



wwPDB EM Validation Summary Report ⓘ

Aug 23, 2026 – 09:25 am BST

PDB ID : 8OIT / pdb_00008oit
EMDB ID : EMD-16899
Title : 39S human mitochondrial large ribosomal subunit with mtRF1 and P-site tRNA
Authors : Saurer, M.; Leibundgut, M.; Scaiola, A.; Schoenhut, T.; Ban, N.
Deposited on : 2023-03-23
Resolution : 2.90 Å(reported)
Based on initial models : ., 7QI4

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:

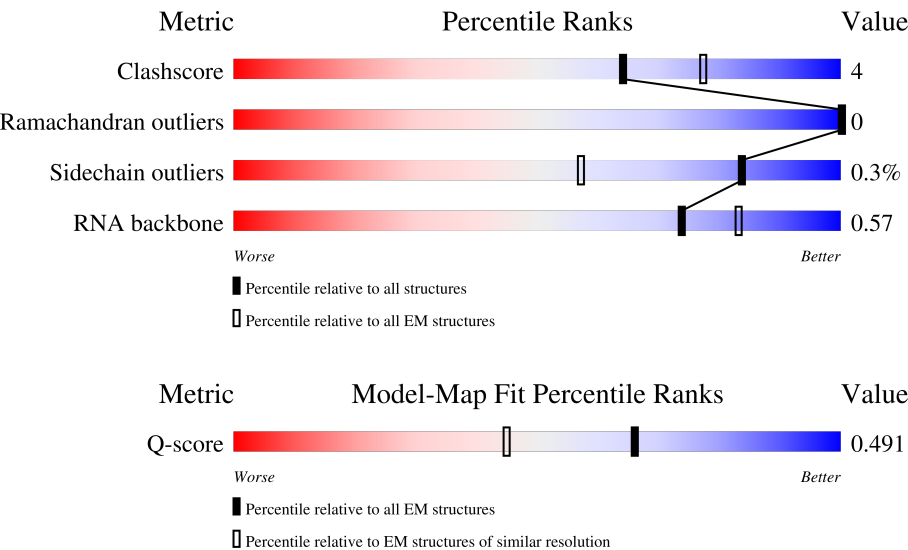
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.90 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	B1	198	
1	B2	198	
1	B3	198	

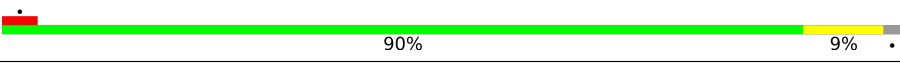
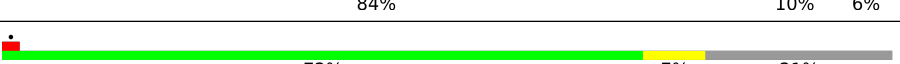
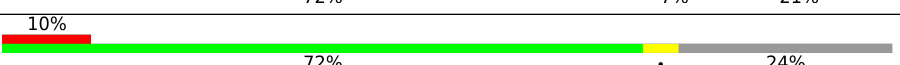
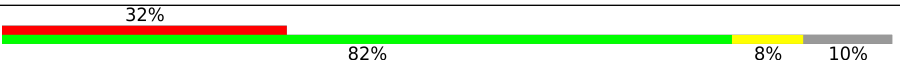
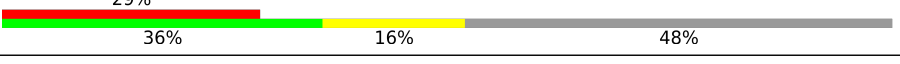
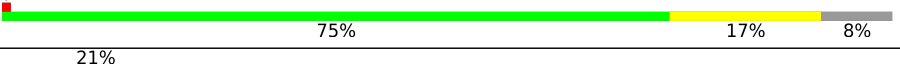
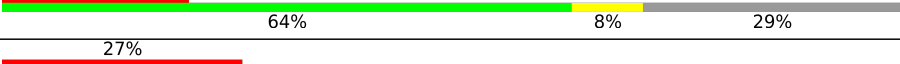
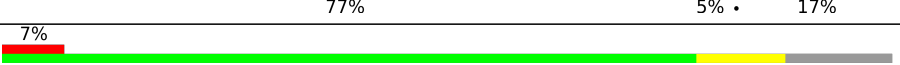
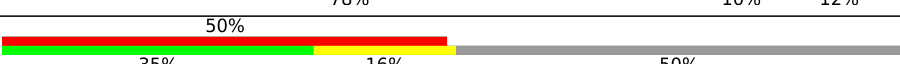
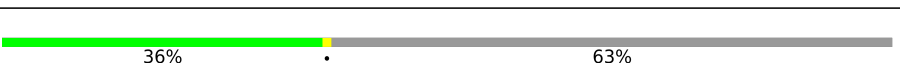
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Mol	Chain	Length	Quality of chain
1	B4	198	
1	B5	198	
1	B6	198	
2	B7	3	
3	B8	1561	
4	B9	72	
5	BA	206	
6	BB	153	
7	BC	216	
8	BD	148	
9	BE	256	
10	BF	250	
11	BG	161	
12	BH	188	
13	BI	65	
14	BJ	92	
15	BK	188	
16	BL	305	
17	BM	348	
18	BN	311	
19	BO	267	
20	BP	261	
21	BQ	192	
22	BR	178	
23	BS	145	

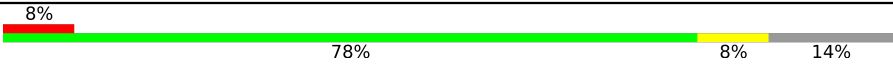
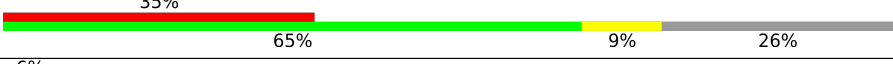
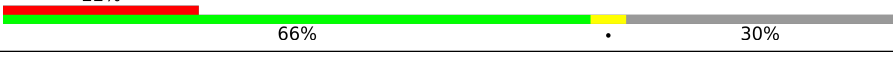
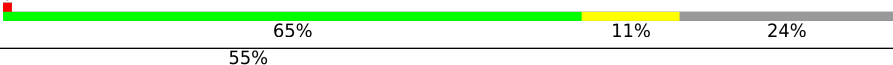
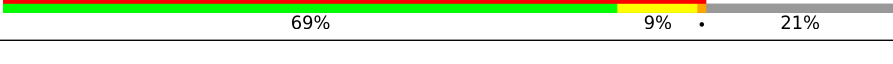
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Mol	Chain	Length	Quality of chain
24	BT	296	
25	BU	251	
26	BV	175	
27	BW	180	
28	BX	292	
29	BY	149	
30	BZ	205	
31	Ba	123	
32	Bb	112	
33	Bc	138	
34	Bd	128	
35	Be	102	
36	Bf	206	
37	Bg	222	
38	Bh	196	
39	Bi	439	
40	Bj	325	
41	Bl	103	
42	Bm	423	
43	Bn	380	
44	Bo	338	
45	Bp	206	
46	Bq	137	
47	Br	142	
48	Bs	215	

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Mol	Chain	Length	Quality of chain
49	Bt	332	
50	Bu	306	
51	Bv	279	
52	Bw	212	
53	Bx	166	
54	By	158	
55	Bz	128	
56	AG	71	
57	Aa	484	

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 113095 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 L12, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	B1	46	Total	C	N	O	0	0
			354	228	56	70		
1	B2	32	Total	C	N	O	0	0
			257	168	40	49		
1	B3	32	Total	C	N	O	0	0
			257	168	40	49		
1	B4	31	Total	C	N	O	0	0
			245	159	39	47		
1	B5	31	Total	C	N	O	0	0
			245	159	39	47		
1	B6	31	Total	C	N	O	0	0
			245	159	39	47		

- Molecule 2 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B7	3	Total	C	N	O	P	0	0
			62	28	11	20	3		

- Molecule 3 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B8	1558	Total	C	N	O	P	0	0
			33070	14843	5963	10706	1558		

- Molecule 4 is a RNA chain called CP Val-tRNA(Val).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B9	72	Total	C	N	O	P	0	0
			1524	685	269	498	72		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B9	70	C	G	conflict	GB NC_012920.1
B9	72	A	U	conflict	GB NC_012920.1

- Molecule 5 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 6 is a protein called 39S ribosomal protein L23, mitochondrial.

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

- Molecule 7 is a protein called 39S ribosomal protein L24, mitochondrial.

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

- Molecule 8 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	BD	116	Total	C	N	O	S	0	0
			904	577	171	153	3		

- Molecule 9 is a protein called 39S ribosomal protein L28, mitochondrial.

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

- Molecule 10 is a protein called 39S ribosomal protein L47, mitochondrial.

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

- Molecule 11 is a protein called 39S ribosomal protein L30, mitochondrial.

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

- Molecule 12 is a protein called 39S ribosomal protein L32, mitochondrial.

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

- Molecule 13 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BI	56	Total	C	N	O	S	0	0
			464	296	89	77	2		

- Molecule 14 is a protein called 39S ribosomal protein L34, mitochondrial.

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

- Molecule 15 is a protein called 39S ribosomal protein L35, mitochondrial.

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

- Molecule 16 is a protein called 39S ribosomal protein L2, mitochondrial.

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

- Molecule 17 is a protein called 39S ribosomal protein L3, mitochondrial.

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

- Molecule 18 is a protein called 39S ribosomal protein L4, mitochondrial.

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

- Molecule 19 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BO	202	Total	C	N	O	S	0	0
			1661	1067	304	286	4		

- Molecule 20 is a protein called 39S ribosomal protein L10, mitochondrial.

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

- Molecule 21 is a protein called 39S ribosomal protein L11, mitochondrial.

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

- Molecule 22 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 23 is a protein called 39S ribosomal protein L14, mitochondrial.

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

- Molecule 24 is a protein called 39S ribosomal protein L15, mitochondrial.

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

- Molecule 25 is a protein called 39S ribosomal protein L16, mitochondrial.

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

- Molecule 26 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 27 is a protein called 39S ribosomal protein L18, mitochondrial.

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

- Molecule 28 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BX	224	Total	C	N	O	S	0	0
			1866	1194	330	333	9		

- Molecule 29 is a protein called 39S ribosomal protein L20, mitochondrial.

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

- Molecule 30 is a protein called 39S ribosomal protein L21, mitochondrial.

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

- Molecule 31 is a protein called 39S ribosomal protein L52, mitochondrial.

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

- Molecule 32 is a protein called 39S ribosomal protein L53, mitochondrial.

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

- Molecule 33 is a protein called 39S ribosomal protein L54, mitochondrial.

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

- Molecule 34 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Bd	66	Total	C	N	O	S	0	0
			550	338	114	96	2		

- Molecule 35 is a protein called Ribosomal protein 63, mitochondrial.

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

- Molecule 36 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

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

- Molecule 37 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Bg	161	Total	C	N	O	S	0	0
			1350	841	260	244	5		

- Molecule 38 is a protein called 39S ribosomal protein S18a, mitochondrial.

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

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

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

- Molecule 40 is a protein called 39S ribosomal protein L1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Bj	164	Total	C	N	O	S	0	0
			1327	856	217	250	4		

- Molecule 41 is a protein called 39S ribosomal protein L36, mitochondrial.

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

- Molecule 42 is a protein called 39S ribosomal protein L37, mitochondrial.

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

- Molecule 43 is a protein called 39S ribosomal protein L38, mitochondrial.

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

- Molecule 44 is a protein called 39S ribosomal protein L39, mitochondrial.

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

- Molecule 45 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Bp	147	Total	C	N	O	S	0	0
			1243	790	218	233	2		

- Molecule 46 is a protein called 39S ribosomal protein L41, mitochondrial.

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

- Molecule 47 is a protein called 39S ribosomal protein L42, mitochondrial.

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

- Molecule 48 is a protein called Large ribosomal subunit protein mL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Bs	151	Total	C	N	O	S	0	0
			1196	744	231	218	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bs	2	ACE	-	acetylation	UNP Q8N983

- Molecule 49 is a protein called 39S ribosomal protein L44, mitochondrial.

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

- Molecule 50 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Bu	241	Total	C	N	O	S	0	0
			1985	1273	340	359	13		

- Molecule 51 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Bv	238	Total	C	N	O	S	0	0
			1931	1222	339	364	6		

- Molecule 52 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Bw	157	Total	C	N	O	S	0	0
			1252	799	207	242	4		

- Molecule 53 is a protein called 39S ribosomal protein L49, mitochondrial.

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

- Molecule 54 is a protein called 39S ribosomal protein L50, mitochondrial.

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

- Molecule 55 is a protein called 39S ribosomal protein L51, mitochondrial.

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

- Molecule 56 is a RNA chain called P-site Met-tRNA(Met).

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AG	71	Total	C	N	O	P	0	0
			1504	674	264	495	71		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AG	69	C	-	insertion	GB NC_012920.1
AG	70	C	-	insertion	GB NC_012920.1

- Molecule 57 is a protein called Peptide chain release factor 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Aa	381	Total	C	N	O	S	0	0
			3114	1940	569	592	13		

There are 41 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Aa	311	ALA	GLY	engineered mutation	UNP O75570
Aa	312	ALA	GLY	engineered mutation	UNP O75570
Aa	446	GLY	-	expression tag	UNP O75570
Aa	447	GLY	-	expression tag	UNP O75570
Aa	448	SER	-	expression tag	UNP O75570
Aa	449	GLY	-	expression tag	UNP O75570
Aa	450	GLY	-	expression tag	UNP O75570
Aa	451	SER	-	expression tag	UNP O75570
Aa	452	GLY	-	expression tag	UNP O75570
Aa	453	GLY	-	expression tag	UNP O75570
Aa	454	SER	-	expression tag	UNP O75570
Aa	455	GLY	-	expression tag	UNP O75570
Aa	456	GLY	-	expression tag	UNP O75570
Aa	457	SER	-	expression tag	UNP O75570
Aa	458	GLY	-	expression tag	UNP O75570
Aa	459	GLY	-	expression tag	UNP O75570
Aa	460	SER	-	expression tag	UNP O75570
Aa	461	GLY	-	expression tag	UNP O75570
Aa	462	GLY	-	expression tag	UNP O75570
Aa	463	ASP	-	expression tag	UNP O75570
Aa	464	TYR	-	expression tag	UNP O75570
Aa	465	LYS	-	expression tag	UNP O75570
Aa	466	ASP	-	expression tag	UNP O75570
Aa	467	HIS	-	expression tag	UNP O75570
Aa	468	ASP	-	expression tag	UNP O75570
Aa	469	GLY	-	expression tag	UNP O75570
Aa	470	ASP	-	expression tag	UNP O75570
Aa	471	TYR	-	expression tag	UNP O75570
Aa	472	LYS	-	expression tag	UNP O75570
Aa	473	ASP	-	expression tag	UNP O75570
Aa	474	HIS	-	expression tag	UNP O75570
Aa	475	ASP	-	expression tag	UNP O75570
Aa	476	ILE	-	expression tag	UNP O75570
Aa	477	ASP	-	expression tag	UNP O75570
Aa	478	TYR	-	expression tag	UNP O75570
Aa	479	LYS	-	expression tag	UNP O75570
Aa	480	ASP	-	expression tag	UNP O75570
Aa	481	ASP	-	expression tag	UNP O75570
Aa	482	ASP	-	expression tag	UNP O75570
Aa	483	ASP	-	expression tag	UNP O75570
Aa	484	LYS	-	expression tag	UNP O75570

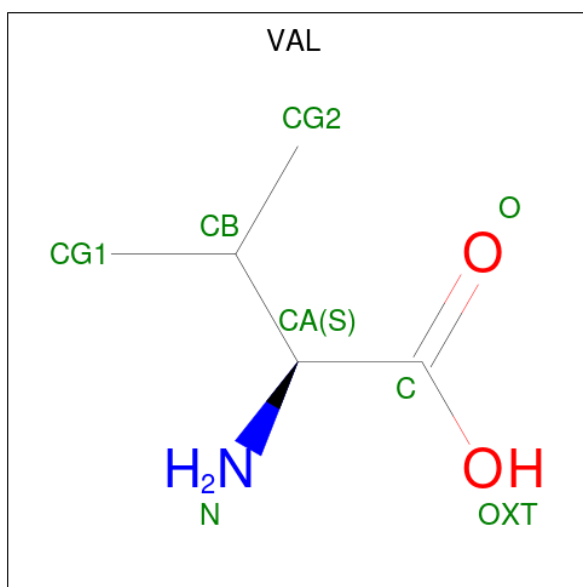
- Molecule 58 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
58	B8	30	Total 30	K 30	0
58	BL	1	Total 1	K 1	0
58	BT	1	Total 1	K 1	0
58	Be	1	Total 1	K 1	0
58	Bn	1	Total 1	K 1	0

- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
59	B8	216	Total 216	Mg 216	0
59	BD	1	Total 1	Mg 1	0
59	BL	3	Total 3	Mg 3	0
59	BN	1	Total 1	Mg 1	0
59	BO	1	Total 1	Mg 1	0
59	BR	1	Total 1	Mg 1	0
59	BT	1	Total 1	Mg 1	0
59	BV	1	Total 1	Mg 1	0
59	Bx	1	Total 1	Mg 1	0
59	AG	1	Total 1	Mg 1	0
59	Aa	1	Total 1	Mg 1	0

- Molecule 60 is VALINE (CCD ID: VAL) (formula: C₅H₁₁NO₂).

