



wwPDB EM Validation Summary Report ⓘ

Oct 6, 2024 – 06:12 PM EDT

PDB ID : 7L08
EMDB ID : EMD-23096
Title : Cryo-EM structure of the human 55S mitoribosome-RRFmt complex.
Authors : Koripella, R.; Agrawal, E.K.; Deep, A.; Agrawal, R.K.
Deposited on : 2020-12-11
Resolution : 3.49 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

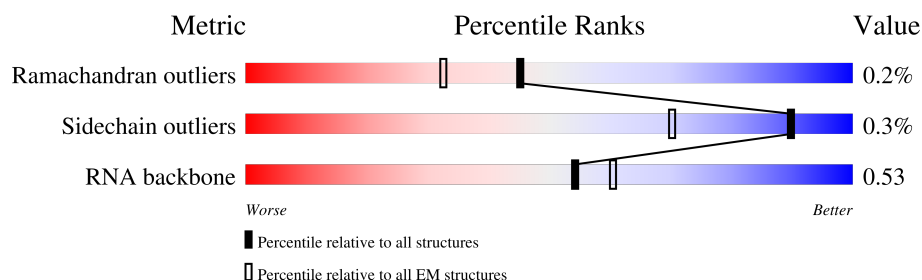
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.49 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	AA	954	
2	AB	296	
3	AC	167	
4	AE	125	
5	AI	194	
6	AJ	138	
7	AK	128	
8	AM	137	

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Mol	Chain	Length	Quality of chain
9	AN	130	
10	AO	258	
11	AP	142	
12	AQ	87	
13	AT	173	
14	AW	187	
15	AX	398	
16	A2	118	
17	AH	201	
18	AL	257	
19	AR	360	
20	AS	190	
21	AU	205	
22	AV	414	
23	AY	395	
24	AZ	106	
25	A1	323	
26	A0	218	
27	A3	199	
28	A4	689	
29	AD	430	
30	AF	242	
31	AG	396	
32	A	1559	
33	B	73	











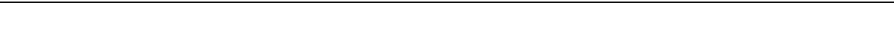

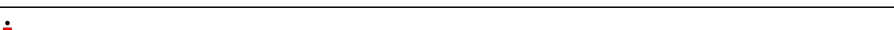
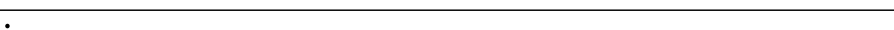











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Mol	Chain	Length	Quality of chain
34	D	305	
35	F	311	
36	H	267	
37	K	178	
38	L	145	
39	M	296	
40	O	175	
41	R	149	
42	S	205	
43	T	212	
44	W	148	
45	X	256	
46	Y	250	
47	Z	161	
48	0	188	
49	1	65	
50	2	92	
51	3	188	
52	4	103	
53	8	206	
54	b	155	
55	e	279	
56	g	166	
57	i	128	
58	j	123	

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Mol	Chain	Length	Quality of chain
59	m	128	
60	o	102	
61	q	222	
62	r	196	
63	J	192	
64	I	261	
65	N	251	
66	P	179	
67	U	153	
68	V	216	
69	E	348	
70	5	423	
71	6	380	
72	7	338	
73	9	137	
74	a	142	
75	c	332	
76	d	306	
77	f	194	
78	h	158	
79	k	112	
80	l	138	
81	p	206	
82	s	439	
83	Q	292	

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Mol	Chain	Length	Quality of chain
84	u	65	<div><div></div><div>28%</div><div></div><div>100%</div></div>
85	TA	198	<div><div></div><div>6%</div><div>23%</div><div></div><div>77%</div></div>
85	TB	198	<div><div></div><div>13%</div><div></div><div>86%</div></div>
86	z	204	<div><div></div><div>18%</div><div></div><div>93%</div><div></div><div></div></div>

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 168922 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 12S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	944	Total	C	N	O	P	0	0
			20030	8980	3612	6494	944		

- Molecule 2 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	220	Total	C	N	O	S	0	0
			1787	1141	324	312	10		

- Molecule 3 is a protein called 28S ribosomal protein S24, mitochondrial.

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

- Molecule 4 is a protein called 28S ribosomal protein S6, mitochondrial.

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

- Molecule 5 is a protein called 28S ribosomal protein S11, mitochondrial.

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

- Molecule 6 is a protein called 28S ribosomal protein S12, mitochondrial.

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

- Molecule 7 is a protein called 28S ribosomal protein S14, mitochondrial.

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

- Molecule 8 is a protein called 28S ribosomal protein S16, mitochondrial.

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

- Molecule 9 is a protein called 28S ribosomal protein S17, mitochondrial.

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

- Molecule 10 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AO	190	Total	C	N	O	S	0	0
			1570	998	291	274	7		

- Molecule 11 is a protein called 28S ribosomal protein S18c, mitochondrial.

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

- Molecule 12 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AQ	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
AQ	50	ARG	CYS	variant	UNP P82921

- Molecule 13 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AT	168	Total	C	N	O	S	0	0
			1371	877	239	244	11		

- Molecule 14 is a protein called 28S ribosomal protein S28, mitochondrial.

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

- Molecule 15 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AX	353	Total	C	N	O	S	0	0
			2860	1828	503	518	11		

- Molecule 16 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	A2	116	Total	C	N	O	S	0	0
			925	574	181	162	8		

- Molecule 17 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AH	122	Total	C	N	O	S	0	0
			1014	656	172	183	3		

- Molecule 18 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AL	174	Total	C	N	O	S	0	0
			1451	924	271	249	7		

- Molecule 19 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AR	292	Total	C	N	O	S	0	0
			2388	1521	410	449	8		

- Molecule 20 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AS	135	Total	C	N	O	S	0	0
			1111	716	198	196	1		

- Molecule 21 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	177	Total	C	N	O	S	0	0
			1499	922	305	268	4		

- Molecule 22 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	367	Total	C	N	O	S	0	0
			3009	1931	502	564	12		

- Molecule 23 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AY	120	Total	C	N	O	S	0	0
			1016	657	167	190	2		

- Molecule 24 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AZ	99	Total	C	N	O	S	0	0
			833	531	152	146	4		

- Molecule 25 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A1	275	Total	C	N	O	S	0	0
			2231	1414	380	426	11		

- Molecule 26 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A0	214	Total	C	N	O	S	0	0
			1781	1125	341	310	5		

- Molecule 27 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A3	72	Total	C	N	O	S	0	0
			639	409	137	92	1		

- Molecule 28 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	A4	549	Total	C	N	O	S	0	0
			3010	1841	573	593	3		

- Molecule 29 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AD	343	Total	C	N	O	S	0	0
			2731	1713	518	487	13		

- Molecule 30 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AF	208	Total	C	N	O	S	0	0
			1724	1103	312	298	11		

- Molecule 31 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AG	315	Total	C	N	O	S	0	0
			2587	1640	462	471	14		

- Molecule 32 is a RNA chain called 16S RRNA.

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

- Molecule 33 is a RNA chain called tRNAVAL.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1601	C	-	insertion	GB 1896813692

- Molecule 34 is a protein called 39S ribosomal protein L2, mitochondrial.

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

- Molecule 35 is a protein called 39S ribosomal protein L4, mitochondrial.

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

- Molecule 36 is a protein called 39S ribosomal protein L9, mitochondrial.

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

- Molecule 37 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 38 is a protein called 39S ribosomal protein L14, mitochondrial.

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

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

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

- Molecule 40 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 41 is a protein called 39S ribosomal protein L20, mitochondrial.

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

- Molecule 42 is a protein called 39S ribosomal protein L21, mitochondrial.

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

- Molecule 43 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 44 is a protein called 39S ribosomal protein L27, mitochondrial.

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

- Molecule 45 is a protein called 39S ribosomal protein L28, mitochondrial.

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

There are 3 discrepancies between the modelled and reference sequences:

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

- Molecule 46 is a protein called 39S ribosomal protein L47, mitochondrial.

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

- Molecule 47 is a protein called 39S ribosomal protein L30, mitochondrial.

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

- Molecule 48 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	0	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 49 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	1	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

- Molecule 50 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2	46	Total	C	N	O	S	0	0
			376	233	83	59	1		

- Molecule 51 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 52 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	38	Total	C	N	O	S	0	0
			342	217	72	49	4		

- Molecule 53 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	8	99	Total	C	N	O	S	0	0
			836	535	144	155	2		

- Molecule 54 is a protein called 39S ribosomal protein L43, mitochondrial.

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

- Molecule 55 is a protein called 39S ribosomal protein L46, mitochondrial.

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

- Molecule 56 is a protein called 39S ribosomal protein L49, mitochondrial.

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

- Molecule 57 is a protein called 39S ribosomal protein L51, mitochondrial.

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

- Molecule 58 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
58	j	93	Total	C	N	O	S	0	0
			740	460	143	135	2		

- Molecule 59 is a protein called 39S ribosomal protein L55, mitochondrial.

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

- Molecule 60 is a protein called Ribosomal protein 63, mitochondrial.

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

- Molecule 61 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

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

- Molecule 62 is a protein called 39S ribosomal protein S18a, mitochondrial.

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

- Molecule 63 is a protein called 39S ribosomal protein L11, mitochondrial.

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

- Molecule 64 is a protein called 39S ribosomal protein L10, mitochondrial.

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

- Molecule 65 is a protein called 39S ribosomal protein L16, mitochondrial.

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

- Molecule 66 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

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

- Molecule 67 is a protein called 39S ribosomal protein L23, mitochondrial.

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

- Molecule 68 is a protein called 39S ribosomal protein L24, mitochondrial.

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

- Molecule 69 is a protein called 39S ribosomal protein L3, mitochondrial.

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

- Molecule 70 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	5	393	Total	C	N	O	S	0	0
			3205	2070	559	565	11		

- Molecule 71 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	6	354	Total	C	N	O	S	0	0
			2948	1881	525	533	9		

- Molecule 72 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	7	297	Total	C	N	O	S	0	0
			2410	1540	409	443	18		

- Molecule 73 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	9	124	Total	C	N	O	S	0	0
			997	644	170	181	2		

- Molecule 74 is a protein called 39S ribosomal protein L42, mitochondrial.

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

- Molecule 75 is a protein called 39S ribosomal protein L44, mitochondrial.

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

- Molecule 76 is a protein called 39S ribosomal protein L45, mitochondrial.

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

- Molecule 77 is a protein called 39S ribosomal protein L48, mitochondrial.

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

- Molecule 78 is a protein called 39S ribosomal protein L50, mitochondrial.

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

- Molecule 79 is a protein called 39S ribosomal protein L53, mitochondrial.

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

- Molecule 80 is a protein called 39S ribosomal protein L54, mitochondrial.

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

- Molecule 81 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

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

- Molecule 82 is a protein called 39S ribosomal protein S30, mitochondrial.

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

- Molecule 83 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Q	227	Total	C	N	O	S	0	0
			1894	1211	338	336	9		

- Molecule 84 is a protein called P-site finger.

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

- Molecule 85 is a protein called 39S ribosomal protein L12, mitochondrial.

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

- Molecule 86 is a protein called Ribosome-recycling factor, mitochondrial.

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

- Molecule 87 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	AA	27	Total	Mg	0
			27	27	
87	AG	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
87	A	94	Total 94	Mg 94	0
87	D	1	Total 1	Mg 1	0
87	M	1	Total 1	Mg 1	0
87	W	1	Total 1	Mg 1	0
87	g	1	Total 1	Mg 1	0
87	E	1	Total 1	Mg 1	0

- Molecule 88 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
88	AB	1	Total 1	Zn 1	0
88	AO	1	Total 1	Zn 1	0
88	AP	1	Total 1	Zn 1	0
88	AT	1	Total 1	Zn 1	0
88	0	1	Total 1	Zn 1	0
88	4	1	Total 1	Zn 1	0
88	r	1	Total 1	Zn 1	0

- Molecule 89 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

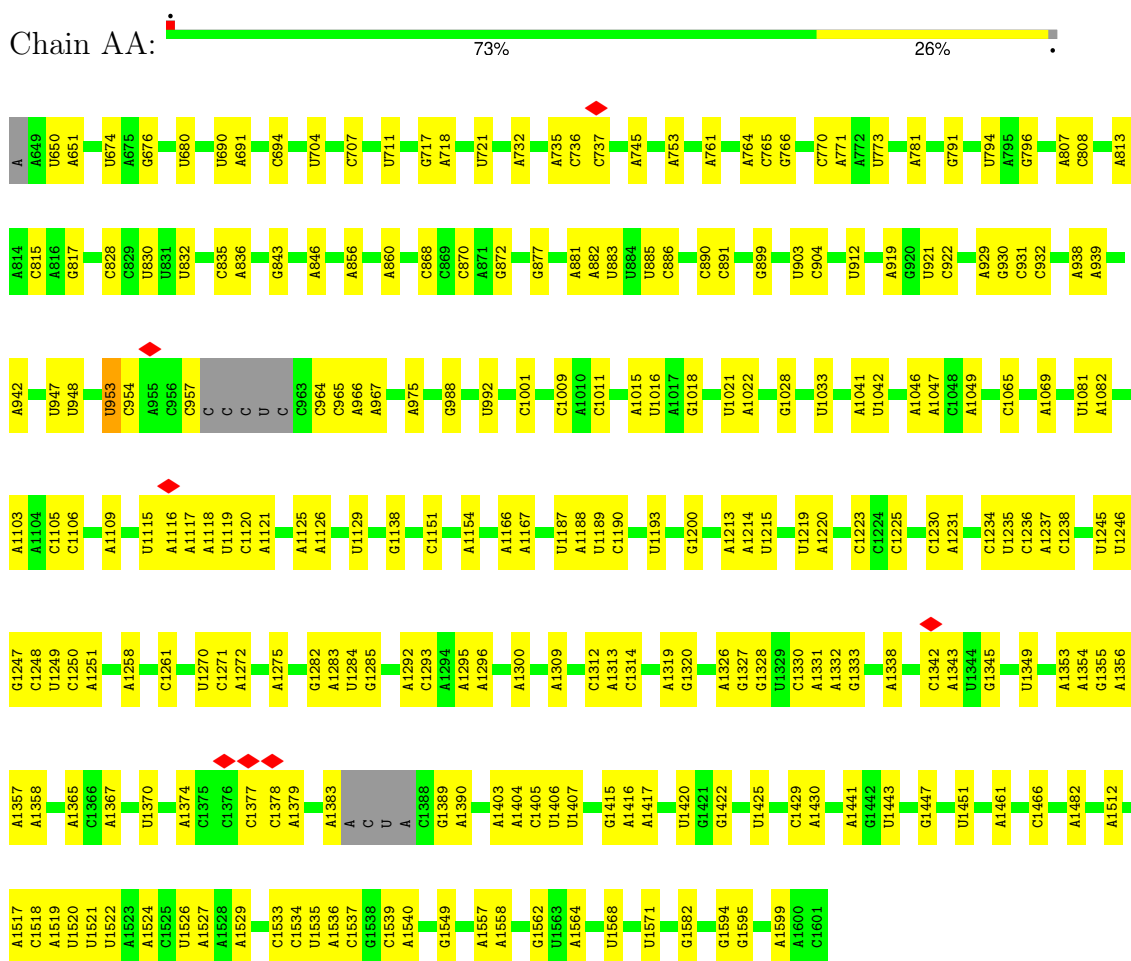


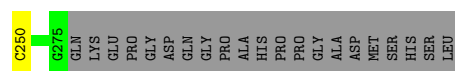
Mol	Chain	Residues	Atoms					AltConf
89	AX	1	Total	C	N	O	P	0
			28	10	5	11	2	

