wwPDB EM Validation Summary Report (i)

Nov 4, 2023 – 03:34 PM EDT

PDB ID	:	6WOO
EMDB ID	:	EMD-21859
Title	:	CryoEM structure of yeast 80S ribosome with Met-tRNAiMet, eIF5B, and GDP
Authors	:	Wang, J.; Wang, J.; Puglisi, J.; Fernandez, I.S.
Deposited on	:	2020-04-25
Resolution	:	2.90 Å(reported)
Based on initial model	:	4V8Y

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

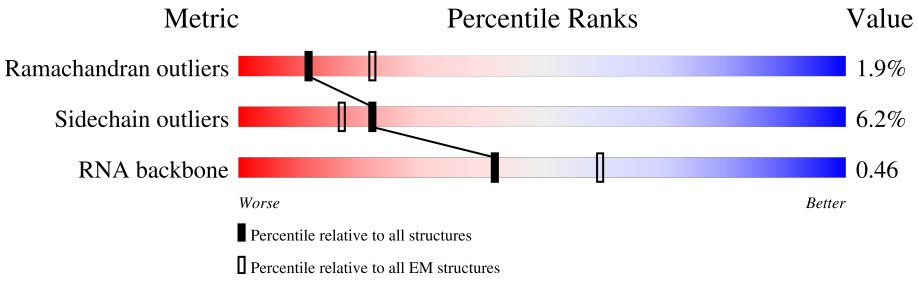
EMDB validation analysis	:	0.0.1.dev70
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	5	3271	10% 75% 25%
2	7	121	83% 17%
3	8	157	78% 22%
4	A	249	6% 92% 7%
5	B	384	9% 94% 6%
6	C	359	6% 91% 9%
7	D	295	23% 92% 8%
8	E	175	16% 84% 5% 11%

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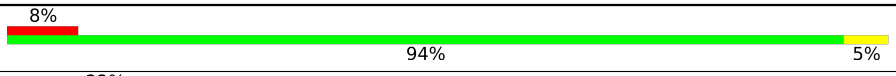
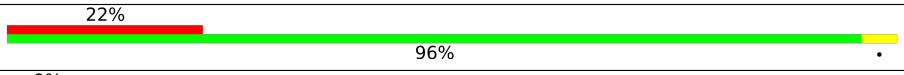
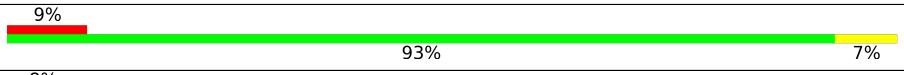
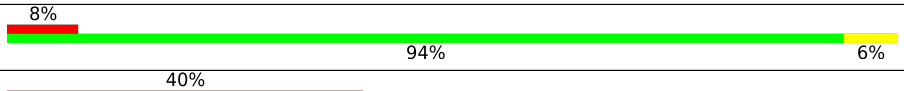
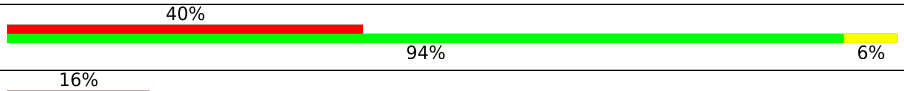
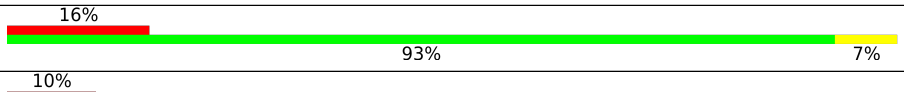
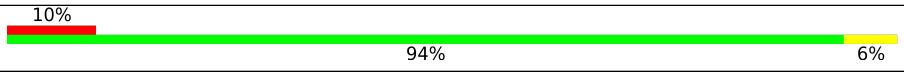
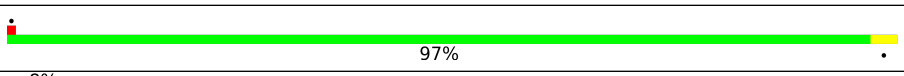
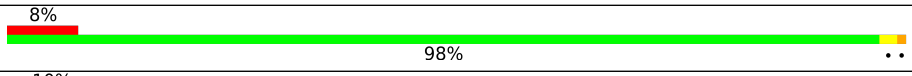
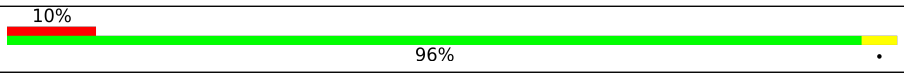
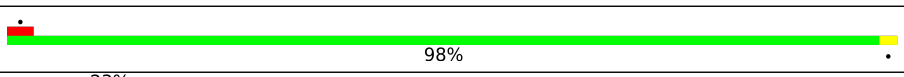
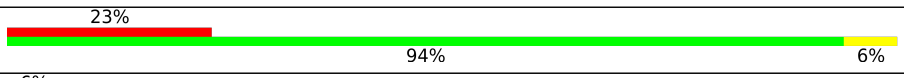
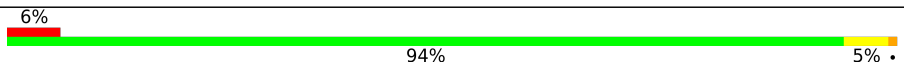
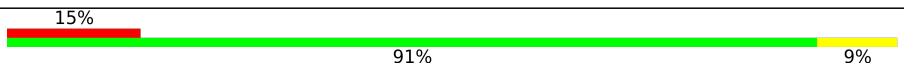
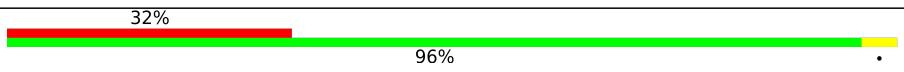
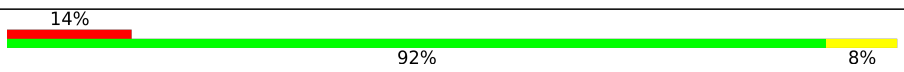
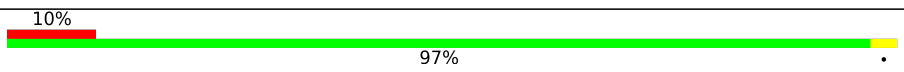
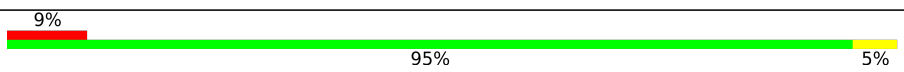
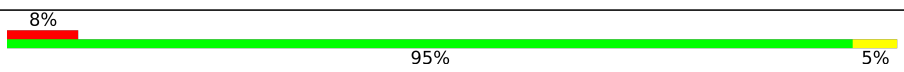
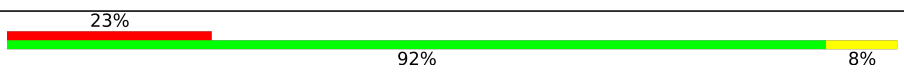
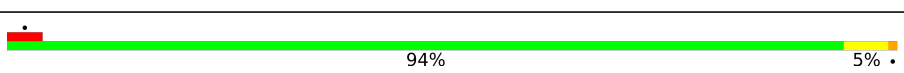
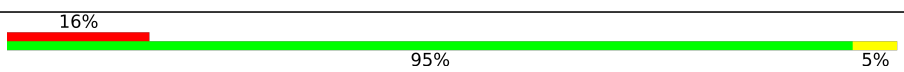
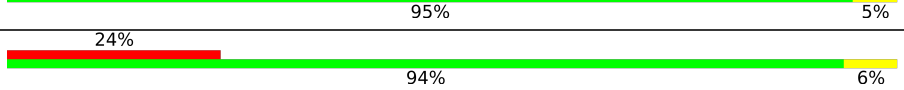
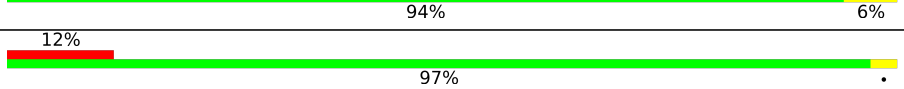
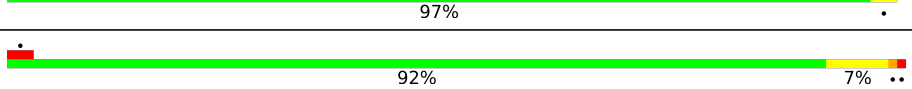
Mol	Chain	Length	Quality of chain
9	F	222	
10	G	233	
11	H	191	
12	I	216	
13	J	168	
14	L	198	
15	M	136	
16	N	202	
17	O	197	
18	P	180	
19	Q	184	
20	R	188	
21	S	169	
22	T	158	
23	U	100	
24	V	132	
25	W	62	
26	X	121	
27	Y	125	
28	Z	134	
29	a	147	
30	b	57	
31	c	97	
32	d	106	
33	e	122	

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Mol	Chain	Length	Quality of chain
34	f	105	96%
35	g	121	19% 88% 12%
36	h	116	5% 98%
37	i	98	13% 92% 7%
38	j	85	96%
39	k	76	50% 89% 9%
40	l	49	94% 6%
41	m	51	8% 100%
42	n	23	26% 91% 9%
43	o	101	10% 85% 15%
44	p	87	10% 90% 9%
45	q	217	100% 86% 13%
46	r	195	95% 85% 15%
47	K	152	95% 97%
48	AA	206	36% 94% 6%
49	BB	214	25% 93% 7%
50	CC	217	15% 93% 6%
51	DD	223	35% 92% 8%
52	EE	257	13% 93% 7%
53	FF	206	21% 89% 8%
54	GG	226	42% 97%
55	HH	184	74% 93% 6%
56	II	199	31% 84% 10% 6%
57	JJ	182	19% 93% 5%
58	KK	96	35% 82% 18%

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Mol	Chain	Length	Quality of chain
59	LL	145	25% 97%
60	MM	124	99% 93% 7%
61	NN	150	33% 94% 5%
62	OO	127	13% 90% 10%
63	PP	103	33% 92% 8%
64	QQ	141	15% 91% 9%
65	RR	123	53% 91% 9%
66	SS	136	23% 93% 7%
67	TT	143	17% 92% 7%
68	UU	106	44% 98%
69	VV	87	25% 92% 8%
70	WW	129	10% 93% 7%
71	XX	144	10% 91% 9%
72	YY	134	26% 97%
73	ZZ	70	36% 96%
74	aa	97	13% 90% 10%
75	bb	81	44% 90% 10%
76	cc	63	21% 94% 6%
77	dd	53	9% 91% 9%
78	ee	53	25% 94% 6%
79	ff	57	70% 72% 5% 23%
80	gg	318	60% 92% 8%
81	2	1796	15% 68% 31%
82	1	600	29% 87% 12%
83	3	76	14% 78% 22%

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Mol	Chain	Length	Quality of chain
84	4	6	100%

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
87	U6A	3	101	-	X	-	-

2 Entry composition (i)

There are 88 unique types of molecules in this entry. The entry contains 211119 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 RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	5	3271	69936	31236	12597	22832	3271	0	0

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	7	121	2579	1152	461	845	121	0	0

- Molecule 3 is a RNA chain called 5.8S ribosomal rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	8	157	3333	1491	584	1101	157	0	0

- Molecule 4 is a protein called uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A	249	1893	1178	384	330	1	0	0

- Molecule 5 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	384	3065	1946	582	529	8	0	0

- Molecule 6 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C	359	2735	1723	520	489	3	0	0

- Molecule 7 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	295	Total	C	N	O	S	0	0
			2370	1498	413	457	2		

- Molecule 8 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 9 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 10 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	233	Total	C	N	O	S	0	0
			1809	1154	324	328	3		

- Molecule 11 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	191	Total	C	N	O	S	0	0
			1524	966	274	280	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	191	GLU	-	insertion	UNP P51401

- Molecule 12 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	216	Total	C	N	O	S	0	0
			1750	1109	331	303	7		

- Molecule 13 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	168	Total	C	N	O	S	0	0
			1344	841	251	248	4		

- Molecule 14 is a protein called eL13.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	L	198	Total	C	N	O	0	0
			1584	988	323	273		

- Molecule 15 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	136	Total	C	N	O	S	0	0
			1054	675	199	178	2		

- Molecule 16 is a protein called eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	202	Total	C	N	O	S	0	0
			1711	1071	359	280	1		

- Molecule 17 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 18 is a protein called uL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	P	180	Total	C	N	O	0	0
			1427	887	284	256		

- Molecule 19 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	184	Total	C	N	O	S	0	0
			1437	906	289	240	2		

- Molecule 20 is a protein called eL19.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	R	188	Total 1521	C 935	N 326	O 260	0	0

- Molecule 21 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	169	Total 1422	C 916	N 262	O 241	S 3	0	0

- Molecule 22 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	158	Total 1268	C 799	N 245	O 220	S 4	0	0

- Molecule 23 is a protein called eL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	U	100	Total 796	C 516	N 131	O 149	0	0

- Molecule 24 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	132	Total 978	C 614	N 184	O 173	S 7	0	0

- Molecule 25 is a protein called eL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	W	62	Total 513	C 331	N 101	O 81	0	0

- Molecule 26 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	121	Total 968	C 623	N 170	O 173	S 2	0	0

- Molecule 27 is a protein called uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	Y	125	Total 988	C 622	N 191	O 175	0	0

- Molecule 28 is a protein called eL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	Z	134	Total 1087	C 707	N 201	O 179	0	0

- Molecule 29 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	147	Total 1168	C 746	N 230	O 189	S 3	0	0

- Molecule 30 is a protein called eL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	b	57	Total 457	C 286	N 99	O 72	0	0

- Molecule 31 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	97	Total 743	C 479	N 124	O 139	S 1	0	0

- Molecule 32 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	106	Total 865	C 550	N 165	O 149	S 1	0	0

- Molecule 33 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	122	Total 988	C 626	N 200	O 161	S 1	0	0

- Molecule 34 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	105	Total	C	N	O	S	0	0
			842	534	164	143	1		

- Molecule 35 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	121	Total	C	N	O	S	0	0
			954	592	194	164	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	122	LYS	-	insertion	UNP P87262

- Molecule 36 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	116	Total	C	N	O	S	0	0
			950	603	182	164	1		

- Molecule 37 is a protein called eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	98	Total	C	N	O	S	0	0
			764	477	155	130	2		

- Molecule 38 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	85	Total	C	N	O	S	0	0
			673	410	147	111	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
j	84	LYS	-	insertion	UNP P49166
j	85	ALA	-	insertion	UNP P49166
j	86	GLN	-	insertion	UNP P49166

- Molecule 39 is a protein called eL38.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	k	76	Total	C	N	O	0	0
			607	388	114	105		

- Molecule 40 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	49	Total	C	N	O	S	0	0
			428	266	96	64	2		

- Molecule 41 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	51	Total	C	N	O	S	0	0
			409	253	85	66	5		

- Molecule 42 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	23	Total	C	N	O	S	0	0
			218	133	60	24	1		

- Molecule 43 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	101	Total	C	N	O	S	0	0
			814	511	165	133	5		

- Molecule 44 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	87	Total	C	N	O	S	0	0
			668	413	134	115	6		

- Molecule 45 is a protein called uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	217	Total	C	N	O	S	0	0
			1718	1097	299	312	10		

- Molecule 46 is a protein called uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	r	195	Total	C	N	O	S	0	0
			1512	968	261	279	4		

- Molecule 47 is a protein called L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	K	147	Total	C	N	O	0	0
			735	441	147	147		

- Molecule 48 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AA	206	Total	C	N	O	S	0	0
			1615	1037	286	290	2		

- Molecule 49 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BB	214	Total	C	N	O	S	0	0
			1716	1086	314	312	4		

- Molecule 50 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	CC	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 51 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	DD	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 52 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	EE	257	Total	C	N	O	S	0	0
			2047	1303	385	356	3		

- Molecule 53 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	FF	201	Total	C	N	O	S	0	0
			1588	996	295	294	3		

- Molecule 54 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	GG	226	Total	C	N	O	S	0	0
			1820	1142	350	325	3		

- Molecule 55 is a protein called eS7.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	HH	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 56 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	II	187	Total	C	N	O	S	0	0
			1480	919	296	263	2		

- Molecule 57 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	JJ	182	Total	C	N	O	S	0	0
			1477	933	288	255	1		

- Molecule 58 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	KK	96	Total	C	N	O	S	0	0
			818	530	133	153	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
KK	89	ALA	GLY	conflict	UNP Q08745

- Molecule 59 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	LL	145	Total	C	N	O	S	0	0
			1166	746	220	197	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LL	146	THR	-	insertion	UNP P0CX47

- Molecule 60 is a protein called eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	MM	124	Total	C	N	O	S	0	0
			934	587	165	180	2		

- Molecule 61 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	NN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 62 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	OO	127	Total	C	N	O	S	0	0
			941	578	186	174	3		

- Molecule 63 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	PP	103	Total	C	N	O	S	0	0
			814	520	149	138	7		

- Molecule 64 is a protein called uS19.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	QQ	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 65 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	RR	123	Total	C	N	O	S	0	0
			989	619	186	182	2		

- Molecule 66 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SS	136	Total	C	N	O	S	0	0
			1121	700	223	196	2		

- Molecule 67 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	TT	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 68 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	UU	106	Total	C	N	O	S	0	0
			847	535	154	157	1		

- Molecule 69 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	VV	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 70 is a protein called uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	WW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 71 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	XX	144	Total	C	N	O	S	0	0
			1123	710	220	190	3		

- Molecule 72 is a protein called eS24.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	YY	134	Total 1073	C 676	N 208	O 189	0	0

- Molecule 73 is a protein called eS25.

Mol	Chain	Residues	Atoms				AltConf	Trace
73	ZZ	70	Total 563	C 360	N 104	O 99	0	0

- Molecule 74 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	aa	97	Total 769	C 475	N 160	O 129	S 5	0	0

- Molecule 75 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	bb	81	Total 610	C 382	N 110	O 113	S 5	0	0

- Molecule 76 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	cc	63	Total 497	C 306	N 99	O 91	S 1	0	0

- Molecule 77 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	dd	53	Total 443	C 275	N 92	O 72	S 4	0	0

- Molecule 78 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	ee	53	Total 426	C 268	N 88	O 69	S 1	0	0

- Molecule 79 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	ff	44	Total	C	N	O	S	0	0
			344	216	68	56	4		

- Molecule 80 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	gg	318	Total	C	N	O	S	0	0
			2444	1546	419	471	8		

- Molecule 81 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	2	1780	Total	C	N	O	P	0	0
			37790	16890	6651	12469	1780		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	677	A	G	conflict	GB 1329886537
2	678	U	A	conflict	GB 1329886537

- Molecule 82 is a protein called eIF5B.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	1	600	Total	C	N	O	S	0	0
			4704	2989	801	893	21		

- Molecule 83 is a RNA chain called Met-tRNA-iMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	3	76	Total	C	N	O	P	0	0
			1630	726	302	526	76		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	17	G	-	insertion	GB 176433

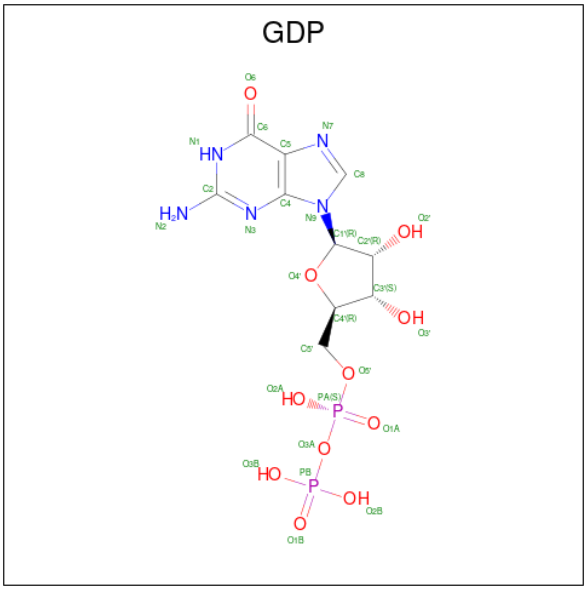
- Molecule 84 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	4	6	Total	C	N	O	P	0	0
			131	59	27	39	6		

- Molecule 85 is ZINC ION (three-letter code: ZN) (formula: Zn).

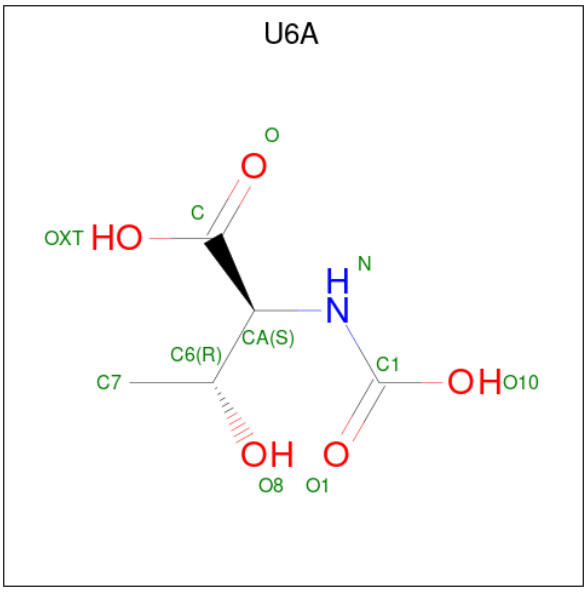
Mol	Chain	Residues	Atoms		AltConf
85	j	1	Total	Zn	0
			1	1	
85	m	1	Total	Zn	0
			1	1	
85	o	1	Total	Zn	0
			1	1	
85	aa	1	Total	Zn	0
			1	1	
85	bb	1	Total	Zn	0
			1	1	
85	ff	1	Total	Zn	0
			1	1	

- Molecule 86 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



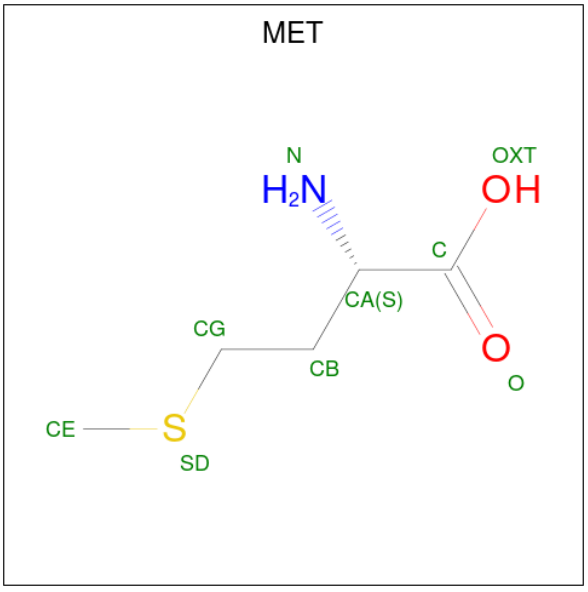
Mol	Chain	Residues	Atoms					AltConf
86	1	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 87 is N-carboxy-L-threonine (three-letter code: U6A) (formula: $C_5H_9NO_5$).



