wwPDB EM Validation Summary Report (i)

Nov 7, 2026 – 10:03 am GMT

PDB ID	:	9TCO / pdb_00009tco
EMDB ID	:	EMD-55794
Title	:	Structural characterization of hibernating ribosomes in the Gram-negative pathogen Klebsiella quasipneumoniae with E-site tRNA and no bS21
Authors	:	Vasanthakrishnan, R.K.B.S.; Olivier, D.; Sophie, C.; Yann, L.C.; Sylvie, G.D.; Sassi, M.; Emmanuel, G.; Reynald, G.
Deposited on	:	2025-11-21
Resolution	:	2.70 Å(reported)
Based on initial model	:	8B0X

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 (i) 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 (1)) were used in the production of this report:

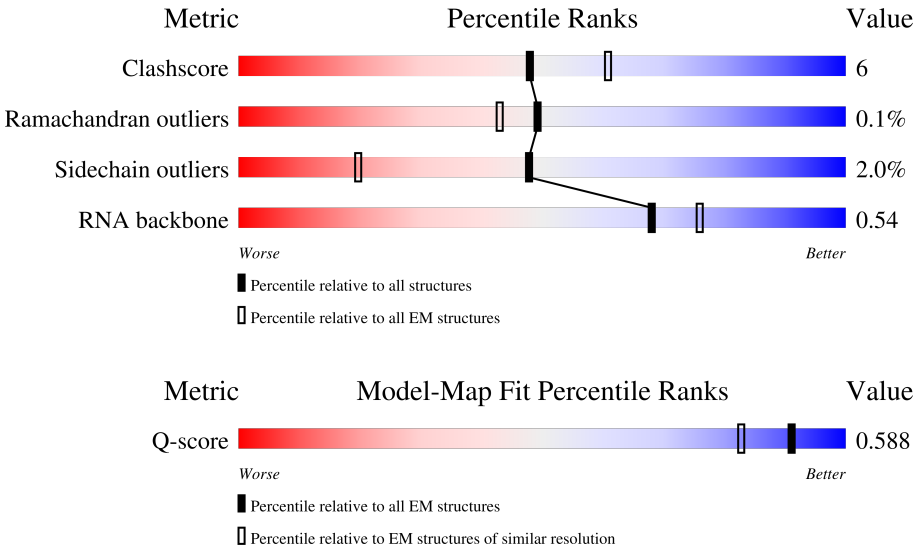
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal 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

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

The reported resolution of this entry is 2.70 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.



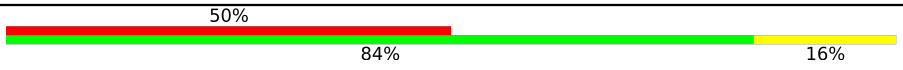
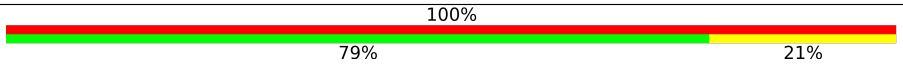
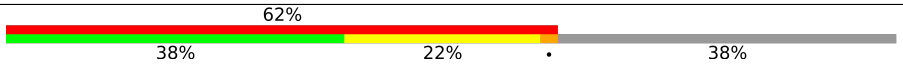
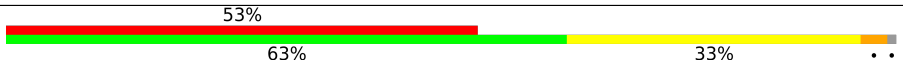
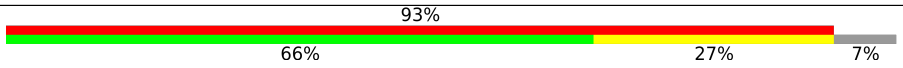
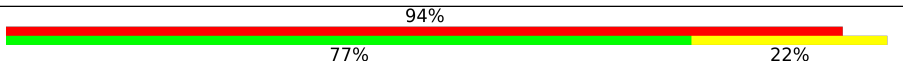
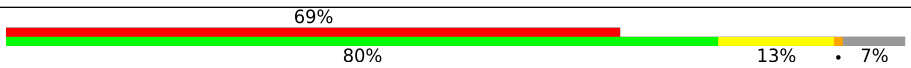
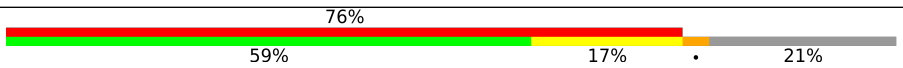
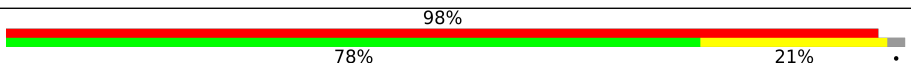
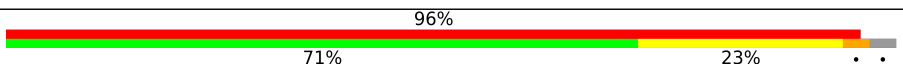
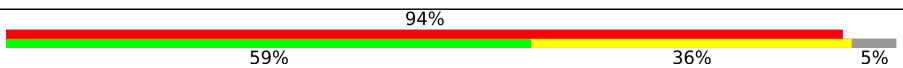
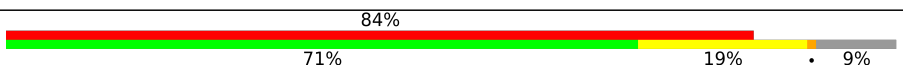
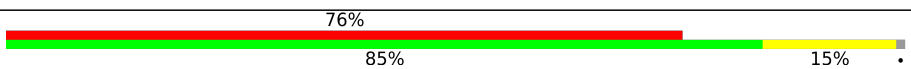
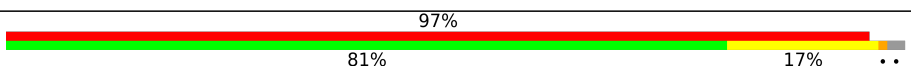
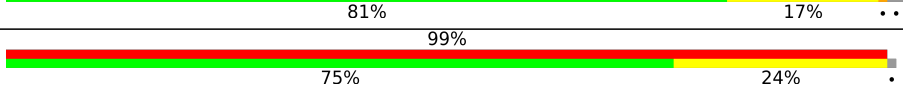
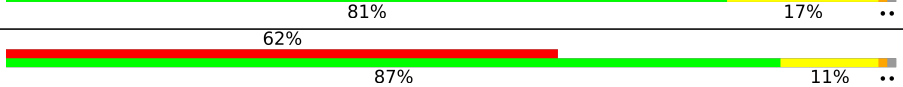
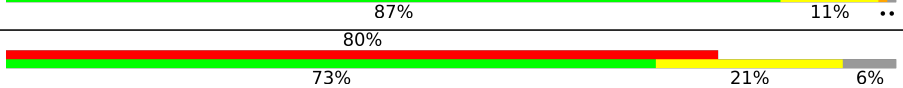
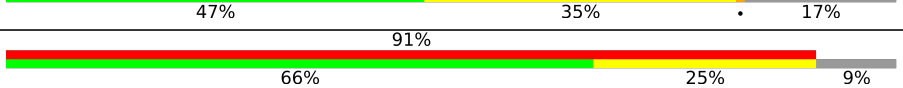
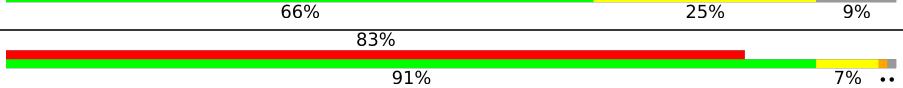
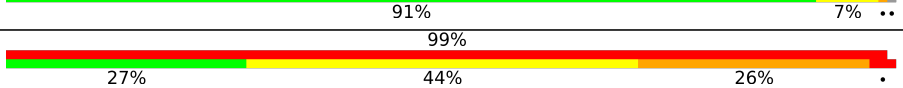
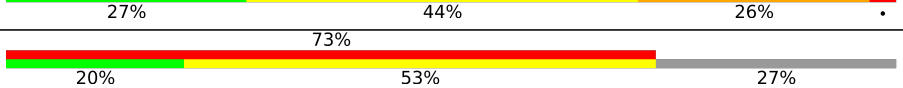
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10327 (2.20 - 3.20)

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	0	55	51% 73% 20% 7%
2	1	46	20% 76% 24%
3	2	65	18% 85% 14%

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Mol	Chain	Length	Quality of chain
4	3	38	
5	4	70	
6	5	234	
7	A	1550	
8	B	241	
9	C	232	
10	D	206	
11	E	167	
12	F	131	
13	G	156	
14	H	130	
15	I	130	
16	J	103	
17	K	129	
18	L	124	
19	M	118	
20	N	101	
21	O	89	
22	P	82	
23	Q	84	
24	R	75	
25	S	92	
26	T	87	
27	V	77	
28	W	15	

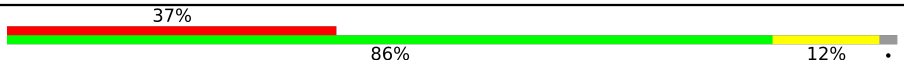
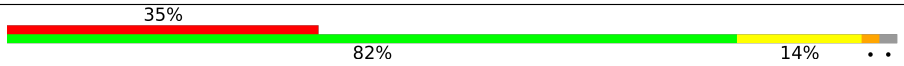
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Mol	Chain	Length	Quality of chain
29	X	111	87% 69% 18% 12%
30	a	2923	22% 66% 29%
31	b	116	48% 79% 19%
32	c	273	30% 91% 8%
33	d	209	29% 88% 12%
34	e	201	51% 85% 14%
35	f	179	98% 84% 15%
36	g	177	96% 82% 16%
37	h	149	99% 69% 30%
38	i	142	31% 88% 12%
39	j	123	40% 87% 13%
40	k	144	43% 84% 16%
41	l	136	48% 86% 13%
42	m	128	16% 82% 11% 7%
43	n	117	72% 73% 26%
44	o	115	44% 85% 14%
45	p	118	27% 90% 9%
46	q	103	53% 80% 20%
47	r	110	31% 89% 11%
48	s	100	47% 86% 7% 7%
49	t	104	68% 84% 13%
50	u	94	70% 90% 10%
51	v	85	21% 76% 15% 8%
52	w	78	42% 88% 10%
53	x	63	73% 73% 25%

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Mol	Chain	Length	Quality of chain
54	y	59	
55	z	57	

2 Entry composition (i)

There are 58 unique types of molecules in this entry. The entry contains 146071 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	51	418	268	76	73	1	0	0

- Molecule 2 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	46	377	228	90	57	2	0	0

- Molecule 3 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	64	504	323	105	74	2	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	38	302	185	65	48	4	0	0

- Molecule 5 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	70	540	333	103	98	6	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	5	146	1105	688	204	211	2	0	0

- Molecule 7 is a RNA chain called 16S rRNA (1538-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	1538	Total	C	N	O	P	0	0
			33009	14730	6051	10690	1538		

- Molecule 8 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	224	Total	C	N	O	S	0	0
			1749	1106	315	320	8		

- Molecule 9 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	206	Total	C	N	O	S	0	0
			1623	1028	305	287	3		

- Molecule 10 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	205	Total	C	N	O	S	0	0
			1644	1025	316	298	5		

- Molecule 11 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	156	Total	C	N	O	S	0	0
			1155	719	219	211	6		

- Molecule 12 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	103	Total	C	N	O	S	0	0
			832	524	151	150	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	62	MET	LEU	variant	UNP A0A2N4W582

- Molecule 13 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	153	Total	C	N	O	S	0	0
			1204	751	231	218	4		

- Molecule 14 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	129	Total	C	N	O	S	0	0
			977	616	171	184	6		

- Molecule 15 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	126	Total	C	N	O	S	0	0
			1010	628	202	177	3		

- Molecule 16 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	98	Total	C	N	O	S	0	0
			788	493	151	143	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	117	Total	C	N	O	S	0	0
			878	541	173	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	modified residue	UNP A0A1C1EGM1

- Molecule 18 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	123	Total	C	N	O	S	0	0
			958	592	196	165	5		

- Molecule 19 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	116	Total	C	N	O	S	0	0
			907	564	181	158	4		

- Molecule 20 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	100	Total	C	N	O	S	0	0
			805	500	164	138	3		

- Molecule 21 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	O	88	Total	C	N	O	S	0	0
			710	438	144	127	1		

- Molecule 22 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	81	Total	C	N	O	S	0	0
			636	397	127	111	1		

- Molecule 23 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	79	Total	C	N	O	S	0	0
			639	402	121	112	4		

- Molecule 24 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	R	62	Total	C	N	O	0	0
			507	321	94	92		

- Molecule 25 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	84	Total	C	N	O	S	0	0
			667	426	127	112	2		

- Molecule 26 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	86	Total	C	N	O	S	0	0
			669	413	138	115	3		

- Molecule 27 is a RNA chain called E site tRNA (77-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
27	V	77	Total	C	N	O	P	S	0	0
			1644	734	297	535	77	1		

- Molecule 28 is a RNA chain called Non Stop mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	11	Total	C	N	O	P	0	0
			242	107	46	78	11		

- Molecule 29 is a protein called Ribosomal subunit interface protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	98	Total	C	N	O	S	0	0
			778	484	149	142	3		

- Molecule 30 is a RNA chain called 23S rRNA (2901-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	2901	Total	C	N	O	P	0	0
			62284	27795	11452	20136	2901		

- Molecule 31 is a RNA chain called 5S rRNA (119-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	116	Total	C	N	O	P	0	0
			2483	1106	453	808	116		

- Molecule 32 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	271	Total	C	N	O	S	0	0
			2080	1286	423	364	7		

- Molecule 33 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	209	Total	C	N	O	S	0	0
			1567	981	289	294	3		

- Molecule 34 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	e	201	Total	C	N	O	S	0	0
			1554	975	284	290	5		

- Molecule 35 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 36 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	176	Total	C	N	O	S	0	0
			1319	830	243	244	2		

- Molecule 37 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	148	Total	C	N	O	S	0	0
			1099	693	197	208	1		

- Molecule 38 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	142	Total	C	N	O	S	0	0
			1134	716	211	202	5		

- Molecule 39 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	123	Total	C	N	O	S	0	0
			947	594	181	166	6		

- Molecule 40 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	144	Total	C	N	O	S	0	0
			1063	658	211	191	3		

- Molecule 41 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	136	Total	C	N	O	S	0	0
			1074	685	204	179	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
l	82	MS6	MET	modified residue	UNP A0A1C1EGZ5

- Molecule 42 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	119	Total	C	N	O	S	0	0
			950	588	195	162	5		

- Molecule 43 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 44 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 45 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 46 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	103	Total 816	C 517	N 153	O 144	S 2	0	0

- Molecule 47 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	110	Total 855	C 530	N 166	O 156	S 3	0	0

- Molecule 48 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	93	Total 739	C 467	N 139	O 131	S 2	0	0

- Molecule 49 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	t	102	Total 779	C 492	N 146	O 141	0	0

- Molecule 50 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	u	94	Total 749	C 477	N 136	O 134	S 2	0	0

- Molecule 51 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	v	78	Total 592	C 367	N 118	O 106	S 1	0	0

- Molecule 52 is a protein called Large ribosomal subunit protein bL28.

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

- Molecule 53 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	62	Total 499	C 308	N 98	O 92	S 1	0	0

- Molecule 54 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	y	58	Total 447	C 279	N 87	O 79	S 2	0	0

- Molecule 55 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	56	Total 443	C 269	N 94	O 79	S 1	0	0

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	3	1	Total 1	Zn 1	0
56	4	1	Total 1	Zn 1	0

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	A	94	Total 94	Mg 94	0
57	N	1	Total 1	Mg 1	0
57	Q	1	Total 1	Mg 1	0
57	a	253	Total 253	Mg 253	0
57	b	5	Total 5	Mg 5	0
57	c	2	Total 2	Mg 2	0
57	p	2	Total 2	Mg 2	0
57	z	1	Total 1	Mg 1	0

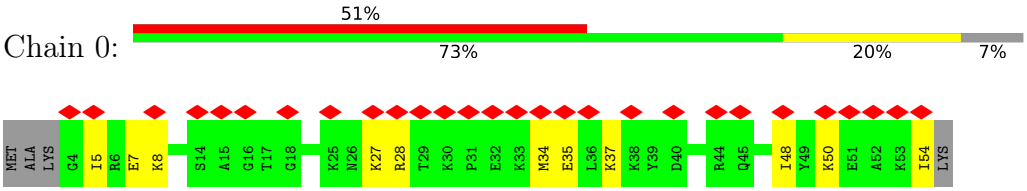
- Molecule 58 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	AltConf
58	A	46	Total K 46 46	0
58	L	1	Total K 1 1	0
58	a	114	Total K 114 114	0
58	b	1	Total K 1 1	0
58	c	4	Total K 4 4	0
58	d	1	Total K 1 1	0
58	e	1	Total K 1 1	0
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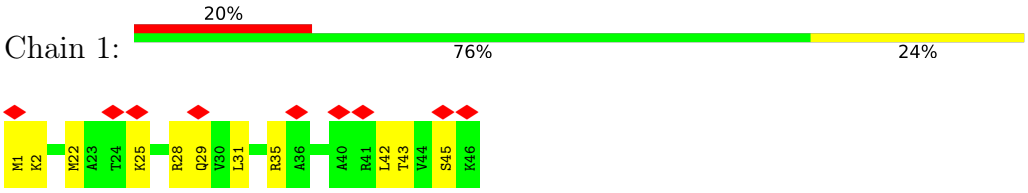
3 Residue-property plots (i)

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.

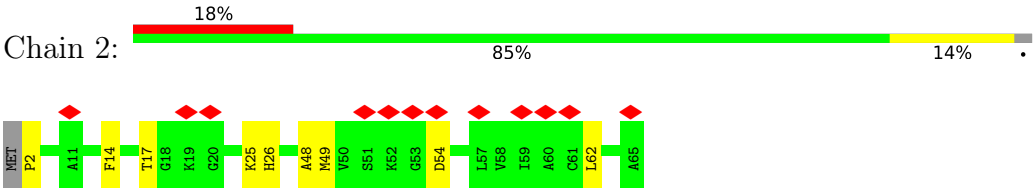
• Molecule 1: Large ribosomal subunit protein bL33



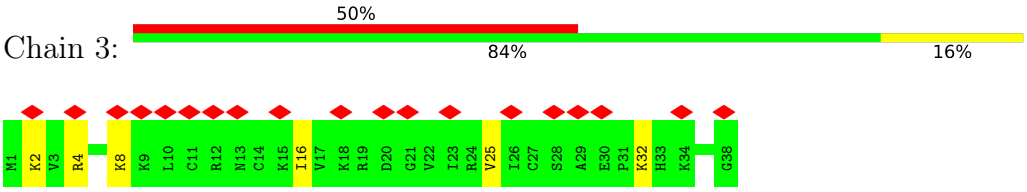
• Molecule 2: Large ribosomal subunit protein bL34



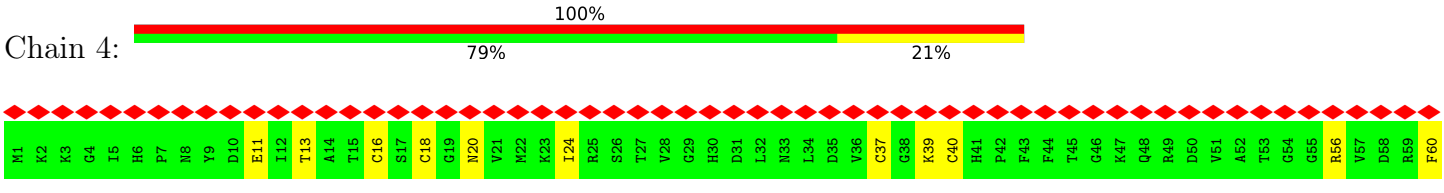
• Molecule 3: Large ribosomal subunit protein bL35



• Molecule 4: Large ribosomal subunit protein bL36



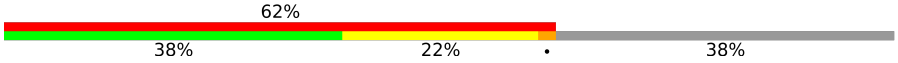
• Molecule 5: Large ribosomal subunit protein bL31

