wwPDB EM Validation Summary Report ⓘ

Sep 16, 2026 – 05:05 AM EDT

PDB ID	:	6C4I / pdb_00006c4i
EMDB ID	:	EMD-7341
Title	:	Conformation of methylated GGQ in the peptidyl transferase center during translation termination
Authors	:	Zeng, F.; Jin, H.
Deposited on	:	2018-01-12
Resolution	:	3.24 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:

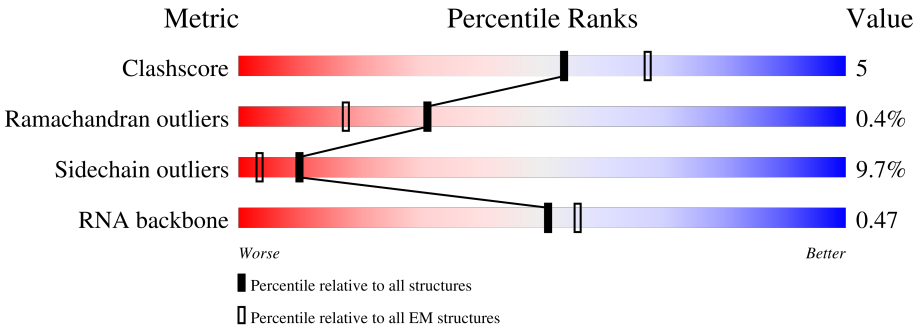
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

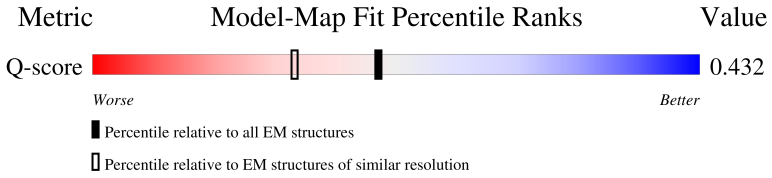
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.24 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.





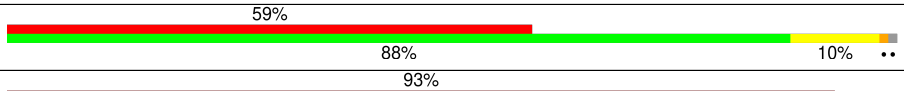
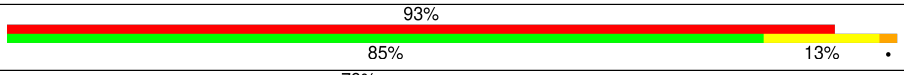
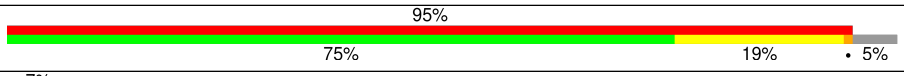
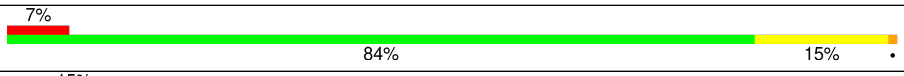
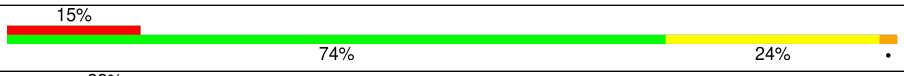
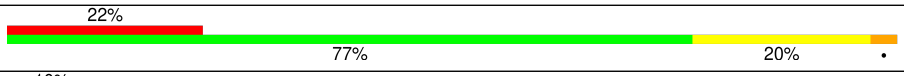
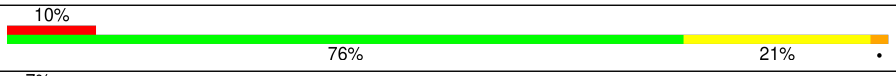
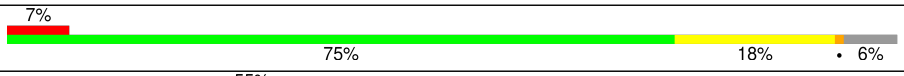
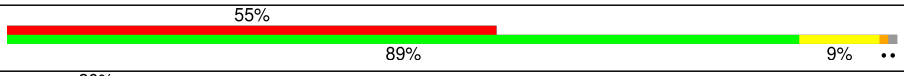
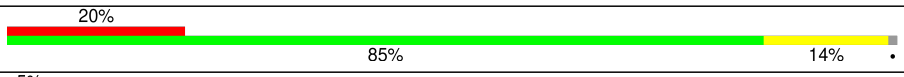
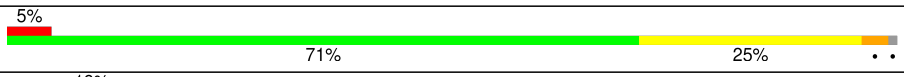
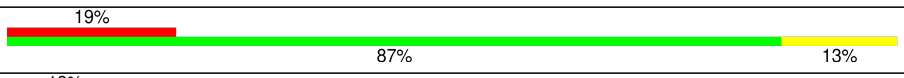
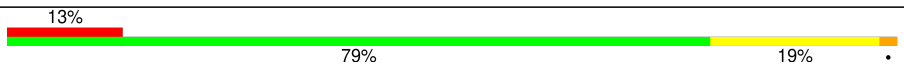
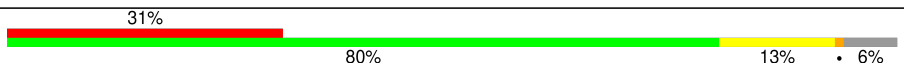
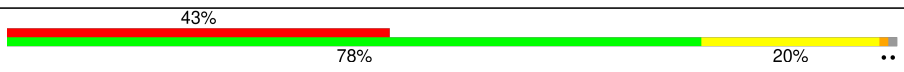
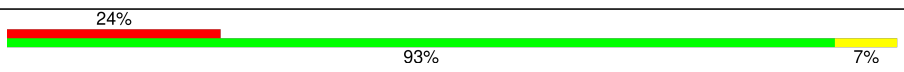
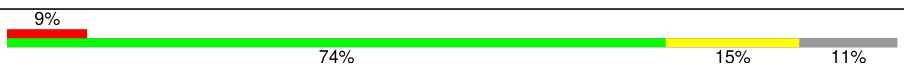
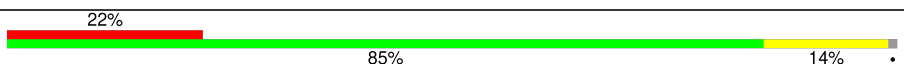
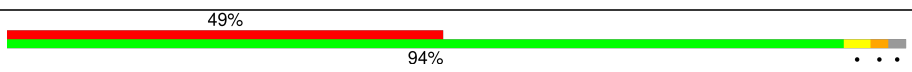
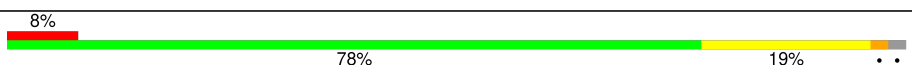
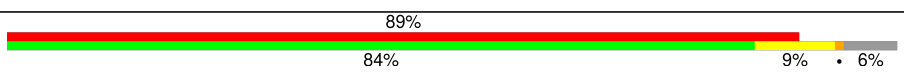
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14594 (2.74 - 3.74)

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 <=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	2904	14% 61% 34% 5%
2	B	120	28% 76% 22% .
3	C	273	8% 78% 21% ..

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Mol	Chain	Length	Quality of chain
4	D	209	
5	E	201	
6	F	177	
7	G	177	
8	H	149	
9	I	165	
10	J	142	
11	K	142	
12	L	123	
13	M	144	
14	N	136	
15	O	127	
16	P	117	
17	Q	115	
18	R	118	
19	S	103	
20	T	110	
21	U	100	
22	V	104	
23	W	94	
24	X	85	
25	Y	78	
26	Z	63	
27	0	59	
28	1	70	

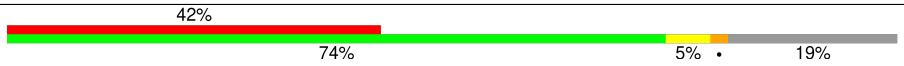
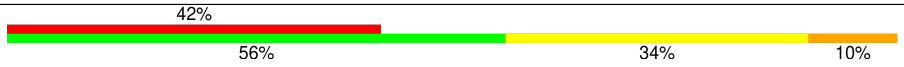
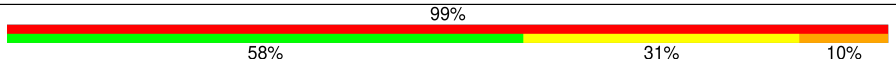
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Mol	Chain	Length	Quality of chain
29	2	57	14% 84% 14%
30	3	52	27% 87% 13%
31	4	46	7% 78% 17%
32	5	65	8% 85% 11%
33	6	38	11% 87% 11%
34	a	1534	49% 63% 34%
35	b	241	92% 84% 8% 7%
36	c	233	84% 81% 6% 11%
37	d	206	96% 84% 16%
38	e	167	77% 77% 14% 7%
39	f	135	55% 61% 13% 23%
40	g	179	81% 72% 10% 15%
41	h	130	83% 87% 11%
42	i	130	95% 80% 15%
43	j	103	96% 73% 17% 5%
44	k	129	50% 74% 15% 9%
45	l	124	52% 77% 19%
46	m	118	92% 78% 17%
47	n	101	98% 82% 14%
48	o	89	49% 78% 16% 6%
49	p	82	90% 88% 11%
50	q	84	76% 74% 20% 5%
51	r	66	70% 82% 18%
52	s	92	90% 74% 14% 10%
53	t	87	84% 84% 10% 5%

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Mol	Chain	Length	Quality of chain
54	u	71	
55	v	384	
56	w	57	
57	x	77	
57	y	77	
58	z	18	

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
1	G7M	A	2069	-	-	X	-
45	0TD	l	89	-	X	X	-

2 Entry composition (i)

There are 61 unique types of molecules in this entry. The entry contains 151446 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 RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	2904	62356	27825	11472	20155	2904	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	887	A	U	conflict	GB 687670942

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	120	2569	1144	468	837	120	0	0

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	271	2082	1288	423	364	7	0	0

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	209	1565	979	288	294	4	0	0

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	201	1552	974	283	290	5	0	0

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	130	Total	C	N	O	S	0	0
			980	620	174	182	4		

- Molecule 10 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	135	Total	C	N	O	S	0	0
			984	622	171	185	6		

- Molecule 11 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 13 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 14 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 16 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 17 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 18 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 19 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 20 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	V	103	Total	C	N	O	0	0
			788	498	148	142		

- Molecule 23 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 25 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	0	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	2	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	3	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	6	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 34 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	1534	Total	C	N	O	P	0	0
			32929	14693	6041	10661	1534		

- Molecule 35 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 36 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 37 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	d	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 38 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 39 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	f	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 40 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	g	152	Total	C	N	O	S	0	0
			1191	741	230	216	4		

- Molecule 41 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	h	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 42 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	i	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 43 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	j	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 44 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	k	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 45 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	l	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 46 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	m	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 47 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	n	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 48 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	o	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 49 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	p	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 50 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 51 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 52 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 53 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	t	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 54 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 55 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	v	362	Total	C	N	O	S	0	0
			2869	1765	504	590	10		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	-18	ALA	-	expression tag	UNP P07012
v	-17	HIS	-	expression tag	UNP P07012
v	-16	HIS	-	expression tag	UNP P07012
v	-15	HIS	-	expression tag	UNP P07012
v	-14	HIS	-	expression tag	UNP P07012
v	-13	HIS	-	expression tag	UNP P07012
v	-12	HIS	-	expression tag	UNP P07012
v	-11	SER	-	expression tag	UNP P07012
v	-10	ALA	-	expression tag	UNP P07012
v	-9	ALA	-	expression tag	UNP P07012
v	-8	LEU	-	expression tag	UNP P07012
v	-7	GLU	-	expression tag	UNP P07012
v	-6	VAL	-	expression tag	UNP P07012
v	-5	LEU	-	expression tag	UNP P07012
v	-4	PHE	-	expression tag	UNP P07012
v	-3	GLN	-	expression tag	UNP P07012
v	-2	GLY	-	expression tag	UNP P07012
v	-1	PRO	-	expression tag	UNP P07012
v	0	GLY	-	expression tag	UNP P07012

- Molecule 56 is a protein called Alternative ribosome-rescue factor A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	w	46	Total	C	N	O	S	0	0
			377	234	77	64	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	-1	GLY	-	expression tag	UNP P36675
w	0	SER	-	expression tag	UNP P36675

- Molecule 57 is a RNA chain called E-site or P-site tRNA fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	x	77	Total	C	N	O	P	0	0
			1643	732	297	537	77		

Continued on next page...

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Mol	Chain	Residues	Atoms					AltConf	Trace
57	y	77	Total 1640	C 732	N 297	O 535	P 76	0	0

- Molecule 58 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	z	5	Total 109	C 49	N 22	O 33	P 5	0	0

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

Mol	Chain	Residues	Atoms		AltConf
59	A	230	Total 230	Mg 230	0
59	B	5	Total 5	Mg 5	0
59	C	1	Total 1	Mg 1	0
59	D	1	Total 1	Mg 1	0
59	O	2	Total 2	Mg 2	0
59	2	1	Total 1	Mg 1	0
59	a	71	Total 71	Mg 71	0
59	d	1	Total 1	Mg 1	0
59	n	1	Total 1	Mg 1	0
59	x	4	Total 4	Mg 4	0

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
60	1	1	Total 1	Zn 1	0
60	6	1	Total 1	Zn 1	0

- Molecule 61 is water.

Mol	Chain	Residues	Atoms		AltConf
61	C	2	Total	O	0
			2	2	

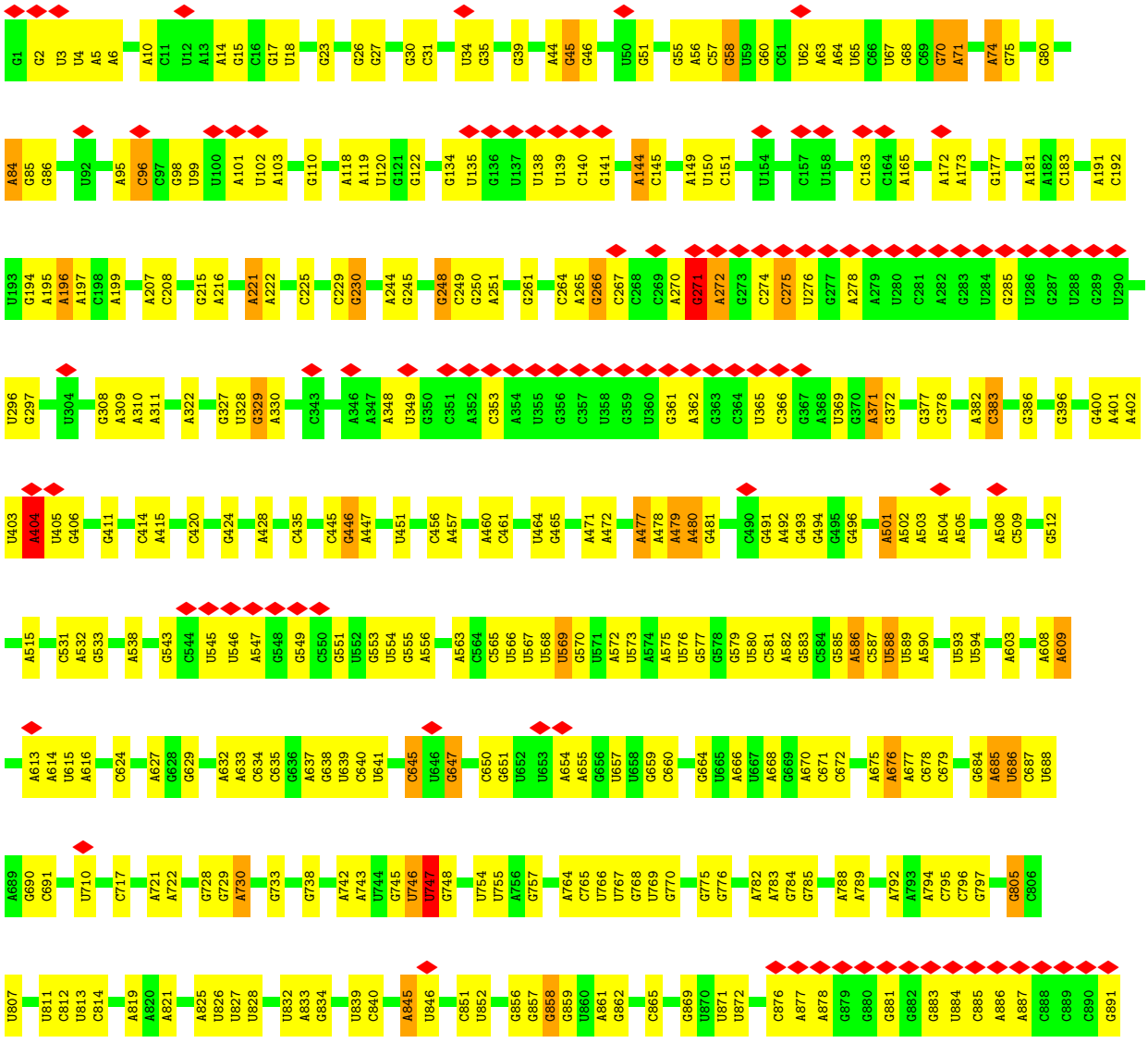
3 Residue-property plots (i)

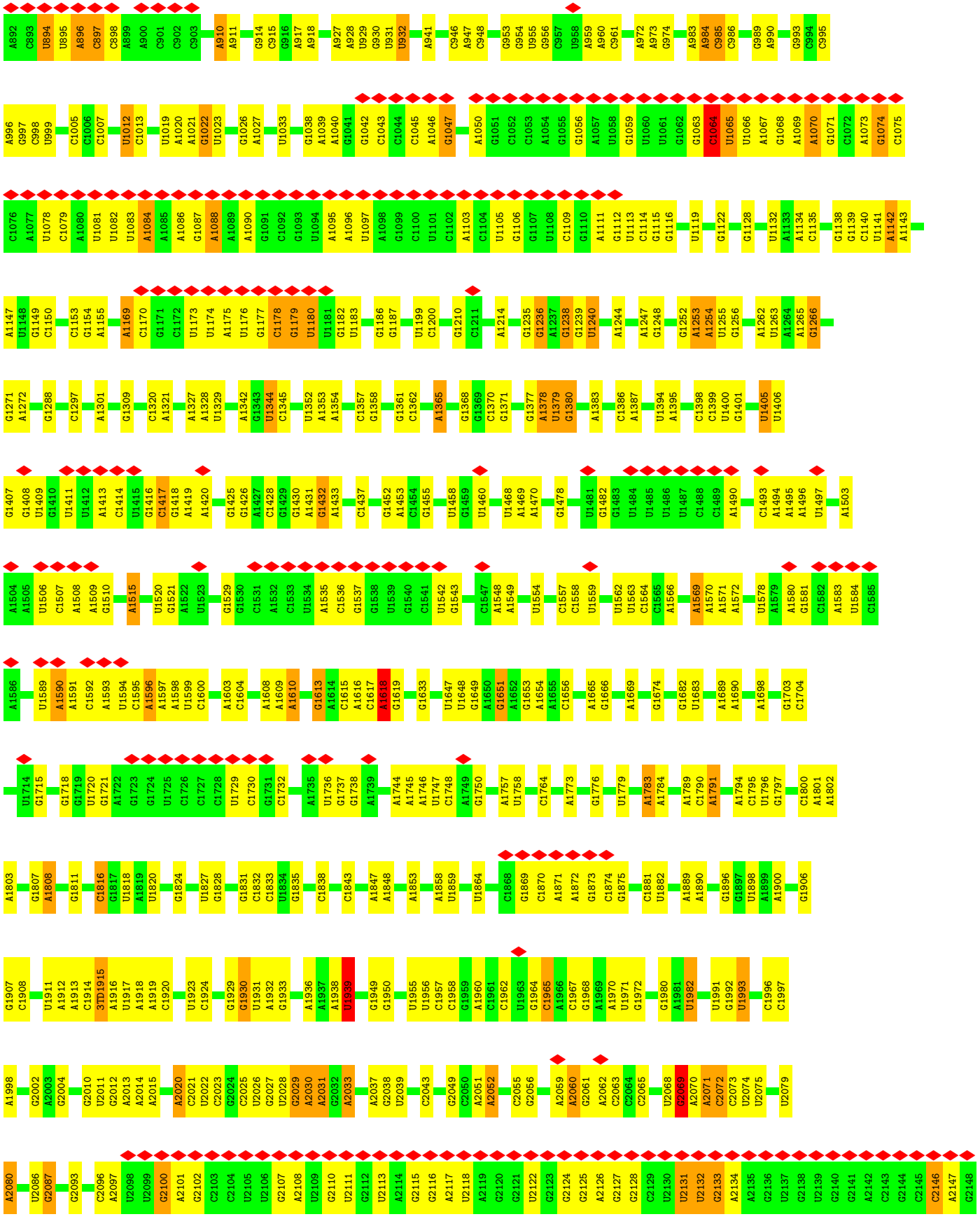
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

