



wwPDB EM Validation Summary Report ⓘ

Oct 12, 2024 – 04:29 PM EDT

PDB ID : 6NU3
EMDB ID : EMD-0515
Title : Structural insights into unique features of the human mitochondrial ribosome recycling
Authors : Sharma, M.R.; Koripella, R.K.; Agrawal, R.K.
Deposited on : 2019-01-30
Resolution : 4.40 Å(reported)
Based on initial model : 3J9M

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:

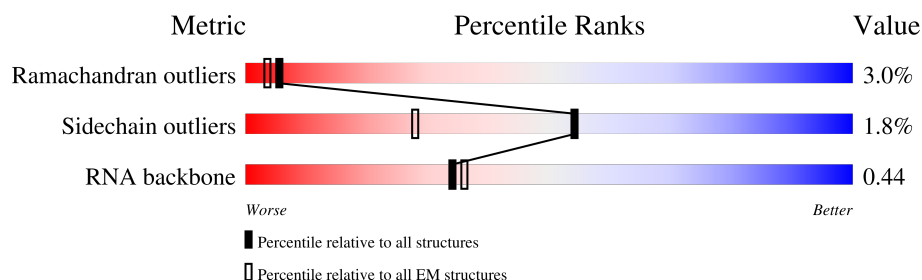
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 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 4.40 Å.

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



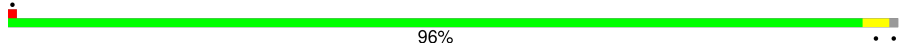

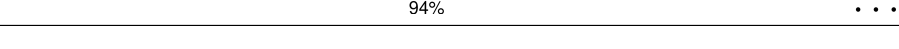
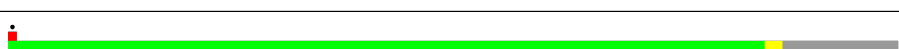

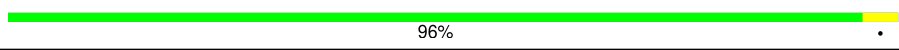
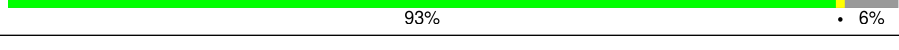
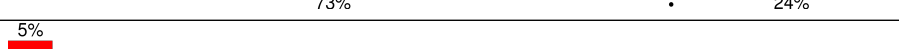



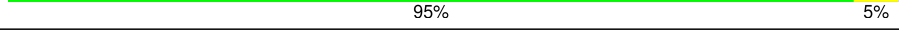

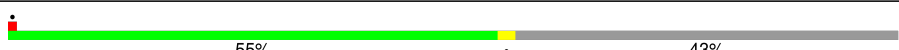


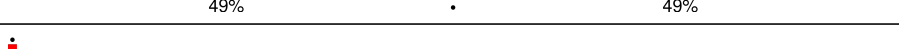







Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	A	1472	
2	B	56	
3	D	305	
4	E	348	
5	F	311	
6	H	267	
7	I	261	
8	J	192	

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Mol	Chain	Length	Quality of chain
9	K	178	
10	L	145	
11	M	296	
12	N	251	
13	O	175	
14	P	180	
15	Q	219	
16	R	149	
17	S	205	
18	T	206	
19	U	153	
20	V	216	
21	W	148	
22	X	243	
23	Y	250	
24	Z	161	
25	0	188	
26	1	65	
27	2	92	
28	3	188	
29	4	103	
30	5	394	
31	6	380	
32	7	338	
33	8	206	

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Mol	Chain	Length	Quality of chain
34	9	137	
35	a	142	
36	b	215	
37	c	332	
38	d	306	
39	e	279	
40	f	212	
41	g	166	
42	h	158	
43	i	128	
44	j	123	
45	k	112	
46	l	138	
47	m	128	
48	o	102	
49	p	206	
50	q	222	
51	r	196	
52	s	439	
53	t	28	
54	u	2	
55	AA	923	
56	AB	296	
57	AC	167	
58	AD	430	

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Mol	Chain	Length	Quality of chain
59	AE	125	
60	AF	242	
61	AG	396	
62	AH	201	
63	AI	194	
64	AJ	138	
65	AK	128	
66	AL	257	
67	AM	137	
68	AN	130	
69	AO	185	
70	AP	142	
71	AQ	86	
72	AR	360	
73	AS	190	
74	AT	173	
75	AU	205	
76	AV	414	
77	AW	187	
78	AX	398	
79	AY	395	
80	AZ	106	
81	A0	225	
82	A1	323	
83	A2	118	

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Mol	Chain	Length	Quality of chain
84	A3	199	<div><div></div><div>34%</div><div></div><div>65%</div></div>
85	A4	474	<div><div></div><div>20%</div><div></div><div>86%</div><div></div><div>13%</div></div>

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 291640 atoms, of which 133281 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	1472	Total	C	H	N	O	P	0	0
			47126	14025	15865	5642	10122	1472		

- Molecule 2 is a RNA chain called mt-tRNAVal.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	56	Total	C	H	N	O	P	0	0
			1794	534	603	214	387	56		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
3	D	236	Total	C	H	N	O	S	0	0
			3738	1145	1896	373	315	9		

- Molecule 4 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	E	300	Total	C	H	N	O	S	0	0
			4743	1523	2378	410	422	10		

- Molecule 5 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	F	250	Total	C	H	N	O	S	0	0
			4058	1294	2045	365	348	6		

- Molecule 6 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	H	95	Total	C	H	N	O		0	0
			1616	498	832	152	134			

- Molecule 7 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	I	158	Total	C	H	N	O	S	0	0
			2652	828	1369	235	210	10		

- Molecule 8 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	J	140	Total	C	H	N	O	S	0	0
			2202	680	1141	192	187	2		

- Molecule 9 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	K	177	Total	C	H	N	O	S	0	0
			2899	934	1448	259	251	7		

- Molecule 10 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	L	115	Total	C	H	N	O	S	0	0
			1830	559	941	171	154	5		

- Molecule 11 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	M	287	Total	C	H	N	O	S	0	0
			4683	1472	2378	425	402	6		

- Molecule 12 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	N	205	Total	C	H	N	O	S	0	0
			3335	1056	1681	308	280	10		

- Molecule 13 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	O	152	Total	C	H	N	O	S	0	0
			2528	784	1283	239	215	7		

- Molecule 14 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	P	133	Total	C	H	N	O	S	0	0
			2161	677	1081	209	189	5		

- Molecule 15 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	Q	219	Total	C	H	N	O	S	0	0
			3681	1168	1859	322	323	9		

- Molecule 16 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	R	140	Total	C	H	N	O	S	0	0
			2367	732	1214	231	186	4		

- Molecule 17 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	S	156	Total	C	H	N	O	S	0	0
			2573	806	1322	222	219	4		

- Molecule 18 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	T	166	Total	C	H	N	O	S	0	0
			2778	875	1410	254	232	7		

- Molecule 19 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	U	111	Total	C	H	N	O	S	0	0
			1857	591	935	176	153	2		

- Molecule 20 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	V	189	Total	C	H	N	O	S	0	0
			3109	987	1558	278	278	8		

- Molecule 21 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	W	111	Total	C	H	N	O	S	0	0
			1769	558	898	164	146	3		

- Molecule 22 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	X	243	Total	C	H	N	O	S	0	0
			4062	1317	2027	351	362	5		

- Molecule 23 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	Y	176	Total	C	H	N	O	S	0	0
			3078	970	1561	291	252	4		

- Molecule 24 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	Z	120	Total	C	H	N	O	S	0	0
			2008	626	1030	183	166	3		

- Molecule 25 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	0	108	Total	C	H	N	O	S	0	0
			1784	545	904	172	157	6		

- Molecule 26 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	1	52	Total	C	H	N	O	S	0	0
			908	278	475	83	70	2		

- Molecule 27 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	2	46	Total	C	H	N	O	S	0	0
			782	233	406	83	59	1		

- Molecule 28 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	3	95	Total	C	H	N	O	S	0	0
			1714	539	883	162	127	3		

- Molecule 29 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	4	36	Total	C	H	N	O	S	0	0
			667	203	345	70	46	3		

- Molecule 30 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	5	376	Total	C	H	N	O	S	0	0
			6123	1987	3059	529	538	10		

- Molecule 31 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	6	325	Total	C	H	N	O	S	0	0
			5086	1692	2450	465	470	9		

- Molecule 32 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	7	266	Total	C	H	N	O	S	0	0
			4331	1383	2173	371	388	16		

- Molecule 33 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	8	99	Total	C	H	N	O	S	0	0
			1680	535	844	144	155	2		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
34	9	109	Total	C	H	N	O	S	0	0
			1751	565	878	152	154	2		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
35	a	82	Total	C	H	N	O	S	0	0
			1344	434	658	124	123	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
36	b	148	Total	C	H	N	O	S	0	0
			2358	733	1180	229	213	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
37	c	275	Total	C	H	N	O	S	0	0
			4437	1415	2220	383	410	9		

- Molecule 38 is a protein called cDNA FLJ61100, highly similar to 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	d	162	Total	C	H	N	O	S	0	0
			2690	870	1343	234	235	8		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
39	e	217	Total	C	H	N	O	S	0	0
			3529	1124	1767	310	323	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
40	f	131	Total	C	H	N	O	S	0	0
			2083	663	1044	169	203	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
41	g	129	Total	C	H	N	O	S	0	0
			2123	690	1056	185	190	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	h	100	Total	C	H	N	O	S	
			1633	524	806	146	155	2	
								0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	i	97	Total	C	H	N	O	S	
			1684	532	857	165	126	4	
								0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	j	85	Total	C	H	N	O	S	
			1357	423	673	133	126	2	
								0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	k	84	Total	C	H	N	O	S	
			1311	407	656	122	121	5	
								0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	l	23	Total	C	H	N	O		
			448	137	227	52	32		
								0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	m	45	Total	C	H	N	O	S	
			759	232	387	76	62	2	
								0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	o	94	Total	C	H	N	O	S	
			1601	501	804	165	128	3	
								0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
49	p	127	Total	C	H	N	O	S	0	0
			2141	661	1083	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	q	128	Total	C	H	N	O	S	0	0
			2125	671	1049	208	192	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
51	r	146	Total	C	H	N	O	S	0	0
			2424	764	1221	232	199	8		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
52	s	370	Total	C	H	N	O	S	0	0
			6058	1946	3022	542	534	14		

- Molecule 53 is a protein called Unknown protein/protein extension.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	t	28	Total	C	H	N	O		
			170	84	30	28	28	0	0

- Molecule 54 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	u	2	Total	C	H	N	O	P	0	0
			65	19	23	8	13	2		

- Molecule 55 is a RNA chain called 12S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	AA	923	Total	C	H	N	O	P	0	0
			29558	8790	9952	3535	6358	923		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
56	AB	217	Total	C	H	N	O	S	0	0
			3534	1131	1766	321	306	10		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
57	AC	132	Total	C	H	N	O	S	0	0
			2170	699	1088	195	184	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
58	AD	322	Total	C	H	N	O	S	0	0
			5153	1611	2596	476	457	13		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
59	AE	122	Total	C	H	N	O	S	0	0
			1973	614	1001	177	177	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
60	AF	201	Total	C	H	N	O	S	0	0
			3384	1069	1716	305	283	11		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
61	AG	305	Total	C	H	N	O	S	0	0
			5019	1599	2503	448	455	14		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
62	AH	122	Total	C	H	N	O	S	0	0
			2023	643	1024	168	185	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
63	AI	136	Total	C	H	N	O	S	0	0
			2063	637	1052	192	178	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
64	AJ	108	Total	C	H	N	O	S	0	0
			1725	521	887	169	142	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
65	AK	101	Total	C	H	N	O	S	0	0
			1746	537	885	179	140	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
66	AL	164	Total	C	H	N	O	S	0	0
			2854	883	1472	257	235	7		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
67	AM	116	Total	C	H	N	O	S	0	0
			1871	582	951	182	150	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
68	AN	107	Total	C	H	N	O	S	0	0
			1754	549	908	153	141	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
69	AO	185	Total	C	H	N	O	S	0	0
			3016	970	1488	285	267	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
70	AP	96	Total	C	H	N	O	S	0	0
			1578	498	804	133	135	8		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
71	AQ	86	Total	C	H	N	O	S	0	0
			1476	455	741	147	124	9		

- Molecule 72 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	AR	242	Total	C	H	N	O	S	0	0
			4039	1285	2031	343	372	8		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
73	AS	126	Total	C	H	N	O	S	0	0
			2079	673	1037	183	185	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
74	AT	162	Total	C	H	N	O	S	0	0
			2674	850	1344	231	238	11		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
75	AU	173	Total	C	H	N	O	S	0	0
			2932	900	1471	294	263	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
76	AV	328	Total	C	H	N	O	S	0	0
			5392	1737	2690	452	502	11		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
77	AW	97	Total	C	H	N	O	S	0	0
			1551	486	785	137	139	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
78	AX	316	Total	C	H	N	O	S	0	0
			5051	1625	2520	440	455	11		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
79	AY	108	Total	C	H	N	O	S	0	0
			1773	593	859	150	169	2		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
80	AZ	87	Total	C	H	N	O	S	0	0
			1487	473	747	133	130	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
81	A0	201	Total	C	H	N	O	S	0	0
			3369	1065	1685	322	292	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
82	A1	256	Total	C	H	N	O	S	0	0
			4173	1321	2097	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	A2	116	Total	C	H	N	O	S	0	0
			1887	574	962	181	162	8		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
84	A3	69	Total	C	H	N	O	S	0	0
			1292	393	682	130	86	1		

- Molecule 85 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial,mS39.

