wwPDB EM Validation Summary Report (i)

Nov 7, 2026 – 10:02 am GMT

PDB ID	:	9TAP / pdb_00009tap
EMDB ID	:	EMD-55754
Title	:	Structural characterization of hibernating ribosomes in the Gram-negative pathogen Acinetobacter baumannii with no 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 (1)) were used in the production of this report:

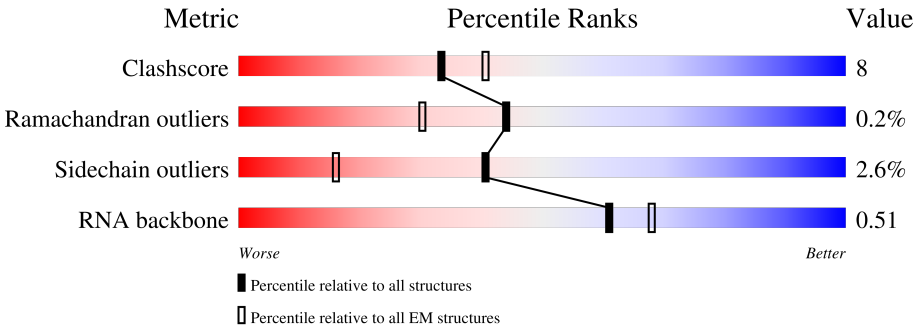
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal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

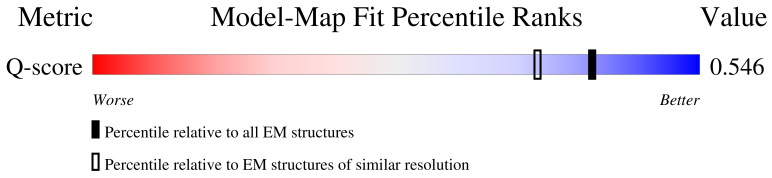
1 Overall quality at a glance (i)

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	73% 71% 29%
2	1	44	20% 86% 14%
3	2	64	33% 78% 20%

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Mol	Chain	Length	Quality of chain
4	3	38	68% 82% 18%
5	4	74	96% 61% 32%
6	A	1537	71% 52% 41% 7%
7	B	250	92% 60% 29% 8%
8	C	250	84% 68% 17% 14%
9	D	208	99% 76% 22%
10	E	165	80% 73% 21% 6%
11	F	127	83% 65% 17% 17%
12	G	156	98% 72% 26%
13	H	131	94% 79% 21%
14	I	128	99% 72% 27%
15	J	103	94% 74% 23%
16	K	128	91% 66% 23% 9%
17	L	124	94% 75% 23%
18	M	118	97% 73% 25%
19	N	101	98% 71% 28%
20	O	89	87% 74% 25%
21	P	83	96% 83% 14%
22	Q	85	91% 61% 31% 7%
23	R	75	88% 65% 21% 12%
24	S	91	92% 71% 19% 8%
25	T	88	95% 75% 22%
26	W	15	67% 47% 13% 7% 33%
27	X	116	85% 68% 22% 10%
28	a	2893	27% 55% 39% 6%

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Mol	Chain	Length	Quality of chain
29	b	115	67% 70% 25% 5%
30	c	274	39% 85% 14%
31	d	212	37% 81% 18%
32	e	200	62% 90% 10%
33	f	178	99% 60% 37%
34	g	177	98% 76% 21%
35	h	148	41% 26% 14% 59%
36	i	142	36% 80% 20%
37	j	122	60% 88% 11%
38	k	146	56% 82% 18%
39	l	137	69% 80% 20%
40	m	125	23% 85% 10% 5%
41	n	116	90% 76% 22%
42	o	122	51% 80% 14%
43	p	119	34% 86% 13%
44	q	103	64% 83% 17%
45	r	109	40% 86% 13%
46	s	106	65% 68% 19% 13%
47	t	105	88% 84% 14%
48	u	98	83% 83% 16%
49	v	85	34% 86% 5% 8%
50	w	78	54% 86% 13%
51	x	65	88% 66% 28% 5%
52	y	58	45% 74% 24%
53	z	61	41% 72% 16% 11%

2 Entry composition (i)

There are 56 unique types of molecules in this entry. The entry contains 142374 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 (1537-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	1536	Total	C	N	O	P	0	0
			32947	14705	6016	10690	1536		

- 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 705	C 434	N 144	O 126	S 1	0	0

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

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

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

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

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

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

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

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

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

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

- Molecule 26 is a RNA chain called non-STOP mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	10	Total 219	C 97	N 41	O 71	P 10	0	0

- 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 RNA (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	1	Total	K	0
			1	1	
54	3	1	Total	K	0
			1	1	
54	A	47	Total	K	0
			47	47	

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Mol	Chain	Residues	Atoms	AltConf
54	L	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
56	p	1	Total Mg 1 1	0

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

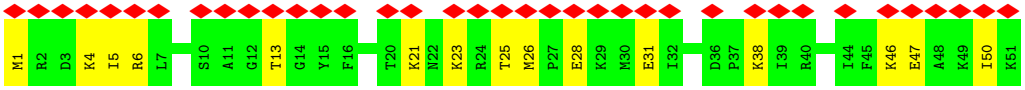
3 Residue-property plots (i)

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:

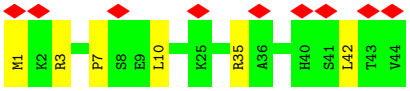




• Molecule 2: Large ribosomal subunit protein bL34

Chain 1:

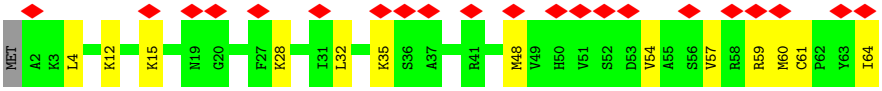




• Molecule 3: Large ribosomal subunit protein bL35

Chain 2:

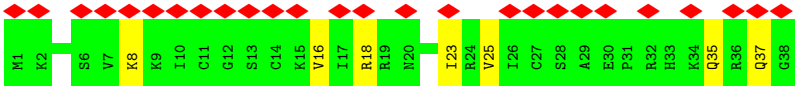




• Molecule 4: Large ribosomal subunit protein bL36

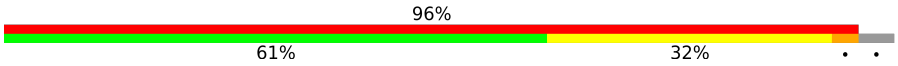
Chain 3:

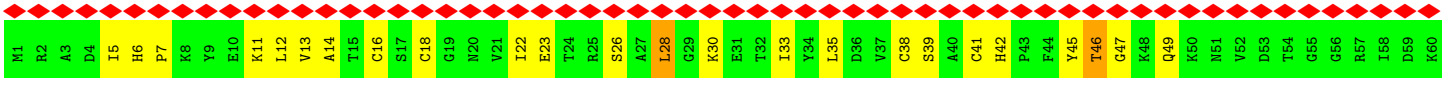


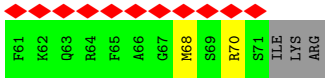


• Molecule 5: Large ribosomal subunit protein bL31

Chain 4:



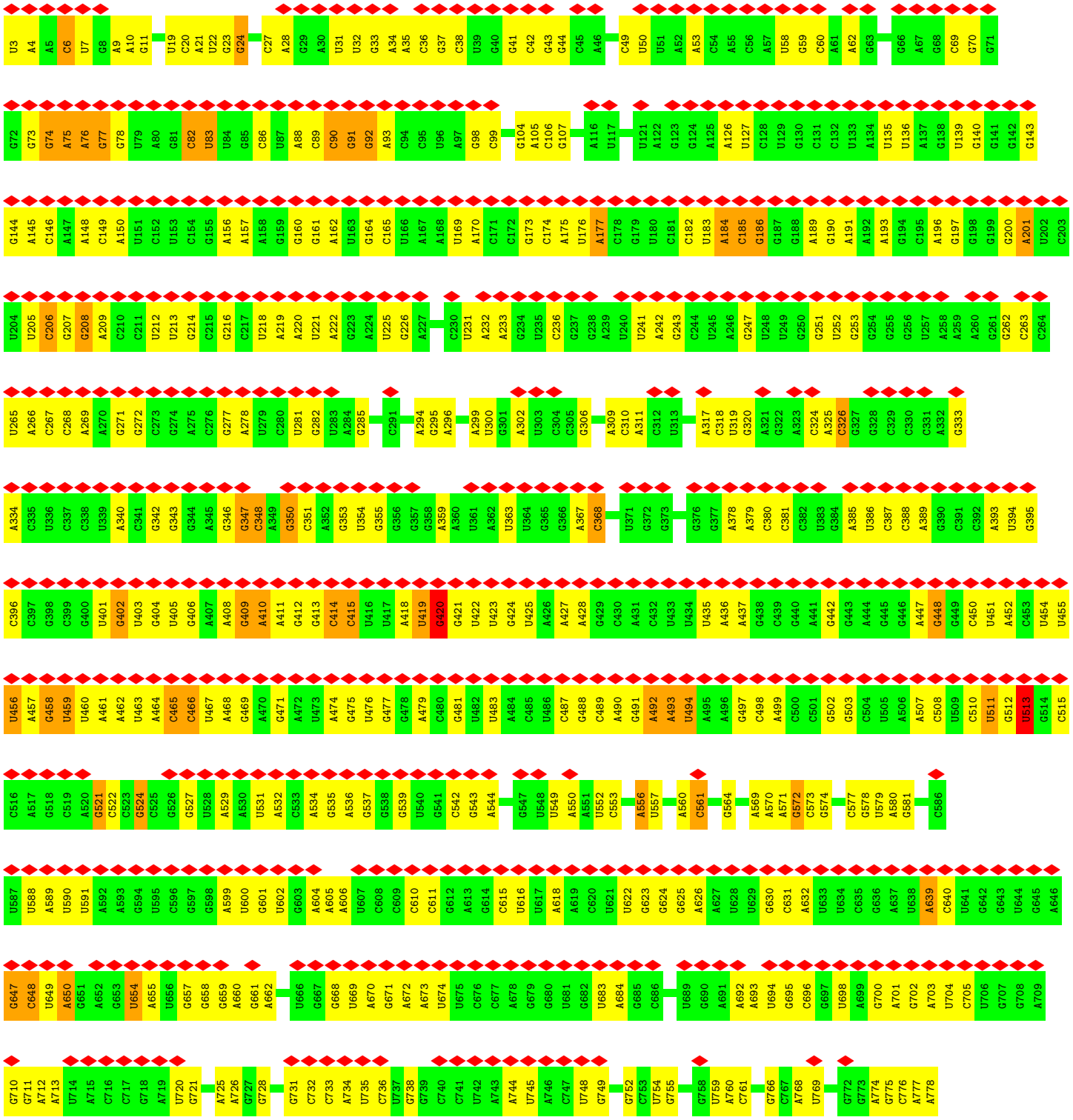


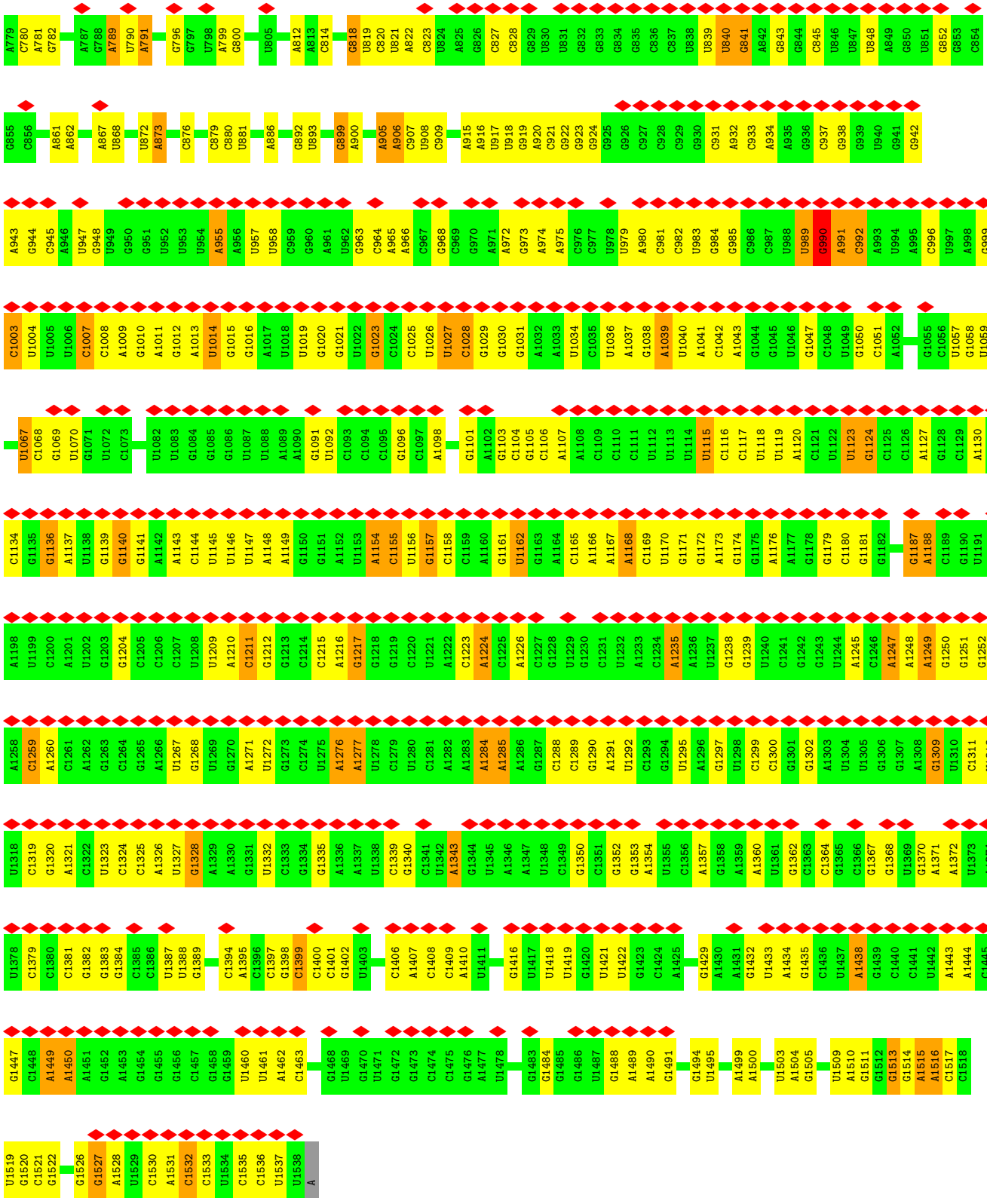


• Molecule 6: 16S rRNA (1537-MER)

Chain A:

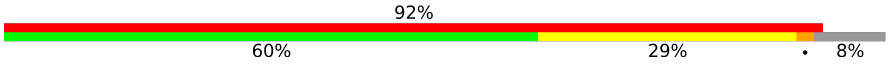






• Molecule 7: Small ribosomal subunit protein uS2

Chain B:

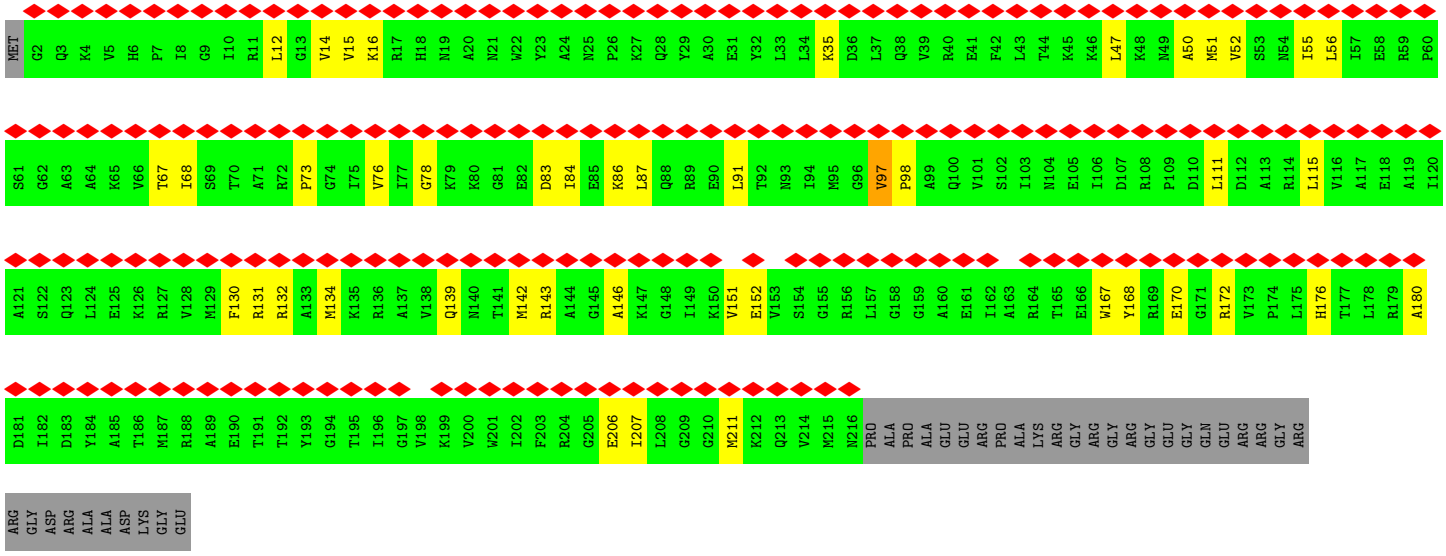




• Molecule 8: Small ribosomal subunit protein uS3

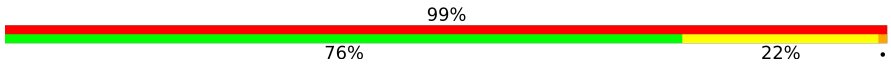
Chain C:

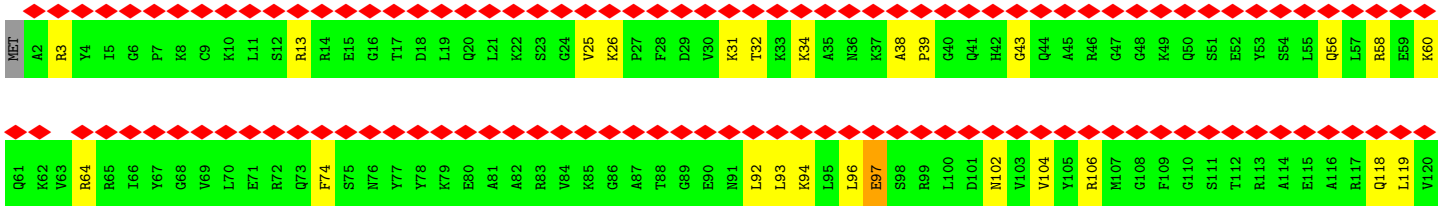


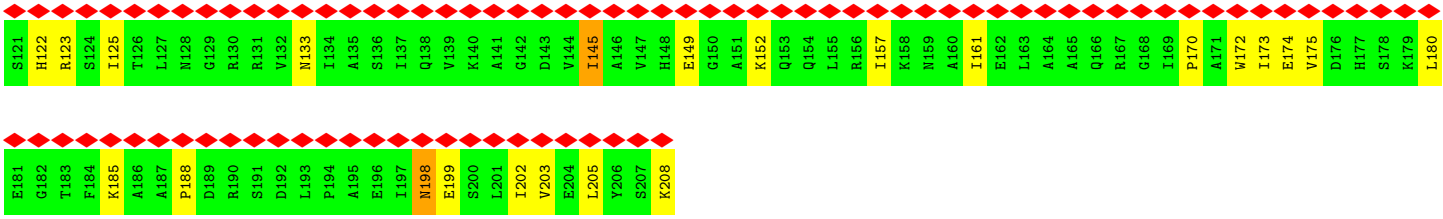


• Molecule 9: Small ribosomal subunit protein uS4

Chain D:



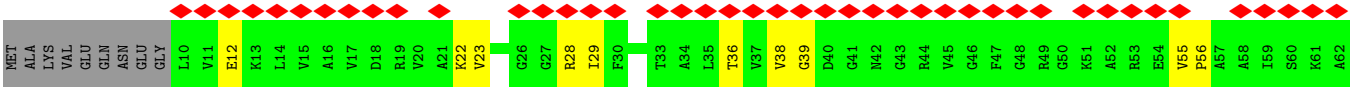


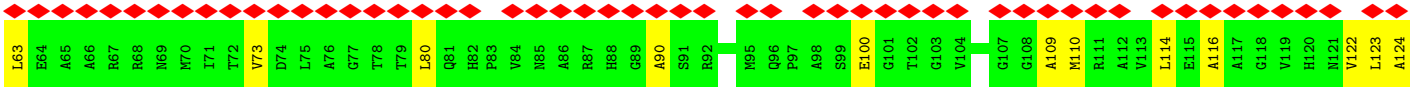


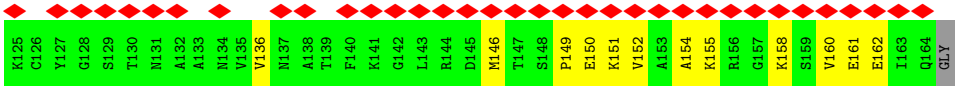
• Molecule 10: Small ribosomal subunit protein uS5

Chain E:





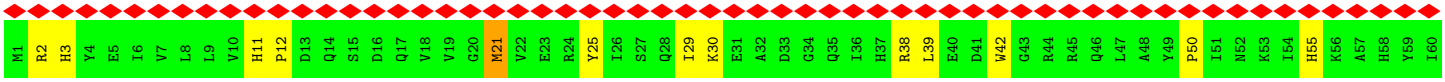


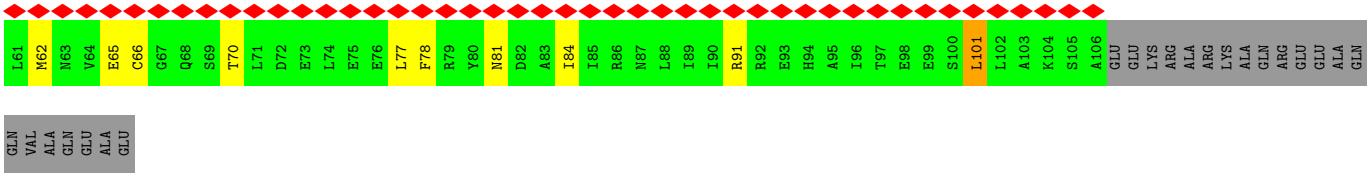


• Molecule 11: Small ribosomal subunit protein bS6

Chain F:

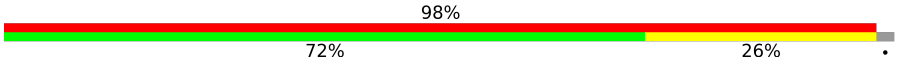


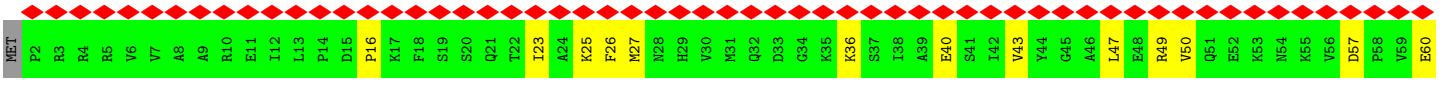




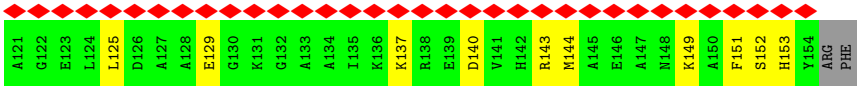
• Molecule 12: Small ribosomal subunit protein uS7

Chain G:



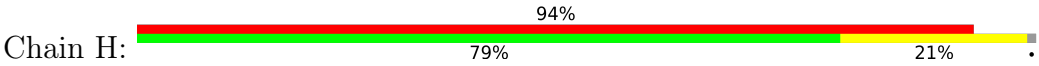


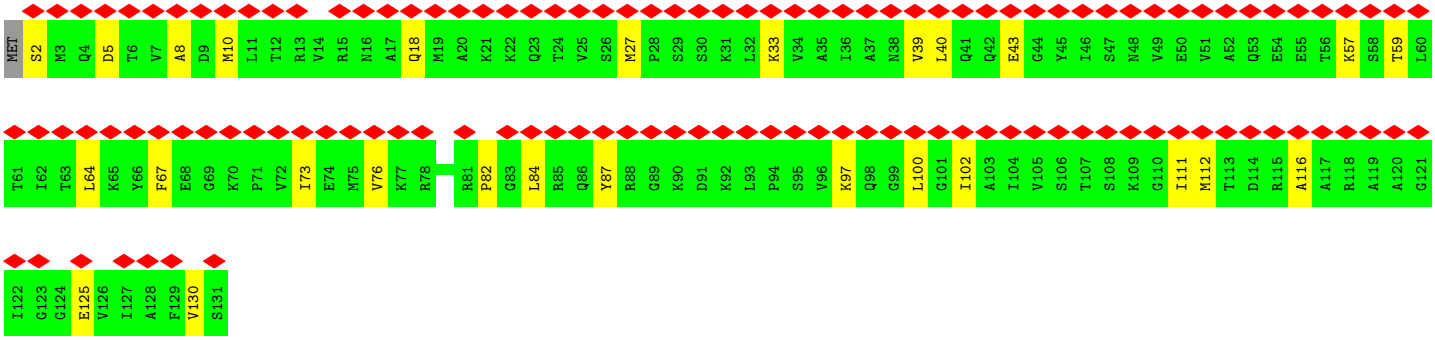




• Molecule 13: Small ribosomal subunit protein uS8

Chain H:

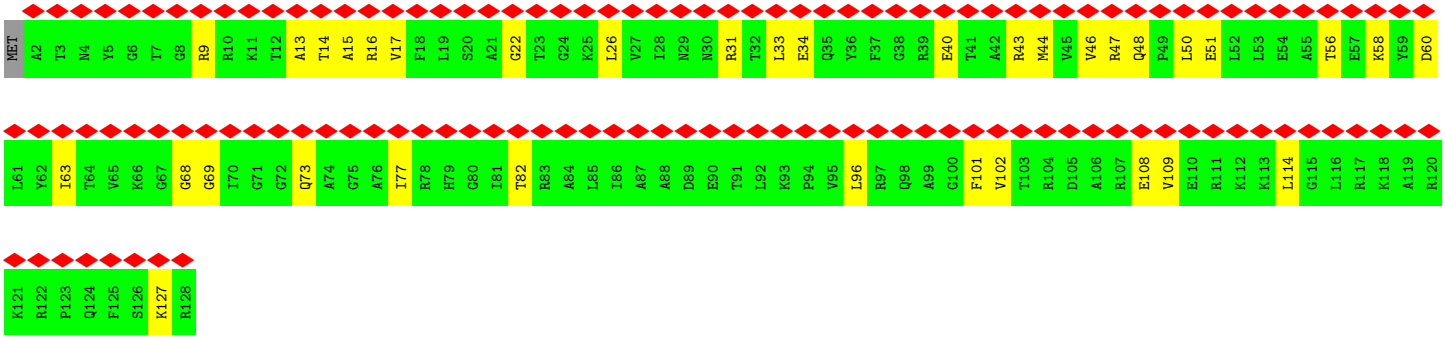




• Molecule 14: Small ribosomal subunit protein uS9

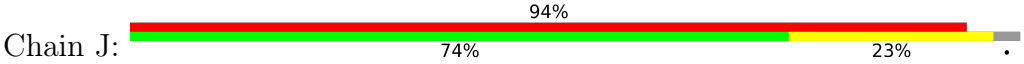
Chain I:

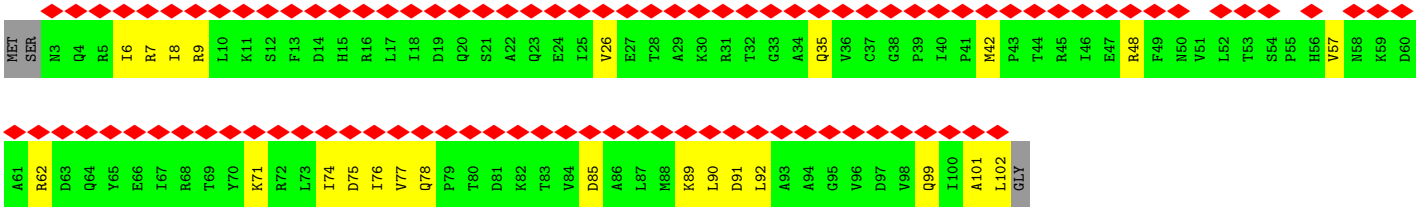




• Molecule 15: Small ribosomal subunit protein uS10

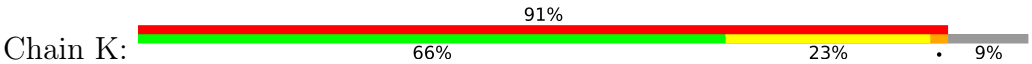
Chain J:



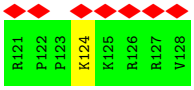


• Molecule 16: Small ribosomal subunit protein uS11

Chain K:

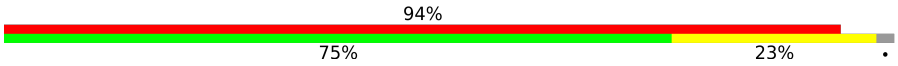


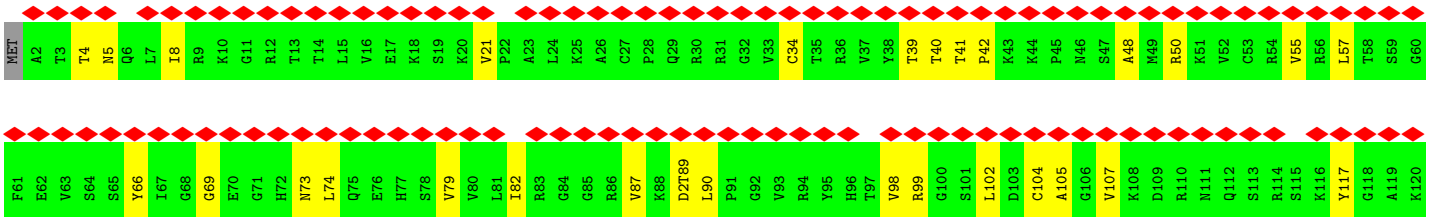




• Molecule 17: Small ribosomal subunit protein uS12

Chain L:

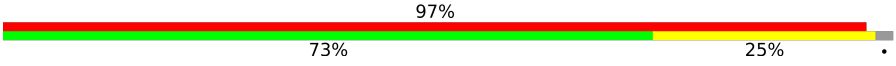


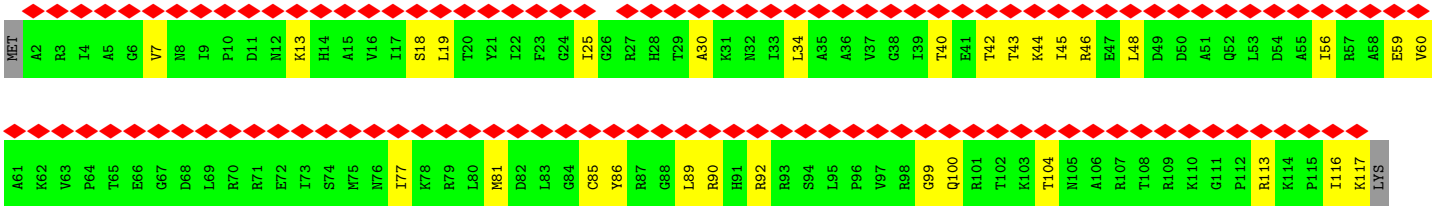




• Molecule 18: Small ribosomal subunit protein uS13

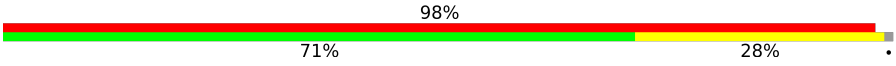
Chain M:

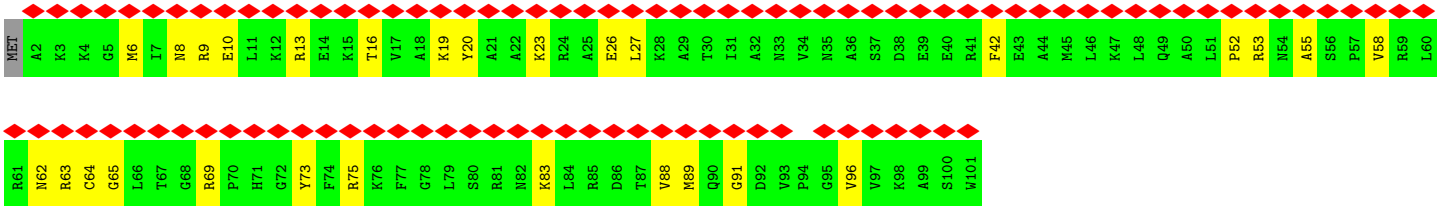




• Molecule 19: Small ribosomal subunit protein uS14

Chain N:

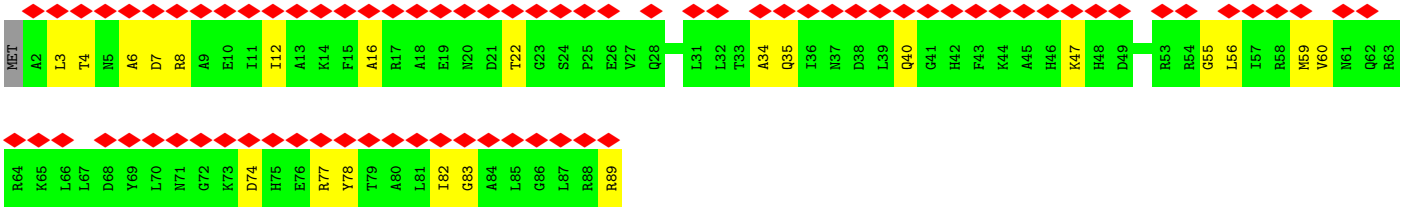




• Molecule 20: Small ribosomal subunit protein uS15

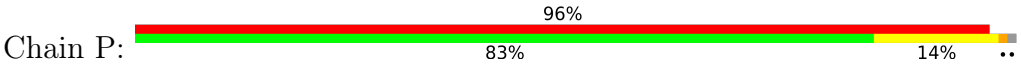
Chain O:

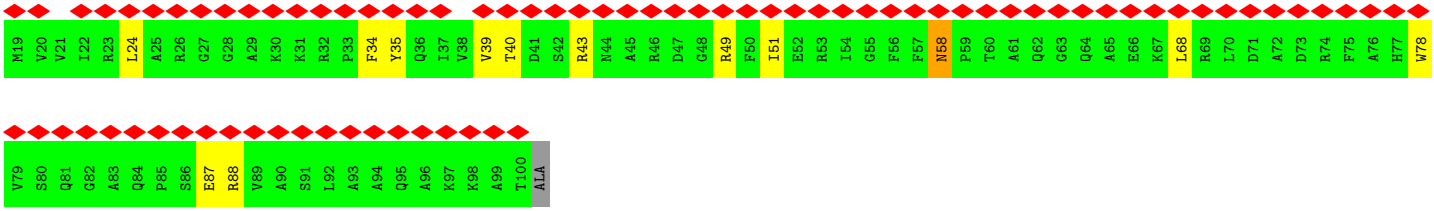




• Molecule 21: Small ribosomal subunit protein bS16

Chain P:

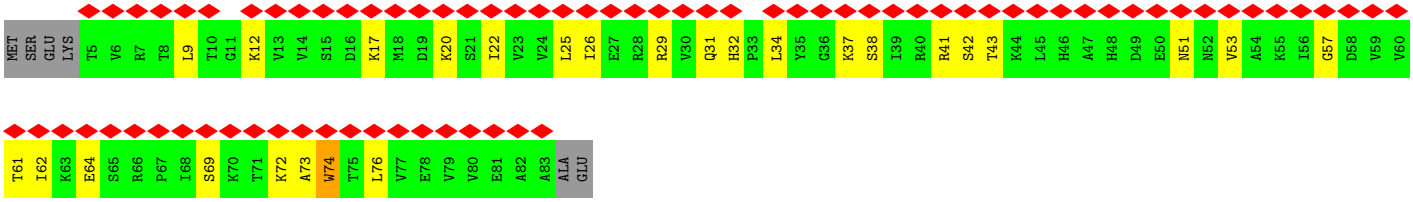




• Molecule 22: Small ribosomal subunit protein uS17

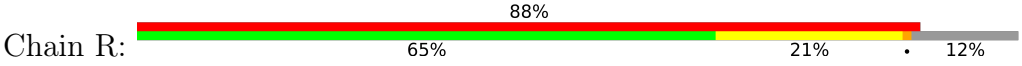
Chain Q:

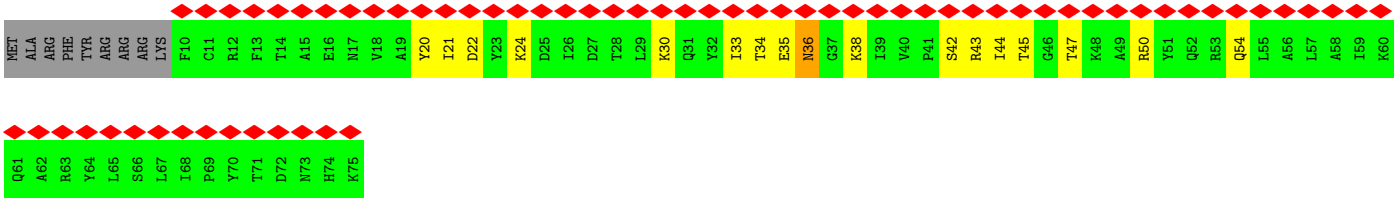




• Molecule 23: Small ribosomal subunit protein bS18

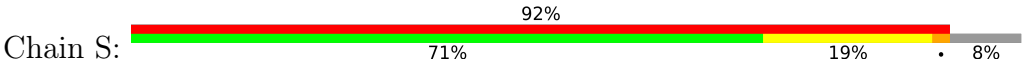
Chain R:

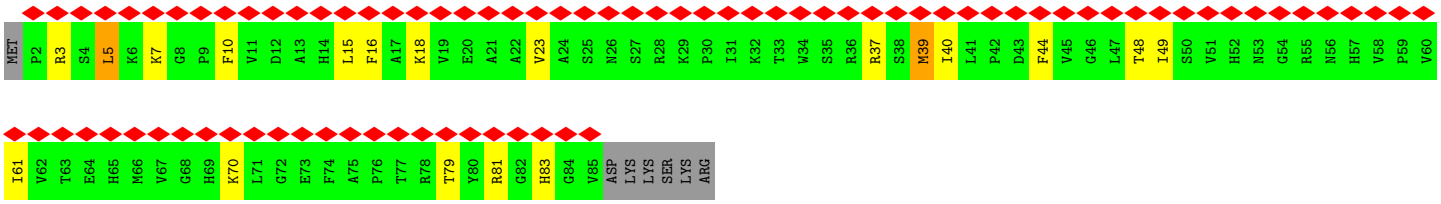




• Molecule 24: Small ribosomal subunit protein uS19

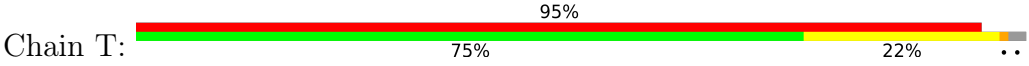
Chain S:

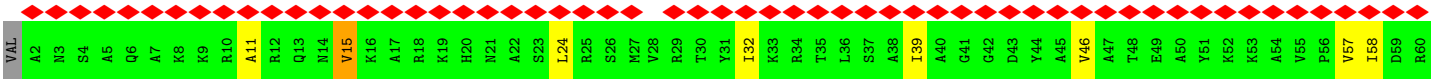




• Molecule 25: 30S ribosomal protein bS20

Chain T:

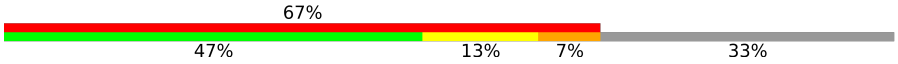


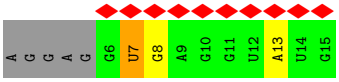




• Molecule 26: non-STOP mRNA

Chain W:

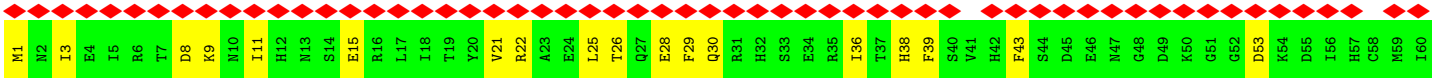


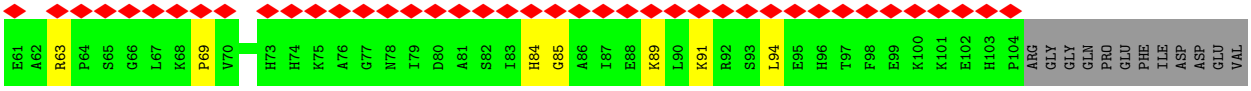


• Molecule 27: Putative ribosomal subunit interface protein

Chain X:



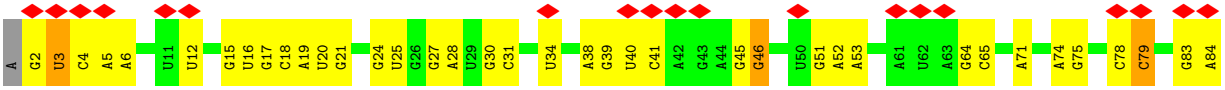


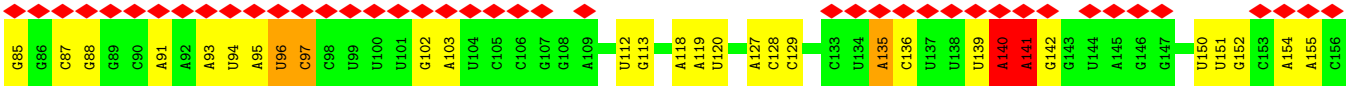


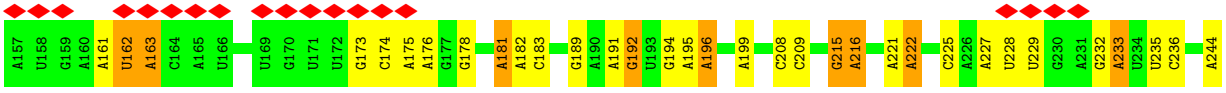
• Molecule 28: 23S rRNA (2890-MER)

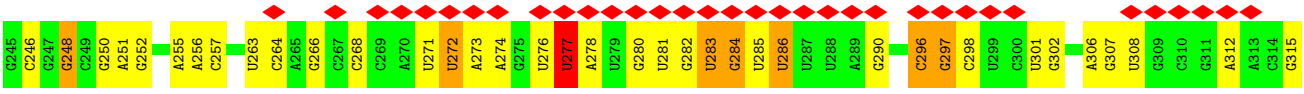
Chain a:



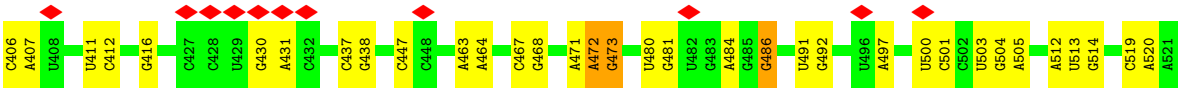


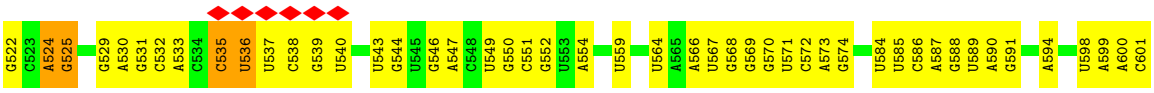


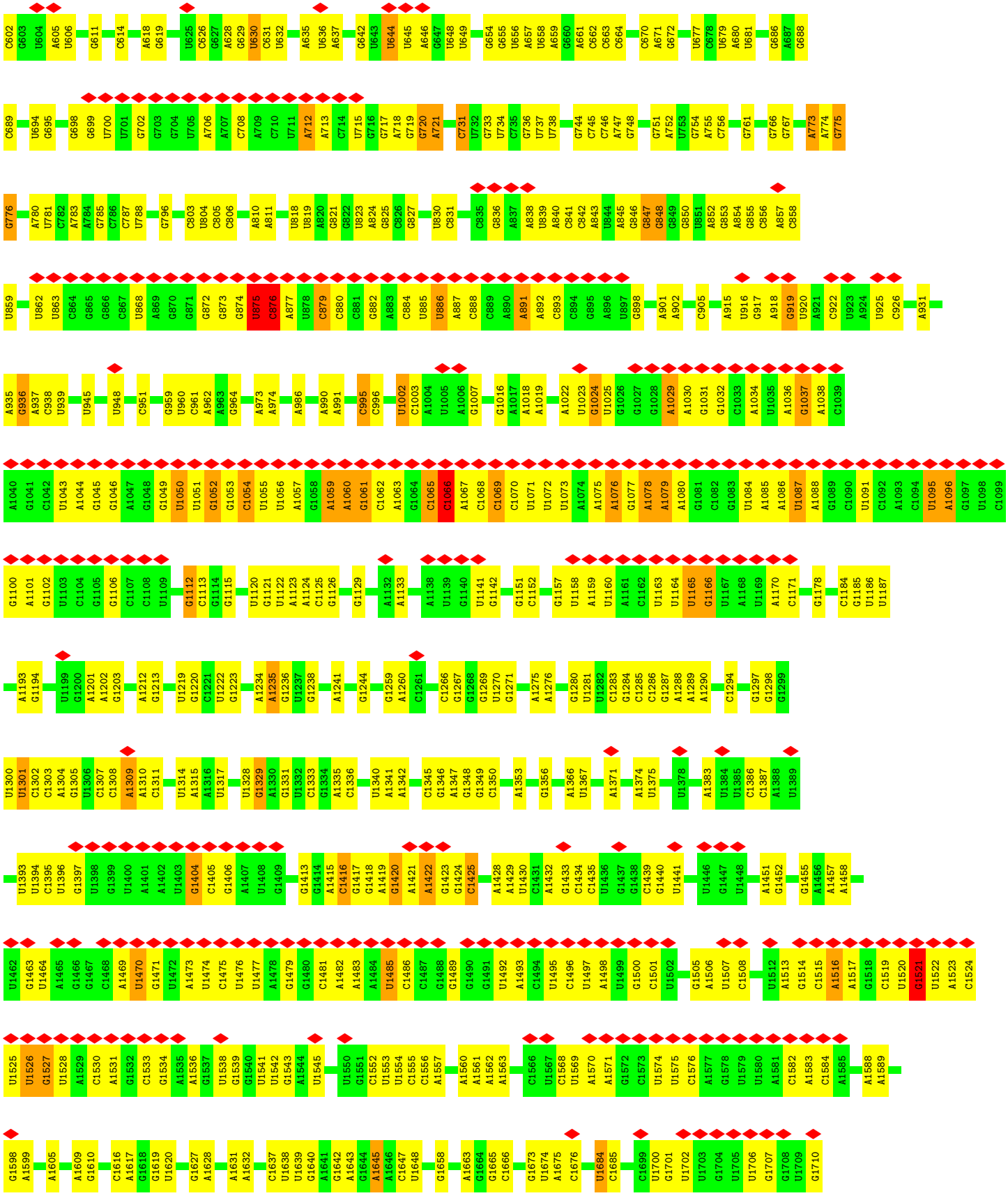


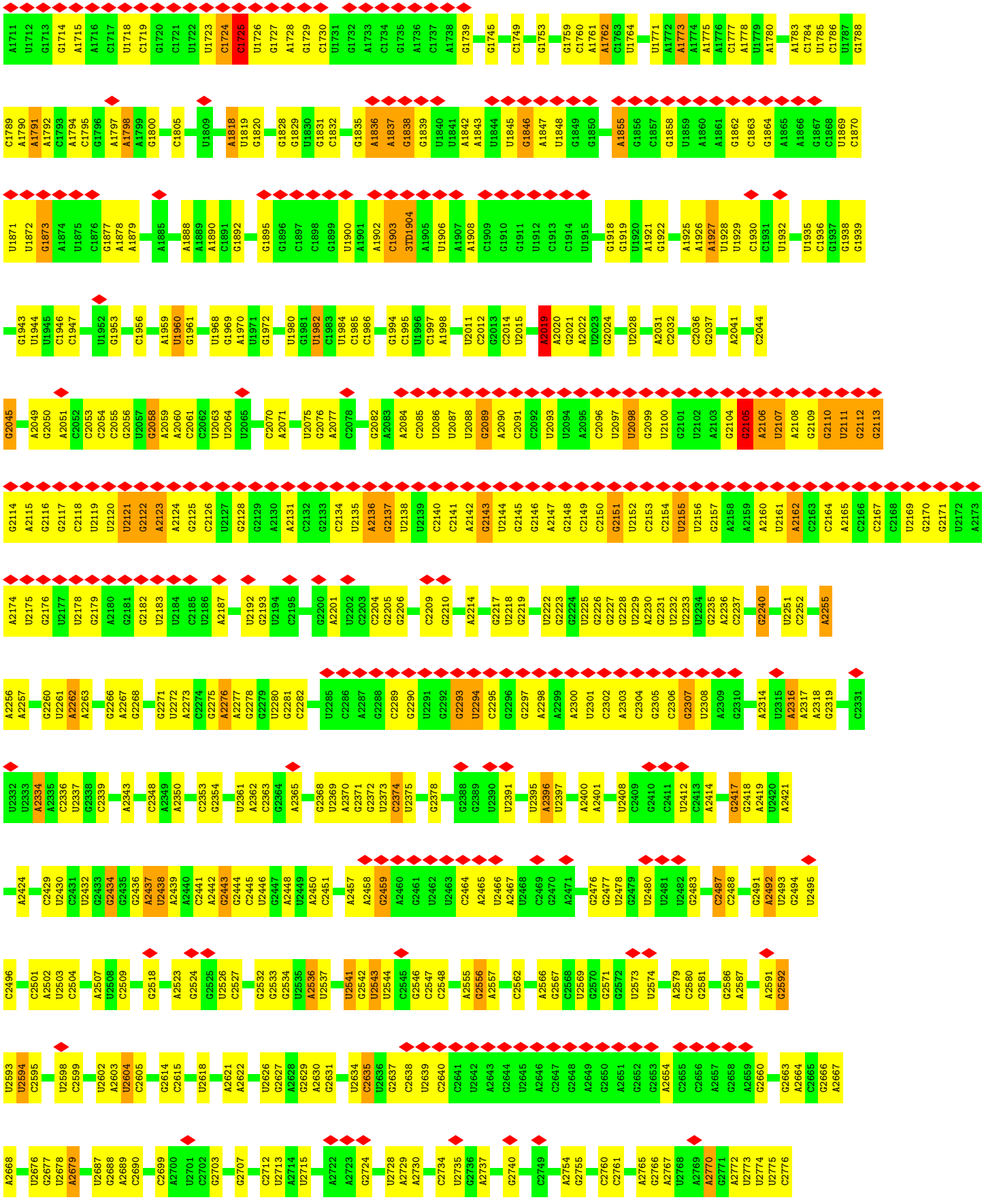


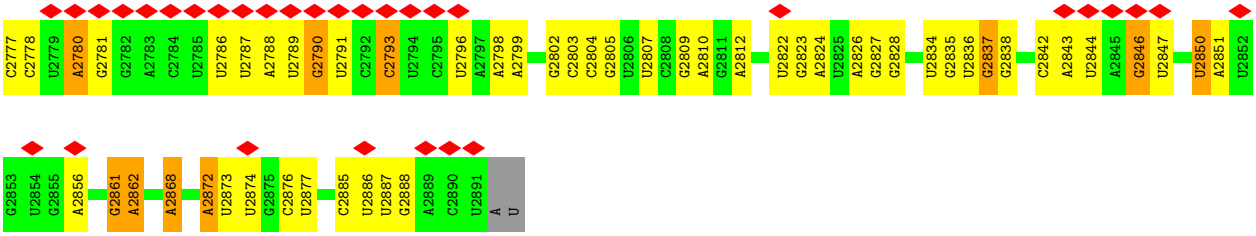








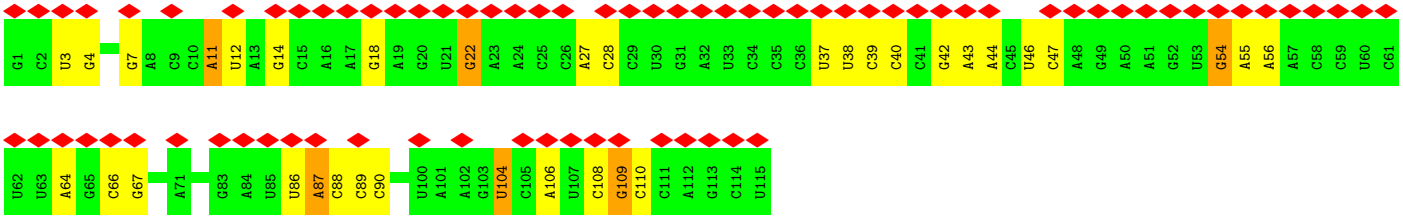




• Molecule 29: RNA (115-MER)