Mol	Chain	Residues	Atoms				AltConf
87	3	1	Total	C	N	O	0
			10	5	1	4	

- Molecule 88 is METHIONINE (three-letter code: MET) (formula: $C_5H_{11}NO_2S$).



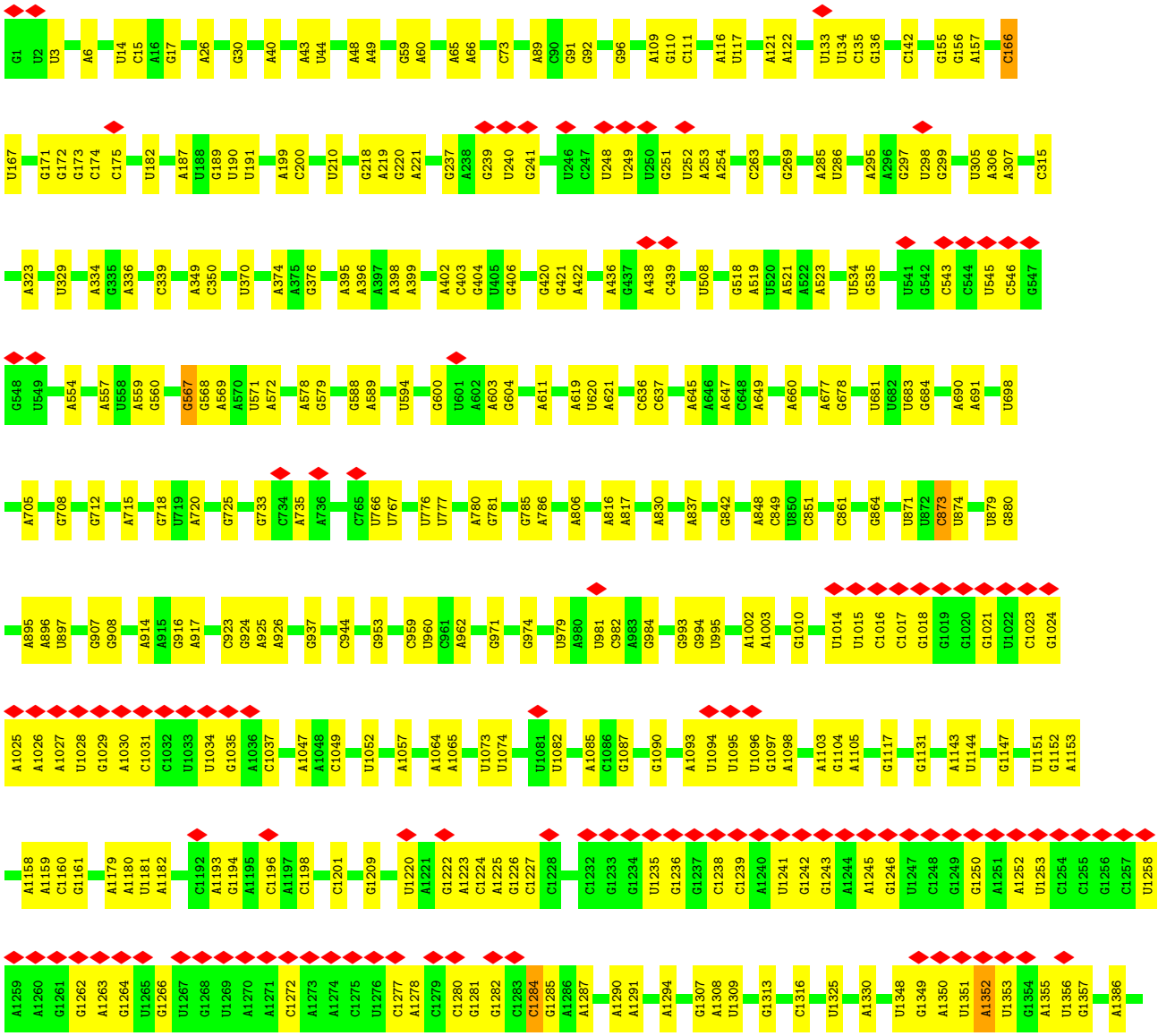
Mol	Chain	Residues	Atoms					AltConf
88	3	1	Total	C	N	O	S	0
			8	5	1	1	1	

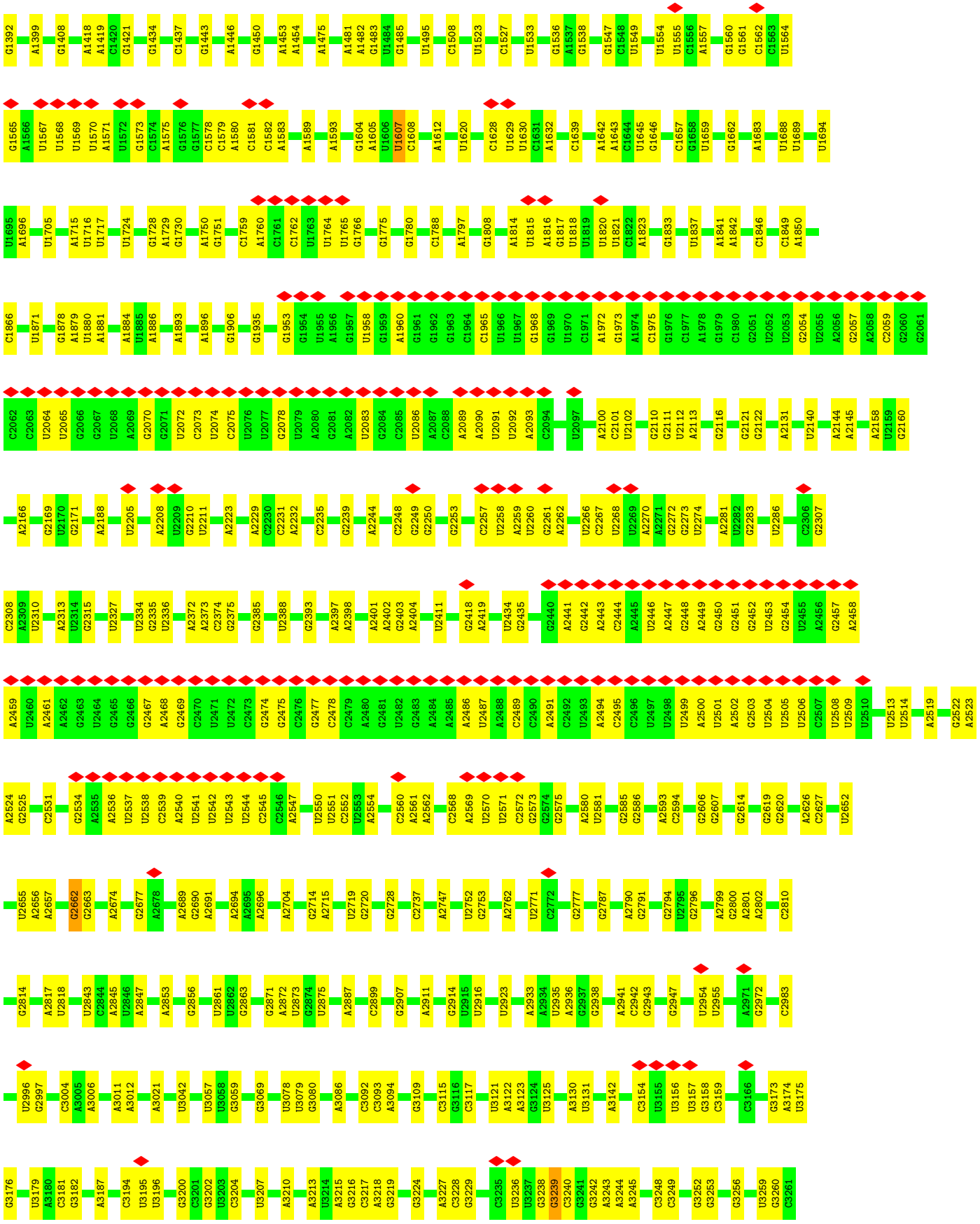
3 Residue-property plots (i)

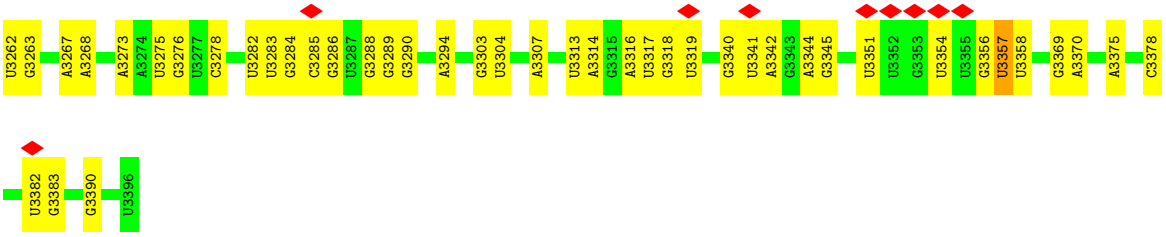
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 25S ribosomal RNA

Chain 5:

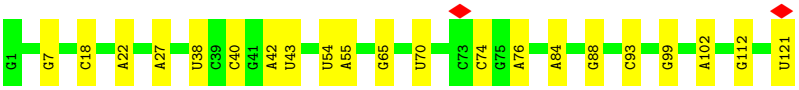



G1392 A1399 G1408 A1418 A1419 C1420 G1421 G1434 C1437 G1443 A1446 G1450 A1453 A1454 A1475 A1481 A1482 G1483 U1484 G1485 U1495 C1508 U1523 C1527 U1533 G1536 A1537 G1538 G1547 C1548 U1549 U1554 U1555 C1556 A1557 G1560 G1561 C1562 C1563 U1564
G1565 A1566 U1567 U1568 U1569 U1570 A1571 U1572 G1573 C1574 A1575 G1576 G1577 C1578 C1579 A1580 C1581 C1582 A1583 A1589 A1593 G1604 A1605 U1606 U1607 C1608 A1612 U1620 C1628 U1629 U1630 C1631 A1632 C1639 A1642 A1643 C1644 U1645 G1646 C1657 G1658 U1659 G1662 A1683 U1688 U1689 U1694
U1695 A1696 U1705 A1715 U1716 U1717 U1724 G1728 A1729 G1730 A1750 G1751 C1759 A1760 C1761 C1762 U1763 U1764 U1765 G1766 G1775 G1780 C1788 A1797 G1808 A1814 U1815 A1816 G1817 U1818 U1819 U1820 U1821 C1822 A1823 G1833 U1837 A1841 A1842 C1846 C1849 A1850
C1866 U1871 G1878 A1879 U1880 A1881 A1884 U1885 A1886 A1893 A1896 G1906 G1935 G1953 G1954 U1955 A1956 G1957 U1958 G1959 A1960 G1961 G1962 G1963 C1964 C1965 U1966 U1967 G1968 G1969 U1970 C1971 A1972 G1973 A1974 C1975 G1976 C1977 A1978 G1979 C1980 G2051 U2052 U2053 G2054 U2055 A2056 G2057 A2058 C2059 G2060 G2061
C2062 C2063 U2064 U2065 G2066 G2067 U2068 A2069 G2070 G2071 U2072 C2073 U2074 C2075 U2076 U2077 G2078 U2079 A2080 G2081 A2082 U2083 G2084 C2085 U2086 A2087 C2088 A2089 A2090 U2091 U2092 A2093 C2094 U2097 A2100 C2101 U2102 G2110 G2111 U2112 A2113 G2116 G2121 G2122 A2131 U2140 A2144 A2145 A2158 U2159 G2160
A2166 G2169 U2170 G2171 A2188 U2205 A2208 U2209 G2210 U2211 A2223 A2229 C2230 C2231 A2232 C2235 G2239 A2244 C2248 G2249 G2250 G2253 C2257 U2258 A2259 U2260 G2261 A2262 U2266 C2267 U2268 U2269 A2270 A2271 G2272 G2273 U2274 A2281 U2282 G2283 U2286 C2306 G2307
C2308 A2309 U2310 A2313 U2314 G2315 U2327 U2334 G2335 U2336 A2372 A2373 C2374 G2375 G2385 U2388 G2393 A2397 A2398 A2401 A2402 G2403 A2404 U2411 G2418 A2419 U2434 G2435 G2440 A2441 G2442 A2443 C2444 A2445 U2446 A2447 G2448 A2449 G2450 G2451 G2452 U2453 G2454 U2455 A2456 G2457 A2458
A2459 U2460 A2461 A2462 G2463 U2464 G2465 G2466 G2467 A2468 G2469 C2470 U2471 U2472 C2473 G2474 G2475 C2476 G2477 C2478 C2479 A2480 G2481 U2482 G2483 A2484 A2485 A2486 U2487 A2488 C2489 C2490 A2491 C2492 U2493 A2494 C2495 C2496 U2497 U2498 U2499 A2500 U2501 A2502 G2503 U2504 U2505 U2506 C2507 U2508 U2509 U2510 U2513 U2514 A2519 G2522 A2523
A2524 G2525 C2531 G2534 A2535 A2536 U2537 U2538 C2539 A2540 U2541 U2542 U2543 U2544 C2545 C2546 A2547 U2550 U2551 C2552 U2553 A2554 C2560 A2561 A2562 C2568 A2569 U2570 U2571 C2572 G2573 G2574 G2575 A2580 U2581 G2585 G2586 A2593 C2594 G2606 G2607 G2614 G2619 G2620 A2626 C2627 U2652
U2655 A2656 A2657 G2662 G2663 A2674 G2677 A2678 A2689 G2690 A2691 A2694 A2695 A2696 A2704 G2714 A2715 U2719 G2720 G2728 C2737 A2747 U2752 G2753 A2762 U2771 C2772 G2777 G2787 A2790 G2791 G2794 U2795 G2796 A2799 G2800 A2801 A2802 C2810
G2814 A2817 U2818 U2843 C2844 A2845 U2846 A2847 A2853 G2856 U2861 U2862 G2863 G2871 A2872 U2873 G2874 U2875 A2887 C2899 G2907 A2911 G2914 U2915 U2916 U2923 A2933 A2934 U2935 A2936 G2937 G2938 A2941 C2942 G2943 G2947 U2954 U2955 A2971 G2972 C2983
U2996 G2997 C3004 A3005 A3006 A3011 A3012 A3021 U3042 U3057 U3058 G3059 G3069 U3078 U3079 G3080 A3086 C3092 C3093 A3094 G3109 C3115 G3116 C3117 U3121 A3122 A3123 G3124 U3125 A3130 U3131 A3142 C3154 U3155 U3156 U3157 G3158 C3159 C3166 G3173 A3174 U3175
G3176 U3179 A3180 C3181 G3182 A3187 C3194 U3195 U3196 G3200 C3201 G3202 U3203 C3204 U3207 A3210 A3213 U3214 A3215 G3216 C3217 A3218 G3219 G3224 A3227 C3228 G3229 C3235 U3236 U3237 G3238 G3239 C3240 G3241 G3242 A3243 A3244 A3245 C3248 C3249 G3252 G3253 G3256 U3259 G3260 C3261



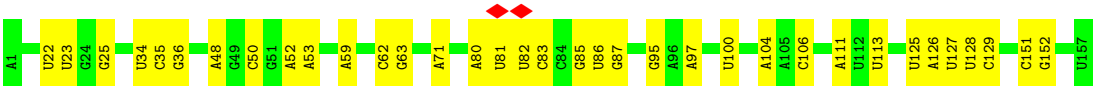
• Molecule 2: 5S ribosomal RNA

Chain 7:



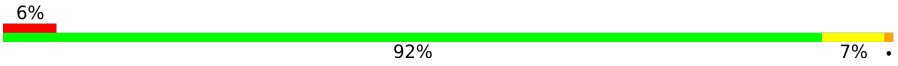
• Molecule 3: 5.8S ribosomal rRNA

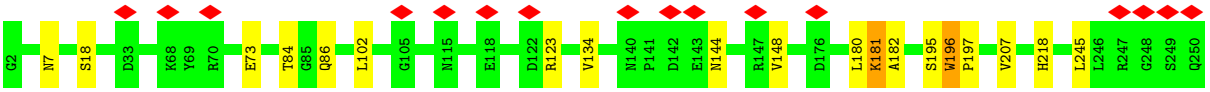
Chain 8:



• Molecule 4: uL2

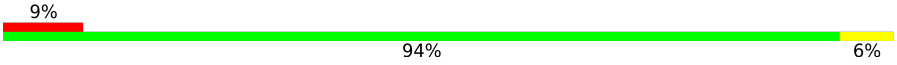
Chain A:

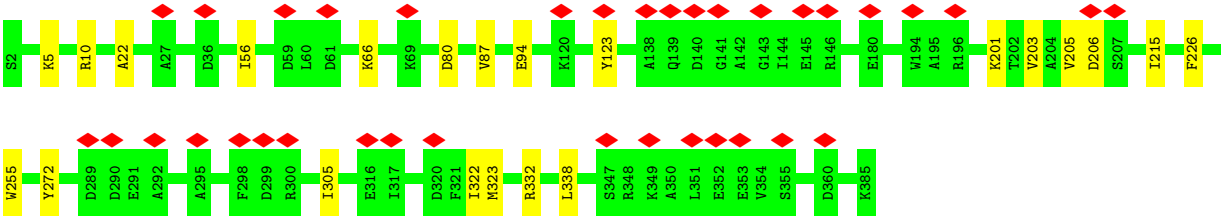




• Molecule 5: uL3

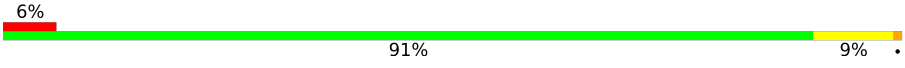
Chain B:

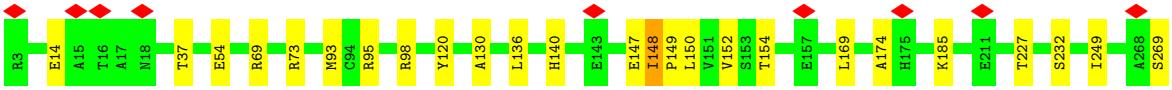


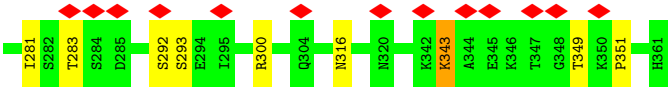


• Molecule 6: uL4

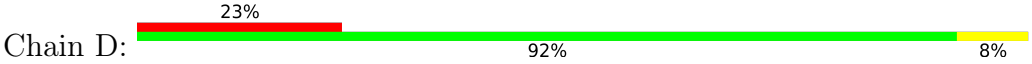
Chain C:

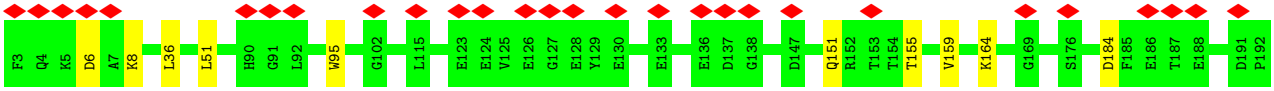


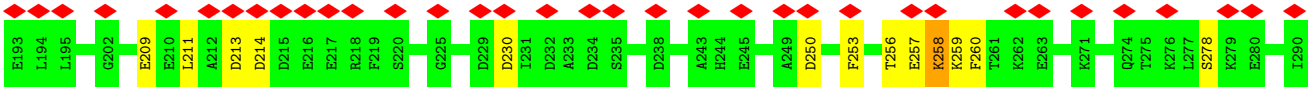


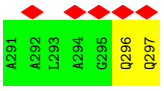


• Molecule 7: uL18

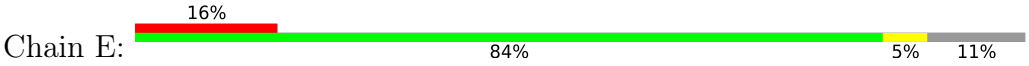


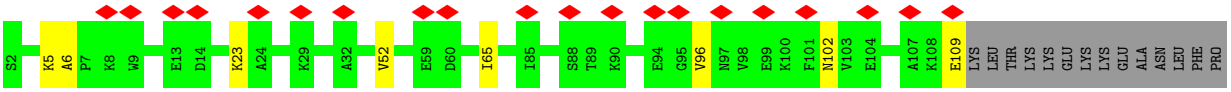


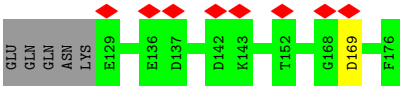




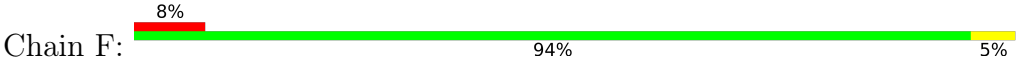
• Molecule 8: eL6

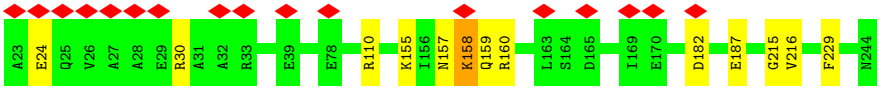




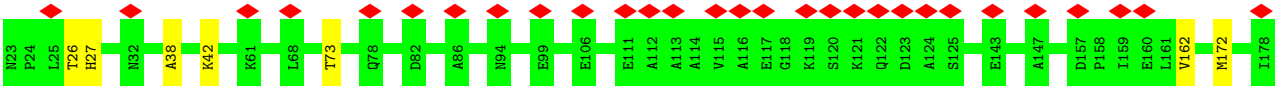


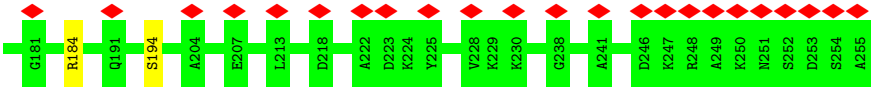
• Molecule 9: uL30





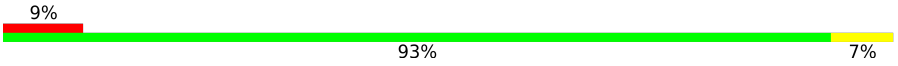
• Molecule 10: eL8

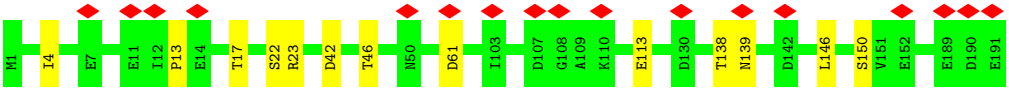




• Molecule 11: uL6

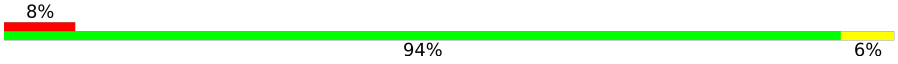
Chain H:

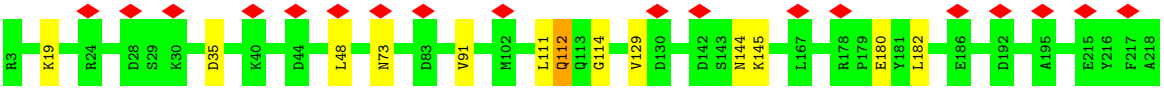




• Molecule 12: uL16

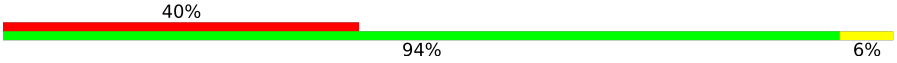
Chain I:

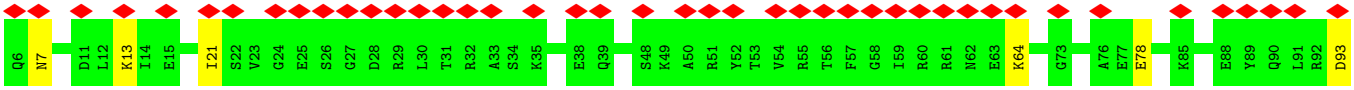


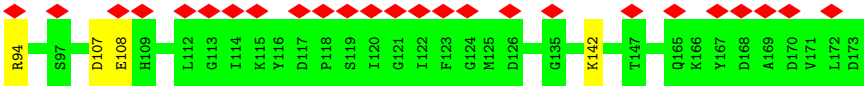


• Molecule 13: uL5

Chain J:

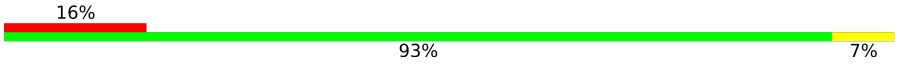


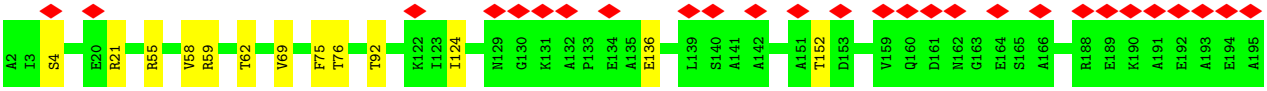


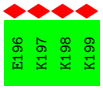


• Molecule 14: eL13

Chain L:

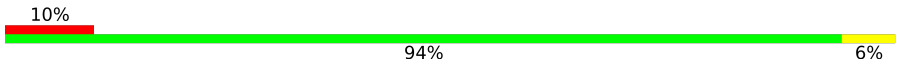


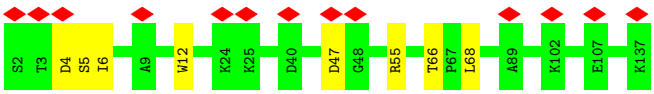




• Molecule 15: eL14

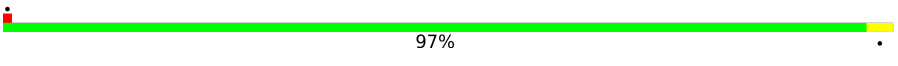
Chain M:

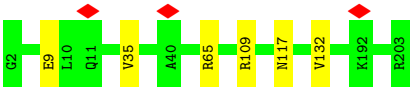




• Molecule 16: eL15

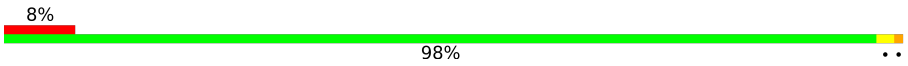
Chain N:

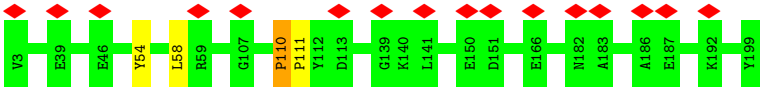




• Molecule 17: uL13

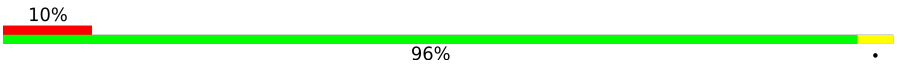
Chain O:

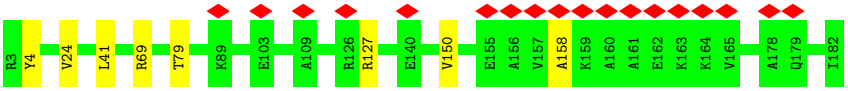




• Molecule 18: uL22

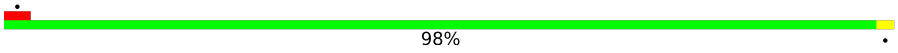
Chain P:

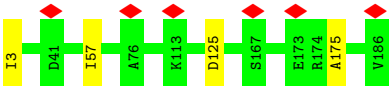




• Molecule 19: eL18

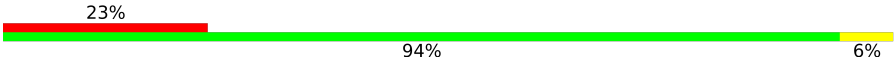
Chain Q:

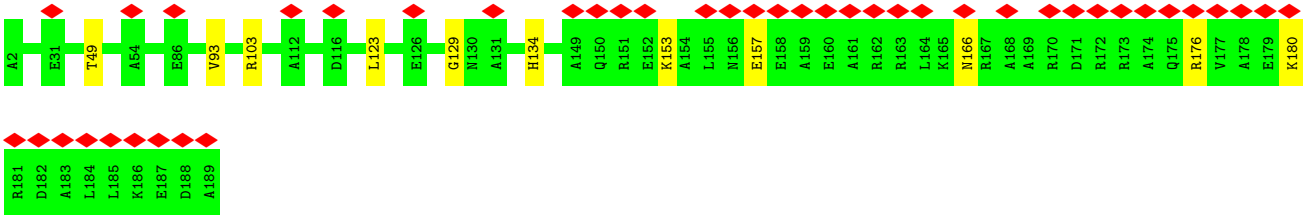




• Molecule 20: eL19

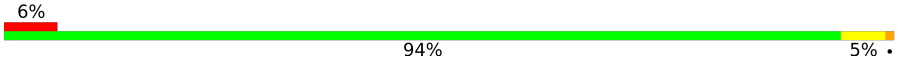
Chain R:

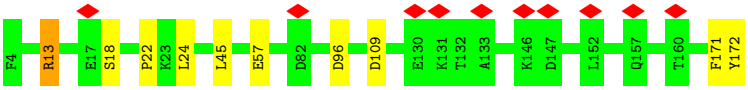




• Molecule 21: eL20

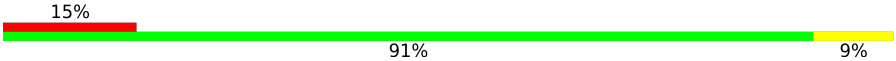
Chain S:

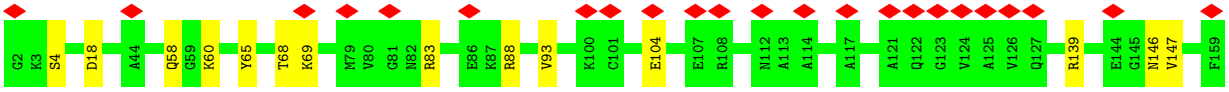




• Molecule 22: eL21

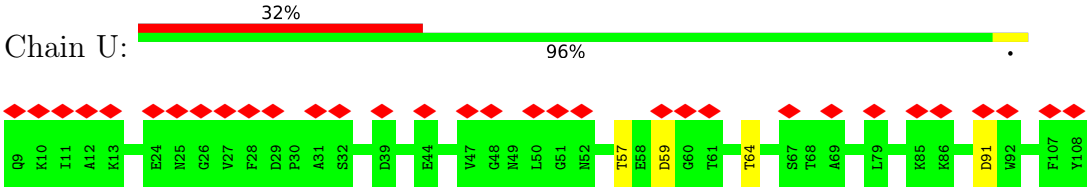
Chain T:





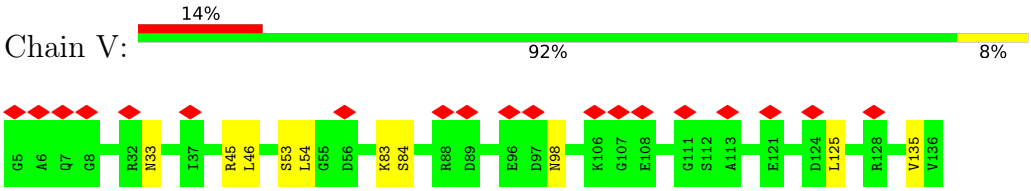
• Molecule 23: eL22

Chain U:



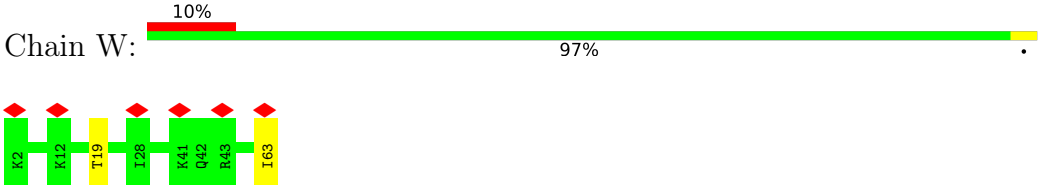
• Molecule 24: uL14

Chain V:



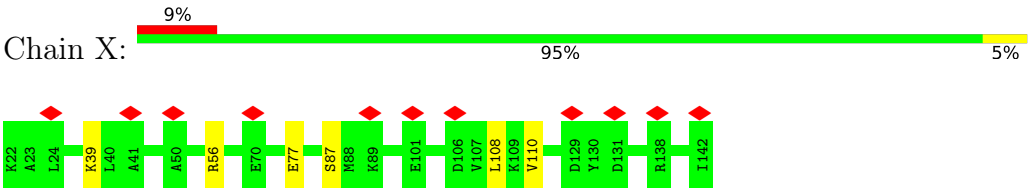
• Molecule 25: eL24

Chain W:



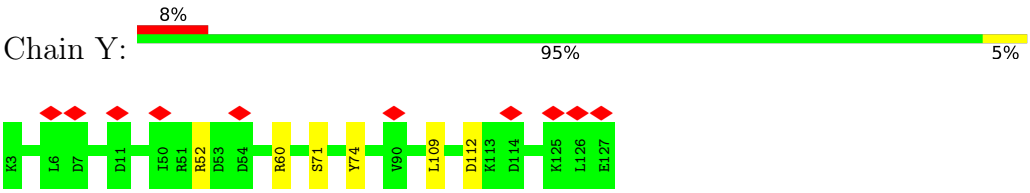
• Molecule 26: uL23

Chain X:



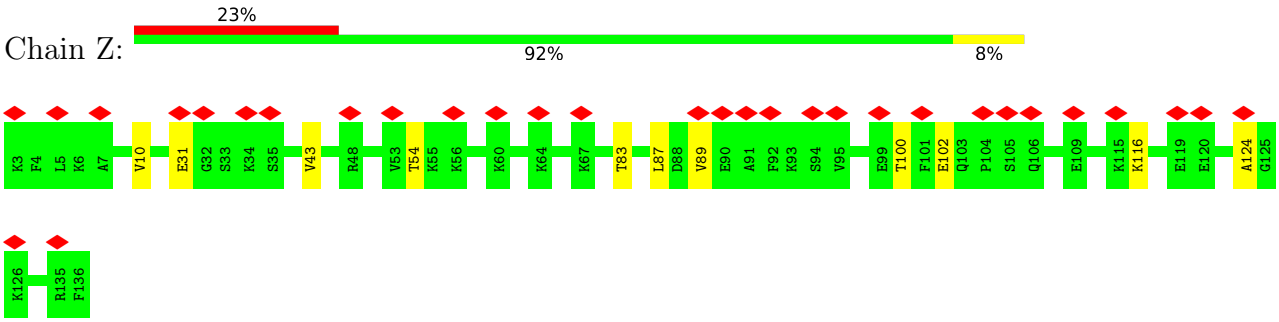
• Molecule 27: uL24

Chain Y:



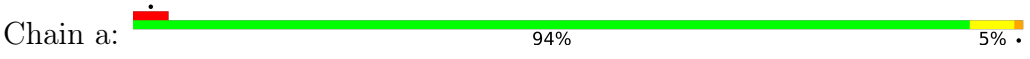
• Molecule 28: eL27

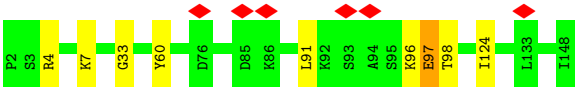
Chain Z:



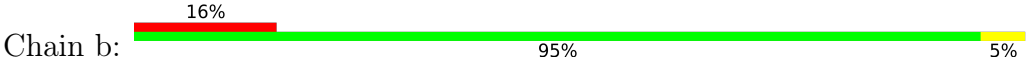
• Molecule 29: uL15

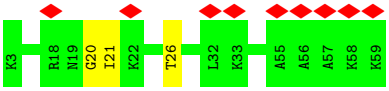
Chain a:



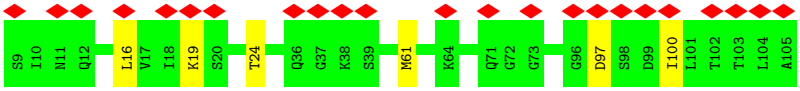


• Molecule 30: eL29

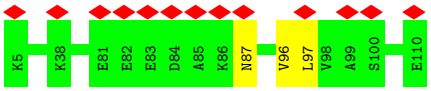




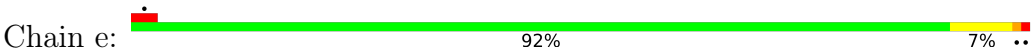
• Molecule 31: eL30

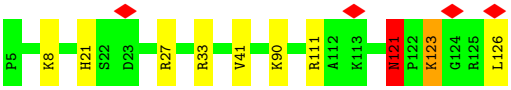


• Molecule 32: eL31



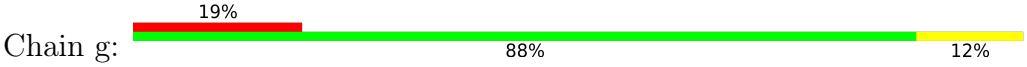
• Molecule 33: eL32

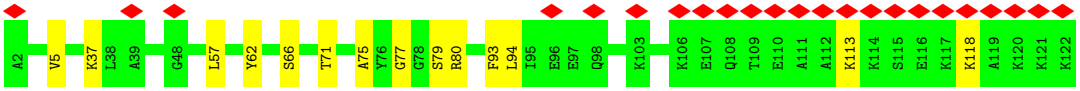




• Molecule 34: eL33

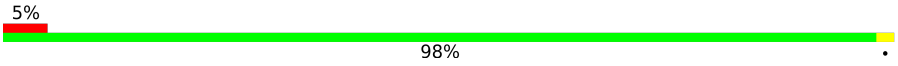
• Molecule 35: eL34

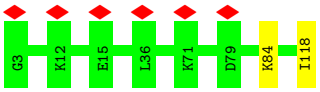




• Molecule 36: uL29

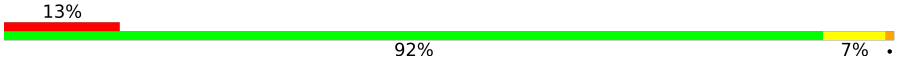
Chain h:

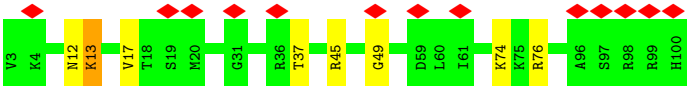




• Molecule 37: eL36

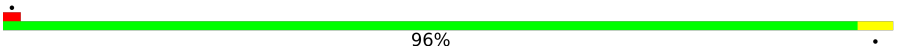
Chain i:

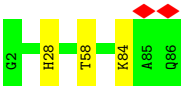




• Molecule 38: eL37

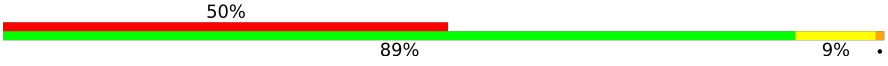
Chain j:

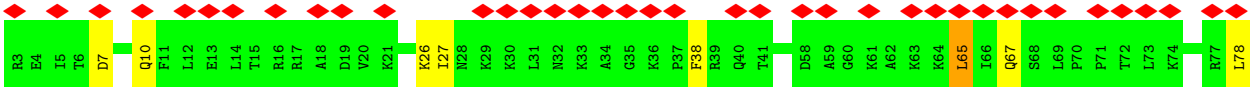




• Molecule 39: eL38

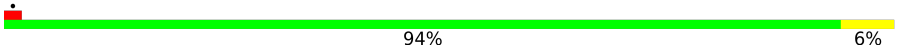
Chain k:

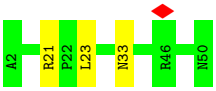




• Molecule 40: eL39

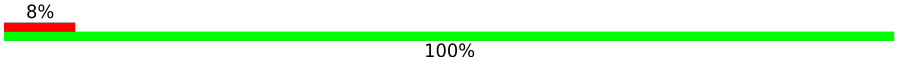
Chain l:

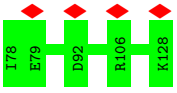




• Molecule 41: eL40

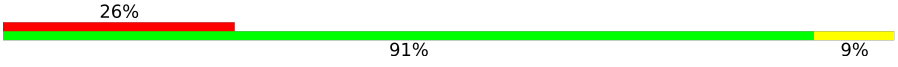
Chain m:

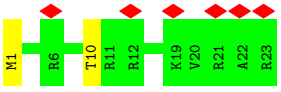




• Molecule 42: eL41

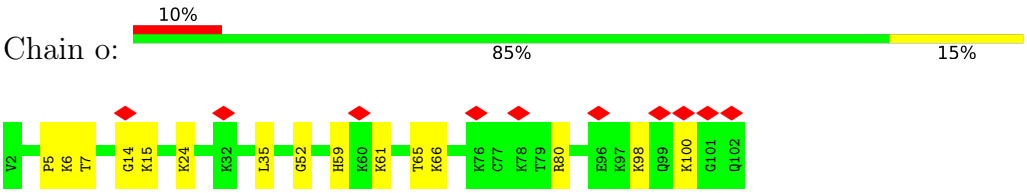
Chain n:





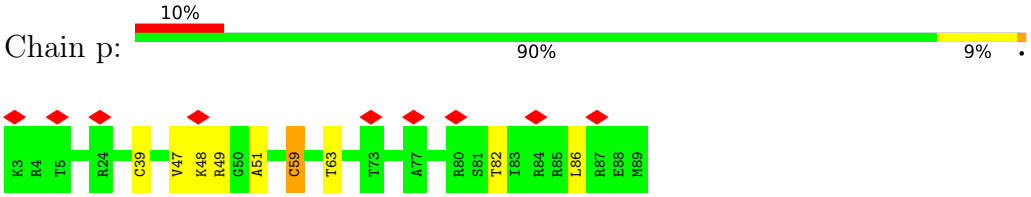
• Molecule 43: eL42

Chain o:



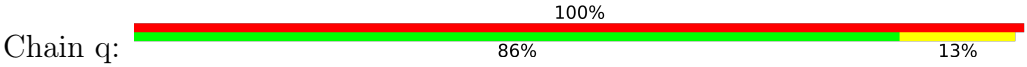
• Molecule 44: eL43

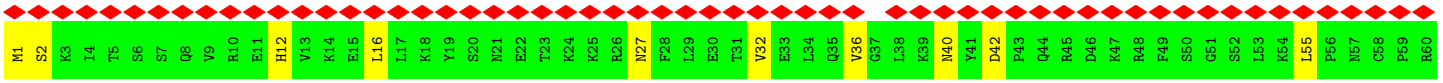
Chain p:

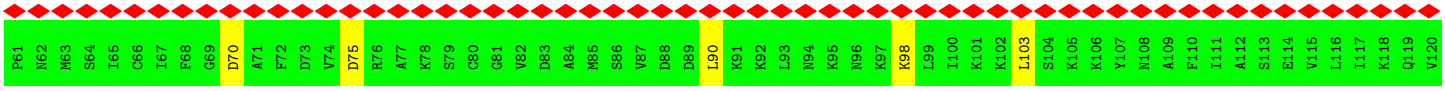


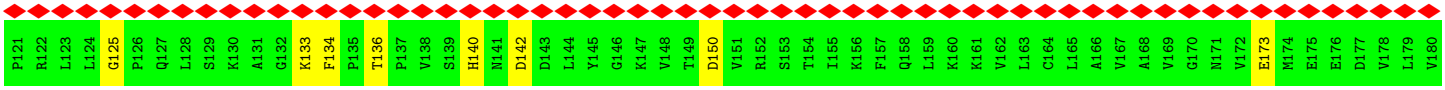
• Molecule 45: uL1

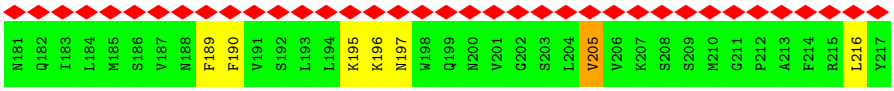
Chain q:





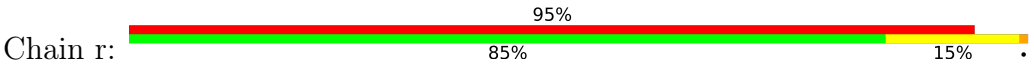


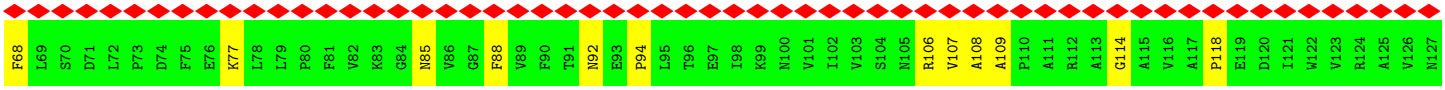


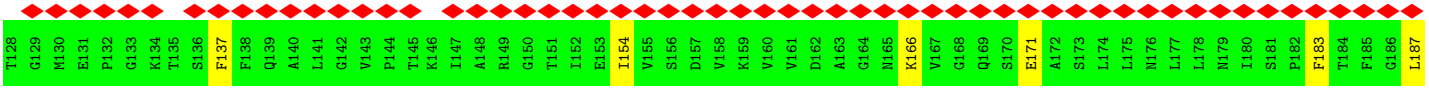


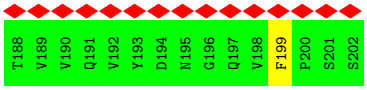
• Molecule 46: uL10

Chain r:



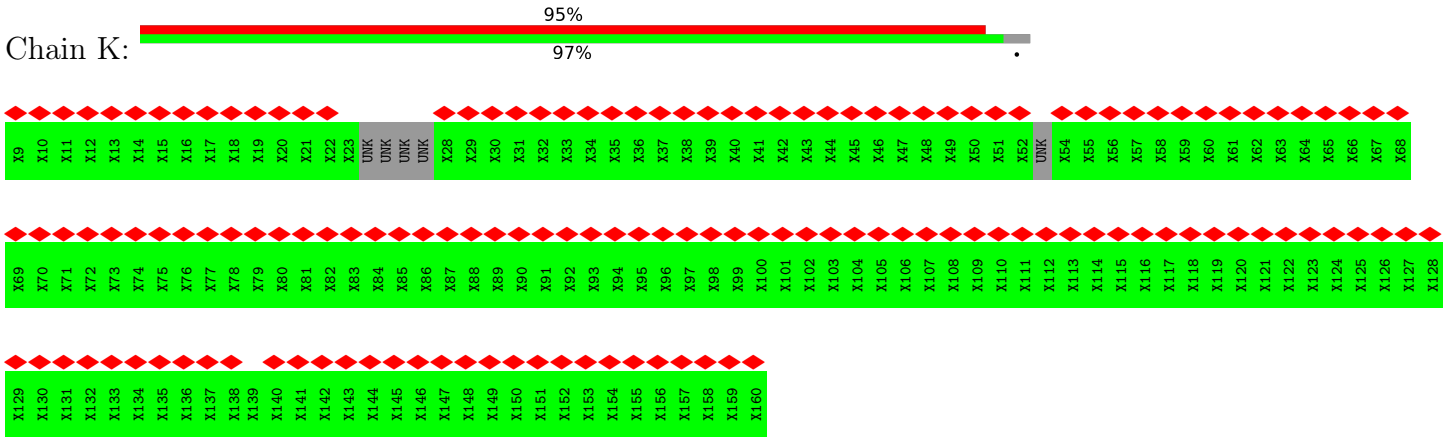






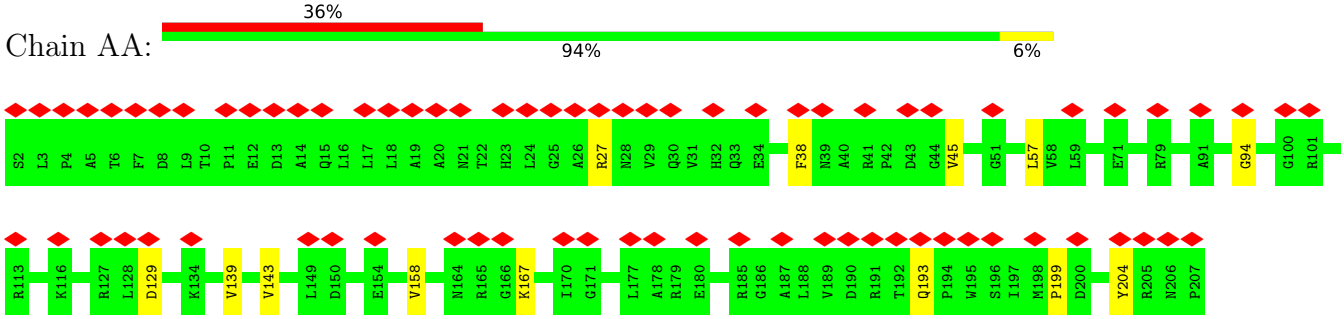
• Molecule 47: L10

Chain K:



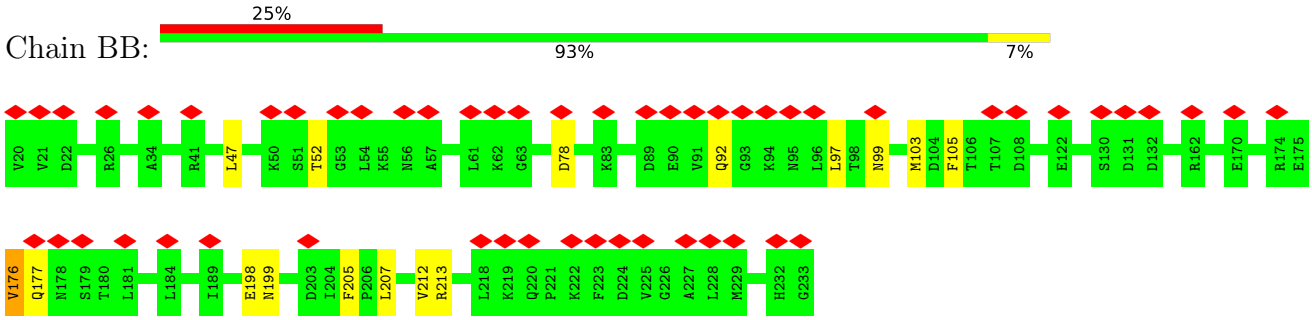
• Molecule 48: uS2

Chain AA:



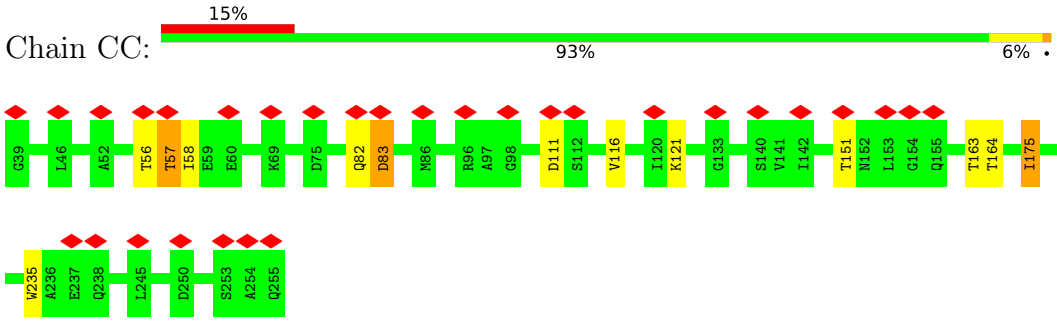
• Molecule 49: eS1

Chain BB:



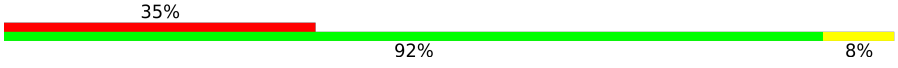
• Molecule 50: uS5

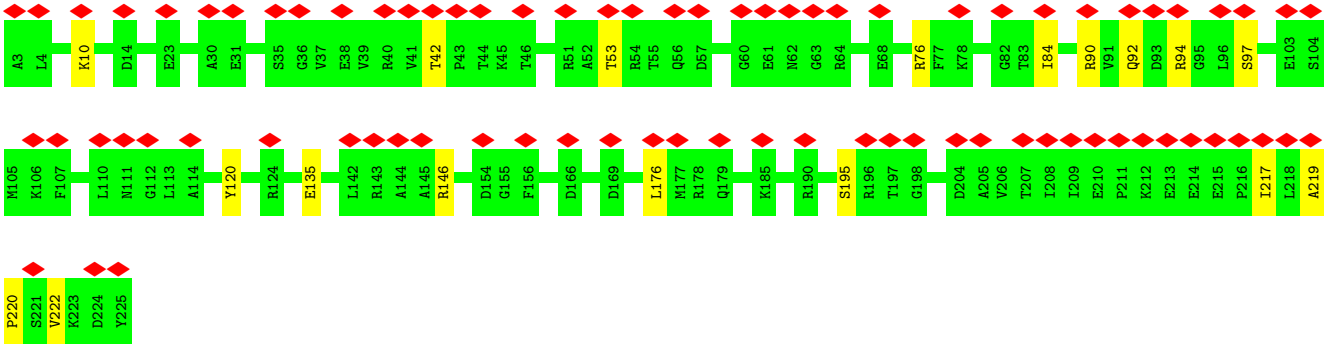
Chain CC:



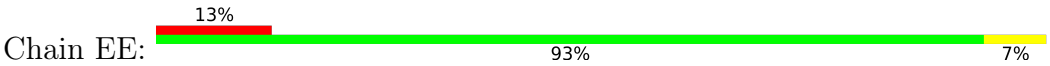
• Molecule 51: uS3

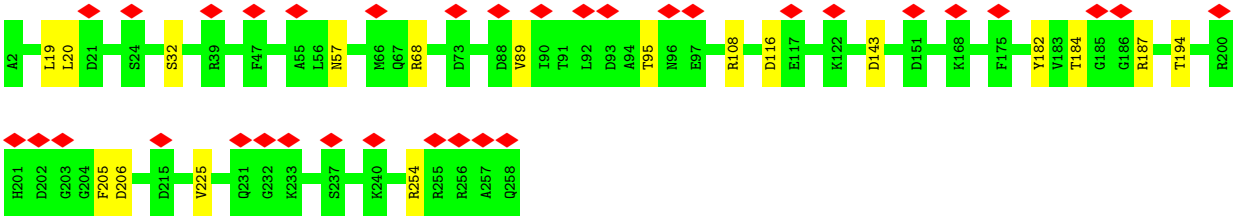
Chain DD:



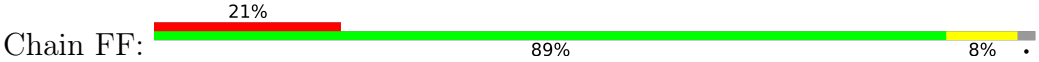


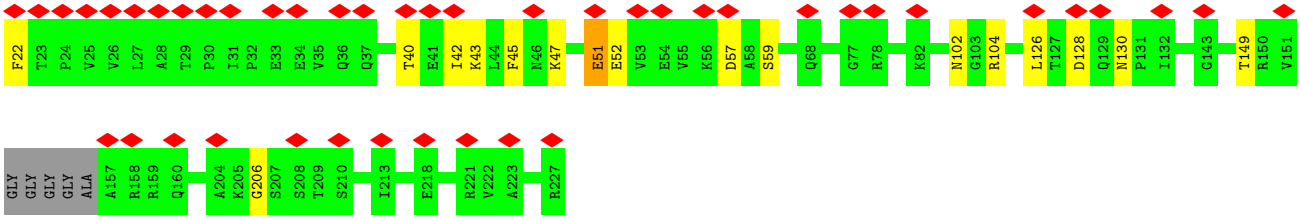
• Molecule 52: eS4



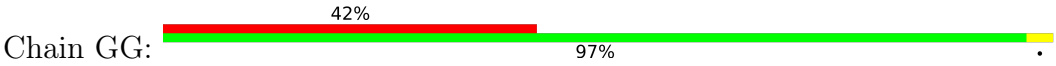


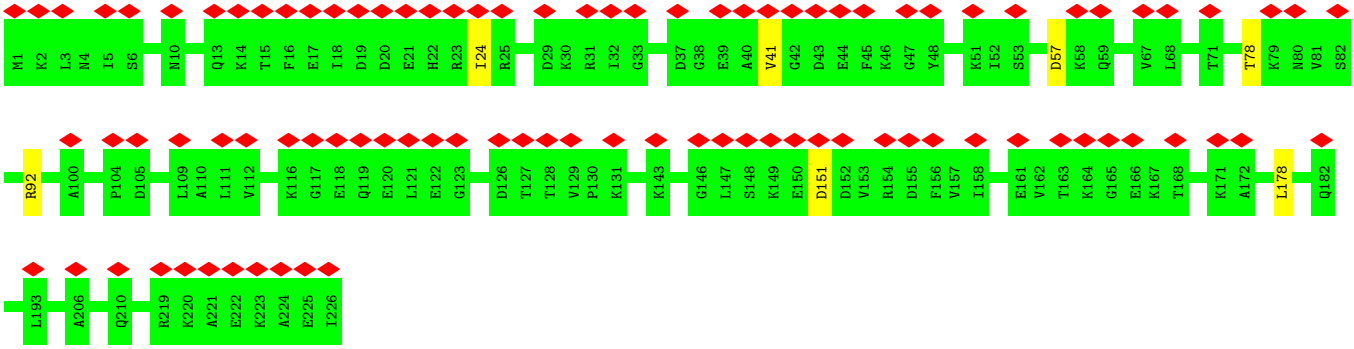
• Molecule 53: uS7





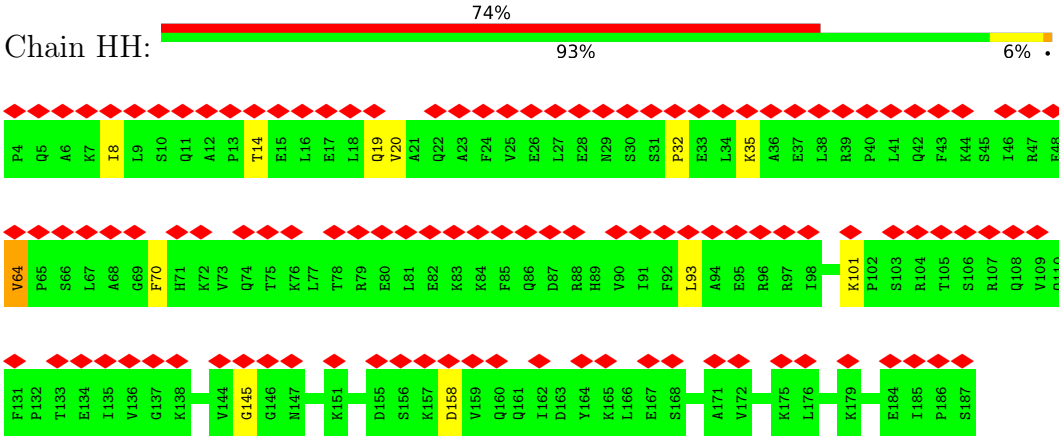
• Molecule 54: eS6





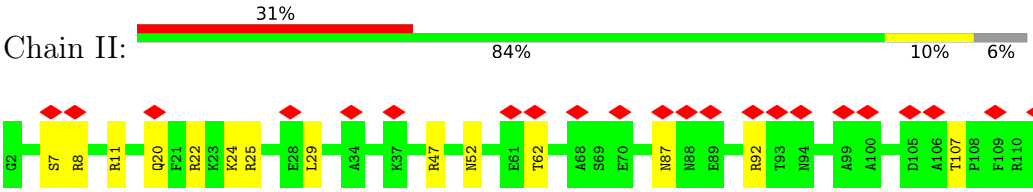
• Molecule 55: eS7

Chain HH:



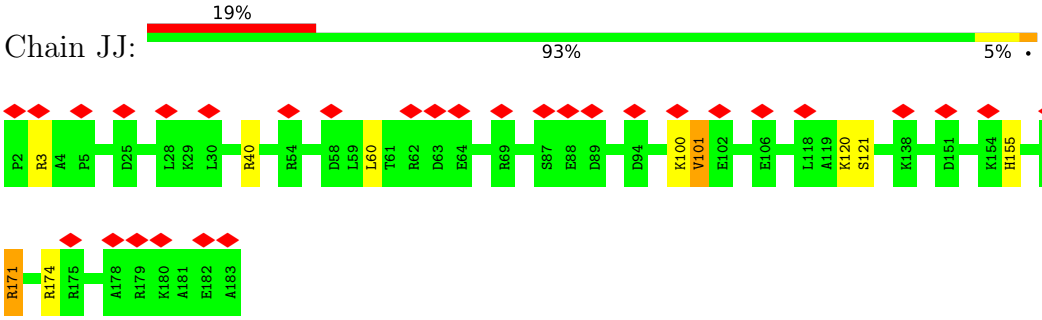
• Molecule 56: eS8

Chain II:



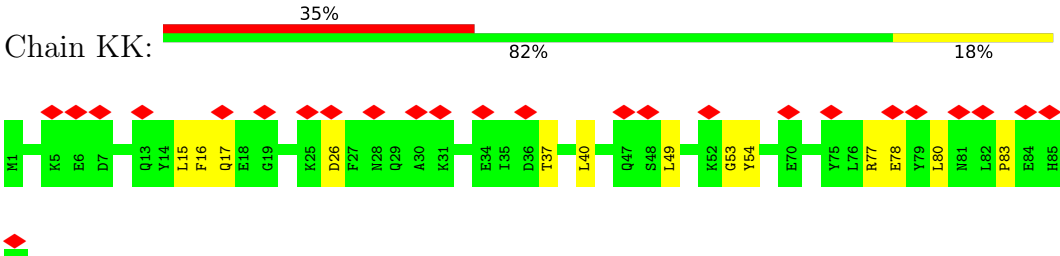
• Molecule 57: uS4

Chain JJ:



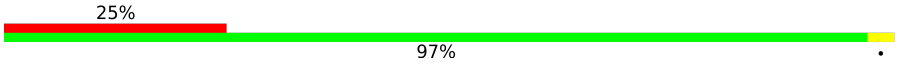
• Molecule 58: eS10

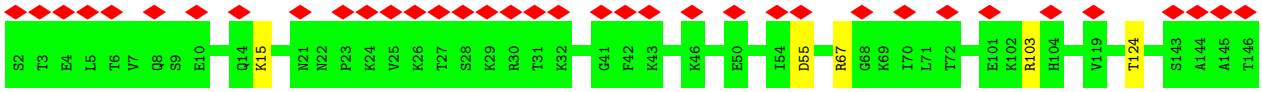
Chain KK:



• Molecule 59: uS17

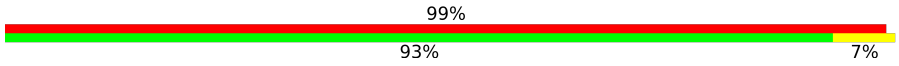
Chain LL:

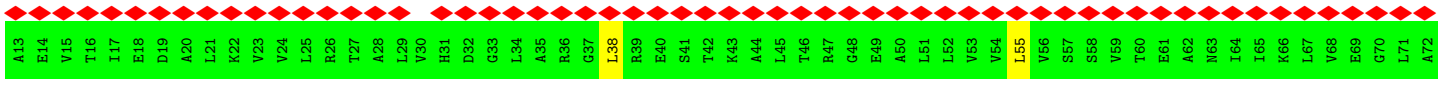


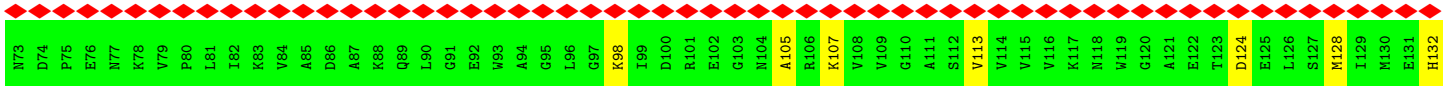


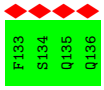
• Molecule 60: eS12

Chain MM:



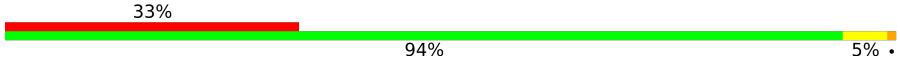


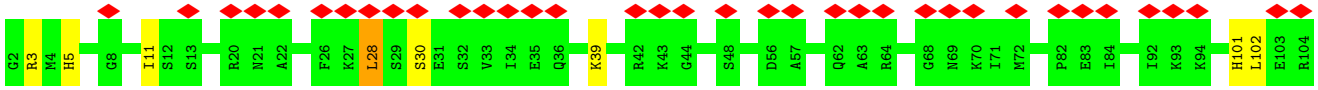


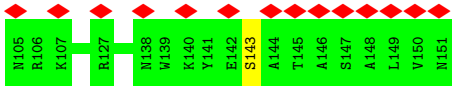


• Molecule 61: uS15

Chain NN:

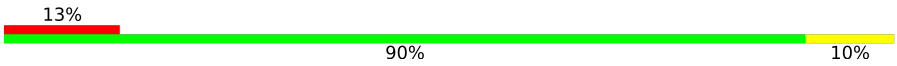


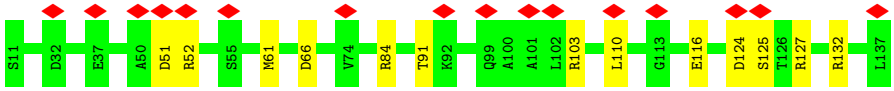




• Molecule 62: uS11

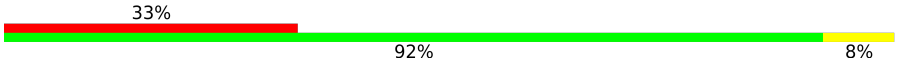
Chain OO:

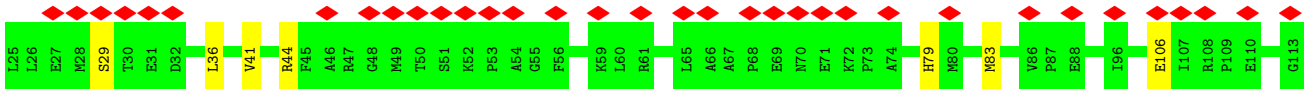




• Molecule 63: uS19

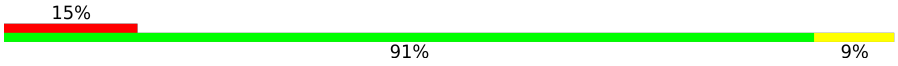
Chain PP:

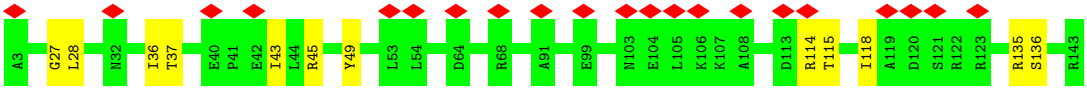




• Molecule 64: uS19

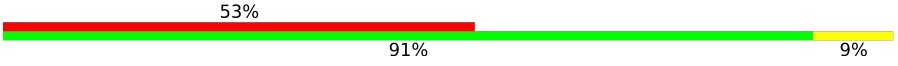
Chain QQ:

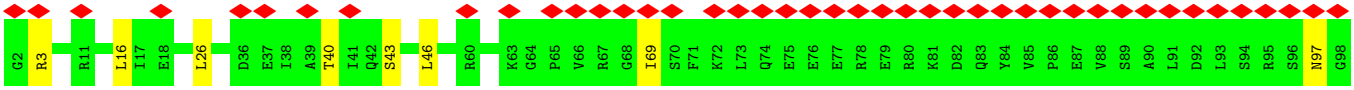


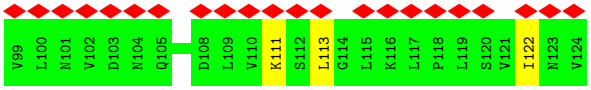


• Molecule 65: eS17

Chain RR:

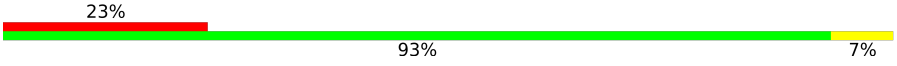


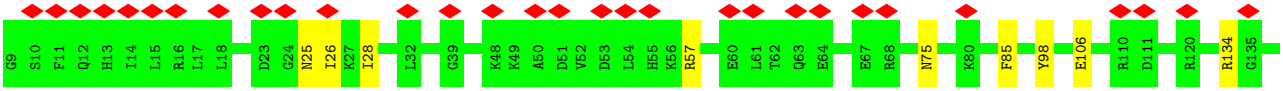




• Molecule 66: uS13

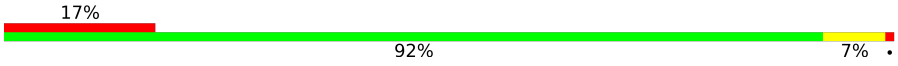
Chain SS:

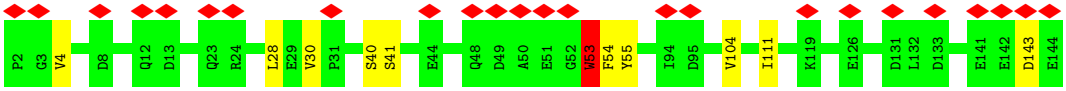




• Molecule 67: eS19

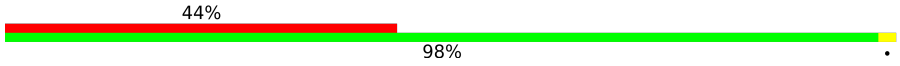
Chain TT:

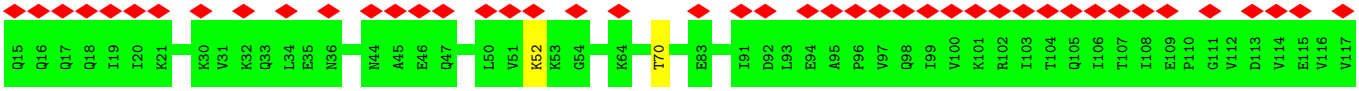




• Molecule 68: uS10

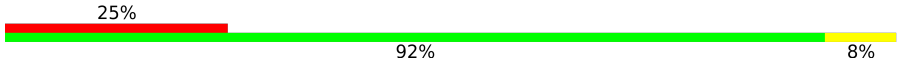
Chain UU:

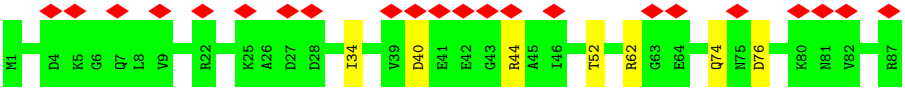




• Molecule 69: eS21

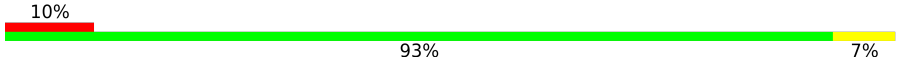
Chain VV:

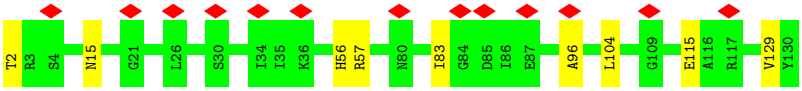




• Molecule 70: uS8

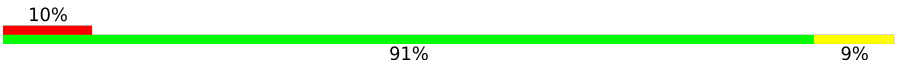
Chain WW:

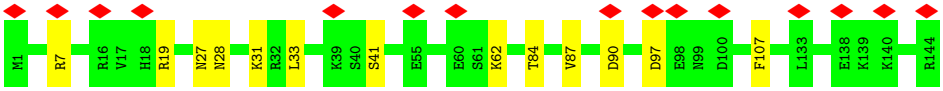




• Molecule 71: uS12

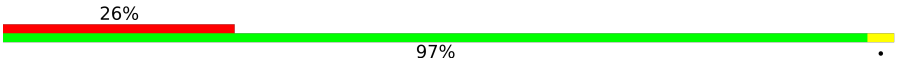
Chain XX:

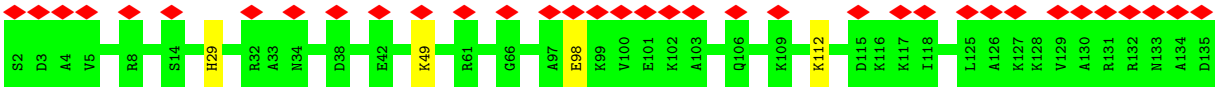




• Molecule 72: eS24

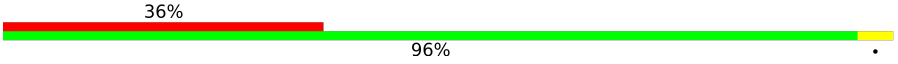
Chain YY:

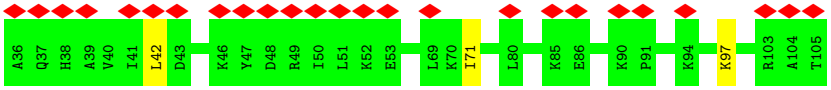




• Molecule 73: eS25

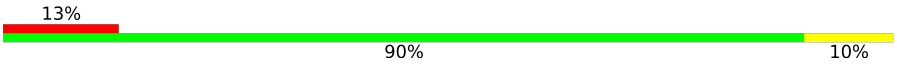
Chain ZZ:

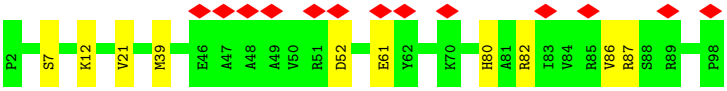




• Molecule 74: eS26

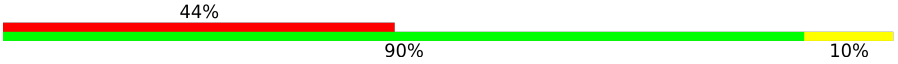
Chain aa:

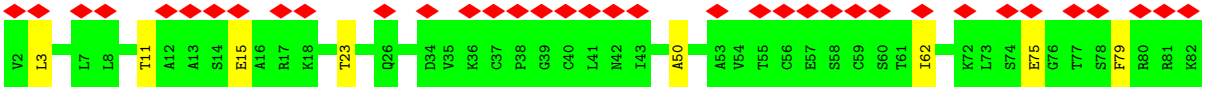




• Molecule 75: eS27

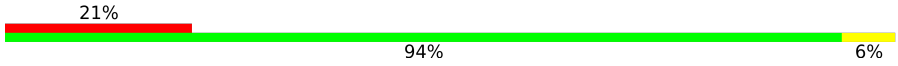
Chain bb:

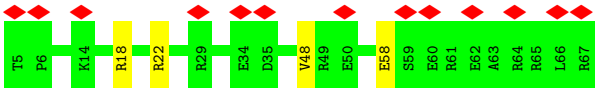




• Molecule 76: eS28

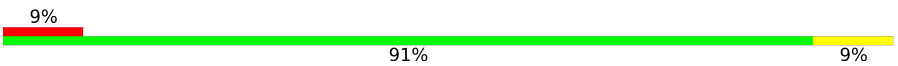
Chain cc:

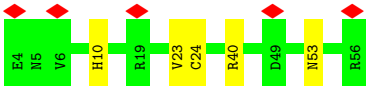




• Molecule 77: uS14

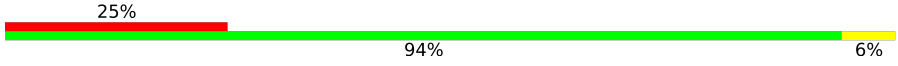
Chain dd:

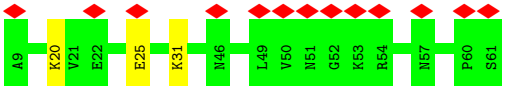




• Molecule 78: eS30

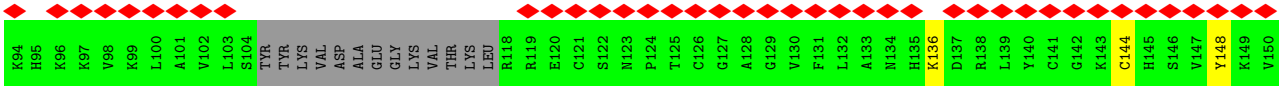
Chain ee:





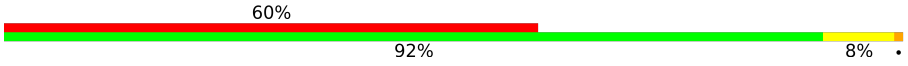
• Molecule 79: eS31

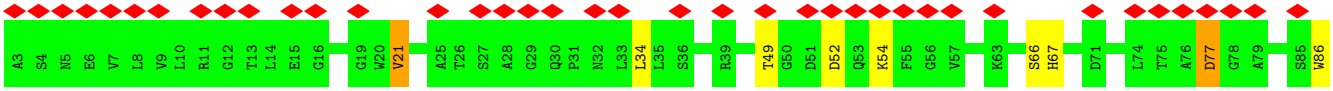
Chain ff:

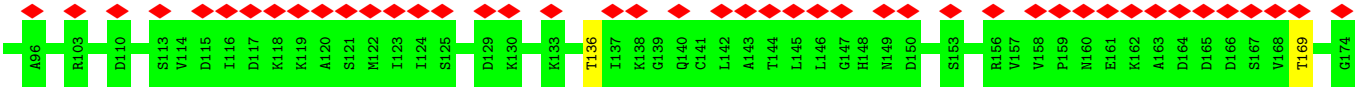


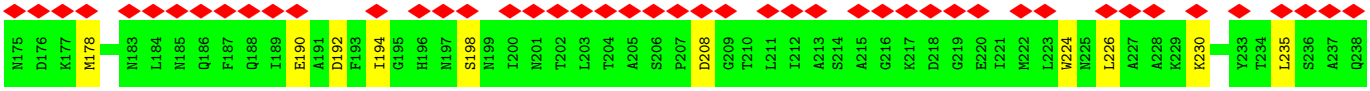
• Molecule 80: RACK1

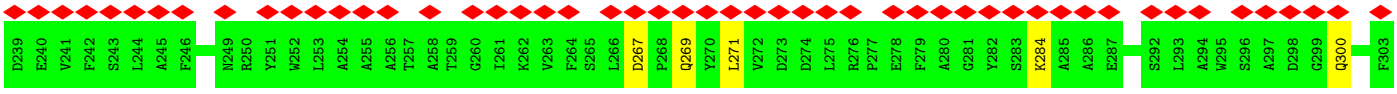
Chain gg:

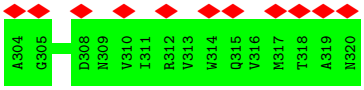






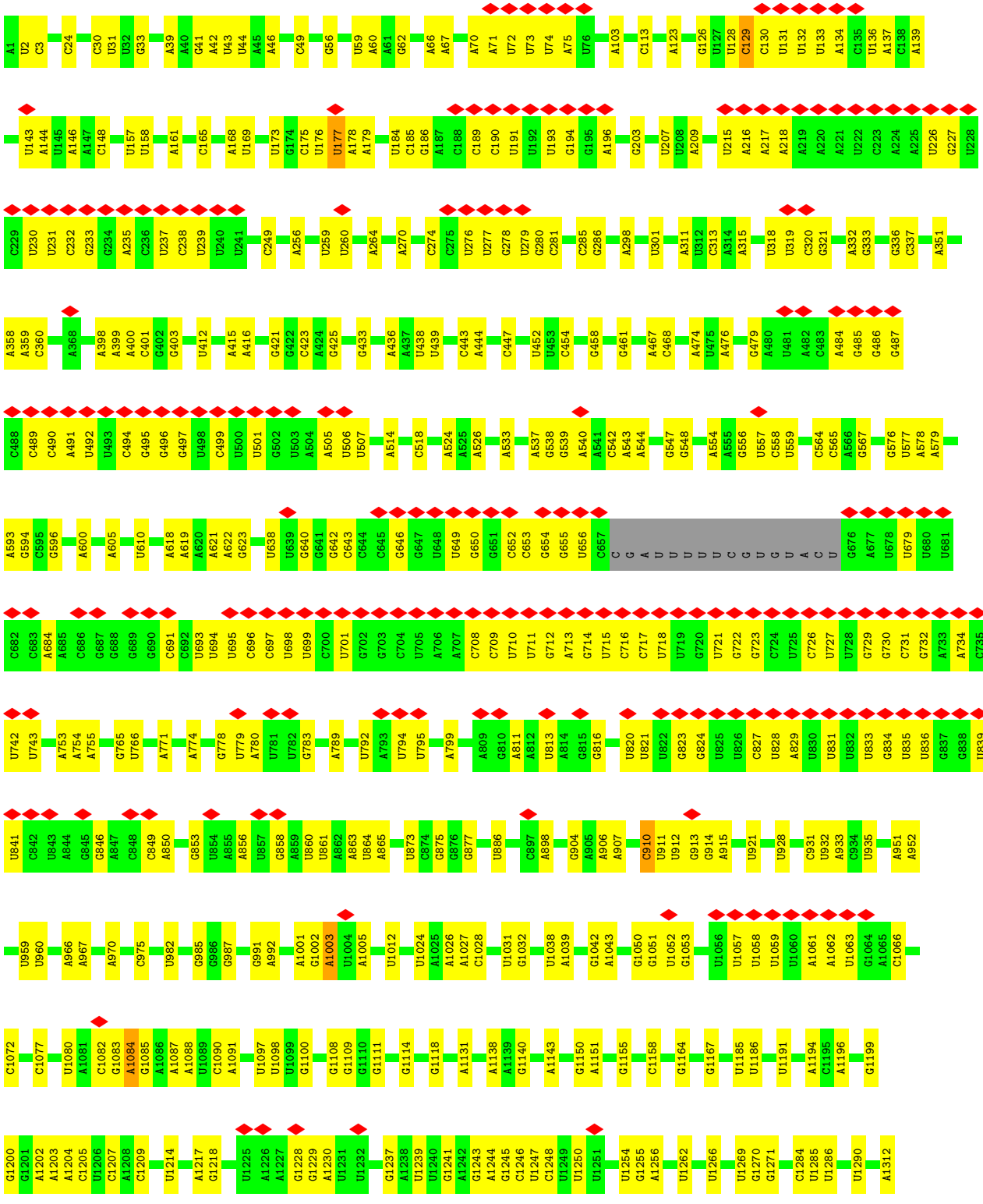


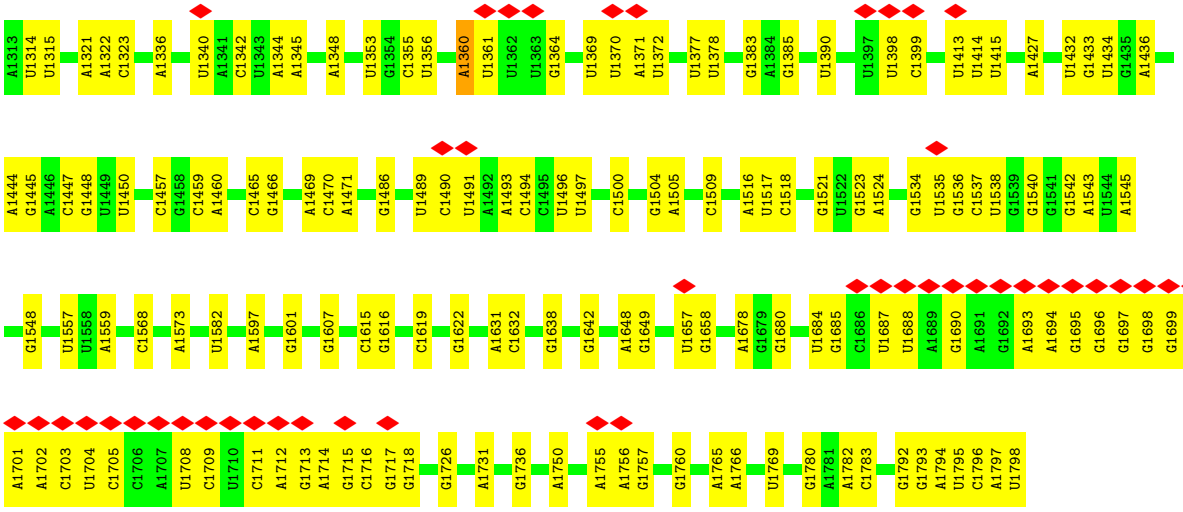




• Molecule 81: 18S ribosomal RNA

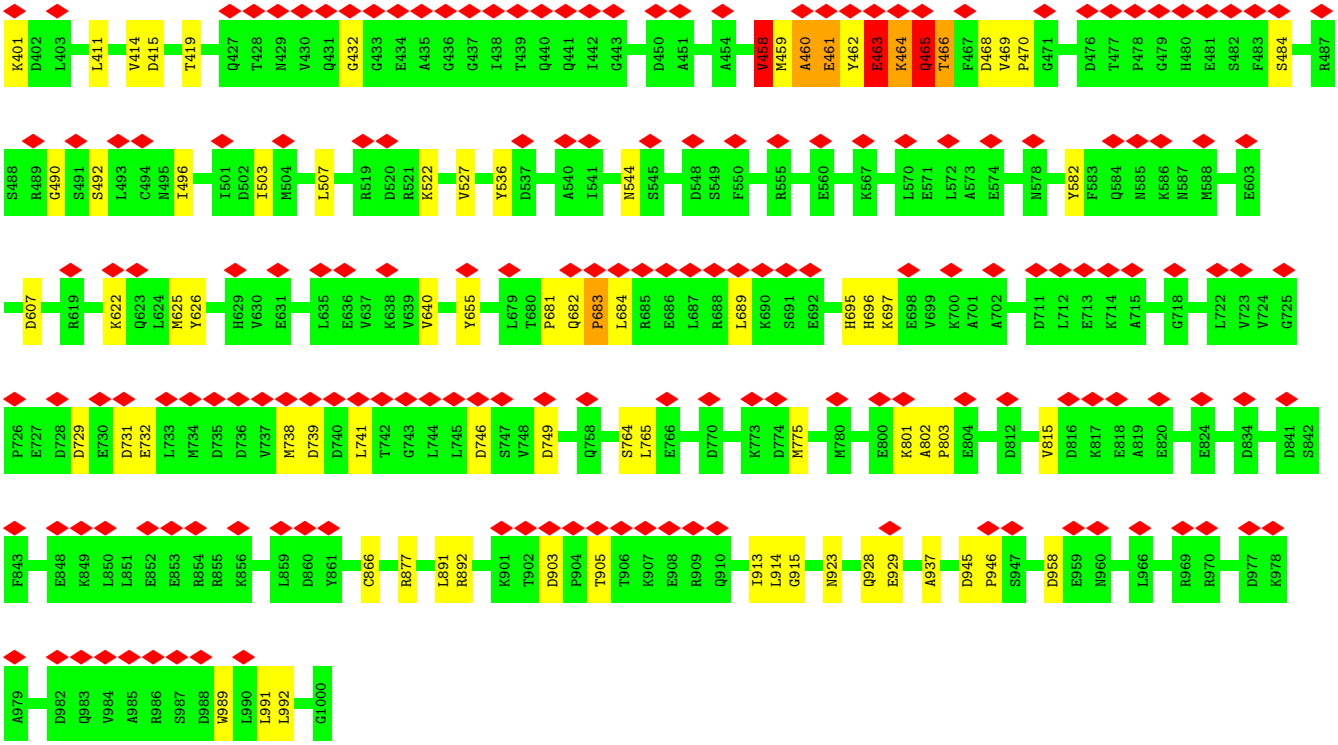
Chain 2:





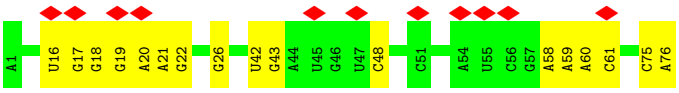
• Molecule 82: eIF5B

Chain 1:



• Molecule 83: Met-tRNA-iMet

Chain 3:



• Molecule 84: mRNA

Chain 4: 

There are no outlier residues recorded for this chain.

