wwPDB EM Validation Summary Report (i)

Nov 7, 2026 – 10:02 am GMT

PDB ID	:	9TA1 / pdb_00009ta1
EMDB ID	:	EMD-55742
Title	:	Structural characterization of hibernating ribosomes in the Gram-negative pathogen Acinetobacter baumannii with bS21 and no E-site tRNA
Authors	:	Vasanthakrishnan, R.K.B.S.; Olivier, D.; Sophie, C.; Yann, L.C.; Sylvie, G.D.; Sassi, M.; Emmanuel, G.; Reynald, G.
Deposited on	:	2025-11-18
Resolution	:	2.90 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 (i)) were used in the production of this report:

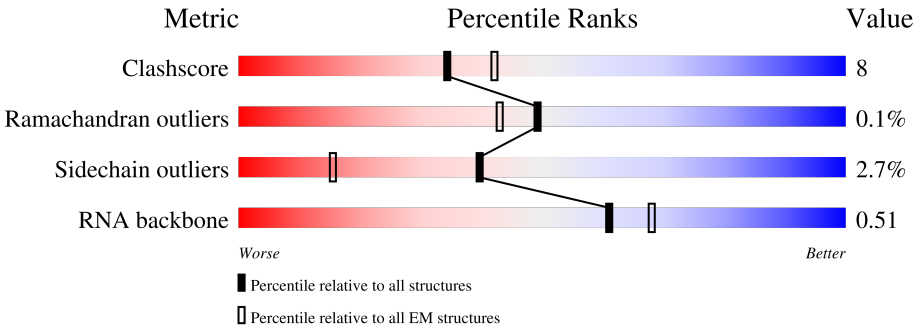
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

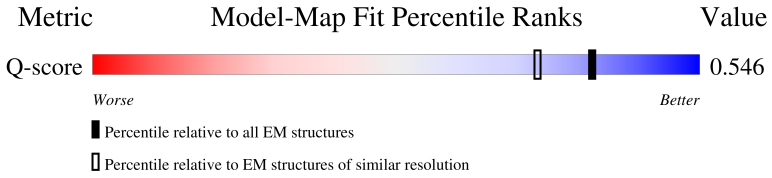
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.90 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	13054 (2.40 - 3.40)

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	0	51	80% 75% 25%
2	1	44	23% 86% 14%
3	2	64	42% 70% 28%

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Mol	Chain	Length	Quality of chain
4	3	38	66% 82% 18%
5	4	74	96% 59% 35%
6	A	1537	54% 56% 37% 7%
7	B	250	90% 67% 23% 8%
8	C	250	79% 70% 16% 14%
9	D	208	98% 74% 25%
10	E	165	73% 78% 16% 6%
11	F	127	80% 62% 18% 17%
12	G	156	98% 68% 29%
13	H	131	73% 79% 19%
14	I	128	97% 80% 20%
15	J	103	92% 53% 43%
16	K	128	77% 67% 22% 9%
17	L	124	86% 74% 22%
18	M	118	98% 71% 25%
19	N	101	97% 68% 31%
20	O	89	81% 80% 18%
21	P	83	88% 78% 19%
22	Q	85	87% 78% 14% 7%
23	R	75	71% 69% 17% 12%
24	S	91	92% 58% 33% 8%
25	T	88	89% 78% 19%
26	U	71	99% 69% 30%
27	X	116	84% 69% 21% 10%
28	a	2893	30% 56% 38% 6%

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Mol	Chain	Length	Quality of chain
29	b	115	74% 63% 32%
30	c	274	48% 79% 20%
31	d	212	45% 84% 15%
32	e	200	66% 79% 20%
33	f	178	99% 57% 39%
34	g	177	99% 73% 25%
35	h	148	41% 32% 8% 59%
36	i	142	52% 76% 24%
37	j	122	69% 82% 18%
38	k	146	60% 84% 16%
39	l	137	78% 82% 18%
40	m	125	38% 86% 10% 5%
41	n	116	92% 73% 25%
42	o	122	61% 76% 20%
43	p	119	37% 85% 13%
44	q	103	66% 84% 16%
45	r	109	46% 78% 22%
46	s	106	64% 69% 18% 13%
47	t	105	90% 80% 17%
48	u	98	84% 79% 19%
49	v	85	41% 81% 11% 8%
50	w	78	55% 77% 21%
51	x	65	91% 77% 17% 5%
52	y	58	55% 81% 19%
53	z	61	44% 84% 5% 11%

2 Entry composition (i)

There are 56 unique types of molecules in this entry. The entry contains 142578 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
1	0	51	Total	C	N	O	S	0	0
			427	274	77	73	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	44	Total	C	N	O	S	0	0
			363	222	85	54	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	63	Total	C	N	O	S	0	0
			509	319	110	76	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			295	179	64	48	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	71	Total	C	N	O	S	0	0
			552	343	101	102	6		

- Molecule 6 is a RNA chain called 16S rRNA (1529-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	1528	Total	C	N	O	P	0	0
			32785	14632	5993	10632	1528		

- Molecule 7 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	229	Total	C	N	O	S	0	0
			1801	1130	333	332	6		

- Molecule 8 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	215	Total	C	N	O	S	0	0
			1690	1065	318	299	8		

- Molecule 9 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	207	Total	C	N	O	S	0	0
			1631	1017	313	299	2		

- Molecule 10 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	155	Total	C	N	O	S	0	0
			1129	700	217	207	5		

- Molecule 11 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	106	Total	C	N	O	S	0	0
			878	552	160	162	4		

- Molecule 12 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	153	Total	C	N	O	S	0	0
			1210	758	229	216	7		

- Molecule 13 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	130	Total	C	N	O	S	0	0
			985	615	177	187	6		

- Molecule 14 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	127	Total	C	N	O	S	0	0
			995	621	198	175	1		

- Molecule 15 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	100	Total	C	N	O	S	0	0
			801	500	150	148	3		

- Molecule 16 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	117	Total	C	N	O	S	0	0
			862	535	166	160	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	118	IAS	ASN	modified residue	UNP D0CD20

- Molecule 17 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	122	Total	C	N	O	S	0	0
			947	581	193	167	6		

- Molecule 18 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	116	Total	C	N	O	S	0	0
			912	564	186	159	3		

- Molecule 19 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	100	Total	C	N	O	S	0	0
			792	493	158	137	4		

- Molecule 20 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	88	Total	C	N	O	S	0	0
			705	434	144	126	1		

- Molecule 21 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	82	Total	C	N	O	S	0	0
			644	403	128	112	1		

- Molecule 22 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	79	Total	C	N	O	S	0	0
			621	390	116	114	1		

- Molecule 23 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	66	Total	C	N	O	S	0	0
			545	349	96	99	1		

- Molecule 24 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	84	Total	C	N	O	S	0	0
			657	419	127	109	2		

- Molecule 25 is a protein called 30S ribosomal protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	86	Total	C	N	O	S	0	0
			663	409	139	113	2		

- Molecule 26 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	70	Total	C	N	O	S	0	0
			585	367	118	99	1		

- Molecule 27 is a protein called Putative ribosomal subunit interface protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	104	Total	C	N	O	S	0	0
			841	519	161	158	3		

- Molecule 28 is a RNA chain called 23S rRNA (2890-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	2890	Total	C	N	O	P	0	0
			61984	27671	11335	20088	2890		

- Molecule 29 is a RNA chain called 5S rRNA (115-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	115	Total	C	N	O	P	0	0
			2450	1095	440	800	115		

- Molecule 30 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	272	Total	C	N	O	S	0	0
			2111	1302	436	365	8		

- Molecule 31 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	211	Total	C	N	O	S	0	0
			1573	973	297	300	3		

- Molecule 32 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	199	Total	C	N	O	S	0	0
			1511	950	280	276	5		

- Molecule 33 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	177	Total	C	N	O	S	0	0
			1395	886	250	251	8		

- Molecule 34 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	175	Total	C	N	O	S	0	0
			1327	838	238	250	1		

- Molecule 35 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	60	Total	C	N	O	S	0	0
			458	287	84	86	1		

- Molecule 36 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	142	Total	C	N	O	S	0	0
			1125	718	200	203	4		

- Molecule 37 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	122	Total	C	N	O	S	0	0
			946	592	180	169	5		

- Molecule 38 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	146	Total	C	N	O	S	0	0
			1089	673	215	200	1		

- Molecule 39 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	137	Total	C	N	O	S	0	0
			1088	687	210	185	6		

- Molecule 40 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	m	119	Total	C	N	O	S	0	0
			942	590	186	163	3		

- Molecule 41 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	n	115	Total	C	N	O	S	0	0
			865	532	175	157	1		

- Molecule 42 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	o	117	Total	C	N	O	0	0
			919	578	177	164		

- Molecule 43 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	117	Total	C	N	O	S	0	0
			934	589	197	146	2		

- Molecule 44 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	103	Total	C	N	O	S	0	0
			807	506	155	143	3		

- Molecule 45 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	109	Total	C	N	O	S	0	0
			826	514	158	150	4		

- Molecule 46 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	92	Total	C	N	O	S	0	0
			717	457	129	130	1		

- Molecule 47 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	t	103	Total	C	N	O	0	0
			766	476	142	148		

- Molecule 48 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	97	Total	C	N	O	S	0	0
			760	477	143	139	1		

- Molecule 49 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	78	Total	C	N	O	S	0	0
			589	365	113	109	2		

- Molecule 50 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	77	Total	C	N	O	S	0	0
			632	395	130	105	2		

- Molecule 51 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	62	Total	C	N	O	S	0	0
			498	308	96	93	1		

- Molecule 52 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	y	58	Total	C	N	O	S	0	0
			463	286	88	85	4		

- Molecule 53 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	z	54	Total	C	N	O	S	0	0
			447	265	100	81	1		

- Molecule 54 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
54	1	2	Total	K	0
			2	2	
54	A	45	Total	K	0
			45	45	
54	E	1	Total	K	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
54	L	1	Total K 1 1	0
54	M	1	Total K 1 1	0
54	a	111	Total K 111 111	0
54	b	1	Total K 1 1	0
54	c	4	Total K 4 4	0
54	d	2	Total K 2 2	0
54	t	1	Total K 1 1	0

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
55	3	1	Total Zn 1 1	0
55	4	1	Total Zn 1 1	0

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
56	A	96	Total Mg 96 96	0
56	J	1	Total Mg 1 1	0
56	X	1	Total Mg 1 1	0
56	a	249	Total Mg 249 249	0
56	b	5	Total Mg 5 5	0
56	c	2	Total Mg 2 2	0
56	d	1	Total Mg 1 1	0
56	k	1	Total Mg 1 1	0

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Mol	Chain	Residues	Atoms	AltConf
56	p	2	Total Mg 2 2	0
56	v	1	Total Mg 1 1	0
56	z	1	Total Mg 1 1	0

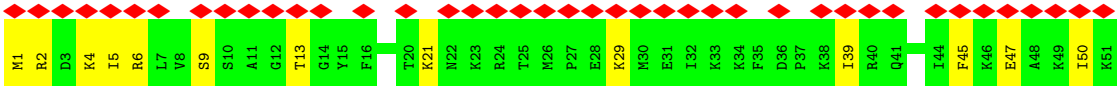
3 Residue-property plots (i)

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: Large ribosomal subunit protein bL33

Chain 0:

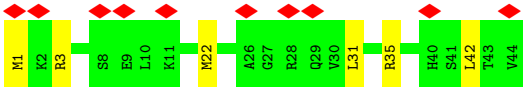




• Molecule 2: Large ribosomal subunit protein bL34

Chain 1:

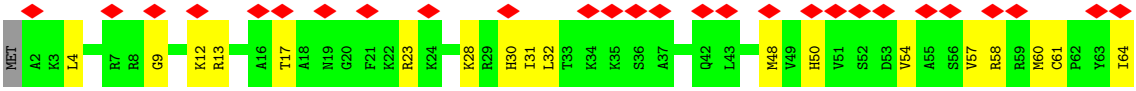




• Molecule 3: Large ribosomal subunit protein bL35

Chain 2:

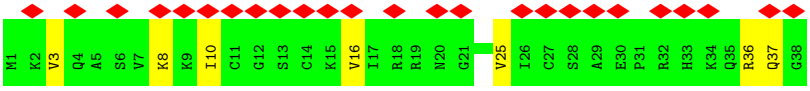




• Molecule 4: Large ribosomal subunit protein bL36

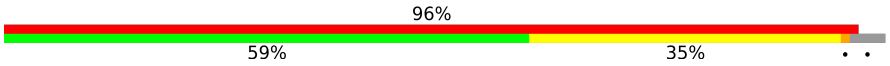
Chain 3:

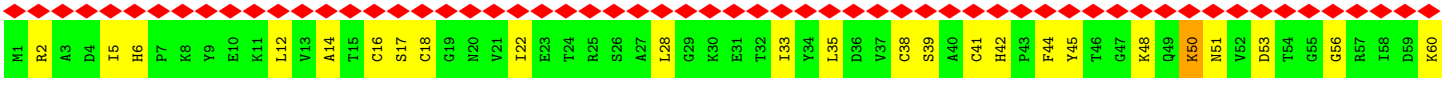


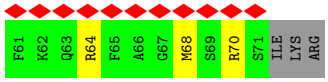


• Molecule 5: Large ribosomal subunit protein bL31

Chain 4:



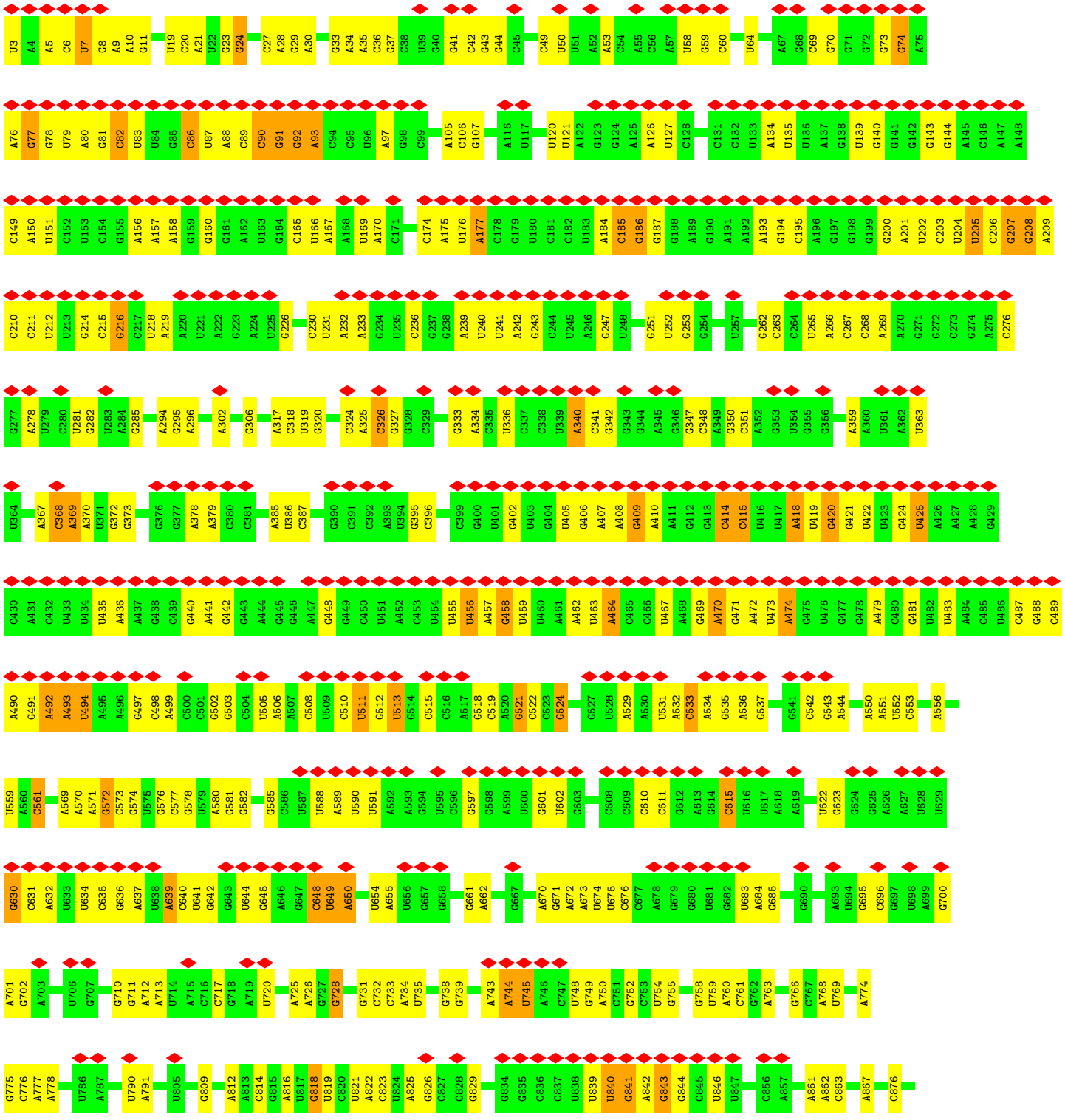


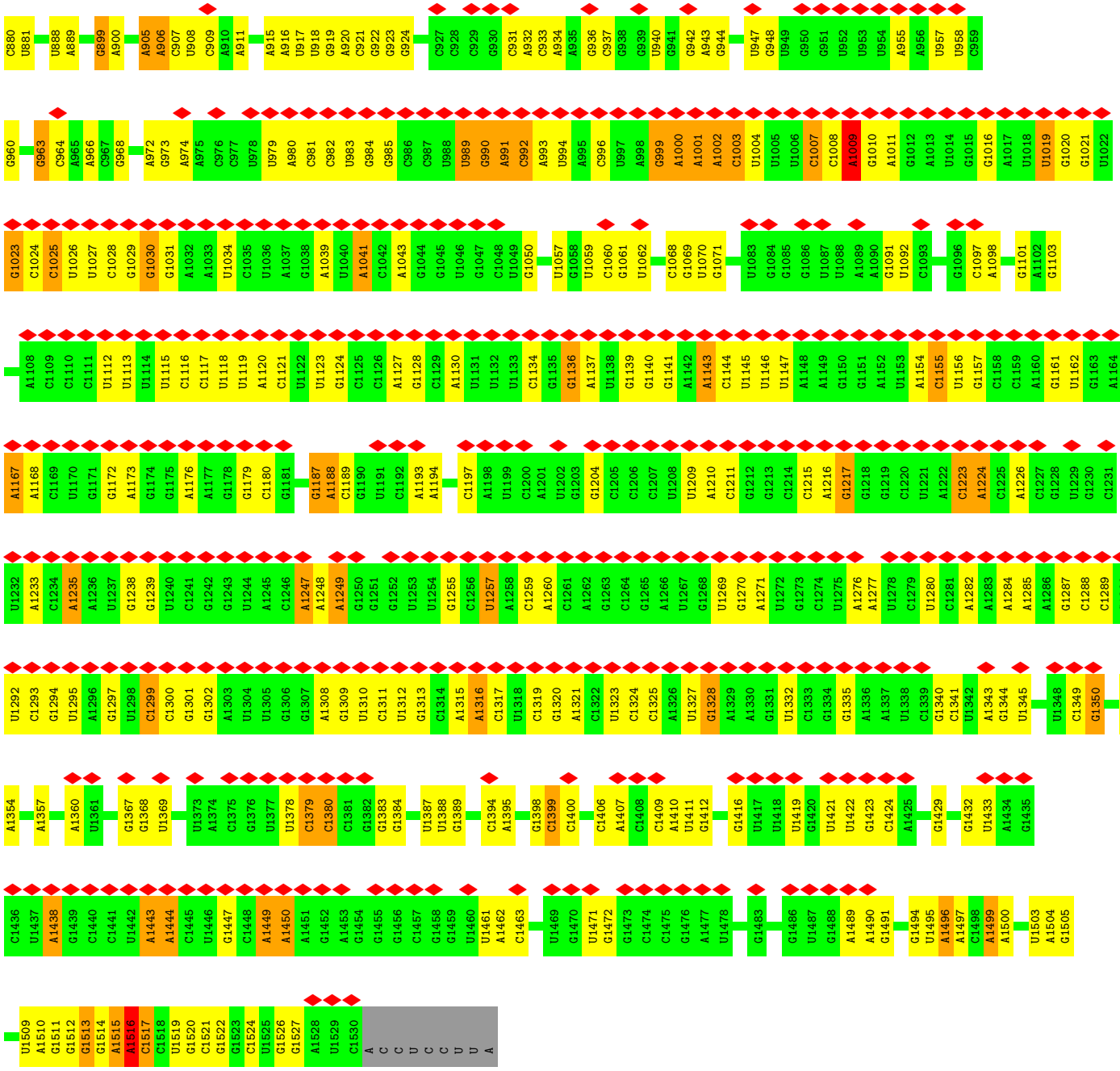


• Molecule 6: 16S rRNA (1529-MER)

