



# wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 11:21 PM UTC

PDB ID : 9HM0 / pdb\_00009hm0  
EMDB ID : EMD-52283  
Title : Translational activator Aep3 in complex with mRNA and the yeast mitochondrial ribosome  
Authors : Carlstrom, A.; Rovensnik, U.; Ott, M.  
Deposited on : 2024-12-06  
Resolution : 3.00 Å (reported)  
Based on initial models : 8OM4, 5MRC, .

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

---

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

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

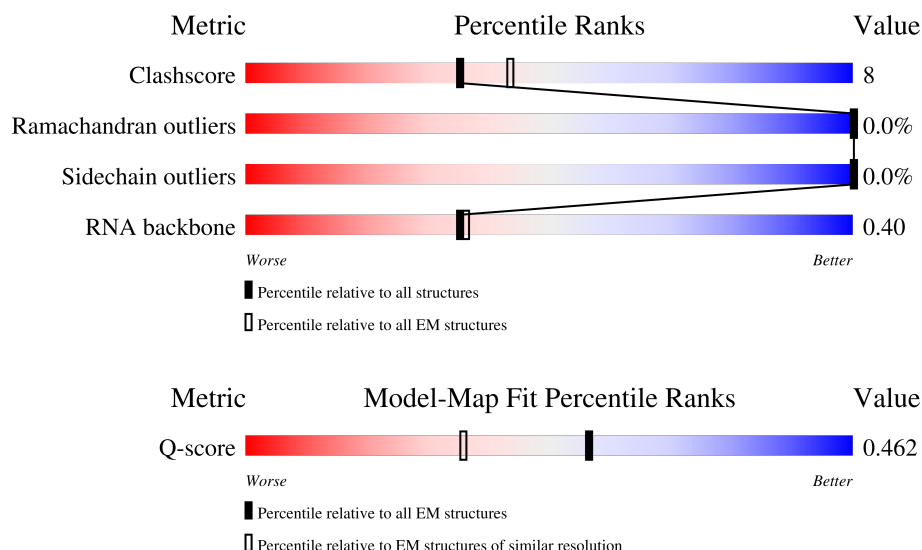
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.00 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  $\geq 3$ , 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	1	111	 18% 11% 71%
2	2	130	 9% 61% 18% 22%
3	3	266	 5% 81% 16% .







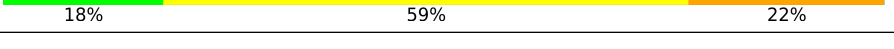
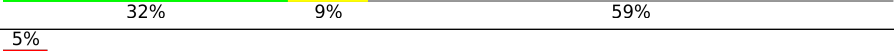
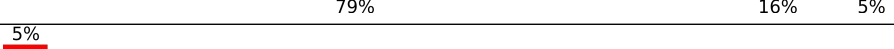
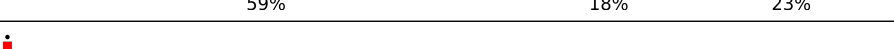
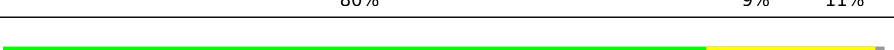

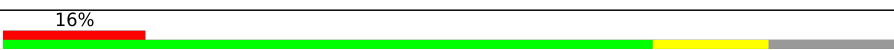

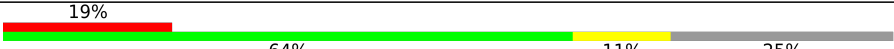





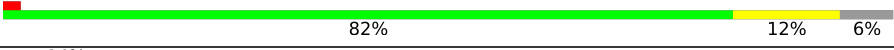
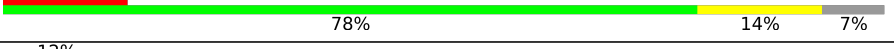
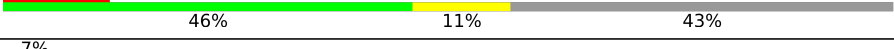
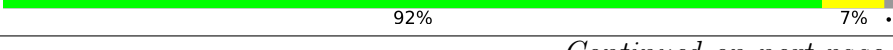

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	4	321	
5	5	339	
6	6	345	
7	7	361	
8	8	500	
9	A	344	
10	B	394	
11	C	398	
12	D	486	
13	E	307	
14	F	131	
15	G	247	
16	H	155	
17	I	278	
18	J	203	
19	K	217	
20	L	153	
21	M	143	
22	N	115	
23	O	286	
24	P	121	
25	Q	237	
26	R	138	
27	S	91	
28	T	177	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	U	264	
30	W	450	
31	X	110	
32	Y	319	
33	Z	95	
34	a	606	
35	t	76	
36	00	93	
37	11	367	
38	22	147	
39	33	146	
40	44	140	
41	55	390	
42	66	281	
43	77	146	
44	88	264	
45	99	253	
46	AA	3296	
47	BB	393	
48	CC	269	
49	DD	286	
50	EE	292	
51	FF	214	
52	GG	139	
53	HH	163	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	II	138	
55	JJ	322	
56	KK	232	
57	LL	238	
58	MM	169	
59	NN	161	
60	OO	309	
61	PP	263	
62	QQ	297	
63	RR	371	
64	SS	258	
65	TT	319	
66	UU	86	
67	V	318	
68	VV	177	
69	WW	183	
70	XX	70	
71	YY	105	
72	ZZ	115	
73	aa	195	
74	bb	157	
75	cc	131	
76	dd	226	
77	r	1649	

## 2 Entry composition

There are 79 unique types of molecules in this entry. The entry contains 213189 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 Small ribosomal subunit protein mS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	32	Total	C	N	O	S	0	0
			288	175	70	41	2		

- Molecule 2 is a protein called Small ribosomal subunit protein mS41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	102	Total	C	N	O	S	0	0
			858	544	161	152	1		

- Molecule 3 is a protein called Small ribosomal subunit protein mS42.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	257	Total	C	N	O	S	0	0
			2063	1326	349	383	5		

- Molecule 4 is a protein called Small ribosomal subunit protein mS43.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	308	Total	C	N	O	S	0	0
			2475	1564	428	473	10		

- Molecule 5 is a protein called Small ribosomal subunit protein mS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	290	Total	C	N	O	S	0	0
			2354	1519	403	428	4		

- Molecule 6 is a protein called Small ribosomal subunit protein mS45.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	319	Total	C	N	O	S	0	0
			2593	1646	467	474	6		

- Molecule 7 is a protein called Small ribosomal subunit protein mS46.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	166	Total	C	N	O	S	0	0
			1337	859	215	260	3		

- Molecule 8 is a protein called Small ribosomal subunit protein mS47.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	467	Total	C	N	O	S	0	0
			3690	2341	621	708	20		

- Molecule 9 is a protein called Small ribosomal subunit protein bS1m.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	343	Total	C	N	O	S	0	0
			2773	1765	497	504	7		

- Molecule 10 is a protein called Small ribosomal subunit protein uS2m.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	344	Total	C	N	O	S	0	0
			2727	1720	468	536	3		

- Molecule 11 is a protein called Small ribosomal subunit protein uS3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	396	Total	C	N	O	S	0	0
			3264	2034	589	608	33		

- Molecule 12 is a protein called Small ribosomal subunit protein uS4m.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	349	Total	C	N	O	S	0	0
			2899	1880	512	502	5		

- Molecule 13 is a protein called Small ribosomal subunit protein uS5m.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	294	Total	C	N	O	S	0	0
			2348	1494	418	428	8		

- Molecule 14 is a protein called Small ribosomal subunit protein bS6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	131	Total	C	N	O	S	0	0
			1055	671	189	191	4		

- Molecule 15 is a protein called Small ribosomal subunit protein uS7m.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	208	Total	C	N	O	S	0	0
			1645	1037	296	307	5		

- Molecule 16 is a protein called Small ribosomal subunit protein uS8m.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	154	Total	C	N	O	S	0	0
			1213	767	217	220	9		

- Molecule 17 is a protein called Small ribosomal subunit protein uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	246	Total	C	N	O	S	0	0
			1974	1258	361	349	6		

- Molecule 18 is a protein called Small ribosomal subunit protein uS10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	188	Total	C	N	O	S	0	0
			1526	976	263	283	4		

- Molecule 19 is a protein called Small ribosomal subunit protein uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	151	Total	C	N	O	S	0	0
			1201	770	210	215	6		

- Molecule 20 is a protein called Small ribosomal subunit protein uS12m.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	125	Total	C	N	O	S	0	0
			954	588	195	167	4		

- Molecule 21 is a protein called Small ribosomal subunit protein uS13m.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	119	Total	C	N	O	S	0	0
			935	591	178	160	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	41	LEU	PHE	conflict	UNP P53937

- Molecule 22 is a protein called Small ribosomal subunit protein uS14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	114	Total	C	N	O	S	0	0
			945	607	181	153	4		

- Molecule 23 is a protein called Small ribosomal subunit protein uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	253	Total	C	N	O	S	0	0
			2069	1292	387	382	8		

- Molecule 24 is a protein called Small ribosomal subunit protein bS16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	120	Total	C	N	O	S	0	0
			951	604	178	167	2		

- Molecule 25 is a protein called Small ribosomal subunit protein uS17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	235	Total	C	N	O	S	0	0
			1923	1203	354	361	5		

- Molecule 26 is a protein called Small ribosomal subunit protein bS18m.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	103	Total	C	N	O	S	0	0
			836	517	166	149	4		

- Molecule 27 is a protein called Small ribosomal subunit protein uS19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	81	Total	C	N	O	S	0	0
			645	414	117	112	2		

- Molecule 28 is a protein called Small ribosomal subunit protein bS21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	101	Total	C	N	O	S	0	0
			837	522	164	146	5		

- Molecule 29 is a protein called Small ribosomal subunit protein mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	237	Total	C	N	O	S	0	0
			1939	1228	339	365	7		

- Molecule 30 is a protein called Small ribosomal subunit protein mS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	W	403	Total	C	N	O	S	0	0
			3231	2081	543	599	8		

- Molecule 31 is a protein called Small ribosomal subunit protein mS33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X	100	Total	C	N	O	S	0	0
			797	509	144	141	3		

- Molecule 32 is a protein called Small ribosomal subunit protein mS35.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	273	Total	C	N	O	S	0	0
			2281	1442	409	426	4		

- Molecule 33 is a protein called Small ribosomal subunit protein mS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Z	94	Total	C	N	O	S	0	0
			739	464	139	130	6		

- Molecule 34 is a protein called ATPase expression protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	562	Total	C	N	O	S	0	0
			4618	2940	823	836	19		

- Molecule 35 is a RNA chain called E/E-site formyl-methionine tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	t	76	Total	C	N	O	P	0	0
			1604	720	271	537	76		

- Molecule 36 is a protein called Large ribosomal subunit protein bL36m.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	00	38	Total	C	N	O	S	0	0
			324	205	66	50	3		

- Molecule 37 is a protein called Large ribosomal subunit protein mL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	11	348	Total	C	N	O	S	0	0
			2875	1847	499	523	6		

- Molecule 38 is a protein called Large ribosomal subunit protein mL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	22	113	Total	C	N	O	S	0	0
			944	597	174	168	5		

- Molecule 39 is a protein called Large ribosomal subunit protein mL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	33	130	Total	C	N	O	S	0	0
			1046	671	189	183	3		

- Molecule 40 is a protein called Large ribosomal subunit protein mL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	44	138	Total	C	N	O	S	0	0
			1117	700	219	193	5		

- Molecule 41 is a protein called Large ribosomal subunit protein mL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	55	324	Total	C	N	O	S	0	0
			2552	1630	431	480	11		

- Molecule 42 is a protein called Large ribosomal subunit protein mL46.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	66	240	Total	C	N	O	S	0	0
			1975	1275	335	363	2		

- Molecule 43 is a protein called Large ribosomal subunit protein mL49.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	77	106	Total	C	N	O	S	0	0
			858	553	151	152	2		

- Molecule 44 is a protein called Large ribosomal subunit protein mL50.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	88	199	Total	C	N	O	S	0	0
			1629	1032	278	315	4		

- Molecule 45 is a protein called Large ribosomal subunit protein mL57.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	99	202	Total	C	N	O	S	0	0
			1587	1014	279	289	5		

- Molecule 46 is a RNA chain called 21S mitochondrial rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AA	2708	Total	C	N	O	P	0	0
			57599	25906	10253	18732	2708		

- Molecule 47 is a protein called Large ribosomal subunit protein uL2m.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BB	330	Total	C	N	O	S	0	0
			2591	1614	518	449	10		

- Molecule 48 is a protein called Large ribosomal subunit protein uL3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CC	249	Total	C	N	O	S	0	0
			1932	1218	360	344	10		

- Molecule 49 is a protein called Large ribosomal subunit protein uL4m.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	DD	258	Total	C	N	O	S	0	0
			2036	1291	364	378	3		

- Molecule 50 is a protein called Large ribosomal subunit protein uL5m.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	EE	274	Total	C	N	O	S	0	0
			2187	1396	391	394	6		

- Molecule 51 is a protein called Large ribosomal subunit protein uL6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	FF	198	Total	C	N	O	S	0	0
			1541	979	276	282	4		

- Molecule 52 is a protein called Large ribosomal subunit protein bL9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	GG	79	Total	C	N	O	S	0	0
			659	418	119	121	1		

- Molecule 53 is a protein called Large ribosomal subunit protein uL13m.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	HH	162	Total	C	N	O	S	0	0
			1292	819	243	226	4		

- Molecule 54 is a protein called Large ribosomal subunit protein uL14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	II	138	Total	C	N	O	S	0	0
			1034	639	195	189	11		

- Molecule 55 is a protein called Large ribosomal subunit protein uL15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	JJ	220	Total	C	N	O	S	0	0
			1746	1119	326	298	3		

- Molecule 56 is a protein called Large ribosomal subunit protein uL16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	KK	195	Total	C	N	O	S	0	0
			1573	1001	297	270	5		

- Molecule 57 is a protein called Large ribosomal subunit protein bL17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LL	237	Total	C	N	O	S	0	0
			1882	1184	345	345	8		

- Molecule 58 is a protein called Large ribosomal subunit protein bL19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	MM	152	Total	C	N	O	S	0	0
			1217	772	224	218	3		

- Molecule 59 is a protein called Large ribosomal subunit protein bL21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	NN	119	Total	C	N	O	S	0	0
			957	604	179	172	2		

- Molecule 60 is a protein called Large ribosomal subunit protein uL22m.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	OO	225	Total	C	N	O	S	0	0
			1826	1169	332	320	5		

- Molecule 61 is a protein called Large ribosomal subunit protein uL23m.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	PP	207	Total	C	N	O	S	0	0
			1729	1104	310	309	6		

- Molecule 62 is a protein called Large ribosomal subunit protein uL24m.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	QQ	296	Total	C	N	O	S	0	0
			2367	1507	413	439	8		

- Molecule 63 is a protein called Large ribosomal subunit protein bL27m.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	RR	337	Total	C	N	O	S	0	0
			2781	1754	506	517	4		

- Molecule 64 is a protein called Large ribosomal subunit protein bL28m.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SS	206	Total	C	N	O	S	0	0
			1712	1103	309	297	3		

- Molecule 65 is a protein called Large ribosomal subunit protein uL29m.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	TT	275	Total	C	N	O	S	0	0
			2255	1428	396	426	5		

- Molecule 66 is a protein called Large ribosomal subunit protein uL30m.

Mol	Chain	Residues	Atoms				AltConf	Trace
66	UU	82	Total	C	N	O	0	0
			639	410	116	113		

- Molecule 67 is a protein called Small ribosomal subunit protein mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	V	290	Total	C	N	O	S	0	0
			2322	1466	411	441	4		

- Molecule 68 is a protein called Large ribosomal subunit protein bL31m.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	VV	104	Total	C	N	O	S	0	0
			805	501	157	146	1		

- Molecule 69 is a protein called Large ribosomal subunit protein bL32m.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	WW	112	Total	C	N	O	S	0	0
			937	587	181	163	6		

- Molecule 70 is a protein called Large ribosomal subunit protein bL33m.

Mol	Chain	Residues	Atoms				AltConf	Trace
70	XX	64	Total	C	N	O	0	0
			512	330	96	86		

- Molecule 71 is a protein called Large ribosomal subunit protein bL34m.

Mol	Chain	Residues	Atoms				AltConf	Trace
71	YY	46	Total	C	N	O	0	0
			385	245	82	58		

- Molecule 72 is a protein called Large ribosomal subunit protein bL35m.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	ZZ	62	Total	C	N	O	S	0	0
			508	322	111	74	1		

- Molecule 73 is a protein called Large ribosomal subunit protein mL58.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	aa	177	Total	C	N	O	S	0	0
			1440	907	267	260	6		

- Molecule 74 is a protein called Large ribosomal subunit protein mL59.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	bb	155	Total	C	N	O	S	0	0
			1299	850	225	221	3		

- Molecule 75 is a protein called Large ribosomal subunit protein mL60.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	cc	119	Total	C	N	O	S	0	0
			1004	645	191	164	4		

- Molecule 76 is a protein called Large ribosomal subunit protein mL67.



Mol	Chain	Residues	Atoms					AltConf	Trace
76	dd	217	Total	C	N	O	S	0	0
			1830	1170	333	320	7		

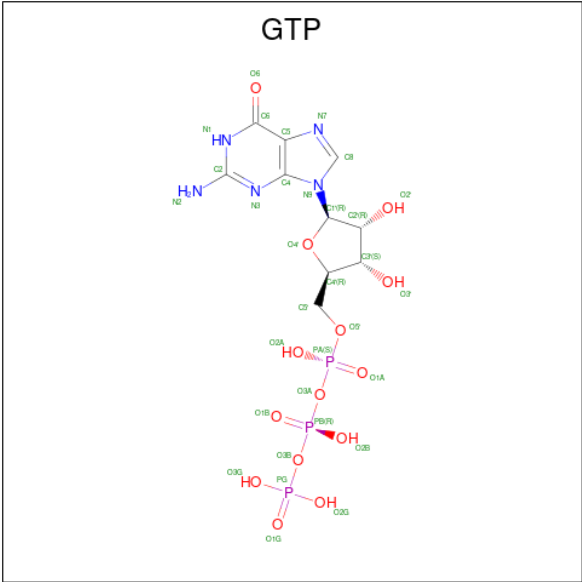
- Molecule 77 is a RNA chain called 15S mitochondrial rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	r	1495	Total	C	N	O	P	0	0
			31749	14277	5600	10377	1495		

- Molecule 78 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
78	1	1	Total	Mg	0
			1	1	
78	B	1	Total	Mg	0
			1	1	
78	E	2	Total	Mg	0
			2	2	
78	K	1	Total	Mg	0
			1	1	
78	M	1	Total	Mg	0
			1	1	
78	P	1	Total	Mg	0
			1	1	
78	W	1	Total	Mg	0
			1	1	
78	AA	194	Total	Mg	0
			194	194	
78	BB	2	Total	Mg	0
			2	2	
78	CC	1	Total	Mg	0
			1	1	
78	NN	1	Total	Mg	0
			1	1	
78	dd	1	Total	Mg	0
			1	1	
78	r	110	Total	Mg	0
			110	110	

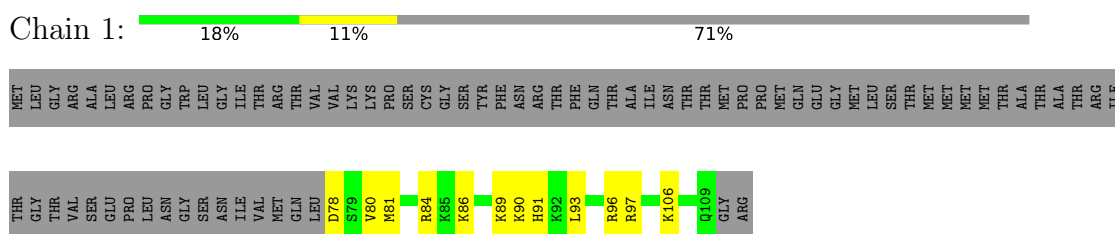
- Molecule 79 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>14</sub>P<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



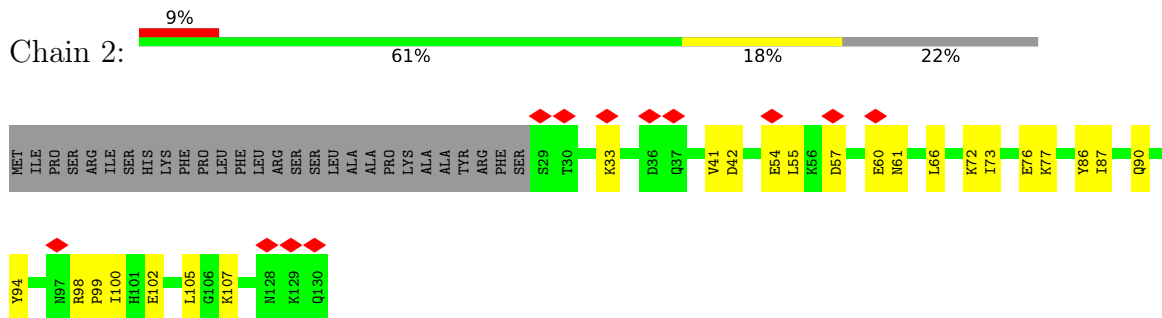
### 3 Residue-property plots

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.