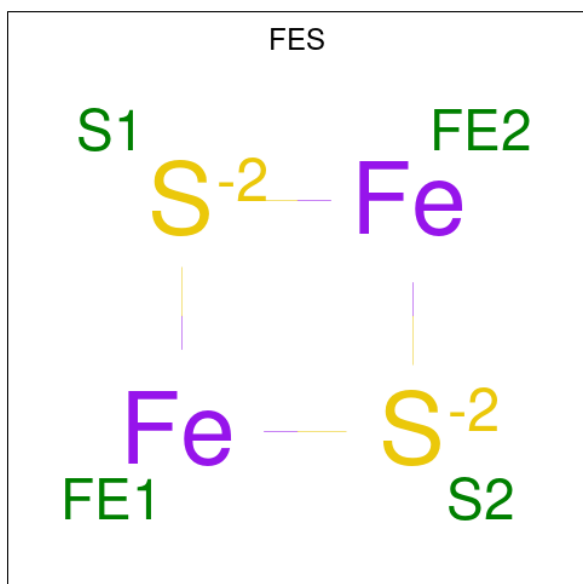


Mol	Chain	Residues	Atoms				AltConf
60	B9	1	Total	C	N	O	0
			7	5	1	1	

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

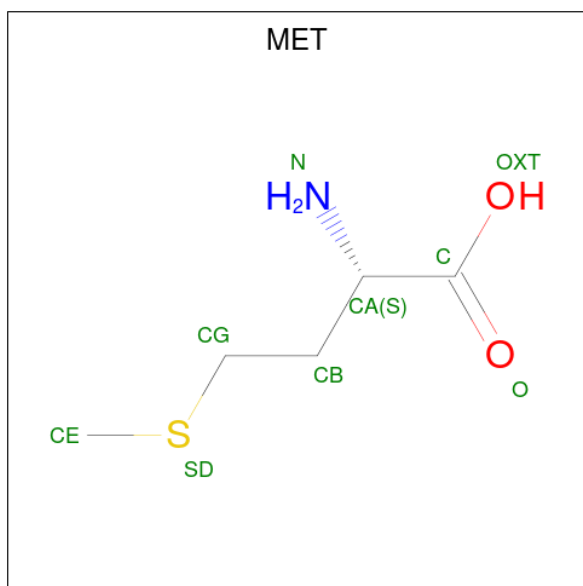
Mol	Chain	Residues	Atoms		AltConf
61	BH	1	Total	Zn	0
			1	1	
61	Bl	1	Total	Zn	0
			1	1	

- Molecule 62 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).

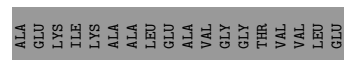
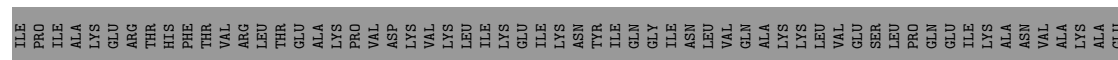
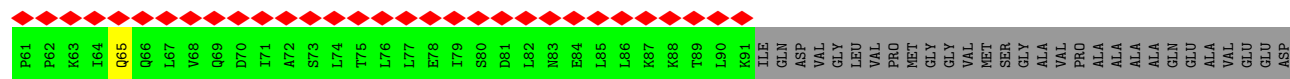


Mol	Chain	Residues	Atoms			AltConf
62	Bh	1	Total	Fe	S	0
			4	2	2	

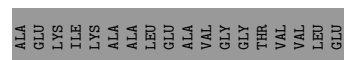
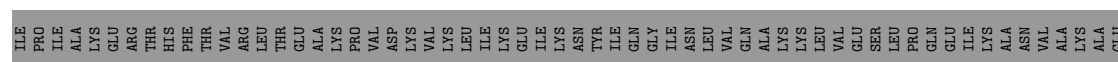
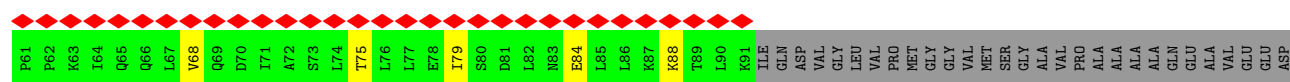
- Molecule 63 is METHIONINE (CCD ID: MET) (formula: $C_5H_{11}NO_2S$).



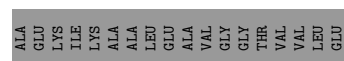
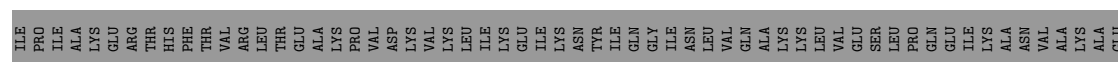
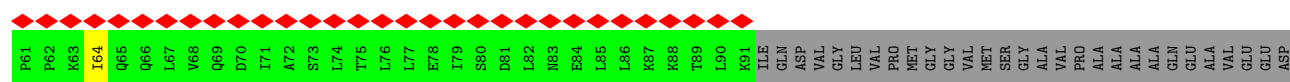
Mol	Chain	Residues	Atoms					AltConf
63	AG	1	Total	C	N	O	S	0
			8	5	1	1	1	



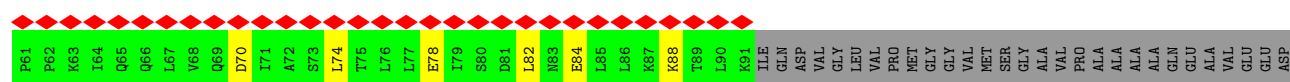
• Molecule 1: 39S ribosomal protein L12, mitochondrial



• Molecule 1: 39S ribosomal protein L12, mitochondrial



• Molecule 1: 39S ribosomal protein L12, mitochondrial

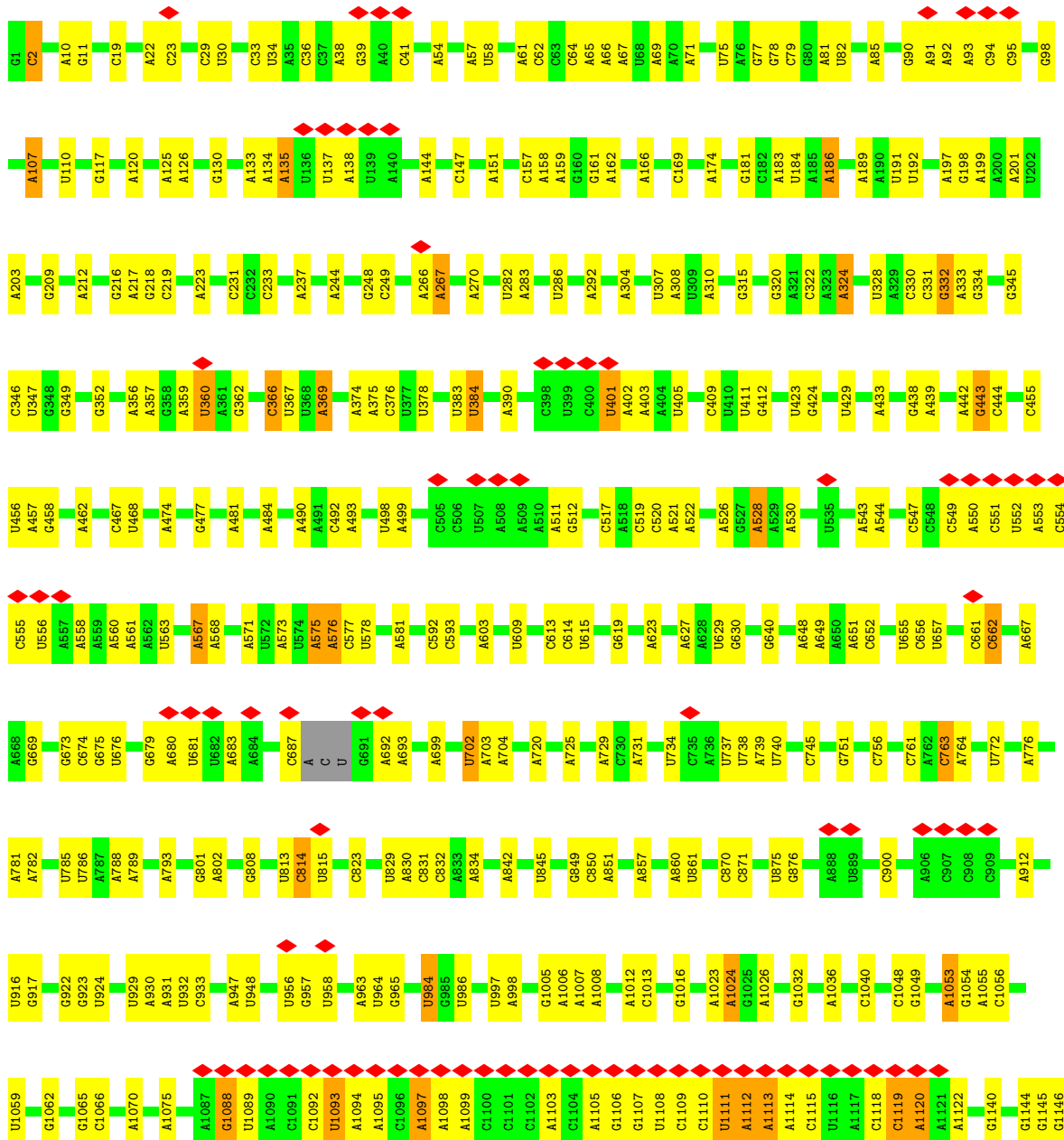


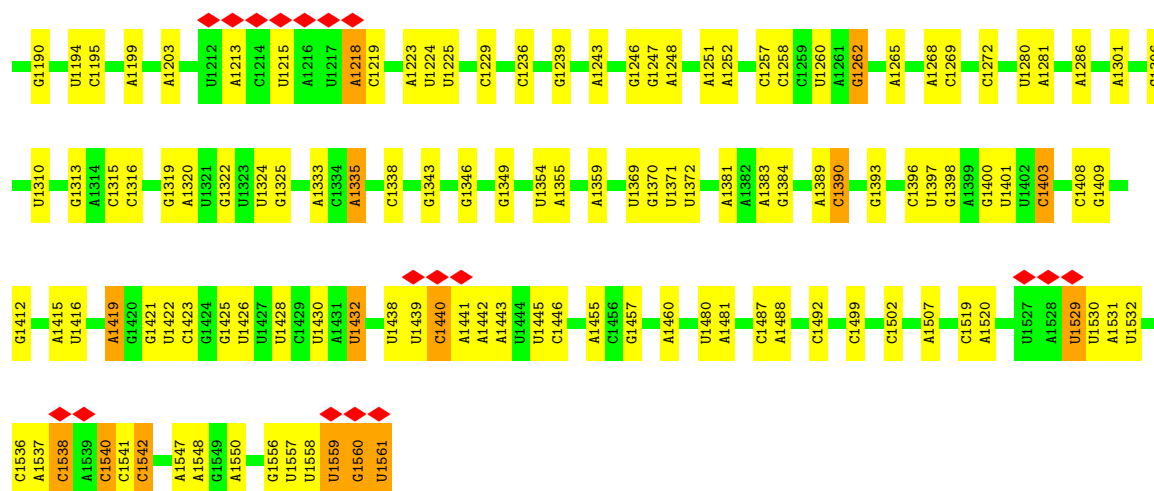
ALA
GLU
LYS
ILE
LYS
ALA
ALA
LEU
GLU
ALA
VAL
GLY
THR
VAL
LEU
GLU

• Molecule 2: E-site tRNA

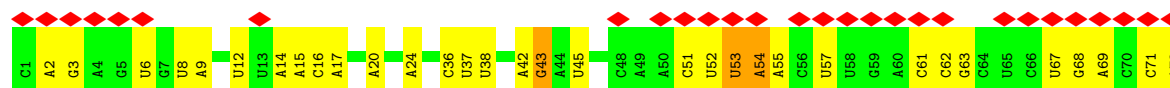
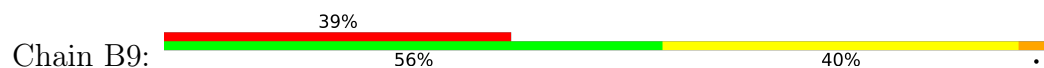


• Molecule 3: 16S rRNA

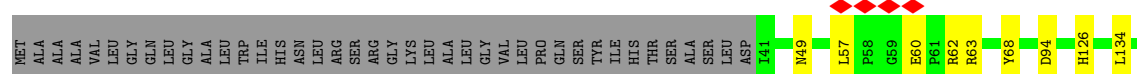
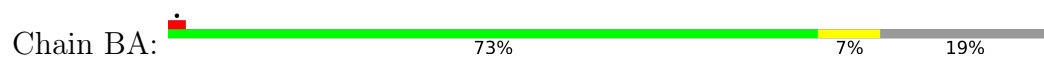




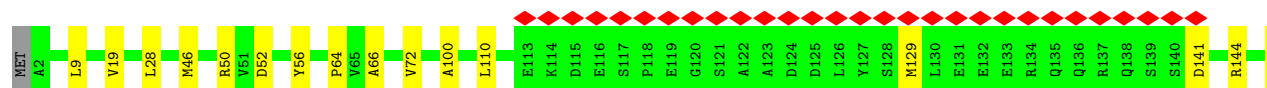
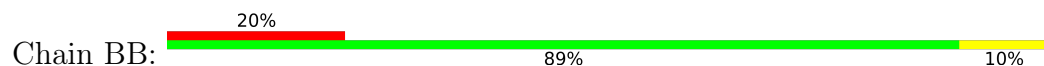
• Molecule 4: CP Val-tRNA(Val)



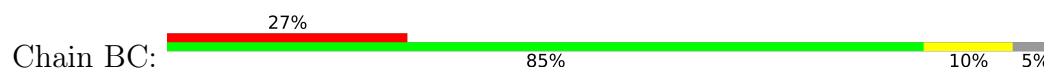
• Molecule 5: 39S ribosomal protein L22, mitochondrial

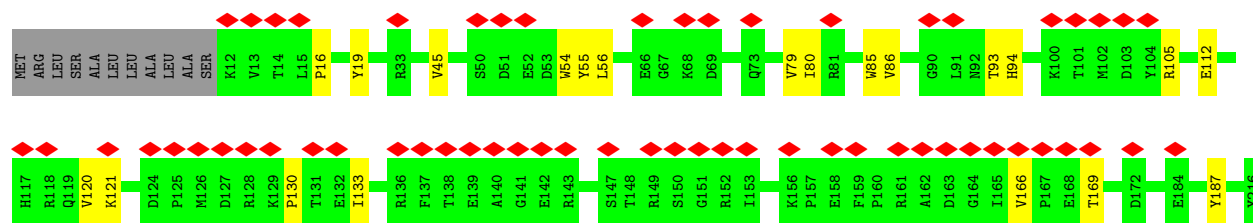


• Molecule 6: 39S ribosomal protein L23, mitochondrial

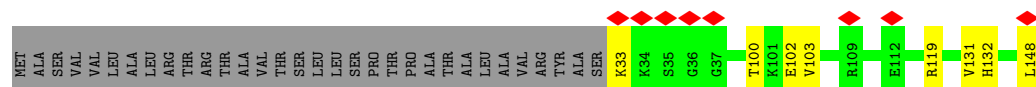
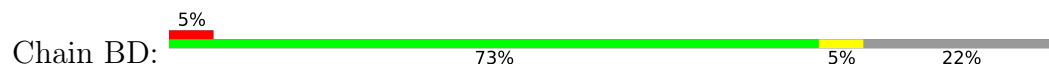


• Molecule 7: 39S ribosomal protein L24, mitochondrial

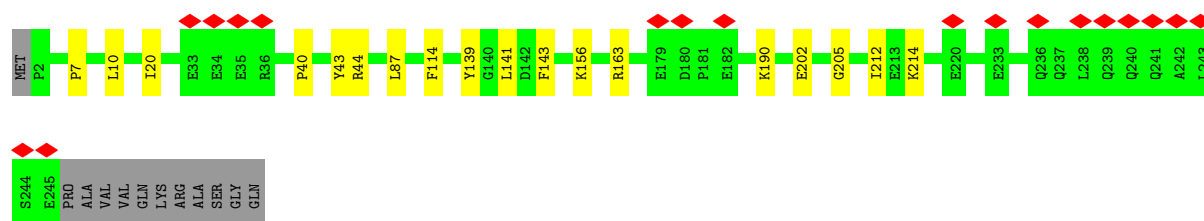
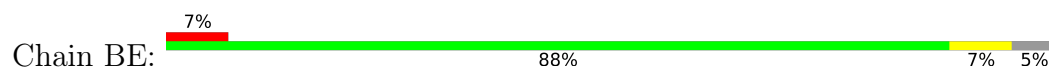




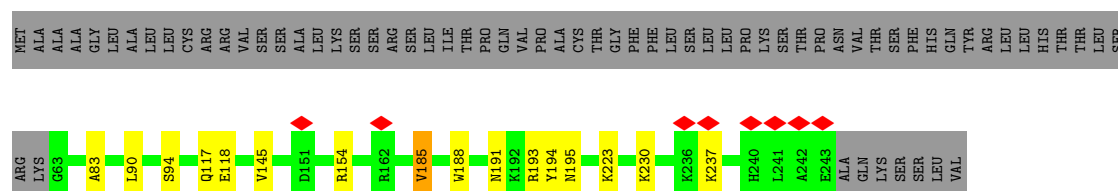
- Molecule 8: 39S ribosomal protein L27, mitochondrial



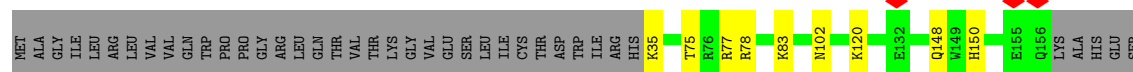
- Molecule 9: 39S ribosomal protein L28, mitochondrial