3 Residue-property plots

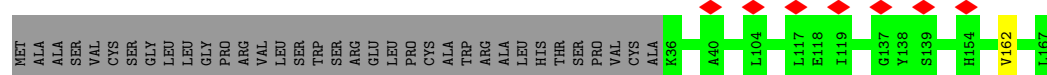
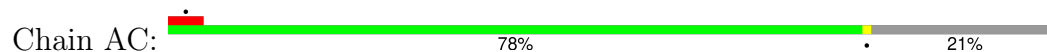
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 12S rRNA

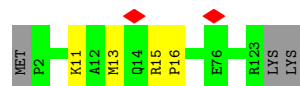




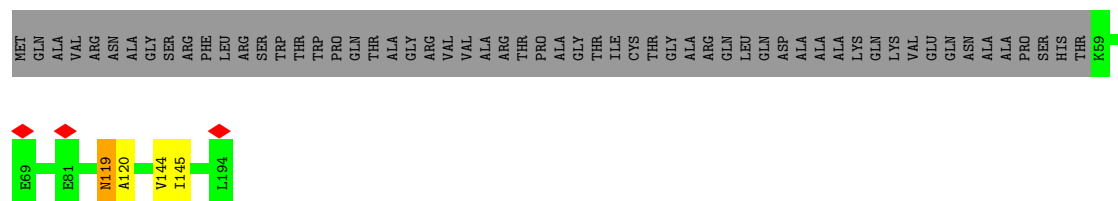
- Molecule 3: 28S ribosomal protein S24, mitochondrial



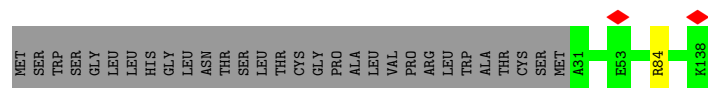
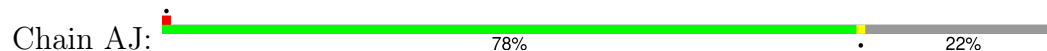
- Molecule 4: 28S ribosomal protein S6, mitochondrial



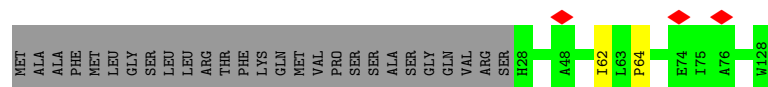
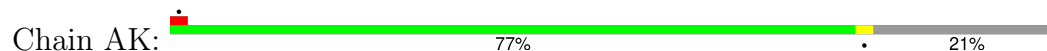
- Molecule 5: 28S ribosomal protein S11, mitochondrial



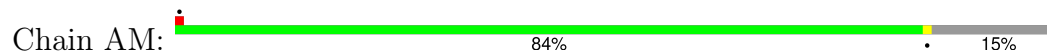
- Molecule 6: 28S ribosomal protein S12, mitochondrial

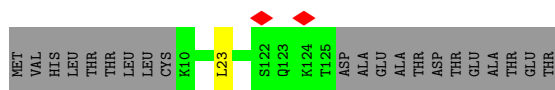


- Molecule 7: 28S ribosomal protein S14, mitochondrial



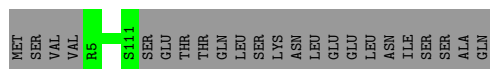
- Molecule 8: 28S ribosomal protein S16, mitochondrial





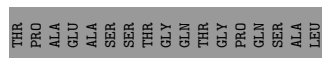
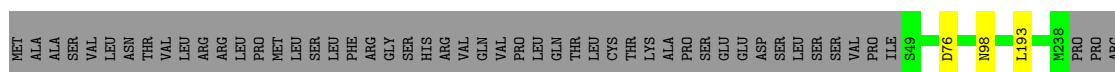
- Molecule 9: 28S ribosomal protein S17, mitochondrial

Chain AN: 82% 18%



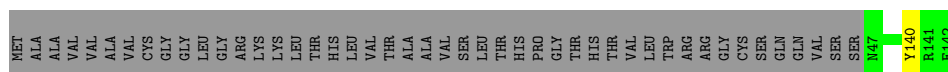
- Molecule 10: 28S ribosomal protein S18b, mitochondrial

Chain AO: 72% 26%



- Molecule 11: 28S ribosomal protein S18c, mitochondrial

Chain AP: 67% 32%



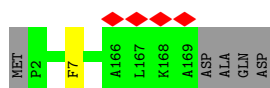
- Molecule 12: 28S ribosomal protein S21, mitochondrial

Chain AQ: 99%



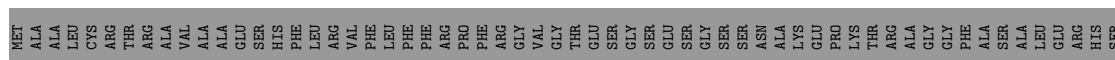
- Molecule 13: 28S ribosomal protein S25, mitochondrial

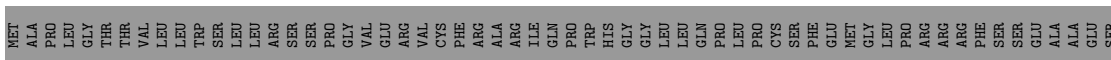
Chain AT: 97%

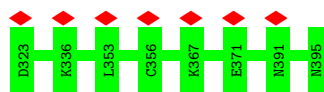


- Molecule 14: 28S ribosomal protein S28, mitochondrial

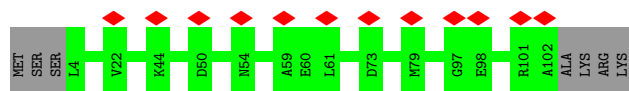
Chain AW: 51% 48%



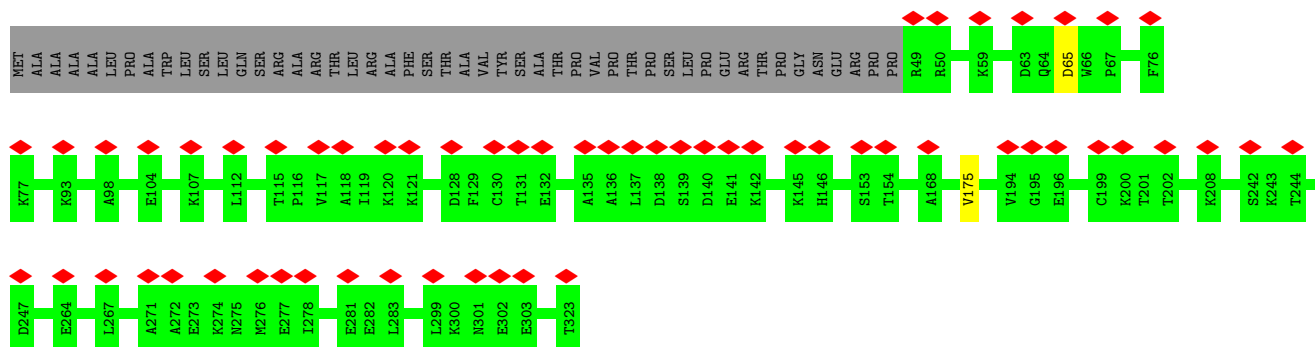
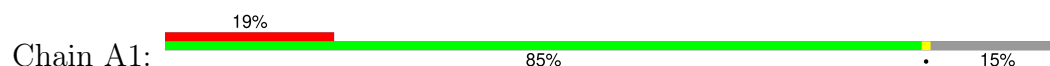




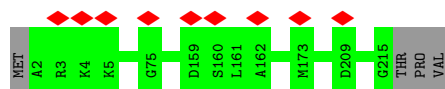
- Molecule 24: 28S ribosomal protein S33, mitochondrial



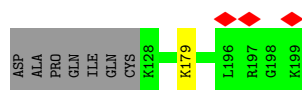
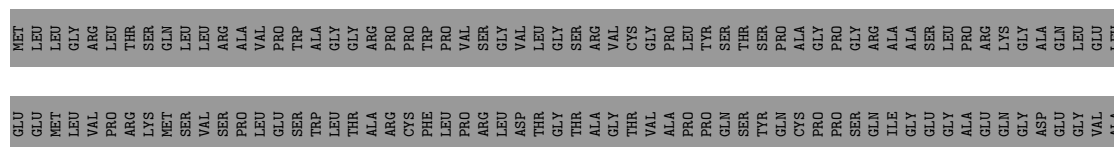
- Molecule 25: 28S ribosomal protein S35, mitochondrial



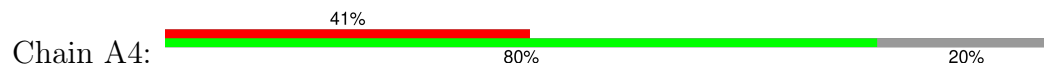
- Molecule 26: 28S ribosomal protein S34, mitochondrial

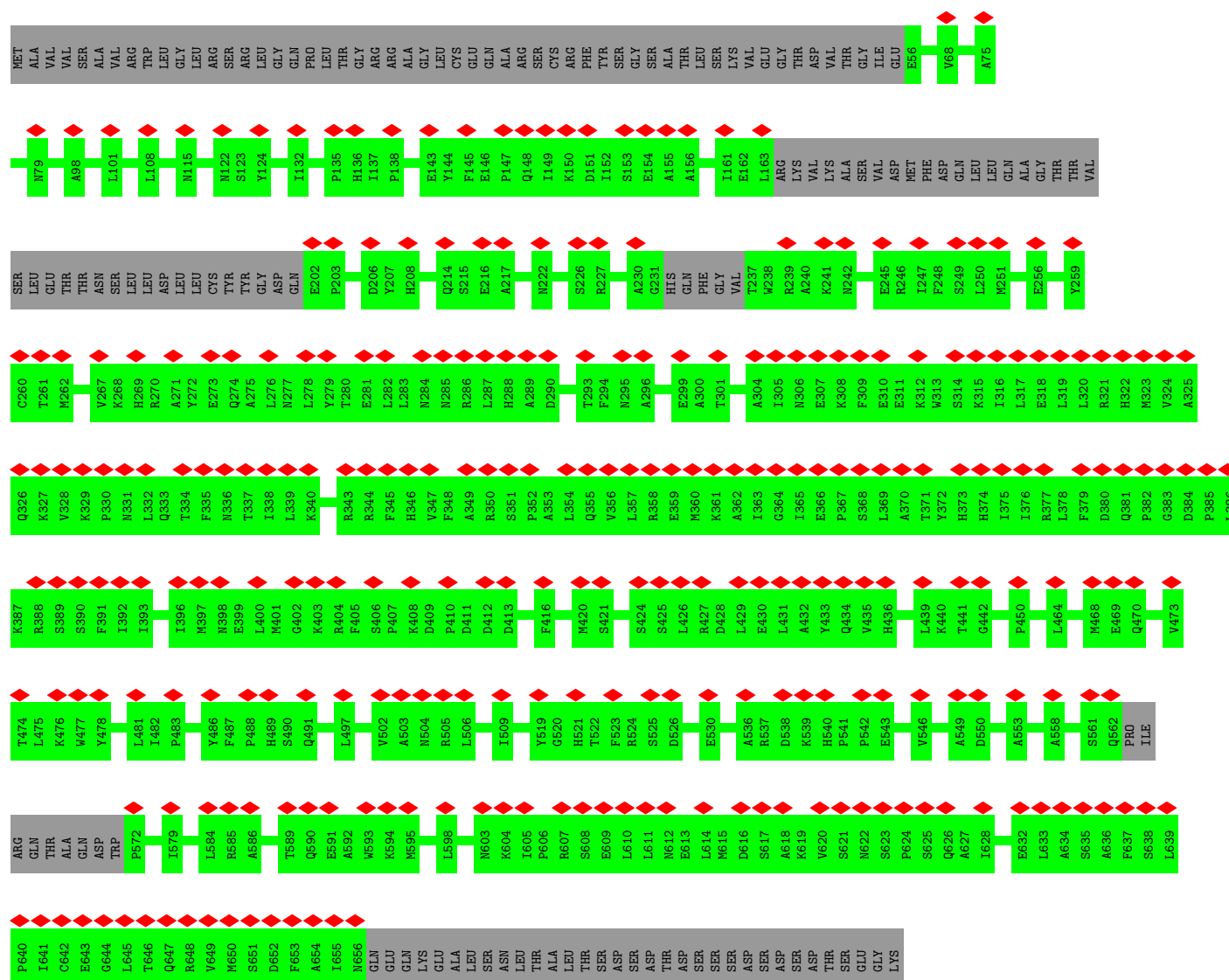


- Molecule 27: Aurora kinase A-interacting protein

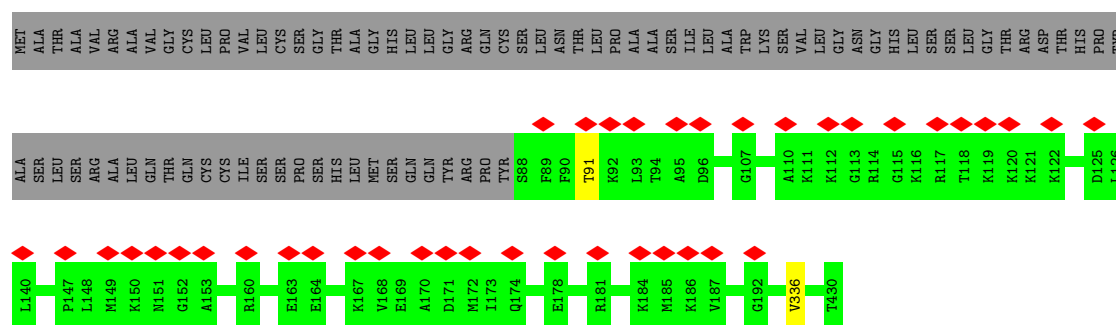
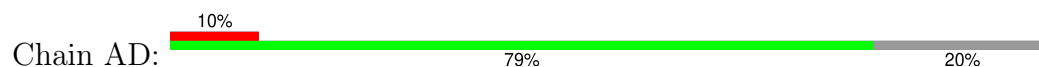


- Molecule 28: Pentatricopeptide repeat domain-containing protein 3, mitochondrial

