



## wwPDB EM Validation Summary Report ⓘ

Dec 6, 2023 – 06:29 pm GMT

PDB ID : 8PK0  
EMDB ID : EMD-17719  
Title : human mitoribosomal large subunit assembly intermediate 1 with GTPBP10-GTPBP7  
Authors : Kummer, E.; Nguyen, T.G.; Ritter, C.  
Deposited on : 2023-06-23  
Resolution : 3.03 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](mailto: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:

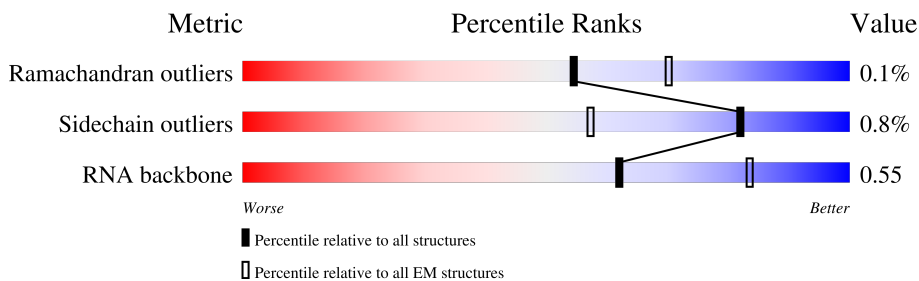
EMDB validation analysis : 0.0.1.dev70  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.03 Å.

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



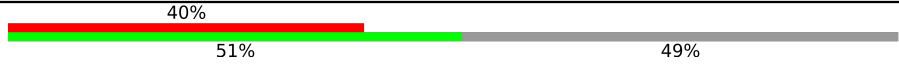



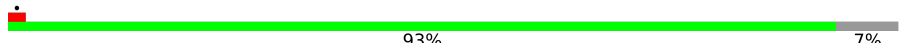
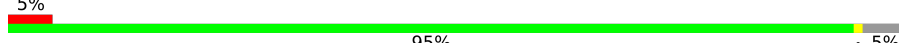

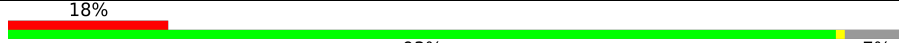
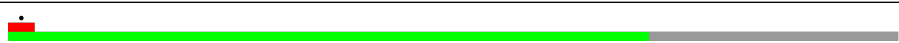

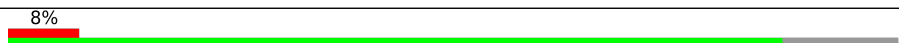


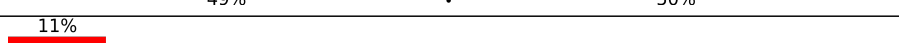
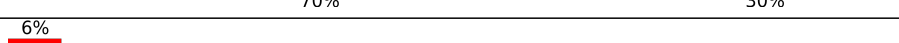
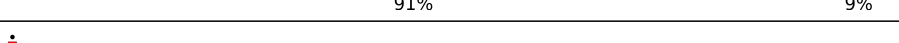
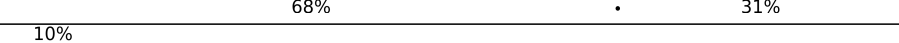
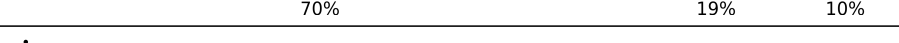
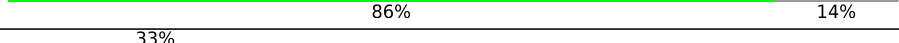






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	0	188	
2	T	206	
3	u	234	
4	1	65	
5	U	153	
6	v	70	
7	2	92	
8	V	216	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	w	156	
10	3	188	
11	W	148	
12	x	384	
13	5	423	
14	X	256	
15	y	381	
16	6	380	
17	Y	250	
18	z	334	
19	7	338	
20	Z	161	
21	8	206	
22	a	142	
23	9	137	
24	b	215	
25	A	1589	
26	c	332	
27	B	72	
28	d	306	
29	D	305	
30	e	279	
31	E	348	
32	f	212	
33	F	311	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	g	166	81% 19%
35	H	267	36% 64%
36	h	158	7% 70% 30%
37	I	261	54% 57% 39%
38	i	128	76% 24%
39	J	192	84% 79% 16%
40	j	123	72% 27%
41	K	178	5% 99%
42	k	112	90% 87% 10%
43	L	145	5% 79% 21%
44	l	138	49% 49% 48%
45	M	296	98%
46	m	128	40% 40% 60%
47	N	251	45% 54% 43%
48	o	102	78% 22%
49	O	175	88% 12%
50	p	206	17% 71% 29%
51	P	180	80% 20%
52	q	222	9% 64% 36%
53	Q	292	75% 24%
54	r	196	19% 82% 17%
55	R	149	94% 6%
56	s	439	88% 12%
57	S	205	78% 21%
58	t	387	40% 81% 16%

## 2 Entry composition i

There are 64 unique types of molecules in this entry. The entry contains 108702 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	110	898	554	176	162	6	0	0

- Molecule 2 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	T	166	1369	875	254	233	7	0	0

- Molecule 3 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	u	126	1044	671	172	191	10	0	0

- Molecule 4 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	1	55	455	290	87	76	2	0	0

- Molecule 5 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	U	152	1251	788	234	226	3	0	0

- Molecule 6 is a protein called MIEF1 upstream open reading frame protein.

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

- Molecule 7 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	2	46	377	233	83	60	1	0	0

- Molecule 8 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	V	205	1676	1068	298	302	8	0	0

- Molecule 9 is a protein called Acyl carrier protein, mitochondrial.

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

- Molecule 10 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	3	95	832	539	162	128	3	0	0

- Molecule 11 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	W	106	835	536	157	139	3	0	0

- Molecule 12 is a protein called 5-methylcytosine rRNA methyltransferase NSUN4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	x	338	2676	1703	467	489	17	0	0

- Molecule 13 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	5	394	3210	2073	560	566	11	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	X	244	Total	C	N	O	S	0	0
			2044	1322	352	365	5		

- Molecule 15 is a protein called Transcription termination factor 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	y	244	Total	C	N	O	S	0	0
			1980	1264	342	362	12		

- Molecule 16 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	6	354	Total	C	N	O	S	0	0
			2948	1881	525	533	9		

- Molecule 17 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Y	181	Total	C	N	O	S	0	0
			1556	995	298	259	4		

- Molecule 18 is a protein called Mitochondrial ribosome-associated GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	z	311	Total	C	N	O	S	0	0
			2443	1549	445	433	16		

- Molecule 19 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	7	294	Total	C	N	O	S	0	0
			2390	1529	405	438	18		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Z	122	Total	C	N	O	S	0	0
			996	636	186	171	3		

- Molecule 21 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	8	102	Total	C	N	O	S	0	0
			860	543	152	163	2		

- Molecule 22 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	a	100	Total	C	N	O	S	0	0
			840	529	152	154	5		

- Molecule 23 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	9	124	Total	C	N	O	S	0	0
			997	644	170	181	2		

- Molecule 24 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	b	149	Total	C	N	O	S	0	0
			1189	739	230	217	3		

- Molecule 25 is a RNA chain called 16S rRNA + pre-H68-71 segment.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A	1423	Total	C	N	O	P	0	0
			30199	13555	5442	9779	1423		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2830	U	G	conflict	GB 1858624182
A	3231	U	-	insertion	GB 1858624182

- Molecule 26 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	c	286	Total	C	N	O	S	0	0
			2299	1470	397	423	9		

- Molecule 27 is a RNA chain called CP tRNA-Val.



Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
27	B	72	1522	683	269	498	72	0	0

- Molecule 28 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	d	255	2088	1335	360	379	14	0	0

- Molecule 29 is a protein called 39S ribosomal protein L2, mitochondrial.

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

- Molecule 30 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	e	228	1848	1174	326	342	6	0	0

- Molecule 31 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	E	305	2406	1545	418	432	11	0	0

- Molecule 32 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	f	150	1196	764	197	231	4	0	0

- Molecule 33 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	F	252	2031	1305	370	350	6	0	0

- Molecule 34 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	g	134	1113	719	193	199	2	0	0

- Molecule 35 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	H	97	802	508	155	139		0	0

- Molecule 36 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	h	110	895	568	156	168	3	0	0

- Molecule 37 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	I	158	871	533	169	166	3	0	0

- Molecule 38 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	i	97	828	532	165	127	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	J	162	798	474	162	162		0	0

- Molecule 40 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	j	90	722	449	140	131	2	0	0

- Molecule 41 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	K	177	Total	C	N	O	S	0	0
			1455	936	259	253	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	101	Total	C	N	O	S	0	0
			502	299	101	102			

- Molecule 43 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	L	115	Total	C	N	O	S	0	0
			890	559	171	155	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	72	Total	C	N	O	S	0	0
			353	209	72	72			

- Molecule 45 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	M	291	Total	C	N	O	S	0	0
			2327	1483	430	408	6		

- Molecule 46 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	m	51	Total	C	N	O	S	0	0
			419	262	82	73	2		

- Molecule 47 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	N	144	Total	C	N	O	S	0	0
			799	485	157	156	1		

- Molecule 48 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	o	80	Total	C	N	O	S	0	0
			677	426	134	114	3		

- Molecule 49 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	O	154	Total	C	N	O	S	0	0
			1259	792	241	219	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	p	147	Total	C	N	O	S	0	0
			1205	748	228	225	4		

- Molecule 51 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	P	144	Total	C	N	O	S	0	0
			1173	733	224	211	5		

- Molecule 52 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	q	141	Total	C	N	O	S	0	0
			1177	732	229	211	5		

- Molecule 53 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Q	221	Total	C	N	O	S	0	0
			1843	1179	327	328	9		

- Molecule 54 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	r	162	Total	C	N	O	S	0	0
			1251	791	243	209	8		

- Molecule 55 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	R	140	Total	C	N	O	S	0	0
			1154	732	231	187	4		

- Molecule 56 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	s	386	Total	C	N	O	S	0	0
			3155	2023	559	559	14		

- Molecule 57 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	S	161	Total	C	N	O	S	0	0
			1293	835	227	227	4		

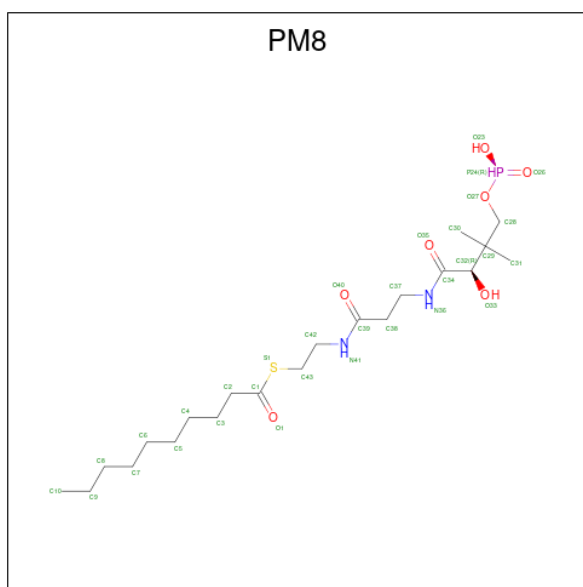
- Molecule 58 is a protein called GTP-binding protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	t	325	Total	C	N	O	S	0	0
			1958	1202	380	372	4		

- Molecule 59 is ZINC ION (three-letter code: ZN) (formula: Zn).

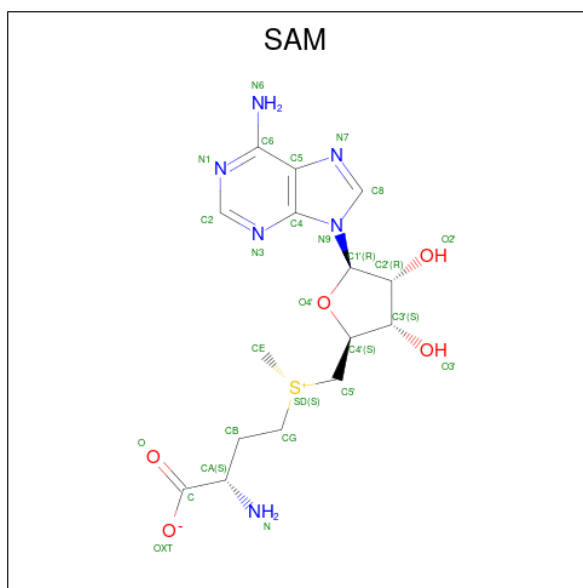
Mol	Chain	Residues	Atoms		AltConf
59	0	1	Total	Zn	0
			1	1	

- Molecule 60 is S-(2-{[N-(2-HYDROXY-4-{[HYDROXY(OXIDO)PHOSPHINO]OXY}-3,3-DIMETHYLBUTANOYL)-BETA-ALANYL]AMINO}ETHYL) DECANETHIOATE (three-letter code: PM8) (formula: C<sub>21</sub>H<sub>41</sub>N<sub>2</sub>O<sub>7</sub>PS).



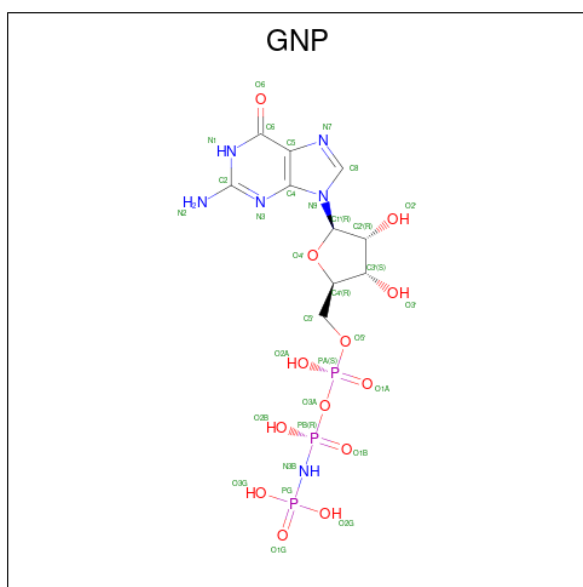
Mol	Chain	Residues	Atoms					AltConf	
			Total	C	N	O	P		S
60	w	1	32	21	2	7	1	1	0

- Molecule 61 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula:  $C_{15}H_{22}N_6O_5S$ ).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
61	x	1	27	15	6	5	1	0

- Molecule 62 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula:  $C_{10}H_{17}N_6O_{13}P_3$ ).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
62	z	1	32	10	6	13	3	0
62	t	1	32	10	6	13	3	0

- Molecule 63 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
63	z	1	1	1	0
63	A	92	92	92	0
63	E	1	1	1	0
63	g	1	1	1	0
63	t	1	1	1	0

- Molecule 64 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
			Total	K	
64	A	10	10	10	0

### 3 Residue-property plots [i](#)

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


- Molecule 1: 39S ribosomal protein L32, mitochondrial

Chain 0:  58% 41%

MET ALA ALA ALA MET LEU VAL LEU VAL VAL SER PRO TRP SER ALA ALA ARG GLY VAL LEU ARG ASN TYR TRP GLU ARG LEU LEU LYS LEU PRO PRO GLN SER ARG PRO PRO TRP TRP GLY PRO ALA ALA VAL VAL GLN GLY PRO PHE MET THR GLU PRO ALA ASN

ASP THR SER GLY SER LYS GLU ASN SER SER LEU LEU ASP SER ILE PHE TRP MET A79 E167 F185 M188

- Molecule 2: 39S ribosomal protein L22, mitochondrial

Chain T:  80% 19%

MET ALA ALA VAL LEU GLY GLN SER LEU ALA ALA TRP ILE HIS ASN LEU ARG SER ARG GLY LYS LEU ALA LEU VAL LEU PRO GLN SER TYR ILE THR SER ALA LEU ASP T41 G59 E181 T185 L206

- Molecule 3: Mitochondrial assembly of ribosomal large subunit protein 1


Chain u:  10% 53% 46%

MET GLY PRO GLY PRO GLY ARG VAL ALA ARG LEU LEU ALA ALA PRO GLY THR MET TRP ARG ALA VAL SER GLU ASP VAL ALA ALA ASP HIS THR PRO ALA ALA GLN ARG LEU PRO VAL VAL GLY ALA CYS ARG ALA CYS THR PRO ASN PHE VAL ARG GLY

LEU HIS SER GLU PRO GLY LEU GLU ARG ALA ALA GLY THR VAL ASN GLU ARG VAL PRO GLU ASP ALA ALA ASP HIS THR PRO LEU LEU VAL R91 R97 E104 D108 R133 H148 K152 R153 D163 T164 D165 D166 G173 E186 I187 A204 Q205 I206 A207 P208

E209 T210 V211 P212 E213 T216 LEU GLY ILE GLU ASP THR SER VAL PRO VAL GLU LEU LYS CYS GLU

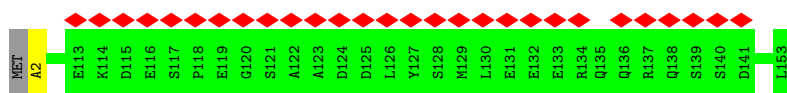
- Molecule 4: 39S ribosomal protein L33, mitochondrial

