



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 11:38 PM UTC

PDB ID : 5M1J / pdb_00005m1j
EMDB ID : EMD-4140
Title : Nonstop ribosomal complex bound with Dom34 and Hbs1
Authors : Hilal, T.; Yamamoto, H.; Loerke, J.; Buerger, J.; Mielke, T.; Spahn, C.M.T.
Deposited on : 2016-10-07
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

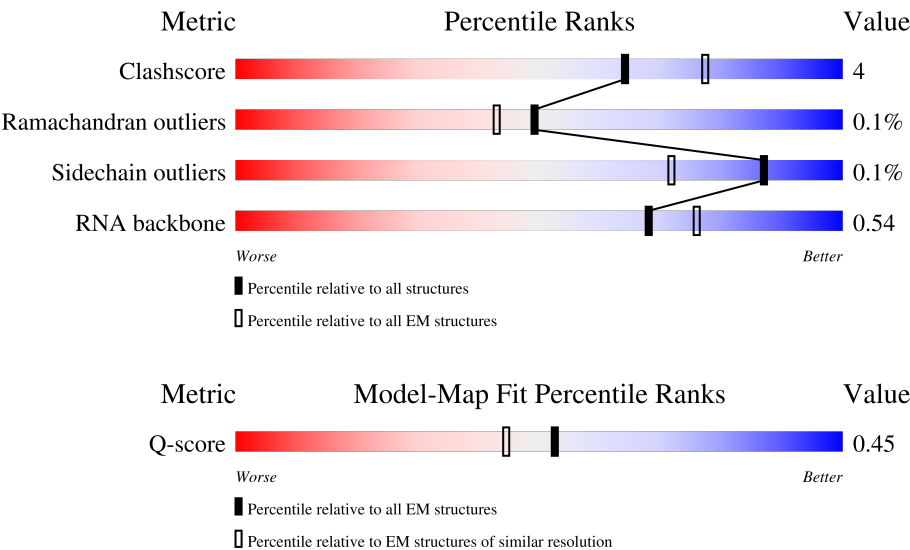
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

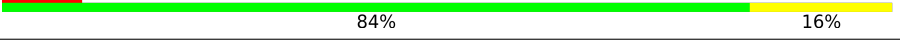
The reported resolution of this entry is 3.30 Å.

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	15087 (2.80 - 3.80)

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	A1	381	
2	A2	207	
3	a2	98	

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Mol	Chain	Length	Quality of chain
4	B2	214	
5	b2	81	
6	C2	217	
7	c2	63	
8	D2	223	
9	d2	53	
10	E2	260	
11	e2	60	
12	F2	206	
13	G2	226	
14	g2	318	
15	H2	184	
16	I2	199	
17	J2	185	
18	K2	96	
19	L2	155	
20	M2	124	
21	N2	150	
22	O2	127	
23	P2	124	
24	Q2	141	
25	R2	125	
26	S2	145	
27	T2	143	
28	U2	107	

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Mol	Chain	Length	Quality of chain
29	V2	87	
30	W2	129	
31	X2	144	
32	Y2	134	
33	Z2	70	
34	22	1798	
35	f2	71	
36	14	3396	
37	34	121	
38	44	158	
39	a5	148	
40	A5	252	
41	b5	58	
42	B5	386	
43	c5	97	
44	C5	361	
45	D5	296	
46	d5	109	
47	e5	127	
48	f5	106	
49	F5	222	
50	g5	112	
51	G5	233	
52	h5	119	
53	H5	191	

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Mol	Chain	Length	Quality of chain
54	i5	99	
55	I5	220	
56	J5	169	
57	j5	87	
58	k5	77	
59	l5	50	
60	L5	193	
61	m5	52	
62	M5	136	
63	N5	203	
64	o5	105	
65	p5	91	
66	P5	183	
67	Q5	185	
68	S5	172	
69	U5	100	
70	V5	136	
71	Z5	135	
72	K5	197	
73	n5	25	
74	R5	188	
75	X5	121	
76	Y5	126	
77	T5	159	
78	E5	175	

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Mol	Chain	Length	Quality of chain
79	W5	98	41% 94% 6%
80	A6	611	64% 74% 14% 12%
81	X7	20	25% 15% 30% 15% 40%
82	A3	76	50% 30% 17%

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 212865 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Protein DOM34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	381	Total	C	N	O	S	0	0
			3058	1976	478	589	15		

- Molecule 2 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A2	207	Total	C	N	O	S	0	0
			1621	1039	286	294	2		

- Molecule 3 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	a2	98	Total	C	N	O	S	0	0
			778	480	162	131	5		

- Molecule 4 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B2	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 5 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	b2	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 6 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C2	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 7 is a protein called 40S ribosomal protein S28-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	c2	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 8 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D2	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 9 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	d2	53	Total	C	N	O	S	0	0
			443	275	92	72	4		

- Molecule 10 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E2	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 11 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	e2	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 12 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F2	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 13 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G2	226	Total	C	N	O	S	0	0
			1820	1142	350	325	3		

- Molecule 14 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	g2	318	Total	C	N	O	S	0	0
			2445	1546	419	472	8		

- Molecule 15 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H2	184	Total	C	N	O	S	0	0
			1481	951	265	265			

- Molecule 16 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I2	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 17 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	J2	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 18 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	K2	96	Total	C	N	O	S	0	0
			817	529	133	153	2		

- Molecule 19 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L2	155	Total	C	N	O	S	0	0
			1244	798	235	208	3		

- Molecule 20 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M2	124	Total	C	N	O	S	0	0
			934	587	165	180	2		

- Molecule 21 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	N2	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 22 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	O2	127	Total	C	N	O	S	0	0
			941	578	186	174	3		

- Molecule 23 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	P2	124	Total	C	N	O	S	0	0
			991	631	187	166	7		

- Molecule 24 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Q2	141	Total	C	N	O		0	0
			1105	708	203	194			

- Molecule 25 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	R2	125	Total	C	N	O	S	0	0
			1000	625	188	185	2		

- Molecule 26 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	S2	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 27 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	T2	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 28 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	U2	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 29 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	V2	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 30 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	W2	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 31 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X2	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 32 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	Y2	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 33 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Z2	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 34 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	22	1781	Total	C	N	O	P	0	0
			37948	16965	6715	12487	1781		

- Molecule 35 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	f2	71	Total	C	N	O	S	0	0
			497	309	93	91	4		

- Molecule 36 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	14	3295	Total	C	N	O	P	0	0
			70476	31477	12696	23008	3295		

- Molecule 37 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	34	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 38 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	44	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 39 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	a5	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 40 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A5	252	Total	C	N	O	S	0	0
			1918	1193	389	335	1		

- Molecule 41 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	b5	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 42 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	B5	386	Total	C	N	O	S	0	0
			3081	1956	584	533	8		

- Molecule 43 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	c5	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 44 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	C5	361	Total	C	N	O	S	0	0
			2749	1730	522	494	3		

- Molecule 45 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	D5	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 46 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	d5	109	Total	C	N	O	S	0	0
			890	565	168	156	1		

- Molecule 47 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	e5	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 48 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	f5	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 49 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	F5	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 50 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	g5	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 51 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	G5	233	Total	C	N	O	S	0	0
			1817	1159	326	329	3		

- Molecule 52 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	h5	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 53 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	H5	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 54 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	i5	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 55 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	I5	211	Total	C	N	O	S	0	0
			1717	1089	325	297	6		

- Molecule 56 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	J5	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 57 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	j5	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 58 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	k5	77	Total	C	N	O		0	0
			612	391	115	106			

- Molecule 59 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	l5	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 60 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	L5	193	Total	C	N	O		0	0
			1543	962	315	266			

- Molecule 61 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	m5	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 62 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	M5	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 63 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	N5	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 64 is a protein called 60S ribosomal protein L42-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	o5	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 65 is a protein called 60S ribosomal protein L43-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	p5	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 66 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	P5	183	Total	C	N	O	S	0	0
			1442	896	287	259			

- Molecule 67 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Q5	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 68 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	S5	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 69 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	U5	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 70 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	V5	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 71 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Z5	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 72 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	K5	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 73 is a protein called 60S ribosomal protein L41-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	n5	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 74 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	R5	188	Total	C	N	O		0	0
			1521	935	326	260			

- Molecule 75 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	X5	121	Total	C	N	O	S	0	0
			968	623	170	173	2		

- Molecule 76 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Y5	126	Total	C	N	O		0	0
			993	625	192	176			

- Molecule 77 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	T5	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 78 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	E5	157	Total	C	N	O	S	0	0
			1248	806	224	217	1		

- Molecule 79 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	W5	98	Total	C	N	O	S	0	0
			800	508	159	132	1		

- Molecule 80 is a protein called Protein HBS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	A6	539	Total	C	N	O	S	0	0
			4279	2712	723	827	17		

- Molecule 81 is a RNA chain called nonstop mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	X7	12	Total	C	N	O	P	0	0
			259	116	49	82	12		

- Molecule 82 is a RNA chain called yeast Phe-tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	A3	76	Total	C	N	O	P	0	0
			1651	745	294	536	76		

- Molecule 83 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
83	a2	1	Total	Zn	0
			1	1	
83	b2	1	Total	Zn	0
			1	1	
83	d2	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
83	f2	1	Total 1	Zn 1	0
83	j5	1	Total 1	Zn 1	0
83	m5	1	Total 1	Zn 1	0
83	o5	1	Total 1	Zn 1	0
83	p5	1	Total 1	Zn 1	0

- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
84	B2	1	Total 1	Mg 1	0
84	C2	2	Total 2	Mg 2	0
84	d2	1	Total 1	Mg 1	0
84	E2	2	Total 2	Mg 2	0
84	F2	2	Total 2	Mg 2	0
84	I2	2	Total 2	Mg 2	0
84	J2	1	Total 1	Mg 1	0
84	L2	1	Total 1	Mg 1	0
84	N2	2	Total 2	Mg 2	0
84	Q2	1	Total 1	Mg 1	0
84	S2	4	Total 4	Mg 4	0
84	T2	1	Total 1	Mg 1	0
84	U2	1	Total 1	Mg 1	0
84	X2	3	Total 3	Mg 3	0

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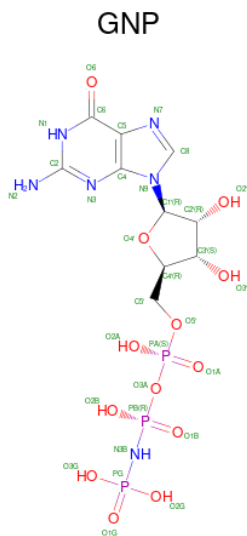
Mol	Chain	Residues	Atoms		AltConf
84	Y2	1	Total 1	Mg 1	0
84	22	177	Total 177	Mg 177	0
84	14	701	Total 701	Mg 701	0
84	34	16	Total 16	Mg 16	0
84	44	34	Total 34	Mg 34	0
84	a5	3	Total 3	Mg 3	0
84	A5	6	Total 6	Mg 6	0
84	b5	1	Total 1	Mg 1	0
84	B5	5	Total 5	Mg 5	0
84	C5	8	Total 8	Mg 8	0
84	D5	1	Total 1	Mg 1	0
84	d5	3	Total 3	Mg 3	0
84	e5	3	Total 3	Mg 3	0
84	f5	1	Total 1	Mg 1	0
84	F5	4	Total 4	Mg 4	0
84	I5	4	Total 4	Mg 4	0
84	J5	2	Total 2	Mg 2	0
84	j5	7	Total 7	Mg 7	0
84	l5	1	Total 1	Mg 1	0
84	L5	4	Total 4	Mg 4	0
84	m5	3	Total 3	Mg 3	0

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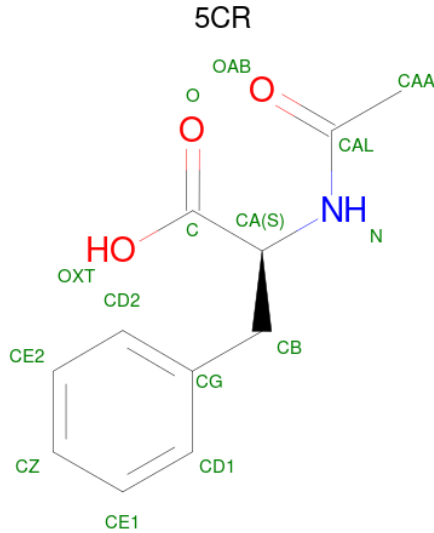
Mol	Chain	Residues	Atoms		AltConf
84	M5	1	Total 1	Mg 1	0
84	N5	7	Total 7	Mg 7	0
84	o5	3	Total 3	Mg 3	0
84	P5	7	Total 7	Mg 7	0
84	Q5	4	Total 4	Mg 4	0
84	S5	4	Total 4	Mg 4	0
84	V5	3	Total 3	Mg 3	0
84	K5	5	Total 5	Mg 5	0
84	R5	3	Total 3	Mg 3	0
84	Y5	2	Total 2	Mg 2	0
84	T5	1	Total 1	Mg 1	0
84	E5	1	Total 1	Mg 1	0
84	A6	2	Total 2	Mg 2	0
84	A3	6	Total 6	Mg 6	0

- Molecule 85 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
85	A6	1	Total	C	N	O	P	0
			32	10	6	13	3	

- Molecule 86 is N-acetyl-L-phenylalanine (CCD ID: 5CR) (formula: $C_{11}H_{13}NO_3$).



