



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 10:42 AM UTC

PDB ID : 7A5K / pdb_00007a5k
EMDB ID : EMD-11646
Title : Structure of the human mitoribosome in the post translocation state bound to mtEF-G1
Authors : Desai, N.; Yang, H.; Chandrasekaran, V.; Kazi, R.; Minczuk, M.; Ramakrishnan, V.
Deposited on : 2020-08-21
Resolution : 3.70 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

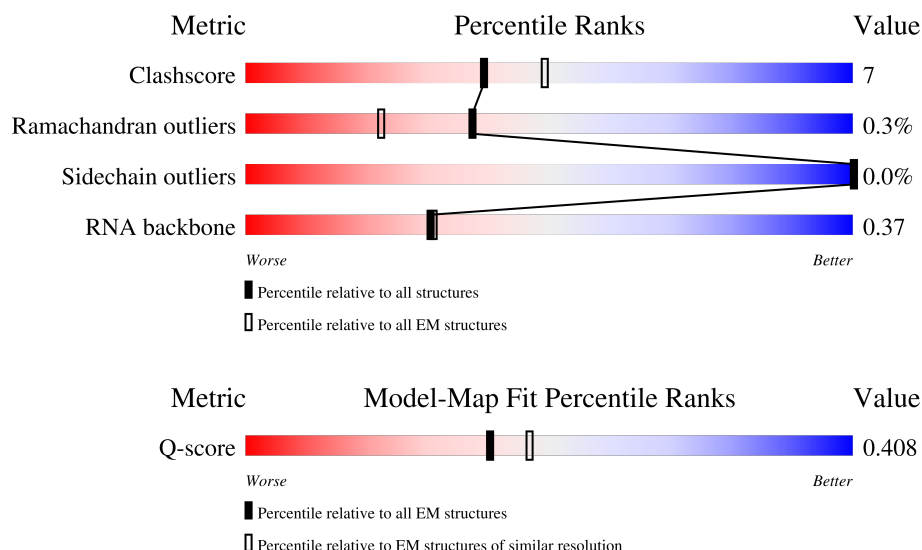
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.70 Å.

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



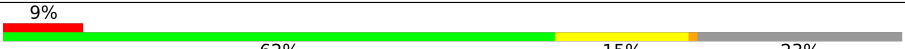
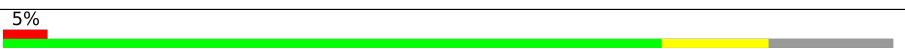
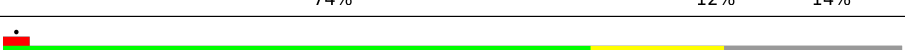
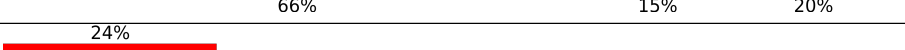
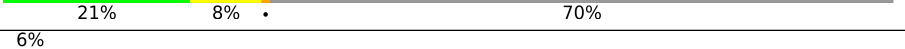
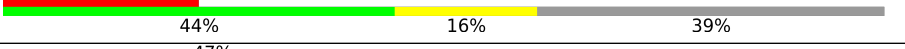
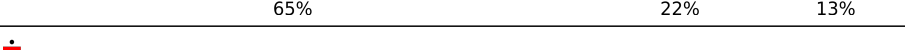
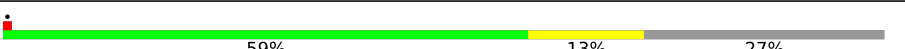
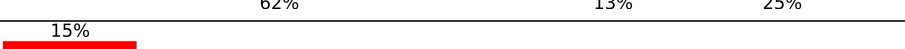
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

Mol	Chain	Length	Quality of chain
1	r1	751	
2	Y2	29	
3	8	1559	

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Mol	Chain	Length	Quality of chain
3	A3	1559	
4	B3	73	
5	D3	305	
6	E3	348	
7	F3	311	
8	D	267	
8	H3	267	
9	I3	261	
10	J3	192	
11	K3	178	
12	L3	145	
13	M3	296	
14	N3	251	
15	O3	175	
16	P3	179	
17	Q3	292	
18	R3	149	
19	S3	205	
20	T3	212	
21	U3	153	
22	V3	216	
23	W3	148	
24	X3	256	
25	Y3	250	
26	Z3	161	

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Mol	Chain	Length	Quality of chain
27	03	188	
28	13	65	
29	23	92	
30	33	188	
31	43	103	
32	53	423	
33	63	380	
34	73	338	
35	93	137	
36	a3	142	
37	b3	155	
38	c3	332	
39	d3	306	
40	e3	279	
41	f3	194	
42	g3	166	
43	h3	158	
44	i3	128	
45	j3	123	
46	k3	112	
47	l3	138	
48	m3	128	
49	o3	102	
50	p3	206	
51	q3	222	

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Mol	Chain	Length	Quality of chain
52	r3	196	
53	s3	439	
54	u3	2	
55	A5	435	
56	B6	296	
57	C6	167	
58	D6	430	
59	E6	125	
60	F6	242	
61	G6	396	
62	H6	201	
63	I6	194	
64	J6	138	
65	K6	128	
66	L6	257	
67	M6	137	
68	N6	130	
69	O6	258	
70	P6	142	
71	Q6	87	
72	R6	360	
73	S6	190	
74	T6	173	
75	U6	205	
76	V6	414	

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Mol	Chain	Length	Quality of chain
77	W6	187	
78	X6	398	
79	Y6	395	
80	Z6	106	
81	a6	218	
82	b6	323	
83	c6	118	
84	d6	199	
85	e6	689	
86	A6	954	
87	24	73	
87	FE	73	
88	A	206	
89	n	286	
90	B	28	

2 Entry composition

There are 95 unique types of molecules in this entry. The entry contains 171122 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 Elongation factor G, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	r1	696	Total	C	N	O	S	0	0
			5452	3435	940	1044	33		

- Molecule 2 is a protein called nascent chain.

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

- Molecule 3 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A3	1503	Total	C	N	O	P	0	0
			31913	14319	5761	10330	1503		
3	8	8	Total	C	N	O	P	0	0
			175	79	37	51	8		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A3	3107	U	UNK	conflict	GB 1025814679
8	663	U	UNK	conflict	GB 1025814679

- Molecule 4 is a RNA chain called mt-tRNAVal.

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

- Molecule 5 is a protein called 39S ribosomal protein L2, mitochondrial.

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

- Molecule 6 is a protein called 39S ribosomal protein L3, mitochondrial.

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

- Molecule 7 is a protein called 39S ribosomal protein L4, mitochondrial.

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

- Molecule 8 is a protein called 39S ribosomal protein L9, mitochondrial.

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

- Molecule 9 is a protein called 39S ribosomal protein L10, mitochondrial.

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

- Molecule 10 is a protein called 39S ribosomal protein L11, mitochondrial.

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

- Molecule 11 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 12 is a protein called 39S ribosomal protein L14, mitochondrial.

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

- Molecule 13 is a protein called 39S ribosomal protein L15, mitochondrial.

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

- Molecule 14 is a protein called 39S ribosomal protein L16, mitochondrial.

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

- Molecule 15 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 16 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

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

- Molecule 17 is a protein called 39S ribosomal protein L19, mitochondrial.

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

- Molecule 18 is a protein called 39S ribosomal protein L20, mitochondrial.

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

- Molecule 19 is a protein called 39S ribosomal protein L21, mitochondrial.

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

- Molecule 20 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 21 is a protein called 39S ribosomal protein L23, mitochondrial.

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

- Molecule 22 is a protein called 39S ribosomal protein L24, mitochondrial.

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

- Molecule 23 is a protein called 39S ribosomal protein L27, mitochondrial.

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

- Molecule 24 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	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 25 is a protein called 39S ribosomal protein L47, mitochondrial.

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

- Molecule 26 is a protein called 39S ribosomal protein L30, mitochondrial.

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

- Molecule 27 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	03	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 28 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	13	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

- Molecule 29 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	23	46	Total	C	N	O	S	0	0
			376	233	83	59	1		

- Molecule 30 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	33	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 31 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	43	36	Total	C	N	O	S	0	0
			322	203	70	46	3		

- Molecule 32 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	53	376	Total	C	N	O	S	0	0
			3064	1987	529	538	10		

- Molecule 33 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	63	325	Total	C	N	O	S	0	0
			2636	1692	465	470	9		

- Molecule 34 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	73	266	Total	C	N	O	S	0	0
			2158	1383	371	388	16		

- Molecule 35 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	93	109	Total	C	N	O	S	0	0
			873	565	152	154	2		

- Molecule 36 is a protein called 39S ribosomal protein L42, mitochondrial.

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

- Molecule 37 is a protein called 39S ribosomal protein L43, mitochondrial.

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

- Molecule 38 is a protein called 39S ribosomal protein L44, mitochondrial.

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

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

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

- Molecule 40 is a protein called 39S ribosomal protein L46, mitochondrial.

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

- Molecule 41 is a protein called 39S ribosomal protein L48, mitochondrial.

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

- Molecule 42 is a protein called 39S ribosomal protein L49, mitochondrial.

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

- Molecule 43 is a protein called 39S ribosomal protein L50, mitochondrial.

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

- Molecule 44 is a protein called 39S ribosomal protein L51, mitochondrial.

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

- Molecule 45 is a protein called cDNA FLJ76418, highly similar to Homo sapiens mitochondrial ribosomal protein L52 (MRPL52), transcript variant 1, mRNA.

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

- Molecule 46 is a protein called 39S ribosomal protein L53, mitochondrial.

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

- Molecule 47 is a protein called 39S ribosomal protein L54, mitochondrial.

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

- Molecule 48 is a protein called 39S ribosomal protein L55, mitochondrial.

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

- Molecule 49 is a protein called Ribosomal protein 63, mitochondrial.

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

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

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

- Molecule 51 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

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

- Molecule 52 is a protein called 39S ribosomal protein S18a, mitochondrial.

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

- Molecule 53 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	s3	370	Total	C	N	O	S	0	0
			3036	1946	542	534	14		

- Molecule 54 is a RNA chain called RNA.

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

- Molecule 55 is a protein called Mitochondrial inner membrane protein OXA1L.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	A5	28	Total	C	N	O	0	0
			136	80	28	28		

- Molecule 56 is a protein called 28S ribosomal protein S2, mitochondrial.

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

- Molecule 57 is a protein called 28S ribosomal protein S24, mitochondrial.

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

- Molecule 58 is a protein called 28S ribosomal protein S5, mitochondrial.

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

- Molecule 59 is a protein called 28S ribosomal protein S6, mitochondrial.

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

- Molecule 60 is a protein called 28S ribosomal protein S7, mitochondrial.

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

- Molecule 61 is a protein called 28S ribosomal protein S9, mitochondrial.

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

- Molecule 62 is a protein called 28S ribosomal protein S10, mitochondrial.

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

- Molecule 63 is a protein called 28S ribosomal protein S11, mitochondrial.

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

- Molecule 64 is a protein called 28S ribosomal protein S12, mitochondrial.

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

- Molecule 65 is a protein called 28S ribosomal protein S14, mitochondrial.

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

- Molecule 66 is a protein called 28S ribosomal protein S15, mitochondrial.

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

- Molecule 67 is a protein called 28S ribosomal protein S16, mitochondrial.

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

- Molecule 68 is a protein called 28S ribosomal protein S17, mitochondrial.

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

- Molecule 69 is a protein called 28S ribosomal protein S18b, mitochondrial.

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

- Molecule 70 is a protein called 28S ribosomal protein S18c, mitochondrial.

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

- Molecule 71 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	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 72 is a protein called 28S ribosomal protein S22, mitochondrial.

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

- Molecule 73 is a protein called 28S ribosomal protein S23, mitochondrial.

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

- Molecule 74 is a protein called 28S ribosomal protein S25, mitochondrial.

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

- Molecule 75 is a protein called 28S ribosomal protein S26, mitochondrial.

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

- Molecule 76 is a protein called 28S ribosomal protein S27, mitochondrial.

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

- Molecule 77 is a protein called 28S ribosomal protein S28, mitochondrial.

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

- Molecule 78 is a protein called 28S ribosomal protein S29, mitochondrial.

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

- Molecule 79 is a protein called 28S ribosomal protein S31, mitochondrial.

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

- Molecule 80 is a protein called 28S ribosomal protein S33, mitochondrial.

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

- Molecule 81 is a protein called 28S ribosomal protein S34, mitochondrial.

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

- Molecule 82 is a protein called 28S ribosomal protein S35, mitochondrial.

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

- Molecule 83 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

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

- Molecule 84 is a protein called Aurora kinase A-interacting protein.

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

- Molecule 85 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

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

- Molecule 86 is a RNA chain called 12S rRNA.

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

- Molecule 87 is a RNA chain called mt-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	24	73	Total	C	N	O	P	0	0
			1547	696	280	499	72		
87	FE	73	Total	C	N	O	P	0	0
			1547	696	280	499	72		

- 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		

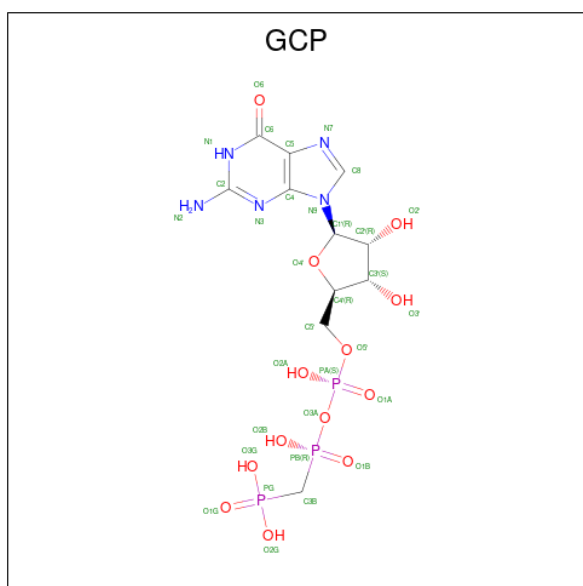
- Molecule 89 is a protein called 39S ribosomal protein L1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	n	218	Total	C	N	O	S	0	0
			1744	1121	294	324	5		

- Molecule 90 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
90	B	28	Total	C	N	O	0	0
			140	84	28	28		

- Molecule 91 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).

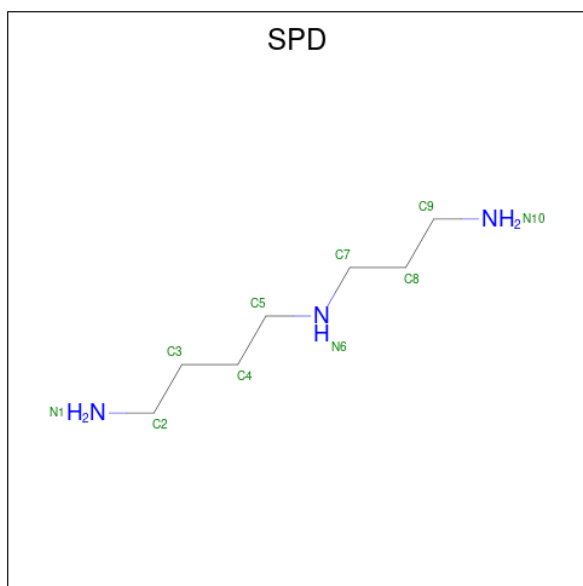


Mol	Chain	Residues	Atoms					AltConf
91	r1	1	Total	C	N	O	P	0
			32	11	5	13	3	

- Molecule 92 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
92	r1	1	Total	Mg	0
			1	1	
92	A3	95	Total	Mg	0
			95	95	
92	D3	1	Total	Mg	0
			1	1	
92	E3	1	Total	Mg	0
			1	1	
92	M3	1	Total	Mg	0
			1	1	
92	g3	1	Total	Mg	0
			1	1	
92	A6	28	Total	Mg	0
			28	28	

- Molecule 93 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).

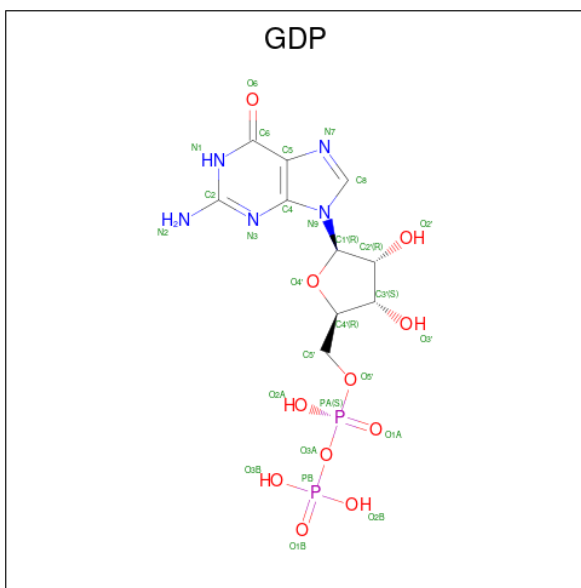


Mol	Chain	Residues	Atoms			AltConf
93	A3	1	Total	C	N	0
			10	7	3	

- Molecule 94 is ZINC ION (CCD ID: 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	

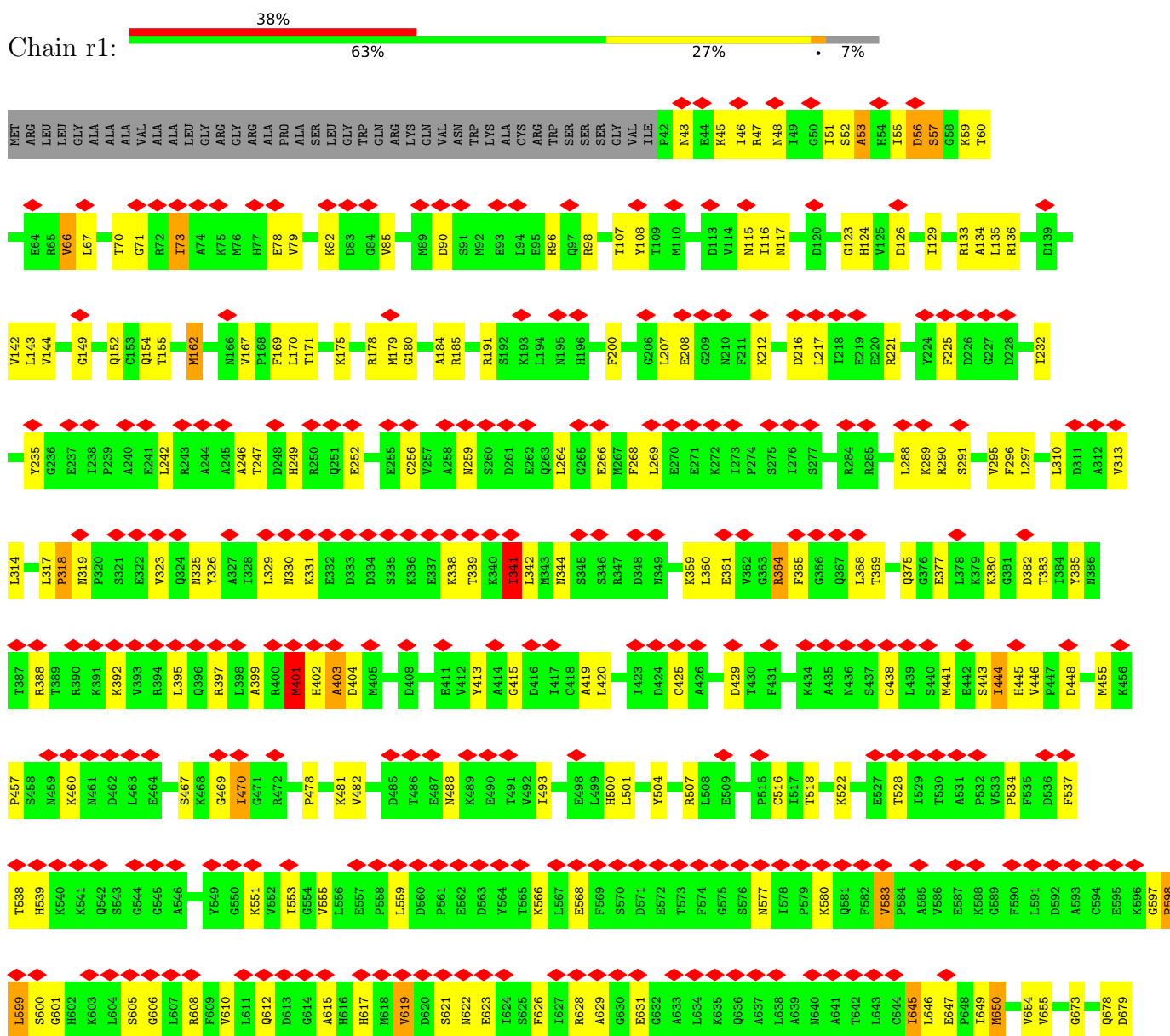
- Molecule 95 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



3 Residue-property plots

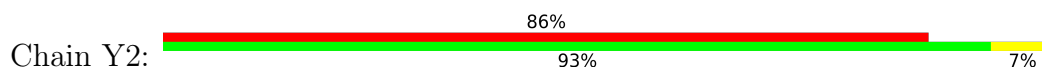
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

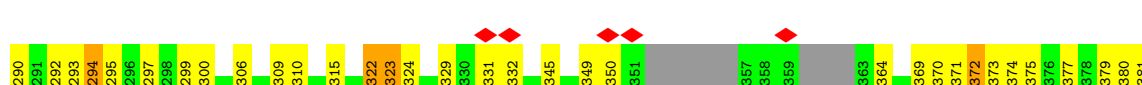
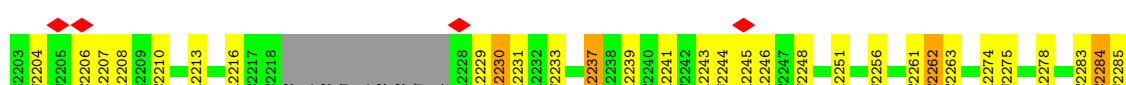
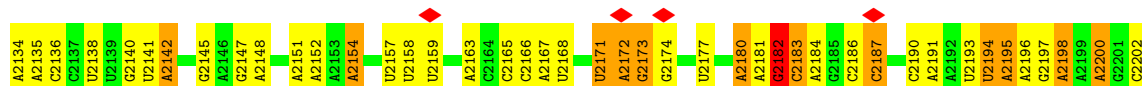
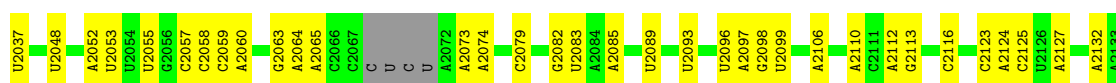
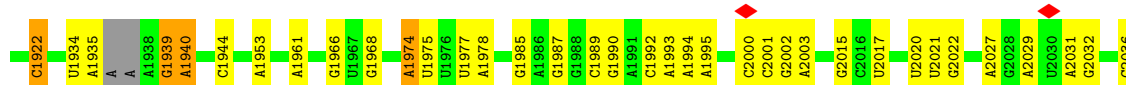
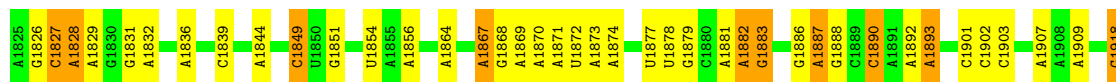
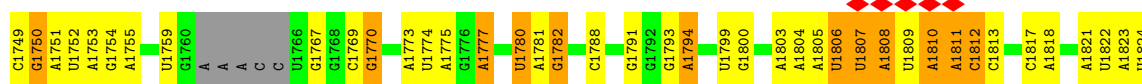