Chain 1:  12% 85% 15%

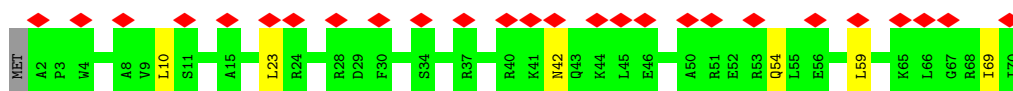
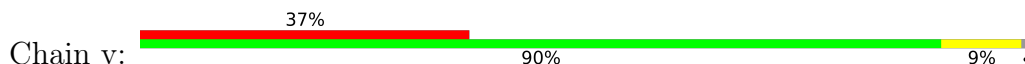




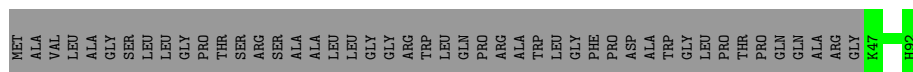
• Molecule 5: 39S ribosomal protein L23, mitochondrial



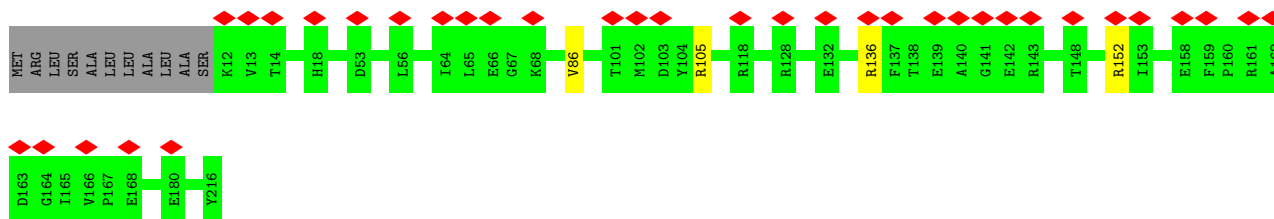
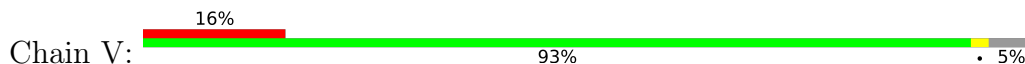
• Molecule 6: MIEF1 upstream open reading frame protein



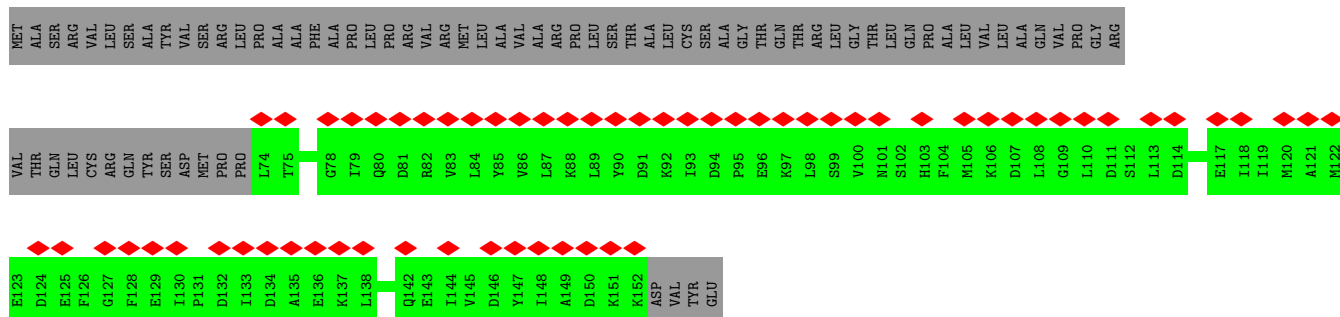
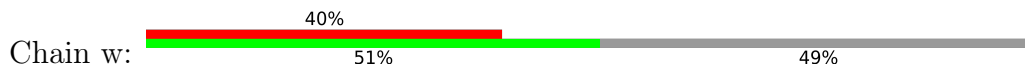
• Molecule 7: 39S ribosomal protein L34, mitochondrial



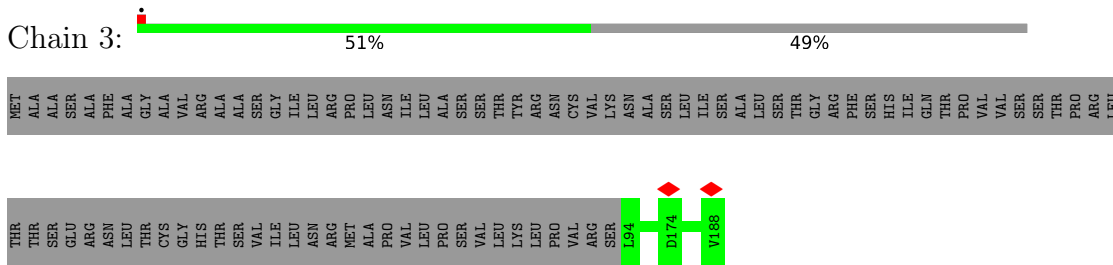
• Molecule 8: 39S ribosomal protein L24, mitochondrial



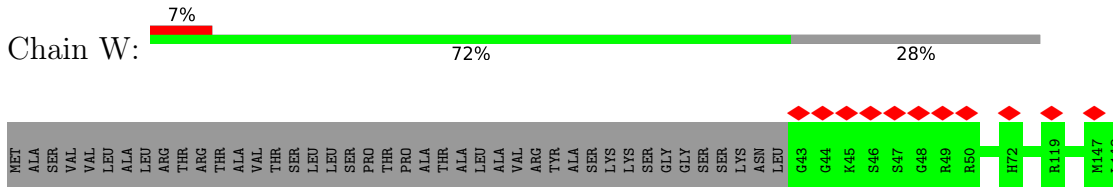
• Molecule 9: Acyl carrier protein, mitochondrial



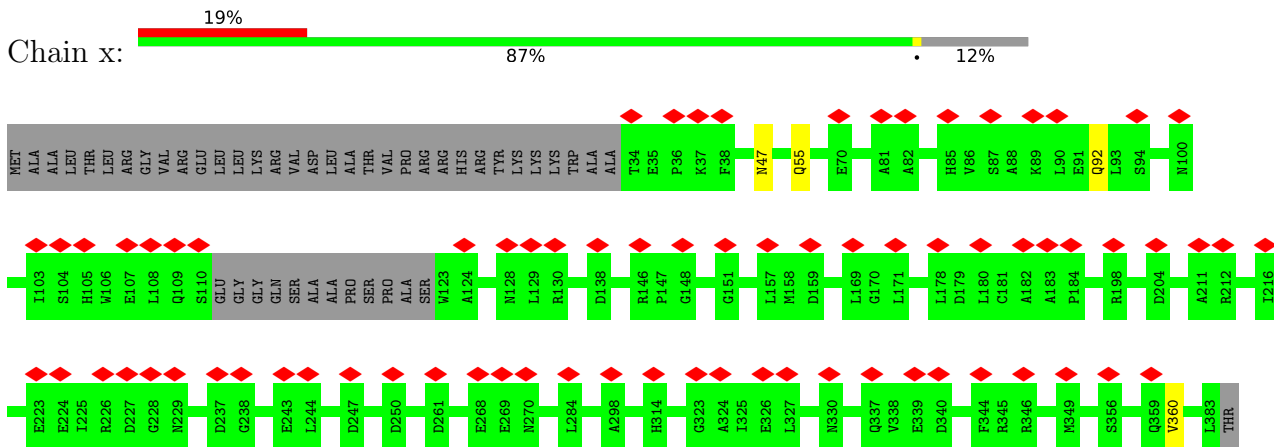
- Molecule 10: 39S ribosomal protein L35, mitochondrial



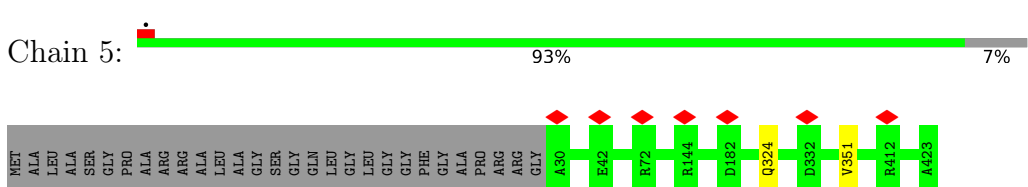
- Molecule 11: 39S ribosomal protein L27, mitochondrial



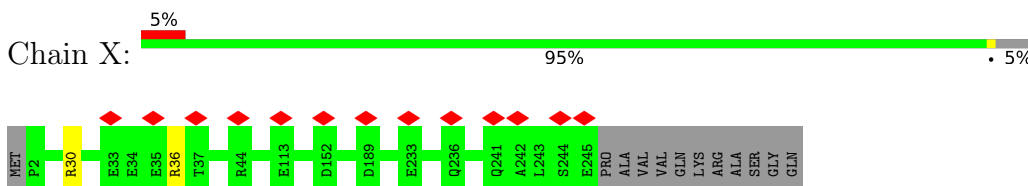
- Molecule 12: 5-methylcytosine rRNA methyltransferase NSUN4



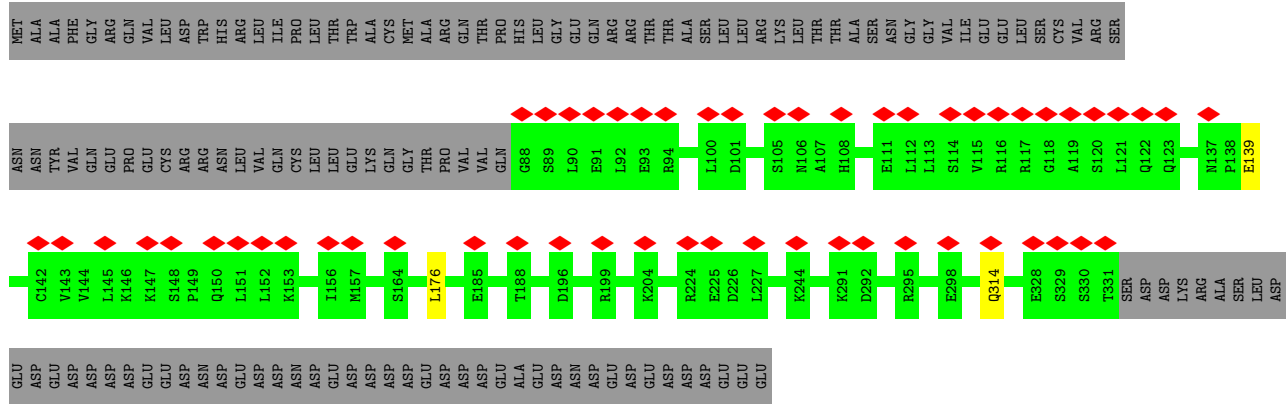
- Molecule 13: 39S ribosomal protein L37, mitochondrial



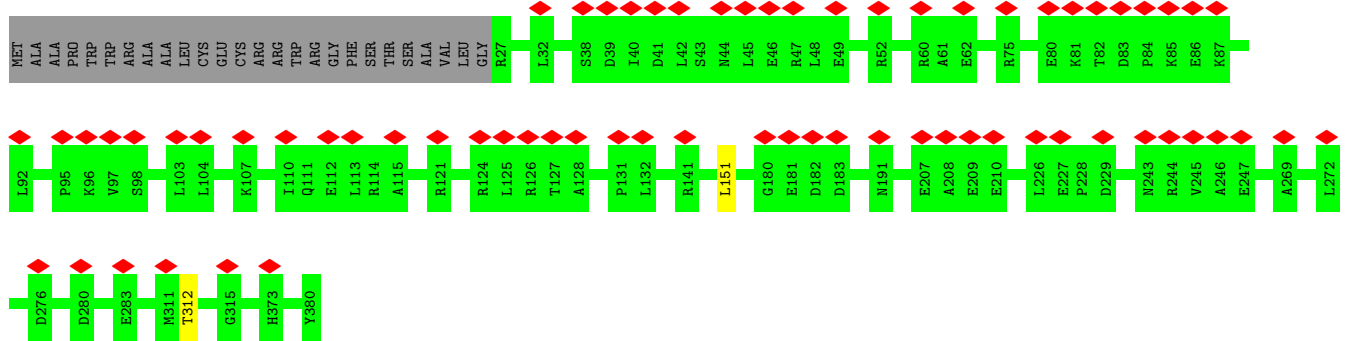
- Molecule 14: 39S ribosomal protein L28, mitochondrial



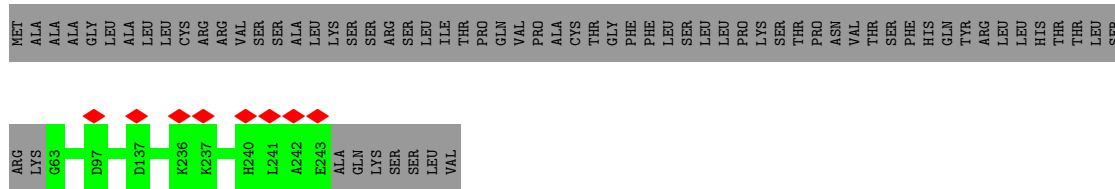
- Molecule 15: Transcription termination factor 4, mitochondrial



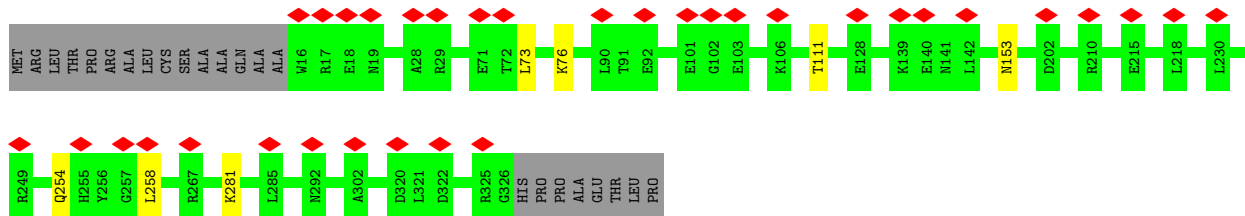
• Molecule 16: 39S ribosomal protein L38, mitochondrial



• Molecule 17: 39S ribosomal protein L47, mitochondrial

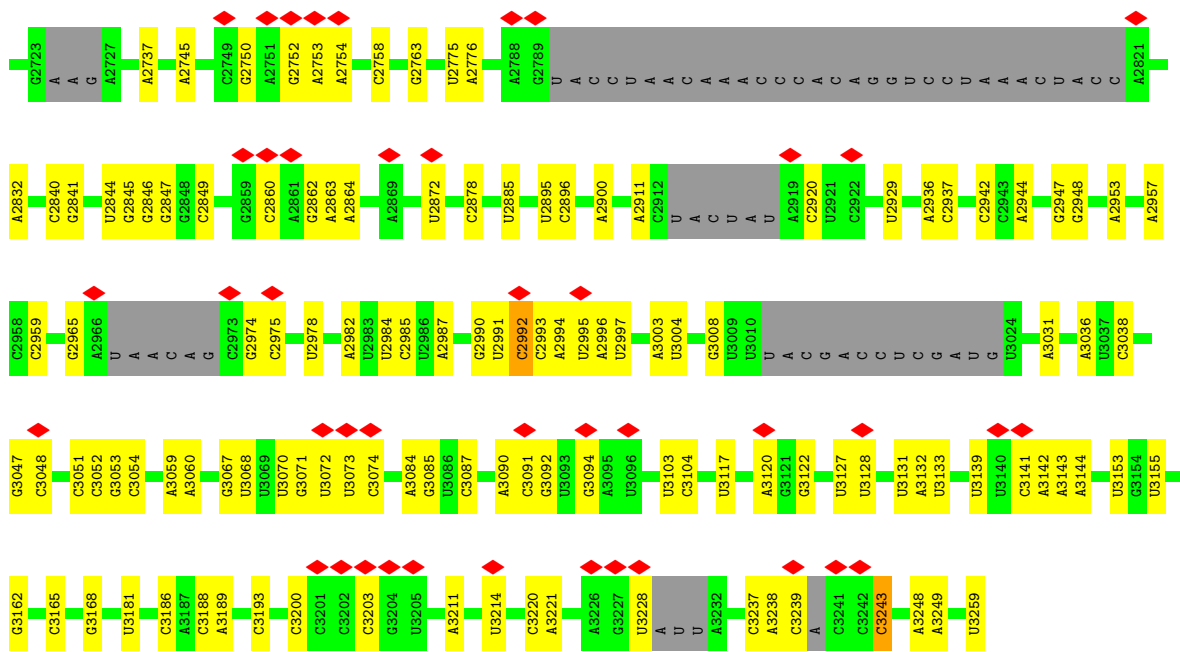


• Molecule 18: Mitochondrial ribosome-associated GTPase 1

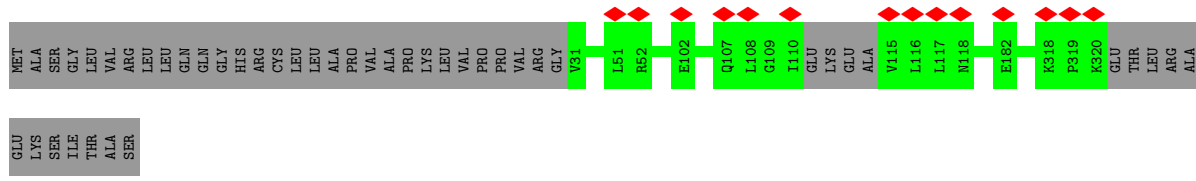
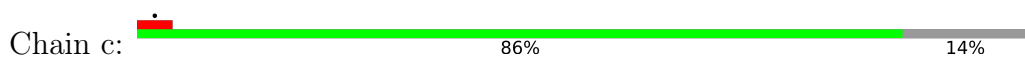