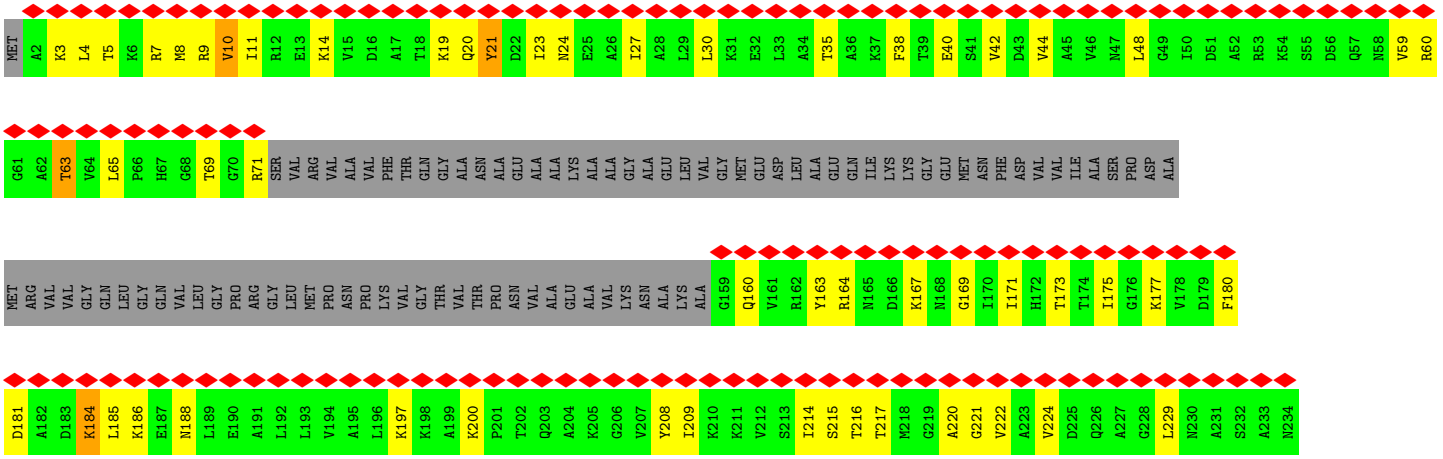




• Molecule 6: Large ribosomal subunit protein uL1

Chain 5:

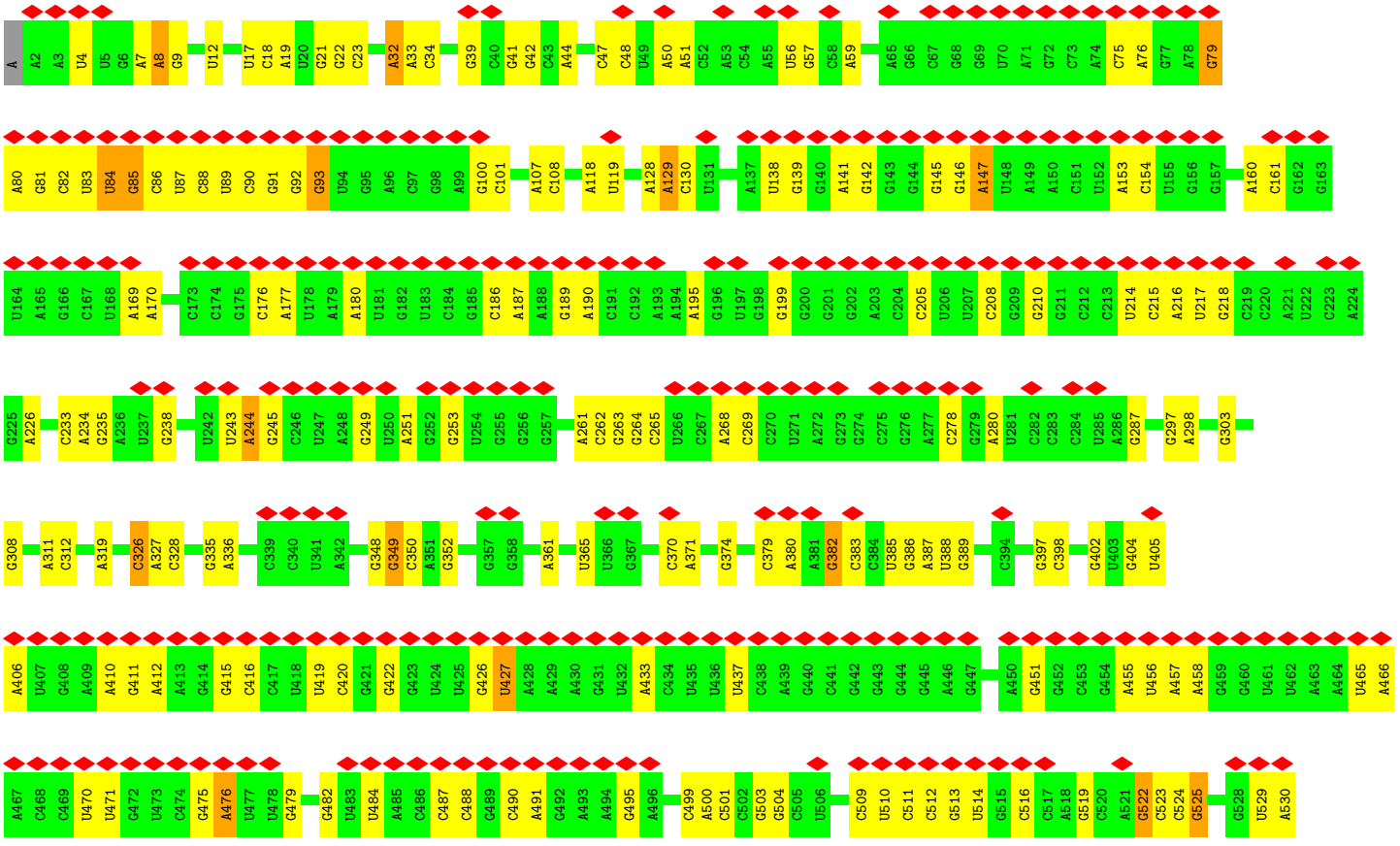


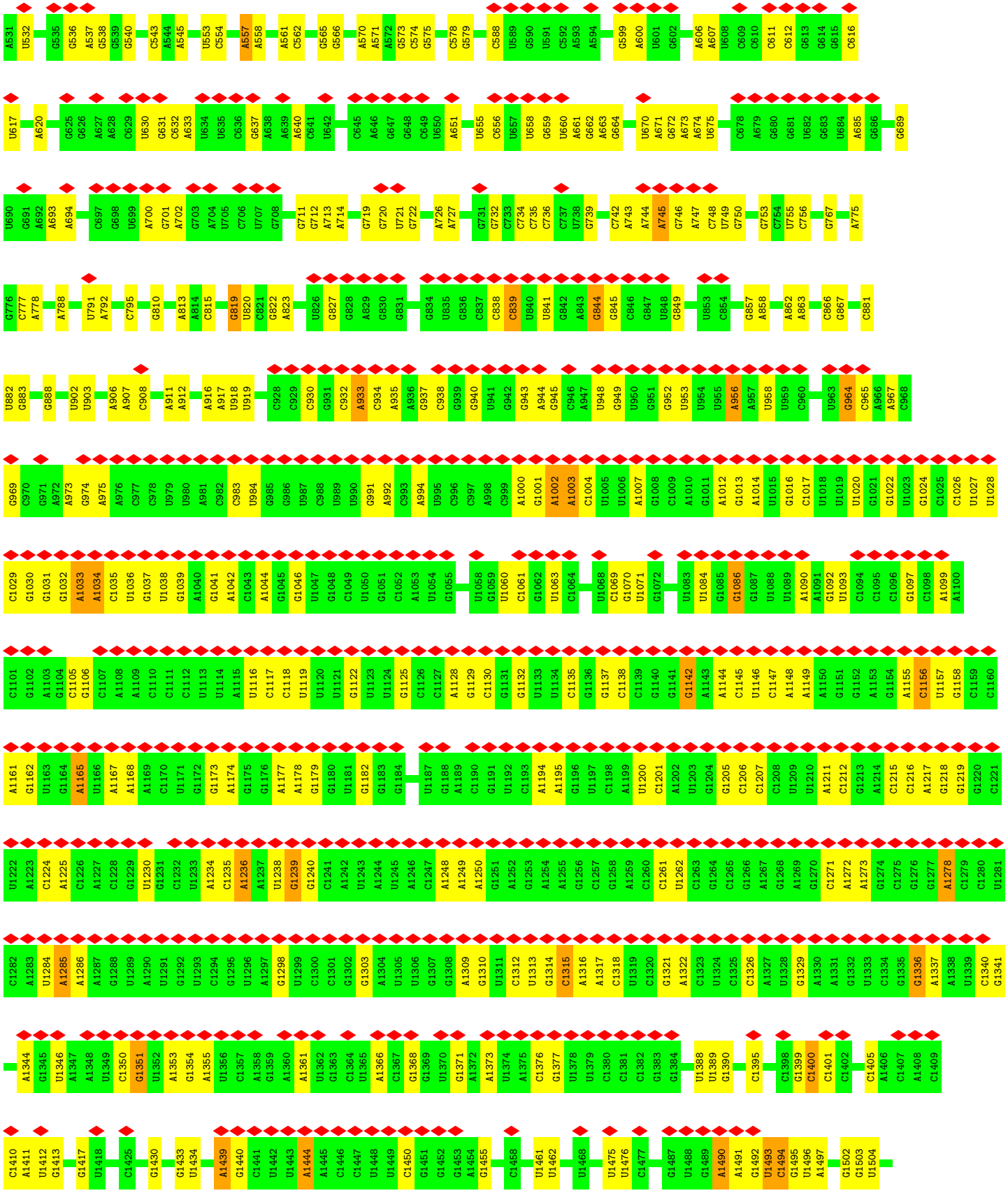


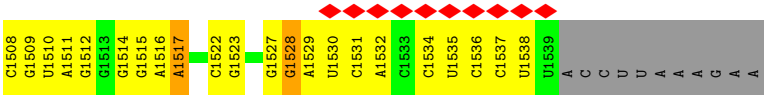
• Molecule 7: 16S rRNA (1538-MER)

Chain A:



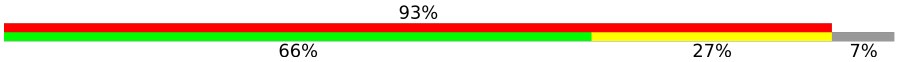



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U617 A620 G625 G626 A627 A628 C629 U630 G631 C632 A633 U634 U635 C636 G637 A638 A639 A640 C641 U642 C645 A646 G647 G648 C649 U650 A651 U655 C656 U657 U658 G659 U660 A661 G662 A663 G664 U670 A671 G672 A673 A674 U675 C678 A679 G680 G681 U682 G683 U684 A685 G686 G689
U690 G691 A692 A693 A694 C697 G698 U699 A700 G701 A702 G703 A704 U705 C706 U707 G708 G711 G712 A713 A714 G719 G720 U721 G722 A726 A727 G731 G732 C733 C734 C735 C736 C737 U738 G739 C742 A743 A744 A745 G746 A747 C748 U749 G750 G753 G754 U755 C756 G767 A775
G776 C777 A778 A788 U791 A792 C795 G810 A813 A814 C815 G819 U820 C821 G822 A823 U826 G827 G828 A829 G830 G831 G834 U835 G836 C837 C838 C839 U840 U841 G842 A843 G844 G845 C846 G847 U848 G849 U853 C854 G857 A858 A862 A863 C866 G867 C881
U882 G883 G888 U902 U903 A906 A907 C908 A911 A912 A916 A917 U918 U919 C928 C929 C930 G931 C932 A933 C934 A935 A936 G937 C938 G939 G940 U941 G942 G943 A944 G945 C946 A947 U948 G949 U950 G951 G952 U953 U954 U955 A956 A957 U958 U959 C960 U963 G964 C965 A966 A967 C968
G969 C970 G971 A972 A973 G974 A975 A976 C977 C978 U979 U980 A981 C982 C983 U984 G985 G986 U987 C988 U989 U990 G991 A992 C993 A994 U995 C996 C997 A998 C999 A1000 G1001 A1002 A1003 C1004 U1005 U1006 A1007 G1008 C1009 A1010 G1011 A1012 G1013 A1014 U1015 G1016 C1017 U1018 U1019 U1020 G1021 G1022 U1023 G1024 C1025 C1026 U1027 U1028
C1029 G1030 G1031 G1032 A1033 A1034 C1035 U1036 G1037 U1038 G1039 A1040 G1041 A1042 C1043 A1044 G1045 G1046 U1047 G1048 C1049 U1050 G1051 C1052 A1053 U1054 G1055 U1058 G1059 U1060 C1061 G1062 U1063 C1064 U1068 C1069 G1070 U1071 G1072 U1083 U1084 G1085 G1086 G1087 U1088 U1089 A1090 A1091 G1092 U1093 C1094 C1095 C1096 G1097 C1098 A1099 A1100
C1101 G1102 A1103 G1104 C1105 G1106 C1107 A1108 A1109 C1110 C1111 C1112 U1113 U1114 A1115 U1116 C1117 C1118 U1119 U1120 U1121 G1122 U1123 U1124 G1125 C1126 C1127 A1128 G1129 C1130 G1131 G1132 U1133 U1134 C1135 G1136 G1137 C1138 C1139 G1140 G1141 G1142 A1143 A1144 C1145 U1146 C1147 A1148 A1149 A1150 G1151 G1152 A1153 G1154 A1155 C1156 U1157 G1158 C1159 C1160
A1161 G1162 U1163 G1164 A1165 A1166 U1166 A1167 A1168 A1169 C1170 U1171 G1172 G1173 A1174 G1175 G1176 A1177 A1178 G1179 G1180 U1181 G1182 G1183 G1184 U1187 G1188 A1189 C1190 G1191 U1192 C1193 A1194 A1195 G1196 U1197 C1198 A1199 U1200 C1201 A1202 U1203 G1204 G1205 C1206 C1207 C1208 U1209 U1210 A1211 C1212 G1213 A1214 C1215 C1216 A1217 G1218 G1219 G1220 C1221
U1222 A1223 C1224 A1225 C1226 A1227 C1228 G1229 U1230 G1231 C1232 U1233 A1234 C1235 A1236 A1237 U1238 G1239 G1240 C1241 A1242 U1243 A1244 U1245 A1246 C1247 A1248 A1249 A1250 G1251 A1252 G1253 A1254 A1255 G1256 C1257 G1258 A1259 C1260 C1261 U1262 C1263 G1264 C1265 G1266 A1267 G1268 A1269 G1270 C1271 A1272 A1273 G1274 C1275 G1276 G1277 A1278 C1279 C1280 U1281
C1282 A1283 U1284 A1285 A1286 A1287 G1288 U1289 A1290 U1291 G1292 U1293 C1294 G1295 U1296 A1297 G1298 U1299 C1300 C1301 G1302 G1303 A1304 U1305 U1306 G1307 G1308 A1309 G1310 U1311 C1312 U1313 G1314 C1315 A1316 A1317 C1318 U1319 C1320 G1321 A1322 C1323 U1324 C1325 C1326 A1327 U1328 G1329 A1330 A1331 G1332 U1333 C1334 G1335 G1336 A1337 A1338 U1339 C1340 G1341
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• Molecule 8: Small ribosomal subunit protein uS2

Chain B:

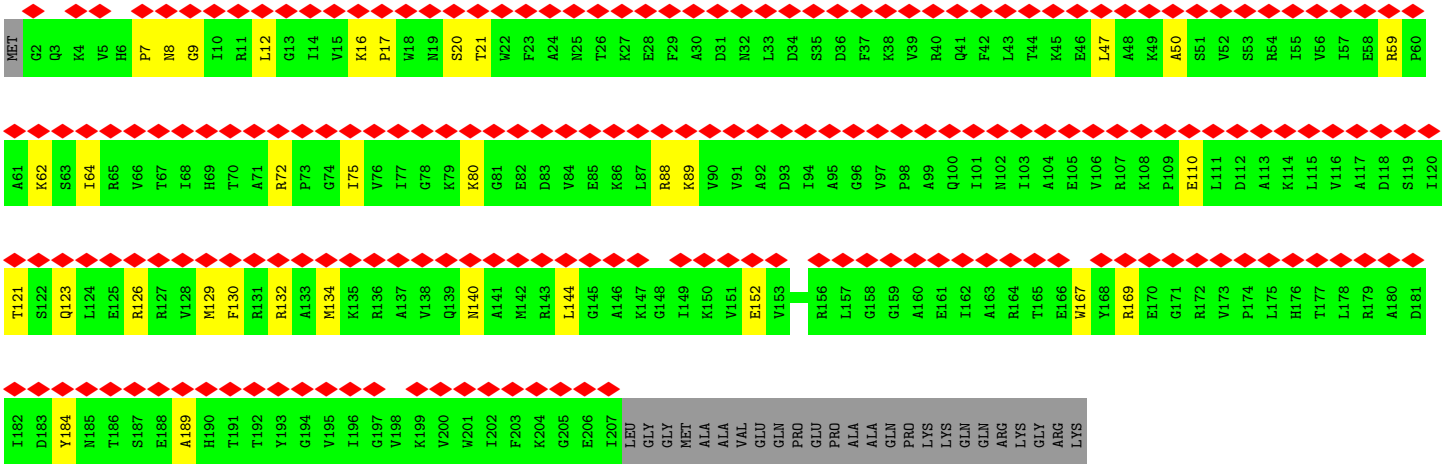




• Molecule 9: Small ribosomal subunit protein uS3

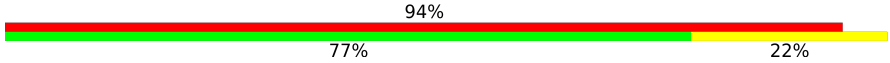
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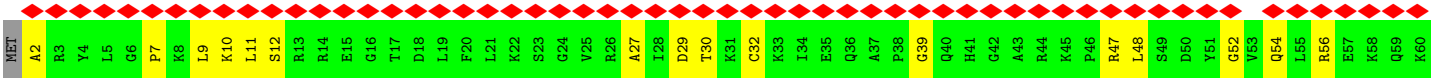


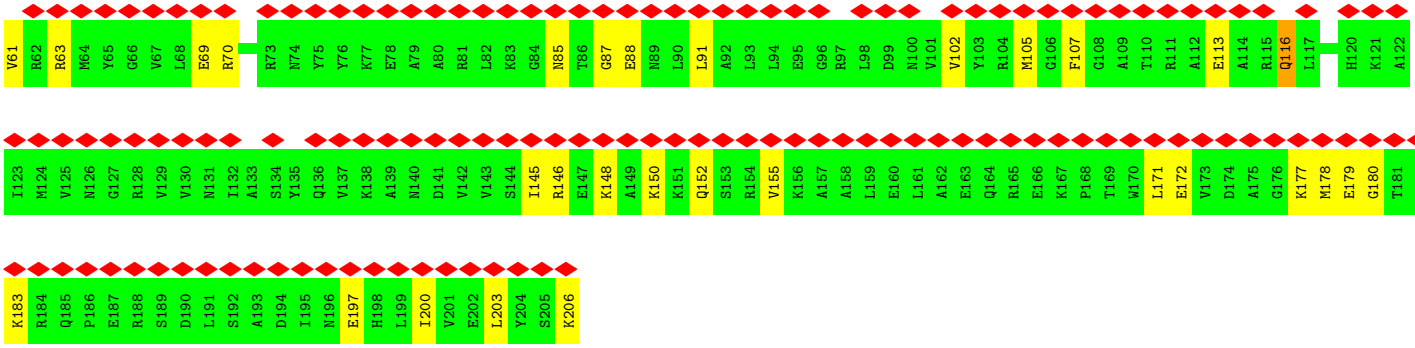


• Molecule 10: Small ribosomal subunit protein uS4

Chain D:



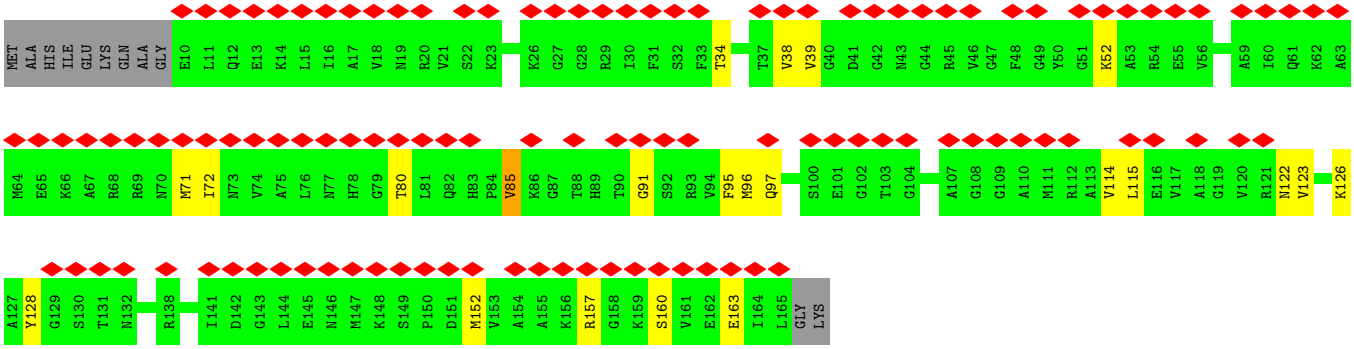




• Molecule 11: Small ribosomal subunit protein uS5

Chain E:

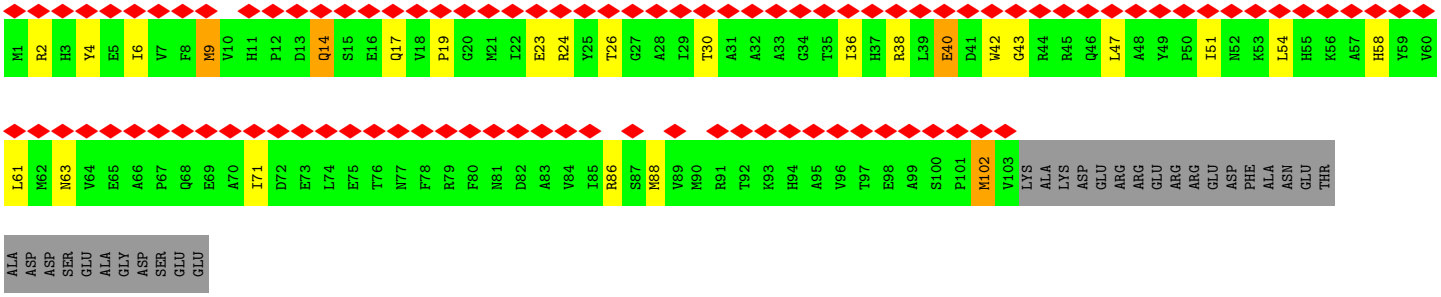




• Molecule 12: Small ribosomal subunit protein bS6

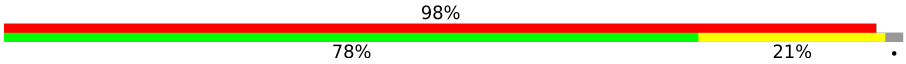
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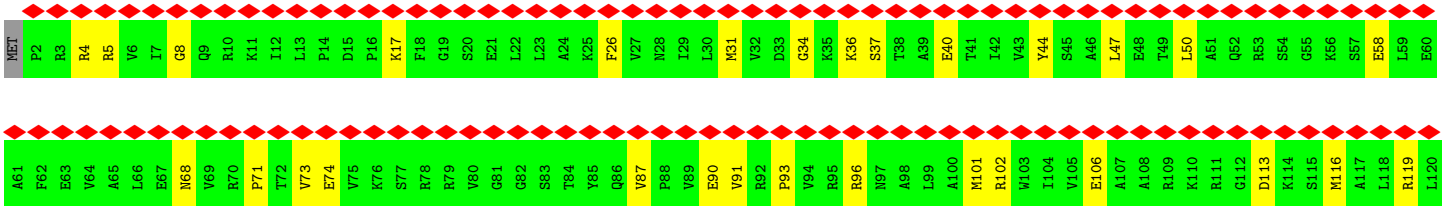


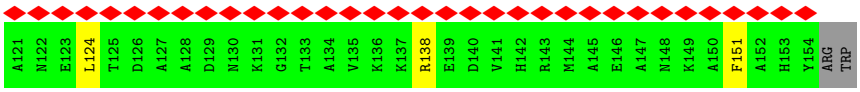


• Molecule 13: Small ribosomal subunit protein uS7

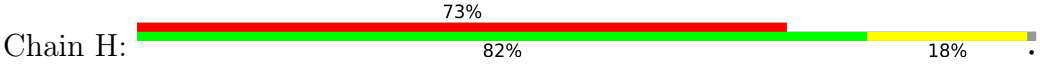
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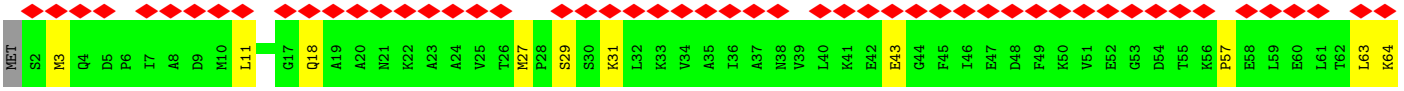


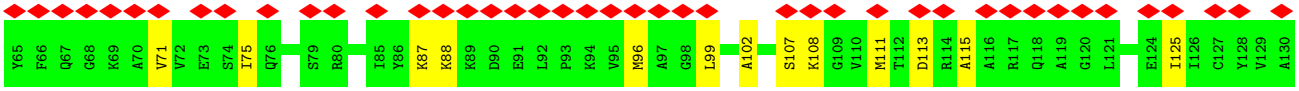




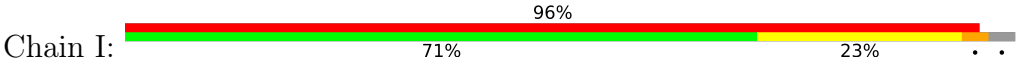
• Molecule 14: Small ribosomal subunit protein uS8

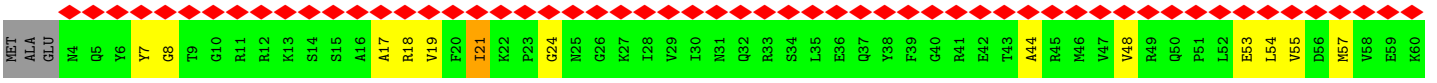


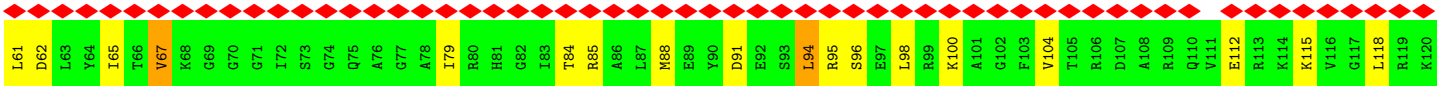


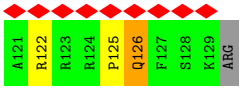


• Molecule 15: Small ribosomal subunit protein uS9

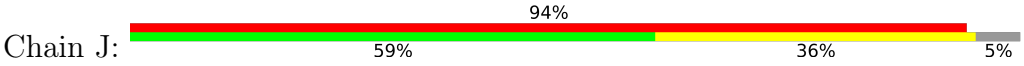


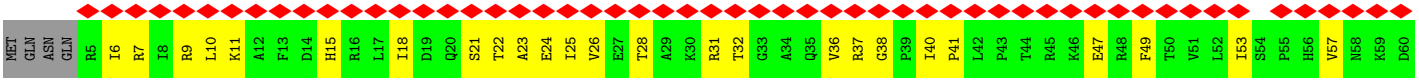


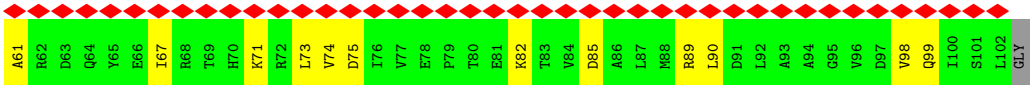




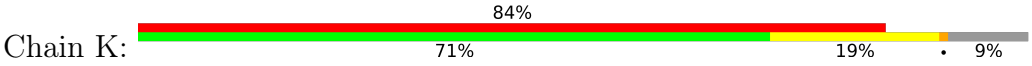
• Molecule 16: Small ribosomal subunit protein uS10

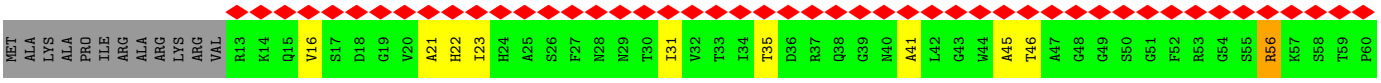






• Molecule 17: Small ribosomal subunit protein uS11



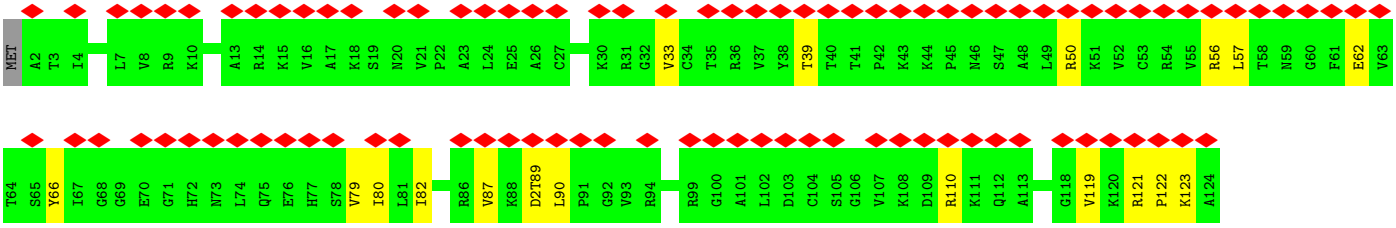




• Molecule 18: Small ribosomal subunit protein uS12

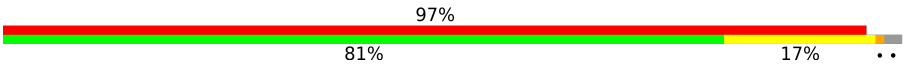
Chain L:

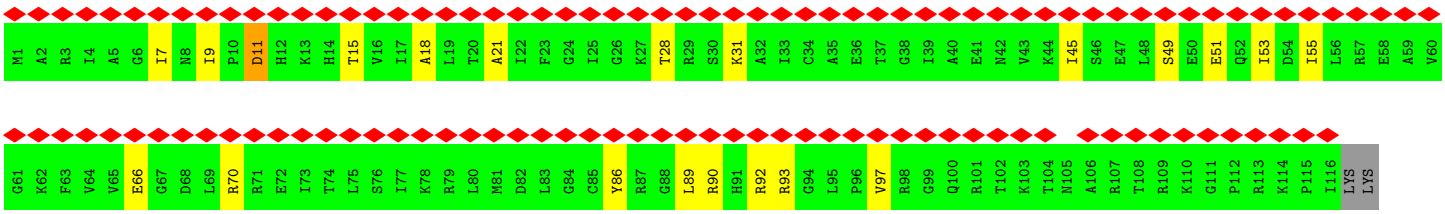




• Molecule 19: Small ribosomal subunit protein uS13

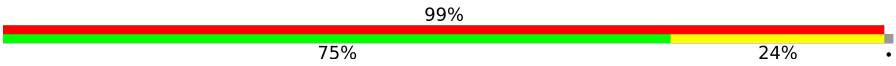
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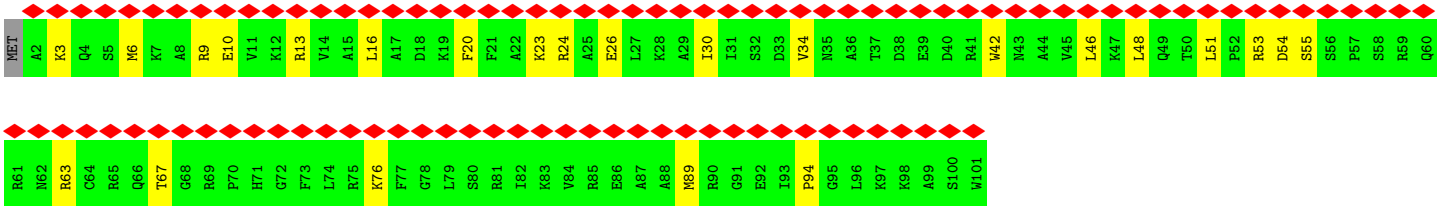




• Molecule 20: Small ribosomal subunit protein uS14

Chain N:

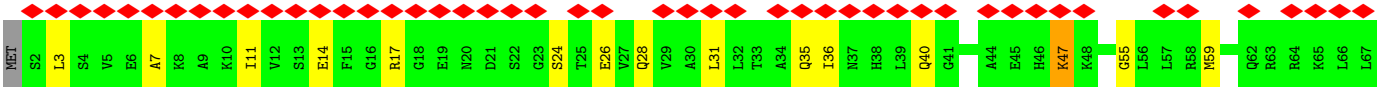


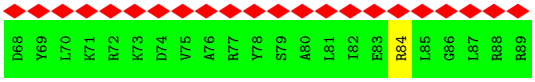


• Molecule 21: Small ribosomal subunit protein uS15

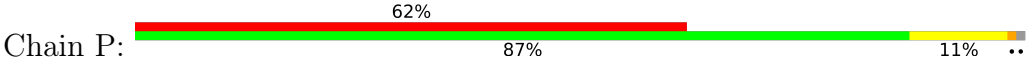
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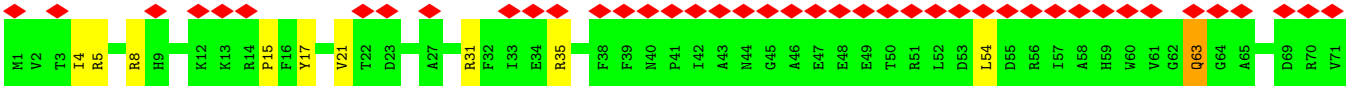


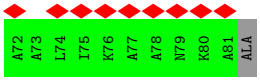




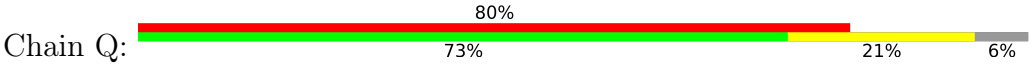
• Molecule 22: Small ribosomal subunit protein bS16

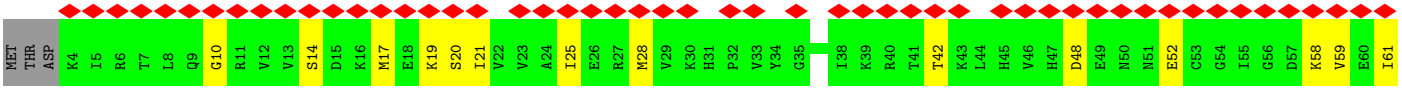


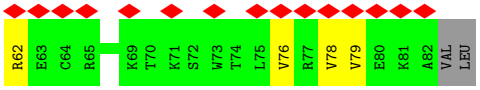




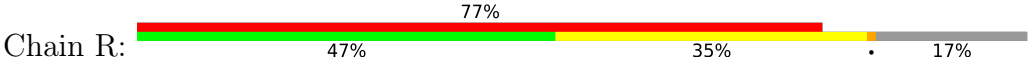
• Molecule 23: Small ribosomal subunit protein uS17

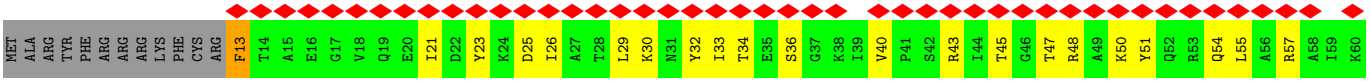


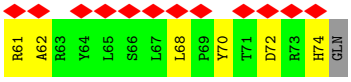




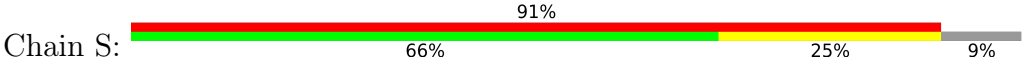
• Molecule 24: Small ribosomal subunit protein bS18

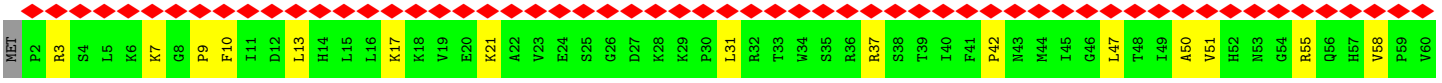


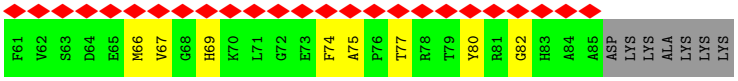




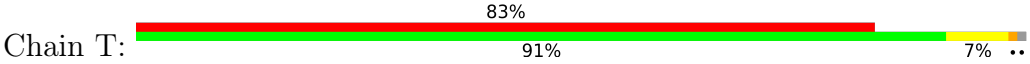
• Molecule 25: Small ribosomal subunit protein uS19

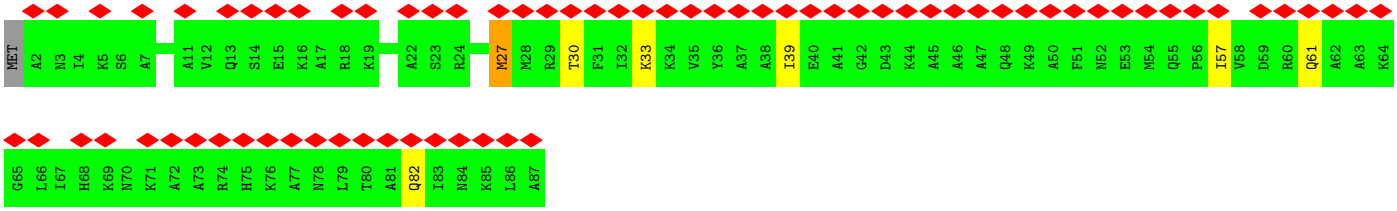




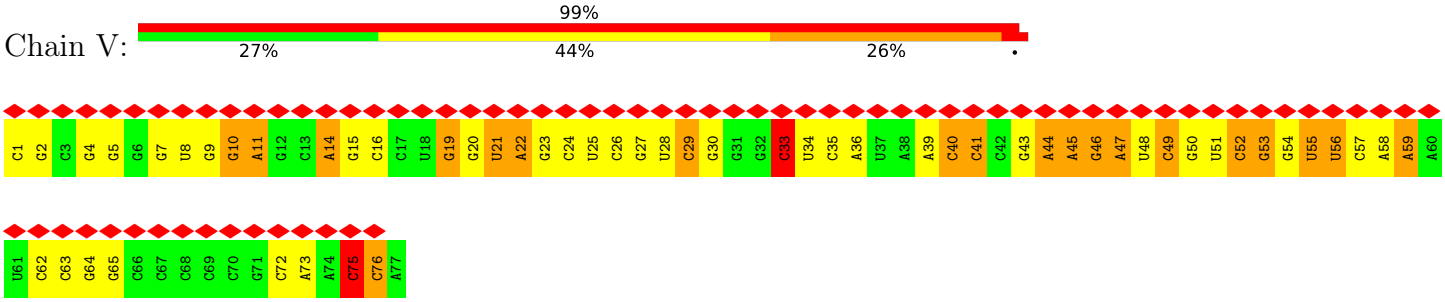


• Molecule 26: Small ribosomal subunit protein bS20

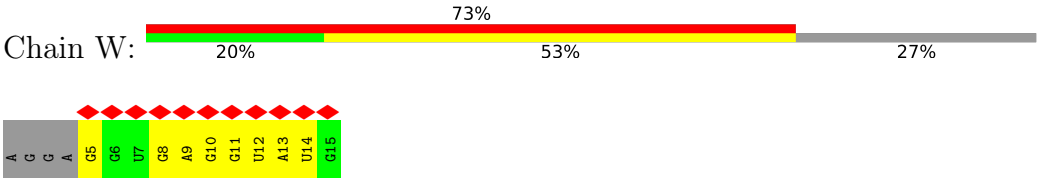




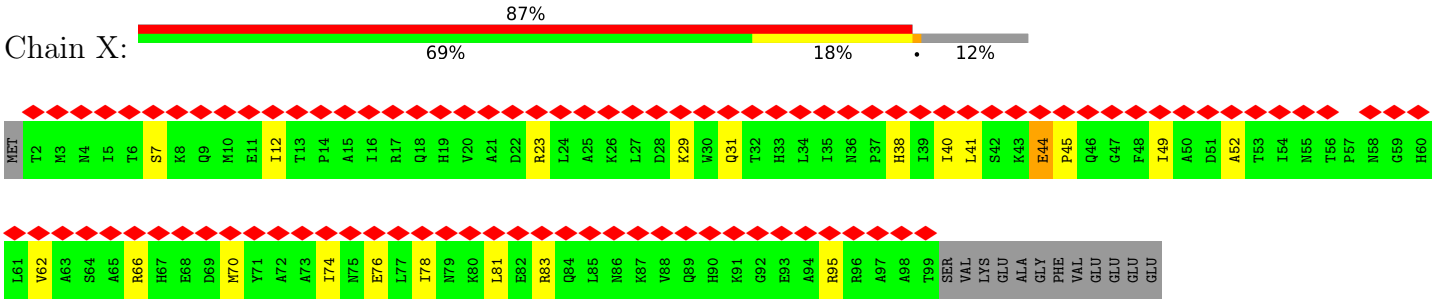
• Molecule 27: E site tRNA (77-MER)



