



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 08:36 am BST

PDB ID : 7A5G
EMDB ID : EMD-11642
Title : Structure of the elongating human mitoribosome bound to mtEF-Tu.GMPPCP and A/T mt-tRNA
Authors : Desai, N.; Yang, H.; Chandrasekaran, V.; Kazi, R.; Minczuk, M.; Ramakrishnan, V.
Deposited on : 2020-08-21
Resolution : 4.33 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:

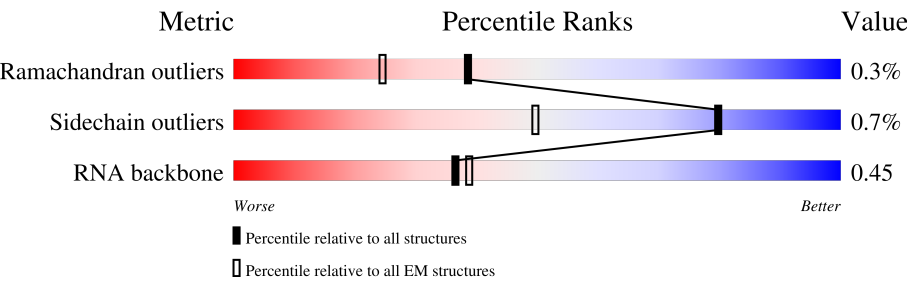
EMDB validation analysis : 0.0.1.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : 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

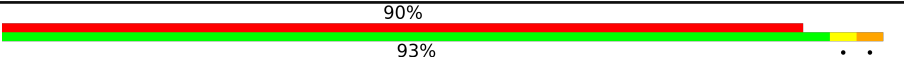




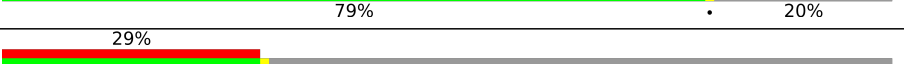

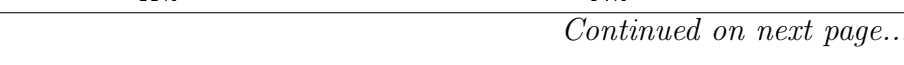
The reported resolution of this entry is 4.33 Å.

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	Y2	29	
2	A3	1559	
3	B3	69	
4	D3	305	
5	E3	348	
6	F3	311	
7	D	267	
7	H3	267	

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Mol	Chain	Length	Quality of chain
8	I3	261	
9	J3	192	
10	K3	178	
11	L3	145	
12	M3	296	
13	N3	251	
14	O3	175	
15	P3	180	
16	Q3	292	
17	R3	149	
18	S3	205	
19	T3	206	
20	U3	153	
21	V3	216	
22	W3	148	
23	X3	256	
24	Y3	250	
25	Z3	161	
26	O3	188	
27	13	65	
28	23	92	
29	33	188	
30	43	103	
31	53	423	
32	63	380	

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Mol	Chain	Length	Quality of chain
33	73	338	
34	93	137	
35	a3	142	
36	b3	215	
37	c3	332	
38	d3	306	
39	e3	279	
40	f3	212	
41	g3	166	
42	h3	158	
43	i3	128	
44	j3	123	
45	k3	112	
46	l3	138	
47	m3	128	
48	o3	102	
49	p3	206	
50	q3	222	
51	r3	196	
52	s3	467	
52	t3	467	
53	u3	2	
54	A5	28	
55	B6	296	
56	C6	167	

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Mol	Chain	Length	Quality of chain
57	D6	430	
58	E6	125	
59	F6	242	
60	G6	396	
61	H6	201	
62	I6	194	
63	J6	138	
64	K6	128	
65	L6	257	
66	M6	137	
67	N6	130	
68	O6	258	
69	P6	142	
70	Q6	87	
71	R6	360	
72	S6	190	
73	T6	173	
74	U6	205	
75	V6	414	
76	W6	187	
77	X6	398	
78	Y6	395	
79	Z6	106	
80	a6	218	
81	b6	323	

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Mol	Chain	Length	Quality of chain
82	c6	118	
83	d6	199	
84	e6	689	
85	A6	954	
86	24	73	
86	C	73	
87	i4	10	
88	A	206	
89	Z	452	
90	j	76	
91	n	229	

2 Entry composition

There are 101 unique types of molecules in this entry. The entry contains 170507 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 nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	Y2	29	Total	C	N	O	0	0
			145	87	29	29		

- Molecule 2 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A3	1503	Total	C	N	O	P	0	0
			31913	14319	5761	10330	1503		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A3	3107	U	UNK	conflict	GB 1025814679

- Molecule 3 is a RNA chain called mt-tRNAVal.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B3	56	Total	C	N	O	P	0	0
			1191	534	214	387	56		

- Molecule 4 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D3	236	Total	C	N	O	S	0	0
			1842	1145	373	315	9		

- Molecule 5 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E3	300	Total	C	N	O	S	0	0
			2365	1523	410	422	10		

- Molecule 6 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F3	250	Total	C	N	O	S	0	0
			2013	1294	365	348	6		

- Molecule 7 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H3	95	Total	C	N	O		0	0
			784	498	152	134			
7	D	80	Total	C	N	O	S	0	0
			648	421	111	112	4		

- Molecule 8 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I3	158	Total	C	N	O	S	0	0
			1283	828	235	210	10		

- Molecule 9 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J3	140	Total	C	N	O	S	0	0
			1061	680	192	187	2		

- Molecule 10 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K3	177	Total	C	N	O	S	0	0
			1451	934	259	251	7		

- Molecule 11 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L3	115	Total	C	N	O	S	0	0
			889	559	171	154	5		

- Molecule 12 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M3	287	Total	C	N	O	S	0	0
			2305	1472	425	402	6		

- Molecule 13 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N3	205	Total	C	N	O	S	0	0
			1654	1056	308	280	10		

- Molecule 14 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O3	152	Total	C	N	O	S	0	0
			1245	784	239	215	7		

- Molecule 15 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P3	133	Total	C	N	O	S	0	0
			1080	677	209	189	5		

- Molecule 16 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q3	219	Total	C	N	O	S	0	0
			1822	1168	322	323	9		

- Molecule 17 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R3	140	Total	C	N	O	S	0	0
			1153	732	231	186	4		

- Molecule 18 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S3	156	Total	C	N	O	S	0	0
			1251	806	222	219	4		

- Molecule 19 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T3	166	Total	C	N	O	S	0	0
			1368	875	254	232	7		

- Molecule 20 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U3	111	Total	C	N	O	S	0	0
			922	591	176	153	2		

- Molecule 21 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V3	189	Total	C	N	O	S	0	0
			1551	987	278	278	8		

- Molecule 22 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W3	111	Total	C	N	O	S	0	0
			871	558	164	146	3		

- Molecule 23 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X3	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
X3	148	ALA	THR	conflict	UNP Q13084
X3	149	SER	PRO	conflict	UNP Q13084
X3	150	GLY	LYS	conflict	UNP Q13084

- Molecule 24 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y3	176	Total	C	N	O	S	0	0
			1517	970	291	252	4		

- Molecule 25 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z3	120	Total	C	N	O	S	0	0
			978	626	183	166	3		

- Molecule 26 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	03	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 27 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	13	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

- Molecule 28 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	23	46	Total	C	N	O	S	0	0
			376	233	83	59	1		

- Molecule 29 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	33	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 30 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	43	36	Total	C	N	O	S	0	0
			322	203	70	46	3		

- Molecule 31 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	53	376	Total	C	N	O	S	0	0
			3064	1987	529	538	10		

- Molecule 32 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	63	325	Total	C	N	O	S	0	0
			2636	1692	465	470	9		

- Molecule 33 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	73	266	Total	C	N	O	S	0	0
			2158	1383	371	388	16		

- Molecule 34 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	93	109	Total	C	N	O	S	0	0
			873	565	152	154	2		

- Molecule 35 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a3	82	Total	C	N	O	S	0	0
			686	434	124	123	5		

- Molecule 36 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	b3	148	Total	C	N	O	S	0	0
			1178	733	229	213	3		

- Molecule 37 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	c3	275	Total	C	N	O	S	0	0
			2217	1415	383	410	9		

- Molecule 38 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	d3	162	Total	C	N	O	S	0	0
			1347	870	234	235	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e3	217	Total	C	N	O	S	0	0
			1762	1124	310	323	5		

- Molecule 40 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	f3	131	Total	C	N	O	S	0	0
			1039	663	169	203	4		

- Molecule 41 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	g3	129	Total	C	N	O	S	0	0
			1067	690	185	190	2		

- Molecule 42 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	h3	100	Total	C	N	O	S	0	0
			827	524	146	155	2		

- Molecule 43 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	i3	97	Total	C	N	O	S	0	0
			827	532	165	126	4		

- Molecule 44 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	j3	85	Total	C	N	O	S	0	0
			684	423	133	126	2		

- Molecule 45 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	k3	84	Total	C	N	O	S	0	0
			655	407	122	121	5		

- Molecule 46 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	l3	23	Total	C	N	O	0	0
			221	137	52	32		

- Molecule 47 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	m3	45	Total	C	N	O	S	0	0
			372	232	76	62	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	o3	94	Total	C	N	O	S	0	0
			797	501	165	128	3		

- Molecule 49 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	p3	127	Total	C	N	O	S	0	0
			1058	661	201	192	4		

- Molecule 50 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	q3	128	Total	C	N	O	S	0	0
			1076	671	208	192	5		

- Molecule 51 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r3	146	Total	C	N	O	S	0	0
			1203	764	232	199	8		

- Molecule 52 is a protein called 39S ribosomal protein S30, mitochondrial, 39S ribosomal protein S30, mitochondrial, mL65.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s3	370	Total	C	N	O	S	0	0
			3036	1946	542	534	14		
52	t3	28	Total	C	N	O		0	0
			140	84	28	28			

- Molecule 53 is a RNA chain called RNA (5'-R(P*CP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u3	2	Total	C	N	O	P	0	0
			42	19	8	13	2		

- Molecule 54 is a protein called Oxa1L tail.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	A5	28	Total	C	N	O	0	0
			140	84	28	28		

- Molecule 55 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	B6	217	Total	C	N	O	S	0	0
			1768	1131	321	306	10		

- Molecule 56 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	C6	132	Total	C	N	O	S	0	0
			1082	699	195	184	4		

- Molecule 57 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	D6	322	Total	C	N	O	S	0	0
			2557	1611	476	457	13		

- Molecule 58 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	E6	122	Total	C	N	O	S	0	0
			972	614	177	177	4		

- Molecule 59 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	F6	201	Total	C	N	O	S	0	0
			1668	1069	305	283	11		

- Molecule 60 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	G6	305	Total	C	N	O	S	0	0
			2516	1599	448	455	14		

- Molecule 61 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	H6	122	Total	C	N	O	S	0	0
			999	643	168	185	3		

- Molecule 62 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	I6	136	Total	C	N	O	S	0	0
			1011	637	192	178	4		

- Molecule 63 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	J6	108	Total	C	N	O	S	0	0
			838	521	169	142	6		

- Molecule 64 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	K6	101	Total	C	N	O	S	0	0
			861	537	179	140	5		

- Molecule 65 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	L6	164	Total	C	N	O	S	0	0
			1382	883	257	235	7		

- Molecule 66 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	M6	116	Total	C	N	O	S	0	0
			920	582	182	150	6		

- Molecule 67 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	N6	107	Total	C	N	O	S	0	0
			846	549	153	141	3		

- Molecule 68 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	O6	185	Total	C	N	O	S	0	0
			1528	970	285	267	6		

- Molecule 69 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	P6	96	Total	C	N	O	S	0	0
			774	498	133	135	8		

- Molecule 70 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Q6	86	Total	C	N	O	S	0	0
			740	458	150	124	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q6	50	ARG	CYS	conflict	UNP P82921

- Molecule 71 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	R6	242	Total	C	N	O	S	0	0
			2008	1285	343	372	8		

- Molecule 72 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	S6	126	Total	C	N	O	S	0	0
			1042	673	183	185	1		

- Molecule 73 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	T6	162	Total	C	N	O	S	0	0
			1330	850	231	238	11		

- Molecule 74 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	U6	173	Total	C	N	O	S	0	0
			1461	900	294	263	4		

- Molecule 75 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	V6	328	Total	C	N	O	S	0	0
			2702	1737	452	502	11		

- Molecule 76 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	W6	97	Total	C	N	O	S	0	0
			766	486	137	139	4		

- Molecule 77 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	X6	316	Total	C	N	O	S	0	0
			2531	1625	440	455	11		

- Molecule 78 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Y6	108	Total	C	N	O	S	0	0
			914	593	150	169	2		

- Molecule 79 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Z6	87	Total	C	N	O	S	0	0
			740	473	133	130	4		

- Molecule 80 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	a6	201	Total	C	N	O	S	0	0
			1684	1065	322	292	5		

- Molecule 81 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	b6	256	Total	C	N	O	S	0	0
			2076	1321	350	395	10		

- Molecule 82 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	c6	116	Total	C	N	O	S	0	0
			925	574	181	162	8		

- Molecule 83 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	d6	69	Total	C	N	O	S	0	0
			610	393	130	86	1		

- Molecule 84 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	e6	414	Total	C	N	O	S	0	0
			2838	1805	490	529	14		

- Molecule 85 is a RNA chain called 12S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	A6	928	Total	C	N	O	P	0	0
			19716	8840	3560	6388	928		

- Molecule 86 is a RNA chain called P tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	24	73	Total	C	N	O	P	0	0
			1547	696	280	499	72		
86	C	73	Total	C	N	O	P	0	0
			1547	696	280	499	72		

- Molecule 87 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	i4	10	Total	C	N	O	P	0	0
			216	97	41	68	10		

- Molecule 88 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	A	162	Total	C	N	O	S	0	0
			1375	876	247	249	3		

- Molecule 89 is a protein called Elongation factor Tu, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	Z	394	Total	C	N	O	S	0	0
			3042	1923	538	566	15		

- Molecule 90 is a RNA chain called E tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	j	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

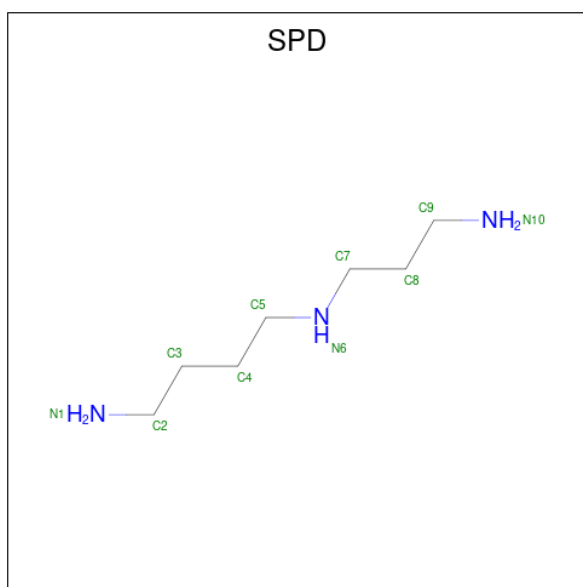
- Molecule 91 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	n	228	Total	C	N	O	S	4	0
			1767	1121	321	322	3		

- Molecule 92 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
92	A3	95	Total	Mg	0
			95	95	
92	D3	1	Total	Mg	0
			1	1	
92	M3	1	Total	Mg	0
			1	1	
92	g3	1	Total	Mg	0
			1	1	
92	o3	1	Total	Mg	0
			1	1	
92	A6	28	Total	Mg	0
			28	28	
92	n	1	Total	Mg	0
			1	1	

- Molecule 93 is SPERMIDINE (three-letter code: SPD) (formula: C₇H₁₉N₃).

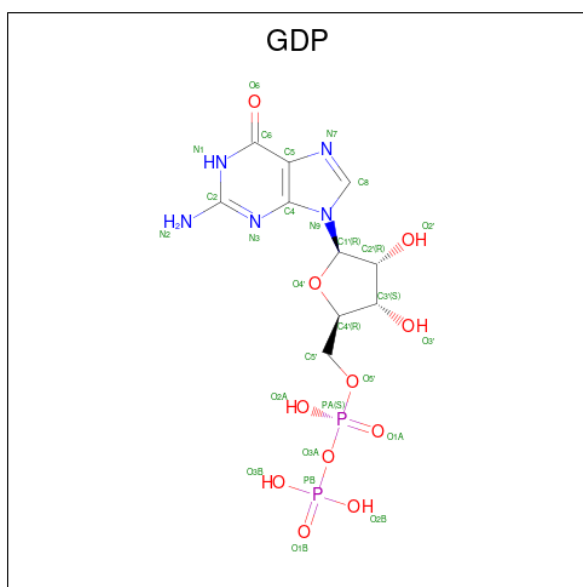


Mol	Chain	Residues	Atoms			AltConf
93	A3	1	Total	C	N	0
			10	7	3	

- Molecule 94 is ZINC ION (three-letter code: ZN) (formula: Zn).

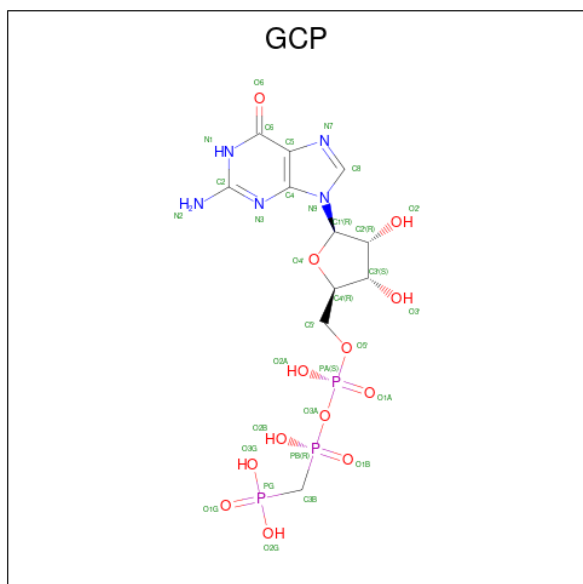
Mol	Chain	Residues	Atoms		AltConf
94	03	1	Total	Zn	0
			1	1	
94	43	1	Total	Zn	0
			1	1	
94	r3	1	Total	Zn	0
			1	1	
94	B6	1	Total	Zn	0
			1	1	
94	O6	1	Total	Zn	0
			1	1	
94	P6	1	Total	Zn	0
			1	1	
94	T6	1	Total	Zn	0
			1	1	

- Molecule 95 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					AltConf
95	X6	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 96 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).

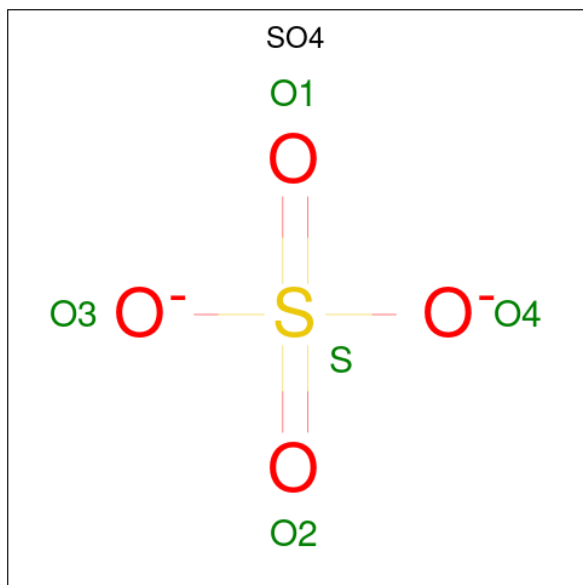


Mol	Chain	Residues	Atoms					AltConf
96	Z	1	Total	C	N	O	P	0
			32	11	5	13	3	

- Molecule 97 is SODIUM ION (three-letter code: NA) (formula: Na).

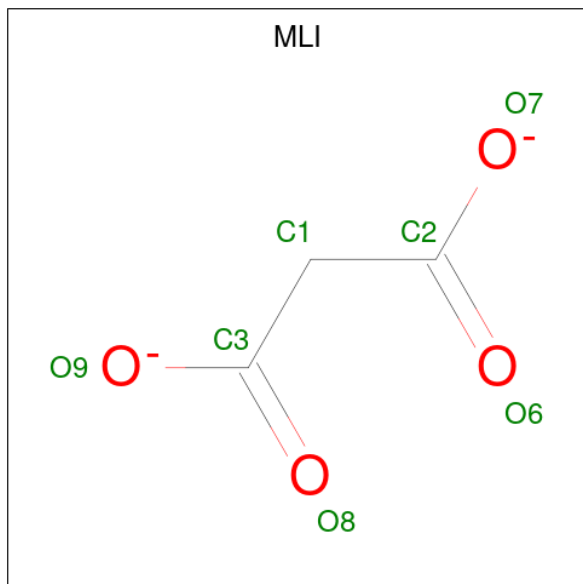
Mol	Chain	Residues	Atoms		AltConf
97	D	2	Total	Na	0
			2	2	
97	n	2	Total	Na	0
			2	2	

- Molecule 98 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			AltConf
98	n	1	Total	O	S	0
			5	4	1	

- Molecule 99 is MALONATE ION (three-letter code: MLI) (formula: C₃H₂O₄).



Mol	Chain	Residues	Atoms			AltConf
99	n	1	Total	C	O	0
			7	3	4	
99	n	1	Total	C	O	0
			7	3	4	
99	n	1	Total	C	O	0
			7	3	4	

- Molecule 100 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		AltConf
100	n	2	Total	Cl	0
			2	2	

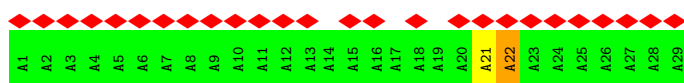
- Molecule 101 is water.

Mol	Chain	Residues	Atoms		AltConf
101	A3	3	Total	O	0
			3	3	
101	D	9	Total	O	0
			9	9	
101	n	67	Total	O	0
			67	67	

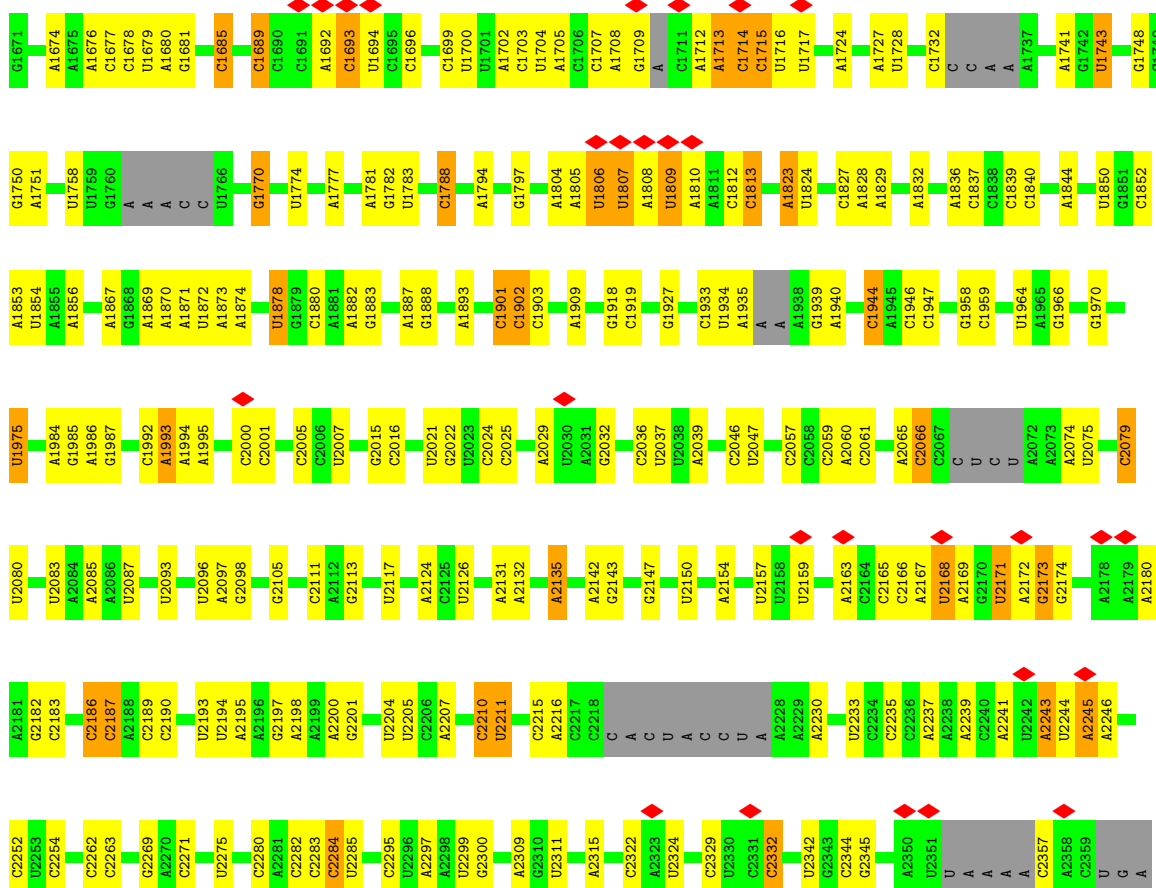
3 Residue-property plots

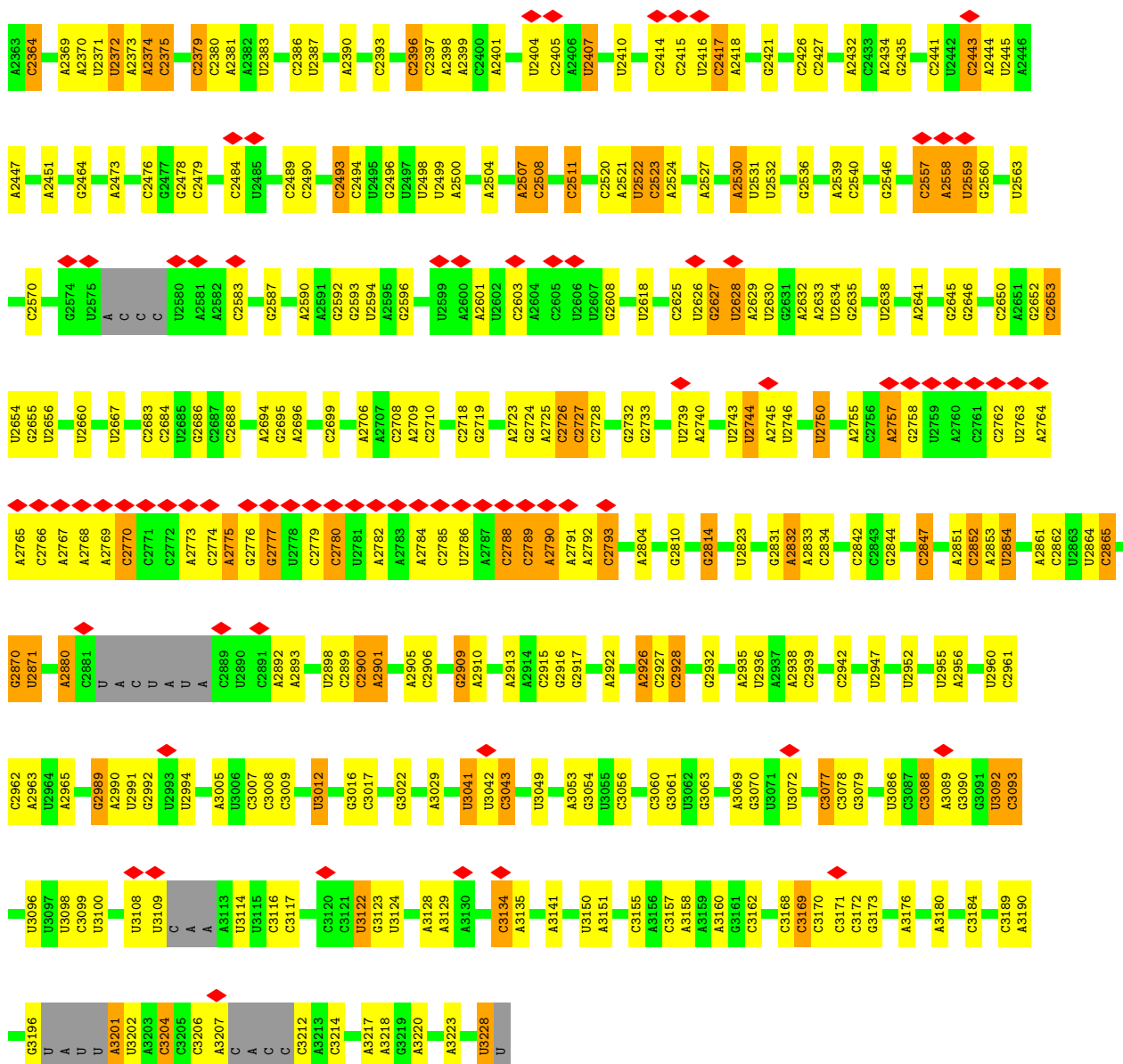
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: nascent chain