Mol	Chain	Residues	Atoms						AltConf	Trace
85	A4	414	Total	C	H	N	O	S	0	0
			5097	1805	2259	490	529	14		

- Molecule 86 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	A	97	Total	Mg	0
			97	97	
86	M	1	Total	Mg	0
			1	1	
86	g	1	Total	Mg	0
			1	1	
86	AA	28	Total	Mg	0
			28	28	

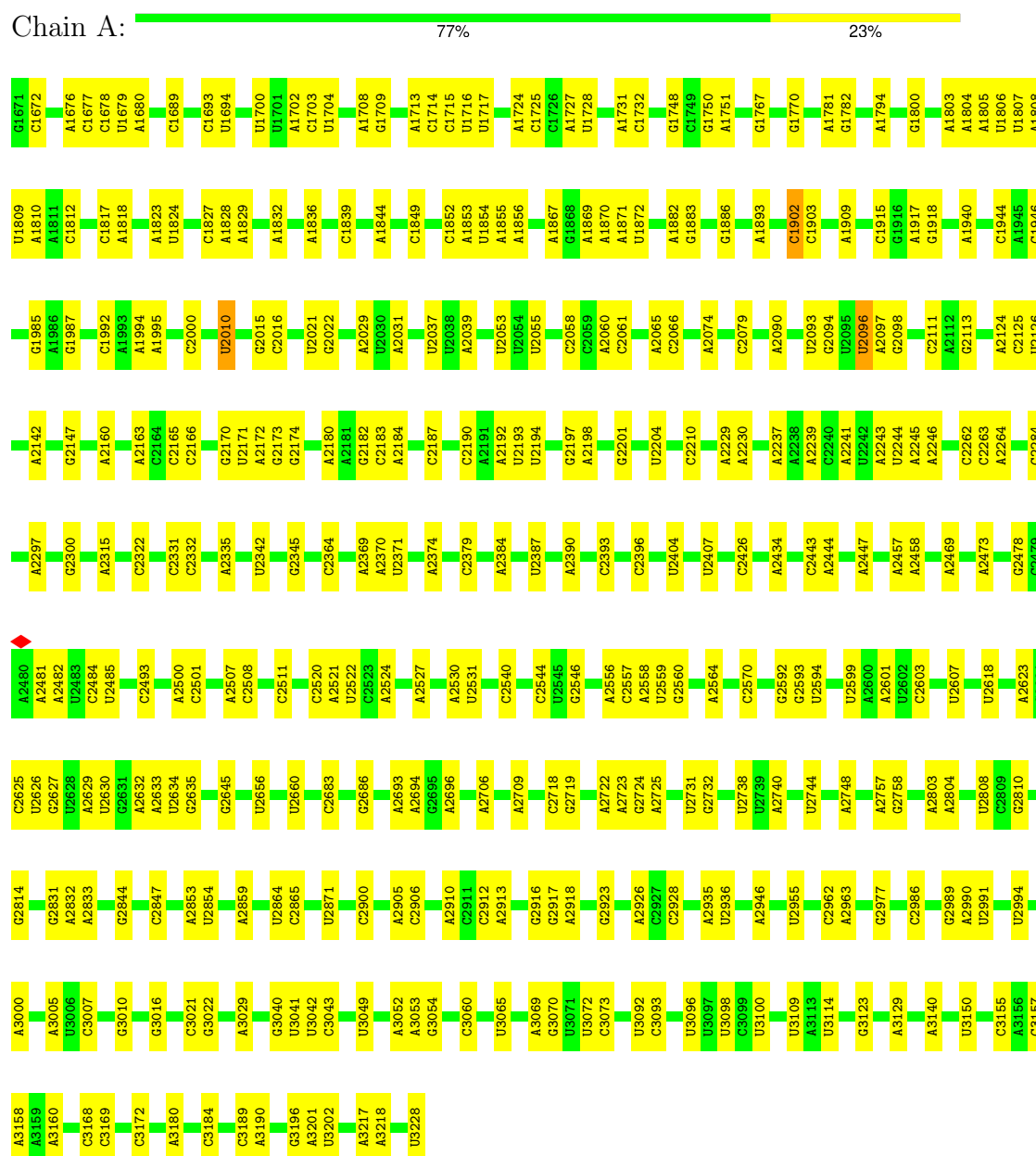
- Molecule 87 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	0	1	Total	Zn	0
			1	1	
87	4	1	Total	Zn	0
			1	1	
87	r	1	Total	Zn	0
			1	1	
87	AB	1	Total	Zn	0
			1	1	
87	AO	1	Total	Zn	0
			1	1	
87	AP	1	Total	Zn	0
			1	1	
87	AT	1	Total	Zn	0
			1	1	


3 Residue-property plots

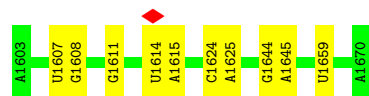
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S rRNA



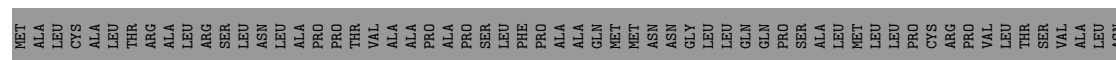
- Molecule 2: mt-tRNAVal

Chain B:  82% 18%




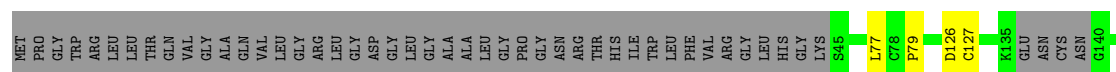
- Molecule 3: 39S ribosomal protein L2, mitochondrial

Chain D:  75% 23%



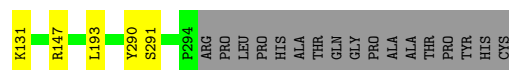
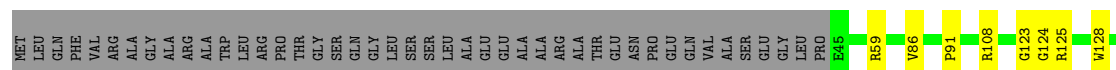
- Molecule 4: 39S ribosomal protein L3, mitochondrial

Chain E:  84% 14%



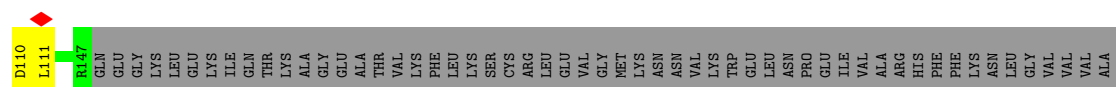
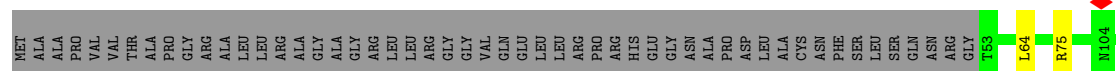
- Molecule 5: 39S ribosomal protein L4, mitochondrial

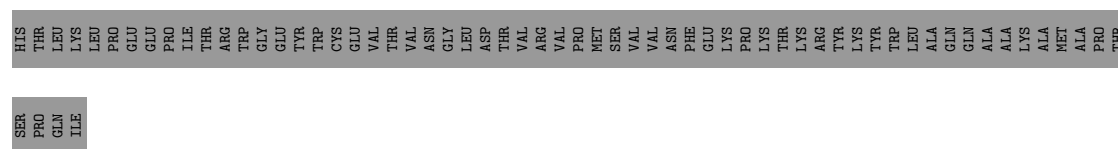
Chain F:  76% 20%



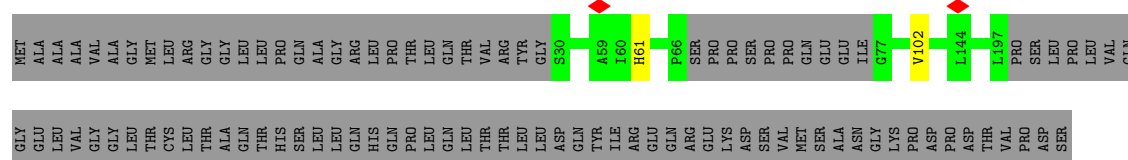
- Molecule 6: 39S ribosomal protein L9, mitochondrial

Chain H:  34% 64%

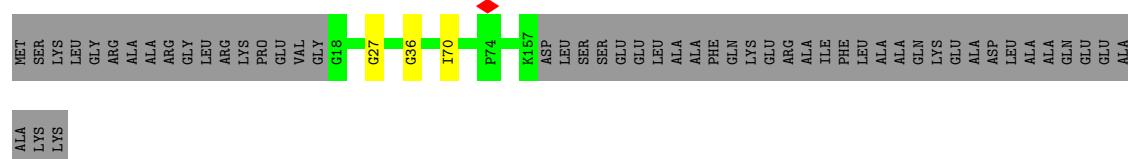




• Molecule 7: 39S ribosomal protein L10, mitochondrial



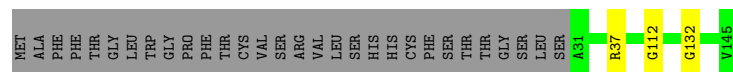
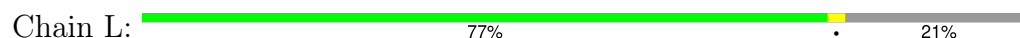
• Molecule 8: 39S ribosomal protein L11, mitochondrial



• Molecule 9: 39S ribosomal protein L13, mitochondrial



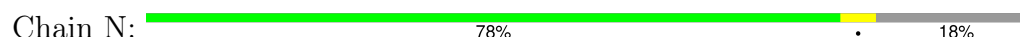
• Molecule 10: 39S ribosomal protein L14, mitochondrial

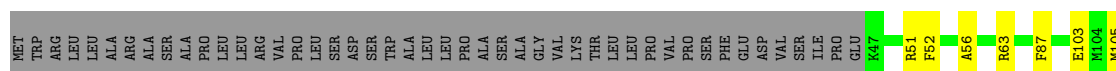


• Molecule 11: 39S ribosomal protein L15, mitochondrial

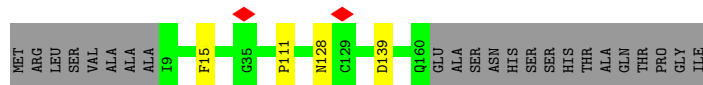
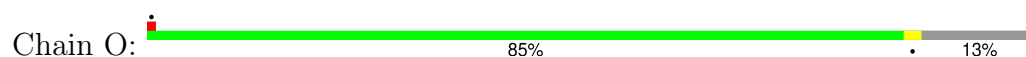


• Molecule 12: 39S ribosomal protein L16, mitochondrial

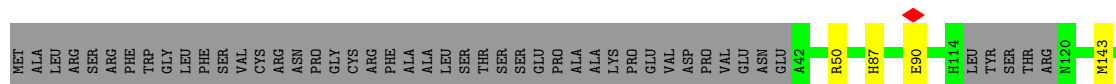




- Molecule 13: 39S ribosomal protein L17, mitochondrial



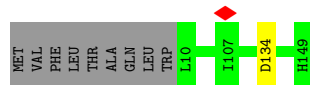
- Molecule 14: 39S ribosomal protein L18, mitochondrial



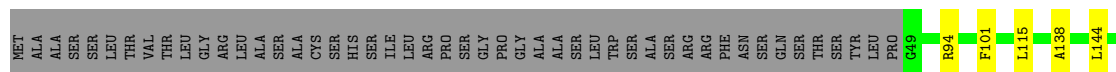
- Molecule 15: 39S ribosomal protein L19, mitochondrial



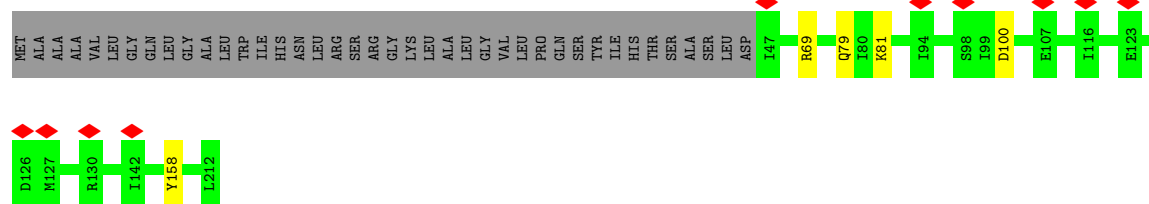
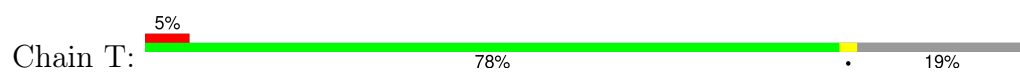
- Molecule 16: 39S ribosomal protein L20, mitochondrial



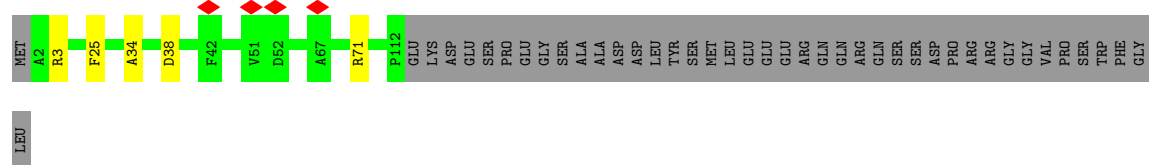
- Molecule 17: 39S ribosomal protein L21, mitochondrial



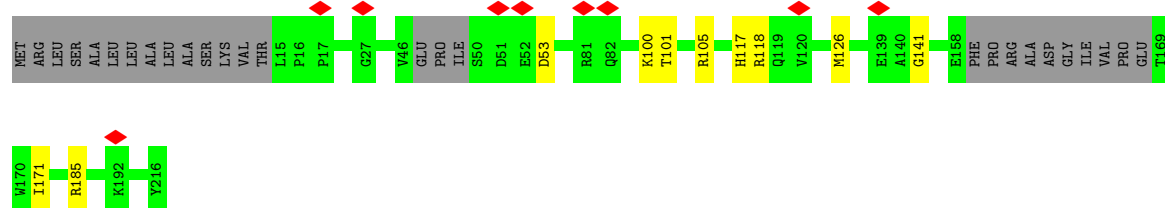
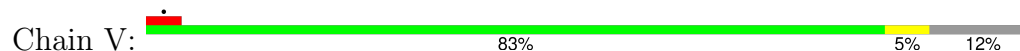
- Molecule 18: 39S ribosomal protein L22, mitochondrial



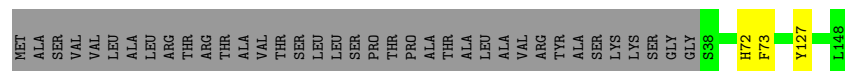
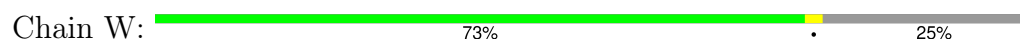
- Molecule 19: 39S ribosomal protein L23, mitochondrial



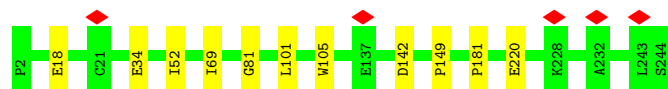
- Molecule 20: 39S ribosomal protein L24, mitochondrial



- Molecule 21: 39S ribosomal protein L27, mitochondrial



- Molecule 22: 39S ribosomal protein L28, mitochondrial

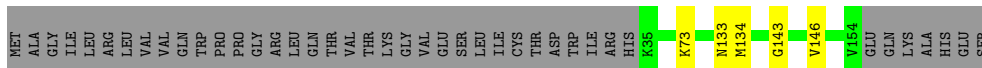


- Molecule 23: 39S ribosomal protein L47, mitochondrial

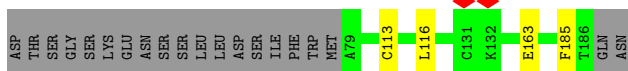
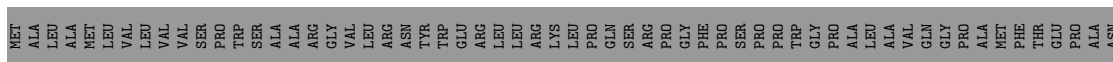




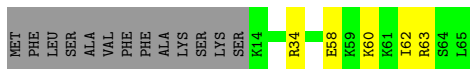
- Chain Z: 71% . 25%



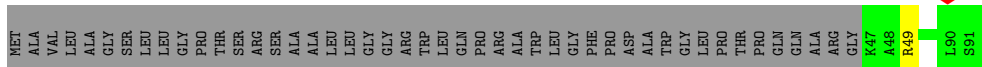
- Chain 0:  55% . 43%



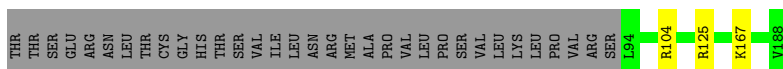
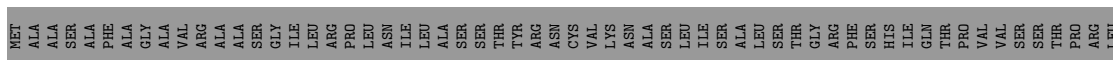
- Chain 1:



- Chain 2:  49% . 50%



- Chain 3: 49% . 49%



- Chain 4: 35% 65%

MET ALA ASN PHE ILE ARG LYS MET VAL ASN PRO LEU LEU TYR SER ARG HIS THR VAL LYS PRO PRO ARG ALA LEU SER PHE LEU PHE GLY SER ARG ARG ALA ALA PRO VAL ALA VAL VAL ARG SER LEU SER PRO PRO GLY LEU PRO HIS LEU

LEU PRO ALA ALA GLY PHE K67 Q86 Q102 MET


- Molecule 30: 39S ribosomal protein L37, mitochondrial

Chain 5:  90% 5% 5%

ALA Y51 V35 E2 I58 P68 P77 H94 A103 E130 D141 ASP PRO ARG ASN HIS LEU GLU ASN Q150 C177 D182 E216 S217 L218 N250 H251 V252 I263 D264 I270 I271 D272 P286 K296 A297 G319 N331 D332 D348

L355 Q358 D365 CYS ASN GLU G369 L373 D377 S378 D379 Q380 L381 L382 Y383 T392 LYS LYS ARG VAL V398 F414 L415 A416 L419 H420 G421 A422 ALA


- Molecule 31: 39S ribosomal protein L38, mitochondrial

Chain 6:  81% 5% 14%

MET ALA ALA PRO TRP ARG ALA ALA LEU CYS GLU CYS ARG TRP ARG TRP ARG GLY PHE THR SER ALA VAL LEU GLY R27 S38 S43 R60 R72 G79 LYS THR ASP PRO LYS GLU ILE ASP GLY LEU PRO PRO VAL R99 E118 GLU

E120 R124 R127 V130 R159 A165 L173 E209 GLU GLY SER L213 P228 H234 H235 Q277 S282 GLU ASP ALA ARG P287 R299 H307 A314 F318 L334 H351 H359 H373 G378 Y380

- Molecule 32: 39S ribosomal protein L39, mitochondrial

Chain 7:  77% 21%

MET GLU ALA LEU MET GLY SER ARG ALA ALA ARG LEU TRP LEU VAL ALA PRO GLY GLY GLY ILE LYS TRP GLN ARG PHE ILE ALA THR SER SER ALA GLN LEU S36 T62 K72 T73 D74 P75 L119 T129 F130 K131 F138 LYS ASP GLU TYR MET VAL N165 L185

ASP SER LYS LEU ASP GLY TRP H193 K234 Q246 N247 P248 E249 R250 I251 P270 S273 I274 E279 W285 LEU GLN THR GLN THR SER SER ALA SER LEU I294 H309 F310 K322 MET VAL THR GLU ASP GLN SER LYS ALA THR GLU LYS CYS THR SER THR


- Molecule 33: 39S ribosomal protein L40, mitochondrial

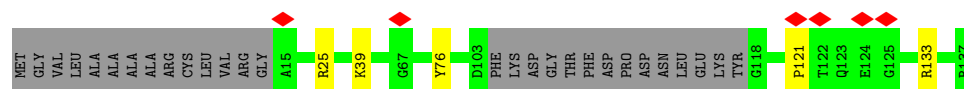
Chain 8:  48% 52%

MET THR ALA SER VAL LEU ARG SER SER SER ILE LEU LEU LEU ARG ARG PRO THR LEU SER SER GLY LEU LEU GLU LEU TRP THR THR GLN THR GLN LEU ARG GLN THR THR HIS GLN ALA SER SER LEU LEU SER PHE TRP GLU ILE LEU PRO MET ARG SER GLU PHE LYS LYS VAL ASP PRO LYS LYS

ASP GLN GLU ALA LYS GLY ARG LEU LYS SER ARG SER ILE ARG ILE ARG LYS LEU GLU THR LYS ALA THR GLN I83 P181 ILE PRO ASN TYR GLN PRO PRO GLY ARG TYR ASN ASP ILE THR LYS VAL THR THR GLN VAL GLU PHE LYS ARG

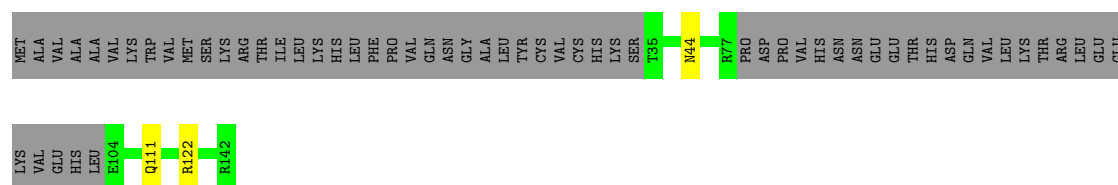
- Molecule 34: 39S ribosomal protein L41, mitochondrial

Chain 9:  76% 20%



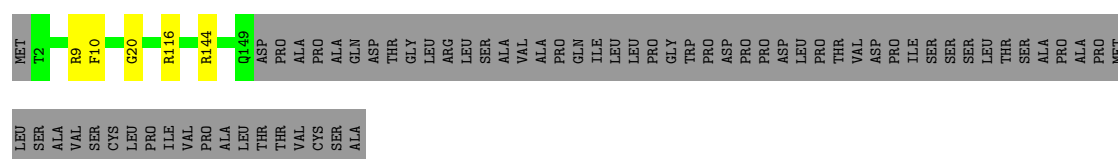
- Molecule 35: 39S ribosomal protein L42, mitochondrial

Chain a:  56% 42%




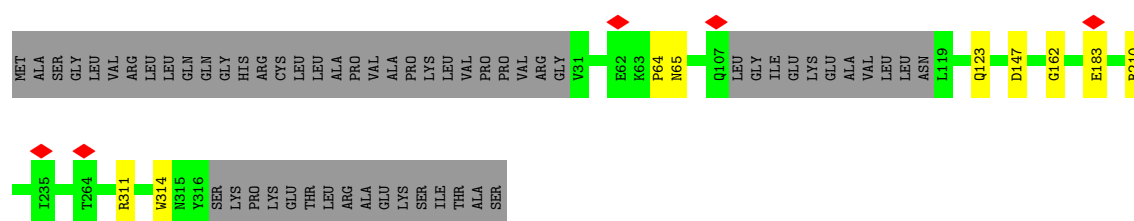
- Molecule 36: 39S ribosomal protein L43, mitochondrial

Chain b:  67% 31%



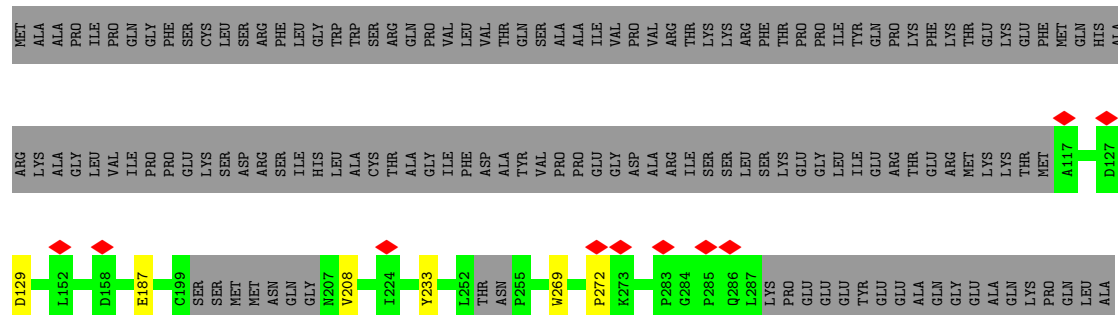
- Molecule 37: 39S ribosomal protein L44, mitochondrial

Chain c:  80% 17%



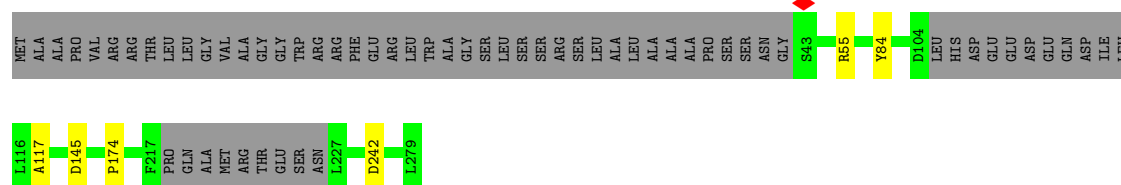
- Molecule 38: cDNA FLJ61100, highly similar to 39S ribosomal protein L45, mitochondrial

Chain d:  51% 47%



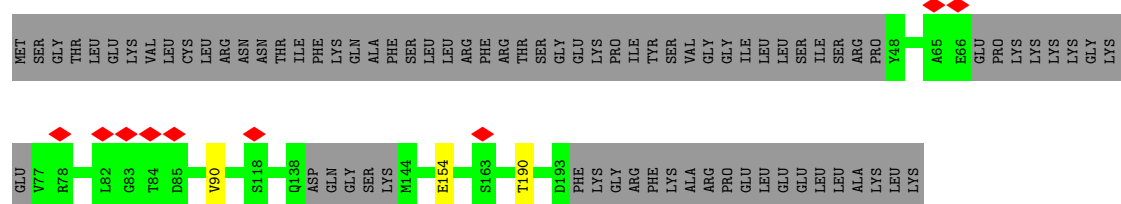
- Molecule 39: 39S ribosomal protein L46, mitochondrial

Chain e:  76% 22%



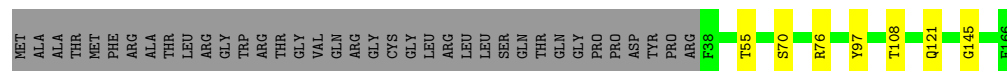
- Molecule 40: 39S ribosomal protein L48, mitochondrial

Chain f:  60% 38%



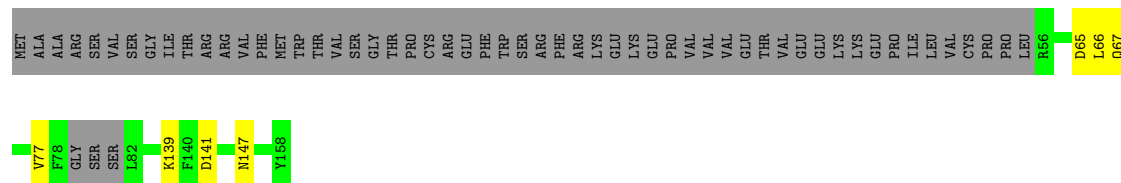
- Molecule 41: 39S ribosomal protein L49, mitochondrial

Chain g:  73% 22%



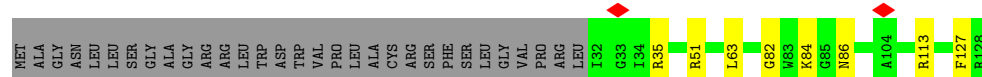
- Molecule 42: 39S ribosomal protein L50, mitochondrial

Chain h:  59% 37%



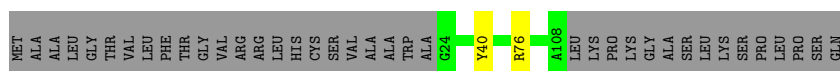
- Molecule 43: 39S ribosomal protein L51, mitochondrial

Chain i:  70% 24%



- Molecule 44: 39S ribosomal protein L52, mitochondrial

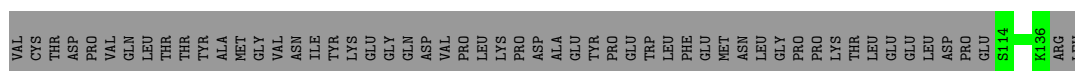
Chain j:  67% 31%



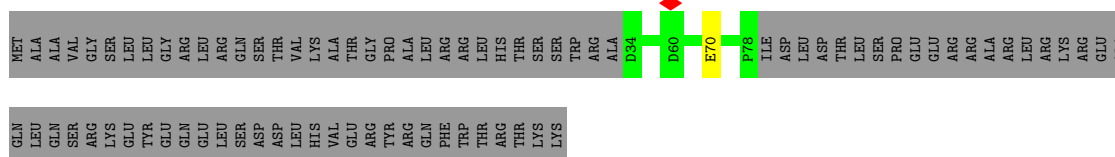
- Molecule 45: 39S ribosomal protein L53, mitochondrial



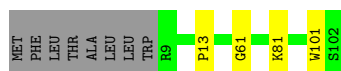
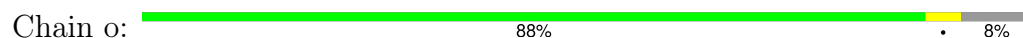
- Molecule 46: 39S ribosomal protein L54, mitochondrial



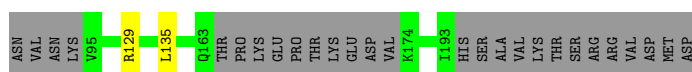
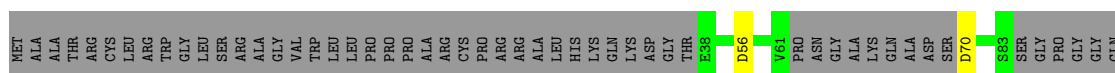
- Molecule 47: 39S ribosomal protein L55, mitochondrial



- Molecule 48: Ribosomal protein 63, mitochondrial

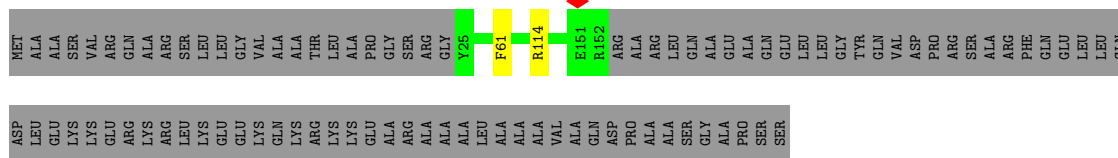


- Molecule 49: Peptidyl-tRNA hydrolase ICT1, mitochondrial



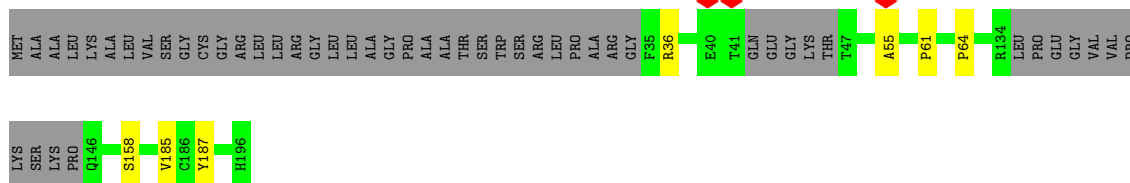
- Molecule 50: Growth arrest and DNA damage-inducible proteins-interacting protein 1

Chain q:  57% 42%




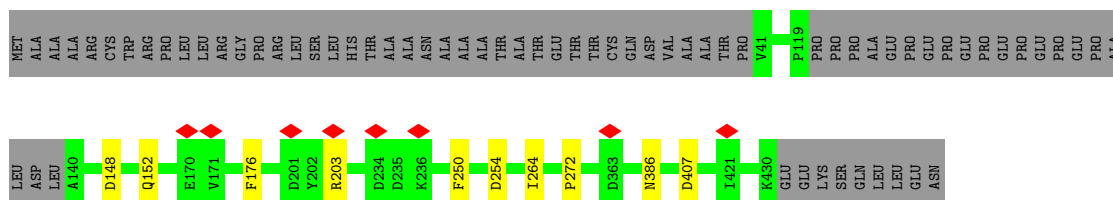
- Molecule 51: 39S ribosomal protein S18a, mitochondrial

Chain r:  71% 26%



- Molecule 52: 39S ribosomal protein S30, mitochondrial

Chain s:  82% 16%



- Molecule 53: Unknown protein/protein extension

Chain t:  100%

There are no outlier residues recorded for this chain.