Chain A:

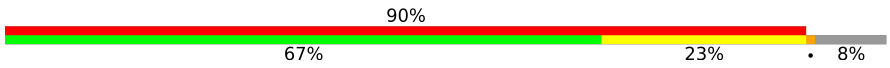


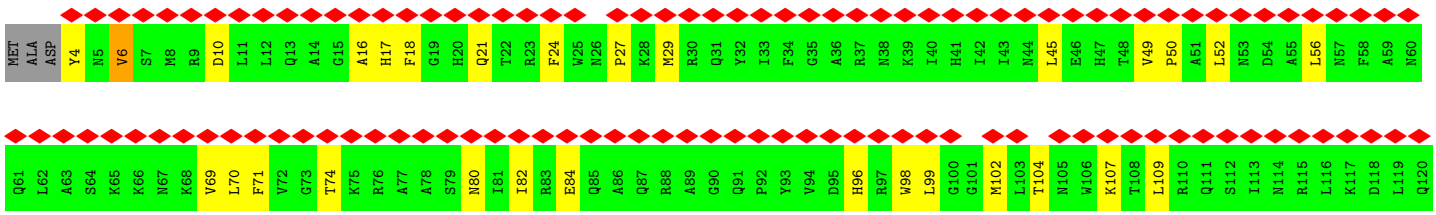


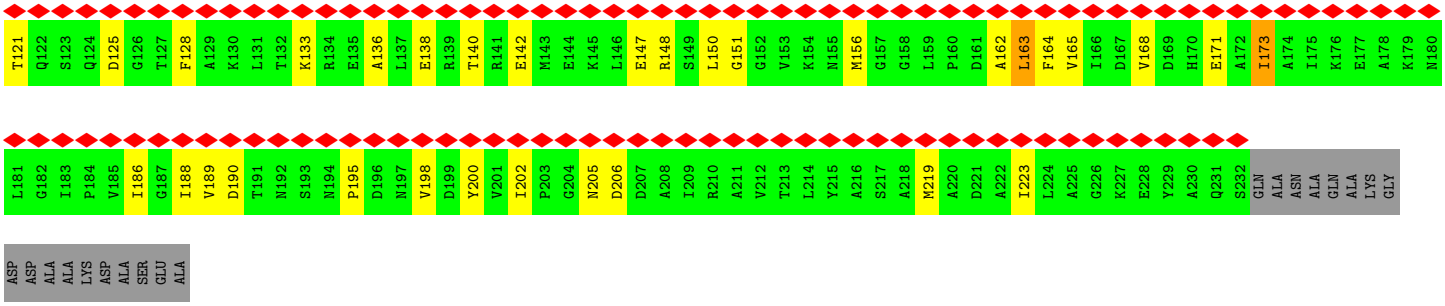


• Molecule 7: Small ribosomal subunit protein uS2

Chain B:



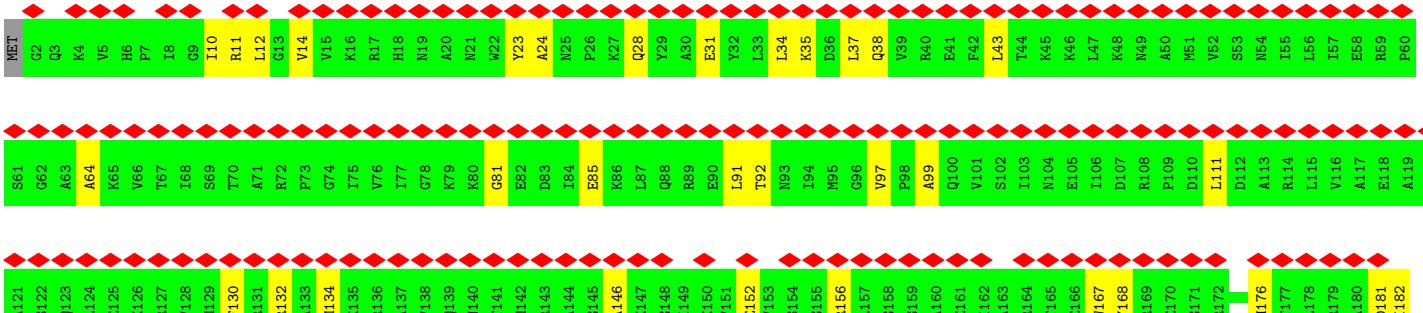




• Molecule 8: Small ribosomal subunit protein uS3

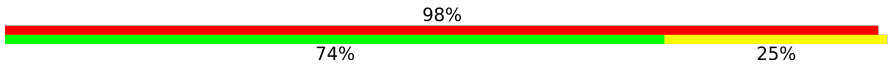
Chain C:





• Molecule 9: Small ribosomal subunit protein uS4

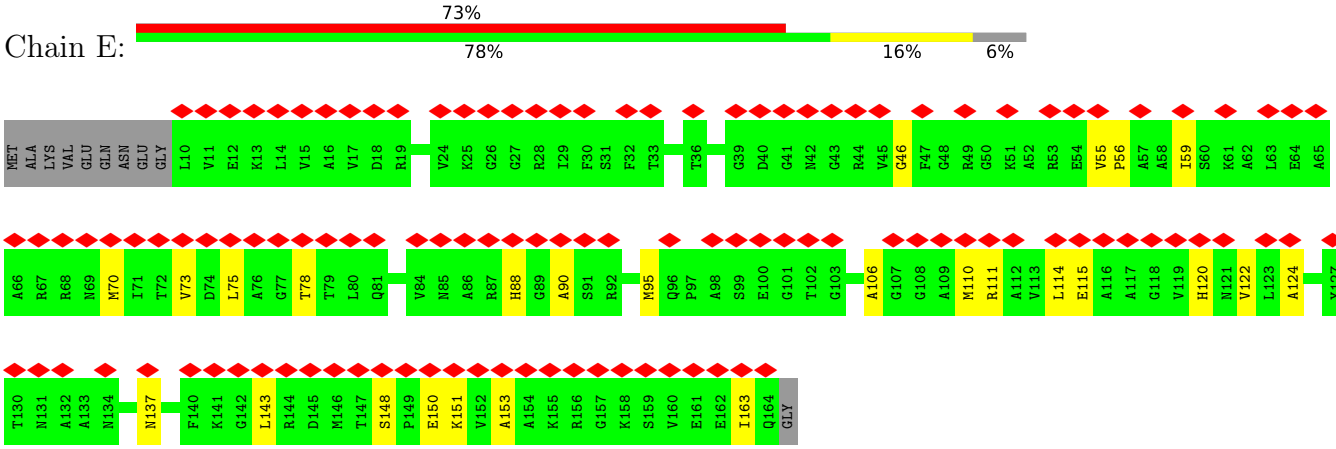
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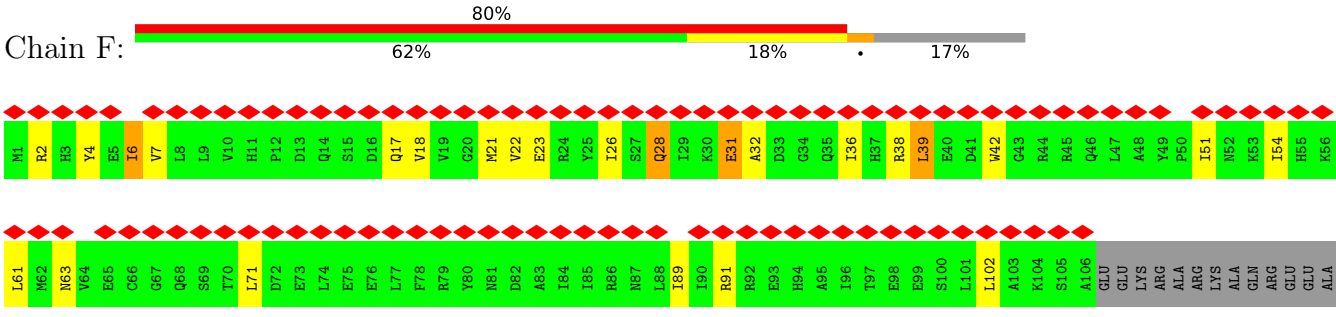
• Molecule 10: Small ribosomal subunit protein uS5

Chain E:



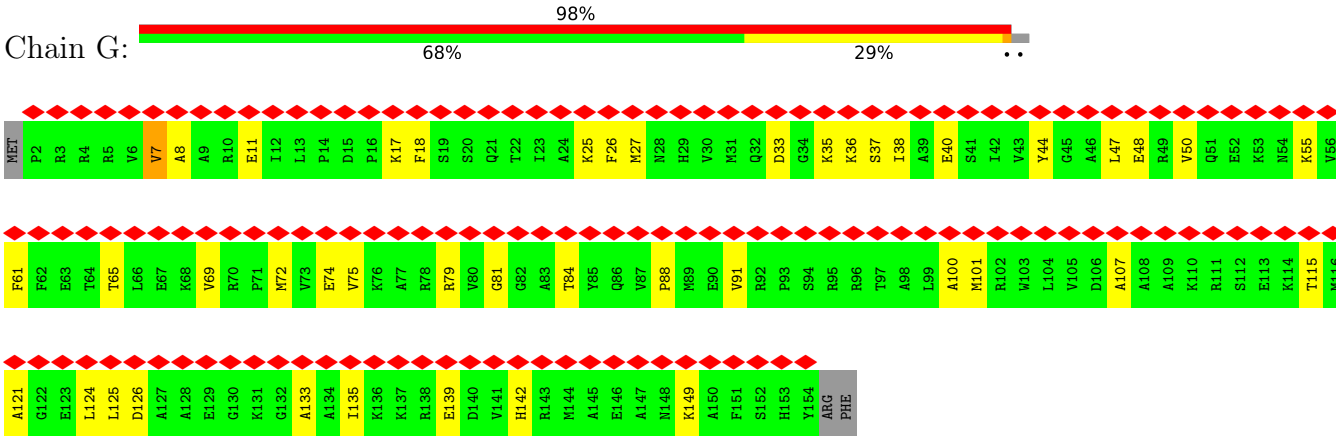
• Molecule 11: Small ribosomal subunit protein bS6

Chain F:



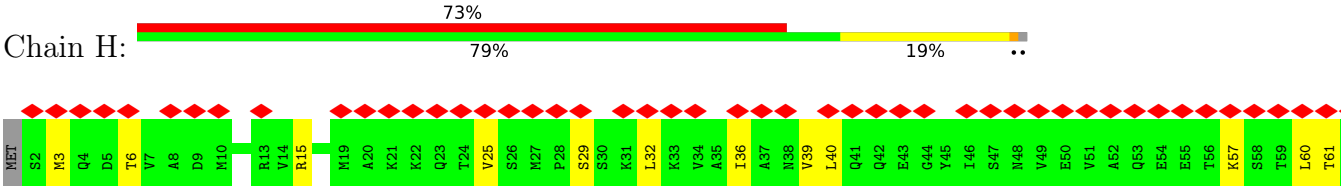
• Molecule 12: Small ribosomal subunit protein uS7

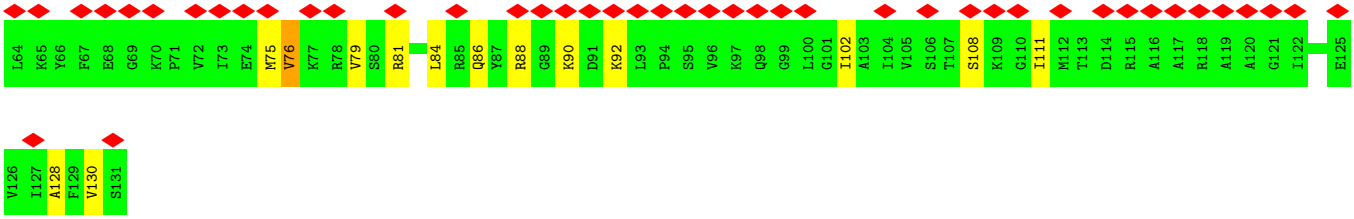
Chain G:



• Molecule 13: Small ribosomal subunit protein uS8

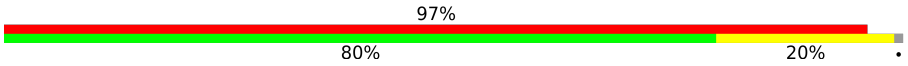
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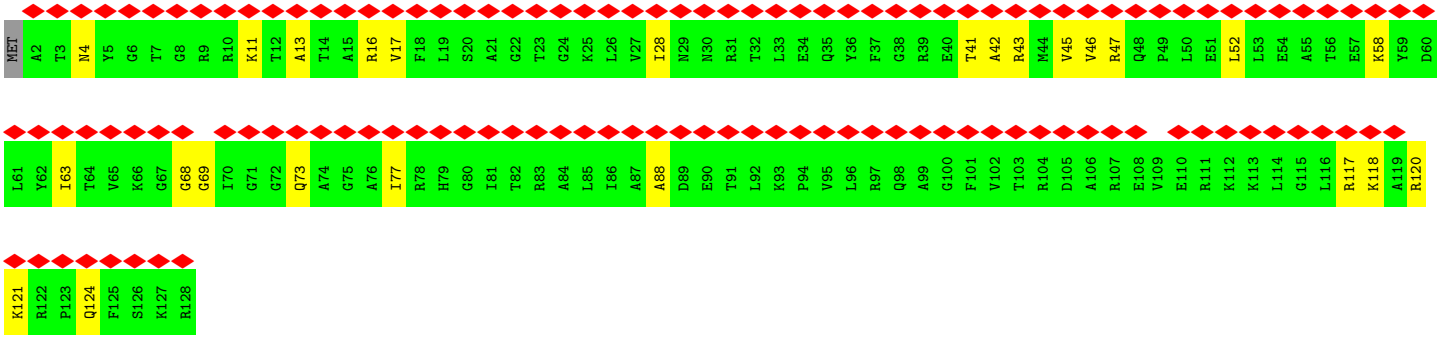




• Molecule 14: Small ribosomal subunit protein uS9

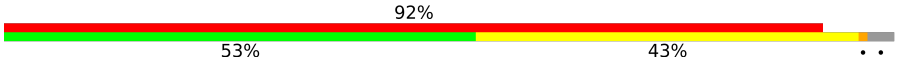
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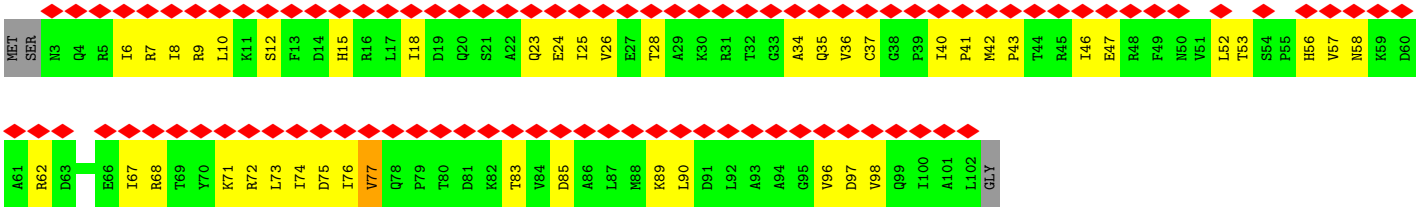




• Molecule 15: Small ribosomal subunit protein uS10

Chain J:

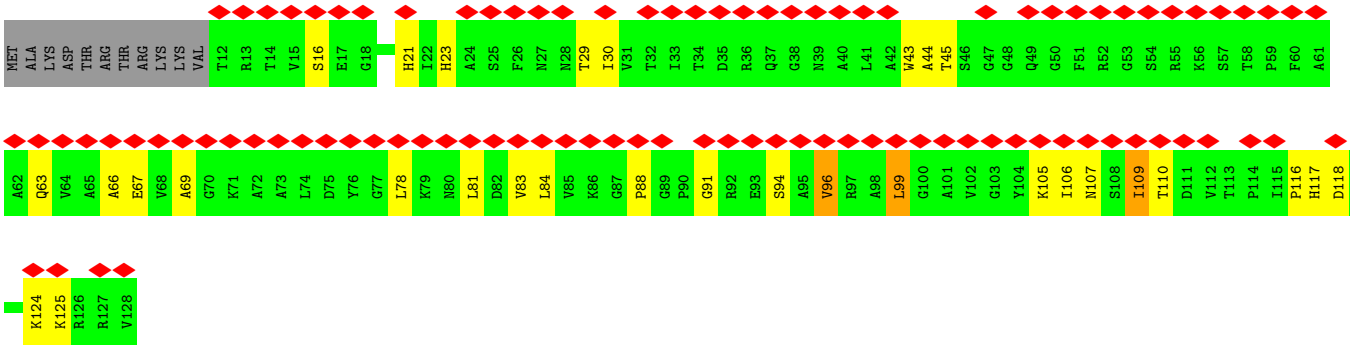




• Molecule 16: Small ribosomal subunit protein uS11

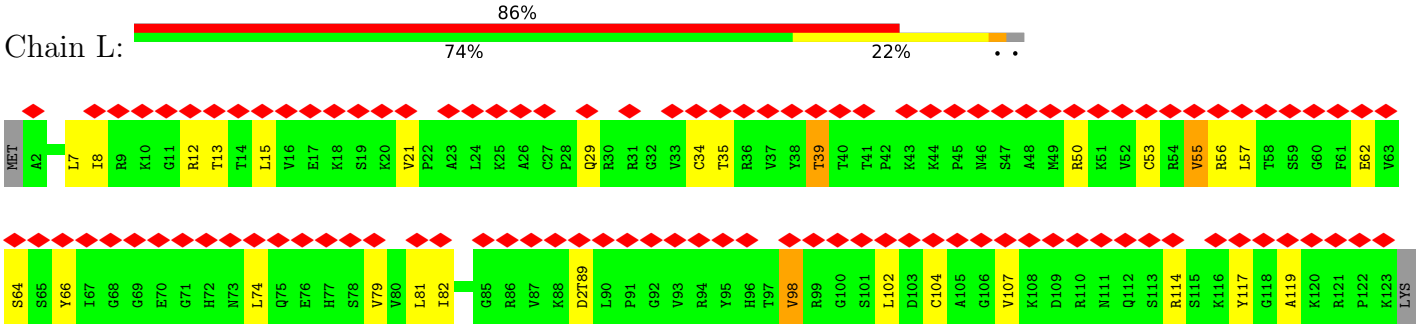
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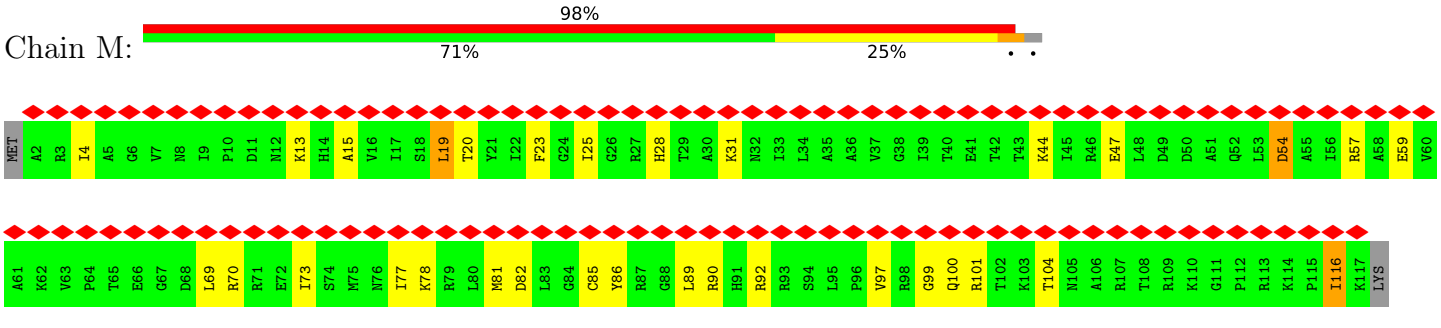
• Molecule 17: Small ribosomal subunit protein uS12

Chain L:



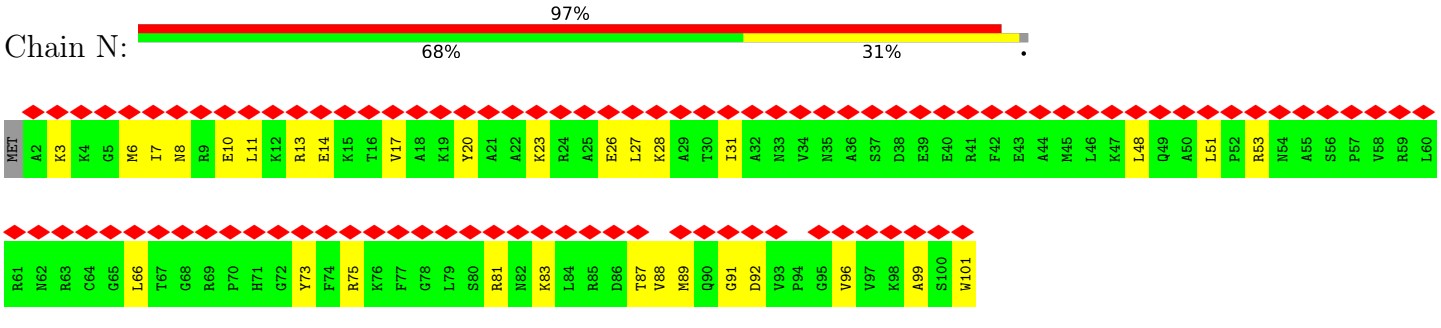
• Molecule 18: Small ribosomal subunit protein uS13

Chain M:



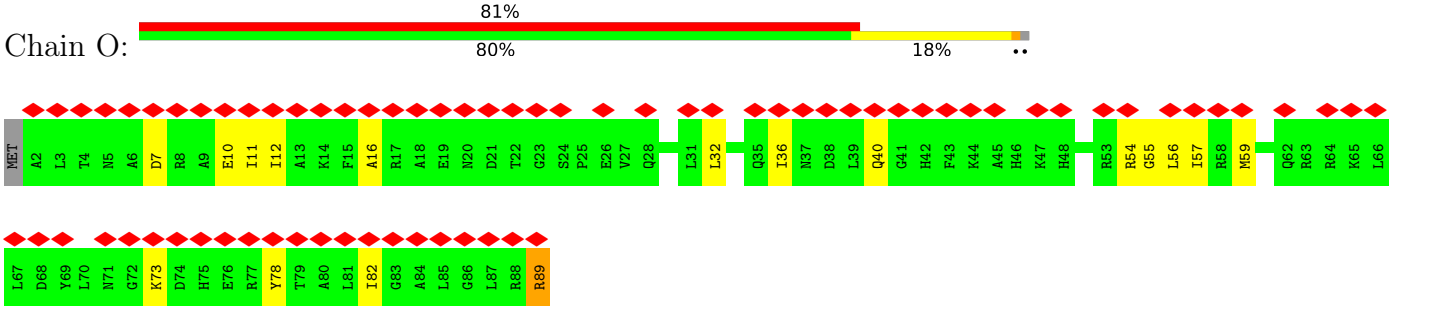
• Molecule 19: Small ribosomal subunit protein uS14

Chain N:



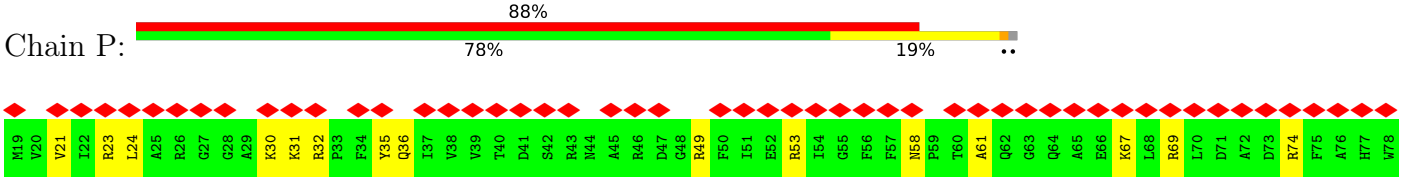
• Molecule 20: Small ribosomal subunit protein uS15

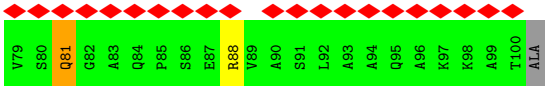
Chain O:



• Molecule 21: Small ribosomal subunit protein bS16

Chain P:

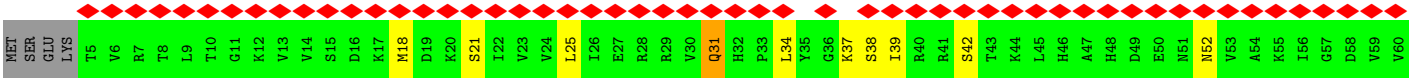


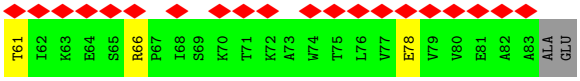


• Molecule 22: Small ribosomal subunit protein uS17

Chain Q:



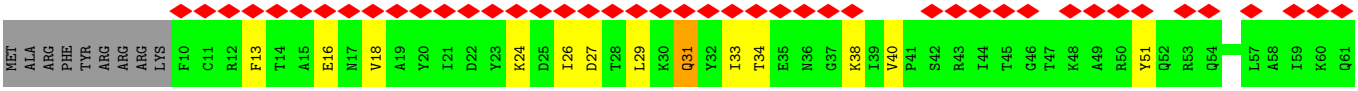


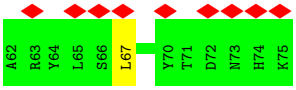


• Molecule 23: Small ribosomal subunit protein bS18

Chain R:

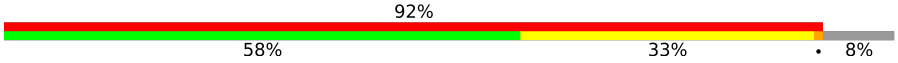


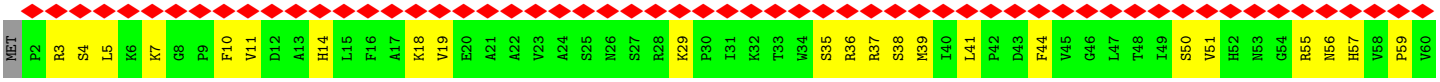


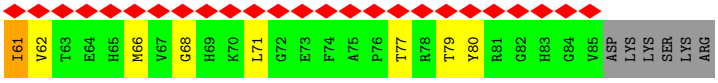


• Molecule 24: Small ribosomal subunit protein uS19

Chain S:

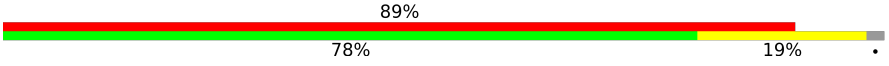


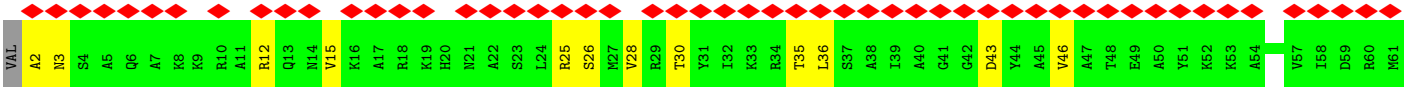


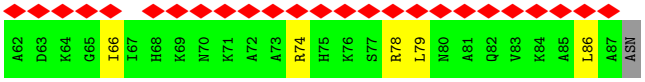


• Molecule 25: 30S ribosomal protein bS20

Chain T:

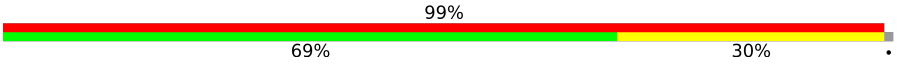


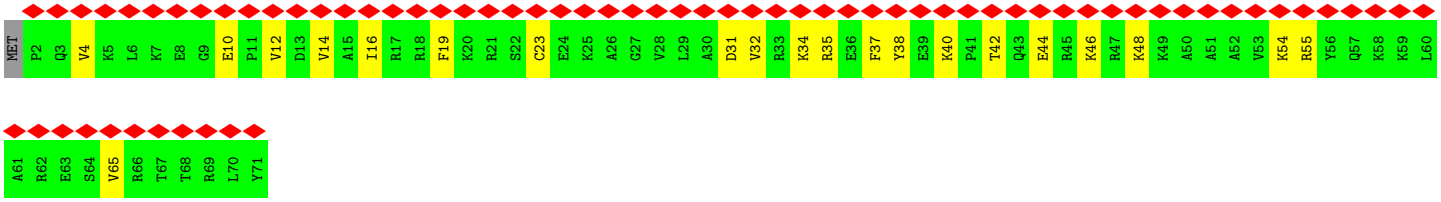




• Molecule 26: Small ribosomal subunit protein bS21

Chain U:





• Molecule 27: Putative ribosomal subunit interface protein

Chain X:

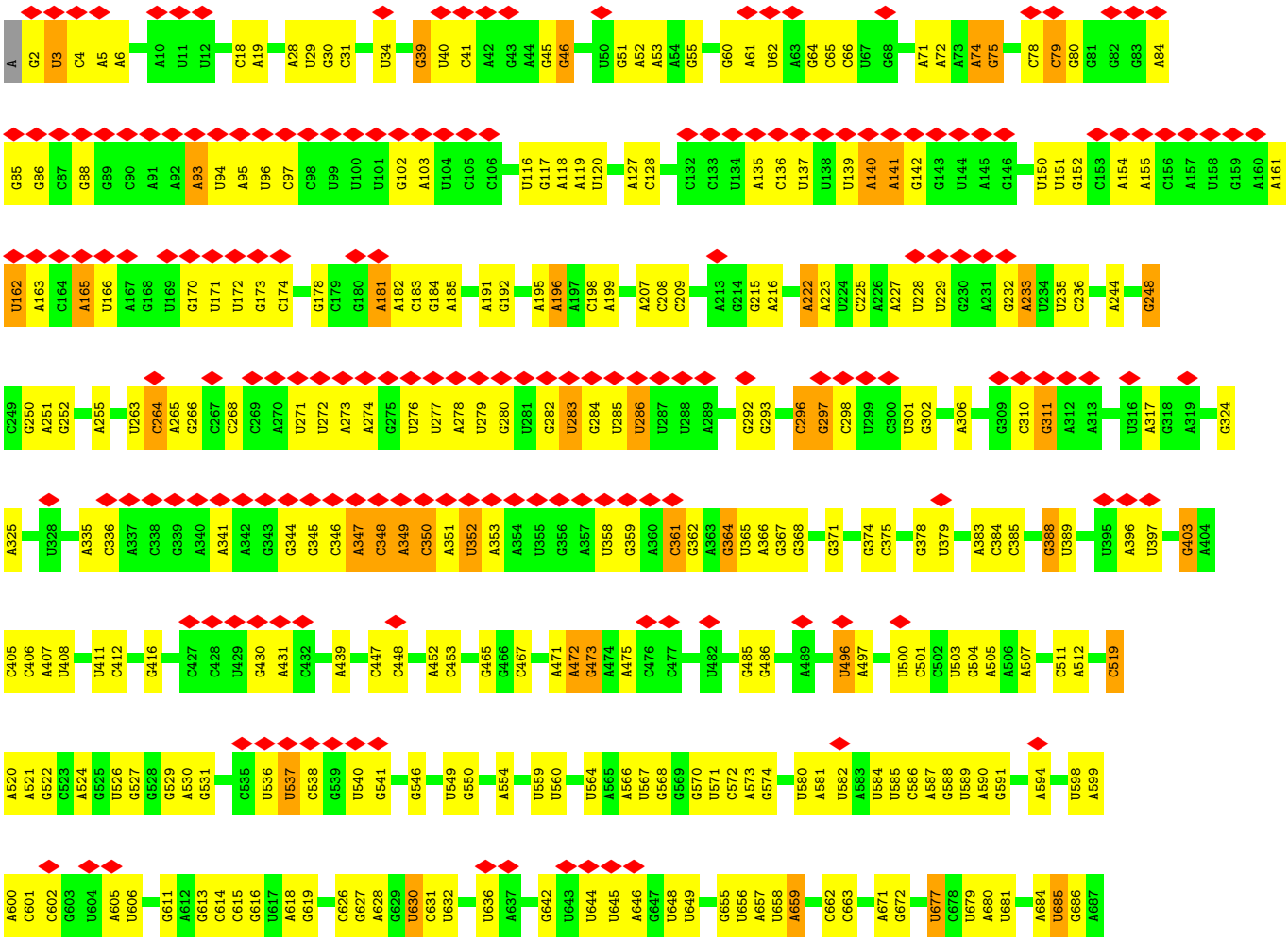


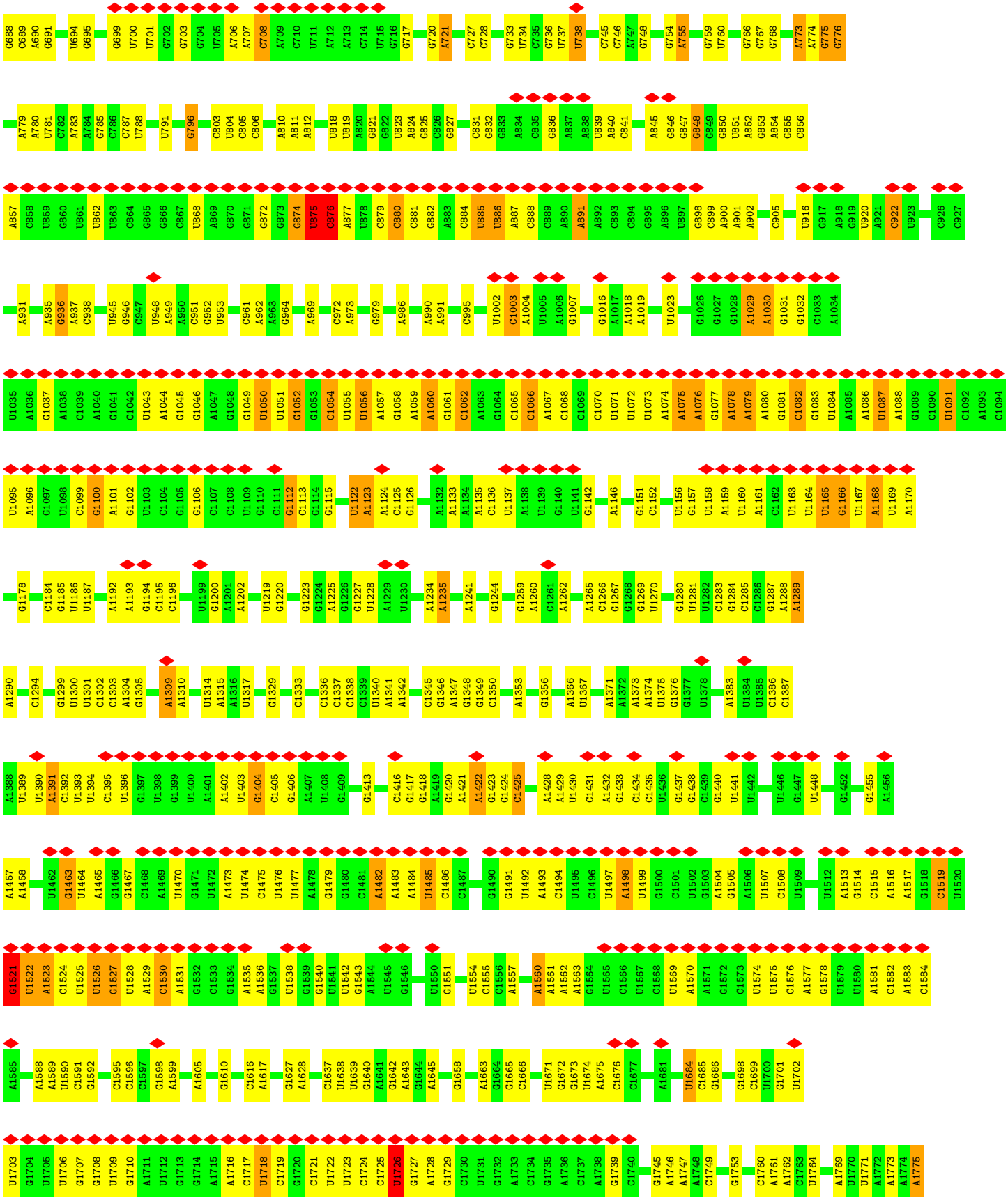


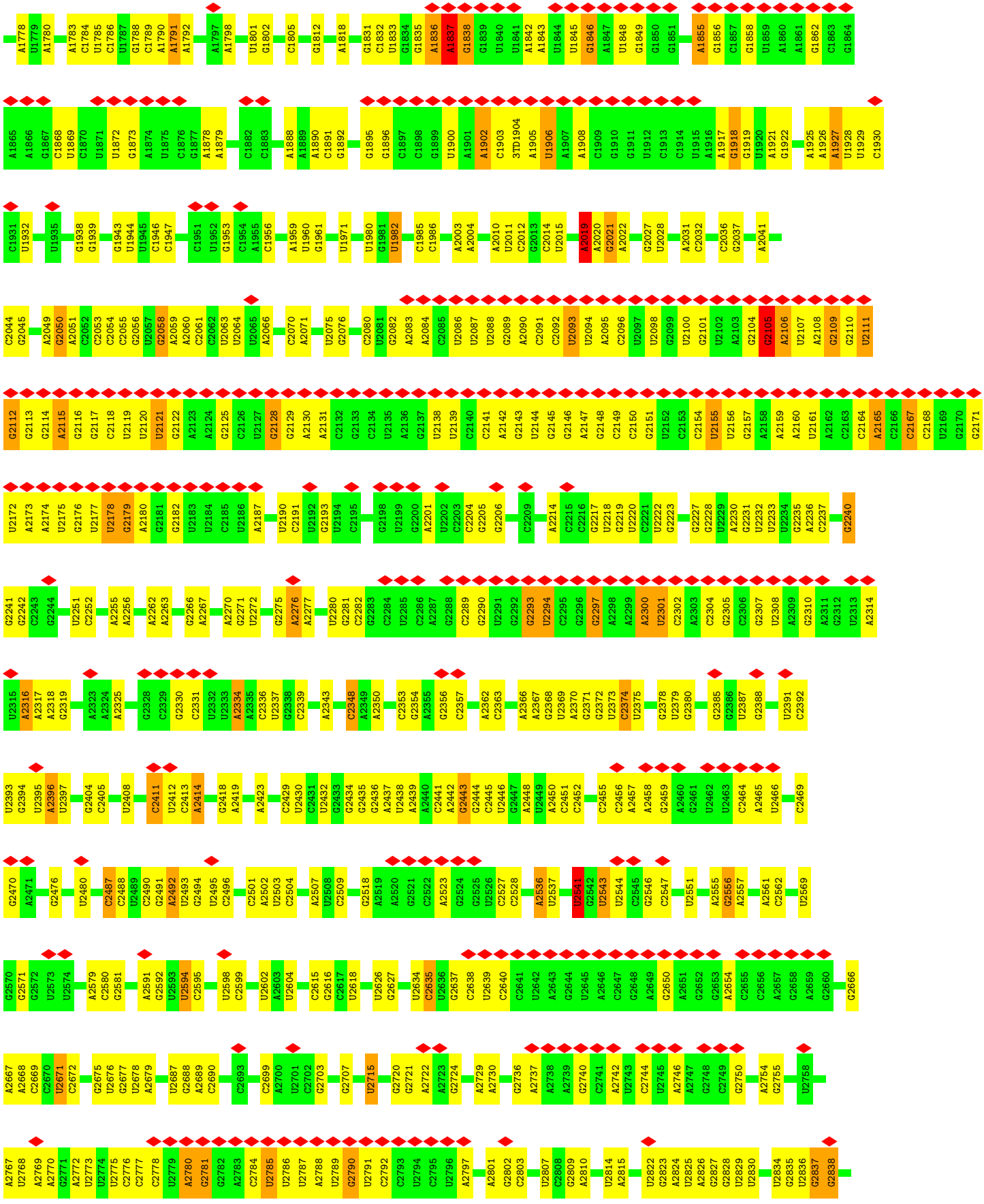
• Molecule 28: 23S rRNA (2890-MER)

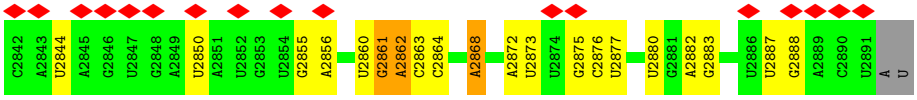
Chain a:






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A779 A780 U781 C782 A783 A784 G785 C786 C787 U788 U791 G796 C803 U804 C805 C806 A810 A811 A812 U818 U819 A820 G821 C822 U823 A824 G825 C826 G827 C831 G832 G833 A834 C835 G836 A837 A838 U839 A840 C841 A845 G846 G847 G848 G849 G850 U851 A852 G853 A854 G855 C856
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U1703 G1704 U1705 U1706 G1707 G1708 U1709 G1710 A1711 U1712 G1713 G1714 A1715 A1716 C1717 U1718 C1719 G1720 C1721 U1722 U1723 C1724 C1725 U1726 G1727 A1728 G1729 C1730 U1731 G1732 A1733 C1734 G1735 A1736 C1737 A1738 G1739 C1740 G1745 A1746 A1747 A1748 C1749 G1753 C1760 A1761 A1762 C1763 U1764 A1769 U1770 U1771 A1772 A1773 A1774 A1775

