



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:59 PM UTC

PDB ID : 7O9M / pdb_00007o9m
EMDB ID : EMD-12764
Title : Human mitochondrial ribosome large subunit assembly intermediate with MTERF4-NSUN4, MRM2, MTG1 and the MALSU module
Authors : Valentin Gese, G.; Hallberg, B.M.
Deposited on : 2021-04-16
Resolution : 2.60 Å(reported)
Based on initial model : 5OOL

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:

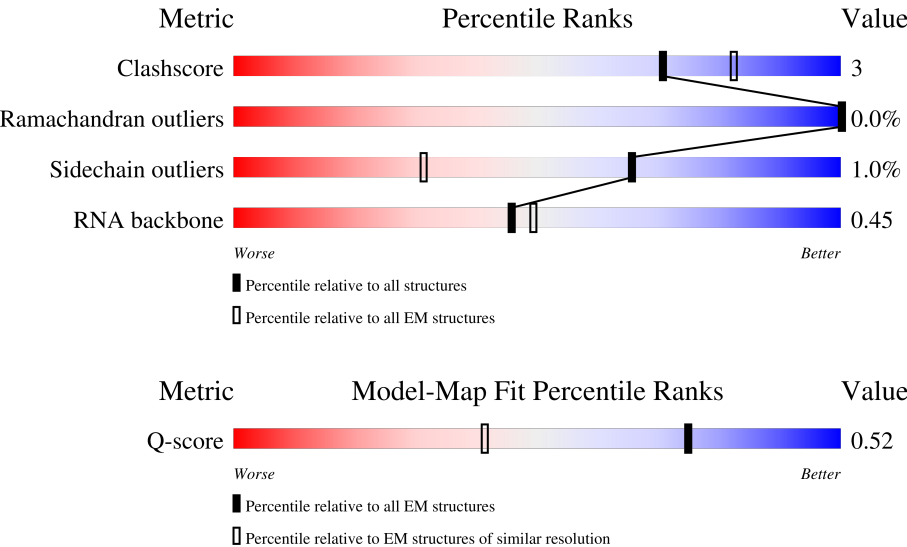
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.60 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.



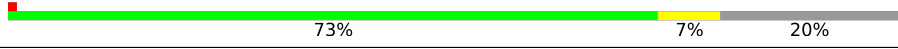
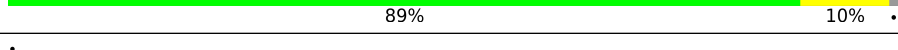
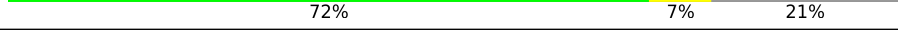
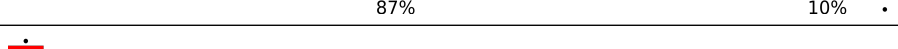
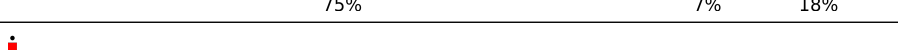
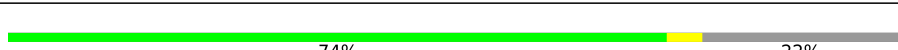
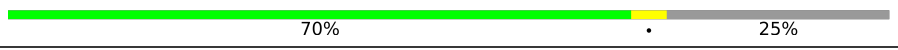
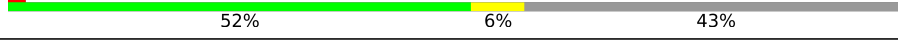
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8728 (2.10 - 3.10)

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

Mol	Chain	Length	Quality of chain
1	A	1559	7% 59% 28% 5% 8%
2	B	69	52% 29% 13%
3	C	333	68% 63% 9% 28%

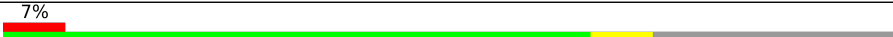
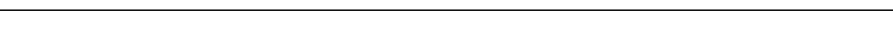
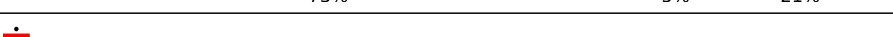
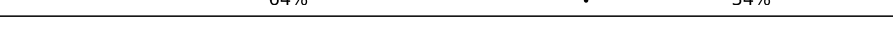
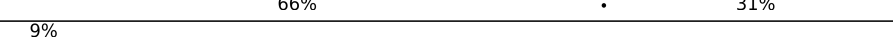
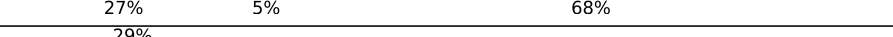
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Mol	Chain	Length	Quality of chain
4	D	305	
5	E	348	
6	F	311	
7	H	267	
8	I	261	
9	J	192	
10	K	178	
11	L	145	
12	M	296	
13	N	251	
14	O	175	
15	P	179	
16	Q	292	
17	R	149	
18	S	205	
19	T	212	
20	U	153	
21	V	216	
22	W	148	
23	X	256	
24	Y	250	
25	Z	161	
26	a	142	
27	0	188	
28	1	65	

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Mol	Chain	Length	Quality of chain
29	2	92	
30	3	188	
31	4	103	
32	5	423	
33	6	380	
34	7	338	
35	8	206	
36	9	137	
37	b	215	
38	c	332	
39	d	302	
40	e	279	
41	f	212	
42	g	166	
43	h	158	
44	i	128	
45	j	123	
46	k	112	
47	l	138	
48	m	128	
49	o	102	
50	p	205	
51	q	222	
52	r	196	
53	s	439	

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Mol	Chain	Length	Quality of chain
54	n	246	
55	A1	384	
56	A2	381	
57	v	70	
58	u	234	
59	t1	198	
59	t2	198	
59	t3	198	
59	t4	198	
59	t5	198	
59	t6	198	
60	w	156	
61	UNK	26	

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 110030 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1441	Total	C	N	O	P	0	2
			30552	13711	5512	9889	1440		

- Molecule 2 is a RNA chain called MT-TRNAVAL.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	60	Total	C	N	O	P	0	0
			1275	572	230	413	60		

- Molecule 3 is a protein called Mitochondrial ribosome-associated GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	240	Total	C	N	O	S	0	0
			1878	1195	330	342	11		

- Molecule 4 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	238	Total	C	N	O	S	0	0
			1859	1157	376	317	9		

- Molecule 5 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	304	Total	C	N	O	S	0	0
			2396	1539	416	430	11		

- Molecule 6 is a protein called 39S ribosomal protein L4, mitochondrial.

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

- Molecule 7 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	H	90	Total	C	N	O	0	0
			749	477	146	126		

- Molecule 8 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	205	Total	C	N	O	S	0	0
			1646	1059	293	283	11		

- Molecule 9 is a protein called 39S ribosomal protein L11, mitochondrial.

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

- Molecule 10 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 11 is a protein called 39S ribosomal protein L14, mitochondrial.

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

- Molecule 12 is a protein called 39S ribosomal protein L15, mitochondrial.

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

- Molecule 13 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	206	Total	C	N	O	S	0	0
			1676	1076	302	289	9		

- Molecule 14 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 15 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	141	Total	C	N	O	S	0	0
			1148	719	221	203	5		

- Molecule 16 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	217	Total	C	N	O	S	0	0
			1805	1159	317	320	9		

- Molecule 17 is a protein called 39S ribosomal protein L20, mitochondrial.

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

- Molecule 18 is a protein called 39S ribosomal protein L21, mitochondrial.

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

- Molecule 19 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 20 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	139	Total	C	N	O	S	0	0
			1154	734	220	197	3		

- Molecule 21 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	202	Total	C	N	O	S	0	0
			1652	1053	294	297	8		

- Molecule 22 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	101	Total	C	N	O	S	0	0
			805	520	151	131	3		

- Molecule 23 is a protein called 39S ribosomal protein L28, mitochondrial.

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

- Molecule 24 is a protein called 39S ribosomal protein L47, mitochondrial.

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

- Molecule 25 is a protein called 39S ribosomal protein L30, mitochondrial.

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

- Molecule 26 is a protein called 39S ribosomal protein L42, mitochondrial.

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	2	45	Total	C	N	O	S	0	0
			367	227	81	58	1		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4	38	Total	C	N	O	S	0	0
			342	217	72	49	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5	392	Total	C	N	O	S	0	0
			3199	2067	558	563	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	6	324	Total	C	N	O	S	0	0
			2723	1743	488	484	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	7	287	Total	C	N	O	S	0	0
			2334	1495	397	425	17		

- Molecule 35 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	8	85	Total	C	N	O	S	0	0
			719	454	129	134	2		

- Molecule 36 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	9	123	Total	C	N	O	S	0	0
			992	642	169	179	2		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	c	286	Total	C	N	O	S	0	0
			2300	1469	396	426	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	d	220	Total	C	N	O	S	0	0
			1819	1170	310	327	12		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	f	130	Total	C	N	O	S	0	0
			1044	669	172	200	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	g	131	Total	C	N	O	S	0	0
			1085	701	190	192	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	h	105	Total	C	N	O	S	0	0
			862	548	151	160	3		

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

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

- Molecule 45 is a protein called 39S ribosomal protein L52, mitochondrial.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	k	95	Total	C	N	O	S	0	0
			732	456	139	132	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	l	44	Total	C	N	O	S	0	0
			395	251	76	67	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	m	42	Total	C	N	O	S	0	0
			345	216	70	57	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	o	80	Total	C	N	O	S	0	0
			670	423	131	113	3		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	q	135	Total	C	N	O	S	0	0
			1134	705	222	202	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
52	r	157	Total	C	N	O	S	0	0
			1283	817	245	213	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
53	s	372	Total	C	N	O	S	0	0
			3052	1956	544	538	14		

- Molecule 54 is a protein called rRNA methyltransferase 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	n	215	Total	C	N	O	S	0	0
			1667	1055	303	303	6		

- Molecule 55 is a protein called 5-methylcytosine rRNA methyltransferase NSUN4.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	A1	335	Total	C	N	O	S	0	0
			2652	1690	463	482	17		

- Molecule 56 is a protein called Transcription termination factor 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	A2	238	Total	C	N	O	S	0	0
			1942	1244	336	350	12		

- Molecule 57 is a protein called MIEF1 upstream open reading frame protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	v	69	Total	C	N	O		0	0
			589	372	116	101			

- Molecule 58 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	u	129	Total	C	N	O	S	0	0
			1064	685	175	194	10		

- Molecule 59 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	t1	46	Total	C	N	O		0	0
			354	228	56	70			
59	t2	30	Total	C	N	O		0	0
			238	154	38	46			
59	t3	30	Total	C	N	O		0	0
			238	154	38	46			
59	t4	29	Total	C	N	O		0	0
			229	148	36	45			
59	t6	27	Total	C	N	O		0	0
			214	137	34	43			
59	t5	29	Total	C	N	O		0	0
			229	148	36	45			

- Molecule 60 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	w	87	Total	C	N	O	S	0	0
			705	452	103	144	6		

- Molecule 61 is a protein called Unknown residues.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	UNK	26	Total	C	N	O		0	0
			130	78	26	26			

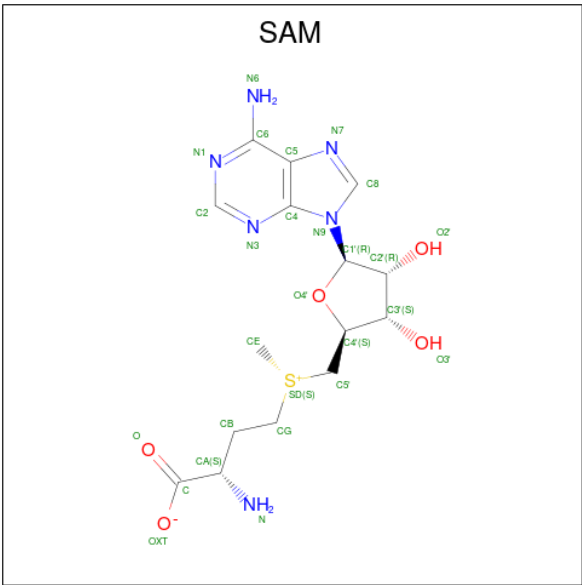
- | Mol | Chain | Residues | Atoms | AltConf |
|-----|-------|----------|---------------------|---------|
| 62 | A | 101 | Total Mg
101 101 | 0 |
| 62 | D | 1 | Total Mg
1 1 | 0 |
| 62 | F | 1 | Total Mg
1 1 | 0 |
| 62 | n | 1 | Total Mg
1 1 | 0 |

-
- The image displays the chemical structure of GDP (Guanosine Diphosphate). It consists of a guanine base (a purine derivative) linked to a ribose sugar, which is in turn linked to two phosphate groups. The guanine base is shown with its characteristic fused ring system, including the amino group at the 2-position. The ribose sugar is a five-membered ring with hydroxyl groups at the 2' and 3' positions. The two phosphate groups are connected by a pyrophosphate linkage, with the second phosphate group being the terminal one. The structure is labeled with various atoms and bonds, including the nitrogenous base (Guanine), the sugar (Ribose), and the phosphate groups (Phosphate 1 and Phosphate 2).

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

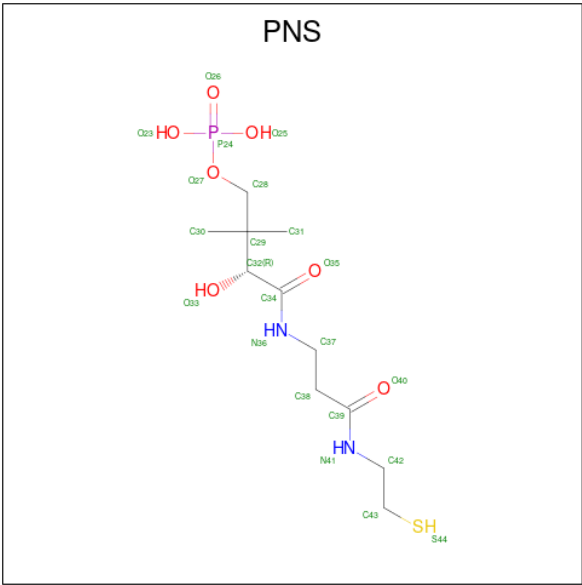
- | Mol | Chain | Residues | Atoms | AltConf |
|-----|-------|----------|-----------------|---------|
| 64 | 0 | 1 | Total Zn
1 1 | 0 |
| 64 | 4 | 1 | Total Zn
1 1 | 0 |

- WORLDWIDE
PDB
PROTEIN DATA BANK



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
65	A1	1	27	15	6	5	1	0

- Molecule 66 is 4'-PHOSPHOPANTETHEINE (CCD ID: PNS) (formula: C₁₁H₂₃N₂O₇PS).