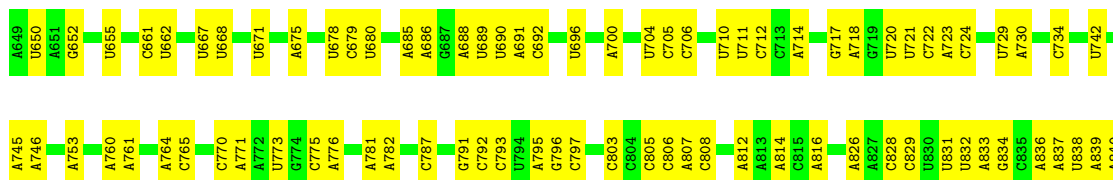
- Molecule 54: E-site tRNA

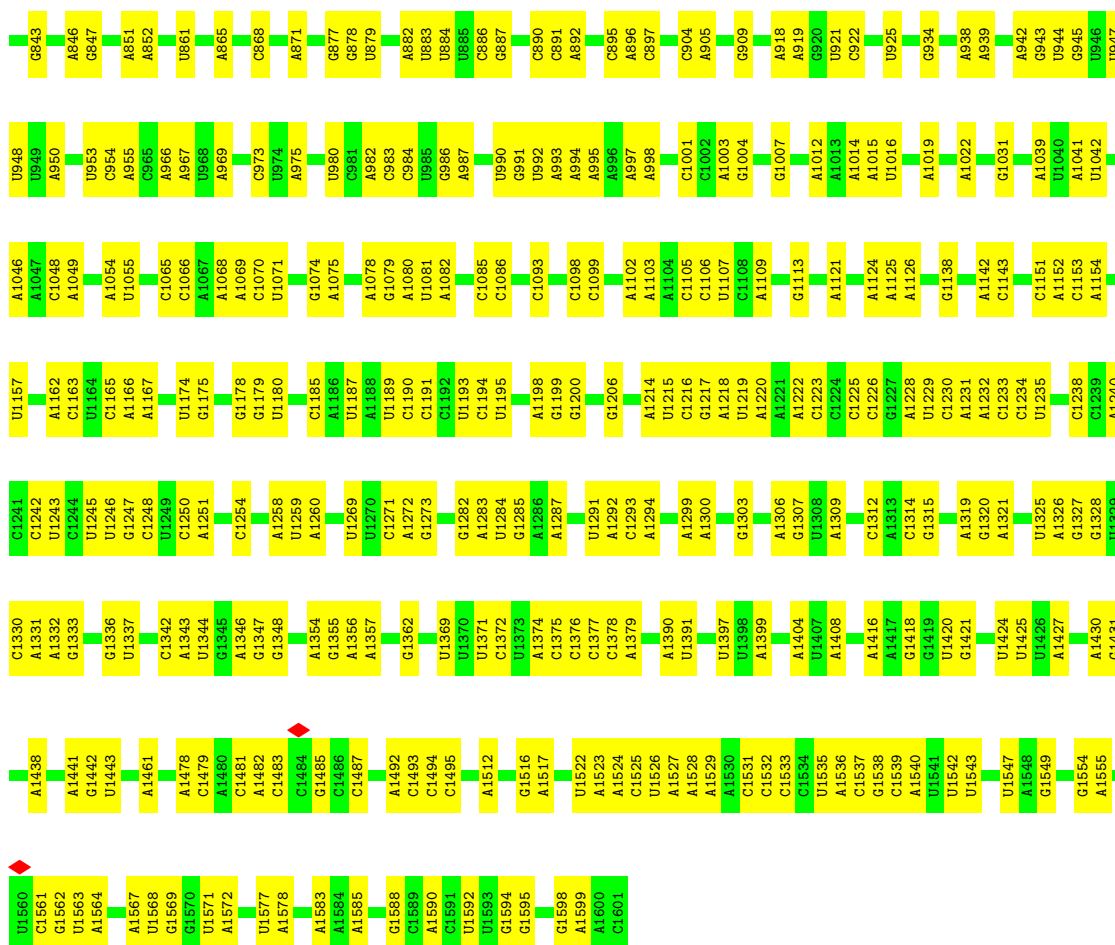
Chain u:  100%

There are no outlier residues recorded for this chain.

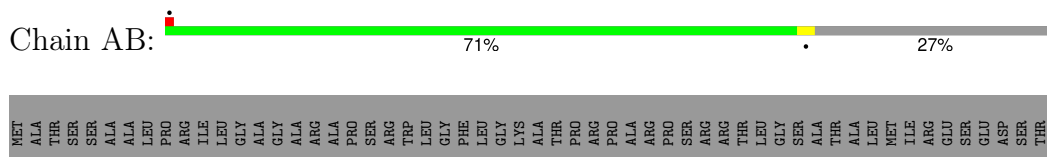
- Molecule 55: 12S rRNA

Chain AA:  58% 42%

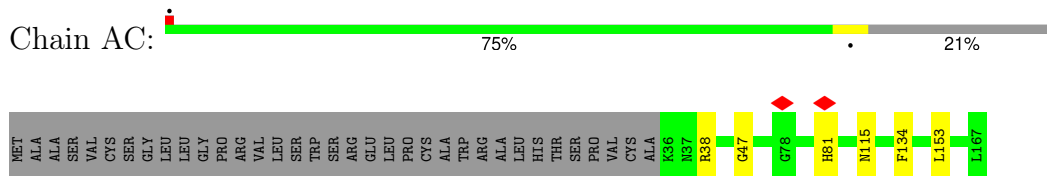




- Molecule 56: 28S ribosomal protein S2, mitochondrial



- Molecule 57: 28S ribosomal protein S24, mitochondrial



- Molecule 58: 28S ribosomal protein S5, mitochondrial



MET ALA THR ALA VAL ARG VAL ALA GLY CYS LEU PRO VAL LEU CYS THR ALA GLY HIS LEU ARG GLN SER LEU THR PRO ASN LEU THR PRO ALA ALA SER ILE LEU ALA TRP LYS SER VAL LEU GLY ASN HIS LEU SER SER SER LEU THR

ALA SER LEU SER ARG ALA LEU GLN THR CYS GLN CYS CYS ILE SER SER PRO SER HIS LEU MET SER HIS GLN GLN TYR ARG PRO TYR S88 T94 A104 G107 GLY ALA SER ILE LYS LYS LYS LYS ARG GLY THR LYS LYS LYS LYS ASP L126 N127 R128 G129 P147 K150


ASN GLY V154 Q159 K167 A170 D171 M172 V179 D180 K183 K184 M186 K186 V193 E213 A233 K234 R237 E283 R284 H288 T288 L290 K299 K332 R388 G389 P397 E398 R419 R427 A428 A429 T430

- Molecule 59: 28S ribosomal protein S6, mitochondrial

Chain AE:  6% 90% 6% ..

MET P2 Q14 R15 L22 T25 R32 G33 R45 D67 P71 A74 V75 E76 M78 V79 S83 E101 E106 K122 R123 LYS


- Molecule 60: 28S ribosomal protein S7, mitochondrial

Chain AF:  5% 80% 17%

MET ALA ALA PRO VAL LYS VAL ALA ALA ARG GLY TRP SER GLY LEU ALA LEU GLY VAL ARG ARG ALA VAL LEU GLN LEU PRO GLY LEU THR GLN VAL ARG S35 R36 Y37 K53 PRO VAL GLU GLU THR E61 A117 R120 K125 A128 A129 S130 A131 I156

G157 L158 V159 L162 G165 V172 F181 R198 K228 M229 V242

- Molecule 61: 28S ribosomal protein S9, mitochondrial

Chain AG:  11% 72% 23%

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

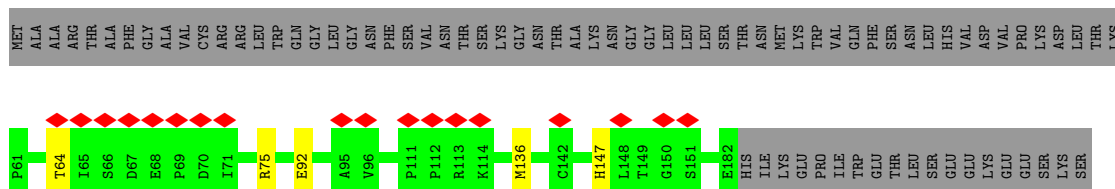
VAL PRO THR SER LYS ARG GLU THR TYR E71 D72 F73 E79 G93 E94 D95 F99 E102 D105 R106 M125 K126 Q130 R134 A137 E142 P146 G154 Q175 SER HIS LEU GLN ALA LYS SER LEU LEU PRO GLU LYS THR VAL THR ARG ASP

VAL ILE GLY SER R198 I201 K202 E203 E204 L205 E206 E207 M208 E226 Q232 A235 A236 E239 R243 R246 S247 V248 T249 L256 Q261 Y262 D263 E264 Q265 G266 M267 K271 K280 A281 E282 H288 M296 G297 I298 Q301 K325 T331 V332 S333

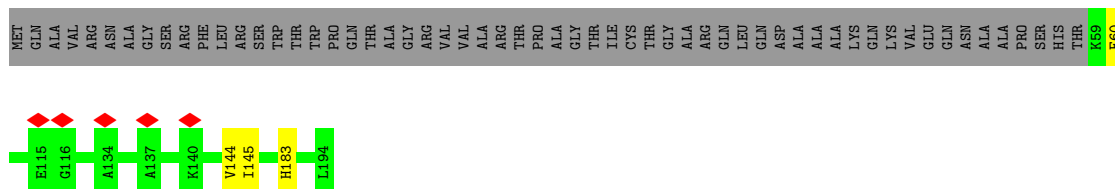
G334 G335 G336 F355 L369 R375 A387 T392 R396

- Molecule 62: 28S ribosomal protein S10, mitochondrial

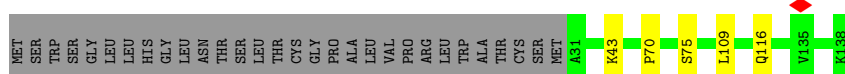
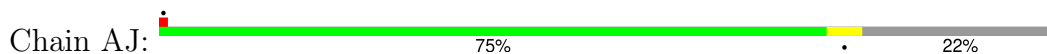
Chain AH:  9% 58% 39%



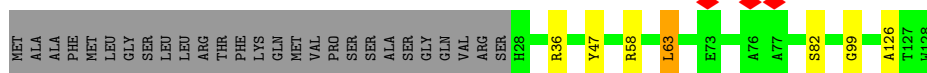
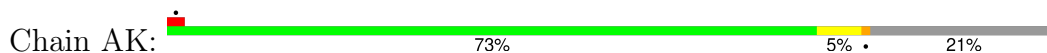
- Molecule 63: 28S ribosomal protein S11, mitochondrial



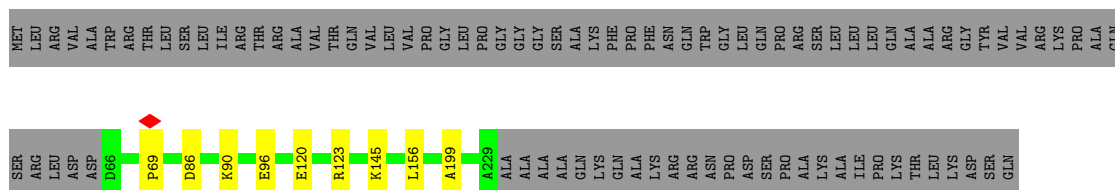
- Molecule 64: 28S ribosomal protein S12, mitochondrial



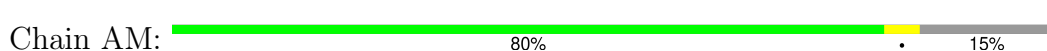
- Molecule 65: 28S ribosomal protein S14, mitochondrial




- Molecule 66: 28S ribosomal protein S15, mitochondrial



- Molecule 67: 28S ribosomal protein S16, mitochondrial



- Molecule 68: 28S ribosomal protein S17, mitochondrial

Chain AN:  78% 5% 18%



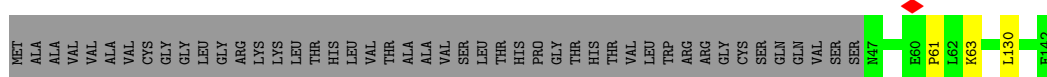
- Molecule 69: 28S ribosomal protein S18b, mitochondrial

Chain AO:  92% 8%



- Molecule 70: 28S ribosomal protein S18c, mitochondrial

Chain AP:  65% 32%



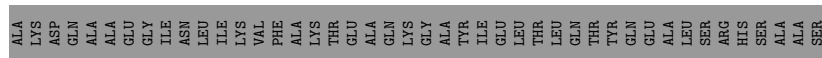
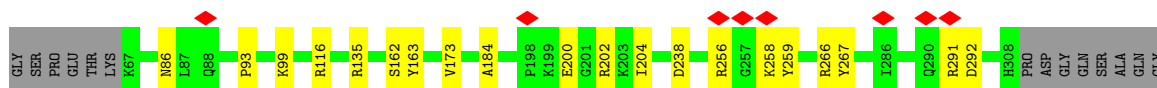
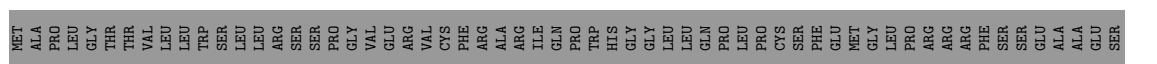
- Molecule 71: 28S ribosomal protein S21, mitochondrial

Chain AQ:  94% 6%



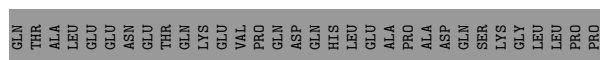
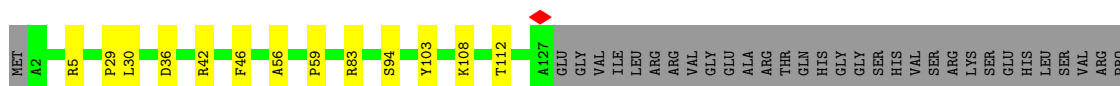
- Molecule 72: 28S ribosomal protein S22, mitochondrial

