



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:59 PM UTC

PDB ID : 7ODR / pdb_00007odr
EMDB ID : EMD-12845
Title : State A of the human mitoribosomal large subunit assembly intermediate
Authors : Lenarcic, T.; Jaskolowski, M.; Leibundgut, M.; Scaiola, A.; Schoenhut, T.;
Saurer, M.; Lee, R.G.; Rackham, O.; Filipovska, A.; Ban, N.
Deposited on : 2021-04-30
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

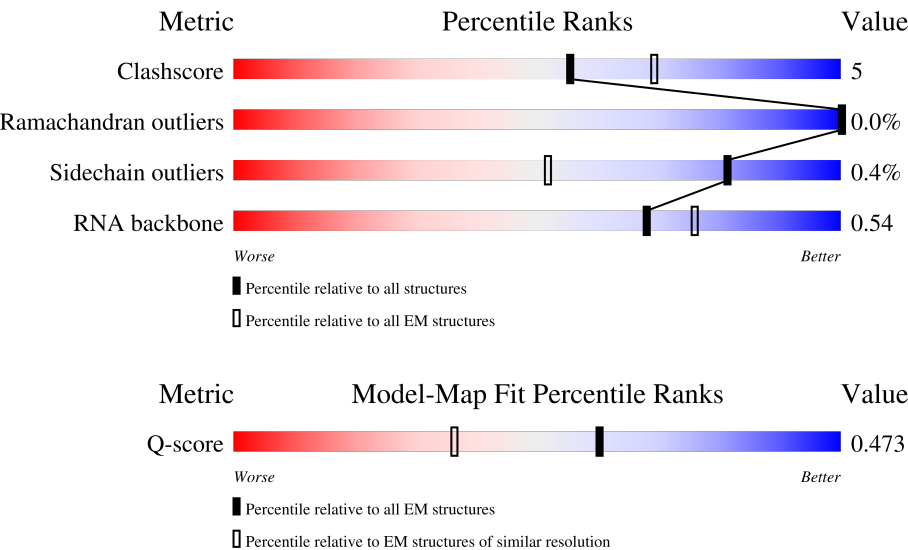
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.90 Å.

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



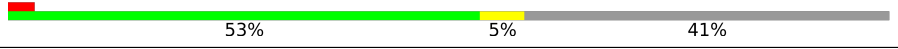
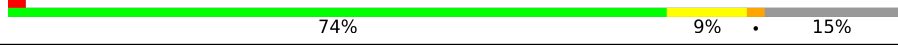
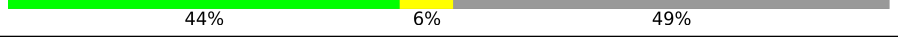
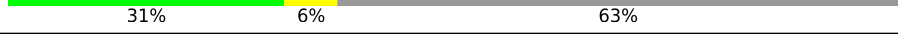
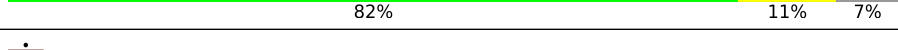
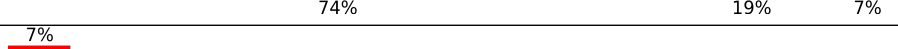
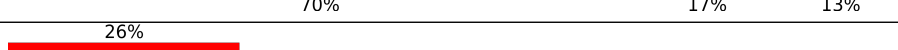
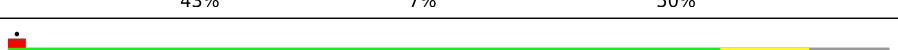
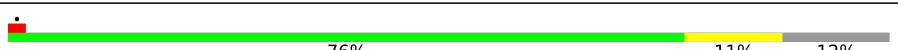
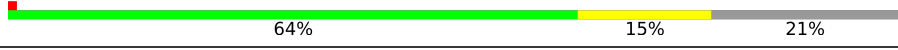
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	u	234	
2	v	70	
3	w	156	

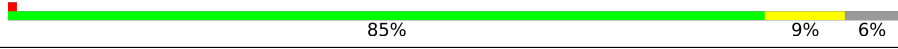
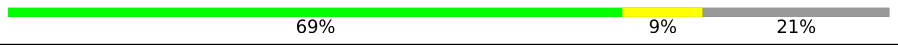
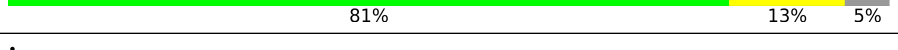
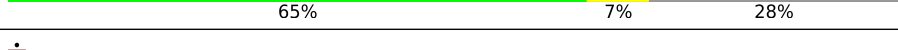
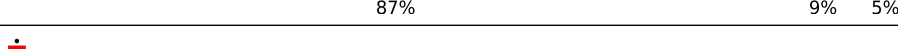
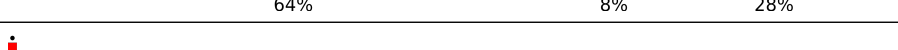
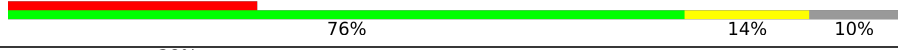
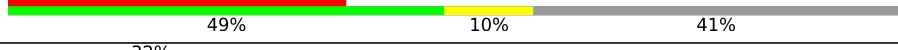
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Mol	Chain	Length	Quality of chain
4	x	384	
5	y	381	
6	0	188	
7	1	65	
8	2	92	
9	3	188	
10	4	103	
11	5	423	
12	6	380	
13	7	338	
14	8	206	
15	9	137	
16	A	1590	
17	B	72	
18	D	305	
19	E	348	
20	F	311	
21	H	267	
22	I	261	
23	J	192	
24	K	178	
25	L	145	
26	M	296	
27	N	251	
28	O	175	

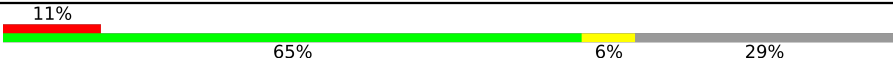
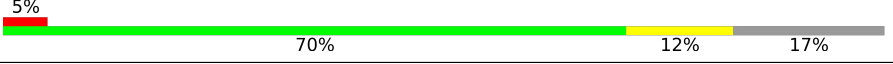
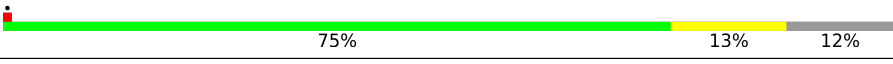
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Mol	Chain	Length	Quality of chain
29	P	180	
30	Q	292	
31	R	149	
32	S	205	
33	T	206	
34	U	153	
35	V	216	
36	W	148	
37	X	256	
38	Y	250	
39	Z	161	
40	a	142	
41	b	215	
42	c	332	
43	d	306	
44	e	279	
45	f	212	
46	g	166	
47	h	158	
48	i	128	
49	j	123	
50	k	112	
51	l	138	
52	m	128	
53	o	102	

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Mol	Chain	Length	Quality of chain
54	p	206	
55	q	222	
56	r	196	
57	s	439	

2 Entry composition [i](#)

There are 63 unique types of molecules in this entry. The entry contains 107464 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	u	110	Total	C	N	O	S	0	0
			919	591	154	164	10		

- Molecule 2 is a protein called MIEF1 upstream open reading frame protein.

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

- Molecule 3 is a protein called Acyl carrier protein, mitochondrial.

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

- Molecule 4 is a protein called 5-methylcytosine rRNA methyltransferase NSUN4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	x	336	Total	C	N	O	S	0	0
			2660	1694	465	484	17		

- Molecule 5 is a protein called Transcription termination factor 4, mitochondrial.

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

- Molecule 6 is a protein called 39S ribosomal protein L32, mitochondrial.

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

- Molecule 7 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	1	55	Total	C	N	O	S	0	0
			455	290	87	76	2		

- Molecule 8 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	2	46	Total	C	N	O	S	0	0
			377	233	83	60	1		

- Molecule 9 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	3	95	Total	C	N	O	S	0	0
			832	539	162	128	3		

- Molecule 10 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	4	38	Total	C	N	O	S	0	0
			342	217	72	49	4		

- Molecule 11 is a protein called 39S ribosomal protein L37, mitochondrial.

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

- Molecule 12 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	6	354	Total	C	N	O	S	0	0
			2948	1881	525	533	9		

- Molecule 13 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	7	294	Total	C	N	O	S	0	0
			2390	1529	405	438	18		

- Molecule 14 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	8	102	Total	C	N	O	S	0	0
			860	543	152	163	2		

- Molecule 15 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	9	124	Total	C	N	O	S	0	0
			997	644	170	181	2		

- Molecule 16 is a RNA chain called 16S mitochondrial rRNA, DNA (31-MER),16S mitochondrial rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	A	1448	Total	C	N	O	P	0	0
			30460	13658	5442	9912	1448		

- Molecule 17 is a RNA chain called mitochondrial tRNAVal.

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

- Molecule 18 is a protein called 39S ribosomal protein L2, mitochondrial.

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

- Molecule 19 is a protein called 39S ribosomal protein L3, mitochondrial.

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

- Molecule 20 is a protein called 39S ribosomal protein L4, mitochondrial.

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

- Molecule 21 is a protein called 39S ribosomal protein L9, mitochondrial.

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

- Molecule 22 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	I	163	Total	C	N	O	S	0	0
			1324	854	240	220	10		

- Molecule 23 is a protein called 39S ribosomal protein L11, mitochondrial.

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

- Molecule 24 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 25 is a protein called 39S ribosomal protein L14, mitochondrial.

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

- Molecule 26 is a protein called 39S ribosomal protein L15, mitochondrial.

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

- Molecule 27 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	N	212	Total	C	N	O	S	0	0
			1723	1107	310	297	9		

- Molecule 28 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 29 is a protein called 39S ribosomal protein L18, mitochondrial.

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

- Molecule 30 is a protein called 39S ribosomal protein L19, mitochondrial.

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

- Molecule 31 is a protein called 39S ribosomal protein L20, mitochondrial.

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

- Molecule 32 is a protein called 39S ribosomal protein L21, mitochondrial.

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

- Molecule 33 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 34 is a protein called 39S ribosomal protein L23, mitochondrial.

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

- Molecule 35 is a protein called 39S ribosomal protein L24, mitochondrial.

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

- Molecule 36 is a protein called 39S ribosomal protein L27, mitochondrial.

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

- Molecule 37 is a protein called 39S ribosomal protein L28, mitochondrial.

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

- Molecule 38 is a protein called 39S ribosomal protein L47, mitochondrial.

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

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

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

- Molecule 40 is a protein called 39S ribosomal protein L42, mitochondrial.

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

- Molecule 41 is a protein called 39S ribosomal protein L43, mitochondrial.

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

- Molecule 42 is a protein called 39S ribosomal protein L44, mitochondrial.

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

- Molecule 43 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	d	259	Total	C	N	O	S	0	0
			2124	1357	369	384	14		

- Molecule 44 is a protein called 39S ribosomal protein L46, mitochondrial.

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

- Molecule 45 is a protein called 39S ribosomal protein L48, mitochondrial.

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

- Molecule 46 is a protein called 39S ribosomal protein L49, mitochondrial.

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

- Molecule 47 is a protein called 39S ribosomal protein L50, mitochondrial.

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

- Molecule 48 is a protein called 39S ribosomal protein L51, mitochondrial.

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

- Molecule 49 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	j	94	Total	C	N	O	S	0	0
			745	463	144	136	2		

- Molecule 50 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	k	101	Total	C	N	O	S	0	0
			774	479	148	142	5		

- Molecule 51 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	l	82	Total	C	N	O	S	0	0
			688	437	120	128	3		

- Molecule 52 is a protein called 39S ribosomal protein L55, mitochondrial.

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

- Molecule 53 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	o	94	Total	C	N	O	S	0	0
			798	501	165	129	3		

- Molecule 54 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

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

- Molecule 55 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

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

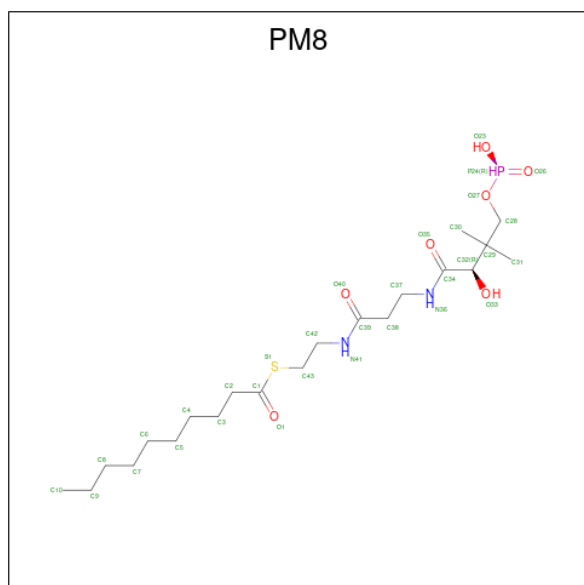
- Molecule 56 is a protein called 39S ribosomal protein S18a, mitochondrial.

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

- Molecule 57 is a protein called 39S ribosomal protein S30, mitochondrial.

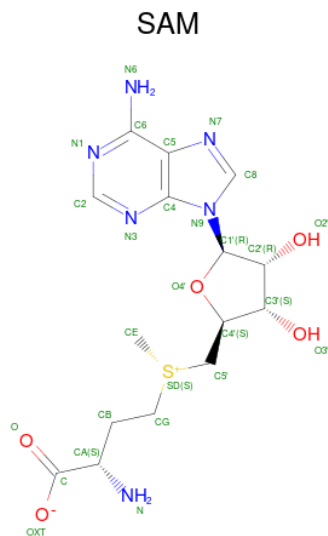
Mol	Chain	Residues	Atoms					AltConf	Trace
57	s	386	Total	C	N	O	S	0	0
			3155	2023	559	559	14		

- Molecule 58 is S-(2-{[N-(2-HYDROXY-4-{[HYDROXY(OXIDO)PHOSPHINO]OXY}-3,3-DIMETHYLBUTANOYL)-BETA-ALANYL]AMINO}ETHYL) DECANETHIOATE (CCD ID: PM8) (formula: C₂₁H₄₁N₂O₇PS).



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

- Molecule 59 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: C₁₅H₂₂N₆O₅S).