Mol	Chain	Residues	Atoms				AltConf
86	A3	1	Total	C	N	O	0
			14	11	1	2	

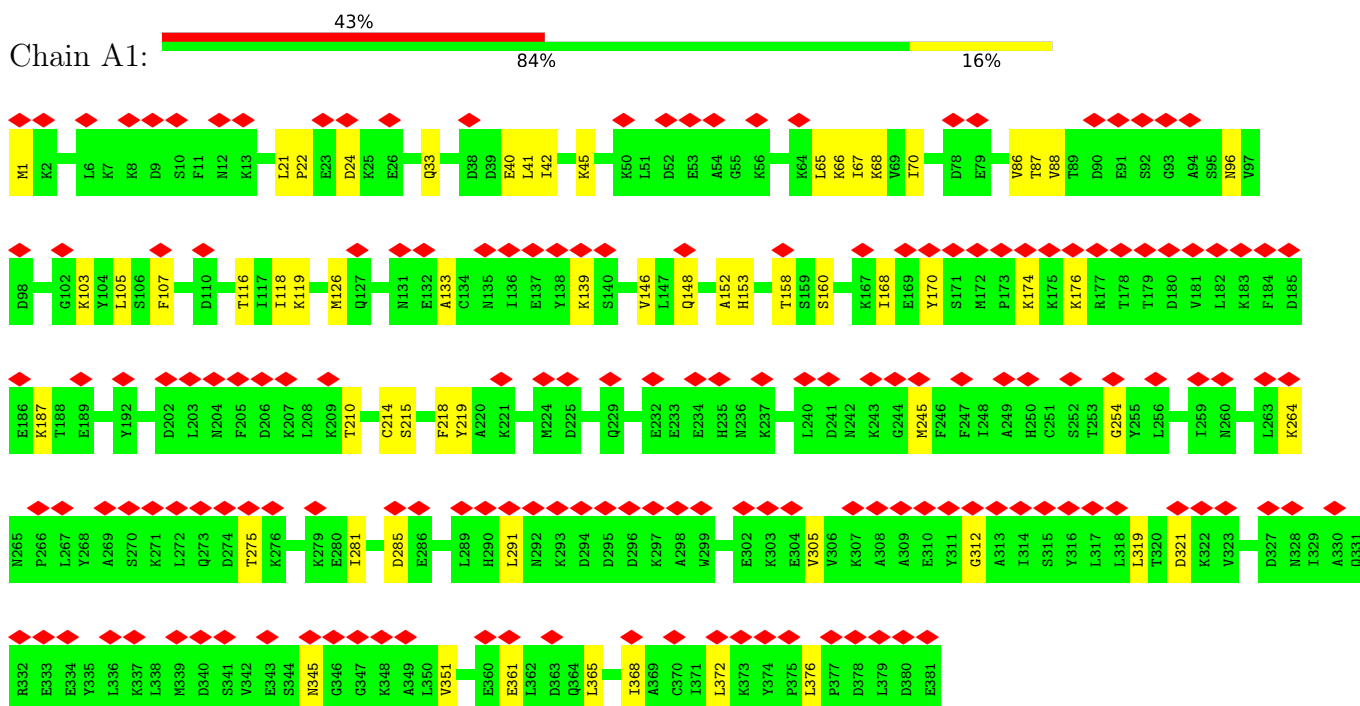
- Molecule 87 is water.

Mol	Chain	Residues	Atoms		AltConf
87	A1	7	Total 7	O 7	0
87	A6	6	Total 6	O 6	0

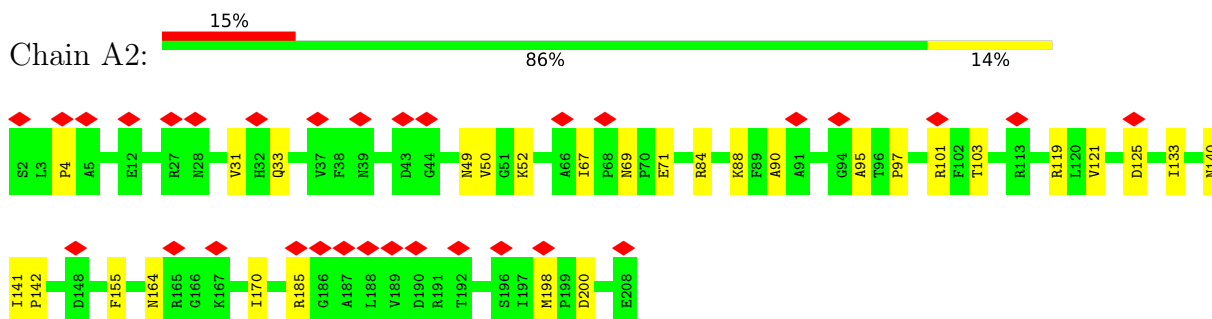
3 Residue-property plots

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.

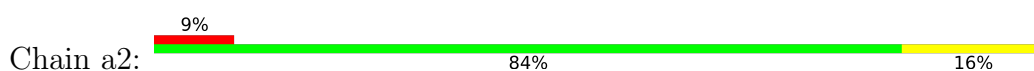
• Molecule 1: Protein DOM34

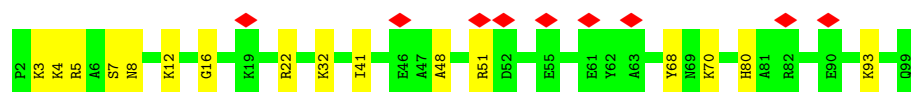


• Molecule 2: 40S ribosomal protein S0-A

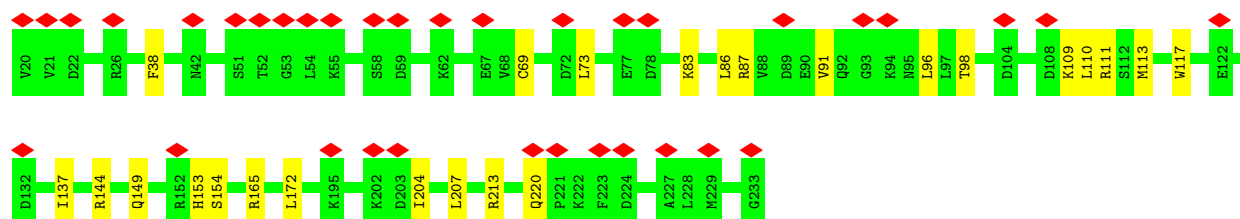
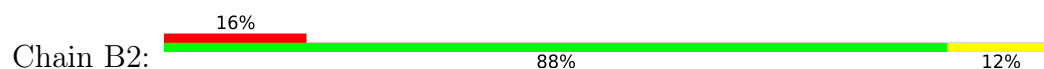


• Molecule 3: 40S ribosomal protein S26-B

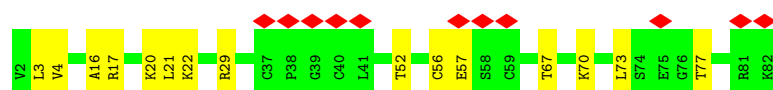
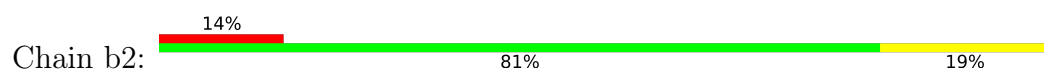




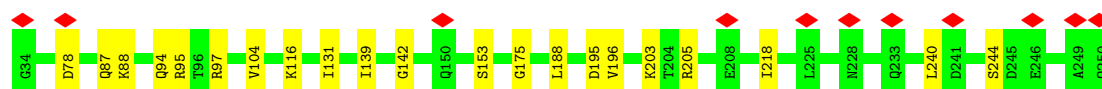
- Molecule 4: 40S ribosomal protein S1-A



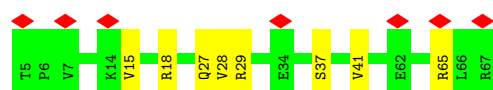
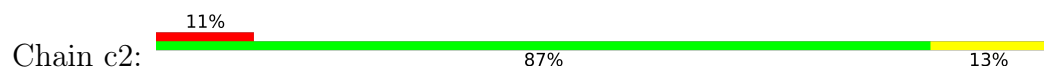
- Molecule 5: 40S ribosomal protein S27-A



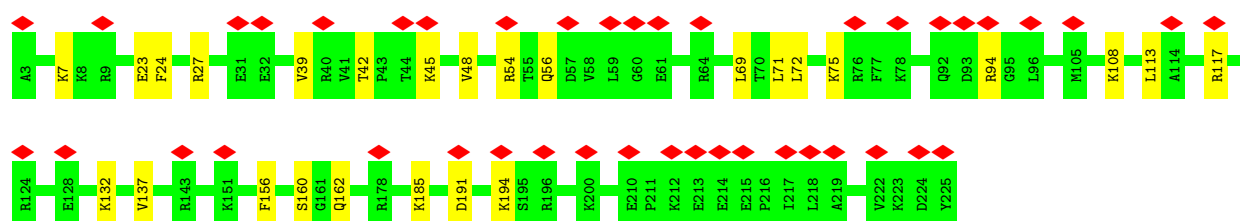
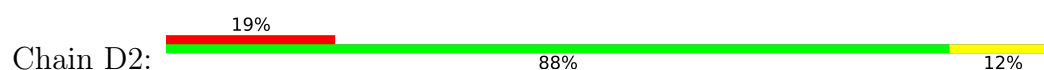
- Molecule 6: 40S ribosomal protein S2



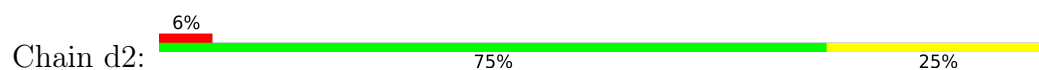
- Molecule 7: 40S ribosomal protein S28-B



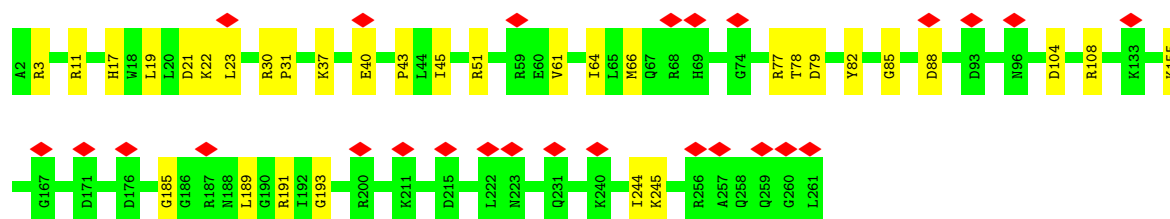
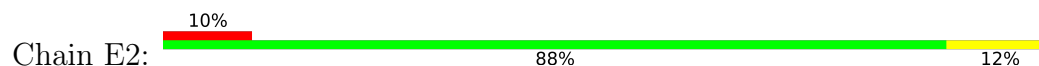
- Molecule 8: 40S ribosomal protein S3



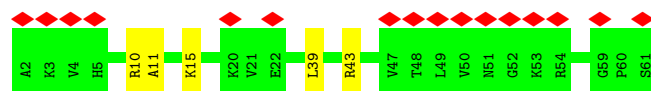
- Molecule 9: 40S ribosomal protein S29-A



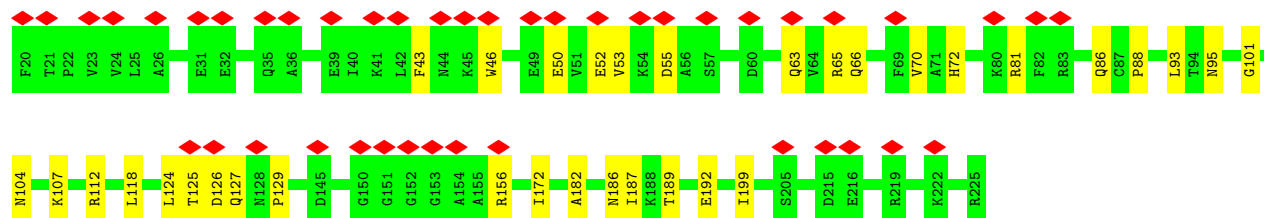
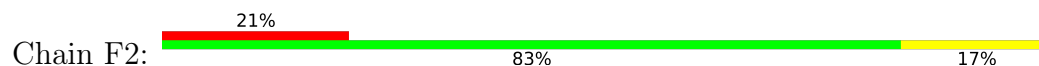
- Molecule 10: 40S ribosomal protein S4-A



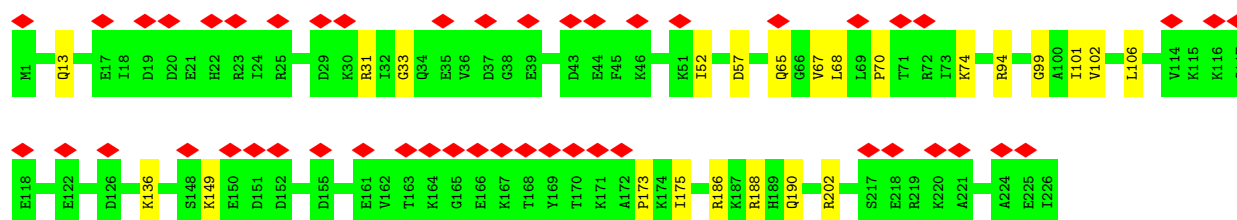
- Molecule 11: 40S ribosomal protein S30-A



