



wwPDB EM Validation Summary Report ⓘ

Nov 9, 2024 – 11:50 PM EST

PDB ID : 7L20
EMDB ID : EMD-23121
Title : Cryo-EM structure of the human 39S mitoribosomal subunit in complex with RRFmt and EF-G2mt.
Authors : Agrawal, E.; Koripella, R.
Deposited on : 2020-12-15
Resolution : 3.15 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.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

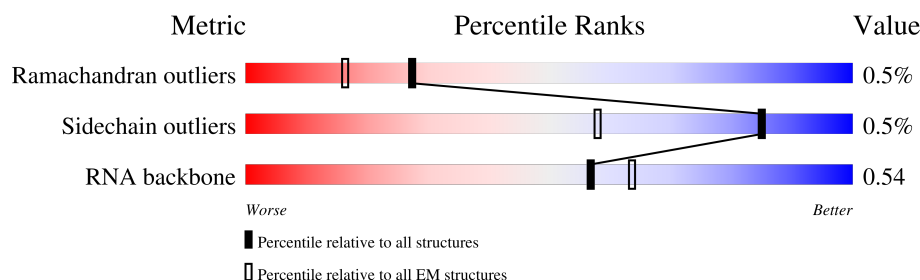
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.15 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1559	
2	B	73	
3	D	305	
4	F	311	
5	H	267	
6	K	178	
7	L	145	
8	M	296	

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Mol	Chain	Length	Quality of chain
9	O	175	
10	R	149	
11	S	205	
12	T	212	
13	W	148	
14	X	256	
15	Y	250	
16	Z	161	
17	0	188	
18	1	65	
19	2	92	
20	3	188	
21	4	103	
22	8	206	
23	b	155	
24	e	279	
25	g	166	
26	i	128	
27	j	123	
28	m	128	
29	o	102	
30	q	222	
31	r	196	
32	J	192	
33	I	261	

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Mol	Chain	Length	Quality of chain
34	N	251	
35	P	179	
36	U	153	
37	V	216	
38	E	348	
39	5	423	
40	6	380	
41	7	338	
42	9	137	
43	a	142	
44	c	332	
45	d	306	
46	f	194	
47	h	158	
48	k	112	
49	l	138	
50	p	206	
51	s	439	
52	Q	292	
53	u	65	
54	TA	198	
54	TB	198	
54	TC	198	
55	z	204	
56	w	696	

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 110234 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 RNA chain called 16S rRNA mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1527	Total	C	N	O	P	0	0
			32395	14536	5844	10488	1527		

- Molecule 2 is a RNA chain called tRNAval.

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

- Molecule 3 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	239	Total	C	N	O	S	0	0
			1866	1162	377	318	9		

- Molecule 4 is a protein called 39S ribosomal protein L4, mitochondrial.

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

- Molecule 5 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	H	98	Total	C	N	O	0	0
			806	510	156	140		

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

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

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

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

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

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

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

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

- Molecule 10 is a protein called 39S ribosomal protein L20, mitochondrial.

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

- Molecule 11 is a protein called 39S ribosomal protein L21, mitochondrial.

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

- Molecule 12 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 13 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	W	111	Total	C	N	O	S	0	0
			871	558	164	146	3		

- Molecule 14 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	X	243	Total	C	N	O	S	0	0
			2027	1310	350	362	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	148	ALA	THR	variant	UNP Q13084
X	149	SER	PRO	variant	UNP Q13084
X	150	GLY	LYS	variant	UNP Q13084

- Molecule 15 is a protein called 39S ribosomal protein L47, mitochondrial.

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

- Molecule 16 is a protein called 39S ribosomal protein L30, mitochondrial.

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

- Molecule 17 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	0	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 18 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	1	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

- Molecule 19 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	2	46	Total	C	N	O	S	0	0
			376	233	83	59	1		

- Molecule 20 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 21 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	4	38	Total	C	N	O	S	0	0
			342	217	72	49	4		

- Molecule 22 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	8	99	Total	C	N	O	S	0	0
			836	535	144	155	2		

- Molecule 23 is a protein called 39S ribosomal protein L43, mitochondrial.

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

- Molecule 24 is a protein called 39S ribosomal protein L46, mitochondrial.

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

- Molecule 25 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	g	132	Total	C	N	O	S	0	0
			1096	709	191	194	2		

- Molecule 26 is a protein called 39S ribosomal protein L51, mitochondrial.

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

- Molecule 27 is a protein called cDNA FLJ76418, highly similar to Homo sapiens mitochondrial ribosomal protein L52 (MRPL52), transcript variant 1, mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	j	93	Total	C	N	O	S	0	0
			740	460	143	135	2		

- Molecule 28 is a protein called 39S ribosomal protein L55, mitochondrial.

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

- Molecule 29 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	o	94	Total	C	N	O	S	0	0
			797	501	165	128	3		

- Molecule 30 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	q	168	Total	C	N	O	S	0	0
			1293	801	254	233	5		

- Molecule 31 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	r	162	Total	C	N	O	S	0	0
			1322	839	252	223	8		

- Molecule 32 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	J	175	Total	C	N	O	S	0	0
			1330	847	237	244	2		

- Molecule 33 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	I	179	Total	C	N	O	S	0	0
			1435	925	258	242	10		

- Molecule 34 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	N	222	Total	C	N	O	S	0	0
			1786	1143	326	307	10		

- Molecule 35 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	P	143	Total	C	N	O	S	0	0
			1165	729	223	208	5		

- Molecule 36 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	U	152	Total	C	N	O	S	0	0
			1222	773	233	213	3		

- Molecule 37 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	V	206	Total	C	N	O	S	0	0
			1682	1071	299	304	8		

- Molecule 38 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	E	306	Total	C	N	O	S	0	0
			2410	1547	419	433	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	5	393	Total	C	N	O	S	0	0
			3205	2070	559	565	11		

- Molecule 40 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	6	354	Total	C	N	O	S	0	0
			2948	1881	525	533	9		

- Molecule 41 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	7	297	Total	C	N	O	S	0	0
			2410	1540	409	443	18		

- Molecule 42 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	9	124	Total	C	N	O	S	0	0
			997	644	170	181	2		

- Molecule 43 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	a	108	Total	C	N	O	S	0	0
			896	560	162	169	5		

- Molecule 44 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	c	289	Total	C	N	O	S	0	0
			2322	1483	400	430	9		

- Molecule 45 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	d	257	Total	C	N	O	S	0	0
			2075	1326	363	372	14		

- Molecule 46 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	f	146	Total	C	N	O	S	0	0
			1126	714	186	222	4		

- Molecule 47 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	h	110	Total	C	N	O	S	0	0
			894	568	156	167	3		

- Molecule 48 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	k	96	Total	C	N	O	S	0	0
			743	462	143	133	5		

- Molecule 49 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	l	72	Total	C	N	O	S	0	0
			619	394	112	111	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	p	152	Total	C	N	O	S	0	0
			1227	762	232	229	4		

- Molecule 51 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	393	Total	C	N	O	S	0	0
			3178	2036	565	563	14		

- Molecule 52 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Q	220	Total	C	N	O	S	0	0
			1834	1174	326	325	9		

- Molecule 53 is a protein called 39 S P-site finger.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	u	65	Total	C	N	O	0	0
			325	195	65	65		

- Molecule 54 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	TA	45	Total	C	N	O	0	0
			345	222	54	69		
54	TB	27	Total	C	N	O	0	0
			213	137	33	43		
54	TC	71	Total	C	N	O	0	0
			352	210	71	71		

- Molecule 55 is a protein called Ribosome-recycling factor, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	197	Total	C	N	O	S	0	0
			1525	942	274	301	8		

- Molecule 56 is a protein called Ribosome-releasing factor 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	w	696	Total	C	N	O	S	0	0
			5422	3424	932	1042	24		

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	86	LEU	THR	conflict	UNP Q969S9
w	90	VAL	ILE	conflict	UNP Q969S9
w	94	THR	SER	conflict	UNP Q969S9
w	197	ASP	MET	conflict	UNP Q969S9
w	216	ARG	LYS	conflict	UNP Q969S9
w	?	-	ALA	deletion	UNP Q969S9
w	?	-	ALA	deletion	UNP Q969S9
w	?	-	ALA	deletion	UNP Q969S9
w	?	-	ARG	deletion	UNP Q969S9
w	?	-	ARG	deletion	UNP Q969S9
w	?	-	ALA	deletion	UNP Q969S9
w	?	-	GLU	deletion	UNP Q969S9
w	?	-	ARG	deletion	UNP Q969S9
w	?	-	GLU	deletion	UNP Q969S9
w	?	-	GLY	deletion	UNP Q969S9
w	?	-	GLU	deletion	UNP Q969S9
w	?	-	LYS	deletion	UNP Q969S9
w	?	-	LYS	deletion	UNP Q969S9
w	?	-	HIS	deletion	UNP Q969S9
w	?	-	ARG	deletion	UNP Q969S9
w	?	-	GLN	deletion	UNP Q969S9
w	?	-	ASN	deletion	UNP Q969S9
w	?	-	ASN	deletion	UNP Q969S9
w	?	-	GLU	deletion	UNP Q969S9
w	?	-	ALA	deletion	UNP Q969S9
w	?	-	GLU	deletion	UNP Q969S9
w	?	-	ARG	deletion	UNP Q969S9

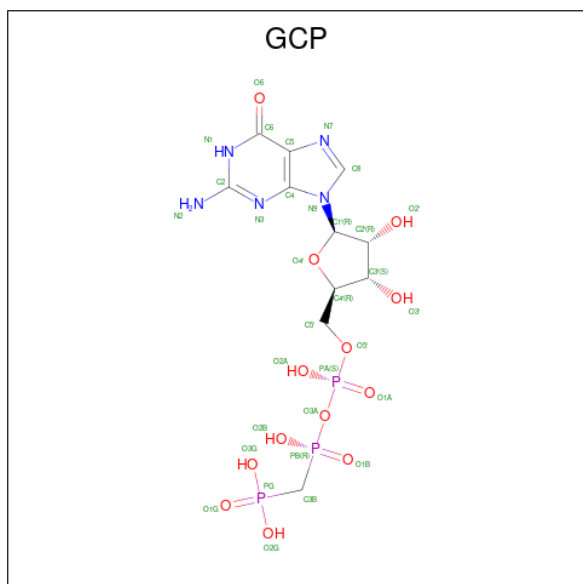
- Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	A	97	Total 97	Mg 97	0
57	D	1	Total 1	Mg 1	0
57	W	1	Total 1	Mg 1	0
57	g	1	Total 1	Mg 1	0
57	E	1	Total 1	Mg 1	0
57	w	1	Total 1	Mg 1	0

- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 59 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).

