



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 09:20 PM UTC

PDB ID : 7AM2 / pdb_00007am2
EMDB ID : EMD-11821
Title : Intermediate assembly of the Large subunit from Leishmania major mitochondrial ribosome
Authors : Soufari, H.; Waltz, F.; Parrot, C.; Bochler, A.; Hashem, Y.
Deposited on : 2020-10-07
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

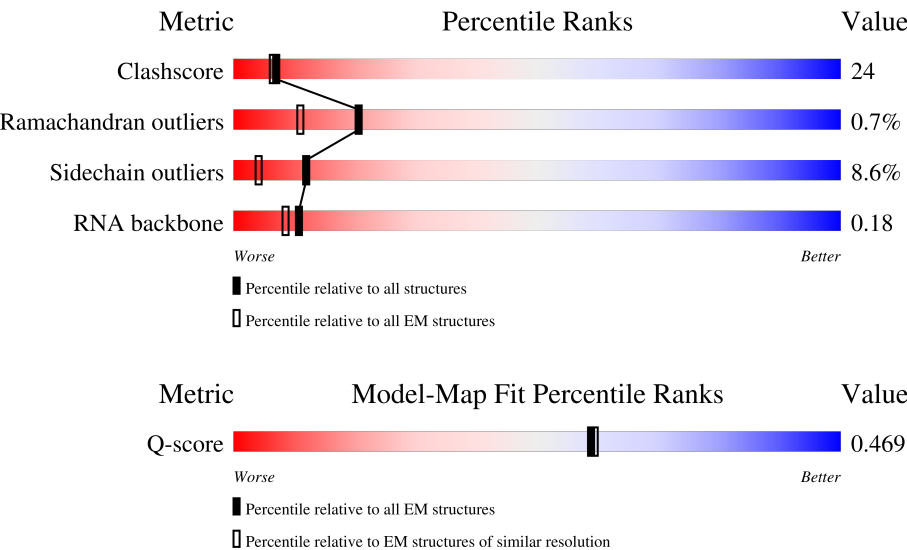
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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

Mol	Chain	Length	Quality of chain
1	A	467	45%29%24%
2	B	436	63%34%
3	C	262	42%34%5%19%

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Mol	Chain	Length	Quality of chain
4	E	346	
5	F	171	
6	G	374	
7	I	305	
8	J	144	
9	K	194	
10	L	186	
11	M	279	
12	N	252	
13	O	476	
14	Q	234	
15	R	480	
16	S	409	
17	T	83	
18	V	151	
19	Z	197	
20	BA	167	
21	CA	618	
22	UA	203	
23	BB	156	
24	CB	202	
25	BK	893	
26	BQ	445	
27	BN	344	
28	BE	118	

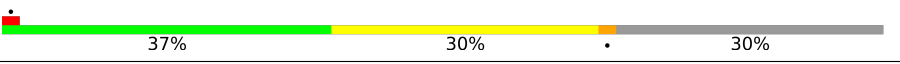
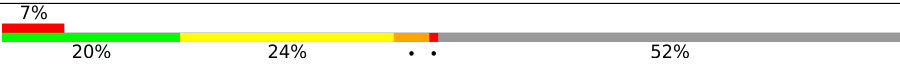
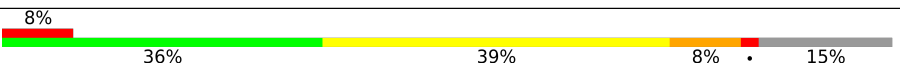
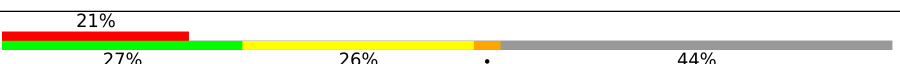
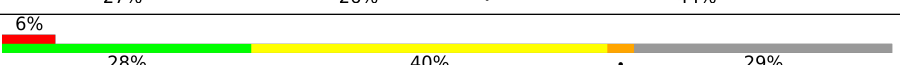
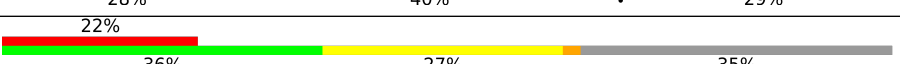
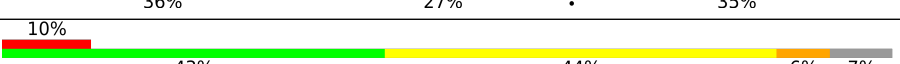
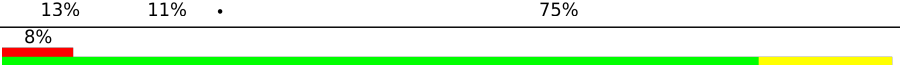
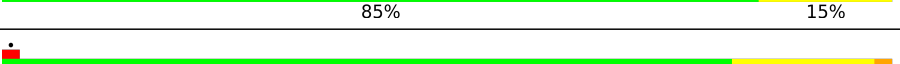
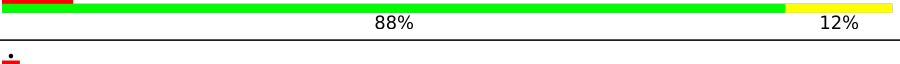
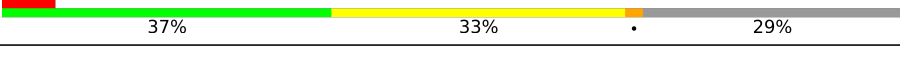
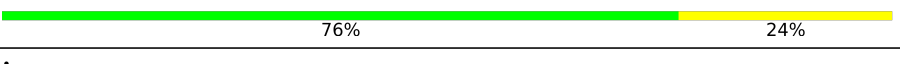
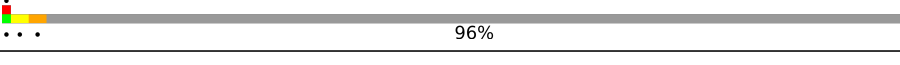
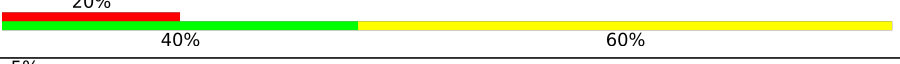
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Mol	Chain	Length	Quality of chain
29	BO	190	
30	At	183	
31	Au	186	
32	Ae	311	
33	Af	155	
34	Ah	570	
35	Ap	240	
36	Al	346	
37	Ab	262	
38	Aa	195	
39	BP	254	
40	Az	152	
41	Am	340	
42	As	249	
43	BG	1347	
44	Ad	237	
45	Aw	187	
46	BH	229	
47	Aj	503	
48	Ar	205	
49	An	331	
50	BF	109	
51	Av	192	
52	BM	457	
53	Ag	244	

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Mol	Chain	Length	Quality of chain
54	Bl	266	
55	Ax	216	
56	BS	416	
57	BX	569	
57	BY	569	
58	BZ	413	
59	CC	150	
60	CD	126	
61	BT	464	
62	BU	497	
63	BW	776	
64	BV	787	
65	U7	40	
66	U6	187	
67	U1	46	
68	U3	75	
69	U4	136	
70	U5	94	
71	BR	301	
72	U2	37	
73	1	19000	
74	R1	3	
75	R2	35	
76	R5	5	
77	U8	59	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
78	GTP	BU	501	-	-	X	-

2 Entry composition

There are 79 unique types of molecules in this entry. The entry contains 139535 atoms, of which 12 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 Ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	356	Total	C	N	O	S	0	0
			2909	1877	482	535	15		

- Molecule 2 is a protein called uL4m.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	435	Total	C	N	O	S	0	0
			3513	2237	615	642	19		

- Molecule 3 is a protein called RIBOSOMAL_L9 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	212	Total	C	N	O	S	0	0
			1772	1144	303	321	4		

- Molecule 4 is a protein called Putative ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	225	Total	C	N	O	S	0	0
			1818	1176	319	314	9		

- Molecule 5 is a protein called 50S ribosomal protein L13-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	147	Total	C	N	O	S	0	0
			1231	788	223	210	10		

- Molecule 6 is a protein called Ribosomal_L18e/L15P domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	334	Total	C	N	O	S	0	0
			2767	1765	505	489	8		

- Molecule 7 is a protein called Putative 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	257	Total	C	N	O	S	0	0
			2153	1362	406	372	13		

- Molecule 8 is a protein called bL19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	141	Total	C	N	O	S	0	0
			1146	727	211	202	6		

- Molecule 9 is a protein called bL20m.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	179	Total	C	N	O	S	0	0
			1467	910	289	258	10		

- Molecule 10 is a protein called bL21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	178	Total	C	N	O	S	0	0
			1419	907	257	250	5		

- Molecule 11 is a protein called uL22m.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	259	Total	C	N	O	S	0	0
			2116	1345	385	371	15		

- Molecule 12 is a protein called uL23m.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	189	Total	C	N	O	S	0	0
			1599	1031	296	269	3		

- Molecule 13 is a protein called uL24m.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	300	Total	C	N	O	S	0	0
			2477	1561	446	463	7		

- Molecule 14 is a protein called bL28m.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	217	Total	C	N	O	S	0	0
			1785	1127	331	316	11		

- Molecule 15 is a protein called uL29m.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	472	Total	C	N	O	S	0	0
			3755	2377	662	704	12		

- Molecule 16 is a protein called uL30m.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	150	Total	C	N	O	S	0	0
			1244	782	247	207	8		

- Molecule 17 is a protein called bL32m.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	T	55	Total	C	N	O	S	0	0
			487	311	93	78	5		

- Molecule 18 is a protein called bL35m.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	141	Total	C	N	O	S	0	0
			1202	755	242	197	8		

- Molecule 19 is a protein called mL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Z	113	Total	C	N	O	S	0	0
			907	582	167	154	4		

- Molecule 20 is a protein called mL94.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BA	106	Total	C	N	O	S	0	0
			786	489	144	149	4		

- Molecule 21 is a protein called TRUD domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CA	537	Total	C	N	O	S	0	0
			4230	2664	783	765	18		

- Molecule 22 is a protein called UA.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	UA	203	Total	C	N	O	0	0
			1015	609	203	203		

- Molecule 23 is a protein called mL95.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	BB	106	Total	C	N	O	0	0
			894	574	168	152		

- Molecule 24 is a protein called RNA uridylyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	CB	135	Total	C	N	O	S	0	0
			1074	673	192	201	8		

- Molecule 25 is a protein called mL67.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BK	694	Total	C	N	O	S	0	0
			5419	3421	975	1002	21		

- Molecule 26 is a protein called mL71.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BQ	413	Total	C	N	O	S	0	0
			3230	2031	571	615	13		

- Molecule 27 is a protein called mL81.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BN	196	Total	C	N	O	S	0	0
			1507	939	275	286	7		

- Molecule 28 is a protein called mL98.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	BE	37	Total	C	N	O	0	0
			325	210	55	60		

- Molecule 29 is a protein called Putative ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BO	158	Total	C	N	O	S	0	0
			1281	805	258	209	9		

- Molecule 30 is a protein called mL86.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	At	165	Total	C	N	O	S	0	0
			1346	824	260	254	8		

- Molecule 31 is a protein called mL87.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Au	80	Total	C	N	O	S	0	0
			681	432	135	109	5		

- Molecule 32 is a protein called mL53.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ae	290	Total	C	N	O	S	0	0
			2354	1523	417	403	11		

- Molecule 33 is a protein called mL63.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Af	145	Total	C	N	O	S	0	0
			1192	748	228	215	1		

- Molecule 34 is a protein called mL68.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ah	399	Total	C	N	O	S	0	0
			3242	2062	567	596	17		

- Molecule 35 is a protein called mL80.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ap	214	Total	C	N	O	S	0	0
			1775	1111	327	328	9		

- Molecule 36 is a protein called mL74.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Al	228	Total	C	N	O	S	0	0
			1857	1188	321	342	6		

- Molecule 37 is a protein called L51_S25_CI-B8 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ab	168	Total	C	N	O	S	0	0
			1413	886	268	254	5		

- Molecule 38 is a protein called mL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Aa	135	Total	C	N	O	S	0	0
			1076	670	202	199	5		

- Molecule 39 is a protein called mL52,mL52.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BP	131	Total	C	N	O	S	0	0
			1070	682	194	193	1		

- Molecule 40 is a protein called mL93.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Az	130	Total	C	N	O	S	0	0
			1150	739	205	201	5		

- Molecule 41 is a protein called mL75.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Am	296	Total	C	N	O	S	0	0
			2435	1553	435	431	16		

- Molecule 42 is a protein called mL85.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	As	144	Total	C	N	O	S	0	0
			1187	734	225	223	5		

- Molecule 43 is a protein called mL100.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BG	85	Total	C	N	O	S	0	0
			675	423	126	119	7		

- Molecule 44 is a protein called mL49.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ad	189	Total	C	N	O	S	0	0
			1502	969	264	262	7		

- Molecule 45 is a protein called mL89.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Aw	185	Total	C	N	O	S	0	0
			1509	949	289	268	3		

- Molecule 46 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BH	181	Total	C	N	O	S	0	0
			1394	885	244	257	8		

- Molecule 47 is a protein called mL72.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Aj	342	Total	C	N	O	S	0	0
			2777	1762	512	492	11		

- Molecule 48 is a protein called mL84.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ar	195	Total	C	N	O	S	0	0
			1644	1054	295	288	7		

- Molecule 49 is a protein called mL76.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	An	238	Total	C	N	O	S	0	0
			1946	1222	357	363	4		

- Molecule 50 is a protein called mL99.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BF	79	Total	C	N	O	S	0	0
			661	413	128	118	2		

- Molecule 51 is a protein called mL88.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Av	100	Total	C	N	O	S	0	0
			828	530	142	151	5		

- Molecule 52 is a protein called mL70.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BM	389	Total	C	N	O	S	0	0
			3069	1954	548	551	16		

- Molecule 53 is a protein called mL59/64.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ag	124	Total	C	N	O	S	0	0
			1031	656	189	181	5		

- Molecule 54 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Bl	186	Total	C	N	O	S	0	0
			1409	895	242	264	8		

- Molecule 55 is a protein called LIM zinc-binding domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Ax	167	Total	C	N	O	S	0	0
			1388	876	268	233	11		

- Molecule 56 is a protein called DNAj-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BS	125	Total	C	N	O	S	0	0
			978	624	177	173	4		

- Molecule 57 is a protein called SpoU_methylase domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BY	275	Total	C	N	O	S	0	0
			2111	1317	384	401	9		
57	BX	272	Total	C	N	O	S	0	0
			2086	1301	381	396	8		

- Molecule 58 is a protein called Pseudouridylate synthase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BZ	351	Total	C	N	O	S	0	0
			2829	1810	514	493	12		

- Molecule 59 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	CC	84	Total	C	N	O	S	0	0
			668	429	104	134	1		

- Molecule 60 is a protein called L0R8F8.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	CD	90	Total	C	N	O	S	0	0
			761	475	146	136	4		

- Molecule 61 is a protein called G domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	BT	300	Total	C	N	O	S	0	0
			2346	1487	419	425	15		

- Molecule 62 is a protein called GTPase Der.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	BU	463	Total	C	N	O	S	0	0
			3680	2315	654	691	20		

- Molecule 63 is a protein called DEAD/DEAH box helicase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	BW	447	Total	C	N	O	S	0	0
			3589	2282	661	622	24		

- Molecule 64 is a protein called G domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	BV	199	Total	C	N	O	S	0	0
			1596	1016	292	282	6		

- Molecule 65 is a protein called mL78.

Mol	Chain	Residues	Atoms				AltConf	Trace
65	U7	40	Total	C	N	O	0	0
			200	120	40	40		

- Molecule 66 is a protein called U6.

Mol	Chain	Residues	Atoms				AltConf	Trace
66	U6	187	Total	C	N	O	0	0
			935	561	187	187		

- Molecule 67 is a protein called U1.

Mol	Chain	Residues	Atoms				AltConf	Trace
67	U1	46	Total	C	N	O	0	0
			230	138	46	46		

- Molecule 68 is a protein called U3.

Mol	Chain	Residues	Atoms				AltConf	Trace
68	U3	75	Total	C	N	O	0	0
			375	225	75	75		

- Molecule 69 is a protein called U4.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	U4	136	Total	C	N	O	0	0
			680	408	136	136		

- Molecule 70 is a protein called U5.

Mol	Chain	Residues	Atoms				AltConf	Trace
70	U5	94	Total	C	N	O	0	0
			470	282	94	94		

- Molecule 71 is a protein called mL78.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	BR	214	Total	C	N	O	S	0	0
			1703	1071	329	300	3		

- Molecule 72 is a protein called U2.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	U2	37	Total	C	N	O	0	0
			185	111	37	37		

- Molecule 73 is a RNA chain called Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	1	797	Total	C	N	O	P	0	0
			16777	7564	2796	5622	795		

- Molecule 74 is a RNA chain called R1.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	R1	3	Total	C	N	O	P	0	0
			62	28	9	22	3		

- Molecule 75 is a RNA chain called R2.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	R2	34	Total	C	N	O	P	0	0
			665	306	68	258	33		

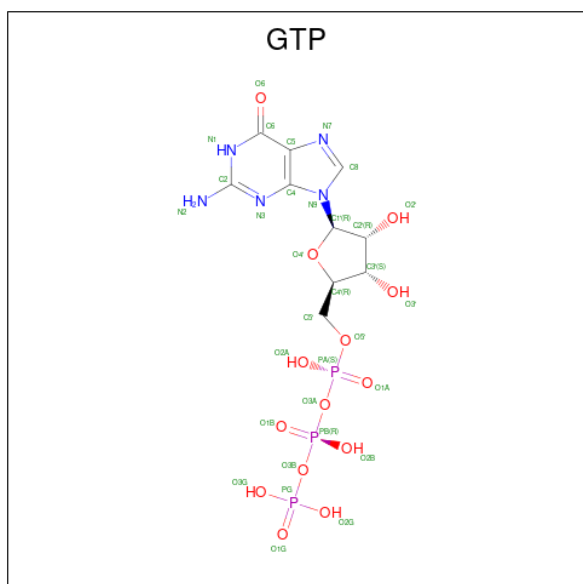
- Molecule 76 is a RNA chain called R5.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	R5	5	Total	C	N	O	P	0	0
			100	45	10	40	5		

- Molecule 77 is a protein called U8.

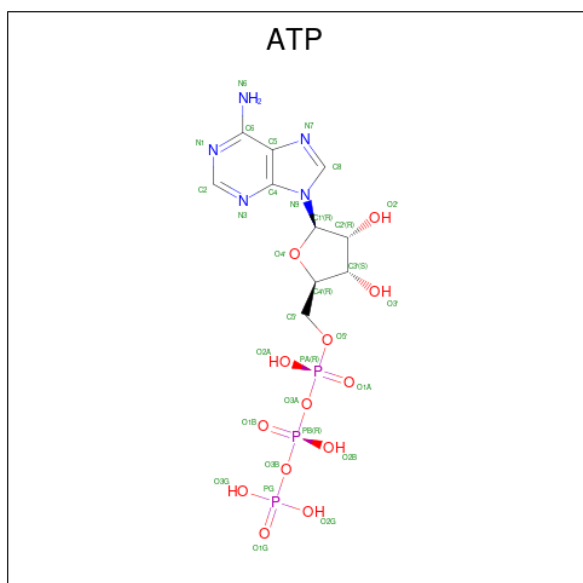
Mol	Chain	Residues	Atoms				AltConf	Trace
77	U8	59	Total	C	N	O	0	0
			295	177	59	59		

- Molecule 78 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).