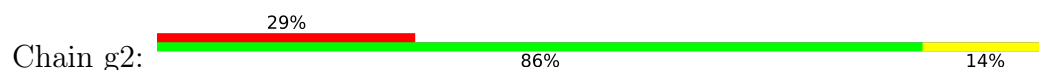
- Molecule 12: 40S ribosomal protein S5

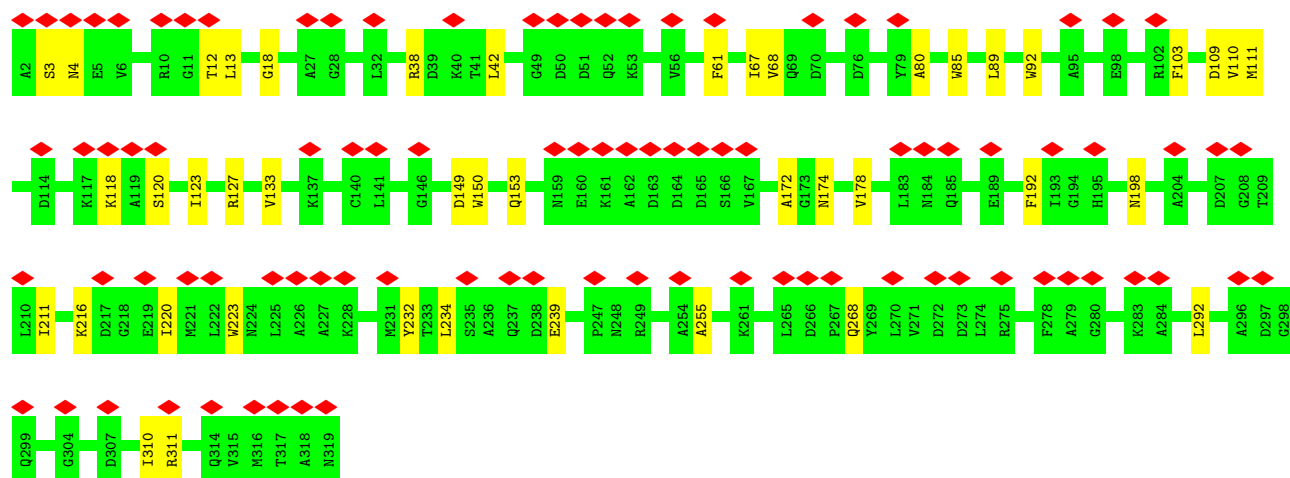


- Molecule 13: 40S ribosomal protein S6-A

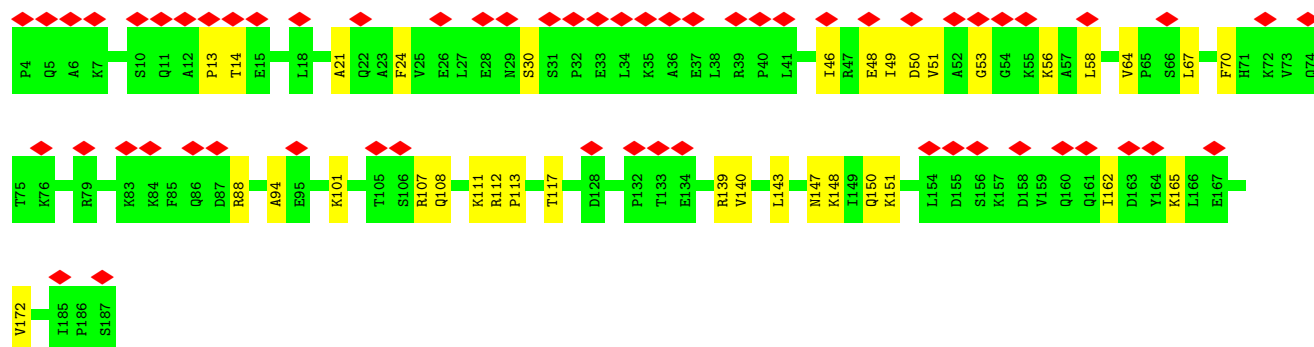
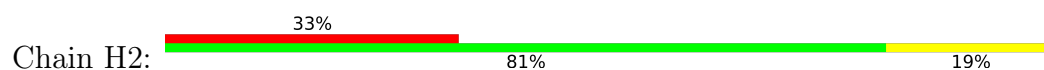


- Molecule 14: Guanine nucleotide-binding protein subunit beta-like protein

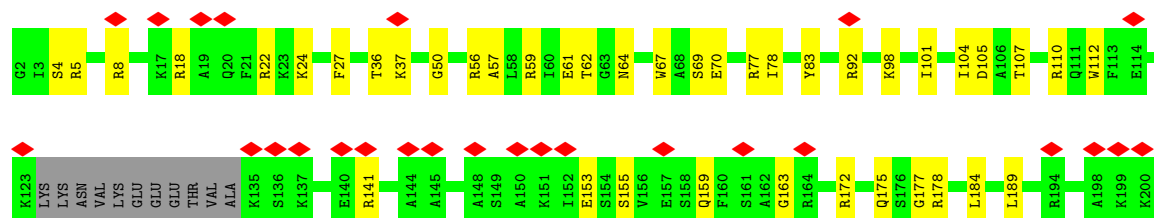
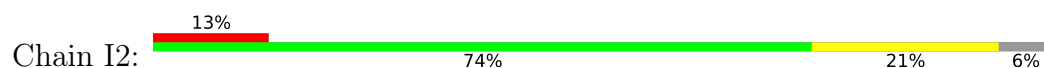




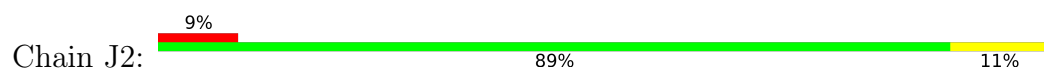
- Molecule 15: 40S ribosomal protein S7-A



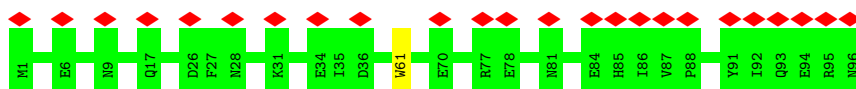
- Molecule 16: 40S ribosomal protein S8-A



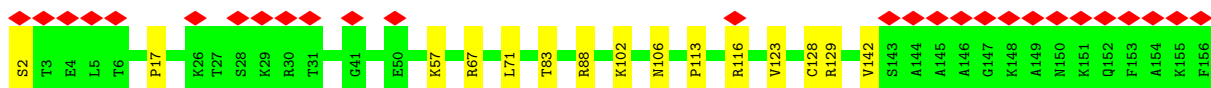
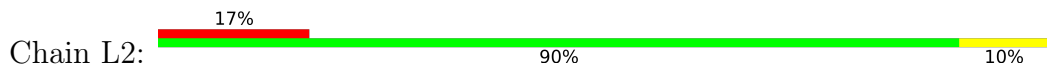
- Molecule 17: 40S ribosomal protein S9-A



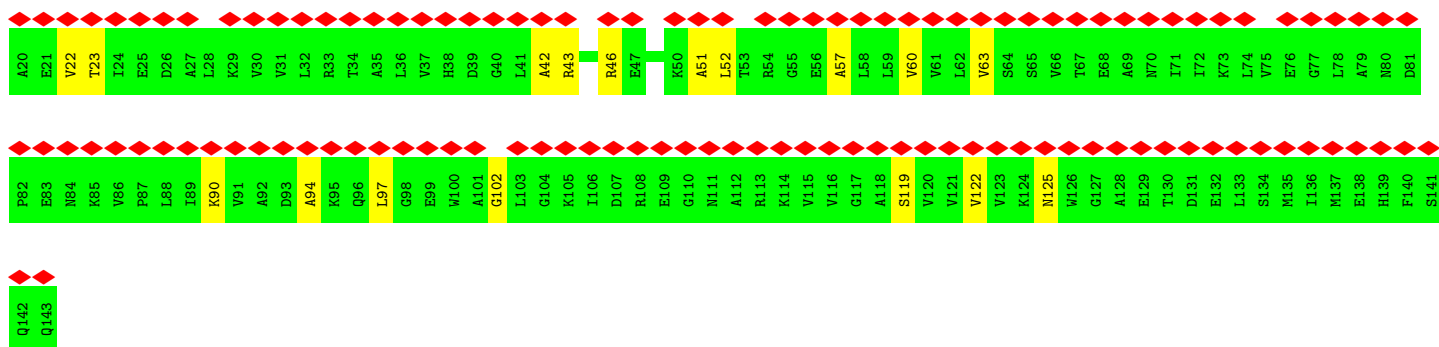
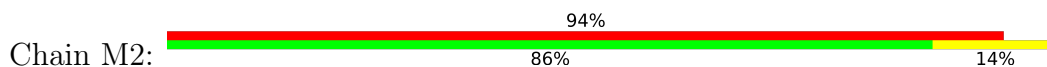
- Molecule 18: 40S ribosomal protein S10-A



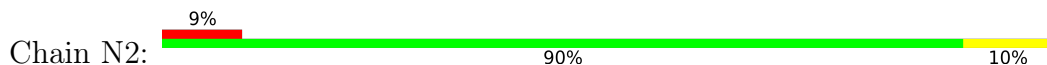
• Molecule 19: 40S ribosomal protein S11-A



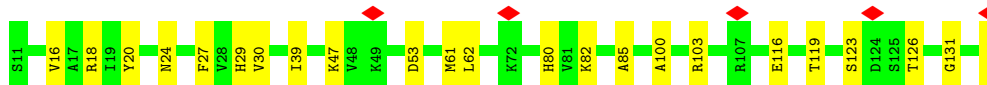
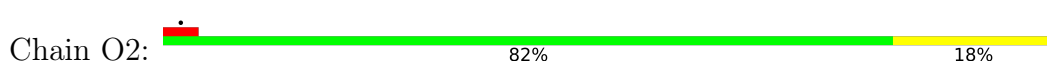
• Molecule 20: 40S ribosomal protein S12



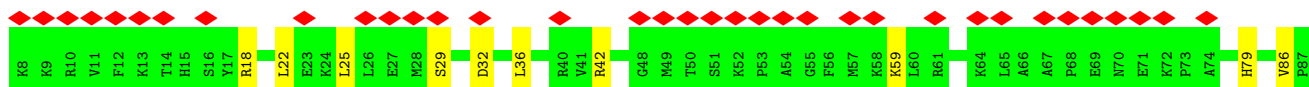
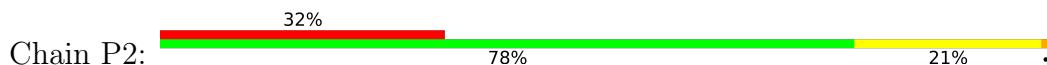
• Molecule 21: 40S ribosomal protein S13



• Molecule 22: 40S ribosomal protein S14-A

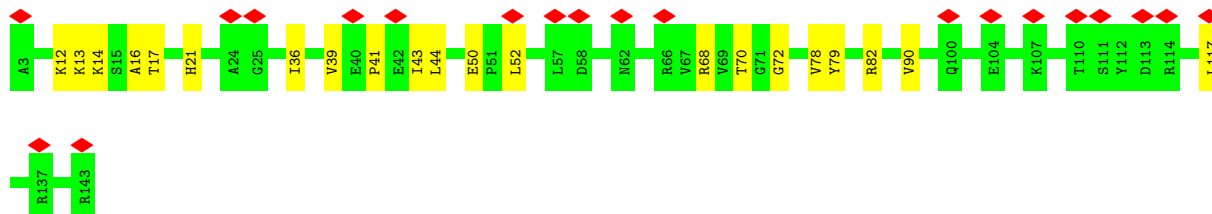
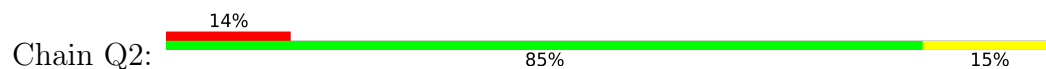


• Molecule 23: 40S ribosomal protein S15

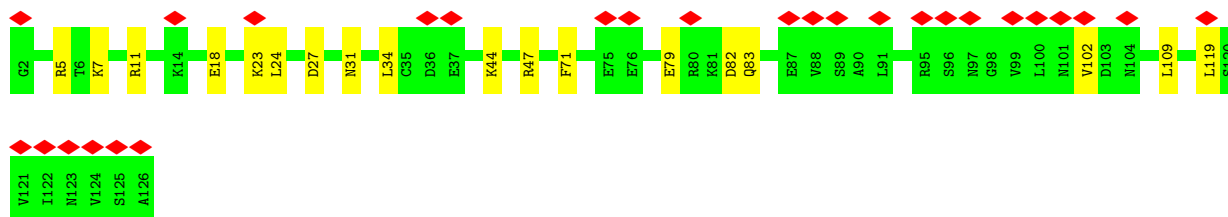
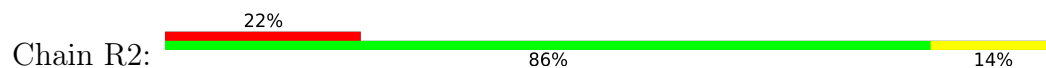




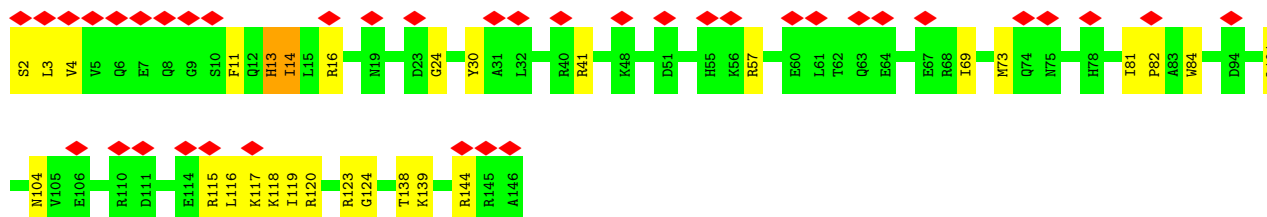
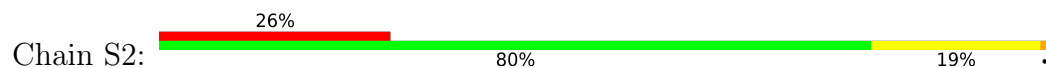
- Molecule 24: 40S ribosomal protein S16-A



