



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 04:09 PM UTC

PDB ID : 6WOO / pdb_00006woo
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 ⓘ symbol.

The types of validation reports are described at

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

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

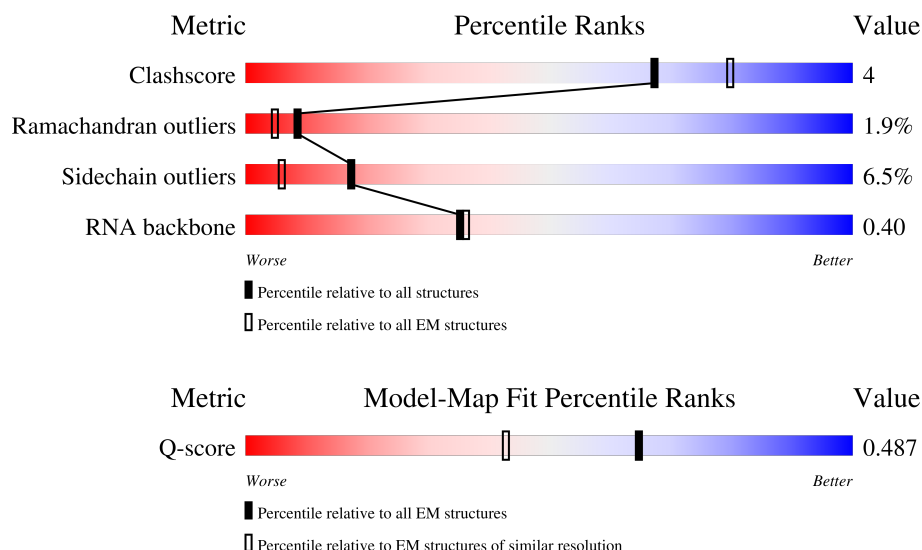
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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

Mol	Chain	Length	Quality of chain
1	5	3271	
2	7	121	
3	8	157	

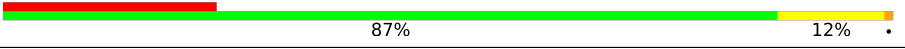
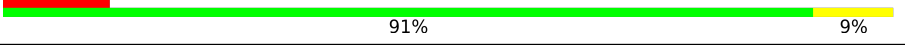
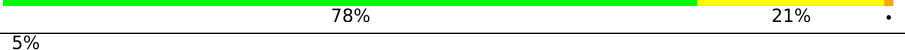
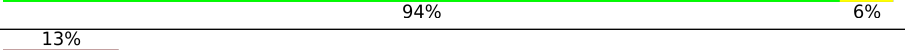
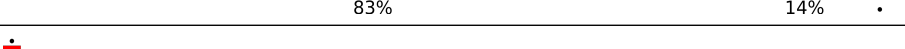
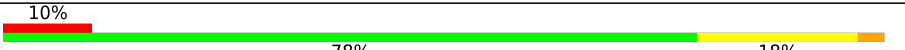
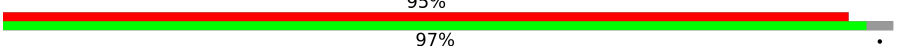
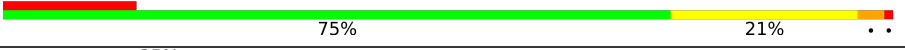
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Mol	Chain	Length	Quality of chain
4	A	249	
5	B	384	
6	C	359	
7	D	295	
8	E	175	
9	F	222	
10	G	233	
11	H	191	
12	I	216	
13	J	168	
14	L	198	
15	M	136	
16	N	202	
17	O	197	
18	P	180	
19	Q	184	
20	R	188	
21	S	169	
22	T	158	
23	U	100	
24	V	132	
25	W	62	
26	X	121	
27	Y	125	
28	Z	134	

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Mol	Chain	Length	Quality of chain
29	a	147	
30	b	57	
31	c	97	
32	d	106	
33	e	122	
34	f	105	
35	g	121	
36	h	116	
37	i	98	
38	j	85	
39	k	76	
40	l	49	
41	m	51	
42	n	23	
43	o	101	
44	p	87	
45	q	217	
46	r	195	
47	K	152	
48	AA	206	
49	BB	214	
50	CC	217	
51	DD	223	
52	EE	257	
53	FF	206	

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Mol	Chain	Length	Quality of chain
54	GG	226	
55	HH	184	
56	II	199	
57	JJ	182	
58	KK	96	
59	LL	145	
60	MM	124	
61	NN	150	
62	OO	127	
63	PP	103	
64	QQ	141	
65	RR	123	
66	SS	136	
67	TT	143	
68	UU	106	
69	VV	87	
70	WW	129	
71	XX	144	
72	YY	134	
73	ZZ	70	
74	aa	97	
75	bb	81	
76	cc	63	
77	dd	53	
78	ee	53	

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Mol	Chain	Length	Quality of chain
79	ff	57	
80	gg	318	
81	2	1796	
82	1	600	
83	3	76	
84	4	6	

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
85	ZN	aa	500	-	-	X	-
87	U6A	3	101	-	X	-	-

2 Entry composition

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
1	5	3271	Total	C	N	O	P	0	0
			69936	31236	12597	22832	3271		

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

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

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

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

- Molecule 4 is a protein called uL2.

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

- Molecule 5 is a protein called uL3.

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

- Molecule 6 is a protein called uL4.

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

- 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	C	N	O	0	0
			1521	935	326	260		

- Molecule 21 is a protein called eL20.

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

- Molecule 22 is a protein called eL21.

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

- Molecule 23 is a protein called eL22.

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

- Molecule 24 is a protein called uL14.

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

- Molecule 25 is a protein called eL24.

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

- Molecule 26 is a protein called uL23.

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

- Molecule 27 is a protein called uL24.

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

- Molecule 28 is a protein called eL27.

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

- Molecule 29 is a protein called uL15.

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

- Molecule 30 is a protein called eL29.

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

- Molecule 31 is a protein called eL30.

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

- Molecule 32 is a protein called eL31.

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

- Molecule 33 is a protein called eL32.

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

- 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	S	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	S	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	C	N	O	0	0
			1073	676	208	189		

- Molecule 73 is a protein called eS25.

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

- Molecule 74 is a protein called eS26.

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

- Molecule 75 is a protein called eS27.

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

- Molecule 76 is a protein called eS28.

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

- Molecule 77 is a protein called uS14.

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

- Molecule 78 is a protein called eS30.

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

- 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

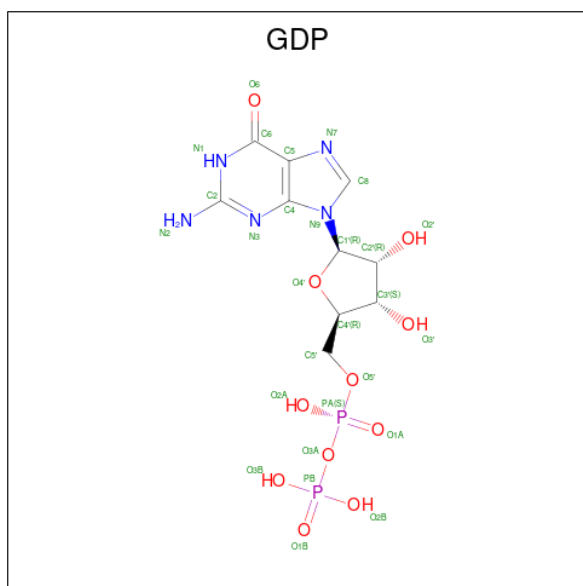
- Molecule 84 is a RNA chain called mRNA.

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 (CCD ID: ZN) (formula: Zn).

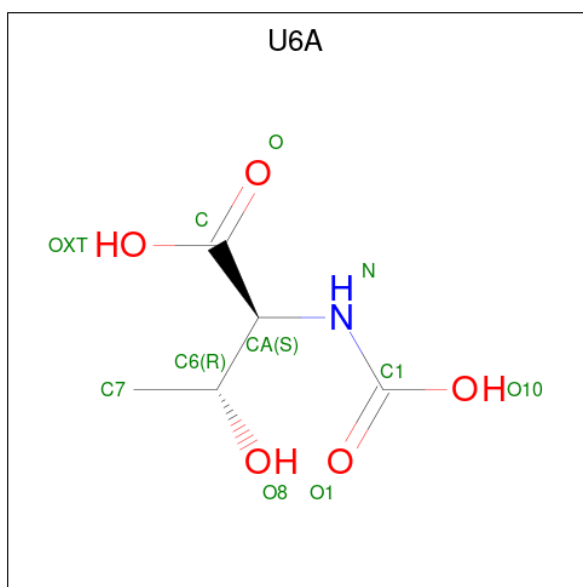
Mol	Chain	Residues	Atoms		AltConf
85	j	1	Total	Zn	0
			1	1	
85	m	1	Total	Zn	0
			1	1	
85	o	1	Total	Zn	0
			1	1	
85	aa	1	Total	Zn	0
			1	1	
85	bb	1	Total	Zn	0
			1	1	
85	ff	1	Total	Zn	0
			1	1	

- Molecule 86 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



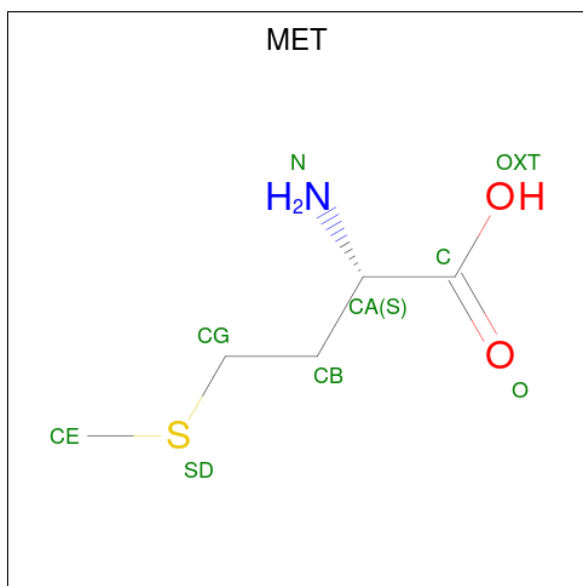
Mol	Chain	Residues	Atoms					AltConf
86	1	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 87 is N-carboxy-L-threonine (CCD ID: U6A) (formula: C₅H₉NO₅).



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

- Molecule 88 is METHIONINE (CCD ID: MET) (formula: $C_5H_{11}NO_2S$).

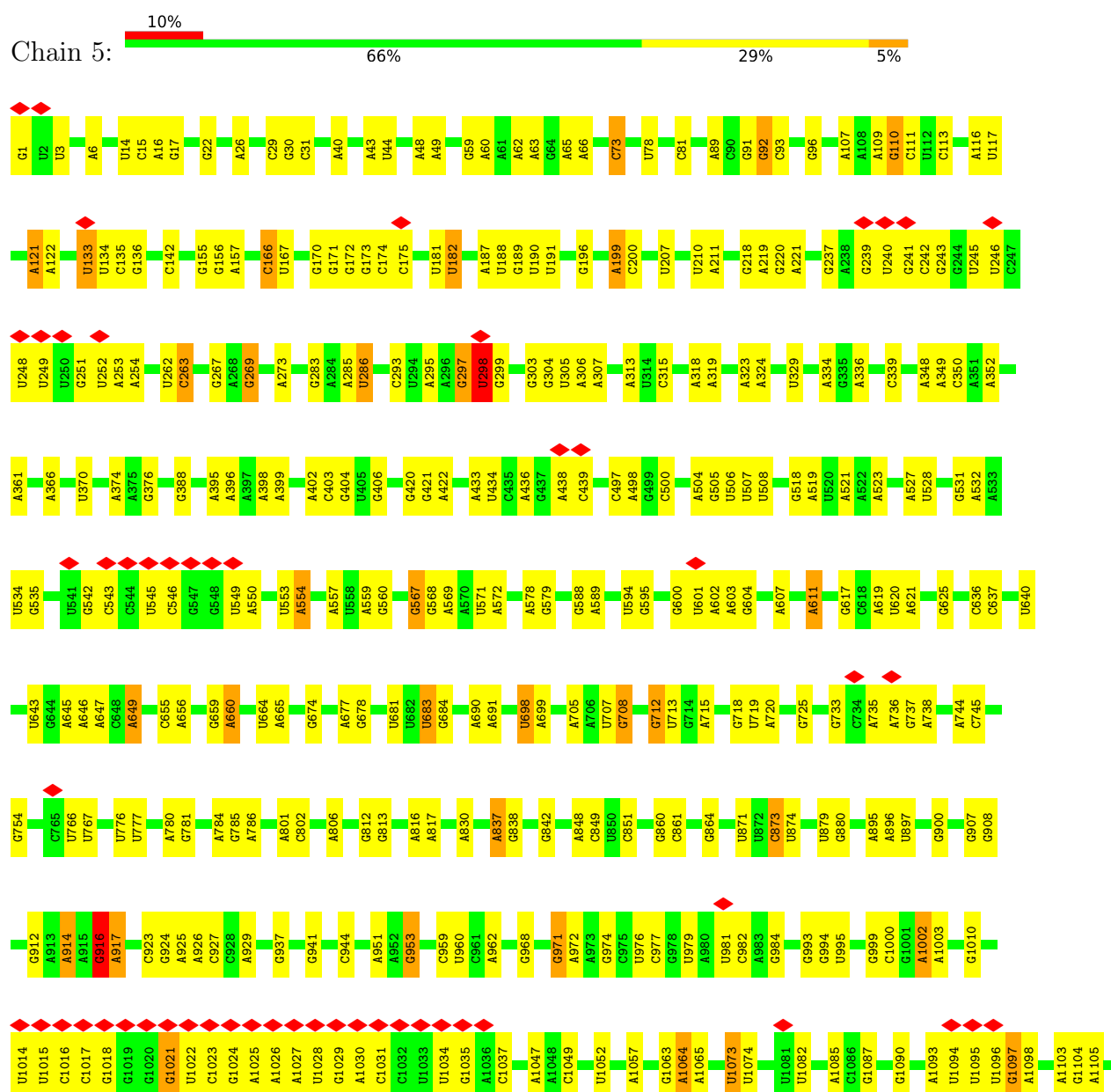


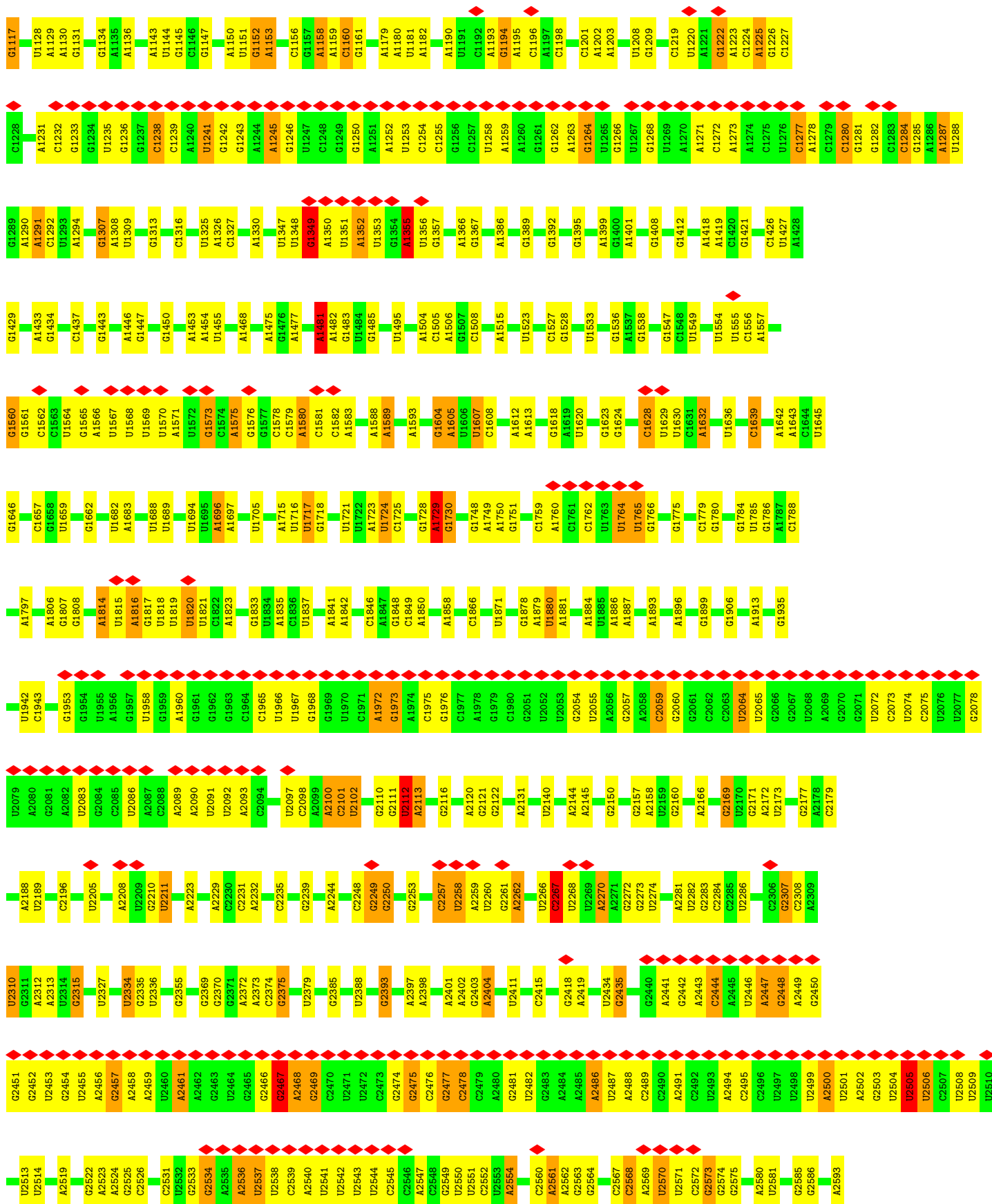
Mol	Chain	Residues	Atoms					AltConf
88	3	1	Total	C	N	O	S	0
			8	5	1	1	1	

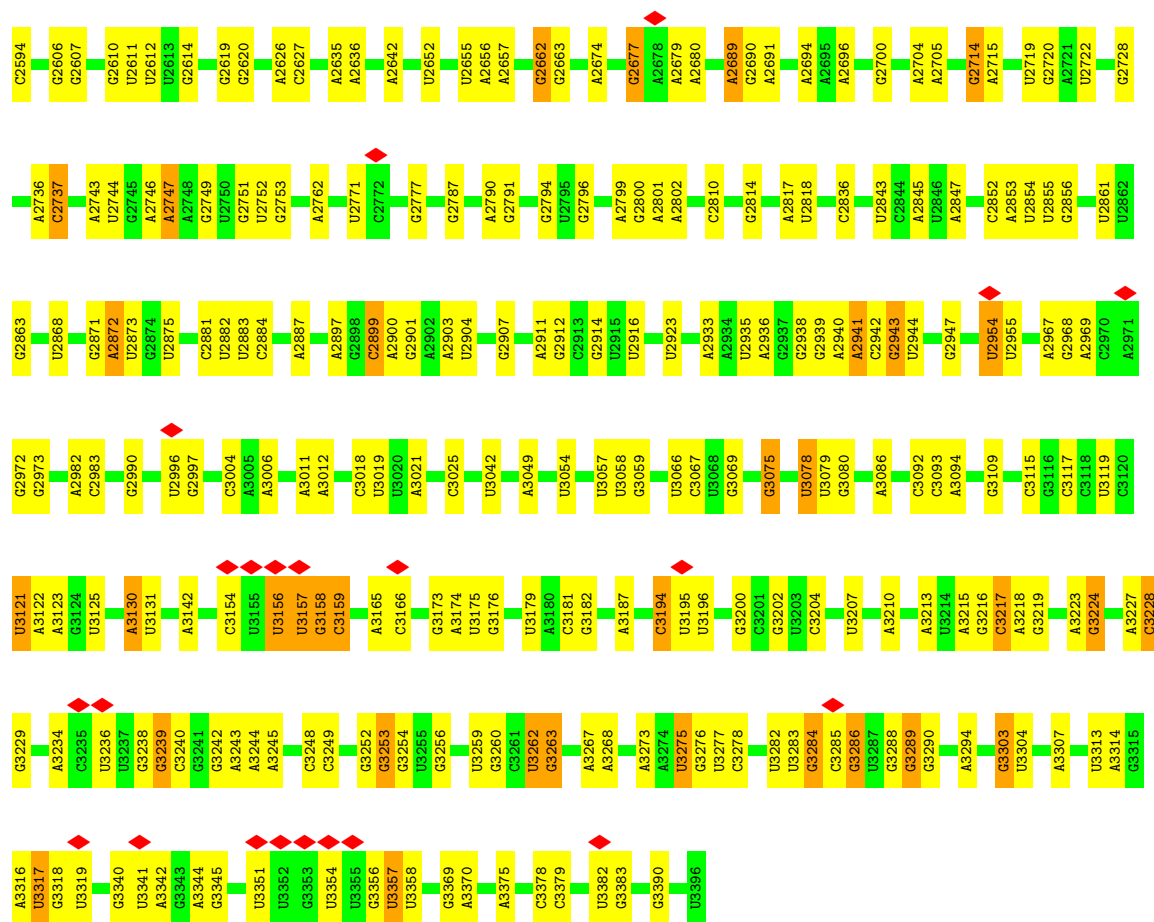
3 Residue-property plots

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



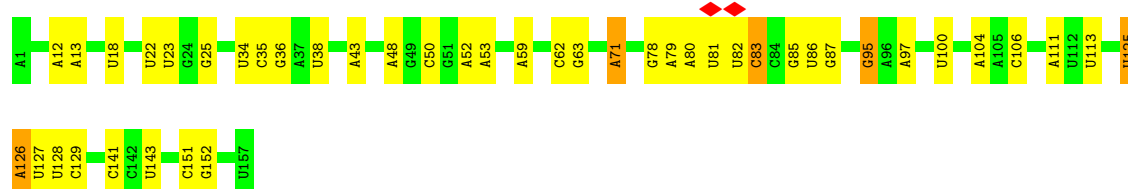




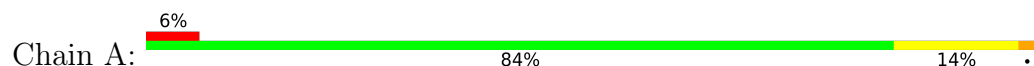
• Molecule 2: 5S ribosomal RNA

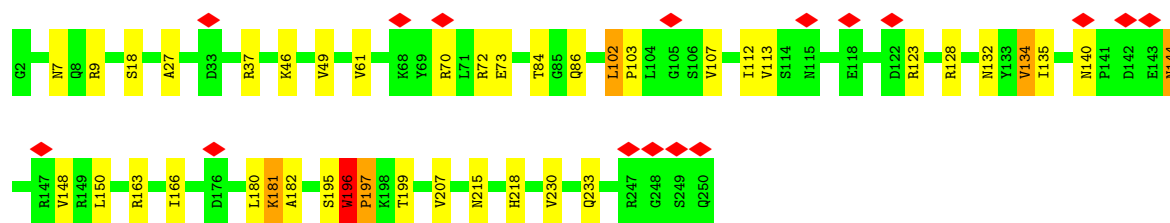


• Molecule 3: 5.8S ribosomal rRNA

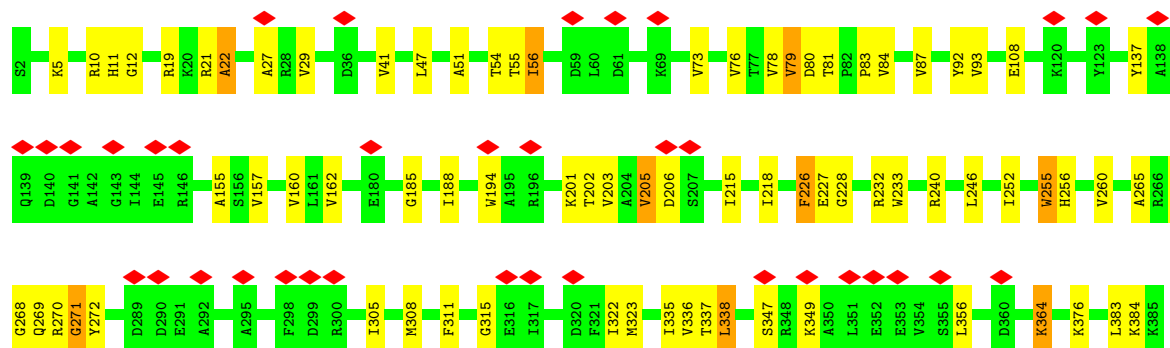
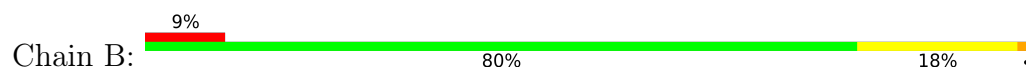


