



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 12:08 PM UTC

PDB ID : 3JAI / pdb_00003jai
EMDB ID : EMD-3040
Title : Structure of a mammalian ribosomal termination complex with ABCE1, eRF1(AAQ), and the UGA stop codon
Authors : Brown, A.; Shao, S.; Murray, J.; Hegde, R.S.; Ramakrishnan, V.
Deposited on : 2015-06-10
Resolution : 3.65 Å (reported)
Based on initial models : 1DT9, 4V51, 3BK7, 3J92, 3J7P

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

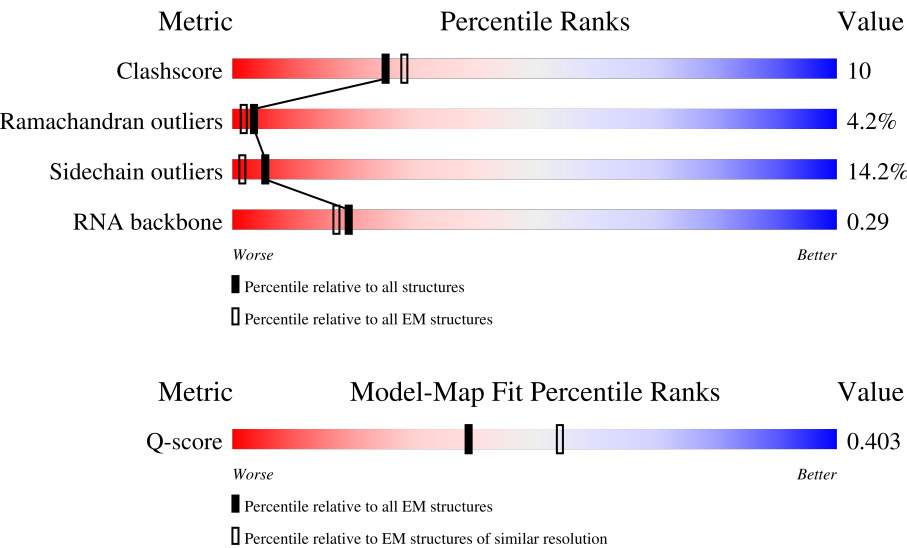
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.65 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.



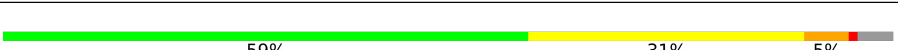
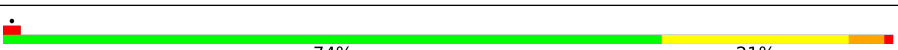
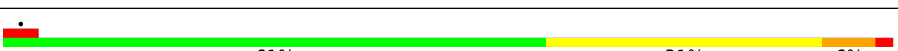
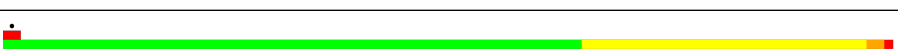
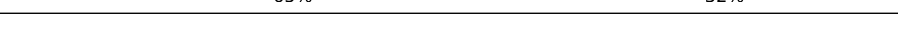
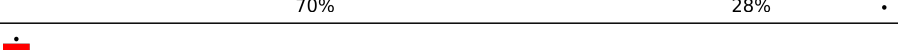
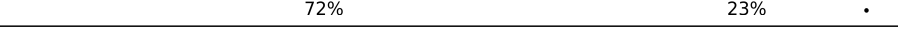
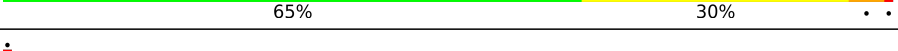
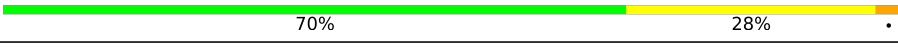
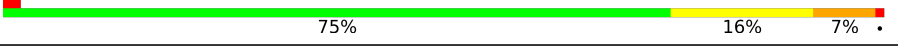
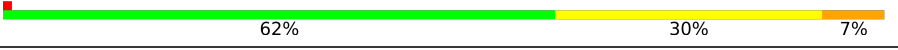
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	9087 (3.33 - 4.33)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	244	61%33%6%
2	B	394	65%27%6%
3	C	361	66%27%7%

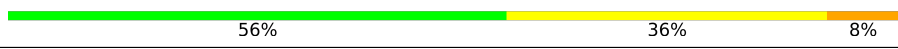
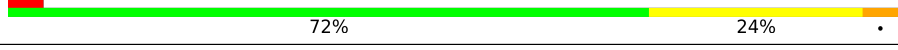
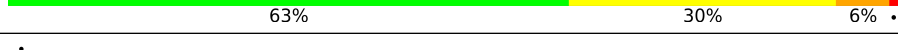
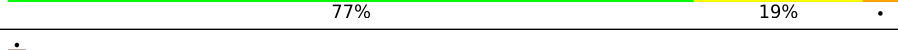
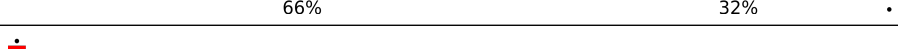
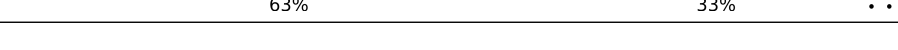
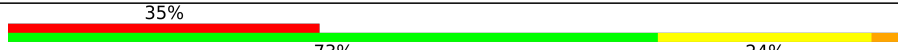
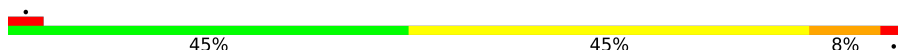
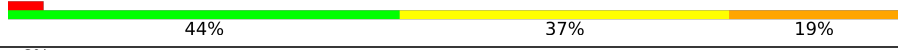
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Mol	Chain	Length	Quality of chain
4	D	292	
5	E	248	
6	F	225	
7	G	241	
8	H	190	
9	I	213	
10	J	169	
11	L	210	
12	M	138	
13	N	203	
14	O	199	
15	P	153	
16	Q	187	
17	R	180	
18	S	175	
19	T	159	
20	U	99	
21	V	131	
22	W	63	
23	X	119	
24	Y	134	
25	Z	135	
26	a	147	
27	b	75	
28	c	94	

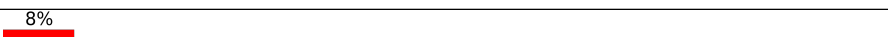
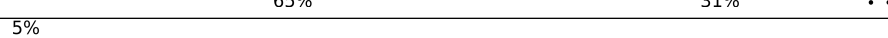
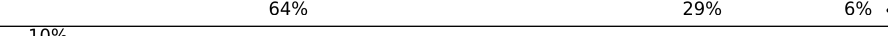
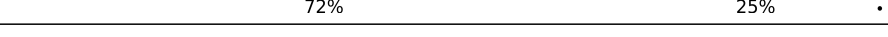
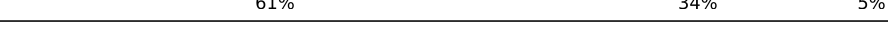
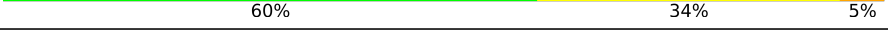
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Mol	Chain	Length	Quality of chain
29	d	107	
30	e	128	
31	f	109	
32	g	114	
33	h	122	
34	i	102	
35	j	86	
36	k	69	
37	l	50	
38	m	52	
39	n	23	
40	o	104	
41	p	91	
42	r	125	
43	s	198	
44	t	163	
45	1	15	
46	2	76	
47	3	75	
48	5	3662	
49	7	120	
50	8	156	
51	9	1719	
52	AA	208	
53	BB	213	

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Mol	Chain	Length	Quality of chain
54	CC	218	
55	DD	227	
56	EE	262	
57	FF	191	
58	GG	237	
59	HH	189	
60	II	206	
61	JJ	185	
62	KK	98	
63	LL	152	
64	MM	124	
65	NN	150	
66	OO	136	
67	PP	127	
68	QQ	141	
69	RR	129	
70	SS	137	
71	TT	141	
72	UU	104	
73	VV	83	
74	WW	129	
75	XX	141	
76	YY	126	
77	ZZ	75	
78	aa	98	

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Mol	Chain	Length	Quality of chain
79	bb	83	
80	cc	61	
81	dd	53	
82	ee	57	
83	ff	68	
84	gg	313	
85	hh	12	
86	ii	416	
87	jj	594	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
89	ZN	ff	200	-	-	X	-
89	ZN	m	201	-	-	X	-
90	SF4	jj	600	-	-	X	-
90	SF4	jj	601	-	-	X	-

2 Entry composition

There are 91 unique types of molecules in this entry. The entry contains 226453 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 uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	394	Total	C	N	O	S	0	0
			3148	2007	591	537	13		

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	361	Total	C	N	O	S	0	0
			2875	1808	576	477	14		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	361	LYS	-	expression tag	UNP G1SVW5
C	362	SER	-	expression tag	UNP G1SVW5

- Molecule 4 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	292	Total	C	N	O	S	0	0
			2386	1509	437	426	14		

- Molecule 5 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	236	Total	C	N	O	S	0	0
			1898	1215	362	318	3		

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	241	Total	C	N	O	S	0	0
			1934	1233	371	326	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	191	GLY	CYS	conflict	UNP G1STW0

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	204	Total	C	N	O	S	0	0
			1655	1051	319	272	13		

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	169	Total	C	N	O	S	0	0
			1353	855	252	240	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	210	Total	C	N	O	S	0	0
			1703	1065	354	280	4		

- Molecule 12 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 13 is a protein called eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	199	Total	C	N	O	S	0	0
			1638	1056	321	256	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 21 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 24 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	75	Total	C	N	O	S	0	0
			609	378	130	98	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 34 is a protein called eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	125	Total	C	N	O	S	0	0
			1001	621	206	168	6		

- Molecule 43 is a protein called uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	198	Total	C	N	O	S	0	0
			1523	969	265	280	9		

- Molecule 44 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	163	Total	C	N	O	S	0	0
			1238	773	230	230	5		

- Molecule 45 is a protein called peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	1	15	Total	C	N	O	S	0	0
			125	82	20	22	1		

- Molecule 46 is a RNA chain called tRNA(Val).

Mol	Chain	Residues	Atoms					AltConf	Trace
46	2	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

- Molecule 47 is a RNA chain called tRNA(Lys).

Mol	Chain	Residues	Atoms					AltConf	Trace
47	3	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 48 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

- Molecule 49 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 50 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 51 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	9	1719	Total	C	N	O	P	0	0
			36680	16371	6586	12005	1718		

- Molecule 52 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AA	208	Total	C	N	O	S	0	0
			1642	1045	289	300	8		

- Molecule 53 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 54 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CC	218	Total	C	N	O	S	0	0
			1692	1102	287	296	7		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CC	194	ARG	HIS	conflict	UNP G1TUT9
CC	228	GLY	SER	conflict	UNP G1TUT9

- Molecule 55 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	DD	227	Total	C	N	O	S	0	0
			1764	1124	317	315	8		

- Molecule 56 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	EE	262	Total	C	N	O	S	0	0
			2073	1323	384	357	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EE	25	GLY	SER	conflict	UNP G1TK17

- Molecule 57 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	FF	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 58 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	GG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 59 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	HH	189	Total	C	N	O	S	0	0
			1521	969	280	271	1		

- Molecule 60 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	II	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
II	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 61 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	JJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 62 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	KK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 63 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	LL	152	Total	C	N	O	S	0	0
			1238	788	232	212	6		

- Molecule 64 is a protein called eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	MM	124	Total	C	N	O	S	0	0
			958	600	170	179	9		

- Molecule 65 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	NN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 66 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	OO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 67 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	PP	127	Total	C	N	O	S	0	0
			1060	673	201	179	7		

- Molecule 68 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	QQ	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 69 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	RR	129	Total	C	N	O	S	0	0
			1047	658	193	191	5		

- Molecule 70 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SS	137	Total	C	N	O	S	0	0
			1139	714	231	193	1		

- Molecule 71 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	TT	141	Total	C	N	O	S	0	0
			1102	692	212	195	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TT	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 72 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	UU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 73 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	VV	83	Total	C	N	O	S	0	0
			636	394	118	119	5		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
VV	3	ASN	SER	conflict	UNP G1TM82
VV	4	ASP	ASN	conflict	UNP G1TM82
VV	50	PHE	SER	conflict	UNP G1TM82
VV	75	ALA	SER	conflict	UNP G1TM82

- Molecule 74 is a protein called uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	WW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 75 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	XX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 76 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	YY	126	Total	C	N	O	S	0	0
			1023	646	200	172	5		

- Molecule 77 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	ZZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 78 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	aa	98	Total	C	N	O	S	0	0
			781	486	161	129	5		

- Molecule 79 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	bb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 80 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	cc	61	Total	C	N	O	S	0	0
			475	290	92	91	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
cc	18	ILE	LEU	conflict	UNP G1TIB4
cc	20	LYS	ARG	conflict	UNP G1TIB4
cc	40	HIS	ARG	conflict	UNP G1TIB4
cc	42	THR	ILE	conflict	UNP G1TIB4

- Molecule 81 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	dd	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 82 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	ee	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 83 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	ff	62	Total	C	N	O	S	0	0
			520	331	98	85	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ff	?	-	VAL	deletion	UNP G1SK22

- Molecule 84 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	gg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 85 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	hh	12	Total	C	N	O	P	0	0
			257	115	46	84	12		

- Molecule 86 is a protein called eRF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	ii	416	Total	C	N	O	S	0	0
			3280	2087	559	623	11		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ii	183	ALA	GLY	engineered mutation	UNP P62495
ii	184	ALA	GLY	engineered mutation	UNP P62495

- Molecule 87 is a protein called ABCE1.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	jj	577	Total	C	N	O	S	0	0
			4551	2910	780	830	31		

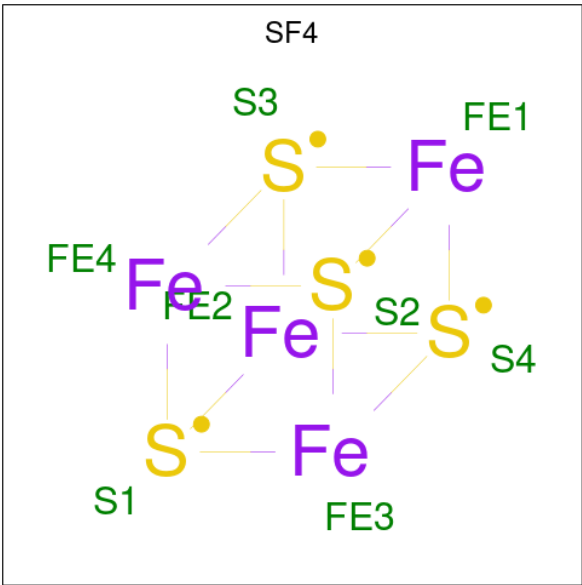
- Molecule 88 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
88	C	1	Total 1	Mg 1	0
88	I	1	Total 1	Mg 1	0
88	P	1	Total 1	Mg 1	0
88	V	1	Total 1	Mg 1	0
88	g	1	Total 1	Mg 1	0
88	5	147	Total 147	Mg 147	0
88	7	5	Total 5	Mg 5	0
88	8	2	Total 2	Mg 2	0
88	9	35	Total 35	Mg 35	0
88	hh	1	Total 1	Mg 1	0

- Molecule 89 is ZINC ION (CCD ID: ZN) (formula: Zn).

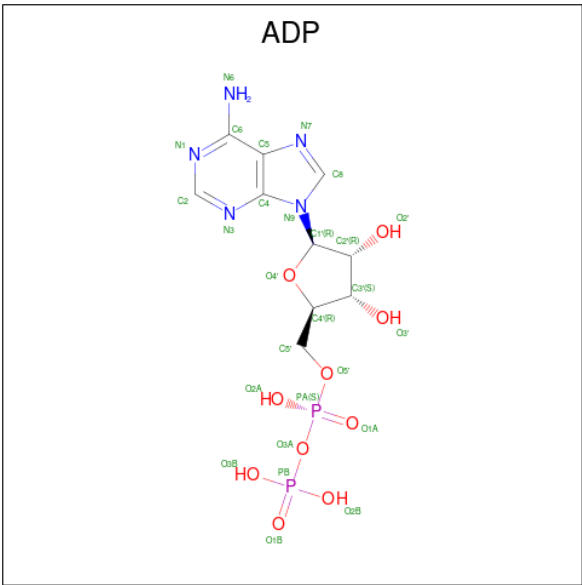
Mol	Chain	Residues	Atoms		AltConf
89	g	1	Total 1	Zn 1	0
89	j	1	Total 1	Zn 1	0
89	m	1	Total 1	Zn 1	0
89	o	1	Total 1	Zn 1	0
89	p	1	Total 1	Zn 1	0
89	aa	1	Total 1	Zn 1	0
89	dd	1	Total 1	Zn 1	0
89	ff	1	Total 1	Zn 1	0

- Molecule 90 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			AltConf
90	jj	1	Total	Fe	S	0
			8	4	4	
90	jj	1	Total	Fe	S	0
			8	4	4	

- Molecule 91 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

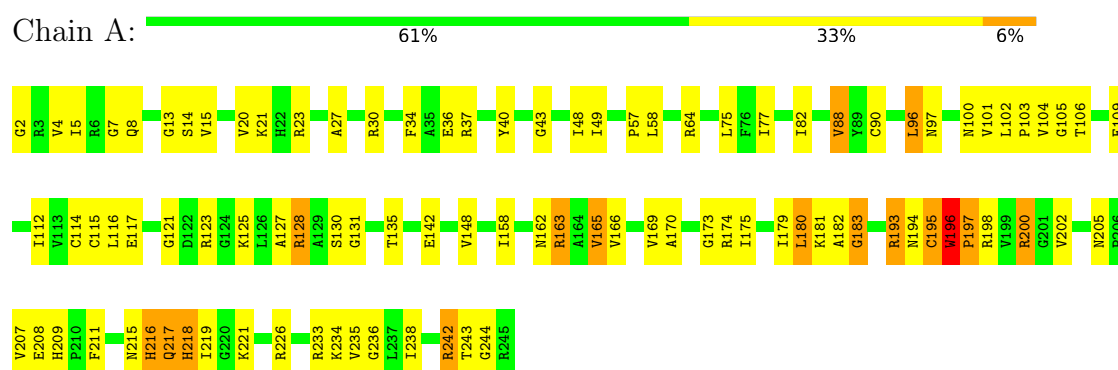


Mol	Chain	Residues	Atoms					AltConf
91	jj	1	Total 27	C 10	N 5	O 10	P 2	0
91	jj	1	Total 27	C 10	N 5	O 10	P 2	0

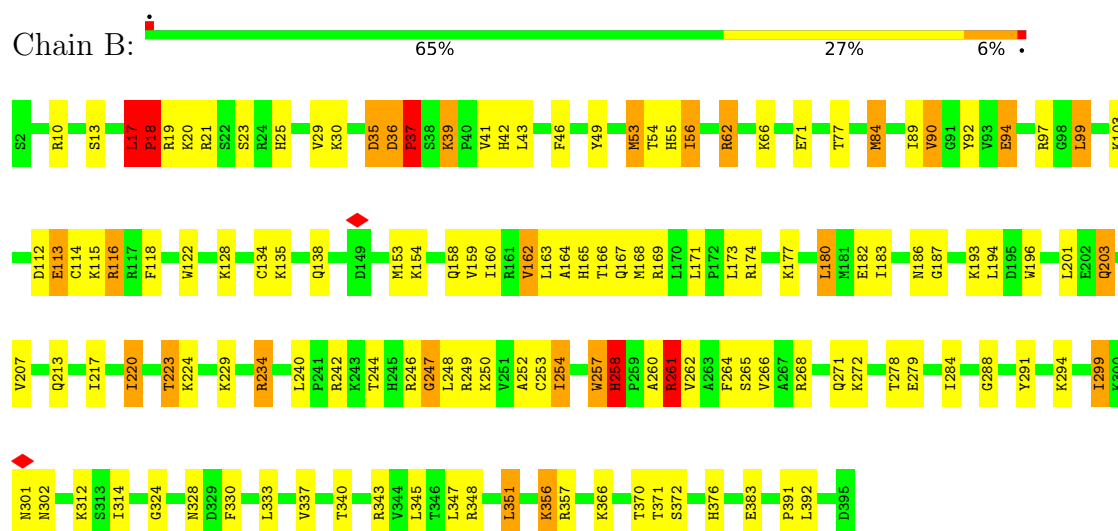
3 Residue-property plots [i](#)

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.