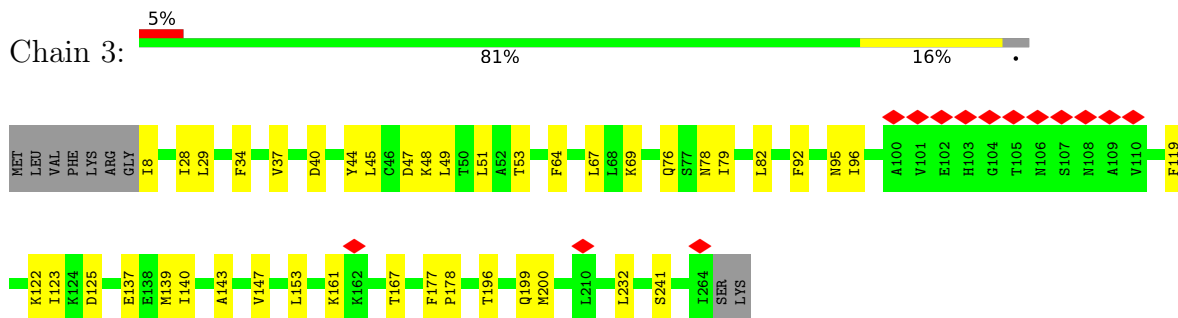
- Molecule 1: Small ribosomal subunit protein mS38



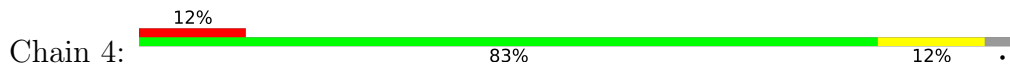
- Molecule 2: Small ribosomal subunit protein mS41



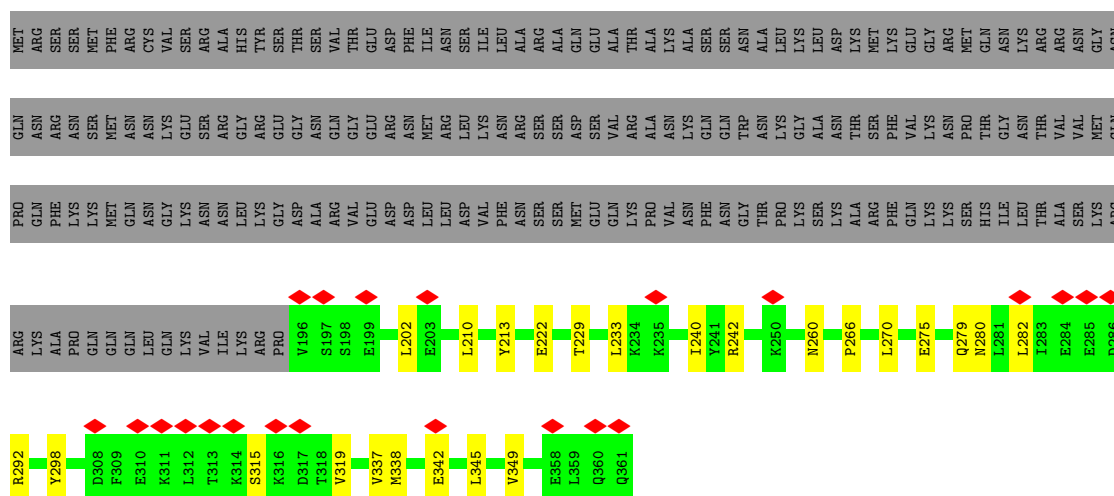
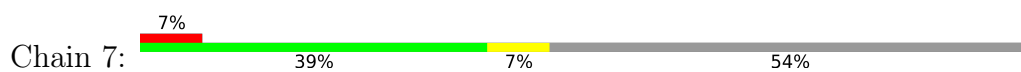
- Molecule 3: Small ribosomal subunit protein mS42



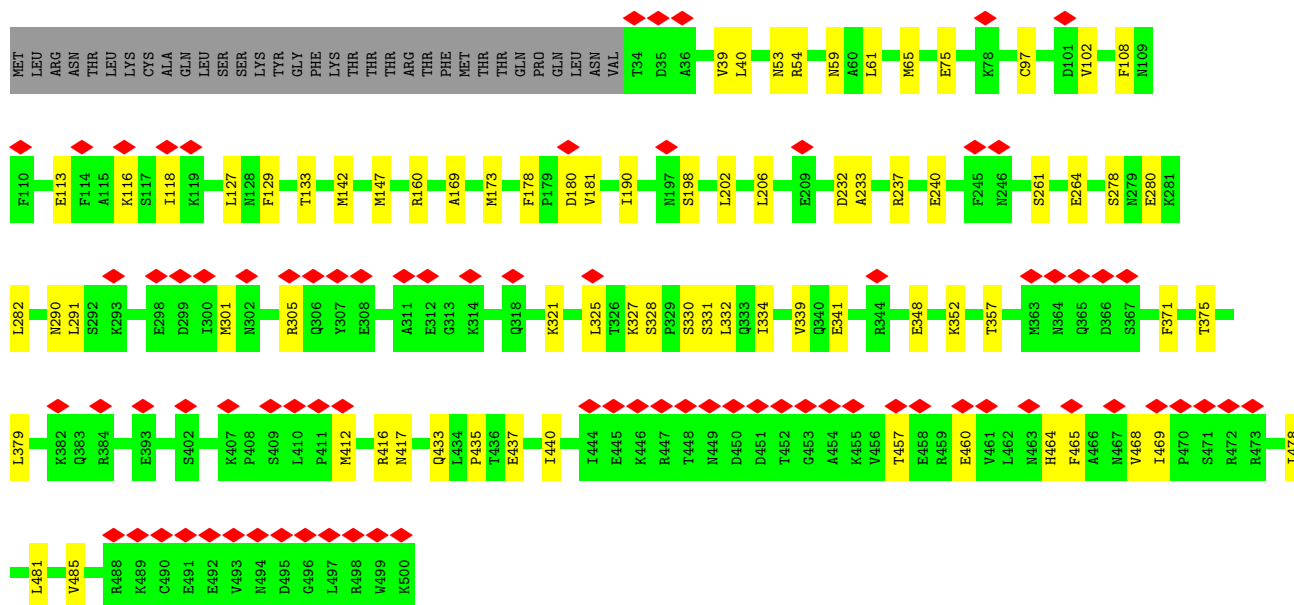
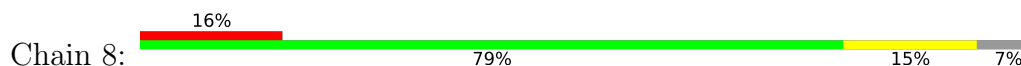
- Molecule 4: Small ribosomal subunit protein mS43



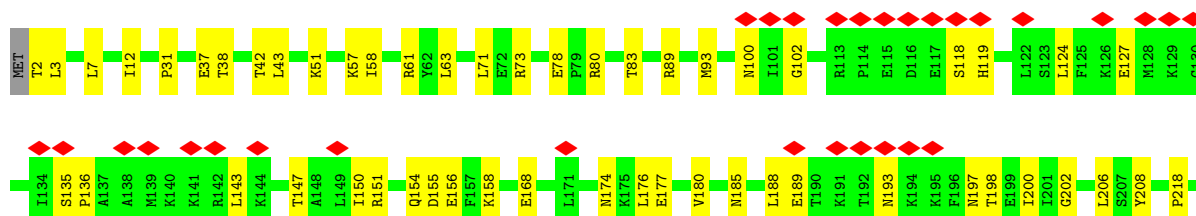
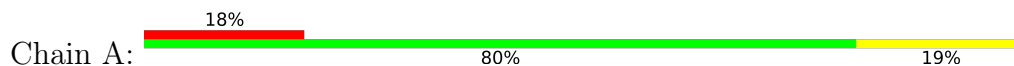




• Molecule 8: Small ribosomal subunit protein mS47

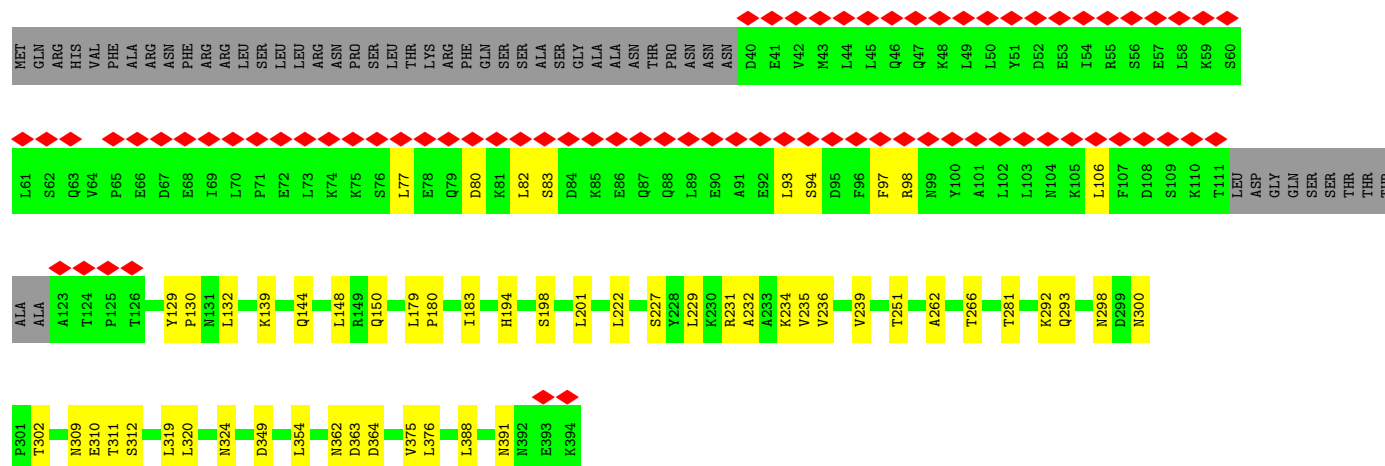
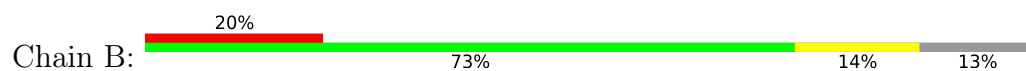


• Molecule 9: Small ribosomal subunit protein bS1m

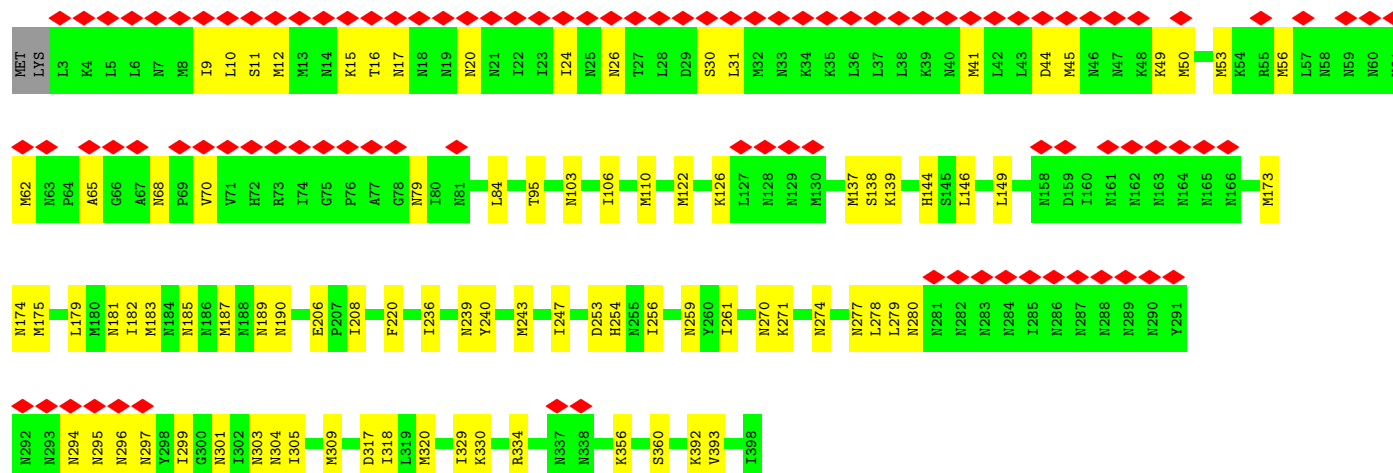
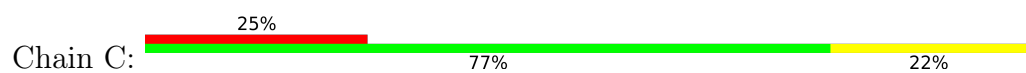




- Molecule 10: Small ribosomal subunit protein uS2m

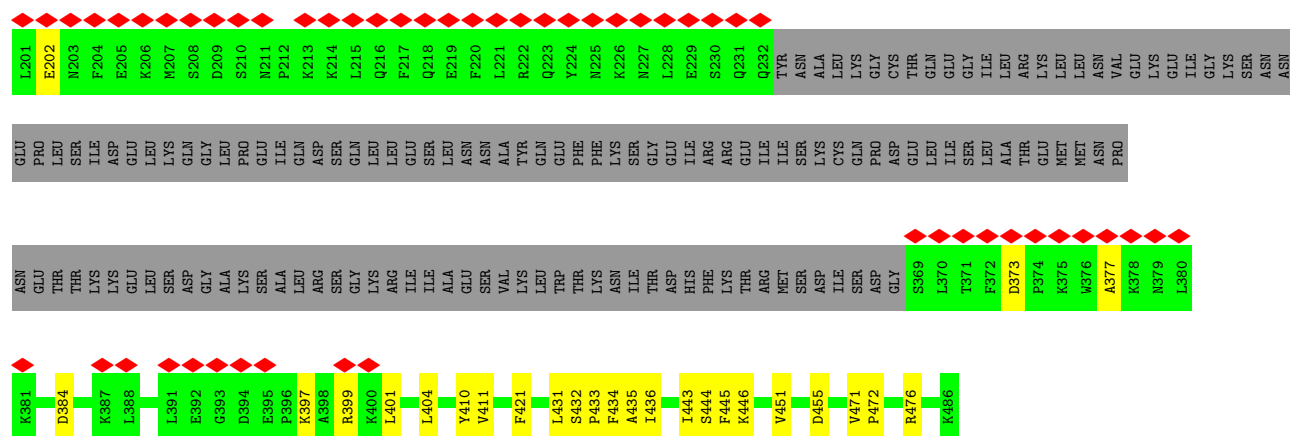


- Molecule 11: Small ribosomal subunit protein uS3m

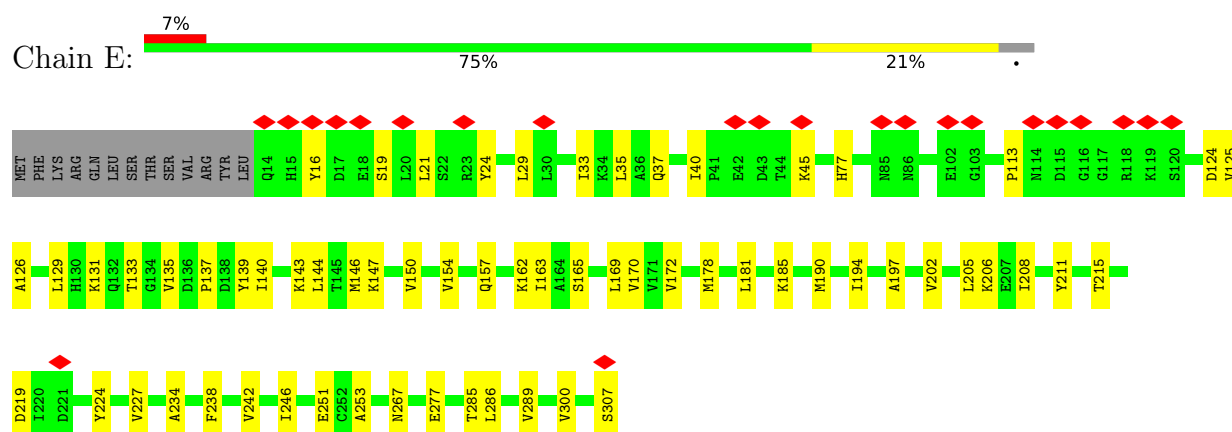


- Molecule 12: Small ribosomal subunit protein uS4m

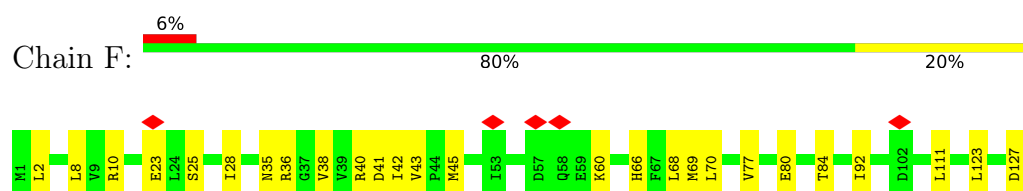




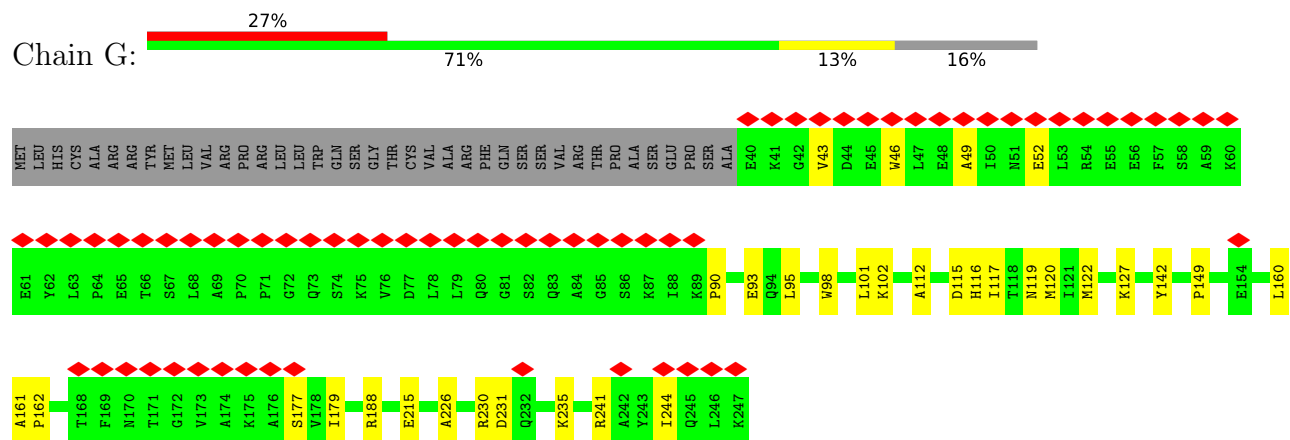
• Molecule 13: Small ribosomal subunit protein uS5m




• Molecule 14: Small ribosomal subunit protein bS6m

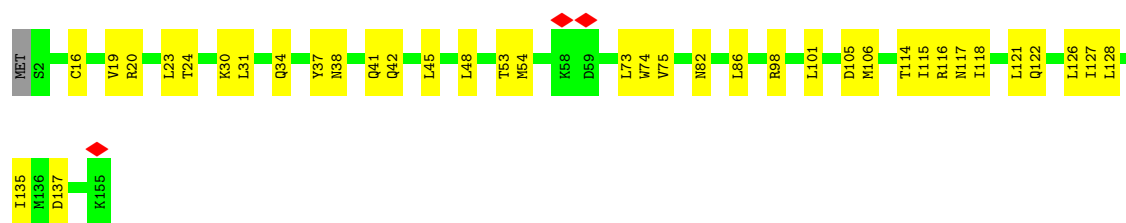


• Molecule 15: Small ribosomal subunit protein uS7m



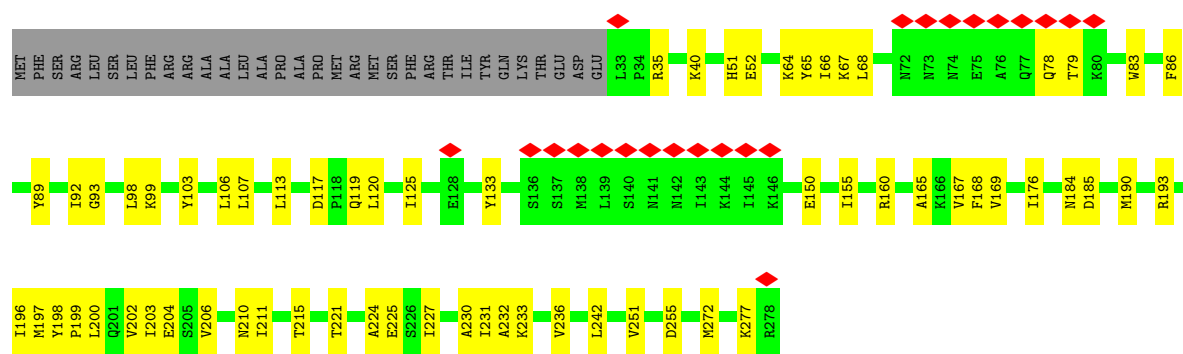
- Molecule 16: Small ribosomal subunit protein uS8m

Chain H: 



