



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 10:36 AM UTC

PDB ID : 9CN3 / pdb_00009cn3
EMDB ID : EMD-45757
Title : Human 39S mitoribosome in complex with antibiotic Linezolid
Authors : Raskar, T.; Bibel, B.; Galonic Fujimori, D.; Fraser, J.
Deposited on : 2024-07-15
Resolution : 2.62 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

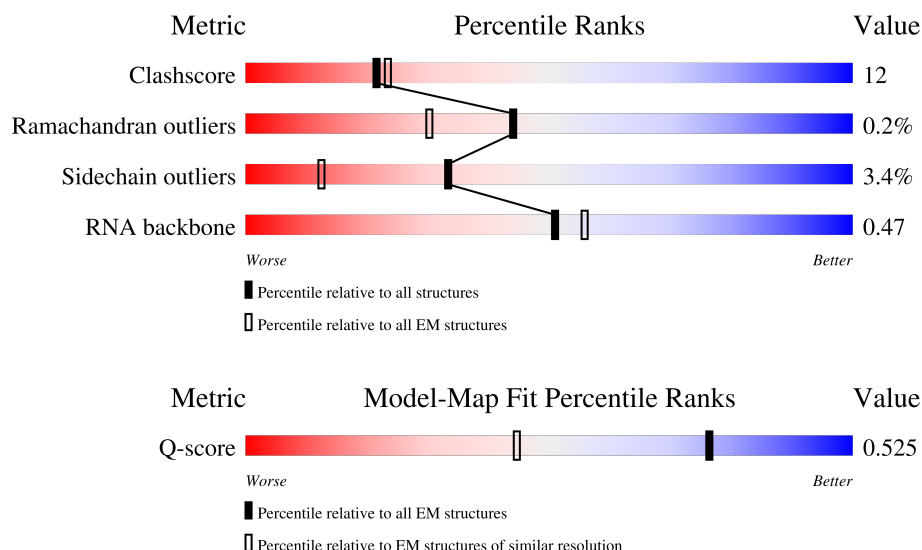
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.62 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.



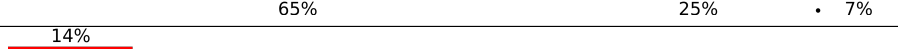
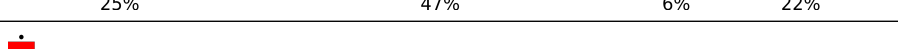
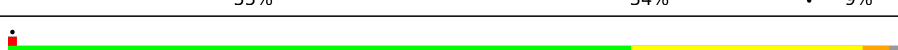
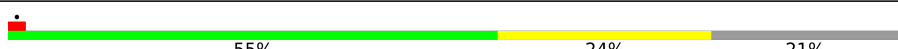
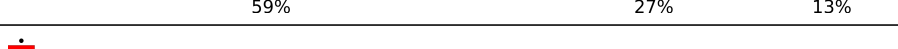
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8810 (2.12 - 3.12)

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	0	188	
2	1	65	
3	2	92	

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Mol	Chain	Length	Quality of chain
4	3	188	
5	4	103	
6	5	423	
7	6	380	
8	7	338	
9	8	206	
10	9	137	
11	A	1559	
12	B	72	
13	D	305	
14	E	348	
15	F	311	
16	H	267	
17	I	261	
18	J	192	
19	K	178	
20	L	145	
21	M	296	
22	N	251	
23	O	175	
24	P	179	
25	Q	292	
26	R	149	
27	S	205	
28	T	212	

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Mol	Chain	Length	Quality of chain
29	U	153	
30	V	216	
31	W	148	
32	X	256	
33	Y	250	
34	Z	161	
35	a	142	
36	b	155	
37	c	332	
38	d	306	
39	e	279	
40	f	194	
41	g	166	
42	h	158	
43	i	128	
44	j	123	
45	k	112	
46	l	138	
47	m	128	
48	o	102	
49	p	206	
50	q	222	
51	r	196	
52	s	439	
53	u	710	

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Mol	Chain	Length	Quality of chain
54	TA	198	23%17%6%77%
54	TB	198	14%10%86%
54	TC	198	36%36%64%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 107417 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 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 2 is a protein called 39S ribosomal protein L33, mitochondrial.

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

- Molecule 3 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			376	233	83	59	1		

- Molecule 4 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 5 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			342	217	72	49	4		

- Molecule 6 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	393	Total	C	N	O	S	0	0
			3205	2070	559	565	11		

- Molecule 7 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	354	Total	C	N	O	S	0	0
			2948	1881	525	533	9		

- Molecule 8 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	297	Total	C	N	O	S	0	0
			2410	1540	409	443	18		

- Molecule 9 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	99	Total	C	N	O	S	0	0
			836	535	144	155	2		

- Molecule 10 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	9	124	Total	C	N	O	S	0	0
			997	644	170	181	2		

- Molecule 11 is a RNA chain called 16S rRNA.

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

- Molecule 12 is a RNA chain called tRNA.

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

- Molecule 13 is a protein called 39S ribosomal protein L2, mitochondrial.

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

- Molecule 14 is a protein called 39S ribosomal protein L3, mitochondrial.

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

- Molecule 15 is a protein called 39S ribosomal protein L4, mitochondrial.

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

- Molecule 16 is a protein called 39S ribosomal protein L9, mitochondrial.

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

- Molecule 17 is a protein called 39S ribosomal protein L10, mitochondrial.

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

- Molecule 18 is a protein called 39S ribosomal protein L11, mitochondrial.

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

- Molecule 19 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 20 is a protein called 39S ribosomal protein L14, mitochondrial.

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

- Molecule 21 is a protein called 39S ribosomal protein L15, mitochondrial.

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

- Molecule 22 is a protein called 39S ribosomal protein L16, mitochondrial.

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

- Molecule 23 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 24 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

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

- Molecule 25 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	220	Total	C	N	O	S	0	0
			1834	1174	326	325	9		

- Molecule 26 is a protein called 39S ribosomal protein L20, mitochondrial.

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

- Molecule 27 is a protein called 39S ribosomal protein L21, mitochondrial.

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

- Molecule 28 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 29 is a protein called 39S ribosomal protein L23, mitochondrial.

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

- Molecule 30 is a protein called 39S ribosomal protein L24, mitochondrial.

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

- Molecule 31 is a protein called 39S ribosomal protein L27, mitochondrial.

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

- Molecule 32 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X	243	Total	C	N	O	S	0	0
			2035	1317	351	362	5		

- Molecule 33 is a protein called 39S ribosomal protein L47, mitochondrial.

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

- Molecule 34 is a protein called 39S ribosomal protein L30, mitochondrial.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 44 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
44	j	93	Total	C	N	O	S	0	0
			740	460	143	135	2		

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	q	168	Total	C	N	O	S	0	0
			1294	801	255	233	5		

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

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

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

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

- Molecule 53 is a protein called P-site finger.

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

- Molecule 54 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	TA	45	Total	C	N	O	0	0
			345	222	54	69		
54	TB	27	Total	C	N	O	0	0
			213	137	33	43		
54	TC	71	Total	C	N	O	0	0
			352	210	71	71		

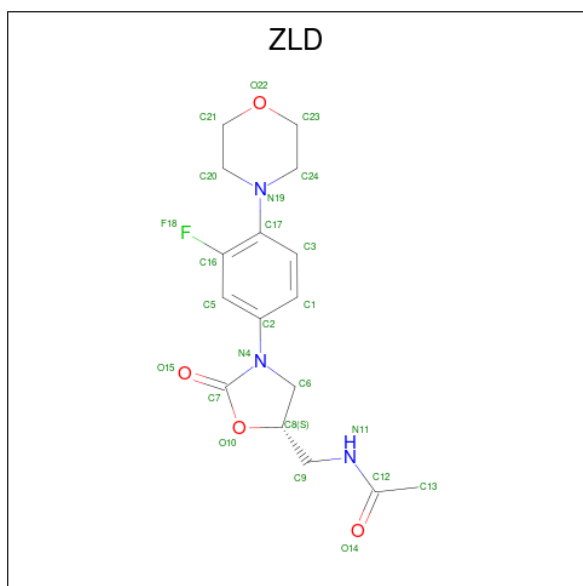
- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	0	1	Total	Zn	0
			1	1	
55	4	1	Total	Zn	0
			1	1	
55	r	1	Total	Zn	0
			1	1	

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	A	100	Total	Mg	0
			100	100	
56	D	1	Total	Mg	0
			1	1	
56	g	1	Total	Mg	0
			1	1	

- Molecule 57 is N-{[(5S)-3-(3-fluoro-4-morpholin-4-ylphenyl)-2-oxo-1,3-oxazolidin-5-yl]methyl}acetamide (CCD ID: ZLD) (formula: C₁₆H₂₀FN₃O₄).



Mol	Chain	Residues	Atoms					AltConf
57	A	1	Total	C	F	N	O	0
			24	16	1	3	4	

- Molecule 58 is water.

Mol	Chain	Residues	Atoms		AltConf
58	0	16	Total 16	O 16	0
58	1	8	Total 8	O 8	0
58	2	10	Total 10	O 10	0
58	3	15	Total 15	O 15	0
58	4	7	Total 7	O 7	0
58	5	63	Total 63	O 63	0
58	6	99	Total 99	O 99	0
58	7	96	Total 96	O 96	0
58	8	44	Total 44	O 44	0
58	9	23	Total 23	O 23	0
58	A	1975	Total 1975	O 1975	0
58	B	99	Total 99	O 99	0
58	D	31	Total 31	O 31	0
58	E	51	Total 51	O 51	0
58	F	24	Total 24	O 24	0
58	H	29	Total 29	O 29	0
58	I	62	Total 62	O 62	0
58	J	107	Total 107	O 107	0
58	K	28	Total 28	O 28	0
58	L	14	Total 14	O 14	0
58	M	39	Total 39	O 39	0
58	N	49	Total 49	O 49	0

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Mol	Chain	Residues	Atoms		AltConf
58	O	26	Total 26	O 26	0
58	P	34	Total 34	O 34	0
58	Q	50	Total 50	O 50	0
58	R	20	Total 20	O 20	0
58	S	27	Total 27	O 27	0
58	T	29	Total 29	O 29	0
58	U	35	Total 35	O 35	0
58	V	37	Total 37	O 37	0
58	W	19	Total 19	O 19	0
58	X	30	Total 30	O 30	0
58	Y	22	Total 22	O 22	0
58	Z	27	Total 27	O 27	0
58	a	18	Total 18	O 18	0
58	b	34	Total 34	O 34	0
58	c	21	Total 21	O 21	0
58	d	10	Total 10	O 10	0
58	e	196	Total 196	O 196	0
58	f	59	Total 59	O 59	0
58	g	27	Total 27	O 27	0
58	h	36	Total 36	O 36	0
58	i	28	Total 28	O 28	0

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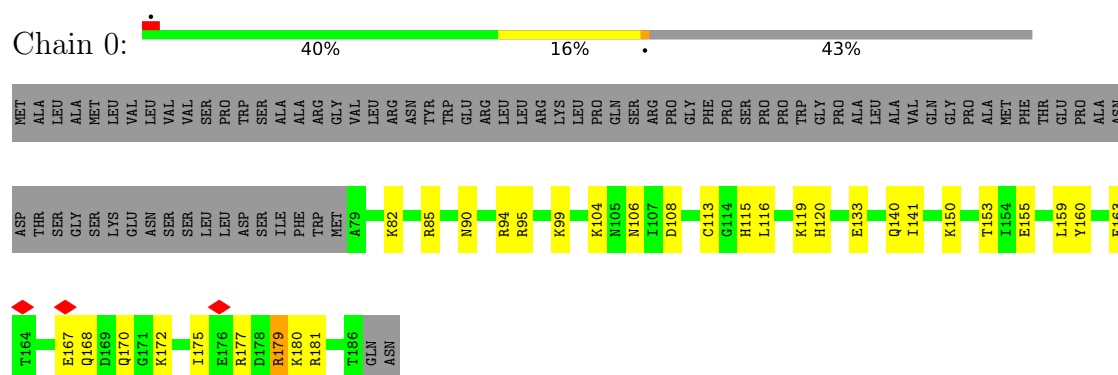
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Mol	Chain	Residues	Atoms		AltConf
58	j	24	Total 24	O 24	0
58	k	32	Total 32	O 32	0
58	l	50	Total 50	O 50	0
58	m	33	Total 33	O 33	0
58	o	18	Total 18	O 18	0
58	p	57	Total 57	O 57	0
58	q	6	Total 6	O 6	0
58	r	44	Total 44	O 44	0
58	s	57	Total 57	O 57	0
58	u	32	Total 32	O 32	0
58	TA	43	Total 43	O 43	0
58	TB	22	Total 22	O 22	0
58	TC	37	Total 37	O 37	0

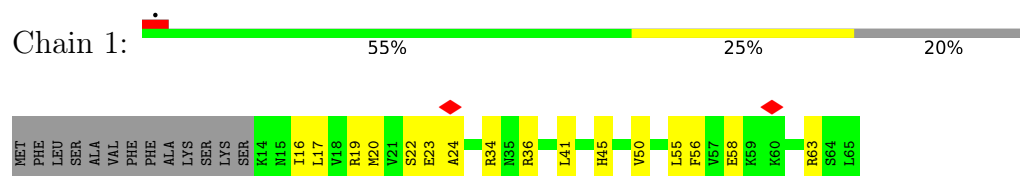
3 Residue-property plots [i](#)

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.

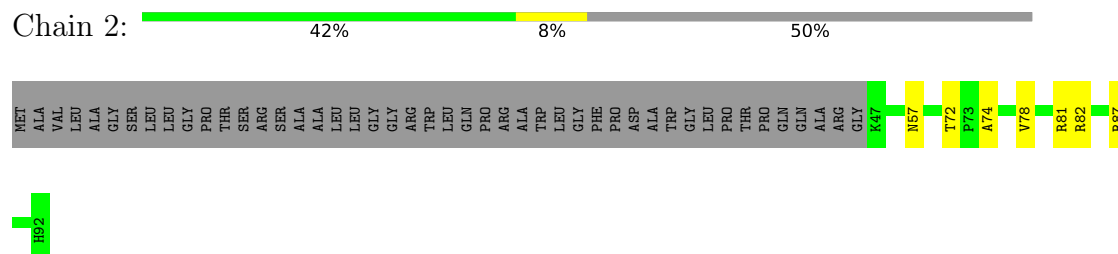
- Molecule 1: 39S ribosomal protein L32, mitochondrial



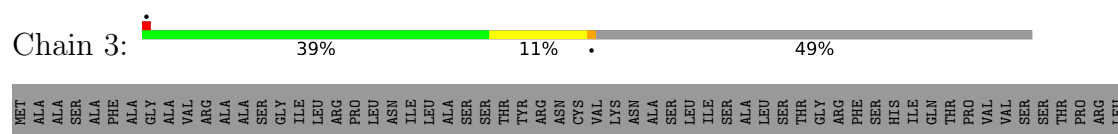
- Molecule 2: 39S ribosomal protein L33, mitochondrial

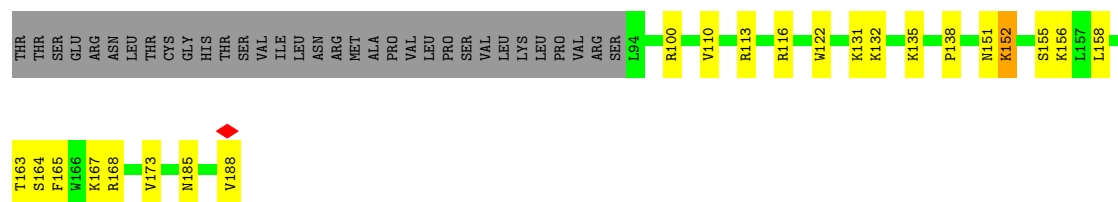


- Molecule 3: 39S ribosomal protein L34, mitochondrial



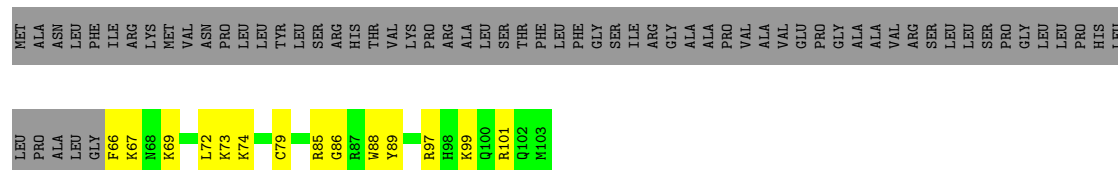
- Molecule 4: 39S ribosomal protein L35, mitochondrial





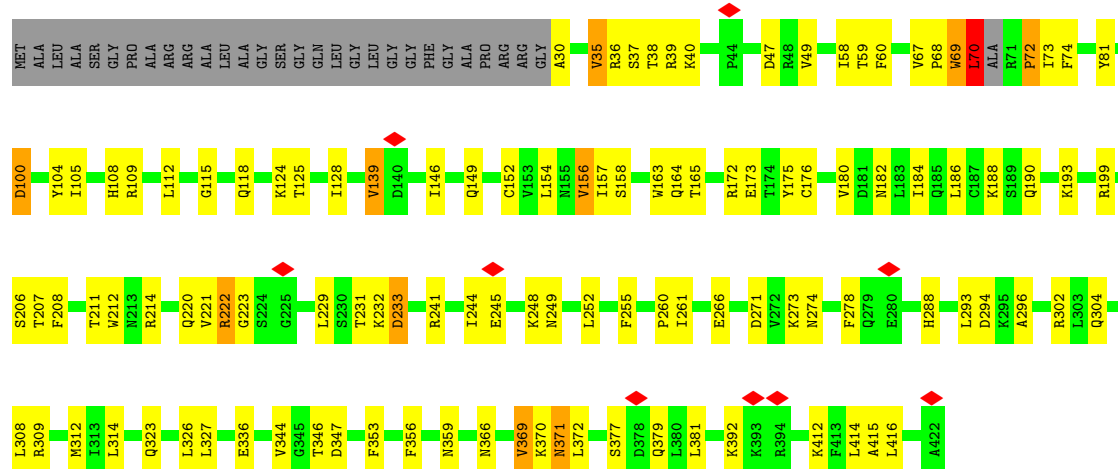
- Molecule 5: 39S ribosomal protein L36, mitochondrial