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

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
60	0	1	Total 1	Zn 1	0
60	4	1	Total 1	Zn 1	0

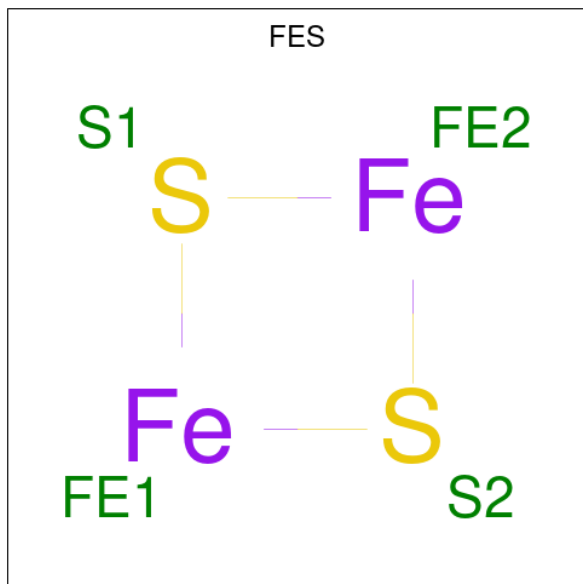
- Molecule 61 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
61	9	1	Total 1	Mg 1	0
61	A	92	Total 92	Mg 92	0
61	D	1	Total 1	Mg 1	0
61	M	1	Total 1	Mg 1	0
61	O	1	Total 1	Mg 1	0
61	g	1	Total 1	Mg 1	0

- Molecule 62 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
62	A	2	Total	K	0
			2	2	

- Molecule 63 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



Mol	Chain	Residues	Atoms			AltConf
63	r	1	Total	Fe	S	0
			4	2	2	

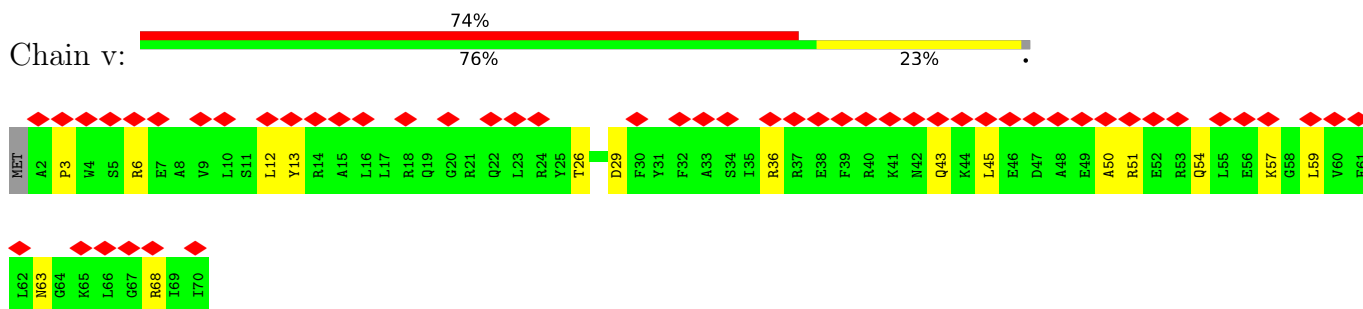
3 Residue-property plots

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: Mitochondrial assembly of ribosomal large subunit protein 1



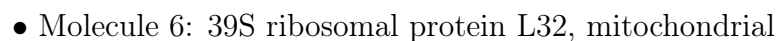
- Molecule 2: MIEF1 upstream open reading frame protein

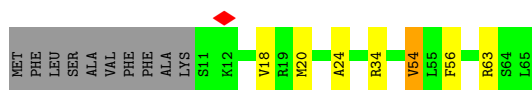


- Molecule 3: Acyl carrier protein, mitochondrial

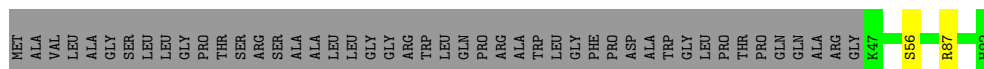


Chain x: 69% 19% 12%

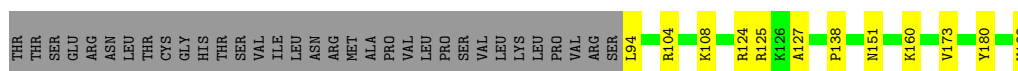




- Molecule 8: 39S ribosomal protein L34, mitochondrial



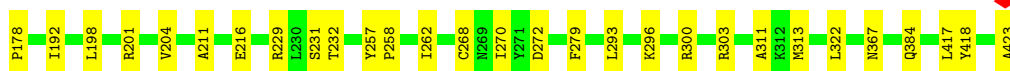
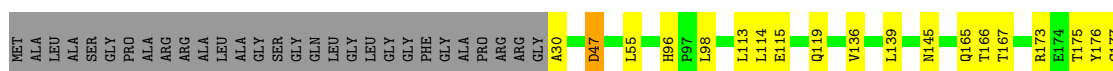
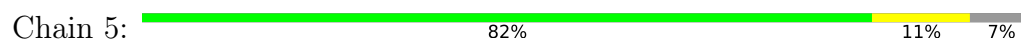
- Molecule 9: 39S ribosomal protein L35, mitochondrial



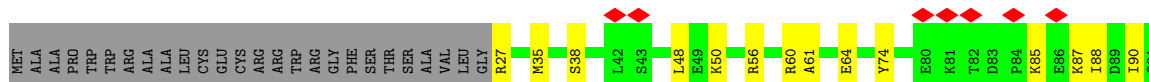
- Molecule 10: 39S ribosomal protein L36, mitochondrial

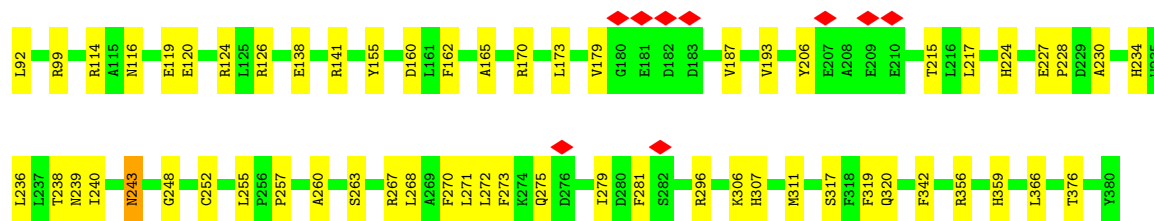


- Molecule 11: 39S ribosomal protein L37, mitochondrial

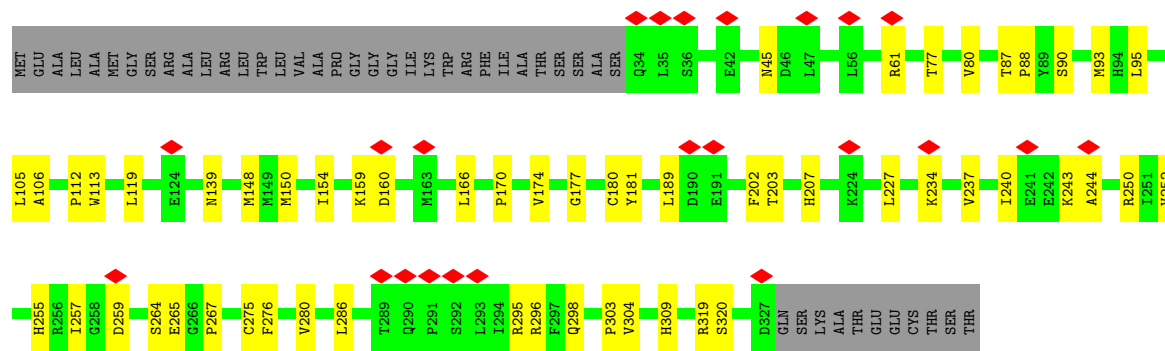


- Molecule 12: 39S ribosomal protein L38, mitochondrial

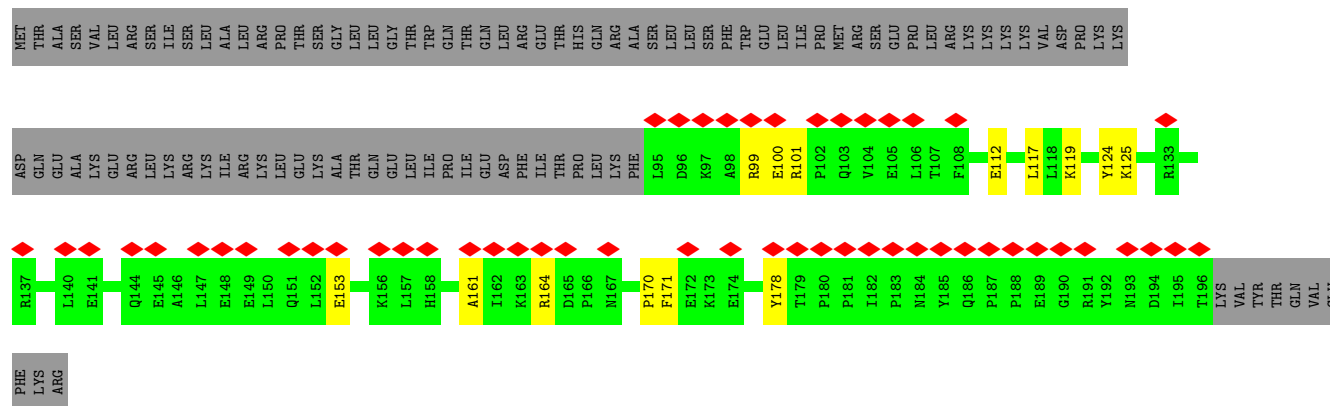
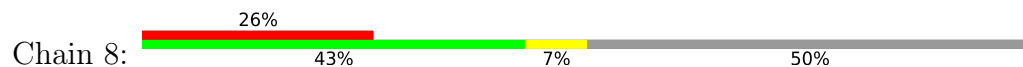




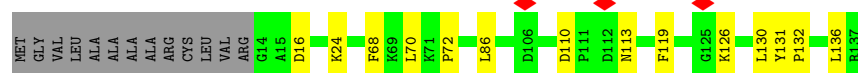
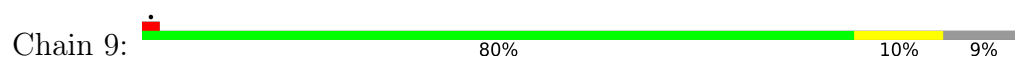
- Molecule 13: 39S ribosomal protein L39, mitochondrial



- Molecule 14: 39S ribosomal protein L40, mitochondrial



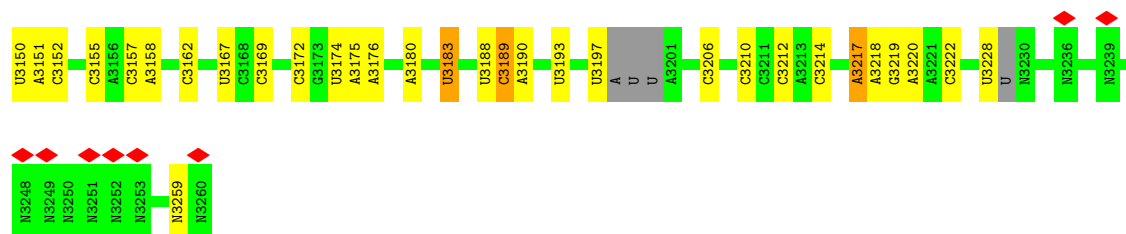
- Molecule 15: 39S ribosomal protein L41, mitochondrial



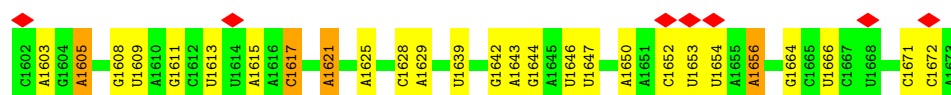
- Molecule 16: 16S mitochondrial rRNA, DNA (31-MER), 16S mitochondrial rRNA



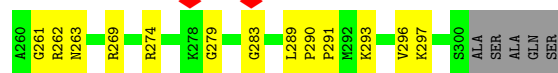
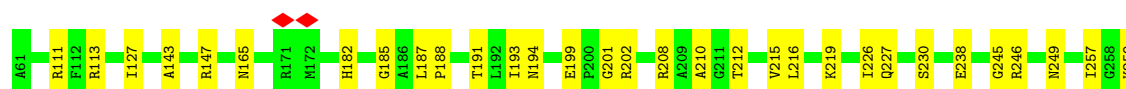
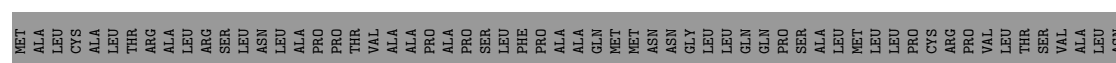
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C3021	A2921	U	C2718	C	G2300	C2210	C2125	C2001	A1773	U1673
U3024	A2922	C	G2719	A2432	G2309	U2211	U2126	G2002	A1777	C1678
A3025	U2925	U	G2720	A2442	A2306	C2212	A2127	A2003	U1780	C1689
U3041	A2926	U	G2721	U2443	G2310	A2216	A2131	G2015	A1781	C1693
U3042	A2927	A	G2724	C2443	A2321	C2217	A2132	C2016	G1782	C1693
C3043	C2927	A	A2725	A2444	C2322	C	A2136	U2017	G1787	A1697
C3043	C2928	A	U2726	U2445	C2322	C	A2137	G2018	A1790	C1698
A3051	C2929	U	G2727	A2446	U2324	A	U2138	G2019	G1791	C1699
A3052	U2930	U	C2728	G2449	U2325	U	A2144	G2022	G1792	U1700
A3053	A2935	G	U2729	A2450	C2328	C	A2147	G1886	G1793	C1703
G3054	U	G	G2732	A2451	C2332	A	C2151	A2029	A1887	U1704
C3056	A	U	G2733	A2452	G2345	U2228	A2154	U2030	A1889	A1795
C3056	C2939	A	U2734	G2453	U2346	A2230	A2155	A2031	A1891	U1798
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C3073	C2962	A	U2754	A2468	A2354	A2238	A2177	A2040	U1807	A1712
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C3077	G2975	U	C2756	G2470	A2356	C2240	A2180	A2065	A1809	A1724
G3082	U2975	C	U2757	G2478	C2359	A2241	A2181	A1936	C1827	A1727
U3083	U2980	C	G2758	C2493	U2360	U2242	C2182	A1937	A1828	U1728
A3084	A2981	U	A	U2499	G2361	U2244	C2183	A1938	A1829	A1731
A3085	C2982	C	A	A2500	A2362	A2246	A2184	G1939	A1830	A1737
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U3097	A	C	A2506	A2507	A2390	U2256	A2179	G1973	A1828	U1745
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A3101	G	A	C2511	A2512	U2392	C2259	C2182	U1977	A1830	G1747
U3102	U2993	U	A2512	G2519	C2393	A2260	C2183	A1978	G1831	G1748
C3103	U2994	C	G2519	C2520	A2394	C2261	A2184	U1979	C1749	C1749
U3104	G2995	G	C2520	A2521	A2395	C2262	A2184	U1980	G1750	A1751
U3109	U2998	U	A2521	A2527	C2396	C2263	A2191	A1980	A1836	U1752
C3110	A3000	C	A2527	G2528	A2401	U2277	U2194	A1984	A1844	A1753
A3111	A3005	A	U2528	U2529	C2405	U2277	A2195	G1985	A1853	G1754
A3113	C3008	U	U2529	A2530	A2406	C2283	A2196	A1986	A1854	A1755
A3126	U2910	C	A2530	U2531	U2407	C2284	G2197	G1987	A1855	G1760
G3132	C2911	U	U2531	U2531	U2408	U2285	A2198	G1990	A1859	A1761
G3132	G3013	A	U2531	U2531	U2409	U2287	A2199	C1991	A1860	A1762
G3132	G3014	C	U2531	U2531	U2410	U2287	A2200	G1992	U1861	A1763
A3141	U3015	A	C2540	C2541	U2410	A2293	G2201	A1993	U1862	C1764
A3141	G3016	C	C2541	C2541	U2410	A2294	C2202	A1994	A1863	C1765
A3141	G3016	U	C2541	C2541	U2410	A2294	U2204	A1995	A1864	G1770
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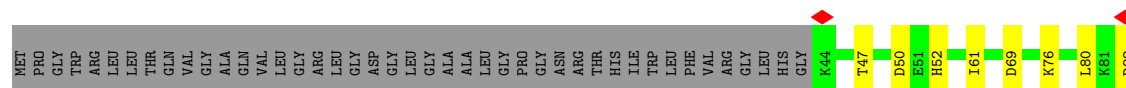
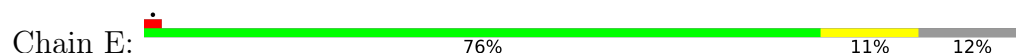
- Molecule 17: mitochondrial tRNA^{Val}