• Molecule 4: uL2

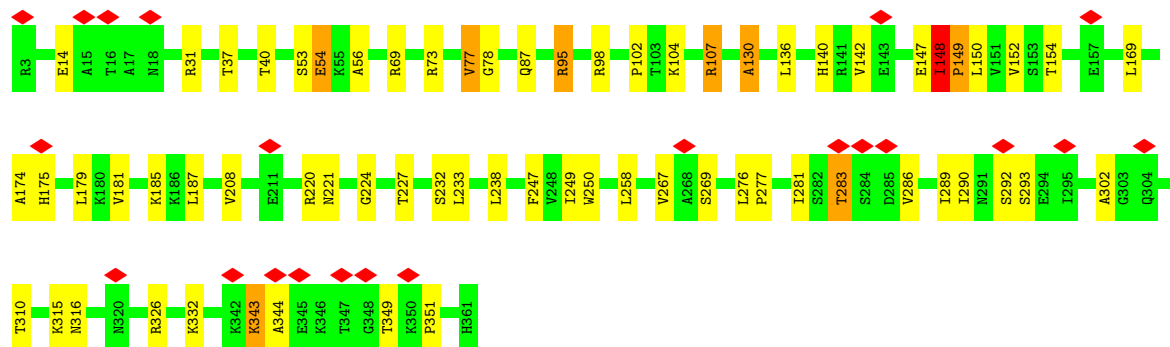
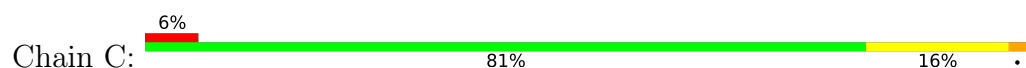




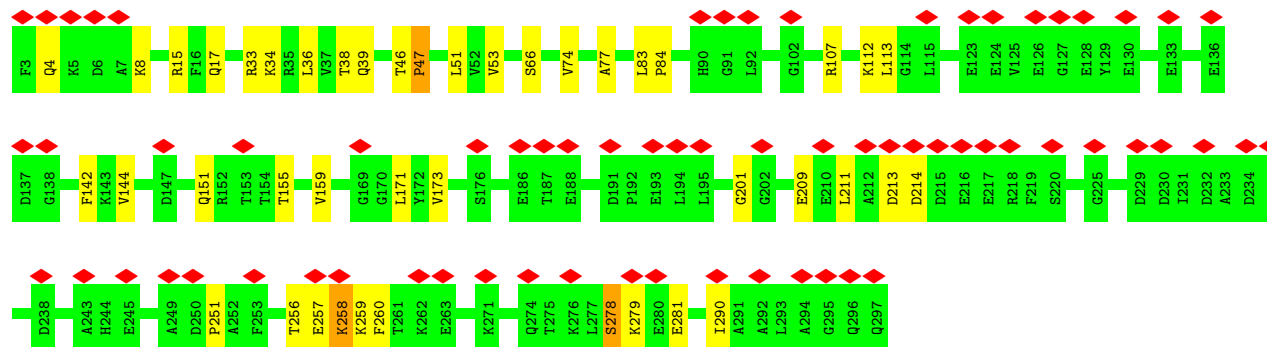
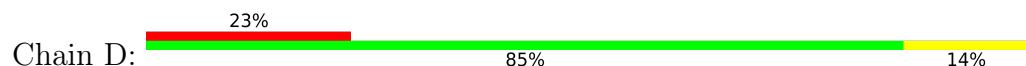
• Molecule 5: uL3



• Molecule 6: uL4

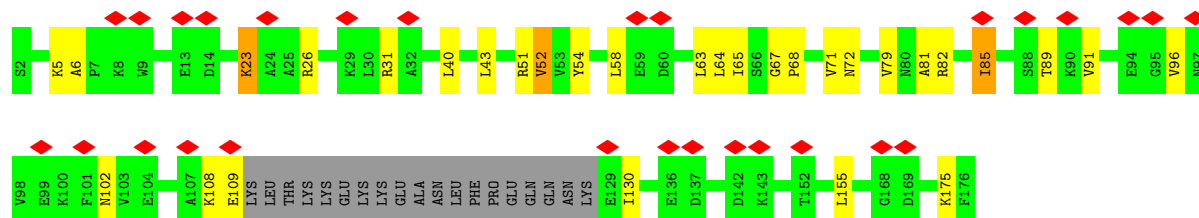


• Molecule 7: uL18



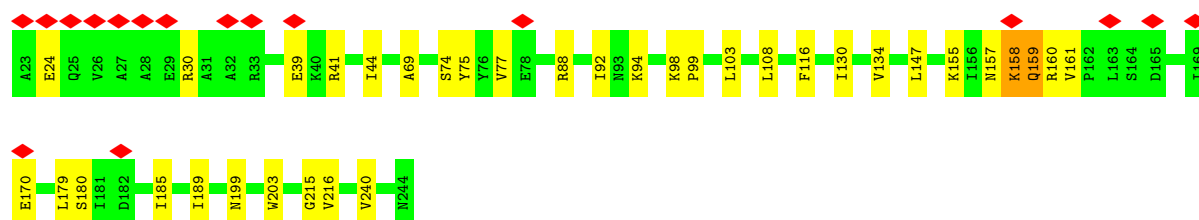
- Molecule 8: eL6

Chain E: 

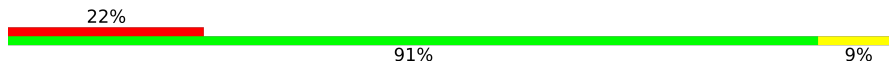


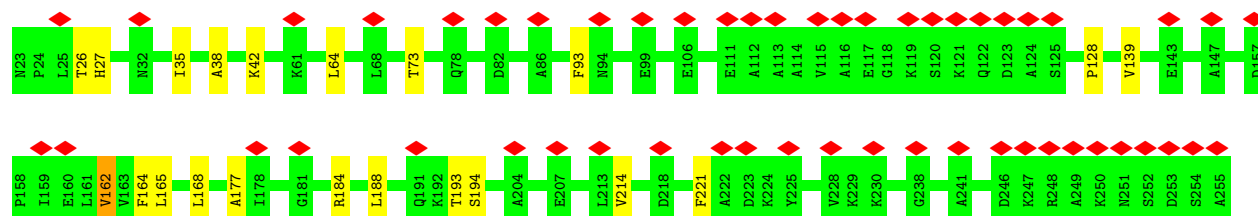
- Molecule 9: uL30

Chain F: 



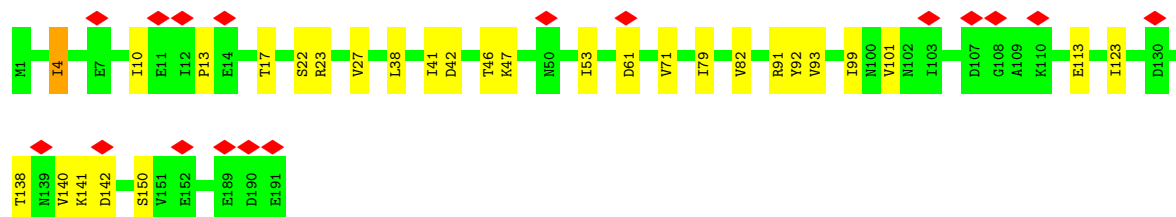
- Molecule 10: eL8

Chain G: 



- Molecule 11: uL6

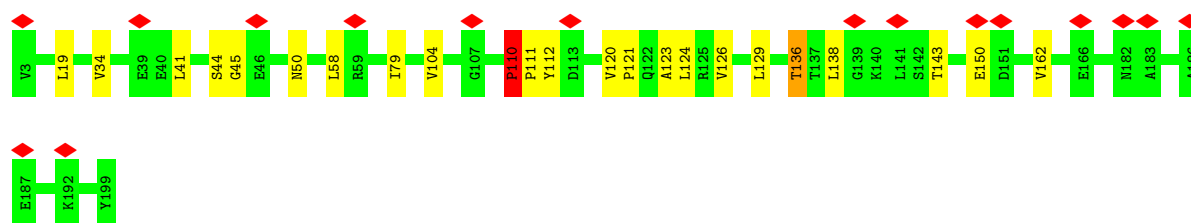
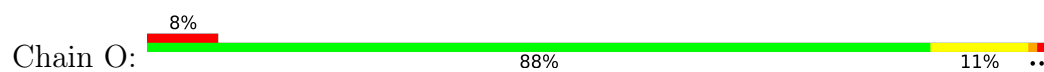
Chain H: 



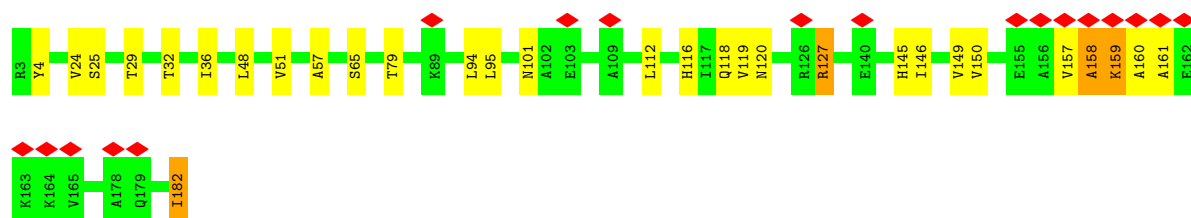
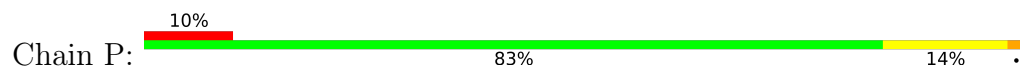
- Molecule 12: uL16

Chain I: 

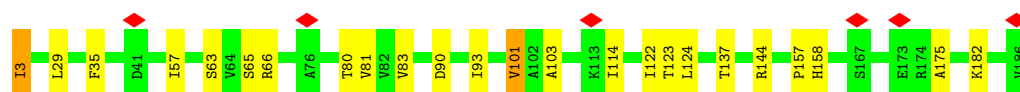
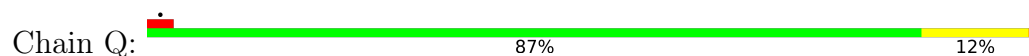




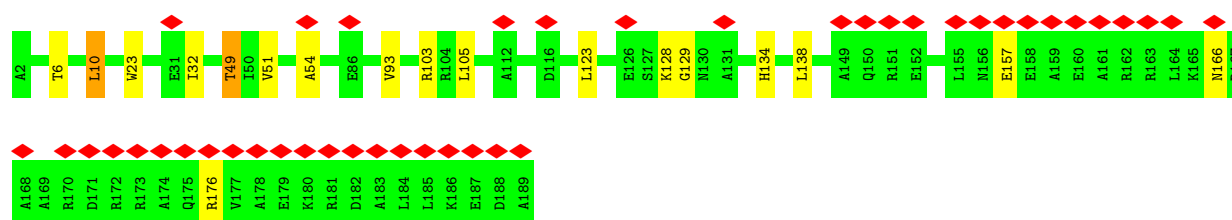
- Molecule 18: uL22



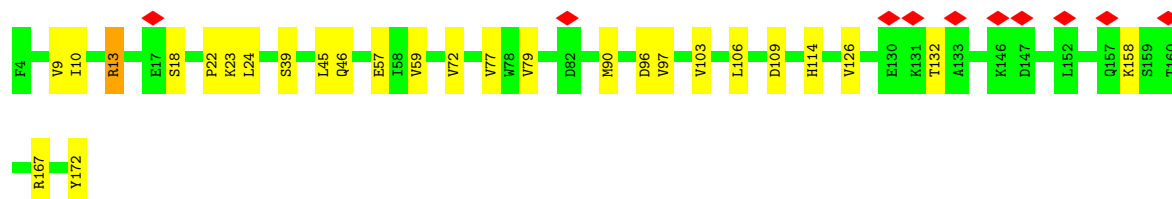
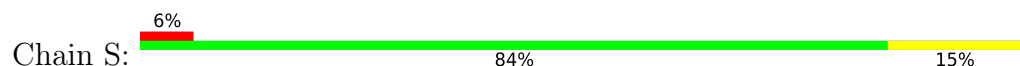
- Molecule 19: eL18



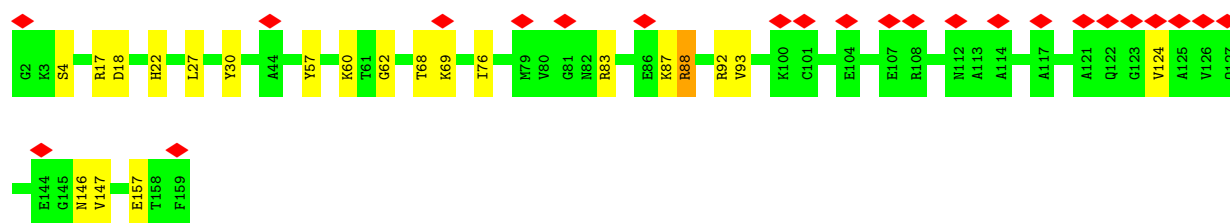
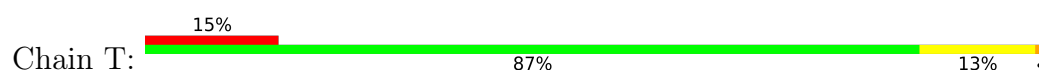
- Molecule 20: eL19



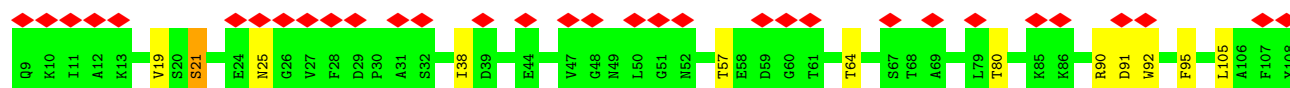
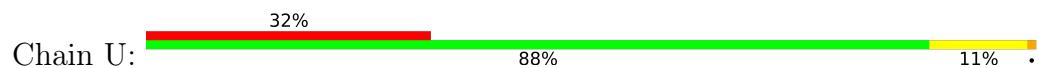
- Molecule 21: eL20



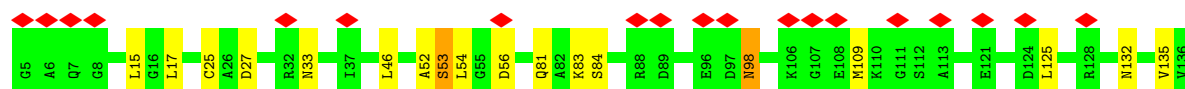
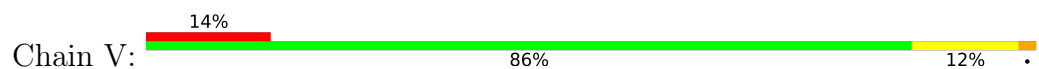
- Molecule 22: eL21



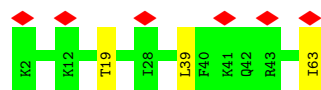
• Molecule 23: eL22



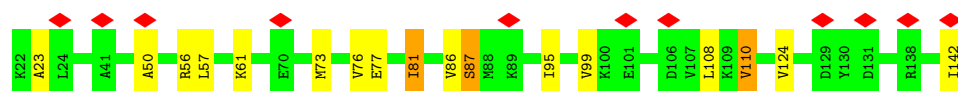
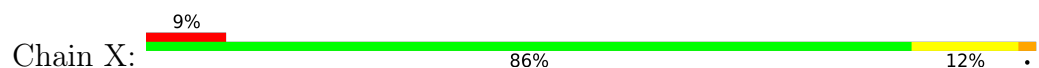
• Molecule 24: uL14



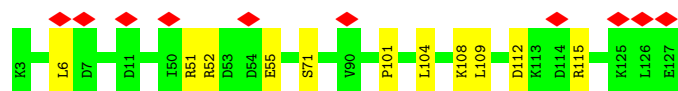
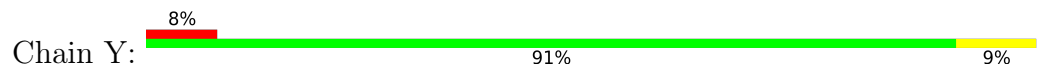
• Molecule 25: eL24



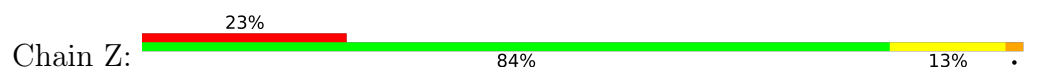
• Molecule 26: uL23

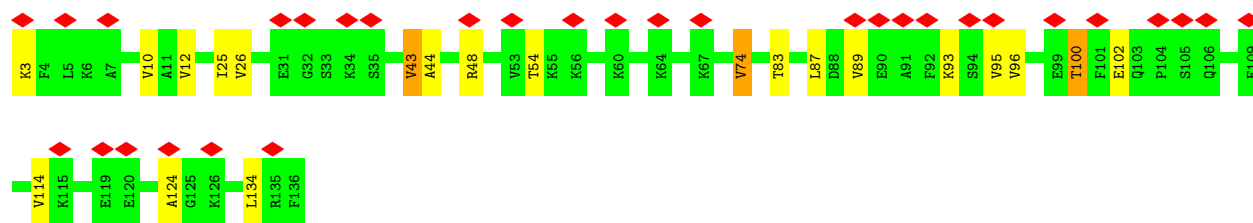


• Molecule 27: uL24

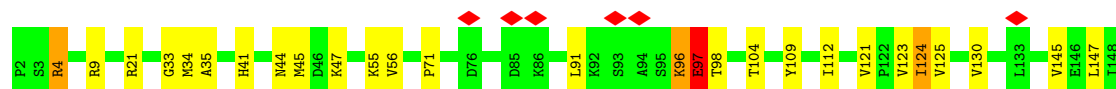
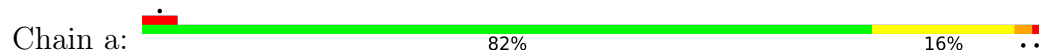


• Molecule 28: eL27

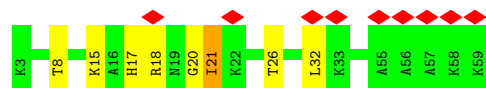
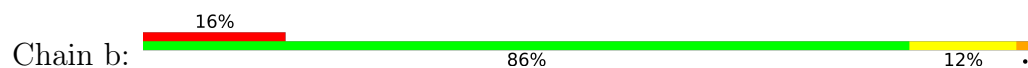