Chain b:

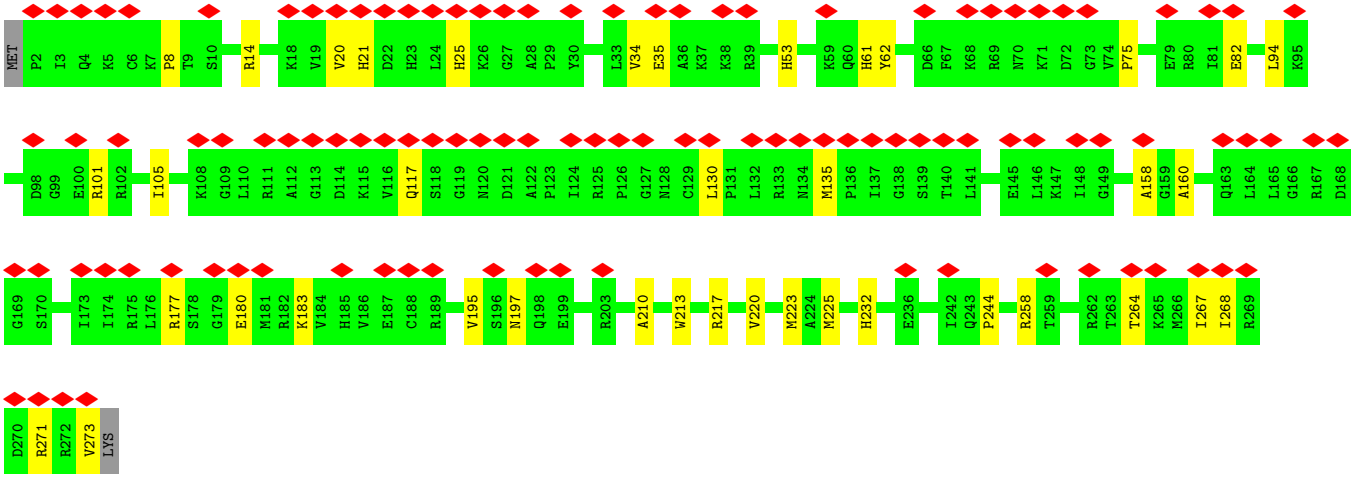




• Molecule 30: Large ribosomal subunit protein uL2

Chain c:

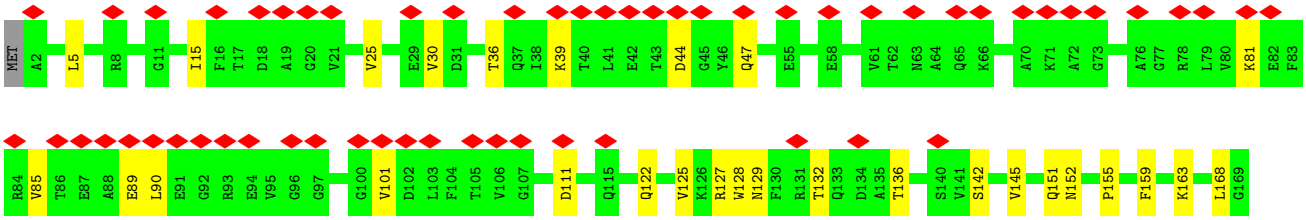


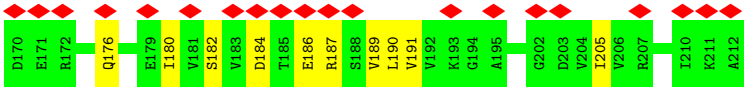


• Molecule 31: Large ribosomal subunit protein uL3

Chain d:

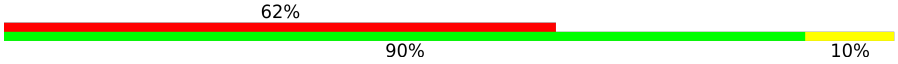


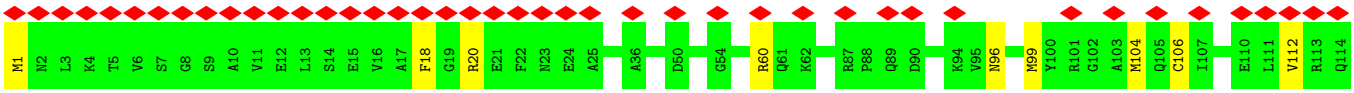


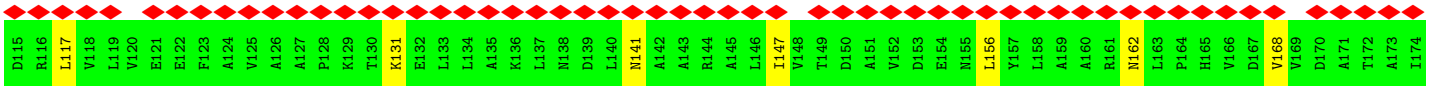


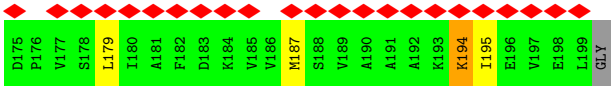
• Molecule 32: Large ribosomal subunit protein uL4

Chain e:



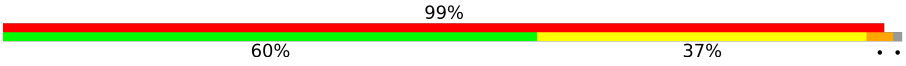


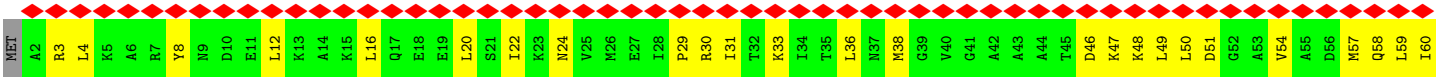


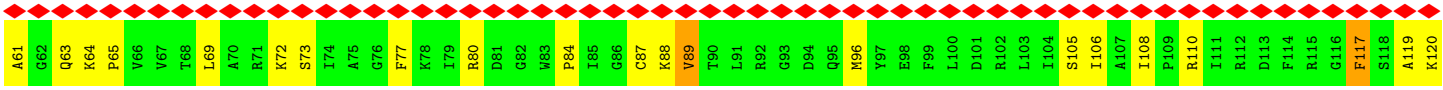


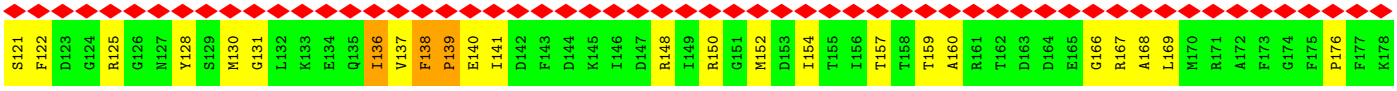
• Molecule 33: Large ribosomal subunit protein uL5

Chain f:



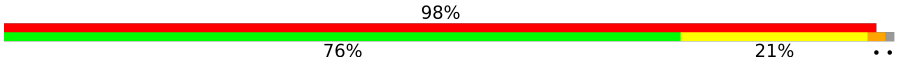




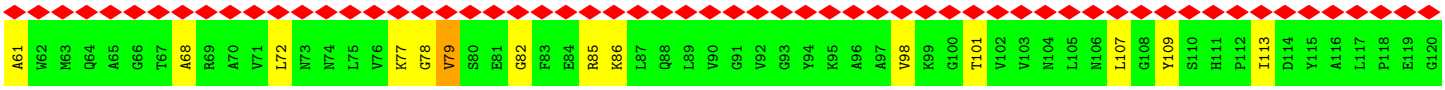


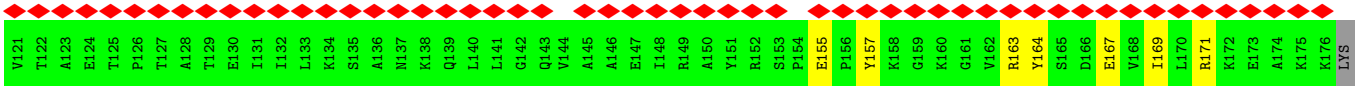
• Molecule 34: Large ribosomal subunit protein uL6

Chain g:





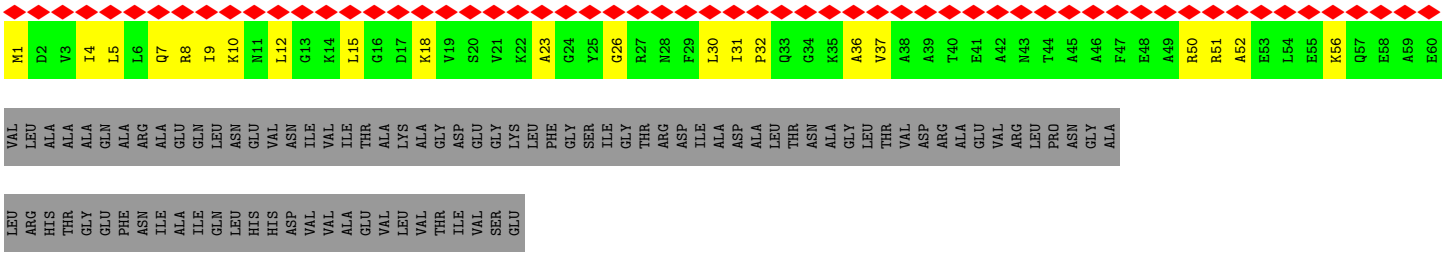




• Molecule 35: Large ribosomal subunit protein bL9

Chain h:

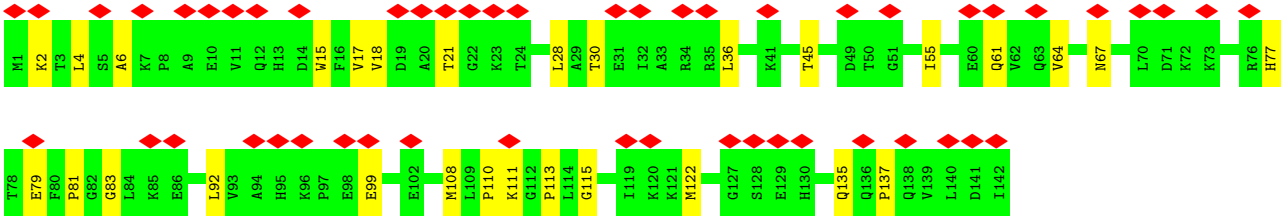




• Molecule 36: Large ribosomal subunit protein uL13

Chain i:

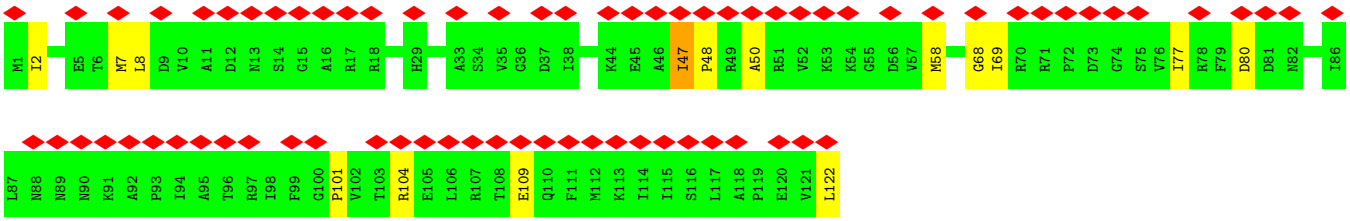




• Molecule 37: Large ribosomal subunit protein uL14

Chain j:

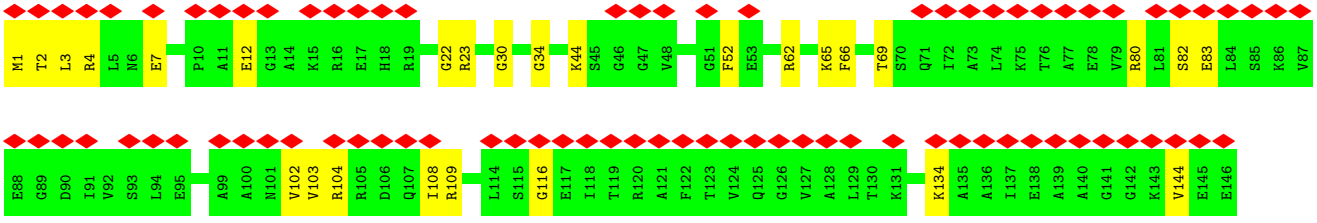




• Molecule 38: Large ribosomal subunit protein uL15

Chain k:

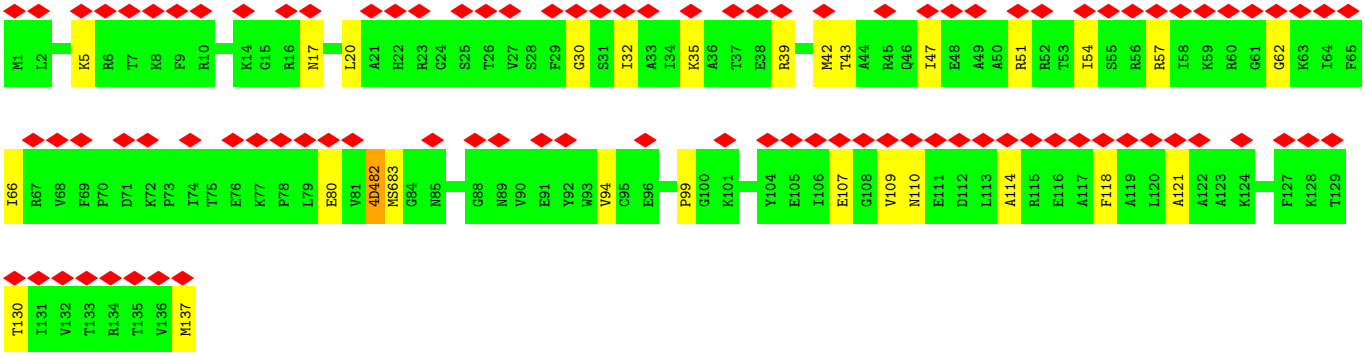




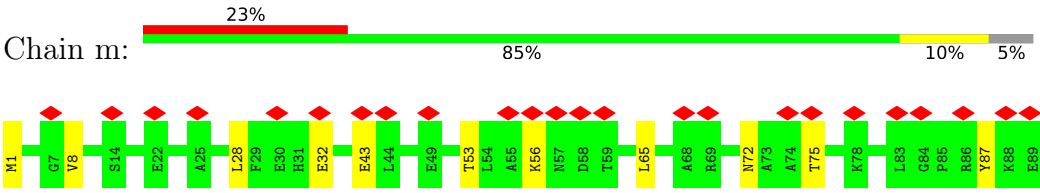
• Molecule 39: Large ribosomal subunit protein uL16

Chain l:

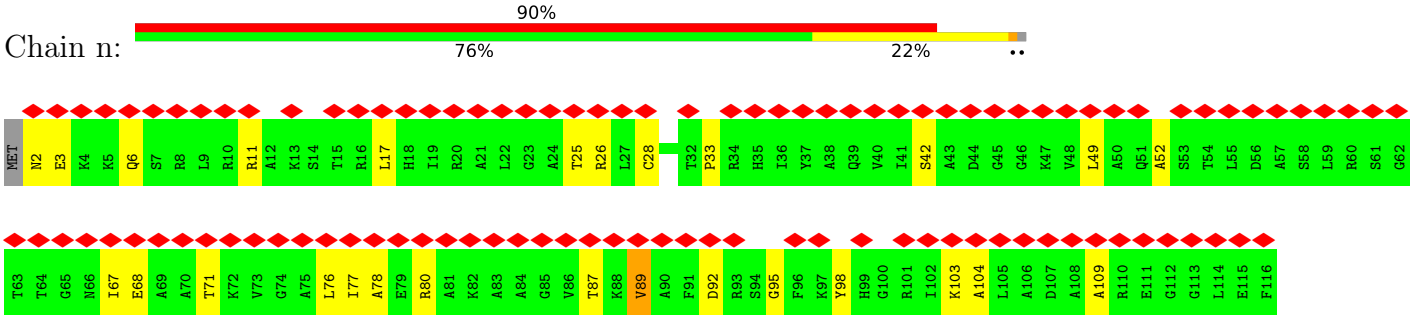




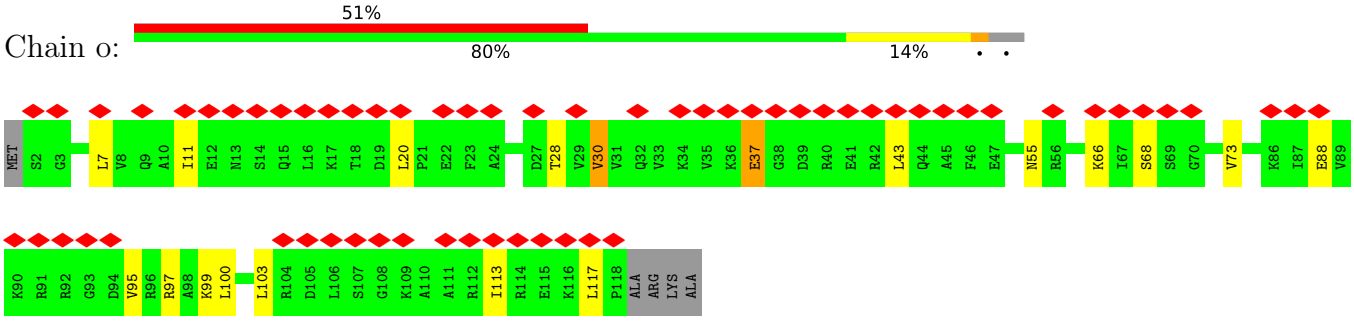
• Molecule 40: Large ribosomal subunit protein bL17