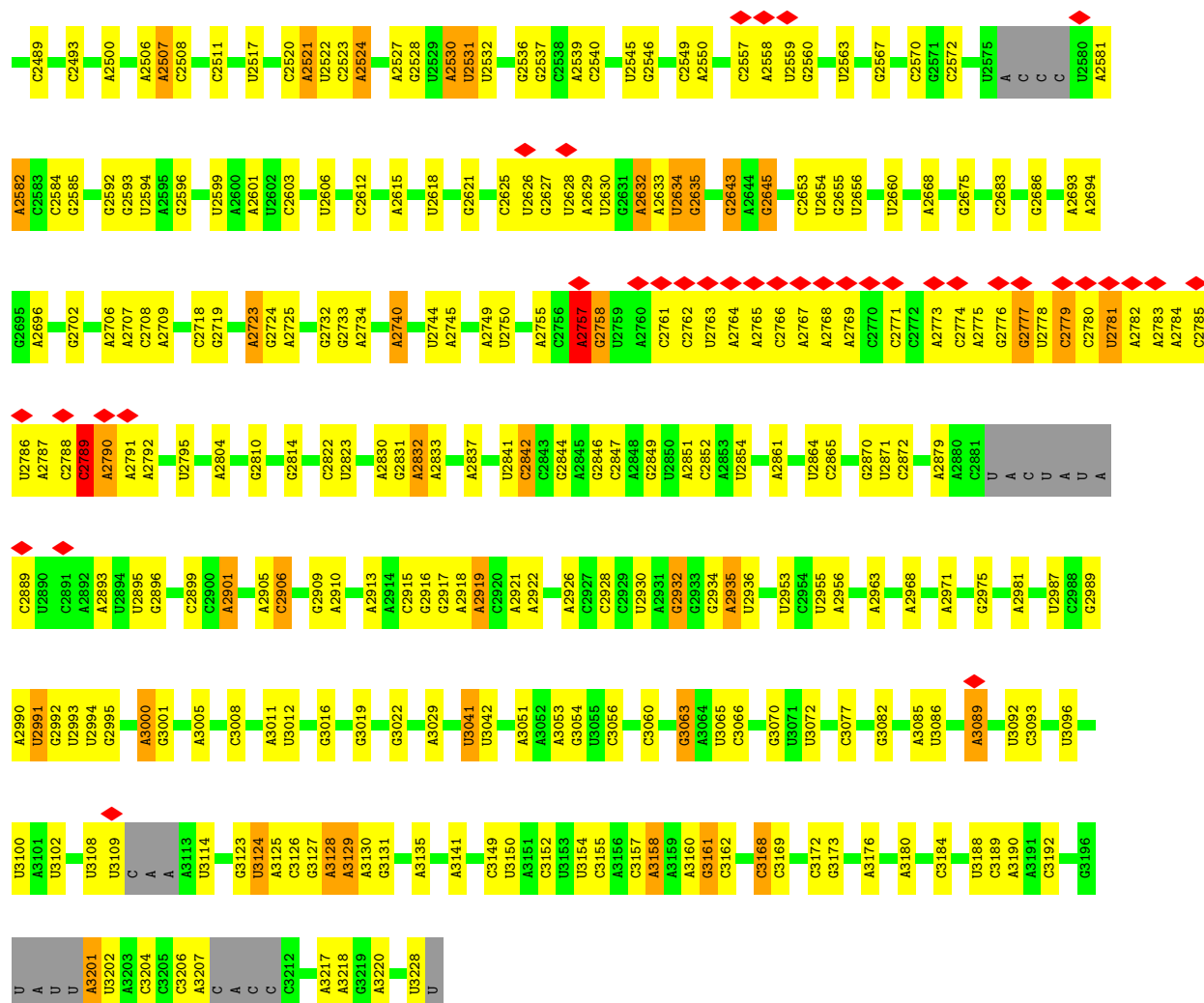


- Molecule 2: nascent chain



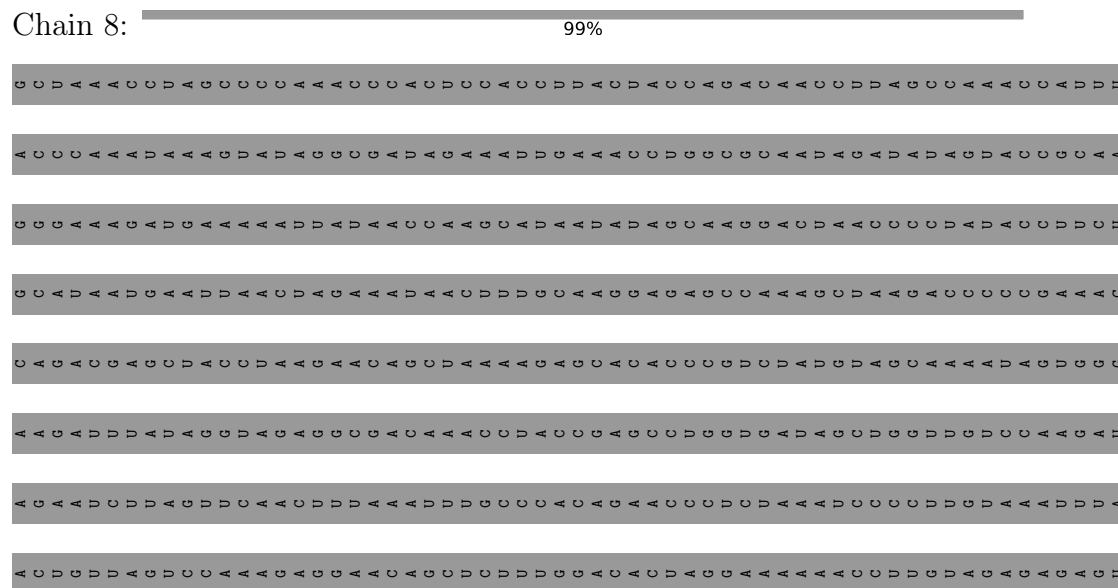
- Molecule 3: 16S rRNA

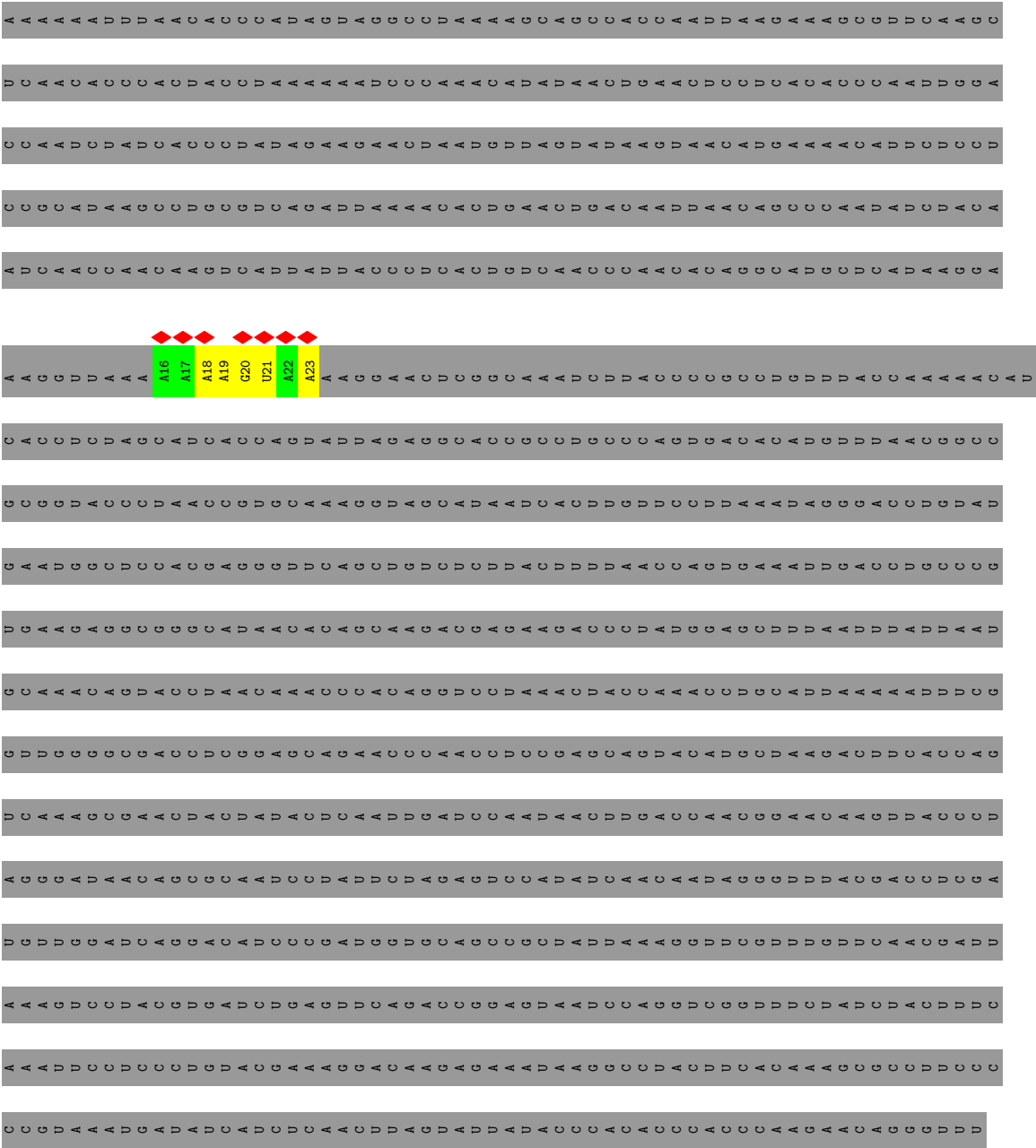




- Molecule 3: 16S rRNA

Chain 8:

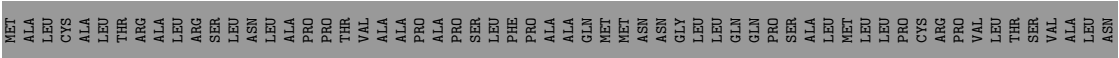


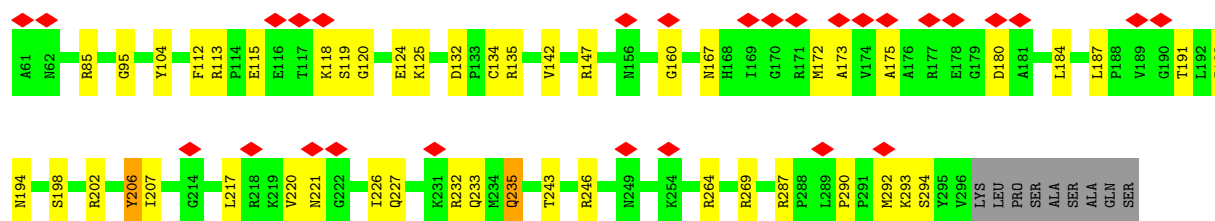


● Molecule 4: mt-tRNAVal

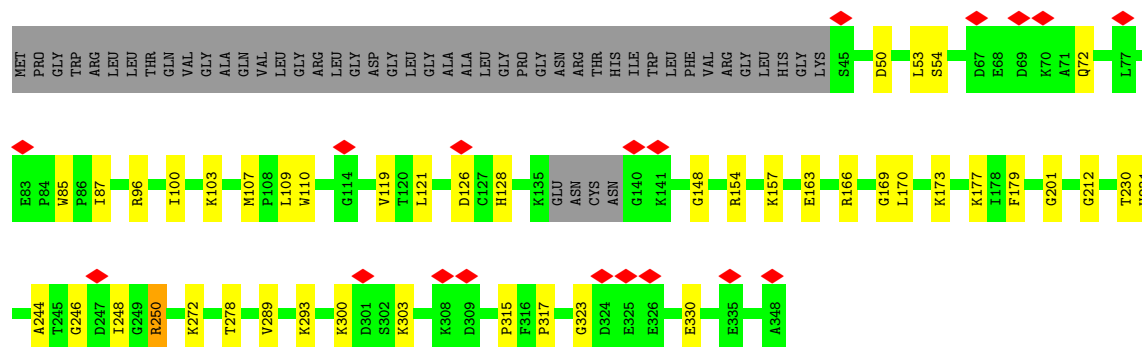
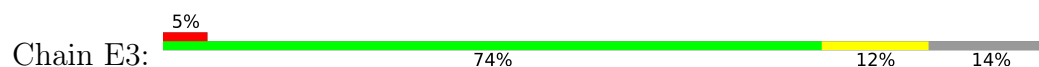


● Molecule 5: 39S ribosomal protein L2, mitochondrial

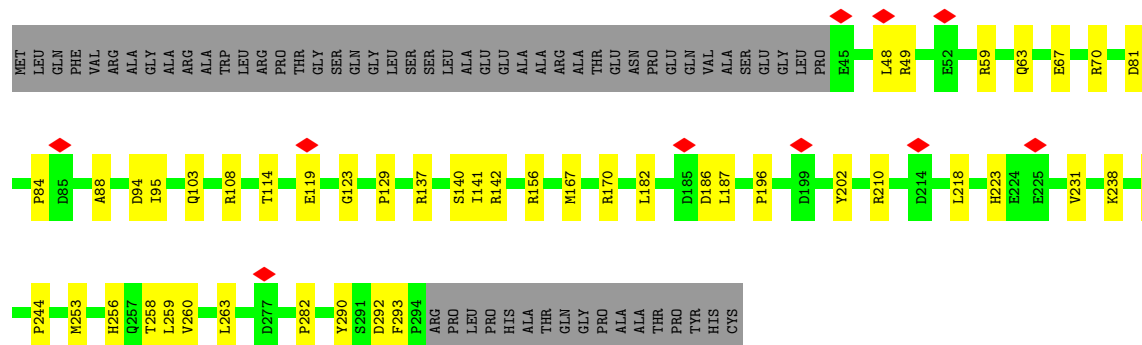




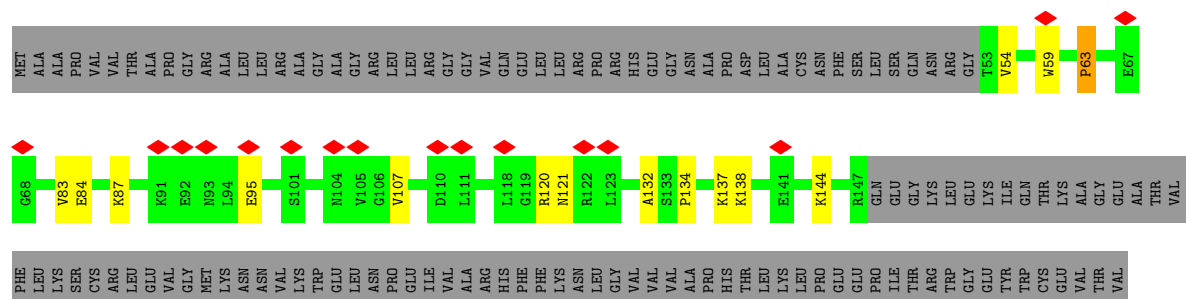
• Molecule 6: 39S ribosomal protein L3, mitochondrial



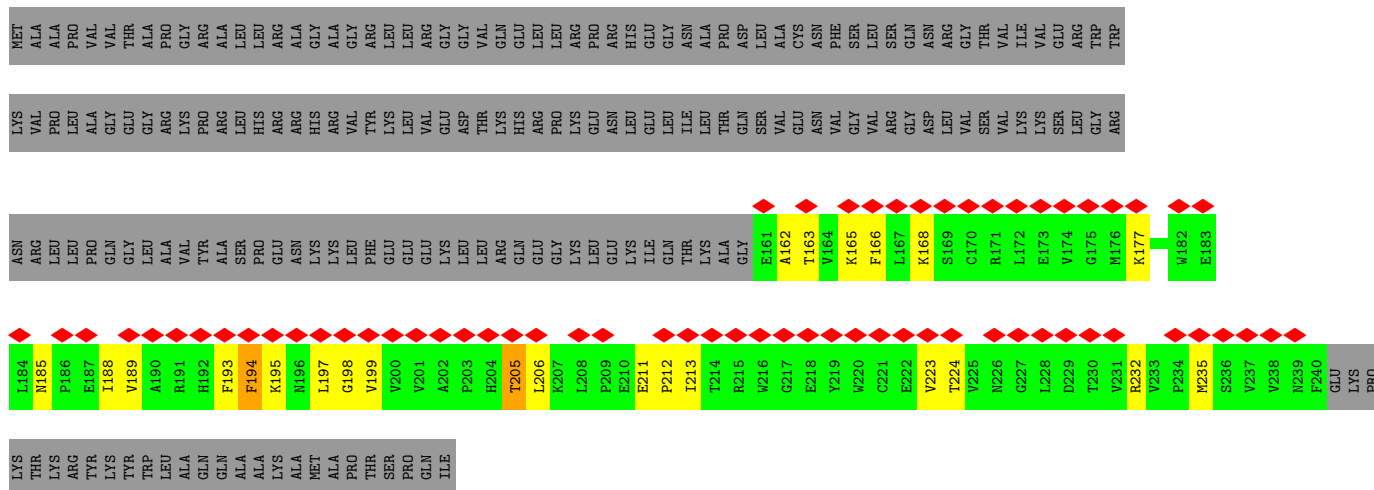
• Molecule 7: 39S ribosomal protein L4, mitochondrial



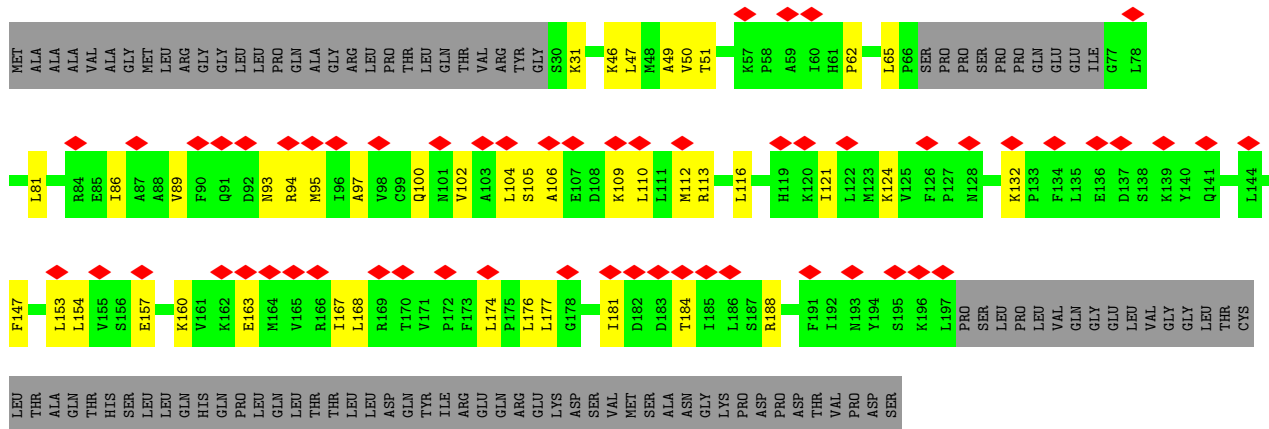
• Molecule 8: 39S ribosomal protein L9, mitochondrial



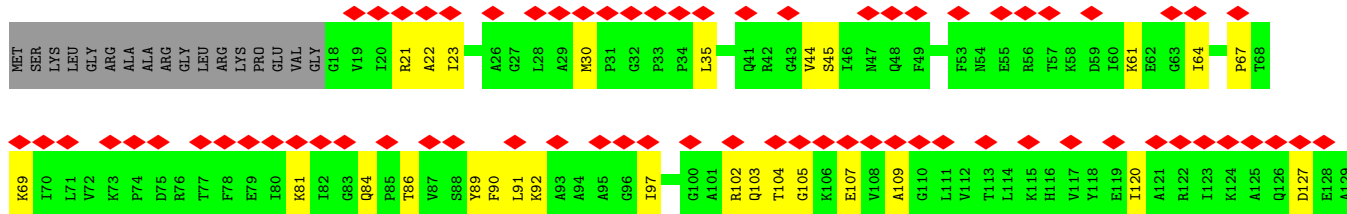
Chain D:

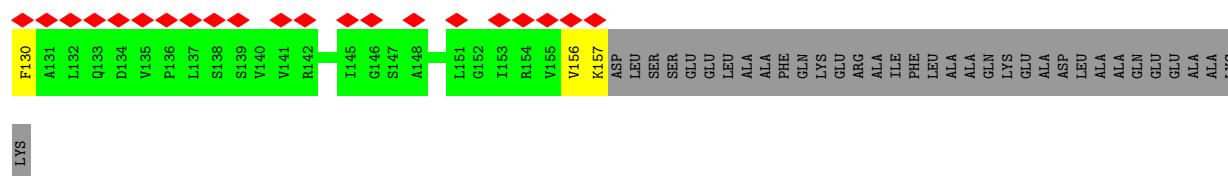


Chain I3:

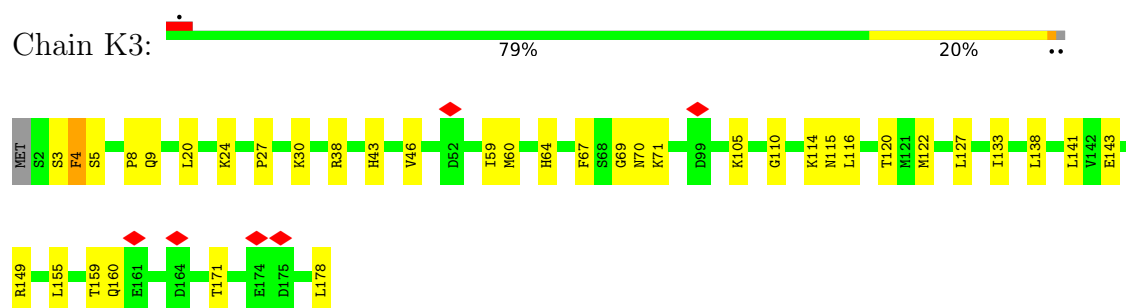


Chain J3:

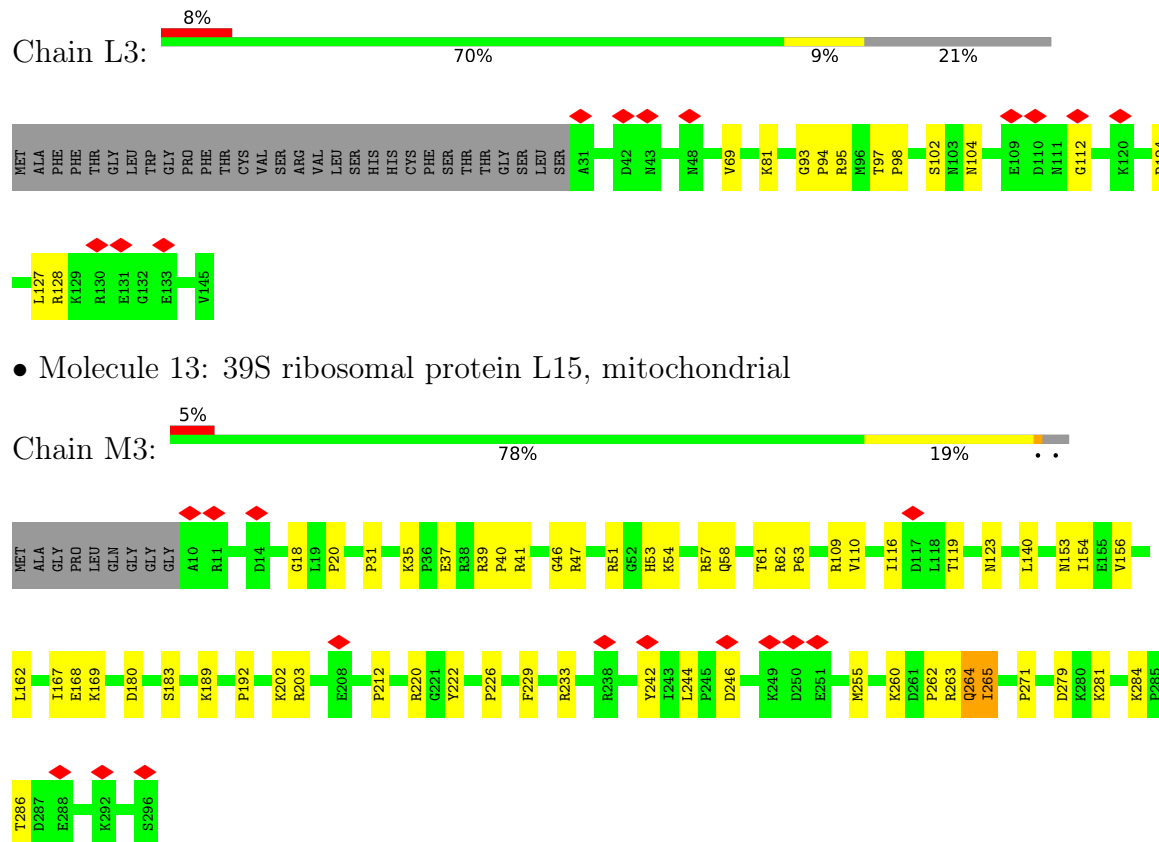




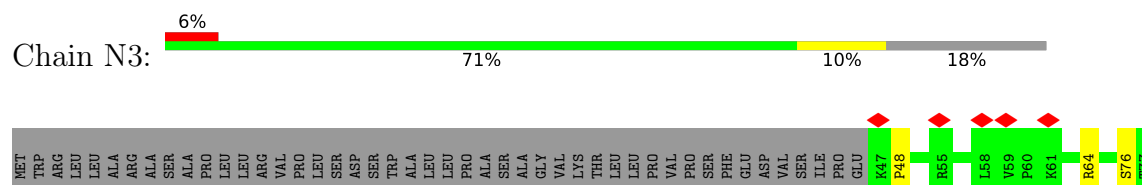
- Molecule 11: 39S ribosomal protein L13, mitochondrial



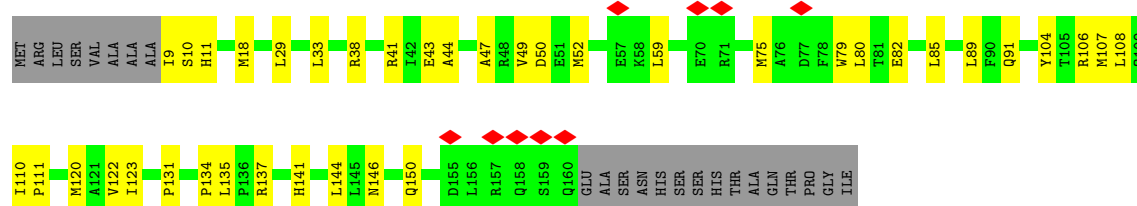
- Molecule 12: 39S ribosomal protein L14, mitochondrial



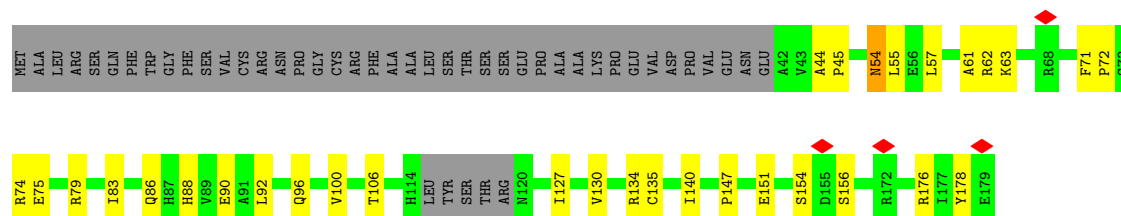
- Molecule 13: 39S ribosomal protein L15, mitochondrial



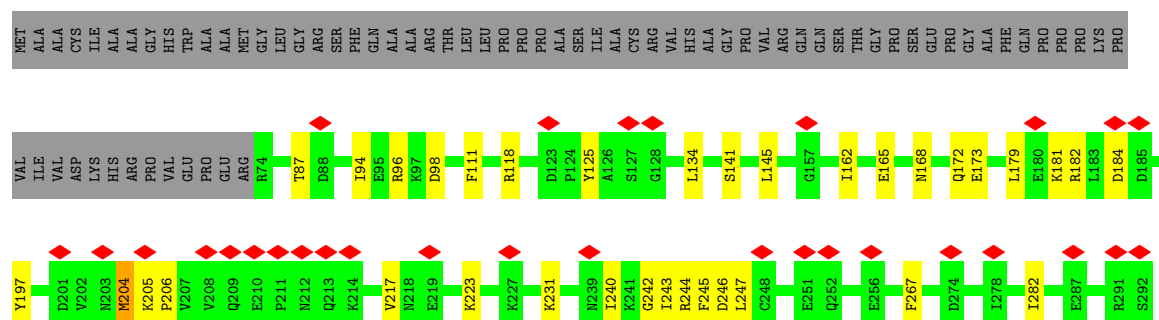
- Molecule 15: 39S ribosomal protein L17, mitochondrial



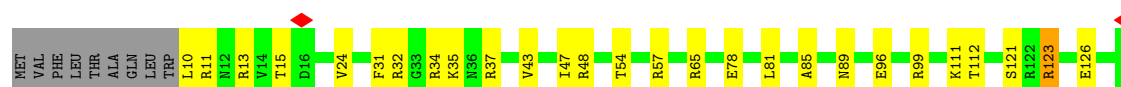
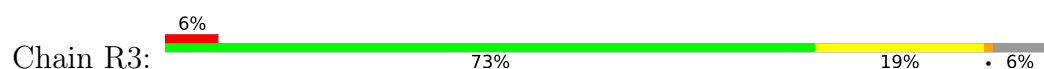
- Molecule 16: Mitochondrial ribosomal protein L18, isoform CRA b

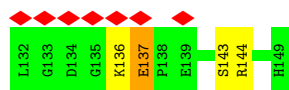


- Molecule 17: 39S ribosomal protein L19, mitochondrial

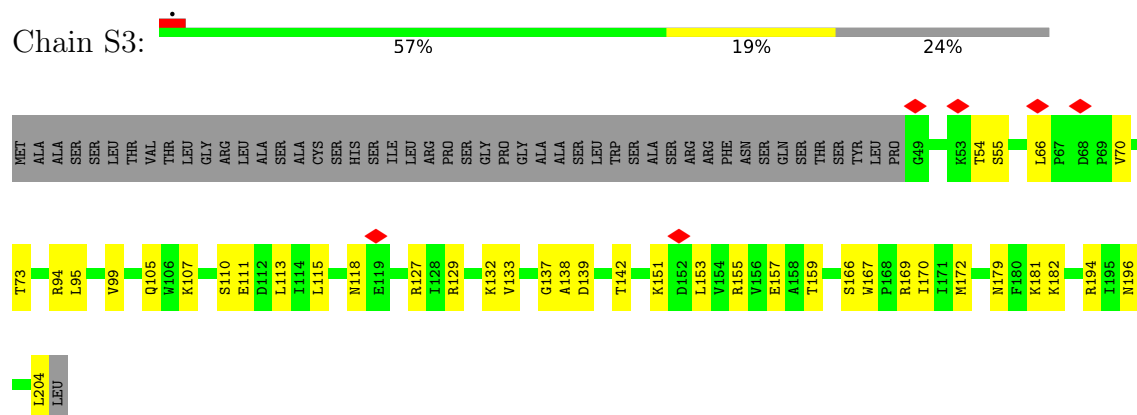


- Molecule 18: 39S ribosomal protein L20, mitochondrial

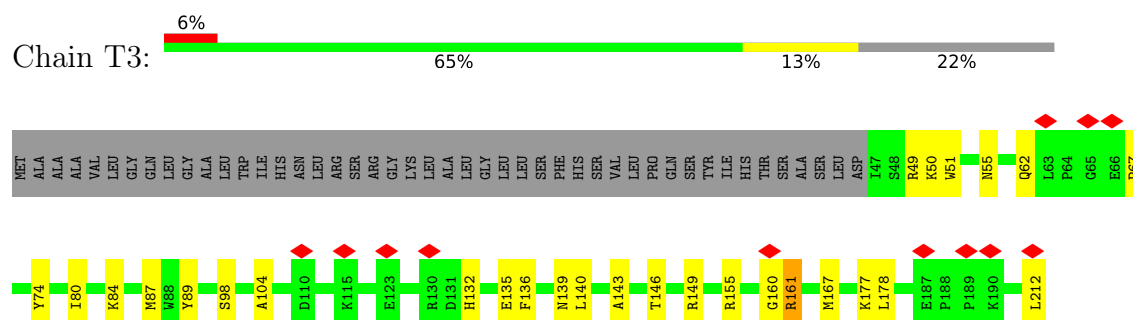




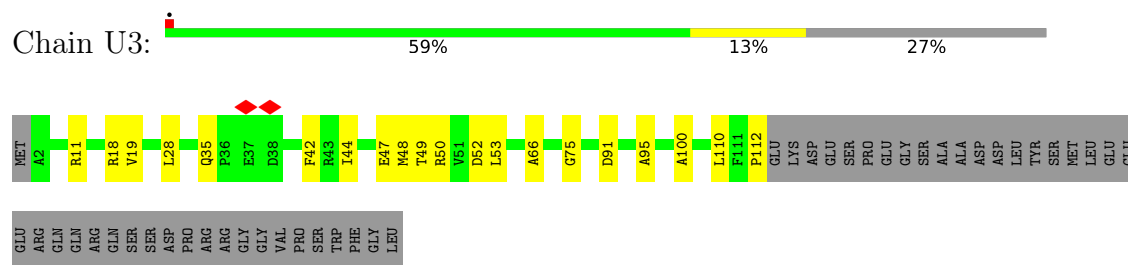
- Molecule 19: 39S ribosomal protein L21, mitochondrial