Chain 4: 23% 14% 63%



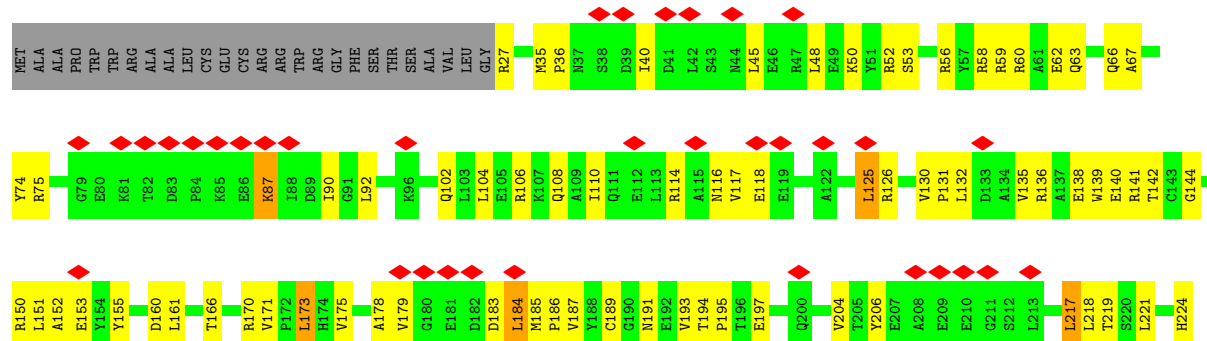
- Molecule 6: 39S ribosomal protein L37, mitochondrial

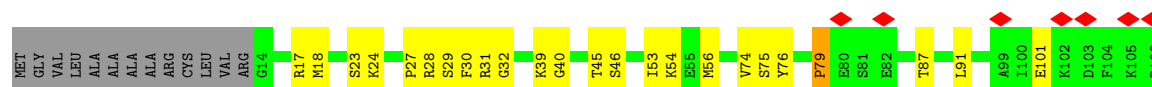
Chain 5: 65% 25% 7%

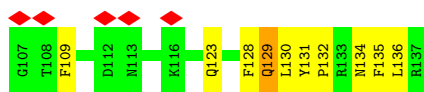


- Molecule 7: 39S ribosomal protein L38, mitochondrial

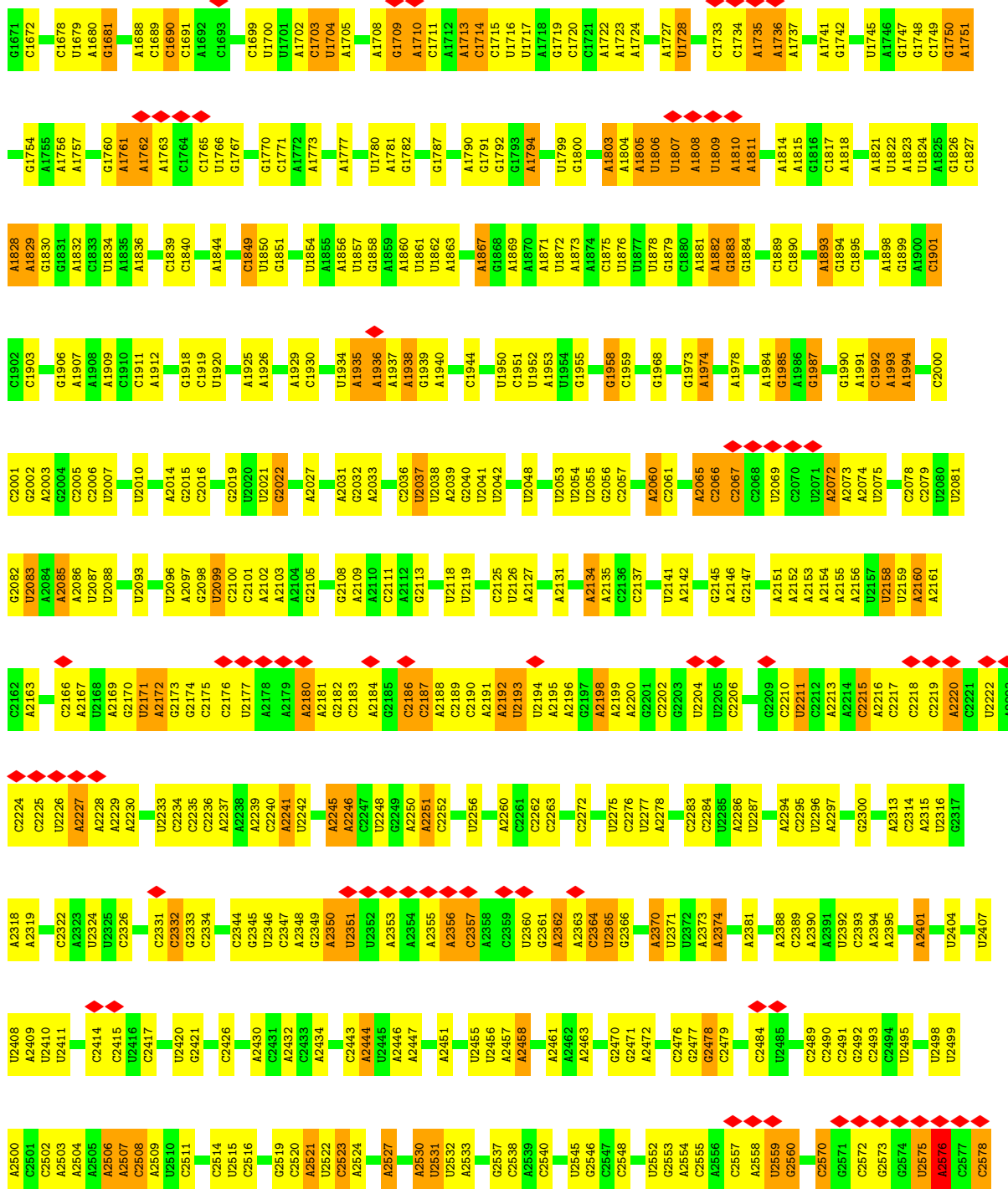
Chain 6: 14% 55% 36% 7%

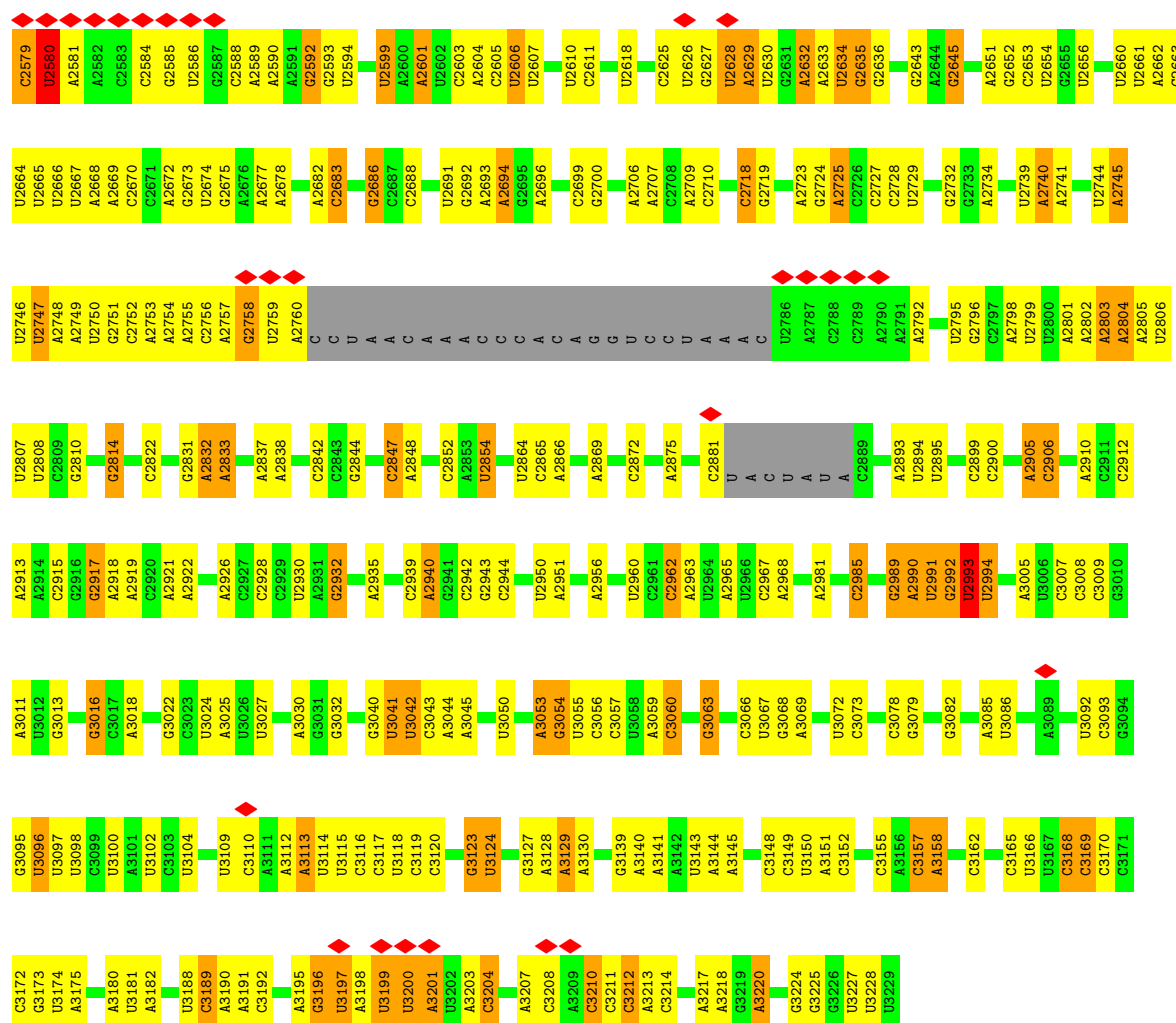




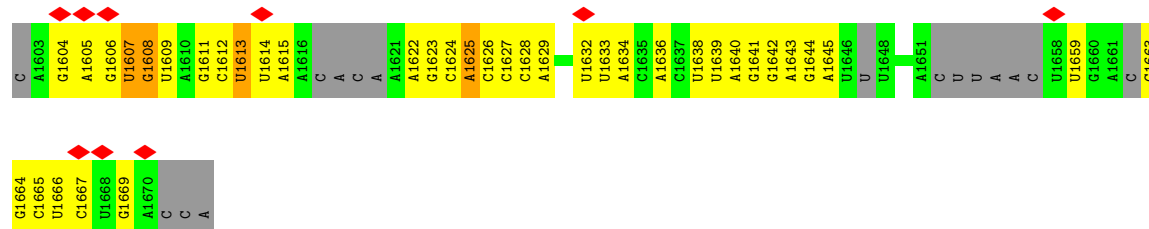


• Molecule 11: 16S rRNA

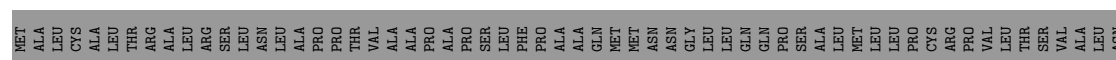


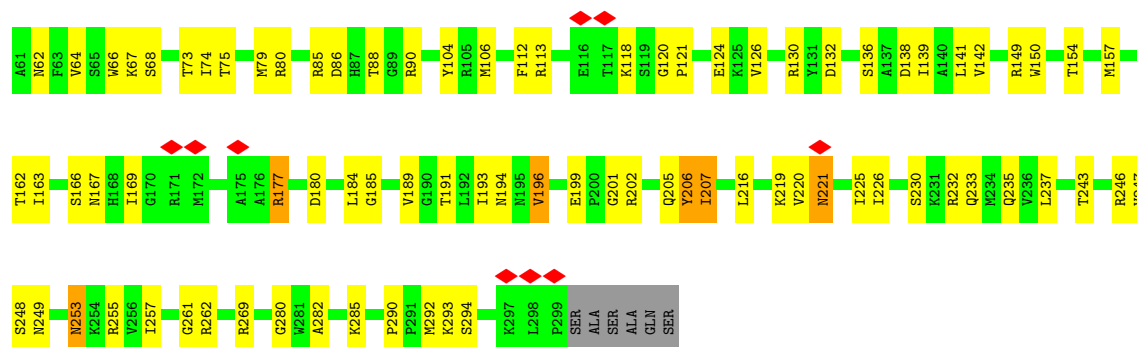


• Molecule 12: tRNA



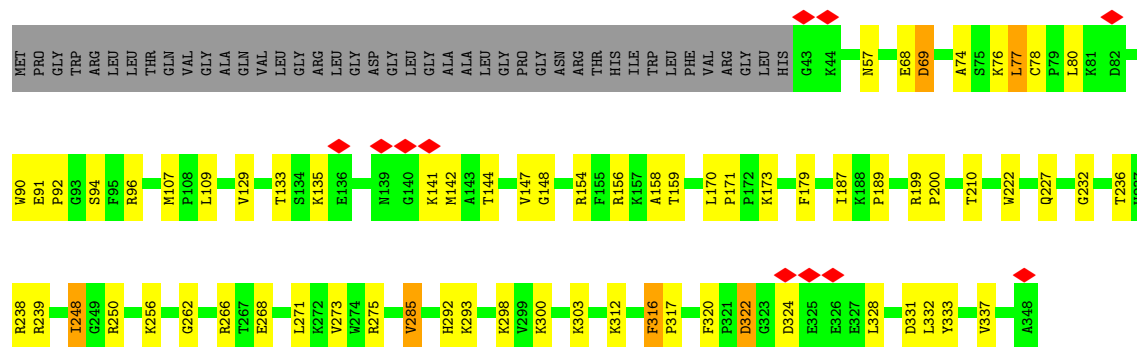
• Molecule 13: 39S ribosomal protein L2, mitochondrial





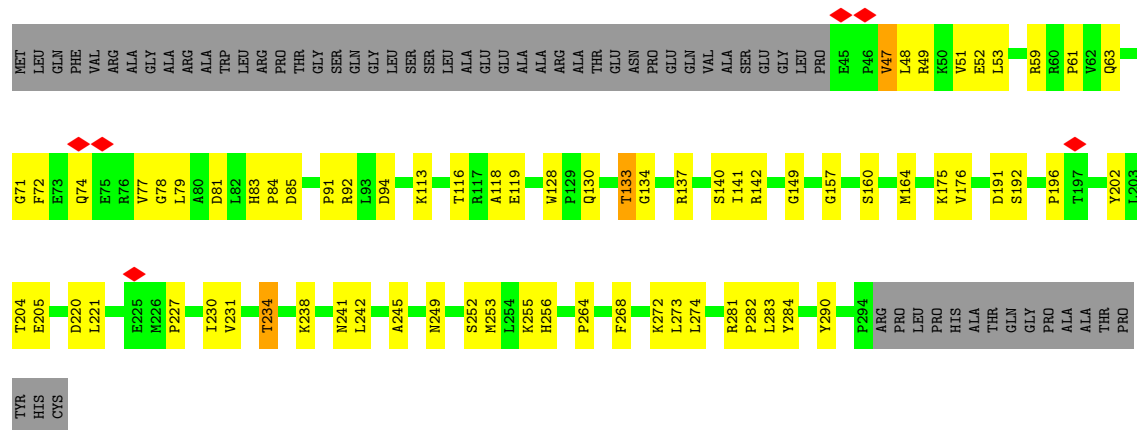
• Molecule 14: 39S ribosomal protein L3, mitochondrial

Chain E: 68% 18% 12%



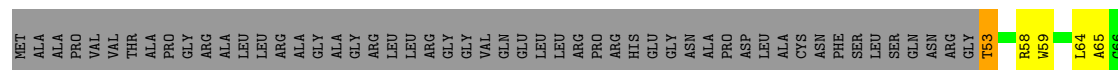
• Molecule 15: 39S ribosomal protein L4, mitochondrial