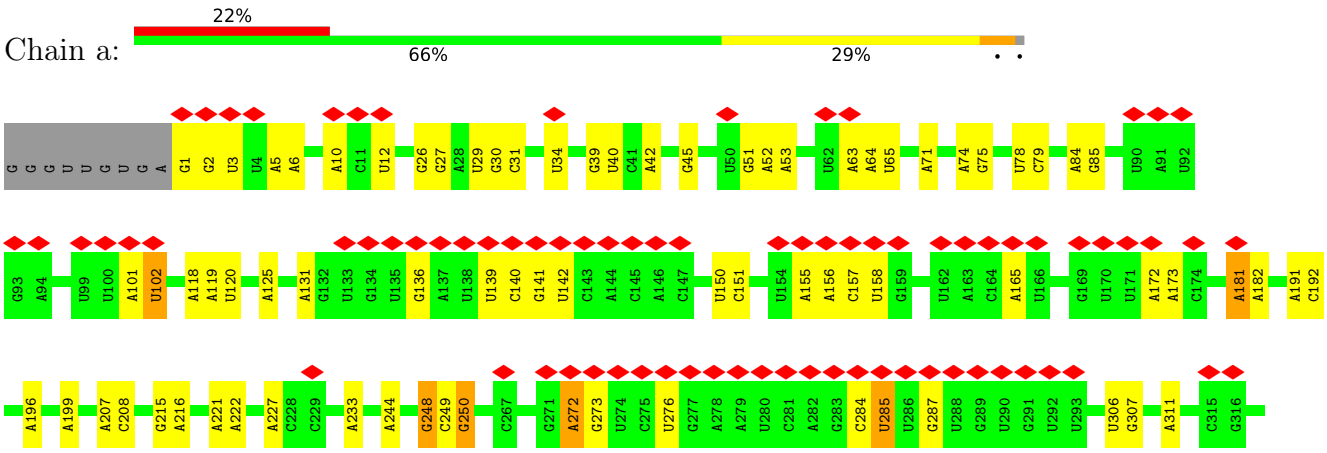
• Molecule 28: Non Stop mRNA

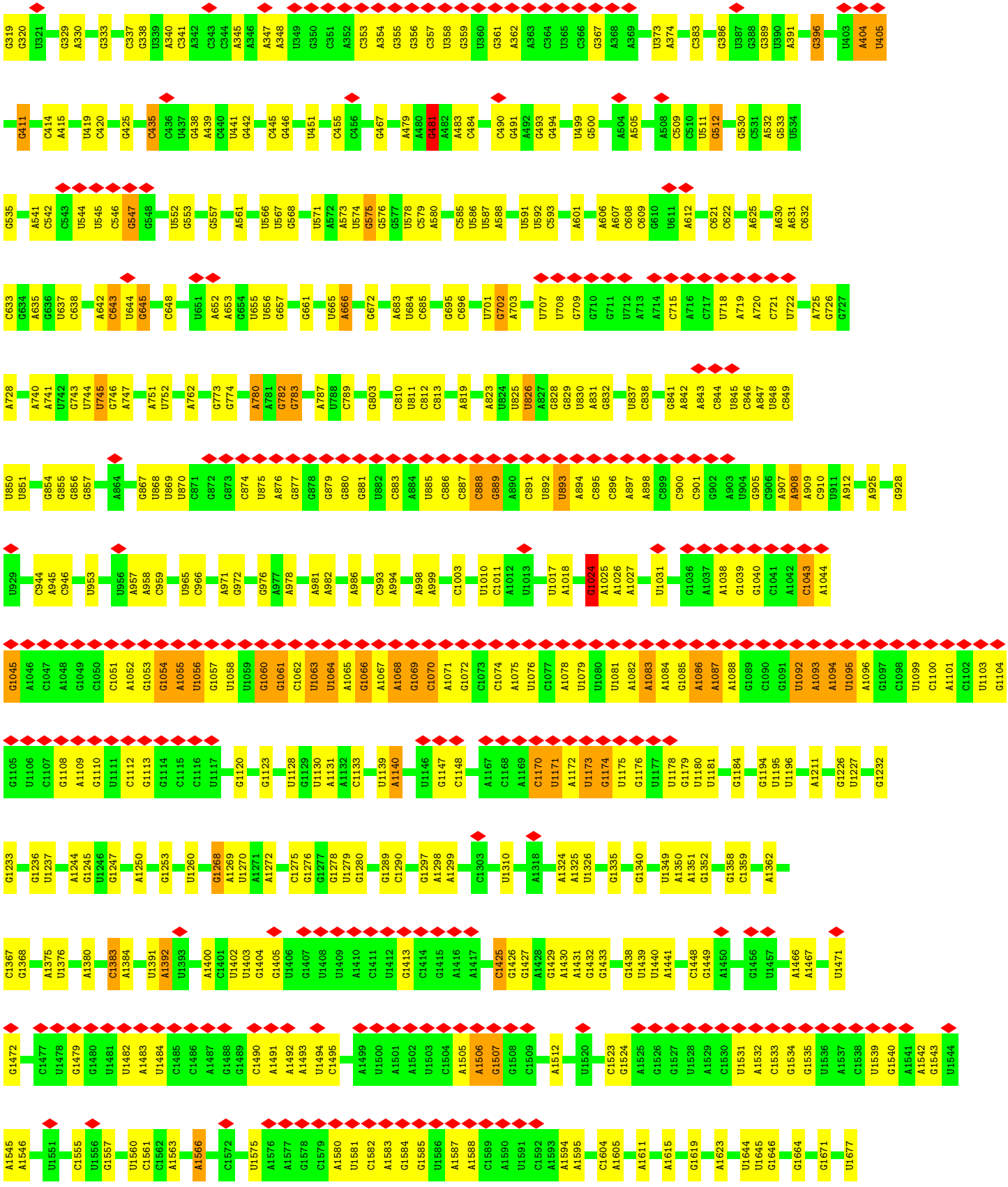


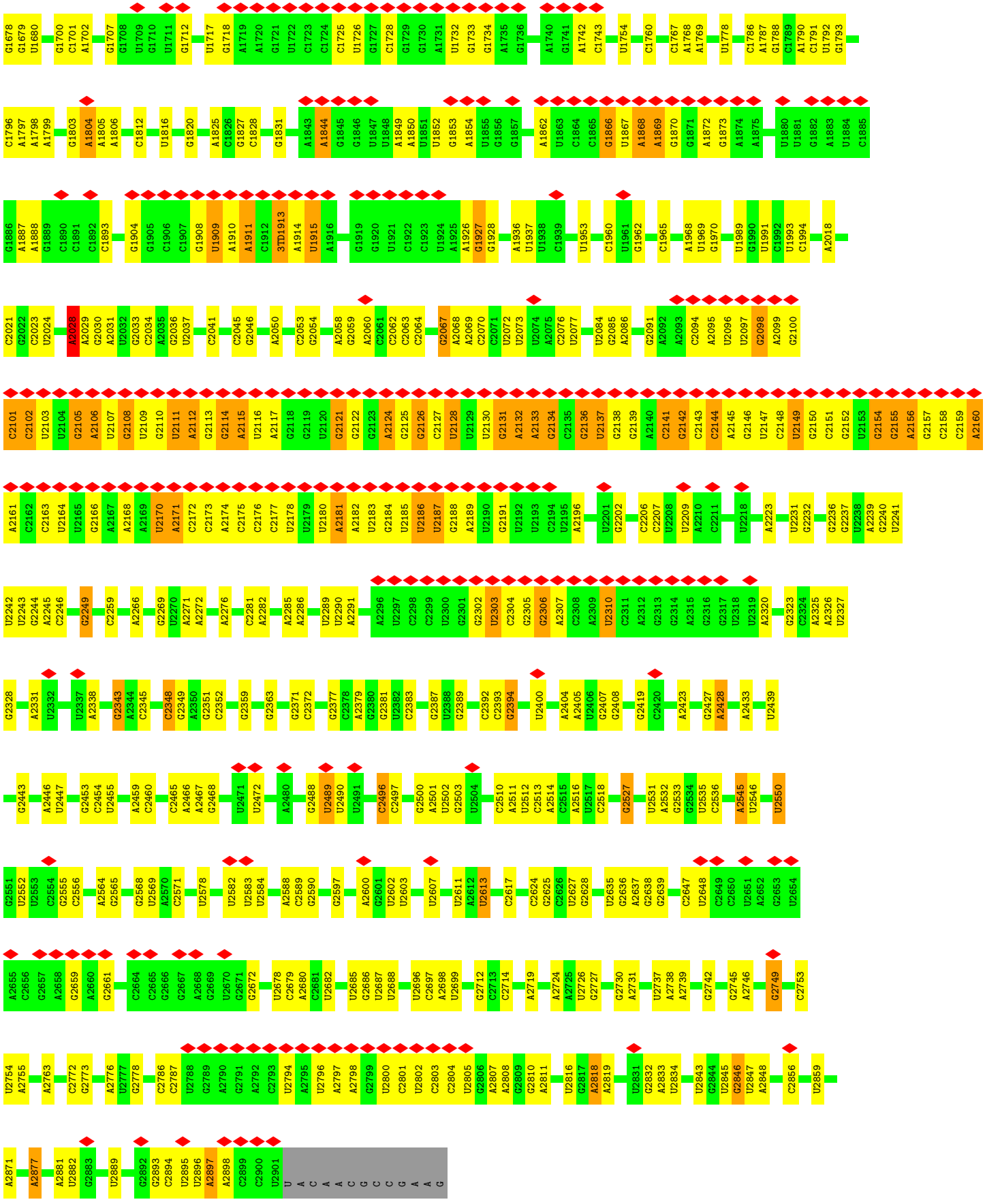
• Molecule 29: Ribosomal subunit interface protein



• Molecule 30: 23S rRNA (2901-MER)

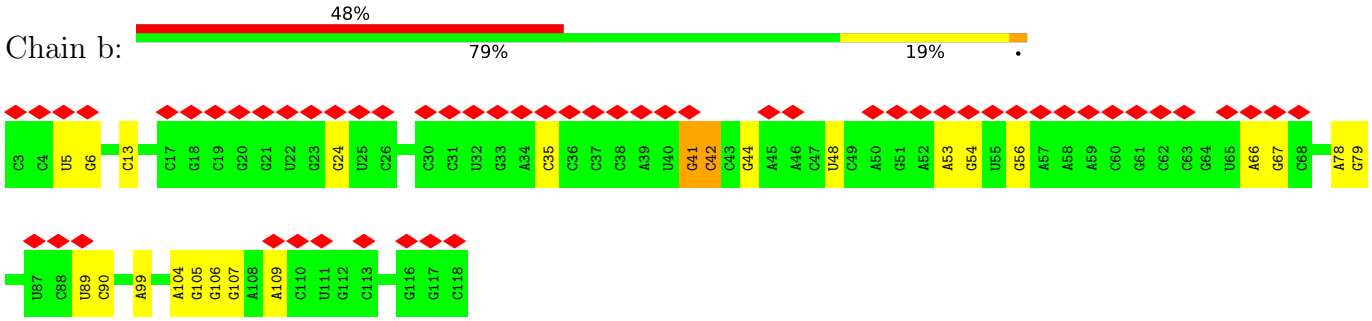





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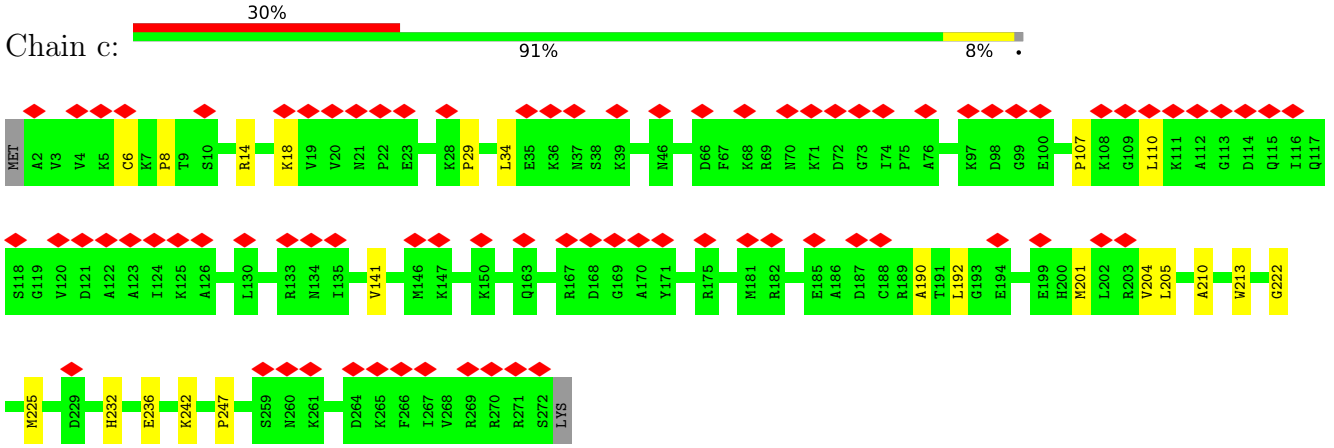
• Molecule 31: 5S rRNA (119-MER)

Chain b:



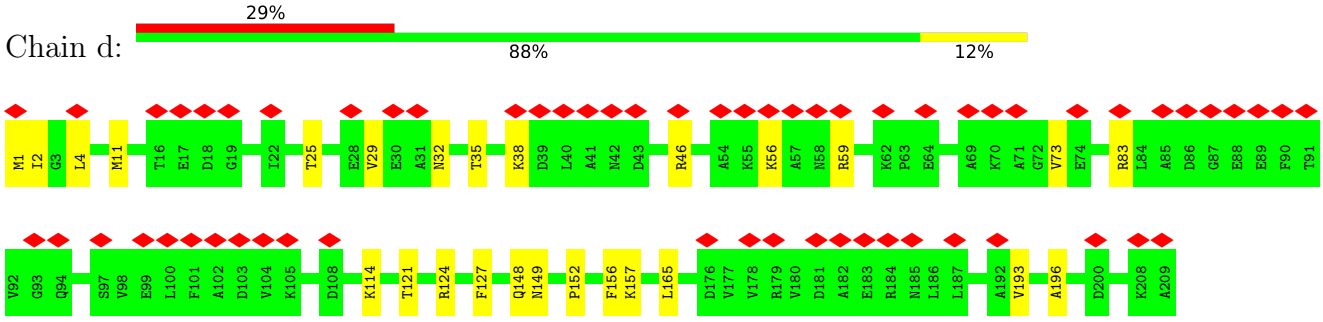
• Molecule 32: Large ribosomal subunit protein uL2

Chain c:



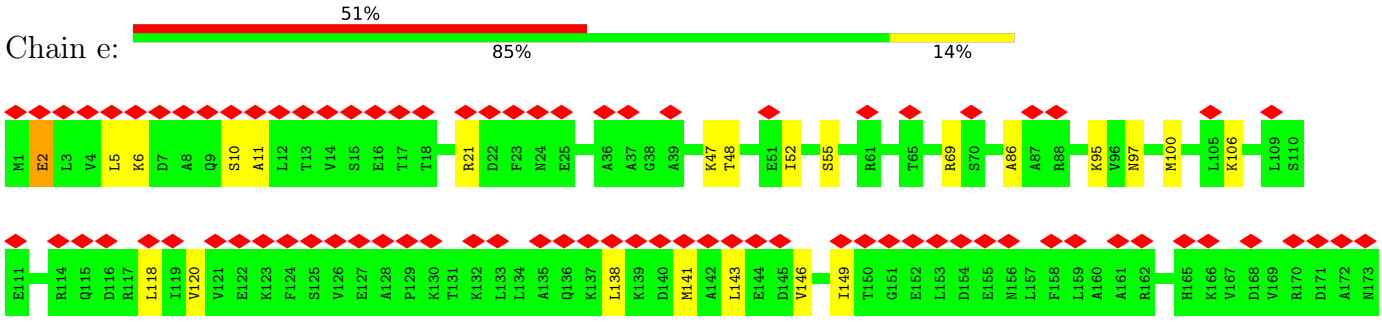
• Molecule 33: Large ribosomal subunit protein uL3

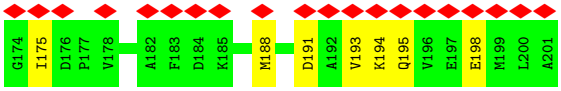
Chain d:



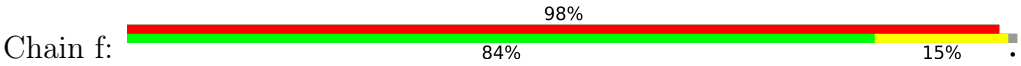
• Molecule 34: Large ribosomal subunit protein uL4

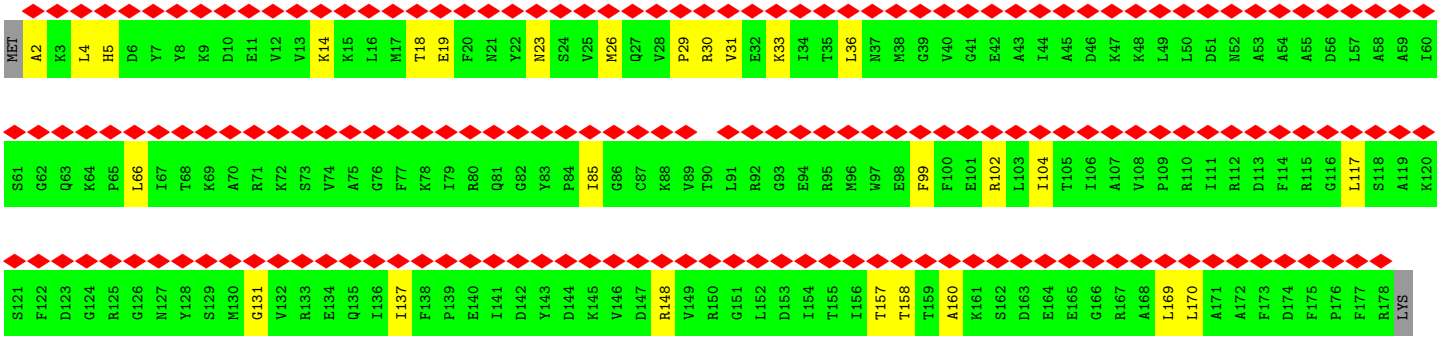
Chain e:



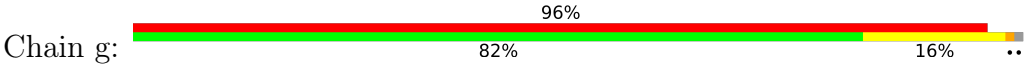


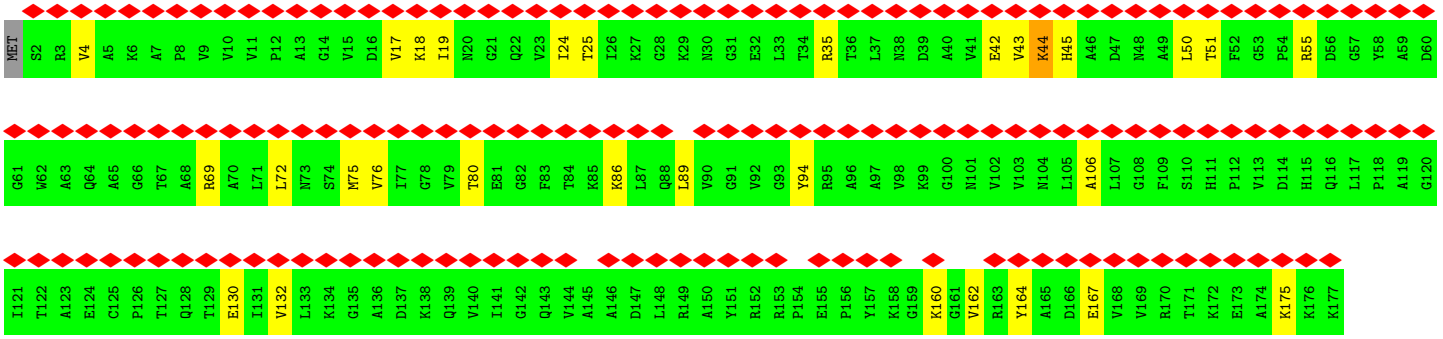
• Molecule 35: Large ribosomal subunit protein uL5





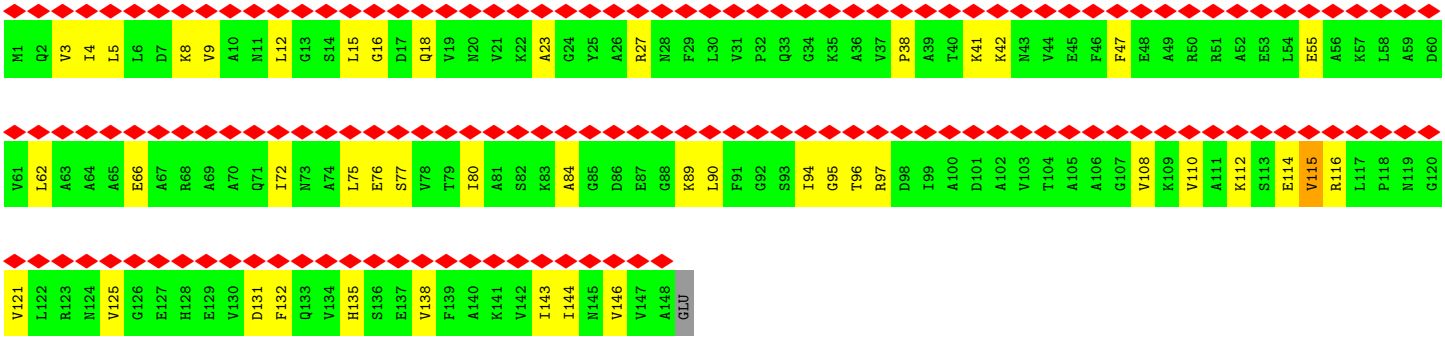
• Molecule 36: Large ribosomal subunit protein uL6