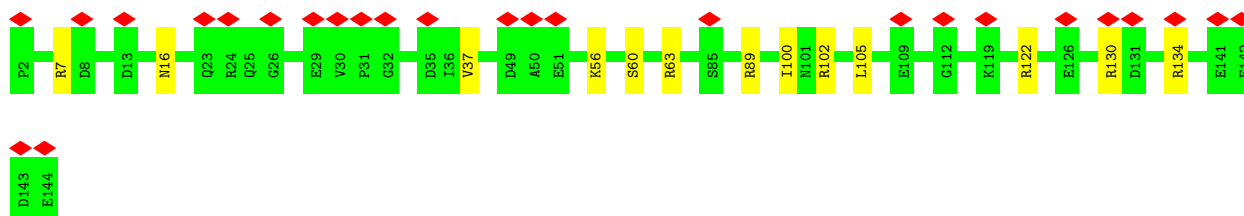
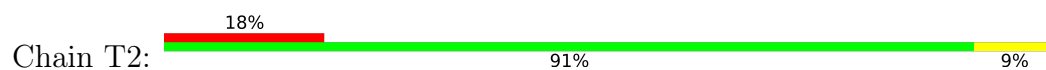
- Molecule 25: 40S ribosomal protein S17-B



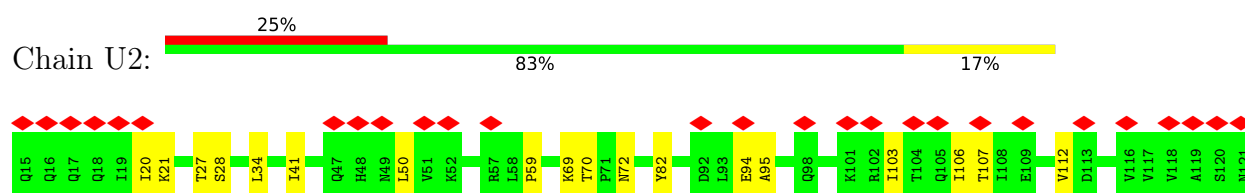
- Molecule 26: 40S ribosomal protein S18-A



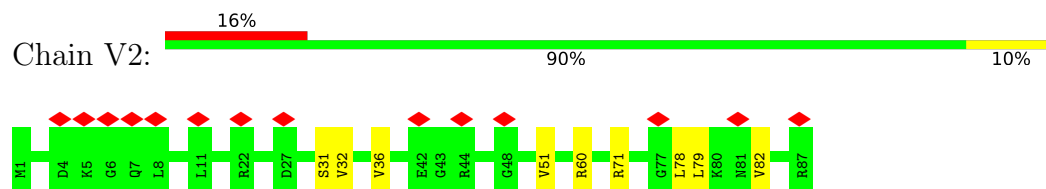
- Molecule 27: 40S ribosomal protein S19-A



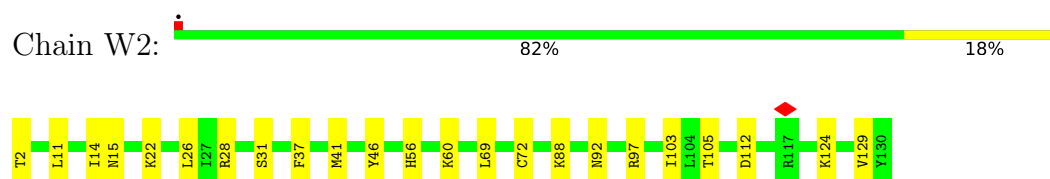
- Molecule 28: 40S ribosomal protein S20



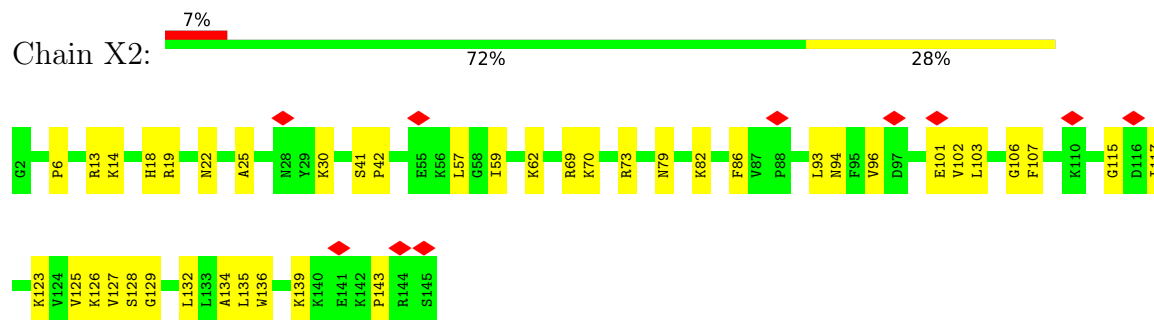
- Molecule 29: 40S ribosomal protein S21-A



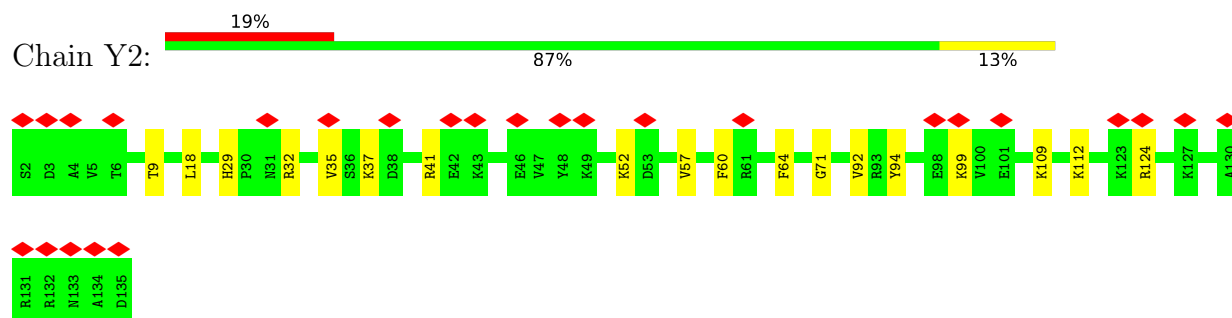
- Molecule 30: 40S ribosomal protein S22-A



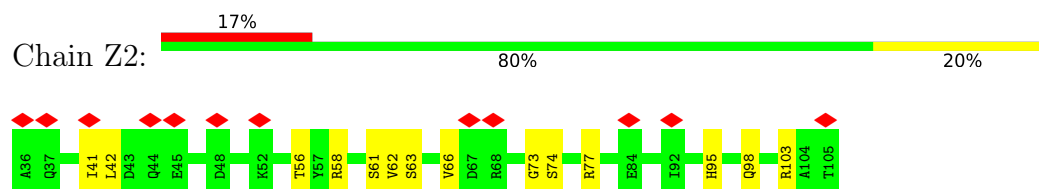
- Molecule 31: 40S ribosomal protein S23-A



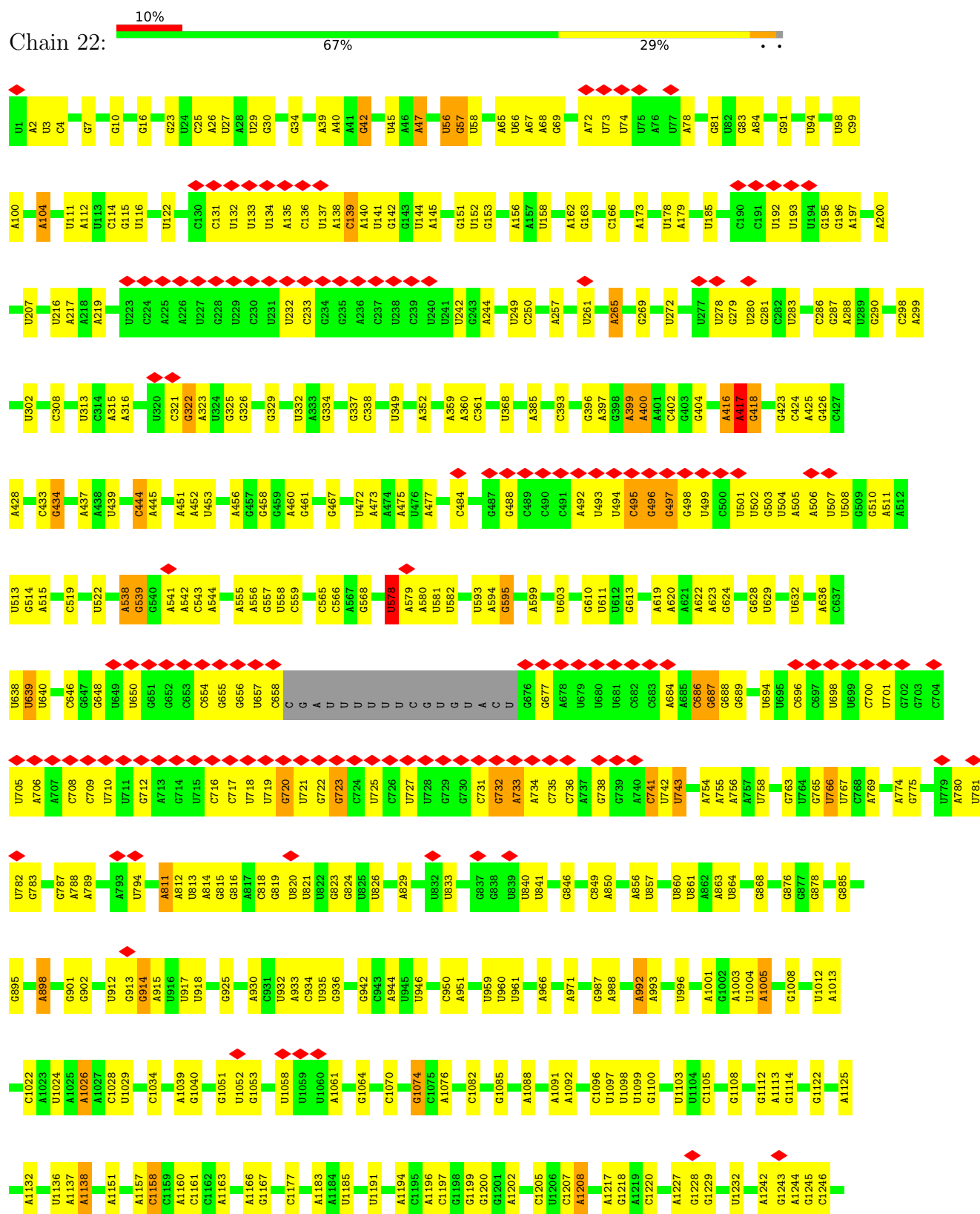
- Molecule 32: 40S ribosomal protein S24-A

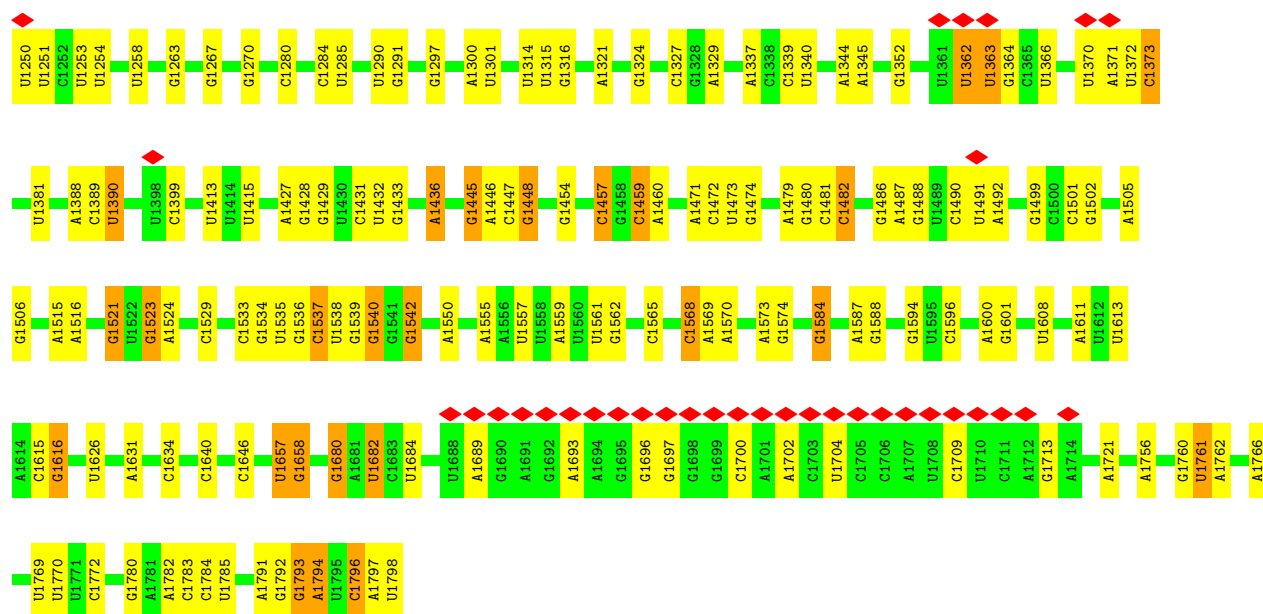


- Molecule 33: 40S ribosomal protein S25-A

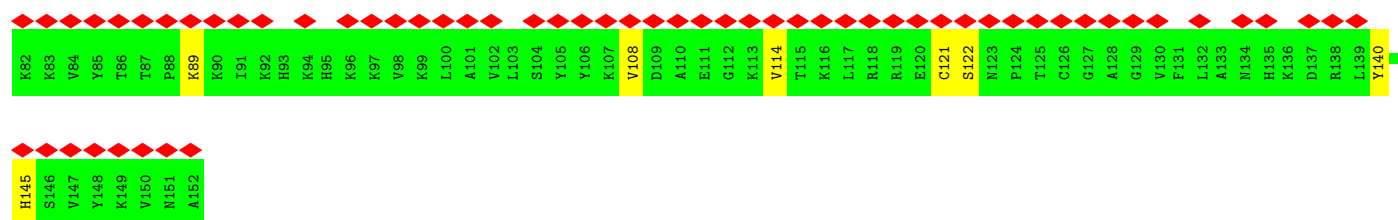
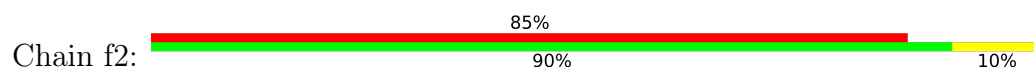