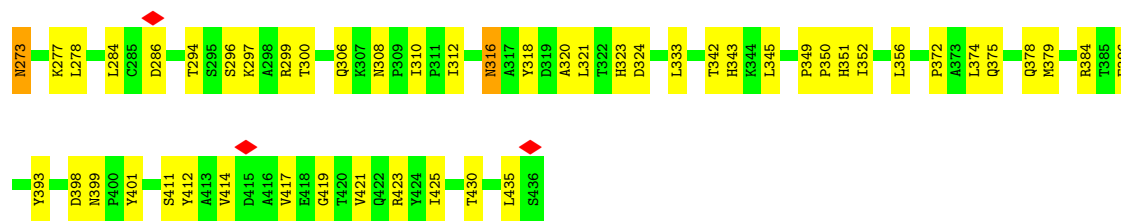


Mol	Chain	Residues	Atoms					AltConf
78	BU	1	Total	C	N	O	P	0
			32	10	5	14	3	

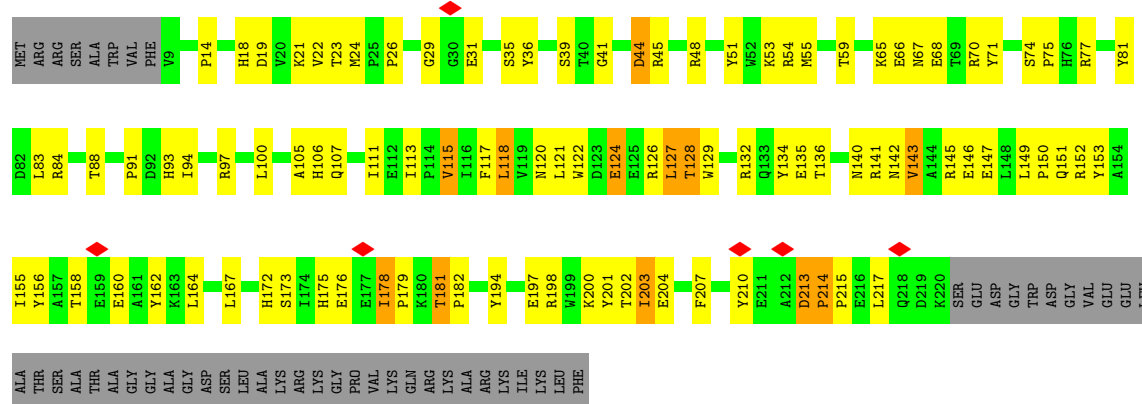
- Molecule 79 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



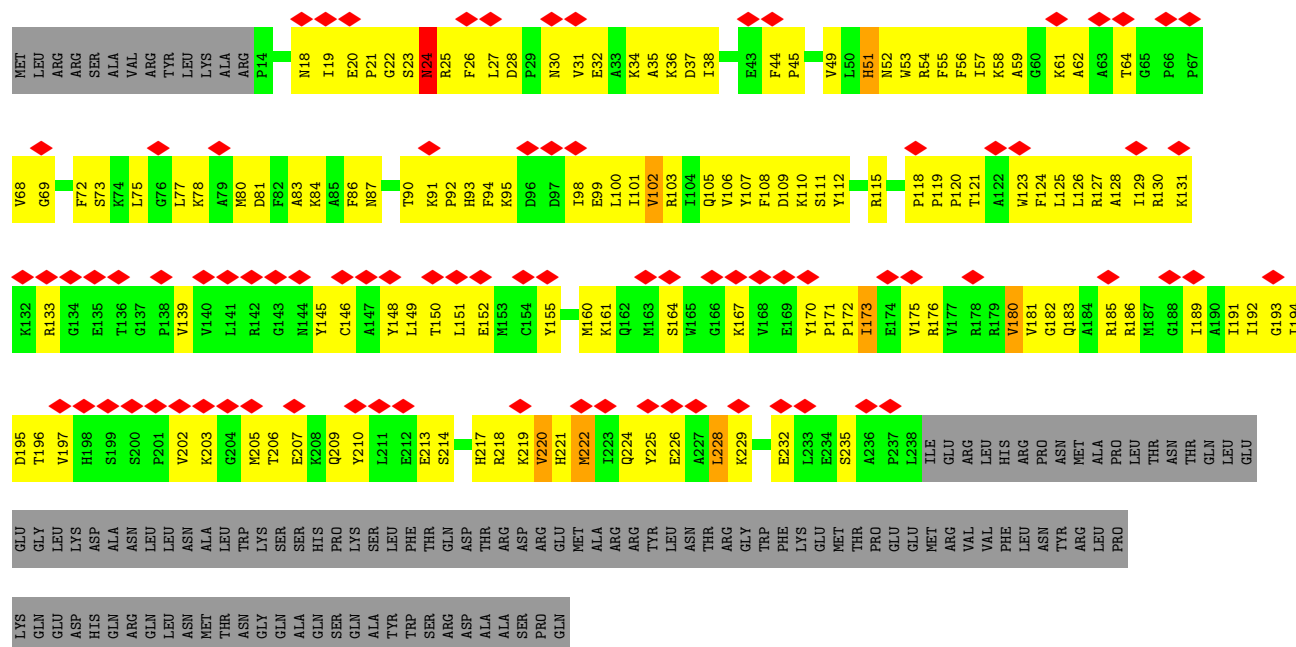
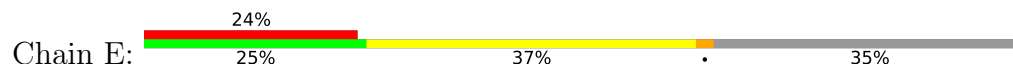
Mol	Chain	Residues	Atoms						AltConf
79	BW	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	



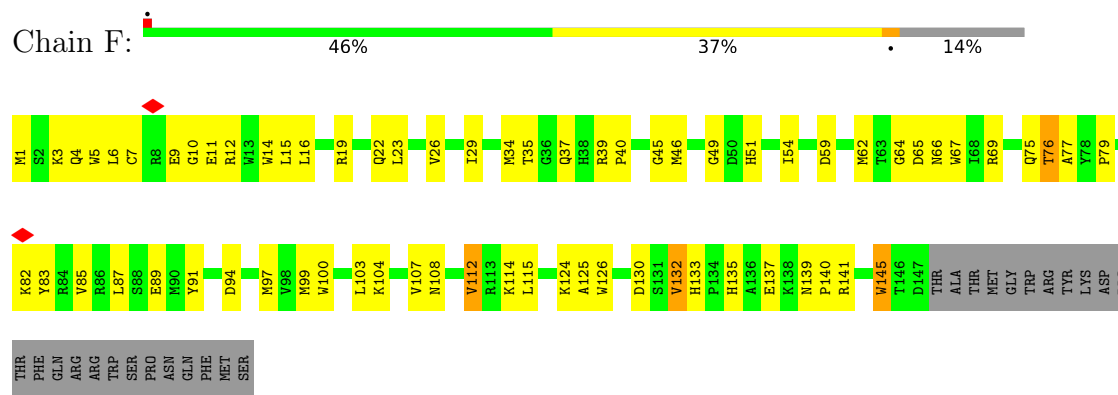
• Molecule 3: RIBOSOMAL_L9 domain-containing protein



• Molecule 4: Putative ribosomal protein L11



• Molecule 5: 50S ribosomal protein L13-like protein



PRO
GLN
LYS
TYR

• Molecule 8: bL19m

Chain J:  35% 50% 12% ..

MET G1 R4 E5 R6 T7 F11 F12 R15 F19 F20 S21 S22 L23 L24 R27 T28 Q29 R30 A31 I37 S41 M42 K43 P44 A45 K46 H47 T48 K49 E50 Q51 V52 T53 O54 S55 P56 S58 C59 N60 F61 E62 Y63 N64 P65 R66 P67 V68 R69 L70 L71 G72

T73 V74 M75 D76 A77 T79 E80 S81 T82 S83 R84 R85 G86 G87 L88 K89 Y90 Y91 A92 R93 S94 N98 M99 M100 L101 W102 I103 P104 A105 G106 N107 P108 K109 L110 L111 A112 E113 V114 T115 O116 A117 K118 S119 F120 S121 H122 Y123 L124 D125 R126 R127 S128 S129 E130 L131 L132

R139 A140 R141 MET LYS

• Molecule 9: bL20m

Chain K:  54% 36% 8% ..

MET LEU ARG SER THR VAL LEU Y10 Y11 R12 A13 T14 L20 M23 L24 R25 G26 R27 E31 R32 K33 V34 R38 I39 T40 F41 L42 M43 Q46 T47 R50 V51 E52 R59 V62 V66 D67 S68 A69 H73 G74 S75 D76 W77 R81 N82 D83

L84 N88 L89 Y102 E103 P104 L105 F107 R108 A109 V110 M111 E112 R117 P121 P122 P123 P124 M125 T126 A127 Q128 E132 T136 R137 P138 E139 D140 A144 H145 P146 A147 A148 R149 E153 E157 R158 M159 T162 G163 R164 S165 D166 V167 L168 Q169 R170 E171 G172

P173 R174 T175 W179 A182 L188 GLY SER ALA GLN LYS

• Molecule 10: bL21m

Chain L:  58% 34% ..

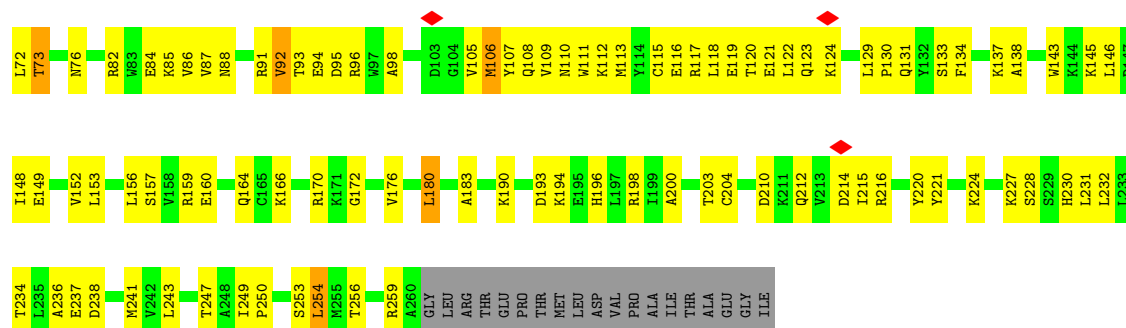
MET L2 L16 K21 F22 V25 N29 S35 D38 V39 V42 Q43 R44 Q52 I53 A54 L55 M60 V61 G62 G63 P64 R65 P66 T67 G70 R71 P72 L73 L74 V77 R78 T80 A81 D82 Q86 K87 R88 R89 R90 N91 V92 V93 S94 T98

R105 W106 L107 Q110 T114 I115 L116 R117 T118 R119 E120 Y123 E124 P125 T126 V127 V128 G129 E130 K133 L139 R140 D141 D145 Y146 H147 P148 N149 P150 V151 F152 D156 L160 K164 D165 W166 N167 K168 E171 E177 M178 N179 GLU ALA PRO THR LYS

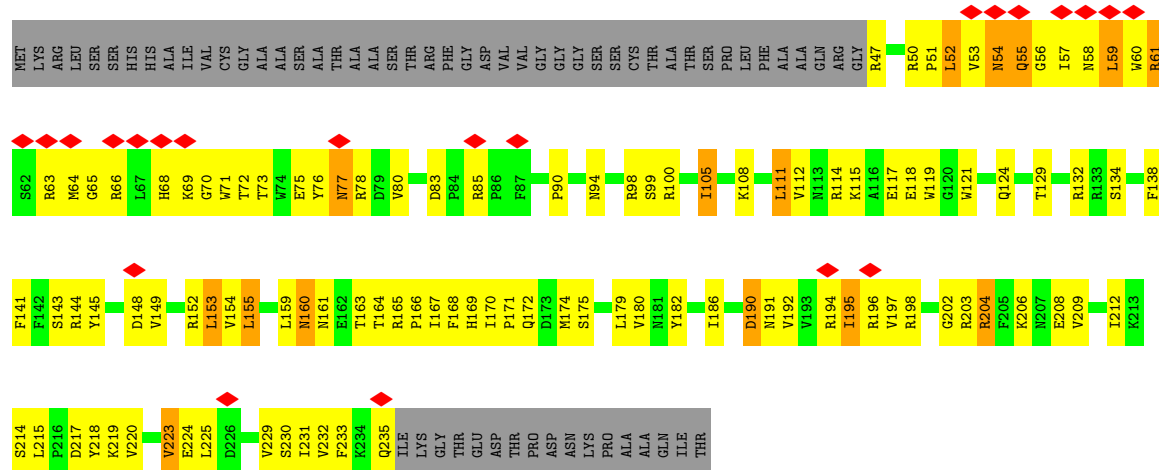
• Molecule 11: uL22m

Chain M:  43% 48% 7% ..

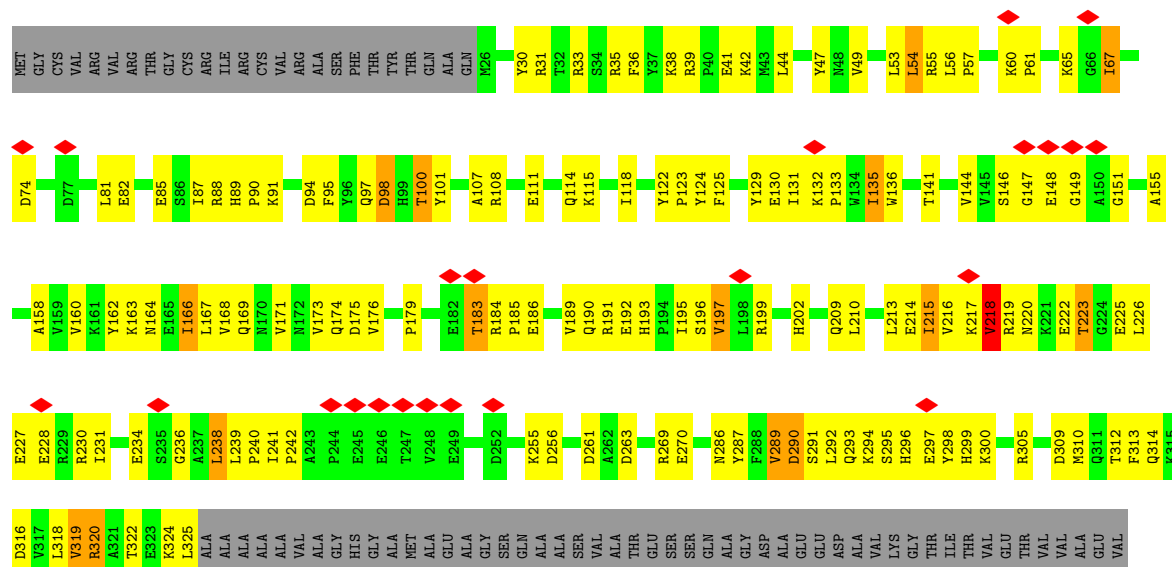
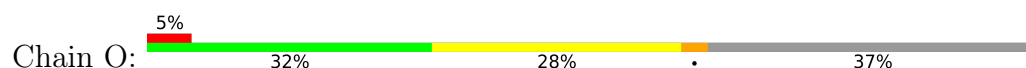
MET P2 R7 Y8 I10 G11 L12 R13 P14 A15 P16 K17 R18 Q19 N20 L26 Q29 K30 H31 Y32 A33 R34 E35 L36 W37 K39 R40 Q41 Y42 Y43 S44 T45 R46 P47 I50 Q51 K52 S56 T57 P58 R59 I60 L61 L62 D63 R64 T65 L66 W67 R68 S69 G70 W71

