



wwPDB EM Validation Summary Report ⓘ

Nov 17, 2024 – 12:57 PM EST

PDB ID : 3JAI
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 : 4V51, 3J92, 1DT9, 3BK7, 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.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

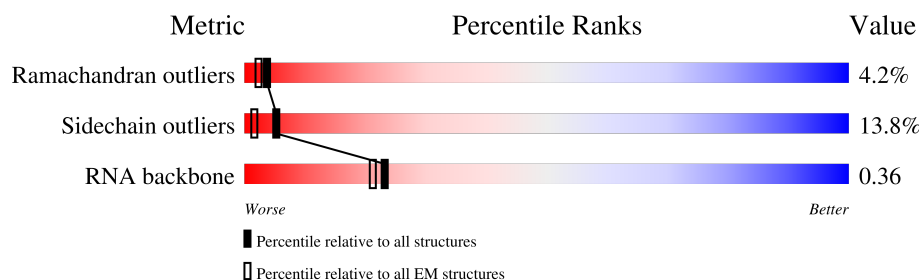
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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.













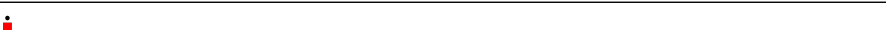

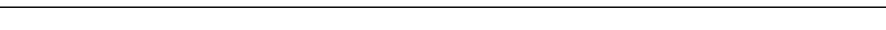
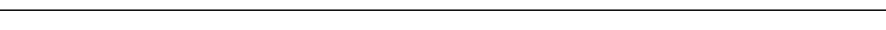











Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	
2	B	394	
3	C	361	
4	D	292	
5	E	248	
6	F	225	
7	G	241	
8	H	190	



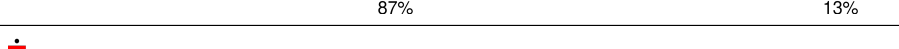
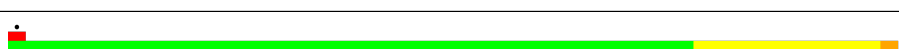







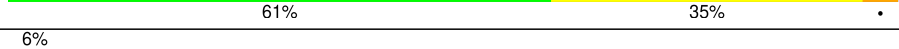

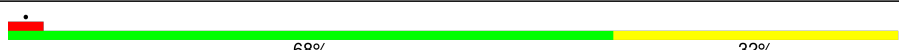


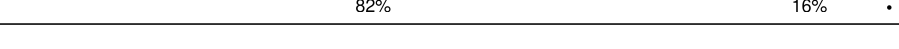







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Mol	Chain	Length	Quality of chain
9	I	213	 84% 11%
10	J	169	 86% 12%
11	L	210	 80% 18%
12	M	138	 91% 9%
13	N	203	 88% 11%
14	O	199	 83% 17%
15	P	153	 88% 12%
16	Q	187	 87% 13%
17	R	180	 87% 13%
18	S	175	 86% 12%
19	T	159	 83% 16%
20	U	99	 87% 12%
21	V	131	 85% 15%
22	W	63	 89% 10%
23	X	119	 87% 13%
24	Y	134	 84% 14%
25	Z	135	 84% 16%
26	a	147	 88% 9%
27	b	75	 13% 85% 13%
28	c	94	 85% 15%
29	d	107	 81% 17%
30	e	128	 82% 17%
31	f	109	 82% 17%
32	g	114	 82% 18%
33	h	122	 85% 14%

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Mol	Chain	Length	Quality of chain
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	
54	CC	218	
55	DD	227	
56	EE	262	
57	FF	191	
58	GG	237	


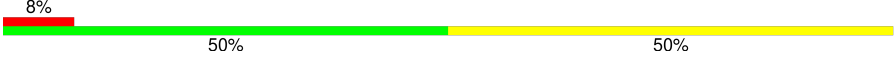

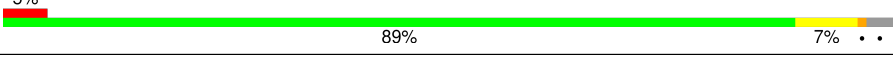
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Mol	Chain	Length	Quality of chain
59	HH	189	
60	II	206	
61	JJ	185	
62	KK	98	
63	LL	152	
64	MM	124	
65	NN	150	
66	OO	136	
67	PP	127	
68	QQ	141	
69	RR	129	
70	SS	137	
71	TT	141	
72	UU	104	
73	VV	83	
74	WW	129	
75	XX	141	
76	YY	126	
77	ZZ	75	
78	aa	98	
79	bb	83	
80	cc	61	
81	dd	53	
82	ee	57	
83	ff	68	

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Mol	Chain	Length	Quality of chain
84	gg	313	
85	hh	12	
86	ii	416	
87	jj	594	

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		

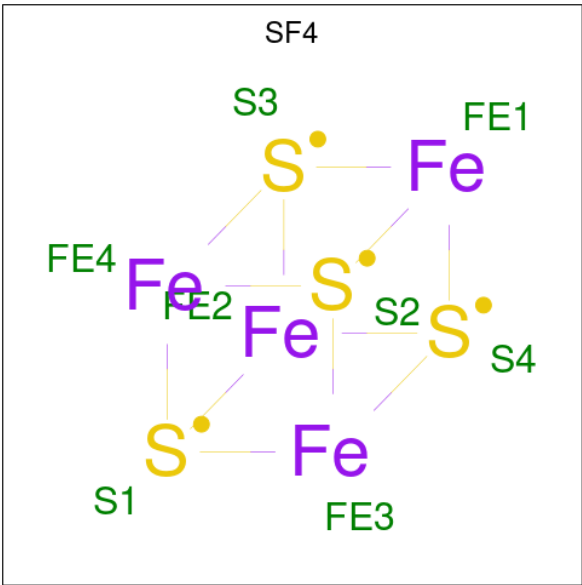
- Molecule 88 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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 (three-letter code: ZN) (formula: Zn).

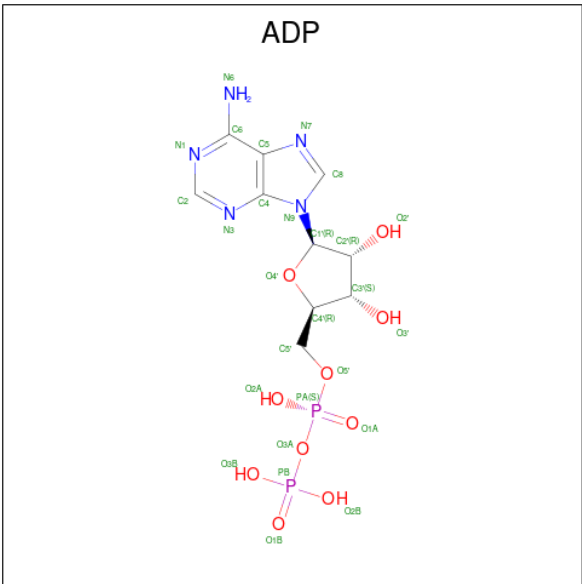
Mol	Chain	Residues	Atoms		AltConf
89	g	1	Total 1	Zn 1	0
89	j	1	Total 1	Zn 1	0
89	m	1	Total 1	Zn 1	0
89	o	1	Total 1	Zn 1	0
89	p	1	Total 1	Zn 1	0
89	aa	1	Total 1	Zn 1	0
89	dd	1	Total 1	Zn 1	0
89	ff	1	Total 1	Zn 1	0

- Molecule 90 is IRON/SULFUR CLUSTER (three-letter code: 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 (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



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

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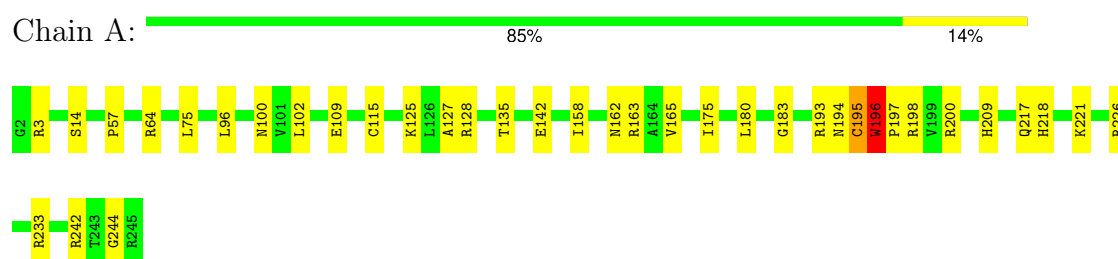
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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
91	jj	1	27	10	5	10	2	0

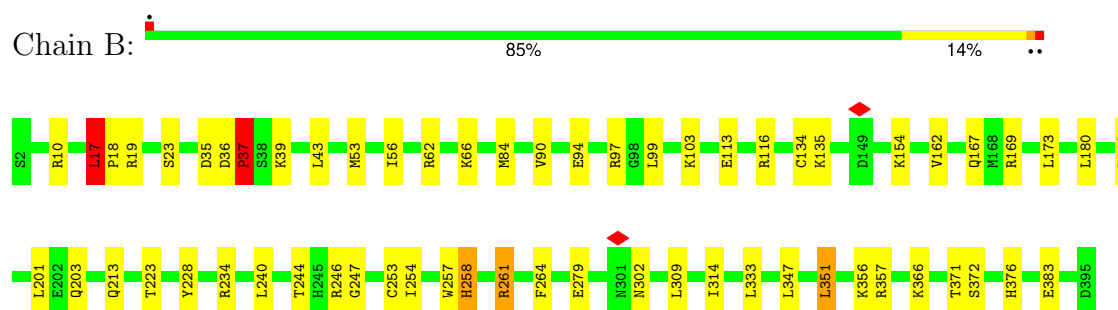
3 Residue-property plots [i](#)

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.

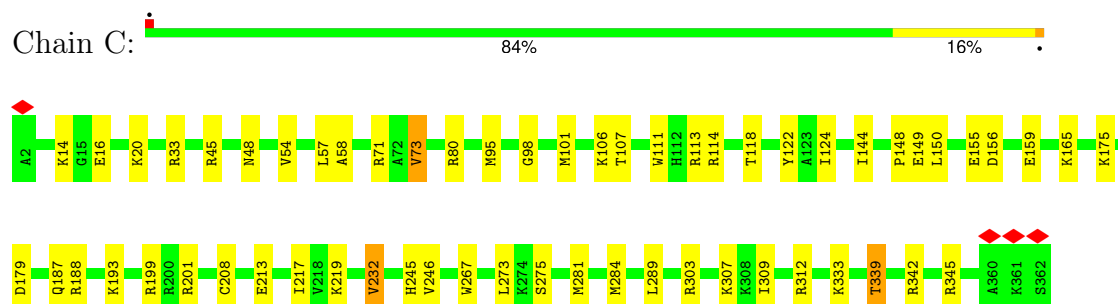
• Molecule 1: uL2



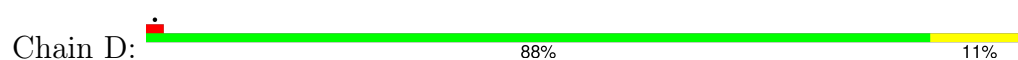
• Molecule 2: uL3

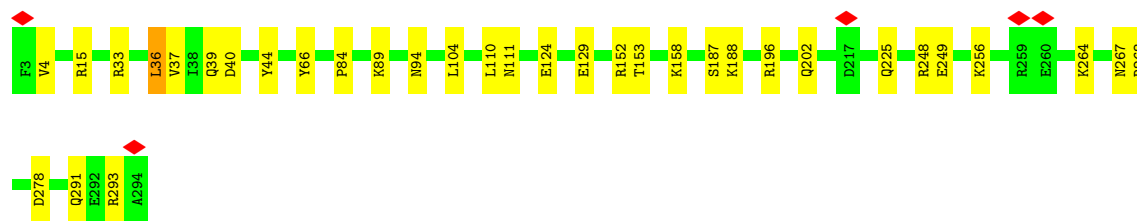


• Molecule 3: uL4

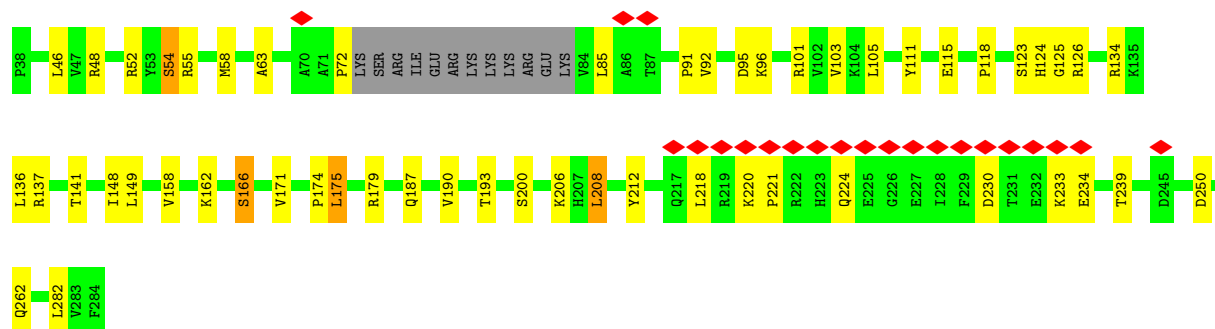
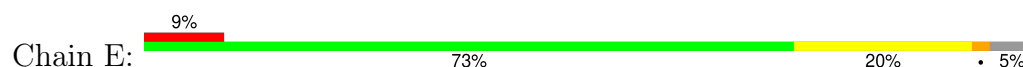


• Molecule 4: uL18





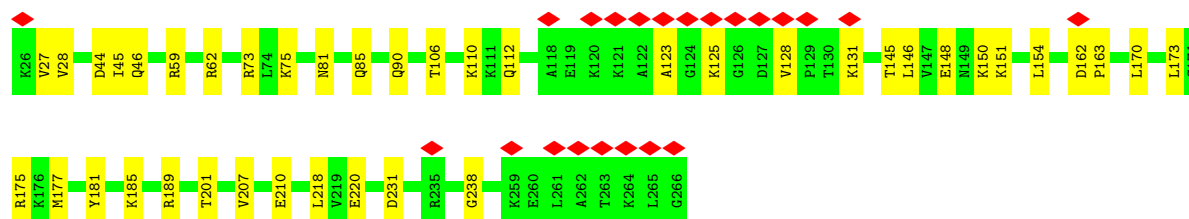
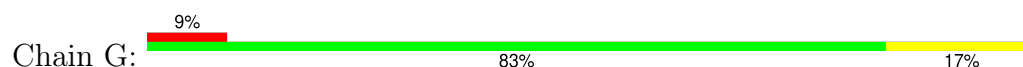
• Molecule 5: eL6



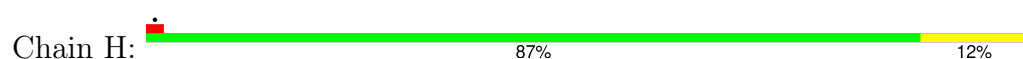
• Molecule 6: uL30



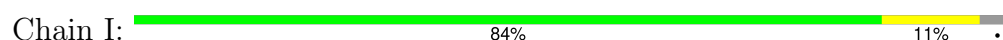
• Molecule 7: eL8

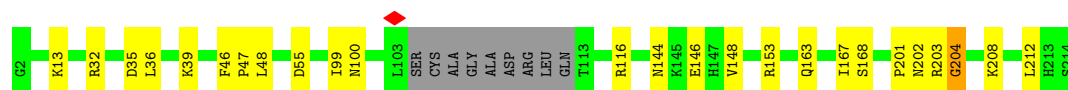


• Molecule 8: uL6

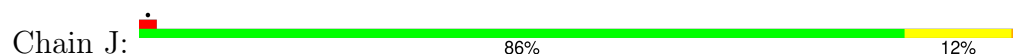


• Molecule 9: uL16

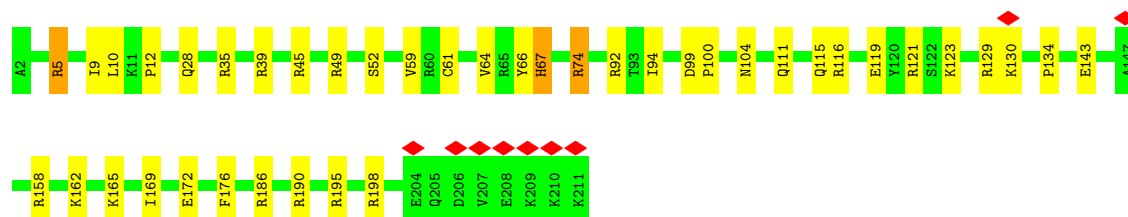
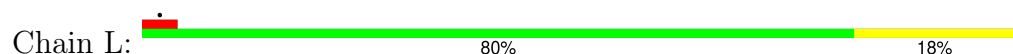