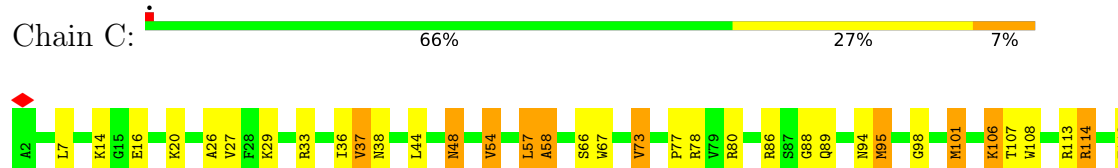
• Molecule 1: uL2

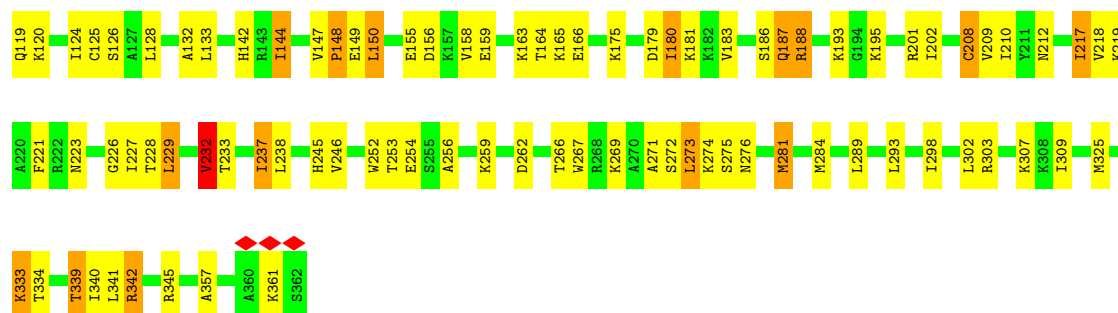


• Molecule 2: uL3

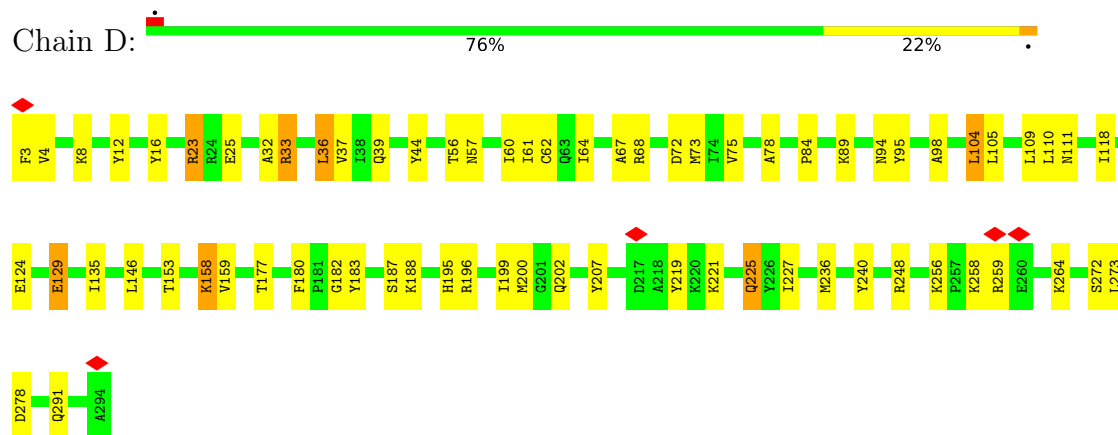


• Molecule 3: uL4

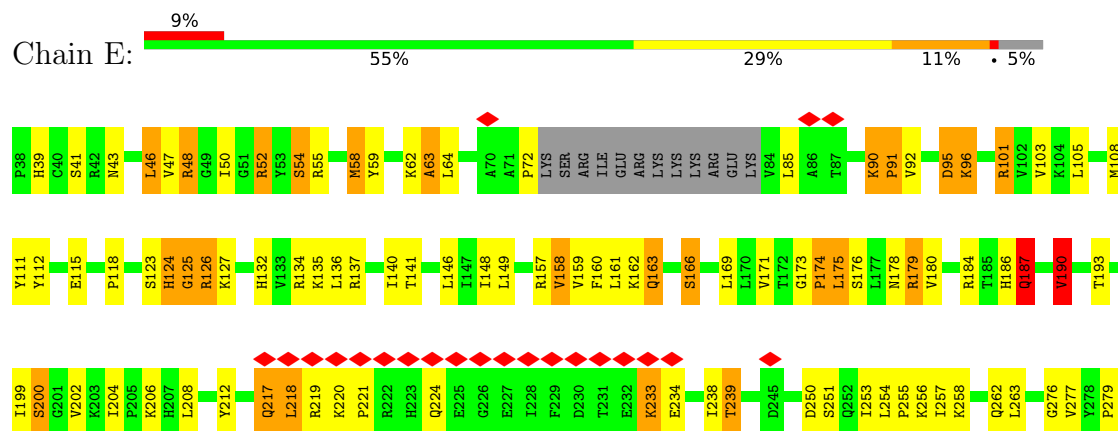




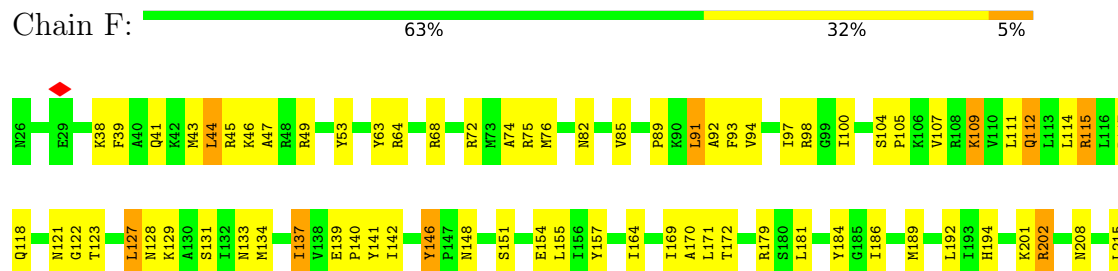
• Molecule 4: uL18

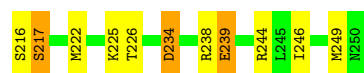


• Molecule 5: eL6

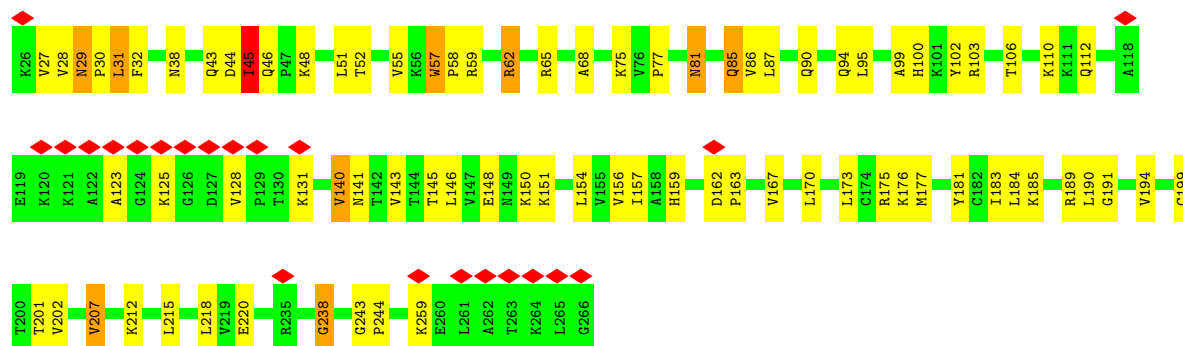


• Molecule 6: uL30

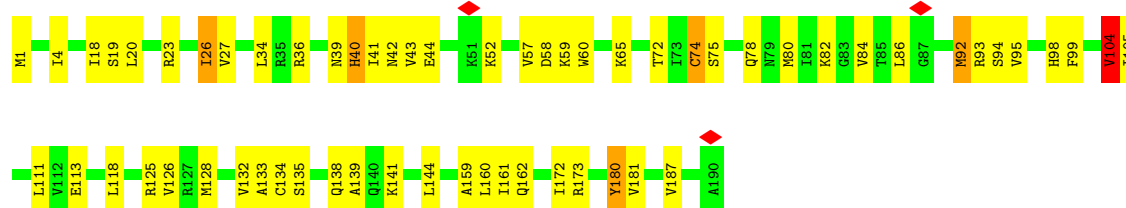




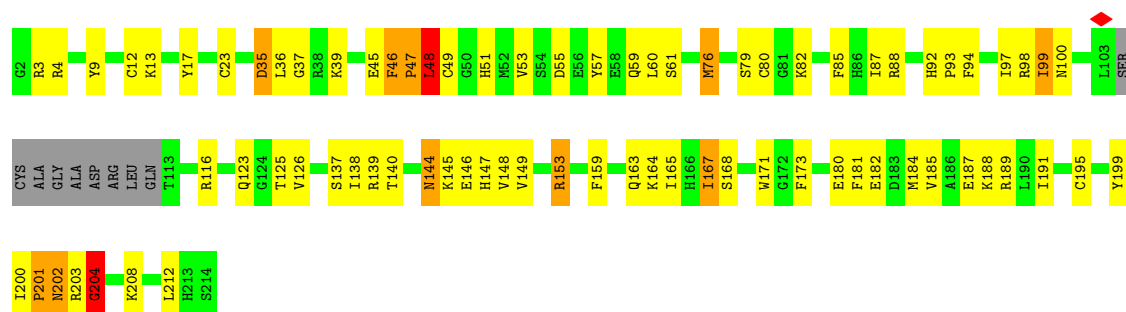
• Molecule 7: eL8



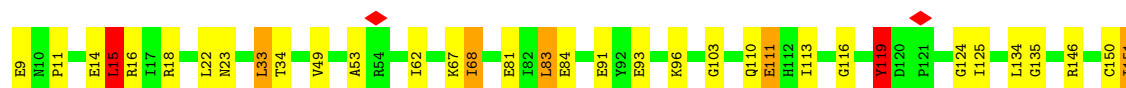
• Molecule 8: uL6



• Molecule 9: uL16

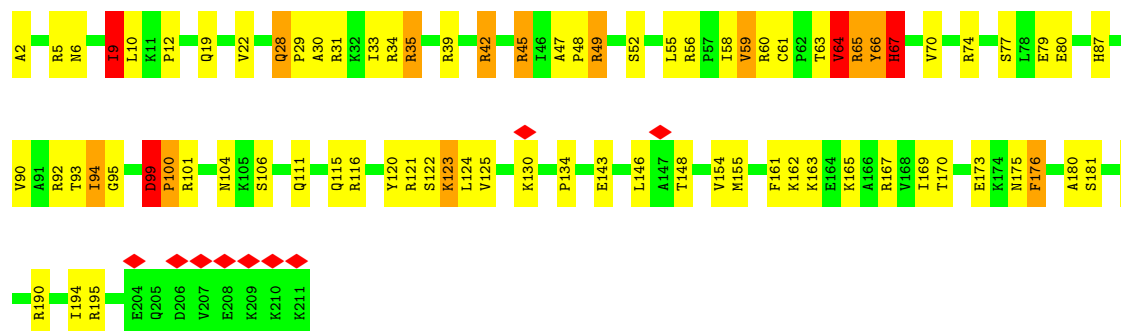


• Molecule 10: uL5

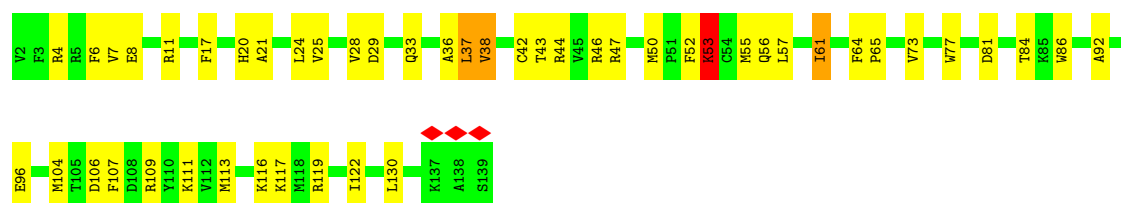




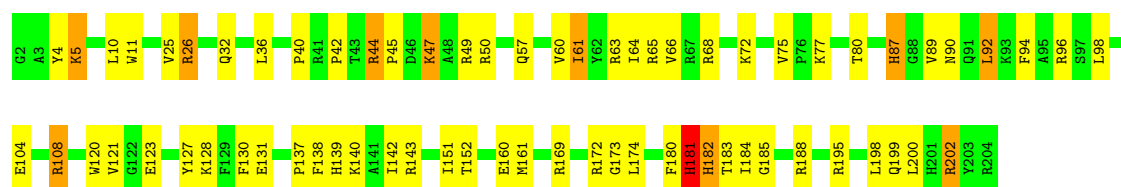
• Molecule 11: eL13



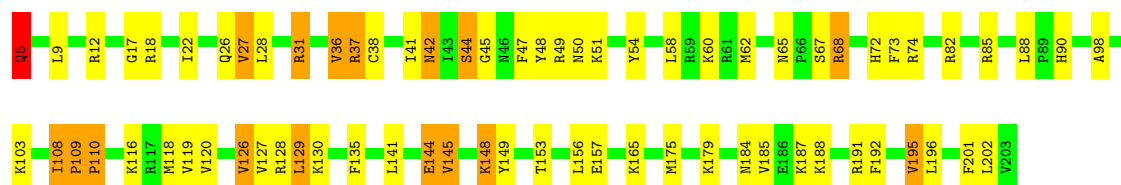
• Molecule 12: eL14



• Molecule 13: eL15



• Molecule 14: uL13



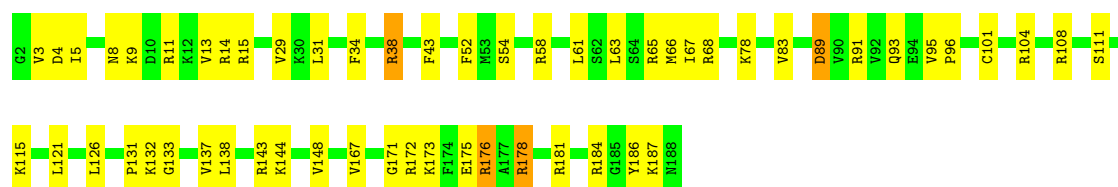
• Molecule 15: uL22

Chain P:  71% 24% 6%



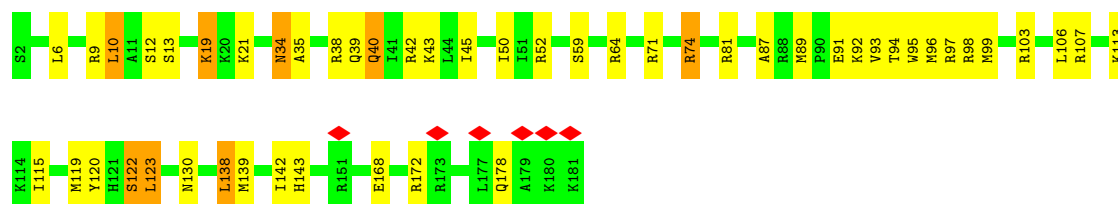
• Molecule 16: eL18

Chain Q:  70% 28% 2%



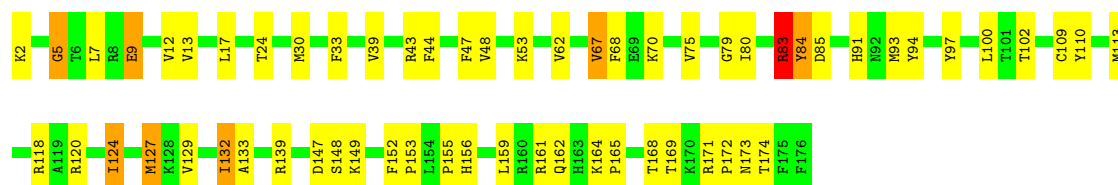
• Molecule 17: eL19

Chain R:  72% 23% 5%



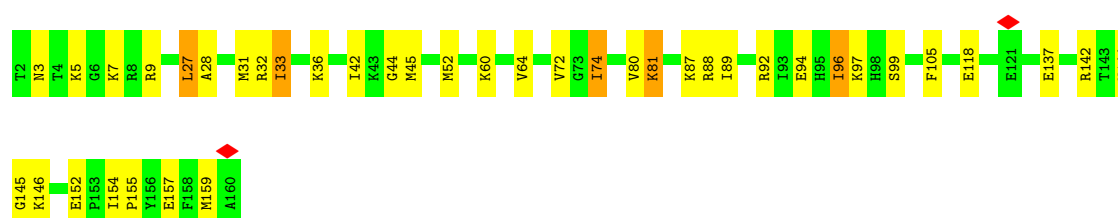
• Molecule 18: eL20

Chain S:  65% 30% 5%



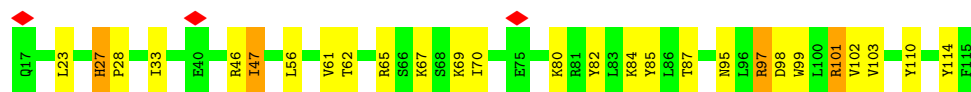
• Molecule 19: eL21

Chain T:  75% 22% 3%



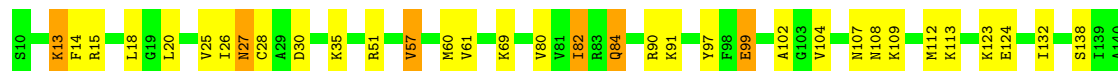
- Molecule 20: eL22

Chain U: 



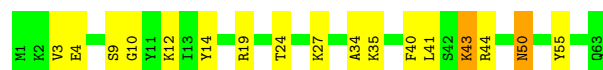
- Molecule 21: uL14

Chain V: 



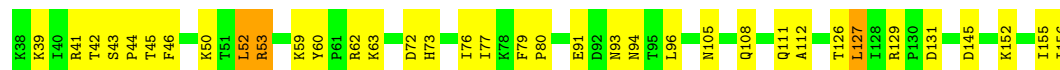
- Molecule 22: eL24

Chain W: 



- Molecule 23: uL23

Chain X: 



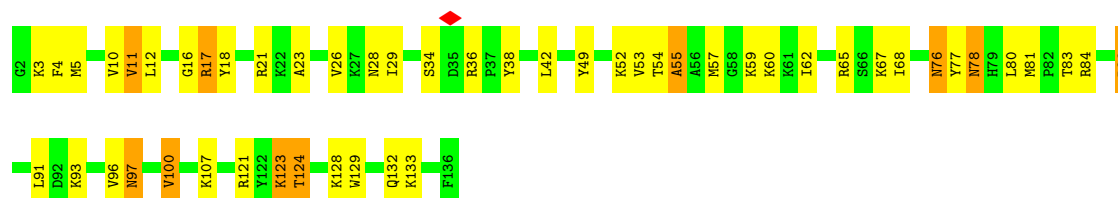
- Molecule 24: uL24

Chain Y: 



- Molecule 25: eL27

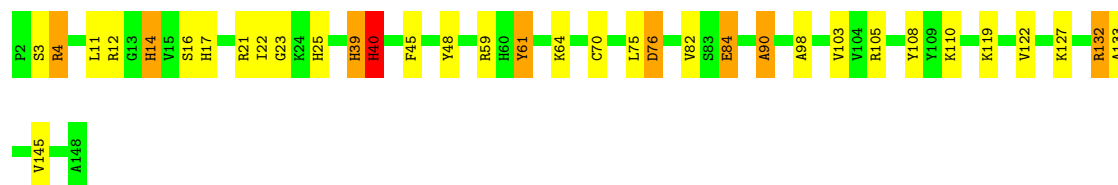
Chain Z: 



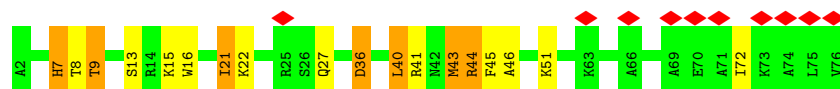
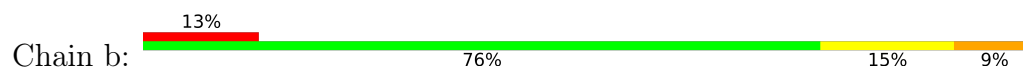
- Molecule 26: uL15

Chain a: 