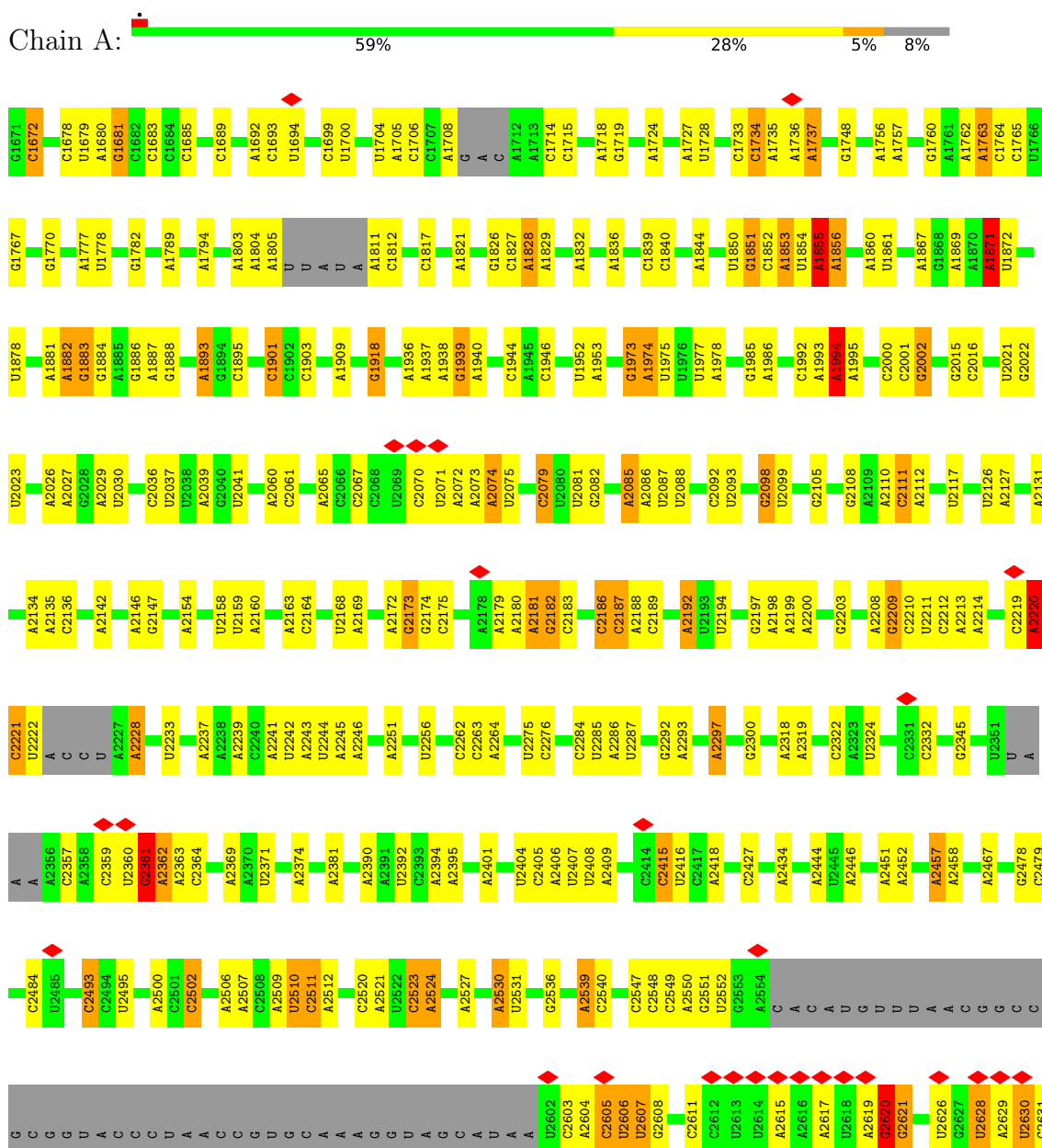


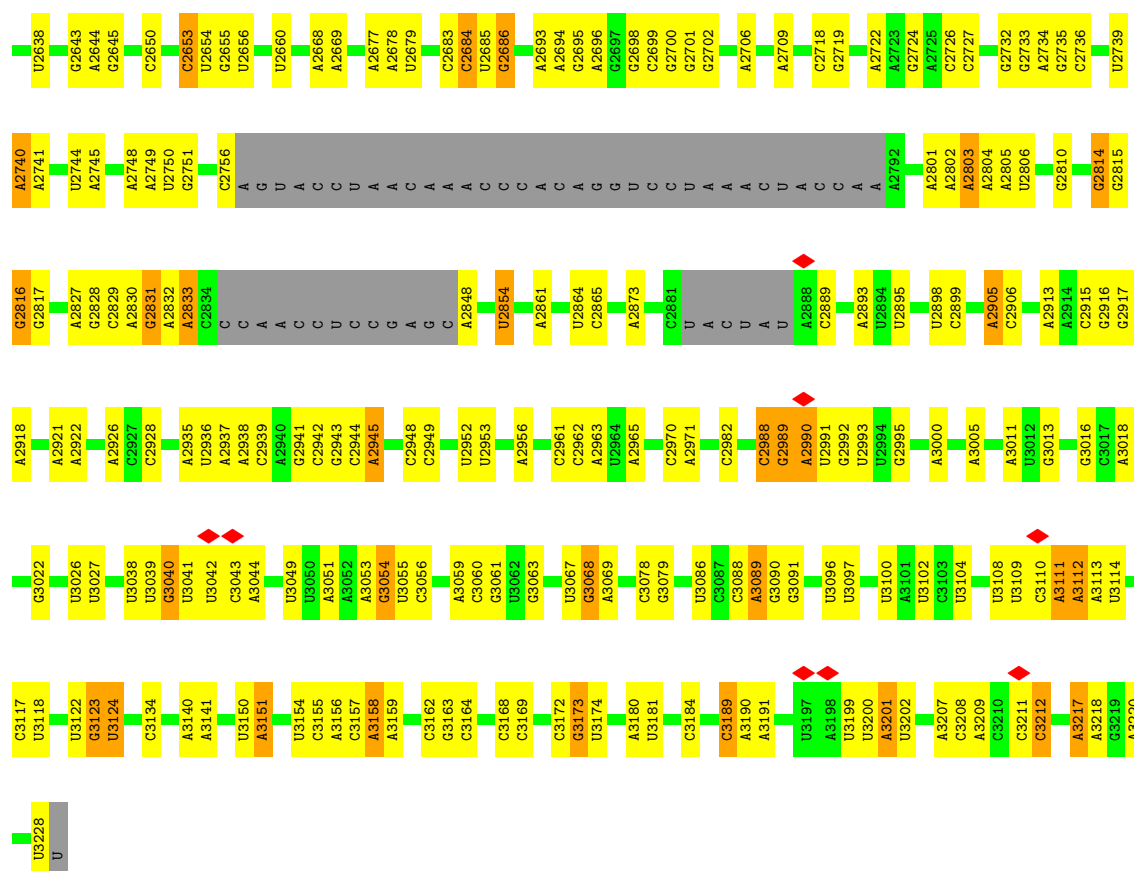
Mol	Chain	Residues	Atoms						AltConf
			Total	C	N	O	P	S	
66	w	1	21	11	2	6	1	1	0

3 Residue-property plots

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

• Molecule 1: 16S rRNA

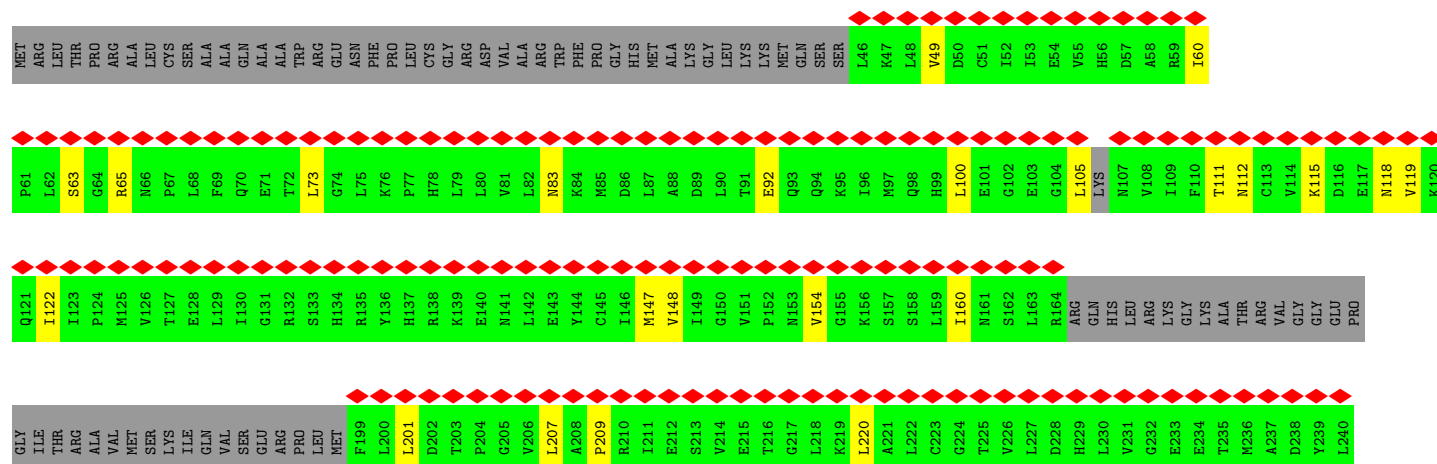




• Molecule 2: MT-TRNAVAL



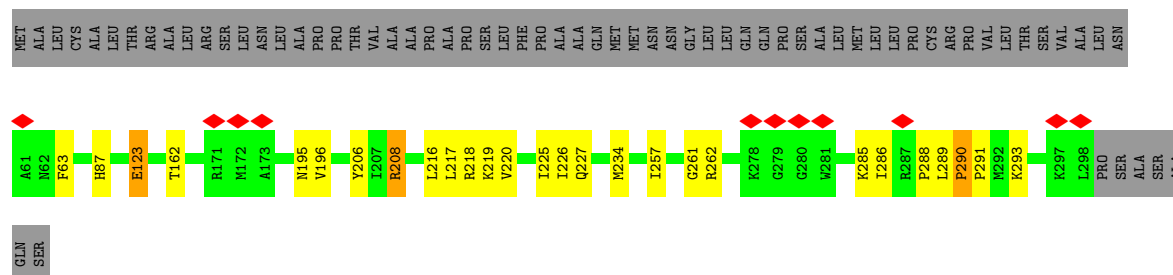
• Molecule 3: Mitochondrial ribosome-associated GTPase 1





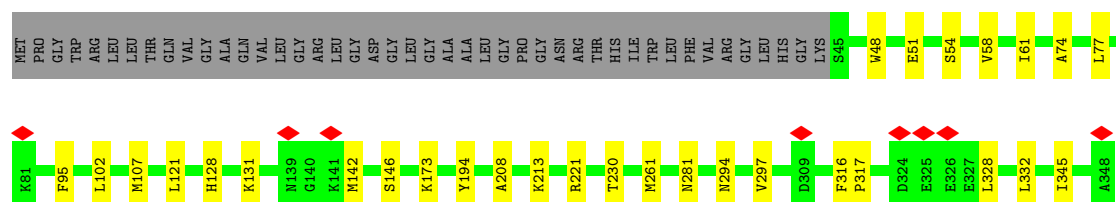
- Molecule 4: 39S ribosomal protein L2, mitochondrial

Chain D: 69% 8% 22%



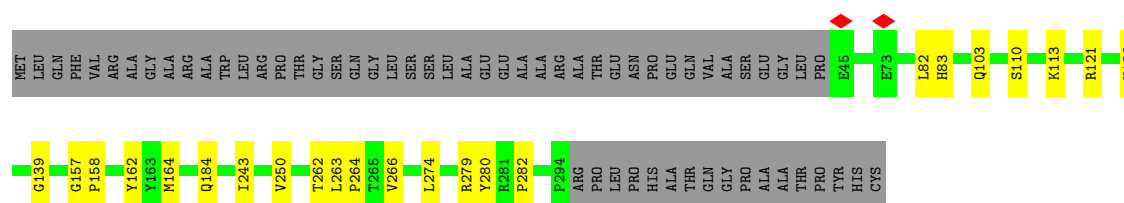
- Molecule 5: 39S ribosomal protein L3, mitochondrial

Chain E: 79% 9% 13%



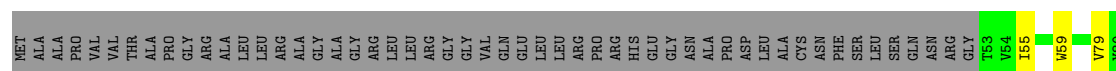
- Molecule 6: 39S ribosomal protein L4, mitochondrial

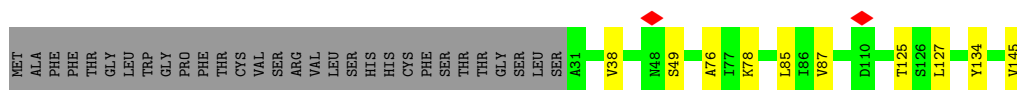
Chain F: 73% 7% 20%



- Molecule 7: 39S ribosomal protein L9, mitochondrial

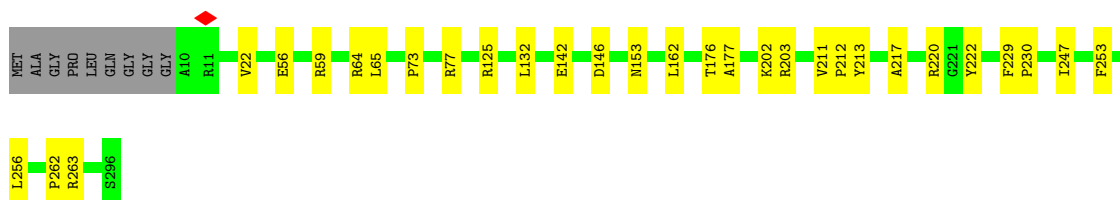
Chain H: 30% 66%





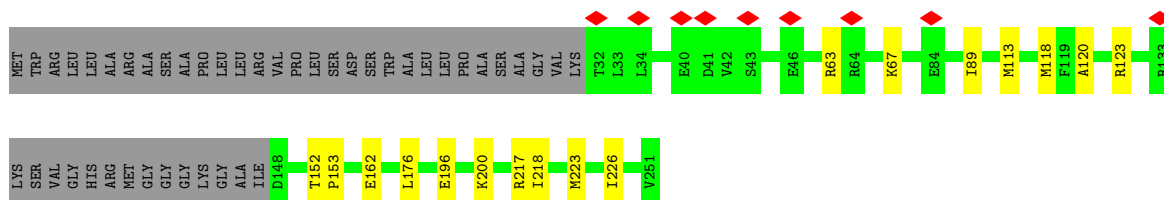
- Molecule 12: 39S ribosomal protein L15, mitochondrial

Chain M: 87% 10% .



