



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 04:34 PM UTC

PDB ID : 7O9K / pdb_00007o9k
EMDB ID : EMD-12763
Title : Human mitochondrial ribosome large subunit assembly intermediate with MTERF4-NSUN4, MRM2, MTG1, the MALSU module, GTPBP5 and mtEF-Tu
Authors : Valentin Gese, G.; Hallberg, B.M.
Deposited on : 2021-04-16
Resolution : 3.10 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:

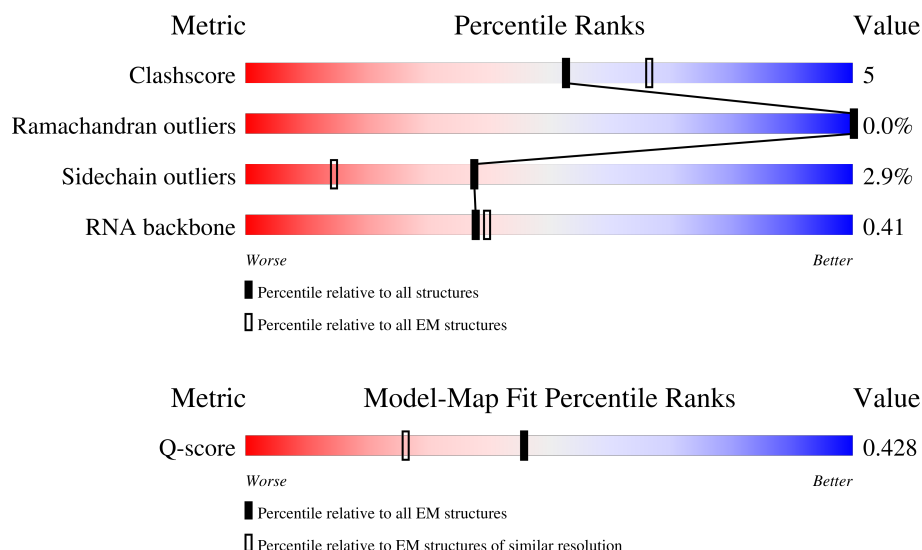
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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	a	142	

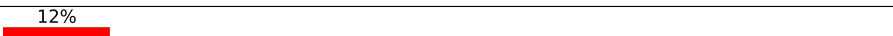
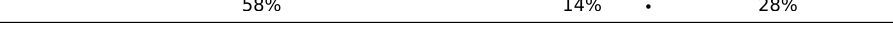
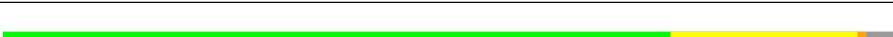
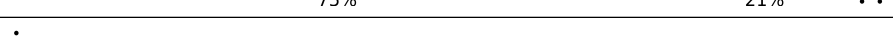
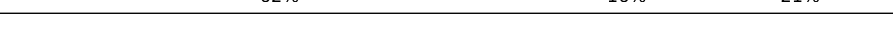
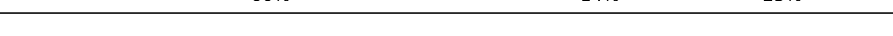
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Mol	Chain	Length	Quality of chain
3	1	65	
4	2	92	
5	3	188	
6	4	103	
7	5	423	
8	6	380	
9	7	338	
10	8	206	
11	9	137	
12	A	1559	
13	A1	384	
14	B	69	
15	A2	381	
16	C	334	
17	D	305	
18	E	348	
19	F	311	
20	FF	198	
20	t1	198	
20	t2	198	
20	t3	198	
20	t4	198	
20	t5	198	
20	t6	198	
21	G	414	

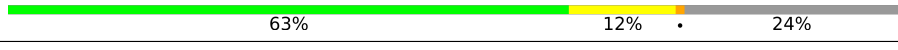
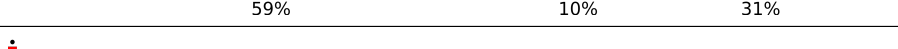
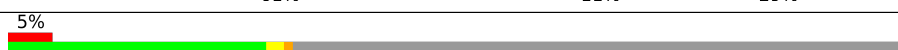
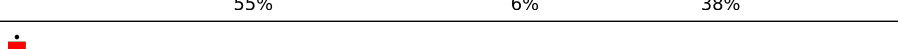
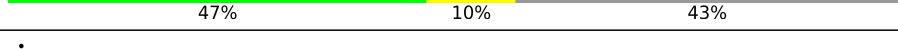
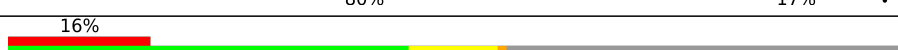
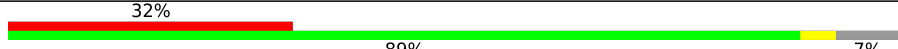
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Mol	Chain	Length	Quality of chain
22	H	267	
23	I	261	
24	J	192	
25	K	178	
26	L	145	
27	M	296	
28	N	251	
29	O	175	
30	P	179	
31	Q	292	
32	R	149	
33	S	205	
34	T	212	
35	U	153	
36	V	216	
37	W	148	
38	X	256	
39	Y	250	
40	Z	161	
41	b	215	
42	c	332	
43	d	306	
44	e	279	
45	f	212	
46	g	166	

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Mol	Chain	Length	Quality of chain
47	h	158	
48	i	128	
49	j	123	
50	k	112	
51	l	138	
52	m	128	
53	n	246	
54	o	102	
55	p	206	
56	q	222	
57	r	196	
58	s	439	
59	t	452	
60	u	234	
61	v	70	
62	w	156	
63	UNK	28	

2 Entry composition

There are 70 unique types of molecules in this entry. The entry contains 115679 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 L42, mitochondrial.

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

- Molecule 3 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

- Molecule 4 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	2	45	Total	C	N	O	S	0	0
			367	227	81	58	1		

- Molecule 5 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 6 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	4	38	Total	C	N	O	S	0	0
			342	217	72	49	4		

- Molecule 7 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	5	392	Total	C	N	O	S	0	0
			3199	2067	558	563	11		

- Molecule 8 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	6	331	Total	C	N	O	S	0	0
			2692	1723	480	480	9		

- Molecule 9 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	7	290	Total	C	N	O	S	0	0
			2356	1509	400	429	18		

- Molecule 10 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	8	85	Total	C	N	O	S	0	0
			719	454	129	134	2		

- Molecule 11 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	9	123	Total	C	N	O	S	0	0
			992	642	169	179	2		

- Molecule 12 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	A	1436	Total	C	N	O	P	0	0
			30486	13680	5498	9872	1436		

- Molecule 13 is a protein called 5-methylcytosine rRNA methyltransferase NSUN4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A1	344	Total	C	N	O	S	0	0
			2731	1743	476	495	17		

- Molecule 14 is a RNA chain called MT-TRNAVAL.

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

- Molecule 15 is a protein called Transcription termination factor 4, mitochondrial.

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

- Molecule 16 is a protein called Mitochondrial ribosome-associated GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	C	255	Total	C	N	O	S	0	0
			1990	1267	349	360	14		

- Molecule 17 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	D	237	Total	C	N	O	S	0	0
			1851	1151	375	316	9		

- Molecule 18 is a protein called 39S ribosomal protein L3, mitochondrial.

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

- Molecule 19 is a protein called 39S ribosomal protein L4, mitochondrial.

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

- Molecule 20 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	FF	70	Total	C	N	O	0	0
			540	348	92	100		
20	t1	46	Total	C	N	O	0	0
			354	228	56	70		
20	t2	30	Total	C	N	O	0	0
			238	154	38	46		

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Mol	Chain	Residues	Atoms				AltConf	Trace
20	t3	30	Total	C	N	O	0	0
			238	154	38	46		
20	t4	29	Total	C	N	O	0	0
			229	148	36	45		
20	t5	29	Total	C	N	O	0	0
			229	148	36	45		
20	t6	27	Total	C	N	O	0	0
			214	137	34	43		

- Molecule 21 is a protein called Mitochondrial ribosome-associated GTPase 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	G	337	Total	C	N	O	S	0	0
			2549	1608	466	467	8		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	407	ASP	-	expression tag	UNP Q9H4K7
G	408	TYR	-	expression tag	UNP Q9H4K7
G	409	LYS	-	expression tag	UNP Q9H4K7
G	410	ASP	-	expression tag	UNP Q9H4K7
G	411	ASP	-	expression tag	UNP Q9H4K7
G	412	ASP	-	expression tag	UNP Q9H4K7
G	413	ASP	-	expression tag	UNP Q9H4K7
G	414	LYS	-	expression tag	UNP Q9H4K7

- Molecule 22 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	H	95	Total	C	N	O	0	0
			784	498	152	134		

- Molecule 23 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	I	212	Total	C	N	O	S	0	0
			1695	1088	304	292	11		

- Molecule 24 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	J	138	Total	C	N	O	S	0	0
			1050	673	190	185	2		

- Molecule 25 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 26 is a protein called 39S ribosomal protein L14, mitochondrial.

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

- Molecule 27 is a protein called 39S ribosomal protein L15, mitochondrial.

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

- Molecule 28 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	N	179	Total	C	N	O	S	0	0
			1457	930	267	251	9		

- Molecule 29 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 30 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

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

- Molecule 31 is a protein called 39S ribosomal protein L19, mitochondrial.

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

- Molecule 32 is a protein called 39S ribosomal protein L20, mitochondrial.

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

- Molecule 33 is a protein called 39S ribosomal protein L21, mitochondrial.

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

- Molecule 34 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 35 is a protein called 39S ribosomal protein L23, mitochondrial.

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

- Molecule 36 is a protein called 39S ribosomal protein L24, mitochondrial.

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

- Molecule 37 is a protein called 39S ribosomal protein L27, mitochondrial.

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

- Molecule 38 is a protein called 39S ribosomal protein L28, mitochondrial.

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

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

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

- Molecule 40 is a protein called 39S ribosomal protein L30, mitochondrial.

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	c	275	Total	C	N	O	S	0	0
			2217	1415	383	410	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	d	223	Total	C	N	O	S	0	0
			1847	1187	317	330	13		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	f	123	Total	C	N	O	S	0	0
			979	625	164	187	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	g	129	Total	C	N	O	S	0	0
			1067	690	185	190	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	h	107	Total	C	N	O	S	0	0
			871	551	153	164	3		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	k	80	Total	C	N	O	S	0	0
			627	392	116	114	5		

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
52	m	35	Total	C	N	O	0	0
			287	180	57	50		

- Molecule 53 is a protein called rRNA methyltransferase 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	n	189	Total	C	N	O	S	0	0
			1450	917	259	268	6		

- Molecule 54 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	o	91	Total	C	N	O	S	0	0
			771	487	156	125	3		

- Molecule 55 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

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

- Molecule 56 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

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

- Molecule 57 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	r	155	Total	C	N	O	S	0	0
			1268	806	243	211	8		

- Molecule 58 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	s	370	Total	C	N	O	S	0	0
			3036	1946	542	534	14		

- Molecule 59 is a protein called Elongation factor Tu, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	t	381	Total	C	N	O	S	0	0
			2939	1860	519	545	15		

- Molecule 60 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	u	133	Total	C	N	O	S	0	0
			1092	702	181	199	10		

- Molecule 61 is a protein called MIEF1 upstream open reading frame protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	v	68	Total	C	N	O		0	0
			584	369	115	100			

- Molecule 62 is a protein called Acyl carrier protein, mitochondrial.

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

- Molecule 63 is a protein called UNK.

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

- Molecule 64 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 65 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

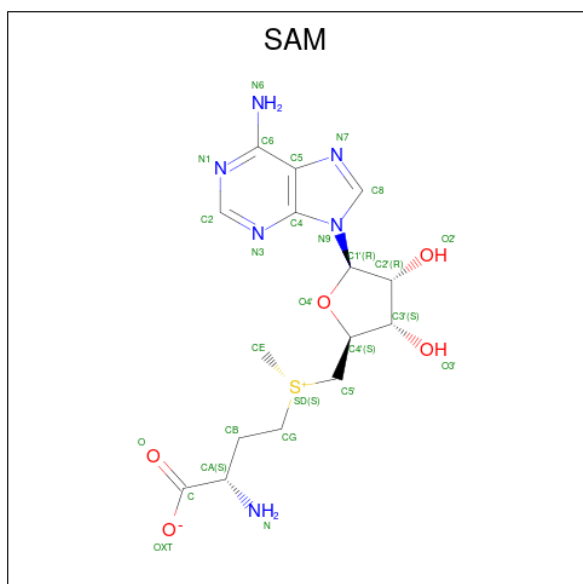
Mol	Chain	Residues	Atoms		AltConf
65	A	85	Total	Mg	0
			85	85	
65	D	1	Total	Mg	0
			1	1	

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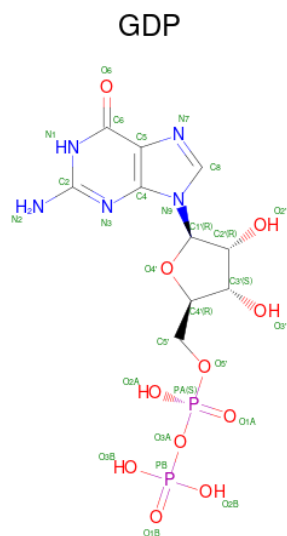
Mol	Chain	Residues	Atoms		AltConf
65	E	1	Total	Mg	0
			1	1	
65	G	2	Total	Mg	0
			2	2	
65	M	1	Total	Mg	0
			1	1	
65	W	1	Total	Mg	0
			1	1	
65	g	1	Total	Mg	0
			1	1	
65	t	1	Total	Mg	0
			1	1	

- Molecule 66 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



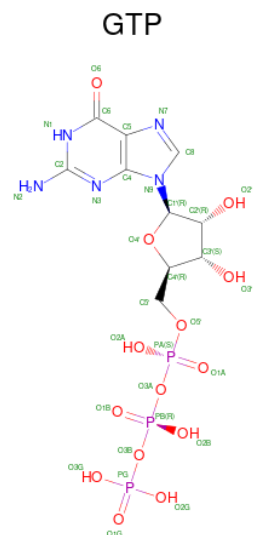
Mol	Chain	Residues	Atoms					AltConf
66	A1	1	Total	C	N	O	S	0
			27	15	6	5	1	

- Molecule 67 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



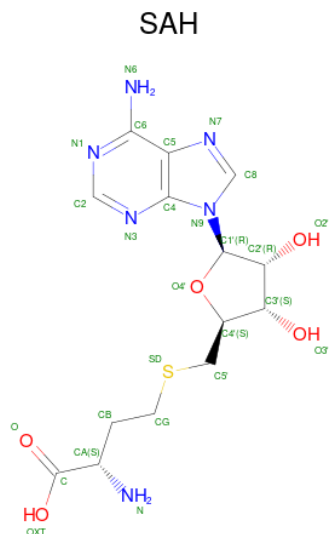
Mol	Chain	Residues	Atoms					AltConf
67	C	1	Total 28	C 10	N 5	O 11	P 2	0
67	t	1	Total 28	C 10	N 5	O 11	P 2	0

- Molecule 68 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $\text{C}_{10}\text{H}_{16}\text{N}_5\text{O}_{14}\text{P}_3$).



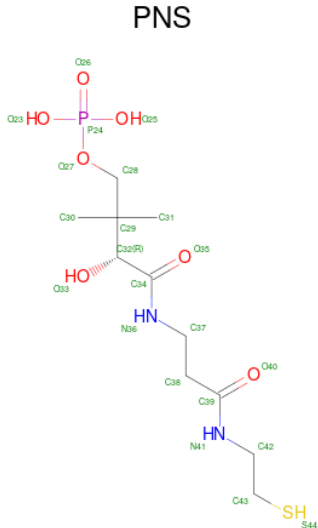
Mol	Chain	Residues	Atoms					AltConf
68	G	1	Total 32	C 10	N 5	O 14	P 3	0

- Molecule 69 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



Mol	Chain	Residues	Atoms					AltConf
69	n	1	Total 26	C 14	N 6	O 5	S 1	0

- Molecule 70 is 4'-PHOSPHOPANTETHEINE (CCD ID: PNS) (formula: $C_{11}H_{23}N_2O_7PS$).

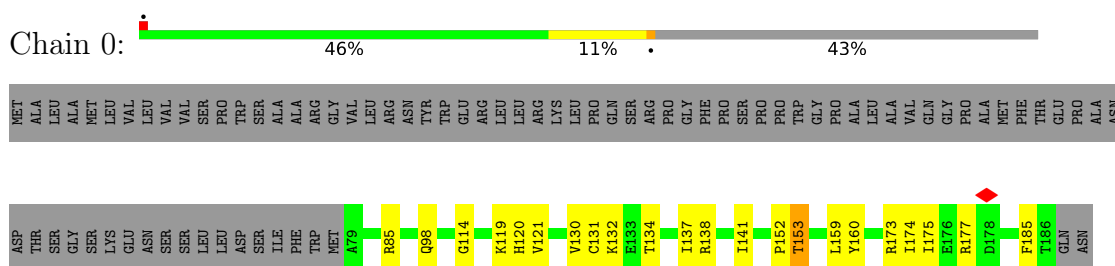


Mol	Chain	Residues	Atoms					AltConf	
70	w	1	Total 21	C 11	N 2	O 6	P 1	S 1	0

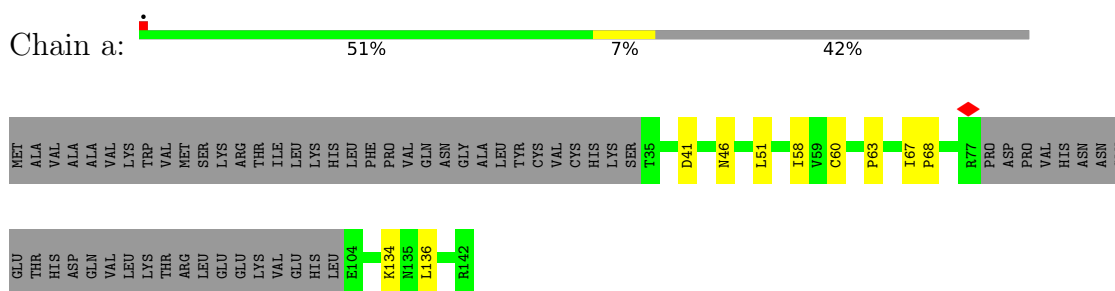
3 Residue-property plots [i](#)

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.