Chain F: 58% 22% 20%

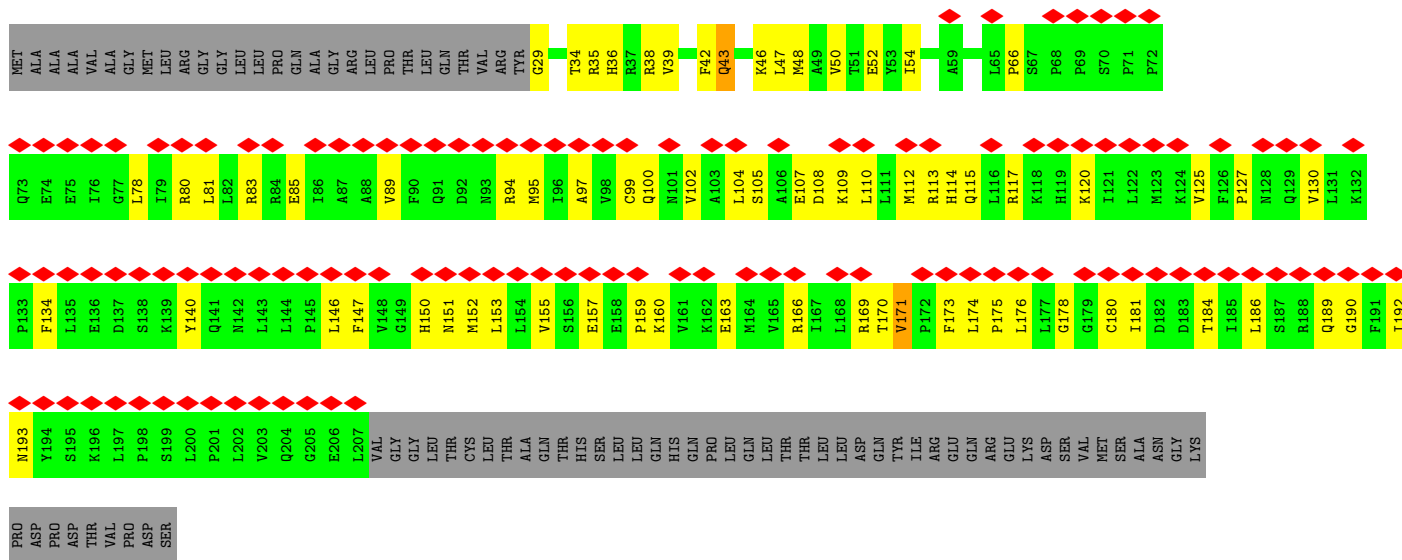


• Molecule 16: 39S ribosomal protein L9, mitochondrial

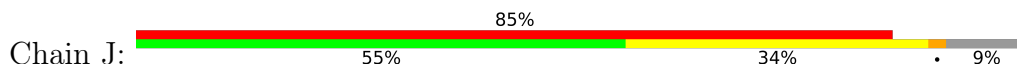
Chain H: 24% 12% 63%



- Molecule 17: 39S ribosomal protein L10, mitochondrial

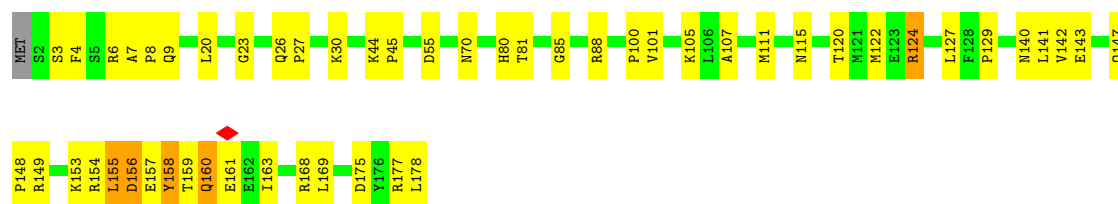


- Molecule 18: 39S ribosomal protein L11, mitochondrial



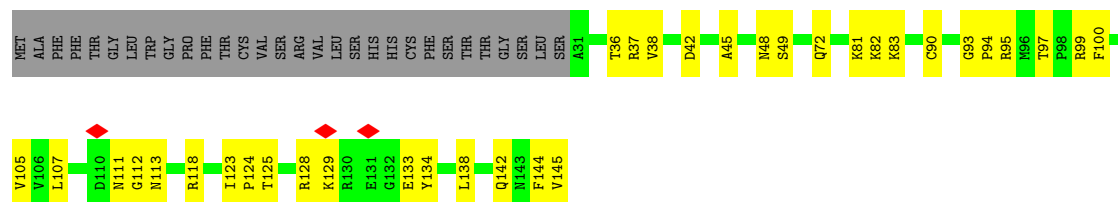
- Molecule 19: 39S ribosomal protein L13, mitochondrial

Chain K:  70% 26% ..



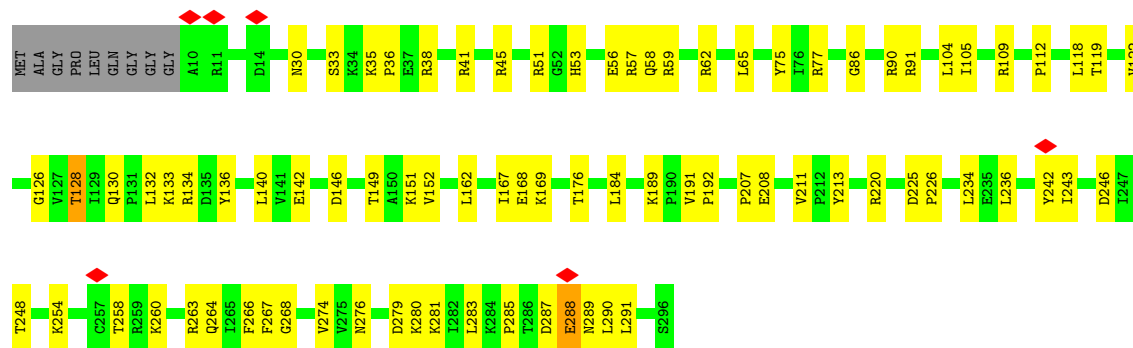
- Molecule 20: 39S ribosomal protein L14, mitochondrial

Chain L:  55% 24% 21%



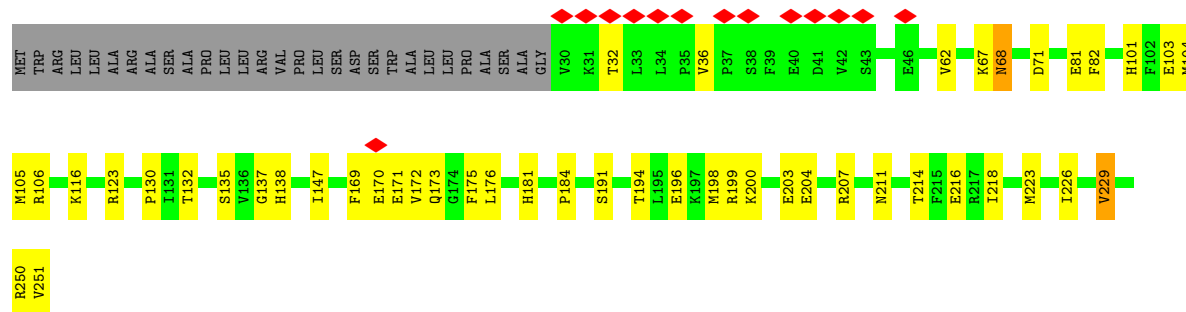
- Molecule 21: 39S ribosomal protein L15, mitochondrial

Chain M:  69% 27% ..

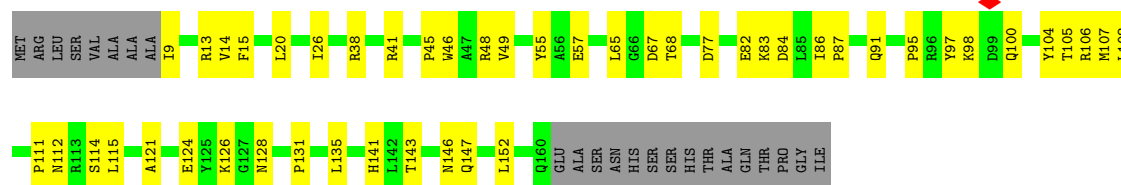


- Molecule 22: 39S ribosomal protein L16, mitochondrial

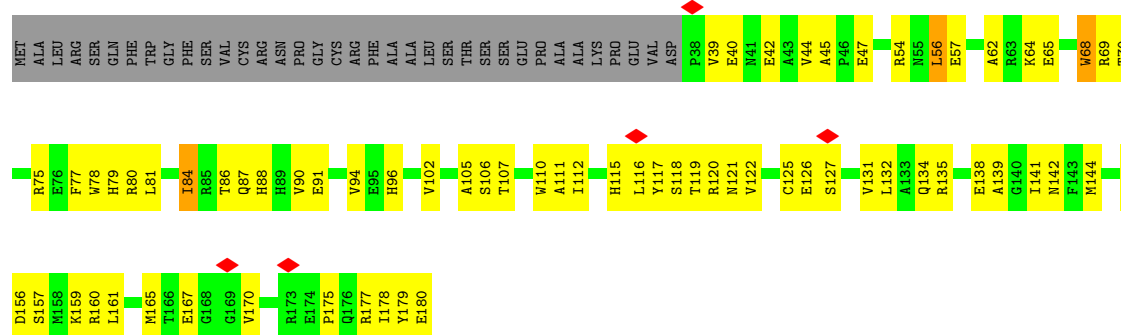
Chain N:  6% 69% 18% 12%



- Molecule 23: 39S ribosomal protein L17, mitochondrial



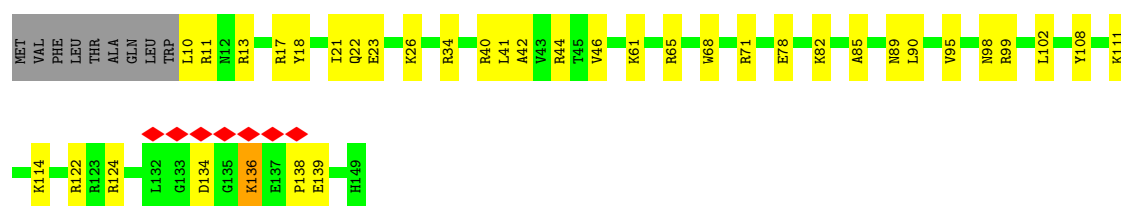
- Molecule 24: Mitochondrial ribosomal protein L18, isoform CRA_b



- Molecule 25: 39S ribosomal protein L19, mitochondrial

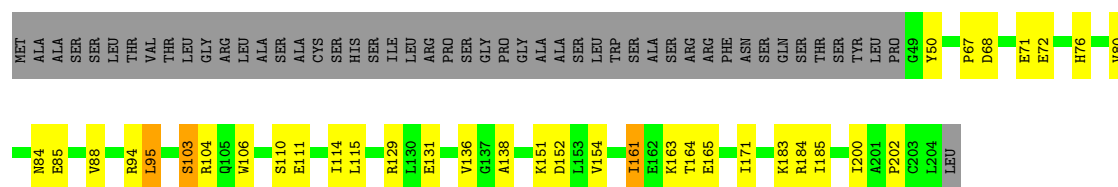


- Molecule 26: 39S ribosomal protein L20, mitochondrial



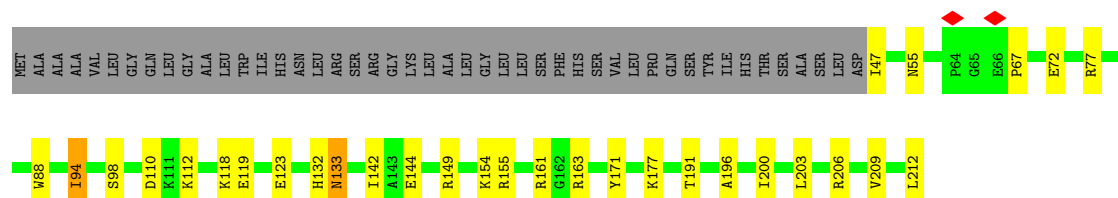
- Molecule 27: 39S ribosomal protein L21, mitochondrial

Chain S: 



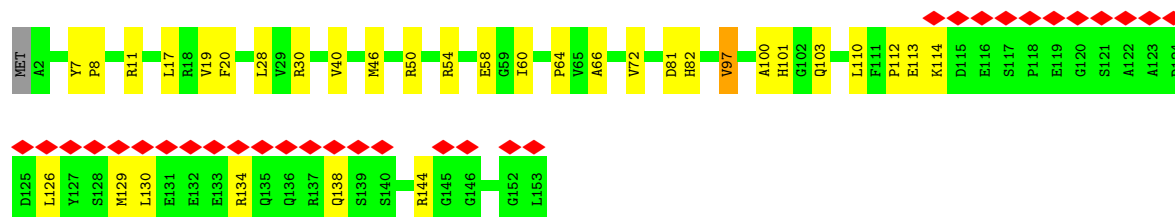
- Molecule 28: 39S ribosomal protein L22, mitochondrial

Chain T: 



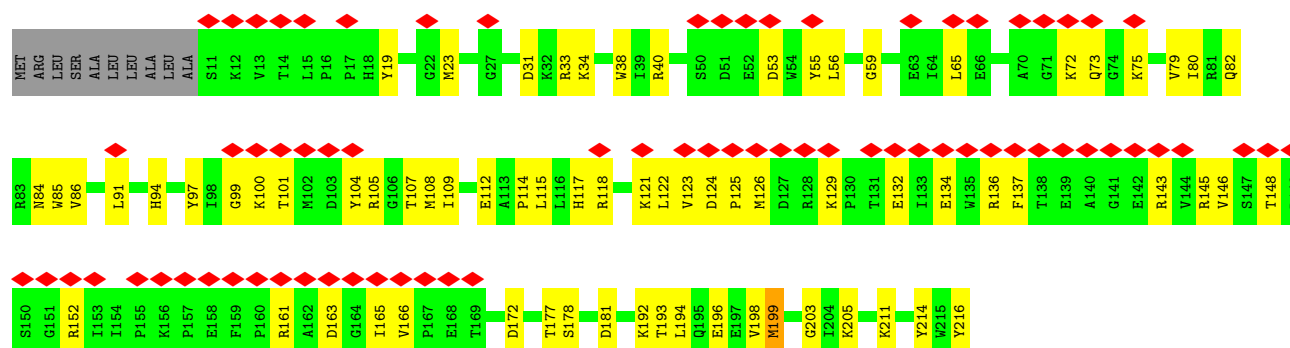
- Molecule 29: 39S ribosomal protein L23, mitochondrial

Chain U: 



- Molecule 30: 39S ribosomal protein L24, mitochondrial

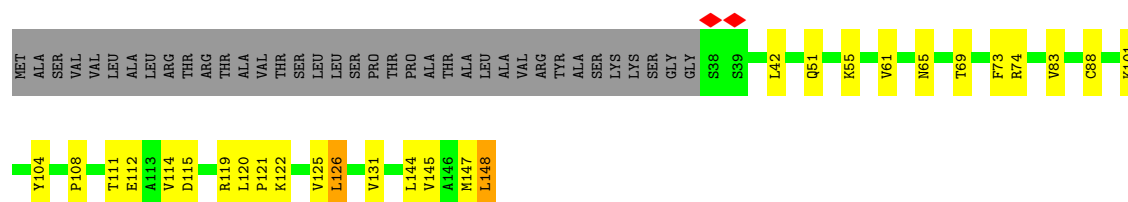
Chain V: 



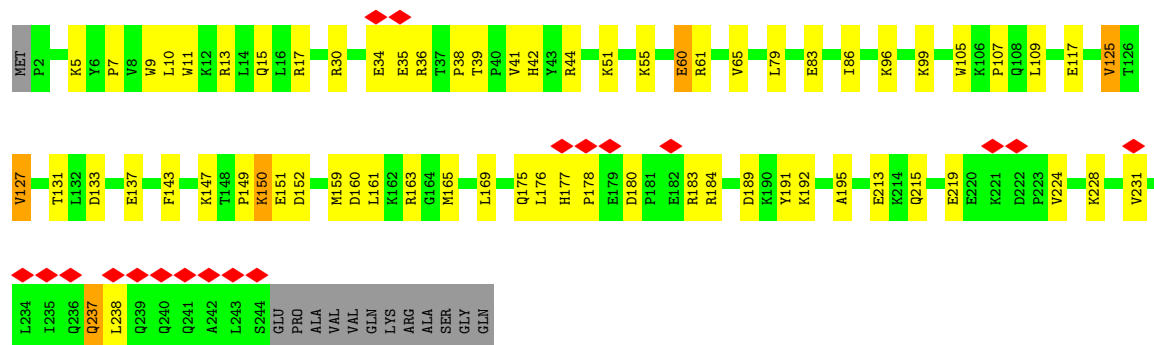
- Molecule 31: 39S ribosomal protein L27, mitochondrial

Chain W: 

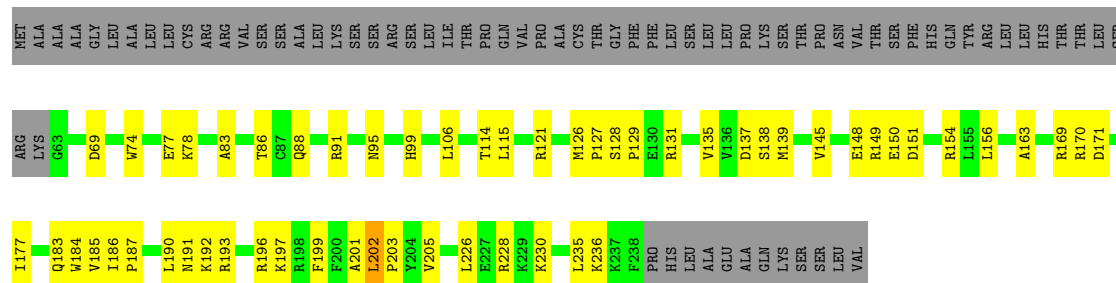




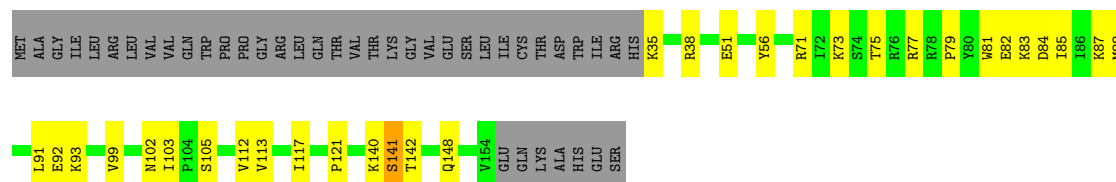
- Molecule 32: 39S ribosomal protein L28, mitochondrial