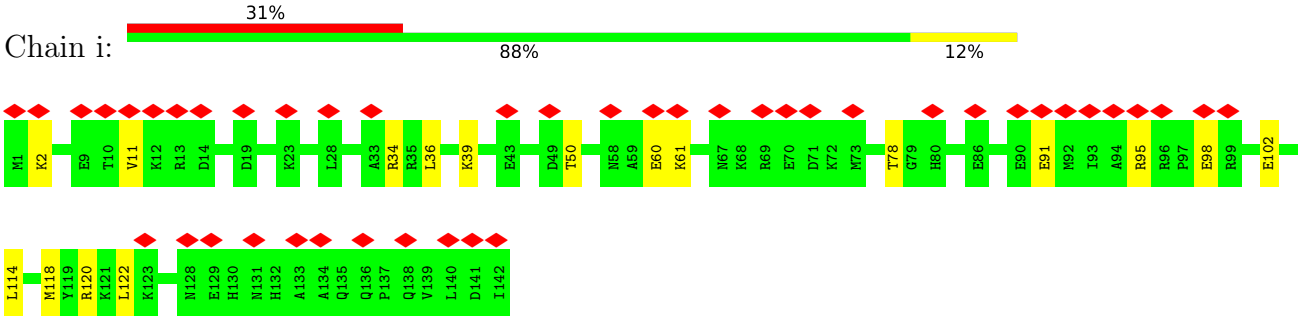
• Molecule 37: Large ribosomal subunit protein bL9





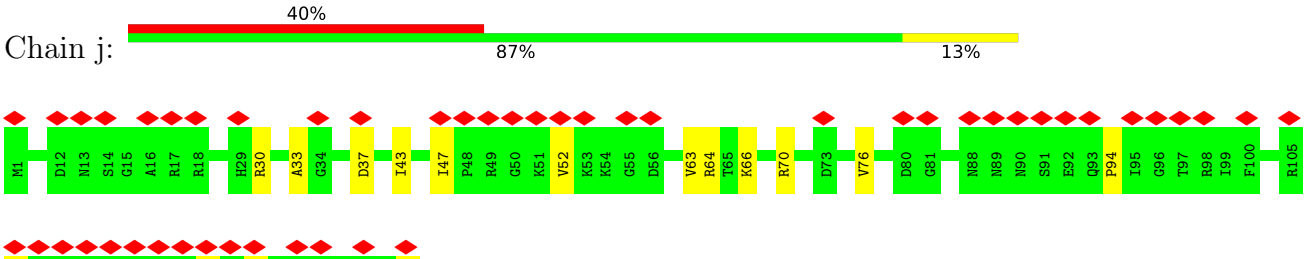
• Molecule 38: Large ribosomal subunit protein uL13

Chain i:



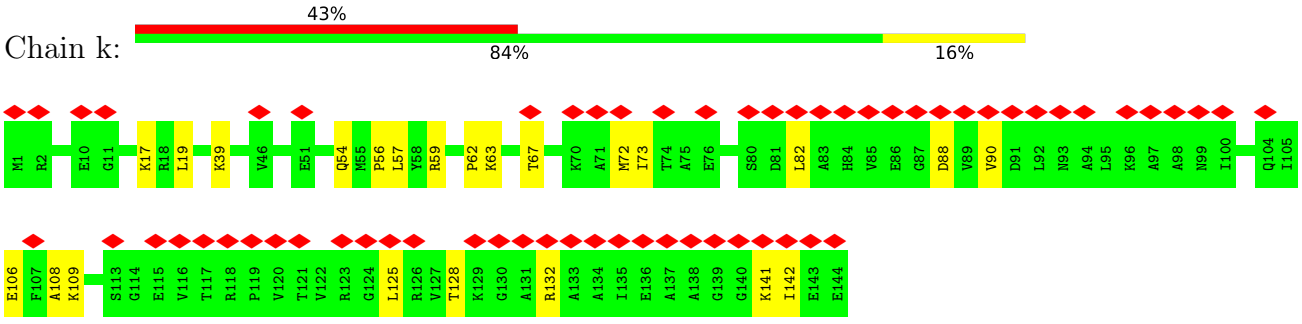
• Molecule 39: Large ribosomal subunit protein uL14

Chain j:



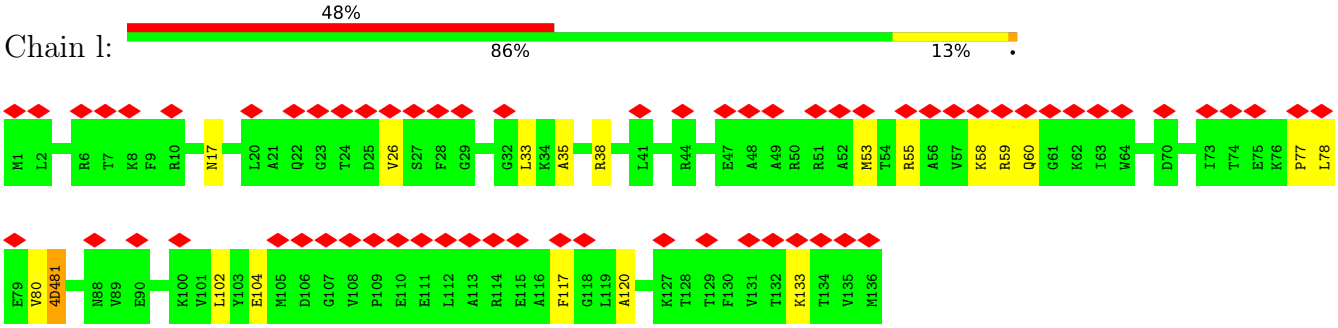
• Molecule 40: Large ribosomal subunit protein uL15

Chain k:



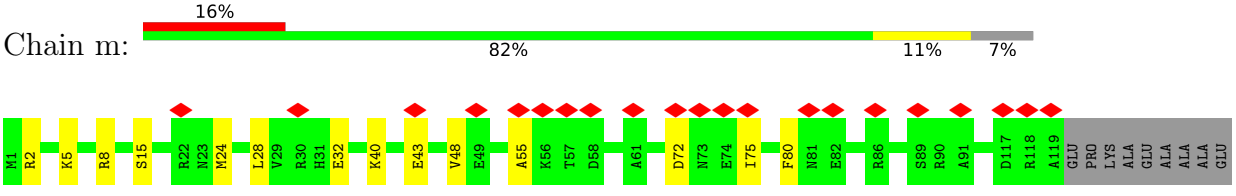
• Molecule 41: Large ribosomal subunit protein uL16

Chain l:



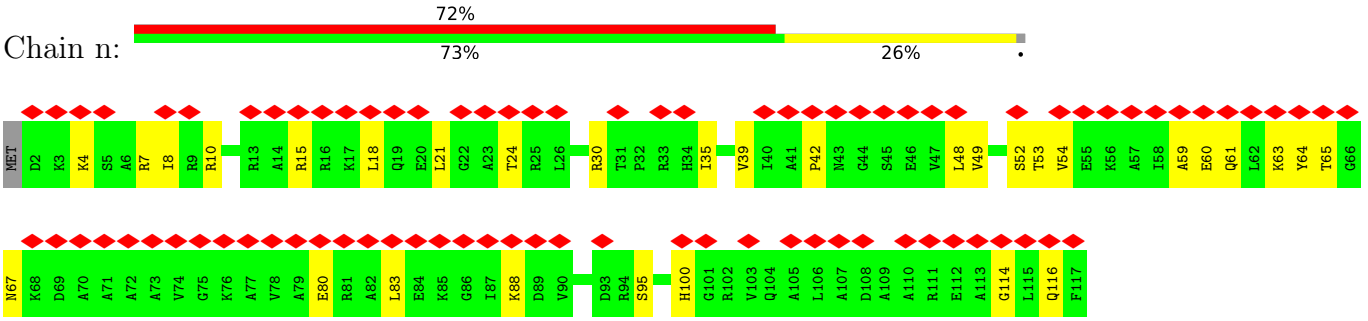
• Molecule 42: Large ribosomal subunit protein bL17

Chain m:



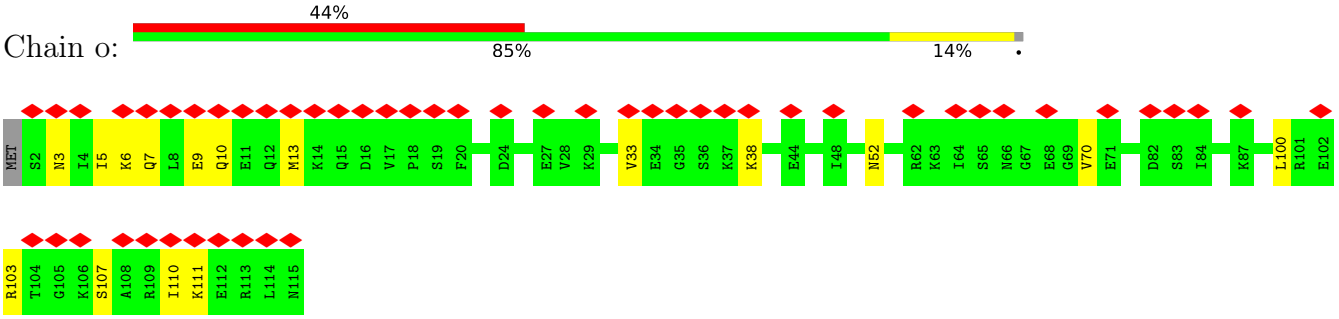
• Molecule 43: Large ribosomal subunit protein uL18

Chain n:



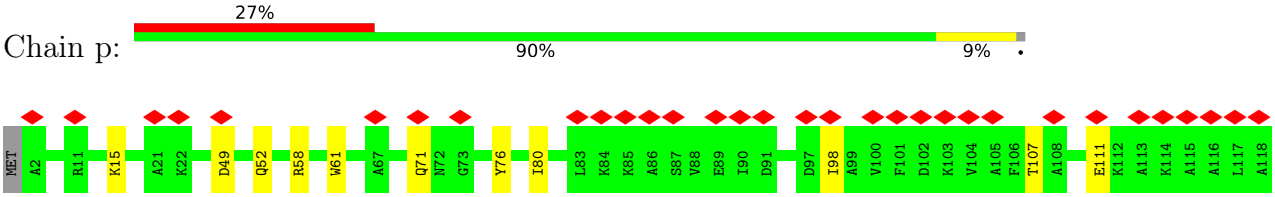
• Molecule 44: Large ribosomal subunit protein bL19

Chain o:



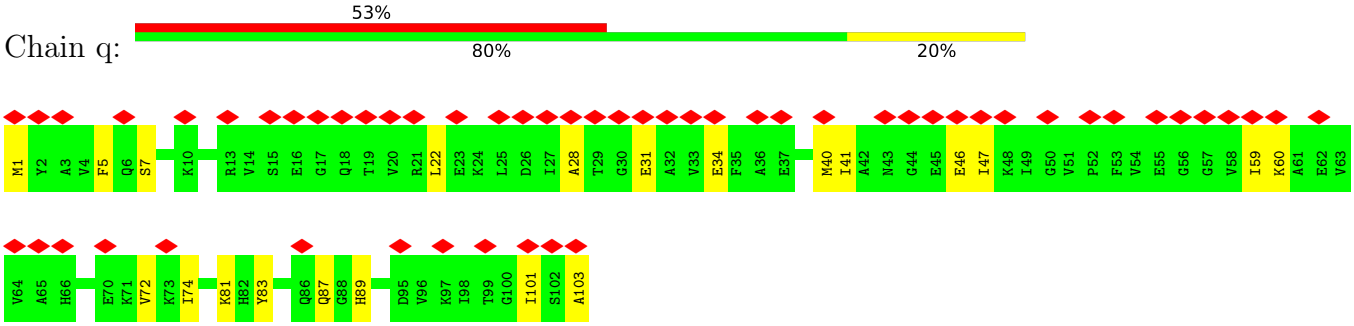
• Molecule 45: Large ribosomal subunit protein bL20

Chain p:



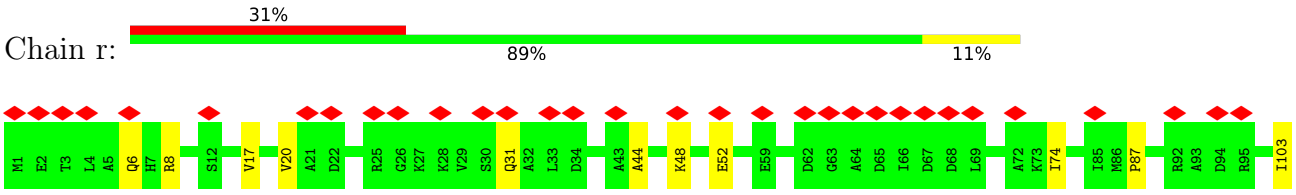
• Molecule 46: Large ribosomal subunit protein bL21

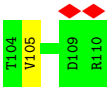
Chain q:



• Molecule 47: Large ribosomal subunit protein uL22

Chain r:

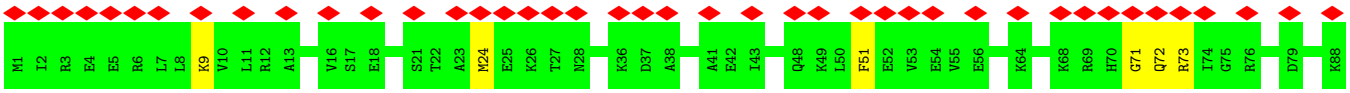


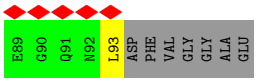


• Molecule 48: Large ribosomal subunit protein uL23

Chain s:



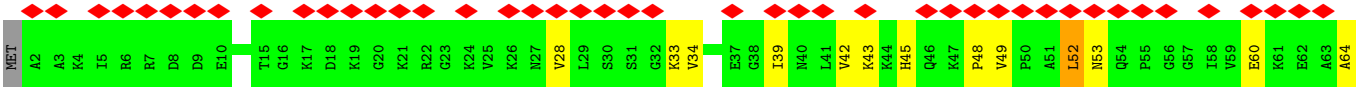


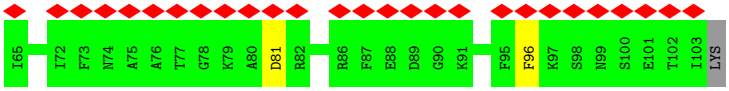


• Molecule 49: Large ribosomal subunit protein uL24

Chain t:

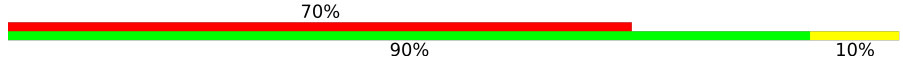


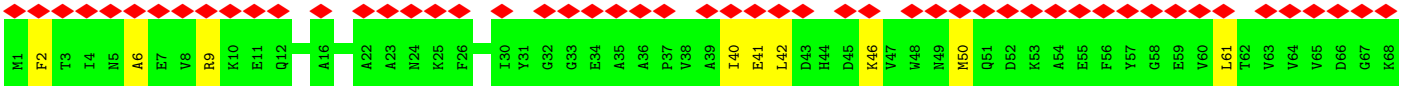


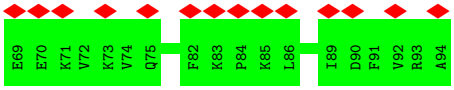


• Molecule 50: Large ribosomal subunit protein bL25

Chain u:



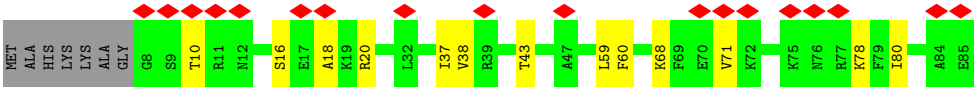




• Molecule 51: Large ribosomal subunit protein bL27

Chain v:

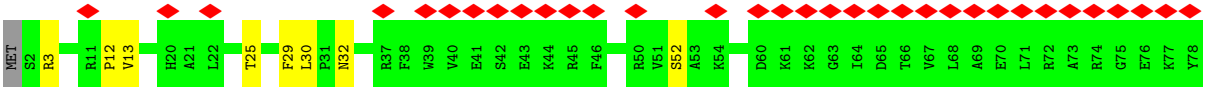




• Molecule 52: Large ribosomal subunit protein bL28

Chain w:

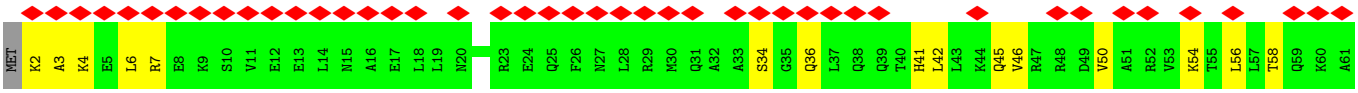




• Molecule 53: Large ribosomal subunit protein uL29

Chain x:



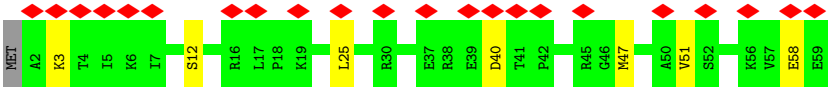




• Molecule 54: Large ribosomal subunit protein uL30

Chain y:

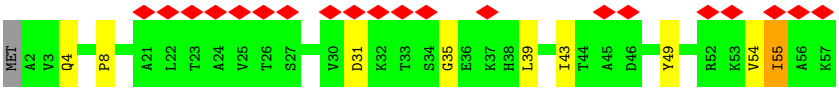




• Molecule 55: Large ribosomal subunit protein bL32

Chain z:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	56981	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 ($e^-/Å^2$)	35	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.014	Depositor
Minimum map value	-0.993	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.063	Depositor
Recommended contour level	0.55	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OMU, PSU, 5MC, 4SU, 2MA, G7M, IAS, D2T, 6MZ, MEQ, OMG, K, 3TD, MA6, ZN, 4D4, H2U, 1MG, OMC, UR3, 2MG, 4OC, MS6, 5MU, 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	0	0.30	0/425	0.39	0/566
2	1	0.35	0/380	0.38	0/498
3	2	0.32	0/513	0.33	0/676
4	3	0.29	0/303	0.34	0/397
5	4	0.19	0/550	0.43	0/734
6	5	0.17	0/1112	0.39	0/1492
7	A	0.61	0/36680	0.74	3/57215 (0.0%)
8	B	0.16	0/1780	0.38	0/2398
9	C	0.20	0/1650	0.32	0/2223
10	D	0.22	0/1665	0.28	0/2225
11	E	0.26	0/1168	0.29	0/1570
12	F	0.22	0/851	0.35	0/1152
13	G	0.21	0/1220	0.36	0/1638
14	H	0.25	0/987	0.34	0/1323
15	I	0.20	0/1022	0.33	0/1361
16	J	0.22	0/798	0.44	0/1078
17	K	0.22	0/885	0.37	0/1192
18	L	0.27	0/961	0.33	0/1287
19	M	0.19	0/916	0.36	0/1225
20	N	0.21	0/817	0.31	0/1088
21	O	0.24	0/718	0.31	0/955
22	P	0.26	0/646	0.32	0/870
23	Q	0.24	0/647	0.39	0/865
24	R	0.24	0/515	0.36	0/693
25	S	0.19	0/684	0.31	0/920
26	T	0.24	0/675	0.30	0/894
27	V	0.36	0/1724	0.83	2/2687 (0.1%)
28	W	0.37	0/271	0.86	0/422
29	X	0.20	0/791	0.38	0/1069
30	a	0.77	0/69183	0.79	14/107924 (0.0%)
31	b	0.62	0/2776	0.73	0/4328

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	c	0.32	0/2118	0.33	0/2846
33	d	0.31	0/1577	0.33	0/2122
34	e	0.30	0/1573	0.35	0/2115
35	f	0.22	0/1434	0.35	0/1926
36	g	0.23	0/1339	0.35	0/1811
37	h	0.18	0/1110	0.39	0/1500
38	i	0.30	0/1157	0.30	0/1556
39	j	0.30	0/956	0.37	0/1281
40	k	0.30	0/1073	0.32	0/1427
41	l	0.30	0/1072	0.33	0/1434
42	m	0.32	0/963	0.35	0/1288
43	n	0.25	0/902	0.40	0/1209
44	o	0.30	0/929	0.32	0/1242
45	p	0.35	0/960	0.33	0/1278
46	q	0.31	0/829	0.38	0/1106
47	r	0.30	0/862	0.33	0/1154
48	s	0.27	0/745	0.35	0/996
49	t	0.26	0/787	0.36	1/1051 (0.1%)
50	u	0.26	0/763	0.39	0/1024
51	v	0.32	0/599	0.36	0/795
52	w	0.31	0/635	0.32	0/848
53	x	0.25	0/500	0.31	0/665
54	y	0.27	0/451	0.37	0/603
55	z	0.30	0/449	0.35	0/597
All	All	0.61	0/157096	0.69	20/234839 (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
41	l	0	1

There are no bond length outliers.