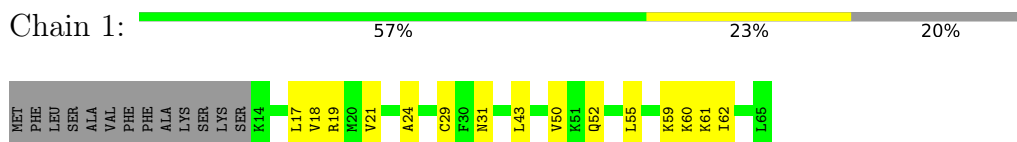
- Molecule 1: 39S ribosomal protein L32, mitochondrial



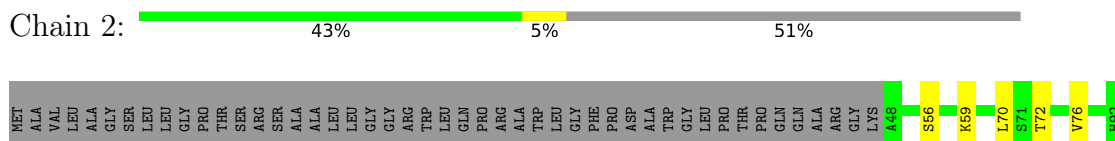
- Molecule 2: 39S ribosomal protein L42, mitochondrial



- Molecule 3: 39S ribosomal protein L33, mitochondrial

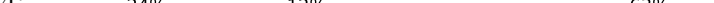


- Molecule 4: 39S ribosomal protein L34, mitochondrial



- Molecule 5: 39S ribosomal protein L35, mitochondrial

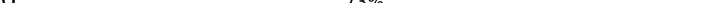
T153	S154	V158	THR	THR	GLU	ARG	ASN	LEU	THR	CYS	GLY	HIS	THR	SER	VAL	ILE	LEU	ASN	ARG	ARG	PRO	ALA	ASN	PRO	VAL	LEU	PRO	SER	VAL	LEU	LYS	PRO	VAL	ARG	SER	L94	S98	K103	R104	K105	T106	V107	K108	I111	D112	R113	F114	L115	T137	P138	F149	K156	L157	M161	T162	THR	THR	GLN	THR	PRO	VAL	VAL	SER	SER	THR	PRO	THR	ARG	THR	ALA	ALA	SER	PHE	SER	HIS	ILE	LEU	LEU	SER	THR	THR	GLY	ARG	ALA	ASN	LYS	VAL	CYS	ASN	ARG	TYR	THR	SER	SER	SER	ALA	LEU	ILE	ASN	PRO	ARG	LEU	VAL	GLY	ALA	ALA	PHE	ALA	SER	ALA	MET
------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain 4:  24% 12% 63%

LEU	PRO	ALA	ASN	GLY	F66		V71	L72	C76		C79		Y80	L81	V82	K83	R84	H85	G86		V90		H93	K99	M103																								
MET	ALA	ASN	PHE	TLE	ARG	LYS	MET	VAL	ASN	PRO	LEU	LEU	TYR	LEU	SER	ARG	HIS	THR	VAL	LYS	PRO	ARG	ALA	LEU	SER	THR	LEU	PHE	GLY	SER	ILE	ARG	GLY	ALA	ALA	VAL	GLU	PRO	GLY	ALA	LEU	LEU	SER	PRO	GLY	LEU	PRO	HIS	LEU

- Chain 5: 78% 14% • 7%

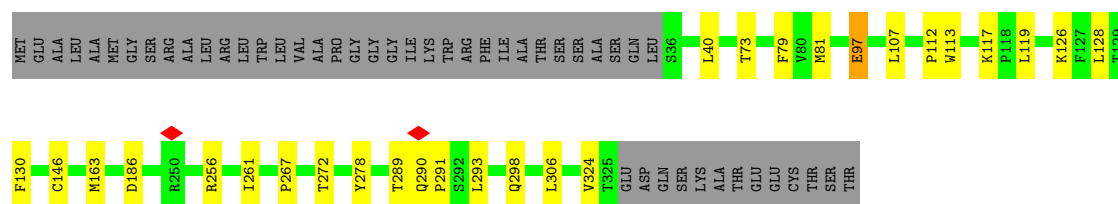
H302	L121	MET
R303	L122	ALA
R310	L123	LEU
L315	T124	ALA
F316	K125	SER
A317	T126	GLY
P339	L127	PRO
V342	L128	ALA
Q343		ARG
F357	L132	ARG
L364	P133	ALA
D365	V136	LEU
N372	L139	ALA
S378	Q165	GLY
I392	E174	GLN
A422	T175	LEU
ALA	V176	GLY
	V179	PHE
	T180	GLY
	V181	ALA
	I185	PRO
	L193	ARG
	R215	ARG
	L220	GLY
	G224	ALA
	A228	YS1
	R229	E42
	L230	L46
	T238	I52
	I239	P53
	F256	G54
	L259	L55
	Q280	M64
	H289	R80
	T290	P91
	L291	F107
	Y292	H108
	K296	H109
	A297	R110
	N298	L113
	L299	L114
	R300	E115
	T301	G116
		V117
		K118
		Q119

- Chain 6:  73% 14% • 13%

[illegible]

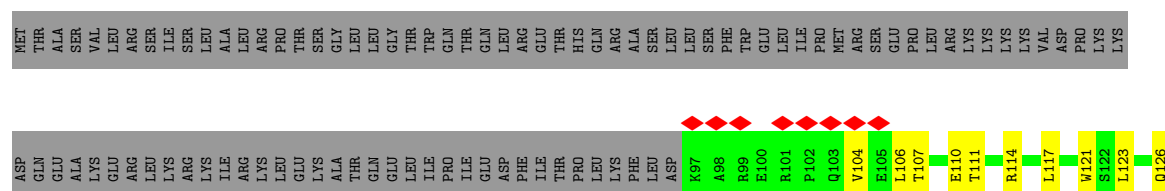
- 
- WORLD WIDE
PDB
PROTEIN DATA BANK

Chain 7:  78% 8% 14%



- Molecule 10: 39S ribosomal protein L40, mitochondrial

Chain 8:  7% 33% 8% 59%



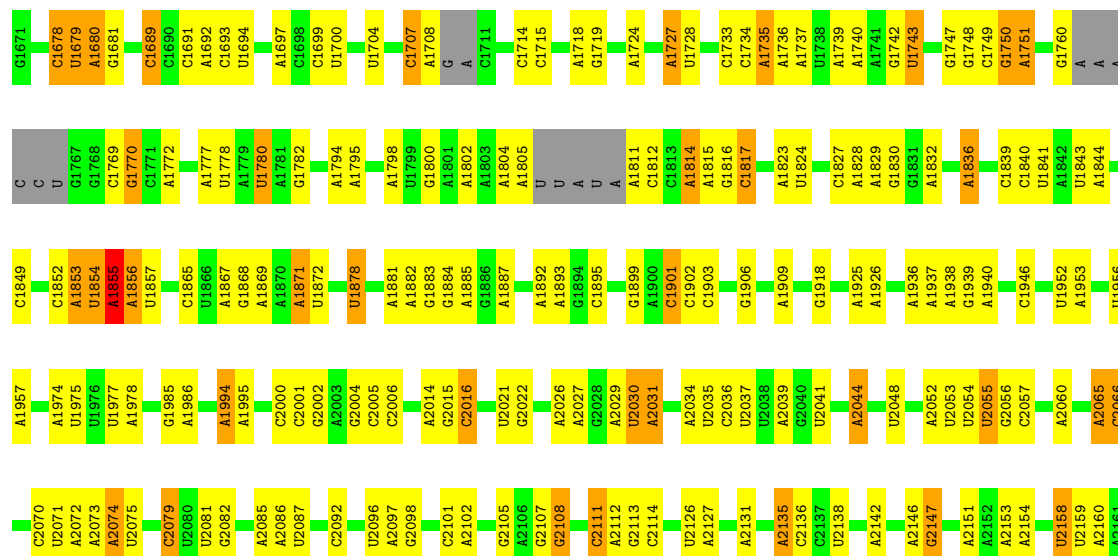
- Molecule 11: 39S ribosomal protein L41, mitochondrial

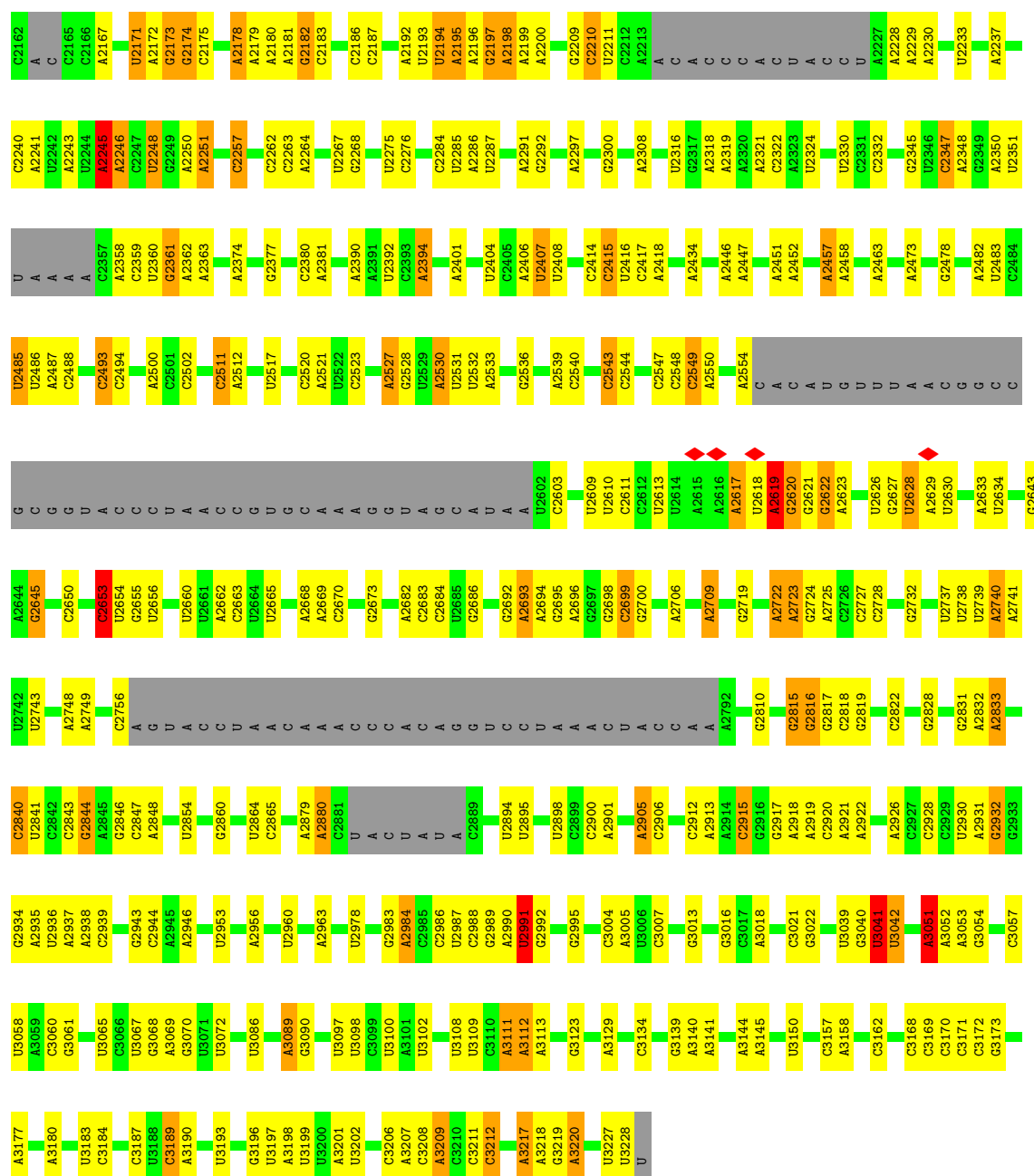
Chain 9:  77% 12% 10%



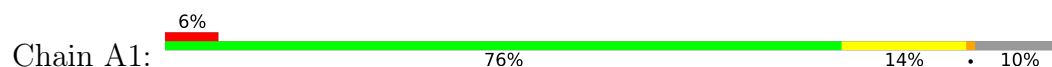
- Molecule 12: 16S rRNA

Chain A:  57% 28% 6% 8%

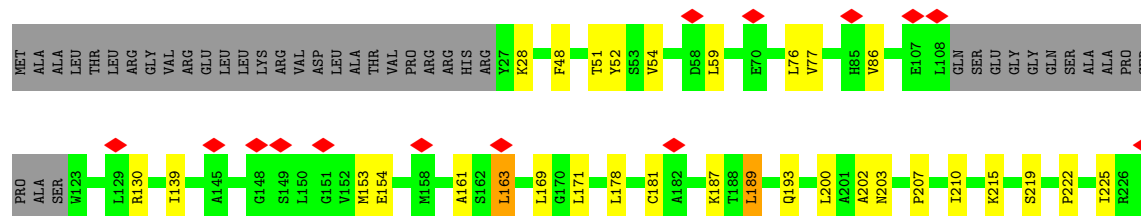




• Molecule 13: 5-methylcytosine rRNA methyltransferase NSUN4

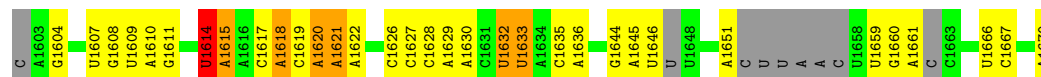
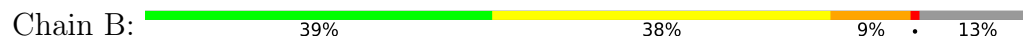


Chain A1:

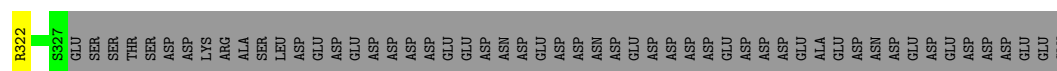
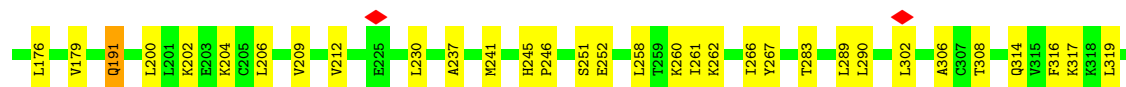
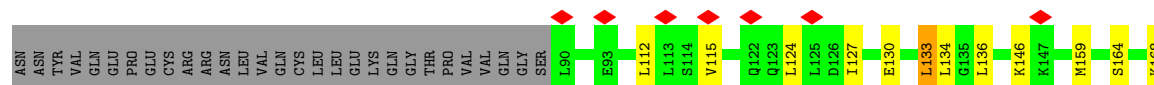
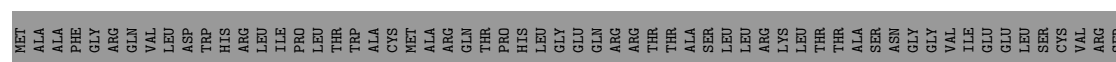




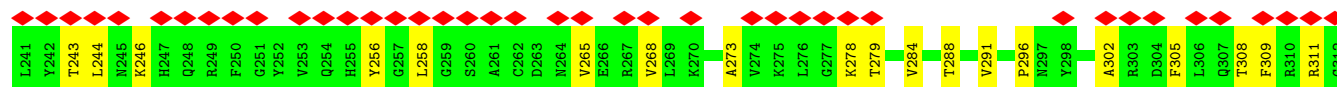
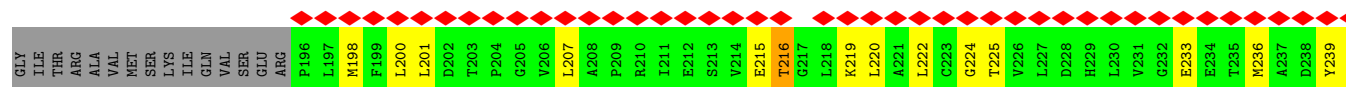
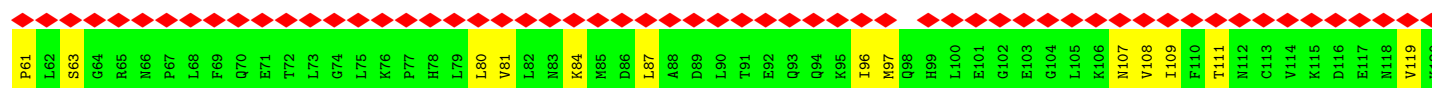
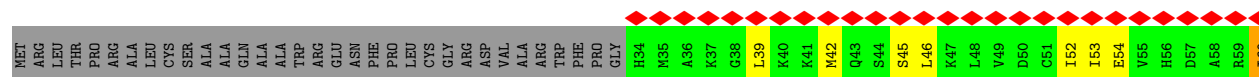
• Molecule 14: MT-TRNAVAL

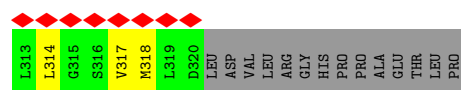


• Molecule 15: Transcription termination factor 4, mitochondrial

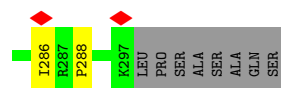
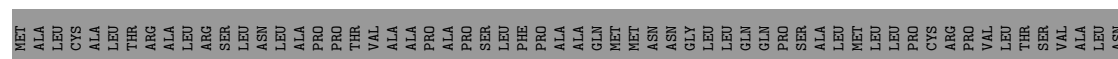


• Molecule 16: Mitochondrial ribosome-associated GTPase 1

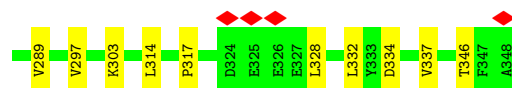
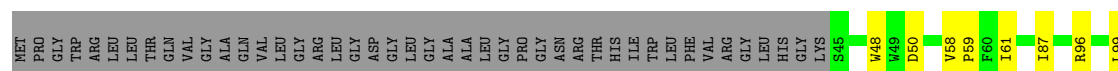




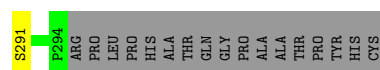
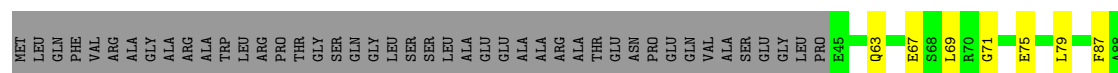
- Molecule 17: 39S ribosomal protein L2, mitochondrial