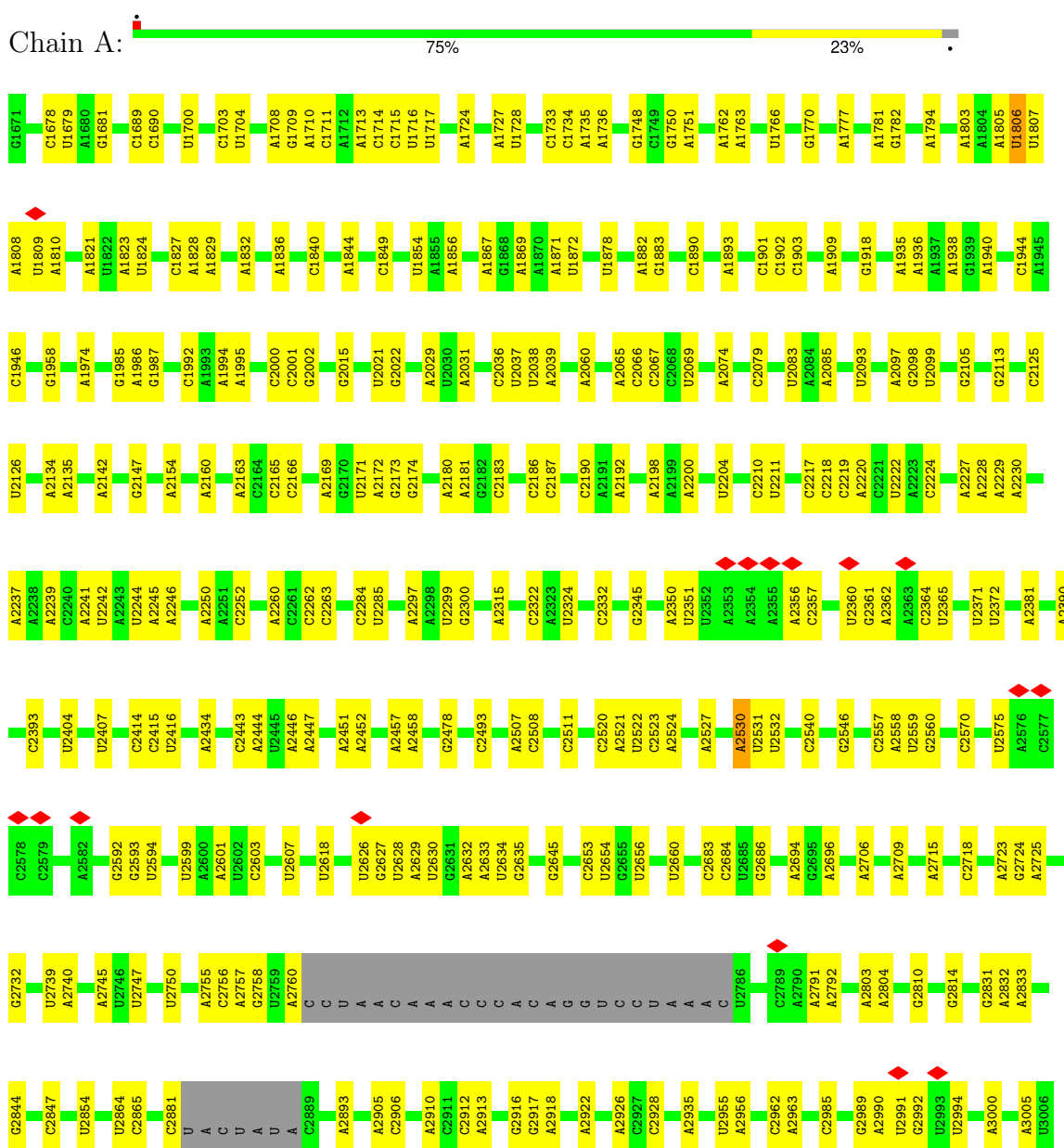


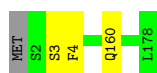
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
59	w	1	32	11	5	13	3	0

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.

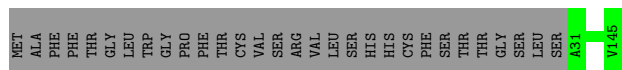
• Molecule 1: 16S rRNA mitochondrial





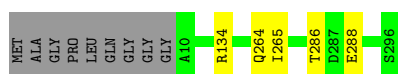
- Molecule 7: 39S ribosomal protein L14, mitochondrial

Chain L: 79% 21%



- Molecule 8: 39S ribosomal protein L15, mitochondrial

Chain M: 95% . .



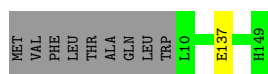
- Molecule 9: 39S ribosomal protein L17, mitochondrial

Chain O: 86% . 13%



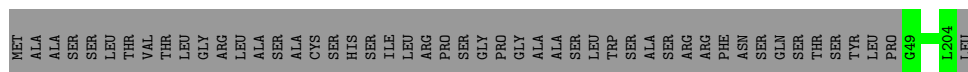
- Molecule 10: 39S ribosomal protein L20, mitochondrial

Chain R: 93% . 6%



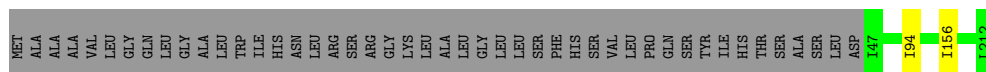
- Molecule 11: 39S ribosomal protein L21, mitochondrial

Chain S: 76% 24%



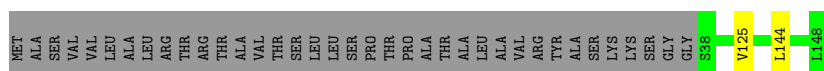
- Molecule 12: 39S ribosomal protein L22, mitochondrial

Chain T: 77% . 22%

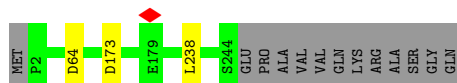


- Molecule 13: 39S ribosomal protein L27, mitochondrial

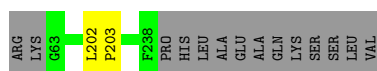
Chain W: 74% . 25%



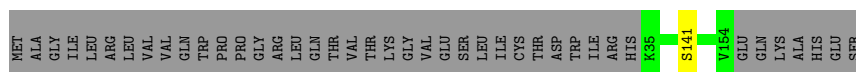
- Molecule 14: 39S ribosomal protein L28, mitochondrial



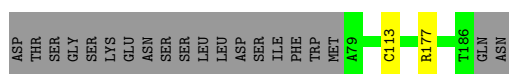
- Molecule 15: 39S ribosomal protein L47, mitochondrial



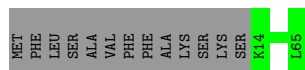
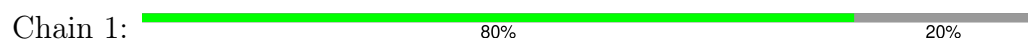
- Molecule 16: 39S ribosomal protein L30, mitochondrial



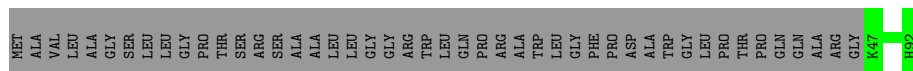
- Molecule 17: 39S ribosomal protein L32, mitochondrial



- Molecule 18: 39S ribosomal protein L33, mitochondrial

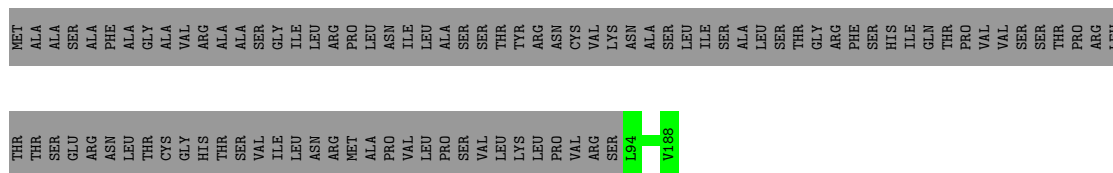


- Molecule 19: 39S ribosomal protein L34, mitochondrial



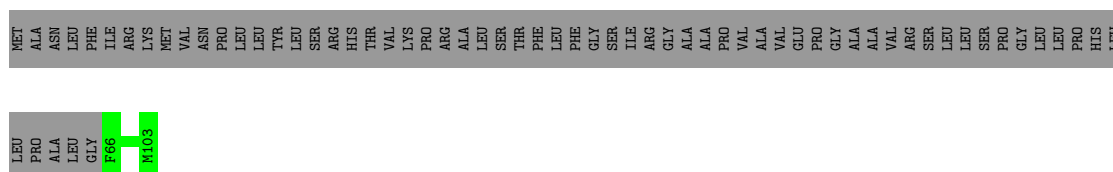
- Molecule 20: 39S ribosomal protein L35, mitochondrial

Chain 3:  51% 49%



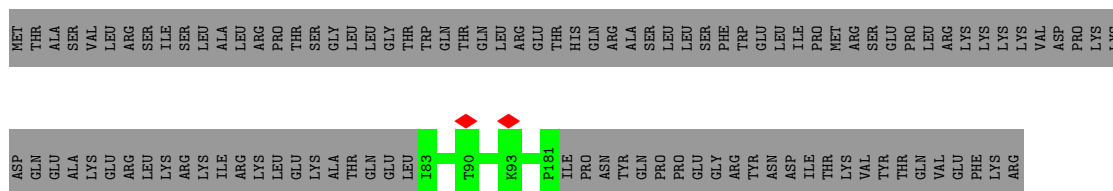
- Molecule 21: 39S ribosomal protein L36, mitochondrial

Chain 4:  37% 63%



- Molecule 22: 39S ribosomal protein L40, mitochondrial

Chain 8:  48% 52%




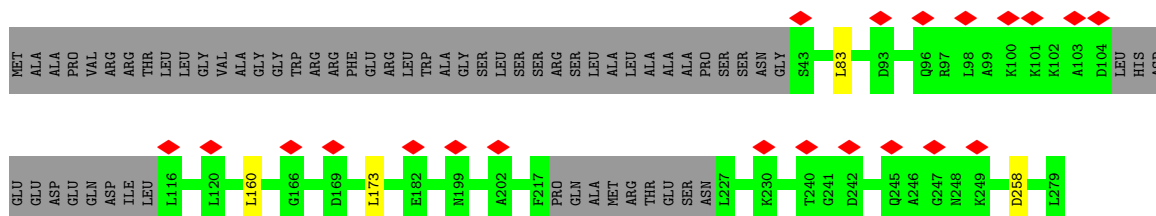
- Molecule 23: 39S ribosomal protein L43, mitochondrial

Chain b:  95% 5%




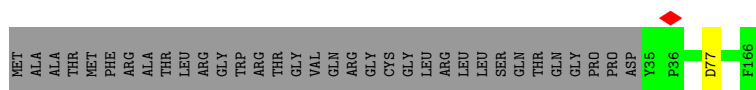
- Molecule 24: 39S ribosomal protein L46, mitochondrial

Chain e:  8% 76% 22%



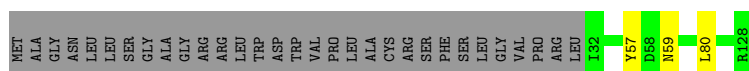
- Molecule 25: 39S ribosomal protein L49, mitochondrial

Chain g:  79% 20%



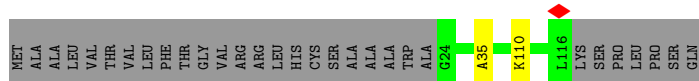
- Molecule 26: 39S ribosomal protein L51, mitochondrial

Chain i: 73% 24%



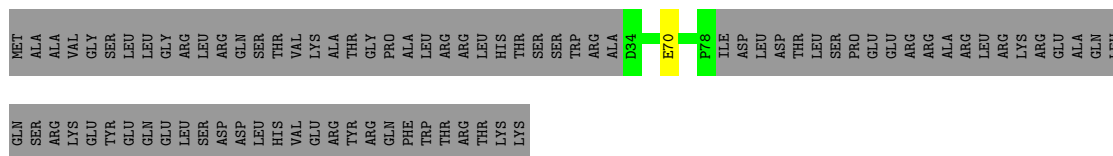
- Molecule 27: cDNA FLJ76418, highly similar to Homo sapiens mitochondrial ribosomal protein L52 (MRPL52), transcript variant 1, mRNA