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
30	a	2098	G	OP1-P-O3'	-10.75	75.74	108.00
30	a	2098	G	OP2-P-O3'	-9.72	78.84	108.00
30	a	1310	U	C2-N1-C1'	6.81	125.88	117.70
30	a	1024	G	O5'-C5'-C4'	5.94	114.15	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
30	a	1056	U	C2-N1-C1'	5.76	124.61	117.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
41	l	81	4D4	Mainchain

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	0	418	0	449	6	0
2	1	377	0	418	7	0
3	2	504	0	572	7	0
4	3	302	0	340	4	0
5	4	540	0	537	11	0
6	5	1105	0	1165	37	0
7	A	33009	0	16626	313	0
8	B	1749	0	1774	43	0
9	C	1623	0	1696	24	0
10	D	1644	0	1706	33	0
11	E	1155	0	1206	12	0
12	F	832	0	821	14	0
13	G	1204	0	1255	23	0
14	H	977	0	1031	16	0
15	I	1010	0	1057	21	0
16	J	788	0	830	22	0
17	K	878	0	884	16	0
18	L	958	0	1019	9	0
19	M	907	0	977	16	0
20	N	805	0	846	20	0
21	O	710	0	735	10	0
22	P	636	0	649	9	0
23	Q	639	0	684	10	0
24	R	507	0	525	21	0
25	S	667	0	691	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	T	669	0	717	5	0
27	V	1644	0	841	41	0
28	W	242	0	119	9	0
29	X	778	0	793	14	0
30	a	62284	0	31325	483	0
31	b	2483	0	1258	11	0
32	c	2080	0	2151	14	0
33	d	1567	0	1619	16	0
34	e	1554	0	1620	18	0
35	f	1410	0	1444	14	0
36	g	1319	0	1367	19	0
37	h	1099	0	1139	32	0
38	i	1134	0	1161	11	0
39	j	947	0	1025	10	0
40	k	1063	0	1130	15	0
41	l	1074	0	1138	11	0
42	m	950	0	994	7	0
43	n	892	0	923	19	0
44	o	917	0	962	9	0
45	p	947	0	1019	6	0
46	q	816	0	841	12	0
47	r	855	0	915	6	0
48	s	739	0	809	4	0
49	t	779	0	830	9	0
50	u	749	0	763	5	0
51	v	592	0	612	7	0
52	w	625	0	652	5	0
53	x	499	0	534	10	0
54	y	447	0	484	4	0
55	z	443	0	458	6	0
56	3	1	0	0	0	0
56	4	1	0	0	0	0
57	A	94	0	0	0	0
57	N	1	0	0	0	0
57	Q	1	0	0	0	0
57	a	253	0	0	0	0
57	b	5	0	0	0	0
57	c	2	0	0	0	0
57	p	2	0	0	0	0
57	z	1	0	0	0	0
58	A	46	0	0	0	0
58	L	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	a	114	0	0	0	0
58	b	1	0	0	0	0
58	c	4	0	0	0	0
58	d	1	0	0	0	0
58	e	1	0	0	0	0
58	f	1	0	0	0	0
All	All	146071	0	98136	1431	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 6.

The worst 5 of 1431 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)
7:A:76:A:N6	7:A:91:G:H1	1.40	1.19
30:a:879:G:H1	30:a:893:U:H3	1.04	1.01
37:h:94:ILE:HG13	37:h:146:VAL:HG11	1.47	0.97
30:a:285:U:H3	30:a:355:G:H1	0.92	0.92
12:F:9:MET:HE2	12:F:86:ARG:HB3	1.52	0.90

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	49/55 (89%)	48 (98%)	1 (2%)	0	100	100
2	1	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
3	2	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
4	3	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
5	4	68/70 (97%)	58 (85%)	10 (15%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	5	142/234 (61%)	132 (93%)	10 (7%)	0	100	100
8	B	222/241 (92%)	204 (92%)	18 (8%)	0	100	100
9	C	204/232 (88%)	199 (98%)	5 (2%)	0	100	100
10	D	203/206 (98%)	200 (98%)	3 (2%)	0	100	100
11	E	154/167 (92%)	146 (95%)	8 (5%)	0	100	100
12	F	101/131 (77%)	99 (98%)	2 (2%)	0	100	100
13	G	151/156 (97%)	146 (97%)	5 (3%)	0	100	100
14	H	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
15	I	124/130 (95%)	121 (98%)	3 (2%)	0	100	100
16	J	96/103 (93%)	91 (95%)	4 (4%)	1 (1%)	12	32
17	K	113/129 (88%)	107 (95%)	6 (5%)	0	100	100
18	L	120/124 (97%)	117 (98%)	3 (2%)	0	100	100
19	M	114/118 (97%)	108 (95%)	6 (5%)	0	100	100
20	N	98/101 (97%)	98 (100%)	0	0	100	100
21	O	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
22	P	79/82 (96%)	76 (96%)	3 (4%)	0	100	100
23	Q	77/84 (92%)	73 (95%)	4 (5%)	0	100	100
24	R	60/75 (80%)	59 (98%)	1 (2%)	0	100	100
25	S	82/92 (89%)	80 (98%)	2 (2%)	0	100	100
26	T	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
29	X	96/111 (86%)	94 (98%)	2 (2%)	0	100	100
32	c	269/273 (98%)	262 (97%)	7 (3%)	0	100	100
33	d	206/209 (99%)	202 (98%)	3 (2%)	1 (0%)	24	48
34	e	199/201 (99%)	197 (99%)	2 (1%)	0	100	100
35	f	175/179 (98%)	165 (94%)	10 (6%)	0	100	100
36	g	174/177 (98%)	168 (97%)	6 (3%)	0	100	100
37	h	146/149 (98%)	135 (92%)	10 (7%)	1 (1%)	18	41
38	i	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
39	j	121/123 (98%)	115 (95%)	6 (5%)	0	100	100
40	k	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
41	l	132/136 (97%)	129 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	m	117/128 (91%)	112 (96%)	5 (4%)	0	100	100
43	n	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
44	o	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
45	p	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
46	q	101/103 (98%)	98 (97%)	3 (3%)	0	100	100
47	r	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
48	s	91/100 (91%)	88 (97%)	3 (3%)	0	100	100
49	t	100/104 (96%)	96 (96%)	4 (4%)	0	100	100
50	u	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
51	v	76/85 (89%)	74 (97%)	2 (3%)	0	100	100
52	w	75/78 (96%)	75 (100%)	0	0	100	100
53	x	60/63 (95%)	59 (98%)	1 (2%)	0	100	100
54	y	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
55	z	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
All	All	5767/6160 (94%)	5571 (97%)	193 (3%)	3 (0%)	49	73

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
37	h	115	VAL
16	J	57	VAL
33	d	149	ASN

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	
1	0	46/49 (94%)	45 (98%)	1 (2%)	45	74
2	1	38/38 (100%)	38 (100%)	0	100	100
3	2	51/52 (98%)	51 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3	34/34 (100%)	34 (100%)	0	100	100
5	4	60/60 (100%)	58 (97%)	2 (3%)	33	63
6	5	116/180 (64%)	108 (93%)	8 (7%)	14	34
8	B	185/198 (93%)	180 (97%)	5 (3%)	39	69
9	C	170/189 (90%)	169 (99%)	1 (1%)	78	91
10	D	171/172 (99%)	167 (98%)	4 (2%)	44	73
11	E	119/126 (94%)	117 (98%)	2 (2%)	53	79
12	F	88/111 (79%)	82 (93%)	6 (7%)	14	35
13	G	126/129 (98%)	125 (99%)	1 (1%)	73	88
14	H	104/105 (99%)	104 (100%)	0	100	100
15	I	104/107 (97%)	99 (95%)	5 (5%)	23	50
16	J	87/91 (96%)	82 (94%)	5 (6%)	18	43
17	K	89/98 (91%)	88 (99%)	1 (1%)	65	85
18	L	102/103 (99%)	100 (98%)	2 (2%)	48	76
19	M	96/98 (98%)	92 (96%)	4 (4%)	26	55
20	N	83/84 (99%)	82 (99%)	1 (1%)	63	84
21	O	75/76 (99%)	74 (99%)	1 (1%)	61	83
22	P	63/63 (100%)	62 (98%)	1 (2%)	55	80
23	Q	73/78 (94%)	70 (96%)	3 (4%)	27	56
24	R	53/65 (82%)	50 (94%)	3 (6%)	18	43
25	S	72/79 (91%)	72 (100%)	0	100	100
26	T	65/66 (98%)	64 (98%)	1 (2%)	57	81
29	X	83/94 (88%)	79 (95%)	4 (5%)	23	50
32	c	215/217 (99%)	214 (100%)	1 (0%)	81	92
33	d	163/163 (100%)	163 (100%)	0	100	100
34	e	165/165 (100%)	163 (99%)	2 (1%)	63	84
35	f	148/150 (99%)	141 (95%)	7 (5%)	23	51
36	g	135/136 (99%)	133 (98%)	2 (2%)	57	81
37	h	112/113 (99%)	110 (98%)	2 (2%)	51	78
38	i	116/116 (100%)	116 (100%)	0	100	100
39	j	104/104 (100%)	102 (98%)	2 (2%)	50	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
40	k	105/105 (100%)	103 (98%)	2 (2%)	50 77
41	l	107/107 (100%)	106 (99%)	1 (1%)	70 87
42	m	98/103 (95%)	96 (98%)	2 (2%)	48 76
43	n	86/87 (99%)	84 (98%)	2 (2%)	44 73
44	o	99/100 (99%)	98 (99%)	1 (1%)	68 86
45	p	89/90 (99%)	88 (99%)	1 (1%)	65 85
46	q	83/83 (100%)	83 (100%)	0	100 100
47	r	92/92 (100%)	91 (99%)	1 (1%)	65 85
48	s	80/84 (95%)	79 (99%)	1 (1%)	61 83
49	t	83/85 (98%)	82 (99%)	1 (1%)	63 84
50	u	76/76 (100%)	76 (100%)	0	100 100
51	v	60/64 (94%)	57 (95%)	3 (5%)	22 48
52	w	67/68 (98%)	66 (98%)	1 (2%)	57 81
53	x	53/54 (98%)	53 (100%)	0	100 100
54	y	48/49 (98%)	47 (98%)	1 (2%)	47 75
55	z	47/48 (98%)	46 (98%)	1 (2%)	47 75
All	All	4784/5004 (96%)	4689 (98%)	95 (2%)	48 76

5 of 95 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	X	31	GLN
36	g	44	LYS
29	X	76	GLU
35	f	23	ASN
39	j	47	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
38	i	136	GLN
52	w	36	HIS
39	j	88	ASN
43	n	98	GLN
54	y	9	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	V	76/77 (98%)	27 (35%)	2 (2%)
28	W	10/15 (66%)	1 (10%)	0
30	a	2898/2923 (99%)	422 (14%)	0
31	b	115/116 (99%)	12 (10%)	0
7	A	1537/1550 (99%)	196 (12%)	2 (0%)
All	All	4636/4681 (99%)	658 (14%)	4 (0%)

5 of 658 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	4	U
7	A	7	A
7	A	8	A
7	A	9	G
7	A	32	A

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A	1033	A
7	A	1492	G
27	V	20	G
27	V	75	C

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

45 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	$\#\|Z\| > 2$
30	2MA	a	2501	30,58,57	22,25,26	1.34	3 (13%)	33,37,40	2.07	8 (24%)
7	MA6	A	1516	7	23,26,27	1.26	3 (13%)	34,38,41	2.24	9 (26%)
7	UR3	A	1496	7	19,22,23	2.57	6 (31%)	26,32,35	1.27	2 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
30	1MG	a	743	30	22,26,27	2.54	6 (27%)	33,39,42	1.99	6 (18%)
7	5MC	A	1405	7	18,22,23	1.94	6 (33%)	26,32,35	1.30	2 (7%)
30	6MZ	a	2028	30	22,25,26	2.47	4 (18%)	30,36,39	2.37	9 (30%)
7	4OC	A	1400	7	20,23,24	2.21	3 (15%)	26,32,35	0.99	2 (7%)
7	5MC	A	965	7	18,22,23	1.91	5 (27%)	26,32,35	1.26	2 (7%)
30	G7M	a	2067	30,58	23,26,27	2.21	5 (21%)	35,39,42	1.91	7 (20%)
30	PSU	a	953	30	18,21,22	2.13	7 (38%)	22,30,33	1.89	3 (13%)
30	H2U	a	2447	30	18,21,22	4.04	5 (27%)	21,30,33	5.34	6 (28%)
7	G7M	A	525	58,7	23,26,27	2.17	5 (21%)	35,39,42	1.91	7 (20%)
27	5MU	V	55	27	19,22,23	2.35	7 (36%)	28,32,35	3.77	10 (35%)
17	IAS	K	119	17	6,7,8	1.77	1 (16%)	6,8,10	2.61	2 (33%)
30	2MG	a	1831	30	23,26,27	2.59	7 (30%)	32,38,41	2.11	10 (31%)
30	3TD	a	1913	-	18,22,23	2.89	7 (38%)	22,32,35	1.71	3 (13%)
30	PSU	a	2455	30	18,21,22	2.24	9 (50%)	22,30,33	1.97	5 (22%)
7	2MG	A	1514	7	23,26,27	2.57	7 (30%)	32,38,41	2.16	11 (34%)
41	4D4	l	81	41	9,11,12	0.82	0	8,13,15	1.84	2 (25%)
30	6MZ	a	1615	30	22,25,26	2.39	3 (13%)	30,36,39	2.35	9 (30%)
41	MS6	l	82	41	5,7,8	0.65	0	2,7,9	1.45	0
30	PSU	a	1909	30	18,21,22	2.09	8 (44%)	22,30,33	1.84	3 (13%)
18	D2T	L	89	18	7,9,10	1.19	1 (14%)	6,11,13	1.56	1 (16%)
30	OMG	a	2249	30,58	23,26,27	2.35	6 (26%)	33,38,41	1.86	10 (30%)
30	2MG	a	2443	30	23,26,27	2.58	7 (30%)	32,38,41	2.11	11 (34%)
30	PSU	a	744	30,57	18,21,22	2.09	8 (44%)	22,30,33	1.81	3 (13%)
7	PSU	A	514	7	18,21,22	2.06	8 (44%)	22,30,33	1.81	5 (22%)
30	PSU	a	2502	30,58	18,21,22	2.18	7 (38%)	22,30,33	1.86	4 (18%)
30	PSU	a	2578	30	18,21,22	2.24	9 (50%)	22,30,33	1.99	5 (22%)
30	PSU	a	2602	30	18,21,22	2.18	8 (44%)	22,30,33	1.90	4 (18%)
33	MEQ	d	150	33	8,9,10	0.94	0	5,10,12	0.69	0
27	H2U	V	21	27	18,21,22	4.36	5 (27%)	21,30,33	4.81	6 (28%)
30	5MC	a	1960	30,58	18,22,23	1.92	6 (33%)	26,32,35	1.26	2 (7%)
7	2MG	A	1205	7	23,26,27	2.58	4 (17%)	32,38,41	2.09	9 (28%)
27	PSU	V	56	27	18,21,22	1.95	7 (38%)	22,30,33	1.80	3 (13%)
30	5MU	a	745	30	19,22,23	2.53	7 (36%)	28,32,35	3.99	12 (42%)
30	5MU	a	1937	30,58	19,22,23	2.65	7 (36%)	28,32,35	3.72	10 (35%)
27	OMC	V	33	27	19,22,23	1.73	3 (15%)	26,31,34	0.94	2 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
30	OMU	a	2550	30,58,57	19,22,23	2.69	7 (36%)	26,31,34	1.74	5 (19%)
7	2MG	A	964	7	23,26,27	2.60	5 (21%)	32,38,41	2.03	9 (28%)
30	OMC	a	2496	30,57	19,22,23	1.84	4 (21%)	26,31,34	1.14	2 (7%)
30	PSU	a	1915	30	18,21,22	2.09	7 (38%)	22,30,33	1.83	5 (22%)
7	MA6	A	1517	7	23,26,27	1.27	3 (13%)	34,38,41	2.33	9 (26%)
30	PSU	a	2603	30	18,21,22	2.14	7 (38%)	22,30,33	1.90	3 (13%)
27	4SU	V	8	27	18,21,22	3.69	8 (44%)	26,30,33	2.20	5 (19%)

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
30	2MA	a	2501	30,58,57	-	2/7/25/26	0/3/3/3
7	MA6	A	1516	7	-	0/11/29/30	0/3/3/3
7	UR3	A	1496	7	-	0/7/25/26	0/2/2/2
30	1MG	a	743	30	-	0/7/25/26	0/3/3/3
7	5MC	A	1405	7	-	0/7/25/26	0/2/2/2
30	6MZ	a	2028	30	-	2/9/27/28	0/3/3/3
7	4OC	A	1400	7	-	0/9/29/30	0/2/2/2
7	5MC	A	965	7	-	0/7/25/26	0/2/2/2
30	G7M	a	2067	30,58	-	3/7/25/26	0/3/3/3
30	PSU	a	953	30	-	0/7/25/26	0/2/2/2
30	H2U	a	2447	30	-	0/7/38/39	0/2/2/2
7	G7M	A	525	58,7	-	2/7/25/26	0/3/3/3
27	5MU	V	55	27	-	0/7/25/26	0/2/2/2
17	IAS	K	119	17	-	1/7/7/8	-
30	2MG	a	1831	30	-	2/9/27/28	0/3/3/3
30	3TD	a	1913	-	-	0/7/25/26	0/2/2/2
30	PSU	a	2455	30	-	0/7/25/26	0/2/2/2
7	2MG	A	1514	7	-	0/9/27/28	0/3/3/3
41	4D4	l	81	41	-	3/11/12/14	-
30	6MZ	a	1615	30	-	0/9/27/28	0/3/3/3
41	MS6	l	82	41	-	2/4/6/8	-
30	PSU	a	1909	30	-	0/7/25/26	0/2/2/2
18	D2T	L	89	18	-	4/7/12/14	-
30	OMG	a	2249	30,58	-	1/9/27/28	0/3/3/3
30	2MG	a	2443	30	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	PSU	a	744	30,57	-	1/7/25/26	0/2/2/2
7	PSU	A	514	7	-	0/7/25/26	0/2/2/2
30	PSU	a	2502	30,58	-	2/7/25/26	0/2/2/2
30	PSU	a	2578	30	-	0/7/25/26	0/2/2/2
30	PSU	a	2602	30	-	0/7/25/26	0/2/2/2
33	MEQ	d	150	33	-	2/8/9/11	-
27	H2U	V	21	27	-	6/7/38/39	0/2/2/2
30	5MC	a	1960	30,58	-	0/7/25/26	0/2/2/2
7	2MG	A	1205	7	-	2/9/27/28	0/3/3/3
27	PSU	V	56	27	-	0/7/25/26	0/2/2/2
30	5MU	a	745	30	-	0/7/25/26	0/2/2/2
30	5MU	a	1937	30,58	-	0/7/25/26	0/2/2/2
27	OMC	V	33	27	-	2/9/27/28	0/2/2/2
30	OMU	a	2550	30,58,57	-	0/9/27/28	0/2/2/2
7	2MG	A	964	7	-	0/9/27/28	0/3/3/3
30	OMC	a	2496	30,57	-	1/9/27/28	0/2/2/2
30	PSU	a	1915	30	-	0/7/25/26	0/2/2/2
7	MA6	A	1517	7	-	4/11/29/30	0/3/3/3
30	PSU	a	2603	30	-	0/7/25/26	0/2/2/2
27	4SU	V	8	27	-	0/7/25/26	0/2/2/2

The worst 5 of 241 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	V	21	H2U	O4-C4	10.18	1.44	1.23
30	a	2447	H2U	O4-C4	9.98	1.43	1.23
30	a	2028	6MZ	C6-N6	9.94	1.45	1.34
30	a	1615	6MZ	C6-N6	9.74	1.44	1.34
27	V	21	H2U	C2-N1	9.19	1.48	1.35

The worst 5 of 243 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
30	a	2447	H2U	C4-N3-C2	-17.36	111.39	125.79
27	V	21	H2U	C4-N3-C2	-13.77	114.37	125.79
27	V	21	H2U	O2-C2-N1	-11.11	109.16	123.11
30	a	2447	H2U	O2-C2-N1	-10.63	109.77	123.11
30	a	745	5MU	C5M-C5-C4	9.40	129.11	118.77

There are no chirality outliers.