- Molecule 18: 39S ribosomal protein L3, mitochondrial

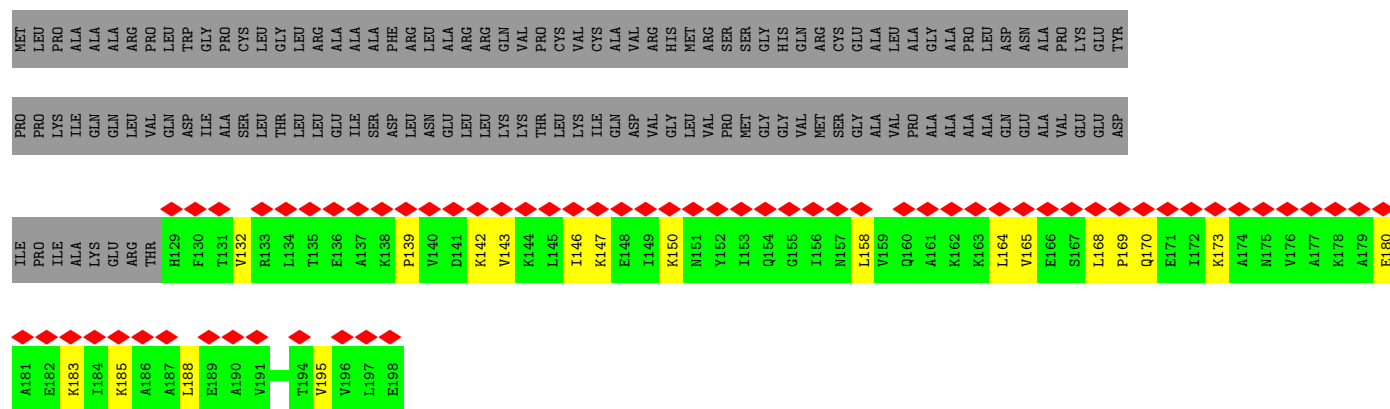


- Molecule 19: 39S ribosomal protein L4, mitochondrial

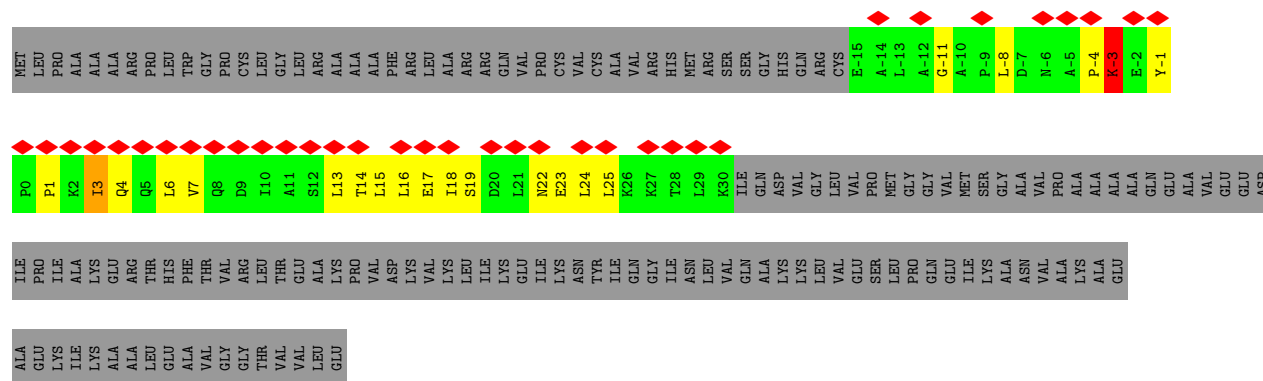


- Molecule 20: 39S ribosomal protein L12, mitochondrial

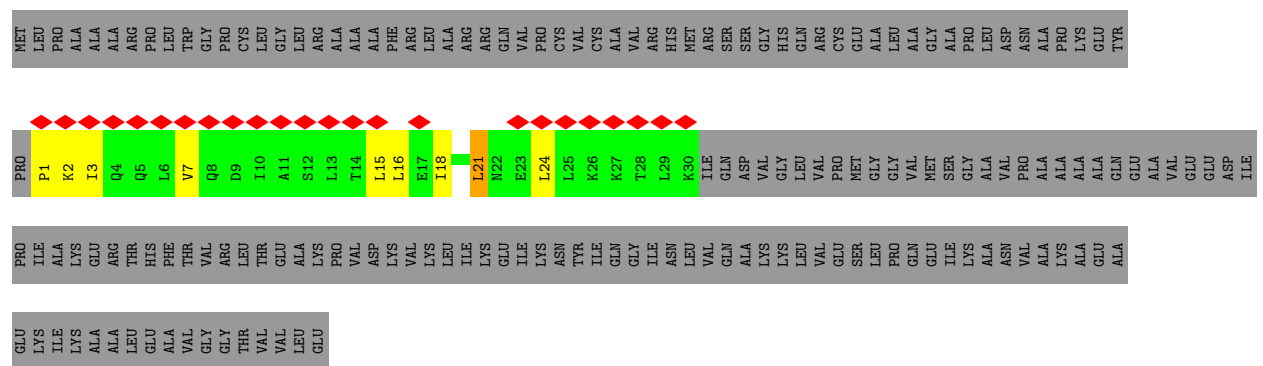




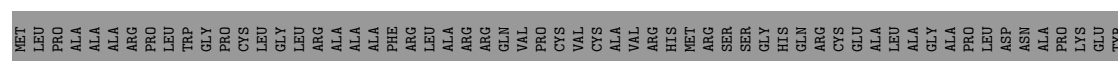
• Molecule 20: 39S ribosomal protein L12, mitochondrial

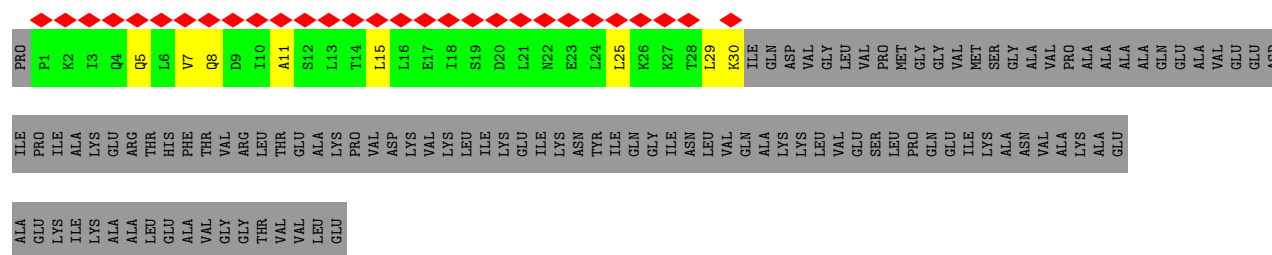


• Molecule 20: 39S ribosomal protein L12, mitochondrial

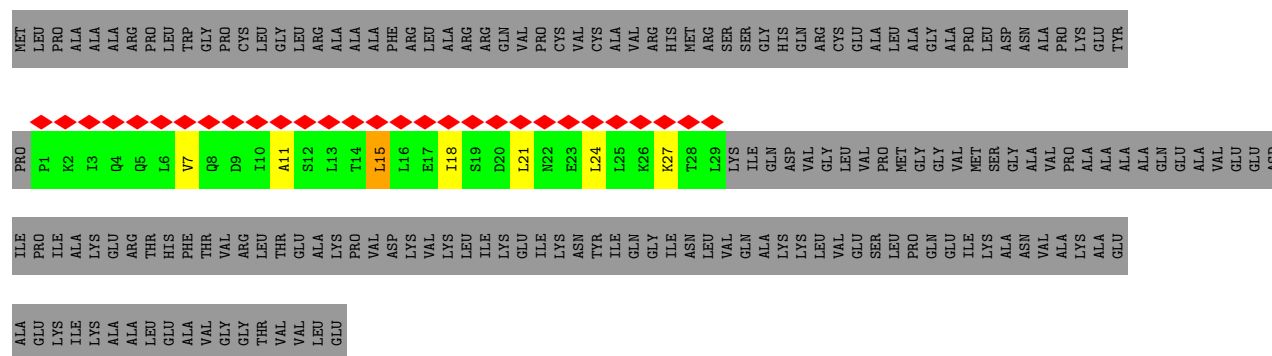


• Molecule 20: 39S ribosomal protein L12, mitochondrial

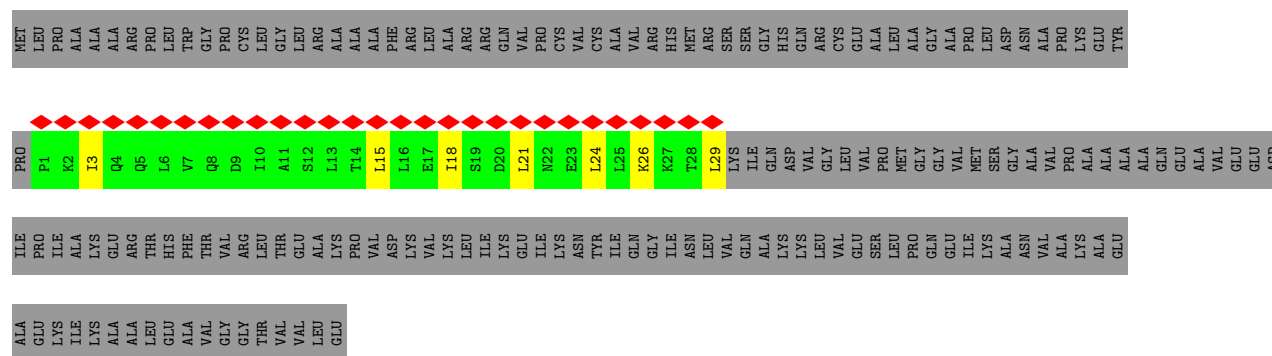




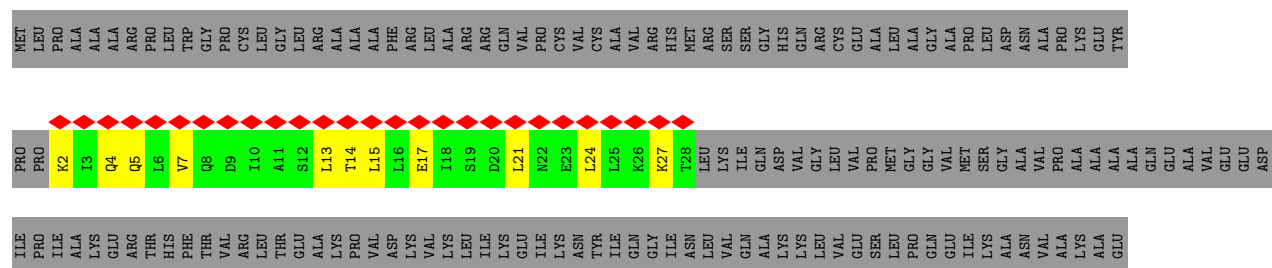
• Molecule 20: 39S ribosomal protein L12, mitochondrial



• Molecule 20: 39S ribosomal protein L12, mitochondrial



• Molecule 20: 39S ribosomal protein L12, mitochondrial



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

• Molecule 21: Mitochondrial ribosome-associated GTPase 2

Chain G:  66% 14% 19%

MET
ALA
PRO
LYS
ALA
ARG
CYS
PHE
SER
ALA
ARG
LEU
VAL
ARG
THR
VAL
PHE
GLN
GLY
VAL
GLY
HIS
TRP
ALA
LEU
SER
THR
TRP
ALA
GLY
LEU
LYS
PRO
SER
ARG
LEU
PRO
GLN
ARG
ALA
SER
LEU
ALA
LYS
HIS
GLN
GLU
LEU
PRO
G59

L62
L63
L68
V73
R76
Q86
A87
S90
G102
G105
G108
Q121
V128
V157
P158
K164
E165
R168
V169
H192
R193
F194
F195
P203
V204
T205
C206
T207
P208
A227
G228
M229
A235
L241
R242
P249
A250
V251
F256
T257

P261
I265
L272
V276
I282
I283
H284
G285
A286
H287
G291
L292
L297
H299
I300
D311
L312
D323
S336
A341
K346
I347
R360
D361
H362
L363
G364
Q365
E366
V367
V369
L370
H384
L385
K386
V387
L388
Y389
D390
A391
Y392
A393
E394
A395

GLU
LEU
GLY
GLN
GLY
ARG
GLN
PRO
LEU
TRP
TRP
ASP
LYS
ASP
ASP
LYS

• Molecule 22: 39S ribosomal protein L9, mitochondrial

Chain H:  34% 64%

MET
ALA
ALA
PRO
VAL
VAL
THR
ALA
PRO
GLY
ARG
ALA
LEU
LEU
ARG
GLY
ALA
GLY
ARG
GLY
VAL
GLN
GLU
LEU
LEU
ARG
GLY
VAL
GLY
ASN
PRO
HIS
GLY
ASN
GLY
ALA
PRO
ASP
LEU
LEU
ALA
CYS
ASN
PHE
SER
SER
GLN
ASN
ARG
GLY
T53
V54
I55
V107
R108
Y131

L145
L146
R147
GLN
GLY
GLY
LYS
GLU
GLY
LEU
ILE
THR
GLY
LYS
GLY
ALA
GLY
ALA
THR
VAL
VAL
LYS
PHE
ASN
GLY
LEU
SER
CYS
ARG
THR
VAL
VAL
PRO
MET
SER
VAL
ASN
PHE
GLY
LEU
LYS
TRP
GLU
LYS
PRO
GLY
ILE
VAL
ALA
ARG
HIS
PHE
PHE
LYS
ASN
ALA
LYS
GLY
VAL
VAL
VAL
PRO

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

SER
PRO
GLN
ILE

• Molecule 23: 39S ribosomal protein L10, mitochondrial

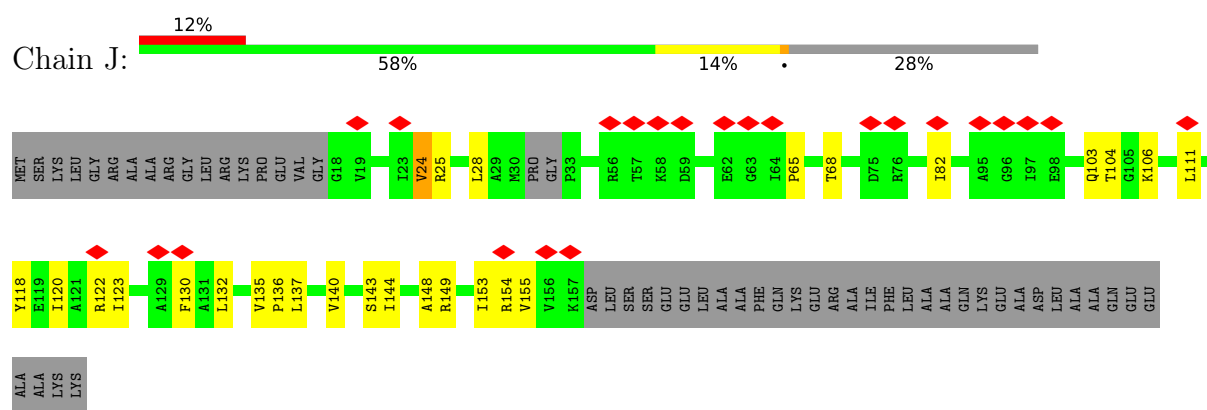
Chain I:  21% 65% 16% 19%

MET
ALA
ALA
VAL
ALA
GLY
MET
LEU
ARG
GLY
LEU
LEU
PRO
GLN
ALA
GLY
ARG
LEU
PRO
THR
LEU
LEU
GLN
THR
VAL
ARG
TYR
G29
V39
L47
V50
P69
S70
P71
P72
Q73
E74
E75
I76
G77
L78
R83
A97
M101
E107
L116
I121
L144

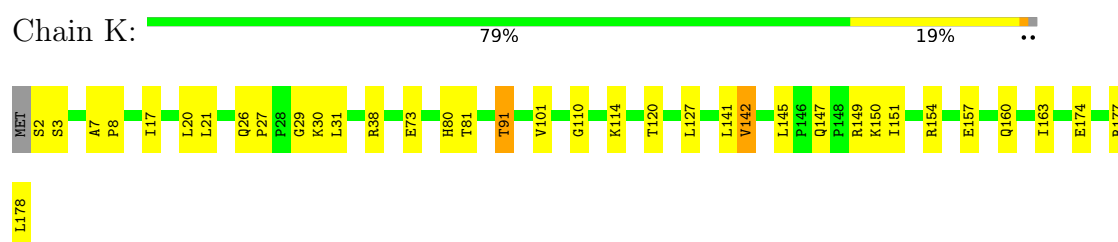
P145
L146
L154
L176
L177
G178
D182
I185
L186
S187
R188
Y194
S195
K196
L197
P198
S199
L200
P201
L202
V203
Q204
G205
E206
L207
V208
G209
G210
L211
T212
C213
L214
T215
A216
Q217
T218
H219
S220
L221
L222
Q223
H224
Q225
P226
L227
Q228
L229
T230
T231
L232
L233
D234
Q235
V236
I237

R238
E239
Q240
ARG
GLY
LYS
ASP
SER
VAL
MET
SER
SER
ALA
ASN
GLY
LYS
PRO
ASP
PRO
ASP
THR
VAL
PRO
PRO
ASP
SER

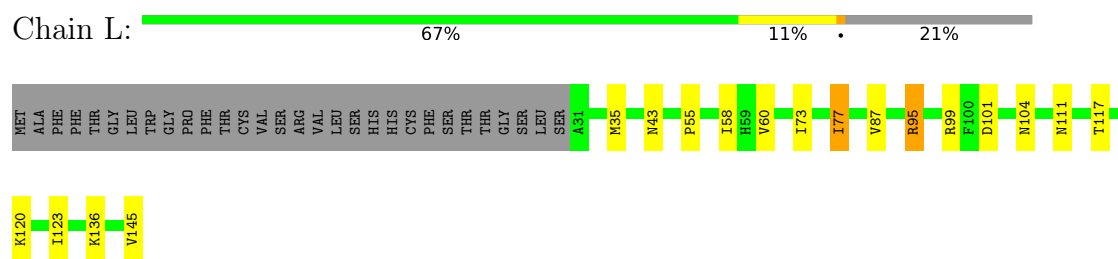
• Molecule 24: 39S ribosomal protein L11, mitochondrial



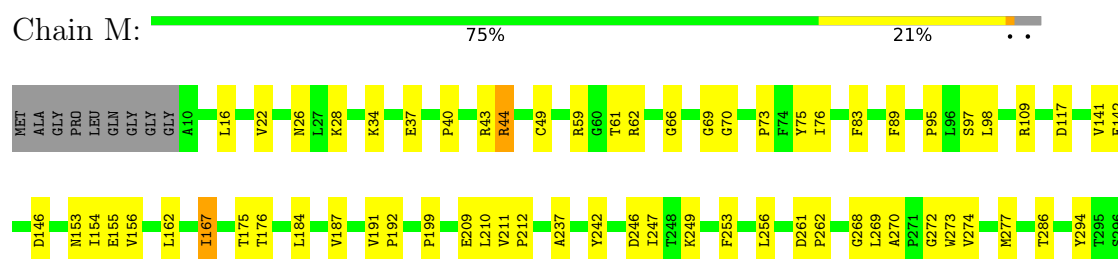
- Molecule 25: 39S ribosomal protein L13, mitochondrial