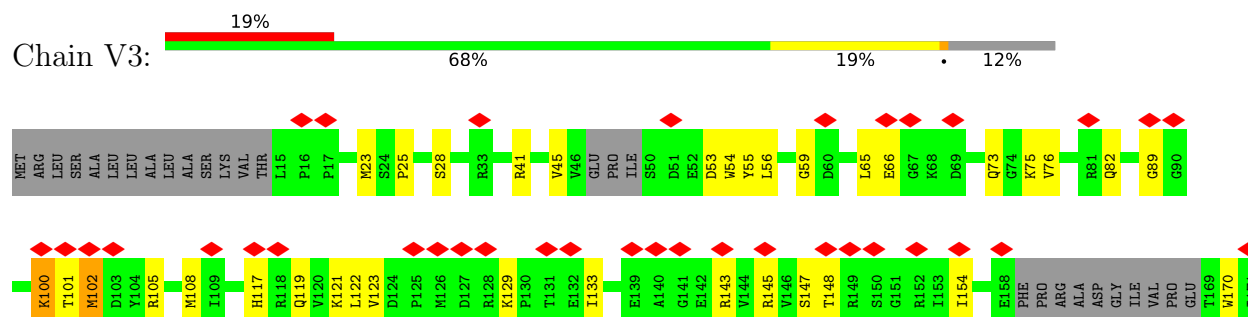
- Molecule 20: 39S ribosomal protein L22, mitochondrial

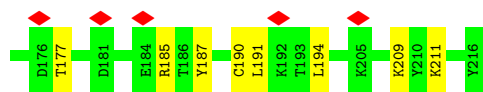


- Molecule 21: 39S ribosomal protein L23, mitochondrial



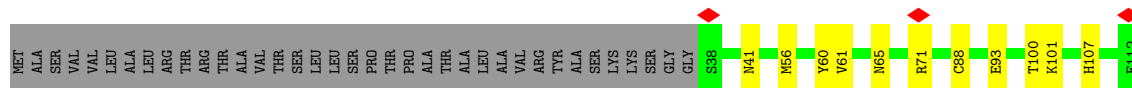
- Molecule 22: 39S ribosomal protein L24, mitochondrial





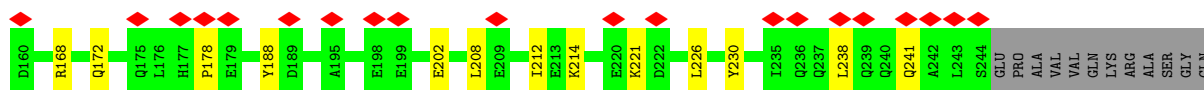
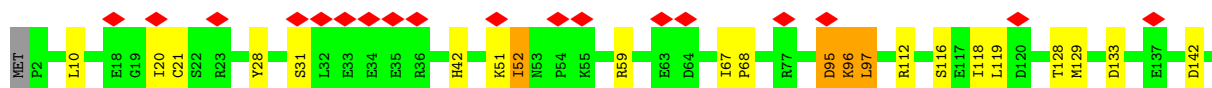
- Molecule 23: 39S ribosomal protein L27, mitochondrial

Chain W3: 62% 13% 25%



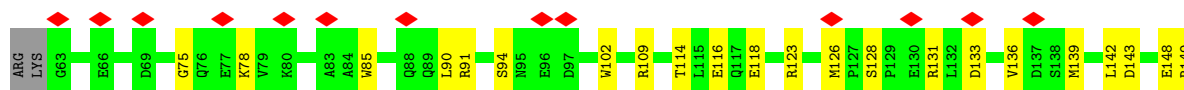
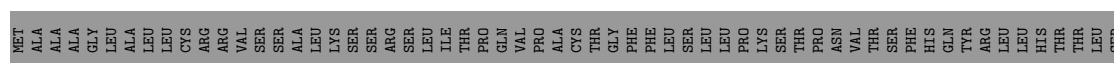
- Molecule 24: 39S ribosomal protein L28, mitochondrial

Chain X3: 15% 81% 12% 5%



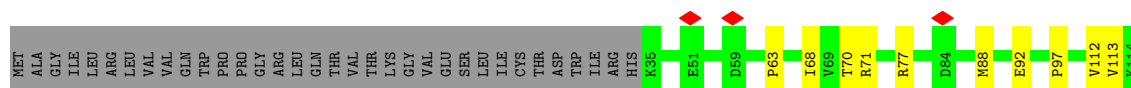
- Molecule 25: 39S ribosomal protein L47, mitochondrial

Chain Y3: 8% 57% 14% 30%



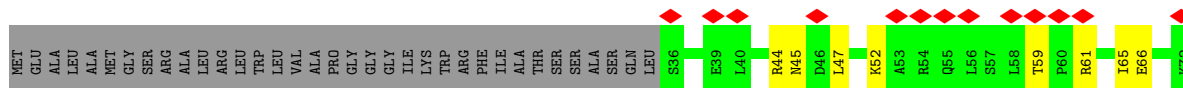
- Molecule 26: 39S ribosomal protein L30, mitochondrial

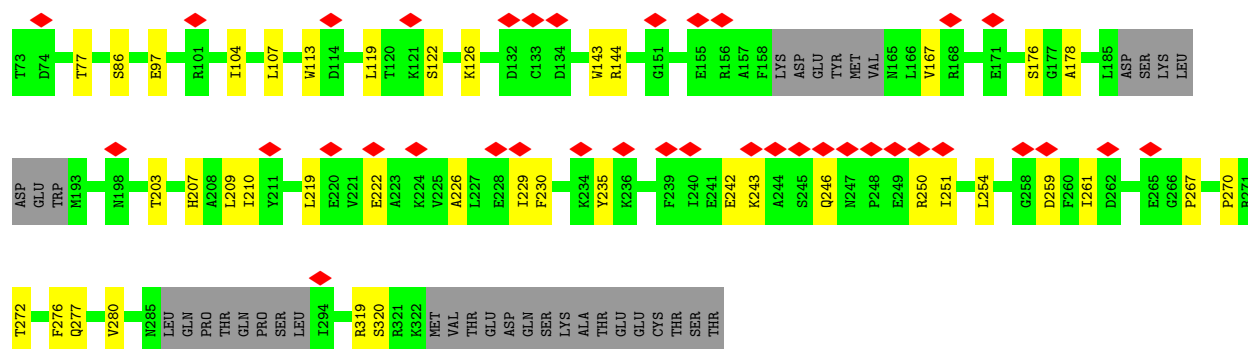
Chain Z3: 63% 11% 25%



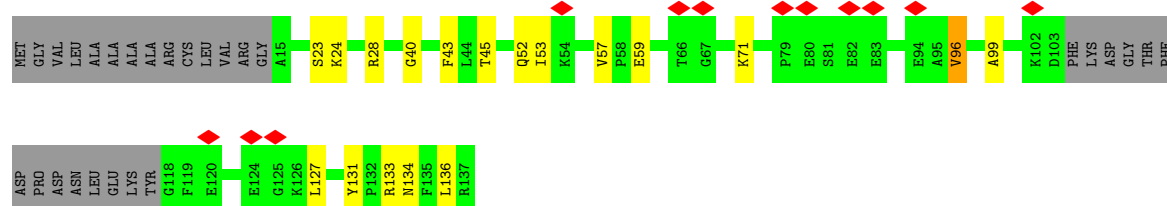
Chain 03:



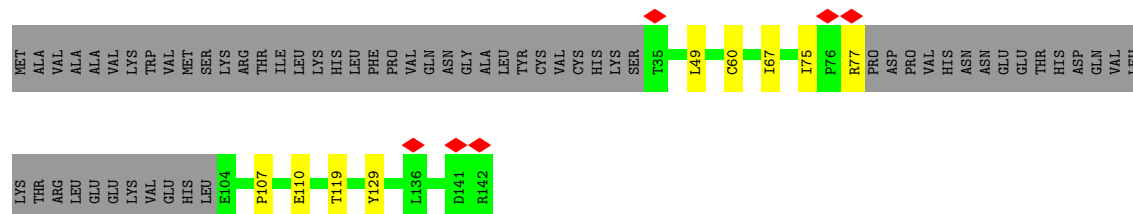




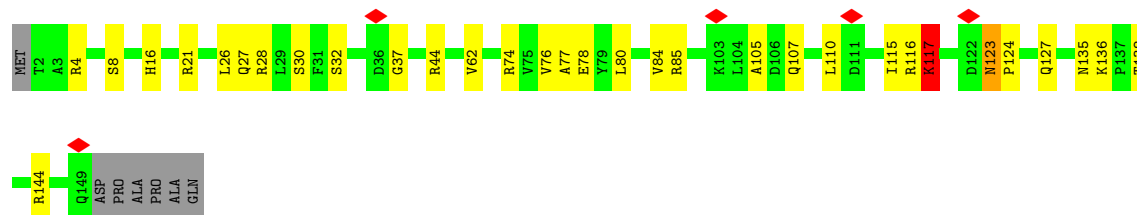
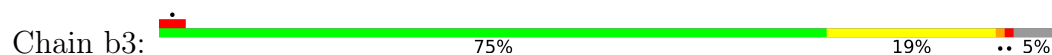
- Molecule 35: 39S ribosomal protein L41, mitochondrial



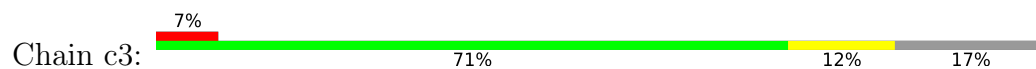
- Molecule 36: 39S ribosomal protein L42, mitochondrial

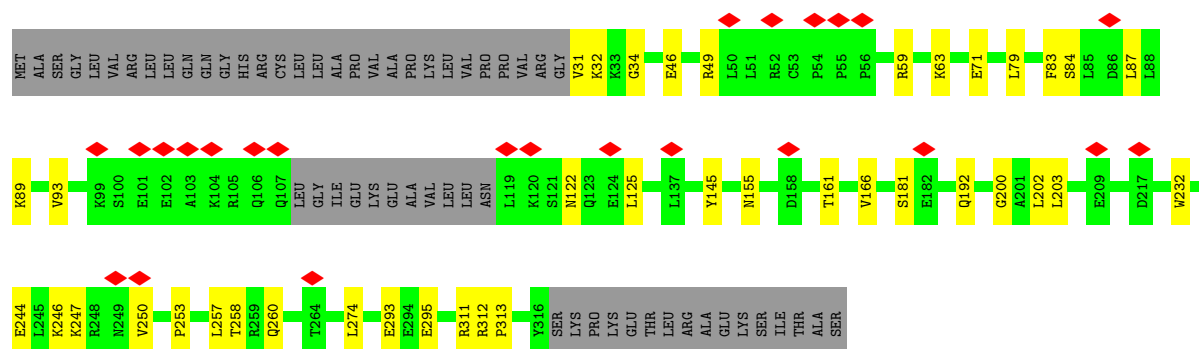


- Molecule 37: 39S ribosomal protein L43, mitochondrial

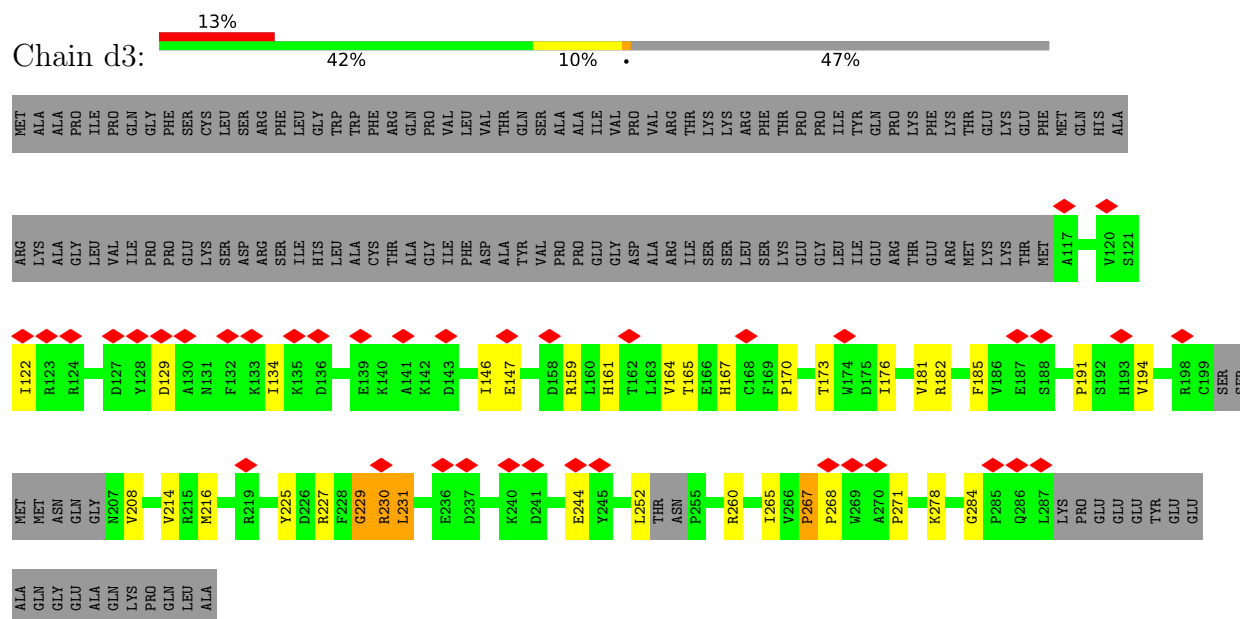


- Molecule 38: 39S ribosomal protein L44, mitochondrial

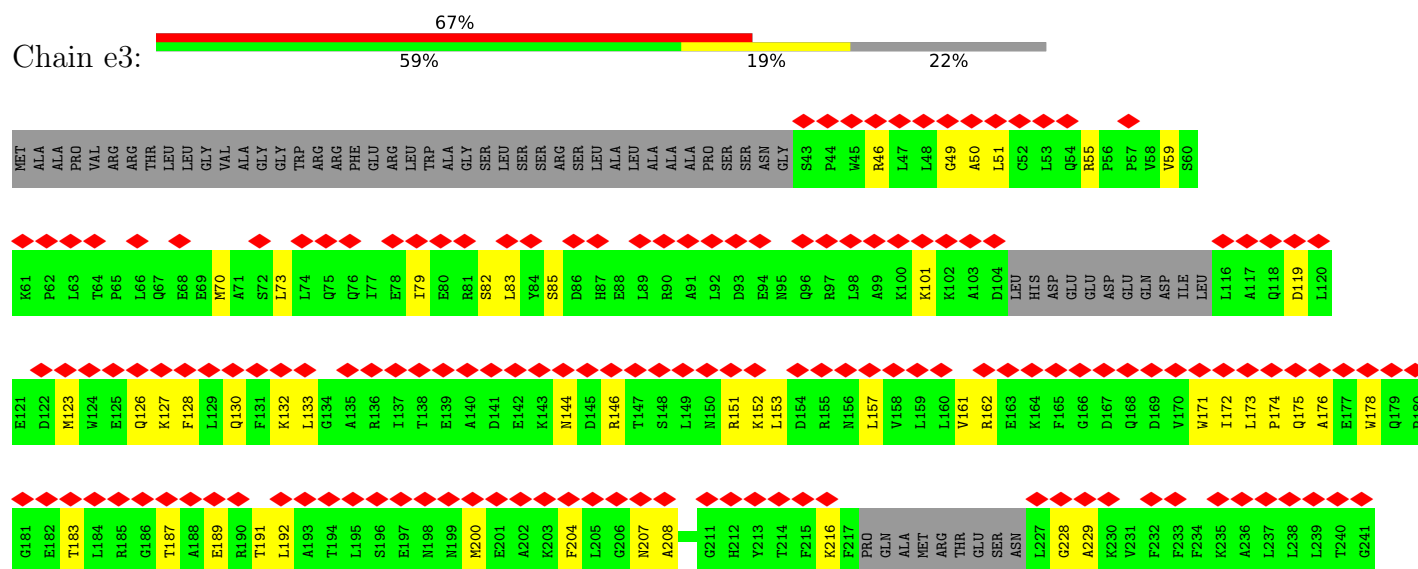


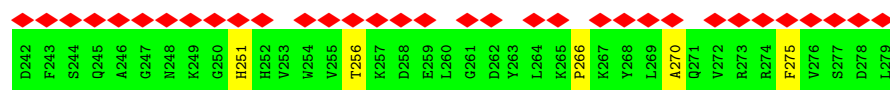


- Molecule 39: 39S ribosomal protein L45, mitochondrial

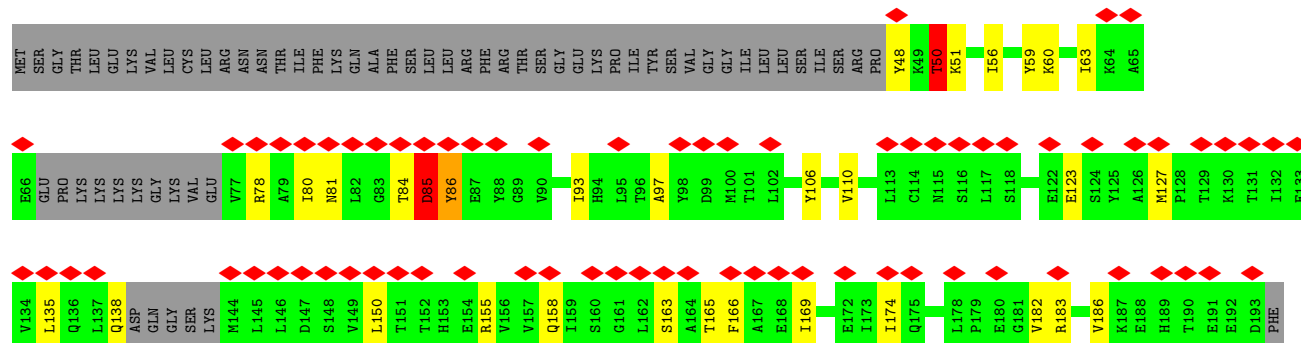
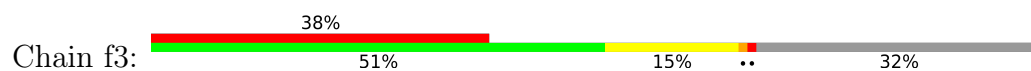


- Molecule 40: 39S ribosomal protein L46, mitochondrial

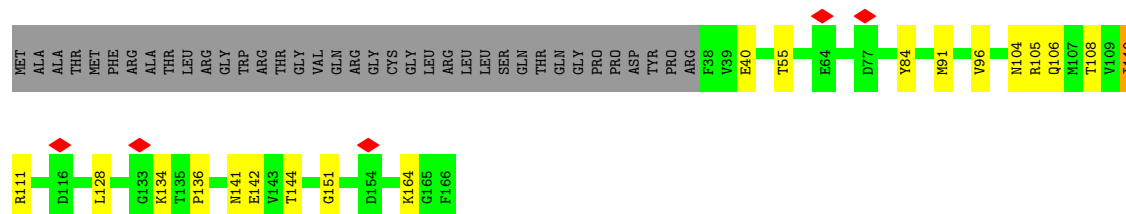




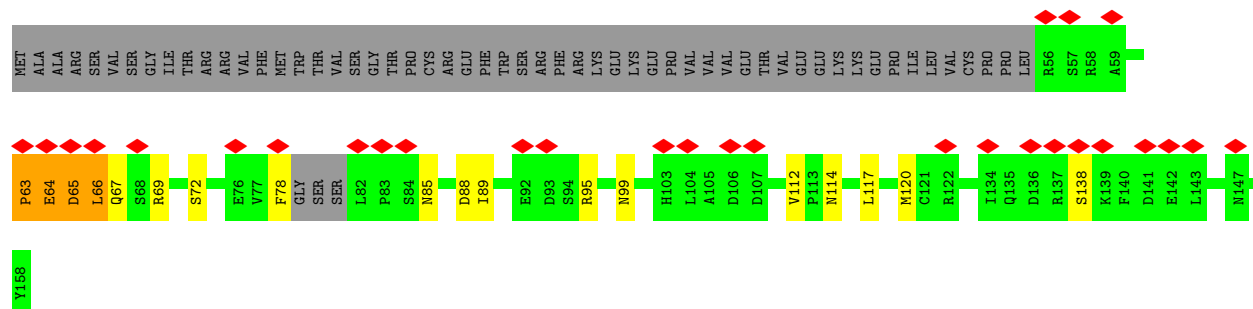
- Molecule 41: 39S ribosomal protein L48, mitochondrial



- Molecule 42: 39S ribosomal protein L49, mitochondrial



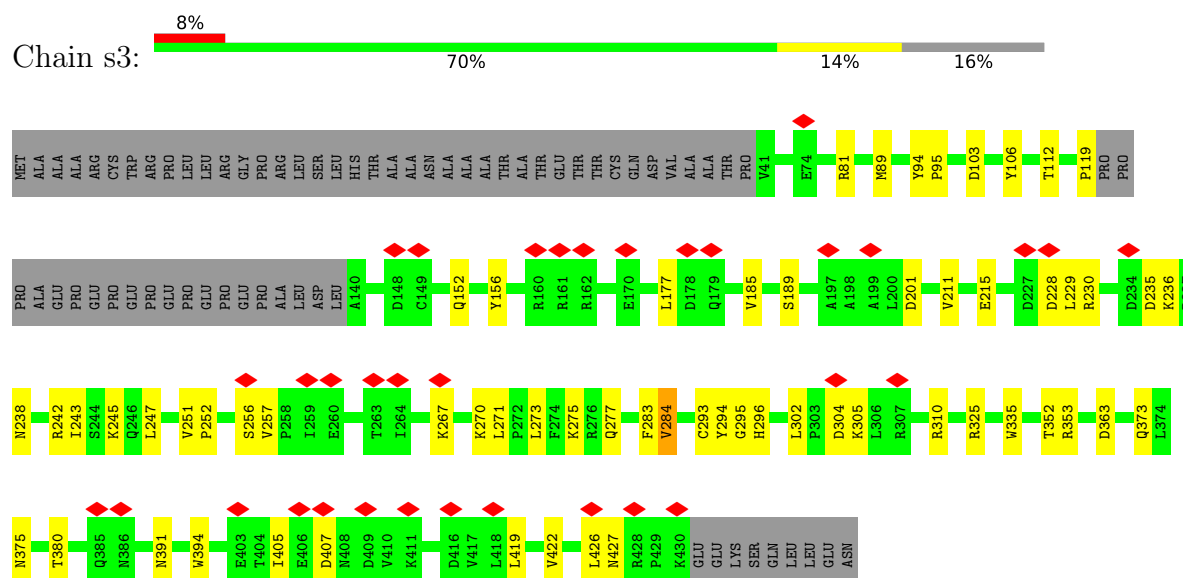
- Molecule 43: 39S ribosomal protein L50, mitochondrial



- Molecule 44: 39S ribosomal protein L51, mitochondrial



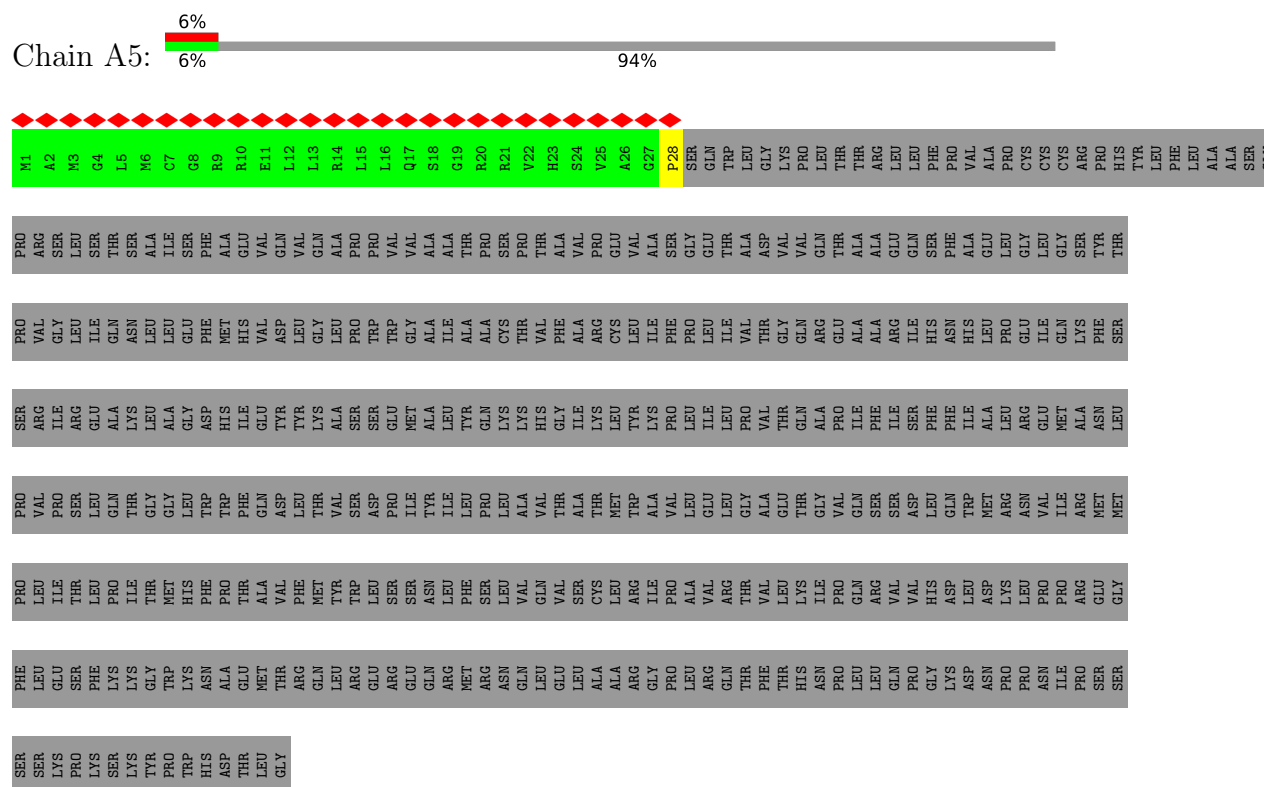
- Molecule 53: 39S ribosomal protein S30, mitochondrial