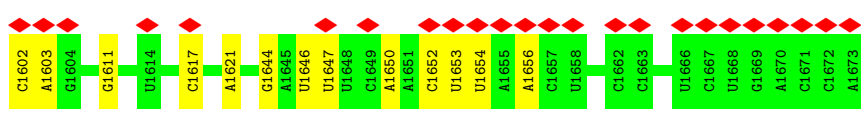
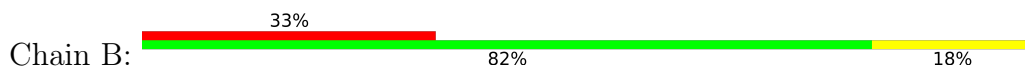




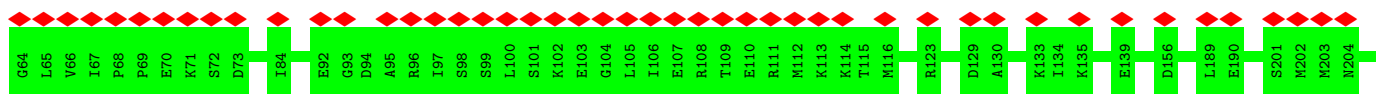
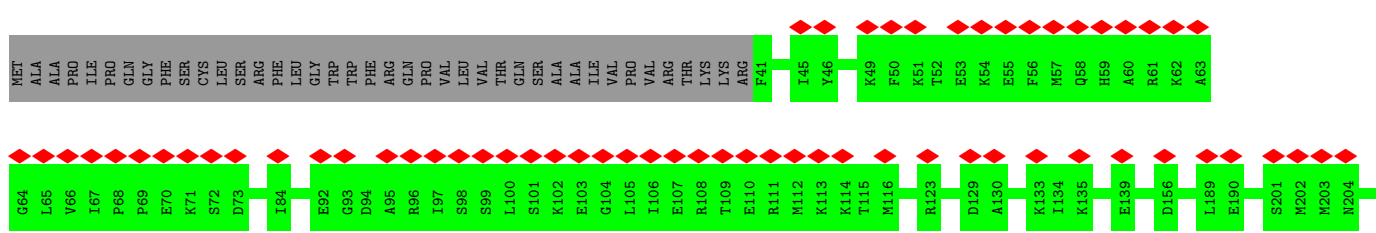
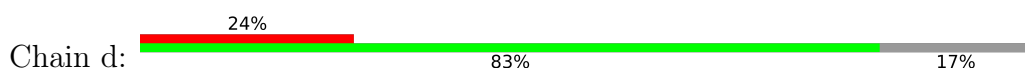
• Molecule 26: 39S ribosomal protein L44, mitochondrial

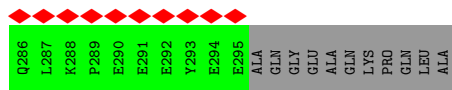


• Molecule 27: CP tRNA-Val

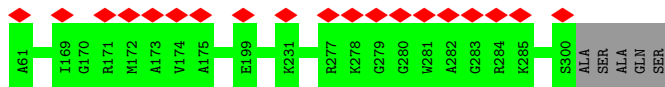
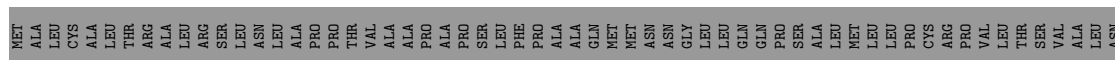
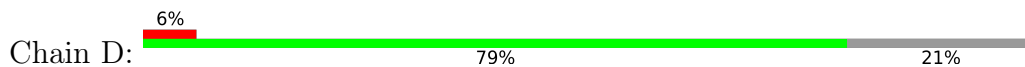


• Molecule 28: 39S ribosomal protein L45, mitochondrial

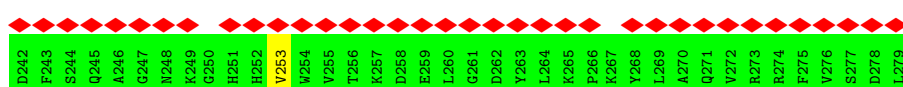
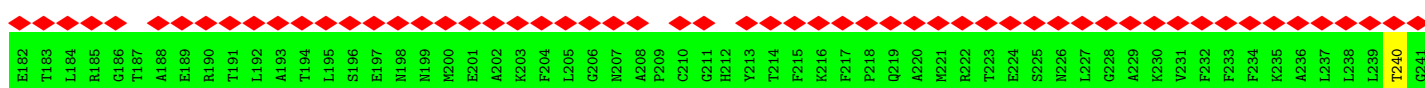
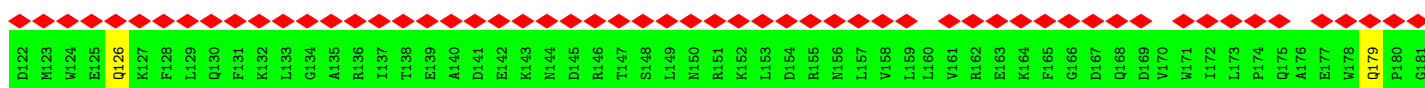
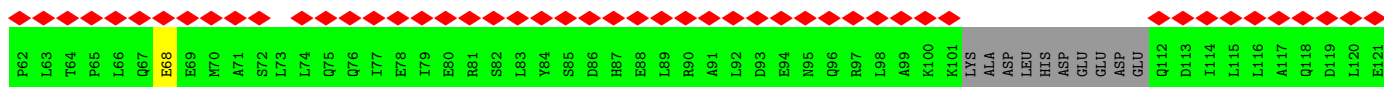
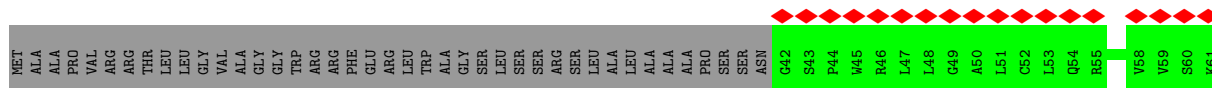
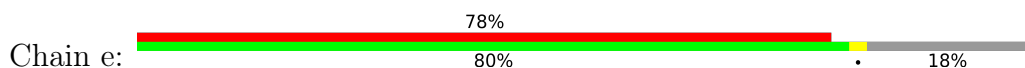




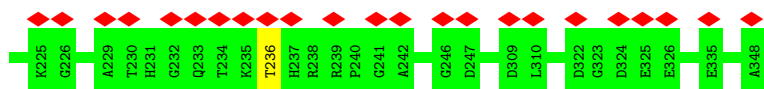
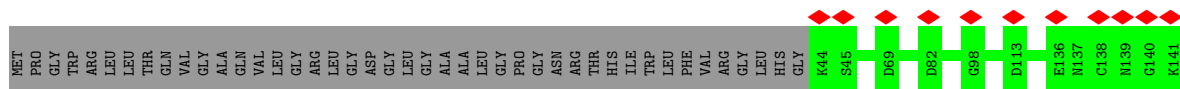
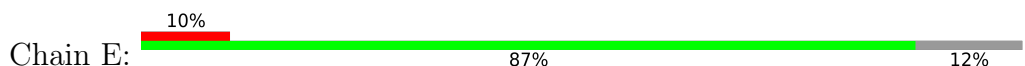
• Molecule 29: 39S ribosomal protein L2, mitochondrial



• Molecule 30: 39S ribosomal protein L46, mitochondrial

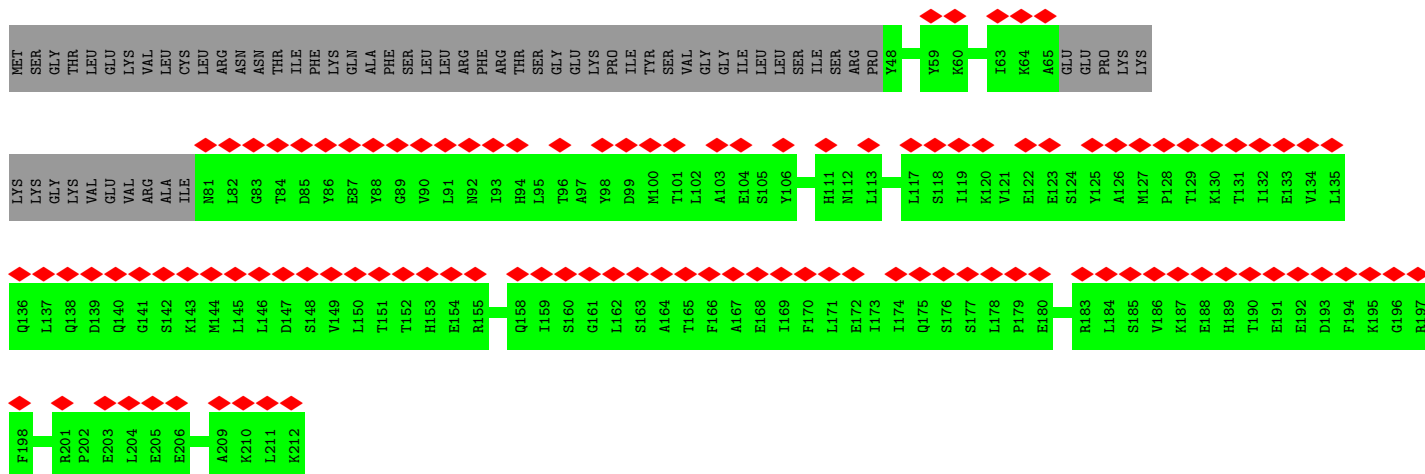


• Molecule 31: 39S ribosomal protein L3, mitochondrial

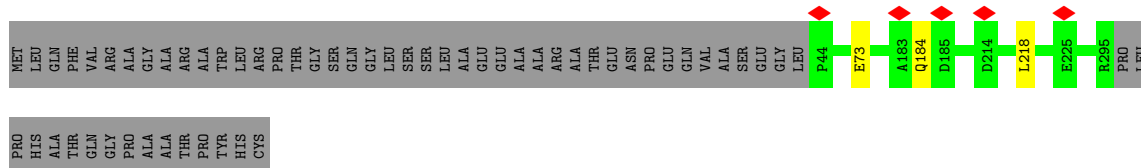
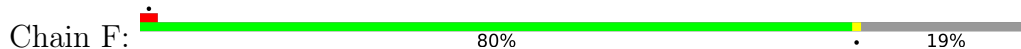


• Molecule 32: 39S ribosomal protein L48, mitochondrial

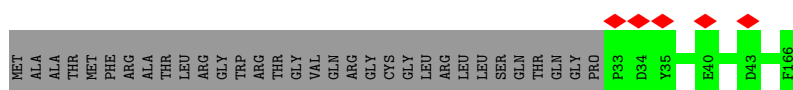
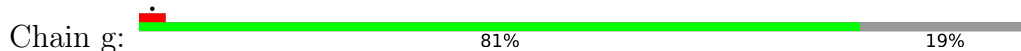




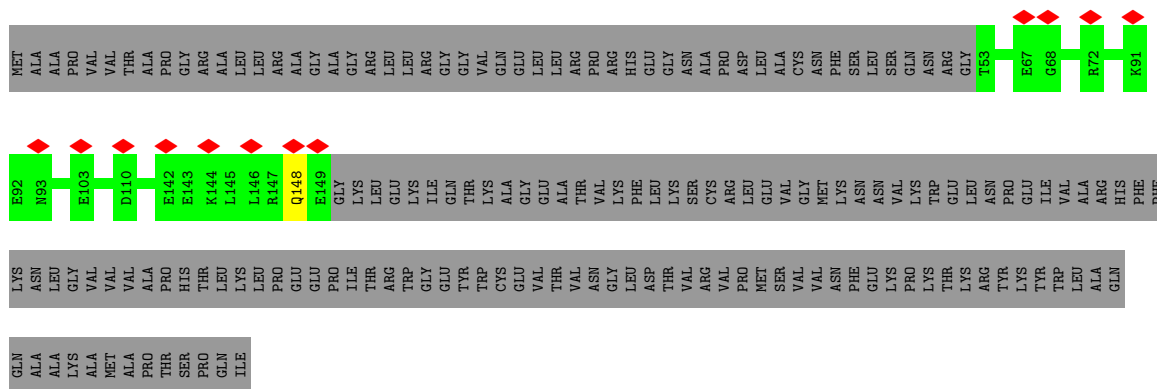
- Molecule 33: 39S ribosomal protein L4, mitochondrial



- Molecule 34: 39S ribosomal protein L49, mitochondrial

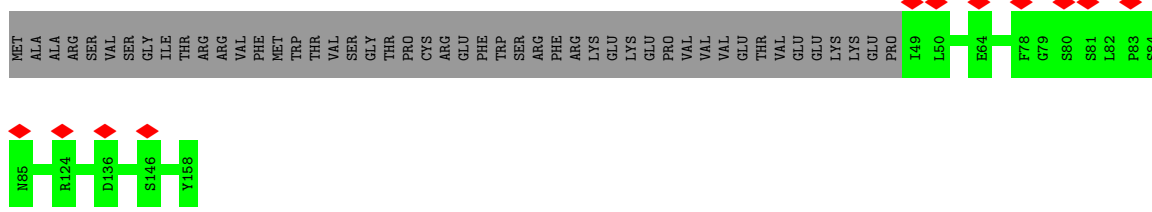


- Molecule 35: 39S ribosomal protein L9, mitochondrial

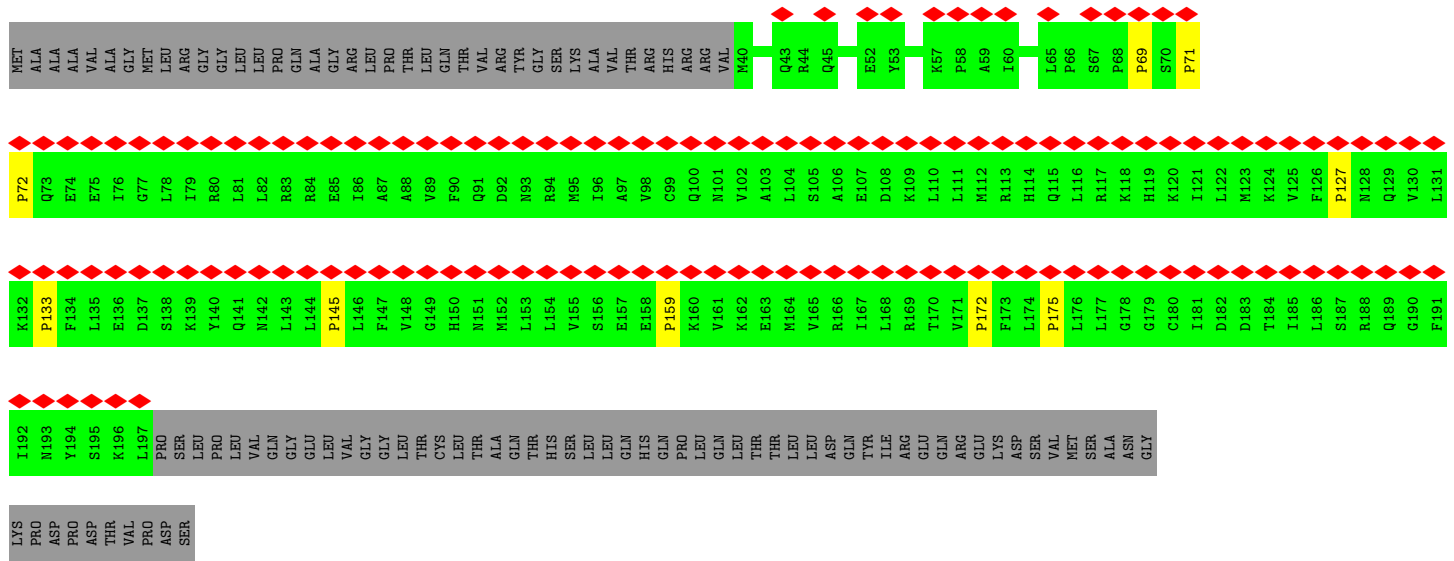


- Molecule 36: 39S ribosomal protein L50, mitochondrial

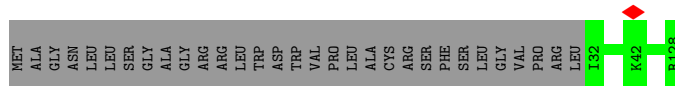
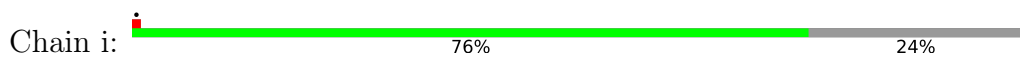