Chain AR:  62% 6% 33%




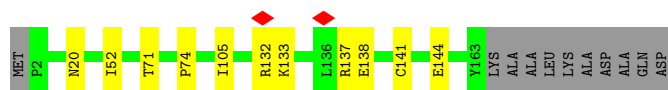
- Molecule 73: 28S ribosomal protein S23, mitochondrial

Chain AS:  59% 7% 34%




- Molecule 74: 28S ribosomal protein S25, mitochondrial

Chain AT:  87% 6% 6%




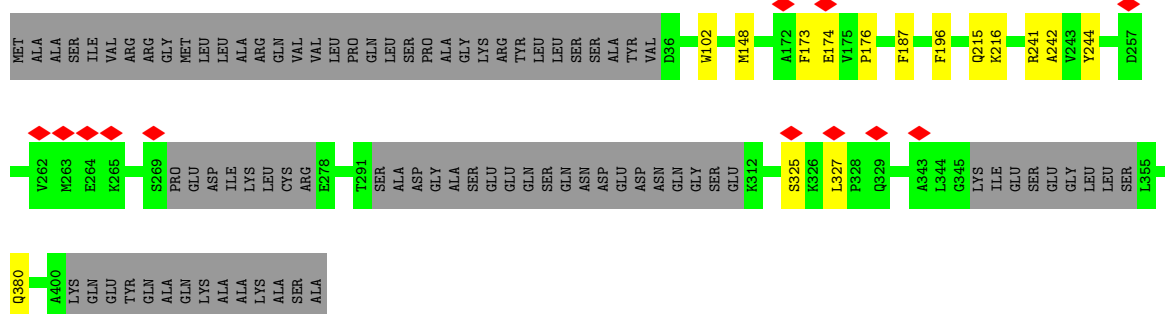
- Molecule 75: 28S ribosomal protein S26, mitochondrial

Chain AU:  80% 16%



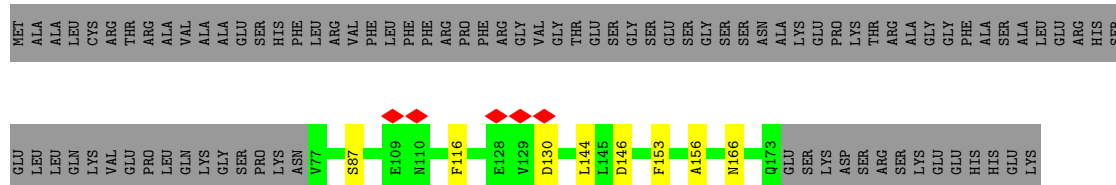
- Molecule 76: 28S ribosomal protein S27, mitochondrial

Chain AV:  76% 21%




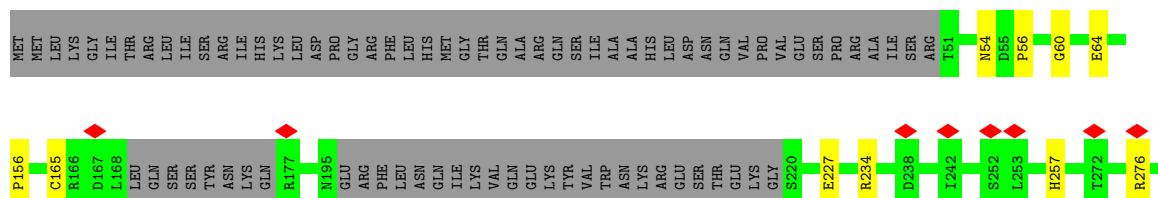
- Molecule 77: 28S ribosomal protein S28, mitochondrial

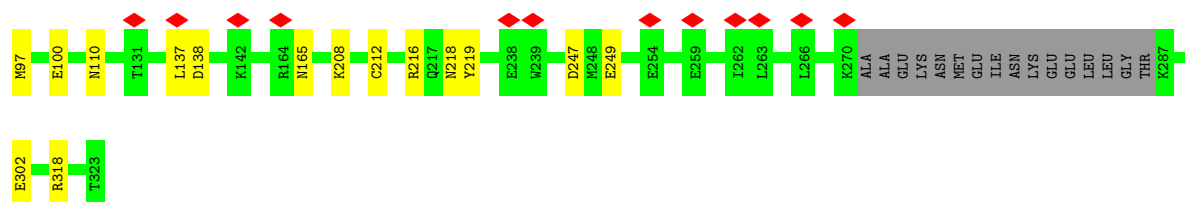
Chain AW:  48% 48%



- Molecule 78: 28S ribosomal protein S29, mitochondrial

Chain AX:  5% 76% 21%

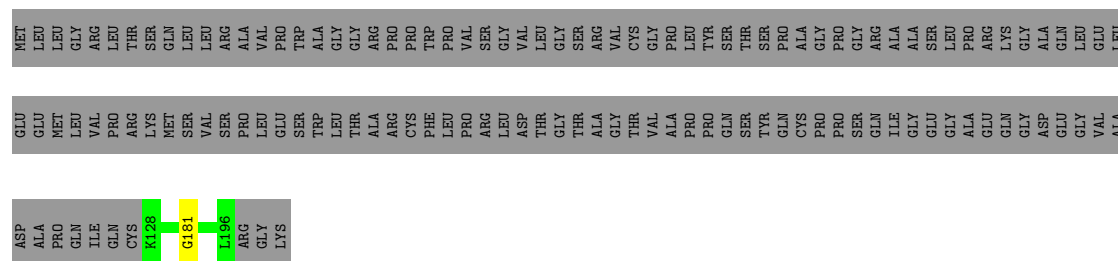




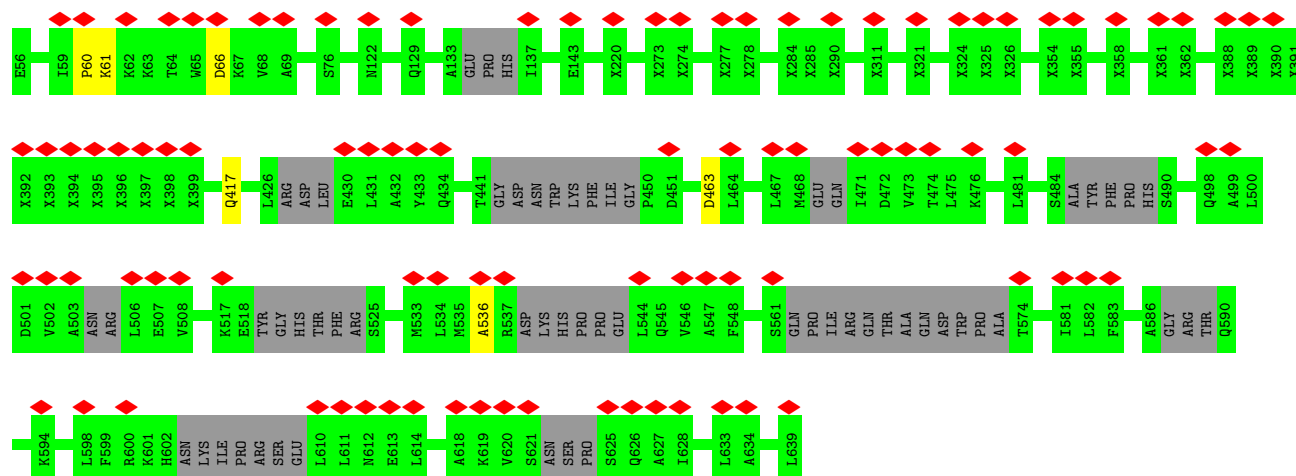
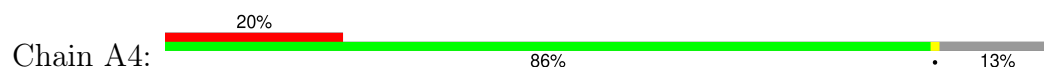
- Molecule 83: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1



- Molecule 84: Aurora kinase A-interacting protein



- Molecule 85: Pentatricopeptide repeat domain-containing protein 3, mitochondrial, mS39



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	26195	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.462	Depositor
Minimum map value	-0.346	Depositor
Average map value	0.022	Depositor
Map value standard deviation	0.095	Depositor
Recommended contour level	0.165	Depositor
Map size (\AA)	414.2, 414.2, 414.2	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.09, 1.09, 1.09	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.14	0/34967	0.72	7/54407 (0.0%)
2	B	0.13	0/1328	0.70	0/2056
3	D	0.23	0/1879	0.41	0/2527
4	E	0.23	0/2433	0.39	0/3299
5	F	0.23	0/2071	0.37	0/2817
6	H	0.22	0/798	0.40	0/1073
7	I	0.23	0/1308	0.37	0/1761
8	J	0.24	0/1077	0.39	0/1452
9	K	0.23	0/1495	0.36	0/2029
10	L	0.23	0/904	0.41	0/1218
11	M	0.24	0/2359	0.37	0/3185
12	N	0.24	0/1697	0.39	0/2281
13	O	0.23	0/1269	0.36	0/1708
14	P	0.23	0/1103	0.39	0/1491
15	Q	0.23	0/1863	0.37	0/2509
16	R	0.23	0/1174	0.35	0/1572
17	S	0.23	0/1276	0.41	0/1729
18	T	0.23	0/1402	0.36	0/1886
19	U	0.24	0/946	0.39	0/1283
20	V	0.22	0/1590	0.39	0/2151
21	W	0.23	0/893	0.39	0/1204
22	X	0.23	0/2090	0.35	0/2825
23	Y	0.23	0/1552	0.34	0/2079
24	Z	0.23	0/1003	0.38	0/1354
25	0	0.23	0/895	0.38	0/1201
26	1	0.23	0/438	0.40	0/583
27	2	0.23	0/382	0.36	0/507
28	3	0.23	0/852	0.38	0/1136
29	4	0.21	0/329	0.39	0/435
30	5	0.23	0/3154	0.38	0/4295
31	6	0.23	0/2722	0.36	0/3709
32	7	0.23	0/2207	0.36	0/2978

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	8	0.23	0/855	0.33	0/1152
34	9	0.25	0/896	0.37	0/1205
35	a	0.22	0/709	0.39	0/963
36	b	0.23	0/1202	0.39	0/1626
37	c	0.24	0/2264	0.36	0/3059
38	d	0.22	0/1385	0.38	0/1877
39	e	0.23	0/1797	0.36	0/2422
40	f	0.23	0/1055	0.40	0/1427
41	g	0.24	0/1102	0.37	0/1503
42	h	0.22	0/847	0.37	0/1150
43	i	0.23	0/849	0.34	0/1135
44	j	0.23	0/698	0.35	0/940
45	k	0.23	0/665	0.37	0/897
46	l	0.20	0/226	0.30	0/299
47	m	0.22	0/379	0.39	0/510
48	o	0.22	0/818	0.35	0/1097
49	p	0.22	0/1071	0.37	0/1433
50	q	0.23	0/1107	0.33	0/1498
51	r	0.22	0/1238	0.36	0/1676
52	s	0.23	0/3114	0.38	0/4225
54	u	0.06	0/46	0.61	0/69
55	AA	0.16	0/21926	0.75	5/34121 (0.0%)
56	AB	0.24	0/1811	0.38	0/2451
57	AC	0.23	0/1112	0.36	0/1505
58	AD	0.23	0/2607	0.39	0/3498
59	AE	0.23	0/989	0.41	0/1335
60	AF	0.23	0/1708	0.37	0/2291
61	AG	0.23	0/2570	0.36	0/3443
62	AH	0.23	0/1019	0.39	0/1379
63	AI	0.24	0/1031	0.40	0/1390
64	AJ	0.23	0/854	0.39	0/1148
65	AK	0.21	0/879	0.38	0/1182
66	AL	0.23	0/1406	0.35	0/1878
67	AM	0.23	0/941	0.38	0/1265
68	AN	0.22	0/864	0.39	0/1169
69	AO	0.24	0/1580	0.40	1/2150 (0.0%)
70	AP	0.23	0/791	0.36	0/1062
71	AQ	0.23	0/747	0.38	0/995
72	AR	0.23	0/2050	0.36	0/2770
73	AS	0.24	0/1069	0.36	0/1441
74	AT	0.24	0/1361	0.38	0/1829
75	AU	0.22	0/1482	0.36	0/1987
76	AV	0.23	0/2758	0.34	0/3724

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
77	AW	0.24	0/778	0.39	0/1048
78	AX	0.23	0/2596	0.37	0/3519
79	AY	0.24	0/943	0.32	0/1274
80	AZ	0.23	0/757	0.34	0/1011
81	A0	0.22	0/1727	0.38	0/2338
82	A1	0.23	0/2121	0.37	0/2873
83	A2	0.23	0/939	0.39	0/1256
84	A3	0.22	0/621	0.36	0/820
85	A4	0.23	0/2137	0.32	0/2872
All	All	0.21	0/165953	0.54	13/235927 (0.0%)

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2010	U	C5-C4-O4	9.58	131.65	125.90
1	A	2010	U	N3-C4-O4	-8.86	113.20	119.40
1	A	1693	C	C2-N1-C1'	6.97	126.46	118.80
1	A	1902	C	C2-N1-C1'	6.15	125.56	118.80
1	A	1693	C	N1-C2-O2	5.83	122.40	118.90

There are no chirality outliers.

There are no planarity outliers.