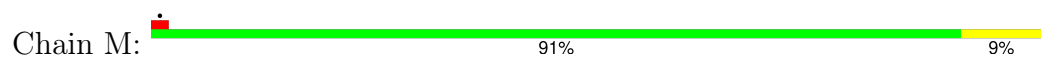
- Molecule 10: uL5



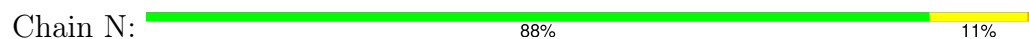
- Molecule 11: eL13



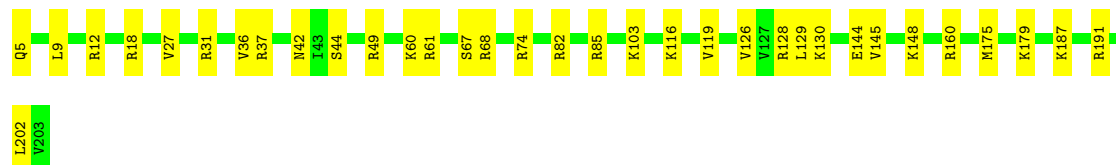
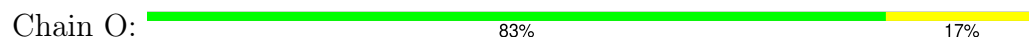
- Molecule 12: eL14



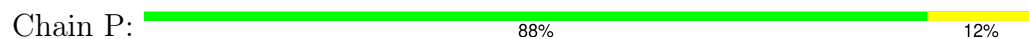
- Molecule 13: eL15



- Molecule 14: uL13

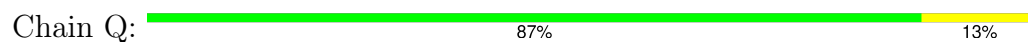


- Molecule 15: uL22

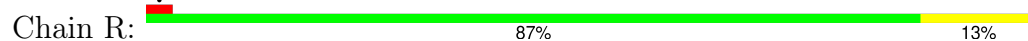




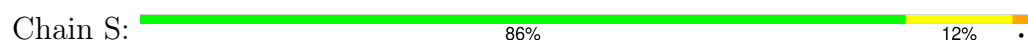
- Molecule 16: eL18



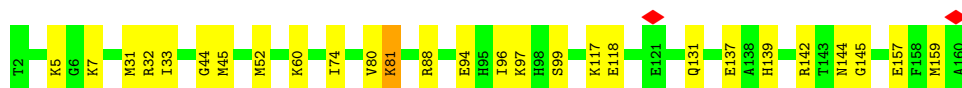
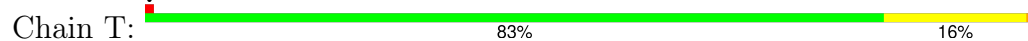
- Molecule 17: eL19



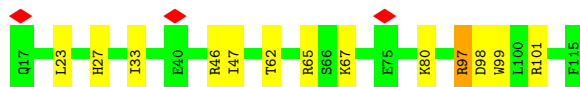
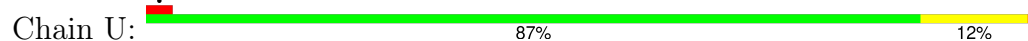
- Molecule 18: eL20



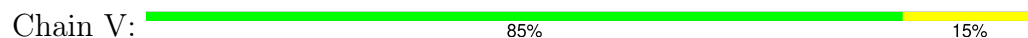
- Molecule 19: eL21



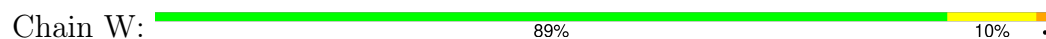
- Molecule 20: eL22

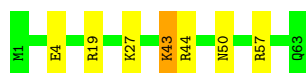


- Molecule 21: uL14



- Molecule 22: eL24





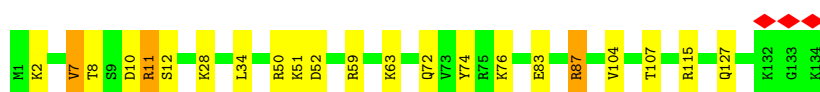
• Molecule 23: uL23

Chain X: 87% 13%



• Molecule 24: uL24

Chain Y: 84% 14% .



• Molecule 25: eL27

Chain Z: 84% 16%



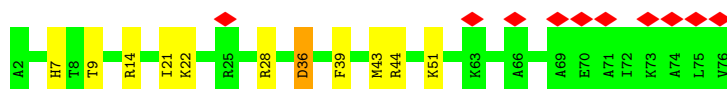
• Molecule 26: uL15

Chain a: 88% 9% .



• Molecule 27: eL29

Chain b: 13% 85% 13% .



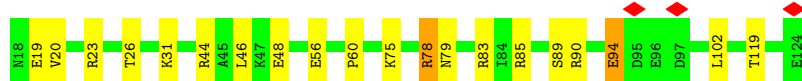
• Molecule 28: eL30

Chain c: 85% 15%

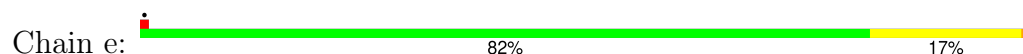


• Molecule 29: eL31

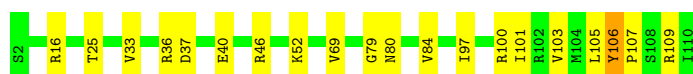
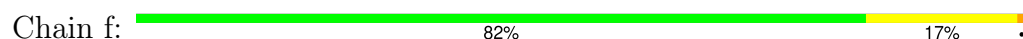
Chain d: 81% 17% .



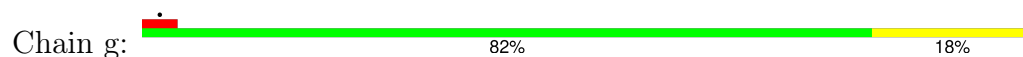
• Molecule 30: eL32



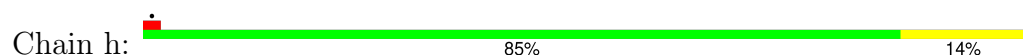
• Molecule 31: eL33



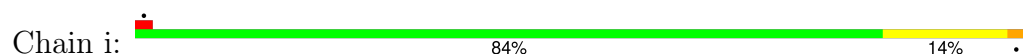
• Molecule 32: eL34



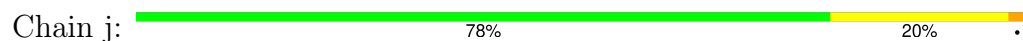
• Molecule 33: uL29



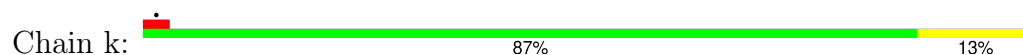
• Molecule 34: eL36



• Molecule 35: eL37

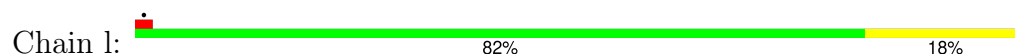


• Molecule 36: eL38

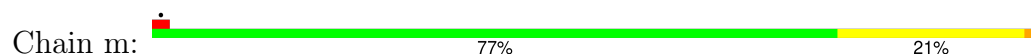




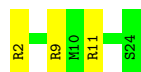
• Molecule 37: eL39



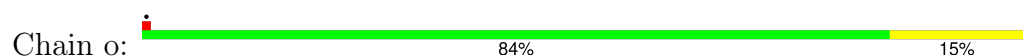
• Molecule 38: eL40



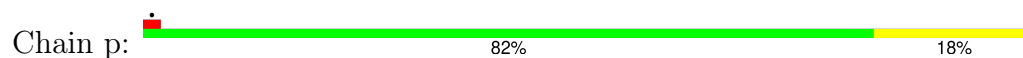
• Molecule 39: eL41



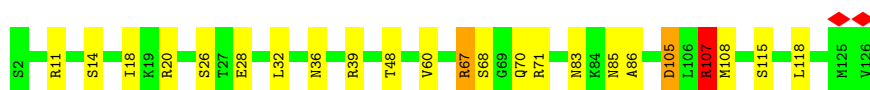
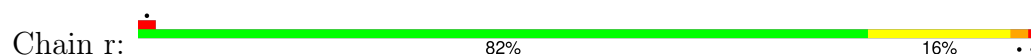
• Molecule 40: eL42



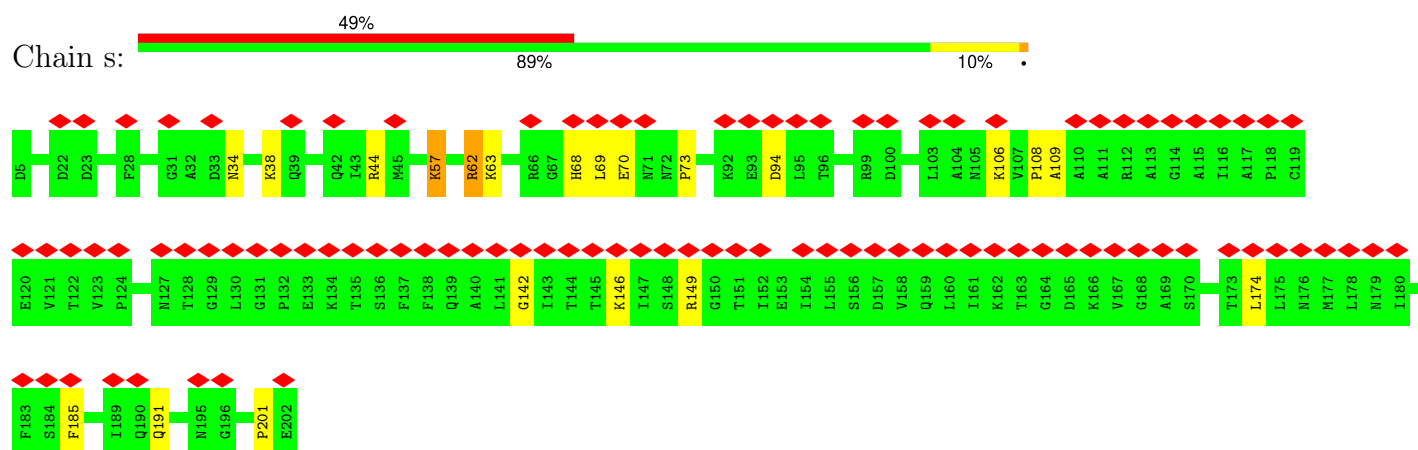
• Molecule 41: eL43



• Molecule 42: eL28



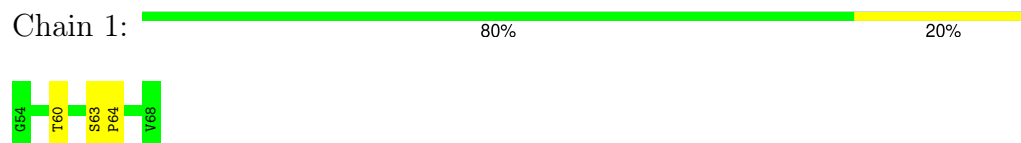
• Molecule 43: uL10



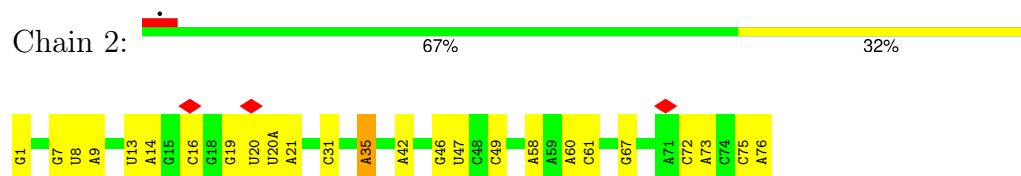
- Molecule 44: uL11



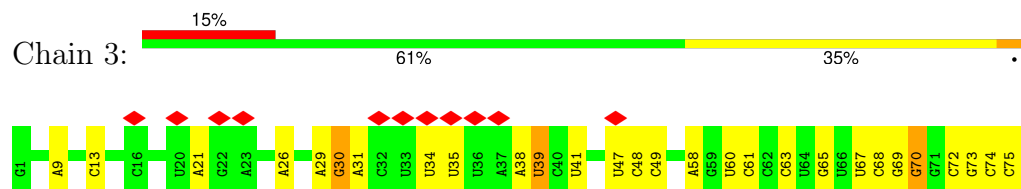
- Molecule 45: peptide



- Molecule 46: tRNA(Val)

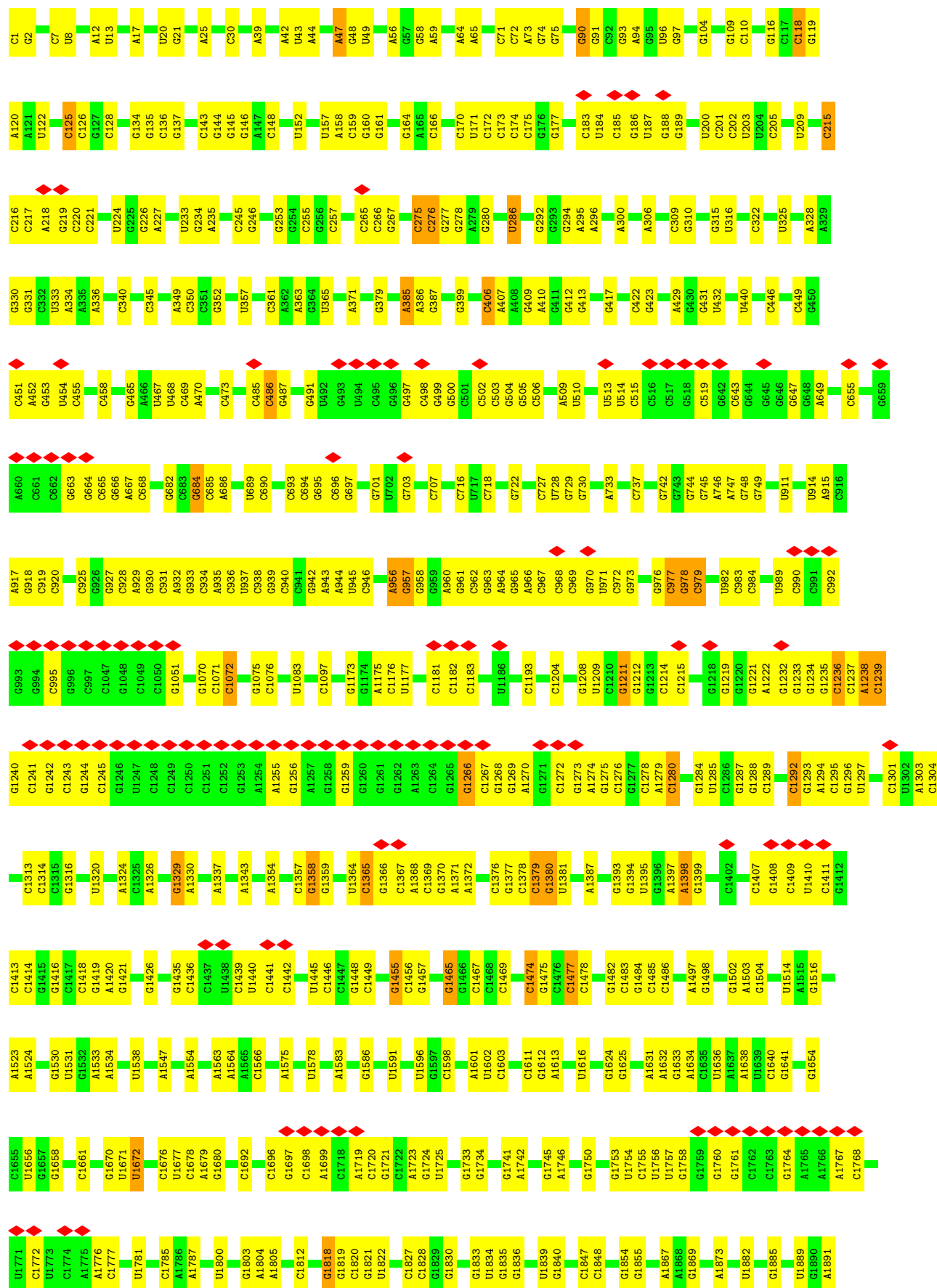


- Molecule 47: tRNA(Lys)

