wwPDB EM Validation Summary Report

Nov 11, 2026 – 10:43 AM JST

PDB ID	:	24NV / pdb_000024nv
EMDB ID	:	EMD-69708
Title	:	P-tRNA bound M. smegmatis 70S ribosome
Authors	:	Sengupta, J.; Dhur, A.; Baid, P.; Srinivasan, K.
Deposited on	:	2026-03-12
Resolution	:	3.90 Å(reported)
Based on initial model	:	5O61

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:

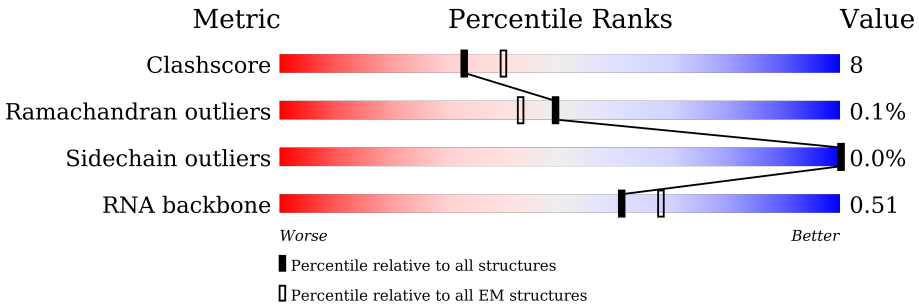
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

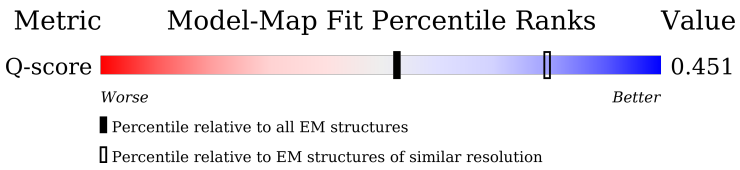
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.90 Å.

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





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	2	76	5% 55% 37% 8%
2	3	24	12% 83% 12% ·
3	4	8	25% 62% 12% 25%

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Mol	Chain	Length	Quality of chain
4	B	118	68% 27% 5%
5	C	275	12% 52% 23% 24%
6	D	201	14% 63% 36%
7	E	214	7% 64% 21% 16%
8	F	96	8% 64% 36%
9	G	156	6% 77% 22%
10	H	132	80% 19%
11	I	150	55% 29% 16%
12	J	101	22% 69% 27%
13	K	138	63% 20% 17%
14	L	124	9% 69% 29%
15	M	124	8% 61% 31% 6%
16	N	61	79% 20%
17	O	89	72% 27%
18	P	156	6% 46% 26% 28%
19	Q	98	9% 57% 39%
20	R	84	6% 65% 12% 23%
21	S	93	5% 65% 24% 12%
22	T	86	8% 64% 35%
23	U	100	8% 78% 19%
24	V	277	81% 52% 30% 18%
25	W	215	15% 73% 16% 11%
26	X	88	6% 70% 19% 10%
27	Y	64	83% 16%
28	Z	77	68% 16% 17%

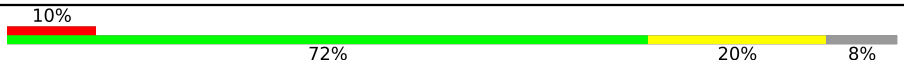
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Mol	Chain	Length	Quality of chain
29	a	61	82% 15%
30	b	57	82% 12% 5%
31	c	55	5% 64% 25% 11%
32	d	47	81% 17%
33	e	64	81% 17%
34	f	37	76% 24%
35	g	75	43% 21% 36%
36	i	278	83% 16%
37	j	217	83% 16%
38	k	215	85% 13%
39	l	187	6% 61% 36%
40	m	179	9% 76% 22%
41	n	151	56% 75% 25%
42	q	147	85% 14%
43	r	122	83% 17%
44	s	147	82% 16%
45	t	138	78% 21%
46	u	199	46% 13% 41%
47	v	127	77% 22%
48	w	113	6% 84% 16%
49	x	129	81% 15%
50	y	103	84% 13%
51	z	153	66% 8% 25%
52	o	142	92% 53% 41% 6%
53	p	175	72% 47% 25% 28%

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Mol	Chain	Length	Quality of chain
54	1	105	
55	h	3120	
56	A	1528	

2 Entry composition (i)

There are 58 unique types of molecules in this entry. The entry contains 149767 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 P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	76	1614	721	287	531	75	0	0

- Molecule 2 is a protein called 50S ribosomal protein bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	3	23	189	111	50	28	0	0

- Molecule 3 is a RNA chain called mRNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	4	8	173	78	35	52	8	0	0

- Molecule 4 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	B	118	2522	1126	468	810	118	0	0

- Molecule 5 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	C	208	1660	1036	322	298	4	0	0

- Molecule 6 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	D	200	1641	1028	316	295	2	0	0

- Molecule 7 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

- Molecule 8 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 9 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

- Molecule 10 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 11 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	I	126	Total	C	N	O	0	0
			994	630	194	170		

- Molecule 12 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	99	Total	C	N	O	S	0	0
			788	495	146	144	3		

- Molecule 13 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 14 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	122	Total 958	C 594	N 197	O 165	S 2	0	0

- Molecule 15 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	116	Total 935	C 572	N 191	O 169	S 3	0	0

- Molecule 16 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	60	Total 477	C 302	N 97	O 73	S 5	0	0

- Molecule 17 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	O	88	Total 720	C 449	N 147	O 124	0	0

- Molecule 18 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	P	113	Total 891	C 570	N 162	O 159	0	0

- Molecule 19 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	94	Total 748	C 469	N 142	O 135	S 2	0	0

- Molecule 20 is a protein called 30S ribosomal protein S18 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	65	Total 513	C 318	N 102	O 90	S 3	0	0

- Molecule 21 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 22 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	T	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 24 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 25 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 27 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 28 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 29 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	a	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 31 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 32 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 33 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	e	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 34 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 35 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 36 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 37 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 38 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 39 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 40 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	m	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 41 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	n	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 42 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	q	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 43 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	r	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 44 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	s	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 45 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	t	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 46 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 47 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	v	126	Total	C	N	O	0	0
			956	586	199	171		

- Molecule 48 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	w	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 49 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	x	124	Total 988	C 613	N 203	O 172	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
50	y	100	Total 754	C 478	N 137	O 139	0	0

- Molecule 51 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	z	114	Total 873	C 543	N 171	O 159	0	0

- Molecule 52 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	o	133	Total 990	C 625	N 175	O 187	S 3	0	0

- Molecule 53 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	p	126	Total 918	C 580	N 156	O 180	S 2	0	0

- Molecule 54 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	1	97	Total 732	C 456	N 137	O 137	S 2	0	0

- Molecule 55 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	h	3084	Total 66232	C 29522	N 12183	O 21443	P 3084	0	0

- Molecule 56 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	A	1511	Total 32439	C 14448	N 5930	O 10550	P 1511	0	0

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
57	F	1	Total 1	Mg 1	0
57	R	1	Total 1	Mg 1	0
57	X	1	Total 1	Mg 1	0
57	i	3	Total 3	Mg 3	0
57	l	1	Total 1	Mg 1	0
57	t	1	Total 1	Mg 1	0
57	z	1	Total 1	Mg 1	0
57	h	3	Total 3	Mg 3	0

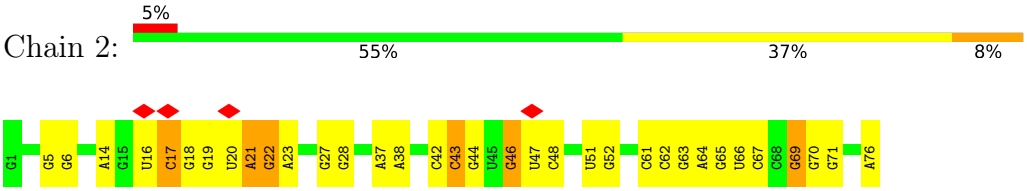
- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
58	N	1	Total 1	Zn 1	0
58	R	1	Total 1	Zn 1	0
58	Y	1	Total 1	Zn 1	0
58	c	1	Total 1	Zn 1	0
58	f	1	Total 1	Zn 1	0
58	g	1	Total 1	Zn 1	0

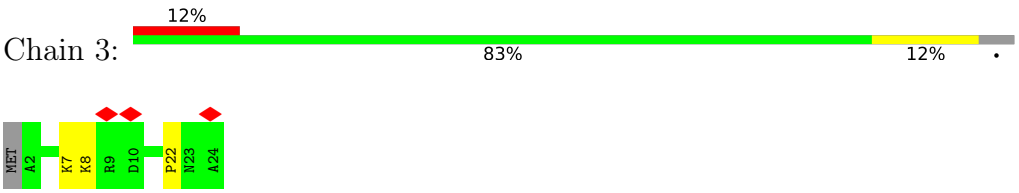
3 Residue-property plots (i)

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.

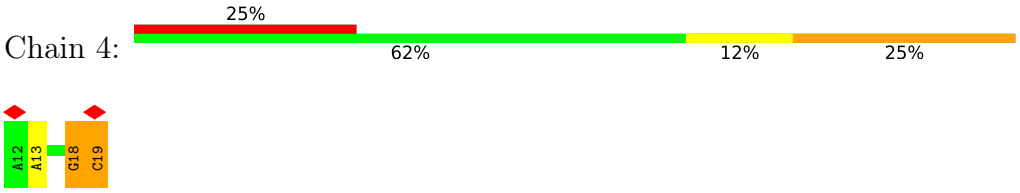
• Molecule 1: P-site tRNA



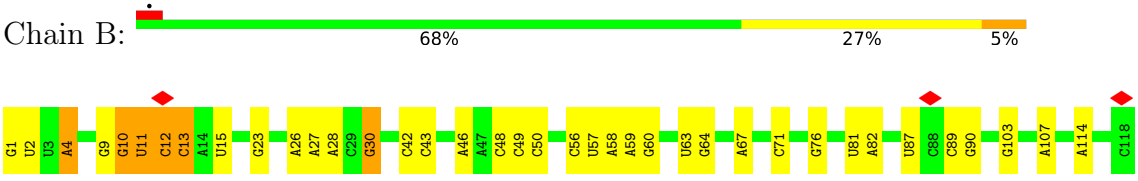
• Molecule 2: 50S ribosomal protein bL37



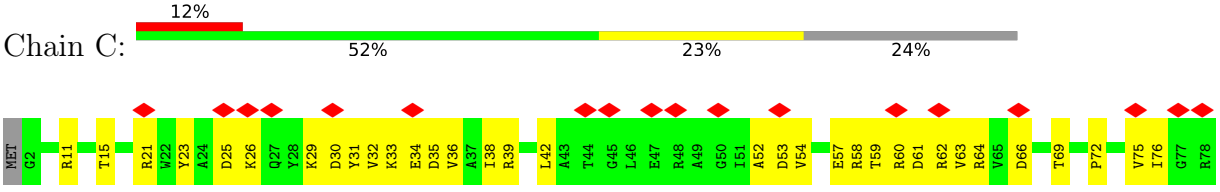
• Molecule 3: mRNA fragment

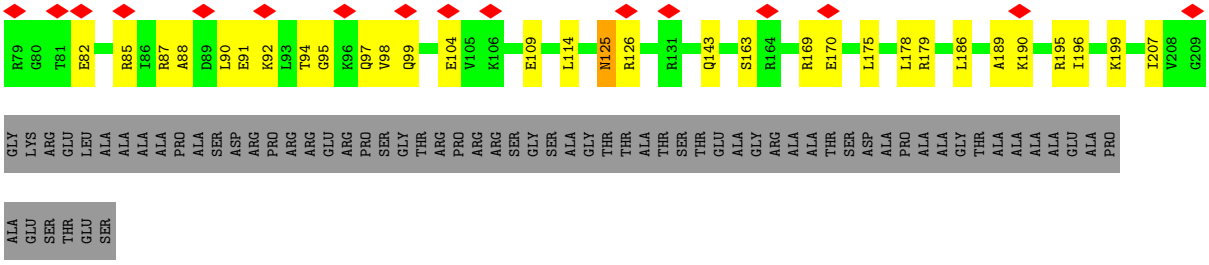


• Molecule 4: 5S ribosomal RNA



• Molecule 5: 30S ribosomal protein S3

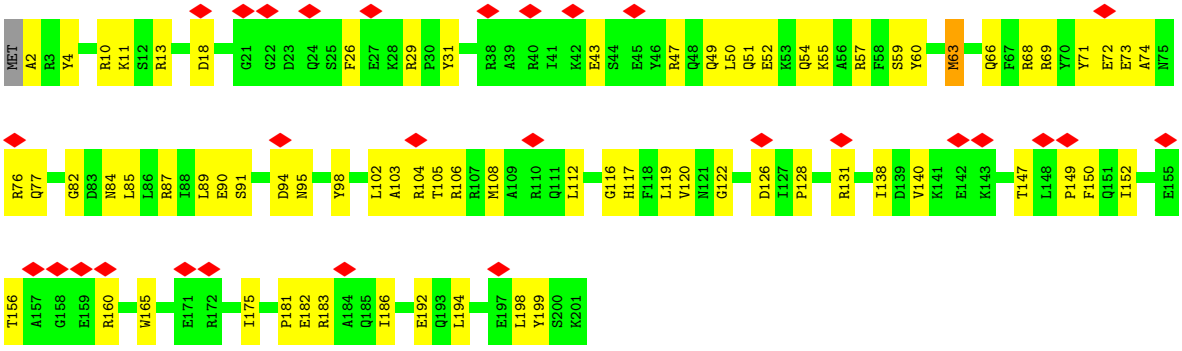




• Molecule 6: 30S ribosomal protein S4

Chain D:

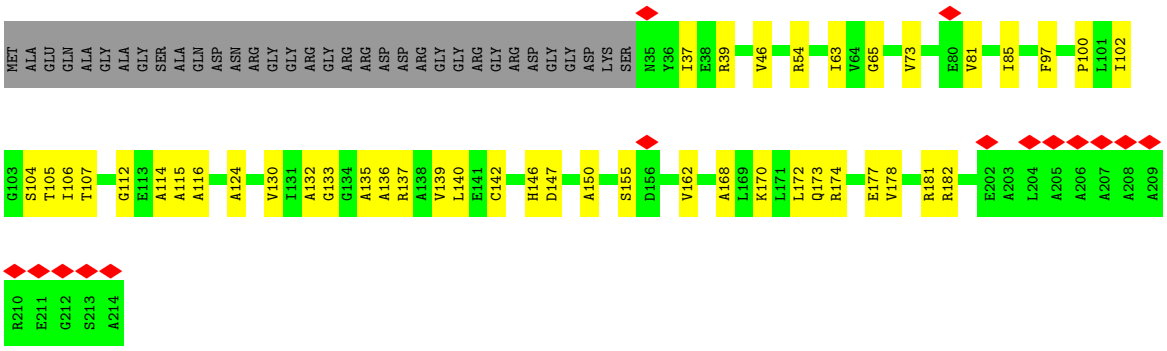




• Molecule 7: 30S ribosomal protein S5

Chain E:

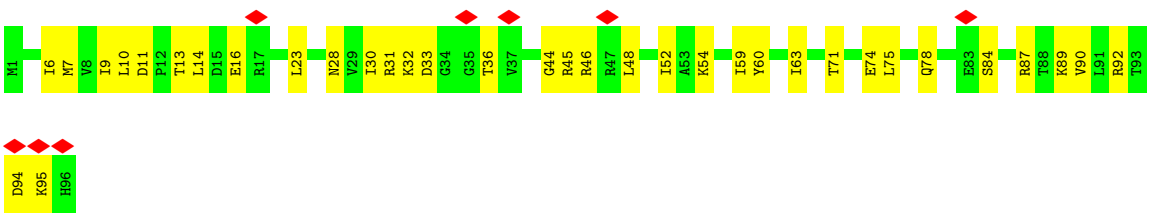




• Molecule 8: Small ribosomal subunit protein bS6

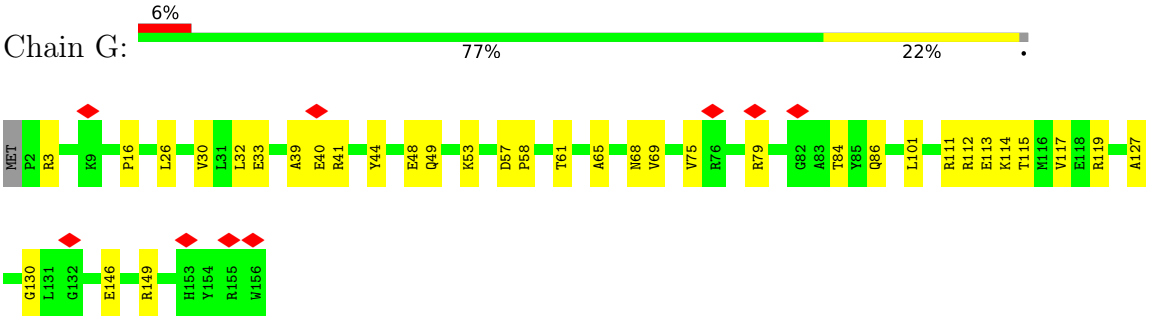
Chain F:





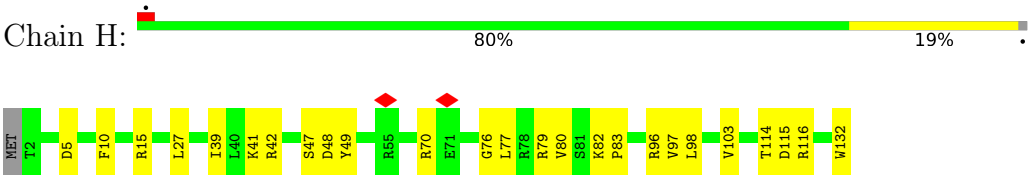
• Molecule 9: 30S ribosomal protein S7

Chain G:



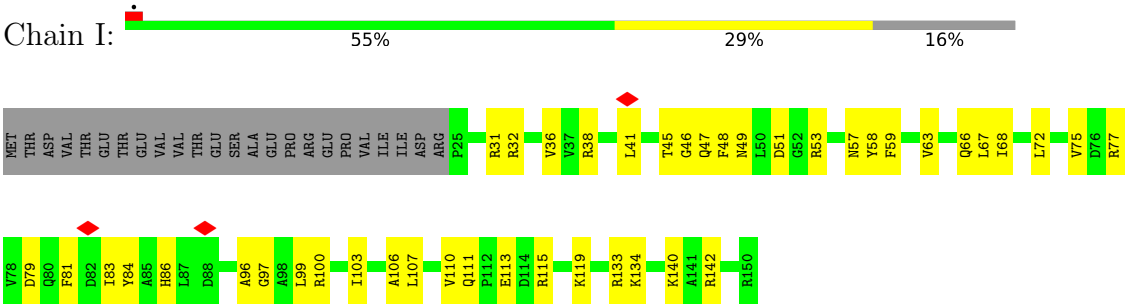
• Molecule 10: 30S ribosomal protein S8

Chain H:



• Molecule 11: 30S ribosomal protein S9

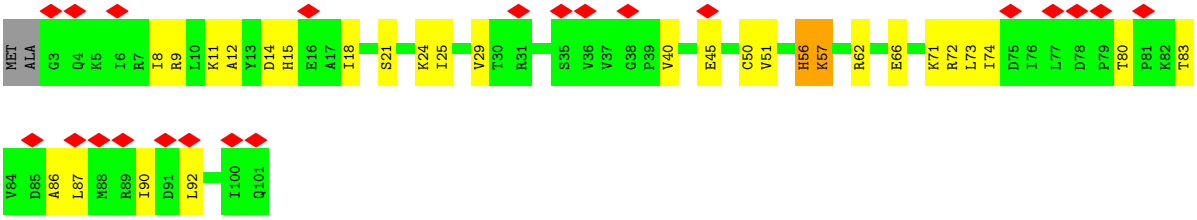
Chain I:



• Molecule 12: 30S ribosomal protein S10

Chain J:

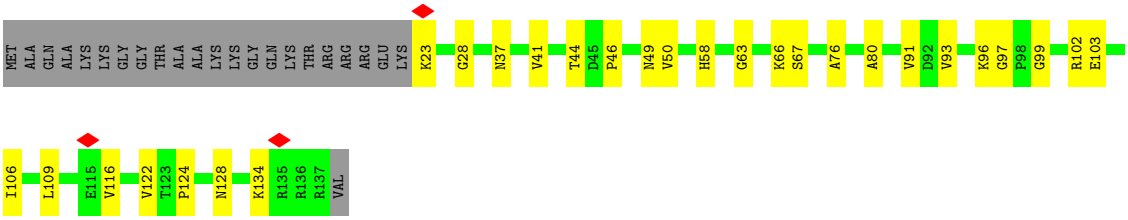




• Molecule 13: 30S ribosomal protein S11

Chain K:

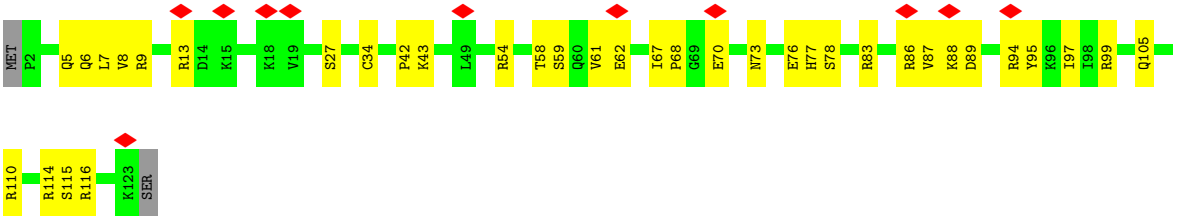




• Molecule 14: 30S ribosomal protein S12

Chain L:

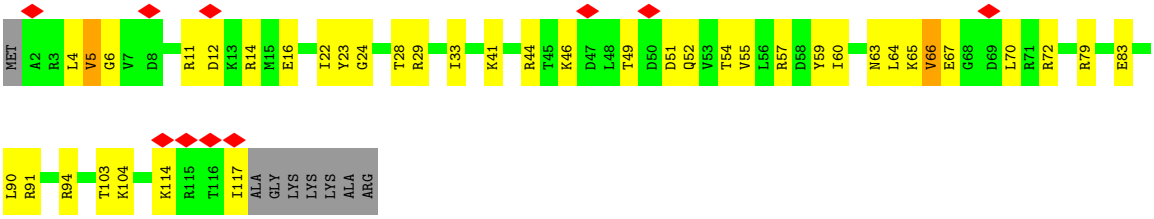




• Molecule 15: 30S ribosomal protein S13

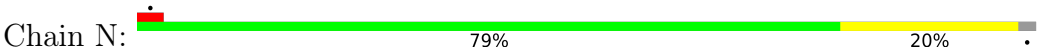
Chain M:





• Molecule 16: 30S ribosomal protein S14 type Z

Chain N:

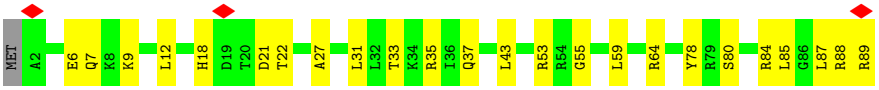




• Molecule 17: 30S ribosomal protein S15

Chain O:

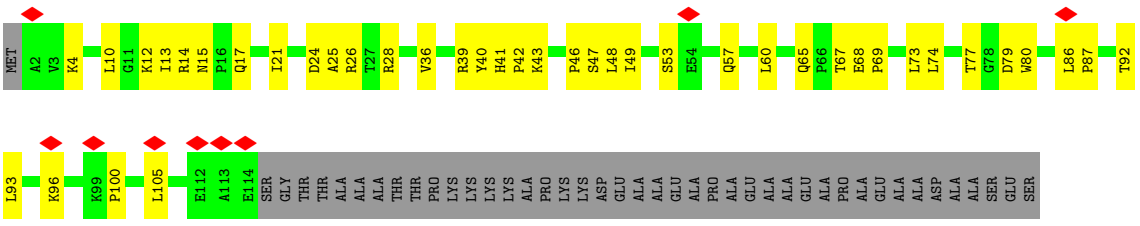




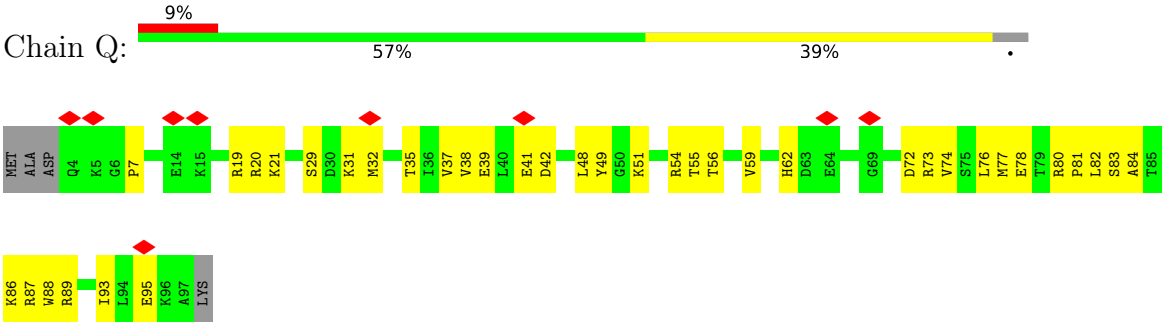
• Molecule 18: 30S ribosomal protein S16

Chain P:

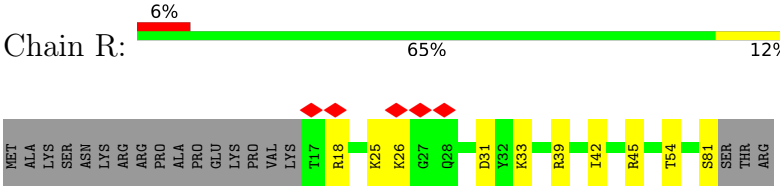




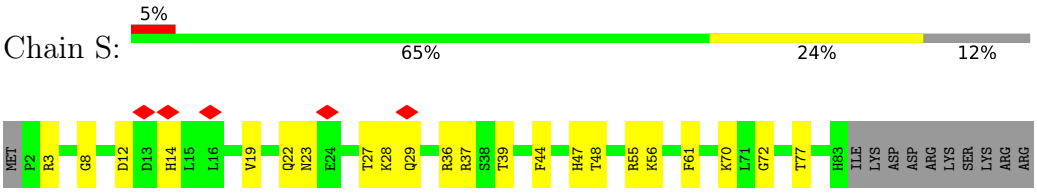
• Molecule 19: 30S ribosomal protein S17



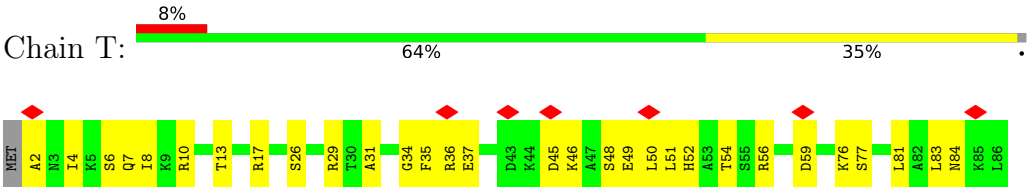
• Molecule 20: 30S ribosomal protein S18 2



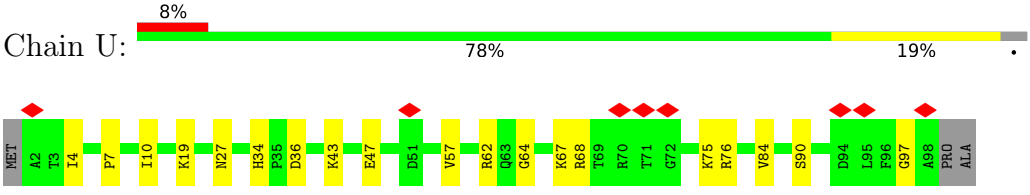
• Molecule 21: 30S ribosomal protein S19



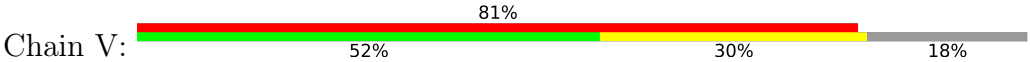
• Molecule 22: 30S ribosomal protein S20



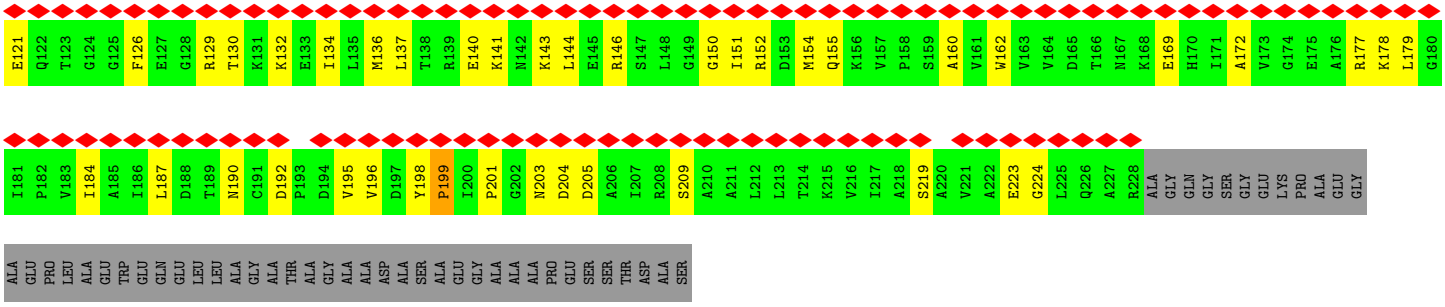
• Molecule 23: 50S ribosomal protein L23



• Molecule 24: 30S ribosomal protein S2

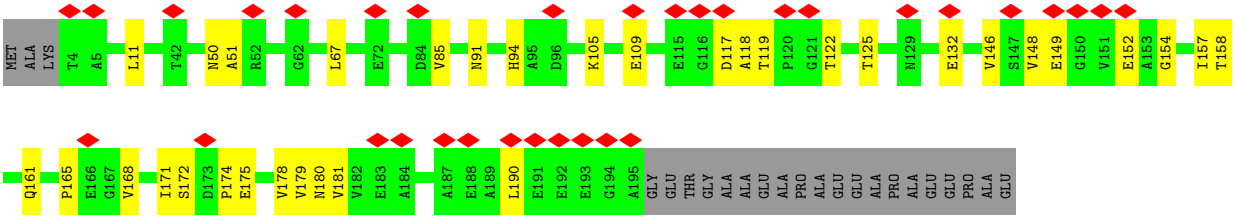






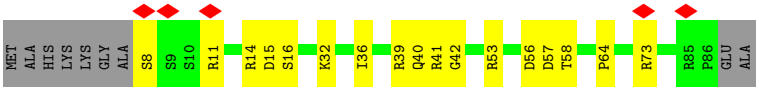
• Molecule 25: 50S ribosomal protein L25