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	107000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.258	Depositor
Minimum map value	-0.092	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.042	Depositor
Map size (Å)	424.8, 424.8, 424.8	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.416, 1.416, 1.416	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, U6A, GDP

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	5	0.27	0/78264	0.70	10/121981 (0.0%)
2	7	0.24	0/2883	0.68	0/4491
3	8	0.26	0/3724	0.69	0/5798
4	A	0.66	0/1927	0.84	0/2589
5	B	0.65	0/3136	0.83	0/4217
6	C	0.66	0/2787	0.84	1/3773 (0.0%)
7	D	0.67	0/2420	0.80	0/3264
8	E	0.67	0/1260	0.80	0/1694
9	F	0.65	0/1821	0.81	0/2451
10	G	0.67	0/1841	0.79	0/2486
11	H	0.67	0/1545	0.82	0/2081
12	I	0.65	0/1787	0.81	0/2397
13	J	0.68	0/1365	0.82	0/1831
14	L	0.65	0/1609	0.86	0/2158
15	M	0.67	0/1069	0.83	0/1439
16	N	0.62	0/1748	0.82	0/2343
17	O	0.65	0/1585	0.80	0/2128
18	P	0.66	0/1450	0.84	0/1947
19	Q	0.65	0/1461	0.82	0/1960
20	R	0.67	0/1538	0.84	0/2050
21	S	0.63	0/1457	0.81	0/1958
22	T	0.66	0/1292	0.82	0/1732
23	U	0.68	0/812	0.80	0/1099
24	V	0.67	0/993	0.83	0/1335
25	W	0.65	0/525	0.81	0/697
26	X	0.65	0/983	0.78	0/1325
27	Y	0.67	0/999	0.82	0/1334
28	Z	0.66	0/1113	0.82	0/1490
29	a	0.63	0/1199	0.82	0/1605
30	b	0.64	0/468	0.82	0/622
31	c	0.70	0/751	0.79	0/1008
32	d	0.66	0/879	0.80	0/1179

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
33	e	0.66	0/1009	0.85	1/1349 (0.1%)
34	f	0.64	0/860	0.82	0/1157
35	g	0.67	0/964	0.86	0/1282
36	h	0.66	0/959	0.82	0/1276
37	i	0.68	0/770	0.86	0/1021
38	j	0.65	0/688	0.88	0/912
39	k	0.69	1/613 (0.2%)	0.87	0/819
40	l	0.63	0/435	0.80	0/577
41	m	0.64	0/415	0.82	0/551
42	n	0.64	0/219	0.95	0/281
43	o	0.63	0/826	0.84	0/1090
44	p	0.70	0/675	0.86	0/898
45	q	0.71	0/1744	0.84	0/2339
46	r	0.71	0/1538	0.86	0/2079
48	AA	0.66	0/1656	0.81	0/2266
49	BB	0.68	0/1742	0.81	0/2346
50	CC	0.68	0/1665	0.81	1/2263 (0.0%)
51	DD	0.69	0/1759	0.83	0/2368
52	EE	0.66	0/2088	0.82	0/2811
53	FF	0.68	0/1607	0.82	0/2172
54	GG	0.67	0/1844	0.83	0/2464
55	HH	0.68	0/1506	0.83	0/2028
56	II	0.67	0/1505	0.87	0/2010
57	JJ	0.67	0/1502	0.83	0/2013
58	KK	0.66	0/838	0.79	0/1133
59	LL	0.66	0/1192	0.82	0/1608
60	MM	0.74	0/942	0.85	0/1274
61	NN	0.68	0/1215	0.81	0/1638
62	OO	0.69	0/952	0.87	0/1279
63	PP	0.67	0/831	0.81	0/1117
64	QQ	0.67	0/1125	0.83	0/1510
65	RR	0.69	0/998	0.84	0/1337
66	SS	0.67	0/1140	0.84	0/1532
67	TT	0.68	0/1130	0.82	0/1517
68	UU	0.69	0/857	0.82	0/1158
69	VV	0.69	0/693	0.84	0/935
70	WW	0.67	0/1038	0.84	0/1395
71	XX	0.66	0/1141	0.82	0/1520
72	YY	0.68	0/1087	0.83	0/1449
73	ZZ	0.69	0/571	0.82	0/768
74	aa	0.66	0/782	0.87	0/1047
75	bb	0.70	0/620	0.83	0/838
76	cc	0.68	0/499	0.87	0/670

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
77	dd	0.66	0/453	0.85	0/602
78	ee	0.65	0/433	0.81	0/576
79	ff	0.69	0/349	0.88	0/463
80	gg	0.68	0/2495	0.81	0/3392
81	2	0.25	0/42249	0.69	6/65802 (0.0%)
82	1	0.96	30/4776 (0.6%)	0.93	12/6454 (0.2%)
83	3	0.21	0/1823	0.67	0/2842
84	4	0.23	0/147	0.61	0/227
All	All	0.49	31/225656 (0.0%)	0.75	31/330917 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	A	0	1
6	C	0	2
7	D	0	1
9	F	0	2
11	H	0	1
13	J	0	1
17	O	0	1
21	S	0	1
30	b	0	1
33	e	0	1
34	f	0	1
37	i	0	1
39	k	0	1
44	p	0	2
46	r	0	3
49	BB	0	1
50	CC	0	1
51	DD	0	1
52	EE	0	1
53	FF	0	2
54	GG	0	1
55	HH	0	1
56	II	0	3
57	JJ	0	1
58	KK	0	1
59	LL	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
64	QQ	0	2
66	SS	0	1
67	TT	0	1
71	XX	0	2
72	YY	0	1
82	1	0	7
All	All	0	48

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	1	463	GLU	CD-OE1	-13.34	1.10	1.25
82	1	458	VAL	CA-C	-10.00	1.26	1.52
82	1	461	GLU	C-O	-9.97	1.04	1.23
82	1	459	MET	CA-CB	-9.84	1.32	1.53
82	1	462	TYR	CB-CG	-9.81	1.36	1.51

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
82	1	458	VAL	CG1-CB-CG2	-9.46	95.76	110.90
82	1	464	LYS	N-CA-C	9.16	135.74	111.00
82	1	463	GLU	CB-CA-C	-9.05	92.30	110.40
82	1	461	GLU	N-CA-CB	-8.50	95.31	110.60
1	5	1607	U	C2'-C3'-O3'	8.22	127.58	109.50

There are no chirality outliers.

5 of 48 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	196	TRP	Peptide
6	C	148	ILE	Peptide
6	C	349	THR	Peptide
7	D	258	LYS	Peptide
9	F	157	ASN	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
4	A	247/249 (99%)	223 (90%)	17 (7%)	7 (3%)	5 19
5	B	382/384 (100%)	325 (85%)	54 (14%)	3 (1%)	19 51
6	C	357/359 (99%)	287 (80%)	54 (15%)	16 (4%)	2 9
7	D	293/295 (99%)	266 (91%)	24 (8%)	3 (1%)	15 45
8	E	152/175 (87%)	142 (93%)	8 (5%)	2 (1%)	12 37
9	F	220/222 (99%)	194 (88%)	22 (10%)	4 (2%)	8 29
10	G	231/233 (99%)	210 (91%)	19 (8%)	2 (1%)	17 48
11	H	189/191 (99%)	165 (87%)	21 (11%)	3 (2%)	9 32
12	I	214/216 (99%)	191 (89%)	18 (8%)	5 (2%)	6 23
13	J	166/168 (99%)	149 (90%)	16 (10%)	1 (1%)	25 58
14	L	196/198 (99%)	173 (88%)	19 (10%)	4 (2%)	7 27
15	M	134/136 (98%)	118 (88%)	14 (10%)	2 (2%)	10 34
16	N	200/202 (99%)	183 (92%)	16 (8%)	1 (0%)	29 61
17	O	195/197 (99%)	184 (94%)	9 (5%)	2 (1%)	15 45
18	P	178/180 (99%)	158 (89%)	18 (10%)	2 (1%)	14 42
19	Q	182/184 (99%)	169 (93%)	12 (7%)	1 (0%)	29 61
20	R	186/188 (99%)	174 (94%)	11 (6%)	1 (0%)	29 61
21	S	167/169 (99%)	152 (91%)	12 (7%)	3 (2%)	8 29
22	T	156/158 (99%)	141 (90%)	13 (8%)	2 (1%)	12 37
23	U	98/100 (98%)	89 (91%)	9 (9%)	0	100 100
24	V	130/132 (98%)	115 (88%)	13 (10%)	2 (2%)	10 34
25	W	60/62 (97%)	54 (90%)	6 (10%)	0	100 100
26	X	119/121 (98%)	108 (91%)	10 (8%)	1 (1%)	19 51
27	Y	123/125 (98%)	111 (90%)	12 (10%)	0	100 100
28	Z	132/134 (98%)	114 (86%)	16 (12%)	2 (2%)	10 34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
29	a	145/147 (99%)	122 (84%)	19 (13%)	4 (3%)	5 19
30	b	55/57 (96%)	46 (84%)	7 (13%)	2 (4%)	3 14
31	c	95/97 (98%)	91 (96%)	4 (4%)	0	100 100
32	d	104/106 (98%)	99 (95%)	5 (5%)	0	100 100
33	e	120/122 (98%)	110 (92%)	8 (7%)	2 (2%)	9 31
34	f	103/105 (98%)	92 (89%)	9 (9%)	2 (2%)	8 28
35	g	119/121 (98%)	106 (89%)	10 (8%)	3 (2%)	5 21
36	h	114/116 (98%)	108 (95%)	5 (4%)	1 (1%)	17 48
37	i	94/98 (96%)	79 (84%)	13 (14%)	2 (2%)	7 26
38	j	83/85 (98%)	75 (90%)	8 (10%)	0	100 100
39	k	74/76 (97%)	64 (86%)	10 (14%)	0	100 100
40	l	47/49 (96%)	39 (83%)	7 (15%)	1 (2%)	7 26
41	m	49/51 (96%)	46 (94%)	3 (6%)	0	100 100
42	n	21/23 (91%)	19 (90%)	2 (10%)	0	100 100
43	o	99/101 (98%)	79 (80%)	12 (12%)	8 (8%)	1 2
44	p	85/87 (98%)	70 (82%)	12 (14%)	3 (4%)	3 14
45	q	213/217 (98%)	163 (76%)	45 (21%)	5 (2%)	6 23
46	r	191/195 (98%)	144 (75%)	41 (22%)	6 (3%)	4 16
48	AA	204/206 (99%)	166 (81%)	31 (15%)	7 (3%)	3 15
49	BB	212/214 (99%)	187 (88%)	23 (11%)	2 (1%)	17 48
50	CC	215/217 (99%)	188 (87%)	21 (10%)	6 (3%)	5 19
51	DD	221/223 (99%)	189 (86%)	26 (12%)	6 (3%)	5 19
52	EE	255/257 (99%)	217 (85%)	33 (13%)	5 (2%)	7 27
53	FF	197/206 (96%)	155 (79%)	36 (18%)	6 (3%)	4 17
54	GG	224/226 (99%)	201 (90%)	22 (10%)	1 (0%)	34 66
55	HH	182/184 (99%)	157 (86%)	22 (12%)	3 (2%)	9 32
56	II	183/199 (92%)	153 (84%)	25 (14%)	5 (3%)	5 19
57	JJ	180/182 (99%)	156 (87%)	17 (9%)	7 (4%)	3 12
58	KK	94/96 (98%)	81 (86%)	10 (11%)	3 (3%)	4 16
59	LL	143/145 (99%)	127 (89%)	15 (10%)	1 (1%)	22 54
60	MM	122/124 (98%)	85 (70%)	34 (28%)	3 (2%)	5 21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
61	NN	148/150 (99%)	137 (93%)	7 (5%)	4 (3%)	5 19
62	OO	125/127 (98%)	106 (85%)	16 (13%)	3 (2%)	6 22
63	PP	101/103 (98%)	88 (87%)	12 (12%)	1 (1%)	15 45
64	QQ	139/141 (99%)	126 (91%)	11 (8%)	2 (1%)	11 36
65	RR	119/123 (97%)	99 (83%)	19 (16%)	1 (1%)	19 51
66	SS	134/136 (98%)	116 (87%)	17 (13%)	1 (1%)	22 54
67	TT	141/143 (99%)	128 (91%)	10 (7%)	3 (2%)	7 26
68	UU	104/106 (98%)	94 (90%)	10 (10%)	0	100 100
69	VV	85/87 (98%)	71 (84%)	14 (16%)	0	100 100
70	WW	127/129 (98%)	114 (90%)	10 (8%)	3 (2%)	6 22
71	XX	142/144 (99%)	125 (88%)	14 (10%)	3 (2%)	7 26
72	YY	132/134 (98%)	119 (90%)	12 (9%)	1 (1%)	19 51
73	ZZ	68/70 (97%)	59 (87%)	8 (12%)	1 (2%)	10 34
74	aa	95/97 (98%)	76 (80%)	14 (15%)	5 (5%)	2 6
75	bb	79/81 (98%)	63 (80%)	15 (19%)	1 (1%)	12 37
76	cc	61/63 (97%)	54 (88%)	7 (12%)	0	100 100
77	dd	51/53 (96%)	49 (96%)	2 (4%)	0	100 100
78	ee	51/53 (96%)	44 (86%)	7 (14%)	0	100 100
79	ff	40/57 (70%)	20 (50%)	19 (48%)	1 (2%)	5 21
80	gg	312/318 (98%)	265 (85%)	43 (14%)	4 (1%)	12 37
82	1	598/600 (100%)	476 (80%)	94 (16%)	28 (5%)	2 8
All	All	11802/12025 (98%)	10238 (87%)	1339 (11%)	225 (2%)	11 28

5 of 225 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	181	LYS
4	A	196	TRP
6	C	54	GLU
6	C	148	ILE
6	C	316	ASN

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
4	A	191/191 (100%)	178 (93%)	13 (7%)	16 42
5	B	320/320 (100%)	301 (94%)	19 (6%)	19 49
6	C	286/286 (100%)	269 (94%)	17 (6%)	19 49
7	D	244/244 (100%)	222 (91%)	22 (9%)	9 29
8	E	134/152 (88%)	127 (95%)	7 (5%)	23 55
9	F	186/186 (100%)	178 (96%)	8 (4%)	29 62
10	G	189/191 (99%)	182 (96%)	7 (4%)	34 68
11	H	172/172 (100%)	163 (95%)	9 (5%)	23 55
12	I	184/185 (100%)	175 (95%)	9 (5%)	25 57
13	J	146/146 (100%)	138 (94%)	8 (6%)	21 53
14	L	158/158 (100%)	149 (94%)	9 (6%)	20 51
15	M	108/108 (100%)	102 (94%)	6 (6%)	21 52
16	N	174/174 (100%)	169 (97%)	5 (3%)	42 76
17	O	160/160 (100%)	158 (99%)	2 (1%)	69 90
18	P	145/145 (100%)	139 (96%)	6 (4%)	30 64
19	Q	150/150 (100%)	147 (98%)	3 (2%)	55 82
20	R	153/153 (100%)	143 (94%)	10 (6%)	17 45
21	S	154/154 (100%)	147 (96%)	7 (4%)	27 61
22	T	135/135 (100%)	123 (91%)	12 (9%)	9 29
23	U	87/87 (100%)	83 (95%)	4 (5%)	27 60
24	V	101/101 (100%)	93 (92%)	8 (8%)	12 34
25	W	54/54 (100%)	52 (96%)	2 (4%)	34 68
26	X	105/105 (100%)	100 (95%)	5 (5%)	25 58
27	Y	109/109 (100%)	103 (94%)	6 (6%)	21 53
28	Z	115/115 (100%)	106 (92%)	9 (8%)	12 34
29	a	118/118 (100%)	112 (95%)	6 (5%)	24 56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
30	b	46/46 (100%)	46 (100%)	0	100 100
31	c	81/81 (100%)	75 (93%)	6 (7%)	13 38
32	d	93/93 (100%)	90 (97%)	3 (3%)	39 73
33	e	106/106 (100%)	97 (92%)	9 (8%)	10 31
34	f	89/89 (100%)	87 (98%)	2 (2%)	52 81
35	g	103/103 (100%)	92 (89%)	11 (11%)	6 20
36	h	103/103 (100%)	102 (99%)	1 (1%)	76 92
37	i	80/80 (100%)	74 (92%)	6 (8%)	13 37
38	j	69/69 (100%)	66 (96%)	3 (4%)	29 62
39	k	68/68 (100%)	61 (90%)	7 (10%)	7 22
40	l	44/44 (100%)	42 (96%)	2 (4%)	27 61
41	m	46/46 (100%)	46 (100%)	0	100 100
42	n	21/21 (100%)	19 (90%)	2 (10%)	8 26
43	o	87/87 (100%)	80 (92%)	7 (8%)	12 33
44	p	69/69 (100%)	64 (93%)	5 (7%)	14 39
45	q	198/198 (100%)	172 (87%)	26 (13%)	4 12
46	r	165/165 (100%)	143 (87%)	22 (13%)	4 11
48	AA	173/173 (100%)	167 (96%)	6 (4%)	36 70
49	BB	192/192 (100%)	178 (93%)	14 (7%)	14 38
50	CC	176/176 (100%)	165 (94%)	11 (6%)	18 46
51	DD	182/182 (100%)	171 (94%)	11 (6%)	19 49
52	EE	219/219 (100%)	207 (94%)	12 (6%)	21 53
53	FF	173/173 (100%)	163 (94%)	10 (6%)	20 50
54	GG	193/193 (100%)	188 (97%)	5 (3%)	46 77
55	HH	165/165 (100%)	156 (94%)	9 (6%)	21 53
56	II	149/160 (93%)	138 (93%)	11 (7%)	13 38
57	JJ	156/156 (100%)	148 (95%)	8 (5%)	24 56
58	KK	89/89 (100%)	76 (85%)	13 (15%)	3 9
59	LL	130/130 (100%)	127 (98%)	3 (2%)	50 80
60	MM	100/100 (100%)	94 (94%)	6 (6%)	19 49
61	NN	127/127 (100%)	121 (95%)	6 (5%)	26 59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
62	OO	96/96 (100%)	86 (90%)	10 (10%)	7 21
63	PP	86/86 (100%)	79 (92%)	7 (8%)	11 33
64	QQ	117/117 (100%)	109 (93%)	8 (7%)	16 42
65	RR	112/112 (100%)	102 (91%)	10 (9%)	9 29
66	SS	120/120 (100%)	113 (94%)	7 (6%)	20 50
67	TT	115/115 (100%)	106 (92%)	9 (8%)	12 34
68	UU	99/99 (100%)	97 (98%)	2 (2%)	55 82
69	VV	74/74 (100%)	67 (90%)	7 (10%)	8 26
70	WW	110/110 (100%)	104 (94%)	6 (6%)	21 53
71	XX	119/119 (100%)	111 (93%)	8 (7%)	16 43
72	YY	112/112 (100%)	110 (98%)	2 (2%)	59 85
73	ZZ	61/61 (100%)	59 (97%)	2 (3%)	38 72
74	aa	83/83 (100%)	78 (94%)	5 (6%)	19 49
75	bb	70/70 (100%)	63 (90%)	7 (10%)	7 23
76	cc	56/56 (100%)	52 (93%)	4 (7%)	14 40
77	dd	47/47 (100%)	42 (89%)	5 (11%)	6 20
78	ee	46/46 (100%)	43 (94%)	3 (6%)	17 45
79	ff	38/49 (78%)	36 (95%)	2 (5%)	22 54
80	gg	261/261 (100%)	237 (91%)	24 (9%)	9 27
82	1	524/524 (100%)	479 (91%)	45 (9%)	10 30
All	All	10116/10159 (100%)	9487 (94%)	629 (6%)	22 47

5 of 629 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
62	OO	125	SER
80	gg	194	ILE
64	QQ	43	ILE
62	OO	124	ASP
70	WW	115	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 122 such sidechains are listed below:

Mol	Chain	Res	Type
33	e	31	ASN
73	ZZ	95	HIS
48	AA	83	GLN
72	YY	110	GLN
82	1	569	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3250/3271 (99%)	786 (24%)	76 (2%)
2	7	120/121 (99%)	21 (17%)	0
3	8	156/157 (99%)	34 (21%)	2 (1%)
81	2	1767/1796 (98%)	554 (31%)	32 (1%)
83	3	75/76 (98%)	17 (22%)	0
84	4	5/6 (83%)	0	0
All	All	5373/5427 (99%)	1412 (26%)	110 (2%)

5 of 1412 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	3	U
1	5	6	A
1	5	14	U
1	5	15	C
1	5	17	G

5 of 110 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	2941	A
1	5	3289	G
81	2	1755	A
81	2	1344	A
1	5	3057	U

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 6 are monoatomic - leaving 3 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	$\#\|Z\| > 2$
87	U6A	3	101	83	9,9,10	1.95	2 (22%)	10,11,13	2.55	1 (10%)
88	MET	3	102	83	6,7,8	0.46	0	2,7,9	2.12	1 (50%)
86	GDP	1	1101	-	24,30,30	0.96	1 (4%)	30,47,47	1.39	4 (13%)

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
87	U6A	3	101	83	-	10/11/11/12	-
88	MET	3	102	83	-	1/5/6/8	-
86	GDP	1	1101	-	-	3/12/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	3	101	U6A	O1-C1	4.49	1.36	1.22
87	3	101	U6A	CA-N	2.80	1.49	1.45
86	1	1101	GDP	C6-N1	-2.41	1.34	1.37

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	3	101	U6A	O1-C1-N	7.50	145.02	125.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
88	3	102	MET	CE-SD-CG	2.95	110.52	100.40
86	1	1101	GDP	C3'-C2'-C1'	2.90	105.35	100.98
86	1	1101	GDP	PA-O3A-PB	-2.75	123.38	132.83
86	1	1101	GDP	C8-N7-C5	2.75	108.22	102.99

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

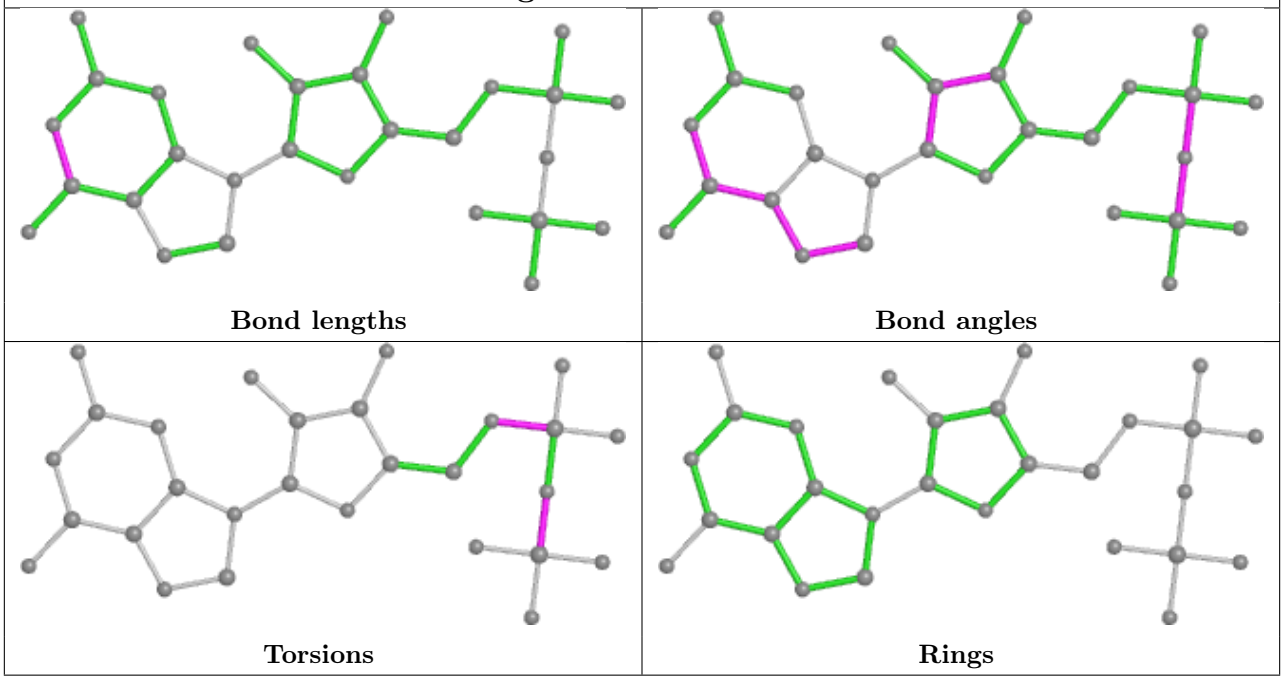
Mol	Chain	Res	Type	Atoms
86	1	1101	GDP	PA-O3A-PB-O2B
86	1	1101	GDP	C5'-O5'-PA-O1A
87	3	101	U6A	O1-C1-N-CA
87	3	101	U6A	C7-C6-CA-C
87	3	101	U6A	O8-C6-CA-C

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 then 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.