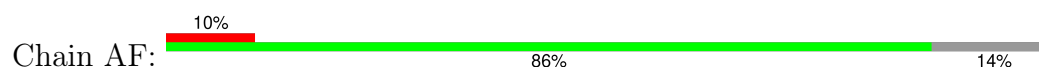


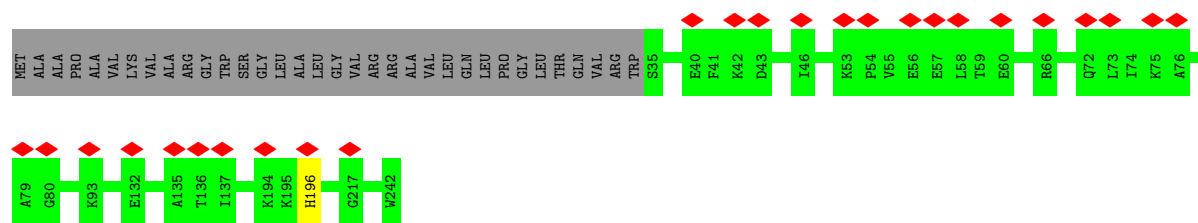


• Molecule 29: 28S ribosomal protein S5, mitochondrial

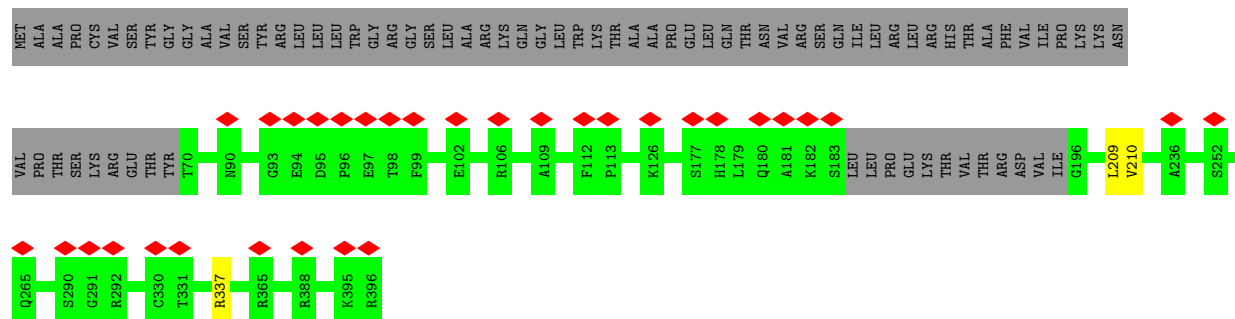
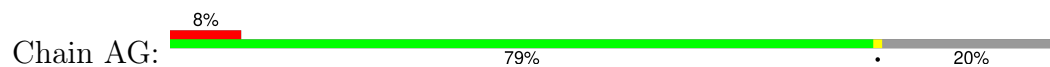


• Molecule 30: 28S ribosomal protein S7, mitochondrial

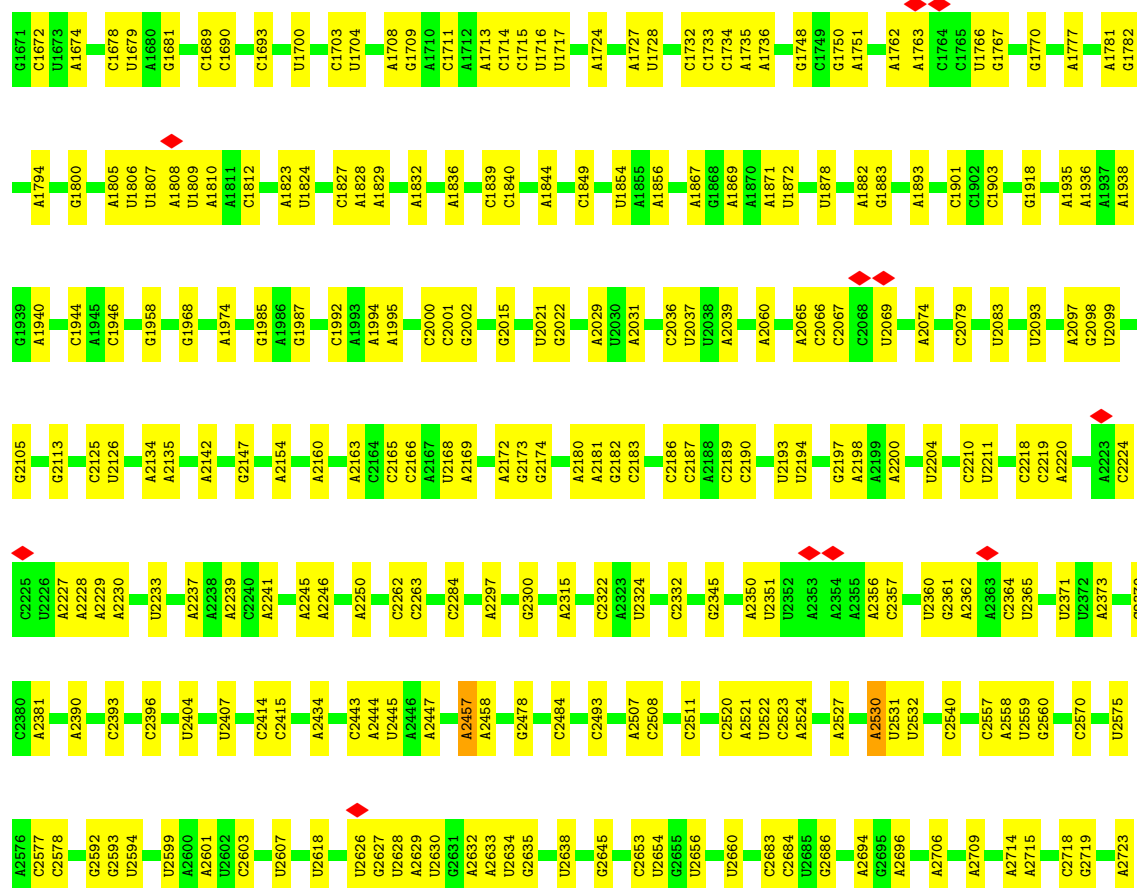
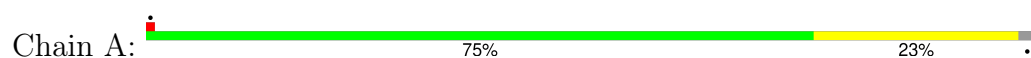


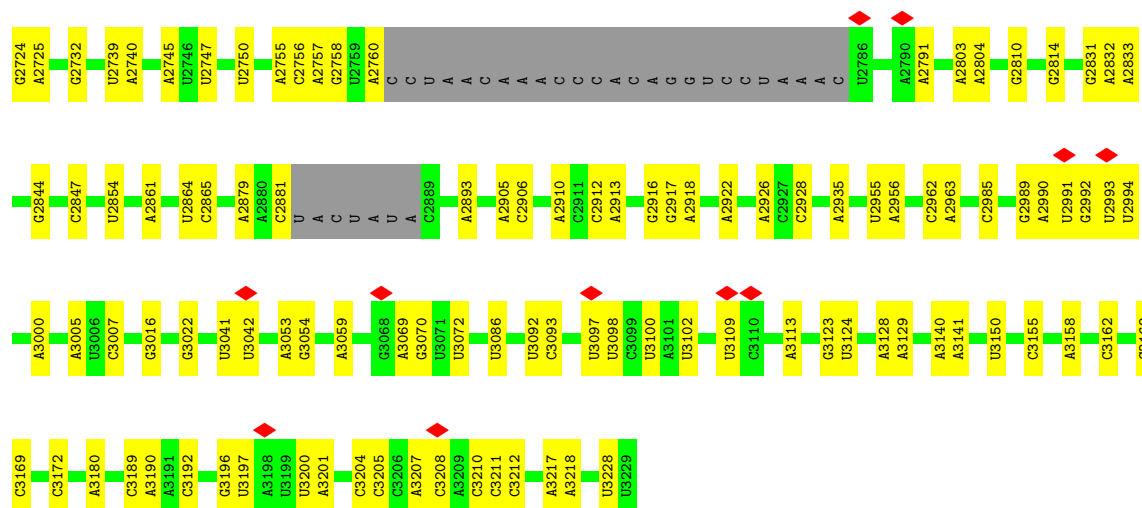


- Molecule 31: 28S ribosomal protein S9, mitochondrial

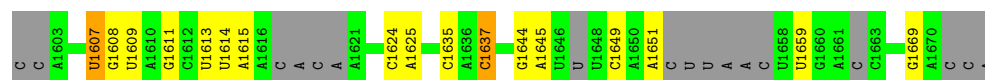


- Molecule 32: 16S RRNA

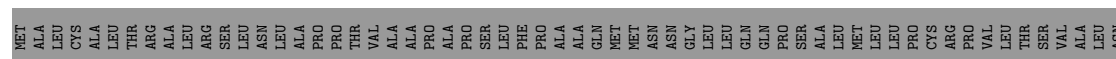
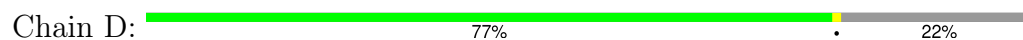




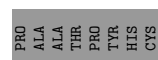
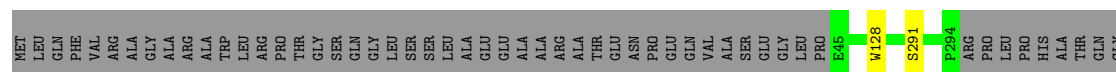
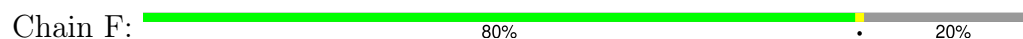
• Molecule 33: tRNAVAL



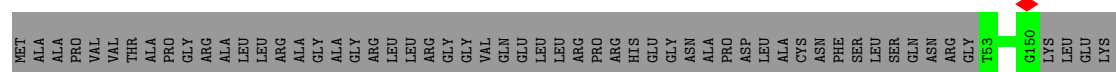
• Molecule 34: 39S ribosomal protein L2, mitochondrial



• Molecule 35: 39S ribosomal protein L4, mitochondrial



• Molecule 36: 39S ribosomal protein L9, mitochondrial



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


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

- Molecule 37: 39S ribosomal protein L13, mitochondrial

Chain K:  98%

MET
S2
S3
F4
S5
Q160
L178

- Molecule 38: 39S ribosomal protein L14, mitochondrial

Chain L:  79% 21%


MET
ALA
PHE
PHE
GLY
THR
GLY
LEU
TRP
GLY
PHE
PRO
THR
CYS
VAL
SER
ARG
VAL
LEU
SER
HIS
CYS
PHE
SER
THR
GLY
SER
LEU
SER
A31
V38
V145

- Molecule 39: 39S ribosomal protein L15, mitochondrial

Chain M:  94%

MET
ALA
GLY
PRO
LEU
GLN
GLY
GLY
A10
P20
V110
R134
D180
Q284
I285
T286
D287
E288
S295

- Molecule 40: 39S ribosomal protein L17, mitochondrial

Chain O:  86% 13%

MET
ARG
LEU
SER
VAL
ALA
ALA
TRP
I9
I110
D160
GLU
ALA
SER
ASN
HIS
SER
HIS
ALA
GLN
THR
PRO
GLY
ILE

- Molecule 41: 39S ribosomal protein L20, mitochondrial

Chain R:  93% 6%


MET
VAL
PHE
LEU
THR
ALA
GLN
LEU
TRP
L10
E137
H149

- Molecule 42: 39S ribosomal protein L21, mitochondrial

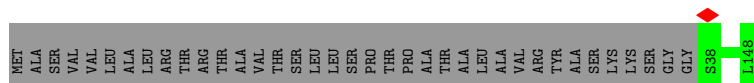
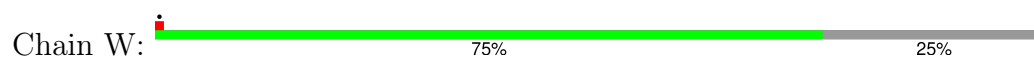
Chain S:  76% 24%

MET
ALA
ALA
SER
SER
LEU
THR
VAL
THR
VAL
LEU
GLY
ARG
LEU
ALA
SER
CYS
SER
HIS
ILE
LEU
ARG
PRO
SER
GLY
PRO
GLY
ALA
ALA
SER
LEU
TRP
SER
ALA
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SER
THR
SER
TYR
LEU
PRO
G49
L204
LEU

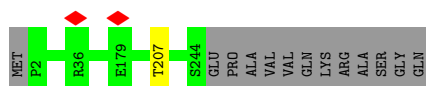
- Molecule 43: 39S ribosomal protein L22, mitochondrial

Chain T:  78% 22%

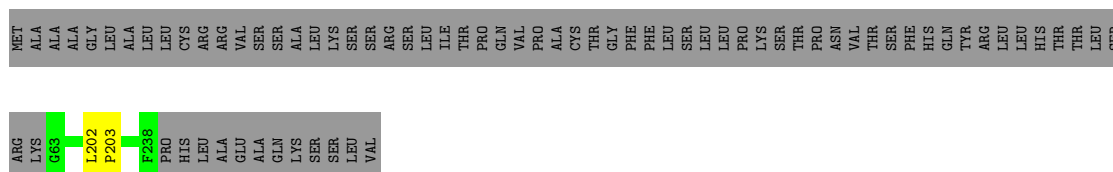
- Molecule 44: 39S ribosomal protein L27, mitochondrial



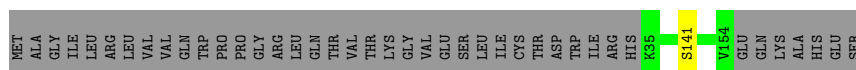
- Molecule 45: 39S ribosomal protein L28, mitochondrial



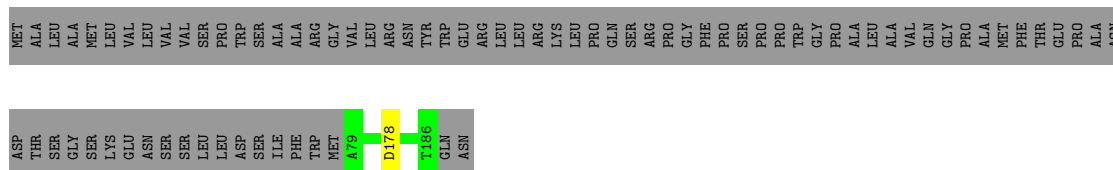
- Molecule 46: 39S ribosomal protein L47, mitochondrial



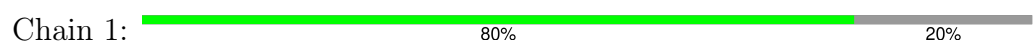
- Molecule 47: 39S ribosomal protein L30, mitochondrial



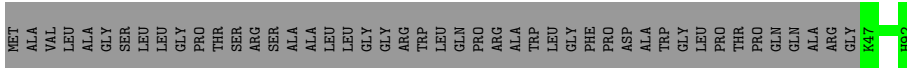
- Molecule 48: 39S ribosomal protein L32, mitochondrial



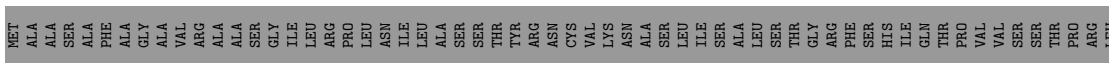
- Molecule 49: 39S ribosomal protein L33, mitochondrial



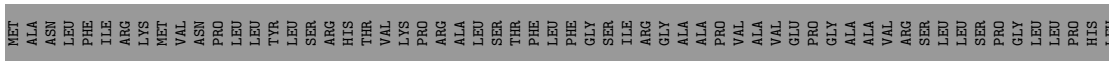
- Molecule 50: 39S ribosomal protein L34, mitochondrial



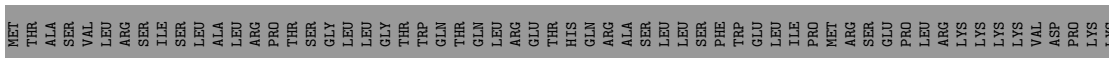
- Molecule 51: 39S ribosomal protein L35, mitochondrial



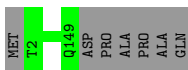
- Molecule 52: 39S ribosomal protein L36, mitochondrial



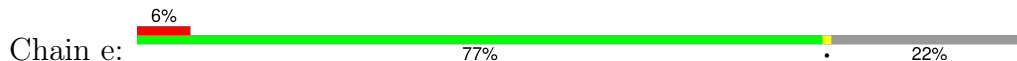
- Molecule 53: 39S ribosomal protein L40, mitochondrial