- Molecule 13: 39S ribosomal protein L16, mitochondrial

Chain N: 75% 7% 18%



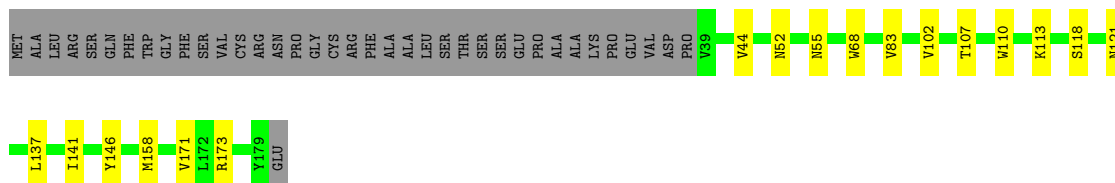
- Molecule 14: 39S ribosomal protein L17, mitochondrial

Chain O: 78% 9% 13%



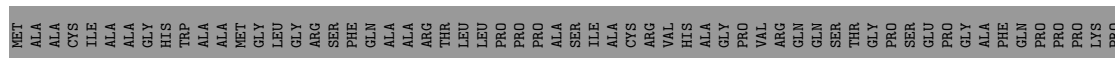
- Molecule 15: Mitochondrial ribosomal protein L18, isoform CRA_b

Chain P: 69% 9% 21%



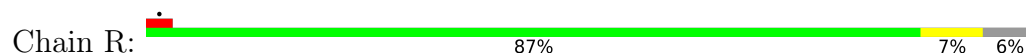
- Molecule 16: 39S ribosomal protein L19, mitochondrial

Chain Q: 68% 6% 26%

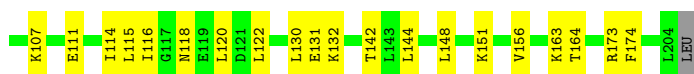
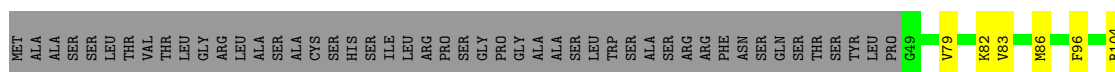




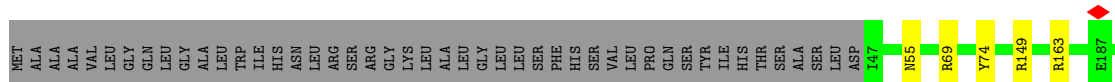
- Molecule 17: 39S ribosomal protein L20, mitochondrial



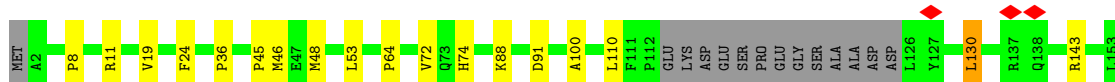
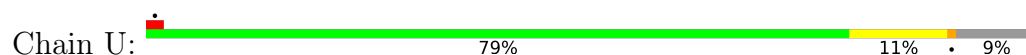
- Molecule 18: 39S ribosomal protein L21, mitochondrial



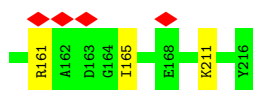
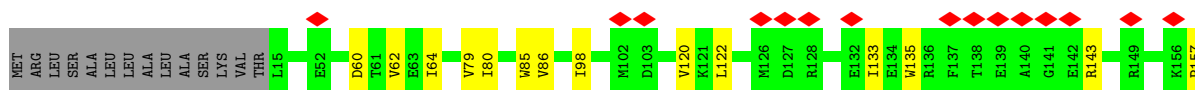
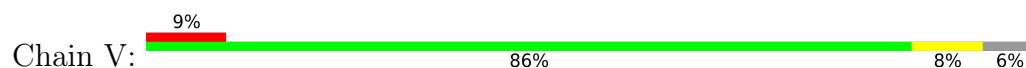
- Molecule 19: 39S ribosomal protein L22, mitochondrial



- Molecule 20: 39S ribosomal protein L23, mitochondrial

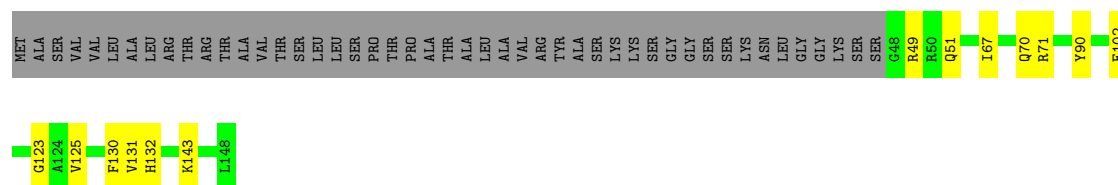


- Molecule 21: 39S ribosomal protein L24, mitochondrial



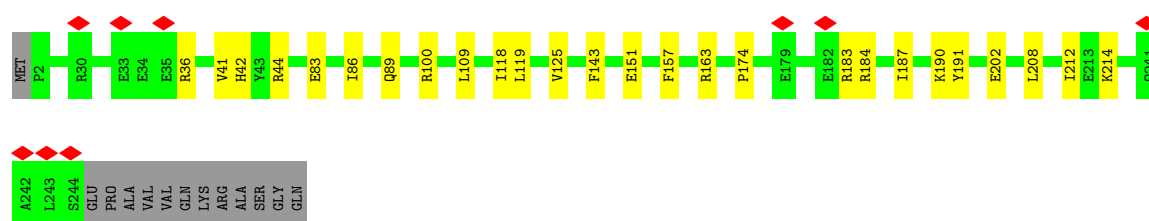
- Molecule 22: 39S ribosomal protein L27, mitochondrial

Chain W:  59% 9% 32%



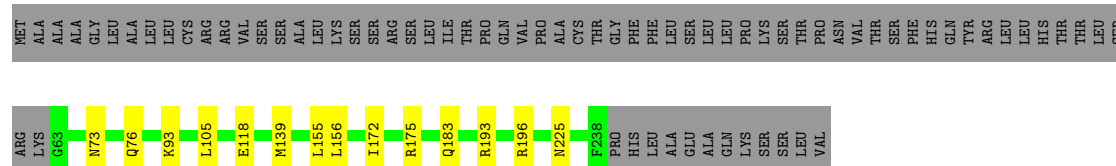
- Molecule 23: 39S ribosomal protein L28, mitochondrial

Chain X:  85% 10% 5%



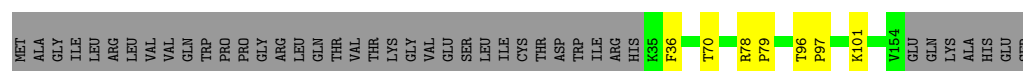
- Molecule 24: 39S ribosomal protein L47, mitochondrial

Chain Y:  65% 6% 30%



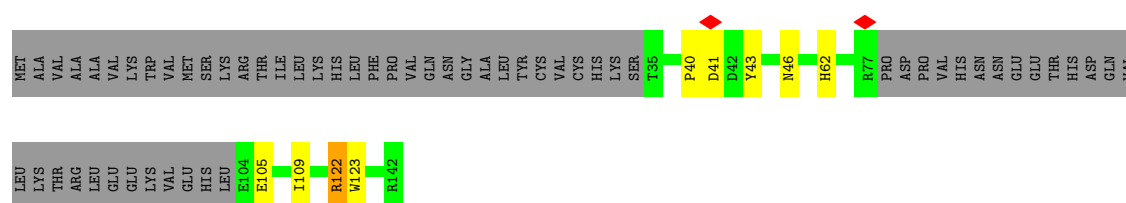
- Molecule 25: 39S ribosomal protein L30, mitochondrial

Chain Z:  70% 25%



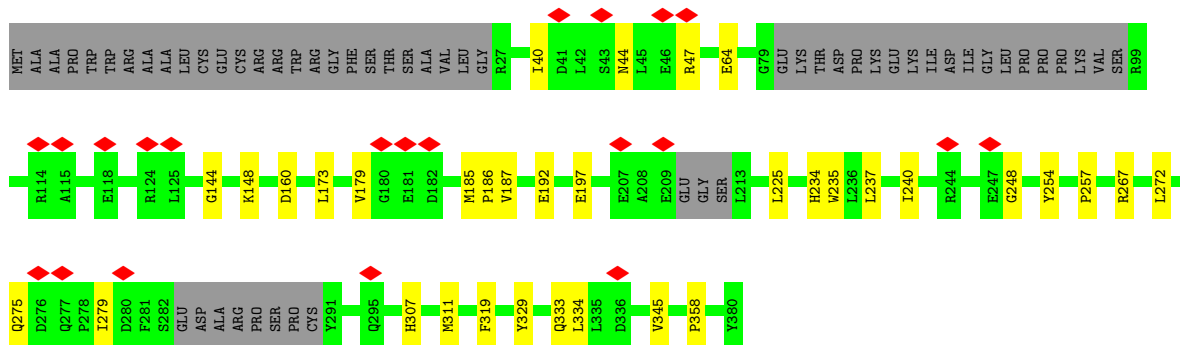
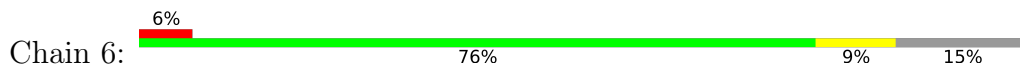
- Molecule 26: 39S ribosomal protein L42, mitochondrial

Chain a:  51% 6% 42%

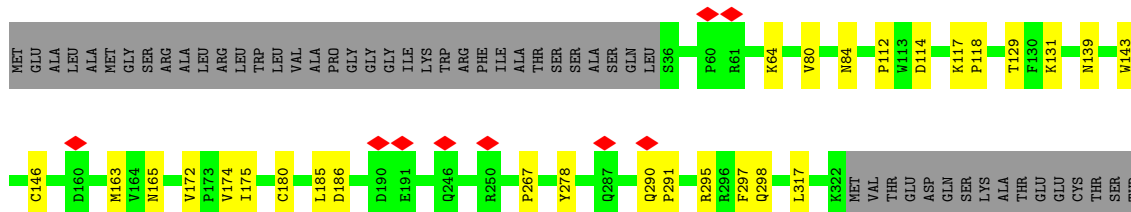
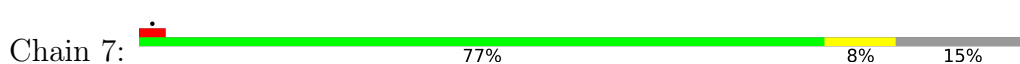


- Molecule 27: 39S ribosomal protein L32, mitochondrial

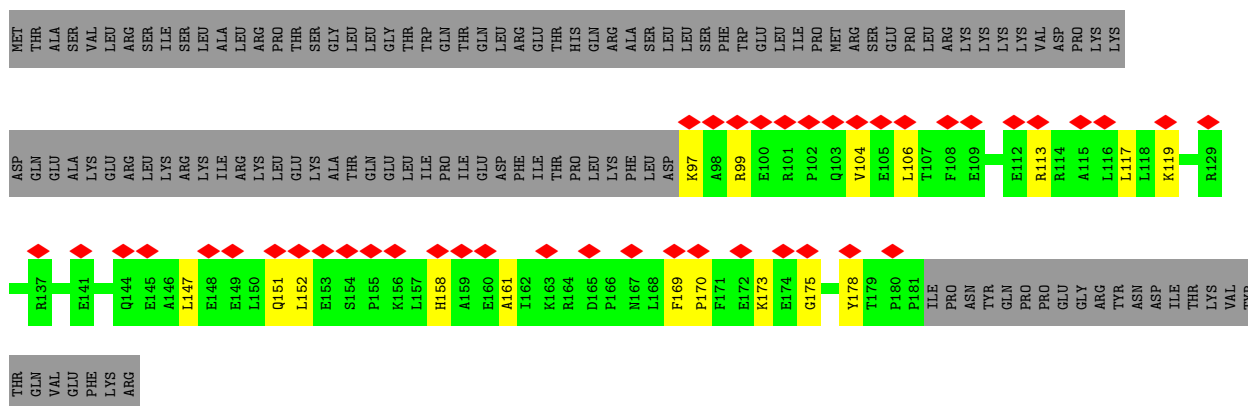
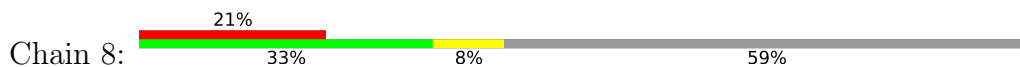
- Molecule 33: 39S ribosomal protein L38, mitochondrial



- Molecule 34: 39S ribosomal protein L39, mitochondrial

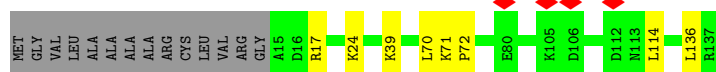


- Molecule 35: 39S ribosomal protein L40, mitochondrial



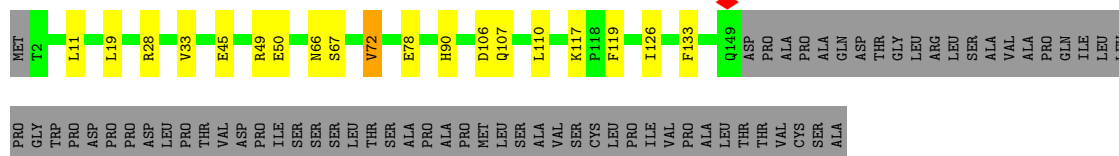
- Molecule 36: 39S ribosomal protein L41, mitochondrial

Chain 9: 



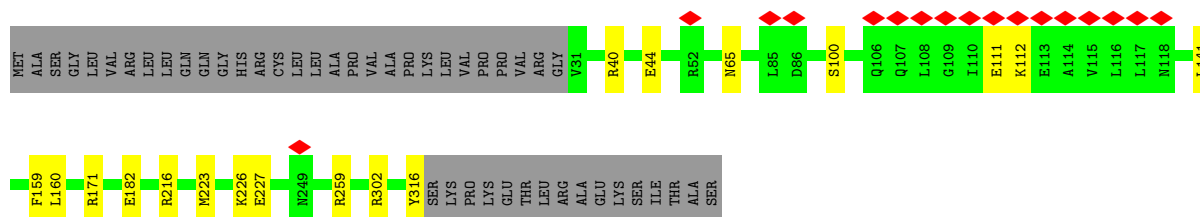
- Molecule 37: 39S ribosomal protein L43, mitochondrial

Chain b: 



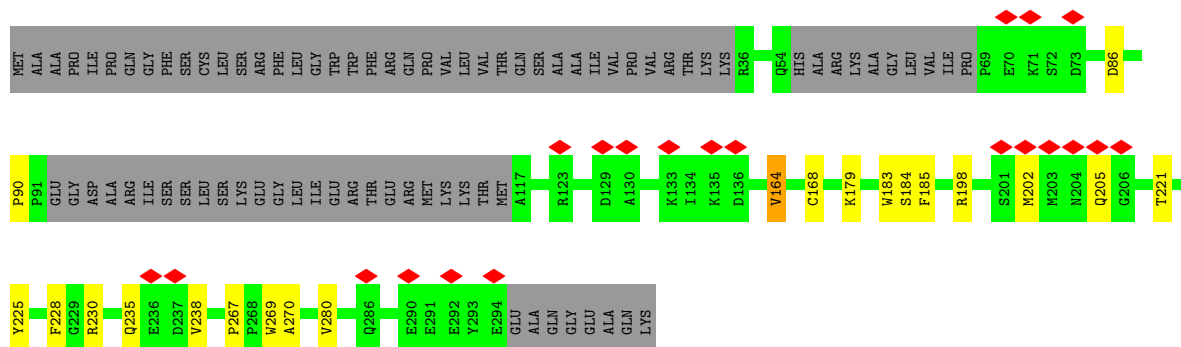
- Molecule 38: 39S ribosomal protein L44, mitochondrial

Chain c: 



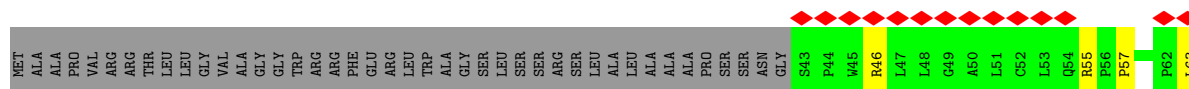
- Molecule 39: 39S ribosomal protein L45, mitochondrial

Chain d: 



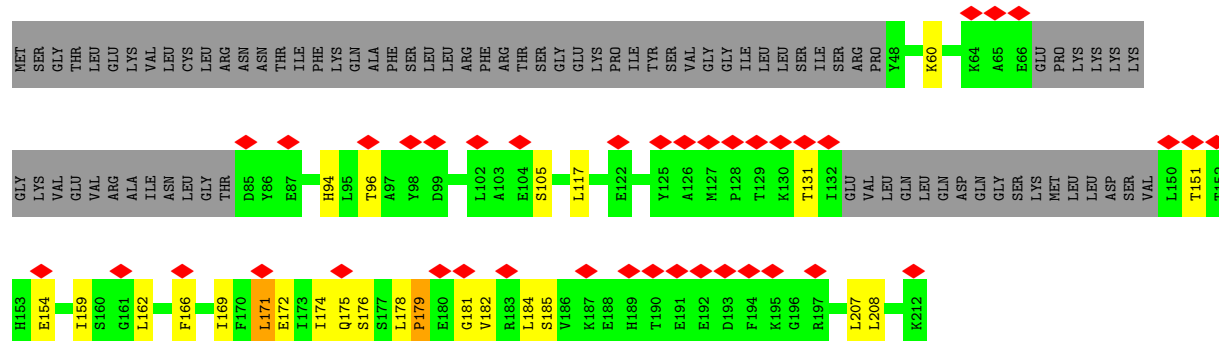
- Molecule 40: 39S ribosomal protein L46, mitochondrial

Chain e: 