• Molecule 34: 18S ribosomal RNA

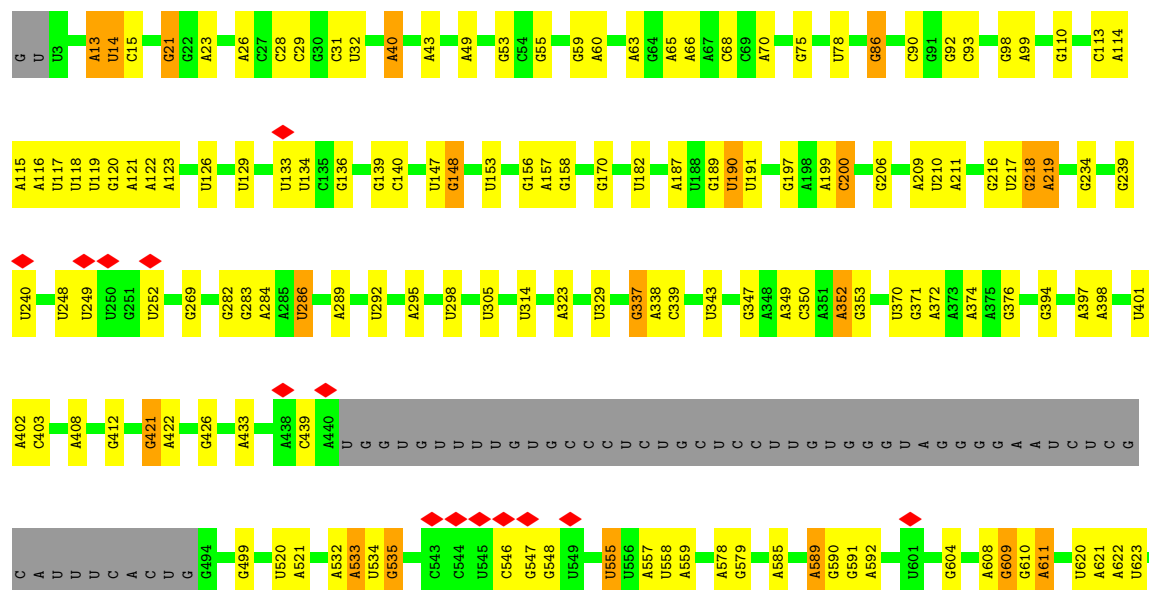




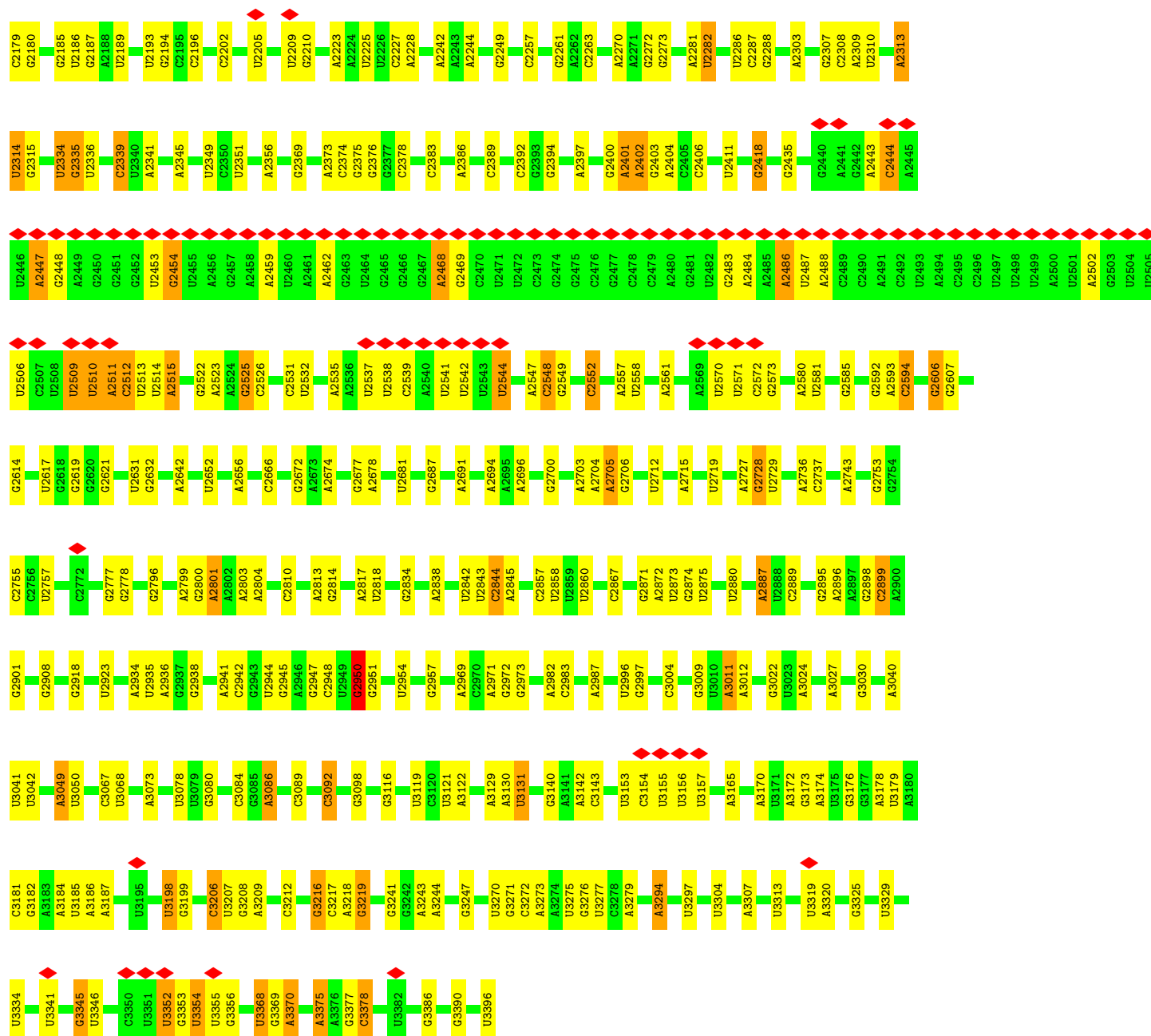
• Molecule 35: Ubiquitin-40S ribosomal protein S31



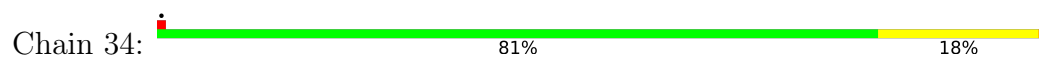
• Molecule 36: 25S ribosomal RNA



U2085	A2086	C2087	A2088	A2089	U2090	U2091	A2092	C2093	C2094	G2095	C2098	A2099	A2107	G2110	G2111	A2112	C2113	C2114	G2115	A2117	C2118	G2121	G2122	A2131	U2137	A2138	A2139	U2140	U2141	A2142	A2143	A2144	A2145	C2146	U2149	G2150	U2159	G2160	C2163	A2168	G2169	U2170	G2174	U2175	U2176	G2177	A2178												
G	A	C	U	A	C	U	U	G	C2034	G2035	U2036	G2037	C2038	C2039	U2040	U2041	U2042	U2043	U2044	G2045	U2046	A2047	G2048	A2049	C2050	G2051	C2052	C2053	C2054	U2055	U2056	G2057	C2058	U2059	A2060	G2061	G2062	U2063	C2064	U2065	G2066	U2067	U2068	G2069	U2070	A2071	G2072	A2073	C2074	G2075	G2076	U2077	C2078	G2079	C2080	U2081	U2082	C2083	C2084
C1965	U1966	U1967	G1968	G1969	U1970	C1971	A1972	G1973	A1974	C1975	G1976	C1977	A1978	G1979	C1980	G1981	G1982	G1983	C1984	G1985	U1986	G1987	C	U	U	U	U	G	A	C	U	U	C	U	U	G	G	U	U	G	G	U	U	C	U	U	C	U	U	A	U	G	G	C	G				
A1841	C1846	A1847	G1848	C1849	A1850	C1857	A1858	G1863	C1866	A1867	G1868	G1875	G1878	A1879	U1880	A1893	G1899	A1900	A1901	C1902	G1906	C1907	A1908	U1920	A1932	G1940	C1941	U1942	C1943	U1944	G1948	G1949	G1953	G1954	U1955	A1956	G1957	U1958	G1959	A1960	G1961	G1962	G1963	C1964															
U1705	A1714	A1715	U1716	U1724	C1725	A1729	G1730	G1736	A1741	U1742	G1747	G1748	A1749	A1750	G1751	A1752	A1760	C1761	C1762	U1763	U1764	U1765	G1766	G1770	G1775	G1778	C1779	G1780	G1786	C1793	G1794	U1795	G1796	A1797	G1808	A1814	U1815	A1816	G1817	U1820	U1821	A1835	C1836																
A1559	G1560	G1561	C1562	C1563	A1566	U1567	U1568	U1569	U1570	A1571	U1572	G1573	C1574	A1575	G1576	G1577	C1581	C1582	A1583	A1588	A1589	A1593	A1594	U1595	C1596	A1602	A1603	G1604	A1605	U1606	U1607	U1629	U1630	G1634	G1635	A1638	C1639	A1642	A1643	C1644	U1645	A1656	C1657	A1683	U1694														
A1418	A1419	C1420	G1421	A1428	G1429	U1430	G1434	A1435	U1436	C1437	A1446	G1447	U1455	U1463	A1467	U1470	A1474	G1480	A1481	A1482	G1483	G1486	G1487	G1488	A1491	G1492	G1493	U1494	U1495	C1496	C1508	G1521	U1522	U1523	A1524	G1528	G1547	U1553	U1554	U1555	C1556	A1557	A1558																
A1278	C1279	G1282	C1283	G1284	U1285	A1286	A1287	A1302	G1307	A1308	U1309	G1313	G1314	U1315	C1316	A1317	G1323	U1324	U1325	A1330	U1331	U1334	U1348	G1349	U1350	U1351	A1352	U1353	G1354	A1355	U1356	G1357	U1361	G1374	C1385	A1386	G1387	G1389	A1390	C1391	G1392	A1399	G1400	G1408															
G1209	U1210	G1213	U1214	G1222	C1227	C1228	G1229	G1230	A1231	C1232	G1233	G1234	U1235	G1236	G1237	C1238	C1239	A1240	U1241	G1242	G1243	A1244	U1245	G1246	U1247	C1248	G1249	G1250	A1251	A1252	U1253	C1254	G1255	G1256	C1257	U1258	A1259	U1260	G1261	G1262	A1263	G1264	U1265	G1266	U1267	G1268	U1269	A1270	A1271	C1272	A1273	A1274	C1275	U1276	C1277				
A1065	A1075	C1076	U1081	A1084	A1093	U1094	U1095	U1096	A1097	A1098	A1103	G1104	U1114	G1115	G1116	G1117	G1127	A1130	G1131	G1134	U1144	G1145	A1150	U1151	G1152	A1153	C1156	A1158	A1159	C1160	A1180	U1181	A1184	C1189	C1192	C1196	C1201	A1205	C1206																				
C959	U960	G963	C969	G974	G978	U979	A980	U981	G982	G984	G999	G1000	G1001	A1002	A1006	G1010	C981	U874	U879	G880	A896	G908	G909	G910	C911	A914	A915	G916	A917	U922	A925	G934	G937	C938	U939	G940	C944	A1047	A1048	C1049	U1050	A1055	A1064																
U827	A828	C833	C837	C838	U842	A849	C855	G858	U864	G868	G874	A877	U881	A890	A891	A892	A893	C896	A705	G712	U713	G714	A715	G727	G728	G733	C734	A735	A736	G742	G763	U764	C765	U766	U767	U776	U777	G781																					