- Molecule 33: 39S ribosomal protein L47, mitochondrial

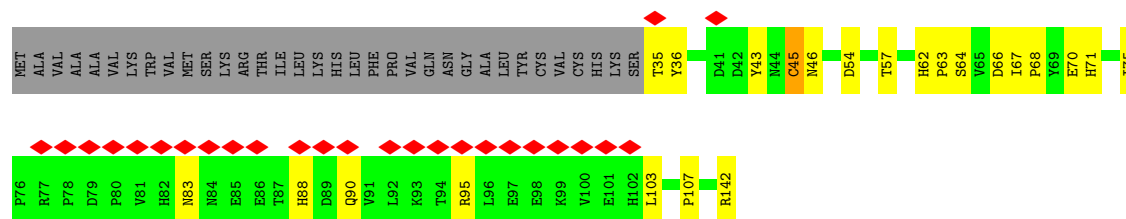


- Molecule 34: 39S ribosomal protein L30, mitochondrial



- Molecule 35: 39S ribosomal protein L42, mitochondrial





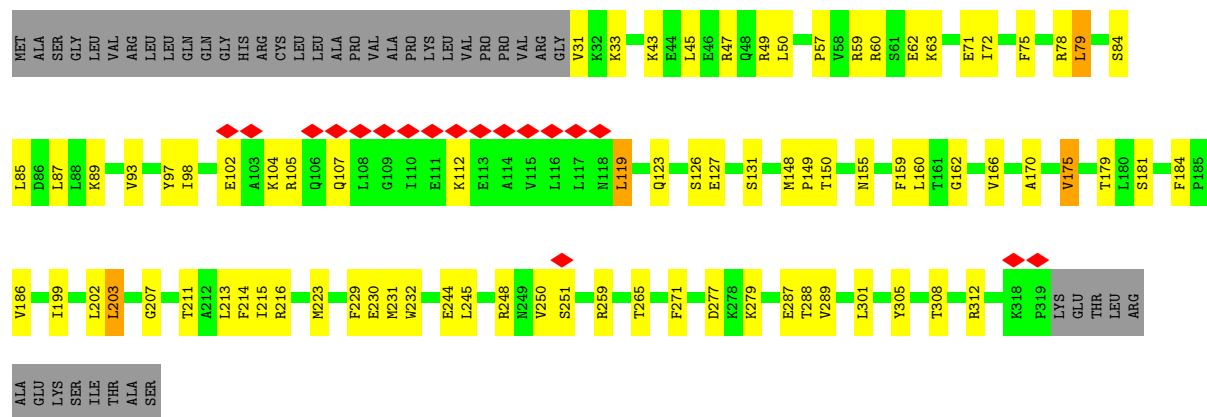
- Molecule 36: 39S ribosomal protein L43, mitochondrial

Chain b: 71% 24% 5%



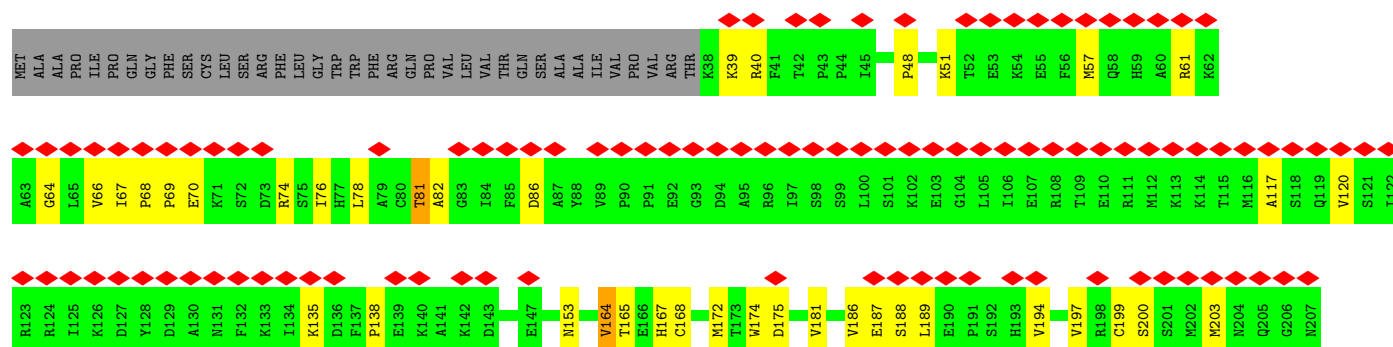
- Molecule 37: 39S ribosomal protein L44, mitochondrial

Chain c: 5% 63% 23% 13%

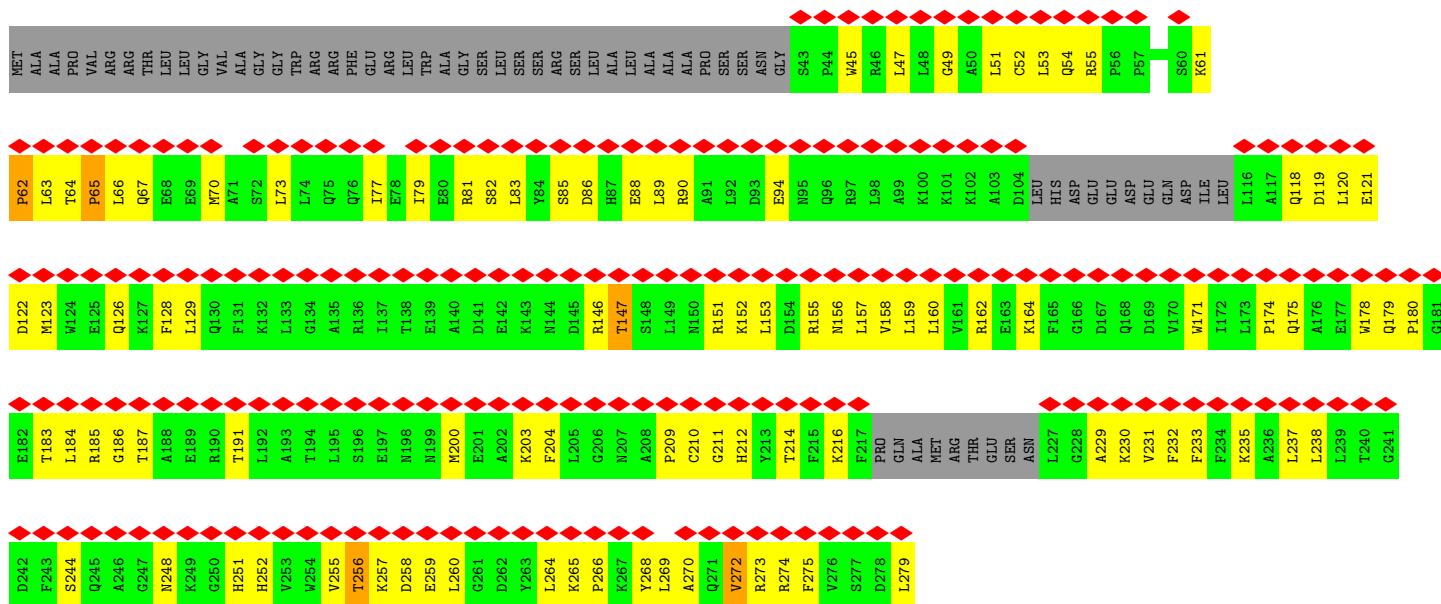
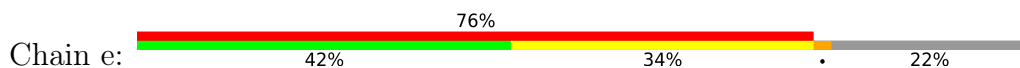


- Molecule 38: 39S ribosomal protein L45, mitochondrial

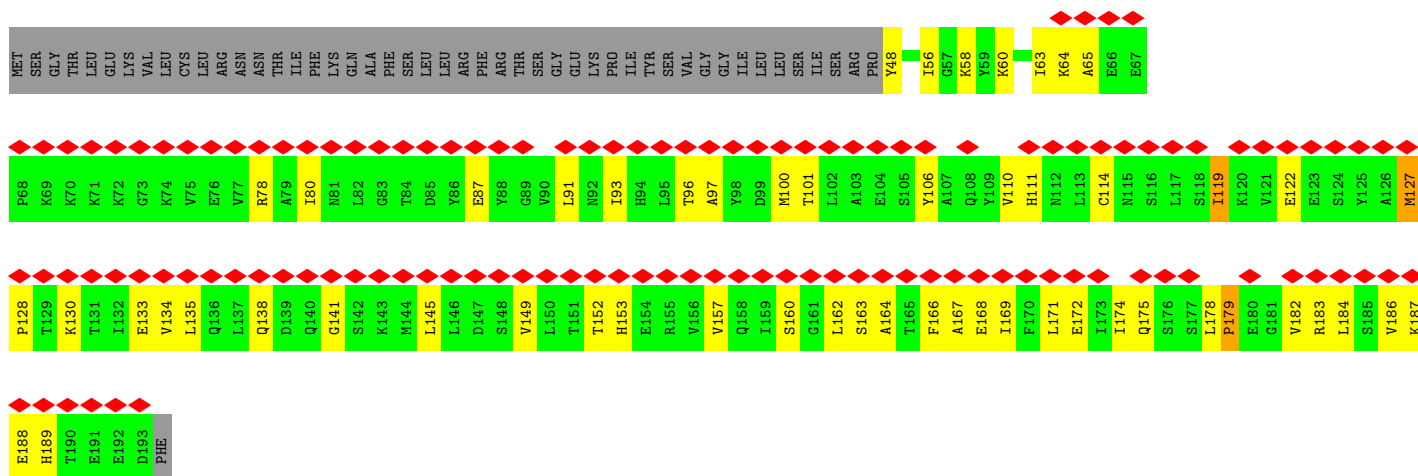
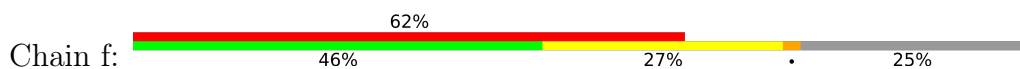
Chain d: 42% 61% 22% 16%



- Molecule 39: 39S ribosomal protein L46, mitochondrial

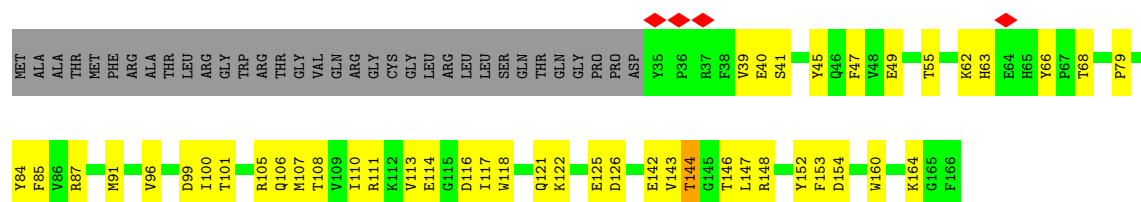


- Molecule 40: 39S ribosomal protein L48, mitochondrial

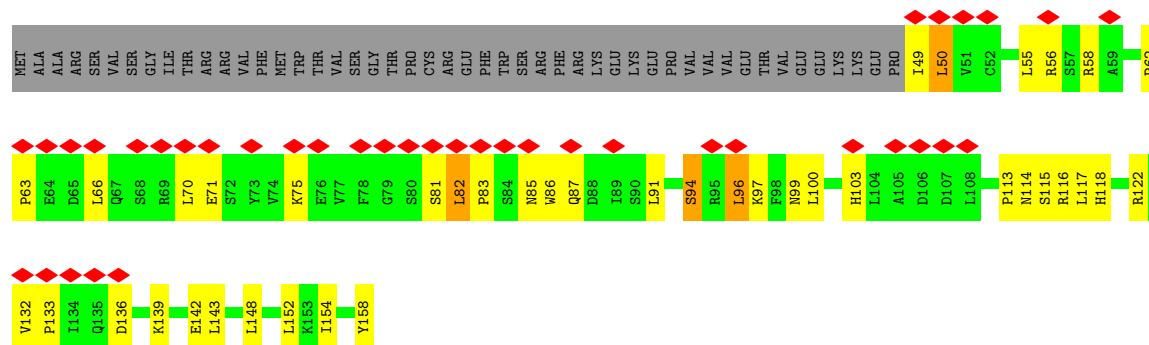


- Molecule 41: 39S ribosomal protein L49, mitochondrial

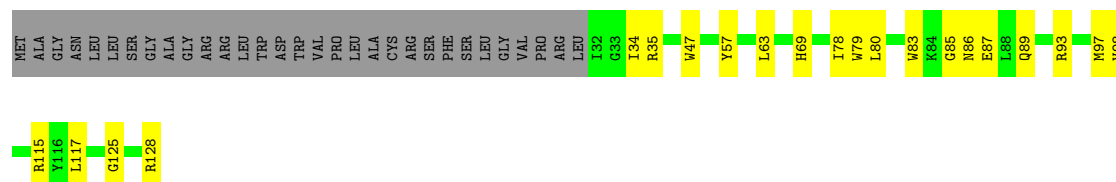




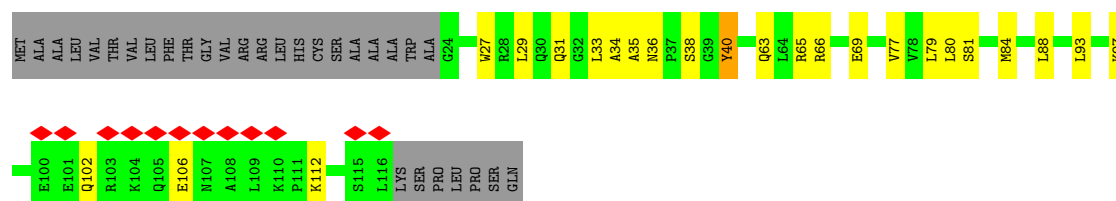
- Molecule 42: 39S ribosomal protein L50, mitochondrial



- Molecule 43: 39S ribosomal protein L51, mitochondrial

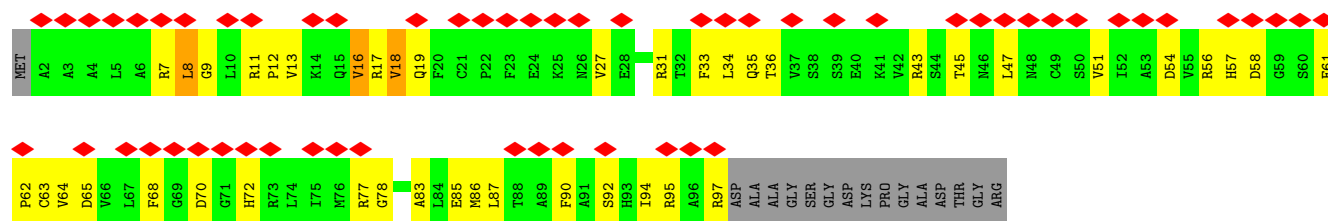


- Molecule 44: cDNA FLJ76418, highly similar to Homo sapiens mitochondrial ribosomal protein L52 (MRPL52), transcript variant 1, mRNA

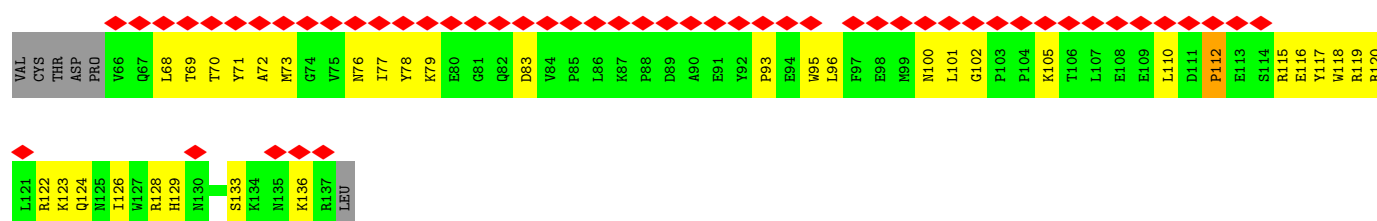
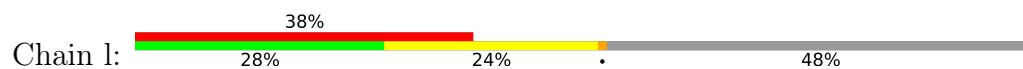


- Molecule 45: 39S ribosomal protein L53, mitochondrial

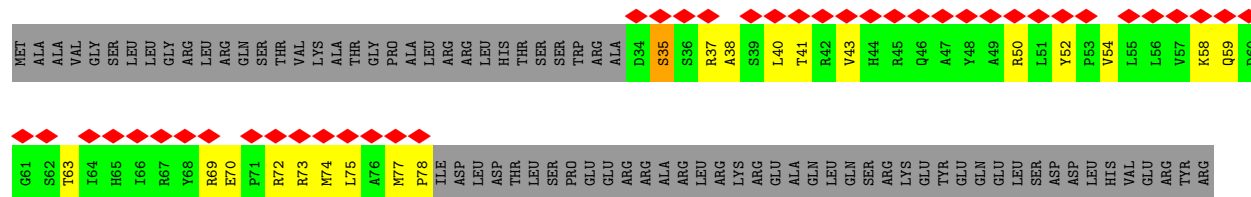




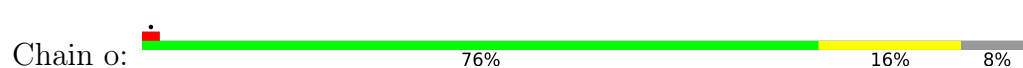
• Molecule 46: 39S ribosomal protein L54, mitochondrial



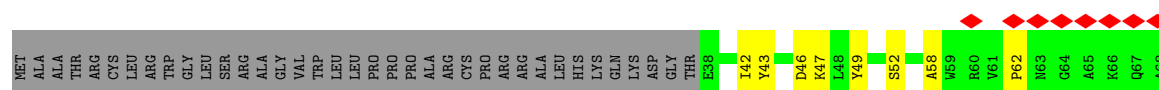
• Molecule 47: 39S ribosomal protein L55, mitochondrial