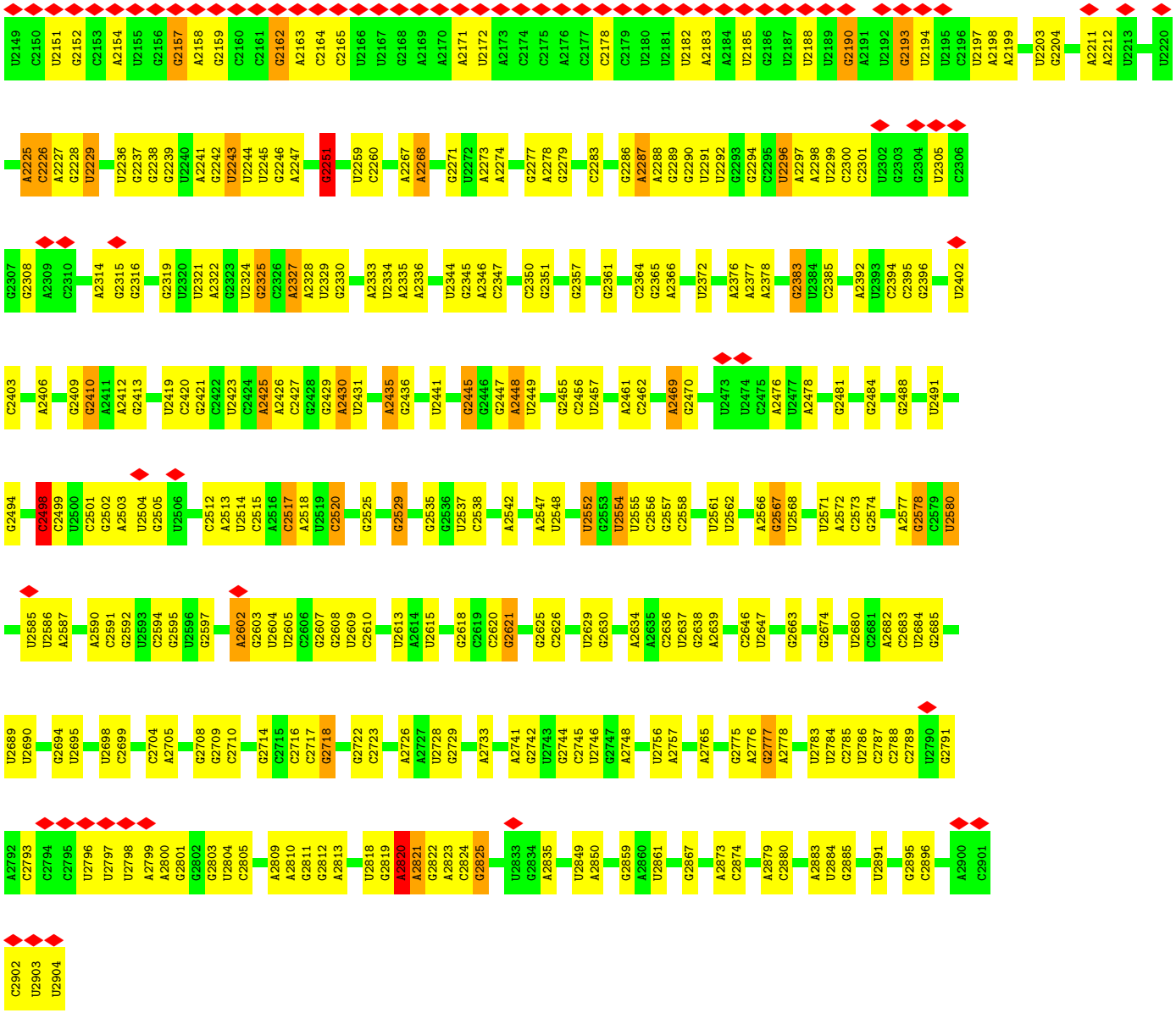
- Molecule 1: 23S rRNA

Chain A:





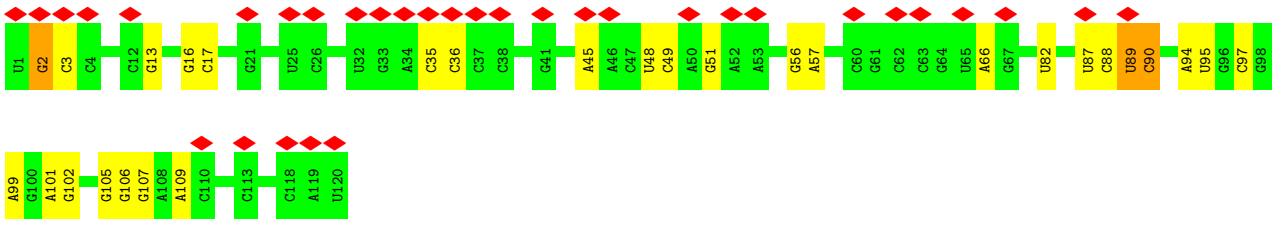

A892 C893 U894 U895 A896 C897 C898 A899 A900 C901 C902 C903 A910 A911 G914 C915 G916 A917 A918 A927 A928 U929 G930 U931 U932 A941 C946 A947 C948 G953 G954 U955 G956 C957 U958 A959 A960 C961 A972 A973 G974 A983 A984 C985 C986 G989 A990 G993 C994 C995
A996 G997 C998 U999 C1005 C1006 C1007 U1012 C1013 U1019 A1020 A1021 G1022 U1023 G1026 A1027 U1033 G1038 A1039 A1040 G1041 G1042 C1043 C1044 C1045 A1046 G1047 A1050 G1051 C1052 C1053 A1054 G1055 G1056 A1057 U1058 G1059 U1060 U1061 G1062 G1063 C1064 U1065 U1066 A1067 G1068 A1069 A1070 G1071 C1072 A1073 G1074 C1075
C1076 A1077 U1078 C1079 A1080 U1081 U1082 U1083 A1084 A1085 A1086 G1087 A1088 A1089 A1090 C1091 C1092 G1093 U1094 A1095 A1096 U1097 A1098 G1099 C1100 U1101 C1102 A1103 C1104 U1105 G1106 G1107 U1108 C1109 G1110 A1111 G1112 U1113 C1114 G1115 G1116 U1119 G1122 G1128 U1132 A1133 A1134 C1135 G1138 G1139 C1140 U1141 A1142 A1143
A1147 U1148 G1149 C1150 C1153 G1154 A1155 A1169 C1170 G1171 C1172 U1173 U1174 A1175 U1176 G1177 C1178 G1179 U1180 U1181 G1182 U1183 G1186 G1187 U1199 C1200 G1210 C1211 A1214 G1235 G1236 A1237 G1238 G1239 U1240 A1244 A1247 G1248 G1252 A1253 A1254 U1255 G1256 A1262 U1263 A1264 A1265 G1266
G1271 A1272 G1288 C1297 A1301 G1309 C1320 A1321 A1327 A1328 U1329 A1342 G1343 U1344 C1345 U1352 A1353 A1354 C1357 G1358 G1361 C1362 A1365 G1368 G1369 C1370 G1371 G1377 A1378 U1379 G1380 A1383 C1386 A1387 U1394 A1395 C1398 C1399 U1400 G1401 U1405 U1406
G1407 G1408 U1409 G1410 U1411 U1412 A1413 C1414 U1415 G1416 C1417 G1418 A1419 A1420 G1425 G1426 A1427 C1428 G1429 G1430 A1431 G1432 A1433 C1437 G1452 A1453 C1454 G1455 U1458 G1459 U1460 U1468 A1469 A1470 G1478 U1481 G1482 G1483 U1484 U1485 U1486 U1487 C1488 C1489 A1490 C1493 A1494 A1495 A1496 U1497 A1503
A1504 A1505 U1506 C1507 A1508 A1509 G1510 A1515 U1520 G1521 A1522 U1523 G1529 G1530 C1531 A1532 C1533 U1534 A1535 C1536 G1537 G1538 U1539 G1540 C1541 U1542 G1543 C1547 A1548 A1549 U1554 C1557 C1558 U1559 U1562 U1563 C1564 C1565 A1566 A1569 A1570 A1571 A1572 U1578 A1579 A1580 G1581 C1582 A1583 U1584 C1585
A1586 U1589 A1590 A1591 C1592 A1593 U1594 C1595 A1596 A1597 A1598 U1599 C1600 A1603 C1604 A1608 A1609 A1610 G1613 A1614 C1615 A1616 C1617 A1618 G1619 G1633 U1647 U1648 G1649 A1650 G1651 A1652 G1653 A1654 A1655 C1656 A1665 G1666 A1669 G1674 G1682 U1683 A1689 A1690 A1698 G1703 C1704
U1714 G1715 G1718 G1719 U1720 G1721 A1722 G1723 G1724 U1725 C1726 C1727 C1728 U1729 C1730 G1731 C1732 A1735 U1736 G1737 G1738 A1739 A1744 A1745 A1746 U1747 C1748 A1749 G1750 A1757 U1758 C1764 A1773 G1776 U1779 A1783 A1784 A1789 C1790 A1791 A1794 C1795 U1796 G1797 C1800 A1801 A1802
A1803 G1807 A1808 G1811 C1816 G1817 U1818 A1819 U1820 G1824 U1827 G1828 G1831 C1832 C1833 U1834 G1835 C1838 C1843 A1847 A1848 A1853 A1858 U1859 U1864 C1868 G1869 C1870 A1871 A1872 G1873 C1874 G1875 C1881 U1882 A1889 A1890 G1896 G1897 U1898 A1899 A1900 G1906
G1907 C1908 U1911 A1912 A1913 C1914 3TD1915 A1916 U1917 A1918 A1919 C1920 U1923 C1924 G1929 G1930 U1931 A1932 G1933 A1936 A1937 A1938 U1939 G1949 G1950 U1955 U1956 C1957 C1958 G1959 A1960 C1961 C1962 U1963 G1964 C1965 A1966 C1967 G1968 A1969 A1970 U1971 G1972 G1980 A1981 U1982 U1991 G1992 U1993 C1996 C1997
A1998 G2002 A2003 G2004 G2010 U2011 G2012 A2013 A2014 A2015 A2020 C2021 U2022 C2023 G2024 C2025 U2026 G2027 U2028 G2029 A2030 A2031 G2032 A2033 A2037 G2038 U2039 C2043 G2049 C2050 A2051 A2052 C2055 G2056 A2059 A2060 G2061 A2062 C2063 C2064 C2065 U2068 G2069 A2070 A2071 C2072 C2073 U2074 U2075 U2079
A2080 U2086 G2087 C2093 C2096 A2097 U2098 U2099 G2100 A2101 C2102 C2103 C2104 U2105 U2106 G2107 A2108 U2109 G2110 U2111 G2112 U2113 A2114 G2115 G2116 A2117 U2118 A2119 G2120 G2121 U2122 G2123 G2124 G2125 A2126 G2127 G2128 C2129 U2130 U2131 U2132 G2133 A2134 A2135 G2136 U2137 G2138 U2139 G2140 G2141 A2142 C2143 G2144 C2145 C2146 A2147 G2148



• Molecule 2: 5S rRNA

Chain B:

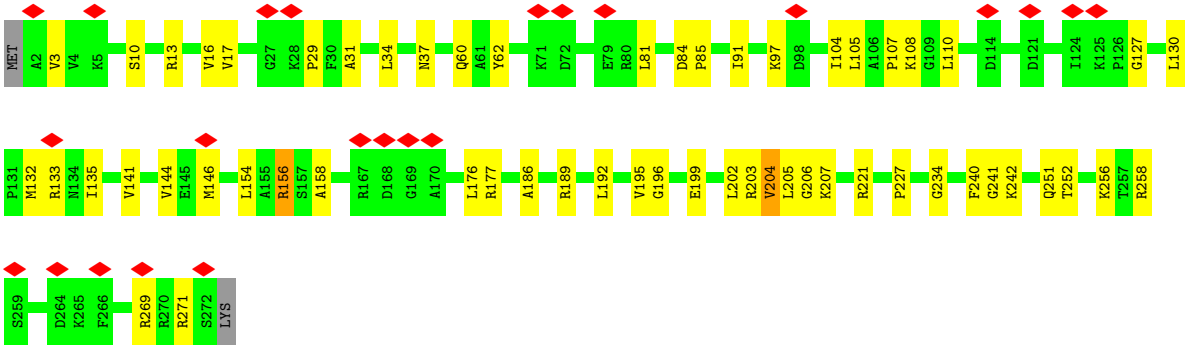




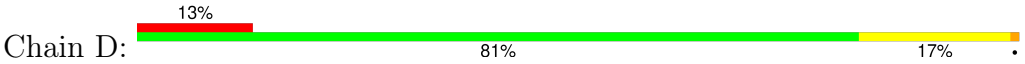
• Molecule 3: 50S ribosomal protein L2

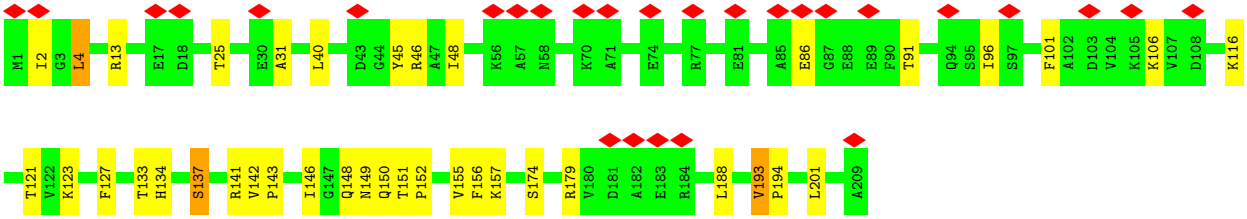
Chain C:



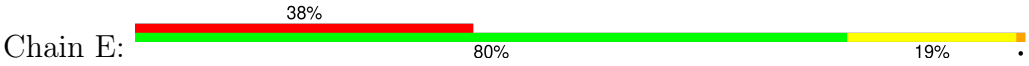


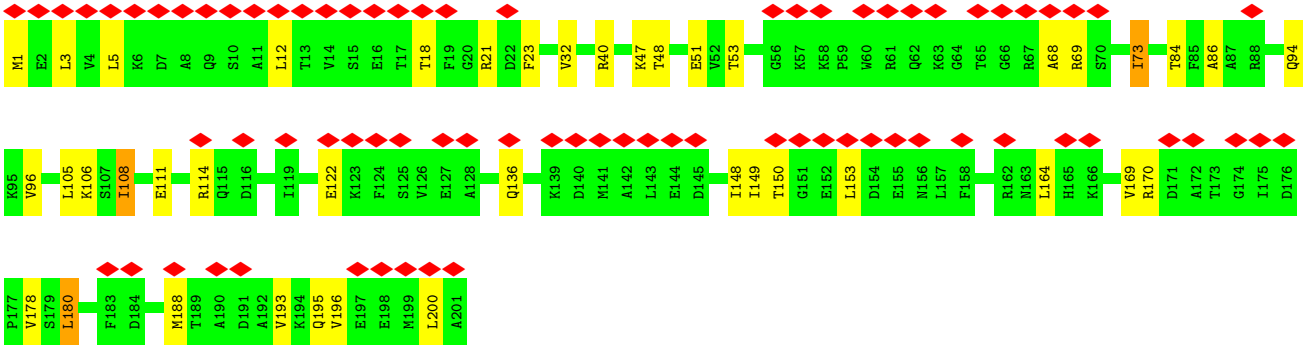
• Molecule 4: 50S ribosomal protein L3



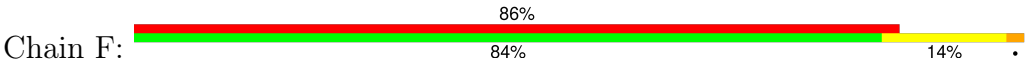


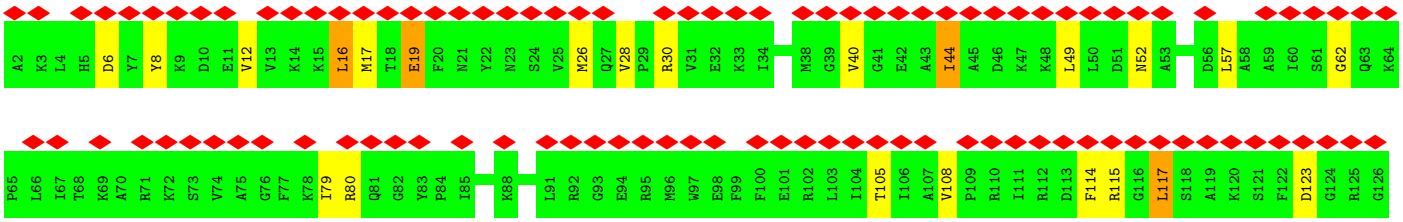
• Molecule 5: 50S ribosomal protein L4

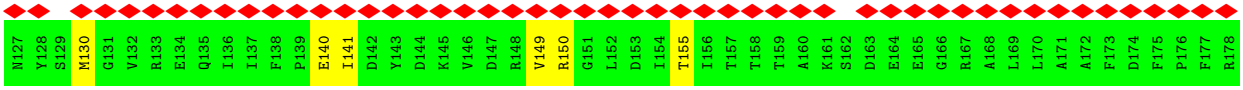




• Molecule 6: 50S ribosomal protein L5



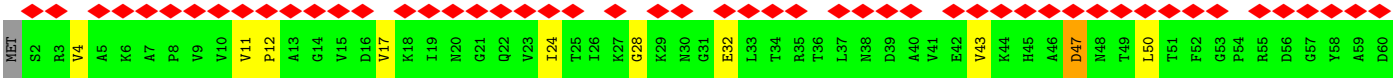


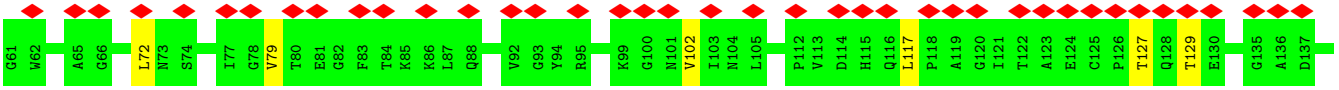


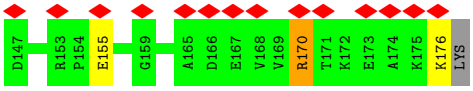
• Molecule 7: 50S ribosomal protein L6

Chain G:



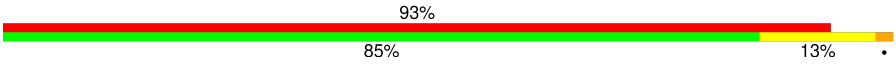


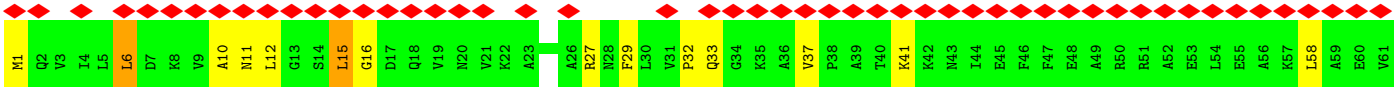


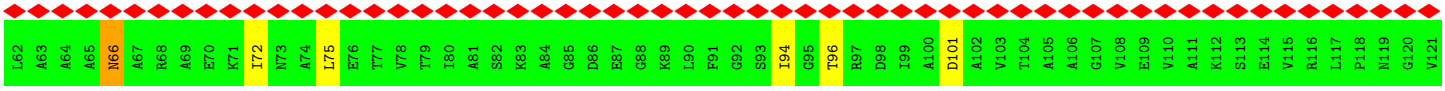


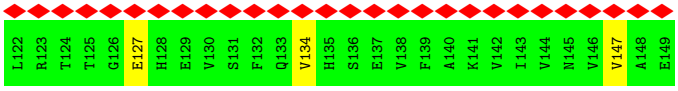
• Molecule 8: 50S ribosomal protein L9

Chain H:





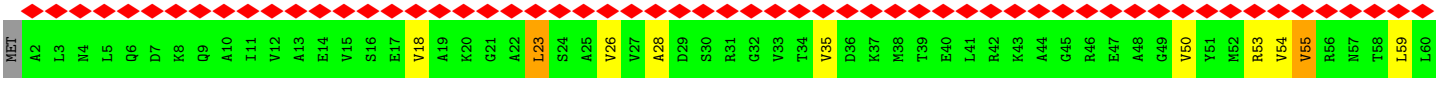


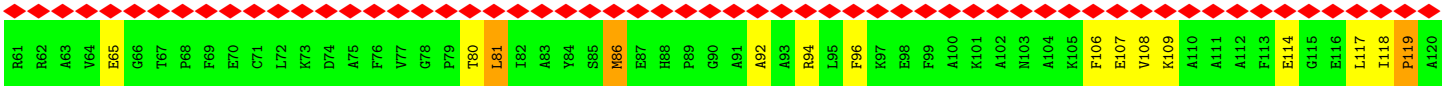


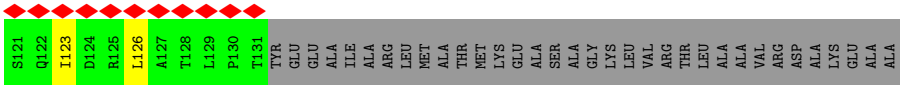
• Molecule 9: 50S ribosomal protein L10

Chain I:



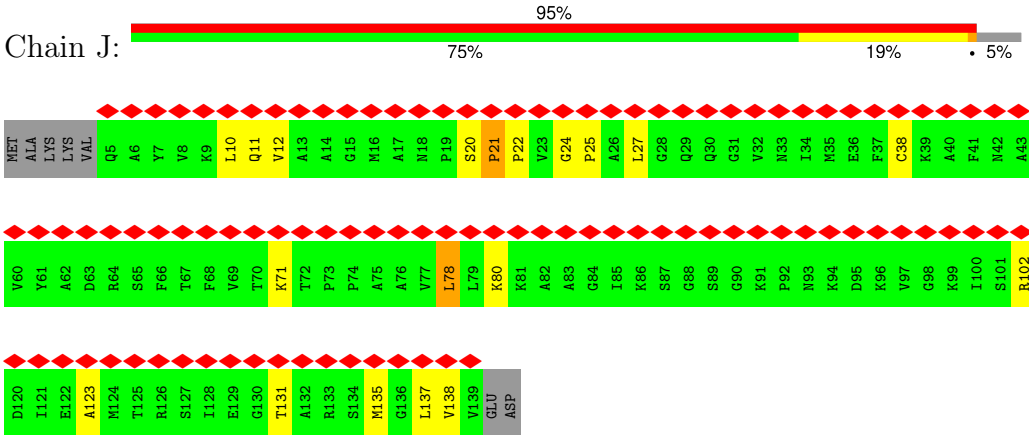






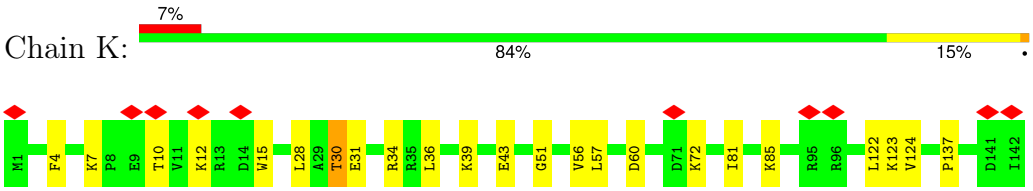
• Molecule 10: 50S ribosomal protein L11

Chain J:



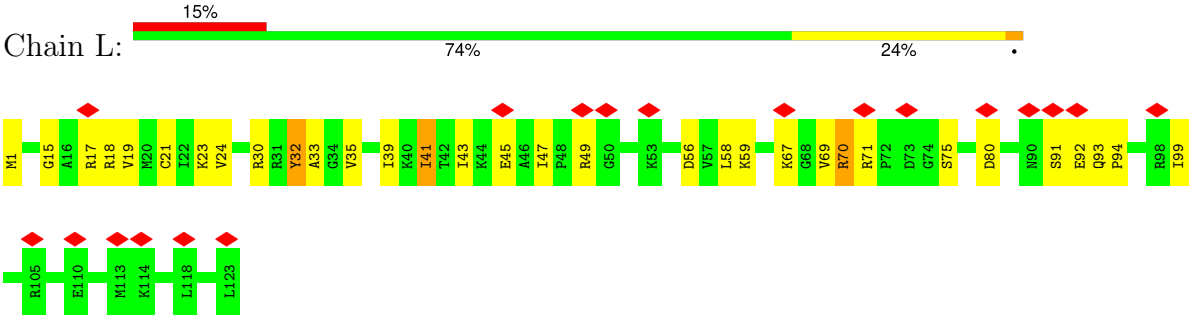
• Molecule 11: 50S ribosomal protein L13

Chain K:



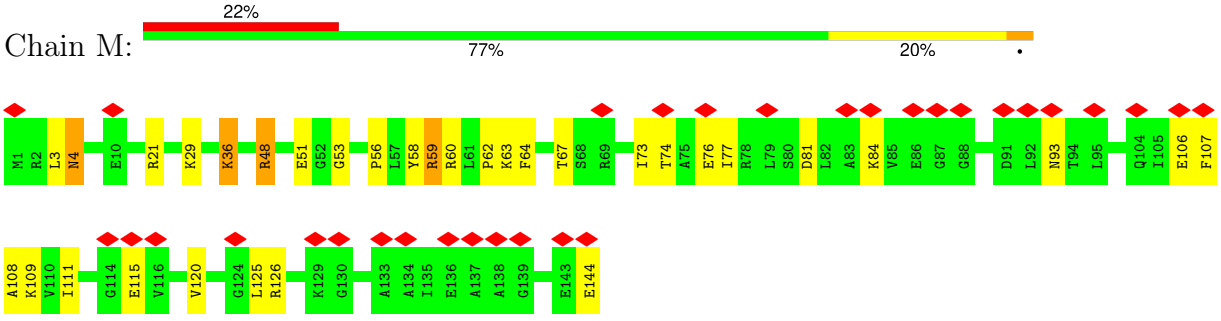
• Molecule 12: 50S ribosomal protein L14

Chain L:



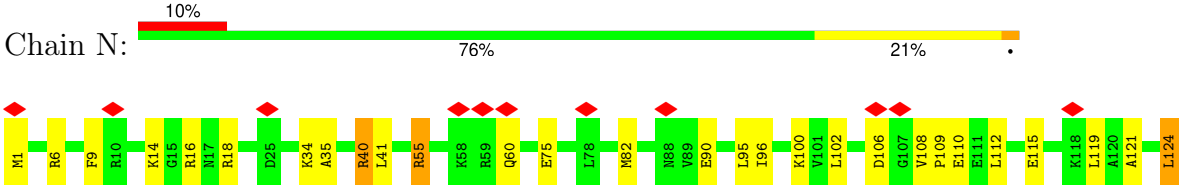
• Molecule 13: 50S ribosomal protein L15

Chain M:



• Molecule 14: 50S ribosomal protein L16

Chain N:

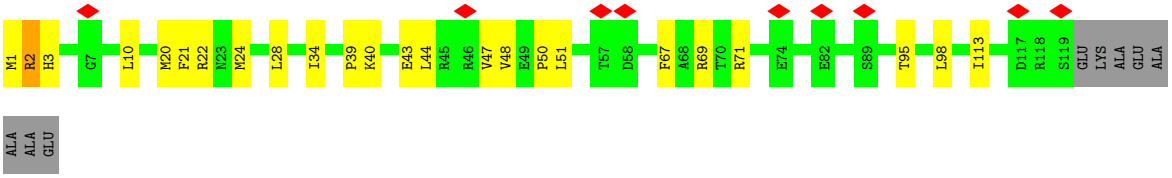




• Molecule 15: 50S ribosomal protein L17

Chain O:

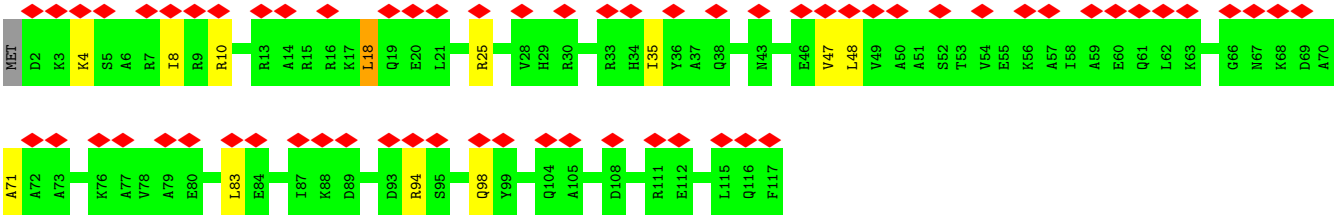




• Molecule 16: 50S ribosomal protein L18

Chain P:

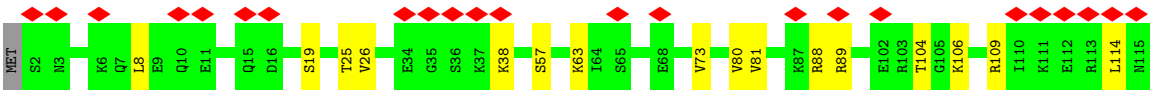




• Molecule 17: 50S ribosomal protein L19

Chain Q:

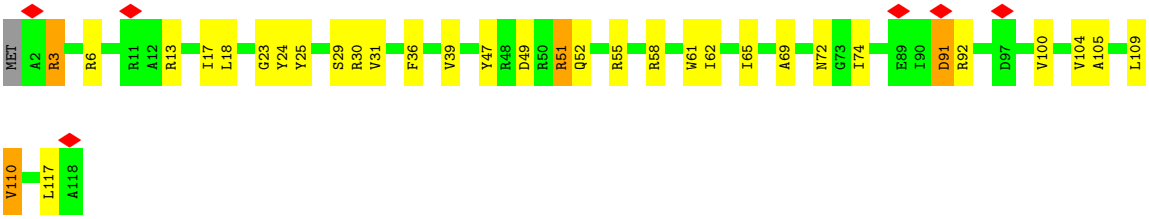




• Molecule 18: 50S ribosomal protein L20

Chain R:

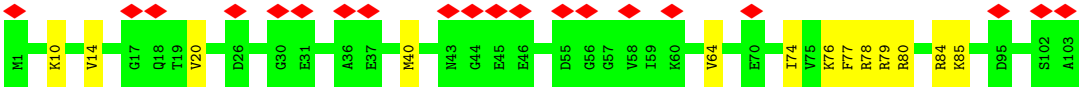




• Molecule 19: 50S ribosomal protein L21

Chain S:

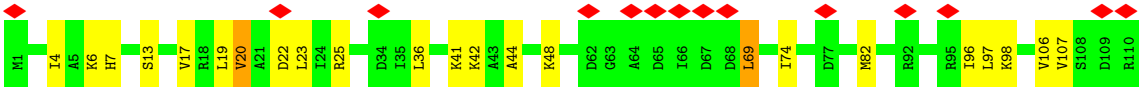




• Molecule 20: 50S ribosomal protein L22

Chain T:

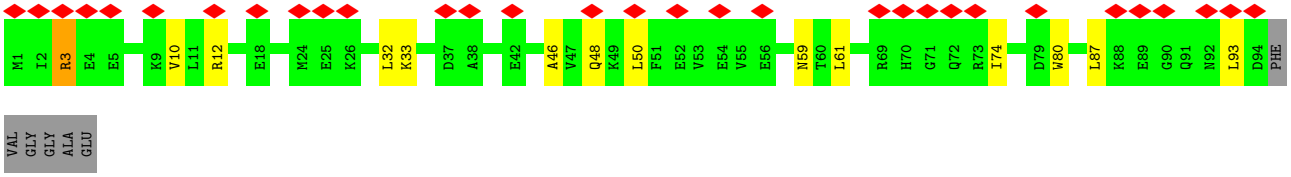




• Molecule 21: 50S ribosomal protein L23

Chain U:

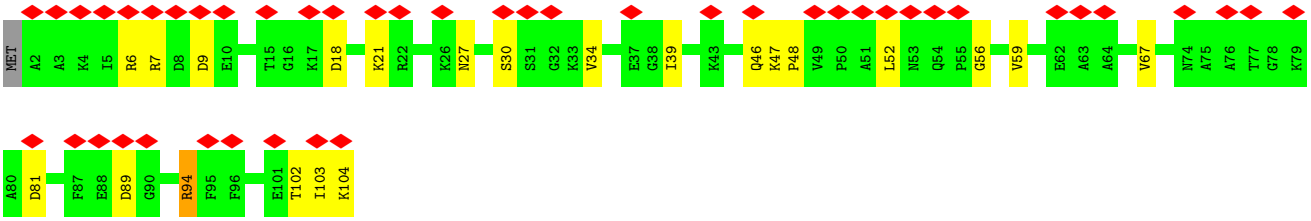




• Molecule 22: 50S ribosomal protein L24

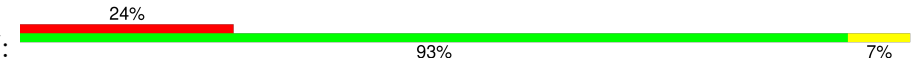
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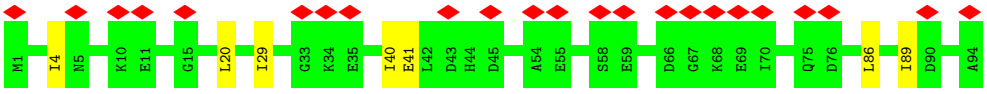




• Molecule 23: 50S ribosomal protein L25

Chain W:

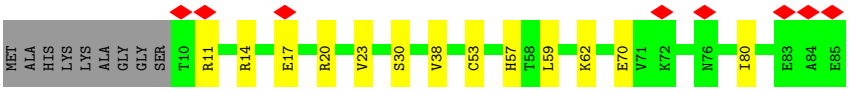




• Molecule 24: 50S ribosomal protein L27

Chain X:

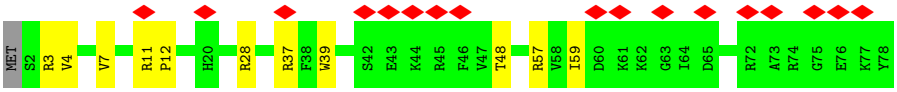




• Molecule 25: 50S ribosomal protein L28

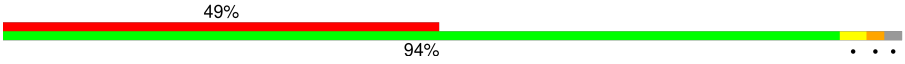
Chain Y:

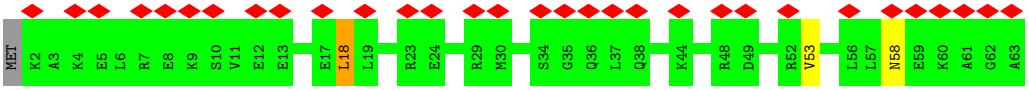




• Molecule 26: 50S ribosomal protein L29

Chain Z:

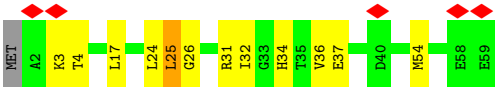




• Molecule 27: 50S ribosomal protein L30

Chain 0:

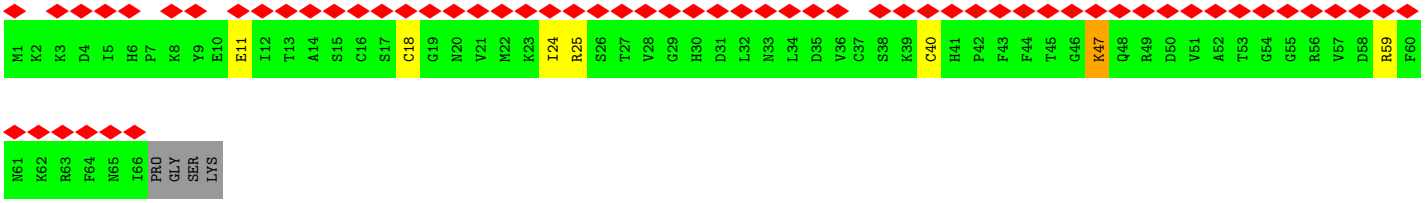




• Molecule 28: 50S ribosomal protein L31

Chain 1:

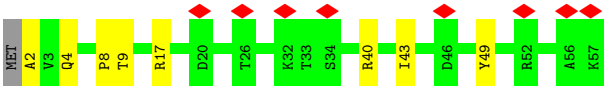




• Molecule 29: 50S ribosomal protein L32

Chain 2:

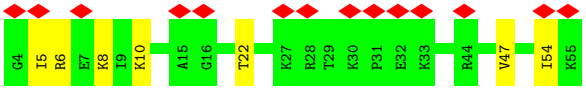




• Molecule 30: 50S ribosomal protein L33

Chain 3:

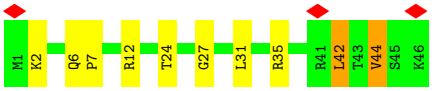




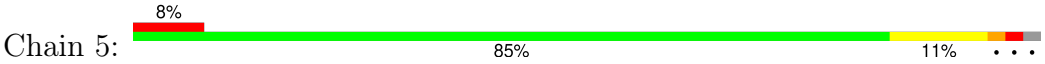
• Molecule 31: 50S ribosomal protein L34

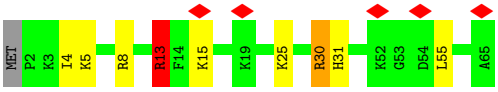
Chain 4:



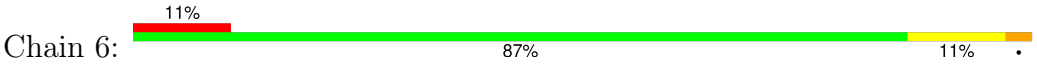


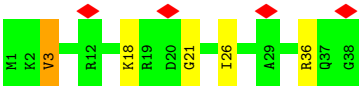
• Molecule 32: 50S ribosomal protein L35





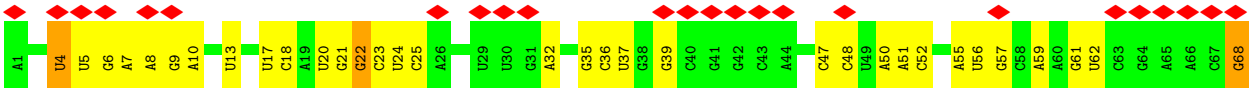
• Molecule 33: 50S ribosomal protein L36