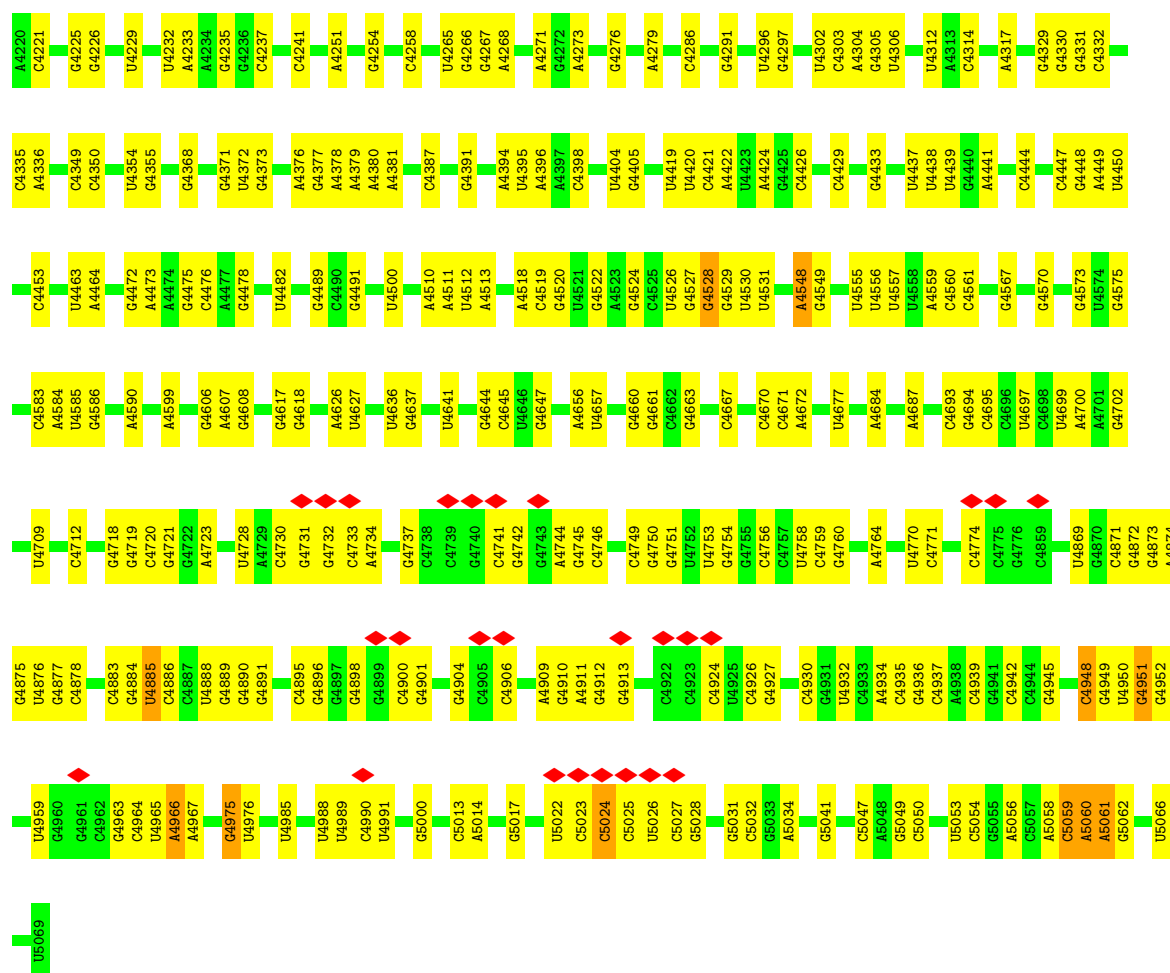


- Molecule 48: 28S ribosomal RNA

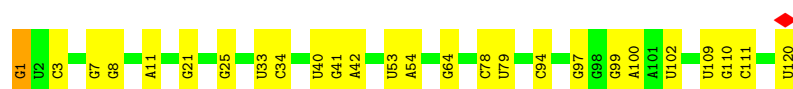
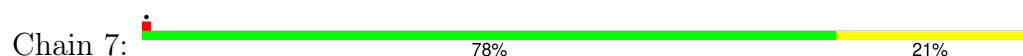




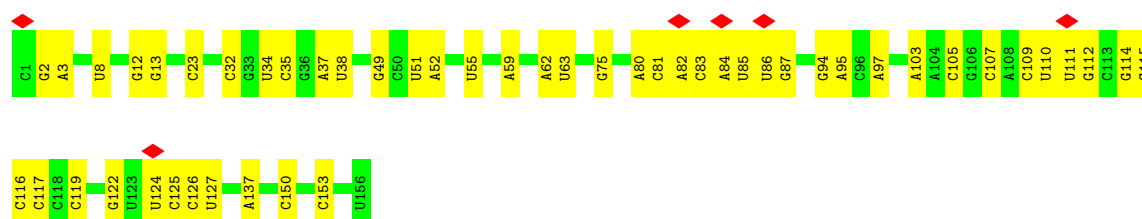
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A3905	A3785	G2897	U2763	G2649	G2400	C2258	A1991	C1893
A3906	G3669	G2898	U2767	G2658	A2401	C2259	A1992	C1894
G3907	G3670	G2898	C2768	G2661	G2416	U2090	C1983	A1897
U3912	G3671	G2902	U2769	G2662	A2417	G2261	U1997	C1898
G3913	G3672	G2903	C2770	G2669	G2421	G2262	A1998	C1899
U3914	G3673	U2904	C2771	G2670	G2422	C2263	G2001	C1900
U3915	G3674	G2905	C2772	C2676	A2423	C2264	A2002	G1910
G3916	U3680	G2906	C2777	A2676	G2424	C2265	G2003	A1917
G3917	G3681	G2907	G2778	A2676	U2425	C2266	U2004	U1918
G3918	A3682	G2908	A2787	G2686	U2426	U2267	G2005	G1919
U3925	A3692	U2908	U2788	G2687	A2428	A2268	U2008	C1920
G3926	G3696	G2909	A2789	G2688	G2433	G2270	G2009	C1921
U3927	U3697	C2910	U2790	G2689	G2433	A2271	G2011	G1922
G3938	G3698	U3583	C2794	G2694	C2437	G2275	C2011	A1923
G3939	U3698	G3584	A2795	A2695	U2440	C2276	G2018	A1929
A3943	U3709	G3585	G2796	A2696	C2441	C2277	C2019	U1930
G3946	A3710	G3586	C2797	A2697	G2442	A2278	U2020	C1931
A3947	A3711	G3587	A2798	A2697	G2443	C2279	G2021	A1939
C3948	A3712	C3587	U2798	G2703	G2443	G2288	C2022	G1940
A3949	U3713	C3588	C2802	G2703	U2447	C2289	C2023	U1947
U4069	A3717	G3589	A2806	U2707	U2447	C2295	G2024	G1948
U4070	A3718	G3590	U2807	U2708	G2450	C2296	A2025	A1956
A4073	A3719	C3591	G2808	U2708	U2467	C2297	A2026	U1957
C4074	U3729	G3592	A2815	C2709	U2468	G2298	U2027	A1958
U4075	G3827	C3593	G2815	C2710	C2469	C2301	C2028	U1959
G4076	C3828	G3594	U2820	G2711	G2470	A2313	A2040	A1960
A4084	A3829	U3595	G2821	C2712	G2471	G2314	A2041	G1961
A4085	G3830	G3596	C2822	C2713	A2472	G2332	G2046	A1962
G4086	A3831	G3597	G2822	G2714	A2473	C2333	A2047	C1963
G4087	G3832	C3598	A2825	G2715	G2474	C2335	U2054	A1964
A4088	U3833	G3605	U2826	C2716	G2475	U2344	G2055	G1965
G4091	G3834	G3609	G2827	G2721	U2485	G2348	G1968	G1969
G4092	A3835	G3615	U2828	G2722	C2488	C2351	A2057	G1972
G4093	G3836	U3616	U2829	G2723	U2489	G2360	G2058	G1973
G4094	A3837	G3625	G2838	A2724	U2490	A2374	C2062	U1974
G4095	G3838	G3626	U2839	G2725	C2491	G2374	G2063	G1975
G4097	G3839	G3627	G2842	G2726	U2495	G2384	G2064	G1976
C4100	G3889	G3628	U2843	U2734	U2495	A2370	C2067	U1980
C4101	A3890	A3629	A2844	G2741	G2502	A2391	C2068	G1981
C4102	G3891	G3630	A2845	U2742	G2503	G2391	A2069	G1982
C4103	U3770	A3635	G2846	A2743	C2504	G2394	U2070	A1984
G4104	U3773	U3644	A2850	A2744	C2505	A2396	A2071	G1985
A4105	A3774	G3661	G2855	G2754	G2506	A2397	C2072	U1986
A4106	A3775	G3662	A2858	A2756	A2507	G2398	G2079	C1987
A4107	G3776	G3663	G2859	A2757	A2511	C2246	C2083	G1988
A4108	G3777	G3664	U2862	U2760	A2512	C2247	C2084	
A4109			U2874	U2761	G2514	C2248		
A4110						C2249		
						C2250		
						G2251		
						G2252		
						A2253		
						G2254		
						G2255		
						C2256		



• Molecule 49: 5S ribosomal RNA



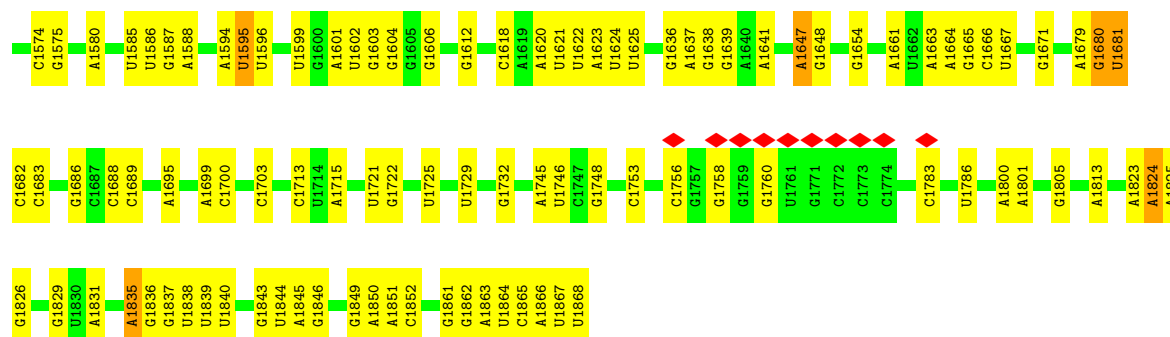
• Molecule 50: 5.8S ribosomal RNA



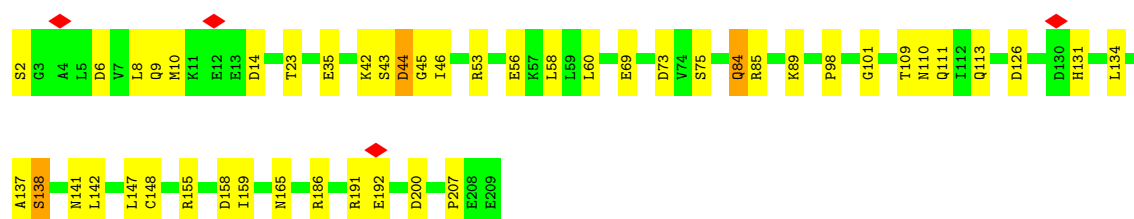
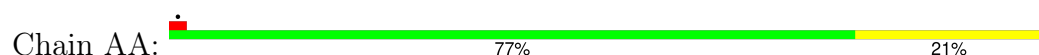
• Molecule 51: 18S ribosomal RNA



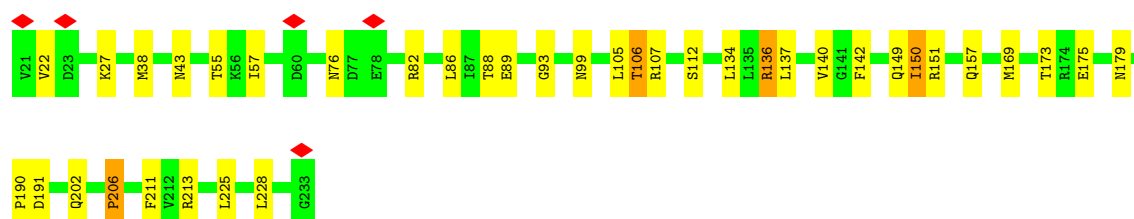
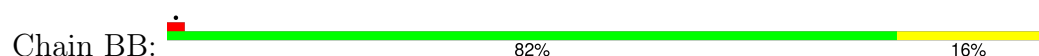




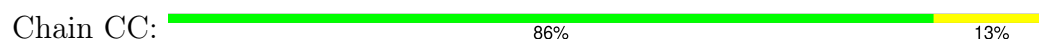
• Molecule 52: uS2



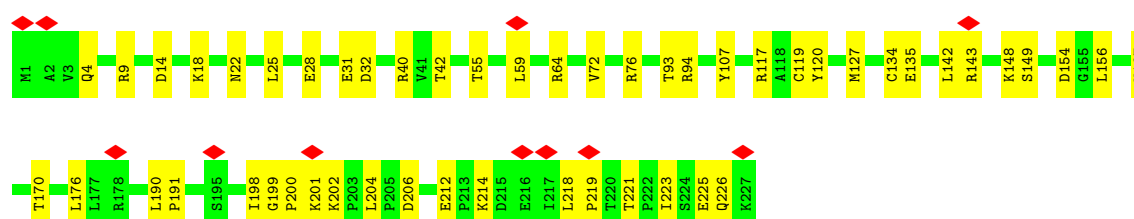
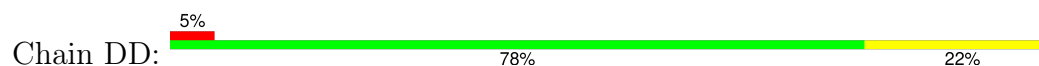
• Molecule 53: eS1