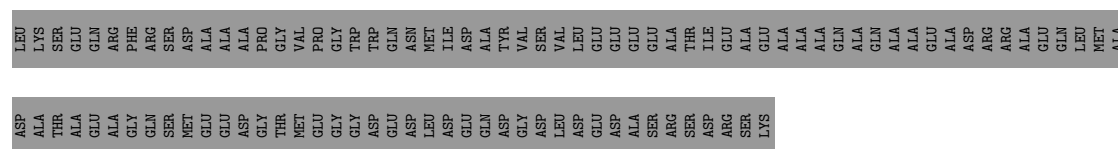


• Molecule 12: uL23m

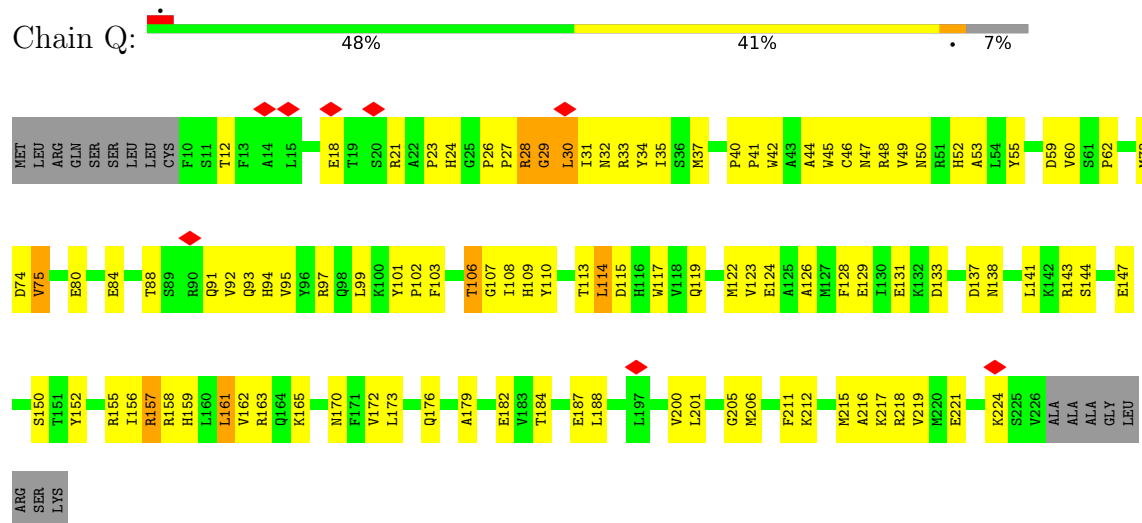


• Molecule 13: uL24m

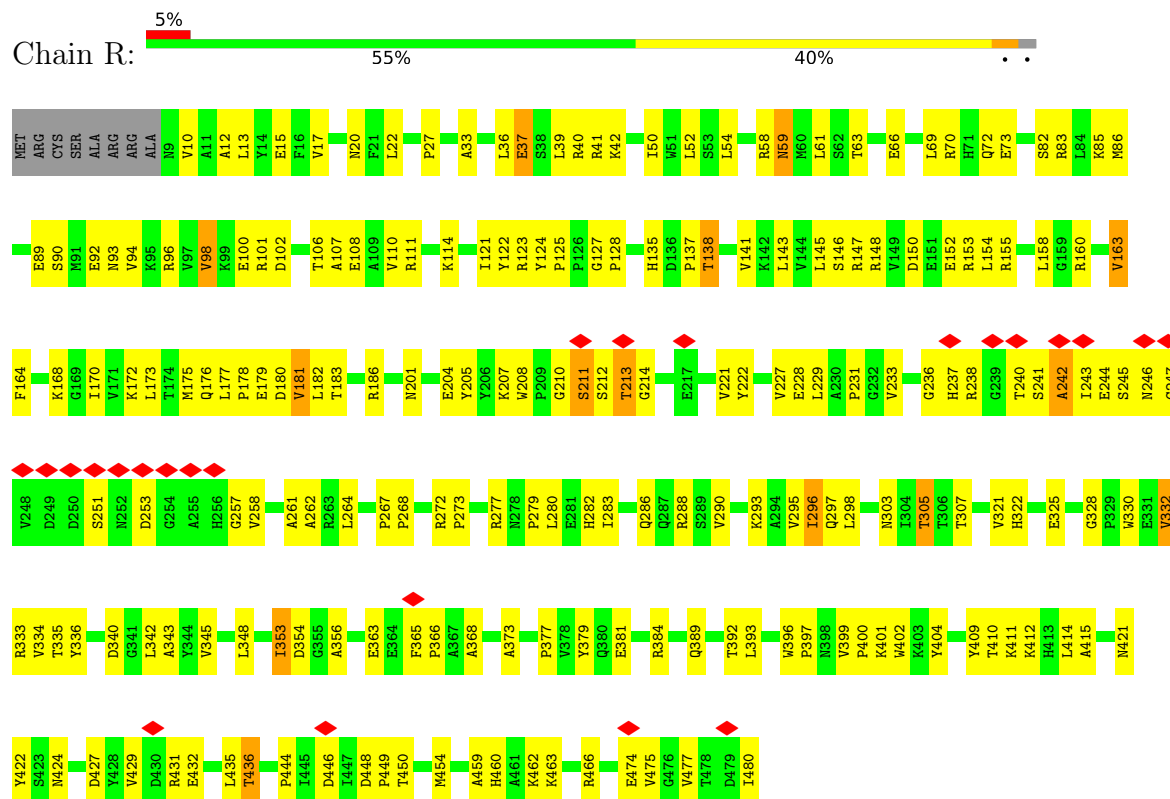




• Molecule 14: bL28m

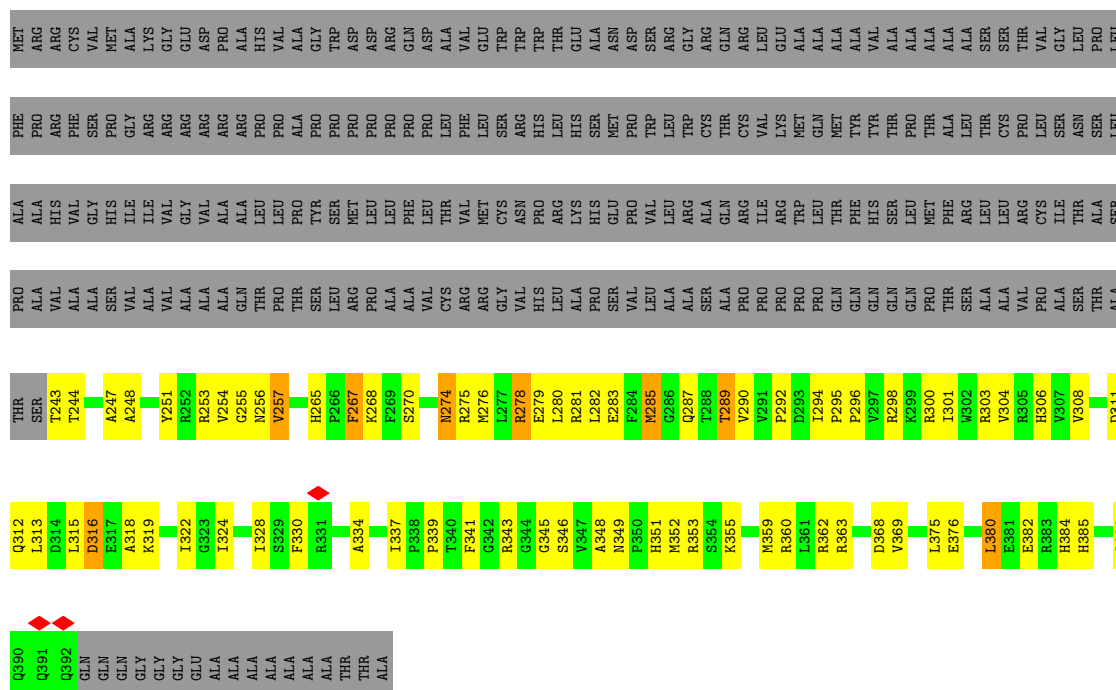


• Molecule 15: uL29m



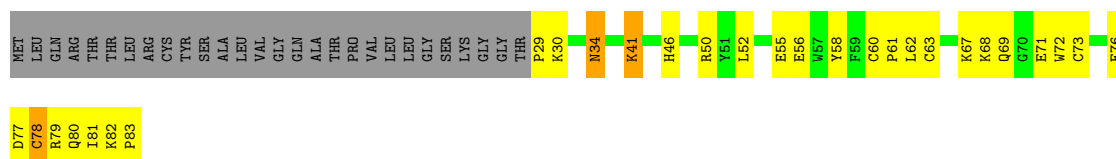
• Molecule 16: uL30m





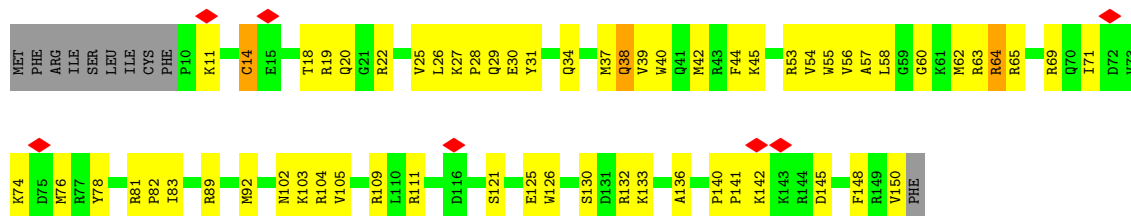
• Molecule 17: bL32m

Chain T: 33% 30% 34%



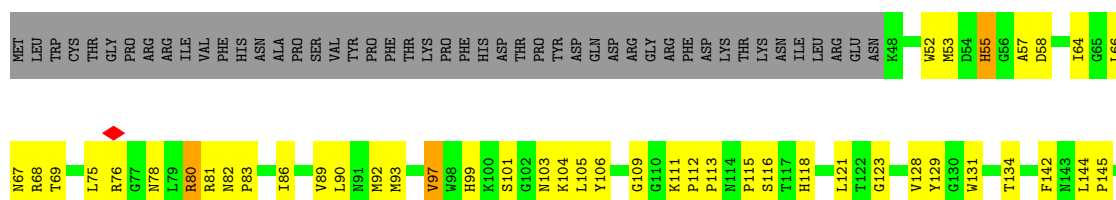
• Molecule 18: bL35m

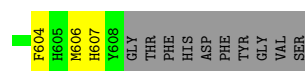
Chain V: 5% 53% 38% 7%



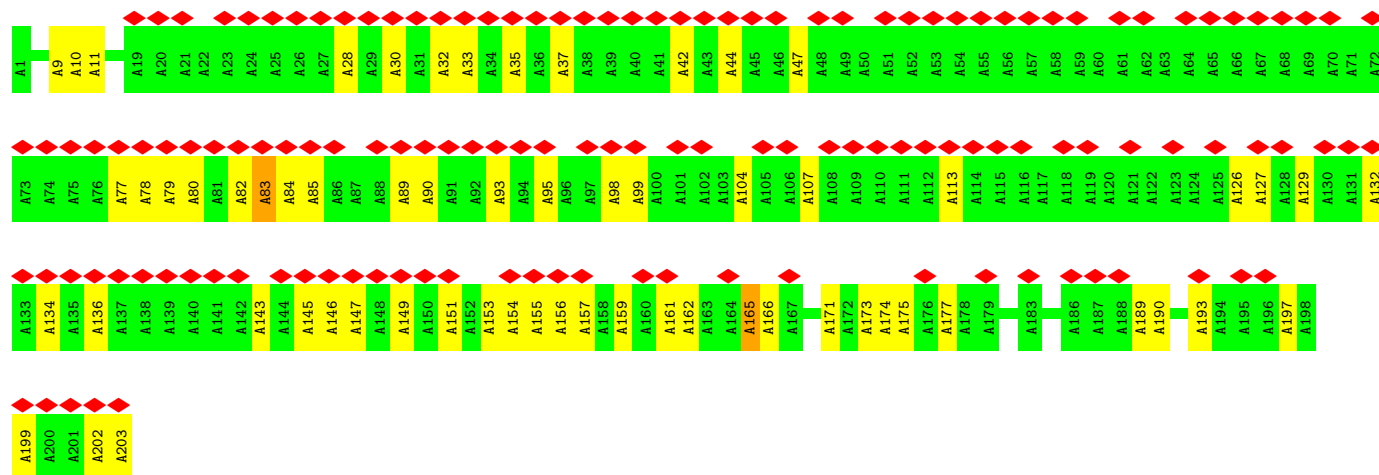
• Molecule 19: mL41

Chain Z: 30% 26% 43%

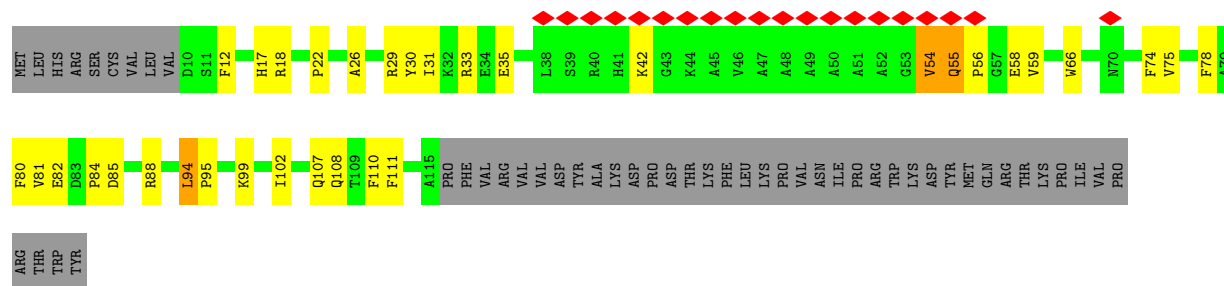




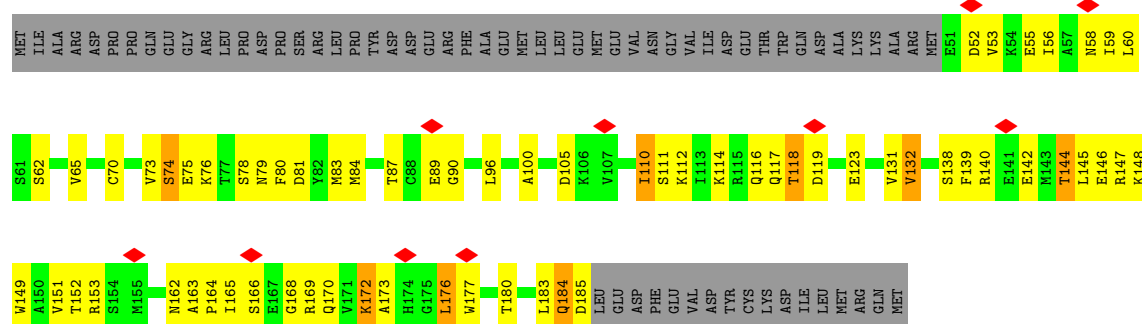
• Molecule 22: UA



• Molecule 23: mL95



• Molecule 24: RNA uridylyltransferase



• Molecule 25: mL67

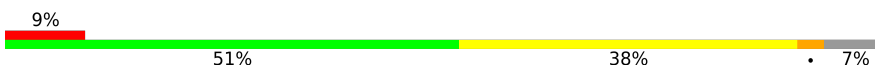
Chain BK:



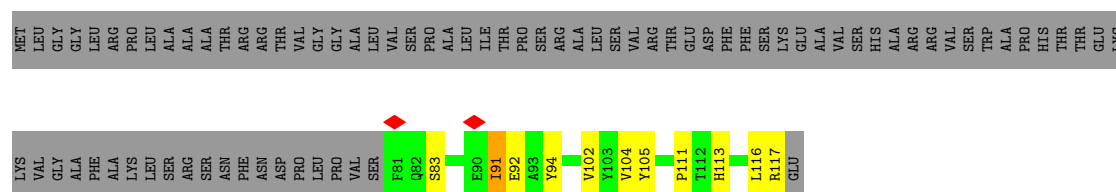
MET	ASP	GLU	T196	N304	THR	L454	T537	R620	D696	L775	P850
ARG	ALA	THR	V197	R309	ASN	R455	E538	V621	R697	T776	LEU
PHE	SER	ALA	L198		ARG	A456	L539	H622	A698	S777	ARG
ASP	MET	THR	D199		F371	H457	L540		L699	T778	GLN
ASN	PHE	SER		Y312	K375	A460	L543	T626	D700	D779	CYS
ALA	GLY	VAL	A202	H314	S376	P461	K546	L627	I701	D780	VAL
PRO	PRO	GLY	T203	P315	E377	S462		V628	W702		D853
PRO	VAL	LEU	R214	R316	D378	T463	D559	N630	S703		A861
PRO	ARG	SER	R217	G317	G379	S464	V560	L631	Y704		F864
PRO	LEU	THR	E218	V318	I380	L465	L563	D632	L705		Y865
PRO	ARG	THR		N319	L384	T466	R564	V637	E707		T866
PRO	ASN	SER		R320	K384	P467	R564	A791	R710		P867
PRO	VAL	VAL	L222	T321	S388	T468	A565	N639	A791		R868
GLU	PRO	THR		G322	G389	L469	V566	V640	M714		H869
ALA	ASP	GLY	N228	G323	V390	F470	P567	F641	R793		W869
ALA	ILE	ALA	G229	H324	V390	C471	H568	L642	P715		P870
GLY	ALA	GLU	Q231	V325	D393	E472	H569	L644	D718		K795
SER	GLU	PRO	L230	T327	G394	R473	A570	H644	L722		E796
THR	GLU	ASP	Q231	T327	G394	R473	A570	H644	L722		L797
THR	ALA	GLU	F232	R329	K395	D474	D571	S645	Y721		R798
THR	ARG	GLU	L233	A330	V400	D475	E574	S646	H723		H802
SER	ARG	LEU	K236	L331	R575	L401	R575	S649	H723		H803
SER	ALA	LEU	L237	L332	L404	L404	L576	R650	T727		H804
THR	LYS	SER	K239	D333	L404	A482	A577	C651	Y728		Y805
ALA	ALA	ARG	Y240	F334	L408	Q483	E578	L655	C729		W806
ALA	ALA	ALA	G241	E336	L408	S484	Q579	L655	D730		H807
SER	GLN	PRO	R242	E336	W412	L485	R580	V656	E731		Q807
ALA	GLN	ASP	S243	D337	W412	T486	A581	R660	R735		VAL
LEU	PRO	ALA	V246	X338	W415	R489	E582	R661	L735		PRO
PRO	PRO	GLN		V339	W415	R489	E582	R661	L735		ALA
ARG	ARG	ASP	T251	T340	L419	F493	A583	R662	A739		ASN
VAL	GLY	GLU	L156	S341	L419	F493	P584	R663	Q815		PRO
SER	SER	SER	L156	HIS	V426	V497	P584	S664	T816		PRO
TYR	ALA	ALA		ASN	R427	S498	T589	K666	L742		ALA
ARG	SER	THR	V255	TRP	L428	R499	A590	D667	A743		ALA
THR	THR	GLN	D259	THR			A590	A668	R744		SER
LEU	LEU	GLN		GLY	Y432	R502	S591		D745		GLN
PRO	SER	GLN	H164	GLU	M433	A503	A592	V671	V746		
SER	SER	ASP	L168	ALA	L434	M504	L595	T672	V749		
MET	ALA	ALA	D169	ALA	L435	V505	P596		K750		
TYR	ASP	ASP	V170	VAL	Q436		D597	L676	W751		
PRO	GLY	GLY	L171	ASP	V437		T598	L677	T752		
LYS	ASP	GLN	R175	ASP	M438		A599	A678	T753		
GLU	ASN	GLN	Q183	GLN	M440		A599	L679	W754		
VAL	ALA	GLY	F184	GLY	Q441		A600	Q680	M755		
SER	ALA	SER	W185	SER	R442		V601		S756		
ASP	ALA	ALA	L289	LEU	D442		L602	Y685	S757		
PHE	SER	ALA	V290	LEU	D443		A518	G686	R758		
ILE	SER	SER	K291	ARG	A444		A518	A687	P764		
PRO	LEU	LEU	I292	ARG	L446		D526	T688	Q765		
PHE	TRP	TRP	K297	PRO	D447		V527	E689	H766		
LEU	ALA	ALA		VAL	A448			K690			
PRO	GLU	GLU	E191	PRO	L449			R691	R769		
LEU	LEU	LEU	A192	GLN	L450			R692	G770		
LYS	SER	LYS	R193	HIS	L450			A693	E771		
HIS	GLY	GLY	P303	ALA	Q453			A695	H772		

• Molecule 26: mL71

Chain BQ:



MET	LEU	ARG	GLN	CYS	VAL	VAL	LEU	SER	Y11	D12	R13	G14	S15	W16	A17	S20	K21	Q23	K24	H25	K26	S27	L28	N29	K32	Y35	P40	V47	K48	K49	F50	Y51	G55	E62	R63	F64	F65	B66	L67	P68	E69	F70	S73	Y74	Q75	Q76	Q77	H78	Y79
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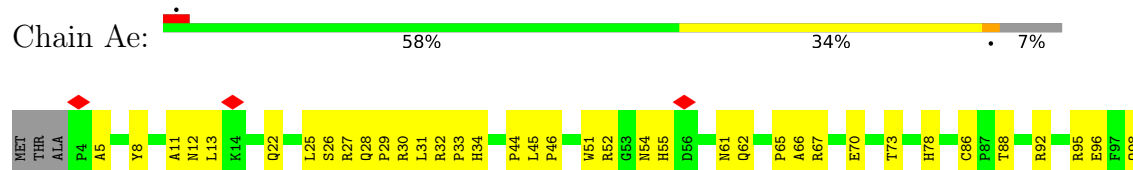


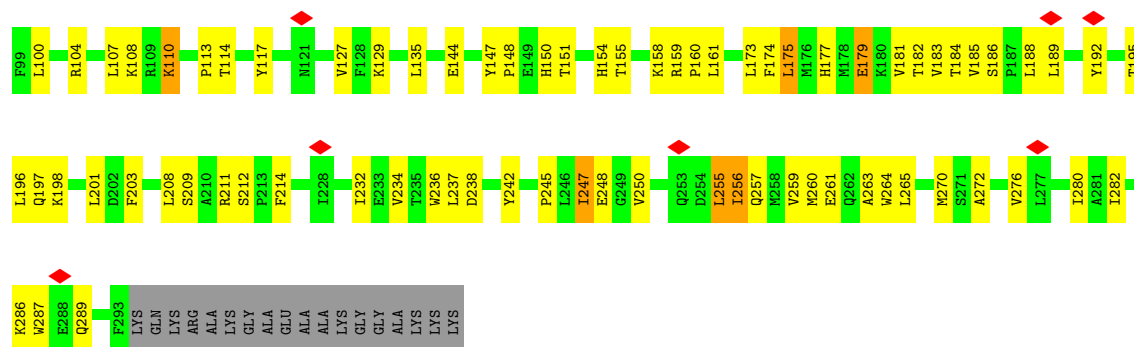
Chain BO:

Chain At:

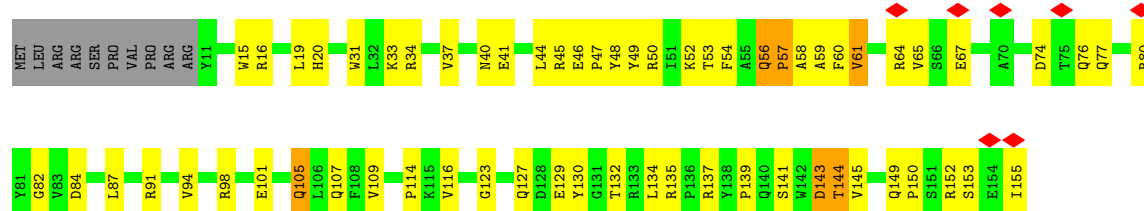
Chain Au:

Chain Ae:

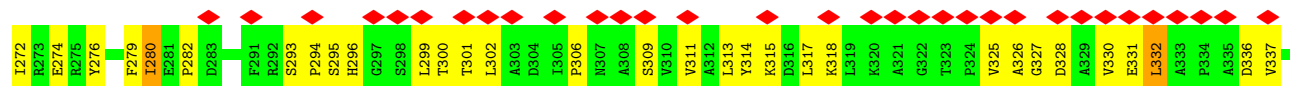
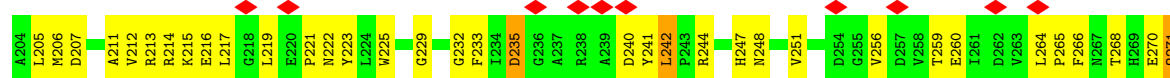
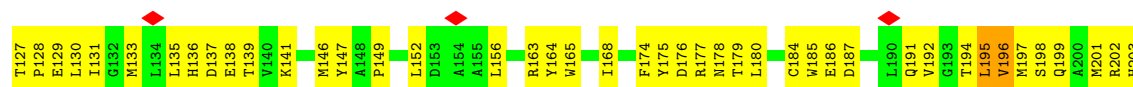
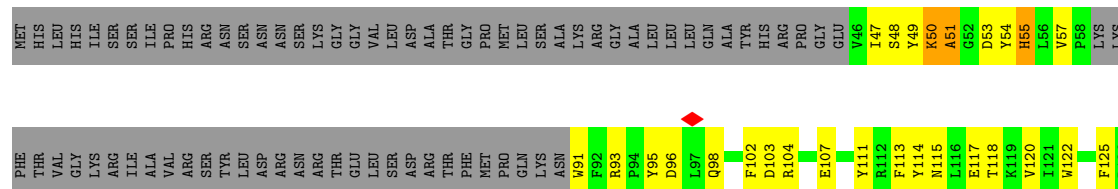


