



wwPDB EM Validation Summary Report ⓘ

Jun 21, 2026 – 12:29 pm BST

PDB ID : 6YDP / pdb_00006ydp
EMDB ID : EMD-10778
Title : 55S mammalian mitochondrial ribosome with mtEFG1 and P site fMet-tRNAMet (POST)
Authors : Kummer, E.; Ban, N.
Deposited on : 2020-03-20
Resolution : 3.00 Å(reported)

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

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

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

The types of validation reports are described at
<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

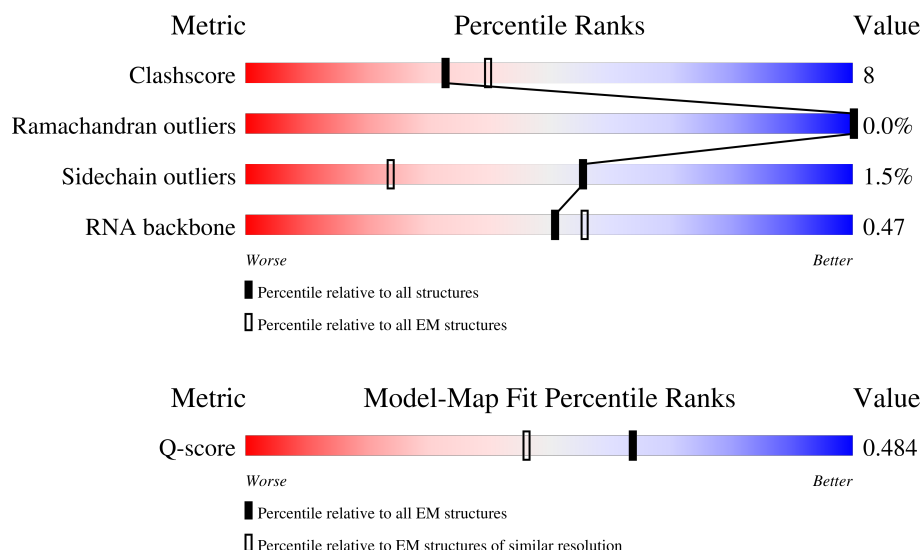
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.00 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.



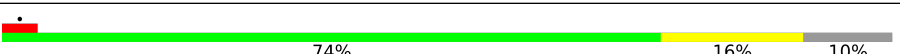
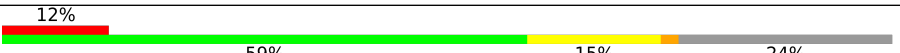
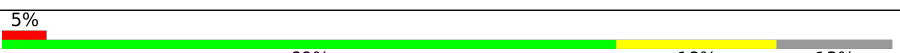
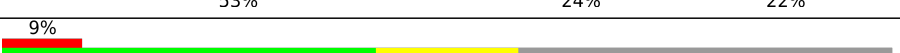
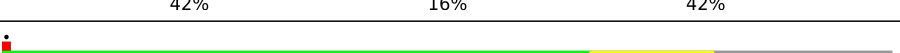
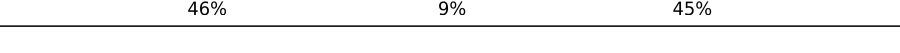
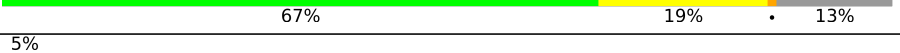
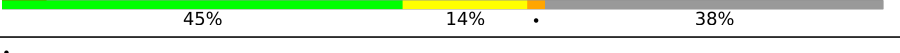
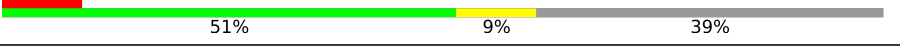
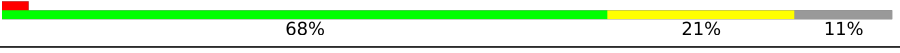
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	B0	148	
2	BU	149	
3	BV	209	

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Mol	Chain	Length	Quality of chain
4	BW	210	
5	BX	150	
6	BY	216	
7	Ba	423	
8	Bb	380	
9	Bc	334	
10	Bd	206	
11	Be	135	
12	Bf	142	
13	Bg	159	
14	Bh	332	
15	Bi	306	
16	Bj	279	
17	Bk	269	
18	Bl	166	
19	Bm	198	
20	Bn	128	
21	Bo	124	
22	Bp	112	
23	Bq	138	
24	Bt	102	
25	Bu	205	
26	Bv	222	
27	Bw	433	
28	B1	256	

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Mol	Chain	Length	Quality of chain
29	Bx	196	
30	AA	16770	
30	BA	16770	
31	AB	289	
32	AC	167	
33	AE	430	
34	AF	276	
35	AG	242	
36	AI	397	
37	AJ	200	
38	AK	196	
39	AL	139	
40	AN	128	
41	AO	239	
42	AP	135	
43	AQ	130	
44	AR	143	
45	AU	87	
46	AV	71	
47	AX	6	
48	AZ	18	
49	Aa	382	
50	Ab	190	
51	Ac	173	
52	Ad	205	

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Mol	Chain	Length	Quality of chain
53	Ae	426	
54	Af	188	
55	B2	252	
56	Ag	410	
57	Ah	387	
58	Ai	106	
59	Aj	218	
60	Ak	325	
61	Am	118	
62	An	199	
63	Ao	699	
64	Ap	258	
65	CL	198	
65	DL	198	
65	EL	198	
65	FL	198	
65	GL	198	
65	HL	198	
65	LL	198	
66	B3	161	
67	B4	126	
68	B5	188	
69	B6	65	
70	B7	95	
71	B8	188	

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Mol	Chain	Length	Quality of chain
72	B9	100	
73	BB	73	
74	BC	722	
75	BD	306	
76	BE	348	
77	BF	294	
78	BI	268	
79	BJ	262	
80	BK	192	
81	BN	178	
82	BO	145	
83	BP	296	
84	BQ	251	
85	BR	169	
86	BS	180	
87	BT	292	

2 Entry composition

There are 95 unique types of molecules in this entry. The entry contains 179513 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Mitochondrial ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B0	110	Total	C	N	O	S	0	0
			857	553	156	145	3		

- Molecule 2 is a protein called Mitochondrial ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	BU	140	Total	C	N	O	S	0	0
			1159	732	239	185	3		

- Molecule 3 is a protein called Mitochondrial ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BV	155	Total	C	N	O	S	0	0
			1231	789	219	219	4		

- Molecule 4 is a protein called uL22m.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	BW	166	Total	C	N	O	S	0	0
			1374	876	258	234	6		

- Molecule 5 is a protein called uL23m.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	BX	149	Total	C	N	O	S	0	0
			1181	752	227	200	2		

- Molecule 6 is a protein called uL24m.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	BY	206	Total	C	N	O	S	0	0
			1678	1056	308	309	5		

- Molecule 7 is a protein called Mitochondrial ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Ba	393	Total	C	N	O	S	0	0
			3173	2040	556	565	12		

- Molecule 8 is a protein called Mitochondrial ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Bb	354	Total	C	N	O	S	0	0
			2952	1876	542	525	9		

- Molecule 9 is a protein called Mitochondrial ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Bc	295	Total	C	N	O	S	0	0
			2408	1541	410	441	16		

- Molecule 10 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Bd	140	Total	C	N	O	S	0	0
			1177	742	213	221	1		

- Molecule 11 is a protein called Mitochondrial ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Be	122	Total	C	N	O	S	0	0
			972	628	168	173	3		

- Molecule 12 is a protein called mL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Bf	108	Total	C	N	O	S	0	0
			827	519	154	150	4		

- Molecule 13 is a protein called Mitochondrial ribosomal protein L43.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Bg	148	Total	C	N	O	S	0	0
			1167	727	225	212	3		

- Molecule 14 is a protein called mL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Bh	289	Total	C	N	O	S	0	0
			2319	1486	399	426	8		

- Molecule 15 is a protein called Mitochondrial ribosomal protein L45.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Bi	260	Total	C	N	O	S	0	0
			2138	1370	379	379	10		

- Molecule 16 is a protein called Mitochondrial ribosomal protein L46.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Bj	217	Total	C	N	O	S	0	0
			1775	1137	311	321	6		

- Molecule 17 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Bk	155	Total	C	N	O	S	0	0
			1246	796	214	231	5		

- Molecule 18 is a protein called Mrpl34.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Bl	133	Total	C	N	O	S	0	0
			1097	709	192	194	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bl	59	ARG	LYS	conflict	UNP A0A0R4J8D6

- Molecule 19 is a protein called Mitochondrial ribosomal protein L50.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Bm	109	Total	C	N	O	S	0	0
			893	568	160	162	3		

- Molecule 20 is a protein called Mitochondrial ribosomal protein L51.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Bn	97	Total	C	N	O	S	0	0
			837	539	166	128	4		

- Molecule 21 is a protein called mL52.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Bo	97	Total	C	N	O	S	0	0
			772	481	148	141	2		

- Molecule 22 is a protein called mL53.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Bp	97	Total	C	N	O	S	0	0
			742	459	143	134	6		

- Molecule 23 is a protein called mL54.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Bq	85	Total	C	N	O	S	0	0
			697	446	128	121	2		

- Molecule 24 is a protein called Mitochondrial ribosomal protein L57.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Bt	94	Total	C	N	O	S	0	0
			780	485	168	126	1		

- Molecule 25 is a protein called mL62 (ICT1).

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Bu	151	Total	C	N	O	S	0	0
			1198	738	233	222	5		

- Molecule 26 is a protein called mL64.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Bv	135	Total	C	N	O	S	0	0
			1131	692	223	211	5		

- Molecule 27 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Bw	387	Total	C	N	O	S	0	0
			3126	2011	548	555	12		

- Molecule 28 is a protein called Mitochondrial ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B1	244	Total	C	N	O	S	0	0
			2036	1315	363	353	5		

- Molecule 29 is a protein called Mitochondrial ribosomal protein S18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Bx	162	Total	C	N	O	S	0	0
			1325	845	249	224	7		

- Molecule 30 is a RNA chain called 12S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AA	960	Total	C	N	O	P	0	0
			20411	9162	3708	6581	960		
30	BA	1544	Total	C	N	O	P	0	0
			32844	14750	5972	10578	1544		

- Molecule 31 is a protein called Mitochondrial ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AB	220	Total	C	N	O	S	0	0
			1762	1126	326	304	6		

- Molecule 32 is a protein called Mitochondrial ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AC	132	Total	C	N	O	S	0	0
			1075	695	195	181	4		

- Molecule 33 is a protein called Mitochondrial ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AE	343	Total	C	N	O	S	0	0
			2732	1707	527	487	11		

- Molecule 34 is a protein called bS6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AF	122	Total	C	N	O	S	0	0
			981	620	178	177	6		

- Molecule 35 is a protein called Mitochondrial ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AG	208	Total	C	N	O	S	0	0
			1721	1097	314	299	11		

- Molecule 36 is a protein called uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AI	328	Total	C	N	O	S	0	0
			2650	1678	478	481	13		

- Molecule 37 is a protein called Mitochondrial ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AJ	140	Total	C	N	O	S	0	0
			1155	746	197	208	4		

- Molecule 38 is a protein called uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	AK	137	Total	C	N	O	S	0	0
			1007	631	193	180	3		

- Molecule 39 is a protein called Mitochondrial ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	AL	109	Total	C	N	O	S	0	0
			840	524	172	138	6		

- Molecule 40 is a protein called Mitochondrial ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AN	101	Total	C	N	O	S	0	0
			858	534	174	144	6		

- Molecule 41 is a protein called uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AO	175	Total	C	N	O	S	0	0
			1448	919	272	248	9		

- Molecule 42 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AP	117	Total	C	N	O	S	0	0
			932	588	184	155	5		

- Molecule 43 is a protein called uS17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AQ	112	Total	C	N	O	S	0	0
			875	568	153	151	3		

- Molecule 44 is a protein called Mitochondrial ribosomal protein S18C.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AR	97	Total	C	N	O	S	0	0
			784	507	132	138	7		

- Molecule 45 is a protein called bS21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AU	86	Total	C	N	O	S	0	0
			734	453	148	125	8		

- Molecule 46 is a RNA chain called fMet-tRNA^{Met} (P site).

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AV	71	Total	C	N	O	P	0	0
			1498	673	264	491	70		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AV	69	C	-	insertion	GB 1208989970
AV	70	C	-	insertion	GB 1208989970
AV	71	A	-	insertion	GB 1208989970

- Molecule 47 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	AX	6	Total	C	N	O	P	0	0
			128	57	22	43	6		

- Molecule 48 is a protein called unknown peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	AZ	18	Total	C	N	O	0	0
			90	54	18	18		

- Molecule 49 is a protein called Mitochondrial ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Aa	292	Total	C	N	O	S	0	0
			2378	1518	409	442	9		

- Molecule 50 is a protein called mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Ab	135	Total	C	N	O	S	0	0
			1101	709	199	192	1		

- Molecule 51 is a protein called Mitochondrial ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ac	169	Total	C	N	O	S	0	0
			1367	876	236	245	10		

- Molecule 52 is a protein called Mitochondrial ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ad	177	Total	C	N	O	S	0	0
			1467	904	288	273	2		

- Molecule 53 is a protein called Mitochondrial ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ae	388	Total	C	N	O	S	0	0
			3109	1971	535	589	14		

- Molecule 54 is a protein called Mitoribosomal protein ms28, mrps28.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Af	99	Total	C	N	O	S	0	0
			778	494	134	146	4		

- Molecule 55 is a protein called Mitochondrial ribosomal protein L47.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	B2	179	Total	C	N	O	S	0	0
			1548	992	290	260	6		

- Molecule 56 is a protein called Death associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Ag	353	Total	C	N	O	S	0	0
			2875	1837	515	513	10		

- Molecule 57 is a protein called Mitochondrial ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Ah	120	Total	C	N	O	S	0	0
			1015	659	168	185	3		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ah	180	UNK	-	insertion	UNP F1RME2
Ah	181	GLN	-	insertion	UNP F1RME2
Ah	182	LYS	-	insertion	UNP F1RME2
Ah	184	GLY	-	insertion	UNP F1RME2
Ah	185	GLU	LYS	conflict	UNP F1RME2
Ah	187	PRO	LYS	conflict	UNP F1RME2
Ah	189	ILE	LEU	conflict	UNP F1RME2
Ah	190	SER	ILE	conflict	UNP F1RME2
Ah	237	SER	-	insertion	UNP F1RME2
Ah	238	PHE	-	insertion	UNP F1RME2

- Molecule 58 is a protein called mS33.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Ai	99	Total	C	N	O	S	0	0
			824	522	156	143	3		

- Molecule 59 is a protein called mS34.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Aj	213	Total	C	N	O	S	0	0
			1788	1131	338	311	8		

- Molecule 60 is a protein called Mitochondrial ribosomal protein S35.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Ak	275	Total	C	N	O	S	0	0
			2222	1414	380	419	9		

- Molecule 61 is a protein called mS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Am	116	Total	C	N	O	S	0	0
			930	577	185	160	8		

- Molecule 62 is a protein called Aurora kinase A interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	An	72	Total	C	N	O	S	0	0
			639	407	139	92	1		

- Molecule 63 is a protein called Pentatricopeptide repeat domain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Ao	572	Total	C	N	O	S	0	0
			4525	2897	770	834	24		

- Molecule 64 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Ap	190	Total	C	N	O	S	0	0
			1564	991	292	273	8		

- Molecule 65 is a protein called Mitochondrial ribosomal protein L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
65	CL	45	Total	C	N	O	0	0
			317	203	52	62		
65	DL	27	Total	C	N	O	0	0
			213	137	33	43		
65	EL	28	Total	C	N	O	0	0
			222	143	35	44		

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Mol	Chain	Residues	Atoms				AltConf	Trace
65	FL	27	Total	C	N	O	0	0
			213	137	33	43		
65	GL	27	Total	C	N	O	0	0
			213	137	33	43		
65	HL	26	Total	C	N	O	0	0
			205	131	32	42		
65	LL	70	Total	C	N	O	0	0
			537	346	93	98		

- Molecule 66 is a protein called uL30m.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	B3	118	Total	C	N	O	S	0	0
			968	622	178	165	3		

- Molecule 67 is a protein called bL31m.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	B4	62	Total	C	N	O	S	0	0
			474	296	94	81	3		

- Molecule 68 is a protein called bL32m.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	B5	110	Total	C	N	O	S	0	0
			902	553	181	162	6		

- Molecule 69 is a protein called bL33m.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	B6	52	Total	C	N	O	S	0	0
			425	274	78	71	2		

- Molecule 70 is a protein called Mitochondrial ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	B7	46	Total	C	N	O	S	0	0
			387	239	89	58	1		

- Molecule 71 is a protein called Mitochondrial ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	B8	95	Total	C	N	O	S	0	0
			833	539	163	129	2		

- Molecule 72 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	B9	38	Total	C	N	O	S	0	0
			335	214	70	47	4		

- Molecule 73 is a RNA chain called CP tRNAPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	BB	67	Total	C	N	O	P	0	0
			1427	640	261	459	67		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BB	72	C	-	insertion	GB 76262549
BB	73	A	-	insertion	GB 76262549

- Molecule 74 is a protein called Elongation factor G, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	BC	694	Total	C	N	O	S	0	0
			5425	3422	935	1035	33		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BC	30	SER	-	expression tag	UNP Q96RP9
BC	31	GLY	-	expression tag	UNP Q96RP9
BC	32	GLY	-	expression tag	UNP Q96RP9
BC	33	SER	-	expression tag	UNP Q96RP9
BC	34	GLY	-	expression tag	UNP Q96RP9
BC	35	SER	-	expression tag	UNP Q96RP9
BC	36	GLY	-	expression tag	UNP Q96RP9

- Molecule 75 is a protein called uL2m.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	BD	240	Total	C	N	O	S	0	0
			1860	1160	371	319	10		

- Molecule 76 is a protein called ICT1.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	BE	307	Total	C	N	O	S	0	0
			2420	1554	426	430	10		

- Molecule 77 is a protein called Mitochondrial ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	BF	250	Total	C	N	O	S	0	0
			2011	1294	367	344	6		

- Molecule 78 is a protein called Mitochondrial ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	BI	98	Total	C	N	O	S	0	0
			805	509	155	141			

- Molecule 79 is a protein called Mitochondrial ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	BJ	212	Total	C	N	O	S	0	0
			1705	1100	306	290	9		

- Molecule 80 is a protein called Mitochondrial ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	BK	176	Total	C	N	O	S	0	0
			1339	851	243	243	2		

- Molecule 81 is a protein called uL13m.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	BN	177	Total	C	N	O	S	0	0
			1444	926	258	253	7		

- Molecule 82 is a protein called uL14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	BO	115	Total	C	N	O	S	0	0
			896	562	176	154	4		

- Molecule 83 is a protein called uL15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	BP	288	Total	C	N	O	S	0	0
			2312	1473	430	403	6		

- Molecule 84 is a protein called uL16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	BQ	222	Total	C	N	O	S	0	0
			1803	1156	331	306	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BQ	237	HIS	TYR	conflict	UNP F1RI89

- Molecule 85 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	BR	153	Total	C	N	O	S	0	0
			1240	777	236	222	5		

- Molecule 86 is a protein called Mitochondrial ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	BS	143	Total	C	N	O	S	0	0
			1168	733	227	204	4		

- Molecule 87 is a protein called Mitochondrial ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	BT	240	Total	C	N	O	S	0	0
			1990	1275	349	357	9		

- Molecule 88 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
88	B0	1	Total 1	Mg 1	0
88	Be	1	Total 1	Mg 1	0
88	Bl	1	Total 1	Mg 1	0
88	Bt	1	Total 1	Mg 1	0
88	AA	101	Total 101	Mg 101	0
88	AB	1	Total 1	Mg 1	0
88	AL	1	Total 1	Mg 1	0
88	AX	1	Total 1	Mg 1	0
88	Ag	1	Total 1	Mg 1	0
88	Am	1	Total 1	Mg 1	0
88	An	1	Total 1	Mg 1	0
88	B3	1	Total 1	Mg 1	0
88	BA	205	Total 205	Mg 205	0
88	BB	1	Total 1	Mg 1	0
88	BC	1	Total 1	Mg 1	0
88	BD	3	Total 3	Mg 3	0
88	BP	2	Total 2	Mg 2	0
88	BQ	1	Total 1	Mg 1	0
88	BR	1	Total 1	Mg 1	0

- Molecule 89 is ZINC ION (CCD ID: ZN) (formula: Zn).

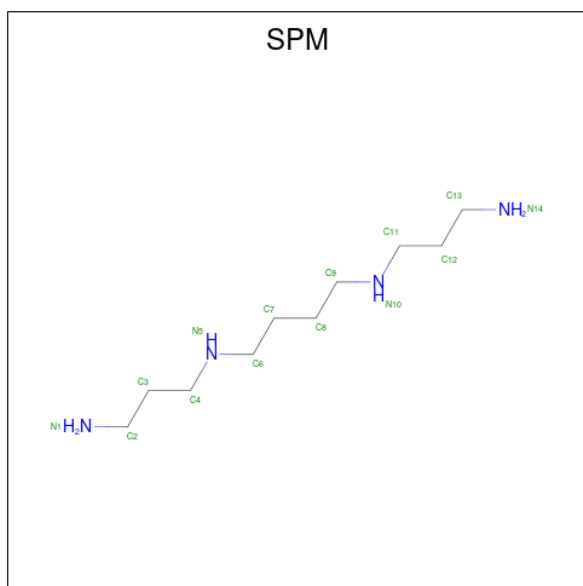
Mol	Chain	Residues	Atoms		AltConf
89	Bx	1	Total 1	Zn 1	0

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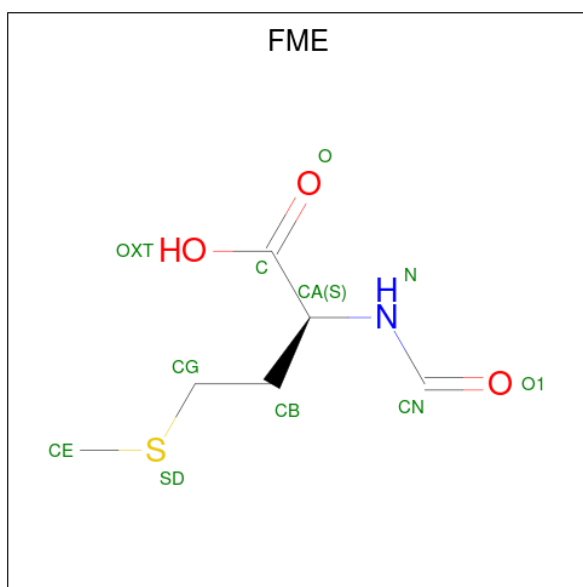
Mol	Chain	Residues	Atoms		AltConf
89	AR	1	Total	Zn	0
			1	1	
89	Ac	1	Total	Zn	0
			1	1	
89	Ap	1	Total	Zn	0
			1	1	
89	B5	1	Total	Zn	0
			1	1	
89	B9	1	Total	Zn	0
			1	1	

- Molecule 90 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$).



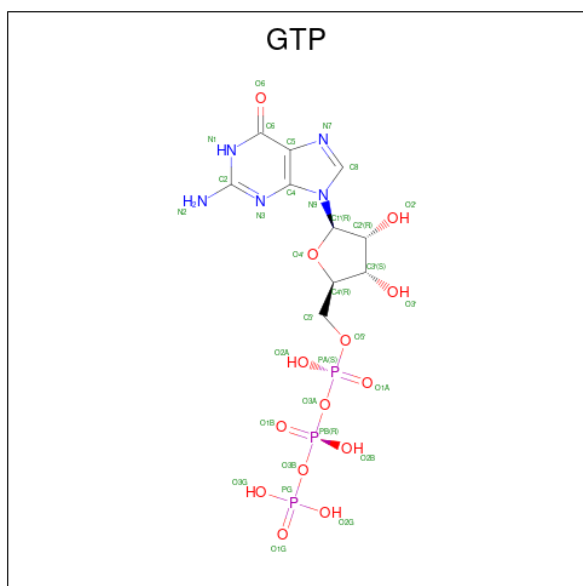
Mol	Chain	Residues	Atoms			AltConf
90	AA	1	Total	C	N	0
			14	10	4	
90	BA	1	Total	C	N	0
			14	10	4	
90	BA	1	Total	C	N	0
			14	10	4	

- Molecule 91 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: $C_6H_{11}NO_3S$) (labeled as "Ligand of Interest" by depositor).



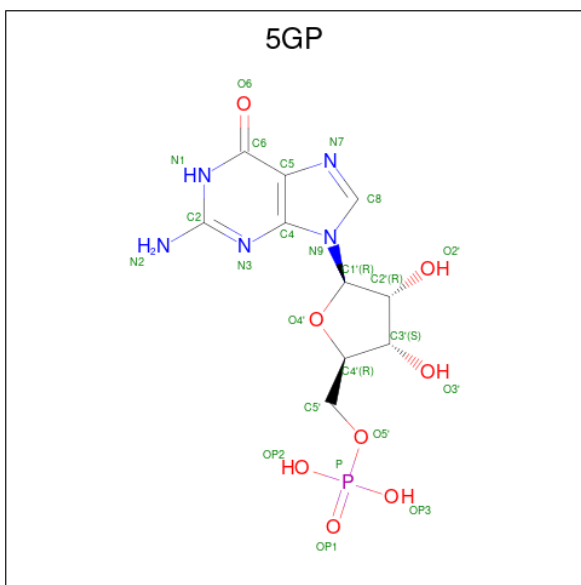
Mol	Chain	Residues	Atoms					AltConf
91	AV	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 92 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



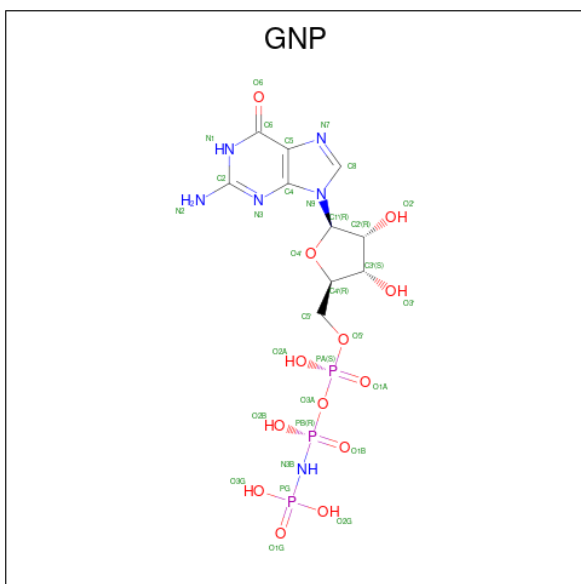
Mol	Chain	Residues	Atoms					AltConf
92	Ag	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 93 is GUANOSINE-5'-MONOPHOSPHATE (CCD ID: 5GP) (formula: $C_{10}H_{14}N_5O_8P$).