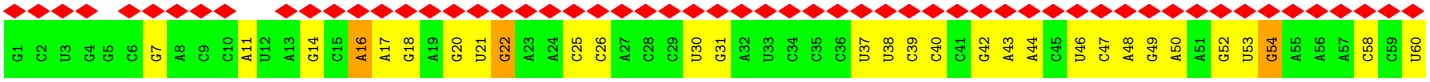

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C2044 G2045 A2049 G2050 A2051 C2052 C2053 C2054 C2055 G2056 U2057 G2058 A2059 A2060 C2061 C2062 U2063 U2064 U2065 A2066 C2070 A2071 U2075 G2076 C2080 U2081 G2082 A2083 A2084 C2085 U2086 U2087 U2088 G2089 A2090 C2091 C2092 U2093 U2094 A2095 C2096 U2097 U2098 G2099 U2100 G2101 U2102 A2103 G2104 G2105 A2106 U2107 A2108 G2109 G2110 U2111
G2112 G2113 G2114 A2115 G2116 G2117 C2118 U2119 U2120 U2121 G2122 A2123 A2124 G2125 C2126 U2127 G2128 G2129 A2130 A2131 C2132 G2133 C2134 U2135 A2136 G2137 U2138 U2139 C2140 C2141 A2142 G2143 U2144 G2145 G2146 A2147 G2148 C2149 C2150 G2151 U2152 C2153 C2154 U2155 U2156 G2157 A2158 A2159 A2160 U2161 A2162 C2163 C2164 A2165 C2166 C2167 C2168 U2169 G2170 G2171
U2172 A2173 A2174 U2175 G2176 U2177 U2178 G2179 A2180 G2181 G2182 U2183 U2184 C2185 U2186 A2187 U2190 C2191 U2192 G2193 U2194 C2195 G2198 U2199 G2200 A2201 U2202 C2203 C2204 G2205 G2206 C2209 A2214 C2215 C2216 G2217 U2218 G2219 U2220 C2221 U2222 G2223 G2227 G2228 U2229 A2230 G2231 U2232 U2233 U2234 G2235 A2236 C2237 G2240
G2241 G2242 C2243 G2244 U2251 C2252 A2255 A2256 A2262 A2263 G2266 A2267 A2270 G2271 U2272 G2275 A2276 A2277 U2280 G2281 C2282 G2283 C2284 U2285 C2286 A2287 G2288 C2289 G2290 U2291 G2292 G2293 U2294 C2295 G2296 G2297 A2298 A2299 A2300 U2301 C2302 A2303 C2304 G2305 C2306 G2307 U2308 A2309 G2310 A2311 G2312 U2313 A2314
U2315 A2316 A2317 A2318 G2319 A2323 A2324 A2325 G2328 C2329 G2330 C2331 U2332 U2333 A2334 A2335 C2336 U2337 G2338 C2339 A2343 C2348 A2349 A2350 C2353 G2354 A2355 G2356 C2357 A2362 C2363 A2366 A2367 G2368 U2369 A2370 G2371 G2372 U2373 C2374 U2375 G2378 U2379 G2380 G2385 G2386 U2387 G2388 U2391 C2392
U2393 G2394 U2395 A2396 U2397 G2404 C2405 U2408 C2411 U2412 C2413 A2414 G2418 A2419 A2423 C2429 U2430 C2431 U2432 G2433 G2434 G2435 G2436 A2437 U2438 A2439 A2440 C2441 A2442 G2443 G2444 C2445 U2446 G2447 A2448 U2449 A2450 C2451 C2452 C2455 C2456 A2457 A2458 G2459 A2460 G2461 U2462 U2463 C2464 A2465 U2466 C2469
G2470 A2471 G2476 U2480 C2487 C2488 U2489 C2490 G2491 A2492 U2493 G2494 U2495 C2496 C2501 A2502 U2503 C2504 A2507 U2508 C2509 G2518 A2519 A2520 G2521 C2522 A2523 G2524 G2525 U2526 C2527 C2528 A2536 U2537 U2541 G2542 U2543 U2544 C2545 G2546 C2547 U2551 A2555 G2556 A2557 A2561 C2562 U2569
G2570 G2571 G2572 U2573 U2574 A2579 C2580 G2581 A2591 G2592 U2593 U2594 C2595 U2598 C2599 U2602 A2603 U2604 C2615 G2616 C2617 U2618 U2626 G2627 U2634 C2635 U2636 G2637 C2638 U2639 C2640 C2641 U2642 A2643 G2644 U2645 A2646 C2647 G2648 A2649 G2650 A2651 G2652 G2653 A2654 C2655 C2656 A2657 G2658 A2659 G2660 G2666
A2667 A2668 C2669 C2670 U2671 C2672 G2675 U2676 G2677 U2678 A2679 U2687 G2688 A2689 C2690 C2693 C2699 A2700 U2701 C2702 G2703 G2707 U2715 G2720 G2721 A2722 A2723 G2724 A2729 A2730 G2736 A2737 A2738 A2739 G2740 C2741 A2742 U2743 C2744 U2745 A2746 A2747 G2748 C2749 G2750 A2754 G2755 U2758
A2767 U2768 A2769 A2770 G2771 A2772 U2773 U2774 U2775 C2776 C2777 C2778 U2779 A2780 G2781 G2782 A2783 C2784 U2785 U2786 U2787 A2788 U2789 G2790 U2791 C2792 C2793 U2794 C2795 U2796 A2797 A2801 G2802 C2803 U2807 C2808 G2809 A2810 U2814 A2815 U2822 G2823 A2824 U2825 A2826 G2827 G2828 U2829 U2830 U2834 G2835 U2836 G2837 G2838

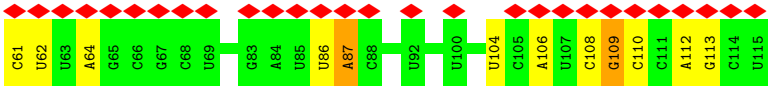


• Molecule 29: 5S rRNA (115-MER)

Chain b:

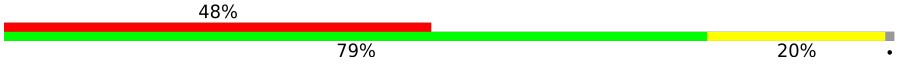


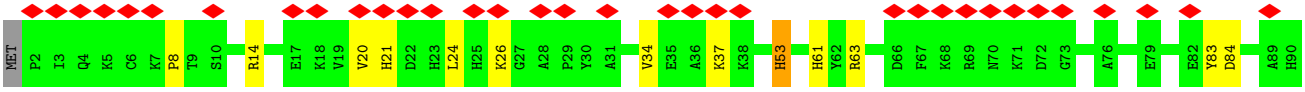


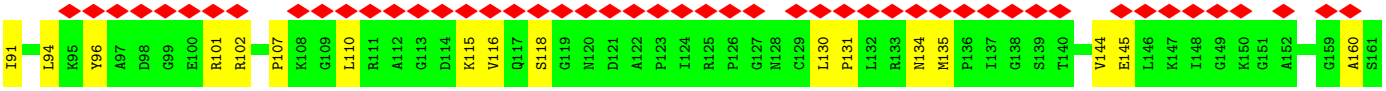


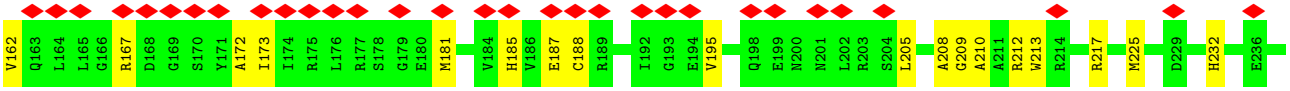
• Molecule 30: Large ribosomal subunit protein uL2

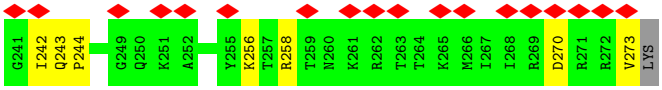
Chain c:







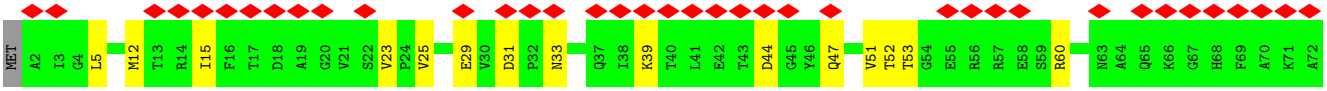


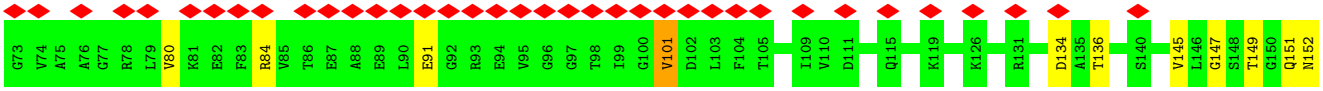


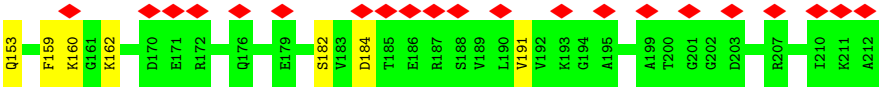
• Molecule 31: Large ribosomal subunit protein uL3

Chain d:



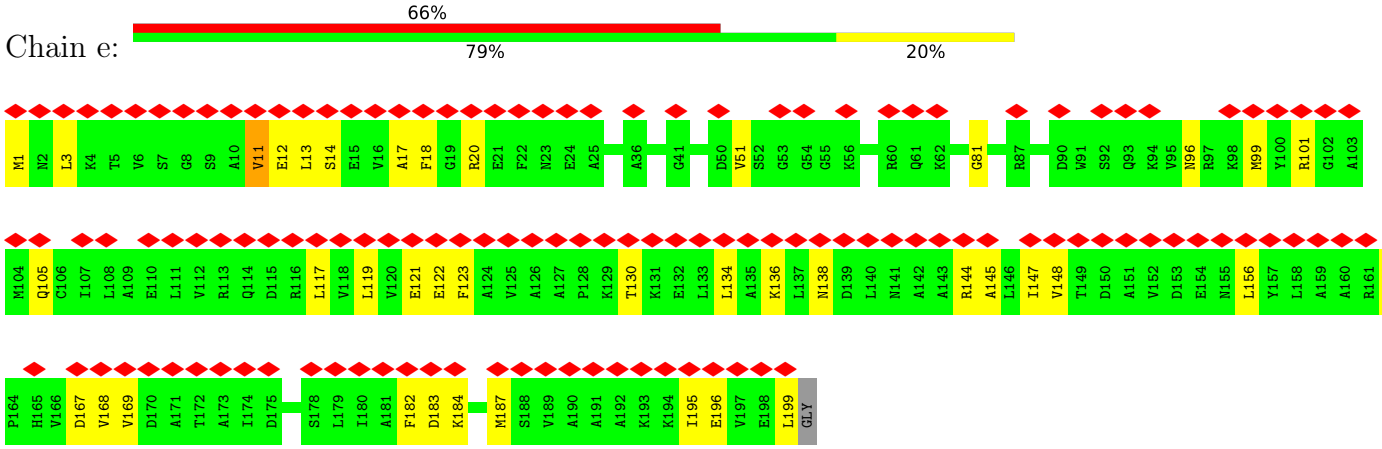






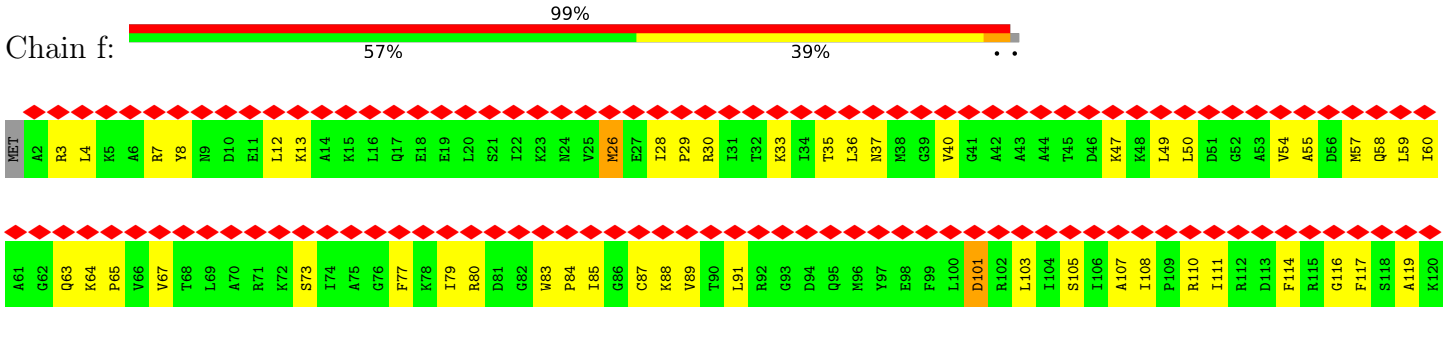
• Molecule 32: Large ribosomal subunit protein uL4

Chain e:



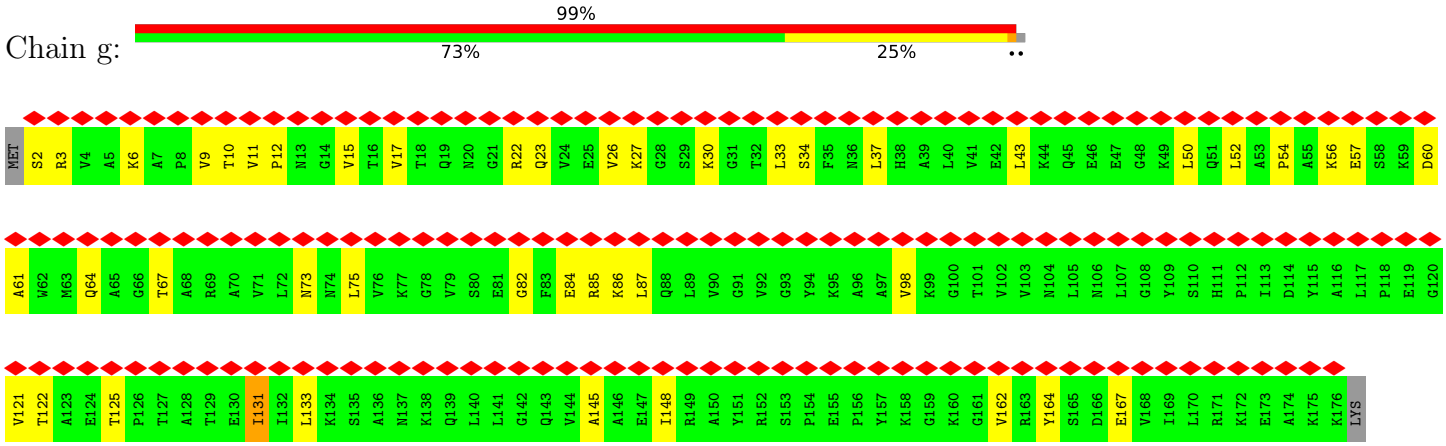
• Molecule 33: Large ribosomal subunit protein uL5

Chain f:



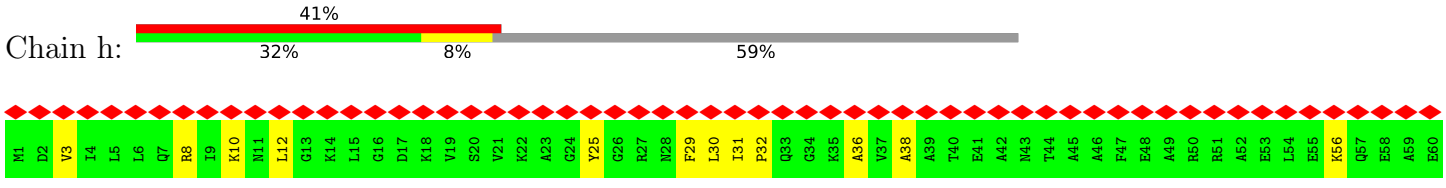
• Molecule 34: Large ribosomal subunit protein uL6

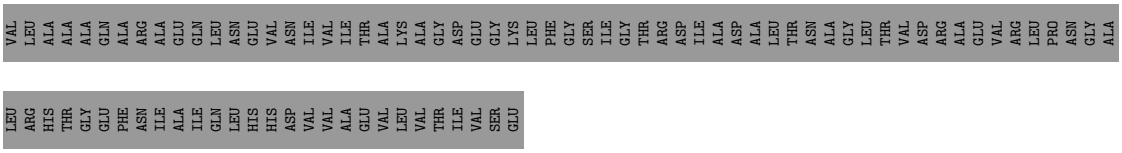
Chain g:



• Molecule 35: Large ribosomal subunit protein bL9

Chain h:

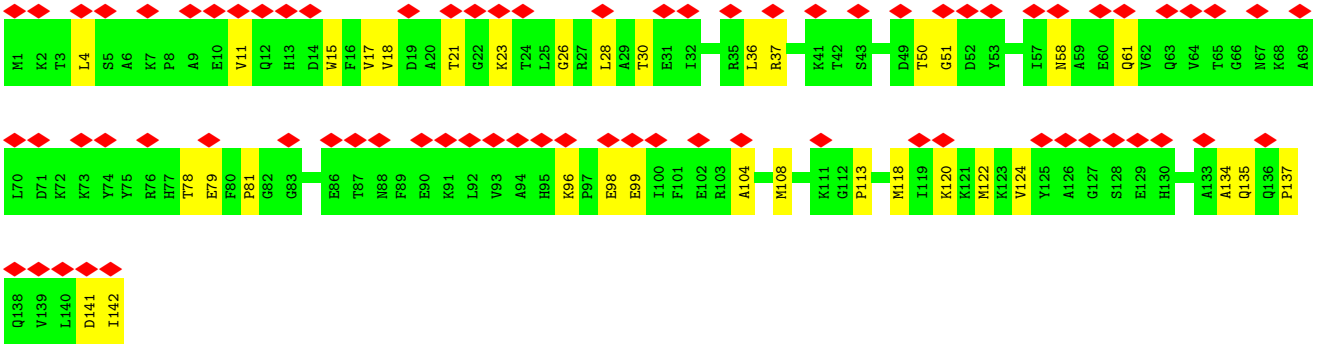




• Molecule 36: Large ribosomal subunit protein uL13

Chain i:

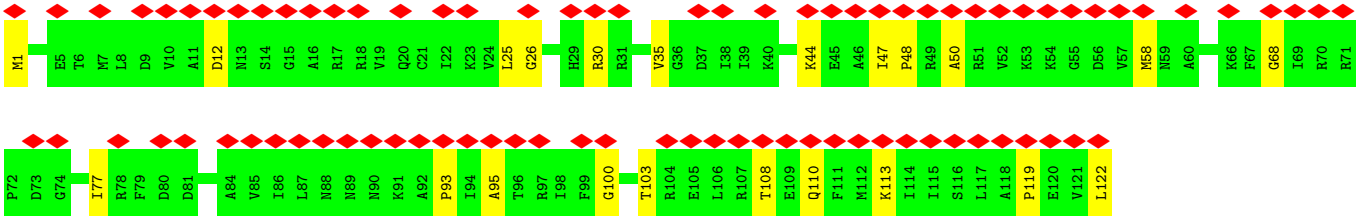




• Molecule 37: Large ribosomal subunit protein uL14

Chain j:

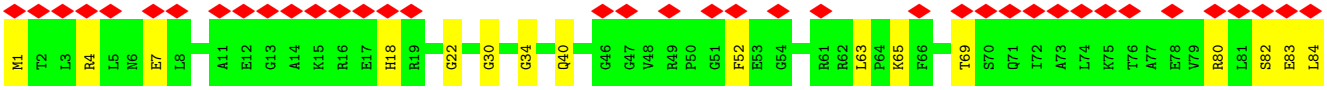


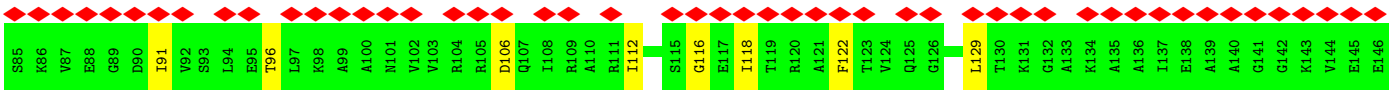


• Molecule 38: Large ribosomal subunit protein uL15

Chain k:



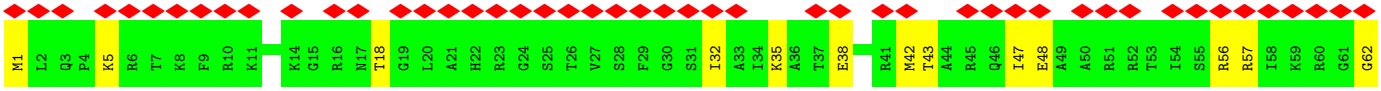


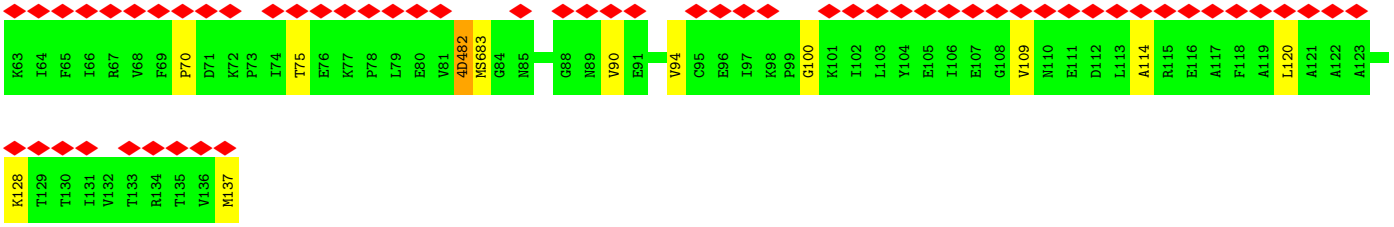


• Molecule 39: Large ribosomal subunit protein uL16

Chain l:



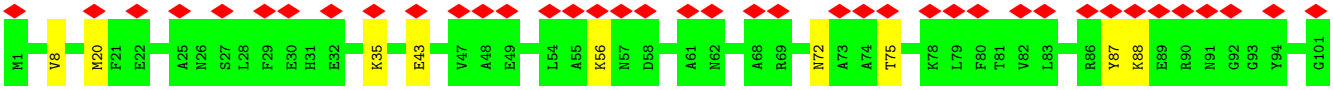




• Molecule 40: Large ribosomal subunit protein bL17

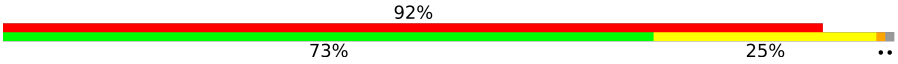
Chain m:

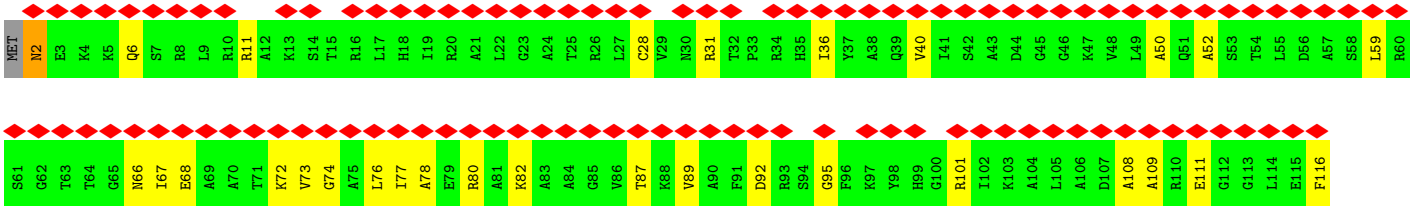




• Molecule 41: Large ribosomal subunit protein uL18

Chain n:

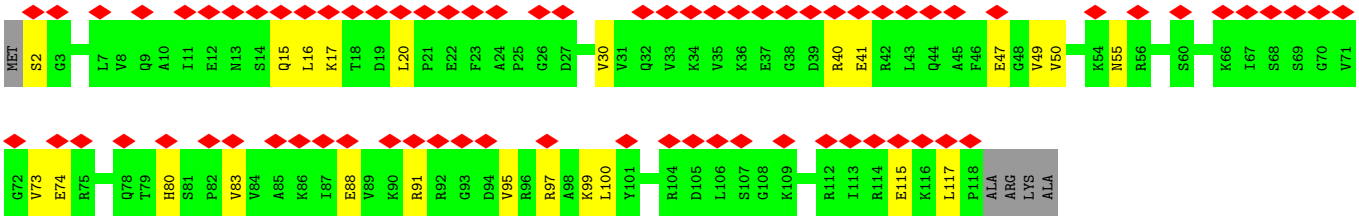




• Molecule 42: Large ribosomal subunit protein bL19

Chain o:

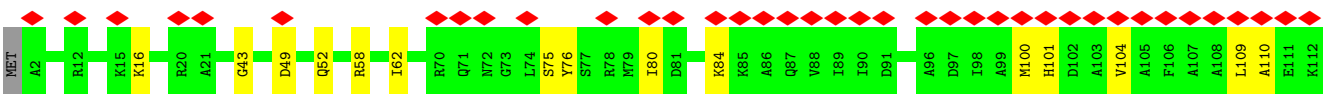


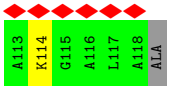


• Molecule 43: Large ribosomal subunit protein bL20

Chain p:



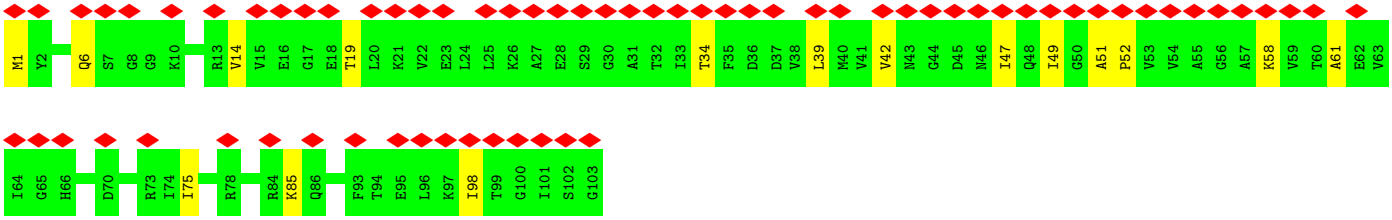




• Molecule 44: Large ribosomal subunit protein bL21

Chain q:

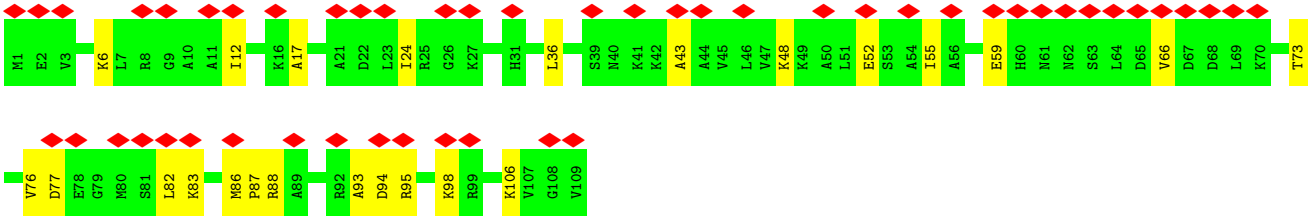




• Molecule 45: Large ribosomal subunit protein uL22

Chain r:

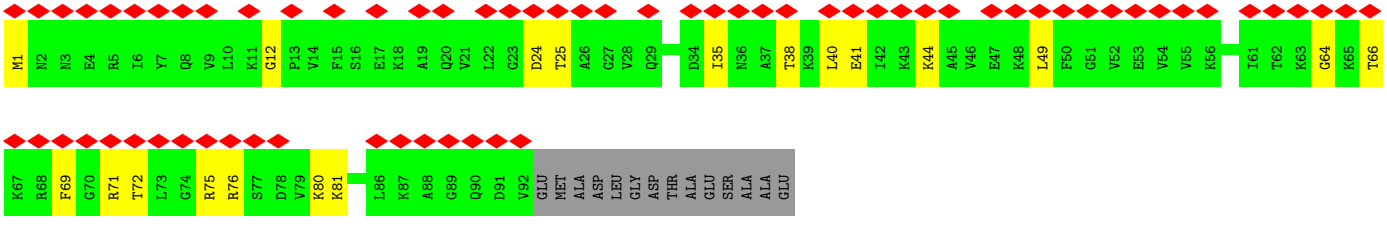




• Molecule 46: Large ribosomal subunit protein uL23

Chain s:

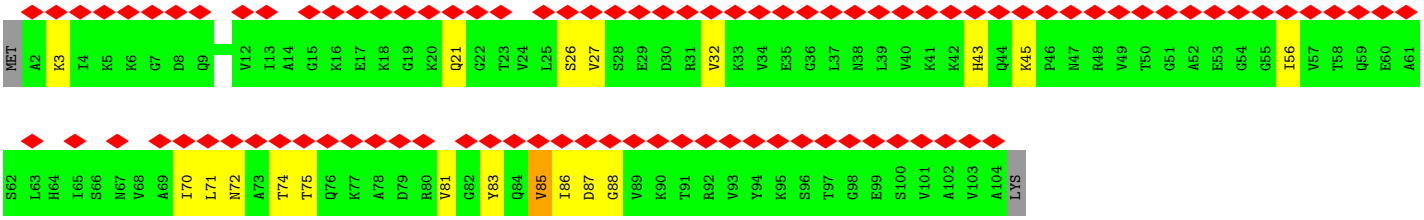




• Molecule 47: Large ribosomal subunit protein uL24

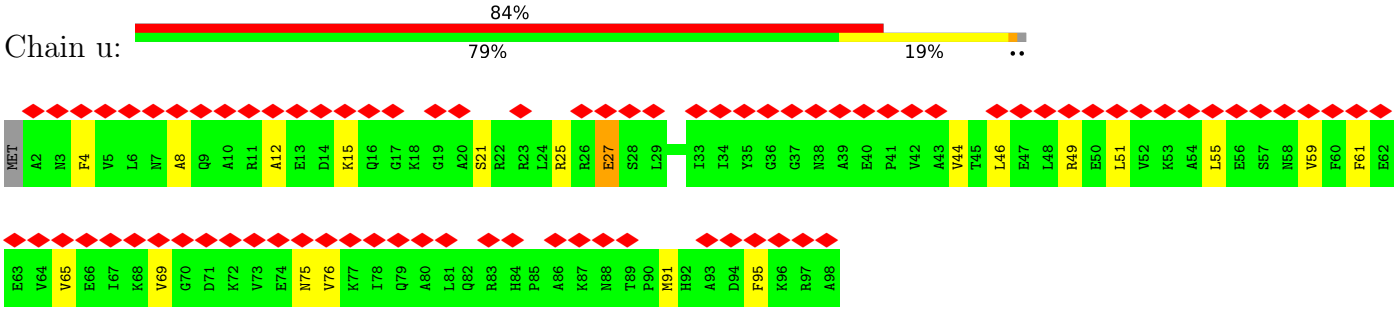
Chain t:





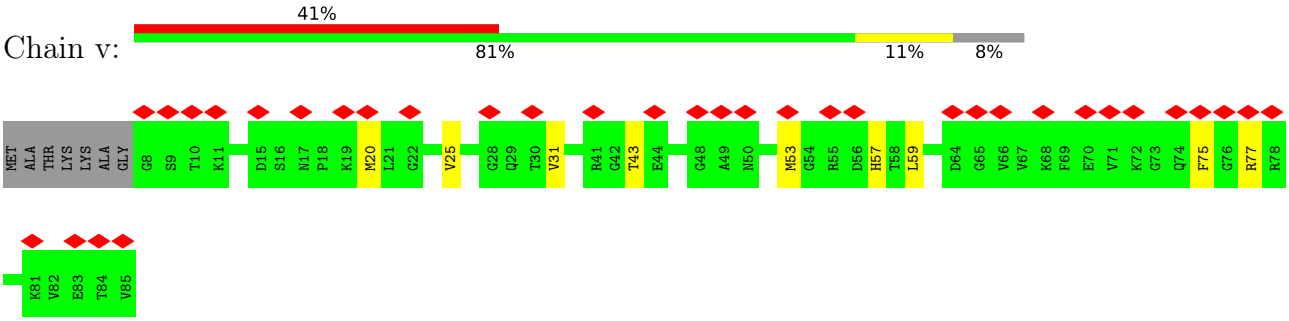
• Molecule 48: Large ribosomal subunit protein bL25

Chain u:



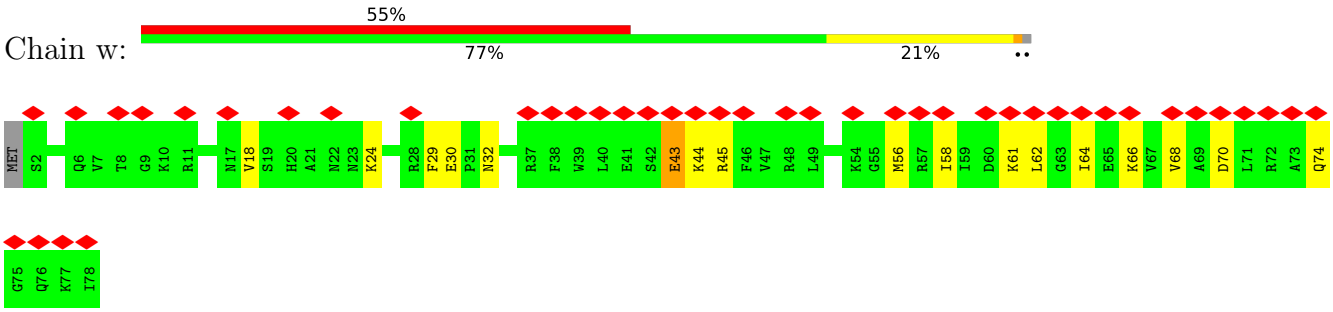
• Molecule 49: Large ribosomal subunit protein bL27

Chain v:



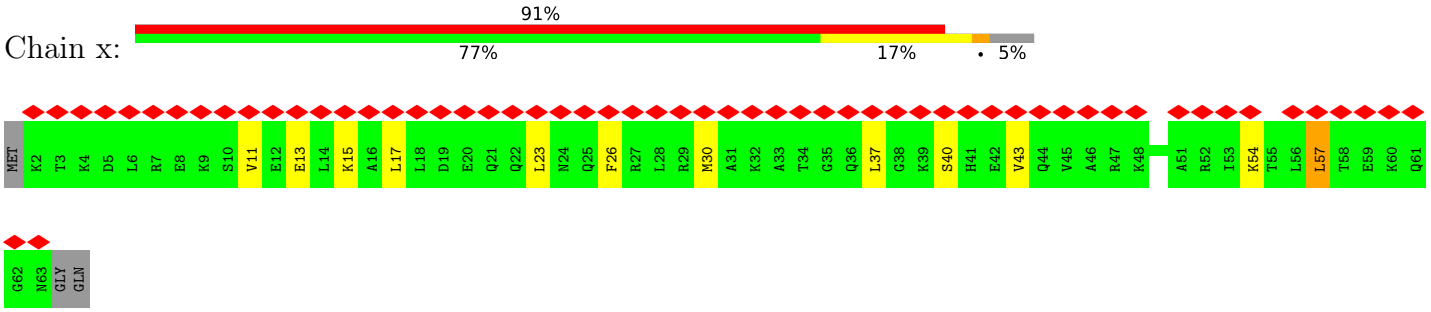
• Molecule 50: Large ribosomal subunit protein bL28

Chain w:



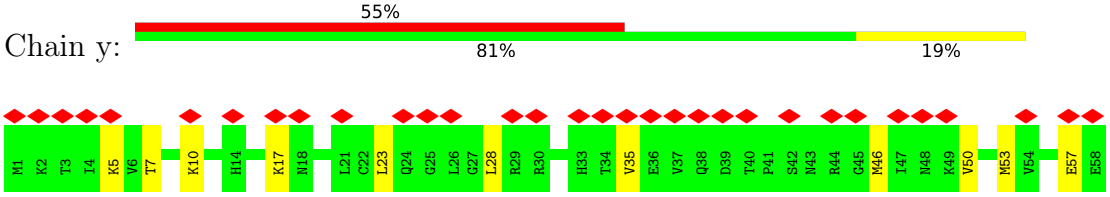
• Molecule 51: Large ribosomal subunit protein uL29

Chain x:

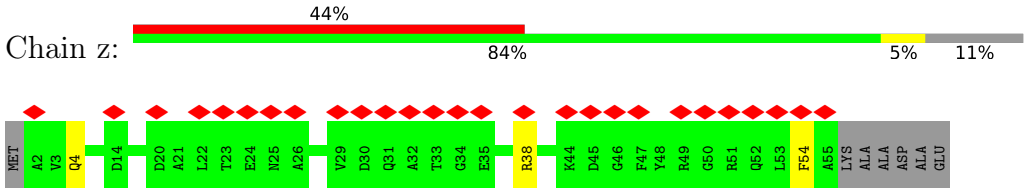


• Molecule 52: Large ribosomal subunit protein uL30

Chain y:



• Molecule 53: Large ribosomal subunit protein bL32



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	17801	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	1.623	Depositor
Minimum map value	-0.590	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.061	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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MA6, OMU, K, IAS, MEQ, ZN, H2U, OMC, 4OC, D2T, PSU, 5MC, MS6, MG, OMG, 6MZ, 3TD, UR3, 4D4, 1MG, G7M, 2MA, 2MG, 5MU

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	0.17	0/434	0.37	0/573
2	1	0.14	0/367	0.35	0/481
3	2	0.15	0/515	0.33	0/678
4	3	0.17	0/296	0.31	0/389
5	4	0.16	0/561	0.47	0/750
6	A	0.30	0/36452	0.76	6/56856 (0.0%)
7	B	0.15	0/1832	0.35	0/2474
8	C	0.14	0/1714	0.31	0/2304
9	D	0.14	0/1653	0.31	0/2213
10	E	0.17	0/1141	0.37	0/1537
11	F	0.15	0/893	0.36	0/1204
12	G	0.15	0/1229	0.36	0/1647
13	H	0.15	0/993	0.32	0/1331
14	I	0.16	0/1006	0.38	0/1346
15	J	0.18	0/811	0.48	0/1096
16	K	0.16	0/869	0.37	0/1175
17	L	0.16	0/949	0.42	0/1270
18	M	0.17	0/922	0.44	0/1237
19	N	0.15	0/803	0.35	0/1071
20	O	0.15	0/715	0.30	0/958
21	P	0.14	0/655	0.33	0/879
22	Q	0.13	0/628	0.37	0/847
23	R	0.16	0/555	0.33	0/749
24	S	0.14	0/675	0.34	0/912
25	T	0.19	0/669	0.31	0/892
26	U	0.17	0/592	0.41	0/784
27	X	0.17	0/858	0.39	0/1150
28	a	0.33	0/68962	0.77	25/107563 (0.0%)
29	b	0.28	0/2739	0.75	0/4266
30	c	0.14	0/2152	0.31	0/2891
31	d	0.16	0/1580	0.31	0/2127

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	e	0.15	0/1532	0.31	0/2068
33	f	0.20	0/1415	0.46	0/1895
34	g	0.14	0/1346	0.32	0/1818
35	h	0.12	0/461	0.37	0/616
36	i	0.16	0/1151	0.35	0/1551
37	j	0.15	0/956	0.33	0/1286
38	k	0.13	0/1097	0.29	0/1461
39	l	0.15	0/1084	0.32	0/1448
40	m	0.14	0/956	0.30	0/1282
41	n	0.15	0/873	0.35	0/1167
42	o	0.15	0/931	0.33	0/1249
43	p	0.18	0/947	0.36	0/1262
44	q	0.15	0/818	0.37	0/1094
45	r	0.16	0/831	0.36	0/1113
46	s	0.15	0/723	0.37	0/967
47	t	0.14	0/770	0.35	0/1034
48	u	0.15	0/770	0.41	1/1036 (0.1%)
49	v	0.14	0/597	0.26	0/798
50	w	0.15	0/642	0.33	0/856
51	x	0.14	0/499	0.39	0/662
52	y	0.16	0/468	0.34	0/624
53	z	0.16	0/453	0.35	0/604
All	All	0.28	0/153540	0.68	32/229541 (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
39	l	0	1

There are no bond length outliers.