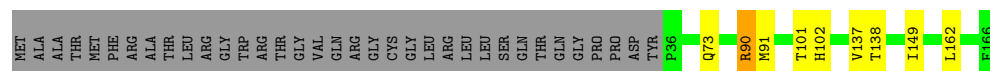




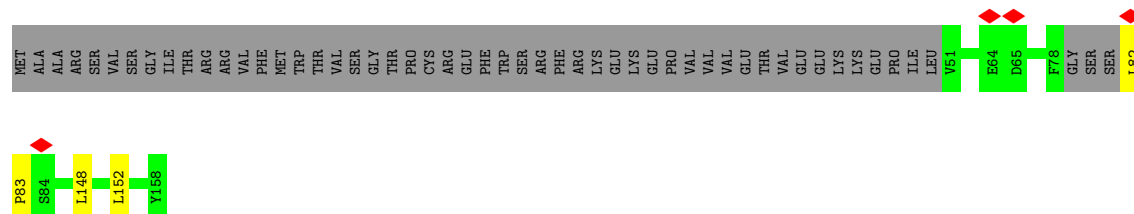
- Molecule 41: 39S ribosomal protein L48, mitochondrial



- Molecule 42: 39S ribosomal protein L49, mitochondrial

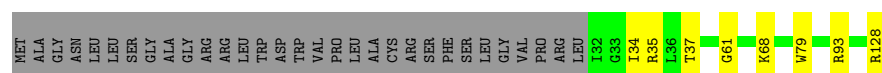


- Molecule 43: 39S ribosomal protein L50, mitochondrial



- Molecule 44: 39S ribosomal protein L51, mitochondrial

Chain i: 



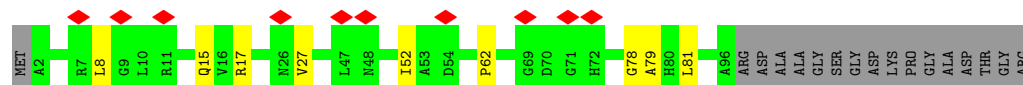
- Molecule 45: 39S ribosomal protein L52, mitochondrial

Chain j: 



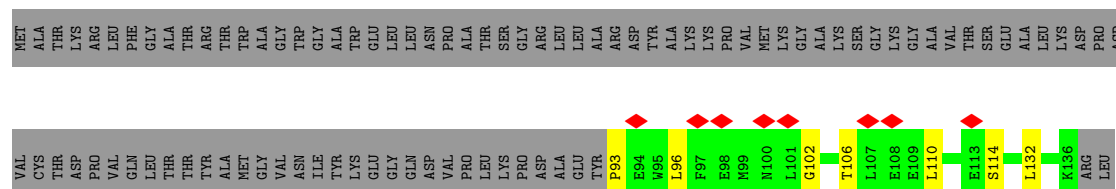
- Molecule 46: 39S ribosomal protein L53, mitochondrial

Chain k: 



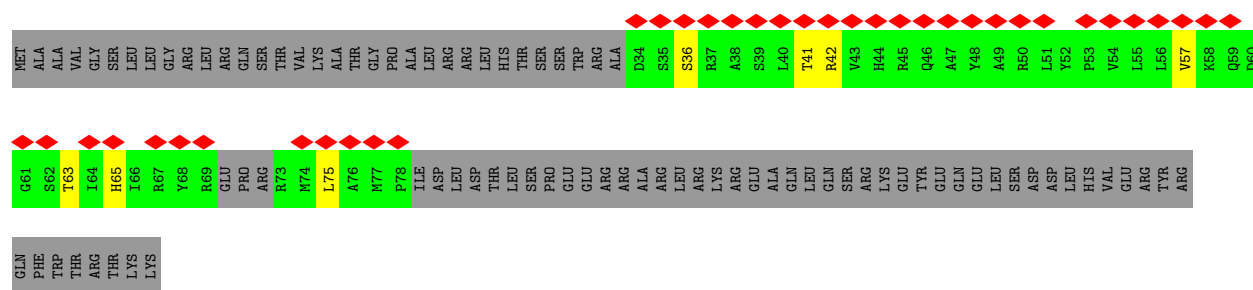
- Molecule 47: 39S ribosomal protein L54, mitochondrial

Chain l: 



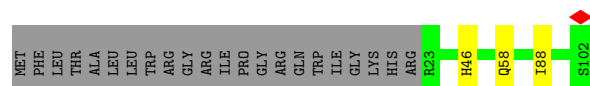
- Molecule 48: 39S ribosomal protein L55, mitochondrial

Chain m: 

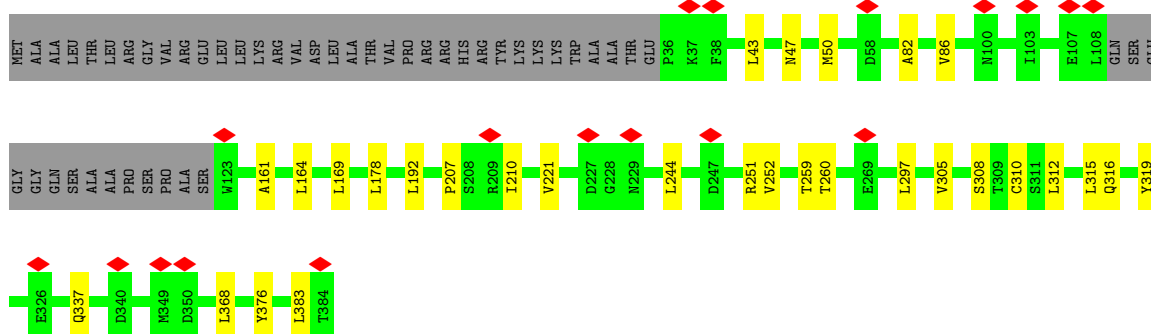
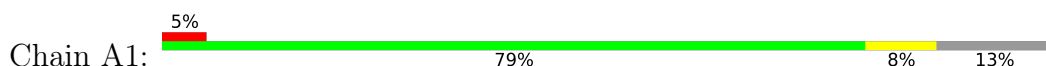


- Molecule 49: Ribosomal protein 63, mitochondrial

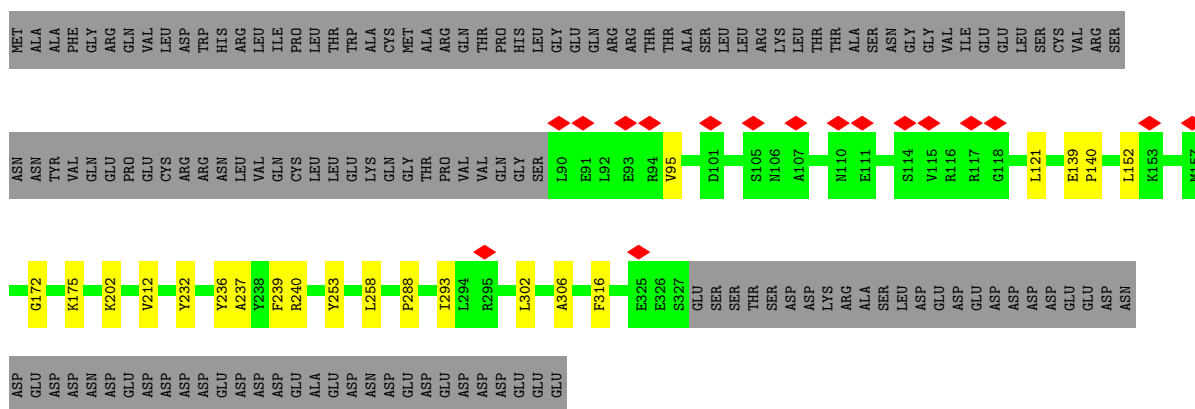
Chain o: 



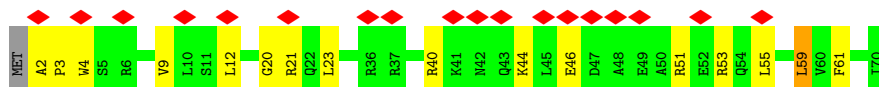
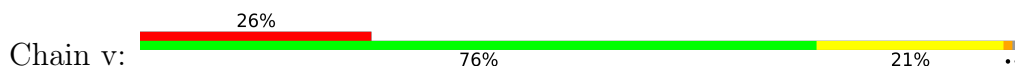
- Molecule 55: 5-methylcytosine rRNA methyltransferase NSUN4



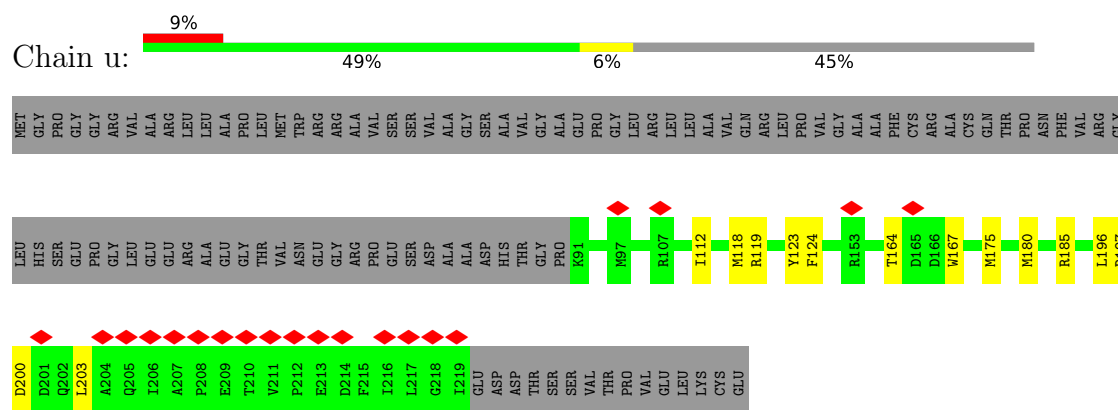
- Molecule 56: Transcription termination factor 4, mitochondrial



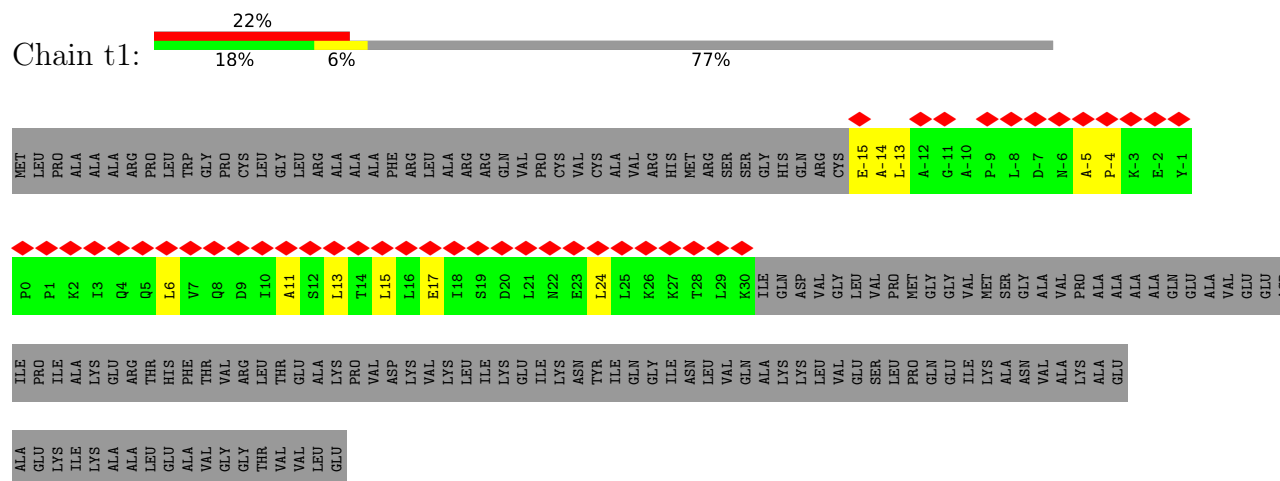
- Molecule 57: MIEF1 upstream open reading frame protein



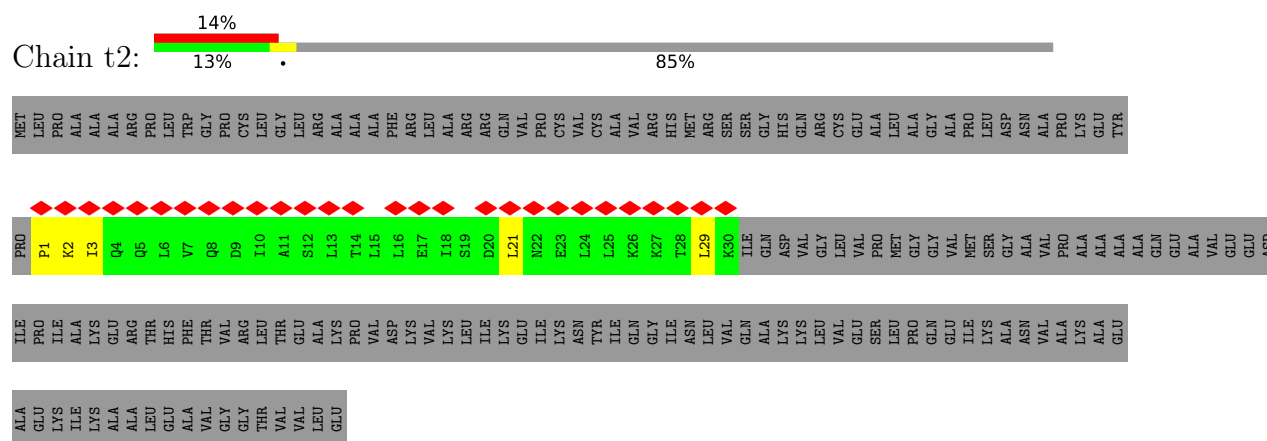
- Molecule 58: Mitochondrial assembly of ribosomal large subunit protein 1



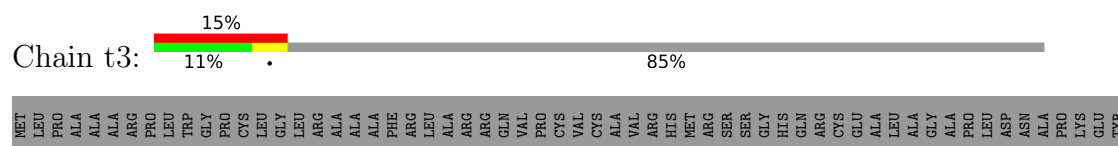
- Molecule 59: 39S ribosomal protein L12, mitochondrial