- Molecule 18: 39S ribosomal protein L2, mitochondrial

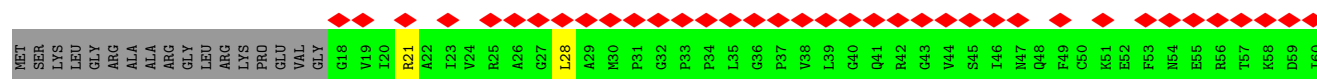


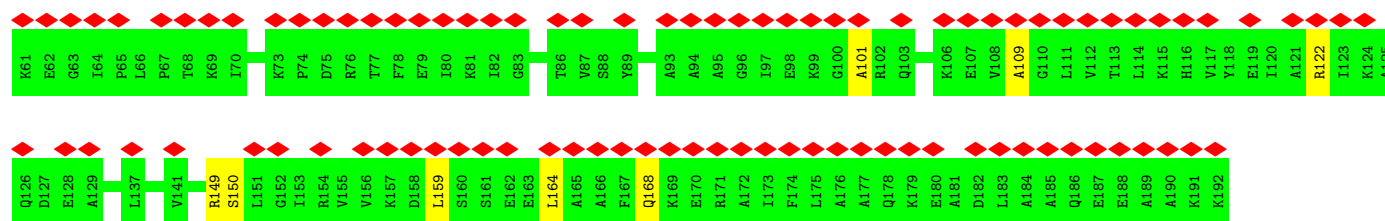
- Molecule 19: 39S ribosomal protein L3, mitochondrial



- Molecule 20: 39S ribosomal protein L4, mitochondrial

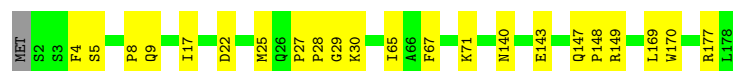






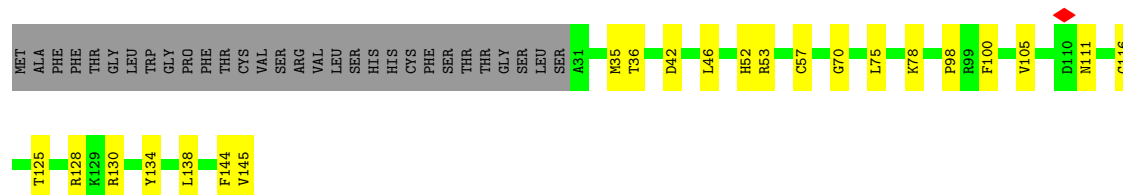
- Molecule 24: 39S ribosomal protein L13, mitochondrial

Chain K: 87% 12% .



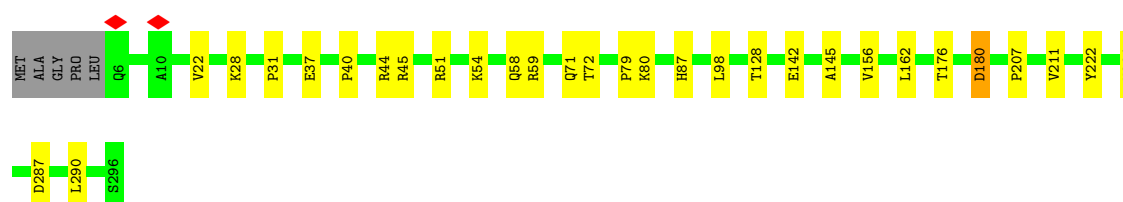
- Molecule 25: 39S ribosomal protein L14, mitochondrial

Chain L: 64% 15% 21%



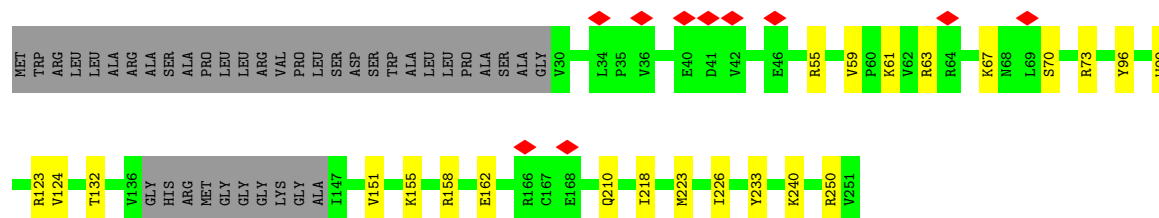
- Molecule 26: 39S ribosomal protein L15, mitochondrial

Chain M: 88% 10% .



- Molecule 27: 39S ribosomal protein L16, mitochondrial

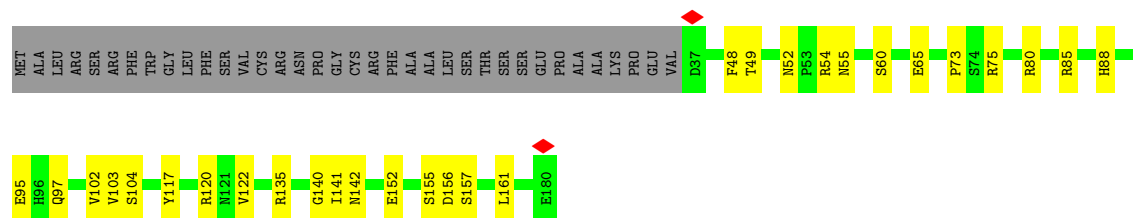
Chain N: 75% 9% 16%



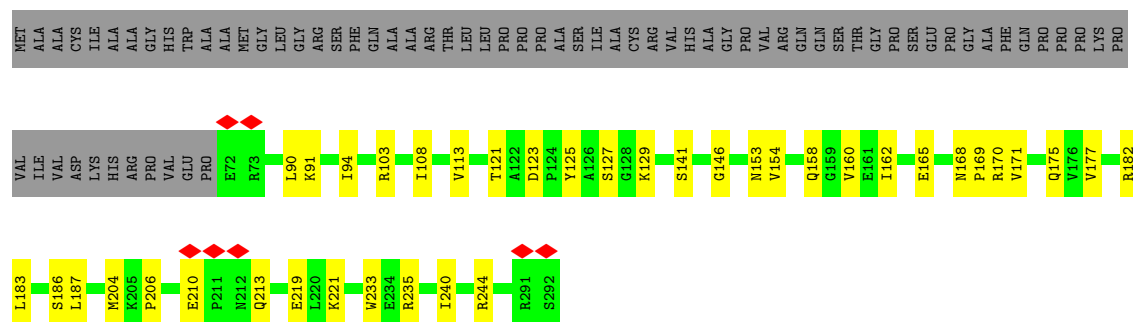
- Molecule 28: 39S ribosomal protein L17, mitochondrial

Chain O: 74% 14% 12%

- Molecule 29: 39S ribosomal protein L18, mitochondrial



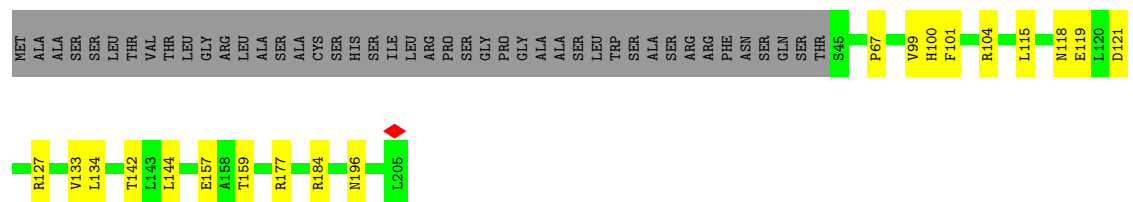
- Molecule 30: 39S ribosomal protein L19, mitochondrial



- Molecule 31: 39S ribosomal protein L20, mitochondrial

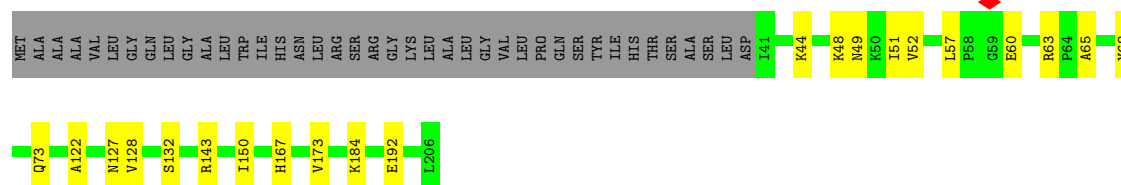


- Molecule 32: 39S ribosomal protein L21, mitochondrial



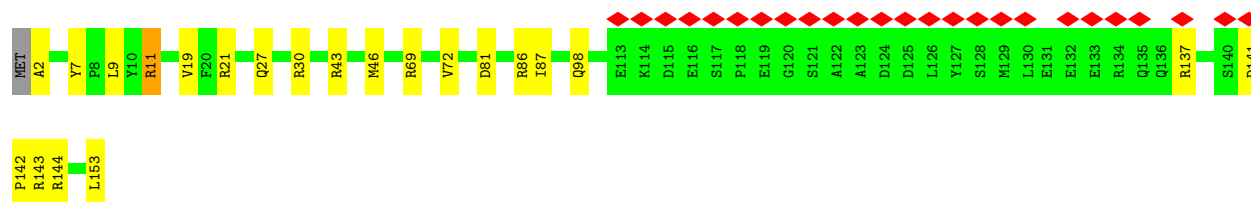
- Molecule 33: 39S ribosomal protein L22, mitochondrial

Chain T:  70% 10% 19%



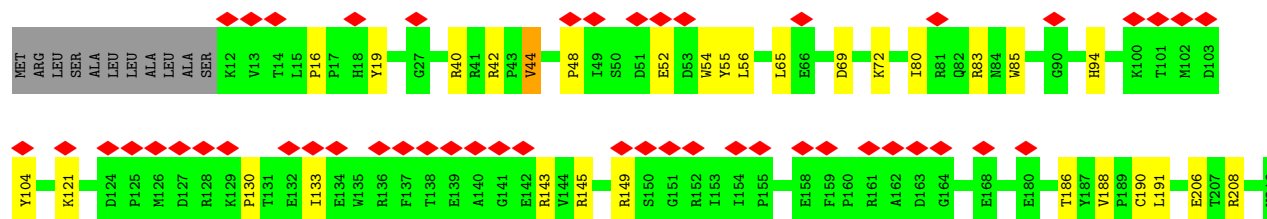
- Molecule 34: 39S ribosomal protein L23, mitochondrial

Chain U:  16% 85% 14% ..