5 of 43 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	L	89	D2T	CG-CB-SB-CB1
18	L	89	D2T	CA-CB-CG-OD1
18	L	89	D2T	CA-CB-CG-OD2
27	V	21	H2U	O4'-C4'-C5'-O5'
27	V	21	H2U	C3'-C4'-C5'-O5'

There are no ring outliers.

10 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	a	2028	6MZ	3	0
7	A	1400	4OC	3	0
27	V	55	5MU	3	0
30	a	1913	3TD	3	0
30	a	2249	OMG	1	0
27	V	56	PSU	1	0
27	V	33	OMC	2	0
30	a	2550	OMU	1	0
7	A	964	2MG	2	0
30	a	1915	PSU	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 530 ligands modelled in this entry, 530 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
30	a	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	a	1912:C	O3'	1913:3TD	P	4.88
1	a	1913:3TD	O3'	1914:A	P	4.35

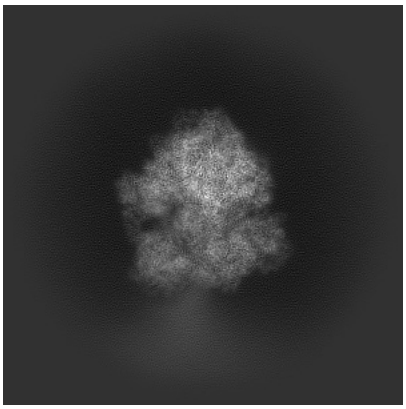
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-55794. These allow visual inspection of the internal detail of the map and identification of artifacts.

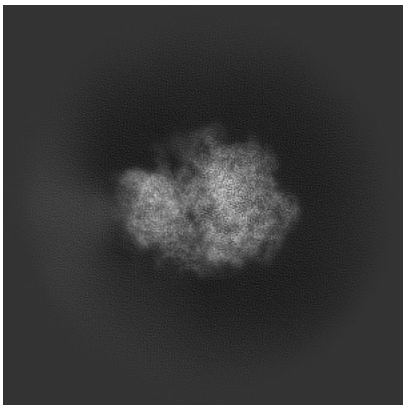
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

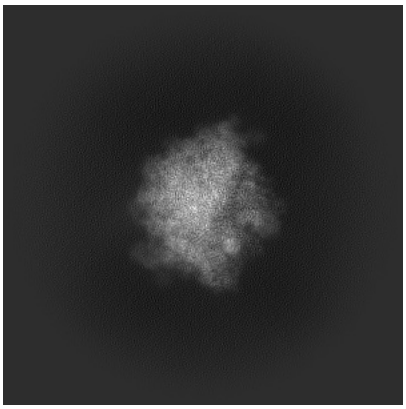
6.1.1 Primary map



X

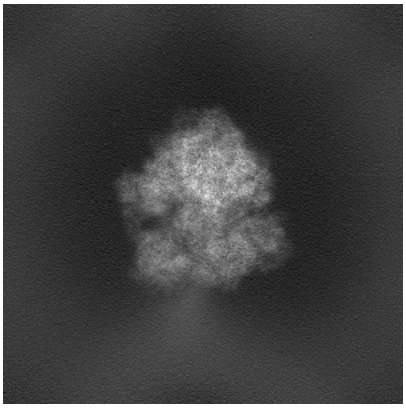


Y

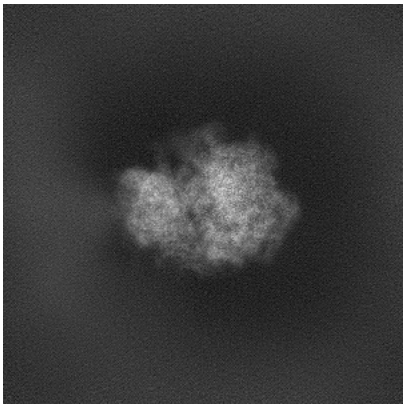


Z

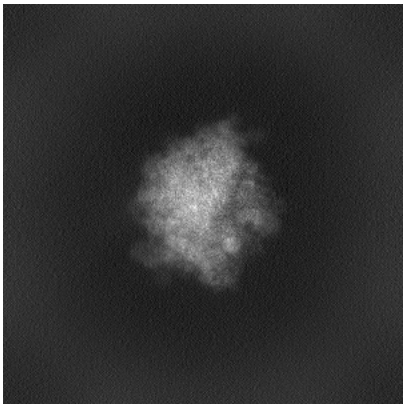
6.1.2 Raw map



X



Y

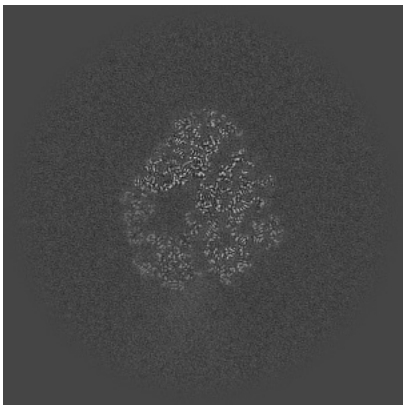


Z

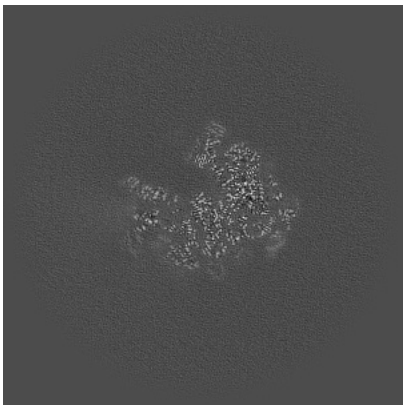
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

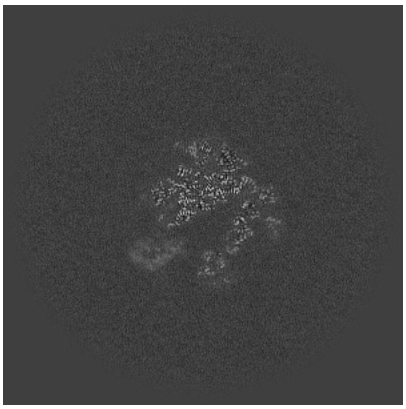
6.2.1 Primary map



X Index: 256

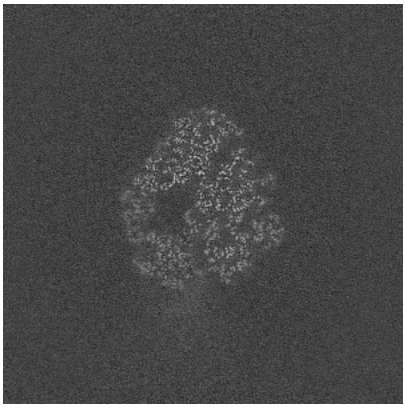


Y Index: 256



Z Index: 256

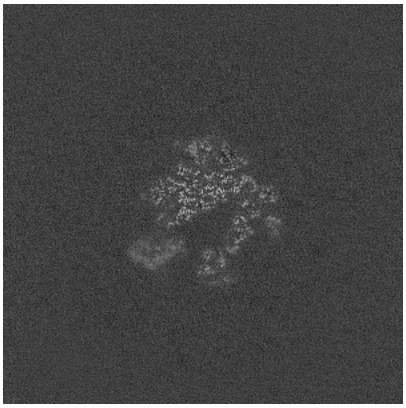
6.2.2 Raw map



X Index: 256



Y Index: 256

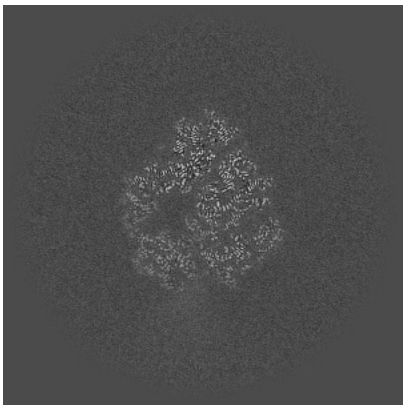


Z Index: 256

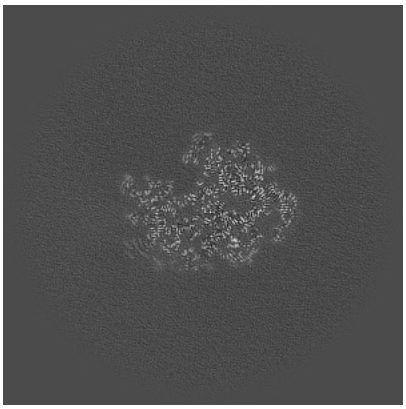
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

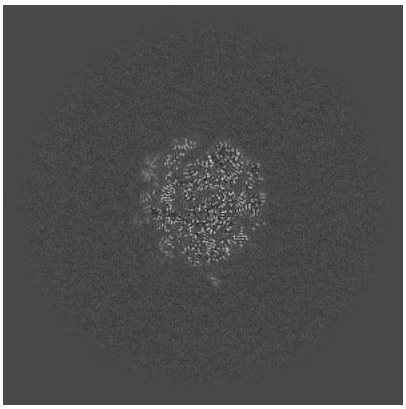
6.3.1 Primary map



X Index: 260

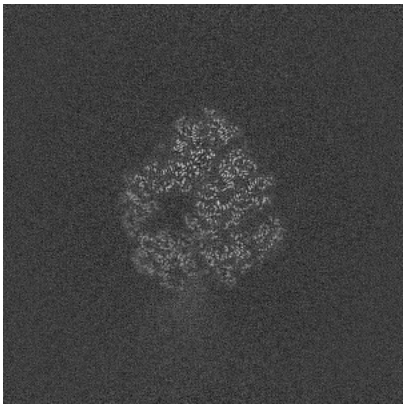


Y Index: 268

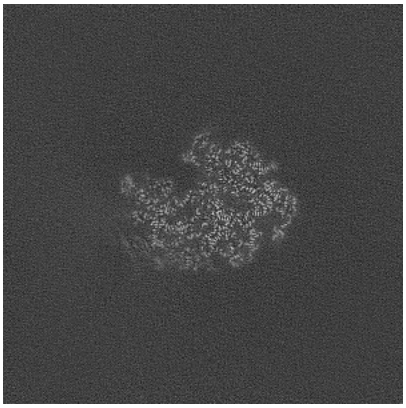


Z Index: 298

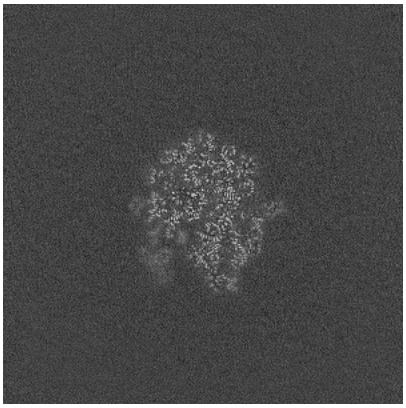
6.3.2 Raw map



X Index: 260



Y Index: 266

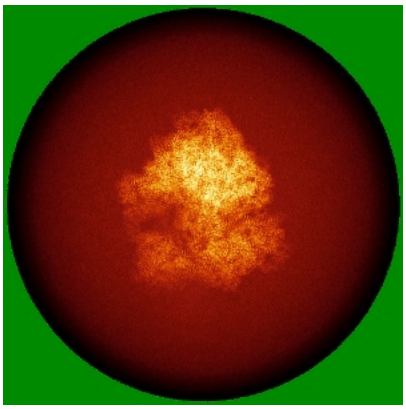


Z Index: 279

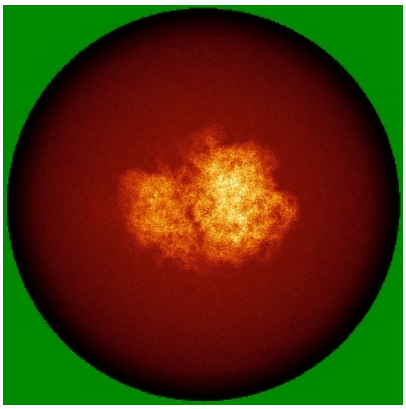
The images above show the largest variance slices of the map in three orthogonal directions.

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

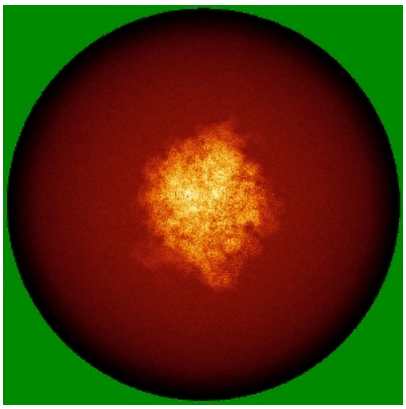
6.4.1 Primary map



X

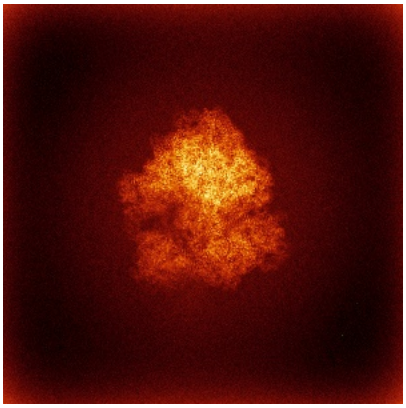


Y

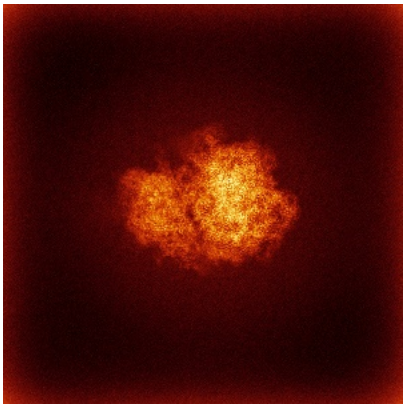


Z

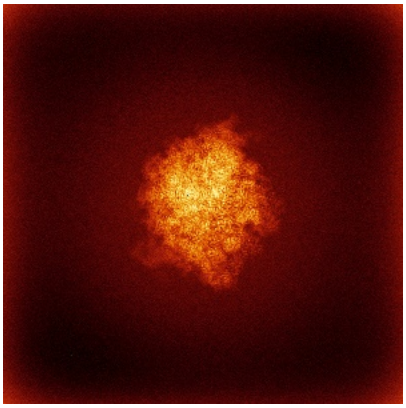
6.4.2 Raw map



X



Y

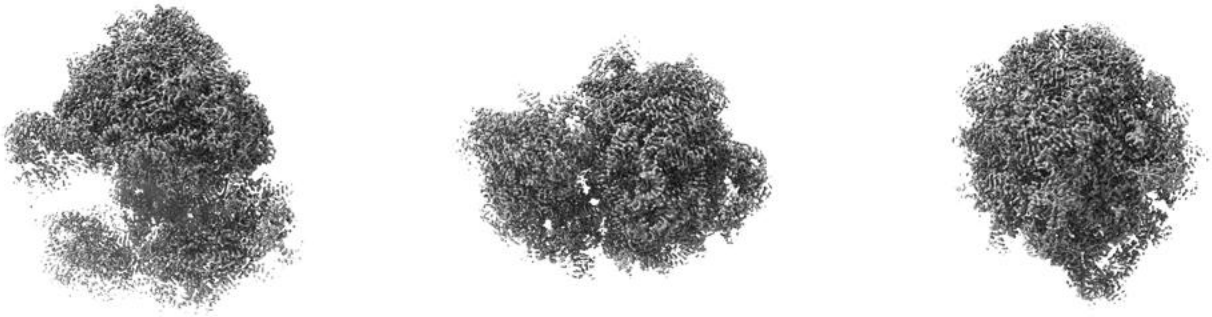


Z

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 0.55. 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.

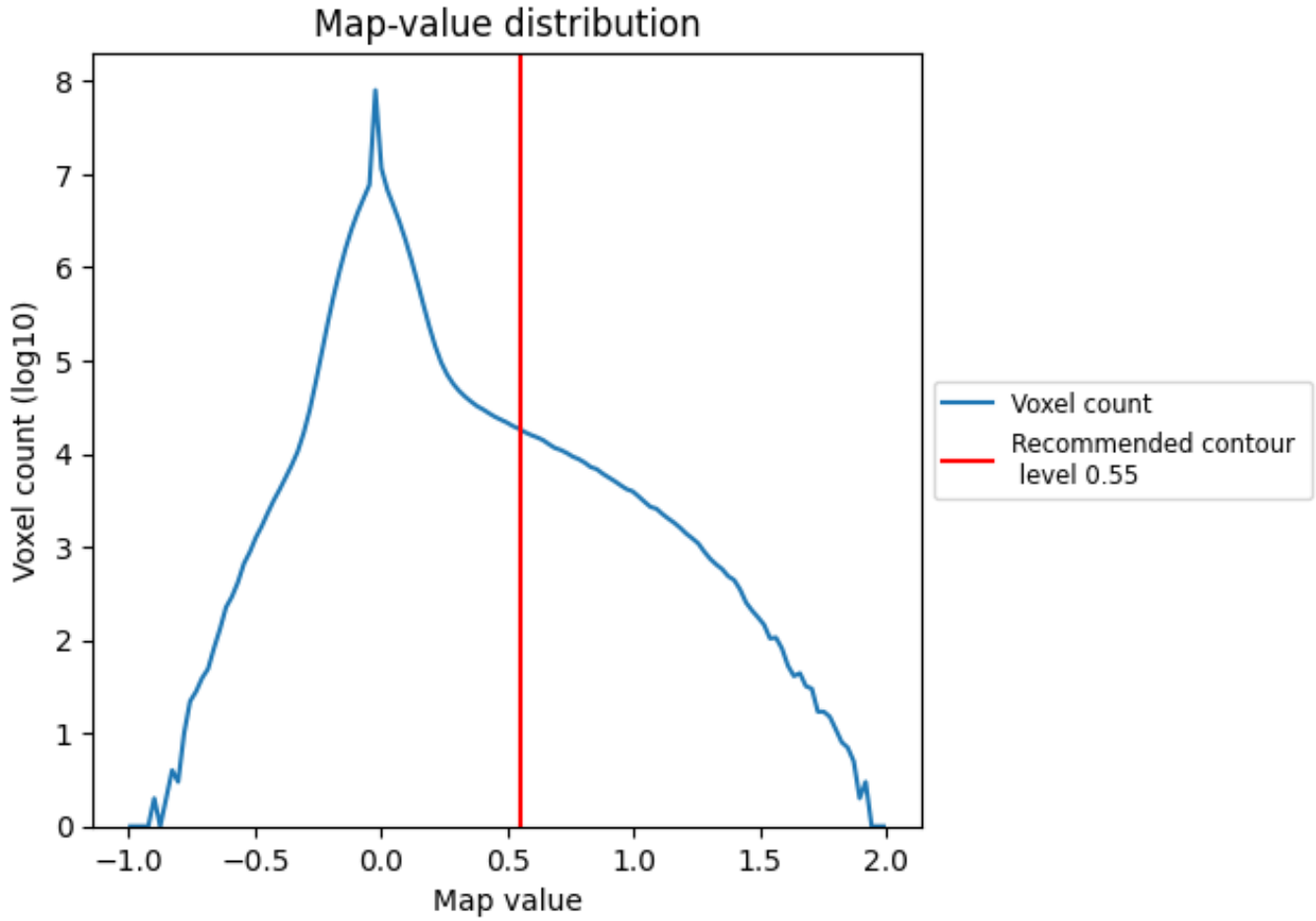
6.6 Mask visualisation (i)

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

7 Map analysis

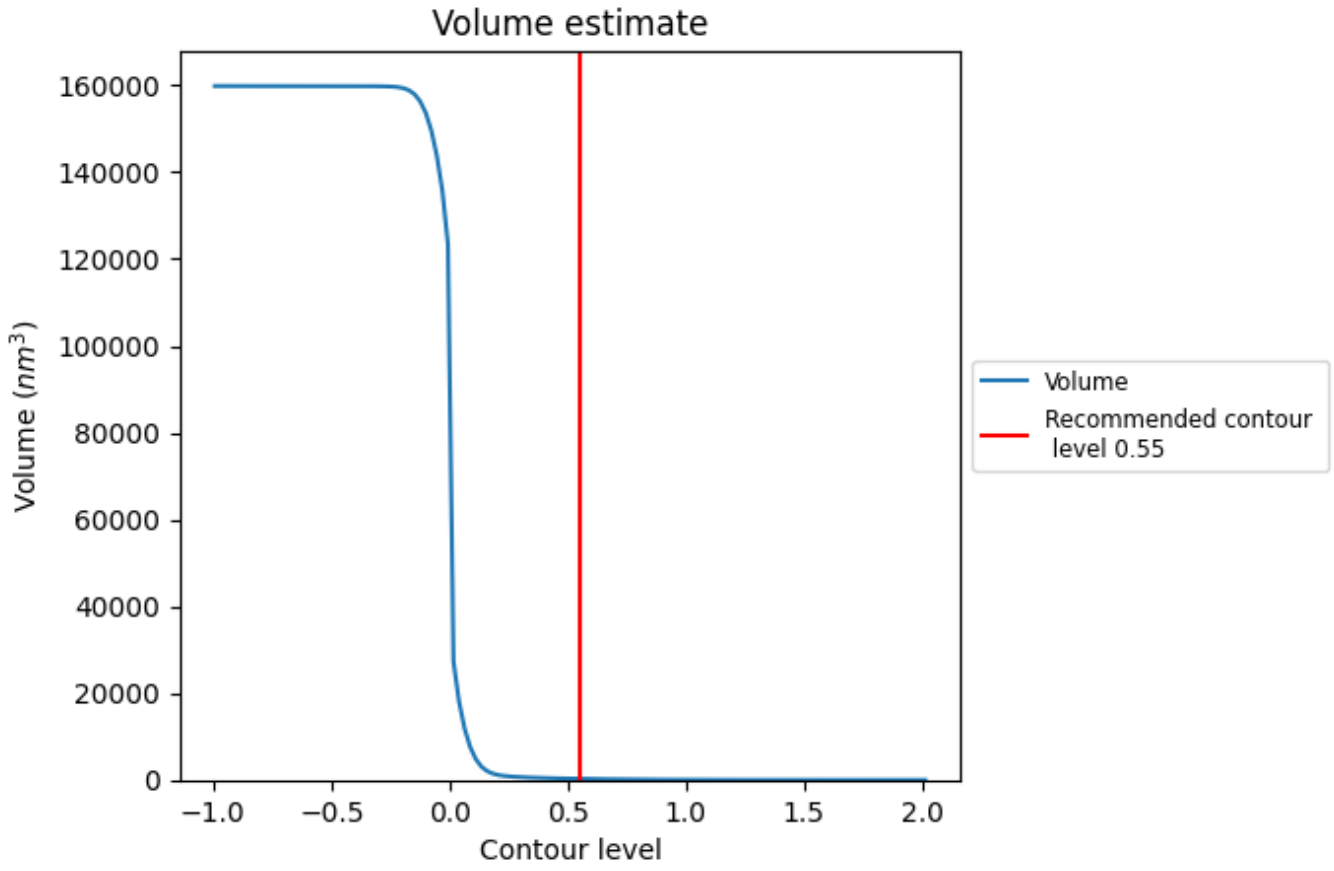
This section contains the results of statistical analysis of the map.