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	a	1301	U	C2-N1-C1'	7.35	126.52	117.70
6	A	415	C	N3-C2-O2	-6.96	117.03	121.90
28	a	781	U	C2-N1-C1'	6.43	125.41	117.70
28	a	875	U	N3-C2-O2	-6.33	117.77	122.20
28	a	2105	G	O5'-C5'-C4'	6.31	114.45	109.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
39	l	82	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	427	0	462	8	0
2	1	363	0	401	7	0
3	2	509	0	566	16	0
4	3	295	0	326	5	0
5	4	552	0	552	21	0
6	A	32785	0	16503	433	0
7	B	1801	0	1814	34	0
8	C	1690	0	1774	27	0
9	D	1631	0	1691	42	0
10	E	1129	0	1172	17	0
11	F	878	0	878	16	0
12	G	1210	0	1255	28	0
13	H	985	0	1047	16	0
14	I	995	0	1053	20	0
15	J	801	0	832	34	0
16	K	862	0	872	20	0
17	L	947	0	997	18	0
18	M	912	0	975	21	0
19	N	792	0	833	22	0
20	O	705	0	712	13	0
21	P	644	0	655	17	0
22	Q	621	0	665	6	0
23	R	545	0	556	10	0
24	S	657	0	675	24	0
25	T	663	0	714	8	0
26	U	585	0	634	13	0
27	X	841	0	824	14	0
28	a	61984	0	31153	729	0
29	b	2450	0	1241	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	c	2111	0	2175	35	0
31	d	1573	0	1611	22	0
32	e	1511	0	1566	24	0
33	f	1395	0	1451	69	0
34	g	1327	0	1386	29	0
35	h	458	0	480	7	0
36	i	1125	0	1148	21	0
37	j	946	0	1007	13	0
38	k	1089	0	1158	16	0
39	l	1088	0	1150	15	0
40	m	942	0	987	8	0
41	n	865	0	905	22	0
42	o	919	0	973	17	0
43	p	934	0	997	12	0
44	q	807	0	842	11	0
45	r	826	0	894	16	0
46	s	717	0	777	12	0
47	t	766	0	816	13	0
48	u	760	0	783	11	0
49	v	589	0	592	5	0
50	w	632	0	667	12	0
51	x	498	0	537	8	0
52	y	463	0	488	5	0
53	z	447	0	435	3	0
54	1	2	0	0	0	0
54	A	45	0	0	0	0
54	E	1	0	0	0	0
54	L	1	0	0	0	0
54	M	1	0	0	0	0
54	a	111	0	0	0	0
54	b	1	0	0	0	0
54	c	4	0	0	0	0
54	d	2	0	0	0	0
54	t	1	0	0	0	0
55	3	1	0	0	0	0
55	4	1	0	0	0	0
56	A	96	0	0	0	0
56	J	1	0	0	0	0
56	X	1	0	0	0	0
56	a	249	0	0	0	0
56	b	5	0	0	0	0
56	c	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	d	1	0	0	0	0
56	k	1	0	0	0	0
56	p	2	0	0	0	0
56	v	1	0	0	0	0
56	z	1	0	0	0	0
All	All	142578	0	95657	1925	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 1925 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)
28:a:872:G:H1	28:a:886:U:H3	1.07	1.00
45:r:83:LYS:HB3	45:r:95:ARG:HH22	1.34	0.93
5:4:38:CYS:SG	5:4:41:CYS:HB3	2.08	0.91
6:A:639:A:H2'	6:A:640:C:H6	1.41	0.85
15:J:57:VAL:HG12	15:J:58:ASN:H	1.41	0.84

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	49/51 (96%)	48 (98%)	1 (2%)	0	100	100
2	1	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
3	2	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
4	3	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
5	4	69/74 (93%)	58 (84%)	10 (14%)	1 (1%)	9	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
7	B	227/250 (91%)	211 (93%)	15 (7%)	1 (0%)	30 59
8	C	213/250 (85%)	207 (97%)	6 (3%)	0	100 100
9	D	205/208 (99%)	199 (97%)	6 (3%)	0	100 100
10	E	153/165 (93%)	150 (98%)	3 (2%)	0	100 100
11	F	104/127 (82%)	100 (96%)	4 (4%)	0	100 100
12	G	151/156 (97%)	143 (95%)	8 (5%)	0	100 100
13	H	128/131 (98%)	124 (97%)	4 (3%)	0	100 100
14	I	125/128 (98%)	118 (94%)	7 (6%)	0	100 100
15	J	98/103 (95%)	94 (96%)	4 (4%)	0	100 100
16	K	113/128 (88%)	107 (95%)	6 (5%)	0	100 100
17	L	119/124 (96%)	114 (96%)	5 (4%)	0	100 100
18	M	114/118 (97%)	109 (96%)	5 (4%)	0	100 100
19	N	98/101 (97%)	93 (95%)	5 (5%)	0	100 100
20	O	86/89 (97%)	84 (98%)	2 (2%)	0	100 100
21	P	80/83 (96%)	79 (99%)	1 (1%)	0	100 100
22	Q	77/85 (91%)	75 (97%)	2 (3%)	0	100 100
23	R	64/75 (85%)	62 (97%)	2 (3%)	0	100 100
24	S	82/91 (90%)	82 (100%)	0	0	100 100
25	T	84/88 (96%)	84 (100%)	0	0	100 100
26	U	68/71 (96%)	66 (97%)	1 (2%)	1 (2%)	8 28
27	X	102/116 (88%)	100 (98%)	2 (2%)	0	100 100
30	c	270/274 (98%)	260 (96%)	10 (4%)	0	100 100
31	d	208/212 (98%)	202 (97%)	5 (2%)	1 (0%)	24 54
32	e	197/200 (98%)	194 (98%)	3 (2%)	0	100 100
33	f	175/178 (98%)	158 (90%)	15 (9%)	2 (1%)	11 36
34	g	173/177 (98%)	164 (95%)	8 (5%)	1 (1%)	21 51
35	h	58/148 (39%)	51 (88%)	7 (12%)	0	100 100
36	i	140/142 (99%)	138 (99%)	2 (1%)	0	100 100
37	j	120/122 (98%)	115 (96%)	5 (4%)	0	100 100
38	k	144/146 (99%)	139 (96%)	5 (4%)	0	100 100
39	l	133/137 (97%)	132 (99%)	1 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	m	117/125 (94%)	115 (98%)	2 (2%)	0	100	100
41	n	113/116 (97%)	109 (96%)	4 (4%)	0	100	100
42	o	115/122 (94%)	113 (98%)	2 (2%)	0	100	100
43	p	115/119 (97%)	115 (100%)	0	0	100	100
44	q	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
45	r	107/109 (98%)	105 (98%)	2 (2%)	0	100	100
46	s	90/106 (85%)	88 (98%)	2 (2%)	0	100	100
47	t	101/105 (96%)	93 (92%)	8 (8%)	0	100	100
48	u	95/98 (97%)	90 (95%)	5 (5%)	0	100	100
49	v	76/85 (89%)	72 (95%)	4 (5%)	0	100	100
50	w	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
51	x	60/65 (92%)	59 (98%)	1 (2%)	0	100	100
52	y	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
53	z	52/61 (85%)	50 (96%)	2 (4%)	0	100	100
All	All	5639/6044 (93%)	5427 (96%)	205 (4%)	7 (0%)	49	77

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	4	53	ASP
31	d	152	ASN
7	B	128	PHE
33	f	139	PRO
33	f	137	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	
1	0	47/47 (100%)	47 (100%)	0	100	100
2	1	36/36 (100%)	36 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	2	52/53 (98%)	52 (100%)	0	100	100
4	3	33/33 (100%)	33 (100%)	0	100	100
5	4	60/63 (95%)	58 (97%)	2 (3%)	33	67
7	B	188/200 (94%)	183 (97%)	5 (3%)	39	73
8	C	175/198 (88%)	173 (99%)	2 (1%)	65	88
9	D	170/171 (99%)	168 (99%)	2 (1%)	63	86
10	E	113/120 (94%)	113 (100%)	0	100	100
11	F	95/111 (86%)	89 (94%)	6 (6%)	16	45
12	G	125/128 (98%)	119 (95%)	6 (5%)	23	55
13	H	108/109 (99%)	105 (97%)	3 (3%)	38	72
14	I	99/100 (99%)	98 (99%)	1 (1%)	68	89
15	J	89/91 (98%)	86 (97%)	3 (3%)	32	66
16	K	87/97 (90%)	82 (94%)	5 (6%)	18	49
17	L	103/105 (98%)	95 (92%)	8 (8%)	11	35
18	M	96/98 (98%)	90 (94%)	6 (6%)	16	45
19	N	81/82 (99%)	81 (100%)	0	100	100
20	O	71/72 (99%)	69 (97%)	2 (3%)	38	72
21	P	63/63 (100%)	62 (98%)	1 (2%)	55	83
22	Q	71/76 (93%)	65 (92%)	6 (8%)	10	31
23	R	58/66 (88%)	57 (98%)	1 (2%)	53	82
24	S	71/78 (91%)	67 (94%)	4 (6%)	19	50
25	T	65/67 (97%)	62 (95%)	3 (5%)	24	57
26	U	61/62 (98%)	57 (93%)	4 (7%)	15	43
27	X	92/102 (90%)	91 (99%)	1 (1%)	65	88
30	c	218/220 (99%)	215 (99%)	3 (1%)	59	85
31	d	165/166 (99%)	160 (97%)	5 (3%)	36	70
32	e	155/155 (100%)	152 (98%)	3 (2%)	50	79
33	f	146/147 (99%)	139 (95%)	7 (5%)	23	55
34	g	140/142 (99%)	136 (97%)	4 (3%)	37	71
35	h	45/112 (40%)	44 (98%)	1 (2%)	45	77
36	i	118/118 (100%)	116 (98%)	2 (2%)	53	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
37	j	103/103 (100%)	102 (99%)	1 (1%)	68 89
38	k	108/108 (100%)	107 (99%)	1 (1%)	70 90
39	l	111/111 (100%)	111 (100%)	0	100 100
40	m	96/101 (95%)	96 (100%)	0	100 100
41	n	84/85 (99%)	81 (96%)	3 (4%)	31 65
42	o	99/102 (97%)	97 (98%)	2 (2%)	48 78
43	p	85/86 (99%)	82 (96%)	3 (4%)	32 66
44	q	84/84 (100%)	82 (98%)	2 (2%)	43 75
45	r	88/88 (100%)	87 (99%)	1 (1%)	65 88
46	s	78/87 (90%)	77 (99%)	1 (1%)	61 86
47	t	83/85 (98%)	80 (96%)	3 (4%)	31 65
48	u	79/80 (99%)	75 (95%)	4 (5%)	21 53
49	v	60/64 (94%)	59 (98%)	1 (2%)	53 82
50	w	69/70 (99%)	67 (97%)	2 (3%)	37 71
51	x	54/56 (96%)	51 (94%)	3 (6%)	19 50
52	y	54/54 (100%)	52 (96%)	2 (4%)	30 64
53	z	46/50 (92%)	46 (100%)	0	100 100
All	All	4677/4902 (95%)	4552 (97%)	125 (3%)	40 73

5 of 125 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	Q	78	GLU
47	t	26	SER
30	c	53	HIS
46	s	72	THR
50	w	30	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
30	c	128	ASN
42	o	32	GLN
33	f	135	GLN
36	i	47	HIS

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Mol	Chain	Res	Type
43	p	44	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	a	2889/2893 (99%)	525 (18%)	0
29	b	114/115 (99%)	14 (12%)	0
6	A	1527/1537 (99%)	278 (18%)	12 (0%)
All	All	4530/4545 (99%)	817 (18%)	12 (0%)

5 of 817 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	A	7	U
6	A	9	A
6	A	11	G
6	A	24	G
6	A	34	A

5 of 12 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	A	989	U
6	A	1123	U
6	A	1449	A
6	A	1179	G
6	A	492	A

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

34 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	$\#\|Z\|>2$
6	MA6	A	1516	6	23,26,27	1.18	3 (13%)	34,38,41	2.24	9 (26%)
28	PSU	a	945	28	18,21,22	1.99	7 (38%)	22,30,33	1.89	4 (18%)
28	G7M	a	2058	28	23,26,27	2.19	5 (21%)	35,39,42	1.79	7 (20%)
6	2MG	A	1204	54,6	23,26,27	2.57	4 (17%)	32,38,41	2.03	10 (31%)
6	4OC	A	1399	6	20,23,24	2.26	3 (15%)	26,32,35	0.95	2 (7%)
28	H2U	a	2438	28	18,21,22	4.24	5 (27%)	21,30,33	5.20	7 (33%)
6	PSU	A	513	6	18,21,22	1.97	7 (38%)	22,30,33	1.82	5 (22%)
28	6MZ	a	2019	28	22,25,26	2.38	3 (13%)	30,36,39	2.49	11 (36%)
39	4D4	l	82	39	9,11,12	0.83	0	8,13,15	1.63	2 (25%)
28	2MA	a	2492	28,56,54	22,25,26	1.32	1 (4%)	33,37,40	1.99	8 (24%)
28	PSU	a	2493	28,54	18,21,22	2.01	7 (38%)	22,30,33	1.87	4 (18%)
28	5MU	a	1928	28,54	19,22,23	2.48	7 (36%)	28,32,35	3.88	10 (35%)
28	PSU	a	2594	28	18,21,22	1.96	7 (38%)	22,30,33	1.77	4 (18%)
28	OMU	a	2541	28	19,22,23	2.57	7 (36%)	26,31,34	1.71	5 (19%)
28	2MG	a	2434	28	23,26,27	2.58	6 (26%)	32,38,41	1.99	9 (28%)
28	OMC	a	2487	28,56	19,22,23	1.75	3 (15%)	26,31,34	0.94	2 (7%)
28	PSU	a	737	28,56	18,21,22	1.98	7 (38%)	22,30,33	1.78	3 (13%)
28	PSU	a	2569	28	18,21,22	2.01	8 (44%)	22,30,33	1.95	5 (22%)
28	OMG	a	2240	28,54	23,26,27	2.35	6 (26%)	33,38,41	1.80	9 (27%)
6	UR3	A	1495	6	19,22,23	2.54	6 (31%)	26,32,35	1.30	2 (7%)
16	IAS	K	118	16	6,7,8	1.78	1 (16%)	6,8,10	2.57	1 (16%)
6	5MC	A	964	6	18,22,23	1.87	5 (27%)	26,32,35	1.30	2 (7%)
28	PSU	a	1900	28	18,21,22	1.95	7 (38%)	22,30,33	1.83	4 (18%)
28	3TD	a	1904	28	18,22,23	2.70	7 (38%)	22,32,35	1.79	3 (13%)
6	2MG	A	1513	6	23,26,27	2.58	5 (21%)	32,38,41	2.03	11 (34%)
17	D2T	L	89	17	7,9,10	1.23	1 (14%)	6,11,13	1.59	1 (16%)
28	1MG	a	736	28	22,26,27	2.53	5 (22%)	33,39,42	2.00	7 (21%)
28	PSU	a	1906	28	18,21,22	1.96	7 (38%)	22,30,33	1.85	4 (18%)
31	MEQ	d	153	31	8,9,10	0.85	0	5,10,12	0.83	0
6	2MG	A	963	6	23,26,27	2.57	4 (17%)	32,38,41	2.06	10 (31%)
6	MA6	A	1515	6	23,26,27	1.17	2 (8%)	34,38,41	2.21	9 (26%)
28	PSU	a	2446	28	18,21,22	2.00	7 (38%)	22,30,33	1.86	5 (22%)
39	MS6	l	83	39	5,7,8	0.50	0	2,7,9	1.69	1 (50%)
6	G7M	A	524	54,6	23,26,27	2.20	5 (21%)	35,39,42	1.80	7 (20%)

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
6	MA6	A	1516	6	-	1/11/29/30	0/3/3/3
28	PSU	a	945	28	-	0/7/25/26	0/2/2/2
28	G7M	a	2058	28	-	1/7/25/26	0/3/3/3
6	2MG	A	1204	54,6	-	2/9/27/28	0/3/3/3
6	4OC	A	1399	6	-	0/9/29/30	0/2/2/2
28	H2U	a	2438	28	-	2/7/38/39	0/2/2/2
6	PSU	A	513	6	-	0/7/25/26	0/2/2/2
28	6MZ	a	2019	28	-	2/9/27/28	0/3/3/3
39	4D4	l	82	39	-	2/11/12/14	-
28	2MA	a	2492	28,56,54	-	2/7/25/26	0/3/3/3
28	PSU	a	2493	28,54	-	1/7/25/26	0/2/2/2
28	5MU	a	1928	28,54	-	0/7/25/26	0/2/2/2
28	PSU	a	2594	28	-	0/7/25/26	0/2/2/2
28	OMU	a	2541	28	-	2/9/27/28	0/2/2/2
28	2MG	a	2434	28	-	0/9/27/28	0/3/3/3
28	OMC	a	2487	28,56	-	1/9/27/28	0/2/2/2
28	PSU	a	737	28,56	-	2/7/25/26	0/2/2/2
28	PSU	a	2569	28	-	0/7/25/26	0/2/2/2
28	OMG	a	2240	28,54	-	1/9/27/28	0/3/3/3
6	UR3	A	1495	6	-	0/7/25/26	0/2/2/2
16	IAS	K	118	16	-	4/7/7/8	-
6	5MC	A	964	6	-	0/7/25/26	0/2/2/2
28	PSU	a	1900	28	-	0/7/25/26	0/2/2/2
28	3TD	a	1904	28	-	0/7/25/26	0/2/2/2
6	2MG	A	1513	6	-	0/9/27/28	0/3/3/3
17	D2T	L	89	17	-	3/7/12/14	-
28	1MG	a	736	28	-	0/7/25/26	0/3/3/3
28	PSU	a	1906	28	-	0/7/25/26	0/2/2/2
31	MEQ	d	153	31	-	3/8/9/11	-
6	2MG	A	963	6	-	0/9/27/28	0/3/3/3
6	MA6	A	1515	6	-	0/11/29/30	0/3/3/3
28	PSU	a	2446	28	-	0/7/25/26	0/2/2/2
39	MS6	l	83	39	-	3/4/6/8	-
6	G7M	A	524	54,6	-	3/7/25/26	0/3/3/3

The worst 5 of 158 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	a	2019	6MZ	C6-N6	10.10	1.45	1.34
28	a	2438	H2U	O4-C4	10.07	1.43	1.23
6	A	1513	2MG	O6-C6	9.17	1.41	1.23
6	A	963	2MG	O6-C6	9.16	1.41	1.23
6	A	1204	2MG	O6-C6	9.16	1.41	1.23

The worst 5 of 183 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	a	2438	H2U	C4-N3-C2	-16.44	112.15	125.79
28	a	2438	H2U	O2-C2-N1	-10.79	109.56	123.11
28	a	1928	5MU	C4-N3-C2	-8.85	115.89	127.35
28	a	1928	5MU	N3-C2-N1	8.56	126.25	114.89
28	a	1928	5MU	C5M-C5-C4	8.21	127.80	118.77

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1204	2MG	N1-C2-N2-CM2
6	A	1204	2MG	N3-C2-N2-CM2
16	K	118	IAS	N-CA-CB-CG
28	a	737	PSU	C2'-C1'-C5-C6
28	a	737	PSU	O4'-C1'-C5-C6

There are no ring outliers.

12 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1516	MA6	1	0
6	A	1399	4OC	4	0
6	A	513	PSU	1	0
28	a	2019	6MZ	2	0
28	a	2594	PSU	1	0
28	a	2541	OMU	1	0
28	a	2240	OMG	1	0
6	A	1513	2MG	2	0
28	a	1906	PSU	1	0
31	d	153	MEQ	2	0
6	A	963	2MG	1	0
6	A	1515	MA6	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 531 ligands modelled in this entry, 531 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.

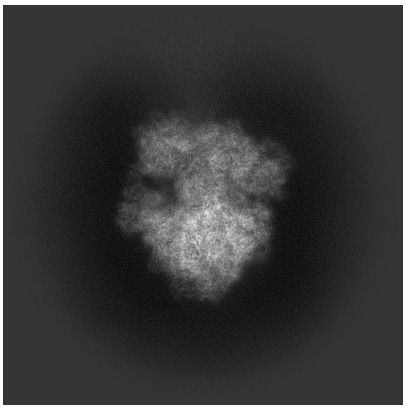
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-55742. These allow visual inspection of the internal detail of the map and identification of artifacts.