Chain j: 74% 24%



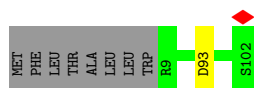
- Molecule 28: 39S ribosomal protein L55, mitochondrial

Chain m: 34% 65%



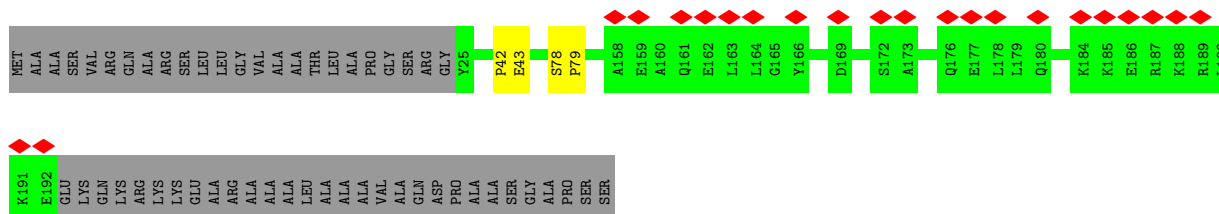
- Molecule 29: Ribosomal protein 63, mitochondrial

Chain o: 91% 8%

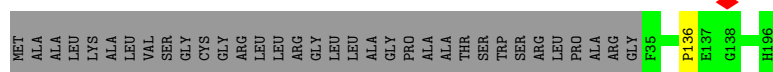
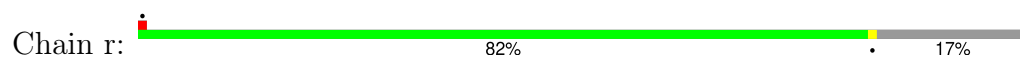


- Molecule 30: Growth arrest and DNA damage-inducible proteins-interacting protein 1

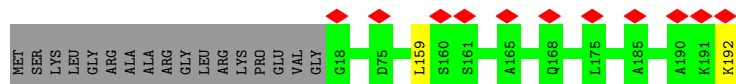
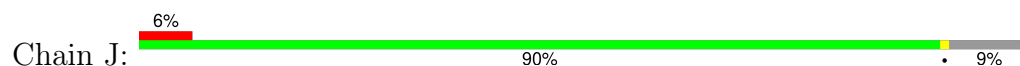
Chain q: 10% 74% 24%



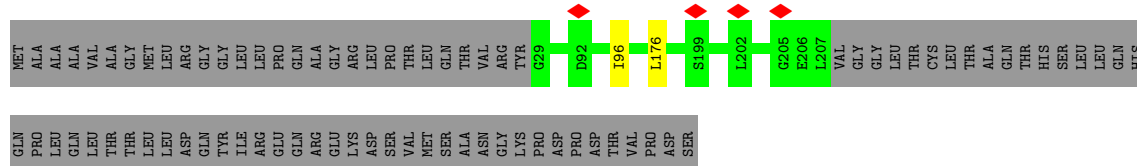
- Molecule 31: 39S ribosomal protein S18a, mitochondrial



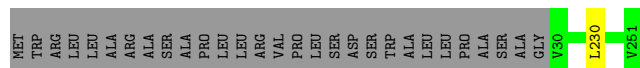
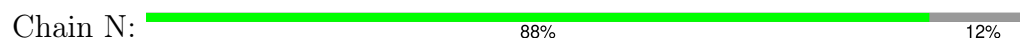
- Molecule 32: 39S ribosomal protein L11, mitochondrial



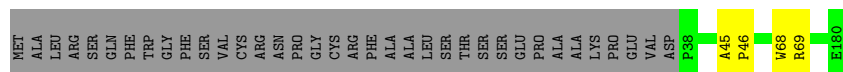
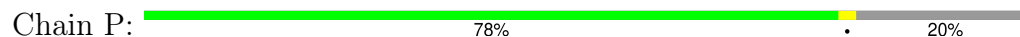
- Molecule 33: 39S ribosomal protein L10, mitochondrial



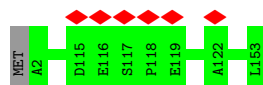
- Molecule 34: 39S ribosomal protein L16, mitochondrial



- Molecule 35: Mitochondrial ribosomal protein L18, isoform CRA_b

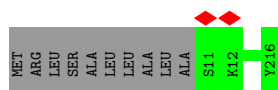


- Molecule 36: 39S ribosomal protein L23, mitochondrial

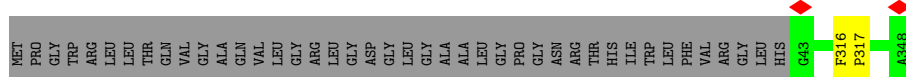
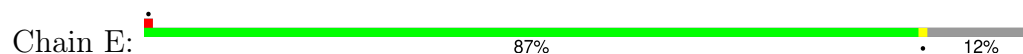


- Molecule 37: 39S ribosomal protein L24, mitochondrial

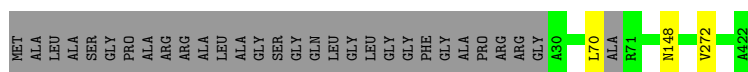




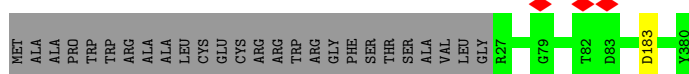
- Molecule 38: 39S ribosomal protein L3, mitochondrial



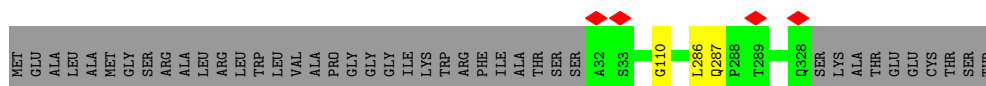
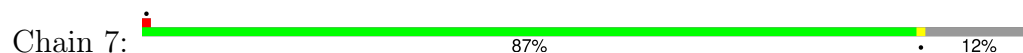
- Molecule 39: 39S ribosomal protein L37, mitochondrial



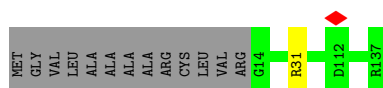
- Molecule 40: 39S ribosomal protein L38, mitochondrial



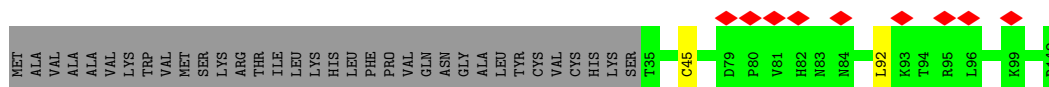
- Molecule 41: 39S ribosomal protein L39, mitochondrial



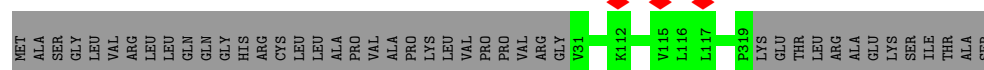
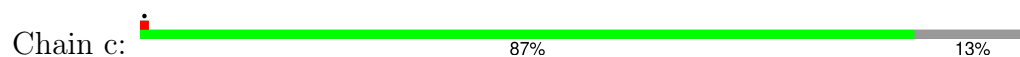
- Molecule 42: 39S ribosomal protein L41, mitochondrial



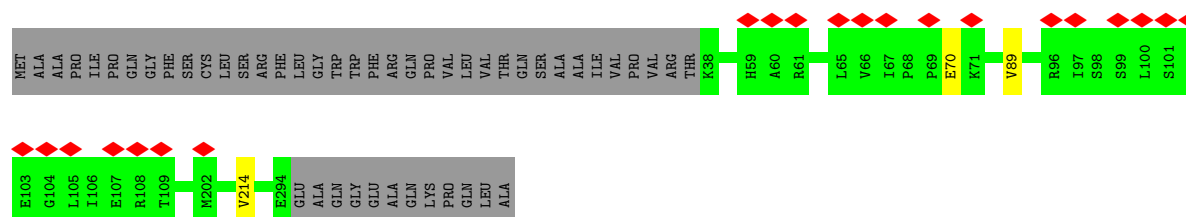
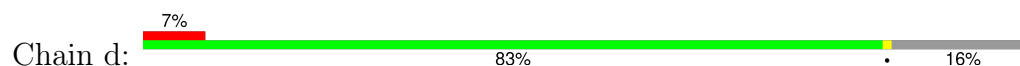
- Molecule 43: 39S ribosomal protein L42, mitochondrial



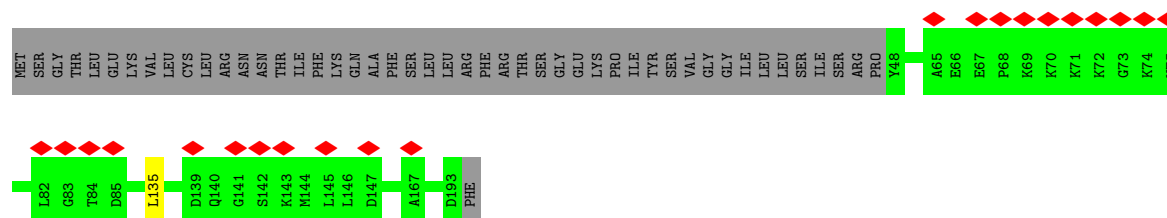
- Molecule 44: 39S ribosomal protein L44, mitochondrial



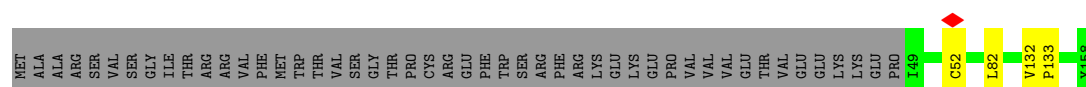
- Molecule 45: 39S ribosomal protein L45, mitochondrial



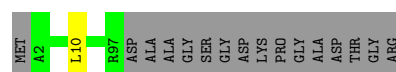
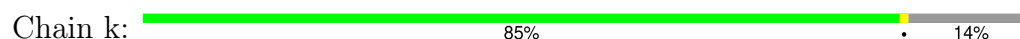
- Molecule 46: 39S ribosomal protein L48, mitochondrial



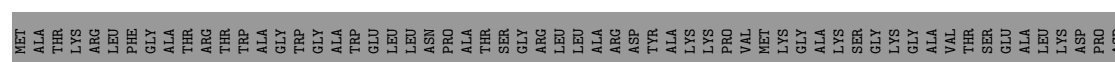
- Molecule 47: 39S ribosomal protein L50, mitochondrial

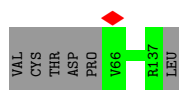


- Molecule 48: 39S ribosomal protein L53, mitochondrial

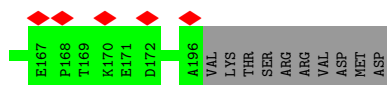
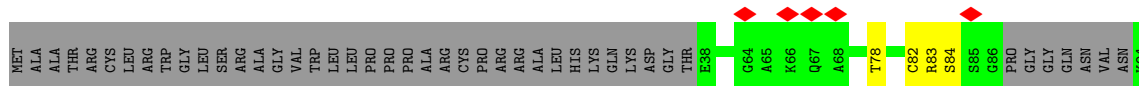