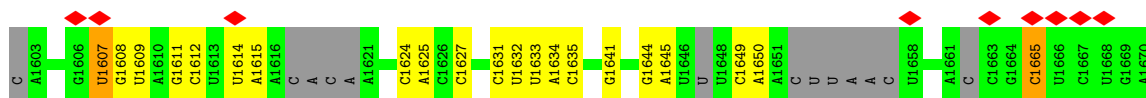


- Molecule 2: 16S rRNA

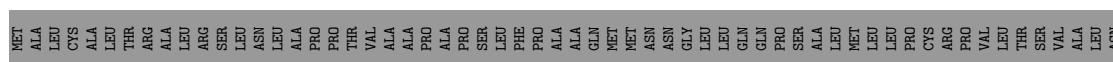
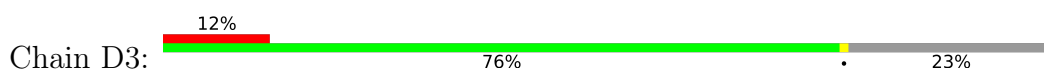


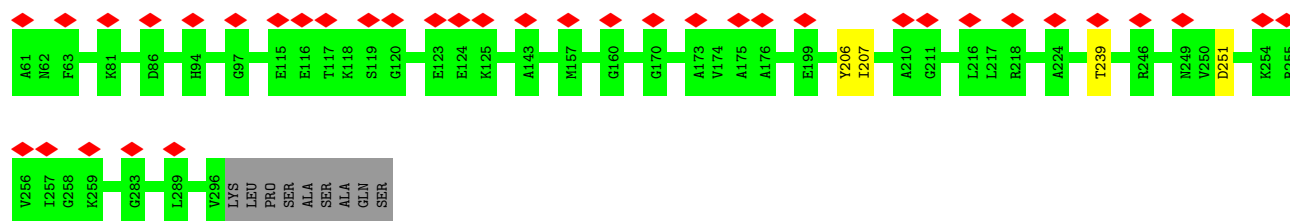


- Molecule 3: mt-tRNAVal



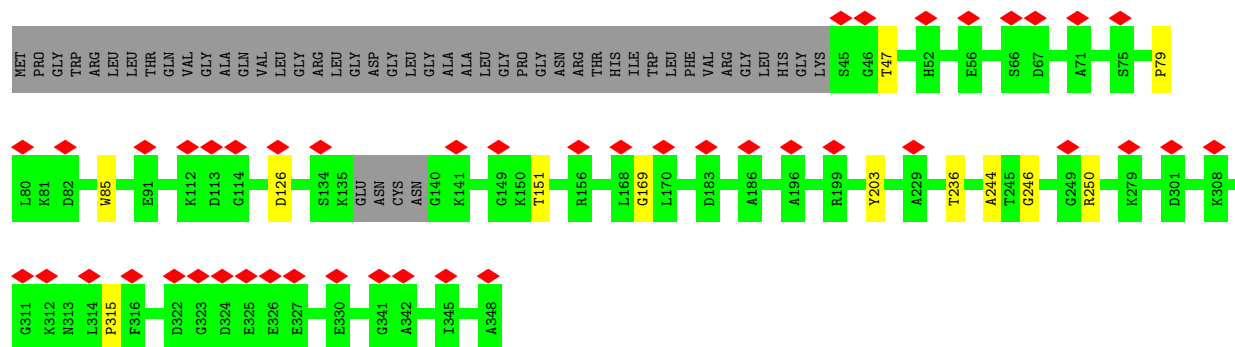
- Molecule 4: 39S ribosomal protein L2, mitochondrial





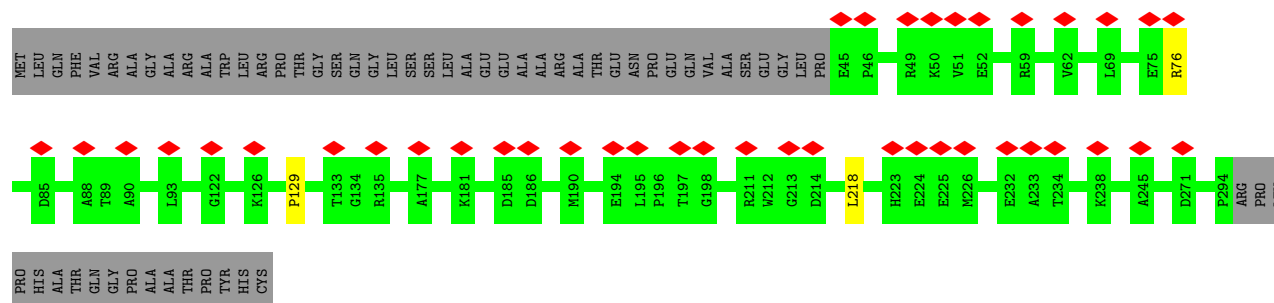
• Molecule 5: 39S ribosomal protein L3, mitochondrial

Chain E3: 13% 83% 14%



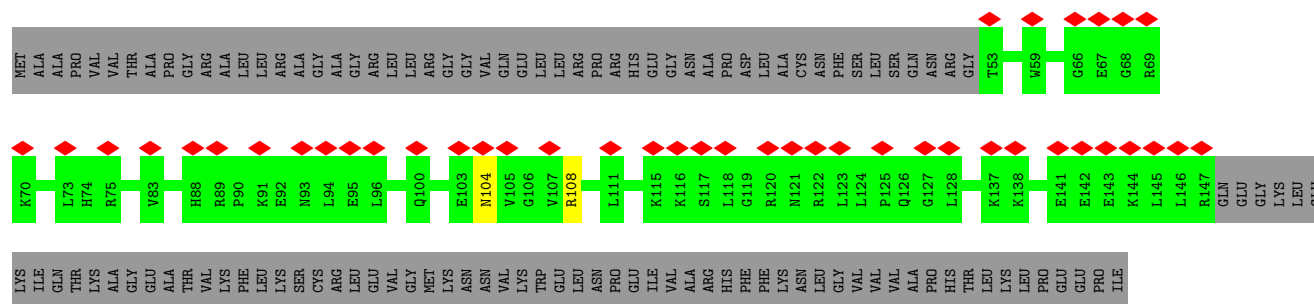
• Molecule 6: 39S ribosomal protein L4, mitochondrial

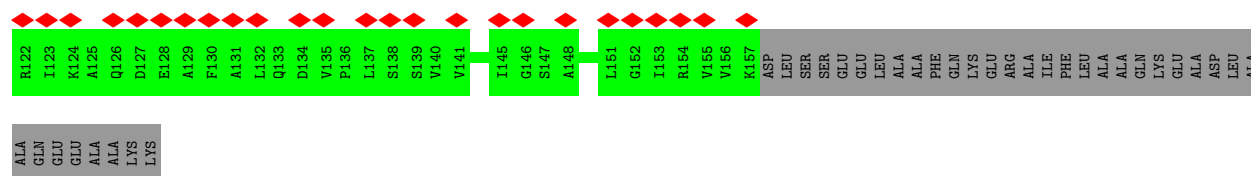
Chain F3: 13% 79% 20%



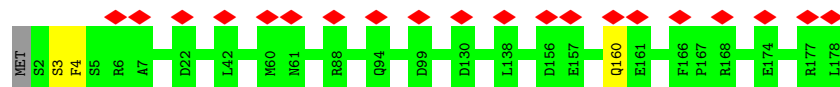
• Molecule 7: 39S ribosomal protein L9, mitochondrial

Chain H3: 16% 35% 64%

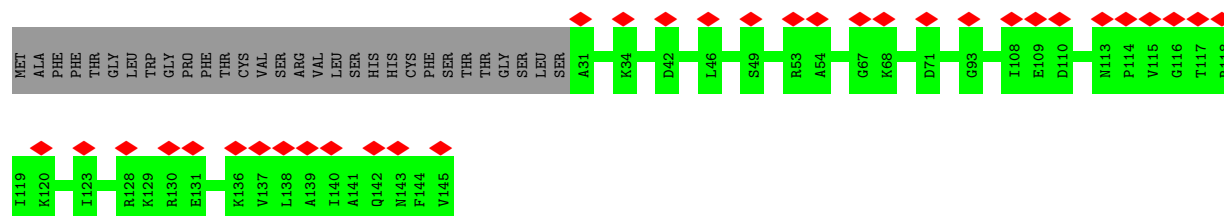
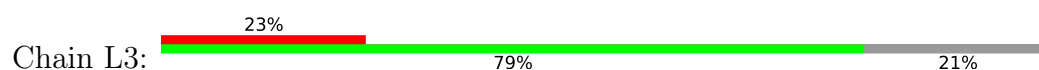




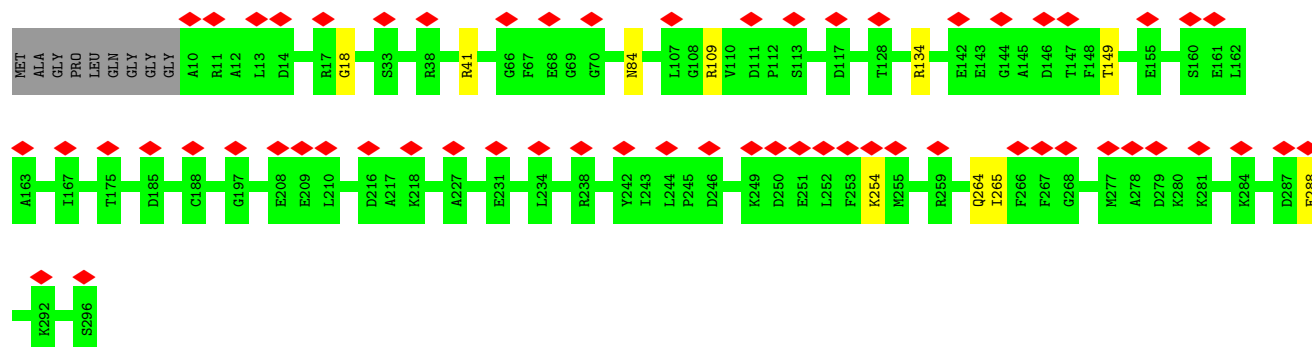
- Molecule 10: 39S ribosomal protein L13, mitochondrial



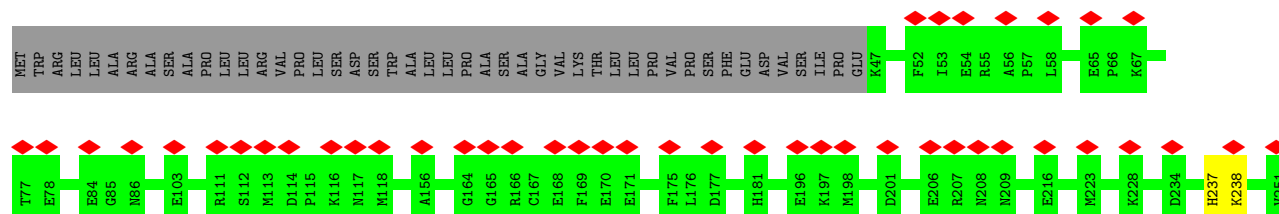
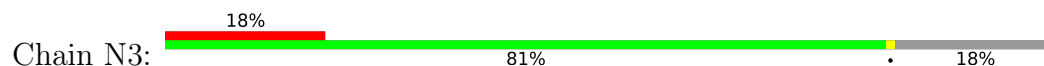
- Molecule 11: 39S ribosomal protein L14, mitochondrial



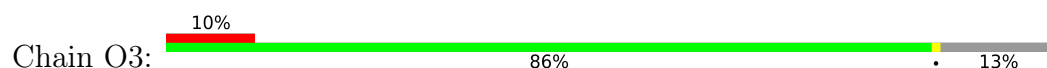
- Molecule 12: 39S ribosomal protein L15, mitochondrial



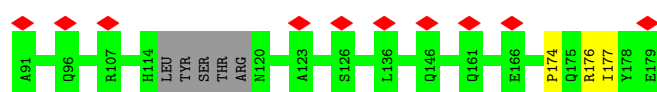
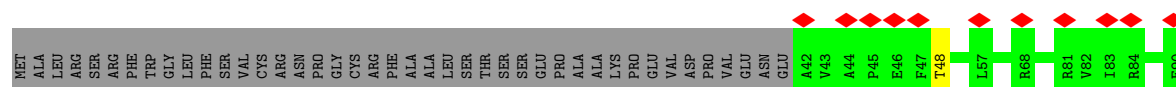
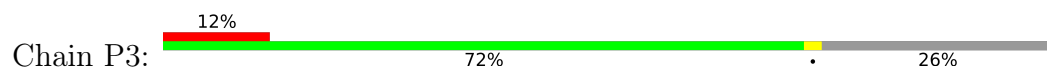
- Molecule 13: 39S ribosomal protein L16, mitochondrial



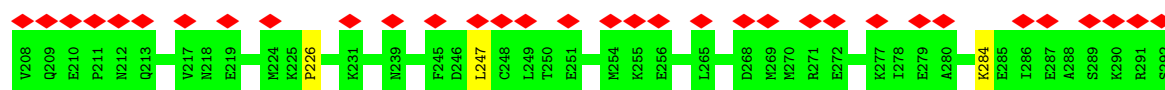
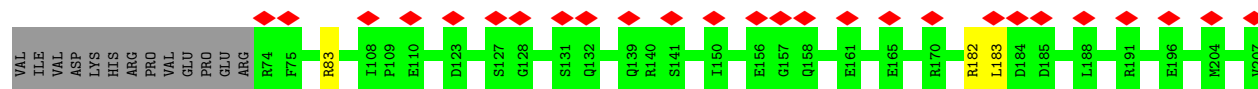
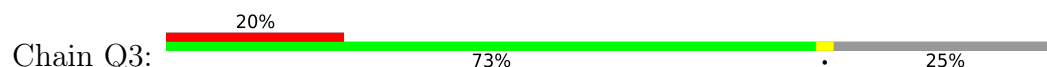
- Molecule 14: 39S ribosomal protein L17, mitochondrial



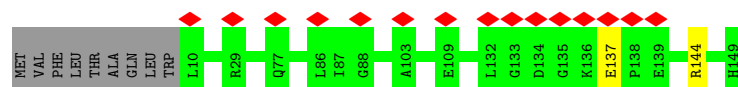
- Molecule 15: 39S ribosomal protein L18, mitochondrial



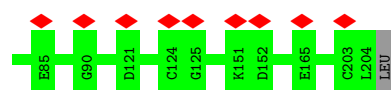
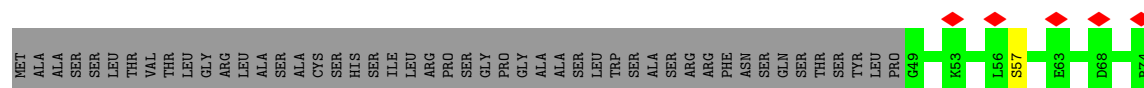
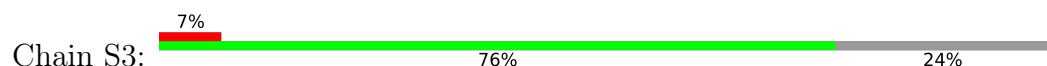
- Molecule 16: 39S ribosomal protein L19, mitochondrial




- Molecule 17: 39S ribosomal protein L20, mitochondrial

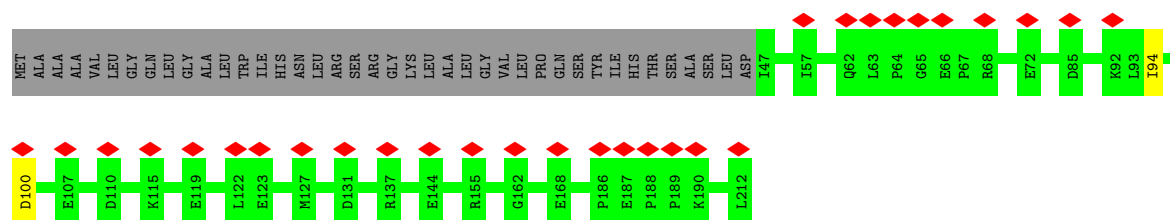


- Molecule 18: 39S ribosomal protein L21, mitochondrial




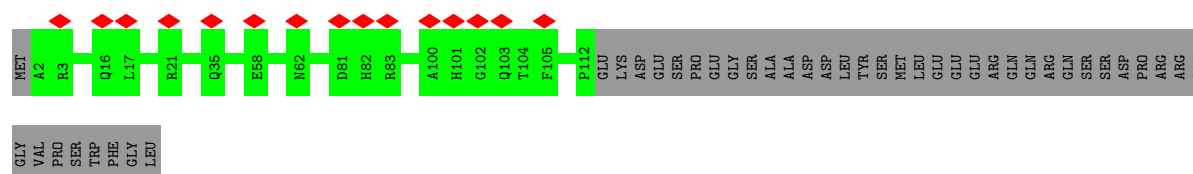
- Molecule 19: 39S ribosomal protein L22, mitochondrial

Chain T3: 




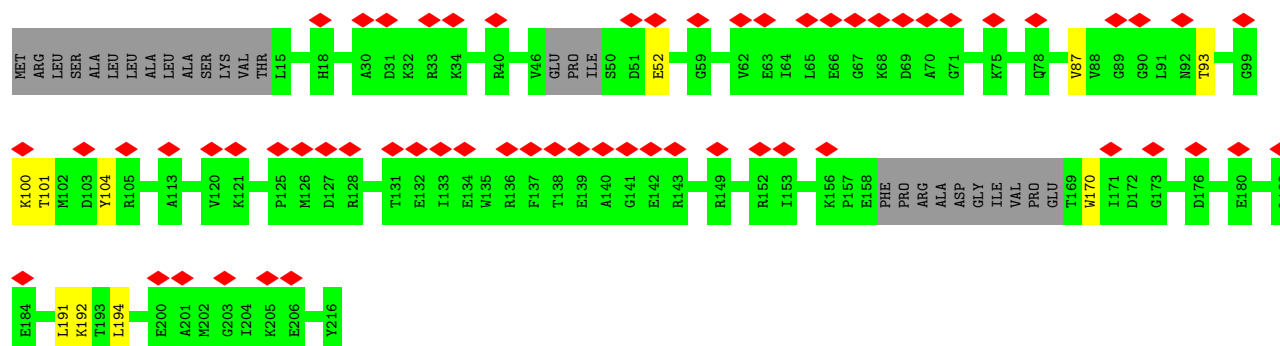
- Molecule 20: 39S ribosomal protein L23, mitochondrial

Chain U3: 




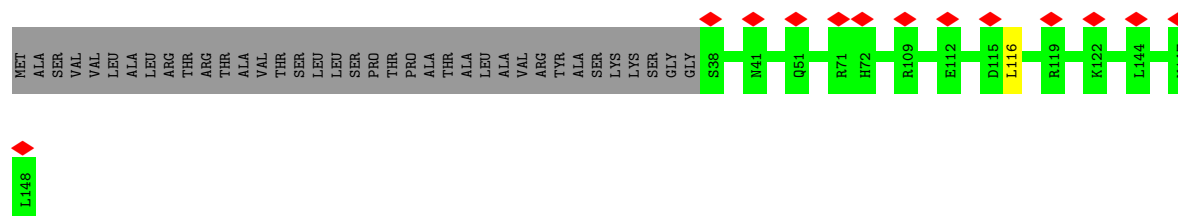
- Molecule 21: 39S ribosomal protein L24, mitochondrial

Chain V3: 



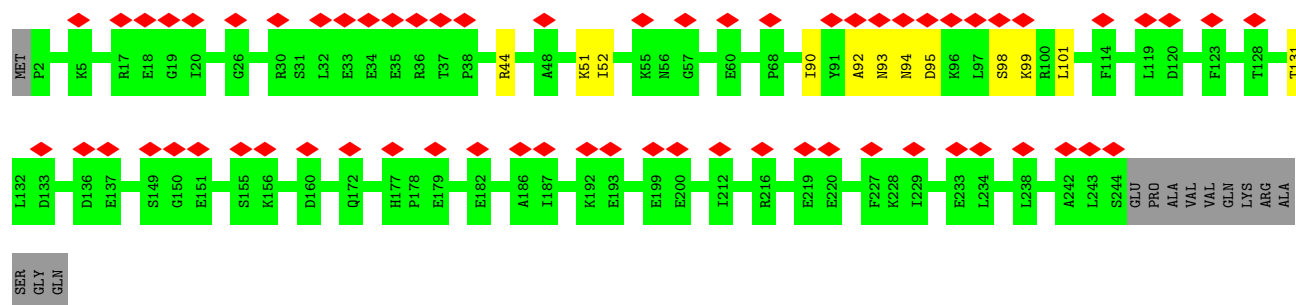
- Molecule 22: 39S ribosomal protein L27, mitochondrial

Chain W3: 

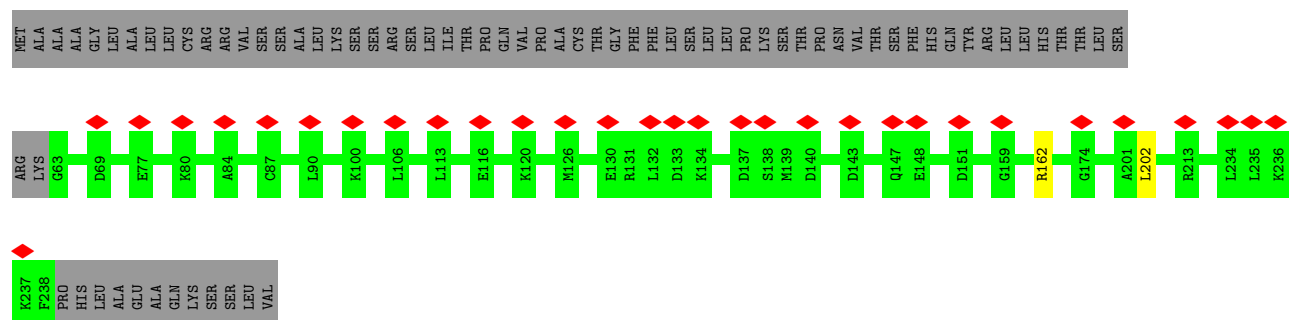


- Molecule 23: 39S ribosomal protein L28, mitochondrial

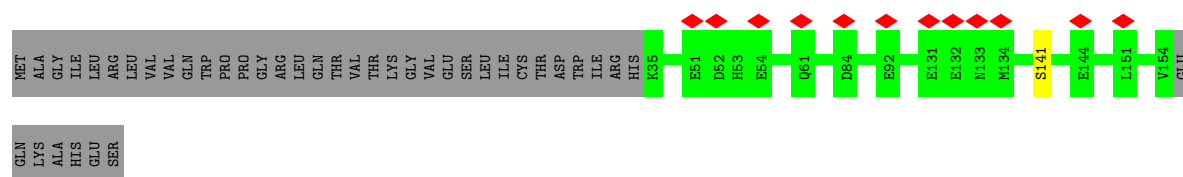
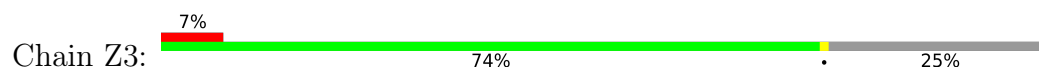
Chain X3: 