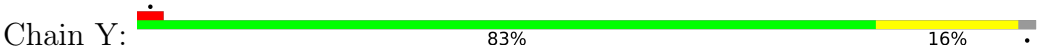


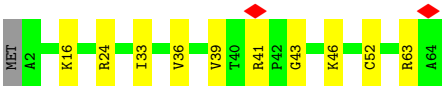
• Molecule 26: 50S ribosomal protein L27





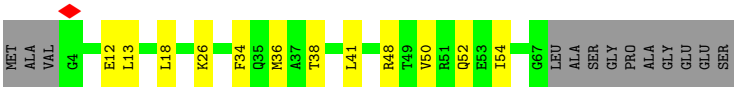
• Molecule 27: 50S ribosomal protein L28



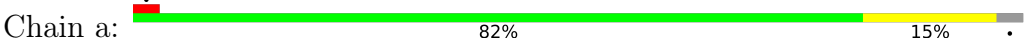


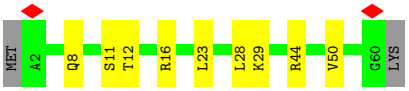
• Molecule 28: 50S ribosomal protein L29





• Molecule 29: 50S ribosomal protein L30

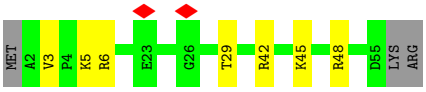




• Molecule 30: 50S ribosomal protein L32

Chain b:

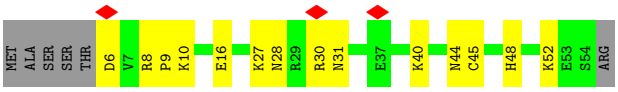




• Molecule 31: 50S ribosomal protein L33 1

Chain c:

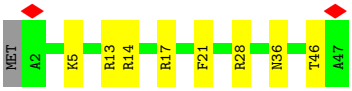




• Molecule 32: 50S ribosomal protein L34

Chain d:

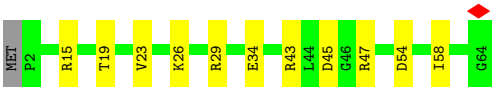




• Molecule 33: 50S ribosomal protein L35

Chain e:

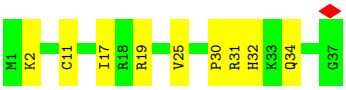




• Molecule 34: 50S ribosomal protein L36

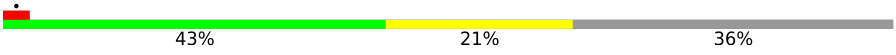
Chain f:

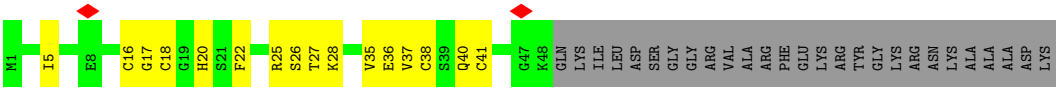




• Molecule 35: 50S ribosomal protein L31

Chain g:

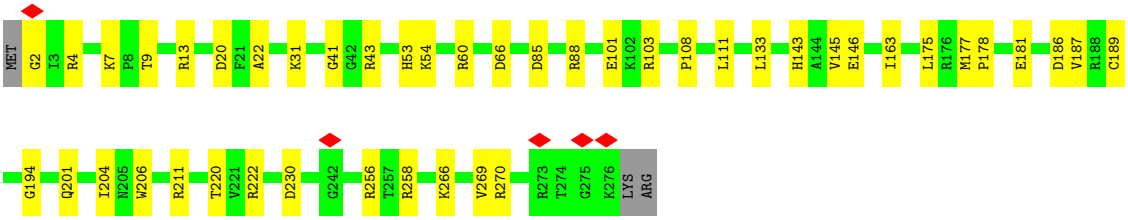




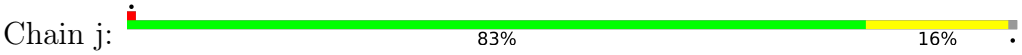
• Molecule 36: 50S ribosomal protein L2

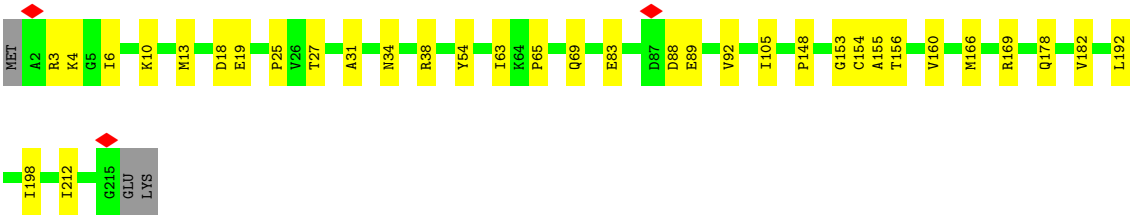
Chain i:



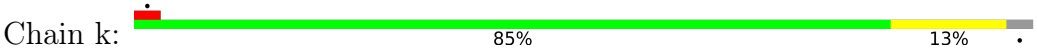


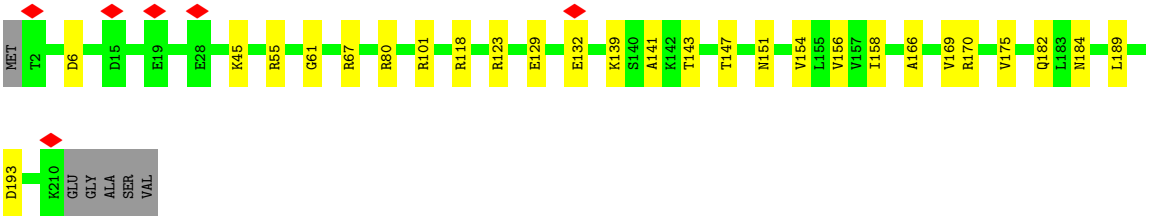
• Molecule 37: 50S ribosomal protein L3





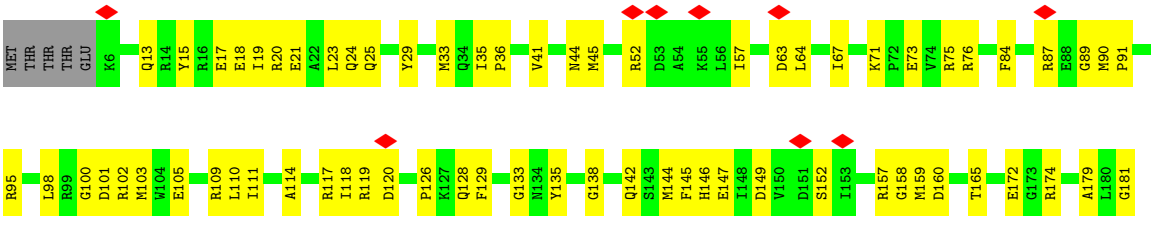
• Molecule 38: 50S ribosomal protein L4



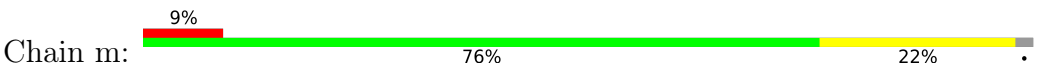


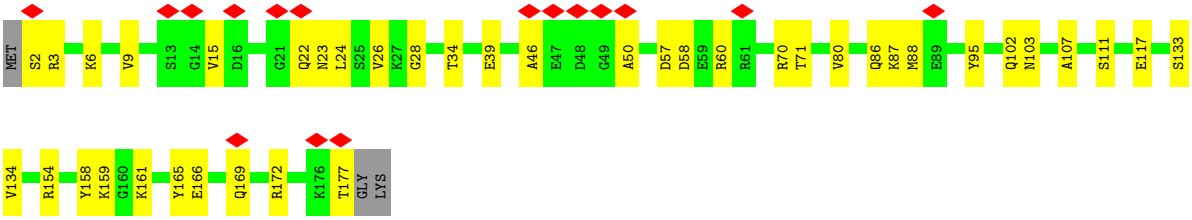
• Molecule 39: 50S ribosomal protein L5





• Molecule 40: 50S ribosomal protein L6

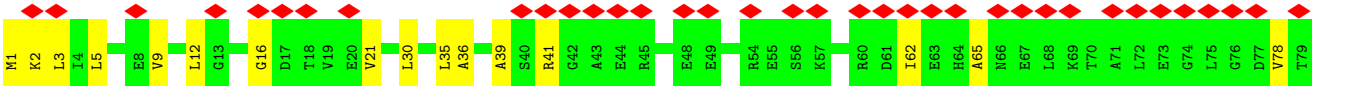


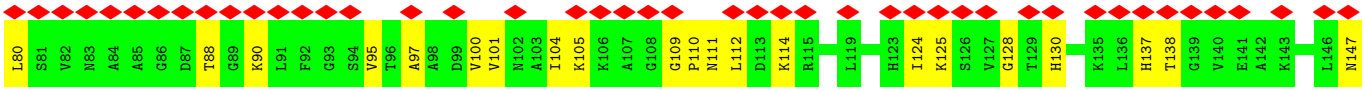


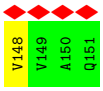
• Molecule 41: 50S ribosomal protein L9

Chain n:





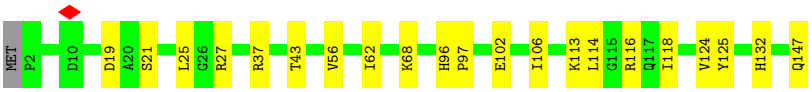




• Molecule 42: 50S ribosomal protein L13

Chain q:

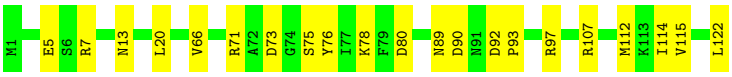




• Molecule 43: 50S ribosomal protein L14

Chain r:

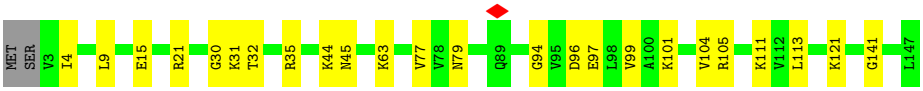




• Molecule 44: 50S ribosomal protein L15

Chain s:

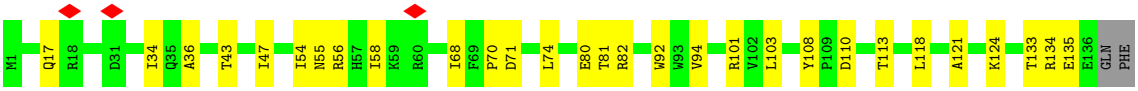




• Molecule 45: 50S ribosomal protein L16

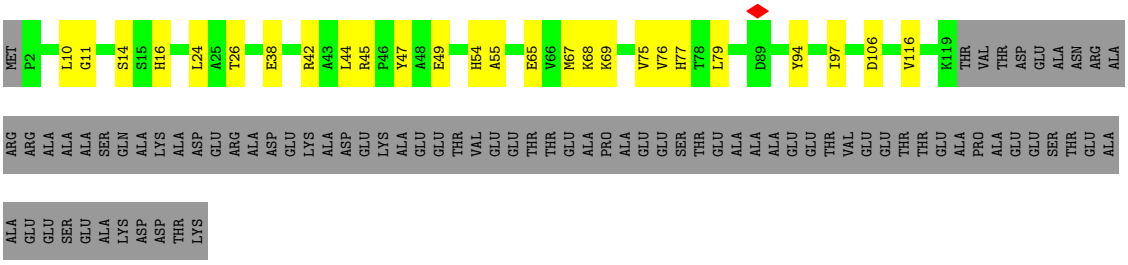
Chain t:



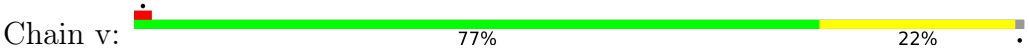


• Molecule 46: 50S ribosomal protein L17



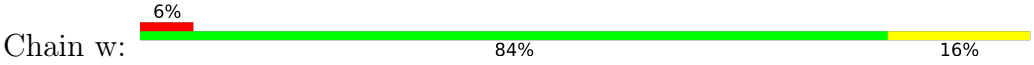


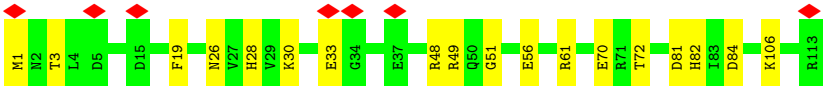
• Molecule 47: 50S ribosomal protein L18



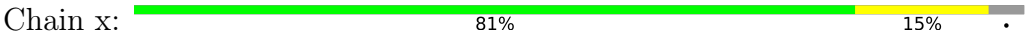


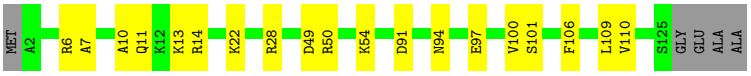
• Molecule 48: 50S ribosomal protein L19



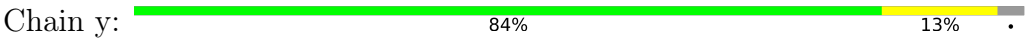


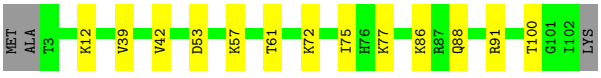
• Molecule 49: 50S ribosomal protein L20





• Molecule 50: 50S ribosomal protein L21





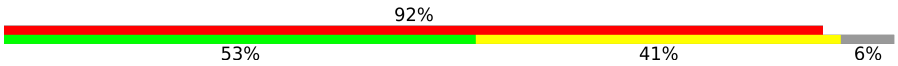
• Molecule 51: 50S ribosomal protein L22

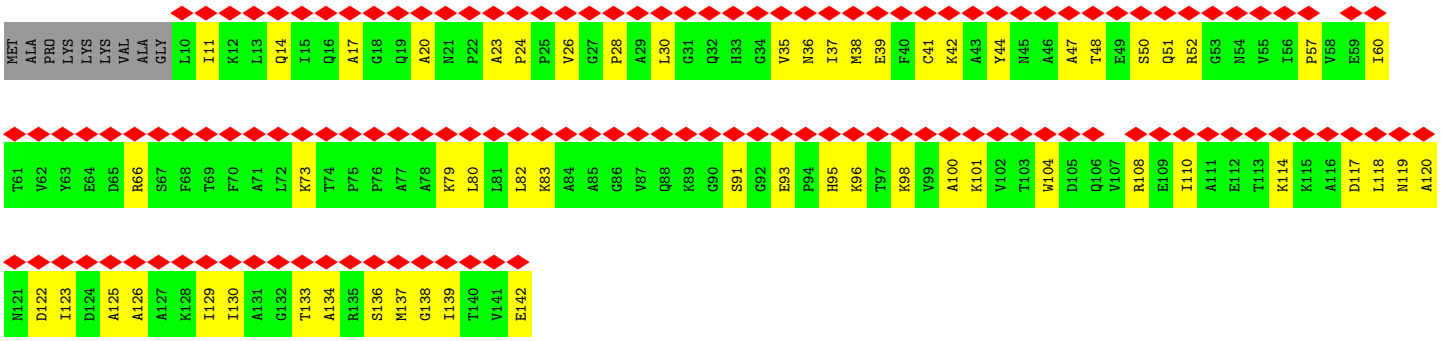




• Molecule 52: 50S ribosomal protein L11

Chain o:

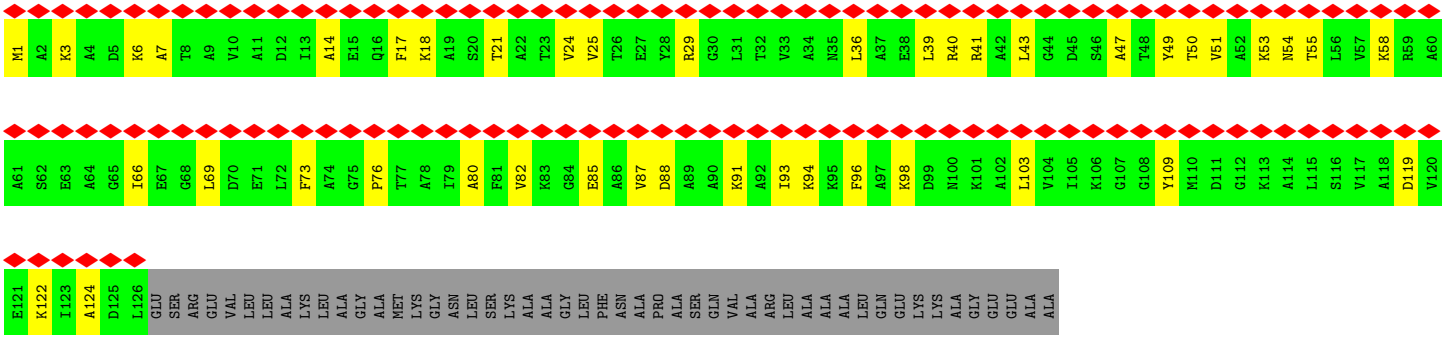




• Molecule 53: 50S ribosomal protein L10

Chain p:

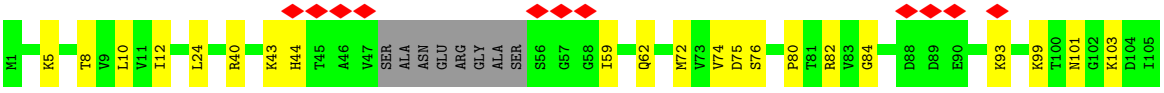




• Molecule 54: Large ribosomal subunit protein uL24

Chain 1:

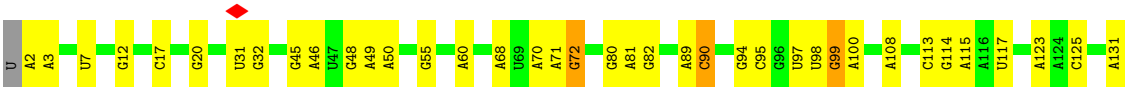


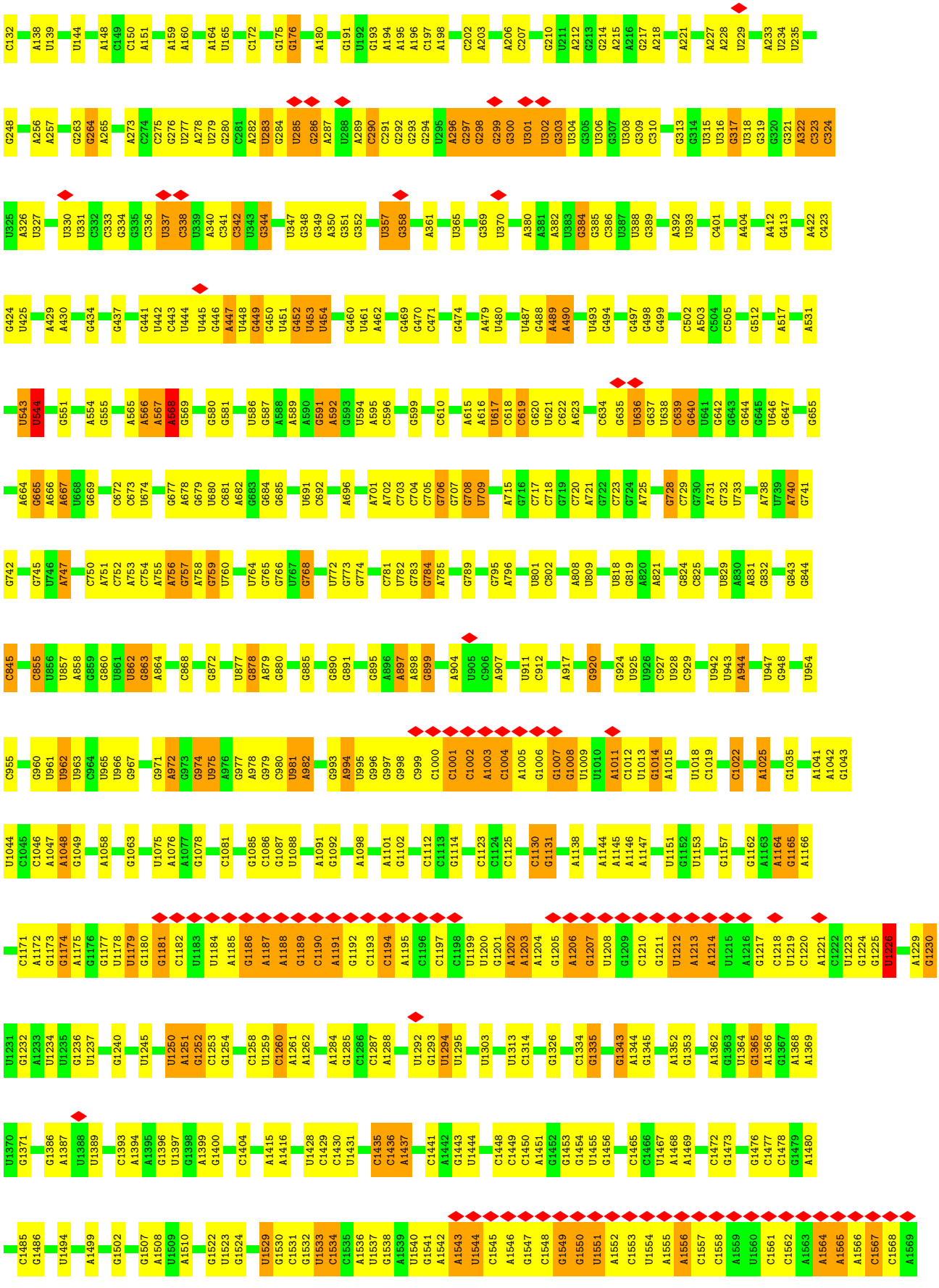


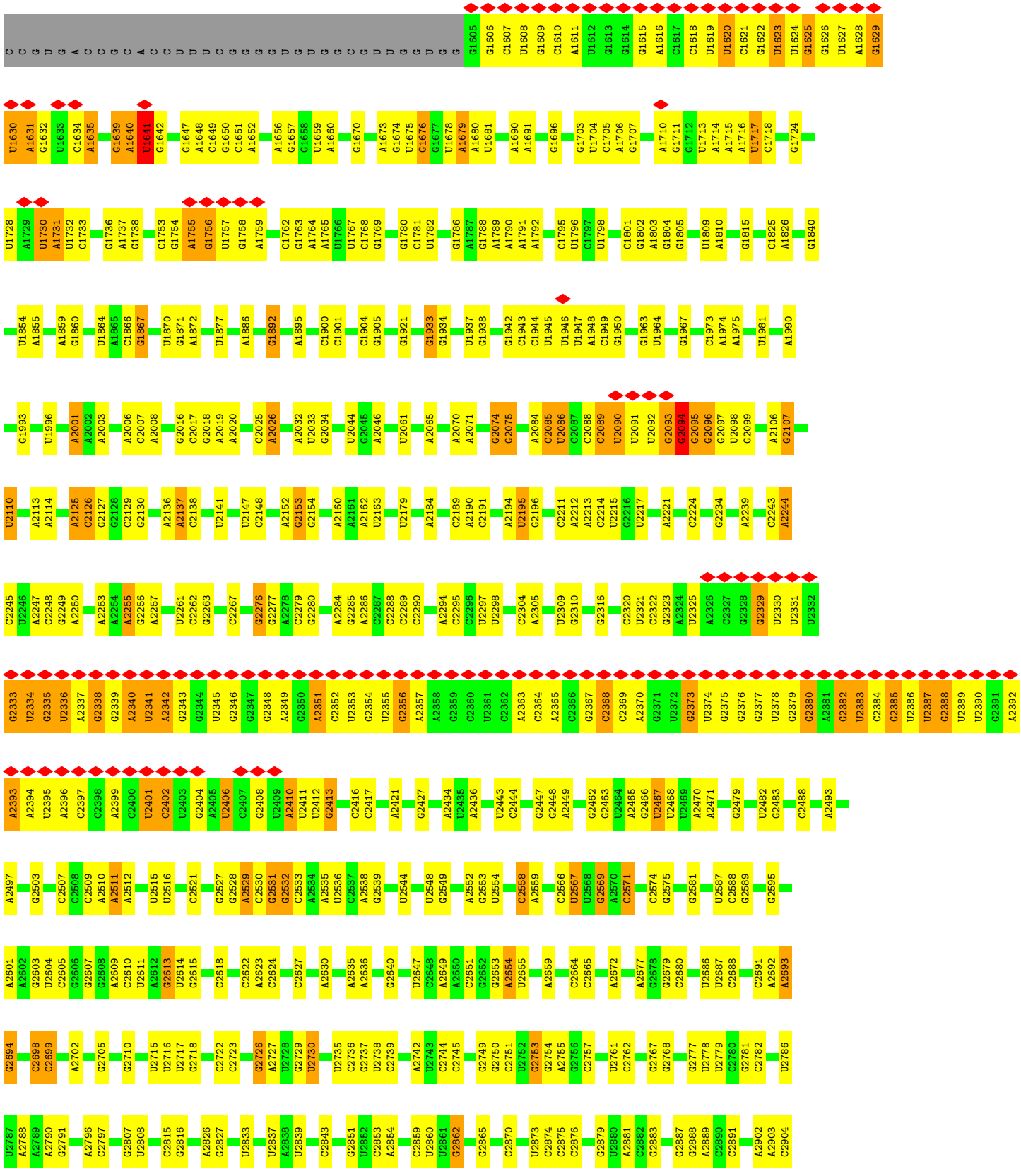
• Molecule 55: 23S ribosomal RNA

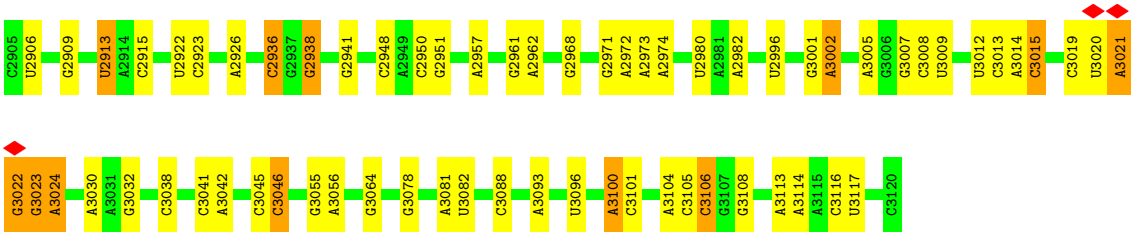
Chain h:







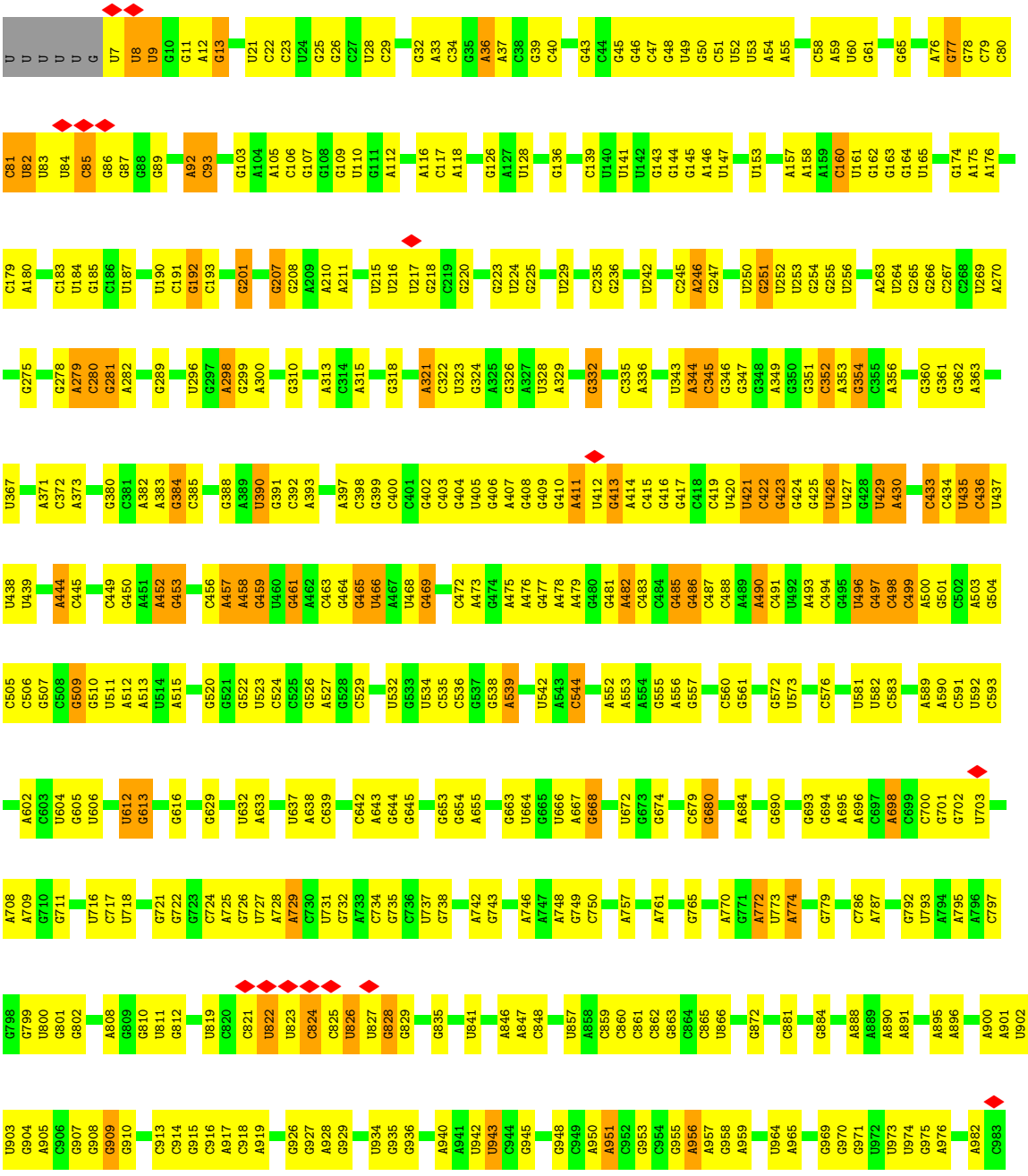


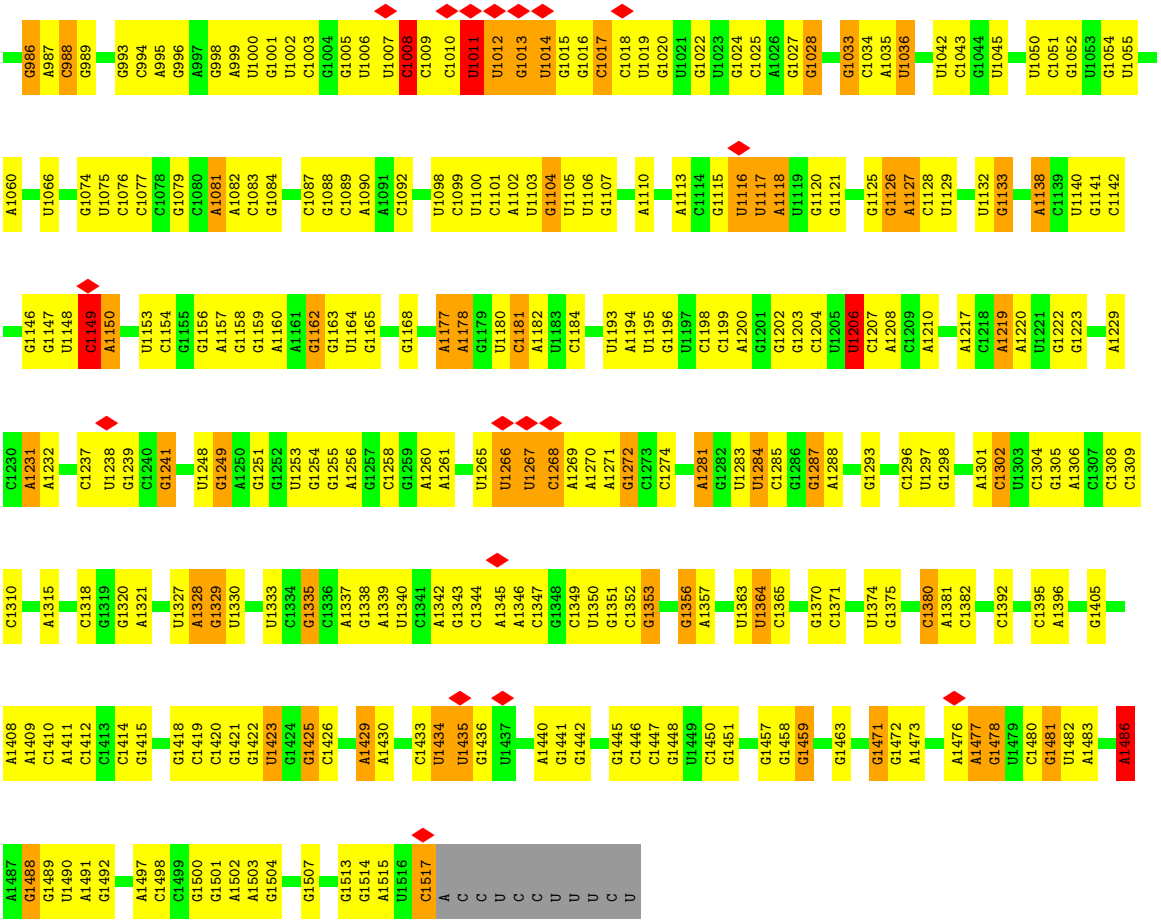


• Molecule 56: 16S ribosomal RNA

Chain A:






G986 A987 C988 G989
G993 C994 A995 G996 A997 G998 A999 U1000 G1001 U1002 C1003 G1004 G1005 U1006 U1007 C1008 C1009 C1010 U1011 U1012 G1013 U1014 G1015 G1016 C1017 C1018 U1019 G1020 U1021 G1022 U1023 G1024 C1025 A1026 G1027 G1028
G1033 C1034 A1035 U1036
U1042 C1043 G1044 U1045
U1050 C1051 G1052 U1053 G1054 U1055
A1060 U1066 G1074 U1075 C1076 C1077 C1078 G1079 C1080 A1081 A1082 C1083 G1084 C1087 G1088 C1089 A1090 A1091 C1092 U1098 C1099 U1100 C1101 A1102 U1103 G1104 U1105 U1106 G1107 A1110 A1113 C1114 G1115 U1116 U1117 A1118 U1119 G1120 G1121 G1125 G1126 A1127 C1128 U1129 U1132 G1133 A1138 C1139 U1140 G1141 C1142
G1146 G1147 U1148 C1149 A1150 U1153 C1154 G1155 G1156 A1157 G1158 G1159 A1160 A1161 G1162 G1163 U1164 G1165 G1168 A1177 A1178 C1179 U1180 C1181 A1182 U1183 C1184 U1193 A1194 U1195 G1196 U1197 C1198 C1199 A1200 G1201 G1202 G1203 C1204 U1205 U1206 C1207 A1208 C1209 A1210 A1217 C1218 A1219 A1220 U1221 G1222 G1223 A1229
C1230 A1231 A1232 C1237 U1238 G1239 C1240 G1241 U1248 G1249 A1250 G1251 G1252 U1253 G1254 G1255 A1256 G1257 C1258 G1259 A1260 A1261 U1265 U1266 U1267 C1268 A1269 A1270 A1271 G1272 C1273 C1274 A1281 G1282 U1283 U1284 C1285 G1286 G1287 A1288 G1293 C1296 U1297 G1298 A1301 C1302 U1303 C1304 G1305 A1306 C1307 C1308 C1309
C1310 A1315 C1318 G1319 G1320 A1321 U1327 A1328 G1329 U1330 U1333 C1334 G1335 C1336 A1337 G1338 A1339 U1340 C1341 A1342 G1343 C1344 A1345 A1346 C1347 G1348 C1349 U1350 G1351 C1352 G1353 G1356 A1357 U1363 U1364 C1365 G1370 C1371 U1374 G1375 C1380 A1381 C1382 C1392 C1395 A1396 G1405
A1408 A1409 C1410 A1411 C1412 C1413 C1414 G1415 G1418 C1419 C1420 G1421 G1422 U1423 G1424 G1425 C1426 A1429 A1430 C1433 U1434 U1435 G1436 U1437 A1440 G1441 G1442 G1445 C1446 C1447 G1448 U1449 C1450 G1451 G1457 G1458 G1459 G1463 G1471 G1472 A1473 A1476 A1477 G1478 U1479 C1480 G1481 U1482 A1483 A1486
A1487 G1488 G1489 U1490 A1491 G1492 A1497 C1498 C1499 G1500 G1501 A1502 A1503 G1504 G1507 G1513 G1514 A1515 U1516 C1517
A C C U C C U U U C U

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	36773	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	20.82	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.209	Depositor
Minimum map value	-0.116	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0336	Depositor
Map size (Å)	449.40002, 449.40002, 449.40002	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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: ZN, MG

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	2	0.34	0/1802	0.78	0/2807
2	3	0.31	0/191	0.50	0/247
3	4	0.33	0/194	0.74	0/300
4	B	0.60	0/2821	0.76	0/4396
5	C	0.24	0/1684	0.51	0/2261
6	D	0.27	0/1672	0.53	0/2251
7	E	0.28	0/1312	0.42	0/1772
8	F	0.27	0/782	0.41	0/1059
9	G	0.22	0/1252	0.43	0/1690
10	H	0.28	0/1025	0.44	0/1385
11	I	0.23	0/1012	0.48	0/1362
12	J	0.24	0/802	0.48	0/1086
13	K	0.27	0/873	0.45	0/1180
14	L	0.28	0/969	0.52	0/1294
15	M	0.26	0/942	0.63	2/1260 (0.2%)
16	N	0.26	0/488	0.46	0/650
17	O	0.28	0/729	0.45	0/977
18	P	0.28	0/908	0.53	0/1226
19	Q	0.26	0/759	0.50	0/1016
20	R	0.27	0/518	0.48	0/693
21	S	0.22	0/680	0.43	0/915
22	T	0.25	0/663	0.45	0/882
23	U	0.32	0/766	0.41	0/1030
24	V	0.29	1/1822 (0.1%)	0.60	3/2457 (0.1%)
25	W	0.24	0/1443	0.38	0/1970
26	X	0.36	0/595	0.49	0/798
27	Y	0.36	0/478	0.45	0/641
28	Z	0.28	0/534	0.41	0/713
29	a	0.33	0/477	0.46	0/640
30	b	0.36	0/427	0.48	0/572
31	c	0.25	0/413	0.42	0/553
32	d	0.37	0/380	0.51	0/500

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	e	0.32	0/507	0.50	0/672
34	f	0.32	0/303	0.40	0/401
35	g	0.24	0/372	0.37	0/503
36	i	0.37	0/2153	0.44	0/2895
37	j	0.35	0/1609	0.47	0/2165
38	k	0.32	0/1592	0.43	0/2153
39	l	0.29	0/1467	0.56	0/1973
40	m	0.25	0/1369	0.44	0/1848
41	n	0.21	0/1027	0.47	0/1398
42	q	0.32	0/1157	0.42	0/1567
43	r	0.33	0/946	0.45	0/1268
44	s	0.33	0/1091	0.53	0/1457
45	t	0.32	0/1118	0.51	0/1506
46	u	0.34	0/945	0.50	0/1267
47	v	0.28	0/966	0.44	0/1298
48	w	0.31	0/921	0.43	0/1236
49	x	0.36	0/1000	0.44	0/1341
50	y	0.30	0/764	0.34	0/1030
51	z	0.33	0/887	0.41	0/1204
52	o	0.22	0/1006	0.50	0/1364
53	p	0.15	0/925	0.37	0/1246
54	1	0.27	0/738	0.40	0/987
55	h	0.73	1/74164 (0.0%)	0.81	38/115718 (0.0%)
56	A	0.57	0/36309	0.78	15/56657 (0.0%)
All	All	0.59	2/162749 (0.0%)	0.72	58/243737 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	D	0	1
12	J	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	V	199	PRO	CG-CD	-7.44	1.25	1.50
55	h	1226	U	O3'-P	6.93	1.69	1.61

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	h	1194	C	C6-N1-C2	12.93	125.47	120.30
24	V	199	PRO	N-CD-CG	-11.43	86.06	103.20
55	h	338	C	N3-C2-O2	-9.60	115.18	121.90
24	V	199	PRO	CA-CB-CG	-8.52	88.31	104.50
55	h	2245	C	C2-N1-C1'	7.89	127.48	118.80

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	D	63	MET	Peptide
12	J	56	HIS	Peptide

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	2	1614	0	823	20	0
2	3	189	0	205	3	0
3	4	173	0	88	1	0
4	B	2522	0	1285	21	0
5	C	1660	0	1707	46	0
6	D	1641	0	1668	67	0
7	E	1296	0	1360	29	0
8	F	771	0	797	24	0
9	G	1232	0	1282	26	0
10	H	1010	0	1046	19	0
11	I	994	0	1050	37	0
12	J	788	0	819	28	0
13	K	855	0	863	20	0
14	L	958	0	1045	31	0
15	M	935	0	986	34	0
16	N	477	0	499	11	0
17	O	720	0	760	17	0
18	P	891	0	935	35	0
19	Q	748	0	795	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	R	513	0	537	7	0
21	S	662	0	677	18	0
22	T	660	0	712	26	0
23	U	756	0	802	15	0
24	V	1793	0	1839	62	0
25	W	1428	0	1443	23	0
26	X	586	0	601	17	0
27	Y	470	0	480	8	0
28	Z	531	0	541	8	0
29	a	474	0	500	6	0
30	b	423	0	463	9	0
31	c	405	0	407	11	0
32	d	377	0	411	6	0
33	e	502	0	541	13	0
34	f	299	0	321	8	0
35	g	364	0	348	13	0
36	i	2110	0	2165	37	0
37	j	1587	0	1630	30	0
38	k	1569	0	1607	23	0
39	l	1445	0	1476	52	0
40	m	1348	0	1399	28	0
41	n	1018	0	988	31	0
42	q	1130	0	1167	15	0
43	r	938	0	1000	15	0
44	s	1078	0	1151	17	0
45	t	1092	0	1128	20	0
46	u	928	0	972	18	0
47	v	956	0	991	20	0
48	w	907	0	938	13	0
49	x	988	0	1038	14	0
50	y	754	0	802	7	0
51	z	873	0	909	9	0
52	o	990	0	1021	44	0
53	p	918	0	959	36	0
54	1	732	0	782	14	0
55	h	66232	0	33325	706	0
56	A	32439	0	16321	493	0
57	F	1	0	0	0	0
57	R	1	0	0	0	0
57	X	1	0	0	0	0
57	h	3	0	0	0	0
57	i	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	l	1	0	0	0	0
57	t	1	0	0	0	0
57	z	1	0	0	0	0
58	N	1	0	0	0	0
58	R	1	0	0	0	0
58	Y	1	0	0	0	0
58	c	1	0	0	0	0
58	f	1	0	0	0	0
58	g	1	0	0	0	0
All	All	149767	0	100405	2070	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 2070 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)
55:h:1177:G:C6	55:h:1206:A:C6	2.56	0.94
55:h:2528:G:H22	55:h:2536:U:H3	1.11	0.94
55:h:2329:G:H1	55:h:2406:U:H3	1.21	0.87
12:J:14:ASP:OD1	12:J:15:HIS:N	2.07	0.86
55:h:3013:C:H5'	55:h:3014:A:H5'	1.58	0.86

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	
2	3	21/24 (88%)	19 (90%)	2 (10%)	0	100	100
5	C	206/275 (75%)	192 (93%)	13 (6%)	1 (0%)	24	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	D	198/201 (98%)	185 (93%)	13 (7%)	0	100	100
7	E	178/214 (83%)	166 (93%)	12 (7%)	0	100	100
8	F	94/96 (98%)	91 (97%)	3 (3%)	0	100	100
9	G	153/156 (98%)	149 (97%)	4 (3%)	0	100	100
10	H	129/132 (98%)	126 (98%)	3 (2%)	0	100	100
11	I	124/150 (83%)	113 (91%)	11 (9%)	0	100	100
12	J	97/101 (96%)	90 (93%)	6 (6%)	1 (1%)	12	45
13	K	113/138 (82%)	107 (95%)	6 (5%)	0	100	100
14	L	120/124 (97%)	111 (92%)	9 (8%)	0	100	100
15	M	114/124 (92%)	106 (93%)	7 (6%)	1 (1%)	14	47
16	N	58/61 (95%)	50 (86%)	8 (14%)	0	100	100
17	O	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
18	P	111/156 (71%)	101 (91%)	10 (9%)	0	100	100
19	Q	92/98 (94%)	89 (97%)	3 (3%)	0	100	100
20	R	63/84 (75%)	61 (97%)	2 (3%)	0	100	100
21	S	80/93 (86%)	77 (96%)	3 (4%)	0	100	100
22	T	83/86 (96%)	83 (100%)	0	0	100	100
23	U	95/100 (95%)	90 (95%)	5 (5%)	0	100	100
24	V	226/277 (82%)	213 (94%)	13 (6%)	0	100	100
25	W	190/215 (88%)	181 (95%)	9 (5%)	0	100	100
26	X	77/88 (88%)	73 (95%)	4 (5%)	0	100	100
27	Y	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
28	Z	62/77 (80%)	61 (98%)	1 (2%)	0	100	100
29	a	57/61 (93%)	53 (93%)	4 (7%)	0	100	100
30	b	52/57 (91%)	50 (96%)	2 (4%)	0	100	100
31	c	47/55 (86%)	45 (96%)	2 (4%)	0	100	100
32	d	44/47 (94%)	44 (100%)	0	0	100	100
33	e	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
34	f	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
35	g	46/75 (61%)	42 (91%)	4 (9%)	0	100	100
36	i	273/278 (98%)	257 (94%)	16 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	j	212/217 (98%)	199 (94%)	13 (6%)	0	100	100
38	k	207/215 (96%)	203 (98%)	4 (2%)	0	100	100
39	l	180/187 (96%)	172 (96%)	8 (4%)	0	100	100
40	m	174/179 (97%)	166 (95%)	8 (5%)	0	100	100
41	n	149/151 (99%)	136 (91%)	13 (9%)	0	100	100
42	q	144/147 (98%)	138 (96%)	6 (4%)	0	100	100
43	r	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
44	s	143/147 (97%)	129 (90%)	14 (10%)	0	100	100
45	t	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
46	u	116/199 (58%)	109 (94%)	7 (6%)	0	100	100
47	v	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
48	w	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
49	x	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
50	y	98/103 (95%)	95 (97%)	3 (3%)	0	100	100
51	z	112/153 (73%)	109 (97%)	3 (3%)	0	100	100
52	o	131/142 (92%)	123 (94%)	8 (6%)	0	100	100
53	p	124/175 (71%)	120 (97%)	4 (3%)	0	100	100
54	1	93/105 (89%)	90 (97%)	3 (3%)	0	100	100
All	All	5940/6646 (89%)	5633 (95%)	304 (5%)	3 (0%)	49	80