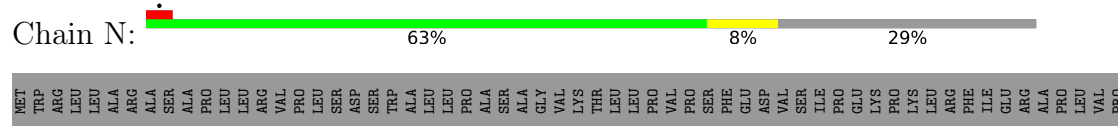
- Molecule 26: 39S ribosomal protein L14, mitochondrial



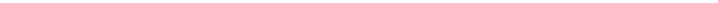
- Molecule 27: 39S ribosomal protein L15, mitochondrial

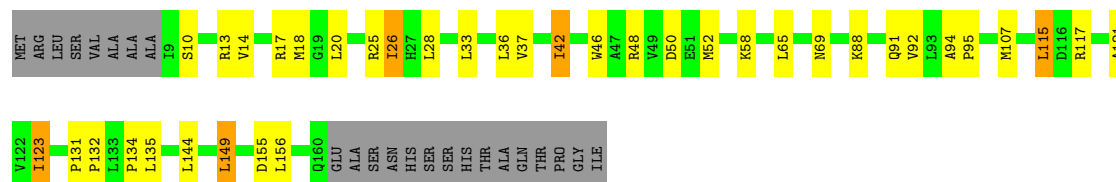


- Molecule 28: 39S ribosomal protein L16, mitochondrial

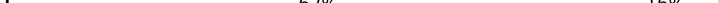


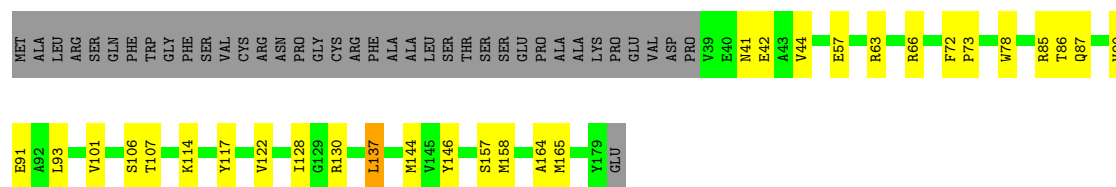
- Molecule 29: 39S ribosomal protein L17, mitochondrial

Chain O:  65% 19% • 13%



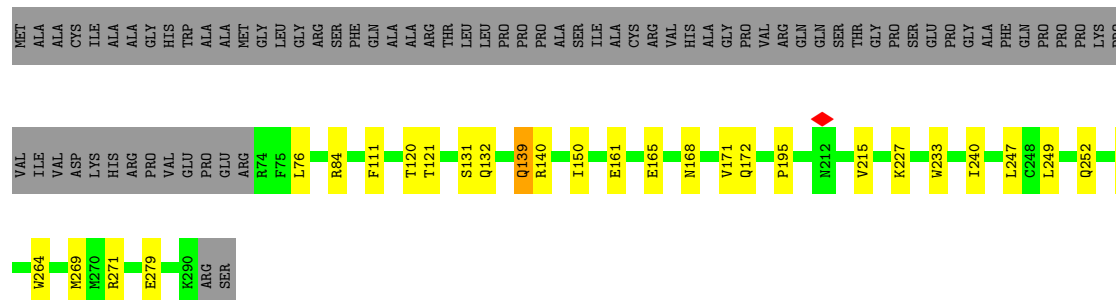
- Molecule 30: Mitochondrial ribosomal protein L18, isoform CRA b

Chain P:  62% 16% 21%



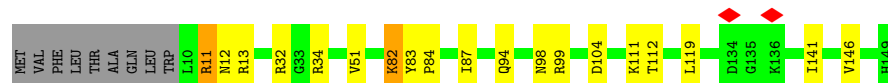
- Molecule 31: 39S ribosomal protein L19, mitochondrial

Chain Q: 65% 9% 26%



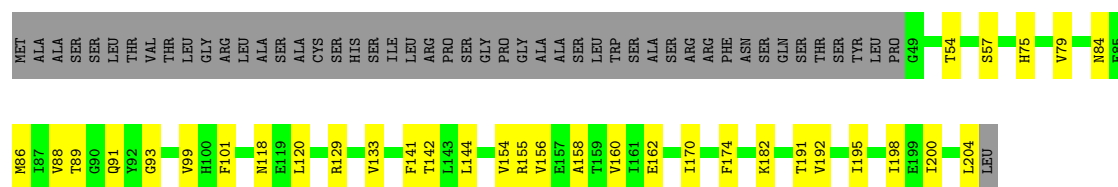
- Molecule 32: 39S ribosomal protein L20, mitochondrial

Chain R: 81% 11% 6%



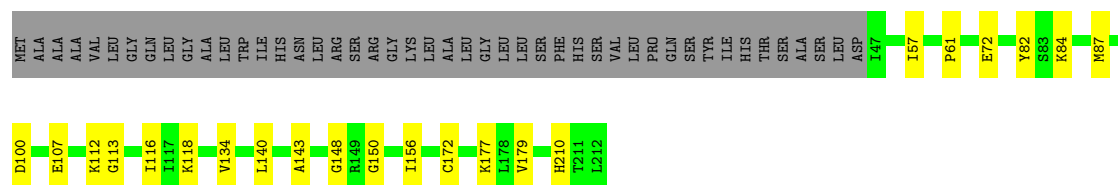
- Molecule 33: 39S ribosomal protein L21, mitochondrial

Chain S:  60% 17% 24%



- Molecule 34: 39S ribosomal protein L22, mitochondrial

Chain T:  68% 10% 22%



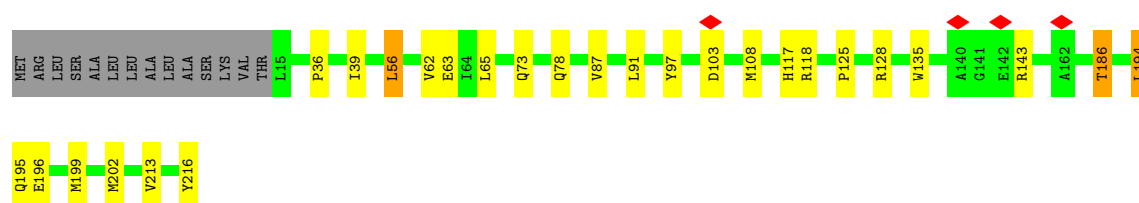
- Molecule 35: 39S ribosomal protein L23, mitochondrial

Chain U:  67% 24% 9%



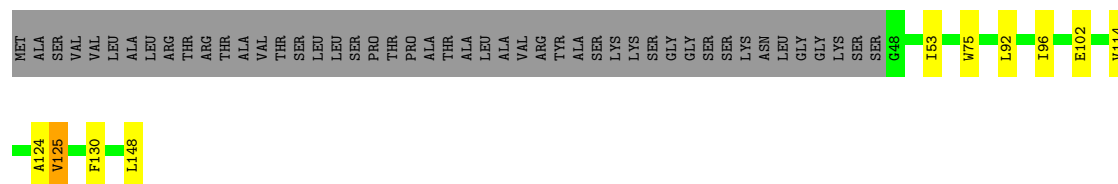
- Molecule 36: 39S ribosomal protein L24, mitochondrial

Chain V:  81% 11% 6%



- Molecule 37: 39S ribosomal protein L27, mitochondrial

Chain W:  61% 6% 32%



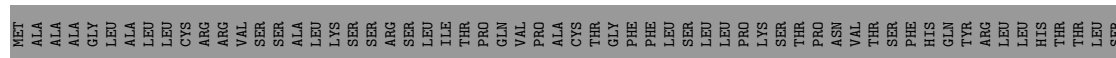
- Molecule 38: 39S ribosomal protein L28, mitochondrial

Chain X:  86% 8% 5%



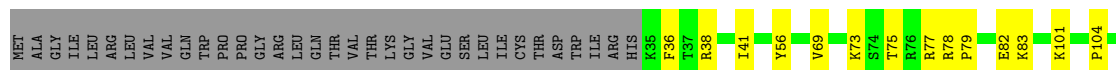
- Molecule 39: 39S ribosomal protein L47, mitochondrial

Chain Y:  61% 9% 30%



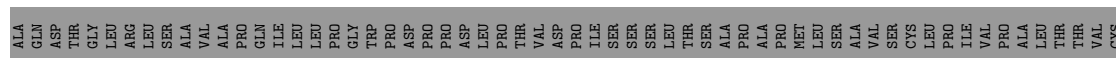
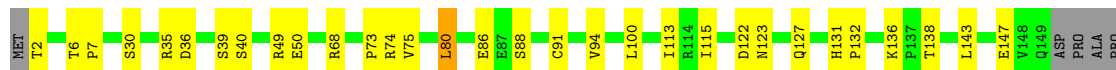
- Molecule 40: 39S ribosomal protein L30, mitochondrial

Chain Z:  60% 14% 25%



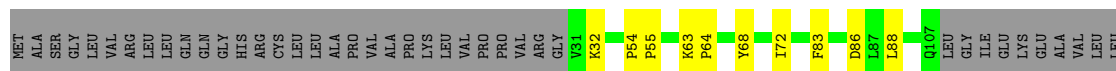
- Molecule 41: 39S ribosomal protein L43, mitochondrial

Chain b:  54% 14% 31%



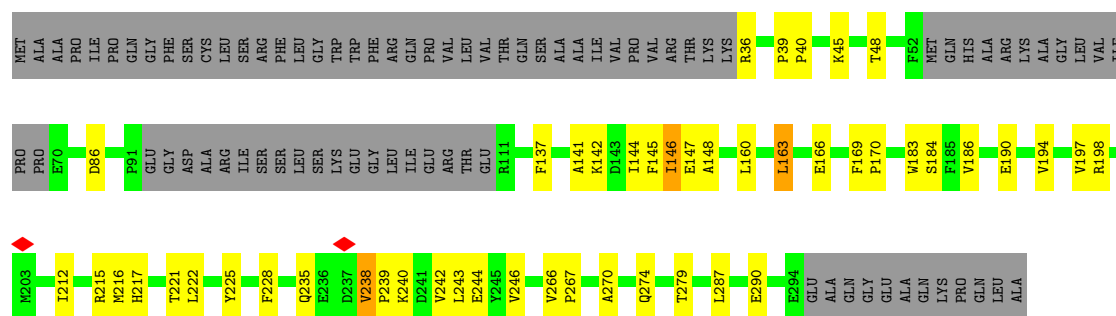
- Molecule 42: 39S ribosomal protein L44, mitochondrial

Chain c:  75% 7% 17%



- Molecule 43: 39S ribosomal protein L45, mitochondrial

Chain d:  57% 15% 27%

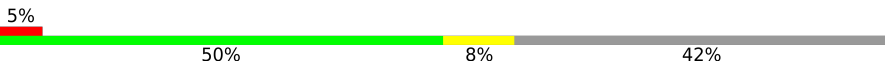


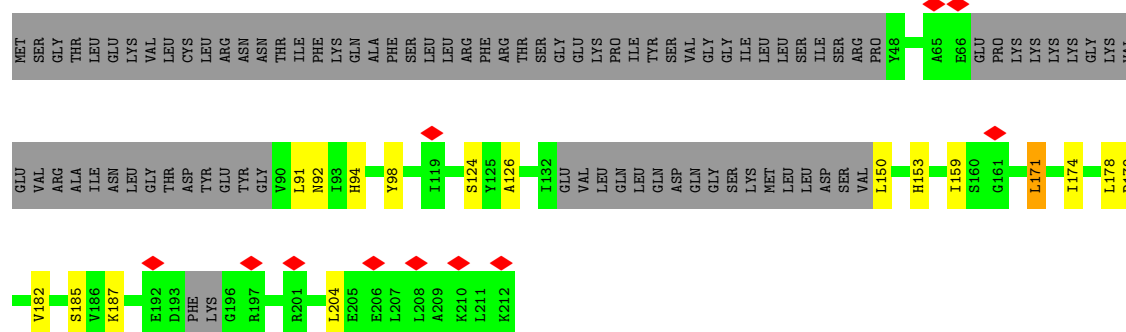
- Molecule 44: 39S ribosomal protein L46, mitochondrial

Chain e:  23% 65% 13% 22%



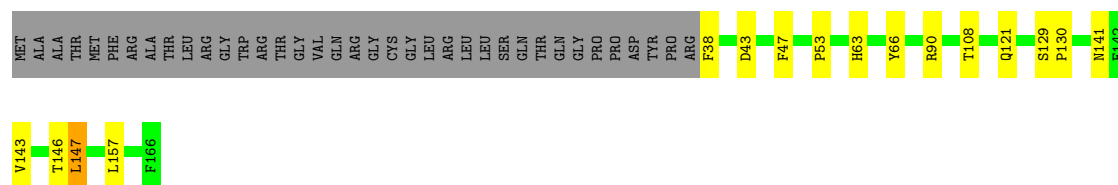
- Molecule 45: 39S ribosomal protein L48, mitochondrial

Chain f:  5% 50% 8% 42%

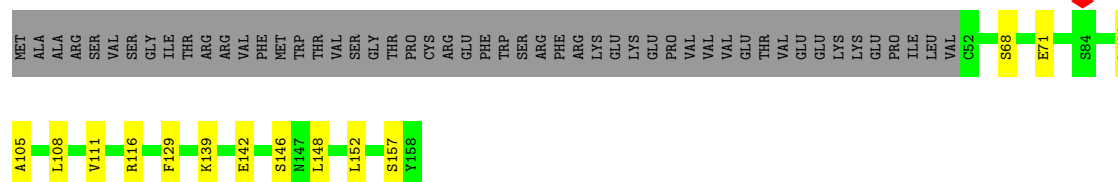


- Molecule 46: 39S ribosomal protein L49, mitochondrial

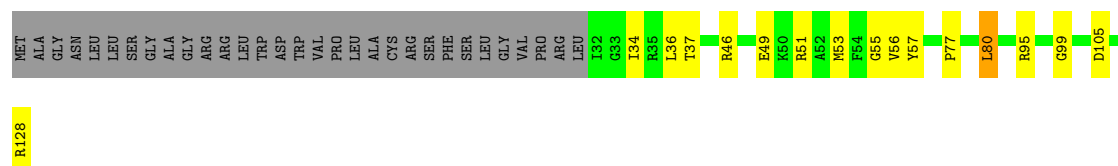
Chain g:  68% 9% 22%



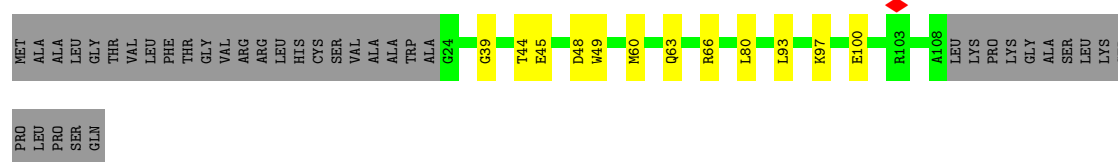
- Molecule 47: 39S ribosomal protein L50, mitochondrial



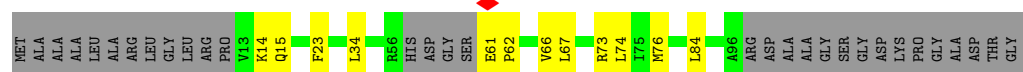
- Molecule 48: 39S ribosomal protein L51, mitochondrial



- Molecule 49: 39S ribosomal protein L52, mitochondrial

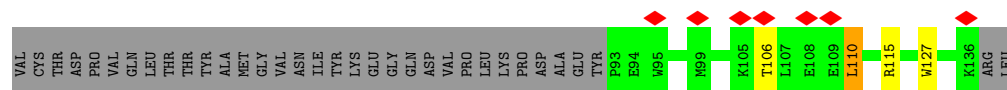


- Molecule 50: 39S ribosomal protein L53, mitochondrial

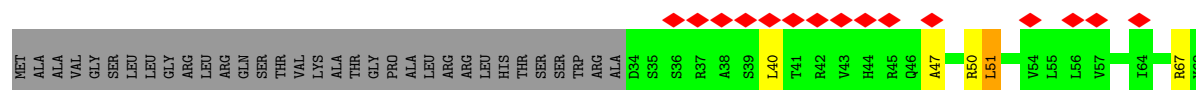


- Molecule 51: 39S ribosomal protein L54, mitochondrial

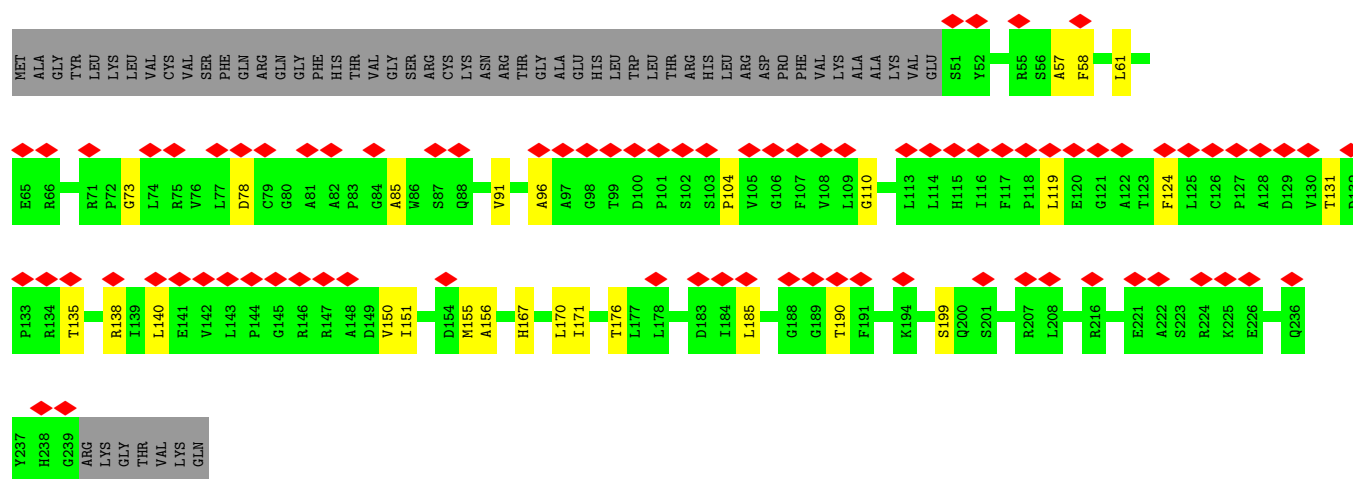




- Molecule 52: 39S ribosomal protein L55, mitochondrial



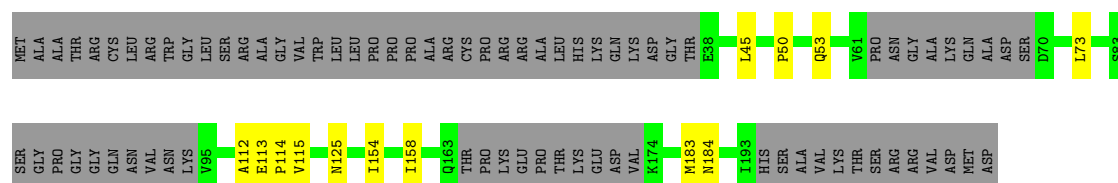
- Molecule 53: rRNA methyltransferase 2, mitochondrial