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	
3	D	234/305 (77%)	197 (84%)	35 (15%)	2 (1%)	14	50
4	E	296/348 (85%)	253 (86%)	34 (12%)	9 (3%)	3	23
5	F	248/311 (80%)	209 (84%)	30 (12%)	9 (4%)	3	21
6	H	93/267 (35%)	85 (91%)	7 (8%)	1 (1%)	12	46
7	I	154/261 (59%)	140 (91%)	12 (8%)	2 (1%)	10	42
8	J	138/192 (72%)	119 (86%)	16 (12%)	3 (2%)	5	30
9	K	175/178 (98%)	152 (87%)	18 (10%)	5 (3%)	3	24
10	L	113/145 (78%)	93 (82%)	17 (15%)	3 (3%)	4	26
11	M	285/296 (96%)	240 (84%)	36 (13%)	9 (3%)	3	22
12	N	203/251 (81%)	181 (89%)	20 (10%)	2 (1%)	13	48
13	O	150/175 (86%)	132 (88%)	15 (10%)	3 (2%)	6	32
14	P	129/180 (72%)	114 (88%)	12 (9%)	3 (2%)	5	29
15	Q	217/219 (99%)	180 (83%)	29 (13%)	8 (4%)	2	20
16	R	138/149 (93%)	125 (91%)	12 (9%)	1 (1%)	19	56
17	S	154/205 (75%)	132 (86%)	19 (12%)	3 (2%)	6	33
18	T	164/206 (80%)	148 (90%)	12 (7%)	4 (2%)	5	28
19	U	109/153 (71%)	92 (84%)	15 (14%)	2 (2%)	7	34
20	V	183/216 (85%)	151 (82%)	24 (13%)	8 (4%)	2	18
21	W	109/148 (74%)	94 (86%)	12 (11%)	3 (3%)	4	25
22	X	241/243 (99%)	201 (83%)	32 (13%)	8 (3%)	3	21
23	Y	174/250 (70%)	157 (90%)	14 (8%)	3 (2%)	7	36
24	Z	118/161 (73%)	100 (85%)	14 (12%)	4 (3%)	3	21
25	0	106/188 (56%)	89 (84%)	14 (13%)	3 (3%)	4	25
26	1	50/65 (77%)	43 (86%)	4 (8%)	3 (6%)	1	13
27	2	44/92 (48%)	40 (91%)	4 (9%)	0	100	100
28	3	93/188 (50%)	86 (92%)	7 (8%)	0	100	100
29	4	34/103 (33%)	33 (97%)	1 (3%)	0	100	100
30	5	368/394 (93%)	308 (84%)	47 (13%)	13 (4%)	3	21
31	6	313/380 (82%)	258 (82%)	45 (14%)	10 (3%)	3	22
32	7	258/338 (76%)	217 (84%)	36 (14%)	5 (2%)	6	33
33	8	97/206 (47%)	88 (91%)	9 (9%)	0	100	100
34	9	105/137 (77%)	90 (86%)	12 (11%)	3 (3%)	3	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	a	78/142 (55%)	72 (92%)	5 (6%)	1 (1%)	10	42
36	b	146/215 (68%)	128 (88%)	16 (11%)	2 (1%)	9	40
37	c	271/332 (82%)	233 (86%)	31 (11%)	7 (3%)	4	26
38	d	156/306 (51%)	132 (85%)	20 (13%)	4 (3%)	4	26
39	e	211/279 (76%)	188 (89%)	20 (10%)	3 (1%)	9	40
40	f	125/212 (59%)	106 (85%)	17 (14%)	2 (2%)	8	37
41	g	127/166 (76%)	106 (84%)	18 (14%)	3 (2%)	5	28
42	h	96/158 (61%)	80 (83%)	11 (12%)	5 (5%)	1	15
43	i	95/128 (74%)	76 (80%)	16 (17%)	3 (3%)	3	22
44	j	83/123 (68%)	77 (93%)	5 (6%)	1 (1%)	11	43
45	k	82/112 (73%)	62 (76%)	12 (15%)	8 (10%)	0	7
46	l	21/138 (15%)	21 (100%)	0	0	100	100
47	m	43/128 (34%)	38 (88%)	5 (12%)	0	100	100
48	o	92/102 (90%)	80 (87%)	8 (9%)	4 (4%)	2	18
49	p	119/206 (58%)	109 (92%)	10 (8%)	0	100	100
50	q	126/222 (57%)	118 (94%)	8 (6%)	0	100	100
51	r	140/196 (71%)	121 (86%)	13 (9%)	6 (4%)	2	18
52	s	366/439 (83%)	315 (86%)	44 (12%)	7 (2%)	6	33
56	AB	215/296 (73%)	186 (86%)	27 (13%)	2 (1%)	14	50
57	AC	130/167 (78%)	97 (75%)	31 (24%)	2 (2%)	8	39
58	AD	316/430 (74%)	255 (81%)	46 (15%)	15 (5%)	2	17
59	AE	120/125 (96%)	87 (72%)	25 (21%)	8 (7%)	1	12
60	AF	197/242 (81%)	168 (85%)	25 (13%)	4 (2%)	6	32
61	AG	301/396 (76%)	245 (81%)	45 (15%)	11 (4%)	2	20
62	AH	120/201 (60%)	93 (78%)	24 (20%)	3 (2%)	4	27
63	AI	134/194 (69%)	106 (79%)	24 (18%)	4 (3%)	3	23
64	AJ	106/138 (77%)	83 (78%)	20 (19%)	3 (3%)	4	25
65	AK	99/128 (77%)	86 (87%)	7 (7%)	6 (6%)	1	13
66	AL	162/257 (63%)	137 (85%)	19 (12%)	6 (4%)	2	20
67	AM	114/137 (83%)	93 (82%)	17 (15%)	4 (4%)	3	21
68	AN	105/130 (81%)	82 (78%)	19 (18%)	4 (4%)	2	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	AO	183/185 (99%)	141 (77%)	33 (18%)	9 (5%)	2	16
70	AP	94/142 (66%)	73 (78%)	18 (19%)	3 (3%)	3	22
71	AQ	84/86 (98%)	77 (92%)	6 (7%)	1 (1%)	11	43
72	AR	240/360 (67%)	171 (71%)	55 (23%)	14 (6%)	1	14
73	AS	124/190 (65%)	102 (82%)	14 (11%)	8 (6%)	1	13
74	AT	160/173 (92%)	130 (81%)	21 (13%)	9 (6%)	1	15
75	AU	171/205 (83%)	152 (89%)	13 (8%)	6 (4%)	3	21
76	AV	320/414 (77%)	267 (83%)	43 (13%)	10 (3%)	3	23
77	AW	95/187 (51%)	65 (68%)	23 (24%)	7 (7%)	1	10
78	AX	310/398 (78%)	253 (82%)	46 (15%)	11 (4%)	3	21
79	AY	106/395 (27%)	86 (81%)	14 (13%)	6 (6%)	1	14
80	AZ	85/106 (80%)	74 (87%)	9 (11%)	2 (2%)	5	28
81	A0	197/225 (88%)	152 (77%)	29 (15%)	16 (8%)	1	9
82	A1	252/323 (78%)	198 (79%)	45 (18%)	9 (4%)	3	21
83	A2	114/118 (97%)	89 (78%)	20 (18%)	5 (4%)	2	18
84	A3	67/199 (34%)	58 (87%)	8 (12%)	1 (2%)	8	39
85	A4	237/474 (50%)	222 (94%)	12 (5%)	3 (1%)	10	42
All	All	12628/17575 (72%)	10637 (84%)	1611 (13%)	380 (3%)	5	23

5 of 380 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	W	73	PHE
22	X	69	ILE
22	X	149	PRO
30	5	263	ILE
30	5	296	LYS

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	
3	D	190/245 (78%)	184 (97%)	6 (3%)	34	55
4	E	255/290 (88%)	255 (100%)	0	100	100
5	F	217/262 (83%)	213 (98%)	4 (2%)	54	71
6	H	86/228 (38%)	83 (96%)	3 (4%)	31	52
7	I	145/232 (62%)	145 (100%)	0	100	100
8	J	113/150 (75%)	113 (100%)	0	100	100
9	K	155/156 (99%)	154 (99%)	1 (1%)	84	88
10	L	98/124 (79%)	98 (100%)	0	100	100
11	M	245/249 (98%)	242 (99%)	3 (1%)	67	79
12	N	172/211 (82%)	164 (95%)	8 (5%)	22	44
13	O	133/150 (89%)	132 (99%)	1 (1%)	79	85
14	P	115/155 (74%)	111 (96%)	4 (4%)	31	52
15	Q	201/201 (100%)	200 (100%)	1 (0%)	86	90
16	R	118/126 (94%)	118 (100%)	0	100	100
17	S	141/180 (78%)	138 (98%)	3 (2%)	48	67
18	T	146/176 (83%)	145 (99%)	1 (1%)	81	87
19	U	99/135 (73%)	96 (97%)	3 (3%)	36	57
20	V	169/191 (88%)	167 (99%)	2 (1%)	67	79
21	W	91/119 (76%)	91 (100%)	0	100	100
22	X	219/219 (100%)	216 (99%)	3 (1%)	62	76
23	Y	159/223 (71%)	159 (100%)	0	100	100
24	Z	111/147 (76%)	110 (99%)	1 (1%)	75	83
25	0	97/164 (59%)	96 (99%)	1 (1%)	73	81
26	1	49/60 (82%)	47 (96%)	2 (4%)	26	48
27	2	40/72 (56%)	39 (98%)	1 (2%)	42	62
28	3	88/166 (53%)	85 (97%)	3 (3%)	32	53
29	4	35/89 (39%)	35 (100%)	0	100	100
30	5	337/353 (96%)	328 (97%)	9 (3%)	40	60
31	6	266/332 (80%)	257 (97%)	9 (3%)	32	53
32	7	242/303 (80%)	240 (99%)	2 (1%)	79	85
33	8	91/190 (48%)	91 (100%)	0	100	100
34	9	91/112 (81%)	89 (98%)	2 (2%)	47	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	a	78/133 (59%)	76 (97%)	2 (3%)	41	61
36	b	130/186 (70%)	127 (98%)	3 (2%)	45	65
37	c	241/288 (84%)	239 (99%)	2 (1%)	79	85
38	d	151/274 (55%)	149 (99%)	2 (1%)	65	77
39	e	188/236 (80%)	185 (98%)	3 (2%)	58	74
40	f	117/188 (62%)	116 (99%)	1 (1%)	75	83
41	g	119/148 (80%)	115 (97%)	4 (3%)	32	53
42	h	95/148 (64%)	93 (98%)	2 (2%)	48	67
43	i	86/110 (78%)	81 (94%)	5 (6%)	17	38
44	j	68/97 (70%)	67 (98%)	1 (2%)	60	75
45	k	74/90 (82%)	74 (100%)	0	100	100
46	l	23/116 (20%)	23 (100%)	0	100	100
47	m	40/113 (35%)	39 (98%)	1 (2%)	42	62
48	o	80/87 (92%)	80 (100%)	0	100	100
49	p	117/181 (65%)	113 (97%)	4 (3%)	32	53
50	q	110/178 (62%)	108 (98%)	2 (2%)	54	71
51	r	133/169 (79%)	132 (99%)	1 (1%)	79	85
52	s	326/381 (86%)	323 (99%)	3 (1%)	75	83
56	AB	191/249 (77%)	187 (98%)	4 (2%)	48	67
57	AC	115/143 (80%)	111 (96%)	4 (4%)	31	52
58	AD	269/357 (75%)	262 (97%)	7 (3%)	41	61
59	AE	104/107 (97%)	102 (98%)	2 (2%)	52	70
60	AF	178/209 (85%)	174 (98%)	4 (2%)	47	66
61	AG	265/342 (78%)	257 (97%)	8 (3%)	36	57
62	AH	112/180 (62%)	110 (98%)	2 (2%)	54	71
63	AI	104/147 (71%)	104 (100%)	0	100	100
64	AJ	93/118 (79%)	91 (98%)	2 (2%)	47	66
65	AK	91/113 (80%)	89 (98%)	2 (2%)	47	66
66	AL	152/226 (67%)	149 (98%)	3 (2%)	50	69
67	AM	95/113 (84%)	93 (98%)	2 (2%)	48	67
68	AN	93/115 (81%)	91 (98%)	2 (2%)	47	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	AO	166/166 (100%)	160 (96%)	6 (4%)	30	52
70	AP	87/123 (71%)	87 (100%)	0	100	100
71	AQ	78/78 (100%)	74 (95%)	4 (5%)	20	42
72	AR	224/318 (70%)	218 (97%)	6 (3%)	40	60
73	AS	109/164 (66%)	104 (95%)	5 (5%)	23	45
74	AT	150/157 (96%)	148 (99%)	2 (1%)	65	77
75	AU	149/174 (86%)	147 (99%)	2 (1%)	65	77
76	AV	295/364 (81%)	290 (98%)	5 (2%)	56	72
77	AW	84/158 (53%)	83 (99%)	1 (1%)	67	79
78	AX	275/351 (78%)	272 (99%)	3 (1%)	70	80
79	AY	99/357 (28%)	99 (100%)	0	100	100
80	AZ	80/95 (84%)	79 (99%)	1 (1%)	65	77
81	A0	176/196 (90%)	172 (98%)	4 (2%)	45	65
82	A1	237/291 (81%)	228 (96%)	9 (4%)	28	50
83	A2	99/101 (98%)	96 (97%)	3 (3%)	36	57
84	A3	63/166 (38%)	63 (100%)	0	100	100
85	A4	226/291 (78%)	223 (99%)	3 (1%)	65	77
All	All	11349/15102 (75%)	11144 (98%)	205 (2%)	54	71

5 of 205 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	AC	134	PHE
65	AK	63	LEU
83	A2	9	ARG
58	AD	237	ARG
61	AG	106	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
52	s	96	GLN
83	A2	90	GLN
58	AD	424	ASN
78	AX	66	GLN

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Mol	Chain	Res	Type
58	AD	165	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1458/1472 (99%)	332 (22%)	23 (1%)
2	B	51/56 (91%)	9 (17%)	1 (1%)
54	u	1/2 (50%)	0	0
55	AA	914/923 (99%)	366 (40%)	24 (2%)
All	All	2424/2453 (98%)	707 (29%)	48 (1%)

5 of 707 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1672	C
1	A	1676	A
1	A	1677	C
1	A	1678	C
1	A	1679	U

5 of 48 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
55	AA	833	A
55	AA	982	A
55	AA	878	G
55	AA	943	G
55	AA	1102	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 134 ligands modelled in this entry, 134 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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
1	A	14
85	A4	13
55	AA	8
2	B	4

The worst 5 of 39 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2218:C	O3'	2228:A	P	41.52
1	A4	399:UNK	C	414:LYS	N	32.07
1	A	2760:A	O3'	2792:A	P	25.98
1	A	1760:G	O3'	1766:U	P	24.98
1	AA	955:A	O3'	965:C	P	24.64

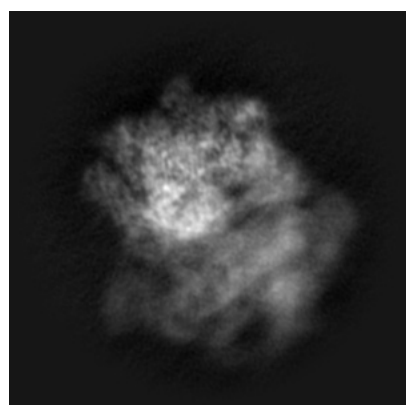
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0515. These allow visual inspection of the internal detail of the map and identification of artifacts.