Mol	Chain	Residues	Atoms					AltConf
93	BA	1	Total	C	N	O	P	0
			24	10	5	8	1	
93	BA	1	Total	C	N	O	P	0
			24	10	5	8	1	

- Molecule 94 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
94	BC	1	Total	C	N	O	P	0
			32	10	6	13	3	

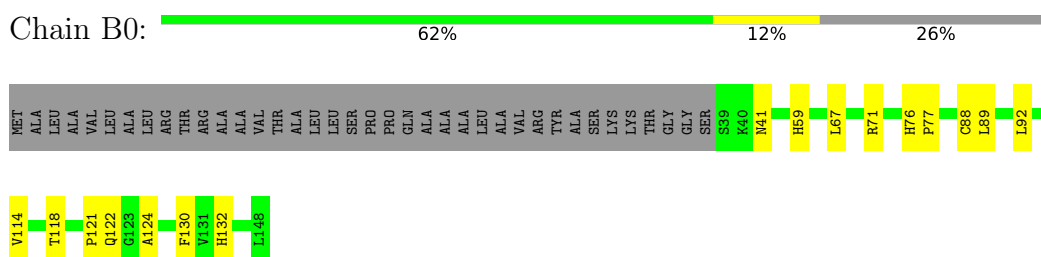
- Molecule 95 is water.

Mol	Chain	Residues	Atoms		AltConf
95	Ag	3	Total 3	O 3	0
95	BC	2	Total 2	O 2	0

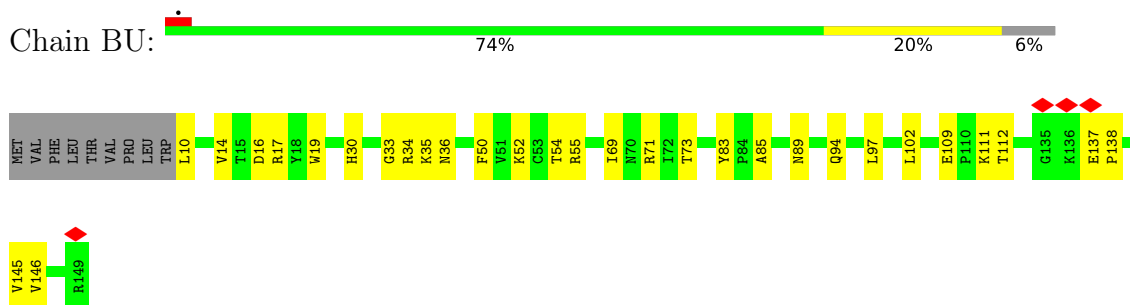
3 Residue-property plots

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

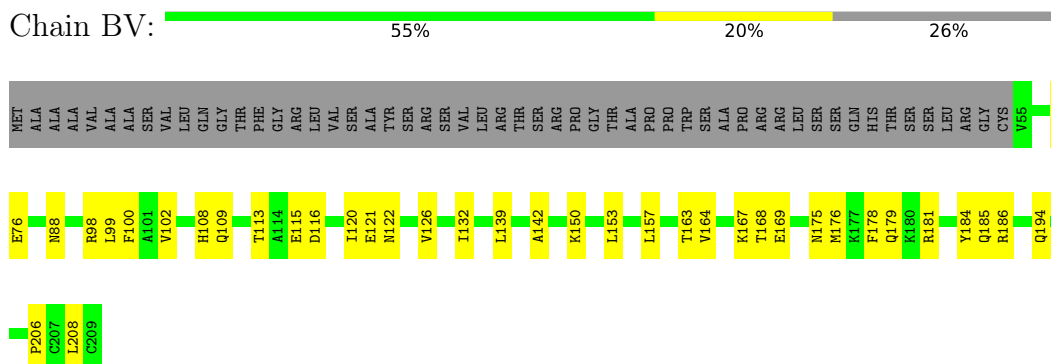
- Molecule 1: Mitochondrial ribosomal protein L27



- Molecule 2: Mitochondrial ribosomal protein L20

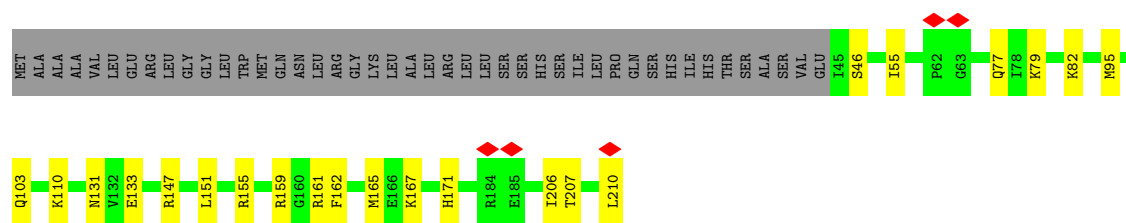


- Molecule 3: Mitochondrial ribosomal protein L21

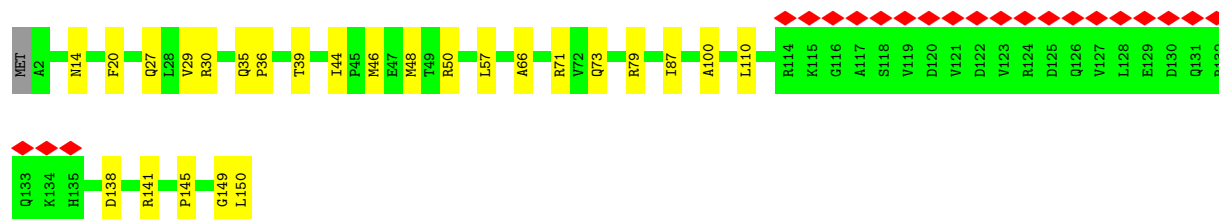
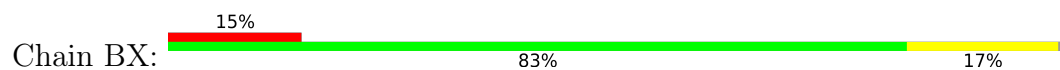


- Molecule 4: uL22m

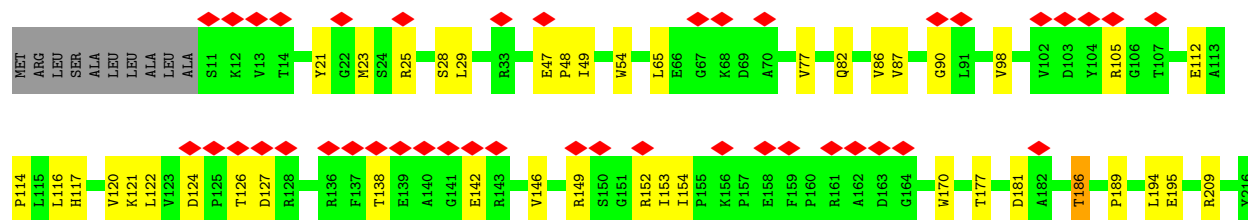
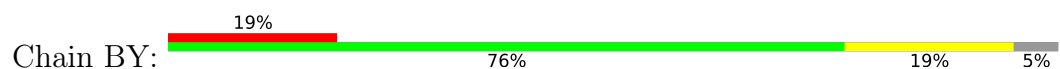




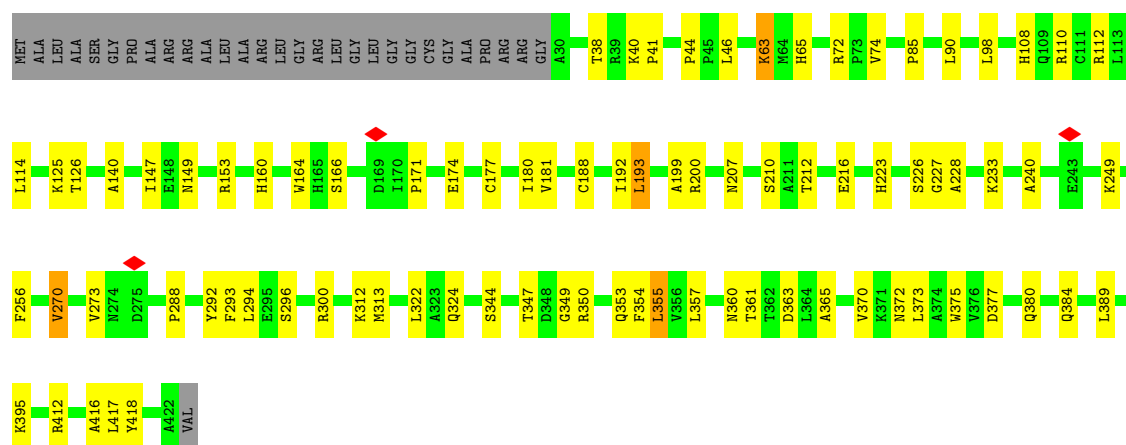
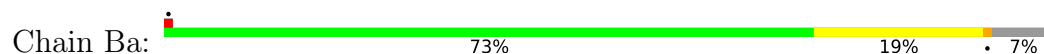
- Molecule 5: uL23m



- Molecule 6: uL24m

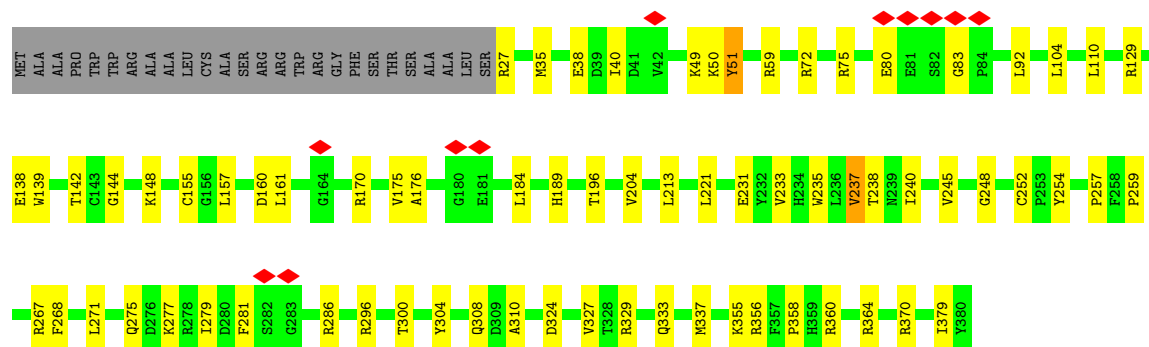


- Molecule 7: Mitochondrial ribosomal protein L37



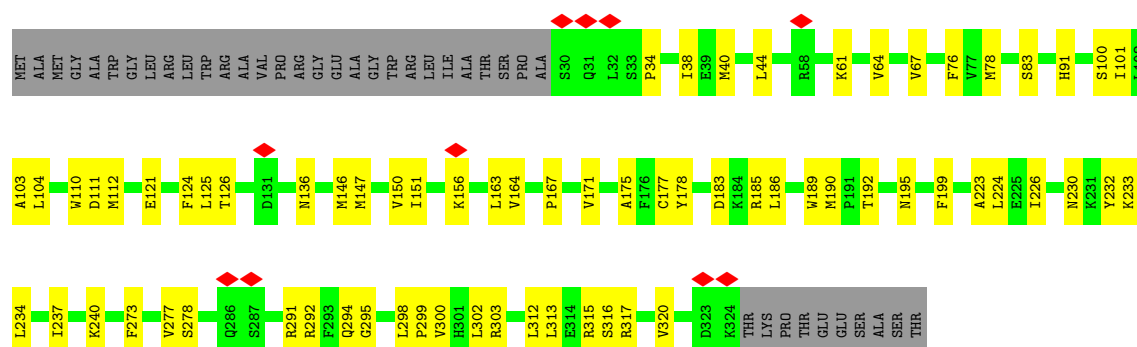
- Molecule 8: Mitochondrial ribosomal protein L38





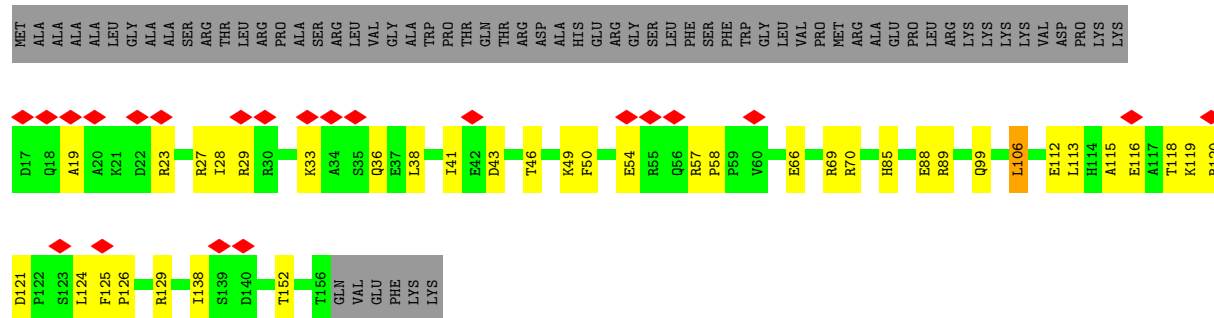
• Molecule 9: Mitochondrial ribosomal protein L39

Chain Bc: 67% 21% 12%



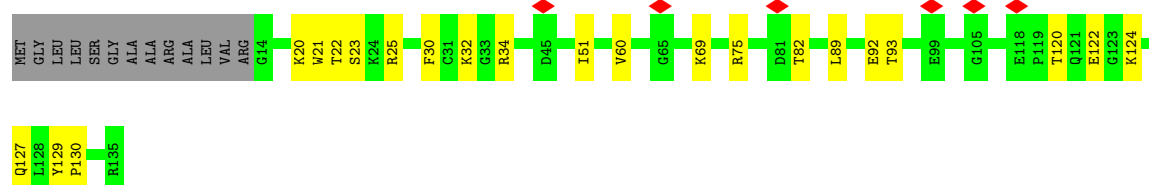
• Molecule 10: Uncharacterized protein

Chain Bd: 11% 50% 18% 32%

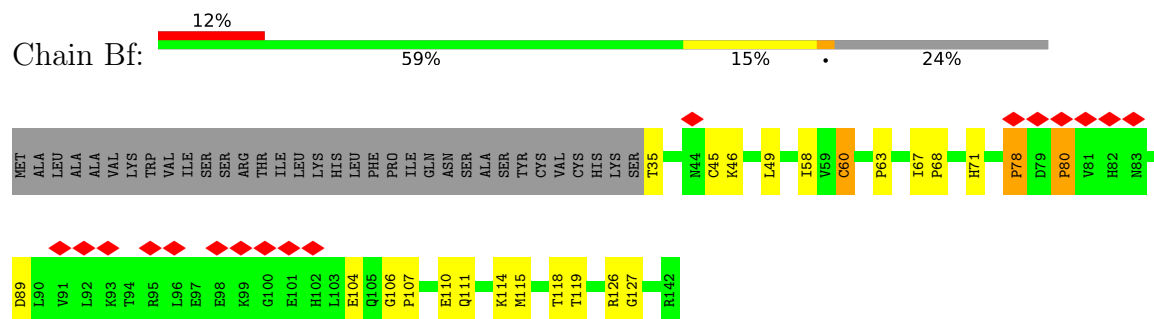


• Molecule 11: Mitochondrial ribosomal protein L41

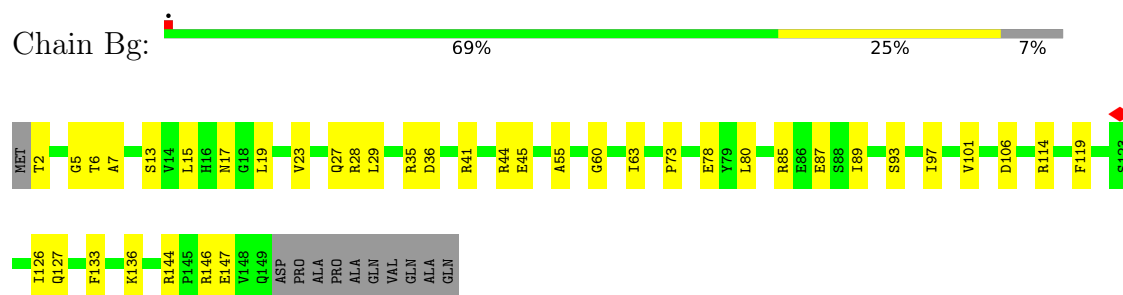
Chain Be: 74% 16% 10%



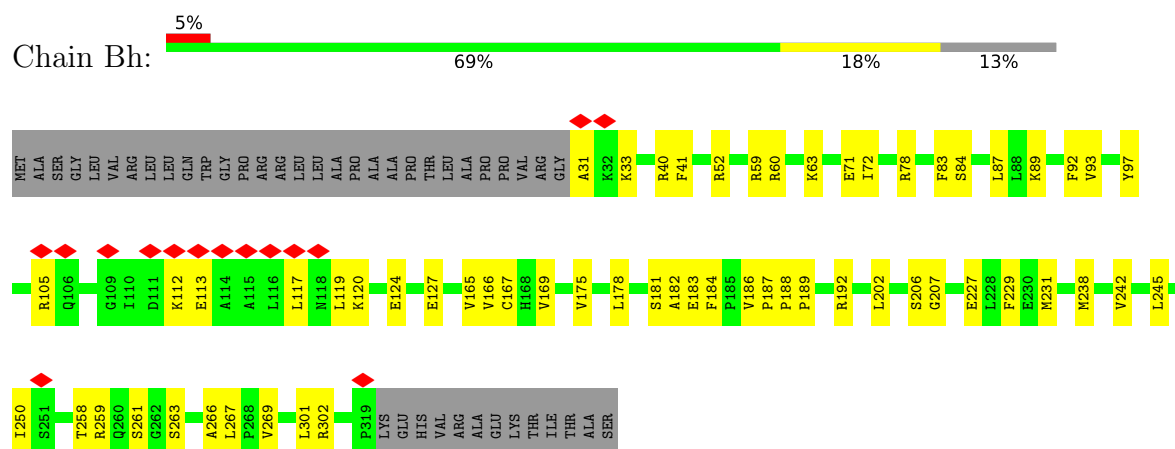
- Molecule 12: mL42



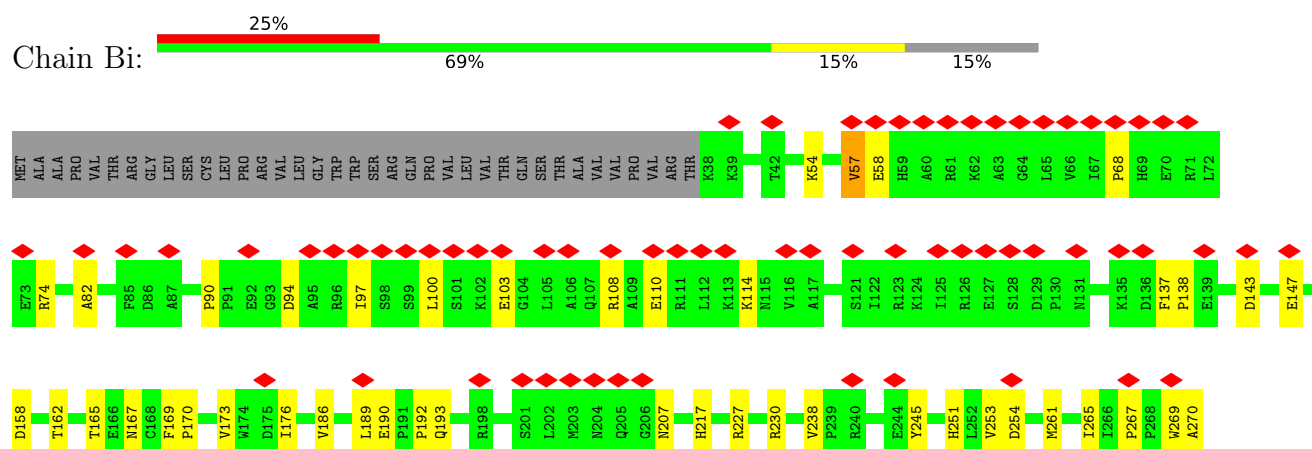
- Molecule 13: Mitochondrial ribosomal protein L43

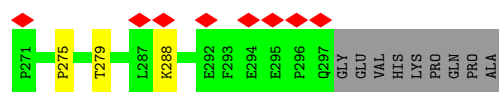


- Molecule 14: mL44

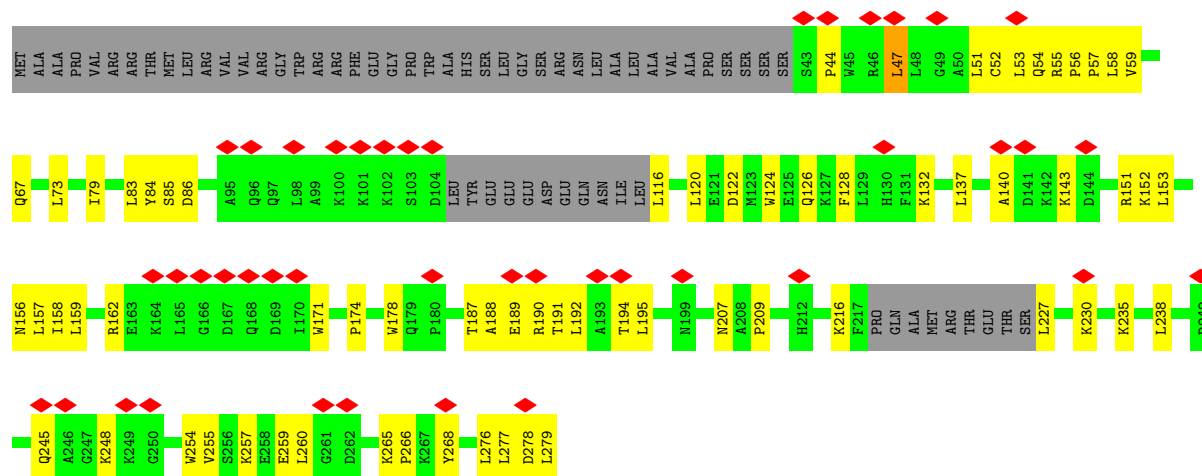


- Molecule 15: Mitochondrial ribosomal protein L45

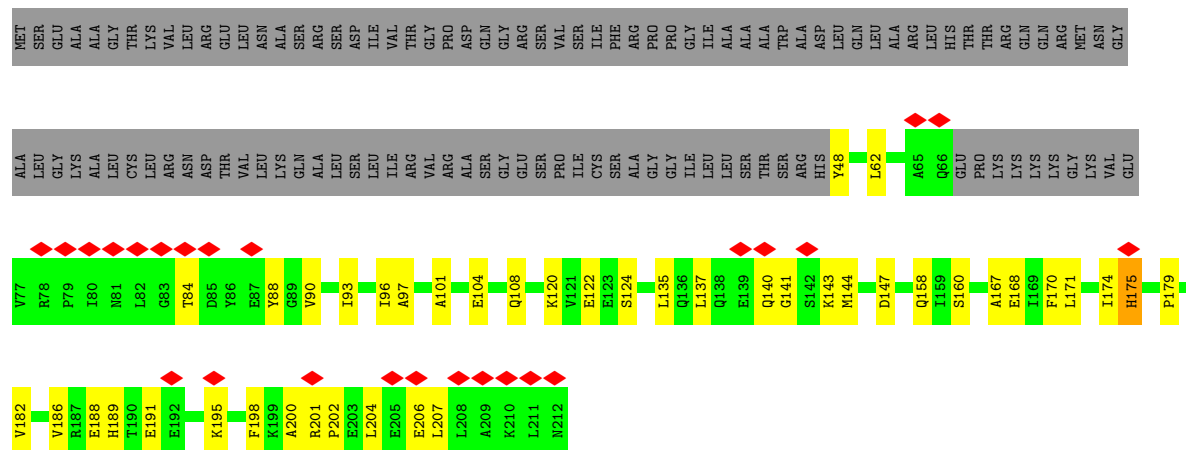
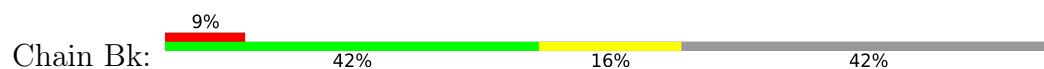




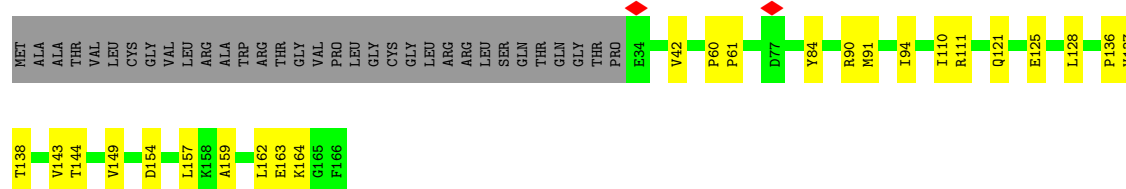
• Molecule 16: Mitochondrial ribosomal protein L46



• Molecule 17: 39S ribosomal protein L48, mitochondrial



• Molecule 18: Mrpl34



- Molecule 19: Mitochondrial ribosomal protein L50



MET VAL ARG ARG LEU ARG GLY LYS ARG GLU CYS THR LEU LEU SER LEU ARG ARG ILE GLY TRP SER TRP VAL THR ALA GLY GLY ILE ARG CYS PHE VAL SER LYS PHE SER LYS MET MET ALA ALA ARG TRP VAL SER GLY LEU ALA ARG ARG ARG LEU THR CYS VAL SER GLY ALA

PRO ARG ARG GLU PHE TRP SER PRO PHE ARG LYS LYS GLN PRO VAL VAL ALA GLU THR VAL GLU VAL LYS LYS PRO GLU THR ILE L51 Q57 S58 R59 P63 D66 L67 R70 L71 E72 V75 G80 S81 S82 V83 P84 S85 Q88 L92 E93 D94 V95 H96