- Molecule 49: 39S ribosomal protein L54, mitochondrial

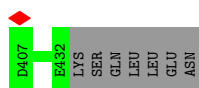
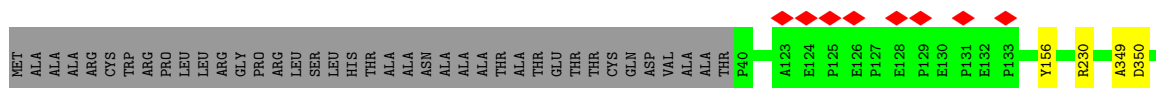
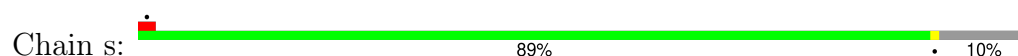




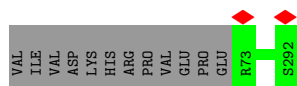
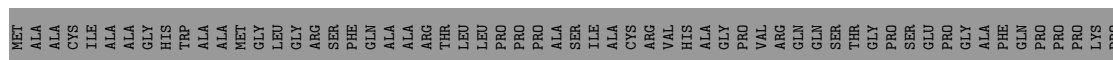
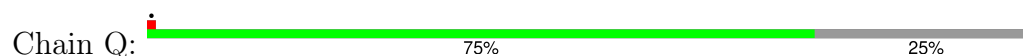
- Molecule 50: Peptidyl-tRNA hydrolase ICT1, mitochondrial



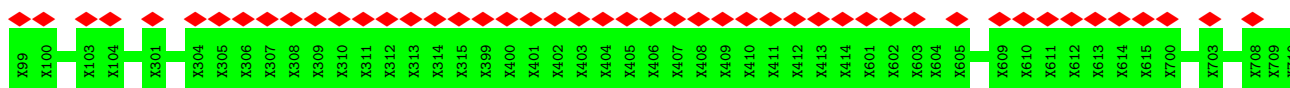
- Molecule 51: 39S ribosomal protein S30, mitochondrial



- Molecule 52: 39S ribosomal protein L19, mitochondrial

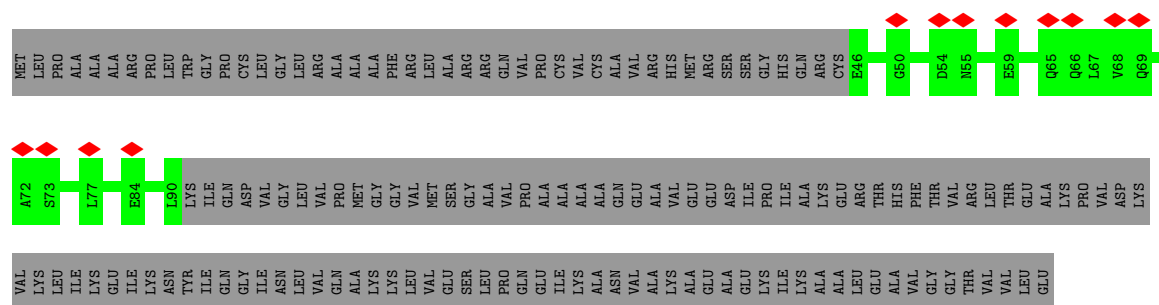


- Molecule 53: 39 S P-site finger



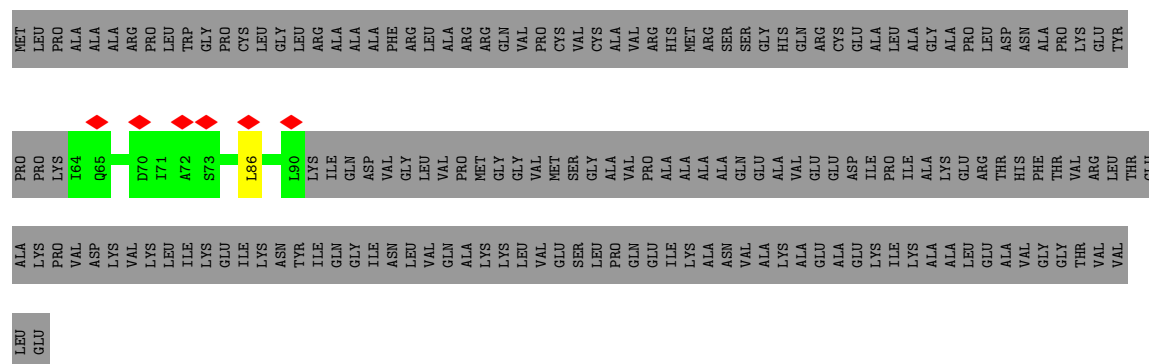
- Molecule 54: 39S ribosomal protein L12, mitochondrial





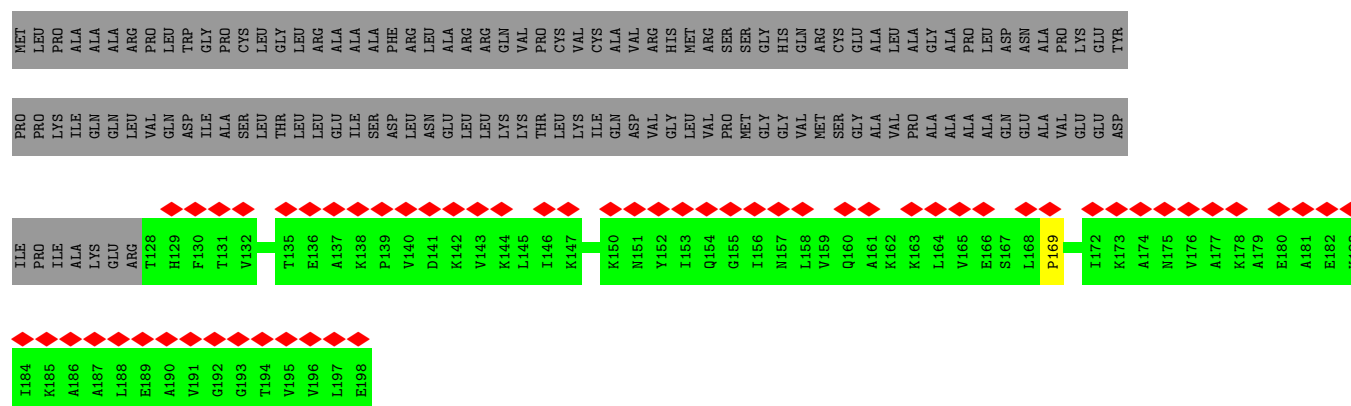
- Molecule 54: 39S ribosomal protein L12, mitochondrial

Chain TB: 13% 86%



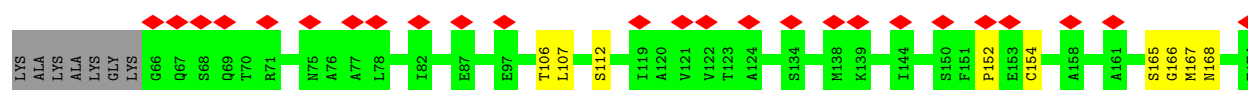
- Molecule 54: 39S ribosomal protein L12, mitochondrial

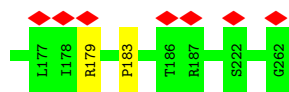
Chain TC: 30% 35% 64%



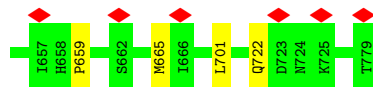
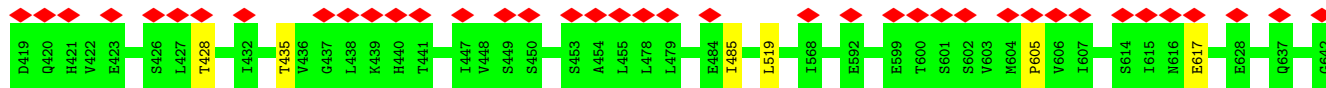
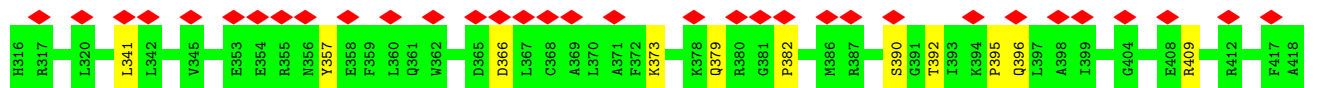
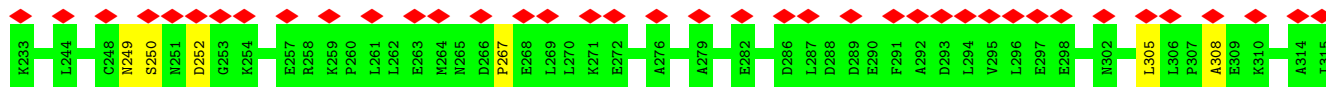
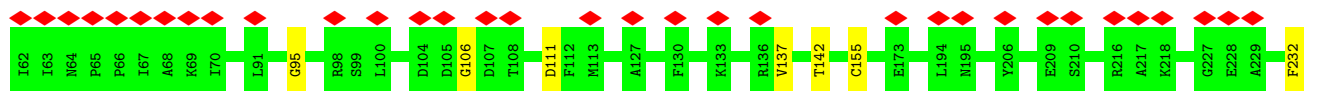
- Molecule 55: Ribosome-recycling factor, mitochondrial

Chain z: 16% 91% 5%





- Molecule 56: Ribosome-releasing factor 2, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	132008	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	71	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	DIRECT ELECTRON DE-16 (4k x 4k)	Depositor
Maximum map value	3.217	Depositor
Minimum map value	-1.964	Depositor
Average map value	-0.004	Depositor
Map value standard deviation	0.126	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	429.30002, 429.30002, 429.30002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07325, 1.07325, 1.07325	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GCP, 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	A	0.18	0/36245	0.77	3/56418 (0.0%)
2	B	0.45	0/1328	1.17	12/2056 (0.6%)
3	D	0.40	0/1904	0.57	0/2561
4	F	0.47	0/2071	0.66	1/2817 (0.0%)
5	H	0.38	0/820	0.70	1/1102 (0.1%)
6	K	0.48	0/1495	0.58	0/2029
7	L	0.42	0/904	0.59	0/1218
8	M	0.45	0/2359	0.62	0/3185
9	O	0.46	0/1269	0.63	0/1708
10	R	0.49	0/1174	0.59	0/1572
11	S	0.43	0/1276	0.62	0/1729
12	T	0.46	0/1402	0.55	0/1886
13	W	0.53	0/893	0.61	0/1204
14	X	0.39	0/2081	0.55	0/2812
15	Y	0.42	0/1552	0.52	0/2079
16	Z	0.44	0/1003	0.60	0/1354
17	0	0.42	0/895	0.61	0/1201
18	1	0.38	0/438	0.60	0/583
19	2	0.49	0/382	0.61	0/507
20	3	0.50	0/852	0.55	0/1136
21	4	0.51	0/350	0.61	0/461
22	8	0.33	0/855	0.56	0/1152
23	b	0.43	0/1202	0.56	0/1626
24	e	0.34	0/1797	0.70	3/2422 (0.1%)
25	g	0.46	0/1132	0.62	0/1543
26	i	0.48	0/849	0.66	1/1135 (0.1%)
27	j	0.44	0/755	0.53	0/1016
28	m	0.29	0/379	0.59	0/510
29	o	0.44	0/818	0.64	1/1097 (0.1%)
30	q	0.34	0/1323	0.55	0/1794
31	r	0.46	0/1362	0.60	0/1846
32	J	0.38	0/1348	0.62	1/1813 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.36	0/1467	0.66	1/1984 (0.1%)
34	N	0.44	1/1833 (0.1%)	0.52	0/2468
35	P	0.40	0/1191	0.60	0/1611
36	U	0.42	0/1252	0.52	0/1697
37	V	0.39	0/1727	0.57	0/2341
38	E	0.44	0/2479	0.58	0/3360
39	5	0.38	0/3300	0.58	2/4495 (0.0%)
40	6	0.39	0/3043	0.54	0/4140
41	7	0.39	0/2467	0.55	1/3337 (0.0%)
42	9	0.41	0/1025	0.57	0/1379
43	a	0.44	1/923 (0.1%)	0.52	1/1254 (0.1%)
44	c	0.39	0/2371	0.54	0/3205
45	d	0.36	0/2132	0.59	0/2887
46	f	0.34	0/1144	0.68	1/1551 (0.1%)
47	h	0.34	0/917	0.56	0/1249
48	k	0.33	0/754	0.65	1/1017 (0.1%)
49	l	0.33	0/636	0.54	0/860
50	p	0.34	0/1246	0.54	0/1675
51	s	0.42	0/3262	0.55	0/4435
52	Q	0.40	0/1875	0.54	0/2523
54	TA	0.27	0/349	0.52	0/475
54	TB	0.28	0/212	0.57	0/286
54	TC	0.23	0/351	0.40	0/488
55	z	0.23	0/1534	0.39	0/2063
56	w	0.24	0/5511	0.44	0/7479
All	All	0.35	2/115514 (0.0%)	0.66	30/163831 (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
3	D	0	1
5	H	0	1
6	K	0	1
8	M	0	2
10	R	0	1
12	T	0	1
16	Z	0	1
17	0	0	1
26	i	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
27	j	0	1
28	m	0	1
30	q	0	1
35	P	0	2
38	E	0	1
41	7	0	1
45	d	0	1
47	h	0	3
50	p	0	2
51	s	0	2
56	w	0	1
All	All	0	26