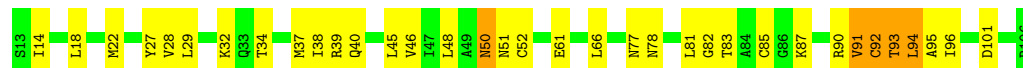




• Molecule 27: eL29



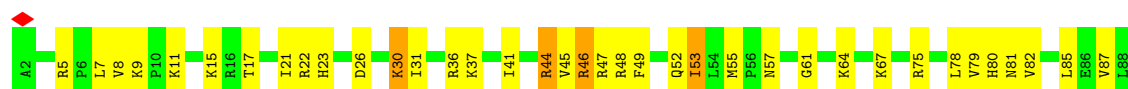
• Molecule 28: eL30



• Molecule 29: eL31

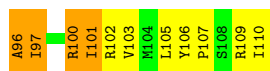


• Molecule 30: eL32

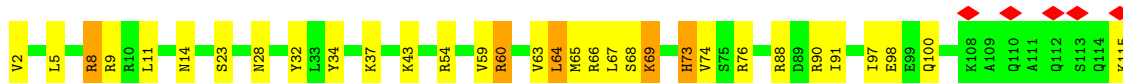


• Molecule 31: eL33

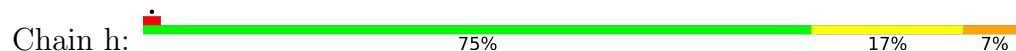




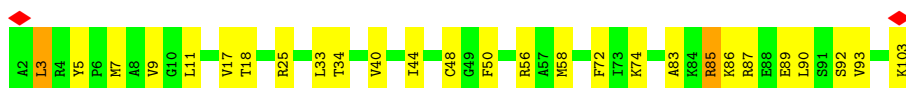
• Molecule 32: eL34



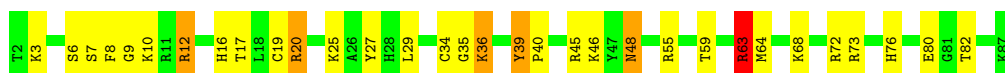
• Molecule 33: uL29



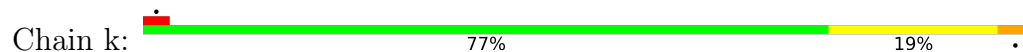
• Molecule 34: eL36



• Molecule 35: eL37



• Molecule 36: eL38

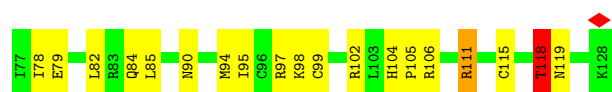


• Molecule 37: eL39

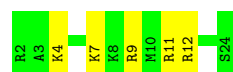
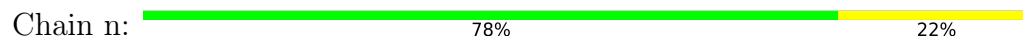


• Molecule 38: eL40

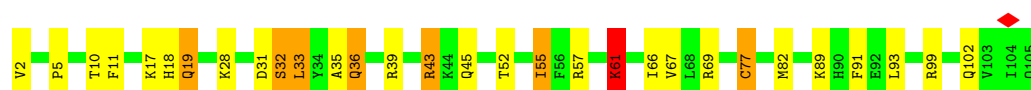




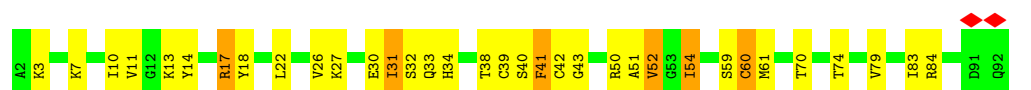
• Molecule 39: eL41



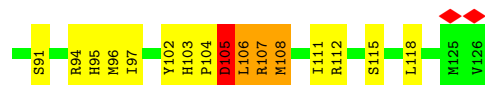
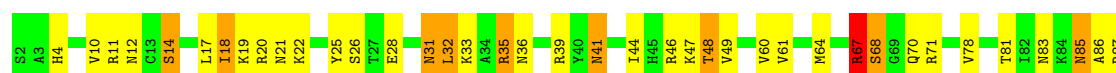
• Molecule 40: eL42



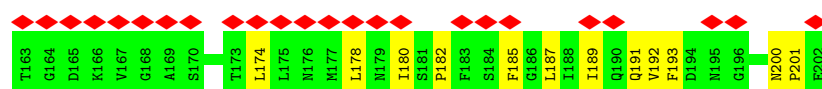
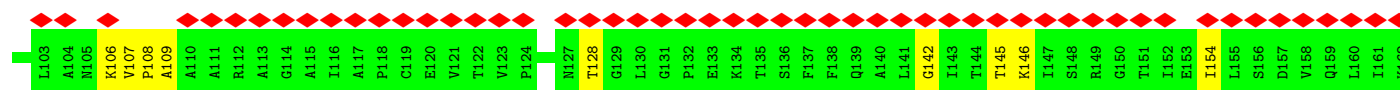
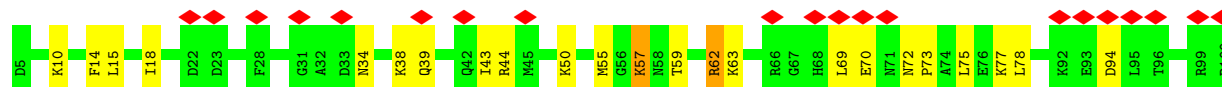
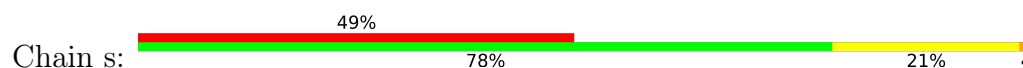
• Molecule 41: eL43



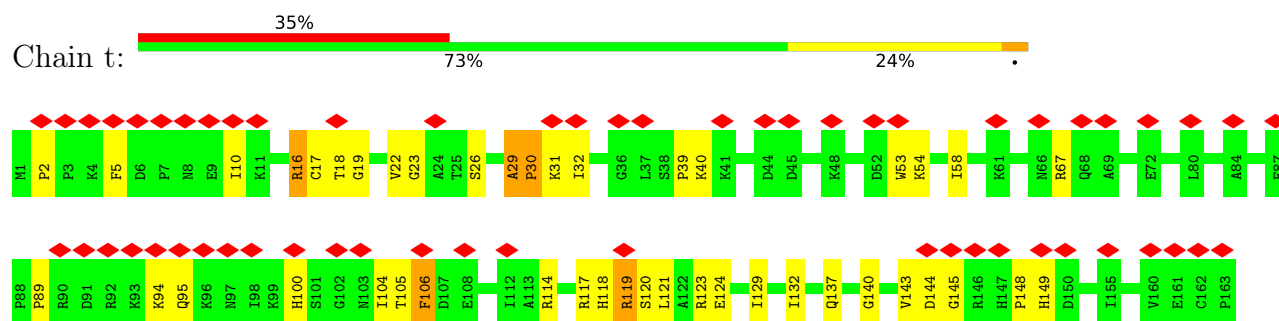
• Molecule 42: eL28



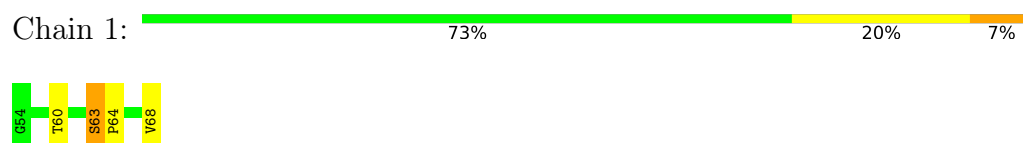
• Molecule 43: uL10



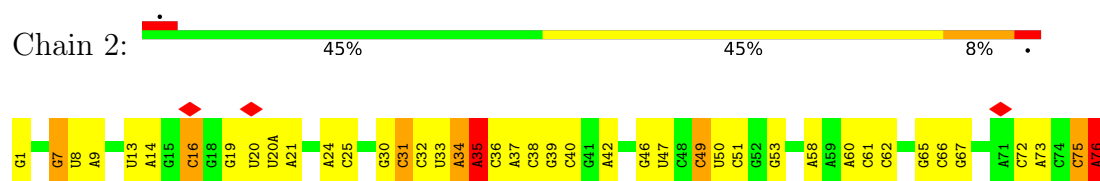
- Molecule 44: uL11



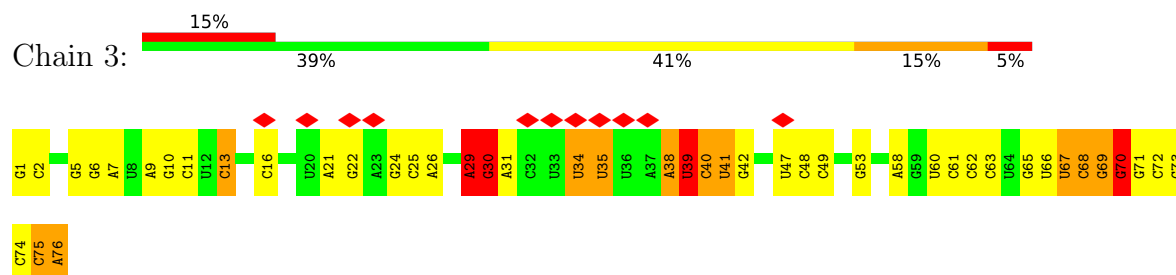
- Molecule 45: peptide



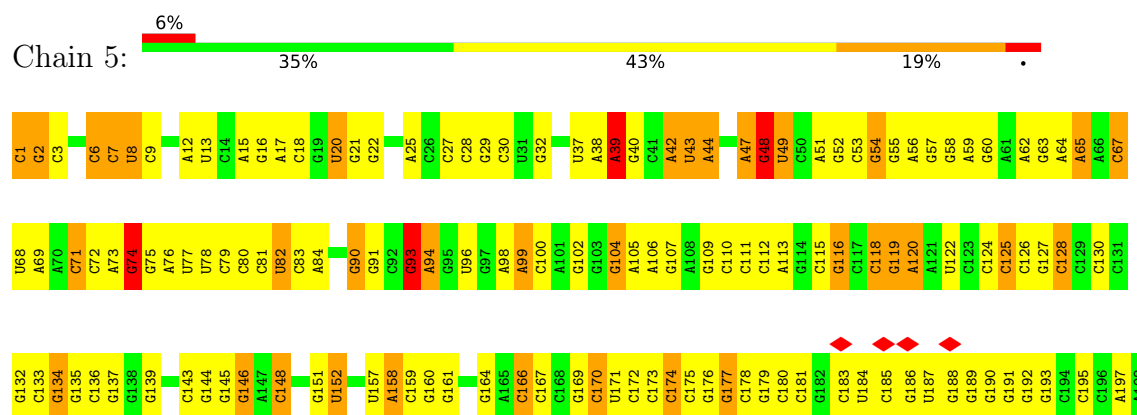
- Molecule 46: tRNA(Val)

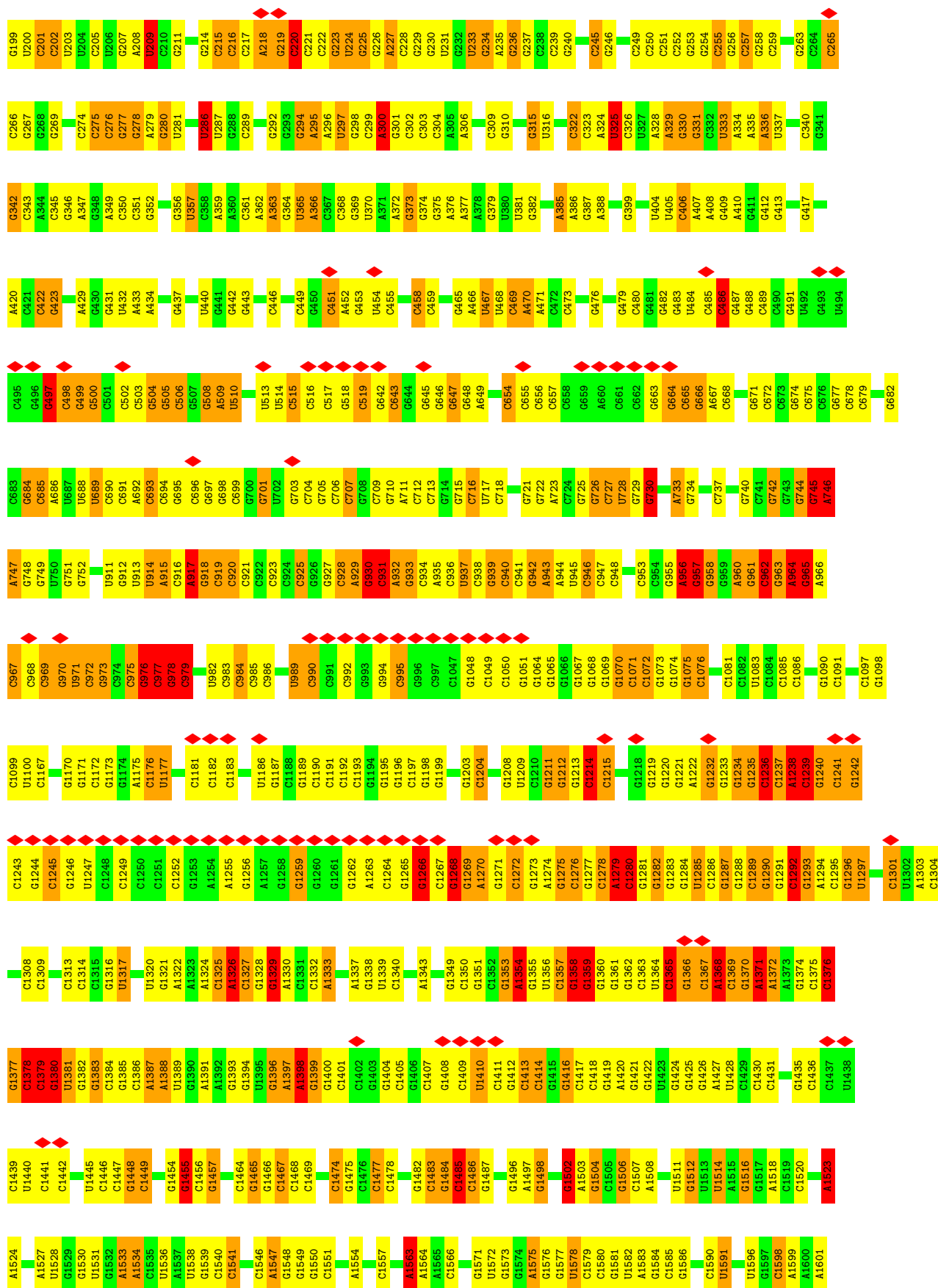


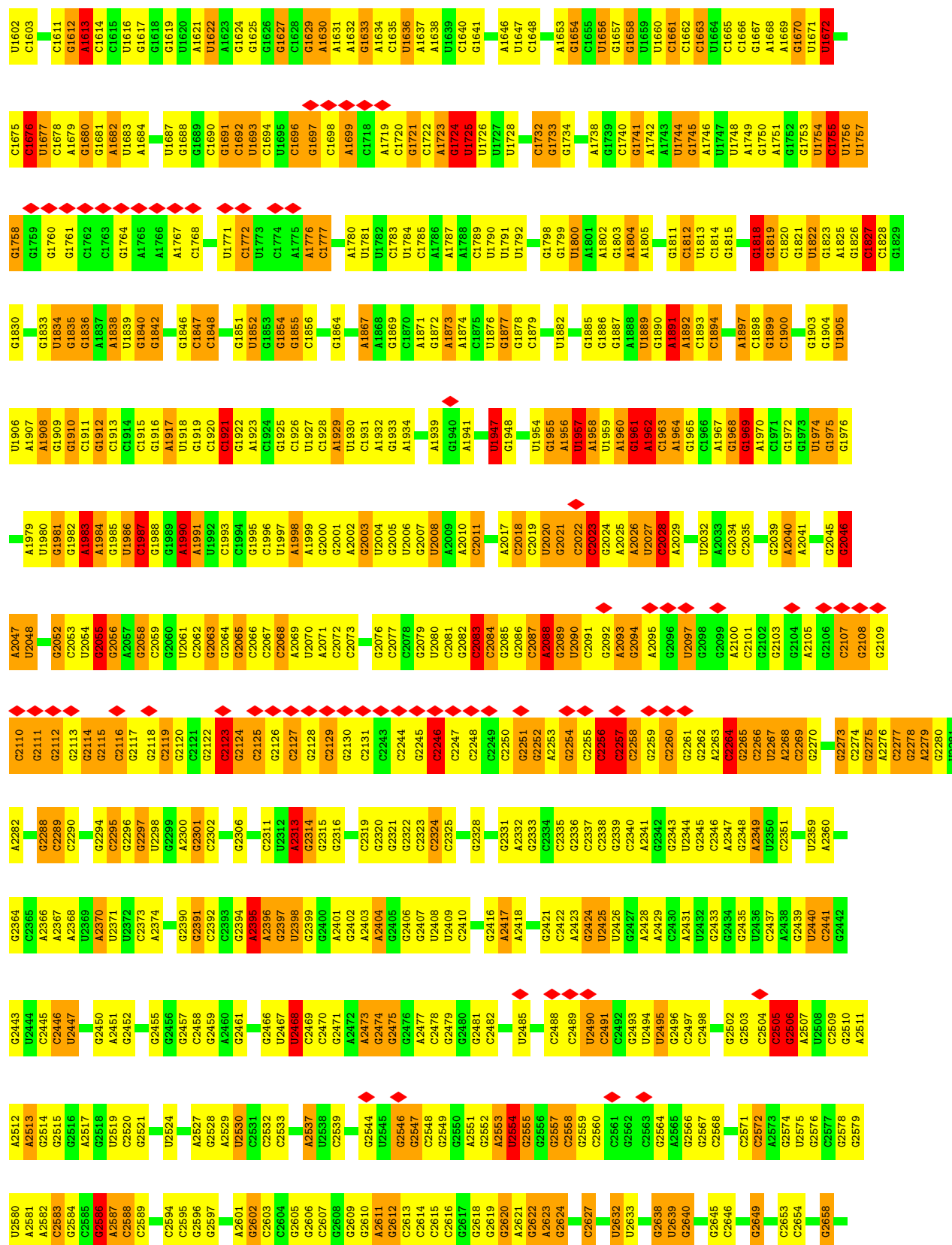
- Molecule 47: tRNA(Lys)