L97 K98 R104 D108 R117 M121 V124 R125 L128 D129 Q136 D137 R138 D142 S147 R148 Y159

- Molecule 20: Mitochondrial ribosomal protein L51



MET ALA GLY SER LEU SER TRP VAL THR GLY ARG GLY LEU TRP GLY ARG LEU PRO LEU THR CYS ARG SER PHE LEU ILE PRO ARG LEU F32 F33 V34 R35 V36 T37 G55 V56 Y57 N65 F66 E67 H69 F70 K71 P77 I78 W79 L80 V83 R113 N122

K126 Y127 R128

- Molecule 21: mL52



MET ALA TRP GLY LEU LEU SER THR VAL ARG ARG LEU HIS CYS GLY THR ALA ALA GLN A23 R28 Q31 E45 D48 D63 R70 A74 R75 R76 V77 V78 L79 L80 K98 E101 E102 E103 K107 K111 Q118 N119 PRO GLN PRO SER

GLN

- Molecule 22: mL53



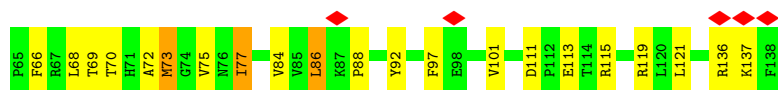
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THR GLY ARG

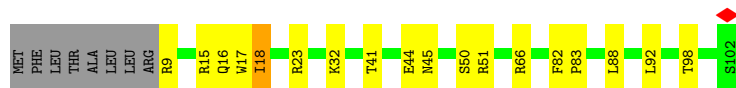
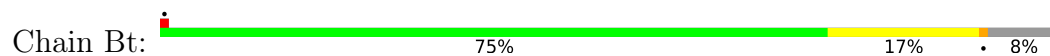
- Molecule 23: mL54



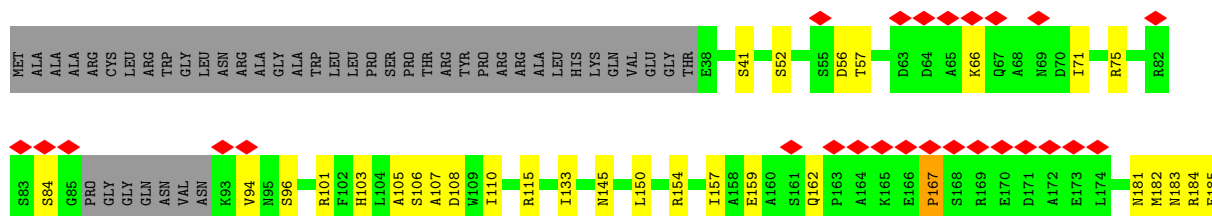
MET ALA ALA ARG ARG LEU PHE GLY PHE ARG ALA ARG SER TRP ALA TRP ARG ALA TRP GLU LEU SER ASP ALA ALA VAL VAL SER GLY ARG LEU HIS VAL ARG ASN TYR ALA LYS ARG PRO VAL ILE LYS GLY GLY LYS GLY LYS VAL VAL VAL GLY E54 P59 C62 T63 D64



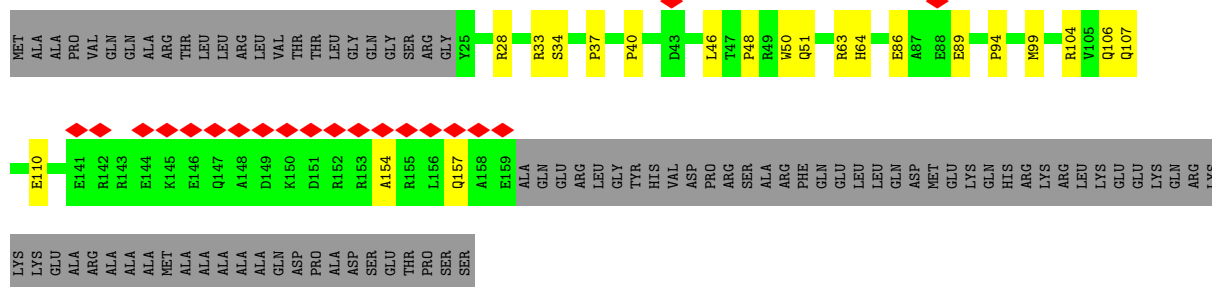
- Molecule 24: Mitochondrial ribosomal protein L57



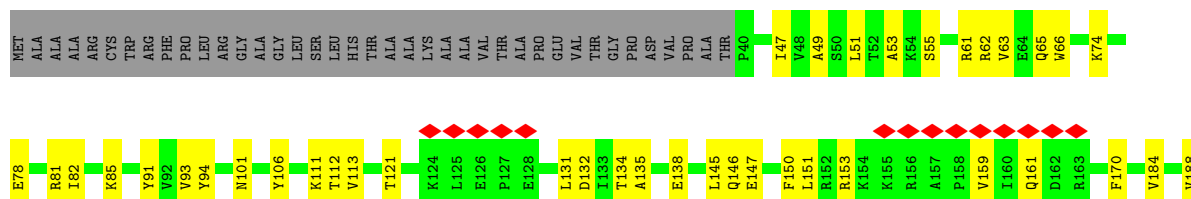
- Molecule 25: mL62 (ICT1)

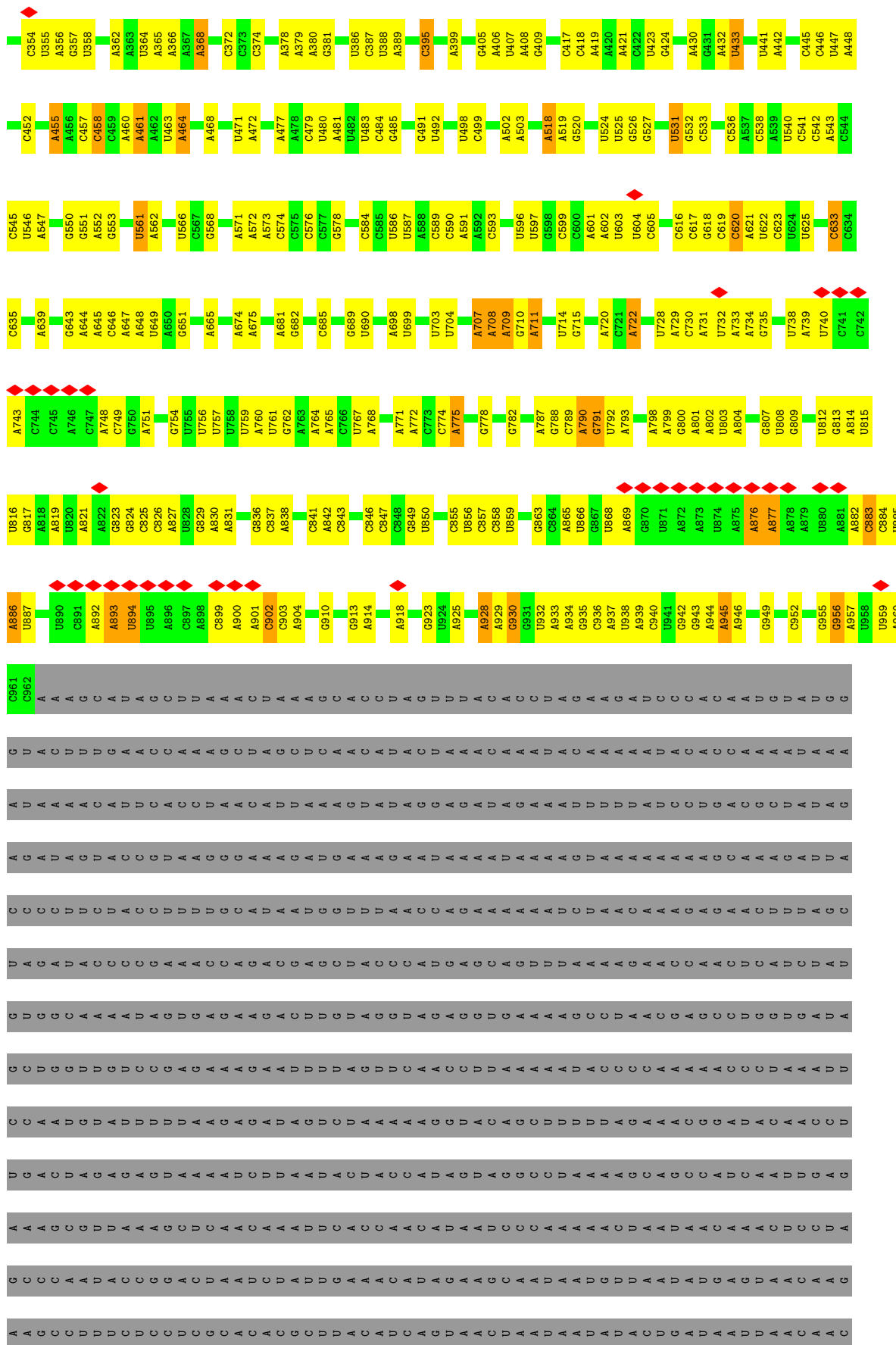


- Molecule 26: mL64



- Molecule 27: 39S ribosomal protein S30, mitochondrial









U A C C A A G C C C U C C U C C G U C C C C U A A A C C U U A A G G A A A U U U A A G G U U U A A C A A C A A G A A G A A G C C U U C A A A G
C U C U A A A G U U A A G U A C A A A A G U A C A C U U U A A C U C C C U G A A A A A C C U A A A G G A C C U U A U C C U A
C A U C A A A U U G A A A U C C A A A A U C A A A C C U U A A A A G C C A A A U C C U C A C C A A G A A U U G G U G G G A
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C U G U C U U A A G A U U A C A A G U C U U A A A U G C U U A A C C A G C C A U U U A C C U A A A U C G U
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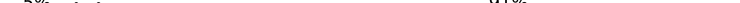
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[illegible]

- Molecule 30: 12S rRNA

Chain BA:  5% . . 91%

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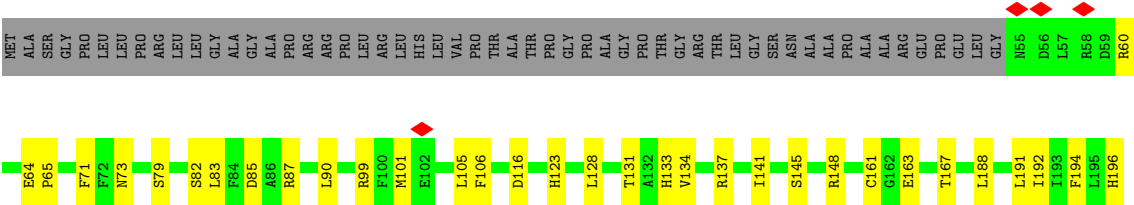
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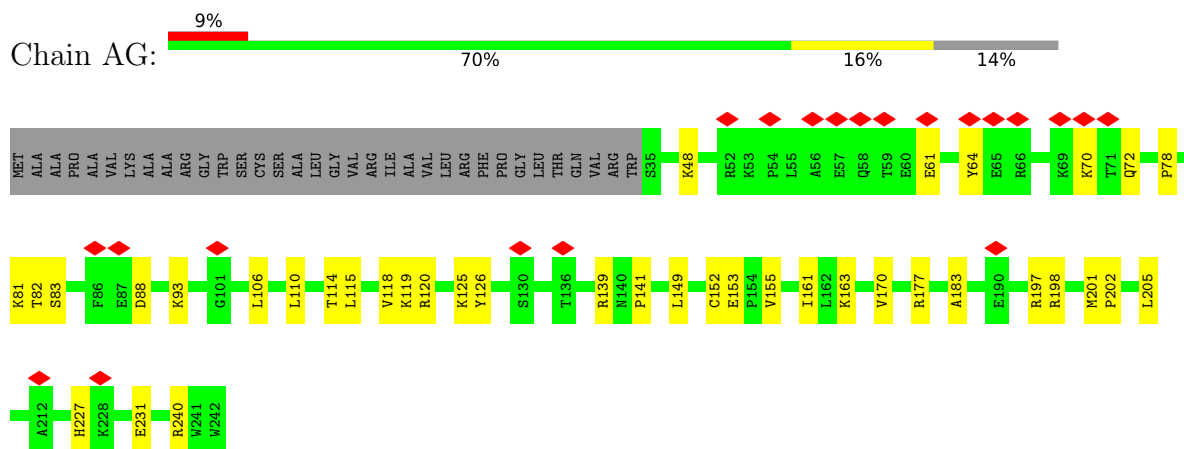


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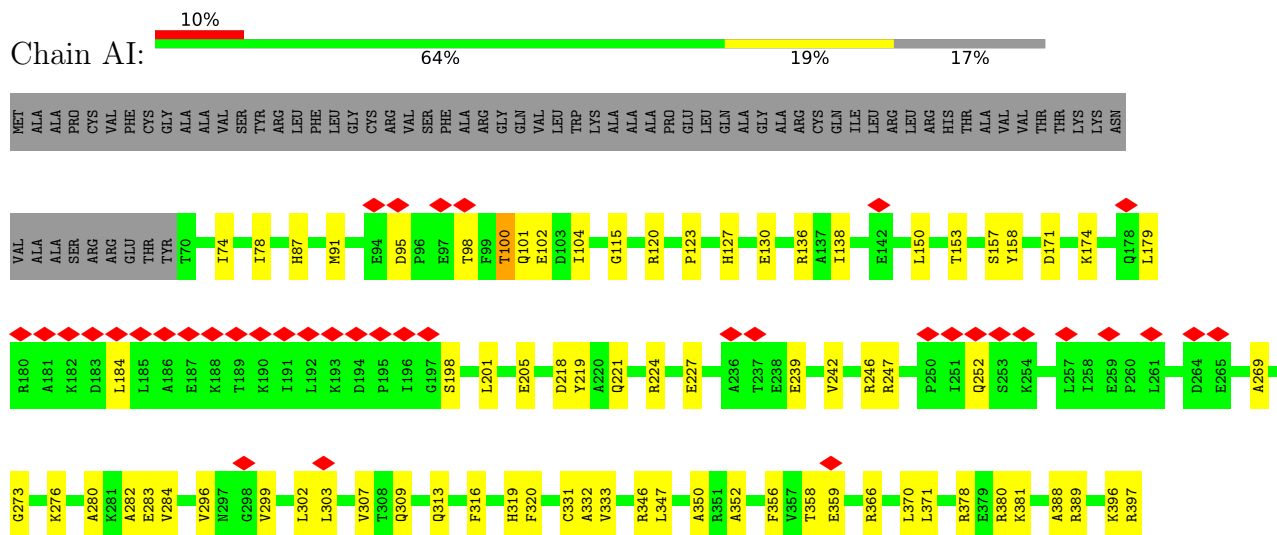
● Molecule 31: Mitochondrial ribosomal protein S2



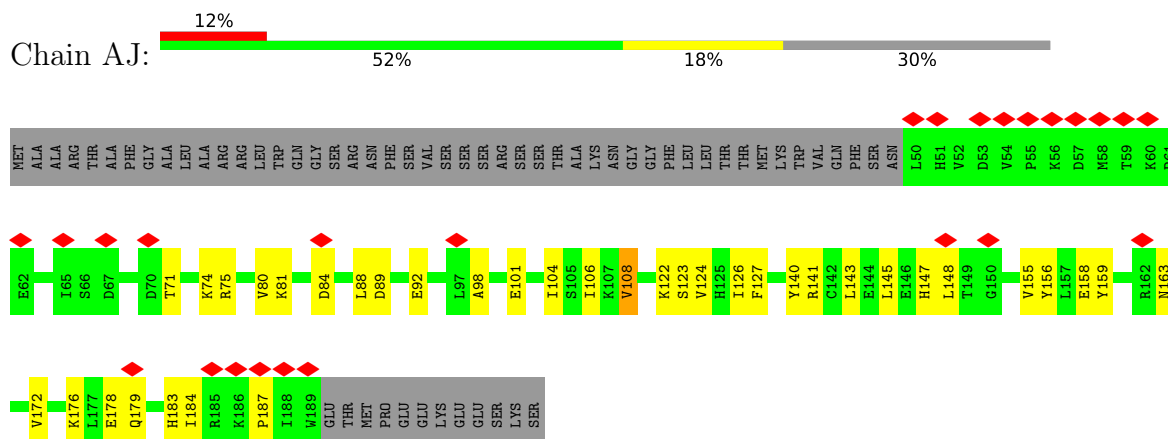
- Molecule 35: Mitochondrial ribosomal protein S7



- Molecule 36: uS9m

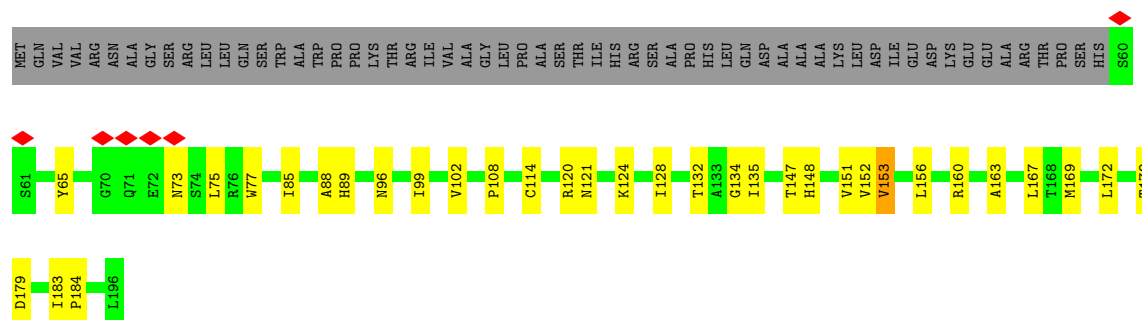


- Molecule 37: Mitochondrial ribosomal protein S10

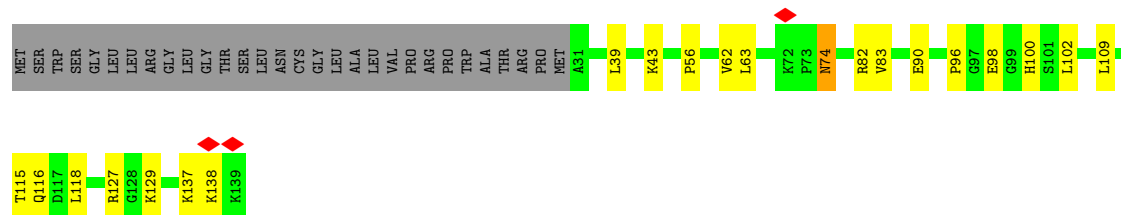


- Molecule 38: uS11m

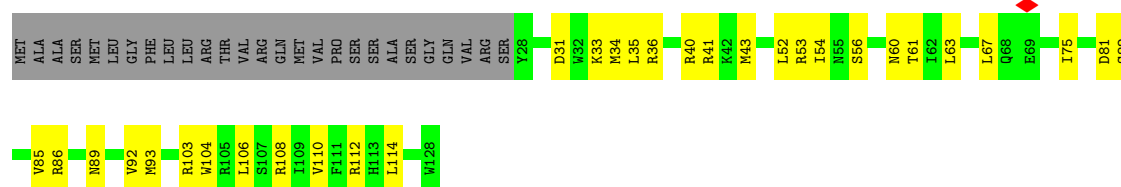




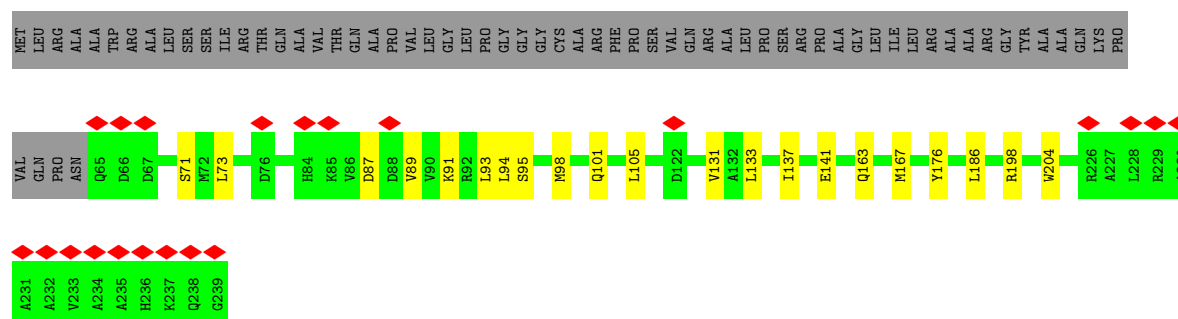
• Molecule 39: Mitochondrial ribosomal protein S12



• Molecule 40: Mitochondrial ribosomal protein S14

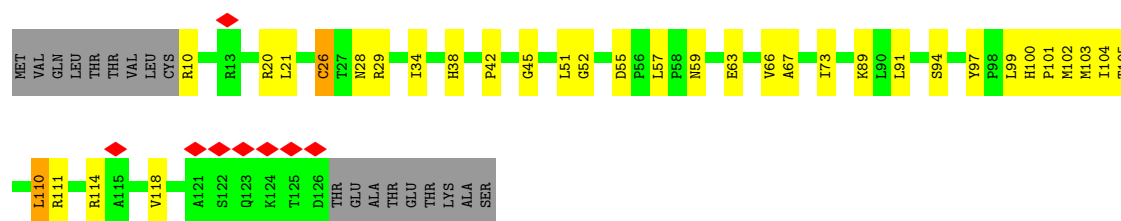


• Molecule 41: uS15m

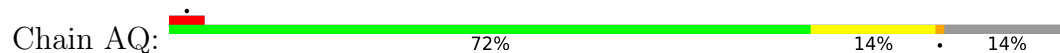


• Molecule 42: 28S ribosomal protein S16, mitochondrial

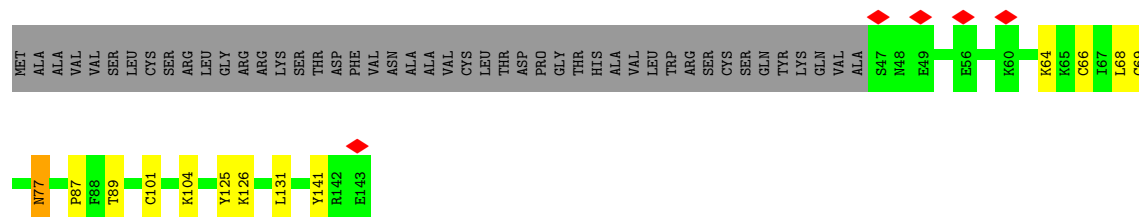




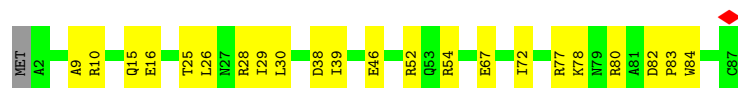
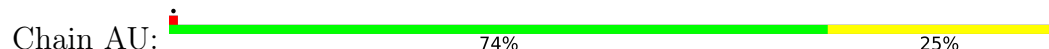
- Molecule 43: uS17m



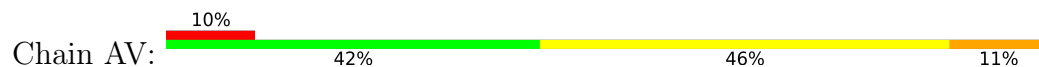
- Molecule 44: Mitochondrial ribosomal protein S18C



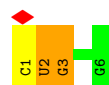
- Molecule 45: bS21m



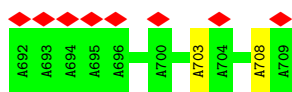
- Molecule 46: fMet-tRNA^{Met} (P site)



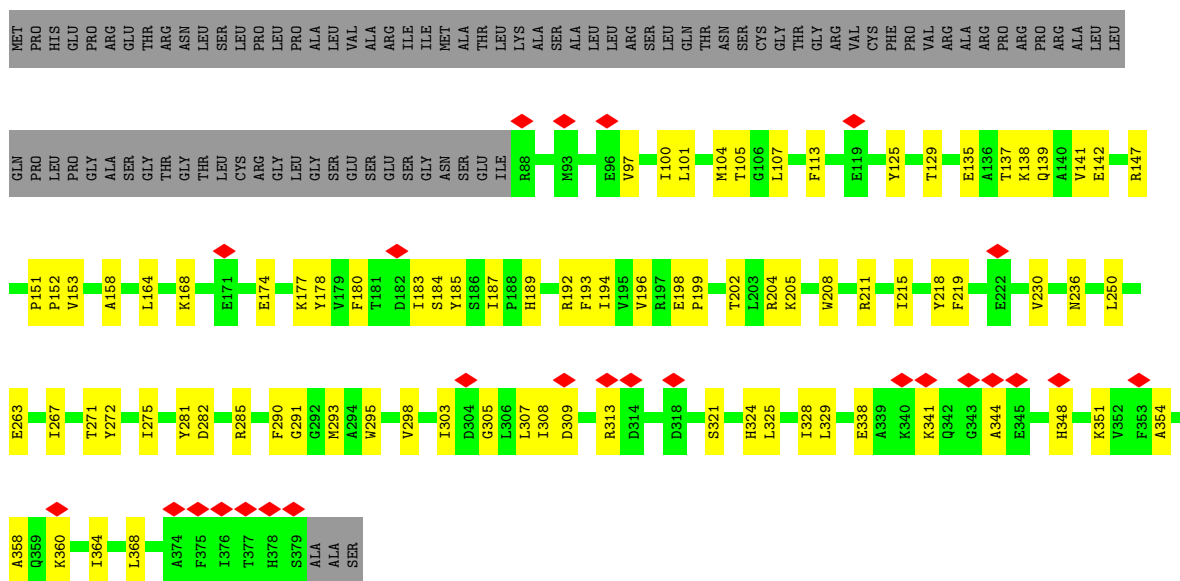
- Molecule 47: mRNA



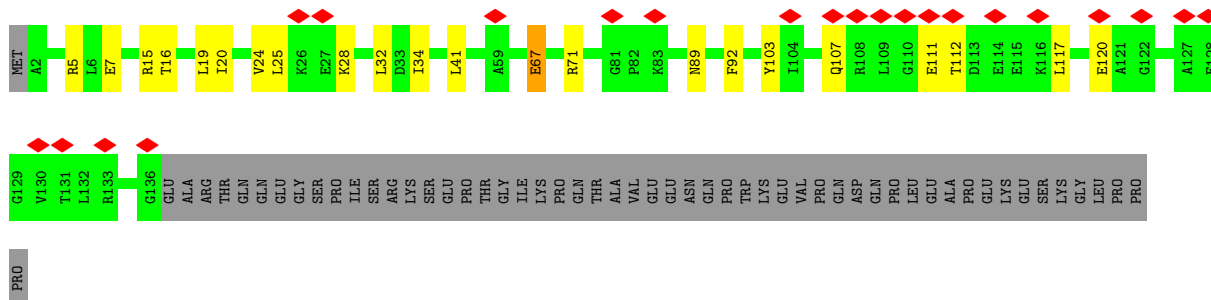
- Molecule 48: unknown peptide



Chain Aa:

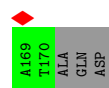


Chain Ab:



Chain Ac: 79% 18%





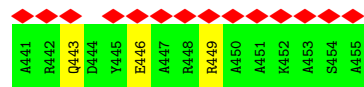
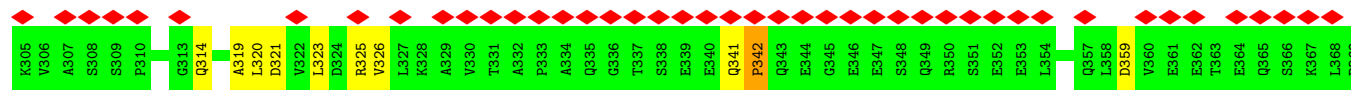
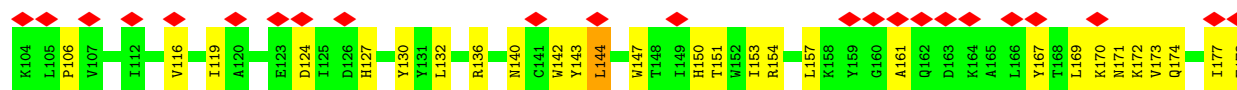
• Molecule 52: Mitochondrial ribosomal protein S26

Chain Ad: 63% 23% 14%



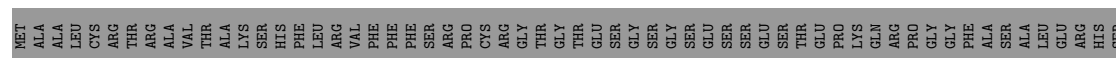
• Molecule 53: Mitochondrial ribosomal protein S27

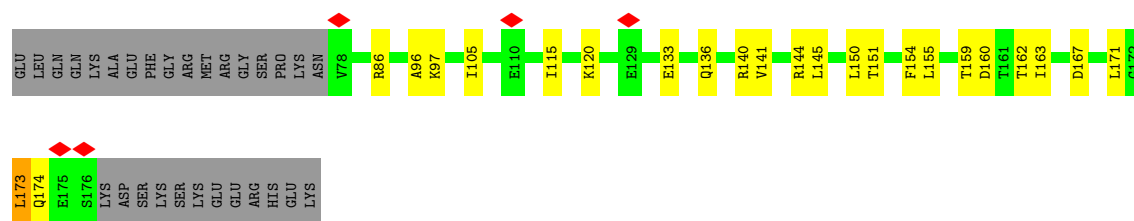
Chain Ae: 42% 63% 27% 9%



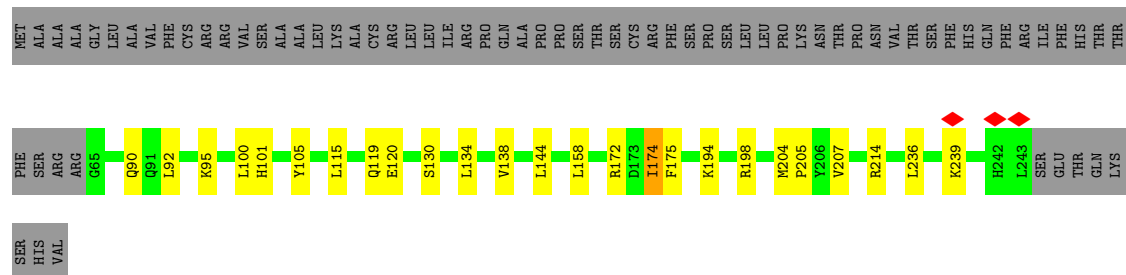
• Molecule 54: Mitoribosomal protein ms28, mrps28

Chain Af: 40% 12% 47%

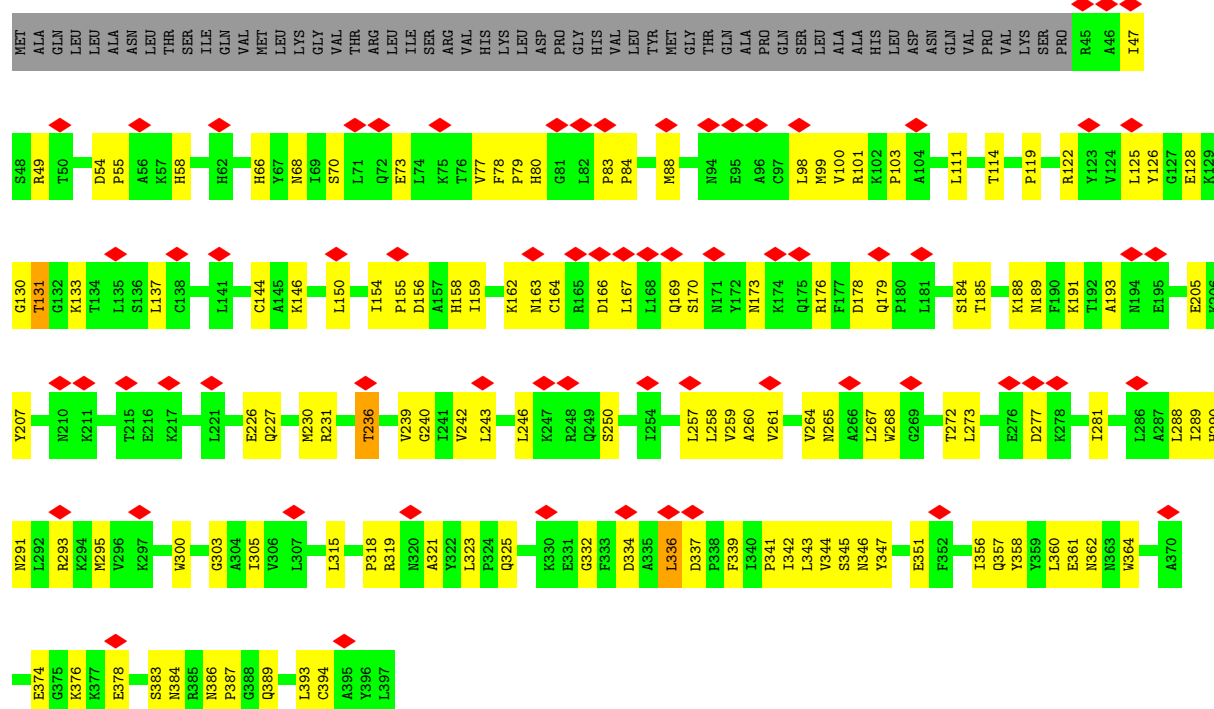




- Molecule 55: Mitochondrial ribosomal protein L47

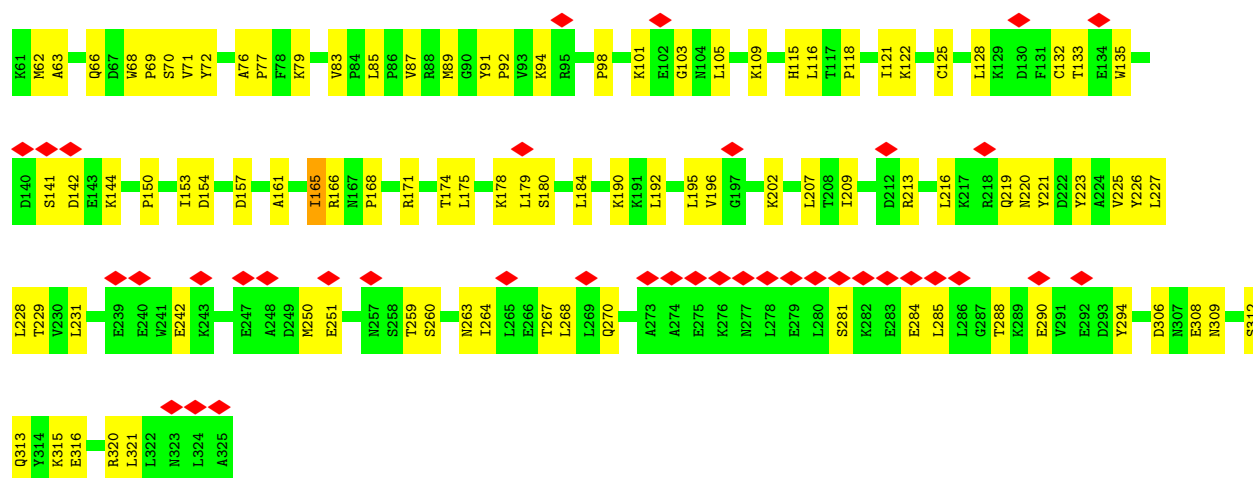


- Molecule 56: Death associated protein 3

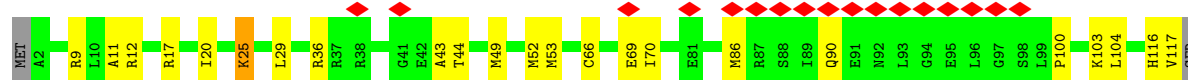
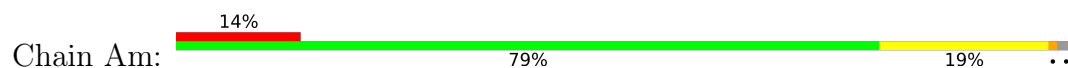


- Molecule 57: Mitochondrial ribosomal protein S31

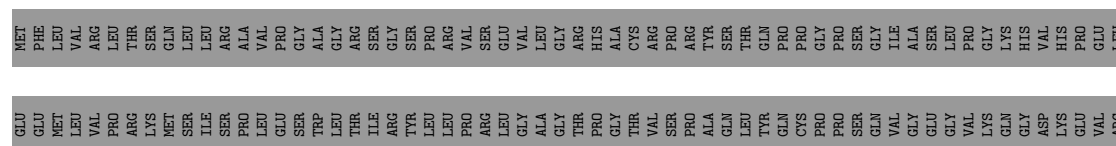




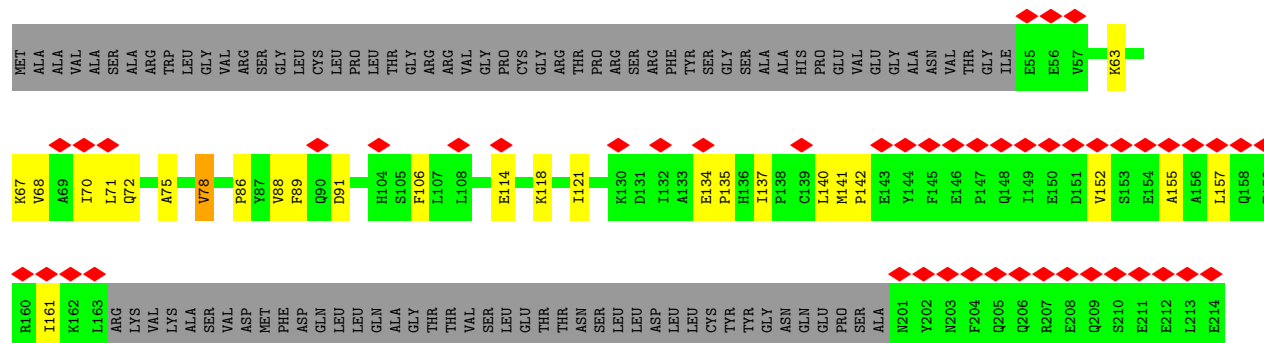
- Molecule 61: mS37

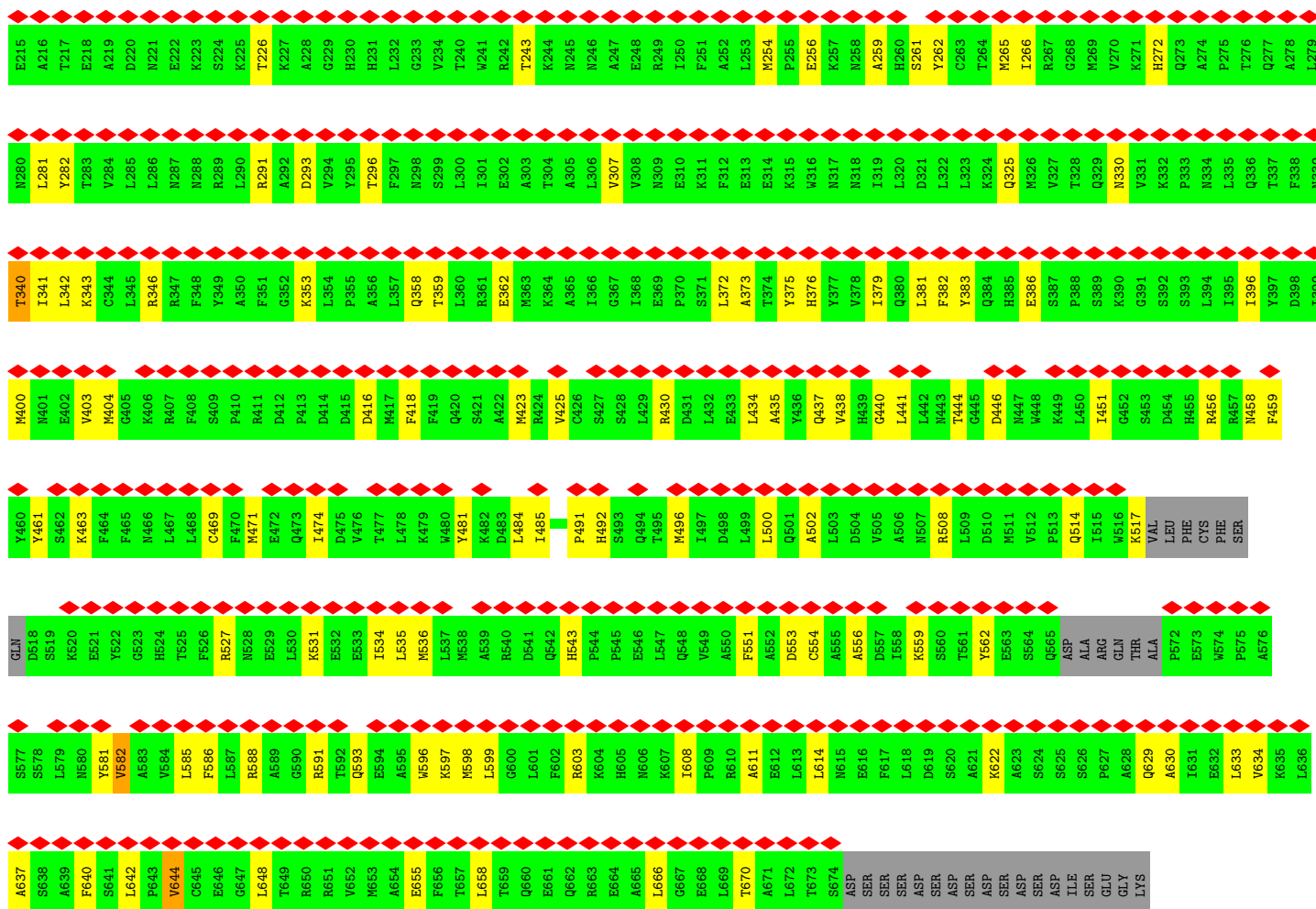


- Molecule 62: Aurora kinase A interacting protein 1



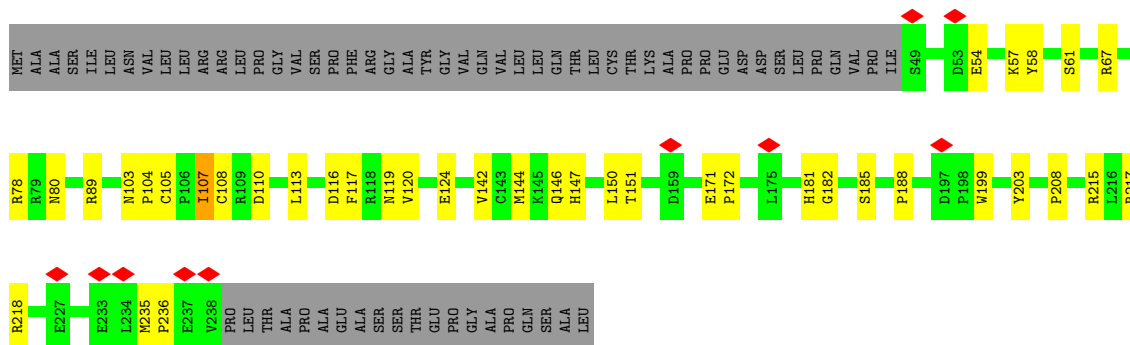
- Molecule 63: Pentatricopeptide repeat domain 3





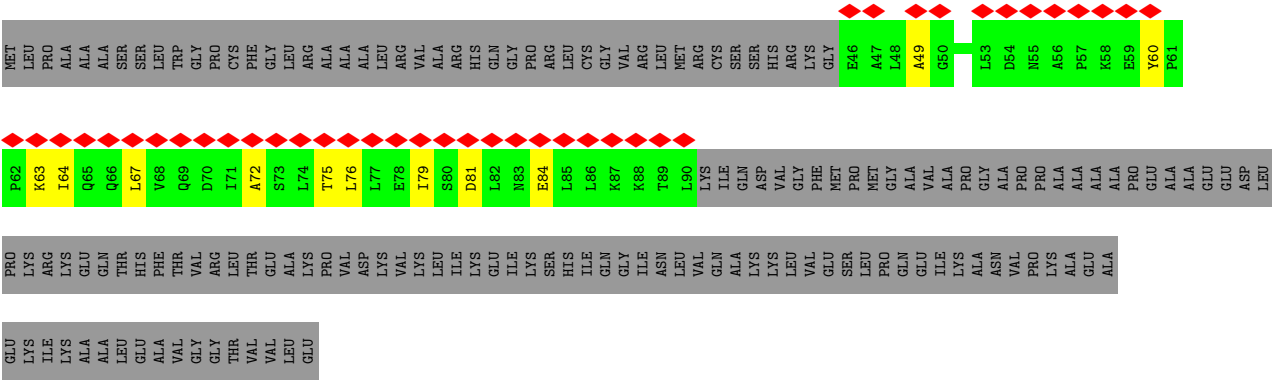
- Molecule 64: 28S ribosomal protein S18b, mitochondrial

Chain Ap: 58% 15% 26%

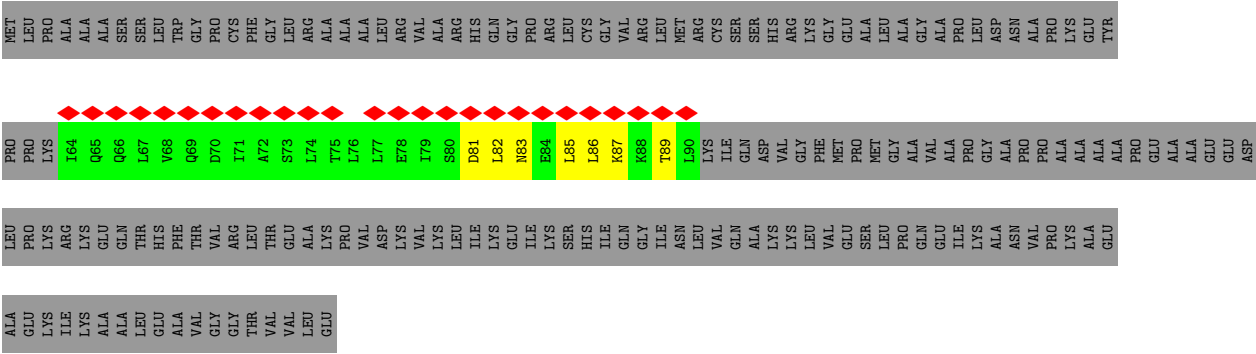


- Molecule 65: Mitochondrial ribosomal protein L12

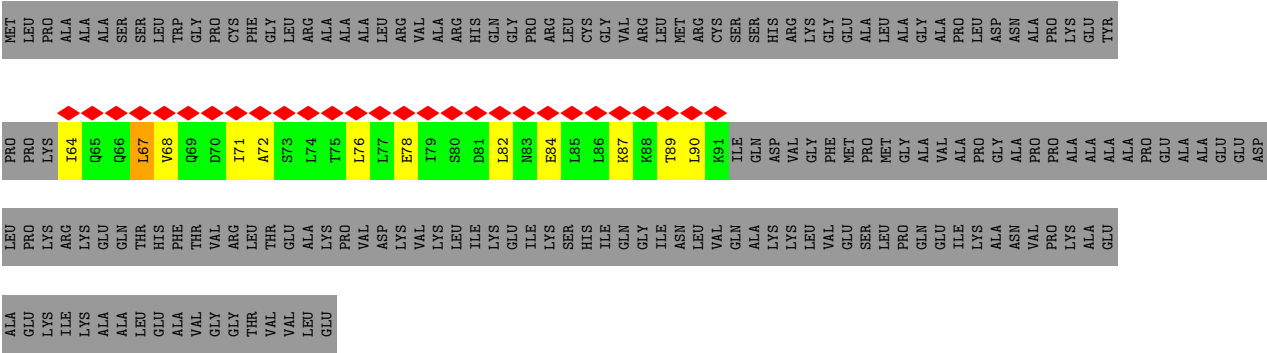
Chain CL: 21% 17% 6% 77%



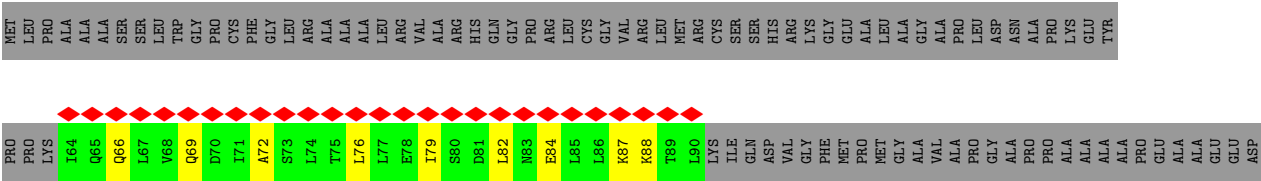
● Molecule 65: Mitochondrial ribosomal protein L12



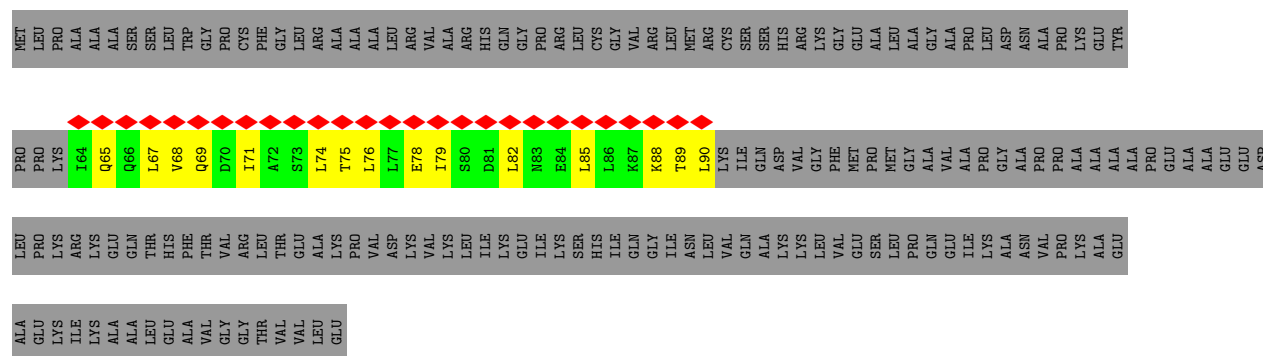
● Molecule 65: Mitochondrial ribosomal protein L12



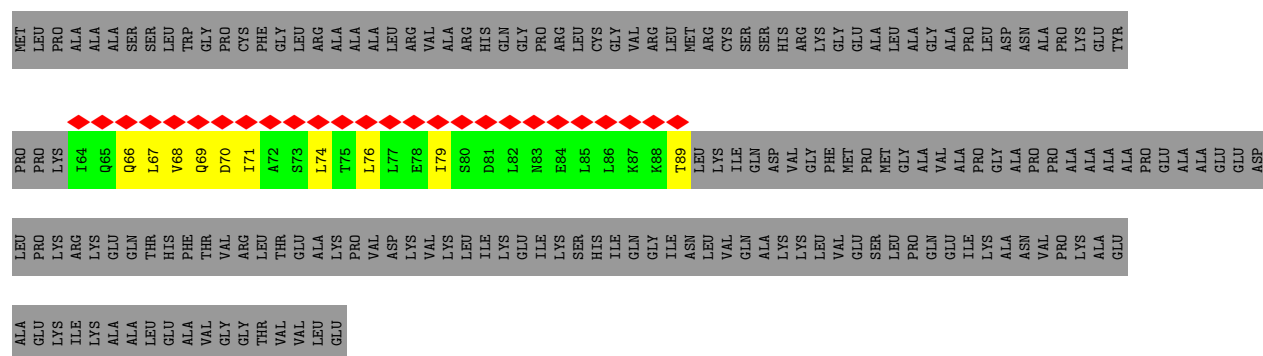
● Molecule 65: Mitochondrial ribosomal protein L12