• Molecule 54: uS5

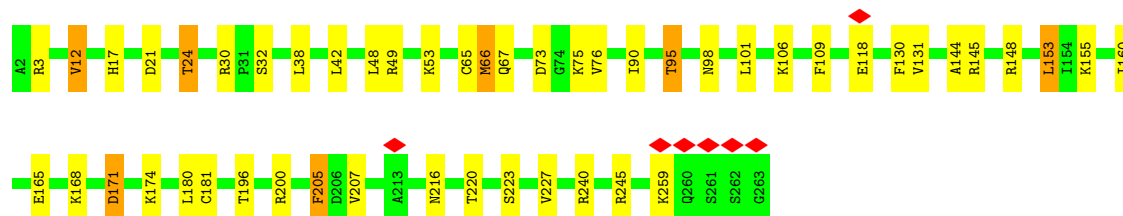


• Molecule 55: uS3




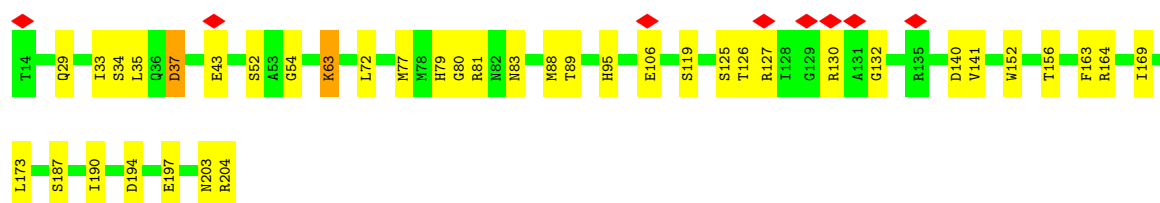
- Molecule 56: eS4

Chain EE:  81% 16%




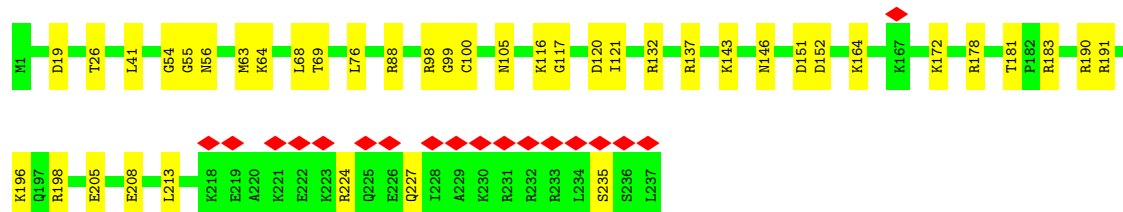
- Molecule 57: uS7

Chain FF:  80% 19%




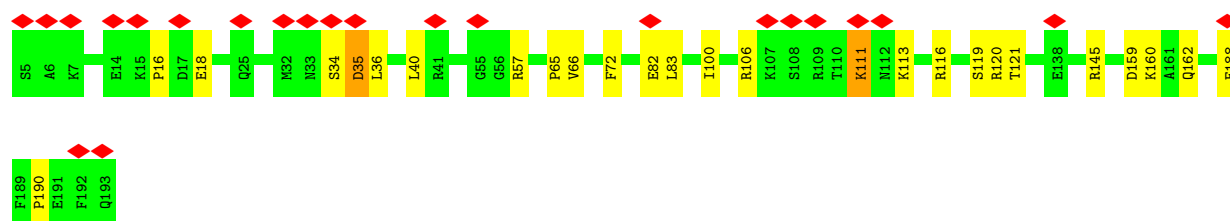
- Molecule 58: eS6

Chain GG:  8% 83% 17%




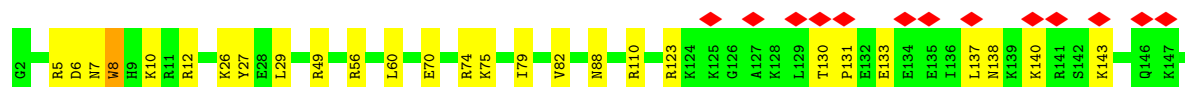
- Molecule 59: eS7

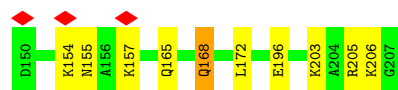
Chain HH:  12% 86% 13%



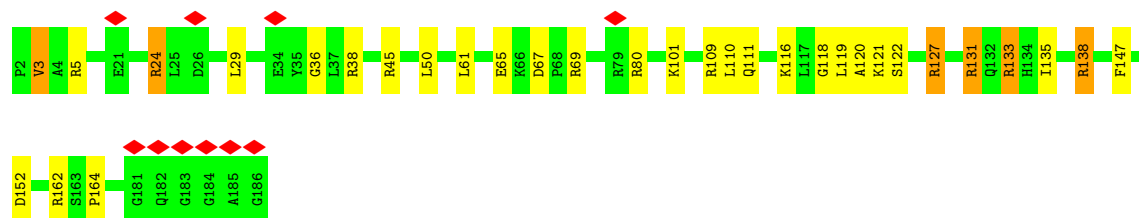
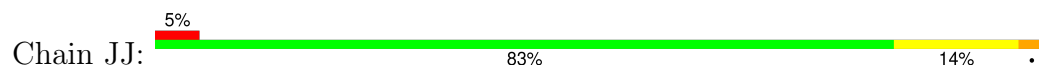
- Molecule 60: eS8

Chain II:  8% 82% 17%

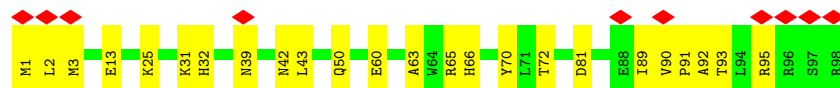
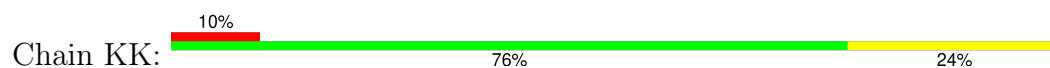




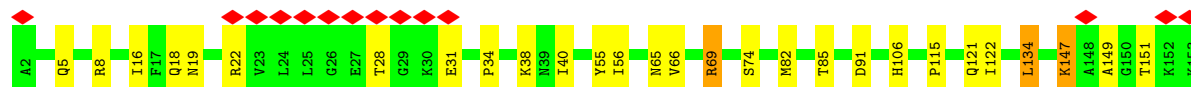
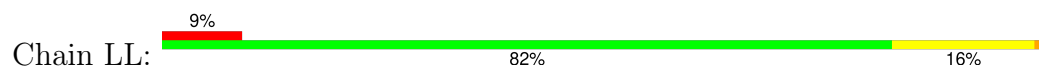
• Molecule 61: uS4



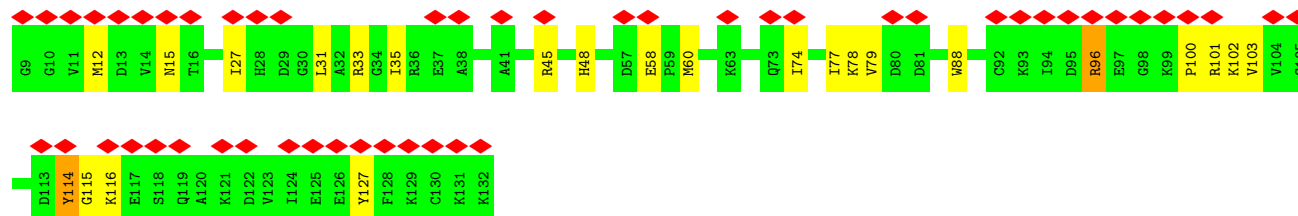
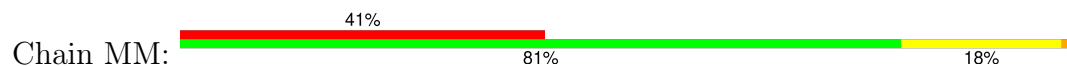
• Molecule 62: eS10



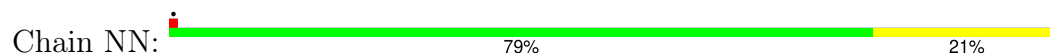
• Molecule 63: uS17



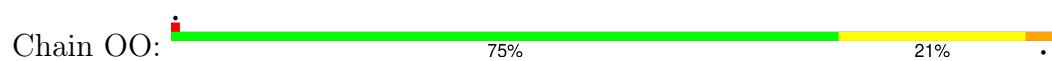
• Molecule 64: eS12



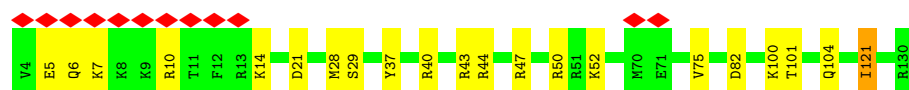
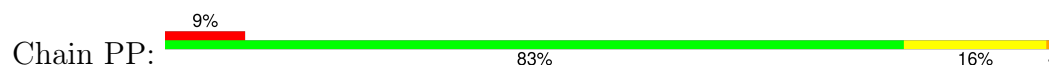
• Molecule 65: uS15



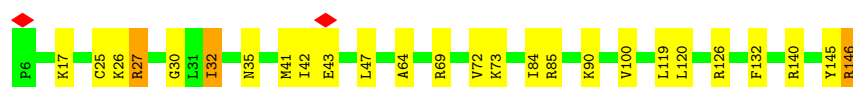
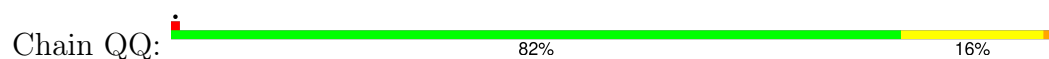
• Molecule 66: uS11



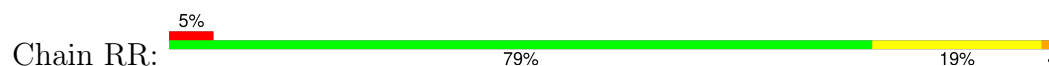
- Molecule 67: uS19



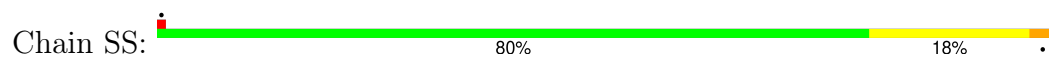
- Molecule 68: uS9



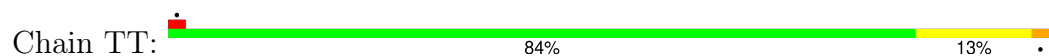
- Molecule 69: eS17



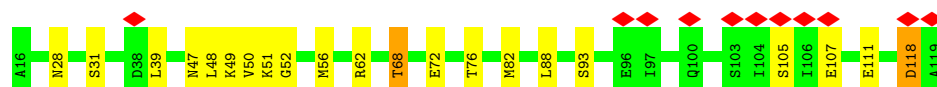
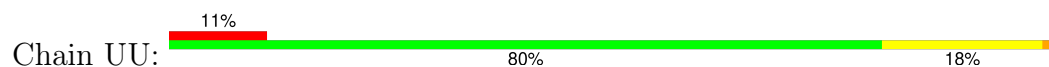
- Molecule 70: uS13




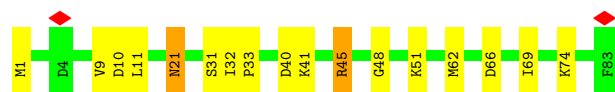
- Molecule 71: eS19



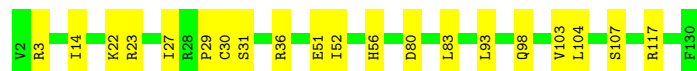
- Molecule 72: uS10




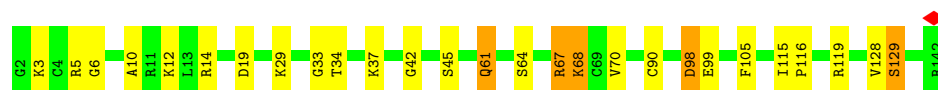
• Molecule 73: eS21

Chain VV:  80% 18%


• Molecule 74: uS8

Chain WW:  84% 16%


• Molecule 75: uS12

Chain XX:  81% 16%


• Molecule 76: eS24

Chain YY:  5% 76% 23%


• Molecule 77: eS25

Chain ZZ:  84% 16%

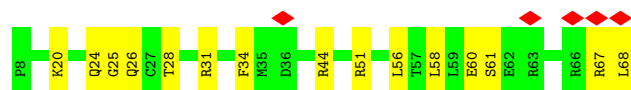
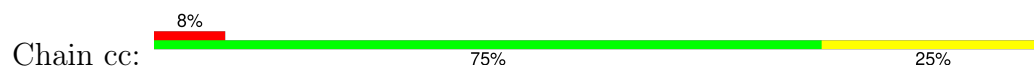
• Molecule 78: eS26

Chain aa:  77% 21%

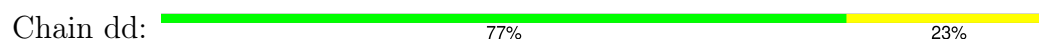
• Molecule 79: eS27

Chain bb:  5% 81% 19%

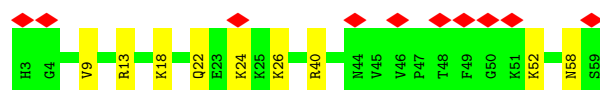
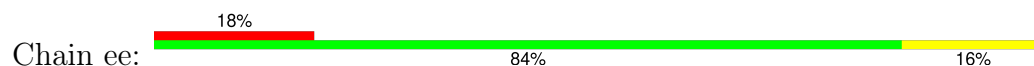
- Molecule 80: eS28



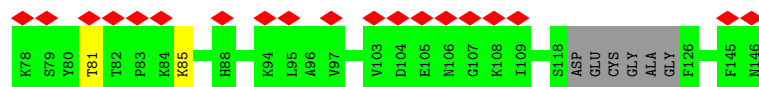
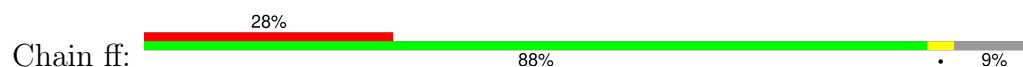
- Molecule 81: uS14



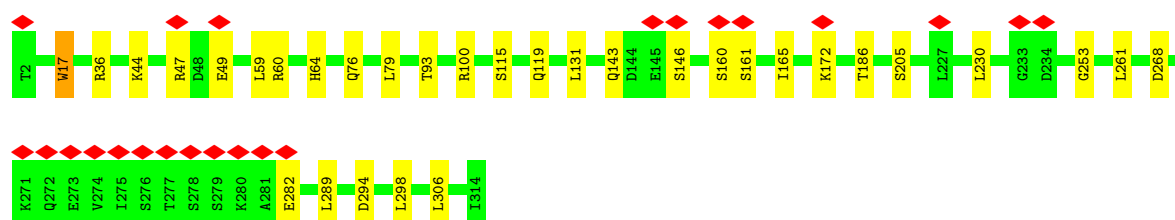
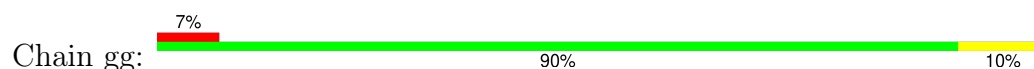
- Molecule 82: eS30