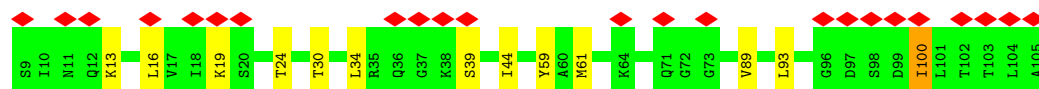
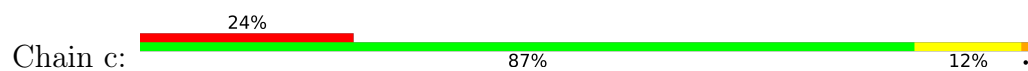
• Molecule 29: uL15



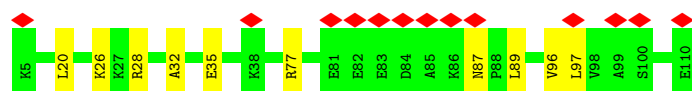
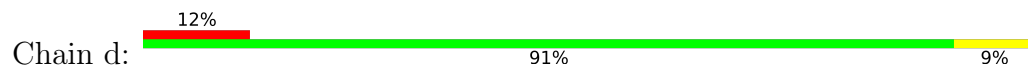
• Molecule 30: eL29



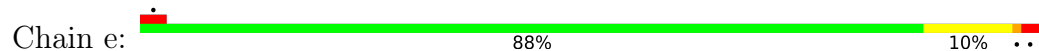
• Molecule 31: eL30



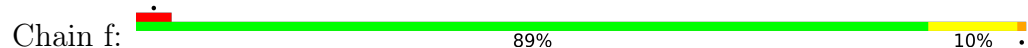
• Molecule 32: eL31

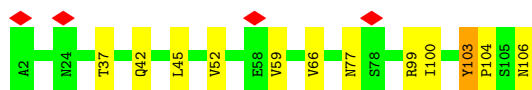


• Molecule 33: eL32

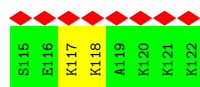
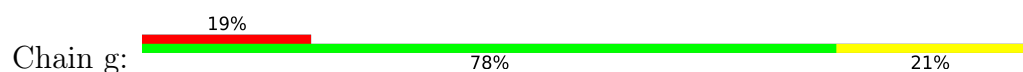


• Molecule 34: eL33





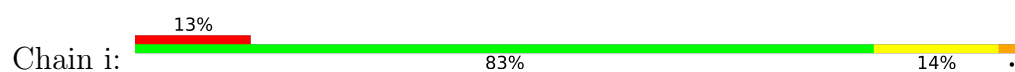
• Molecule 35: eL34



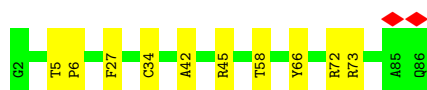
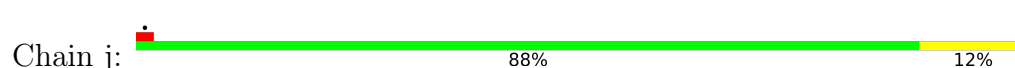
• Molecule 36: uL29



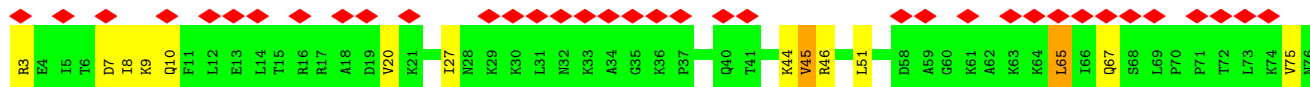
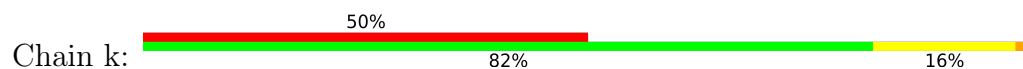
• Molecule 37: eL36



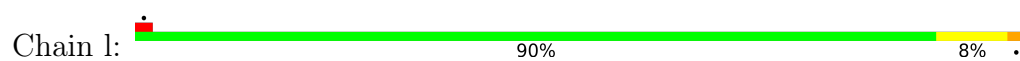
• Molecule 38: eL37



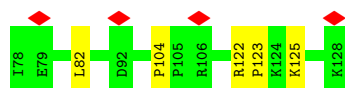
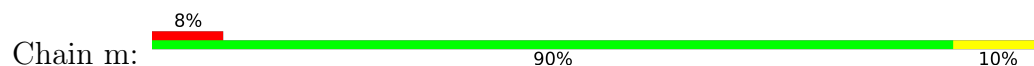
• Molecule 39: eL38



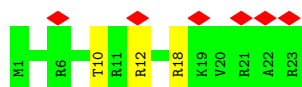
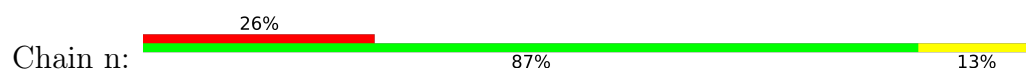
• Molecule 40: eL39



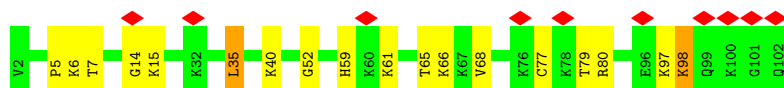
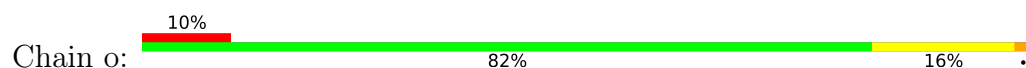
• Molecule 41: eL40



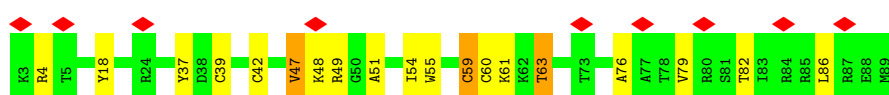
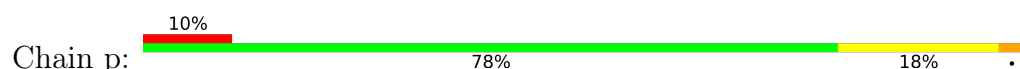
• Molecule 42: eL41



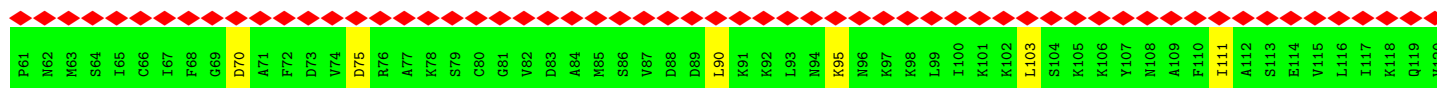
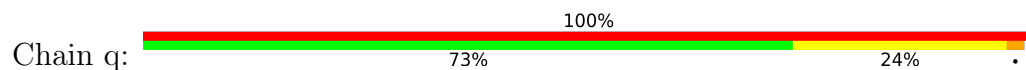
• Molecule 43: eL42



• Molecule 44: eL43

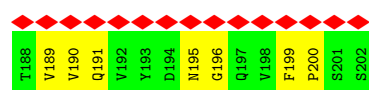
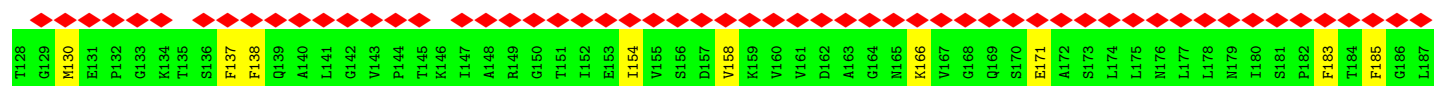
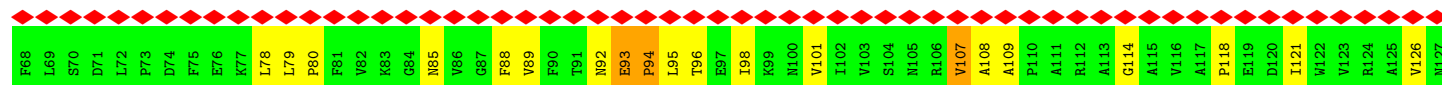


• Molecule 45: uL1

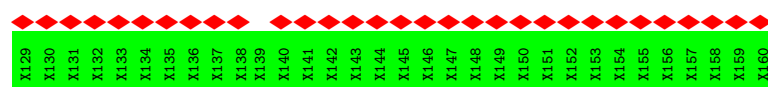
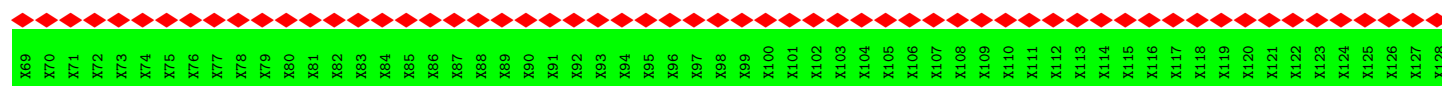
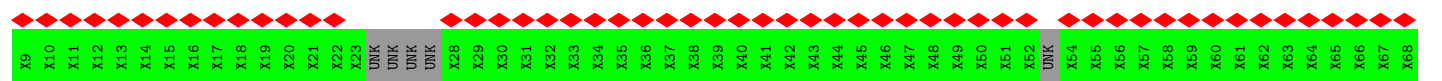




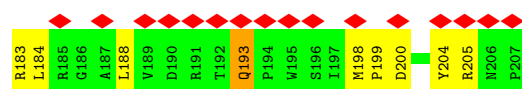
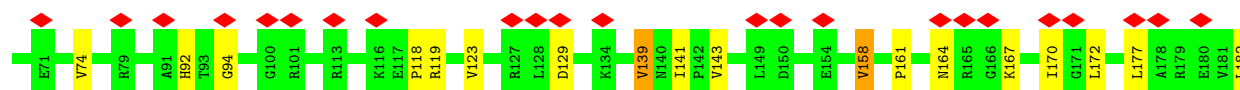
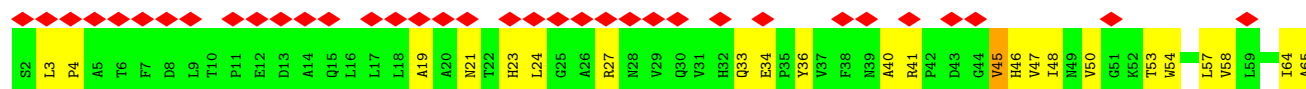
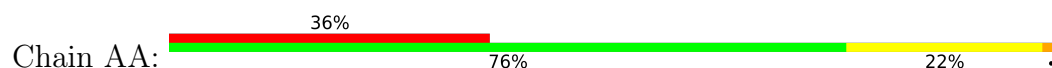
• Molecule 46: uL10



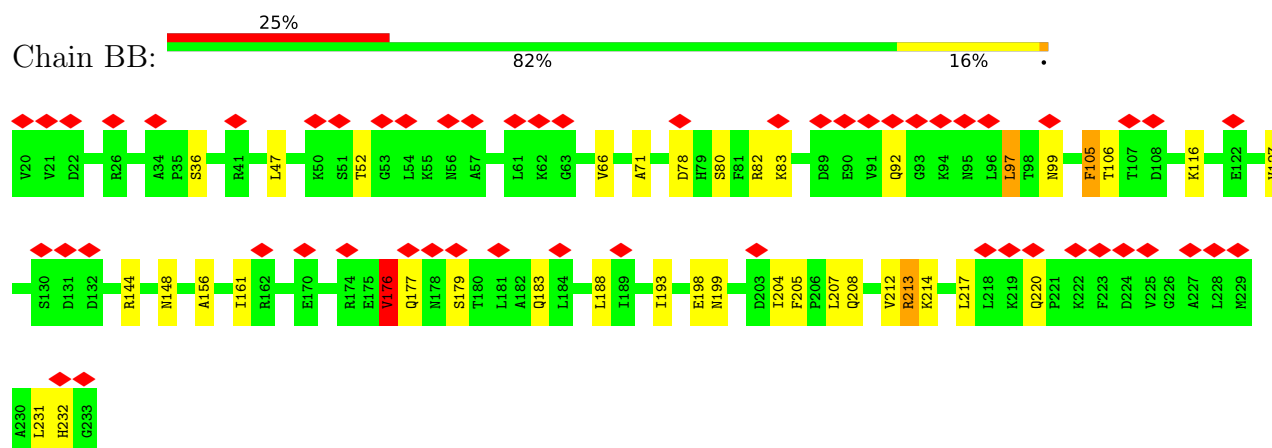
• Molecule 47: L10



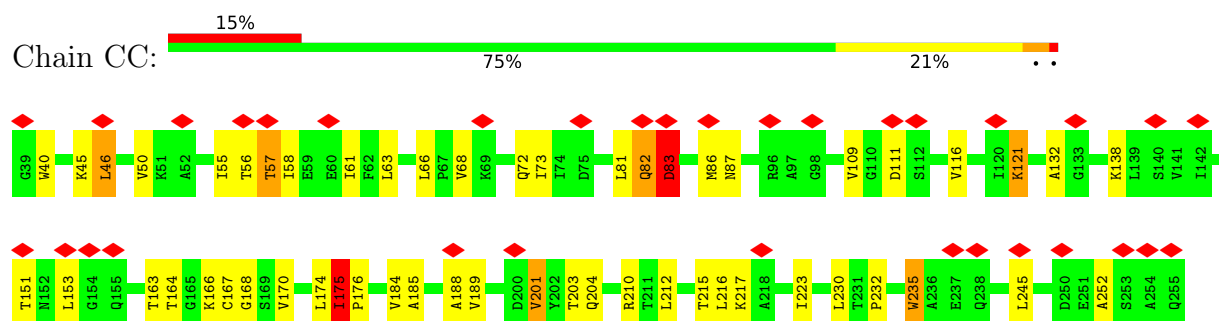
• Molecule 48: uS2



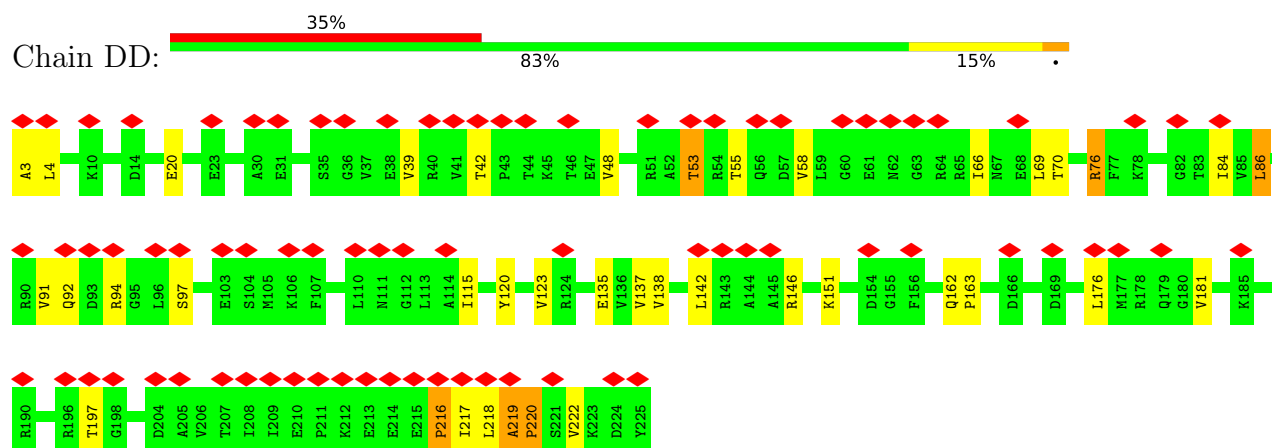
- Molecule 49: eS1



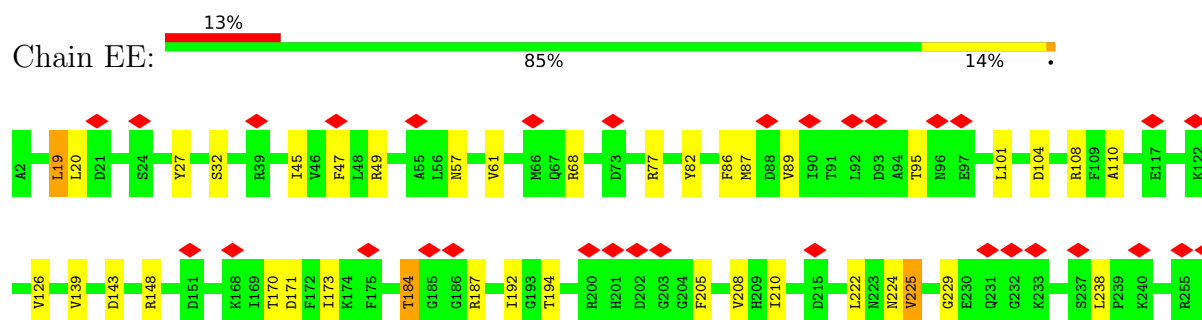
- Molecule 50: uS5



- Molecule 51: uS3

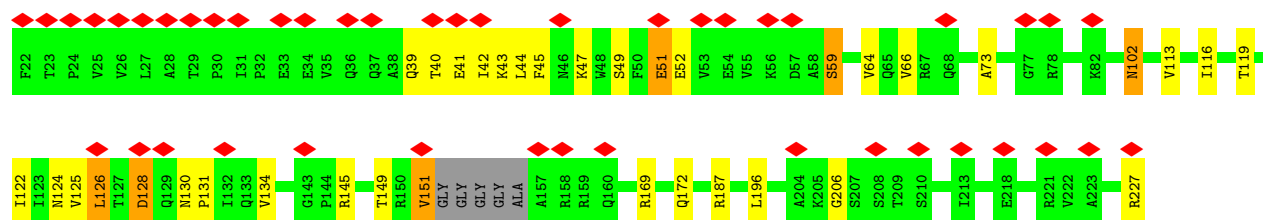
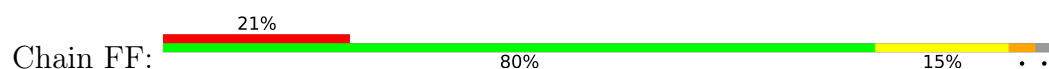


- Molecule 52: eS4

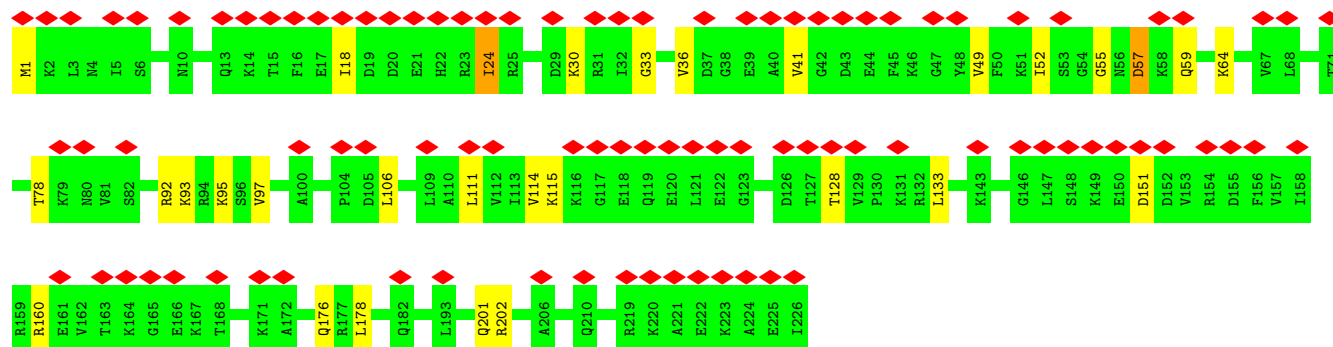
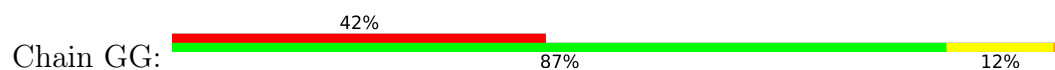




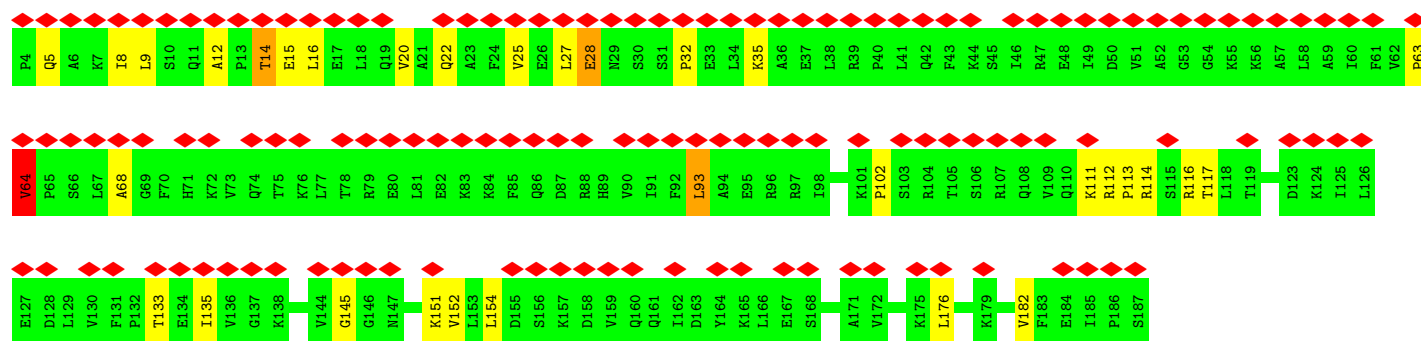
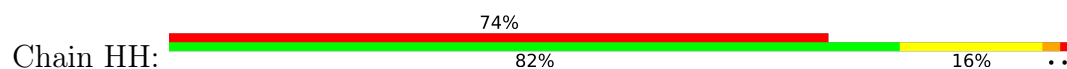
- Molecule 53: uS7