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	J	57	LYS
5	C	125	ASN
15	M	5	VAL

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	
2	3	18/19 (95%)	18 (100%)	0	100	100
5	C	170/212 (80%)	170 (100%)	0	100	100
6	D	175/176 (99%)	175 (100%)	0	100	100
7	E	127/147 (86%)	127 (100%)	0	100	100
8	F	85/85 (100%)	85 (100%)	0	100	100
9	G	131/132 (99%)	131 (100%)	0	100	100
10	H	107/108 (99%)	107 (100%)	0	100	100
11	I	102/125 (82%)	102 (100%)	0	100	100
12	J	89/90 (99%)	89 (100%)	0	100	100
13	K	89/105 (85%)	89 (100%)	0	100	100
14	L	103/105 (98%)	103 (100%)	0	100	100
15	M	99/104 (95%)	99 (100%)	0	100	100
16	N	49/50 (98%)	49 (100%)	0	100	100
17	O	76/77 (99%)	76 (100%)	0	100	100
18	P	92/118 (78%)	91 (99%)	1 (1%)	65	74
19	Q	80/83 (96%)	80 (100%)	0	100	100
20	R	55/72 (76%)	55 (100%)	0	100	100
21	S	73/84 (87%)	73 (100%)	0	100	100
22	T	69/70 (99%)	69 (100%)	0	100	100
23	U	83/85 (98%)	83 (100%)	0	100	100
24	V	191/218 (88%)	191 (100%)	0	100	100
25	W	155/168 (92%)	155 (100%)	0	100	100
26	X	58/63 (92%)	58 (100%)	0	100	100
27	Y	50/51 (98%)	50 (100%)	0	100	100
28	Z	58/66 (88%)	58 (100%)	0	100	100
29	a	52/54 (96%)	52 (100%)	0	100	100
30	b	43/46 (94%)	43 (100%)	0	100	100
31	c	47/52 (90%)	47 (100%)	0	100	100
32	d	35/36 (97%)	35 (100%)	0	100	100
33	e	53/54 (98%)	53 (100%)	0	100	100
34	f	35/35 (100%)	35 (100%)	0	100	100
35	g	43/63 (68%)	43 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	i	215/218 (99%)	215 (100%)	0	100	100
37	j	160/163 (98%)	160 (100%)	0	100	100
38	k	169/173 (98%)	169 (100%)	0	100	100
39	l	151/156 (97%)	151 (100%)	0	100	100
40	m	148/150 (99%)	148 (100%)	0	100	100
41	n	90/116 (78%)	90 (100%)	0	100	100
42	q	119/120 (99%)	119 (100%)	0	100	100
43	r	100/100 (100%)	100 (100%)	0	100	100
44	s	112/114 (98%)	112 (100%)	0	100	100
45	t	114/116 (98%)	114 (100%)	0	100	100
46	u	97/158 (61%)	97 (100%)	0	100	100
47	v	93/94 (99%)	93 (100%)	0	100	100
48	w	100/100 (100%)	100 (100%)	0	100	100
49	x	97/99 (98%)	97 (100%)	0	100	100
50	y	81/83 (98%)	81 (100%)	0	100	100
51	z	90/117 (77%)	90 (100%)	0	100	100
52	o	102/108 (94%)	102 (100%)	0	100	100
53	p	89/120 (74%)	89 (100%)	0	100	100
54	1	81/86 (94%)	81 (100%)	0	100	100
All	All	4900/5344 (92%)	4899 (100%)	1 (0%)	100	100

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

Mol	Chain	Res	Type
18	P	65	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
37	j	69	GLN
41	n	11	HIS
37	j	145	HIS
39	l	24	GLN
42	q	144	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	75/76 (98%)	17 (22%)	0
3	4	7/8 (87%)	2 (28%)	1 (14%)
4	B	117/118 (99%)	18 (15%)	1 (0%)
55	h	3082/3120 (98%)	584 (18%)	0
56	A	1510/1528 (98%)	300 (19%)	14 (0%)
All	All	4791/4850 (98%)	921 (19%)	16 (0%)

5 of 921 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	14	A
1	2	17	C
1	2	19	G
1	2	20	U
1	2	21	A

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
56	A	1477	A
56	A	1435	U
56	A	1007	U
56	A	1149	C
56	A	895	A

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 18 ligands modelled in this entry, 18 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.

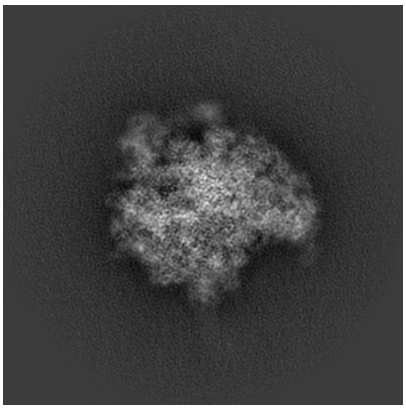
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-69708. These allow visual inspection of the internal detail of the map and identification of artifacts.

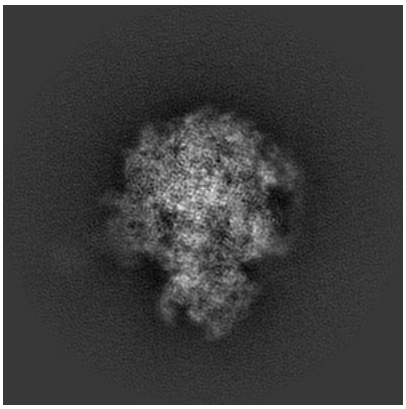
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

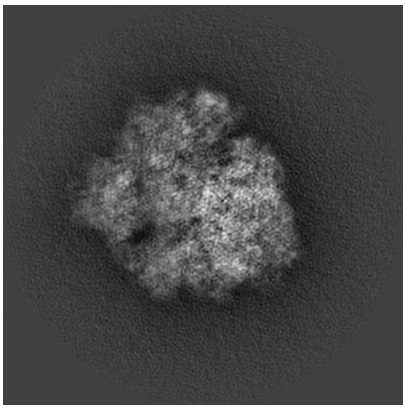
6.1.1 Primary map



X

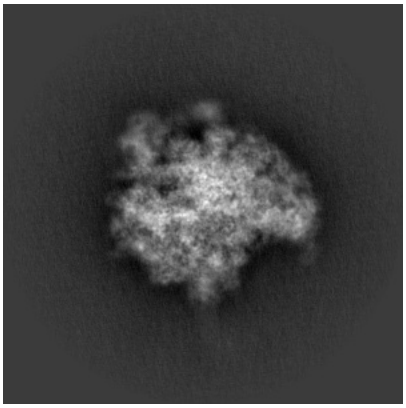


Y

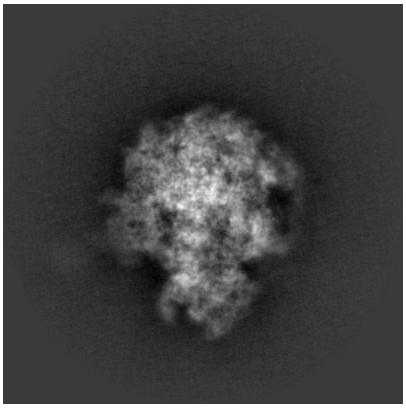


Z

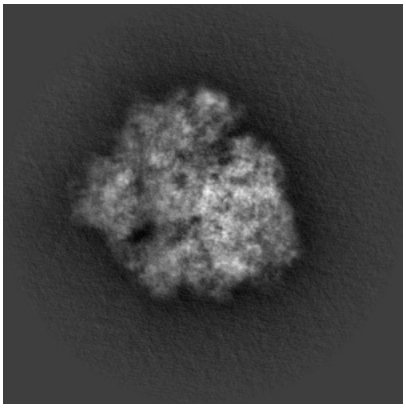
6.1.2 Raw map



X



Y

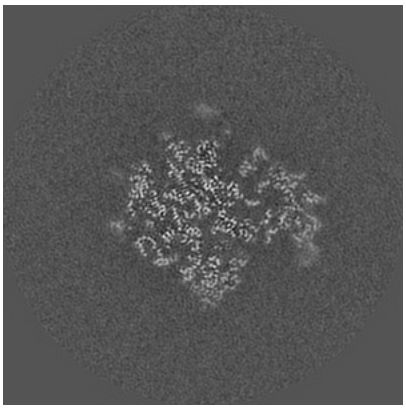


Z

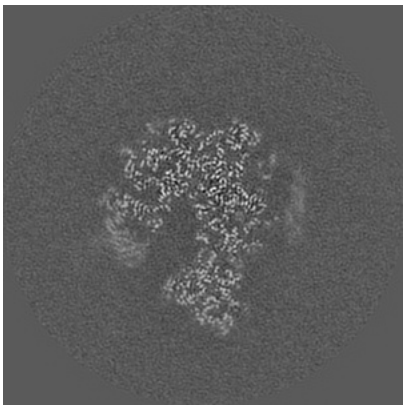
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

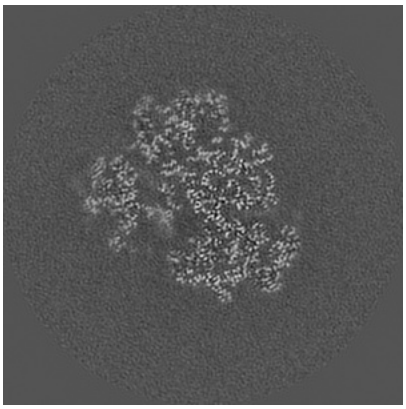
6.2.1 Primary map



X Index: 210

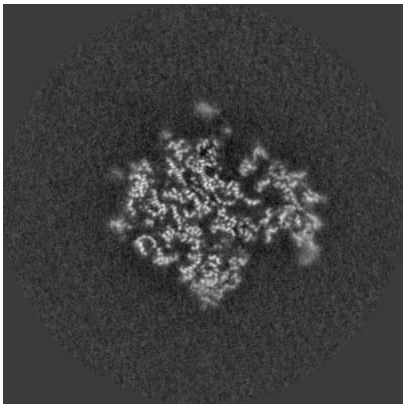


Y Index: 210

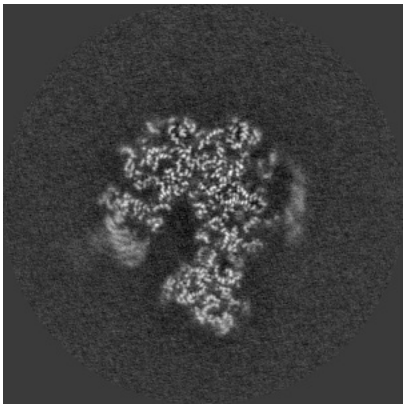


Z Index: 210

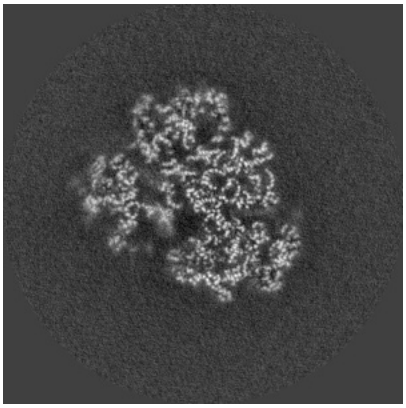
6.2.2 Raw map



X Index: 210



Y Index: 210

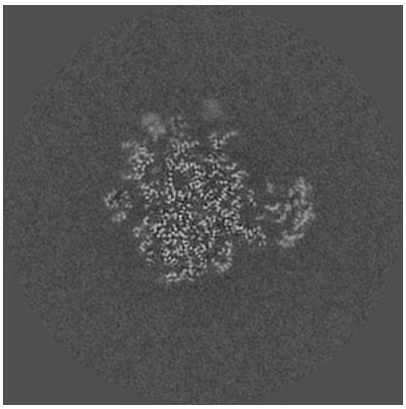


Z Index: 210

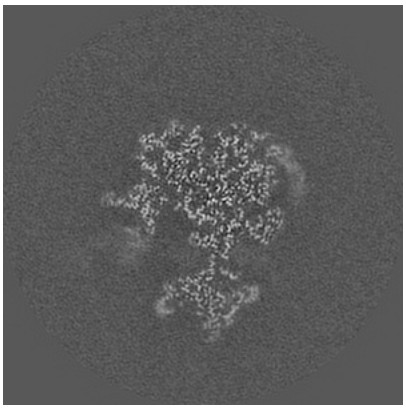
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

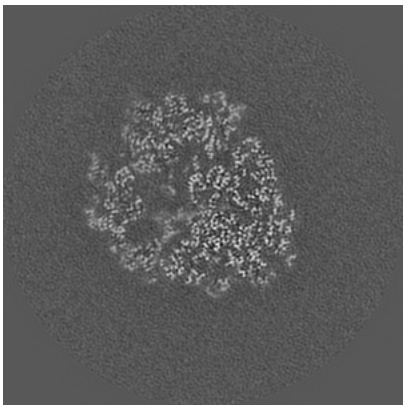
6.3.1 Primary map



X Index: 231

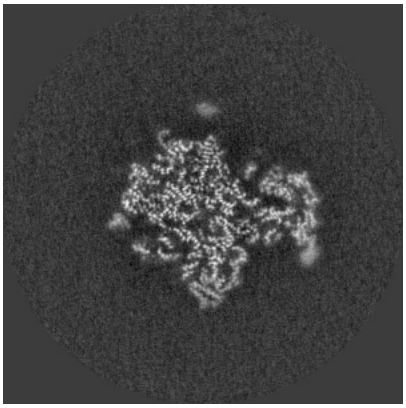


Y Index: 224

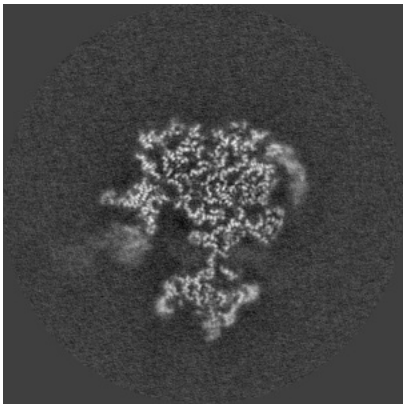


Z Index: 199

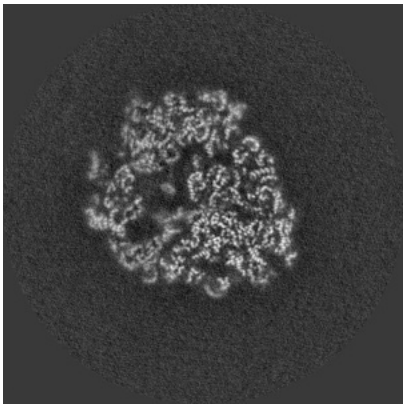
6.3.2 Raw map



X Index: 214



Y Index: 223

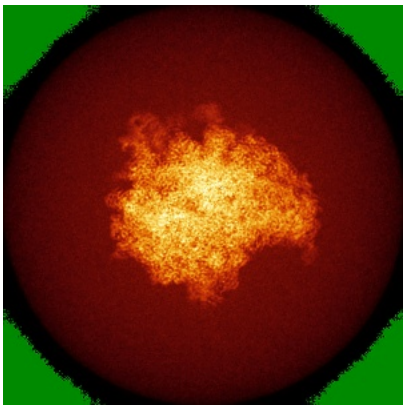


Z Index: 198

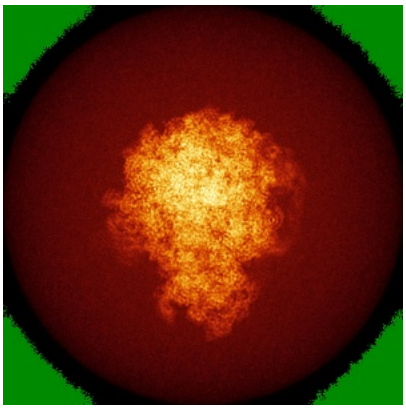
The images above show the largest variance slices of the map in three orthogonal directions.