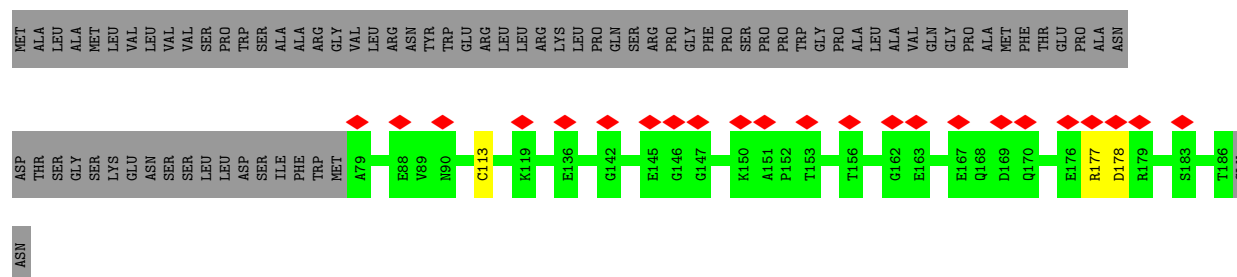
- Molecule 24: 39S ribosomal protein L47, mitochondrial



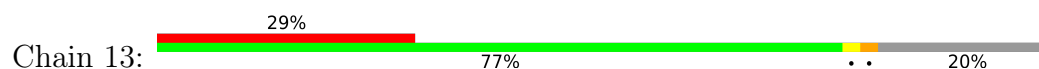
- Molecule 25: 39S ribosomal protein L30, mitochondrial



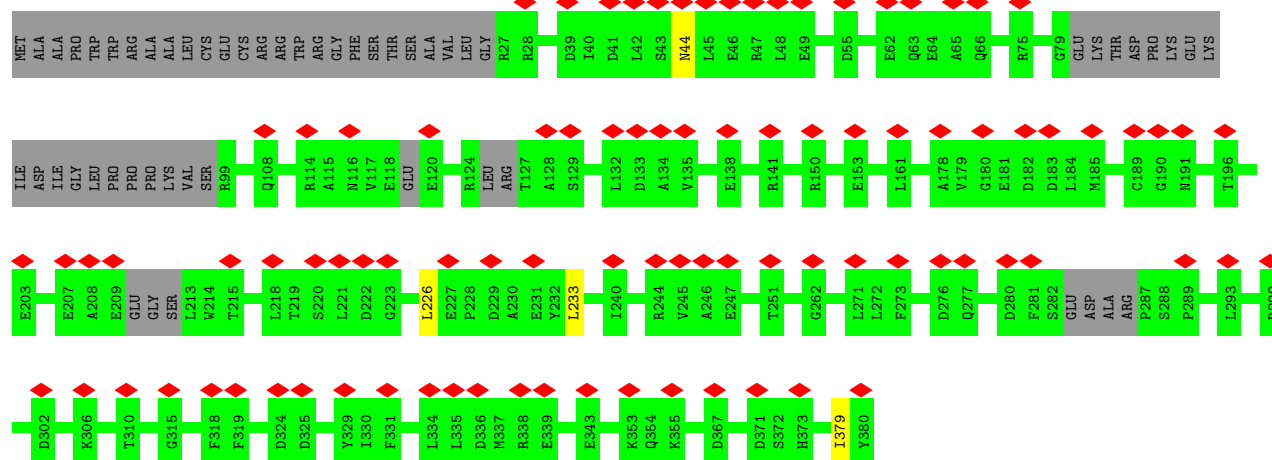
- Molecule 26: 39S ribosomal protein L32, mitochondrial



- Molecule 27: 39S ribosomal protein L33, mitochondrial

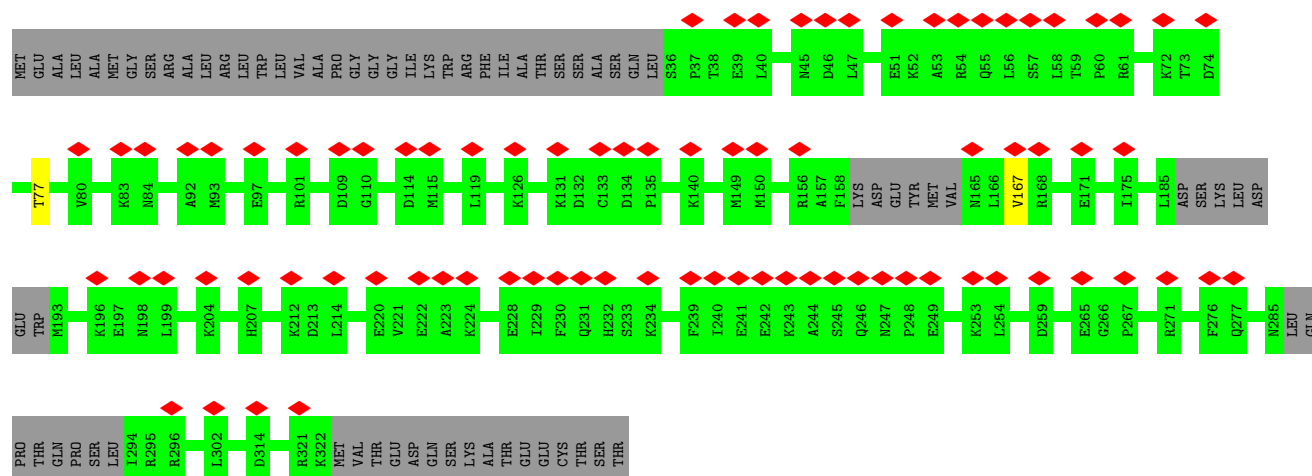


Chain 63: 24% 84% 14%



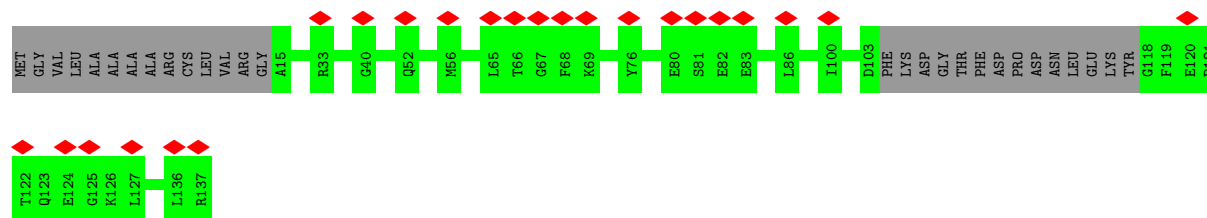
• Molecule 33: 39S ribosomal protein L39, mitochondrial

Chain 73: 25% 78% 21%



• Molecule 34: 39S ribosomal protein L41, mitochondrial

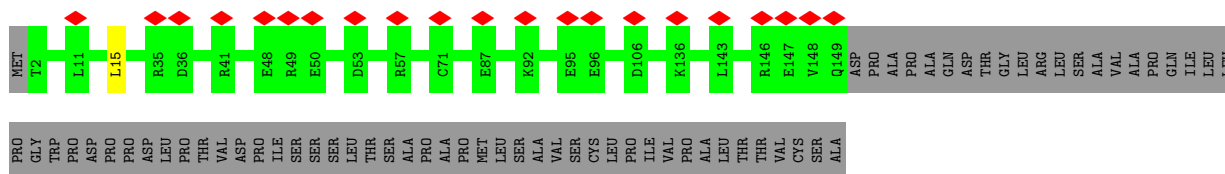
Chain 93: 17% 80% 20%



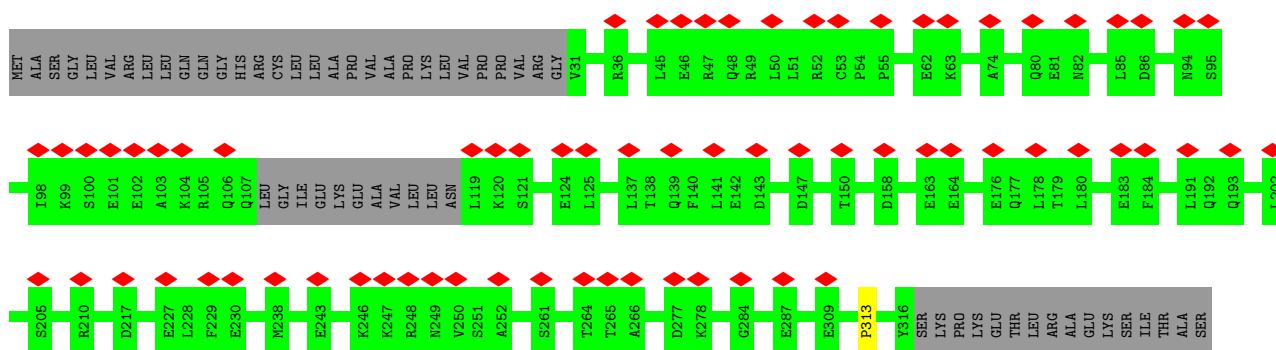
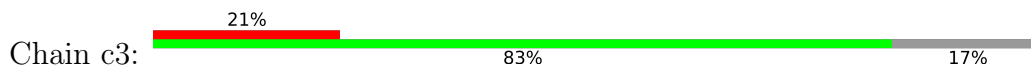
• Molecule 35: 39S ribosomal protein L42, mitochondrial

Chain a3: 14% 58% 42%

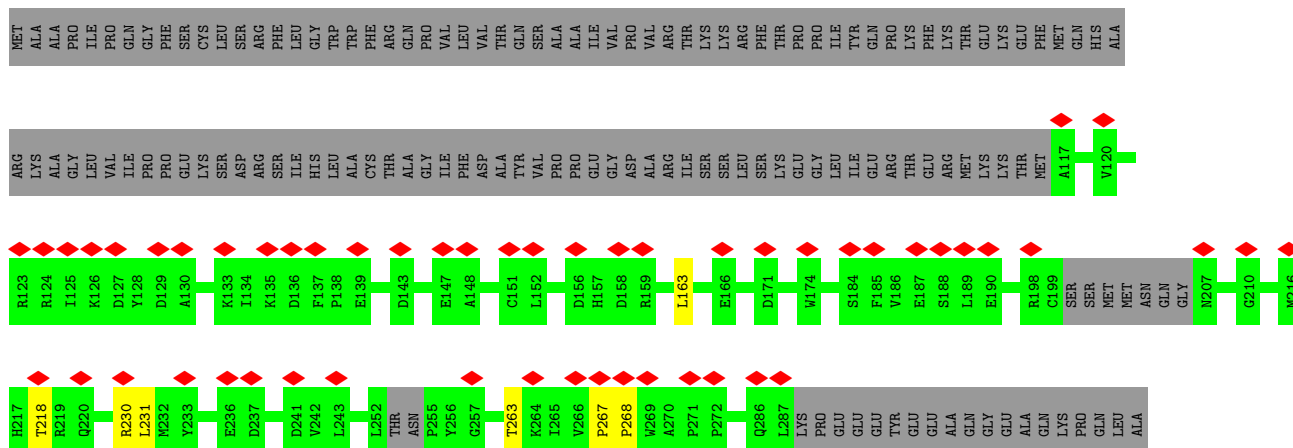
- Molecule 36: 39S ribosomal protein L43, mitochondrial



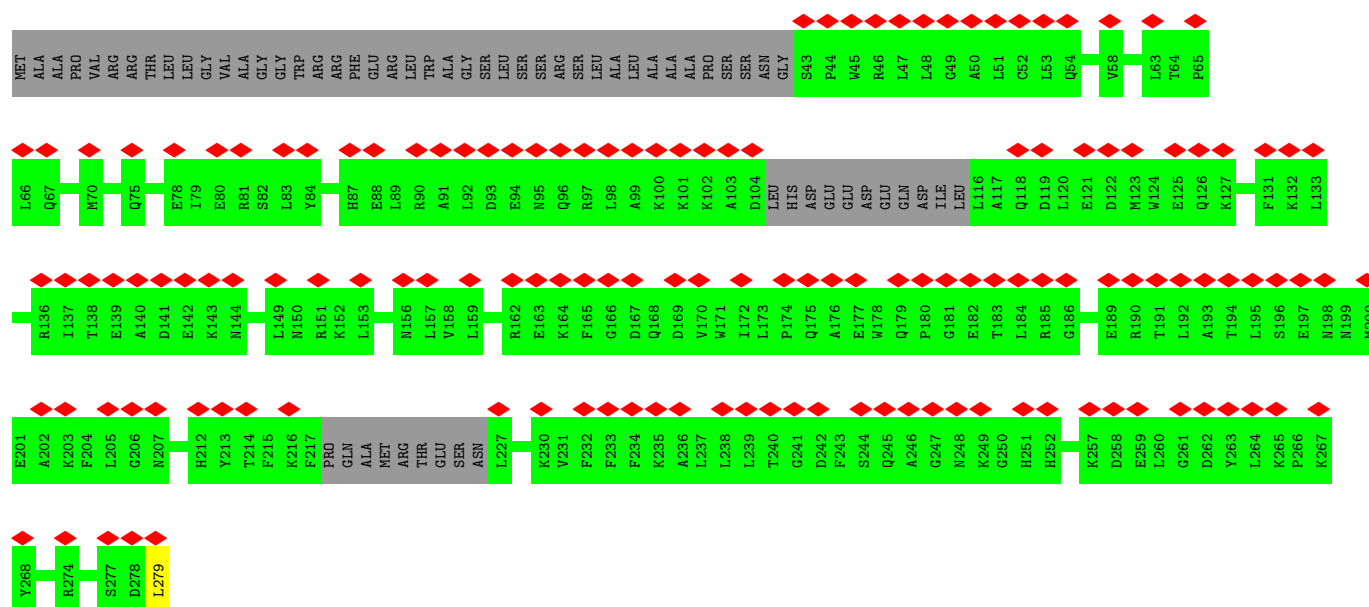
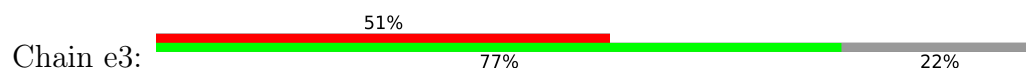
- Molecule 37: 39S ribosomal protein L44, mitochondrial



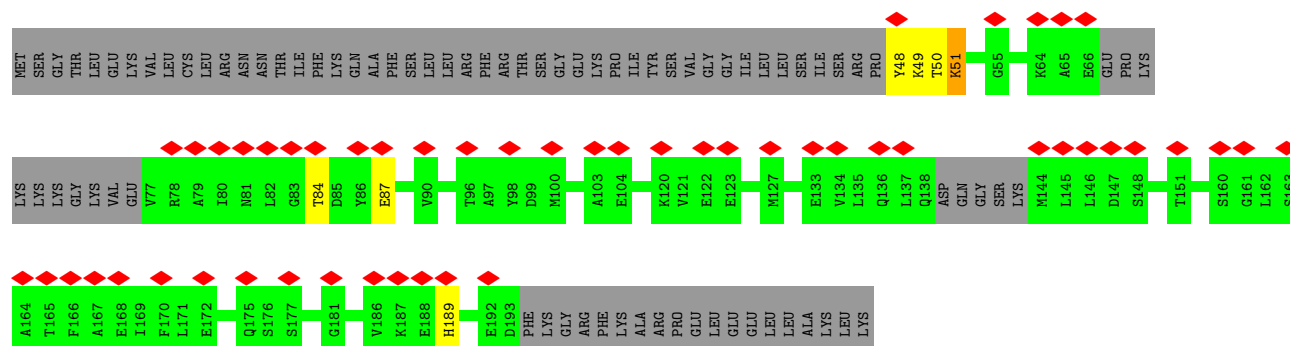
- Molecule 38: 39S ribosomal protein L45, mitochondrial



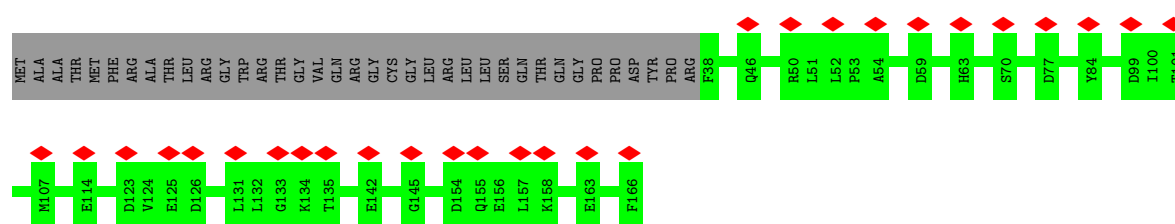
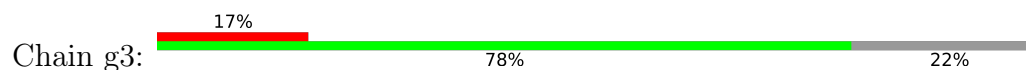
- Molecule 39: 39S ribosomal protein L46, mitochondrial



- Molecule 40: 39S ribosomal protein L48, mitochondrial

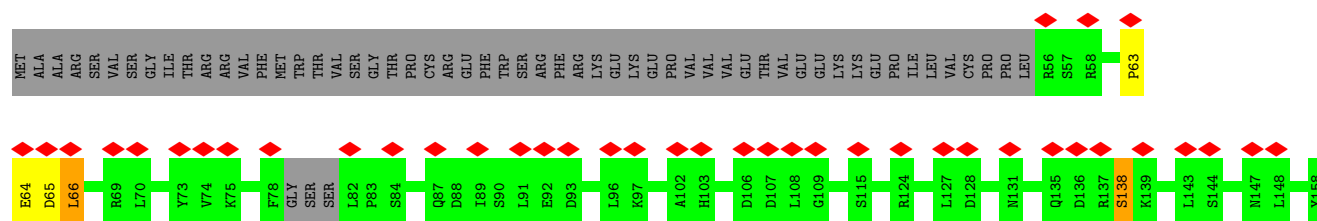


- Molecule 41: 39S ribosomal protein L49, mitochondrial

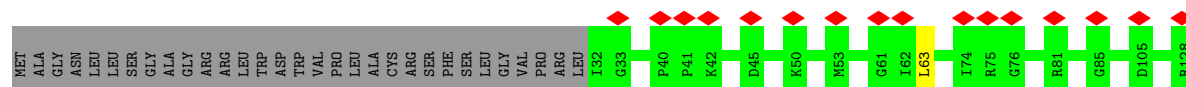
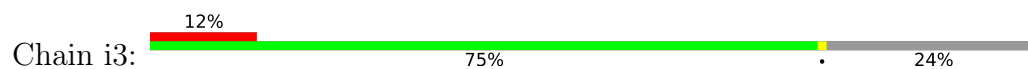


- Molecule 42: 39S ribosomal protein L50, mitochondrial

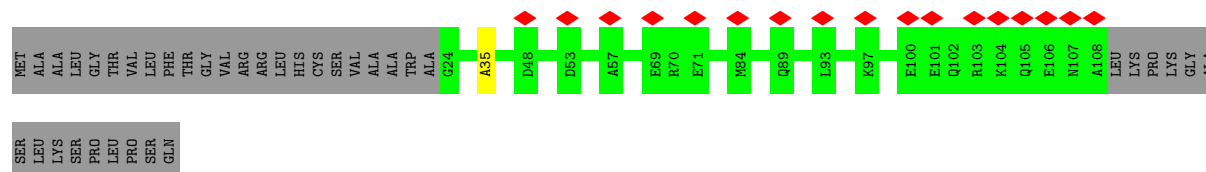




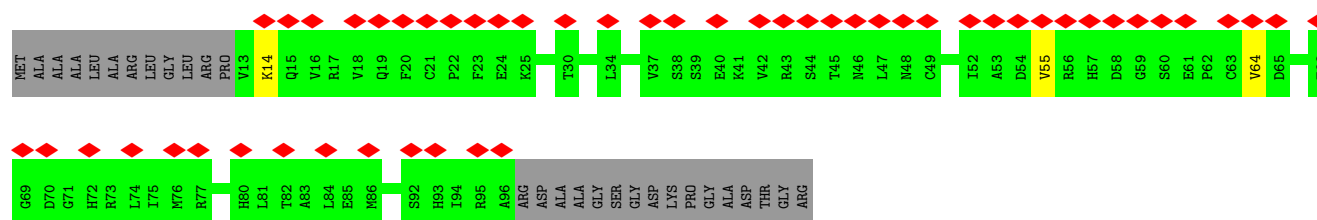
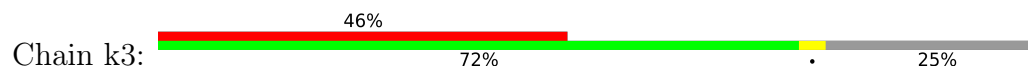
- Molecule 43: 39S ribosomal protein L51, mitochondrial



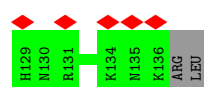
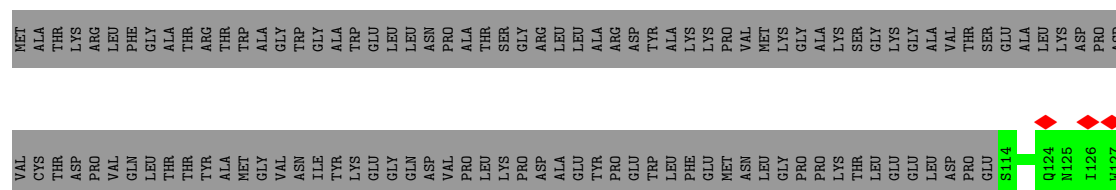
- Molecule 44: 39S ribosomal protein L52, mitochondrial



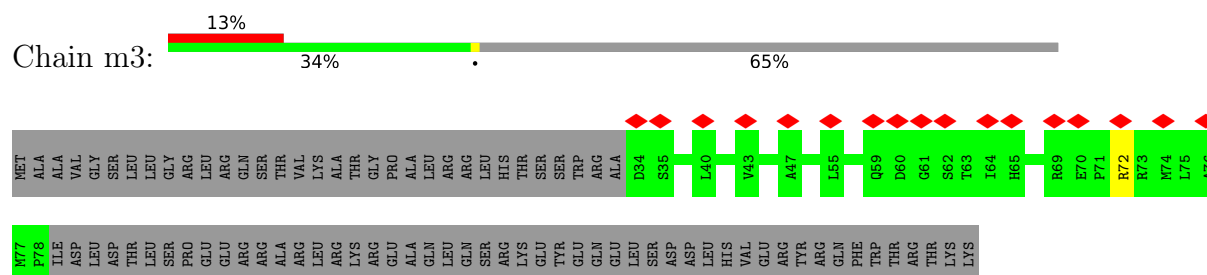
- Molecule 45: 39S ribosomal protein L53, mitochondrial



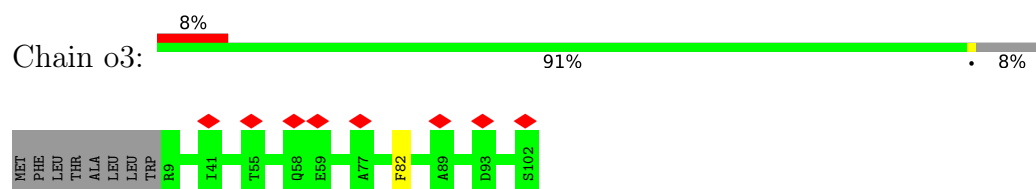
- Molecule 46: 39S ribosomal protein L54, mitochondrial



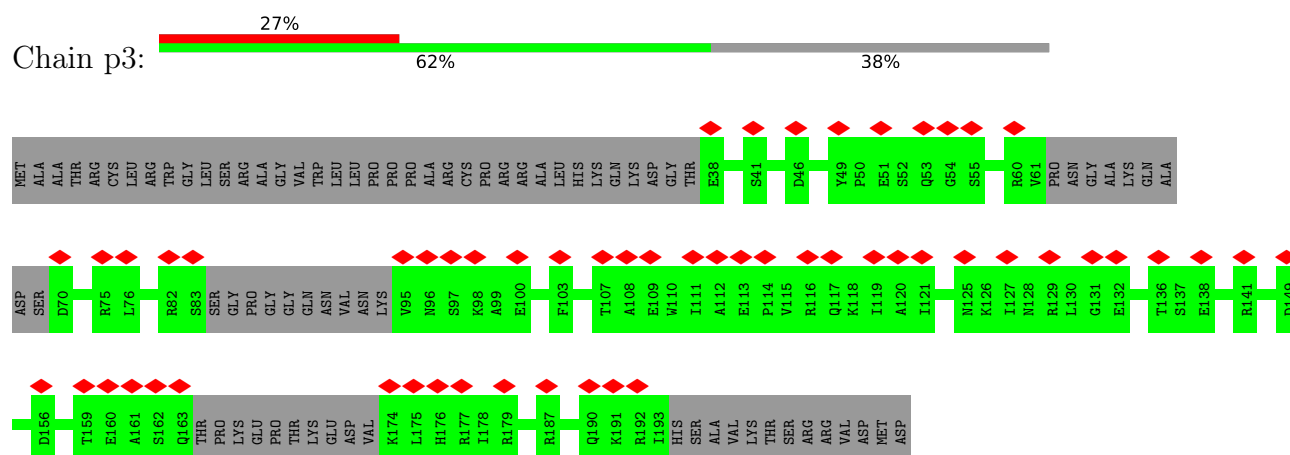
- Molecule 47: 39S ribosomal protein L55, mitochondrial