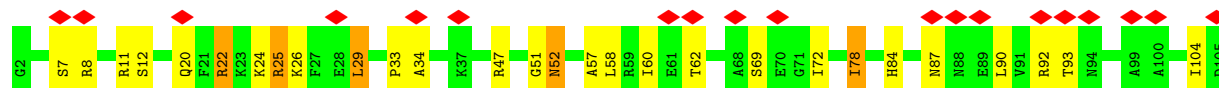
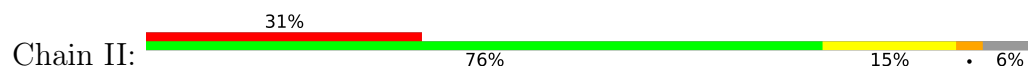
- Molecule 54: eS6

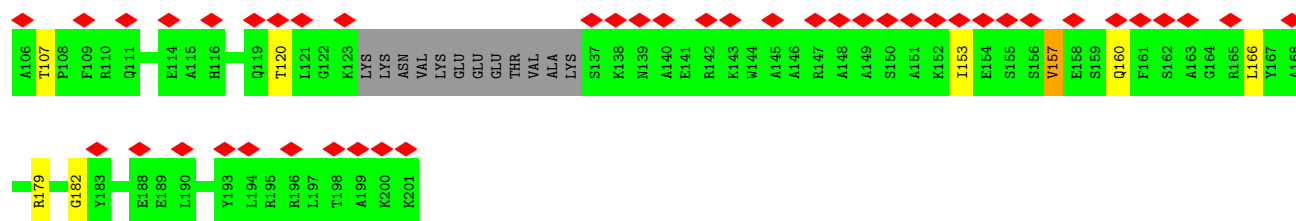


- Molecule 55: eS7

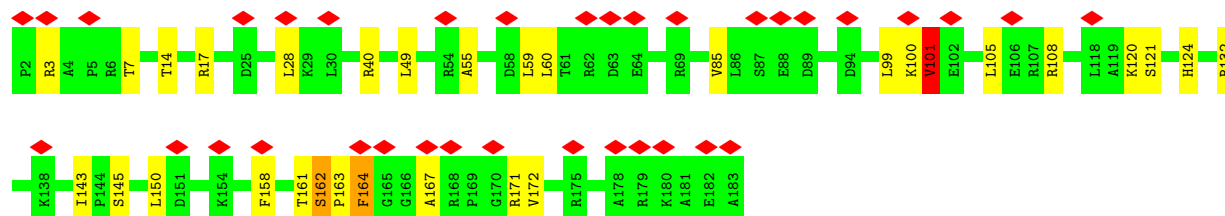
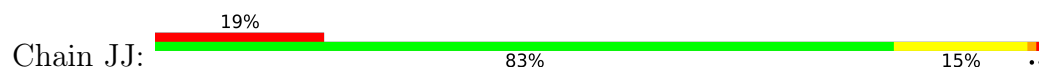


- Molecule 56: eS8

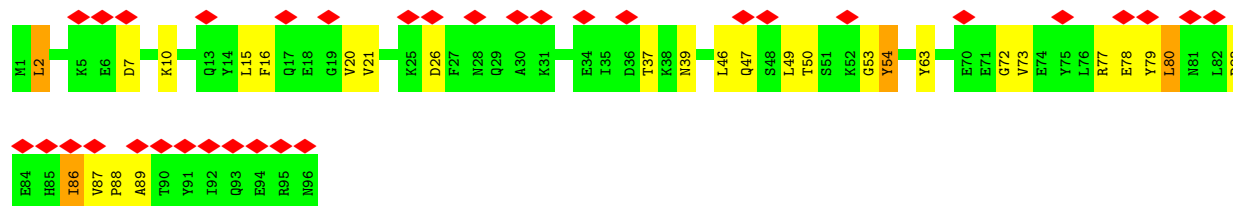
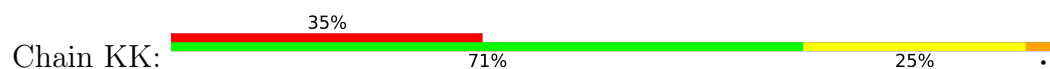




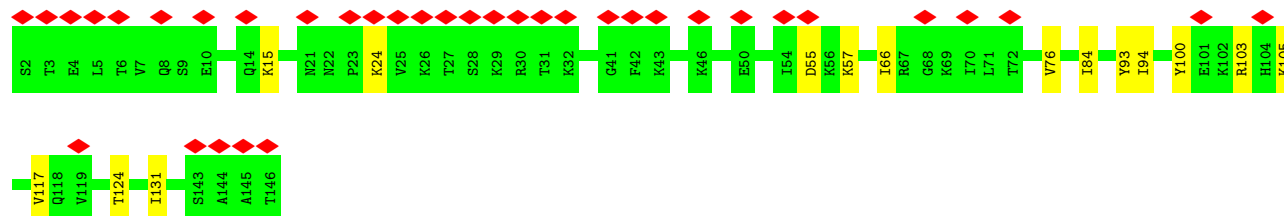
• Molecule 57: uS4



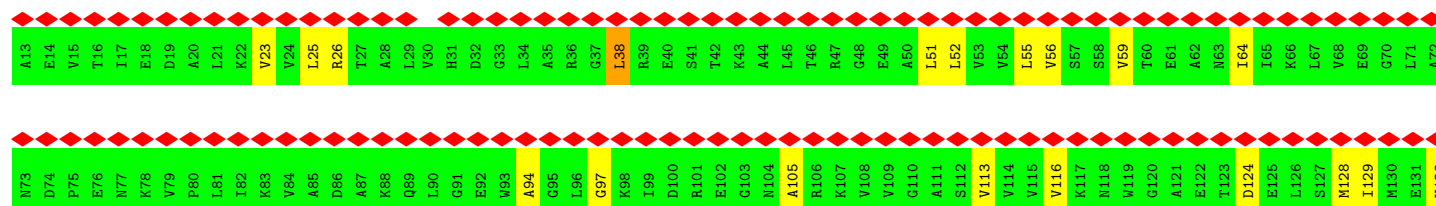
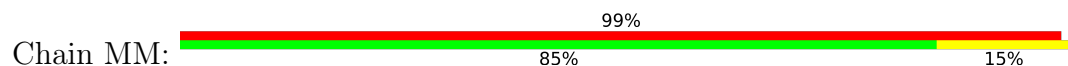
• Molecule 58: eS10

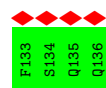


• Molecule 59: uS17

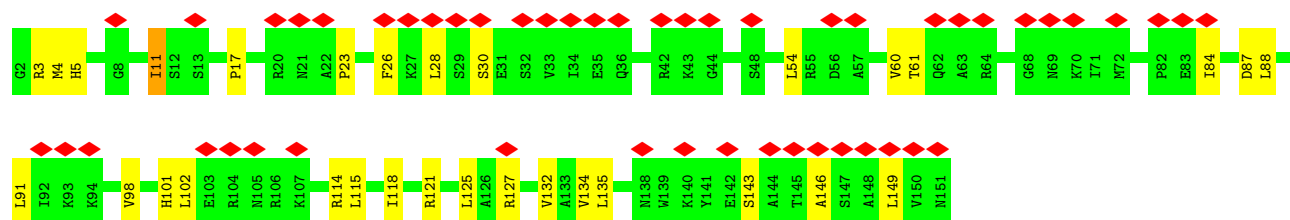
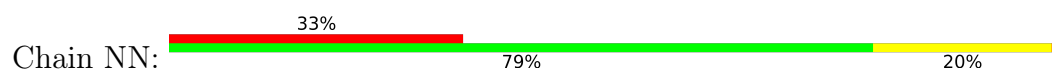


• Molecule 60: eS12

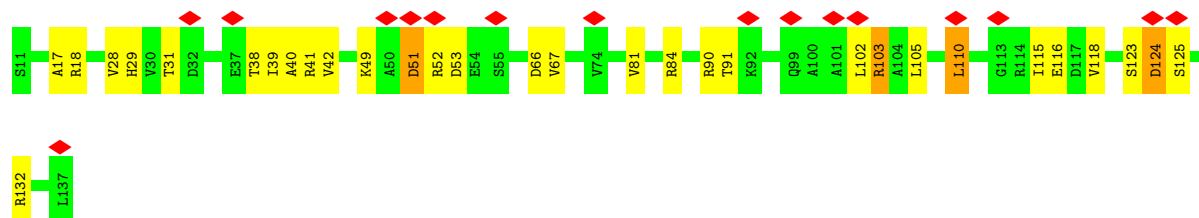
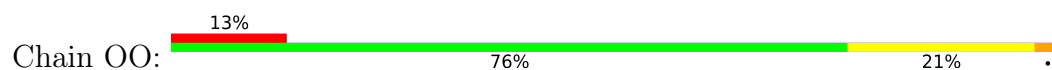




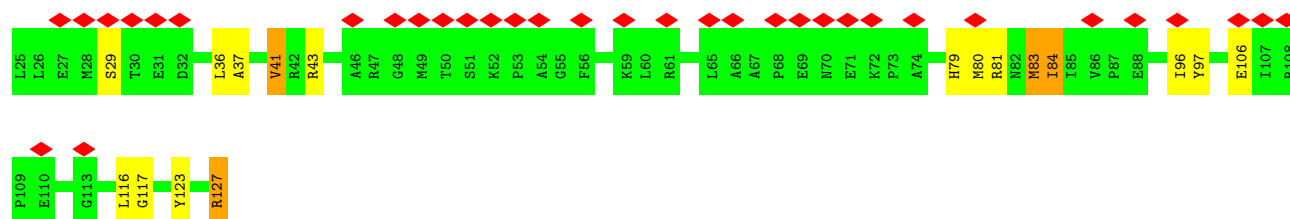
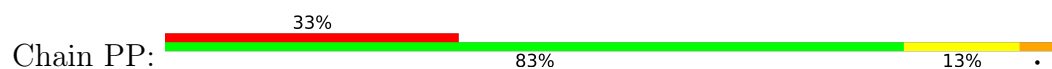
• Molecule 61: uS15



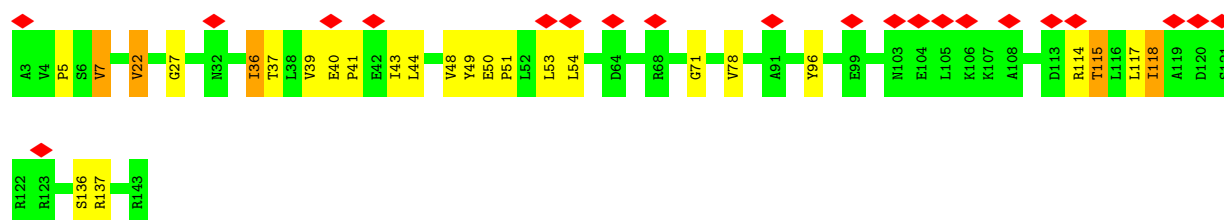
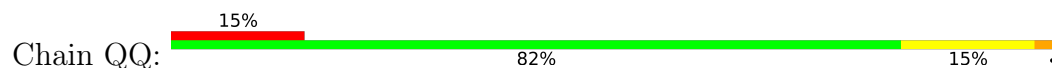
• Molecule 62: uS11



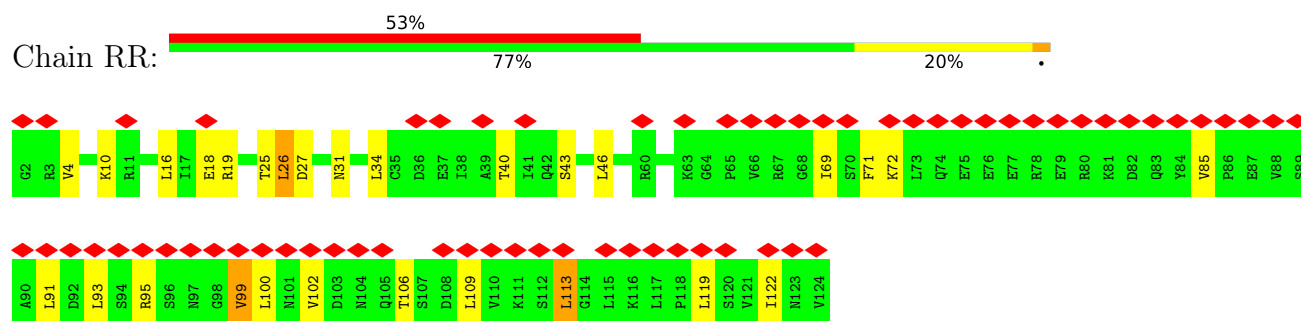
• Molecule 63: uS19



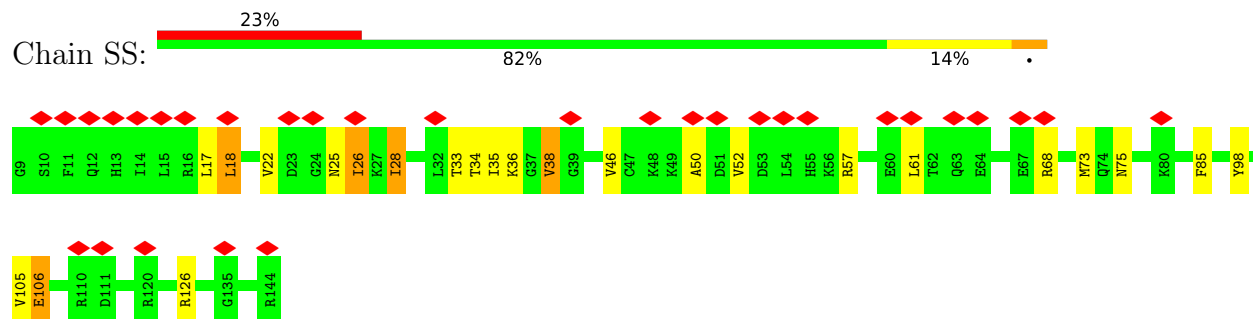
• Molecule 64: uS19



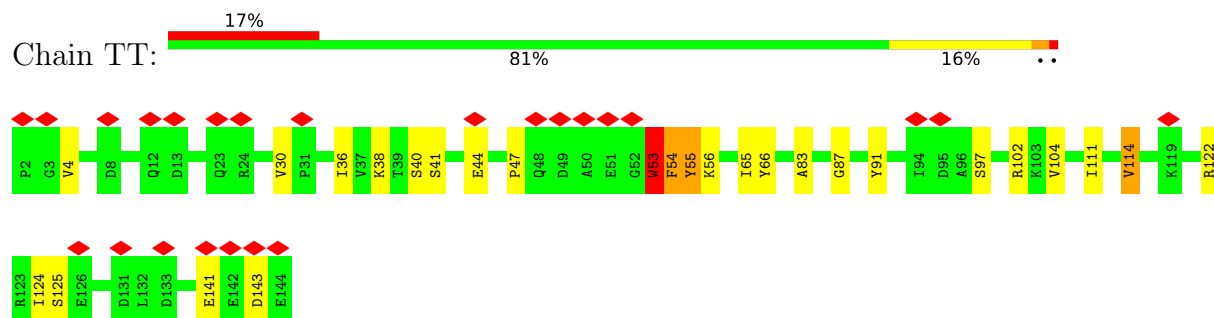
• Molecule 65: eS17



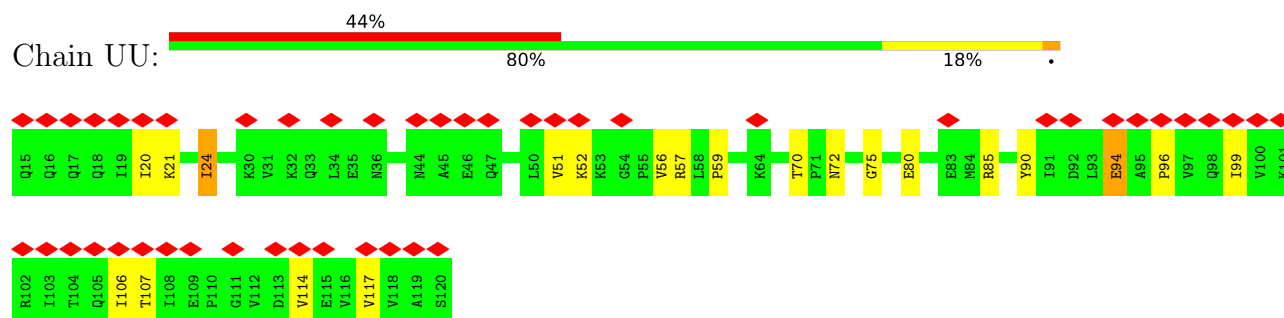
- Molecule 66: uS13



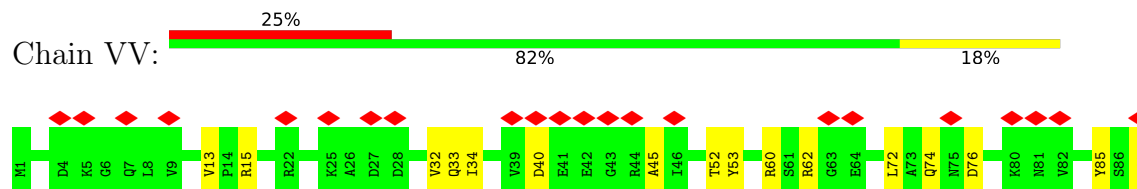
- Molecule 67: eS19



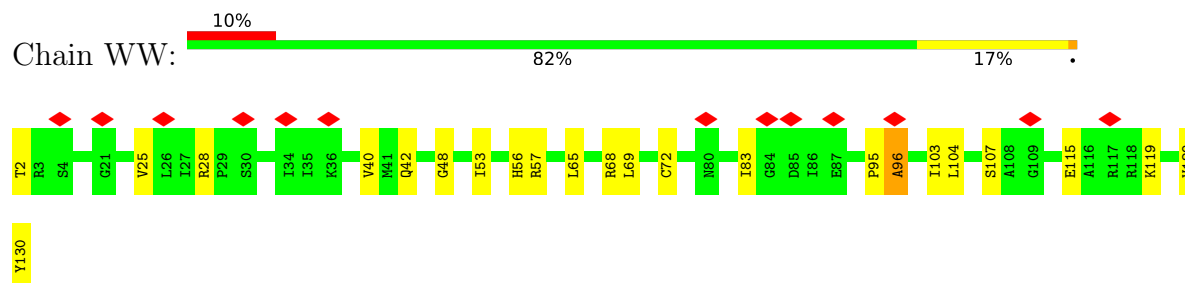
- Molecule 68: uS10



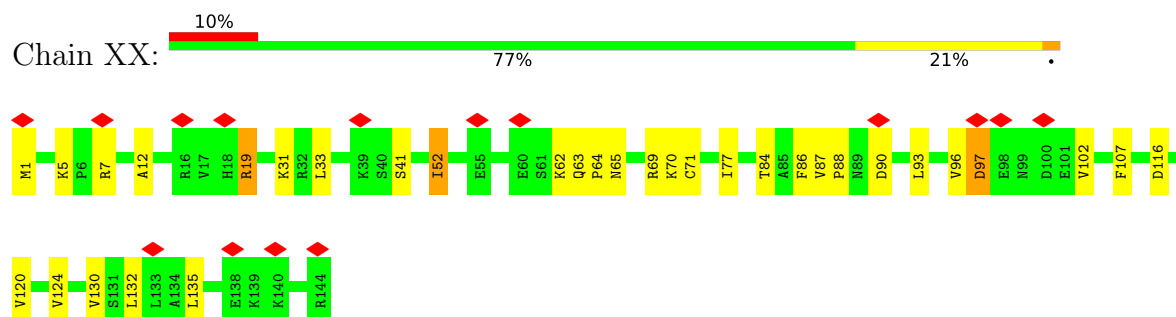
- Molecule 69: eS21



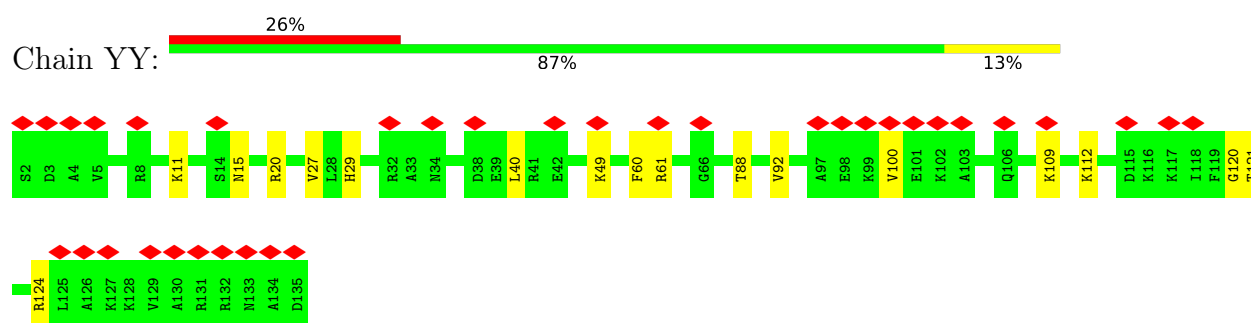
• Molecule 70: uS8



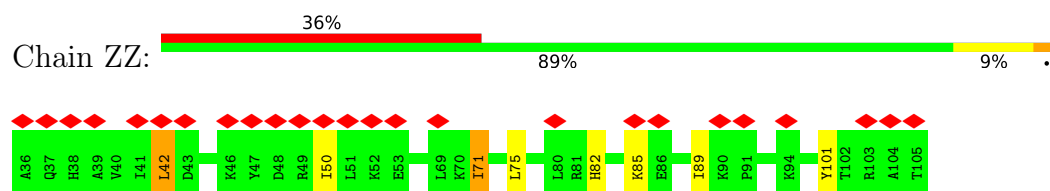
• Molecule 71: uS12



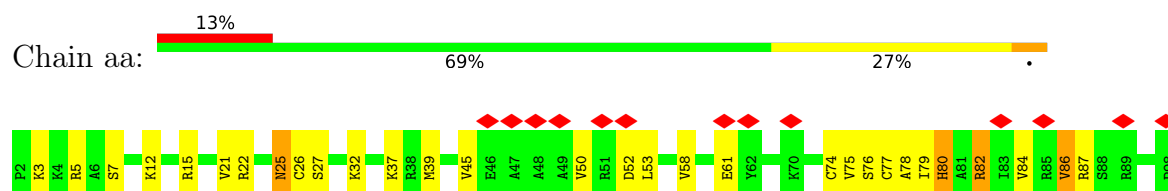
• Molecule 72: eS24



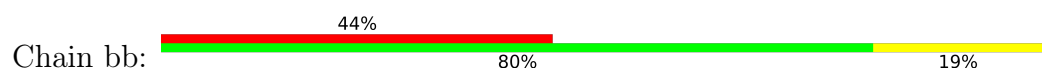
• Molecule 73: eS25

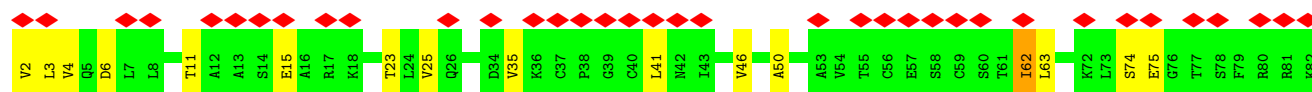


• Molecule 74: eS26

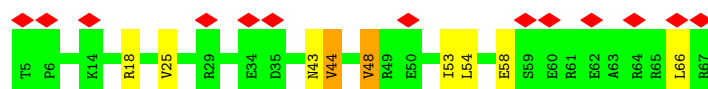
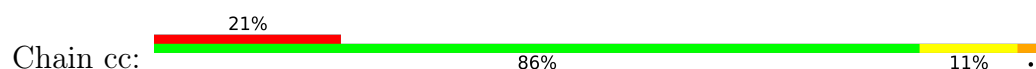