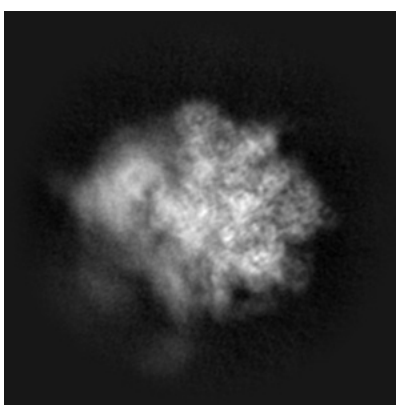
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

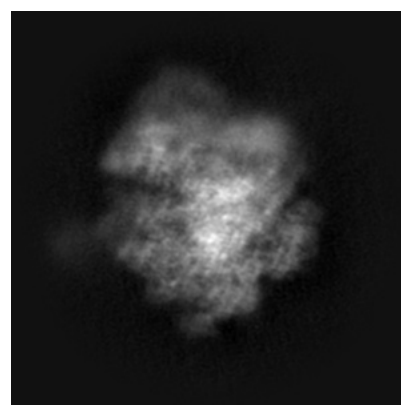
6.1.1 Primary map



X



Y

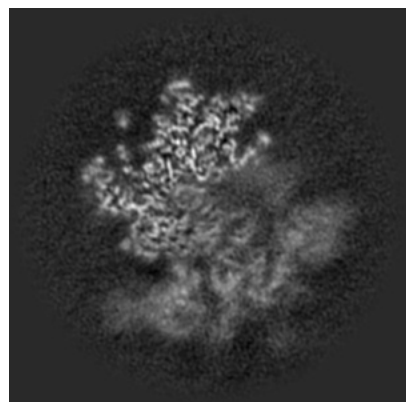


Z

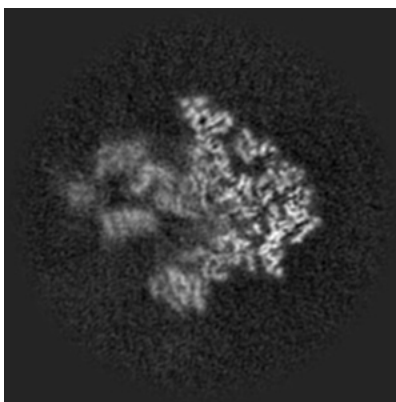
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

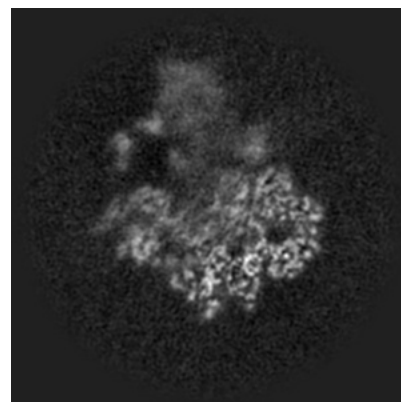
6.2.1 Primary map



X Index: 190



Y Index: 190

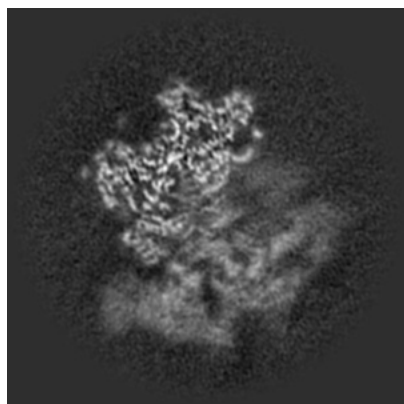


Z Index: 190

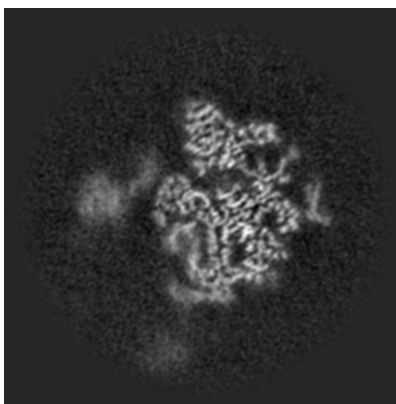
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

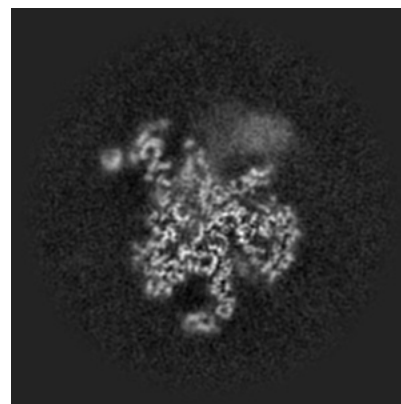
6.3.1 Primary map



X Index: 197



Y Index: 147

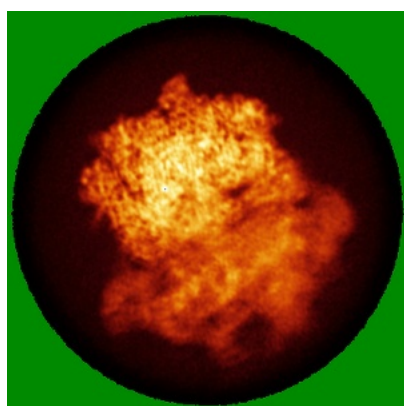


Z Index: 228

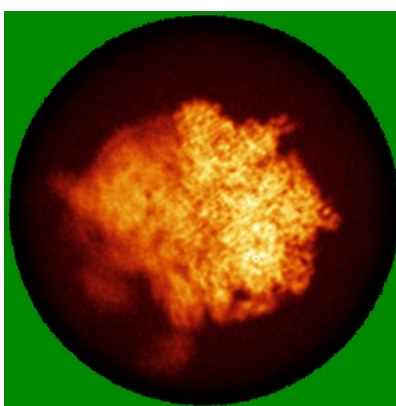
The images above show the largest variance slices of the map in three orthogonal directions.

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

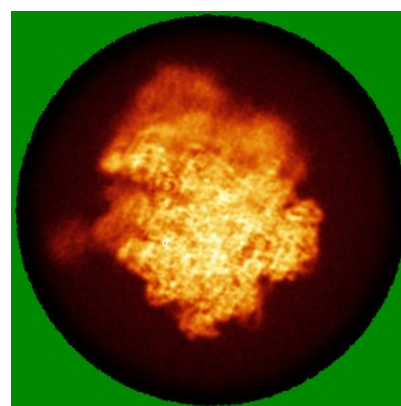
6.4.1 Primary map



X



Y

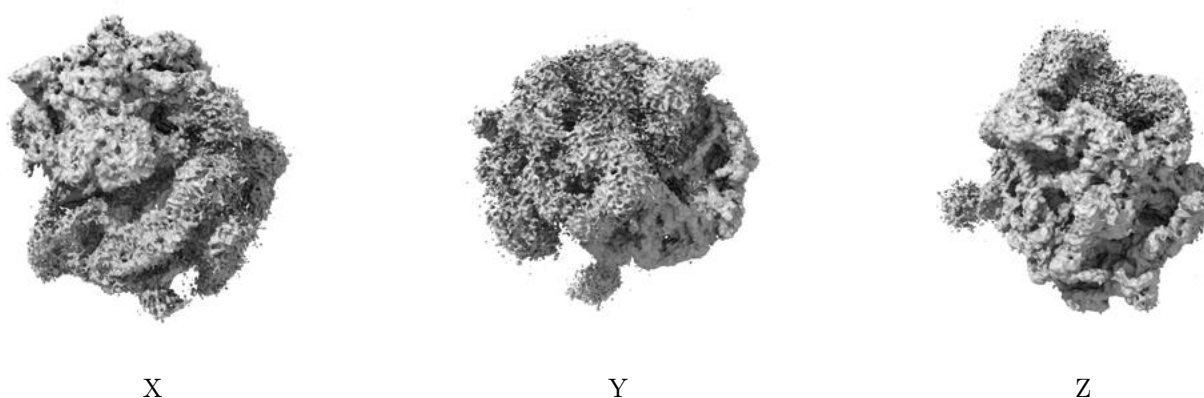


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.165. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

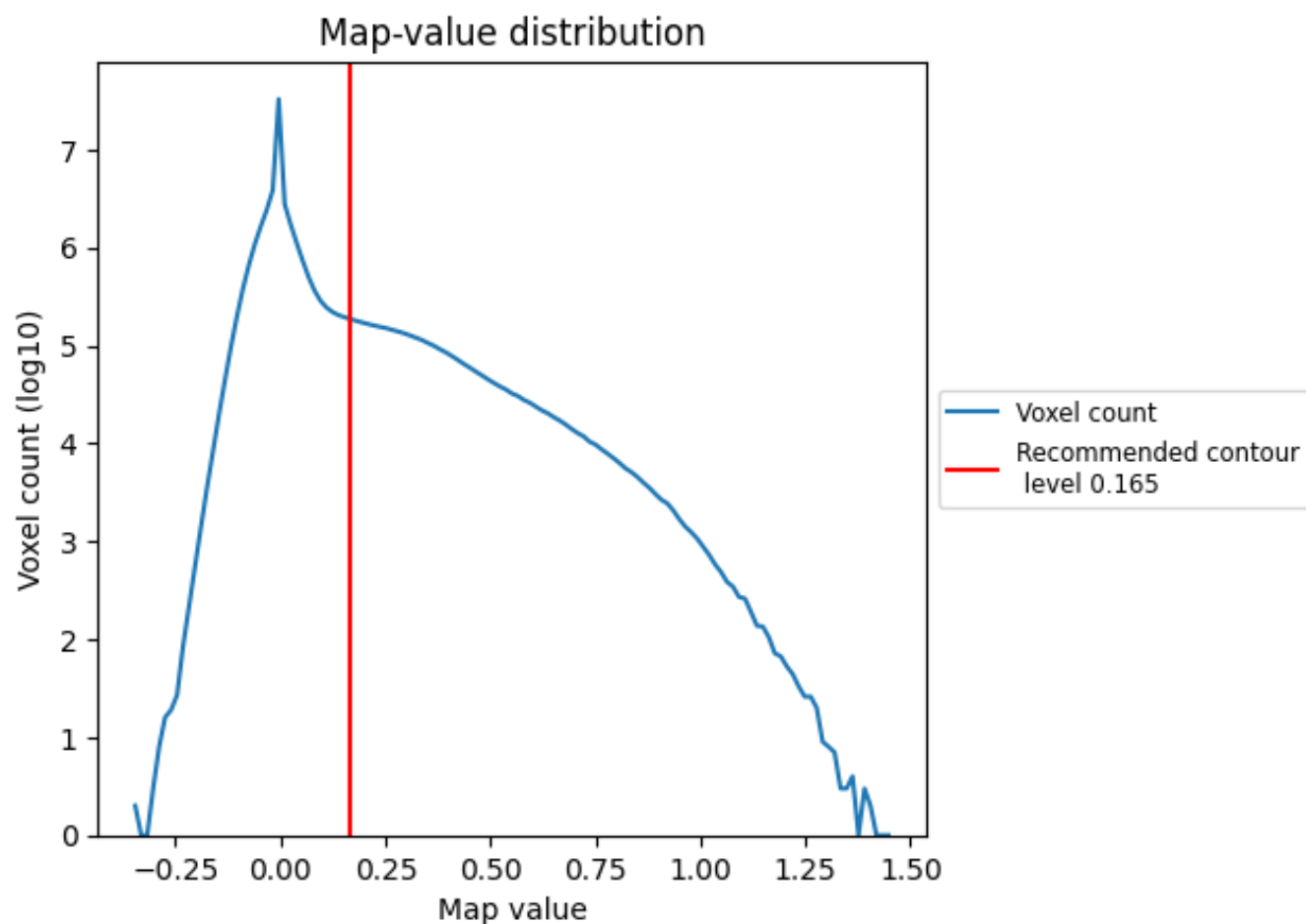
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

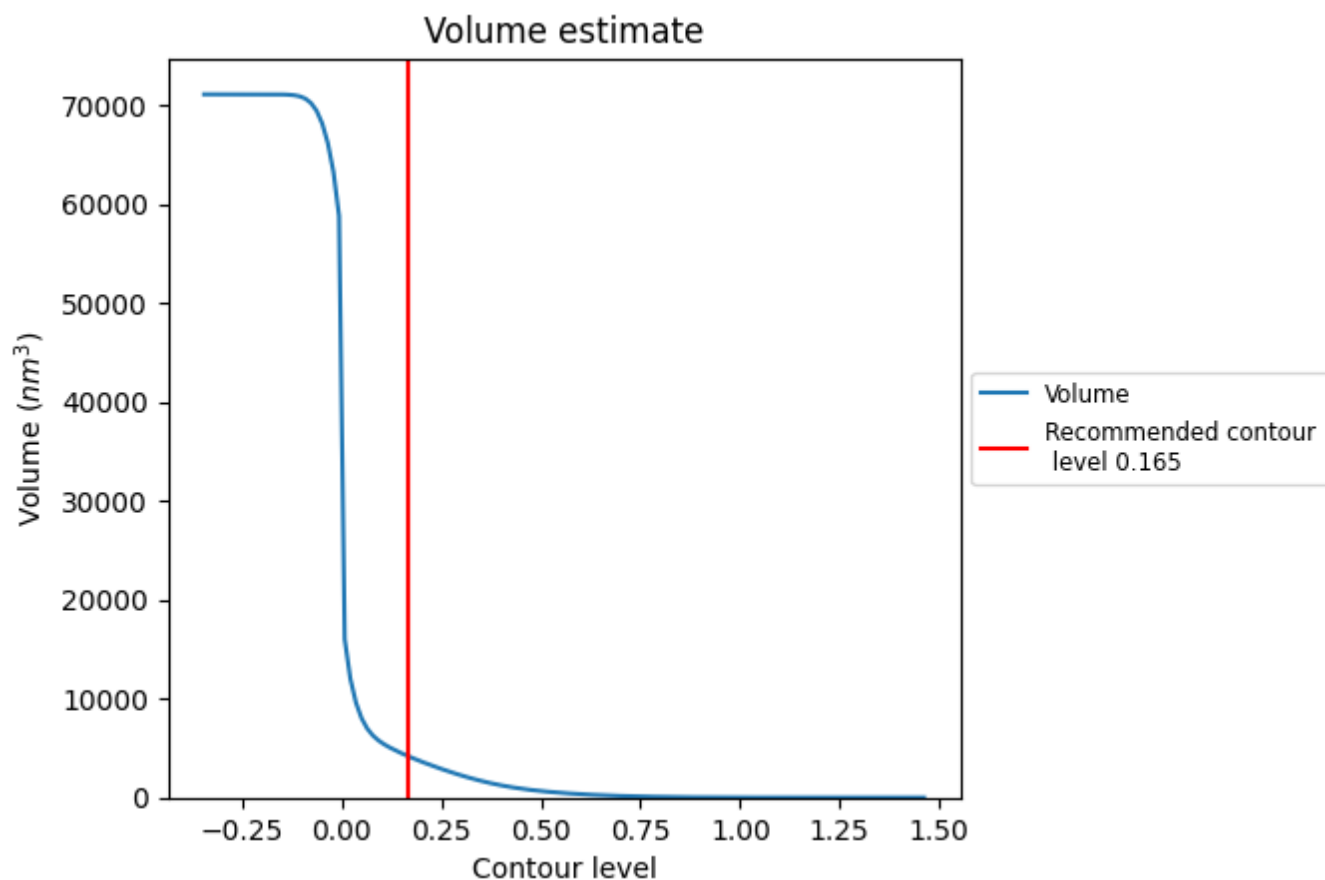
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

