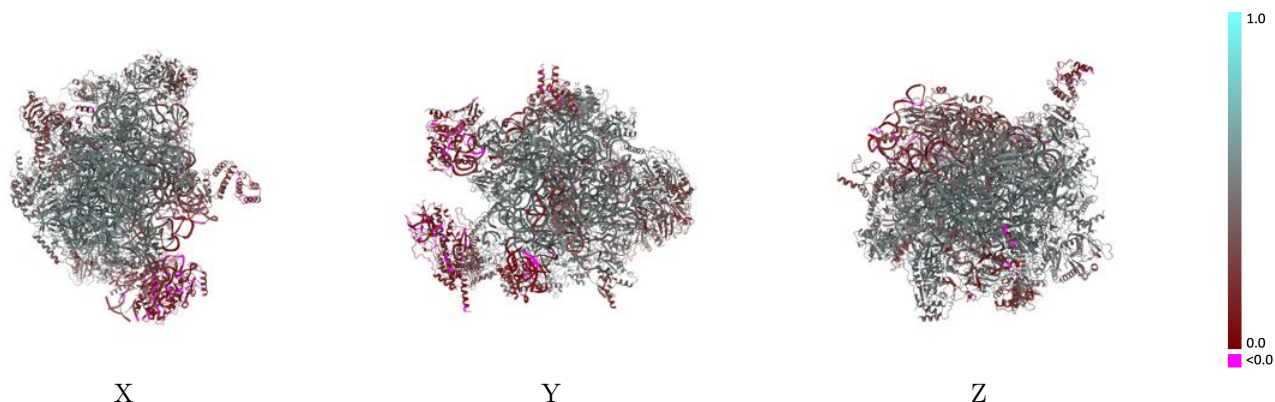
This section contains information regarding the fit between EMDB map EMD-12926 and PDB model 7OID. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



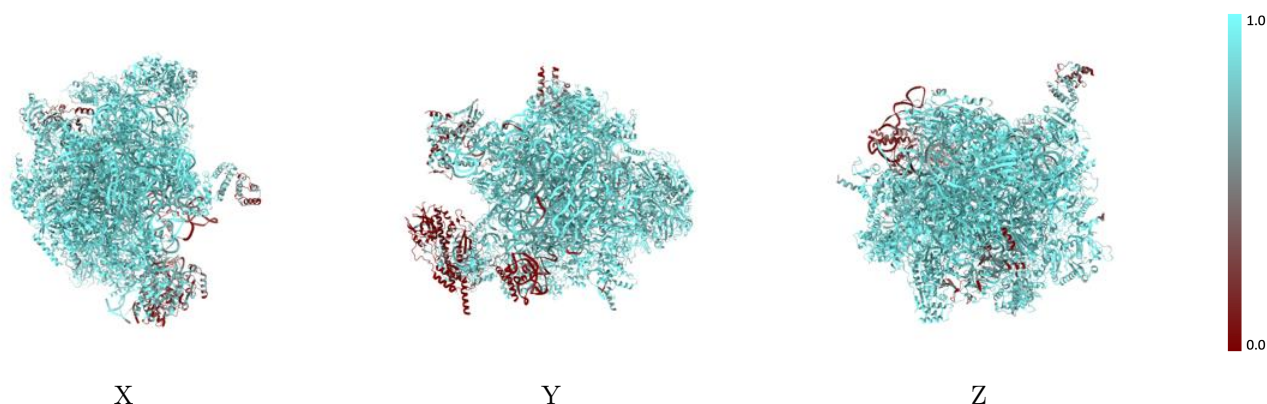
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