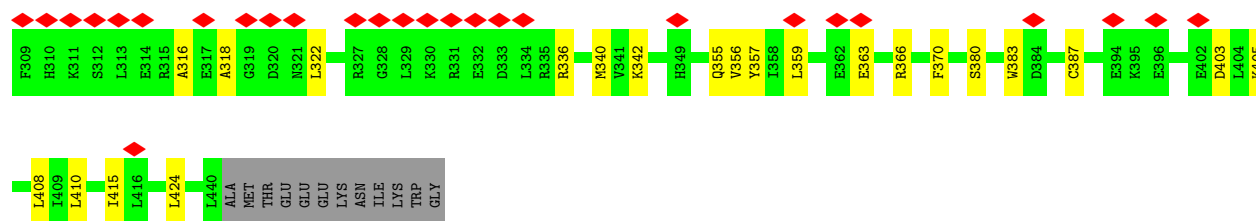
- Molecule 54: Ribosomal protein 63, mitochondrial



- Molecule 55: Peptidyl-tRNA hydrolase ICT1, mitochondrial

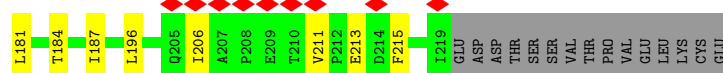
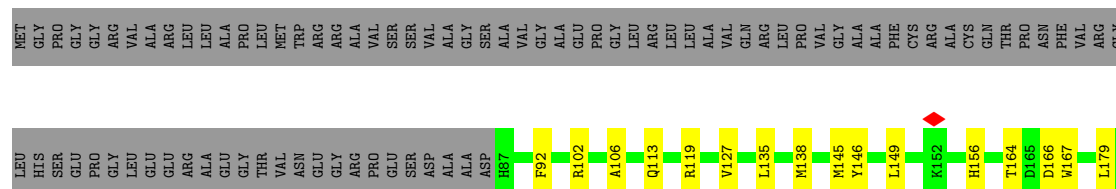


- Molecule 56: Growth arrest and DNA damage-inducible proteins-interacting protein 1



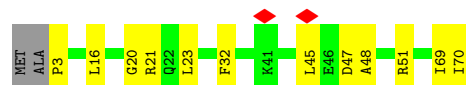
- Molecule 60: Mitochondrial assembly of ribosomal large subunit protein 1

Chain u: 47% 10% 43%



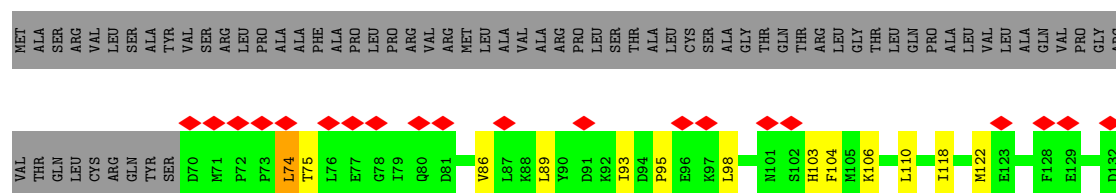
- Molecule 61: MIEF1 upstream open reading frame protein

Chain v: 80% 17% .



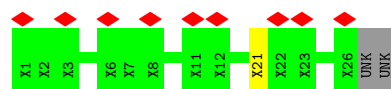
- Molecule 62: Acyl carrier protein, mitochondrial

Chain w: 16% 45% 10% . 44%



- Molecule 63: UNK

Chain UNK: 32% 89% . 7%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39495	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 ($e^-/\text{\AA}^2$)	49.2	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	0.935	Depositor
Minimum map value	-0.278	Depositor
Average map value	0.025	Depositor
Map value standard deviation	0.082	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	221.34, 280.5, 250.92	wwPDB
Map dimensions	246, 275, 217	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: GTP, ZN, MG, SAM, OMG, PNS, SAH, GDP

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	0.44	0/895	1.05	0/1201
2	a	0.49	0/709	1.00	0/963
3	1	0.40	0/438	0.95	0/583
4	2	0.48	0/373	1.11	0/496
5	3	0.41	0/852	0.95	2/1136 (0.2%)
6	4	0.42	0/350	0.98	0/461
7	5	0.46	0/3294	0.99	1/4488 (0.0%)
8	6	0.47	0/2779	1.01	0/3787
9	7	0.43	0/2413	1.04	0/3264
10	8	0.45	0/734	1.14	0/986
11	9	0.45	0/1020	1.04	0/1374
12	A	0.50	0/34076	0.78	31/53028 (0.1%)
13	A1	0.45	0/2795	1.04	0/3792
14	B	0.50	0/1423	0.73	1/2206 (0.0%)
15	A2	0.42	0/1973	1.16	0/2651
16	C	0.43	0/2020	0.66	0/2724
17	D	0.47	0/1888	1.00	1/2538 (0.0%)
18	E	0.45	0/2465	0.99	0/3344
19	F	0.46	0/2071	1.00	0/2817
20	FF	0.44	0/544	1.17	0/730
20	t1	0.66	0/358	0.77	0/486
20	t2	0.10	0/238	0.22	0/319
20	t3	0.09	0/238	0.22	0/319
20	t4	0.10	0/229	0.20	0/308
20	t5	0.10	0/229	0.27	0/308
20	t6	0.10	0/213	0.27	0/286
21	G	0.47	0/2600	1.03	0/3513
22	H	0.44	0/798	1.07	0/1073
23	I	0.46	0/1731	1.02	0/2345
24	J	0.46	0/1064	1.13	0/1431
25	K	0.47	0/1495	1.02	1/2029 (0.0%)
26	L	0.46	0/904	1.00	0/1218

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
27	M	0.44	0/2359	1.04	0/3185
28	N	0.45	0/1494	1.05	0/2010
29	O	0.46	0/1269	1.09	0/1708
30	P	0.43	0/1173	1.05	0/1588
31	Q	0.42	0/1846	1.01	0/2487
32	R	0.45	0/1174	1.06	0/1572
33	S	0.46	0/1276	1.00	0/1729
34	T	0.47	0/1402	0.99	0/1886
35	U	0.45	0/1183	1.00	0/1600
36	V	0.46	0/1697	0.99	0/2302
37	W	0.48	0/827	0.96	0/1118
38	X	0.43	0/2090	1.02	1/2825 (0.0%)
39	Y	0.42	0/1552	1.08	0/2079
40	Z	0.48	0/1003	1.03	0/1354
41	b	0.48	0/1202	1.00	0/1626
42	c	0.44	0/2264	1.11	0/3059
43	d	0.46	0/1899	1.00	0/2569
44	e	0.44	0/1797	1.10	0/2422
45	f	0.45	0/994	1.05	0/1336
46	g	0.47	0/1102	0.96	0/1503
47	h	0.50	0/894	1.06	0/1217
48	i	0.45	0/849	1.00	0/1135
49	j	0.47	0/698	1.17	0/940
50	k	0.47	0/635	1.05	0/855
51	l	0.43	0/407	1.14	0/547
52	m	0.48	0/292	0.93	0/394
53	n	0.46	0/1480	1.05	0/2013
54	o	0.44	0/792	1.05	0/1064
55	p	0.45	0/1071	1.04	0/1433
56	q	0.47	0/1165	1.17	1/1575 (0.1%)
57	r	0.49	0/1305	1.06	1/1767 (0.1%)
58	s	0.44	0/3114	0.97	0/4225
59	t	0.47	0/2992	1.02	0/4047
60	u	0.43	0/1119	1.02	0/1516
61	v	0.39	0/593	1.17	0/788
62	w	0.43	0/717	1.16	0/967
All	All	0.47	0/120935	0.95	40/170645 (0.0%)

There are no bond length outliers.

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	A	2457	A	C2'-C3'-O3'	9.87	124.31	109.50
12	A	2653	C	C4'-C3'-O3'	8.50	125.75	113.00
12	A	1855	A	C2'-C3'-O3'	8.45	126.38	113.70
12	A	3217	A	C4'-C3'-O3'	-8.44	100.34	113.00
12	A	2182	G	C2'-C3'-O3'	8.18	125.97	113.70

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	0	880	0	902	20	0
2	a	686	0	658	9	0
3	1	433	0	475	11	0
4	2	367	0	393	3	0
5	3	831	0	883	13	0
6	4	342	0	361	11	0
7	5	3199	0	3196	33	0
8	6	2692	0	2509	33	0
9	7	2356	0	2368	19	0
10	8	719	0	723	11	0
11	9	992	0	984	14	0
12	A	30486	0	15484	198	0
13	A1	2731	0	2712	32	0
14	B	1275	0	650	13	0
15	A2	1942	0	2035	26	0
16	C	1990	0	2079	50	0
17	D	1851	0	1908	19	0
18	E	2396	0	2402	34	0
19	F	2013	0	2044	37	0
20	FF	540	0	592	12	0
20	t1	354	0	380	24	0
20	t2	238	0	270	25	0
20	t3	238	0	270	10	0
20	t4	229	0	257	8	0
20	t5	229	0	257	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	t6	214	0	236	8	0
21	G	2549	0	2551	39	0
22	H	784	0	832	5	0
23	I	1695	0	1786	48	0
24	J	1050	0	1131	18	0
25	K	1451	0	1448	21	0
26	L	889	0	941	9	0
27	M	2305	0	2378	41	0
28	N	1457	0	1461	13	0
29	O	1245	0	1283	24	0
30	P	1148	0	1148	20	0
31	Q	1805	0	1841	16	0
32	R	1153	0	1214	20	0
33	S	1251	0	1322	21	0
34	T	1368	0	1410	16	0
35	U	1154	0	1154	28	0
36	V	1652	0	1658	17	0
37	W	805	0	828	5	0
38	X	2035	0	2054	17	0
39	Y	1517	0	1561	18	0
40	Z	978	0	1030	15	0
41	b	1178	0	1180	17	0
42	c	2217	0	2220	21	0
43	d	1847	0	1832	35	0
44	e	1762	0	1767	25	0
45	f	979	0	992	9	0
46	g	1067	0	1056	9	0
47	h	871	0	850	9	0
48	i	827	0	857	8	0
49	j	684	0	673	8	0
50	k	627	0	636	8	0
51	l	395	0	391	3	0
52	m	287	0	294	3	0
53	n	1450	0	1450	13	0
54	o	771	0	775	22	0
55	p	1058	0	1083	6	0
56	q	1134	0	1110	10	0
57	r	1268	0	1291	14	0
58	s	3036	0	3022	24	0
59	t	2939	0	3007	34	0
60	u	1092	0	1084	16	0
61	v	584	0	600	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	w	705	0	691	9	0
63	UNK	130	0	28	1	0
64	0	1	0	0	0	0
64	4	1	0	0	0	0
65	A	85	0	0	0	0
65	D	1	0	0	0	0
65	E	1	0	0	0	0
65	G	2	0	0	0	0
65	M	1	0	0	0	0
65	W	1	0	0	0	0
65	g	1	0	0	0	0
65	t	1	0	0	0	0
66	A1	27	0	22	1	0
67	C	28	0	12	0	0
67	t	28	0	12	0	0
68	G	32	0	12	1	0
69	n	26	0	19	0	0
70	w	21	0	21	0	0
All	All	115679	0	101046	1143	0

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

The worst 5 of 1143 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)
23:I:194:TYR:CD1	20:t:2:16:LEU:HD21	1.38	1.55
23:I:194:TYR:CD1	20:t:2:16:LEU:CD2	2.20	1.24
23:I:194:TYR:CE1	20:t:2:16:LEU:HG	1.76	1.19
25:K:21:LEU:HD21	25:K:31:LEU:HD22	1.27	1.10
24:J:25:ARG:HA	24:J:65:PRO:HA	1.28	1.09

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%)	103 (97%)	3 (3%)	0	100	100
2	a	78/142 (55%)	75 (96%)	3 (4%)	0	100	100
3	1	50/65 (77%)	50 (100%)	0	0	100	100
4	2	43/92 (47%)	42 (98%)	1 (2%)	0	100	100
5	3	93/188 (50%)	89 (96%)	4 (4%)	0	100	100
6	4	36/103 (35%)	36 (100%)	0	0	100	100
7	5	390/423 (92%)	376 (96%)	14 (4%)	0	100	100
8	6	323/380 (85%)	310 (96%)	13 (4%)	0	100	100
9	7	288/338 (85%)	274 (95%)	14 (5%)	0	100	100
10	8	83/206 (40%)	75 (90%)	8 (10%)	0	100	100
11	9	121/137 (88%)	117 (97%)	4 (3%)	0	100	100
13	A1	340/384 (88%)	330 (97%)	10 (3%)	0	100	100
15	A2	236/381 (62%)	233 (99%)	3 (1%)	0	100	100
16	C	251/334 (75%)	245 (98%)	6 (2%)	0	100	100
17	D	235/305 (77%)	225 (96%)	10 (4%)	0	100	100
18	E	302/348 (87%)	288 (95%)	14 (5%)	0	100	100
19	F	248/311 (80%)	243 (98%)	5 (2%)	0	100	100
20	FF	68/198 (34%)	65 (96%)	3 (4%)	0	100	100
20	t1	44/198 (22%)	38 (86%)	4 (9%)	2 (4%)	2	12
20	t2	28/198 (14%)	28 (100%)	0	0	100	100
20	t3	28/198 (14%)	28 (100%)	0	0	100	100
20	t4	27/198 (14%)	27 (100%)	0	0	100	100
20	t5	27/198 (14%)	27 (100%)	0	0	100	100
20	t6	25/198 (13%)	24 (96%)	1 (4%)	0	100	100
21	G	335/414 (81%)	316 (94%)	19 (6%)	0	100	100
22	H	93/267 (35%)	91 (98%)	2 (2%)	0	100	100
23	I	210/261 (80%)	207 (99%)	3 (1%)	0	100	100
24	J	134/192 (70%)	127 (95%)	7 (5%)	0	100	100
25	K	175/178 (98%)	173 (99%)	2 (1%)	0	100	100
26	L	113/145 (78%)	107 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	M	285/296 (96%)	279 (98%)	6 (2%)	0	100	100
28	N	175/251 (70%)	170 (97%)	5 (3%)	0	100	100
29	O	150/175 (86%)	144 (96%)	6 (4%)	0	100	100
30	P	139/179 (78%)	137 (99%)	2 (1%)	0	100	100
31	Q	215/292 (74%)	209 (97%)	6 (3%)	0	100	100
32	R	138/149 (93%)	137 (99%)	1 (1%)	0	100	100
33	S	154/205 (75%)	149 (97%)	5 (3%)	0	100	100
34	T	164/212 (77%)	161 (98%)	3 (2%)	0	100	100
35	U	135/153 (88%)	131 (97%)	4 (3%)	0	100	100
36	V	200/216 (93%)	196 (98%)	4 (2%)	0	100	100
37	W	99/148 (67%)	99 (100%)	0	0	100	100
38	X	241/256 (94%)	239 (99%)	2 (1%)	0	100	100
39	Y	174/250 (70%)	170 (98%)	4 (2%)	0	100	100
40	Z	118/161 (73%)	113 (96%)	5 (4%)	0	100	100
41	b	146/215 (68%)	138 (94%)	8 (6%)	0	100	100
42	c	271/332 (82%)	267 (98%)	4 (2%)	0	100	100
43	d	217/306 (71%)	207 (95%)	10 (5%)	0	100	100
44	e	211/279 (76%)	202 (96%)	9 (4%)	0	100	100
45	f	115/212 (54%)	107 (93%)	7 (6%)	1 (1%)	14	44
46	g	127/166 (76%)	125 (98%)	2 (2%)	0	100	100
47	h	105/158 (66%)	101 (96%)	4 (4%)	0	100	100
48	i	95/128 (74%)	92 (97%)	3 (3%)	0	100	100
49	j	83/123 (68%)	82 (99%)	1 (1%)	0	100	100
50	k	76/112 (68%)	73 (96%)	3 (4%)	0	100	100
51	l	42/138 (30%)	42 (100%)	0	0	100	100
52	m	33/128 (26%)	31 (94%)	2 (6%)	0	100	100
53	n	187/246 (76%)	186 (100%)	1 (0%)	0	100	100
54	o	89/102 (87%)	84 (94%)	5 (6%)	0	100	100
55	p	119/206 (58%)	115 (97%)	4 (3%)	0	100	100
56	q	133/222 (60%)	132 (99%)	1 (1%)	0	100	100
57	r	149/196 (76%)	143 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	s	366/439 (83%)	353 (96%)	13 (4%)	0	100	100
59	t	377/452 (83%)	368 (98%)	9 (2%)	0	100	100
60	u	131/234 (56%)	124 (95%)	7 (5%)	0	100	100
61	v	66/70 (94%)	61 (92%)	5 (8%)	0	100	100
62	w	85/156 (54%)	83 (98%)	2 (2%)	0	100	100
All	All	10140/14731 (69%)	9819 (97%)	318 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	t1	-3	LYS
45	f	179	PRO
20	t1	1	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	
1	0	97/164 (59%)	96 (99%)	1 (1%)	68	79
2	a	78/133 (59%)	76 (97%)	2 (3%)	40	68
3	1	49/60 (82%)	47 (96%)	2 (4%)	27	59
4	2	39/72 (54%)	39 (100%)	0	100	100
5	3	88/166 (53%)	83 (94%)	5 (6%)	18	49
6	4	37/89 (42%)	35 (95%)	2 (5%)	20	50
7	5	353/368 (96%)	339 (96%)	14 (4%)	28	60
8	6	271/332 (82%)	262 (97%)	9 (3%)	33	63
9	7	266/303 (88%)	262 (98%)	4 (2%)	57	75
10	8	77/190 (40%)	75 (97%)	2 (3%)	40	68
11	9	104/112 (93%)	101 (97%)	3 (3%)	37	66
13	A1	297/328 (90%)	292 (98%)	5 (2%)	53	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	A2	221/350 (63%)	213 (96%)	8 (4%)	31	62
16	C	224/287 (78%)	220 (98%)	4 (2%)	51	73
17	D	191/245 (78%)	188 (98%)	3 (2%)	55	75
18	E	259/290 (89%)	254 (98%)	5 (2%)	50	73
19	F	217/262 (83%)	211 (97%)	6 (3%)	38	66
20	FF	58/158 (37%)	58 (100%)	0	100	100
20	t1	40/158 (25%)	38 (95%)	2 (5%)	22	53
20	t2	29/158 (18%)	28 (97%)	1 (3%)	32	63
20	t3	29/158 (18%)	29 (100%)	0	100	100
20	t4	28/158 (18%)	27 (96%)	1 (4%)	31	62
20	t5	28/158 (18%)	28 (100%)	0	100	100
20	t6	26/158 (16%)	26 (100%)	0	100	100
21	G	264/328 (80%)	253 (96%)	11 (4%)	26	58
22	H	86/228 (38%)	85 (99%)	1 (1%)	63	78
23	I	194/232 (84%)	190 (98%)	4 (2%)	47	71
24	J	112/150 (75%)	109 (97%)	3 (3%)	39	67
25	K	155/156 (99%)	150 (97%)	5 (3%)	34	64
26	L	98/124 (79%)	91 (93%)	7 (7%)	13	41
27	M	245/249 (98%)	236 (96%)	9 (4%)	30	61
28	N	152/211 (72%)	151 (99%)	1 (1%)	76	82
29	O	133/150 (89%)	121 (91%)	12 (9%)	9	33
30	P	123/154 (80%)	121 (98%)	2 (2%)	55	75
31	Q	199/256 (78%)	192 (96%)	7 (4%)	32	62
32	R	118/126 (94%)	113 (96%)	5 (4%)	26	58
33	S	141/180 (78%)	137 (97%)	4 (3%)	38	66
34	T	146/182 (80%)	144 (99%)	2 (1%)	59	76
35	U	124/135 (92%)	120 (97%)	4 (3%)	34	64
36	V	180/191 (94%)	172 (96%)	8 (4%)	25	56
37	W	83/119 (70%)	79 (95%)	4 (5%)	23	54
38	X	219/229 (96%)	216 (99%)	3 (1%)	59	76
39	Y	159/223 (71%)	156 (98%)	3 (2%)	50	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	Z	111/147 (76%)	105 (95%)	6 (5%)	20	50
41	b	130/186 (70%)	122 (94%)	8 (6%)	16	46
42	c	241/288 (84%)	233 (97%)	8 (3%)	33	63
43	d	207/274 (76%)	199 (96%)	8 (4%)	28	60
44	e	188/236 (80%)	184 (98%)	4 (2%)	47	71
45	f	108/188 (57%)	107 (99%)	1 (1%)	70	80
46	g	119/148 (80%)	116 (98%)	3 (2%)	42	69
47	h	101/148 (68%)	101 (100%)	0	100	100
48	i	86/110 (78%)	79 (92%)	7 (8%)	11	36
49	j	68/97 (70%)	67 (98%)	1 (2%)	57	75
50	k	71/90 (79%)	68 (96%)	3 (4%)	26	58
51	l	43/116 (37%)	42 (98%)	1 (2%)	44	70
52	m	31/113 (27%)	29 (94%)	2 (6%)	15	44
53	n	157/209 (75%)	155 (99%)	2 (1%)	61	77
54	o	78/87 (90%)	74 (95%)	4 (5%)	21	52
55	p	117/181 (65%)	114 (97%)	3 (3%)	40	68
56	q	115/178 (65%)	113 (98%)	2 (2%)	53	74
57	r	141/169 (83%)	135 (96%)	6 (4%)	26	57
58	s	326/381 (86%)	319 (98%)	7 (2%)	47	71
59	t	317/371 (85%)	313 (99%)	4 (1%)	61	77
60	u	123/200 (62%)	120 (98%)	3 (2%)	43	69
61	v	59/60 (98%)	55 (93%)	4 (7%)	14	42
62	w	81/136 (60%)	76 (94%)	5 (6%)	16	46
All	All	9055/12593 (72%)	8789 (97%)	266 (3%)	38	66