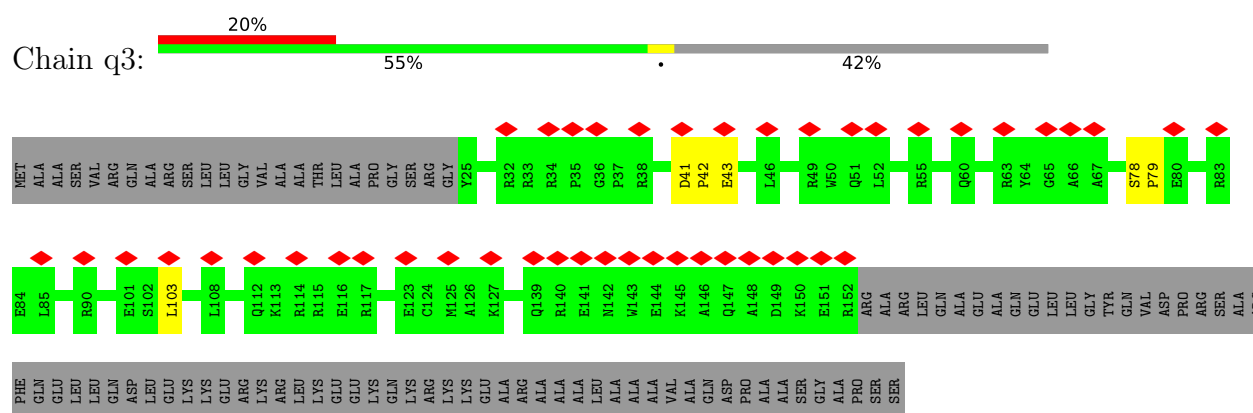
- Molecule 48: Ribosomal protein 63, mitochondrial



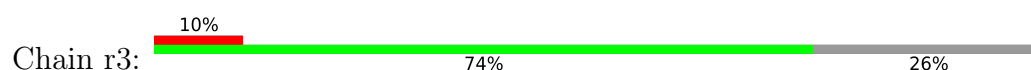
- Molecule 49: Peptidyl-tRNA hydrolase ICT1, mitochondrial

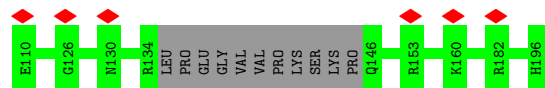


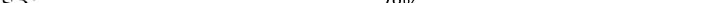
- Molecule 50: Growth arrest and DNA damage-inducible proteins-interacting protein 1

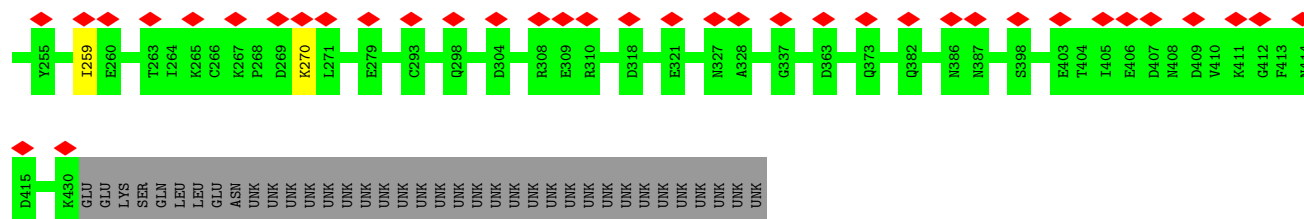


- Molecule 51: 39S ribosomal protein S18a, mitochondrial

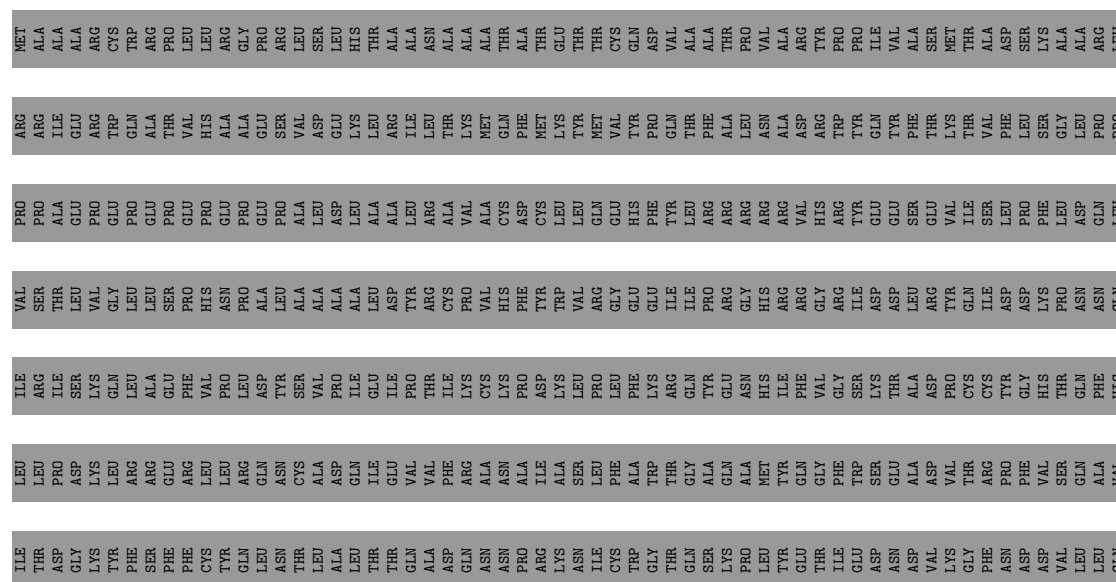


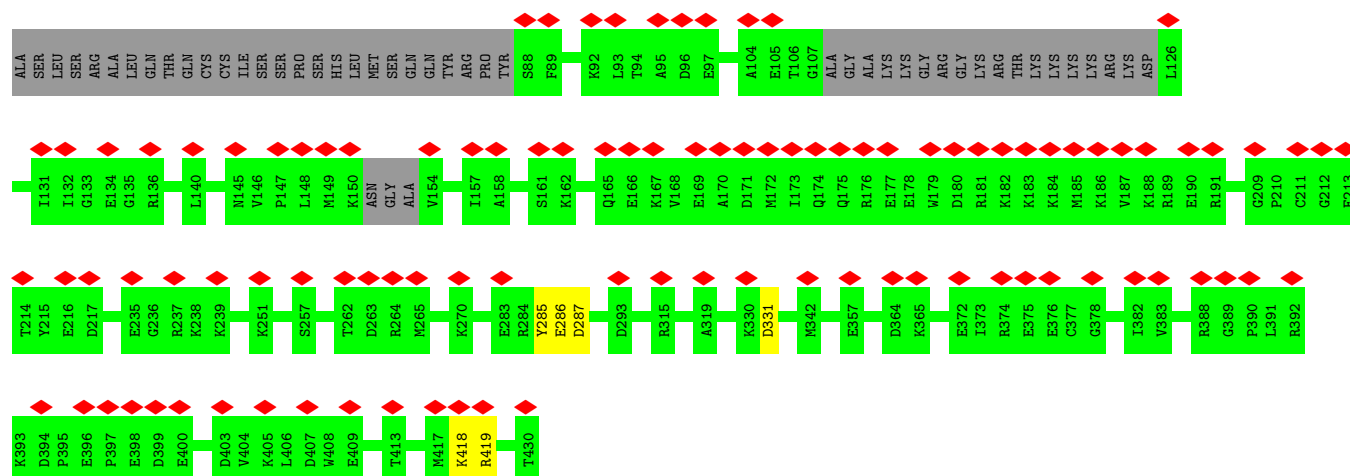


- Chain s3:  14% 78% 21%

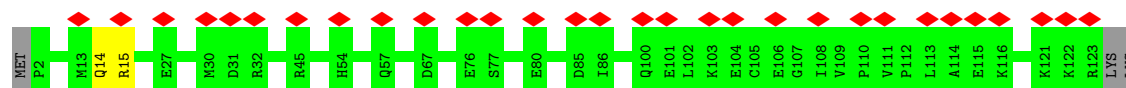


- Chain t3:  5% 6% 94%

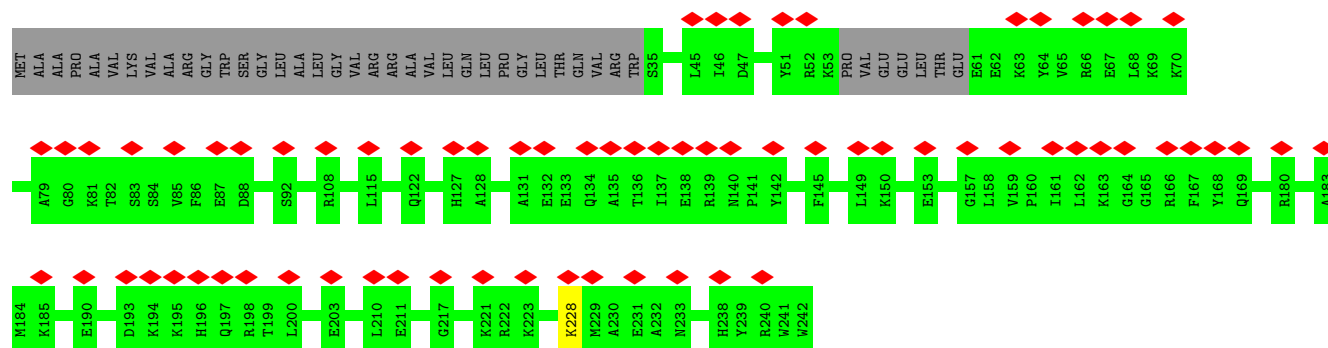
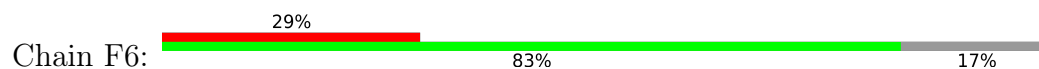




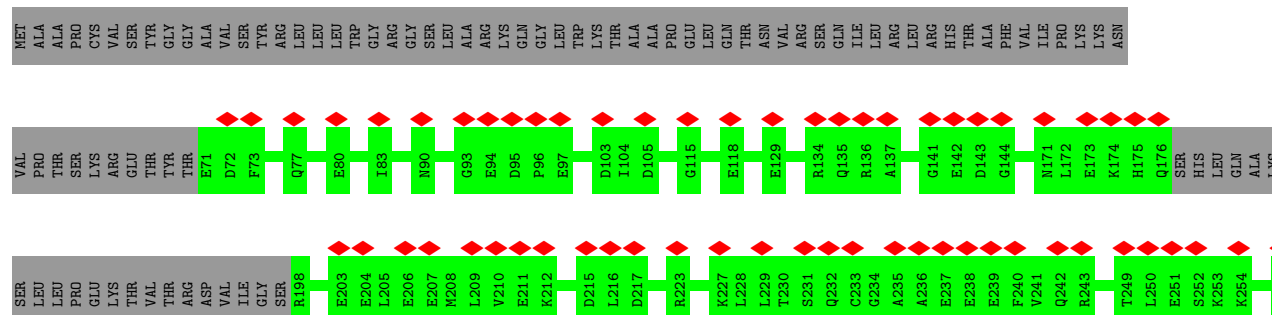
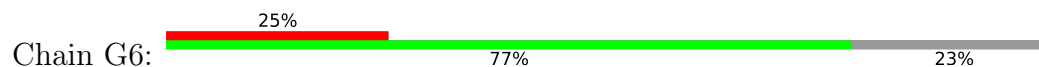
- Molecule 58: 28S ribosomal protein S6, mitochondrial

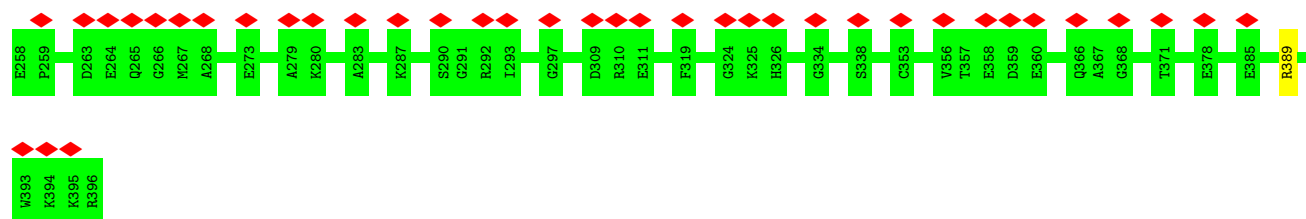


- Molecule 59: 28S ribosomal protein S7, mitochondrial

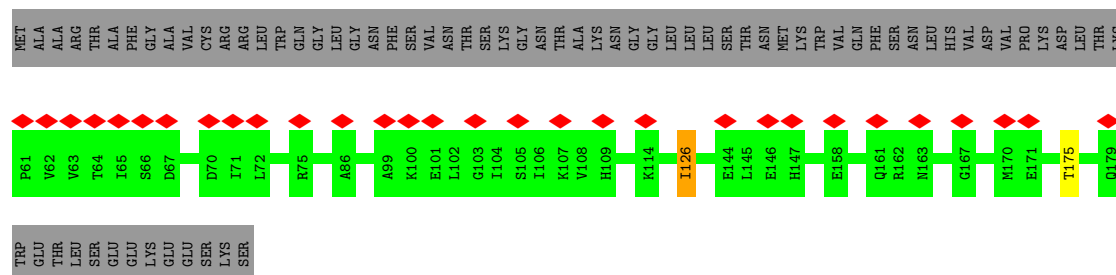


- Molecule 60: 28S ribosomal protein S9, mitochondrial

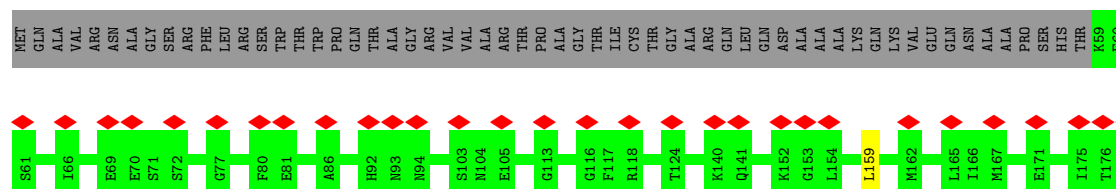




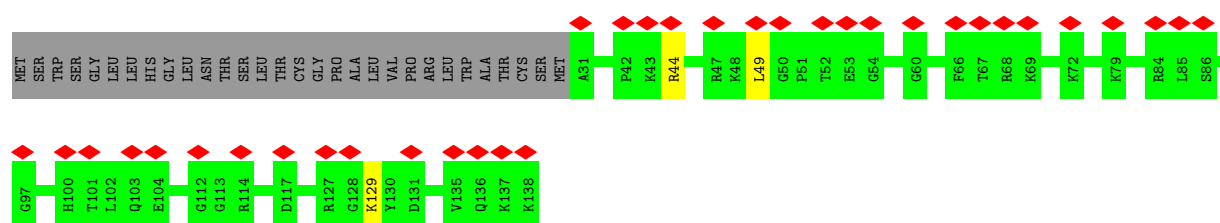
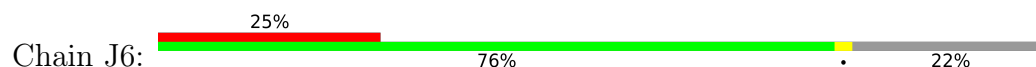
- Molecule 61: 28S ribosomal protein S10, mitochondrial



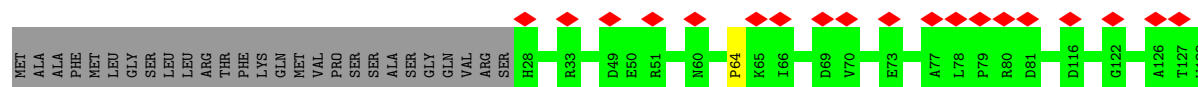
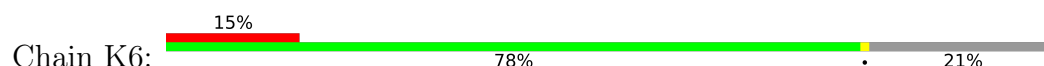
- Molecule 62: 28S ribosomal protein S11, mitochondrial



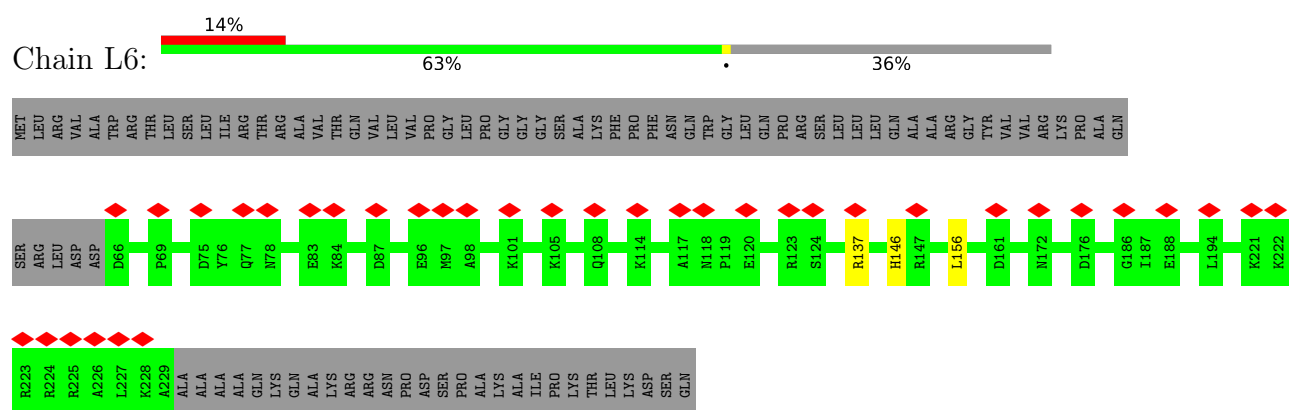
- Molecule 63: 28S ribosomal protein S12, mitochondrial



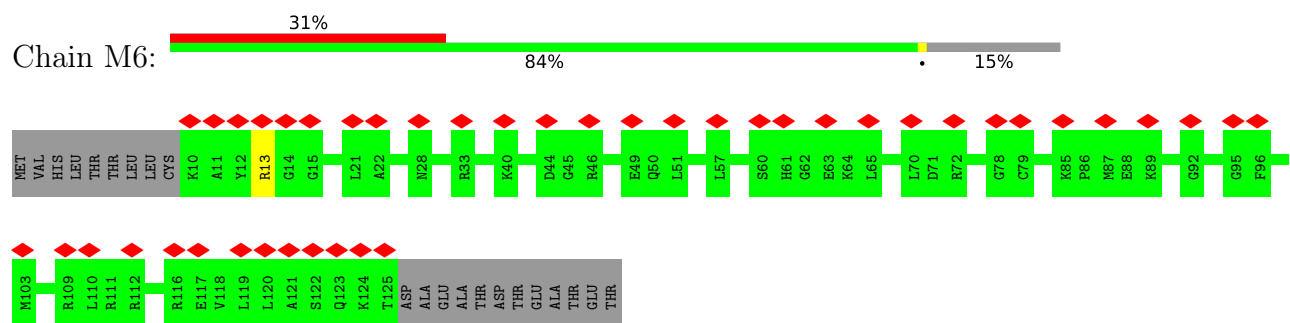
- Molecule 64: 28S ribosomal protein S14, mitochondrial



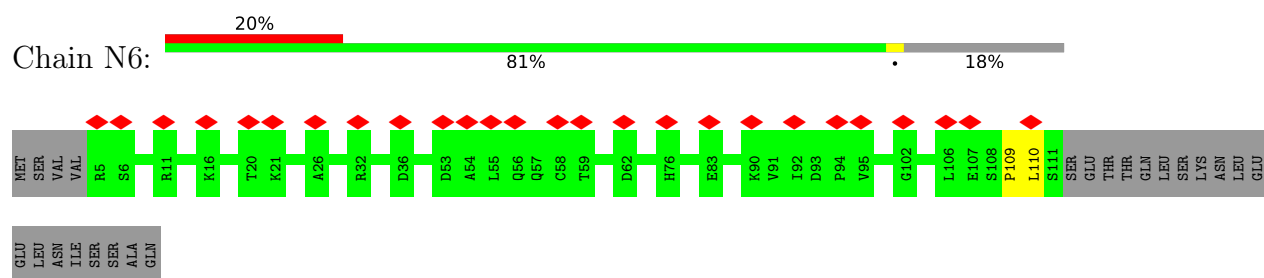
- Molecule 65: 28S ribosomal protein S15, mitochondrial



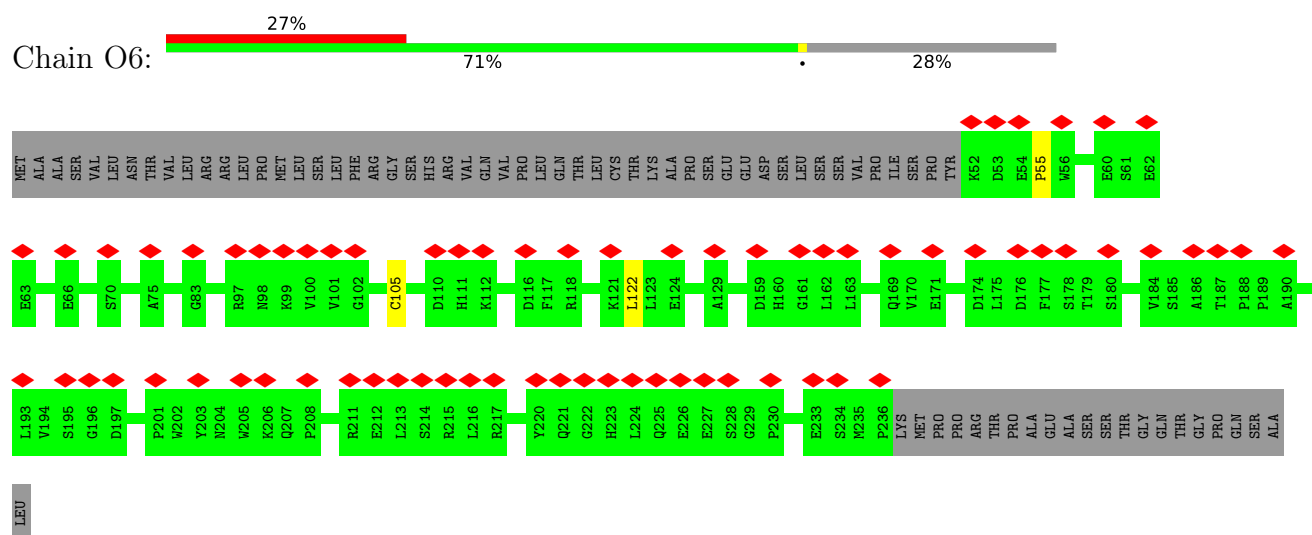
- Molecule 66: 28S ribosomal protein S16, mitochondrial



- Molecule 67: 28S ribosomal protein S17, mitochondrial

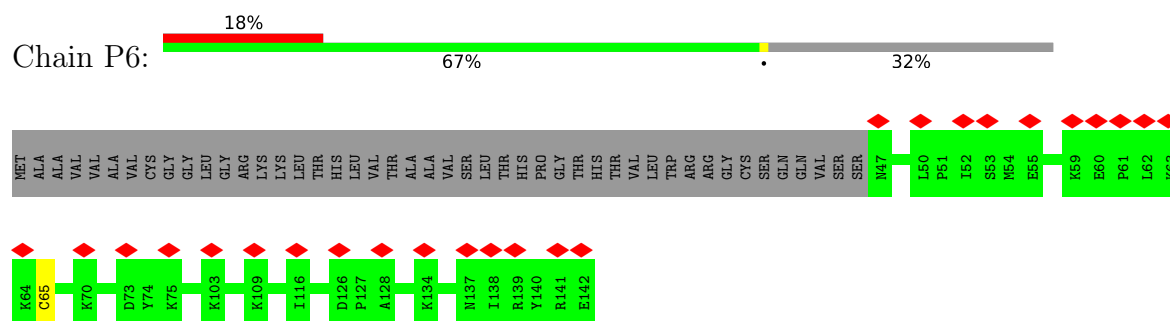


- Molecule 68: 28S ribosomal protein S18b, mitochondrial



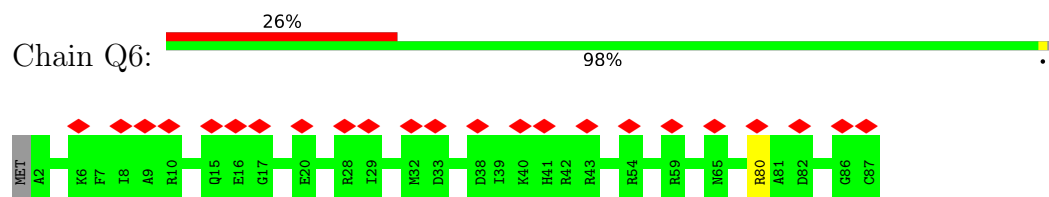
- Molecule 69: 28S ribosomal protein S18c, mitochondrial

Chain P6:



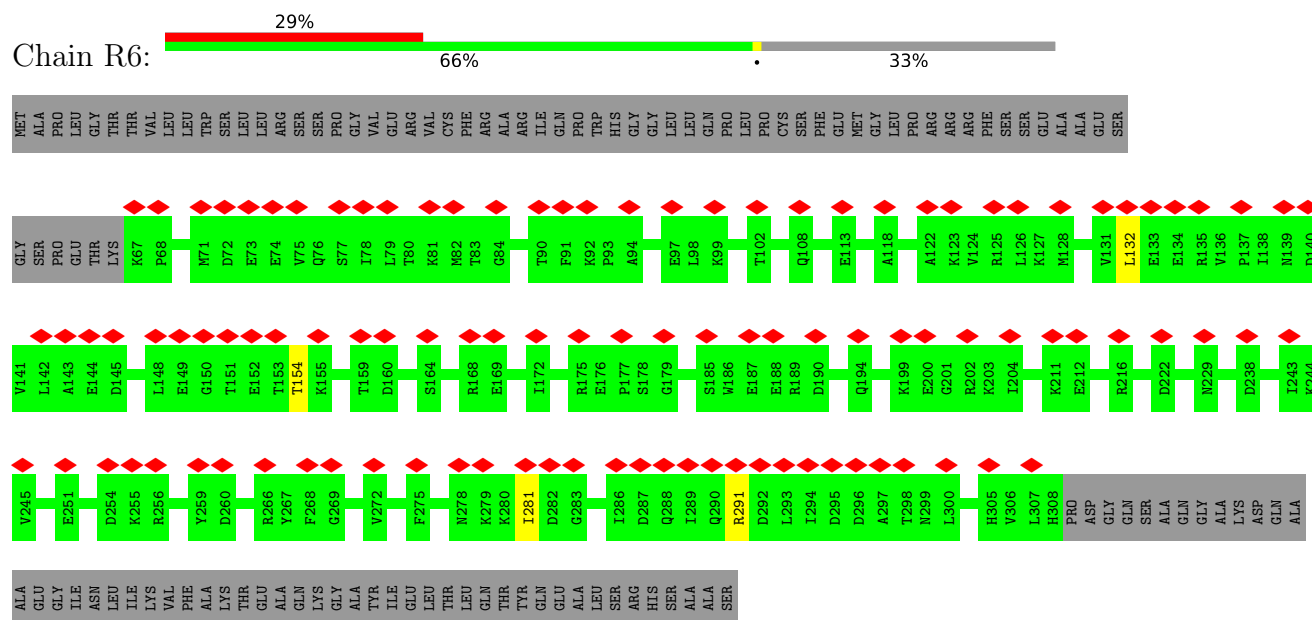
- Molecule 70: 28S ribosomal protein S21, mitochondrial

Chain Q6:



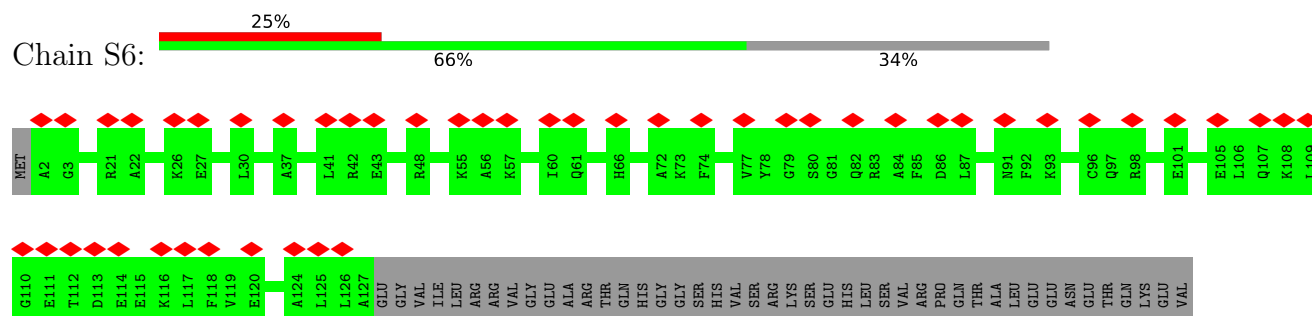
- Molecule 71: 28S ribosomal protein S22, mitochondrial

Chain R6:

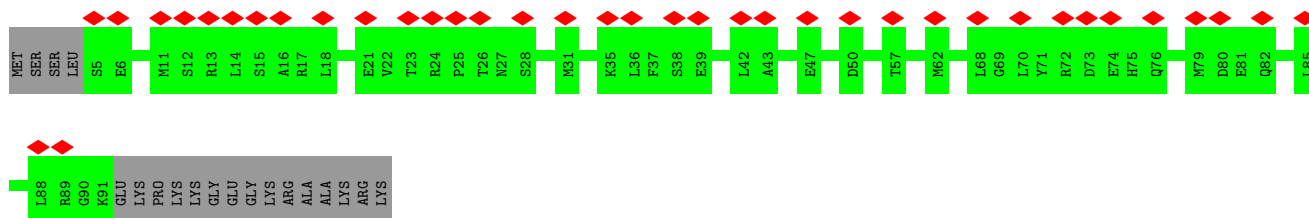
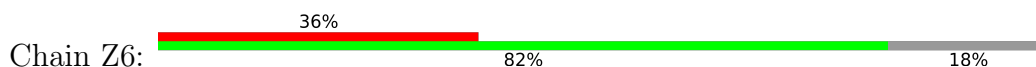


- Molecule 72: 28S ribosomal protein S23, mitochondrial

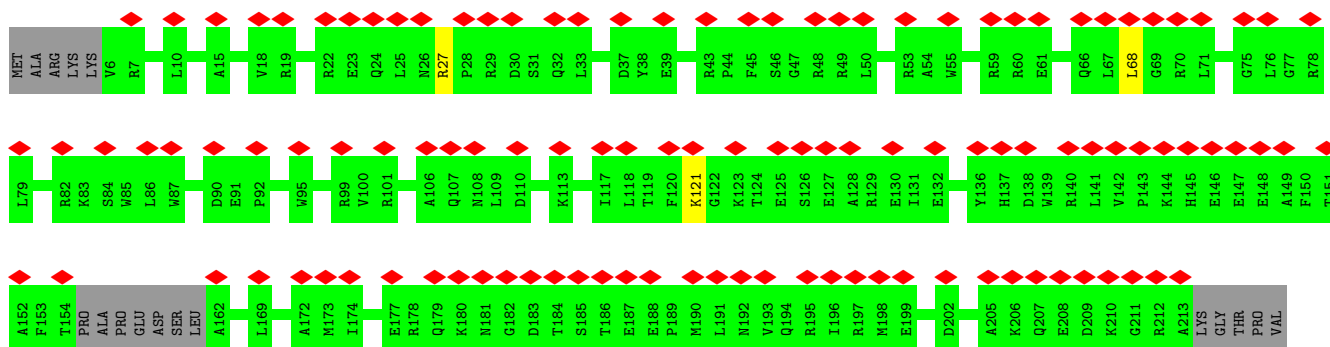
Chain S6:



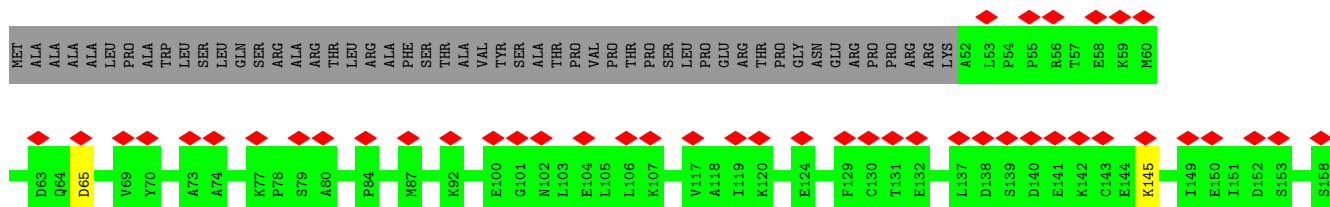
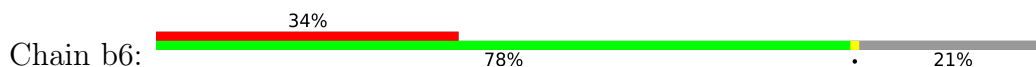
- Molecule 79: 28S ribosomal protein S33, mitochondrial

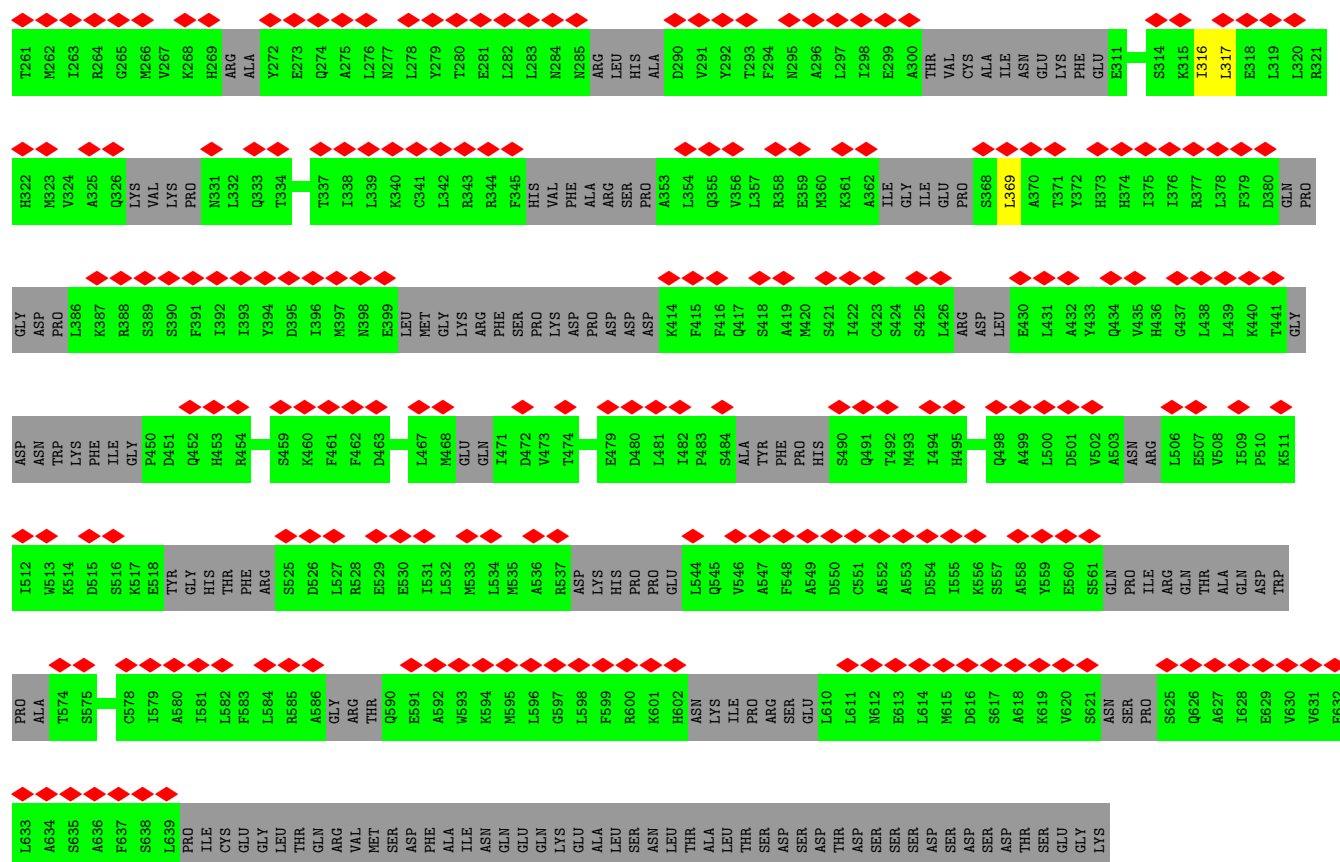


- Molecule 80: 28S ribosomal protein S34, mitochondrial



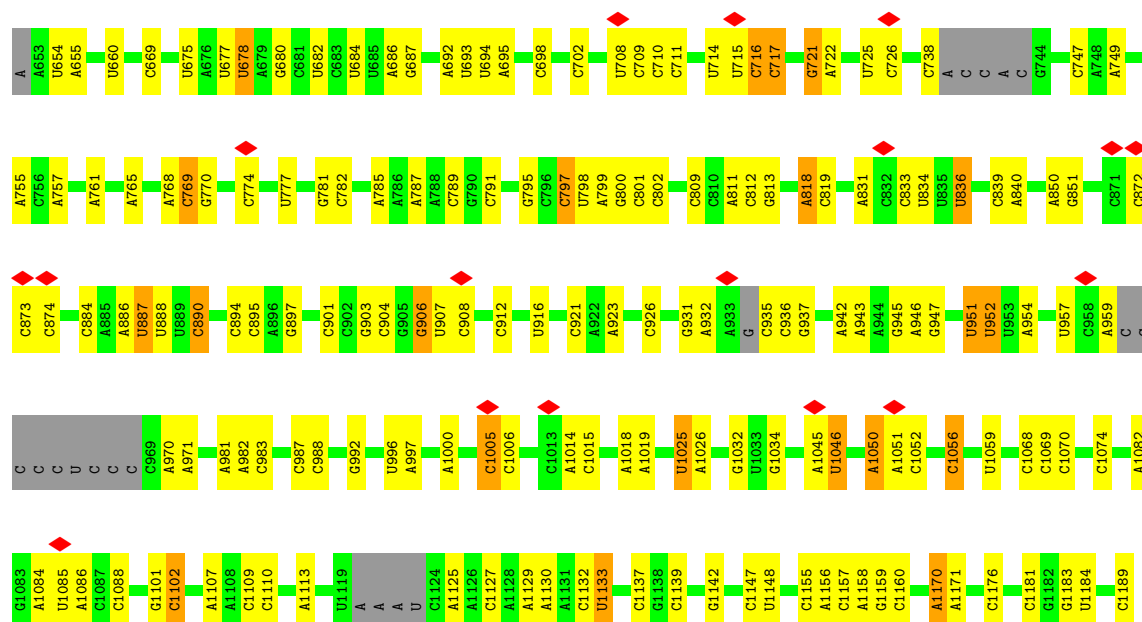
- Molecule 81: 28S ribosomal protein S35, mitochondrial

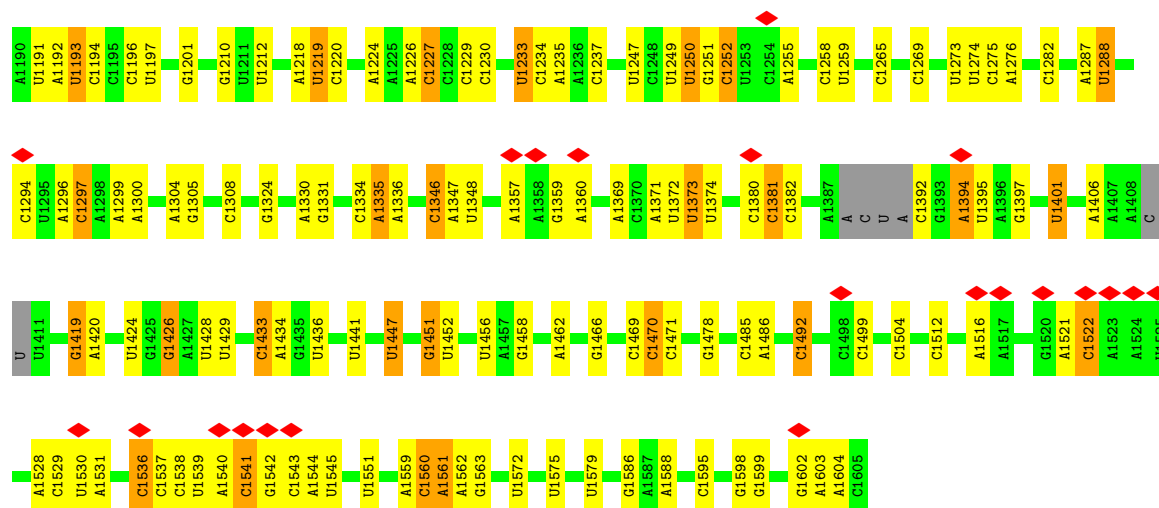




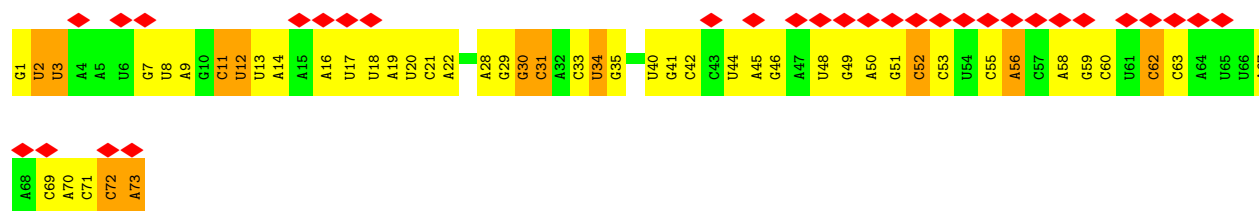
• Molecule 85: 12S rRNA

Chain A6: 65% 27% 5% .

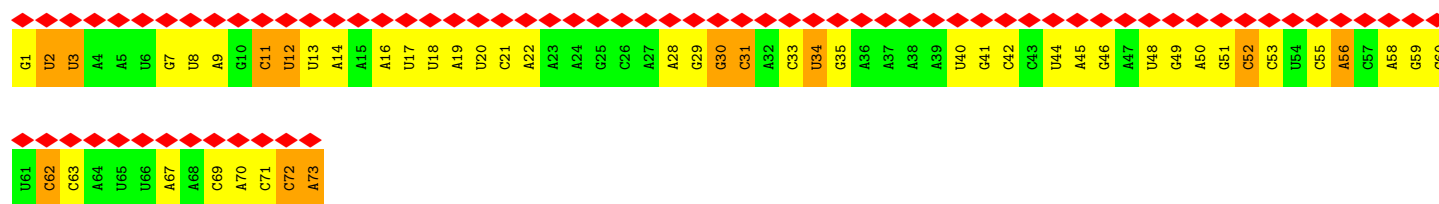




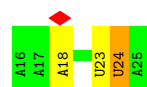
• Molecule 86: P tRNA



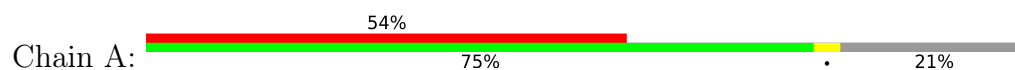
• Molecule 86: P tRNA

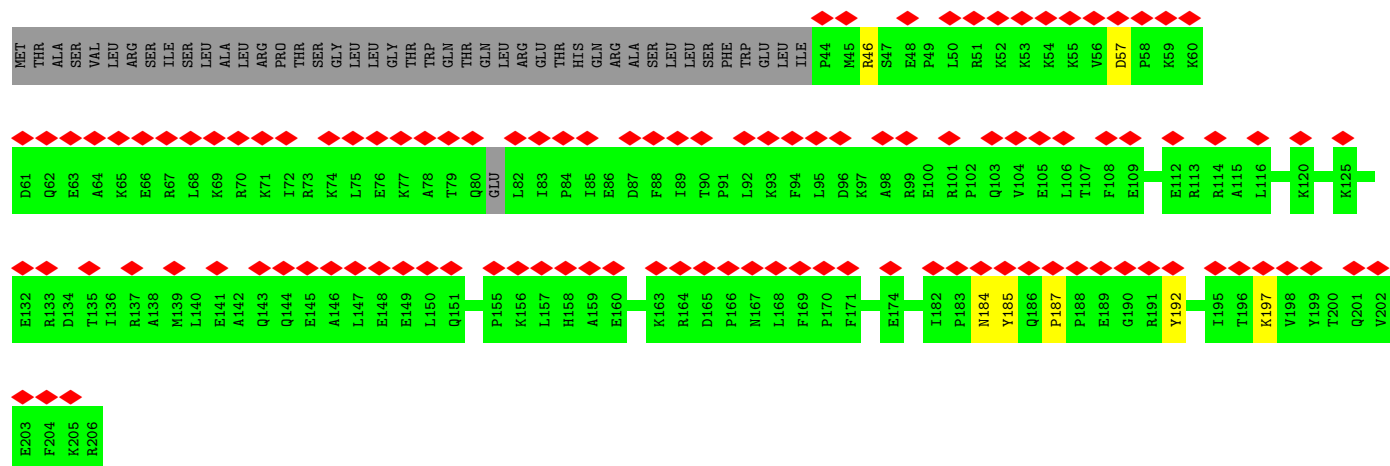


• Molecule 87: mRNA

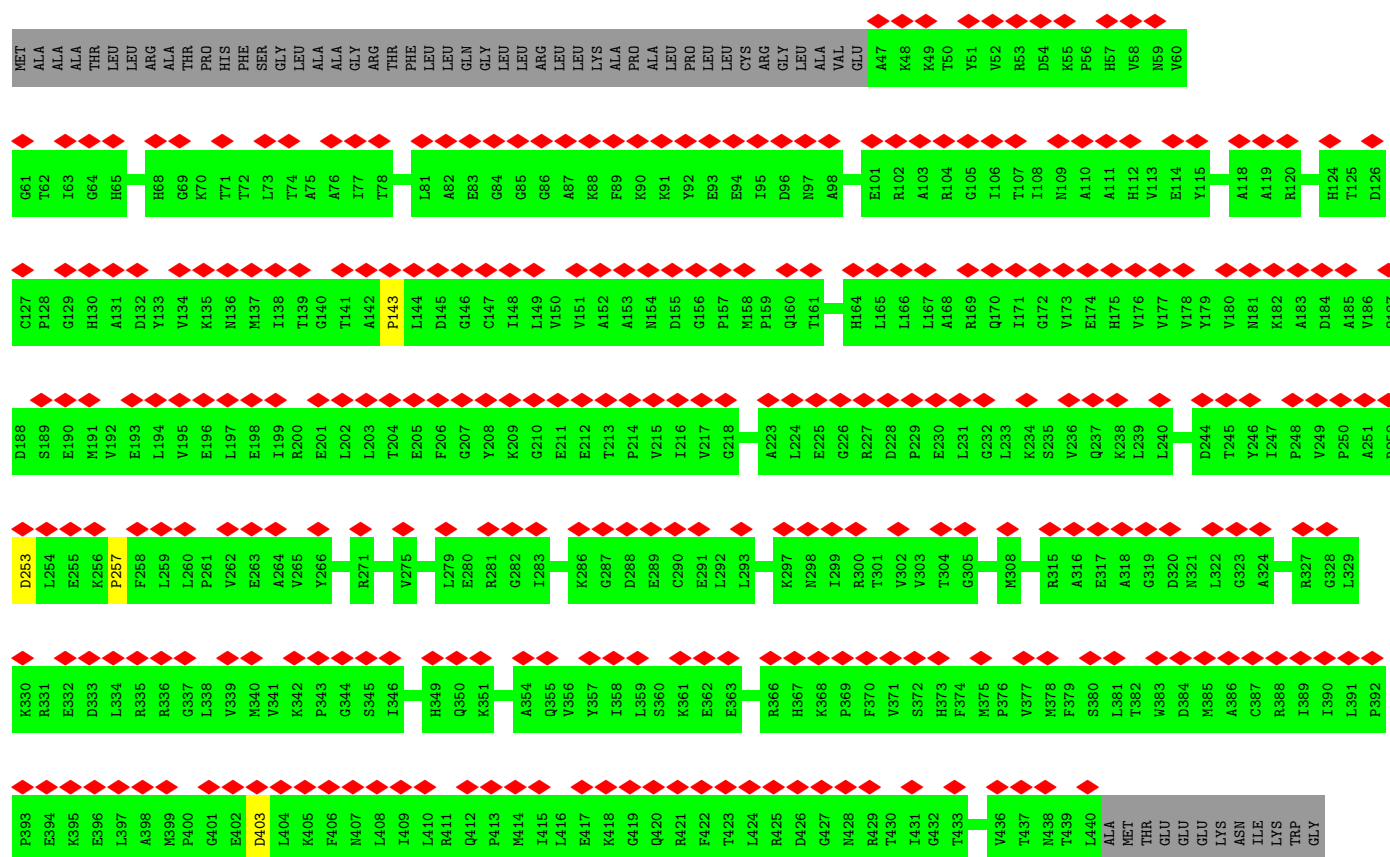
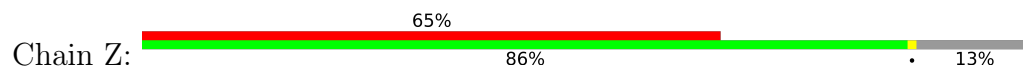