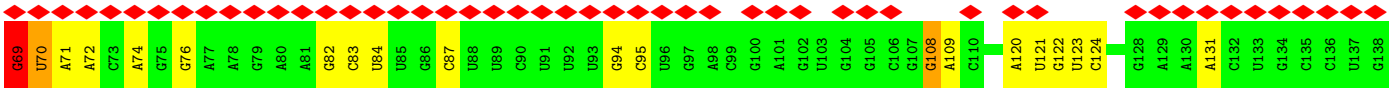


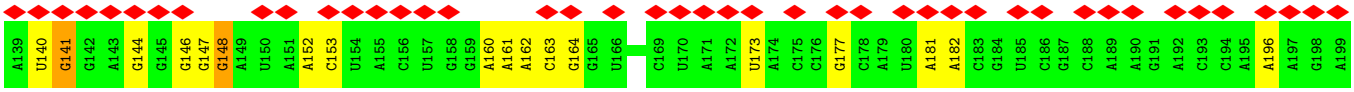


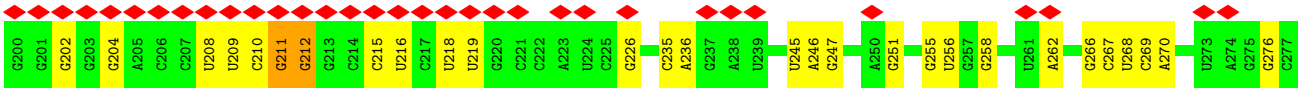
• Molecule 34: 16S rRNA

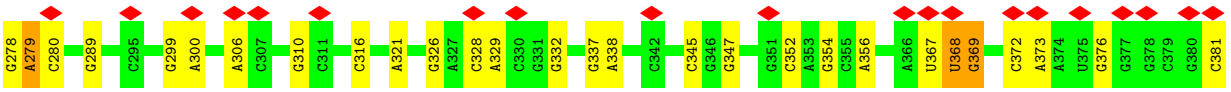


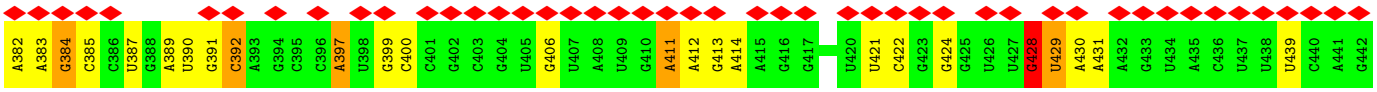


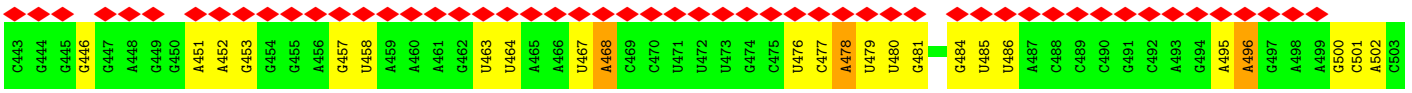


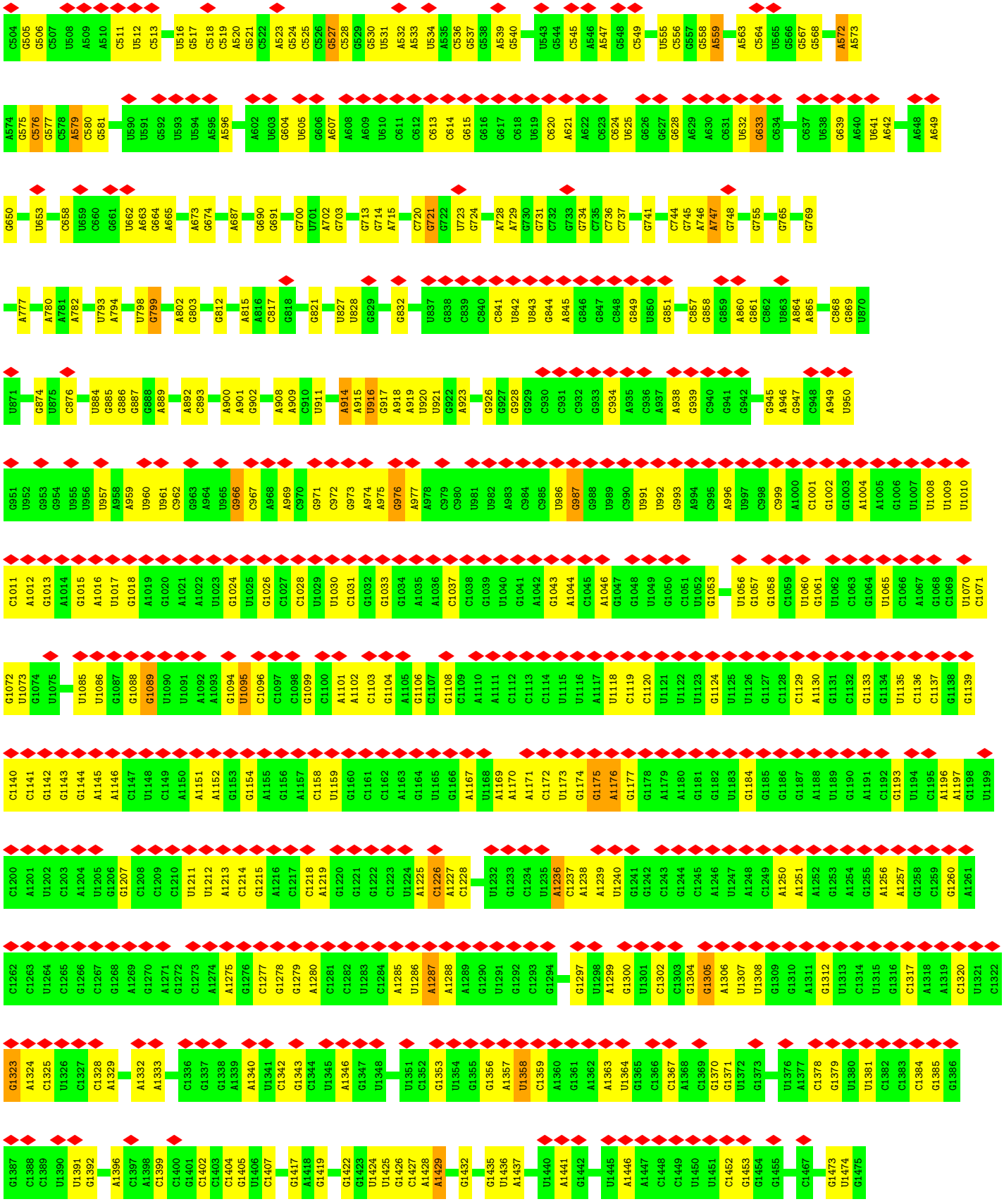


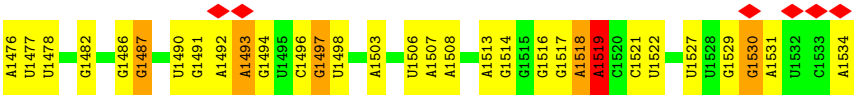






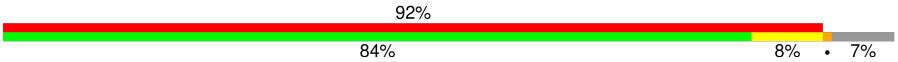


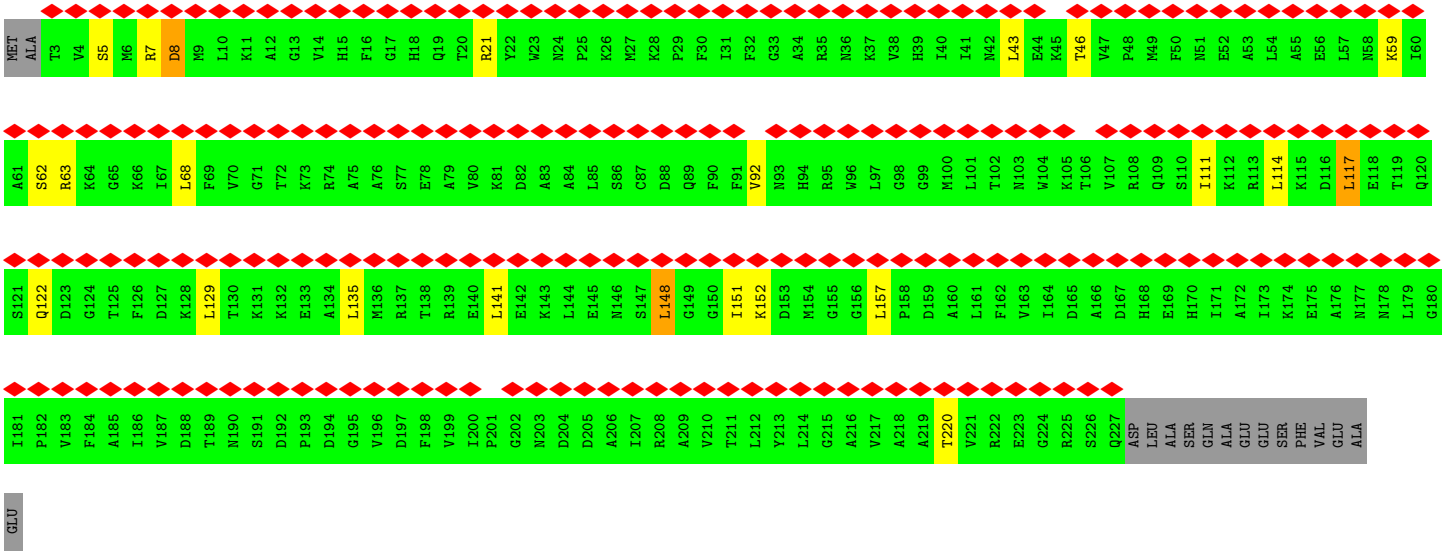

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A574 G575 C576 G577 C578 A579 C580 G581 U590 U591 G592 U593 U594 A595 A596 A602 U603 G604 U605 G606 A607 A608 A609 U610 C611 C612 C613 C614 G615 G616 G617 C618 U619 C620 A621 A622 C623 C624 U625 G626 G627 G628 A629 A630 C631 U632 G633 C634 C637 U638 G639 A640 U641 A642 A648 A649
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G951 U952 G953 G954 U955 U956 U957 A958 A959 U960 U961 C962 G963 A964 U965 G966 C967 A968 A969 C970 G971 C972 G973 A974 A975 G976 A977 A978 C979 C980 U981 U982 A983 C984 C985 U986 G987 G988 U989 C990 U991 U992 G993 A994 C995 A996 U997 C998 C999 A1000 C1001 G1002 G1003 A1004 A1005 G1006 U1007 U1008 U1009 U1010
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C1200 A1201 U1202 C1203 A1204 U1205 G1206 G1207 C1208 C1209 C1210 U1211 U1212 A1213 C1214 G1215 A1216 C1217 C1218 A1219 G1220 G1221 G1222 C1223 U1224 A1225 C1226 A1227 C1228 U1232 G1233 C1234 U1235 A1236 C1237 A1238 A1239 U1240 G1241 G1242 C1243 G1244 C1245 A1246 U1247 A1248 C1249 A1250 A1251 A1252 G1253 A1254 G1255 A1256 A1257 G1258 C1259 G1260 A1261
C1262 C1263 U1264 C1265 G1266 C1267 G1268 A1269 G1270 A1271 G1272 C1273 A1274 A1275 G1276 C1277 G1278 G1279 A1280 C1281 C1282 U1283 C1284 A1285 U1286 A1287 A1288 A1289 G1290 U1291 G1292 C1293 G1294 G1297 U1298 A1299 G1300 U1301 C1302 C1303 G1304 G1305 A1306 U1307 U1308 G1309 G1310 A1311 G1312 U1313 C1314 U1315 G1316 C1317 A1318 A1319 C1320 U1321 C1322
G1323 A1324 C1325 U1326 C1327 C1328 A1329 A1332 A1333 C1336 G1337 G1338 A1339 A1340 U1341 C1342 G1343 C1344 U1345 A1346 G1347 U1348 U1351 C1352 G1353 U1354 G1355 G1356 A1357 U1358 C1359 A1360 G1361 A1362 A1363 U1364 G1365 C1366 C1367 A1368 C1369 G1370 G1371 U1372 G1373 U1376 A1377 C1378 G1379 U1380 U1381 C1382 C1383 C1384 G1385 G1386
G1387 C1388 C1389 U1390 U1391 G1392 A1396 C1397 A1398 C1399 C1400 G1401 C1402 C1403 C1404 G1405 U1406 C1407 G1417 A1418 G1419 G1422 G1423 U1424 U1425 G1426 C1427 A1428 A1429 G1432 G1435 U1436 A1437 U1440 A1441 G1442 U1445 A1446 A1447 C1448 C1449 U1450 U1451 C1452 G1453 G1454 G1455 C1467 G1473 U1474 G1475



• Molecule 35: 30S ribosomal protein S2

Chain b:

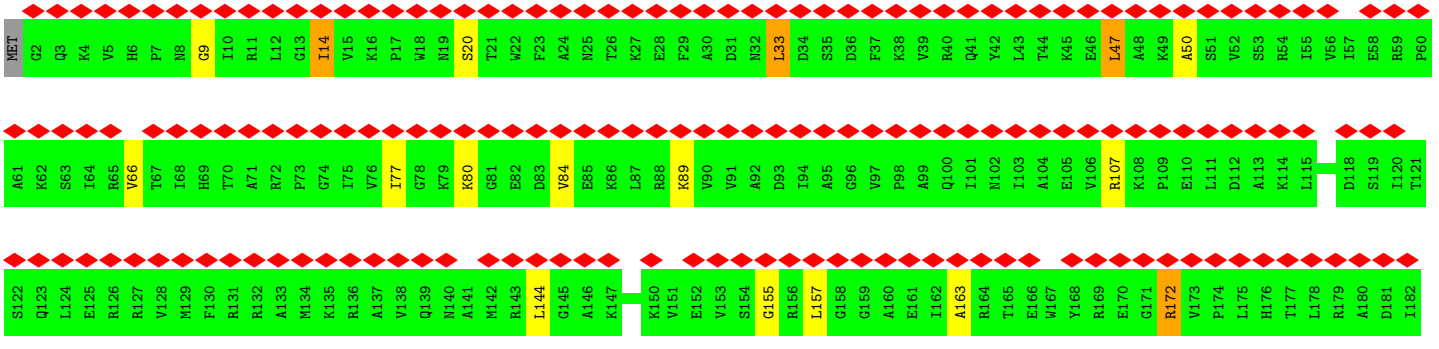




• Molecule 36: 30S ribosomal protein S3

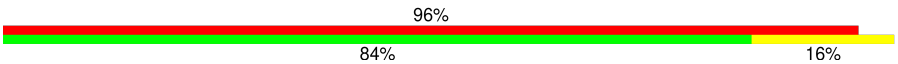
Chain c:

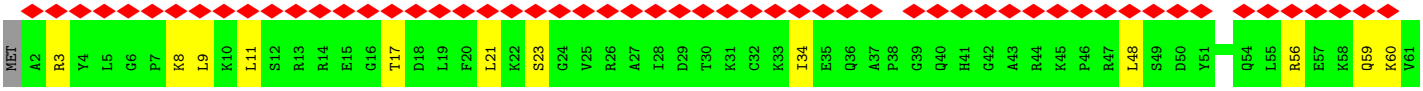


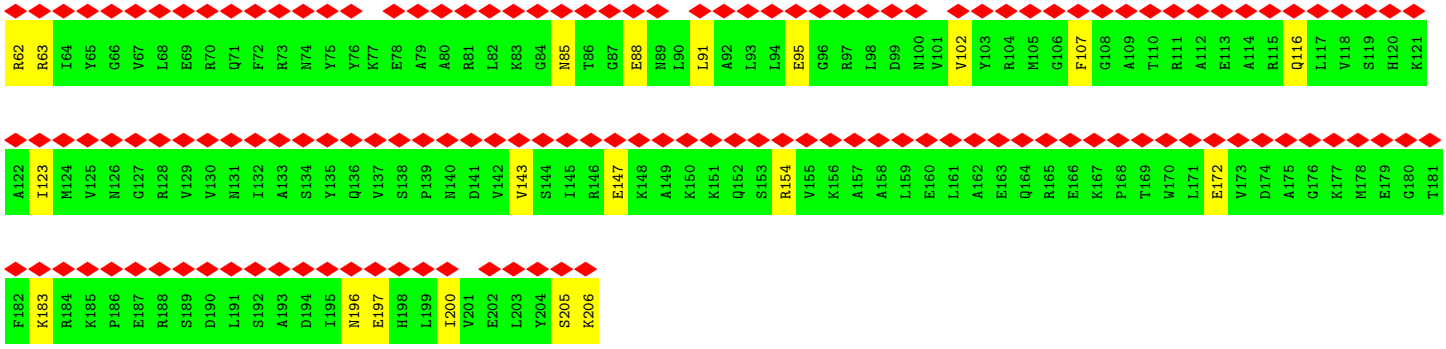


• Molecule 37: 30S ribosomal protein S4

Chain d:



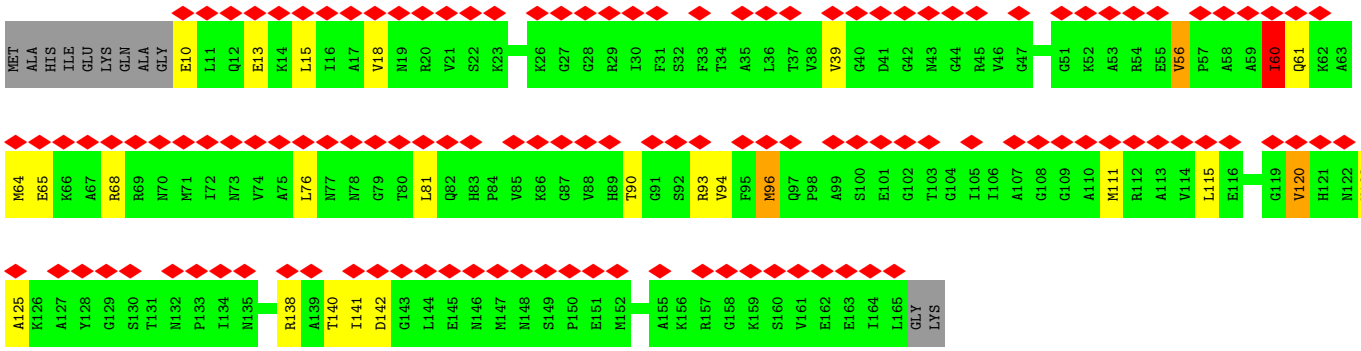




• Molecule 38: 30S ribosomal protein S5

Chain e:

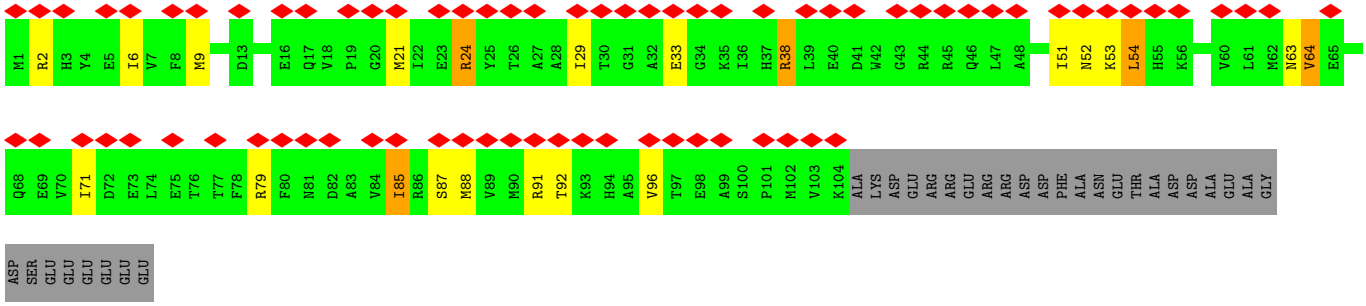




• Molecule 39: 30S ribosomal protein S6

Chain f:

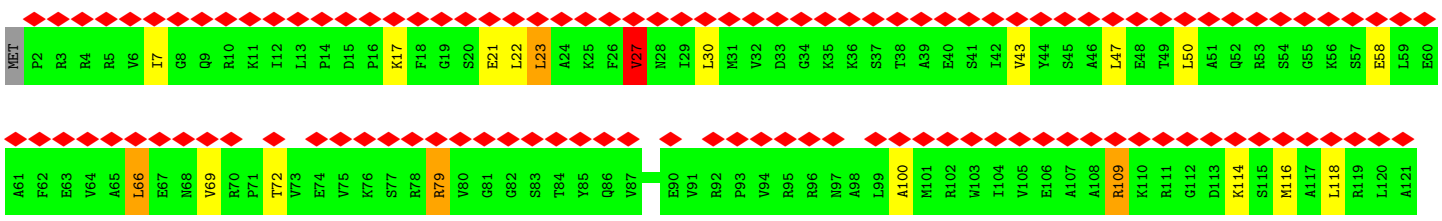


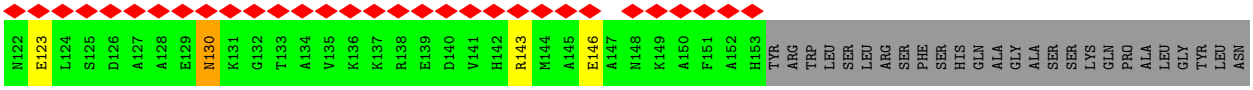


• Molecule 40: 30S ribosomal protein S7

Chain g:



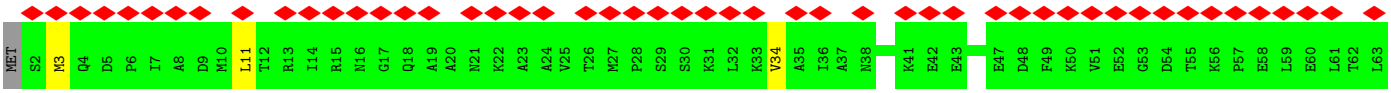


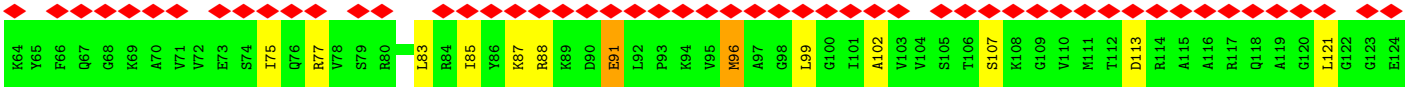


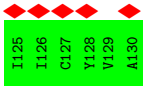
• Molecule 41: 30S ribosomal protein S8

Chain h:



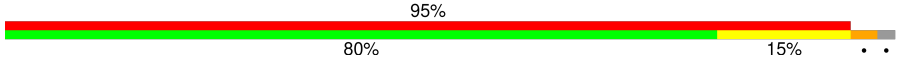


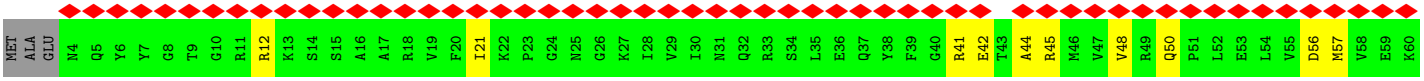


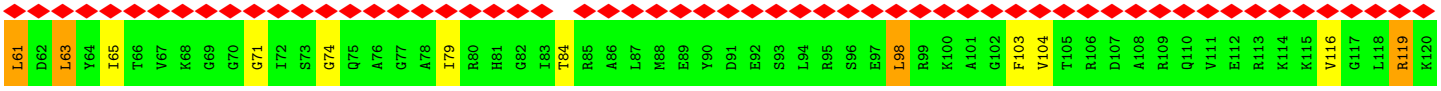


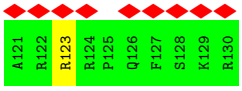
• Molecule 42: 30S ribosomal protein S9

Chain i:



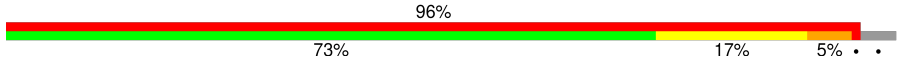


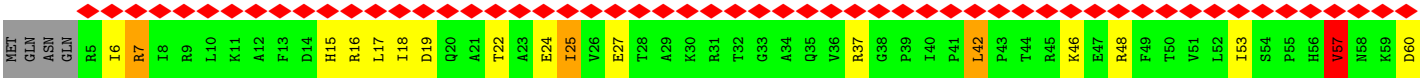


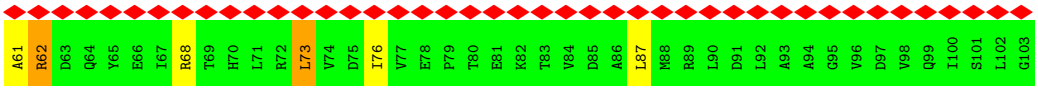


• Molecule 43: 30S ribosomal protein S10

Chain j:

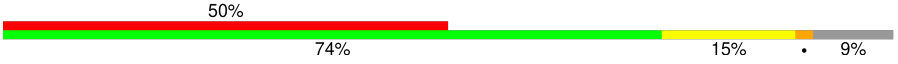


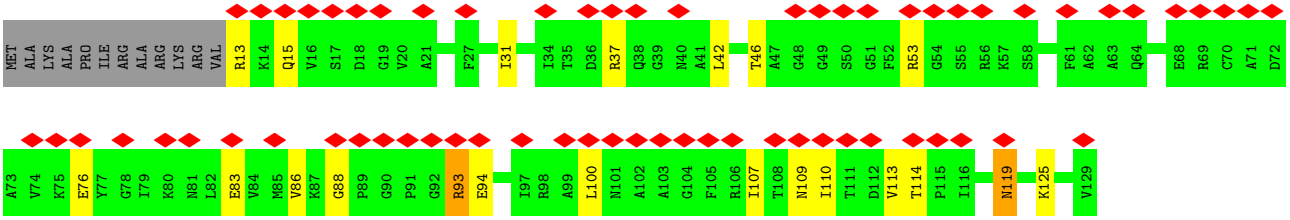




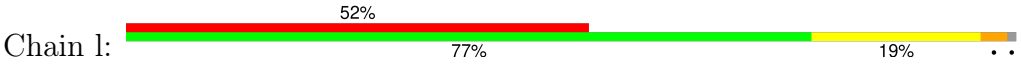
• Molecule 44: 30S ribosomal protein S11

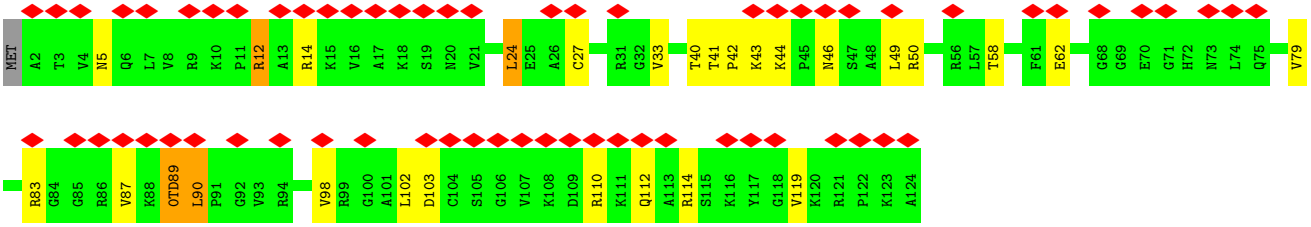
Chain k:



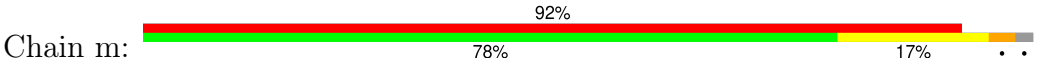


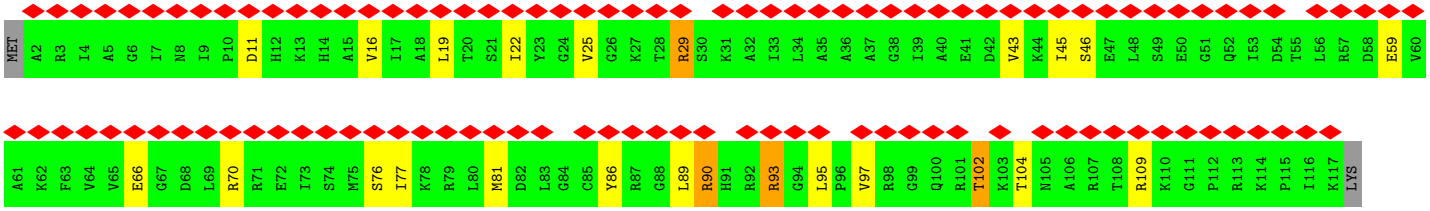
• Molecule 45: 30S ribosomal protein S12



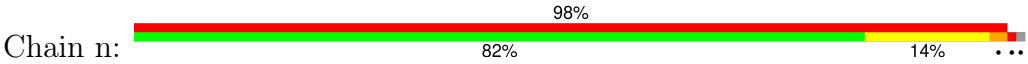


• Molecule 46: 30S ribosomal protein S13



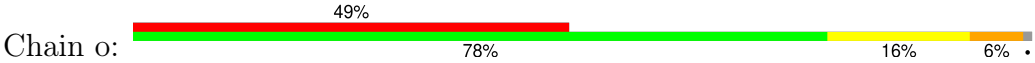


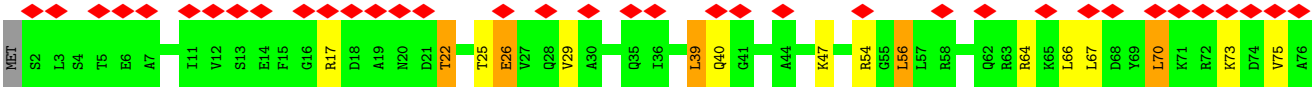
• Molecule 47: 30S ribosomal protein S14

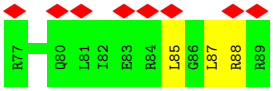




• Molecule 48: 30S ribosomal protein S15



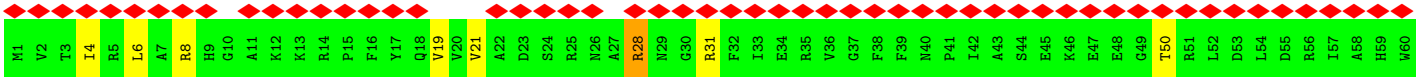


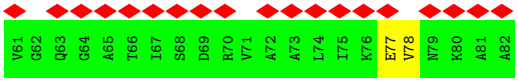


• Molecule 49: 30S ribosomal protein S16

Chain p:



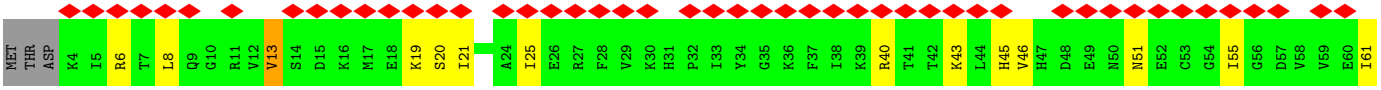


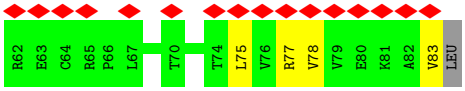


• Molecule 50: 30S ribosomal protein S17

Chain q:



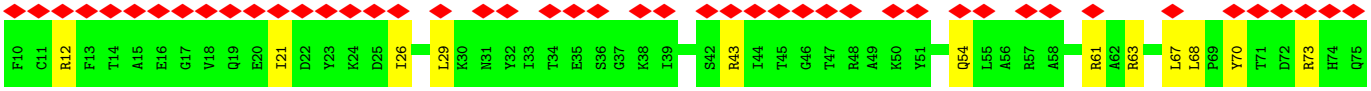




• Molecule 51: 30S ribosomal protein S18

Chain r:

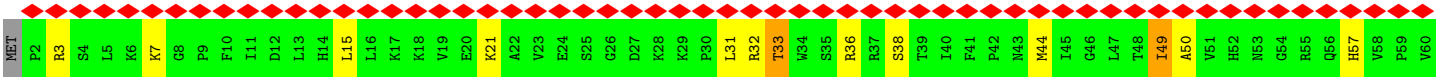


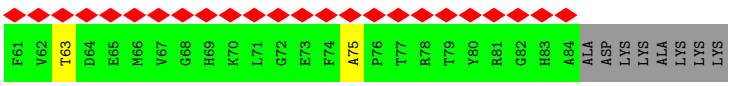


• Molecule 52: 30S ribosomal protein S19

Chain s:



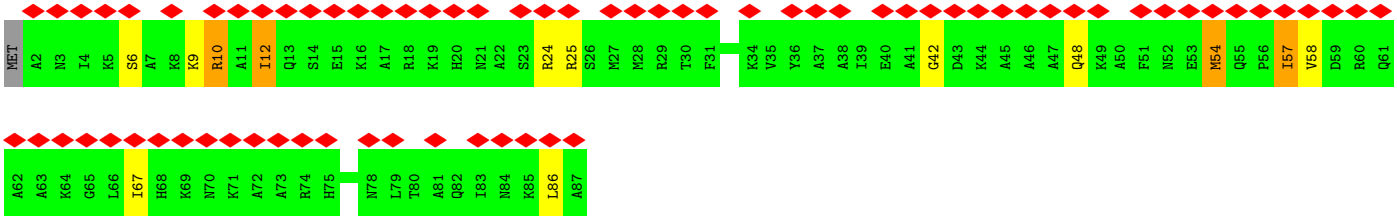




• Molecule 53: 30S ribosomal protein S20

Chain t:

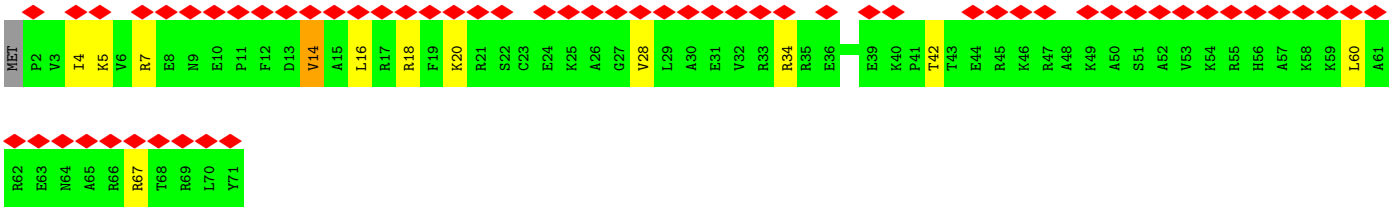




• Molecule 54: 30S ribosomal protein S21

Chain u:

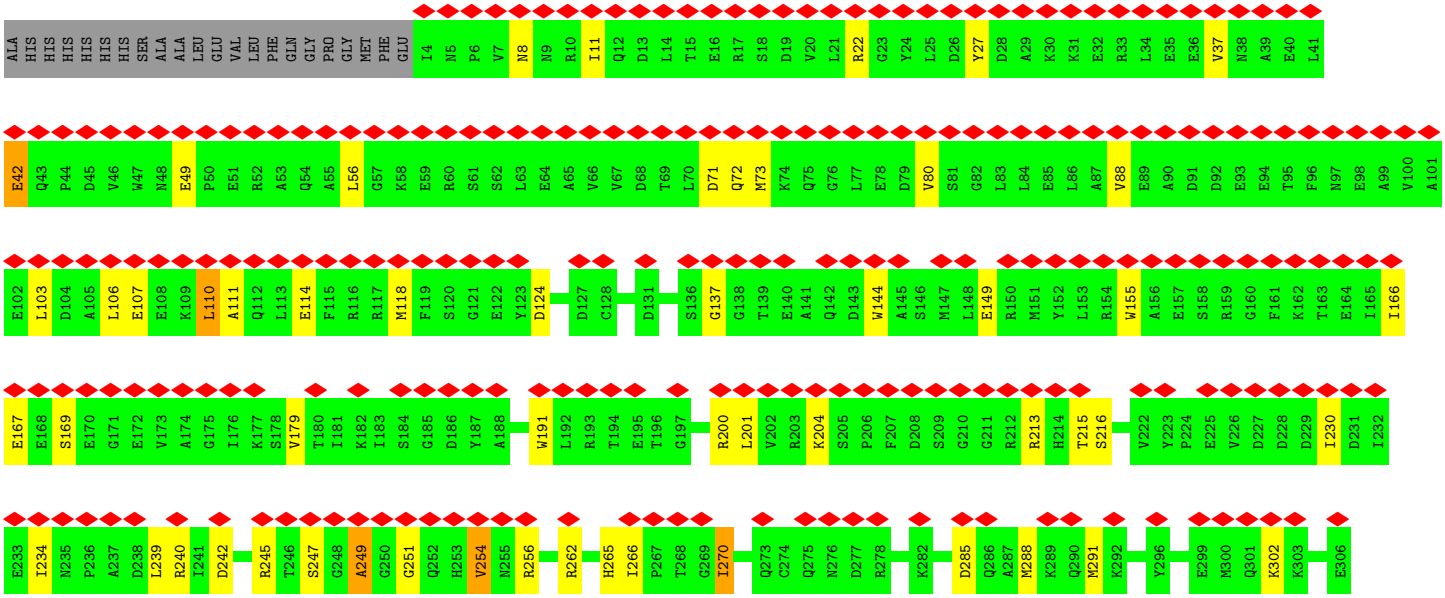




• Molecule 55: Peptide chain release factor 2

Chain v:

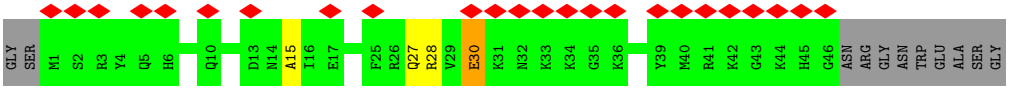




• Molecule 56: Alternative ribosome-rescue factor A

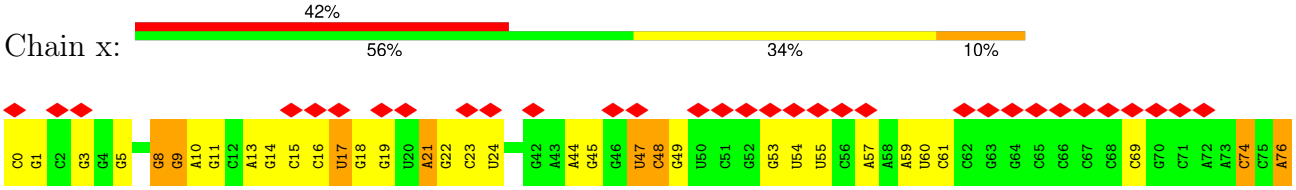
Chain w:





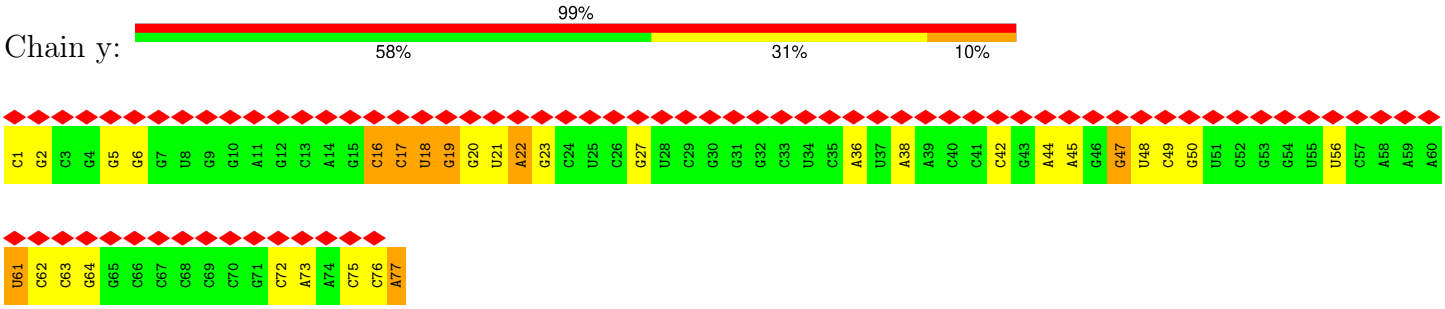
• Molecule 57: E-site or P-site tRNA fMet

Chain x:



• Molecule 57: E-site or P-site tRNA fMet

Chain y:



• Molecule 58: mRNA

Chain z:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	143372	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL 3200FS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	83822	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.448	Depositor
Minimum map value	-0.283	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	460.80002, 460.80002, 460.80002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2, 1.2, 1.2	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 2MA, OMC, MA6, OMU, ZN, G7M, 5MU, MEQ, 1MG, 0TD, 2MG, 6MZ, 4OC, PSU, UR3, 3TD, MG, 5MC, OMG

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	0.38	0/69308	0.73	29/108121 (0.0%)
2	B	0.37	0/2872	0.69	0/4478
3	C	0.47	0/2121	0.89	0/2852
4	D	0.47	0/1586	0.86	0/2134
5	E	0.46	0/1571	1.01	0/2113
6	F	0.51	0/1434	1.00	2/1926 (0.1%)
7	G	0.50	0/1333	0.91	0/1805
8	H	0.56	0/1122	1.00	1/1515 (0.1%)
9	I	0.64	0/993	1.05	0/1340
10	J	0.65	0/998	1.13	1/1348 (0.1%)
11	K	0.52	0/1152	0.97	0/1551
12	L	0.48	0/955	0.90	0/1279
13	M	0.48	0/1062	0.95	0/1413
14	N	0.49	0/1093	0.93	0/1460
15	O	0.48	0/964	1.04	0/1289
16	P	0.47	0/902	1.03	0/1209
17	Q	0.44	0/929	0.82	0/1242
18	R	0.57	0/960	1.05	0/1278
19	S	0.48	0/829	0.77	0/1107
20	T	0.49	0/864	1.01	0/1156
21	U	0.43	0/752	0.89	0/1005
22	V	0.46	0/796	0.84	0/1062
23	W	0.45	0/766	0.85	0/1025
24	X	0.41	0/589	0.78	0/779
25	Y	0.44	0/635	0.83	0/848
26	Z	0.39	0/502	1.06	0/667
27	0	0.42	0/452	0.88	0/605
28	1	0.50	0/531	0.97	0/709
29	2	0.45	0/450	0.85	0/599
30	3	0.44	0/433	0.78	0/576
31	4	0.54	0/380	1.04	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	5	0.45	0/513	1.02	1/676 (0.1%)
33	6	0.42	0/303	0.91	0/397
34	a	0.37	1/36590 (0.0%)	0.69	5/57074 (0.0%)
35	b	0.53	0/1791	1.02	0/2413
36	c	0.51	0/1663	0.97	0/2241
37	d	0.49	0/1665	1.04	3/2227 (0.1%)
38	e	0.54	0/1165	1.04	2/1568 (0.1%)
39	f	0.50	0/867	0.96	0/1171
40	g	0.53	0/1206	1.10	1/1617 (0.1%)
41	h	0.51	0/989	0.96	0/1326
42	i	0.53	0/1034	1.01	0/1375
43	j	0.52	0/800	0.96	1/1082 (0.1%)
44	k	0.47	0/893	0.96	0/1205
45	l	0.48	0/960	0.89	0/1286
46	m	0.54	0/909	1.12	0/1215
47	n	0.48	0/817	1.09	1/1088 (0.1%)
48	o	0.49	0/722	1.12	0/964
49	p	0.51	0/659	0.92	0/884
50	q	0.52	0/657	0.86	0/881
51	r	0.49	0/553	1.01	0/743
52	s	0.52	0/680	0.94	0/915
53	t	0.46	0/675	1.16	0/895
54	u	0.46	0/597	1.07	0/792
55	v	0.49	0/2898	1.02	3/3904 (0.1%)
56	w	0.45	0/383	0.77	0/504
57	x	0.37	0/1835	0.76	4/2859 (0.1%)
57	y	0.38	0/1832	0.70	1/2855 (0.0%)
58	z	0.36	0/122	0.66	0/188
All	All	0.42	1/163112 (0.0%)	0.79	55/243334 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	a	527	G7M	O3'-P	5.36	1.61	1.56

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	2820	A	C4'-C3'-O3'	-8.25	100.62	113.00
1	A	2146	C	C4'-C3'-O3'	7.84	121.16	109.40
1	A	2225	A	C4'-C3'-O3'	7.77	121.06	109.40
1	A	2425	A	C2'-C3'-O3'	7.66	120.98	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
34	a	428	G	C4'-C3'-O3'	7.35	120.42	109.40