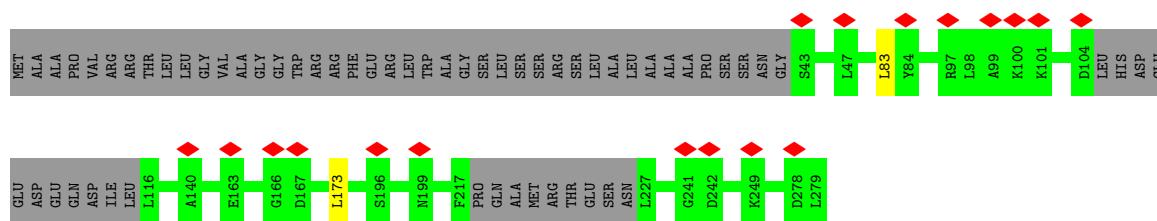


- Molecule 54: 39S ribosomal protein L43, mitochondrial



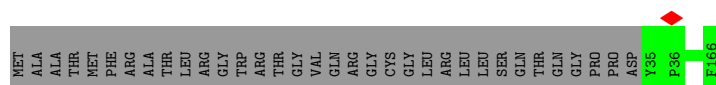
- Molecule 55: 39S ribosomal protein L46, mitochondrial





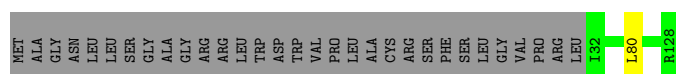
- Molecule 56: 39S ribosomal protein L49, mitochondrial

Chain g: 80% 20%



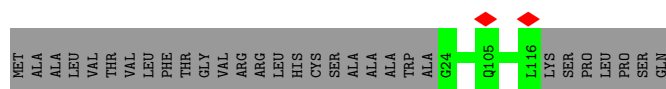
- Molecule 57: 39S ribosomal protein L51, mitochondrial

Chain i: 75% 24%



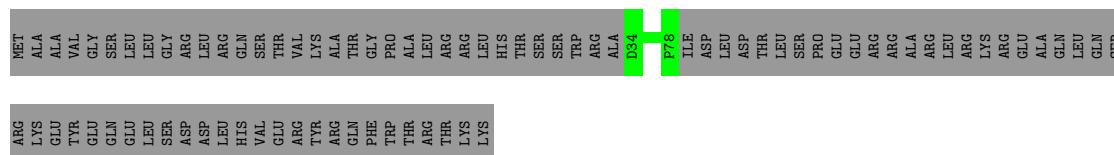
- Molecule 58: cDNA FLJ76418, highly similar to Homo sapiens mitochondrial ribosomal protein L52 (MRPL52), transcript variant 1, mRNA

Chain j: 76% 24%



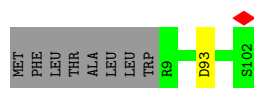
- Molecule 59: 39S ribosomal protein L55, mitochondrial

Chain m: 35% 65%

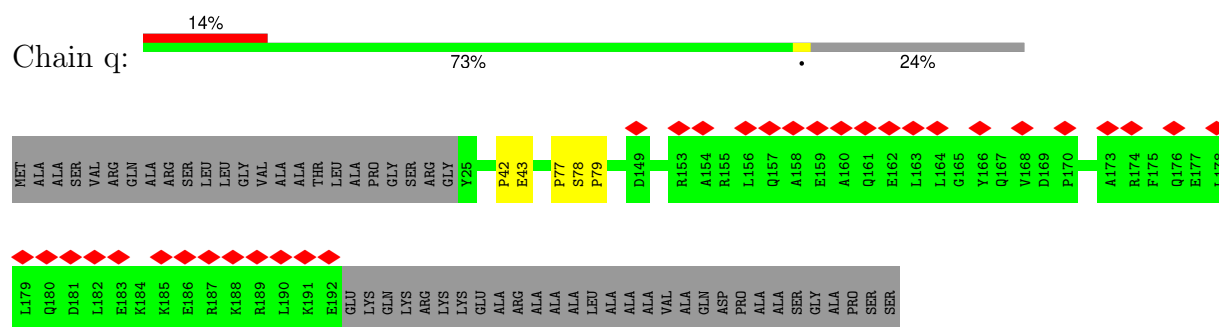


- Molecule 60: Ribosomal protein 63, mitochondrial

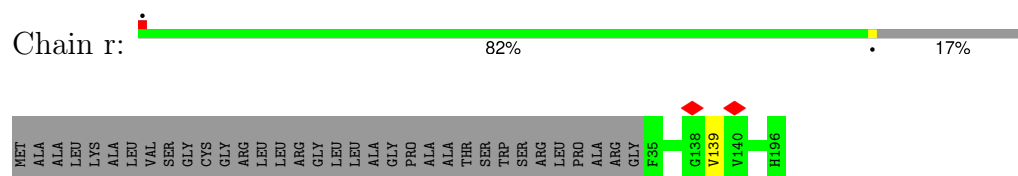
Chain o: 91% 8%



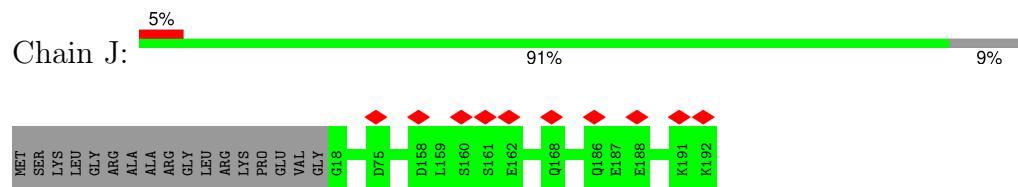
- Molecule 61: Growth arrest and DNA damage-inducible proteins-interacting protein 1



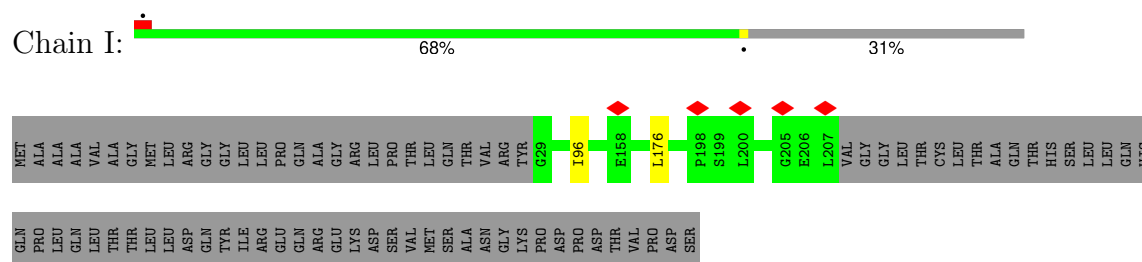
- Molecule 62: 39S ribosomal protein S18a, mitochondrial



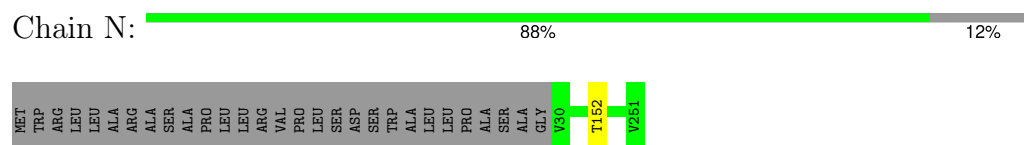
- Molecule 63: 39S ribosomal protein L11, mitochondrial



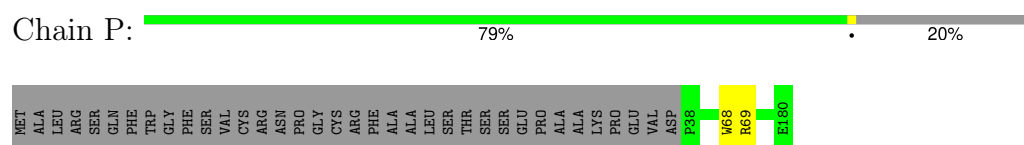
- Molecule 64: 39S ribosomal protein L10, mitochondrial



- Molecule 65: 39S ribosomal protein L16, mitochondrial

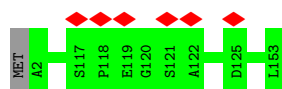


- Molecule 66: Mitochondrial ribosomal protein L18, isoform CRA_b



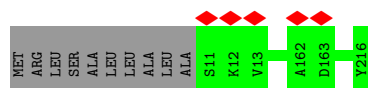
- Molecule 67: 39S ribosomal protein L23, mitochondrial

Chain U:  99%




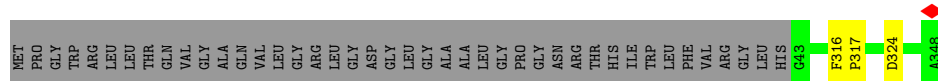
- Molecule 68: 39S ribosomal protein L24, mitochondrial

Chain V:  95%



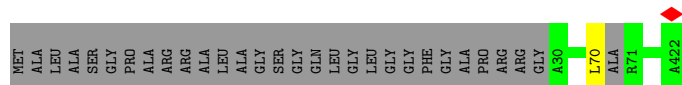
- Molecule 69: 39S ribosomal protein L3, mitochondrial

Chain E:  87%



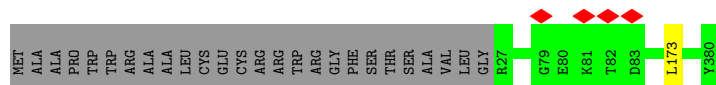
- Molecule 70: 39S ribosomal protein L37, mitochondrial

Chain 5:  93%




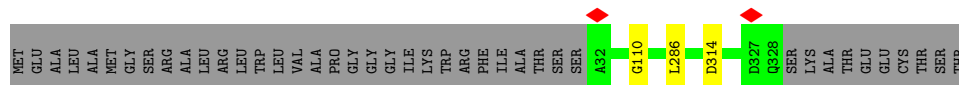
- Molecule 71: 39S ribosomal protein L38, mitochondrial

Chain 6:  93%



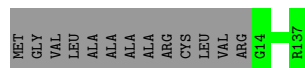
- Molecule 72: 39S ribosomal protein L39, mitochondrial

Chain 7:  87%

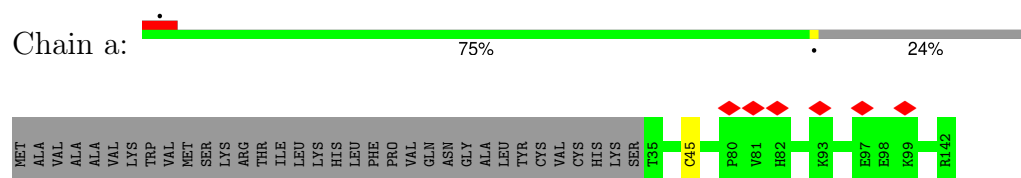


- Molecule 73: 39S ribosomal protein L41, mitochondrial

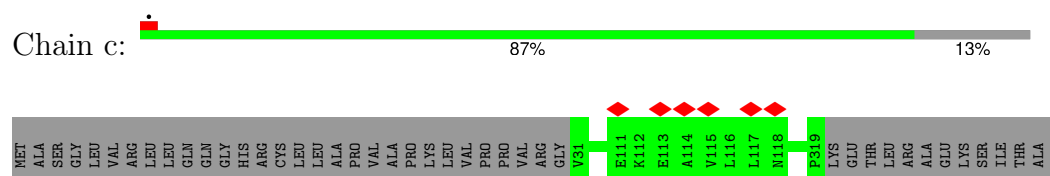
Chain 9:  91%



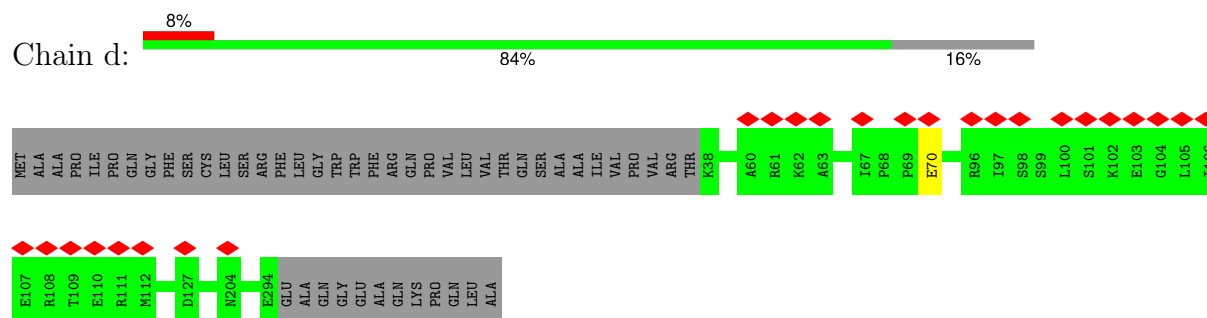
- Molecule 74: 39S ribosomal protein L42, mitochondrial



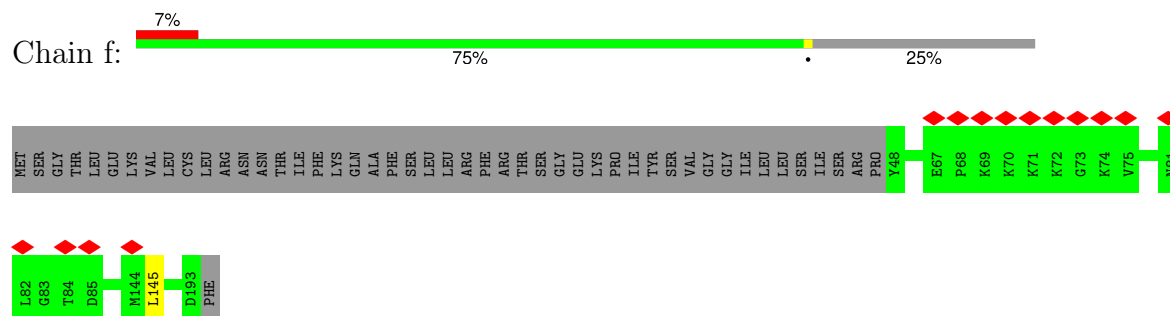
- Molecule 75: 39S ribosomal protein L44, mitochondrial



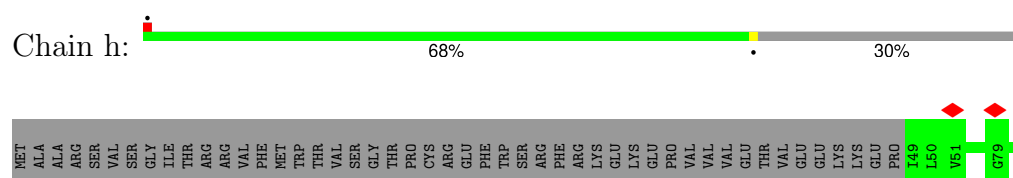
- Molecule 76: 39S ribosomal protein L45, mitochondrial



- Molecule 77: 39S ribosomal protein L48, mitochondrial

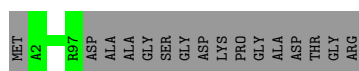


- Molecule 78: 39S ribosomal protein L50, mitochondrial

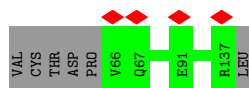


- Molecule 79: 39S ribosomal protein L53, mitochondrial

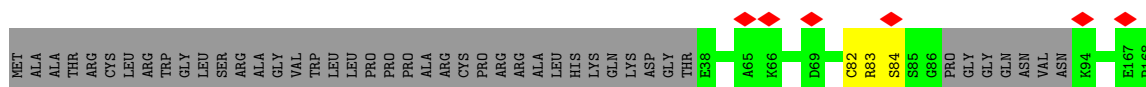
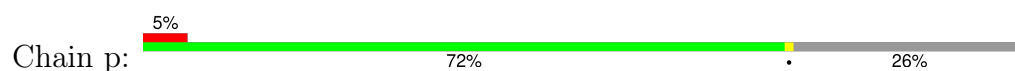