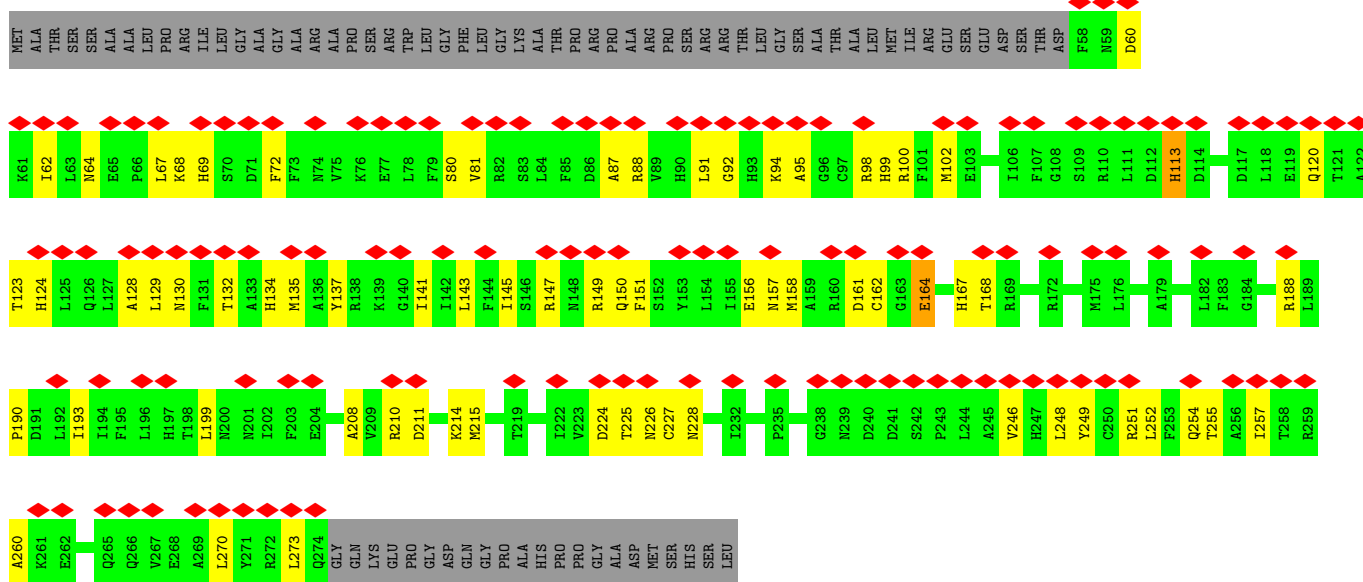
- Molecule 54: RNA



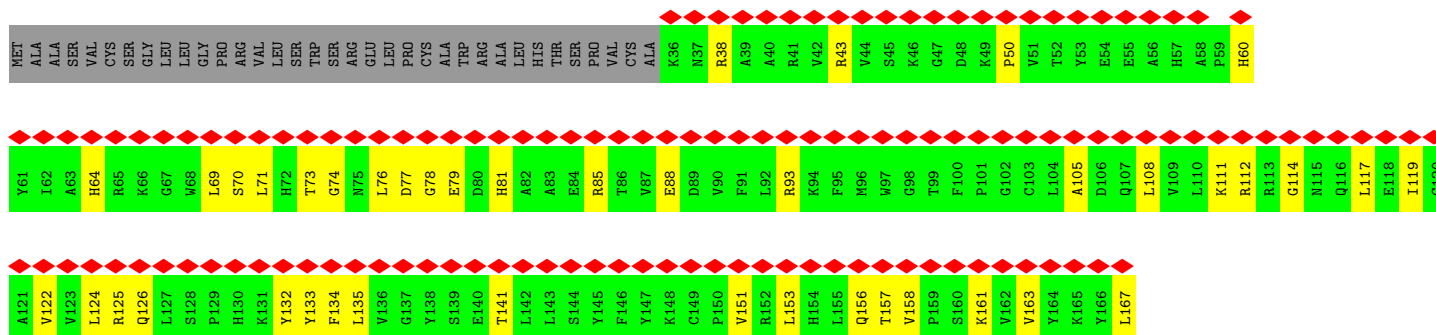
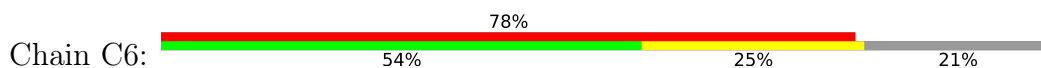
- Molecule 55: Mitochondrial inner membrane protein OXA1L



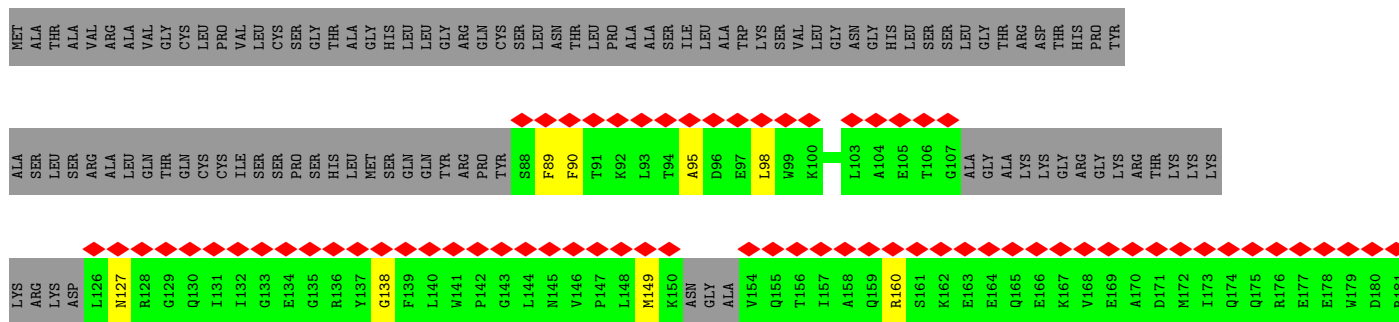
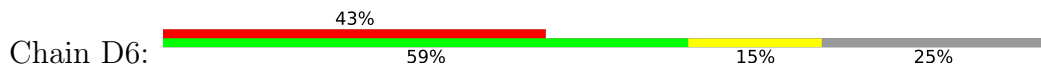
- Molecule 56: 28S ribosomal protein S2, mitochondrial

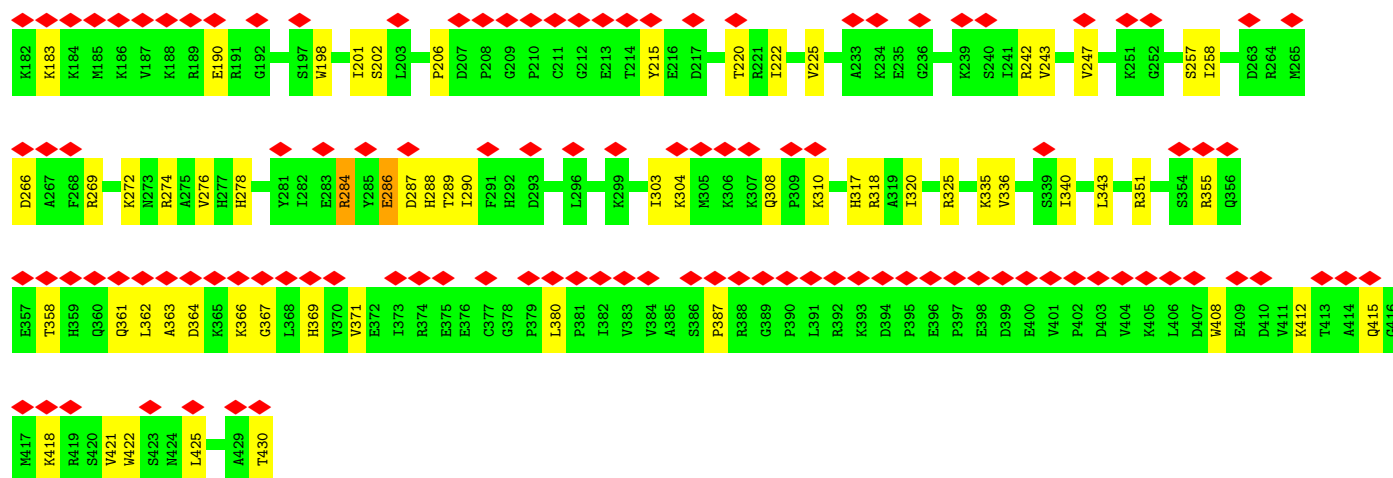


- Molecule 57: 28S ribosomal protein S24, mitochondrial

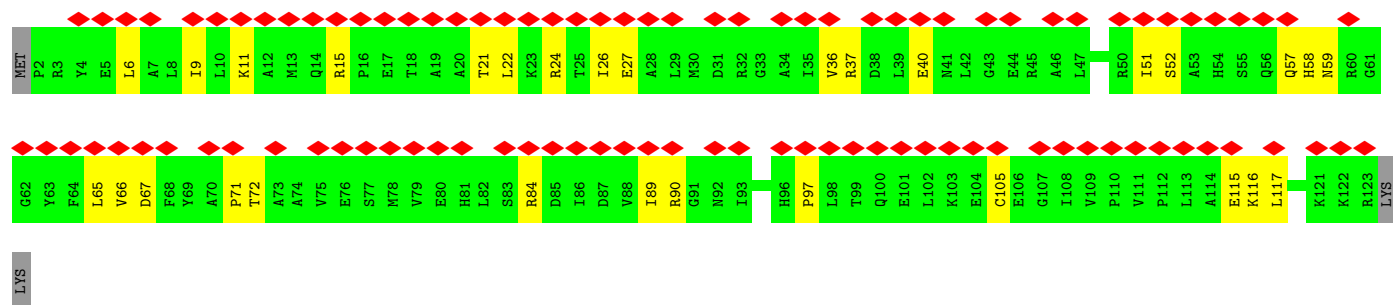
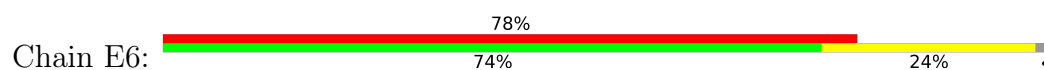


- Molecule 58: 28S ribosomal protein S5, mitochondrial

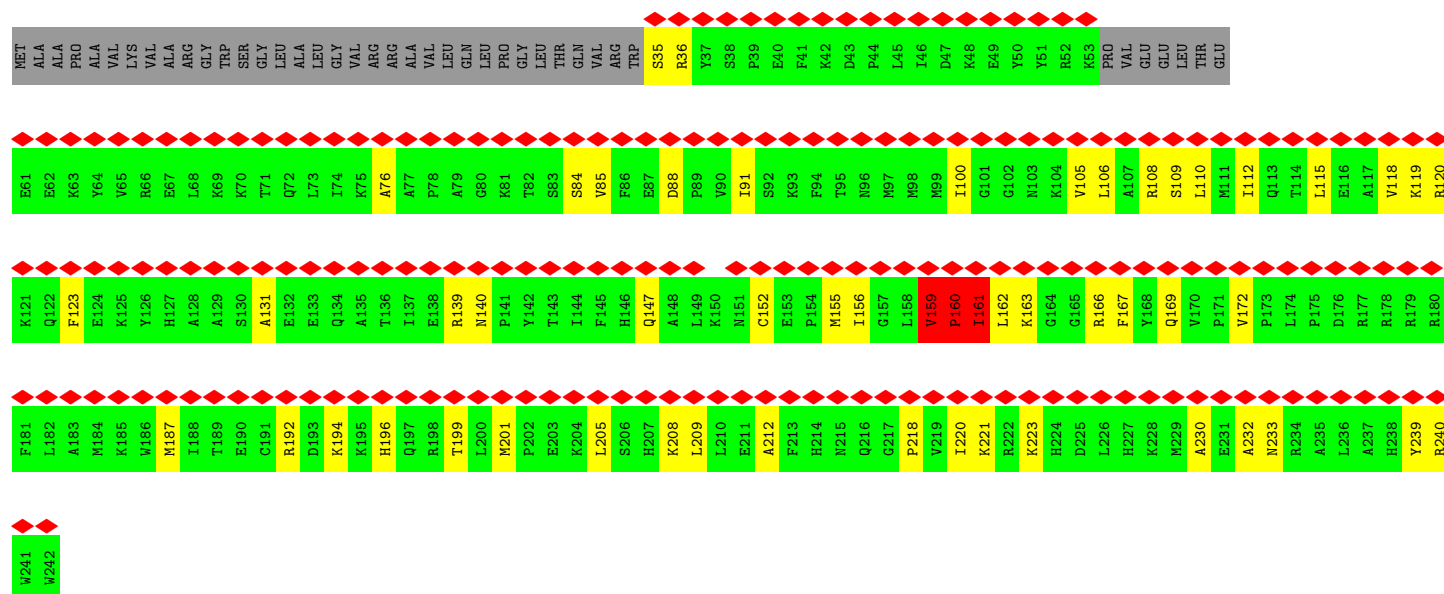
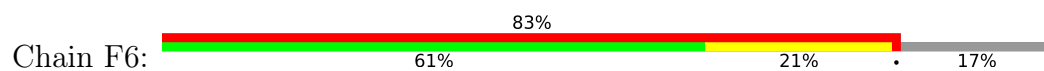




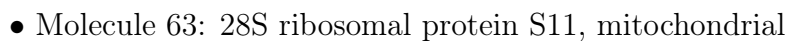
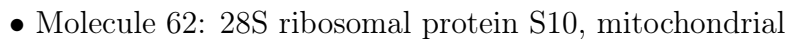
- Molecule 59: 28S ribosomal protein S6, mitochondrial

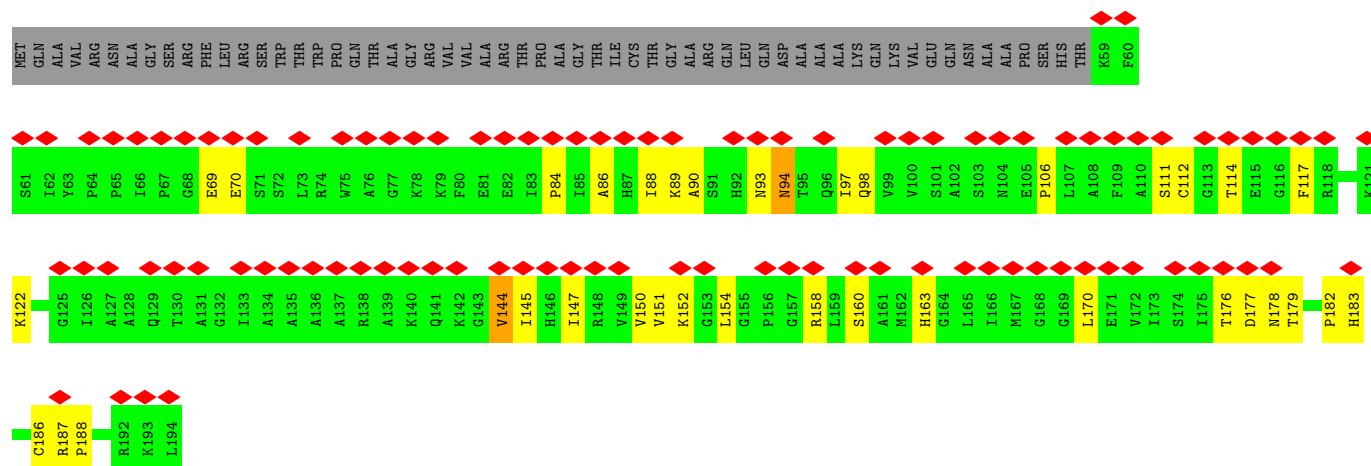


- Molecule 60: 28S ribosomal protein S7, mitochondrial

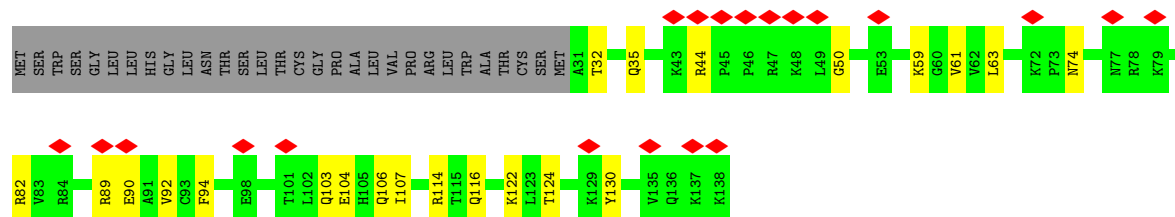


- Chain G6:

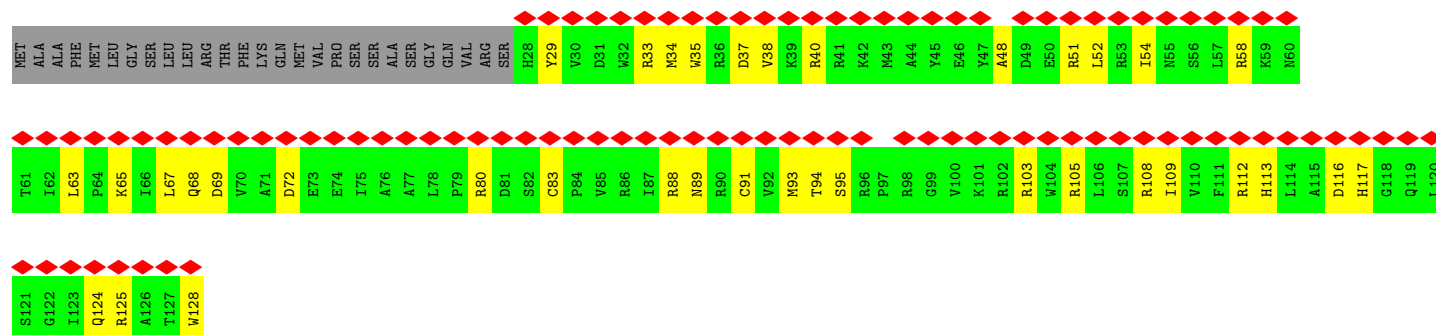
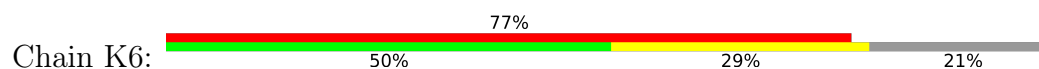




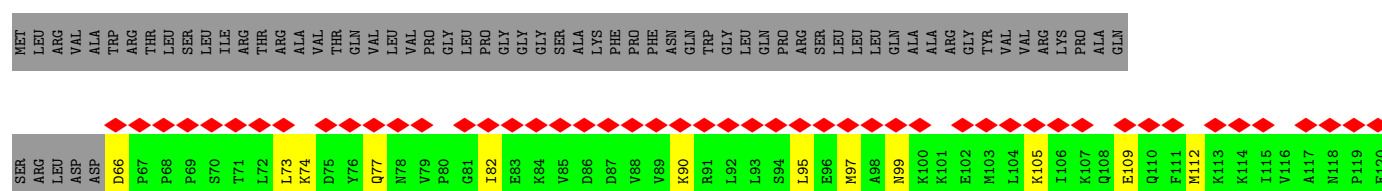
- Molecule 64: 28S ribosomal protein S12, mitochondrial

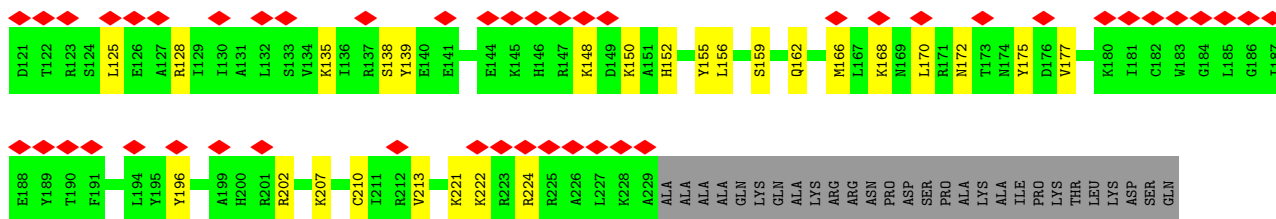


- Molecule 65: 28S ribosomal protein S14, mitochondrial

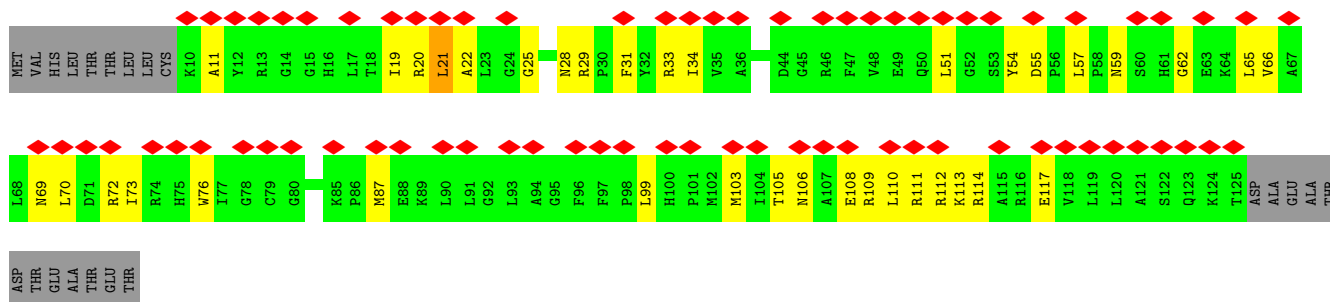


- Molecule 66: 28S ribosomal protein S15, mitochondrial

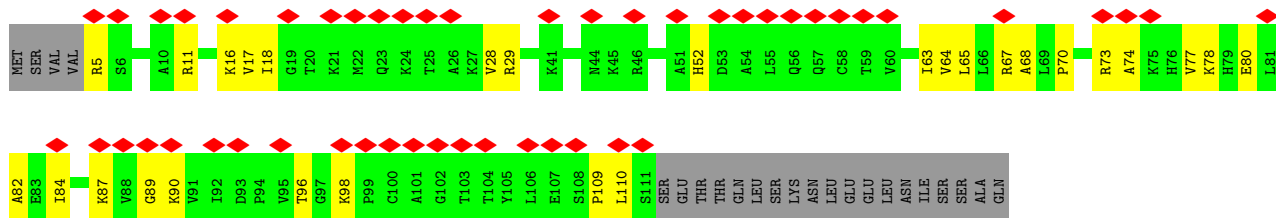
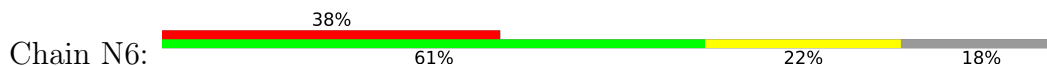




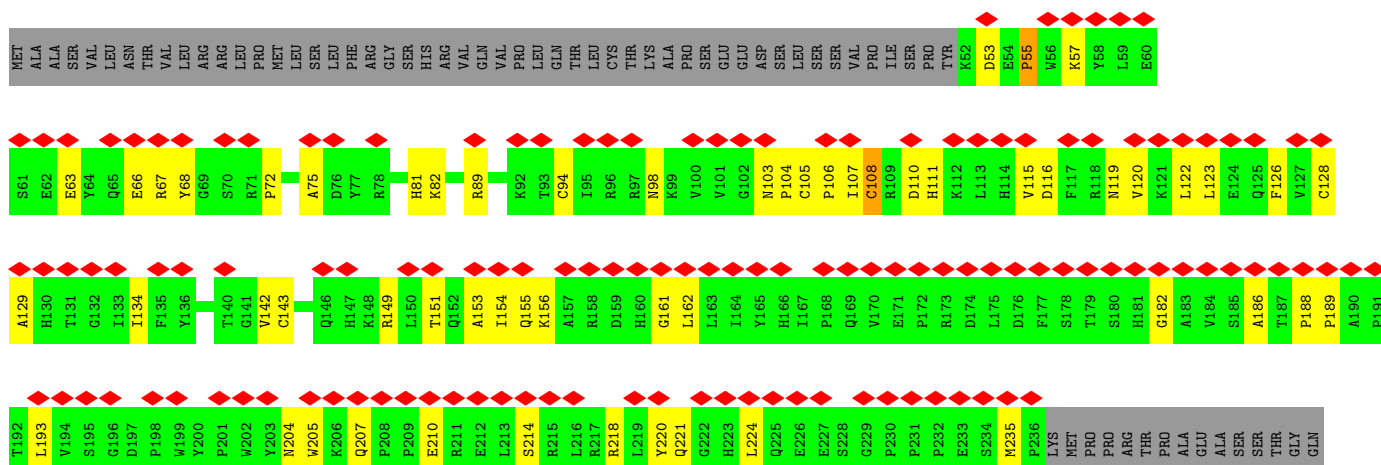
- Molecule 67: 28S ribosomal protein S16, mitochondrial