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.

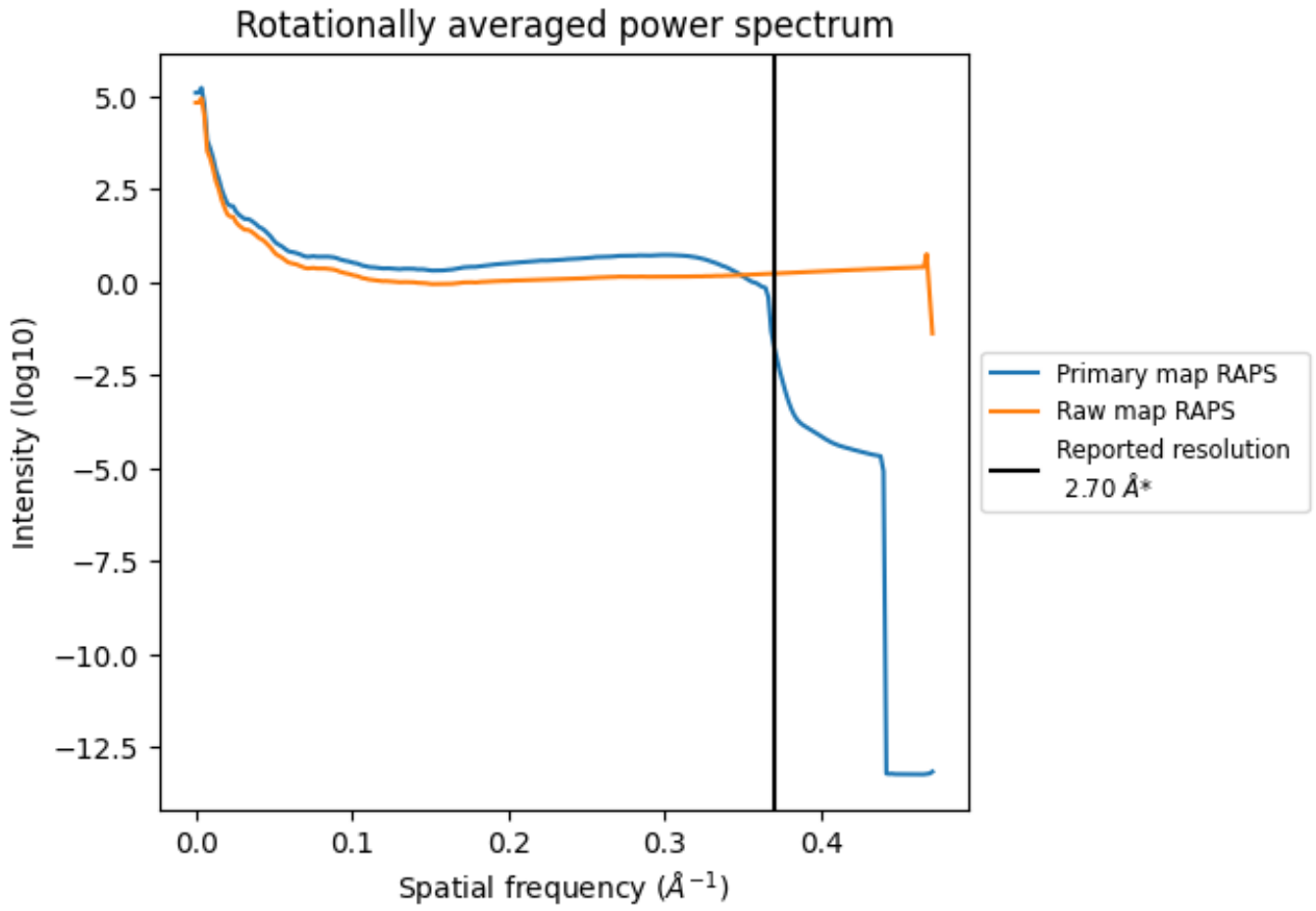
7.2 Volume estimate (i)



The volume at the recommended contour level is 263 nm^3; this corresponds to an approximate mass of 237 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)

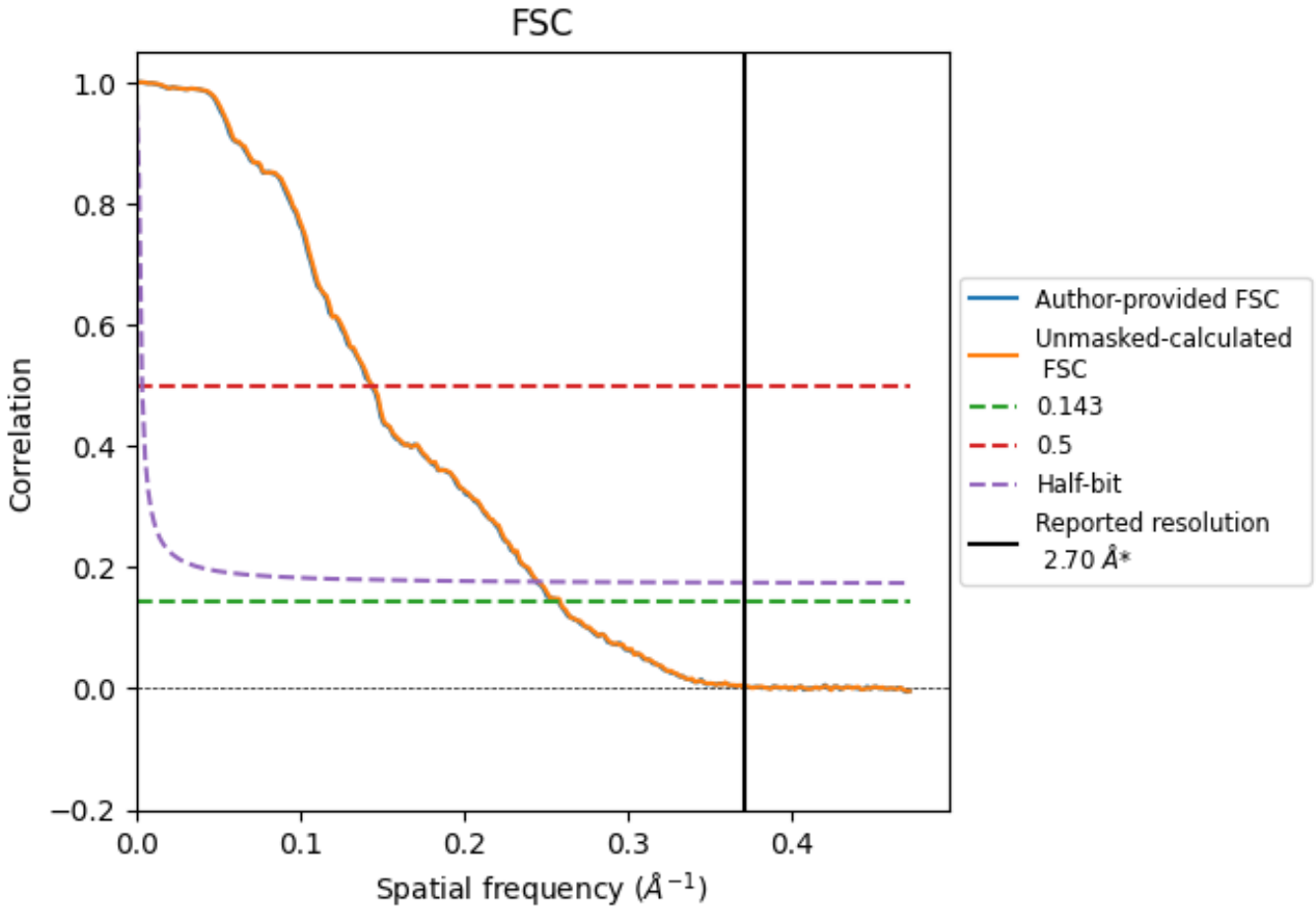


*Reported resolution corresponds to spatial frequency of 0.370 $Å^{-1}$

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 0.370 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	3.88	6.98	4.10
Unmasked-calculated*	3.87	6.94	4.08

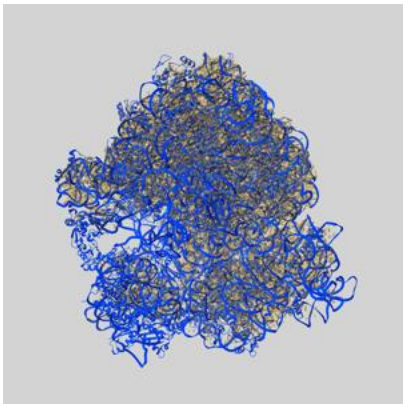
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.88 differs from the reported value 2.7 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.87 differs from the reported value 2.7 by more than 10 %

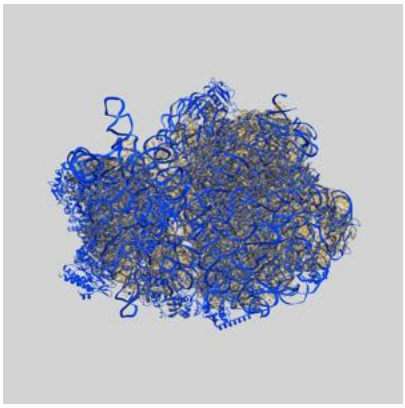
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-55794 and PDB model 9TCO. Per-residue inclusion information can be found in section 3 on page 16.

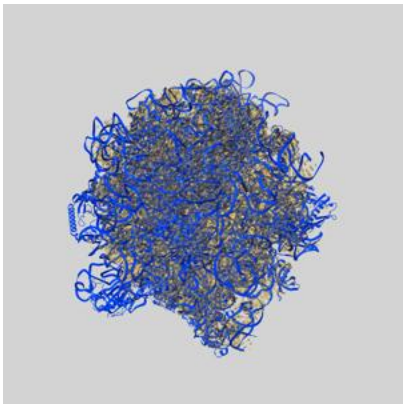
9.1 Map-model overlay



X



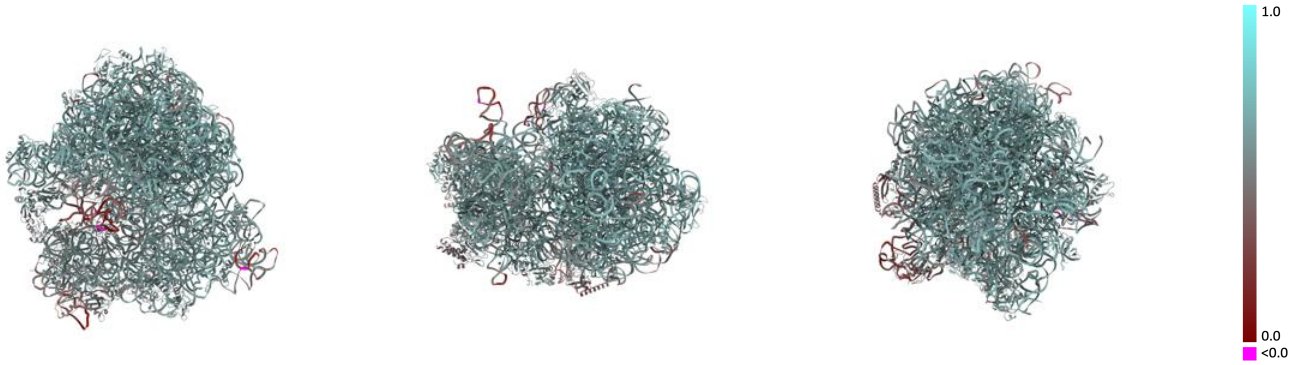
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.55 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.

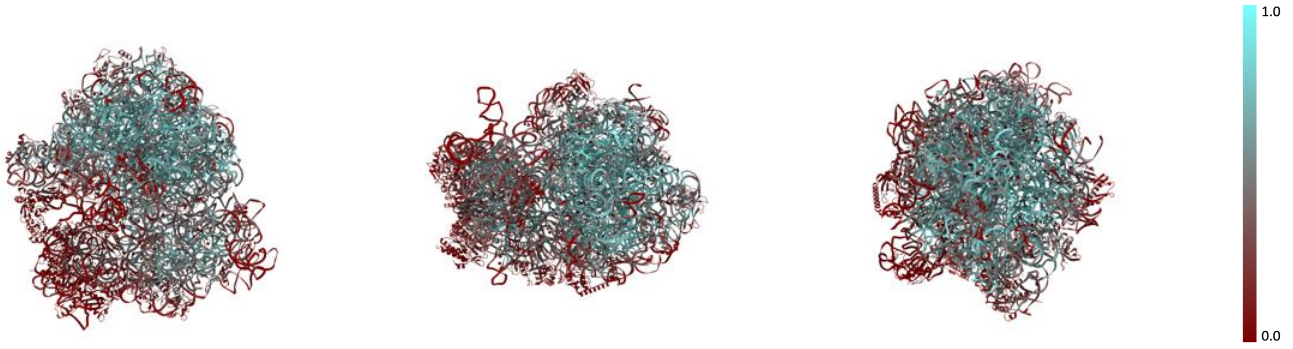
9.2 Q-score mapped to coordinate model (i)



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.

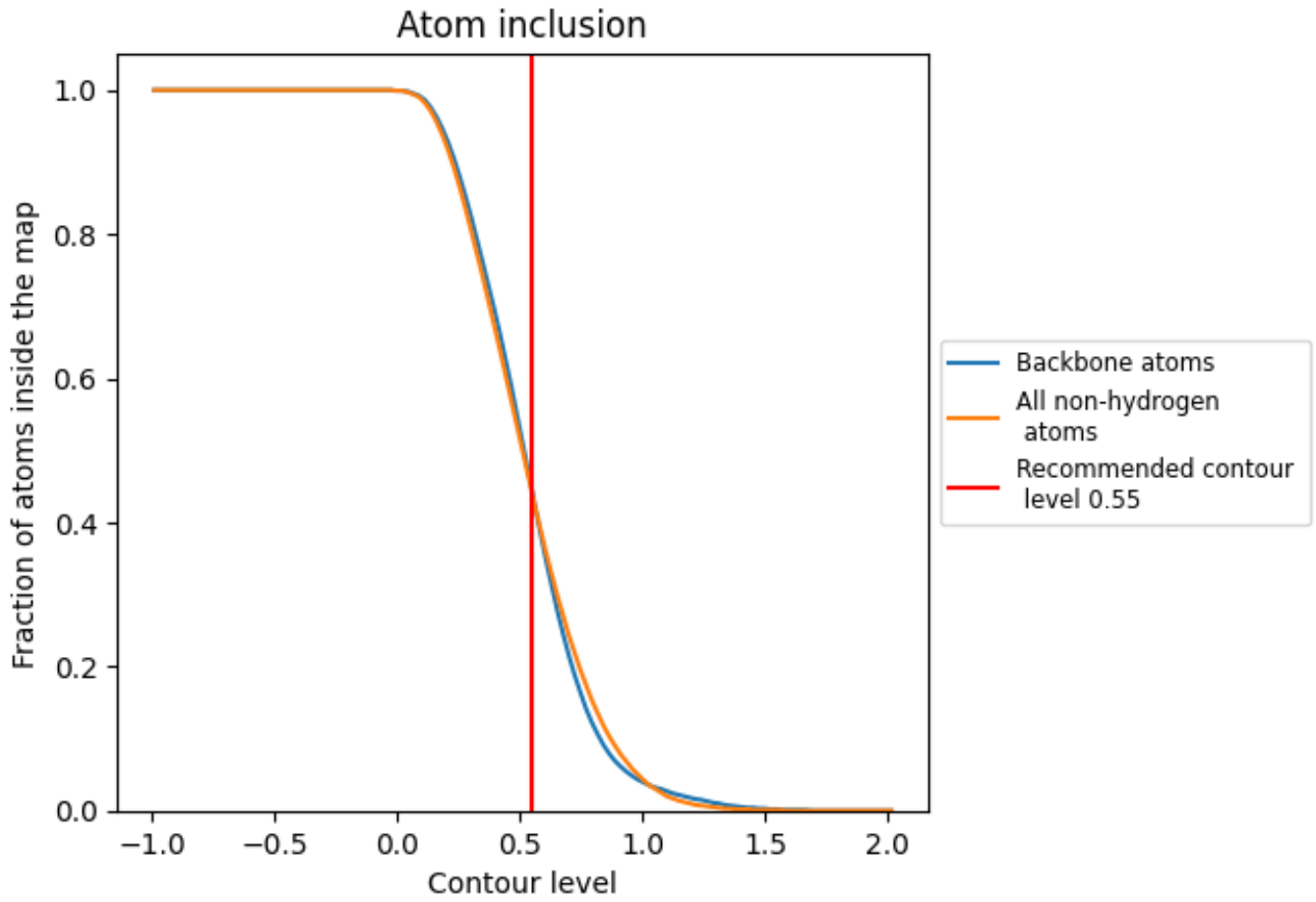
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.55).

9.4 Atom inclusion (i)



At the recommended contour level, 44% of all backbone atoms, 44% 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 (0.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4380	0.5880
0	0.3910	0.6250
1	0.6340	0.6540
2	0.6290	0.6480
3	0.4370	0.6350
4	0.0060	0.4750
5	0.0000	0.4060
A	0.3770	0.5760
B	0.0010	0.4410
C	0.0830	0.5560
D	0.1310	0.5750
E	0.3000	0.6020
F	0.1010	0.5590
G	0.0350	0.5390
H	0.3030	0.6050
I	0.0580	0.5430
J	0.0470	0.4960
K	0.1320	0.5740
L	0.2620	0.6110
M	0.0310	0.5340
N	0.0540	0.5570
O	0.2550	0.6000
P	0.3230	0.5950
Q	0.2180	0.5880
R	0.1520	0.5490
S	0.0060	0.5250
T	0.2650	0.5990
V	0.0120	0.3770
W	0.0000	0.3550
X	0.0580	0.5590
a	0.6010	0.6040
b	0.4260	0.6020
c	0.5340	0.6420
d	0.5120	0.6410
e	0.3950	0.6160



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Chain	Atom inclusion	Q-score
f	0.0550	0.5410
g	0.1040	0.5630
h	0.0100	0.4290
i	0.5210	0.6340
j	0.4480	0.6330
k	0.4630	0.6280
l	0.4270	0.6340
m	0.6050	0.6460
n	0.2780	0.5950
o	0.4510	0.6310
p	0.6010	0.6390
q	0.4190	0.6280
r	0.5010	0.6290
s	0.3730	0.6120
t	0.2910	0.5970
u	0.2930	0.6120
v	0.5520	0.6440
w	0.4580	0.6360
x	0.2650	0.5810
y	0.4530	0.6240
z	0.5130	0.6290