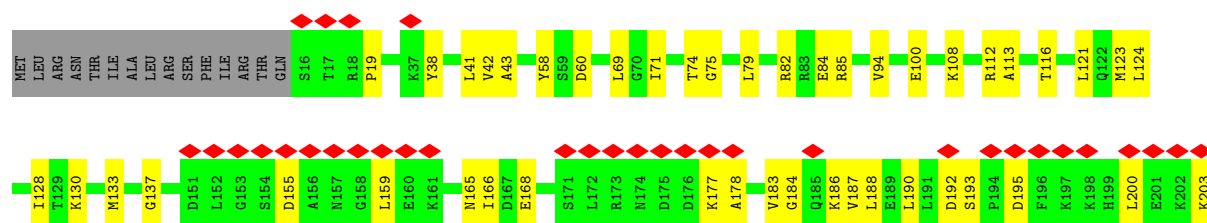
- Molecule 17: Small ribosomal subunit protein uS9m

Chain I: 



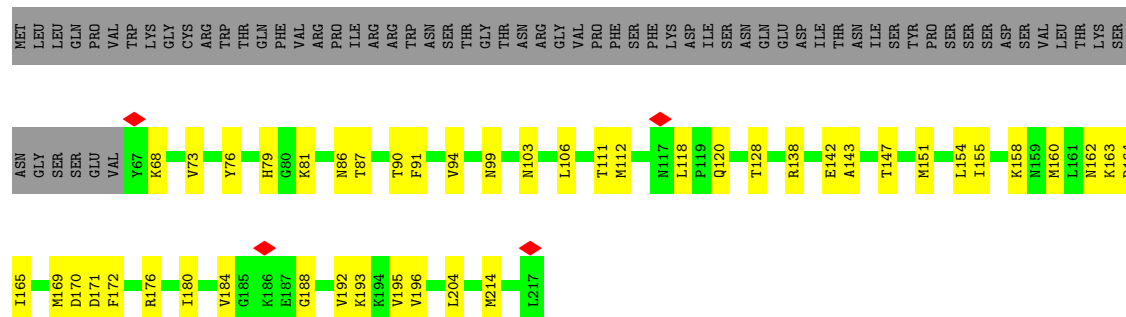
- Molecule 18: Small ribosomal subunit protein uS10m

Chain J: 



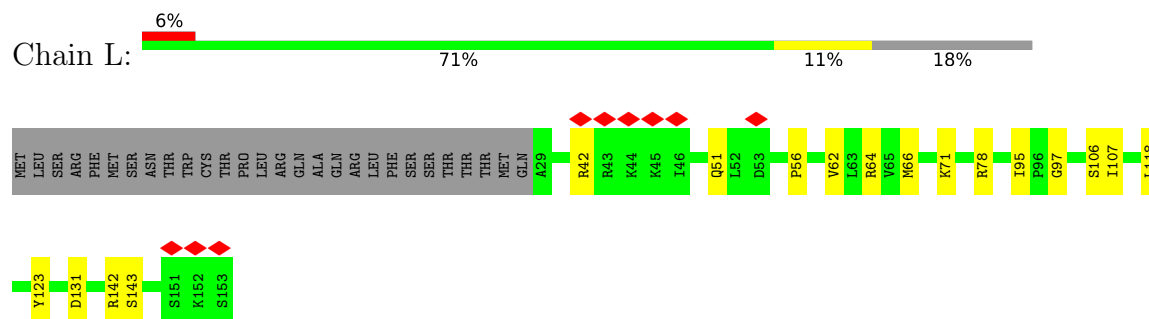
- Molecule 19: Small ribosomal subunit protein uS11m

Chain K: 

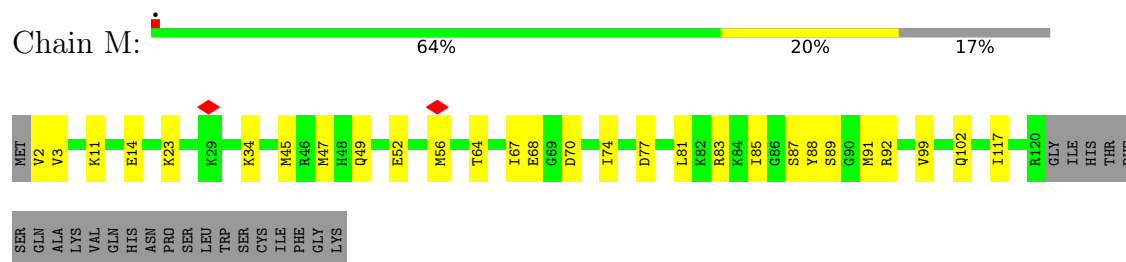




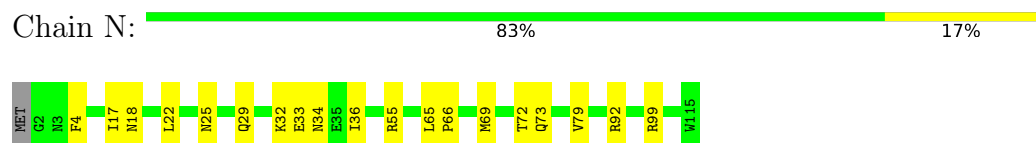
- Molecule 20: Small ribosomal subunit protein uS12m



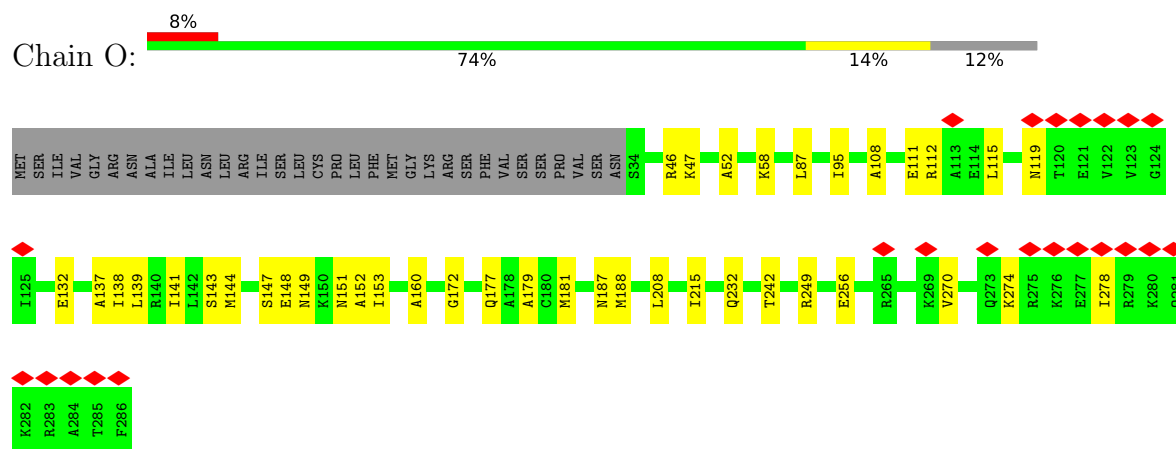
- Molecule 21: Small ribosomal subunit protein uS13m



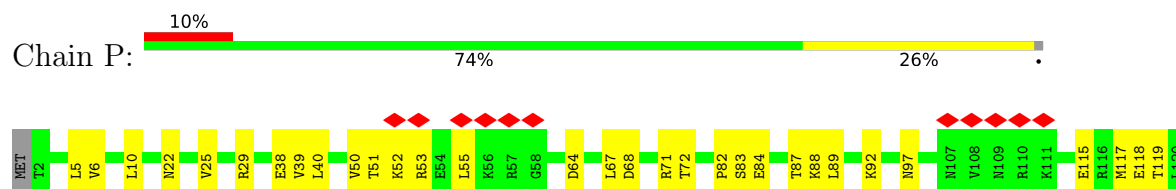
- Molecule 22: Small ribosomal subunit protein uS14m



- Molecule 23: Small ribosomal subunit protein uS15m

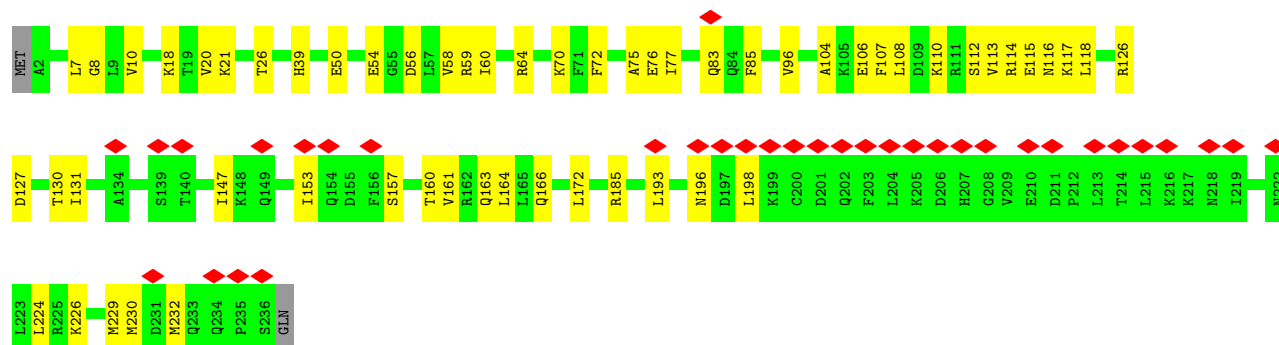
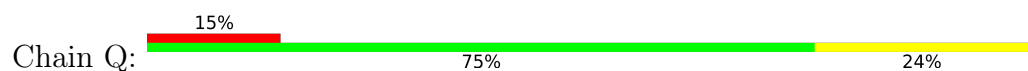


- Molecule 24: Small ribosomal subunit protein bS16m

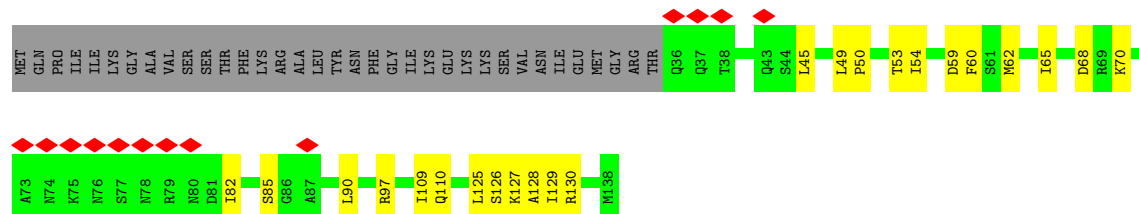




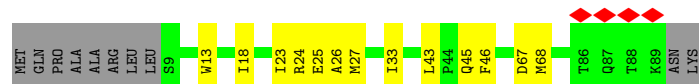
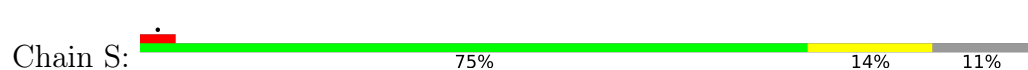
- Molecule 25: Small ribosomal subunit protein uS17m



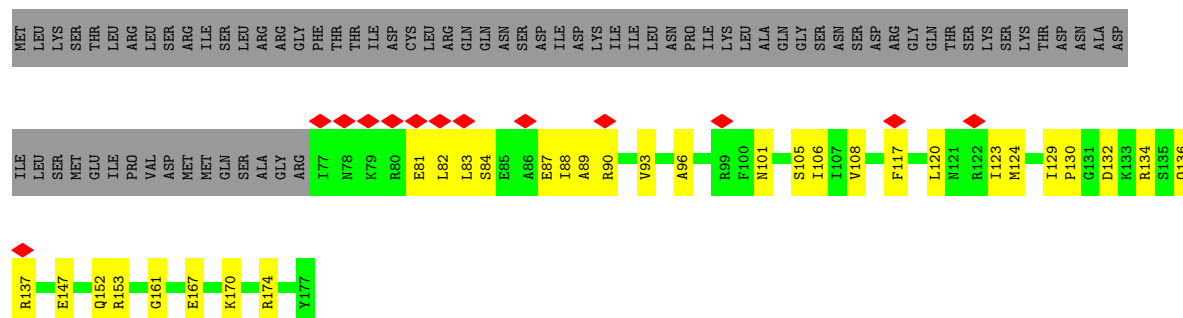
- Molecule 26: Small ribosomal subunit protein bS18m



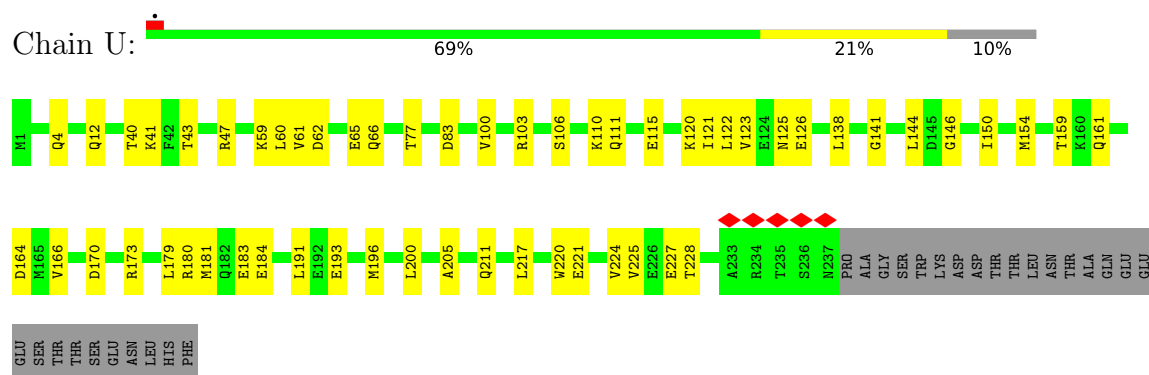
- Molecule 27: Small ribosomal subunit protein uS19m



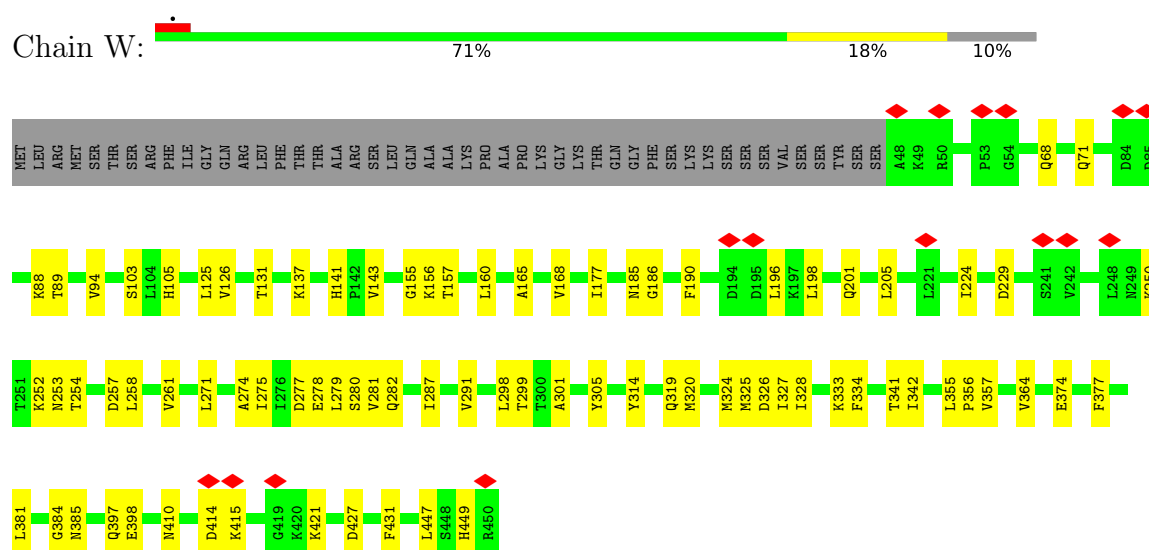
- Molecule 28: Small ribosomal subunit protein bS21m



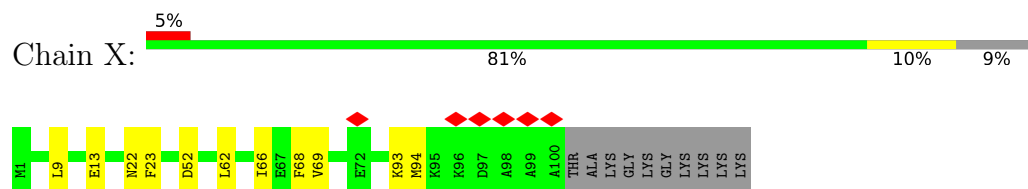
- Molecule 29: Small ribosomal subunit protein mS23



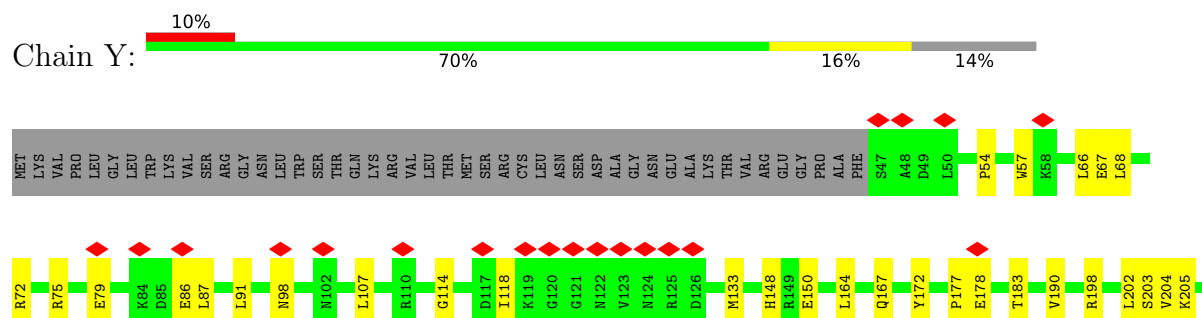
- Molecule 30: Small ribosomal subunit protein mS29



- Molecule 31: Small ribosomal subunit protein mS33

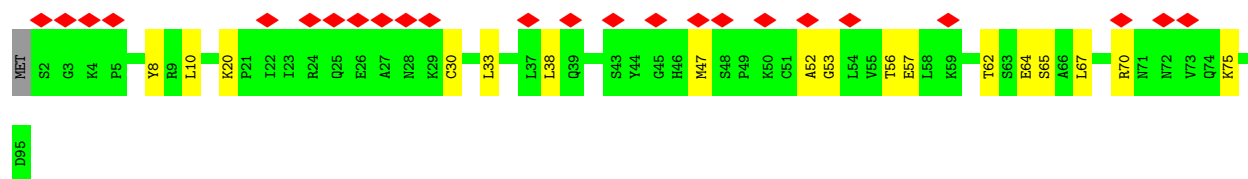
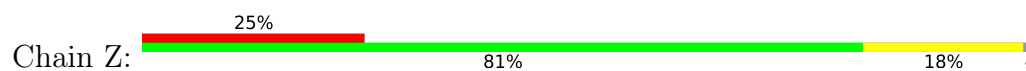


- Molecule 32: Small ribosomal subunit protein mS35

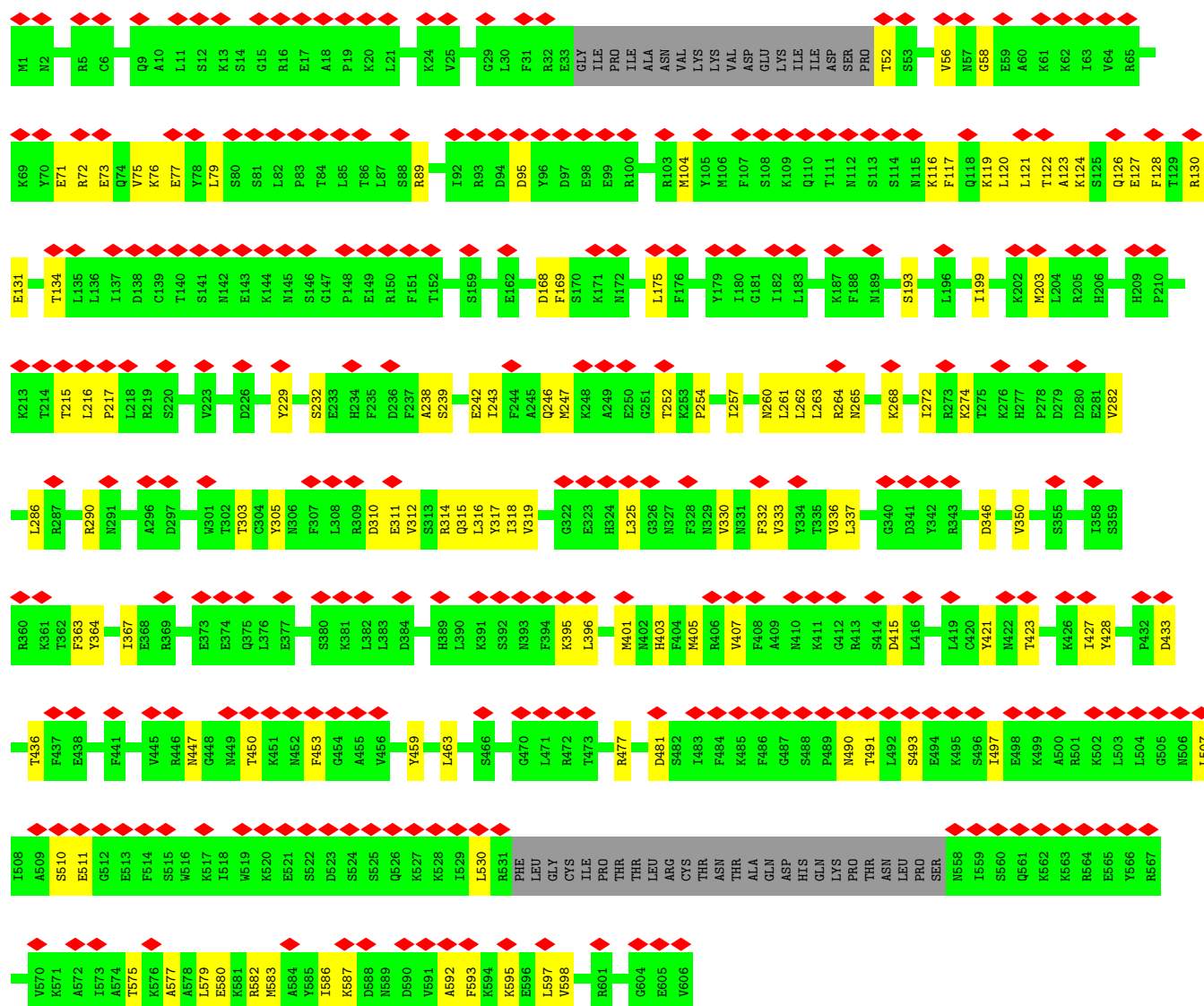
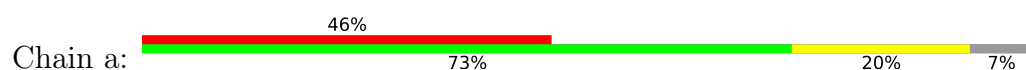