• Molecule 75: eS27

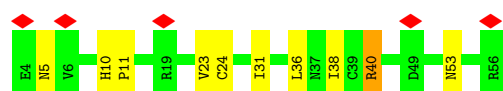
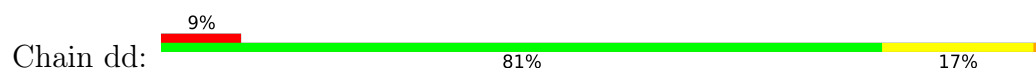




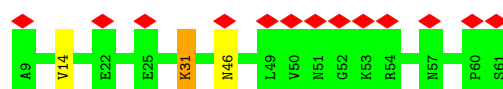
• Molecule 76: eS28



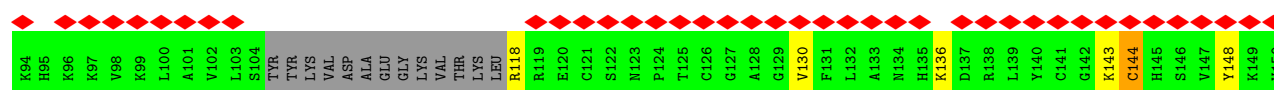
• Molecule 77: uS14



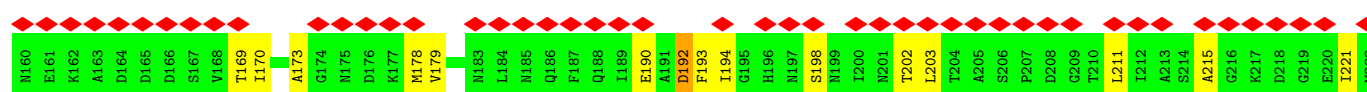
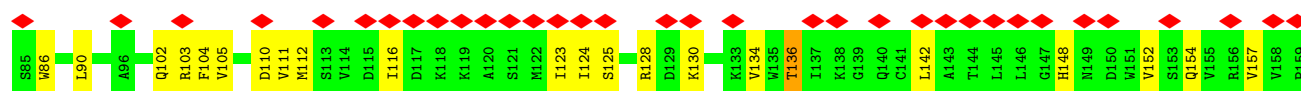
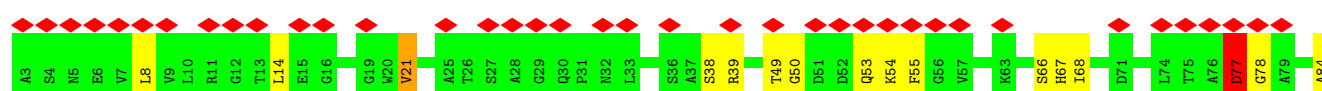
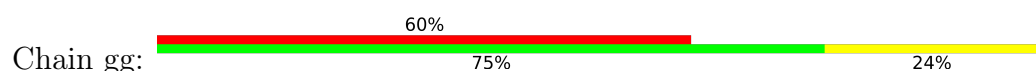
• Molecule 78: eS30

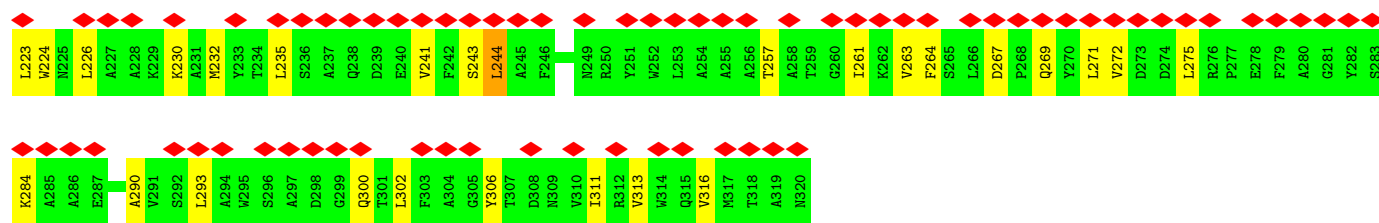


• Molecule 79: eS31

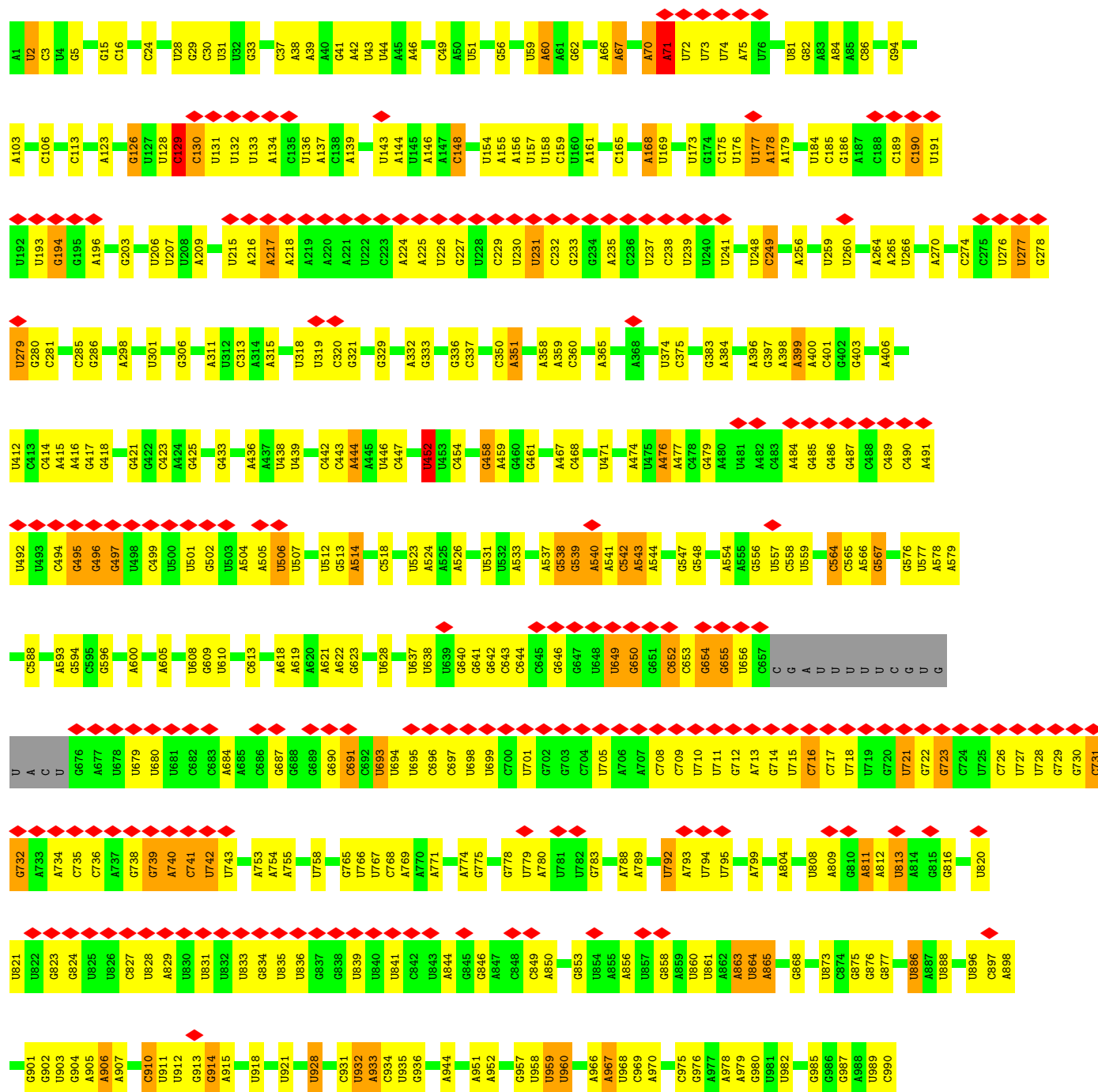


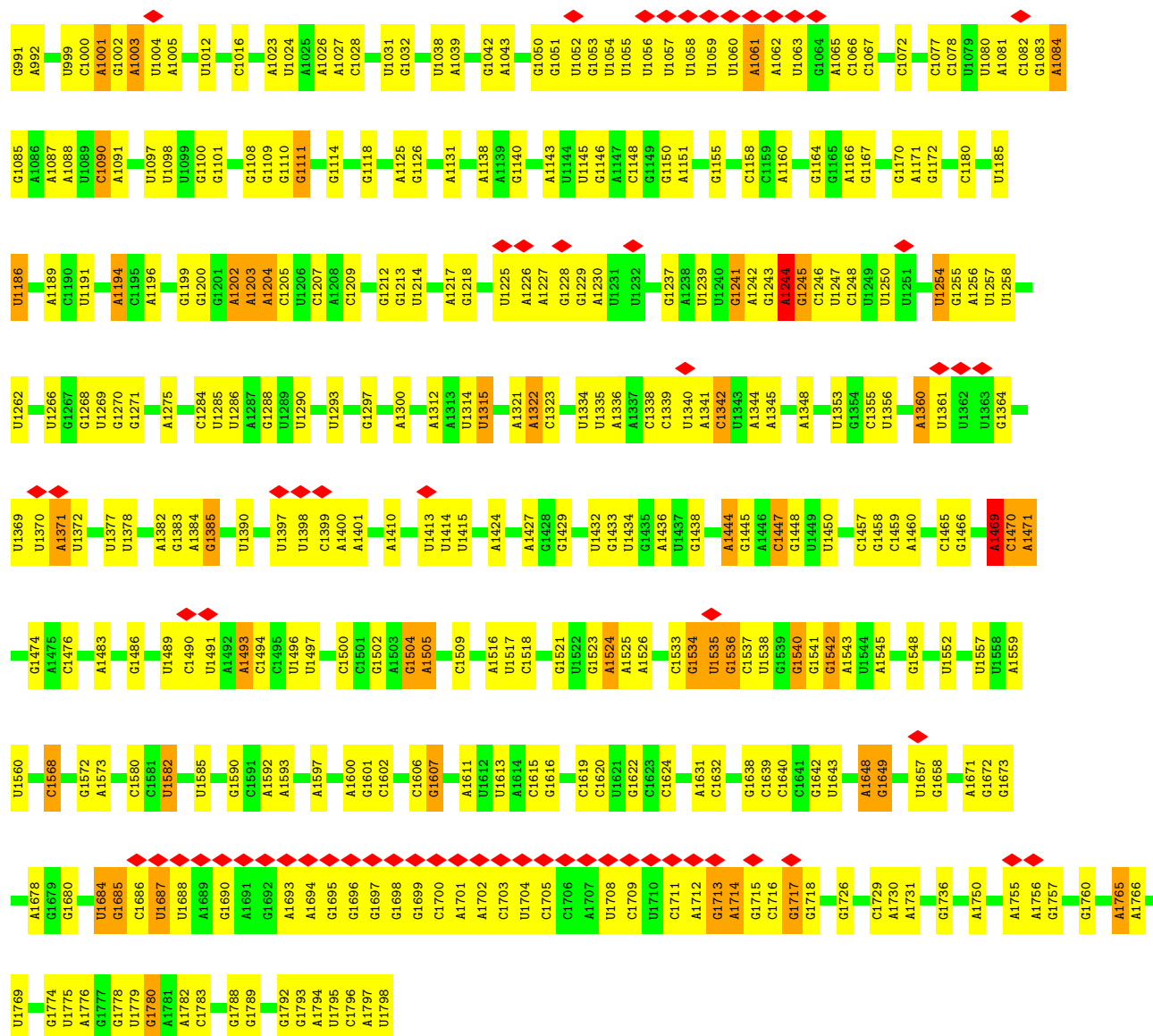
• Molecule 80: RACK1



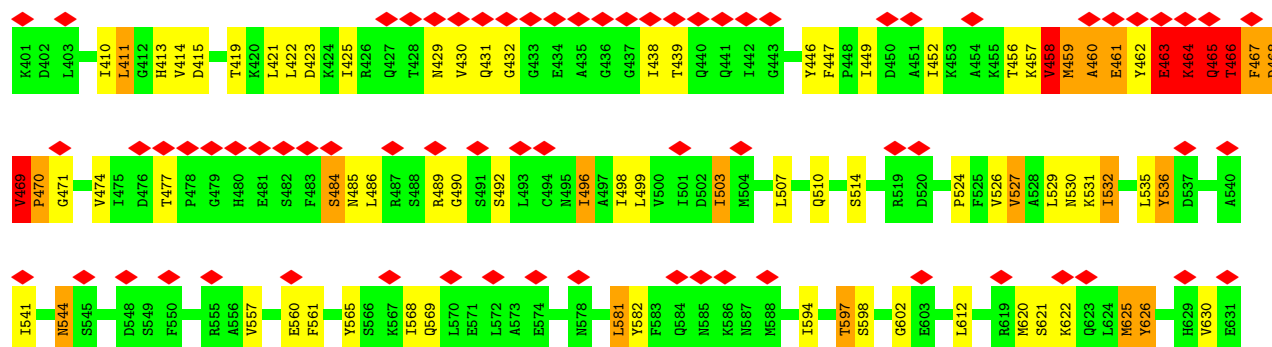


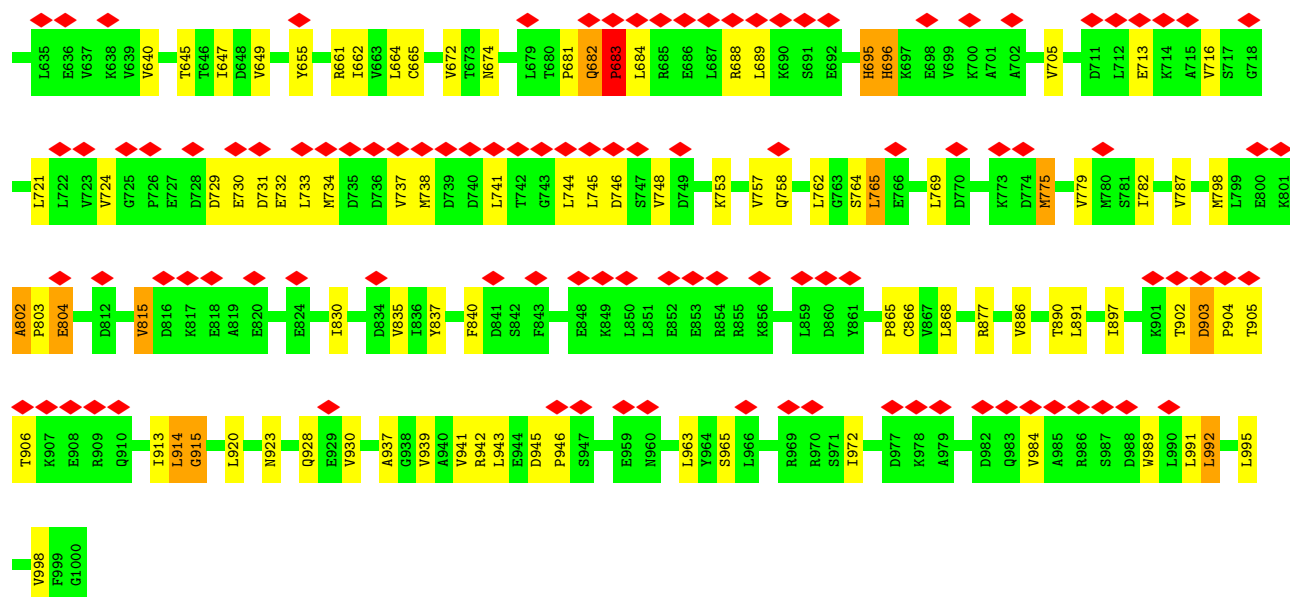
• Molecule 81: 18S ribosomal RNA



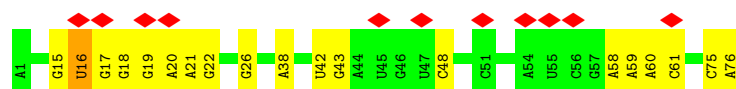
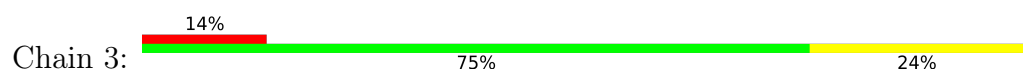


• Molecule 82: eIF5B





- Molecule 83: Met-tRNA-iMet



- Molecule 84: mRNA



There are no outlier residues recorded for this chain.

4 Experimental information

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 ($e^-/\text{\AA}^2$)	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

5.1 Standard geometry

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	0.39	0/78264	0.74	51/121981 (0.0%)
2	7	0.38	0/2883	0.70	1/4491 (0.0%)
3	8	0.37	0/3724	0.72	2/5798 (0.0%)
4	A	1.02	0/1927	1.42	0/2589
5	B	1.02	0/3136	1.41	1/4217 (0.0%)
6	C	1.02	0/2787	1.51	5/3773 (0.1%)
7	D	1.02	0/2420	1.52	3/3264 (0.1%)
8	E	1.04	0/1260	1.43	0/1694
9	F	1.00	0/1821	1.54	0/2451
10	G	1.04	0/1841	1.56	0/2486
11	H	1.03	0/1545	1.41	0/2081
12	I	1.00	0/1787	1.41	0/2397
13	J	1.04	0/1365	1.49	0/1831
14	L	1.02	0/1609	1.54	1/2158 (0.0%)
15	M	1.04	0/1069	1.55	0/1439
16	N	0.96	0/1748	1.46	1/2343 (0.0%)
17	O	0.99	0/1585	1.54	1/2128 (0.0%)
18	P	1.01	0/1450	1.48	0/1947
19	Q	1.01	0/1461	1.47	0/1960
20	R	1.03	0/1538	1.61	2/2050 (0.1%)
21	S	0.98	0/1457	1.33	0/1958
22	T	1.01	0/1292	1.40	0/1732
23	U	1.04	0/812	1.45	0/1099
24	V	1.05	0/993	1.38	0/1335
25	W	1.00	0/525	1.40	0/697
26	X	1.02	0/983	1.46	0/1325
27	Y	1.04	0/999	1.47	0/1334
28	Z	1.01	0/1113	1.48	0/1490
29	a	0.98	0/1199	1.38	0/1605
30	b	1.01	0/468	1.53	0/622
31	c	1.07	0/751	1.54	0/1008
32	d	1.03	0/879	1.38	0/1179

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	1.01	0/1009	1.50	3/1349 (0.2%)
34	f	1.00	1/860 (0.1%)	1.27	0/1157
35	g	1.05	0/964	1.47	0/1282
36	h	1.02	0/959	1.59	0/1276
37	i	1.03	0/770	1.54	0/1021
38	j	0.98	0/688	1.48	0/912
39	k	1.05	0/613	1.39	0/819
40	l	0.97	0/435	1.37	0/577
41	m	1.01	0/415	1.40	0/551
42	n	0.94	0/219	1.52	0/281
43	o	0.98	0/826	1.39	0/1090
44	p	1.05	0/675	1.55	0/898
45	q	1.10	0/1744	1.48	0/2339
46	r	1.08	0/1538	1.45	0/2079
48	AA	1.03	0/1656	1.48	0/2266
49	BB	1.06	0/1742	1.43	0/2346
50	CC	1.05	0/1665	1.50	3/2263 (0.1%)
51	DD	1.05	0/1759	1.46	2/2368 (0.1%)
52	EE	1.03	0/2088	1.38	0/2811
53	FF	1.05	0/1607	1.50	0/2172
54	GG	1.05	0/1844	1.47	1/2464 (0.0%)
55	HH	1.06	0/1506	1.47	2/2028 (0.1%)
56	II	1.03	0/1505	1.50	2/2010 (0.1%)
57	JJ	1.03	0/1502	1.56	0/2013
58	KK	1.02	0/838	1.41	0/1133
59	LL	1.04	0/1192	1.37	0/1608
60	MM	1.13	0/942	1.46	0/1274
61	NN	1.05	0/1215	1.55	0/1638
62	OO	1.07	0/952	1.53	0/1279
63	PP	1.05	0/831	1.42	0/1117
64	QQ	1.05	0/1125	1.45	0/1510
65	RR	1.04	0/998	1.56	0/1337
66	SS	1.03	0/1140	1.51	0/1532
67	TT	1.04	0/1130	1.58	0/1517
68	UU	1.07	0/857	1.45	1/1158 (0.1%)
69	VV	1.03	0/693	1.41	0/935
70	WW	1.04	0/1038	1.50	0/1395
71	XX	1.02	0/1141	1.39	0/1520
72	YY	1.05	0/1087	1.42	0/1449
73	ZZ	1.05	0/571	1.50	0/768
74	aa	1.04	0/782	1.44	0/1047
75	bb	1.09	0/620	1.41	0/838
76	cc	1.07	0/499	1.39	0/670