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	A	62356	0	31381	646	0
2	B	2569	0	1301	10	0
3	C	2082	0	2154	28	0
4	D	1565	0	1616	25	0
5	E	1552	0	1619	18	0
6	F	1410	0	1444	7	0
7	G	1313	0	1358	5	0
8	H	1111	0	1148	8	0
9	I	980	0	1013	10	0
10	J	984	0	1035	12	0
11	K	1129	0	1162	9	0
12	L	946	0	1023	17	0
13	M	1053	0	1129	23	0
14	N	1074	0	1157	14	0
15	O	951	0	994	15	0
16	P	892	0	923	5	0
17	Q	917	0	962	3	0
18	R	947	0	1019	20	0
19	S	816	0	839	5	0
20	T	857	0	922	13	0
21	U	746	0	811	4	0
22	V	788	0	844	7	0
23	W	753	0	780	1	0
24	X	582	0	599	5	0
25	Y	625	0	652	8	0
26	Z	501	0	531	3	0
27	0	448	0	488	8	0
28	1	522	0	522	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	2	444	0	458	7	0
30	3	426	0	464	3	0
31	4	377	0	418	8	0
32	5	504	0	572	8	0
33	6	302	0	340	2	0
34	a	32929	0	16587	282	0
35	b	1760	0	1787	6	0
36	c	1636	0	1710	6	0
37	d	1643	0	1707	10	0
38	e	1152	0	1196	9	0
39	f	848	0	846	9	0
40	g	1191	0	1245	11	0
41	h	979	0	1031	4	0
42	i	1022	0	1070	13	0
43	j	790	0	831	8	0
44	k	877	0	887	8	0
45	l	957	0	1018	16	0
46	m	900	0	965	10	0
47	n	805	0	844	8	0
48	o	714	0	734	4	0
49	p	649	0	666	3	0
50	q	648	0	691	6	0
51	r	544	0	560	6	0
52	s	663	0	688	5	0
53	t	669	0	719	4	0
54	u	589	0	629	5	0
55	v	2869	0	2771	34	0
56	w	377	0	393	4	0
57	x	1643	0	836	17	0
57	y	1640	0	837	24	0
58	z	109	0	55	0	0
59	2	1	0	0	0	0
59	A	230	0	0	0	0
59	B	5	0	0	0	0
59	C	1	0	0	0	0
59	D	1	0	0	0	0
59	O	2	0	0	0	0
59	a	71	0	0	0	0
59	d	1	0	0	0	0
59	n	1	0	0	0	0
59	x	4	0	0	0	0
60	1	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	6	1	0	0	0	0
61	C	2	0	0	0	0
All	All	151446	0	102981	1310	0

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

The worst 5 of 1310 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)
34:a:530:G:H2'	55:v:213:ARG:HH22	1.06	1.10
1:A:2028:U:H2'	1:A:2029:G:H5'	1.29	1.09
1:A:2028:U:C2'	1:A:2029:G:H5'	1.85	1.05
1:A:1353:A:C8	1:A:1378:A:N6	2.25	1.05
57:y:17:C:H4'	57:y:18:U:H5"	1.35	1.03

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
3	C	269/273 (98%)	257 (96%)	11 (4%)	1 (0%)	30 60
4	D	207/209 (99%)	200 (97%)	5 (2%)	2 (1%)	12 42
5	E	199/201 (99%)	193 (97%)	6 (3%)	0	100 100
6	F	175/177 (99%)	165 (94%)	9 (5%)	1 (1%)	21 53
7	G	173/177 (98%)	164 (95%)	8 (5%)	1 (1%)	21 53
8	H	147/149 (99%)	134 (91%)	13 (9%)	0	100 100
9	I	128/165 (78%)	103 (80%)	21 (16%)	4 (3%)	3 19
10	J	133/142 (94%)	119 (90%)	12 (9%)	2 (2%)	8 34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	K	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
12	L	121/123 (98%)	115 (95%)	6 (5%)	0	100	100
13	M	142/144 (99%)	134 (94%)	7 (5%)	1 (1%)	18	50
14	N	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
15	O	117/127 (92%)	106 (91%)	11 (9%)	0	100	100
16	P	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
17	Q	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
18	R	115/118 (98%)	111 (96%)	3 (3%)	1 (1%)	14	44
19	S	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
20	T	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
21	U	92/100 (92%)	92 (100%)	0	0	100	100
22	V	101/104 (97%)	95 (94%)	5 (5%)	1 (1%)	12	42
23	W	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
24	X	74/85 (87%)	69 (93%)	5 (7%)	0	100	100
25	Y	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
26	Z	60/63 (95%)	59 (98%)	1 (2%)	0	100	100
27	0	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	6	31
28	1	64/70 (91%)	61 (95%)	3 (5%)	0	100	100
29	2	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
30	3	50/52 (96%)	50 (100%)	0	0	100	100
31	4	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
32	5	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
33	6	36/38 (95%)	36 (100%)	0	0	100	100
35	b	223/241 (92%)	213 (96%)	10 (4%)	0	100	100
36	c	206/233 (88%)	194 (94%)	10 (5%)	2 (1%)	12	42
37	d	203/206 (98%)	197 (97%)	6 (3%)	0	100	100
38	e	154/167 (92%)	145 (94%)	9 (6%)	0	100	100
39	f	102/135 (76%)	99 (97%)	2 (2%)	1 (1%)	12	42
40	g	150/179 (84%)	145 (97%)	3 (2%)	2 (1%)	9	37
41	h	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
42	i	125/130 (96%)	118 (94%)	5 (4%)	2 (2%)	7	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
43	j	97/103 (94%)	93 (96%)	3 (3%)	1 (1%)	12 42
44	k	115/129 (89%)	106 (92%)	8 (7%)	1 (1%)	14 44
45	l	120/124 (97%)	115 (96%)	5 (4%)	0	100 100
46	m	114/118 (97%)	109 (96%)	5 (4%)	0	100 100
47	n	98/101 (97%)	97 (99%)	1 (1%)	0	100 100
48	o	86/89 (97%)	83 (96%)	3 (4%)	0	100 100
49	p	80/82 (98%)	78 (98%)	2 (2%)	0	100 100
50	q	78/84 (93%)	74 (95%)	4 (5%)	0	100 100
51	r	64/66 (97%)	63 (98%)	1 (2%)	0	100 100
52	s	81/92 (88%)	79 (98%)	2 (2%)	0	100 100
53	t	84/87 (97%)	84 (100%)	0	0	100 100
54	u	68/71 (96%)	67 (98%)	1 (2%)	0	100 100
55	v	359/384 (94%)	346 (96%)	11 (3%)	2 (1%)	21 53
56	w	44/57 (77%)	40 (91%)	4 (9%)	0	100 100
All	All	6273/6647 (94%)	5984 (95%)	263 (4%)	26 (0%)	31 60

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	R	3	ARG
42	i	56	ASP
43	j	57	VAL
4	D	149	ASN
6	F	62	GLY

5.3.2 Protein sidechains (i)

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
3	C	216/218 (99%)	194 (90%)	22 (10%)	7 27
4	D	164/164 (100%)	149 (91%)	15 (9%)	9 31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	165/165 (100%)	145 (88%)	20 (12%)	5	21
6	F	148/148 (100%)	130 (88%)	18 (12%)	5	21
7	G	136/138 (99%)	125 (92%)	11 (8%)	11	37
8	H	114/114 (100%)	98 (86%)	16 (14%)	3	16
9	I	99/123 (80%)	87 (88%)	12 (12%)	5	21
10	J	104/110 (94%)	94 (90%)	10 (10%)	8	30
11	K	116/116 (100%)	104 (90%)	12 (10%)	7	27
12	L	104/104 (100%)	93 (89%)	11 (11%)	6	26
13	M	103/103 (100%)	92 (89%)	11 (11%)	6	25
14	N	109/109 (100%)	95 (87%)	14 (13%)	4	19
15	O	99/103 (96%)	93 (94%)	6 (6%)	17	47
16	P	86/87 (99%)	81 (94%)	5 (6%)	18	48
17	Q	99/100 (99%)	88 (89%)	11 (11%)	6	24
18	R	89/90 (99%)	79 (89%)	10 (11%)	6	24
19	S	84/84 (100%)	78 (93%)	6 (7%)	13	42
20	T	93/93 (100%)	87 (94%)	6 (6%)	15	45
21	U	81/84 (96%)	72 (89%)	9 (11%)	6	24
22	V	84/85 (99%)	74 (88%)	10 (12%)	5	22
23	W	78/78 (100%)	73 (94%)	5 (6%)	16	45
24	X	58/63 (92%)	53 (91%)	5 (9%)	10	34
25	Y	67/68 (98%)	67 (100%)	0	100	100
26	Z	54/55 (98%)	52 (96%)	2 (4%)	30	59
27	0	48/49 (98%)	45 (94%)	3 (6%)	16	46
28	1	59/62 (95%)	56 (95%)	3 (5%)	21	52
29	2	47/48 (98%)	46 (98%)	1 (2%)	47	69
30	3	47/47 (100%)	44 (94%)	3 (6%)	16	45
31	4	38/38 (100%)	35 (92%)	3 (8%)	11	38
32	5	51/52 (98%)	48 (94%)	3 (6%)	18	48
33	6	34/34 (100%)	32 (94%)	2 (6%)	18	48
35	b	187/199 (94%)	173 (92%)	14 (8%)	12	40
36	c	171/190 (90%)	159 (93%)	12 (7%)	14	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
37	d	172/173 (99%)	159 (92%)	13 (8%)	12 39
38	e	119/126 (94%)	104 (87%)	15 (13%)	4 20
39	f	91/116 (78%)	78 (86%)	13 (14%)	3 15
40	g	125/147 (85%)	111 (89%)	14 (11%)	6 24
41	h	104/105 (99%)	94 (90%)	10 (10%)	8 30
42	i	105/107 (98%)	99 (94%)	6 (6%)	18 49
43	j	86/90 (96%)	69 (80%)	17 (20%)	1 7
44	k	90/99 (91%)	79 (88%)	11 (12%)	5 21
45	l	102/103 (99%)	87 (85%)	15 (15%)	3 14
46	m	94/96 (98%)	82 (87%)	12 (13%)	4 19
47	n	83/84 (99%)	74 (89%)	9 (11%)	6 25
48	o	76/77 (99%)	59 (78%)	17 (22%)	1 4
49	p	65/65 (100%)	59 (91%)	6 (9%)	8 31
50	q	74/78 (95%)	65 (88%)	9 (12%)	5 21
51	r	57/57 (100%)	55 (96%)	2 (4%)	32 60
52	s	72/79 (91%)	65 (90%)	7 (10%)	8 30
53	t	65/66 (98%)	55 (85%)	10 (15%)	2 13
54	u	60/61 (98%)	53 (88%)	7 (12%)	5 22
55	v	307/324 (95%)	284 (92%)	23 (8%)	12 40
56	w	39/46 (85%)	38 (97%)	1 (3%)	40 65
All	All	5218/5420 (96%)	4710 (90%)	508 (10%)	10 30

5 of 508 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	V	59	VAL
49	p	6	LEU
36	c	144	LEU
48	o	73	LYS
53	t	54	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 79 such sidechains are listed below:

Mol	Chain	Res	Type
42	i	50	GLN
53	t	13	GLN
42	i	126	GLN
49	p	59	HIS
55	v	253	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2903/2904 (99%)	562 (19%)	75 (2%)
2	B	119/120 (99%)	17 (14%)	1 (0%)
34	a	1531/1534 (99%)	294 (19%)	0
57	x	76/77 (98%)	21 (27%)	0
57	y	76/77 (98%)	19 (25%)	0
58	z	4/18 (22%)	1 (25%)	0
All	All	4709/4730 (99%)	914 (19%)	76 (1%)

5 of 914 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	10	A
1	A	14	A
1	A	15	G
1	A	23	G
1	A	34	U

5 of 76 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1900	A
1	A	2797	U
1	A	2062	A
1	A	2225	A
2	B	87	U

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
34	UR3	a	1498	34	19,22,23	1.19	1 (5%)	26,32,35	1.96	4 (15%)
1	5MU	A	1939	1,59	19,22,23	1.53	6 (31%)	27,32,35	2.37	8 (29%)
34	5MC	a	967	34	19,22,23	1.93	2 (10%)	26,32,35	1.36	4 (15%)
1	PSU	A	1911	1	18,21,22	1.40	2 (11%)	21,30,33	2.00	4 (19%)
1	PSU	A	1917	1	18,21,22	1.41	2 (11%)	21,30,33	2.16	4 (19%)
1	PSU	A	2504	1	18,21,22	1.49	3 (16%)	21,30,33	2.01	4 (19%)
34	2MG	a	1207	34	23,26,27	1.32	4 (17%)	33,38,41	2.27	7 (21%)
1	6MZ	A	2030	1	22,25,26	0.78	0	29,36,39	1.62	6 (20%)
34	MA6	a	1518	34	23,26,27	1.63	5 (21%)	33,38,41	2.31	11 (33%)
34	MA6	a	1519	34	23,26,27	1.67	4 (17%)	33,38,41	2.35	11 (33%)
1	PSU	A	2457	1	18,21,22	1.51	3 (16%)	21,30,33	2.15	5 (23%)
1	OMU	A	2552	1	19,22,23	1.29	3 (15%)	25,31,34	2.02	6 (24%)
1	2MG	A	1835	1	23,26,27	1.33	4 (17%)	33,38,41	2.31	8 (24%)
1	PSU	A	2605	1	18,21,22	1.47	3 (16%)	21,30,33	2.15	5 (23%)
34	2MG	a	1516	34	23,26,27	1.30	4 (17%)	33,38,41	2.28	9 (27%)
34	4OC	a	1402	34	20,23,24	0.85	1 (5%)	25,32,35	1.36	5 (20%)
1	5MC	A	1962	1	19,22,23	1.87	3 (15%)	26,32,35	1.39	4 (15%)
1	PSU	A	746	1,59	18,21,22	1.40	3 (16%)	21,30,33	2.11	4 (19%)
34	G7M	a	527	34	23,26,27	2.37	5 (21%)	34,39,42	3.12	12 (35%)
1	1MG	A	745	1	23,26,27	1.18	4 (17%)	33,39,42	1.85	7 (21%)
34	2MG	a	966	34	23,26,27	1.29	4 (17%)	33,38,41	2.24	6 (18%)
1	OMC	A	2498	1,59	19,22,23	0.85	0	25,31,34	1.05	2 (8%)
1	2MA	A	2503	1,59	22,25,26	1.28	5 (22%)	32,37,40	2.43	10 (31%)
1	2MG	A	2445	1	23,26,27	1.36	4 (17%)	33,38,41	2.12	7 (21%)
1	5MU	A	747	1	19,22,23	1.48	6 (31%)	27,32,35	2.18	7 (25%)
1	OMG	A	2251	1,57	23,26,27	1.25	3 (13%)	32,38,41	2.02	5 (15%)
34	PSU	a	516	34,59	18,21,22	1.41	2 (11%)	21,30,33	2.22	4 (19%)
1	6MZ	A	1618	1	22,25,26	0.73	0	29,36,39	1.40	3 (10%)
1	PSU	A	2580	1	18,21,22	1.52	3 (16%)	21,30,33	2.19	6 (28%)
55	MEQ	v	252	55	8,9,10	0.45	0	5,10,12	0.42	0
45	0TD	l	89	45	8,9,10	8.17	6 (75%)	6,11,13	4.49	4 (66%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	PSU	A	955	1	18,21,22	1.51	2 (11%)	21,30,33	2.39	4 (19%)
1	G7M	A	2069	1	23,26,27	0.90	1 (4%)	34,39,42	2.13	7 (20%)
1	3TD	A	1915	1	19,22,23	2.31	5 (26%)	23,32,35	9.01	6 (26%)
34	5MC	a	1407	34	19,22,23	1.63	2 (10%)	26,32,35	1.30	4 (15%)

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
34	UR3	a	1498	34	-	0/7/25/26	0/2/2/2
1	5MU	A	1939	1,59	-	2/7/25/26	0/2/2/2
34	5MC	a	967	34	-	0/7/25/26	0/2/2/2
1	PSU	A	1911	1	-	0/7/25/26	0/2/2/2
1	PSU	A	1917	1	-	0/7/25/26	0/2/2/2
1	PSU	A	2504	1	-	2/7/25/26	0/2/2/2
34	2MG	a	1207	34	-	0/9/27/28	0/3/3/3
1	6MZ	A	2030	1	-	2/9/27/28	0/3/3/3
34	MA6	a	1518	34	-	2/11/29/30	0/3/3/3
34	MA6	a	1519	34	-	5/11/29/30	0/3/3/3
1	PSU	A	2457	1	-	0/7/25/26	0/2/2/2
1	OMU	A	2552	1	-	0/9/27/28	0/2/2/2
1	2MG	A	1835	1	-	0/9/27/28	0/3/3/3
1	PSU	A	2605	1	-	0/7/25/26	0/2/2/2
34	2MG	a	1516	34	-	0/9/27/28	0/3/3/3
34	4OC	a	1402	34	-	1/9/29/30	0/2/2/2
1	5MC	A	1962	1	-	0/7/25/26	0/2/2/2
1	PSU	A	746	1,59	-	2/7/25/26	0/2/2/2
34	G7M	a	527	34	-	1/7/25/26	0/3/3/3
1	1MG	A	745	1	-	0/7/25/26	0/3/3/3
34	2MG	a	966	34	-	0/9/27/28	0/3/3/3
1	OMC	A	2498	1,59	-	2/9/27/28	0/2/2/2
1	2MA	A	2503	1,59	-	0/7/25/26	0/3/3/3
1	2MG	A	2445	1	-	2/9/27/28	0/3/3/3
1	5MU	A	747	1	-	0/7/25/26	0/2/2/2
1	OMG	A	2251	1,57	-	0/9/27/28	0/3/3/3
34	PSU	a	516	34,59	-	0/7/25/26	0/2/2/2
1	6MZ	A	1618	1	-	4/9/27/28	0/3/3/3
1	PSU	A	2580	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	MEQ	v	252	55	-	2/8/9/11	-
45	0TD	l	89	45	-	3/7/12/14	-
1	PSU	A	955	1	-	0/7/25/26	0/2/2/2
1	G7M	A	2069	1	-	2/7/25/26	0/3/3/3
1	3TD	A	1915	1	-	2/7/25/26	0/2/2/2
34	5MC	a	1407	34	-	0/7/25/26	0/2/2/2

The worst 5 of 105 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	l	89	0TD	CB-SB	-17.26	1.64	1.82
45	l	89	0TD	CB-CA	-14.22	1.50	1.54
34	a	527	G7M	C8-N7	7.61	1.46	1.33
1	A	1915	3TD	C6-C5	-7.14	1.27	1.35
1	A	1962	5MC	C5-C4	7.08	1.49	1.44

The worst 5 of 203 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1915	3TD	C5-C6-N1	29.84	163.57	122.14
1	A	1915	3TD	C6-C5-C4	-27.14	100.00	118.19
1	A	1915	3TD	C1'-C5-C4	9.78	132.45	117.61
1	A	1915	3TD	C6-N1-C2	-9.70	97.10	121.80
34	a	527	G7M	CN7-N7-C8	-9.09	111.02	124.79

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1618	6MZ	C5-C6-N6-C9
1	A	1618	6MZ	N1-C6-N6-C9
1	A	1618	6MZ	O4'-C4'-C5'-O5'
1	A	1618	6MZ	C3'-C4'-C5'-O5'
1	A	1915	3TD	O4'-C1'-C5-C4

There are no ring outliers.

14 monomers are involved in 36 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1939	5MU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	2030	6MZ	4	0
34	a	1518	MA6	3	0
34	a	1519	MA6	3	0
1	A	2552	OMU	2	0
34	a	527	G7M	3	0
1	A	2498	OMC	2	0
1	A	747	5MU	1	0
1	A	2251	OMG	1	0
1	A	1618	6MZ	1	0
1	A	2580	PSU	1	0
45	l	89	0TD	7	0
1	A	2069	G7M	12	0
1	A	1915	3TD	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 319 ligands modelled in this entry, 319 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

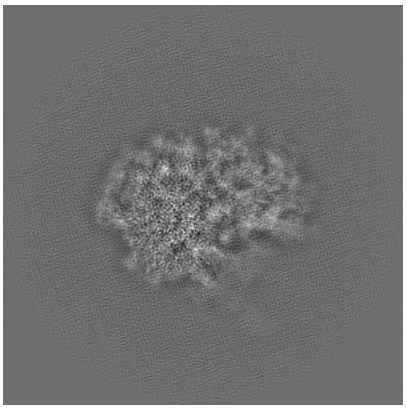
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-7341. These allow visual inspection of the internal detail of the map and identification of artifacts.