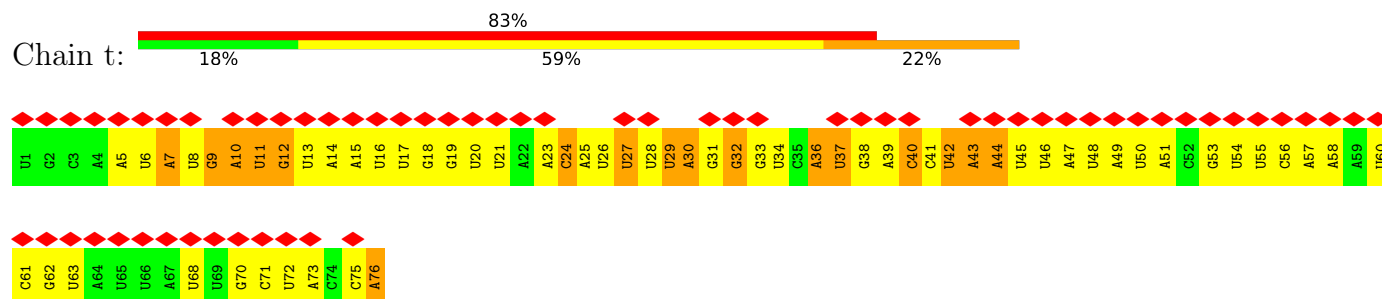
- Molecule 33: Small ribosomal subunit protein mS37



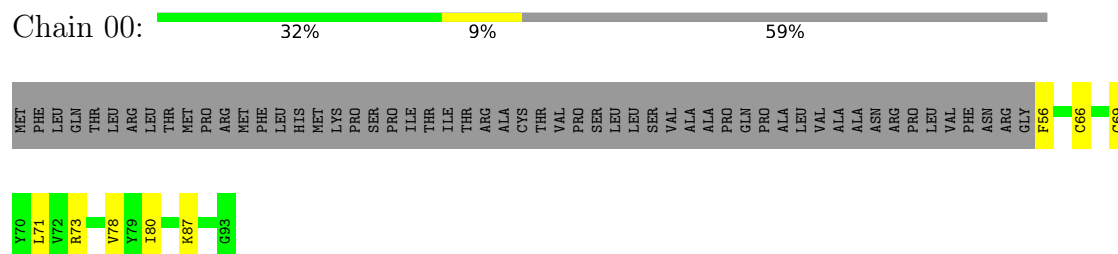
- Molecule 34: ATPase expression protein 3



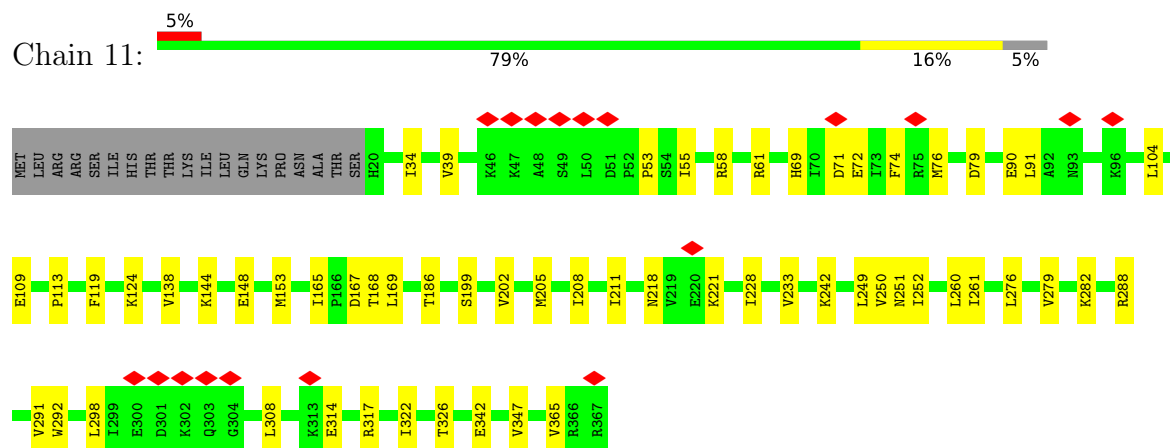
- Molecule 35: E/E-site formyl-methionine tRNA



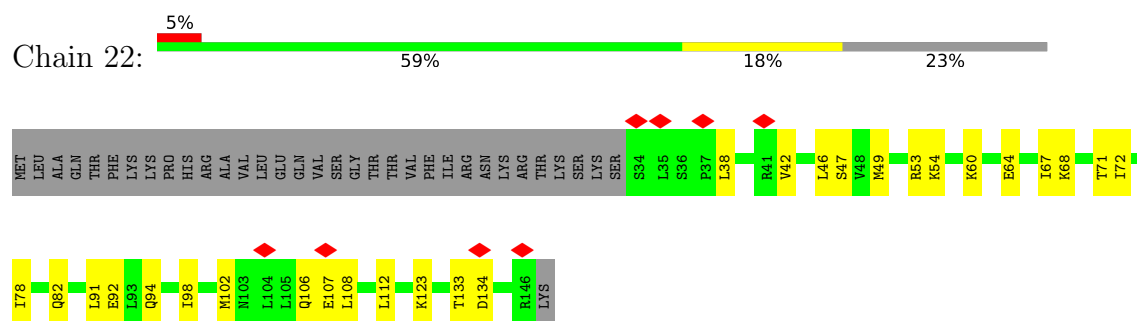
- Molecule 36: Large ribosomal subunit protein bL36m



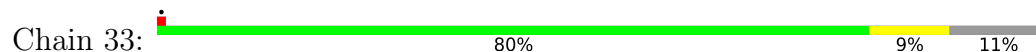
- Molecule 37: Large ribosomal subunit protein mL38



- Molecule 38: Large ribosomal subunit protein mL40



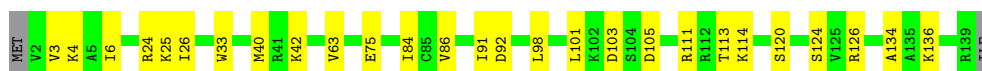
- Molecule 39: Large ribosomal subunit protein mL41





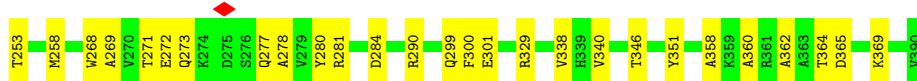
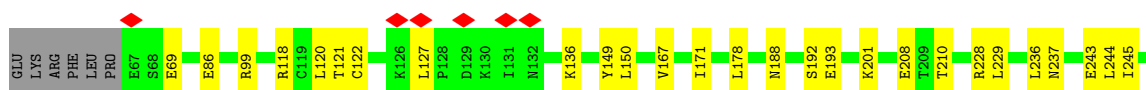
- Molecule 40: Large ribosomal subunit protein mL43

Chain 44: 79% 19%



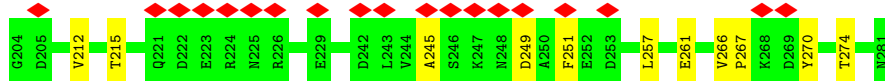
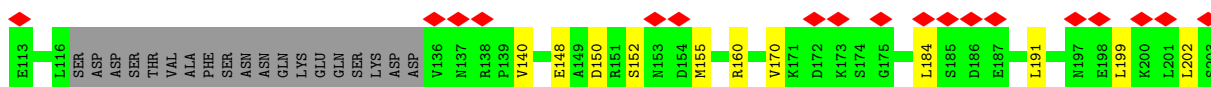
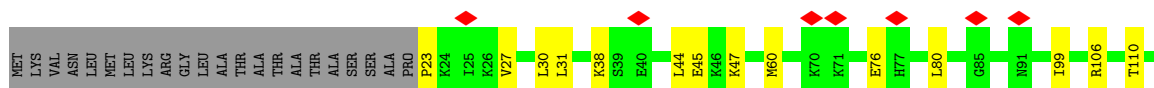
- Molecule 41: Large ribosomal subunit protein mL44

Chain 55: 69% 14% 17%



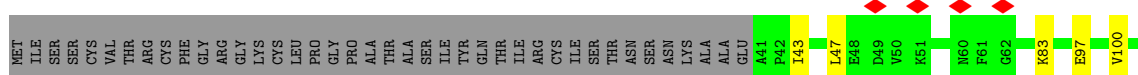
- Molecule 42: Large ribosomal subunit protein mL46

Chain 66: 16% 73% 13% 15%

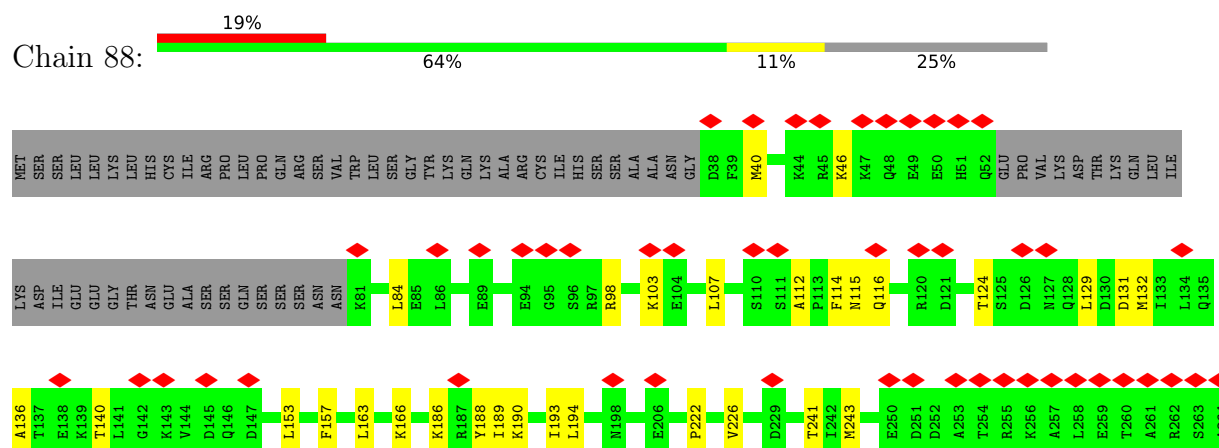


- Molecule 43: Large ribosomal subunit protein mL49

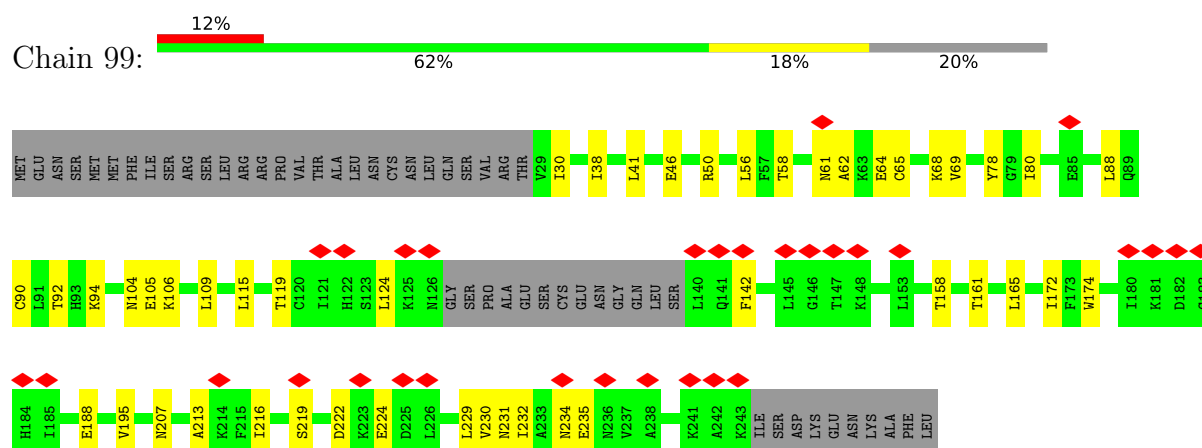
Chain 77: 67% 5% 27%



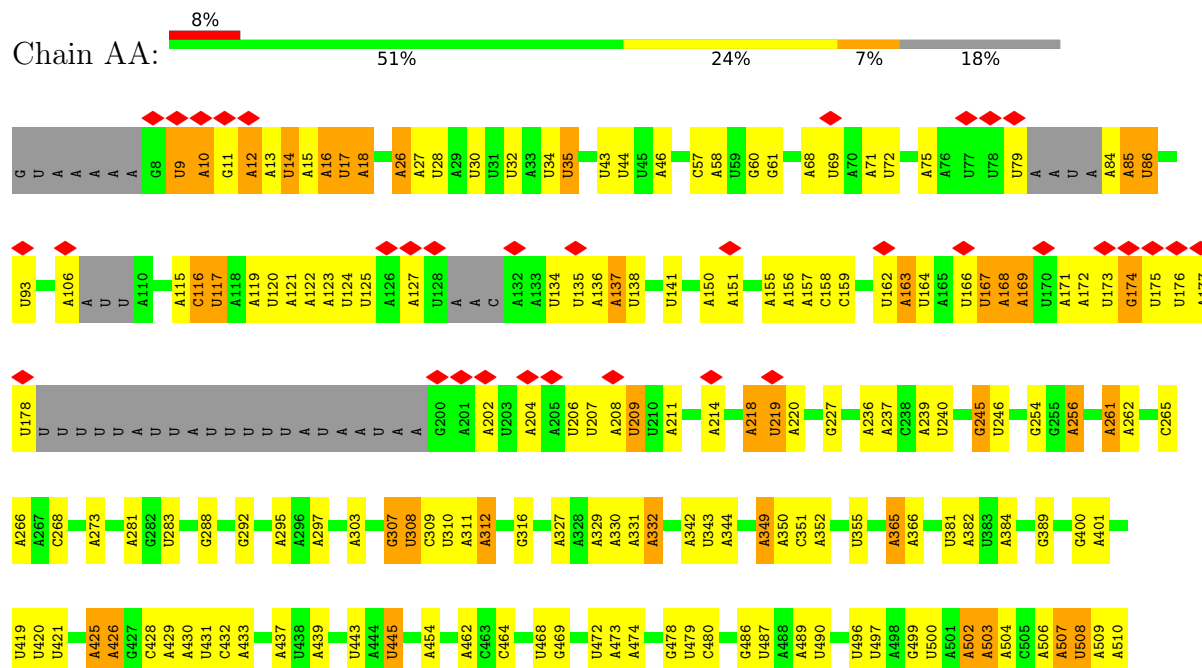
• Molecule 44: Large ribosomal subunit protein mL50



• Molecule 45: Large ribosomal subunit protein mL57



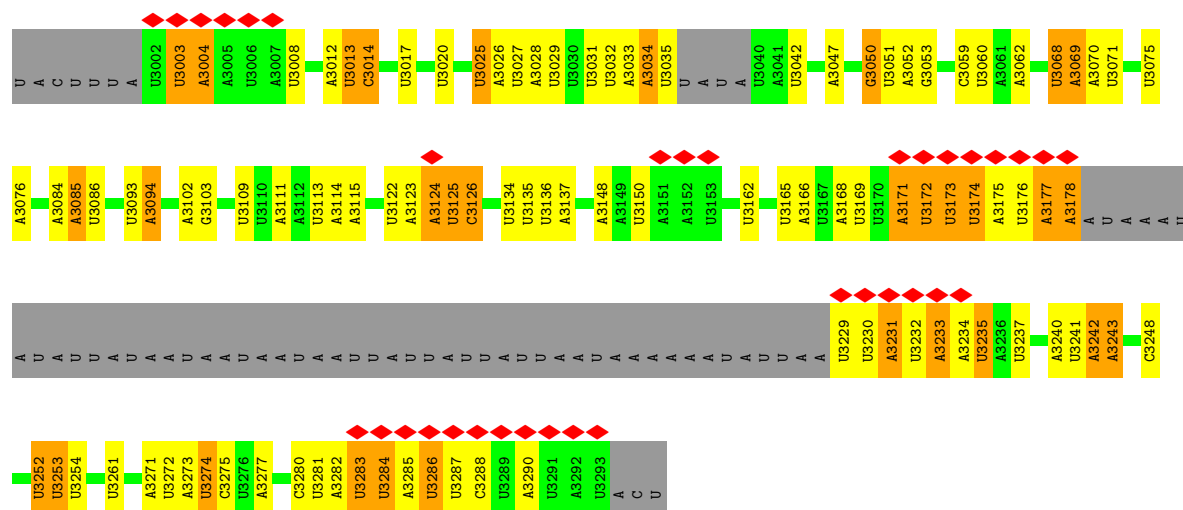
• Molecule 46: 21S mitochondrial rRNA



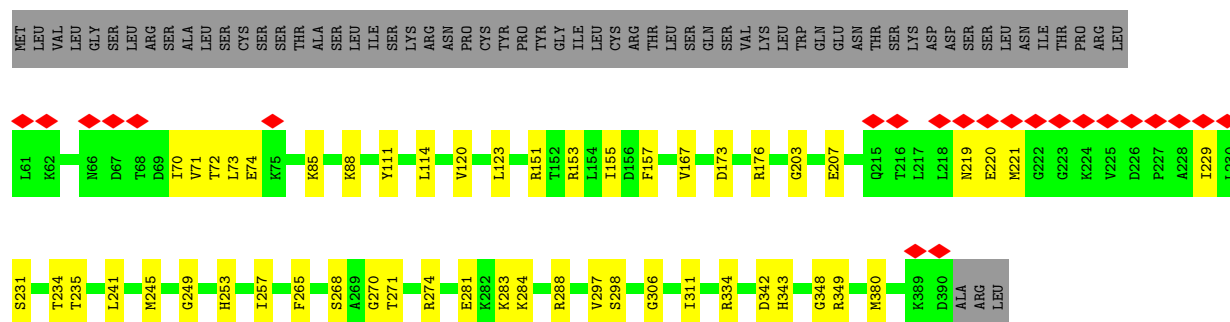
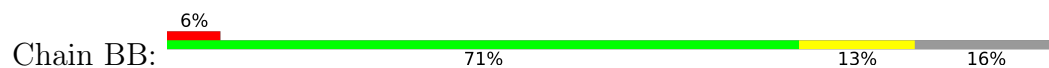




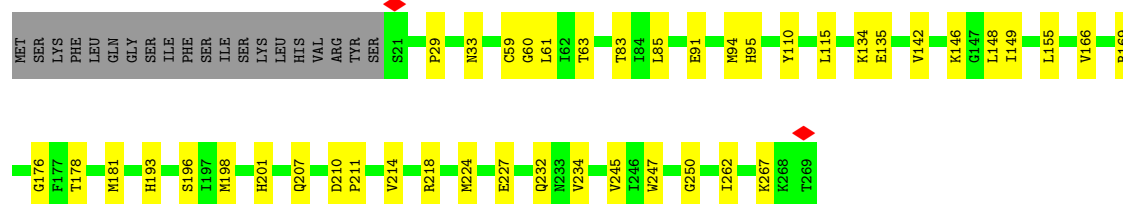
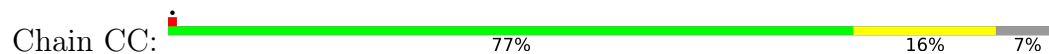




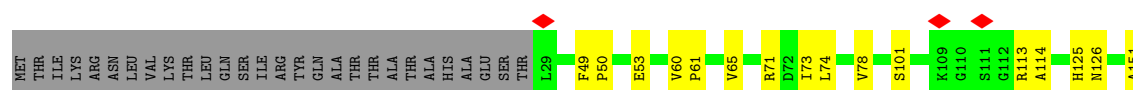
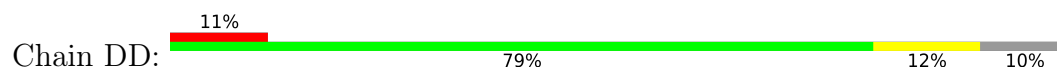
- Molecule 47: Large ribosomal subunit protein uL2m