- Molecule 48: 28S ribosomal RNA



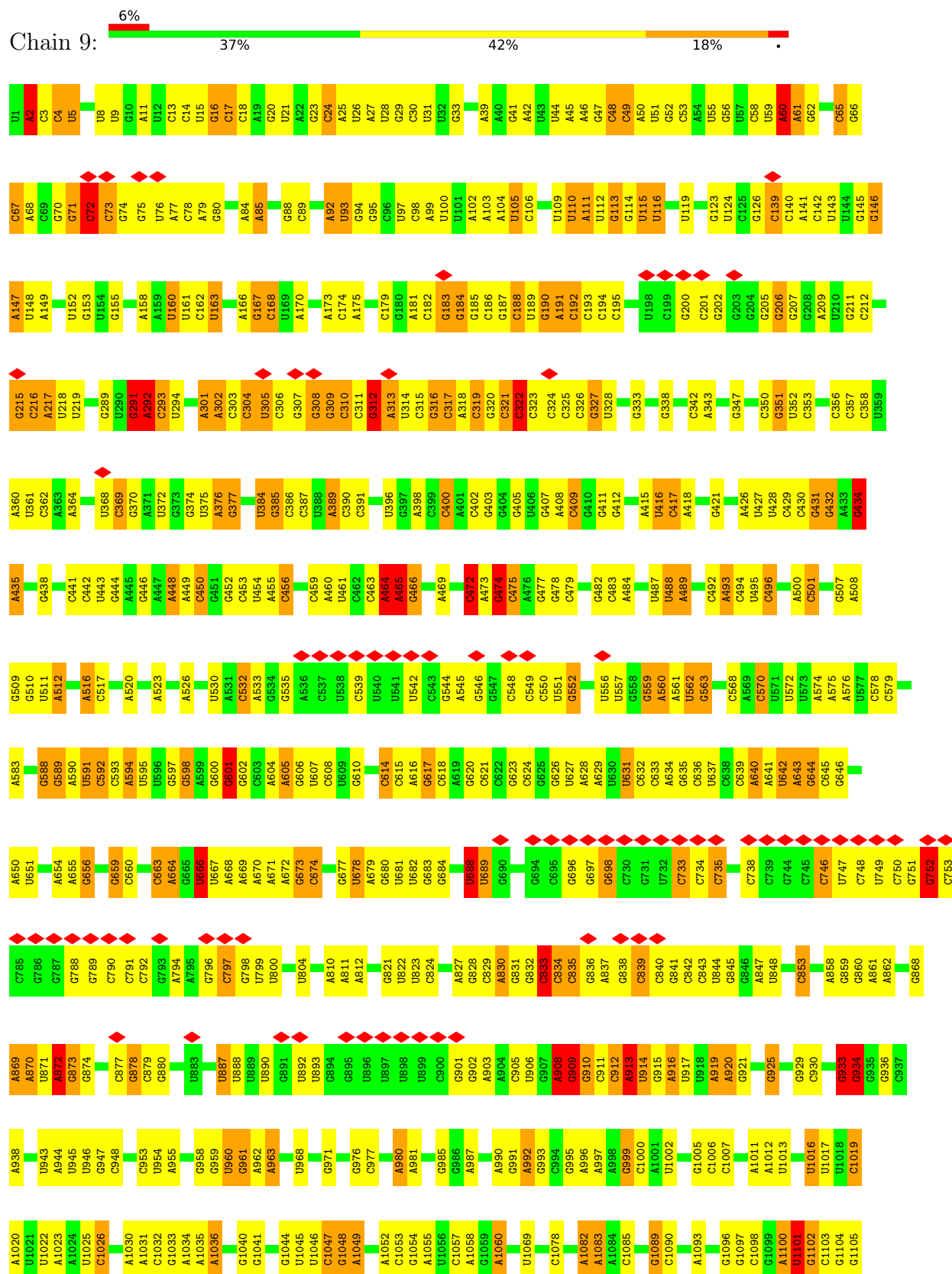


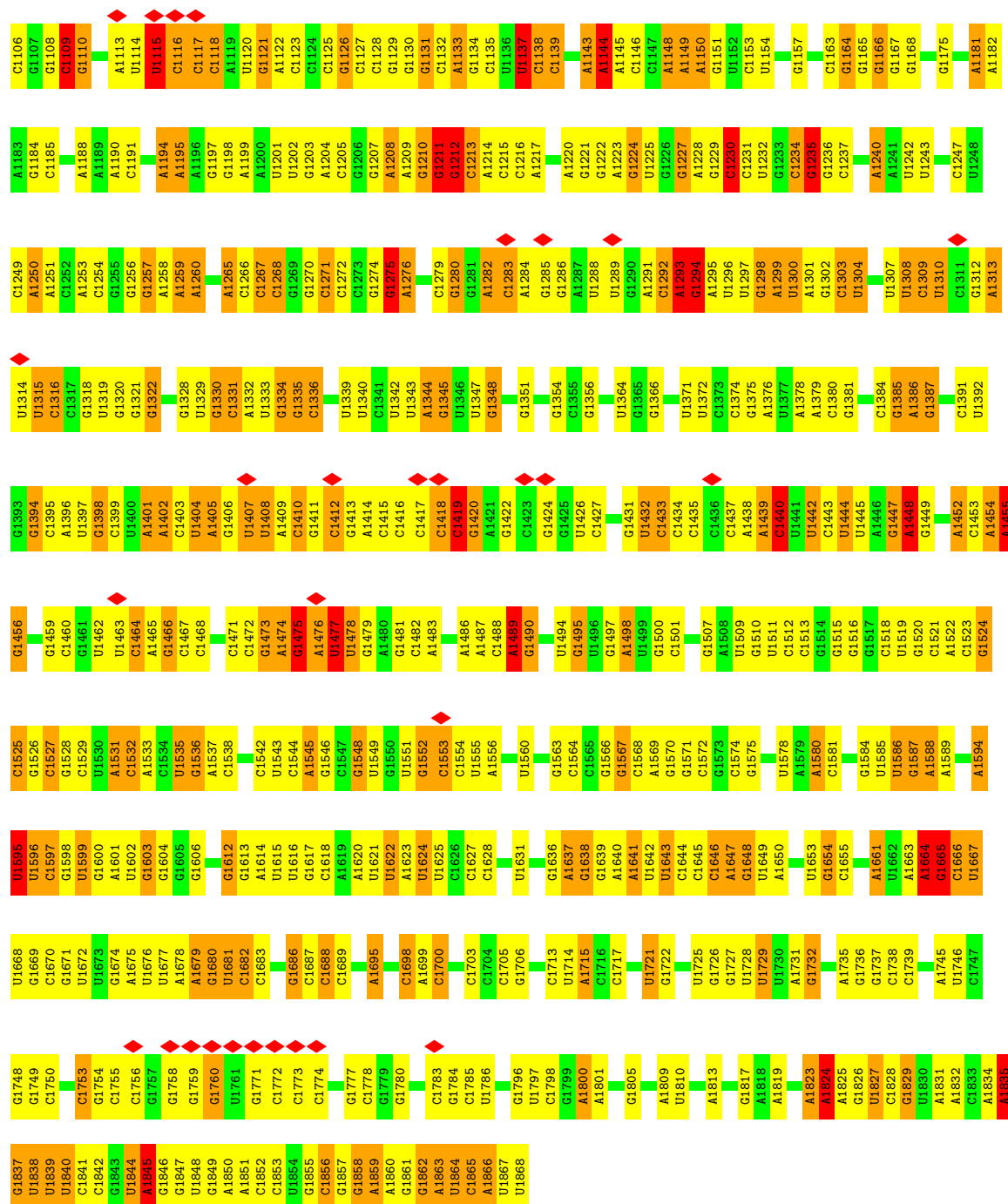






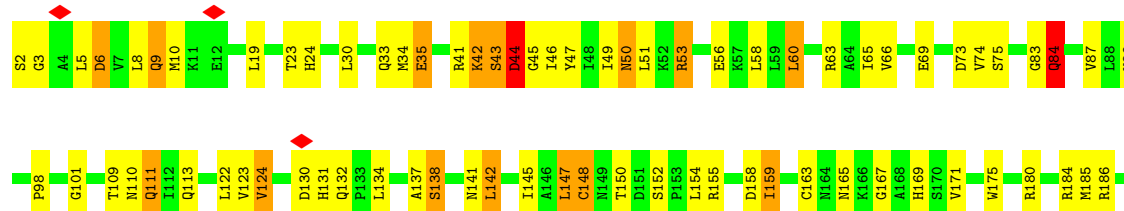
• Molecule 51: 18S ribosomal RNA





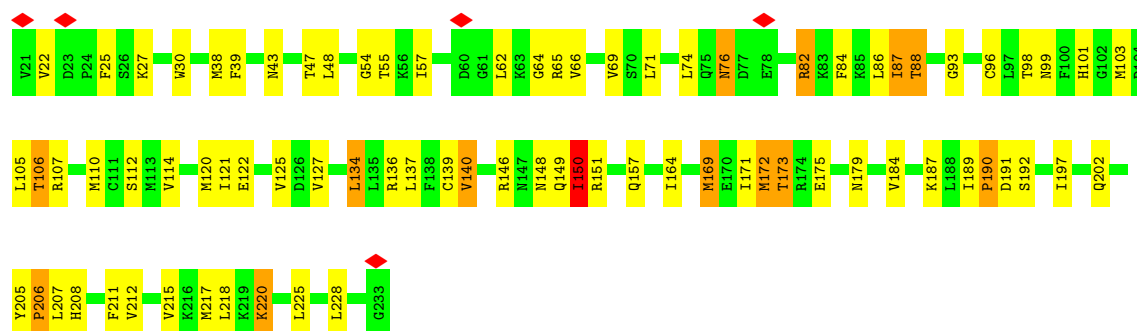
• Molecule 52: uS2

Chain AA: 62% 30% 7%

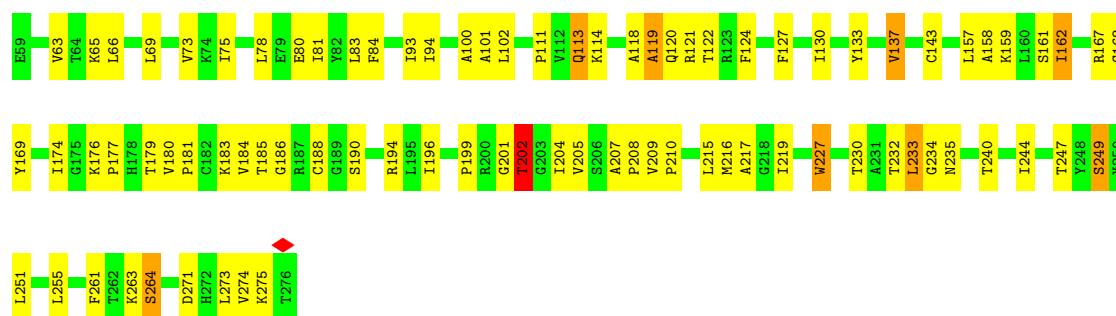




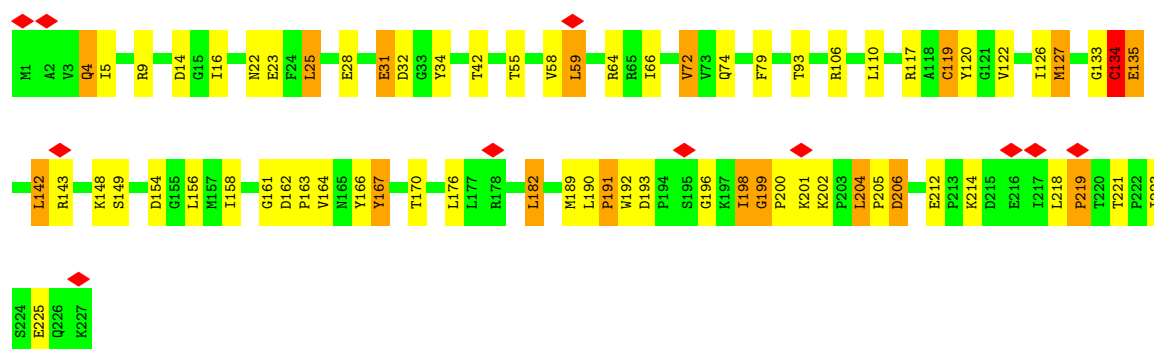
• Molecule 53: eS1



• Molecule 54: uS5

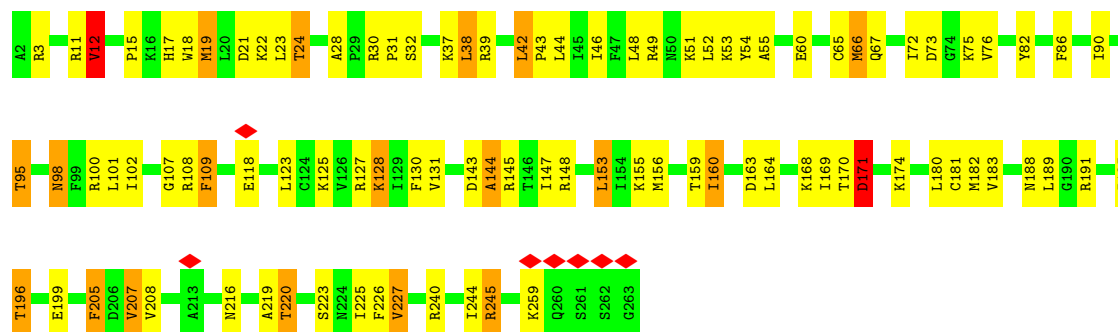


• Molecule 55: uS3

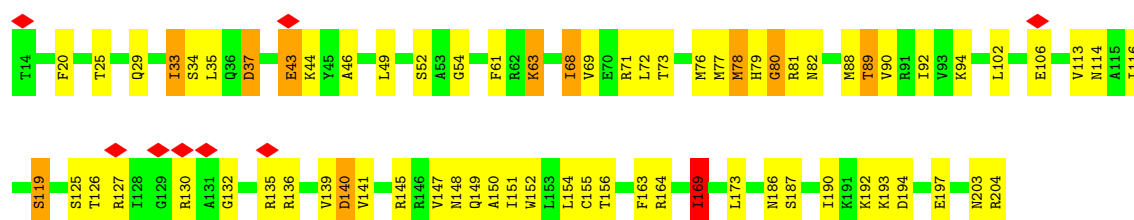


• Molecule 56: eS4

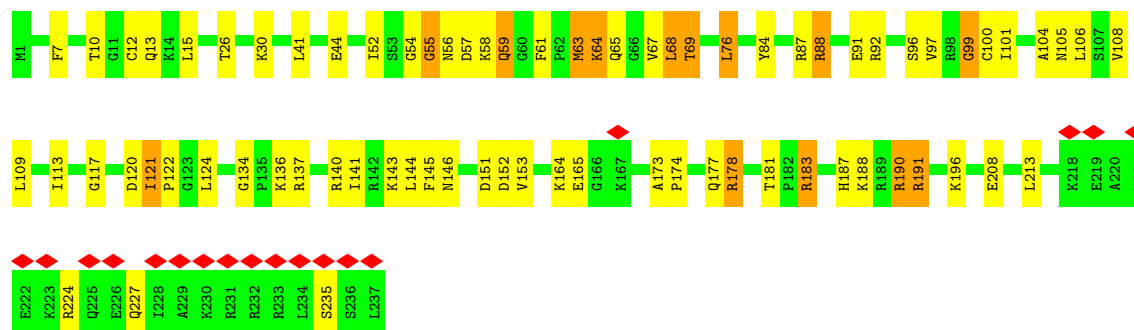




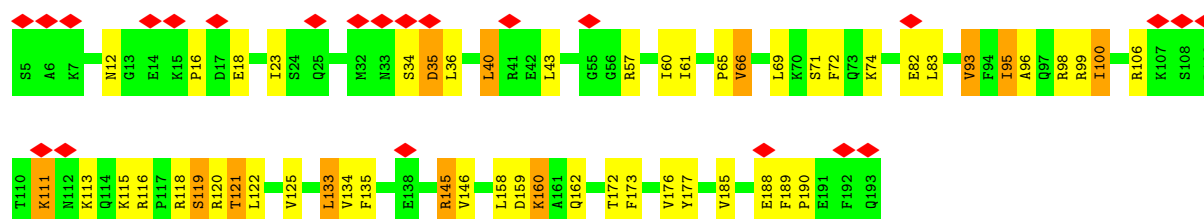
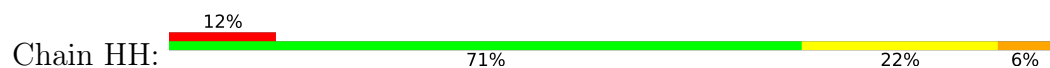
• Molecule 57: uS7



• Molecule 58: eS6

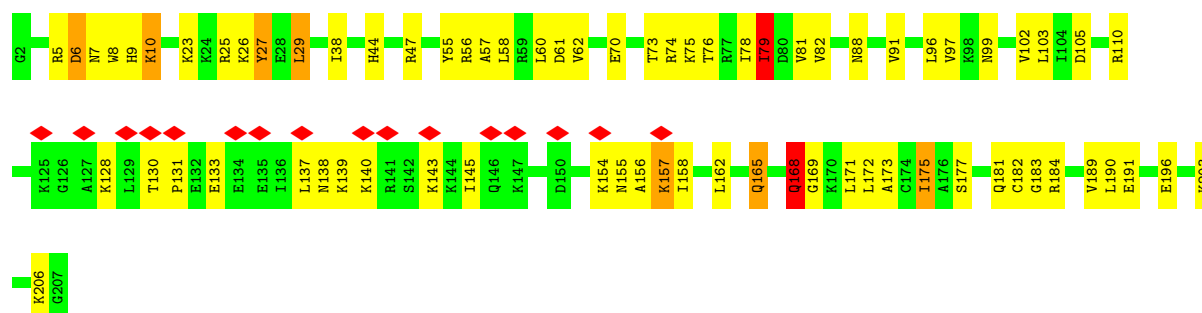


• Molecule 59: eS7

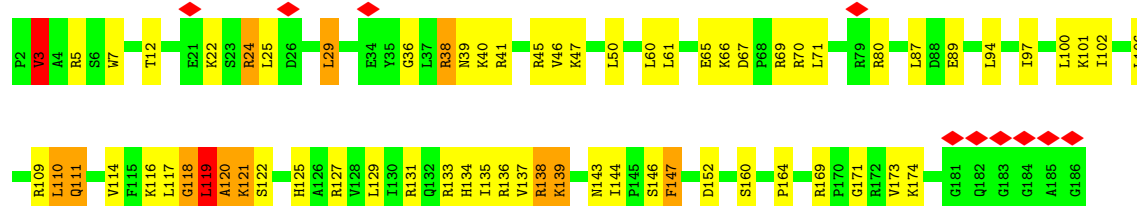


• Molecule 60: eS8

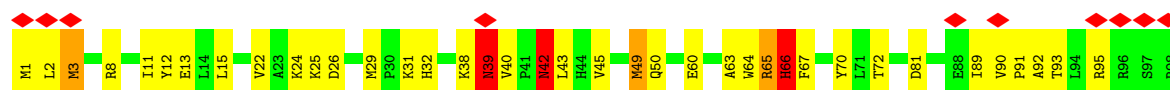




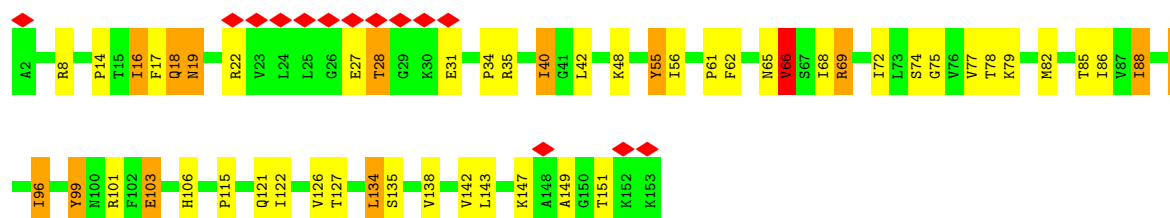
- Molecule 61: uS4



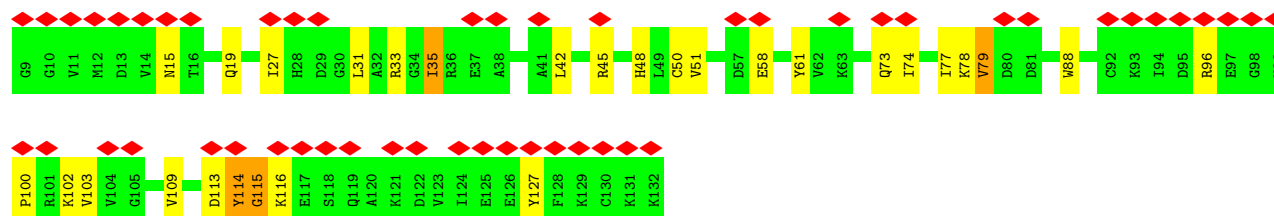
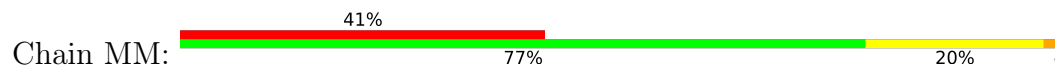
- Molecule 62: eS10



- Molecule 63: uS17

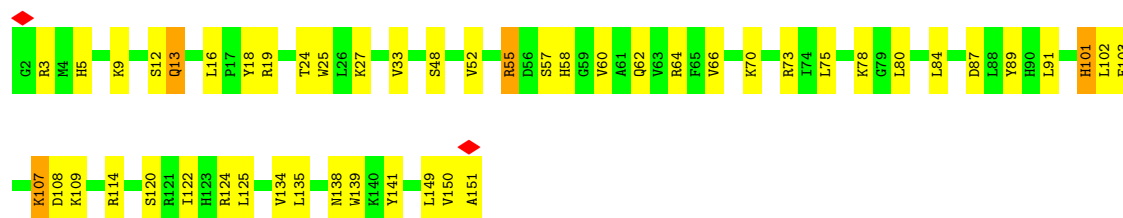


- Molecule 64: eS12



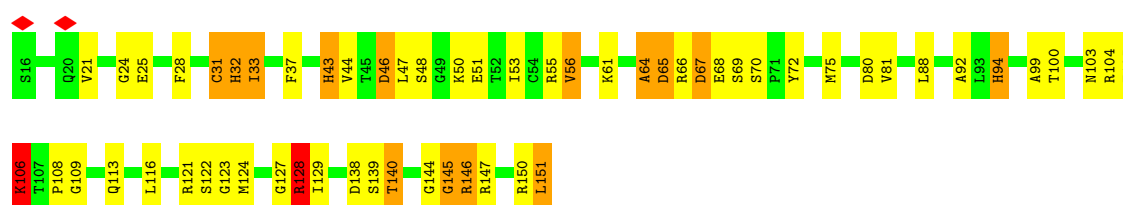
- Molecule 65: uS15

Chain NN:  67% 30% .



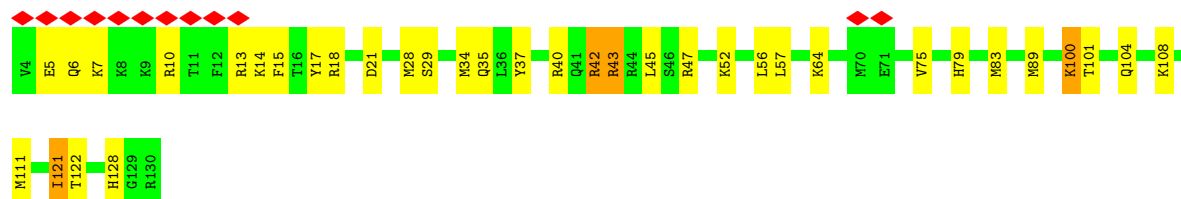
- Molecule 66: uS11

Chain OO:  57% 32% 10% .



- Molecule 67: uS19

Chain PP:  9% 72% 25% .