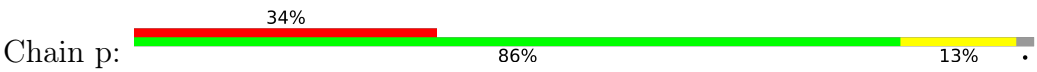
• Molecule 41: Large ribosomal subunit protein uL18

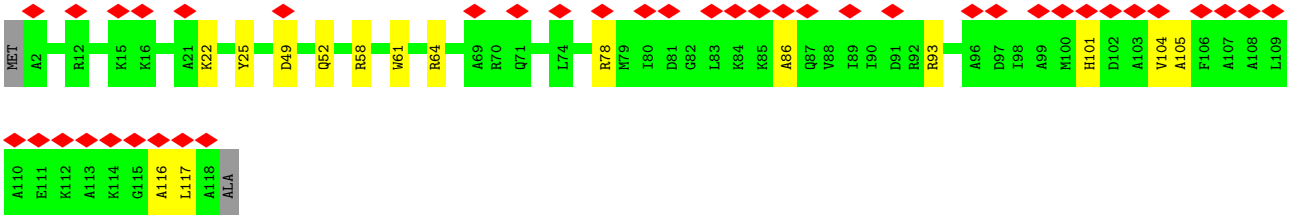


• Molecule 42: Large ribosomal subunit protein bL19

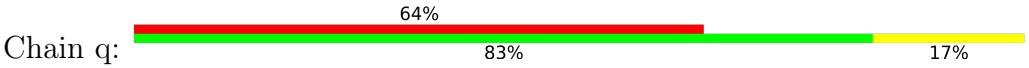


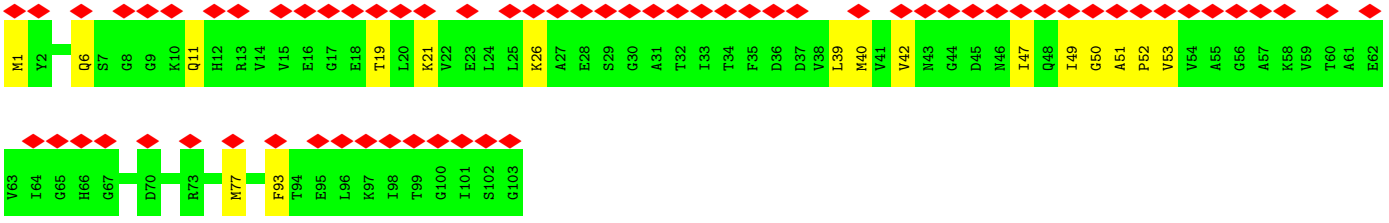
• Molecule 43: Large ribosomal subunit protein bL20



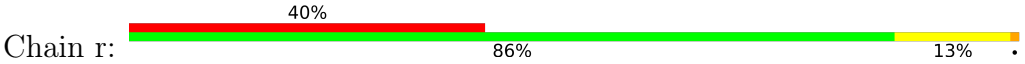


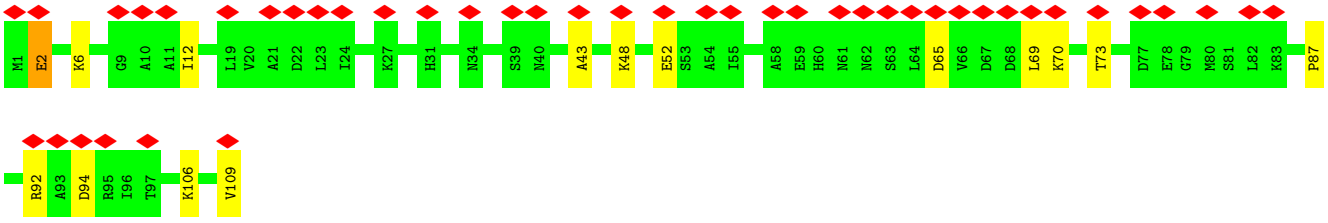
• Molecule 44: Large ribosomal subunit protein bL21





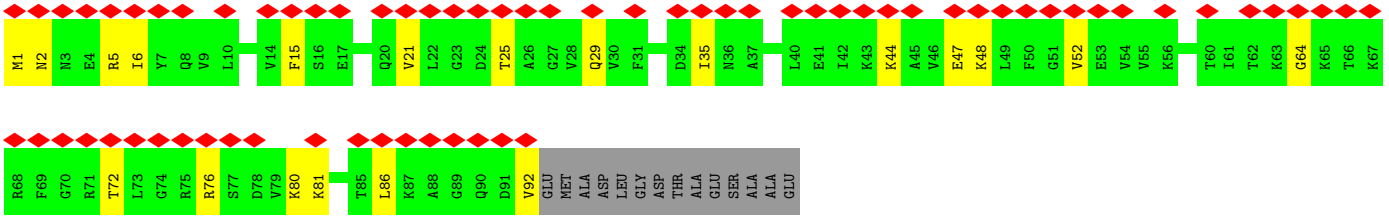
• Molecule 45: Large ribosomal subunit protein uL22



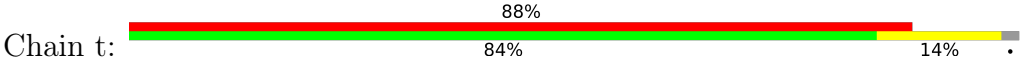


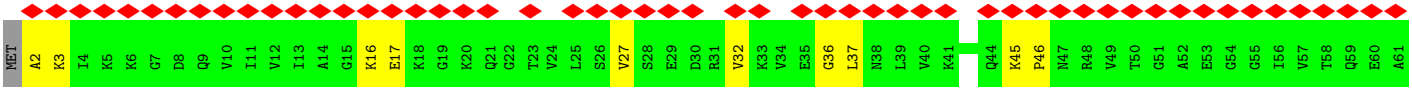
• Molecule 46: Large ribosomal subunit protein uL23

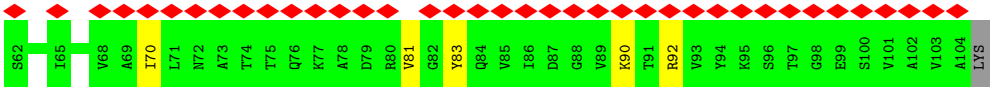




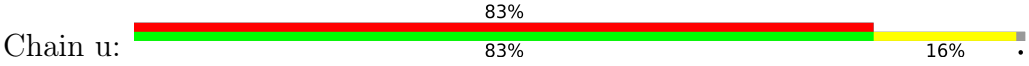
• Molecule 47: Large ribosomal subunit protein uL24

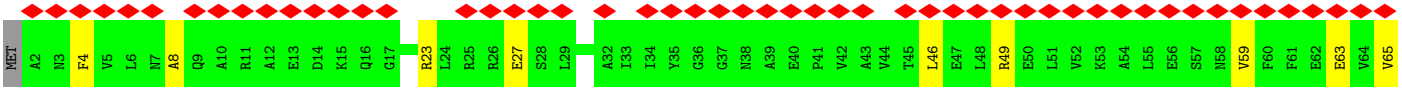


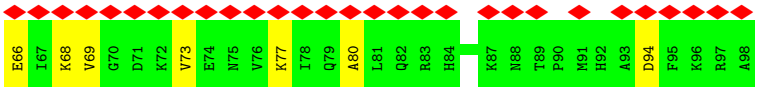




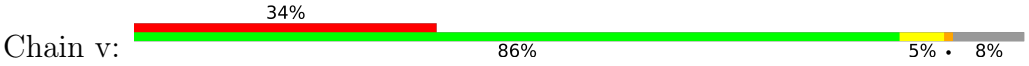
• Molecule 48: Large ribosomal subunit protein bL25

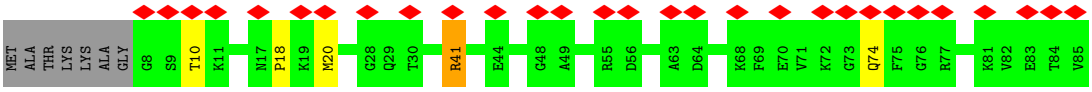




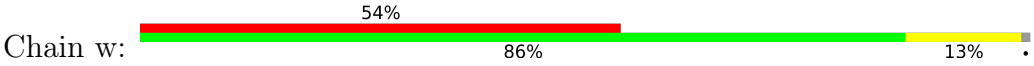


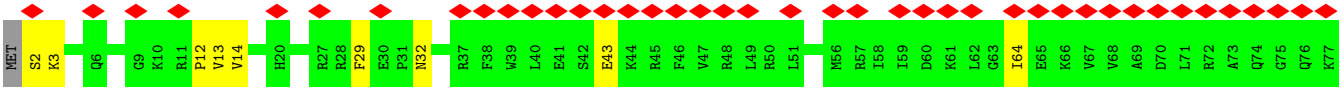
• Molecule 49: Large ribosomal subunit protein bL27





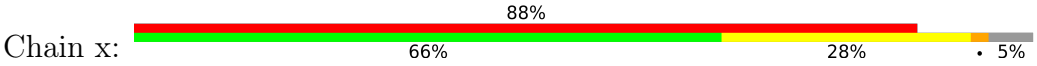
• Molecule 50: Large ribosomal subunit protein bL28

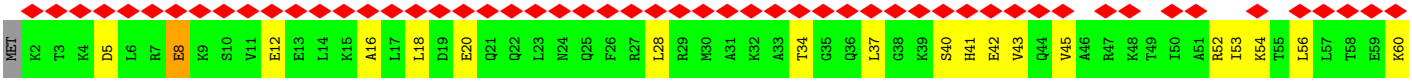


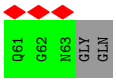




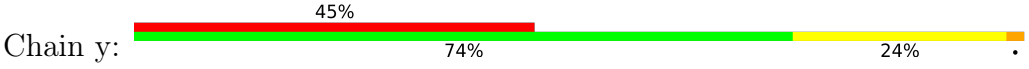
• Molecule 51: Large ribosomal subunit protein uL29

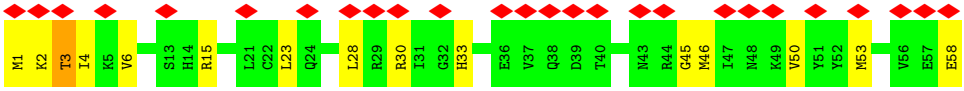






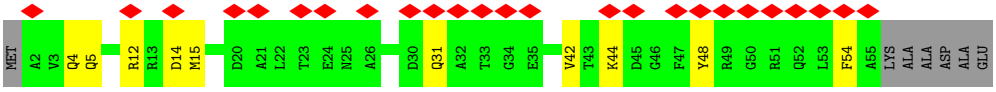
• Molecule 52: Large ribosomal subunit protein uL30





• 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	26517	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	1.666	Depositor
Minimum map value	-0.699	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.059	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: 5MU, IAS, OMU, 1MG, H2U, 2MG, MEQ, G7M, 4OC, MG, 6MZ, OMG, MS6, D2T, OMC, 5MC, 4D4, MA6, K, 2MA, 3TD, ZN, UR3, PSU

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	0.19	0/434	0.51	1/573 (0.2%)
2	1	0.10	0/367	0.27	0/481
3	2	0.11	0/515	0.32	0/678
4	3	0.14	0/296	0.28	0/389
5	4	0.12	0/561	0.37	0/750
6	A	0.26	0/36631	0.75	12/57133 (0.0%)
7	B	0.16	0/1832	0.45	0/2474
8	C	0.13	0/1714	0.31	0/2304
9	D	0.13	0/1653	0.31	0/2213
10	E	0.16	0/1141	0.35	0/1537
11	F	0.13	0/893	0.34	0/1204
12	G	0.15	0/1229	0.36	0/1647
13	H	0.14	0/993	0.38	0/1331
14	I	0.16	0/1006	0.35	0/1346
15	J	0.16	0/811	0.36	0/1096
16	K	0.18	0/869	0.40	0/1175
17	L	0.12	0/949	0.38	0/1270
18	M	0.17	0/922	0.46	0/1237
19	N	0.14	0/803	0.34	0/1071
20	O	0.15	0/715	0.33	0/958
21	P	0.14	0/655	0.33	0/879
22	Q	0.14	0/628	0.40	0/847
23	R	0.12	0/555	0.32	0/749
24	S	0.13	0/675	0.36	0/912
25	T	0.16	0/669	0.29	0/892
26	W	0.27	0/245	0.70	0/381
27	X	0.14	0/858	0.35	0/1150
28	a	0.28	0/68962	0.76	29/107563 (0.0%)
29	b	0.24	0/2739	0.74	0/4266
30	c	0.12	0/2152	0.31	0/2891
31	d	0.14	0/1580	0.31	0/2127

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	e	0.13	0/1532	0.32	0/2068
33	f	0.17	0/1415	0.45	0/1895
34	g	0.10	0/1346	0.28	0/1818
35	h	0.13	0/461	0.38	0/616
36	i	0.13	0/1151	0.32	0/1551
37	j	0.13	0/956	0.30	0/1286
38	k	0.11	0/1097	0.29	0/1461
39	l	0.15	0/1084	0.33	0/1448
40	m	0.13	0/956	0.31	0/1282
41	n	0.10	0/873	0.27	0/1167
42	o	0.12	0/931	0.31	0/1249
43	p	0.14	0/947	0.30	0/1262
44	q	0.13	0/818	0.35	0/1094
45	r	0.13	0/831	0.31	0/1113
46	s	0.12	0/723	0.32	0/967
47	t	0.10	0/770	0.30	0/1034
48	u	0.11	0/770	0.30	0/1036
49	v	0.12	0/597	0.26	0/798
50	w	0.14	0/642	0.33	0/856
51	x	0.12	0/499	0.31	0/662
52	y	0.16	0/468	0.41	0/624
53	z	0.14	0/453	0.36	0/604
All	All	0.24	0/153372	0.67	42/229415 (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
22	Q	0	1
39	l	0	2
All	All	0	3

There are no bond length outliers.

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	1532	C	C6-N1-C2	-8.58	116.87	120.30
6	A	1532	C	N3-C4-C5	-7.57	118.87	121.90
28	a	1066	C	N1-C2-O2	7.23	123.24	118.90
28	a	1301	U	C2-N1-C1'	7.20	126.34	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	415	C	N3-C2-O2	-7.12	116.92	121.90

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
22	Q	41	ARG	Sidechain
39	l	82	4D4	Peptide,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	11	0
2	1	363	0	401	5	0
3	2	509	0	566	11	0
4	3	295	0	325	4	0
5	4	552	0	552	24	0
6	A	32947	0	16584	480	0
7	B	1801	0	1814	58	0
8	C	1690	0	1774	29	0
9	D	1631	0	1691	45	0
10	E	1129	0	1173	21	0
11	F	878	0	878	17	0
12	G	1210	0	1255	30	0
13	H	985	0	1047	19	0
14	I	995	0	1053	29	0
15	J	801	0	832	15	0
16	K	862	0	871	20	0
17	L	947	0	997	17	0
18	M	912	0	975	18	0
19	N	792	0	833	21	0
20	O	705	0	712	16	0
21	P	644	0	655	10	0
22	Q	621	0	665	15	0
23	R	545	0	556	12	0
24	S	657	0	675	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	T	663	0	714	11	0
26	W	219	0	108	2	0
27	X	841	0	824	14	0
28	a	61984	0	31155	757	0
29	b	2450	0	1241	20	0
30	c	2111	0	2175	24	0
31	d	1573	0	1611	23	0
32	e	1511	0	1566	14	0
33	f	1395	0	1451	57	0
34	g	1327	0	1386	25	0
35	h	458	0	480	10	0
36	i	1125	0	1148	23	0
37	j	946	0	1007	11	0
38	k	1089	0	1158	19	0
39	l	1088	0	1150	16	0
40	m	942	0	987	7	0
41	n	865	0	905	13	0
42	o	919	0	973	17	0
43	p	934	0	997	13	0
44	q	807	0	842	12	0
45	r	826	0	894	9	0
46	s	717	0	777	11	0
47	t	766	0	816	9	0
48	u	760	0	783	8	0
49	v	589	0	592	5	0
50	w	632	0	667	9	0
51	x	498	0	537	13	0
52	y	463	0	488	11	0
53	z	447	0	435	8	0
54	1	1	0	0	0	0
54	3	1	0	0	0	0
54	A	47	0	0	0	0
54	L	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
56	d	1	0	0	0	0
56	k	1	0	0	0	0
56	p	1	0	0	0	0
56	s	1	0	0	0	0
56	v	1	0	0	0	0
56	z	1	0	0	0	0
All	All	142374	0	95213	1972	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 1972 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:140:A:HO2'	28:a:141:A:H8	1.04	1.02
6:A:905:A:HO2'	6:A:906:A:H8	1.07	0.95
28:a:467:C:O2	28:a:471:A:N6	2.08	0.85
24:S:3:ARG:HH21	24:S:7:LYS:HG2	1.42	0.83
30:c:130:LEU:HB2	30:c:135:MET:HE2	1.61	0.83