5 of 266 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	q	96	LEU
57	r	159	VAL
61	v	69	ILE
25	K	150	LYS
25	K	2	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 140 such sidechains are listed below:

Mol	Chain	Res	Type
49	j	63	GLN
53	n	214	ASN
58	s	240	GLN
24	J	48	GLN
23	I	225	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	A	1427/1559 (91%)	361 (25%)	54 (3%)
14	B	56/69 (81%)	19 (33%)	2 (3%)
All	All	1483/1628 (91%)	380 (25%)	56 (3%)

5 of 380 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	A	1678	C
12	A	1679	U
12	A	1680	A
12	A	1681	G
12	A	1689	C

5 of 56 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	A	2380	C
14	B	1614	U
12	A	2620	G
14	B	1607	U
12	A	2991	U

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	$\# Z > 2$
12	OMG	A	3040	12	23,26,27	1.23	2 (8%)	32,38,41	2.00	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
12	OMG	A	3040	12	-	2/9/27/28	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	A	3040	OMG	C5-C4	3.61	1.48	1.38
12	A	3040	OMG	C5-N7	-2.08	1.34	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	A	3040	OMG	C5-C4-N3	-5.84	119.10	128.39
12	A	3040	OMG	C2-N3-C4	4.95	120.82	112.30
12	A	3040	OMG	N9-C4-N3	4.24	134.43	125.95
12	A	3040	OMG	C2'-C1'-N9	-3.41	107.77	114.24
12	A	3040	OMG	C6-C5-N7	3.01	135.77	130.29

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	A	3040	OMG	O4'-C1'-N9-C4
12	A	3040	OMG	O4'-C1'-N9-C8

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 101 ligands modelled in this entry, 95 are monoatomic - leaving 6 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
70	PNS	w	201	62	14,20,21	0.35	0	18,26,29	0.74	0
69	SAH	n	301	-	27,28,28	0.49	1 (3%)	36,40,40	0.74	1 (2%)
66	SAM	A1	401	-	27,29,29	0.50	1 (3%)	34,42,42	0.76	1 (2%)
67	GDP	C	401	-	29,30,30	1.17	3 (10%)	45,47,47	1.77	7 (15%)
68	GTP	G	502	65	33,34,34	0.57	0	50,54,54	0.55	0
67	GDP	t	501	65	29,30,30	1.17	3 (10%)	45,47,47	1.84	8 (17%)

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
70	PNS	w	201	62	-	16/24/26/27	-
69	SAH	n	301	-	-	10/15/31/31	0/3/3/3
66	SAM	A1	401	-	-	6/17/33/33	0/3/3/3
67	GDP	C	401	-	-	0/16/32/32	0/3/3/3
68	GTP	G	502	65	-	2/22/38/38	0/3/3/3
67	GDP	t	501	65	-	0/16/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	t	501	GDP	C5-C4	3.38	1.48	1.38
67	C	401	GDP	C5-C4	3.17	1.47	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	C	401	GDP	C6-N1	-2.40	1.34	1.38
69	n	301	SAH	OXT-C	-2.20	1.23	1.30
66	A1	401	SAM	OXT-C	-2.13	1.23	1.30

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	t	501	GDP	C5-C4-N3	-6.35	118.28	128.39
67	C	401	GDP	C5-C4-N3	-6.27	118.41	128.39
67	t	501	GDP	C2-N3-C4	5.36	121.52	112.30
67	C	401	GDP	C2-N3-C4	5.13	121.14	112.30
67	t	501	GDP	N9-C4-N3	4.72	135.38	125.95

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

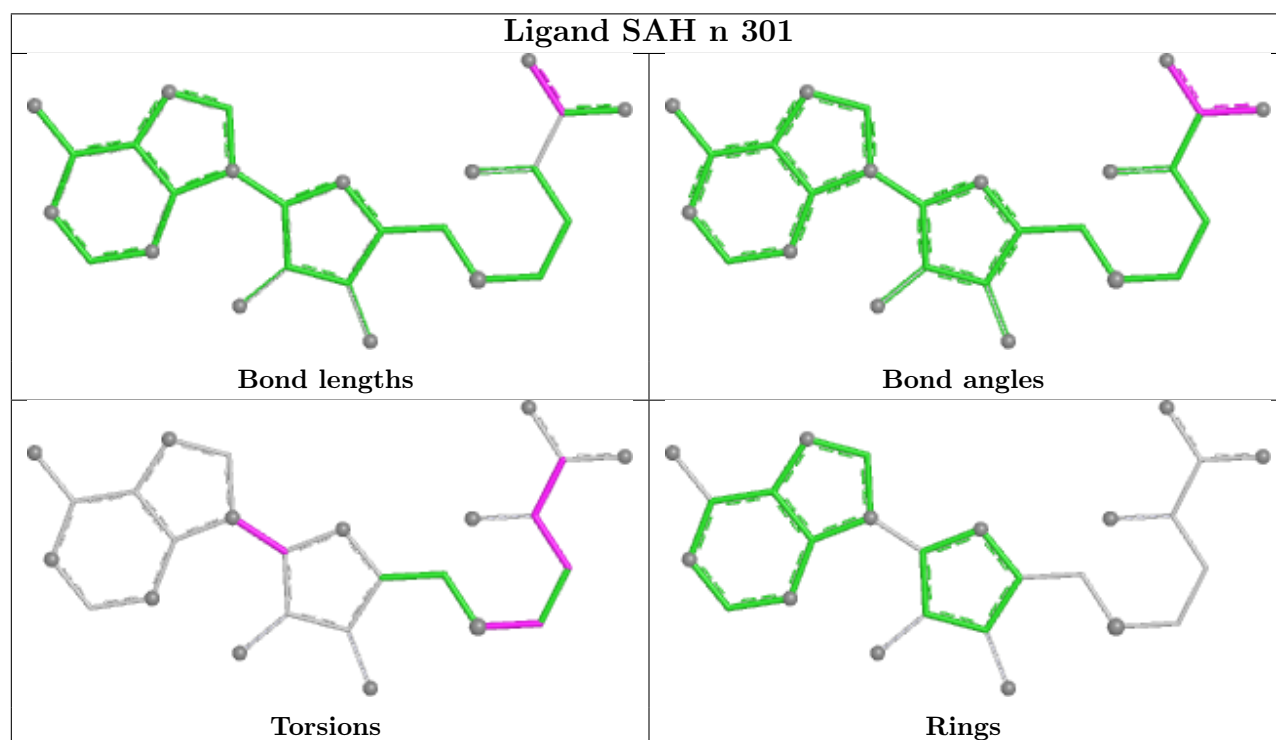
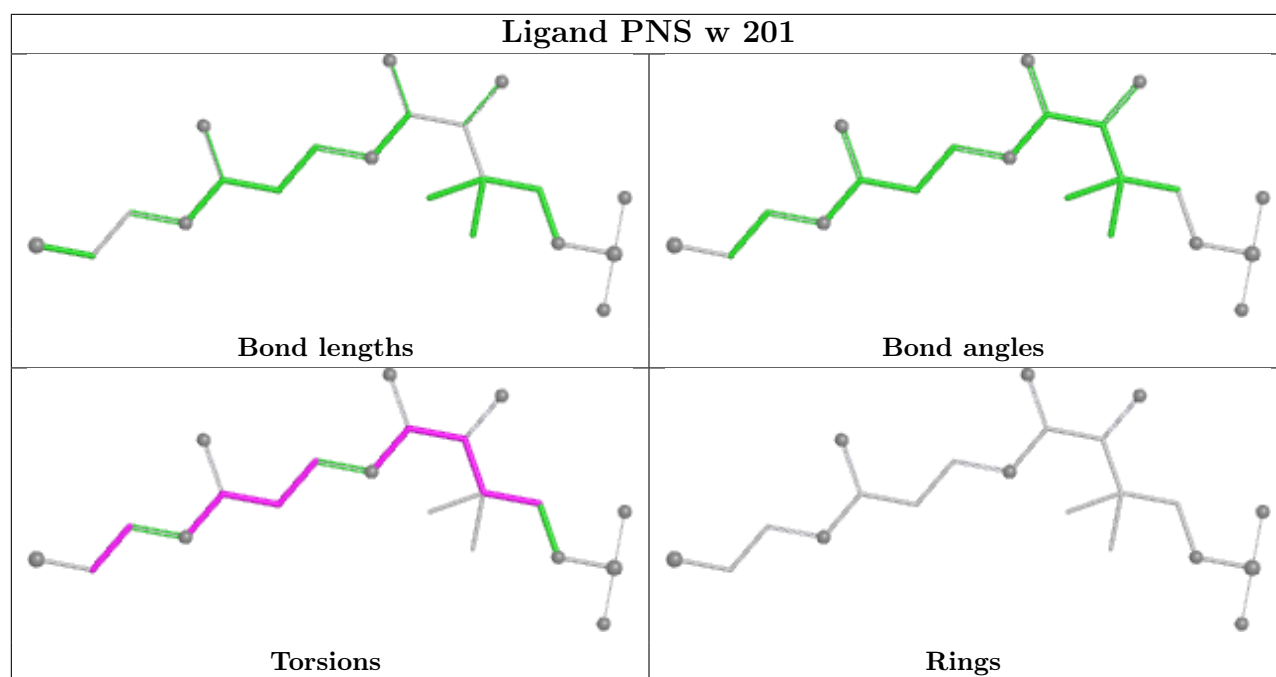
Mol	Chain	Res	Type	Atoms
66	A1	401	SAM	N-CA-CB-CG
66	A1	401	SAM	CA-CB-CG-SD
66	A1	401	SAM	C4'-C5'-SD-CE
66	A1	401	SAM	C2'-C1'-N9-C8
69	n	301	SAH	O-C-CA-N

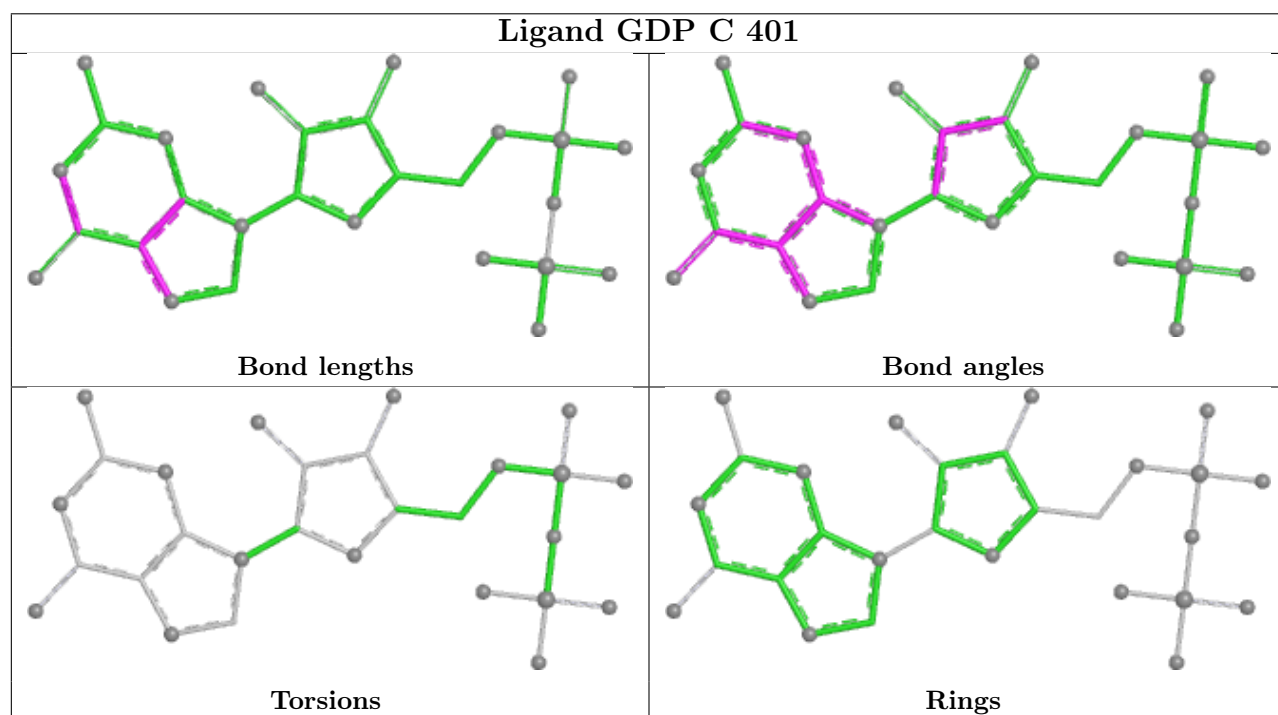
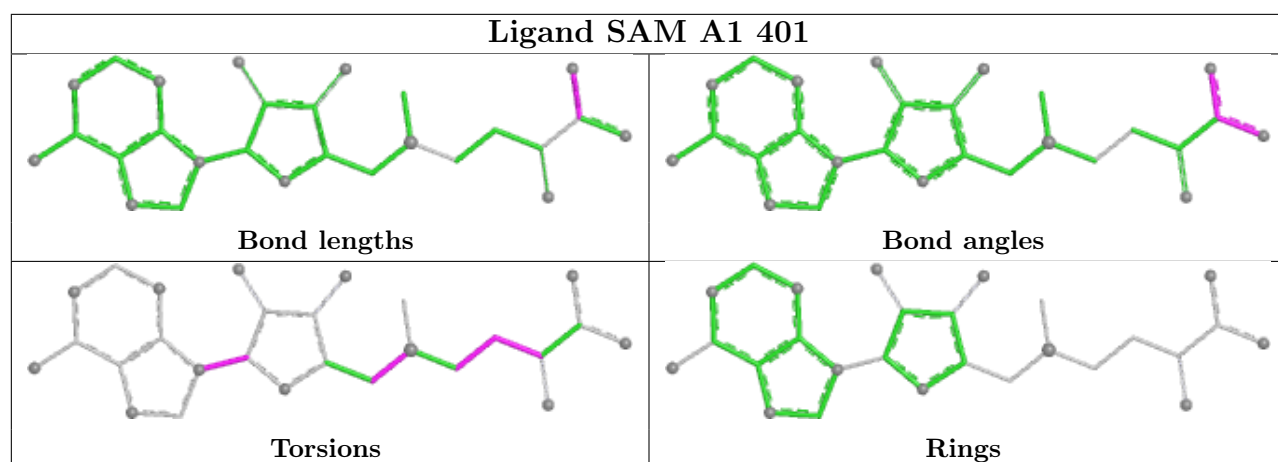
There are no ring outliers.