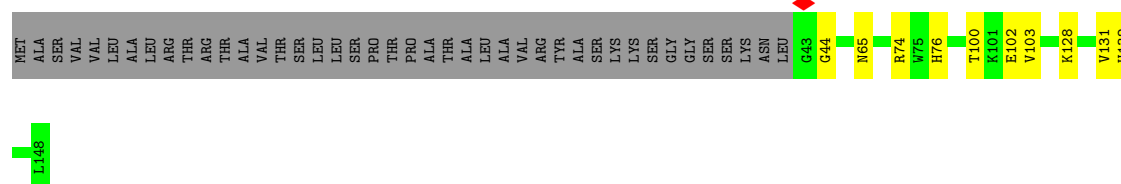
- Molecule 35: 39S ribosomal protein L24, mitochondrial

Chain V:  23% 81% 13% 5%



- Molecule 36: 39S ribosomal protein L27, mitochondrial

Chain W:  65% 7% 28%



- Molecule 37: 39S ribosomal protein L28, mitochondrial

Chain X:  87% 9% 5%



SER
GLY
GLN

- Molecule 38: 39S ribosomal protein L47, mitochondrial

Chain Y:



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

ARG LYS 963 V104 R121 M126 P127 S128 P129 E130 R131 D143 E148 R154 R162 M191 K192 R193 Y194 N195 L202 P203 Y204 L226 K230 L234 H240 L241 A242 E243 ALA GLN LYS SER SER LEU VAL

- Molecule 39: 39S ribosomal protein L30, mitochondrial

Chain Z:



MET ALA GLY ILE LEU ARG LEU VAL TRP VAL TRP MET GLN TRP LYS PRO PRO GLY ARG ALA LEU GLN THR VAL THR LYS GLY VAL GLU SER LEU ILE CYS THR ASP TRP ILE ARG HIS K35 F36 H53 H64 K65 L66 H67 R77 R78 P79 V99 S105 L122 M134 E155 Q156 LYS ALA

HIS
GLU
SER

- Molecule 40: 39S ribosomal protein L42, mitochondrial

Chain a:



MET ALA VAL ALA ALA VAL LYS VAL VAL VAL MET SER LYS THR THR ILE LEU LYS HIS LEU PHE PRO VAL VAL GLN ASN GLY ALA LEU TYR CYS VAL CYS HIS LYS SER T35 Y36 P40 D41 Y42 Y43 Y44 C45 Y46 L51 I58 H62 V65 R77 P78 D79 PRO VAL HIS ASN

ASN GLU GLU THR H88 D89 K93 T94 R95 L96 E97 E98 K99 V100 E104 P107 R142

- Molecule 41: 39S ribosomal protein L43, mitochondrial

Chain b:



MET T2 A3 R4 L11 L26 Q27 R28 L29 S30 S34 R35 D36 G42 A43 R44 R49 E50 E59 V72 V75 V76 A77 E78 H90 C91 K92 S93 V94 A105 S125 I126 Q127 N135 K136 Q149 D150 PRO ALA PRO PRO ALA ALA GLN ASP THR THR GLY LEU ARG LEU SER

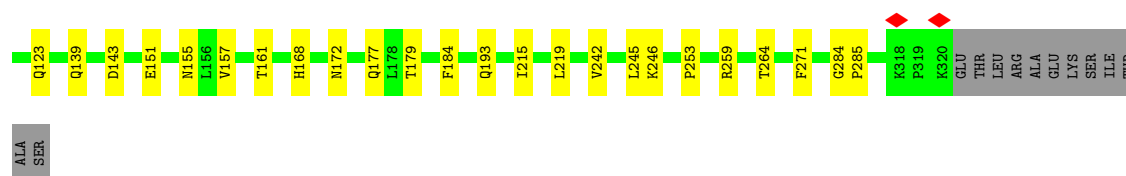
ALA VAL ALA PRO PRO GLE LEU LEU PRO PRO GLN TRP MET PRO ASP PRO ASP LEU LEU THR THR ASP VAL ASP ILE SER SER SER LEU THR VAL PRO PRO VAL V31 E44 Q48 R52 P57 E71 F92 E102 A103 K104 Q107 L108 G109 I110 GLU LYS GLU ALA V115 L116 L117 N118

- Molecule 42: 39S ribosomal protein L44, mitochondrial

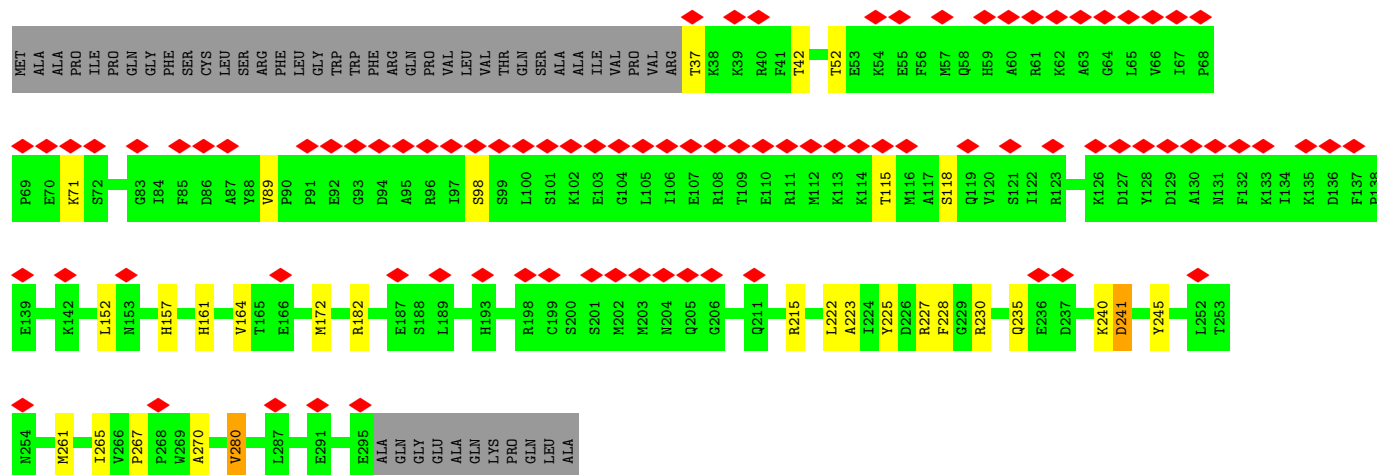
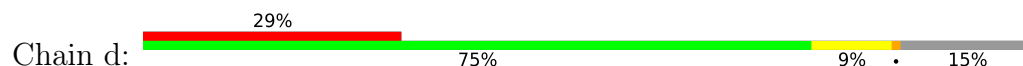
Chain c:



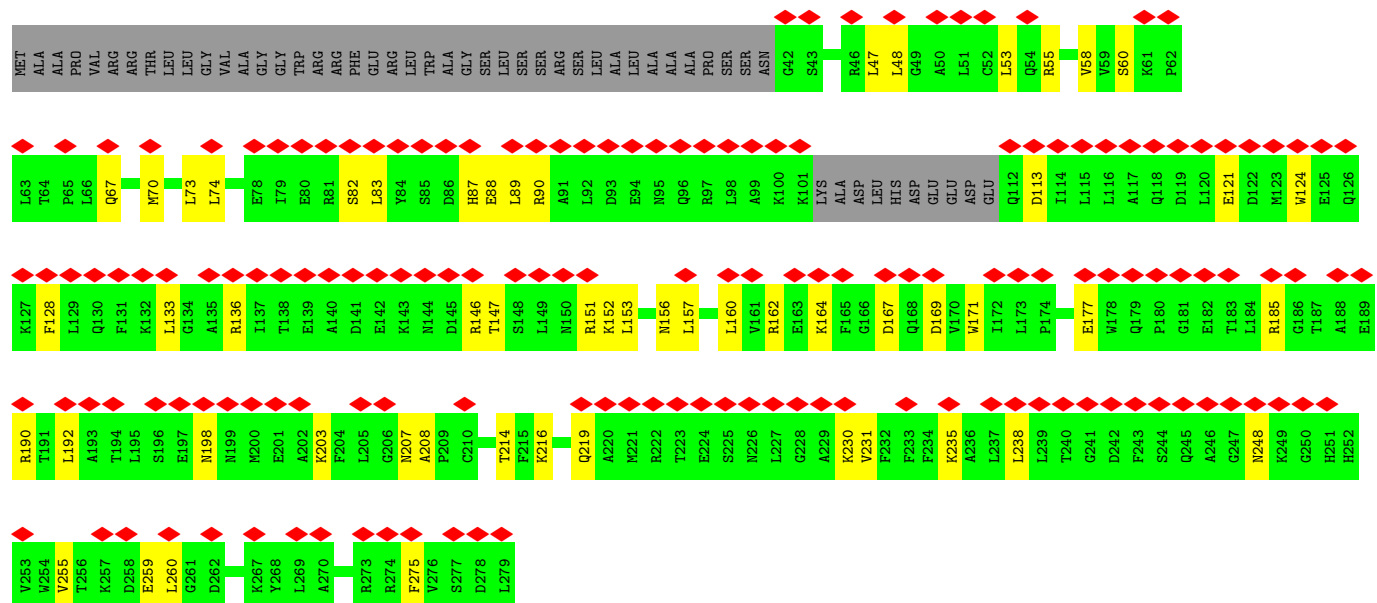
MET ALA SER GLY LEU VAL ARG LEU LEU LEU GLN GLN GLY HIS ARG CYS LEU LEU LEU ALA PRO VAL VAL ALA PRO PRO LYS LEU VAL PRO PRO VAL ARG GLY V31 E44 Q48 R52 P57 E71 F92 E102 A103 K104 Q107 L108 G109 I110 GLU LYS GLU ALA V115 L116 L117 N118



- Molecule 43: 39S ribosomal protein L45, mitochondrial

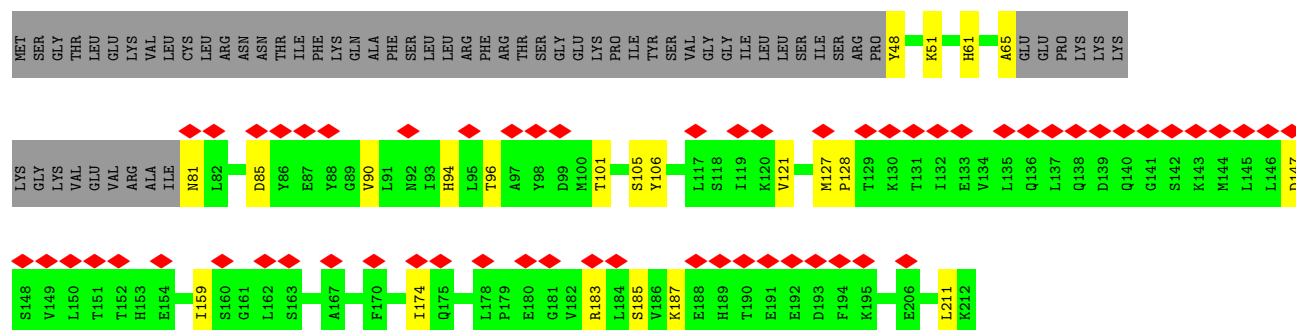


- Molecule 44: 39S ribosomal protein L46, mitochondrial

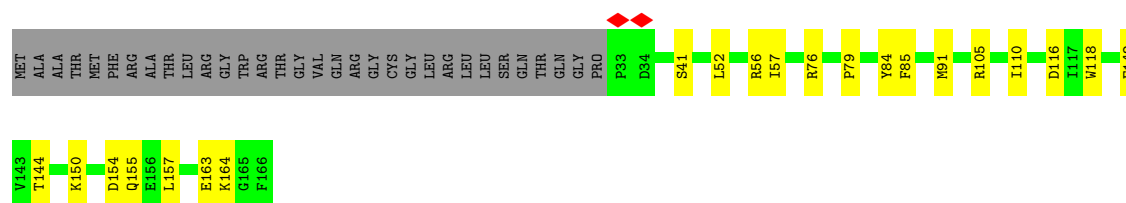


- Molecule 45: 39S ribosomal protein L48, mitochondrial

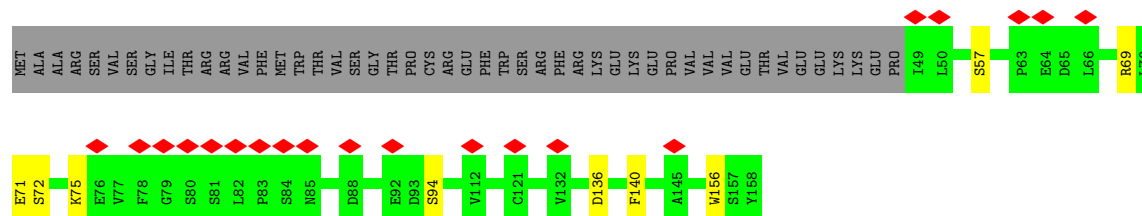




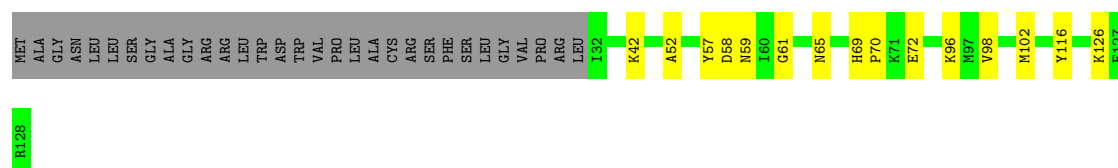
- Molecule 46: 39S ribosomal protein L49, mitochondrial



- Molecule 47: 39S ribosomal protein L50, mitochondrial



- Molecule 48: 39S ribosomal protein L51, mitochondrial



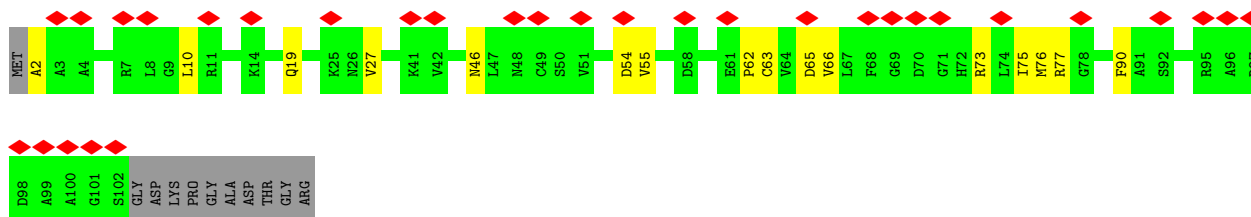
- Molecule 49: 39S ribosomal protein L52, mitochondrial



LEU
PRO
SER
GLN

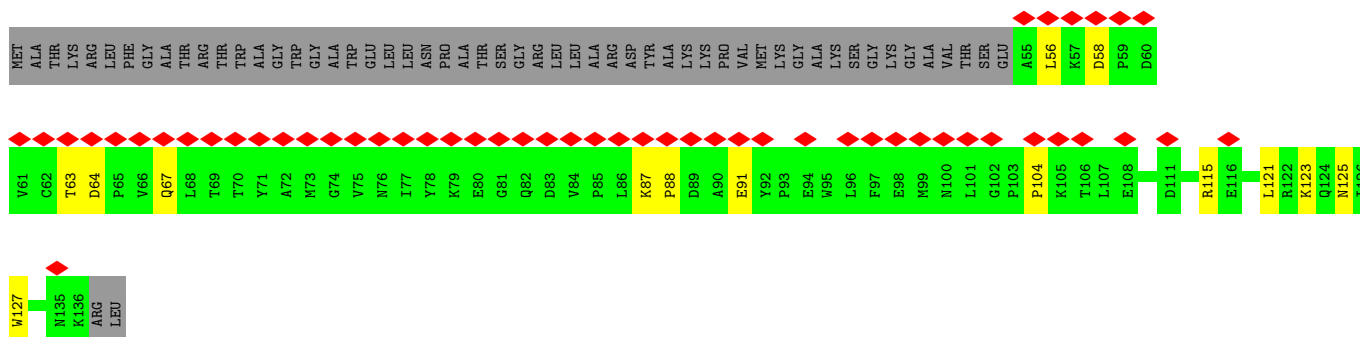
- Molecule 50: 39S ribosomal protein L53, mitochondrial

Chain k: 