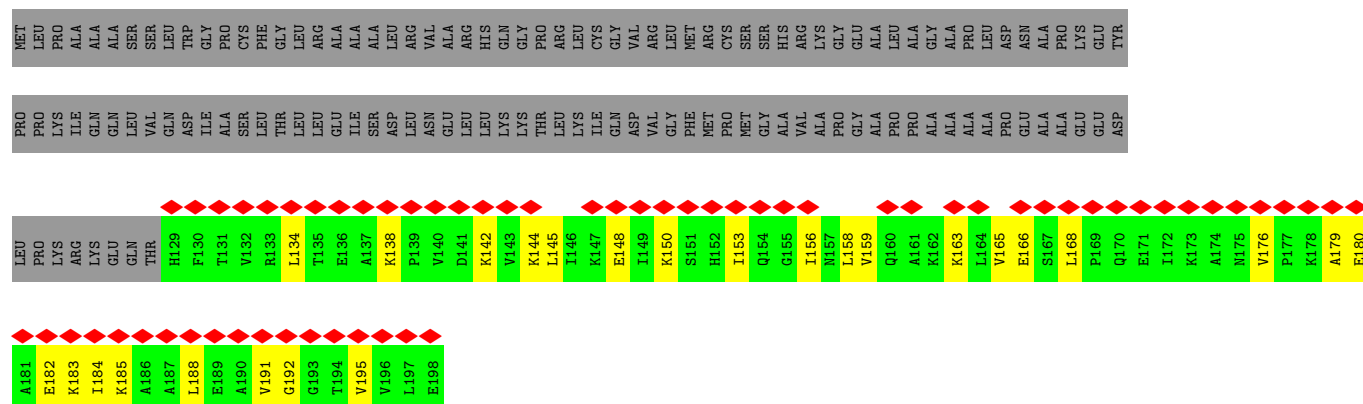
- Molecule 65: Mitochondrial ribosomal protein L12



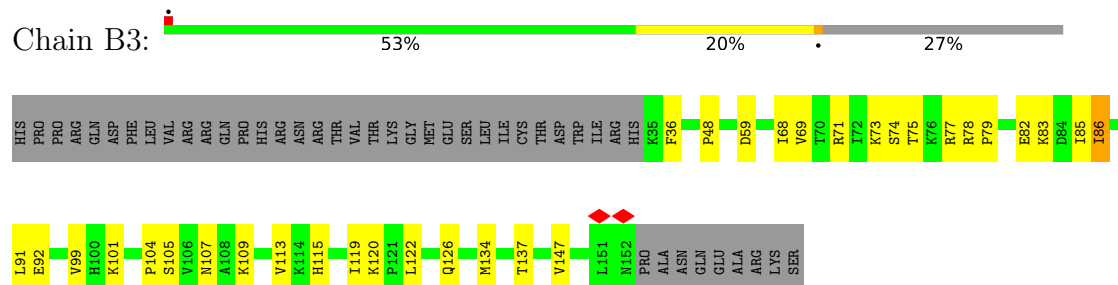
- Molecule 65: Mitochondrial ribosomal protein L12



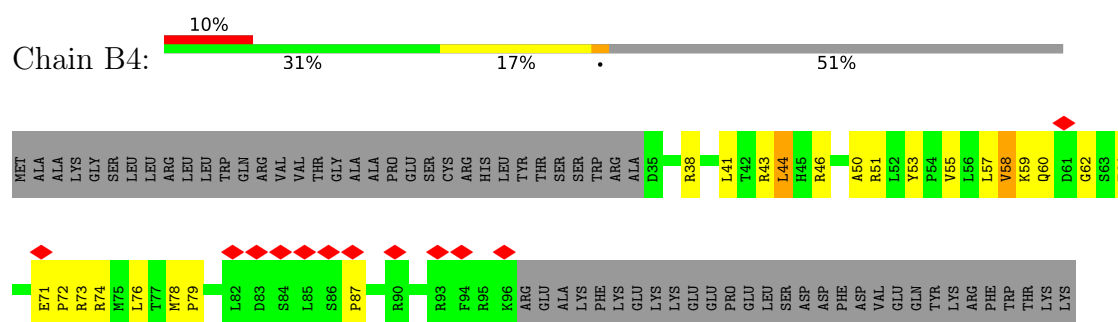
- Molecule 65: Mitochondrial ribosomal protein L12



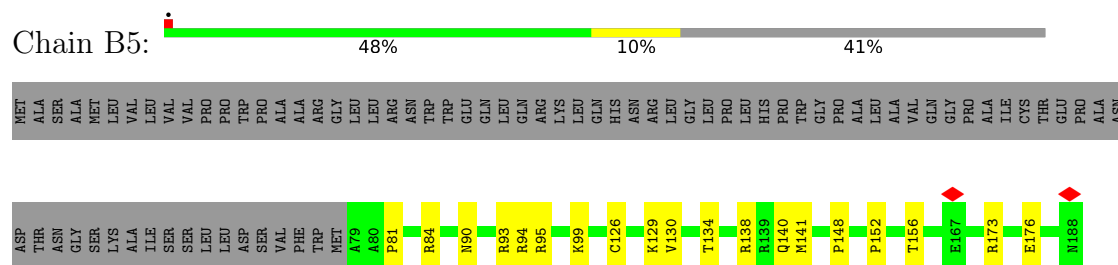
- Molecule 66: uL30m



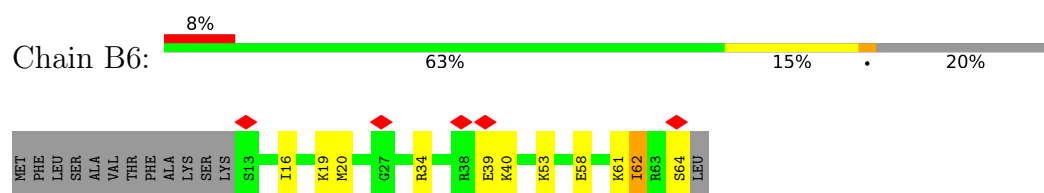
- Molecule 67: bL31m



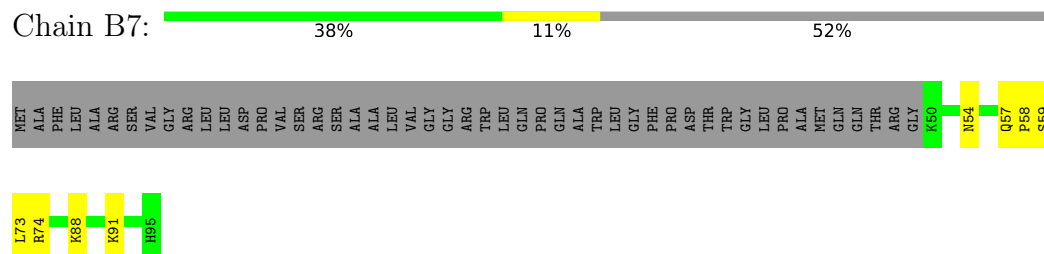
- Molecule 68: bL32m



- Molecule 69: bL33m



- Molecule 70: Mitochondrial ribosomal protein L34



- Molecule 71: Mitochondrial ribosomal protein L35

Device Type	Percentage
Smartphone	43%
Tablet	7%
Feature phone	49%

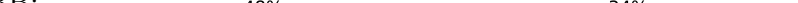


- Molecule 72: Ribosomal protein

Response	Percentage
Yes	31%
No	7%
Don't know	62%

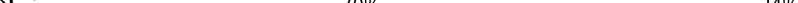


- Molecule 73: CP tRNAPhe

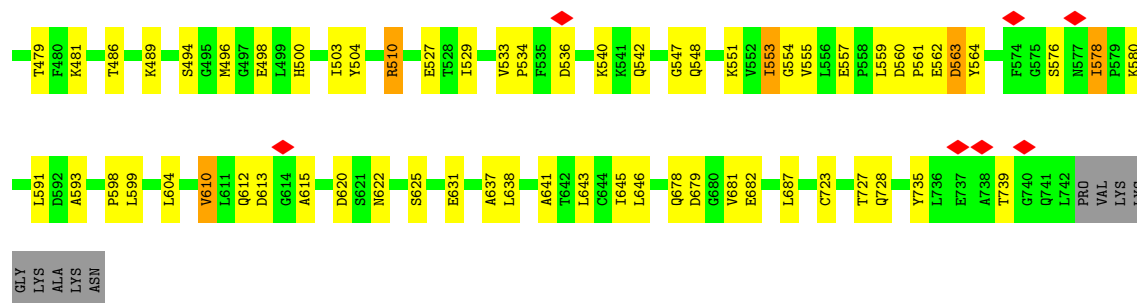
Chain BB: 



- Molecule 74: Elongation factor G, mitochondrial

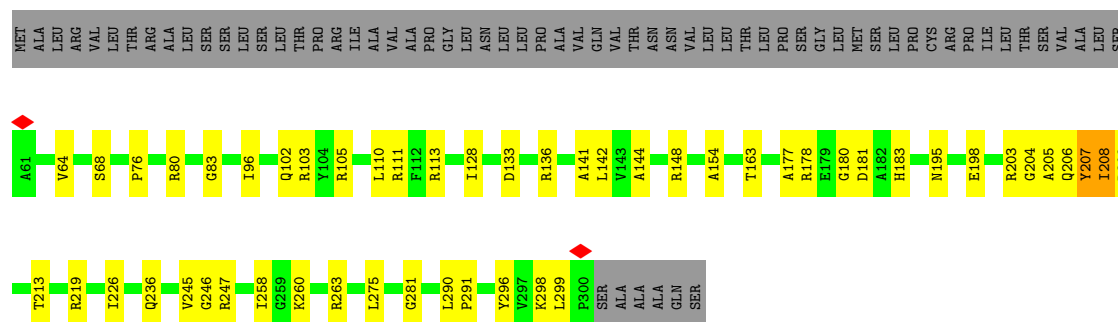
Chain BC: 





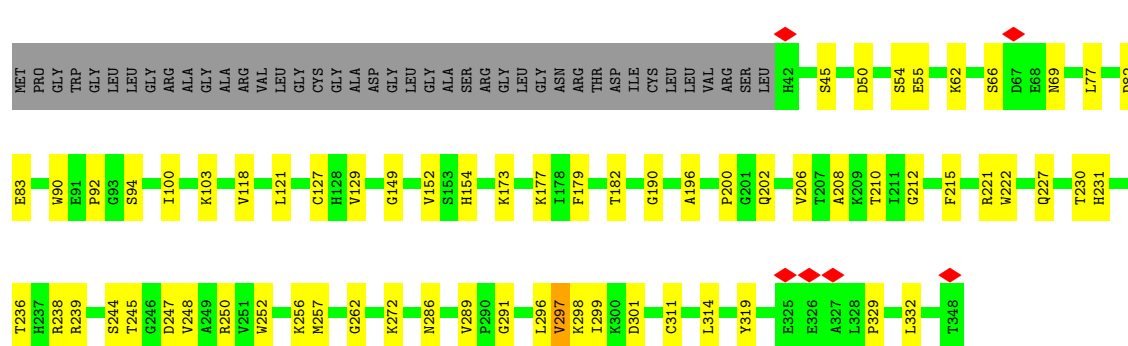
• Molecule 75: uL2m

Chain BD: 61% 16% 22%



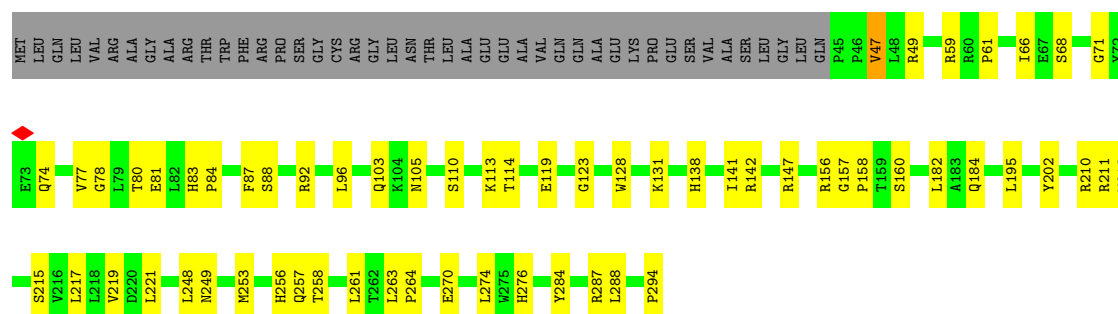
• Molecule 76: ICT1

Chain BE: 69% 19% 12%



• Molecule 77: Mitochondrial ribosomal protein L4

Chain BF: 64% 21% 15%



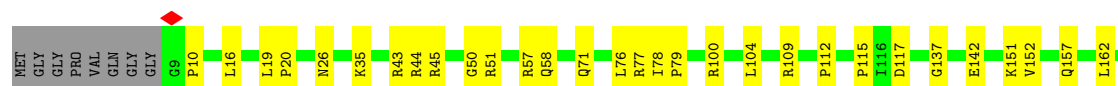
- Molecule 82: uL14m

Chain BO: 



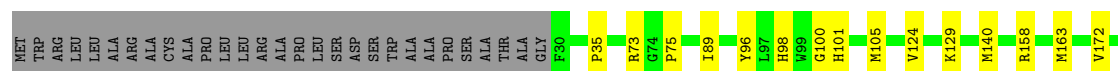
- Molecule 83: uL15m

Chain BP: 



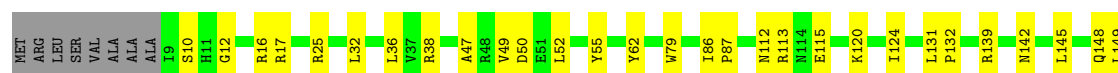
- Molecule 84: uL16m

Chain BQ: 



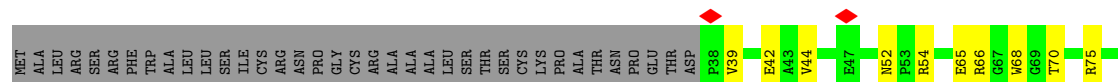
- Molecule 85: Uncharacterized protein

Chain BR: 



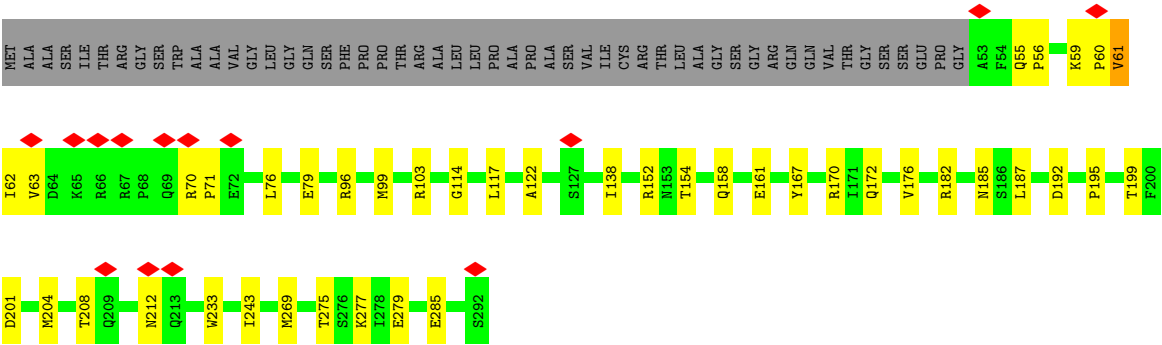
- Molecule 86: Mitochondrial ribosomal protein L18

Chain BS: 





• Molecule 87: Mitochondrial ribosomal protein L19



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	97764	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.676	Depositor
Minimum map value	-0.297	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	444.8, 444.8, 444.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.39, 1.39, 1.39	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5GP, GNP, SPM, MG, GTP, ZN, FME

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	B0	0.12	0/880	0.26	0/1189
2	BU	0.13	0/1179	0.32	0/1578
3	BV	0.12	0/1256	0.29	0/1706
4	BW	0.12	0/1407	0.28	0/1891
5	BX	0.13	0/1211	0.31	0/1646
6	BY	0.10	0/1719	0.29	0/2329
7	Ba	0.11	0/3267	0.28	0/4455
8	Bb	0.12	0/3047	0.30	0/4139
9	Bc	0.10	0/2464	0.27	0/3330
10	Bd	0.12	0/1203	0.30	0/1622
11	Be	0.10	0/1000	0.27	0/1345
12	Bf	0.13	0/851	0.47	2/1159 (0.2%)
13	Bg	0.13	0/1191	0.32	0/1614
14	Bh	0.11	0/2372	0.29	0/3211
15	Bi	0.11	0/2199	0.29	0/2980
16	Bj	0.11	0/1811	0.30	0/2436
17	Bk	0.13	0/1270	0.30	0/1714
18	Bl	0.11	0/1135	0.28	0/1549
19	Bm	0.10	0/917	0.25	0/1248
20	Bn	0.12	0/860	0.32	0/1150
21	Bo	0.11	0/787	0.26	0/1056
22	Bp	0.11	0/752	0.36	0/1013
23	Bq	0.13	0/717	0.39	1/971 (0.1%)
24	Bt	0.13	0/798	0.33	0/1073
25	Bu	0.10	0/1214	0.36	1/1630 (0.1%)
26	Bv	0.11	0/1157	0.29	0/1560
27	Bw	0.12	0/3206	0.29	0/4354
28	B1	0.10	0/2093	0.26	0/2835
29	Bx	0.13	0/1364	0.30	0/1849
30	AA	0.09	0/22851	0.21	0/35576
30	BA	0.13	0/36784	0.25	0/57270
31	AB	0.13	0/1804	0.34	0/2445

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	AC	0.12	0/1105	0.33	0/1496
33	AE	0.12	0/2784	0.30	0/3732
34	AF	0.13	0/999	0.33	0/1347
35	AG	0.11	0/1763	0.28	0/2368
36	AI	0.12	0/2706	0.31	0/3632
37	AJ	0.12	0/1181	0.30	0/1597
38	AK	0.11	0/1027	0.29	0/1389
39	AL	0.11	0/858	0.30	0/1152
40	AN	0.12	0/874	0.33	0/1171
41	AO	0.13	0/1473	0.33	0/1970
42	AP	0.13	0/954	0.35	0/1284
43	AQ	0.09	0/894	0.25	0/1213
44	AR	0.12	0/802	0.32	0/1079
45	AU	0.12	0/745	0.32	0/993
46	AV	0.12	0/1673	0.26	0/2602
47	AX	0.13	0/142	0.33	0/219
48	AZ	0.05	0/89	0.19	0/123
49	Aa	0.12	0/2428	0.30	0/3279
50	Ab	0.12	0/1126	0.31	0/1514
51	Ac	0.13	0/1399	0.30	0/1881
52	Ad	0.14	0/1490	0.34	0/2005
53	Ae	0.14	0/3171	0.38	1/4292 (0.0%)
54	Af	0.11	0/790	0.33	0/1064
55	B2	0.11	0/1586	0.28	0/2123
56	Ag	0.12	0/2945	0.33	0/3984
57	Ah	0.14	0/1045	0.33	0/1409
58	Ai	0.13	0/841	0.35	0/1121
59	Aj	0.11	0/1835	0.31	0/2484
60	Ak	0.12	0/2268	0.31	0/3069
61	Am	0.14	0/947	0.37	0/1268
62	An	0.14	0/650	0.35	0/858
63	Ao	0.13	0/4625	0.33	0/6267
64	Ap	0.11	0/1616	0.29	0/2195
65	CL	0.15	0/319	0.37	0/435
65	DL	0.13	0/212	0.36	0/286
65	EL	0.11	0/221	0.26	0/297
65	FL	0.12	0/212	0.33	0/286
65	GL	0.15	0/212	0.36	0/286
65	HL	0.12	0/204	0.32	0/275
65	LL	0.12	0/542	0.35	0/729
66	B3	0.12	0/993	0.30	0/1341
67	B4	0.11	0/481	0.41	1/653 (0.2%)
68	B5	0.12	0/917	0.29	0/1227

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
69	B6	0.10	0/430	0.27	0/570
70	B7	0.13	0/395	0.31	0/524
71	B8	0.12	0/853	0.28	0/1136
72	B9	0.12	0/342	0.30	0/450
73	BB	0.08	0/1595	0.21	0/2475
74	BC	0.16	0/5522	0.36	0/7451
75	BD	0.12	0/1898	0.32	0/2555
76	BE	0.11	0/2493	0.28	0/3387
77	BF	0.12	0/2069	0.29	0/2816
78	BI	0.12	0/819	0.32	0/1101
79	BJ	0.10	0/1742	0.32	0/2358
80	BK	0.10	0/1359	0.28	0/1828
81	BN	0.12	0/1487	0.27	0/2017
82	BO	0.11	0/912	0.29	0/1231
83	BP	0.12	0/2368	0.30	0/3198
84	BQ	0.12	0/1850	0.29	0/2491
85	BR	0.12	0/1262	0.31	0/1700
86	BS	0.12	0/1197	0.34	0/1624
87	BT	0.15	0/2039	0.31	0/2754
All	All	0.12	0/188542	0.29	6/267584 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
75	BD	0	1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	Bf	80	PRO	N-CA-CB	7.58	111.20	103.25
53	Ae	342	PRO	N-CA-CB	7.40	111.02	103.25
12	Bf	78	PRO	N-CA-CB	7.39	111.01	103.25
25	Bu	167	PRO	N-CA-CB	7.38	110.99	103.25
23	Bq	59	PRO	N-CA-CB	6.62	110.20	103.25

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
75	BD	207	TYR	Peptide

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	B0	857	0	878	15	0
2	BU	1159	0	1228	26	0
3	BV	1231	0	1278	31	0
4	BW	1374	0	1405	19	0
5	BX	1181	0	1139	17	0
6	BY	1678	0	1683	28	0
7	Ba	3173	0	3153	52	0
8	Bb	2952	0	2840	47	0
9	Bc	2408	0	2415	45	0
10	Bd	1177	0	1182	36	0
11	Be	972	0	971	17	0
12	Bf	827	0	736	13	0
13	Bg	1167	0	1173	32	0
14	Bh	2319	0	2332	45	0
15	Bi	2138	0	2139	33	0
16	Bj	1775	0	1797	48	0
17	Bk	1246	0	1251	34	0
18	Bl	1097	0	1080	17	0
19	Bm	893	0	878	14	0
20	Bn	837	0	860	16	0
21	Bo	772	0	773	12	0
22	Bp	742	0	749	16	0
23	Bq	697	0	659	22	0
24	Bt	780	0	792	18	0
25	Bu	1198	0	1192	18	0
26	Bv	1131	0	1093	14	0
27	Bw	3126	0	3153	53	0
28	B1	2036	0	2058	30	0
29	Bx	1325	0	1354	24	0
30	AA	20411	0	10346	297	0
30	BA	32844	0	16618	419	0
31	AB	1762	0	1774	38	0
32	AC	1075	0	1087	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	AE	2732	0	2773	52	0
34	AF	981	0	1012	19	0
35	AG	1721	0	1747	29	0
36	AI	2650	0	2613	49	0
37	AJ	1155	0	1193	34	0
38	AK	1007	0	1042	23	0
39	AL	840	0	890	14	0
40	AN	858	0	883	29	0
41	AO	1448	0	1536	15	0
42	AP	932	0	951	30	0
43	AQ	875	0	931	13	0
44	AR	784	0	813	10	0
45	AU	734	0	745	18	0
46	AV	1498	0	765	22	0
47	AX	128	0	65	2	0
48	AZ	90	0	89	2	0
49	Aa	2378	0	2392	54	0
50	Ab	1101	0	1118	16	0
51	Ac	1367	0	1385	24	0
52	Ad	1467	0	1466	29	0
53	Ae	3109	0	3029	83	0
54	Af	778	0	791	18	0
55	B2	1548	0	1583	22	0
56	Ag	2875	0	2886	86	0
57	Ah	1015	0	969	38	0
58	Ai	824	0	842	20	0
59	Aj	1788	0	1799	43	0
60	Ak	2222	0	2270	90	0
61	Am	930	0	959	17	0
62	An	639	0	709	10	0
63	Ao	4525	0	4433	93	0
64	Ap	1564	0	1531	26	0
65	CL	317	0	309	9	0
65	DL	213	0	234	6	0
65	EL	222	0	247	10	0
65	FL	213	0	234	7	0
65	GL	213	0	234	10	0
65	HL	205	0	223	7	0
65	LL	537	0	591	15	0
66	B3	968	0	1018	27	0
67	B4	474	0	454	22	0
68	B5	902	0	916	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	B6	425	0	471	8	0
70	B7	387	0	413	11	0
71	B8	833	0	883	11	0
72	B9	335	0	359	7	0
73	BB	1427	0	726	19	0
74	BC	5425	0	5412	120	0
75	BD	1860	0	1923	35	0
76	BE	2420	0	2418	43	0
77	BF	2011	0	2049	50	0
78	BI	805	0	845	10	0
79	BJ	1705	0	1804	42	0
80	BK	1339	0	1407	35	0
81	BN	1444	0	1437	19	0
82	BO	896	0	946	15	0
83	BP	2312	0	2373	45	0
84	BQ	1803	0	1841	24	0
85	BR	1240	0	1260	24	0
86	BS	1168	0	1159	29	0
87	BT	1990	0	2017	31	0
88	AA	101	0	0	0	0
88	AB	1	0	0	0	0
88	AL	1	0	0	0	0
88	AX	1	0	0	0	0
88	Ag	1	0	0	0	0
88	Am	1	0	0	0	0
88	An	1	0	0	0	0
88	B0	1	0	0	0	0
88	B3	1	0	0	0	0
88	BA	205	0	0	0	0
88	BB	1	0	0	0	0
88	BC	1	0	0	0	0
88	BD	3	0	0	0	0
88	BP	2	0	0	0	0
88	BQ	1	0	0	0	0
88	BR	1	0	0	0	0
88	Be	1	0	0	0	0
88	Bl	1	0	0	0	0
88	Bt	1	0	0	0	0
89	AR	1	0	0	0	0
89	Ac	1	0	0	0	0
89	Ap	1	0	0	0	0
89	B5	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
89	B9	1	0	0	0	0
89	Bx	1	0	0	0	0
90	AA	14	0	0	0	0
90	BA	28	0	0	0	0
91	AV	10	0	10	1	0
92	Ag	32	0	12	0	0
93	BA	48	0	0	0	0
94	BC	32	0	13	0	0
95	Ag	3	0	0	0	0
95	BC	2	0	0	0	0
All	All	179513	0	152514	2743	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 8.