- Molecule 10: 39S ribosomal protein L47, mitochondrial



- Molecule 11: 39S ribosomal protein L30, mitochondrial



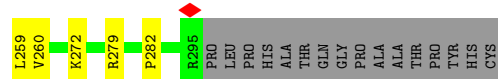
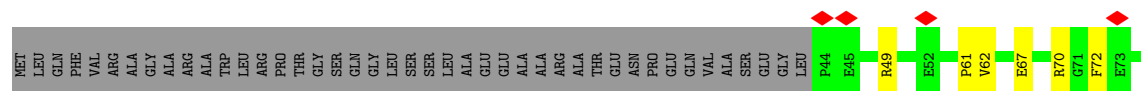
- Molecule 12: 39S ribosomal protein L32, mitochondrial





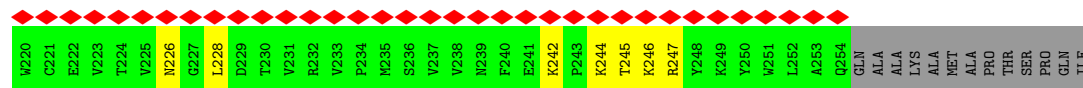
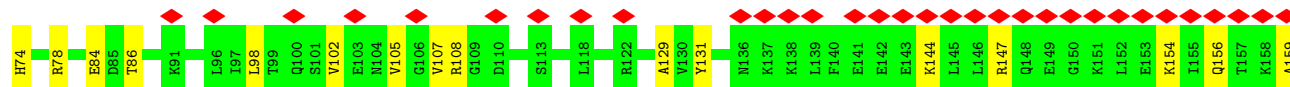
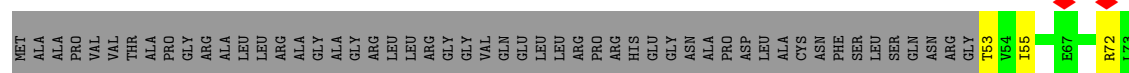
- Molecule 18: 39S ribosomal protein L4, mitochondrial

Chain BN: 67% 14% 19%



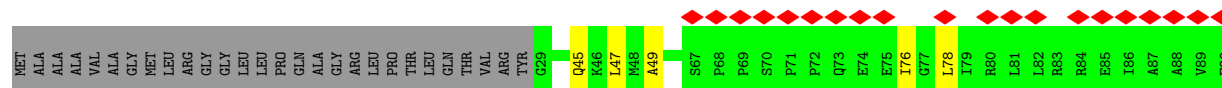
- Molecule 19: 39S ribosomal protein L9, mitochondrial

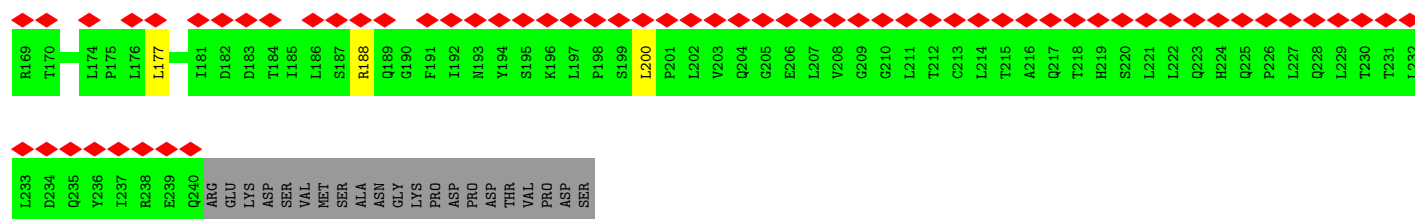
Chain BO: 48% 61% 15% 24%



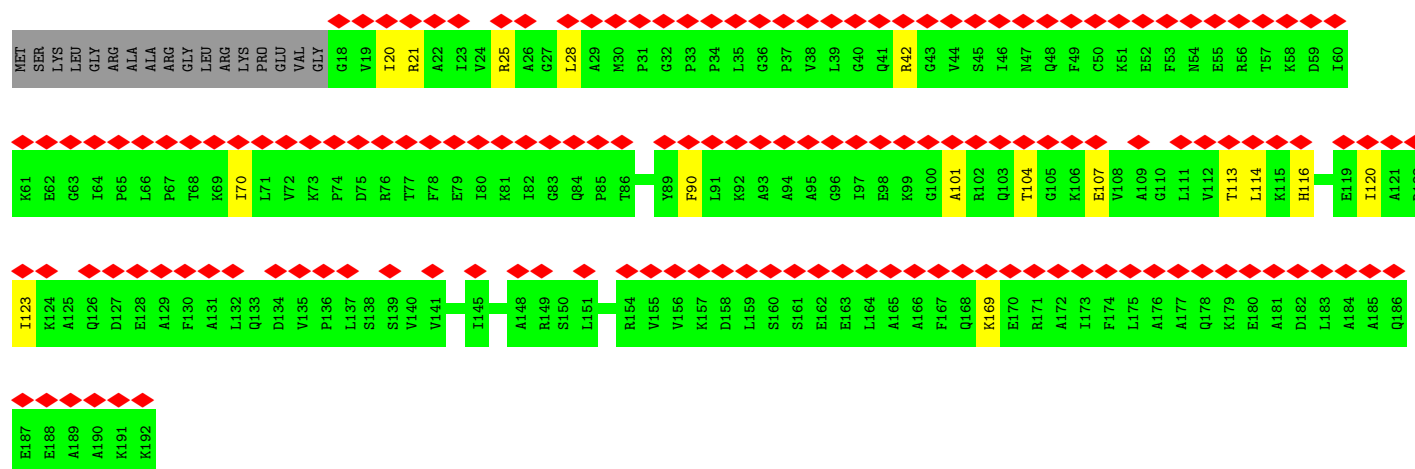
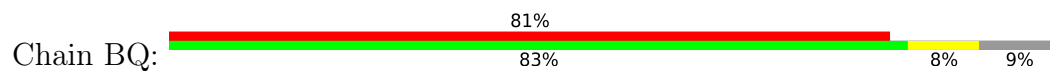
- Molecule 20: 39S ribosomal protein L10, mitochondrial

Chain BP: 46% 75% 7% 19%

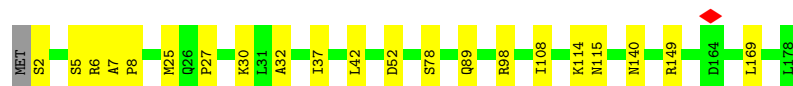
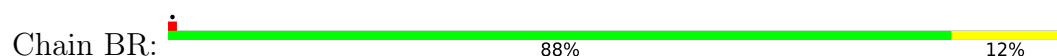




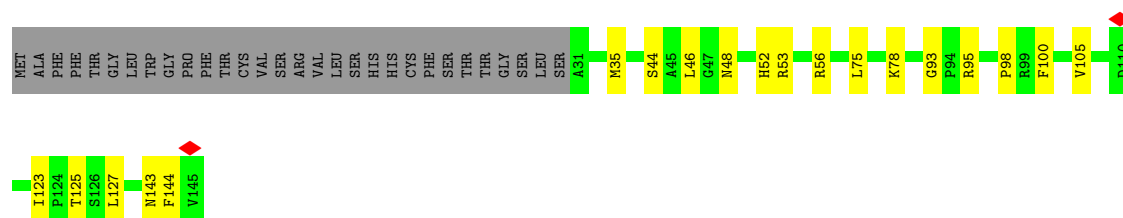
- Molecule 21: 39S ribosomal protein L11, mitochondrial



- Molecule 22: 39S ribosomal protein L13, mitochondrial

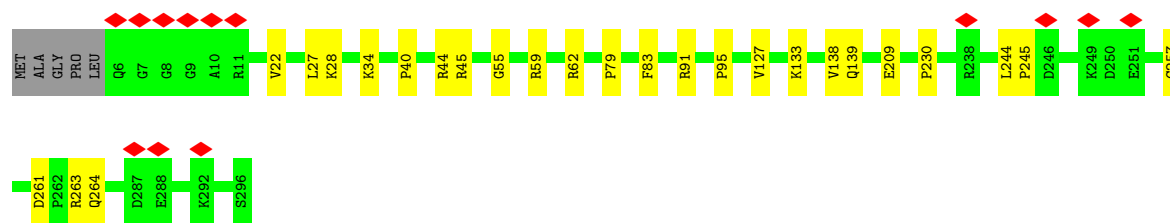


- Molecule 23: 39S ribosomal protein L14, mitochondrial

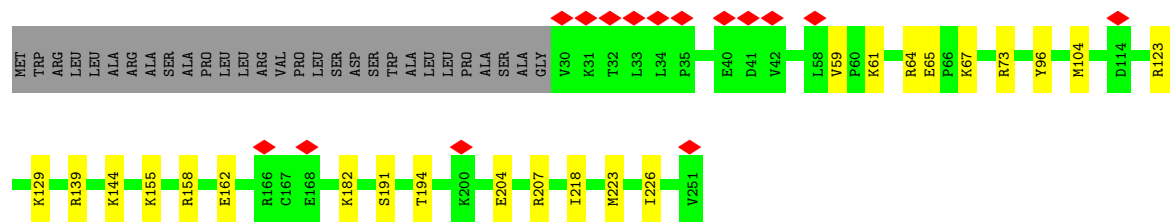
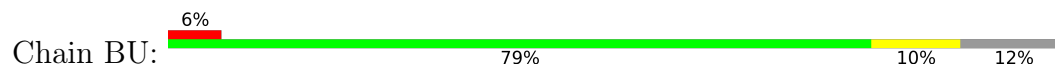


- Molecule 24: 39S ribosomal protein L15, mitochondrial

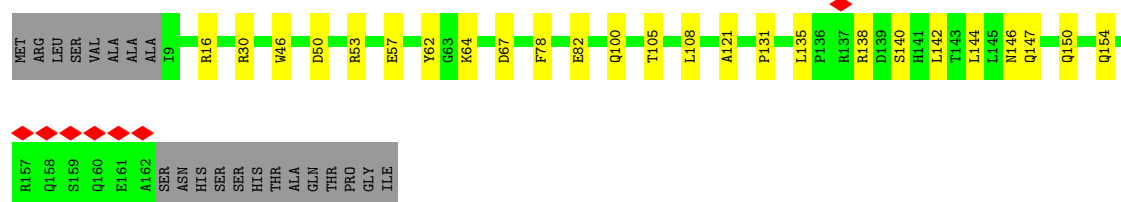
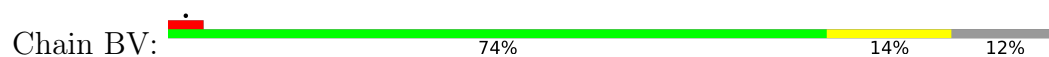




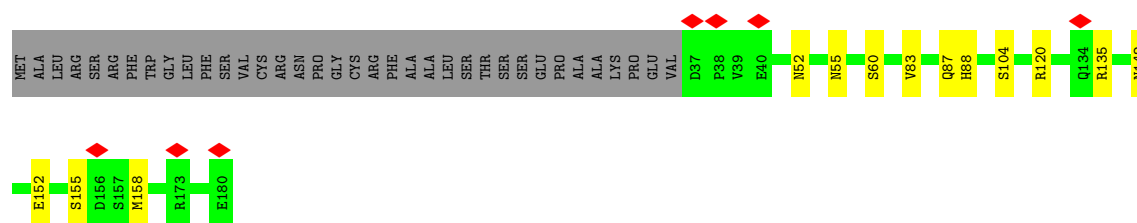
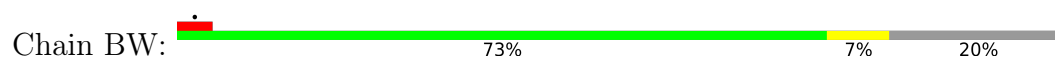
- Molecule 25: 39S ribosomal protein L16, mitochondrial



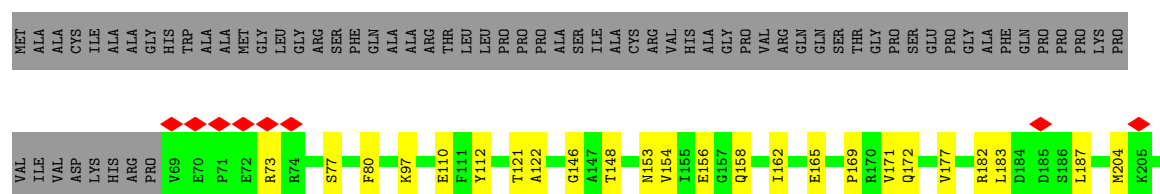
- Molecule 26: 39S ribosomal protein L17, mitochondrial



- Molecule 27: 39S ribosomal protein L18, mitochondrial

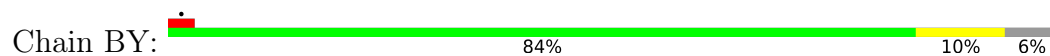


- Molecule 28: 39S ribosomal protein L19, mitochondrial

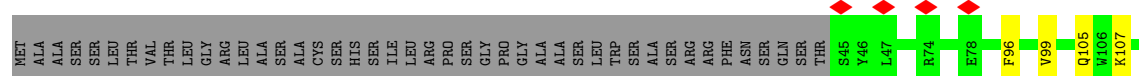
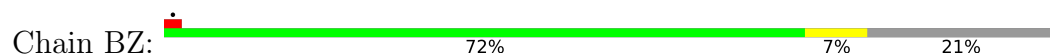




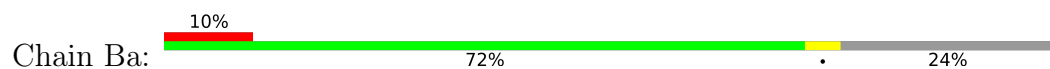
- Molecule 29: 39S ribosomal protein L20, mitochondrial



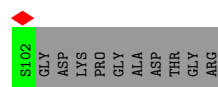
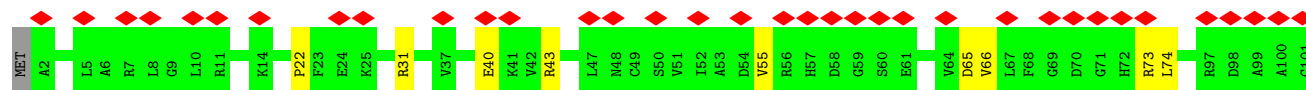
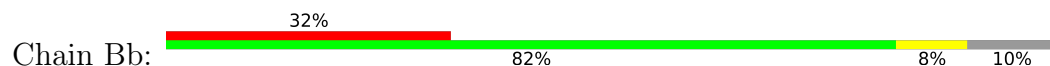
- Molecule 30: 39S ribosomal protein L21, mitochondrial



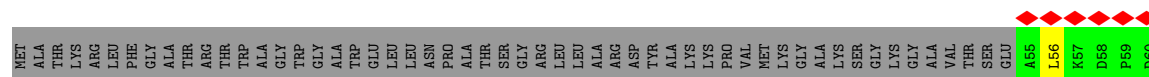
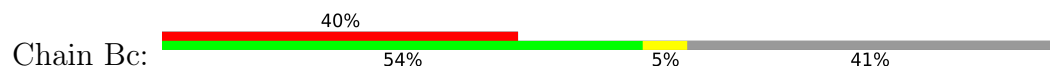
- Molecule 31: 39S ribosomal protein L52, mitochondrial

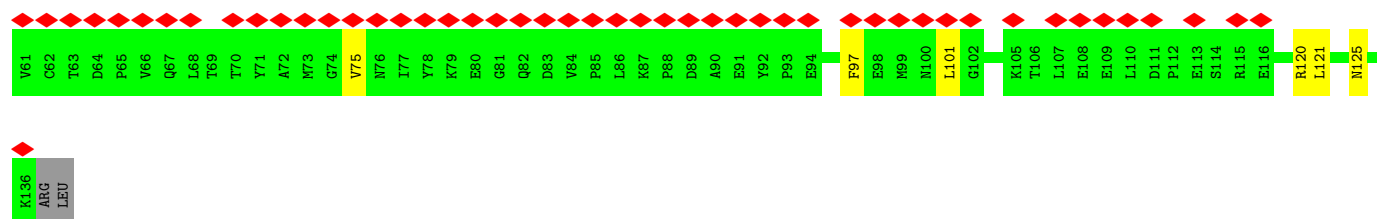


- Molecule 32: 39S ribosomal protein L53, mitochondrial

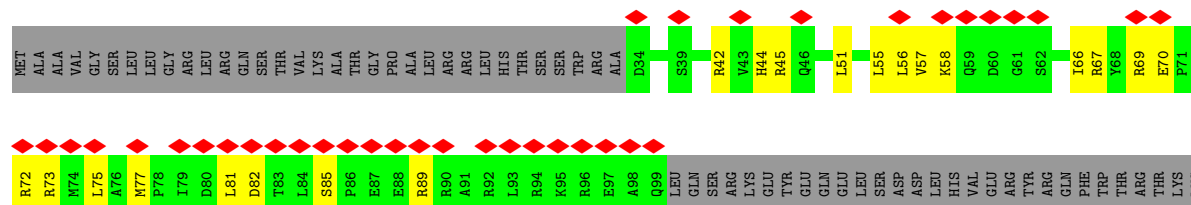
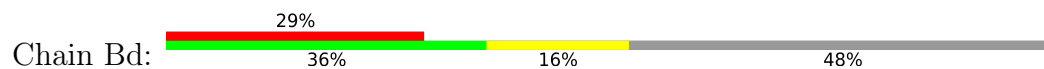