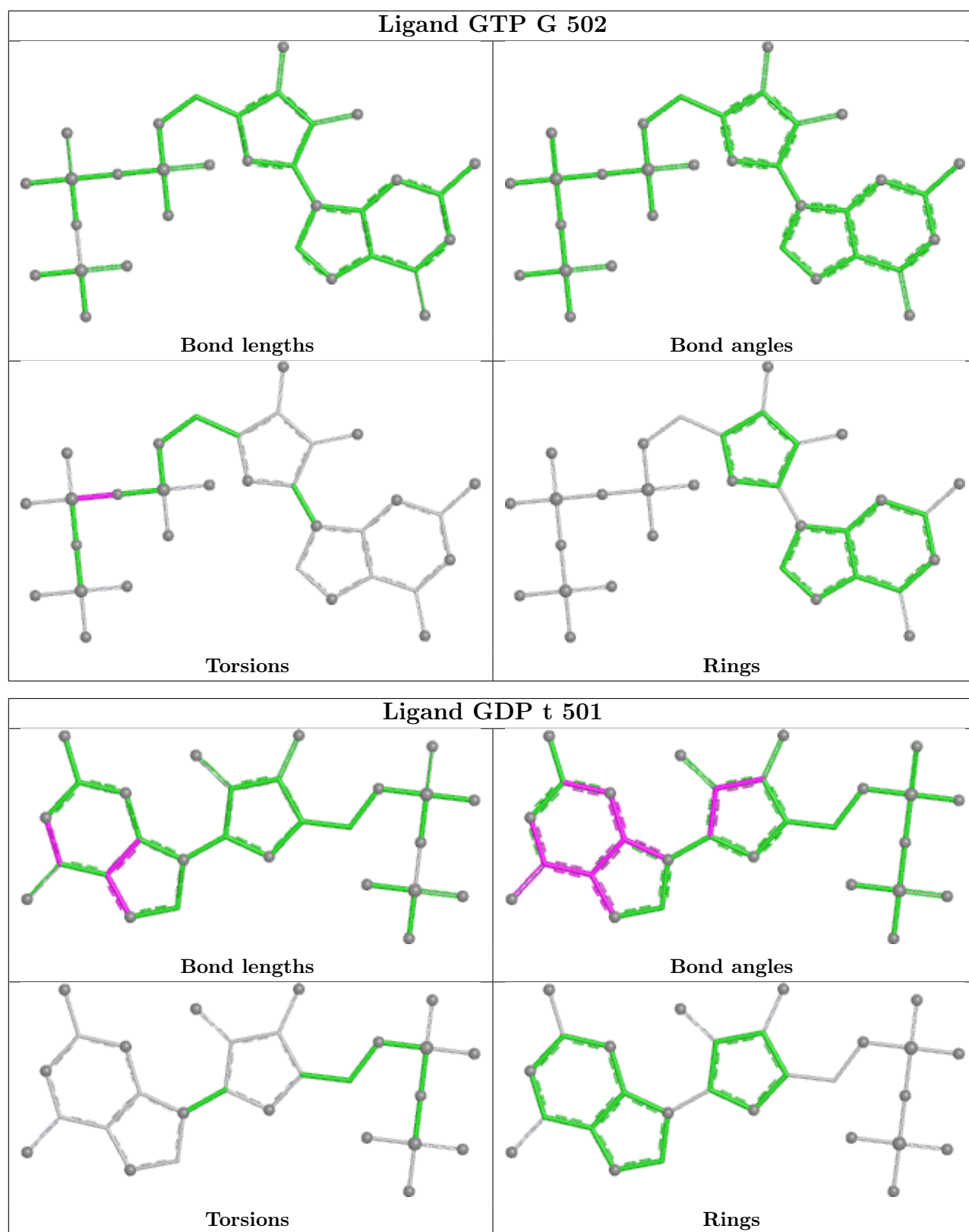
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
66	A1	401	SAM	1	0
68	G	502	GTP	1	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

There are no chain breaks in this entry.

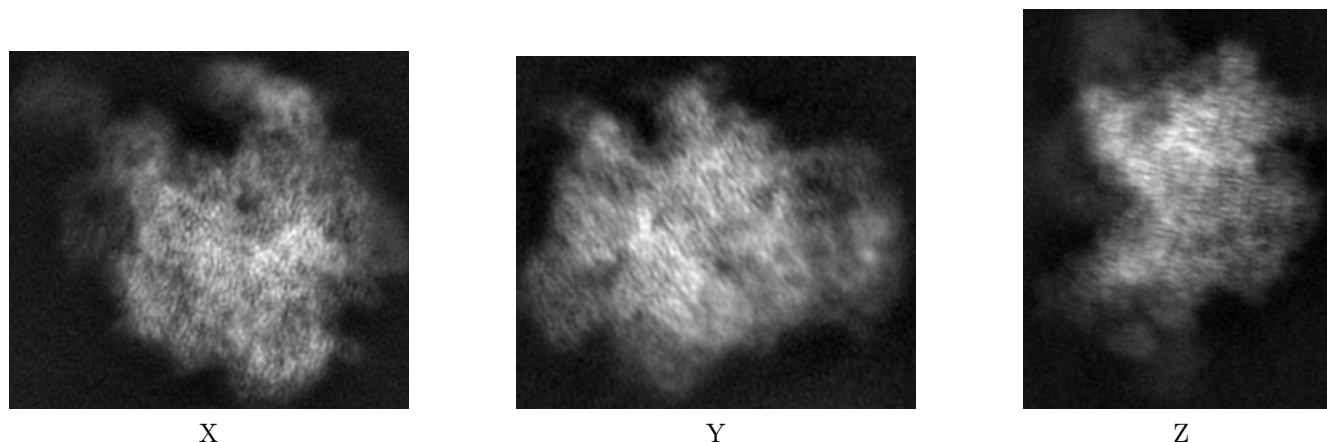
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12763. These allow visual inspection of the internal detail of the map and identification of artifacts.

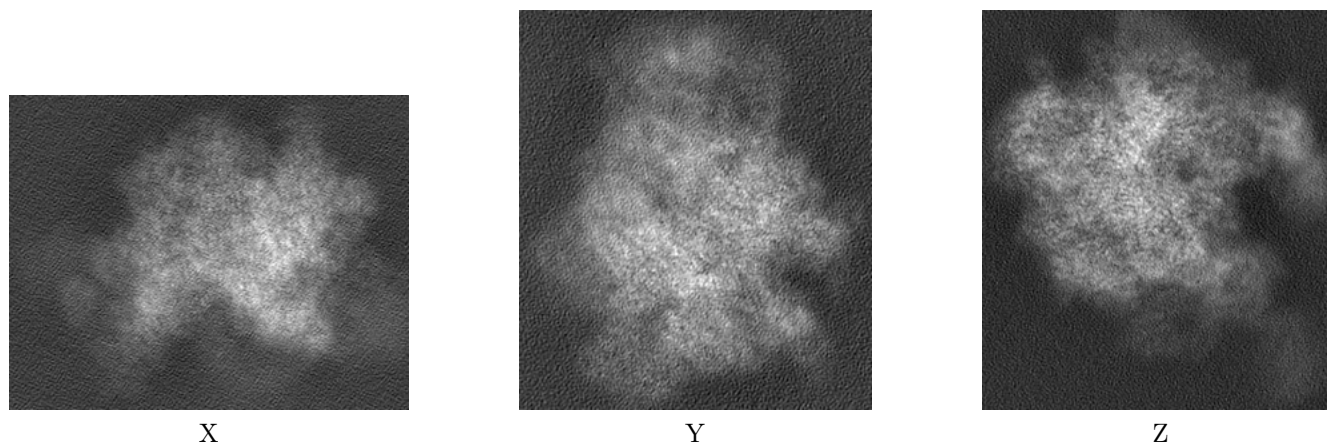
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



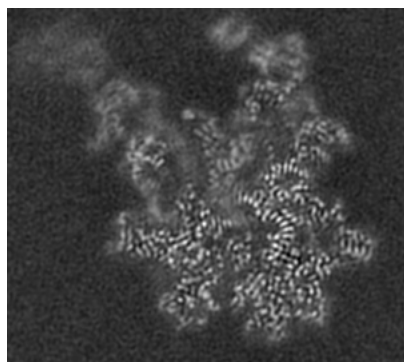
6.1.2 Raw map



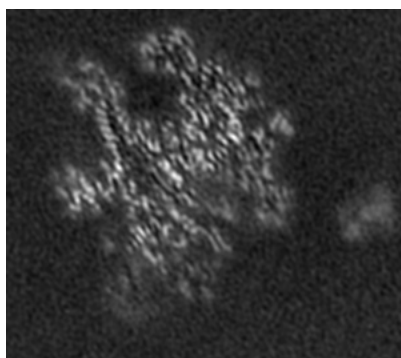
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

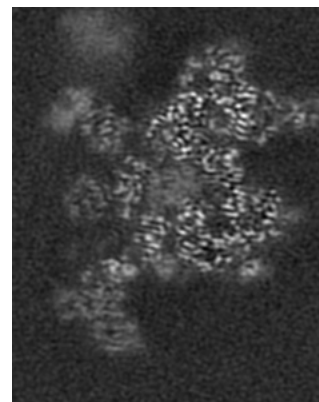
6.2.1 Primary map



X Index: 108

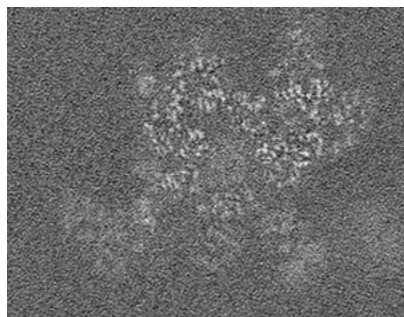


Y Index: 137

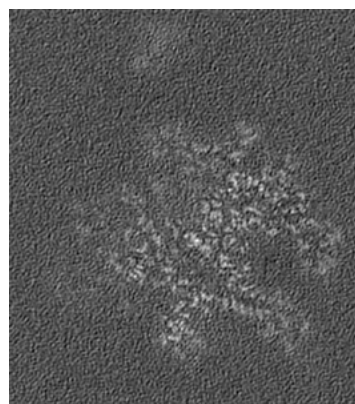


Z Index: 123

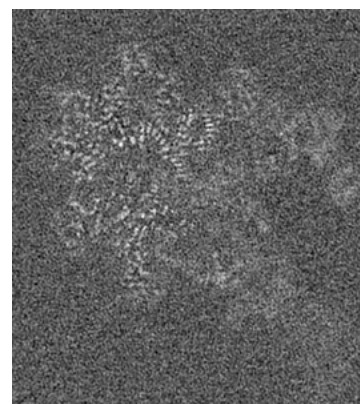
6.2.2 Raw map



X Index: 123



Y Index: 138

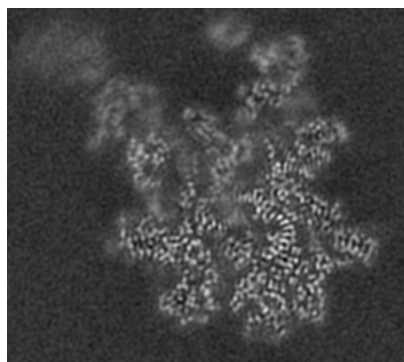


Z Index: 108

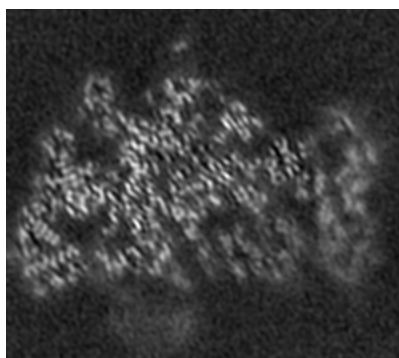
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

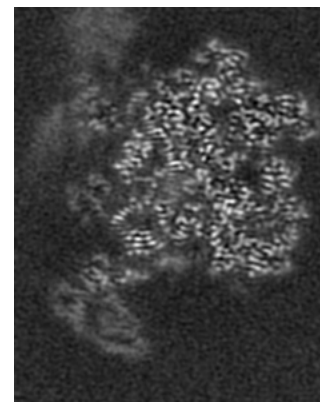
6.3.1 Primary map



X Index: 106

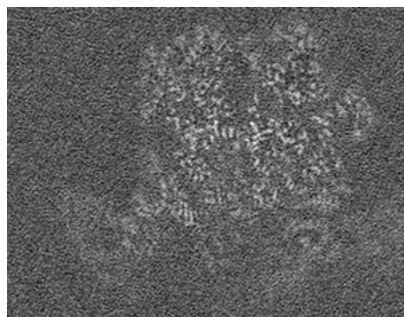


Y Index: 181

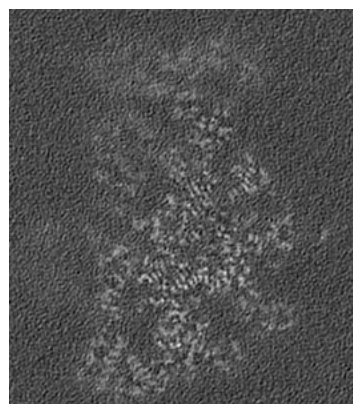


Z Index: 113

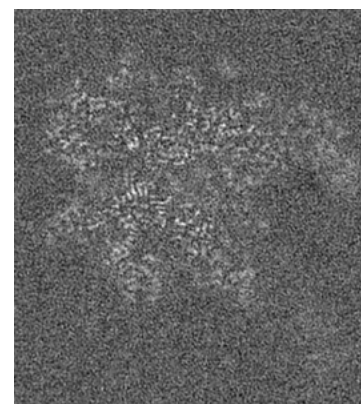
6.3.2 Raw map



X Index: 110



Y Index: 182

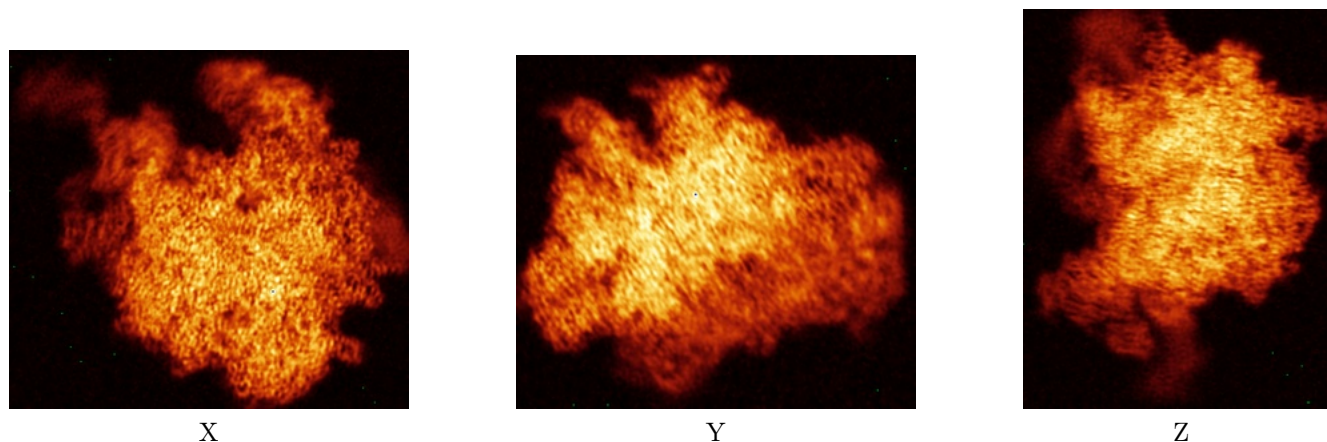


Z Index: 117

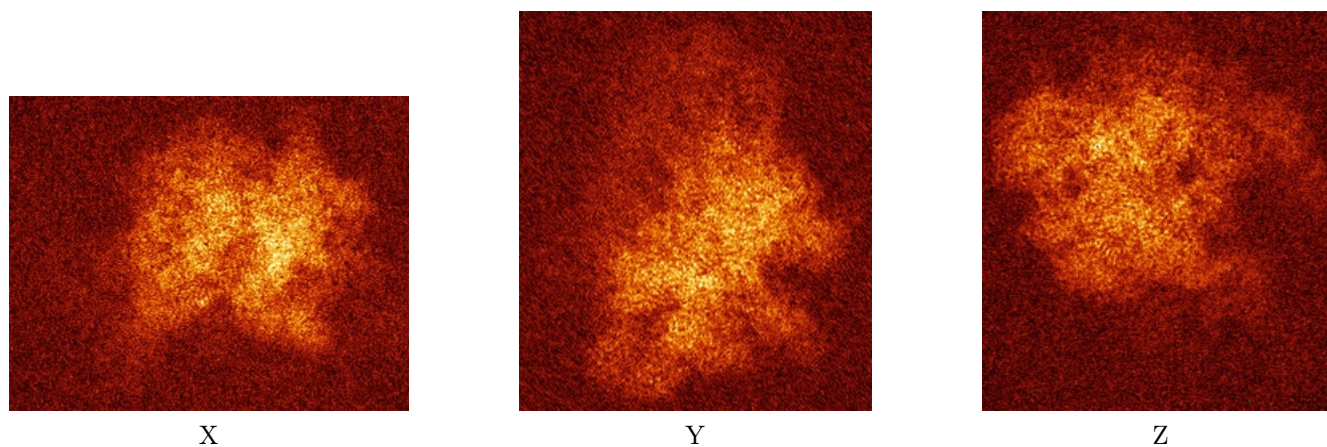
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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.

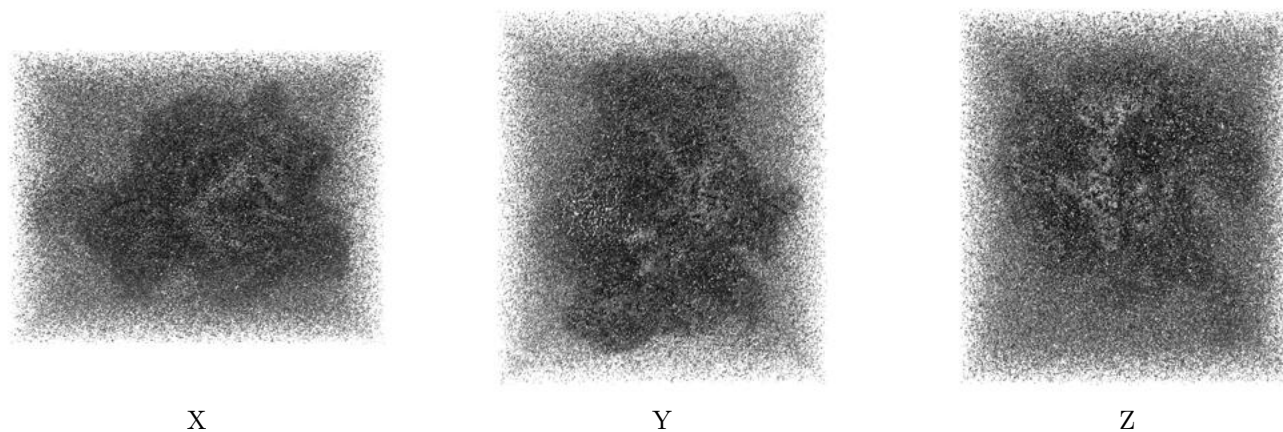
6.5 Orthogonal surface views [i](#)

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.