The worst 5 of 2743 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)
30:AA:405:G:H1	30:AA:452:C:HO2'	1.03	1.01
65:LL:159:VAL:HG11	74:BC:255:GLU:HB2	1.57	0.87
14:Bh:166:VAL:HG11	14:Bh:192:ARG:HG3	1.60	0.84
7:Ba:41:PRO:HG2	30:BA:42:C:H41	1.45	0.81
2:BU:137:GLU:HG2	2:BU:138:PRO:HD3	1.61	0.80

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B0	108/148 (73%)	106 (98%)	2 (2%)	0	100	100
2	BU	138/149 (93%)	138 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	BV	153/209 (73%)	150 (98%)	3 (2%)	0	100	100
4	BW	164/210 (78%)	159 (97%)	5 (3%)	0	100	100
5	BX	147/150 (98%)	143 (97%)	4 (3%)	0	100	100
6	BY	204/216 (94%)	197 (97%)	7 (3%)	0	100	100
7	Ba	391/423 (92%)	377 (96%)	14 (4%)	0	100	100
8	Bb	352/380 (93%)	330 (94%)	22 (6%)	0	100	100
9	Bc	293/334 (88%)	276 (94%)	17 (6%)	0	100	100
10	Bd	138/206 (67%)	134 (97%)	4 (3%)	0	100	100
11	Be	120/135 (89%)	115 (96%)	5 (4%)	0	100	100
12	Bf	106/142 (75%)	103 (97%)	1 (1%)	2 (2%)	6	30
13	Bg	146/159 (92%)	135 (92%)	11 (8%)	0	100	100
14	Bh	287/332 (86%)	272 (95%)	15 (5%)	0	100	100
15	Bi	258/306 (84%)	249 (96%)	9 (4%)	0	100	100
16	Bj	211/279 (76%)	204 (97%)	7 (3%)	0	100	100
17	Bk	151/269 (56%)	145 (96%)	6 (4%)	0	100	100
18	Bl	131/166 (79%)	128 (98%)	3 (2%)	0	100	100
19	Bm	107/198 (54%)	105 (98%)	2 (2%)	0	100	100
20	Bn	95/128 (74%)	91 (96%)	4 (4%)	0	100	100
21	Bo	95/124 (77%)	93 (98%)	2 (2%)	0	100	100
22	Bp	95/112 (85%)	91 (96%)	4 (4%)	0	100	100
23	Bq	83/138 (60%)	76 (92%)	7 (8%)	0	100	100
24	Bt	92/102 (90%)	88 (96%)	4 (4%)	0	100	100
25	Bu	147/205 (72%)	139 (95%)	7 (5%)	1 (1%)	18	53
26	Bv	133/222 (60%)	133 (100%)	0	0	100	100
27	Bw	385/433 (89%)	366 (95%)	19 (5%)	0	100	100
28	B1	242/256 (94%)	239 (99%)	3 (1%)	0	100	100
29	Bx	160/196 (82%)	152 (95%)	8 (5%)	0	100	100
31	AB	218/289 (75%)	205 (94%)	13 (6%)	0	100	100
32	AC	130/167 (78%)	123 (95%)	7 (5%)	0	100	100
33	AE	339/430 (79%)	325 (96%)	14 (4%)	0	100	100
34	AF	120/276 (44%)	115 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	AG	206/242 (85%)	203 (98%)	3 (2%)	0	100	100
36	AI	324/397 (82%)	311 (96%)	13 (4%)	0	100	100
37	AJ	138/200 (69%)	128 (93%)	10 (7%)	0	100	100
38	AK	135/196 (69%)	127 (94%)	8 (6%)	0	100	100
39	AL	107/139 (77%)	104 (97%)	3 (3%)	0	100	100
40	AN	99/128 (77%)	96 (97%)	3 (3%)	0	100	100
41	AO	173/239 (72%)	166 (96%)	7 (4%)	0	100	100
42	AP	115/135 (85%)	111 (96%)	4 (4%)	0	100	100
43	AQ	110/130 (85%)	110 (100%)	0	0	100	100
44	AR	95/143 (66%)	93 (98%)	2 (2%)	0	100	100
45	AU	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
48	AZ	16/18 (89%)	16 (100%)	0	0	100	100
49	Aa	290/382 (76%)	285 (98%)	5 (2%)	0	100	100
50	Ab	133/190 (70%)	132 (99%)	1 (1%)	0	100	100
51	Ac	167/173 (96%)	166 (99%)	1 (1%)	0	100	100
52	Ad	175/205 (85%)	174 (99%)	1 (1%)	0	100	100
53	Ae	386/426 (91%)	363 (94%)	21 (5%)	2 (0%)	24	60
54	Af	97/188 (52%)	92 (95%)	5 (5%)	0	100	100
55	B2	177/252 (70%)	173 (98%)	4 (2%)	0	100	100
56	Ag	351/410 (86%)	339 (97%)	12 (3%)	0	100	100
57	Ah	118/387 (30%)	117 (99%)	1 (1%)	0	100	100
58	Ai	97/106 (92%)	95 (98%)	2 (2%)	0	100	100
59	Aj	211/218 (97%)	204 (97%)	7 (3%)	0	100	100
60	Ak	273/325 (84%)	267 (98%)	6 (2%)	0	100	100
61	Am	114/118 (97%)	111 (97%)	3 (3%)	0	100	100
62	An	70/199 (35%)	68 (97%)	2 (3%)	0	100	100
63	Ao	564/699 (81%)	544 (96%)	20 (4%)	0	100	100
64	Ap	188/258 (73%)	183 (97%)	5 (3%)	0	100	100
65	CL	43/198 (22%)	41 (95%)	2 (5%)	0	100	100
65	DL	25/198 (13%)	25 (100%)	0	0	100	100
65	EL	26/198 (13%)	26 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
65	FL	25/198 (13%)	25 (100%)	0	0	100	100
65	GL	25/198 (13%)	25 (100%)	0	0	100	100
65	HL	24/198 (12%)	24 (100%)	0	0	100	100
65	LL	68/198 (34%)	65 (96%)	3 (4%)	0	100	100
66	B3	116/161 (72%)	114 (98%)	2 (2%)	0	100	100
67	B4	60/126 (48%)	51 (85%)	9 (15%)	0	100	100
68	B5	108/188 (57%)	108 (100%)	0	0	100	100
69	B6	50/65 (77%)	50 (100%)	0	0	100	100
70	B7	44/95 (46%)	43 (98%)	1 (2%)	0	100	100
71	B8	93/188 (50%)	92 (99%)	1 (1%)	0	100	100
72	B9	36/100 (36%)	36 (100%)	0	0	100	100
74	BC	688/722 (95%)	628 (91%)	58 (8%)	2 (0%)	36	70
75	BD	238/306 (78%)	230 (97%)	8 (3%)	0	100	100
76	BE	305/348 (88%)	289 (95%)	16 (5%)	0	100	100
77	BF	248/294 (84%)	240 (97%)	8 (3%)	0	100	100
78	BI	96/268 (36%)	94 (98%)	2 (2%)	0	100	100
79	BJ	210/262 (80%)	200 (95%)	10 (5%)	0	100	100
80	BK	174/192 (91%)	165 (95%)	9 (5%)	0	100	100
81	BN	175/178 (98%)	173 (99%)	2 (1%)	0	100	100
82	BO	113/145 (78%)	112 (99%)	1 (1%)	0	100	100
83	BP	286/296 (97%)	276 (96%)	10 (4%)	0	100	100
84	BQ	220/251 (88%)	214 (97%)	6 (3%)	0	100	100
85	BR	151/169 (89%)	144 (95%)	7 (5%)	0	100	100
86	BS	141/180 (78%)	132 (94%)	9 (6%)	0	100	100
87	BT	238/292 (82%)	229 (96%)	9 (4%)	0	100	100
All	All	14978/20291 (74%)	14414 (96%)	557 (4%)	7 (0%)	100	100

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	Bf	78	PRO
12	Bf	80	PRO
25	Bu	167	PRO

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Mol	Chain	Res	Type
53	Ae	342	PRO
74	BC	153	CYS

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	B0	90/115 (78%)	90 (100%)	0	100	100
2	BU	118/127 (93%)	117 (99%)	1 (1%)	73	86
3	BV	136/178 (76%)	136 (100%)	0	100	100
4	BW	144/180 (80%)	143 (99%)	1 (1%)	76	86
5	BX	116/134 (87%)	114 (98%)	2 (2%)	53	78
6	BY	185/192 (96%)	183 (99%)	2 (1%)	65	83
7	Ba	348/365 (95%)	342 (98%)	6 (2%)	53	78
8	Bb	310/328 (94%)	306 (99%)	4 (1%)	61	81
9	Bc	271/299 (91%)	271 (100%)	0	100	100
10	Bd	129/181 (71%)	125 (97%)	4 (3%)	35	68
11	Be	100/108 (93%)	99 (99%)	1 (1%)	68	84
12	Bf	80/133 (60%)	77 (96%)	3 (4%)	29	63
13	Bg	128/136 (94%)	128 (100%)	0	100	100
14	Bh	251/284 (88%)	250 (100%)	1 (0%)	84	90
15	Bi	236/275 (86%)	233 (99%)	3 (1%)	61	81
16	Bj	190/242 (78%)	186 (98%)	4 (2%)	47	75
17	Bk	135/226 (60%)	131 (97%)	4 (3%)	36	69
18	Bl	122/147 (83%)	120 (98%)	2 (2%)	55	79
19	Bm	103/178 (58%)	103 (100%)	0	100	100
20	Bn	88/113 (78%)	87 (99%)	1 (1%)	65	83
21	Bo	77/97 (79%)	76 (99%)	1 (1%)	61	81
22	Bp	79/88 (90%)	77 (98%)	2 (2%)	42	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	Bq	70/114 (61%)	67 (96%)	3 (4%)	26	60
24	Bt	75/82 (92%)	74 (99%)	1 (1%)	61	81
25	Bu	126/177 (71%)	126 (100%)	0	100	100
26	Bv	115/183 (63%)	115 (100%)	0	100	100
27	Bw	340/373 (91%)	332 (98%)	8 (2%)	43	73
28	B1	219/229 (96%)	215 (98%)	4 (2%)	51	77
29	Bx	149/173 (86%)	145 (97%)	4 (3%)	39	71
31	AB	187/233 (80%)	186 (100%)	1 (0%)	81	89
32	AC	115/142 (81%)	112 (97%)	3 (3%)	40	72
33	AE	282/351 (80%)	279 (99%)	3 (1%)	65	83
34	AF	107/210 (51%)	107 (100%)	0	100	100
35	AG	181/205 (88%)	179 (99%)	2 (1%)	65	83
36	AI	273/333 (82%)	272 (100%)	1 (0%)	84	90
37	AJ	130/180 (72%)	127 (98%)	3 (2%)	44	74
38	AK	103/151 (68%)	102 (99%)	1 (1%)	68	84
39	AL	92/116 (79%)	90 (98%)	2 (2%)	45	74
40	AN	92/114 (81%)	92 (100%)	0	100	100
41	AO	159/205 (78%)	158 (99%)	1 (1%)	78	88
42	AP	97/113 (86%)	95 (98%)	2 (2%)	47	75
43	AQ	97/114 (85%)	94 (97%)	3 (3%)	35	68
44	AR	89/127 (70%)	87 (98%)	2 (2%)	45	74
45	AU	77/78 (99%)	76 (99%)	1 (1%)	61	81
49	Aa	258/330 (78%)	254 (98%)	4 (2%)	55	79
50	Ab	113/162 (70%)	110 (97%)	3 (3%)	39	71
51	Ac	152/155 (98%)	150 (99%)	2 (1%)	61	81
52	Ad	149/168 (89%)	145 (97%)	4 (3%)	39	71
53	Ae	325/371 (88%)	320 (98%)	5 (2%)	57	80
54	Af	86/160 (54%)	85 (99%)	1 (1%)	63	82
55	B2	164/228 (72%)	161 (98%)	3 (2%)	51	77
56	Ag	312/361 (86%)	308 (99%)	4 (1%)	61	81
57	Ah	109/346 (32%)	105 (96%)	4 (4%)	30	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	Ai	86/93 (92%)	86 (100%)	0	100	100
59	Aj	188/190 (99%)	188 (100%)	0	100	100
60	Ak	249/289 (86%)	245 (98%)	4 (2%)	55	79
61	Am	100/102 (98%)	98 (98%)	2 (2%)	48	76
62	An	66/174 (38%)	65 (98%)	1 (2%)	57	80
63	Ao	478/611 (78%)	472 (99%)	6 (1%)	61	81
64	Ap	170/225 (76%)	169 (99%)	1 (1%)	78	88
65	CL	30/157 (19%)	30 (100%)	0	100	100
65	DL	26/157 (17%)	26 (100%)	0	100	100
65	EL	27/157 (17%)	26 (96%)	1 (4%)	30	64
65	FL	26/157 (17%)	26 (100%)	0	100	100
65	GL	26/157 (17%)	25 (96%)	1 (4%)	29	63
65	HL	25/157 (16%)	25 (100%)	0	100	100
65	LL	59/157 (38%)	58 (98%)	1 (2%)	53	78
66	B3	110/150 (73%)	109 (99%)	1 (1%)	70	85
67	B4	45/114 (40%)	43 (96%)	2 (4%)	25	60
68	B5	99/163 (61%)	99 (100%)	0	100	100
69	B6	49/60 (82%)	48 (98%)	1 (2%)	48	76
70	B7	41/78 (53%)	40 (98%)	1 (2%)	43	73
71	B8	87/162 (54%)	86 (99%)	1 (1%)	65	83
72	B9	36/77 (47%)	36 (100%)	0	100	100
74	BC	589/609 (97%)	561 (95%)	28 (5%)	23	57
75	BD	193/248 (78%)	191 (99%)	2 (1%)	68	84
76	BE	263/290 (91%)	257 (98%)	6 (2%)	44	74
77	BF	217/251 (86%)	216 (100%)	1 (0%)	81	89
78	BI	88/228 (39%)	87 (99%)	1 (1%)	65	83
79	BJ	192/230 (84%)	190 (99%)	2 (1%)	68	84
80	BK	138/151 (91%)	133 (96%)	5 (4%)	31	65
81	BN	156/157 (99%)	155 (99%)	1 (1%)	78	88
82	BO	99/123 (80%)	99 (100%)	0	100	100
83	BP	245/249 (98%)	244 (100%)	1 (0%)	84	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
84	BQ	190/210 (90%)	190 (100%)	0	100	100
85	BR	132/143 (92%)	131 (99%)	1 (1%)	73	86
86	BS	123/153 (80%)	119 (97%)	4 (3%)	33	67
87	BT	221/258 (86%)	217 (98%)	4 (2%)	51	77
All	All	13148/17297 (76%)	12952 (98%)	196 (2%)	55	80

5 of 196 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	Ah	365	ILE
74	BC	232	ILE
60	Ak	268	LEU
64	Ap	107	ILE
74	BC	328	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 307 such sidechains are listed below:

Mol	Chain	Res	Type
67	B4	37	ASN
81	BN	140	ASN
71	B8	154	GLN
76	BE	154	HIS
85	BR	148	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	AA	958/16770 (5%)	168 (17%)	0
30	BA	1542/16770 (9%)	399 (25%)	2 (0%)
46	AV	70/71 (98%)	20 (28%)	0
47	AX	5/6 (83%)	1 (20%)	1 (20%)
73	BB	64/73 (87%)	15 (23%)	0
All	All	2639/33690 (7%)	603 (22%)	3 (0%)

5 of 603 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	AA	5	A

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Mol	Chain	Res	Type
30	AA	10	U
30	AA	18	G
30	AA	27	U
30	AA	34	U

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
47	AX	2	U
30	BA	48	U
30	BA	1297	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 340 ligands modelled in this entry, 332 are monoatomic - leaving 8 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
93	5GP	BA	15906	-	26,26,26	0.99	2 (7%)	40,40,40	1.80	8 (20%)
90	SPM	BA	15909	-	13,13,13	0.34	0	12,12,12	0.75	0
93	5GP	BA	15907	88	26,26,26	0.99	2 (7%)	40,40,40	1.69	8 (20%)
90	SPM	BA	15908	-	13,13,13	0.30	0	12,12,12	0.80	0
90	SPM	AA	16801	-	13,13,13	0.31	0	12,12,12	0.80	0
92	GTP	Ag	500	88	30,34,34	0.83	1 (3%)	46,54,54	1.80	11 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
91	FME	AV	101	46	8,9,10	0.96	0	7,9,11	0.89	0
94	GNP	BC	1000	88	33,34,34	1.27	5 (15%)	46,54,54	0.72	1 (2%)

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
93	5GP	BA	15906	-	-	1/10/26/26	0/3/3/3
90	SPM	BA	15909	-	-	4/11/11/11	-
93	5GP	BA	15907	88	-	1/10/26/26	0/3/3/3
90	SPM	BA	15908	-	-	3/11/11/11	-
90	SPM	AA	16801	-	-	5/11/11/11	-
92	GTP	Ag	500	88	-	1/22/38/38	0/3/3/3
91	FME	AV	101	46	-	3/7/9/11	-
94	GNP	BC	1000	88	-	2/18/38/38	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
94	BC	1000	GNP	PB-O3A	4.30	1.64	1.59
94	BC	1000	GNP	PB-O1B	3.02	1.50	1.46
94	BC	1000	GNP	PG-N3B	2.91	1.71	1.63
93	BA	15906	5GP	C6-N1	-2.62	1.34	1.38
94	BC	1000	GNP	PG-O1G	2.59	1.50	1.46

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
93	BA	15906	5GP	C5-C4-N3	-6.27	118.29	128.46
93	BA	15907	5GP	C5-C4-N3	-5.65	119.30	128.46
92	Ag	500	GTP	C5-C4-N3	-5.25	119.95	128.46
93	BA	15906	5GP	C2-N3-C4	4.70	120.67	112.30
92	Ag	500	GTP	C2-N3-C4	4.62	120.53	112.30

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

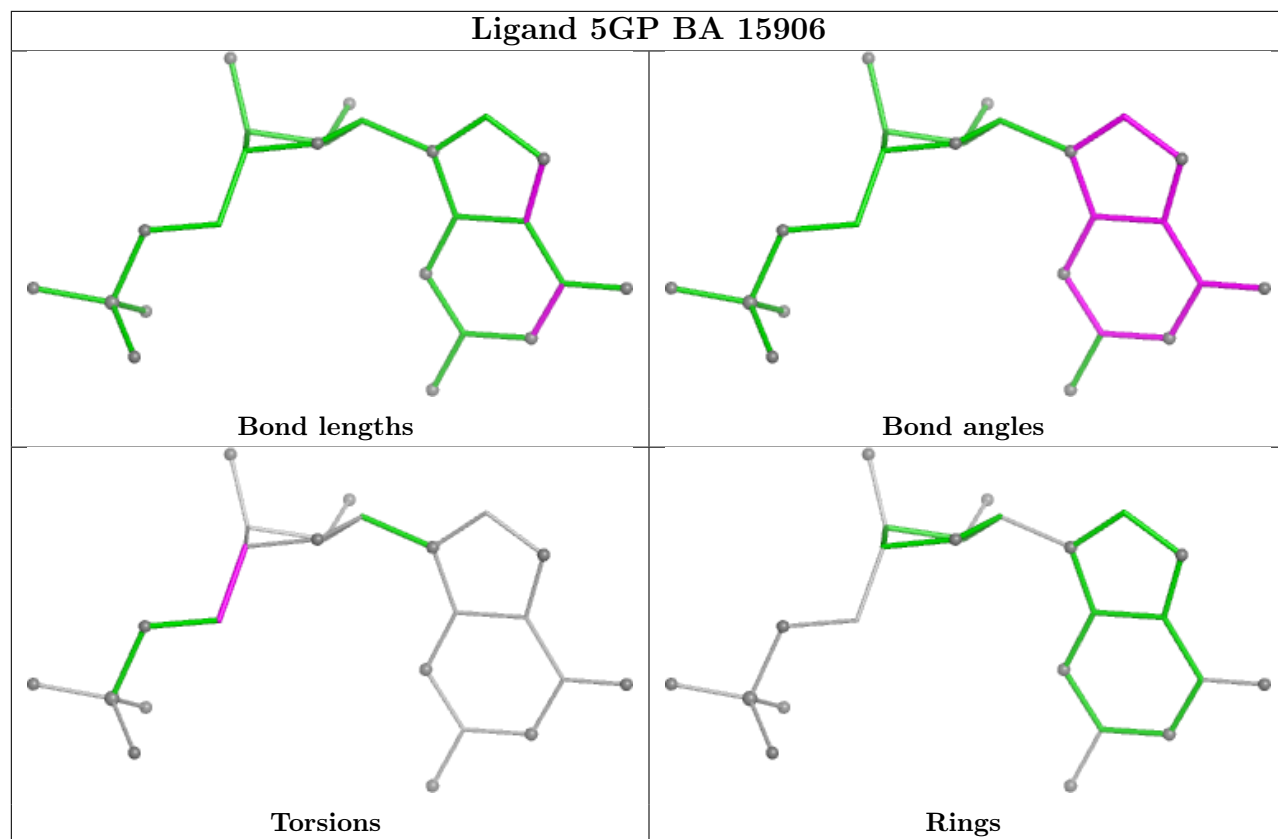
Mol	Chain	Res	Type	Atoms
91	AV	101	FME	C-CA-CB-CG
94	BC	1000	GNP	PG-N3B-PB-O1B
94	BC	1000	GNP	PG-N3B-PB-O3A
90	BA	15908	SPM	C7-C8-C9-N10
91	AV	101	FME	N-CA-CB-CG

There are no ring outliers.

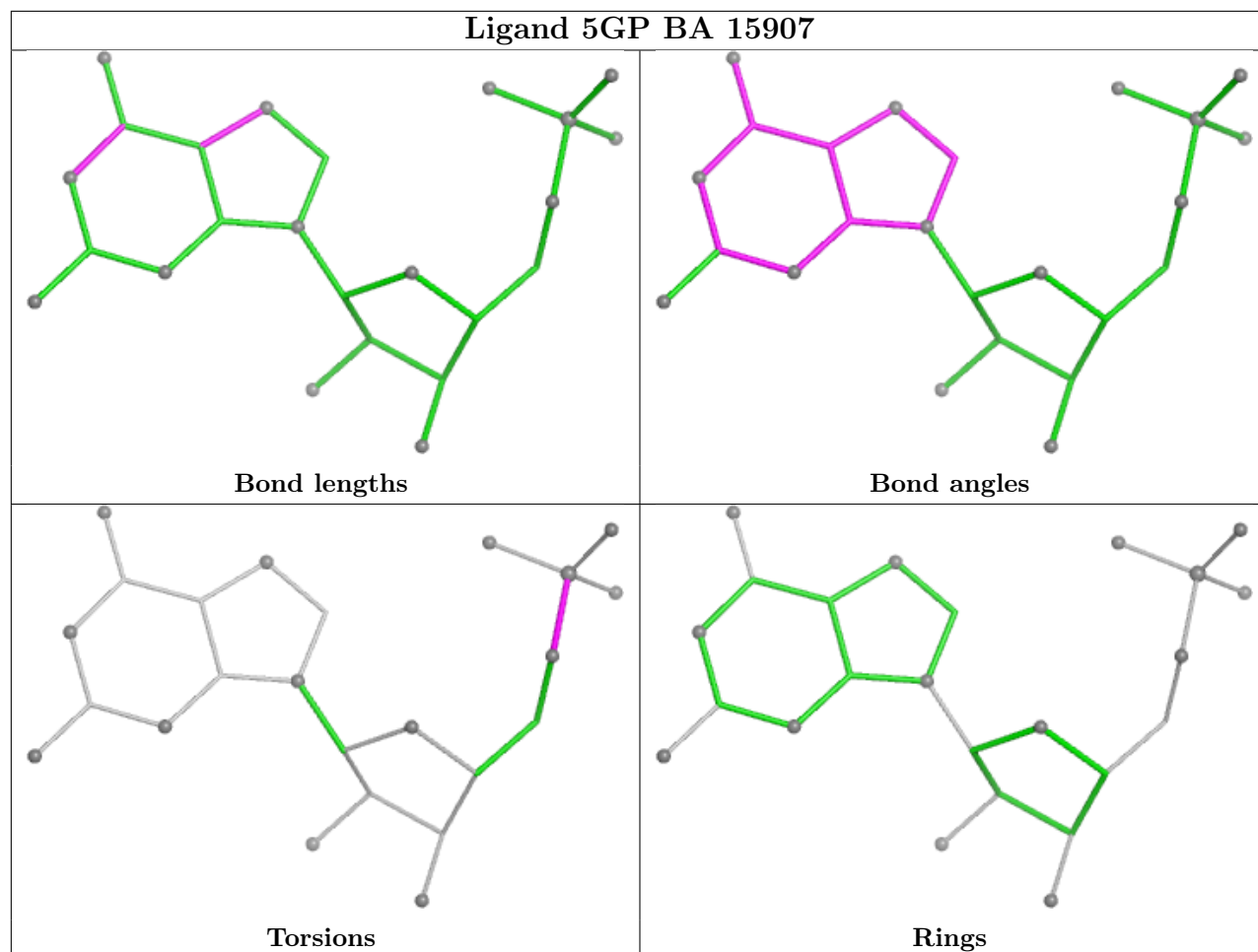
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
91	AV	101	FME	1	0