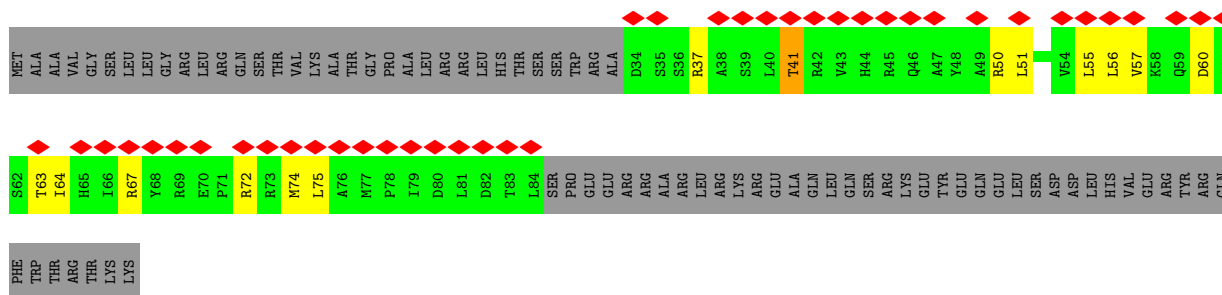
- Molecule 51: 39S ribosomal protein L54, mitochondrial

Chain l: 



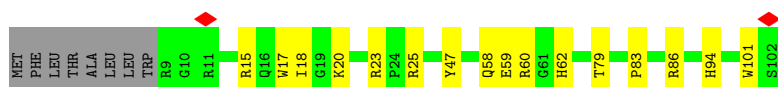
- Molecule 52: 39S ribosomal protein L55, mitochondrial

Chain m: 

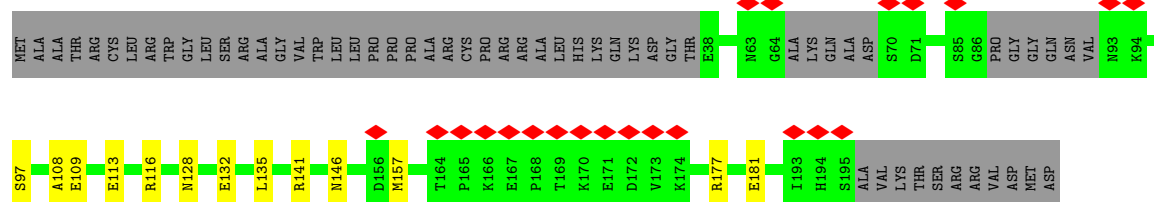


- Molecule 53: Ribosomal protein 63, mitochondrial

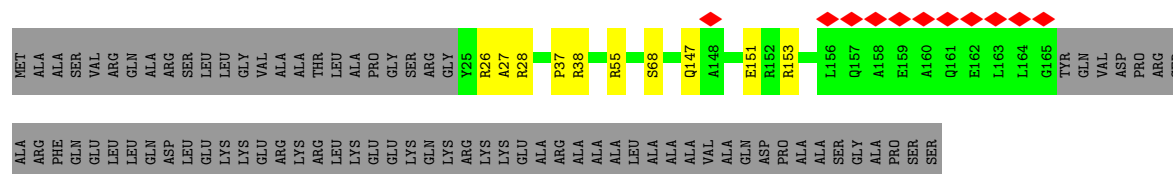
Chain o: 



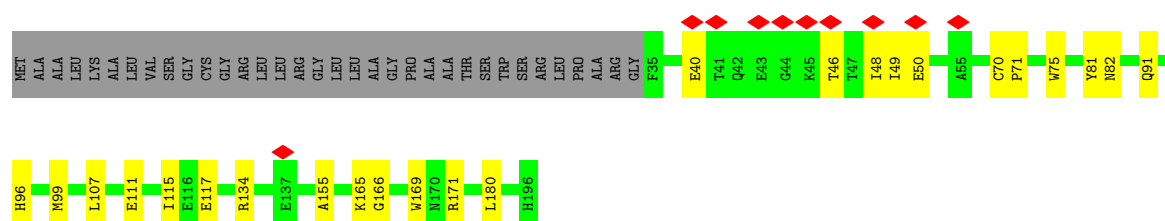
- Molecule 54: Peptidyl-tRNA hydrolase ICT1, mitochondrial



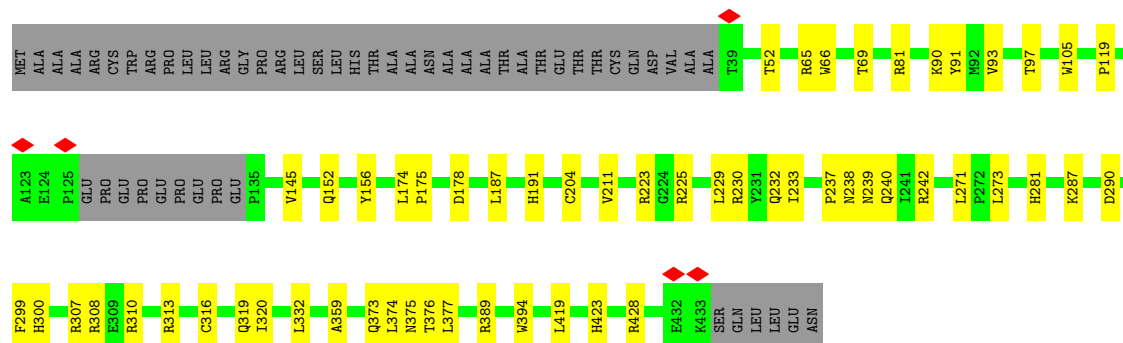
- Molecule 55: Growth arrest and DNA damage-inducible proteins-interacting protein 1



- Molecule 56: 39S ribosomal protein S18a, mitochondrial



- Molecule 57: 39S ribosomal protein S30, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	123267	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.222	Depositor
Minimum map value	-1.532	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.118	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	474.87997, 474.87997, 474.87997	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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, SAC, THC, K, SAM, FES, PM8, AYA, 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	u	0.10	0/941	0.28	0/1270
2	v	0.09	0/597	0.24	0/796
3	w	0.09	0/647	0.28	0/871
4	x	0.10	0/2721	0.28	0/3691
5	y	0.08	0/2011	0.22	0/2702
6	0	0.09	0/913	0.24	0/1224
7	1	0.08	0/460	0.23	0/610
8	2	0.11	0/383	0.24	0/507
9	3	0.11	0/853	0.25	0/1136
10	4	0.10	0/350	0.24	0/461
11	5	0.11	0/3305	0.27	0/4502
12	6	0.11	0/3043	0.27	0/4140
13	7	0.10	0/2447	0.25	0/3310
14	8	0.10	0/880	0.24	0/1188
15	9	0.12	0/1025	0.26	0/1379
16	A	0.09	0/33664	0.16	0/52392
17	B	0.05	0/1700	0.09	0/2641
18	D	0.11	0/1910	0.27	0/2569
19	E	0.11	0/2475	0.26	0/3355
20	F	0.11	0/2090	0.28	0/2842
21	H	0.11	0/816	0.27	0/1097
22	I	0.11	0/1354	0.30	0/1829
23	J	0.09	0/1348	0.28	0/1813
24	K	0.11	0/1490	0.28	0/2021
25	L	0.11	0/905	0.30	0/1218
26	M	0.11	0/2381	0.28	1/3212 (0.0%)
27	N	0.09	0/1768	0.24	0/2383
28	O	0.11	0/1283	0.27	0/1727
29	P	0.10	0/1199	0.27	0/1623
30	Q	0.10	0/1884	0.26	0/2535
31	R	0.10	0/1175	0.24	0/1572
32	S	0.12	0/1320	0.30	0/1789

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	T	0.11	0/1403	0.27	0/1886
34	U	0.11	0/1274	0.27	0/1723
35	V	0.10	0/1721	0.23	0/2333
36	W	0.12	0/857	0.27	0/1155
37	X	0.09	0/2099	0.24	0/2837
38	Y	0.09	0/1593	0.24	0/2136
39	Z	0.11	0/1021	0.27	0/1378
40	a	0.10	0/866	0.25	0/1174
41	b	0.12	0/1203	0.29	0/1627
42	c	0.09	0/2347	0.25	0/3171
43	d	0.10	0/2181	0.26	0/2949
44	e	0.08	0/1885	0.26	0/2542
45	f	0.09	0/1216	0.27	0/1638
46	g	0.12	0/1151	0.29	0/1569
47	h	0.09	0/918	0.23	0/1249
48	i	0.11	0/850	0.25	0/1135
49	j	0.10	0/760	0.24	0/1023
50	k	0.09	0/777	0.23	0/1048
51	l	0.10	0/707	0.27	0/960
52	m	0.08	0/426	0.24	0/575
53	o	0.08	0/819	0.22	0/1097
54	p	0.09	0/1223	0.23	0/1641
55	q	0.08	0/1208	0.20	0/1633
56	r	0.10	0/1362	0.26	0/1846
57	s	0.11	0/3239	0.27	0/4400
All	All	0.10	0/112444	0.23	1/159130 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	M	54	LYS	CB-CA-C	-5.03	109.80	115.79

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	u	919	0	917	13	0
2	v	588	0	604	13	0
3	w	638	0	636	8	0
4	x	2660	0	2640	43	0
5	y	1980	0	2066	33	0
6	0	898	0	916	9	0
7	1	455	0	498	4	0
8	2	377	0	406	2	0
9	3	832	0	883	10	0
10	4	342	0	361	6	0
11	5	3210	0	3206	34	0
12	6	2948	0	2841	56	0
13	7	2390	0	2397	32	0
14	8	860	0	852	15	0
15	9	997	0	987	13	0
16	A	30460	0	15537	256	0
17	B	1522	0	776	13	0
18	D	1872	0	1932	30	0
19	E	2406	0	2415	26	0
20	F	2031	0	2065	44	0
21	H	802	0	846	14	0
22	I	1324	0	1400	16	0
23	J	1330	0	1407	8	0
24	K	1455	0	1452	15	0
25	L	890	0	941	16	0
26	M	2327	0	2395	23	0
27	N	1723	0	1754	15	0
28	O	1259	0	1294	17	0
29	P	1173	0	1165	21	0
30	Q	1843	0	1878	25	0
31	R	1154	0	1214	12	0
32	S	1293	0	1365	15	0
33	T	1369	0	1410	15	0
34	U	1251	0	1232	15	0
35	V	1676	0	1687	20	0
36	W	835	0	858	7	0
37	X	2044	0	2060	15	0
38	Y	1556	0	1597	17	0
39	Z	996	0	1044	8	0
40	a	840	0	810	11	0
41	b	1189	0	1183	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	c	2299	0	2320	17	0
43	d	2124	0	2125	22	0
44	e	1848	0	1849	39	0
45	f	1196	0	1212	13	0
46	g	1113	0	1097	15	0
47	h	895	0	881	5	0
48	i	828	0	857	15	0
49	j	745	0	746	13	0
50	k	774	0	784	12	0
51	l	688	0	674	9	0
52	m	419	0	435	16	0
53	o	798	0	804	18	0
54	p	1205	0	1223	9	0
55	q	1177	0	1154	8	0
56	r	1322	0	1348	20	0
57	s	3155	0	3139	34	0
58	w	32	0	39	5	0
59	x	27	0	22	0	0
60	0	1	0	0	0	0
60	4	1	0	0	0	0
61	9	1	0	0	0	0
61	A	92	0	0	0	0
61	D	1	0	0	0	0
61	M	1	0	0	0	0
61	O	1	0	0	0	0
61	g	1	0	0	0	0
62	A	2	0	0	0	0
63	r	4	0	0	0	0
All	All	107464	0	92636	961	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 961 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:A:2499:U:OP2	16:A:2504:A:N6	2.18	0.76
40:a:41:ASP:HB3	40:a:46:ASN:HD22	1.51	0.75
5:y:162:ARG:NH1	5:y:186:ILE:O	2.19	0.74
4:x:258:CYS:SG	4:x:316:GLN:NE2	2.62	0.73
2:v:45:LEU:HD23	2:v:50:ALA:HB1	1.71	0.72