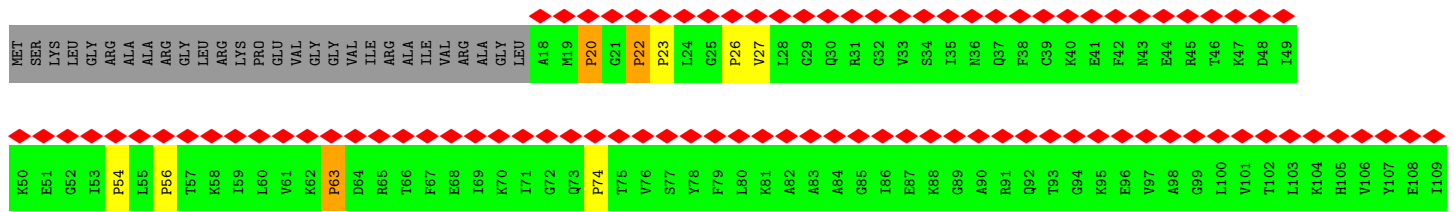
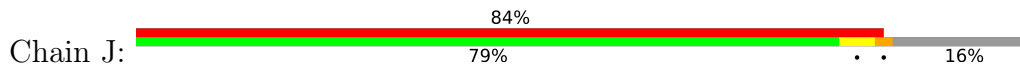
- Molecule 37: 39S ribosomal protein L10, mitochondrial

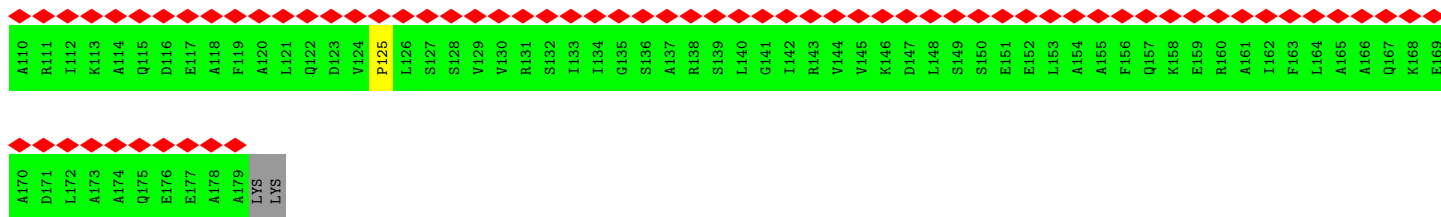


- Molecule 38: 39S ribosomal protein L51, mitochondrial

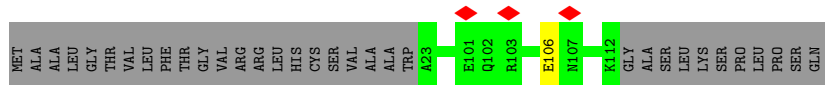


- Molecule 39: 39S ribosomal protein L11, mitochondrial

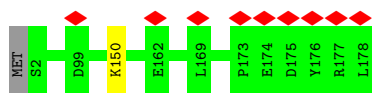




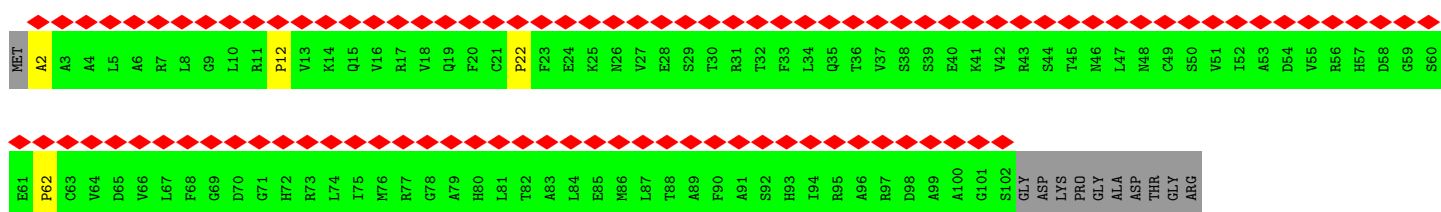
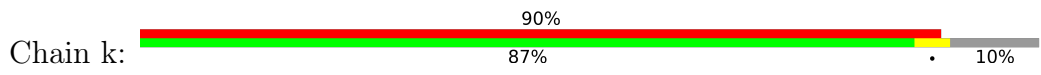
- Molecule 40: 39S ribosomal protein L52, mitochondrial



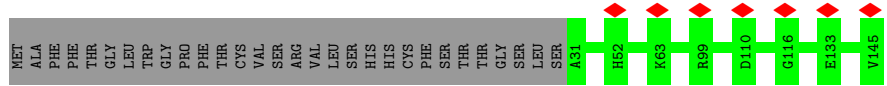
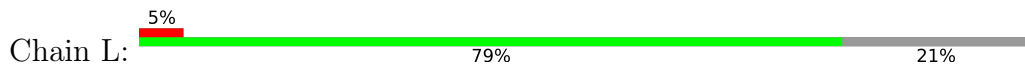
- Molecule 41: 39S ribosomal protein L13, mitochondrial



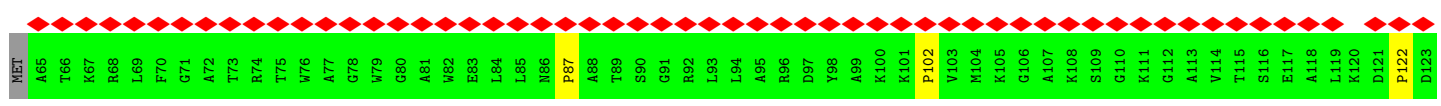
- Molecule 42: 39S ribosomal protein L53, mitochondrial

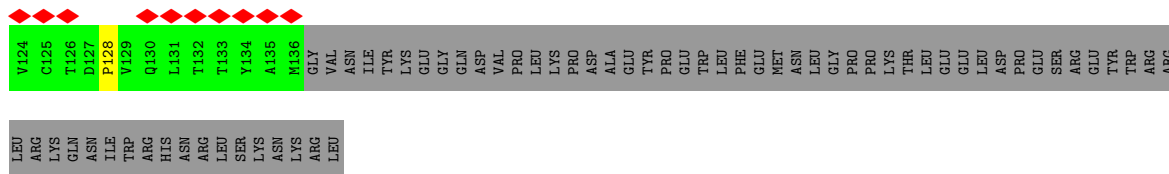


- Molecule 43: 39S ribosomal protein L14, mitochondrial



- Molecule 44: 39S ribosomal protein L54, mitochondrial

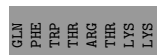
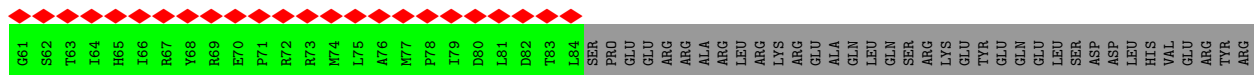
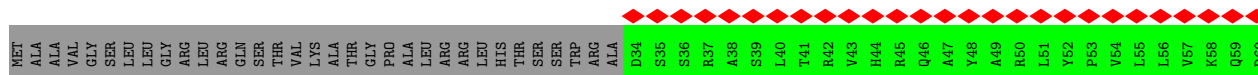




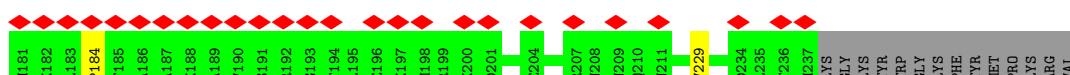
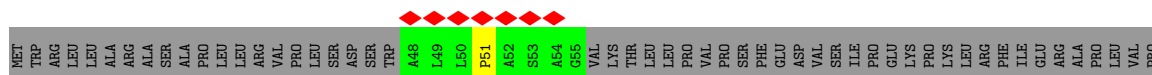
• Molecule 45: 39S ribosomal protein L15, mitochondrial



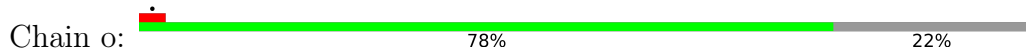
• Molecule 46: 39S ribosomal protein L55, mitochondrial

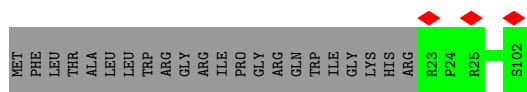


• Molecule 47: 39S ribosomal protein L16, mitochondrial

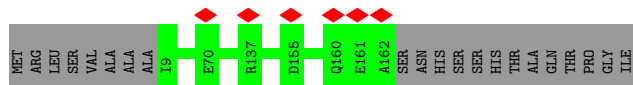
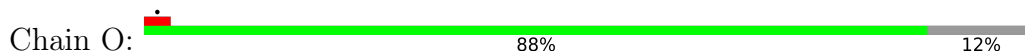


• Molecule 48: Ribosomal protein 63, mitochondrial

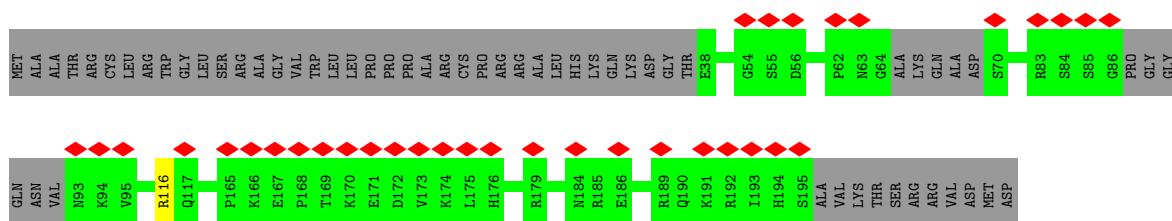




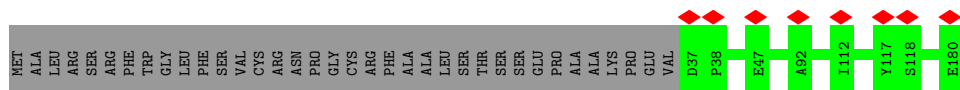
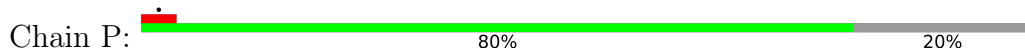
• Molecule 49: 39S ribosomal protein L17, mitochondrial



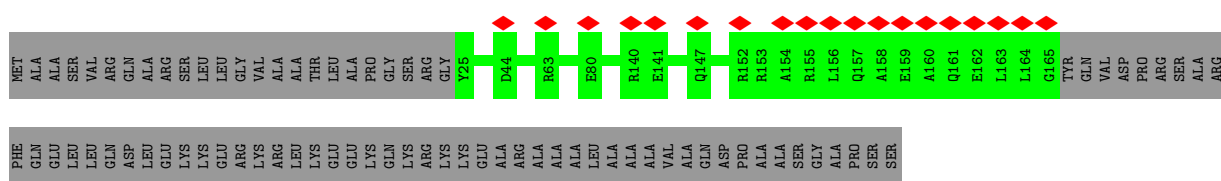
• Molecule 50: Peptidyl-tRNA hydrolase ICT1, mitochondrial



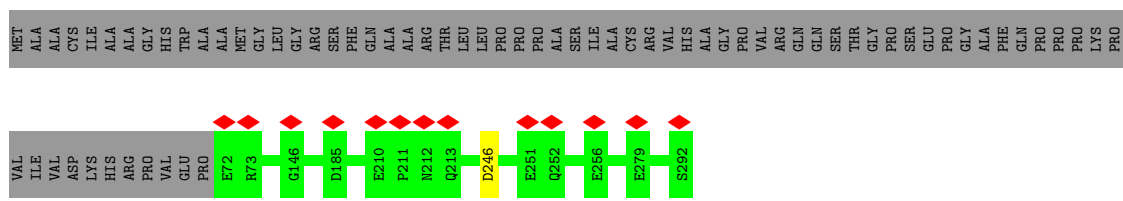
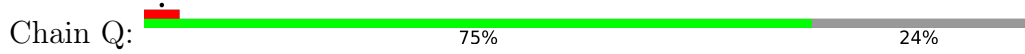
• Molecule 51: 39S ribosomal protein L18, mitochondrial



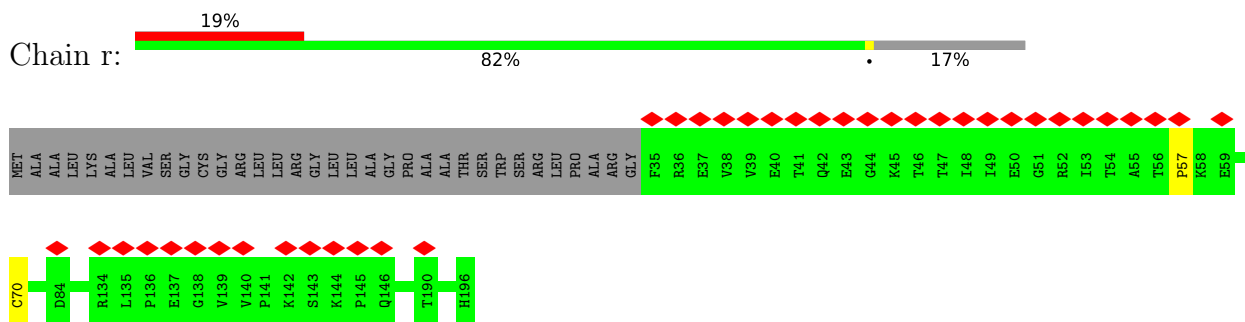
• Molecule 52: Growth arrest and DNA damage-inducible proteins-interacting protein 1



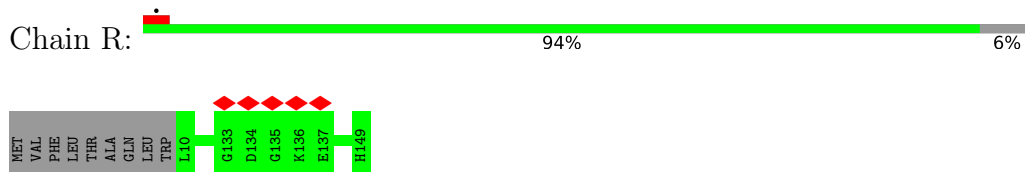
• Molecule 53: 39S ribosomal protein L19, mitochondrial



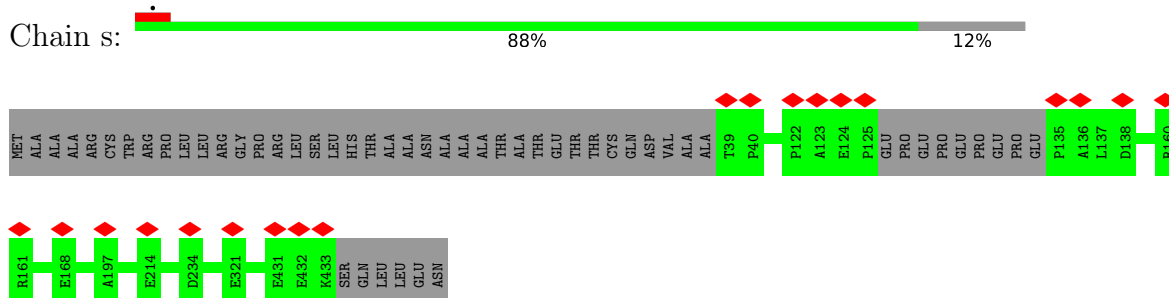
- Molecule 54: 39S ribosomal protein S18a, mitochondrial



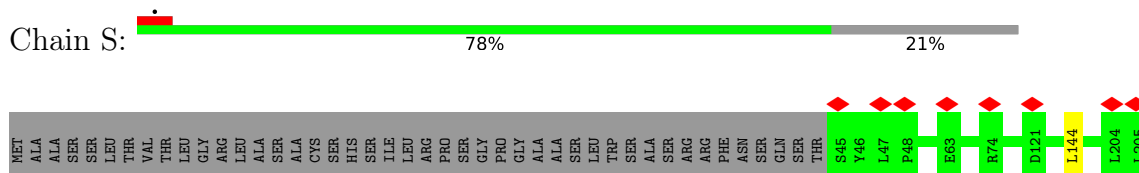
- Molecule 55: 39S ribosomal protein L20, mitochondrial



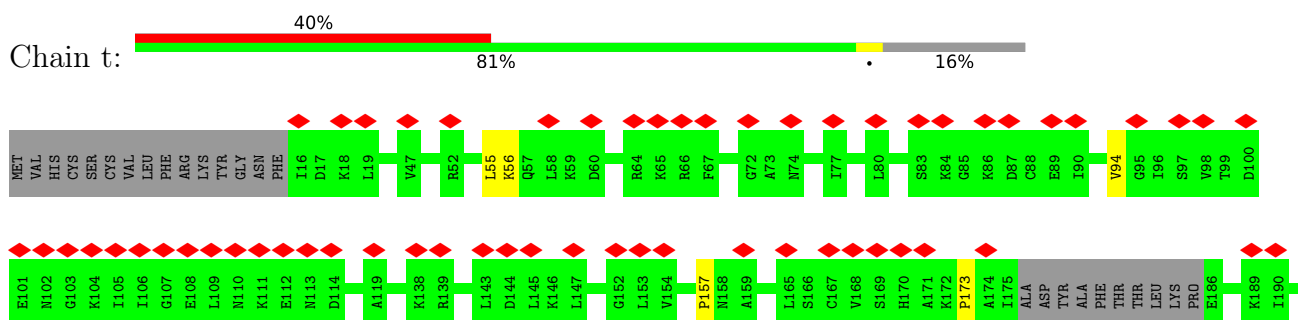
- Molecule 56: 39S ribosomal protein S30, mitochondrial