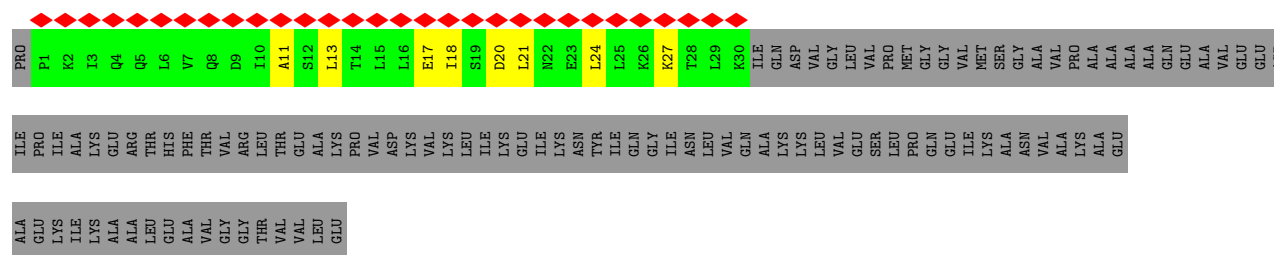


- Molecule 59: 39S ribosomal protein L12, mitochondrial

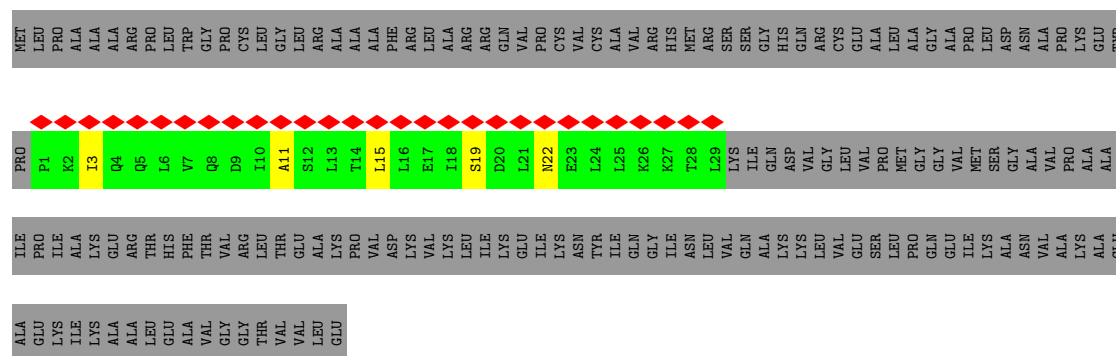


- Molecule 59: 39S ribosomal protein L12, mitochondrial

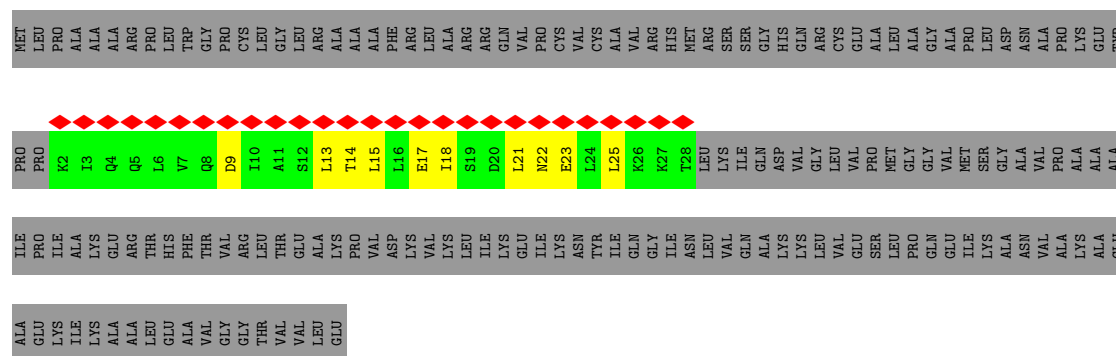




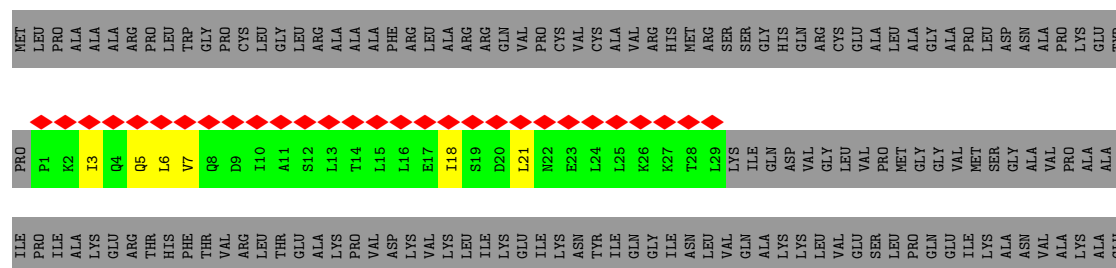
- Molecule 59: 39S ribosomal protein L12, mitochondrial



- Molecule 59: 39S ribosomal protein L12, mitochondrial



- Molecule 59: 39S ribosomal protein L12, mitochondrial



ALA
GLU
LYS
ILE
LYS
ALA
ALA
LEU
GLU
ALA
VAL
GLY
GLY
THR
VAL
LEU
GLU

● Molecule 60: Acyl carrier protein, mitochondrial



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

VAL
THR
GLN
LEU
CYS
ARG
GLN
TYR
SER
D70
M71
P72
P73
L74
T76
L76
E77
G78
I79
Q80
D81
R82
W83
L84
Y85
W86
L87
K88
L89
Y90
D91
K92
I93
D94
P95
E96
K97
L98
S99
V100
N101
S102
H103
F104
M105
K106
D107
L108
G109
L110
D111
S112
L113
E117
M120
A121
M122
E123

D124
E125
F126
G127
F128
E129
I130
P131
D132
I133
D134
A135
E136
K137
L138
M139
Q142
E143
I144
V145
D146
Y147
I148
A149
D150
K151
K152
D153
V154
Y155
E156

● Molecule 61: Unknown residues



X1
X2
X3
X4
X5
X6
X7
X8
X9
X10
X11
X12
X13
X14
X15
X16
X17
X18
X19
X20
X21
X22
X23
X24
X25
X26

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	48646	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48.2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.254	Depositor
Minimum map value	-0.513	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.081	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	215.22, 279.47998, 250.92	wwPDB
Map dimensions	246, 274, 211	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.02, 1.02, 1.02	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.46	0/34198	0.71	21/53222 (0.0%)
2	B	0.50	0/1423	0.71	1/2206 (0.0%)
3	C	0.37	1/1905 (0.1%)	0.87	3/2573 (0.1%)
4	D	0.46	0/1896	0.93	1/2549 (0.0%)
5	E	0.45	0/2465	0.95	0/3344
6	F	0.45	0/2071	1.00	0/2817
7	H	0.44	0/762	1.06	0/1022
8	I	0.46	1/1682 (0.1%)	0.98	0/2280
9	J	0.49	0/1077	1.17	1/1452 (0.1%)
10	K	0.46	0/1495	1.01	0/2029
11	L	0.46	0/904	0.97	0/1218
12	M	0.45	0/2359	1.05	0/3185
13	N	0.46	0/1721	1.04	0/2322
14	O	0.44	0/1269	1.05	0/1708
15	P	0.43	0/1173	0.98	0/1588
16	Q	0.42	0/1846	0.99	0/2487
17	R	0.43	0/1174	1.12	0/1572
18	S	0.44	0/1276	0.95	0/1729
19	T	0.47	0/1402	1.00	0/1886
20	U	0.44	0/1183	0.97	0/1600
21	V	0.46	0/1697	0.98	0/2302
22	W	0.48	0/827	0.92	0/1118
23	X	0.43	0/2090	1.04	0/2825
24	Y	0.41	0/1552	1.08	0/2079
25	Z	0.46	0/1003	0.98	1/1354 (0.1%)
26	a	0.50	0/709	0.99	0/963
27	0	0.44	0/895	1.06	0/1201
28	1	0.40	0/438	0.87	0/583
29	2	0.44	0/373	1.03	0/496
30	3	0.40	0/852	0.93	0/1136
31	4	0.41	0/350	0.82	0/461
32	5	0.46	0/3294	0.98	1/4488 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	6	0.47	0/2809	1.03	0/3818
34	7	0.44	0/2391	1.06	0/3234
35	8	0.46	0/734	1.17	0/986
36	9	0.45	0/1020	1.01	0/1374
37	b	0.47	0/1202	0.98	0/1626
38	c	0.45	0/2348	1.14	0/3174
39	d	0.46	0/1872	0.99	0/2536
40	e	0.44	0/1797	1.05	1/2422 (0.0%)
41	f	0.45	0/1063	1.04	0/1430
42	g	0.46	0/1121	0.96	0/1528
43	h	0.49	0/884	1.07	0/1203
44	i	0.43	0/849	0.97	0/1135
45	j	0.45	0/698	1.16	0/940
46	k	0.46	0/743	1.08	0/1003
47	l	0.41	0/407	1.11	0/547
48	m	0.48	0/350	0.90	0/469
49	o	0.45	0/687	1.07	0/924
50	p	0.44	0/1071	1.07	0/1433
51	q	0.46	0/1165	1.16	0/1575
52	r	0.47	0/1322	1.00	0/1793
53	s	0.44	0/3130	0.99	0/4247
54	n	0.46	0/1703	1.08	0/2314
55	A1	0.45	0/2713	1.02	0/3681
56	A2	0.43	0/1973	1.16	0/2651
57	v	0.41	0/598	1.11	0/796
58	u	0.44	0/1089	1.02	0/1474
59	t1	0.14	0/358	0.25	0/486
59	t2	0.09	0/238	0.25	0/319
59	t3	0.09	0/238	0.22	0/319
59	t4	0.09	0/229	0.19	0/308
59	t5	0.10	0/229	0.33	0/308
59	t6	0.07	0/213	0.21	0/286
60	w	0.43	0/717	1.14	0/967
All	All	0.45	2/115322 (0.0%)	0.92	30/163101 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	209	PRO	C-N	7.23	1.44	1.33
8	I	196	LYS	C-N	-6.30	1.24	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	209	PRO	CA-C-N	-11.35	105.42	123.23
3	C	209	PRO	C-N-CA	-11.35	105.42	123.23
1	A	2457	A	C2'-C3'-O3'	10.04	124.55	109.50
1	A	2182	G	C2'-C3'-O3'	8.65	122.48	109.50
1	A	1994	A	C4'-C3'-O3'	8.64	122.36	109.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	A	30552	0	15539	170	0
2	B	1275	0	650	8	0
3	C	1878	0	1949	19	0
4	D	1859	0	1920	19	0
5	E	2396	0	2402	17	0
6	F	2013	0	2043	16	0
7	H	749	0	798	6	0
8	I	1646	0	1731	21	0
9	J	1061	0	1141	5	0
10	K	1451	0	1448	12	0
11	L	889	0	941	6	0
12	M	2305	0	2378	18	0
13	N	1676	0	1694	12	0
14	O	1245	0	1283	10	0
15	P	1148	0	1148	11	0
16	Q	1805	0	1841	11	0
17	R	1153	0	1214	8	0
18	S	1251	0	1322	17	0
19	T	1368	0	1410	7	0
20	U	1154	0	1154	14	0
21	V	1652	0	1658	11	0
22	W	805	0	829	10	0
23	X	2035	0	2054	16	0
24	Y	1517	0	1561	10	0
25	Z	978	0	1030	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	a	686	0	658	6	0
27	0	880	0	902	7	0
28	1	433	0	475	5	0
29	2	367	0	393	3	0
30	3	831	0	883	5	0
31	4	342	0	361	7	0
32	5	3199	0	3196	34	0
33	6	2723	0	2615	22	0
34	7	2334	0	2343	13	0
35	8	719	0	723	9	0
36	9	992	0	984	6	0
37	b	1178	0	1180	15	0
38	c	2300	0	2313	12	0
39	d	1819	0	1793	12	0
40	e	1762	0	1767	25	0
41	f	1044	0	1046	16	0
42	g	1085	0	1077	5	0
43	h	862	0	845	2	0
44	i	827	0	857	6	0
45	j	684	0	673	2	0
46	k	732	0	745	5	0
47	l	395	0	391	2	0
48	m	345	0	360	4	0
49	o	670	0	665	3	0
50	p	1058	0	1083	8	0
51	q	1134	0	1110	8	0
52	r	1283	0	1310	14	0
53	s	3052	0	3037	25	0
54	n	1667	0	1673	14	0
55	A1	2652	0	2632	15	0
56	A2	1942	0	2035	11	0
57	v	589	0	604	8	0
58	u	1064	0	1060	8	0
59	t1	354	0	380	12	0
59	t2	238	0	270	4	0
59	t3	238	0	270	8	0
59	t4	229	0	257	8	0
59	t5	229	0	257	4	0
59	t6	214	0	236	8	0
60	w	705	0	691	3	0
61	UNK	130	0	28	0	0
62	A	101	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	D	1	0	0	0	0
62	F	1	0	0	0	0
62	n	1	0	0	0	0
63	C	28	0	12	0	0
64	0	1	0	0	0	0
64	4	1	0	0	0	0
65	A1	27	0	22	0	0
66	w	21	0	21	2	0
All	All	110030	0	95371	704	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 3.

The worst 5 of 704 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)
8:I:139:LYS:HG3	59:t1:-15:GLU:O	1.46	1.15
32:5:126:THR:HG22	32:5:372:ASN:HB2	1.46	0.95
20:U:24:PHE:HB2	20:U:45:PRO:HG3	1.60	0.84
32:5:313:MET:HE1	32:5:353:HIS:HB2	1.60	0.82
52:r:99:MET:HE3	52:r:116:GLU:HA	1.62	0.80