• Molecule 88: 39S ribosomal protein L40, mitochondrial

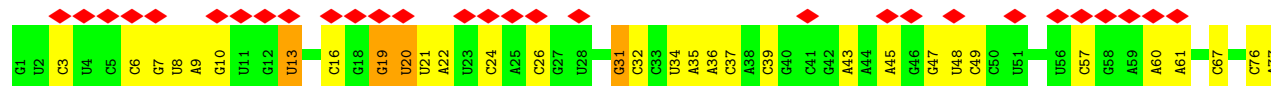




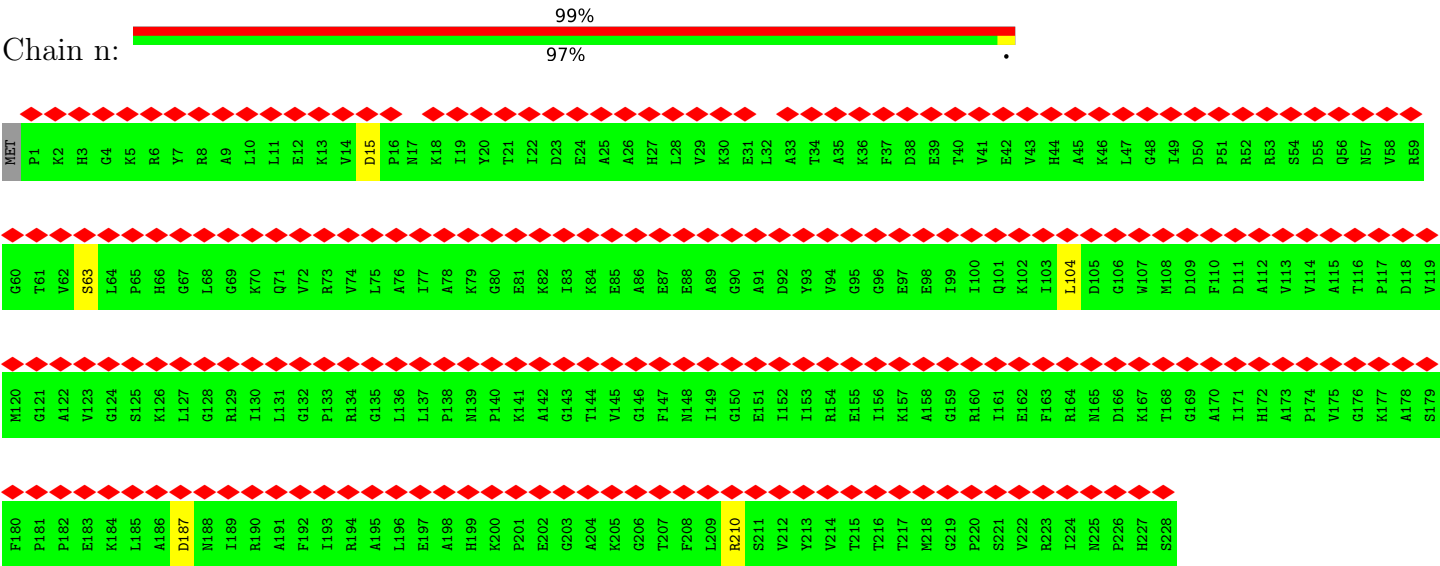
• Molecule 89: Elongation factor Tu, mitochondrial



• Molecule 90: E tRNA



● Molecule 91: 50S ribosomal protein L1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	18188	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.227	Depositor
Minimum map value	-0.130	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	532.48, 532.48, 532.48	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SPD, SO4, ZN, NA, MG, CL, MLI, GDP, GCP

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	Y2	0.31	0/144	0.72	0/200
2	A3	0.95	2/35697 (0.0%)	1.29	424/55544 (0.8%)
3	B3	0.67	0/1328	1.24	12/2056 (0.6%)
4	D3	0.48	0/1879	0.64	2/2527 (0.1%)
5	E3	0.50	0/2433	0.62	0/3299
6	F3	0.48	0/2071	0.65	1/2817 (0.0%)
7	D	0.38	0/665	0.70	0/905
7	H3	0.42	0/798	0.64	0/1073
8	I3	0.37	0/1308	0.58	0/1761
9	J3	0.35	0/1077	0.60	0/1452
10	K3	0.48	0/1495	0.61	0/2029
11	L3	0.44	0/904	0.64	0/1218
12	M3	0.49	0/2359	0.67	0/3185
13	N3	0.48	0/1697	0.60	0/2281
14	O3	0.48	0/1269	0.65	0/1708
15	P3	0.46	0/1103	0.60	0/1491
16	Q3	0.43	0/1863	0.61	1/2509 (0.0%)
17	R3	0.51	0/1174	0.60	0/1572
18	S3	0.52	1/1276 (0.1%)	0.65	0/1729
19	T3	0.50	0/1402	0.58	0/1886
20	U3	0.52	0/946	0.65	0/1283
21	V3	0.45	0/1590	0.68	1/2151 (0.0%)
22	W3	0.54	0/893	0.64	1/1204 (0.1%)
23	X3	0.48	0/2081	0.71	3/2812 (0.1%)
24	Y3	0.45	0/1552	0.57	0/2079
25	Z3	0.46	0/1003	0.62	0/1354
26	O3	0.44	0/895	0.62	0/1201
27	I3	0.40	0/438	0.68	0/583
28	23	0.46	0/382	0.60	0/507
29	33	0.50	0/852	0.61	0/1136
30	43	0.51	0/329	0.56	0/435
31	53	0.46	0/3154	0.66	1/4295 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	63	0.44	0/2722	0.61	2/3709 (0.1%)
33	73	0.44	0/2207	0.60	0/2978
34	93	0.45	0/896	0.60	0/1205
35	a3	0.43	0/709	0.57	0/963
36	b3	0.46	0/1202	0.61	0/1626
37	c3	0.42	0/2264	0.57	0/3059
38	d3	0.41	0/1385	0.70	1/1877 (0.1%)
39	e3	0.36	0/1797	0.66	1/2422 (0.0%)
40	f3	0.50	0/1055	0.78	1/1427 (0.1%)
41	g3	0.49	0/1102	0.62	0/1503
42	h3	0.44	0/847	0.74	3/1150 (0.3%)
43	i3	0.49	0/849	0.66	1/1135 (0.1%)
44	j3	0.44	0/698	0.57	0/940
45	k3	0.35	0/665	0.66	0/897
46	l3	0.38	0/226	0.47	0/299
47	m3	0.38	0/379	0.60	0/510
48	o3	0.47	0/818	0.57	0/1097
49	p3	0.34	0/1071	0.56	0/1433
50	q3	0.41	0/1107	0.57	1/1498 (0.1%)
51	r3	0.46	0/1238	0.56	0/1676
52	s3	0.47	0/3114	0.62	1/4225 (0.0%)
53	u3	0.58	0/46	1.07	0/69
55	B6	0.48	0/1811	0.62	0/2451
56	C6	0.50	0/1112	0.60	0/1505
57	D6	0.44	0/2607	0.64	0/3498
58	E6	0.41	0/989	0.63	1/1335 (0.1%)
59	F6	0.44	0/1708	0.62	0/2291
60	G6	0.43	0/2570	0.59	0/3443
61	H6	0.54	0/1019	0.74	1/1379 (0.1%)
62	I6	0.40	0/1031	0.60	1/1390 (0.1%)
63	J6	0.44	0/854	0.67	1/1148 (0.1%)
64	K6	0.47	0/879	0.59	0/1182
65	L6	0.42	0/1406	0.55	0/1878
66	M6	0.38	0/941	0.61	0/1265
67	N6	0.45	0/864	0.66	1/1169 (0.1%)
68	O6	0.40	0/1580	0.61	2/2150 (0.1%)
69	P6	0.47	0/791	0.63	0/1062
70	Q6	0.47	0/752	0.58	0/1001
71	R6	0.39	0/2050	0.62	0/2770
72	S6	0.43	0/1069	0.59	0/1441
73	T6	0.43	0/1361	0.64	0/1829
74	U6	0.37	0/1482	0.56	0/1987
75	V6	0.36	0/2758	0.64	2/3724 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	W6	0.43	0/778	0.67	0/1048
77	X6	0.41	0/2596	0.69	2/3519 (0.1%)
78	Y6	0.42	0/943	0.60	0/1274
79	Z6	0.41	0/757	0.60	0/1011
80	a6	0.37	0/1727	0.61	1/2338 (0.0%)
81	b6	0.39	0/2121	0.63	0/2873
82	c6	0.43	1/939 (0.1%)	0.59	0/1256
83	d6	0.41	0/621	0.65	0/820
84	e6	0.37	0/2859	0.60	3/3864 (0.1%)
85	A6	0.89	0/22053	1.27	237/34324 (0.7%)
86	24	0.61	0/1731	1.55	47/2693 (1.7%)
86	C	0.60	0/1731	1.55	48/2693 (1.8%)
87	i4	0.84	0/242	1.33	4/375 (1.1%)
88	A	0.40	0/1403	0.68	0/1880
89	Z	0.40	0/3097	0.67	1/4190 (0.0%)
90	j	0.60	0/1805	1.36	29/2809 (1.0%)
91	n	0.34	0/1813	0.65	3/2443 (0.1%)
All	All	0.65	4/179304 (0.0%)	0.95	841/255288 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	Y2	0	2
4	D3	0	1
5	E3	0	7
6	F3	0	1
9	J3	0	1
10	K3	0	1
12	M3	0	2
13	N3	0	1
15	P3	0	2
16	Q3	0	2
17	R3	0	1
19	T3	0	1
21	V3	0	3
23	X3	0	6
24	Y3	0	1
25	Z3	0	1
26	O3	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
27	l3	0	1
31	53	0	4
38	d3	0	3
40	f3	0	6
42	h3	0	2
45	k3	0	2
50	q3	0	1
52	s3	0	2
57	D6	0	2
63	J6	0	1
64	K6	0	1
67	N6	0	1
68	O6	0	1
69	P6	0	1
71	R6	0	3
75	V6	0	1
82	c6	0	2
84	e6	0	1
88	A	0	6
89	Z	0	1
All	All	0	76

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A3	2688	C	C2-O2	-5.81	1.19	1.24
18	S3	57	SER	C-N	-5.78	1.20	1.34
2	A3	1984	A	N7-C5	-5.30	1.36	1.39
82	c6	55	CYS	CB-SG	-5.11	1.73	1.81

The worst 5 of 841 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	24	73	A	N7-C8-N9	15.03	121.31	113.80
86	C	73	A	N7-C8-N9	14.98	121.29	113.80
86	24	73	A	C8-N9-C4	-14.45	100.02	105.80
86	C	73	A	C8-N9-C4	-14.35	100.06	105.80
2	A3	1732	C	N1-C2-O2	13.99	127.30	118.90

There are no chirality outliers.

5 of 76 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D3	206	TYR	Peptide
5	E3	126	ASP	Peptide
5	E3	85	TRP	Peptide
1	Y2	21	ALA	Peptide
1	Y2	22	ALA	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	Y2	27/29 (93%)	20 (74%)	6 (22%)	1 (4%)	2	20
4	D3	234/305 (77%)	215 (92%)	18 (8%)	1 (0%)	30	67
5	E3	296/348 (85%)	262 (88%)	32 (11%)	2 (1%)	19	56
6	F3	248/311 (80%)	228 (92%)	20 (8%)	0	100	100
7	D	78/267 (29%)	66 (85%)	11 (14%)	1 (1%)	10	42
7	H3	93/267 (35%)	83 (89%)	9 (10%)	1 (1%)	12	46
8	I3	154/261 (59%)	147 (96%)	7 (4%)	0	100	100
9	J3	138/192 (72%)	127 (92%)	11 (8%)	0	100	100
10	K3	175/178 (98%)	151 (86%)	22 (13%)	2 (1%)	12	46
11	L3	113/145 (78%)	101 (89%)	12 (11%)	0	100	100
12	M3	285/296 (96%)	255 (90%)	27 (10%)	3 (1%)	12	46
13	N3	203/251 (81%)	186 (92%)	16 (8%)	1 (0%)	25	63
14	O3	150/175 (86%)	131 (87%)	18 (12%)	1 (1%)	19	56
15	P3	129/180 (72%)	117 (91%)	11 (8%)	1 (1%)	16	53
16	Q3	217/292 (74%)	193 (89%)	23 (11%)	1 (0%)	25	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	R3	138/149 (93%)	133 (96%)	5 (4%)	0	100	100
18	S3	154/205 (75%)	138 (90%)	16 (10%)	0	100	100
19	T3	164/206 (80%)	154 (94%)	10 (6%)	0	100	100
20	U3	109/153 (71%)	97 (89%)	12 (11%)	0	100	100
21	V3	183/216 (85%)	156 (85%)	24 (13%)	3 (2%)	8	37
22	W3	109/148 (74%)	103 (94%)	6 (6%)	0	100	100
23	X3	241/256 (94%)	210 (87%)	29 (12%)	2 (1%)	16	53
24	Y3	174/250 (70%)	162 (93%)	12 (7%)	0	100	100
25	Z3	118/161 (73%)	109 (92%)	9 (8%)	0	100	100
26	03	106/188 (56%)	91 (86%)	14 (13%)	1 (1%)	14	50
27	13	50/65 (77%)	46 (92%)	3 (6%)	1 (2%)	6	32
28	23	44/92 (48%)	42 (96%)	2 (4%)	0	100	100
29	33	93/188 (50%)	88 (95%)	5 (5%)	0	100	100
30	43	34/103 (33%)	32 (94%)	2 (6%)	0	100	100
31	53	368/423 (87%)	324 (88%)	42 (11%)	2 (0%)	25	63
32	63	313/380 (82%)	273 (87%)	40 (13%)	0	100	100
33	73	258/338 (76%)	234 (91%)	24 (9%)	0	100	100
34	93	105/137 (77%)	90 (86%)	15 (14%)	0	100	100
35	a3	78/142 (55%)	72 (92%)	6 (8%)	0	100	100
36	b3	146/215 (68%)	131 (90%)	15 (10%)	0	100	100
37	c3	271/332 (82%)	249 (92%)	21 (8%)	1 (0%)	30	67
38	d3	156/306 (51%)	142 (91%)	13 (8%)	1 (1%)	22	59
39	e3	211/279 (76%)	191 (90%)	20 (10%)	0	100	100
40	f3	125/212 (59%)	103 (82%)	21 (17%)	1 (1%)	16	53
41	g3	127/166 (76%)	114 (90%)	13 (10%)	0	100	100
42	h3	96/158 (61%)	86 (90%)	8 (8%)	2 (2%)	5	30
43	i3	95/128 (74%)	85 (90%)	10 (10%)	0	100	100
44	j3	83/123 (68%)	78 (94%)	4 (5%)	1 (1%)	11	43
45	k3	82/112 (73%)	67 (82%)	15 (18%)	0	100	100
46	l3	21/138 (15%)	21 (100%)	0	0	100	100
47	m3	43/128 (34%)	37 (86%)	6 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	o3	92/102 (90%)	85 (92%)	7 (8%)	0	100	100
49	p3	119/206 (58%)	109 (92%)	10 (8%)	0	100	100
50	q3	126/222 (57%)	117 (93%)	6 (5%)	3 (2%)	5	28
51	r3	140/196 (71%)	126 (90%)	14 (10%)	0	100	100
52	s3	366/467 (78%)	334 (91%)	32 (9%)	0	100	100
55	B6	215/296 (73%)	198 (92%)	17 (8%)	0	100	100
56	C6	130/167 (78%)	119 (92%)	11 (8%)	0	100	100
57	D6	316/430 (74%)	282 (89%)	33 (10%)	1 (0%)	37	72
58	E6	120/125 (96%)	113 (94%)	6 (5%)	1 (1%)	16	53
59	F6	197/242 (81%)	184 (93%)	13 (7%)	0	100	100
60	G6	301/396 (76%)	281 (93%)	20 (7%)	0	100	100
61	H6	120/201 (60%)	105 (88%)	14 (12%)	1 (1%)	16	53
62	I6	134/194 (69%)	123 (92%)	11 (8%)	0	100	100
63	J6	106/138 (77%)	95 (90%)	11 (10%)	0	100	100
64	K6	99/128 (77%)	97 (98%)	2 (2%)	0	100	100
65	L6	162/257 (63%)	154 (95%)	8 (5%)	0	100	100
66	M6	114/137 (83%)	103 (90%)	11 (10%)	0	100	100
67	N6	105/130 (81%)	98 (93%)	7 (7%)	0	100	100
68	O6	183/258 (71%)	163 (89%)	20 (11%)	0	100	100
69	P6	94/142 (66%)	84 (89%)	10 (11%)	0	100	100
70	Q6	84/87 (97%)	77 (92%)	7 (8%)	0	100	100
71	R6	240/360 (67%)	211 (88%)	29 (12%)	0	100	100
72	S6	124/190 (65%)	115 (93%)	9 (7%)	0	100	100
73	T6	160/173 (92%)	144 (90%)	16 (10%)	0	100	100
74	U6	171/205 (83%)	164 (96%)	7 (4%)	0	100	100
75	V6	320/414 (77%)	283 (88%)	36 (11%)	1 (0%)	37	72
76	W6	95/187 (51%)	85 (90%)	10 (10%)	0	100	100
77	X6	310/398 (78%)	265 (86%)	43 (14%)	2 (1%)	22	59
78	Y6	106/395 (27%)	97 (92%)	9 (8%)	0	100	100
79	Z6	85/106 (80%)	81 (95%)	4 (5%)	0	100	100
80	a6	197/218 (90%)	182 (92%)	15 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
81	b6	252/323 (78%)	224 (89%)	28 (11%)	0	100	100
82	c6	114/118 (97%)	97 (85%)	17 (15%)	0	100	100
83	d6	67/199 (34%)	63 (94%)	4 (6%)	0	100	100
84	e6	362/689 (52%)	328 (91%)	30 (8%)	4 (1%)	12	46
88	A	158/206 (77%)	142 (90%)	16 (10%)	0	100	100
89	Z	392/452 (87%)	352 (90%)	39 (10%)	1 (0%)	37	72
91	n	230/229 (100%)	209 (91%)	21 (9%)	0	100	100
All	All	13541/18977 (71%)	12229 (90%)	1268 (9%)	44 (0%)	38	72

5 of 44 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
40	f3	51	LYS
50	q3	43	GLU
84	e6	68	VAL
10	K3	160	GLN
12	M3	288	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D3	190/245 (78%)	189 (100%)	1 (0%)	86	90
5	E3	255/290 (88%)	252 (99%)	3 (1%)	67	79
6	F3	217/262 (83%)	216 (100%)	1 (0%)	86	90
7	D	73/228 (32%)	71 (97%)	2 (3%)	40	60
7	H3	86/228 (38%)	85 (99%)	1 (1%)	67	79
8	I3	145/232 (62%)	145 (100%)	0	100	100
9	J3	113/150 (75%)	113 (100%)	0	100	100
10	K3	155/156 (99%)	155 (100%)	0	100	100
11	L3	98/124 (79%)	98 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	M3	245/249 (98%)	240 (98%)	5 (2%)	50	69
13	N3	172/211 (82%)	172 (100%)	0	100	100
14	O3	133/150 (89%)	132 (99%)	1 (1%)	79	85
15	P3	115/155 (74%)	114 (99%)	1 (1%)	75	83
16	Q3	201/256 (78%)	199 (99%)	2 (1%)	73	81
17	R3	118/126 (94%)	117 (99%)	1 (1%)	79	85
18	S3	141/180 (78%)	141 (100%)	0	100	100
19	T3	146/176 (83%)	145 (99%)	1 (1%)	81	87
20	U3	99/135 (73%)	99 (100%)	0	100	100
21	V3	169/191 (88%)	166 (98%)	3 (2%)	54	71
22	W3	91/119 (76%)	91 (100%)	0	100	100
23	X3	217/227 (96%)	215 (99%)	2 (1%)	75	83
24	Y3	159/223 (71%)	158 (99%)	1 (1%)	84	88
25	Z3	111/147 (76%)	111 (100%)	0	100	100
26	03	97/164 (59%)	96 (99%)	1 (1%)	73	81
27	13	49/60 (82%)	48 (98%)	1 (2%)	50	69
28	23	40/72 (56%)	40 (100%)	0	100	100
29	33	88/166 (53%)	88 (100%)	0	100	100
30	43	35/89 (39%)	35 (100%)	0	100	100
31	53	337/368 (92%)	333 (99%)	4 (1%)	67	79
32	63	266/332 (80%)	264 (99%)	2 (1%)	79	85
33	73	242/303 (80%)	240 (99%)	2 (1%)	79	85
34	93	91/112 (81%)	91 (100%)	0	100	100
35	a3	78/133 (59%)	78 (100%)	0	100	100
36	b3	130/186 (70%)	129 (99%)	1 (1%)	79	85
37	c3	241/288 (84%)	241 (100%)	0	100	100
38	d3	151/274 (55%)	149 (99%)	2 (1%)	65	77
39	e3	188/236 (80%)	188 (100%)	0	100	100
40	f3	117/188 (62%)	117 (100%)	0	100	100
41	g3	119/148 (80%)	119 (100%)	0	100	100
42	h3	95/148 (64%)	95 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	i3	86/110 (78%)	86 (100%)	0	100	100
44	j3	68/97 (70%)	68 (100%)	0	100	100
45	k3	74/90 (82%)	73 (99%)	1 (1%)	62	76
46	l3	23/116 (20%)	23 (100%)	0	100	100
47	m3	40/113 (35%)	39 (98%)	1 (2%)	42	62
48	o3	80/87 (92%)	79 (99%)	1 (1%)	65	77
49	p3	117/181 (65%)	117 (100%)	0	100	100
50	q3	110/178 (62%)	109 (99%)	1 (1%)	75	83
51	r3	133/169 (79%)	133 (100%)	0	100	100
52	s3	326/381 (86%)	322 (99%)	4 (1%)	67	79
55	B6	191/249 (77%)	190 (100%)	1 (0%)	86	90
56	C6	115/143 (80%)	113 (98%)	2 (2%)	56	72
57	D6	269/357 (75%)	266 (99%)	3 (1%)	70	80
58	E6	104/107 (97%)	104 (100%)	0	100	100
59	F6	178/209 (85%)	177 (99%)	1 (1%)	84	88
60	G6	265/342 (78%)	264 (100%)	1 (0%)	89	91
61	H6	112/180 (62%)	110 (98%)	2 (2%)	54	71
62	I6	104/147 (71%)	103 (99%)	1 (1%)	73	81
63	J6	93/118 (79%)	92 (99%)	1 (1%)	70	80
64	K6	91/113 (80%)	91 (100%)	0	100	100
65	L6	152/226 (67%)	149 (98%)	3 (2%)	50	69
66	M6	95/113 (84%)	94 (99%)	1 (1%)	70	80
67	N6	93/115 (81%)	93 (100%)	0	100	100
68	O6	166/230 (72%)	166 (100%)	0	100	100
69	P6	87/123 (71%)	87 (100%)	0	100	100
70	Q6	78/79 (99%)	77 (99%)	1 (1%)	65	77
71	R6	224/318 (70%)	223 (100%)	1 (0%)	89	91
72	S6	109/164 (66%)	109 (100%)	0	100	100
73	T6	150/157 (96%)	150 (100%)	0	100	100
74	U6	149/174 (86%)	148 (99%)	1 (1%)	81	87
75	V6	295/364 (81%)	292 (99%)	3 (1%)	73	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
76	W6	84/158 (53%)	83 (99%)	1 (1%)	67	79
77	X6	275/351 (78%)	273 (99%)	2 (1%)	81	87
78	Y6	99/357 (28%)	98 (99%)	1 (1%)	73	81
79	Z6	80/95 (84%)	80 (100%)	0	100	100
80	a6	176/190 (93%)	174 (99%)	2 (1%)	70	80
81	b6	237/291 (81%)	234 (99%)	3 (1%)	65	77
82	c6	99/101 (98%)	97 (98%)	2 (2%)	50	69
83	d6	63/166 (38%)	63 (100%)	0	100	100
84	e6	226/609 (37%)	225 (100%)	1 (0%)	89	91
88	A	151/190 (80%)	150 (99%)	1 (1%)	81	87
89	Z	328/371 (88%)	327 (100%)	1 (0%)	91	92
91	n	184/181 (102%)	181 (98%)	3 (2%)	58	74
All	All	11992/16337 (73%)	11907 (99%)	85 (1%)	80	87

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
65	L6	146	HIS
80	a6	121	LYS
66	M6	13	ARG
75	V6	337	LEU
82	c6	37	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 151 such sidechains are listed below:

Mol	Chain	Res	Type
73	T6	128	ASN
84	e6	122	ASN
74	U6	186	ASN
77	X6	90	GLN
91	n	225	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	A3	1490/1559 (95%)	437 (29%)	31 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	B3	51/69 (73%)	15 (29%)	1 (1%)
53	u3	1/2 (50%)	1 (100%)	0
85	A6	921/954 (96%)	232 (25%)	14 (1%)
86	24	73/73 (100%)	41 (56%)	5 (6%)
86	C	73/73 (100%)	42 (57%)	5 (6%)
87	i4	9/10 (90%)	2 (22%)	0
90	j	74/76 (97%)	23 (31%)	0
All	All	2692/2816 (95%)	793 (29%)	56 (2%)

5 of 793 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	A3	1674	A
2	A3	1676	A
2	A3	1677	C
2	A3	1678	C
2	A3	1679	U

5 of 56 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A3	3041	U
86	C	71	C
85	A6	1025	U
86	C	70	A
86	24	70	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 148 ligands modelled in this entry, 141 are monoatomic - leaving 7 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
99	MLI	n	304	-	6,6,6	1.48	0	7,7,7	1.45	1 (14%)
96	GCP	Z	501	-	27,34,34	3.44	13 (48%)	34,54,54	1.86	7 (20%)
99	MLI	n	303	-	6,6,6	1.33	0	7,7,7	1.34	0
99	MLI	n	302	-	6,6,6	1.36	0	7,7,7	1.30	0
93	SPD	A3	3396	-	9,9,9	0.34	0	8,8,8	0.59	0
95	GDP	X6	500	-	24,30,30	1.05	1 (4%)	30,47,47	1.58	6 (20%)
98	SO4	n	301	-	4,4,4	0.17	0	6,6,6	0.10	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
99	MLI	n	304	-	-	2/4/4/4	-
96	GCP	Z	501	-	-	4/15/38/38	0/3/3/3
99	MLI	n	303	-	-	4/4/4/4	-
99	MLI	n	302	-	-	2/4/4/4	-
93	SPD	A3	3396	-	-	4/7/7/7	-
95	GDP	X6	500	-	-	4/12/32/32	0/3/3/3

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
96	Z	501	GCP	O4'-C4'	8.82	1.64	1.45
96	Z	501	GCP	C3'-C4'	-7.75	1.33	1.53
96	Z	501	GCP	O4'-C1'	-6.89	1.31	1.41
96	Z	501	GCP	O6-C6	5.61	1.38	1.24
96	Z	501	GCP	C2-N2	4.97	1.43	1.33

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
96	Z	501	GCP	C2-N3-C4	4.79	120.83	115.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
95	X6	500	GDP	PA-O3A-PB	-4.57	117.16	132.83
96	Z	501	GCP	N3-C2-N1	-4.57	121.13	127.22
96	Z	501	GCP	C4-C5-C6	-4.05	116.93	120.80
95	X6	500	GDP	C3'-C2'-C1'	3.93	106.90	100.98

There are no chirality outliers.