- Molecule 33: 39S ribosomal protein L54, mitochondrial

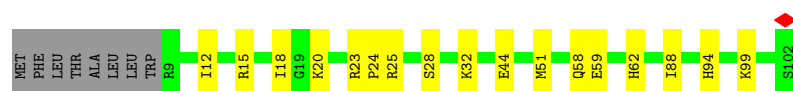
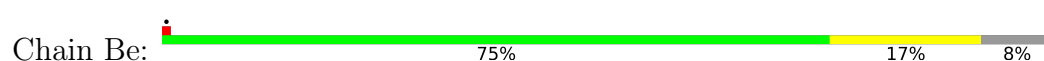




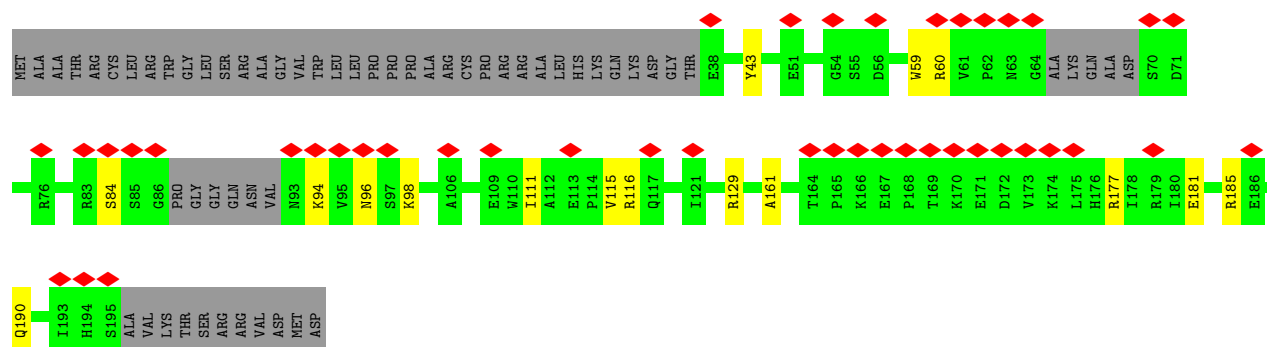
- Molecule 34: 39S ribosomal protein L55, mitochondrial



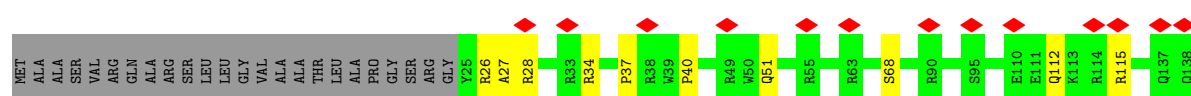
- Molecule 35: Ribosomal protein 63, mitochondrial



- Molecule 36: Peptidyl-tRNA hydrolase ICT1, mitochondrial



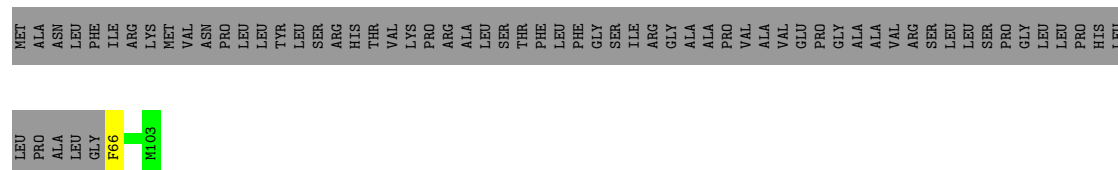
- Molecule 37: Growth arrest and DNA damage-inducible proteins-interacting protein 1





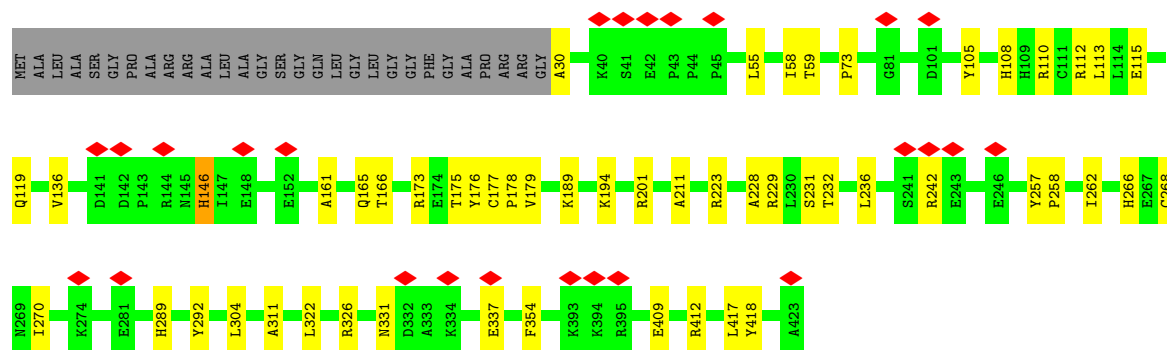
- Molecule 41: 39S ribosomal protein L36, mitochondrial

Chain Bl: 36% 63%



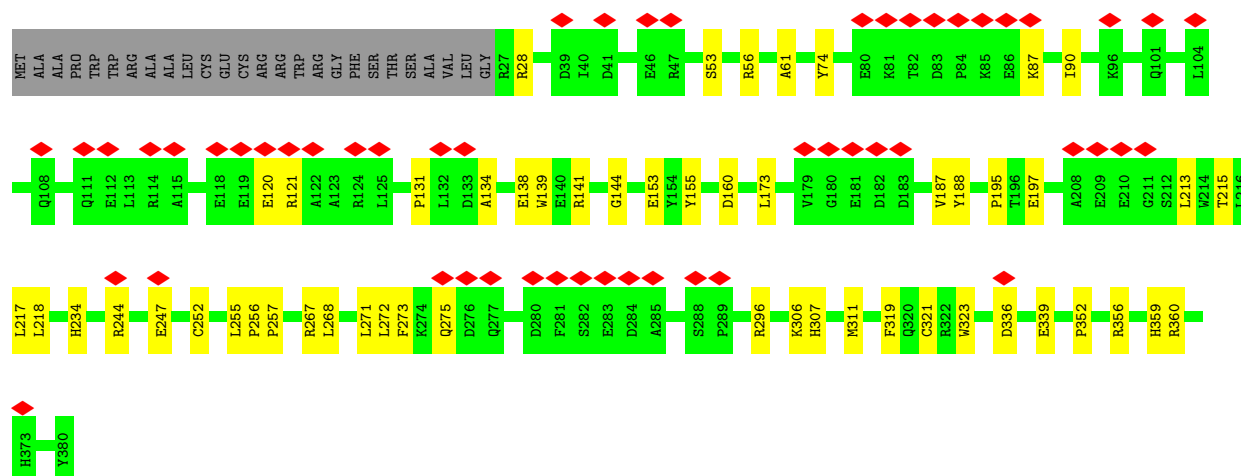
- Molecule 42: 39S ribosomal protein L37, mitochondrial

Chain Bm: 6% 81% 12% 7%



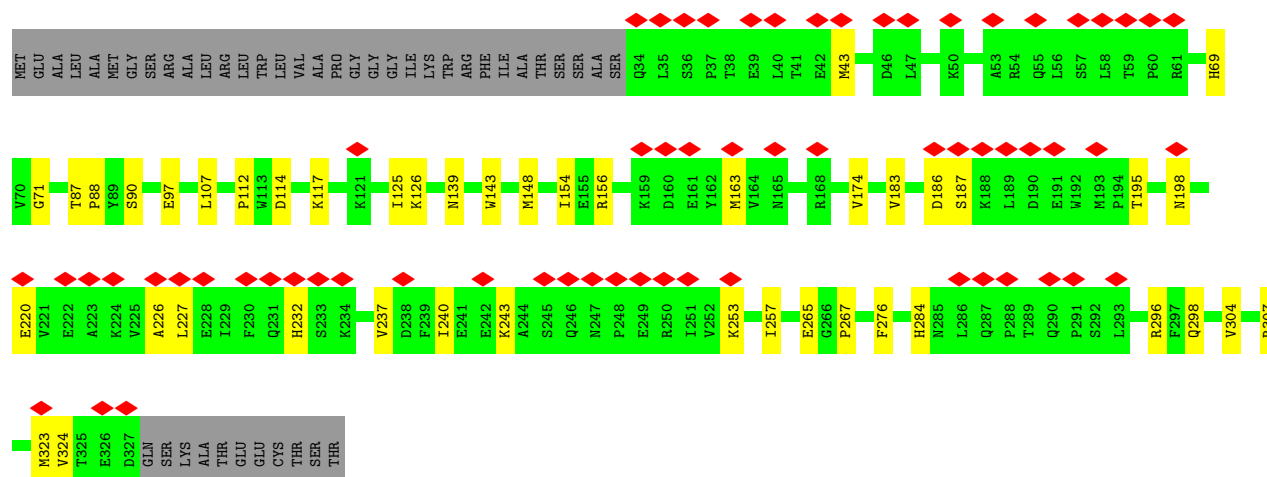
- Molecule 43: 39S ribosomal protein L38, mitochondrial

Chain Bn: 14% 79% 14% 7%



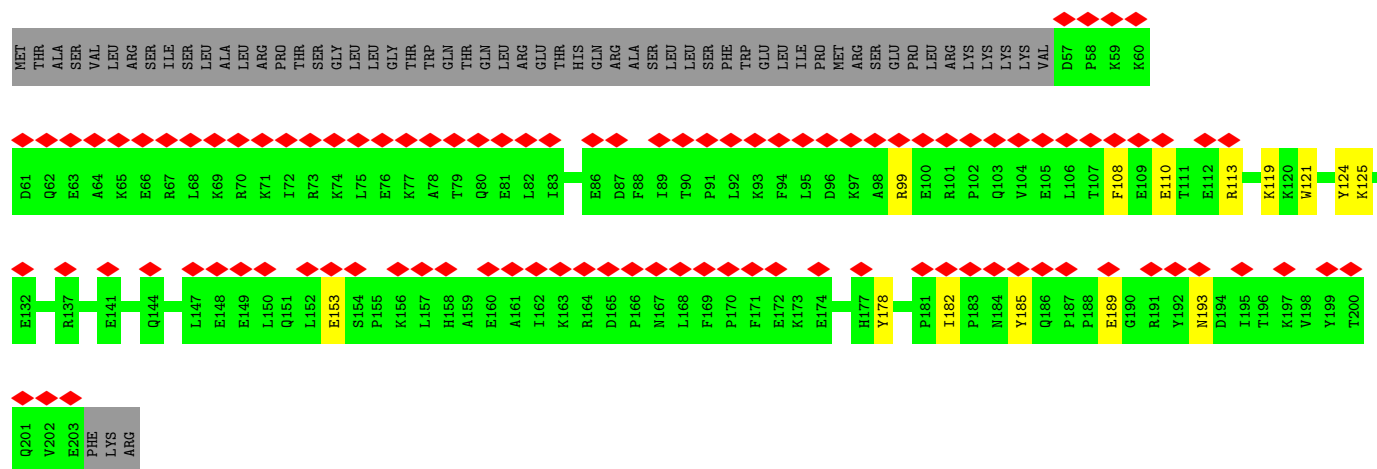
- Molecule 44: 39S ribosomal protein L39, mitochondrial

Chain Bo: 



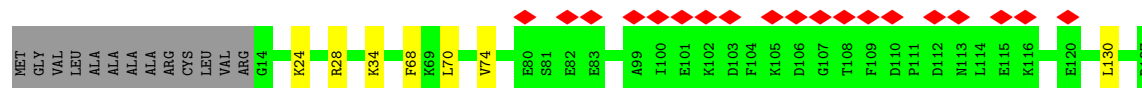
- Molecule 45: 39S ribosomal protein L40, mitochondrial

Chain Bp: 



- Molecule 46: 39S ribosomal protein L41, mitochondrial

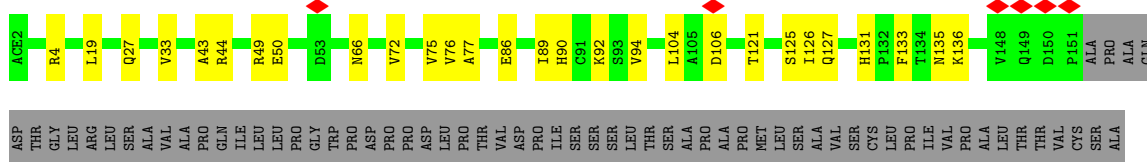
Chain Bq: 



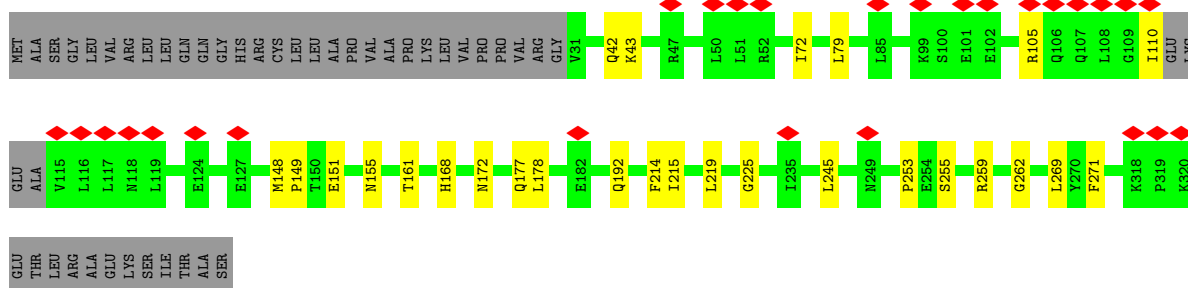
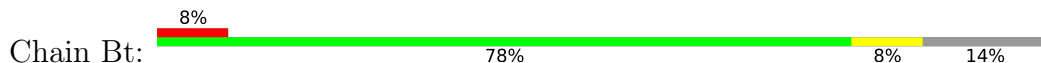
- Molecule 47: 39S ribosomal protein L42, mitochondrial

Chain Br: 

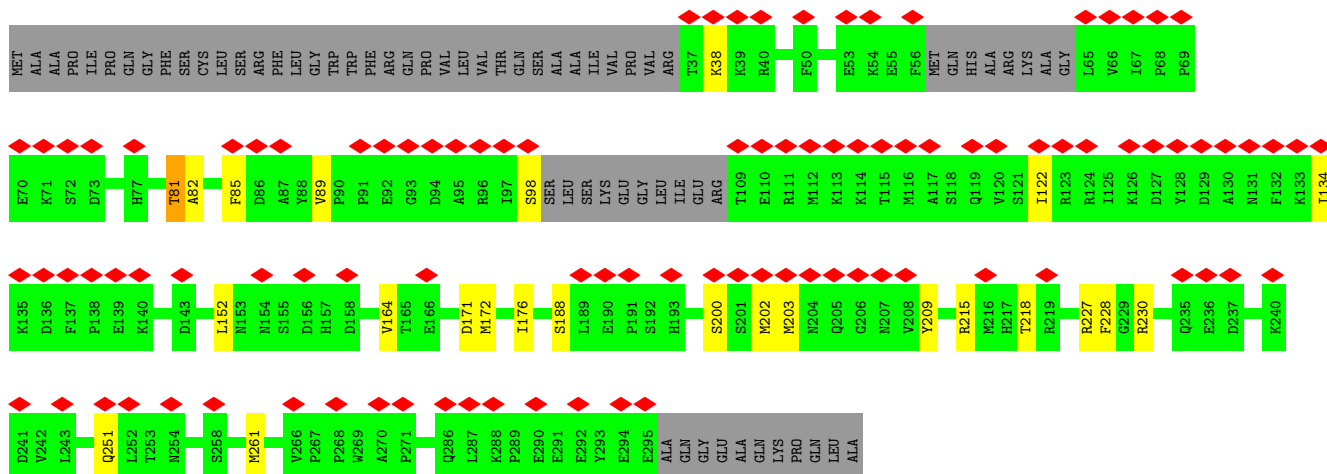
- Molecule 48: Large ribosomal subunit protein mL43