- Molecule 57: 39S ribosomal protein L21, mitochondrial



- Molecule 58: GTP-binding protein 10



I198	S199	V200	A201	D202	L203	P204	G205	L206	I207	E208	H211	M212	N213	K214	H218	L221	K222	E225	R226	Q229	L230	L231	F232	V233	V234	D235	I236	S237	G238	F239	Q240	L241	S242	S243	Q246	T249	A250	F251	E252	T253	I254	I255	L256	E262	L263	Y264	K265	E266	E267	L268	Q269																										
T270	K271	P272	A273	A276	V277	M280	D281	L282	P283	D284	A285	Q286	H290	L296	Q297	M298	P299	K300	D301	F302	L303	H304	L305	F306	E307	K308	N309	M310	I311	P312	E313	R314	T315	V316	E317	F318	Q319	P323	T328	G329	E330	G331	K341	S342	L343	D344	E345	Q346	A347	N348	Q349	E350																									
ASN	ASP	ALA	LEU	HIS	LYS	LYS	GLN	LEU	LEU	ASN	ASN	TRP	ILE	SER	ASP	THR	MET	SER	SER	THR	THR	GLU	PRO	PRO	SER	LYS	HIS	ALA	VAL	THR	THR	SER	LYS	MET	ASP	ASP	ILE	ILE	ASN	ASP	ALA	LEU	HIS	LYS	LYS	GLN	LEU	LEU	ASN	ASN	TRP	ILE	SER	ASP	THR	MET	SER	SER	THR	THR	GLU	PRO	PRO	SER	LYS	HIS	ALA	VAL	THR	THR	SER	LYS	MET	ASP	ASP	ILE	ILE

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31656	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 ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	4.028	Depositor
Minimum map value	-2.106	Depositor
Average map value	-0.004	Depositor
Map value standard deviation	0.160	Depositor
Recommended contour level	0.747	Depositor
Map size ( $\text{\AA}$ )	518.4, 518.4, 518.4	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.08, 1.08, 1.08	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: K, SAC, PM8, THC, AYA, GNP, ZN, SAM, 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	0	0.25	0/913	0.51	0/1224
2	T	0.26	0/1403	0.48	0/1886
3	u	0.25	0/1069	0.48	0/1447
4	1	0.25	0/460	0.54	0/610
5	U	0.26	0/1274	0.52	0/1723
6	v	0.24	0/597	0.55	0/796
7	2	0.23	0/383	0.53	0/507
8	V	0.25	0/1721	0.50	0/2333
9	w	0.25	0/647	0.46	0/871
10	3	0.25	0/853	0.51	0/1136
11	W	0.26	0/857	0.49	0/1155
12	x	0.25	0/2737	0.48	0/3714
13	5	0.25	0/3305	0.47	0/4502
14	X	0.25	0/2099	0.46	0/2837
15	y	0.25	0/2011	0.46	0/2702
16	6	0.25	0/3043	0.50	0/4140
17	Y	0.25	0/1593	0.48	0/2136
18	z	0.24	0/2484	0.48	0/3349
19	7	0.25	0/2447	0.45	0/3310
20	Z	0.24	0/1021	0.47	0/1378
21	8	0.25	0/880	0.50	0/1188
22	a	0.25	0/866	0.49	0/1174
23	9	0.27	0/1025	0.47	0/1379
24	b	0.25	0/1203	0.53	0/1627
25	A	0.25	0/33779	0.77	19/52552 (0.0%)
26	c	0.25	0/2347	0.45	0/3171
27	B	0.31	1/1700 (0.1%)	0.74	0/2641
28	d	0.25	0/2145	0.46	0/2903
29	D	0.25	0/1910	0.55	0/2569
30	e	0.24	0/1885	0.47	0/2542
31	E	0.25	0/2475	0.46	0/3355
32	f	0.24	0/1216	0.44	0/1638



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	F	0.25	0/2090	0.49	0/2842
34	g	0.26	0/1151	0.49	0/1569
35	H	0.24	0/816	0.52	0/1097
36	h	0.24	0/918	0.44	0/1249
37	I	0.26	0/880	0.66	9/1220 (0.7%)
38	i	0.25	0/850	0.50	0/1135
39	J	0.28	0/797	0.72	9/1107 (0.8%)
40	j	0.25	0/737	0.47	0/992
41	K	0.25	0/1490	0.47	0/2021
42	k	0.27	0/493	0.55	3/685 (0.4%)
43	L	0.25	0/905	0.52	0/1218
44	l	0.27	0/352	0.67	4/487 (0.8%)
45	M	0.26	0/2381	0.51	0/3212
46	m	0.23	0/426	0.56	0/575
47	N	0.27	0/803	0.65	6/1105 (0.5%)
48	o	0.25	0/694	0.51	0/931
49	O	0.25	0/1283	0.52	0/1727
50	p	0.24	0/1223	0.49	0/1641
51	P	0.24	0/1199	0.52	0/1623
52	q	0.24	0/1208	0.50	0/1633
53	Q	0.25	0/1884	0.48	0/2535
54	r	0.25	0/1289	0.51	1/1752 (0.1%)
55	R	0.26	0/1175	0.51	0/1572
56	s	0.26	0/3239	0.49	0/4400
57	S	0.25	0/1320	0.50	0/1789
58	t	0.26	0/1971	0.59	8/2684 (0.3%)
All	All	0.25	1/113922 (0.0%)	0.61	59/161296 (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
21	8	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	B	1602	C	OP3-P	-10.60	1.48	1.61

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	1711	C	C2-N1-C1'	9.02	128.73	118.80
25	A	1711	C	N1-C2-O2	8.65	124.09	118.90
39	J	63	PRO	N-CA-CB	8.46	113.45	103.30
25	A	1711	C	N3-C2-O2	-7.38	116.73	121.90
25	A	2992	C	N1-C2-O2	7.37	123.32	118.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	8	169	PHE	Peptide

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	108/188 (57%)	108 (100%)	0	0	100	100
2	T	164/206 (80%)	162 (99%)	2 (1%)	0	100	100
3	u	124/234 (53%)	117 (94%)	7 (6%)	0	100	100
4	1	53/65 (82%)	53 (100%)	0	0	100	100
5	U	150/153 (98%)	148 (99%)	2 (1%)	0	100	100
6	v	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
7	2	44/92 (48%)	44 (100%)	0	0	100	100
8	V	203/216 (94%)	201 (99%)	2 (1%)	0	100	100
9	w	77/156 (49%)	70 (91%)	7 (9%)	0	100	100
10	3	93/188 (50%)	92 (99%)	1 (1%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	W	104/148 (70%)	102 (98%)	2 (2%)	0	100	100
12	x	334/384 (87%)	324 (97%)	10 (3%)	0	100	100
13	5	392/423 (93%)	385 (98%)	7 (2%)	0	100	100
14	X	242/256 (94%)	239 (99%)	3 (1%)	0	100	100
15	y	242/381 (64%)	238 (98%)	4 (2%)	0	100	100
16	6	352/380 (93%)	340 (97%)	12 (3%)	0	100	100
17	Y	179/250 (72%)	178 (99%)	1 (1%)	0	100	100
18	z	309/334 (92%)	302 (98%)	7 (2%)	0	100	100
19	7	292/338 (86%)	281 (96%)	11 (4%)	0	100	100
20	Z	120/161 (74%)	118 (98%)	2 (2%)	0	100	100
21	8	100/206 (48%)	98 (98%)	2 (2%)	0	100	100
22	a	96/142 (68%)	95 (99%)	1 (1%)	0	100	100
23	9	122/137 (89%)	118 (97%)	4 (3%)	0	100	100
24	b	147/215 (68%)	142 (97%)	5 (3%)	0	100	100
26	c	282/332 (85%)	276 (98%)	6 (2%)	0	100	100
28	d	253/306 (83%)	251 (99%)	2 (1%)	0	100	100
29	D	238/305 (78%)	227 (95%)	11 (5%)	0	100	100
30	e	224/279 (80%)	221 (99%)	3 (1%)	0	100	100
31	E	303/348 (87%)	296 (98%)	7 (2%)	0	100	100
32	f	146/212 (69%)	142 (97%)	4 (3%)	0	100	100
33	F	250/311 (80%)	248 (99%)	2 (1%)	0	100	100
34	g	132/166 (80%)	129 (98%)	3 (2%)	0	100	100
35	H	95/267 (36%)	95 (100%)	0	0	100	100
36	h	108/158 (68%)	104 (96%)	4 (4%)	0	100	100
37	I	156/261 (60%)	153 (98%)	3 (2%)	0	100	100
38	i	95/128 (74%)	94 (99%)	1 (1%)	0	100	100
39	J	160/192 (83%)	149 (93%)	7 (4%)	4 (2%)	5	25
40	j	88/123 (72%)	87 (99%)	1 (1%)	0	100	100
41	K	175/178 (98%)	171 (98%)	4 (2%)	0	100	100
42	k	99/112 (88%)	97 (98%)	2 (2%)	0	100	100
43	L	113/145 (78%)	110 (97%)	3 (3%)	0	100	100

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	l	70/138 (51%)	67 (96%)	3 (4%)	0	100	100
45	M	289/296 (98%)	288 (100%)	1 (0%)	0	100	100
46	m	49/128 (38%)	48 (98%)	1 (2%)	0	100	100
47	N	138/251 (55%)	132 (96%)	4 (3%)	2 (1%)	11	40
48	o	78/102 (76%)	78 (100%)	0	0	100	100
49	O	152/175 (87%)	148 (97%)	4 (3%)	0	100	100
50	p	141/206 (68%)	136 (96%)	5 (4%)	0	100	100
51	P	142/180 (79%)	141 (99%)	1 (1%)	0	100	100
52	q	139/222 (63%)	139 (100%)	0	0	100	100
53	Q	219/292 (75%)	217 (99%)	2 (1%)	0	100	100
54	r	160/196 (82%)	159 (99%)	1 (1%)	0	100	100
55	R	138/149 (93%)	137 (99%)	1 (1%)	0	100	100
56	s	382/439 (87%)	374 (98%)	8 (2%)	0	100	100
57	S	159/205 (78%)	158 (99%)	1 (1%)	0	100	100
58	t	321/387 (83%)	307 (96%)	14 (4%)	0	100	100
All	All	9608/12512 (77%)	9398 (98%)	204 (2%)	6 (0%)	54	84

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
39	J	22	PRO
39	J	63	PRO
47	N	114	PRO
39	J	20	PRO
39	J	27	VAL

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	99/164 (60%)	98 (99%)	1 (1%)	76	91

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	T	146/176 (83%)	145 (99%)	1 (1%)	84	93
3	u	118/200 (59%)	115 (98%)	3 (2%)	47	77
4	1	52/60 (87%)	52 (100%)	0	100	100
5	U	134/135 (99%)	134 (100%)	0	100	100
6	v	59/60 (98%)	53 (90%)	6 (10%)	7	26
7	2	40/72 (56%)	40 (100%)	0	100	100
8	V	183/191 (96%)	179 (98%)	4 (2%)	52	79
9	w	73/136 (54%)	73 (100%)	0	100	100
10	3	88/166 (53%)	88 (100%)	0	100	100
11	W	86/119 (72%)	86 (100%)	0	100	100
12	x	293/328 (89%)	289 (99%)	4 (1%)	67	86
13	5	353/368 (96%)	351 (99%)	2 (1%)	86	94
14	X	220/229 (96%)	218 (99%)	2 (1%)	78	91
15	y	226/350 (65%)	223 (99%)	3 (1%)	69	88
16	6	313/332 (94%)	311 (99%)	2 (1%)	86	94
17	Y	163/223 (73%)	163 (100%)	0	100	100
18	z	270/287 (94%)	263 (97%)	7 (3%)	46	76
19	7	270/303 (89%)	269 (100%)	1 (0%)	91	96
20	Z	113/147 (77%)	113 (100%)	0	100	100
21	8	93/190 (49%)	92 (99%)	1 (1%)	73	90
22	a	96/133 (72%)	96 (100%)	0	100	100
23	9	104/112 (93%)	104 (100%)	0	100	100
24	b	130/185 (70%)	129 (99%)	1 (1%)	81	92
26	c	251/288 (87%)	251 (100%)	0	100	100
28	d	233/274 (85%)	233 (100%)	0	100	100
29	D	194/245 (79%)	194 (100%)	0	100	100
30	e	198/236 (84%)	193 (98%)	5 (2%)	47	77
31	E	260/290 (90%)	259 (100%)	1 (0%)	91	96
32	f	133/188 (71%)	133 (100%)	0	100	100
33	F	219/262 (84%)	216 (99%)	3 (1%)	67	86
34	g	124/148 (84%)	124 (100%)	0	100	100

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	H	88/228 (39%)	87 (99%)	1 (1%)	73	90
36	h	104/148 (70%)	104 (100%)	0	100	100
37	I	27/232 (12%)	27 (100%)	0	100	100
38	i	86/110 (78%)	86 (100%)	0	100	100
40	j	72/97 (74%)	71 (99%)	1 (1%)	67	86
41	K	154/155 (99%)	153 (99%)	1 (1%)	86	94
43	L	98/124 (79%)	98 (100%)	0	100	100
45	M	246/249 (99%)	244 (99%)	2 (1%)	81	92
46	m	46/113 (41%)	46 (100%)	0	100	100
47	N	25/211 (12%)	24 (96%)	1 (4%)	31	66
48	o	69/87 (79%)	69 (100%)	0	100	100
49	O	134/150 (89%)	134 (100%)	0	100	100
50	p	135/181 (75%)	134 (99%)	1 (1%)	84	93
51	P	126/155 (81%)	126 (100%)	0	100	100
52	q	119/178 (67%)	119 (100%)	0	100	100
53	Q	203/256 (79%)	202 (100%)	1 (0%)	88	95
54	r	126/169 (75%)	125 (99%)	1 (1%)	81	92
55	R	118/126 (94%)	118 (100%)	0	100	100
56	s	340/381 (89%)	340 (100%)	0	100	100
57	S	146/180 (81%)	145 (99%)	1 (1%)	84	93
58	t	106/331 (32%)	103 (97%)	3 (3%)	43	75
All	All	7902/10458 (76%)	7842 (99%)	60 (1%)	82	92

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	z	73	LEU
54	r	70	CYS
19	7	114	ASP
53	Q	246	ASP
58	t	94	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
13	5	384	GLN
18	z	43	GLN
51	P	142	ASN
50	p	184	ASN
12	x	371	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	A	1409/1589 (88%)	295 (20%)	11 (0%)
27	B	71/72 (98%)	12 (16%)	0
All	All	1480/1661 (89%)	307 (20%)	11 (0%)

5 of 307 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
25	A	1672	C
25	A	1676	A
25	A	1678	C
25	A	1681	G
25	A	1689	C

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	A	2994	A
25	A	2995	U
25	A	3073	U
25	A	3071	G
25	A	2530	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
42	AYA	k	2	42	6,7,8	1.24	1 (16%)	5,8,10	1.22	1 (20%)
5	AYA	U	2	5	6,7,8	1.33	1 (16%)	5,8,10	1.14	1 (20%)
41	SAC	K	2	41	7,8,9	1.00	0	8,9,11	0.88	0
24	THC	b	2	24	8,9,10	1.06	1 (12%)	9,11,13	0.63	0

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
42	AYA	k	2	42	-	0/4/6/8	-
5	AYA	U	2	5	-	1/4/6/8	-
41	SAC	K	2	41	-	3/7/8/10	-
24	THC	b	2	24	-	0/8/10/12	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	U	2	AYA	CA-N	-2.66	1.43	1.46
42	k	2	AYA	CA-N	-2.26	1.44	1.46
24	b	2	THC	CA-N1	-2.21	1.43	1.46

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	k	2	AYA	CB-CA-N	2.58	112.48	109.61
5	U	2	AYA	CB-CA-N	2.43	112.31	109.61

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
41	K	2	SAC	O-C-CA-CB
41	K	2	SAC	N-CA-CB-OG
41	K	2	SAC	C-CA-CB-OG
5	U	2	AYA	C-CA-N-CT

There are no ring outliers.

No monomer is involved in short contacts.



## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 111 ligands modelled in this entry, 107 are monoatomic - leaving 4 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
62	GNP	z	401	18,63	29,34,34	1.58	7 (24%)	33,54,54	2.15	6 (18%)
62	GNP	t	1000	63	29,34,34	1.63	7 (24%)	33,54,54	2.12	6 (18%)
61	SAM	x	401	-	24,29,29	1.21	3 (12%)	23,42,42	1.60	4 (17%)
60	PM8	w	200	9	25,31,31	1.92	6 (24%)	30,38,38	1.82	9 (30%)

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
62	GNP	z	401	18,63	-	6/14/38/38	0/3/3/3
62	GNP	t	1000	63	-	2/14/38/38	0/3/3/3
61	SAM	x	401	-	-	4/12/33/33	0/3/3/3
60	PM8	w	200	9	-	17/36/38/38	-

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	w	200	PM8	C34-N36	6.08	1.46	1.33
60	w	200	PM8	C39-N41	5.23	1.45	1.33
62	t	1000	GNP	PB-O3A	4.55	1.64	1.59
62	z	401	GNP	PB-O3A	4.27	1.64	1.59
61	x	401	SAM	C2-N3	4.00	1.38	1.32

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	z	401	GNP	C5-C6-N1	-8.53	111.77	123.43
62	t	1000	GNP	C5-C6-N1	-8.41	111.93	123.43
62	t	1000	GNP	C2-N1-C6	5.86	125.25	115.93
62	z	401	GNP	C2-N1-C6	5.86	125.24	115.93
60	w	200	PM8	C2-C1-S1	5.74	120.14	113.46

There are no chirality outliers.