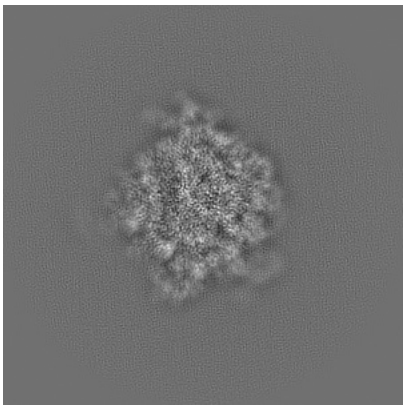
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

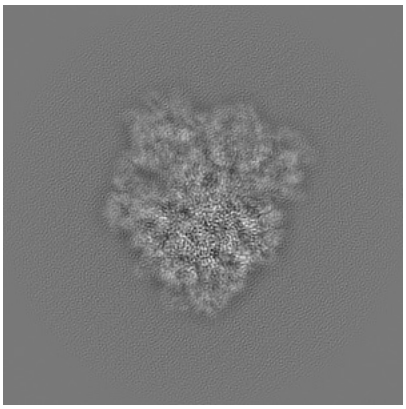
6.1.1 Primary map



X

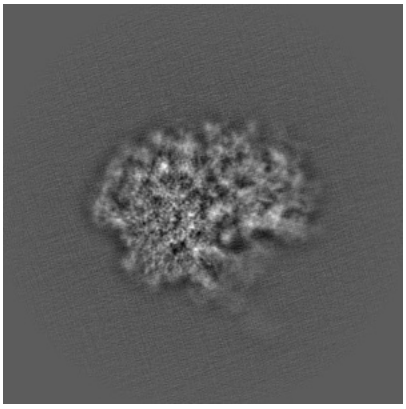


Y

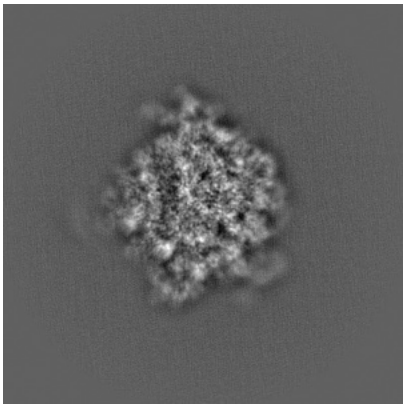


Z

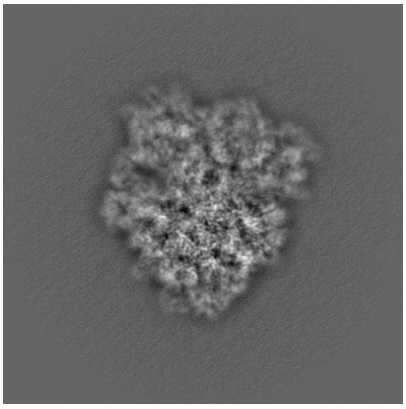
6.1.2 Raw map



X



Y

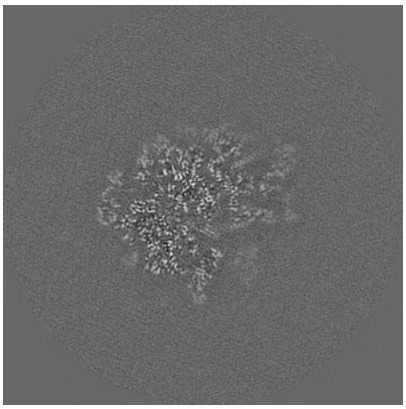


Z

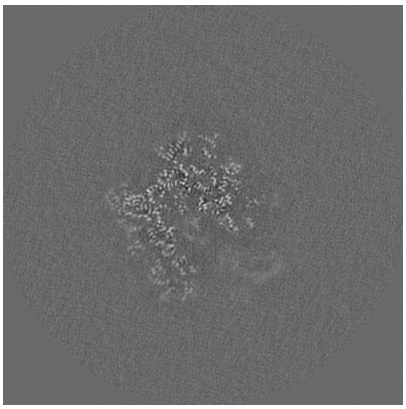
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

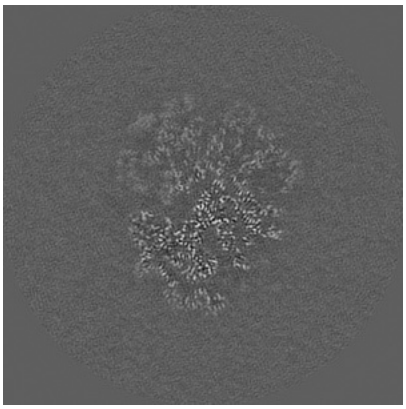
6.2.1 Primary map



X Index: 192

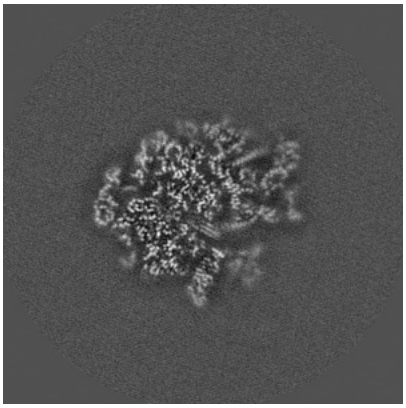


Y Index: 192

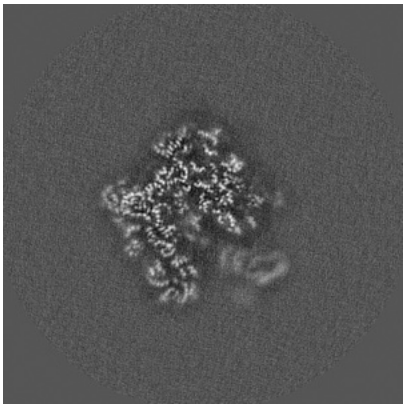


Z Index: 192

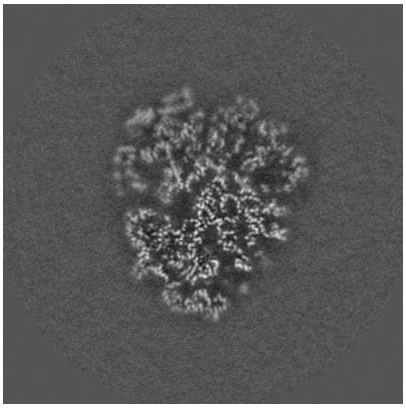
6.2.2 Raw map



X Index: 192



Y Index: 192

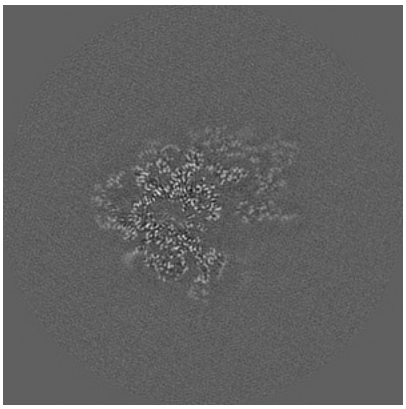


Z Index: 192

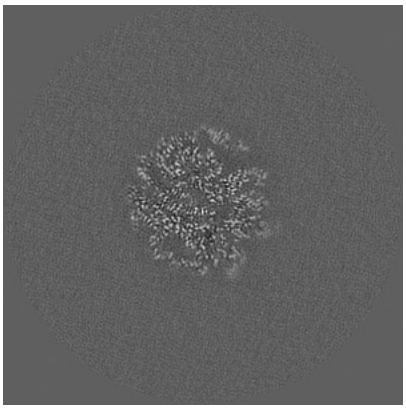
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

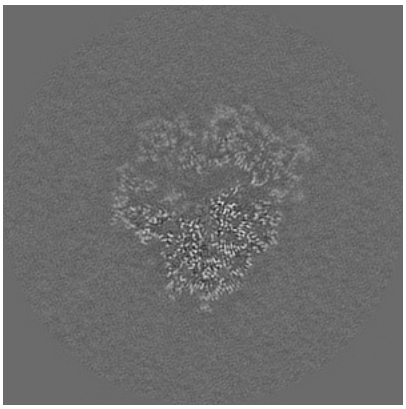
6.3.1 Primary map



X Index: 198

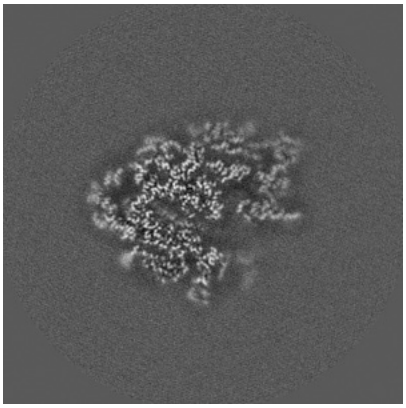


Y Index: 158

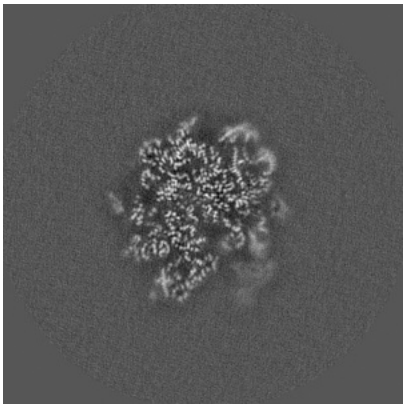


Z Index: 176

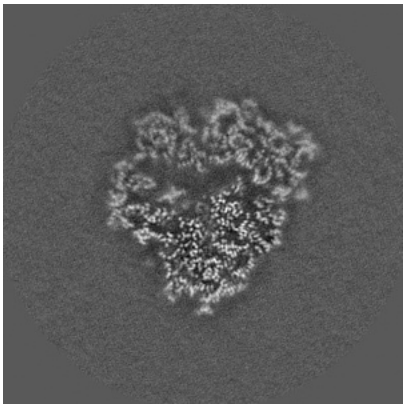
6.3.2 Raw map



X Index: 198



Y Index: 177

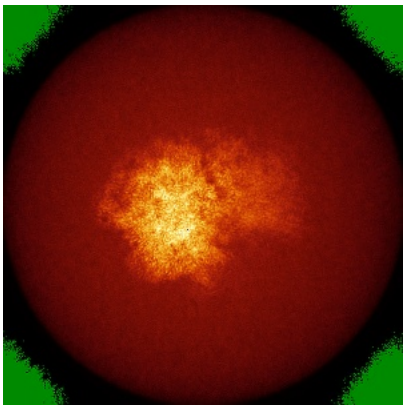


Z Index: 176

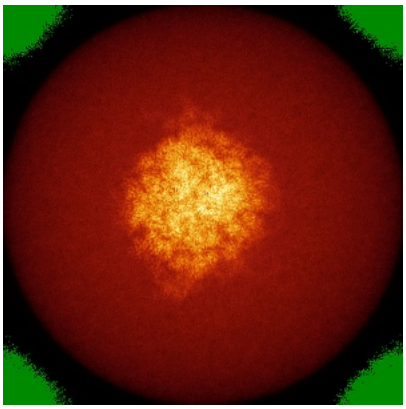
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

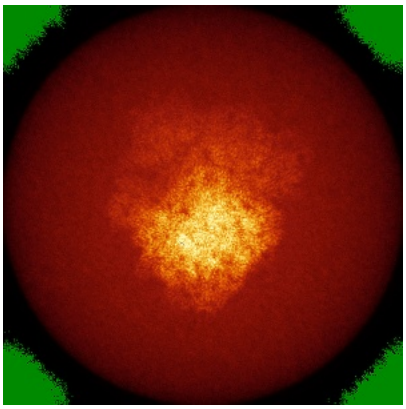
6.4.1 Primary map



X

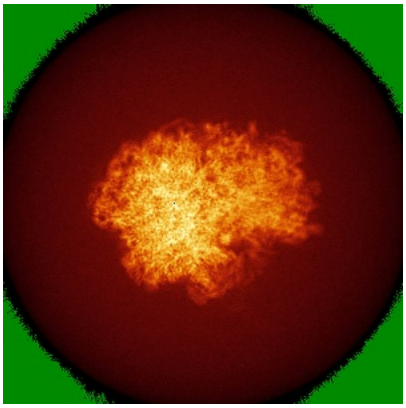


Y

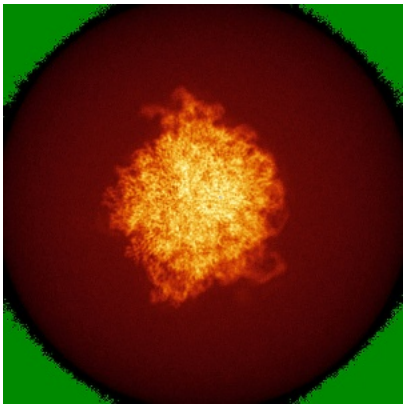


Z

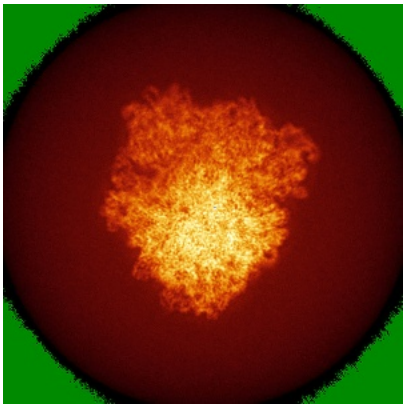
6.4.2 Raw map



X



Y

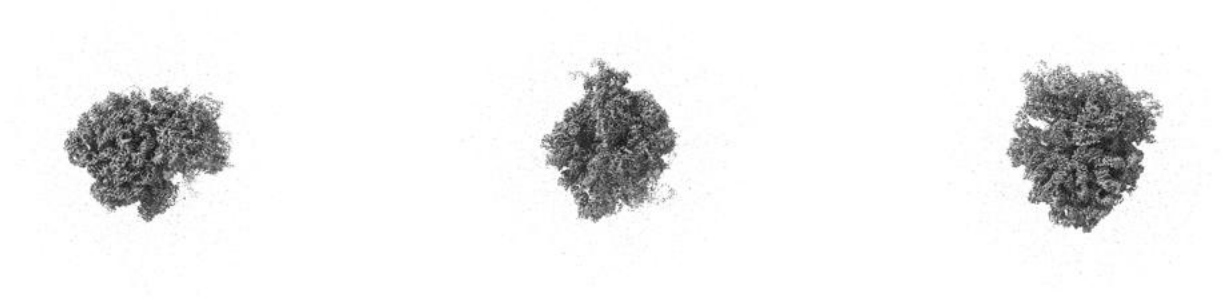


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

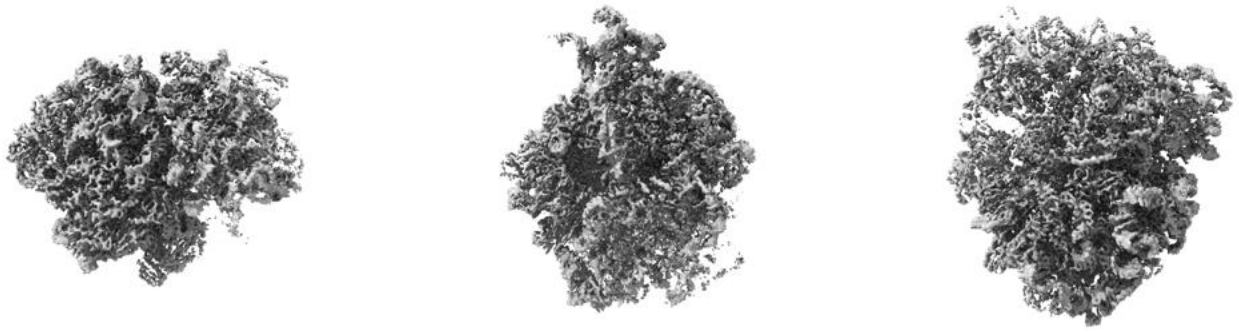
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

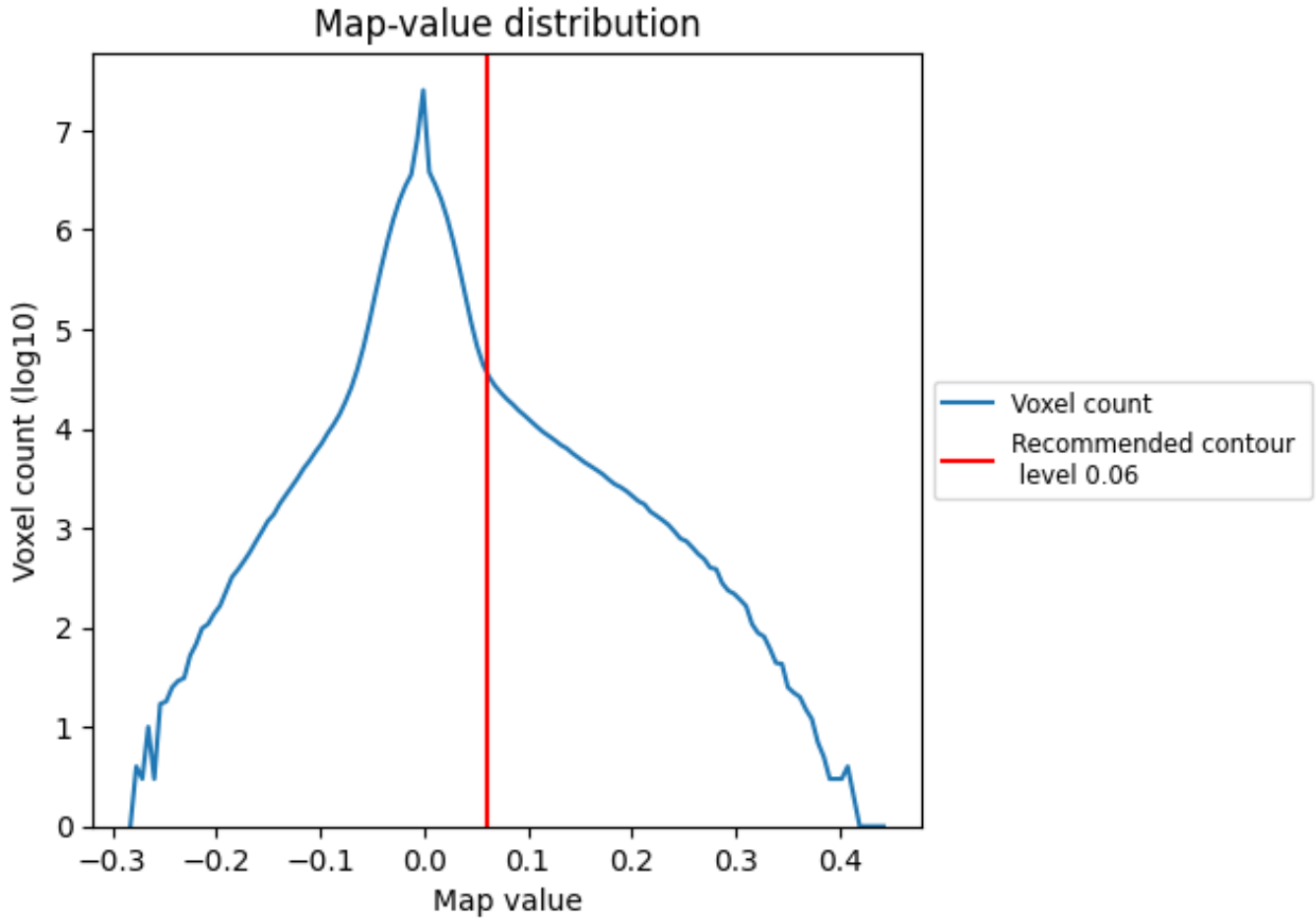
6.6 Mask visualisation (i)