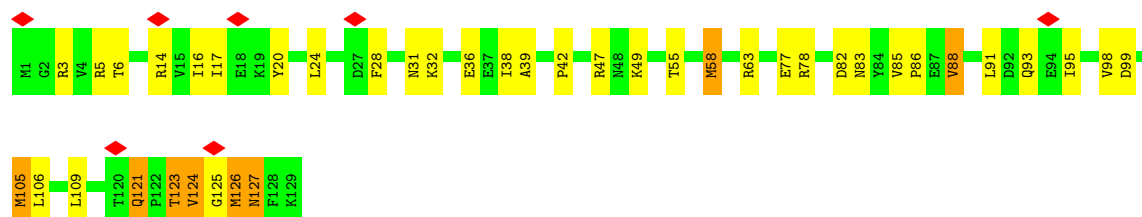
- Molecule 68: uS9

Chain QQ:  74% 21% . .



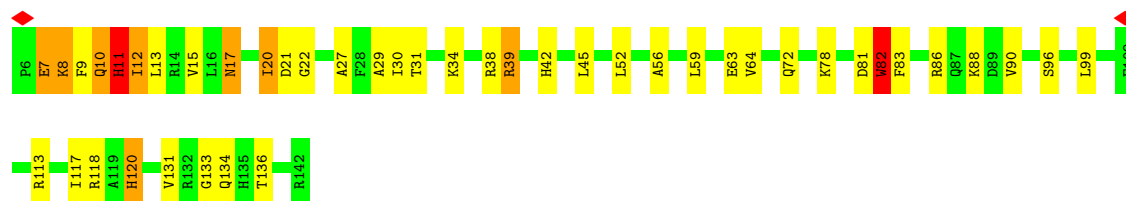
- Molecule 69: eS17

Chain RR:  5% 68% 26% 6%



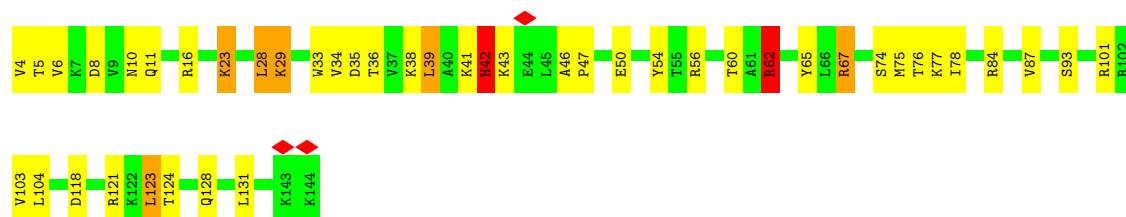
- Molecule 70: uS13

Chain SS:  68% 25% 6%



- Molecule 71: eS19

Chain TT:  68% 26%



- Molecule 72: uS10

Chain UU:  11% 77% 21%



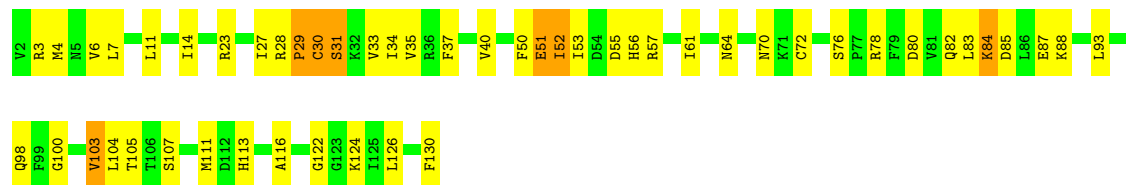
- Molecule 73: eS21

Chain VV:  61% 34% 5%



- Molecule 74: uS8

Chain WW:  60% 34% 5%

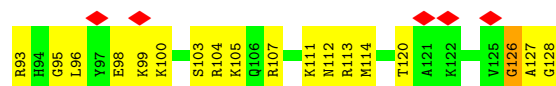
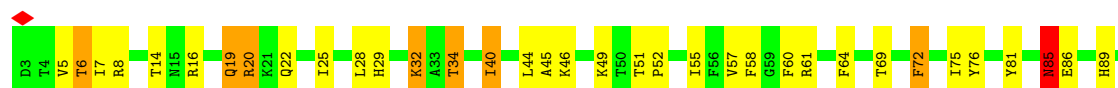


- Molecule 75: uS12

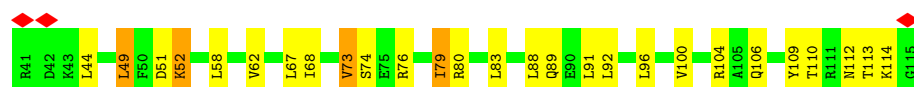
Chain XX:  70% 25%



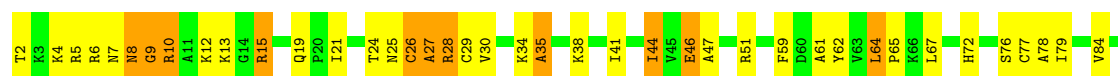
• Molecule 76: eS24



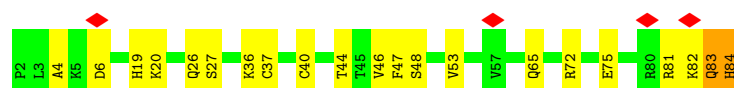
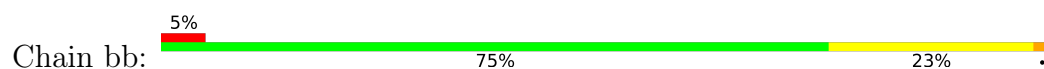
• Molecule 77: eS25



• Molecule 78: eS26



• Molecule 79: eS27



• Molecule 80: eS28



- Molecule 81: uS14

Chain dd: 



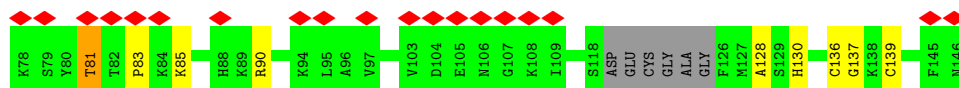
- Molecule 82: eS30

Chain ee: 



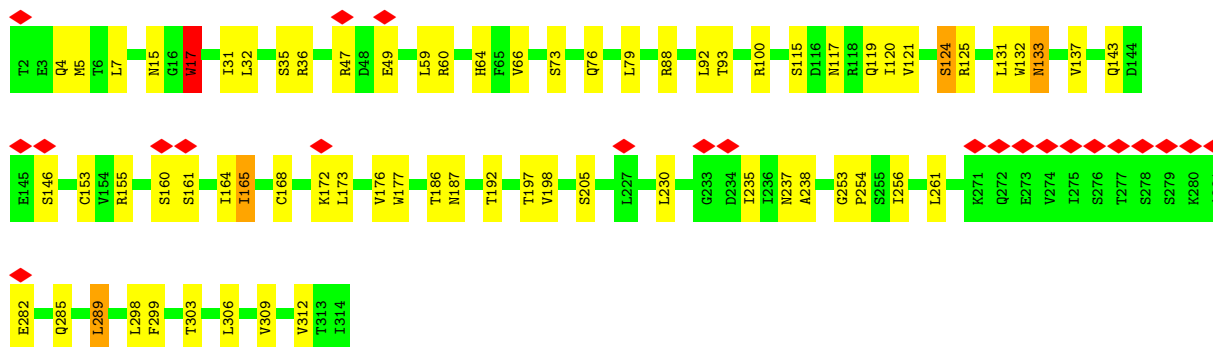
- Molecule 83: eS31

Chain ff: 



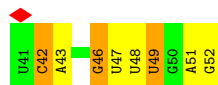
- Molecule 84: RACK1

Chain gg: 



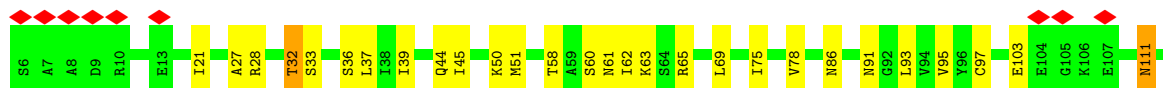
- Molecule 85: mRNA

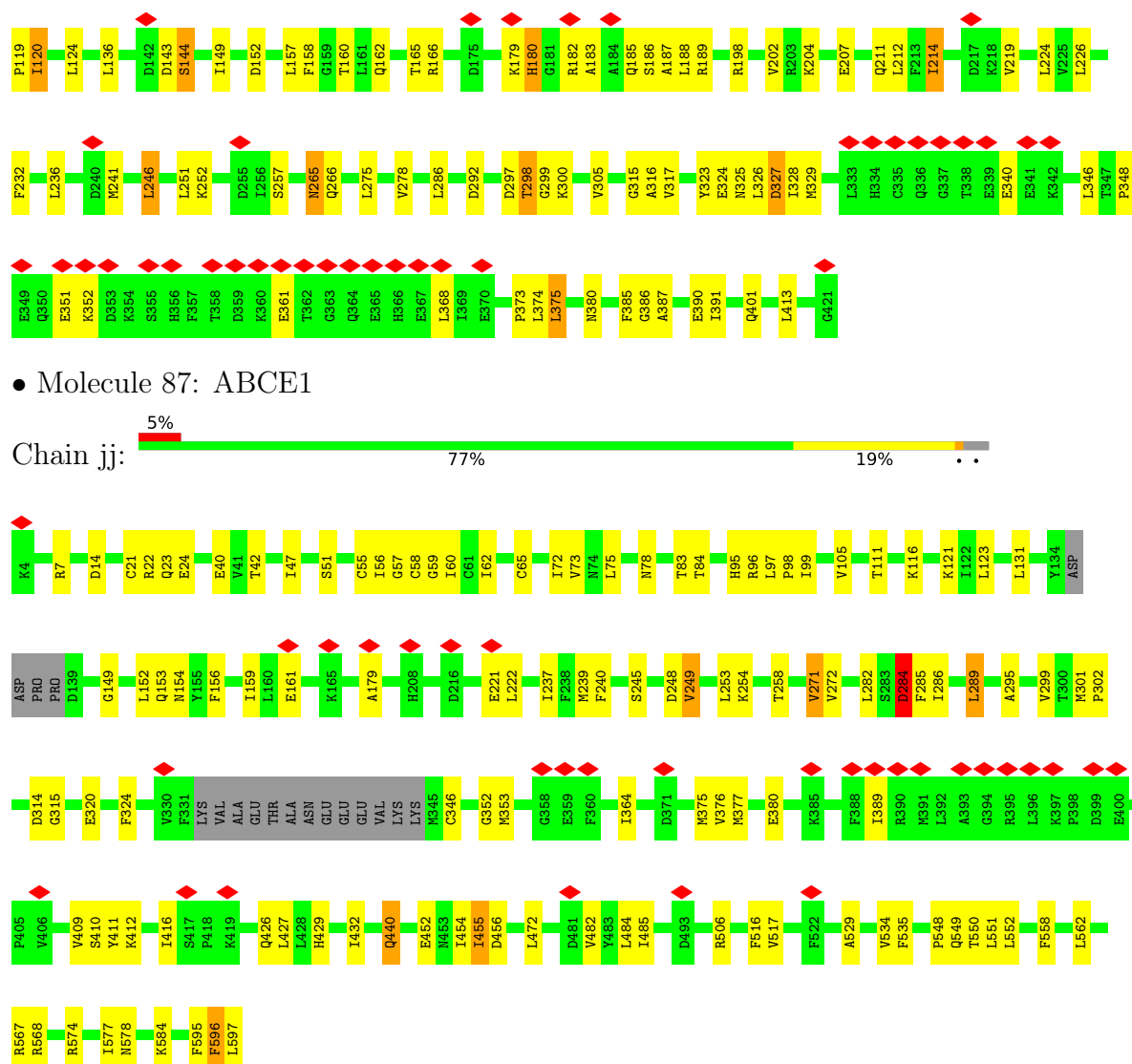
Chain hh: 



- Molecule 86: eRF1

Chain ii: 





• Molecule 87: ABCE1

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	22058	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1700	Depositor
Maximum defocus (nm)	3600	Depositor
Magnification	104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.719	Depositor
Minimum map value	-0.488	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.07	Depositor
Map size ($\text{\AA}$)	562.8, 562.8, 562.8	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3399999, 1.3399999, 1.3399999	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SF4, MG, ADP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.93	2/1906 (0.1%)	1.05	4/2556 (0.2%)
2	B	0.82	5/3216 (0.2%)	1.05	11/4311 (0.3%)
3	C	0.87	5/2929 (0.2%)	1.07	11/3935 (0.3%)
4	D	0.65	1/2432 (0.0%)	0.95	0/3257
5	E	0.77	5/1936 (0.3%)	1.08	9/2600 (0.3%)
6	F	0.87	4/1905 (0.2%)	1.02	2/2539 (0.1%)
7	G	0.79	3/1967 (0.2%)	1.03	8/2647 (0.3%)
8	H	0.70	1/1535 (0.1%)	0.95	0/2063
9	I	0.73	2/1693 (0.1%)	0.99	4/2260 (0.2%)
10	J	0.62	1/1376 (0.1%)	0.90	1/1841 (0.1%)
11	L	0.82	2/1734 (0.1%)	1.00	4/2317 (0.2%)
12	M	0.75	1/1158 (0.1%)	0.98	2/1547 (0.1%)
13	N	0.92	1/1746 (0.1%)	1.14	4/2338 (0.2%)
14	O	0.87	2/1671 (0.1%)	1.11	8/2234 (0.4%)
15	P	0.91	3/1268 (0.2%)	1.06	4/1701 (0.2%)
16	Q	0.84	1/1530 (0.1%)	1.04	2/2041 (0.1%)
17	R	0.75	1/1524 (0.1%)	0.96	0/2013
18	S	0.85	1/1493 (0.1%)	1.02	4/2002 (0.2%)
19	T	0.71	0/1326	0.95	2/1770 (0.1%)
20	U	0.63	1/822 (0.1%)	0.86	0/1103
21	V	0.81	0/993	1.01	1/1332 (0.1%)
22	W	0.73	0/541	0.96	2/720 (0.3%)
23	X	0.74	0/993	0.96	1/1334 (0.1%)
24	Y	0.75	0/1132	1.02	5/1504 (0.3%)
25	Z	0.79	3/1130 (0.3%)	1.04	2/1507 (0.1%)
26	a	0.86	0/1191	1.07	2/1590 (0.1%)
27	b	0.75	1/619 (0.2%)	0.97	0/818
28	c	0.74	1/742 (0.1%)	1.03	1/996 (0.1%)
29	d	0.79	0/903	1.04	1/1216 (0.1%)
30	e	0.81	0/1071	1.05	2/1429 (0.1%)
31	f	0.94	3/895 (0.3%)	1.13	6/1198 (0.5%)
32	g	0.79	1/916 (0.1%)	0.97	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.70	1/1021 (0.1%)	1.01	0/1348
34	i	0.70	0/841	0.95	0/1112
35	j	1.02	3/720 (0.4%)	1.20	5/952 (0.5%)
36	k	0.69	1/575 (0.2%)	1.01	3/761 (0.4%)
37	l	0.85	0/454	1.00	1/599 (0.2%)
38	m	0.73	0/435	1.04	1/575 (0.2%)
39	n	0.77	0/223	0.96	0/284
40	o	0.78	1/864 (0.1%)	0.96	1/1140 (0.1%)
41	p	0.77	0/718	1.07	3/953 (0.3%)
42	r	0.90	3/1017 (0.3%)	1.13	2/1364 (0.1%)
43	s	0.60	1/1547 (0.1%)	0.81	3/2088 (0.1%)
44	t	0.65	1/1257 (0.1%)	0.99	5/1697 (0.3%)
45	1	0.86	0/129	1.18	2/173 (1.2%)
46	2	0.40	0/1805	0.84	5/2809 (0.2%)
47	3	0.44	0/1777	0.92	11/2763 (0.4%)
48	5	0.51	4/87790 (0.0%)	1.01	557/136937 (0.4%)
49	7	0.48	0/2858	0.87	4/4455 (0.1%)
50	8	0.50	0/3701	0.94	11/5766 (0.2%)
51	9	0.47	2/41013 (0.0%)	0.95	164/63919 (0.3%)
52	AA	0.71	3/1679 (0.2%)	0.99	2/2283 (0.1%)
53	BB	0.71	2/1756 (0.1%)	1.02	6/2350 (0.3%)
54	CC	0.70	1/1730 (0.1%)	1.02	4/2344 (0.2%)
55	DD	0.63	1/1792 (0.1%)	0.93	1/2412 (0.0%)
56	EE	0.66	0/2115	1.05	3/2843 (0.1%)
57	FF	0.71	2/1531 (0.1%)	1.01	5/2059 (0.2%)
58	GG	0.67	3/1946 (0.2%)	0.92	2/2590 (0.1%)
59	HH	0.63	1/1544 (0.1%)	0.94	1/2068 (0.0%)
60	II	0.72	0/1715	0.98	4/2287 (0.2%)
61	JJ	0.71	2/1550 (0.1%)	1.03	0/2069
62	KK	0.73	2/851 (0.2%)	1.02	3/1147 (0.3%)
63	LL	0.77	1/1259 (0.1%)	1.02	4/1684 (0.2%)
64	MM	0.69	2/968 (0.2%)	0.92	0/1296
65	NN	0.75	3/1232 (0.2%)	1.05	4/1656 (0.2%)
66	OO	0.83	3/1029 (0.3%)	1.15	7/1380 (0.5%)
67	PP	0.69	3/1079 (0.3%)	1.00	4/1437 (0.3%)
68	QQ	0.68	1/1142 (0.1%)	0.93	1/1528 (0.1%)
69	RR	0.66	1/1060 (0.1%)	0.93	0/1421
70	SS	0.65	1/1157 (0.1%)	0.97	2/1548 (0.1%)
71	TT	0.68	1/1120 (0.1%)	1.03	2/1499 (0.1%)
72	UU	0.66	1/831 (0.1%)	0.93	1/1115 (0.1%)
73	VV	0.71	1/645 (0.2%)	1.01	0/865
74	WW	0.82	3/1051 (0.3%)	1.04	4/1406 (0.3%)
75	XX	0.81	3/1116 (0.3%)	1.08	3/1490 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	YY	0.69	3/1040 (0.3%)	0.95	2/1382 (0.1%)
77	ZZ	0.67	1/604 (0.2%)	0.99	1/810 (0.1%)
78	aa	0.75	0/794	1.06	1/1065 (0.1%)
79	bb	0.57	0/665	0.86	1/891 (0.1%)
80	cc	0.74	1/478 (0.2%)	0.99	0/640
81	dd	0.77	1/455 (0.2%)	0.98	0/603
82	ee	0.75	1/462 (0.2%)	0.93	0/607
83	ff	0.53	0/531	0.70	0/703
84	gg	0.61	4/2493 (0.2%)	0.84	4/3394 (0.1%)
85	hh	0.48	0/287	0.94	1/445 (0.2%)
86	ii	0.62	5/3333 (0.2%)	0.94	6/4483 (0.1%)
87	jj	0.57	2/4633 (0.0%)	0.92	3/6249 (0.0%)
All	All	0.61	127/242711 (0.1%)	0.99	963/355683 (0.3%)

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
1	A	0	2
2	B	0	6
3	C	0	5
4	D	0	1
5	E	0	4
7	G	0	1
9	I	0	4
11	L	0	1
14	O	0	3
18	S	0	2
19	T	0	1
21	V	0	1
23	X	0	1
24	Y	0	1
26	a	0	2
31	f	0	1
33	h	0	1
36	k	0	1
38	m	0	1
42	r	0	1
51	9	0	3
52	AA	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
53	BB	0	3
55	DD	0	1
56	EE	0	2
57	FF	0	1
59	HH	0	1
61	JJ	0	1
63	LL	0	2
66	OO	0	2
68	QQ	0	1
70	SS	0	3
71	TT	0	1
72	UU	0	2
73	VV	0	1
74	WW	0	1
75	XX	0	1
76	YY	0	1
78	aa	0	2
86	ii	0	3
87	jj	0	2
All	All	0	76

The worst 5 of 127 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	5	957	G	O3'-P	7.88	1.73	1.61
48	5	3859	G	O3'-P	-6.46	1.51	1.61
48	5	1847	C	O3'-P	-6.28	1.51	1.61
7	G	29	ASN	C-N	6.22	1.39	1.33
35	j	48	ASN	CG-OD1	6.13	1.35	1.23

The worst 5 of 963 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	5	1965	G	P-O3'-C3'	15.99	144.18	120.20
48	5	4975	G	C2'-C3'-O3'	15.61	132.91	109.50
48	5	1358	G	C4'-C3'-O3'	14.12	134.18	113.00
48	5	2022	C	C4'-C3'-O3'	13.60	133.40	113.00
48	5	1847	C	C4'-C3'-O3'	-12.98	93.53	113.00

There are no chirality outliers.