- Molecule 83: eS31



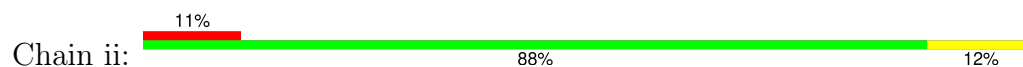
- Molecule 84: RACK1

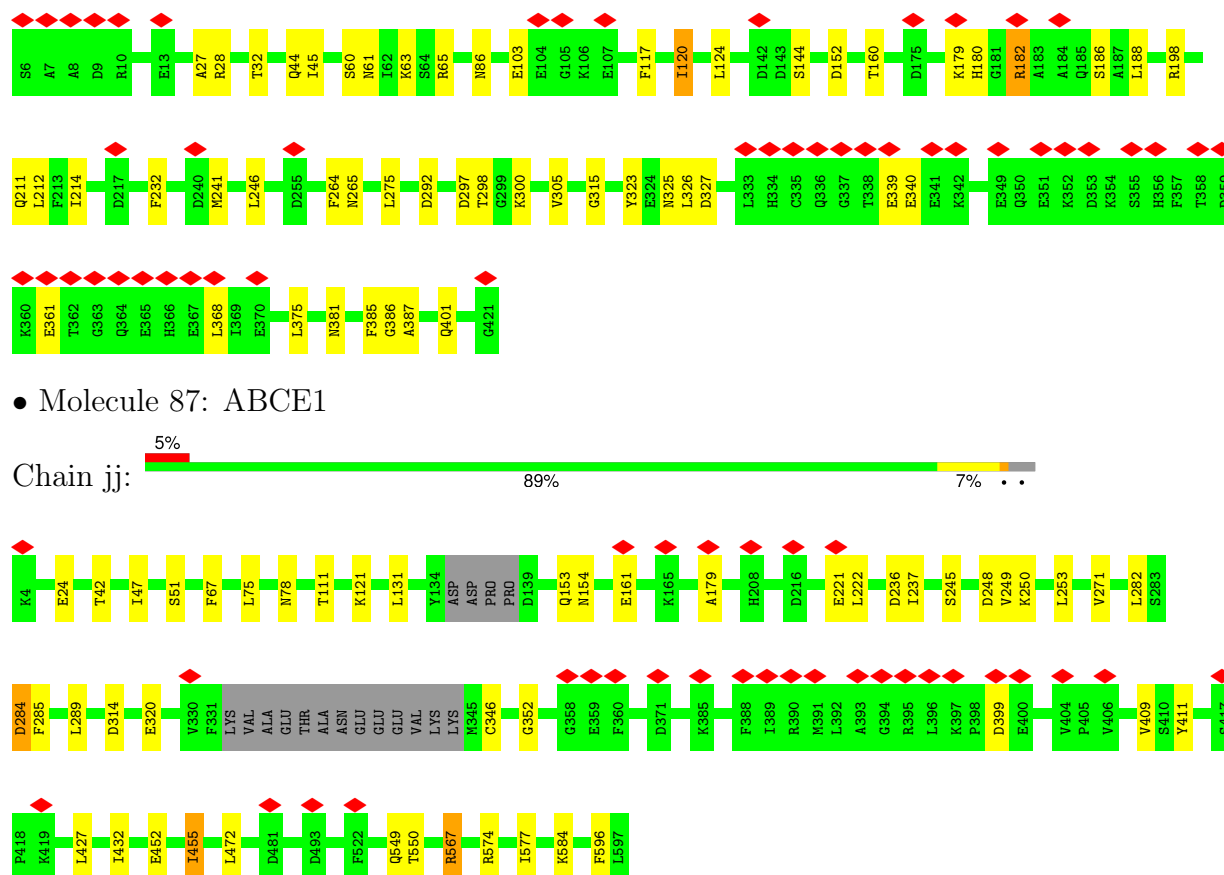


- Molecule 85: mRNA



- Molecule 86: eRF1





• 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 (\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 (\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: SF4, ZN, 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	0.68	0/1906	0.94	1/2556 (0.0%)
2	B	0.62	0/3216	0.89	4/4311 (0.1%)
3	C	0.65	1/2929 (0.0%)	0.91	5/3935 (0.1%)
4	D	0.50	0/2432	0.76	1/3257 (0.0%)
5	E	0.54	0/1936	0.87	2/2600 (0.1%)
6	F	0.64	0/1905	0.88	2/2539 (0.1%)
7	G	0.55	0/1967	0.83	2/2647 (0.1%)
8	H	0.51	0/1535	0.84	1/2063 (0.0%)
9	I	0.55	0/1693	0.79	1/2260 (0.0%)
10	J	0.49	0/1376	0.80	2/1841 (0.1%)
11	L	0.59	0/1734	0.92	2/2317 (0.1%)
12	M	0.55	0/1158	0.80	0/1547
13	N	0.67	0/1746	0.99	3/2338 (0.1%)
14	O	0.63	0/1671	0.88	0/2234
15	P	0.67	0/1268	0.87	0/1701
16	Q	0.62	0/1530	0.94	0/2041
17	R	0.54	0/1524	0.88	2/2013 (0.1%)
18	S	0.63	0/1493	0.93	6/2002 (0.3%)
19	T	0.53	0/1326	0.80	0/1770
20	U	0.48	0/822	0.75	0/1103
21	V	0.59	0/993	0.84	0/1332
22	W	0.57	0/541	0.86	2/720 (0.3%)
23	X	0.55	0/993	0.84	1/1334 (0.1%)
24	Y	0.54	0/1132	0.90	1/1504 (0.1%)
25	Z	0.58	0/1130	0.84	0/1507
26	a	0.65	0/1191	0.91	1/1590 (0.1%)
27	b	0.56	0/619	0.79	1/818 (0.1%)
28	c	0.55	0/742	0.79	0/996
29	d	0.55	0/903	0.90	1/1216 (0.1%)
30	e	0.59	0/1071	0.93	1/1429 (0.1%)
31	f	0.70	0/895	0.95	0/1198
32	g	0.59	0/916	0.90	3/1220 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.51	0/1021	0.84	1/1348 (0.1%)
34	i	0.52	0/841	0.87	2/1112 (0.2%)
35	j	0.73	1/720 (0.1%)	1.09	4/952 (0.4%)
36	k	0.54	0/575	0.79	0/761
37	l	0.66	0/454	0.91	0/599
38	m	0.51	0/435	0.86	0/575
39	n	0.56	0/223	1.00	1/284 (0.4%)
40	o	0.59	0/864	0.86	0/1140
41	p	0.57	0/718	0.82	0/953
42	r	0.63	0/1017	0.91	2/1364 (0.1%)
43	s	0.41	0/1547	0.60	0/2088
44	t	0.41	0/1257	0.70	0/1697
45	1	0.60	0/129	0.78	0/173
46	2	0.32	0/1805	0.76	3/2809 (0.1%)
47	3	0.34	0/1777	0.88	5/2763 (0.2%)
48	5	0.52	20/87790 (0.0%)	0.86	109/136937 (0.1%)
49	7	0.47	0/2858	0.74	1/4455 (0.0%)
50	8	0.53	0/3701	0.78	0/5766
51	9	0.45	10/41013 (0.0%)	0.82	41/63919 (0.1%)
52	AA	0.51	0/1679	0.78	0/2283
53	BB	0.54	0/1756	0.81	1/2350 (0.0%)
54	CC	0.52	0/1730	0.84	1/2344 (0.0%)
55	DD	0.47	0/1792	0.77	0/2412
56	EE	0.49	0/2115	0.87	0/2843
57	FF	0.52	0/1531	0.82	0/2059
58	GG	0.49	0/1946	0.80	0/2590
59	HH	0.46	0/1544	0.74	0/2068
60	II	0.52	0/1715	0.86	1/2287 (0.0%)
61	JJ	0.52	0/1550	0.91	3/2069 (0.1%)
62	KK	0.51	0/851	0.78	0/1147
63	LL	0.54	0/1259	0.85	0/1684
64	MM	0.48	0/968	0.65	0/1296
65	NN	0.52	0/1232	0.83	0/1656
66	OO	0.59	0/1029	0.98	2/1380 (0.1%)
67	PP	0.48	0/1079	0.79	0/1437
68	QQ	0.51	0/1142	0.82	1/1528 (0.1%)
69	RR	0.49	0/1060	0.76	0/1421
70	SS	0.47	0/1157	0.86	1/1548 (0.1%)
71	TT	0.51	0/1120	0.84	3/1499 (0.2%)
72	UU	0.48	0/831	0.75	0/1115
73	VV	0.53	0/645	0.83	0/865
74	WW	0.59	0/1051	0.88	0/1406
75	XX	0.58	0/1116	0.90	1/1490 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	YY	0.51	0/1040	0.80	0/1382
77	ZZ	0.49	0/604	0.82	0/810
78	aa	0.53	0/794	0.87	0/1065
79	bb	0.43	0/665	0.71	0/891
80	cc	0.57	0/478	0.88	0/640
81	dd	0.61	0/455	0.92	1/603 (0.2%)
82	ee	0.57	0/462	0.84	1/607 (0.2%)
83	ff	0.39	0/531	0.65	0/703
84	gg	0.45	0/2493	0.70	1/3394 (0.0%)
85	hh	0.47	0/287	0.78	0/445
86	ii	0.45	0/3333	0.67	1/4483 (0.0%)
87	jj	0.42	0/4633	0.70	3/6249 (0.0%)
All	All	0.52	32/242711 (0.0%)	0.84	235/355683 (0.1%)

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 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	5	957	G	O3'-P	9.85	1.73	1.61
48	5	3859	G	O3'-P	-8.08	1.51	1.61
48	5	1847	C	O3'-P	-7.85	1.51	1.61
48	5	956	A	O3'-P	7.22	1.69	1.61
51	9	677	G	O3'-P	-6.35	1.53	1.61

The worst 5 of 235 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	5	1965	G	P-O3'-C3'	20.40	144.18	119.70
48	5	3753	G	N9-C1'-C2'	-13.34	96.66	114.00
51	9	1235	G	N9-C1'-C2'	-12.87	97.27	114.00
47	3	70	G	N9-C1'-C2'	-12.35	97.94	114.00
51	9	1212	G	N9-C1'-C2'	-11.52	99.03	114.00

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 [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	22
2	B	392/394 (100%)	338 (86%)	44 (11%)	10 (3%)	4	27
3	C	359/361 (99%)	302 (84%)	48 (13%)	9 (2%)	4	28
4	D	290/292 (99%)	255 (88%)	31 (11%)	4 (1%)	9	37
5	E	232/248 (94%)	172 (74%)	37 (16%)	23 (10%)	0	6
6	F	223/225 (99%)	204 (92%)	18 (8%)	1 (0%)	30	62
7	G	239/241 (99%)	205 (86%)	26 (11%)	8 (3%)	3	24
8	H	188/190 (99%)	161 (86%)	25 (13%)	2 (1%)	12	42
9	I	200/213 (94%)	178 (89%)	17 (8%)	5 (2%)	4	28
10	J	167/169 (99%)	141 (84%)	18 (11%)	8 (5%)	2	17
11	L	208/210 (99%)	174 (84%)	25 (12%)	9 (4%)	2	19
12	M	136/138 (99%)	123 (90%)	12 (9%)	1 (1%)	19	51
13	N	201/203 (99%)	167 (83%)	32 (16%)	2 (1%)	13	44
14	O	197/199 (99%)	176 (89%)	20 (10%)	1 (0%)	25	57
15	P	151/153 (99%)	134 (89%)	13 (9%)	4 (3%)	4	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	Q	185/187 (99%)	161 (87%)	20 (11%)	4 (2%)	5	30
17	R	178/180 (99%)	151 (85%)	25 (14%)	2 (1%)	12	42
18	S	173/175 (99%)	151 (87%)	18 (10%)	4 (2%)	5	29
19	T	157/159 (99%)	137 (87%)	17 (11%)	3 (2%)	6	33
20	U	97/99 (98%)	82 (84%)	11 (11%)	4 (4%)	2	20
21	V	129/131 (98%)	110 (85%)	19 (15%)	0	100	100
22	W	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	8	35
23	X	117/119 (98%)	106 (91%)	9 (8%)	2 (2%)	7	34
24	Y	132/134 (98%)	114 (86%)	13 (10%)	5 (4%)	2	21
25	Z	133/135 (98%)	113 (85%)	14 (10%)	6 (4%)	2	18
26	a	145/147 (99%)	114 (79%)	24 (17%)	7 (5%)	2	17
27	b	73/75 (97%)	65 (89%)	5 (7%)	3 (4%)	2	20
28	c	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
29	d	105/107 (98%)	86 (82%)	17 (16%)	2 (2%)	6	33
30	e	126/128 (98%)	110 (87%)	12 (10%)	4 (3%)	3	24
31	f	107/109 (98%)	88 (82%)	12 (11%)	7 (6%)	1	13
32	g	112/114 (98%)	97 (87%)	13 (12%)	2 (2%)	7	33
33	h	120/122 (98%)	106 (88%)	10 (8%)	4 (3%)	3	24
34	i	100/102 (98%)	87 (87%)	11 (11%)	2 (2%)	6	32
35	j	84/86 (98%)	73 (87%)	8 (10%)	3 (4%)	3	22
36	k	67/69 (97%)	53 (79%)	10 (15%)	4 (6%)	1	14
37	l	48/50 (96%)	41 (85%)	5 (10%)	2 (4%)	2	19
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	21
41	p	89/91 (98%)	75 (84%)	9 (10%)	5 (6%)	1	15
42	r	123/125 (98%)	104 (85%)	10 (8%)	9 (7%)	1	11
43	s	196/198 (99%)	163 (83%)	21 (11%)	12 (6%)	1	14
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	9
52	AA	206/208 (99%)	153 (74%)	37 (18%)	16 (8%)	1	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	BB	211/213 (99%)	165 (78%)	34 (16%)	12 (6%)	1	15
54	CC	216/218 (99%)	184 (85%)	22 (10%)	10 (5%)	2	18
55	DD	225/227 (99%)	184 (82%)	30 (13%)	11 (5%)	2	17
56	EE	260/262 (99%)	197 (76%)	43 (16%)	20 (8%)	1	9
57	FF	189/191 (99%)	156 (82%)	22 (12%)	11 (6%)	1	14
58	GG	235/237 (99%)	198 (84%)	29 (12%)	8 (3%)	3	24
59	HH	187/189 (99%)	144 (77%)	30 (16%)	13 (7%)	1	11
60	II	204/206 (99%)	169 (83%)	25 (12%)	10 (5%)	2	17
61	JJ	183/185 (99%)	152 (83%)	19 (10%)	12 (7%)	1	13
62	KK	96/98 (98%)	65 (68%)	20 (21%)	11 (12%)	0	4
63	LL	150/152 (99%)	125 (83%)	16 (11%)	9 (6%)	1	14
64	MM	122/124 (98%)	87 (71%)	25 (20%)	10 (8%)	1	8
65	NN	148/150 (99%)	121 (82%)	21 (14%)	6 (4%)	2	20
66	OO	134/136 (98%)	96 (72%)	24 (18%)	14 (10%)	0	5
67	PP	125/127 (98%)	102 (82%)	20 (16%)	3 (2%)	5	28
68	QQ	139/141 (99%)	115 (83%)	14 (10%)	10 (7%)	1	11
69	RR	127/129 (98%)	100 (79%)	18 (14%)	9 (7%)	1	11
70	SS	135/137 (98%)	110 (82%)	15 (11%)	10 (7%)	1	10
71	TT	139/141 (99%)	127 (91%)	9 (6%)	3 (2%)	5	30
72	UU	102/104 (98%)	84 (82%)	12 (12%)	6 (6%)	1	14
73	VV	81/83 (98%)	65 (80%)	9 (11%)	7 (9%)	0	8
74	WW	127/129 (98%)	101 (80%)	21 (16%)	5 (4%)	2	21
75	XX	139/141 (99%)	122 (88%)	8 (6%)	9 (6%)	1	13
76	YY	124/126 (98%)	100 (81%)	15 (12%)	9 (7%)	1	11
77	ZZ	73/75 (97%)	58 (80%)	11 (15%)	4 (6%)	1	15
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	10
80	cc	59/61 (97%)	47 (80%)	11 (19%)	1 (2%)	7	34
81	dd	51/53 (96%)	40 (78%)	11 (22%)	0	100	100
82	ee	55/57 (96%)	39 (71%)	14 (26%)	2 (4%)	3	22
83	ff	58/68 (85%)	49 (84%)	8 (14%)	1 (2%)	7	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
84	gg	311/313 (99%)	263 (85%)	40 (13%)	8 (3%)	4	27
86	ii	414/416 (100%)	378 (91%)	25 (6%)	11 (3%)	4	27
87	jj	569/594 (96%)	501 (88%)	54 (10%)	14 (2%)	4	28
All	All	12492/12708 (98%)	10443 (84%)	1523 (12%)	526 (4%)	4	19