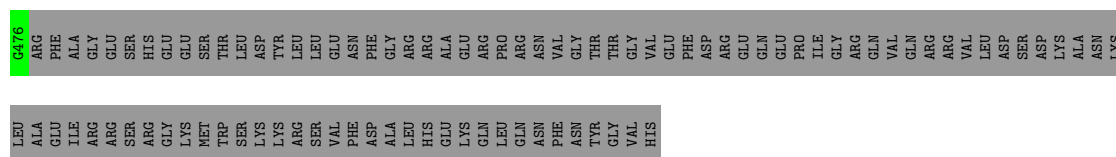


• Molecule 33: mL63

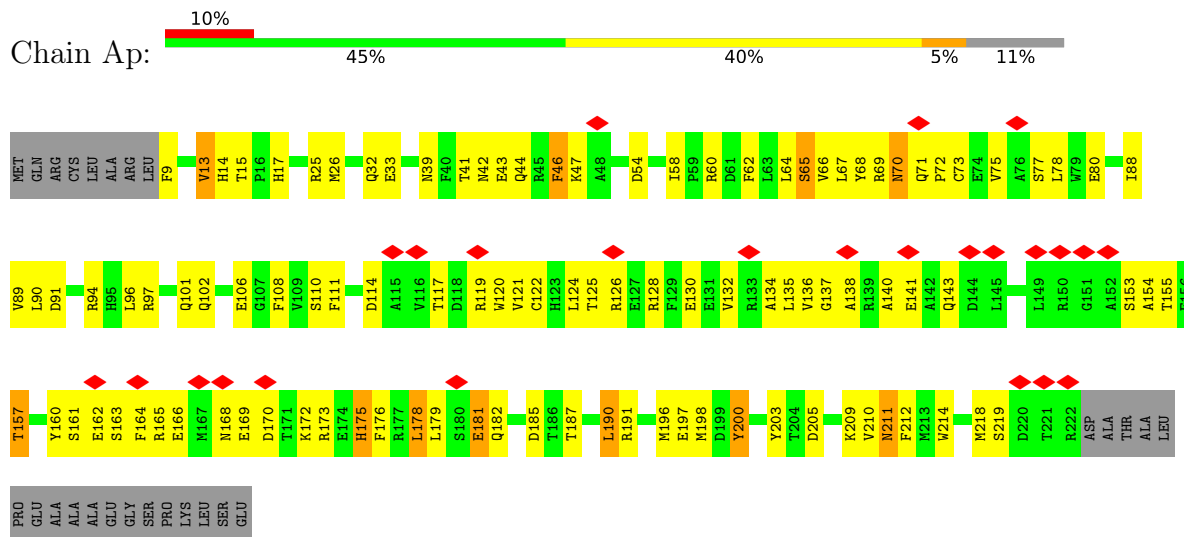


• Molecule 34: mL68

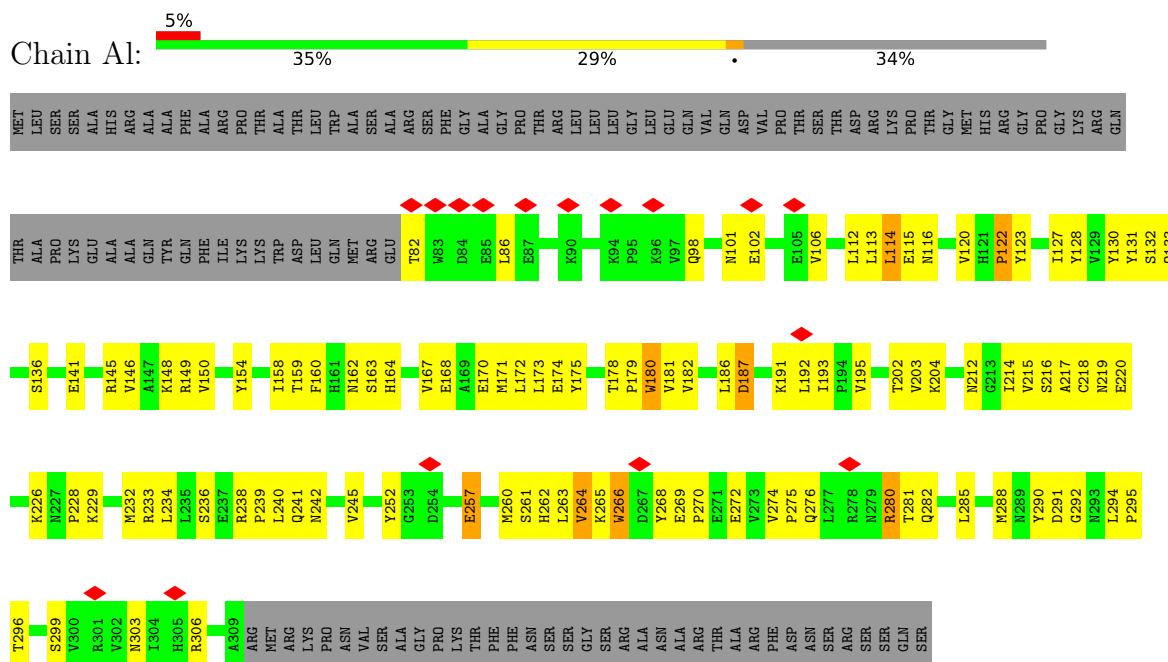




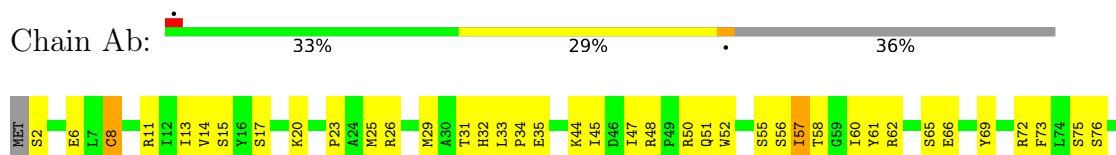
• Molecule 35: mL80

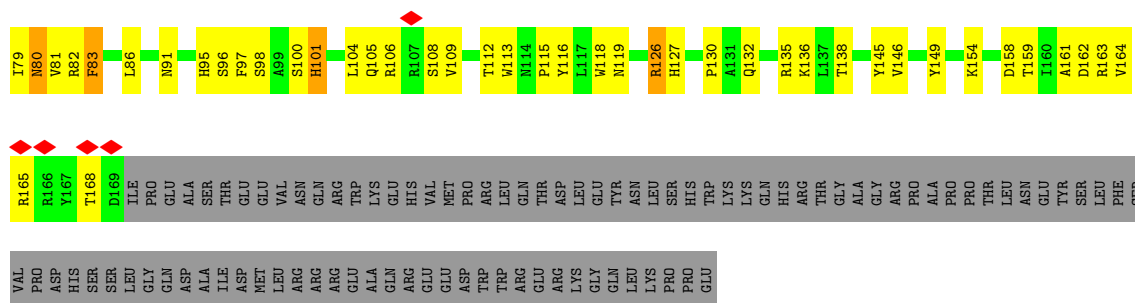


• Molecule 36: mL74

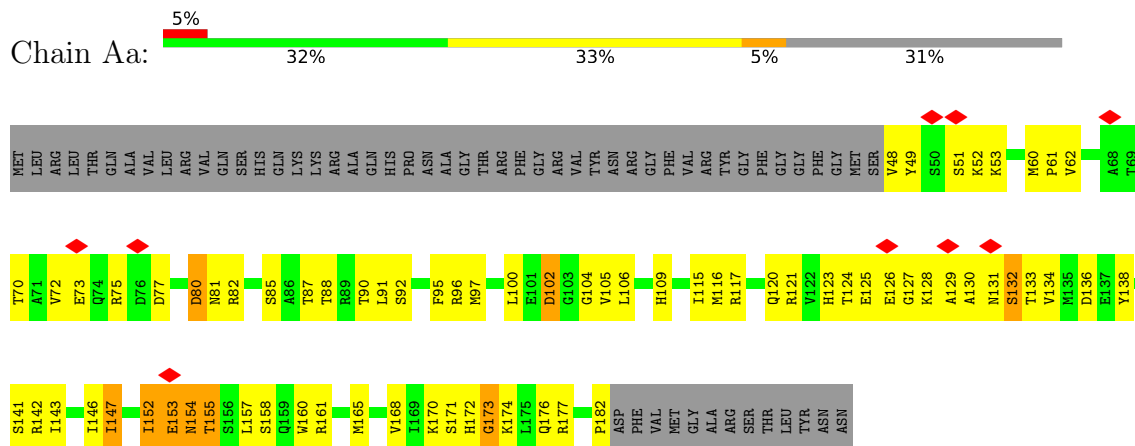


• Molecule 37: L51_S25_CI-B8 domain-containing protein

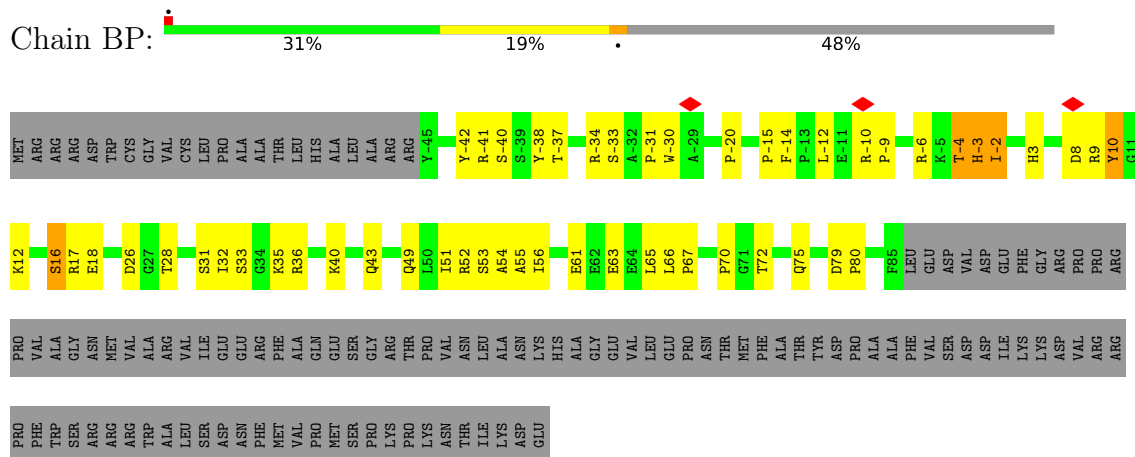




• Molecule 38: mL42



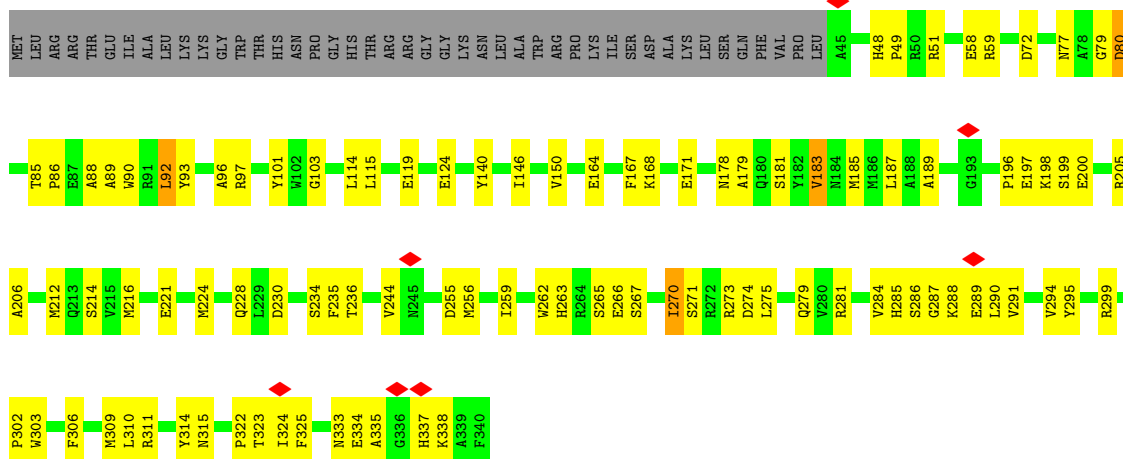
• Molecule 39: mL52,mL52



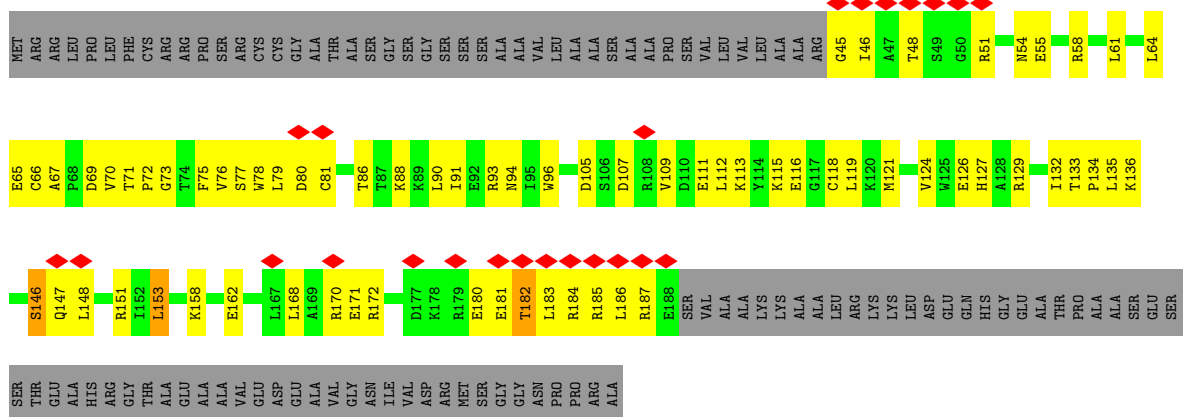
• Molecule 40: mL93



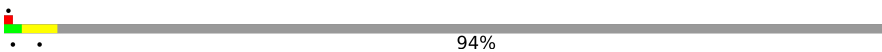
Chain Am:



Chain As:



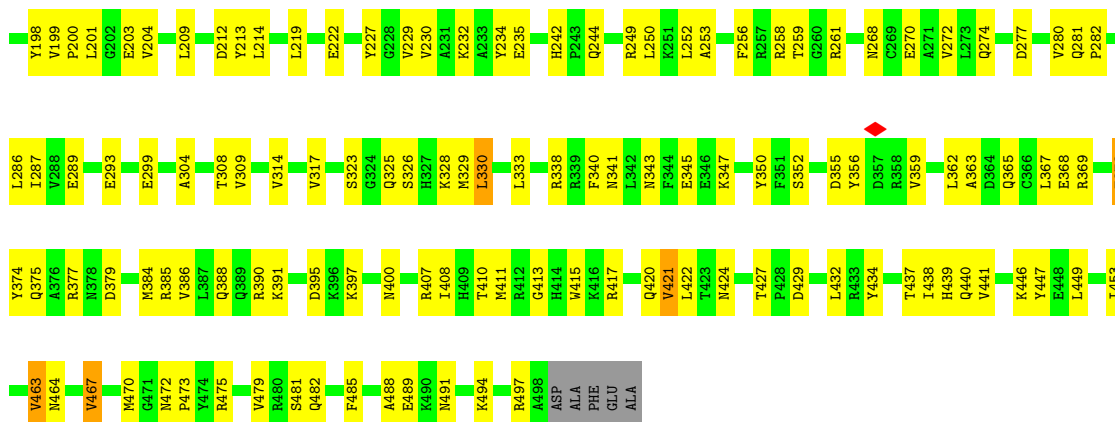
Chain BG:



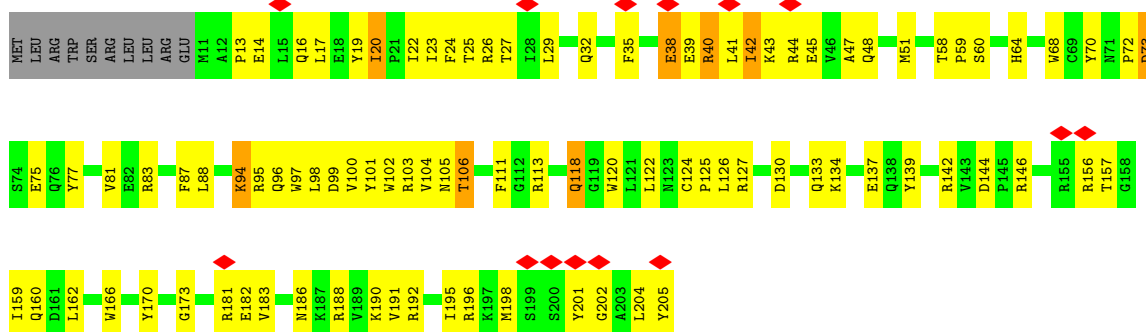
K1327	Q1328	R1329	S1330	G1331	K1332	I1333	A1334	S1335	Q1336	P1337	L1338	M1339	E1340	V1341	C1342	K1344	ASN	GLU	PHE																															
A1261	H1263	P1264	G1266	D1267	Q1268	I1269	L1270	L1271	V1272	S1273	M1274	S1275	F1276	T1277	L1280	L1281	T1282	R1283	T1284	D1285	P1288	K1289	G1290	D1291	R1292	T1295	F1296	M1299	S1300	V1301	M1304	R1307	M1308	P1309	Y1310	K1311	P1312	V1313	D1314	T1315	P1316	G1317	S1318	P1319	Y1320	A1321	T1322	L1323	Y1324	M1325

Chain Ad:

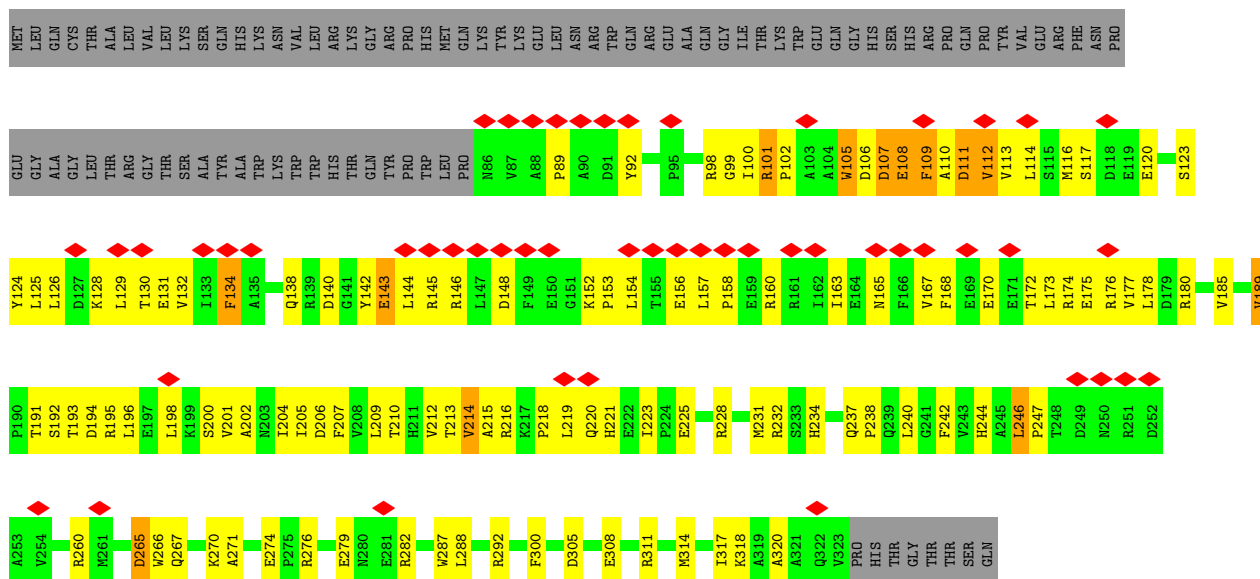




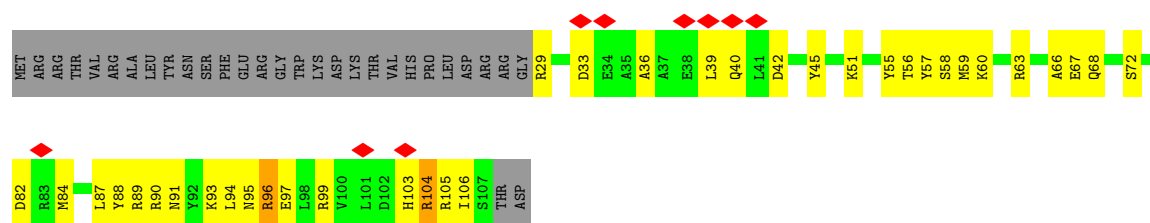
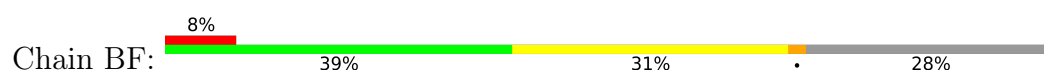
• Molecule 48: mL84



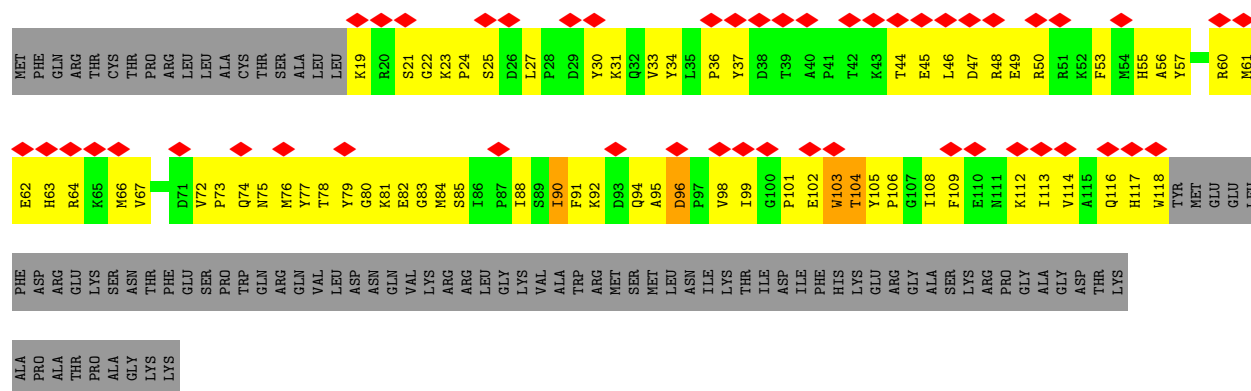
• Molecule 49: mL76



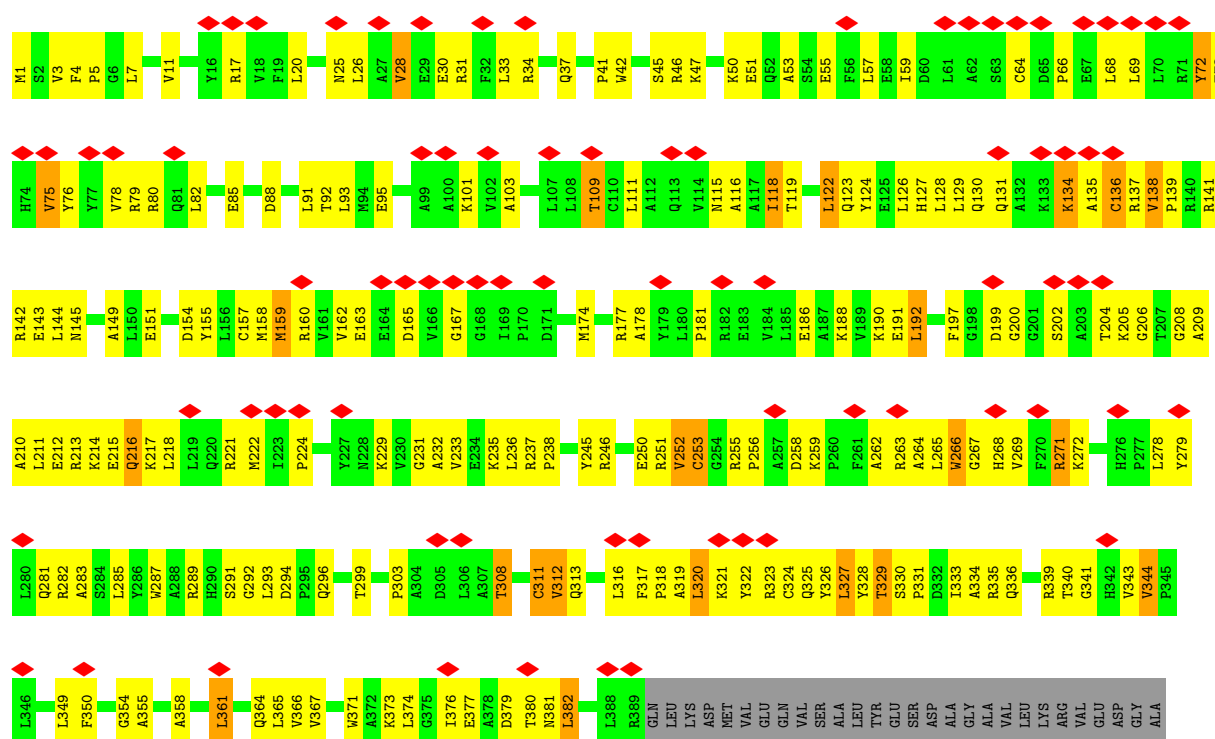
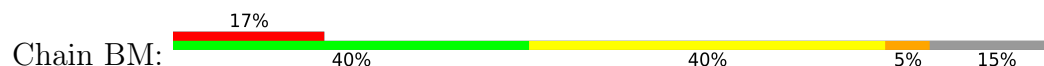
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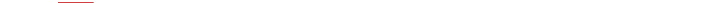


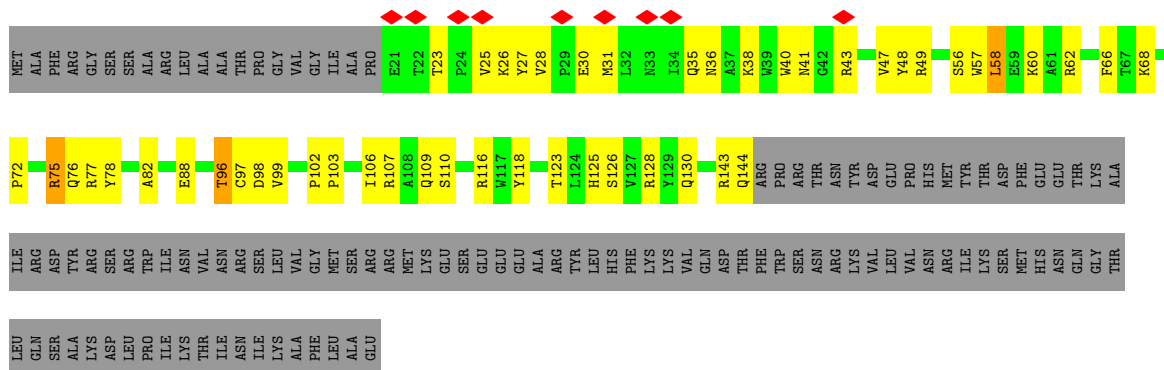
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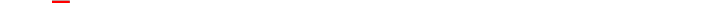