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	2	61/64 (95%)	58 (95%)	3 (5%)	0	100	100
4	3	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
5	4	69/74 (93%)	54 (78%)	15 (22%)	0	100	100
7	B	227/250 (91%)	208 (92%)	17 (8%)	2 (1%)	14	41
8	C	213/250 (85%)	208 (98%)	5 (2%)	0	100	100
9	D	205/208 (99%)	198 (97%)	7 (3%)	0	100	100
10	E	153/165 (93%)	148 (97%)	5 (3%)	0	100	100
11	F	104/127 (82%)	102 (98%)	2 (2%)	0	100	100
12	G	151/156 (97%)	144 (95%)	7 (5%)	0	100	100
13	H	128/131 (98%)	122 (95%)	6 (5%)	0	100	100
14	I	125/128 (98%)	118 (94%)	7 (6%)	0	100	100
15	J	98/103 (95%)	95 (97%)	3 (3%)	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%)	110 (96%)	4 (4%)	0	100	100
19	N	98/101 (97%)	91 (93%)	7 (7%)	0	100	100
20	O	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
21	P	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
22	Q	77/85 (91%)	75 (97%)	1 (1%)	1 (1%)	9	32
23	R	64/75 (85%)	64 (100%)	0	0	100	100
24	S	82/91 (90%)	80 (98%)	2 (2%)	0	100	100
25	T	84/88 (96%)	84 (100%)	0	0	100	100
27	X	102/116 (88%)	100 (98%)	2 (2%)	0	100	100
30	c	270/274 (98%)	262 (97%)	8 (3%)	0	100	100
31	d	208/212 (98%)	202 (97%)	5 (2%)	1 (0%)	24	54
32	e	197/200 (98%)	193 (98%)	4 (2%)	0	100	100
33	f	175/178 (98%)	159 (91%)	13 (7%)	3 (2%)	7	26
34	g	173/177 (98%)	167 (96%)	5 (3%)	1 (1%)	21	51
35	h	58/148 (39%)	54 (93%)	4 (7%)	0	100	100
36	i	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
37	j	120/122 (98%)	115 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	k	144/146 (99%)	140 (97%)	4 (3%)	0	100	100
39	l	133/137 (97%)	130 (98%)	3 (2%)	0	100	100
40	m	117/125 (94%)	115 (98%)	2 (2%)	0	100	100
41	n	113/116 (97%)	109 (96%)	3 (3%)	1 (1%)	14	41
42	o	115/122 (94%)	112 (97%)	3 (3%)	0	100	100
43	p	115/119 (97%)	114 (99%)	1 (1%)	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%)	87 (97%)	3 (3%)	0	100	100
47	t	101/105 (96%)	98 (97%)	3 (3%)	0	100	100
48	u	95/98 (97%)	90 (95%)	5 (5%)	0	100	100
49	v	76/85 (89%)	74 (97%)	2 (3%)	0	100	100
50	w	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
51	x	60/65 (92%)	56 (93%)	4 (7%)	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	5571/5973 (93%)	5355 (96%)	207 (4%)	9 (0%)	44	72

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
31	d	152	ASN
33	f	136	ILE
7	B	128	PHE
7	B	38	ASN
33	f	72	LYS

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
3	2	52/53 (98%)	51 (98%)	1 (2%)	50	79
4	3	33/33 (100%)	31 (94%)	2 (6%)	17	46
5	4	60/63 (95%)	58 (97%)	2 (3%)	33	67
7	B	188/200 (94%)	176 (94%)	12 (6%)	16	44
8	C	175/198 (88%)	172 (98%)	3 (2%)	53	82
9	D	170/171 (99%)	166 (98%)	4 (2%)	43	75
10	E	113/120 (94%)	109 (96%)	4 (4%)	32	66
11	F	95/111 (86%)	92 (97%)	3 (3%)	34	68
12	G	125/128 (98%)	124 (99%)	1 (1%)	73	90
13	H	108/109 (99%)	106 (98%)	2 (2%)	50	79
14	I	99/100 (99%)	98 (99%)	1 (1%)	68	89
15	J	89/91 (98%)	85 (96%)	4 (4%)	24	58
16	K	87/97 (90%)	85 (98%)	2 (2%)	44	76
17	L	103/105 (98%)	99 (96%)	4 (4%)	28	63
18	M	96/98 (98%)	92 (96%)	4 (4%)	26	60
19	N	81/82 (99%)	80 (99%)	1 (1%)	63	86
20	O	71/72 (99%)	70 (99%)	1 (1%)	59	85
21	P	63/63 (100%)	61 (97%)	2 (3%)	34	68
22	Q	71/76 (93%)	67 (94%)	4 (6%)	19	50
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%)	63 (97%)	2 (3%)	35	69
27	X	92/102 (90%)	90 (98%)	2 (2%)	45	77
30	c	218/220 (99%)	217 (100%)	1 (0%)	81	93
31	d	165/166 (99%)	162 (98%)	3 (2%)	51	80
32	e	155/155 (100%)	153 (99%)	2 (1%)	61	86
33	f	146/147 (99%)	139 (95%)	7 (5%)	23	55
34	g	140/142 (99%)	134 (96%)	6 (4%)	26	60
35	h	45/112 (40%)	42 (93%)	3 (7%)	15	43
36	i	118/118 (100%)	115 (98%)	3 (2%)	42	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	j	103/103 (100%)	99 (96%)	4 (4%)	28	63
38	k	108/108 (100%)	107 (99%)	1 (1%)	70	90
39	l	111/111 (100%)	109 (98%)	2 (2%)	51	80
40	m	96/101 (95%)	94 (98%)	2 (2%)	47	77
41	n	84/85 (99%)	80 (95%)	4 (5%)	23	55
42	o	99/102 (97%)	96 (97%)	3 (3%)	36	70
43	p	85/86 (99%)	85 (100%)	0	100	100
44	q	84/84 (100%)	83 (99%)	1 (1%)	63	86
45	r	88/88 (100%)	87 (99%)	1 (1%)	65	88
46	s	78/87 (90%)	76 (97%)	2 (3%)	40	73
47	t	83/85 (98%)	82 (99%)	1 (1%)	63	86
48	u	79/80 (99%)	77 (98%)	2 (2%)	42	74
49	v	60/64 (94%)	58 (97%)	2 (3%)	33	67
50	w	69/70 (99%)	67 (97%)	2 (3%)	37	71
51	x	54/56 (96%)	53 (98%)	1 (2%)	50	79
52	y	54/54 (100%)	53 (98%)	1 (2%)	50	79
53	z	46/50 (92%)	45 (98%)	1 (2%)	45	77
All	All	4616/4840 (95%)	4495 (97%)	121 (3%)	41	73

5 of 121 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	R	36	ASN
46	s	72	THR
32	e	194	LYS
46	s	2	ASN
51	x	8	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
30	c	4	GLN
35	h	33	GLN
49	v	57	HIS
30	c	53	HIS

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Mol	Chain	Res	Type
33	f	24	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	W	9/15 (60%)	2 (22%)	0
28	a	2889/2893 (99%)	536 (18%)	0
29	b	114/115 (99%)	14 (12%)	0
6	A	1535/1537 (99%)	272 (17%)	12 (0%)
All	All	4547/4560 (99%)	824 (18%)	12 (0%)

5 of 824 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	A	6	C
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	618	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	$\#\|Z\|>2$
28	2MA	a	2492	28,56,54	22,25,26	1.31	1 (4%)	33,37,40	2.02	7 (21%)
6	2MG	A	1204	6,54	23,26,27	2.57	4 (17%)	32,38,41	2.09	10 (31%)
28	G7M	a	2058	28	23,26,27	2.16	5 (21%)	35,39,42	1.84	7 (20%)
6	MA6	A	1515	6	23,26,27	1.16	2 (8%)	34,38,41	2.25	9 (26%)
6	MA6	A	1516	6	23,26,27	1.16	3 (13%)	34,38,41	2.28	9 (26%)
28	PSU	a	2446	28	18,21,22	1.97	7 (38%)	22,30,33	1.82	4 (18%)
28	OMC	a	2487	28,56	19,22,23	1.72	3 (15%)	26,31,34	1.02	2 (7%)
28	PSU	a	945	28	18,21,22	1.95	7 (38%)	22,30,33	1.86	4 (18%)
28	6MZ	a	2019	28	22,25,26	2.41	3 (13%)	30,36,39	2.33	10 (33%)
6	2MG	A	1513	6	23,26,27	2.57	4 (17%)	32,38,41	2.09	9 (28%)
28	1MG	a	736	28	22,26,27	2.50	5 (22%)	33,39,42	1.99	7 (21%)
6	G7M	A	524	6,54	23,26,27	2.17	5 (21%)	35,39,42	1.80	7 (20%)
28	PSU	a	2594	28	18,21,22	1.93	7 (38%)	22,30,33	1.77	4 (18%)
39	4D4	l	82	39	9,11,12	0.83	0	8,13,15	1.62	2 (25%)
28	PSU	a	2569	28	18,21,22	1.98	8 (44%)	22,30,33	1.87	4 (18%)
28	PSU	a	1900	28	18,21,22	1.93	7 (38%)	22,30,33	1.82	3 (13%)
17	D2T	L	89	17	7,9,10	1.26	1 (14%)	6,11,13	1.52	1 (16%)
28	3TD	a	1904	28	18,22,23	2.71	7 (38%)	22,32,35	1.73	2 (9%)
6	PSU	A	513	6	18,21,22	1.98	8 (44%)	22,30,33	1.81	5 (22%)
16	IAS	K	118	16	6,7,8	1.80	1 (16%)	6,8,10	2.36	1 (16%)
28	OMU	a	2541	28	19,22,23	2.56	7 (36%)	26,31,34	1.73	5 (19%)
28	PSU	a	2493	28,54	18,21,22	1.96	7 (38%)	22,30,33	1.81	3 (13%)
39	MS6	l	83	39	5,7,8	0.50	0	2,7,9	1.71	1 (50%)
28	2MG	a	2434	28	23,26,27	2.58	6 (26%)	32,38,41	2.02	11 (34%)
28	H2U	a	2438	28	18,21,22	4.27	5 (27%)	21,30,33	5.18	7 (33%)
6	UR3	A	1495	6	19,22,23	2.54	7 (36%)	26,32,35	1.30	2 (7%)
31	MEQ	d	153	31	8,9,10	0.84	0	5,10,12	0.60	0
6	5MC	A	964	6	18,22,23	1.86	5 (27%)	26,32,35	1.33	2 (7%)
28	PSU	a	737	28,56	18,21,22	1.95	7 (38%)	22,30,33	1.78	3 (13%)
6	2MG	A	963	6	23,26,27	2.56	4 (17%)	32,38,41	2.08	11 (34%)
6	4OC	A	1399	6	20,23,24	2.26	4 (20%)	26,32,35	1.00	2 (7%)
28	PSU	a	1906	28	18,21,22	1.95	7 (38%)	22,30,33	1.81	3 (13%)
28	5MU	a	1928	28,54	19,22,23	2.43	7 (36%)	28,32,35	3.81	10 (35%)
28	OMG	a	2240	28,54	23,26,27	2.35	6 (26%)	33,38,41	1.81	10 (30%)

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

The worst 5 of 160 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	a	2019	6MZ	C6-N6	10.35	1.45	1.34
28	a	2438	H2U	O4-C4	10.10	1.43	1.23
6	A	1513	2MG	O6-C6	9.21	1.41	1.23
6	A	1204	2MG	O6-C6	9.18	1.41	1.23
6	A	963	2MG	O6-C6	9.13	1.41	1.23

The worst 5 of 177 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	a	2438	H2U	C4-N3-C2	-16.20	112.35	125.79
28	a	2438	H2U	O2-C2-N1	-10.74	109.63	123.11
28	a	1928	5MU	C4-N3-C2	-8.87	115.86	127.35
28	a	1928	5MU	N3-C2-N1	8.55	126.24	114.89
28	a	1928	5MU	C5-C6-N1	-8.08	115.03	123.34

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	963	2MG	N3-C2-N2-CM2
6	A	1204	2MG	N1-C2-N2-CM2
6	A	1204	2MG	N3-C2-N2-CM2
17	L	89	D2T	CG-CB-SB-CB1
17	L	89	D2T	CA-CB-CG-OD1

There are no ring outliers.

10 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1515	MA6	1	0
28	a	2019	6MZ	2	0
6	A	1513	2MG	1	0
28	a	2594	PSU	4	0
28	a	1904	3TD	1	0
6	A	513	PSU	1	0
16	K	118	IAS	1	0
28	a	2438	H2U	1	0
6	A	1399	4OC	2	0
28	a	2240	OMG	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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
16	K	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	118:IAS	CG	119:GLY	N	1.79

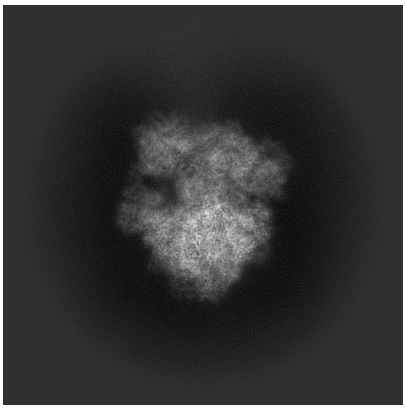
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-55754. These allow visual inspection of the internal detail of the map and identification of artifacts.

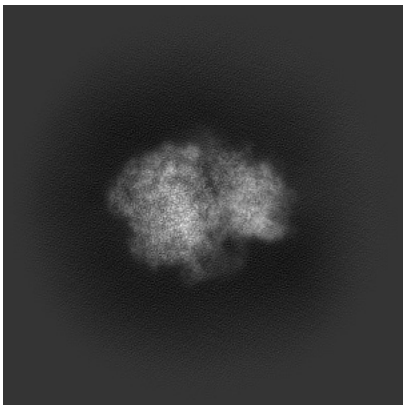
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

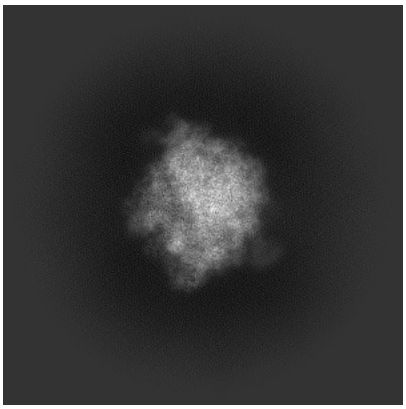
6.1.1 Primary map



X

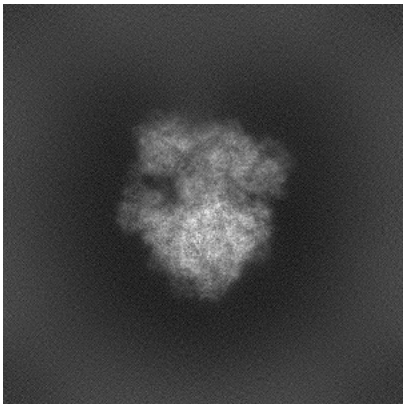


Y

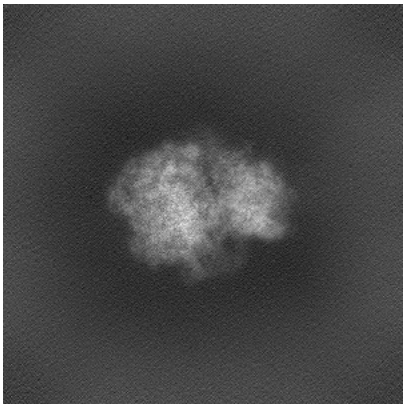


Z

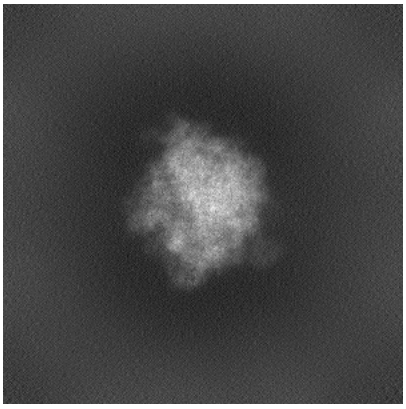
6.1.2 Raw map



X



Y

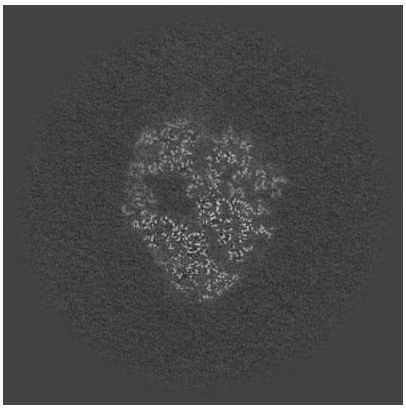


Z

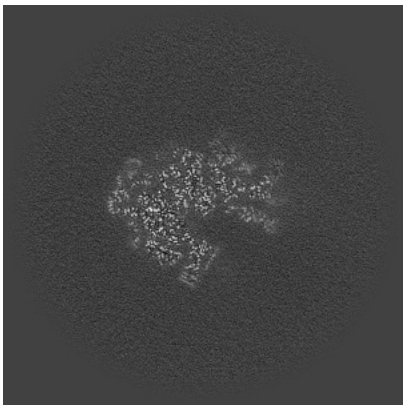
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