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%)	159 (85%)	28 (15%)	2	14
2	B	336/342 (98%)	288 (86%)	48 (14%)	2	15
3	C	301/301 (100%)	258 (86%)	43 (14%)	2	15
4	D	247/247 (100%)	218 (88%)	29 (12%)	4	21
5	E	208/221 (94%)	179 (86%)	29 (14%)	3	16
6	F	194/195 (100%)	169 (87%)	25 (13%)	3	17
7	G	206/206 (100%)	176 (85%)	30 (15%)	2	14
8	H	169/169 (100%)	147 (87%)	22 (13%)	3	17
9	I	174/180 (97%)	158 (91%)	16 (9%)	7	29
10	J	142/142 (100%)	127 (89%)	15 (11%)	5	24
11	L	176/176 (100%)	144 (82%)	32 (18%)	1	8
12	M	117/117 (100%)	104 (89%)	13 (11%)	5	22
13	N	171/171 (100%)	149 (87%)	22 (13%)	3	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	O	171/171 (100%)	141 (82%)	30 (18%)	1	9
15	P	134/134 (100%)	118 (88%)	16 (12%)	4	20
16	Q	163/163 (100%)	142 (87%)	21 (13%)	3	17
17	R	159/159 (100%)	139 (87%)	20 (13%)	3	18
18	S	156/156 (100%)	137 (88%)	19 (12%)	4	19
19	T	139/139 (100%)	115 (83%)	24 (17%)	1	10
20	U	89/89 (100%)	79 (89%)	10 (11%)	5	22
21	V	101/101 (100%)	82 (81%)	19 (19%)	1	7
22	W	55/55 (100%)	49 (89%)	6 (11%)	5	23
23	X	107/107 (100%)	95 (89%)	12 (11%)	5	22
24	Y	124/124 (100%)	106 (86%)	18 (14%)	2	14
25	Z	117/117 (100%)	101 (86%)	16 (14%)	3	16
26	a	119/119 (100%)	108 (91%)	11 (9%)	7	29
27	b	62/62 (100%)	54 (87%)	8 (13%)	3	17
28	c	79/79 (100%)	65 (82%)	14 (18%)	1	9
29	d	98/98 (100%)	79 (81%)	19 (19%)	1	7
30	e	114/114 (100%)	95 (83%)	19 (17%)	2	11
31	f	88/88 (100%)	75 (85%)	13 (15%)	2	14
32	g	98/98 (100%)	81 (83%)	17 (17%)	1	10
33	h	109/109 (100%)	96 (88%)	13 (12%)	4	20
34	i	86/86 (100%)	72 (84%)	14 (16%)	2	11
35	j	73/73 (100%)	57 (78%)	16 (22%)	1	5
36	k	64/64 (100%)	60 (94%)	4 (6%)	15	41
37	l	47/47 (100%)	40 (85%)	7 (15%)	2	14
38	m	48/48 (100%)	36 (75%)	12 (25%)	0	3
39	n	22/22 (100%)	20 (91%)	2 (9%)	7	29
40	o	92/92 (100%)	78 (85%)	14 (15%)	2	13
41	p	74/74 (100%)	63 (85%)	11 (15%)	2	14
42	r	109/109 (100%)	93 (85%)	16 (15%)	2	14
43	s	166/166 (100%)	155 (93%)	11 (7%)	14	39
44	t	136/136 (100%)	126 (93%)	10 (7%)	11	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	1	13/13 (100%)	11 (85%)	2 (15%)	2	13
52	AA	174/174 (100%)	142 (82%)	32 (18%)	1	8
53	BB	194/194 (100%)	168 (87%)	26 (13%)	3	16
54	CC	183/183 (100%)	162 (88%)	21 (12%)	4	21
55	DD	190/190 (100%)	151 (80%)	39 (20%)	1	6
56	EE	223/223 (100%)	188 (84%)	35 (16%)	2	13
57	FF	161/161 (100%)	132 (82%)	29 (18%)	1	9
58	GG	207/207 (100%)	174 (84%)	33 (16%)	2	12
59	HH	169/169 (100%)	155 (92%)	14 (8%)	9	32
60	II	178/178 (100%)	150 (84%)	28 (16%)	2	13
61	JJ	161/161 (100%)	139 (86%)	22 (14%)	3	16
62	KK	89/89 (100%)	76 (85%)	13 (15%)	2	14
63	LL	136/136 (100%)	116 (85%)	20 (15%)	2	14
64	MM	104/104 (100%)	88 (85%)	16 (15%)	2	13
65	NN	130/130 (100%)	104 (80%)	26 (20%)	1	6
66	OO	106/106 (100%)	84 (79%)	22 (21%)	1	6
67	PP	116/116 (100%)	97 (84%)	19 (16%)	2	11
68	QQ	117/117 (100%)	100 (86%)	17 (14%)	2	14
69	RR	117/117 (100%)	96 (82%)	21 (18%)	1	9
70	SS	119/119 (100%)	101 (85%)	18 (15%)	2	14
71	TT	112/112 (100%)	94 (84%)	18 (16%)	2	12
72	UU	94/94 (100%)	79 (84%)	15 (16%)	2	12
73	VV	67/67 (100%)	56 (84%)	11 (16%)	2	11
74	WW	112/112 (100%)	98 (88%)	14 (12%)	3	18
75	XX	113/113 (100%)	92 (81%)	21 (19%)	1	8
76	YY	108/108 (100%)	87 (81%)	21 (19%)	1	7
77	ZZ	66/66 (100%)	58 (88%)	8 (12%)	4	19
78	aa	85/85 (100%)	74 (87%)	11 (13%)	3	17
79	bb	75/75 (100%)	65 (87%)	10 (13%)	3	17
80	cc	54/54 (100%)	40 (74%)	14 (26%)	0	3
81	dd	47/47 (100%)	36 (77%)	11 (23%)	0	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
82	ee	47/47 (100%)	41 (87%)	6 (13%)	3	18
83	ff	58/61 (95%)	57 (98%)	1 (2%)	56	73
84	gg	272/272 (100%)	248 (91%)	24 (9%)	8	30
86	ii	358/358 (100%)	319 (89%)	39 (11%)	5	23
87	jj	507/522 (97%)	475 (94%)	32 (6%)	15	41
All	All	10889/10933 (100%)	9386 (86%)	1503 (14%)	5	16

5 of 1503 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	EE	67	GLN
65	NN	114	ARG
57	FF	72	LEU
56	EE	66	MET
60	II	88	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
5	E	217	GLN
11	L	175	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
46	2	74/76 (97%)	24 (32%)	0
47	3	72/75 (96%)	28 (38%)	6 (8%)
48	5	3645/3662 (99%)	1236 (33%)	291 (7%)
49	7	120/120 (100%)	24 (20%)	2 (1%)
50	8	155/156 (99%)	49 (31%)	6 (3%)
51	9	1710/1719 (99%)	614 (35%)	115 (6%)
85	hh	11/12 (91%)	6 (54%)	0
All	All	5787/5820 (99%)	1981 (34%)	420 (7%)

5 of 1981 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
46	2	7	G

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Mol	Chain	Res	Type
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	$\# Z > 2$
91	ADP	jj	603	-	24,29,29	1.06	3 (12%)	29,45,45	1.31	2 (6%)
91	ADP	jj	602	-	24,29,29	1.03	3 (12%)	29,45,45	1.30	3 (10%)
90	SF4	jj	601	87	0,12,12	-	-	-		
90	SF4	jj	600	87	0,12,12	-	-	-		

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
91	ADP	jj	603	-	-	2/12/32/32	0/3/3/3
91	ADP	jj	602	-	-	0/12/32/32	0/3/3/3
90	SF4	jj	601	87	-	-	0/6/5/5
90	SF4	jj	600	87	-	-	0/6/5/5

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
91	jj	603	ADP	C2-N3	2.32	1.35	1.32
91	jj	602	ADP	C2-N3	2.30	1.35	1.32
91	jj	603	ADP	PA-O3A	2.29	1.62	1.59
91	jj	602	ADP	PA-O3A	2.21	1.61	1.59
91	jj	603	ADP	O4'-C1'	2.15	1.43	1.40

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
91	jj	602	ADP	N3-C2-N1	-4.34	122.78	128.67
91	jj	603	ADP	N3-C2-N1	-4.28	122.86	128.67
91	jj	602	ADP	C4-C5-N7	-2.84	106.34	109.34
91	jj	603	ADP	C4-C5-N7	-2.81	106.37	109.34
91	jj	602	ADP	O4'-C1'-N9	2.10	111.53	108.75

There are no chirality outliers.

All (2) torsion outliers are listed below:

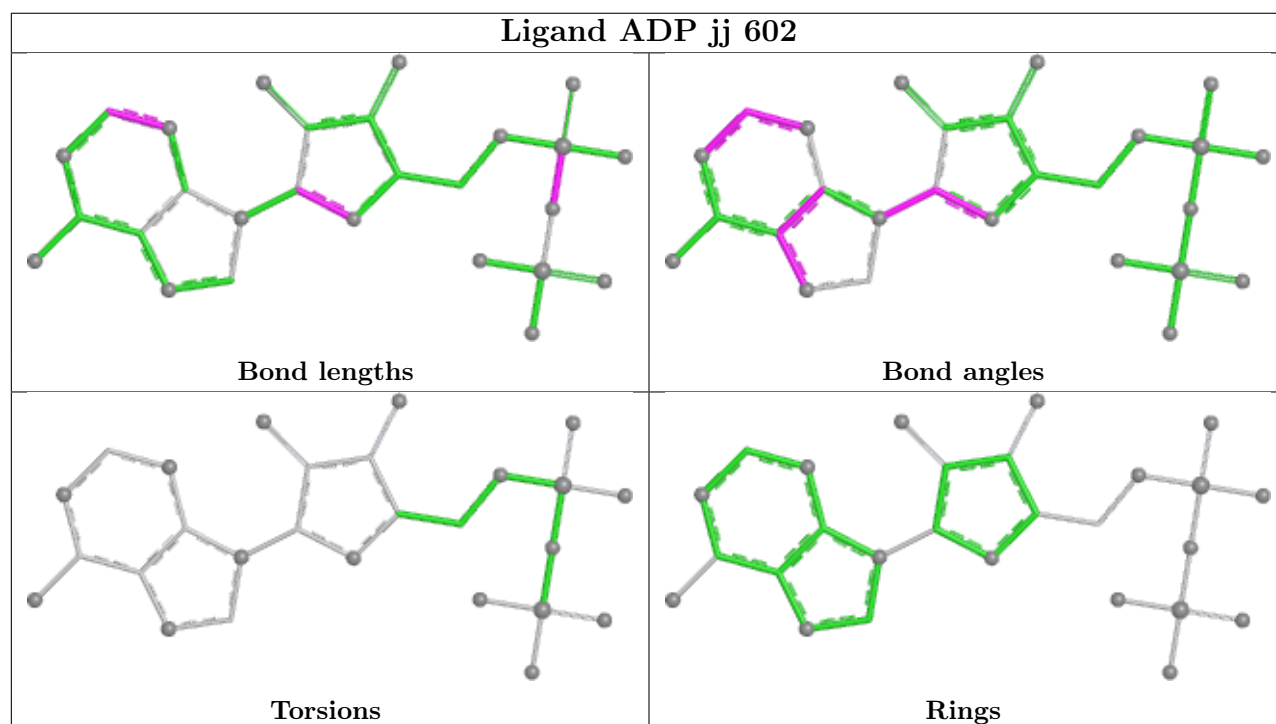
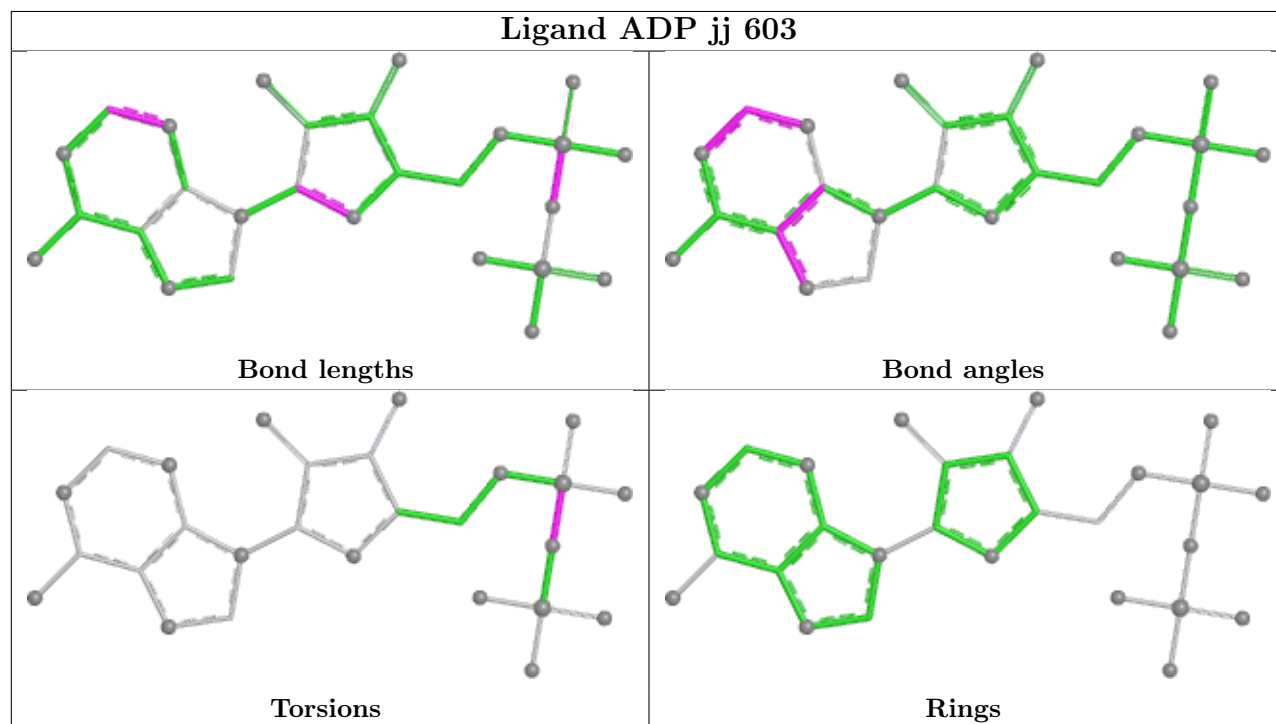
Mol	Chain	Res	Type	Atoms
91	jj	603	ADP	PB-O3A-PA-O1A
91	jj	603	ADP	PB-O3A-PA-O2A

There are no ring outliers.

No monomer is involved in short contacts.

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

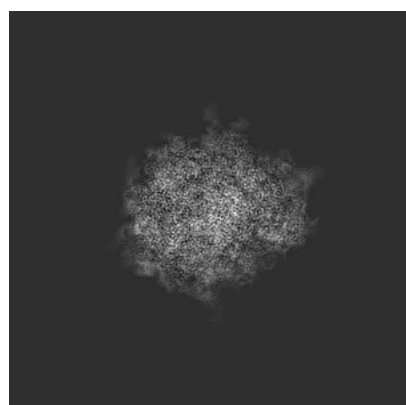
6 Map visualisation [i](#)

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.