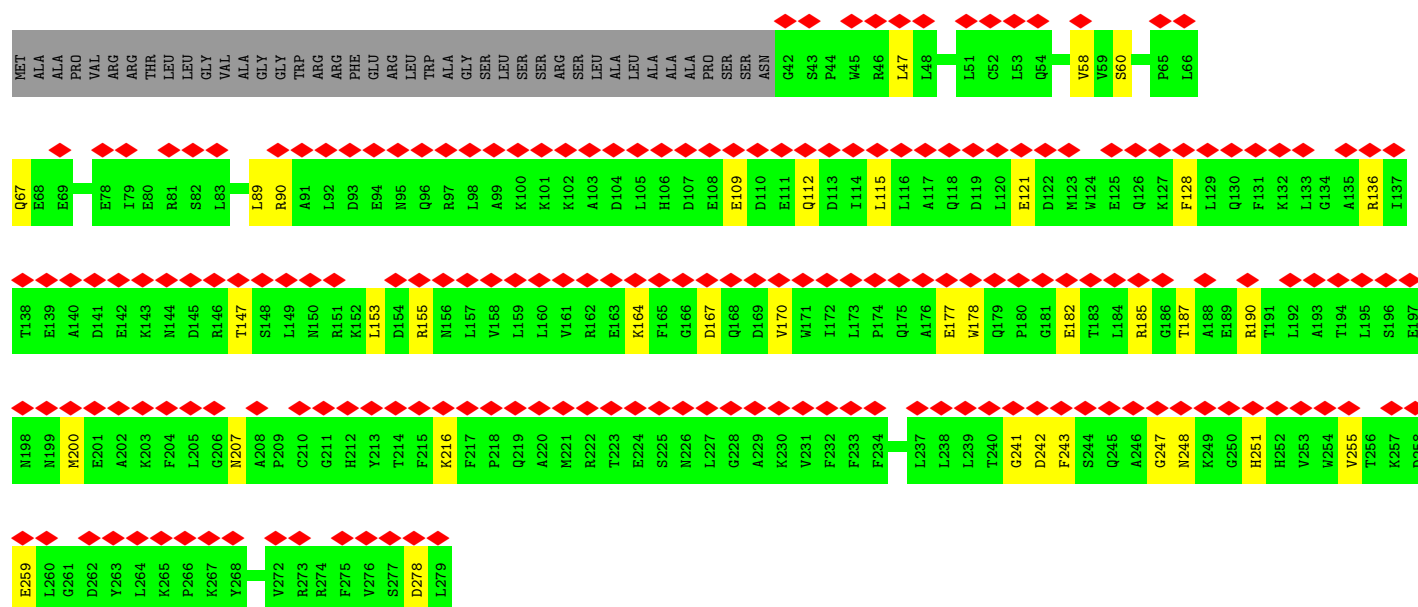
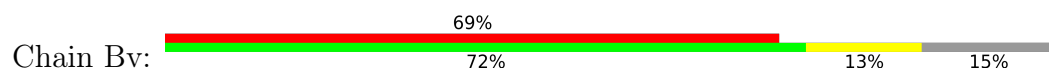
- Molecule 49: 39S ribosomal protein L44, mitochondrial



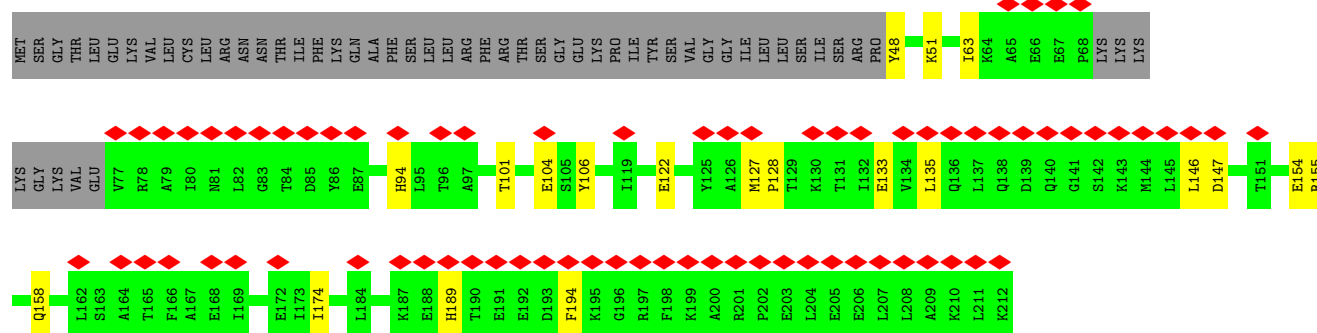
- Molecule 50: 39S ribosomal protein L45, mitochondrial



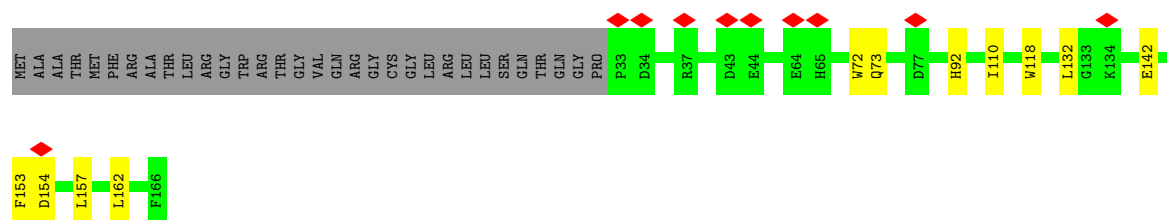
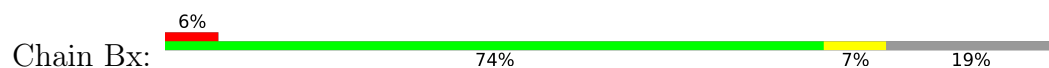
- Molecule 51: 39S ribosomal protein L46, mitochondrial



- Molecule 52: 39S ribosomal protein L48, mitochondrial



- Molecule 53: 39S ribosomal protein L49, mitochondrial



- Molecule 54: 39S ribosomal protein L50, mitochondrial



ASP
ASP
ASP
LYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	41288	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.267	Depositor
Minimum map value	-1.999	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.146	Depositor
Recommended contour level	0.75	Depositor
Map size ($\text{\AA}$)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 1MA, SAC, K, 2MG, ZN, MG, FES, RSQ, AYA, OMU, OMG, PSU, ACE

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	B1	0.07	0/358	0.16	0/486
1	B2	0.08	0/259	0.18	0/350
1	B3	0.07	0/259	0.17	0/350
1	B4	0.05	0/246	0.14	0/331
1	B5	0.06	0/246	0.16	0/331
1	B6	0.06	0/246	0.16	0/331
2	B7	0.05	0/68	0.11	0/103
3	B8	0.09	0/36876	0.15	0/57402
4	B9	0.07	0/1627	0.13	0/2527
5	BA	0.09	0/1403	0.20	0/1886
6	BB	0.09	0/1274	0.20	0/1723
7	BC	0.08	0/1721	0.19	0/2333
8	BD	0.09	0/926	0.20	0/1244
9	BE	0.08	0/2099	0.18	0/2837
10	BF	0.08	0/1593	0.17	0/2136
11	BG	0.09	0/1021	0.21	0/1378
12	BH	0.08	0/913	0.18	0/1224
13	BI	0.08	0/469	0.20	0/621
14	BJ	0.09	0/383	0.20	0/507
15	BK	0.09	0/853	0.20	0/1136
16	BL	0.09	0/1896	0.20	0/2549
17	BM	0.09	0/2475	0.22	0/3355
18	BN	0.09	0/2090	0.21	0/2842
19	BO	0.08	0/1698	0.22	0/2292
20	BP	0.08	0/1731	0.20	0/2345
21	BQ	0.06	0/1348	0.17	0/1813
22	BR	0.09	0/1490	0.21	0/2021
23	BS	0.08	0/905	0.21	0/1218
24	BT	0.09	0/2381	0.21	0/3212
25	BU	0.08	0/1833	0.19	0/2468
26	BV	0.09	0/1283	0.20	0/1727
27	BW	0.08	0/1199	0.20	0/1623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
28	BX	0.08	0/1908	0.20	0/2569
29	BY	0.09	0/1175	0.18	0/1572
30	BZ	0.09	0/1320	0.23	0/1789
31	Ba	0.07	0/760	0.17	0/1023
32	Bb	0.07	0/777	0.17	0/1048
33	Bc	0.06	0/707	0.17	0/960
34	Bd	0.06	0/558	0.18	0/749
35	Be	0.09	0/819	0.20	0/1097
36	Bf	0.07	0/1223	0.17	0/1641
37	Bg	0.07	0/1384	0.17	0/1869
38	Bh	0.09	0/1362	0.22	0/1846
39	Bi	0.09	0/3239	0.20	0/4400
40	Bj	0.08	0/1354	0.22	0/1831
41	Bl	0.10	0/350	0.21	0/461
42	Bm	0.09	0/3305	0.20	0/4502
43	Bn	0.08	0/3043	0.20	0/4140
44	Bo	0.07	0/2447	0.19	0/3310
45	Bp	0.06	0/1269	0.16	0/1708
46	Bq	0.08	0/1025	0.20	0/1379
47	Br	0.09	0/866	0.23	0/1174
48	Bs	0.10	0/1219	0.22	0/1651
49	Bt	0.07	0/2347	0.19	0/3171
50	Bu	0.08	0/2039	0.20	0/2759
51	Bv	0.06	0/1970	0.17	0/2658
52	Bw	0.07	0/1273	0.17	0/1716
53	Bx	0.09	0/1151	0.21	0/1569
54	By	0.06	0/918	0.16	0/1249
55	Bz	0.10	0/850	0.21	0/1135
56	AG	0.09	0/1588	0.19	0/2466
57	Aa	0.12	0/3162	0.25	0/4253
All	All	0.09	0/118577	0.18	0/168396

There are no bond length outliers.

There are no bond angle outliers.

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	B1	354	0	377	3	0
1	B2	257	0	283	3	0
1	B3	257	0	283	1	0
1	B4	245	0	275	3	0
1	B5	245	0	275	1	0
1	B6	245	0	275	4	0
2	B7	62	0	34	0	0
3	B8	33070	0	16795	227	0
4	B9	1524	0	778	20	0
5	BA	1369	0	1410	11	0
6	BB	1251	0	1232	10	0
7	BC	1676	0	1687	14	0
8	BD	904	0	935	7	0
9	BE	2044	0	2060	13	0
10	BF	1556	0	1597	13	0
11	BG	996	0	1044	7	0
12	BH	898	0	916	5	0
13	BI	464	0	511	6	0
14	BJ	377	0	406	2	0
15	BK	832	0	883	12	0
16	BL	1859	0	1920	17	0
17	BM	2406	0	2415	21	0
18	BN	2031	0	2065	31	0
19	BO	1661	0	1734	32	0
20	BP	1695	0	1785	14	0
21	BQ	1330	0	1407	13	0
22	BR	1455	0	1452	14	0
23	BS	890	0	941	12	0
24	BT	2327	0	2395	20	0
25	BU	1786	0	1817	16	0
26	BV	1259	0	1294	18	0
27	BW	1173	0	1165	10	0
28	BX	1866	0	1900	22	0
29	BY	1154	0	1214	14	0
30	BZ	1293	0	1365	11	0
31	Ba	745	0	746	5	0
32	Bb	774	0	784	7	0
33	Bc	688	0	674	7	0
34	Bd	550	0	572	14	0
35	Be	798	0	804	14	0
36	Bf	1205	0	1223	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	Bg	1350	0	1327	10	0
38	Bh	1322	0	1348	8	0
39	Bi	3155	0	3139	26	0
40	Bj	1327	0	1353	42	0
41	Bl	342	0	361	1	0
42	Bm	3210	0	3206	34	0
43	Bn	2948	0	2841	36	0
44	Bo	2390	0	2397	26	0
45	Bp	1243	0	1265	11	0
46	Bq	997	0	987	6	0
47	Br	840	0	810	7	0
48	Bs	1196	0	1195	21	0
49	Bt	2299	0	2320	18	0
50	Bu	1985	0	1976	16	0
51	Bv	1931	0	1916	24	0
52	Bw	1252	0	1269	14	0
53	Bx	1113	0	1097	7	0
54	By	895	0	881	6	0
55	Bz	828	0	857	11	0
56	AG	1504	0	764	20	0
57	Aa	3114	0	3115	35	0
58	B8	30	0	0	0	0
58	BL	1	0	0	0	0
58	BT	1	0	0	0	0
58	Be	1	0	0	0	0
58	Bn	1	0	0	0	0
59	AG	1	0	0	0	0
59	Aa	1	0	0	0	0
59	B8	216	0	0	0	0
59	BD	1	0	0	0	0
59	BL	3	0	0	0	0
59	BN	1	0	0	0	0
59	BO	1	0	0	0	0
59	BR	1	0	0	0	0
59	BT	1	0	0	0	0
59	BV	1	0	0	0	0
59	Bx	1	0	0	0	0
60	B9	7	0	8	0	0
61	BH	1	0	0	0	0
61	Bl	1	0	0	0	0
62	Bh	4	0	0	1	0
63	AG	8	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	113095	0	96168	812	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 4.

The worst 5 of 812 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)
3:B8:1401:U:H5''	57:Aa:310:ALA:HA	1.51	0.93
4:B9:6:U:H3	4:B9:63:G:H1	1.18	0.91
3:B8:1343:G:HO2'	41:Bl:66:PHE:N	1.72	0.85
3:B8:1107:G:N3	19:BO:179:ASN:ND2	2.30	0.79
3:B8:1111:U:O2	40:Bj:296:ARG:NH2	2.17	0.78

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	
1	B1	44/198 (22%)	44 (100%)	0	0	100	100
1	B2	30/198 (15%)	30 (100%)	0	0	100	100
1	B3	30/198 (15%)	29 (97%)	1 (3%)	0	100	100
1	B4	29/198 (15%)	29 (100%)	0	0	100	100
1	B5	29/198 (15%)	29 (100%)	0	0	100	100
1	B6	29/198 (15%)	29 (100%)	0	0	100	100
5	BA	164/206 (80%)	162 (99%)	2 (1%)	0	100	100
6	BB	150/153 (98%)	148 (99%)	2 (1%)	0	100	100
7	BC	203/216 (94%)	201 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	BD	114/148 (77%)	113 (99%)	1 (1%)	0	100	100
9	BE	242/256 (94%)	240 (99%)	2 (1%)	0	100	100
10	BF	179/250 (72%)	178 (99%)	1 (1%)	0	100	100
11	BG	120/161 (74%)	119 (99%)	1 (1%)	0	100	100
12	BH	108/188 (57%)	108 (100%)	0	0	100	100
13	BI	54/65 (83%)	53 (98%)	1 (2%)	0	100	100
14	BJ	44/92 (48%)	43 (98%)	1 (2%)	0	100	100
15	BK	93/188 (50%)	92 (99%)	1 (1%)	0	100	100
16	BL	236/305 (77%)	230 (98%)	6 (2%)	0	100	100
17	BM	303/348 (87%)	300 (99%)	3 (1%)	0	100	100
18	BN	250/311 (80%)	246 (98%)	4 (2%)	0	100	100
19	BO	200/267 (75%)	193 (96%)	7 (4%)	0	100	100
20	BP	210/261 (80%)	205 (98%)	5 (2%)	0	100	100
21	BQ	173/192 (90%)	172 (99%)	1 (1%)	0	100	100
22	BR	175/178 (98%)	174 (99%)	1 (1%)	0	100	100
23	BS	113/145 (78%)	113 (100%)	0	0	100	100
24	BT	289/296 (98%)	285 (99%)	4 (1%)	0	100	100
25	BU	220/251 (88%)	219 (100%)	1 (0%)	0	100	100
26	BV	152/175 (87%)	149 (98%)	3 (2%)	0	100	100
27	BW	142/180 (79%)	139 (98%)	3 (2%)	0	100	100
28	BX	222/292 (76%)	220 (99%)	2 (1%)	0	100	100
29	BY	138/149 (93%)	137 (99%)	1 (1%)	0	100	100
30	BZ	159/205 (78%)	158 (99%)	1 (1%)	0	100	100
31	Ba	92/123 (75%)	91 (99%)	1 (1%)	0	100	100
32	Bb	99/112 (88%)	99 (100%)	0	0	100	100
33	Bc	80/138 (58%)	80 (100%)	0	0	100	100
34	Bd	64/128 (50%)	64 (100%)	0	0	100	100
35	Be	92/102 (90%)	92 (100%)	0	0	100	100
36	Bf	141/206 (68%)	140 (99%)	1 (1%)	0	100	100
37	Bg	159/222 (72%)	158 (99%)	1 (1%)	0	100	100
38	Bh	160/196 (82%)	158 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	Bi	382/439 (87%)	377 (99%)	5 (1%)	0	100	100
40	Bj	160/325 (49%)	156 (98%)	4 (2%)	0	100	100
41	Bl	36/103 (35%)	36 (100%)	0	0	100	100
42	Bm	392/423 (93%)	388 (99%)	4 (1%)	0	100	100
43	Bn	352/380 (93%)	343 (97%)	9 (3%)	0	100	100
44	Bo	292/338 (86%)	285 (98%)	7 (2%)	0	100	100
45	Bp	145/206 (70%)	145 (100%)	0	0	100	100
46	Bq	122/137 (89%)	120 (98%)	2 (2%)	0	100	100
47	Br	96/142 (68%)	96 (100%)	0	0	100	100
48	Bs	149/215 (69%)	146 (98%)	3 (2%)	0	100	100
49	Bt	282/332 (85%)	278 (99%)	4 (1%)	0	100	100
50	Bu	235/306 (77%)	233 (99%)	2 (1%)	0	100	100
51	Bv	236/279 (85%)	230 (98%)	6 (2%)	0	100	100
52	Bw	153/212 (72%)	151 (99%)	2 (1%)	0	100	100
53	Bx	132/166 (80%)	129 (98%)	3 (2%)	0	100	100
54	By	108/158 (68%)	107 (99%)	1 (1%)	0	100	100
55	Bz	95/128 (74%)	95 (100%)	0	0	100	100
57	Aa	379/484 (78%)	376 (99%)	3 (1%)	0	100	100
All	All	9277/12666 (73%)	9160 (99%)	117 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	B1	40/158 (25%)	40 (100%)	0	100	100
1	B2	31/158 (20%)	31 (100%)	0	100	100
1	B3	31/158 (20%)	31 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B4	30/158 (19%)	30 (100%)	0	100	100
1	B5	30/158 (19%)	30 (100%)	0	100	100
1	B6	30/158 (19%)	30 (100%)	0	100	100
5	BA	146/176 (83%)	146 (100%)	0	100	100
6	BB	134/135 (99%)	132 (98%)	2 (2%)	57	84
7	BC	183/191 (96%)	183 (100%)	0	100	100
8	BD	94/119 (79%)	93 (99%)	1 (1%)	65	88
9	BE	220/229 (96%)	220 (100%)	0	100	100
10	BF	163/223 (73%)	162 (99%)	1 (1%)	78	93
11	BG	113/147 (77%)	113 (100%)	0	100	100
12	BH	99/164 (60%)	99 (100%)	0	100	100
13	BI	53/60 (88%)	53 (100%)	0	100	100
14	BJ	40/72 (56%)	40 (100%)	0	100	100
15	BK	88/166 (53%)	88 (100%)	0	100	100
16	BL	192/245 (78%)	191 (100%)	1 (0%)	81	93
17	BM	260/290 (90%)	259 (100%)	1 (0%)	84	94
18	BN	219/262 (84%)	219 (100%)	0	100	100
19	BO	182/228 (80%)	181 (100%)	1 (0%)	81	93
20	BP	194/232 (84%)	194 (100%)	0	100	100
21	BQ	138/150 (92%)	138 (100%)	0	100	100
22	BR	154/155 (99%)	154 (100%)	0	100	100
23	BS	98/124 (79%)	98 (100%)	0	100	100
24	BT	246/249 (99%)	246 (100%)	0	100	100
25	BU	189/211 (90%)	188 (100%)	1 (0%)	81	93
26	BV	134/150 (89%)	134 (100%)	0	100	100
27	BW	126/155 (81%)	126 (100%)	0	100	100
28	BX	206/256 (80%)	206 (100%)	0	100	100
29	BY	118/126 (94%)	118 (100%)	0	100	100
30	BZ	146/180 (81%)	146 (100%)	0	100	100
31	Ba	74/97 (76%)	74 (100%)	0	100	100
32	Bb	83/90 (92%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	Bc	76/116 (66%)	76 (100%)	0	100	100
34	Bd	59/113 (52%)	59 (100%)	0	100	100
35	Be	80/87 (92%)	80 (100%)	0	100	100
36	Bf	135/181 (75%)	135 (100%)	0	100	100
37	Bg	138/178 (78%)	138 (100%)	0	100	100
38	Bh	147/169 (87%)	146 (99%)	1 (1%)	76	92
39	Bi	340/381 (89%)	339 (100%)	1 (0%)	86	96
40	Bj	150/287 (52%)	150 (100%)	0	100	100
41	Bl	37/89 (42%)	37 (100%)	0	100	100
42	Bm	353/368 (96%)	352 (100%)	1 (0%)	86	96
43	Bn	313/332 (94%)	313 (100%)	0	100	100
44	Bo	270/303 (89%)	269 (100%)	1 (0%)	84	94
45	Bp	136/190 (72%)	136 (100%)	0	100	100
46	Bq	104/112 (93%)	104 (100%)	0	100	100
47	Br	96/133 (72%)	96 (100%)	0	100	100
48	Bs	132/185 (71%)	130 (98%)	2 (2%)	57	84
49	Bt	251/288 (87%)	251 (100%)	0	100	100
50	Bu	223/274 (81%)	221 (99%)	2 (1%)	70	90
51	Bv	207/236 (88%)	207 (100%)	0	100	100
52	Bw	139/188 (74%)	139 (100%)	0	100	100
53	Bx	124/148 (84%)	124 (100%)	0	100	100
54	By	104/148 (70%)	104 (100%)	0	100	100
55	Bz	86/110 (78%)	85 (99%)	1 (1%)	63	86
57	Aa	338/427 (79%)	333 (98%)	5 (2%)	57	84
All	All	8322/10873 (76%)	8300 (100%)	22 (0%)	84	96