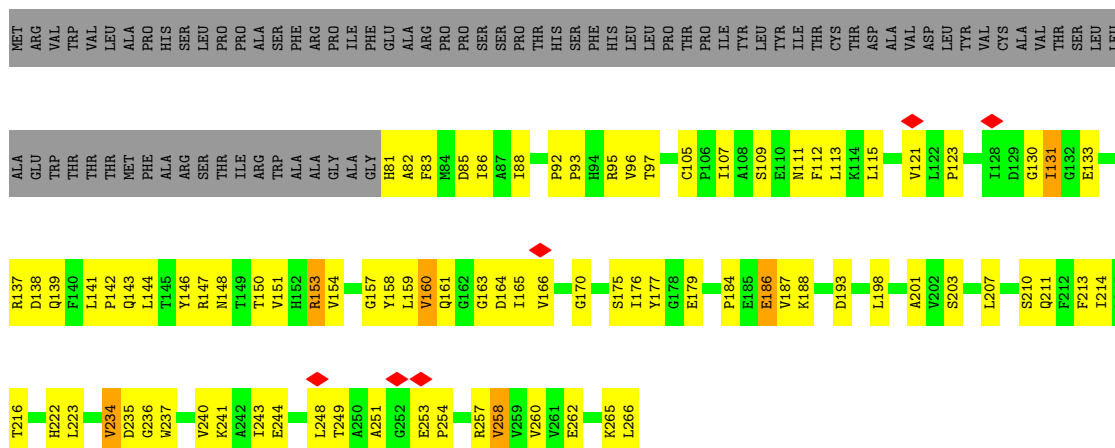
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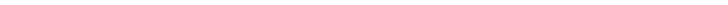


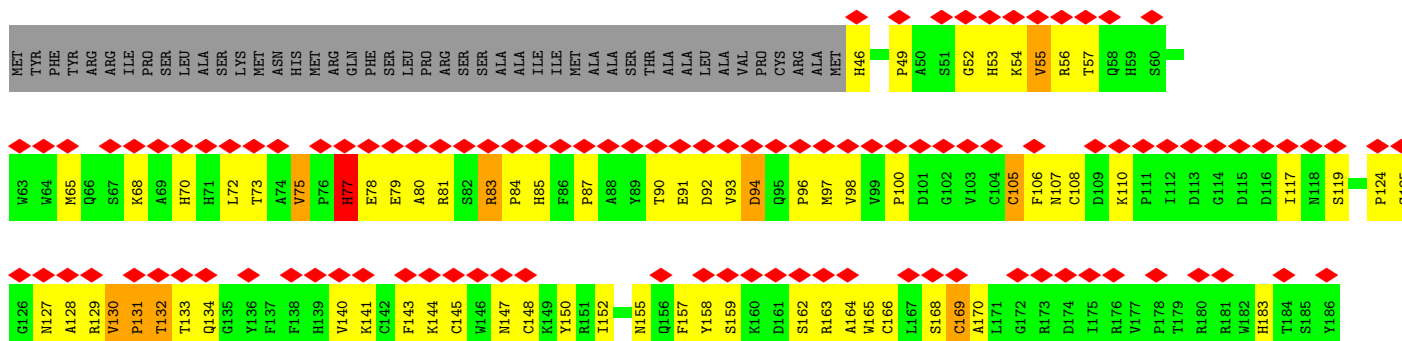
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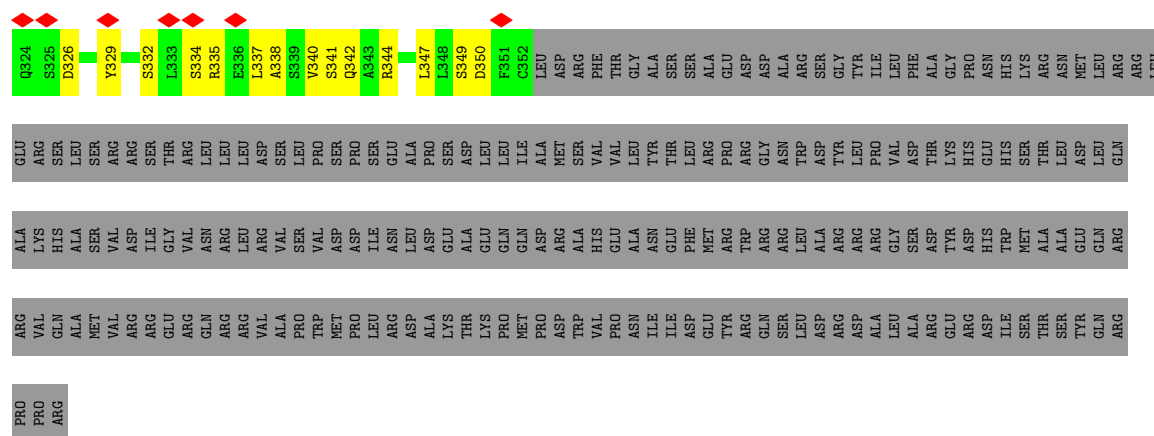
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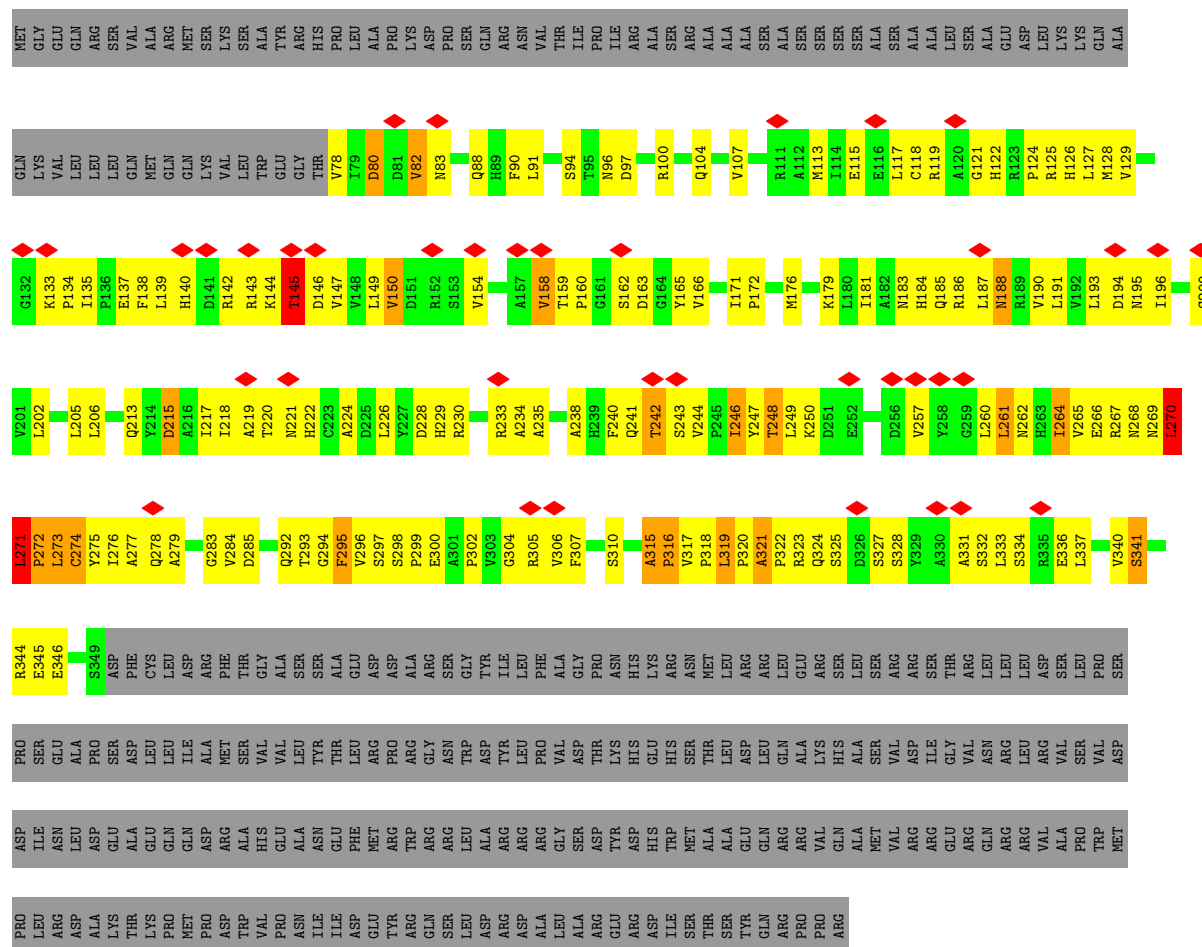
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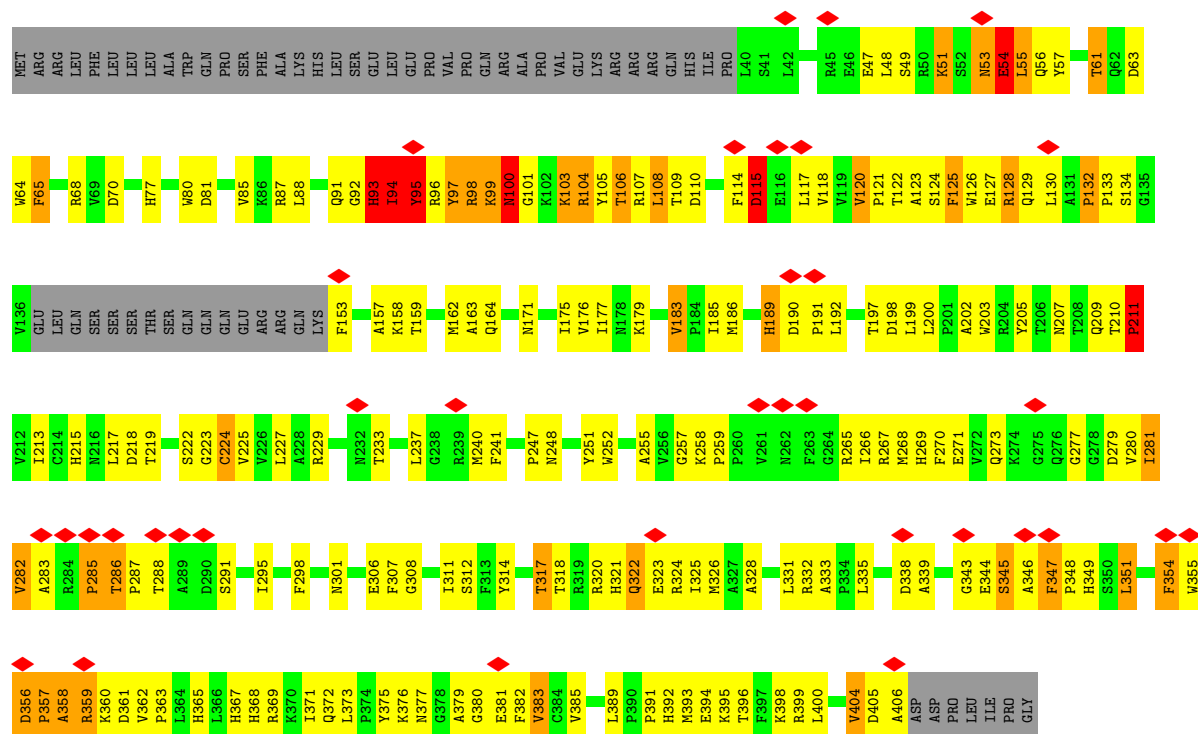


• Molecule 57: SpoU_methylase domain-containing protein

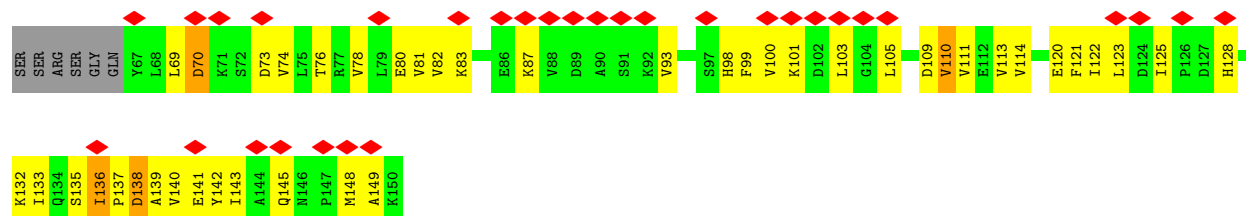
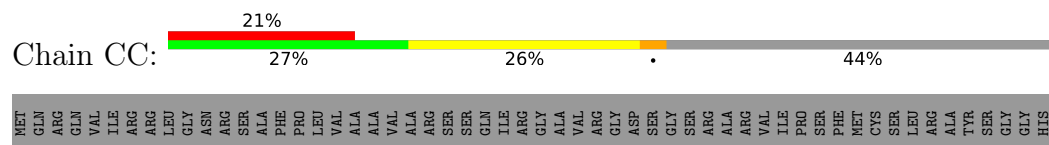


• Molecule 58: Pseudouridylate synthase-like protein

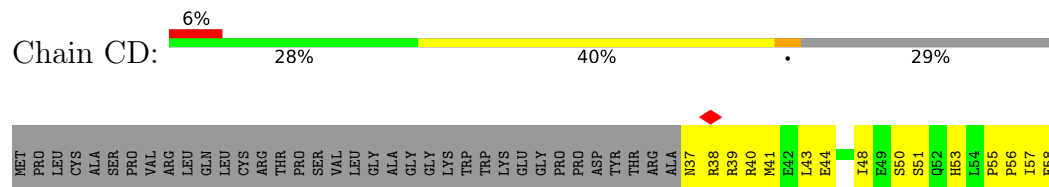




• Molecule 59: Acyl carrier protein

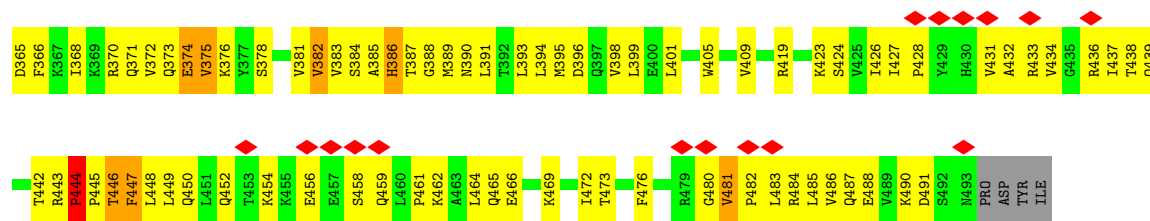


• Molecule 60: L0R8F8

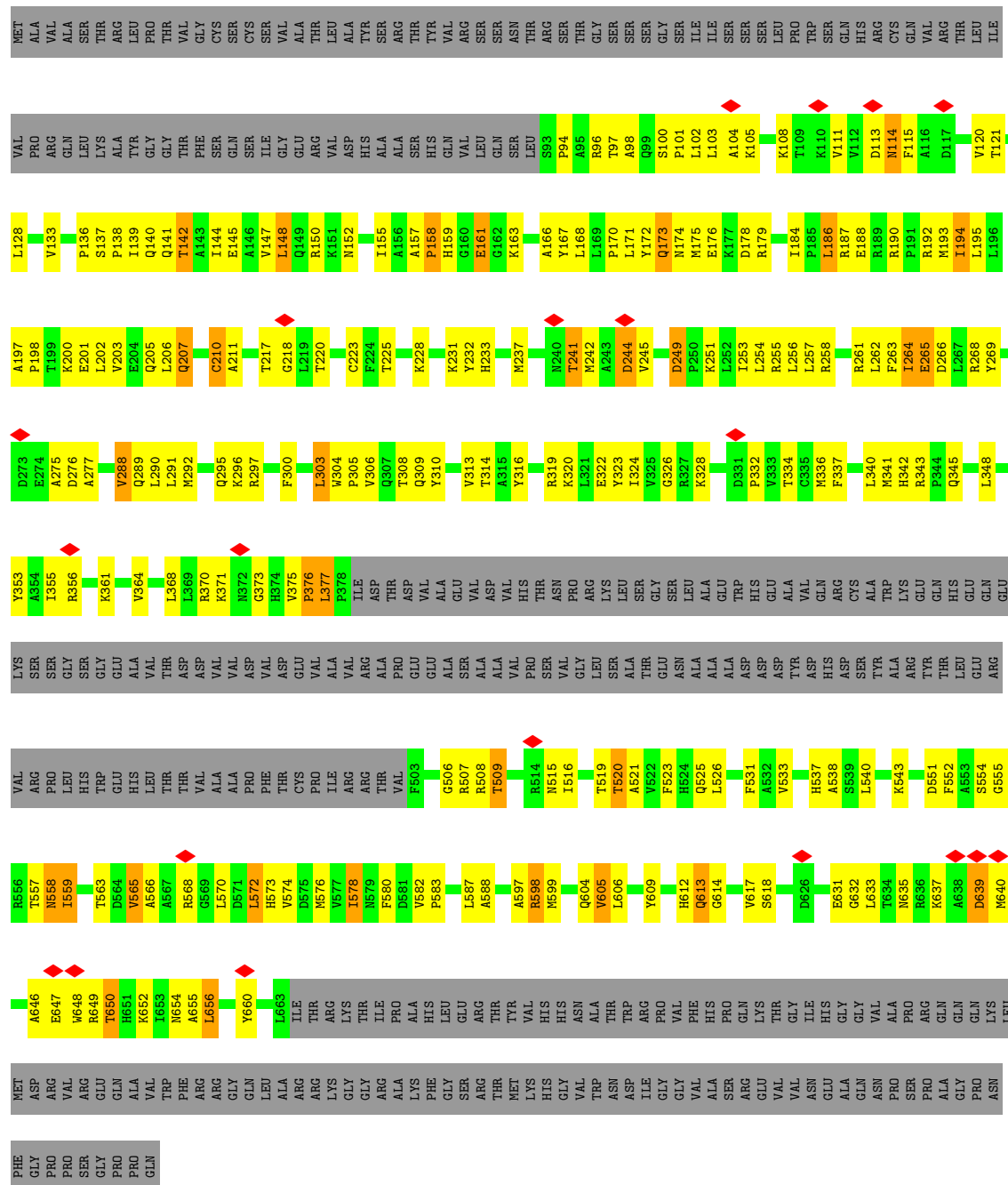
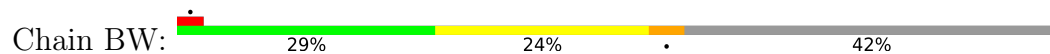


• Molecule 61: G domain-containing protein

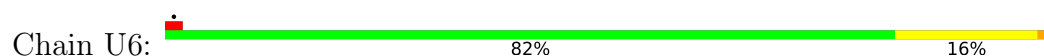




• Molecule 63: DEAD/DEAH box helicase-like protein

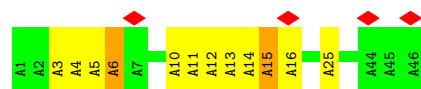
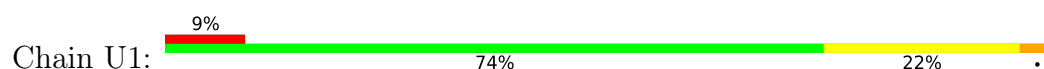


• Molecule 64: G domain-containing protein





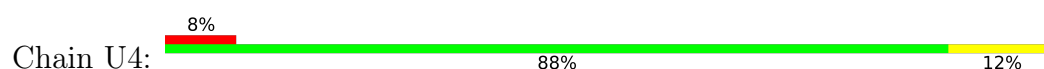
• Molecule 67: U1



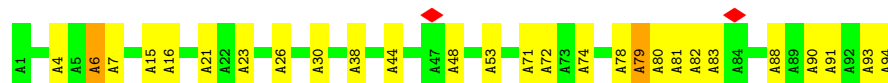
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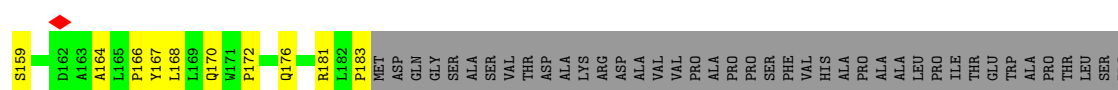
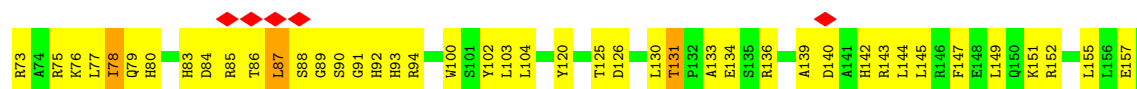
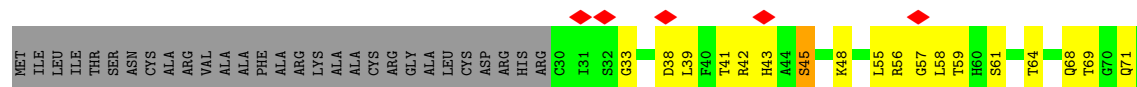
• Molecule 69: U4