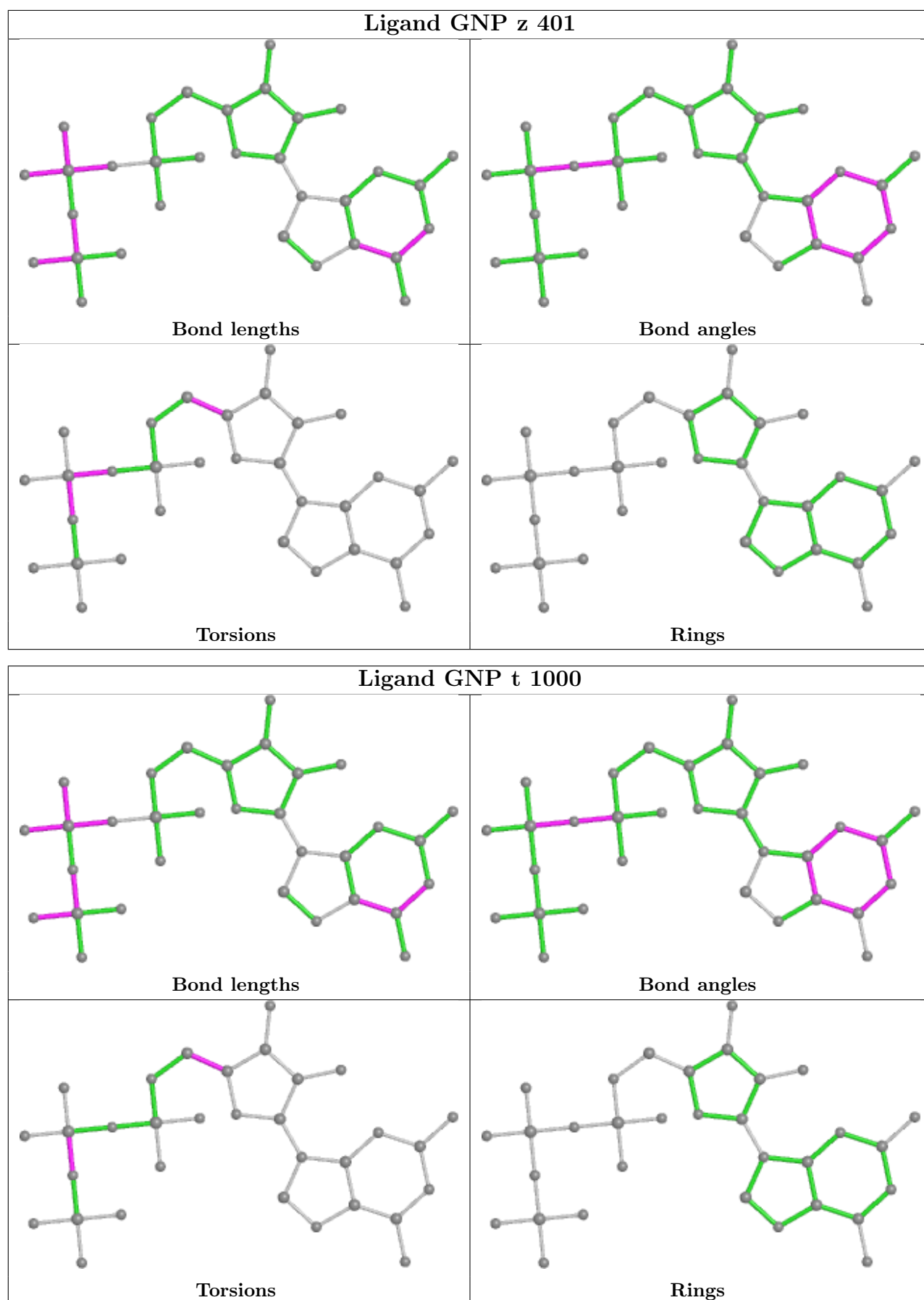
5 of 29 torsion outliers are listed below:

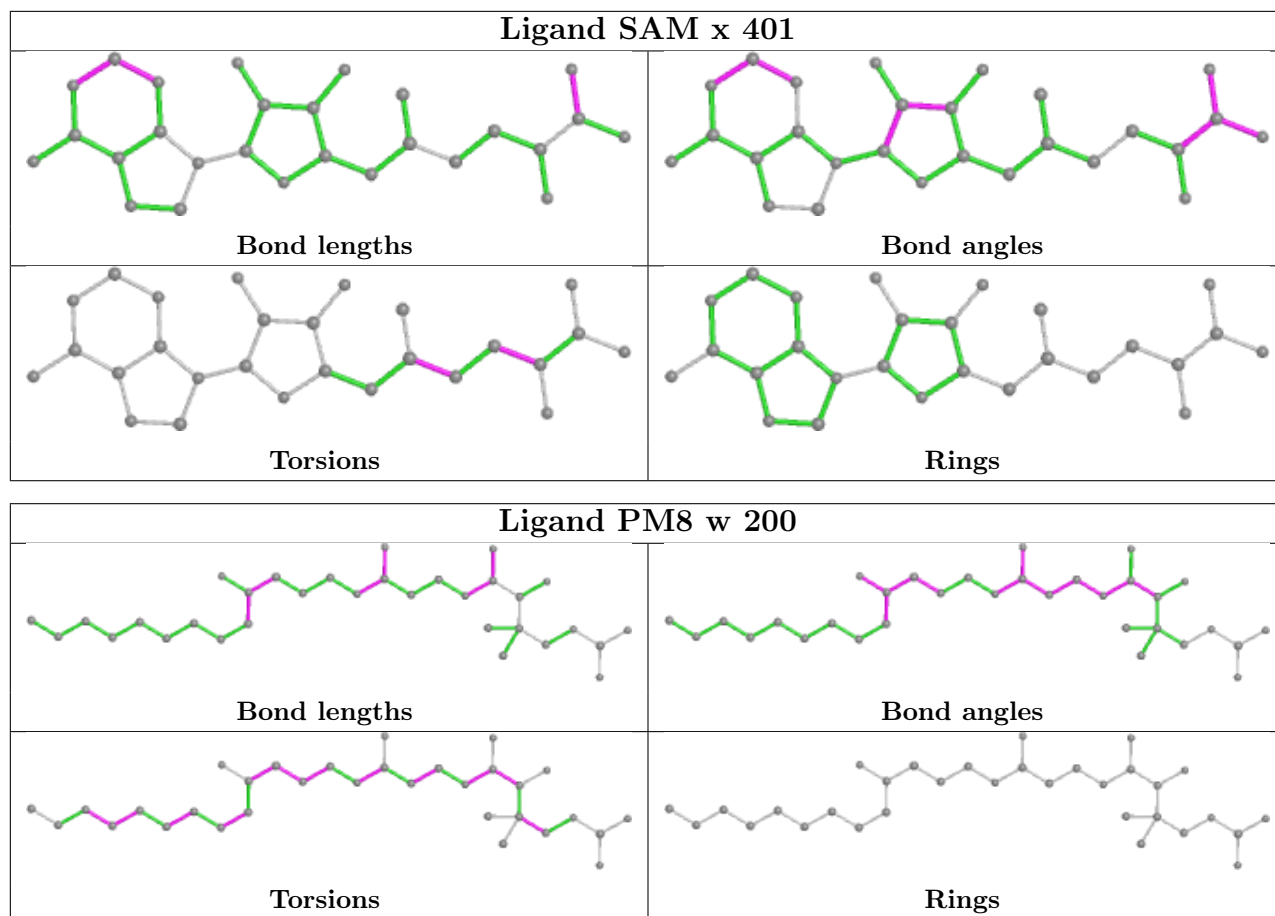
Mol	Chain	Res	Type	Atoms
60	w	200	PM8	O27-C28-C29-C32
60	w	200	PM8	C32-C34-N36-C37
60	w	200	PM8	N36-C37-C38-C39
60	w	200	PM8	N41-C42-C43-S1
60	w	200	PM8	C1-C2-C3-C4

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 [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
25	A	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2554:U	O3'	2555:A	P	17.72
1	A	2570:U	O3'	2571:A	P	17.44
1	A	2547:C	O3'	2548:U	P	12.62

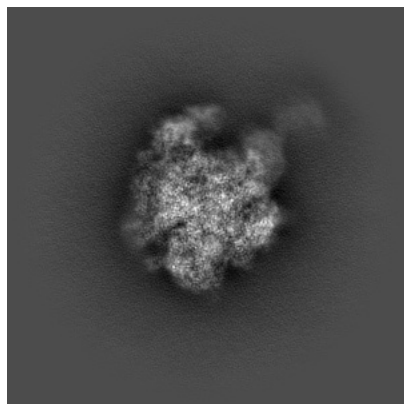
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17719. These allow visual inspection of the internal detail of the map and identification of artifacts.

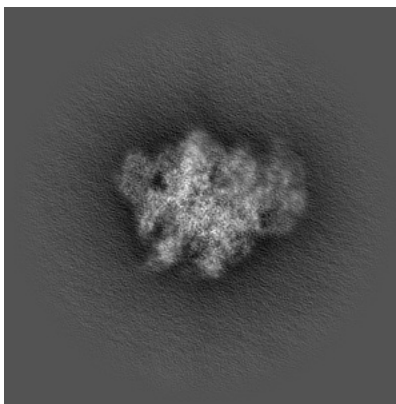
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

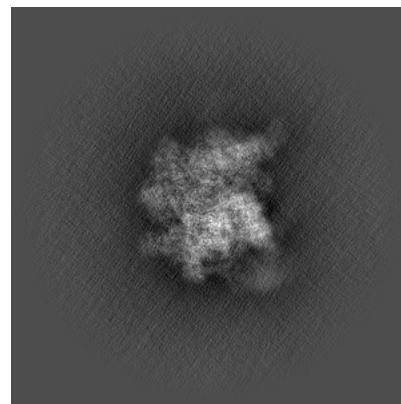
#### 6.1.1 Primary map



X

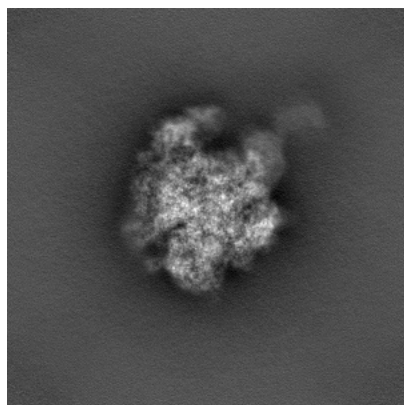


Y

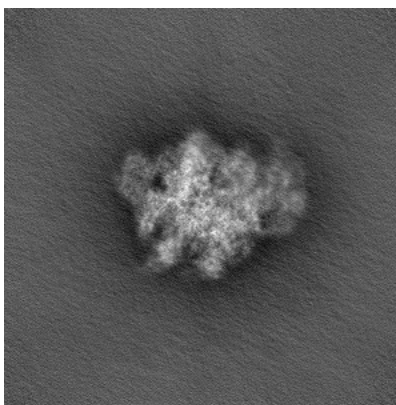


Z

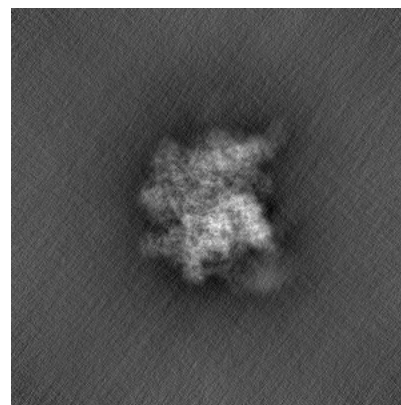
#### 6.1.2 Raw map



X



Y

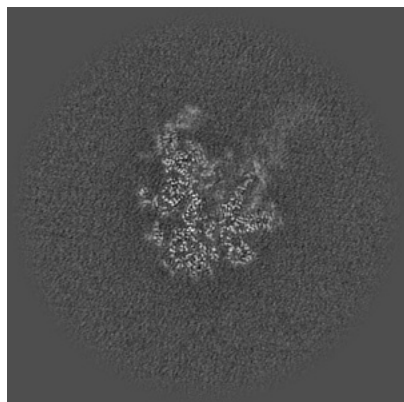


Z

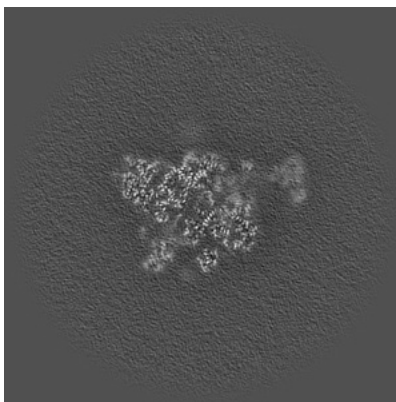
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

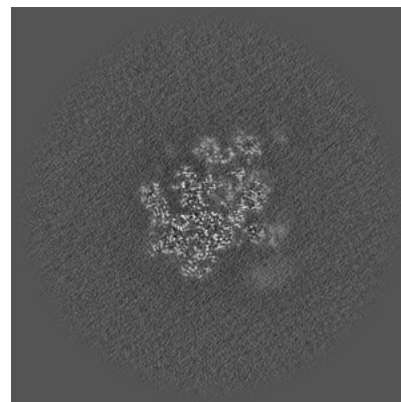
### 6.2.1 Primary map



X Index: 240

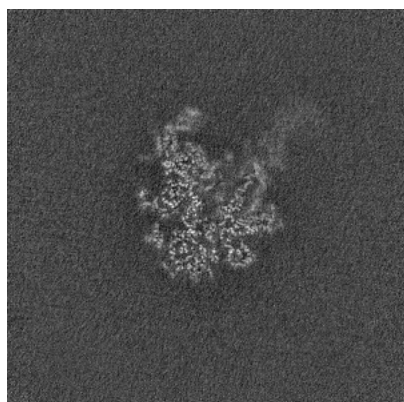


Y Index: 240

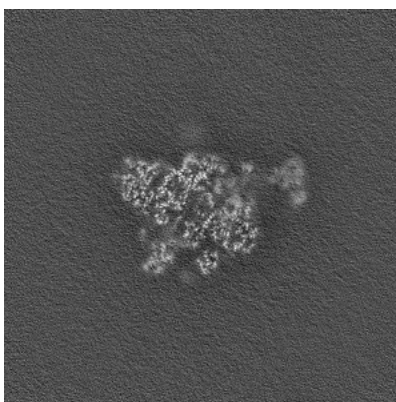


Z Index: 240

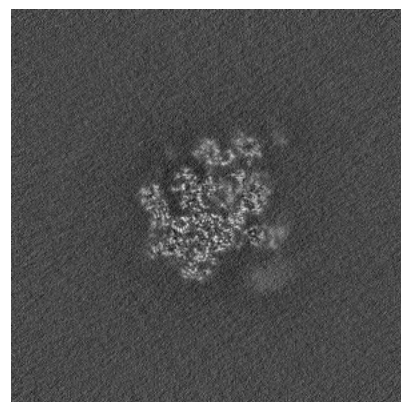
### 6.2.2 Raw map



X Index: 240



Y Index: 240

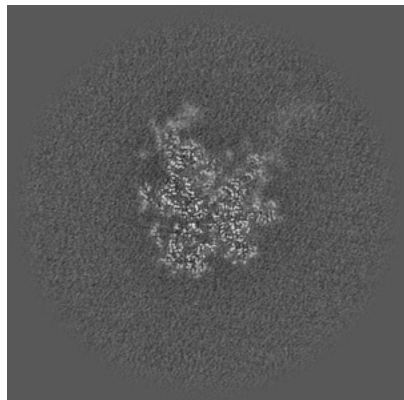


Z Index: 240

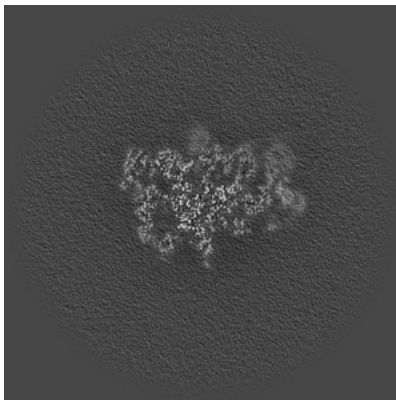
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

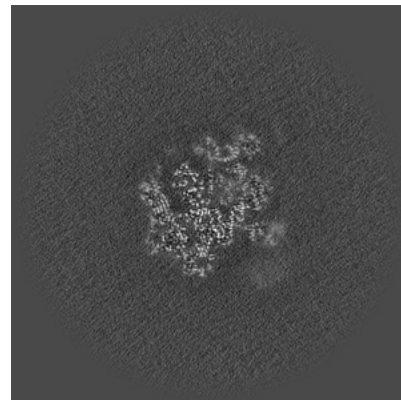
### 6.3.1 Primary map



X Index: 237

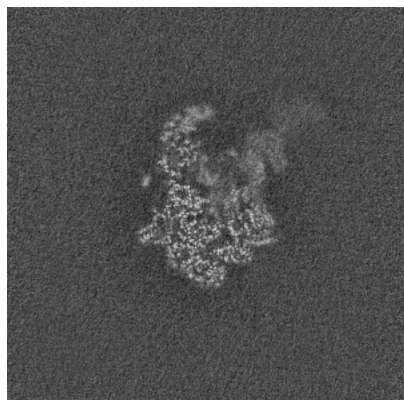


Y Index: 217

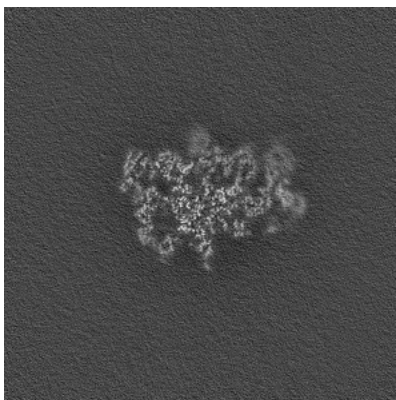


Z Index: 242

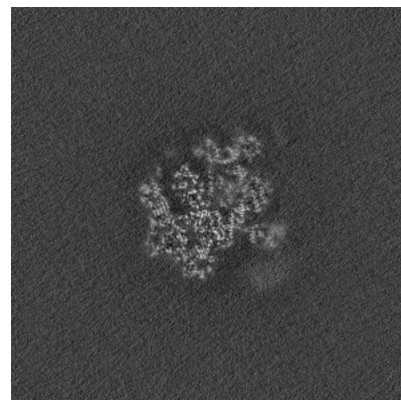
### 6.3.2 Raw map



X Index: 250



Y Index: 217

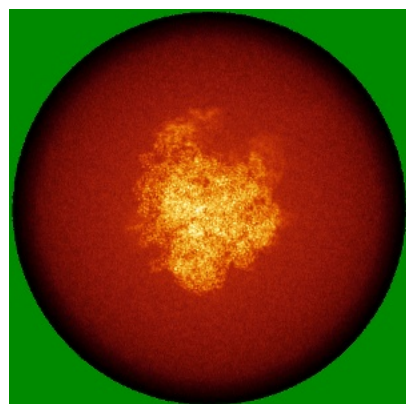


Z Index: 242

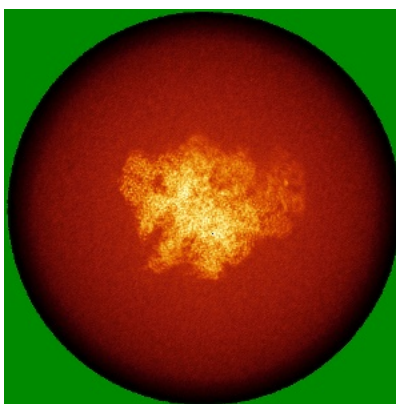
The images above show the largest variance slices of the map in three orthogonal directions.