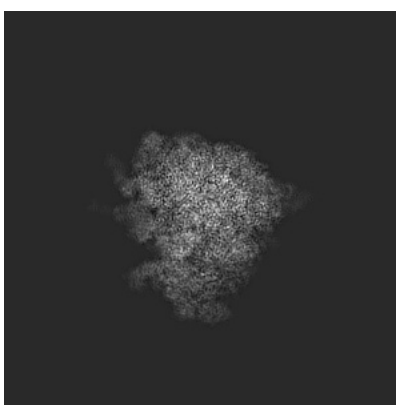
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

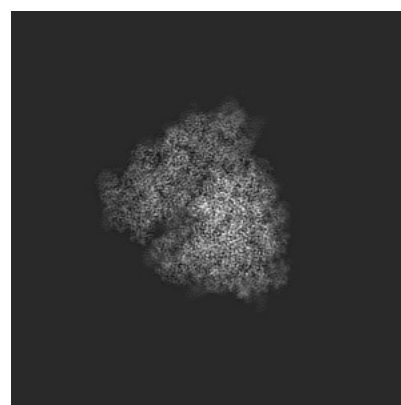
6.1.1 Primary map



X



Y



Z

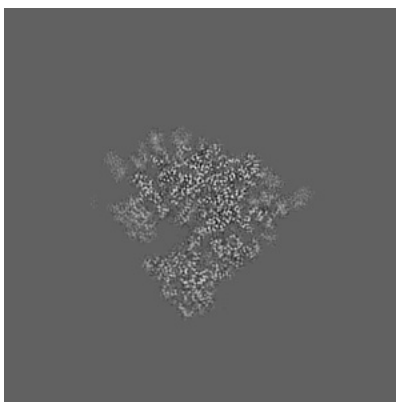
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

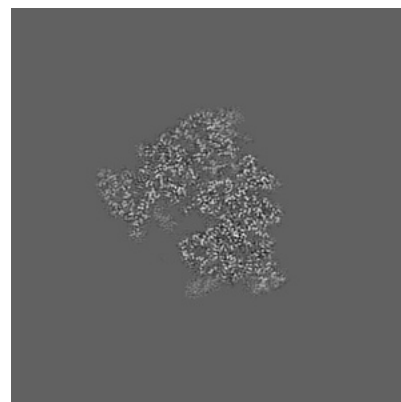
6.2.1 Primary map



X Index: 210



Y Index: 210

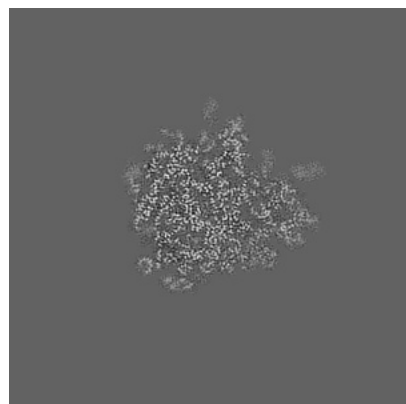


Z Index: 210

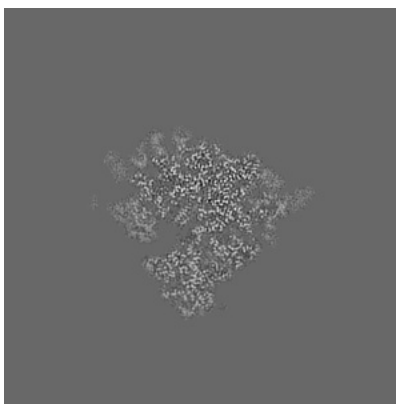
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

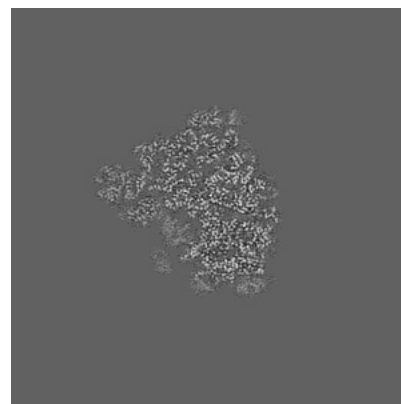
6.3.1 Primary map



X Index: 225



Y Index: 211

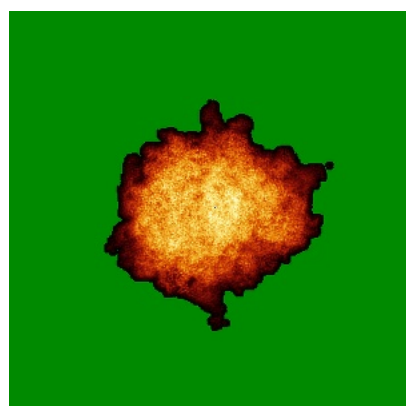


Z Index: 220

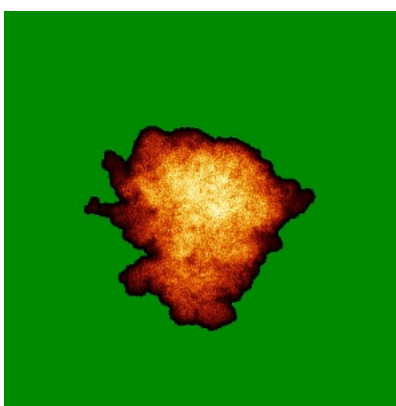
The images above show the largest variance slices of the map in three orthogonal directions.

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

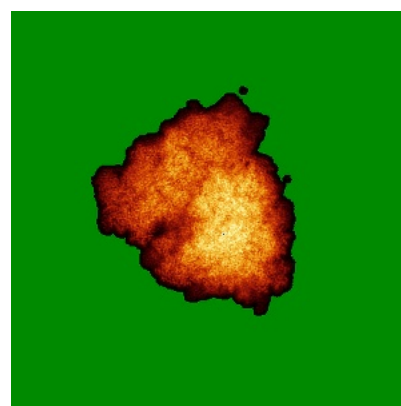
6.4.1 Primary map



X



Y

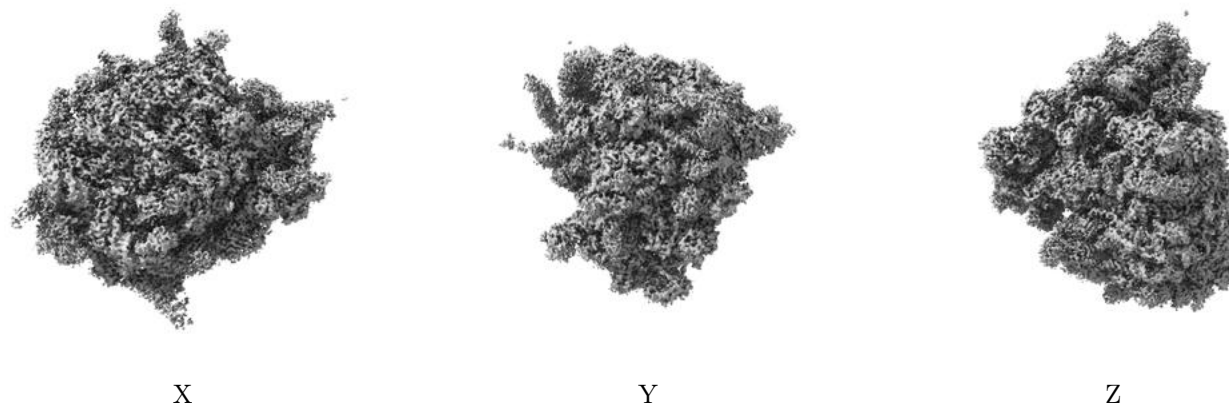


Z

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.

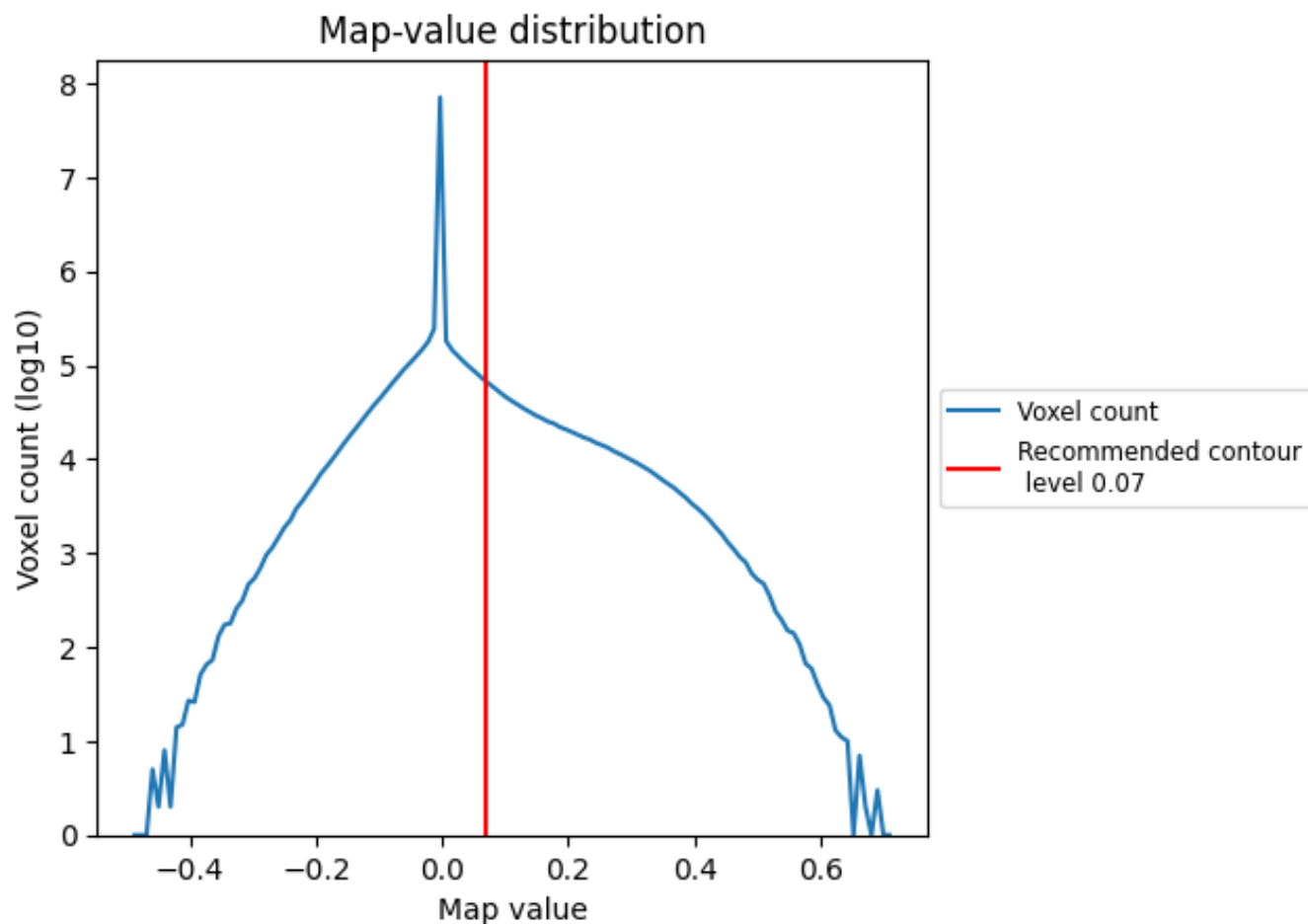
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

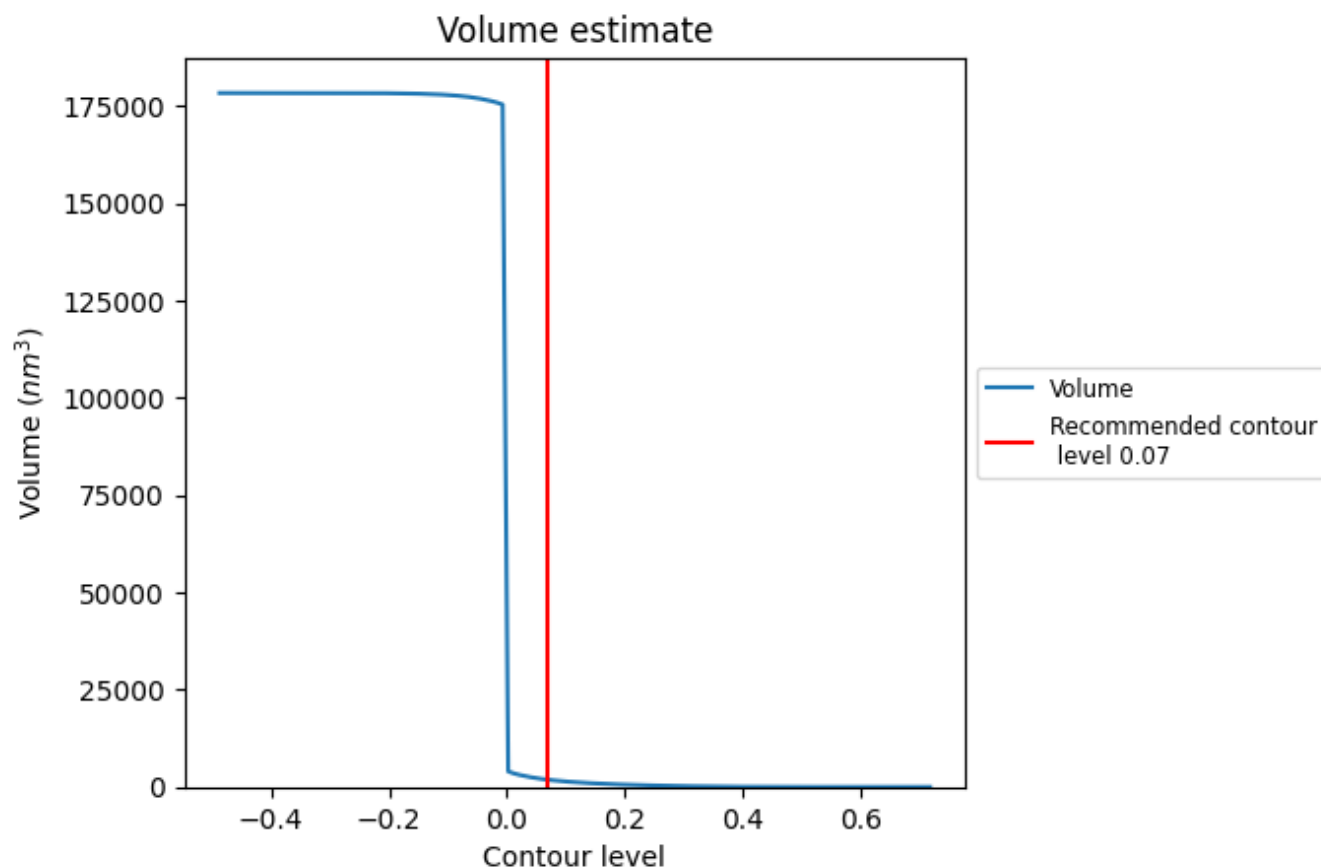
This section contains the results of statistical analysis of the map.

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.