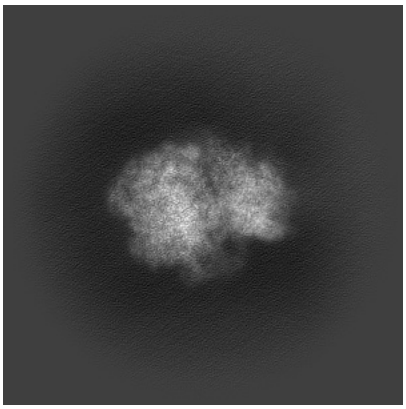
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

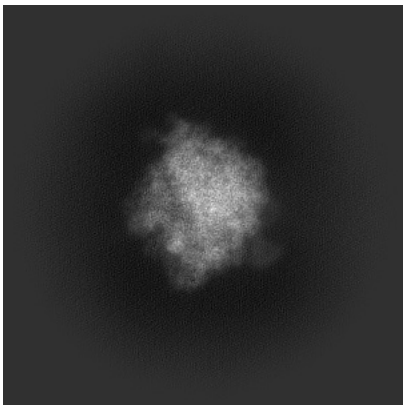
6.1.1 Primary map



X

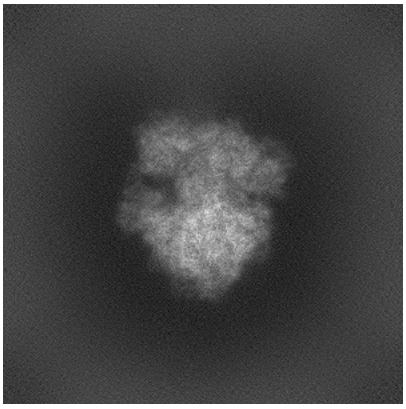


Y

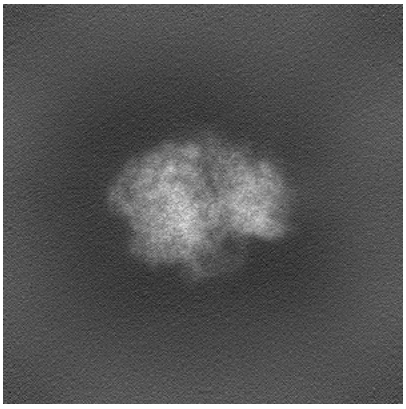


Z

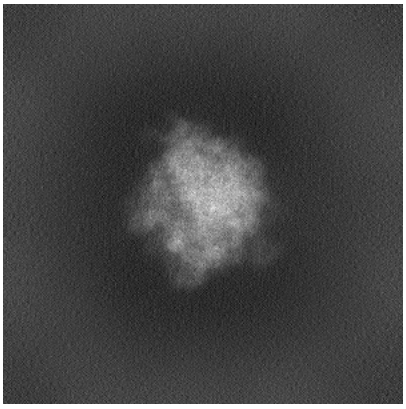
6.1.2 Raw map



X



Y

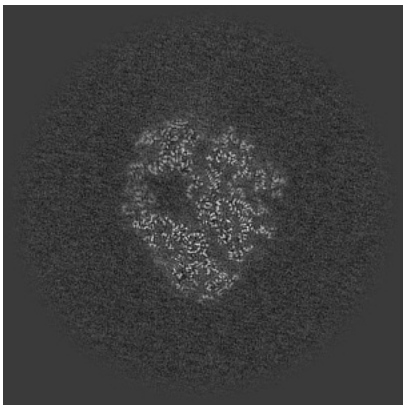


Z

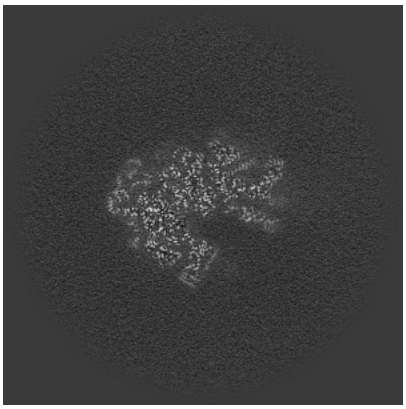
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

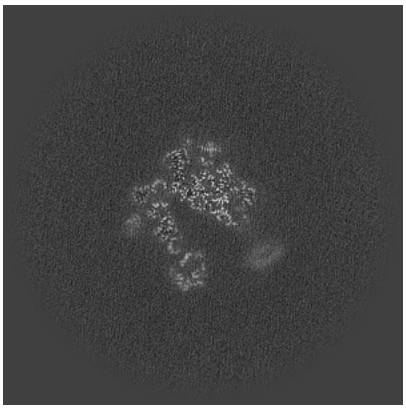
6.2.1 Primary map



X Index: 256

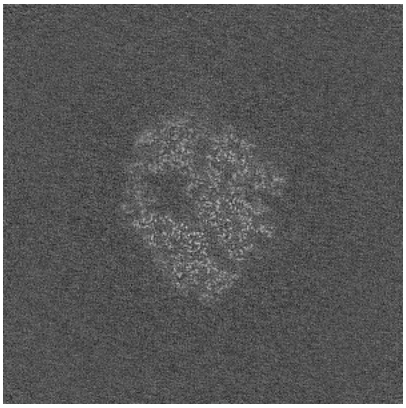


Y Index: 256

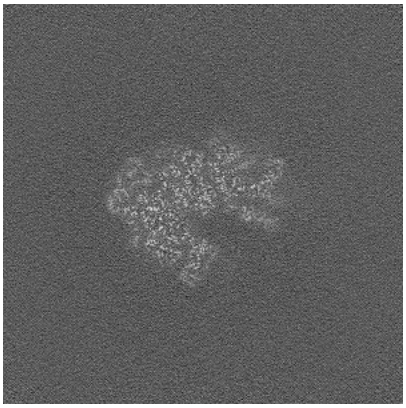


Z Index: 256

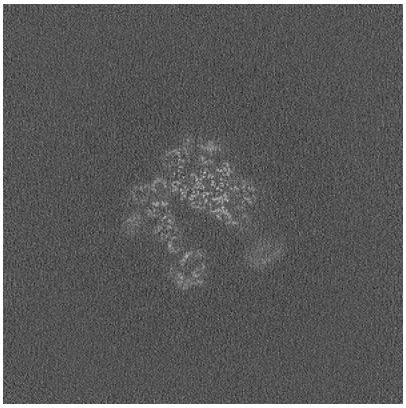
6.2.2 Raw map



X Index: 256



Y Index: 256

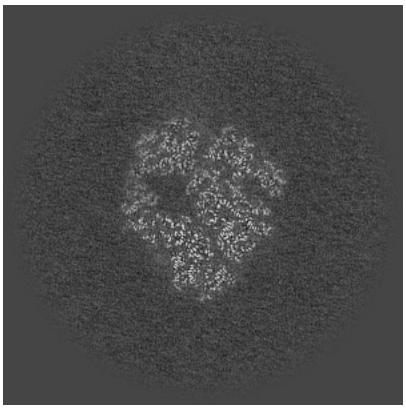


Z Index: 256

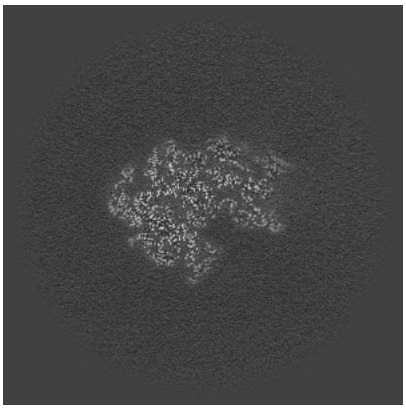
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

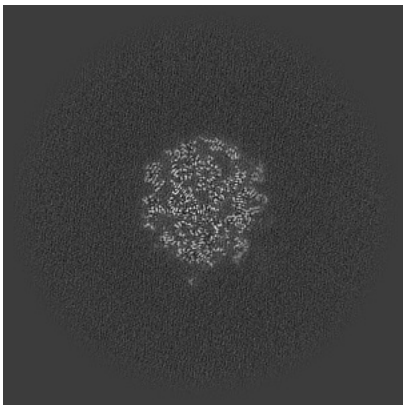
6.3.1 Primary map



X Index: 253

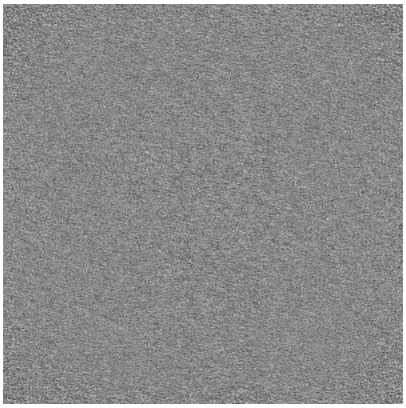


Y Index: 263

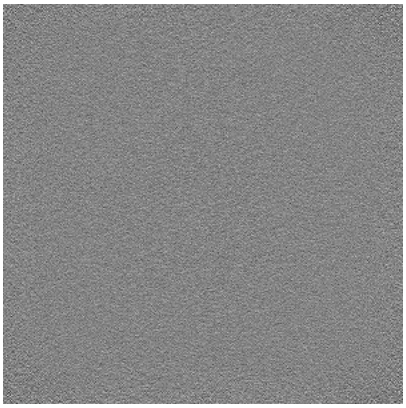


Z Index: 216

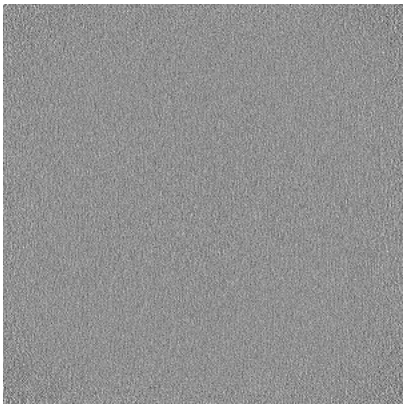
6.3.2 Raw map



X Index: 0



Y Index: 0

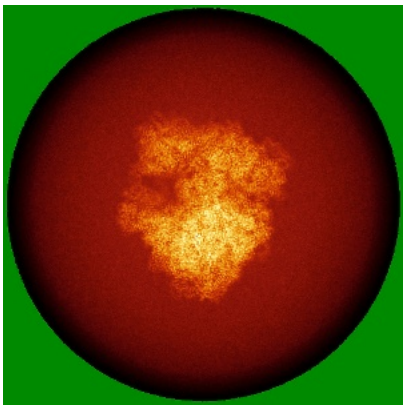


Z Index: 0

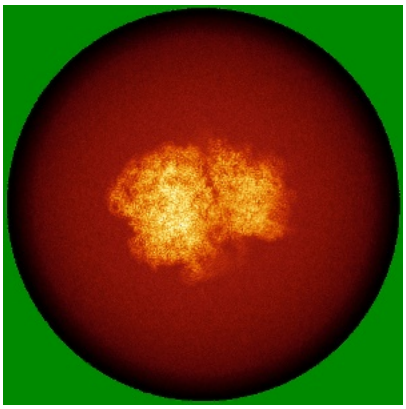
The images above show the largest variance slices of the map in three orthogonal directions.

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

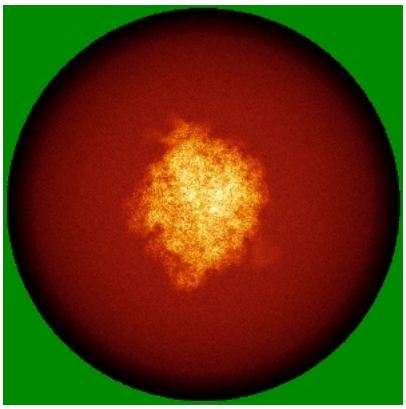
6.4.1 Primary map



X

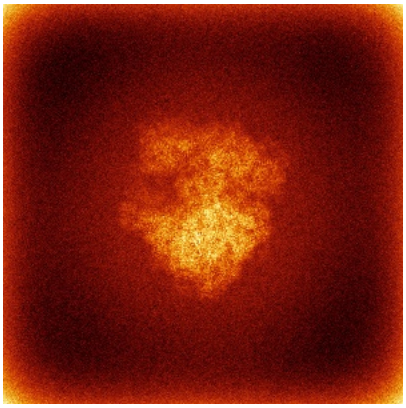


Y

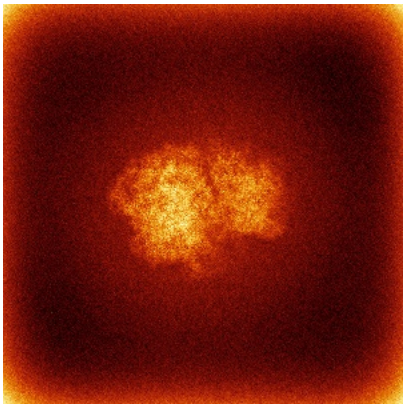


Z

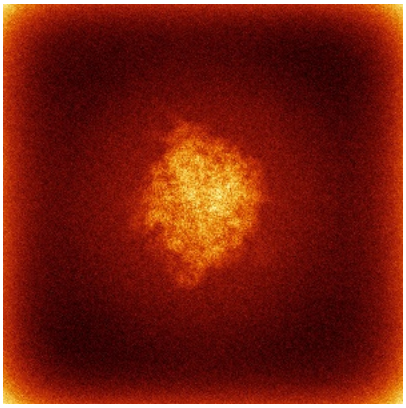
6.4.2 Raw map



X



Y

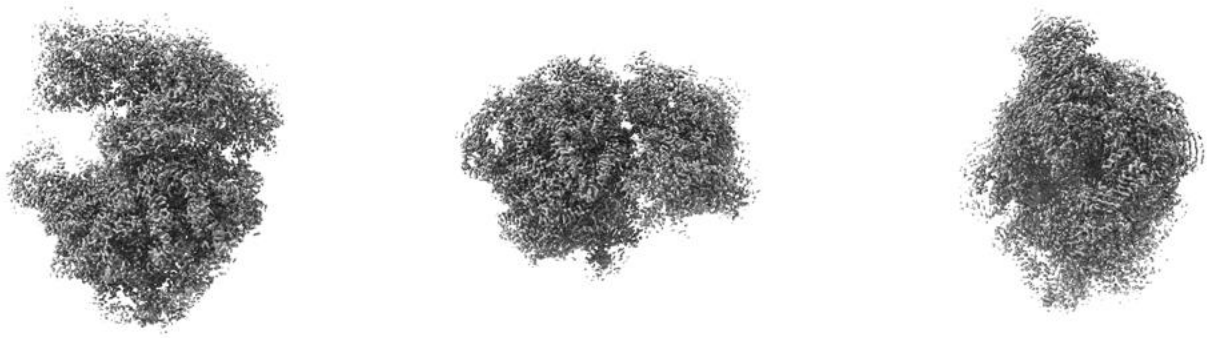


Z

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)

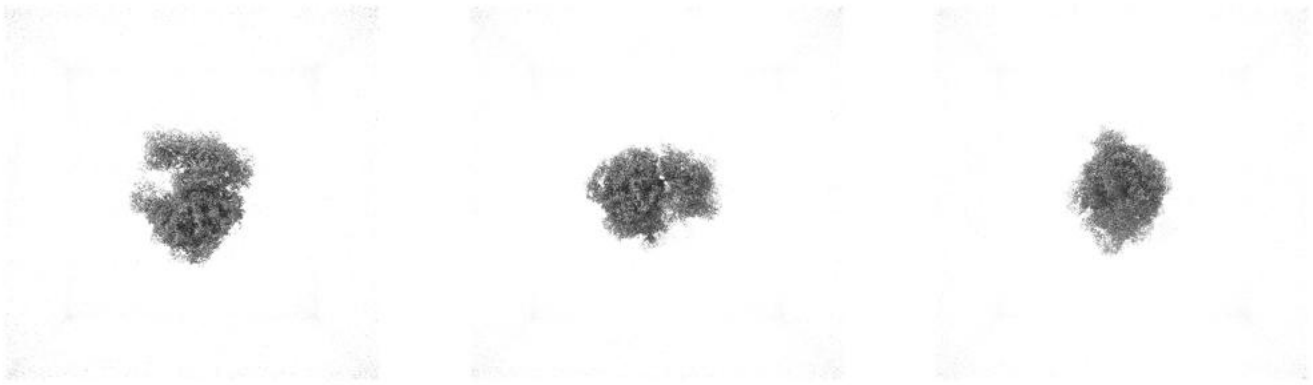
6.5.1 Primary map



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.

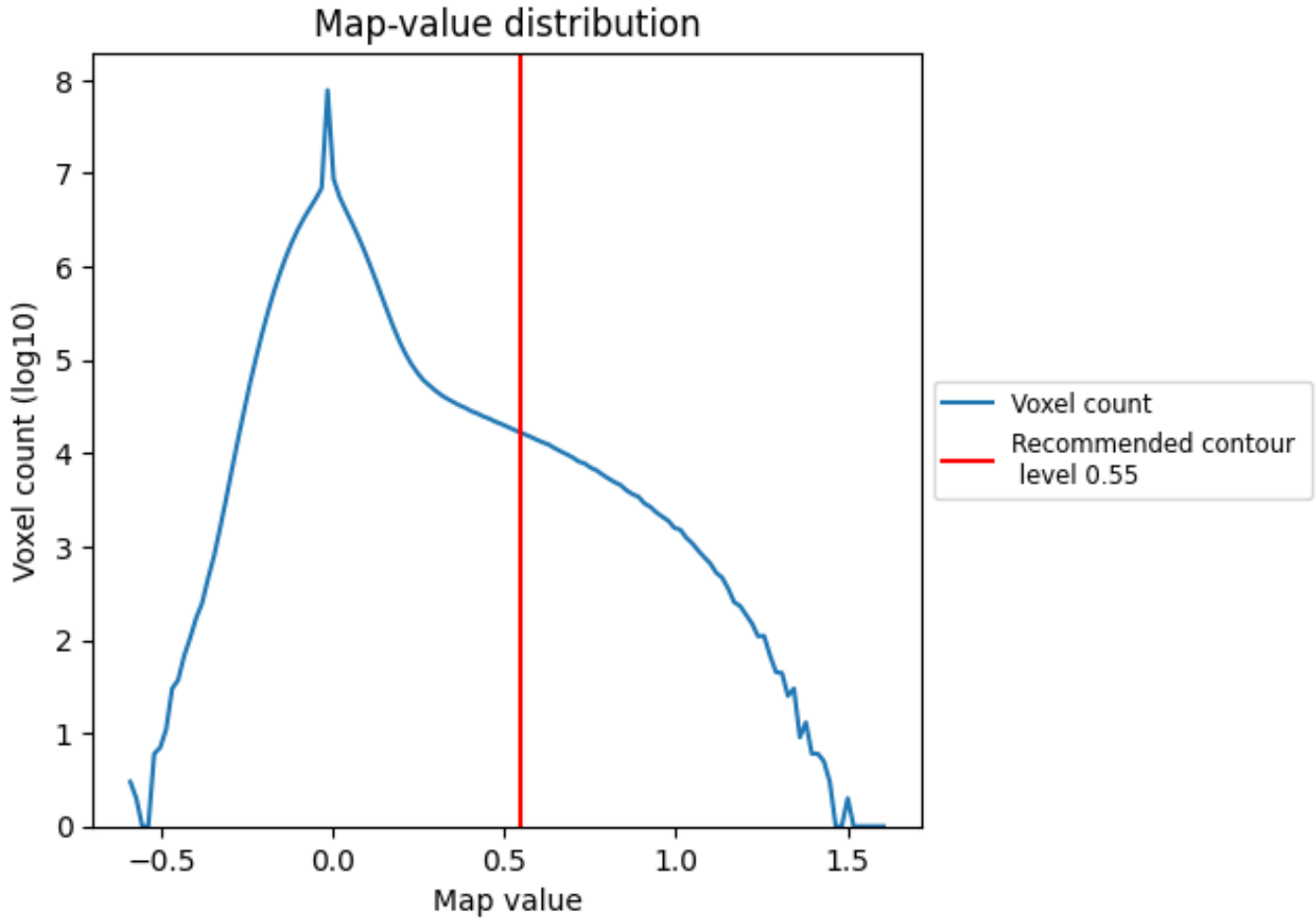
6.6 Mask visualisation (i)

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

7 Map analysis

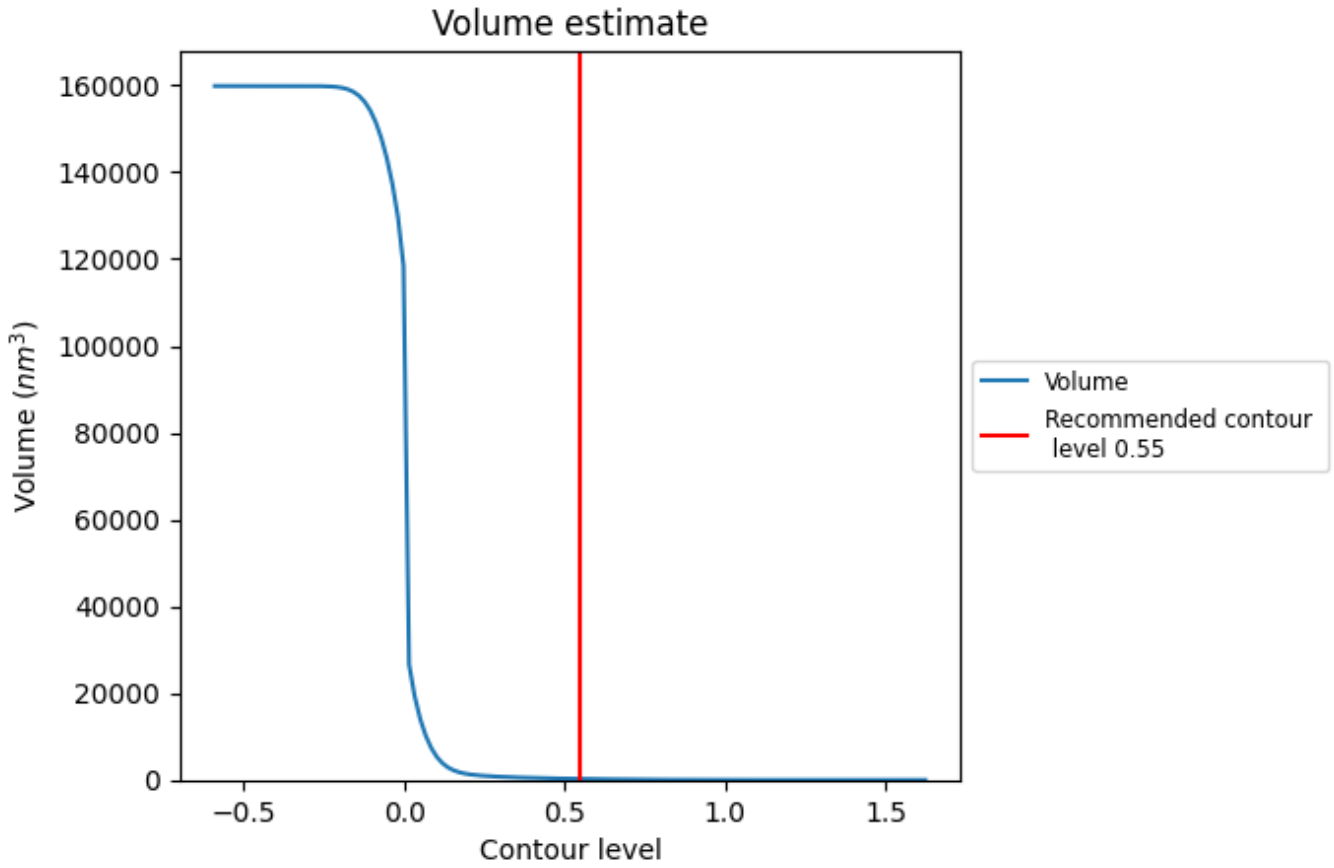
This section contains the results of statistical analysis of the map.