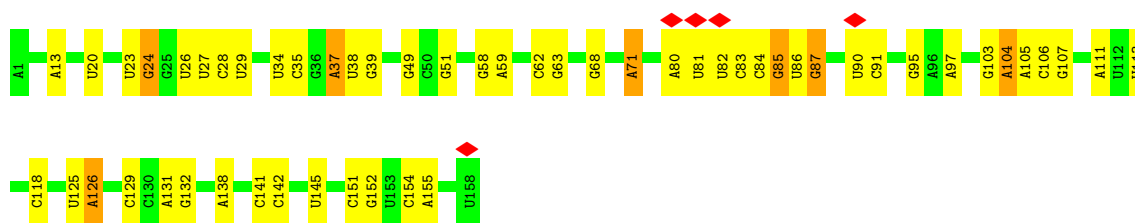


• Molecule 37: 5S ribosomal RNA

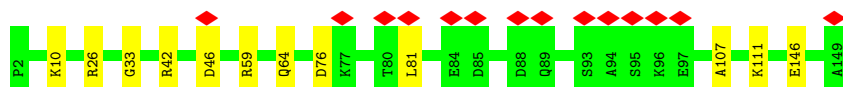


• Molecule 38: 5.8S ribosomal RNA

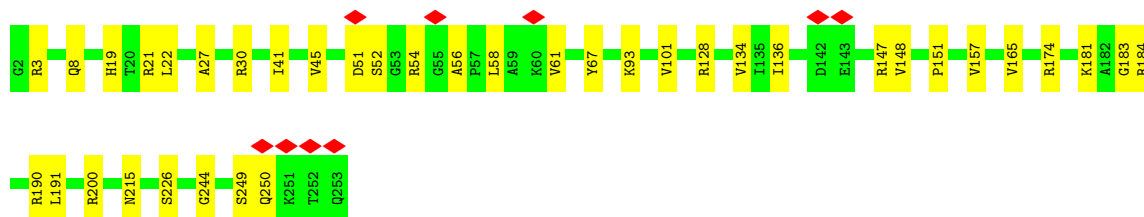
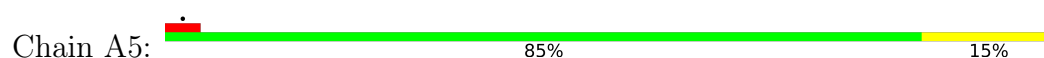




- Molecule 39: 60S ribosomal protein L28



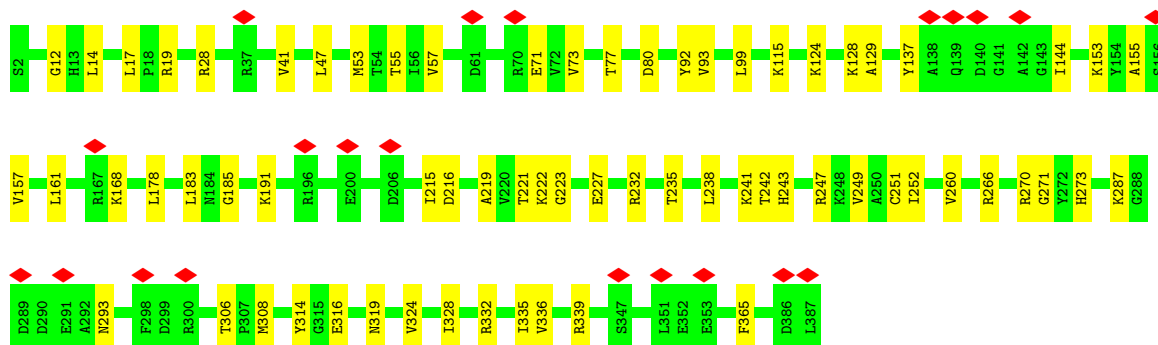
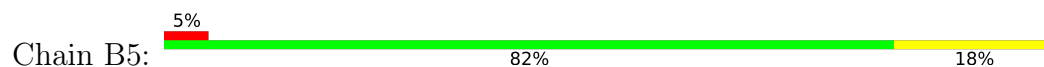
- Molecule 40: 60S ribosomal protein L2-A



- Molecule 41: 60S ribosomal protein L29



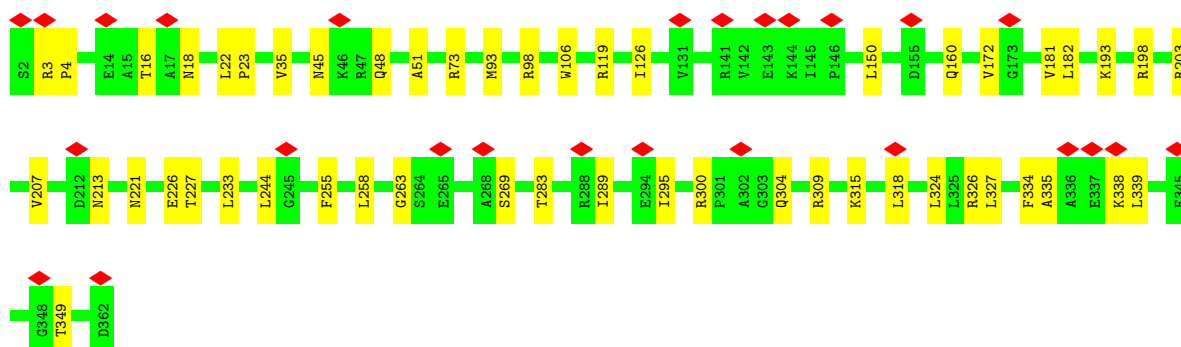
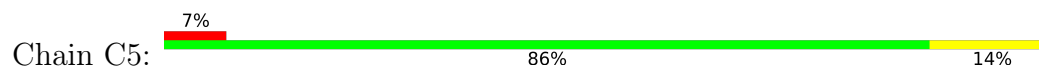
- Molecule 42: 60S ribosomal protein L3



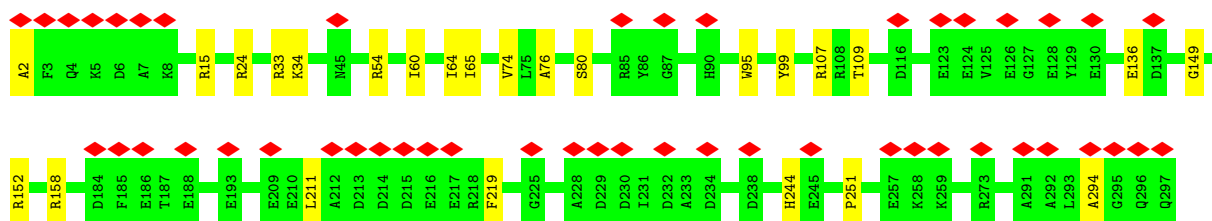
- Molecule 43: 60S ribosomal protein L30



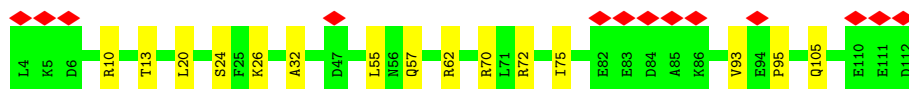
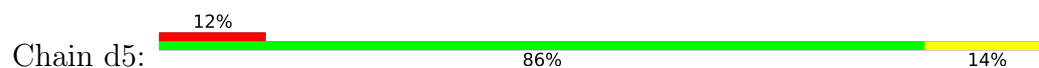
- Molecule 44: 60S ribosomal protein L4-A



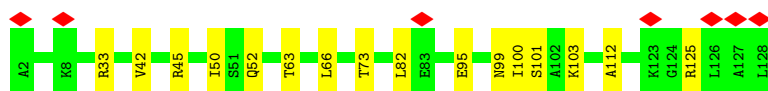
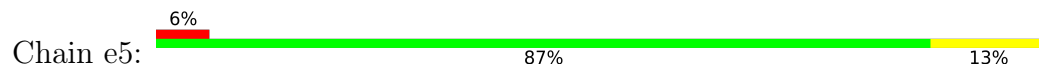
- Molecule 45: 60S ribosomal protein L5



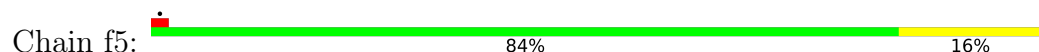
- Molecule 46: 60S ribosomal protein L31-A

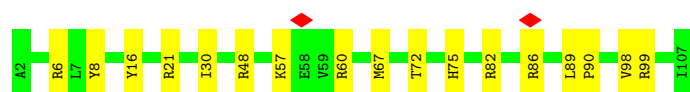


- Molecule 47: 60S ribosomal protein L32

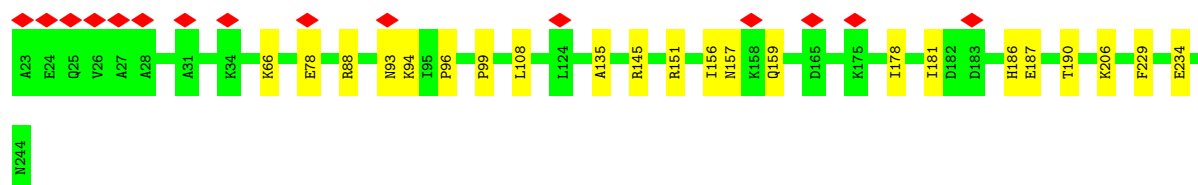
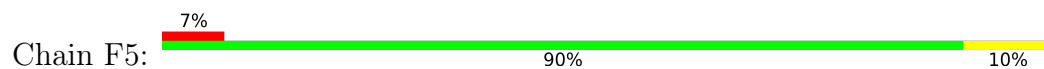


- Molecule 48: 60S ribosomal protein L33-A

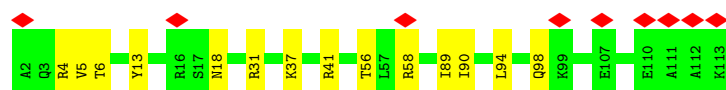
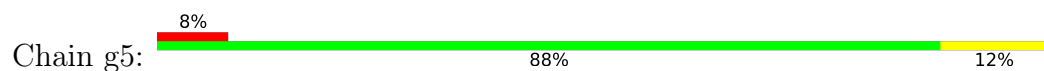




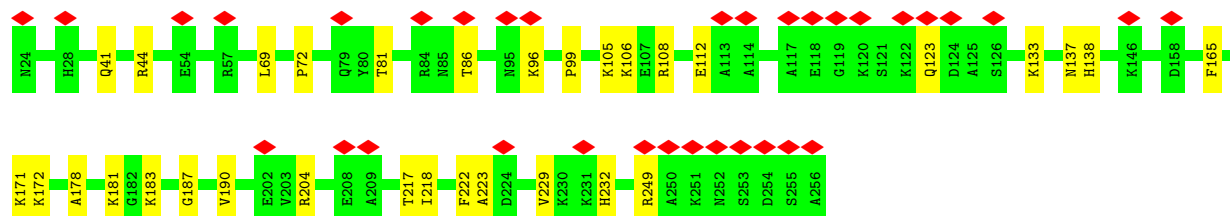
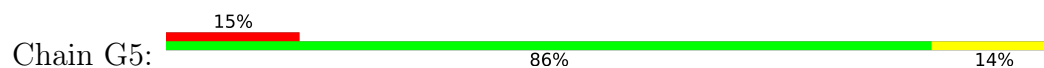
- Molecule 49: 60S ribosomal protein L7-A



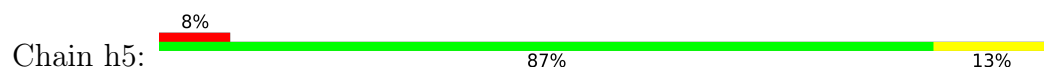
- Molecule 50: 60S ribosomal protein L34-A



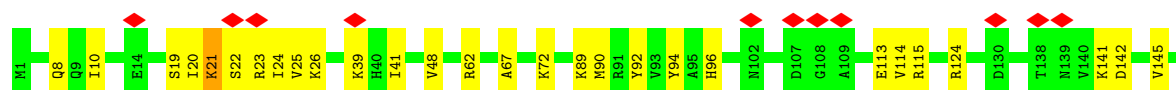
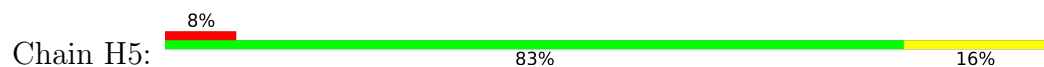
- Molecule 51: 60S ribosomal protein L8-A

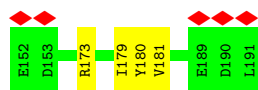


- Molecule 52: 60S ribosomal protein L35-A

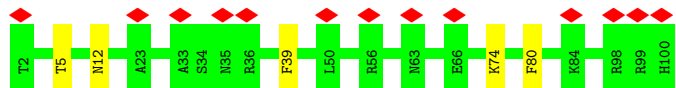


- Molecule 53: 60S ribosomal protein L9-A

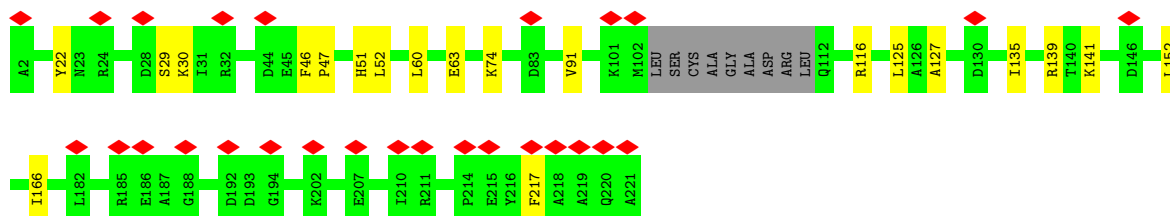
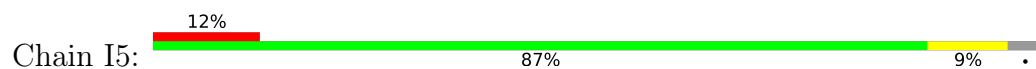