- Molecule 68: 28S ribosomal protein S17, mitochondrial

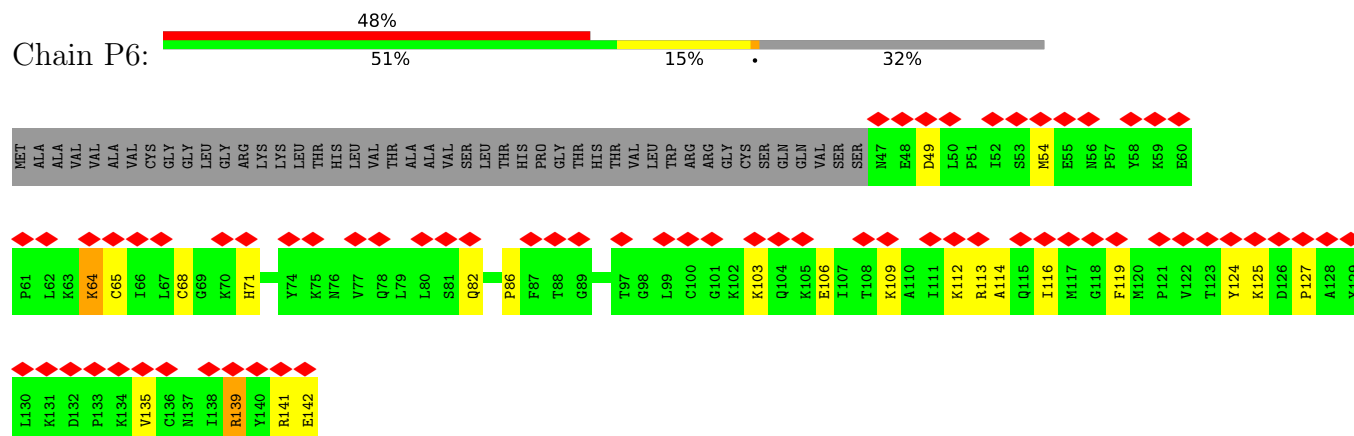


- Molecule 69: 28S ribosomal protein S18b, mitochondrial

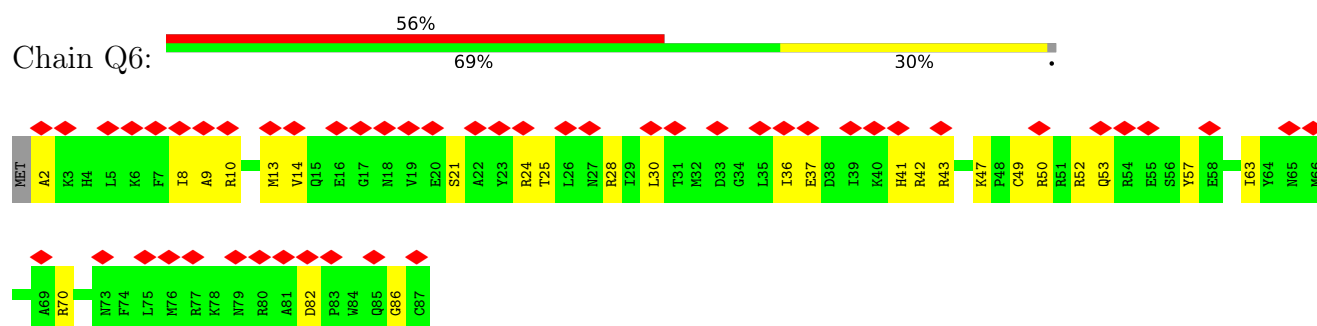


THR
GLY
PRO
GLN
SER
ALA
LEU

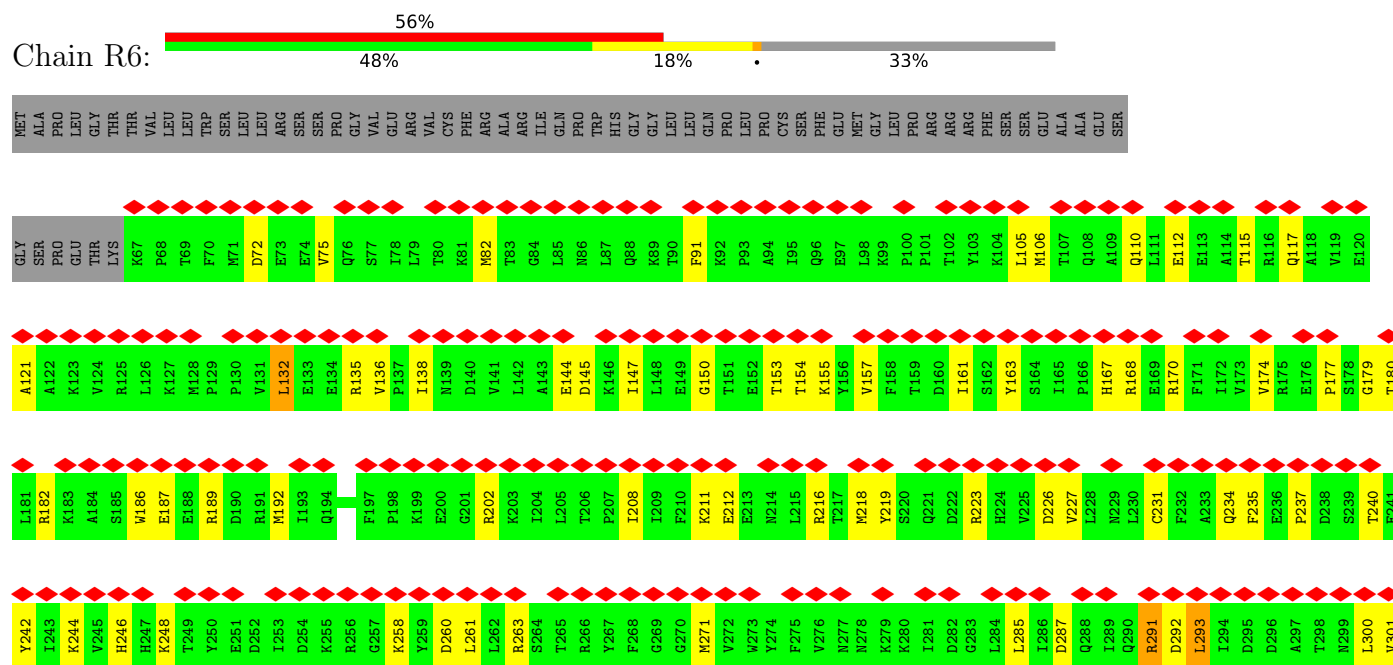
- Molecule 70: 28S ribosomal protein S18c, mitochondrial

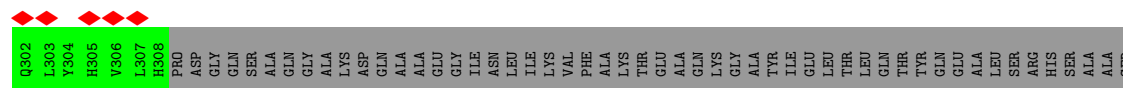


- Molecule 71: 28S ribosomal protein S21, mitochondrial



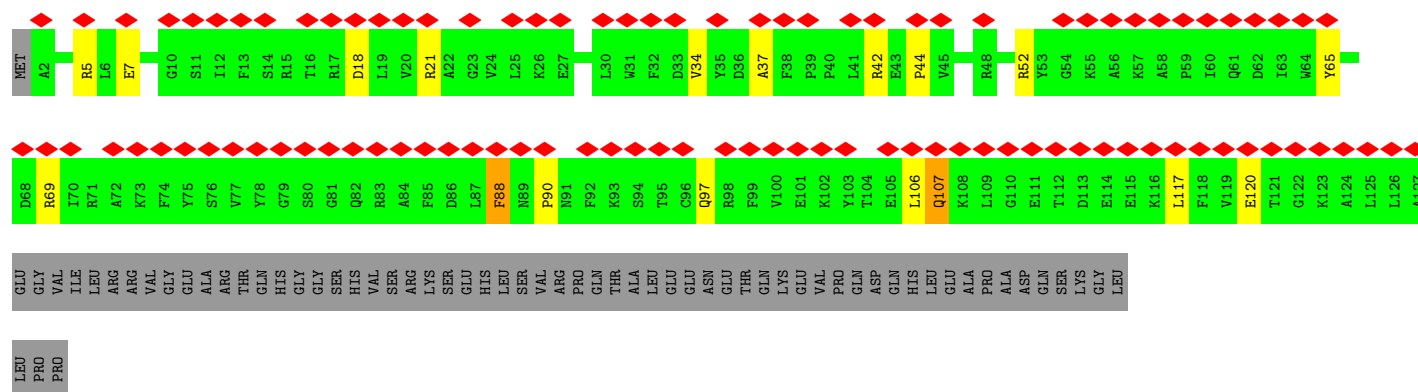
- Molecule 72: 28S ribosomal protein S22, mitochondrial





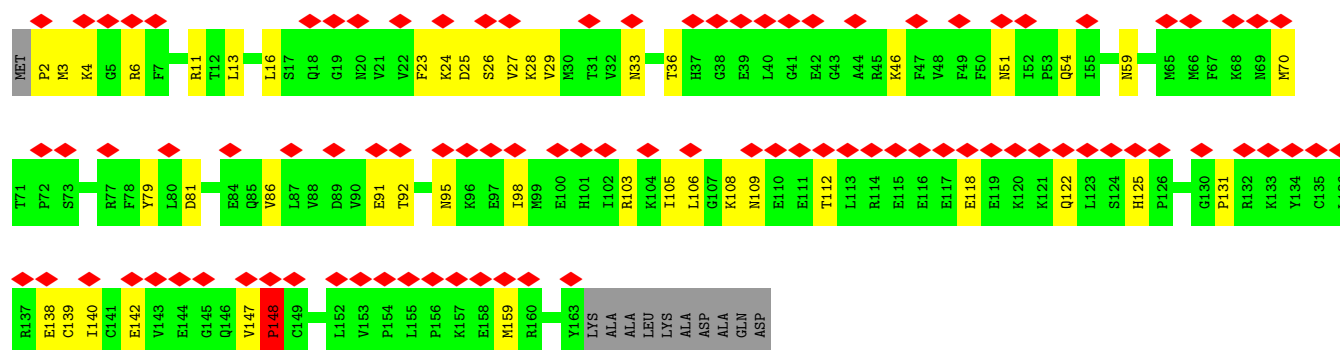
- Molecule 73: 28S ribosomal protein S23, mitochondrial

Chain S6: 52%
57% 8% 34%



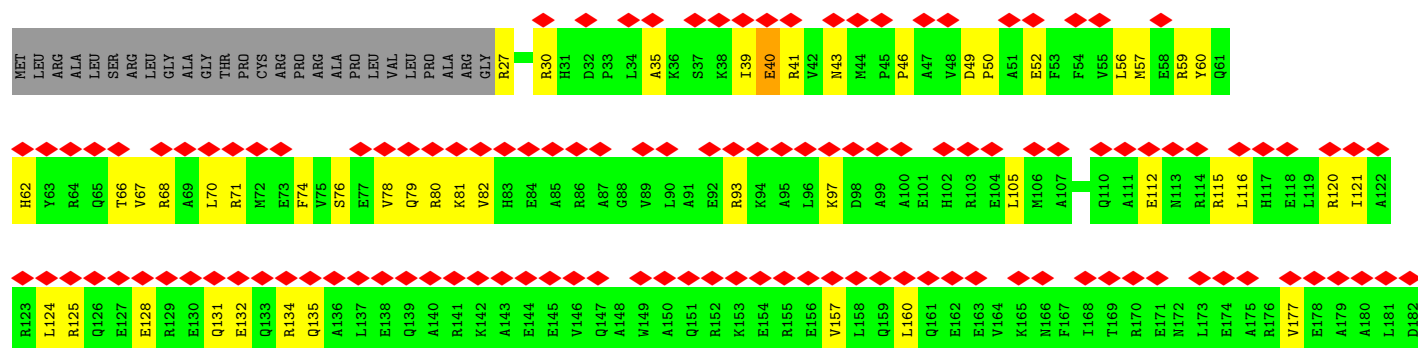
- Molecule 74: 28S ribosomal protein S25, mitochondrial

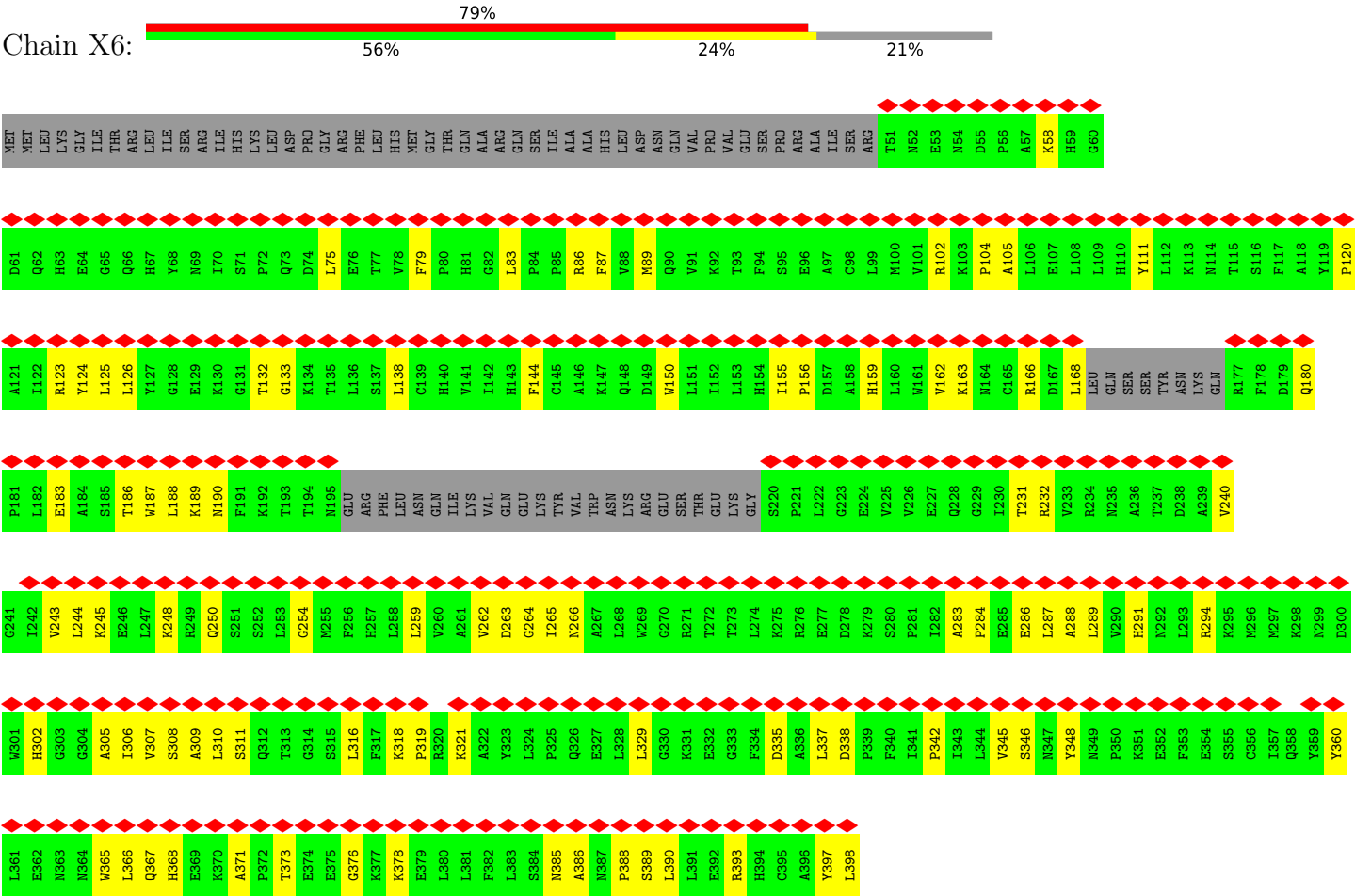
Chain T6: 54%
68% 25% 6%



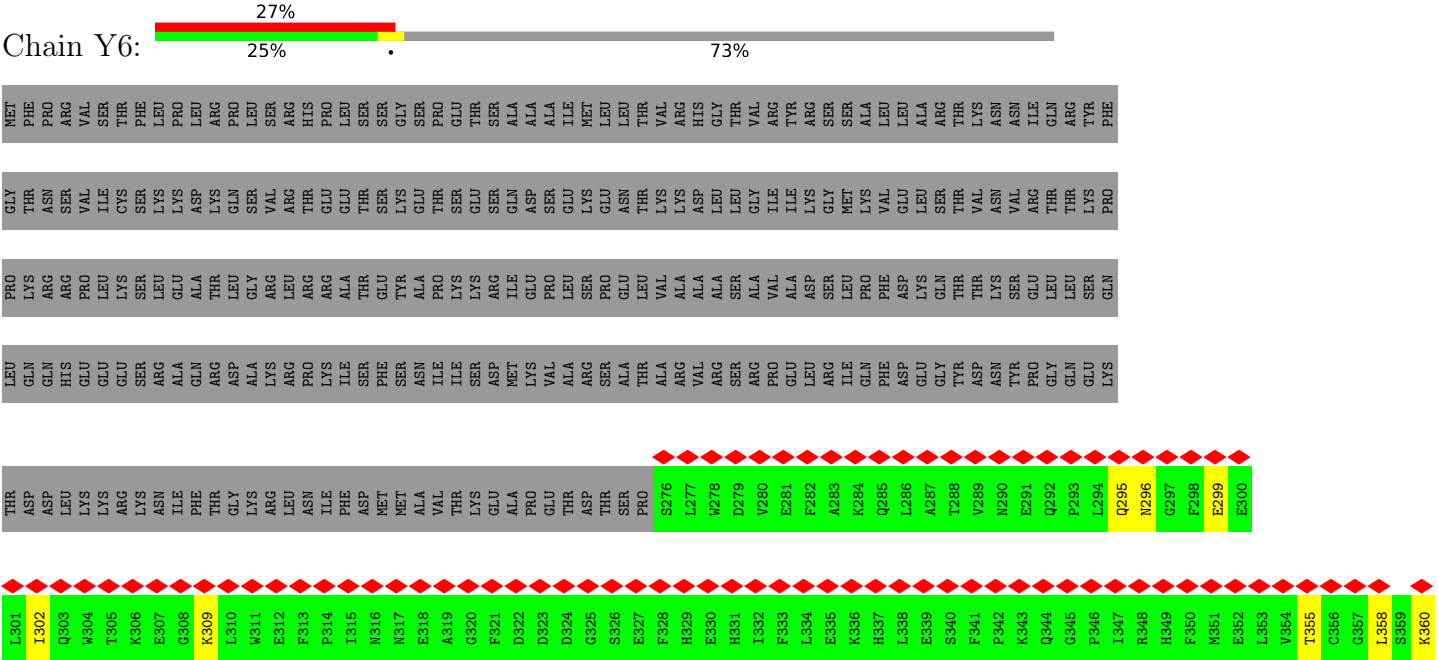
- Molecule 75: 28S ribosomal protein S26, mitochondrial

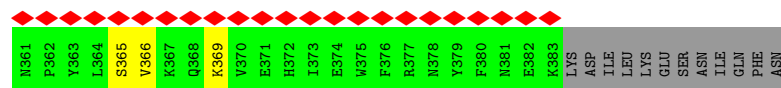
Chain U6: 66%
60% 24% 16%



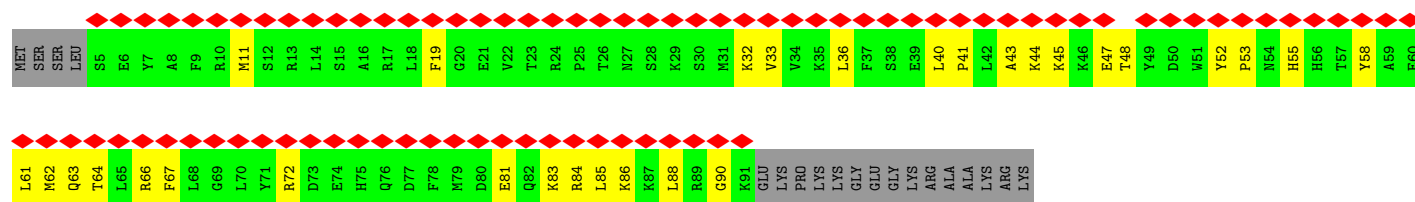
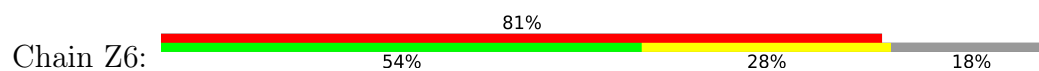


● Molecule 79: 28S ribosomal protein S31, mitochondrial

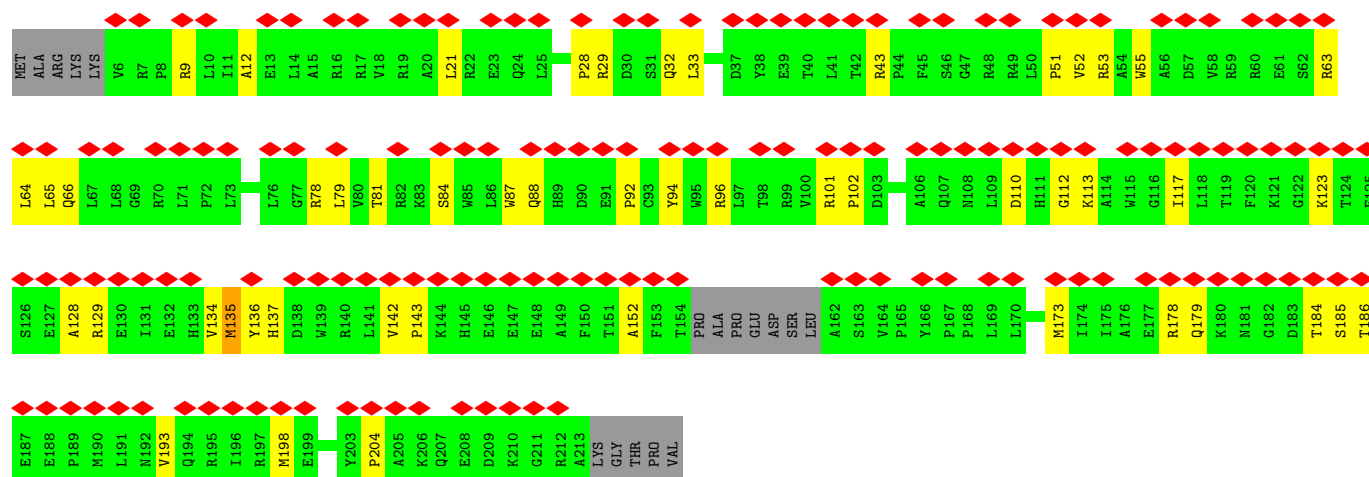




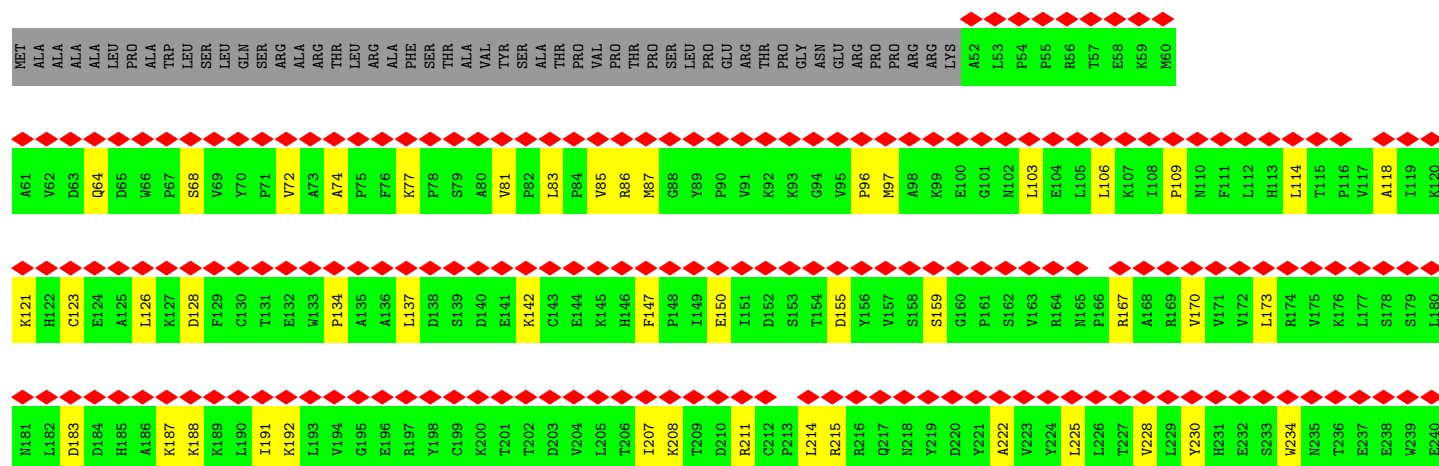
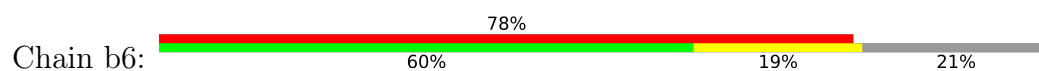
- Molecule 80: 28S ribosomal protein S33, mitochondrial



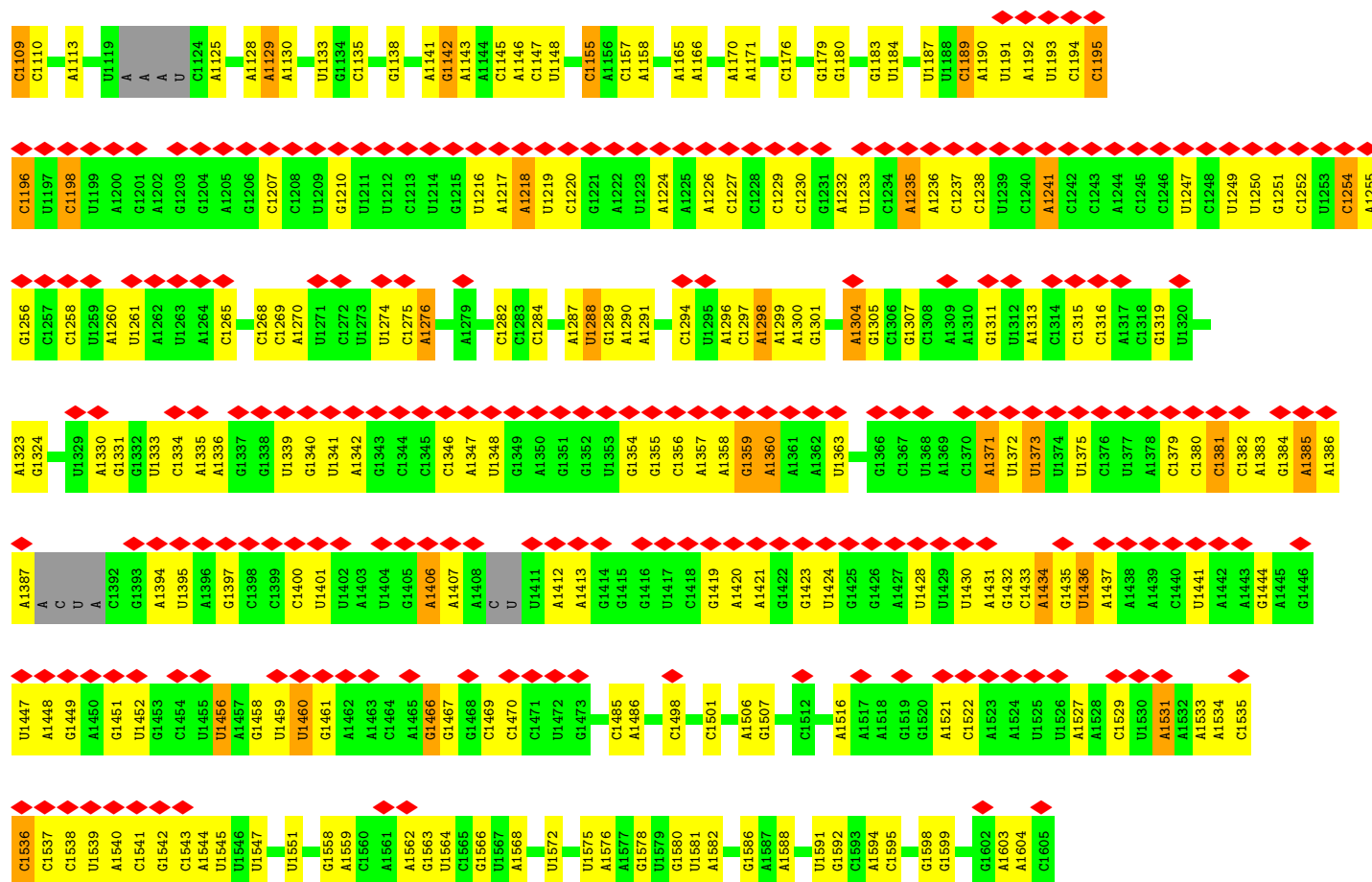
- Molecule 81: 28S ribosomal protein S34, mitochondrial



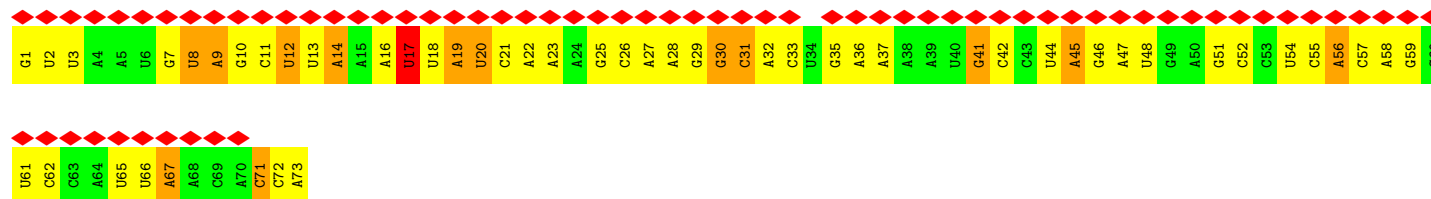
- Molecule 82: 28S ribosomal protein S35, mitochondrial