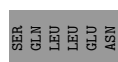
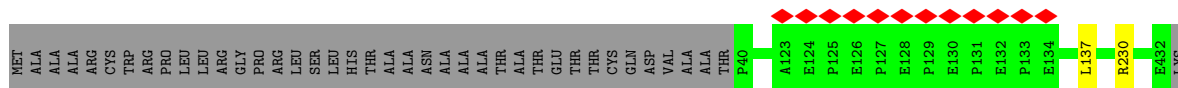
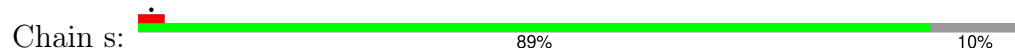
- Molecule 80: 39S ribosomal protein L54, mitochondrial



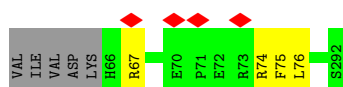
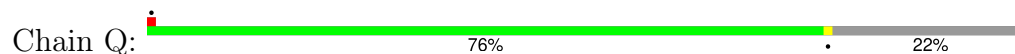
- Molecule 81: Peptidyl-tRNA hydrolase ICT1, mitochondrial



- Molecule 82: 39S ribosomal protein S30, mitochondrial

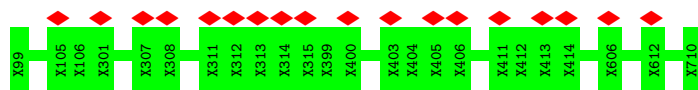


- Molecule 83: 39S ribosomal protein L19, mitochondrial



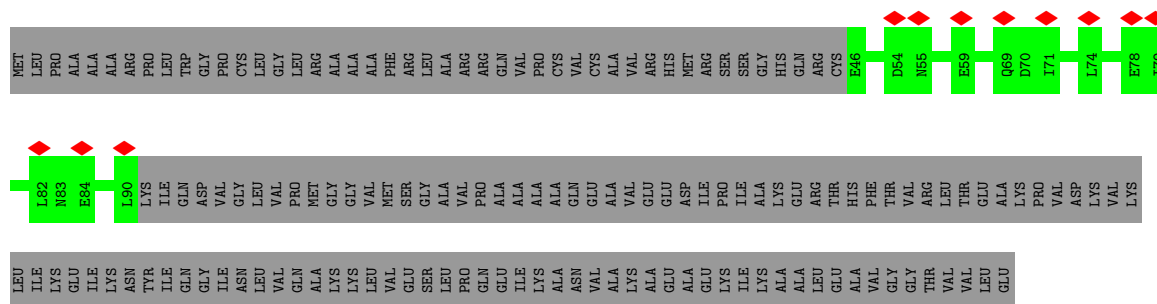
- Molecule 84: P-site finger





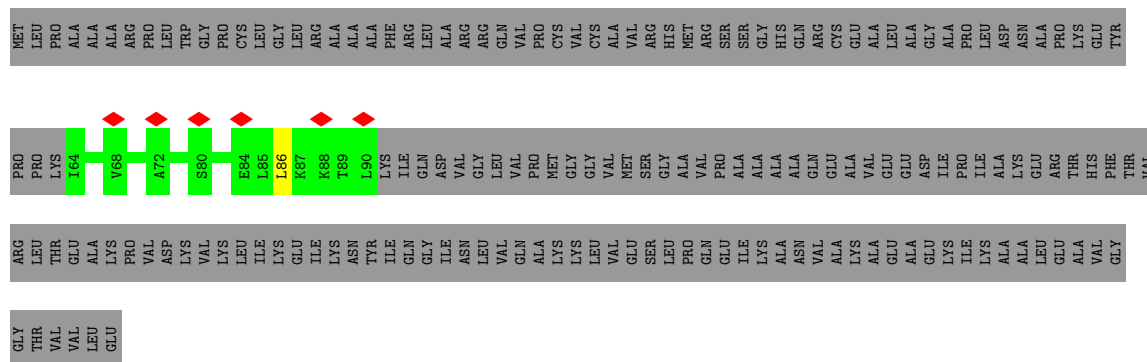
- Molecule 85: 39S ribosomal protein L12, mitochondrial

Chain TA: 6% 23% 77%



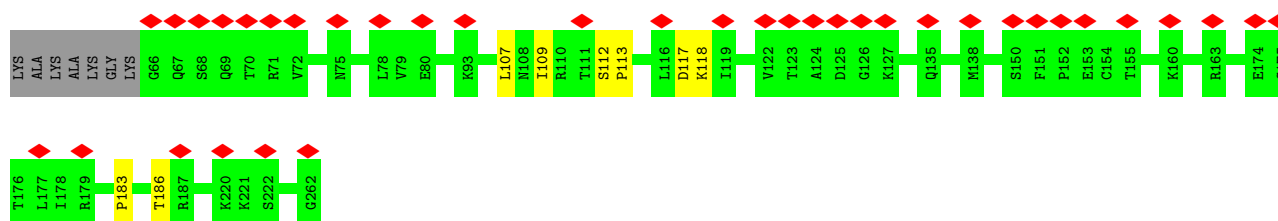
- Molecule 85: 39S ribosomal protein L12, mitochondrial

Chain TB: 13% 86%



- Molecule 86: Ribosome-recycling factor, mitochondrial

Chain z: 18% 93%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	93212	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 ($e^-/\text{\AA}^2$)	69.2	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	2.359	Depositor
Minimum map value	-1.343	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.110	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	429.30002, 429.30002, 429.30002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07325, 1.07325, 1.07325	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, GDP, 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	AA	0.17	0/22406	0.76	1/34881 (0.0%)
2	AB	0.44	0/1830	0.59	0/2477
3	AC	0.38	0/1112	0.58	0/1505
4	AE	0.41	0/989	0.69	0/1335
5	AI	0.40	0/1031	0.62	0/1390
6	AJ	0.53	0/854	0.72	0/1148
7	AK	0.38	0/879	0.63	1/1182 (0.1%)
8	AM	0.42	0/941	0.63	0/1265
9	AN	0.47	0/864	0.63	0/1169
10	AO	0.43	0/1624	0.59	0/2209
11	AP	0.46	0/791	0.62	0/1062
12	AQ	0.46	0/752	0.55	0/1001
13	AT	0.49	0/1402	0.59	0/1883
14	AW	0.42	0/778	0.66	0/1048
15	AX	0.37	0/2932	0.64	0/3968
16	A2	0.41	0/939	0.66	0/1256
17	AH	0.38	0/1037	0.64	3/1403 (0.2%)
18	AL	0.42	0/1475	0.59	1/1970 (0.1%)
19	AR	0.39	0/2435	0.58	1/3288 (0.0%)
20	AS	0.45	0/1138	0.62	0/1533
21	AU	0.39	0/1521	0.54	0/2039
22	AV	0.38	0/3071	0.67	1/4147 (0.0%)
23	AY	0.38	0/1046	0.57	0/1410
24	AZ	0.39	0/851	0.65	0/1133
25	A1	0.36	0/2277	0.59	0/3079
26	A0	0.40	0/1827	0.59	0/2473
27	A3	0.52	0/650	0.65	0/855
28	A4	0.27	0/3028	0.47	0/4197
29	AD	0.45	0/2783	0.61	0/3724
30	AF	0.39	0/1765	0.60	0/2369
31	AG	0.39	0/2642	0.59	0/3538
32	A	0.17	0/36245	0.75	3/56418 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	B	0.36	0/1328	1.10	8/2056 (0.4%)
34	D	0.30	0/1904	0.53	0/2561
35	F	0.34	0/2071	0.57	1/2817 (0.0%)
36	H	0.29	0/820	0.59	0/1102
37	K	0.31	0/1495	0.52	0/2029
38	L	0.31	0/904	0.54	0/1218
39	M	0.32	0/2359	0.58	1/3185 (0.0%)
40	O	0.31	0/1269	0.54	0/1708
41	R	0.33	0/1174	0.54	0/1572
42	S	0.31	0/1276	0.59	0/1729
43	T	0.32	0/1402	0.52	0/1886
44	W	0.34	0/893	0.56	0/1204
45	X	0.30	0/2081	0.53	0/2812
46	Y	0.30	0/1552	0.50	0/2079
47	Z	0.30	0/1003	0.53	0/1354
48	0	0.29	0/895	0.56	0/1201
49	1	0.28	0/438	0.52	0/583
50	2	0.30	0/382	0.51	0/507
51	3	0.33	0/852	0.51	0/1136
52	4	0.33	0/350	0.51	0/461
53	8	0.31	0/855	0.59	1/1152 (0.1%)
54	b	0.31	0/1202	0.51	0/1626
55	e	0.31	0/1797	0.65	2/2422 (0.1%)
56	g	0.31	0/1132	0.55	0/1543
57	i	0.34	0/849	0.60	1/1135 (0.1%)
58	j	0.33	0/755	0.48	0/1016
59	m	0.26	0/379	0.56	0/510
60	o	0.31	0/818	0.56	1/1097 (0.1%)
61	q	0.29	0/1323	0.52	0/1794
62	r	0.32	0/1362	0.55	0/1846
63	J	0.30	0/1348	0.58	0/1813
64	I	0.29	0/1467	0.63	1/1984 (0.1%)
65	N	0.31	0/1833	0.50	0/2468
66	P	0.30	0/1191	0.56	0/1611
67	U	0.32	0/1252	0.49	0/1697
68	V	0.30	0/1727	0.52	0/2341
69	E	0.31	0/2479	0.53	0/3360
70	5	0.30	0/3300	0.54	1/4495 (0.0%)
71	6	0.30	0/3043	0.51	0/4140
72	7	0.30	0/2467	0.54	2/3337 (0.1%)
73	9	0.32	0/1025	0.51	0/1379
74	a	0.32	0/923	0.51	0/1254
75	c	0.30	0/2371	0.50	0/3205

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	d	0.30	0/2132	0.55	0/2887
77	f	0.33	0/1144	0.64	1/1551 (0.1%)
78	h	0.29	0/917	0.57	0/1249
79	k	0.27	0/754	0.59	0/1017
80	l	0.30	0/636	0.52	0/860
81	p	0.28	0/1246	0.54	0/1675
82	s	0.32	0/3262	0.53	1/4435 (0.0%)
83	Q	0.31	0/1938	0.54	0/2610
85	TA	0.27	0/349	0.53	0/475
85	TB	0.28	0/212	0.57	0/286
86	z	0.23	0/1534	0.38	0/2063
All	All	0.30	0/177385	0.65	32/251888 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AB	0	1
4	AE	0	2
5	AI	0	2
7	AK	0	1
10	AO	0	1
11	AP	0	1
14	AW	0	1
15	AX	0	1
31	AG	0	1
34	D	0	1
37	K	0	2
39	M	0	4
40	O	0	1
41	R	0	1
43	T	0	1
46	Y	0	1
47	Z	0	1
61	q	0	2
66	P	0	1
69	E	0	1
76	d	0	1
78	h	0	2
81	p	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
83	Q	0	1
All	All	0	33

There are no bond length outliers.

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	AL	71	LEU	CA-CB-CG	8.11	133.95	115.30
22	AV	364	LEU	CA-CB-CG	6.78	130.89	115.30
72	7	314	ASP	CB-CG-OD1	6.70	124.33	118.30
33	B	1635	C	N1-C2-O2	6.43	122.76	118.90
77	f	145	LEU	CA-CB-CG	6.02	129.15	115.30

There are no chirality outliers.

5 of 33 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	172	ARG	Peptide
4	AE	11	LYS	Peptide
4	AE	13	MET	Peptide
5	AI	119	ASN	Peptide
5	AI	144	VAL	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	218/296 (74%)	204 (94%)	14 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AC	130/167 (78%)	124 (95%)	6 (5%)	0	100	100
4	AE	120/125 (96%)	110 (92%)	8 (7%)	2 (2%)	7	36
5	AI	134/194 (69%)	118 (88%)	13 (10%)	3 (2%)	5	31
6	AJ	106/138 (77%)	87 (82%)	19 (18%)	0	100	100
7	AK	99/128 (77%)	93 (94%)	6 (6%)	0	100	100
8	AM	114/137 (83%)	103 (90%)	11 (10%)	0	100	100
9	AN	105/130 (81%)	90 (86%)	15 (14%)	0	100	100
10	AO	188/258 (73%)	176 (94%)	12 (6%)	0	100	100
11	AP	94/142 (66%)	88 (94%)	6 (6%)	0	100	100
12	AQ	84/87 (97%)	77 (92%)	7 (8%)	0	100	100
13	AT	166/173 (96%)	160 (96%)	6 (4%)	0	100	100
14	AW	95/187 (51%)	82 (86%)	13 (14%)	0	100	100
15	AX	351/398 (88%)	329 (94%)	22 (6%)	0	100	100
16	A2	114/118 (97%)	105 (92%)	9 (8%)	0	100	100
17	AH	120/201 (60%)	109 (91%)	11 (9%)	0	100	100
18	AL	172/257 (67%)	164 (95%)	8 (5%)	0	100	100
19	AR	290/360 (81%)	276 (95%)	14 (5%)	0	100	100
20	AS	133/190 (70%)	127 (96%)	6 (4%)	0	100	100
21	AU	175/205 (85%)	170 (97%)	5 (3%)	0	100	100
22	AV	363/414 (88%)	321 (88%)	42 (12%)	0	100	100
23	AY	118/395 (30%)	111 (94%)	7 (6%)	0	100	100
24	AZ	97/106 (92%)	87 (90%)	10 (10%)	0	100	100
25	A1	273/323 (84%)	257 (94%)	16 (6%)	0	100	100
26	A0	212/218 (97%)	199 (94%)	13 (6%)	0	100	100
27	A3	70/199 (35%)	68 (97%)	2 (3%)	0	100	100
28	A4	541/689 (78%)	502 (93%)	39 (7%)	0	100	100
29	AD	341/430 (79%)	316 (93%)	25 (7%)	0	100	100
30	AF	206/242 (85%)	193 (94%)	13 (6%)	0	100	100
31	AG	311/396 (78%)	294 (94%)	16 (5%)	1 (0%)	37	68
34	D	237/305 (78%)	224 (94%)	12 (5%)	1 (0%)	30	64
35	F	248/311 (80%)	227 (92%)	20 (8%)	1 (0%)	30	64