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
77	dd	0.99	0/453	1.45	0/602
78	ee	1.02	0/433	1.37	0/576
79	ff	1.06	0/349	1.40	0/463
80	gg	1.06	0/2495	1.35	0/3392
81	2	0.38	0/42249	0.73	23/65802 (0.0%)
82	1	1.35	36/4776 (0.8%)	1.53	25/6454 (0.4%)
83	3	0.37	0/1823	0.68	0/2842
84	4	0.39	0/147	0.72	0/227
All	All	0.75	37/225656 (0.0%)	1.08	130/330917 (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

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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 37 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	1	458	VAL	CA-C	-20.21	1.26	1.52
82	1	461	GLU	C-O	-15.54	1.04	1.24
82	1	459	MET	C-O	-13.48	1.06	1.24
82	1	458	VAL	C-O	-12.80	1.05	1.24
82	1	459	MET	CA-CB	-12.59	1.32	1.53

The worst 5 of 130 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	1607	U	C2'-C3'-O3'	12.05	127.58	109.50
82	1	464	LYS	N-CA-C	11.71	135.74	110.80
82	1	462	TYR	CA-C-O	-10.19	108.06	118.97
82	1	469	VAL	CA-C-N	10.12	132.49	119.84
82	1	469	VAL	C-N-CA	10.12	132.49	119.84

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 [\(i\)](#)

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5	69936	0	35154	281	0
2	7	2579	0	1304	9	0
3	8	3333	0	1685	11	0
4	A	1893	0	1959	19	0
5	B	3065	0	3150	42	0
6	C	2735	0	2854	28	0
7	D	2370	0	2320	19	0
8	E	1239	0	1326	14	0
9	F	1784	0	1862	19	0
10	G	1809	0	1891	7	0
11	H	1524	0	1587	11	0
12	I	1750	0	1788	13	0
13	J	1344	0	1370	8	0
14	L	1584	0	1658	16	0
15	M	1054	0	1149	11	0
16	N	1711	0	1766	19	0
17	O	1555	0	1659	8	0
18	P	1427	0	1470	19	0
19	Q	1437	0	1540	15	0
20	R	1521	0	1617	6	0
21	S	1422	0	1463	14	0
22	T	1268	0	1312	11	0
23	U	796	0	812	5	0
24	V	978	0	1025	6	0
25	W	513	0	539	0	0
26	X	968	0	1036	8	0
27	Y	988	0	1076	5	0
28	Z	1087	0	1150	7	0
29	a	1168	0	1210	15	0
30	b	457	0	486	4	0
31	c	743	0	797	4	0
32	d	865	0	917	4	0
33	e	988	0	1054	12	0
34	f	842	0	869	3	0
35	g	954	0	1039	9	0
36	h	950	0	1055	4	0
37	i	764	0	841	10	0
38	j	673	0	677	7	0
39	k	607	0	677	12	0
40	l	428	0	464	2	0
41	m	409	0	444	4	0
42	n	218	0	266	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	o	814	0	881	3	0
44	p	668	0	711	10	0
45	q	1718	0	1810	19	0
46	r	1512	0	1546	29	0
47	K	735	0	178	0	0
48	AA	1615	0	1631	29	0
49	BB	1716	0	1786	16	0
50	CC	1635	0	1723	26	0
51	DD	1734	0	1817	14	0
52	EE	2047	0	2132	17	0
53	FF	1588	0	1657	14	0
54	GG	1820	0	1918	18	0
55	HH	1481	0	1572	14	0
56	II	1480	0	1512	14	0
57	JJ	1477	0	1559	13	0
58	KK	818	0	806	12	0
59	LL	1166	0	1232	7	0
60	MM	934	0	975	11	0
61	NN	1192	0	1255	15	0
62	OO	941	0	979	16	0
63	PP	814	0	850	12	0
64	QQ	1105	0	1166	13	0
65	RR	989	0	1052	16	0
66	SS	1121	0	1148	16	0
67	TT	1112	0	1124	13	0
68	UU	847	0	911	10	0
69	VV	684	0	672	6	0
70	WW	1021	0	1060	12	0
71	XX	1123	0	1203	15	0
72	YY	1073	0	1132	11	0
73	ZZ	563	0	603	6	0
74	aa	769	0	816	14	0
75	bb	610	0	633	6	0
76	cc	497	0	535	5	0
77	dd	443	0	433	5	0
78	ee	426	0	472	4	0
79	ff	344	0	360	2	0
80	gg	2444	0	2399	37	0
81	2	37790	0	19024	231	0
82	1	4704	0	4839	116	0
83	3	1630	0	824	3	0
84	4	131	0	66	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
85	aa	1	0	0	2	0
85	bb	1	0	0	0	0
85	ff	1	0	0	0	0
85	j	1	0	0	0	0
85	m	1	0	0	0	0
85	o	1	0	0	0	0
86	1	28	0	12	0	0
87	3	10	0	0	0	0
88	3	8	0	8	0	0
All	All	211119	0	157340	1327	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 1327 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:1:423:ASP:OD1	82:1:429:ASN:HA	1.06	1.24
82:1:423:ASP:OD1	82:1:429:ASN:CA	2.01	1.09
82:1:464:LYS:H	82:1:464:LYS:HD2	1.29	0.98
82:1:565:TYR:CE1	82:1:581:LEU:HD13	1.99	0.98
82:1:423:ASP:CG	82:1:429:ASN:HA	1.92	0.94

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	A	247/249 (99%)	223 (90%)	17 (7%)	7 (3%)	4	15
5	B	382/384 (100%)	325 (85%)	54 (14%)	3 (1%)	16	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	C	357/359 (99%)	287 (80%)	54 (15%)	16 (4%)	2	8
7	D	293/295 (99%)	266 (91%)	24 (8%)	3 (1%)	12	39
8	E	152/175 (87%)	142 (93%)	8 (5%)	2 (1%)	9	32
9	F	220/222 (99%)	194 (88%)	22 (10%)	4 (2%)	6	25
10	G	231/233 (99%)	210 (91%)	19 (8%)	2 (1%)	14	41
11	H	189/191 (99%)	165 (87%)	21 (11%)	3 (2%)	7	27
12	I	214/216 (99%)	191 (89%)	18 (8%)	5 (2%)	5	19
13	J	166/168 (99%)	149 (90%)	16 (10%)	1 (1%)	21	51
14	L	196/198 (99%)	173 (88%)	19 (10%)	4 (2%)	6	22
15	M	134/136 (98%)	118 (88%)	14 (10%)	2 (2%)	8	28
16	N	200/202 (99%)	183 (92%)	16 (8%)	1 (0%)	24	54
17	O	195/197 (99%)	184 (94%)	9 (5%)	2 (1%)	12	39
18	P	178/180 (99%)	158 (89%)	18 (10%)	2 (1%)	11	36
19	Q	182/184 (99%)	169 (93%)	12 (7%)	1 (0%)	24	54
20	R	186/188 (99%)	174 (94%)	11 (6%)	1 (0%)	24	54
21	S	167/169 (99%)	152 (91%)	12 (7%)	3 (2%)	6	25
22	T	156/158 (99%)	141 (90%)	13 (8%)	2 (1%)	9	32
23	U	98/100 (98%)	89 (91%)	9 (9%)	0	100	100
24	V	130/132 (98%)	115 (88%)	13 (10%)	2 (2%)	8	28
25	W	60/62 (97%)	54 (90%)	6 (10%)	0	100	100
26	X	119/121 (98%)	108 (91%)	10 (8%)	1 (1%)	16	44
27	Y	123/125 (98%)	111 (90%)	12 (10%)	0	100	100
28	Z	132/134 (98%)	114 (86%)	16 (12%)	2 (2%)	8	28
29	a	145/147 (99%)	122 (84%)	19 (13%)	4 (3%)	4	15
30	b	55/57 (96%)	46 (84%)	7 (13%)	2 (4%)	2	11
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%)	7	26
34	f	103/105 (98%)	92 (89%)	9 (9%)	2 (2%)	6	23
35	g	119/121 (98%)	106 (89%)	10 (8%)	3 (2%)	4	17
36	h	114/116 (98%)	108 (95%)	5 (4%)	1 (1%)	14	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	i	94/98 (96%)	79 (84%)	13 (14%)	2 (2%)	5	21
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%)	5	21
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	1
44	p	85/87 (98%)	70 (82%)	12 (14%)	3 (4%)	3	12
45	q	213/217 (98%)	163 (76%)	45 (21%)	5 (2%)	5	19
46	r	191/195 (98%)	144 (75%)	41 (22%)	6 (3%)	3	14
48	AA	204/206 (99%)	166 (81%)	31 (15%)	7 (3%)	3	12
49	BB	212/214 (99%)	187 (88%)	23 (11%)	2 (1%)	14	41
50	CC	215/217 (99%)	188 (87%)	21 (10%)	6 (3%)	4	15
51	DD	221/223 (99%)	189 (86%)	26 (12%)	6 (3%)	4	16
52	EE	255/257 (99%)	217 (85%)	33 (13%)	5 (2%)	6	22
53	FF	197/206 (96%)	155 (79%)	36 (18%)	6 (3%)	3	14
54	GG	224/226 (99%)	201 (90%)	22 (10%)	1 (0%)	30	59
55	HH	182/184 (99%)	157 (86%)	22 (12%)	3 (2%)	7	27
56	II	183/199 (92%)	153 (84%)	25 (14%)	5 (3%)	4	16
57	JJ	180/182 (99%)	156 (87%)	17 (9%)	7 (4%)	2	10
58	KK	94/96 (98%)	81 (86%)	10 (11%)	3 (3%)	3	13
59	LL	143/145 (99%)	127 (89%)	15 (10%)	1 (1%)	18	48
60	MM	122/124 (98%)	85 (70%)	34 (28%)	3 (2%)	4	17
61	NN	148/150 (99%)	137 (93%)	7 (5%)	4 (3%)	4	16
62	OO	125/127 (98%)	106 (85%)	16 (13%)	3 (2%)	4	18
63	PP	101/103 (98%)	88 (87%)	12 (12%)	1 (1%)	12	39
64	QQ	139/141 (99%)	126 (91%)	11 (8%)	2 (1%)	9	30
65	RR	119/123 (97%)	99 (83%)	19 (16%)	1 (1%)	16	44
66	SS	134/136 (98%)	116 (87%)	17 (13%)	1 (1%)	18	48
67	TT	141/143 (99%)	128 (91%)	10 (7%)	3 (2%)	5	21
68	UU	104/106 (98%)	94 (90%)	10 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	VV	85/87 (98%)	71 (84%)	14 (16%)	0	100	100
70	WW	127/129 (98%)	114 (90%)	10 (8%)	3 (2%)	4	18
71	XX	142/144 (99%)	125 (88%)	14 (10%)	3 (2%)	5	21
72	YY	132/134 (98%)	119 (90%)	12 (9%)	1 (1%)	16	44
73	ZZ	68/70 (97%)	59 (87%)	8 (12%)	1 (2%)	8	28
74	aa	95/97 (98%)	76 (80%)	14 (15%)	5 (5%)	1	5
75	bb	79/81 (98%)	63 (80%)	15 (19%)	1 (1%)	9	32
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%)	4	17
80	gg	312/318 (98%)	265 (85%)	43 (14%)	4 (1%)	9	32
82	1	598/600 (100%)	476 (80%)	94 (16%)	28 (5%)	2	7
All	All	11802/12025 (98%)	10238 (87%)	1339 (11%)	225 (2%)	8	23

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 ⓘ

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%)	175 (92%)	16 (8%)	10	31
5	B	320/320 (100%)	297 (93%)	23 (7%)	13	39
6	C	286/286 (100%)	268 (94%)	18 (6%)	16	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	D	244/244 (100%)	226 (93%)	18 (7%)	13	38
8	E	134/152 (88%)	123 (92%)	11 (8%)	10	32
9	F	186/186 (100%)	183 (98%)	3 (2%)	55	83
10	G	189/191 (99%)	179 (95%)	10 (5%)	20	52
11	H	172/172 (100%)	161 (94%)	11 (6%)	16	44
12	I	184/185 (100%)	173 (94%)	11 (6%)	17	47
13	J	146/146 (100%)	139 (95%)	7 (5%)	23	55
14	L	158/158 (100%)	151 (96%)	7 (4%)	25	59
15	M	108/108 (100%)	101 (94%)	7 (6%)	15	44
16	N	174/174 (100%)	168 (97%)	6 (3%)	32	66
17	O	160/160 (100%)	154 (96%)	6 (4%)	29	64
18	P	145/145 (100%)	136 (94%)	9 (6%)	16	46
19	Q	150/150 (100%)	146 (97%)	4 (3%)	39	73
20	R	153/153 (100%)	144 (94%)	9 (6%)	18	48
21	S	154/154 (100%)	144 (94%)	10 (6%)	15	44
22	T	135/135 (100%)	126 (93%)	9 (7%)	15	43
23	U	87/87 (100%)	82 (94%)	5 (6%)	18	49
24	V	101/101 (100%)	94 (93%)	7 (7%)	14	41
25	W	54/54 (100%)	51 (94%)	3 (6%)	19	50
26	X	105/105 (100%)	99 (94%)	6 (6%)	18	49
27	Y	109/109 (100%)	105 (96%)	4 (4%)	30	64
28	Z	115/115 (100%)	104 (90%)	11 (10%)	8	26
29	a	118/118 (100%)	112 (95%)	6 (5%)	21	53
30	b	46/46 (100%)	45 (98%)	1 (2%)	45	77
31	c	81/81 (100%)	75 (93%)	6 (7%)	13	38
32	d	93/93 (100%)	89 (96%)	4 (4%)	26	60
33	e	106/106 (100%)	101 (95%)	5 (5%)	23	56
34	f	89/89 (100%)	84 (94%)	5 (6%)	19	50
35	g	103/103 (100%)	91 (88%)	12 (12%)	5	17
36	h	103/103 (100%)	102 (99%)	1 (1%)	68	89
37	i	80/80 (100%)	75 (94%)	5 (6%)	16	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	j	69/69 (100%)	68 (99%)	1 (1%)	59	85
39	k	68/68 (100%)	61 (90%)	7 (10%)	7	23
40	l	44/44 (100%)	43 (98%)	1 (2%)	44	76
41	m	46/46 (100%)	46 (100%)	0	100	100
42	n	21/21 (100%)	20 (95%)	1 (5%)	23	55
43	o	87/87 (100%)	81 (93%)	6 (7%)	14	41
44	p	69/69 (100%)	65 (94%)	4 (6%)	18	49
45	q	198/198 (100%)	173 (87%)	25 (13%)	4	14
46	r	165/165 (100%)	146 (88%)	19 (12%)	5	18
48	AA	173/173 (100%)	164 (95%)	9 (5%)	21	52
49	BB	192/192 (100%)	178 (93%)	14 (7%)	13	38
50	CC	176/176 (100%)	161 (92%)	15 (8%)	10	31
51	DD	182/182 (100%)	169 (93%)	13 (7%)	13	40
52	EE	219/219 (100%)	212 (97%)	7 (3%)	34	68
53	FF	173/173 (100%)	161 (93%)	12 (7%)	14	41
54	GG	193/193 (100%)	185 (96%)	8 (4%)	27	61
55	HH	165/165 (100%)	158 (96%)	7 (4%)	26	60
56	II	149/160 (93%)	138 (93%)	11 (7%)	13	38
57	JJ	156/156 (100%)	147 (94%)	9 (6%)	18	49
58	KK	89/89 (100%)	77 (86%)	12 (14%)	4	12
59	LL	130/130 (100%)	127 (98%)	3 (2%)	44	76
60	MM	100/100 (100%)	93 (93%)	7 (7%)	14	40
61	NN	127/127 (100%)	122 (96%)	5 (4%)	28	63
62	OO	96/96 (100%)	84 (88%)	12 (12%)	4	15
63	PP	86/86 (100%)	80 (93%)	6 (7%)	14	40
64	QQ	117/117 (100%)	110 (94%)	7 (6%)	17	47
65	RR	112/112 (100%)	101 (90%)	11 (10%)	7	25
66	SS	120/120 (100%)	112 (93%)	8 (7%)	15	43
67	TT	115/115 (100%)	103 (90%)	12 (10%)	7	23
68	UU	99/99 (100%)	92 (93%)	7 (7%)	13	40
69	VV	74/74 (100%)	67 (90%)	7 (10%)	8	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	WW	110/110 (100%)	105 (96%)	5 (4%)	24	58
71	XX	119/119 (100%)	112 (94%)	7 (6%)	18	48
72	YY	112/112 (100%)	111 (99%)	1 (1%)	70	90
73	ZZ	61/61 (100%)	60 (98%)	1 (2%)	55	83
74	aa	83/83 (100%)	72 (87%)	11 (13%)	4	12
75	bb	70/70 (100%)	62 (89%)	8 (11%)	5	18
76	cc	56/56 (100%)	52 (93%)	4 (7%)	13	40
77	dd	47/47 (100%)	43 (92%)	4 (8%)	10	31
78	ee	46/46 (100%)	45 (98%)	1 (2%)	45	77
79	ff	38/49 (78%)	36 (95%)	2 (5%)	20	52
80	gg	261/261 (100%)	238 (91%)	23 (9%)	9	29
82	1	524/524 (100%)	477 (91%)	47 (9%)	9	28
All	All	10116/10159 (100%)	9460 (94%)	656 (6%)	17	44

5 of 656 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
60	MM	55	LEU
75	bb	62	ILE
62	OO	91	THR
60	MM	51	LEU
67	TT	41	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 190 such sidechains are listed below:

Mol	Chain	Res	Type
51	DD	22	ASN
58	KK	96	ASN
51	DD	165	ASN
53	FF	141	ASN
62	OO	29	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3250/3271 (99%)	798 (24%)	76 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	7	120/121 (99%)	21 (17%)	0
3	8	156/157 (99%)	34 (21%)	2 (1%)
81	2	1770/1796 (98%)	559 (31%)	32 (1%)
83	3	75/76 (98%)	17 (22%)	0
84	4	5/6 (83%)	0	0
All	All	5376/5427 (99%)	1429 (26%)	110 (2%)

5 of 1429 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 oligosaccharides 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
88	MET	3	102	83	6,7,8	0.48	0	2,7,9	1.44	0
87	U6A	3	101	83	9,9,10	1.69	2 (22%)	10,11,13	2.60	1 (10%)
86	GDP	1	1101	-	29,30,30	1.15	3 (10%)	45,47,47	1.87	7 (15%)

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
88	MET	3	102	83	-	1/5/6/8	-
87	U6A	3	101	83	-	10/11/11/12	-
86	GDP	1	1101	-	-	3/16/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	3	101	U6A	O1-C1	3.32	1.36	1.22
86	1	1101	GDP	C5-C4	3.01	1.47	1.38
87	3	101	U6A	CA-N	2.80	1.49	1.45
86	1	1101	GDP	C6-N1	-2.44	1.34	1.38
86	1	1101	GDP	C5-N7	-2.19	1.34	1.39

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	3	101	U6A	O1-C1-N	7.63	145.02	125.32
86	1	1101	GDP	C5-C4-N3	-6.25	118.44	128.39
86	1	1101	GDP	C2-N3-C4	5.12	121.13	112.30
86	1	1101	GDP	N9-C4-N3	4.49	134.94	125.95
86	1	1101	GDP	C6-C5-N7	3.42	136.51	130.29

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

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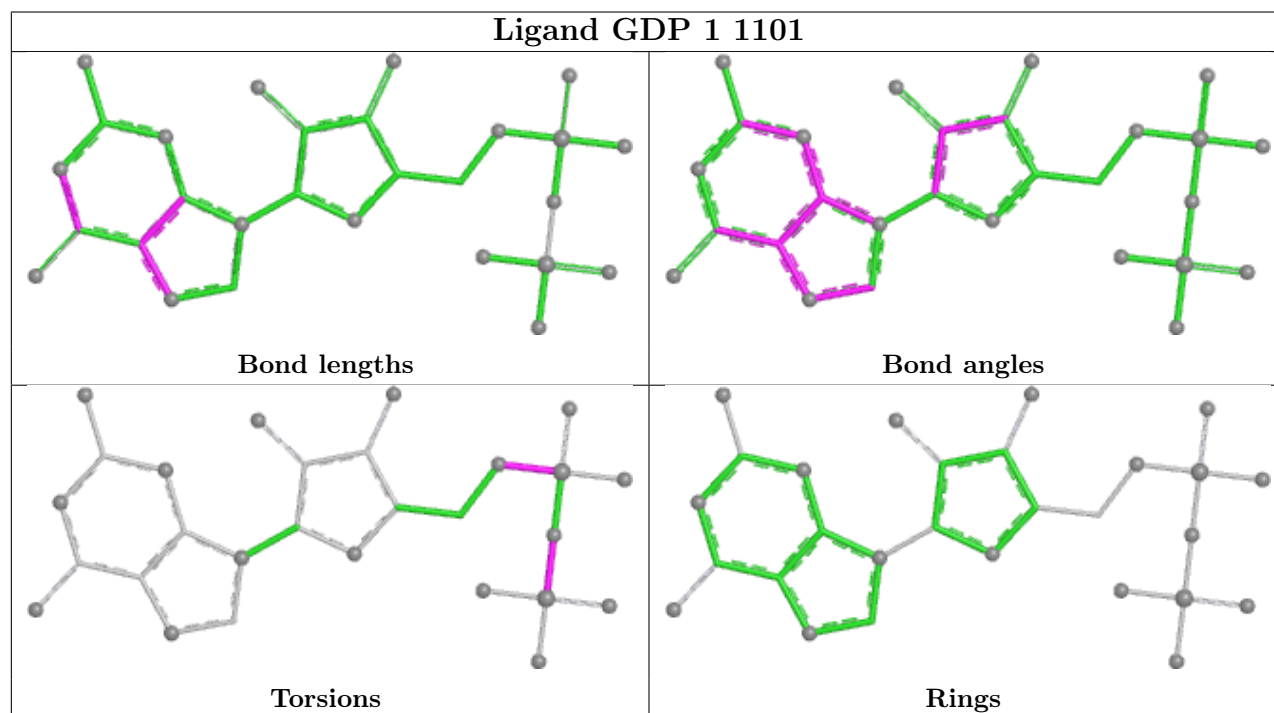
Continued from previous page...