5 of 76 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	195	CYS	Peptide
1	A	196	TRP	Peptide
2	B	17	LEU	Peptide
2	B	35	ASP	Peptide
2	B	36	ASP	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1868	0	1959	51	0
2	B	3148	0	3267	75	0
3	C	2875	0	3049	71	0
4	D	2386	0	2419	35	0
5	E	1898	0	2035	75	0
6	F	1870	0	1994	49	0
7	G	1934	0	2087	43	0
8	H	1516	0	1597	31	0
9	I	1655	0	1704	63	0
10	J	1353	0	1386	18	0
11	L	1703	0	1820	68	0
12	M	1137	0	1211	34	0
13	N	1701	0	1749	47	0
14	O	1638	0	1777	40	0
15	P	1242	0	1269	16	0
16	Q	1506	0	1623	22	0
17	R	1508	0	1664	31	0
18	S	1454	0	1496	35	0
19	T	1298	0	1366	12	0
20	U	808	0	831	10	0
21	V	979	0	1039	12	0
22	W	528	0	541	7	0
23	X	976	0	1053	23	0
24	Y	1115	0	1205	13	0
25	Z	1107	0	1182	23	0
26	a	1162	0	1209	20	0
27	b	609	0	650	9	0
28	c	732	0	769	18	0
29	d	888	0	930	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	e	1053	0	1147	29	0
31	f	876	0	912	29	0
32	g	906	0	998	14	0
33	h	1013	0	1147	30	0
34	i	830	0	916	12	0
35	j	705	0	738	16	0
36	k	569	0	637	3	0
37	l	444	0	483	6	0
38	m	429	0	467	10	0
39	n	222	0	264	6	0
40	o	851	0	922	12	0
41	p	708	0	756	18	0
42	r	1001	0	1060	58	0
43	s	1523	0	1577	30	0
44	t	1238	0	1295	10	0
45	1	125	0	117	2	0
46	2	1616	0	824	23	0
47	3	1593	0	811	47	0
48	5	78486	0	39663	1657	0
49	7	2558	0	1296	31	0
50	8	3314	0	1683	58	0
51	9	36680	0	18530	739	0
52	AA	1642	0	1646	33	0
53	BB	1729	0	1803	32	0
54	CC	1692	0	1780	46	0
55	DD	1764	0	1863	27	0
56	EE	2073	0	2175	47	0
57	FF	1509	0	1563	29	0
58	GG	1923	0	2089	32	0
59	HH	1521	0	1616	27	0
60	II	1686	0	1772	34	0
61	JJ	1525	0	1640	32	0
62	KK	827	0	854	14	0
63	LL	1238	0	1315	21	0
64	MM	958	0	993	4	0
65	NN	1208	0	1294	13	0
66	OO	1016	0	1039	29	0
67	PP	1060	0	1120	14	0
68	QQ	1124	0	1193	12	0
69	RR	1047	0	1103	16	0
70	SS	1139	0	1191	16	0
71	TT	1102	0	1142	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	UU	821	0	883	2	0
73	VV	636	0	634	14	0
74	WW	1034	0	1080	22	0
75	XX	1098	0	1167	11	0
76	YY	1023	0	1090	19	0
77	ZZ	598	0	656	9	0
78	aa	781	0	829	23	0
79	bb	651	0	672	7	0
80	cc	475	0	497	7	0
81	dd	445	0	439	13	0
82	ee	457	0	502	5	0
83	ff	520	0	536	13	0
84	gg	2436	0	2393	20	0
85	hh	257	0	129	3	0
86	ii	3280	0	3326	42	0
87	jj	4551	0	4687	75	0
88	5	147	0	0	0	0
88	7	5	0	0	0	0
88	8	2	0	0	0	0
88	9	35	0	0	0	0
88	C	1	0	0	0	0
88	I	1	0	0	0	0
88	P	1	0	0	0	0
88	V	1	0	0	0	0
88	g	1	0	0	0	0
88	hh	1	0	0	0	0
89	aa	1	0	0	1	0
89	dd	1	0	0	0	0
89	ff	1	0	0	2	0
89	g	1	0	0	0	0
89	j	1	0	0	0	0
89	m	1	0	0	2	0
89	o	1	0	0	0	0
89	p	1	0	0	0	0
90	jj	16	0	0	7	0
91	jj	54	0	24	0	0
All	All	226453	0	169859	4093	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 10.

The worst 5 of 4093 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)
9:I:191:ILE:HD12	9:I:200:ILE:CD1	1.25	1.59
9:I:191:ILE:CD1	9:I:200:ILE:HD12	1.17	1.55
87:jj:568:ARG:CD	87:jj:597:LEU:O	1.66	1.42
5:E:279:PRO:HG2	31:f:7:CYS:SG	1.60	1.41
42:r:103:HIS:ND1	42:r:106:LEU:CD2	1.85	1.38

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	A	242/244 (99%)	199 (82%)	34 (14%)	9 (4%)	2	19
2	B	392/394 (100%)	338 (86%)	44 (11%)	10 (3%)	4	24
3	C	359/361 (99%)	302 (84%)	48 (13%)	9 (2%)	4	25
4	D	290/292 (99%)	255 (88%)	31 (11%)	4 (1%)	9	34
5	E	232/248 (94%)	172 (74%)	37 (16%)	23 (10%)	0	5
6	F	223/225 (99%)	204 (92%)	18 (8%)	1 (0%)	30	58
7	G	239/241 (99%)	205 (86%)	26 (11%)	8 (3%)	3	21
8	H	188/190 (99%)	161 (86%)	25 (13%)	2 (1%)	11	39
9	I	200/213 (94%)	178 (89%)	17 (8%)	5 (2%)	4	25
10	J	167/169 (99%)	141 (84%)	18 (11%)	8 (5%)	2	14
11	L	208/210 (99%)	174 (84%)	25 (12%)	9 (4%)	2	16
12	M	136/138 (99%)	123 (90%)	12 (9%)	1 (1%)	18	48
13	N	201/203 (99%)	167 (83%)	32 (16%)	2 (1%)	12	41
14	O	197/199 (99%)	176 (89%)	20 (10%)	1 (0%)	24	55
15	P	151/153 (99%)	134 (89%)	13 (9%)	4 (3%)	4	24
16	Q	185/187 (99%)	161 (87%)	20 (11%)	4 (2%)	5	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	R	178/180 (99%)	151 (85%)	25 (14%)	2 (1%)	11	39
18	S	173/175 (99%)	151 (87%)	18 (10%)	4 (2%)	5	26
19	T	157/159 (99%)	137 (87%)	17 (11%)	3 (2%)	6	30
20	U	97/99 (98%)	82 (84%)	11 (11%)	4 (4%)	2	17
21	V	129/131 (98%)	110 (85%)	19 (15%)	0	100	100
22	W	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	7	32
23	X	117/119 (98%)	106 (91%)	9 (8%)	2 (2%)	7	31
24	Y	132/134 (98%)	114 (86%)	13 (10%)	5 (4%)	2	18
25	Z	133/135 (98%)	113 (85%)	14 (10%)	6 (4%)	2	15
26	a	145/147 (99%)	114 (79%)	24 (17%)	7 (5%)	2	14
27	b	73/75 (97%)	65 (89%)	5 (7%)	3 (4%)	2	17
28	c	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
29	d	105/107 (98%)	86 (82%)	17 (16%)	2 (2%)	6	30
30	e	126/128 (98%)	110 (87%)	12 (10%)	4 (3%)	3	21
31	f	107/109 (98%)	88 (82%)	12 (11%)	7 (6%)	1	11
32	g	112/114 (98%)	97 (87%)	13 (12%)	2 (2%)	6	30
33	h	120/122 (98%)	106 (88%)	10 (8%)	4 (3%)	3	21
34	i	100/102 (98%)	87 (87%)	11 (11%)	2 (2%)	6	29
35	j	84/86 (98%)	73 (87%)	8 (10%)	3 (4%)	2	19
36	k	67/69 (97%)	53 (79%)	10 (15%)	4 (6%)	1	12
37	l	48/50 (96%)	41 (85%)	5 (10%)	2 (4%)	2	16
38	m	50/52 (96%)	43 (86%)	7 (14%)	0	100	100
39	n	21/23 (91%)	21 (100%)	0	0	100	100
40	o	102/104 (98%)	79 (78%)	19 (19%)	4 (4%)	2	18
41	p	89/91 (98%)	75 (84%)	9 (10%)	5 (6%)	1	13
42	r	123/125 (98%)	104 (85%)	10 (8%)	9 (7%)	1	8
43	s	196/198 (99%)	163 (83%)	21 (11%)	12 (6%)	1	11
44	t	161/163 (99%)	100 (62%)	36 (22%)	25 (16%)	0	2
45	1	13/15 (87%)	10 (77%)	2 (15%)	1 (8%)	1	7
52	AA	206/208 (99%)	153 (74%)	37 (18%)	16 (8%)	1	7
53	BB	211/213 (99%)	165 (78%)	34 (16%)	12 (6%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	CC	216/218 (99%)	184 (85%)	22 (10%)	10 (5%)	2	15
55	DD	225/227 (99%)	184 (82%)	30 (13%)	11 (5%)	1	14
56	EE	260/262 (99%)	197 (76%)	43 (16%)	20 (8%)	1	7
57	FF	189/191 (99%)	156 (82%)	22 (12%)	11 (6%)	1	12
58	GG	235/237 (99%)	198 (84%)	29 (12%)	8 (3%)	3	21
59	HH	187/189 (99%)	144 (77%)	30 (16%)	13 (7%)	1	9
60	II	204/206 (99%)	169 (83%)	25 (12%)	10 (5%)	1	14
61	JJ	183/185 (99%)	152 (83%)	19 (10%)	12 (7%)	1	10
62	KK	96/98 (98%)	65 (68%)	20 (21%)	11 (12%)	0	3
63	LL	150/152 (99%)	125 (83%)	16 (11%)	9 (6%)	1	12
64	MM	122/124 (98%)	87 (71%)	25 (20%)	10 (8%)	0	6
65	NN	148/150 (99%)	121 (82%)	21 (14%)	6 (4%)	2	17
66	OO	134/136 (98%)	96 (72%)	24 (18%)	14 (10%)	0	4
67	PP	125/127 (98%)	102 (82%)	20 (16%)	3 (2%)	4	25
68	QQ	139/141 (99%)	115 (83%)	14 (10%)	10 (7%)	1	9
69	RR	127/129 (98%)	100 (79%)	18 (14%)	9 (7%)	1	9
70	SS	135/137 (98%)	110 (82%)	15 (11%)	10 (7%)	1	8
71	TT	139/141 (99%)	127 (91%)	9 (6%)	3 (2%)	5	27
72	UU	102/104 (98%)	84 (82%)	12 (12%)	6 (6%)	1	12
73	VV	81/83 (98%)	65 (80%)	9 (11%)	7 (9%)	0	6
74	WW	127/129 (98%)	101 (80%)	21 (16%)	5 (4%)	2	18
75	XX	139/141 (99%)	122 (88%)	8 (6%)	9 (6%)	1	11
76	YY	124/126 (98%)	100 (81%)	15 (12%)	9 (7%)	1	8
77	ZZ	73/75 (97%)	58 (80%)	11 (15%)	4 (6%)	1	13
78	aa	96/98 (98%)	76 (79%)	8 (8%)	12 (12%)	0	3
79	bb	81/83 (98%)	59 (73%)	16 (20%)	6 (7%)	1	8
80	cc	59/61 (97%)	47 (80%)	11 (19%)	1 (2%)	7	31
81	dd	51/53 (96%)	40 (78%)	11 (22%)	0	100	100
82	ee	55/57 (96%)	39 (71%)	14 (26%)	2 (4%)	2	19
83	ff	58/68 (85%)	49 (84%)	8 (14%)	1 (2%)	7	31
84	gg	311/313 (99%)	263 (85%)	40 (13%)	8 (3%)	4	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
86	ii	414/416 (100%)	378 (91%)	25 (6%)	11 (3%)	4	24
87	jj	569/594 (96%)	501 (88%)	54 (10%)	14 (2%)	4	25
All	All	12492/12708 (98%)	10443 (84%)	1523 (12%)	526 (4%)	3	16

5 of 526 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	14	SER
1	A	196	TRP
1	A	197	PRO
2	B	37	PRO
2	B	302	ASN

5.3.2 Protein sidechains ⓘ

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	A	187/187 (100%)	157 (84%)	30 (16%)	2	14
2	B	336/342 (98%)	285 (85%)	51 (15%)	3	15
3	C	301/301 (100%)	259 (86%)	42 (14%)	3	17
4	D	247/247 (100%)	219 (89%)	28 (11%)	5	24
5	E	208/221 (94%)	178 (86%)	30 (14%)	3	16
6	F	194/195 (100%)	171 (88%)	23 (12%)	5	22
7	G	206/206 (100%)	173 (84%)	33 (16%)	2	14
8	H	169/169 (100%)	144 (85%)	25 (15%)	3	16
9	I	174/180 (97%)	155 (89%)	19 (11%)	6	25
10	J	142/142 (100%)	124 (87%)	18 (13%)	4	20
11	L	176/176 (100%)	149 (85%)	27 (15%)	3	14
12	M	117/117 (100%)	103 (88%)	14 (12%)	5	22
13	N	171/171 (100%)	149 (87%)	22 (13%)	4	19
14	O	171/171 (100%)	143 (84%)	28 (16%)	2	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	P	134/134 (100%)	116 (87%)	18 (13%)	4	19
16	Q	163/163 (100%)	139 (85%)	24 (15%)	3	16
17	R	159/159 (100%)	138 (87%)	21 (13%)	4	19
18	S	156/156 (100%)	134 (86%)	22 (14%)	3	17
19	T	139/139 (100%)	115 (83%)	24 (17%)	2	12
20	U	89/89 (100%)	79 (89%)	10 (11%)	6	24
21	V	101/101 (100%)	82 (81%)	19 (19%)	1	9
22	W	55/55 (100%)	49 (89%)	6 (11%)	6	25
23	X	107/107 (100%)	92 (86%)	15 (14%)	3	17
24	Y	124/124 (100%)	106 (86%)	18 (14%)	3	16
25	Z	117/117 (100%)	97 (83%)	20 (17%)	2	12
26	a	119/119 (100%)	108 (91%)	11 (9%)	8	30
27	b	62/62 (100%)	53 (86%)	9 (14%)	3	16
28	c	79/79 (100%)	65 (82%)	14 (18%)	2	11
29	d	98/98 (100%)	78 (80%)	20 (20%)	1	7
30	e	114/114 (100%)	91 (80%)	23 (20%)	1	8
31	f	88/88 (100%)	75 (85%)	13 (15%)	3	16
32	g	98/98 (100%)	81 (83%)	17 (17%)	2	12
33	h	109/109 (100%)	95 (87%)	14 (13%)	4	20
34	i	86/86 (100%)	75 (87%)	11 (13%)	4	20
35	j	73/73 (100%)	60 (82%)	13 (18%)	2	11
36	k	64/64 (100%)	58 (91%)	6 (9%)	8	30
37	l	47/47 (100%)	40 (85%)	7 (15%)	3	15
38	m	48/48 (100%)	39 (81%)	9 (19%)	1	9
39	n	22/22 (100%)	21 (96%)	1 (4%)	24	48
40	o	92/92 (100%)	76 (83%)	16 (17%)	2	11
41	p	74/74 (100%)	65 (88%)	9 (12%)	5	21
42	r	109/109 (100%)	89 (82%)	20 (18%)	2	10
43	s	166/166 (100%)	155 (93%)	11 (7%)	15	40
44	t	136/136 (100%)	130 (96%)	6 (4%)	25	49
45	l	13/13 (100%)	11 (85%)	2 (15%)	2	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	AA	174/174 (100%)	143 (82%)	31 (18%)	2	11
53	BB	194/194 (100%)	163 (84%)	31 (16%)	2	14
54	CC	183/183 (100%)	164 (90%)	19 (10%)	7	27
55	DD	190/190 (100%)	154 (81%)	36 (19%)	1	9
56	EE	223/223 (100%)	189 (85%)	34 (15%)	3	15
57	FF	161/161 (100%)	132 (82%)	29 (18%)	2	11
58	GG	207/207 (100%)	178 (86%)	29 (14%)	3	17
59	HH	169/169 (100%)	152 (90%)	17 (10%)	7	28
60	II	178/178 (100%)	147 (83%)	31 (17%)	2	11
61	JJ	161/161 (100%)	135 (84%)	26 (16%)	2	13
62	KK	89/89 (100%)	74 (83%)	15 (17%)	2	12
63	LL	136/136 (100%)	111 (82%)	25 (18%)	1	10
64	MM	104/104 (100%)	90 (86%)	14 (14%)	4	18
65	NN	130/130 (100%)	104 (80%)	26 (20%)	1	8
66	OO	106/106 (100%)	88 (83%)	18 (17%)	2	12
67	PP	116/116 (100%)	98 (84%)	18 (16%)	2	14
68	QQ	117/117 (100%)	100 (86%)	17 (14%)	3	16
69	RR	117/117 (100%)	97 (83%)	20 (17%)	2	12
70	SS	119/119 (100%)	97 (82%)	22 (18%)	1	10
71	TT	112/112 (100%)	91 (81%)	21 (19%)	1	9
72	UU	94/94 (100%)	82 (87%)	12 (13%)	4	20
73	VV	67/67 (100%)	57 (85%)	10 (15%)	3	15
74	WW	112/112 (100%)	97 (87%)	15 (13%)	4	19
75	XX	113/113 (100%)	93 (82%)	20 (18%)	2	11
76	YY	108/108 (100%)	86 (80%)	22 (20%)	1	7
77	ZZ	66/66 (100%)	55 (83%)	11 (17%)	2	13
78	aa	85/85 (100%)	74 (87%)	11 (13%)	4	19
79	bb	75/75 (100%)	66 (88%)	9 (12%)	5	22
80	cc	54/54 (100%)	40 (74%)	14 (26%)	0	4
81	dd	47/47 (100%)	35 (74%)	12 (26%)	0	4
82	ee	47/47 (100%)	41 (87%)	6 (13%)	4	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
83	ff	58/61 (95%)	56 (97%)	2 (3%)	32	53
84	gg	272/272 (100%)	247 (91%)	25 (9%)	8	30
86	ii	358/358 (100%)	314 (88%)	44 (12%)	4	21
87	jj	507/522 (97%)	469 (92%)	38 (8%)	12	37
All	All	10889/10933 (100%)	9340 (86%)	1549 (14%)	5	17

5 of 1549 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
55	DD	170	THR
64	MM	42	LEU
56	EE	130	PHE
55	DD	167	TYR
59	HH	121	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 129 such sidechains are listed below:

Mol	Chain	Res	Type
79	bb	29	ASN
84	gg	178	ASN
27	b	17	HIS
26	a	60	HIS
84	gg	285	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
46	2	74/76 (97%)	24 (32%)	0
47	3	72/75 (96%)	29 (40%)	6 (8%)
48	5	3650/3662 (99%)	1260 (34%)	291 (7%)
49	7	120/120 (100%)	25 (20%)	2 (1%)
50	8	155/156 (99%)	49 (31%)	6 (3%)
51	9	1712/1719 (99%)	623 (36%)	115 (6%)
85	hh	11/12 (91%)	6 (54%)	0
All	All	5794/5820 (99%)	2016 (34%)	420 (7%)

5 of 2016 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
46	2	7	G
46	2	8	U
46	2	9	A
46	2	13	U
46	2	14	A

5 of 420 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	5	3904	G
48	5	4951	G
51	9	1489	A
48	5	4119	C
48	5	4510	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 207 ligands modelled in this entry, 203 are monoatomic - leaving 4 for Mogul analysis.

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	$\# Z > 2$
90	SF4	jj	600	87	0,12,12	-	-	-		
90	SF4	jj	601	87	0,12,12	-	-	-		
91	ADP	jj	603	-	28,29,29	1.52	5 (17%)	43,45,45	1.91	11 (25%)
91	ADP	jj	602	-	28,29,29	1.51	5 (17%)	43,45,45	1.90	11 (25%)

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
90	SF4	jj	600	87	-	-	0/6/5/5
91	ADP	jj	602	-	-	0/16/32/32	0/3/3/3
91	ADP	jj	603	-	-	2/16/32/32	0/3/3/3
90	SF4	jj	601	87	-	-	0/6/5/5

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
91	jj	602	ADP	C5-C4	4.98	1.48	1.39
91	jj	603	ADP	C5-C4	4.96	1.47	1.39
91	jj	603	ADP	C5-C6	3.01	1.49	1.41
91	jj	602	ADP	C5-C6	2.96	1.49	1.41
91	jj	602	ADP	C8-N7	2.50	1.36	1.31

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
91	jj	603	ADP	C5-C4-N3	-5.90	118.60	126.72
91	jj	602	ADP	C5-C4-N3	-5.87	118.64	126.72
91	jj	603	ADP	N3-C4-N9	4.63	135.04	127.17
91	jj	602	ADP	N3-C4-N9	4.61	135.00	127.17
91	jj	602	ADP	C2-N3-C4	3.95	121.48	111.83

There are no chirality outliers.