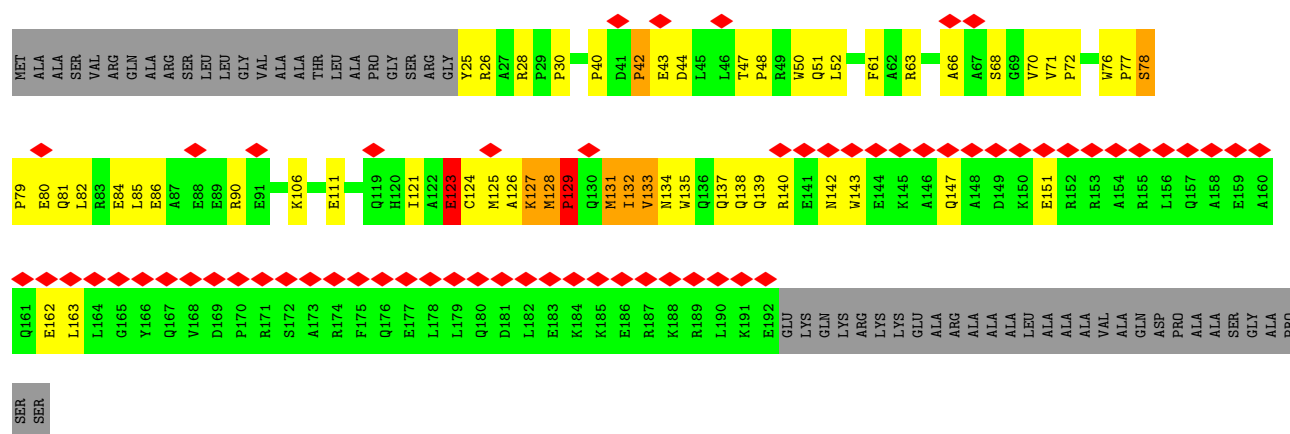
• Molecule 48: Ribosomal protein 63, mitochondrial



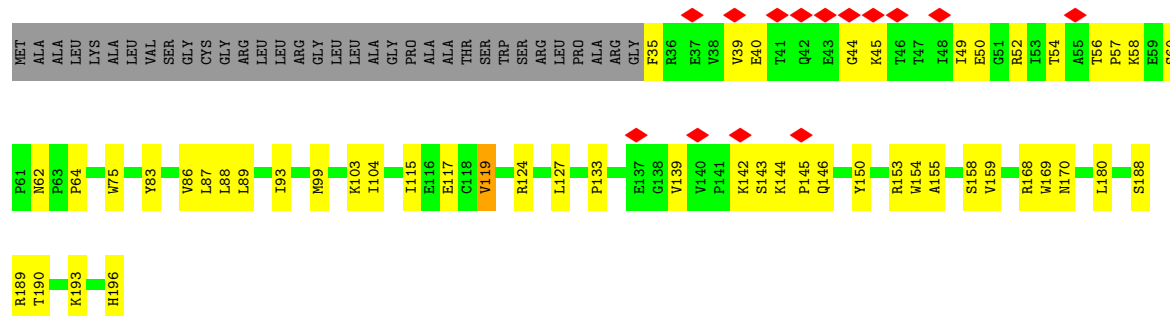
• Molecule 49: Peptidyl-tRNA hydrolase ICT1, mitochondrial



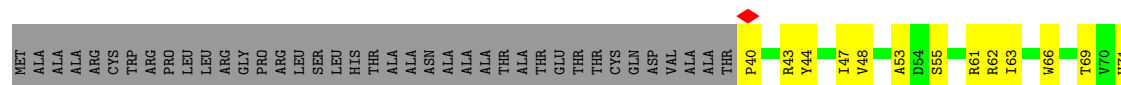
- Molecule 50: Growth arrest and DNA damage-inducible proteins-interacting protein 1

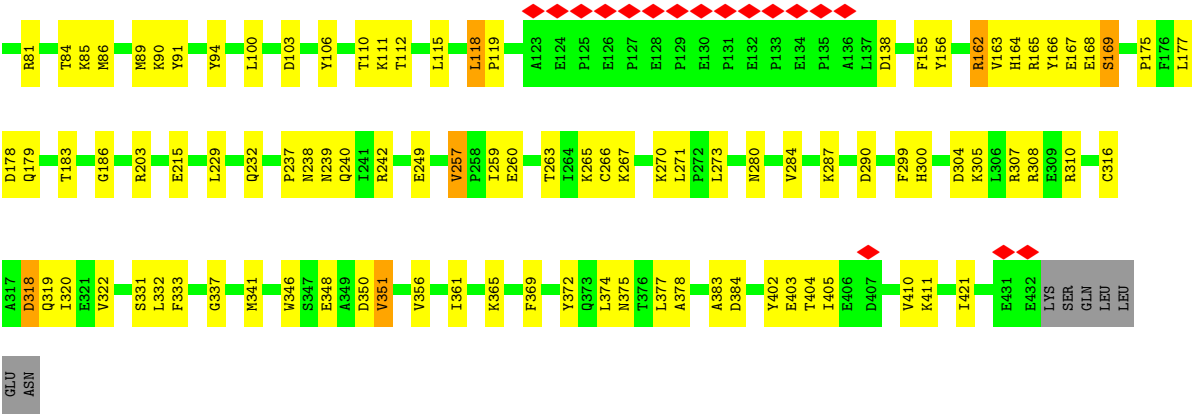


- Molecule 51: 39S ribosomal protein S18a, mitochondrial

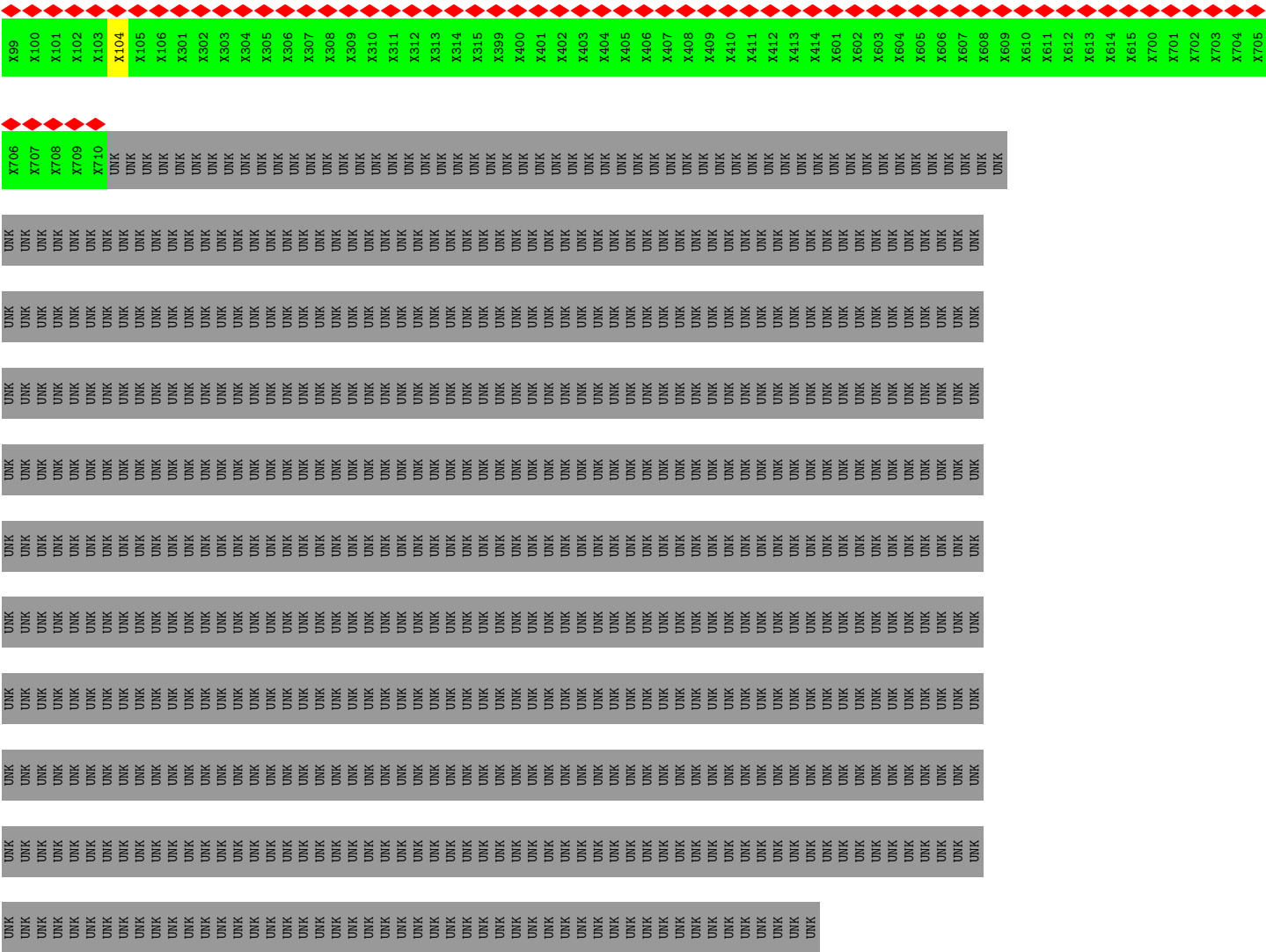


- Molecule 52: 39S ribosomal protein S30, mitochondrial





• Molecule 53: P-site finger



• Molecule 54: 39S ribosomal protein L12, mitochondrial

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	347872	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	21	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.661	Depositor
Minimum map value	-2.742	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.096	Depositor
Recommended contour level	0.38	Depositor
Map size (Å)	484.4, 484.4, 484.4	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.865, 0.865, 0.865	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0	0.19	0/895	0.41	0/1201
2	1	0.16	0/438	0.42	0/583
3	2	0.18	0/382	0.29	0/507
4	3	0.18	0/852	0.32	0/1136
5	4	0.14	0/350	0.36	0/461
6	5	0.21	0/3300	0.40	0/4495
7	6	0.20	0/3043	0.51	3/4140 (0.1%)
8	7	0.14	0/2467	0.36	0/3337
9	8	0.15	0/855	0.36	0/1152
10	9	0.19	0/1025	0.42	1/1379 (0.1%)
11	A	0.33	9/36246 (0.0%)	0.33	4/56422 (0.0%)
12	B	0.10	0/1328	0.25	0/2056
13	D	0.16	0/1904	0.37	0/2561
14	E	0.15	0/2479	0.37	0/3360
15	F	0.18	0/2071	0.42	0/2817
16	H	0.17	0/820	0.46	0/1102
17	I	0.48	2/1467 (0.1%)	0.78	4/1984 (0.2%)
18	J	0.87	6/1348 (0.4%)	1.35	11/1813 (0.6%)
19	K	0.19	0/1495	0.41	0/2029
20	L	0.17	0/904	0.45	2/1218 (0.2%)
21	M	0.19	0/2359	0.44	0/3185
22	N	0.17	0/1833	0.39	0/2468
23	O	0.18	0/1269	0.38	0/1708
24	P	0.19	0/1191	0.47	0/1611
25	Q	0.15	0/1875	0.34	0/2523
26	R	0.21	0/1174	0.43	0/1572
27	S	0.19	0/1276	0.39	0/1729
28	T	0.20	0/1402	0.39	1/1886 (0.1%)
29	U	0.18	0/1252	0.38	0/1697
30	V	0.14	0/1727	0.40	0/2341
31	W	0.18	0/893	0.40	0/1204
32	X	0.21	0/2090	0.41	0/2825

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Y	0.16	0/1552	0.34	0/2079
34	Z	0.18	0/1003	0.37	0/1354
35	a	0.16	0/923	0.34	0/1254
36	b	0.17	0/1202	0.36	0/1626
37	c	0.16	0/2371	0.32	0/3205
38	d	0.72	3/2132 (0.1%)	0.78	5/2887 (0.2%)
39	e	0.59	3/1797 (0.2%)	0.95	6/2422 (0.2%)
40	f	0.19	0/1144	0.54	2/1551 (0.1%)
41	g	0.18	0/1132	0.43	0/1543
42	h	0.16	0/917	0.43	0/1249
43	i	0.21	0/849	0.41	0/1135
44	j	0.16	0/755	0.38	0/1016
45	k	0.44	2/754 (0.3%)	0.88	4/1017 (0.4%)
46	l	0.68	1/636 (0.2%)	1.04	4/860 (0.5%)
47	m	0.15	0/379	0.40	0/510
48	o	0.17	0/818	0.43	0/1097
49	p	0.18	0/1246	0.49	1/1675 (0.1%)
50	q	0.35	1/1325 (0.1%)	0.55	1/1799 (0.1%)
51	r	0.17	0/1362	0.39	0/1846
52	s	0.17	0/3262	0.39	2/4435 (0.0%)
54	TA	1.34	3/349 (0.9%)	2.02	5/475 (1.1%)
54	TB	0.12	0/212	0.36	0/286
54	TC	0.09	0/351	0.24	0/488
All	All	0.31	30/108481 (0.0%)	0.46	56/154311 (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
13	D	0	1
14	E	0	1
19	K	0	1
24	P	0	1
33	Y	0	1
34	Z	0	1
42	h	0	2
49	p	0	1
50	q	0	1
All	All	0	10

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	d	268	PRO	CG-CD	-30.05	0.48	1.50
11	A	2576	A	C6-N1	23.35	1.82	1.35
18	J	136	PRO	CG-CD	-22.68	0.73	1.50
11	A	2576	A	N1-C2	22.25	1.78	1.34
54	TA	52	PRO	CG-CD	-21.99	0.76	1.50

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	TA	52	PRO	N-CD-CG	-32.86	53.91	103.20
38	d	268	PRO	N-CD-CG	-28.97	59.74	103.20
39	e	62	PRO	N-CD-CG	-28.41	60.59	103.20
18	J	136	PRO	N-CD-CG	-25.46	65.00	103.20
39	e	62	PRO	CA-CB-CG	-21.30	64.02	104.50

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	D	206	TYR	Peptide
14	E	316	PHE	Peptide
19	K	3	SER	Peptide
24	P	68	TRP	Peptide
33	Y	202	LEU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	880	0	902	27	0
2	1	433	0	475	17	0
3	2	376	0	406	5	0
4	3	831	0	883	16	0
5	4	342	0	361	12	0
6	5	3205	0	3201	81	0
7	6	2948	0	2841	122	0
8	7	2410	0	2415	63	0
9	8	836	0	844	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	9	997	0	987	34	0
11	A	32395	0	16450	495	0
12	B	1191	0	607	41	0
13	D	1866	0	1927	60	0
14	E	2410	0	2418	47	0
15	F	2013	0	2044	57	0
16	H	806	0	849	27	0
17	I	1435	0	1521	58	0
18	J	1330	0	1407	62	0
19	K	1451	0	1448	40	0
20	L	889	0	941	23	0
21	M	2305	0	2378	67	0
22	N	1786	0	1817	41	0
23	O	1245	0	1283	35	0
24	P	1165	0	1162	54	0
25	Q	1834	0	1872	34	0
26	R	1153	0	1214	30	0
27	S	1251	0	1322	28	0
28	T	1368	0	1410	19	0
29	U	1222	0	1187	31	0
30	V	1682	0	1692	61	0
31	W	871	0	898	21	0
32	X	2035	0	2054	43	0
33	Y	1517	0	1561	42	0
34	Z	978	0	1030	24	0
35	a	896	0	847	19	0
36	b	1178	0	1180	35	0
37	c	2322	0	2338	55	0
38	d	2075	0	2037	49	0
39	e	1762	0	1767	94	0
40	f	1126	0	1106	51	0
41	g	1096	0	1081	35	0
42	h	894	0	881	34	0
43	i	827	0	857	18	0
44	j	740	0	741	20	0
45	k	743	0	758	33	0
46	l	619	0	611	29	0
47	m	372	0	387	31	0
48	o	797	0	804	15	0
49	p	1227	0	1239	51	0
50	q	1294	0	1178	58	0
51	r	1322	0	1349	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	s	3178	0	3124	73	0
53	u	325	0	77	1	0
54	TA	345	0	364	10	0
54	TB	213	0	234	8	0
54	TC	352	0	169	0	0
55	0	1	0	0	0	0
55	4	1	0	0	0	0
55	r	1	0	0	0	0
56	A	100	0	0	0	0
56	D	1	0	0	0	0
56	g	1	0	0	0	0
57	A	24	0	20	3	0
58	0	16	0	0	1	0
58	1	8	0	0	0	0
58	2	10	0	0	0	0
58	3	15	0	0	1	0
58	4	7	0	0	0	0
58	5	63	0	0	1	0
58	6	99	0	0	2	0
58	7	96	0	0	7	0
58	8	44	0	0	3	0
58	9	23	0	0	0	0
58	A	1975	0	0	11	0
58	B	99	0	0	3	0
58	D	31	0	0	1	0
58	E	51	0	0	0	0
58	F	24	0	0	2	0
58	H	29	0	0	1	0
58	I	62	0	0	6	0
58	J	107	0	0	5	0
58	K	28	0	0	0	0
58	L	14	0	0	1	0
58	M	39	0	0	0	0
58	N	49	0	0	0	0
58	O	26	0	0	0	0
58	P	34	0	0	2	0
58	Q	50	0	0	1	0
58	R	20	0	0	3	0
58	S	27	0	0	0	0
58	T	29	0	0	0	0
58	TA	43	0	0	0	0
58	TB	22	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	TC	37	0	0	0	0
58	U	35	0	0	1	0
58	V	37	0	0	2	0
58	W	19	0	0	0	0
58	X	30	0	0	2	0
58	Y	22	0	0	1	0
58	Z	27	0	0	2	0
58	a	18	0	0	1	0
58	b	34	0	0	1	0
58	c	21	0	0	0	0
58	d	10	0	0	0	0
58	e	196	0	0	11	0
58	f	59	0	0	4	0
58	g	27	0	0	1	0
58	h	36	0	0	2	0
58	i	28	0	0	0	0
58	j	24	0	0	1	0
58	k	32	0	0	2	0
58	l	50	0	0	2	0
58	m	33	0	0	3	0
58	o	18	0	0	0	0
58	p	57	0	0	2	0
58	q	6	0	0	0	0
58	r	44	0	0	1	0
58	s	57	0	0	1	0
58	u	32	0	0	0	0
All	All	107417	0	86956	2218	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 12.