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	H	96/267 (36%)	88 (92%)	8 (8%)	0	100	100
37	K	175/178 (98%)	157 (90%)	17 (10%)	1 (1%)	22	56
38	L	113/145 (78%)	103 (91%)	10 (9%)	0	100	100
39	M	285/296 (96%)	251 (88%)	32 (11%)	2 (1%)	19	53
40	O	150/175 (86%)	135 (90%)	15 (10%)	0	100	100
41	R	138/149 (93%)	131 (95%)	7 (5%)	0	100	100
42	S	154/205 (75%)	146 (95%)	8 (5%)	0	100	100
43	T	164/212 (77%)	157 (96%)	7 (4%)	0	100	100
44	W	109/148 (74%)	104 (95%)	5 (5%)	0	100	100
45	X	241/256 (94%)	220 (91%)	21 (9%)	0	100	100
46	Y	174/250 (70%)	166 (95%)	7 (4%)	1 (1%)	22	56
47	Z	118/161 (73%)	110 (93%)	8 (7%)	0	100	100
48	0	106/188 (56%)	92 (87%)	14 (13%)	0	100	100
49	1	50/65 (77%)	46 (92%)	4 (8%)	0	100	100
50	2	44/92 (48%)	43 (98%)	1 (2%)	0	100	100
51	3	93/188 (50%)	90 (97%)	3 (3%)	0	100	100
52	4	36/103 (35%)	36 (100%)	0	0	100	100
53	8	97/206 (47%)	94 (97%)	3 (3%)	0	100	100
54	b	146/155 (94%)	135 (92%)	11 (8%)	0	100	100
55	e	211/279 (76%)	200 (95%)	11 (5%)	0	100	100
56	g	130/166 (78%)	125 (96%)	5 (4%)	0	100	100
57	i	95/128 (74%)	88 (93%)	7 (7%)	0	100	100
58	j	91/123 (74%)	85 (93%)	6 (7%)	0	100	100
59	m	43/128 (34%)	38 (88%)	5 (12%)	0	100	100
60	o	92/102 (90%)	86 (94%)	6 (6%)	0	100	100
61	q	164/222 (74%)	151 (92%)	10 (6%)	3 (2%)	7	35
62	r	160/196 (82%)	149 (93%)	11 (7%)	0	100	100
63	J	173/192 (90%)	165 (95%)	8 (5%)	0	100	100
64	I	177/261 (68%)	163 (92%)	14 (8%)	0	100	100
65	N	220/251 (88%)	216 (98%)	4 (2%)	0	100	100
66	P	141/179 (79%)	129 (92%)	11 (8%)	1 (1%)	19	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	U	150/153 (98%)	144 (96%)	6 (4%)	0	100	100
68	V	204/216 (94%)	195 (96%)	9 (4%)	0	100	100
69	E	304/348 (87%)	286 (94%)	17 (6%)	1 (0%)	37	68
70	5	391/423 (92%)	376 (96%)	15 (4%)	0	100	100
71	6	352/380 (93%)	329 (94%)	23 (6%)	0	100	100
72	7	295/338 (87%)	280 (95%)	14 (5%)	1 (0%)	37	68
73	9	122/137 (89%)	114 (93%)	8 (7%)	0	100	100
74	a	106/142 (75%)	104 (98%)	2 (2%)	0	100	100
75	c	287/332 (86%)	276 (96%)	11 (4%)	0	100	100
76	d	255/306 (83%)	234 (92%)	21 (8%)	0	100	100
77	f	144/194 (74%)	135 (94%)	9 (6%)	0	100	100
78	h	108/158 (68%)	101 (94%)	7 (6%)	0	100	100
79	k	94/112 (84%)	92 (98%)	2 (2%)	0	100	100
80	l	70/138 (51%)	63 (90%)	7 (10%)	0	100	100
81	p	148/206 (72%)	140 (95%)	7 (5%)	1 (1%)	19	53
82	s	391/439 (89%)	362 (93%)	29 (7%)	0	100	100
83	Q	225/292 (77%)	215 (96%)	8 (4%)	2 (1%)	14	49
85	TA	43/198 (22%)	35 (81%)	8 (19%)	0	100	100
85	TB	25/198 (13%)	24 (96%)	1 (4%)	0	100	100
86	z	195/204 (96%)	166 (85%)	23 (12%)	6 (3%)	3	26
All	All	14120/18499 (76%)	13161 (93%)	932 (7%)	27 (0%)	45	75

5 of 27 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	AI	120	ALA
66	P	69	ARG
83	Q	74	ARG
37	K	160	GLN
39	M	288	GLU

5.3.2 Protein sidechains ⓘ

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	193/249 (78%)	191 (99%)	2 (1%)	73	84
3	AC	115/143 (80%)	114 (99%)	1 (1%)	75	86
4	AE	104/107 (97%)	104 (100%)	0	100	100
5	AI	104/147 (71%)	104 (100%)	0	100	100
6	AJ	93/118 (79%)	92 (99%)	1 (1%)	70	83
7	AK	91/113 (80%)	91 (100%)	0	100	100
8	AM	95/113 (84%)	94 (99%)	1 (1%)	70	83
9	AN	93/115 (81%)	93 (100%)	0	100	100
10	AO	171/230 (74%)	169 (99%)	2 (1%)	67	82
11	AP	87/123 (71%)	87 (100%)	0	100	100
12	AQ	78/79 (99%)	78 (100%)	0	100	100
13	AT	153/157 (98%)	152 (99%)	1 (1%)	81	89
14	AW	84/158 (53%)	84 (100%)	0	100	100
15	AX	312/351 (89%)	310 (99%)	2 (1%)	84	91
16	A2	99/101 (98%)	99 (100%)	0	100	100
17	AH	112/180 (62%)	111 (99%)	1 (1%)	75	86
18	AL	157/226 (70%)	157 (100%)	0	100	100
19	AR	262/318 (82%)	260 (99%)	2 (1%)	79	88
20	AS	116/164 (71%)	116 (100%)	0	100	100
21	AU	153/174 (88%)	152 (99%)	1 (1%)	81	89
22	AV	328/364 (90%)	326 (99%)	2 (1%)	84	91
23	AY	111/357 (31%)	111 (100%)	0	100	100
24	AZ	89/95 (94%)	89 (100%)	0	100	100
25	A1	253/291 (87%)	251 (99%)	2 (1%)	79	88
26	A0	186/190 (98%)	186 (100%)	0	100	100
27	A3	66/166 (40%)	65 (98%)	1 (2%)	60	77
28	A4	83/609 (14%)	83 (100%)	0	100	100
29	AD	286/357 (80%)	284 (99%)	2 (1%)	81	89
30	AF	185/209 (88%)	184 (100%)	1 (0%)	86	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	AG	273/342 (80%)	272 (100%)	1 (0%)	89	95
34	D	193/245 (79%)	192 (100%)	1 (0%)	86	93
35	F	217/262 (83%)	217 (100%)	0	100	100
36	H	88/228 (39%)	88 (100%)	0	100	100
37	K	155/156 (99%)	155 (100%)	0	100	100
38	L	98/124 (79%)	97 (99%)	1 (1%)	73	84
39	M	245/249 (98%)	244 (100%)	1 (0%)	89	95
40	O	133/150 (89%)	133 (100%)	0	100	100
41	R	118/126 (94%)	118 (100%)	0	100	100
42	S	141/180 (78%)	141 (100%)	0	100	100
43	T	146/182 (80%)	146 (100%)	0	100	100
44	W	91/119 (76%)	91 (100%)	0	100	100
45	X	217/227 (96%)	216 (100%)	1 (0%)	86	93
46	Y	159/223 (71%)	159 (100%)	0	100	100
47	Z	111/147 (76%)	111 (100%)	0	100	100
48	0	97/164 (59%)	96 (99%)	1 (1%)	73	84
49	1	49/60 (82%)	49 (100%)	0	100	100
50	2	40/72 (56%)	40 (100%)	0	100	100
51	3	88/166 (53%)	88 (100%)	0	100	100
52	4	37/89 (42%)	37 (100%)	0	100	100
53	8	91/190 (48%)	90 (99%)	1 (1%)	70	83
54	b	130/135 (96%)	130 (100%)	0	100	100
55	e	188/236 (80%)	188 (100%)	0	100	100
56	g	122/148 (82%)	122 (100%)	0	100	100
57	i	86/110 (78%)	86 (100%)	0	100	100
58	j	74/97 (76%)	74 (100%)	0	100	100
59	m	40/113 (35%)	40 (100%)	0	100	100
60	o	80/87 (92%)	80 (100%)	0	100	100
61	q	113/178 (64%)	113 (100%)	0	100	100
62	r	147/169 (87%)	146 (99%)	1 (1%)	81	89
63	J	138/150 (92%)	138 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
64	I	164/232 (71%)	163 (99%)	1 (1%)	84	91
65	N	189/211 (90%)	188 (100%)	1 (0%)	86	93
66	P	125/154 (81%)	125 (100%)	0	100	100
67	U	125/135 (93%)	125 (100%)	0	100	100
68	V	184/191 (96%)	184 (100%)	0	100	100
69	E	260/290 (90%)	259 (100%)	1 (0%)	89	95
70	5	353/368 (96%)	353 (100%)	0	100	100
71	6	313/332 (94%)	312 (100%)	1 (0%)	91	96
72	7	272/303 (90%)	272 (100%)	0	100	100
73	9	104/112 (93%)	104 (100%)	0	100	100
74	a	101/133 (76%)	100 (99%)	1 (1%)	73	84
75	c	253/288 (88%)	253 (100%)	0	100	100
76	d	224/274 (82%)	224 (100%)	0	100	100
77	f	122/173 (70%)	122 (100%)	0	100	100
78	h	104/148 (70%)	104 (100%)	0	100	100
79	k	81/90 (90%)	81 (100%)	0	100	100
80	l	67/116 (58%)	67 (100%)	0	100	100
81	p	134/181 (74%)	134 (100%)	0	100	100
82	s	336/381 (88%)	335 (100%)	1 (0%)	91	96
83	Q	209/256 (82%)	208 (100%)	1 (0%)	86	93
85	TA	39/158 (25%)	39 (100%)	0	100	100
85	TB	26/158 (16%)	25 (96%)	1 (4%)	28	57
86	z	175/179 (98%)	173 (99%)	2 (1%)	70	83
All	All	12124/15991 (76%)	12084 (100%)	40 (0%)	90	96

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
53	8	178	TYR
82	s	230	ARG
62	r	139	VAL
69	E	324	ASP
85	TB	86	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 174 such sidechains are listed below:

Mol	Chain	Res	Type
54	b	90	HIS
68	V	84	ASN
55	e	248	ASN
62	r	96	HIS
71	6	320	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	940/954 (98%)	237 (25%)	12 (1%)
32	A	1522/1559 (97%)	349 (22%)	27 (1%)
33	B	51/73 (69%)	14 (27%)	1 (1%)
All	All	2513/2586 (97%)	600 (23%)	40 (1%)

5 of 600 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	650	U
1	AA	651	A
1	AA	674	U
1	AA	676	G
1	AA	680	U

5 of 40 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
32	A	2507	A
32	A	3041	U
32	A	2530	A
32	A	2653	C
32	A	3123	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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 135 ligands modelled in this entry, 134 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
89	GDP	AX	500	15	25,30,30	1.12	0	30,47,47	1.45	5 (16%)

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
89	GDP	AX	500	15	-	2/12/32/32	0/3/3/3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	AX	500	GDP	C8-N7-C5	3.04	107.73	102.55
89	AX	500	GDP	O3B-PB-O3A	2.64	113.48	104.64
89	AX	500	GDP	O6-C6-N1	2.37	123.43	120.62
89	AX	500	GDP	O3'-C3'-C4'	2.29	117.66	111.08
89	AX	500	GDP	O6-C6-C5	-2.20	119.96	124.32

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
89	AX	500	GDP	C5'-O5'-PA-O3A

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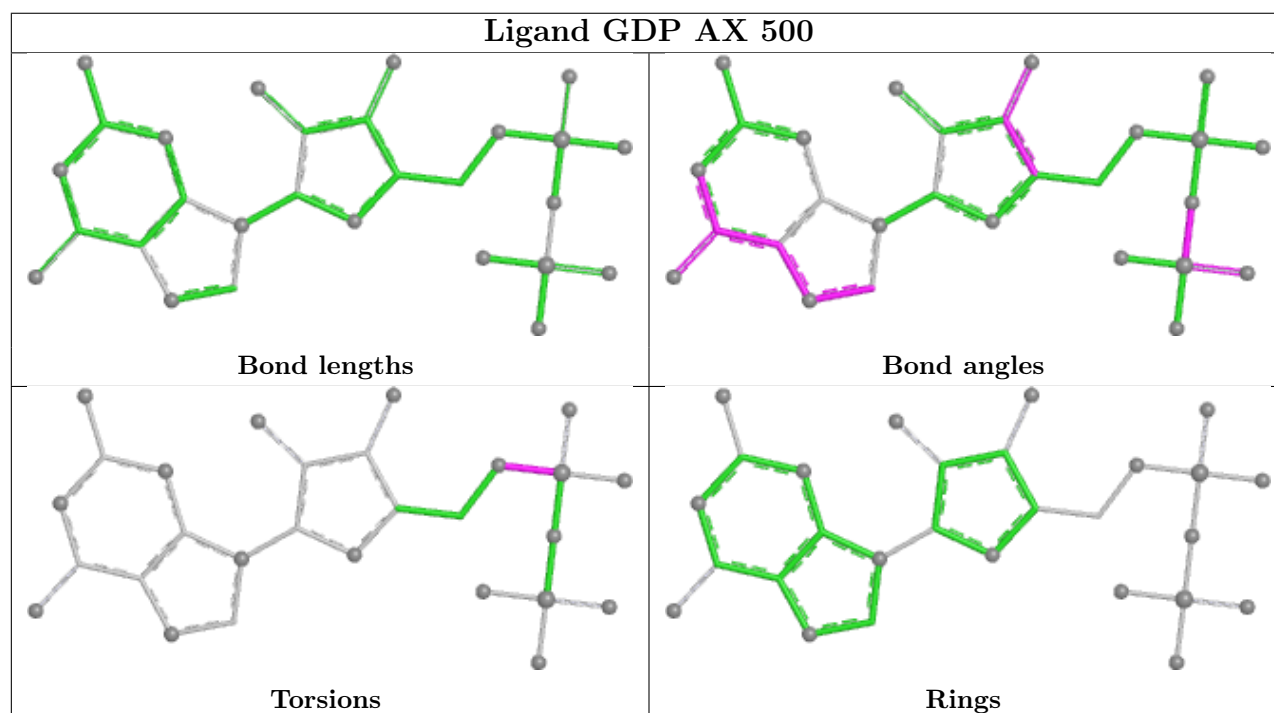
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Mol	Chain	Res	Type	Atoms
89	AX	500	GDP	C5'-O5'-PA-O1A

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
84	u	4
32	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	u	414:UNK	C	601:UNK	N	48.75
1	u	106:UNK	C	301:UNK	N	32.31
1	u	315:UNK	C	399:UNK	N	23.19
1	u	615:UNK	C	700:UNK	N	20.56
1	A	2580:U	O3'	2581:A	P	3.48

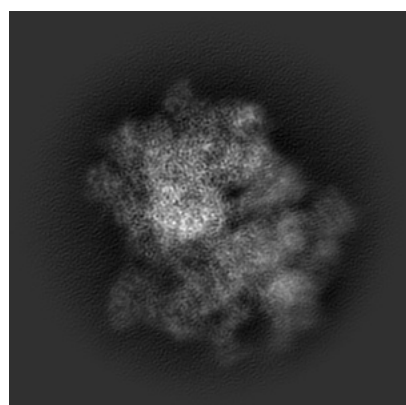
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23096. These allow visual inspection of the internal detail of the map and identification of artifacts.