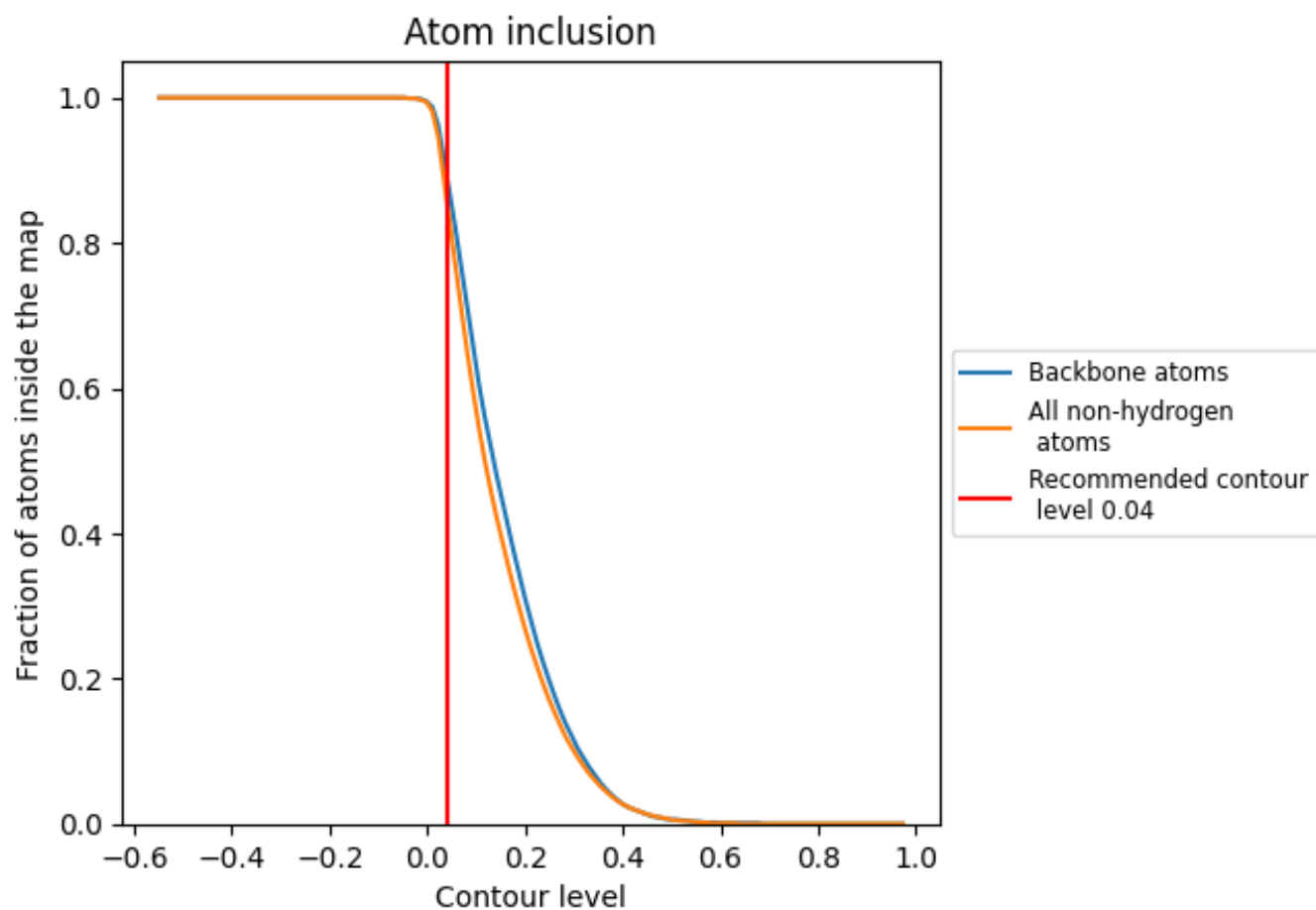
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 86% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8560	 0.4290
0	 0.9320	 0.4950
1	 0.7860	 0.2170
2	 0.9700	 0.5770
3	 0.9700	 0.5670
4	 0.9740	 0.5030
5	 0.8270	 0.3580
6	 0.8840	 0.3890
7	 0.9010	 0.4220
8	 0.1400	 0.1470
9	 0.9150	 0.4500
A	 0.9440	 0.4660
B	 0.8380	 0.2300
D	 0.8710	 0.4200
E	 0.9490	 0.5060
F	 0.9560	 0.5370
H	 0.8640	 0.4200
I	 0.6800	 0.2380
J	 0.4590	 0.1140
K	 0.9500	 0.5270
L	 0.9290	 0.4890
M	 0.9610	 0.5340
N	 0.9520	 0.5040
O	 0.9420	 0.5090
P	 0.9100	 0.4240
Q	 0.9300	 0.4840
R	 0.9070	 0.5130
S	 0.9280	 0.5110
T	 0.9610	 0.5320
U	 0.8690	 0.4510
V	 0.5660	 0.2700
W	 0.9450	 0.5280
X	 0.9310	 0.4790
Y	 0.9260	 0.4760
Z	 0.9220	 0.5110



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Chain	Atom inclusion	Q-score
a	 0.9630	 0.5170
b	 0.9570	 0.5210
c	 0.9350	 0.4800
d	 0.7050	 0.2860
e	 0.0180	 0.1000
f	 0.2500	 0.2060
g	 0.9550	 0.5170
h	 0.8970	 0.4000
i	 0.9540	 0.5560
j	 0.9360	 0.4850
k	 0.7680	 0.2300
l	 0.7960	 0.1800
m	 0.0030	 0.0760
o	 0.9540	 0.5370
p	 0.9090	 0.4520
q	 0.6280	 0.3440
r	 0.9280	 0.4850
s	 0.9260	 0.4710
u	 0.8720	 0.3690
v	 0.7090	 0.2550
w	 0.3600	 0.1620
z	 0.1260	 0.0760