All (2) torsion outliers are listed below:

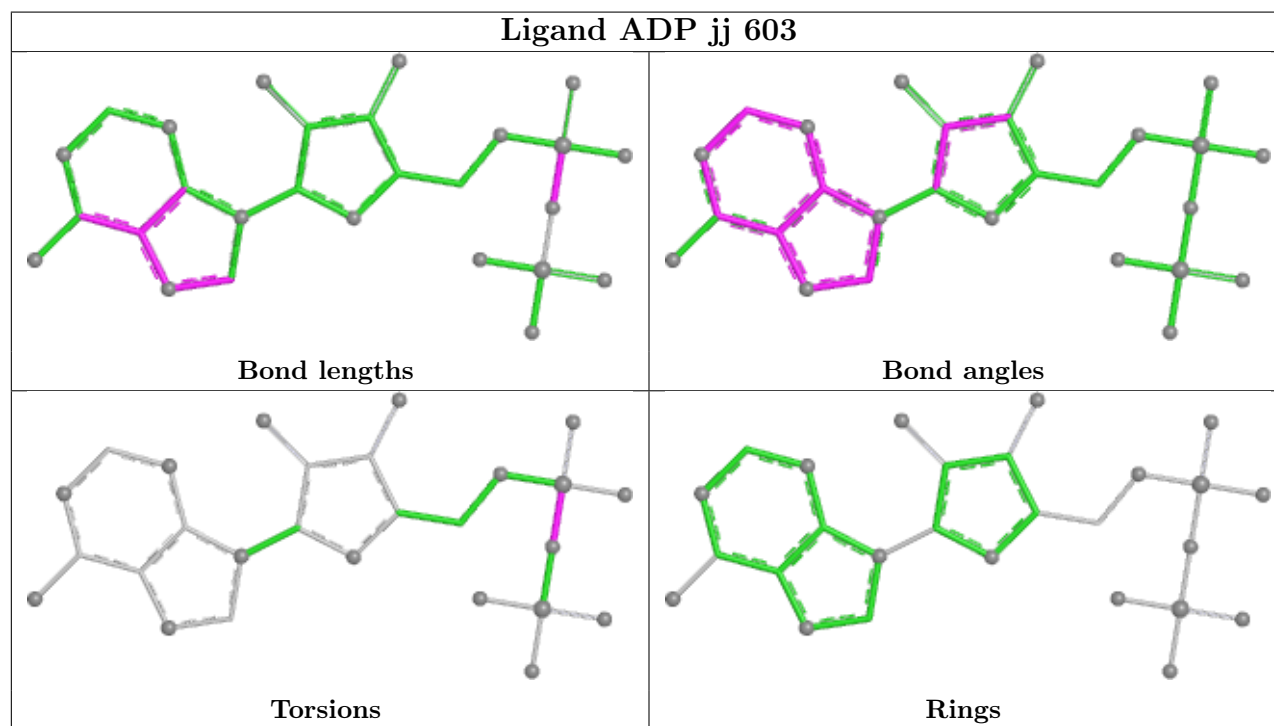
Mol	Chain	Res	Type	Atoms
91	jj	603	ADP	PB-O3A-PA-O1A
91	jj	603	ADP	PB-O3A-PA-O2A

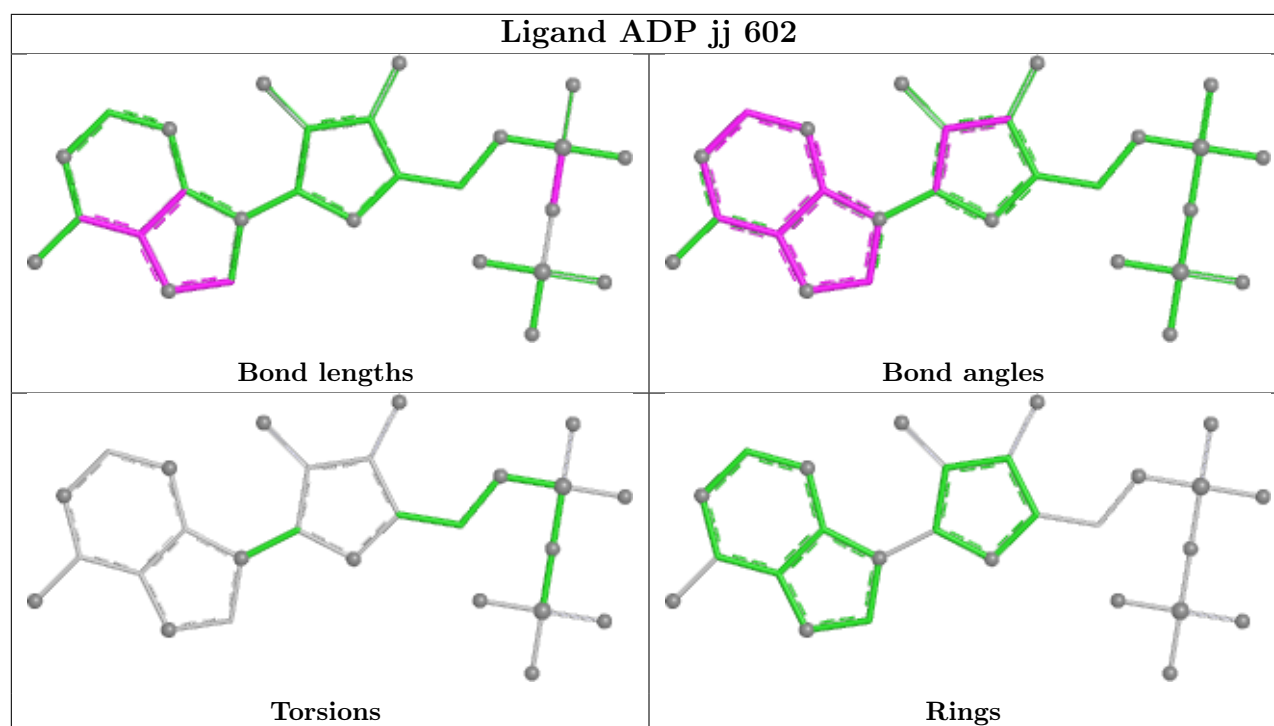
There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
90	jj	600	SF4	3	0
90	jj	601	SF4	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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
48	5	16
51	9	8
47	3	2
46	2	1
87	jj	1

The worst 5 of 28 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	9	753:C	O3'	785:C	P	23.51
1	9	126:G	O3'	139:C	P	21.53
1	9	698:G	O3'	730:C	P	20.02
1	5	4776:G	O3'	4859:C	P	17.98
1	9	1761:U	O3'	1771:G	P	17.66

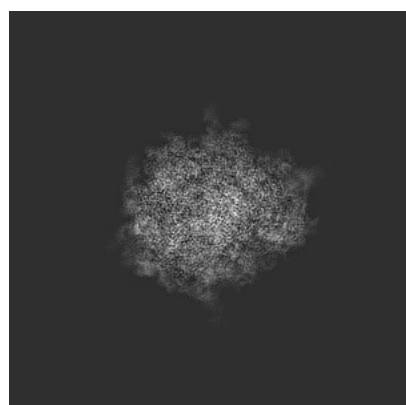
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3040. These allow visual inspection of the internal detail of the map and identification of artifacts.

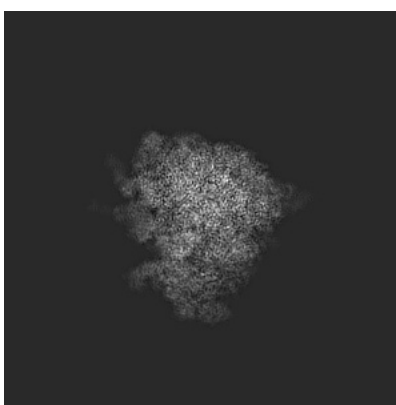
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

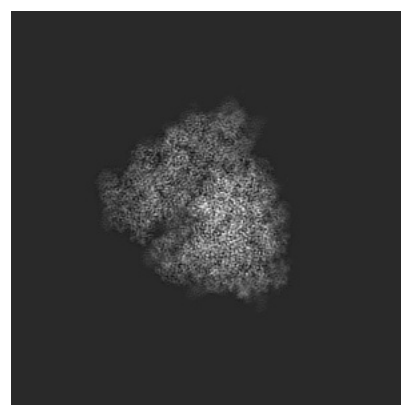
6.1.1 Primary map



X



Y



Z

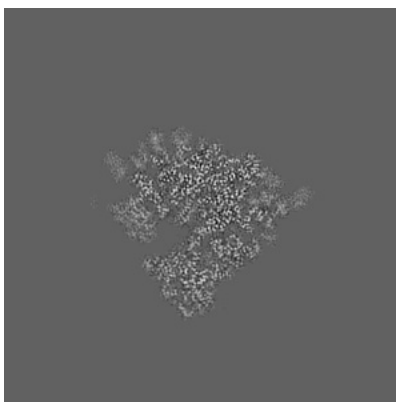
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

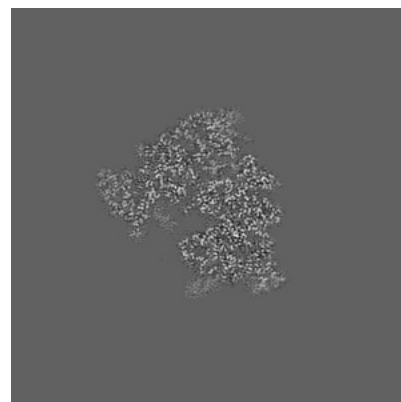
6.2.1 Primary map



X Index: 210



Y Index: 210

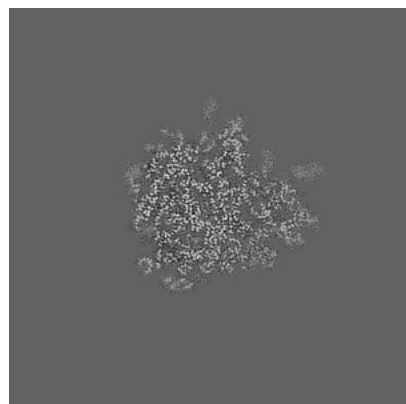


Z Index: 210

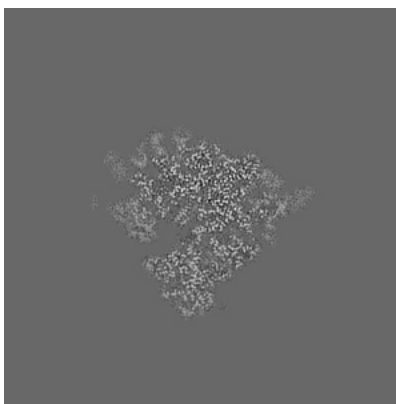
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

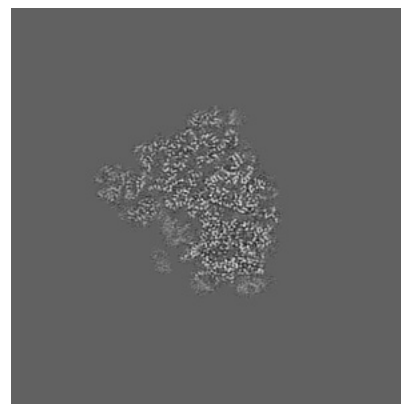
6.3.1 Primary map



X Index: 225



Y Index: 211

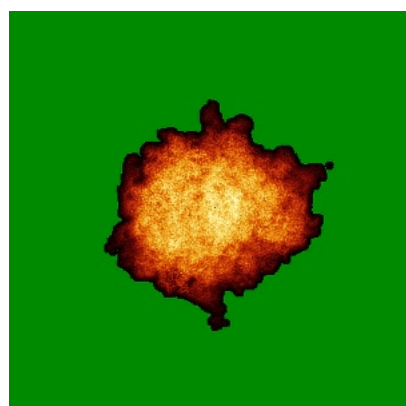


Z Index: 220

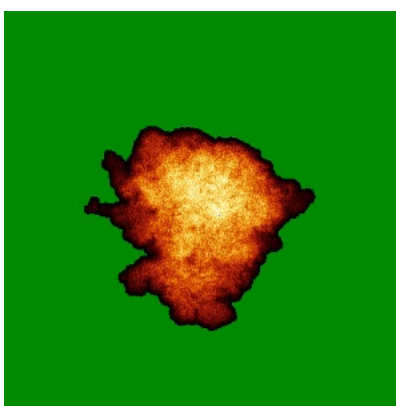
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

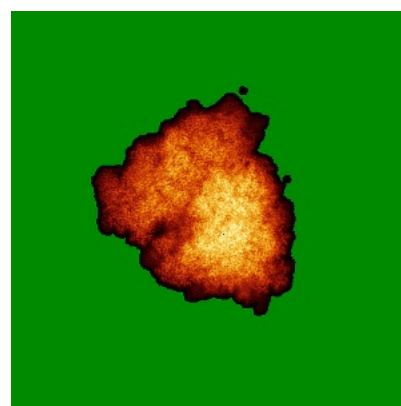
6.4.1 Primary map



X



Y

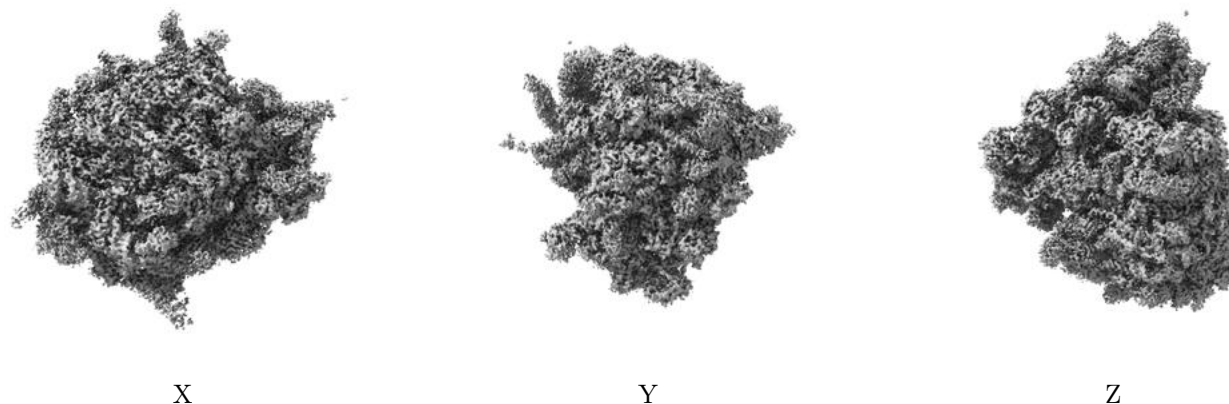


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

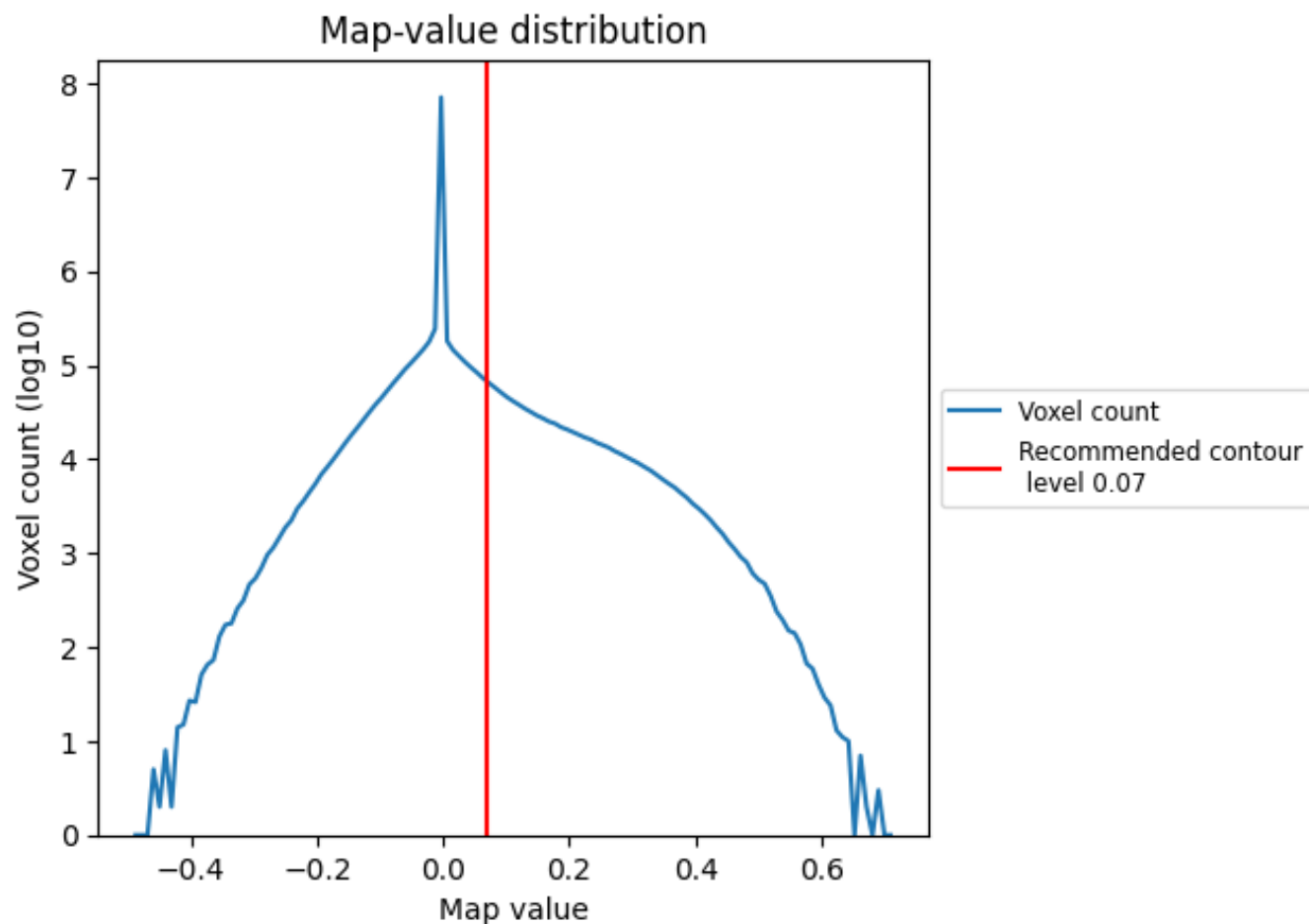
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

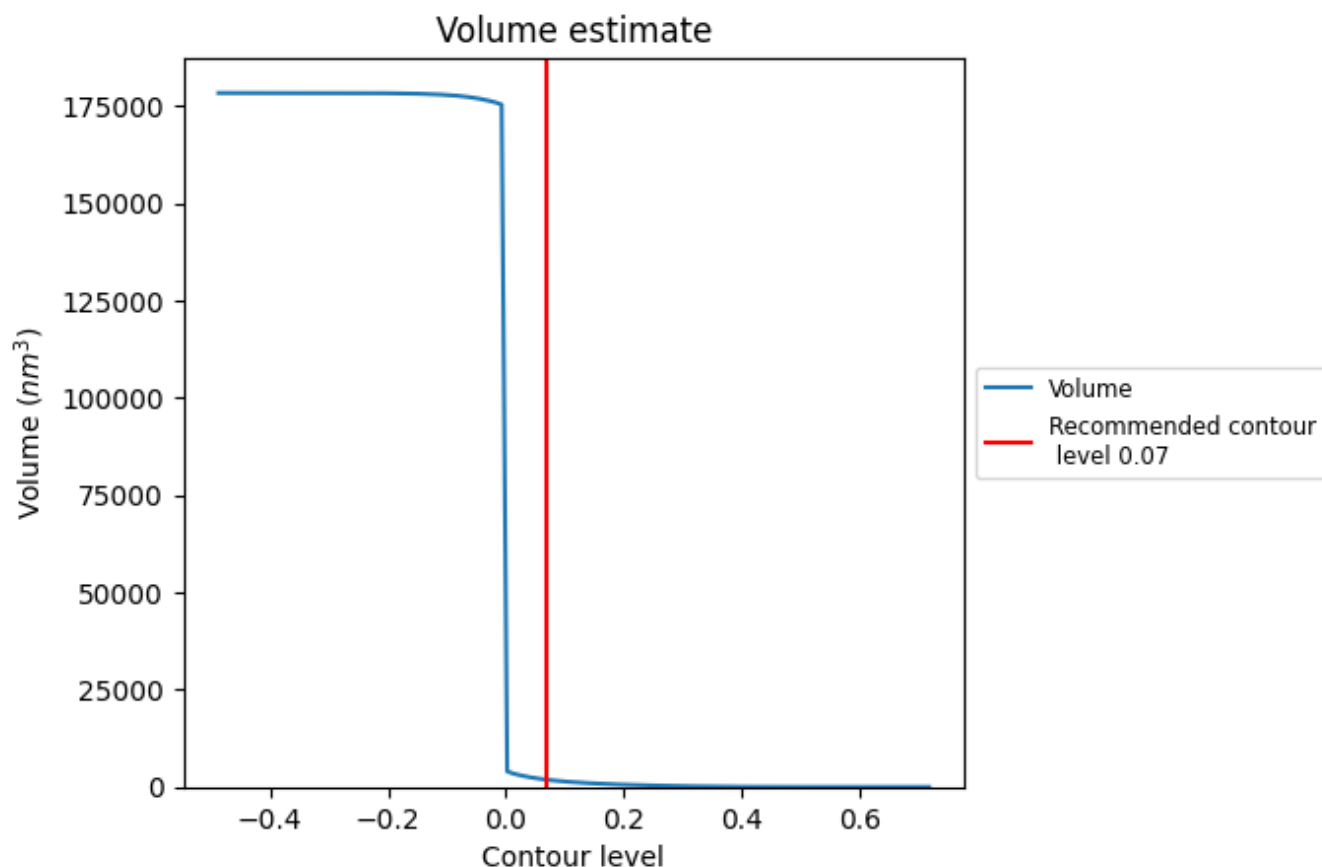
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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.