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	Bu	81	THR
57	Aa	194	THR
55	Bz	43	VAL
57	Aa	199	ILE
19	BO	102	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 103 such sidechains are listed below:

Mol	Chain	Res	Type
39	Bi	314	GLN
44	Bo	198	ASN
57	Aa	124	GLN
39	Bi	358	GLN
42	Bm	165	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B7	2/3 (66%)	1 (50%)	0
3	B8	1556/1561 (99%)	236 (15%)	1 (0%)
4	B9	71/72 (98%)	11 (15%)	0
56	AG	70/71 (98%)	11 (15%)	0
All	All	1699/1707 (99%)	259 (15%)	1 (0%)

5 of 259 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B7	76	A
3	B8	2	C
3	B8	11	G
3	B8	19	C
3	B8	22	A

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	B8	575	A

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

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

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

RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
56	PSU	AG	24	56	18,21,22	1.32	2 (11%)	22,30,33	1.82	3 (13%)
56	PSU	AG	46	56	18,21,22	1.37	2 (11%)	22,30,33	1.83	3 (13%)
3	OMG	B8	1145	58,56,3	23,26,27	1.19	3 (13%)	33,38,41	1.87	6 (18%)
4	PSU	B9	37	4	18,21,22	1.34	2 (11%)	22,30,33	1.83	3 (13%)
4	2MG	B9	10	4	23,26,27	0.47	0	32,38,41	0.52	0
3	PSU	B8	1397	3	18,21,22	1.38	2 (11%)	22,30,33	1.84	3 (13%)
22	SAC	BR	2	22	7,8,9	0.54	0	8,9,11	0.95	1 (12%)
4	1MA	B9	9	4	21,25,26	0.51	0	31,37,40	0.77	1 (3%)
3	1MA	B8	947	3	21,25,26	0.46	0	31,37,40	0.73	1 (3%)
56	RSQ	AG	31	56	20,23,24	0.56	0	26,33,36	1.16	2 (7%)
3	OMG	B8	1370	3	23,26,27	1.19	3 (13%)	33,38,41	1.88	6 (18%)
3	OMU	B8	1369	58,3	19,22,23	1.19	2 (10%)	26,31,34	1.68	5 (19%)
56	PSU	AG	51	56	18,21,22	1.37	2 (11%)	22,30,33	1.79	3 (13%)
6	AYA	BB	2	6	6,7,8	0.80	0	5,8,10	0.37	0
32	AYA	Bb	2	32	6,7,8	0.68	0	5,8,10	0.41	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
56	PSU	AG	24	56	-	0/7/25/26	0/2/2/2
56	PSU	AG	46	56	-	0/7/25/26	0/2/2/2
3	OMG	B8	1145	58,56,3	-	0/9/27/28	0/3/3/3
4	PSU	B9	37	4	-	0/7/25/26	0/2/2/2
4	2MG	B9	10	4	-	0/9/27/28	0/3/3/3
3	PSU	B8	1397	3	-	0/7/25/26	0/2/2/2
22	SAC	BR	2	22	-	0/7/8/10	-
4	1MA	B9	9	4	-	0/7/25/26	0/3/3/3
3	1MA	B8	947	3	-	0/7/25/26	0/3/3/3
56	RSQ	AG	31	56	-	2/9/27/28	0/2/2/2
3	OMG	B8	1370	3	-	0/9/27/28	0/3/3/3
3	OMU	B8	1369	58,3	-	0/9/27/28	0/2/2/2
56	PSU	AG	51	56	-	2/7/25/26	0/2/2/2
6	AYA	BB	2	6	-	1/4/6/8	-
32	AYA	Bb	2	32	-	3/4/6/8	-

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	AG	46	PSU	C6-C5	3.34	1.39	1.35
56	AG	51	PSU	C6-C5	3.33	1.39	1.35
4	B9	37	PSU	C6-C5	3.17	1.39	1.35
56	AG	24	PSU	C6-C5	3.16	1.39	1.35
3	B8	1397	PSU	C6-C5	3.10	1.38	1.35

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B8	1397	PSU	N1-C2-N3	5.92	121.84	115.13
3	B8	1145	OMG	C5-C4-N3	-5.86	118.96	128.46
3	B8	1370	OMG	C5-C4-N3	-5.84	118.99	128.46
56	AG	46	PSU	N1-C2-N3	5.78	121.68	115.13
4	B9	37	PSU	N1-C2-N3	5.75	121.64	115.13

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
56	AG	51	PSU	O4'-C1'-C5-C4
56	AG	51	PSU	O4'-C1'-C5-C6
32	Bb	2	AYA	OT-CT-N-CA
32	Bb	2	AYA	CM-CT-N-CA
56	AG	31	RSQ	C2'-C1'-N1-C2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	AG	31	RSQ	1	0
56	AG	51	PSU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 267 ligands modelled in this entry, 264 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	$\# Z > 2$
60	VAL	B9	101	4	4,6,7	0.53	0	6,7,9	0.90	0
63	MET	AG	101	56	6,7,8	0.46	0	2,7,9	0.13	0
62	FES	Bh	201	38,20	0,4,4	-	-	-		

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
60	VAL	B9	101	4	-	3/5/6/8	-
63	MET	AG	101	56	-	1/5/6/8	-
62	FES	Bh	201	38,20	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	B9	101	VAL	N-CA-CB-CG2
60	B9	101	VAL	C-CA-CB-CG1
60	B9	101	VAL	C-CA-CB-CG2
63	AG	101	MET	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
62	Bh	201	FES	1	0

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.

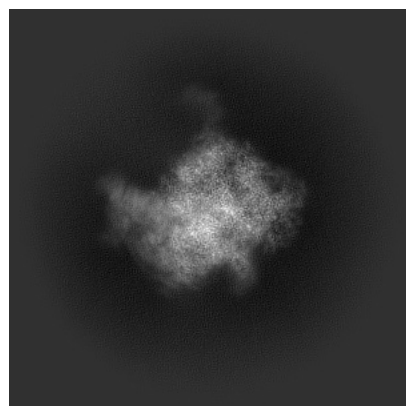
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16899. These allow visual inspection of the internal detail of the map and identification of artifacts.

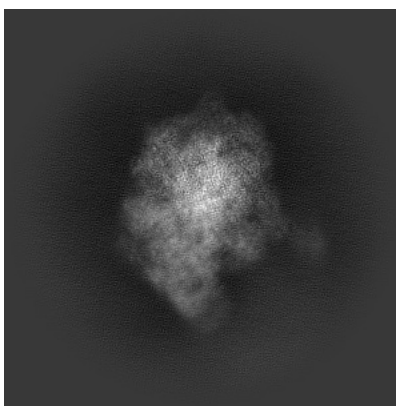
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

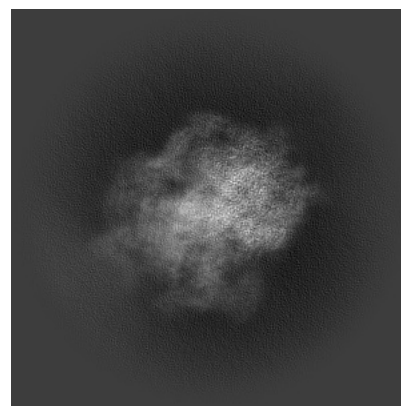
6.1.1 Primary map



X

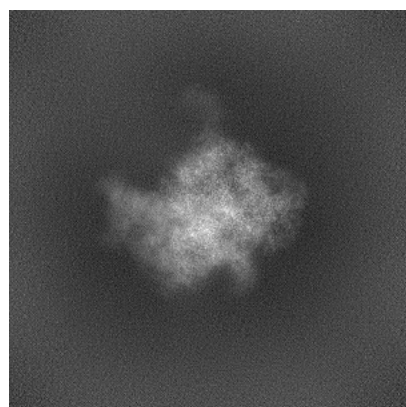


Y

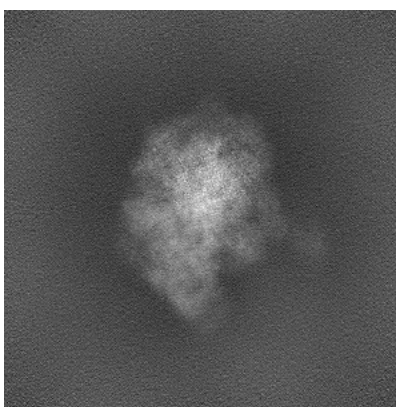


Z

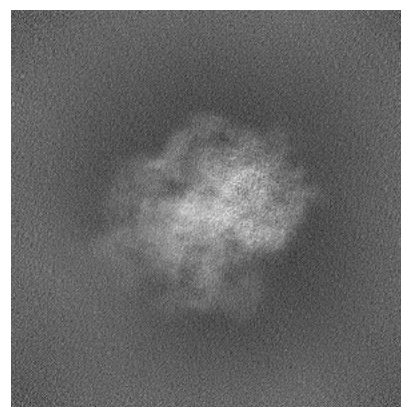
6.1.2 Raw map



X



Y

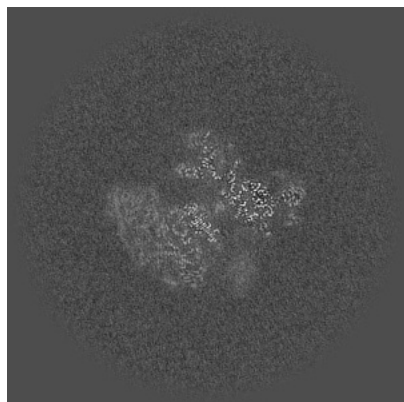


Z

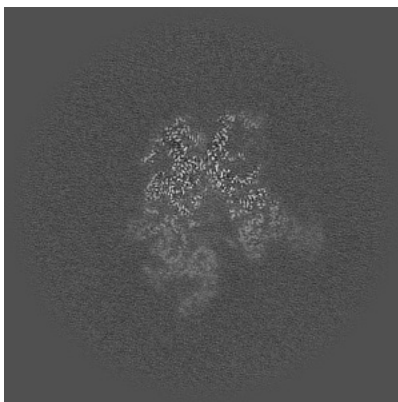
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

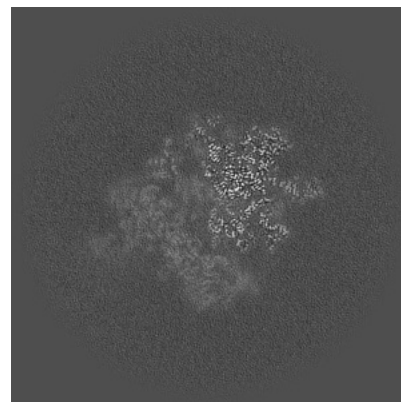
6.2.1 Primary map



X Index: 256

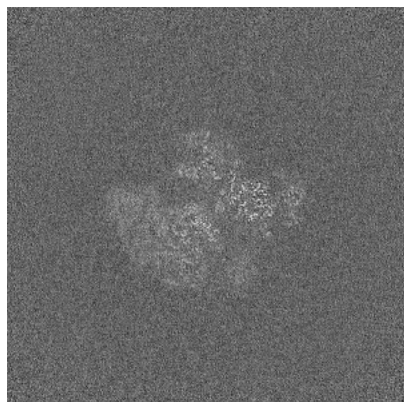


Y Index: 256

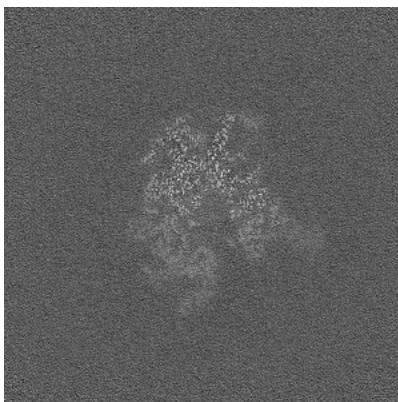


Z Index: 256

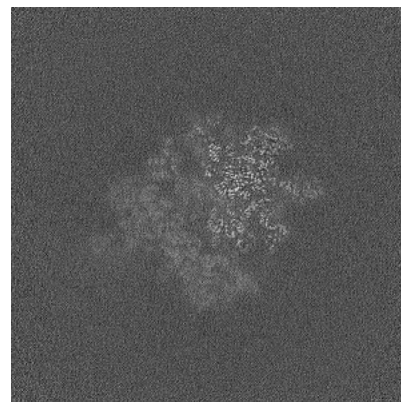
6.2.2 Raw map



X Index: 256



Y Index: 256

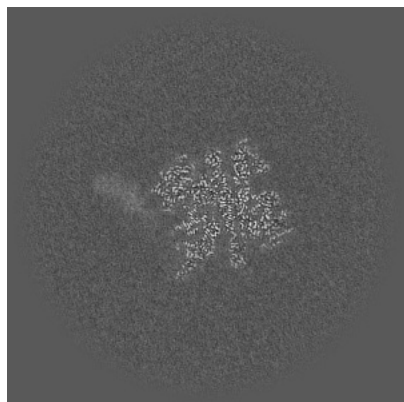


Z Index: 256

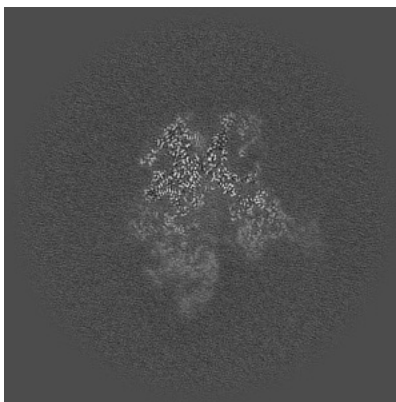
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