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	u	108/234 (46%)	104 (96%)	4 (4%)	0	100	100
2	v	67/70 (96%)	67 (100%)	0	0	100	100
3	w	77/156 (49%)	73 (95%)	4 (5%)	0	100	100
4	x	332/384 (86%)	328 (99%)	4 (1%)	0	100	100
5	y	242/381 (64%)	240 (99%)	2 (1%)	0	100	100
6	0	108/188 (57%)	108 (100%)	0	0	100	100
7	1	53/65 (82%)	52 (98%)	1 (2%)	0	100	100
8	2	44/92 (48%)	42 (96%)	2 (4%)	0	100	100
9	3	93/188 (50%)	92 (99%)	1 (1%)	0	100	100
10	4	36/103 (35%)	36 (100%)	0	0	100	100
11	5	392/423 (93%)	389 (99%)	3 (1%)	0	100	100
12	6	352/380 (93%)	346 (98%)	6 (2%)	0	100	100
13	7	292/338 (86%)	287 (98%)	5 (2%)	0	100	100
14	8	100/206 (48%)	100 (100%)	0	0	100	100
15	9	122/137 (89%)	121 (99%)	1 (1%)	0	100	100
18	D	238/305 (78%)	234 (98%)	4 (2%)	0	100	100
19	E	303/348 (87%)	298 (98%)	4 (1%)	1 (0%)	36	65
20	F	250/311 (80%)	248 (99%)	2 (1%)	0	100	100
21	H	95/267 (36%)	94 (99%)	1 (1%)	0	100	100
22	I	161/261 (62%)	159 (99%)	2 (1%)	0	100	100
23	J	173/192 (90%)	172 (99%)	1 (1%)	0	100	100
24	K	175/178 (98%)	174 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	L	113/145 (78%)	113 (100%)	0	0	100	100
26	M	289/296 (98%)	287 (99%)	2 (1%)	0	100	100
27	N	208/251 (83%)	206 (99%)	2 (1%)	0	100	100
28	O	152/175 (87%)	150 (99%)	2 (1%)	0	100	100
29	P	142/180 (79%)	138 (97%)	4 (3%)	0	100	100
30	Q	219/292 (75%)	219 (100%)	0	0	100	100
31	R	138/149 (93%)	137 (99%)	1 (1%)	0	100	100
32	S	159/205 (78%)	159 (100%)	0	0	100	100
33	T	164/206 (80%)	164 (100%)	0	0	100	100
34	U	150/153 (98%)	148 (99%)	2 (1%)	0	100	100
35	V	203/216 (94%)	202 (100%)	1 (0%)	0	100	100
36	W	104/148 (70%)	102 (98%)	2 (2%)	0	100	100
37	X	242/256 (94%)	241 (100%)	1 (0%)	0	100	100
38	Y	179/250 (72%)	178 (99%)	1 (1%)	0	100	100
39	Z	120/161 (74%)	118 (98%)	2 (2%)	0	100	100
40	a	96/142 (68%)	95 (99%)	1 (1%)	0	100	100
41	b	147/215 (68%)	145 (99%)	2 (1%)	0	100	100
42	c	282/332 (85%)	280 (99%)	2 (1%)	0	100	100
43	d	257/306 (84%)	255 (99%)	2 (1%)	0	100	100
44	e	224/279 (80%)	219 (98%)	5 (2%)	0	100	100
45	f	146/212 (69%)	143 (98%)	3 (2%)	0	100	100
46	g	132/166 (80%)	131 (99%)	1 (1%)	0	100	100
47	h	108/158 (68%)	106 (98%)	2 (2%)	0	100	100
48	i	95/128 (74%)	95 (100%)	0	0	100	100
49	j	92/123 (75%)	92 (100%)	0	0	100	100
50	k	99/112 (88%)	97 (98%)	2 (2%)	0	100	100
51	l	80/138 (58%)	80 (100%)	0	0	100	100
52	m	49/128 (38%)	49 (100%)	0	0	100	100
53	o	92/102 (90%)	92 (100%)	0	0	100	100
54	p	141/206 (68%)	139 (99%)	2 (1%)	0	100	100
55	q	139/222 (63%)	139 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	r	160/196 (82%)	158 (99%)	2 (1%)	0	100	100
57	s	382/439 (87%)	374 (98%)	8 (2%)	0	100	100
All	All	9116/11894 (77%)	9015 (99%)	100 (1%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	E	150	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	
1	u	104/200 (52%)	101 (97%)	3 (3%)	37	71
2	v	59/60 (98%)	59 (100%)	0	100	100
3	w	73/136 (54%)	73 (100%)	0	100	100
4	x	291/328 (89%)	288 (99%)	3 (1%)	68	89
5	y	226/350 (65%)	225 (100%)	1 (0%)	84	94
6	0	99/164 (60%)	99 (100%)	0	100	100
7	1	52/60 (87%)	51 (98%)	1 (2%)	50	79
8	2	40/72 (56%)	40 (100%)	0	100	100
9	3	88/166 (53%)	87 (99%)	1 (1%)	65	88
10	4	37/89 (42%)	37 (100%)	0	100	100
11	5	353/368 (96%)	352 (100%)	1 (0%)	86	96
12	6	313/332 (94%)	311 (99%)	2 (1%)	78	93
13	7	270/303 (89%)	269 (100%)	1 (0%)	84	94
14	8	93/190 (49%)	93 (100%)	0	100	100
15	9	104/112 (93%)	104 (100%)	0	100	100
18	D	194/245 (79%)	194 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	E	260/290 (90%)	260 (100%)	0	100	100
20	F	219/262 (84%)	219 (100%)	0	100	100
21	H	88/228 (39%)	87 (99%)	1 (1%)	65	88
22	I	151/232 (65%)	151 (100%)	0	100	100
23	J	138/150 (92%)	138 (100%)	0	100	100
24	K	154/155 (99%)	153 (99%)	1 (1%)	78	93
25	L	98/124 (79%)	98 (100%)	0	100	100
26	M	246/249 (99%)	244 (99%)	2 (1%)	73	90
27	N	185/211 (88%)	183 (99%)	2 (1%)	65	88
28	O	134/150 (89%)	134 (100%)	0	100	100
29	P	126/155 (81%)	125 (99%)	1 (1%)	73	90
30	Q	203/256 (79%)	202 (100%)	1 (0%)	81	93
31	R	118/126 (94%)	118 (100%)	0	100	100
32	S	146/180 (81%)	146 (100%)	0	100	100
33	T	146/176 (83%)	146 (100%)	0	100	100
34	U	134/135 (99%)	132 (98%)	2 (2%)	57	84
35	V	183/191 (96%)	180 (98%)	3 (2%)	55	83
36	W	86/119 (72%)	85 (99%)	1 (1%)	63	86
37	X	220/229 (96%)	220 (100%)	0	100	100
38	Y	163/223 (73%)	163 (100%)	0	100	100
39	Z	113/147 (77%)	112 (99%)	1 (1%)	70	90
40	a	96/133 (72%)	96 (100%)	0	100	100
41	b	130/185 (70%)	129 (99%)	1 (1%)	73	90
42	c	251/288 (87%)	251 (100%)	0	100	100
43	d	237/274 (86%)	234 (99%)	3 (1%)	61	86
44	e	198/236 (84%)	198 (100%)	0	100	100
45	f	133/188 (71%)	132 (99%)	1 (1%)	73	90
46	g	124/148 (84%)	124 (100%)	0	100	100
47	h	104/148 (70%)	104 (100%)	0	100	100
48	i	86/110 (78%)	86 (100%)	0	100	100
49	j	74/97 (76%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	k	83/90 (92%)	83 (100%)	0	100	100
51	l	76/116 (66%)	75 (99%)	1 (1%)	61	86
52	m	46/113 (41%)	45 (98%)	1 (2%)	45	77
53	o	80/87 (92%)	80 (100%)	0	100	100
54	p	135/181 (75%)	135 (100%)	0	100	100
55	q	119/178 (67%)	119 (100%)	0	100	100
56	r	147/169 (87%)	147 (100%)	0	100	100
57	s	340/381 (89%)	339 (100%)	1 (0%)	86	96
All	All	8166/10285 (79%)	8130 (100%)	36 (0%)	81	94

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	b	75	VAL
57	s	97	THR
43	d	89	VAL
45	f	211	LEU
13	7	234	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 97 such sidechains are listed below:

Mol	Chain	Res	Type
35	V	73	GLN
43	d	157	HIS
37	X	89	GLN
40	a	46	ASN
44	e	75	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	A	1409/1590 (88%)	246 (17%)	1 (0%)
17	B	71/72 (98%)	13 (18%)	0
All	All	1480/1662 (89%)	259 (17%)	1 (0%)

5 of 259 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
16	A	1689	C
16	A	1693	C
16	A	1699	C
16	A	1700	U
16	A	1704	U

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	A	2030	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
24	SAC	K	2	24	7,8,9	1.04	0	7,9,11	0.90	0
50	AYA	k	2	50	6,7,8	1.24	1 (16%)	6,8,10	1.18	1 (16%)
41	THC	b	2	41	8,9,10	1.10	1 (12%)	10,11,13	1.28	2 (20%)
34	AYA	U	2	34	6,7,8	1.30	1 (16%)	6,8,10	1.09	1 (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
24	SAC	K	2	24	-	2/7/8/10	-
50	AYA	k	2	50	-	1/5/6/8	-
41	THC	b	2	41	-	0/9/10/12	-
34	AYA	U	2	34	-	0/5/6/8	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	U	2	AYA	CA-N	-2.50	1.43	1.46
41	b	2	THC	CA-N1	-2.22	1.43	1.46
50	k	2	AYA	CA-N	-2.20	1.44	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	k	2	AYA	CB-CA-N	2.61	112.63	109.68
34	U	2	AYA	CB-CA-N	2.48	112.48	109.68
41	b	2	THC	CB-CA-C	-2.44	107.51	111.55
41	b	2	THC	C-CA-N1	2.41	113.60	109.80

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	K	2	SAC	N-CA-CB-OG
24	K	2	SAC	C-CA-CB-OG
50	k	2	AYA	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
41	b	2	THC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 104 ligands modelled in this entry, 101 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
59	SAM	x	401	-	27,29,29	1.11	4 (14%)	34,42,42	2.01	8 (23%)
63	FES	r	201	56,22	0,4,4	-	-	-		
58	PM8	w	200	3	26,31,31	0.25	0	30,38,38	0.43	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	SAM	x	401	-	-	8/17/33/33	0/3/3/3
63	FES	r	201	56,22	-	-	0/1/1/1
58	PM8	w	200	3	-	13/36/38/38	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	x	401	SAM	C2-N3	2.60	1.38	1.33
59	x	401	SAM	C2-N1	2.56	1.38	1.33
59	x	401	SAM	OXT-C	-2.26	1.23	1.30
59	x	401	SAM	C8-N7	2.11	1.35	1.31

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	x	401	SAM	N3-C2-N1	-5.57	120.16	128.58
59	x	401	SAM	C5-C4-N3	-4.68	120.27	126.72
59	x	401	SAM	N9-C8-N7	-3.82	108.51	113.94
59	x	401	SAM	C2-N3-C4	3.48	120.34	111.83
59	x	401	SAM	C5-N7-C8	3.38	108.76	103.45

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

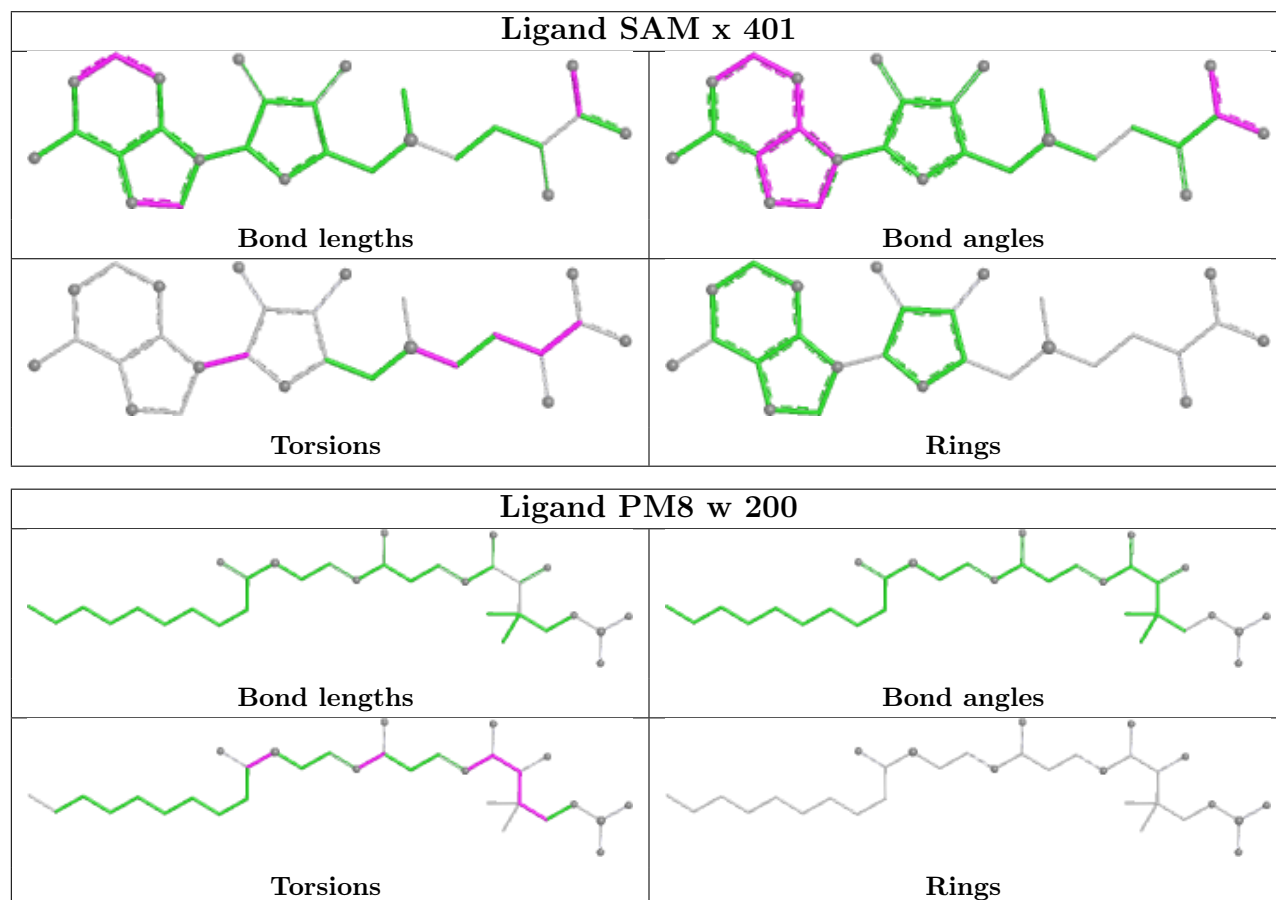
Mol	Chain	Res	Type	Atoms
58	w	200	PM8	O27-C28-C29-C30
58	w	200	PM8	O27-C28-C29-C31
58	w	200	PM8	O27-C28-C29-C32
58	w	200	PM8	C32-C34-N36-C37
58	w	200	PM8	O1-C1-S1-C43

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	w	200	PM8	5	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
16	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	3251:N	O3'	3252:N	P	17.10
1	A	3236:N	O3'	3237:N	P	13.81

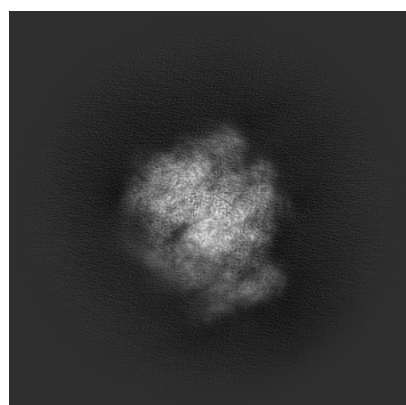
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12845. These allow visual inspection of the internal detail of the map and identification of artifacts.