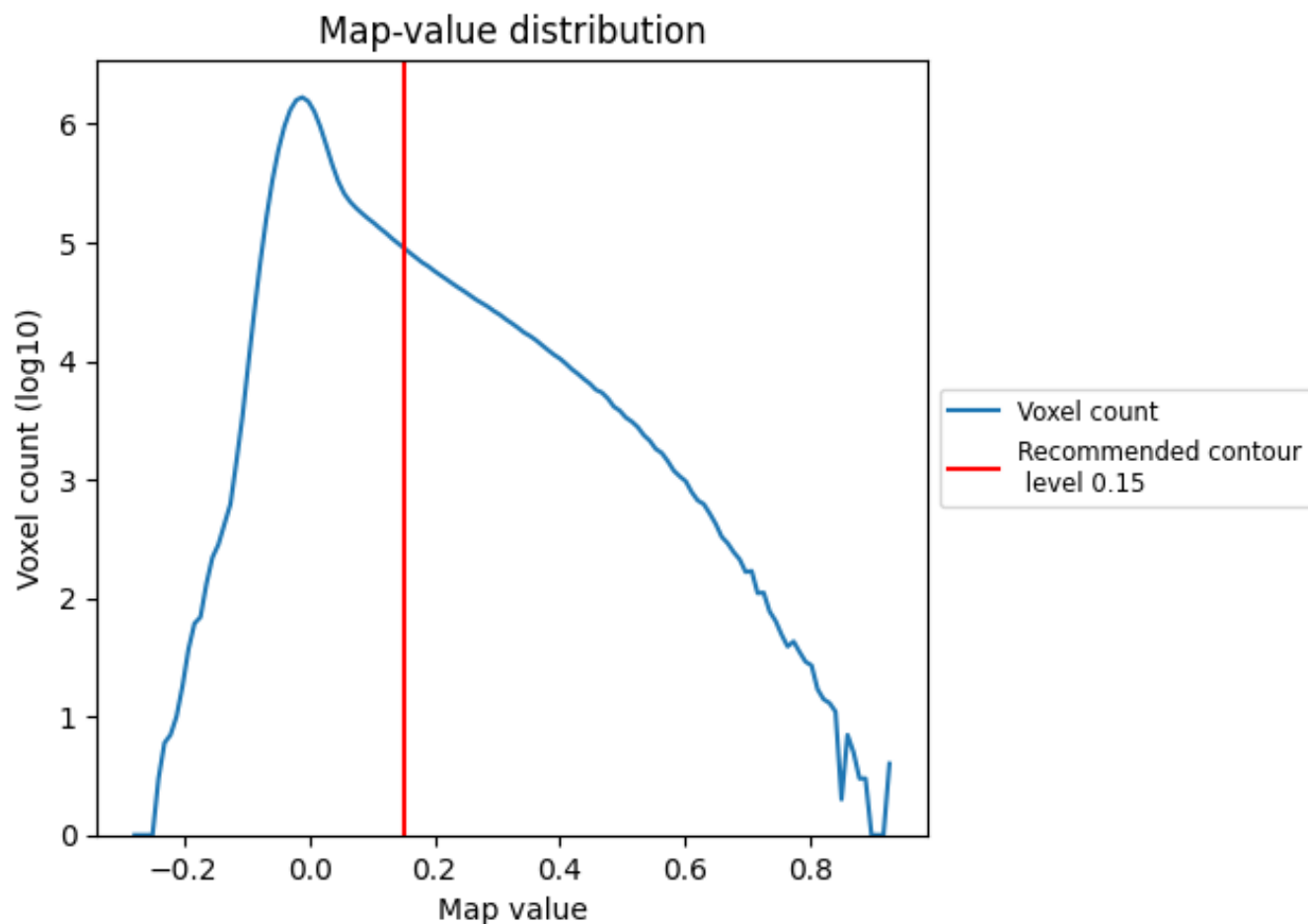
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

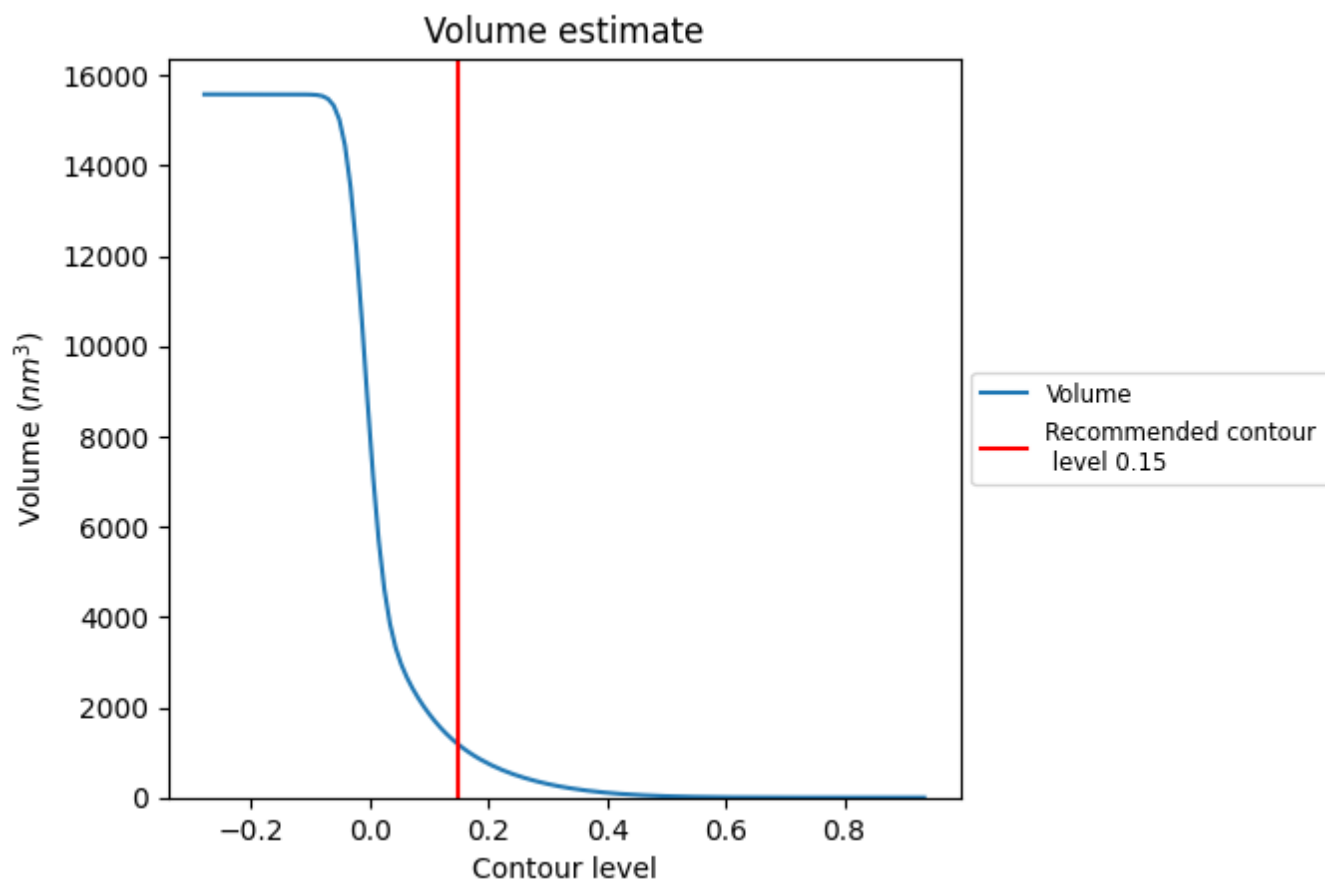
This section contains the results of statistical analysis of the map.

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 1174 nm³; this corresponds to an approximate mass of 1061 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.

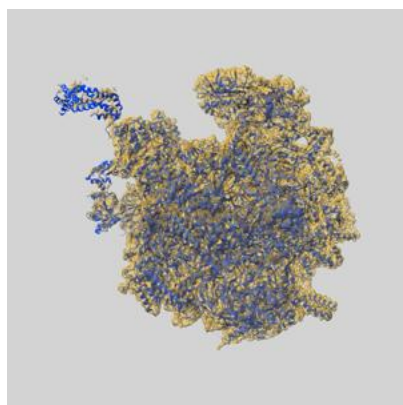
8 Fourier-Shell correlation

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

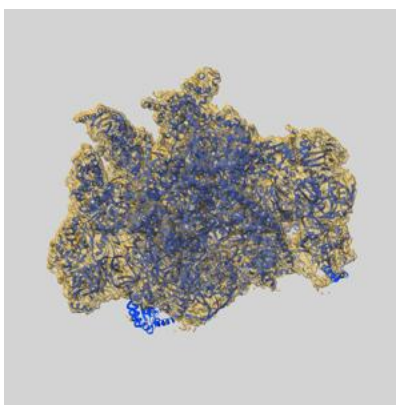
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12763 and PDB model 7O9K. Per-residue inclusion information can be found in section [3](#) on page [19](#).

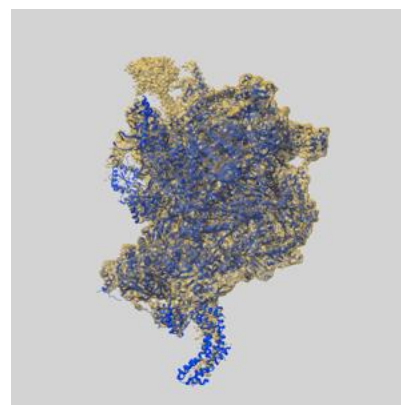
9.1 Map-model overlay [i](#)



X



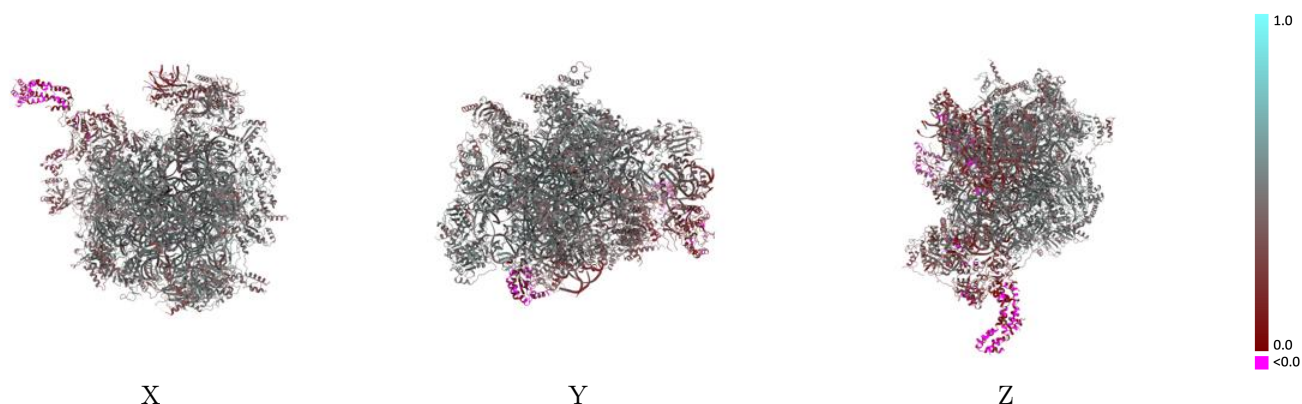
Y



Z

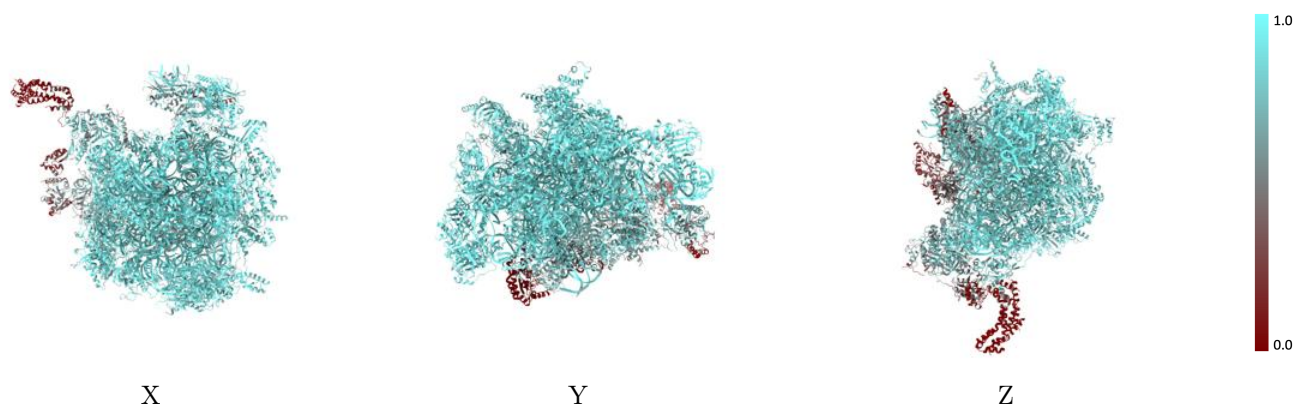
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



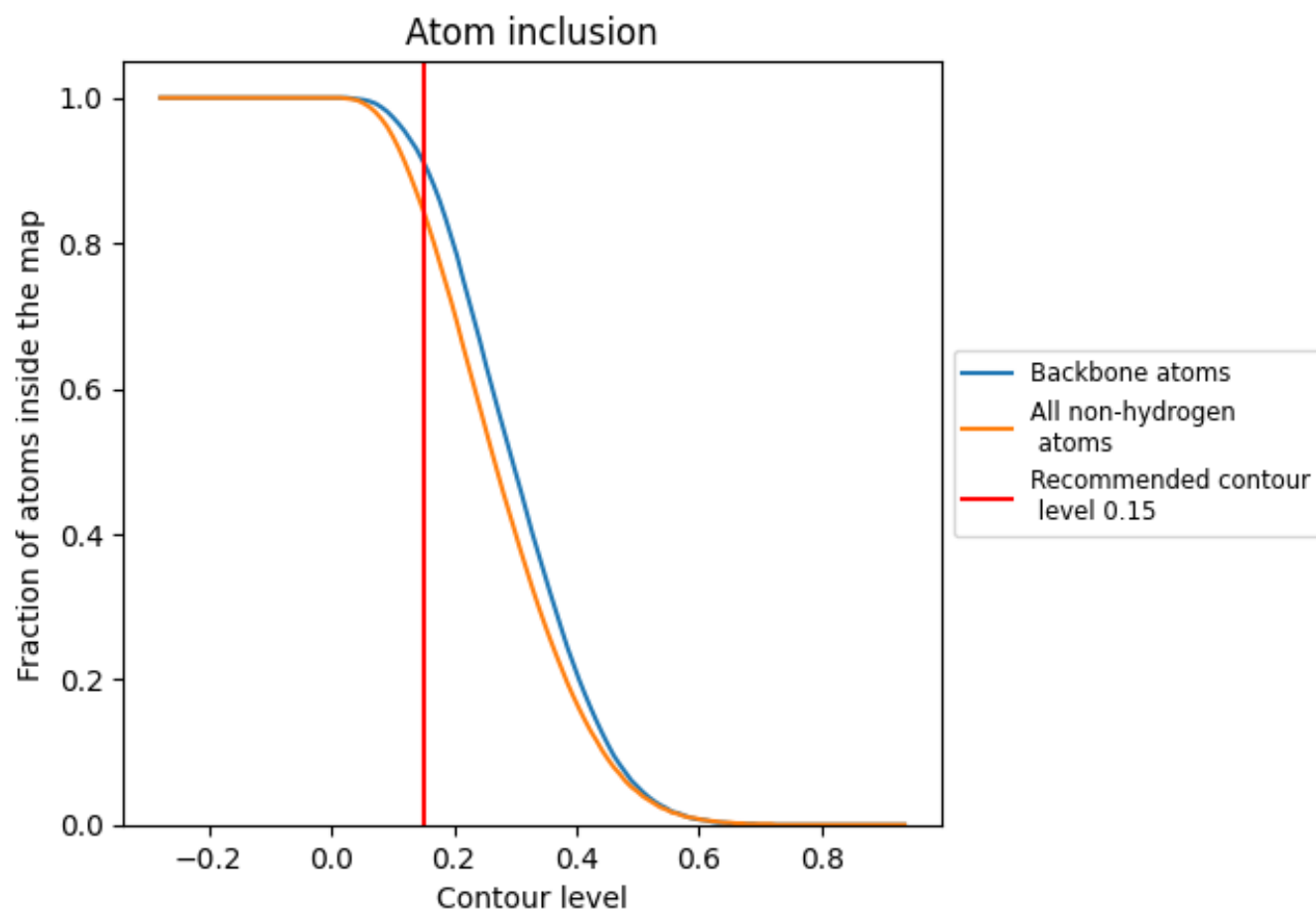
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 84% 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	 0.8450	 0.4280
0	 0.9100	 0.4650
1	 0.8620	 0.4650
2	 0.9540	 0.5310
3	 0.9510	 0.5170
4	 0.8870	 0.4770
5	 0.9150	 0.4760
6	 0.9120	 0.4280
7	 0.8580	 0.4310
8	 0.6190	 0.2450
9	 0.9060	 0.4700
A	 0.9740	 0.4660
A1	 0.7460	 0.4070
A2	 0.7390	 0.4000
B	 0.9570	 0.3150
C	 0.1210	 0.1320
D	 0.9000	 0.4820
E	 0.9110	 0.4810
F	 0.9200	 0.4910
FF	 0.1140	 0.1840
G	 0.7600	 0.4150
H	 0.8470	 0.4470
I	 0.5970	 0.2430
J	 0.6770	 0.1950
K	 0.9350	 0.4990
L	 0.8630	 0.4870
M	 0.9310	 0.4880
N	 0.8120	 0.3930
O	 0.9360	 0.4960
P	 0.9200	 0.4410
Q	 0.8980	 0.4750
R	 0.9350	 0.5020
S	 0.8990	 0.4880
T	 0.9120	 0.5010
U	 0.9310	 0.4860



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Chain	Atom inclusion	Q-score
UNK	 0.6080	 0.2820
V	 0.8450	 0.4210
W	 0.8990	 0.4920
X	 0.8850	 0.4680
Y	 0.9160	 0.4760
Z	 0.9120	 0.4900
a	 0.9140	 0.4930
b	 0.9200	 0.4970
c	 0.8740	 0.4610
d	 0.8420	 0.4170
e	 0.5650	 0.2060
f	 0.6870	 0.3080
g	 0.9360	 0.4810
h	 0.8560	 0.4230
i	 0.9420	 0.5120
j	 0.8910	 0.4660
k	 0.8240	 0.3110
l	 0.7390	 0.2770
m	 0.5150	 0.1920
n	 0.4320	 0.4110
o	 0.9070	 0.4640
p	 0.8880	 0.4230
q	 0.8270	 0.3940
r	 0.9100	 0.4670
s	 0.9390	 0.4910
t	 0.4820	 0.3220
t1	 0.2380	 0.1210
t2	 0.2230	 0.1260
t3	 0.0500	 0.0150
t4	 0.0220	 0.0060
t5	 0.0040	 0.0220
t6	 0.0050	 -0.0020
u	 0.7700	 0.4430
v	 0.7520	 0.4020
w	 0.5010	 0.2740