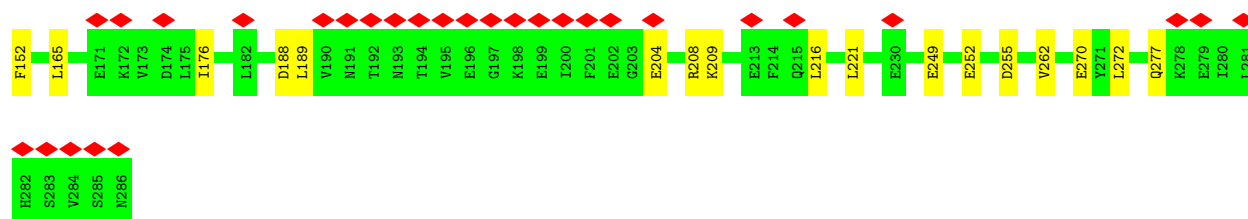


- Molecule 48: Large ribosomal subunit protein uL3m

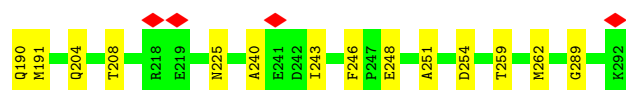
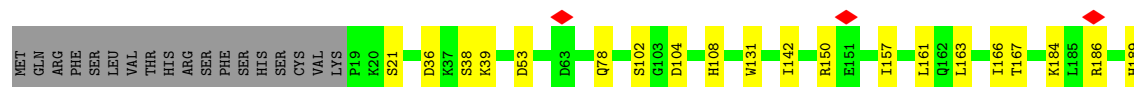
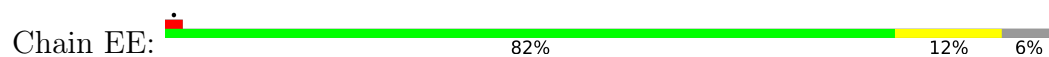


- Molecule 49: Large ribosomal subunit protein uL4m

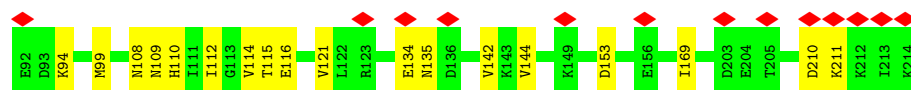
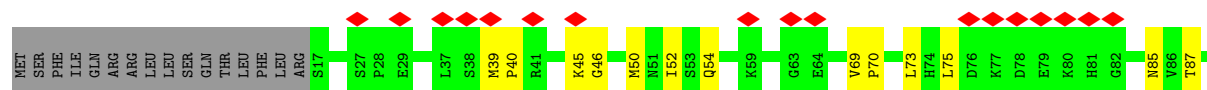
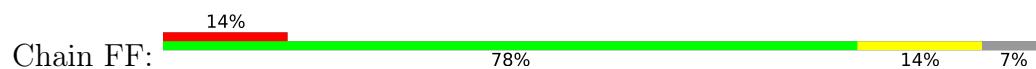




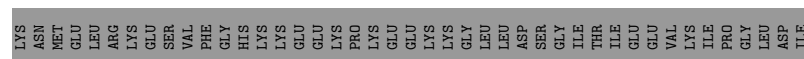
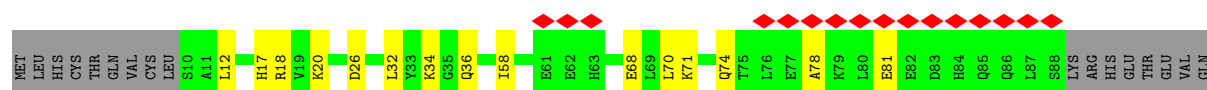
- Molecule 50: Large ribosomal subunit protein uL5m



- Molecule 51: Large ribosomal subunit protein uL6m



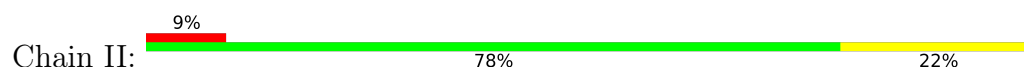
- Molecule 52: Large ribosomal subunit protein bL9m

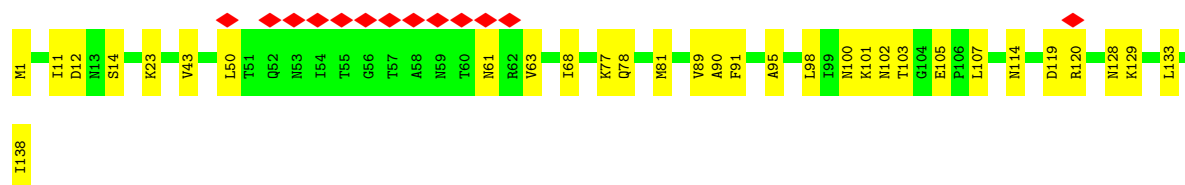


- Molecule 53: Large ribosomal subunit protein uL13m



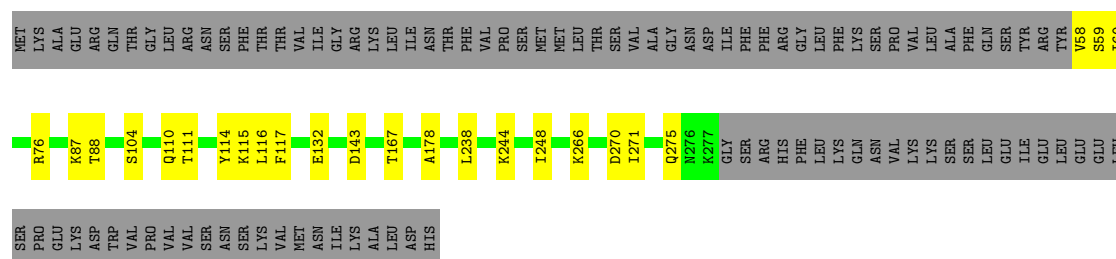
- Molecule 54: Large ribosomal subunit protein uL14m





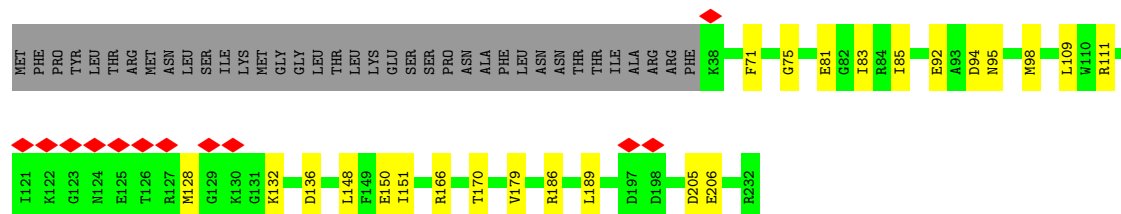
- Molecule 55: Large ribosomal subunit protein uL15m

Chain JJ:



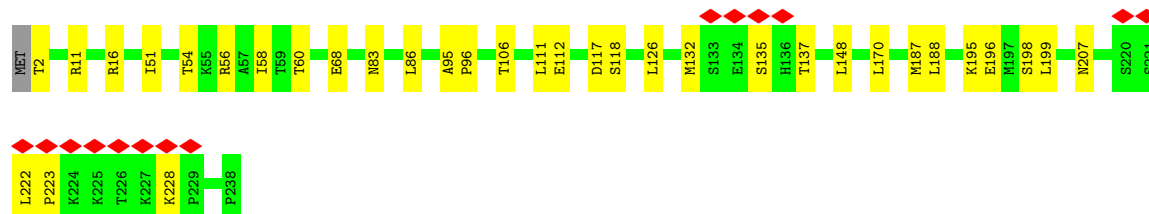
- Molecule 56: Large ribosomal subunit protein uL16m

Chain KK:



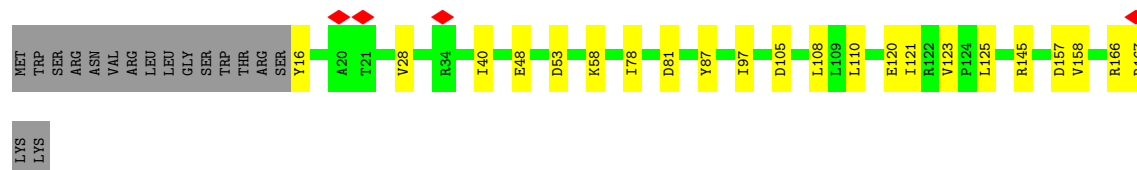
- Molecule 57: Large ribosomal subunit protein bL17m

Chain LL:

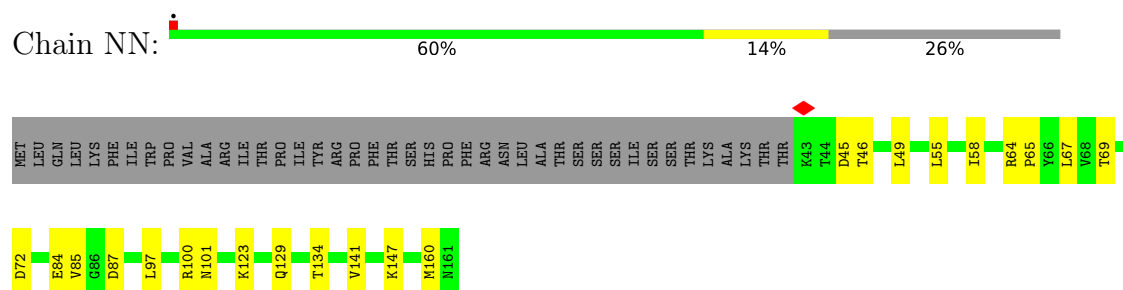


- Molecule 58: Large ribosomal subunit protein bL19m

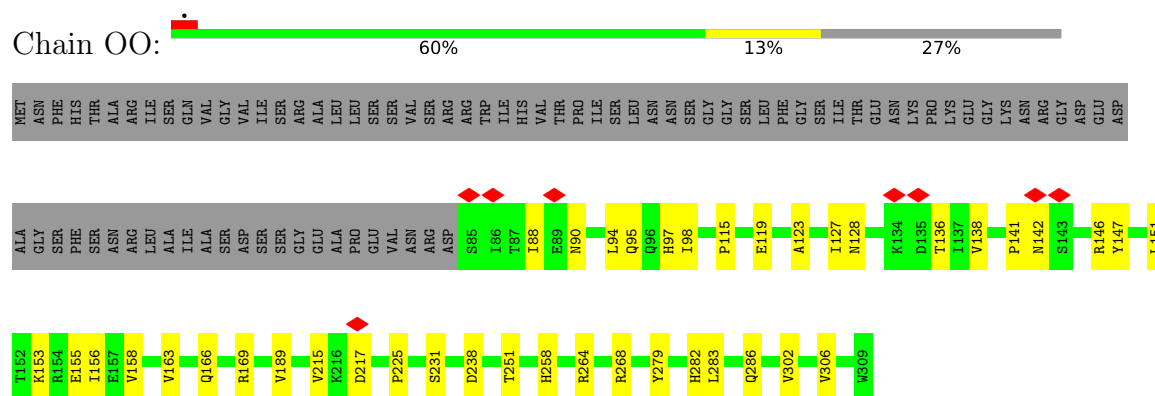
Chain MM:



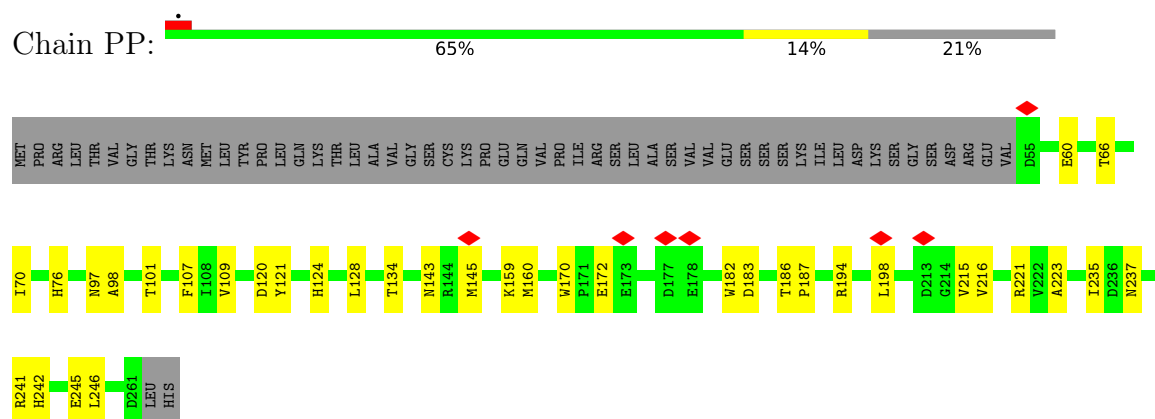
- Molecule 59: Large ribosomal subunit protein bL21m



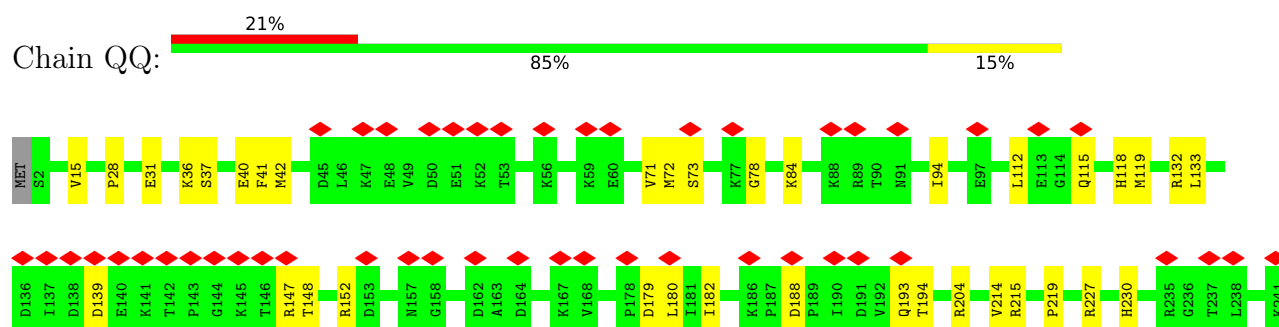
- Molecule 60: Large ribosomal subunit protein uL22m



- Molecule 61: Large ribosomal subunit protein uL23m




- Molecule 62: Large ribosomal subunit protein uL24m






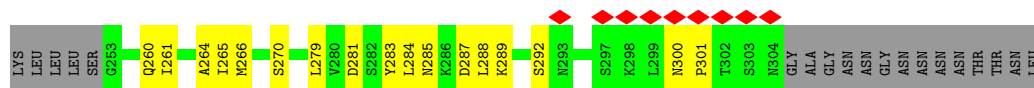
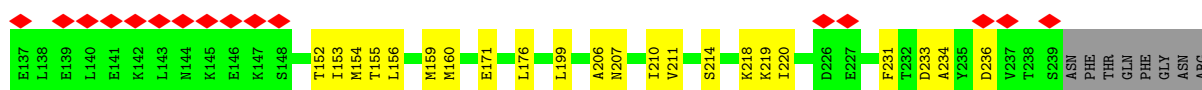
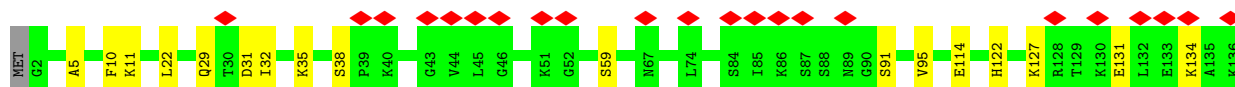
- Molecule 66: Large ribosomal subunit protein uL30m

Chain UU: 



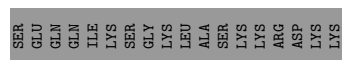
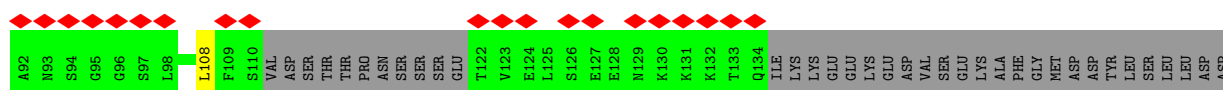
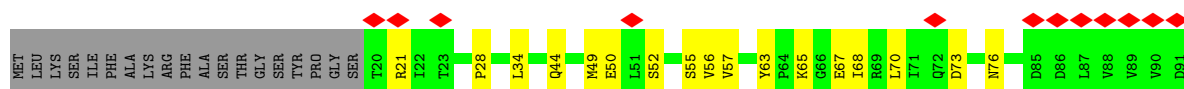
- Molecule 67: Small ribosomal subunit protein mS26

Chain V: 



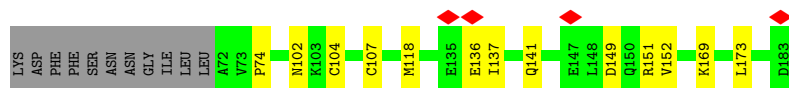
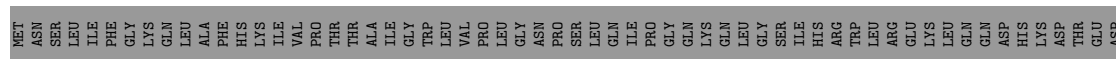
- Molecule 68: Large ribosomal subunit protein bL31m

Chain VV: 



- Molecule 69: Large ribosomal subunit protein bL32m

Chain WW: 

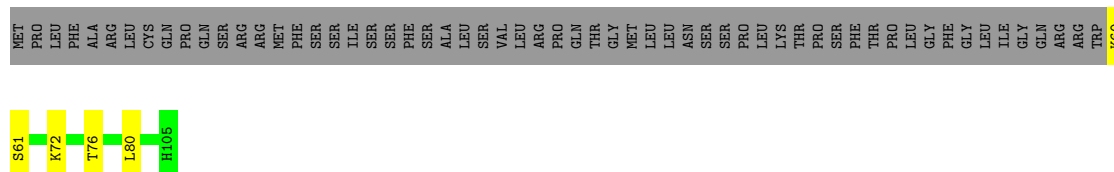
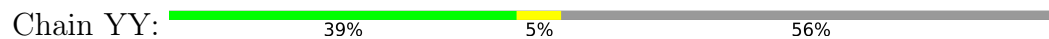


- Molecule 70: Large ribosomal subunit protein bL33m

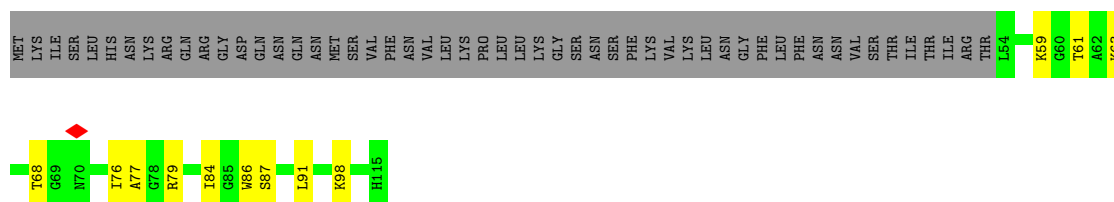
Chain XX: 



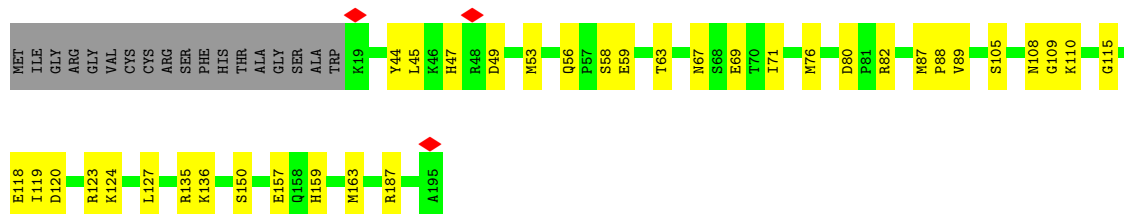
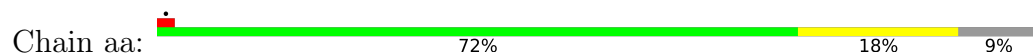
- Molecule 71: Large ribosomal subunit protein bL34m



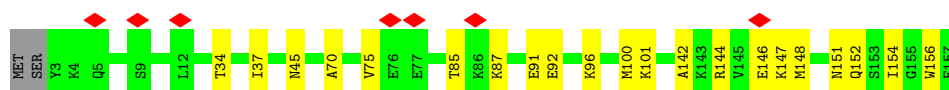
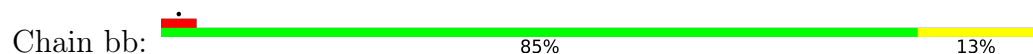
- Molecule 72: Large ribosomal subunit protein bL35m



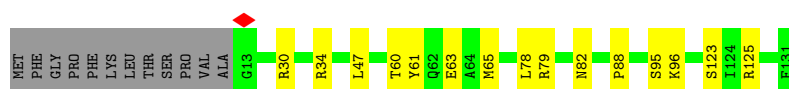
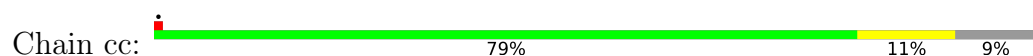
- Molecule 73: Large ribosomal subunit protein mL58