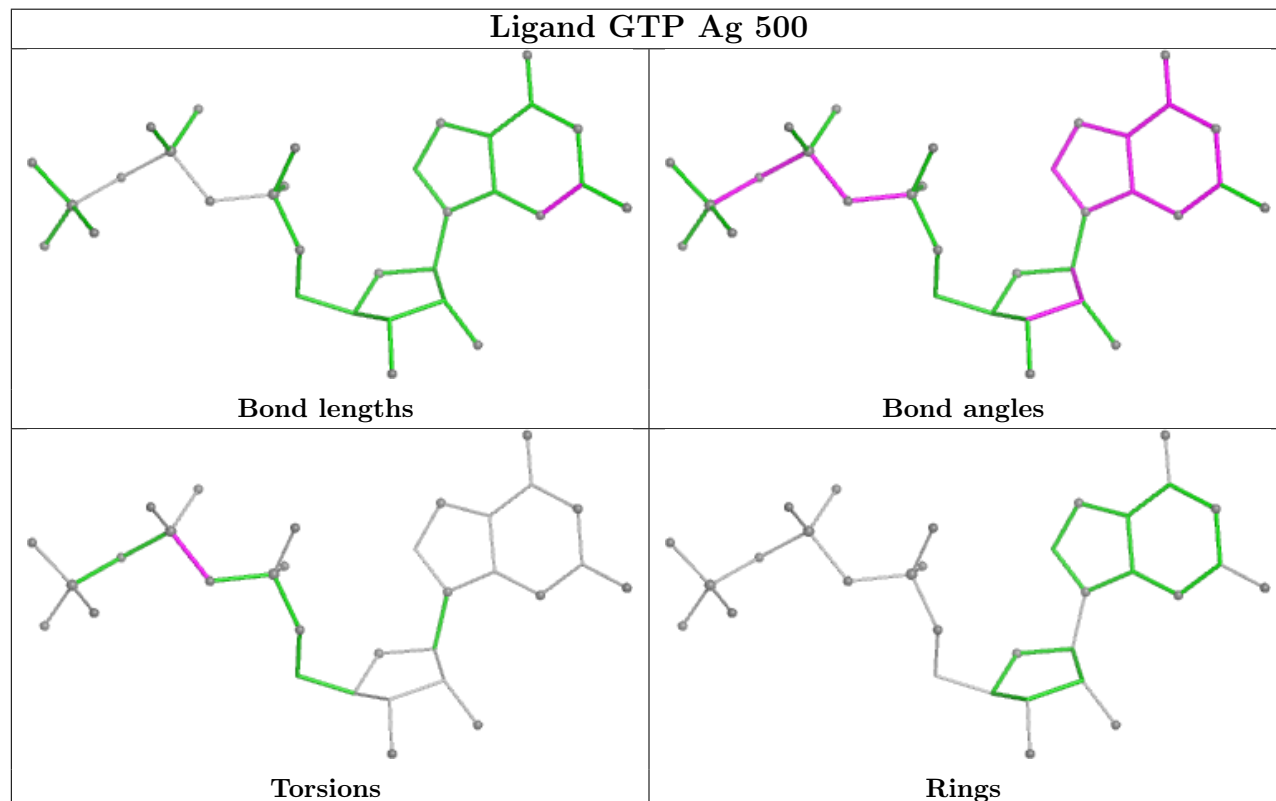
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

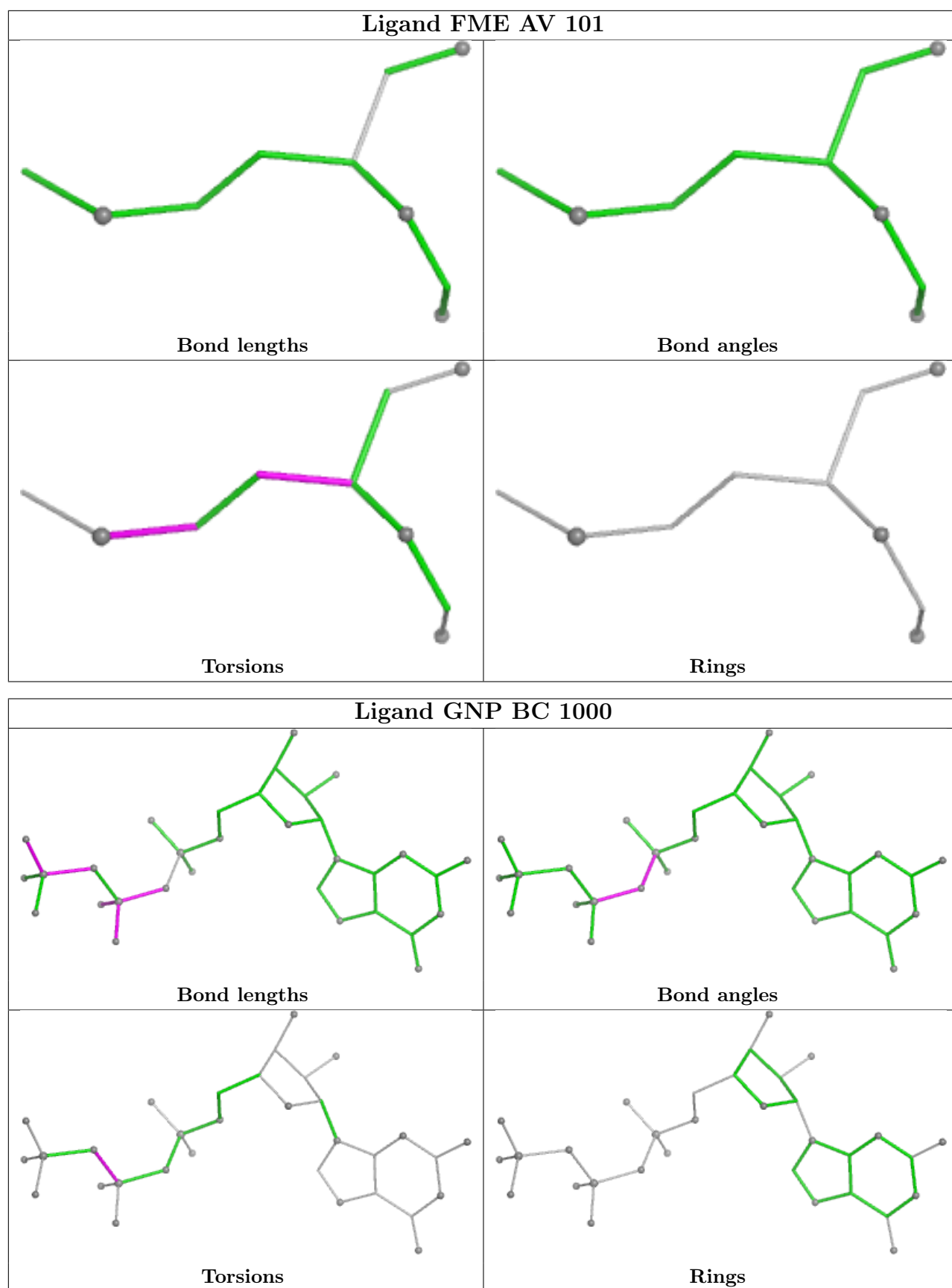


Ligand 5GP BA 15907



Ligand GTP Ag 500





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
63	Ao	1
30	AA	1
33	AE	1
36	AI	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Ao	234:VAL	C	240:THR	N	8.13
1	AA	532:G	O3'	533:C	P	4.55
1	AE	188:LYS	C	189:ARG	N	3.53
1	AI	249:ILE	C	250:PRO	N	3.18

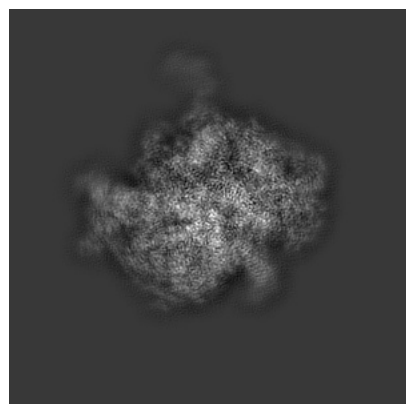
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10778. These allow visual inspection of the internal detail of the map and identification of artifacts.

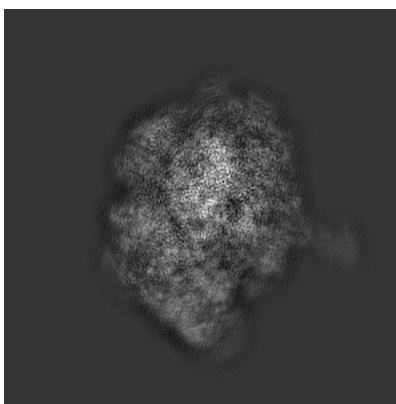
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

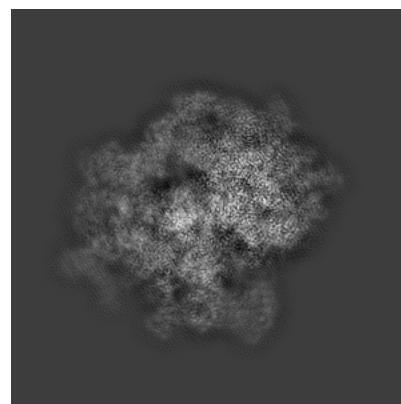
6.1.1 Primary map



X

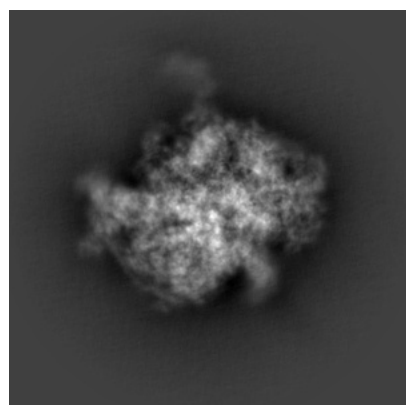


Y

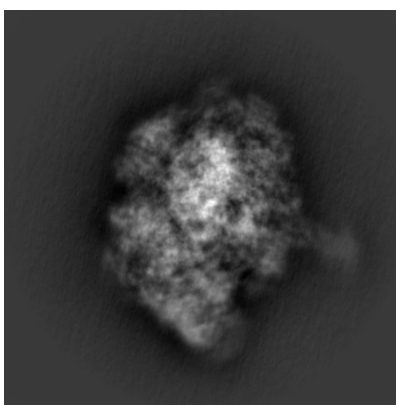


Z

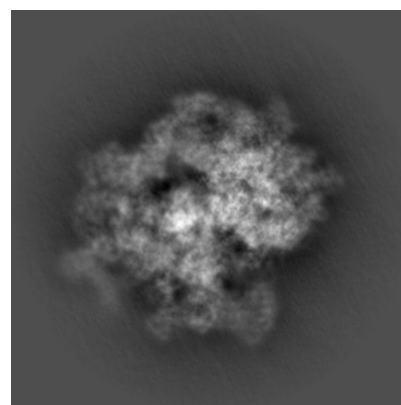
6.1.2 Raw map



X



Y

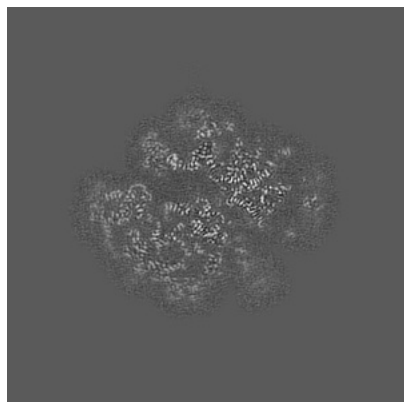


Z

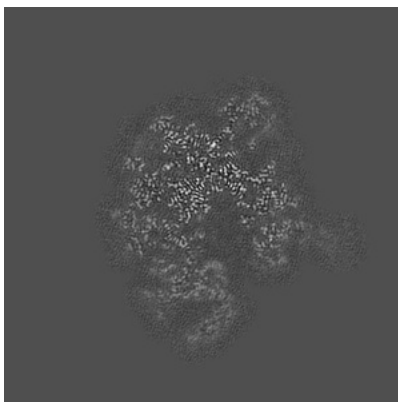
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

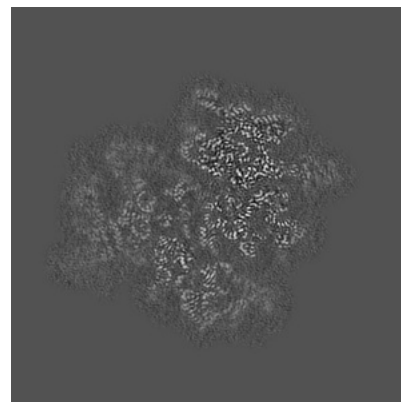
6.2.1 Primary map



X Index: 160

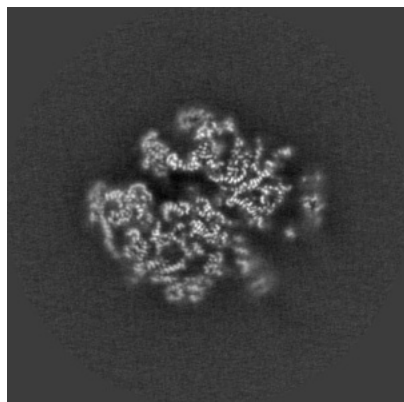


Y Index: 160

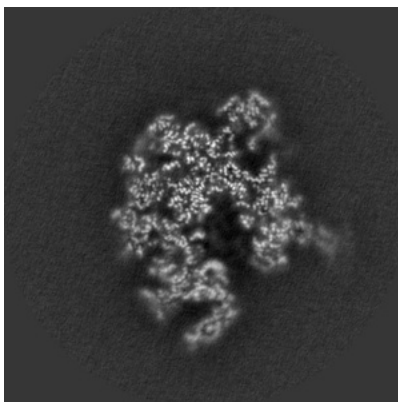


Z Index: 160

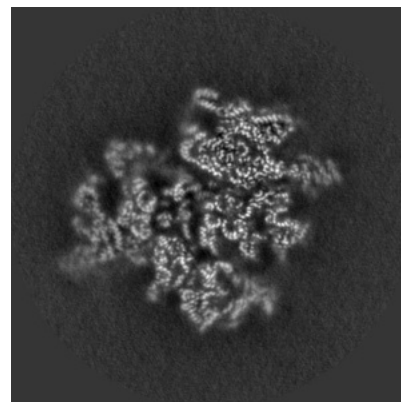
6.2.2 Raw map



X Index: 160



Y Index: 160

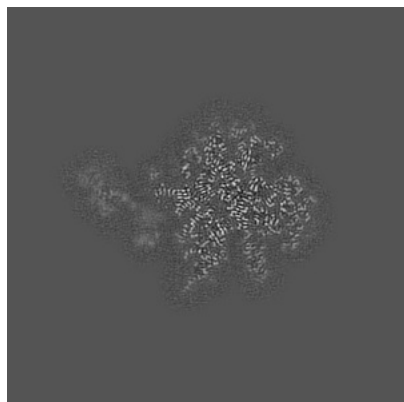


Z Index: 160

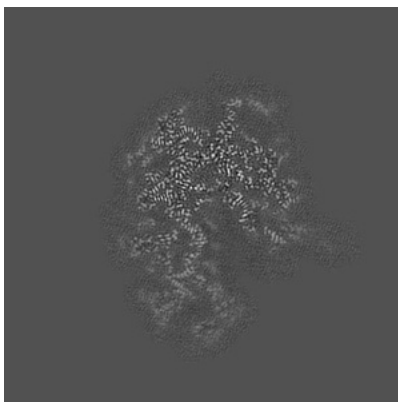
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

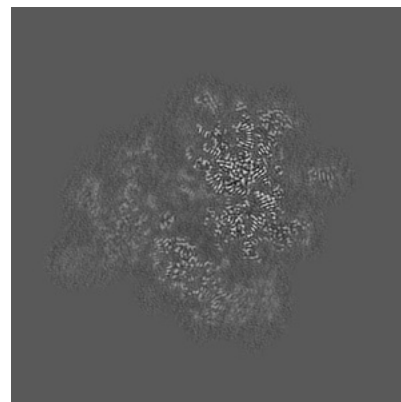
6.3.1 Primary map



X Index: 182

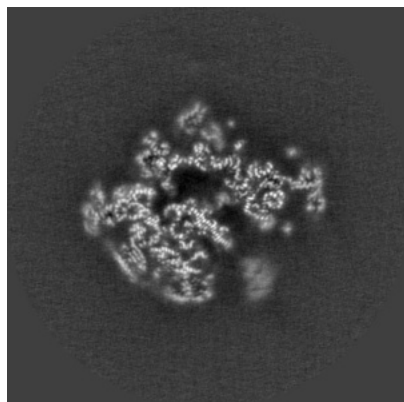


Y Index: 166

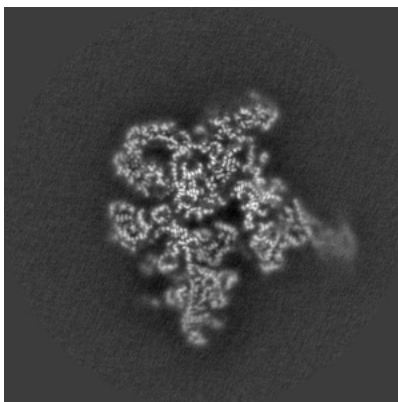


Z Index: 166

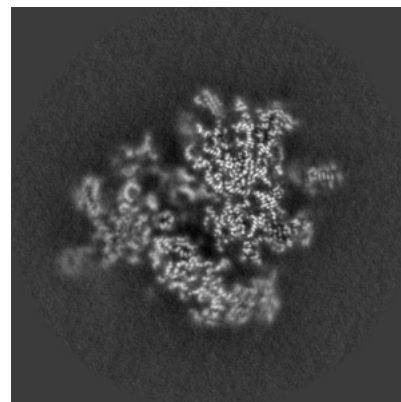
6.3.2 Raw map



X Index: 154



Y Index: 150

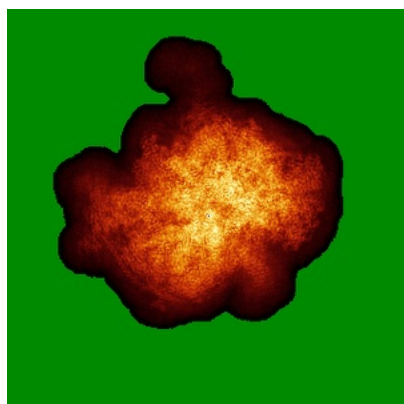


Z Index: 166

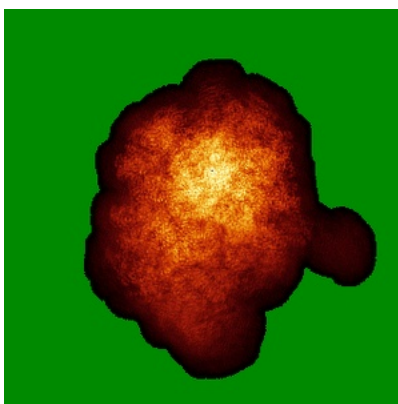
The images above show the largest variance slices of the map in three orthogonal directions.

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

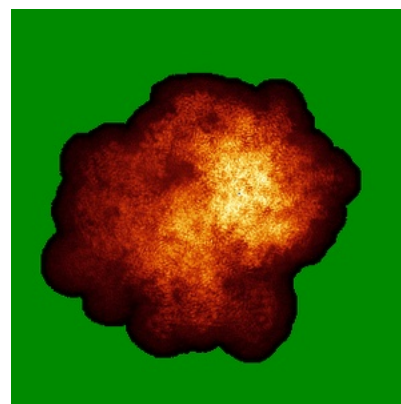
6.4.1 Primary map



X



Y

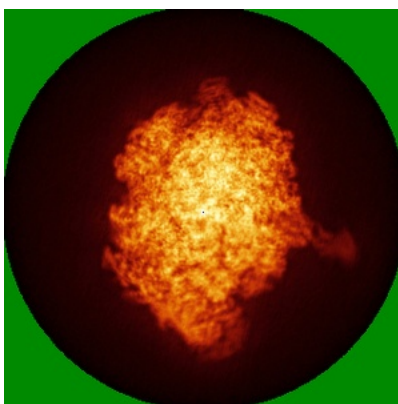


Z

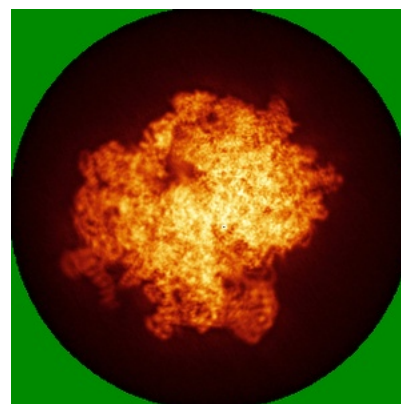
6.4.2 Raw map



X



Y

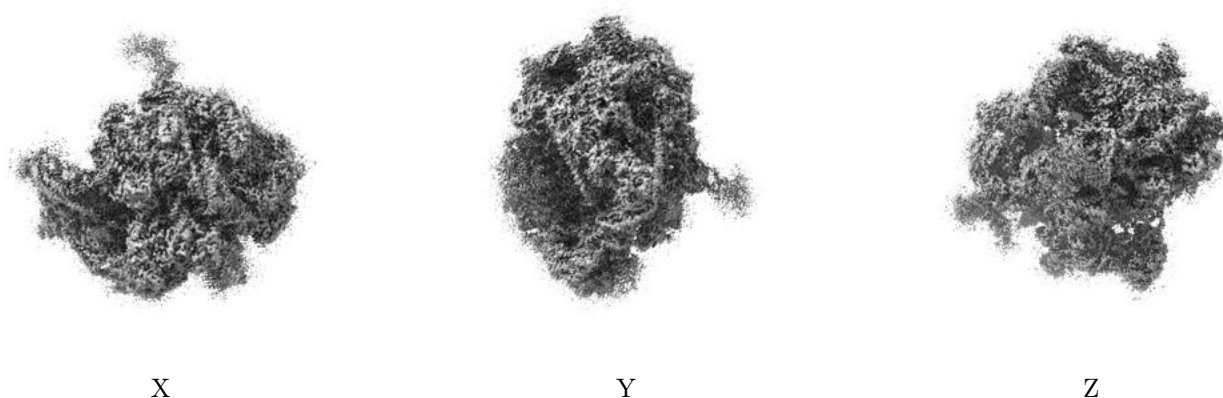


Z

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.

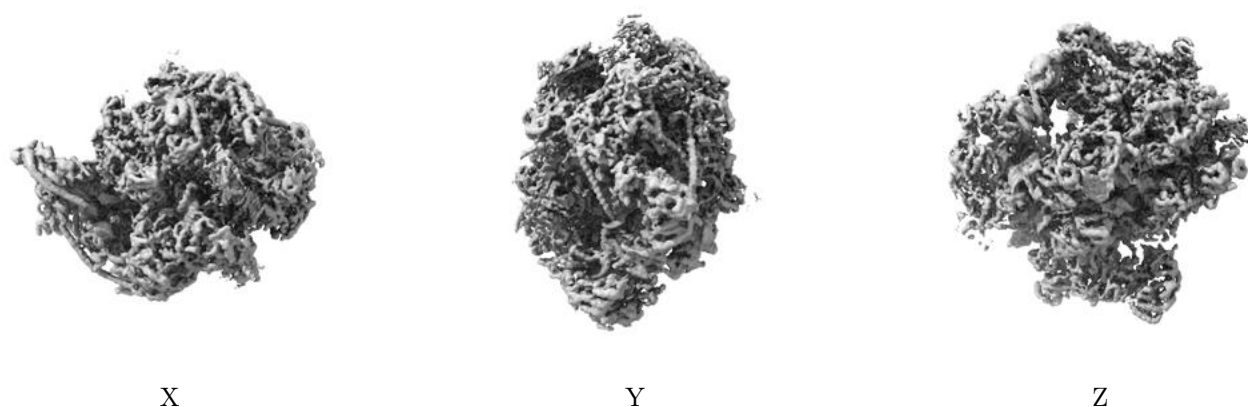
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.045. 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.