• Molecule 70: U5

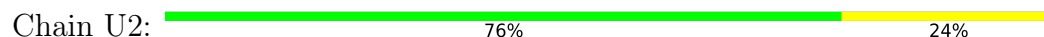


• Molecule 71: mL78

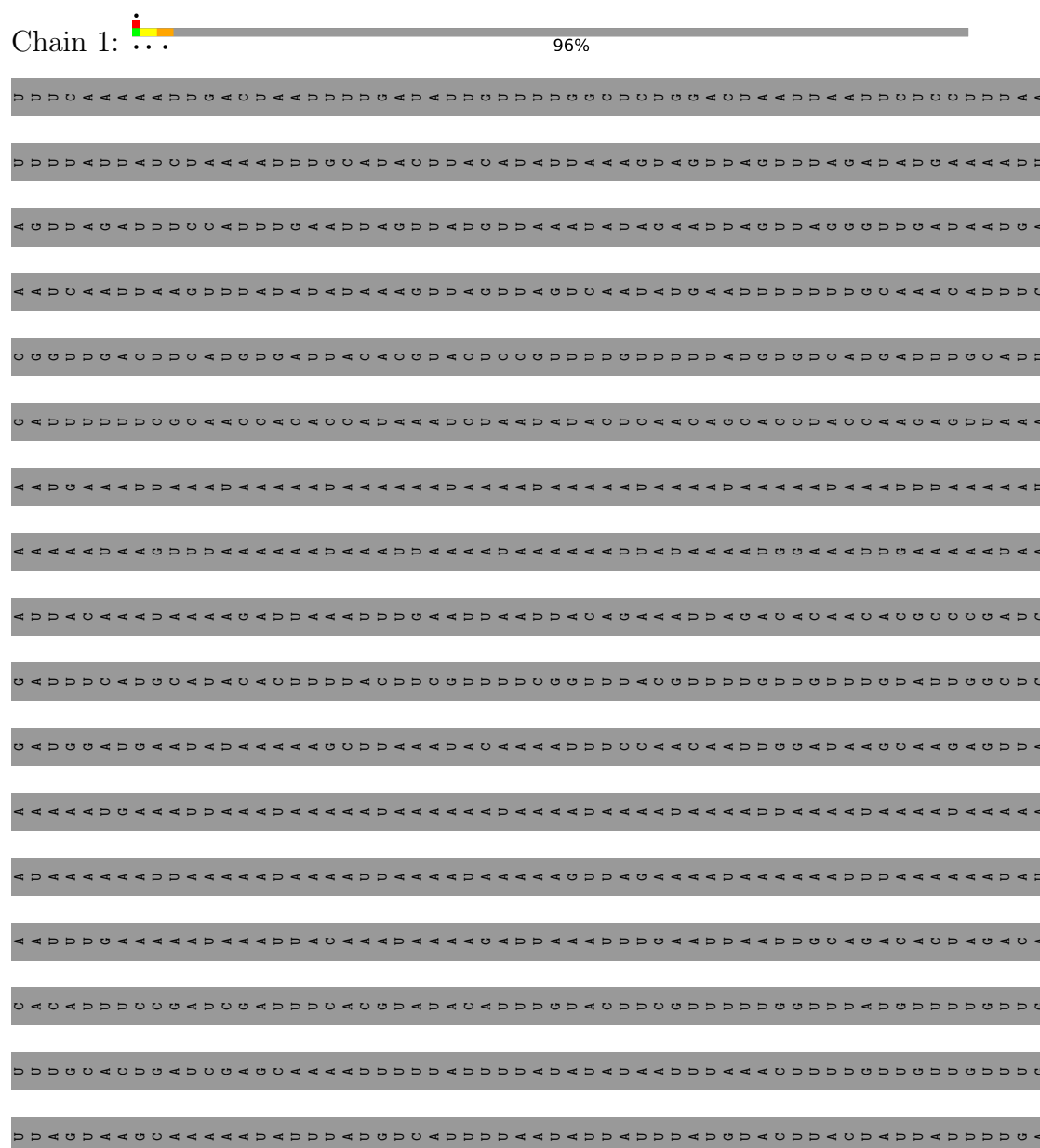




- Molecule 72: U2



- Molecule 73: Ribosomal RNA







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U C G C C A C A C C C C A C G A A A A A C A A A A A U U U G C A C G C C A A C A A A A A U U U G A A A A A A A A A C

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A C A C

C A C G A A C A G

U A U G A A C C A U

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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	59200	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	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	0.222	Depositor
Minimum map value	-0.120	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	489.6, 489.6, 489.6	wwPDB
Map dimensions	408, 408, 408	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2, 1.2, 1.2	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, ATP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.36	0/3011	0.45	0/4097
2	B	0.89	1/3623 (0.0%)	0.44	1/4931 (0.0%)
3	C	0.33	0/1831	0.49	2/2498 (0.1%)
4	E	0.26	0/1864	0.47	0/2512
5	F	0.39	0/1272	0.47	0/1730
6	G	0.51	0/2857	0.82	15/3879 (0.4%)
7	I	0.33	0/2220	0.45	0/2998
8	J	0.60	0/1175	1.01	3/1582 (0.2%)
9	K	0.37	0/1499	0.44	0/2026
10	L	0.34	0/1452	0.45	0/1970
11	M	0.37	0/2168	0.47	0/2928
12	N	0.44	0/1650	0.68	2/2242 (0.1%)
13	O	0.31	0/2529	0.49	0/3422
14	Q	0.39	0/1827	0.57	1/2463 (0.0%)
15	R	0.28	0/3852	0.44	0/5243
16	S	0.36	0/1271	0.45	0/1712
17	T	0.39	0/501	0.50	0/665
18	V	0.40	0/1231	0.51	0/1645
19	Z	0.32	0/940	0.45	0/1279
20	BA	0.23	0/797	0.43	0/1084
21	CA	0.37	0/4341	0.66	10/5889 (0.2%)
22	UA	0.42	0/1014	1.05	6/1418 (0.4%)
23	BB	0.47	0/922	0.65	0/1248
24	CB	0.25	0/1092	0.52	0/1477
25	BK	0.34	0/5536	0.58	6/7536 (0.1%)
26	BQ	0.28	0/3310	0.44	0/4478
27	BN	0.40	0/1539	0.73	4/2093 (0.2%)
28	BE	0.30	0/337	0.52	0/458
29	BO	0.31	0/1311	0.56	0/1766
30	At	0.34	0/1373	0.45	0/1848
31	Au	0.27	0/702	0.41	0/943
32	Ae	0.30	0/2436	0.43	0/3316

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Af	0.45	0/1228	0.65	1/1671 (0.1%)
34	Ah	0.22	0/3327	0.43	0/4518
35	Ap	0.22	0/1819	0.39	0/2458
36	Al	0.35	0/1909	0.55	0/2606
37	Ab	0.37	0/1454	0.44	0/1966
38	Aa	0.31	0/1103	0.52	0/1498
39	BP	0.33	0/1109	0.47	0/1507
40	Az	0.36	0/1192	0.43	0/1613
41	Am	0.35	0/2508	0.51	1/3392 (0.0%)
42	As	0.28	0/1204	0.53	2/1622 (0.1%)
43	BG	0.24	0/692	0.61	1/935 (0.1%)
44	Ad	0.51	0/1547	0.79	5/2097 (0.2%)
45	Aw	1.01	2/1552 (0.1%)	0.64	1/2107 (0.0%)
46	BH	0.31	0/1430	0.41	0/1937
47	Aj	0.32	0/2837	0.43	0/3821
48	Ar	0.30	0/1689	0.53	0/2280
49	An	0.28	0/1990	0.57	4/2701 (0.1%)
50	BF	0.25	0/675	0.51	0/907
51	Av	0.29	0/853	0.60	1/1152 (0.1%)
52	BM	0.19	0/3136	0.42	0/4259
53	Ag	0.35	0/1063	0.44	0/1442
54	Bl	0.21	0/1440	0.40	0/1953
55	Ax	0.27	0/1439	0.60	1/1952 (0.1%)
56	BS	0.33	0/1016	0.57	0/1388
57	BX	0.35	0/2126	0.82	6/2892 (0.2%)
57	BY	0.24	0/2152	0.52	1/2927 (0.0%)
58	BZ	0.49	0/2911	0.89	17/3954 (0.4%)
59	CC	0.18	0/679	0.41	0/921
60	CD	0.23	0/774	0.56	0/1034
61	BT	0.21	0/2399	0.50	0/3255
62	BU	0.38	0/3739	0.67	7/5052 (0.1%)
63	BW	0.43	0/3658	0.65	0/4940
64	BV	0.27	0/1634	0.57	0/2212
66	U6	0.67	0/934	1.03	1/1306 (0.1%)
67	U1	0.61	0/229	1.03	0/319
68	U3	0.51	0/374	0.88	2/522 (0.4%)
69	U4	0.18	0/679	0.44	0/949
70	U5	0.33	0/469	0.74	0/655
71	BR	0.29	0/1745	0.48	0/2370
72	U2	0.37	0/184	0.73	0/256
73	1	0.54	15/18754 (0.1%)	0.56	7/29135 (0.0%)
74	R1	0.42	0/68	0.92	0/103
75	R2	0.35	0/729	1.12	10/1111 (0.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	R5	0.33	0/109	0.61	0/166
77	U8	1.29	0/294	1.74	1/410 (0.2%)
All	All	0.42	18/144335 (0.0%)	0.58	119/199647 (0.1%)

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
6	G	1	0
14	Q	0	1
57	BX	0	1
66	U6	0	2
70	U5	0	3
All	All	1	7

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	194	LYS	CE-NZ	48.95	2.96	1.49
45	Aw	81	ARG	CD-NE	30.26	1.88	1.46
45	Aw	81	ARG	NE-CZ	21.91	1.57	1.33
73	1	106	A	C6-N1	21.73	1.79	1.35
73	1	106	A	N1-C2	21.59	1.77	1.34

The worst 5 of 119 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	BX	272	PRO	N-CA-C	21.57	143.51	113.53
45	Aw	81	ARG	CD-NE-CZ	21.11	153.95	124.40
6	G	311	PRO	N-CA-C	11.29	135.74	112.47
57	BX	270	LEU	N-CA-C	-10.08	100.30	111.28
44	Ad	123	PRO	N-CA-C	-9.98	95.66	111.03

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	G	310	HIS	CA

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
57	BX	295	PHE	Peptide
14	Q	23	PRO	Mainchain
70	U5	6	ALA	Peptide
66	U6	34	ALA	Peptide
66	U6	68	ALA	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	A	2909	0	2723	115	0
2	B	3513	0	3413	165	0
3	C	1772	0	1734	85	0
4	E	1818	0	1867	158	0
5	F	1231	0	1205	72	0
6	G	2767	0	2676	180	0
7	I	2153	0	2089	112	0
8	J	1146	0	1148	108	0
9	K	1467	0	1469	69	0
10	L	1419	0	1443	53	0
11	M	2116	0	2150	125	0
12	N	1599	0	1591	133	0
13	O	2477	0	2477	143	0
14	Q	1785	0	1784	127	0
15	R	3755	0	3722	183	0
16	S	1244	0	1272	72	0
17	T	487	0	495	34	0
18	V	1202	0	1224	76	0
19	Z	907	0	896	45	0
20	BA	786	0	812	48	0
21	CA	4230	0	4140	262	0
22	UA	1015	0	1017	42	0
23	BB	894	0	872	51	0
24	CB	1074	0	1076	70	0
25	BK	5419	0	5423	281	0
26	BQ	3230	0	3136	164	0
27	BN	1507	0	1479	127	0
28	BE	325	0	296	10	0
29	BO	1281	0	1287	95	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	At	1346	0	1299	72	0
31	Au	681	0	673	25	0
32	Ae	2354	0	2324	90	0
33	Af	1192	0	1165	75	0
34	Ah	3242	0	3132	168	0
35	Ap	1775	0	1699	90	0
36	Al	1857	0	1823	89	0
37	Ab	1413	0	1353	86	0
38	Aa	1076	0	1058	64	0
39	BP	1070	0	1019	52	0
40	Az	1150	0	1082	54	0
41	Am	2435	0	2356	79	0
42	As	1187	0	1203	65	0
43	BG	675	0	675	51	0
44	Ad	1502	0	1488	100	0
45	Aw	1509	0	1470	93	0
46	BH	1394	0	1350	51	0
47	Aj	2777	0	2778	120	0
48	Ar	1644	0	1608	93	0
49	An	1946	0	1905	118	0
50	BF	661	0	655	30	0
51	Av	828	0	811	87	0
52	BM	3069	0	3105	183	0
53	Ag	1031	0	999	49	0
54	Bl	1409	0	1400	69	0
55	Ax	1388	0	1305	87	0
56	BS	978	0	941	70	0
57	BX	2086	0	2075	156	0
57	BY	2111	0	2093	144	0
58	BZ	2829	0	2808	233	0
59	CC	668	0	668	32	0
60	CD	761	0	775	49	0
61	BT	2346	0	2366	105	0
62	BU	3680	0	3731	240	0
63	BW	3589	0	3714	195	0
64	BV	1596	0	1586	89	0
65	U7	200	0	48	5	0
66	U6	935	0	937	28	0
67	U1	230	0	232	18	0
68	U3	375	0	377	16	0
69	U4	680	0	682	11	0
70	U5	470	0	472	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
71	BR	1703	0	1703	95	0
72	U2	185	0	187	18	0
73	1	16777	0	8400	800	0
74	R1	62	0	32	10	0
75	R2	665	0	344	43	0
76	R5	100	0	51	5	0
77	U8	295	0	297	54	0
78	BU	32	0	12	9	0
79	BW	31	12	12	4	0
All	All	139523	12	129194	6399	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 24.

The worst 5 of 6399 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)
73:1:106:A:N3	73:1:106:A:C2	1.74	1.55
45:Aw:81:ARG:NE	73:1:106:A:C2	1.71	1.54
45:Aw:81:ARG:NE	73:1:106:A:C6	1.75	1.51
73:1:106:A:C6	73:1:106:A:N1	1.79	1.49
73:1:106:A:N3	73:1:106:A:C4	1.76	1.49

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	354/467 (76%)	298 (84%)	55 (16%)	1 (0%)	36	65
2	B	433/436 (99%)	387 (89%)	46 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	210/262 (80%)	182 (87%)	27 (13%)	1 (0%)	24	54
4	E	223/346 (64%)	192 (86%)	30 (14%)	1 (0%)	30	59
5	F	145/171 (85%)	125 (86%)	20 (14%)	0	100	100
6	G	332/374 (89%)	289 (87%)	36 (11%)	7 (2%)	5	24
7	I	255/305 (84%)	218 (86%)	37 (14%)	0	100	100
8	J	139/144 (96%)	108 (78%)	27 (19%)	4 (3%)	3	19
9	K	177/194 (91%)	159 (90%)	18 (10%)	0	100	100
10	L	176/186 (95%)	159 (90%)	17 (10%)	0	100	100
11	M	257/279 (92%)	218 (85%)	39 (15%)	0	100	100
12	N	187/252 (74%)	154 (82%)	29 (16%)	4 (2%)	5	24
13	O	298/476 (63%)	267 (90%)	30 (10%)	1 (0%)	36	65
14	Q	215/234 (92%)	191 (89%)	23 (11%)	1 (0%)	24	54
15	R	470/480 (98%)	410 (87%)	59 (13%)	1 (0%)	43	71
16	S	148/409 (36%)	135 (91%)	13 (9%)	0	100	100
17	T	53/83 (64%)	47 (89%)	6 (11%)	0	100	100
18	V	139/151 (92%)	114 (82%)	25 (18%)	0	100	100
19	Z	111/197 (56%)	95 (86%)	16 (14%)	0	100	100
20	BA	104/167 (62%)	85 (82%)	19 (18%)	0	100	100
21	CA	535/618 (87%)	417 (78%)	113 (21%)	5 (1%)	14	42
22	UA	201/203 (99%)	167 (83%)	30 (15%)	4 (2%)	6	25
23	BB	104/156 (67%)	87 (84%)	17 (16%)	0	100	100
24	CB	133/202 (66%)	95 (71%)	38 (29%)	0	100	100
25	BK	690/893 (77%)	608 (88%)	78 (11%)	4 (1%)	21	50
26	BQ	409/445 (92%)	362 (88%)	46 (11%)	1 (0%)	43	71
27	BN	192/344 (56%)	163 (85%)	27 (14%)	2 (1%)	12	40
28	BE	35/118 (30%)	26 (74%)	9 (26%)	0	100	100
29	BO	154/190 (81%)	108 (70%)	44 (29%)	2 (1%)	9	33
30	At	163/183 (89%)	136 (83%)	27 (17%)	0	100	100
31	Au	78/186 (42%)	72 (92%)	6 (8%)	0	100	100
32	Ae	288/311 (93%)	243 (84%)	45 (16%)	0	100	100
33	Af	143/155 (92%)	126 (88%)	17 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	Ah	395/570 (69%)	347 (88%)	46 (12%)	2 (0%)	24	54
35	Ap	212/240 (88%)	193 (91%)	19 (9%)	0	100	100
36	Al	226/346 (65%)	197 (87%)	27 (12%)	2 (1%)	14	42
37	Ab	166/262 (63%)	148 (89%)	18 (11%)	0	100	100
38	Aa	133/195 (68%)	106 (80%)	23 (17%)	4 (3%)	3	18
39	BP	129/254 (51%)	105 (81%)	23 (18%)	1 (1%)	16	44
40	Az	128/152 (84%)	121 (94%)	7 (6%)	0	100	100
41	Am	294/340 (86%)	265 (90%)	29 (10%)	0	100	100
42	As	142/249 (57%)	125 (88%)	17 (12%)	0	100	100
43	BG	83/1347 (6%)	64 (77%)	17 (20%)	2 (2%)	4	22
44	Ad	185/237 (78%)	165 (89%)	20 (11%)	0	100	100
45	Aw	183/187 (98%)	160 (87%)	23 (13%)	0	100	100
46	BH	179/229 (78%)	158 (88%)	20 (11%)	1 (1%)	21	50
47	Aj	338/503 (67%)	303 (90%)	35 (10%)	0	100	100
48	Ar	193/205 (94%)	148 (77%)	45 (23%)	0	100	100
49	An	236/331 (71%)	206 (87%)	28 (12%)	2 (1%)	16	44
50	BF	77/109 (71%)	65 (84%)	12 (16%)	0	100	100
51	Av	98/192 (51%)	75 (76%)	23 (24%)	0	100	100
52	BM	387/457 (85%)	345 (89%)	42 (11%)	0	100	100
53	Ag	122/244 (50%)	105 (86%)	17 (14%)	0	100	100
54	Bl	184/266 (69%)	164 (89%)	20 (11%)	0	100	100
55	Ax	165/216 (76%)	122 (74%)	39 (24%)	4 (2%)	4	22
56	BS	121/416 (29%)	100 (83%)	21 (17%)	0	100	100
57	BX	270/569 (48%)	202 (75%)	64 (24%)	4 (2%)	8	30
57	BY	273/569 (48%)	214 (78%)	58 (21%)	1 (0%)	30	59
58	BZ	347/413 (84%)	277 (80%)	60 (17%)	10 (3%)	3	19
59	CC	82/150 (55%)	76 (93%)	6 (7%)	0	100	100
60	CD	88/126 (70%)	70 (80%)	17 (19%)	1 (1%)	11	38
61	BT	298/464 (64%)	235 (79%)	62 (21%)	1 (0%)	36	65
62	BU	461/497 (93%)	373 (81%)	85 (18%)	3 (1%)	18	47
63	BW	443/776 (57%)	359 (81%)	76 (17%)	8 (2%)	6	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
64	BV	195/787 (25%)	151 (77%)	42 (22%)	2 (1%)	12	40
66	U6	185/187 (99%)	138 (75%)	43 (23%)	4 (2%)	5	24
67	U1	44/46 (96%)	34 (77%)	8 (18%)	2 (4%)	2	12
68	U3	73/75 (97%)	55 (75%)	17 (23%)	1 (1%)	9	31
69	U4	134/136 (98%)	120 (90%)	14 (10%)	0	100	100
70	U5	92/94 (98%)	52 (56%)	38 (41%)	2 (2%)	5	24
71	BR	210/301 (70%)	178 (85%)	32 (15%)	0	100	100
72	U2	35/37 (95%)	24 (69%)	11 (31%)	0	100	100
77	U8	57/59 (97%)	34 (60%)	8 (14%)	15 (26%)	0	0
All	All	15214/22450 (68%)	12822 (84%)	2281 (15%)	111 (1%)	20	47

5 of 111 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	G	310	HIS
6	G	311	PRO
6	G	333	ILE
8	J	60	ASN
12	N	77	ASN

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	A	305/394 (77%)	282 (92%)	23 (8%)	12	38
2	B	380/381 (100%)	351 (92%)	29 (8%)	12	38
3	C	190/227 (84%)	172 (90%)	18 (10%)	8	29
4	E	193/301 (64%)	176 (91%)	17 (9%)	9	31
5	F	130/152 (86%)	124 (95%)	6 (5%)	24	50
6	G	290/323 (90%)	267 (92%)	23 (8%)	11	36
7	I	223/262 (85%)	211 (95%)	12 (5%)	20	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	J	119/122 (98%)	101 (85%)	18 (15%)	3	11
9	K	151/162 (93%)	138 (91%)	13 (9%)	10	33
10	L	151/158 (96%)	130 (86%)	21 (14%)	3	14
11	M	226/242 (93%)	206 (91%)	20 (9%)	9	31
12	N	175/220 (80%)	153 (87%)	22 (13%)	4	18
13	O	272/397 (68%)	246 (90%)	26 (10%)	8	28
14	Q	191/204 (94%)	179 (94%)	12 (6%)	16	42
15	R	406/412 (98%)	370 (91%)	36 (9%)	9	31
16	S	135/336 (40%)	123 (91%)	12 (9%)	9	31
17	T	52/74 (70%)	47 (90%)	5 (10%)	8	28
18	V	125/135 (93%)	116 (93%)	9 (7%)	13	39
19	Z	97/172 (56%)	89 (92%)	8 (8%)	10	35
20	BA	86/135 (64%)	78 (91%)	8 (9%)	8	29
21	CA	446/501 (89%)	390 (87%)	56 (13%)	4	18
23	BB	91/140 (65%)	87 (96%)	4 (4%)	25	51
24	CB	118/179 (66%)	104 (88%)	14 (12%)	5	19
25	BK	582/739 (79%)	518 (89%)	64 (11%)	6	22
26	BQ	347/375 (92%)	322 (93%)	25 (7%)	13	39
27	BN	159/280 (57%)	143 (90%)	16 (10%)	7	25
28	BE	35/100 (35%)	31 (89%)	4 (11%)	5	21
29	BO	136/158 (86%)	118 (87%)	18 (13%)	4	16
30	At	140/153 (92%)	132 (94%)	8 (6%)	18	45
31	Au	69/164 (42%)	65 (94%)	4 (6%)	18	45
32	Ae	249/261 (95%)	229 (92%)	20 (8%)	11	36
33	Af	125/135 (93%)	117 (94%)	8 (6%)	16	42
34	Ah	337/485 (70%)	307 (91%)	30 (9%)	9	31
35	Ap	189/208 (91%)	172 (91%)	17 (9%)	9	30
36	Al	204/299 (68%)	185 (91%)	19 (9%)	8	29
37	Ab	150/235 (64%)	138 (92%)	12 (8%)	11	36
38	Aa	118/166 (71%)	104 (88%)	14 (12%)	5	19
39	BP	110/215 (51%)	100 (91%)	10 (9%)	9	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	Az	123/143 (86%)	115 (94%)	8 (6%)	15	42
41	Am	250/287 (87%)	236 (94%)	14 (6%)	19	46
42	As	131/204 (64%)	123 (94%)	8 (6%)	17	43
43	BG	77/1047 (7%)	71 (92%)	6 (8%)	11	37
44	Ad	159/193 (82%)	150 (94%)	9 (6%)	18	45
45	Aw	157/159 (99%)	146 (93%)	11 (7%)	14	40
46	BH	150/189 (79%)	144 (96%)	6 (4%)	28	53
47	Aj	287/420 (68%)	272 (95%)	15 (5%)	21	48
48	Ar	169/179 (94%)	157 (93%)	12 (7%)	13	39
49	An	208/289 (72%)	195 (94%)	13 (6%)	16	42
50	BF	68/95 (72%)	65 (96%)	3 (4%)	25	51
51	Av	90/169 (53%)	85 (94%)	5 (6%)	19	46
52	BM	319/370 (86%)	284 (89%)	35 (11%)	6	22
53	Ag	106/211 (50%)	97 (92%)	9 (8%)	10	33
54	Bl	153/221 (69%)	142 (93%)	11 (7%)	13	39
55	Ax	150/190 (79%)	142 (95%)	8 (5%)	20	47
56	BS	103/328 (31%)	95 (92%)	8 (8%)	11	37
57	BX	226/483 (47%)	201 (89%)	25 (11%)	6	21
57	BY	229/483 (47%)	208 (91%)	21 (9%)	8	29
58	BZ	305/363 (84%)	268 (88%)	37 (12%)	5	19
59	CC	77/129 (60%)	70 (91%)	7 (9%)	9	30
60	CD	83/112 (74%)	77 (93%)	6 (7%)	13	39
61	BT	257/398 (65%)	237 (92%)	20 (8%)	11	37
62	BU	401/431 (93%)	357 (89%)	44 (11%)	6	22
63	BW	386/661 (58%)	344 (89%)	42 (11%)	6	22
64	BV	172/644 (27%)	164 (95%)	8 (5%)	23	50
71	BR	177/241 (73%)	167 (94%)	10 (6%)	19	46
All	All	12515/18241 (69%)	11433 (91%)	1082 (9%)	12	33