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

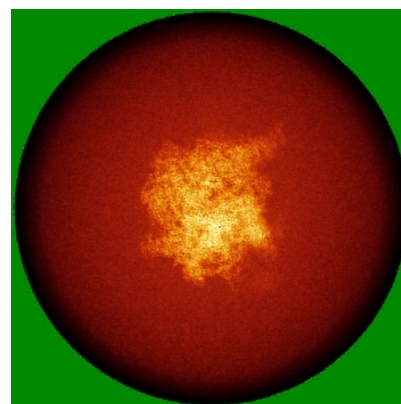
### 6.4.1 Primary map



X

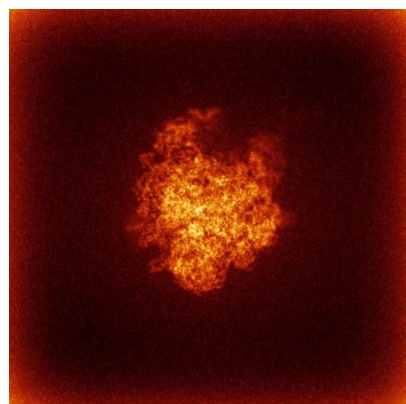


Y

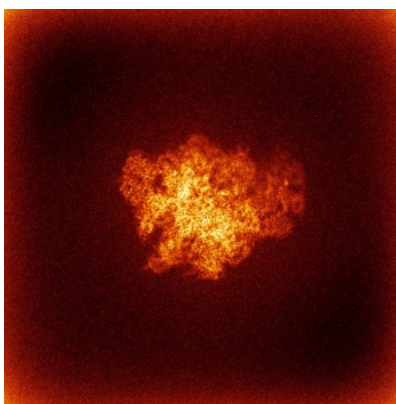


Z

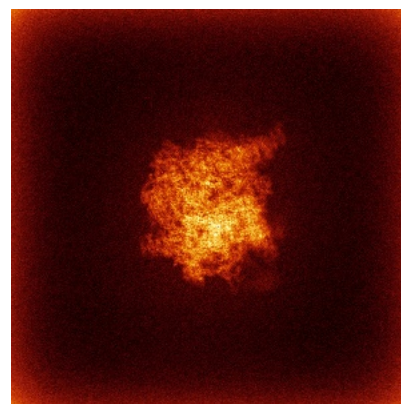
### 6.4.2 Raw map



X



Y



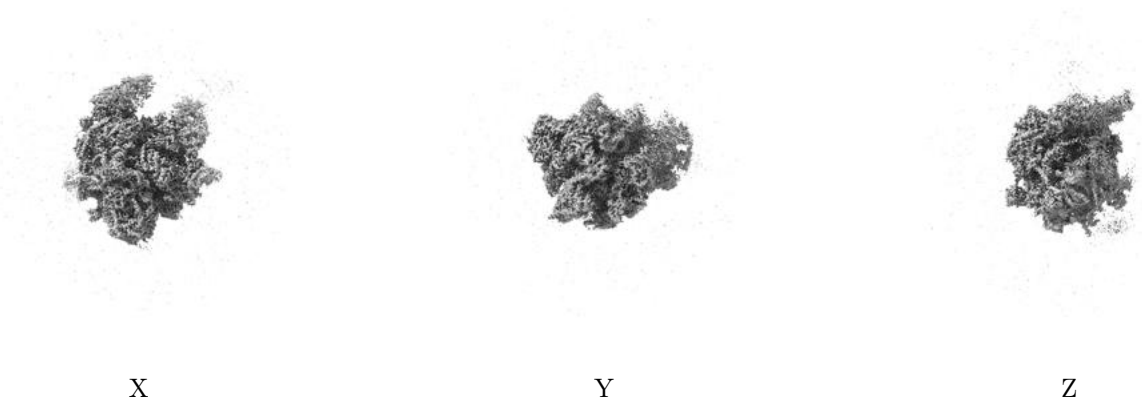
Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.



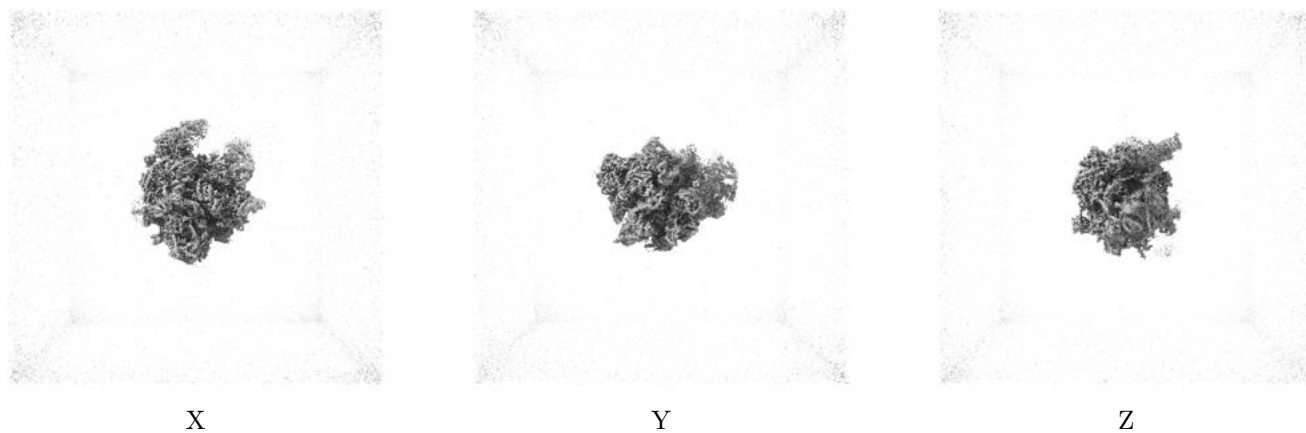
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.747. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

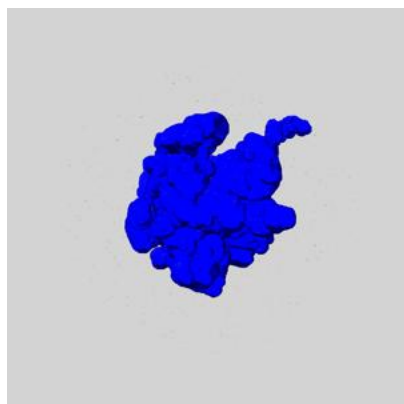
## 6.6 Mask visualisation [i](#)

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

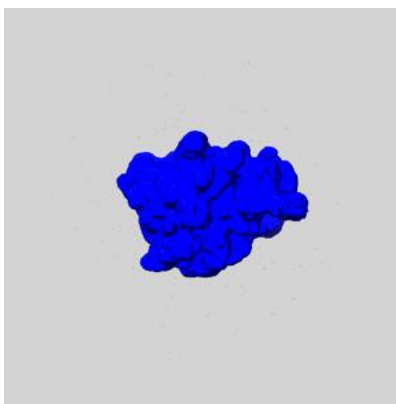
A mask typically either:

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

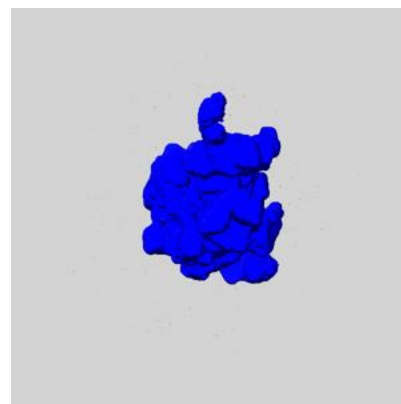
### 6.6.1 emd\_17719\_msk\_1.map [i](#)



X



Y

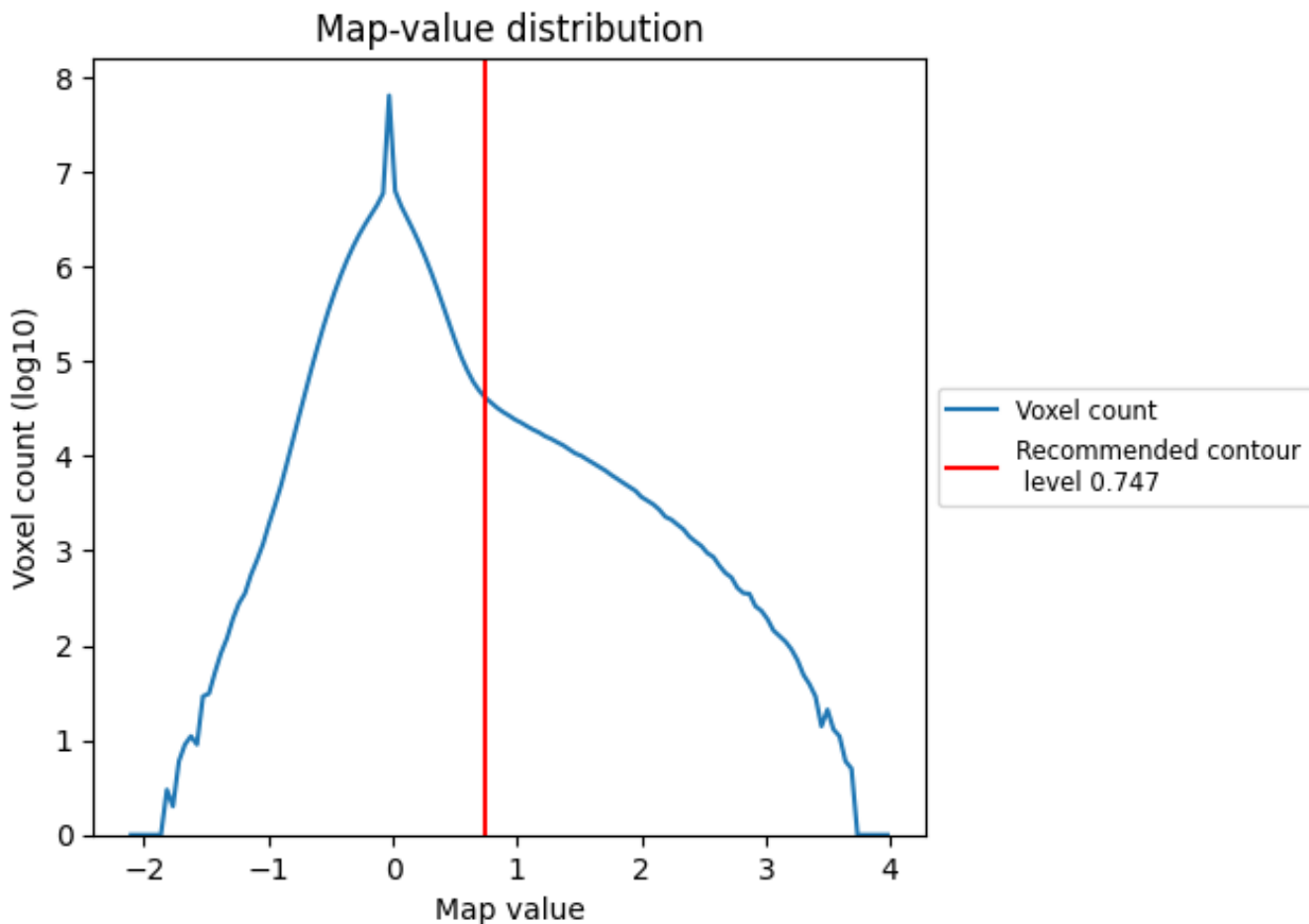


Z

## 7 Map analysis [i](#)

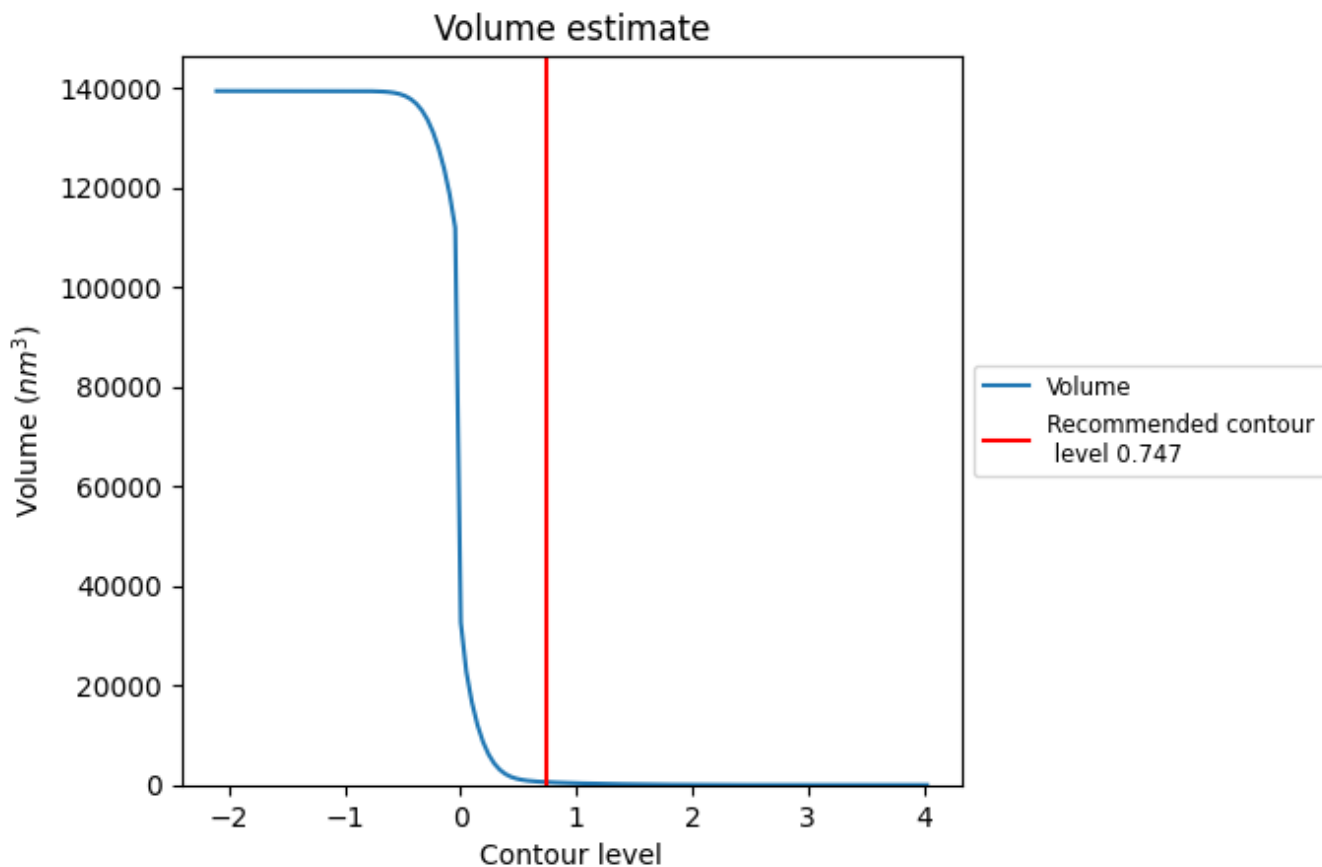
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