Mol	Chain	Res	Type	Atoms
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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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

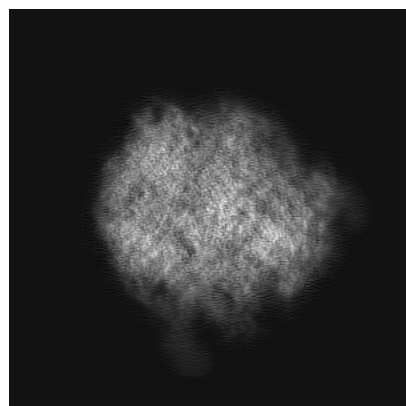
6 Map visualisation [i](#)

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.

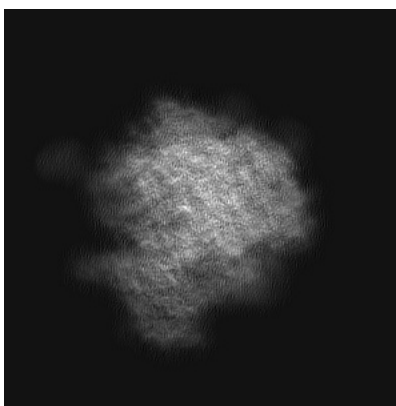
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

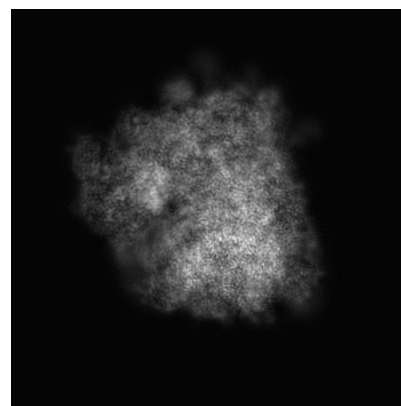
6.1.1 Primary map



X

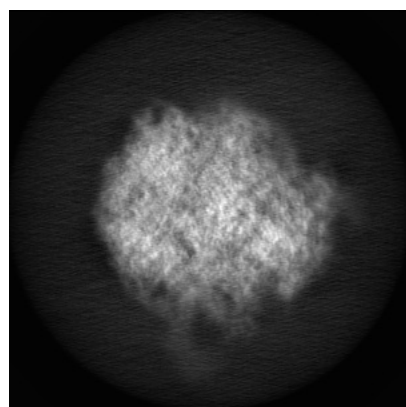


Y

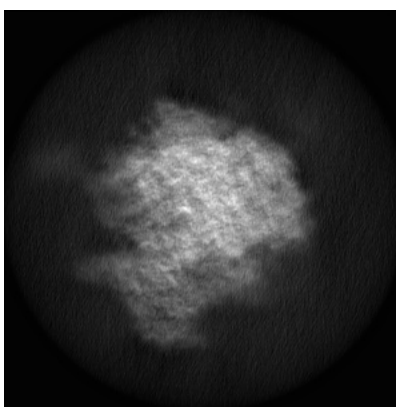


Z

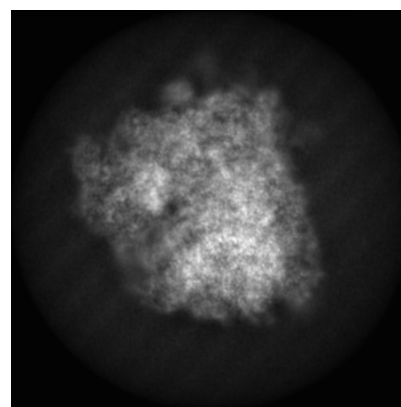
6.1.2 Raw map



X



Y

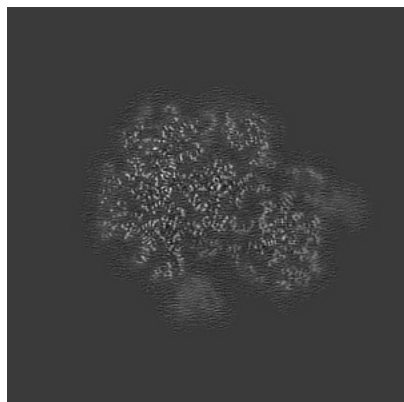


Z

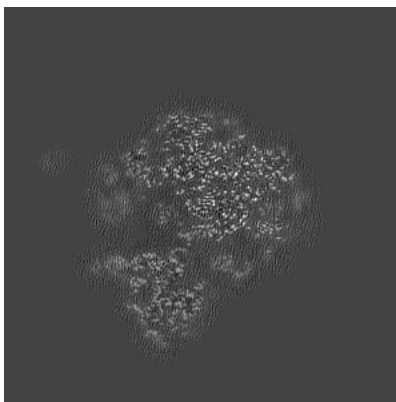
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

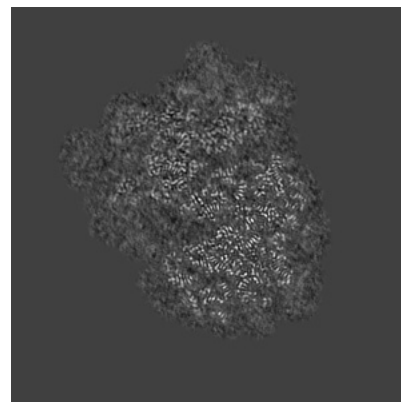
6.2.1 Primary map



X Index: 150

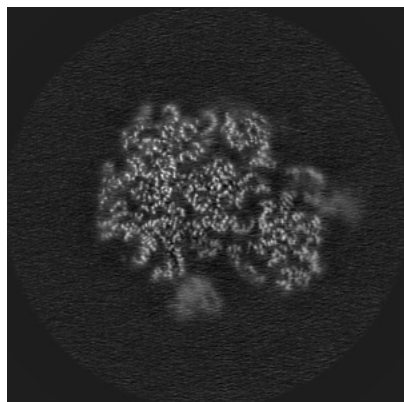


Y Index: 150

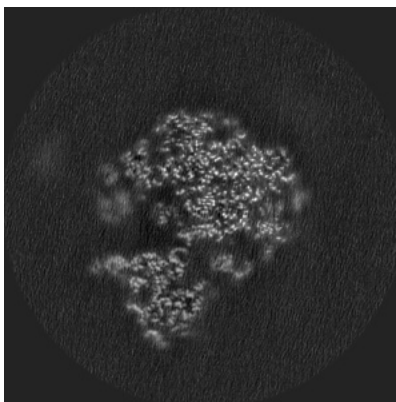


Z Index: 150

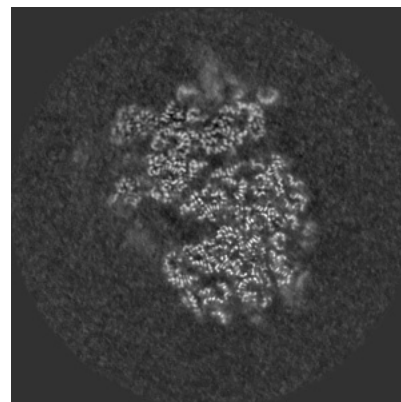
6.2.2 Raw map



X Index: 150



Y Index: 150

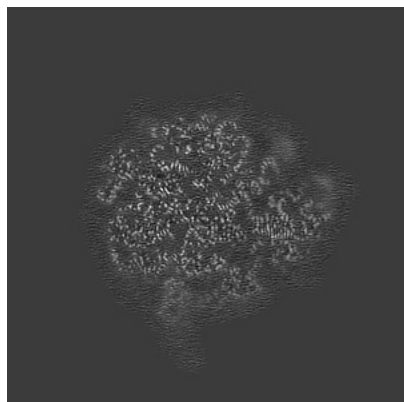


Z Index: 150

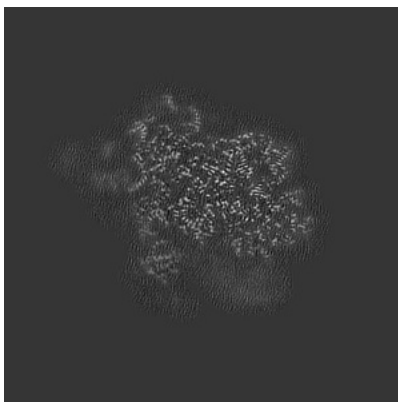
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

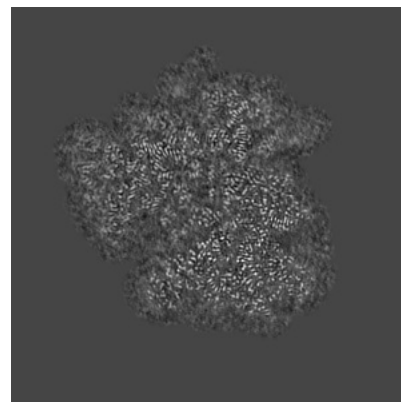
6.3.1 Primary map



X Index: 172

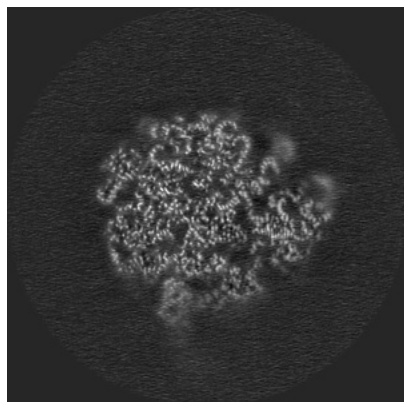


Y Index: 117

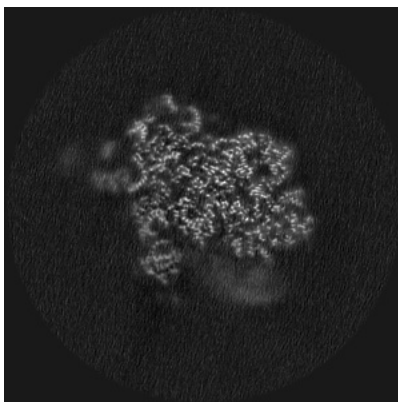


Z Index: 132

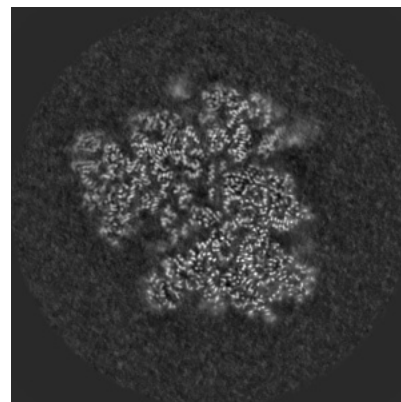
6.3.2 Raw map



X Index: 172



Y Index: 117

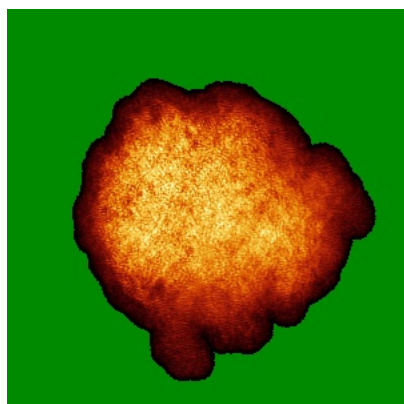


Z Index: 132

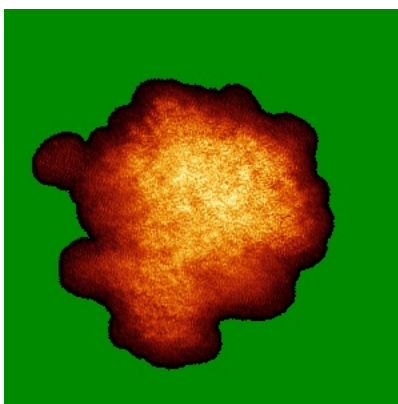
The images above show the largest variance slices of the map in three orthogonal directions.

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

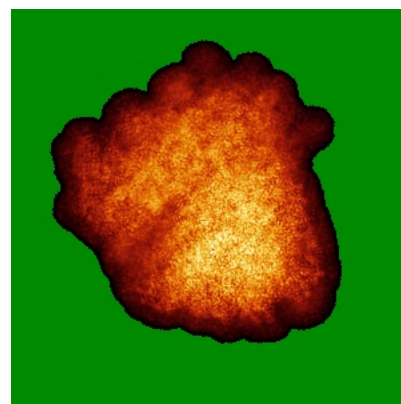
6.4.1 Primary map



X

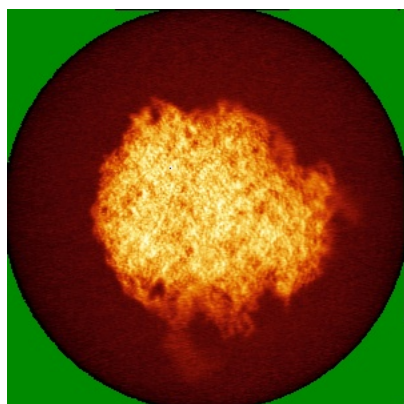


Y

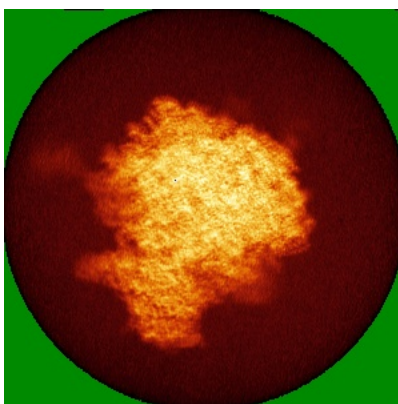


Z

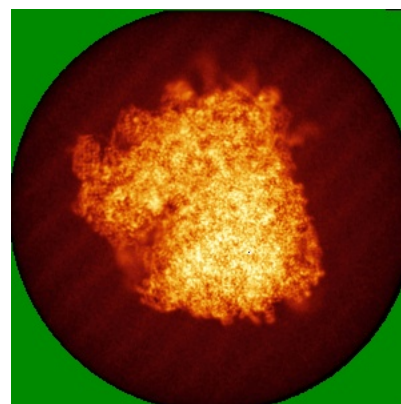
6.4.2 Raw map



X



Y

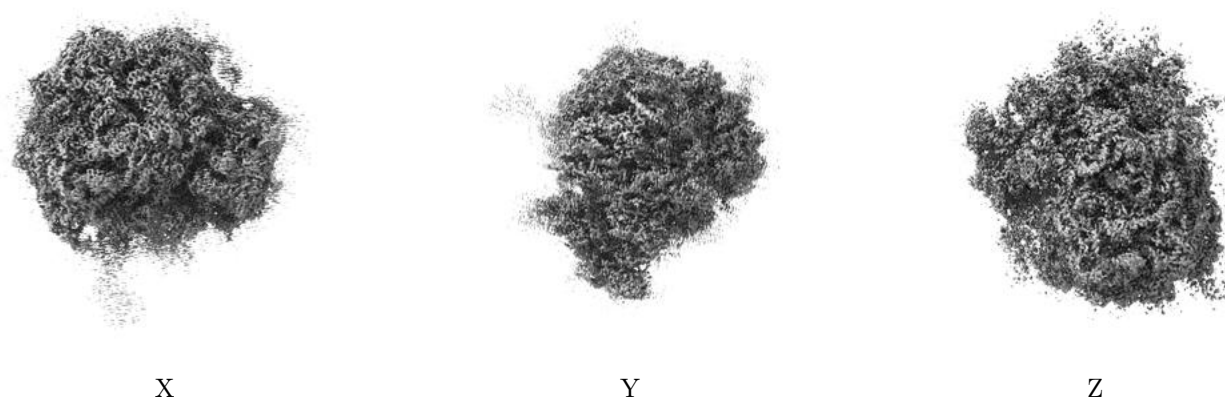


Z

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



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



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.

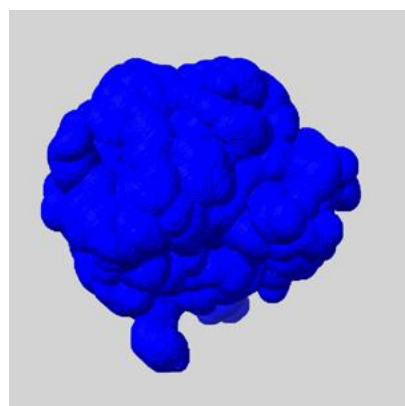
6.6 Mask visualisation [i](#)

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

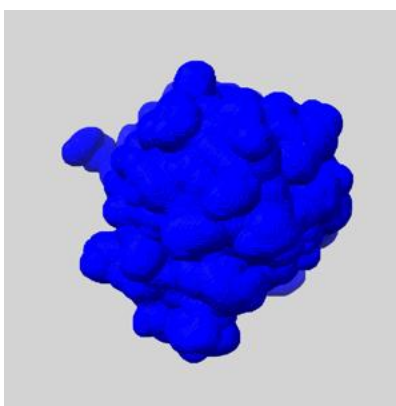
A mask typically either:

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

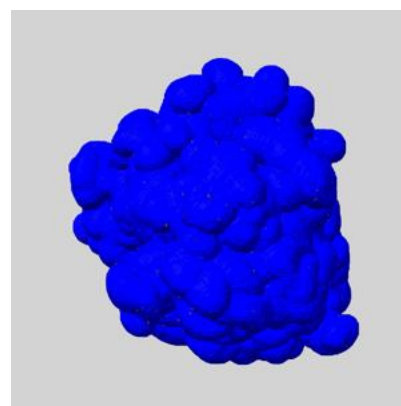
6.6.1 emd_21859_msk_1.map [i](#)