5 of 1082 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
58	BZ	125	PHE

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Mol	Chain	Res	Type
60	CD	60	THR
58	BZ	120	VAL
63	BW	244	ASP
21	CA	534	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 320 such sidechains are listed below:

Mol	Chain	Res	Type
47	Aj	388	GLN
58	BZ	329	HIS
49	An	122	GLN
56	BS	292	GLN
62	BU	325	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
73	1	790/19000 (4%)	466 (58%)	77 (9%)
74	R1	2/3 (66%)	2 (100%)	1 (50%)
75	R2	32/35 (91%)	24 (75%)	10 (31%)
76	R5	4/5 (80%)	0	0
All	All	828/19043 (4%)	492 (59%)	88 (10%)

5 of 492 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
73	1	35	U
73	1	36	U
73	1	39	U
73	1	41	A
73	1	42	A

5 of 88 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
73	1	590	A
73	1	1097	A
73	1	594	U
73	1	916	G
73	1	1172	A

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](#)

2 ligands 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	$\# Z > 2$
79	ATP	BW	801	-	32,33,33	0.50	0	48,52,52	0.65	0
78	GTP	BU	501	-	33,34,34	0.61	0	50,54,54	0.69	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
79	ATP	BW	801	-	-	1/22/38/38	0/3/3/3
78	GTP	BU	501	-	-	7/22/38/38	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
78	BU	501	GTP	O4'-C4'-C3'	-2.59	100.02	105.15

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
78	BU	501	GTP	PB-O3A-PA-O5'
78	BU	501	GTP	C5'-O5'-PA-O3A
78	BU	501	GTP	C5'-O5'-PA-O2A
78	BU	501	GTP	O4'-C1'-N9-C4
78	BU	501	GTP	O4'-C4'-C5'-O5'

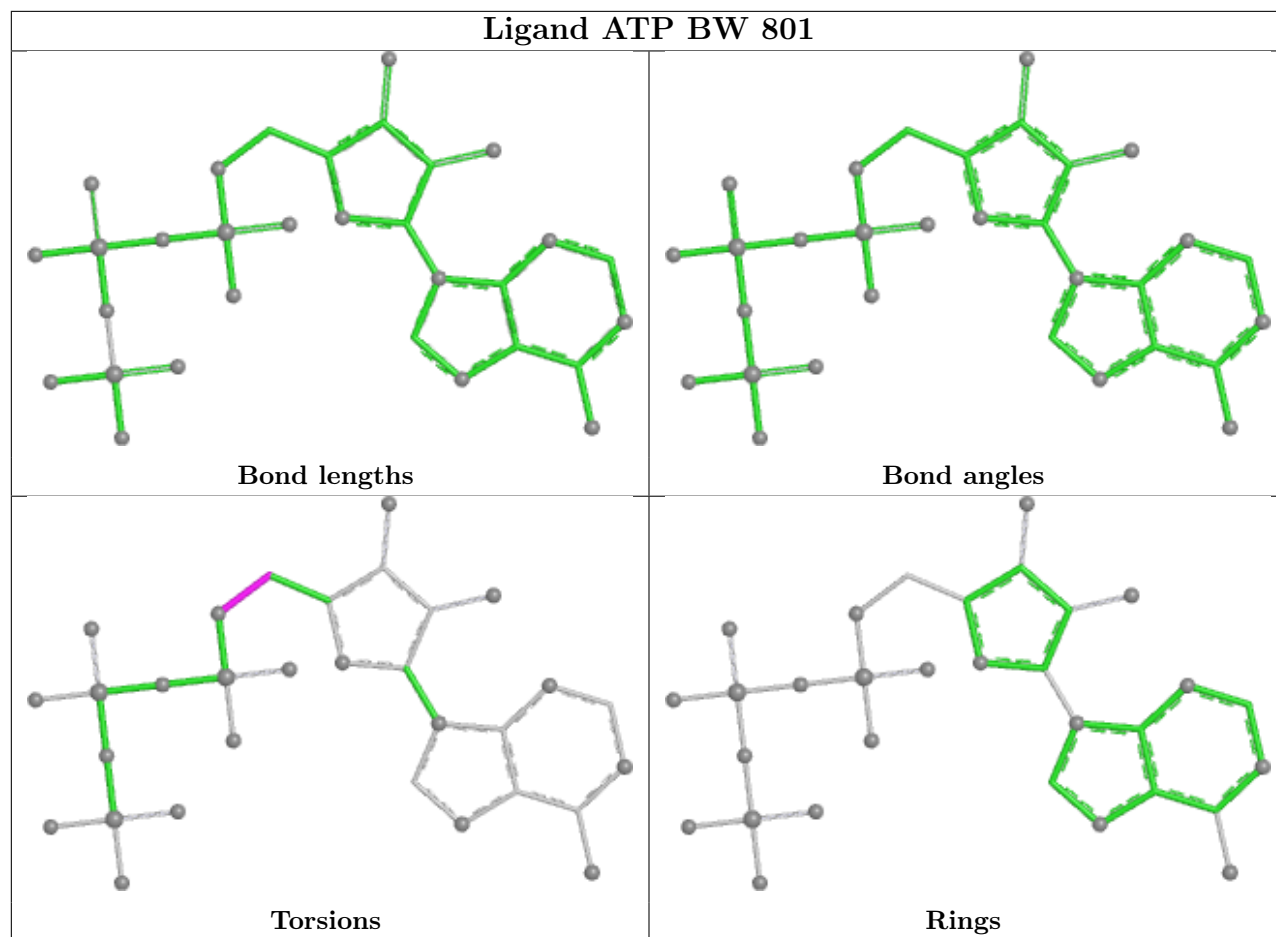
There are no ring outliers.

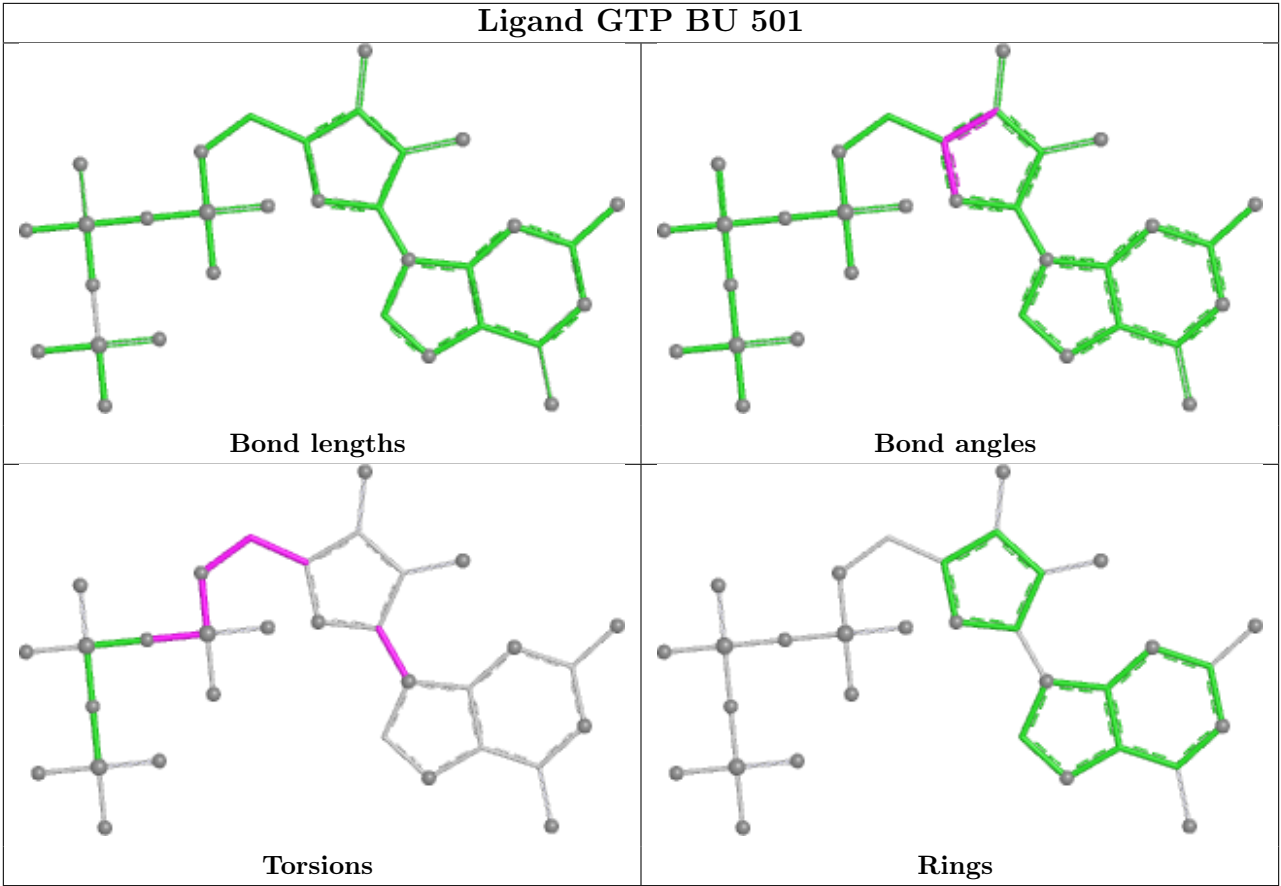
2 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
79	BW	801	ATP	4	0
78	BU	501	GTP	9	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 ATP BW 801





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
75	R2	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R2	21:U	O3'	122:U	P	84.98
1	R2	134:U	O3'	235:U	P	16.60

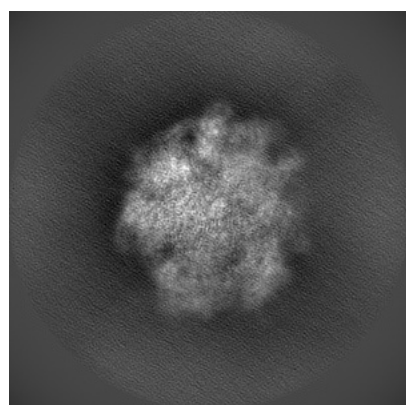
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11821. These allow visual inspection of the internal detail of the map and identification of artifacts.

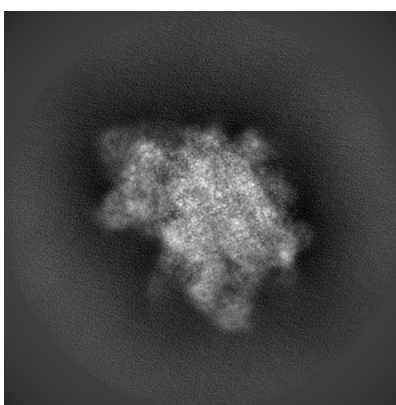
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

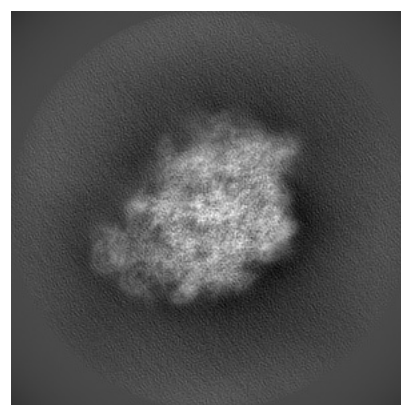
6.1.1 Primary map



X



Y

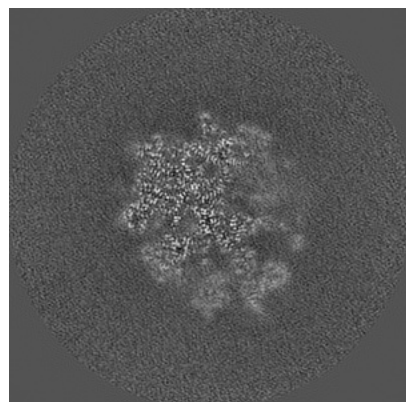


Z

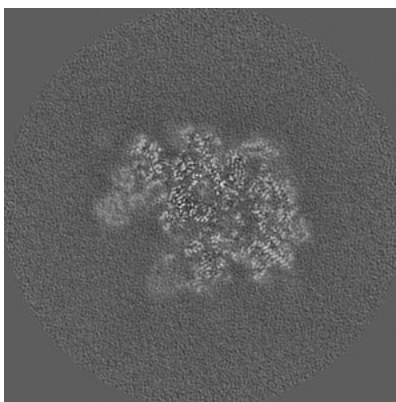
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

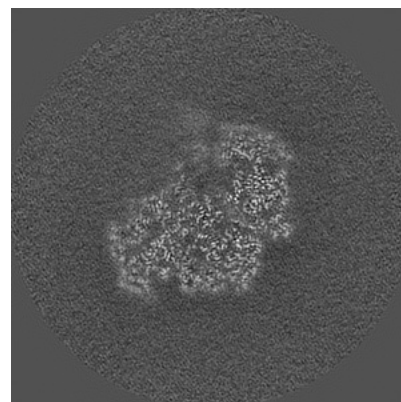
6.2.1 Primary map



X Index: 204



Y Index: 204

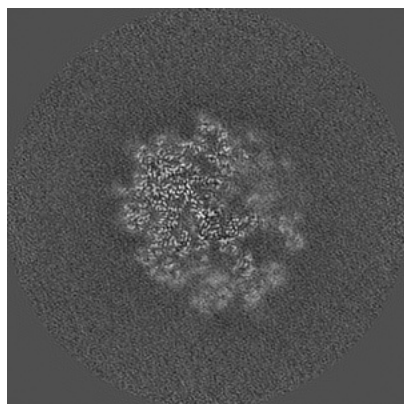


Z Index: 204

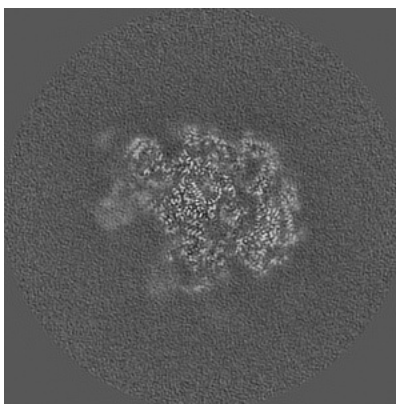
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

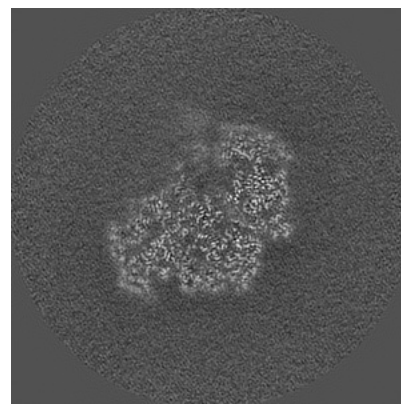
6.3.1 Primary map



X Index: 208



Y Index: 198

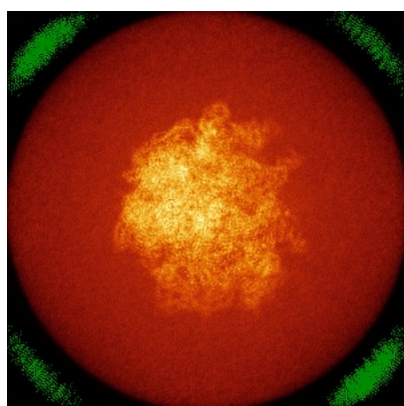


Z Index: 204

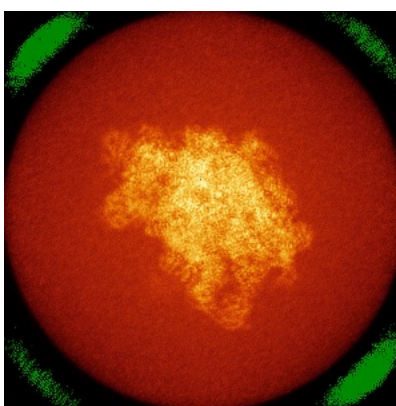
The images above show the largest variance slices of the map in three orthogonal directions.

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

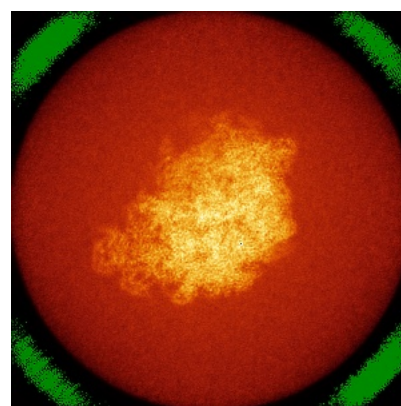
6.4.1 Primary map



X



Y

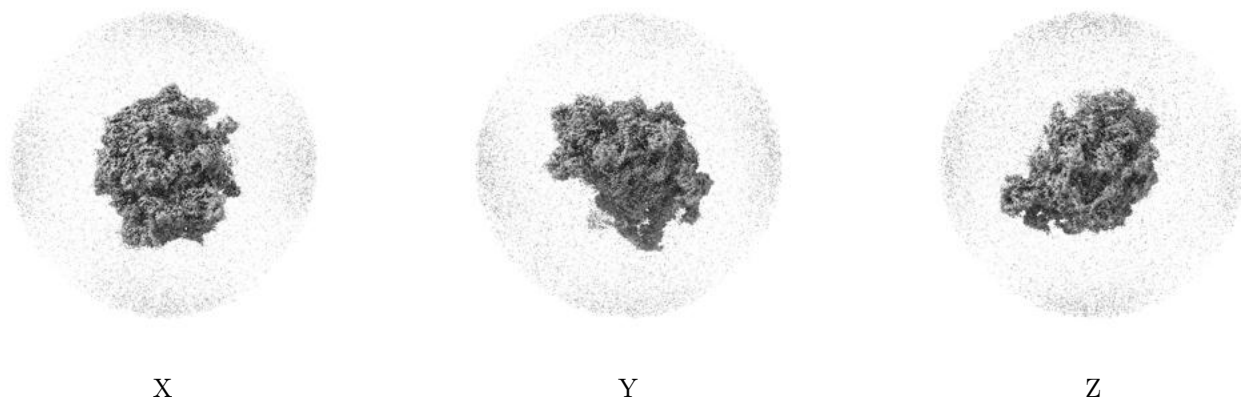


Z

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 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