The worst 5 of 2218 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)
11:A:2576:A:C5	11:A:2576:A:C6	1.77	1.65
11:A:2576:A:C4	11:A:2576:A:N3	1.78	1.52
11:A:2576:A:N3	11:A:2576:A:C2	1.75	1.51
11:A:2576:A:C2	11:A:2576:A:N1	1.78	1.48
11:A:2576:A:C6	11:A:2576:A:N1	1.82	1.47

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	0	106/188 (56%)	94 (89%)	12 (11%)	0	100	100
2	1	50/65 (77%)	47 (94%)	3 (6%)	0	100	100
3	2	44/92 (48%)	43 (98%)	1 (2%)	0	100	100
4	3	93/188 (50%)	92 (99%)	1 (1%)	0	100	100
5	4	36/103 (35%)	35 (97%)	1 (3%)	0	100	100
6	5	391/423 (92%)	373 (95%)	16 (4%)	2 (0%)	24	44
7	6	352/380 (93%)	324 (92%)	28 (8%)	0	100	100
8	7	295/338 (87%)	279 (95%)	15 (5%)	1 (0%)	36	56
9	8	97/206 (47%)	91 (94%)	6 (6%)	0	100	100
10	9	122/137 (89%)	116 (95%)	6 (5%)	0	100	100
13	D	237/305 (78%)	225 (95%)	11 (5%)	1 (0%)	30	49
14	E	304/348 (87%)	283 (93%)	20 (7%)	1 (0%)	36	56
15	F	248/311 (80%)	228 (92%)	20 (8%)	0	100	100
16	H	96/267 (36%)	87 (91%)	9 (9%)	0	100	100
17	I	177/261 (68%)	164 (93%)	13 (7%)	0	100	100
18	J	173/192 (90%)	162 (94%)	10 (6%)	1 (1%)	21	39
19	K	175/178 (98%)	157 (90%)	17 (10%)	1 (1%)	21	39
20	L	113/145 (78%)	103 (91%)	10 (9%)	0	100	100
21	M	285/296 (96%)	254 (89%)	30 (10%)	1 (0%)	30	49
22	N	220/251 (88%)	217 (99%)	3 (1%)	0	100	100
23	O	150/175 (86%)	132 (88%)	18 (12%)	0	100	100
24	P	141/179 (79%)	130 (92%)	10 (7%)	1 (1%)	18	35
25	Q	218/292 (75%)	211 (97%)	7 (3%)	0	100	100
26	R	138/149 (93%)	128 (93%)	10 (7%)	0	100	100
27	S	154/205 (75%)	147 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	T	164/212 (77%)	157 (96%)	7 (4%)	0	100	100
29	U	150/153 (98%)	144 (96%)	6 (4%)	0	100	100
30	V	204/216 (94%)	200 (98%)	4 (2%)	0	100	100
31	W	109/148 (74%)	103 (94%)	6 (6%)	0	100	100
32	X	241/256 (94%)	226 (94%)	15 (6%)	0	100	100
33	Y	174/250 (70%)	164 (94%)	10 (6%)	0	100	100
34	Z	118/161 (73%)	109 (92%)	9 (8%)	0	100	100
35	a	106/142 (75%)	103 (97%)	3 (3%)	0	100	100
36	b	146/155 (94%)	139 (95%)	7 (5%)	0	100	100
37	c	287/332 (86%)	265 (92%)	22 (8%)	0	100	100
38	d	255/306 (83%)	241 (94%)	14 (6%)	0	100	100
39	e	211/279 (76%)	194 (92%)	17 (8%)	0	100	100
40	f	144/194 (74%)	136 (94%)	8 (6%)	0	100	100
41	g	130/166 (78%)	121 (93%)	9 (7%)	0	100	100
42	h	108/158 (68%)	99 (92%)	9 (8%)	0	100	100
43	i	95/128 (74%)	91 (96%)	4 (4%)	0	100	100
44	j	91/123 (74%)	87 (96%)	4 (4%)	0	100	100
45	k	94/112 (84%)	90 (96%)	4 (4%)	0	100	100
46	l	70/138 (51%)	62 (89%)	8 (11%)	0	100	100
47	m	43/128 (34%)	39 (91%)	4 (9%)	0	100	100
48	o	92/102 (90%)	86 (94%)	6 (6%)	0	100	100
49	p	148/206 (72%)	134 (90%)	14 (10%)	0	100	100
50	q	166/222 (75%)	154 (93%)	6 (4%)	6 (4%)	2	3
51	r	160/196 (82%)	150 (94%)	10 (6%)	0	100	100
52	s	391/439 (89%)	364 (93%)	27 (7%)	0	100	100
54	TA	43/198 (22%)	39 (91%)	4 (9%)	0	100	100
54	TB	25/198 (13%)	24 (96%)	1 (4%)	0	100	100
54	TC	69/198 (35%)	64 (93%)	5 (7%)	0	100	100
All	All	8449/11190 (76%)	7907 (94%)	527 (6%)	15 (0%)	44	64

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	5	70	LEU
24	P	69	ARG
50	q	43	GLU
50	q	132	ILE
19	K	160	GLN

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	0	97/164 (59%)	95 (98%)	2 (2%)	47	72
2	1	49/60 (82%)	49 (100%)	0	100	100
3	2	40/72 (56%)	40 (100%)	0	100	100
4	3	88/166 (53%)	85 (97%)	3 (3%)	32	58
5	4	37/89 (42%)	36 (97%)	1 (3%)	39	65
6	5	353/368 (96%)	333 (94%)	20 (6%)	18	38
7	6	313/332 (94%)	299 (96%)	14 (4%)	24	48
8	7	272/303 (90%)	264 (97%)	8 (3%)	37	63
9	8	91/190 (48%)	89 (98%)	2 (2%)	45	70
10	9	104/112 (93%)	100 (96%)	4 (4%)	29	54
13	D	193/245 (79%)	184 (95%)	9 (5%)	23	46
14	E	260/290 (90%)	251 (96%)	9 (4%)	32	57
15	F	217/262 (83%)	213 (98%)	4 (2%)	51	75
16	H	88/228 (39%)	84 (96%)	4 (4%)	24	48
17	I	164/232 (71%)	158 (96%)	6 (4%)	30	55
18	J	138/150 (92%)	132 (96%)	6 (4%)	26	49
19	K	155/156 (99%)	151 (97%)	4 (3%)	40	66
20	L	98/124 (79%)	95 (97%)	3 (3%)	35	61
21	M	245/249 (98%)	241 (98%)	4 (2%)	55	78
22	N	189/211 (90%)	184 (97%)	5 (3%)	40	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	O	133/150 (89%)	131 (98%)	2 (2%)	57	79
24	P	125/154 (81%)	121 (97%)	4 (3%)	34	60
25	Q	202/256 (79%)	201 (100%)	1 (0%)	81	91
26	R	118/126 (94%)	116 (98%)	2 (2%)	53	76
27	S	141/180 (78%)	136 (96%)	5 (4%)	32	57
28	T	146/182 (80%)	138 (94%)	8 (6%)	19	39
29	U	125/135 (93%)	123 (98%)	2 (2%)	55	78
30	V	184/191 (96%)	179 (97%)	5 (3%)	39	65
31	W	91/119 (76%)	86 (94%)	5 (6%)	19	39
32	X	219/229 (96%)	210 (96%)	9 (4%)	27	52
33	Y	159/223 (71%)	155 (98%)	4 (2%)	42	68
34	Z	111/147 (76%)	108 (97%)	3 (3%)	39	65
35	a	101/133 (76%)	97 (96%)	4 (4%)	28	53
36	b	130/135 (96%)	127 (98%)	3 (2%)	44	69
37	c	253/288 (88%)	244 (96%)	9 (4%)	31	56
38	d	224/274 (82%)	214 (96%)	10 (4%)	24	48
39	e	188/236 (80%)	183 (97%)	5 (3%)	39	65
40	f	122/173 (70%)	117 (96%)	5 (4%)	27	52
41	g	122/148 (82%)	118 (97%)	4 (3%)	33	59
42	h	104/148 (70%)	96 (92%)	8 (8%)	12	25
43	i	86/110 (78%)	84 (98%)	2 (2%)	44	69
44	j	74/97 (76%)	72 (97%)	2 (3%)	39	65
45	k	81/90 (90%)	74 (91%)	7 (9%)	10	20
46	l	67/116 (58%)	67 (100%)	0	100	100
47	m	40/113 (35%)	39 (98%)	1 (2%)	42	68
48	o	80/87 (92%)	79 (99%)	1 (1%)	61	81
49	p	134/181 (74%)	127 (95%)	7 (5%)	21	42
50	q	114/178 (64%)	107 (94%)	7 (6%)	17	35
51	r	147/169 (87%)	143 (97%)	4 (3%)	39	65
52	s	336/381 (88%)	324 (96%)	12 (4%)	31	56
54	TA	39/158 (25%)	38 (97%)	1 (3%)	40	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
54	TB	26/158 (16%)	25 (96%)	1 (4%)	29 54
All	All	7413/9468 (78%)	7162 (97%)	251 (3%)	33 58

5 of 251 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	R	95	VAL
49	p	96	ASN
32	X	60	GLU
49	p	42	ILE
51	r	159	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
39	e	248	ASN
44	j	89	GLN
50	q	157	GLN
17	I	100	GLN
17	I	43	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	1523/1559 (97%)	360 (23%)	24 (1%)
12	B	51/72 (70%)	12 (23%)	1 (1%)
All	All	1574/1631 (96%)	372 (23%)	25 (1%)

5 of 372 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	1678	C
11	A	1679	U
11	A	1681	G
11	A	1689	C
11	A	1690	C

5 of 25 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	A	2559	U
11	A	2905	A
12	B	1607	U
11	A	2628	U
11	A	2989	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 106 ligands modelled in this entry, 105 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	$\# Z > 2$
57	ZLD	A	3400	56	26,26,26	0.88	1 (3%)	36,36,36	1.21	2 (5%)

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
57	ZLD	A	3400	56	-	2/13/33/33	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	A	3400	ZLD	C7-N4	-2.31	1.34	1.36

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	A	3400	ZLD	C6-C8-C9	4.30	118.25	113.38
57	A	3400	ZLD	O10-C7-O15	-2.63	119.32	122.40

There are no chirality outliers.

All (2) torsion outliers are listed below:

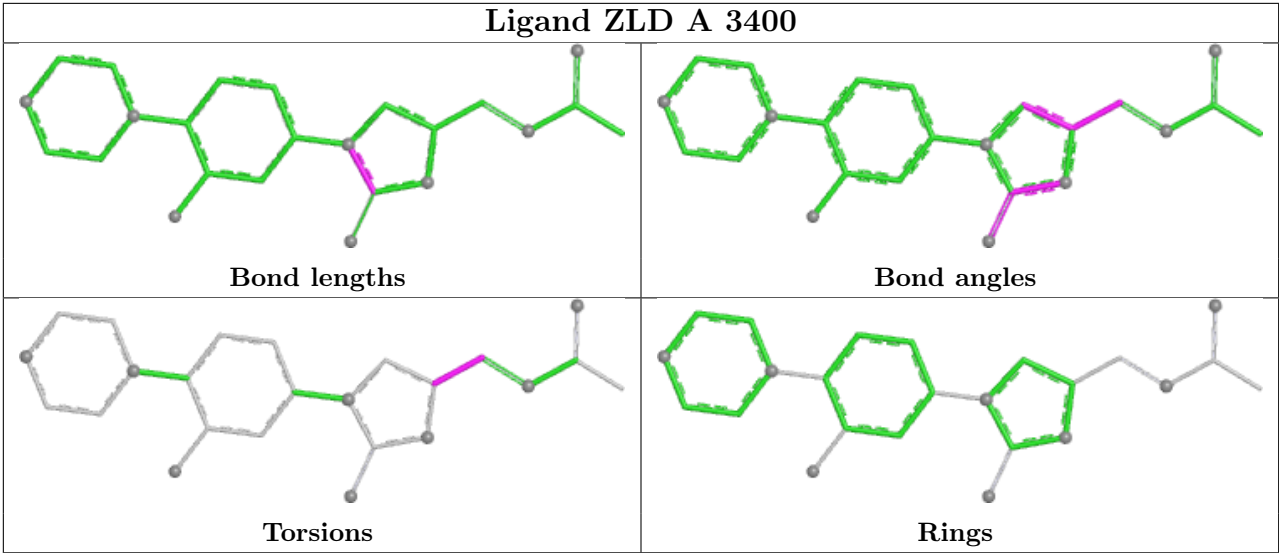
Mol	Chain	Res	Type	Atoms
57	A	3400	ZLD	C6-C8-C9-N11
57	A	3400	ZLD	O10-C8-C9-N11

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	A	3400	ZLD	3	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
53	u	4

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	50.73
1	u	106:UNK	C	301:UNK	N	32.84
1	u	315:UNK	C	399:UNK	N	24.40
1	u	615:UNK	C	700:UNK	N	14.68

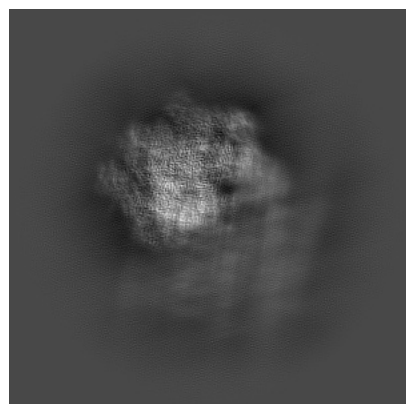
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45757. These allow visual inspection of the internal detail of the map and identification of artifacts.

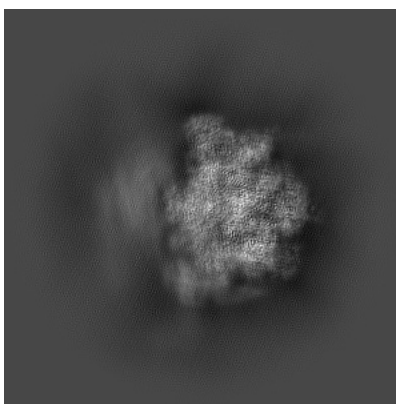
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

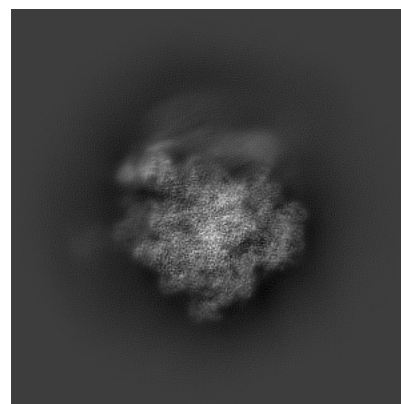
6.1.1 Primary map



X

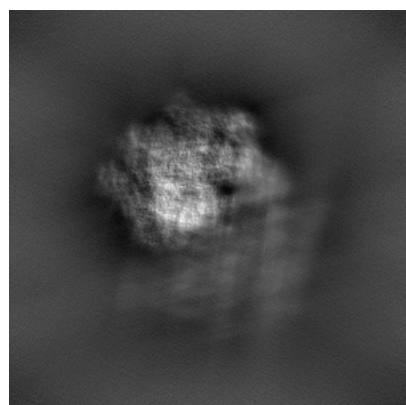


Y

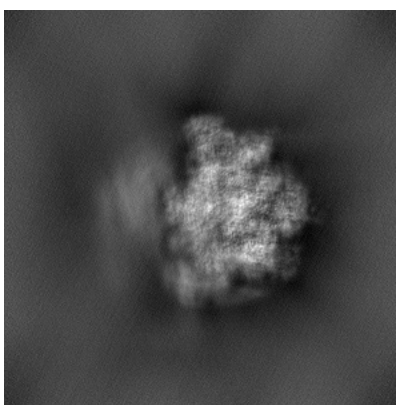


Z

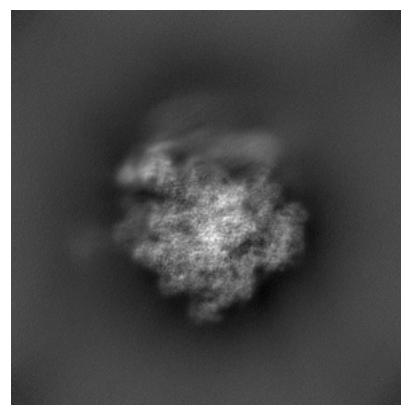
6.1.2 Raw map



X



Y

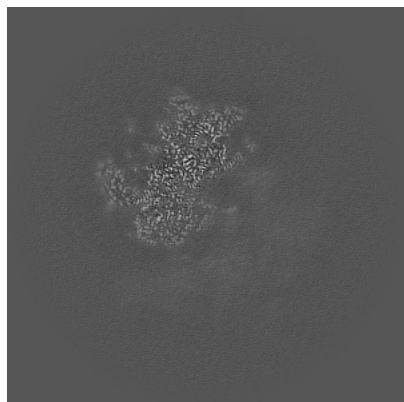


Z

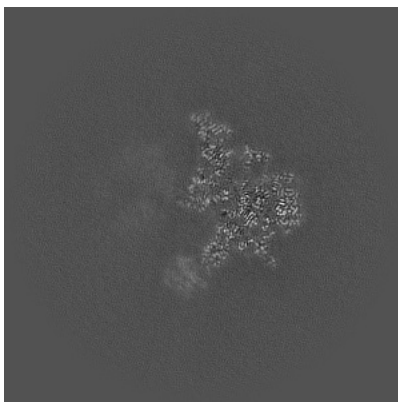
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