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

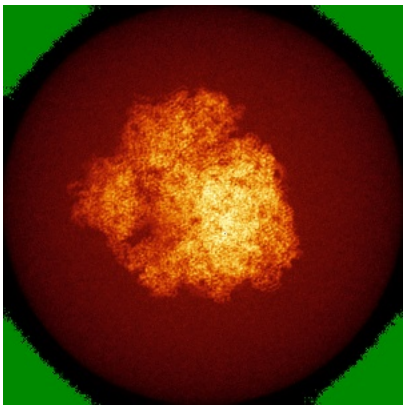
6.4.1 Primary map



X

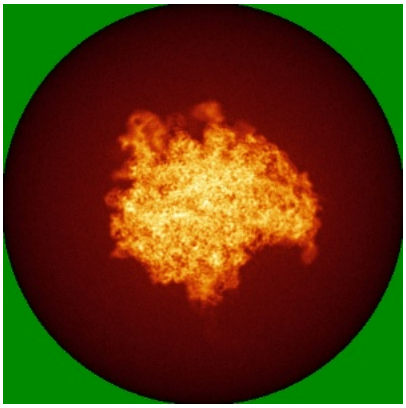


Y

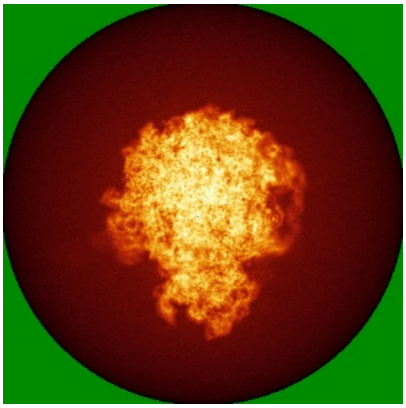


Z

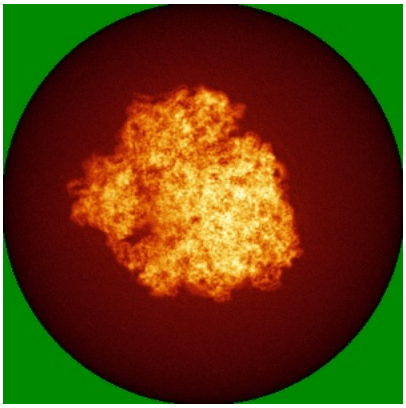
6.4.2 Raw map



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 0.0336. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

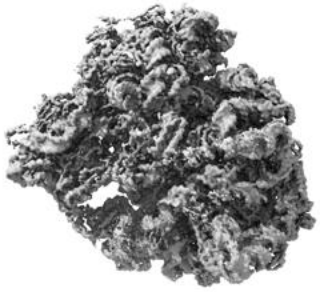
6.5.2 Raw map



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.

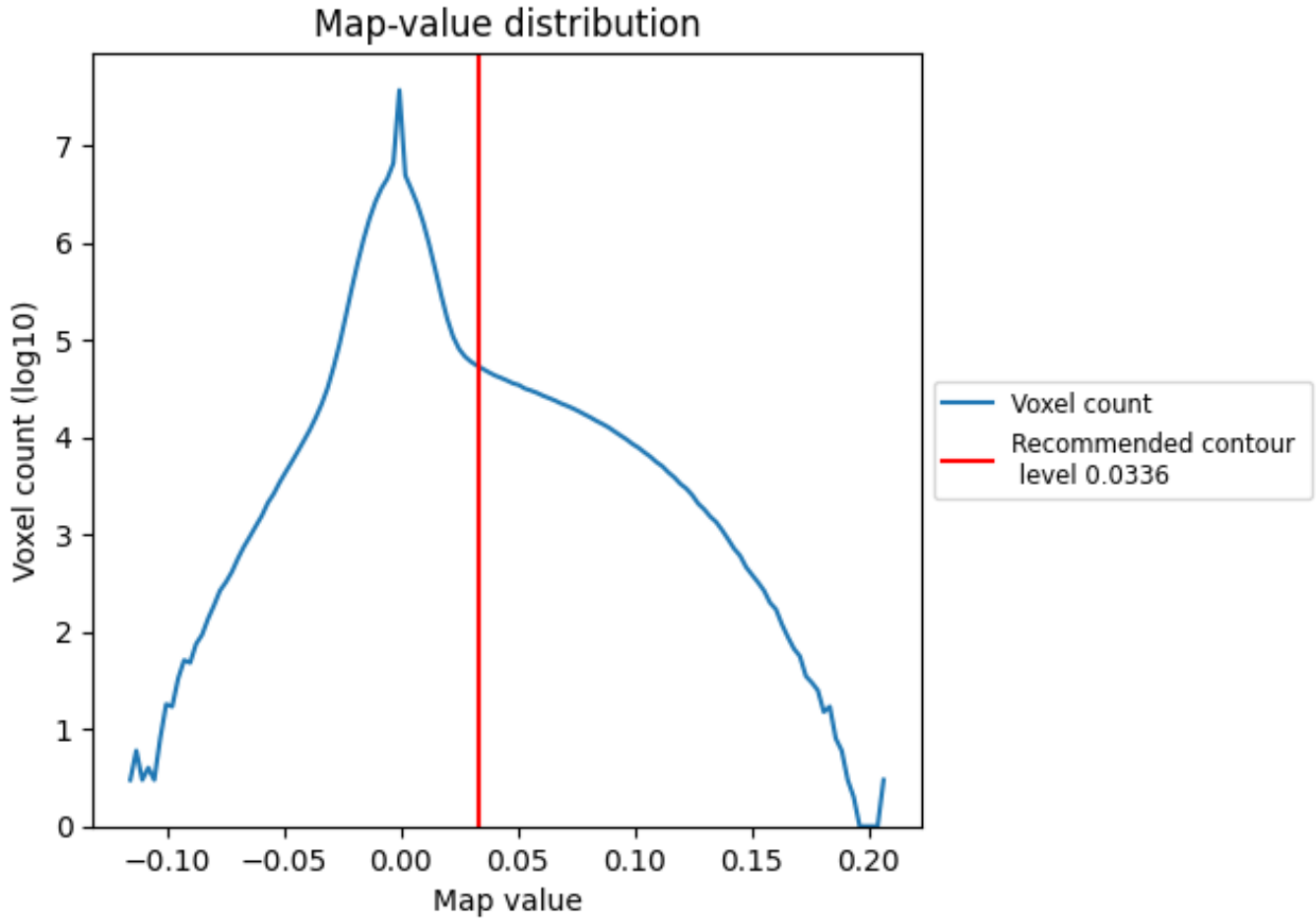
6.6 Mask visualisation (i)

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

7 Map analysis

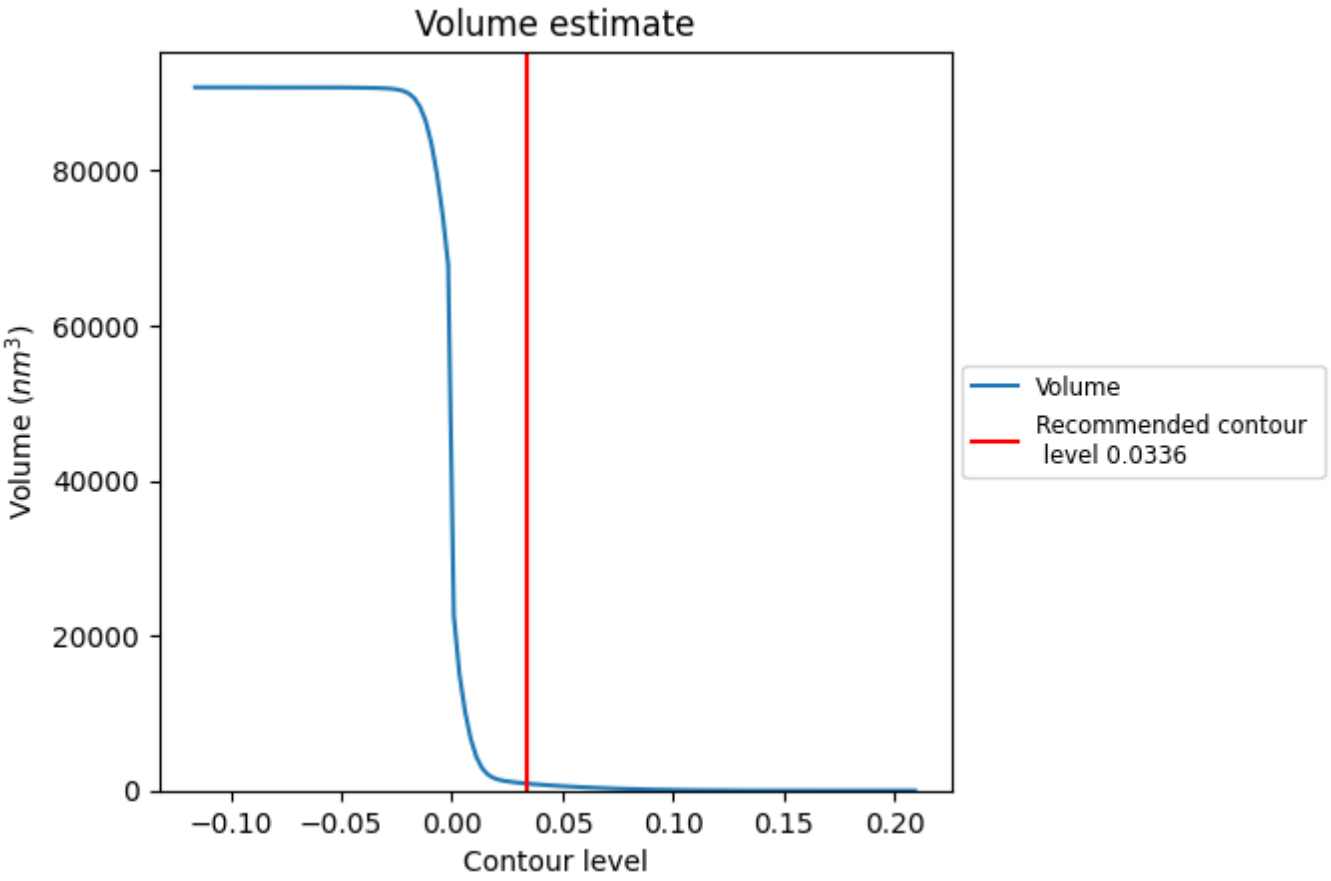
This section contains the results of statistical analysis of the map.

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.

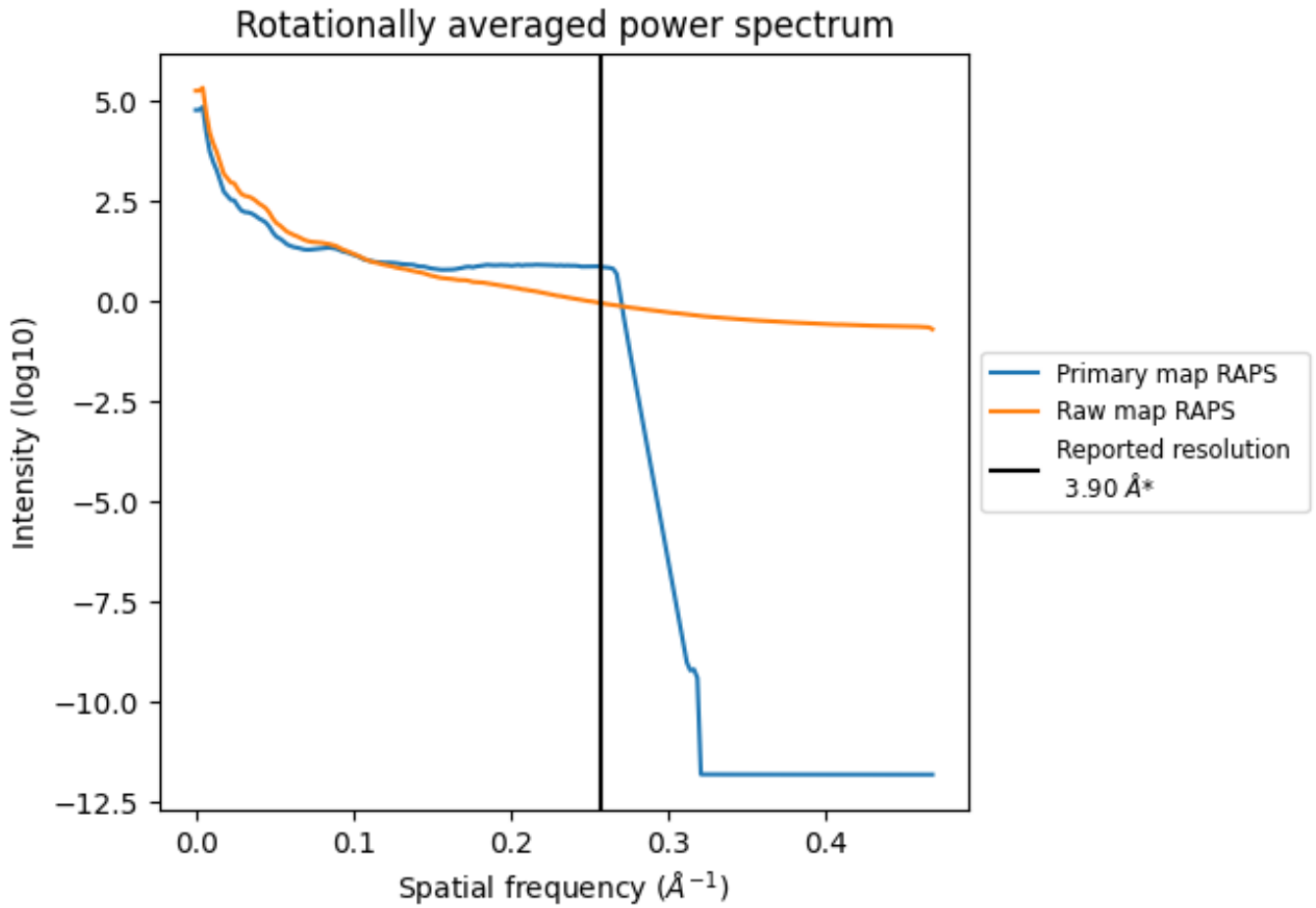
7.2 Volume estimate (i)