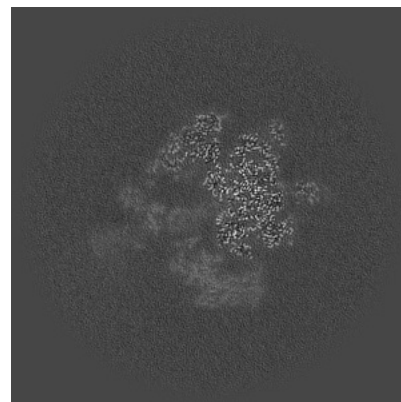
6.3.1 Primary map



X Index: 297

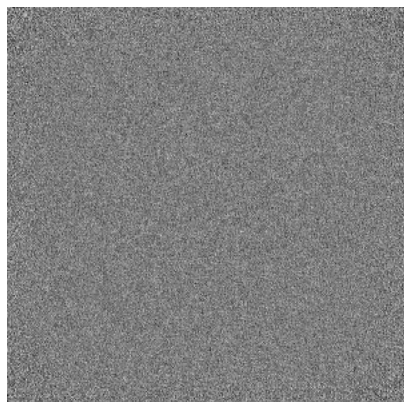


Y Index: 254

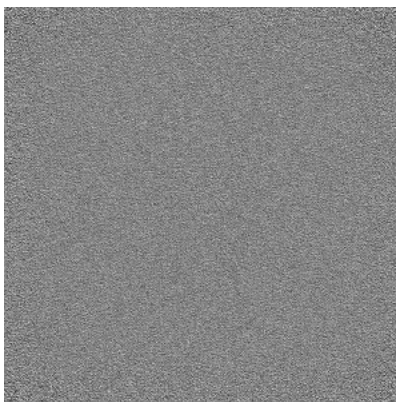


Z Index: 269

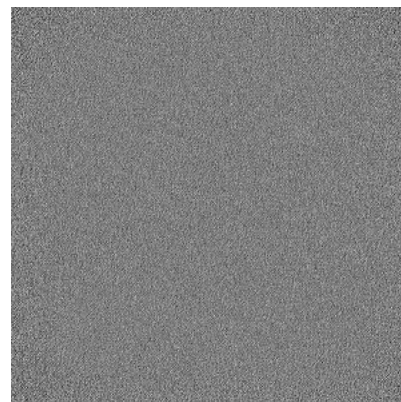
6.3.2 Raw map



X Index: 0



Y Index: 0

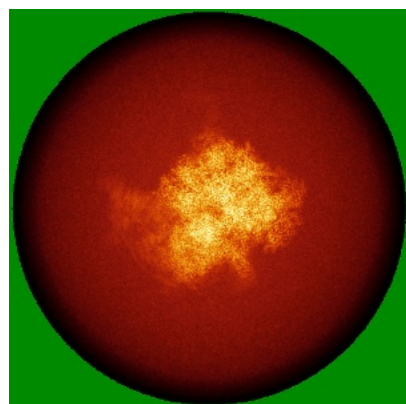


Z Index: 0

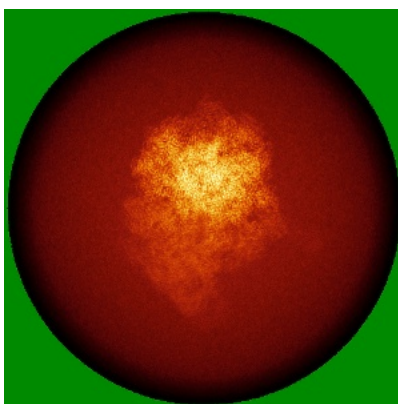
The images above show the largest variance slices of the map in three orthogonal directions.

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

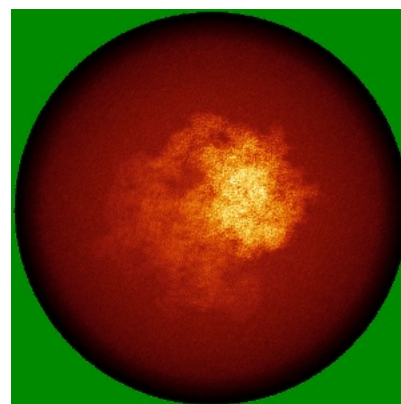
6.4.1 Primary map



X

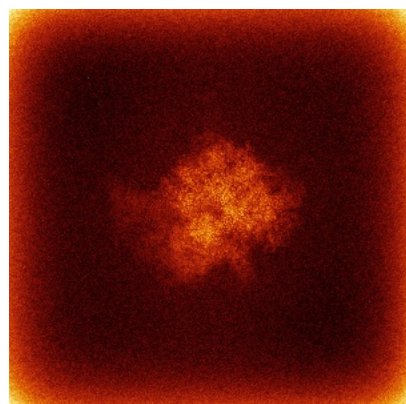


Y

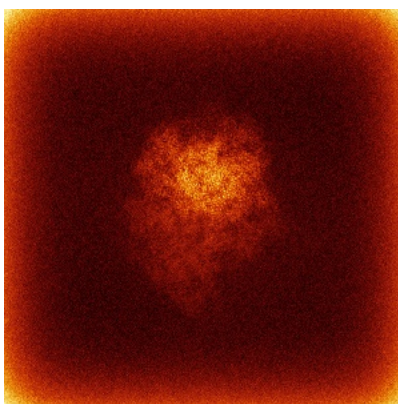


Z

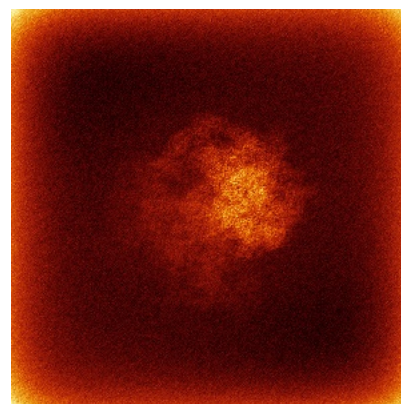
6.4.2 Raw map



X



Y

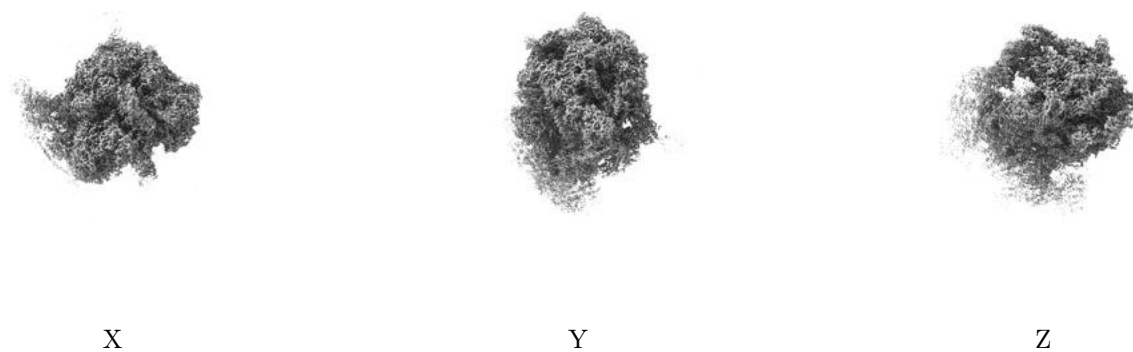


Z

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.

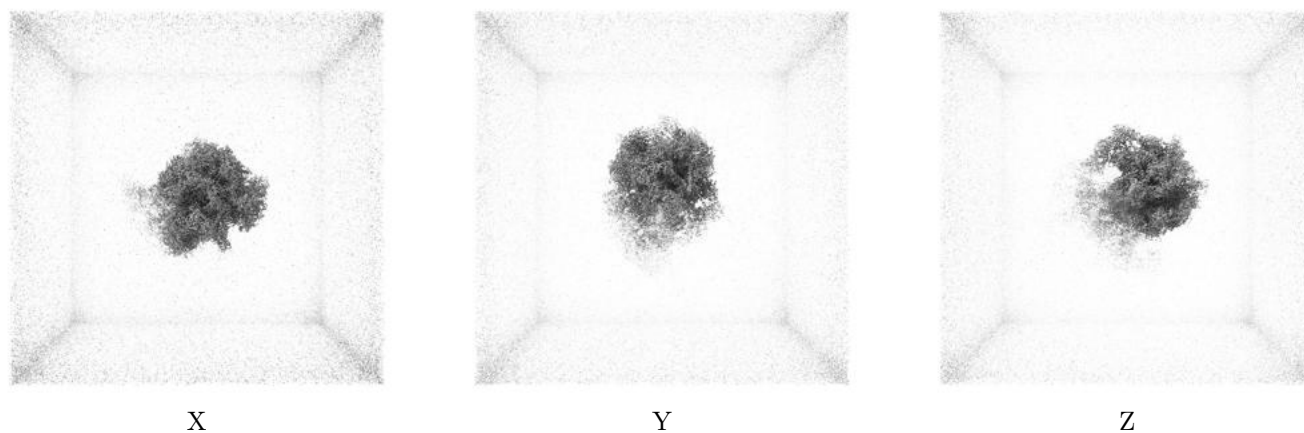
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.75. 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.

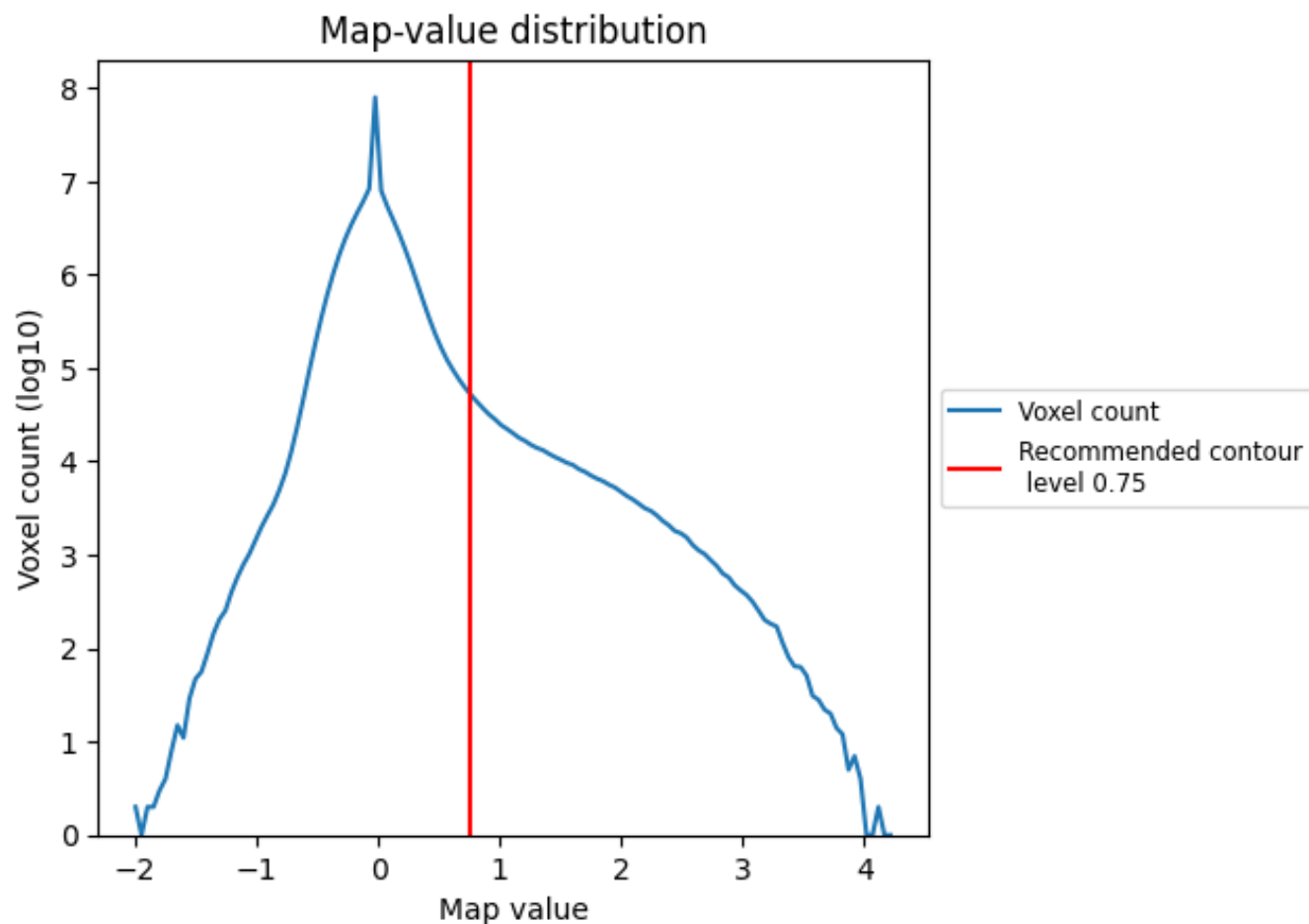
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

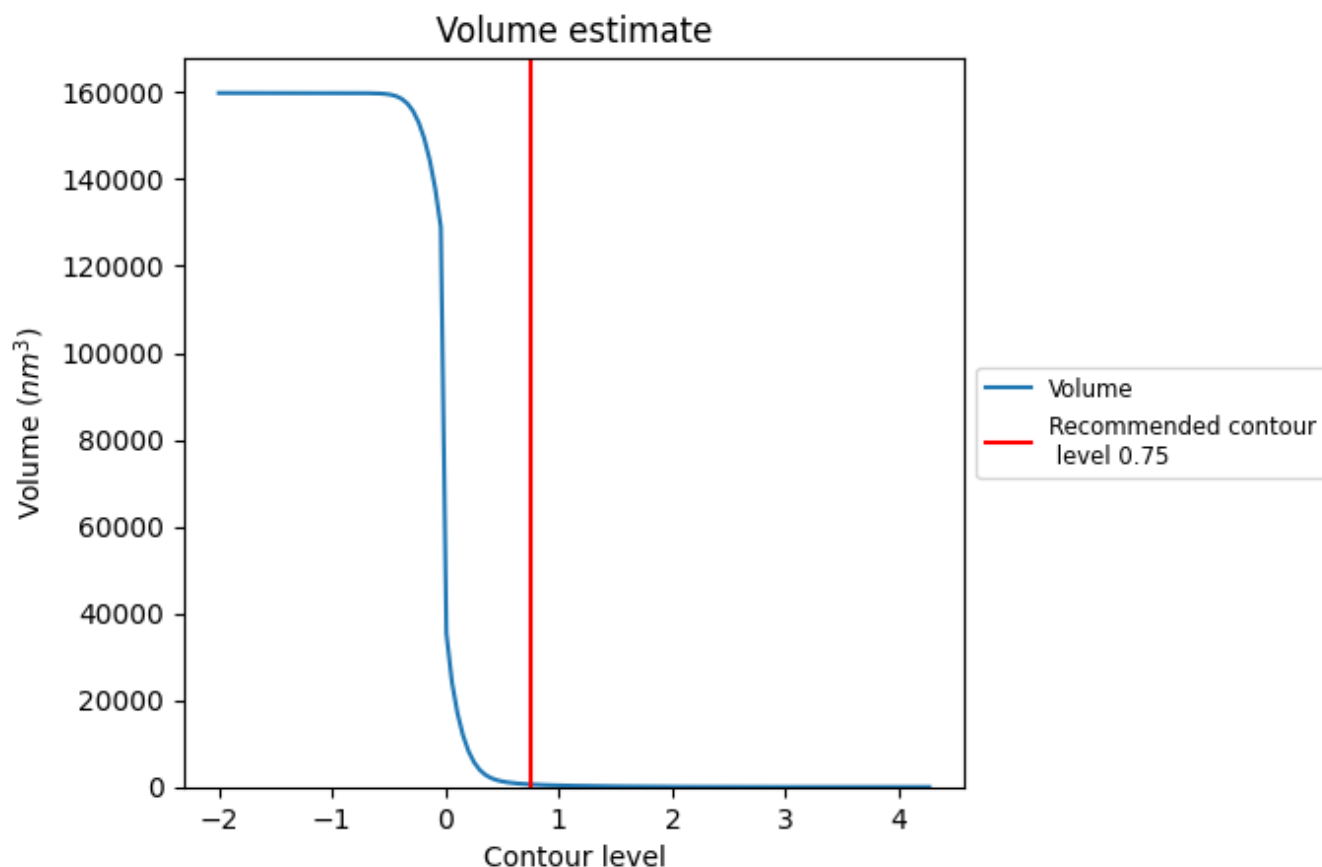
This section contains the results of statistical analysis of the map.

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.