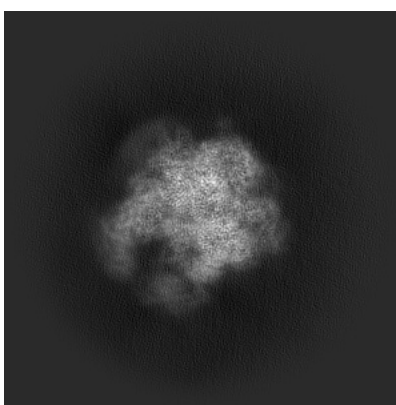
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

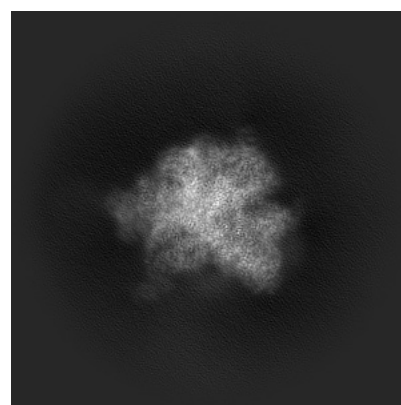
6.1.1 Primary map



X



Y

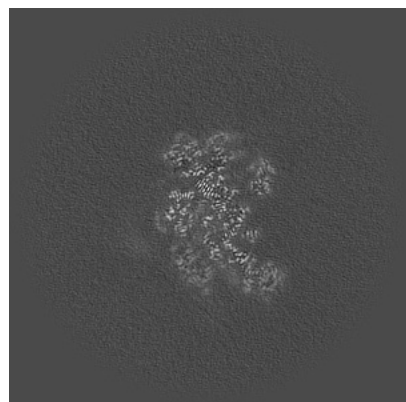


Z

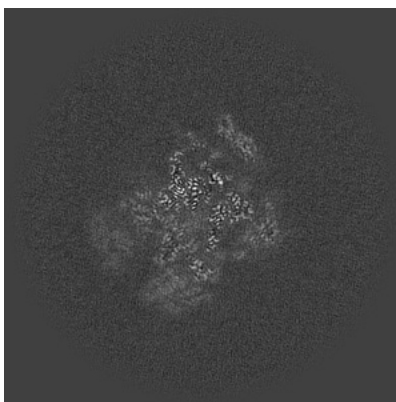
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

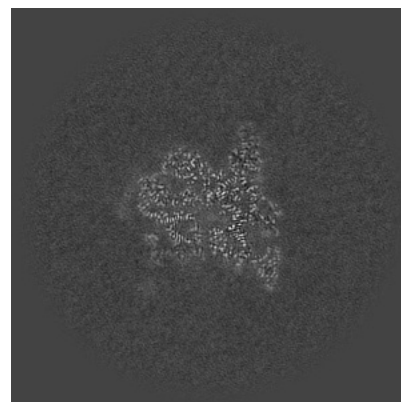
6.2.1 Primary map



X Index: 224



Y Index: 224

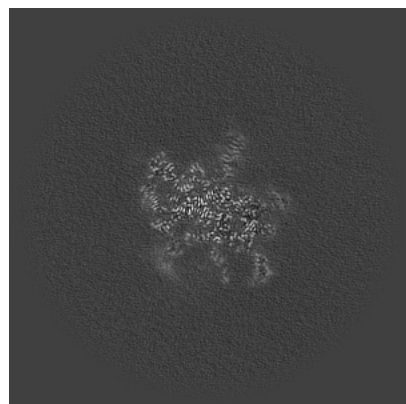


Z Index: 224

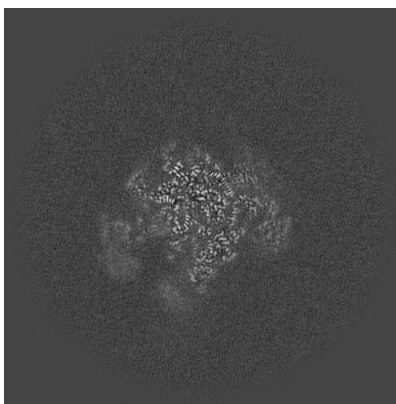
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

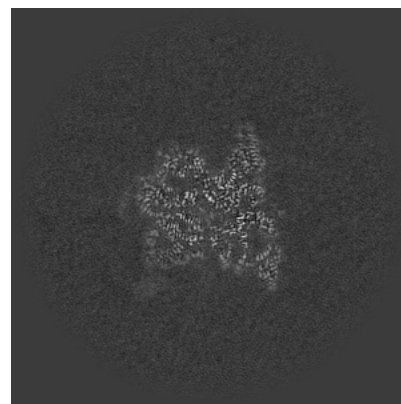
6.3.1 Primary map



X Index: 256



Y Index: 242

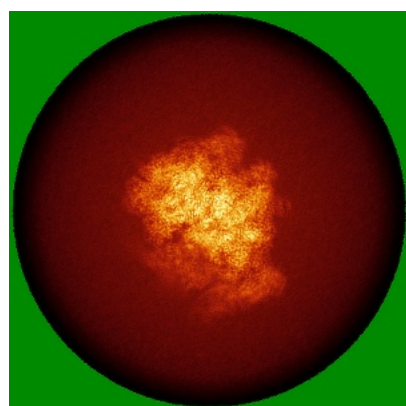


Z Index: 227

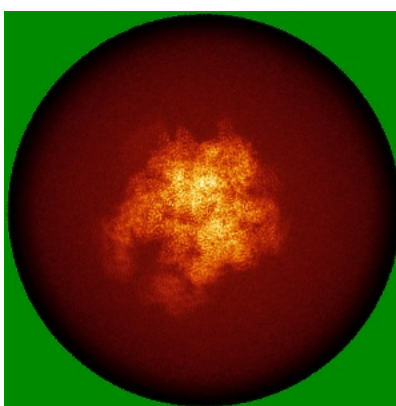
The images above show the largest variance slices of the map in three orthogonal directions.

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

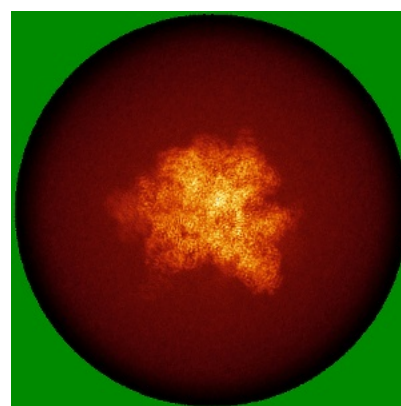
6.4.1 Primary map



X



Y

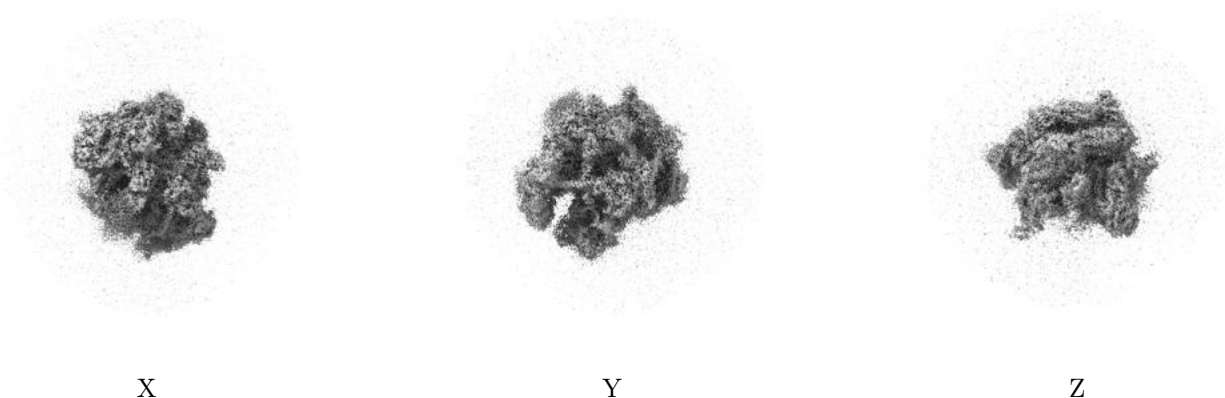


Z

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 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

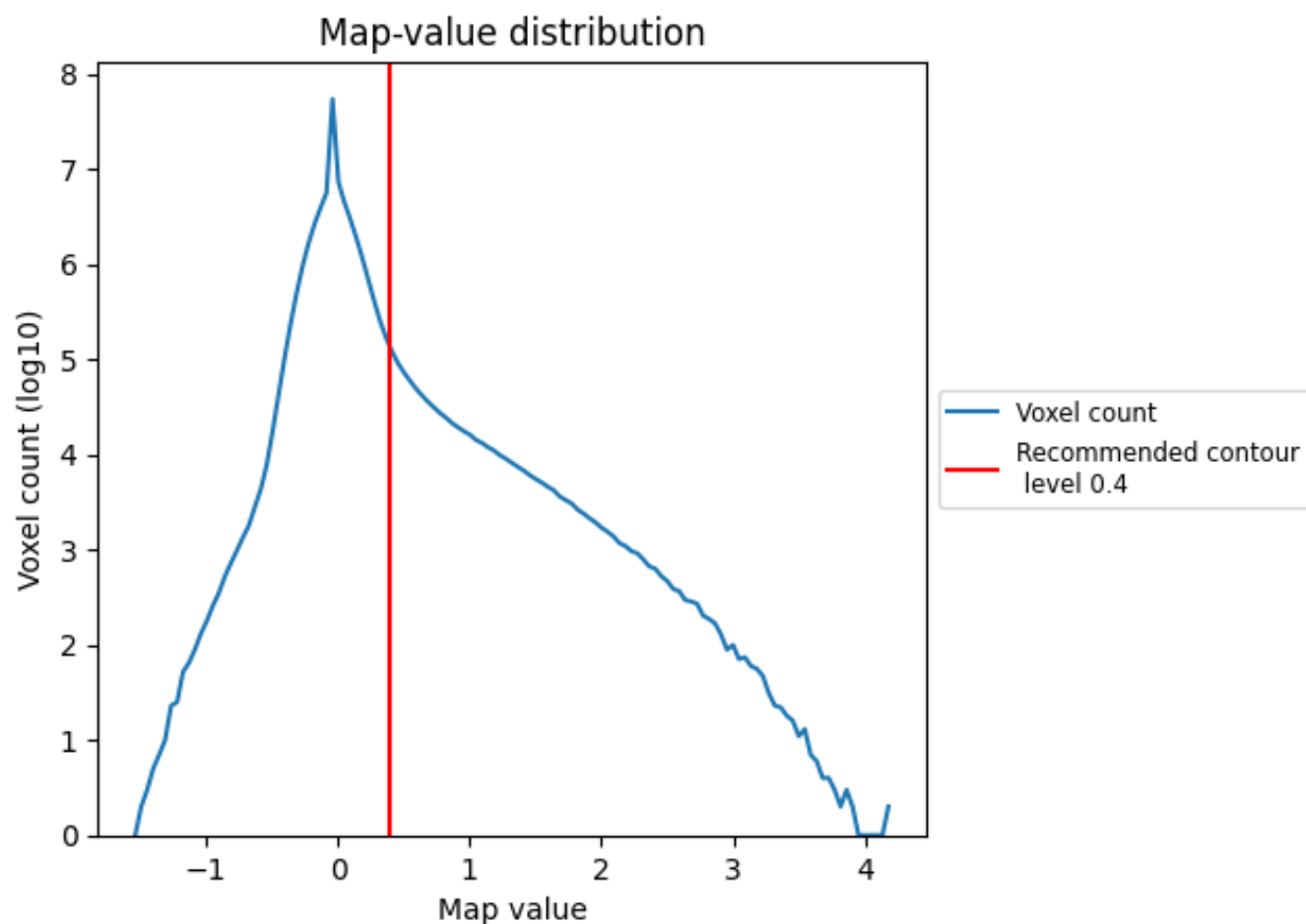
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

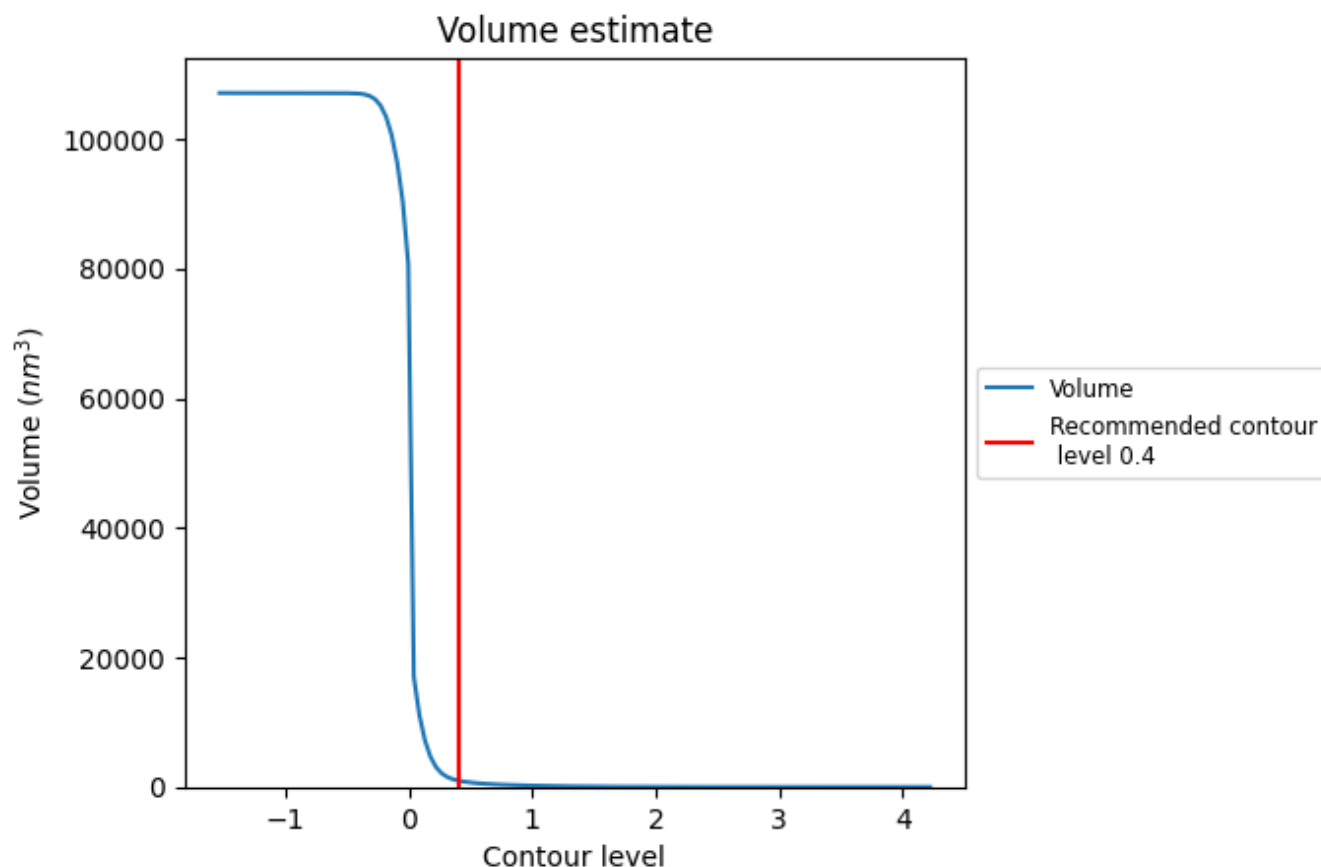
This section contains the results of statistical analysis of the map.

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.