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	N	230	LEU	C-N	-6.33	1.19	1.34
43	a	45	CYS	CB-SG	-5.81	1.72	1.81

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	f	135	LEU	CA-CB-CG	7.00	131.39	115.30
2	B	1633	U	N1-C2-O2	6.91	127.63	122.80
24	e	83	LEU	CA-CB-CG	6.83	131.01	115.30
29	o	93	ASP	CB-CG-OD2	6.53	124.17	118.30
33	I	176	LEU	CA-CB-CG	6.23	129.62	115.30

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	D	206	TYR	Peptide
5	H	86	THR	Peptide
6	K	3	SER	Peptide
8	M	264	GLN	Peptide
8	M	286	THR	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 ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	D	237/305 (78%)	227 (96%)	9 (4%)	1 (0%)	30	61
4	F	248/311 (80%)	226 (91%)	20 (8%)	2 (1%)	16	47
5	H	96/267 (36%)	88 (92%)	8 (8%)	0	100	100
6	K	175/178 (98%)	153 (87%)	20 (11%)	2 (1%)	12	40
7	L	113/145 (78%)	102 (90%)	11 (10%)	0	100	100
8	M	285/296 (96%)	248 (87%)	35 (12%)	2 (1%)	19	51
9	O	150/175 (86%)	133 (89%)	16 (11%)	1 (1%)	19	51
10	R	138/149 (93%)	130 (94%)	8 (6%)	0	100	100
11	S	154/205 (75%)	143 (93%)	11 (7%)	0	100	100
12	T	164/212 (77%)	156 (95%)	8 (5%)	0	100	100
13	W	109/148 (74%)	102 (94%)	7 (6%)	0	100	100
14	X	241/256 (94%)	221 (92%)	20 (8%)	0	100	100
15	Y	174/250 (70%)	165 (95%)	7 (4%)	2 (1%)	12	40
16	Z	118/161 (73%)	110 (93%)	8 (7%)	0	100	100
17	0	106/188 (56%)	92 (87%)	14 (13%)	0	100	100
18	1	50/65 (77%)	45 (90%)	5 (10%)	0	100	100
19	2	44/92 (48%)	43 (98%)	1 (2%)	0	100	100
20	3	93/188 (50%)	89 (96%)	4 (4%)	0	100	100
21	4	36/103 (35%)	34 (94%)	2 (6%)	0	100	100
22	8	97/206 (47%)	95 (98%)	2 (2%)	0	100	100
23	b	146/155 (94%)	135 (92%)	11 (8%)	0	100	100
24	e	211/279 (76%)	203 (96%)	8 (4%)	0	100	100
25	g	130/166 (78%)	122 (94%)	8 (6%)	0	100	100
26	i	95/128 (74%)	88 (93%)	7 (7%)	0	100	100
27	j	91/123 (74%)	84 (92%)	6 (7%)	1 (1%)	12	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	m	43/128 (34%)	37 (86%)	6 (14%)	0	100	100
29	o	92/102 (90%)	85 (92%)	7 (8%)	0	100	100
30	q	164/222 (74%)	153 (93%)	8 (5%)	3 (2%)	7	31
31	r	160/196 (82%)	148 (92%)	11 (7%)	1 (1%)	22	54
32	J	173/192 (90%)	163 (94%)	10 (6%)	0	100	100
33	I	177/261 (68%)	167 (94%)	10 (6%)	0	100	100
34	N	220/251 (88%)	215 (98%)	5 (2%)	0	100	100
35	P	141/179 (79%)	131 (93%)	8 (6%)	2 (1%)	9	36
36	U	150/153 (98%)	141 (94%)	9 (6%)	0	100	100
37	V	204/216 (94%)	194 (95%)	10 (5%)	0	100	100
38	E	304/348 (87%)	283 (93%)	20 (7%)	1 (0%)	37	66
39	5	391/423 (92%)	375 (96%)	16 (4%)	0	100	100
40	6	352/380 (93%)	328 (93%)	24 (7%)	0	100	100
41	7	295/338 (87%)	276 (94%)	18 (6%)	1 (0%)	37	66
42	9	122/137 (89%)	112 (92%)	10 (8%)	0	100	100
43	a	106/142 (75%)	101 (95%)	5 (5%)	0	100	100
44	c	287/332 (86%)	269 (94%)	18 (6%)	0	100	100
45	d	255/306 (83%)	235 (92%)	20 (8%)	0	100	100
46	f	144/194 (74%)	135 (94%)	9 (6%)	0	100	100
47	h	108/158 (68%)	98 (91%)	9 (8%)	1 (1%)	14	45
48	k	94/112 (84%)	88 (94%)	6 (6%)	0	100	100
49	l	70/138 (51%)	63 (90%)	7 (10%)	0	100	100
50	p	148/206 (72%)	139 (94%)	8 (5%)	1 (1%)	19	51
51	s	391/439 (89%)	361 (92%)	29 (7%)	1 (0%)	37	66
52	Q	218/292 (75%)	209 (96%)	9 (4%)	0	100	100
54	TA	43/198 (22%)	35 (81%)	8 (19%)	0	100	100
54	TB	25/198 (13%)	24 (96%)	1 (4%)	0	100	100
54	TC	69/198 (35%)	59 (86%)	9 (13%)	1 (1%)	9	36
55	z	195/204 (96%)	164 (84%)	23 (12%)	8 (4%)	2	14
56	w	692/696 (99%)	583 (84%)	93 (13%)	16 (2%)	5	25
All	All	9334/12090 (77%)	8605 (92%)	682 (7%)	47 (0%)	27	57

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	q	43	GLU
35	P	69	ARG
6	K	160	GLN
38	E	317	PRO
55	z	106	THR

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	
3	D	193/245 (79%)	192 (100%)	1 (0%)	86	92
4	F	217/262 (83%)	216 (100%)	1 (0%)	86	92
5	H	88/228 (39%)	88 (100%)	0	100	100
6	K	155/156 (99%)	155 (100%)	0	100	100
7	L	98/124 (79%)	98 (100%)	0	100	100
8	M	245/249 (98%)	244 (100%)	1 (0%)	89	94
9	O	133/150 (89%)	133 (100%)	0	100	100
10	R	118/126 (94%)	118 (100%)	0	100	100
11	S	141/180 (78%)	141 (100%)	0	100	100
12	T	146/182 (80%)	145 (99%)	1 (1%)	81	90
13	W	91/119 (76%)	89 (98%)	2 (2%)	47	70
14	X	217/227 (96%)	214 (99%)	3 (1%)	62	80
15	Y	159/223 (71%)	159 (100%)	0	100	100
16	Z	111/147 (76%)	111 (100%)	0	100	100
17	0	97/164 (59%)	96 (99%)	1 (1%)	73	85
18	1	49/60 (82%)	49 (100%)	0	100	100
19	2	40/72 (56%)	40 (100%)	0	100	100
20	3	88/166 (53%)	88 (100%)	0	100	100
21	4	37/89 (42%)	37 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	8	91/190 (48%)	91 (100%)	0	100	100
23	b	130/135 (96%)	130 (100%)	0	100	100
24	e	188/236 (80%)	187 (100%)	1 (0%)	86	92
25	g	122/148 (82%)	121 (99%)	1 (1%)	79	89
26	i	86/110 (78%)	85 (99%)	1 (1%)	67	82
27	j	74/97 (76%)	74 (100%)	0	100	100
28	m	40/113 (35%)	40 (100%)	0	100	100
29	o	80/87 (92%)	80 (100%)	0	100	100
30	q	113/178 (64%)	113 (100%)	0	100	100
31	r	147/169 (87%)	147 (100%)	0	100	100
32	J	138/150 (92%)	137 (99%)	1 (1%)	81	90
33	I	164/232 (71%)	163 (99%)	1 (1%)	84	91
34	N	189/211 (90%)	189 (100%)	0	100	100
35	P	125/154 (81%)	125 (100%)	0	100	100
36	U	125/135 (93%)	125 (100%)	0	100	100
37	V	184/191 (96%)	184 (100%)	0	100	100
38	E	260/290 (90%)	260 (100%)	0	100	100
39	5	353/368 (96%)	351 (99%)	2 (1%)	84	91
40	6	313/332 (94%)	312 (100%)	1 (0%)	91	95
41	7	272/303 (90%)	272 (100%)	0	100	100
42	9	104/112 (93%)	103 (99%)	1 (1%)	73	85
43	a	101/133 (76%)	101 (100%)	0	100	100
44	c	253/288 (88%)	253 (100%)	0	100	100
45	d	224/274 (82%)	222 (99%)	2 (1%)	75	87
46	f	122/173 (70%)	122 (100%)	0	100	100
47	h	104/148 (70%)	104 (100%)	0	100	100
48	k	81/90 (90%)	81 (100%)	0	100	100
49	l	67/116 (58%)	67 (100%)	0	100	100
50	p	134/181 (74%)	133 (99%)	1 (1%)	81	90
51	s	336/381 (88%)	335 (100%)	1 (0%)	91	95
52	Q	202/256 (79%)	202 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	TA	39/158 (25%)	39 (100%)	0	100	100
54	TB	26/158 (16%)	25 (96%)	1 (4%)	28	56
55	z	175/179 (98%)	172 (98%)	3 (2%)	56	75
56	w	604/604 (100%)	587 (97%)	17 (3%)	38	64
All	All	8189/10249 (80%)	8145 (100%)	44 (0%)	85	92

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	w	155	CYS
56	w	392	THR
56	w	232	PHE
56	w	341	LEU
56	w	409	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 125 such sidechains are listed below:

Mol	Chain	Res	Type
31	r	184	ASN
55	z	252	HIS
38	E	294	ASN
55	z	131	ASN
56	w	312	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1522/1559 (97%)	349 (22%)	28 (1%)
2	B	51/73 (69%)	13 (25%)	1 (1%)
All	All	1573/1632 (96%)	362 (23%)	29 (1%)

5 of 362 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1678	C
1	A	1679	U
1	A	1681	G
1	A	1689	C
1	A	1690	C

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2245	A
1	A	3196	G
1	A	2507	A
1	A	3041	U
1	A	2457	A

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 106 ligands modelled in this entry, 105 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	GCP	w	801	56,57	27,34,34	1.82	5 (18%)	35,54,54	2.41	10 (28%)

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	GCP	w	801	56,57	-	5/15/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	w	801	GCP	PG-O1G	5.63	1.61	1.50
59	w	801	GCP	C5-C6	4.37	1.49	1.41
59	w	801	GCP	PG-O3G	3.07	1.61	1.55
59	w	801	GCP	PG-O2G	-2.58	1.49	1.55
59	w	801	GCP	PB-O2B	2.26	1.61	1.56

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	w	801	GCP	PB-O3A-PA	-5.88	113.17	132.37
59	w	801	GCP	C2-N1-C6	5.25	123.27	115.96
59	w	801	GCP	C2-N3-C4	4.95	120.82	115.48
59	w	801	GCP	N3-C2-N1	-4.22	121.85	127.21
59	w	801	GCP	O4'-C1'-N9	4.07	114.15	108.75

There are no chirality outliers.