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	234/333 (70%)	231 (99%)	3 (1%)	0	100	100
4	D	236/305 (77%)	229 (97%)	6 (2%)	1 (0%)	30	51
5	E	302/348 (87%)	290 (96%)	12 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	248/311 (80%)	243 (98%)	5 (2%)	0	100	100
7	H	86/267 (32%)	85 (99%)	1 (1%)	0	100	100
8	I	203/261 (78%)	196 (97%)	7 (3%)	0	100	100
9	J	138/192 (72%)	134 (97%)	4 (3%)	0	100	100
10	K	175/178 (98%)	172 (98%)	3 (2%)	0	100	100
11	L	113/145 (78%)	109 (96%)	4 (4%)	0	100	100
12	M	285/296 (96%)	280 (98%)	5 (2%)	0	100	100
13	N	202/251 (80%)	201 (100%)	1 (0%)	0	100	100
14	O	150/175 (86%)	150 (100%)	0	0	100	100
15	P	139/179 (78%)	135 (97%)	4 (3%)	0	100	100
16	Q	215/292 (74%)	210 (98%)	5 (2%)	0	100	100
17	R	138/149 (93%)	137 (99%)	1 (1%)	0	100	100
18	S	154/205 (75%)	151 (98%)	3 (2%)	0	100	100
19	T	164/212 (77%)	160 (98%)	4 (2%)	0	100	100
20	U	135/153 (88%)	132 (98%)	3 (2%)	0	100	100
21	V	200/216 (93%)	196 (98%)	4 (2%)	0	100	100
22	W	99/148 (67%)	94 (95%)	5 (5%)	0	100	100
23	X	241/256 (94%)	235 (98%)	6 (2%)	0	100	100
24	Y	174/250 (70%)	171 (98%)	3 (2%)	0	100	100
25	Z	118/161 (73%)	114 (97%)	4 (3%)	0	100	100
26	a	78/142 (55%)	76 (97%)	2 (3%)	0	100	100
27	0	106/188 (56%)	102 (96%)	4 (4%)	0	100	100
28	1	50/65 (77%)	50 (100%)	0	0	100	100
29	2	43/92 (47%)	42 (98%)	1 (2%)	0	100	100
30	3	93/188 (50%)	91 (98%)	2 (2%)	0	100	100
31	4	36/103 (35%)	36 (100%)	0	0	100	100
32	5	390/423 (92%)	381 (98%)	9 (2%)	0	100	100
33	6	316/380 (83%)	310 (98%)	6 (2%)	0	100	100
34	7	285/338 (84%)	268 (94%)	17 (6%)	0	100	100
35	8	83/206 (40%)	80 (96%)	3 (4%)	0	100	100
36	9	121/137 (88%)	120 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	b	146/215 (68%)	139 (95%)	7 (5%)	0	100	100
38	c	284/332 (86%)	279 (98%)	5 (2%)	0	100	100
39	d	214/302 (71%)	208 (97%)	6 (3%)	0	100	100
40	e	211/279 (76%)	200 (95%)	11 (5%)	0	100	100
41	f	124/212 (58%)	121 (98%)	2 (2%)	1 (1%)	16	34
42	g	129/166 (78%)	125 (97%)	4 (3%)	0	100	100
43	h	101/158 (64%)	100 (99%)	1 (1%)	0	100	100
44	i	95/128 (74%)	91 (96%)	4 (4%)	0	100	100
45	j	83/123 (68%)	83 (100%)	0	0	100	100
46	k	93/112 (83%)	90 (97%)	3 (3%)	0	100	100
47	l	42/138 (30%)	41 (98%)	0	1 (2%)	4	9
48	m	38/128 (30%)	35 (92%)	3 (8%)	0	100	100
49	o	78/102 (76%)	78 (100%)	0	0	100	100
50	p	119/205 (58%)	115 (97%)	4 (3%)	0	100	100
51	q	133/222 (60%)	132 (99%)	1 (1%)	0	100	100
52	r	153/196 (78%)	152 (99%)	1 (1%)	0	100	100
53	s	368/439 (84%)	359 (98%)	8 (2%)	1 (0%)	36	58
54	n	213/246 (87%)	211 (99%)	2 (1%)	0	100	100
55	A1	331/384 (86%)	328 (99%)	3 (1%)	0	100	100
56	A2	236/381 (62%)	233 (99%)	3 (1%)	0	100	100
57	v	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
58	u	127/234 (54%)	125 (98%)	2 (2%)	0	100	100
59	t1	44/198 (22%)	43 (98%)	1 (2%)	0	100	100
59	t2	28/198 (14%)	28 (100%)	0	0	100	100
59	t3	28/198 (14%)	28 (100%)	0	0	100	100
59	t4	27/198 (14%)	27 (100%)	0	0	100	100
59	t5	27/198 (14%)	27 (100%)	0	0	100	100
59	t6	25/198 (13%)	25 (100%)	0	0	100	100
60	w	85/156 (54%)	82 (96%)	3 (4%)	0	100	100
All	All	9399/13661 (69%)	9179 (98%)	216 (2%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
47	l	102	GLY
53	s	272	PRO
4	D	220	VAL
41	f	179	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	211/286 (74%)	207 (98%)	4 (2%)	50	75
4	D	192/245 (78%)	190 (99%)	2 (1%)	68	86
5	E	259/290 (89%)	259 (100%)	0	100	100
6	F	217/262 (83%)	217 (100%)	0	100	100
7	H	82/228 (36%)	82 (100%)	0	100	100
8	I	189/232 (82%)	188 (100%)	1 (0%)	81	92
9	J	113/150 (75%)	111 (98%)	2 (2%)	51	76
10	K	155/156 (99%)	154 (99%)	1 (1%)	78	91
11	L	98/124 (79%)	97 (99%)	1 (1%)	68	86
12	M	245/249 (98%)	242 (99%)	3 (1%)	63	83
13	N	179/211 (85%)	179 (100%)	0	100	100
14	O	133/150 (89%)	133 (100%)	0	100	100
15	P	123/154 (80%)	123 (100%)	0	100	100
16	Q	199/256 (78%)	198 (100%)	1 (0%)	81	92
17	R	118/126 (94%)	116 (98%)	2 (2%)	53	78
18	S	141/180 (78%)	138 (98%)	3 (2%)	47	73
19	T	146/182 (80%)	144 (99%)	2 (1%)	59	81
20	U	124/135 (92%)	123 (99%)	1 (1%)	73	88
21	V	180/191 (94%)	180 (100%)	0	100	100
22	W	83/119 (70%)	83 (100%)	0	100	100
23	X	219/229 (96%)	218 (100%)	1 (0%)	81	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	Y	159/223 (71%)	157 (99%)	2 (1%)	61	82
25	Z	111/147 (76%)	110 (99%)	1 (1%)	70	87
26	a	78/133 (59%)	77 (99%)	1 (1%)	61	82
27	0	97/164 (59%)	97 (100%)	0	100	100
28	1	49/60 (82%)	49 (100%)	0	100	100
29	2	39/72 (54%)	39 (100%)	0	100	100
30	3	88/166 (53%)	87 (99%)	1 (1%)	65	84
31	4	37/89 (42%)	37 (100%)	0	100	100
32	5	353/368 (96%)	350 (99%)	3 (1%)	73	88
33	6	286/332 (86%)	286 (100%)	0	100	100
34	7	263/303 (87%)	260 (99%)	3 (1%)	65	84
35	8	77/190 (40%)	74 (96%)	3 (4%)	28	55
36	9	104/112 (93%)	103 (99%)	1 (1%)	68	86
37	b	130/186 (70%)	128 (98%)	2 (2%)	57	80
38	c	250/288 (87%)	249 (100%)	1 (0%)	84	93
39	d	204/271 (75%)	203 (100%)	1 (0%)	81	92
40	e	188/236 (80%)	185 (98%)	3 (2%)	55	79
41	f	114/188 (61%)	112 (98%)	2 (2%)	51	76
42	g	121/148 (82%)	119 (98%)	2 (2%)	53	78
43	h	100/148 (68%)	100 (100%)	0	100	100
44	i	86/110 (78%)	85 (99%)	1 (1%)	63	83
45	j	68/97 (70%)	66 (97%)	2 (3%)	37	65
46	k	80/90 (89%)	79 (99%)	1 (1%)	61	82
47	l	43/116 (37%)	39 (91%)	4 (9%)	8	18
48	m	37/113 (33%)	34 (92%)	3 (8%)	11	24
49	o	68/87 (78%)	67 (98%)	1 (2%)	57	80
50	p	117/180 (65%)	117 (100%)	0	100	100
51	q	115/178 (65%)	114 (99%)	1 (1%)	70	87
52	r	143/169 (85%)	137 (96%)	6 (4%)	26	52
53	s	328/381 (86%)	326 (99%)	2 (1%)	78	91
54	n	179/209 (86%)	178 (99%)	1 (1%)	78	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	A1	290/328 (88%)	287 (99%)	3 (1%)	68	86
56	A2	221/350 (63%)	220 (100%)	1 (0%)	81	92
57	v	59/60 (98%)	55 (93%)	4 (7%)	14	32
58	u	120/200 (60%)	120 (100%)	0	100	100
59	t1	40/158 (25%)	40 (100%)	0	100	100
59	t2	29/158 (18%)	29 (100%)	0	100	100
59	t3	29/158 (18%)	29 (100%)	0	100	100
59	t4	28/158 (18%)	28 (100%)	0	100	100
59	t5	28/158 (18%)	28 (100%)	0	100	100
59	t6	26/158 (16%)	26 (100%)	0	100	100
60	w	81/136 (60%)	80 (99%)	1 (1%)	63	83
All	All	8469/11731 (72%)	8388 (99%)	81 (1%)	65	86

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	l	132	LEU
54	n	235	THR
48	m	63	THR
52	r	70	CYS
56	A2	152	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 145 such sidechains are listed below:

Mol	Chain	Res	Type
45	j	31	GLN
59	t2	8	GLN
51	q	60	GLN
53	s	420	GLN
16	Q	258	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1434/1559 (91%)	362 (25%)	47 (3%)
2	B	56/69 (81%)	13 (23%)	2 (3%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	1490/1628 (91%)	375 (25%)	49 (3%)

5 of 375 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1672	C
1	A	1678	C
1	A	1679	U
1	A	1681	G
1	A	1685	C

5 of 49 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2605	C
1	A	2744	U
1	A	2620	G
1	A	2653	C
1	A	2905	A

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
1	OMG	A	3040	1	23,26,27	1.23	3 (13%)	32,38,41	2.12	8 (25%)

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
1	OMG	A	3040	1	-	1/9/27/28	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	3040	OMG	C5-C4	3.38	1.48	1.38
1	A	3040	OMG	C6-N1	-2.15	1.34	1.38
1	A	3040	OMG	C5-N7	-2.07	1.34	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3040	OMG	C5-C4-N3	-6.39	118.22	128.39
1	A	3040	OMG	C2-N3-C4	5.33	121.48	112.30
1	A	3040	OMG	N9-C4-N3	4.71	135.36	125.95
1	A	3040	OMG	C6-C5-N7	3.25	136.20	130.29
1	A	3040	OMG	C4-C5-N7	-2.56	106.62	110.67

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	3040	OMG	C1'-C2'-O2'-CM2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	3040	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 109 ligands modelled in this entry, 106 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
63	GDP	C	401	-	29,30,30	1.14	3 (10%)	45,47,47	1.79	5 (11%)
65	SAM	A1	401	-	27,29,29	0.49	1 (3%)	34,42,42	0.71	1 (2%)
66	PNS	w	201	60	14,20,21	0.35	0	18,26,29	0.78	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
63	GDP	C	401	-	-	3/16/32/32	0/3/3/3
65	SAM	A1	401	-	-	5/17/33/33	0/3/3/3
66	PNS	w	201	60	-	12/24/26/27	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
63	C	401	GDP	C5-C4	3.13	1.47	1.38
63	C	401	GDP	C6-N1	-2.40	1.34	1.38
65	A1	401	SAM	OXT-C	-2.18	1.23	1.30
63	C	401	GDP	C5-N7	-2.05	1.35	1.39

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
63	C	401	GDP	C5-C4-N3	-6.08	118.71	128.39
63	C	401	GDP	C2-N3-C4	5.01	120.92	112.30
63	C	401	GDP	N9-C4-N3	4.40	134.75	125.95
63	C	401	GDP	C6-C5-N7	3.40	136.49	130.29
65	A1	401	SAM	OXT-C-O	-2.88	117.55	124.08

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
63	C	401	GDP	C5'-O5'-PA-O3A

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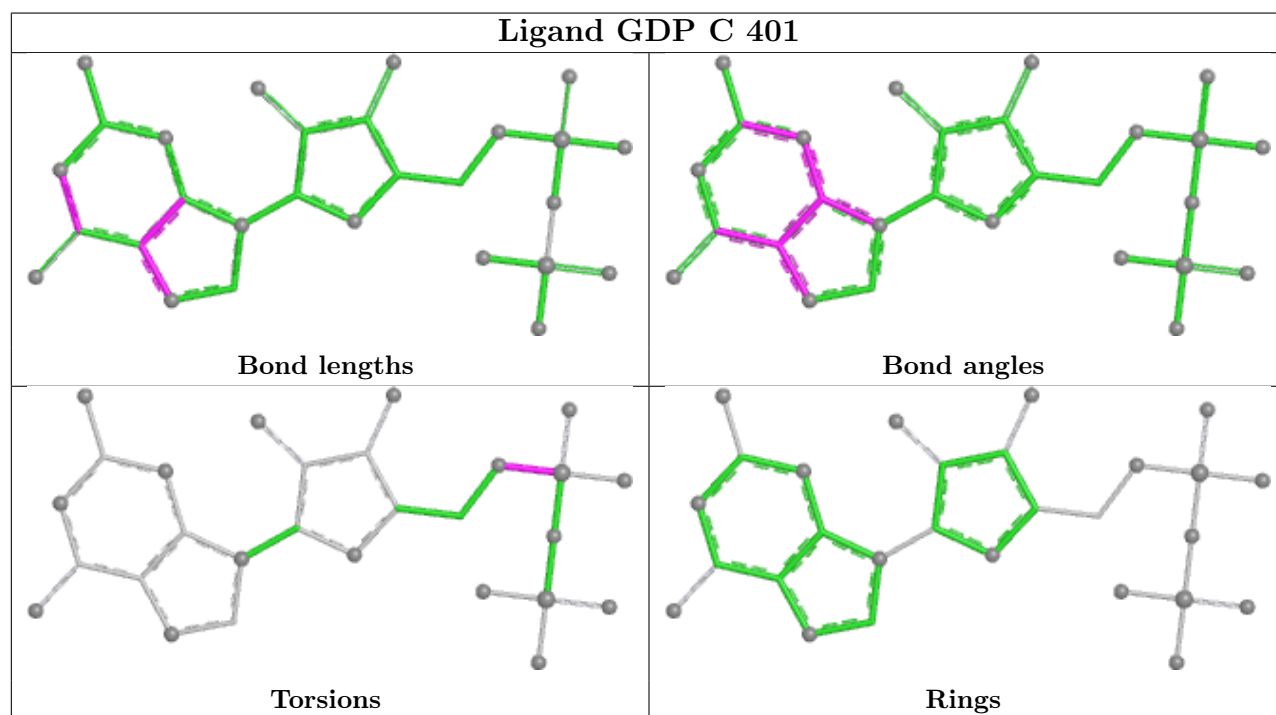
Mol	Chain	Res	Type	Atoms
63	C	401	GDP	C5'-O5'-PA-O1A
63	C	401	GDP	C5'-O5'-PA-O2A
66	w	201	PNS	C28-C29-C32-O33
66	w	201	PNS	C28-C29-C32-C34

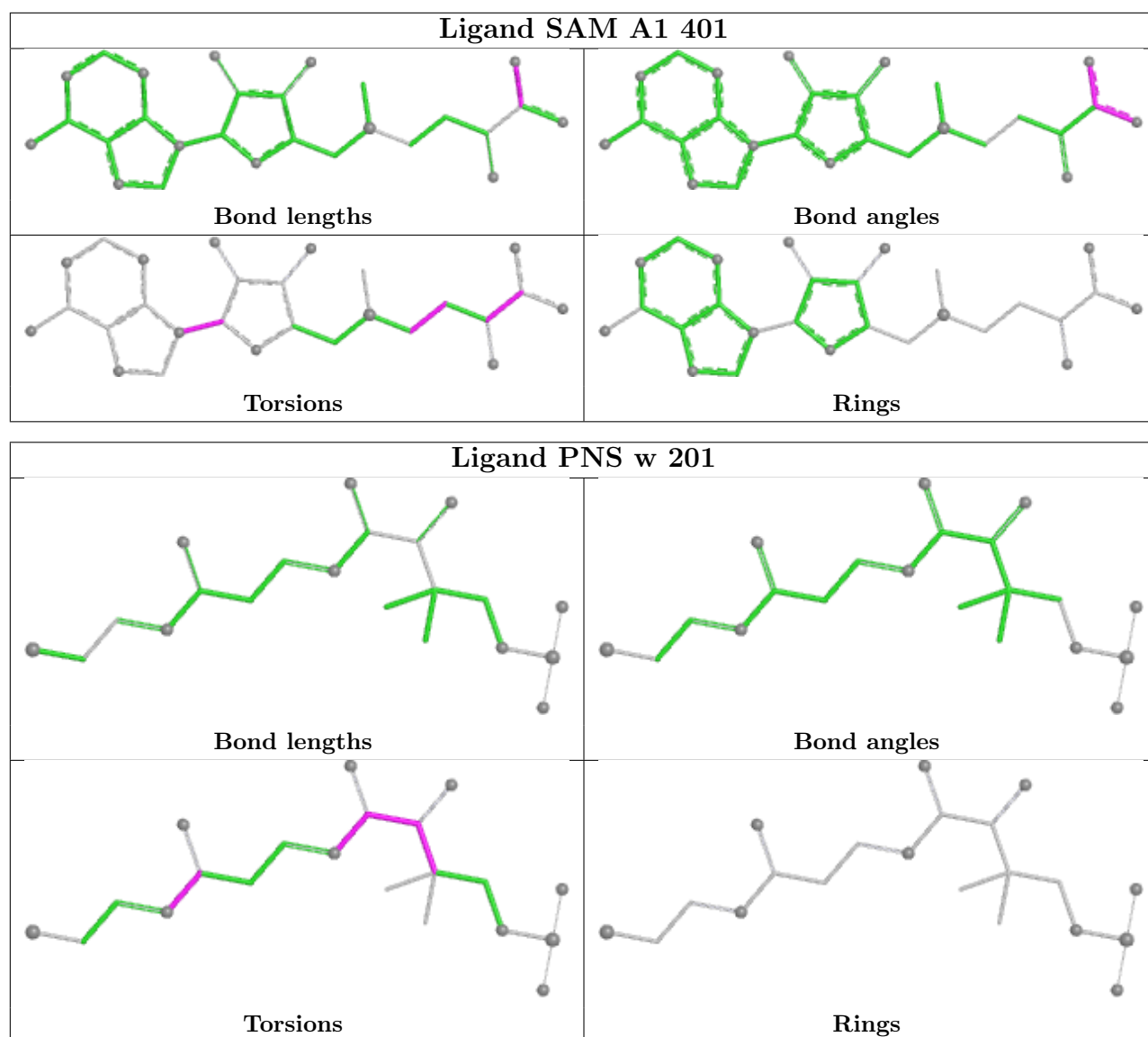
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
66	w	201	PNS	2	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](#)

There are no chain breaks in this entry.