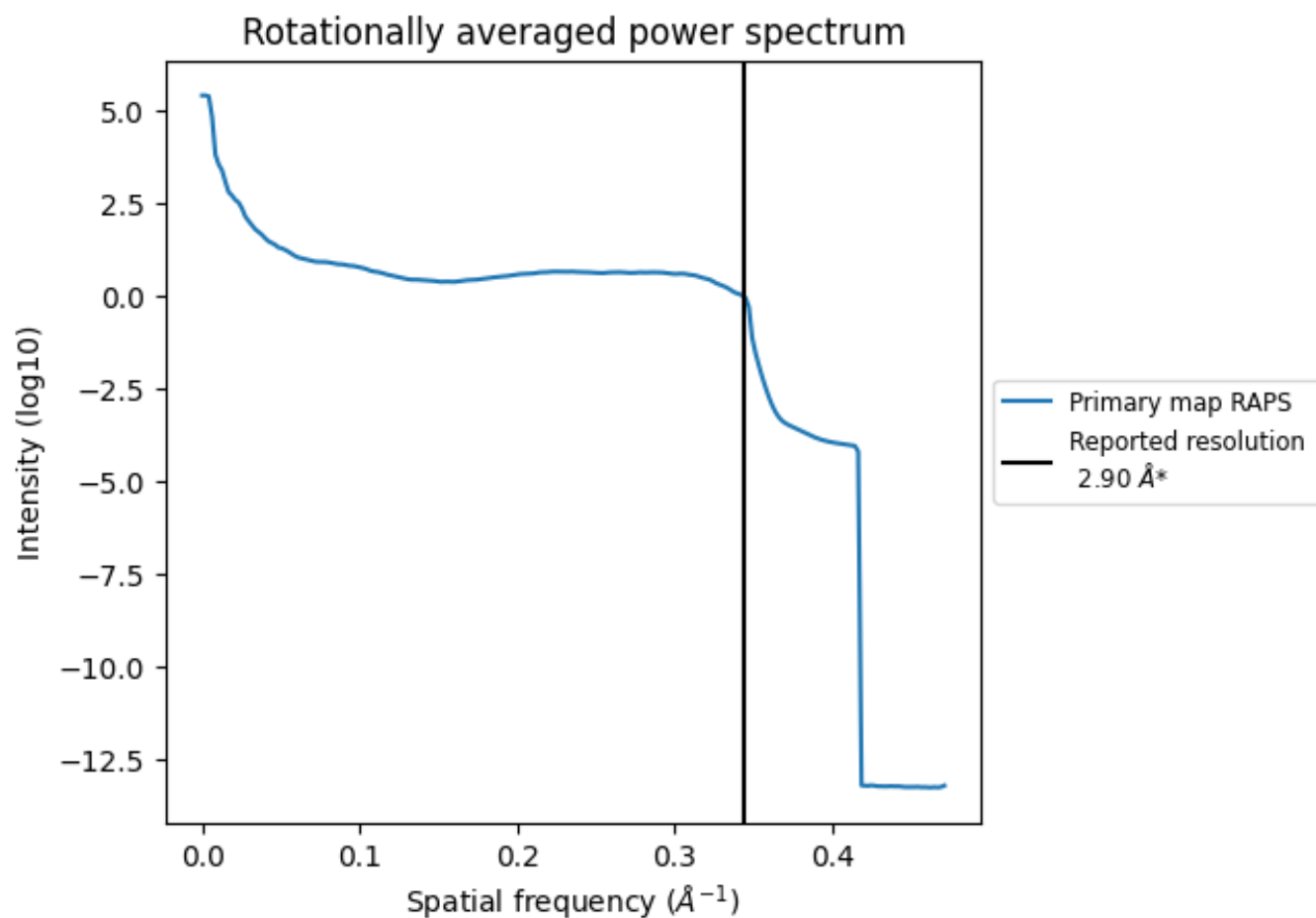
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 985 nm^3 ; this corresponds to an approximate mass of 890 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 0.345 Å⁻¹

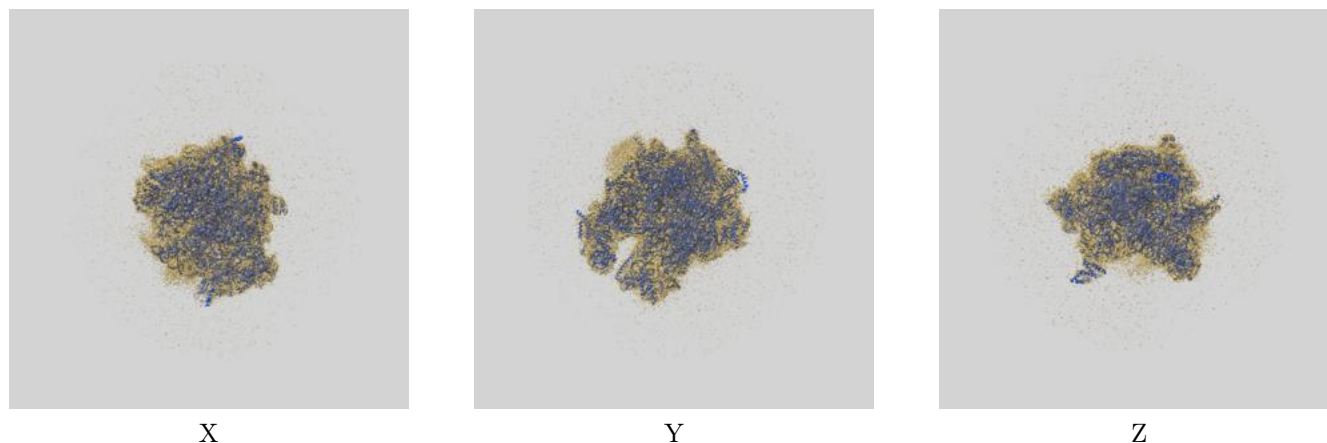
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

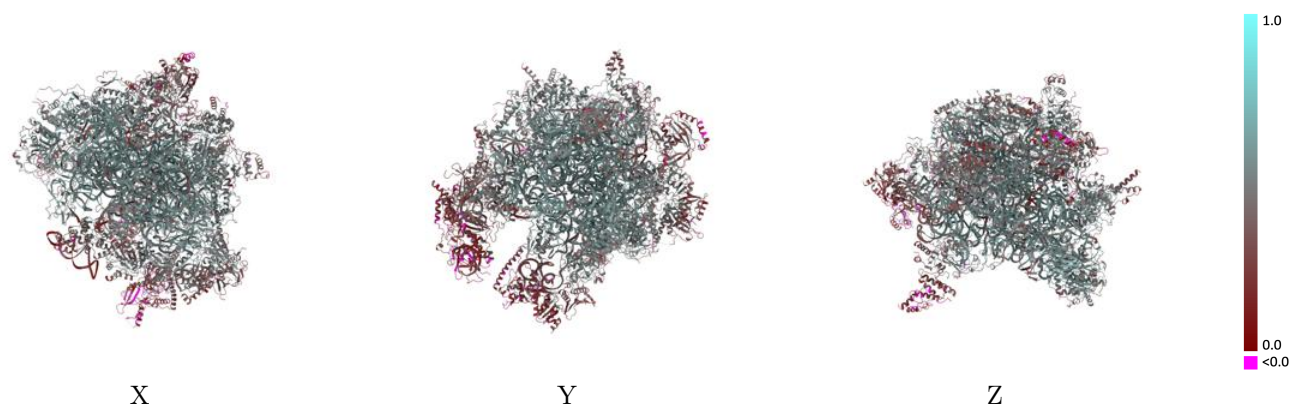
This section contains information regarding the fit between EMDB map EMD-12845 and PDB model 7ODR. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



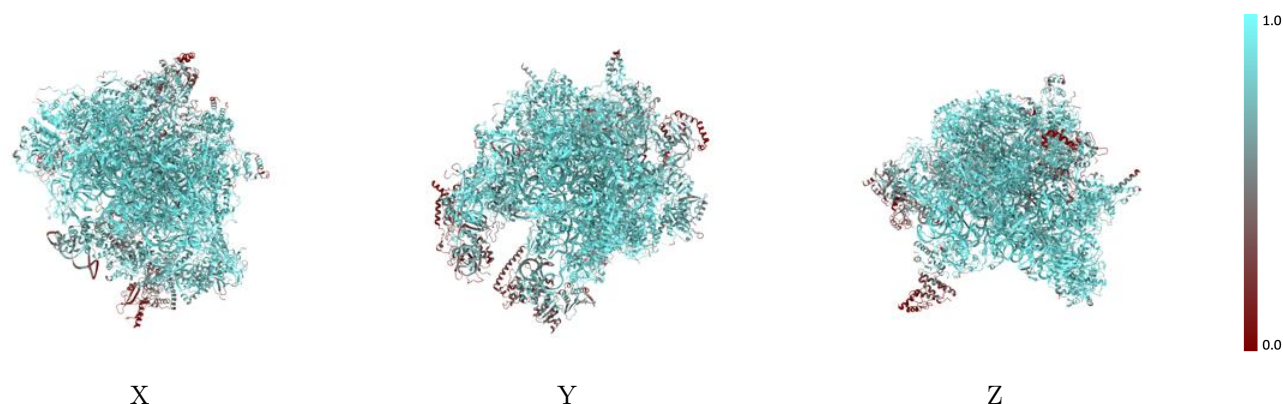
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



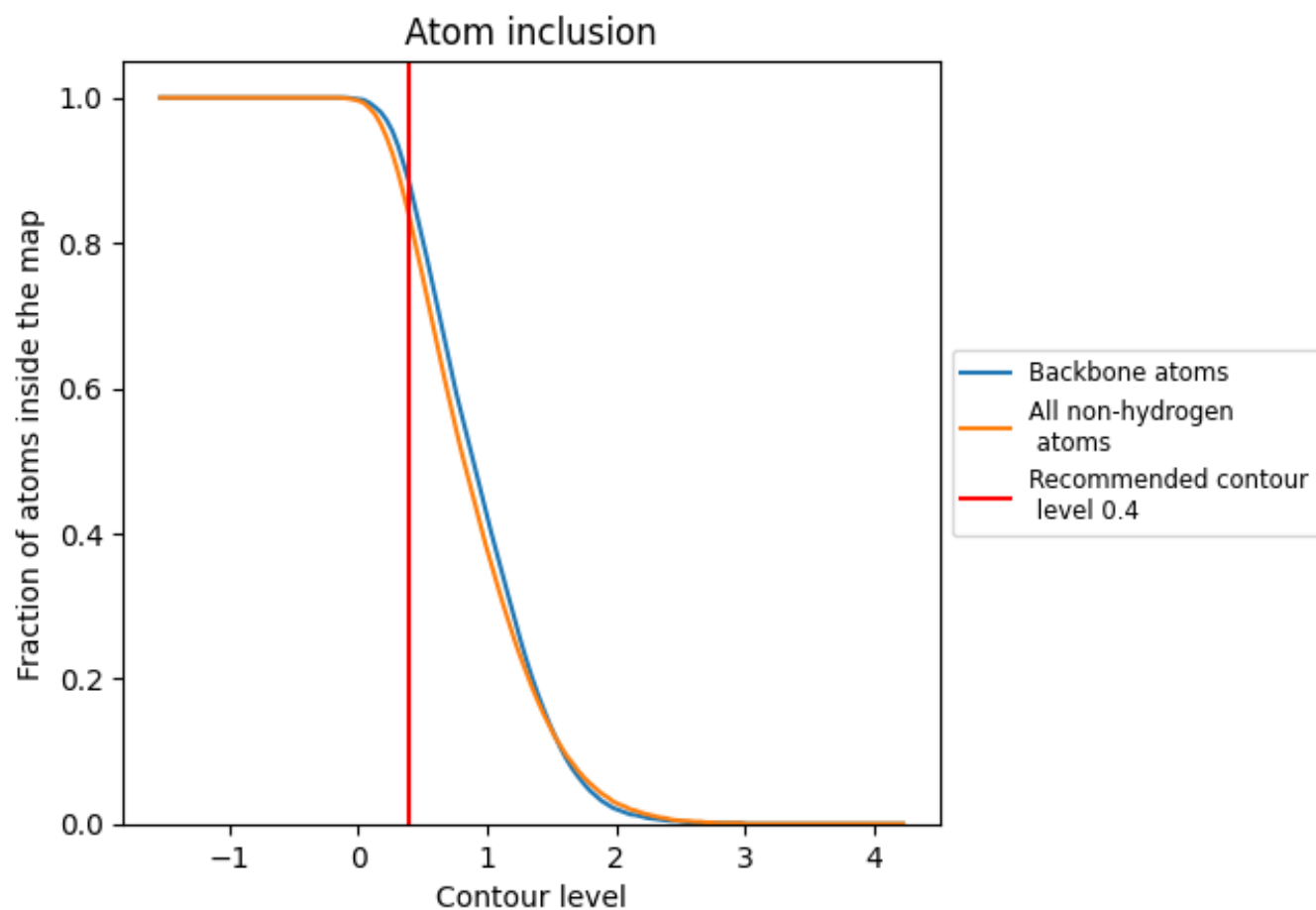
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 83% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8330	 0.4730
0	 0.8600	 0.5060
1	 0.8620	 0.5230
2	 0.9780	 0.6110
3	 0.9700	 0.5930
4	 0.9330	 0.5280
5	 0.8930	 0.5110
6	 0.8300	 0.4200
7	 0.7720	 0.3860
8	 0.4000	 0.2120
9	 0.8600	 0.4840
A	 0.9540	 0.5400
B	 0.7920	 0.2830
D	 0.8960	 0.5290
E	 0.9100	 0.5170
F	 0.8970	 0.5250
H	 0.8210	 0.4780
I	 0.5630	 0.2770
J	 0.2810	 0.1600
K	 0.9310	 0.5430
L	 0.8760	 0.4930
M	 0.9180	 0.5410
N	 0.8220	 0.4720
O	 0.9140	 0.5310
P	 0.8920	 0.4850
Q	 0.8820	 0.4920
R	 0.9320	 0.5610
S	 0.9160	 0.5270
T	 0.9100	 0.5450
U	 0.8100	 0.4800
V	 0.6370	 0.3980
W	 0.9300	 0.5690
X	 0.8610	 0.5120
Y	 0.8860	 0.5180
Z	 0.9070	 0.5550



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Chain	Atom inclusion	Q-score
a	 0.8070	 0.4750
b	 0.9100	 0.5330
c	 0.8340	 0.4610
d	 0.5190	 0.3270
e	 0.2960	 0.1340
f	 0.4860	 0.2730
g	 0.8990	 0.5160
h	 0.6780	 0.3880
i	 0.9490	 0.5720
j	 0.8660	 0.4880
k	 0.5290	 0.2690
l	 0.3600	 0.1960
m	 0.2680	 0.1890
o	 0.8910	 0.5140
p	 0.7180	 0.4100
q	 0.7890	 0.4370
r	 0.8510	 0.4860
s	 0.9060	 0.5320
u	 0.6770	 0.3790
v	 0.2930	 0.2360
w	 0.0680	 0.1330
x	 0.8160	 0.4410
y	 0.7570	 0.4190