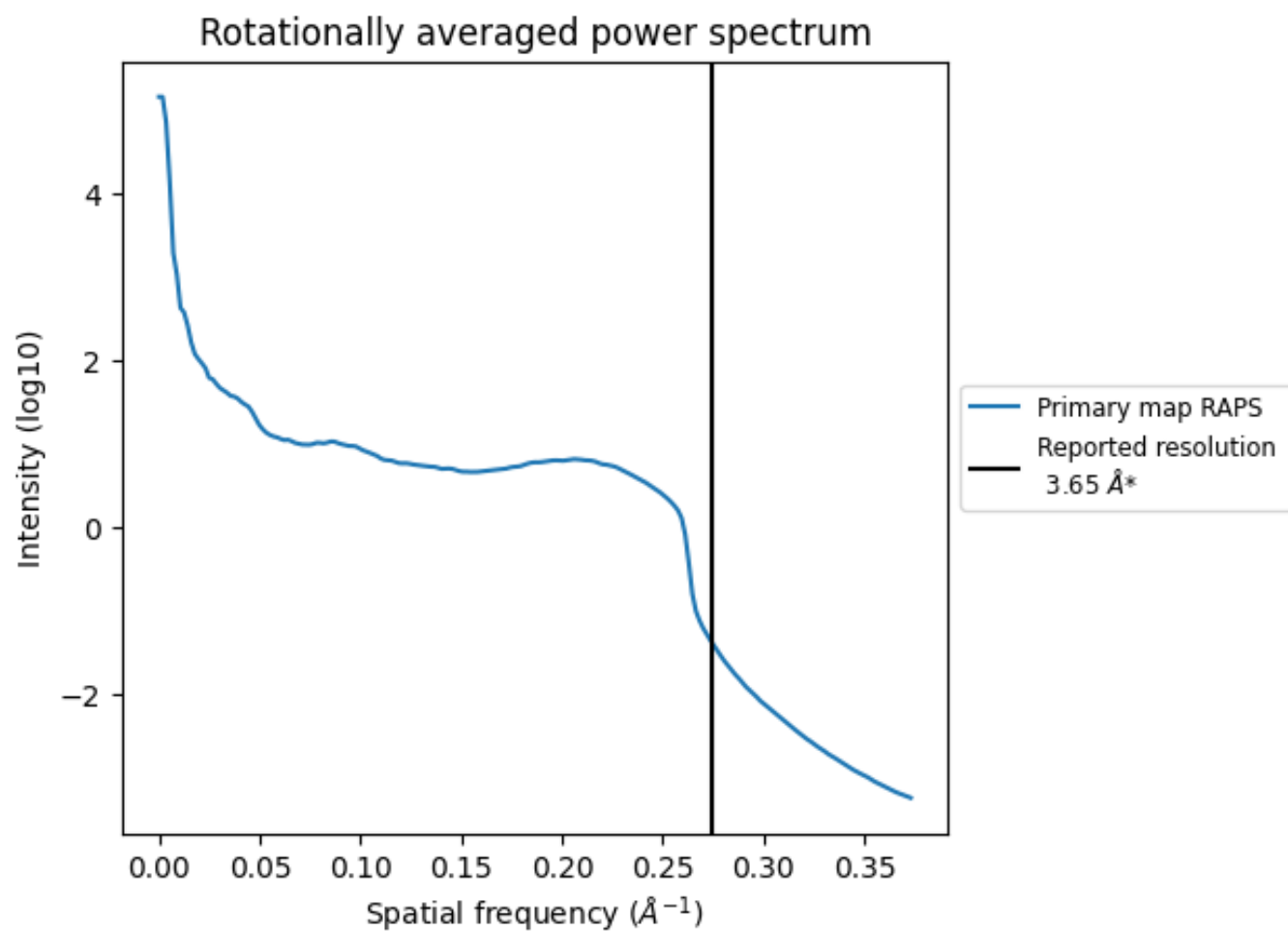
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1855 nm^3 ; this corresponds to an approximate mass of 1676 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 ⓘ

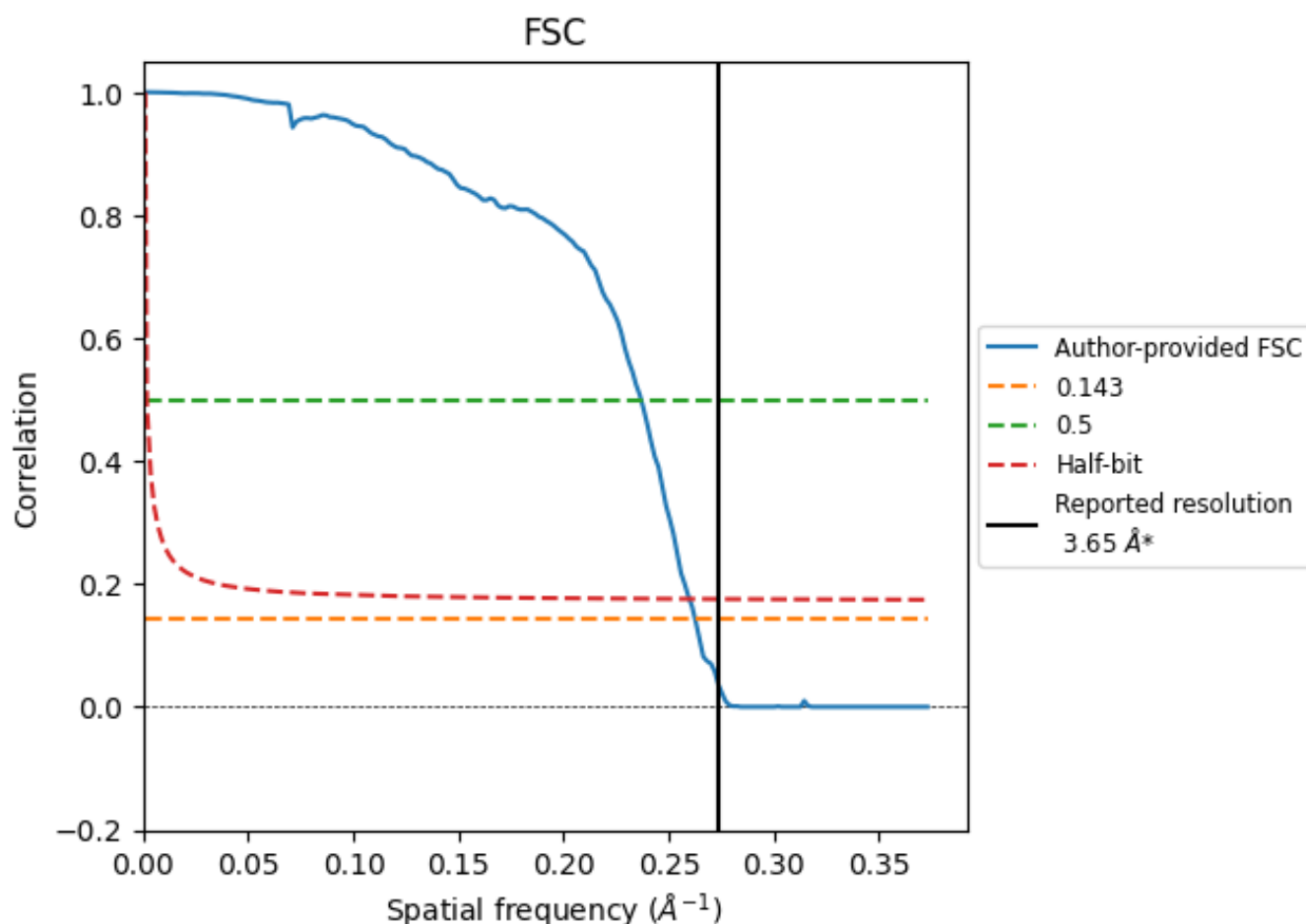


*Reported resolution corresponds to spatial frequency of 0.274 Å⁻¹

8 Fourier-Shell correlation [i](#)

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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.274 Å⁻¹

8.2 Resolution estimates [i](#)

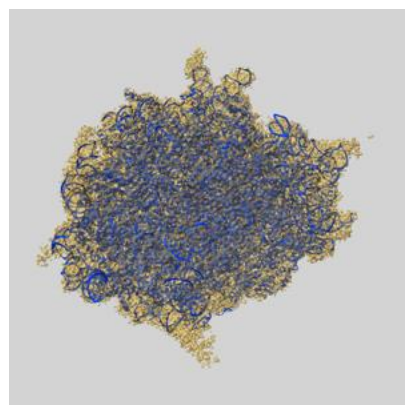
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.65	-	-
Author-provided FSC curve	3.81	4.22	3.85
Unmasked-calculated*	-	-	-

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

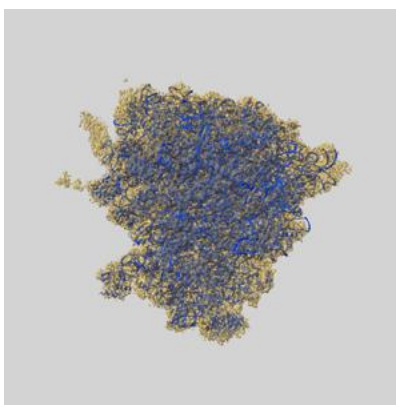
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3040 and PDB model 3JAI. Per-residue inclusion information can be found in section 3 on page 23.

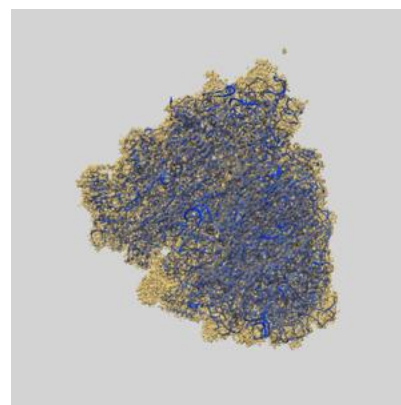
9.1 Map-model overlay [i](#)



X



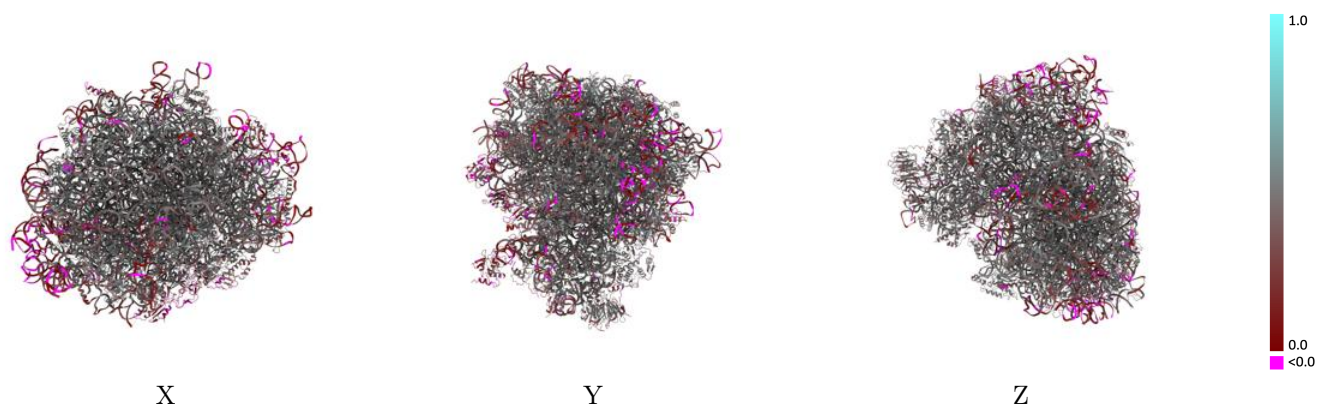
Y



Z

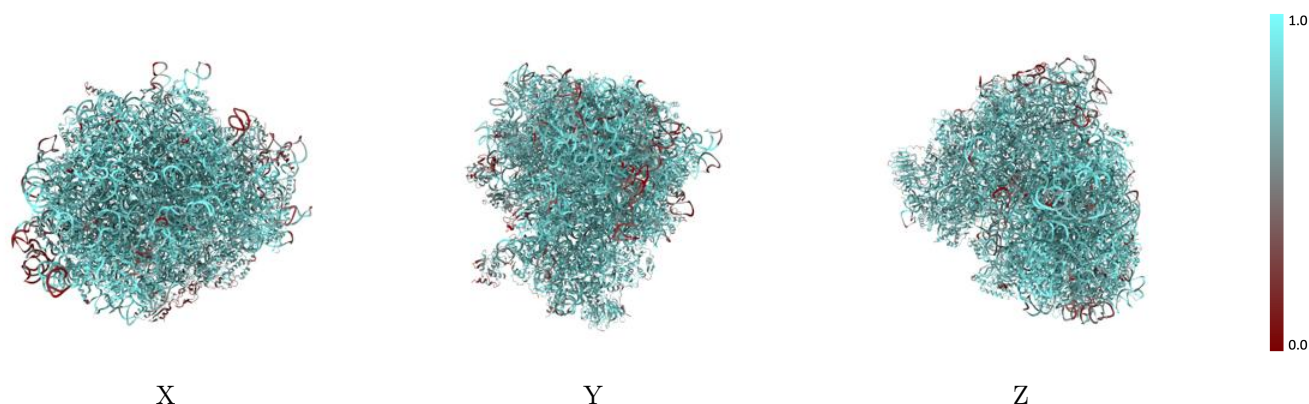
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



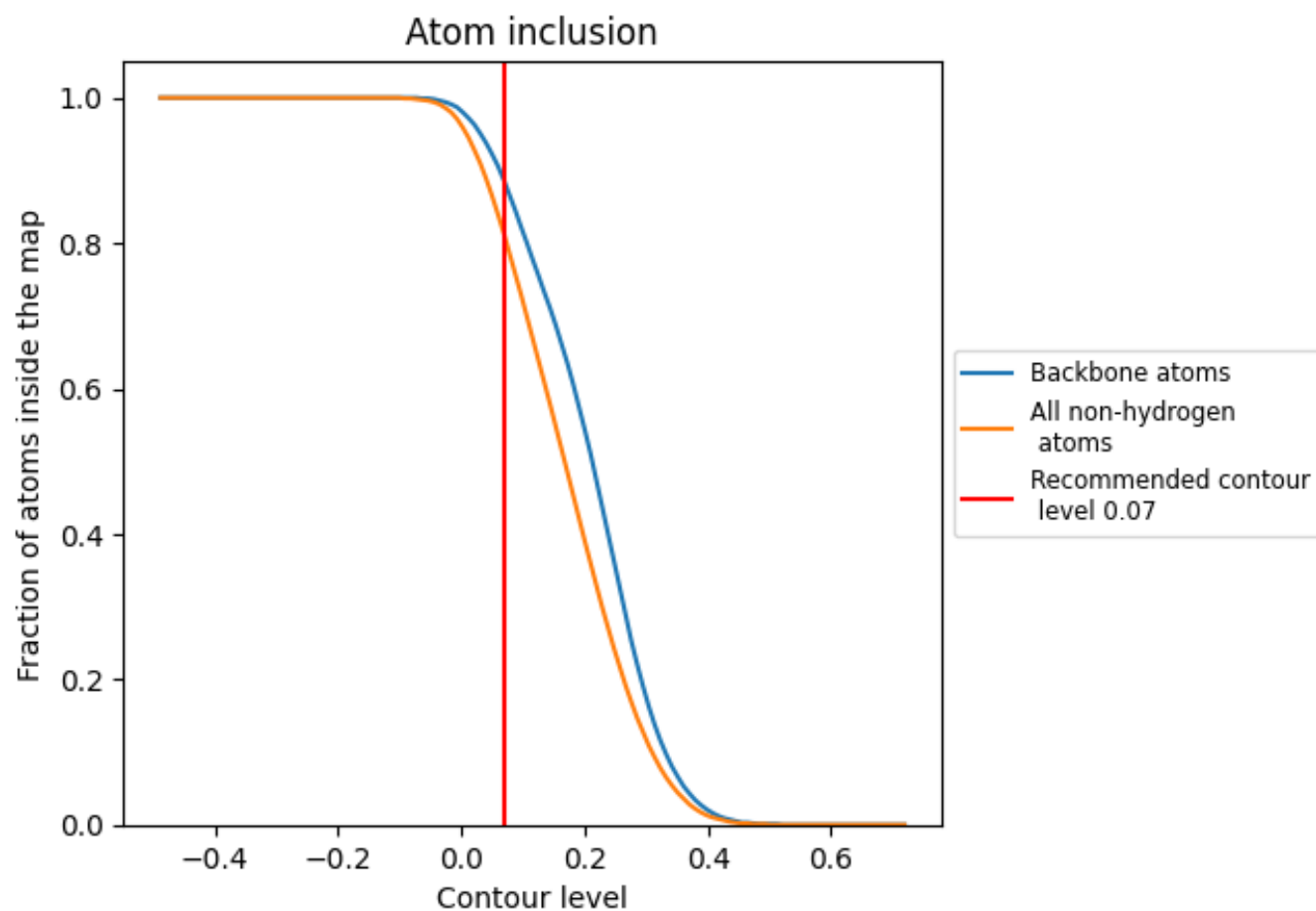
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



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 (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 81% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8110	 0.4030
1	 0.7600	 0.4260
2	 0.8210	 0.3620
3	 0.6600	 0.2310
5	 0.8310	 0.3780
7	 0.9160	 0.4410
8	 0.8640	 0.4060
9	 0.8390	 0.3840
A	 0.8530	 0.4850
AA	 0.8050	 0.4430
B	 0.8470	 0.4800
BB	 0.7990	 0.4590
C	 0.8490	 0.4760
CC	 0.8050	 0.4540
D	 0.8340	 0.4420
DD	 0.7230	 0.4000
E	 0.7650	 0.4120
EE	 0.8080	 0.4570
F	 0.8180	 0.4670
FF	 0.7540	 0.4220
G	 0.7670	 0.4160
GG	 0.7370	 0.3870
H	 0.8130	 0.4640
HH	 0.7020	 0.3610
I	 0.8300	 0.4730
II	 0.7740	 0.4220
J	 0.8020	 0.4350
JJ	 0.7840	 0.4300
KK	 0.7280	 0.3640
L	 0.8120	 0.4400
LL	 0.7710	 0.4380
M	 0.8360	 0.4580
MM	 0.4580	 0.1910
N	 0.8690	 0.4870
NN	 0.8100	 0.4550



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Chain	Atom inclusion	Q-score
O	 0.8390	 0.4720
OO	 0.8200	 0.4590
P	 0.8370	 0.4820
PP	 0.7130	 0.3720
Q	 0.8480	 0.4810
QQ	 0.7840	 0.4440
R	 0.8180	 0.4420
RR	 0.7230	 0.3950
S	 0.8510	 0.4770
SS	 0.7870	 0.4140
T	 0.8350	 0.4690
TT	 0.7950	 0.4250
U	 0.7960	 0.4300
UU	 0.7080	 0.3840
V	 0.8110	 0.4800
VV	 0.7800	 0.4310
W	 0.8330	 0.4770
WW	 0.8360	 0.4740
X	 0.8250	 0.4660
XX	 0.8210	 0.4710
Y	 0.8240	 0.4630
YY	 0.7840	 0.4190
Z	 0.8430	 0.4630
ZZ	 0.7440	 0.3880
a	 0.8680	 0.4870
aa	 0.8340	 0.4750
b	 0.7400	 0.4120
bb	 0.7570	 0.4290
c	 0.8450	 0.4690
cc	 0.7270	 0.4050
d	 0.8330	 0.4680
dd	 0.8220	 0.4600
e	 0.8410	 0.4750
ee	 0.6840	 0.3850
f	 0.8590	 0.4860
ff	 0.5830	 0.2490
g	 0.8220	 0.4560
gg	 0.7070	 0.3880
h	 0.8130	 0.4540
hh	 0.8330	 0.4170
i	 0.8130	 0.4520
ii	 0.6690	 0.3930

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Chain	Atom inclusion	Q-score
j	 0.8860	 0.4830
jj	 0.7110	 0.3920
k	 0.7790	 0.4280
l	 0.8580	 0.4850
m	 0.8410	 0.4610
n	 0.8410	 0.4620
o	 0.8320	 0.4780
p	 0.8330	 0.4680
r	 0.8550	 0.4750
s	 0.4230	 0.1690
t	 0.5070	 0.1640