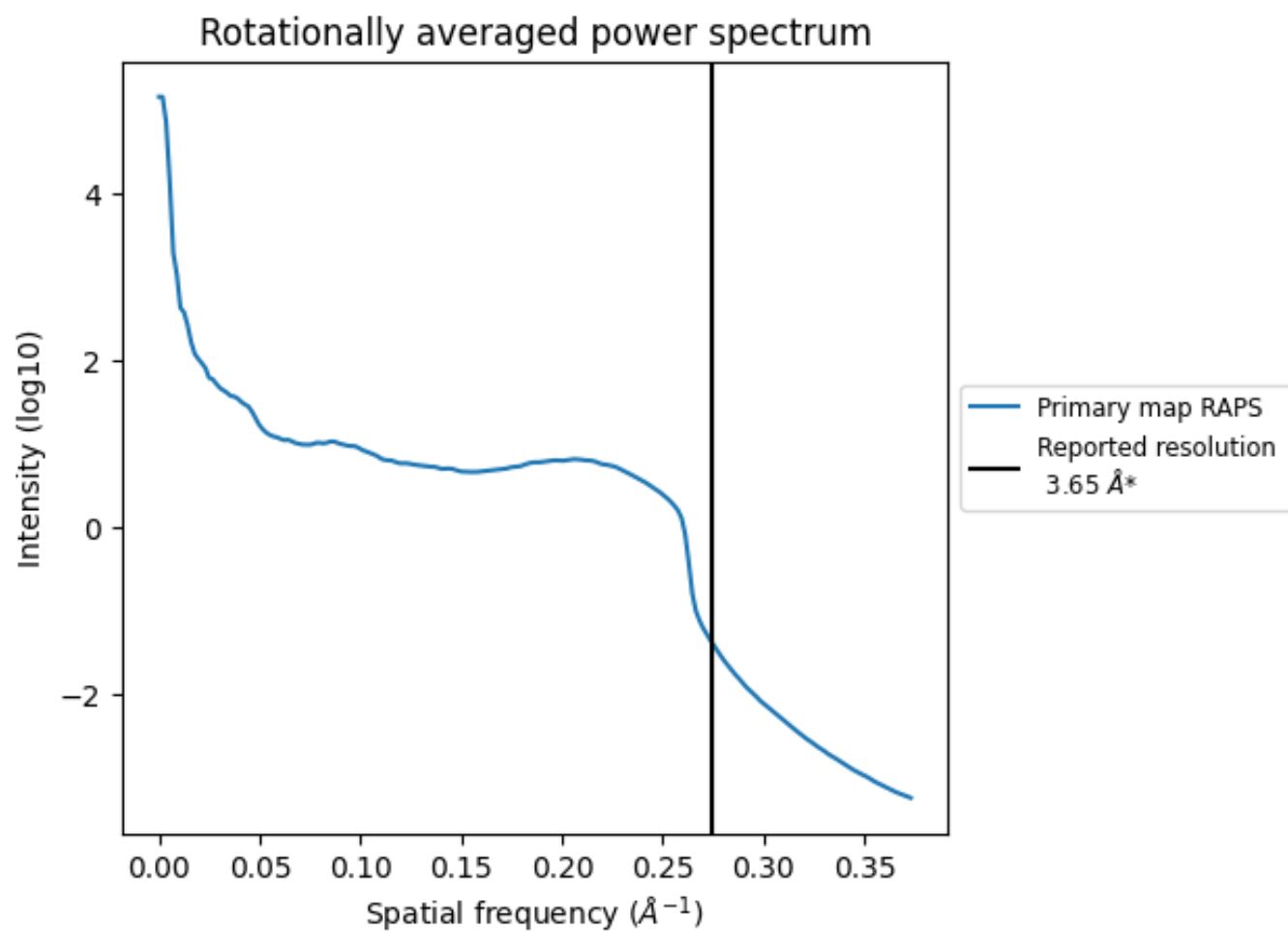
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1855 nm³; 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 ⓘ

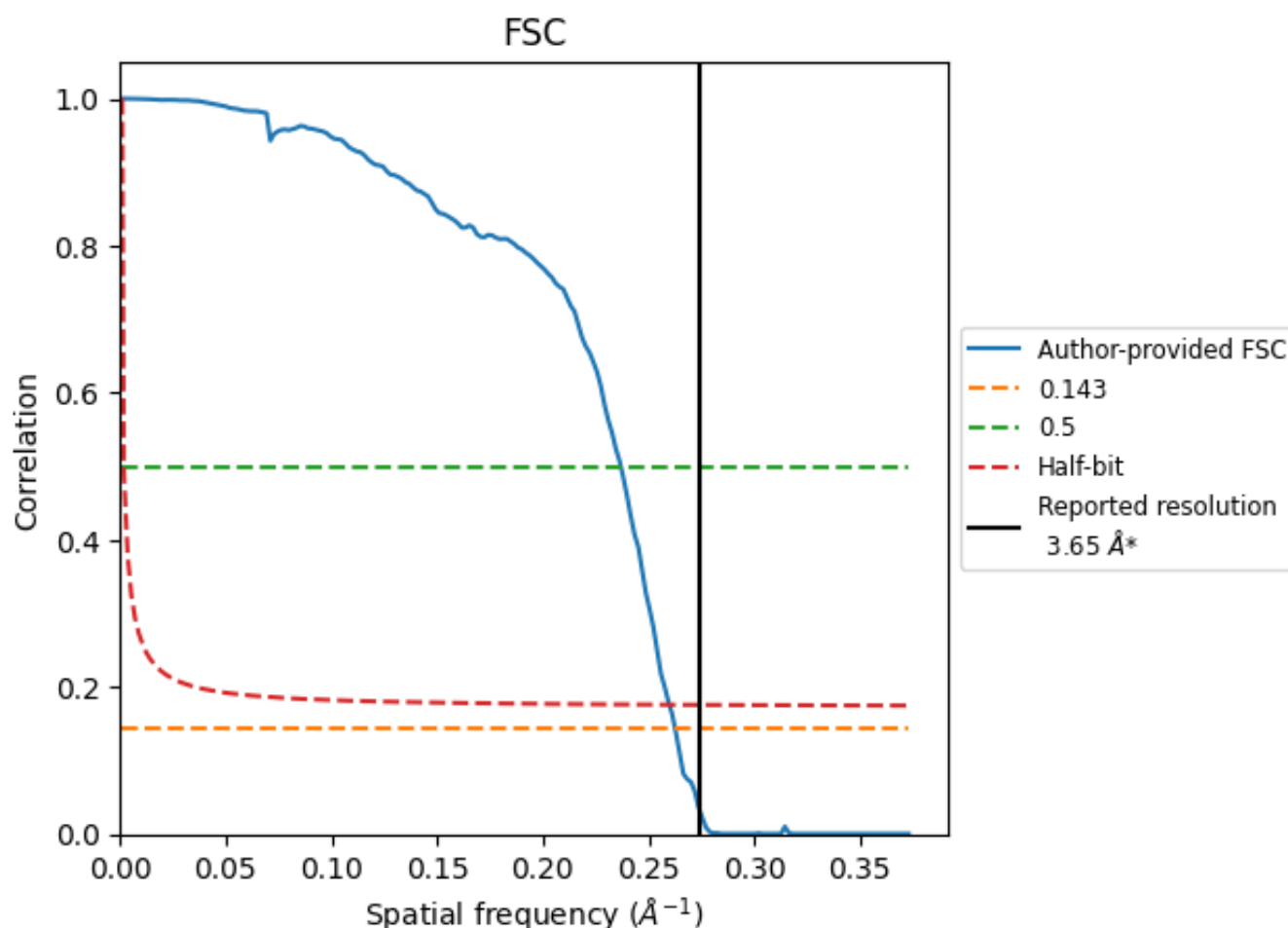


*Reported resolution corresponds to spatial frequency of 0.274 Å⁻¹

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](#)

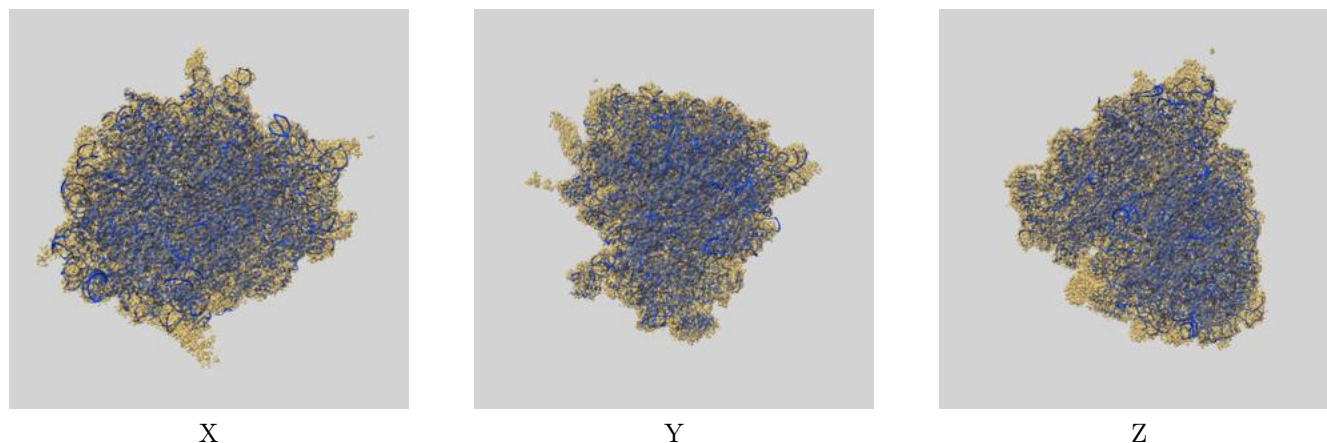
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.65	-	-
Author-provided FSC curve	3.81	4.22	3.85
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

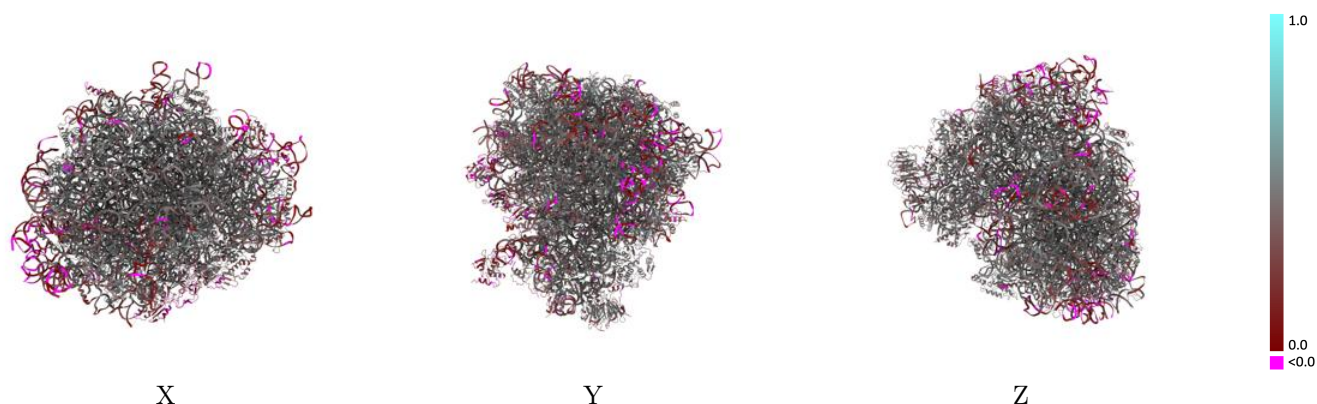
This section contains information regarding the fit between EMDB map EMD-3040 and PDB model 3JAI. Per-residue inclusion information can be found in section 3 on page 24.

9.1 Map-model overlay [i](#)



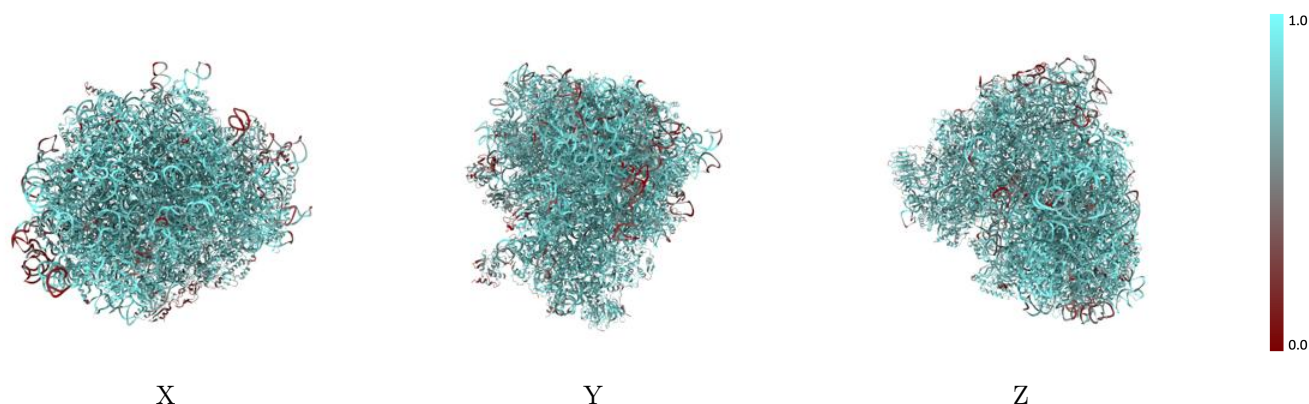
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



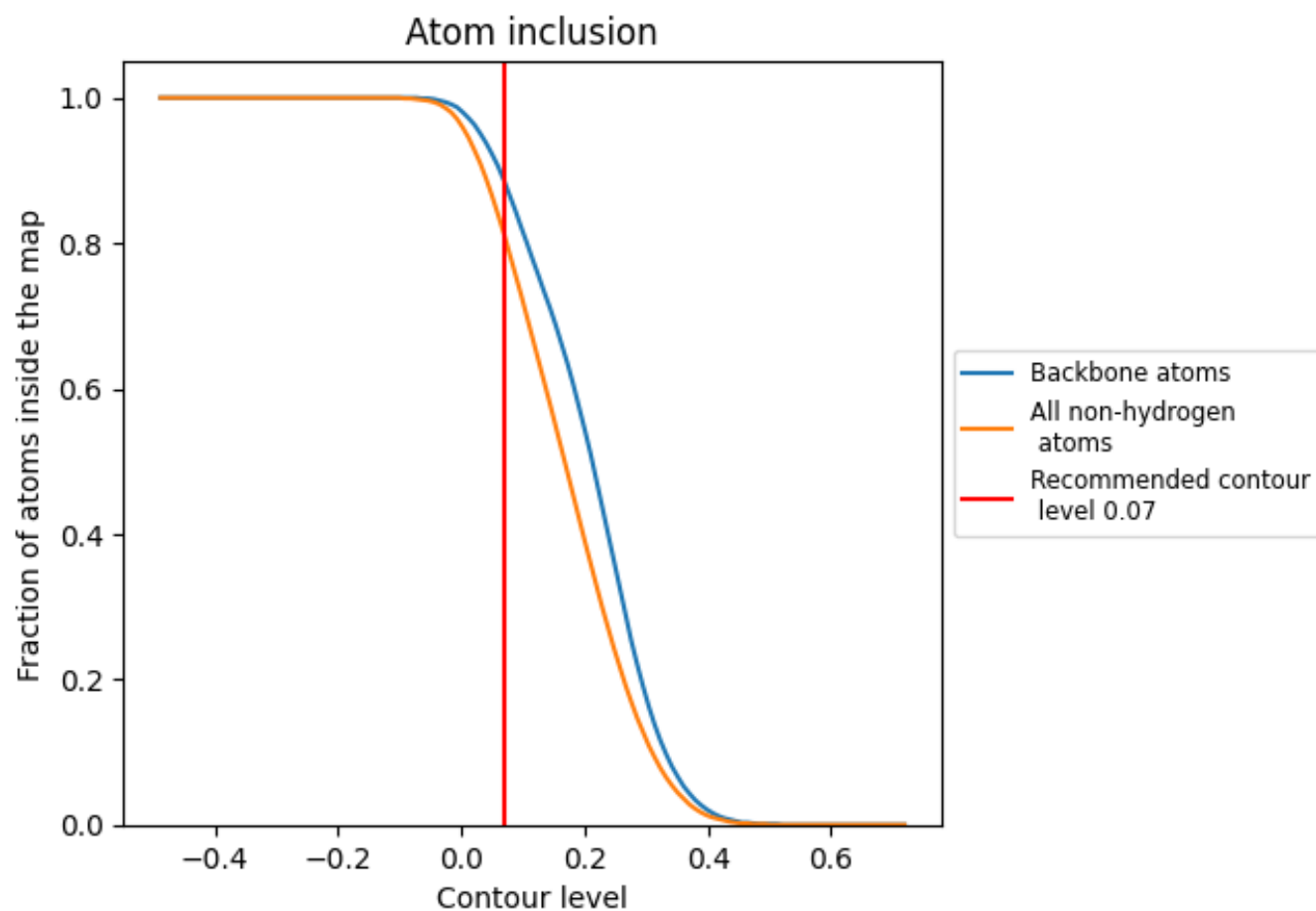
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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