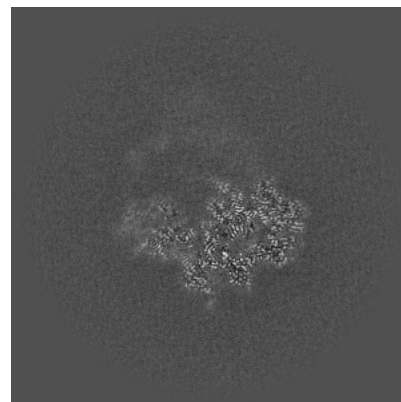
6.2.1 Primary map



X Index: 280

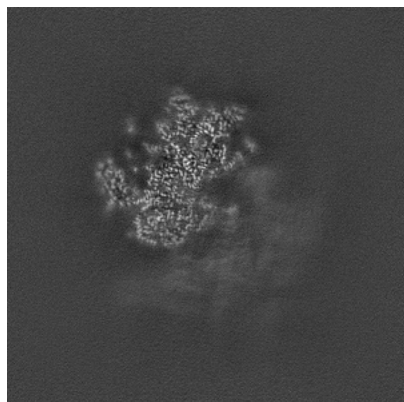


Y Index: 280

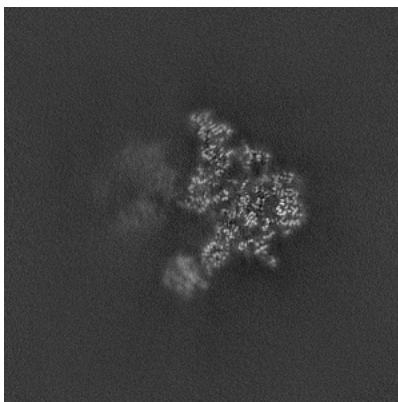


Z Index: 280

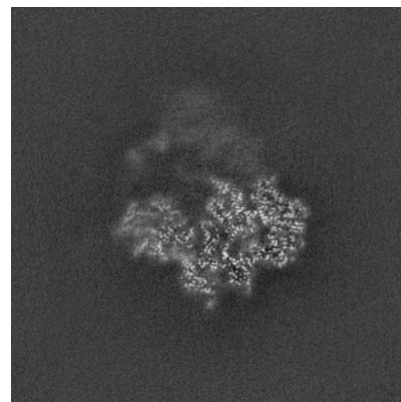
6.2.2 Raw map



X Index: 280



Y Index: 280

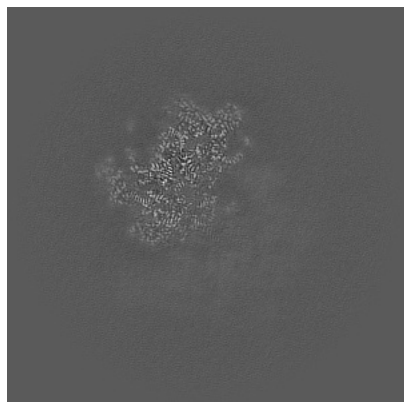


Z Index: 280

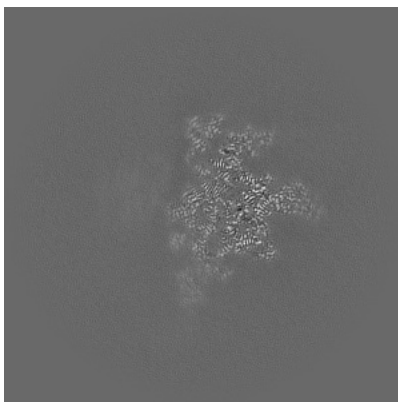
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

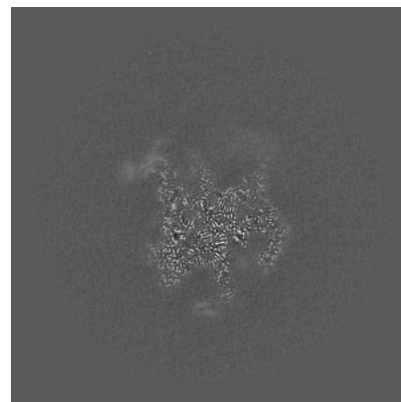
6.3.1 Primary map



X Index: 286

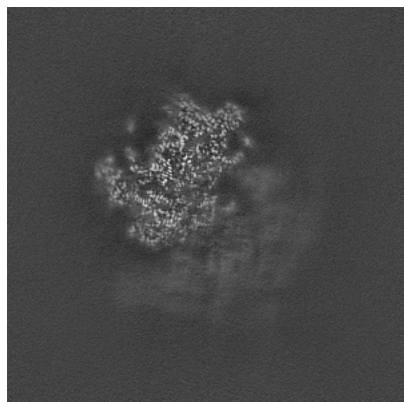


Y Index: 239

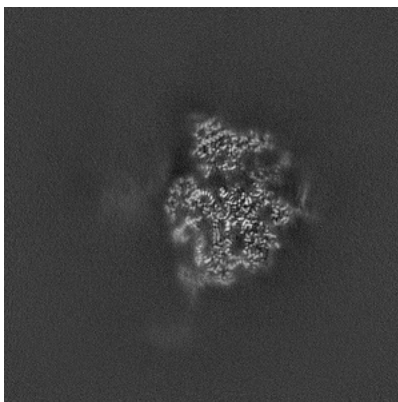


Z Index: 338

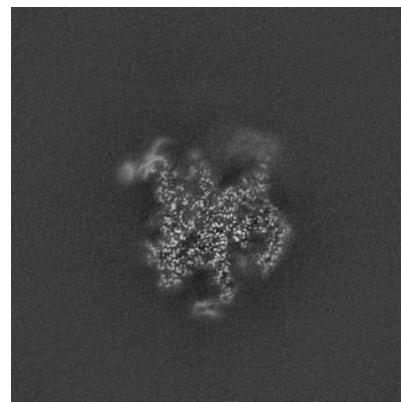
6.3.2 Raw map



X Index: 286



Y Index: 220

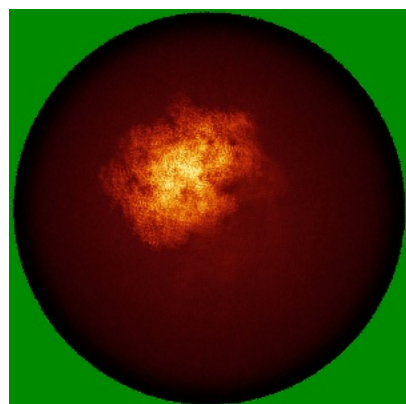


Z Index: 338

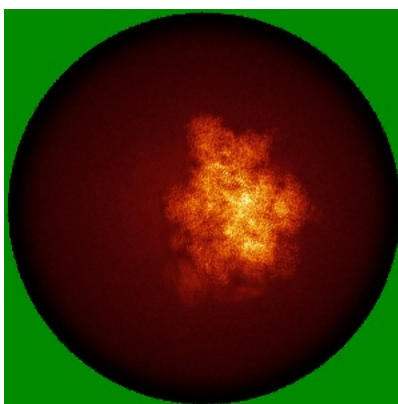
The images above show the largest variance slices of the map in three orthogonal directions.

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

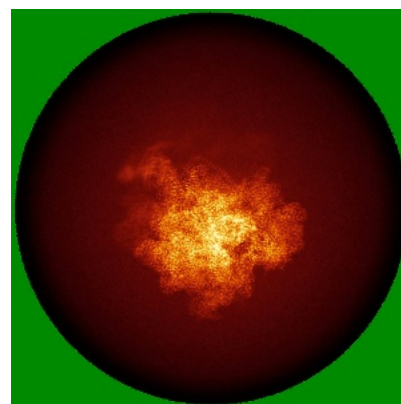
6.4.1 Primary map



X

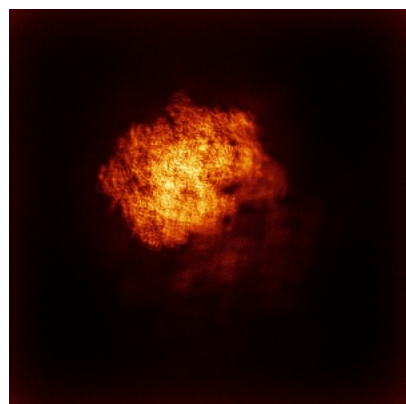


Y

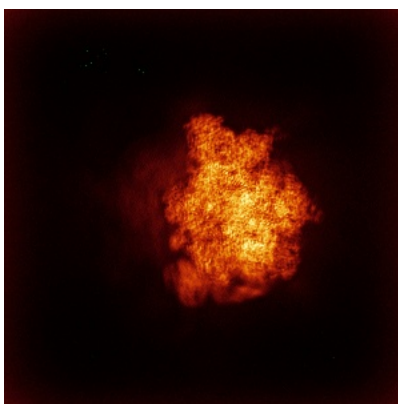


Z

6.4.2 Raw map



X



Y

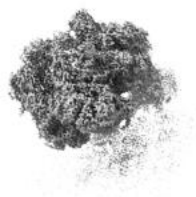


Z

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

6.5 Orthogonal surface views [i](#)

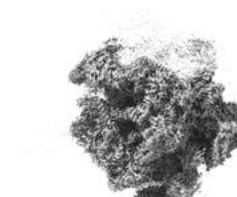
6.5.1 Primary map



X



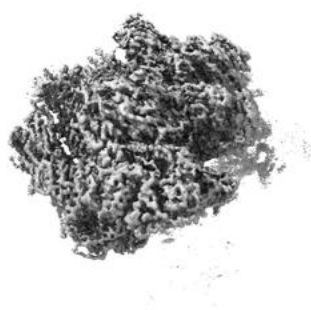
Y



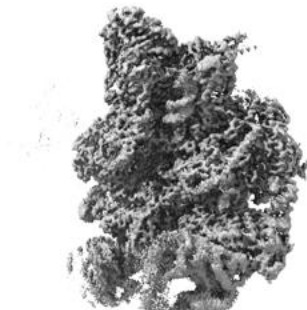
Z

The images above show the 3D surface view of the map at the recommended contour level 0.38. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

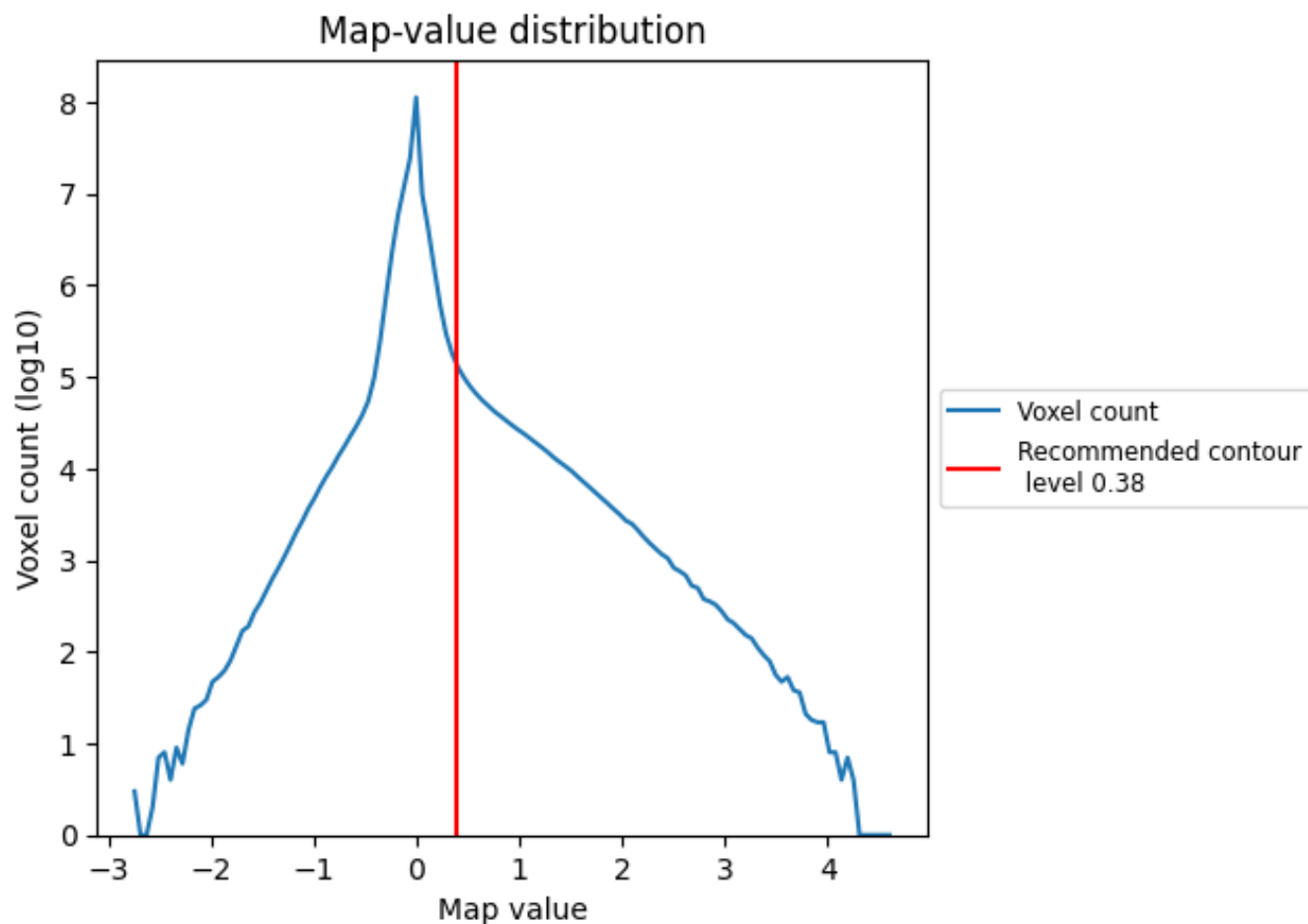
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

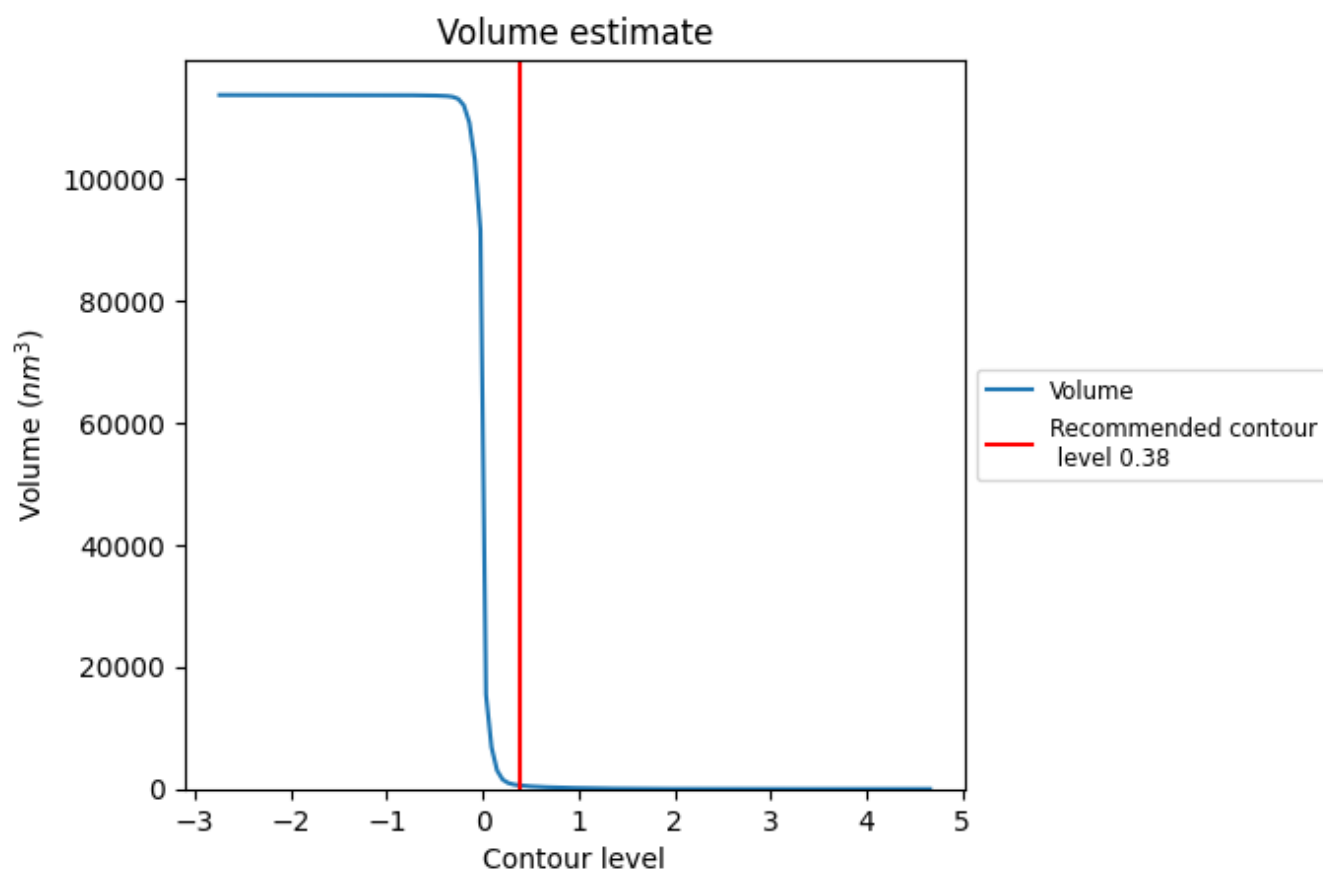
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