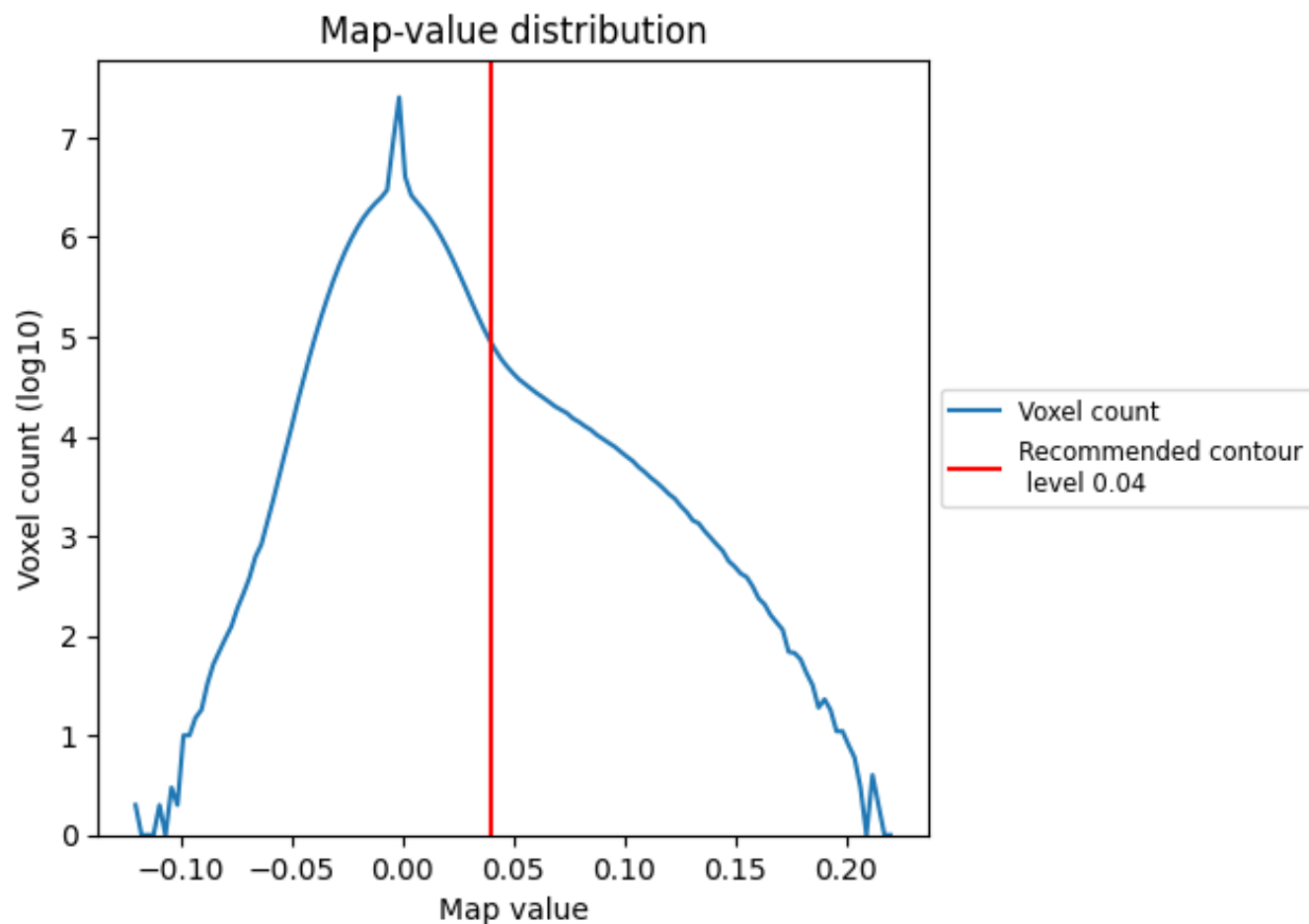
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

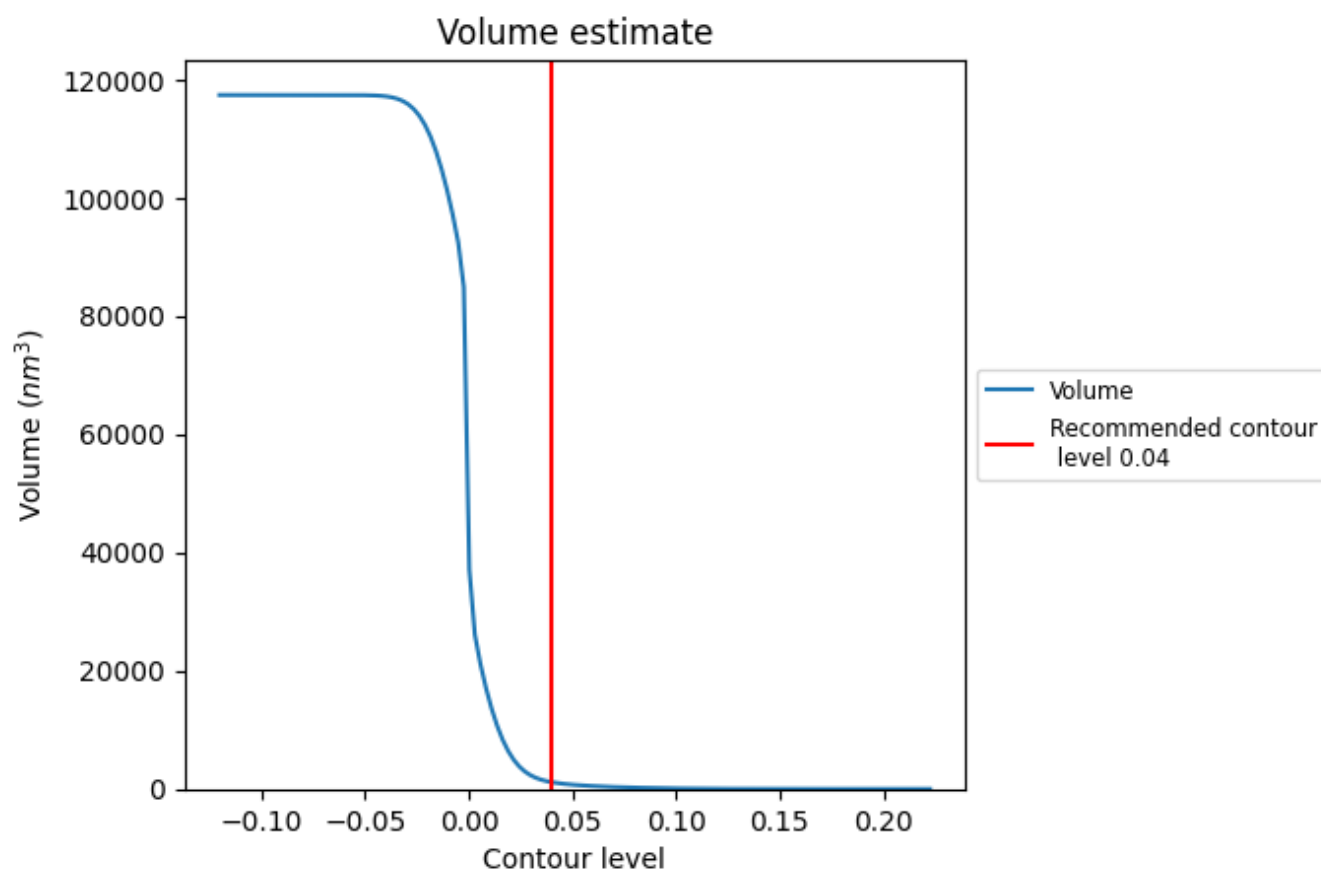
This section contains the results of statistical analysis of the map.

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.

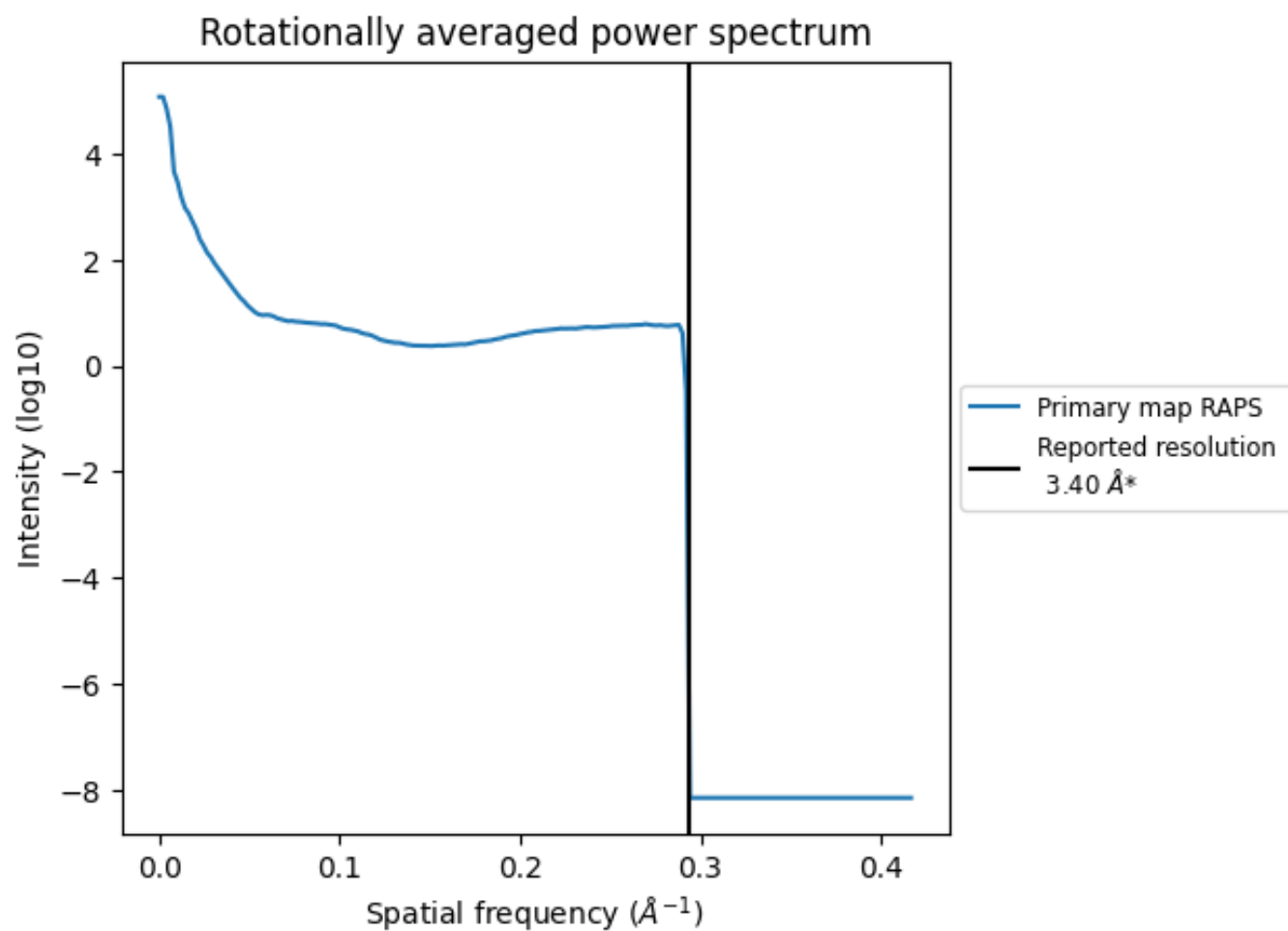
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1146 nm³; this corresponds to an approximate mass of 1035 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 0.294 Å⁻¹

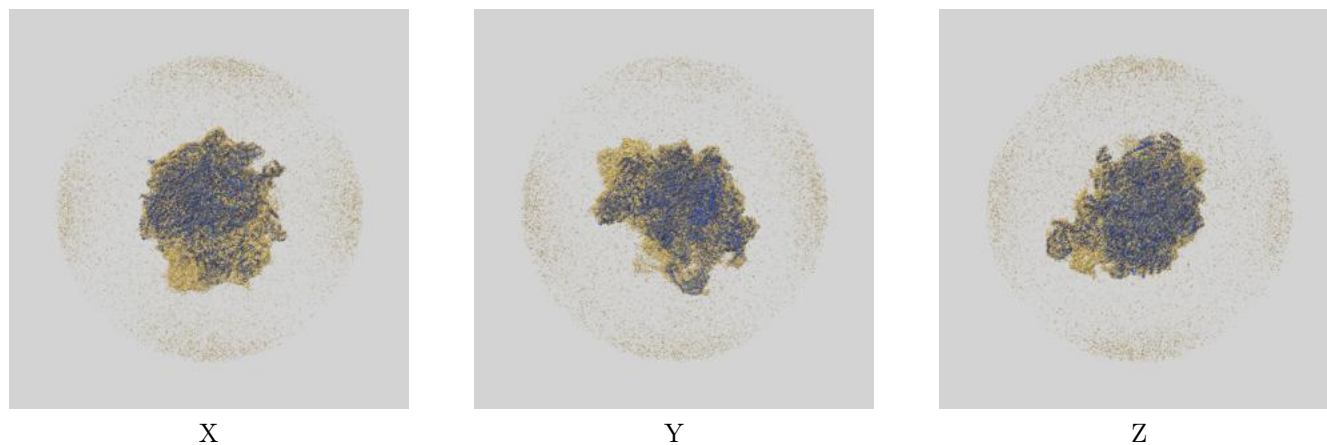
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

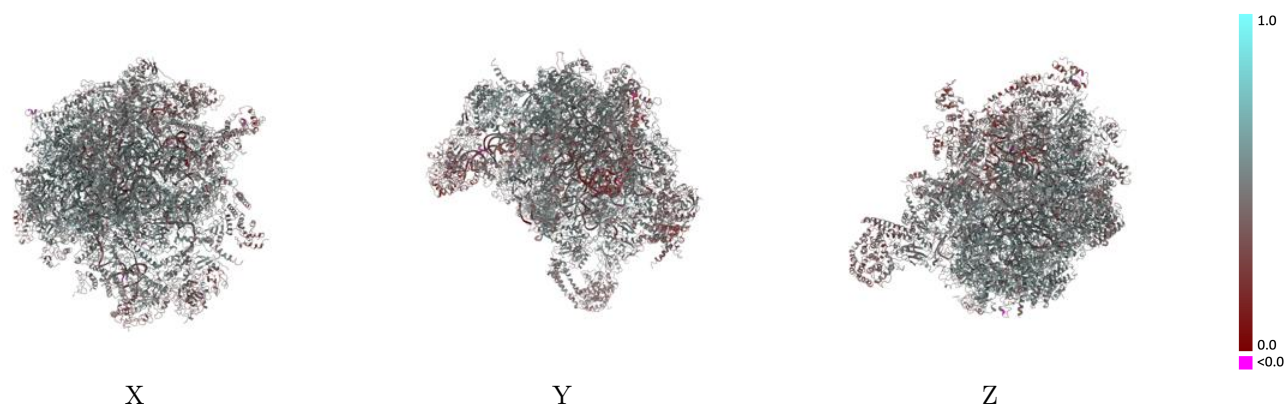
This section contains information regarding the fit between EMDB map EMD-11821 and PDB model 7AM2. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



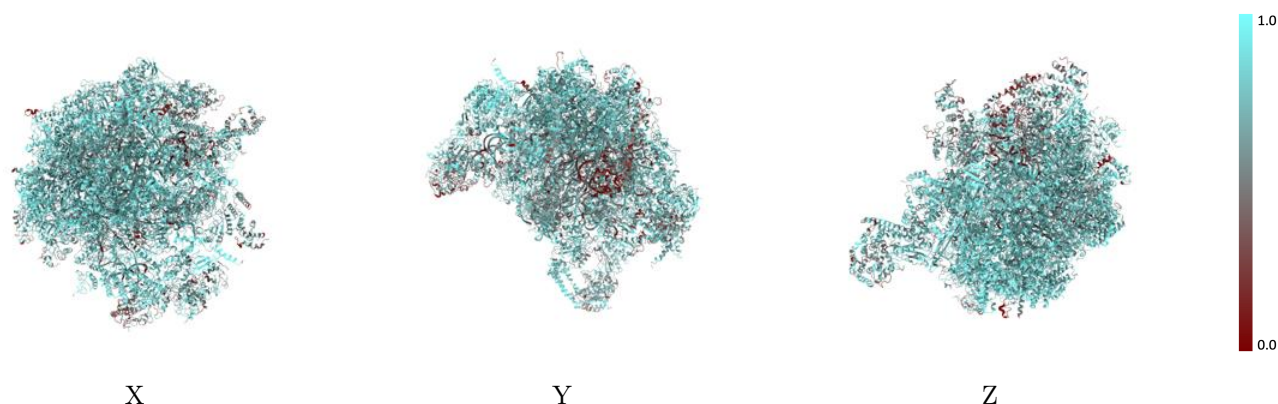
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



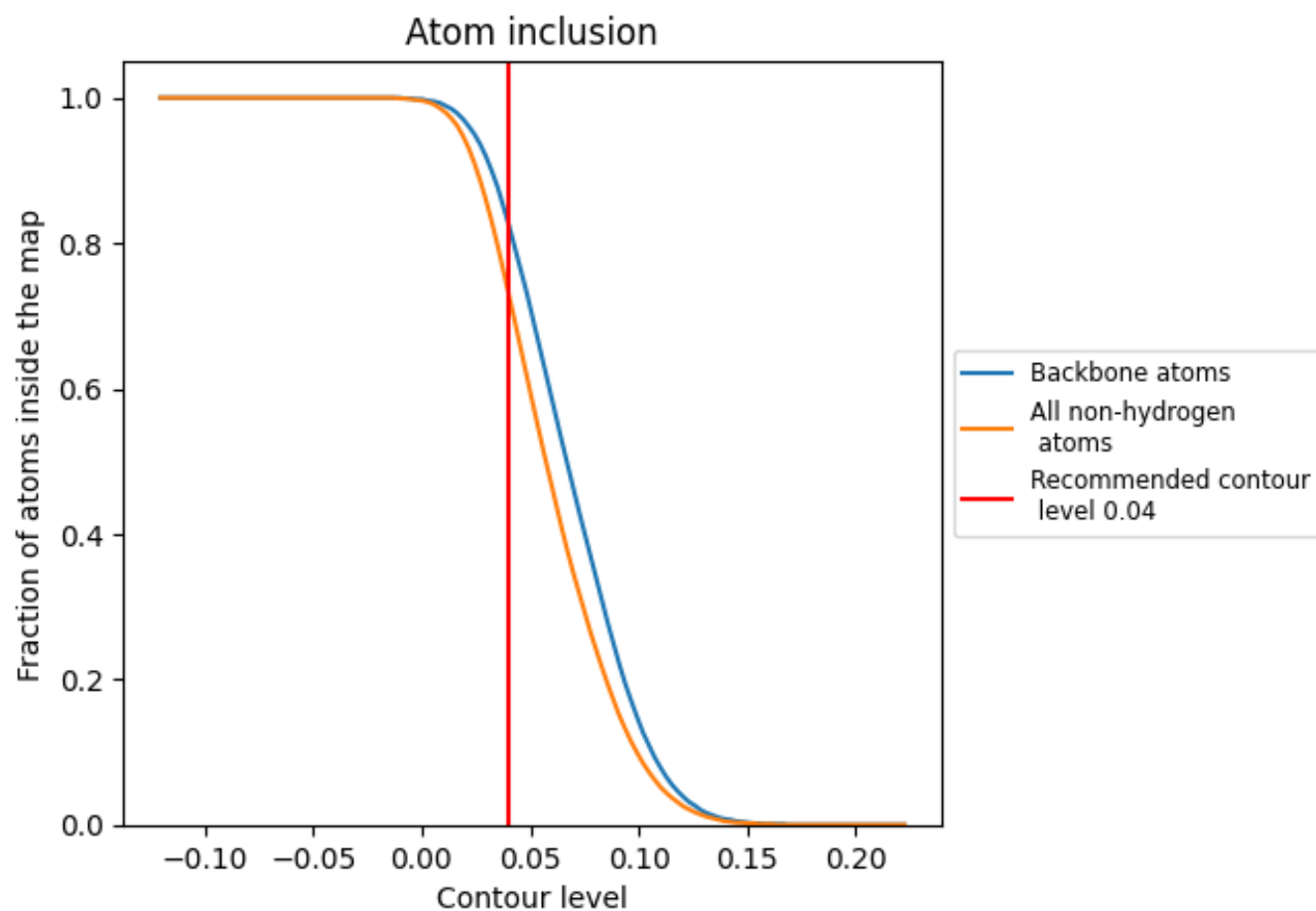
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 73% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7320	 0.4690
1	 0.7180	 0.4210
A	 0.7990	 0.5290
Aa	 0.7820	 0.5070
Ab	 0.8220	 0.5180
Ad	 0.8320	 0.5290
Ae	 0.7890	 0.5050
Af	 0.7710	 0.5090
Ag	 0.8150	 0.5250
Ah	 0.6620	 0.3970
Aj	 0.8210	 0.5190
Al	 0.7450	 0.4990
Am	 0.8200	 0.5130
An	 0.6080	 0.4010
Ap	 0.6860	 0.4290
Ar	 0.7540	 0.4800
As	 0.6880	 0.4540
At	 0.8440	 0.5220
Au	 0.7930	 0.4740
Av	 0.4000	 0.3300
Aw	 0.8590	 0.5230
Ax	 0.2640	 0.3760
Az	 0.8470	 0.5230
B	 0.8400	 0.5370
BA	 0.6560	 0.4420
BB	 0.7040	 0.5030
BE	 0.7550	 0.5050
BF	 0.7080	 0.4870
BG	 0.5940	 0.4300
BH	 0.8280	 0.5060
BK	 0.7860	 0.5000
BM	 0.6160	 0.3750
BN	 0.7360	 0.4700
BO	 0.7050	 0.4770
BP	 0.8190	 0.5310



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Chain	Atom inclusion	Q-score
BQ	 0.7440	 0.4700
BR	 0.7380	 0.4710
BS	 0.5660	 0.4300
BT	 0.5040	 0.4440
BU	 0.6810	 0.4650
BV	 0.5760	 0.4260
BW	 0.7660	 0.5110
BX	 0.6740	 0.4250
BY	 0.5730	 0.3530
BZ	 0.7190	 0.4910
Bl	 0.7890	 0.4370
C	 0.7890	 0.4870
CA	 0.7560	 0.4660
CB	 0.7050	 0.4570
CC	 0.5140	 0.3370
CD	 0.7130	 0.4440
E	 0.4920	 0.3790
F	 0.8040	 0.5490
G	 0.7750	 0.5130
I	 0.7630	 0.4960
J	 0.7840	 0.5040
K	 0.8160	 0.5230
L	 0.8220	 0.5310
M	 0.8150	 0.5270
N	 0.7440	 0.4920
O	 0.7420	 0.4850
Q	 0.7880	 0.4930
R	 0.8080	 0.4870
R1	 0.8550	 0.4300
R2	 0.8290	 0.3970
R5	 0.7100	 0.1690
S	 0.7870	 0.5270
T	 0.8500	 0.5420
U1	 0.8040	 0.4680
U2	 0.8970	 0.5410
U3	 0.8190	 0.4520
U4	 0.8220	 0.4370
U5	 0.8490	 0.5050
U6	 0.8820	 0.4860
U7	 0.8200	 0.4720
U8	 0.8310	 0.5330
UA	 0.3680	 0.3300

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Chain	Atom inclusion	Q-score
V	 0.7790	 0.5250
Z	 0.8030	 0.4950