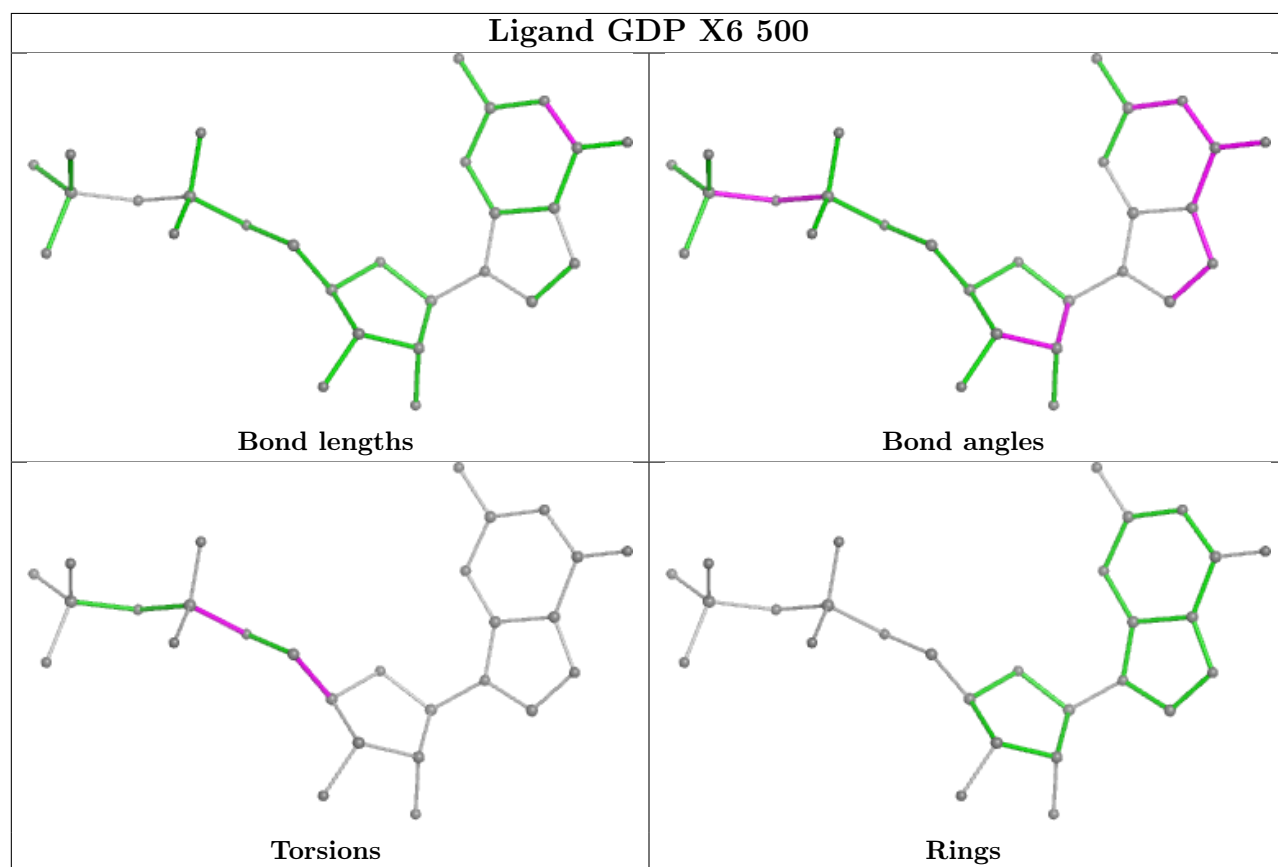
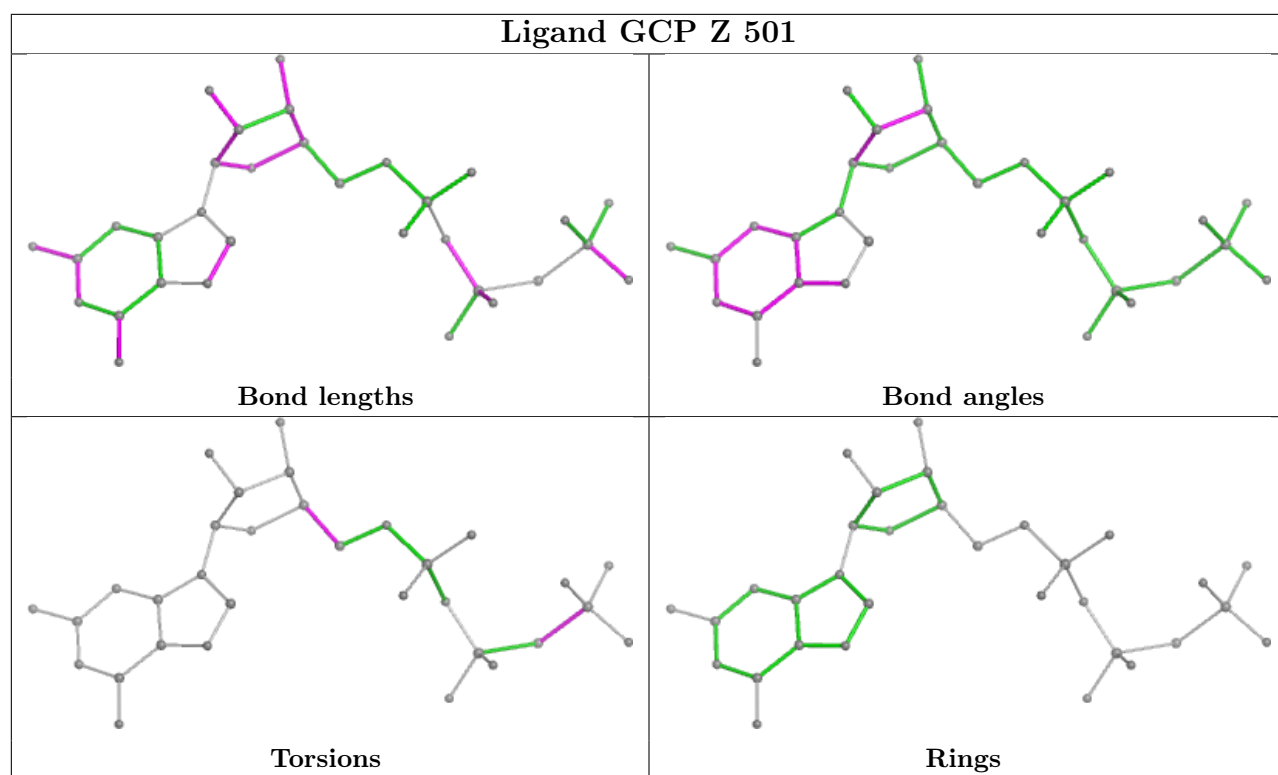
5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
95	X6	500	GDP	C5'-O5'-PA-O1A
96	Z	501	GCP	PB-C3B-PG-O1G
96	Z	501	GCP	PB-C3B-PG-O2G
96	Z	501	GCP	PB-C3B-PG-O3G
95	X6	500	GDP	C3'-C4'-C5'-O5'

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
90	j	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	j	16:C	O3'	18:G	P	5.97

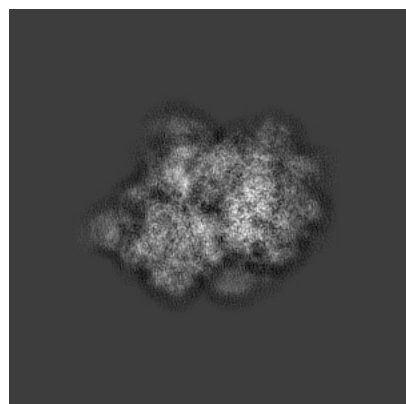
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11642. These allow visual inspection of the internal detail of the map and identification of artifacts.

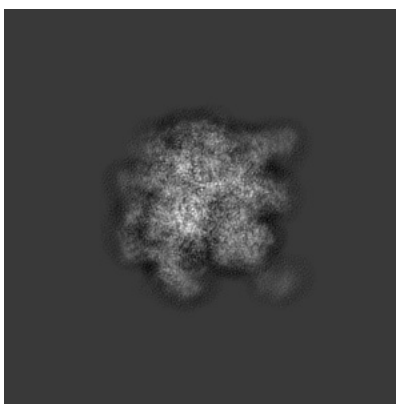
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

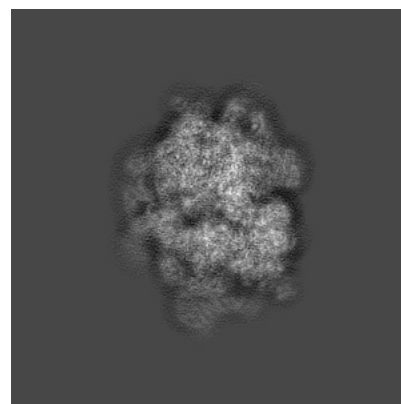
6.1.1 Primary map



X

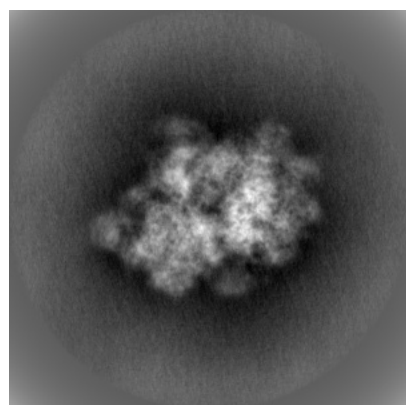


Y

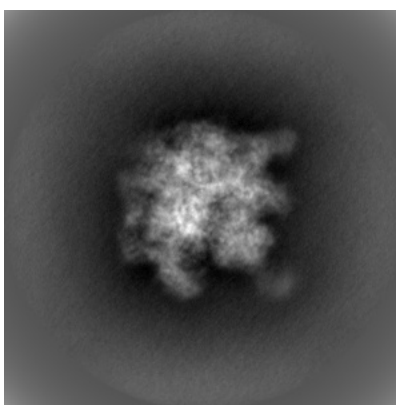


Z

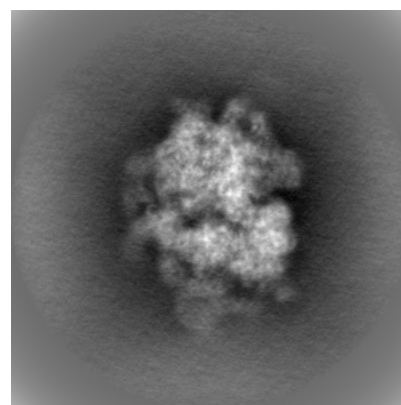
6.1.2 Raw map



X



Y

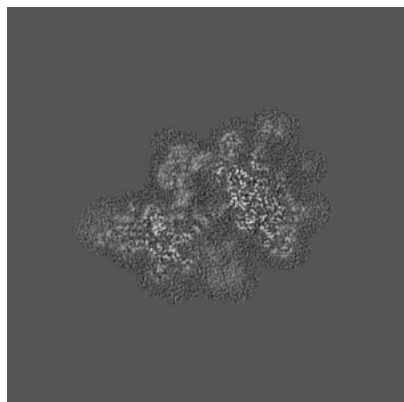


Z

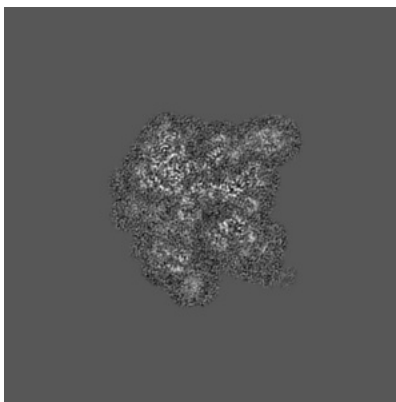
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

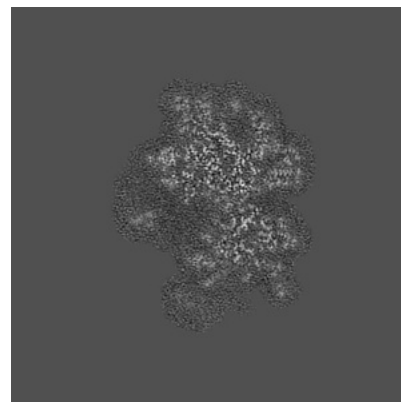
6.2.1 Primary map



X Index: 256

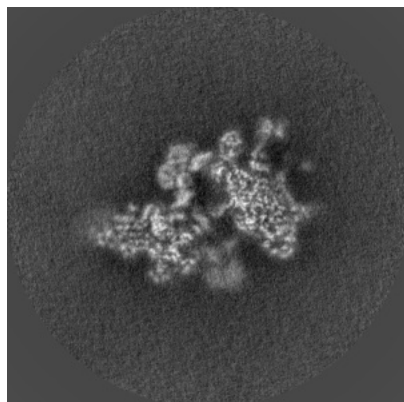


Y Index: 256

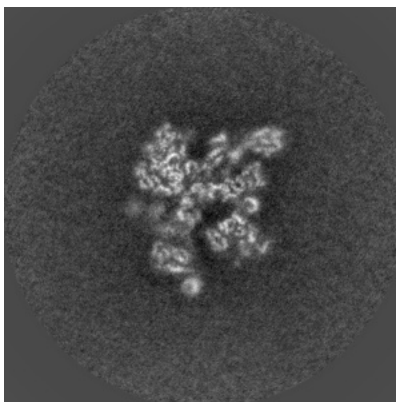


Z Index: 256

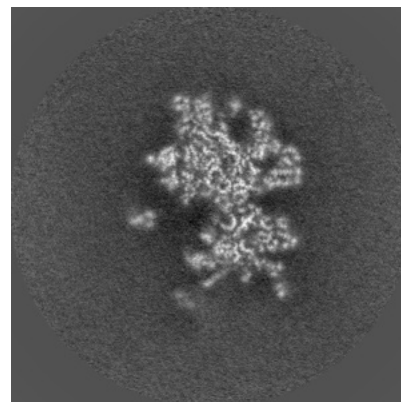
6.2.2 Raw map



X Index: 256



Y Index: 256

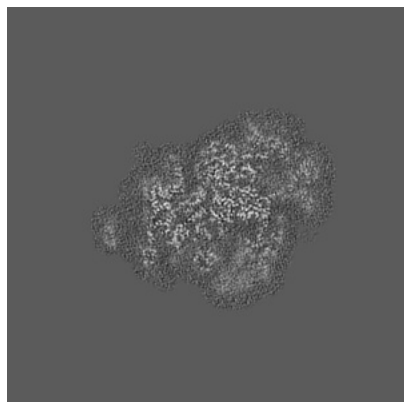


Z Index: 256

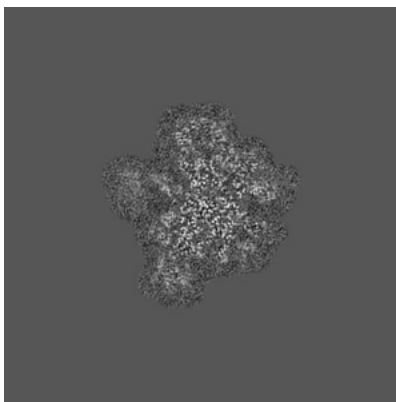
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

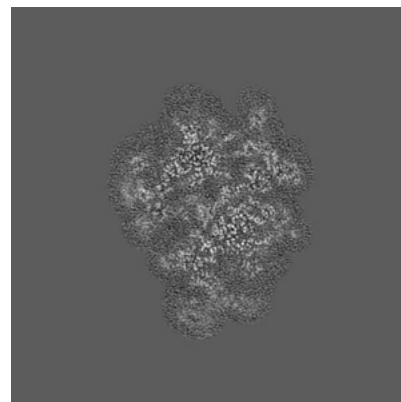
6.3.1 Primary map



X Index: 288

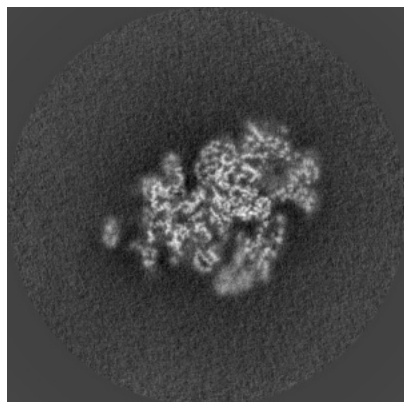


Y Index: 304

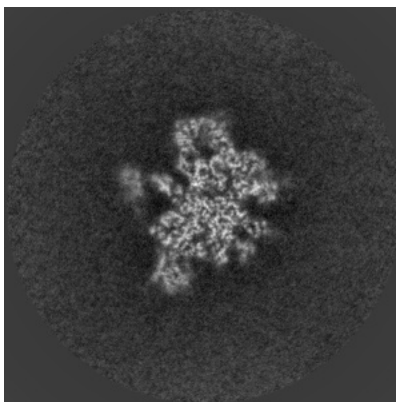


Z Index: 228

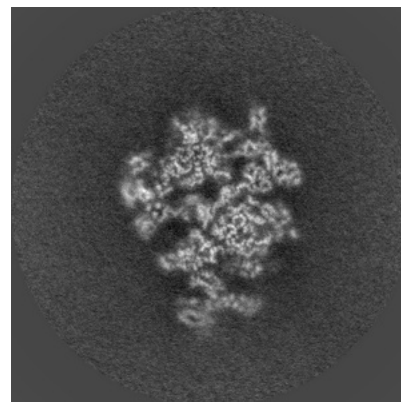
6.3.2 Raw map



X Index: 287



Y Index: 305

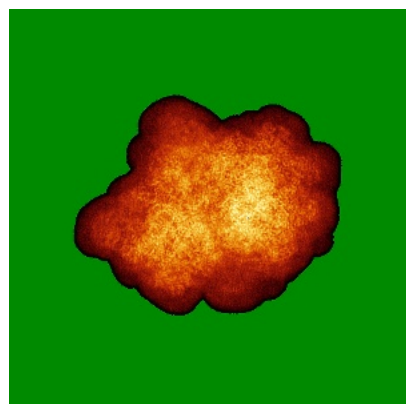


Z Index: 228

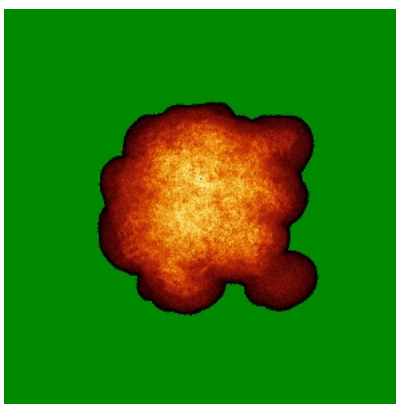
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

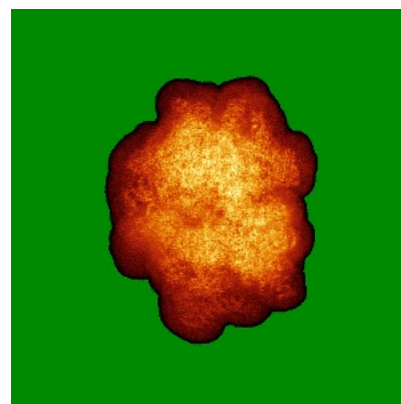
6.4.1 Primary map



X

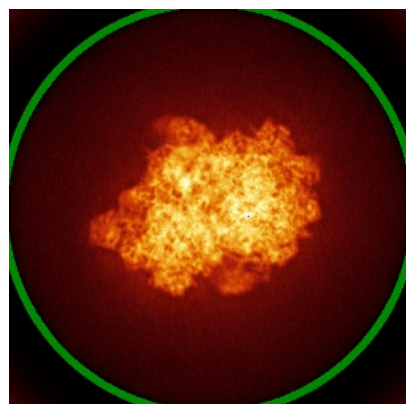


Y

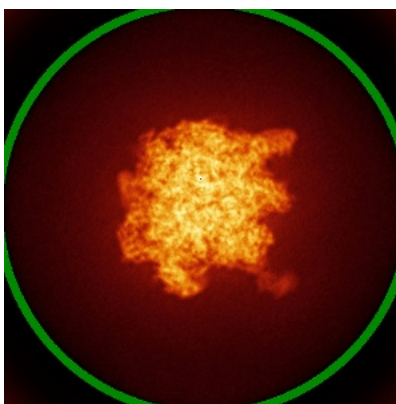


Z

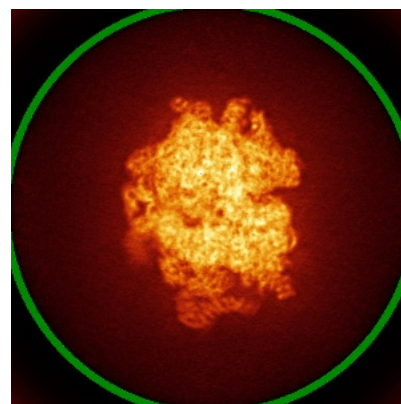
6.4.2 Raw map



X



Y

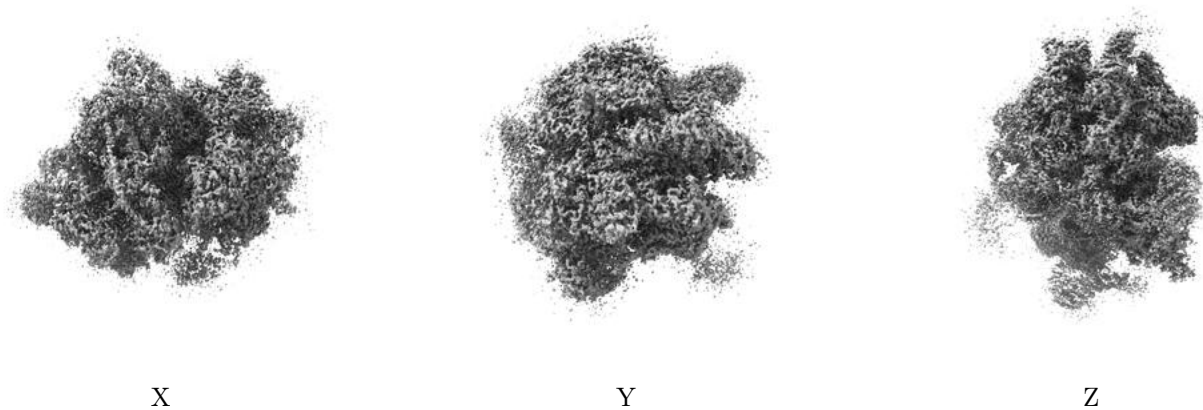


Z

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 0.05. 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.