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.

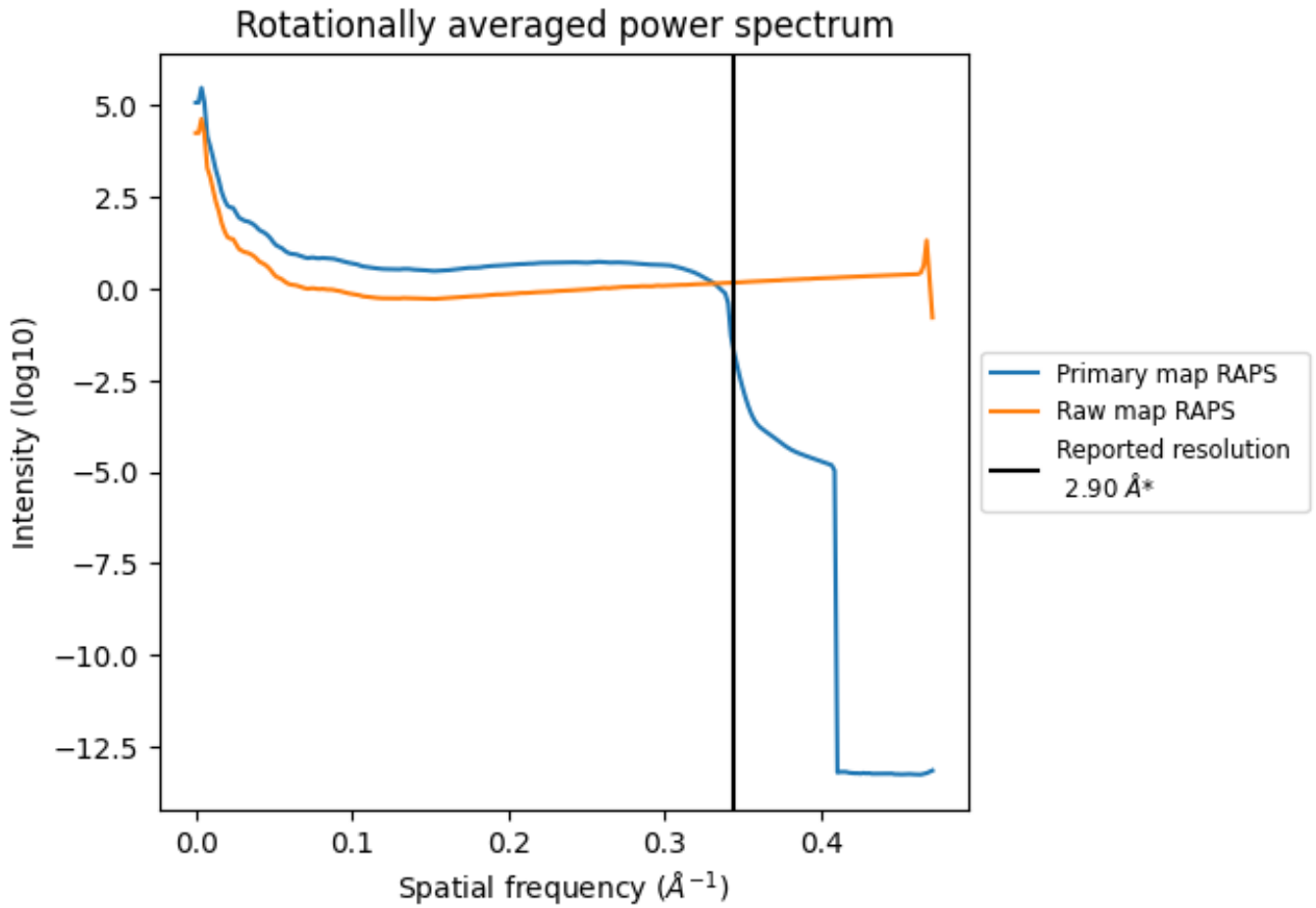
7.2 Volume estimate (i)



The volume at the recommended contour level is 242 nm^3; this corresponds to an approximate mass of 219 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)

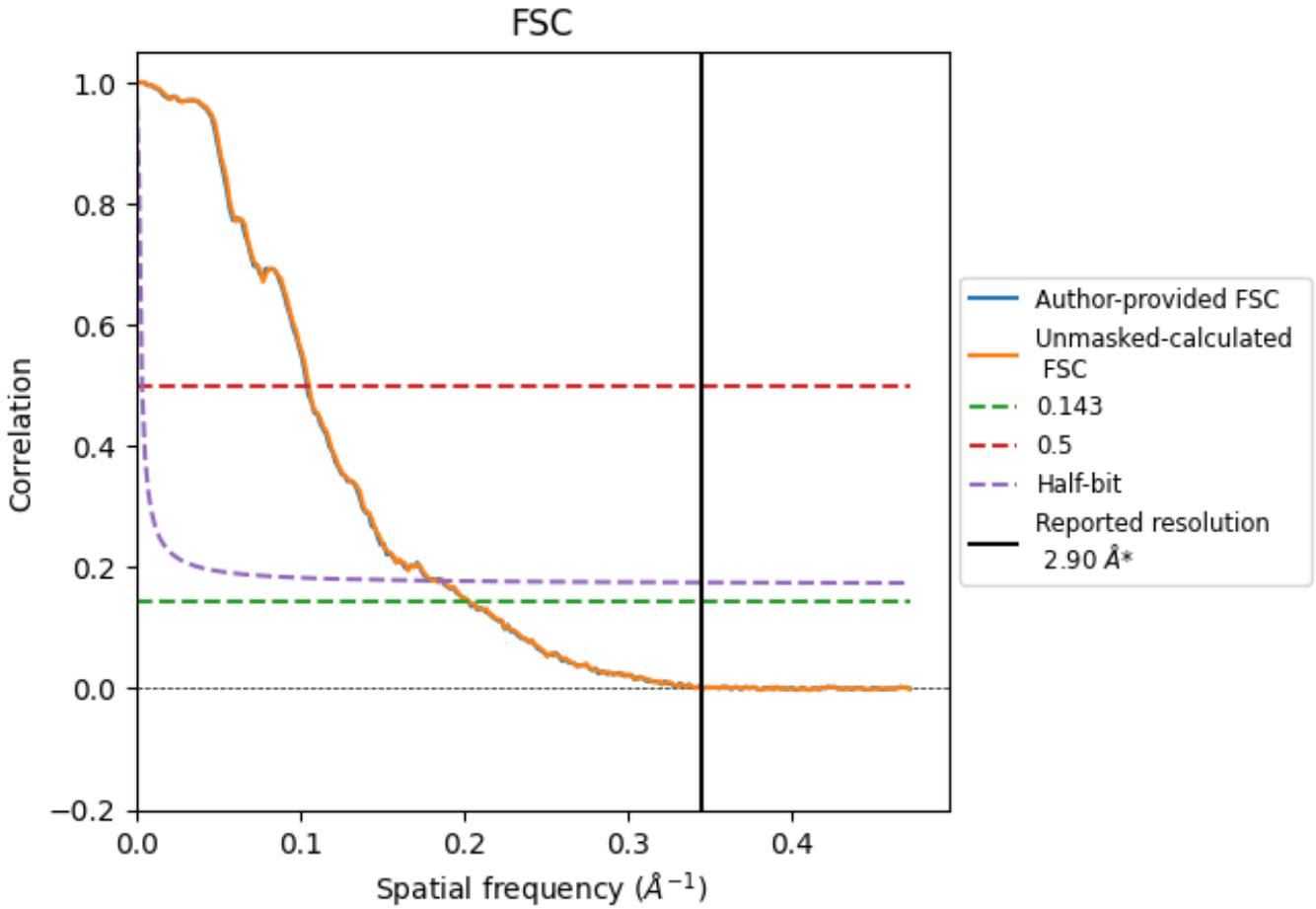


*Reported resolution corresponds to spatial frequency of 0.345 $Å^{-1}$

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 0.345 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	4.93	9.60	5.36
Unmasked-calculated*	4.92	9.50	5.55

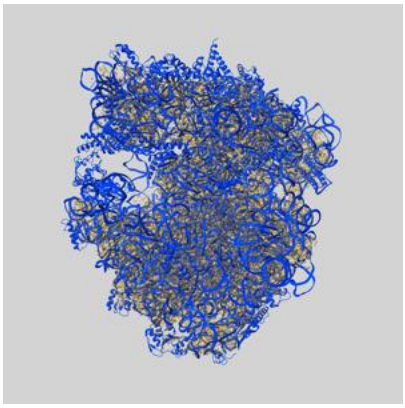
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.93 differs from the reported value 2.9 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.92 differs from the reported value 2.9 by more than 10 %

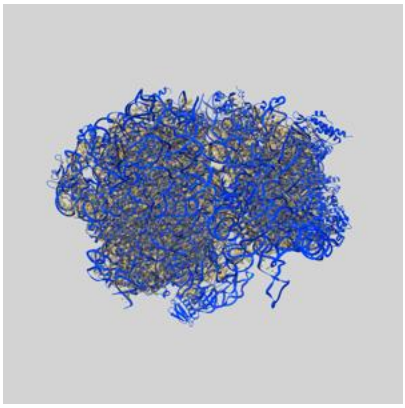
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-55742 and PDB model 9TA1. Per-residue inclusion information can be found in section 3 on page 15.

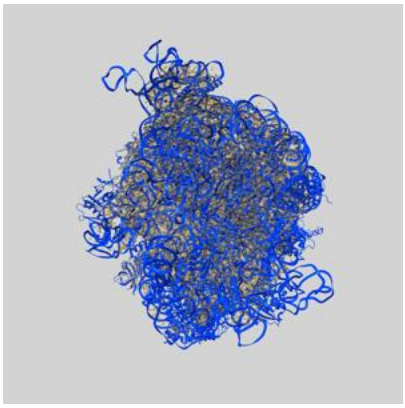
9.1 Map-model overlay



X



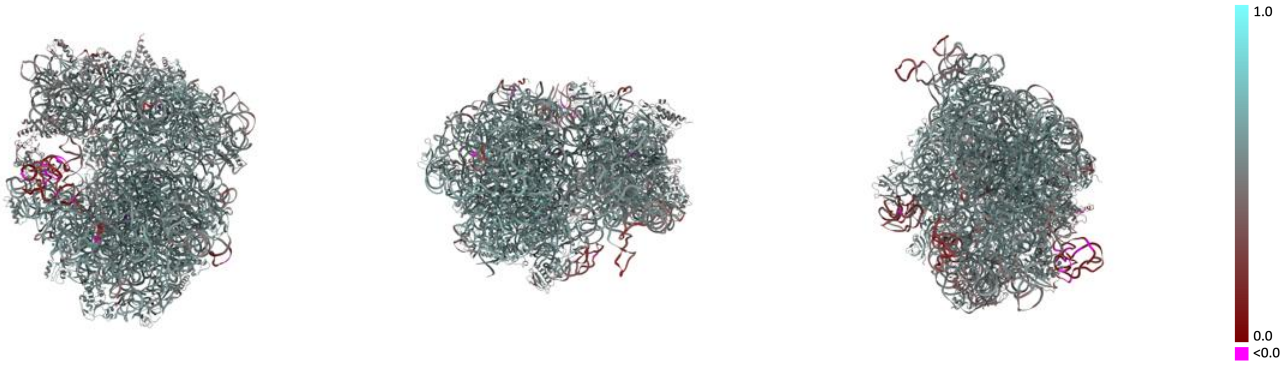
Y



Z

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

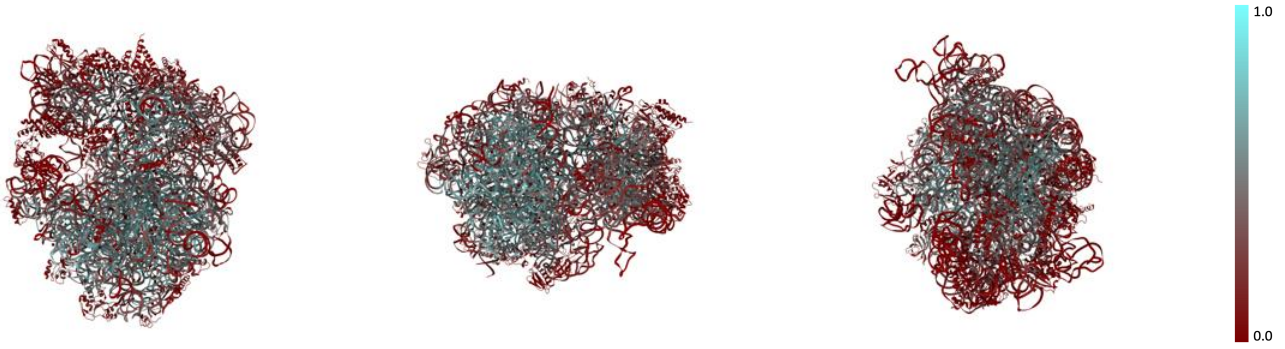
9.2 Q-score mapped to coordinate model (i)



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.

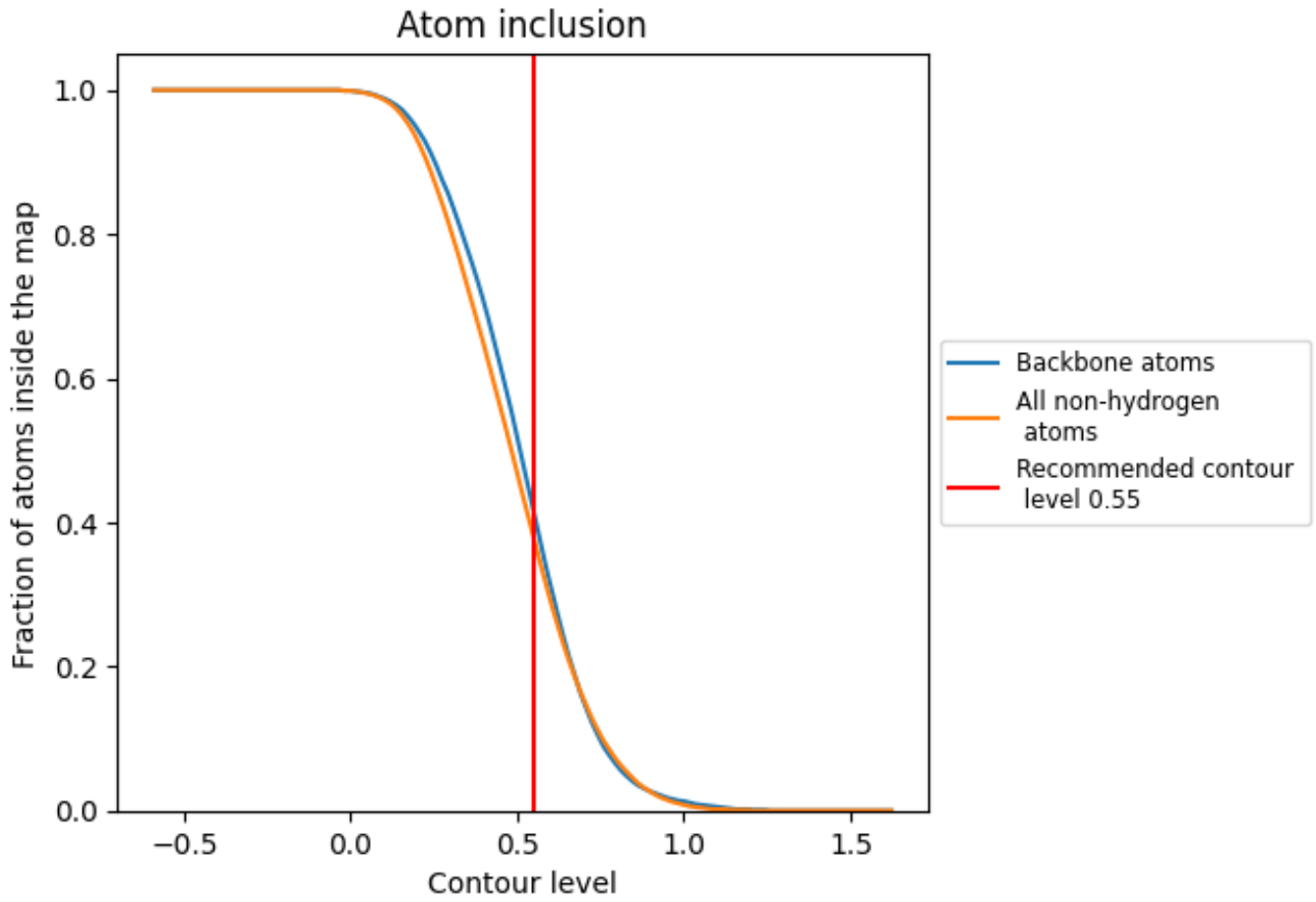
9.3 Atom inclusion mapped to coordinate model (i)



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, 41% of all backbone atoms, 38% 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	0.3770	0.5460
0	0.2230	0.5770
1	0.5620	0.6050
2	0.4470	0.6050
3	0.3460	0.5870
4	0.0000	0.3450
A	0.3620	0.5360
B	0.0530	0.4950
C	0.1400	0.5300
D	0.0980	0.5220
E	0.2830	0.5720
F	0.1180	0.5380
G	0.0290	0.4850
H	0.2710	0.5750
I	0.0990	0.5260
J	0.0950	0.5000
K	0.1990	0.5550
L	0.1760	0.5620
M	0.0270	0.4970
N	0.1020	0.5140
O	0.2430	0.5630
P	0.2220	0.5570
Q	0.1270	0.5520
R	0.2100	0.5370
S	0.0200	0.5080
T	0.2130	0.5550
U	0.0250	0.4850
X	0.1550	0.5290
a	0.4960	0.5500
b	0.2850	0.5430
c	0.4330	0.5990
d	0.4110	0.5880
e	0.2950	0.5770
f	0.0160	0.4800
g	0.0430	0.5230



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Chain	Atom inclusion	Q-score
h	0.0000	0.2760
i	0.4020	0.5890
j	0.2980	0.5860
k	0.3490	0.5810
l	0.2710	0.5760
m	0.4490	0.5980
n	0.1650	0.5440
o	0.3150	0.5840
p	0.4750	0.5940
q	0.3120	0.5860
r	0.4080	0.5860
s	0.2510	0.5650
t	0.1450	0.5390
u	0.1980	0.5640
v	0.4250	0.5990
w	0.3440	0.5840
x	0.1190	0.5260
y	0.3660	0.5890
z	0.4240	0.5880