X



Y

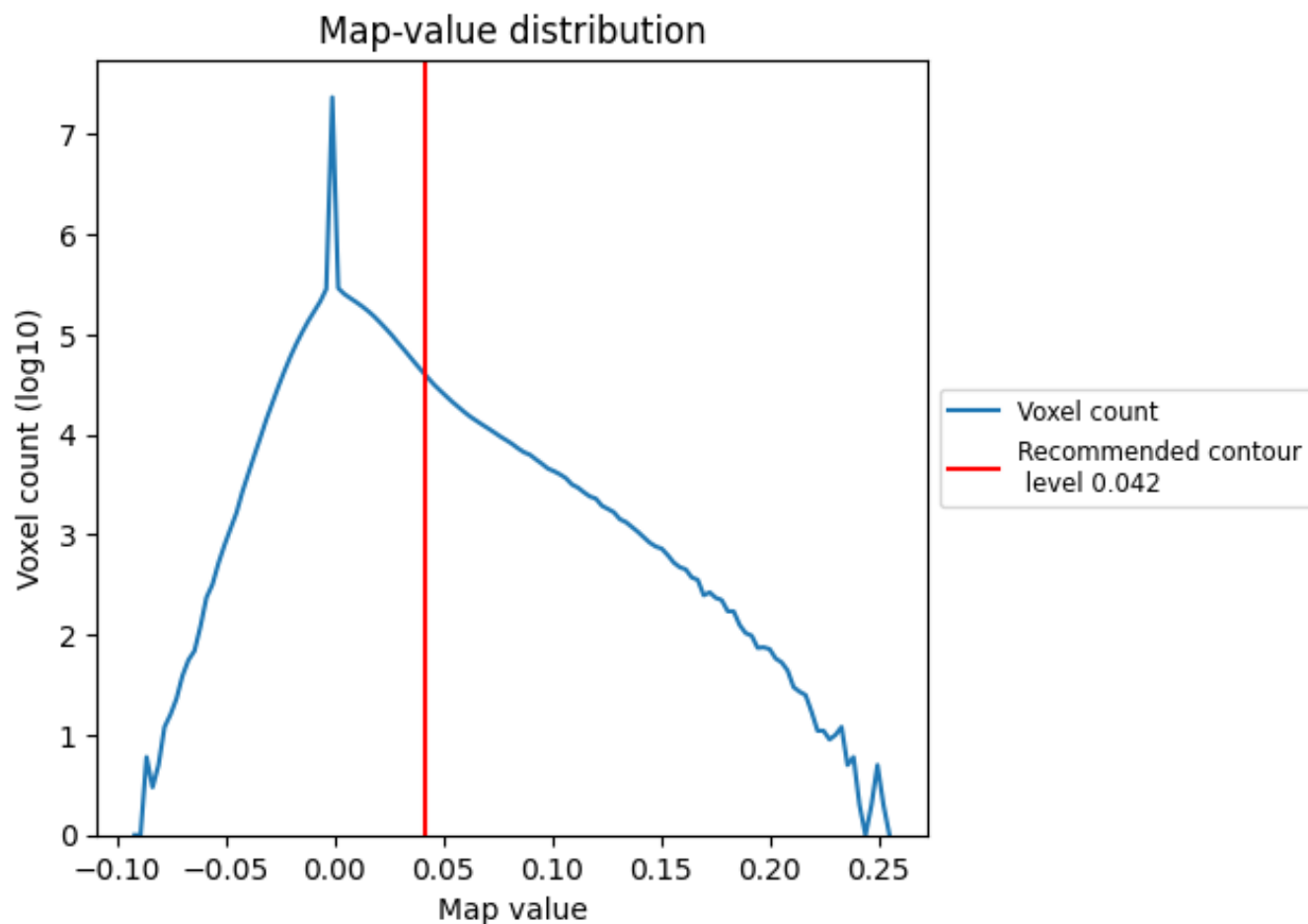


Z

7 Map analysis [i](#)

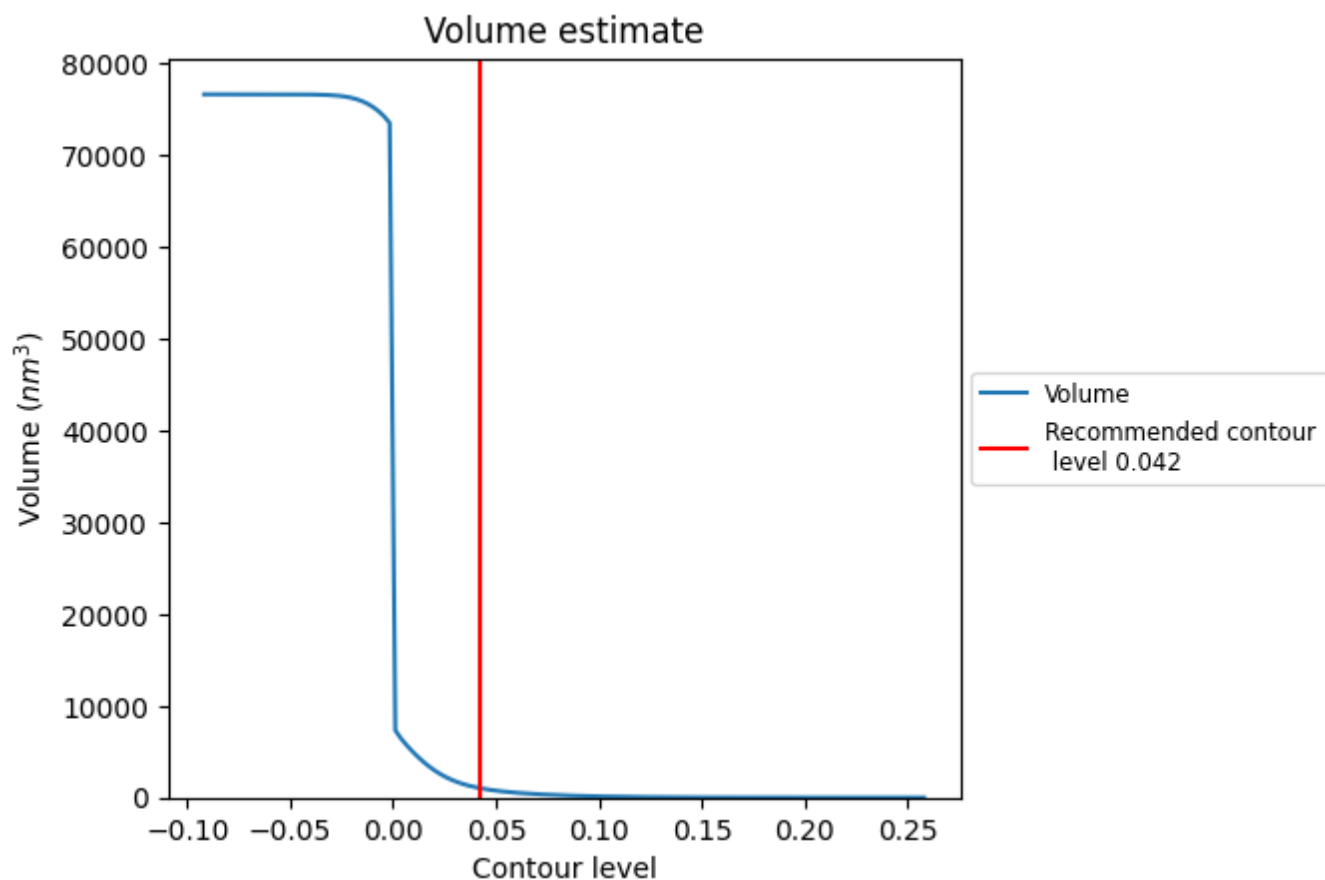
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

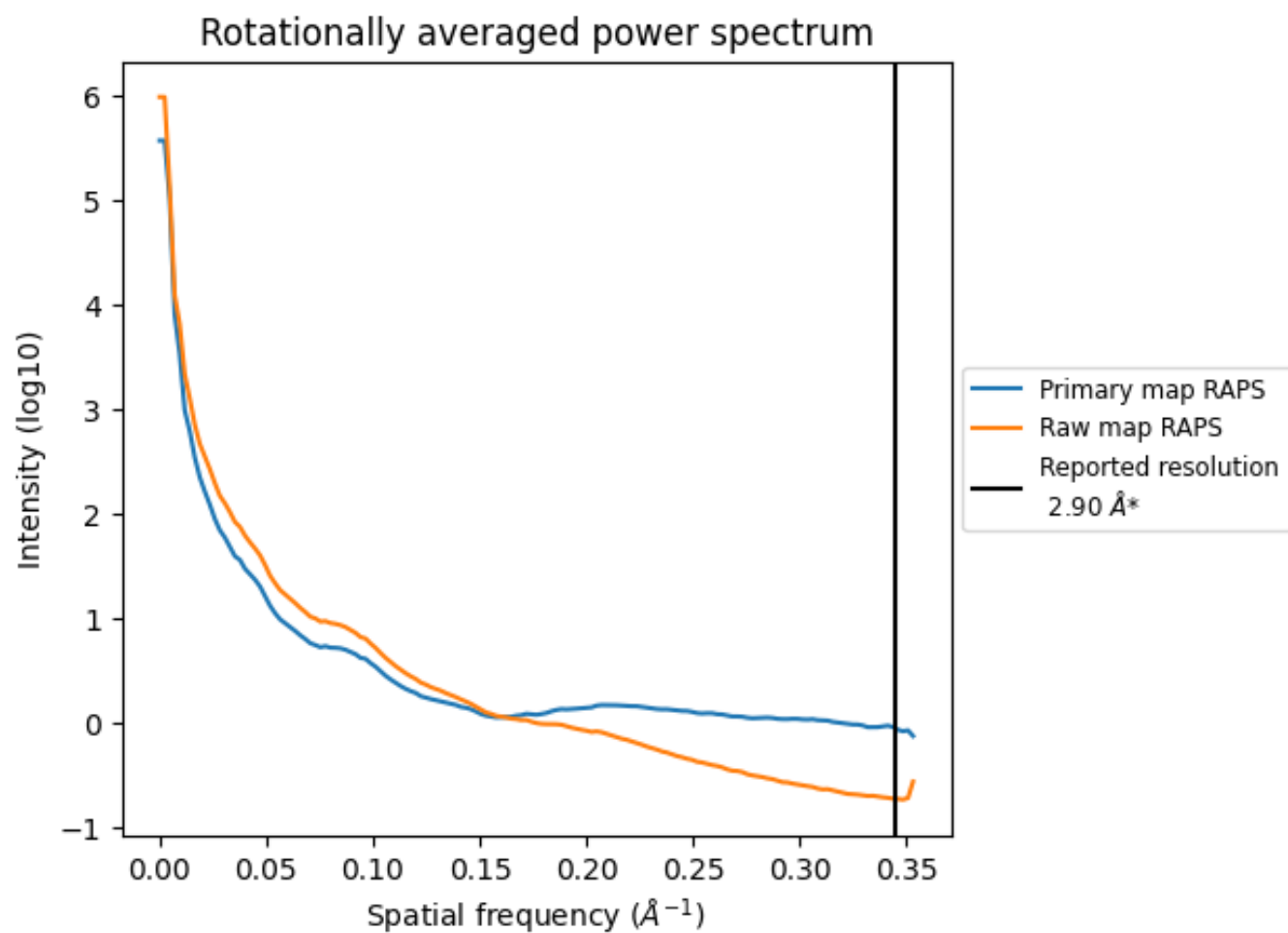
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1033 nm³; 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 ⓘ

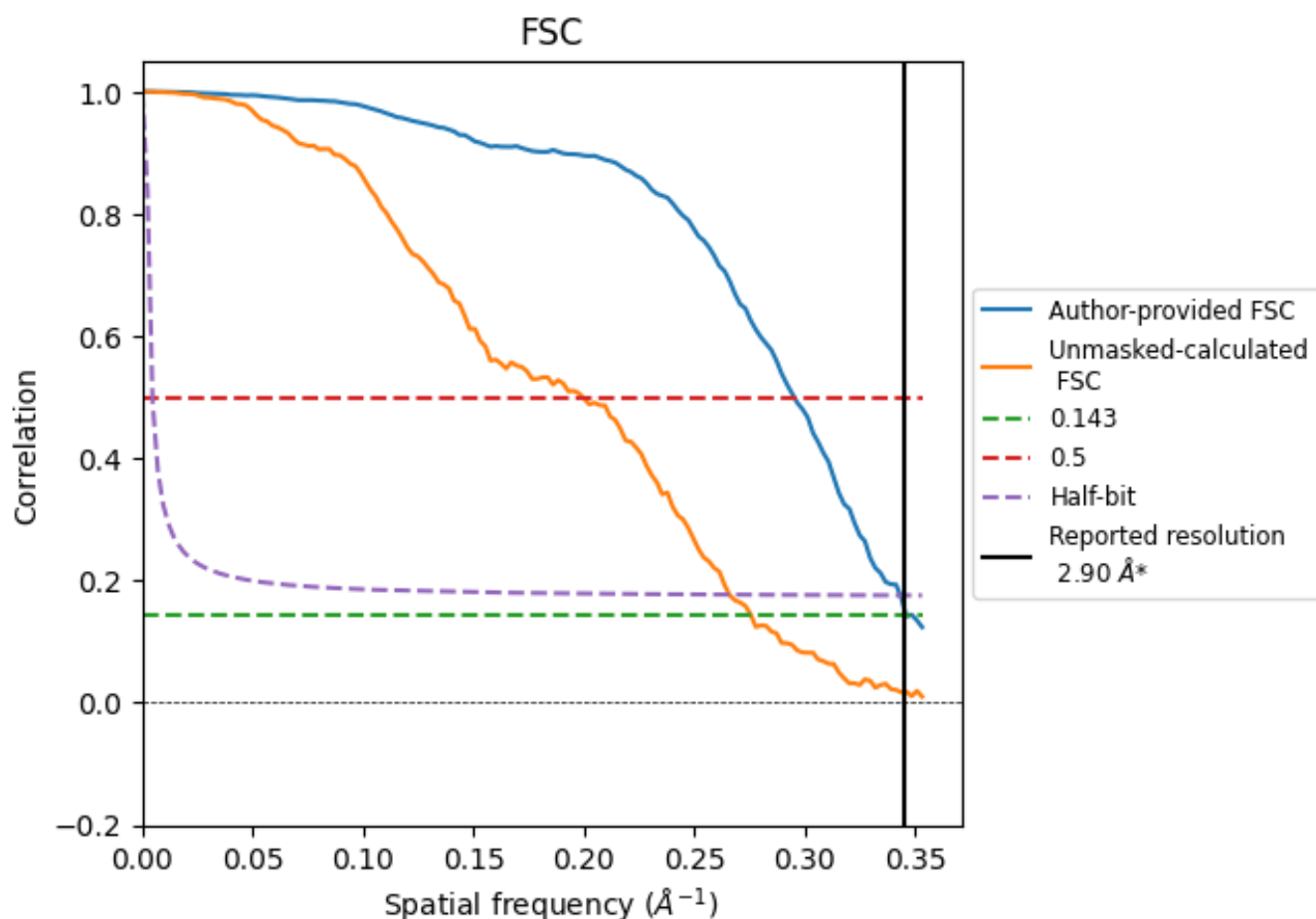


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

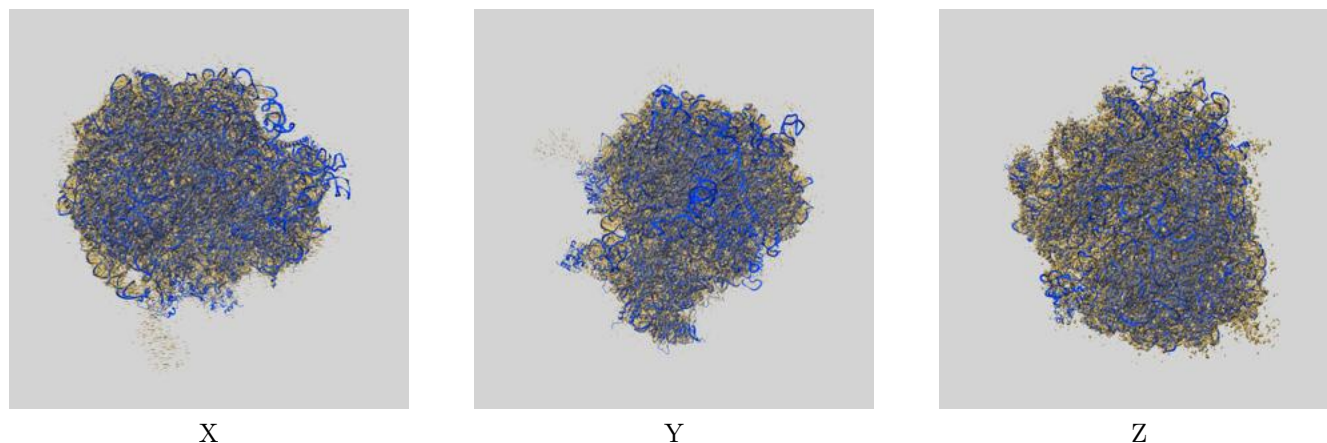
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.89	3.39	2.91
Unmasked-calculated*	3.63	5.02	3.76

*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 [i](#)

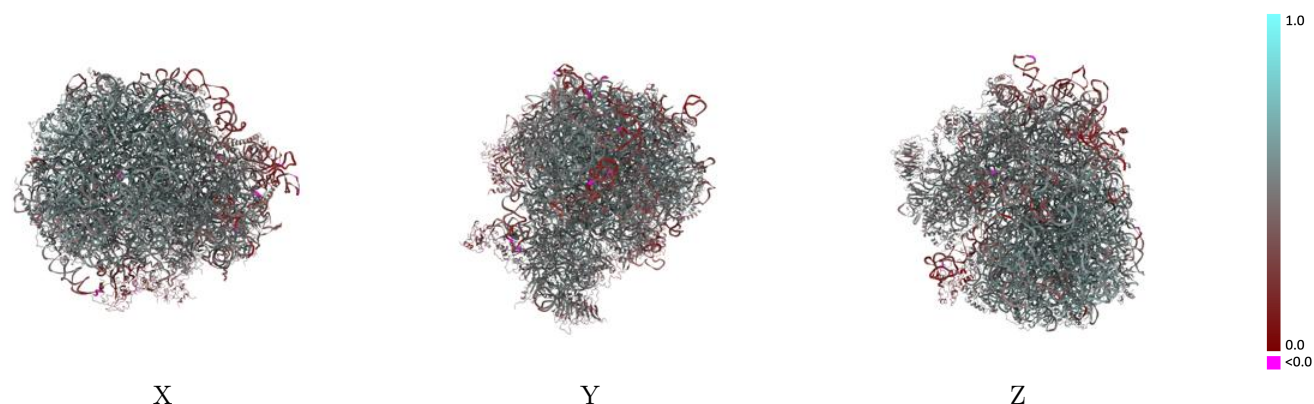
This section contains information regarding the fit between EMDB map EMD-21859 and PDB model 6WOO. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

9.1 Map-model overlay [i](#)



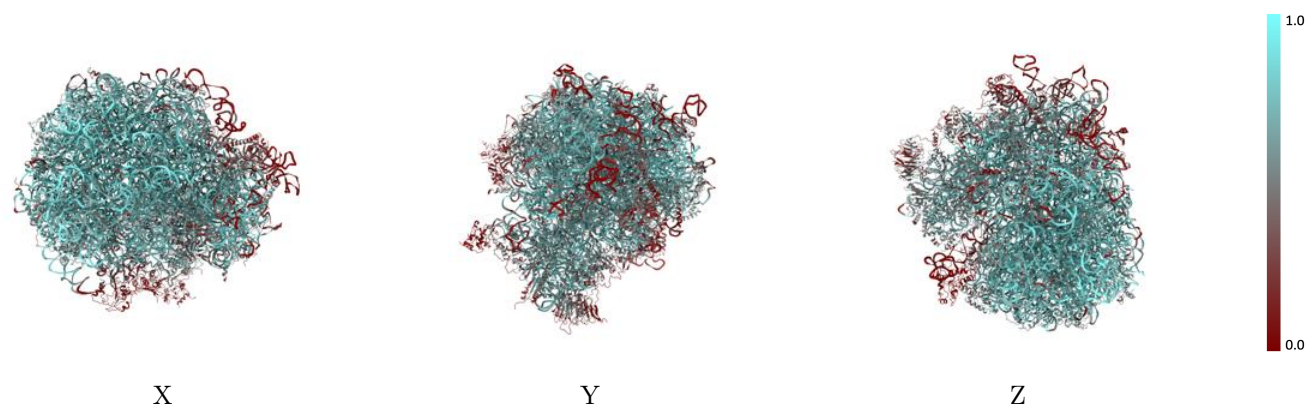
The images above show the 3D surface view of the map at the recommended contour level 0.042 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



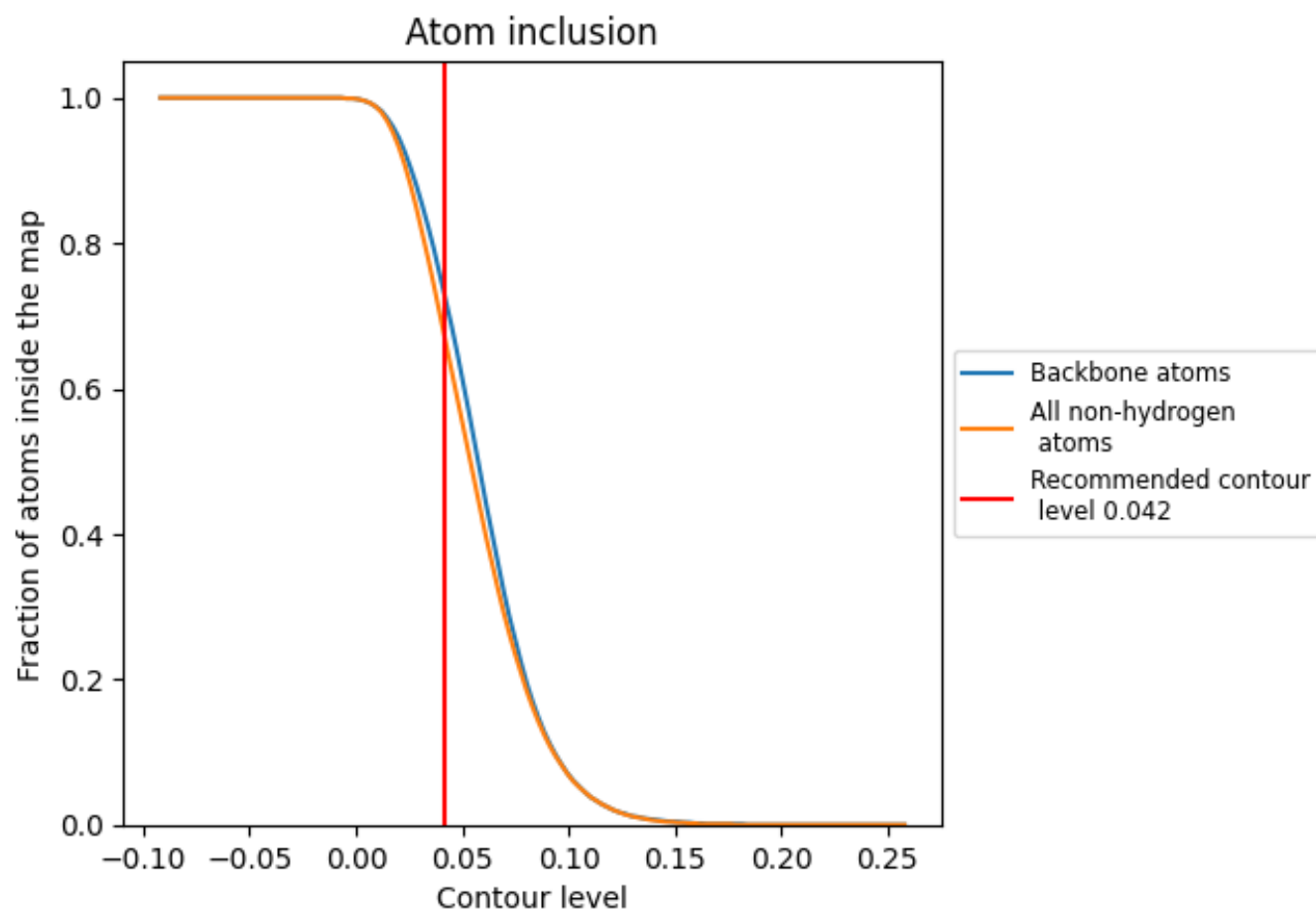
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



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

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 ⓘ

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