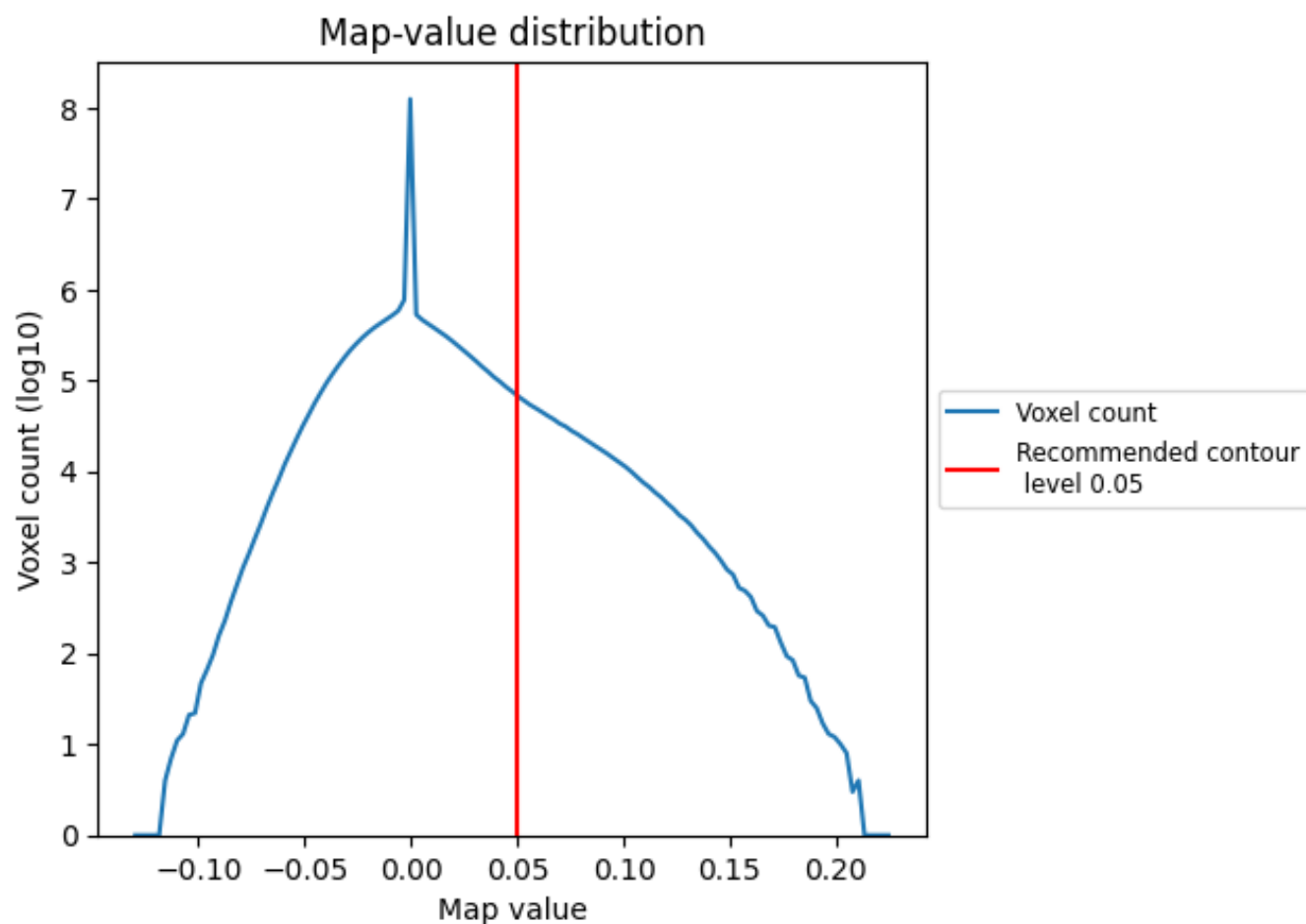
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

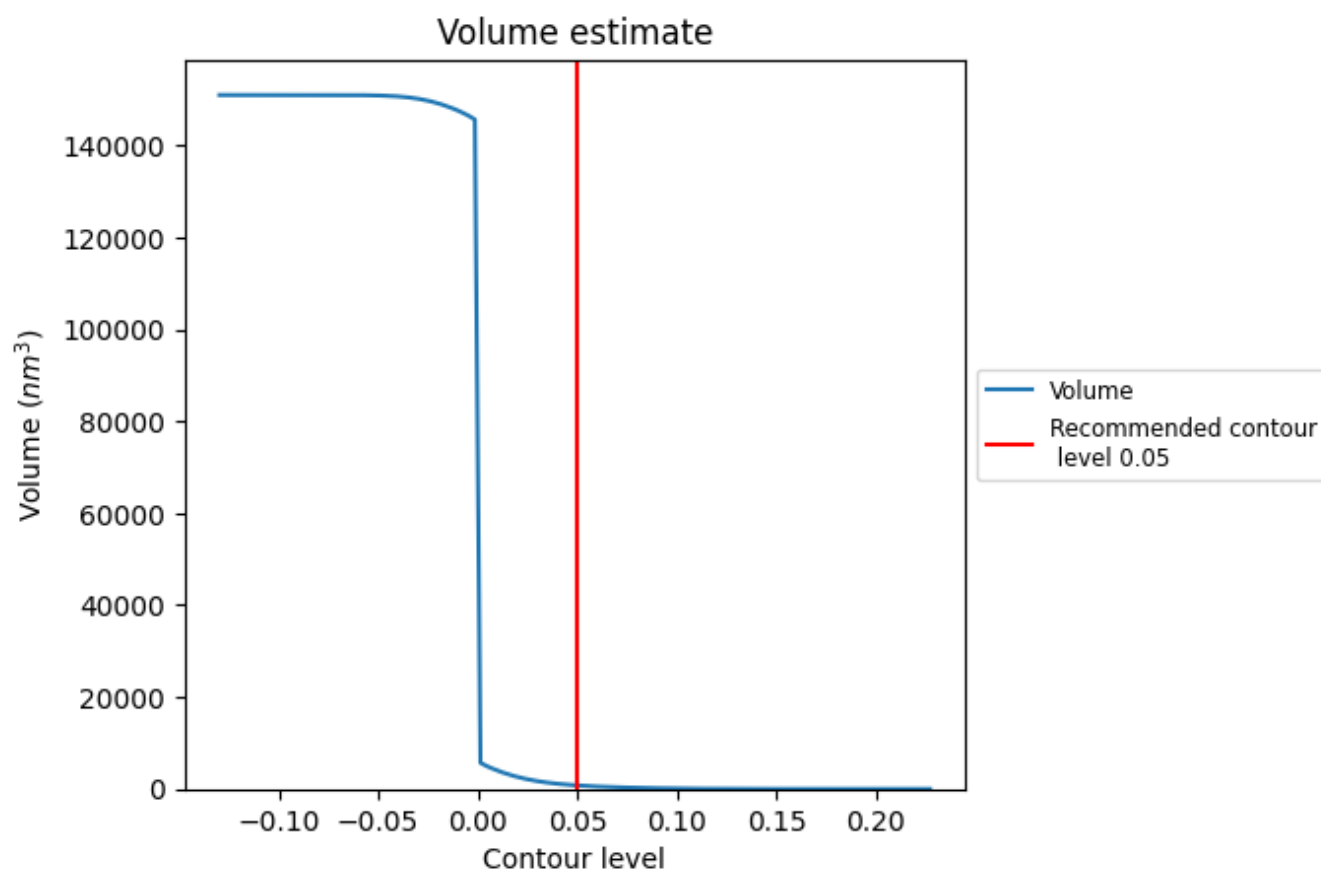
This section contains the results of statistical analysis of the map.

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.

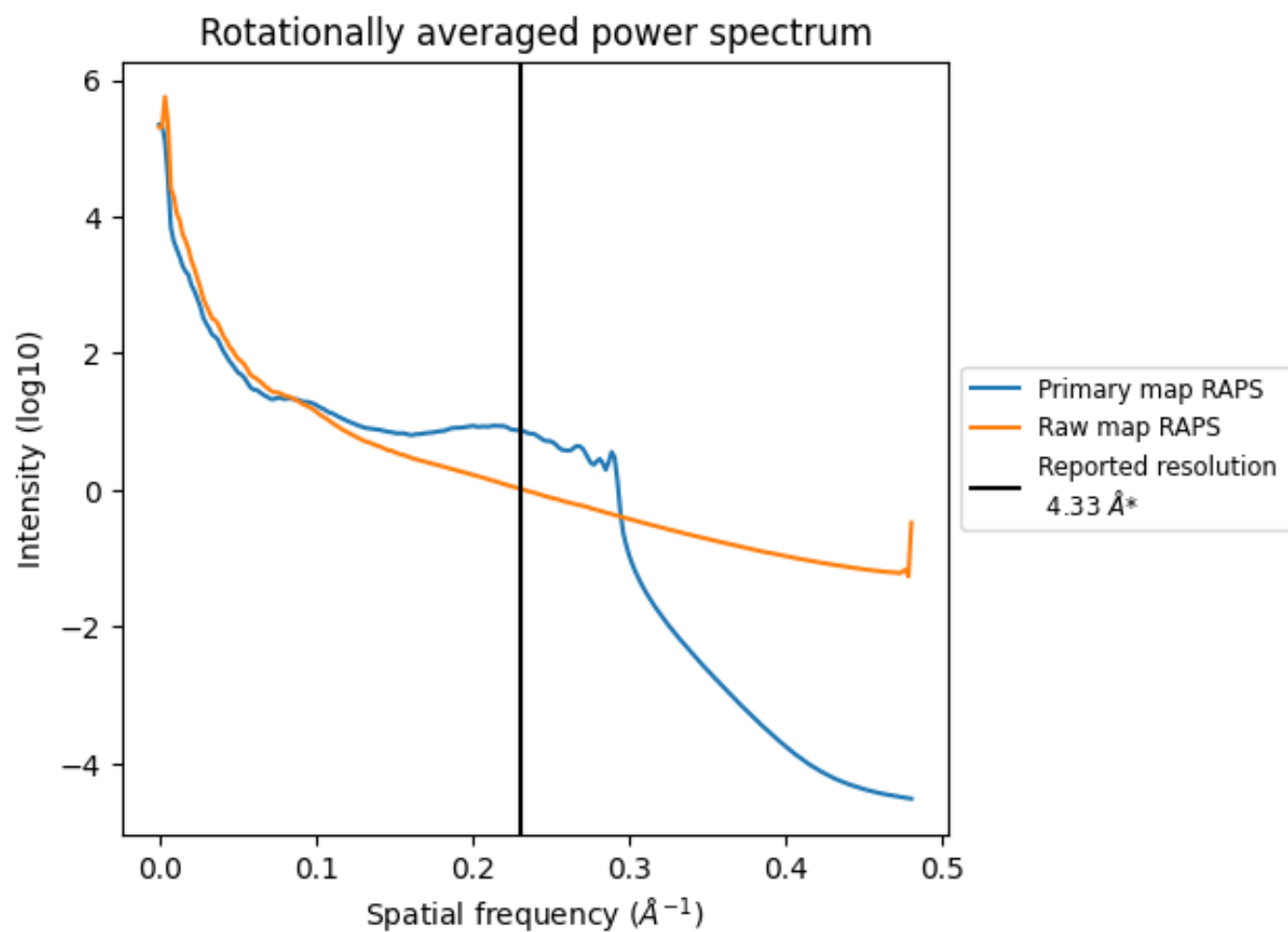
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 775 nm^3 ; this corresponds to an approximate mass of 700 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 ⓘ

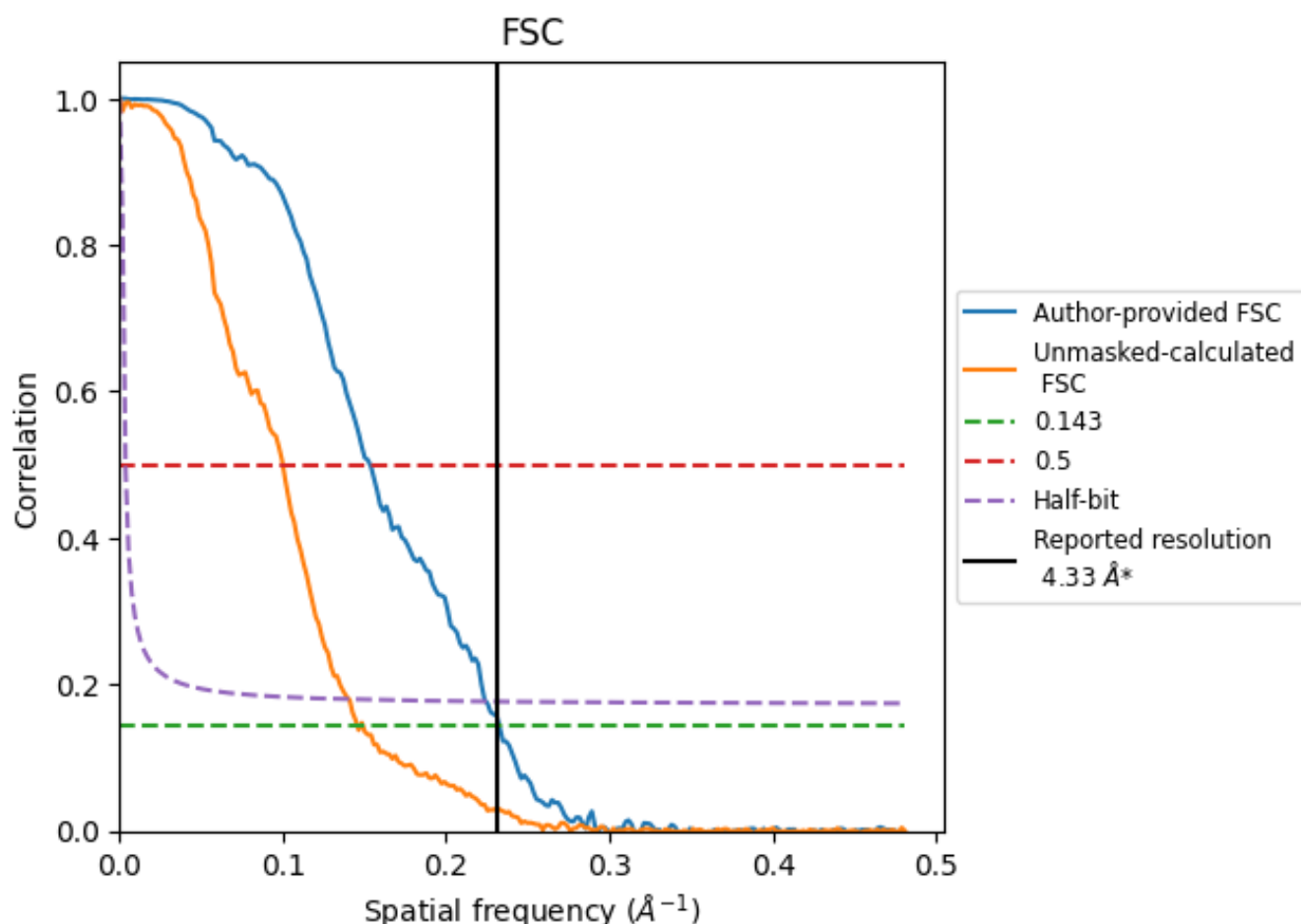


*Reported resolution corresponds to spatial frequency of 0.231 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.231 Å⁻¹

8.2 Resolution estimates [i](#)

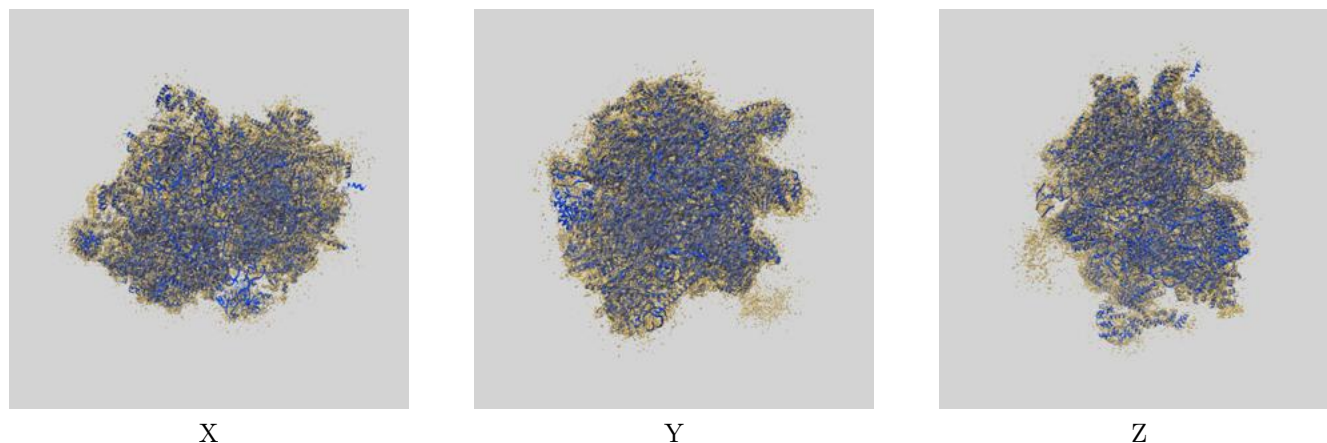
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.33	-	-
Author-provided FSC curve	4.30	6.52	4.46
Unmasked-calculated*	6.86	10.00	7.11

*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 6.86 differs from the reported value 4.33 by more than 10 %

9 Map-model fit [i](#)

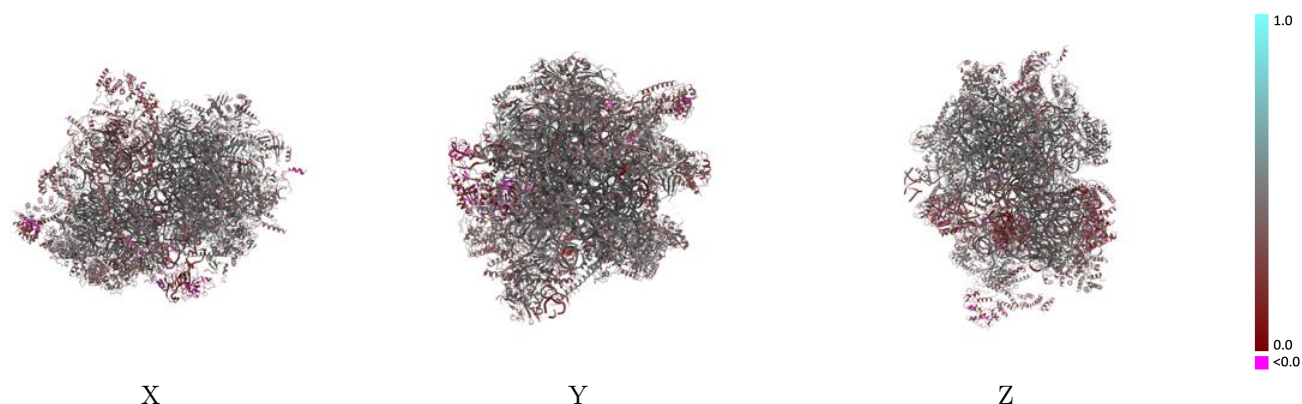
This section contains information regarding the fit between EMDB map EMD-11642 and PDB model 7A5G. Per-residue inclusion information can be found in section [3](#) on page [25](#).

9.1 Map-model overlay [i](#)



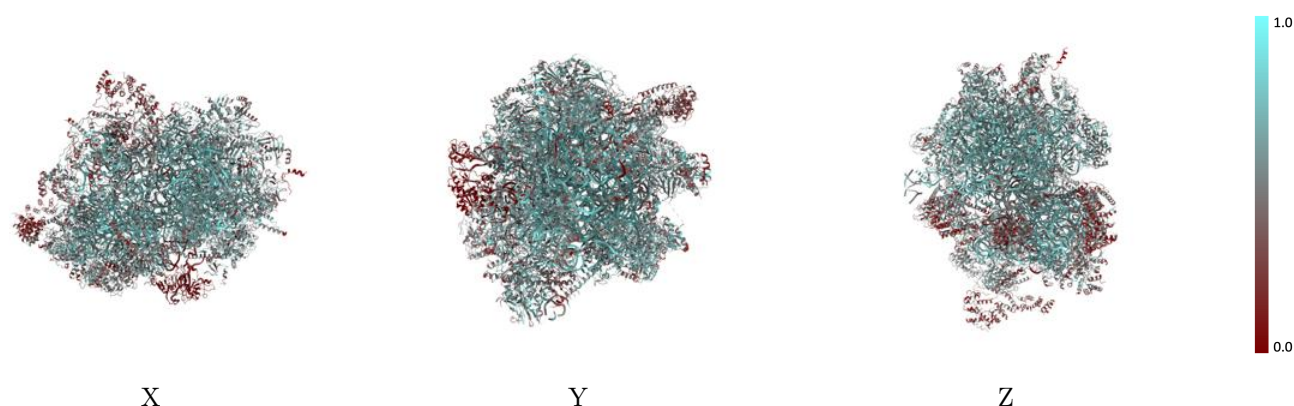
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



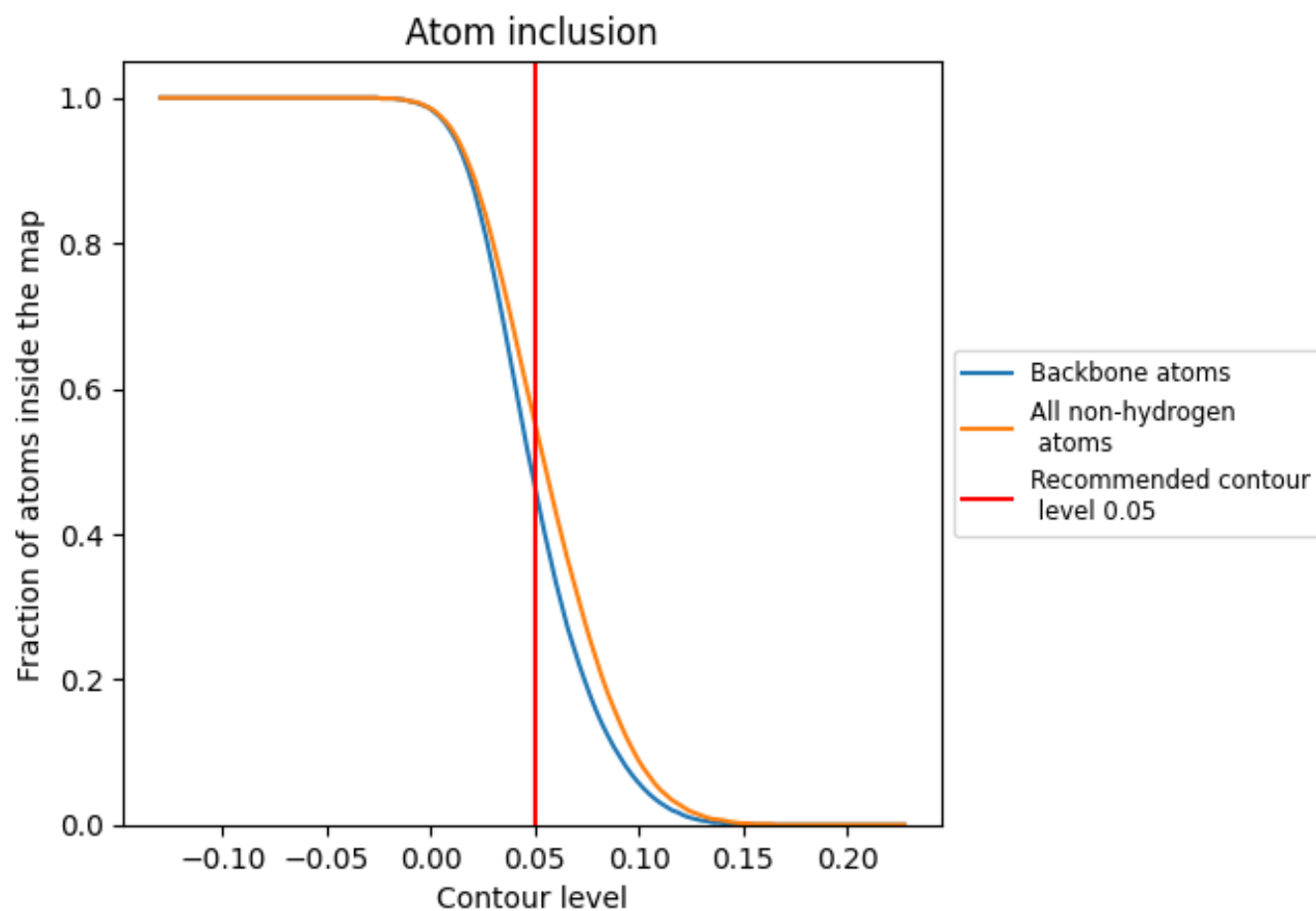
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 46% of all backbone atoms, 55% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5530	 0.4020
03	 0.5490	 0.4420
13	 0.4950	 0.4280
23	 0.6640	 0.4860
24	 0.4210	 0.2530
33	 0.6320	 0.4910
43	 0.6680	 0.4910
53	 0.5790	 0.4320
63	 0.5600	 0.4090
73	 0.5000	 0.3880
93	 0.5610	 0.4350
A	 0.2900	 0.2890
A3	 0.7370	 0.4360
A5	 0.0000	 0.1120
A6	 0.7380	 0.4240
B3	 0.6540	 0.3240
B6	 0.6170	 0.4460
C	 0.0410	 0.0670
C6	 0.5480	 0.4550
D	 0.1030	 0.1770
D3	 0.6270	 0.4780
D6	 0.5020	 0.4360
E3	 0.6030	 0.4540
E6	 0.5290	 0.4340
F3	 0.5860	 0.4510
F6	 0.4730	 0.3890
G6	 0.5030	 0.4060
H3	 0.4600	 0.4020
H6	 0.5140	 0.4260
I3	 0.3610	 0.3280
I6	 0.5340	 0.4380
J3	 0.2250	 0.2590
J6	 0.4910	 0.4530
K3	 0.6190	 0.4640
K6	 0.5970	 0.4460







































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Chain	Atom inclusion	Q-score
L3	 0.5080	 0.4490
L6	 0.5530	 0.4290
M3	 0.5750	 0.4420
M6	 0.4790	 0.3990
N3	 0.5640	 0.4580
N6	 0.5370	 0.4490
O3	 0.5880	 0.4420
O6	 0.4860	 0.3900
P3	 0.5930	 0.4420
P6	 0.5600	 0.4380
Q3	 0.5100	 0.4330
Q6	 0.5500	 0.4380
R3	 0.6200	 0.4690
R6	 0.4360	 0.3750
S3	 0.6210	 0.4670
S6	 0.4820	 0.3990
T3	 0.5790	 0.4650
T6	 0.5500	 0.4280
U3	 0.6000	 0.4570
U6	 0.4530	 0.3560
V3	 0.5020	 0.4020
V6	 0.2740	 0.2700
W3	 0.6360	 0.4890
W6	 0.5440	 0.4300
X3	 0.5290	 0.4150
X6	 0.4640	 0.3570
Y2	 0.1660	 0.2790
Y3	 0.6020	 0.4440
Y6	 0.4290	 0.3500
Z	 0.2600	 0.2600
Z3	 0.6350	 0.4730
Z6	 0.4680	 0.3970
a3	 0.5910	 0.4530
a6	 0.3910	 0.3510
b3	 0.6020	 0.4580
b6	 0.4350	 0.3700
c3	 0.5340	 0.4080
c6	 0.4140	 0.3970
d3	 0.4950	 0.3930
d6	 0.5450	 0.4520
e3	 0.3240	 0.2840
e6	 0.2880	 0.2730

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Chain	Atom inclusion	Q-score
f3	 0.4560	 0.3670
g3	 0.5770	 0.4400
h3	 0.4740	 0.3670
i3	 0.6100	 0.4690
i4	 0.6710	 0.4480
j	 0.4650	 0.2250
j3	 0.5780	 0.4350
k3	 0.3260	 0.2920
l3	 0.5390	 0.3730
m3	 0.4900	 0.4010
n	 0.0510	 0.1720
o3	 0.6430	 0.4760
p3	 0.4580	 0.3880
q3	 0.4910	 0.3990
r3	 0.6450	 0.4590
s3	 0.5800	 0.4340
t3	 0.2070	 0.2150
u3	 0.1910	 0.3380