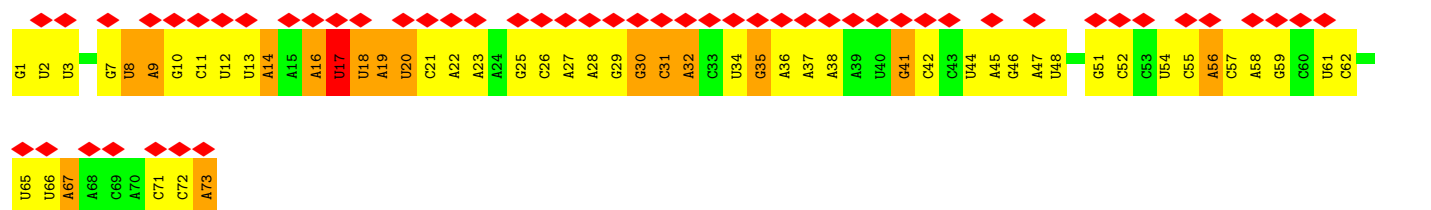
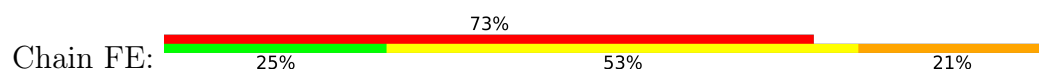




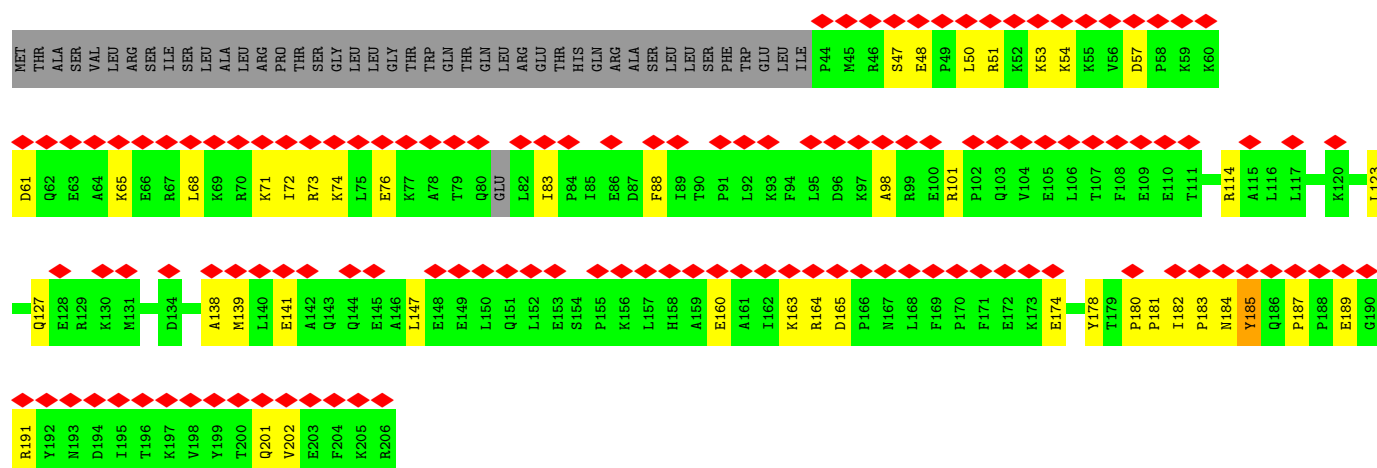
• Molecule 87: mt-tRNA



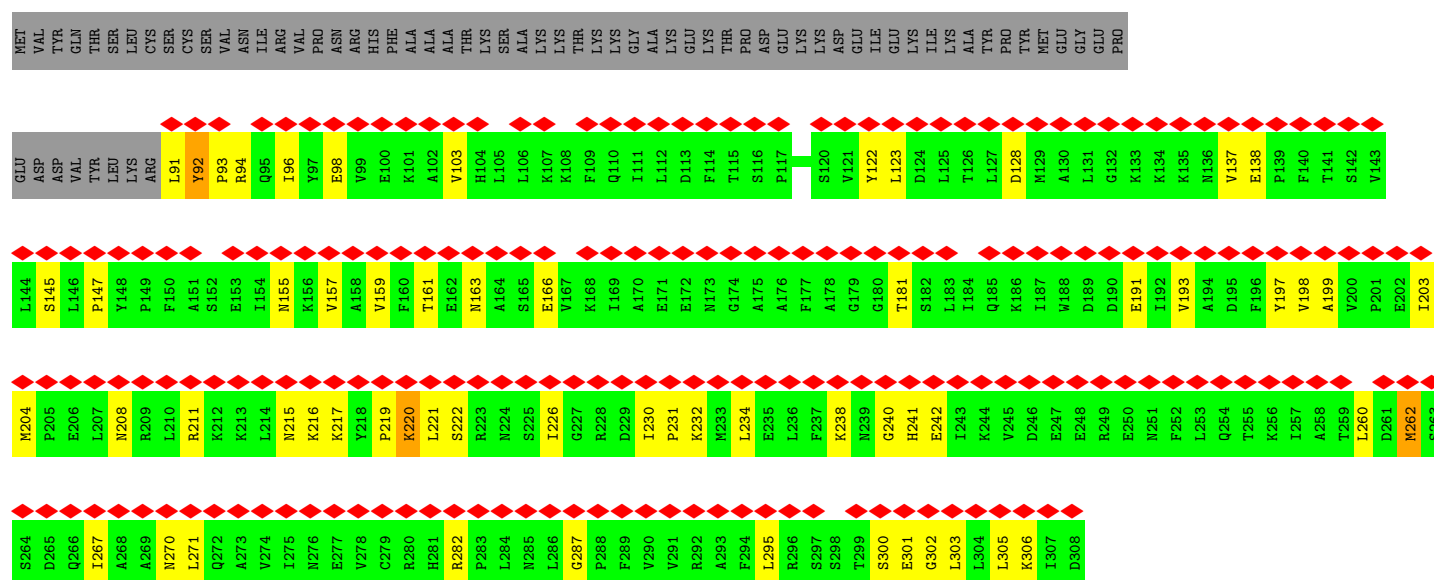
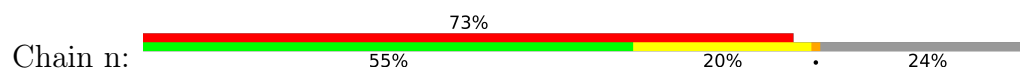
• Molecule 87: mt-tRNA



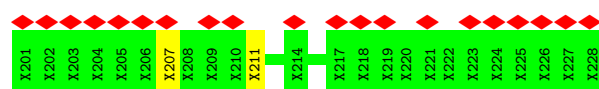
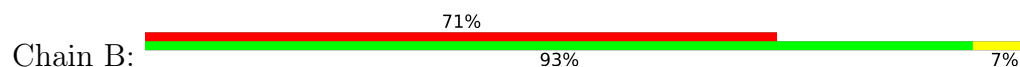
• Molecule 88: 39S ribosomal protein L40, mitochondrial



• Molecule 89: 39S ribosomal protein L1, mitochondrial



• Molecule 90: Unknown protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19767	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	0.294	Depositor
Minimum map value	-0.153	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: MG, GCP, SPD, ZN, GDP

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	r1	0.49	2/5552 (0.0%)	1.19	36/7490 (0.5%)
3	8	0.29	0/197	0.50	0/305
3	A3	0.50	0/35697	0.50	14/55544 (0.0%)
4	B3	0.29	0/1328	0.39	0/2056
5	D3	0.43	0/1879	0.74	1/2527 (0.0%)
6	E3	0.49	0/2433	0.76	6/3299 (0.2%)
7	F3	0.50	0/2071	0.81	0/2817
8	D	3.49	3/665 (0.5%)	1.20	5/905 (0.6%)
8	H3	0.40	0/798	0.80	0/1073
9	I3	0.39	0/1308	0.82	0/1761
10	J3	0.42	0/1077	0.87	0/1452
11	K3	0.54	0/1495	0.74	1/2029 (0.0%)
12	L3	0.46	0/904	0.75	2/1218 (0.2%)
13	M3	0.52	1/2359 (0.0%)	0.82	2/3185 (0.1%)
14	N3	0.50	0/1697	0.82	3/2281 (0.1%)
15	O3	0.51	0/1269	0.80	0/1708
16	P3	0.47	0/1103	0.82	0/1491
17	Q3	0.43	0/1863	0.76	2/2509 (0.1%)
18	R3	0.57	0/1174	0.73	1/1572 (0.1%)
19	S3	0.52	0/1276	0.76	0/1729
20	T3	0.49	0/1402	0.73	1/1886 (0.1%)
21	U3	0.54	0/946	0.75	0/1283
22	V3	0.40	0/1590	0.83	3/2151 (0.1%)
23	W3	0.54	0/893	0.71	0/1204
24	X3	0.42	0/2081	0.86	11/2812 (0.4%)
25	Y3	0.51	1/1552 (0.1%)	0.71	0/2079
26	Z3	0.50	0/1003	0.69	0/1354
27	03	0.45	0/895	0.79	0/1201
28	13	0.45	0/438	0.94	0/583
29	23	0.56	0/382	0.68	0/507
30	33	0.55	0/852	0.67	0/1136
31	43	0.53	0/329	0.64	0/435

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	53	0.42	1/3154 (0.0%)	0.74	3/4295 (0.1%)
33	63	0.43	0/2722	0.78	0/3709
34	73	0.40	0/2207	0.75	1/2978 (0.0%)
35	93	0.41	0/896	0.82	3/1205 (0.2%)
36	a3	0.43	0/709	0.68	0/963
37	b3	0.48	0/1202	0.75	1/1626 (0.1%)
38	c3	0.42	0/2264	0.72	0/3059
39	d3	0.42	0/1385	0.95	8/1877 (0.4%)
40	e3	0.32	0/1797	0.76	0/2422
41	f3	0.44	0/1055	1.09	7/1427 (0.5%)
42	g3	0.55	0/1102	0.77	0/1503
43	h3	0.38	0/847	0.86	4/1150 (0.3%)
44	i3	0.55	0/849	0.76	0/1135
45	j3	0.42	0/698	0.73	0/940
46	k3	0.34	0/665	0.83	0/897
47	l3	0.43	0/226	0.69	0/299
48	m3	0.37	0/379	0.77	0/510
49	o3	0.53	0/818	0.70	0/1097
50	p3	0.34	0/1071	0.67	2/1433 (0.1%)
51	q3	0.37	0/1107	0.70	0/1498
52	r3	0.51	0/1238	0.77	1/1676 (0.1%)
53	s3	0.47	0/3114	0.94	3/4225 (0.1%)
54	u3	0.43	0/46	0.31	0/69
55	A5	0.34	0/135	0.99	1/185 (0.5%)
56	B6	0.36	0/1811	0.80	0/2451
57	C6	0.28	0/1112	0.65	0/1505
58	D6	0.38	0/2607	0.82	4/3498 (0.1%)
59	E6	0.35	0/989	0.80	0/1335
60	F6	0.40	1/1708 (0.1%)	0.83	7/2291 (0.3%)
61	G6	0.33	0/2570	0.76	0/3443
62	H6	0.30	0/1019	0.80	2/1379 (0.1%)
63	I6	0.33	0/1031	0.84	2/1390 (0.1%)
64	J6	0.58	1/854 (0.1%)	0.87	0/1148
65	K6	0.33	0/879	0.79	0/1182
66	L6	0.31	0/1406	0.76	1/1878 (0.1%)
67	M6	0.41	0/941	0.98	3/1265 (0.2%)
68	N6	0.50	1/864 (0.1%)	0.85	3/1169 (0.3%)
69	O6	0.36	0/1580	0.84	1/2150 (0.0%)
70	P6	0.36	0/791	0.84	0/1062
71	Q6	0.38	0/752	0.87	1/1001 (0.1%)
72	R6	0.33	0/2050	0.84	3/2770 (0.1%)
73	S6	0.59	1/1069 (0.1%)	1.12	8/1441 (0.6%)
74	T6	0.40	0/1361	0.89	1/1829 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	U6	0.33	1/1482 (0.1%)	0.75	2/1987 (0.1%)
76	V6	0.30	0/2758	0.78	6/3724 (0.2%)
77	W6	0.31	0/778	0.82	0/1048
78	X6	0.30	0/2596	0.75	0/3519
79	Y6	0.29	0/943	0.70	0/1274
80	Z6	0.27	0/757	0.75	2/1011 (0.2%)
81	a6	0.39	1/1727 (0.1%)	0.85	2/2338 (0.1%)
82	b6	0.31	0/2121	0.83	4/2873 (0.1%)
83	c6	0.32	0/939	0.74	0/1256
84	d6	0.40	0/621	0.78	0/820
85	e6	0.28	0/2859	0.81	3/3864 (0.1%)
86	A6	0.32	0/22053	0.44	0/34324
87	24	0.52	6/1731 (0.3%)	0.51	1/2693 (0.0%)
87	FE	0.52	6/1731 (0.3%)	0.51	1/2693 (0.0%)
88	A	0.34	0/1403	0.91	6/1880 (0.3%)
89	n	3.25	9/1776 (0.5%)	0.90	3/2397 (0.1%)
All	All	0.58	35/179863 (0.0%)	0.71	188/255648 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	r1	0	23
2	Y2	0	2
5	D3	0	1
6	E3	0	5
7	F3	0	2
8	D	0	2
8	H3	0	1
9	I3	0	1
10	J3	0	2
11	K3	0	2
13	M3	0	4
14	N3	0	2
15	O3	0	1
17	Q3	0	1
18	R3	0	1
20	T3	0	1
22	V3	0	2
24	X3	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
26	Z3	0	1
27	03	0	2
28	13	0	2
32	53	0	4
33	63	0	2
35	93	0	1
38	c3	0	1
39	d3	0	5
41	f3	0	4
42	g3	0	1
43	h3	0	2
44	i3	0	1
45	j3	0	1
49	o3	0	1
51	q3	0	1
53	s3	0	2
56	B6	0	1
58	D6	0	4
60	F6	0	4
61	G6	0	1
63	I6	0	2
64	J6	0	1
68	N6	0	1
69	O6	0	3
70	P6	0	3
72	R6	0	3
73	S6	0	1
75	U6	0	2
76	V6	0	2
81	a6	0	1
82	b6	0	1
83	c6	0	1
85	e6	0	2
88	A	0	6
89	n	0	1
All	All	0	125

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	n	220	LYS	CE-NZ	104.36	4.62	1.49
8	D	194	PHE	CB-CG	88.76	3.54	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	n	92	TYR	CD1-CE1	44.49	2.72	1.38
89	n	92	TYR	CD2-CE2	42.39	2.65	1.38
89	n	92	TYR	CE2-CZ	32.60	2.16	1.38

The worst 5 of 188 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	s3	427	ASN	CA-C-N	27.57	159.64	120.49
53	s3	427	ASN	C-N-CA	27.57	159.64	120.49
73	S6	90	PRO	N-CD-CG	-18.72	75.12	103.20
3	A3	2790	A	OP1-P-OP2	-14.48	76.15	119.60
8	D	194	PHE	CA-CB-CG	13.85	127.64	113.80

There are no chirality outliers.

5 of 125 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	r1	162	MET	Peptide
1	r1	53	ALA	Peptide
1	r1	57	SER	Peptide
1	r1	78	GLU	Peptide
1	r1	98	ARG	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	r1	5452	0	5425	125	0
2	Y2	145	0	37	0	0
3	8	175	0	88	2	0
3	A3	31913	0	16215	211	0
4	B3	1191	0	607	3	0
5	D3	1842	0	1895	32	0
6	E3	2365	0	2378	23	0
7	F3	2013	0	2044	32	0
8	D	648	0	657	33	0
8	H3	784	0	832	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	I3	1283	0	1369	33	0
10	J3	1061	0	1141	17	0
11	K3	1451	0	1448	23	0
12	L3	889	0	941	8	0
13	M3	2305	0	2378	42	0
14	N3	1654	0	1681	17	0
15	O3	1245	0	1283	27	0
16	P3	1080	0	1081	20	0
17	Q3	1822	0	1859	25	0
18	R3	1153	0	1214	28	0
19	S3	1251	0	1322	30	0
20	T3	1368	0	1410	19	0
21	U3	922	0	935	16	0
22	V3	1551	0	1558	28	0
23	W3	871	0	898	17	0
24	X3	2027	0	2040	24	0
25	Y3	1517	0	1561	24	0
26	Z3	978	0	1030	12	0
27	03	880	0	902	17	0
28	13	433	0	475	10	0
29	23	376	0	406	7	0
30	33	831	0	883	10	0
31	43	322	0	343	4	0
32	53	3064	0	3059	43	0
33	63	2636	0	2450	27	0
34	73	2158	0	2173	27	0
35	93	873	0	878	13	0
36	a3	686	0	658	9	0
37	b3	1178	0	1180	27	0
38	c3	2217	0	2220	26	0
39	d3	1347	0	1343	18	0
40	e3	1762	0	1767	40	0
41	f3	1039	0	1044	21	0
42	g3	1067	0	1056	15	0
43	h3	827	0	806	11	0
44	i3	827	0	857	11	0
45	j3	684	0	673	10	0
46	k3	655	0	656	15	0
47	l3	221	0	227	4	0
48	m3	372	0	387	12	0
49	o3	797	0	804	15	0
50	p3	1058	0	1083	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	q3	1076	0	1049	15	0
52	r3	1203	0	1220	21	0
53	s3	3036	0	3021	34	0
54	u3	42	0	23	2	0
55	A5	136	0	67	0	0
56	B6	1768	0	1765	51	0
57	C6	1082	0	1088	31	0
58	D6	2557	0	2596	45	0
59	E6	972	0	1000	25	0
60	F6	1668	0	1716	48	0
61	G6	2516	0	2503	54	0
62	H6	999	0	1024	37	0
63	I6	1011	0	1052	33	0
64	J6	838	0	887	16	0
65	K6	861	0	885	33	0
66	L6	1382	0	1472	26	0
67	M6	920	0	951	28	0
68	N6	846	0	908	15	0
69	O6	1528	0	1488	37	0
70	P6	774	0	801	21	0
71	Q6	740	0	754	20	0
72	R6	2008	0	2031	49	0
73	S6	1042	0	1037	15	0
74	T6	1330	0	1342	35	0
75	U6	1461	0	1471	38	0
76	V6	2702	0	2690	45	0
77	W6	766	0	785	16	0
78	X6	2531	0	2520	67	0
79	Y6	914	0	859	10	0
80	Z6	740	0	747	19	0
81	a6	1684	0	1685	40	0
82	b6	2076	0	2097	45	0
83	c6	925	0	962	18	0
84	d6	610	0	682	6	0
85	e6	2838	0	2416	35	0
86	A6	19716	0	10015	155	0
87	24	1547	0	787	20	0
87	FE	1547	0	788	45	0
88	A	1375	0	1426	31	0
89	n	1744	0	1796	74	0
90	B	140	0	32	1	0
91	r1	32	0	14	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
92	A3	95	0	0	0	0
92	A6	28	0	0	0	0
92	D3	1	0	0	0	0
92	E3	1	0	0	0	0
92	M3	1	0	0	0	0
92	g3	1	0	0	0	0
92	r1	1	0	0	0	0
93	A3	10	0	19	0	0
94	O3	1	0	0	0	0
94	43	1	0	0	0	0
94	B6	1	0	0	0	0
94	O6	1	0	0	0	0
94	P6	1	0	0	0	0
94	T6	1	0	0	0	0
94	r3	1	0	0	0	0
95	X6	28	0	12	1	0
All	All	171122	0	144140	2127	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 2127 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
89:n:92:TYR:CG	89:n:92:TYR:CD1	1.99	1.49
89:n:92:TYR:CG	89:n:92:TYR:CD2	2.00	1.47
89:n:92:TYR:CE1	89:n:92:TYR:CZ	2.16	1.34
89:n:92:TYR:CZ	89:n:92:TYR:CE2	2.16	1.33
60:F6:161:ILE:HB	87:FE:30:G:H2'	1.54	0.88

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	r1	694/751 (92%)	523 (75%)	159 (23%)	12 (2%)	7	34
5	D3	234/305 (77%)	216 (92%)	17 (7%)	1 (0%)	30	60
6	E3	296/348 (85%)	258 (87%)	38 (13%)	0	100	100
7	F3	248/311 (80%)	224 (90%)	24 (10%)	0	100	100
8	D	78/267 (29%)	60 (77%)	18 (23%)	0	100	100
8	H3	93/267 (35%)	84 (90%)	9 (10%)	0	100	100
9	I3	154/261 (59%)	145 (94%)	9 (6%)	0	100	100
10	J3	138/192 (72%)	124 (90%)	14 (10%)	0	100	100
11	K3	175/178 (98%)	153 (87%)	19 (11%)	3 (2%)	7	34
12	L3	113/145 (78%)	104 (92%)	9 (8%)	0	100	100
13	M3	285/296 (96%)	254 (89%)	30 (10%)	1 (0%)	30	60
14	N3	203/251 (81%)	189 (93%)	12 (6%)	2 (1%)	12	43
15	O3	150/175 (86%)	130 (87%)	19 (13%)	1 (1%)	18	50
16	P3	129/179 (72%)	118 (92%)	11 (8%)	0	100	100
17	Q3	217/292 (74%)	192 (88%)	25 (12%)	0	100	100
18	R3	138/149 (93%)	128 (93%)	10 (7%)	0	100	100
19	S3	154/205 (75%)	139 (90%)	15 (10%)	0	100	100
20	T3	164/212 (77%)	152 (93%)	12 (7%)	0	100	100
21	U3	109/153 (71%)	96 (88%)	13 (12%)	0	100	100
22	V3	183/216 (85%)	155 (85%)	26 (14%)	2 (1%)	11	42
23	W3	109/148 (74%)	103 (94%)	6 (6%)	0	100	100
24	X3	241/256 (94%)	220 (91%)	20 (8%)	1 (0%)	30	60
25	Y3	174/250 (70%)	161 (92%)	12 (7%)	1 (1%)	21	52
26	Z3	118/161 (73%)	108 (92%)	10 (8%)	0	100	100
27	03	106/188 (56%)	94 (89%)	11 (10%)	1 (1%)	14	45
28	13	50/65 (77%)	46 (92%)	3 (6%)	1 (2%)	6	32
29	23	44/92 (48%)	42 (96%)	2 (4%)	0	100	100
30	33	93/188 (50%)	89 (96%)	4 (4%)	0	100	100
31	43	34/103 (33%)	34 (100%)	0	0	100	100
32	53	368/423 (87%)	326 (89%)	40 (11%)	2 (0%)	24	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	63	313/380 (82%)	283 (90%)	30 (10%)	0	100	100
34	73	258/338 (76%)	233 (90%)	25 (10%)	0	100	100
35	93	105/137 (77%)	88 (84%)	17 (16%)	0	100	100
36	a3	78/142 (55%)	74 (95%)	4 (5%)	0	100	100
37	b3	146/155 (94%)	132 (90%)	13 (9%)	1 (1%)	18	50
38	c3	271/332 (82%)	251 (93%)	20 (7%)	0	100	100
39	d3	156/306 (51%)	139 (89%)	15 (10%)	2 (1%)	9	38
40	e3	211/279 (76%)	193 (92%)	18 (8%)	0	100	100
41	f3	125/194 (64%)	103 (82%)	19 (15%)	3 (2%)	4	29
42	g3	127/166 (76%)	119 (94%)	8 (6%)	0	100	100
43	h3	96/158 (61%)	84 (88%)	11 (12%)	1 (1%)	12	43
44	i3	95/128 (74%)	87 (92%)	8 (8%)	0	100	100
45	j3	83/123 (68%)	78 (94%)	4 (5%)	1 (1%)	10	40
46	k3	82/112 (73%)	66 (80%)	16 (20%)	0	100	100
47	l3	21/138 (15%)	21 (100%)	0	0	100	100
48	m3	43/128 (34%)	36 (84%)	7 (16%)	0	100	100
49	o3	92/102 (90%)	86 (94%)	6 (6%)	0	100	100
50	p3	119/206 (58%)	113 (95%)	6 (5%)	0	100	100
51	q3	126/222 (57%)	119 (94%)	5 (4%)	2 (2%)	7	35
52	r3	140/196 (71%)	125 (89%)	15 (11%)	0	100	100
53	s3	366/439 (83%)	340 (93%)	26 (7%)	0	100	100
55	A5	26/435 (6%)	17 (65%)	9 (35%)	0	100	100
56	B6	215/296 (73%)	200 (93%)	15 (7%)	0	100	100
57	C6	130/167 (78%)	122 (94%)	8 (6%)	0	100	100
58	D6	316/430 (74%)	272 (86%)	44 (14%)	0	100	100
59	E6	120/125 (96%)	113 (94%)	6 (5%)	1 (1%)	16	48
60	F6	197/242 (81%)	182 (92%)	14 (7%)	1 (0%)	24	56
61	G6	301/396 (76%)	276 (92%)	25 (8%)	0	100	100
62	H6	120/201 (60%)	103 (86%)	17 (14%)	0	100	100
63	I6	134/194 (69%)	122 (91%)	12 (9%)	0	100	100
64	J6	106/138 (77%)	93 (88%)	13 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
65	K6	99/128 (77%)	88 (89%)	11 (11%)	0	100	100
66	L6	162/257 (63%)	151 (93%)	11 (7%)	0	100	100
67	M6	114/137 (83%)	100 (88%)	14 (12%)	0	100	100
68	N6	105/130 (81%)	93 (89%)	12 (11%)	0	100	100
69	O6	183/258 (71%)	159 (87%)	24 (13%)	0	100	100
70	P6	94/142 (66%)	82 (87%)	12 (13%)	0	100	100
71	Q6	84/87 (97%)	75 (89%)	9 (11%)	0	100	100
72	R6	240/360 (67%)	210 (88%)	30 (12%)	0	100	100
73	S6	124/190 (65%)	110 (89%)	14 (11%)	0	100	100
74	T6	160/173 (92%)	140 (88%)	19 (12%)	1 (1%)	21	52
75	U6	171/205 (83%)	159 (93%)	12 (7%)	0	100	100
76	V6	320/414 (77%)	287 (90%)	33 (10%)	0	100	100
77	W6	95/187 (51%)	81 (85%)	14 (15%)	0	100	100
78	X6	310/398 (78%)	264 (85%)	45 (14%)	1 (0%)	36	65
79	Y6	106/395 (27%)	96 (91%)	10 (9%)	0	100	100
80	Z6	85/106 (80%)	79 (93%)	6 (7%)	0	100	100
81	a6	197/218 (90%)	174 (88%)	23 (12%)	0	100	100
82	b6	252/323 (78%)	223 (88%)	29 (12%)	0	100	100
83	c6	114/118 (97%)	98 (86%)	15 (13%)	1 (1%)	14	45
84	d6	67/199 (34%)	62 (92%)	5 (8%)	0	100	100
85	e6	362/689 (52%)	328 (91%)	29 (8%)	5 (1%)	9	37
88	A	158/206 (77%)	139 (88%)	19 (12%)	0	100	100
89	n	216/286 (76%)	166 (77%)	50 (23%)	0	100	100
All	All	13828/19638 (70%)	12301 (89%)	1479 (11%)	48 (0%)	37	65

5 of 48 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	r1	365	PHE
1	r1	598	PRO
1	r1	623	GLU
1	r1	724	LEU
1	r1	725	PRO