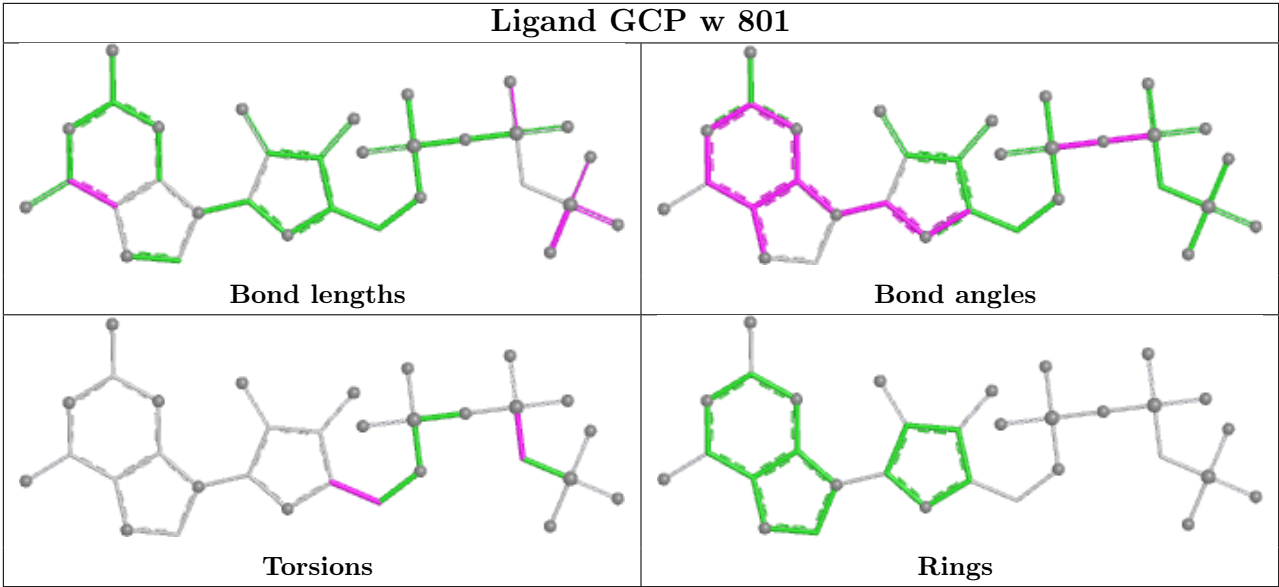
All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	w	801	GCP	PG-C3B-PB-O1B
59	w	801	GCP	PG-C3B-PB-O3A
59	w	801	GCP	O4'-C4'-C5'-O5'
59	w	801	GCP	C3'-C4'-C5'-O5'
59	w	801	GCP	PG-C3B-PB-O2B

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
53	u	4
56	w	1
1	A	1
34	N	1

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	u	414:UNK	C	601:UNK	N	50.84
1	u	106:UNK	C	301:UNK	N	32.66
1	u	315:UNK	C	399:UNK	N	23.91
1	u	615:UNK	C	700:UNK	N	15.49
1	w	455:LEU	C	478:LEU	N	11.53

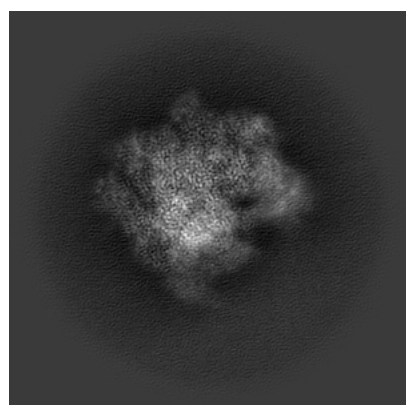
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23121. These allow visual inspection of the internal detail of the map and identification of artifacts.

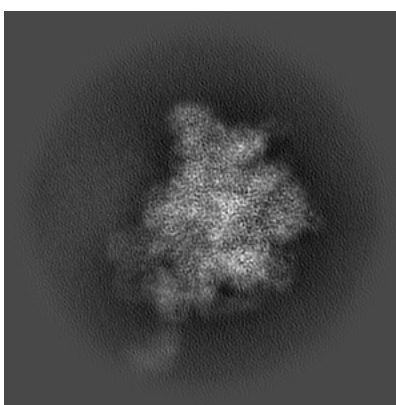
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

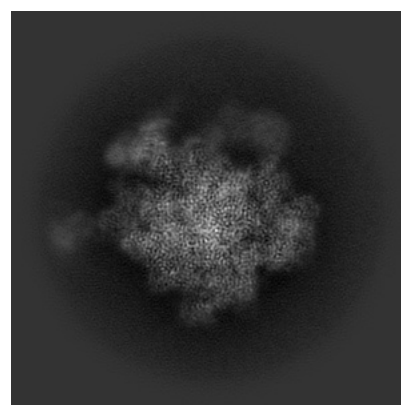
6.1.1 Primary map



X



Y

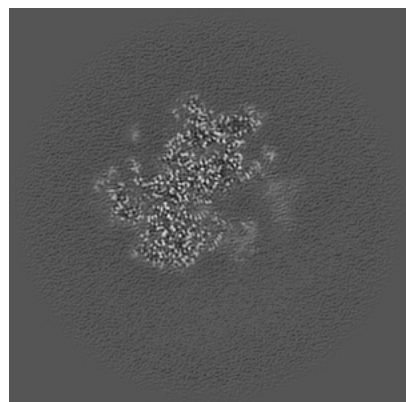


Z

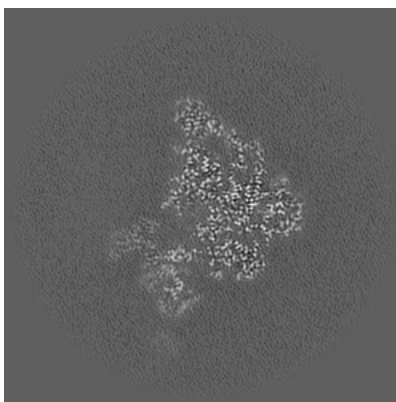
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

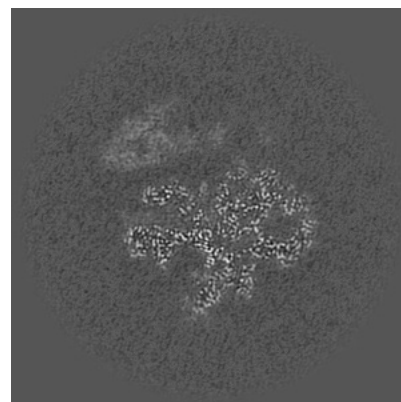
6.2.1 Primary map



X Index: 200



Y Index: 200

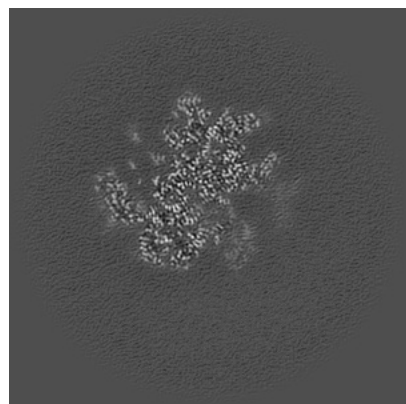


Z Index: 200

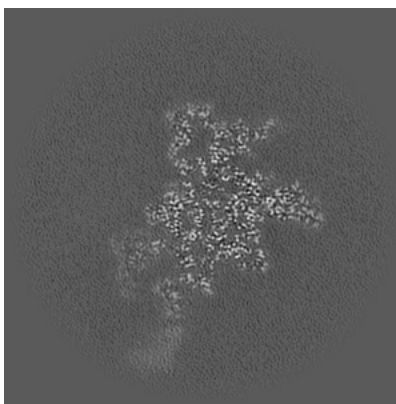
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

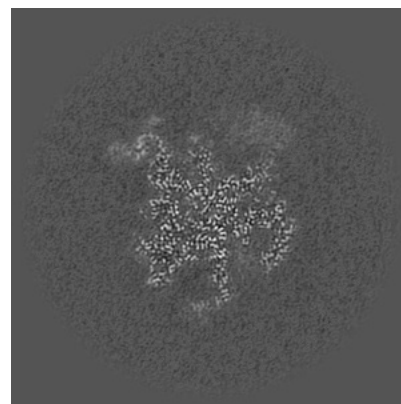
6.3.1 Primary map



X Index: 195



Y Index: 179

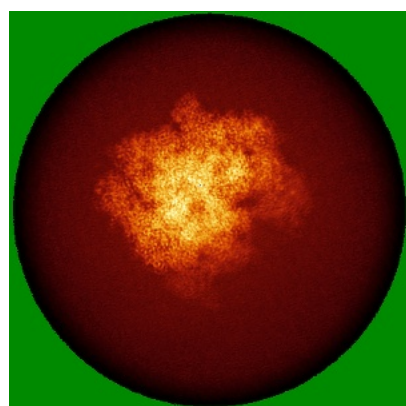


Z Index: 232

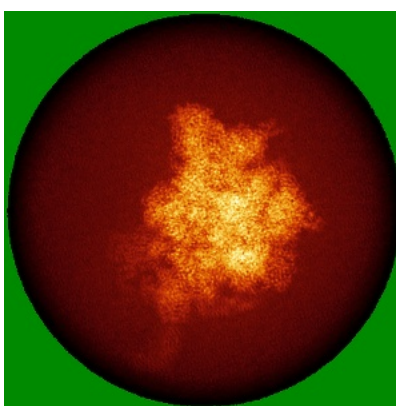
The images above show the largest variance slices of the map in three orthogonal directions.