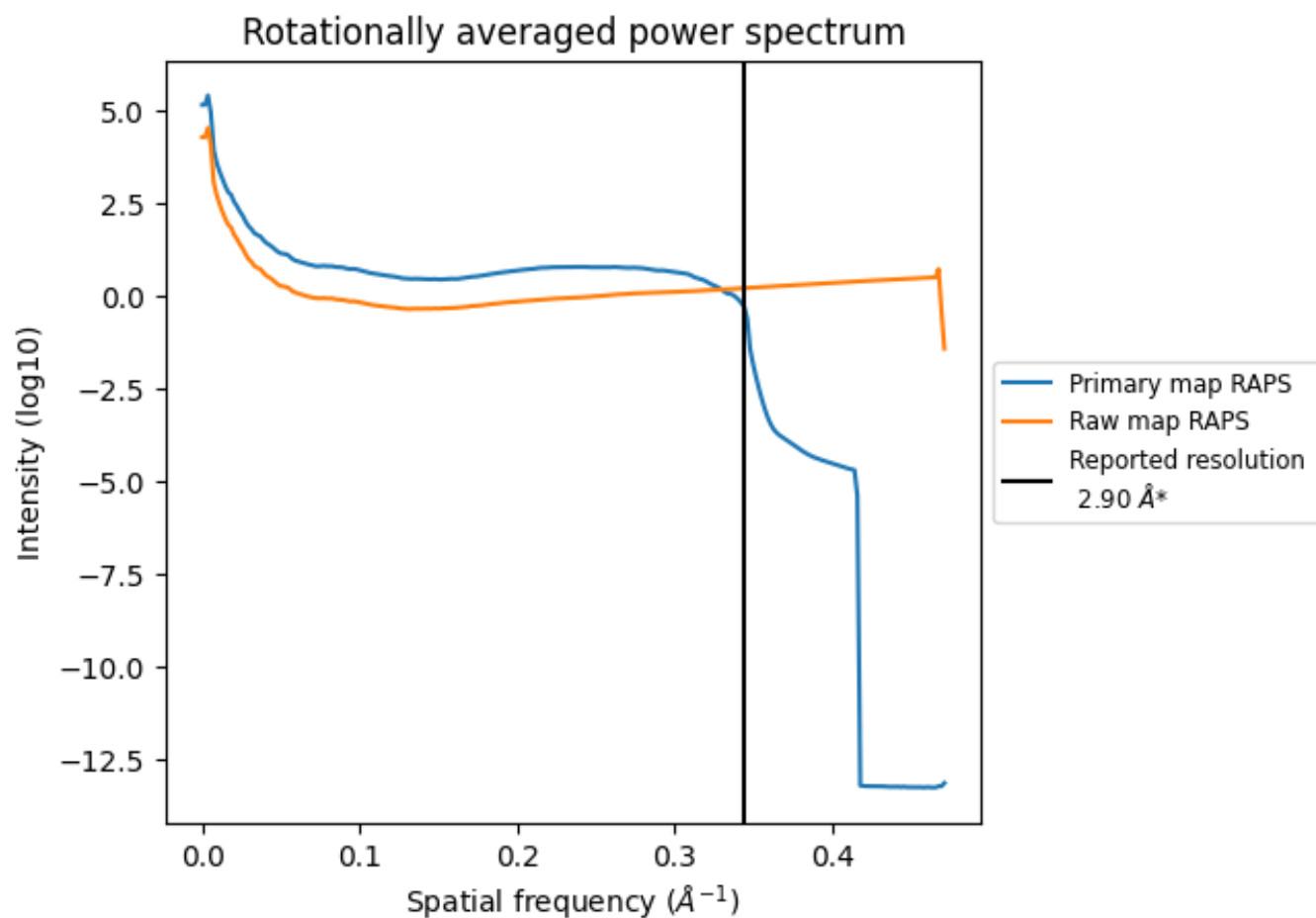
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 590 nm³; this corresponds to an approximate mass of 533 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

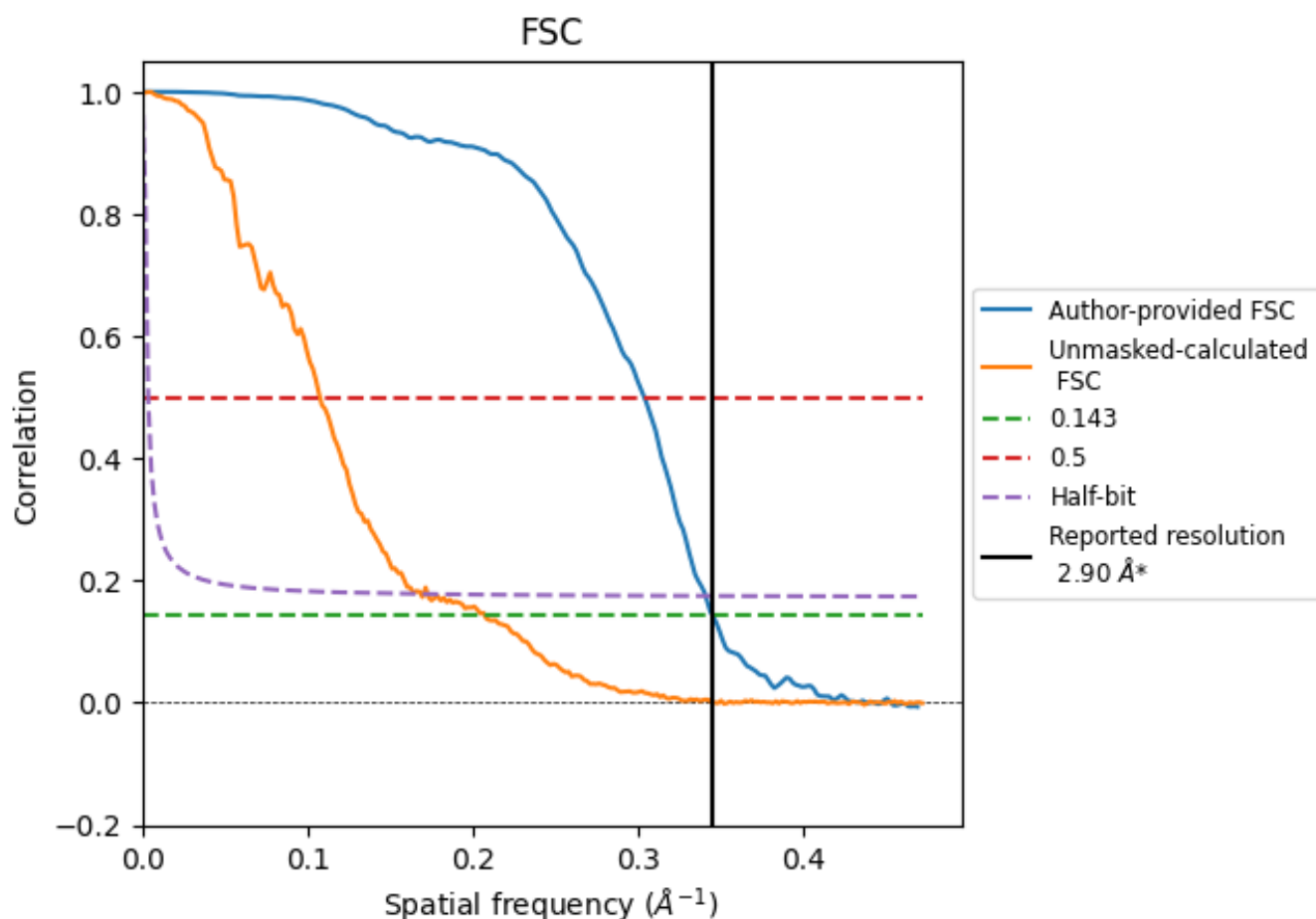


*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

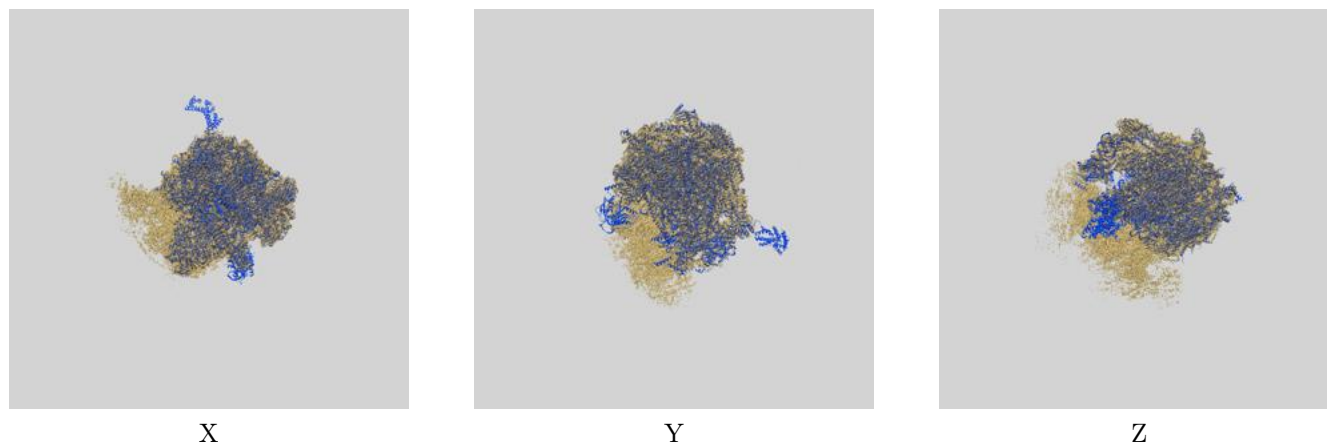
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.90	3.29	2.94
Unmasked-calculated*	4.83	9.30	5.93

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.83 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

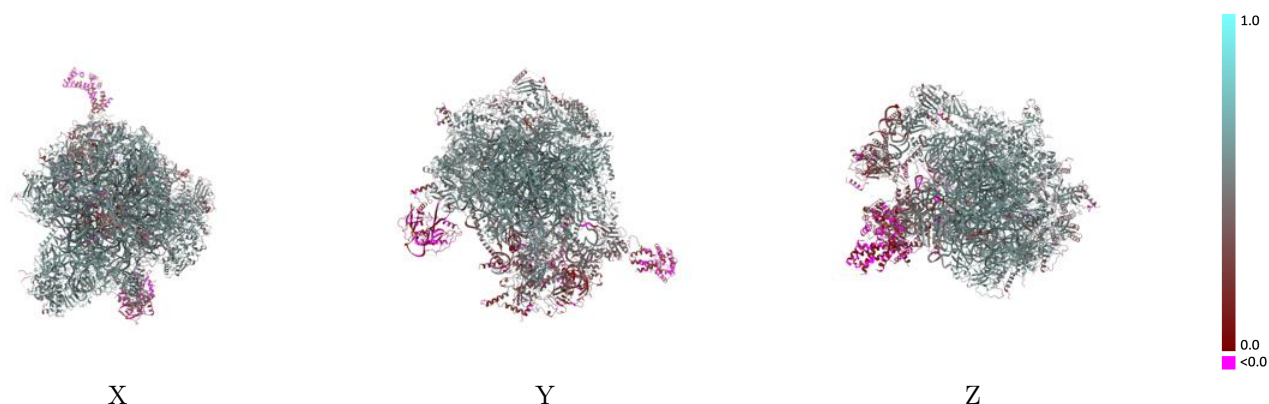
This section contains information regarding the fit between EMDB map EMD-16899 and PDB model 8OIT. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

9.1 Map-model overlay [i](#)



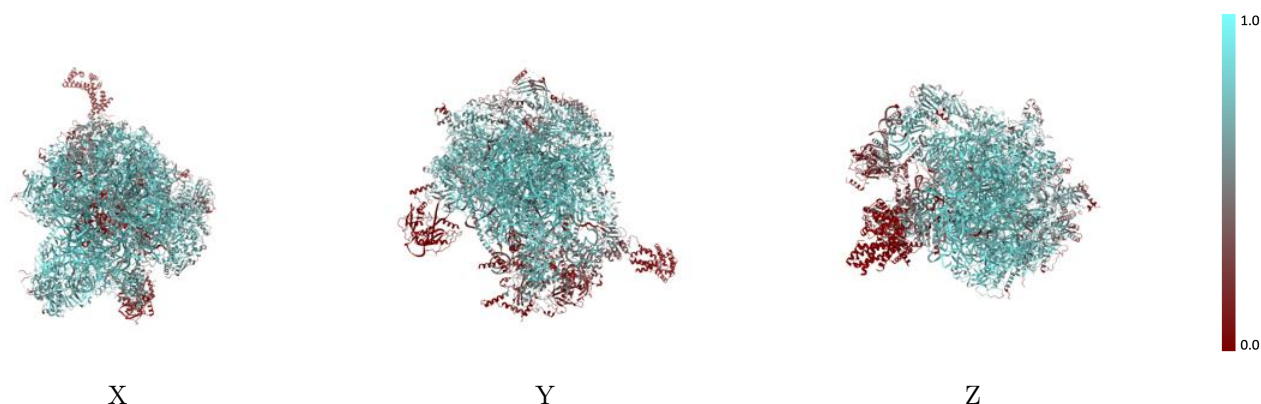
The images above show the 3D surface view of the map at the recommended contour level 0.75 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



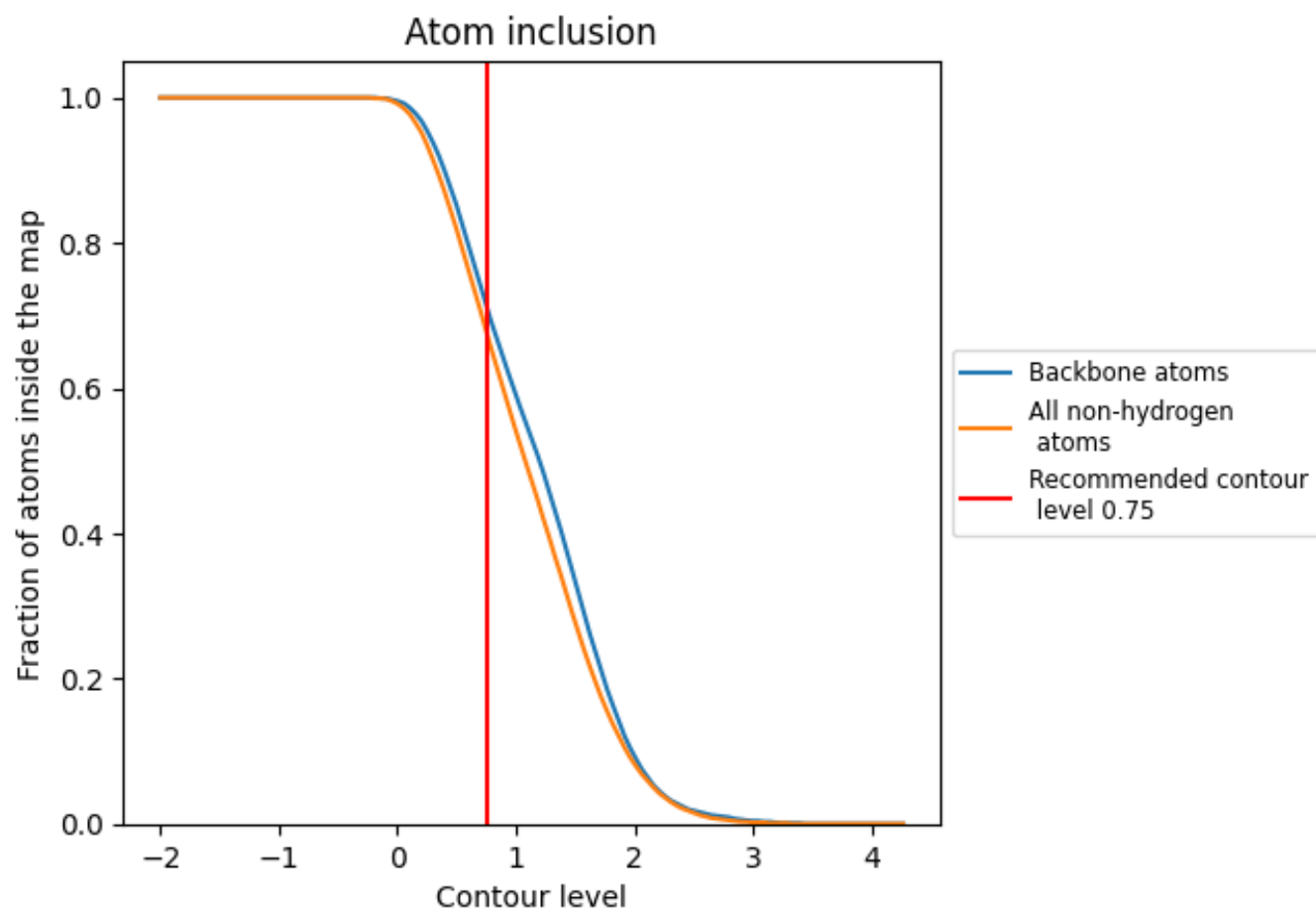
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.75).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 68% 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 (0.75) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6780	 0.4910
AG	 0.3600	 0.3100
Aa	 0.0150	 0.1020
B1	 0.0230	 0.1990
B2	 0.0080	 0.0960
B3	 0.0000	 0.0740
B4	 0.0000	 0.0850
B5	 0.0000	 -0.0030
B6	 0.0000	 0.0050
B7	 0.1290	 0.4350
B8	 0.8620	 0.5550
B9	 0.5550	 0.3740
BA	 0.7920	 0.5740
BB	 0.6950	 0.5180
BC	 0.5170	 0.4850
BD	 0.8150	 0.5780
BE	 0.7160	 0.5340
BF	 0.7450	 0.5540
BG	 0.8010	 0.5690
BH	 0.7130	 0.5520
BI	 0.6900	 0.5230
BJ	 0.8750	 0.6110
BK	 0.8690	 0.6040
BL	 0.8090	 0.5720
BM	 0.8030	 0.5620
BN	 0.7970	 0.5710
BO	 0.2840	 0.2670
BP	 0.3740	 0.3490
BQ	 0.1620	 0.2570
BR	 0.8370	 0.5830
BS	 0.8100	 0.5700
BT	 0.7910	 0.5700
BU	 0.7720	 0.5530
BV	 0.7930	 0.5660
BW	 0.7570	 0.5470



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Chain	Atom inclusion	Q-score
BX	 0.7470	 0.5400
BY	 0.8150	 0.5830
BZ	 0.7850	 0.5660
Ba	 0.6760	 0.5070
Bb	 0.4720	 0.4420
Bc	 0.3020	 0.3210
Bd	 0.3530	 0.3110
Be	 0.8460	 0.5870
Bf	 0.5220	 0.4570
Bg	 0.4640	 0.3870
Bh	 0.7760	 0.5420
Bi	 0.7540	 0.5470
Bj	 0.0030	 0.0410
Bl	 0.8530	 0.5780
Bm	 0.7440	 0.5420
Bn	 0.6680	 0.4950
Bo	 0.5930	 0.4880
Bp	 0.2910	 0.3170
Bq	 0.6800	 0.5170
Br	 0.6560	 0.5020
Bs	 0.7970	 0.5730
Bt	 0.6830	 0.5290
Bu	 0.4640	 0.4540
Bv	 0.2030	 0.2770
Bw	 0.4040	 0.3890
Bx	 0.7410	 0.5500
By	 0.5190	 0.4880
Bz	 0.8530	 0.5910