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	
1	r1	592/630 (94%)	592 (100%)	0	100	100
5	D3	190/245 (78%)	190 (100%)	0	100	100
6	E3	255/290 (88%)	255 (100%)	0	100	100
7	F3	217/262 (83%)	217 (100%)	0	100	100
8	D	73/228 (32%)	73 (100%)	0	100	100
8	H3	86/228 (38%)	86 (100%)	0	100	100
9	I3	145/232 (62%)	145 (100%)	0	100	100
10	J3	113/150 (75%)	113 (100%)	0	100	100
11	K3	155/156 (99%)	154 (99%)	1 (1%)	78	79
12	L3	98/124 (79%)	98 (100%)	0	100	100
13	M3	245/249 (98%)	245 (100%)	0	100	100
14	N3	172/211 (82%)	172 (100%)	0	100	100
15	O3	133/150 (89%)	133 (100%)	0	100	100
16	P3	115/154 (75%)	114 (99%)	1 (1%)	70	75
17	Q3	201/256 (78%)	201 (100%)	0	100	100
18	R3	118/126 (94%)	118 (100%)	0	100	100
19	S3	141/180 (78%)	140 (99%)	1 (1%)	76	77
20	T3	146/182 (80%)	146 (100%)	0	100	100
21	U3	99/135 (73%)	99 (100%)	0	100	100
22	V3	169/191 (88%)	169 (100%)	0	100	100
23	W3	91/119 (76%)	91 (100%)	0	100	100
24	X3	217/227 (96%)	217 (100%)	0	100	100
25	Y3	159/223 (71%)	159 (100%)	0	100	100
26	Z3	111/147 (76%)	111 (100%)	0	100	100
27	03	97/164 (59%)	97 (100%)	0	100	100
28	13	49/60 (82%)	49 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	23	40/72 (56%)	40 (100%)	0	100	100
30	33	88/166 (53%)	88 (100%)	0	100	100
31	43	35/89 (39%)	35 (100%)	0	100	100
32	53	337/368 (92%)	336 (100%)	1 (0%)	86	83
33	63	266/332 (80%)	266 (100%)	0	100	100
34	73	242/303 (80%)	242 (100%)	0	100	100
35	93	91/112 (81%)	91 (100%)	0	100	100
36	a3	78/133 (59%)	78 (100%)	0	100	100
37	b3	130/135 (96%)	129 (99%)	1 (1%)	73	76
38	c3	241/288 (84%)	241 (100%)	0	100	100
39	d3	151/274 (55%)	151 (100%)	0	100	100
40	e3	188/236 (80%)	188 (100%)	0	100	100
41	f3	117/173 (68%)	117 (100%)	0	100	100
42	g3	119/148 (80%)	119 (100%)	0	100	100
43	h3	95/148 (64%)	95 (100%)	0	100	100
44	i3	86/110 (78%)	86 (100%)	0	100	100
45	j3	68/97 (70%)	68 (100%)	0	100	100
46	k3	74/90 (82%)	74 (100%)	0	100	100
47	l3	23/116 (20%)	23 (100%)	0	100	100
48	m3	40/113 (35%)	40 (100%)	0	100	100
49	o3	80/87 (92%)	80 (100%)	0	100	100
50	p3	117/181 (65%)	117 (100%)	0	100	100
51	q3	110/178 (62%)	110 (100%)	0	100	100
52	r3	133/169 (79%)	133 (100%)	0	100	100
53	s3	326/381 (86%)	326 (100%)	0	100	100
56	B6	191/249 (77%)	190 (100%)	1 (0%)	81	80
57	C6	115/143 (80%)	115 (100%)	0	100	100
58	D6	269/357 (75%)	269 (100%)	0	100	100
59	E6	104/107 (97%)	104 (100%)	0	100	100
60	F6	178/209 (85%)	178 (100%)	0	100	100
61	G6	265/342 (78%)	265 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	H6	112/180 (62%)	112 (100%)	0	100	100
63	I6	104/147 (71%)	104 (100%)	0	100	100
64	J6	93/118 (79%)	93 (100%)	0	100	100
65	K6	91/113 (80%)	91 (100%)	0	100	100
66	L6	152/226 (67%)	152 (100%)	0	100	100
67	M6	95/113 (84%)	95 (100%)	0	100	100
68	N6	93/115 (81%)	93 (100%)	0	100	100
69	O6	166/230 (72%)	166 (100%)	0	100	100
70	P6	87/123 (71%)	87 (100%)	0	100	100
71	Q6	78/79 (99%)	78 (100%)	0	100	100
72	R6	224/318 (70%)	224 (100%)	0	100	100
73	S6	109/164 (66%)	109 (100%)	0	100	100
74	T6	150/157 (96%)	150 (100%)	0	100	100
75	U6	149/174 (86%)	149 (100%)	0	100	100
76	V6	295/364 (81%)	295 (100%)	0	100	100
77	W6	84/158 (53%)	84 (100%)	0	100	100
78	X6	275/351 (78%)	275 (100%)	0	100	100
79	Y6	99/357 (28%)	99 (100%)	0	100	100
80	Z6	80/95 (84%)	80 (100%)	0	100	100
81	a6	176/190 (93%)	176 (100%)	0	100	100
82	b6	237/291 (81%)	237 (100%)	0	100	100
83	c6	99/101 (98%)	99 (100%)	0	100	100
84	d6	63/166 (38%)	63 (100%)	0	100	100
85	e6	226/609 (37%)	226 (100%)	0	100	100
88	A	151/190 (80%)	151 (100%)	0	100	100
89	n	194/254 (76%)	194 (100%)	0	100	100
All	All	12266/16608 (74%)	12260 (100%)	6 (0%)	100	100

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	53	275	ASN
37	b3	123	ASN

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Mol	Chain	Res	Type
56	B6	113	HIS
16	P3	54	ASN
11	K3	70	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 122 such sidechains are listed below:

Mol	Chain	Res	Type
48	m3	59	GLN
81	a6	108	ASN
60	F6	146	HIS
79	Y6	303	GLN
88	A	158	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	8	7/1559 (0%)	4 (57%)	0
3	A3	1490/1559 (95%)	415 (27%)	38 (2%)
4	B3	52/73 (71%)	16 (30%)	1 (1%)
54	u3	1/2 (50%)	0	0
86	A6	921/954 (96%)	267 (28%)	14 (1%)
87	24	73/73 (100%)	38 (52%)	1 (1%)
87	FE	73/73 (100%)	38 (52%)	1 (1%)
All	All	2617/4293 (60%)	778 (29%)	55 (2%)

5 of 778 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	A3	1674	A
3	A3	1676	A
3	A3	1678	C
3	A3	1679	U
3	A3	1680	A

5 of 55 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	A3	2788	C
3	A3	3157	C
87	FE	1	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
86	A6	1419	G
3	A3	2789	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 138 ligands modelled in this entry, 135 are monoatomic - leaving 3 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
95	GDP	X6	500	-	29,30,30	1.18	3 (10%)	45,47,47	1.84	8 (17%)
93	SPD	A3	3396	-	9,9,9	0.35	0	8,8,8	0.48	0
91	GCP	r1	801	92	32,34,34	3.34	16 (50%)	49,54,54	4.53	18 (36%)

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
95	GDP	X6	500	-	-	6/16/32/32	0/3/3/3
93	SPD	A3	3396	-	-	6/7/7/7	-
91	GCP	r1	801	92	-	7/19/38/38	0/3/3/3

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
91	r1	801	GCP	O6-C6	8.71	1.40	1.23
91	r1	801	GCP	C2'-C3'	-8.24	1.31	1.53
91	r1	801	GCP	PB-O3A	6.26	1.65	1.58
91	r1	801	GCP	O4'-C1'	-5.48	1.29	1.42
91	r1	801	GCP	C2-N2	5.21	1.46	1.34

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
91	r1	801	GCP	O3G-PG-C3B	-16.88	65.45	106.40
91	r1	801	GCP	O3G-PG-O1G	-14.68	74.41	112.39
91	r1	801	GCP	O1G-PG-C3B	12.89	139.50	111.37
91	r1	801	GCP	O3G-PG-O2G	12.39	143.27	107.96
95	X6	500	GDP	C5-C4-N3	-6.35	118.29	128.39

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

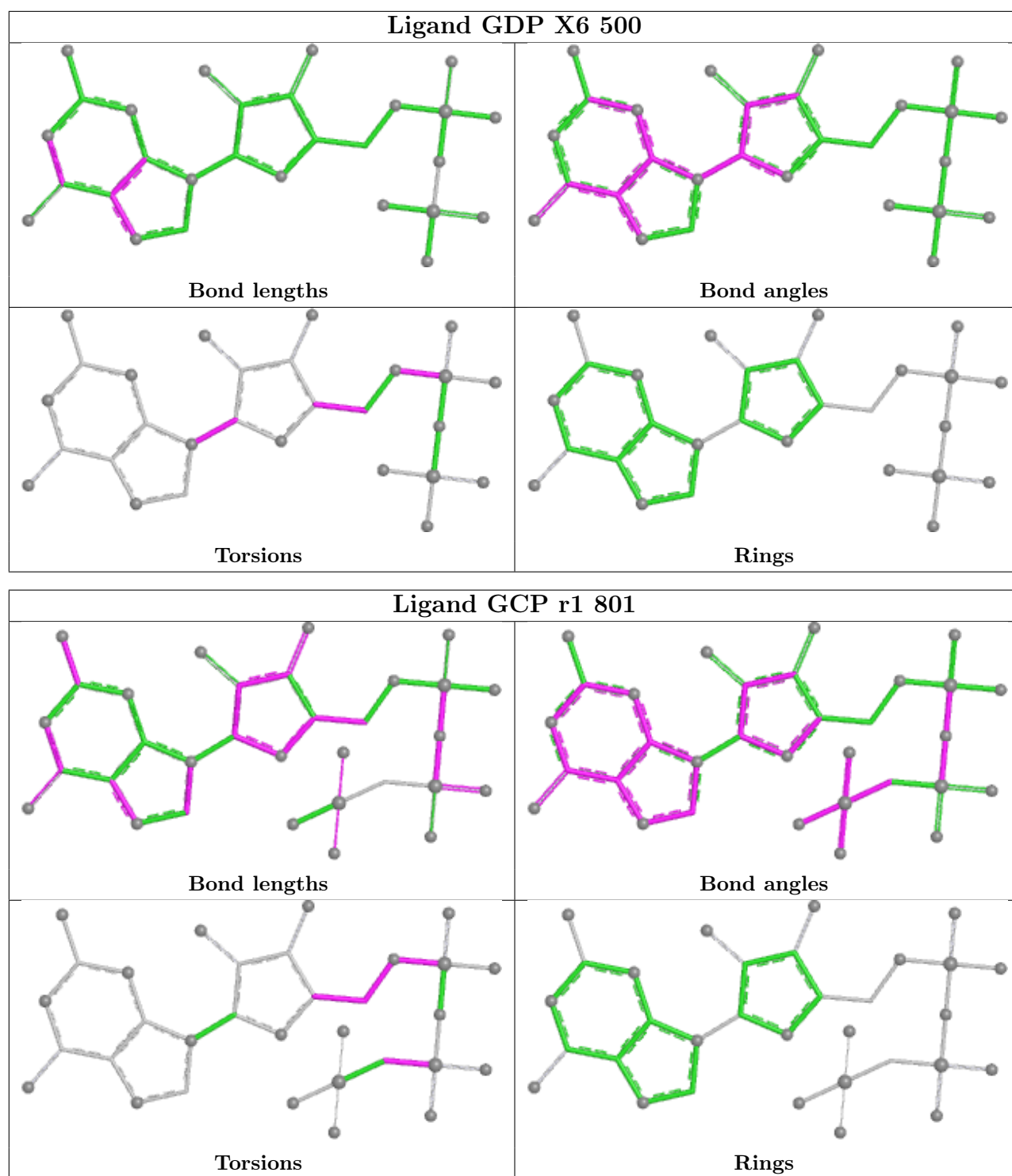
Mol	Chain	Res	Type	Atoms
91	r1	801	GCP	PG-C3B-PB-O1B
91	r1	801	GCP	PG-C3B-PB-O2B
91	r1	801	GCP	PG-C3B-PB-O3A
91	r1	801	GCP	C5'-O5'-PA-O1A
95	X6	500	GDP	C5'-O5'-PA-O3A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
95	X6	500	GDP	1	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
13	M3	1
25	Y3	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	M3	61:THR	C	62:ARG	N	1.19
1	Y3	123:ARG	C	124:LEU	N	1.19

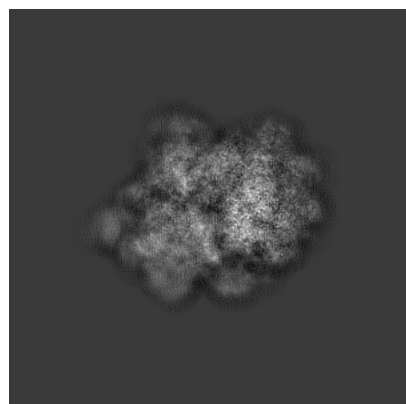
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11646. These allow visual inspection of the internal detail of the map and identification of artifacts.

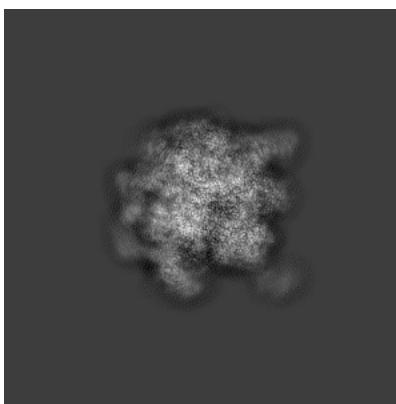
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

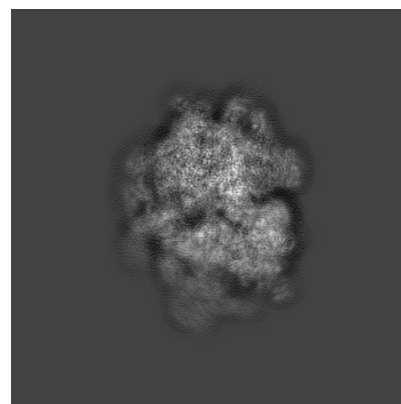
6.1.1 Primary map



X

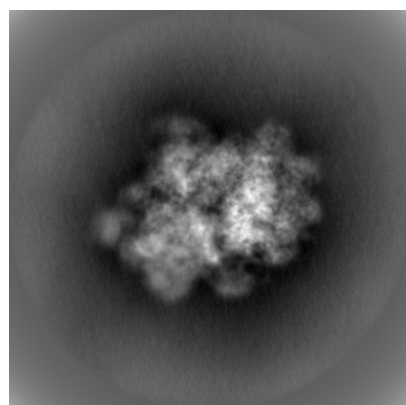


Y

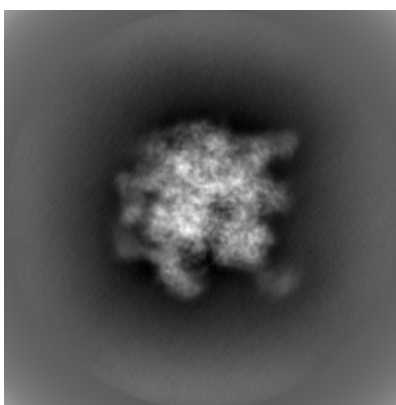


Z

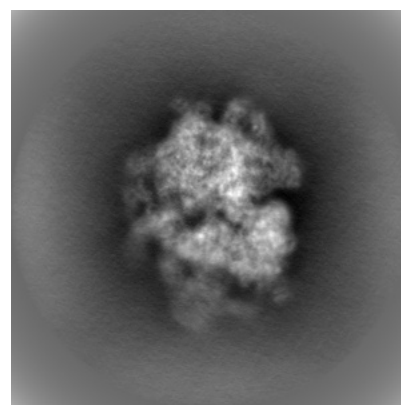
6.1.2 Raw map



X



Y

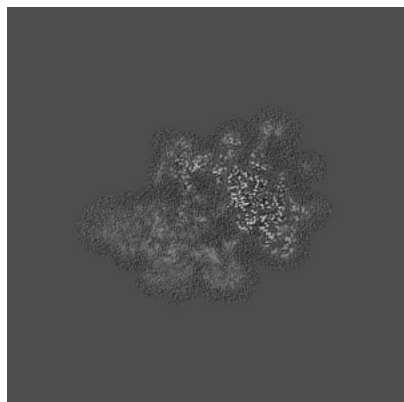


Z

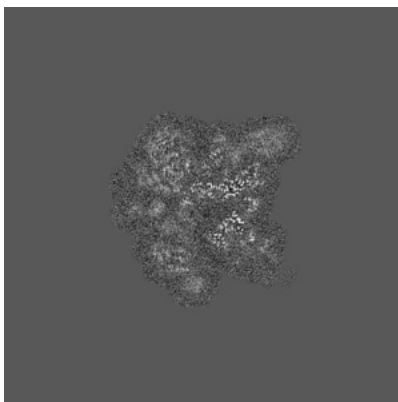
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

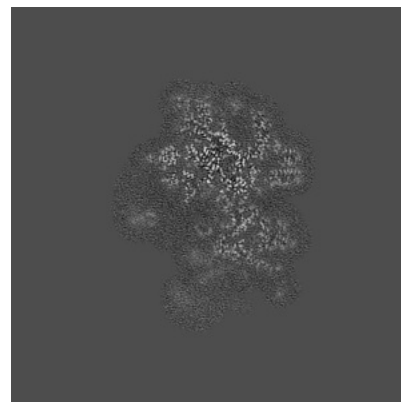
6.2.1 Primary map



X Index: 256

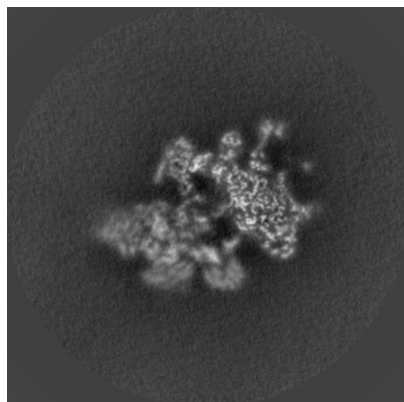


Y Index: 256

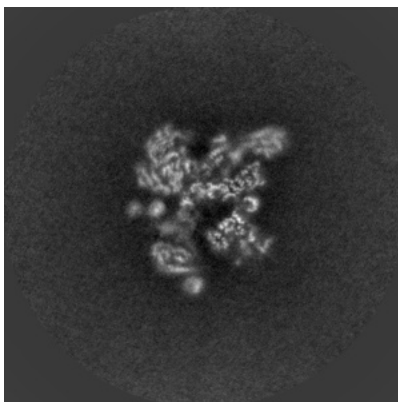


Z Index: 256

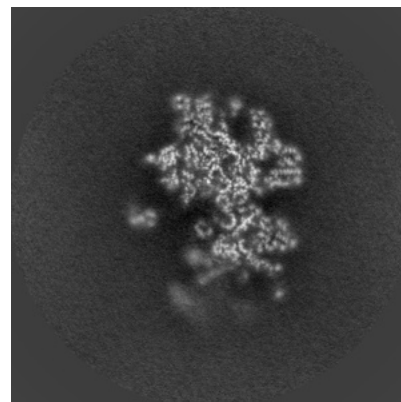
6.2.2 Raw map



X Index: 256



Y Index: 256

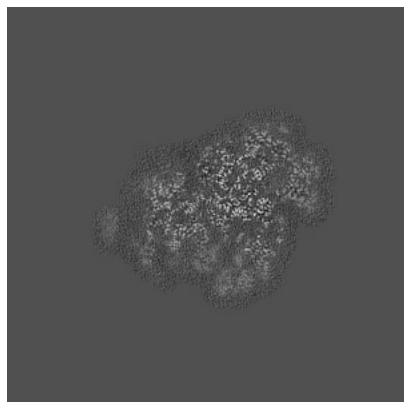


Z Index: 256

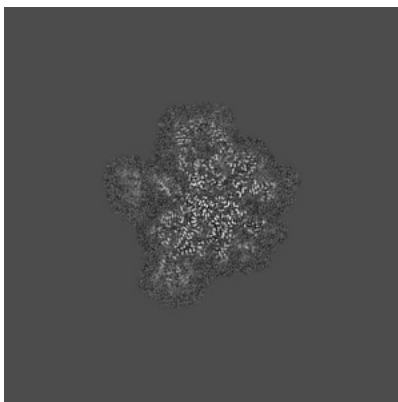
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

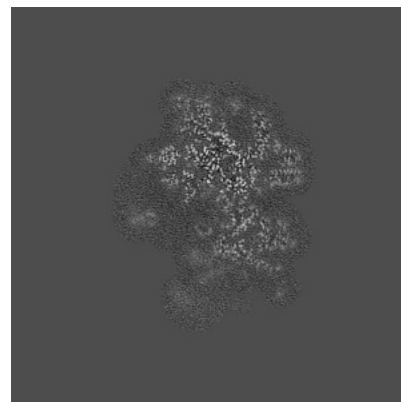
6.3.1 Primary map



X Index: 286

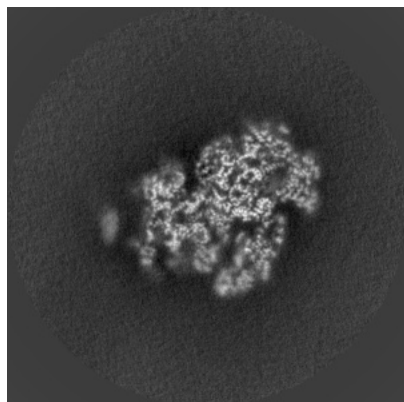


Y Index: 305

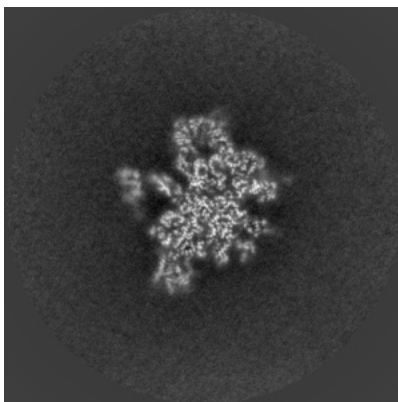


Z Index: 256

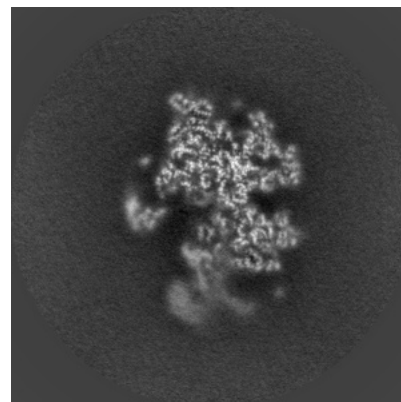
6.3.2 Raw map



X Index: 286



Y Index: 305

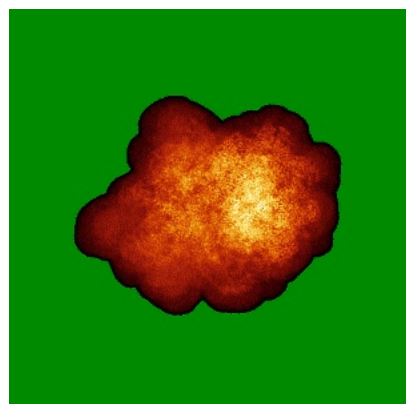


Z Index: 247

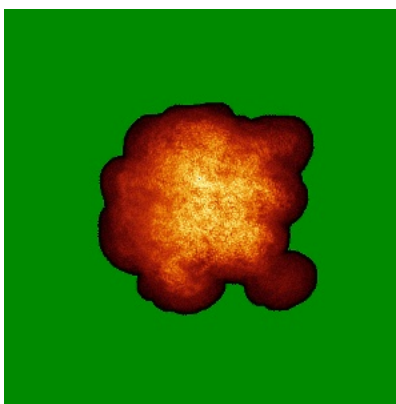
The images above show the largest variance slices of the map in three orthogonal directions.

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

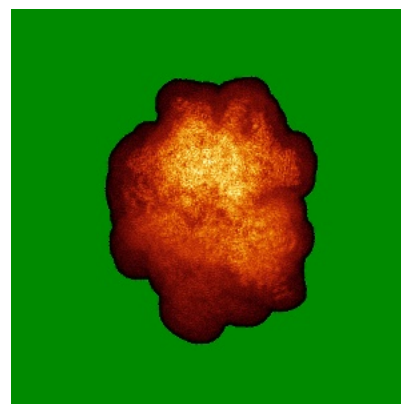
6.4.1 Primary map



X

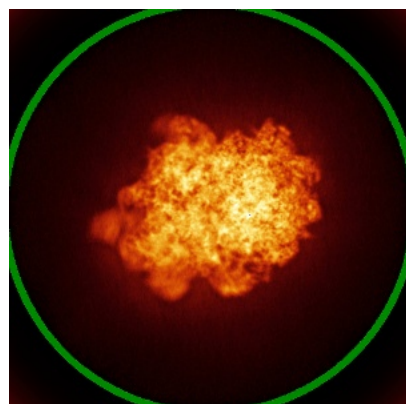


Y

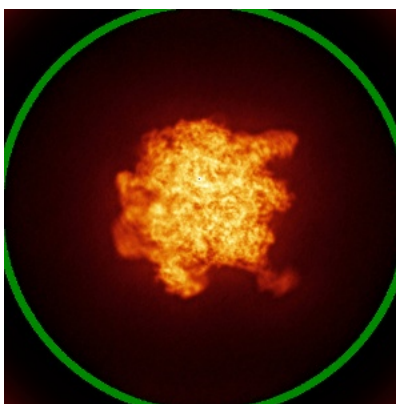


Z

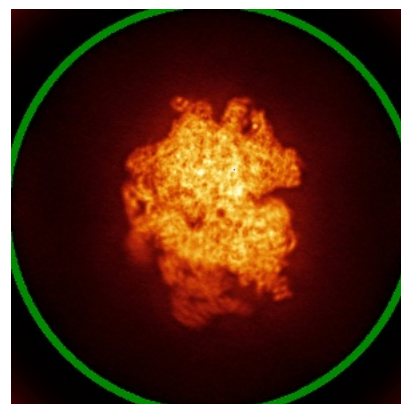
6.4.2 Raw map



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](#)

This section was not generated.