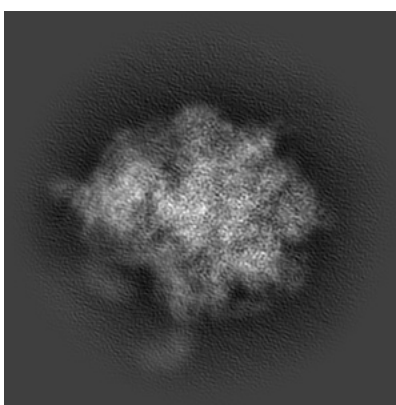
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

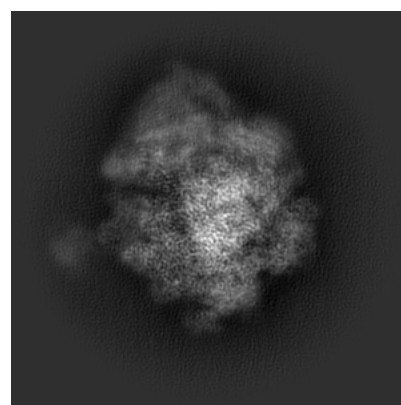
6.1.1 Primary map



X



Y

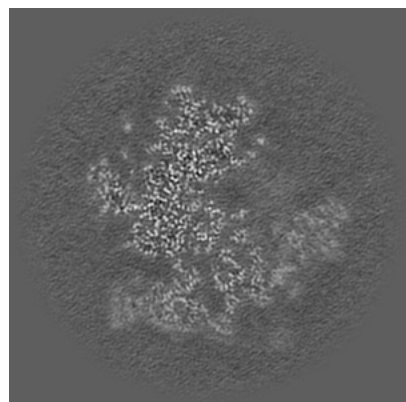


Z

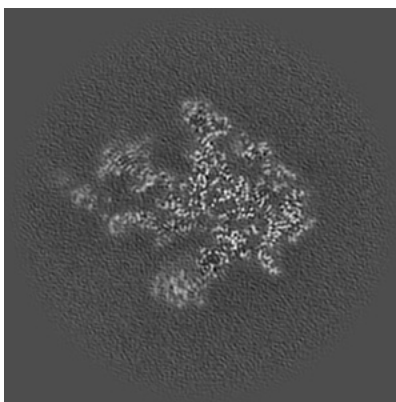
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

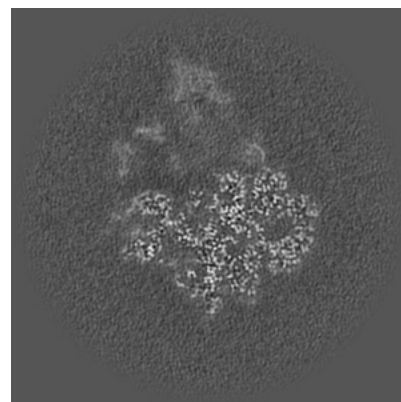
6.2.1 Primary map



X Index: 200



Y Index: 200

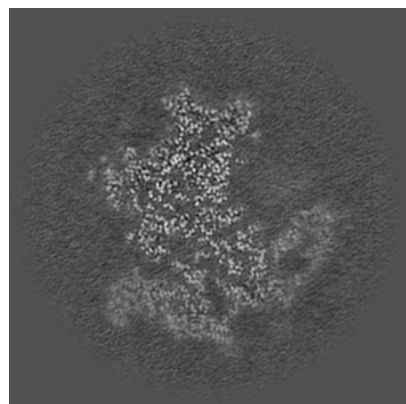


Z Index: 200

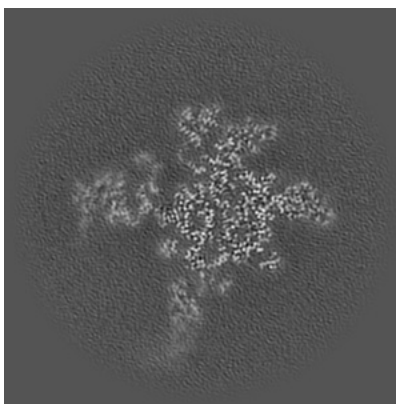
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

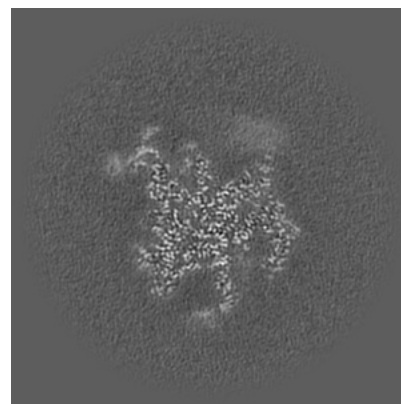
6.3.1 Primary map



X Index: 208



Y Index: 171

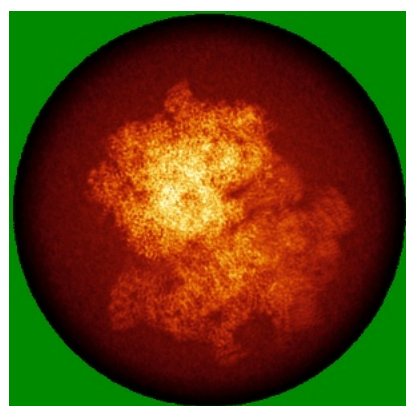


Z Index: 242

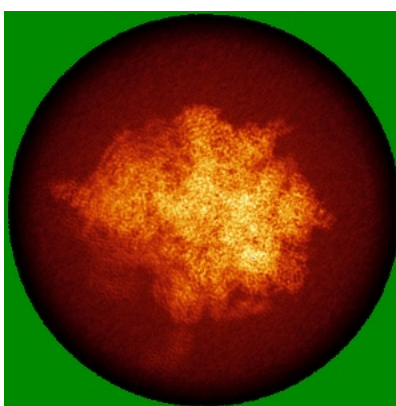
The images above show the largest variance slices of the map in three orthogonal directions.

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

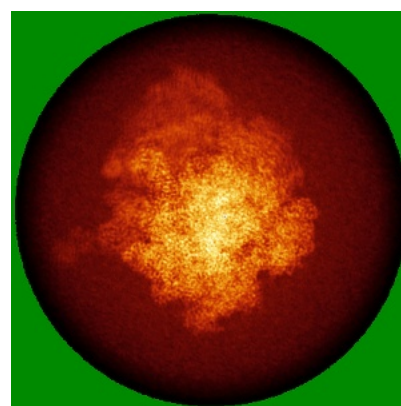
6.4.1 Primary map



X



Y

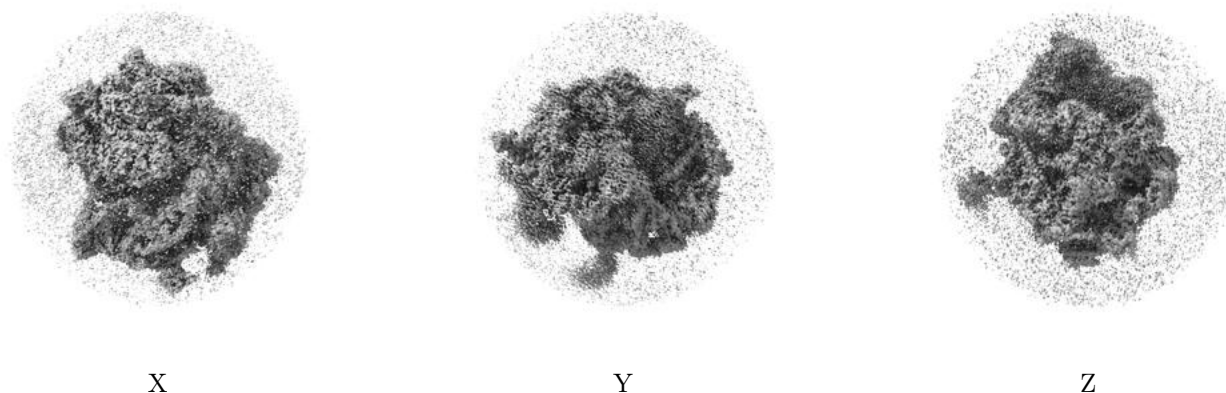


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

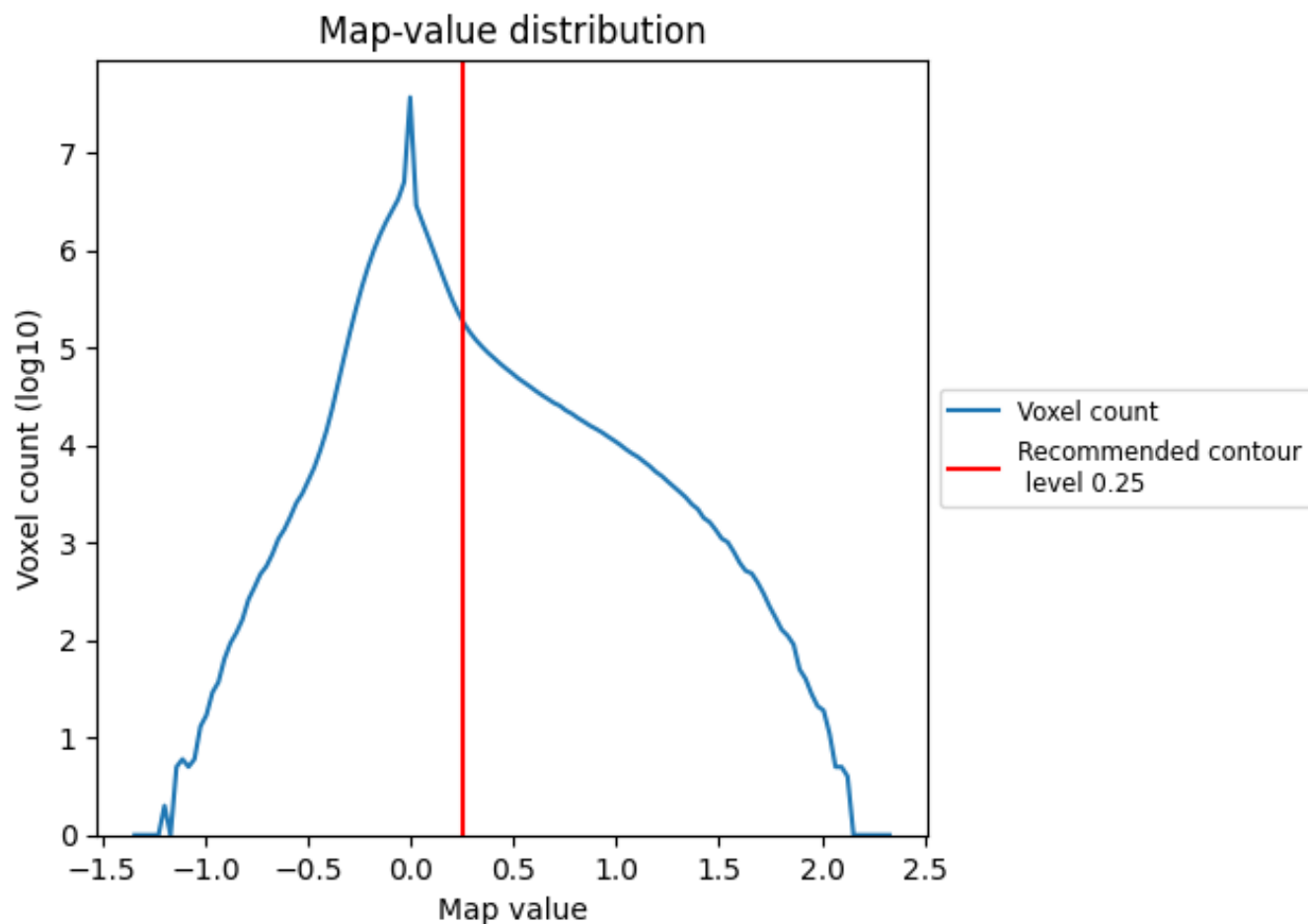
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

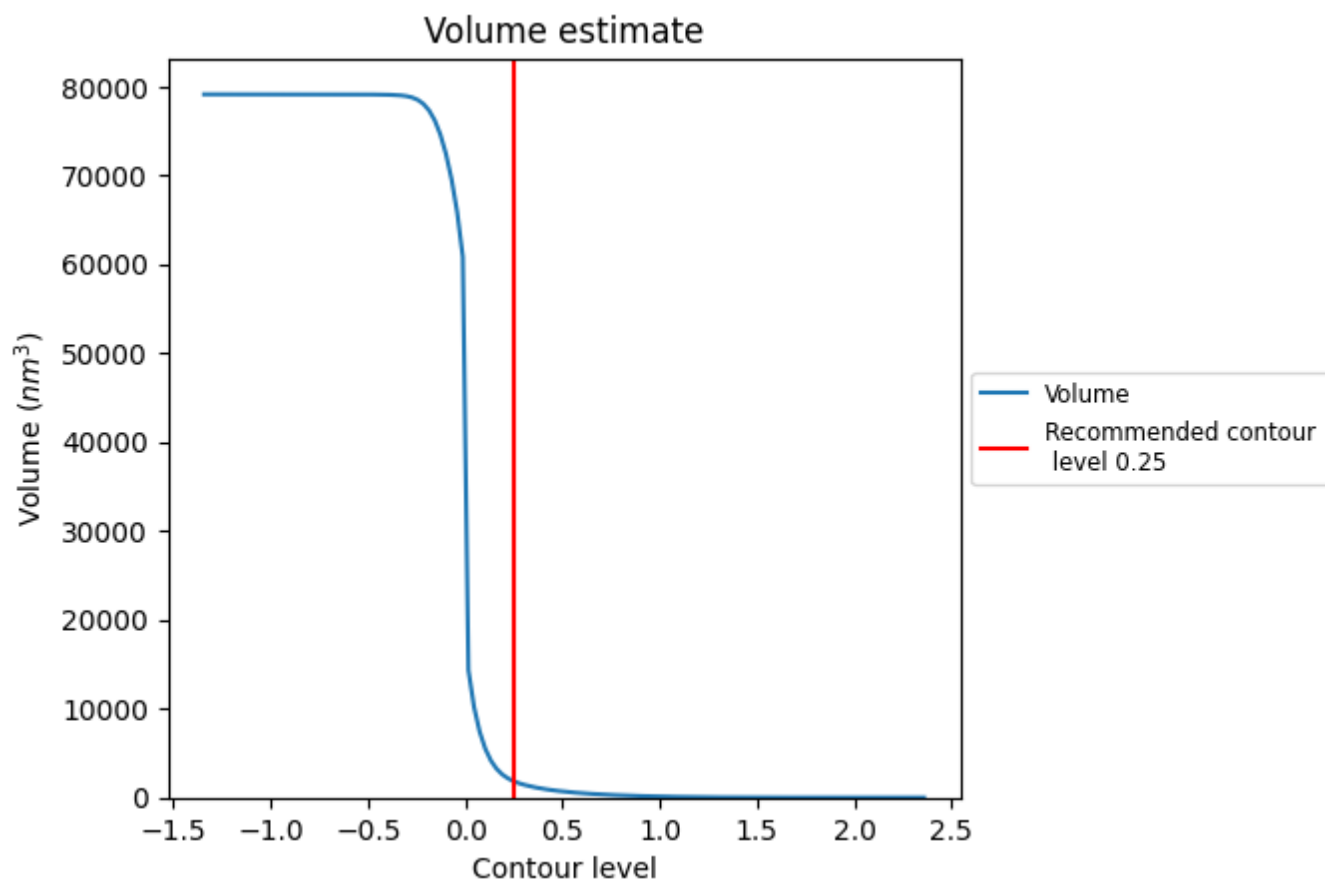
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