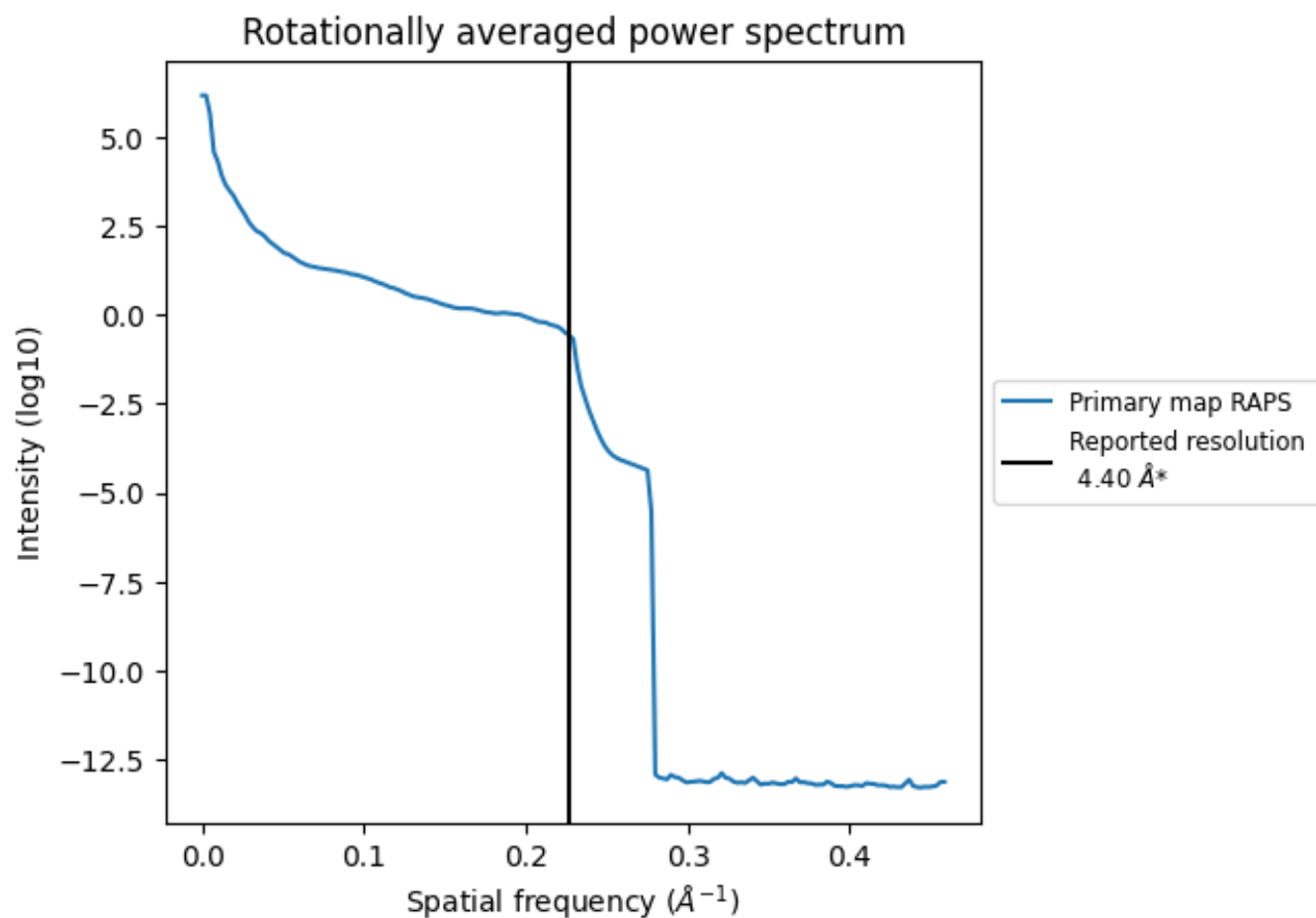
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4210 nm³; this corresponds to an approximate mass of 3803 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 0.227 Å⁻¹

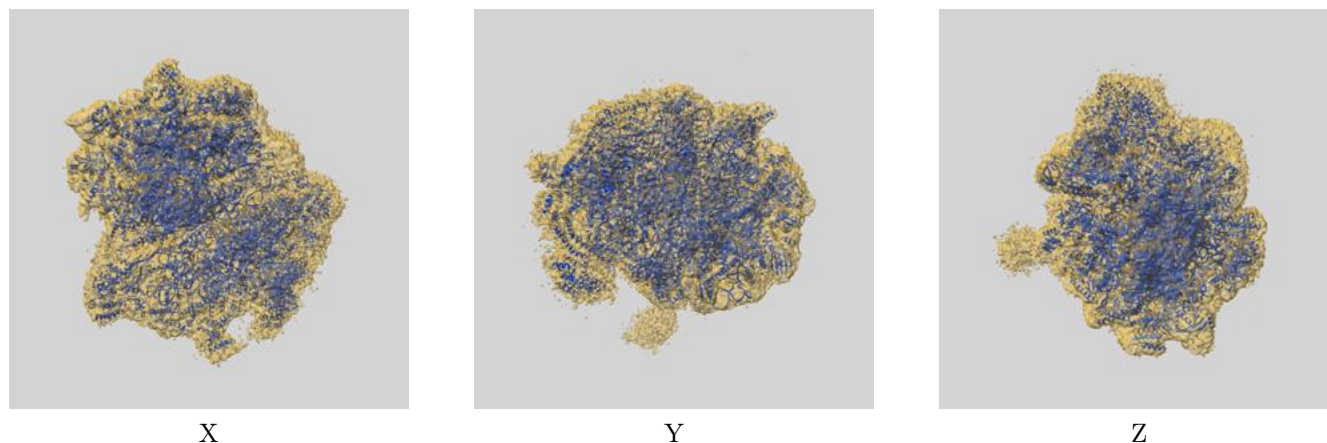
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

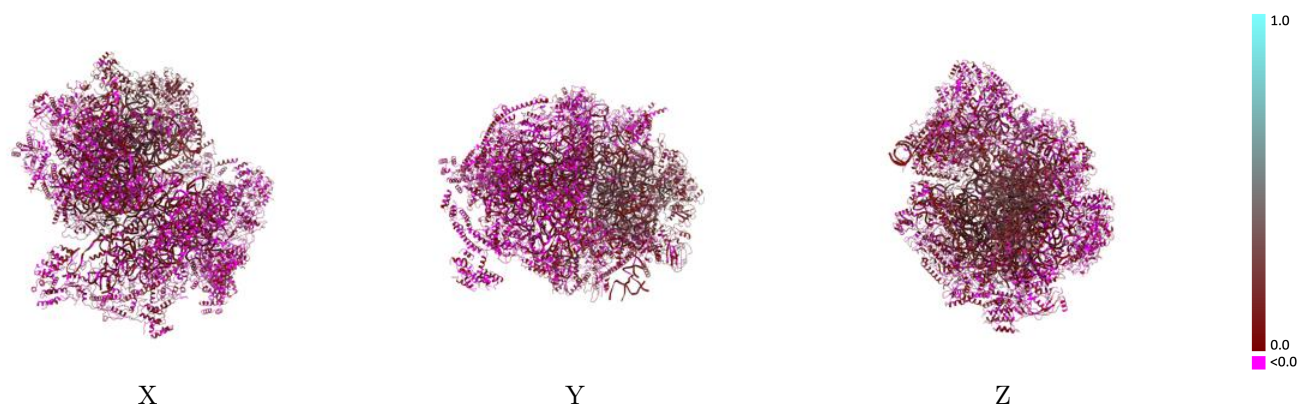
This section contains information regarding the fit between EMDB map EMD-0515 and PDB model 6NU3. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



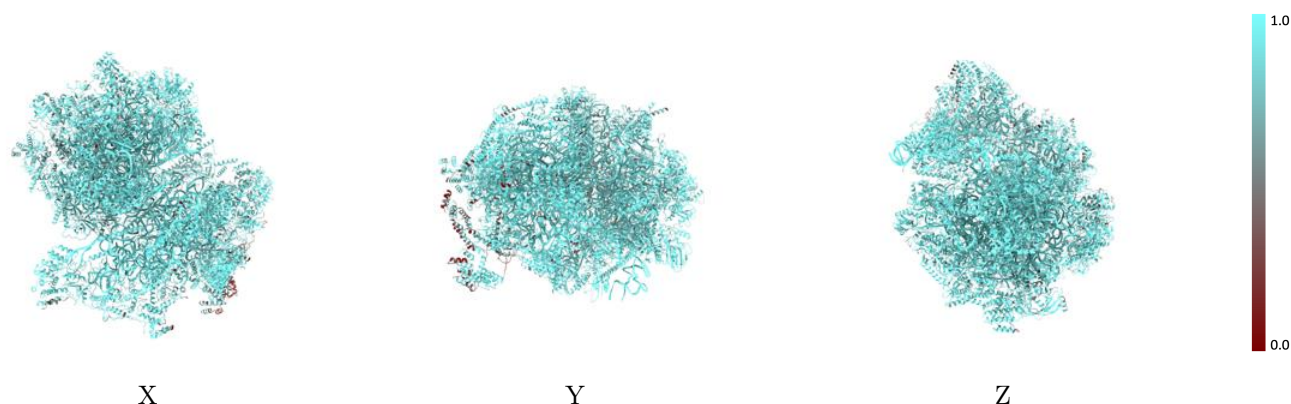
The images above show the 3D surface view of the map at the recommended contour level 0.165 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



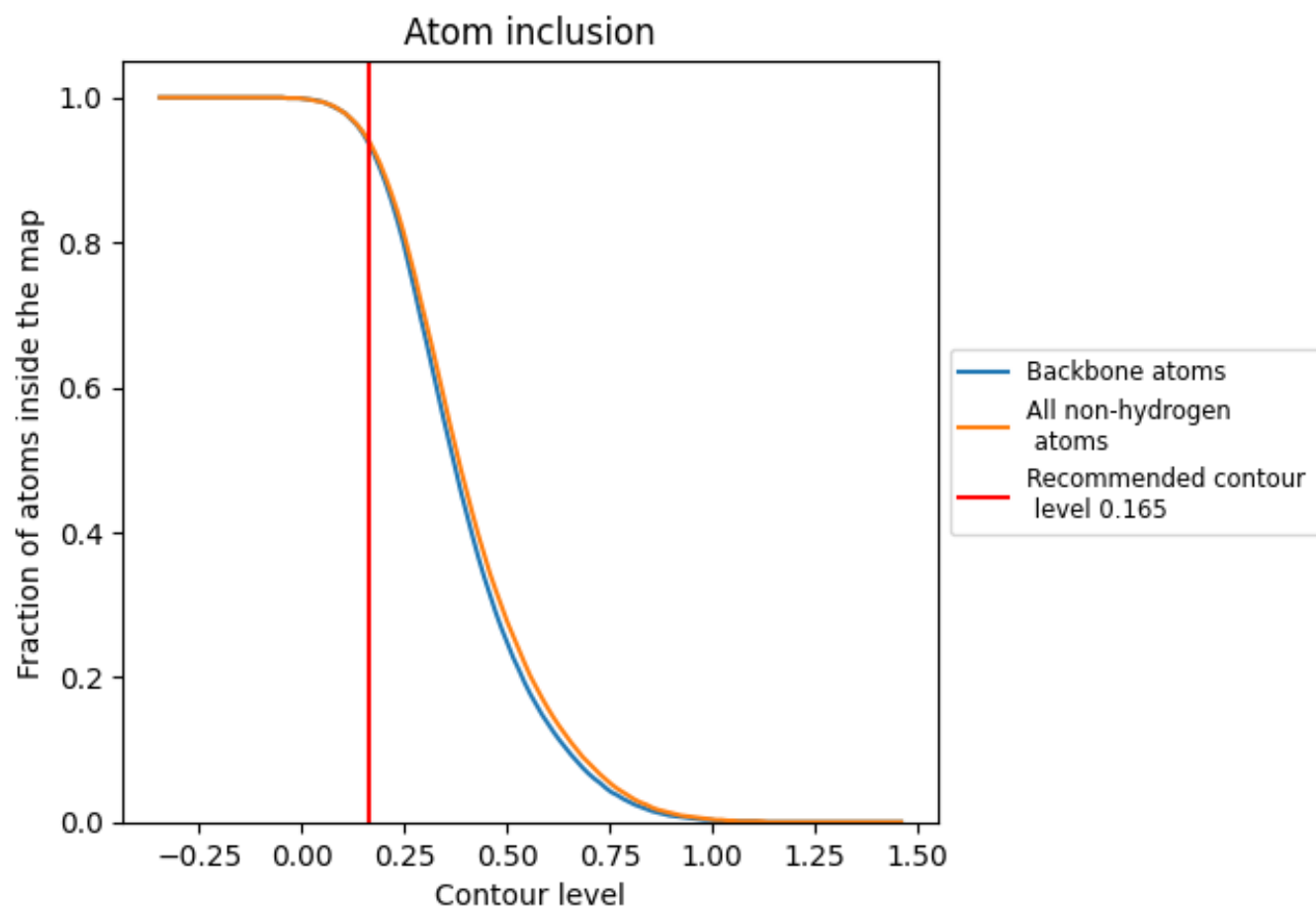
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.165).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 94% 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 (0.165) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9390	 0.0950
0	 0.8660	 0.0450
1	 0.9810	 0.1250
2	 0.8690	 0.0330
3	 0.9500	 0.2510
4	 0.9410	 0.1000
5	 0.9100	 0.0200
6	 0.9570	 0.1670
7	 0.8850	 0.0280
8	 0.9240	 0.0990
9	 0.9060	 0.0340
A	 0.9780	 0.1740
A0	 0.9520	 0.0590
A1	 0.8970	 0.0470
A2	 0.9270	 0.0240
A3	 0.9570	 0.0840
A4	 0.7080	 0.0270
AA	 0.9850	 0.0790
AB	 0.9610	 0.0160
AC	 0.9530	 0.0000
AD	 0.9070	 0.0320
AE	 0.9040	 -0.0190
AF	 0.9200	 0.0140
AG	 0.8240	 0.0350
AH	 0.8380	 0.0050
AI	 0.9470	 0.0130
AJ	 0.9460	 0.1030
AK	 0.9460	 0.0230
AL	 0.9670	 0.0120
AM	 0.9720	 0.0370
AN	 0.9920	 0.0210
AO	 0.9260	 0.0690
AP	 0.9660	 0.0040
AQ	 0.9520	 0.0530
AR	 0.8990	 0.0570





















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Chain	Atom inclusion	Q-score
AS	 0.9610	 0.0230
AT	 0.9560	 0.0710
AU	 0.9500	 0.0690
AV	 0.9300	 0.0550
AW	 0.9320	 -0.0190
AX	 0.8930	 0.0250
AY	 0.8230	 0.0330
AZ	 0.9650	 0.0100
B	 0.9740	 0.1320
D	 0.9090	 0.0250
E	 0.9580	 0.1030
F	 0.9260	 0.1950
H	 0.9040	 0.1250
I	 0.9470	 0.0830
J	 0.9460	 0.0510
K	 0.9300	 0.1070
L	 0.8850	 0.1580
M	 0.9590	 0.2250
N	 0.9480	 0.1690
O	 0.8850	 0.0200
P	 0.9370	 0.1170
Q	 0.9210	 0.1340
R	 0.9210	 0.1100
S	 0.9190	 0.1070
T	 0.8280	 0.0650
U	 0.8770	 -0.0080
V	 0.8630	 0.0610
W	 0.9280	 0.1280
X	 0.9050	 0.1050
Y	 0.9160	 0.0380
Z	 0.9330	 0.1410
a	 0.9430	 0.0870
b	 0.8960	 0.0910
c	 0.8840	 0.0590
d	 0.8810	 0.0520
e	 0.9700	 0.1010
f	 0.8940	 0.1190
g	 0.9690	 0.2690
h	 0.9440	 0.1650
i	 0.9080	 0.1780
j	 0.9210	 0.1190
k	 0.9240	 0.0440

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Chain	Atom inclusion	Q-score
l	 0.9900	 0.1070
m	 0.9210	 0.0360
o	 0.9630	 0.1550
p	 0.9650	 0.1770
q	 0.9390	 0.1990
r	 0.9600	 0.1020
s	 0.8940	 -0.0050
t	 0.9790	 0.1730
u	 1.0000	 0.0970