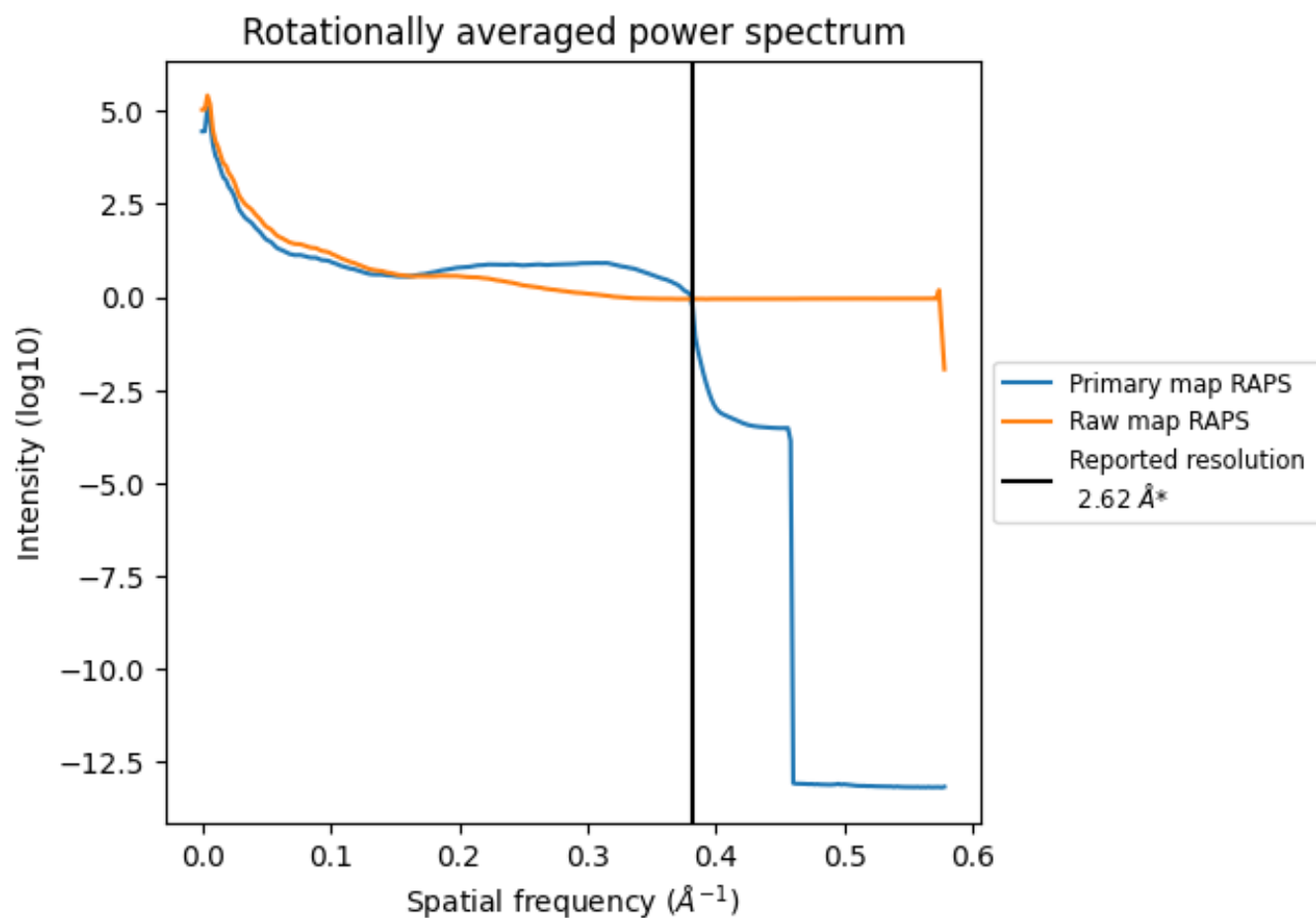
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 592 nm^3 ; this corresponds to an approximate mass of 535 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 ⓘ

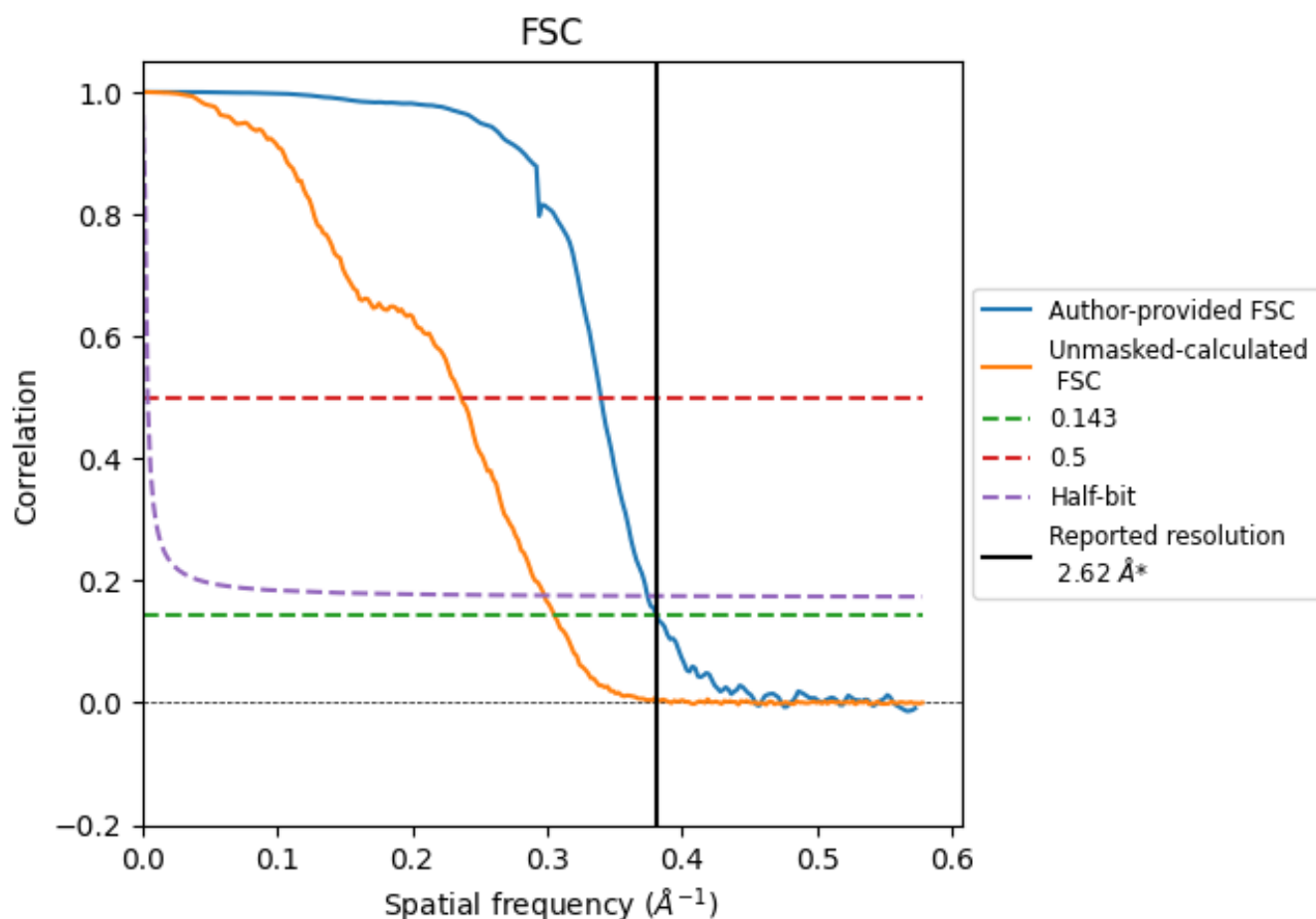


*Reported resolution corresponds to spatial frequency of 0.382 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.382 $\text{\AA}^{-1}$

8.2 Resolution estimates

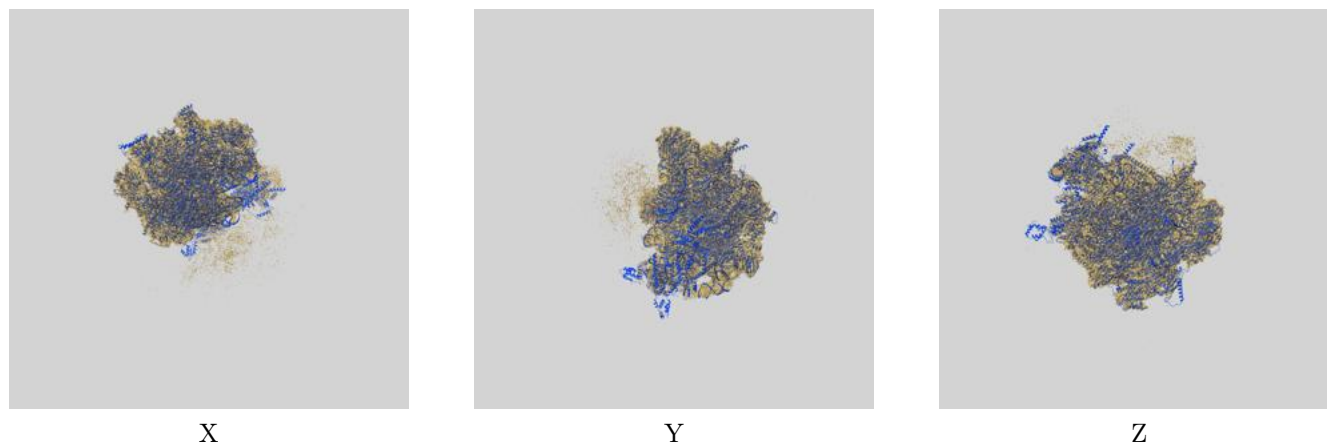
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.62	-	-
Author-provided FSC curve	2.62	2.94	2.67
Unmasked-calculated*	3.27	4.23	3.36

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.27 differs from the reported value 2.62 by more than 10 %

9 Map-model fit [i](#)

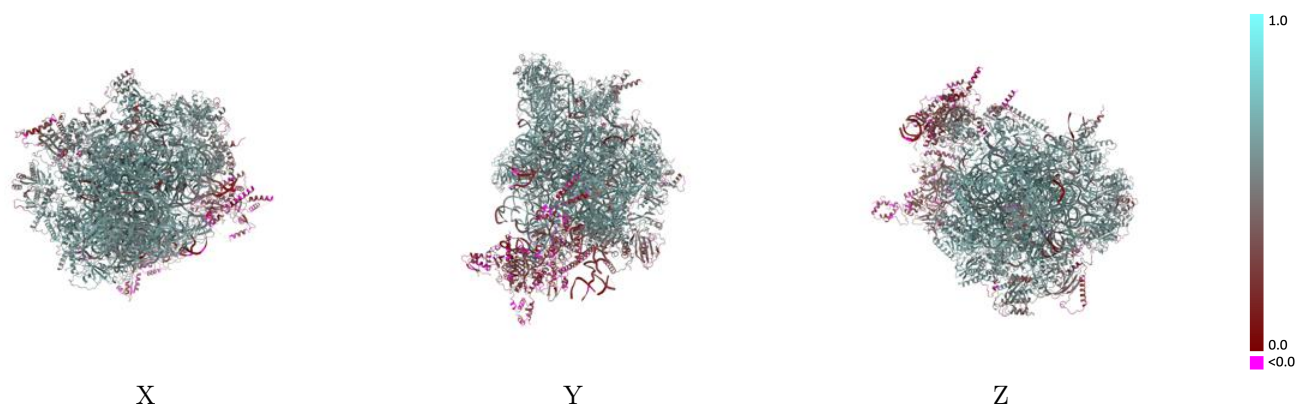
This section contains information regarding the fit between EMDB map EMD-45757 and PDB model 9CN3. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

9.1 Map-model overlay [i](#)



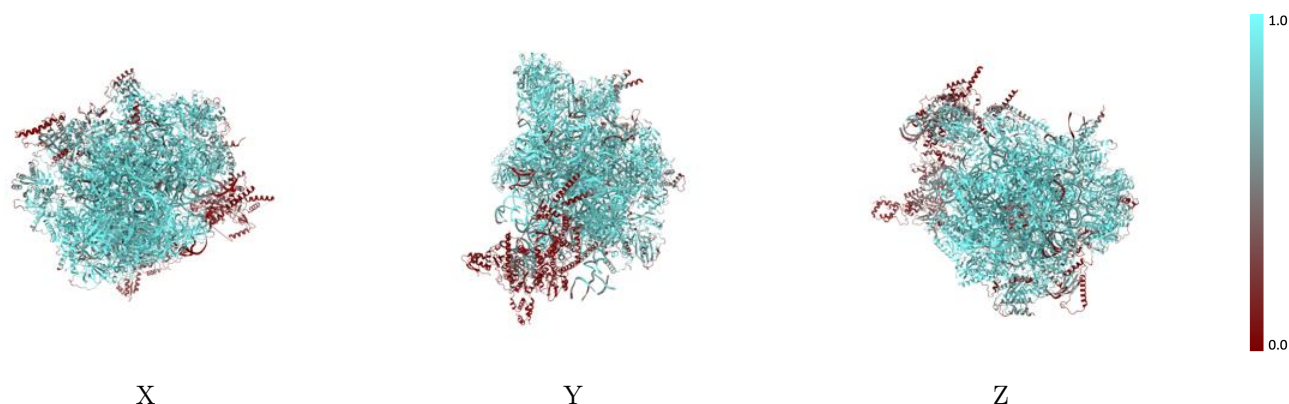
The images above show the 3D surface view of the map at the recommended contour level 0.38 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



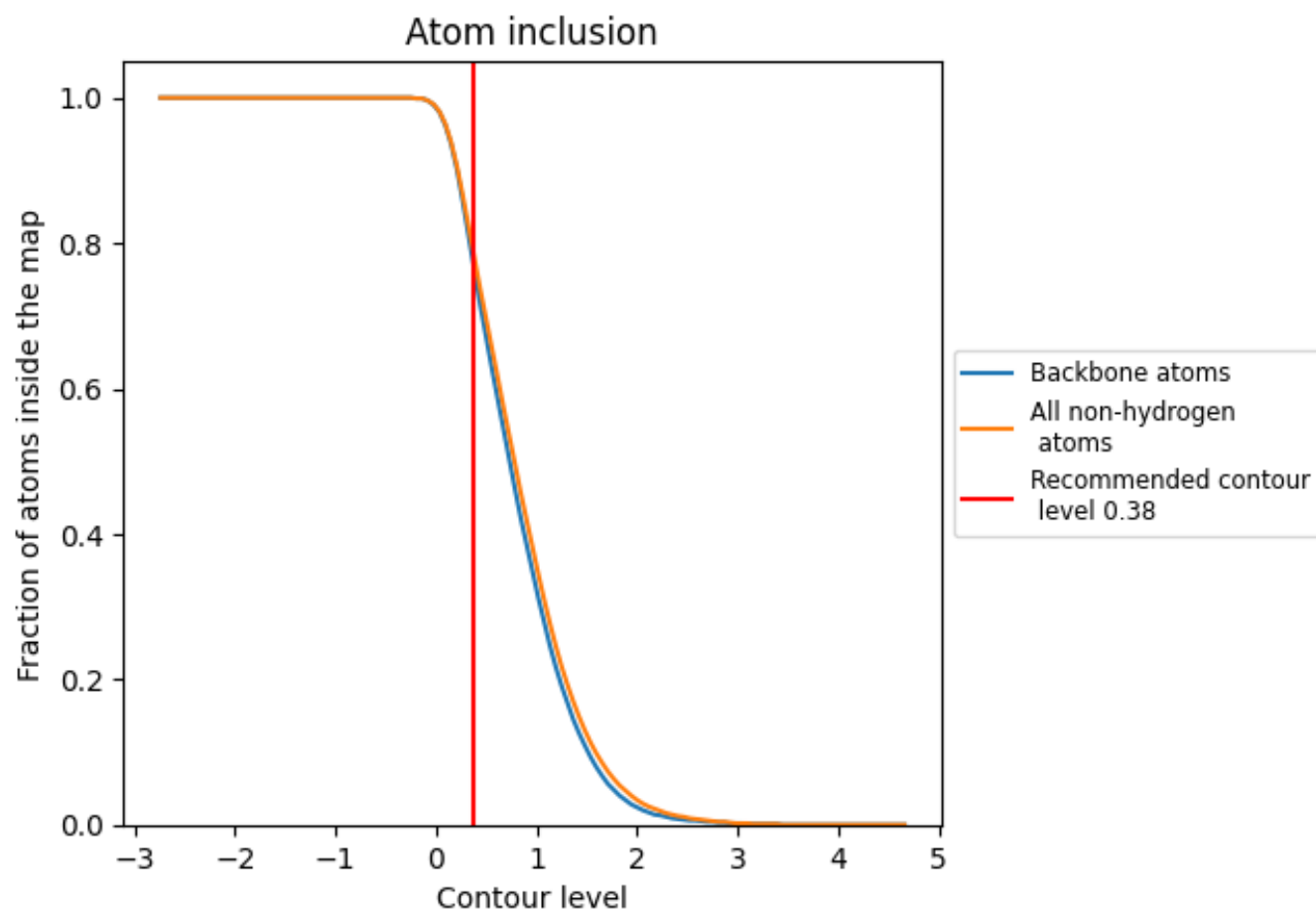
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.38).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 78% 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 (0.38) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7800	 0.5250
0	 0.8840	 0.5860
1	 0.8090	 0.5550
2	 0.9830	 0.6510
3	 0.9640	 0.6510
4	 0.9390	 0.6080
5	 0.8520	 0.5610
6	 0.7050	 0.4490
7	 0.7500	 0.5070
8	 0.1510	 0.1860
9	 0.7750	 0.5410
A	 0.8900	 0.5670
B	 0.6800	 0.2220
D	 0.8750	 0.5870
E	 0.8990	 0.5950
F	 0.9020	 0.6000
H	 0.7490	 0.5100
I	 0.3410	 0.2930
J	 0.1060	 0.1880
K	 0.9370	 0.6170
L	 0.8700	 0.5820
M	 0.8900	 0.5990
N	 0.8590	 0.5830
O	 0.9270	 0.6070
P	 0.8180	 0.5070
Q	 0.8540	 0.5870
R	 0.9320	 0.6180
S	 0.9500	 0.6200
T	 0.9220	 0.6250
TA	 0.0000	 0.1000
TB	 0.0000	 0.0950
TC	 0.0000	 0.0990
U	 0.7970	 0.5530
V	 0.5390	 0.4850
W	 0.9150	 0.6090



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Chain	Atom inclusion	Q-score
X	 0.8270	 0.5680
Y	 0.9100	 0.5990
Z	 0.9450	 0.6270
a	 0.7170	 0.5100
b	 0.9470	 0.6200
c	 0.8330	 0.5610
d	 0.4200	 0.4060
e	 0.0830	 0.1650
f	 0.2070	 0.2670
g	 0.9000	 0.5900
h	 0.5180	 0.4440
i	 0.9430	 0.6320
j	 0.8100	 0.5520
k	 0.3390	 0.2760
l	 0.2530	 0.3000
m	 0.1440	 0.1790
o	 0.9230	 0.6150
p	 0.5740	 0.4420
q	 0.5340	 0.4170
r	 0.8410	 0.5380
s	 0.8790	 0.5800
u	 0.0090	 0.0780