- Molecule 74: Large ribosomal subunit protein mL59

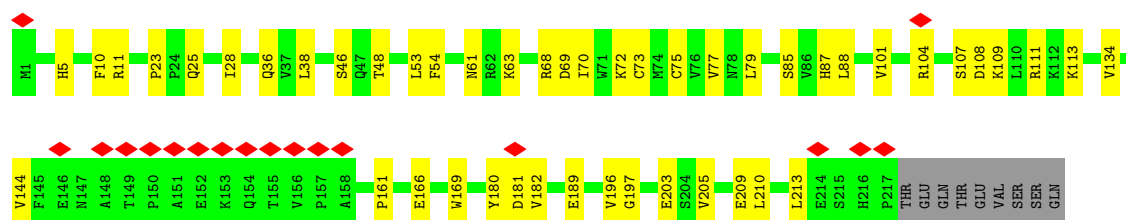
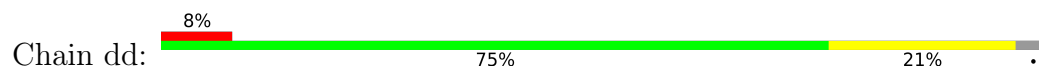


- Molecule 75: Large ribosomal subunit protein mL60

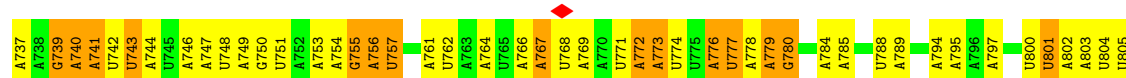
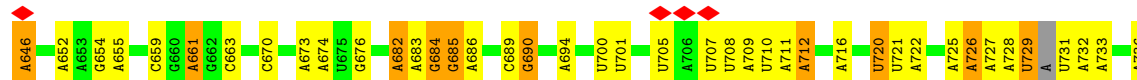
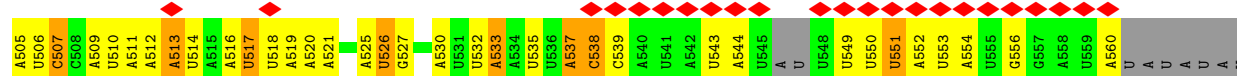
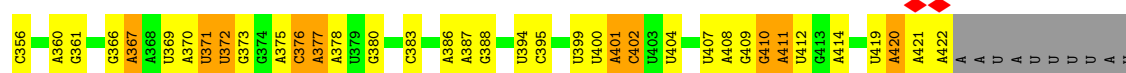
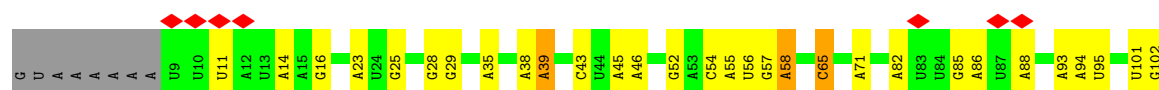




- Chain dd:



- Chain r:



U1599	A1600	G1603	U1604	G1609	A1610	A1611	G1615	G1620	G1621	G1622	G1623	U1624	U1625	A1626	U1627	A1628	A1629	A1630	U1631	A1632	U1633	C1634	A1637	A1638	A1639	U1643	C1644	U1645	U1646	A1647	C1648	A1649																						
U	A	A	U	A	U1537	U1538	U1539	U1540	U1541	A1542	A1543	U1544	U1545	U1546	A1547	U1548	U1549	U1550	U1551	U1552	U1553	U1554	U1555	U1556	A1557	C1561	A1562	G1563	A1564	U1569	U1570	G1573	U1576	U1577	A1578	U1579	U1580	G1583	A1584	A1585	G1586	U1587	U1588	G1589	A1590	A1591	A1592	U1593	C1594	A1595	A1596	G1597	U1598	
A1462	A1465	A1466	U1467	U1471	C1472	A1473	U1474	C1475	A1476	C1477	G1478	C1479	G1480	U1481	U1482	G1483	A1484	A1485	A1486	C1487	A1488	U1494	U1495	A1496	U1497	C1498	U1499	U1503	U1506	U1507	A1508	U1509	A1510	U1511	A1512	A1513	U1514	A1515	U1516	U1517	U1518	U1519	U1520	U1521	A1522	A1523	U1524	A1525	A1526	A1527	U1528	A	U	
U1381	C1382	U1383	A1386	A1387	U1388	C1390	G1391	A1392	U1393	U1394	A1395	U1396	A1397	A1402	A1403	A1404	A1405	G1406	A1407	G1411	C1412	U1413	G1414	G1415	G1422	U1428	A1429	G1430	U1431	A1432	A1437	C1438	G1439	G1442	A1443	A1444	U1445	A1446	U1447	U1448	C1449	U1450	A1451	A1452	C1453	U1454	G1455	U1456	U1457	U1458	C1459			
U1300	A1301	U1302	U1303	U1304	A1309	U1310	A1311	U1312	U1313	U1314	U1318	A1319	A1320	U1321	A1322	U1326	A1327	A1332	U1333	U1334	U1335	U1336	U1337	A1338	U1339	A1344	A1345	U1346	A1347	U1348	A1349	U1350	U1351	U1352	U1355	U1356	A1357	U1358	U1359	A1360	U1361	A1362	U1363	A1364	U1365	U1366	U1367	A1368	U1369	U1375	A1380			
A1229	A1230	U1231	C1232	A1233	U1234	A1235	U1240	C1241	C1242	U1243	U1244	A1245	U1246	A1247	A1248	U1249	A1250	U1251	G1252	G1253	U1255	A1256	A1257	U1258	A1259	G1260	A1261	C1262	U1269	A1270	A1271	U1272	A1273	A1274	A1275	G1278	A1279	U1280	A1281	A1282	U1283	A1284	A1285	U1289	A1290	U1291	A1292	U1293	A1294	A1295	A1296	A1297	U1298	A1299
A1148	A1149	A1158	C1162	A1163	U1164	A1165	U1166	A1167	A1171	A1172	U1173	U1174	U1175	U1176	U1177	A1178	U1179	U1182	A1183	U1192	A1193	U1194	A1195	U1196	U1197	A1198	U1199	A1200	U1201	A1202	U1203	U1204	A1205	A1206	U1207	A1208	U1209	A1210	G1213	A1214	A1215	A1216	G1217	G1218	A1219	A1220	U1221	U1222	G1225	U1226	C1227	A1228		
A1067	A1068	U1069	A1074	U	U	A	U1078	U1079	A1080	U1084	U1085	A1086	U1087	A1088	U1089	C1092	A1093	G1094	G1095	C1096	G1097	U1098	U1099	A1100	C1101	A1102	U1103	U1107	U1111	U1112	G1115	U1116	U1117	U1120	G1121	C1122	A1126	A1127	U1130	A1136	U1137	U1138	A1139	A1140	G1141	U1142	A1145							
G997	A998	C999	U1000	U1001	A1002	A1003	G1004	G1009	U1010	A1011	G1012	U1015	U1018	A1019	U1020	U1021	U1022	A1023	A1024	U1025	U1026	G1027	G1028	A1029	A1030	A1031	C1034	U1035	A1036	C1037	U1041	A1042	A1043	C1044	U1047	C1050	A1051	U1052	A1053	U1054	U1055	U1056	U1057	G1058	A1059	A1060	U1061	A1062	U1063	U1064	A1065	U1066		
A892	A893	A894	U895	U896	U897	U898	U899	A900	U901	U904	A905	U906	U907	U	U	U	A	U913	A918	A925	A930	A931	A936	A937	U940	A941	A946	U949	G953	A954	G955	U956	C964	A965	A972	A973	A974	A986	G987	U883	A984	U885	U886	A987	C995	A996								
A806	A807	A808	U809	U810	U811	U812	A813	A814	C815	U816	G817	A818	C819	A820	U821	U822	G823	A828	U829	A832	A833	U836	A837	G838	A839	A842	G845	A846	G851	C855	U858	A859	U870	C871	U872	A873	G874	U875	U878	A879	A880	A881	G882	U883	A884	U885	U886	A887						

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	22558	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	38	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	165000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.248	Depositor
Minimum map value	-0.087	Depositor
Average map value	0.137	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.22	Depositor
Map size (Å)	529.92, 529.92, 529.92	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82799995, 0.82799995, 0.82799995	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

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	1	0.25	0/288	0.44	0/367
2	2	0.16	0/877	0.36	0/1173
3	3	0.15	0/2114	0.32	0/2872
4	4	0.13	0/2525	0.32	0/3409
5	5	0.14	0/2409	0.33	0/3263
6	6	0.17	0/2655	0.35	0/3583
7	7	0.14	0/1365	0.31	0/1849
8	8	0.13	0/3766	0.30	0/5099
9	A	0.15	0/2831	0.34	1/3811 (0.0%)
10	B	0.18	0/2777	0.36	0/3763
11	C	0.17	0/3313	0.32	0/4470
12	D	0.15	0/2979	0.30	0/4011
13	E	0.18	0/2403	0.37	0/3237
14	F	0.18	0/1068	0.35	0/1430
15	G	0.15	0/1675	0.32	0/2263
16	H	0.19	0/1232	0.34	0/1660
17	I	0.18	0/2012	0.36	0/2707
18	J	0.19	0/1562	0.36	0/2113
19	K	0.16	0/1221	0.41	0/1628
20	L	0.16	0/969	0.29	0/1300
21	M	0.17	0/949	0.40	0/1267
22	N	0.22	0/964	0.35	0/1290
23	O	0.16	0/2093	0.33	0/2796
24	P	0.17	0/967	0.36	0/1307
25	Q	0.14	0/1942	0.33	0/2594
26	R	0.17	0/848	0.32	0/1130
27	S	0.18	0/661	0.32	0/893
28	T	0.18	0/848	0.39	0/1120
29	U	0.17	0/1982	0.35	0/2679
30	W	0.18	0/3297	0.34	0/4456
31	X	0.17	0/811	0.29	0/1084
32	Y	0.16	0/2337	0.29	0/3153

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Z	0.16	0/755	0.36	0/1017
34	a	0.15	0/4707	0.37	0/6313
35	t	0.16	0/1791	0.36	0/2784
36	00	0.20	0/329	0.38	0/432
37	11	0.19	0/2949	0.31	0/3998
38	22	0.19	0/963	0.33	0/1295
39	33	0.20	0/1072	0.34	0/1442
40	44	0.24	0/1138	0.35	0/1526
41	55	0.21	0/2604	0.35	0/3526
42	66	0.14	0/2022	0.29	0/2725
43	77	0.19	0/873	0.31	0/1170
44	88	0.16	0/1659	0.31	0/2230
45	99	0.16	0/1616	0.33	0/2177
46	AA	0.26	0/64517	0.35	0/100356
47	BB	0.20	0/2639	0.33	0/3545
48	CC	0.23	0/1975	0.31	0/2657
49	DD	0.18	0/2077	0.32	0/2814
50	EE	0.18	0/2244	0.31	0/3033
51	FF	0.16	0/1568	0.37	0/2115
52	GG	0.17	0/671	0.33	0/902
53	HH	0.23	0/1319	0.30	0/1771
54	II	0.17	0/1041	0.33	0/1396
55	JJ	0.22	0/1783	0.33	0/2384
56	KK	0.20	0/1606	0.35	0/2148
57	LL	0.20	0/1913	0.32	0/2581
58	MM	0.21	0/1235	0.38	0/1665
59	NN	0.22	0/970	0.33	0/1306
60	OO	0.23	0/1859	0.32	0/2495
61	PP	0.21	0/1773	0.31	0/2390
62	QQ	0.14	0/2420	0.30	0/3267
63	RR	0.18	0/2827	0.32	0/3780
64	SS	0.22	0/1748	0.36	0/2338
65	TT	0.17	0/2311	0.32	0/3135
66	UU	0.21	0/648	0.35	0/870
67	V	0.15	0/2354	0.31	0/3153
68	VV	0.16	0/818	0.28	0/1103
69	WW	0.23	0/955	0.31	0/1273
70	XX	0.25	0/520	0.35	0/696
71	YY	0.25	0/392	0.28	0/515
72	ZZ	0.25	0/522	0.32	0/695
73	aa	0.23	0/1471	0.40	0/1976
74	bb	0.20	0/1333	0.36	0/1783
75	cc	0.22	0/1028	0.29	0/1372

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	dd	0.23	0/1880	0.35	0/2541
77	r	0.21	0/35551	0.37	0/55310
All	All	0.21	0/226186	0.35	1/325777 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	313	PRO	N-CA-CB	6.50	110.08	103.25

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

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	1	288	0	341	14	0
2	2	858	0	865	21	0
3	3	2063	0	2039	29	0
4	4	2475	0	2460	32	0
5	5	2354	0	2401	52	0
6	6	2593	0	2613	64	0
7	7	1337	0	1359	22	0
8	8	3690	0	3680	54	0
9	A	2773	0	2831	63	0
10	B	2727	0	2747	48	0
11	C	3264	0	3253	69	0
12	D	2899	0	2958	49	0
13	E	2348	0	2359	58	0
14	F	1055	0	1129	37	0
15	G	1645	0	1688	25	0
16	H	1213	0	1277	31	0
17	I	1974	0	2062	61	0
18	J	1526	0	1531	46	0
19	K	1201	0	1253	38	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	L	954	0	1010	14	0
21	M	935	0	1000	22	0
22	N	945	0	993	24	0
23	O	2069	0	2139	40	0
24	P	951	0	1010	26	0
25	Q	1923	0	2007	42	0
26	R	836	0	868	24	0
27	S	645	0	667	12	0
28	T	837	0	873	27	0
29	U	1939	0	1929	53	0
30	W	3231	0	3332	60	0
31	X	797	0	842	10	0
32	Y	2281	0	2251	44	0
33	Z	739	0	765	14	0
34	a	4618	0	4694	89	0
35	t	1604	0	808	33	0
36	00	324	0	345	6	0
37	11	2875	0	2881	48	0
38	22	944	0	969	27	0
39	33	1046	0	1071	13	0
40	44	1117	0	1142	26	0
41	55	2552	0	2600	48	0
42	66	1975	0	1993	35	0
43	77	858	0	908	9	0
44	88	1629	0	1633	29	0
45	99	1587	0	1628	34	0
46	AA	57599	0	28881	620	0
47	BB	2591	0	2716	49	0
48	CC	1932	0	1969	36	0
49	DD	2036	0	2075	30	0
50	EE	2187	0	2203	32	0
51	FF	1541	0	1611	24	0
52	GG	659	0	665	9	0
53	HH	1292	0	1334	10	0
54	II	1034	0	1111	27	0
55	JJ	1746	0	1840	19	0
56	KK	1573	0	1629	16	0
57	LL	1882	0	1963	29	0
58	MM	1217	0	1296	23	0
59	NN	957	0	1019	22	0
60	OO	1826	0	1933	31	0
61	PP	1729	0	1724	31	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	QQ	2367	0	2427	42	0
63	RR	2781	0	2864	28	0
64	SS	1712	0	1798	25	0
65	TT	2255	0	2220	42	0
66	UU	639	0	699	12	0
67	V	2322	0	2421	60	0
68	VV	805	0	781	15	0
69	WW	937	0	978	14	0
70	XX	512	0	563	22	0
71	YY	385	0	423	4	0
72	ZZ	508	0	539	11	0
73	aa	1440	0	1473	32	0
74	bb	1299	0	1367	19	0
75	cc	1004	0	1065	10	0
76	dd	1830	0	1827	38	0
77	r	31749	0	15926	487	0
78	1	1	0	0	0	0
78	AA	194	0	0	0	0
78	B	1	0	0	0	0
78	BB	2	0	0	0	0
78	CC	1	0	0	0	0
78	E	2	0	0	0	0
78	K	1	0	0	0	0
78	M	1	0	0	0	0
78	NN	1	0	0	0	0
78	P	1	0	0	0	0
78	W	1	0	0	0	0
78	dd	1	0	0	0	0
78	r	110	0	0	0	0
79	W	32	0	12	2	0
All	All	213189	0	170556	2992	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 2992 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)
68:VV:50:GLU:HG2	68:VV:56:VAL:HG22	1.60	0.84
77:r:1591:A:H3'	77:r:1592:A:H8	1.43	0.83
34:a:282:VAL:O	34:a:286:LEU:HD22	1.79	0.82

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:262:ALA:O	10:B:266:THR:HG22	1.80	0.81
24:P:84:GLU:OE1	24:P:84:GLU:N	2.14	0.81

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	1	30/111 (27%)	30 (100%)	0	0	100	100
2	2	100/130 (77%)	95 (95%)	5 (5%)	0	100	100
3	3	255/266 (96%)	243 (95%)	12 (5%)	0	100	100
4	4	306/321 (95%)	289 (94%)	17 (6%)	0	100	100
5	5	288/339 (85%)	278 (96%)	10 (4%)	0	100	100
6	6	317/345 (92%)	306 (96%)	11 (4%)	0	100	100
7	7	164/361 (45%)	152 (93%)	12 (7%)	0	100	100
8	8	465/500 (93%)	448 (96%)	17 (4%)	0	100	100
9	A	341/344 (99%)	311 (91%)	29 (8%)	1 (0%)	36	70
10	B	340/394 (86%)	327 (96%)	13 (4%)	0	100	100
11	C	394/398 (99%)	371 (94%)	23 (6%)	0	100	100
12	D	345/486 (71%)	339 (98%)	6 (2%)	0	100	100
13	E	292/307 (95%)	278 (95%)	14 (5%)	0	100	100
14	F	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
15	G	206/247 (83%)	194 (94%)	12 (6%)	0	100	100
16	H	152/155 (98%)	147 (97%)	5 (3%)	0	100	100
17	I	244/278 (88%)	230 (94%)	14 (6%)	0	100	100
18	J	186/203 (92%)	176 (95%)	10 (5%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	K	149/217 (69%)	142 (95%)	7 (5%)	0	100	100
20	L	123/153 (80%)	121 (98%)	2 (2%)	0	100	100
21	M	117/143 (82%)	110 (94%)	7 (6%)	0	100	100
22	N	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
23	O	251/286 (88%)	242 (96%)	9 (4%)	0	100	100
24	P	118/121 (98%)	115 (98%)	3 (2%)	0	100	100
25	Q	233/237 (98%)	226 (97%)	7 (3%)	0	100	100
26	R	101/138 (73%)	98 (97%)	3 (3%)	0	100	100
27	S	79/91 (87%)	76 (96%)	3 (4%)	0	100	100
28	T	99/177 (56%)	95 (96%)	4 (4%)	0	100	100
29	U	235/264 (89%)	226 (96%)	9 (4%)	0	100	100
30	W	401/450 (89%)	377 (94%)	24 (6%)	0	100	100
31	X	98/110 (89%)	93 (95%)	5 (5%)	0	100	100
32	Y	271/319 (85%)	262 (97%)	9 (3%)	0	100	100
33	Z	92/95 (97%)	89 (97%)	3 (3%)	0	100	100
34	a	556/606 (92%)	515 (93%)	41 (7%)	0	100	100
36	00	36/93 (39%)	34 (94%)	2 (6%)	0	100	100
37	11	346/367 (94%)	328 (95%)	18 (5%)	0	100	100
38	22	111/147 (76%)	109 (98%)	2 (2%)	0	100	100
39	33	128/146 (88%)	121 (94%)	7 (6%)	0	100	100
40	44	136/140 (97%)	132 (97%)	4 (3%)	0	100	100
41	55	322/390 (83%)	304 (94%)	18 (6%)	0	100	100
42	66	236/281 (84%)	229 (97%)	7 (3%)	0	100	100
43	77	104/146 (71%)	101 (97%)	3 (3%)	0	100	100
44	88	195/264 (74%)	189 (97%)	6 (3%)	0	100	100
45	99	198/253 (78%)	191 (96%)	7 (4%)	0	100	100
47	BB	328/393 (84%)	314 (96%)	14 (4%)	0	100	100
48	CC	247/269 (92%)	233 (94%)	14 (6%)	0	100	100
49	DD	256/286 (90%)	247 (96%)	9 (4%)	0	100	100
50	EE	272/292 (93%)	263 (97%)	9 (3%)	0	100	100
51	FF	196/214 (92%)	181 (92%)	15 (8%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	GG	77/139 (55%)	76 (99%)	1 (1%)	0	100	100
53	HH	160/163 (98%)	159 (99%)	1 (1%)	0	100	100
54	II	136/138 (99%)	126 (93%)	10 (7%)	0	100	100
55	JJ	218/322 (68%)	212 (97%)	6 (3%)	0	100	100
56	KK	193/232 (83%)	188 (97%)	5 (3%)	0	100	100
57	LL	235/238 (99%)	224 (95%)	11 (5%)	0	100	100
58	MM	150/169 (89%)	146 (97%)	4 (3%)	0	100	100
59	NN	117/161 (73%)	112 (96%)	5 (4%)	0	100	100
60	OO	223/309 (72%)	214 (96%)	9 (4%)	0	100	100
61	PP	205/263 (78%)	203 (99%)	2 (1%)	0	100	100
62	QQ	294/297 (99%)	282 (96%)	12 (4%)	0	100	100
63	RR	335/371 (90%)	312 (93%)	23 (7%)	0	100	100
64	SS	202/258 (78%)	192 (95%)	10 (5%)	0	100	100
65	TT	273/319 (86%)	257 (94%)	16 (6%)	0	100	100
66	UU	80/86 (93%)	80 (100%)	0	0	100	100
67	V	286/318 (90%)	279 (98%)	7 (2%)	0	100	100
68	VV	100/177 (56%)	94 (94%)	6 (6%)	0	100	100
69	WW	110/183 (60%)	108 (98%)	2 (2%)	0	100	100
70	XX	62/70 (89%)	61 (98%)	1 (2%)	0	100	100
71	YY	44/105 (42%)	41 (93%)	3 (7%)	0	100	100
72	ZZ	60/115 (52%)	59 (98%)	1 (2%)	0	100	100
73	aa	175/195 (90%)	166 (95%)	9 (5%)	0	100	100
74	bb	153/157 (98%)	145 (95%)	8 (5%)	0	100	100
75	cc	117/131 (89%)	115 (98%)	2 (2%)	0	100	100
76	dd	215/226 (95%)	203 (94%)	12 (6%)	0	100	100
All	All	14920/17661 (84%)	14265 (96%)	654 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	A	313	PRO