Ligand GDP 1 1101



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
1	5	18
81	2	11
80	gg	2
45	q	1
37	i	1
65	RR	1
46	r	1

The worst 5 of 35 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	1980:C	O3'	2051:G	P	18.54
1	5	2083:U	O3'	2084:G	P	11.15
1	5	1954:G	O3'	1955:U	P	7.40
1	5	439:C	O3'	495:G	P	7.21
1	2	856:A	O3'	857:U	P	7.17

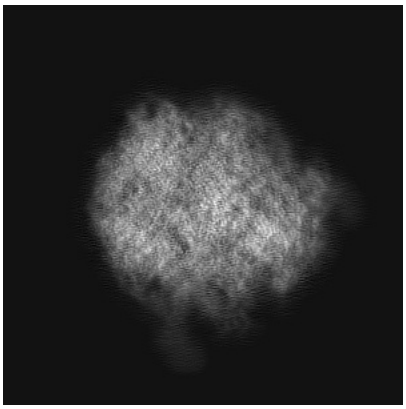
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-21859. These allow visual inspection of the internal detail of the map and identification of artifacts.

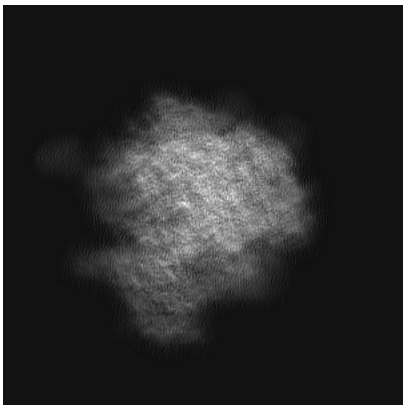
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

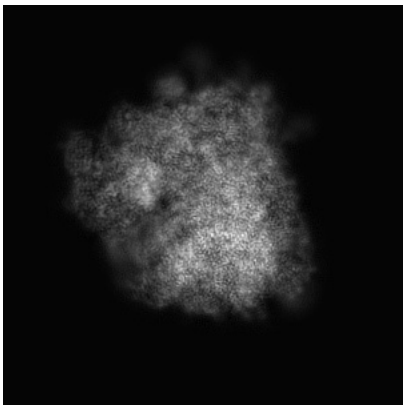
6.1.1 Primary map



X

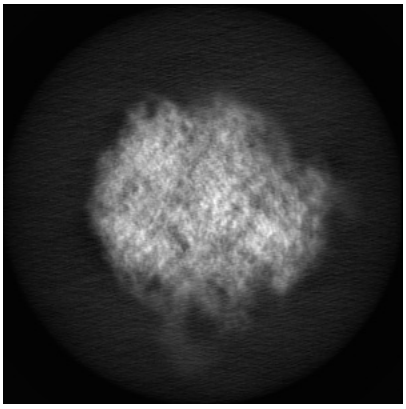


Y

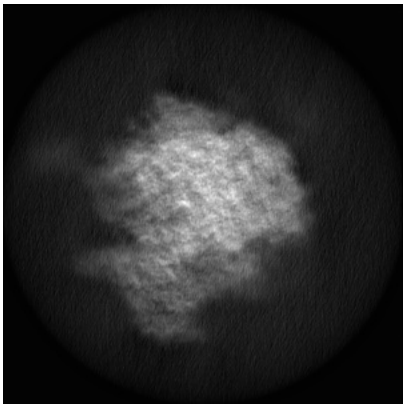


Z

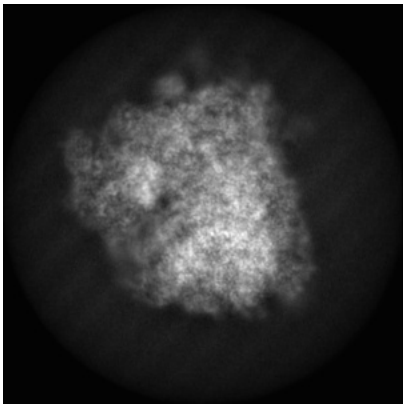
6.1.2 Raw map



X



Y

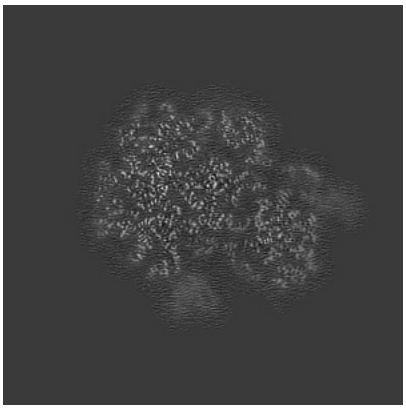


Z

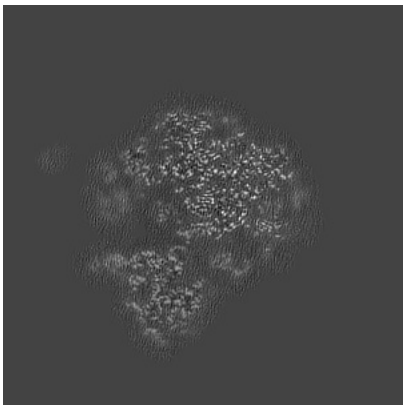
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

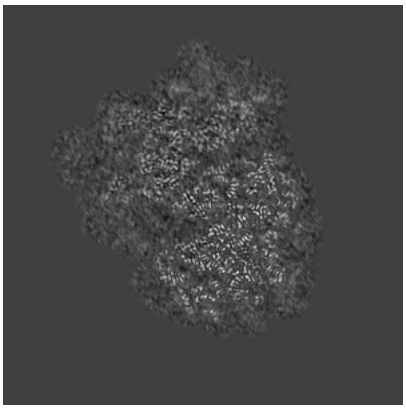
6.2.1 Primary map



X Index: 150

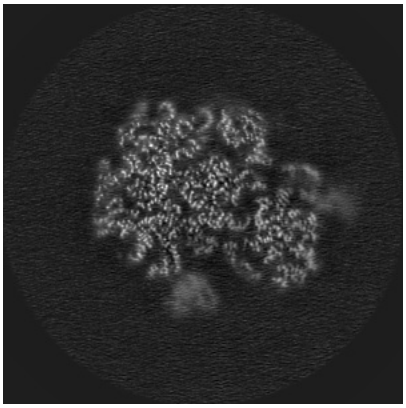


Y Index: 150

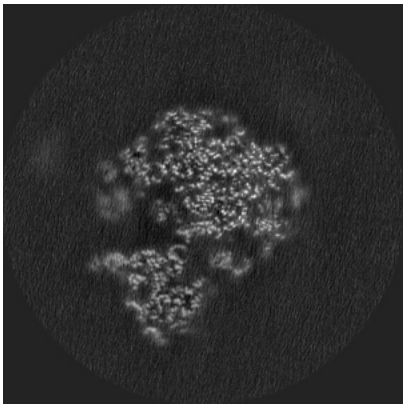


Z Index: 150

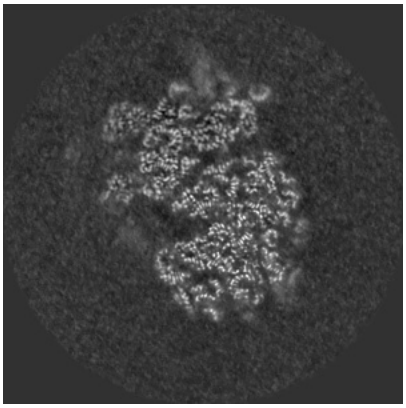
6.2.2 Raw map



X Index: 150



Y Index: 150

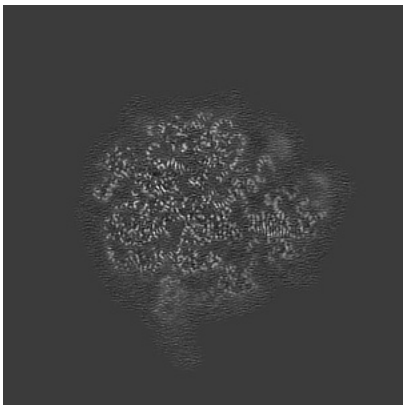


Z Index: 150

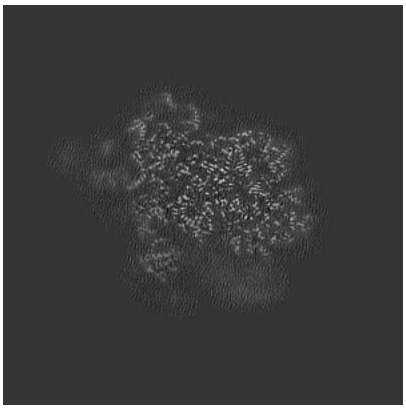
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

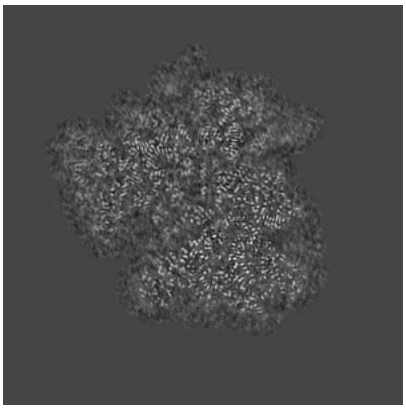
6.3.1 Primary map



X Index: 172

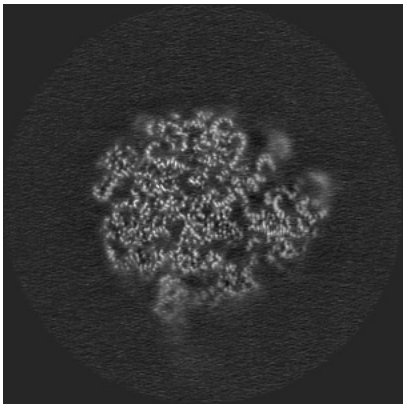


Y Index: 117

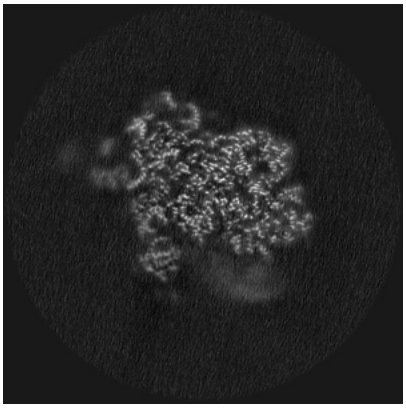


Z Index: 132

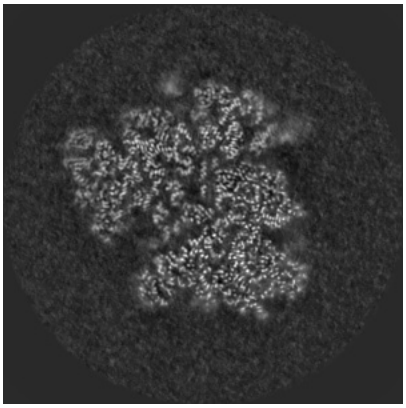
6.3.2 Raw map



X Index: 172



Y Index: 117

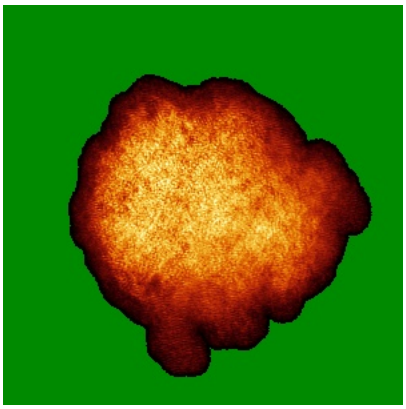


Z Index: 132

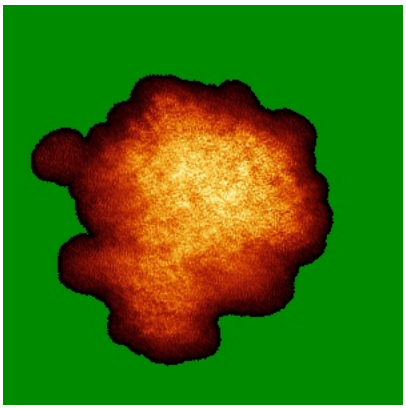
The images above show the largest variance slices of the map in three orthogonal directions.

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

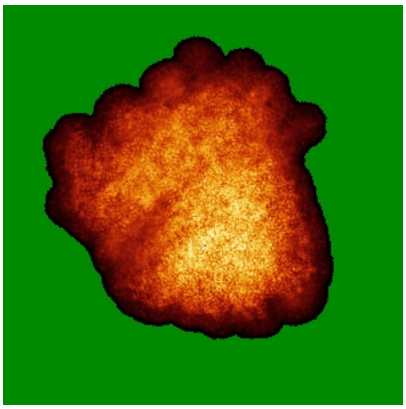
6.4.1 Primary map



X

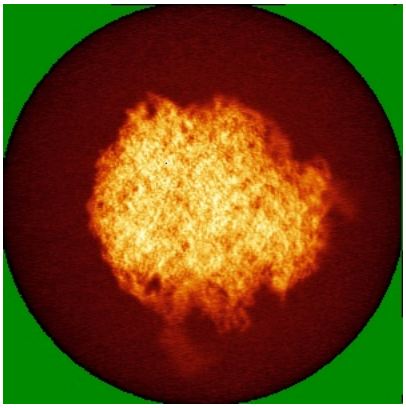


Y

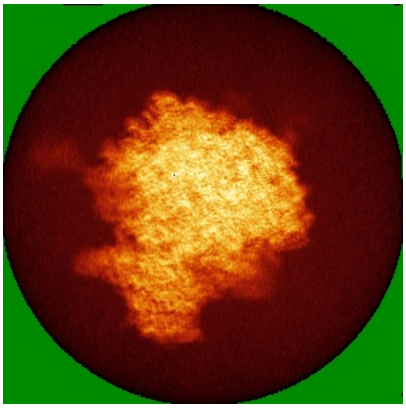


Z

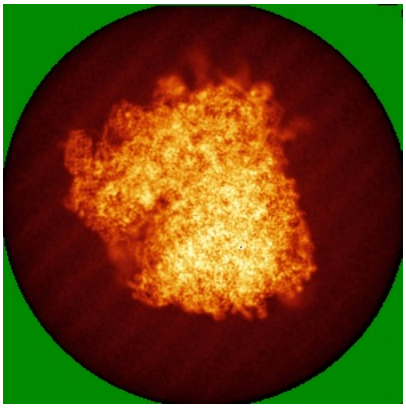
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.042. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X

Y

Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

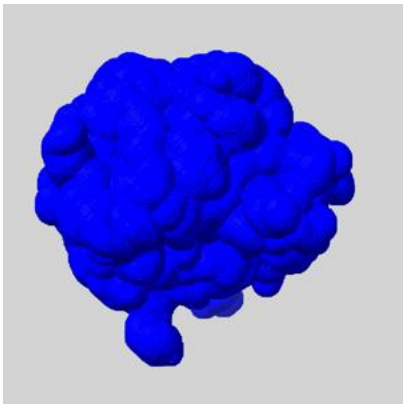
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

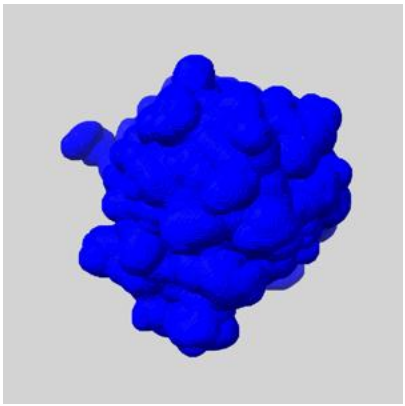
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

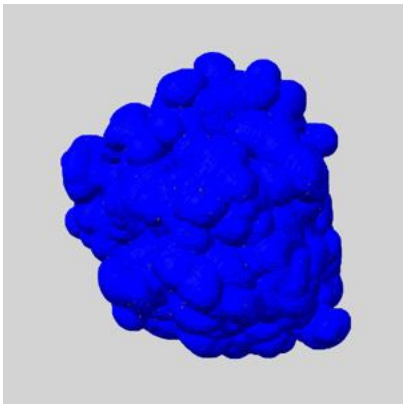
6.6.1 emd_21859_msk_1.map (i)



X



Y

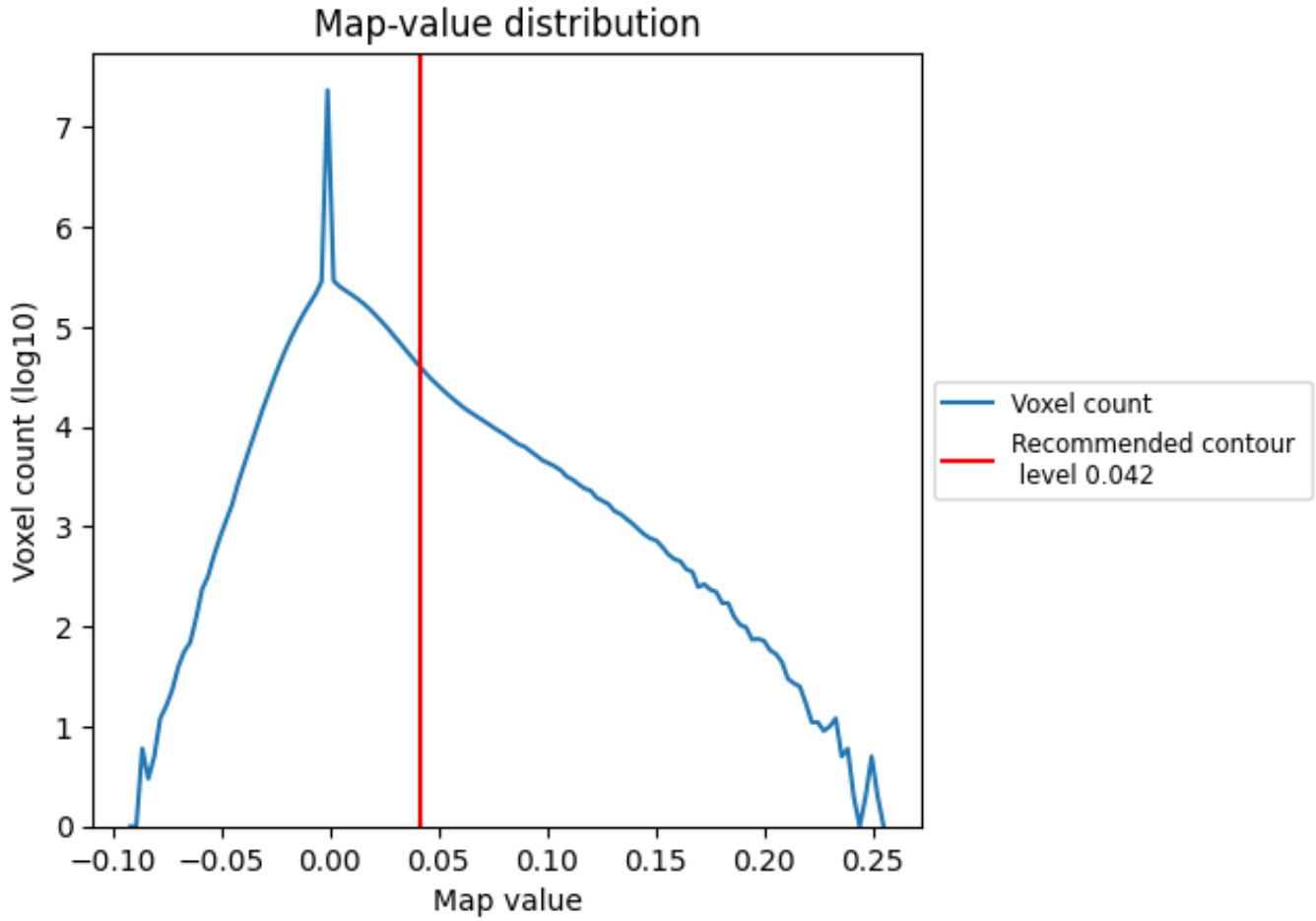


Z

7 Map analysis

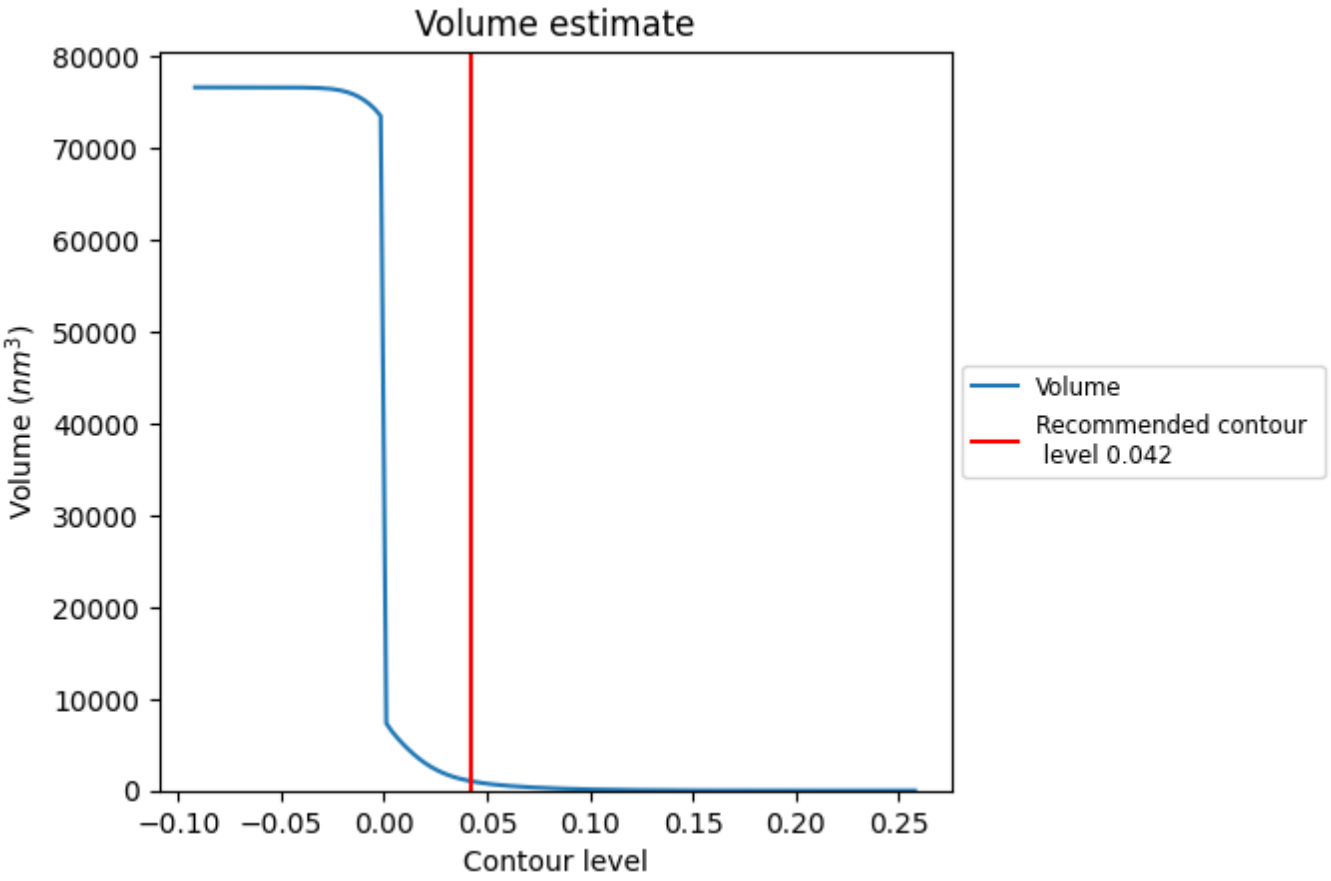
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