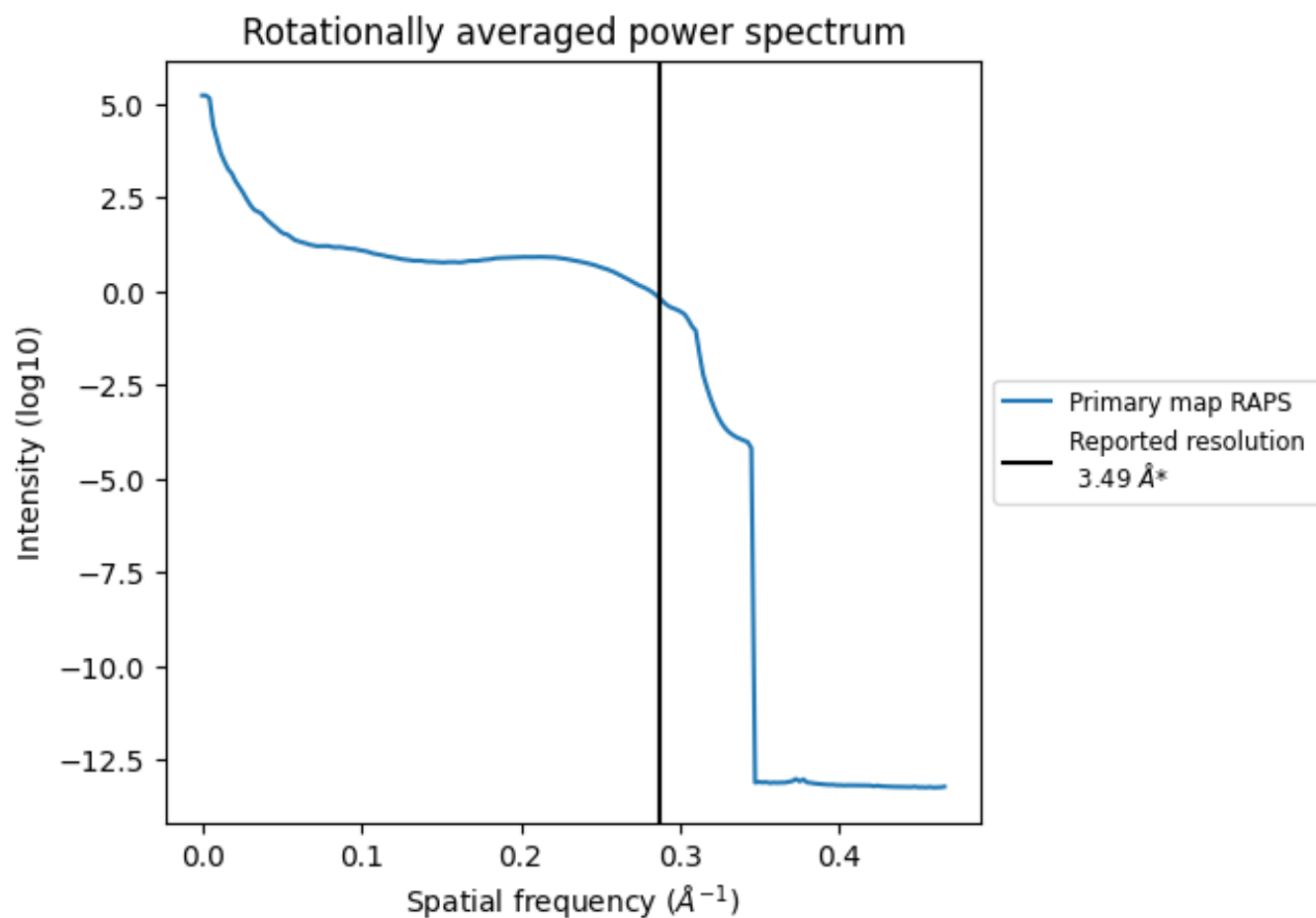
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1834 nm^3 ; this corresponds to an approximate mass of 1656 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 0.287 Å⁻¹

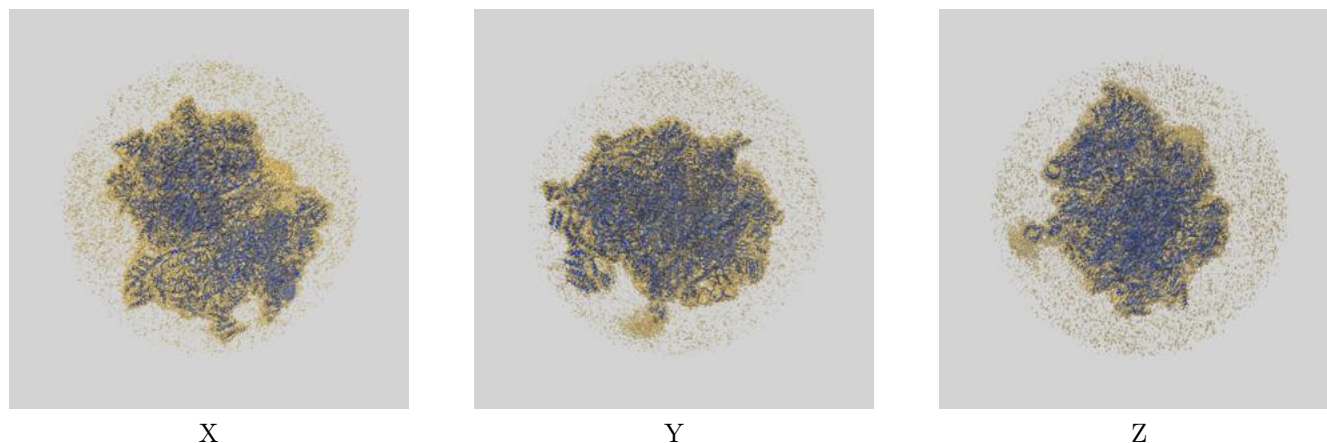
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

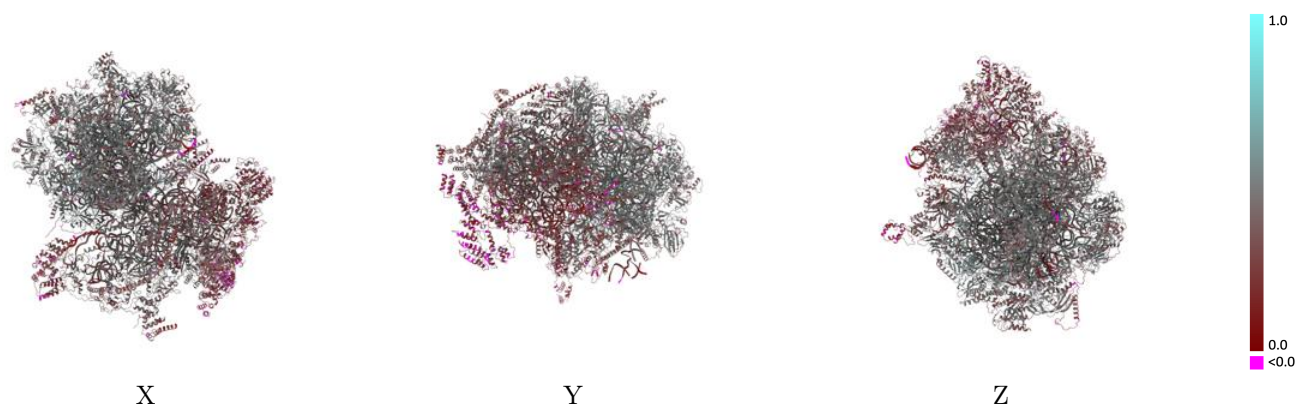
This section contains information regarding the fit between EMDB map EMD-23096 and PDB model 7L08. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay [i](#)



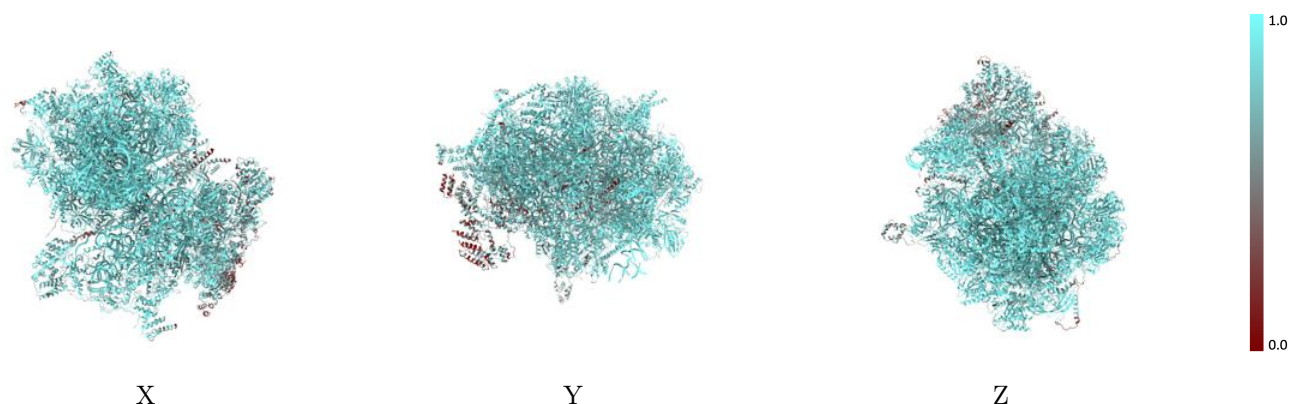
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



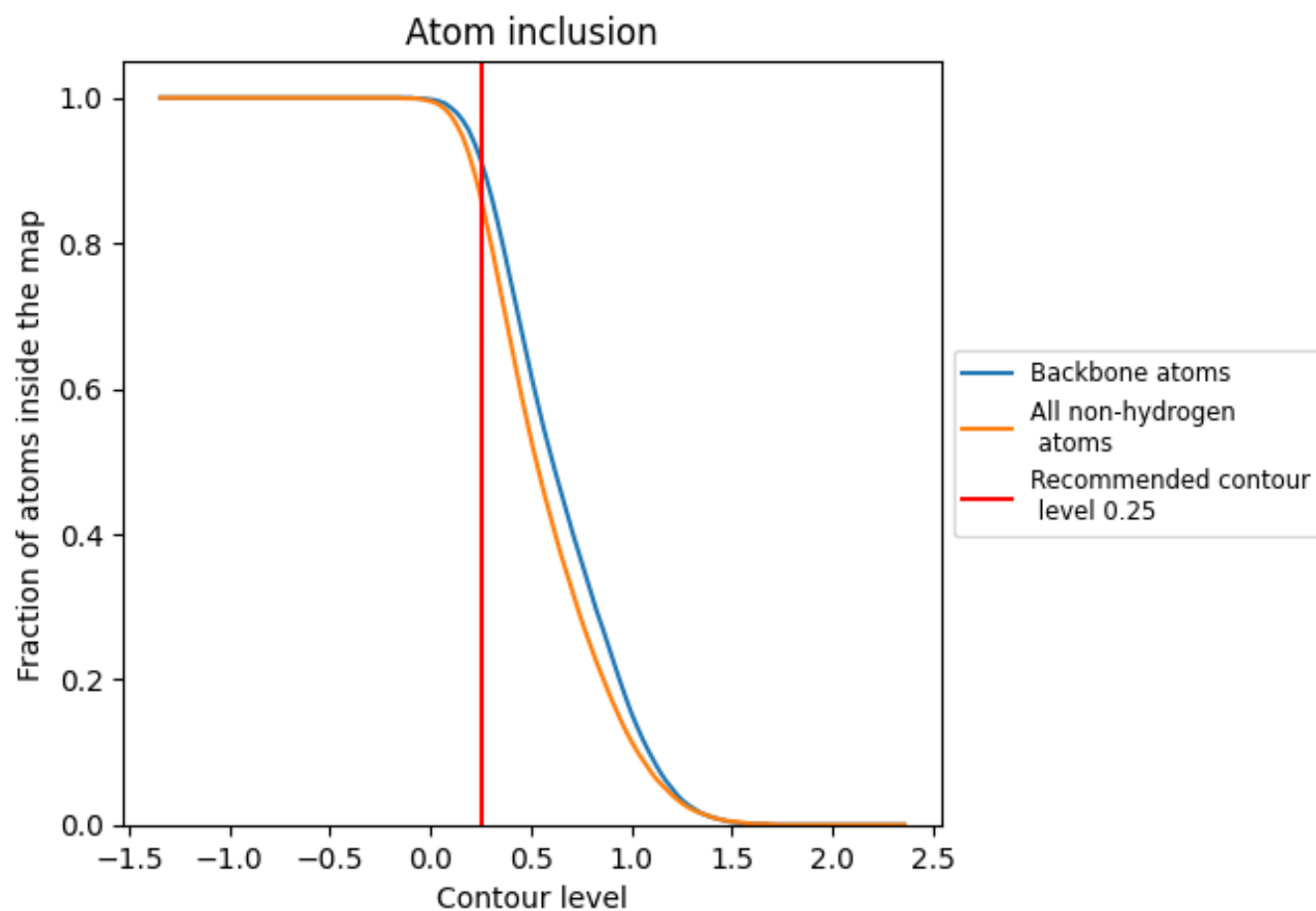
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8640	 0.4000
0	 0.9130	 0.4790
1	 0.9210	 0.4780
2	 0.9190	 0.5070
3	 0.9160	 0.5120
4	 0.9600	 0.5060
5	 0.9290	 0.4570
6	 0.9160	 0.4360
7	 0.8900	 0.4290
8	 0.7930	 0.3160
9	 0.9040	 0.4420
A	 0.9240	 0.4240
A0	 0.8300	 0.3730
A1	 0.6330	 0.2520
A2	 0.7610	 0.3910
A3	 0.8360	 0.4520
A4	 0.4690	 0.1700
AA	 0.9110	 0.3620
AB	 0.8670	 0.3950
AC	 0.7340	 0.2940
AD	 0.7510	 0.4030
AE	 0.8300	 0.3840
AF	 0.7190	 0.3350
AG	 0.7290	 0.3050
AH	 0.7070	 0.2780
AI	 0.8680	 0.3970
AJ	 0.8630	 0.4870
AK	 0.8300	 0.3300
AL	 0.8200	 0.3930
AM	 0.8580	 0.4200
AN	 0.9290	 0.4590
AO	 0.8660	 0.4010
AP	 0.8660	 0.3950
AQ	 0.8820	 0.4130
AR	 0.8210	 0.3610

























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Chain	Atom inclusion	Q-score
AS	 0.8250	 0.3560
AT	 0.8670	 0.4380
AU	 0.8270	 0.3360
AV	 0.7600	 0.2550
AW	 0.8320	 0.3780
AX	 0.7330	 0.2620
AY	 0.6410	 0.2500
AZ	 0.6740	 0.2660
B	 0.9480	 0.3190
D	 0.9220	 0.4950
E	 0.9320	 0.5040
F	 0.9280	 0.4850
H	 0.8990	 0.4370
I	 0.8340	 0.3830
J	 0.7800	 0.2900
K	 0.9440	 0.4980
L	 0.9110	 0.5070
M	 0.9140	 0.4790
N	 0.9190	 0.4960
O	 0.9250	 0.4840
P	 0.9310	 0.4560
Q	 0.8830	 0.4730
R	 0.9110	 0.4940
S	 0.9320	 0.5000
T	 0.9130	 0.5020
TA	 0.5490	 0.1480
TB	 0.6060	 0.2020
U	 0.8960	 0.4540
V	 0.8680	 0.4230
W	 0.9200	 0.5090
X	 0.9050	 0.4650
Y	 0.9150	 0.4550
Z	 0.9250	 0.5080
a	 0.8580	 0.4390
b	 0.9320	 0.4940
c	 0.9120	 0.4580
d	 0.8060	 0.3890
e	 0.7670	 0.2510
f	 0.7770	 0.3610
g	 0.9180	 0.4750
h	 0.8670	 0.3840
i	 0.9130	 0.4900

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Chain	Atom inclusion	Q-score
j	 0.8840	 0.4390
k	 0.8840	 0.4030
l	 0.8090	 0.3270
m	 0.8670	 0.3640
o	 0.9360	 0.5010
p	 0.8370	 0.3880
q	 0.7930	 0.3620
r	 0.9410	 0.4800
s	 0.9150	 0.4620
u	 0.6950	 0.2460
z	 0.6100	 0.3240