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	31/98 (32%)	31 (100%)	0	100	100
2	2	93/117 (80%)	93 (100%)	0	100	100
3	3	232/240 (97%)	232 (100%)	0	100	100
4	4	271/281 (96%)	271 (100%)	0	100	100
5	5	258/303 (85%)	258 (100%)	0	100	100
6	6	289/312 (93%)	289 (100%)	0	100	100
7	7	159/331 (48%)	159 (100%)	0	100	100
8	8	413/444 (93%)	413 (100%)	0	100	100
9	A	307/309 (99%)	307 (100%)	0	100	100
10	B	308/350 (88%)	308 (100%)	0	100	100
11	C	380/385 (99%)	380 (100%)	0	100	100
12	D	314/437 (72%)	314 (100%)	0	100	100
13	E	253/266 (95%)	253 (100%)	0	100	100
14	F	120/120 (100%)	120 (100%)	0	100	100
15	G	177/211 (84%)	177 (100%)	0	100	100
16	H	141/142 (99%)	141 (100%)	0	100	100
17	I	215/245 (88%)	215 (100%)	0	100	100
18	J	169/183 (92%)	169 (100%)	0	100	100
19	K	130/192 (68%)	130 (100%)	0	100	100
20	L	104/131 (79%)	104 (100%)	0	100	100
21	M	100/121 (83%)	100 (100%)	0	100	100
22	N	102/103 (99%)	102 (100%)	0	100	100
23	O	220/250 (88%)	220 (100%)	0	100	100
24	P	105/106 (99%)	105 (100%)	0	100	100
25	Q	216/218 (99%)	216 (100%)	0	100	100
26	R	91/121 (75%)	91 (100%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	S	70/78 (90%)	70 (100%)	0	100	100
28	T	90/159 (57%)	90 (100%)	0	100	100
29	U	212/236 (90%)	212 (100%)	0	100	100
30	W	369/409 (90%)	369 (100%)	0	100	100
31	X	85/92 (92%)	85 (100%)	0	100	100
32	Y	250/289 (86%)	250 (100%)	0	100	100
33	Z	84/85 (99%)	84 (100%)	0	100	100
34	a	511/552 (93%)	511 (100%)	0	100	100
36	00	36/84 (43%)	35 (97%)	1 (3%)	38	70
37	11	323/341 (95%)	323 (100%)	0	100	100
38	22	106/137 (77%)	106 (100%)	0	100	100
39	33	112/126 (89%)	112 (100%)	0	100	100
40	44	121/123 (98%)	121 (100%)	0	100	100
41	55	284/345 (82%)	284 (100%)	0	100	100
42	66	218/252 (86%)	218 (100%)	0	100	100
43	77	95/128 (74%)	95 (100%)	0	100	100
44	88	182/240 (76%)	182 (100%)	0	100	100
45	99	176/222 (79%)	176 (100%)	0	100	100
47	BB	279/337 (83%)	279 (100%)	0	100	100
48	CC	210/229 (92%)	210 (100%)	0	100	100
49	DD	224/248 (90%)	224 (100%)	0	100	100
50	EE	242/260 (93%)	242 (100%)	0	100	100
51	FF	174/190 (92%)	174 (100%)	0	100	100
52	GG	73/129 (57%)	73 (100%)	0	100	100
53	HH	140/141 (99%)	140 (100%)	0	100	100
54	II	117/117 (100%)	117 (100%)	0	100	100
55	JJ	181/274 (66%)	181 (100%)	0	100	100
56	KK	167/200 (84%)	167 (100%)	0	100	100
57	LL	211/212 (100%)	211 (100%)	0	100	100
58	MM	137/153 (90%)	137 (100%)	0	100	100
59	NN	108/147 (74%)	108 (100%)	0	100	100

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
60	OO	200/270 (74%)	200 (100%)	0	100	100
61	PP	185/236 (78%)	185 (100%)	0	100	100
62	QQ	267/268 (100%)	267 (100%)	0	100	100
63	RR	308/337 (91%)	308 (100%)	0	100	100
64	SS	187/231 (81%)	187 (100%)	0	100	100
65	TT	259/298 (87%)	259 (100%)	0	100	100
66	UU	73/77 (95%)	73 (100%)	0	100	100
67	V	264/287 (92%)	264 (100%)	0	100	100
68	VV	83/161 (52%)	83 (100%)	0	100	100
69	WW	104/167 (62%)	104 (100%)	0	100	100
70	XX	56/62 (90%)	56 (100%)	0	100	100
71	YY	40/93 (43%)	40 (100%)	0	100	100
72	ZZ	50/100 (50%)	50 (100%)	0	100	100
73	aa	158/171 (92%)	158 (100%)	0	100	100
74	bb	144/146 (99%)	144 (100%)	0	100	100
75	cc	110/120 (92%)	110 (100%)	0	100	100
76	dd	201/210 (96%)	201 (100%)	0	100	100
All	All	13474/15785 (85%)	13473 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	00	56	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68 such sidechains are listed below:

Mol	Chain	Res	Type
64	SS	170	HIS
65	TT	275	GLN
76	dd	41	GLN
26	R	121	ASN
20	L	33	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	t	75/76 (98%)	54 (72%)	0
46	AA	2681/3296 (81%)	581 (21%)	46 (1%)
77	r	1485/1649 (90%)	519 (34%)	0
All	All	4241/5021 (84%)	1154 (27%)	46 (1%)

5 of 1154 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
35	t	5	A
35	t	6	U
35	t	7	A
35	t	9	G
35	t	10	A

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	AA	1843	U
46	AA	2373	U
46	AA	1892	G
46	AA	2198	U
46	AA	2411	G

## 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 318 ligands modelled in this entry, 317 are monoatomic - leaving 1 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
79	GTP	W	501	78	33,34,34	0.57	0	50,54,54	0.49	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
79	GTP	W	501	78	-	4/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
79	W	501	GTP	O4'-C4'-C5'-O5'
79	W	501	GTP	PB-O3A-PA-O2A
79	W	501	GTP	C4'-C5'-O5'-PA
79	W	501	GTP	PB-O3A-PA-O1A

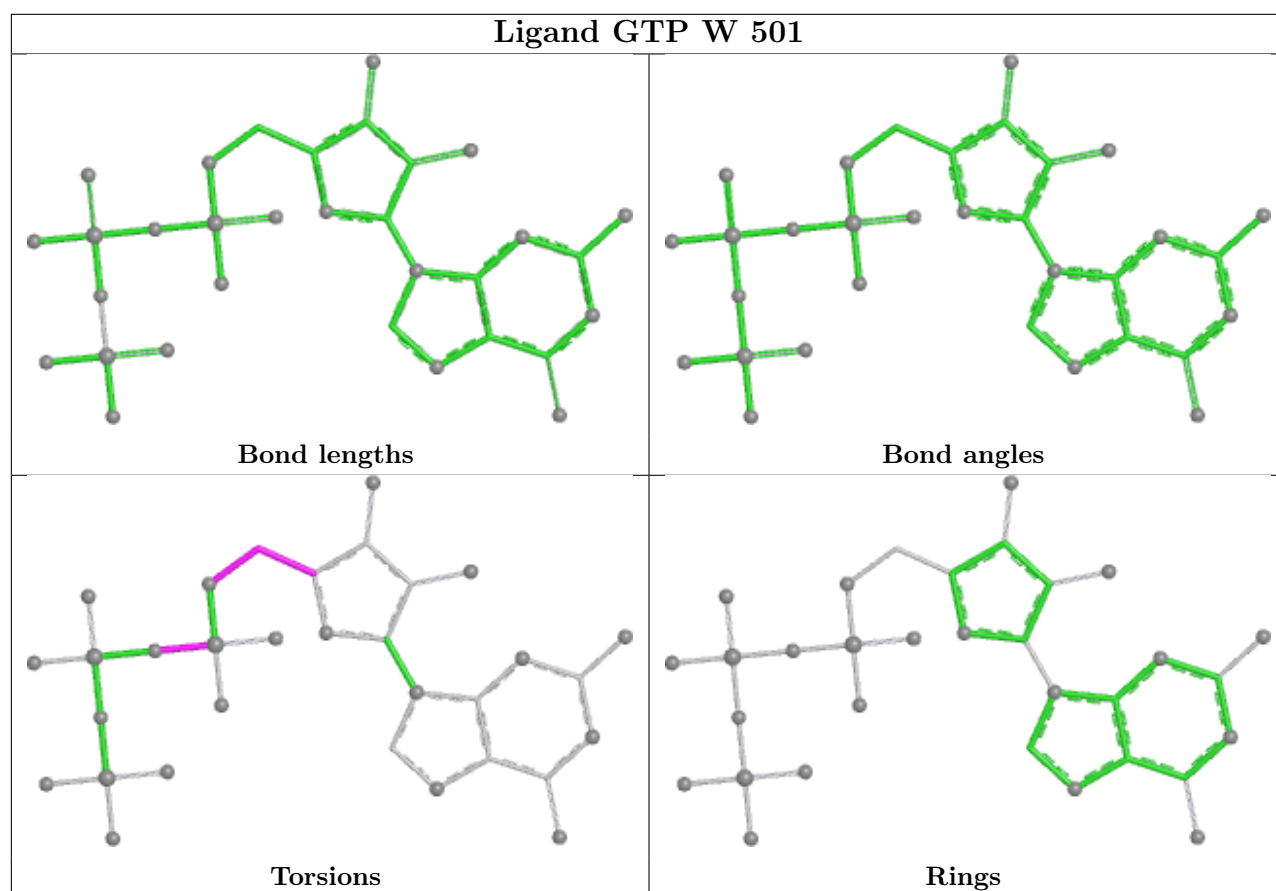
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
79	W	501	GTP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

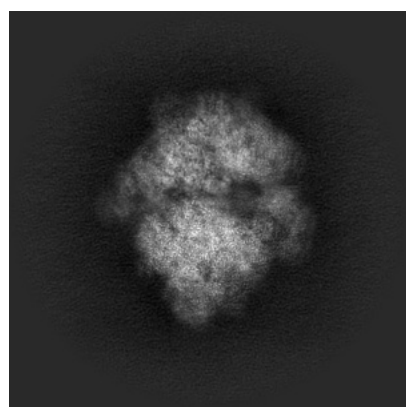
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52283. These allow visual inspection of the internal detail of the map and identification of artifacts.

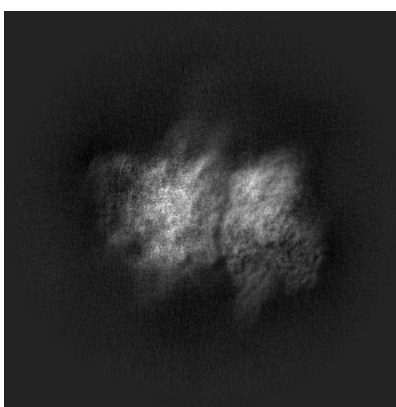
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

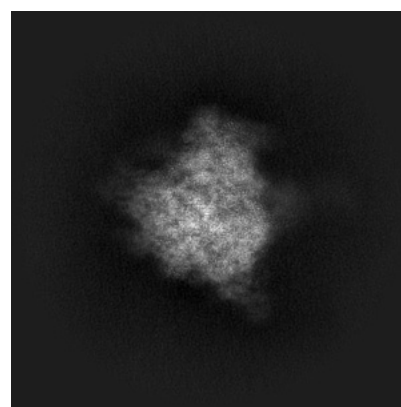
#### 6.1.1 Primary map



X



Y

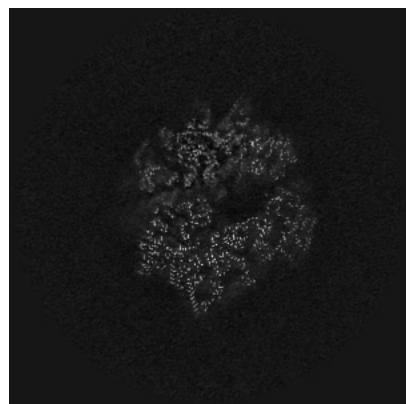


Z

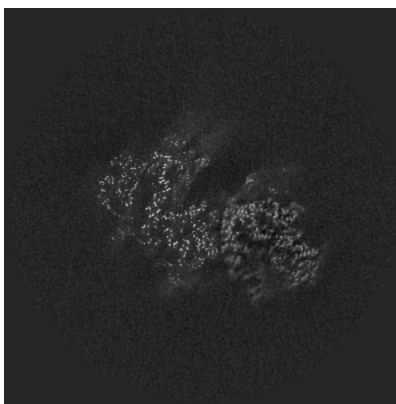
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

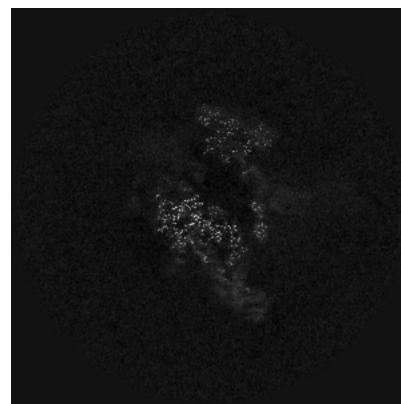
#### 6.2.1 Primary map



X Index: 320



Y Index: 320

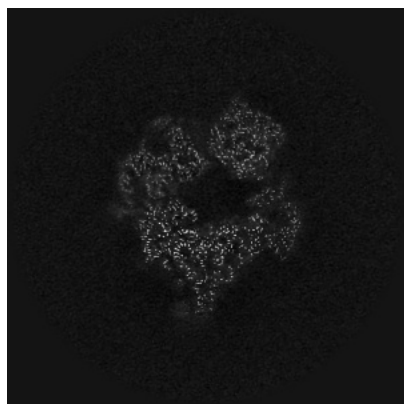


Z Index: 320

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

## 6.3 Largest variance slices [i](#)

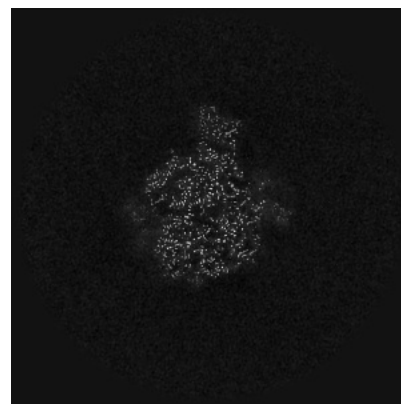
### 6.3.1 Primary map



X Index: 352



Y Index: 296

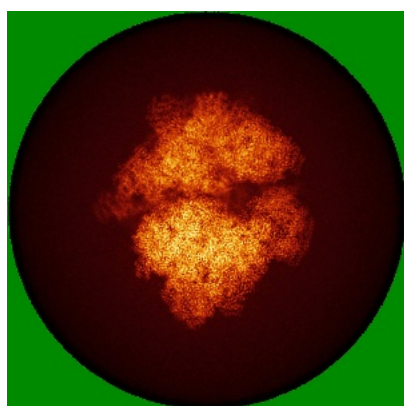


Z Index: 263

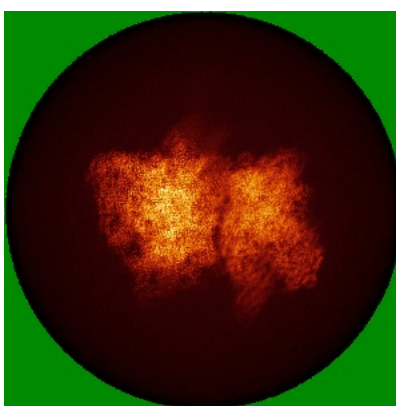
The images above show the largest variance slices of the map in three orthogonal directions.

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

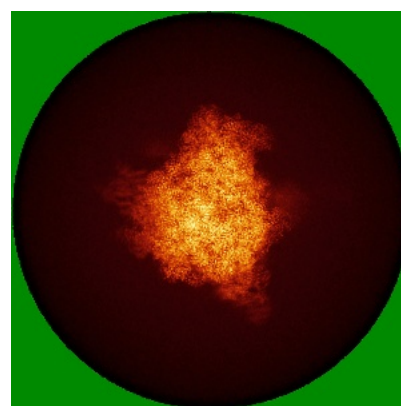
### 6.4.1 Primary map



X



Y

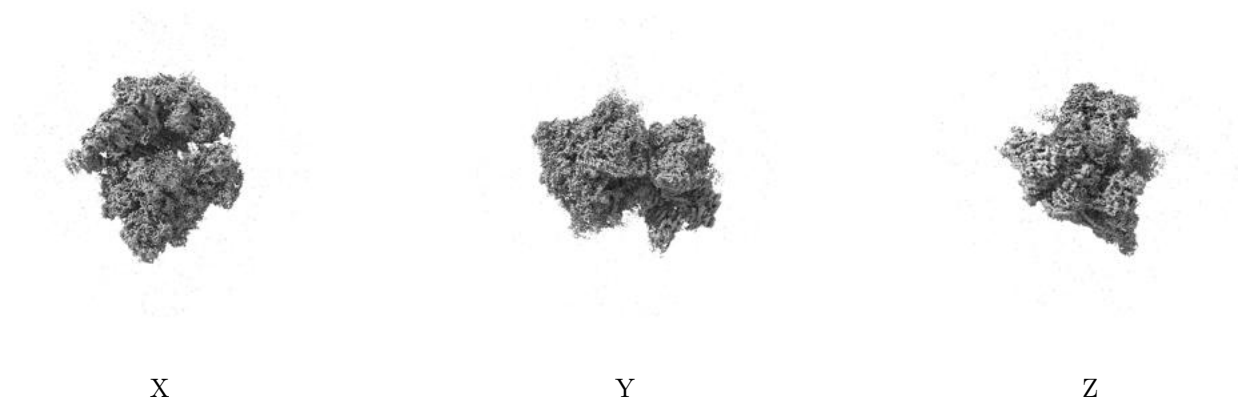


Z

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

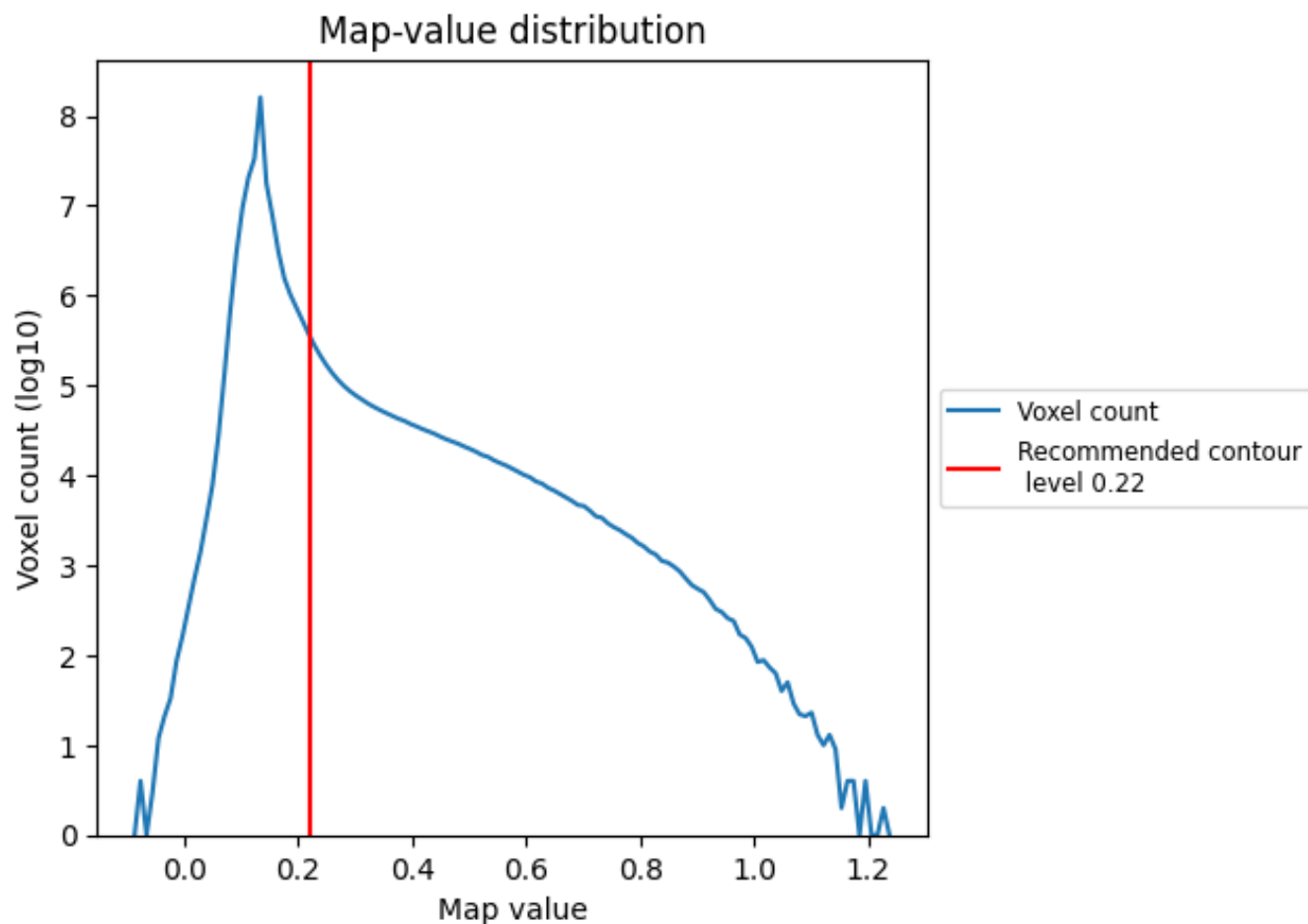
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