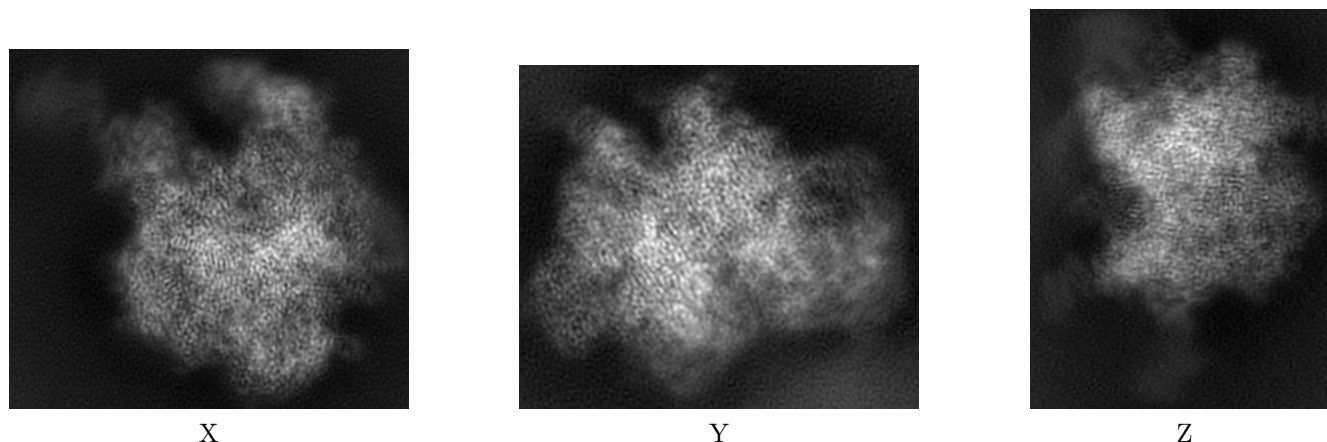
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12764. These allow visual inspection of the internal detail of the map and identification of artifacts.

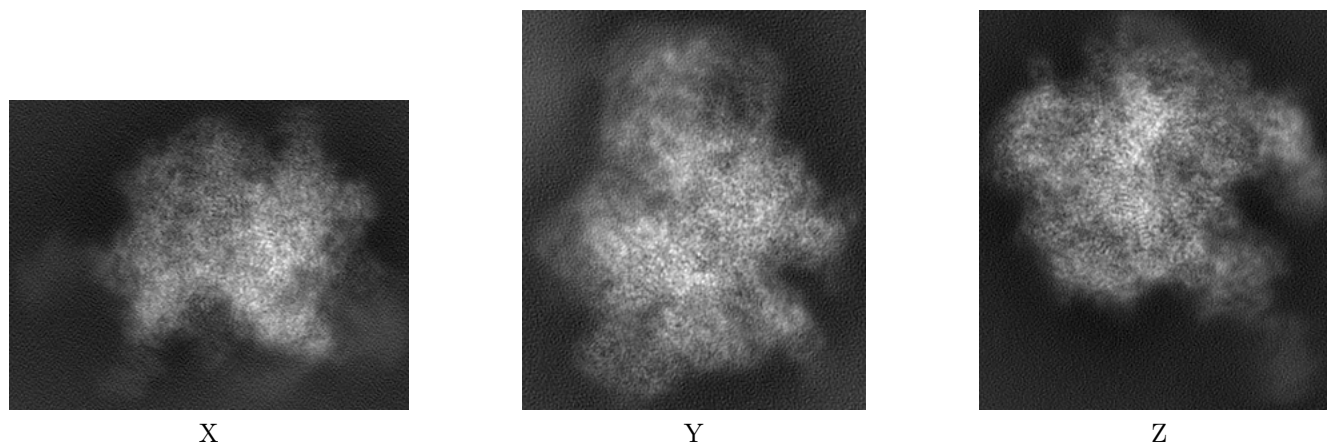
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



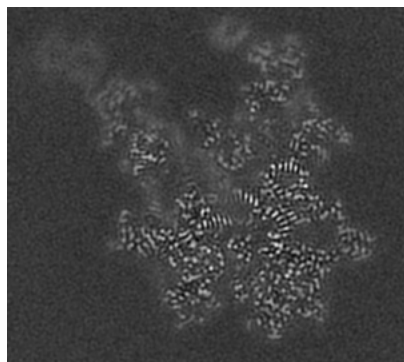
6.1.2 Raw map



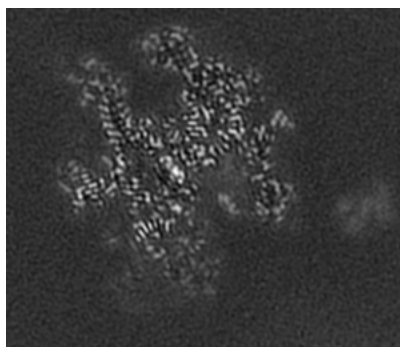
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

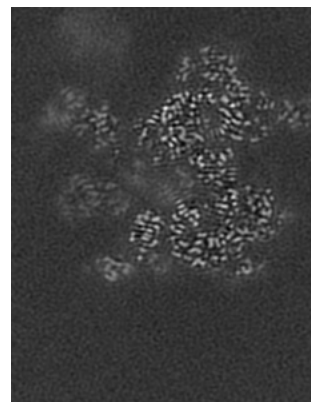
6.2.1 Primary map



X Index: 105

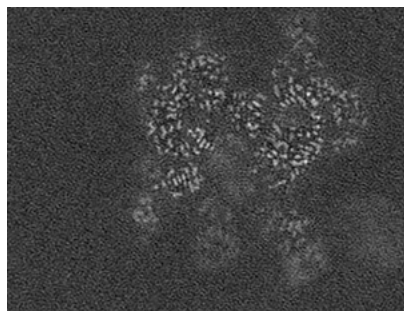


Y Index: 137

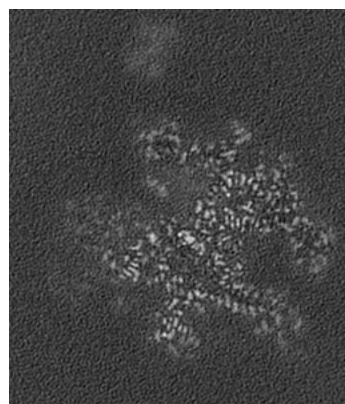


Z Index: 123

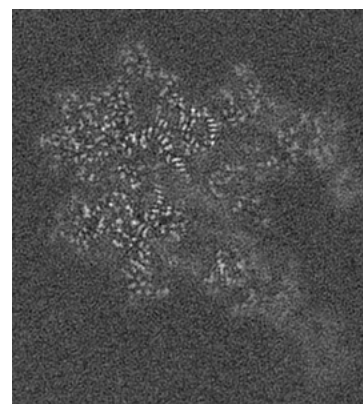
6.2.2 Raw map



X Index: 123



Y Index: 137

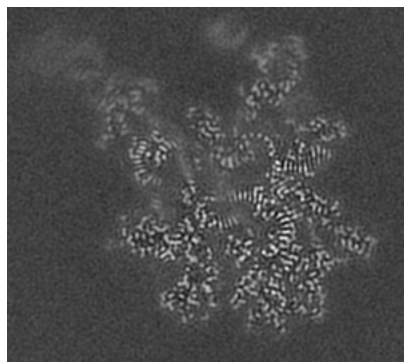


Z Index: 105

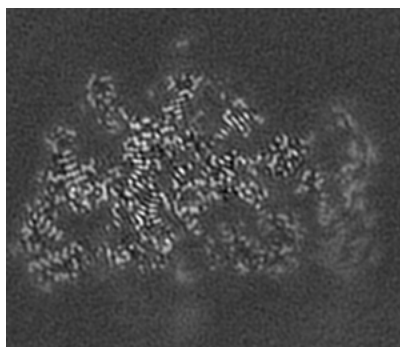
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

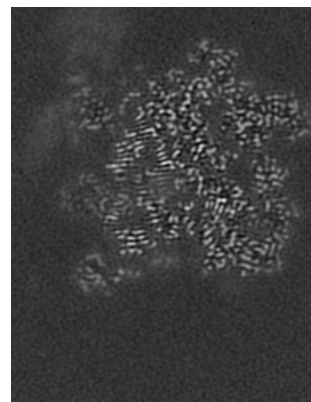
6.3.1 Primary map



X Index: 102

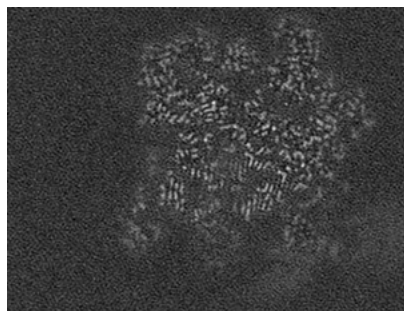


Y Index: 181

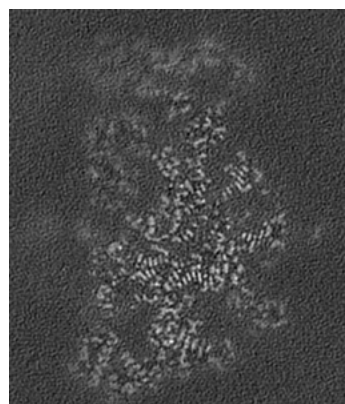


Z Index: 114

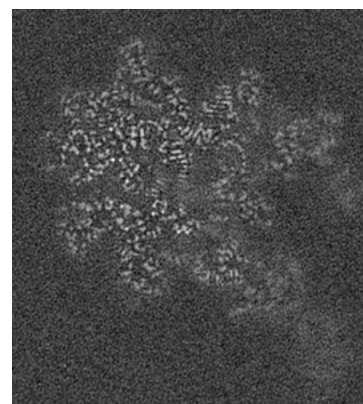
6.3.2 Raw map



X Index: 114



Y Index: 181

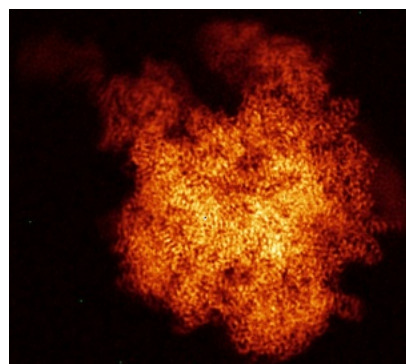


Z Index: 101

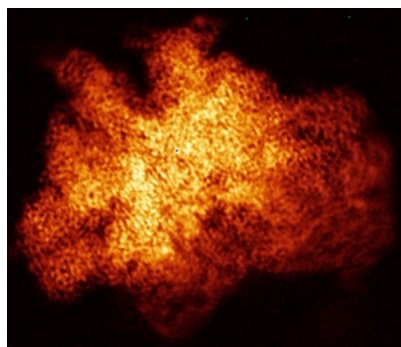
The images above show the largest variance slices of the map in three orthogonal directions.

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

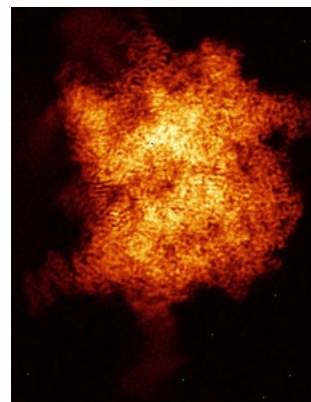
6.4.1 Primary map



X

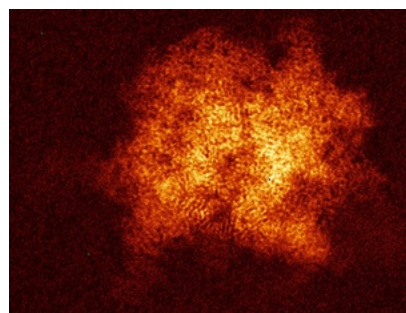


Y

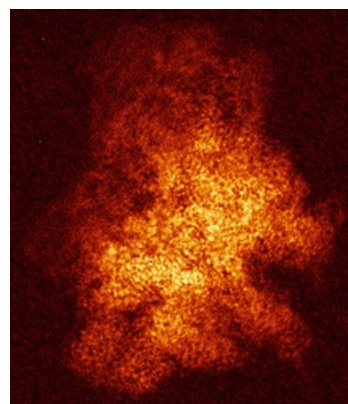


Z

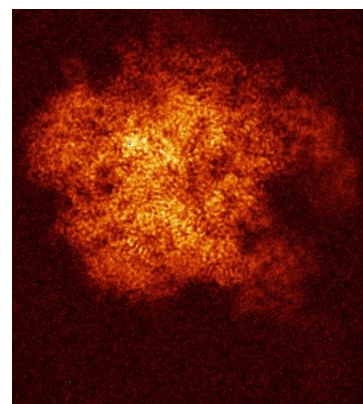
6.4.2 Raw map



X



Y

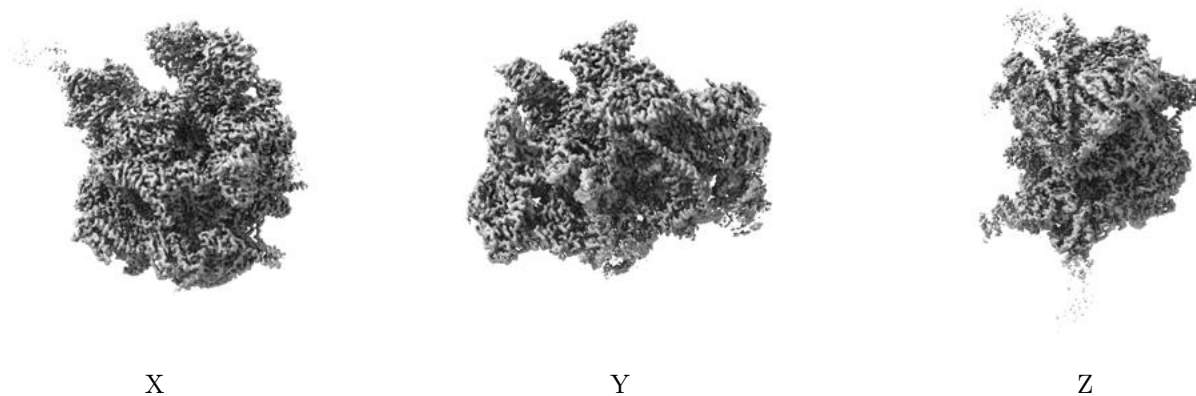


Z

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.

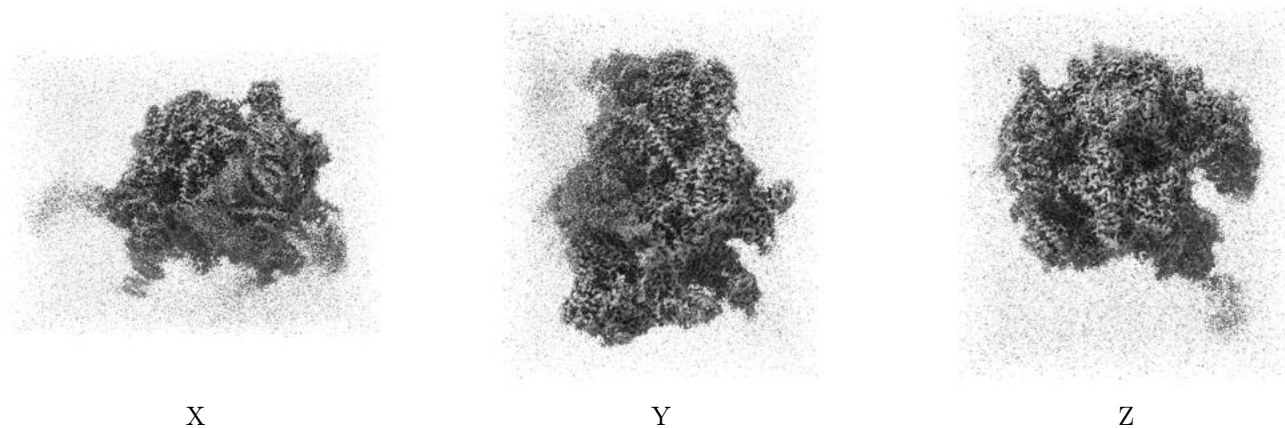
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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



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.