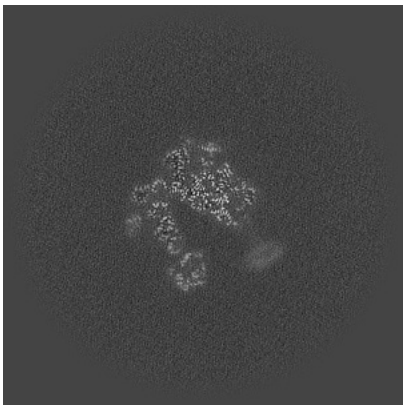
6.2.1 Primary map



X Index: 256

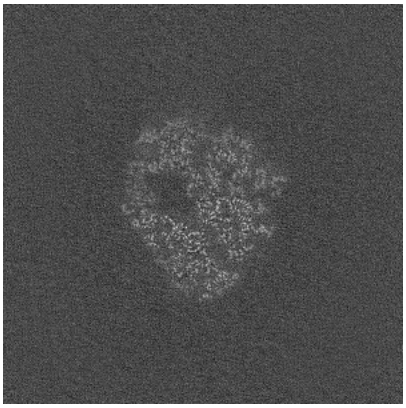


Y Index: 256

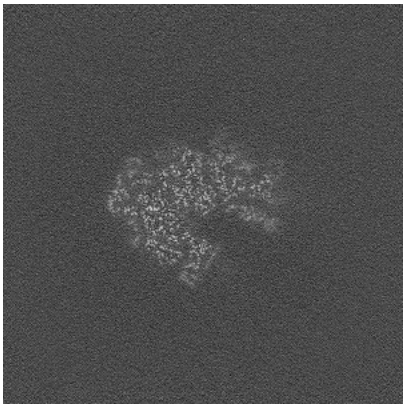


Z Index: 256

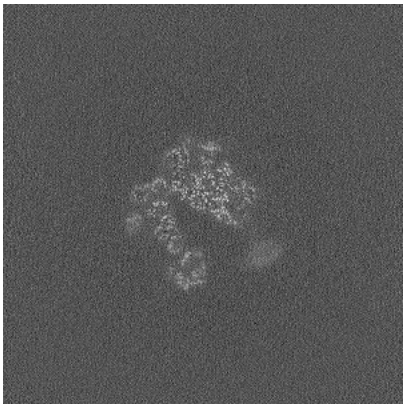
6.2.2 Raw map



X Index: 256



Y Index: 256

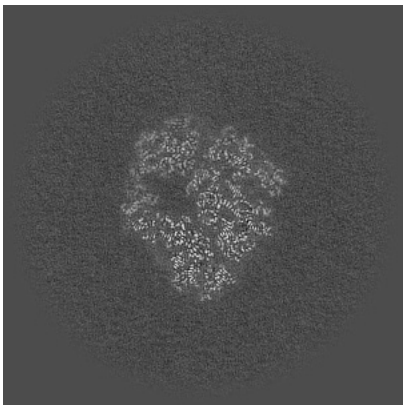


Z Index: 256

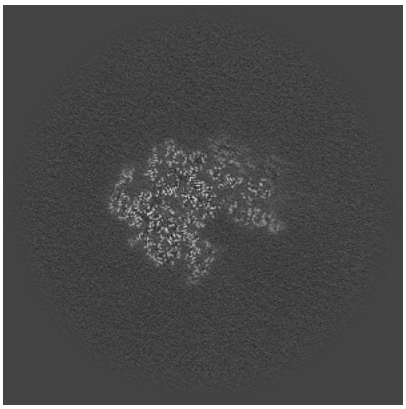
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

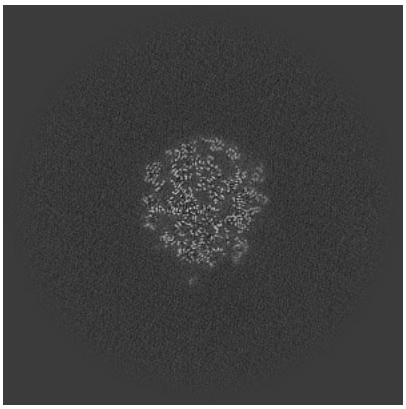
6.3.1 Primary map



X Index: 253

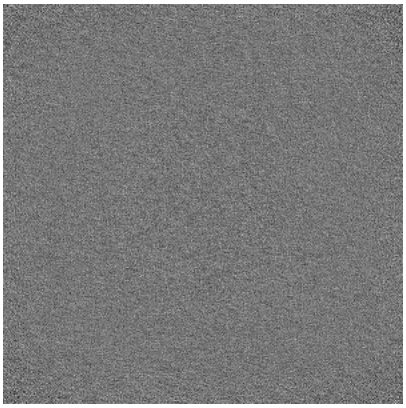


Y Index: 262

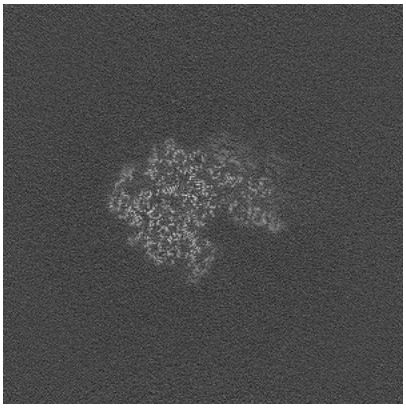


Z Index: 216

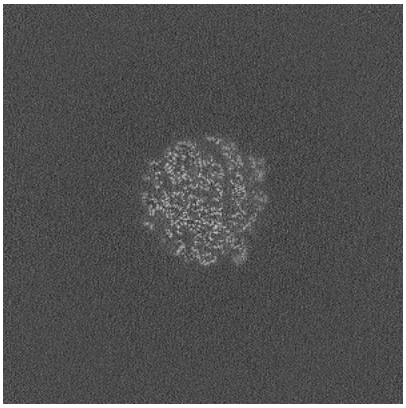
6.3.2 Raw map



X Index: 0



Y Index: 262

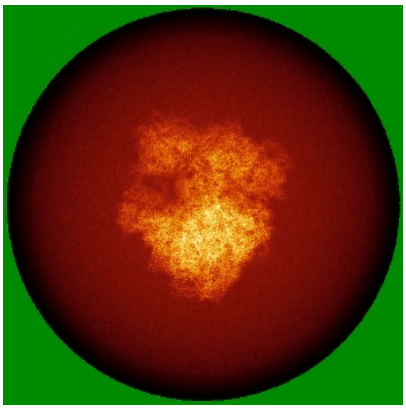


Z Index: 212

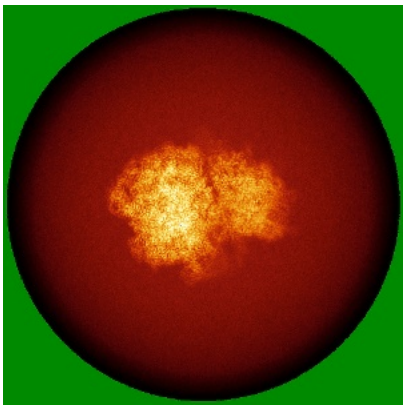
The images above show the largest variance slices of the map in three orthogonal directions.

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

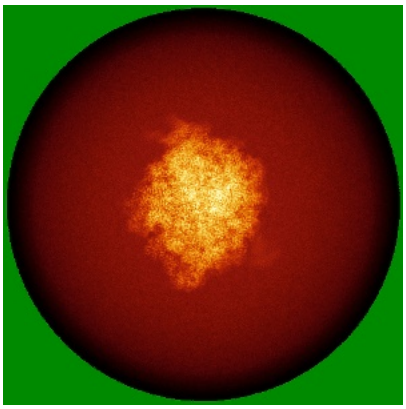
6.4.1 Primary map



X

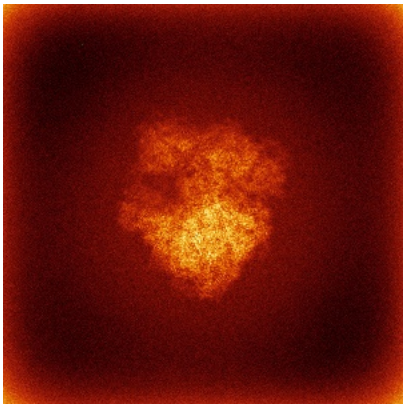


Y

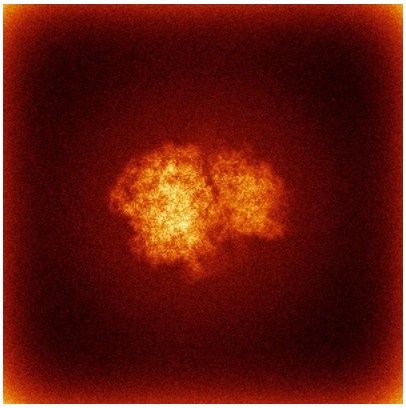


Z

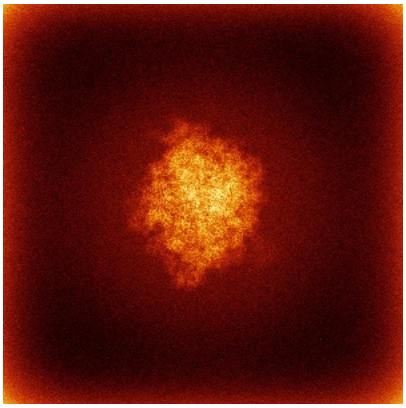
6.4.2 Raw map



X



Y

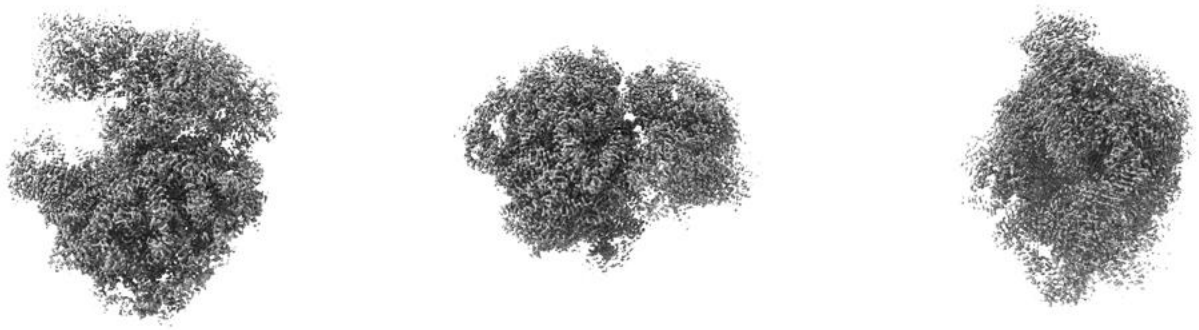


Z

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)

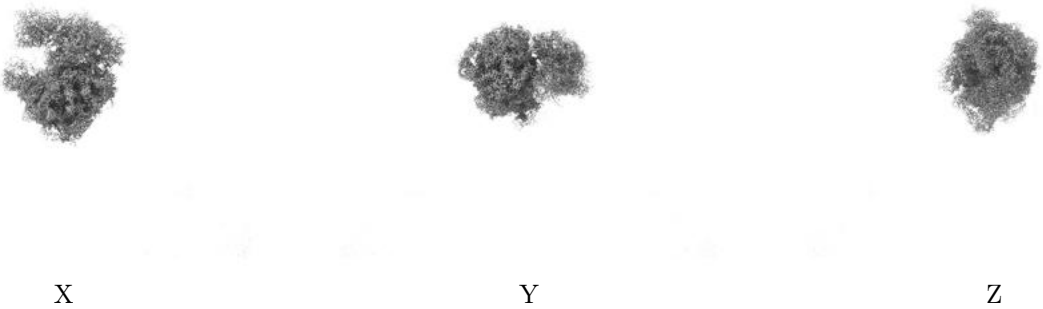
6.5.1 Primary map



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.

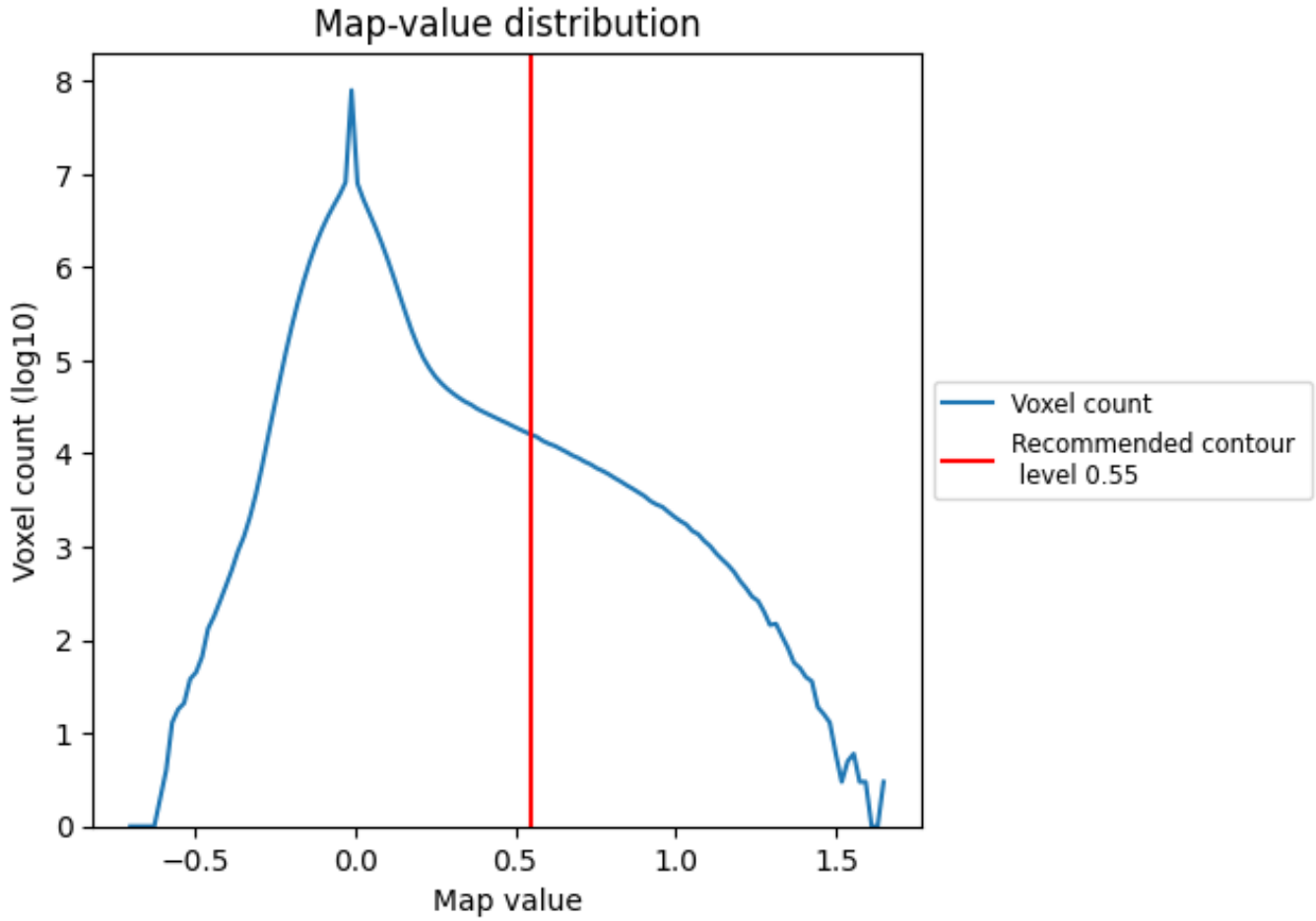
6.6 Mask visualisation (i)

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

7 Map analysis

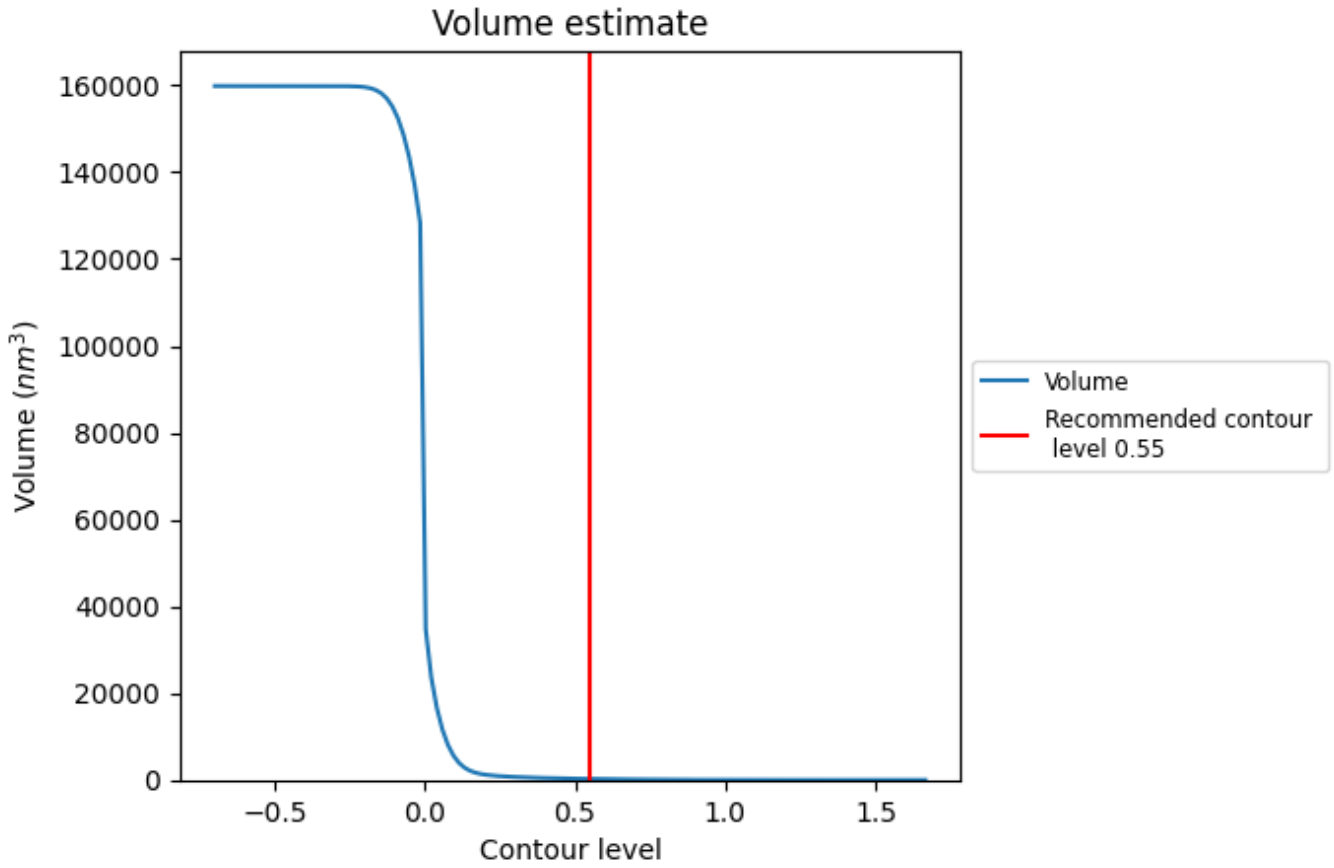
This section contains the results of statistical analysis of the map.

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.