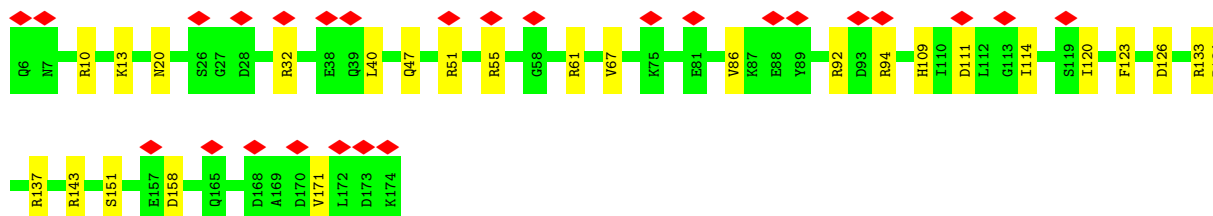
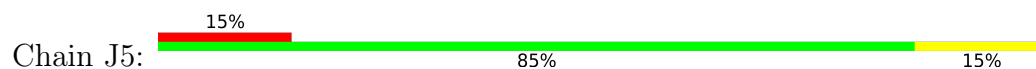
- Molecule 54: 60S ribosomal protein L36-A



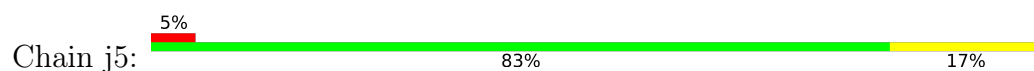
- Molecule 55: 60S ribosomal protein L10



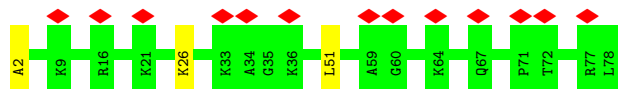
- Molecule 56: 60S ribosomal protein L11-A



- Molecule 57: 60S ribosomal protein L37-A



- Molecule 58: 60S ribosomal protein L38

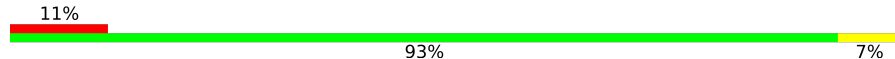


- Molecule 59: 60S ribosomal protein L39

Chain l5:  92% 8%



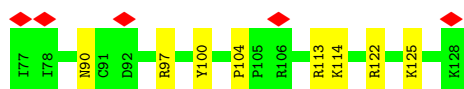
- Molecule 60: 60S ribosomal protein L13-A

Chain L5:  11% 93% 7%



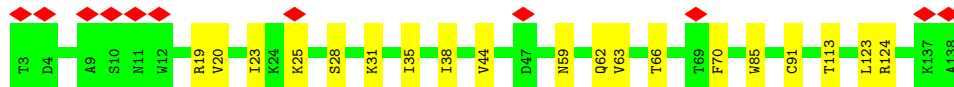
- Molecule 61: Ubiquitin-60S ribosomal protein L40

Chain m5:  10% 85% 15%



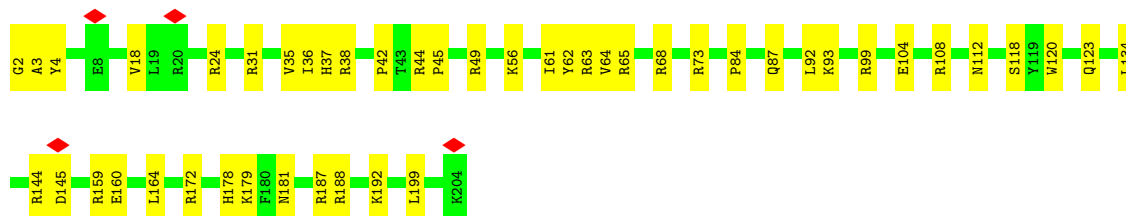
- Molecule 62: 60S ribosomal protein L14-A

Chain M5:  8% 86% 14%

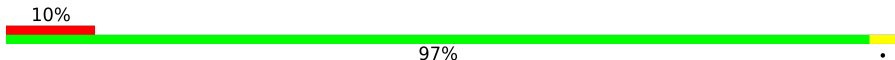


- Molecule 63: 60S ribosomal protein L15-A

Chain N5:  77% 23%

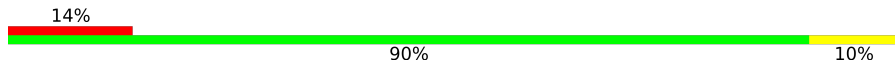


- Molecule 64: 60S ribosomal protein L42-B

Chain o5:  10% 97%

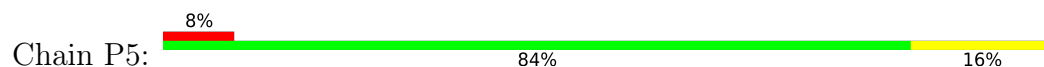


- Molecule 65: 60S ribosomal protein L43-B

Chain p5:  14% 90% 10%



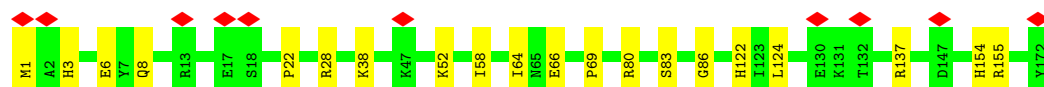
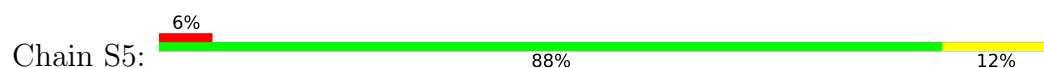
- Molecule 66: 60S ribosomal protein L17-A



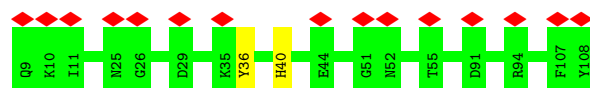
- Molecule 67: 60S ribosomal protein L18-A



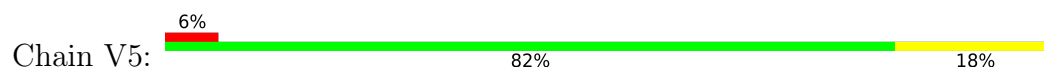
- Molecule 68: 60S ribosomal protein L20-A



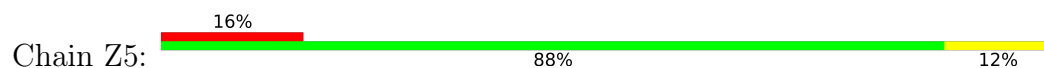
- Molecule 69: 60S ribosomal protein L22-A

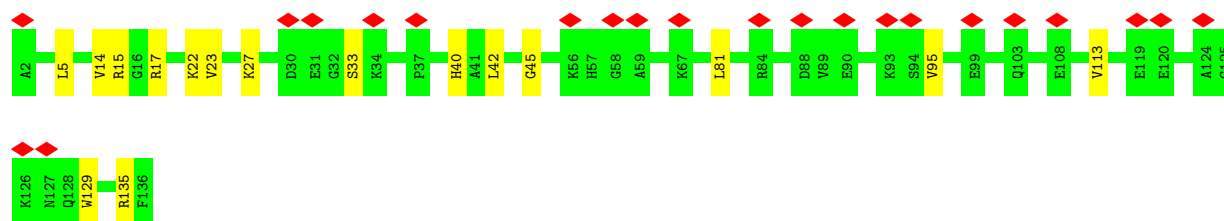


- Molecule 70: 60S ribosomal protein L23-A



- Molecule 71: 60S ribosomal protein L27-A

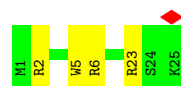
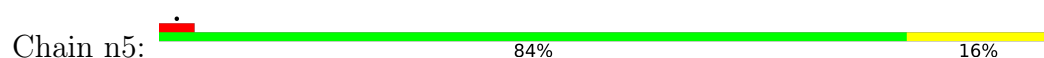




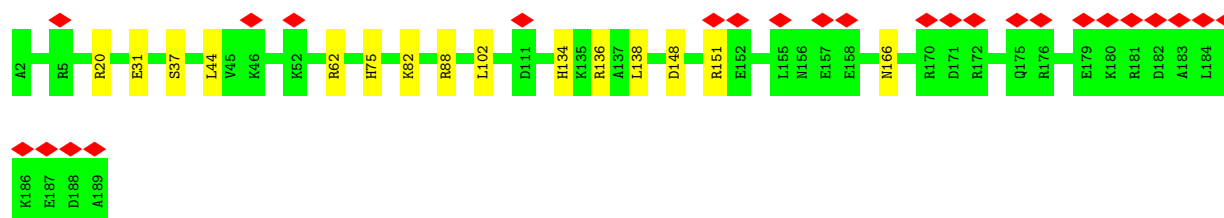
- Molecule 72: 60S ribosomal protein L16-A



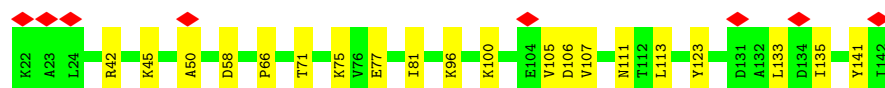
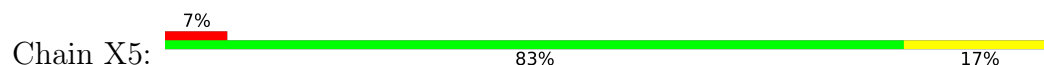
- Molecule 73: 60S ribosomal protein L41-B



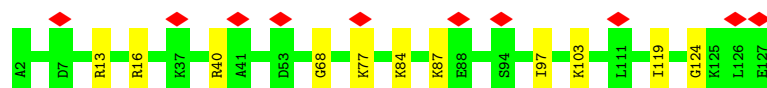
- Molecule 74: 60S ribosomal protein L19-A



- Molecule 75: 60S ribosomal protein L25



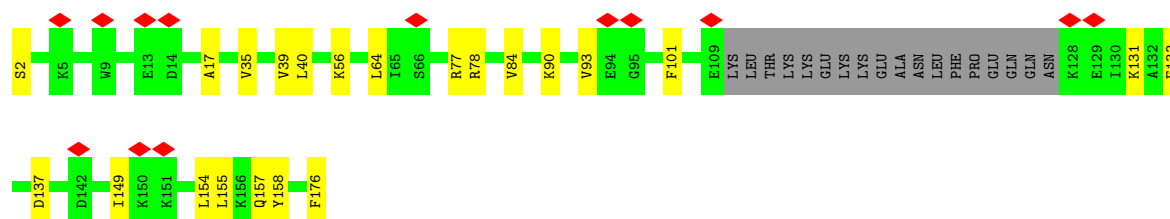
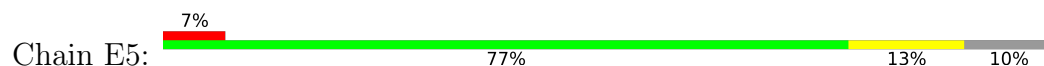
- Molecule 76: 60S ribosomal protein L26-A



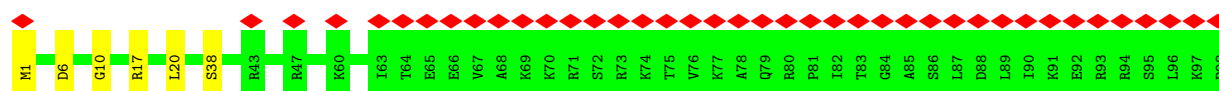
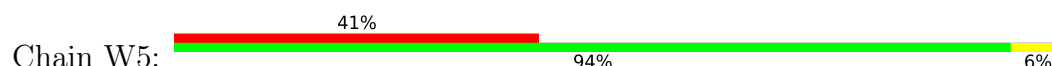
- Molecule 77: 60S ribosomal protein L21-A



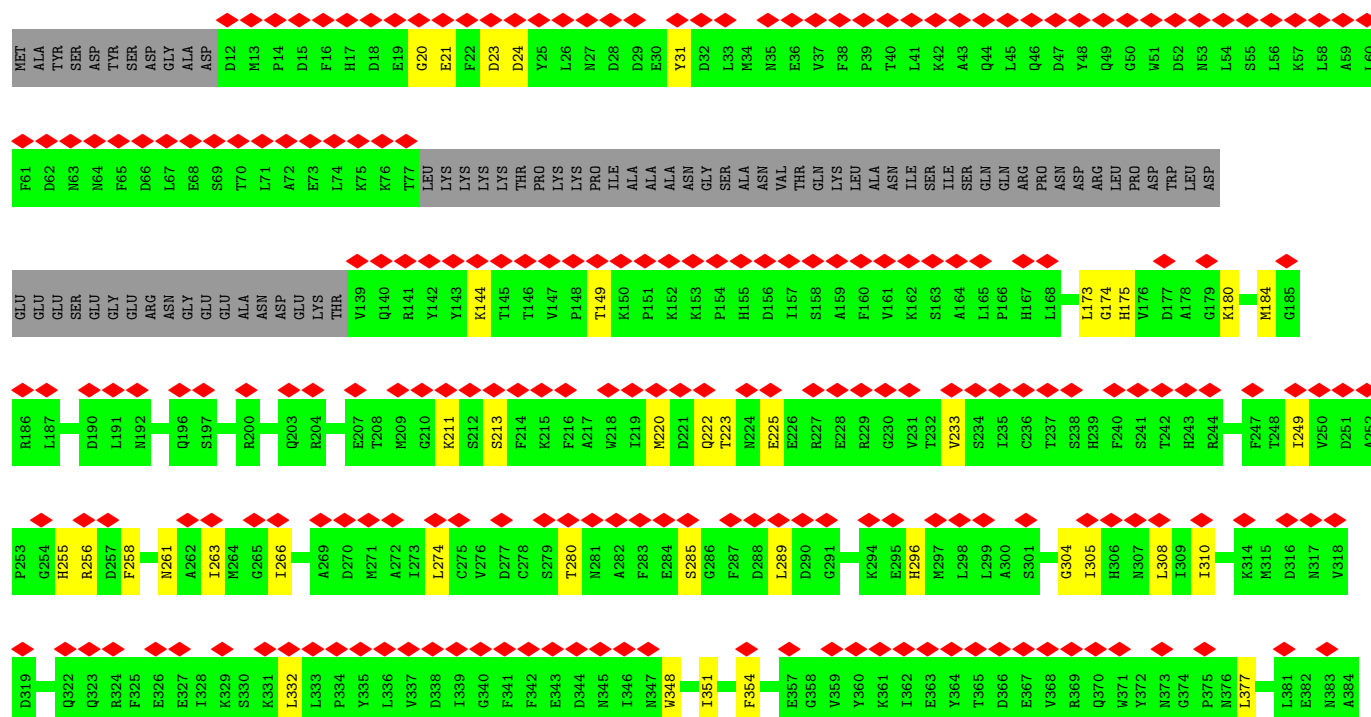
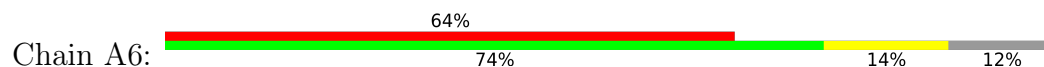
• Molecule 78: 60S ribosomal protein L6-A