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

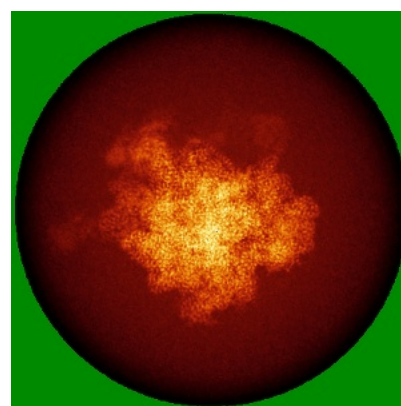
6.4.1 Primary map



X



Y

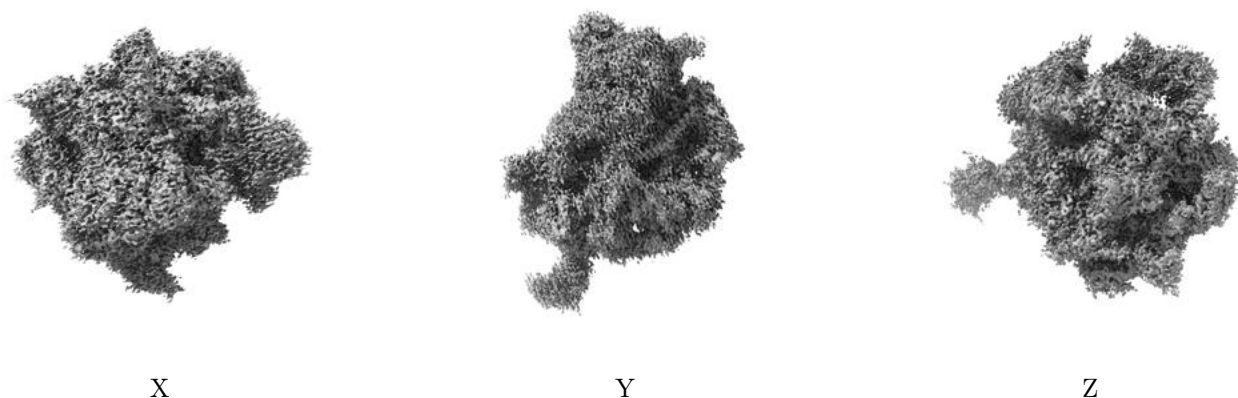


Z

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

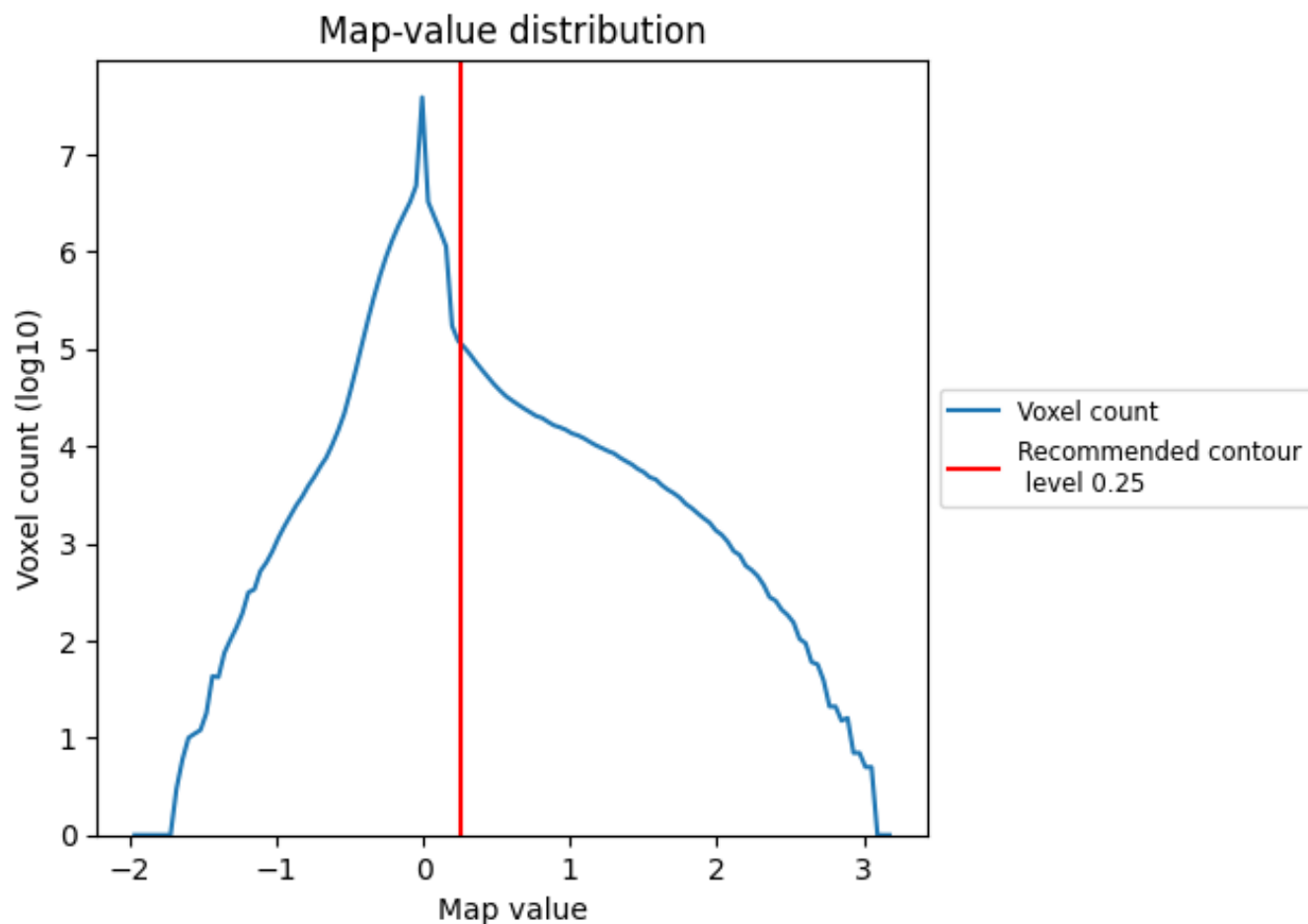
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

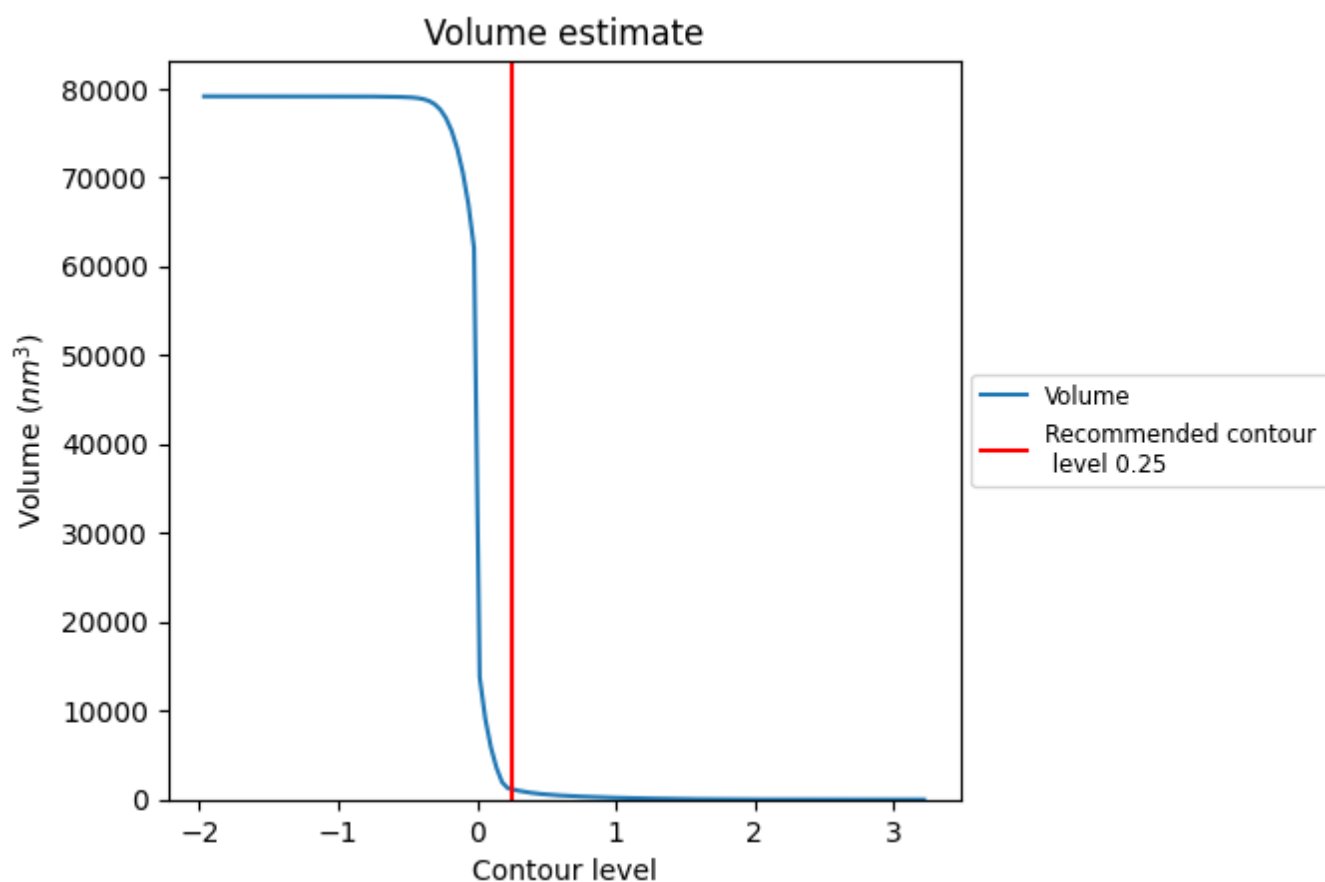
This section contains the results of statistical analysis of the map.

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.

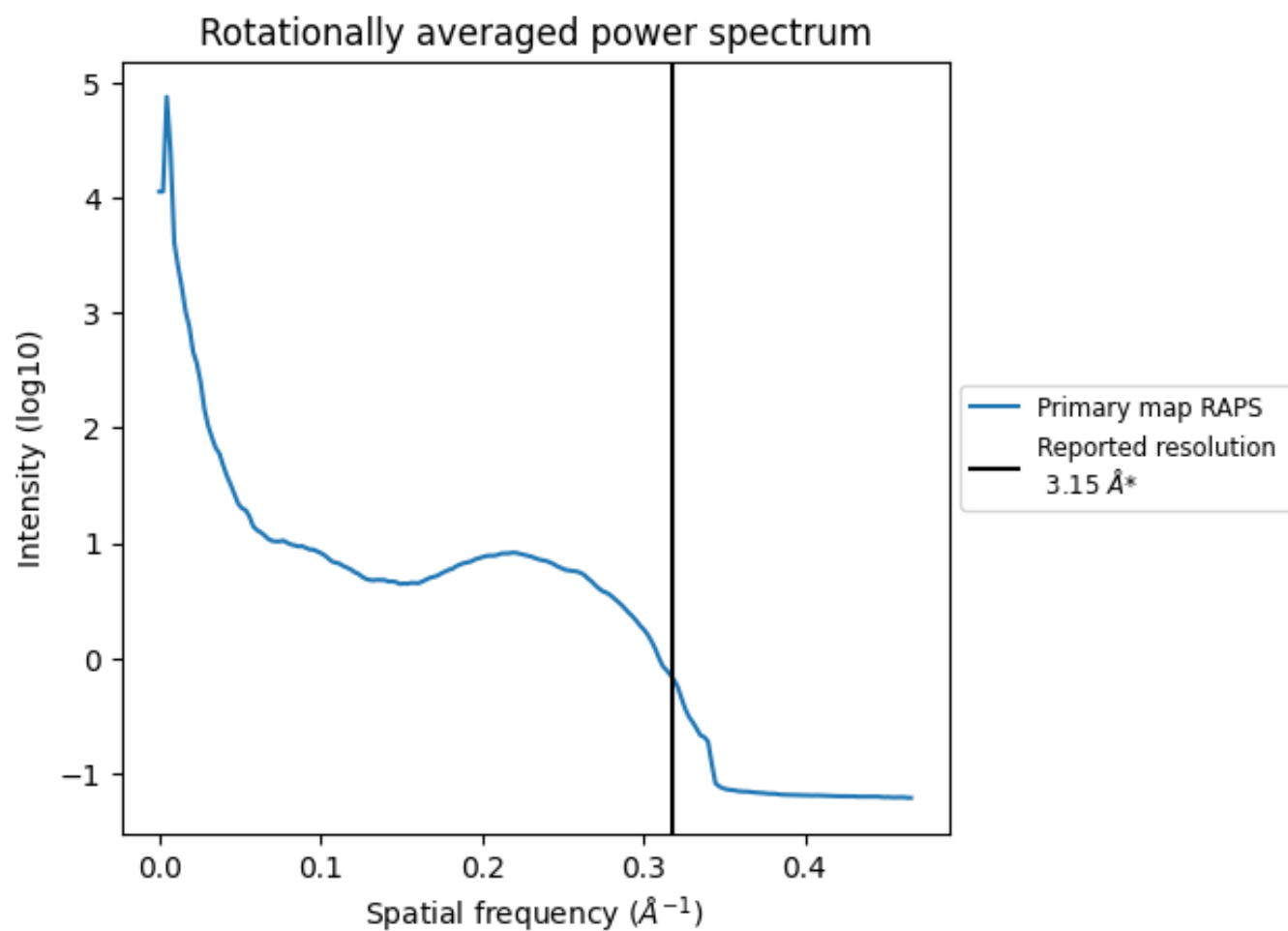
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1170 nm³; this corresponds to an approximate mass of 1057 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.317 \AA^{-1}