The volume at the recommended contour level is 910 nm^3; this corresponds to an approximate mass of 822 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)

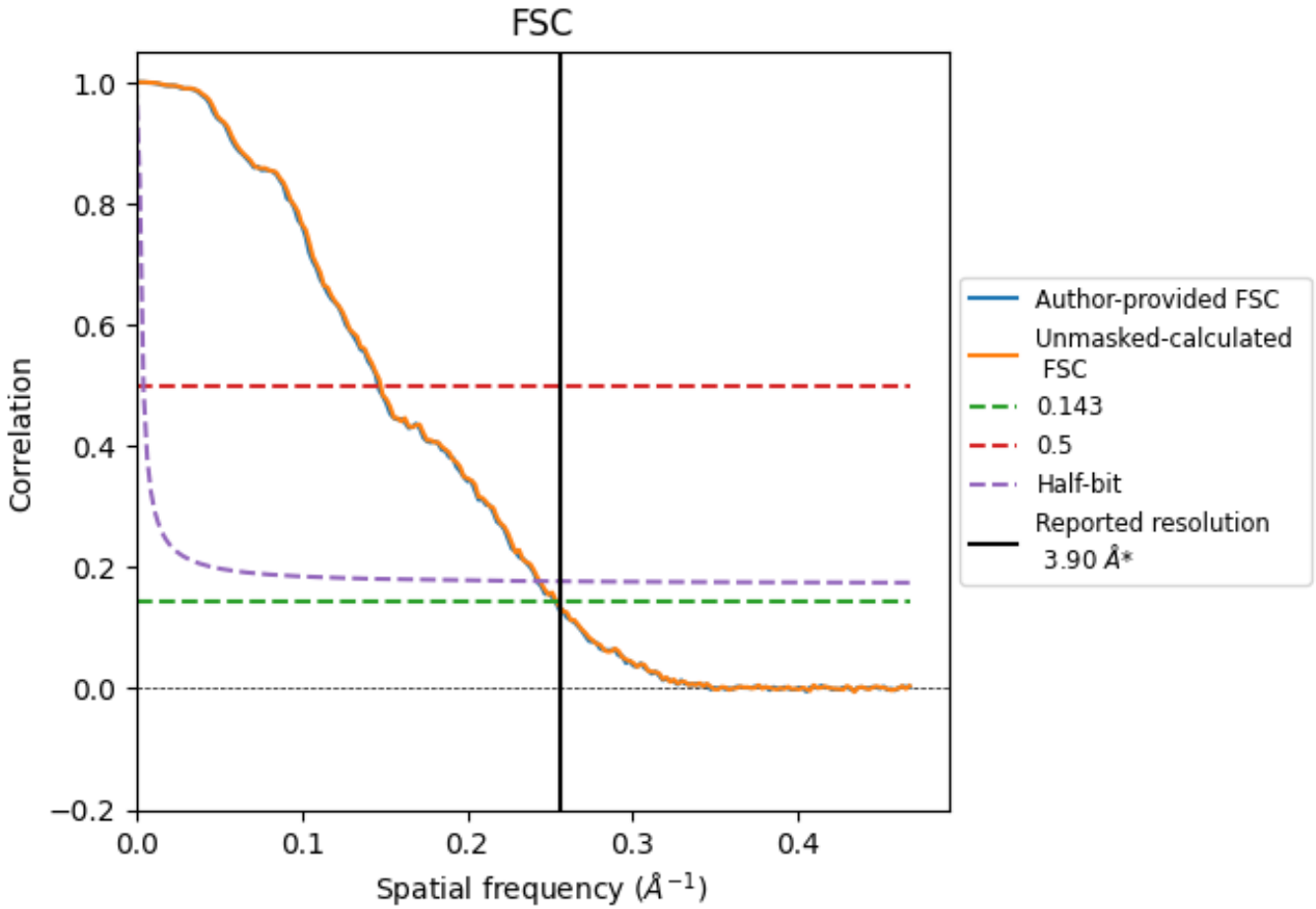


*Reported resolution corresponds to spatial frequency of 0.256 $Å^{-1}$

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 0.256 Å^{-1}

8.2 Resolution estimates (i)

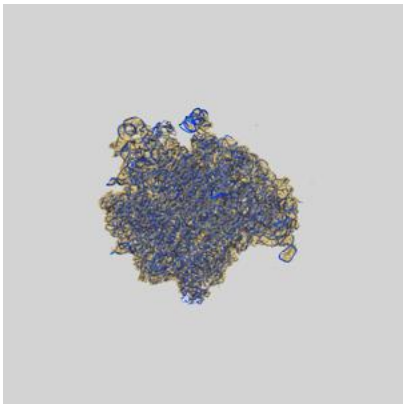
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.95	6.84	4.13
Unmasked-calculated*	3.94	6.77	4.10

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

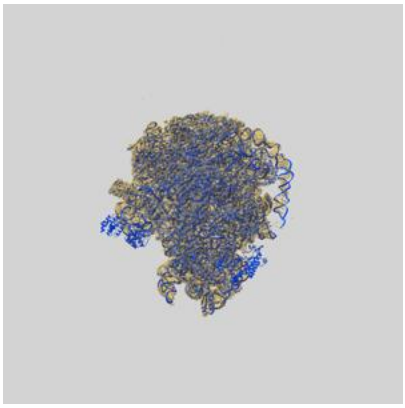
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-69708 and PDB model 24NV. Per-residue inclusion information can be found in section 3 on page 15.

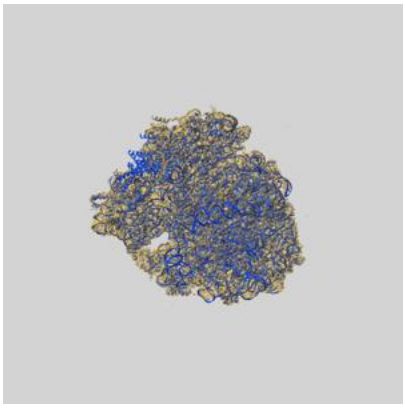
9.1 Map-model overlay



X



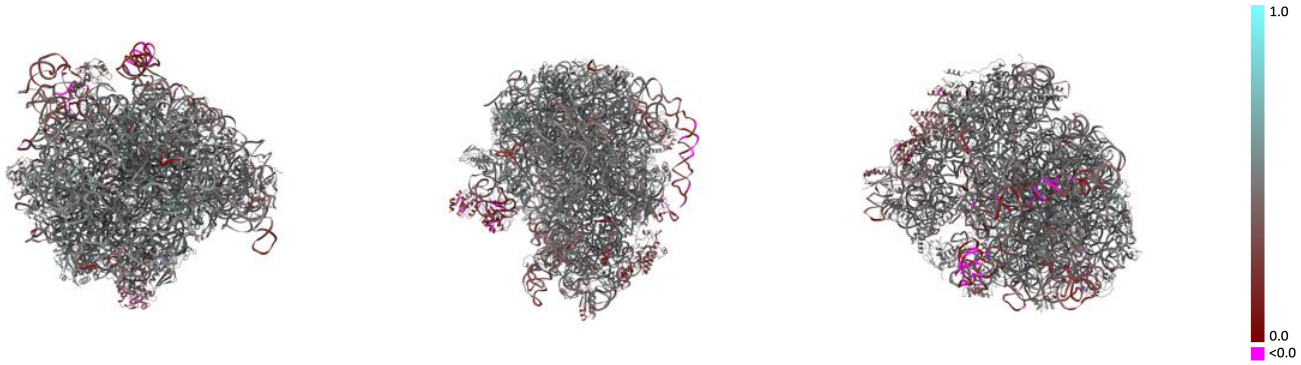
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0336 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

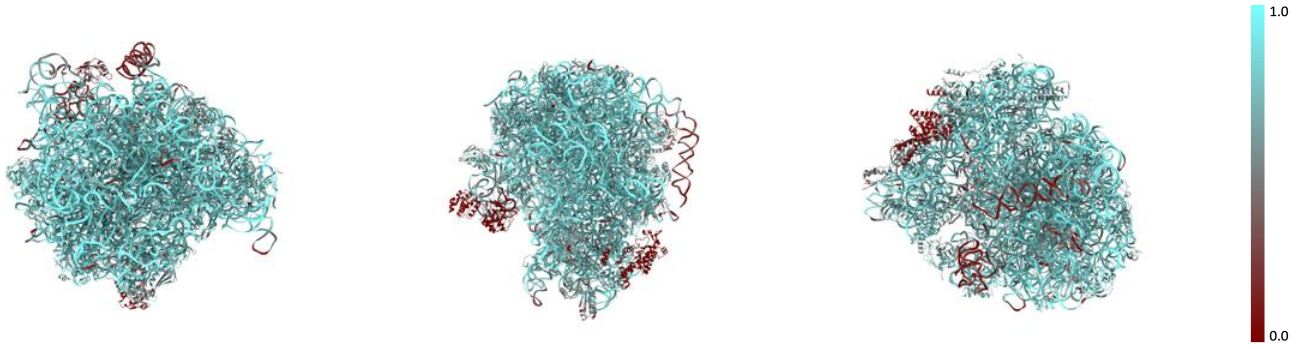
9.2 Q-score mapped to coordinate model (i)



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.

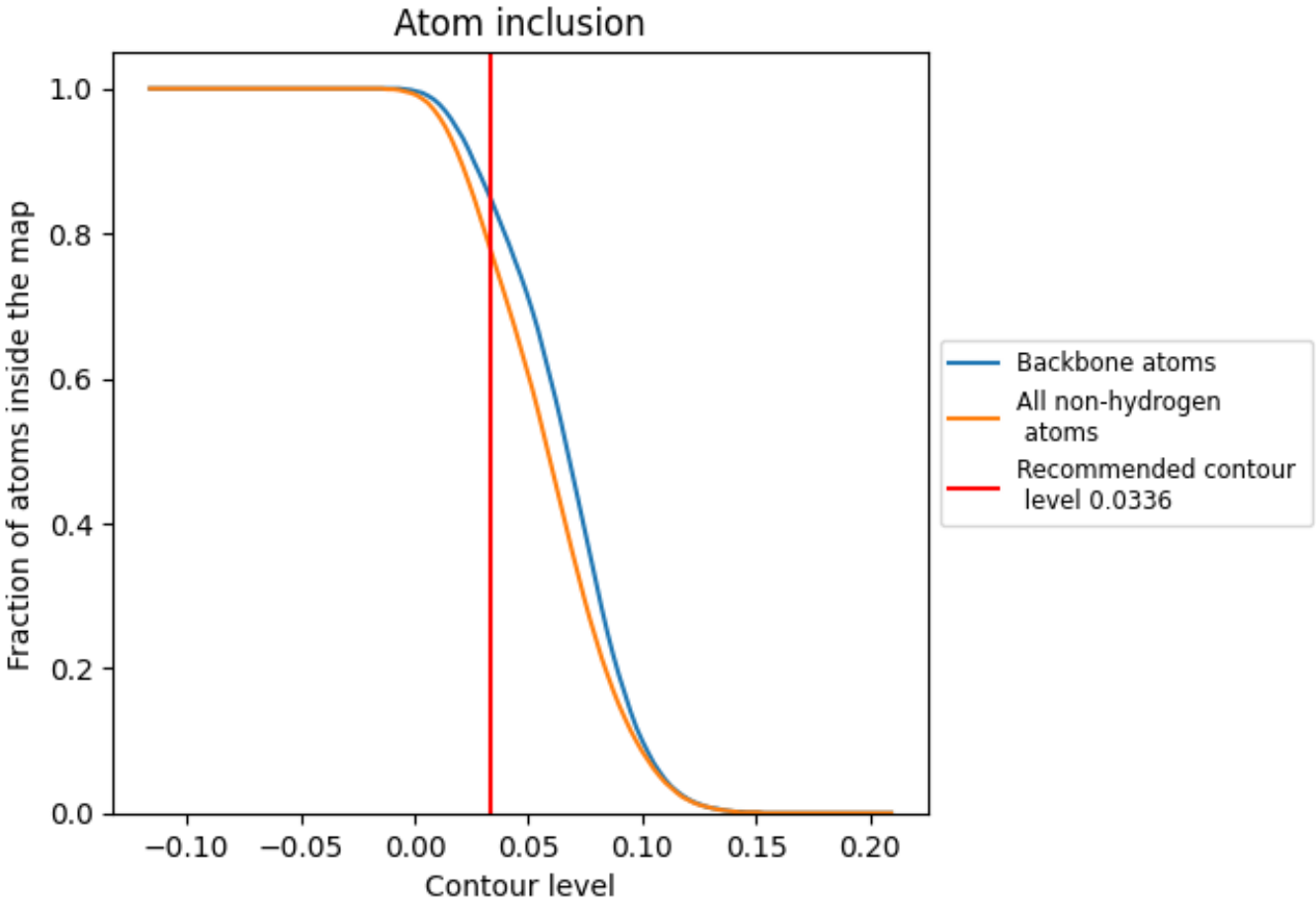
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.0336).

9.4 Atom inclusion (i)



At the recommended contour level, 85% of all backbone atoms, 78% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0336) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7750	0.4510
1	0.6420	0.4720
2	0.7740	0.4270
3	0.6370	0.4900
4	0.5380	0.3630
A	0.8500	0.4520
B	0.8780	0.4660
C	0.6240	0.4300
D	0.6120	0.4300
E	0.6560	0.4640
F	0.6560	0.4510
G	0.6650	0.4530
H	0.7370	0.4920
I	0.6830	0.4590
J	0.5750	0.4110
K	0.6930	0.4750
L	0.6590	0.4880
M	0.6830	0.4540
N	0.7150	0.4960
O	0.7190	0.4750
P	0.6760	0.4480
Q	0.6310	0.4500
R	0.7060	0.4670
S	0.6800	0.4440
T	0.6670	0.4520
U	0.7000	0.4810
V	0.0460	0.3040
W	0.5840	0.4500
X	0.7570	0.5050
Y	0.7530	0.5130
Z	0.7350	0.4630
a	0.7080	0.5060
b	0.7790	0.5060
c	0.6830	0.4930
d	0.7940	0.5170



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
e	0.7290	0.5250
f	0.7330	0.5210
g	0.7310	0.4550
h	0.8270	0.4470
i	0.7590	0.5140
j	0.7780	0.5090
k	0.7510	0.4960
l	0.6910	0.4570
m	0.6580	0.4390
n	0.3500	0.3940
o	0.0440	0.1820
p	0.0140	0.2000
q	0.7760	0.5110
r	0.7260	0.5050
s	0.7630	0.4960
t	0.7190	0.5030
u	0.7760	0.5100
v	0.7430	0.4750
w	0.7070	0.4810
x	0.7950	0.5050
y	0.7770	0.5210
z	0.7620	0.5060