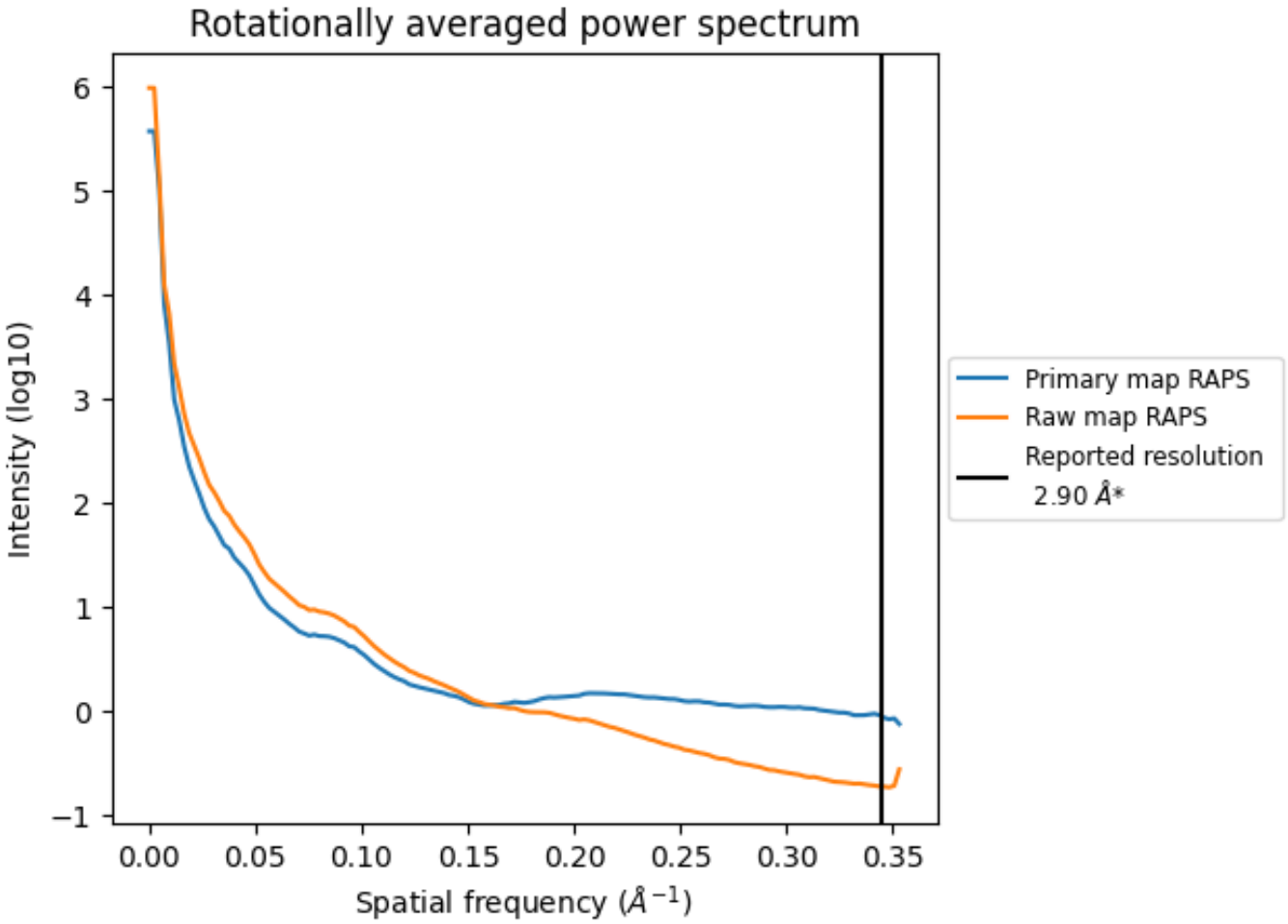
7.2 Volume estimate (i)



The volume at the recommended contour level is 1033 nm^3; this corresponds to an approximate mass of 933 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

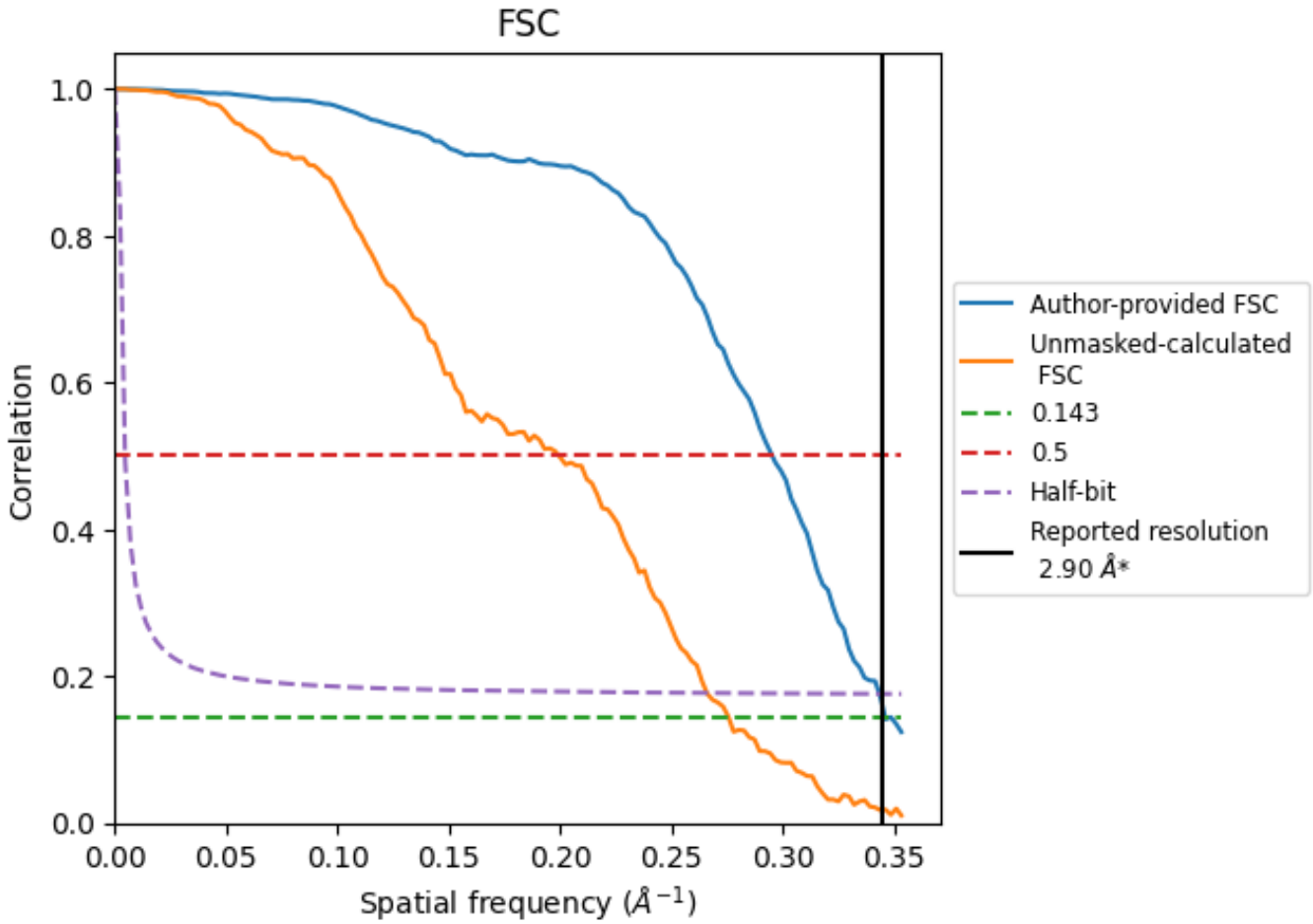


*Reported resolution corresponds to spatial frequency of 0.345 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



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

8.2 Resolution estimates (i)

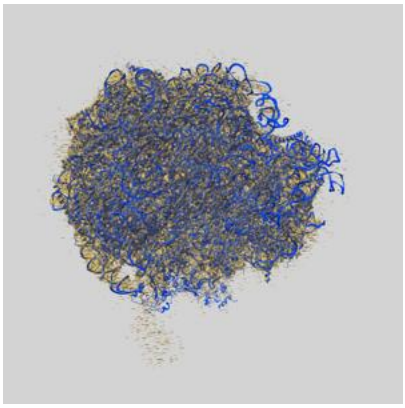
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.89	3.39	2.91
Unmasked-calculated*	3.63	5.02	3.76

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.63 differs from the reported value 2.9 by more than 10 %

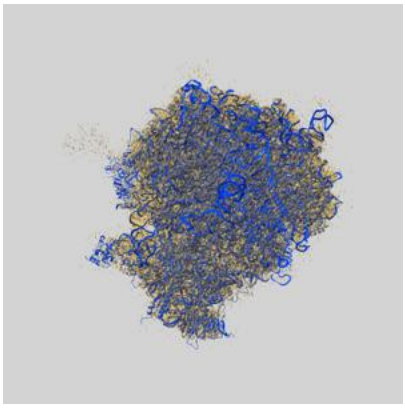
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-21859 and PDB model 6WOO. Per-residue inclusion information can be found in section 3 on page 22.

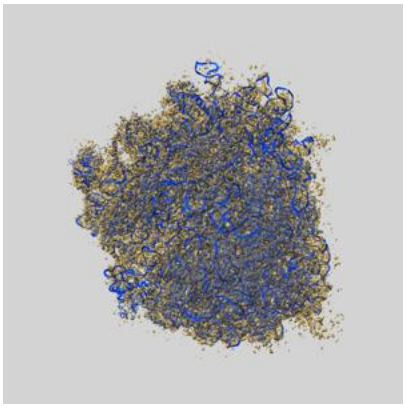
9.1 Map-model overlay



X



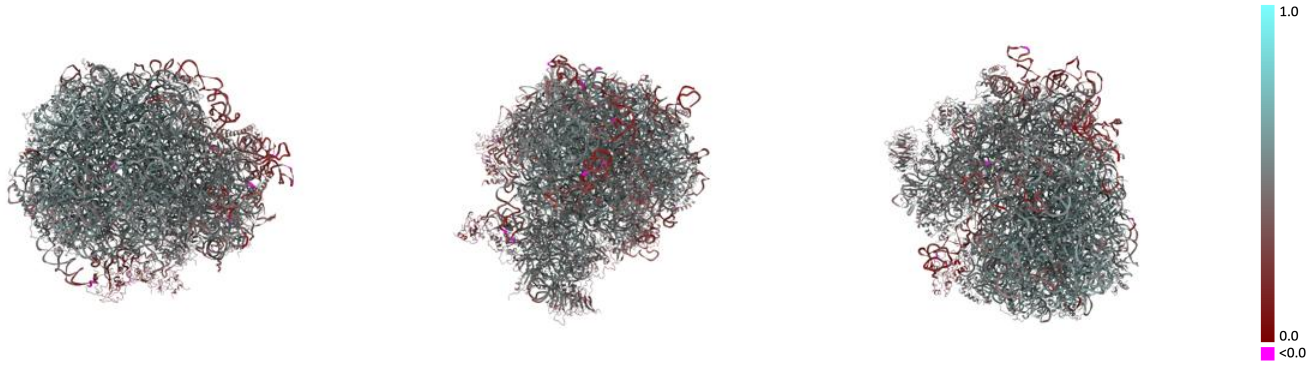
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.042 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

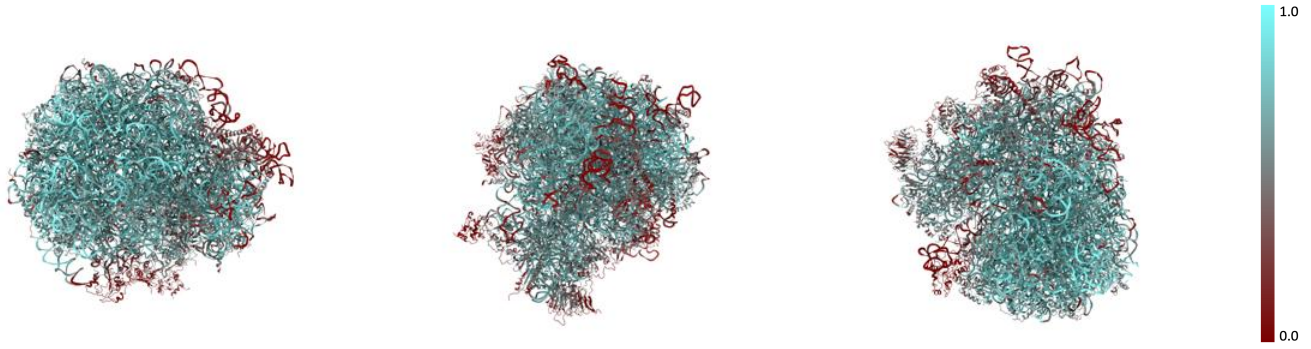
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

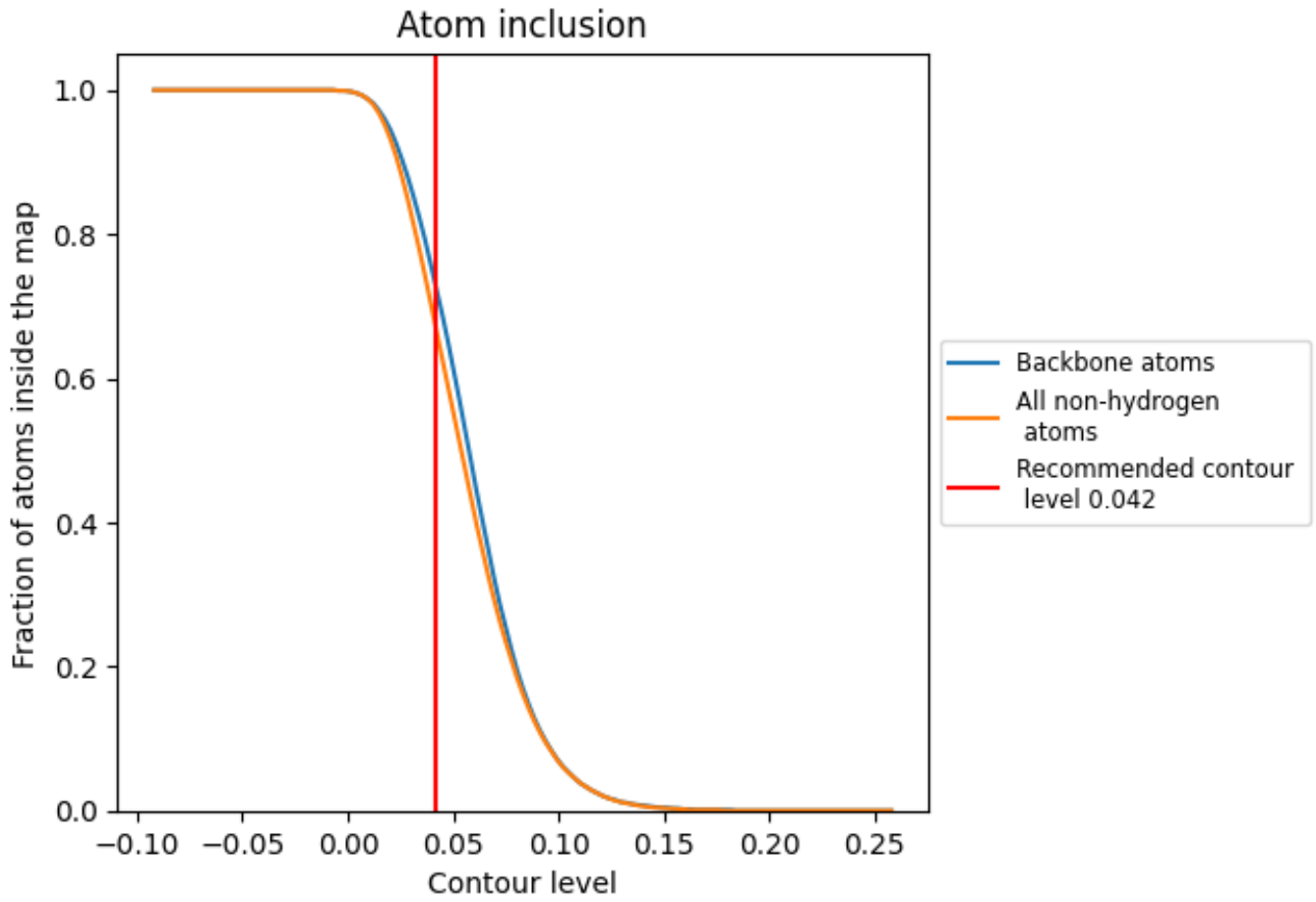
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.042).

9.4 Atom inclusion (i)



At the recommended contour level, 72% of all backbone atoms, 67% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.042) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6670	0.4870
1	0.5100	0.4650
2	0.7060	0.4640
3	0.6180	0.4540
4	0.8170	0.5400
5	0.7780	0.5030
7	0.8310	0.5330
8	0.8590	0.5460
A	0.7070	0.5420
AA	0.4640	0.4490
B	0.6680	0.5200
BB	0.5380	0.4660
C	0.7030	0.5290
CC	0.5750	0.4890
D	0.5690	0.4800
DD	0.4780	0.4570
E	0.6100	0.4800
EE	0.6250	0.5100
F	0.6770	0.5210
FF	0.5530	0.4630
G	0.5660	0.4780
GG	0.4580	0.4370
H	0.6370	0.5020
HH	0.2820	0.4220
I	0.6610	0.5220
II	0.5190	0.4780
J	0.4790	0.4670
JJ	0.6030	0.4770
K	0.0530	0.2380
KK	0.4480	0.4130
L	0.6680	0.5220
LL	0.5460	0.4990
M	0.6290	0.5010
MM	0.0540	0.2660
N	0.7630	0.5580

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Chain	Atom inclusion	Q-score
NN	0.5070	0.4820
O	0.6800	0.5310
OO	0.6100	0.4860
P	0.6890	0.5270
PP	0.5440	0.4390
Q	0.7210	0.5410
QQ	0.5830	0.4990
R	0.5730	0.4900
RR	0.4140	0.4480
S	0.6740	0.5260
SS	0.5680	0.4960
T	0.6450	0.5250
TT	0.5740	0.4920
U	0.4850	0.4440
UU	0.4310	0.4500
V	0.6590	0.5440
VV	0.5060	0.4740
W	0.6400	0.5310
WW	0.6100	0.5140
X	0.6390	0.5150
XX	0.6380	0.5260
Y	0.6740	0.5300
YY	0.5110	0.4650
Z	0.5630	0.4800
ZZ	0.5010	0.4620
a	0.7640	0.5600
aa	0.6530	0.4900
b	0.6290	0.5090
bb	0.4340	0.4650
c	0.5530	0.4570
cc	0.5430	0.4810
d	0.6260	0.5090
dd	0.6700	0.5000
e	0.7180	0.5390
ee	0.5340	0.4690
f	0.7230	0.5520
ff	0.1370	0.3230
g	0.5840	0.4980
gg	0.3410	0.4240
h	0.6540	0.5170
i	0.6220	0.4850
j	0.7760	0.5620

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Chain	Atom inclusion	Q-score
k	0.4500	0.4400
l	0.7300	0.5520
m	0.6770	0.5280
n	0.6400	0.5120
o	0.6680	0.5240
p	0.6440	0.5060
q	0.0230	0.2450
r	0.0940	0.2690