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

7 Map analysis

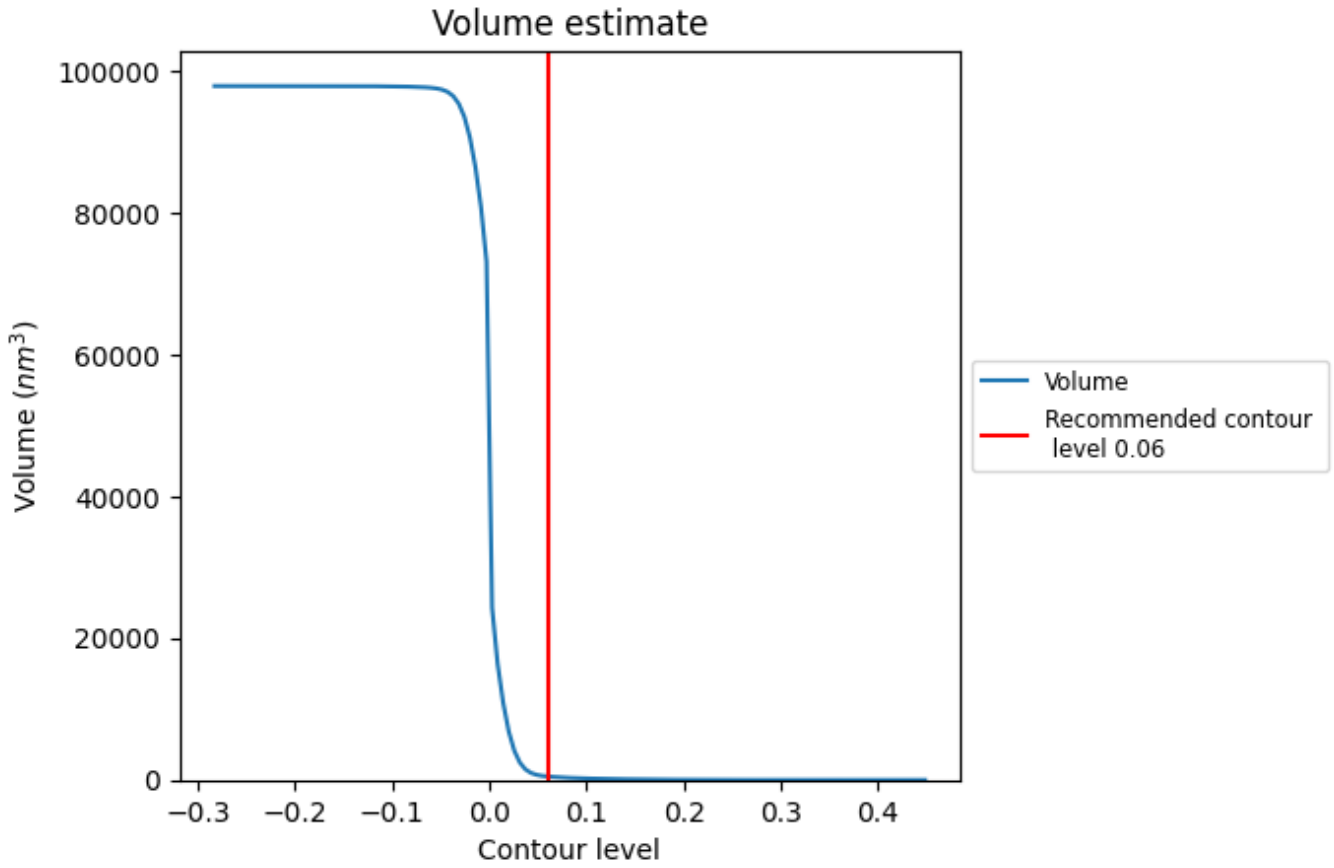
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

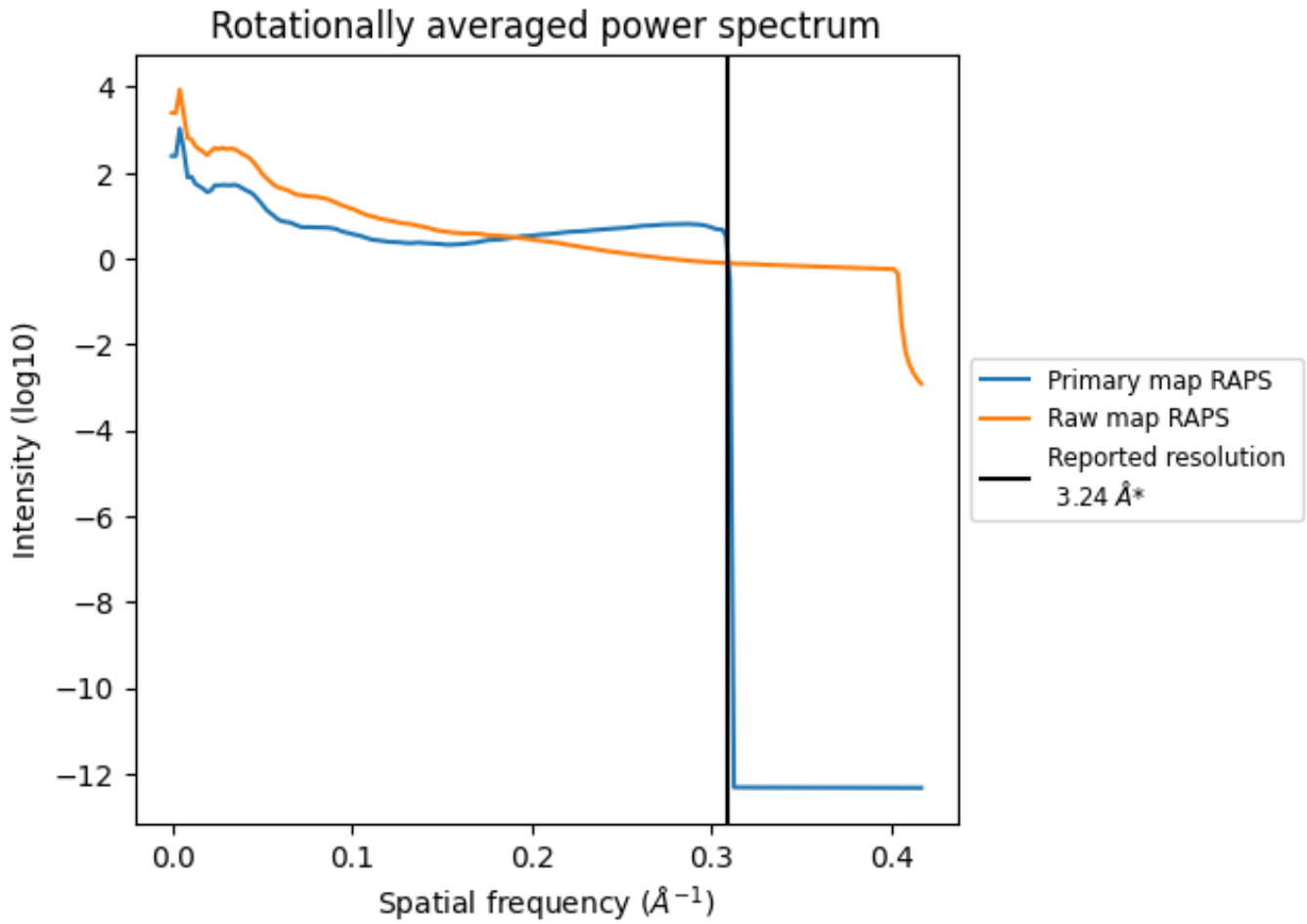
7.2 Volume estimate (i)



The volume at the recommended contour level is 487 nm^3; this corresponds to an approximate mass of 440 kDa.

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

7.3 Rotationally averaged power spectrum (i)

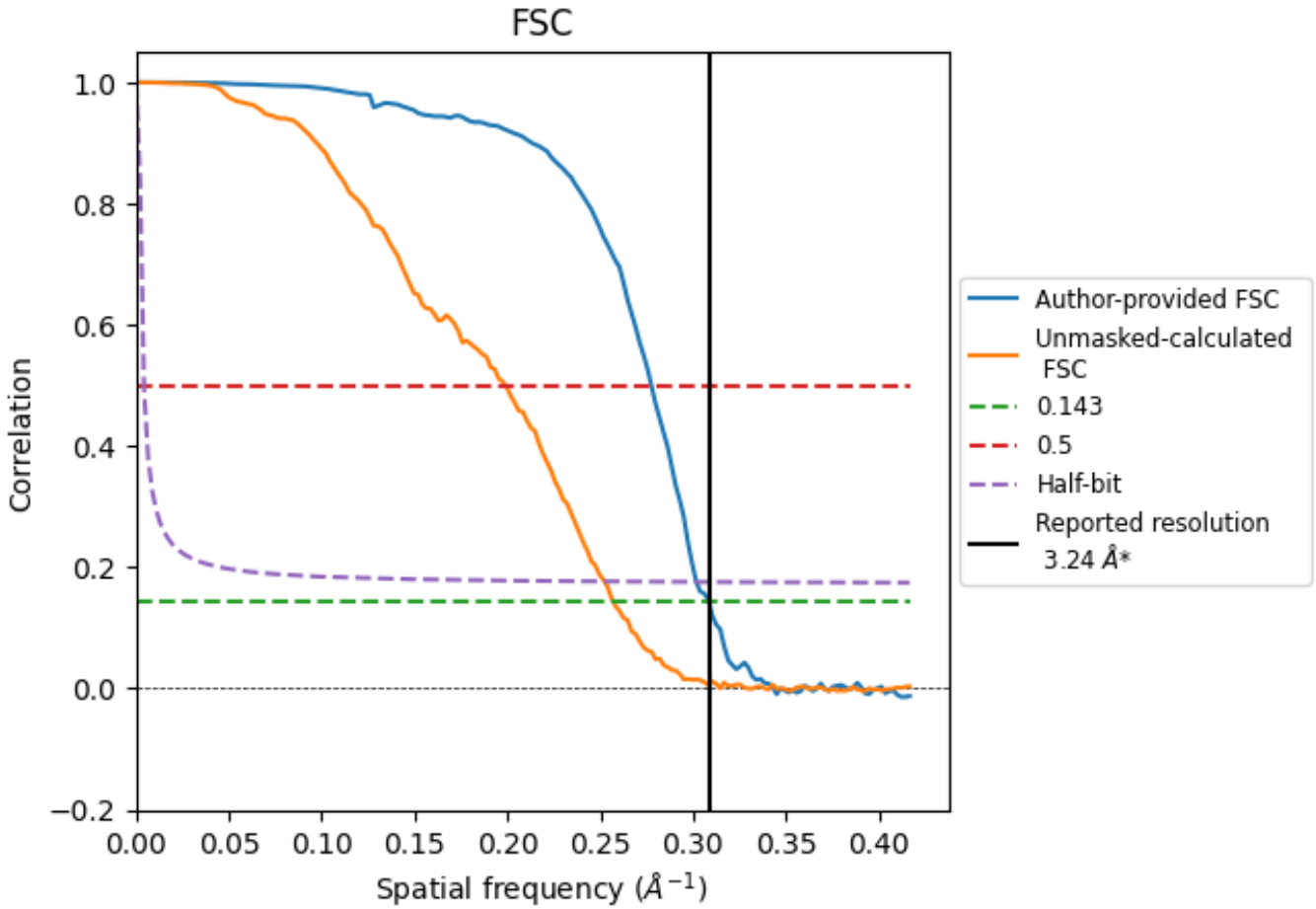


*Reported resolution corresponds to spatial frequency of 0.309 $Å^{-1}$

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.309 Å^{-1}

8.2 Resolution estimates (i)

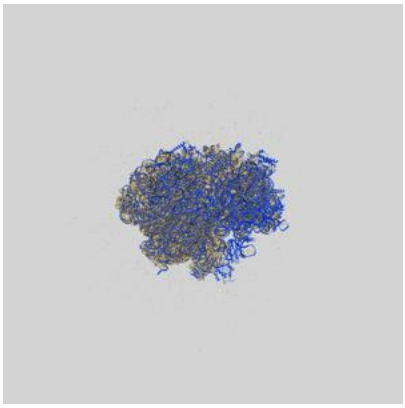
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.24	-	-
Author-provided FSC curve	3.24	3.60	3.31
Unmasked-calculated*	3.89	5.03	3.96

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.89 differs from the reported value 3.24 by more than 10 %

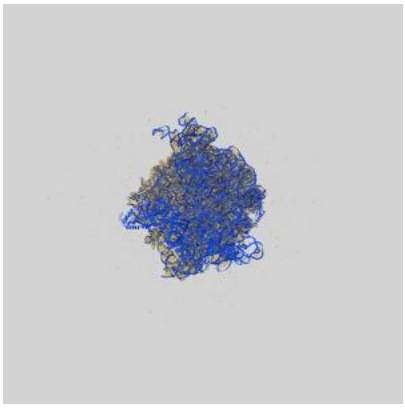
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-7341 and PDB model 6C4I. Per-residue inclusion information can be found in section 3 on page 17.

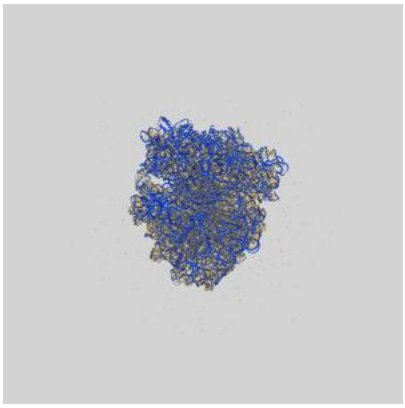
9.1 Map-model overlay



X



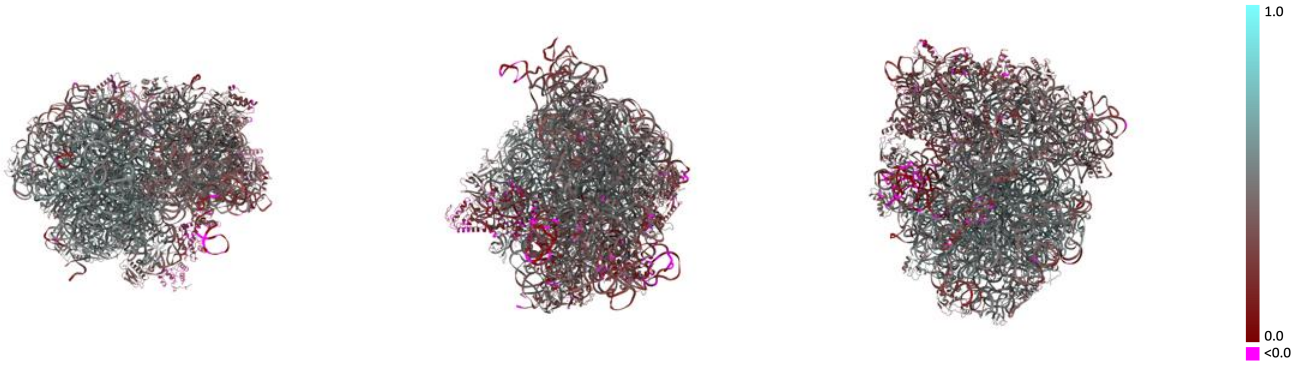
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06 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.

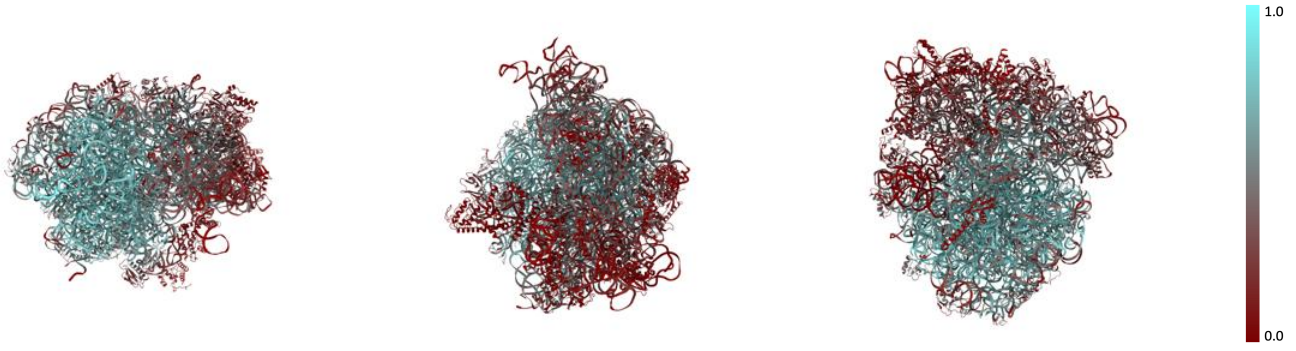
9.2 Q-score mapped to coordinate model



X Y Z

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.

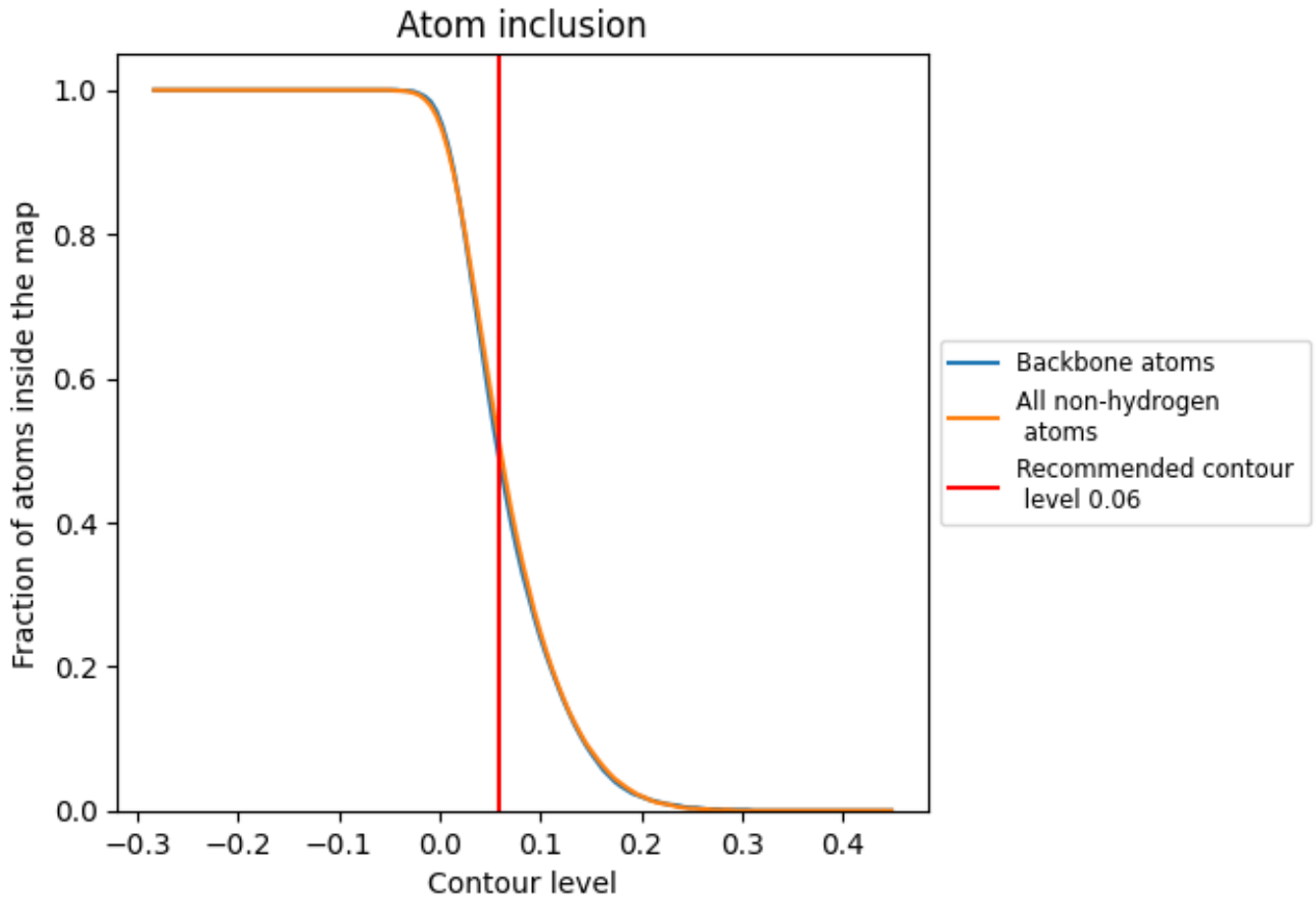
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.06).

9.4 Atom inclusion (i)



At the recommended contour level, 48% of all backbone atoms, 50% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5040	0.4320
0	0.6280	0.4970
1	0.0960	0.2600
2	0.6430	0.5010
3	0.5140	0.4540
4	0.6840	0.5350
5	0.6740	0.5390
6	0.6310	0.5260
A	0.6860	0.4760
B	0.5220	0.4180
C	0.6600	0.5220
D	0.6160	0.5120
E	0.4700	0.4500
F	0.2170	0.3670
G	0.3540	0.3980
H	0.1090	0.2400
I	0.0000	0.0840
J	0.0030	0.0930
K	0.6550	0.5060
L	0.5970	0.5110
M	0.5750	0.4820
N	0.6290	0.5110
O	0.6520	0.5200
P	0.3740	0.4260
Q	0.5730	0.4910
R	0.6870	0.5210
S	0.5870	0.4950
T	0.6160	0.5060
U	0.4860	0.4570
V	0.4200	0.4400
W	0.5540	0.4630
X	0.6240	0.5130
Y	0.5840	0.4980
Z	0.4190	0.4260
a	0.4220	0.4130



Continued on next page...

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Chain	Atom inclusion	Q-score
b	0.1020	0.2890
c	0.1420	0.3450
d	0.1090	0.3380
e	0.2470	0.3960
f	0.3010	0.3780
g	0.1670	0.3090
h	0.2600	0.4010
i	0.0950	0.3210
j	0.0560	0.2800
k	0.3810	0.4260
l	0.3740	0.4500
m	0.1510	0.3300
n	0.1030	0.3430
o	0.3940	0.4060
p	0.2310	0.3920
q	0.2550	0.3990
r	0.2870	0.3540
s	0.1240	0.3480
t	0.2690	0.3820
u	0.1750	0.3240
v	0.1910	0.3170
w	0.3920	0.4690
x	0.4230	0.3990
y	0.0290	0.1220
z	0.3670	0.4340