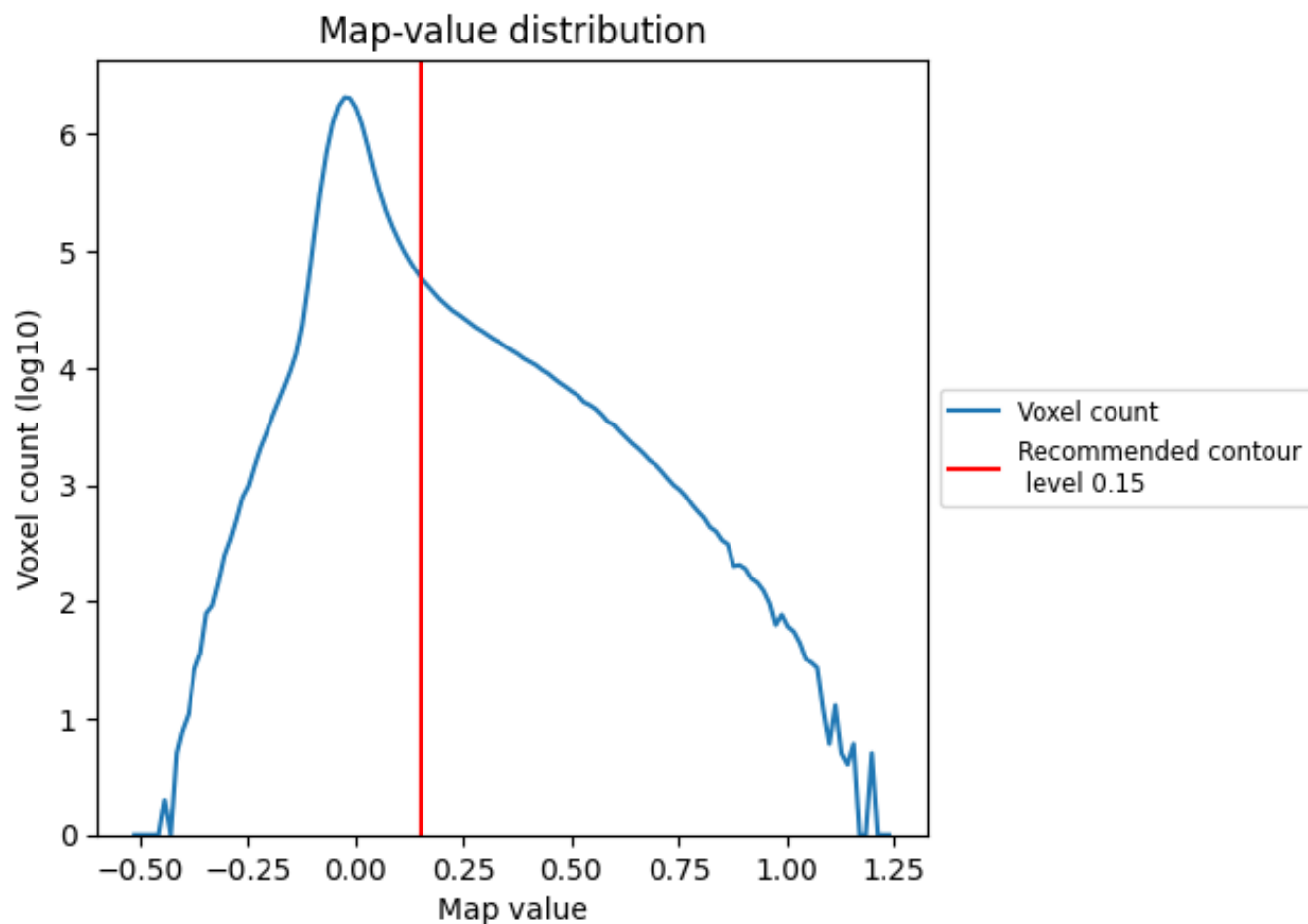
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

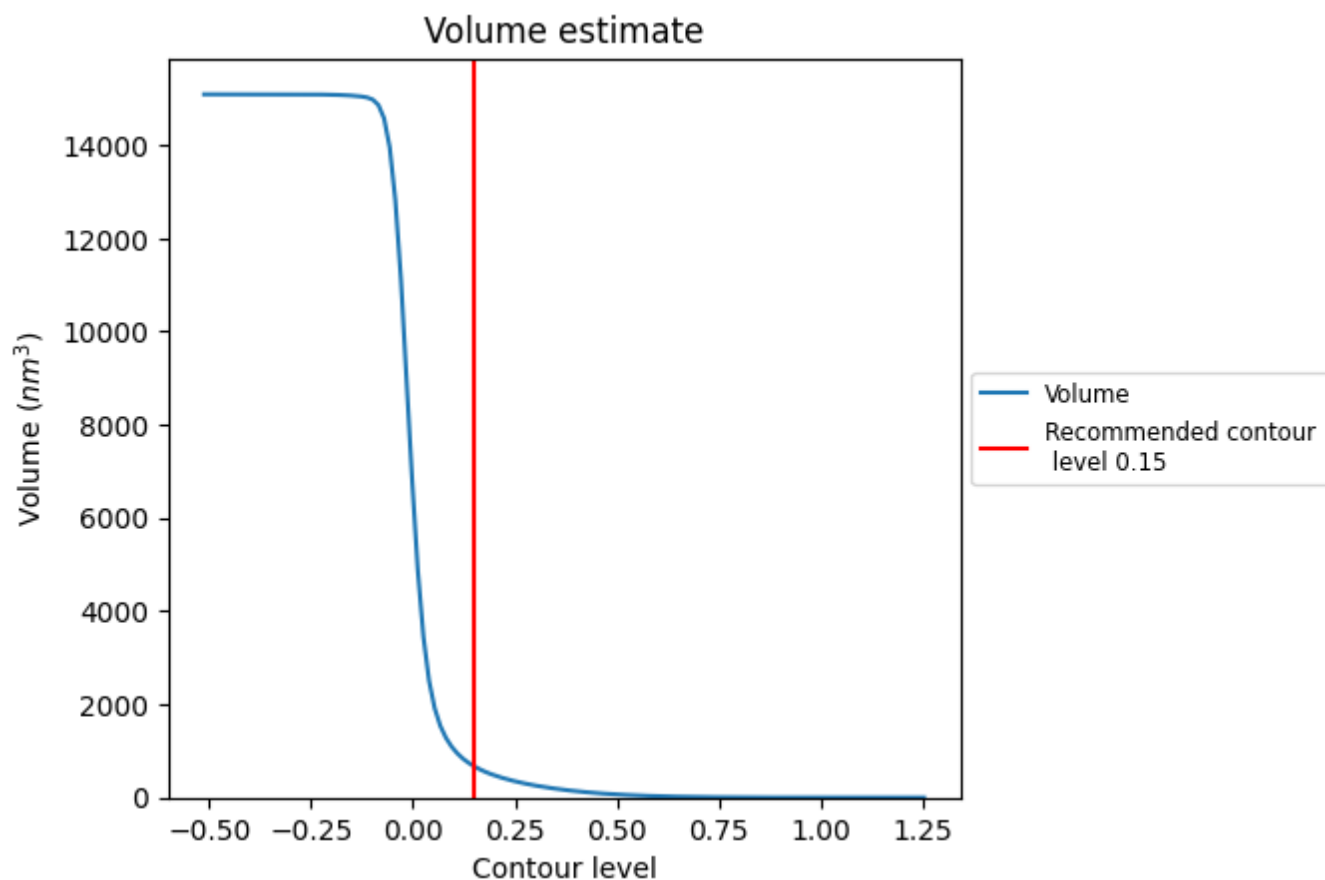
This section contains the results of statistical analysis of the map.

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 671 nm³; this corresponds to an approximate mass of 606 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 [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation ⓘ

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

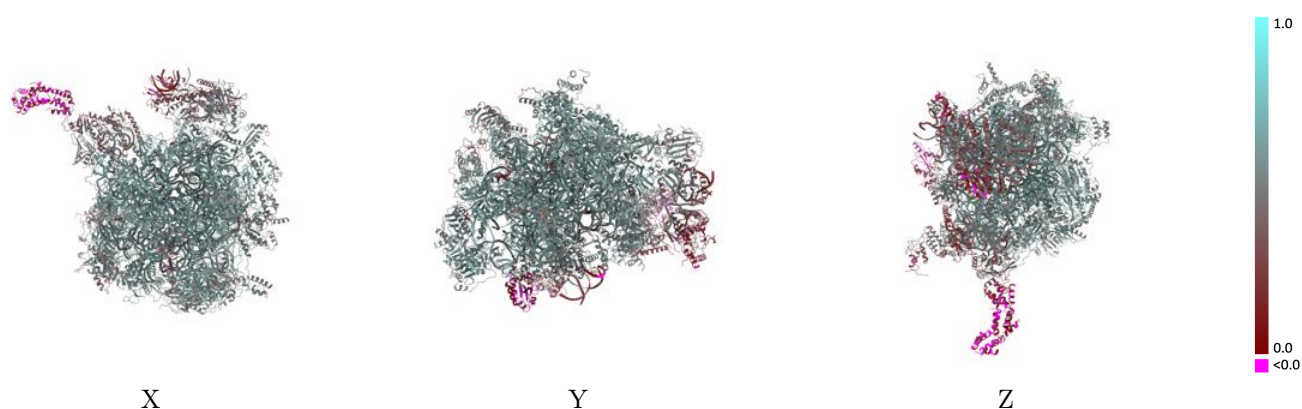
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12764 and PDB model 7O9M. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)

This section was not generated.

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

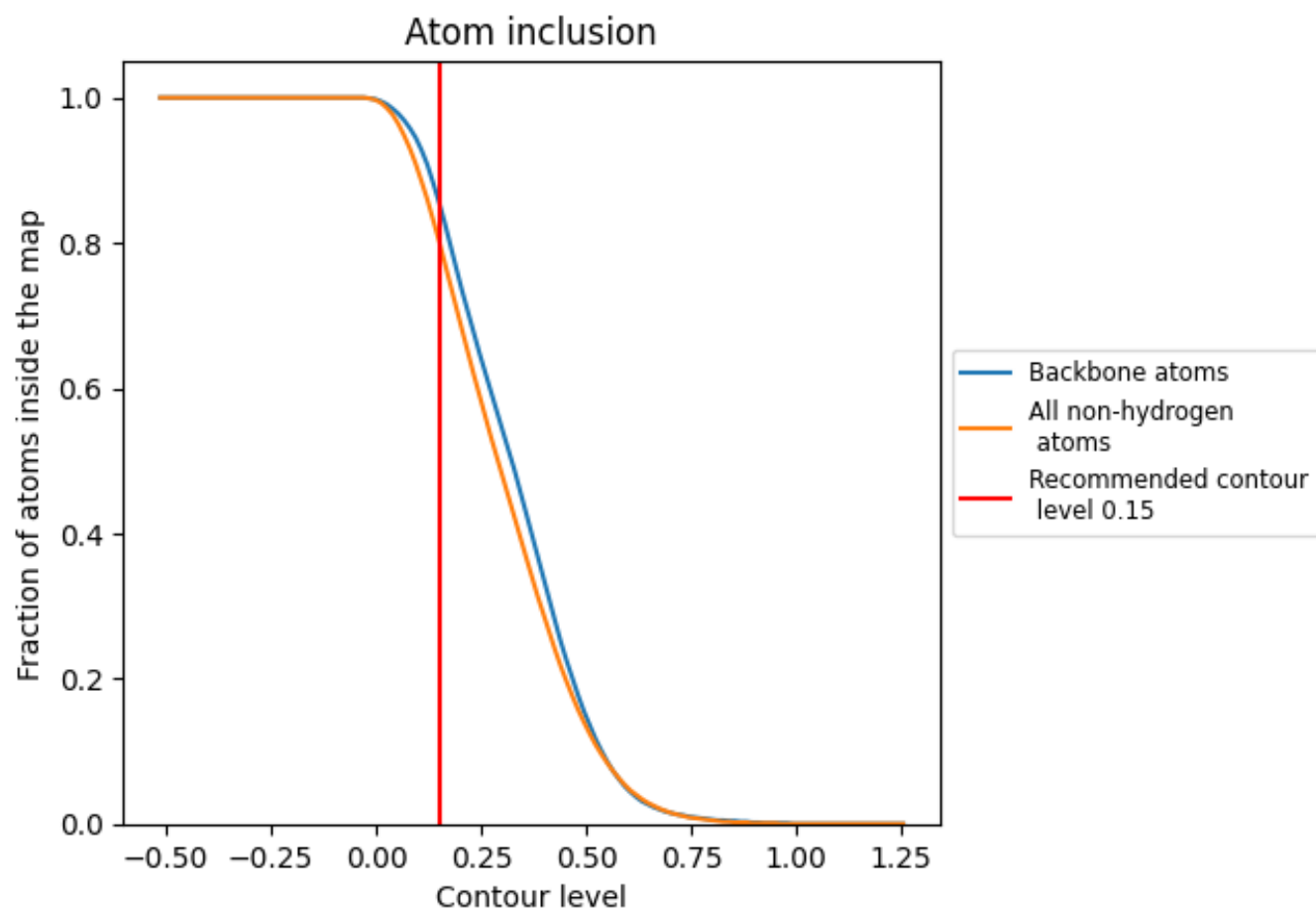


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 80% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8030	 0.5200
0	 0.8640	 0.5660
1	 0.8210	 0.5560
2	 0.9740	 0.6290
3	 0.9540	 0.6120
4	 0.9170	 0.6030
5	 0.8650	 0.5590
6	 0.7810	 0.4920
7	 0.7830	 0.5180
8	 0.3910	 0.2560
9	 0.8300	 0.5560
A	 0.9370	 0.5640
A1	 0.7350	 0.5280
A2	 0.7040	 0.4950
B	 0.7660	 0.3510
C	 0.0400	 0.1520
D	 0.8710	 0.5690
E	 0.8980	 0.5820
F	 0.9070	 0.5880
H	 0.7750	 0.5140
I	 0.4740	 0.3300
J	 0.3600	 0.2510
K	 0.9290	 0.5980
L	 0.8710	 0.5710
M	 0.9090	 0.5830
N	 0.8090	 0.5500
O	 0.8990	 0.5900
P	 0.8350	 0.5340
Q	 0.8560	 0.5670
R	 0.9190	 0.5940
S	 0.9010	 0.5880
T	 0.9180	 0.5960
U	 0.8880	 0.5780
UNK	 0.2850	 0.2430
V	 0.7450	 0.5060



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Chain	Atom inclusion	Q-score
W	 0.9250	 0.5930
X	 0.8400	 0.5550
Y	 0.8720	 0.5770
Z	 0.9010	 0.5930
a	 0.8860	 0.5800
b	 0.9200	 0.5940
c	 0.8110	 0.5460
d	 0.7490	 0.5080
e	 0.1970	 0.1870
f	 0.5390	 0.3900
g	 0.8990	 0.5760
h	 0.7840	 0.5250
i	 0.9360	 0.6050
j	 0.8290	 0.5630
k	 0.6640	 0.4360
l	 0.6410	 0.4200
m	 0.1800	 0.2060
n	 0.4930	 0.4950
o	 0.9010	 0.5850
p	 0.7490	 0.5070
q	 0.7550	 0.5150
r	 0.8740	 0.5600
s	 0.8910	 0.5790
t1	 0.0680	 0.0990
t2	 0.0500	 0.1070
t3	 0.0000	 0.0380
t4	 0.0000	 0.0660
t5	 0.0000	 0.0150
t6	 0.0000	 0.0170
u	 0.6970	 0.5090
v	 0.5950	 0.4160
w	 0.1510	 0.2180