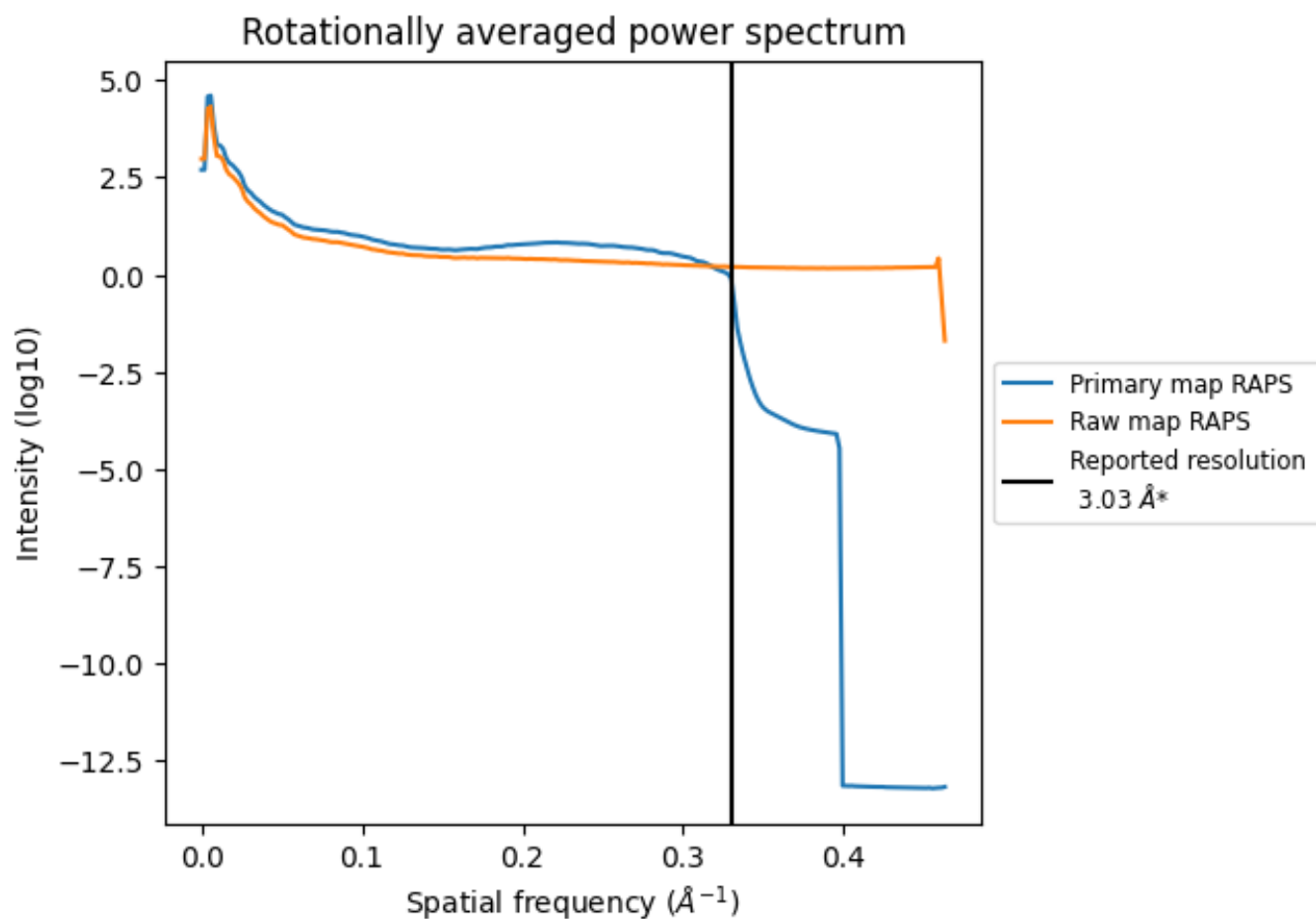
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 564 nm<sup>3</sup>; this corresponds to an approximate mass of 510 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](#)

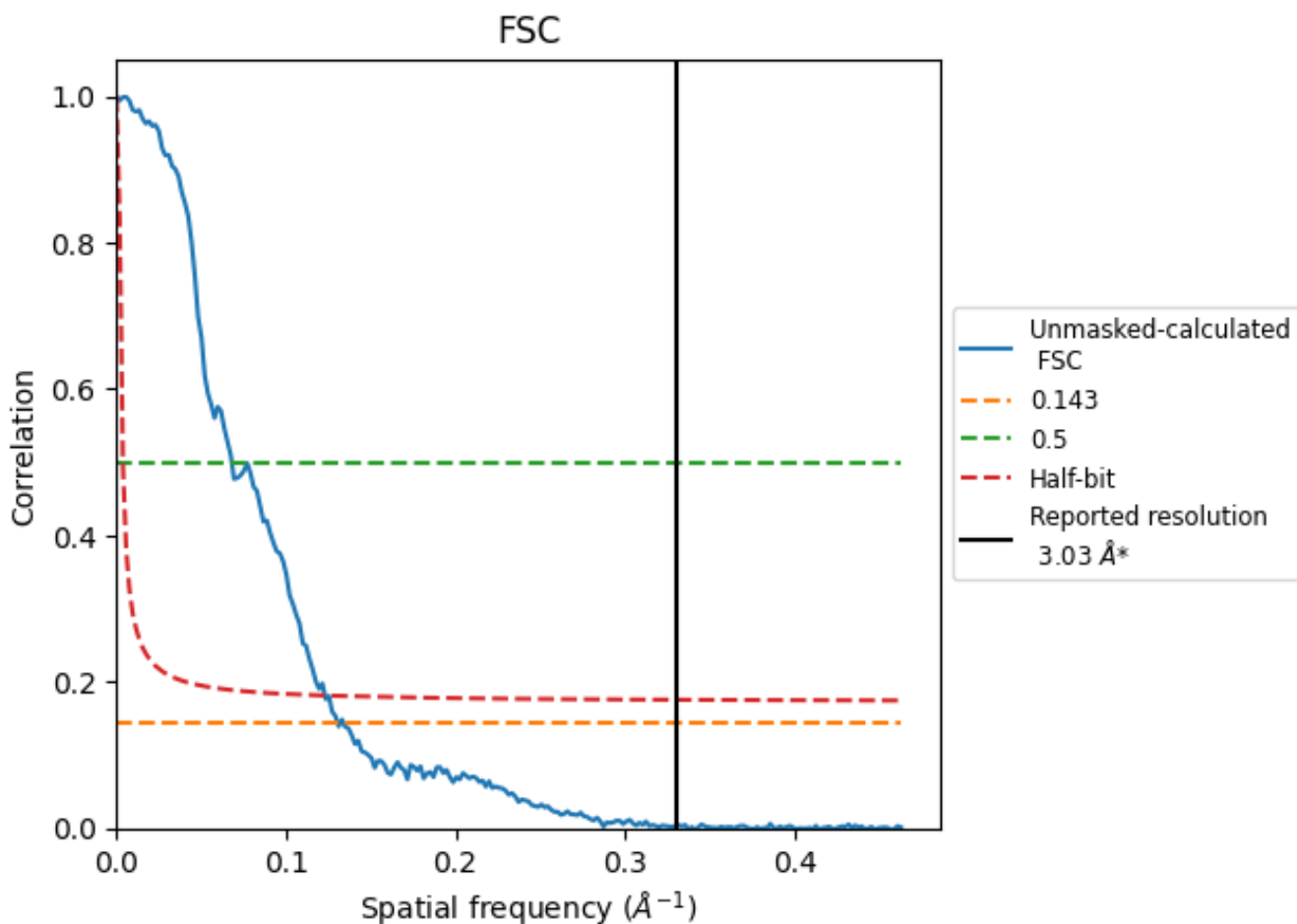


\*Reported resolution corresponds to spatial frequency of 0.330 Å<sup>-1</sup>

## 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 0.330 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

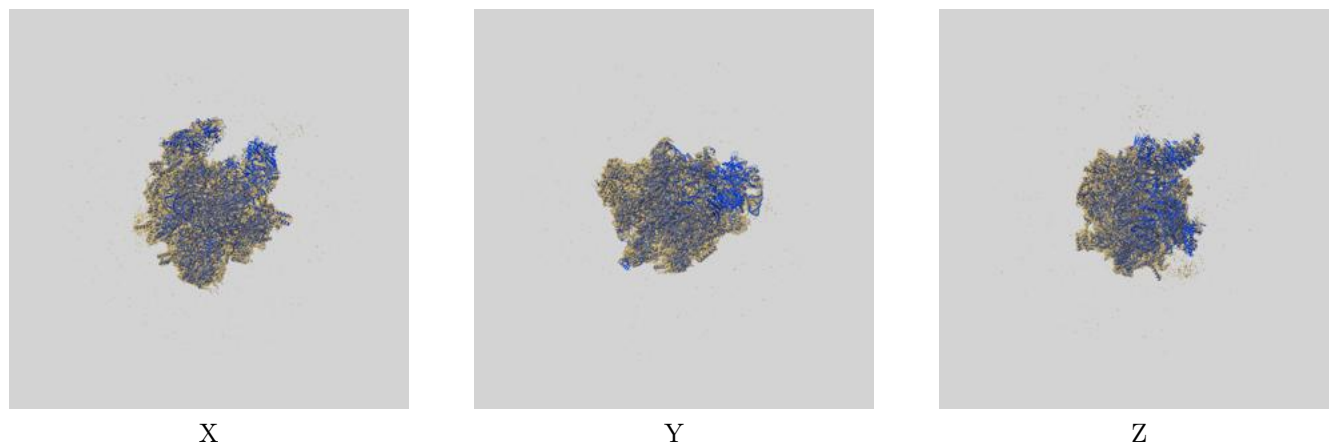
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.03	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.66	14.68	8.13

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.66 differs from the reported value 3.03 by more than 10 %

## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-17719 and PDB model 8PK0. Per-residue inclusion information can be found in section 3 on page 16.

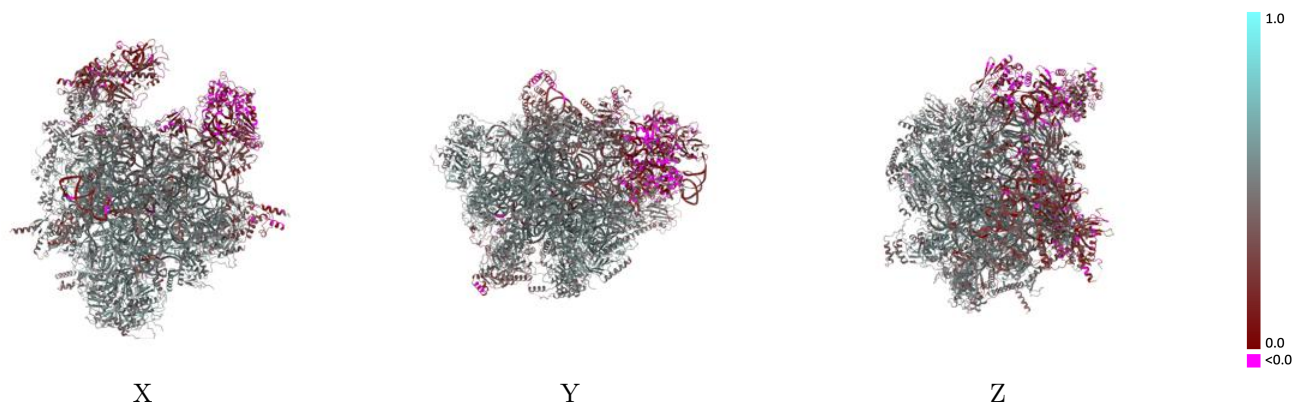
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.747 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](#)

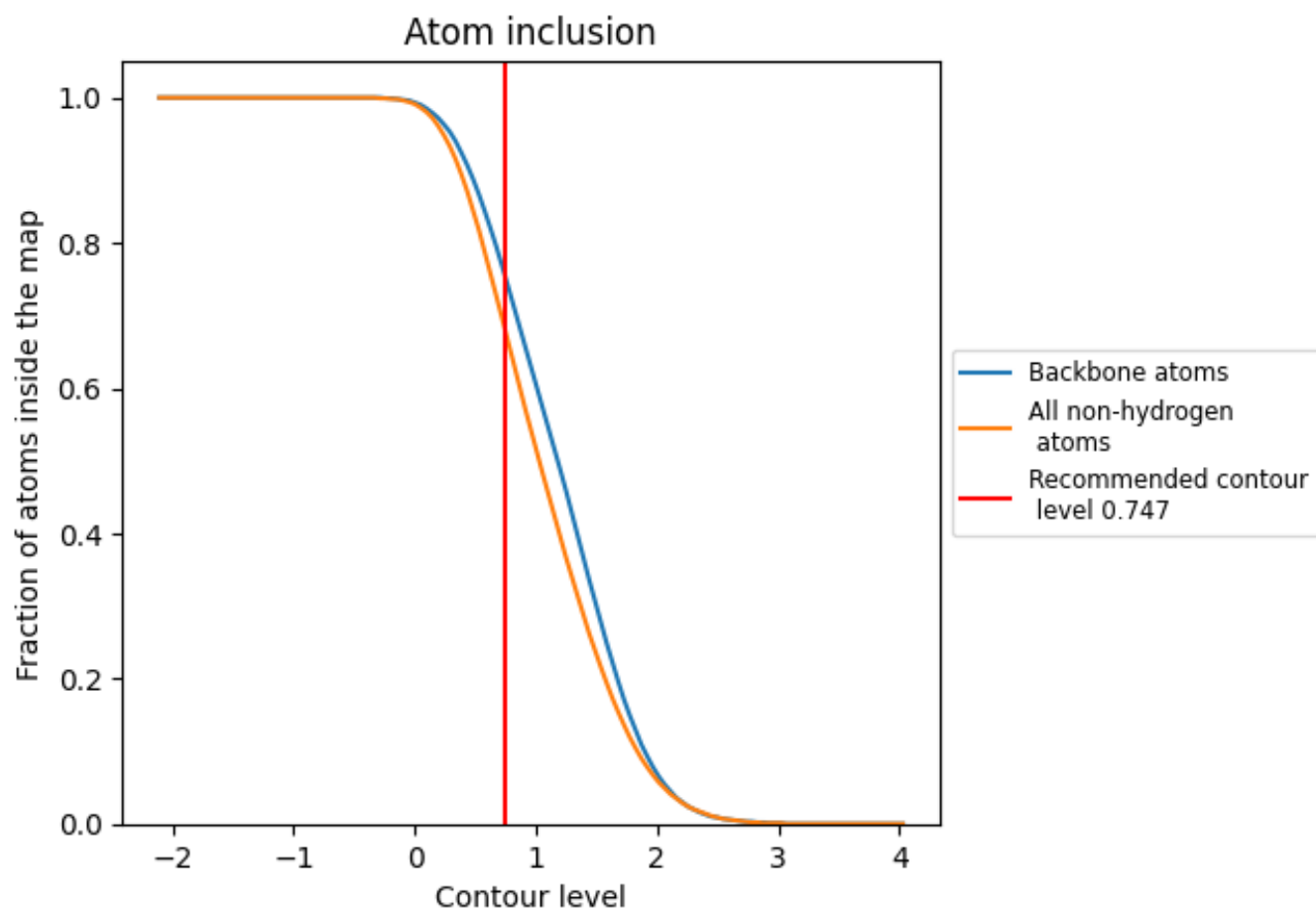


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 68% 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 (0.747) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6800	 0.4550
0	 0.7520	 0.5190
1	 0.6810	 0.4910
2	 0.8310	 0.5780
3	 0.8300	 0.5760
5	 0.7690	 0.5100
6	 0.6210	 0.4180
7	 0.6830	 0.4410
8	 0.2150	 0.2230
9	 0.7520	 0.4980
A	 0.7870	 0.4750
B	 0.5510	 0.2720
D	 0.7420	 0.5150
E	 0.7180	 0.5090
F	 0.8000	 0.5360
H	 0.6490	 0.4750
I	 0.1430	 0.1430
J	 0.0260	 0.0530
K	 0.7580	 0.5220
L	 0.6800	 0.5140
M	 0.7890	 0.5310
N	 0.2550	 0.2650
O	 0.7900	 0.5300
P	 0.6860	 0.4740
Q	 0.7310	 0.4990
R	 0.7900	 0.5420
S	 0.7460	 0.5270
T	 0.7920	 0.5460
U	 0.7050	 0.4860
V	 0.6440	 0.4490
W	 0.7180	 0.5200
X	 0.7470	 0.5140
Y	 0.7580	 0.5170
Z	 0.7330	 0.5180
a	 0.6920	 0.4900



*Continued on next page...*

*Continued from previous page...*

Chain	Atom inclusion	Q-score
b	 0.8000	 0.5300
c	 0.7260	 0.4860
d	 0.5370	 0.3870
e	 0.1180	 0.1790
f	 0.2380	 0.2840
g	 0.7950	 0.5290
h	 0.6800	 0.4390
i	 0.8130	 0.5580
j	 0.7450	 0.4930
k	 0.0380	 0.1050
l	 0.0960	 0.1110
m	 0.0750	 0.1910
o	 0.7440	 0.5120
p	 0.5680	 0.4360
q	 0.6560	 0.4470
r	 0.6340	 0.4350
s	 0.7750	 0.5270
t	 0.4460	 0.3430
u	 0.5710	 0.4150
v	 0.4910	 0.3380
w	 0.2540	 0.2030
x	 0.5790	 0.4350
y	 0.5700	 0.4320
z	 0.6520	 0.4700