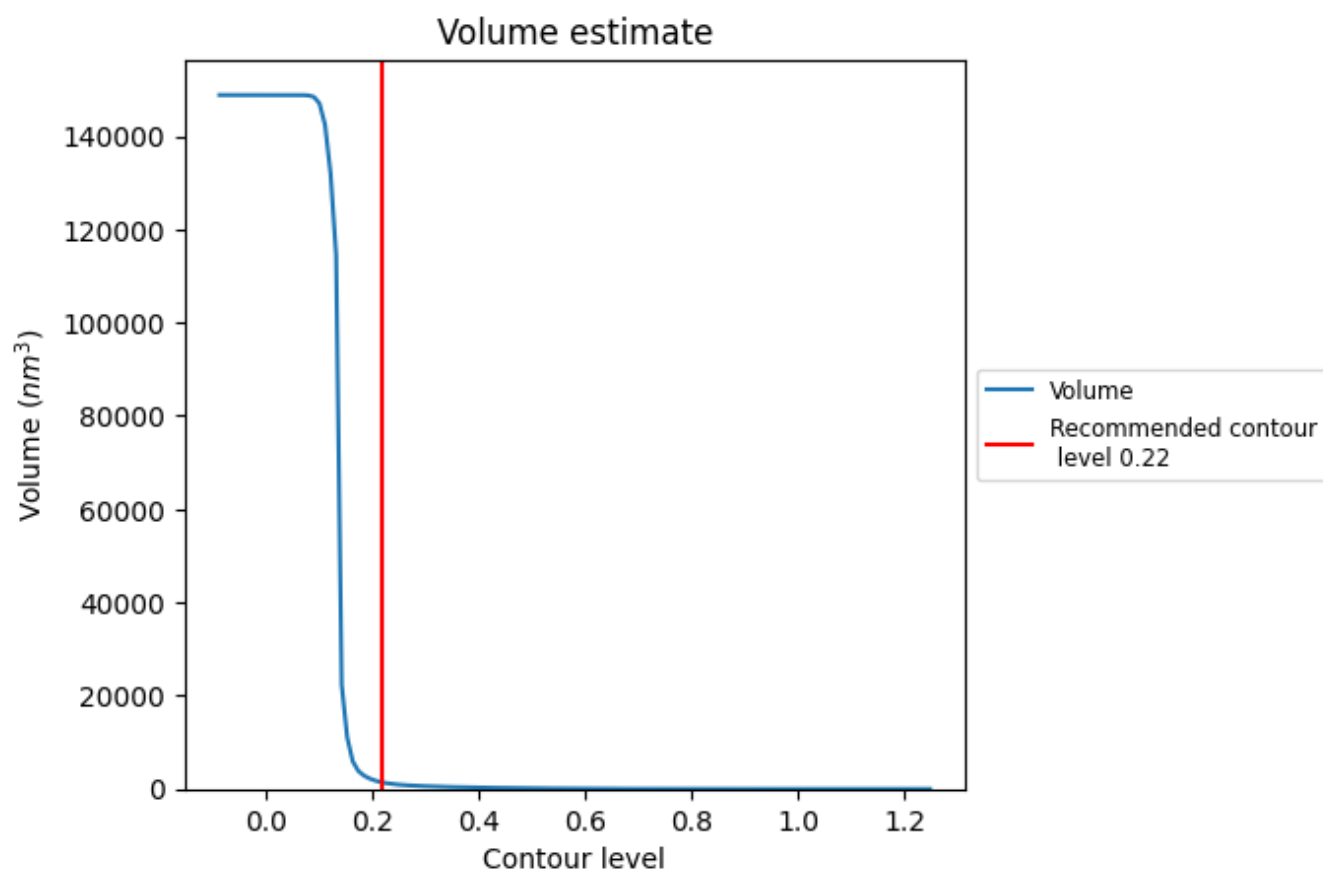
This section contains the results of statistical analysis of the map.

### 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.

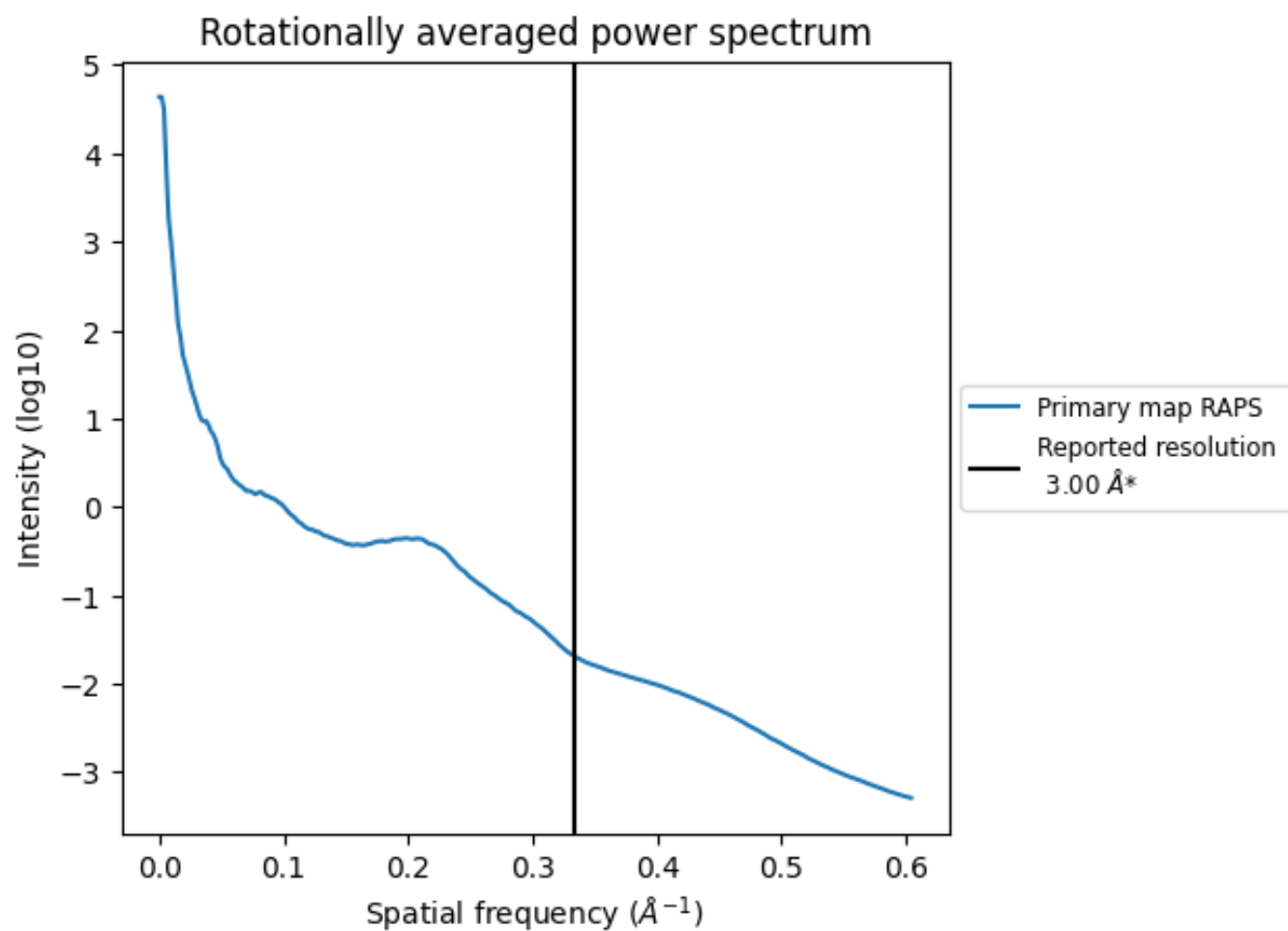
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1388  $\text{nm}^3$ ; this corresponds to an approximate mass of 1253 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 Å<sup>-1</sup>

## 8 Fourier-Shell correlation ⓘ

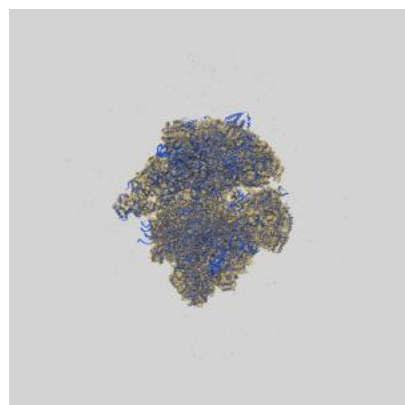
This section was not generated. No FSC curve or half-maps provided.



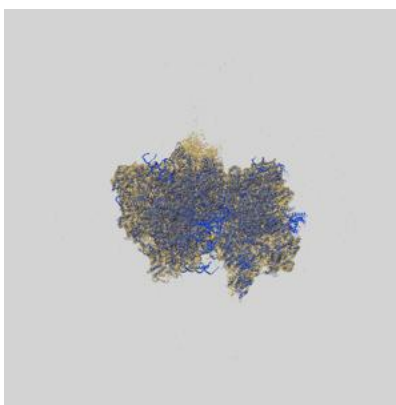
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-52283 and PDB model 9HM0. Per-residue inclusion information can be found in section [3](#) on page [19](#).

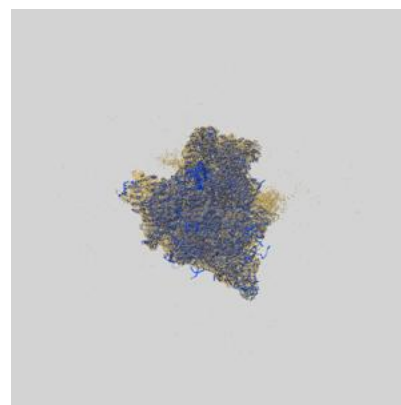
### 9.1 Map-model overlay [i](#)



X



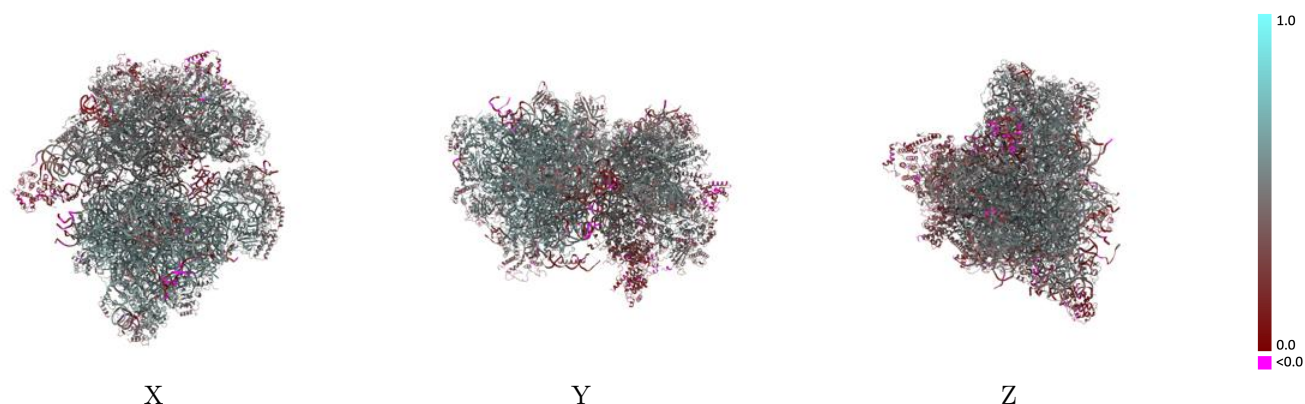
Y



Z

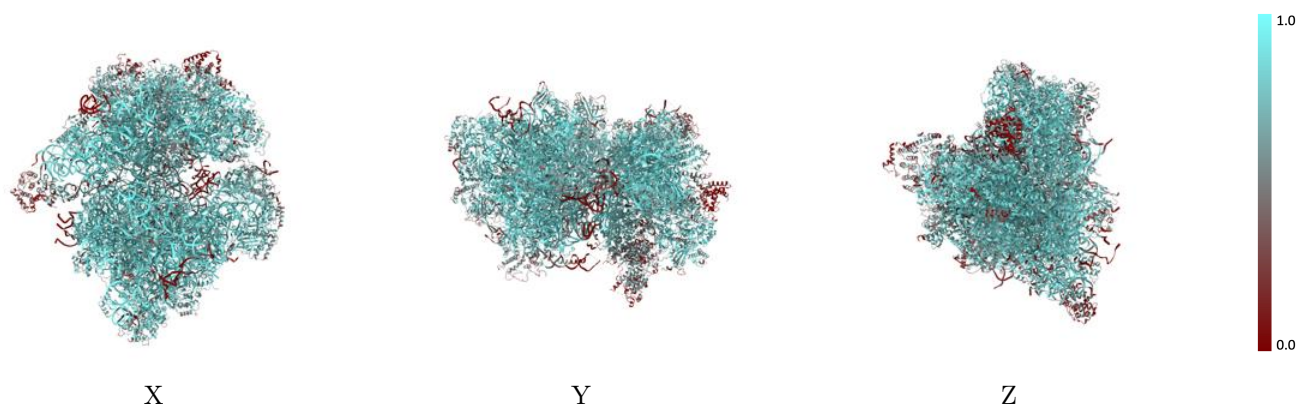
The images above show the 3D surface view of the map at the recommended contour level 0.22 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



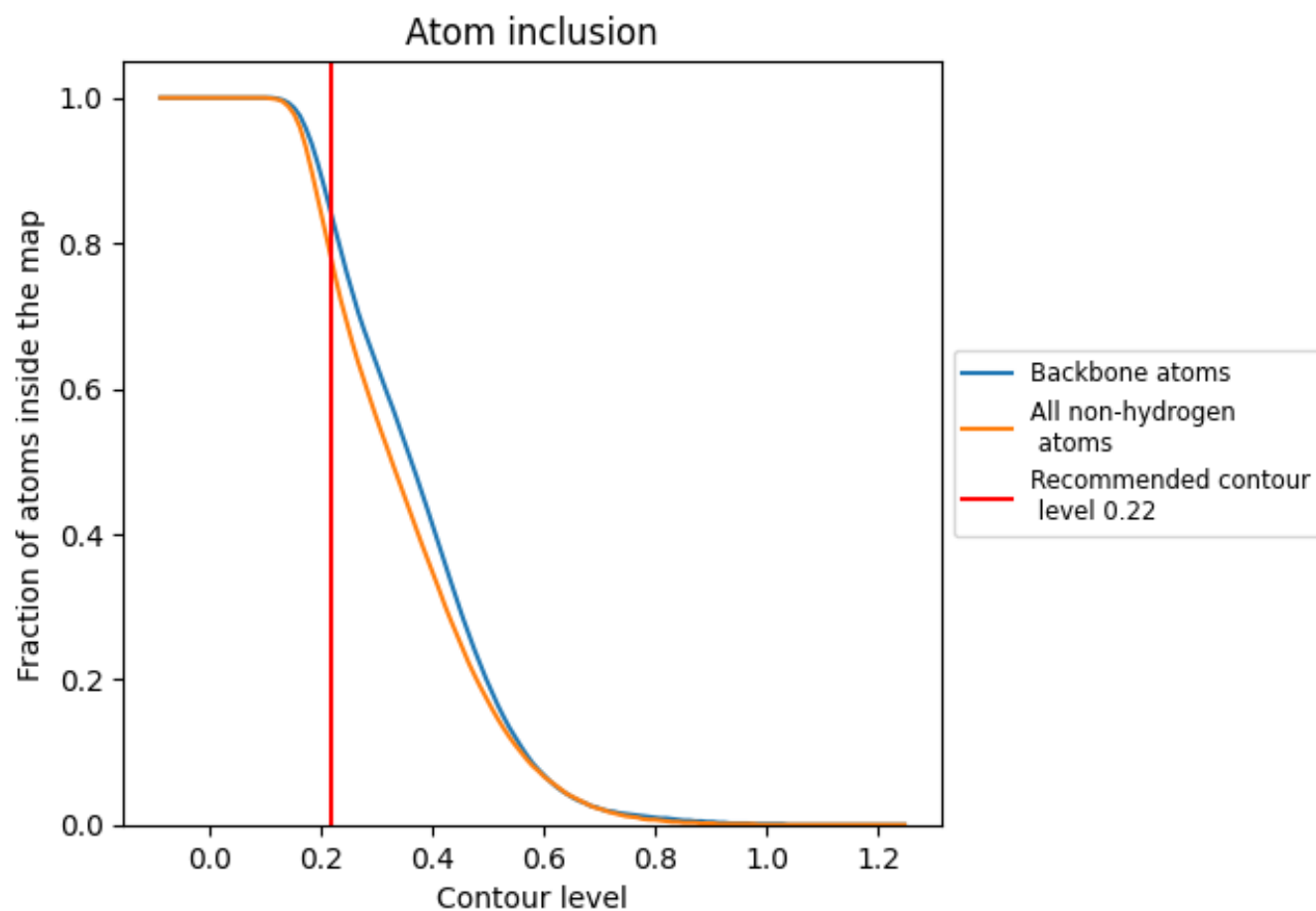
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.22).







































































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 84% of all backbone atoms, 78% 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 (0.22) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7750	 0.4620
00	 0.8840	 0.5560
1	 0.8430	 0.4590
11	 0.7700	 0.5080
2	 0.6960	 0.4100
22	 0.7650	 0.4810
3	 0.7970	 0.4300
33	 0.8150	 0.5320
4	 0.7160	 0.3760
44	 0.8640	 0.5740
5	 0.3380	 0.2070
55	 0.8210	 0.5390
6	 0.7130	 0.4380
66	 0.6200	 0.4300
7	 0.6520	 0.4310
77	 0.8050	 0.5250
8	 0.6150	 0.4250
88	 0.5790	 0.4180
99	 0.6670	 0.4520
A	 0.6750	 0.3750
AA	 0.8410	 0.5020
B	 0.6760	 0.4120
BB	 0.8180	 0.5190
C	 0.6590	 0.4130
CC	 0.8810	 0.5770
D	 0.6850	 0.4200
DD	 0.7140	 0.4890
E	 0.7900	 0.4850
EE	 0.7830	 0.5260
F	 0.7770	 0.4370
FF	 0.6350	 0.4040
G	 0.5420	 0.3670
GG	 0.6630	 0.4650
H	 0.8330	 0.5070
HH	 0.8350	 0.5510





*Continued on next page...*

*Continued from previous page...*

Chain	Atom inclusion	Q-score
I	 0.8030	 0.4660
II	 0.7650	 0.4940
J	 0.7250	 0.4530
JJ	 0.8490	 0.5560
K	 0.7610	 0.4110
KK	 0.8150	 0.5270
L	 0.7850	 0.4930
LL	 0.8120	 0.5380
M	 0.7990	 0.4870
MM	 0.8300	 0.5260
N	 0.8940	 0.5200
NN	 0.8700	 0.5740
O	 0.7740	 0.4210
OO	 0.8150	 0.5460
P	 0.7500	 0.4500
PP	 0.8060	 0.5270
Q	 0.6740	 0.3520
QQ	 0.6040	 0.4270
R	 0.7500	 0.4400
RR	 0.6730	 0.4610
S	 0.7860	 0.4820
SS	 0.6530	 0.4480
T	 0.7090	 0.4030
TT	 0.6390	 0.4090
U	 0.8340	 0.4820
UU	 0.8390	 0.5560
V	 0.6590	 0.3950
VV	 0.5780	 0.4040
W	 0.7600	 0.4720
WW	 0.8440	 0.5560
X	 0.8010	 0.4740
XX	 0.7630	 0.5040
Y	 0.7470	 0.4580
YY	 0.8560	 0.5610
Z	 0.5940	 0.3780
ZZ	 0.8730	 0.5790
a	 0.3940	 0.2240
aa	 0.8030	 0.5240
bb	 0.7780	 0.5040
cc	 0.8600	 0.5620
dd	 0.8120	 0.5200
r	 0.8920	 0.4400

*Continued on next page...*

*Continued from previous page...*

Chain	Atom inclusion	Q-score
t	 0.1750	 0.1680