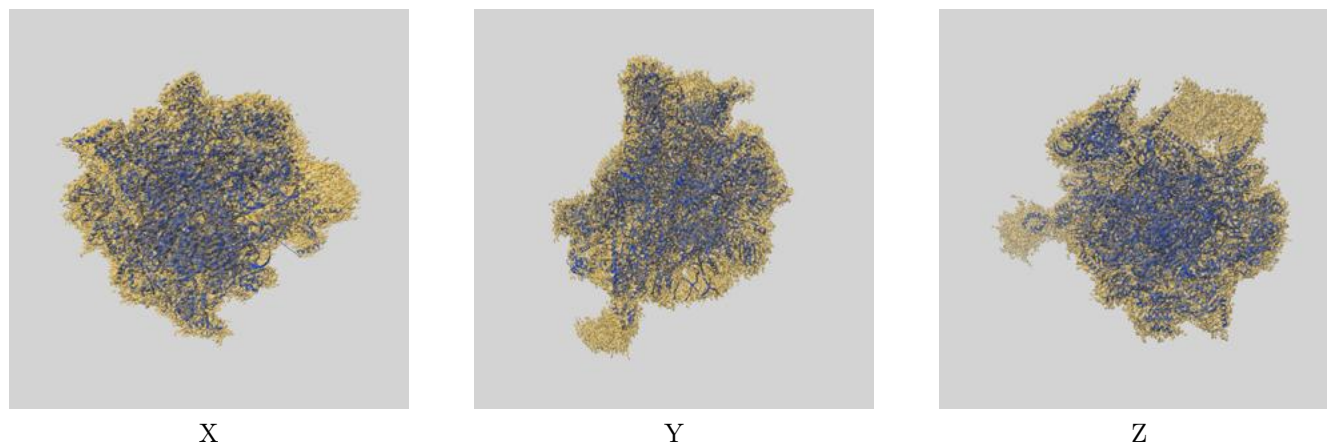
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

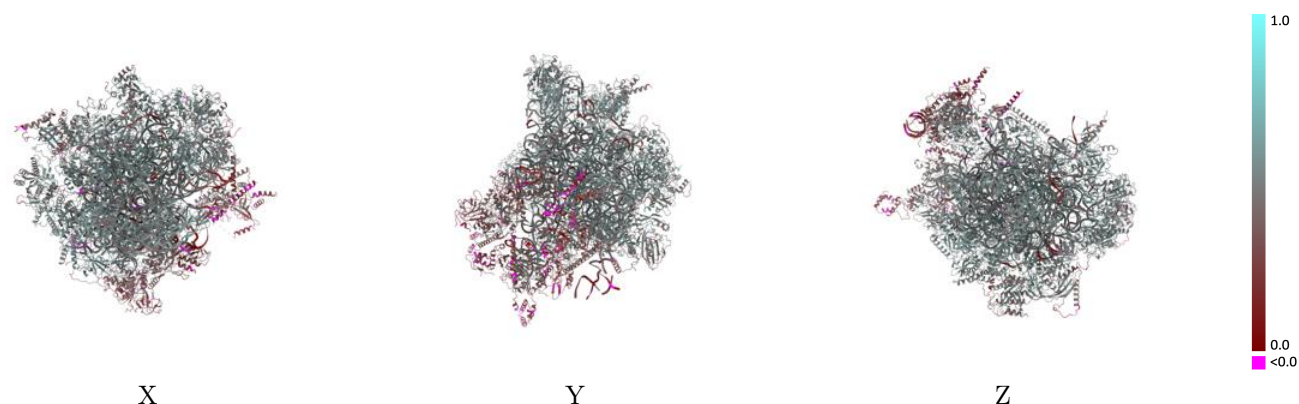
This section contains information regarding the fit between EMDB map EMD-23121 and PDB model 7L20. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.25 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](#)



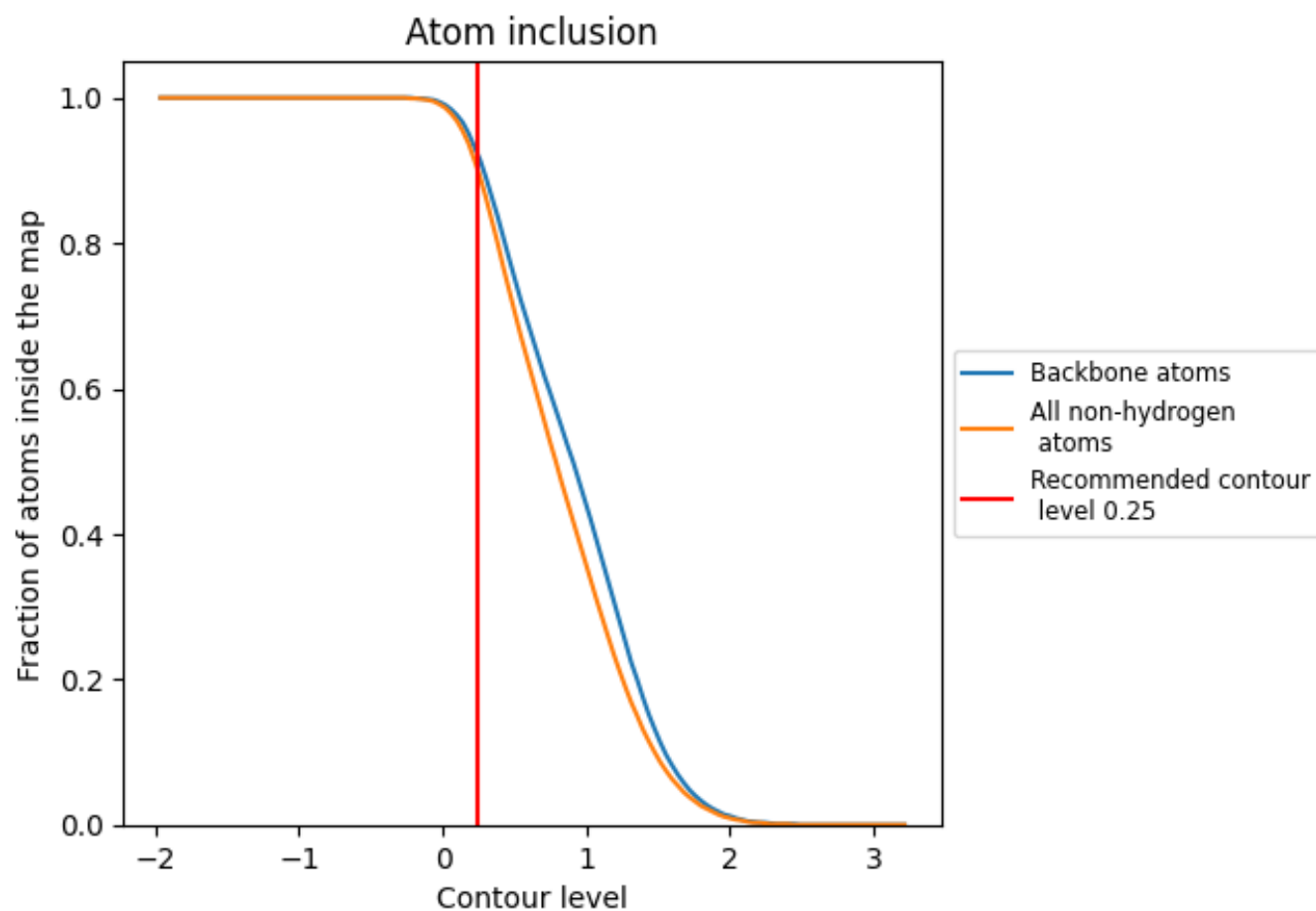
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8980	 0.4720
0	 0.9450	 0.5340
1	 0.9330	 0.5240
2	 0.9610	 0.5740
3	 0.9550	 0.5720
4	 0.9730	 0.5740
5	 0.9530	 0.5150
6	 0.9350	 0.4680
7	 0.9250	 0.4850
8	 0.7820	 0.3180
9	 0.9510	 0.5210
A	 0.9310	 0.4740
B	 0.9370	 0.3360
D	 0.9580	 0.5400
E	 0.9530	 0.5470
F	 0.9550	 0.5400
H	 0.9280	 0.4970
I	 0.8800	 0.4210
J	 0.7820	 0.3140
K	 0.9640	 0.5510
L	 0.9520	 0.5370
M	 0.9580	 0.5410
N	 0.9430	 0.5450
O	 0.9500	 0.5410
P	 0.9520	 0.5080
Q	 0.9480	 0.5380
R	 0.9370	 0.5510
S	 0.9570	 0.5510
T	 0.9480	 0.5530
TA	 0.6080	 0.1640
TB	 0.6010	 0.1610
TC	 0.2590	 0.1400
U	 0.9180	 0.5120
V	 0.9120	 0.4810
W	 0.9380	 0.5500



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Chain	Atom inclusion	Q-score
X	 0.9380	 0.5250
Y	 0.9510	 0.5320
Z	 0.9510	 0.5530
a	 0.8710	 0.4760
b	 0.9560	 0.5480
c	 0.9280	 0.5070
d	 0.8630	 0.4480
e	 0.7420	 0.2390
f	 0.7580	 0.3490
g	 0.9330	 0.5230
h	 0.9190	 0.4730
i	 0.9500	 0.5560
j	 0.9110	 0.5070
k	 0.9160	 0.4430
l	 0.8680	 0.4000
m	 0.8500	 0.3360
o	 0.9400	 0.5430
p	 0.8530	 0.4360
q	 0.8350	 0.4010
r	 0.9550	 0.5280
s	 0.9370	 0.5180
u	 0.3170	 0.0710
w	 0.5880	 0.2990
z	 0.6480	 0.3260