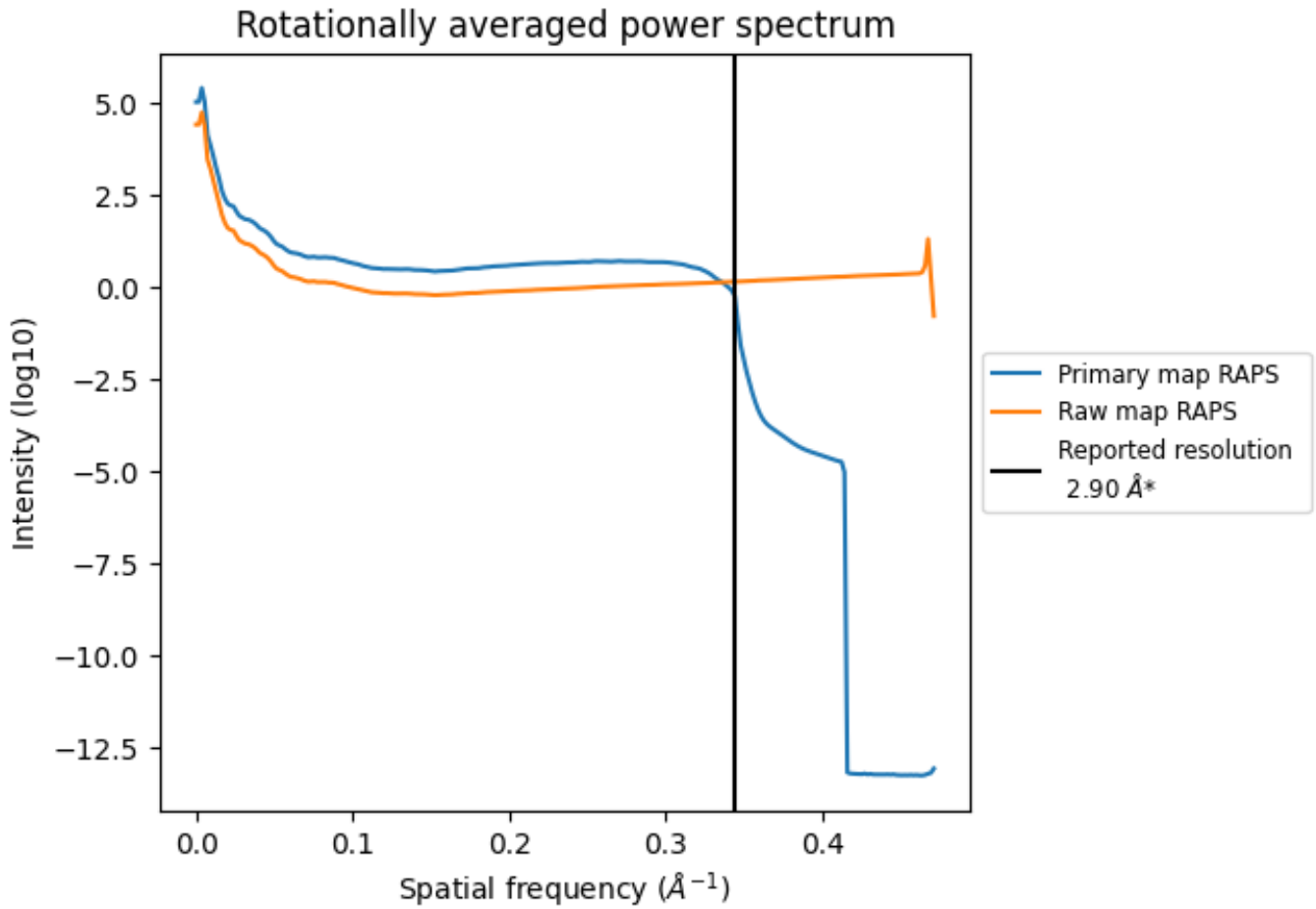
7.2 Volume estimate (i)



The volume at the recommended contour level is 235 nm^3; this corresponds to an approximate mass of 212 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)

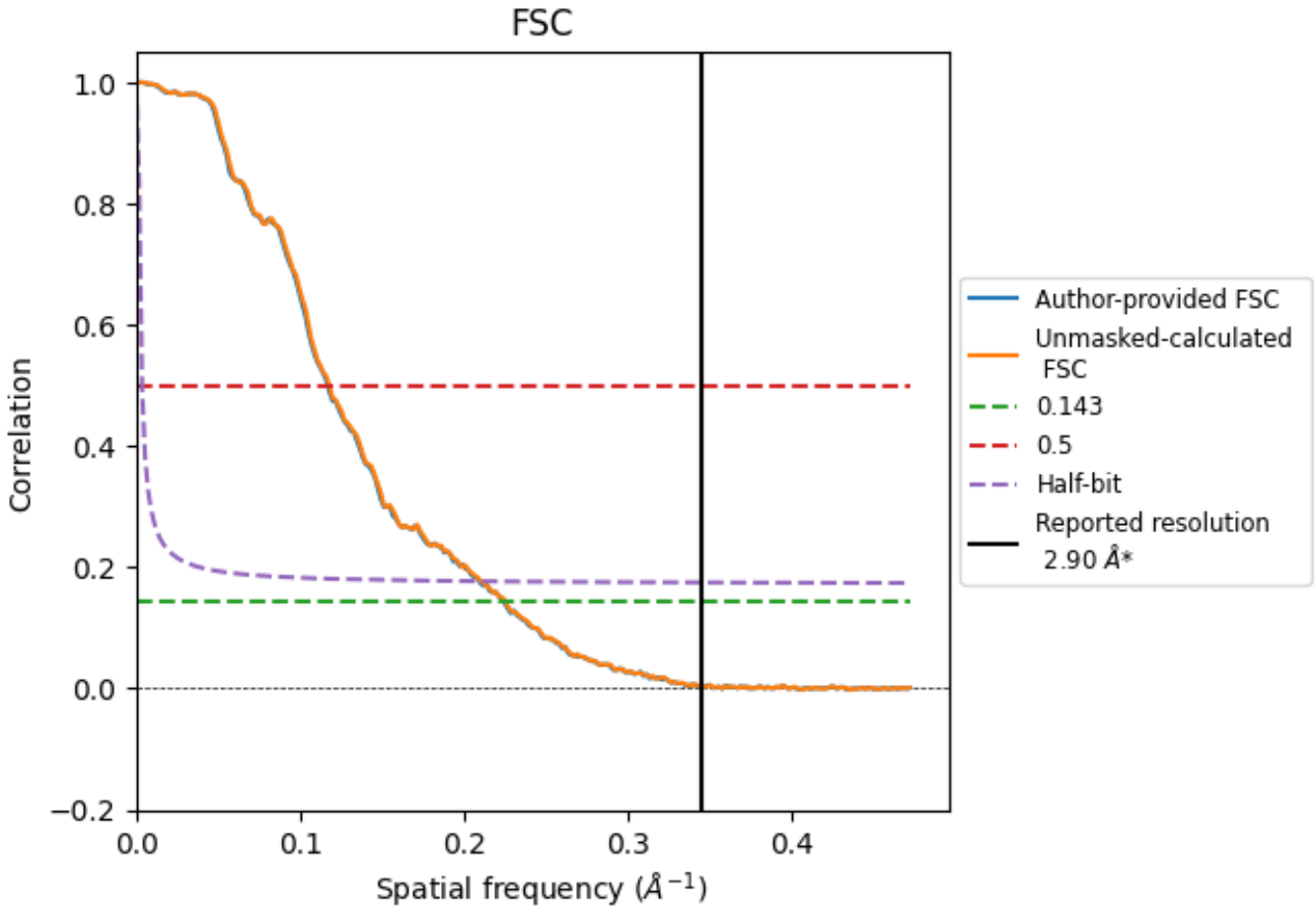


*Reported resolution corresponds to spatial frequency of 0.345 $Å^{-1}$

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	4.46	8.56	4.78
Unmasked-calculated*	4.44	8.48	4.76

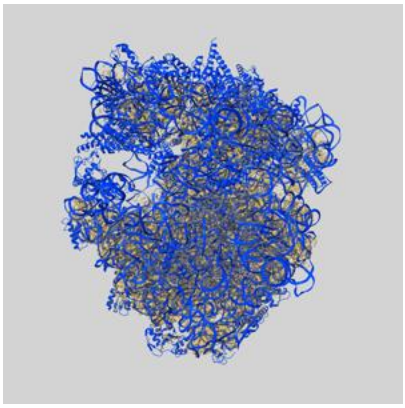
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.46 differs from the reported value 2.9 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.44 differs from the reported value 2.9 by more than 10 %

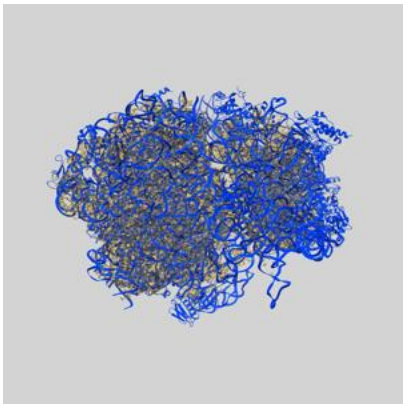
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-55754 and PDB model 9TAP. Per-residue inclusion information can be found in section 3 on page 15.

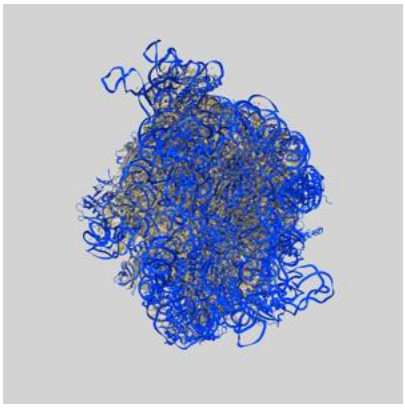
9.1 Map-model overlay



X



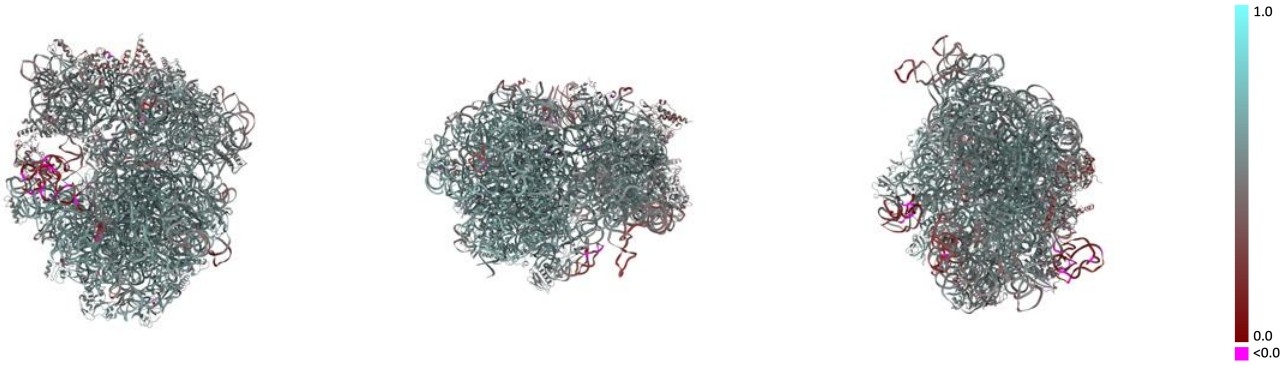
Y



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.

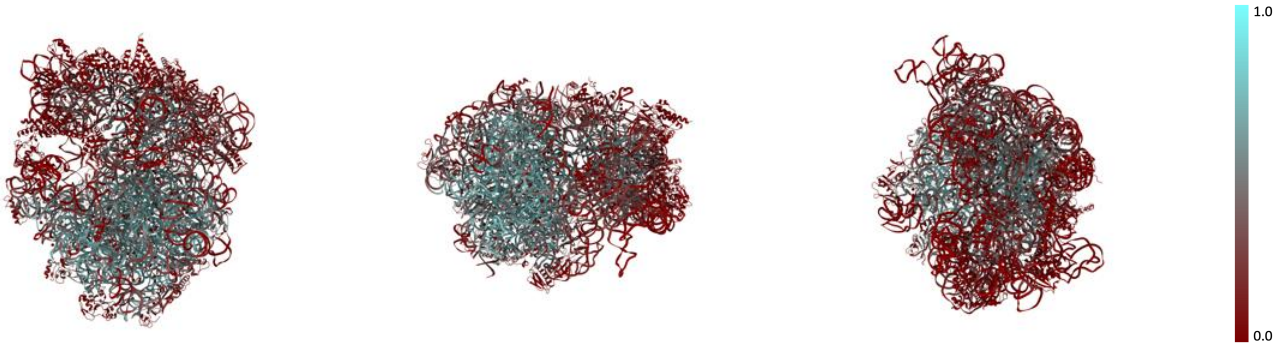
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

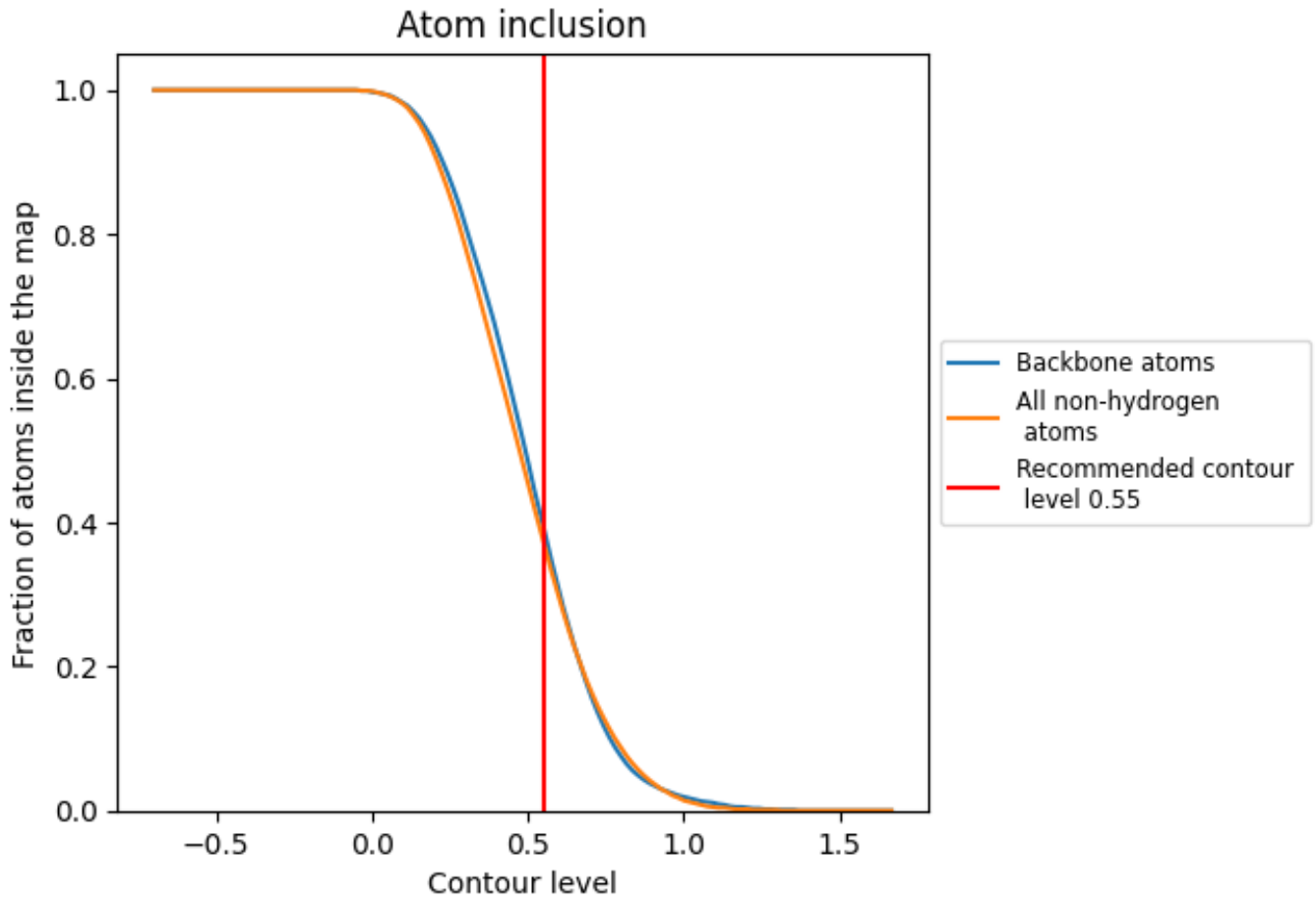
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.55).

9.4 Atom inclusion (i)



At the recommended contour level, 39% of all backbone atoms, 37% 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	0.3720	0.5460
0	0.2760	0.5760
1	0.6130	0.6100
2	0.5000	0.6130
3	0.3480	0.6010
4	0.0000	0.3230
A	0.2820	0.5260
B	0.0000	0.3970
C	0.0850	0.5210
D	0.0290	0.4950
E	0.2120	0.5650
F	0.0000	0.4470
G	0.0030	0.4730
H	0.1400	0.5590
I	0.0490	0.4970
J	0.0670	0.5010
K	0.0640	0.5220
L	0.1070	0.5630
M	0.0160	0.4940
N	0.0540	0.5200
O	0.1770	0.5400
P	0.0970	0.5320
Q	0.0770	0.5390
R	0.0000	0.4540
S	0.0030	0.4950
T	0.1140	0.5440
W	0.0270	0.4660
X	0.1210	0.5390
a	0.5300	0.5600
b	0.3230	0.5570
c	0.4720	0.6050
d	0.4630	0.5980
e	0.3060	0.5860
f	0.0180	0.4670
g	0.0810	0.5390



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
h	0.0000	0.2890
i	0.4670	0.6050
j	0.3350	0.5950
k	0.3890	0.5870
l	0.3210	0.5910
m	0.5190	0.6080
n	0.2110	0.5660
o	0.3670	0.5960
p	0.5390	0.6060
q	0.3430	0.5960
r	0.4550	0.5960
s	0.2890	0.5850
t	0.1650	0.5520
u	0.2260	0.5650
v	0.4840	0.6140
w	0.3650	0.5980
x	0.1660	0.5510
y	0.3970	0.5940
z	0.4660	0.6010