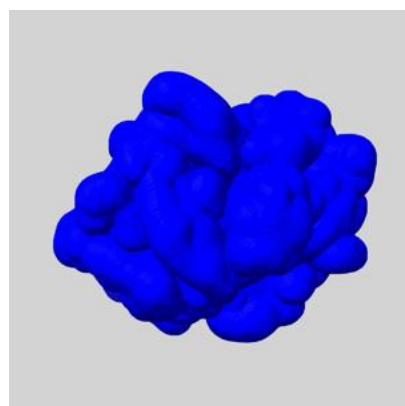
6.6 Mask visualisation [i](#)

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

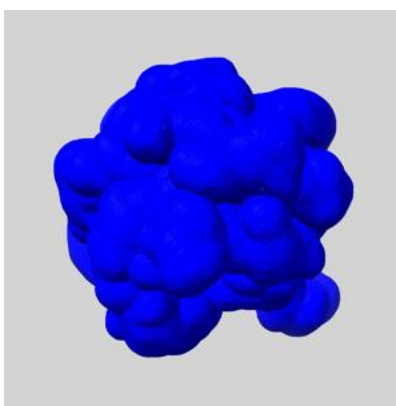
A mask typically either:

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

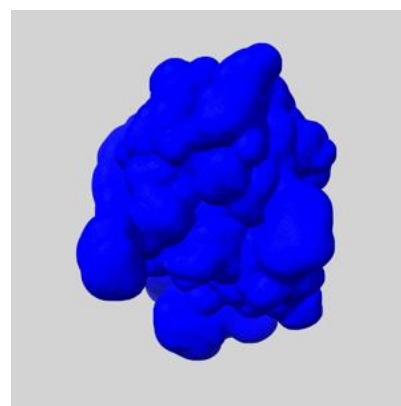
6.6.1 emd_11646_msk_1.map [i](#)



X



Y

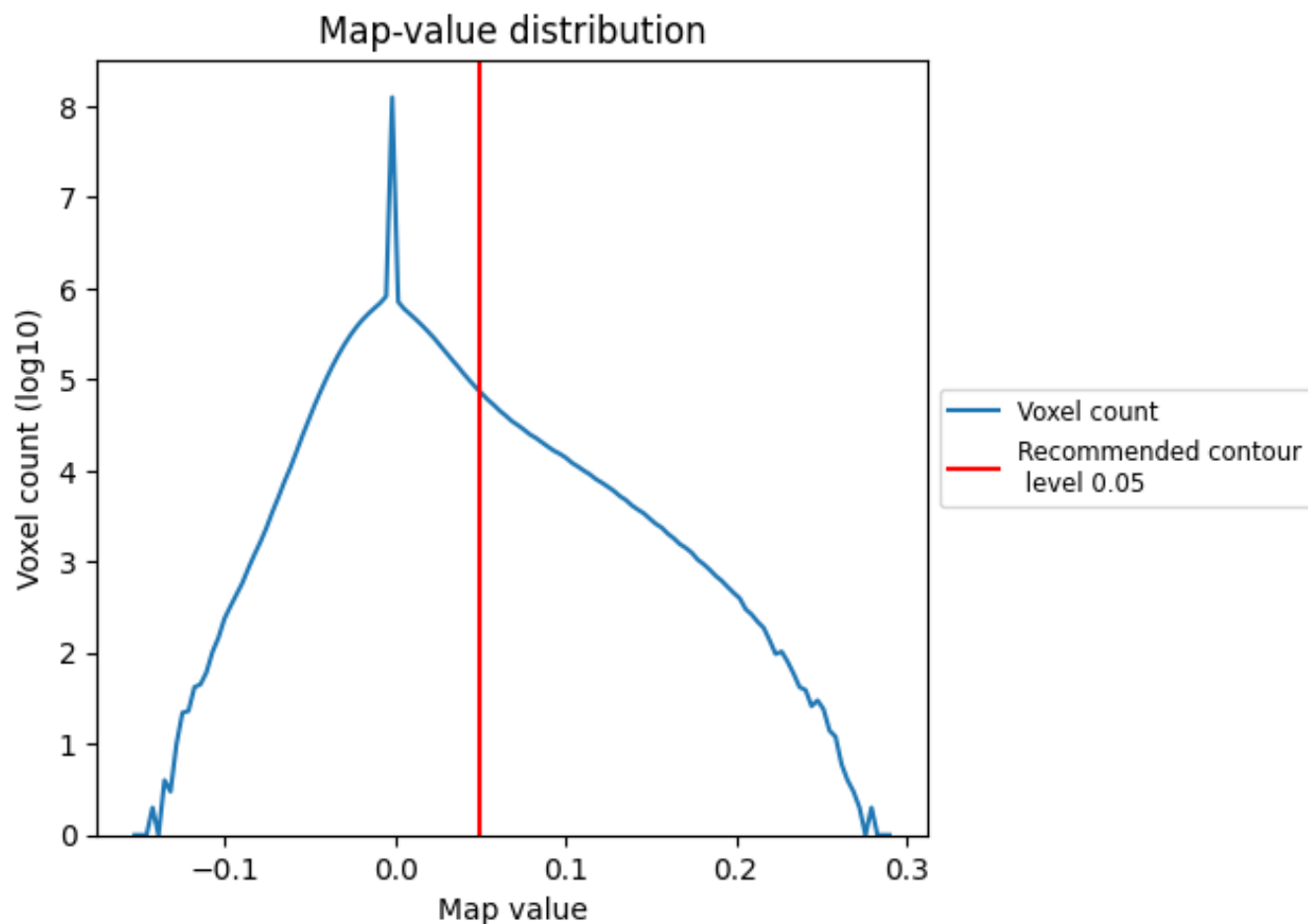


Z

7 Map analysis [i](#)

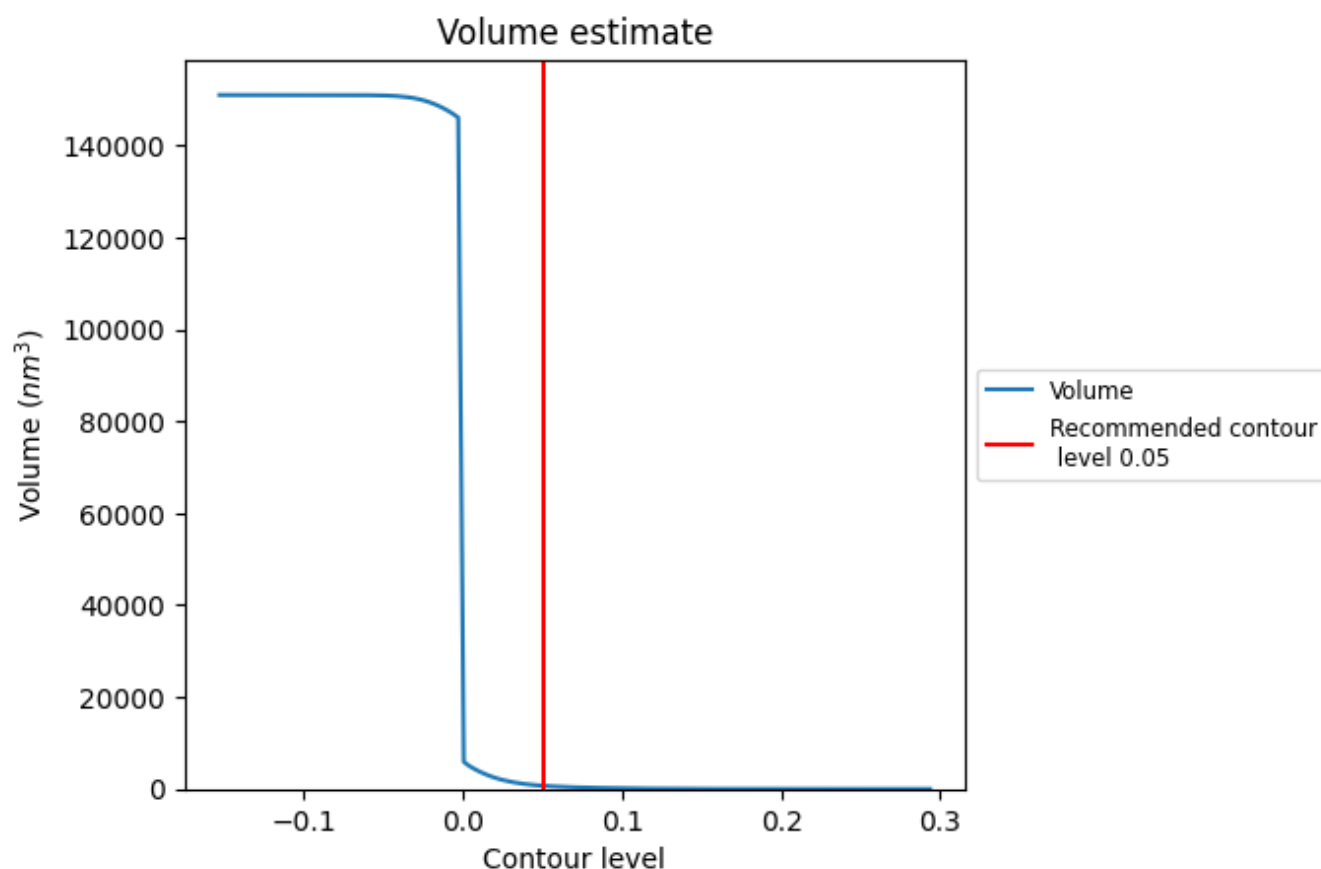
This section contains the results of statistical analysis of the map.

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.

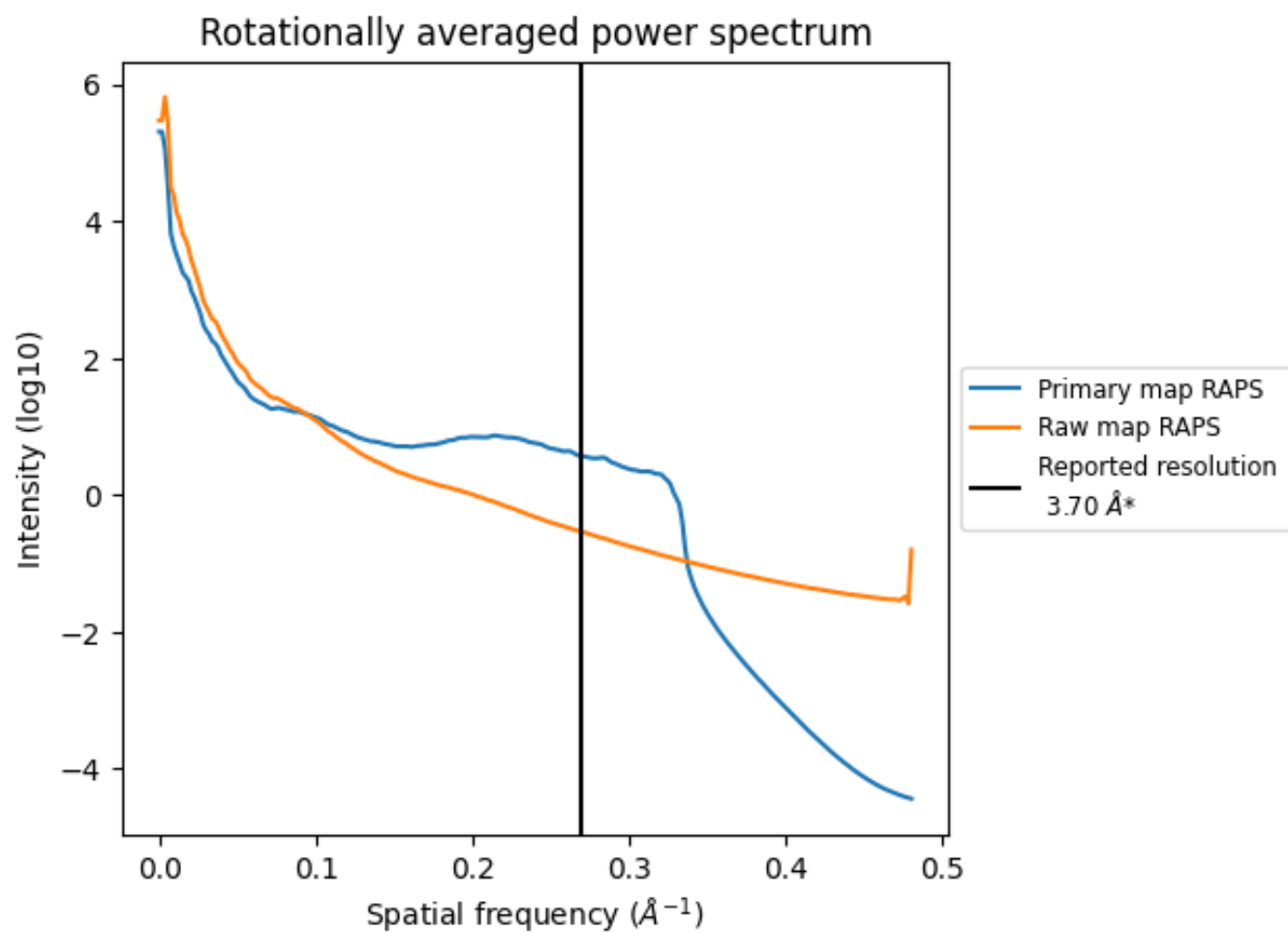
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 706 nm^3 ; this corresponds to an approximate mass of 638 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 ⓘ

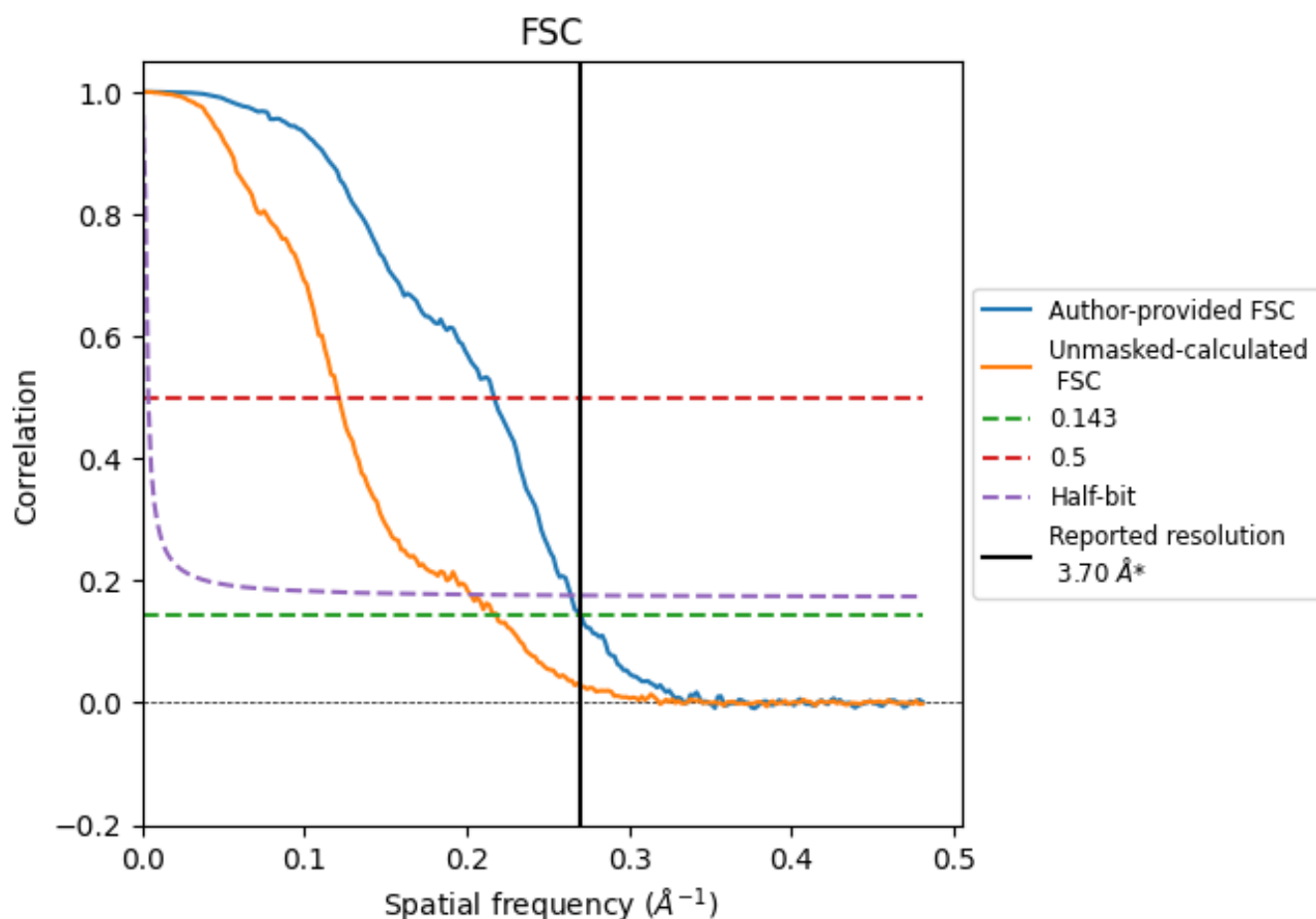


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

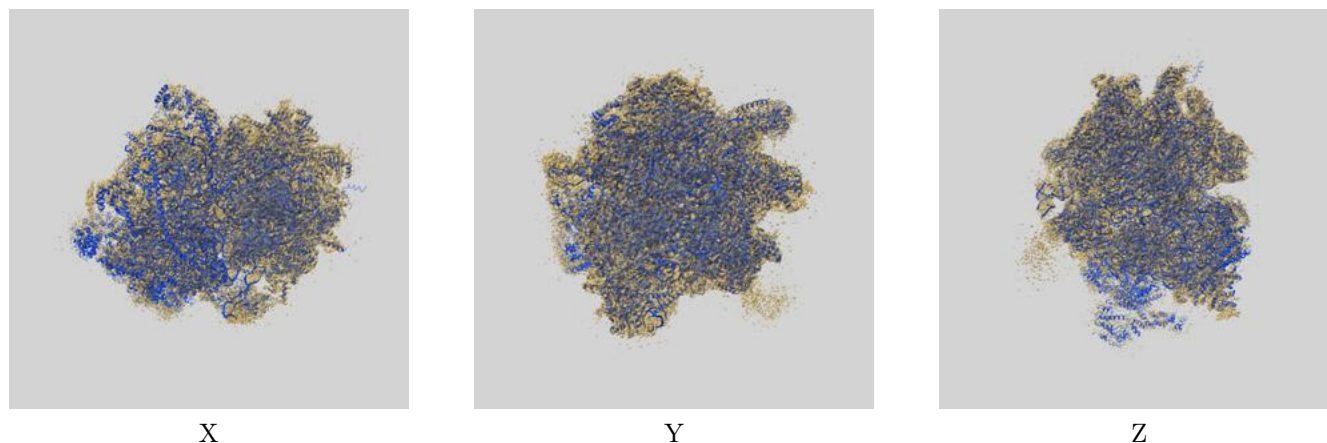
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.70	4.61	3.78
Unmasked-calculated*	4.58	8.26	4.94

*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 4.58 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

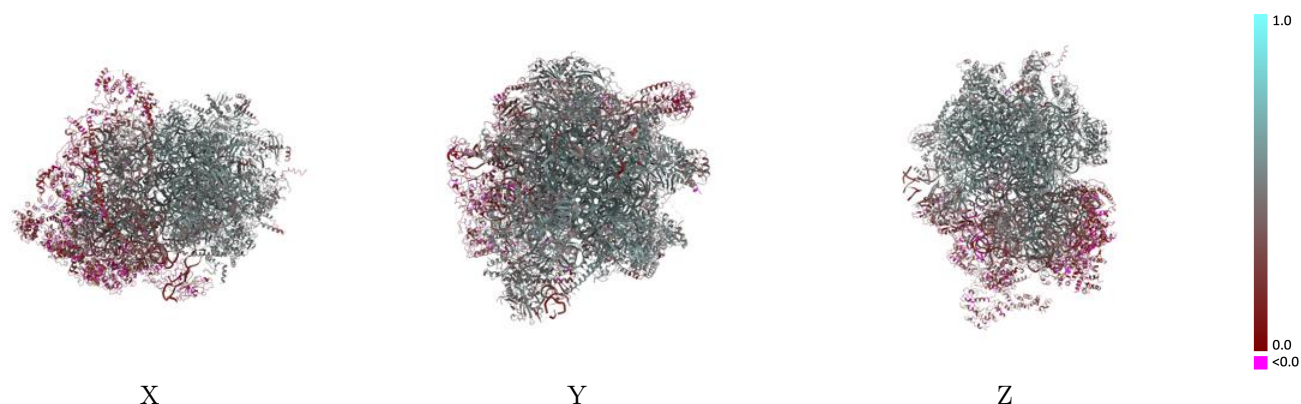
This section contains information regarding the fit between EMDB map EMD-11646 and PDB model 7A5K. Per-residue inclusion information can be found in [section 3](#) on [page 23](#).

9.1 Map-model overlay [i](#)



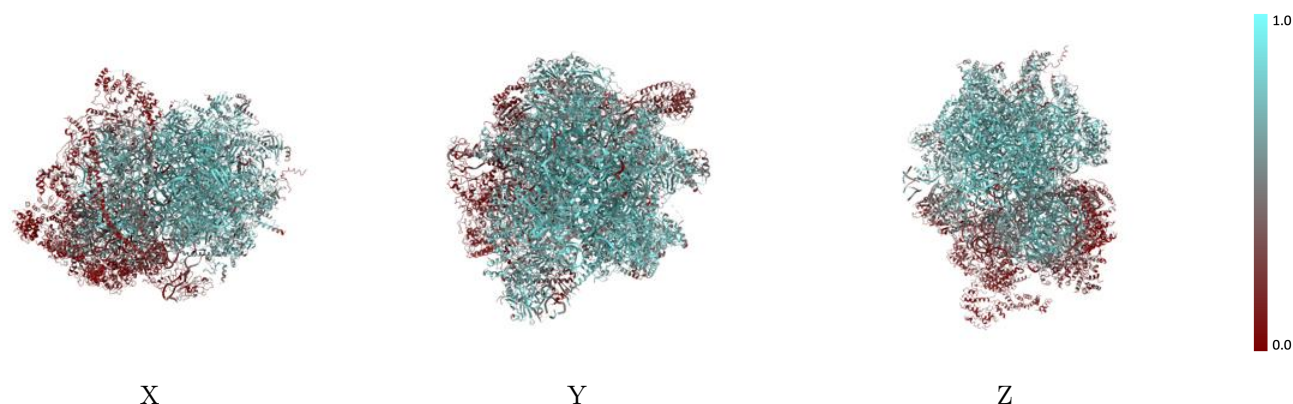
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



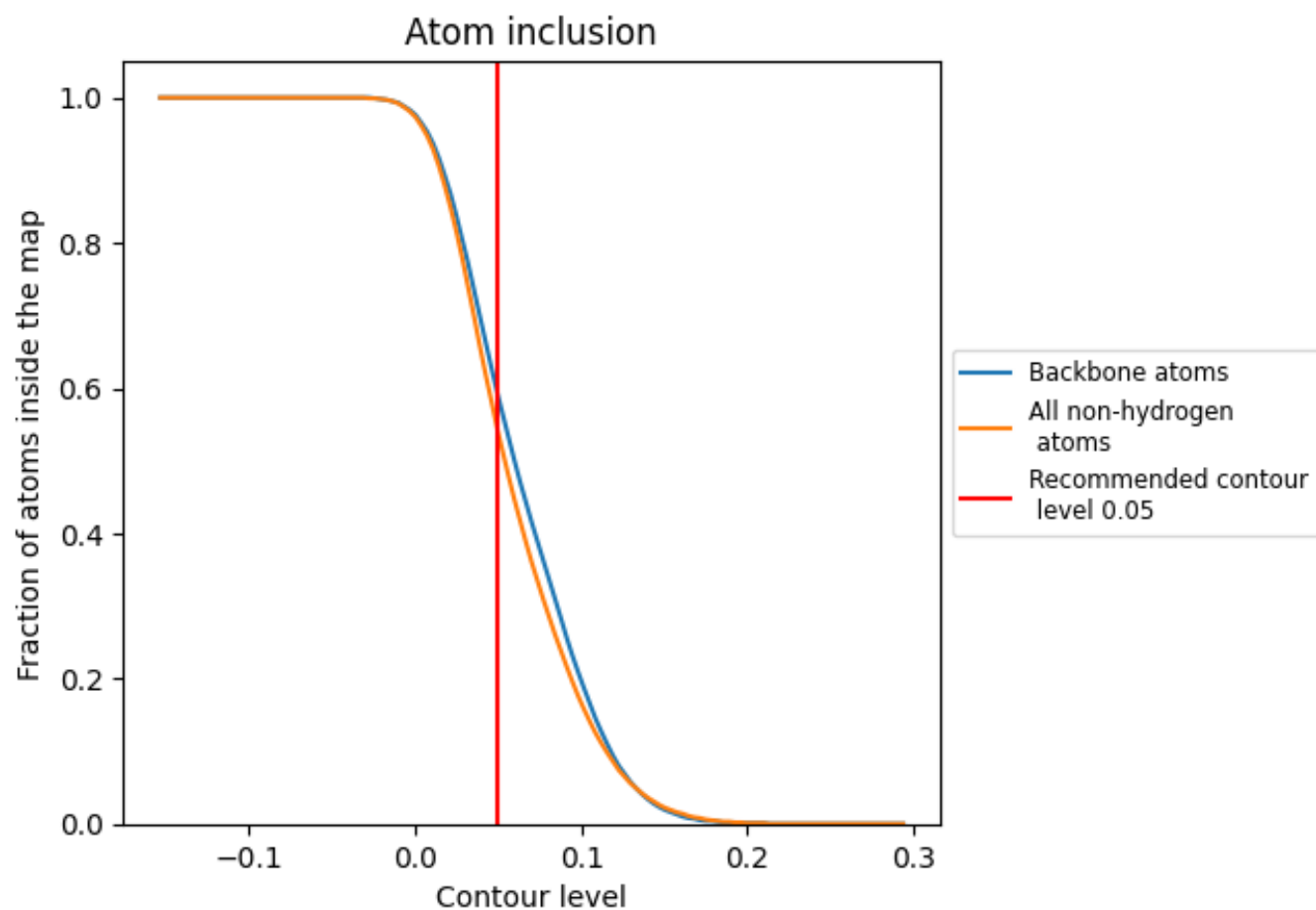
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



At the recommended contour level, 59% of all backbone atoms, 54% 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	 0.5400	 0.4080
03	 0.6660	 0.5020
13	 0.6710	 0.5060
23	 0.7890	 0.5720
24	 0.1140	 0.2090
33	 0.7810	 0.5610
43	 0.7850	 0.5670
53	 0.6440	 0.4830
63	 0.6390	 0.4690
73	 0.6060	 0.4670
8	 0.1490	 0.2980
93	 0.6360	 0.4920
A	 0.2200	 0.2810
A3	 0.8370	 0.5250
A5	 0.0000	 0.1500
A6	 0.5830	 0.3810
B	 0.3000	 0.2660
B3	 0.6330	 0.3450
B6	 0.3390	 0.2780
C6	 0.0750	 0.2080
D	 0.2000	 0.1820
D3	 0.6720	 0.5180
D6	 0.3430	 0.3350
E3	 0.7270	 0.5350
E6	 0.2540	 0.3260
F3	 0.7220	 0.5300
F6	 0.0370	 0.1600
FE	 0.2860	 0.1670
G6	 0.1460	 0.2350
H3	 0.5830	 0.4720
H6	 0.0960	 0.2350
I3	 0.4940	 0.4020
I6	 0.2780	 0.2790
J3	 0.3240	 0.2230
J6	 0.5640	 0.4780



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Chain	Atom inclusion	Q-score
K3	 0.7540	 0.5410
K6	 0.1150	 0.2420
L3	 0.6370	 0.5200
L6	 0.3700	 0.3710
M3	 0.7180	 0.5220
M6	 0.3200	 0.2340
N3	 0.7010	 0.5390
N6	 0.4550	 0.3900
O3	 0.7110	 0.5300
O6	 0.2780	 0.2210
P3	 0.6710	 0.5040
P6	 0.2850	 0.3080
Q3	 0.6370	 0.5090
Q6	 0.4080	 0.3860
R3	 0.7290	 0.5440
R6	 0.1850	 0.1630
S3	 0.7250	 0.5330
S6	 0.2380	 0.2250
T3	 0.7150	 0.5450
T6	 0.3370	 0.2540
U3	 0.7560	 0.5250
U6	 0.2360	 0.2430
V3	 0.5650	 0.4560
V6	 0.1580	 0.1990
W3	 0.7370	 0.5490
W6	 0.1950	 0.2390
X3	 0.6320	 0.4940
X6	 0.0480	 0.1740
Y2	 0.1660	 0.3110
Y3	 0.6990	 0.5070
Y6	 0.0630	 0.1760
Z3	 0.7310	 0.5420
Z6	 0.0770	 0.1940
a3	 0.7130	 0.5240
a6	 0.2410	 0.2380
b3	 0.7140	 0.5250
b6	 0.0750	 0.1920
c3	 0.6530	 0.4930
c6	 0.2300	 0.2880
d3	 0.5690	 0.4410
d6	 0.5450	 0.4610
e3	 0.2200	 0.2680

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Continued from previous page...

Chain	Atom inclusion	Q-score
e6	 0.0490	 0.2010
f3	 0.3720	 0.3680
g3	 0.6990	 0.5070
h3	 0.5670	 0.4430
i3	 0.7470	 0.5450
j3	 0.6660	 0.4960
k3	 0.4540	 0.3670
l3	 0.7140	 0.5040
m3	 0.3600	 0.3560
n	 0.0910	 0.1670
o3	 0.7550	 0.5390
p3	 0.5770	 0.4600
q3	 0.5620	 0.4570
r1	 0.4440	 0.3990
r3	 0.7460	 0.5270
s3	 0.6870	 0.5100
u3	 0.8570	 0.5160