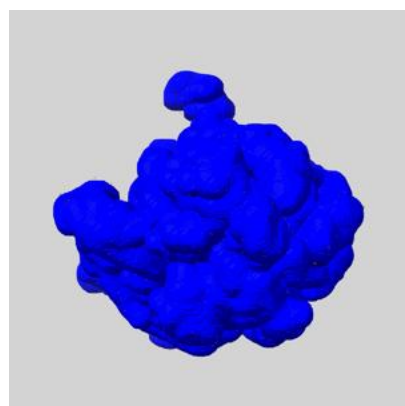
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

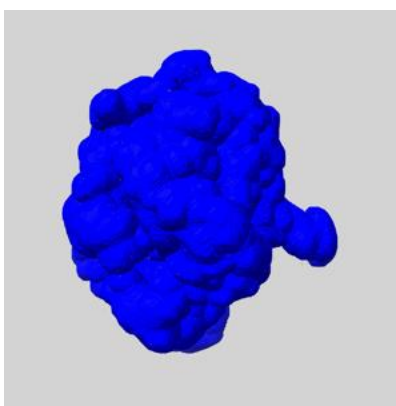
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

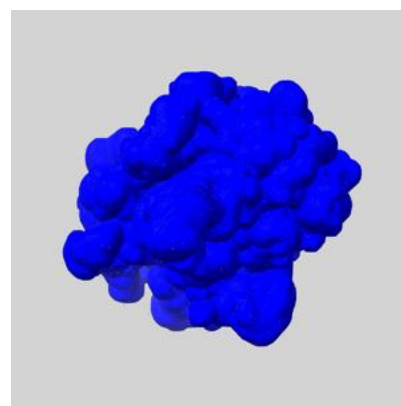
6.6.1 emd_10778_msk_1.map [i](#)



X



Y

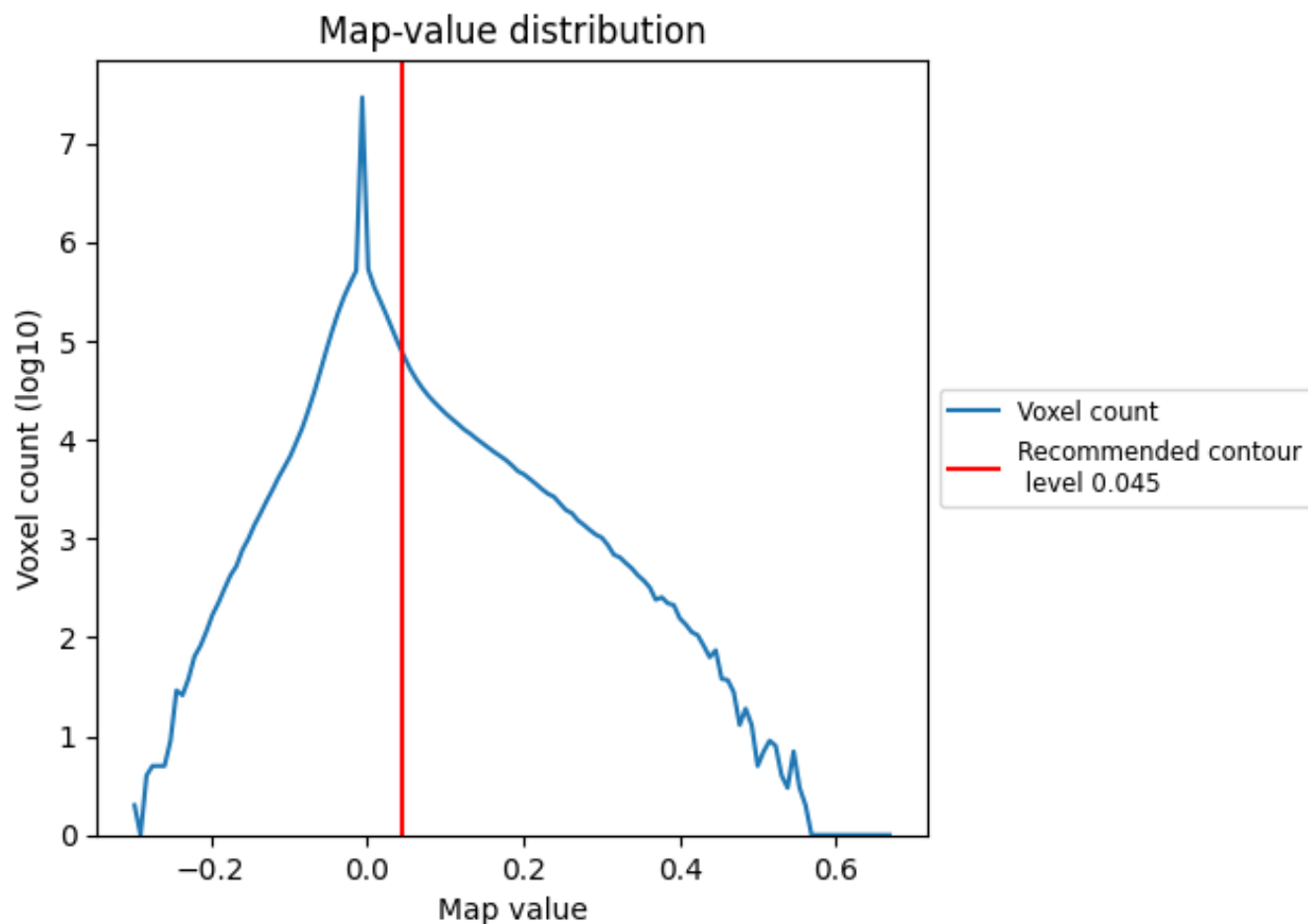


Z

7 Map analysis [i](#)

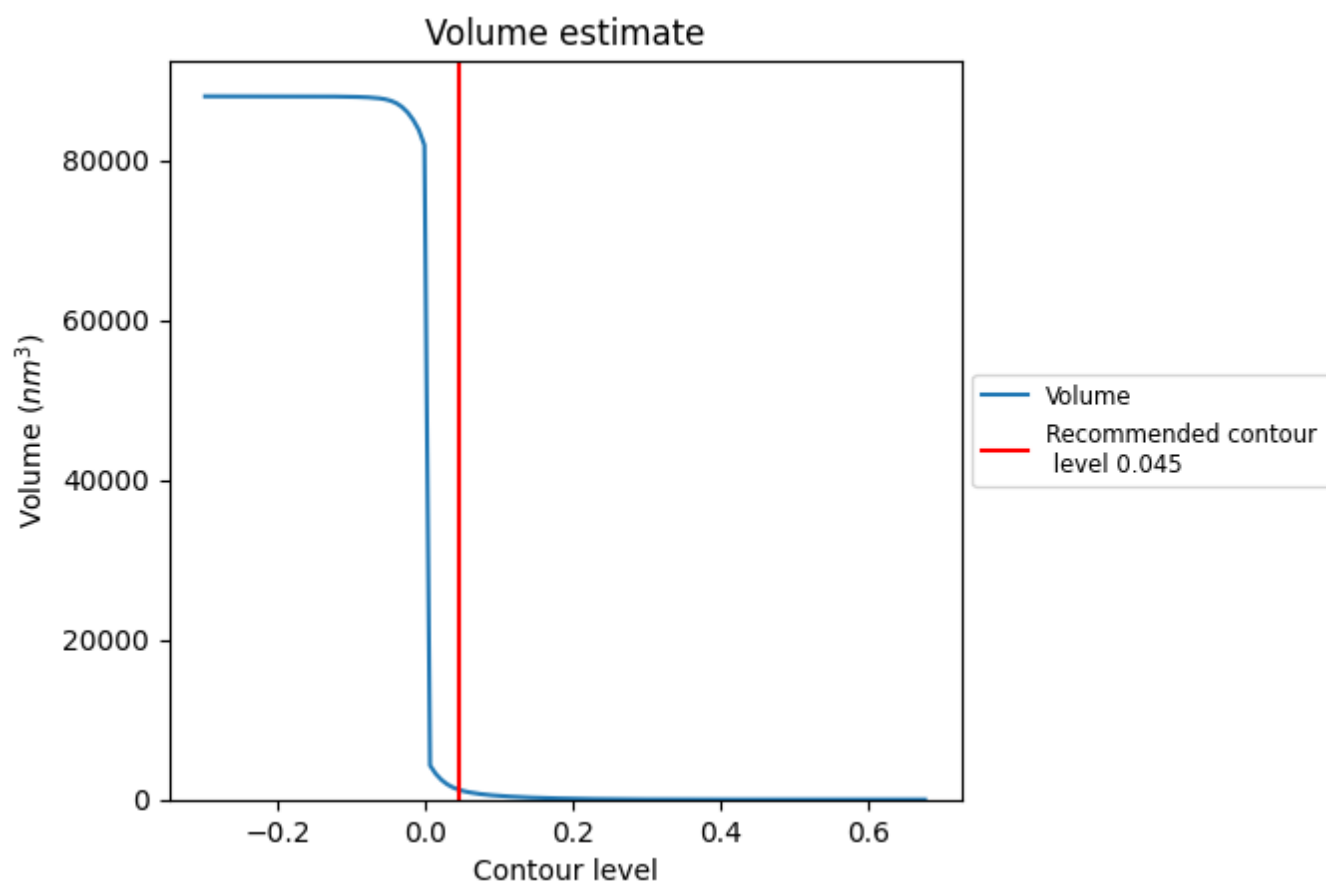
This section contains the results of statistical analysis of the map.

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.

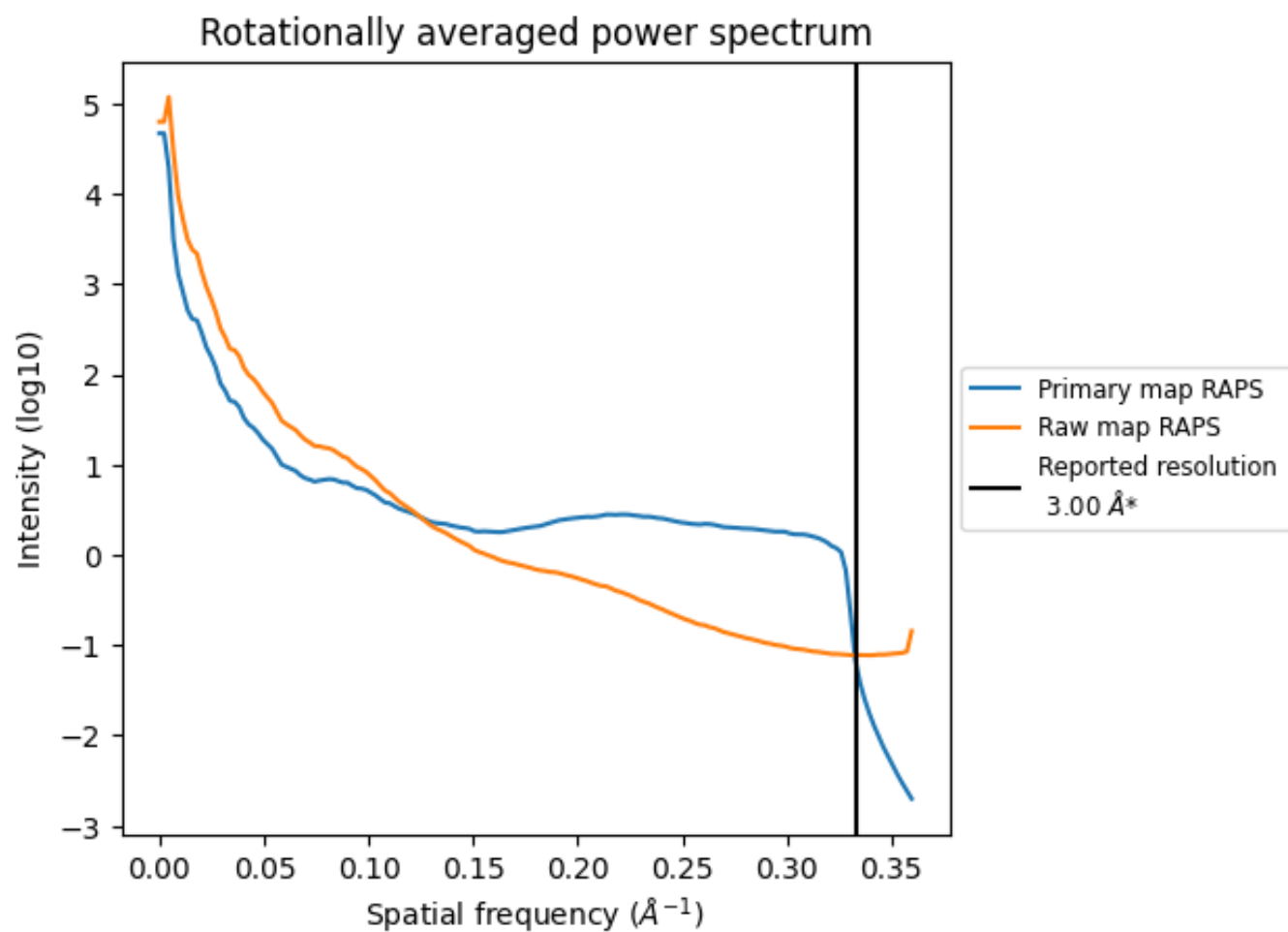
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1257 nm³; this corresponds to an approximate mass of 1135 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 ⓘ

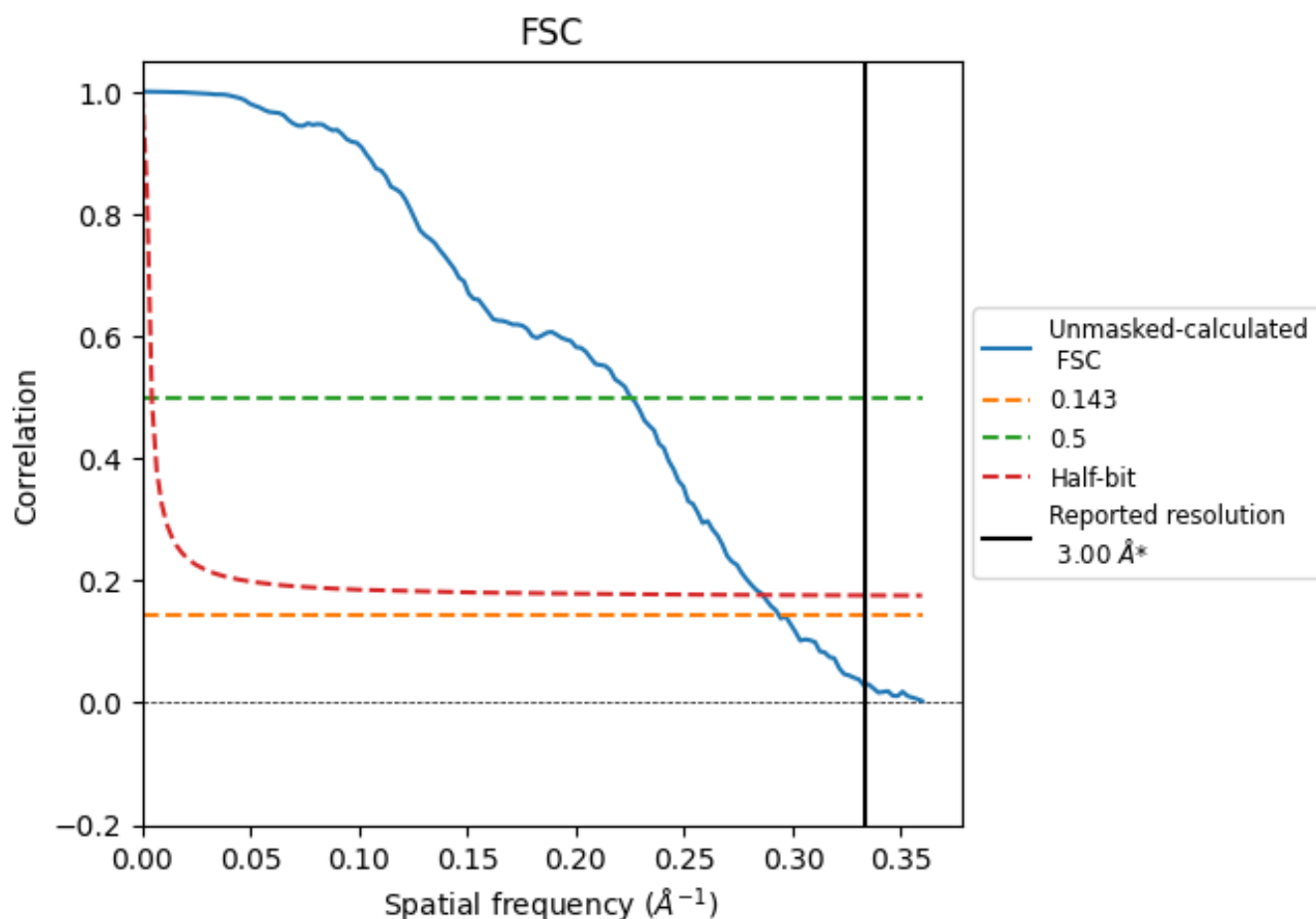


*Reported resolution corresponds to spatial frequency of 0.333 $\text{\AA}^{-1}$

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

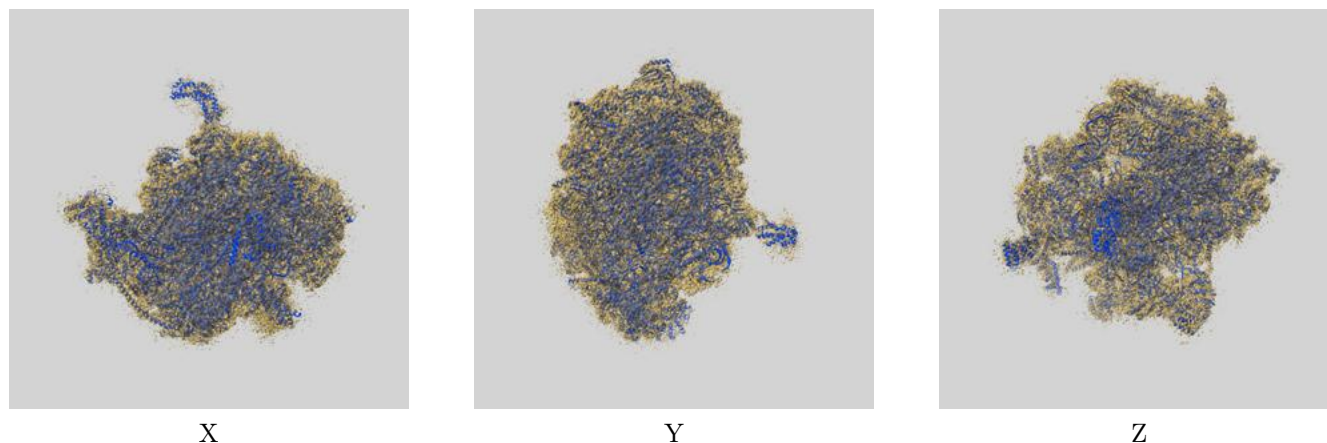
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.41	4.44	3.50

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.41 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

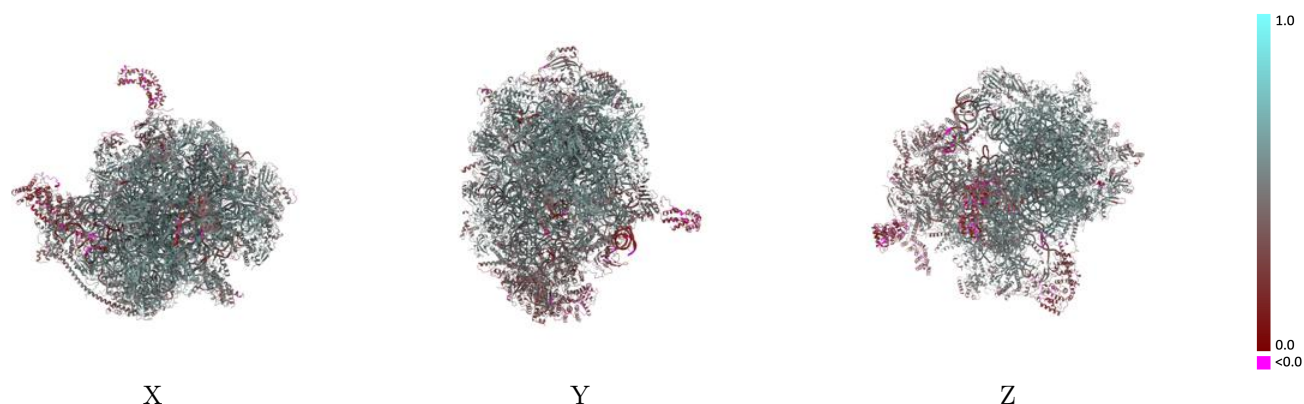
This section contains information regarding the fit between EMDB map EMD-10778 and PDB model 6YDP. Per-residue inclusion information can be found in section [3](#) on page [26](#).

9.1 Map-model overlay [i](#)



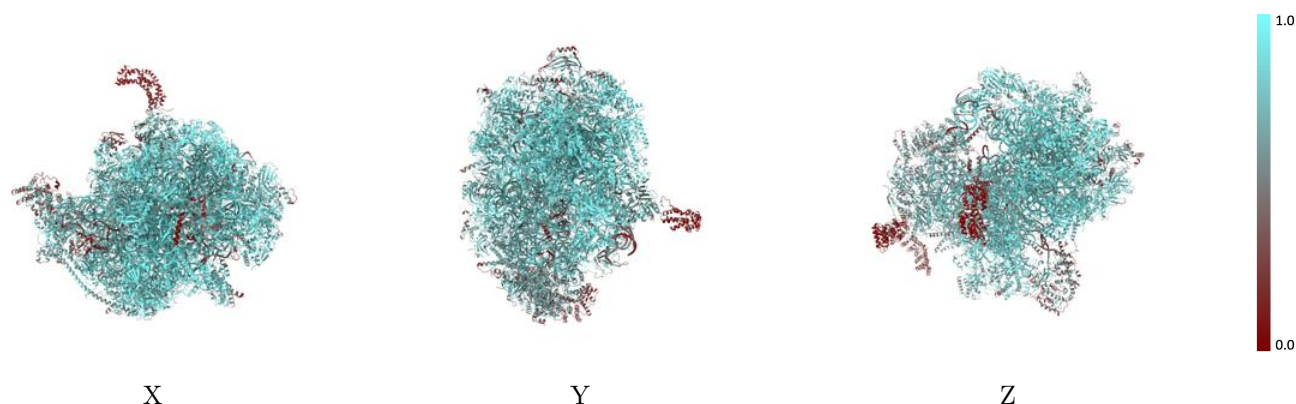
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



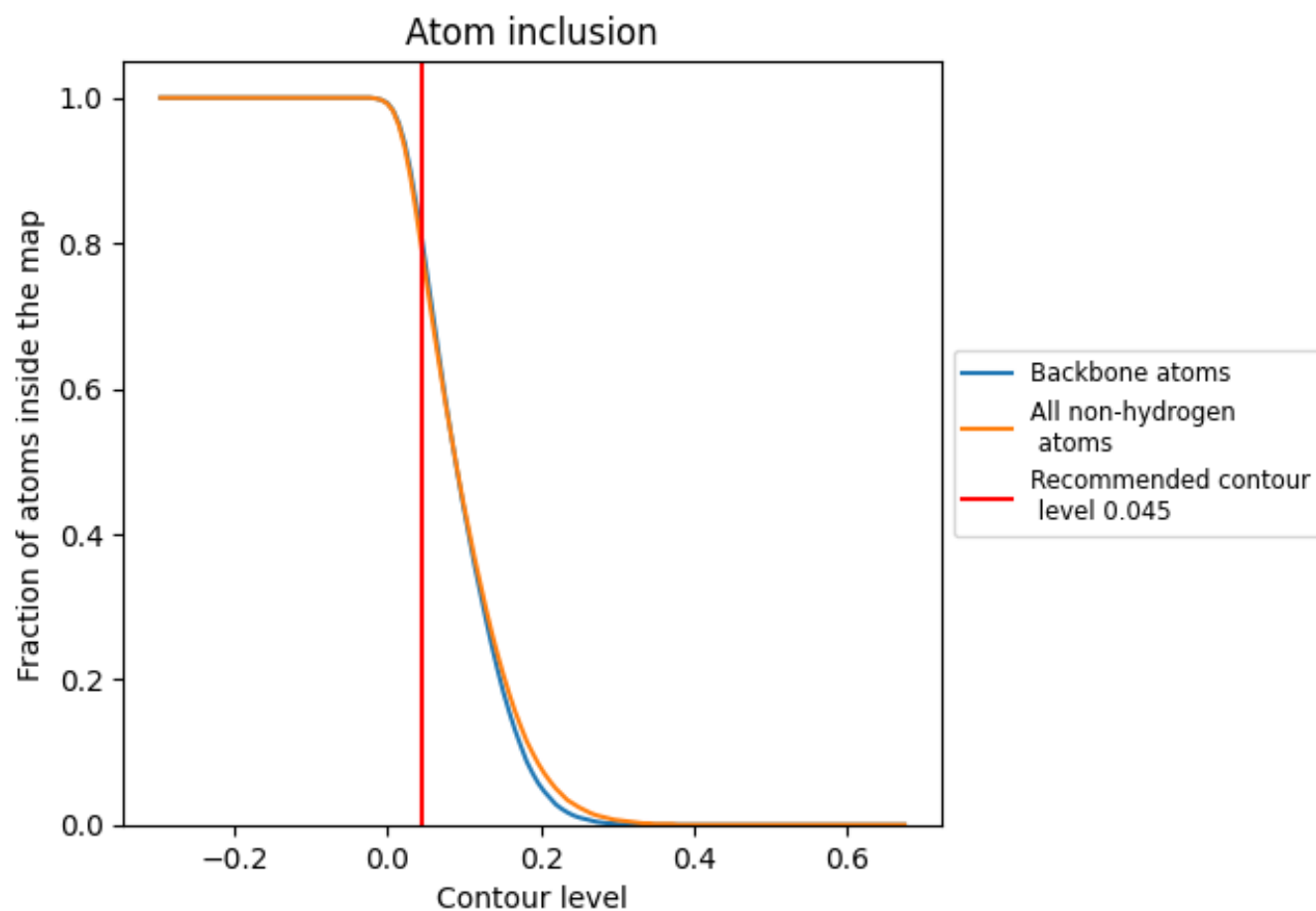
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.045).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 79% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7870	 0.4840
AA	 0.8810	 0.4940
AB	 0.8350	 0.5080
AC	 0.7240	 0.4790
AE	 0.7210	 0.4870
AF	 0.7890	 0.5000
AG	 0.6670	 0.4220
AI	 0.7050	 0.4290
AJ	 0.6520	 0.4140
AK	 0.8200	 0.5130
AL	 0.8460	 0.5520
AN	 0.7370	 0.4570
AO	 0.7190	 0.4720
AP	 0.7920	 0.5000
AQ	 0.8330	 0.5360
AR	 0.8380	 0.5290
AU	 0.8400	 0.5230
AV	 0.7670	 0.4210
AX	 0.7210	 0.4760
AZ	 0.5440	 0.2110
Aa	 0.7300	 0.4330
Ab	 0.7220	 0.4460
Ac	 0.8010	 0.5080
Ad	 0.7400	 0.4310
Ae	 0.4470	 0.2310
Af	 0.7720	 0.4840
Ag	 0.6120	 0.3520
Ah	 0.5300	 0.3420
Ai	 0.6640	 0.4080
Aj	 0.6670	 0.4090
Ak	 0.6180	 0.3740
Am	 0.6820	 0.4650
An	 0.7980	 0.5240
Ao	 0.2040	 0.2230
Ap	 0.8020	 0.4690



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Chain	Atom inclusion	Q-score
B0	 0.9110	 0.5790
B1	 0.7990	 0.5030
B2	 0.8420	 0.5370
B3	 0.8940	 0.5640
B4	 0.7140	 0.4090
B5	 0.8700	 0.5480
B6	 0.7070	 0.4880
B7	 0.9540	 0.6030
B8	 0.9080	 0.5860
B9	 0.9250	 0.5750
BA	 0.9280	 0.5540
BB	 0.6730	 0.3130
BC	 0.8010	 0.5080
BD	 0.8820	 0.5620
BE	 0.8880	 0.5580
BF	 0.8960	 0.5540
BI	 0.7340	 0.4620
BJ	 0.5750	 0.3810
BK	 0.7420	 0.4710
BN	 0.9090	 0.5740
BO	 0.8700	 0.5570
BP	 0.8770	 0.5440
BQ	 0.8810	 0.5630
BR	 0.8920	 0.5570
BS	 0.8770	 0.5330
BT	 0.8150	 0.5240
BU	 0.8840	 0.5610
BV	 0.8780	 0.5500
BW	 0.8800	 0.5700
BX	 0.8050	 0.5160
BY	 0.6380	 0.4530
Ba	 0.8690	 0.5290
Bb	 0.8410	 0.4970
Bc	 0.7950	 0.4810
Bd	 0.6480	 0.3720
Be	 0.8000	 0.4920
Bf	 0.7810	 0.4850
Bg	 0.8860	 0.5620
Bh	 0.8390	 0.5120
Bi	 0.5570	 0.4080
Bj	 0.6080	 0.3060
Bk	 0.6730	 0.4310

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Chain	Atom inclusion	Q-score
Bl	 0.8830	 0.5380
Bm	 0.6080	 0.4340
Bn	 0.9060	 0.5750
Bo	 0.8400	 0.5170
Bp	 0.6590	 0.3810
Bq	 0.7530	 0.4420
Bt	 0.8890	 0.5640
Bu	 0.6700	 0.4230
Bv	 0.6870	 0.4510
Bw	 0.8630	 0.5340
Bx	 0.8420	 0.5150
CL	 0.1140	 0.1270
DL	 0.1450	 0.2010
EL	 0.0720	 0.2050
FL	 0.0190	 0.1690
GL	 0.0420	 0.1720
HL	 0.0540	 0.1950
LL	 0.1830	 0.2320