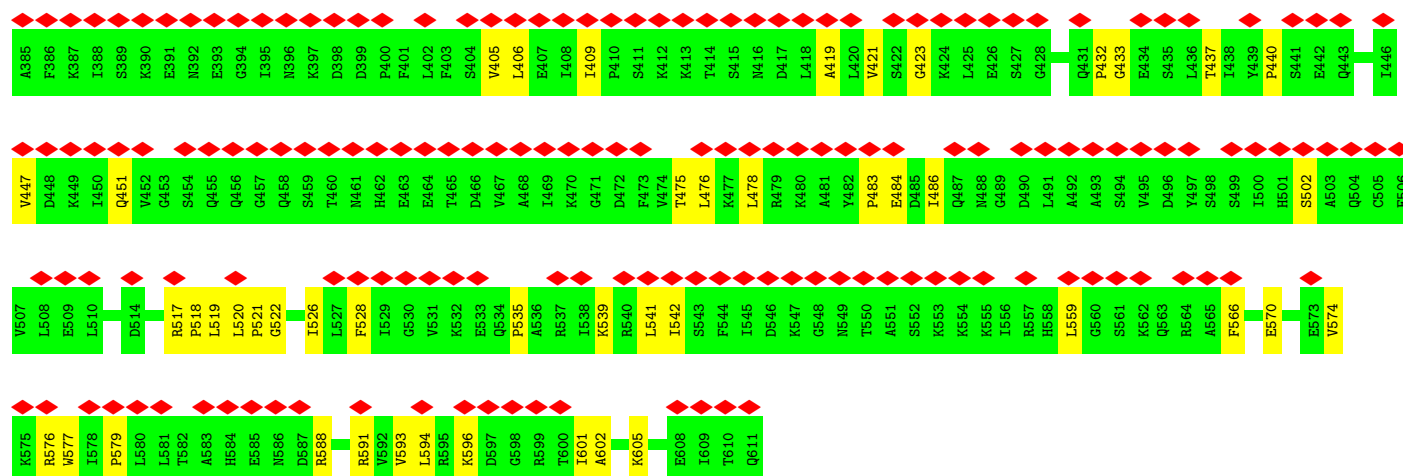


• Molecule 79: 60S ribosomal protein L24-A

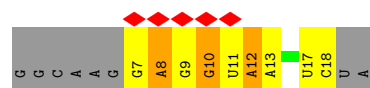


• Molecule 80: Protein HBS1

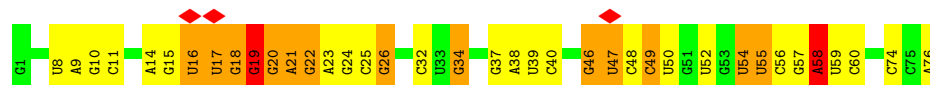




- Molecule 81: nonstop mRNA



- Molecule 82: yeast Phe-tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	73391	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25.0	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	80645	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	21.317	Depositor
Minimum map value	-12.022	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.5	Depositor
Map size ($\text{\AA}$)	409.528, 409.528, 409.528	wwPDB
Map dimensions	412, 412, 412	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.994, 0.994, 0.994	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: M2G, YYG, 7MG, OMC, 5MU, H2U, MG, 5CR, OMG, ZN, 2MG, PSU, 5MC, GNP, 1MA

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	A1	0.17	0/3110	0.53	2/4179 (0.0%)
2	A2	0.20	0/1662	0.61	0/2273
3	a2	0.18	0/791	0.60	2/1059 (0.2%)
4	B2	0.22	0/1735	0.65	0/2335
5	b2	0.17	0/620	0.49	0/838
6	C2	0.19	0/1665	0.52	0/2263
7	c2	0.18	0/499	0.45	0/670
8	D2	0.23	1/1759 (0.1%)	0.55	0/2368
9	d2	0.19	0/453	0.50	0/602
10	E2	0.19	0/2109	0.60	1/2839 (0.0%)
11	e2	0.18	0/483	0.48	0/643
12	F2	0.20	0/1629	0.61	0/2202
13	G2	0.18	0/1844	0.55	0/2464
14	g2	0.15	0/2498	0.45	0/3398
15	H2	0.22	0/1506	0.59	2/2028 (0.1%)
16	I2	0.20	0/1514	0.59	0/2021
17	J2	0.19	0/1519	0.58	0/2035
18	K2	0.18	0/837	0.57	0/1131
19	L2	0.22	0/1272	0.54	0/1712
20	M2	0.25	0/942	0.79	2/1274 (0.2%)
21	N2	0.19	0/1215	0.58	0/1638
22	O2	0.22	0/952	0.64	2/1279 (0.2%)
23	P2	0.36	1/1012 (0.1%)	0.67	1/1356 (0.1%)
24	Q2	0.20	0/1125	0.61	0/1510
25	R2	0.20	0/1010	0.60	0/1355
26	S2	0.22	0/1211	0.66	2/1628 (0.1%)
27	T2	0.20	0/1130	0.55	0/1517
28	U2	0.19	0/865	0.51	0/1169
29	V2	0.18	0/693	0.59	0/935
30	W2	0.19	0/1038	0.54	0/1395
31	X2	0.21	0/1139	0.64	2/1518 (0.1%)
32	Y2	0.17	0/1087	0.55	0/1449

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Z2	0.16	0/571	0.50	0/768
34	22	0.12	0/42444	0.30	7/66138 (0.0%)
35	f2	0.20	0/504	0.66	0/682
36	14	0.12	0/78885	0.29	10/122992 (0.0%)
37	34	0.10	0/2883	0.19	0/4491
38	44	0.11	0/3746	0.26	0/5832
39	a5	0.18	0/1204	0.57	0/1612
40	A5	0.21	0/1952	0.60	0/2622
41	b5	0.18	0/473	0.53	0/629
42	B5	0.18	0/3152	0.53	0/4239
43	c5	0.17	0/751	0.45	0/1008
44	C5	0.20	0/2801	0.59	2/3792 (0.1%)
45	D5	0.17	0/2425	0.56	2/3271 (0.1%)
46	d5	0.22	0/904	0.49	0/1213
47	e5	0.17	0/1041	0.52	0/1394
48	f5	0.17	0/868	0.46	0/1168
49	F5	0.21	0/1821	0.58	0/2451
50	g5	0.17	0/891	0.54	1/1191 (0.1%)
51	G5	0.20	0/1849	0.61	2/2495 (0.1%)
52	h5	0.17	0/978	0.56	2/1301 (0.2%)
53	H5	0.19	0/1539	0.57	2/2073 (0.1%)
54	i5	0.19	0/778	0.61	0/1034
55	I5	0.16	0/1753	0.48	0/2350
56	J5	0.20	0/1374	0.57	0/1842
57	j5	0.20	0/696	0.58	0/923
58	k5	0.17	0/618	0.51	0/826
59	l5	0.19	0/443	0.56	0/588
60	L5	0.20	0/1568	0.62	0/2106
61	m5	0.19	0/423	0.52	0/562
62	M5	0.17	0/1068	0.53	0/1438
63	N5	0.19	0/1757	0.53	0/2354
64	o5	0.16	0/860	0.52	0/1136
65	p5	0.19	0/701	0.57	0/934
66	P5	0.19	0/1465	0.54	0/1968
67	Q5	0.17	0/1465	0.53	0/1965
68	S5	0.18	0/1481	0.55	0/1990
69	U5	0.25	0/812	0.60	0/1099
70	V5	0.18	0/1018	0.46	0/1369
71	Z5	0.18	0/1118	0.51	0/1497
72	K5	0.18	0/1585	0.48	0/2128
73	n5	0.16	0/234	0.52	0/300
74	R5	0.17	0/1538	0.57	0/2050
75	X5	0.17	0/983	0.48	0/1325

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Y5	0.17	0/1004	0.49	0/1341
77	T5	0.18	0/1300	0.53	0/1743
78	E5	0.17	0/1269	0.51	1/1705 (0.1%)
79	W5	0.22	0/814	0.59	0/1081
80	A6	0.17	0/4364	0.46	1/5898 (0.0%)
81	X7	0.33	0/290	0.39	0/450
82	A3	0.38	0/1487	0.48	1/2315 (0.0%)
All	All	0.16	2/226872 (0.0%)	0.42	47/332762 (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
12	F2	0	1
17	J2	0	2
20	M2	0	1
26	S2	0	1
31	X2	0	1
49	F5	0	1
60	L5	0	1
All	All	0	8

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	P2	120	SER	N-CA	7.88	1.55	1.46
8	D2	162	GLN	C-N	5.05	1.39	1.34

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	14	2509	U	C2'-C3'-O3'	8.70	122.55	109.50
36	14	1795	U	N1-C1'-C2'	6.31	121.46	112.00
26	S2	13	HIS	CA-C-N	6.03	132.82	121.97
26	S2	13	HIS	C-N-CA	6.03	132.82	121.97
78	E5	93	VAL	N-CA-C	-5.96	107.48	113.20

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	F2	126	ASP	Peptide
17	J2	133	HIS	Peptide
17	J2	163	PRO	Peptide
20	M2	90	LYS	Peptide
26	S2	13	HIS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A1	3058	0	3134	56	0
2	A2	1621	0	1629	21	0
3	a2	778	0	823	16	0
4	B2	1709	0	1784	14	0
5	b2	610	0	631	11	0
6	C2	1635	0	1723	15	0
7	c2	497	0	535	7	0
8	D2	1734	0	1817	19	0
9	d2	443	0	434	13	0
10	E2	2068	0	2154	22	0
11	e2	475	0	525	4	0
12	F2	1609	0	1674	38	0
13	G2	1820	0	1918	16	0
14	g2	2445	0	2401	24	0
15	H2	1481	0	1572	22	0
16	I2	1489	0	1525	29	0
17	J2	1494	0	1573	13	0
18	K2	817	0	804	2	0
19	L2	1244	0	1314	11	0
20	M2	934	0	975	10	0
21	N2	1192	0	1255	11	0
22	O2	941	0	979	17	0
23	P2	991	0	1035	29	0
24	Q2	1105	0	1166	12	0
25	R2	1000	0	1063	13	0
26	S2	1192	0	1222	38	0
27	T2	1112	0	1124	11	0
28	U2	855	0	917	13	0
29	V2	684	0	672	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	W2	1021	0	1060	16	0
31	X2	1121	0	1196	28	0
32	Y2	1073	0	1132	12	0
33	Z2	563	0	602	68	0
34	22	37948	0	19089	245	0
35	f2	497	0	439	4	0
36	14	70476	0	35381	334	0
37	34	2579	0	1304	13	0
38	44	3353	0	1693	22	0
39	a5	1173	0	1214	11	0
40	A5	1918	0	1986	29	0
41	b5	462	0	491	3	0
42	B5	3081	0	3165	47	0
43	c5	743	0	797	4	0
44	C5	2749	0	2863	38	0
45	D5	2375	0	2324	16	0
46	d5	890	0	938	11	0
47	e5	1020	0	1090	11	0
48	f5	850	0	880	12	0
49	F5	1784	0	1862	13	0
50	g5	881	0	949	8	0
51	G5	1817	0	1908	21	0
52	h5	969	0	1078	11	0
53	H5	1518	0	1587	27	0
54	i5	771	0	849	3	0
55	I5	1717	0	1753	12	0
56	J5	1353	0	1383	40	0
57	j5	681	0	683	13	0
58	k5	612	0	682	3	0
59	l5	436	0	475	5	0
60	L5	1543	0	1608	9	0
61	m5	417	0	455	8	0
62	M5	1053	0	1149	12	0
63	N5	1720	0	1778	36	0
64	o5	847	0	915	2	0
65	p5	694	0	735	5	0
66	P5	1442	0	1485	20	0
67	Q5	1441	0	1542	12	0
68	S5	1445	0	1487	16	0
69	U5	796	0	812	1	0
70	V5	1003	0	1048	17	0
71	Z5	1092	0	1155	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	K5	1555	0	1659	10	0
73	n5	233	0	284	3	0
74	R5	1521	0	1617	13	0
75	X5	968	0	1036	14	0
76	Y5	993	0	1081	8	0
77	T5	1276	0	1323	16	0
78	E5	1248	0	1339	13	0
79	W5	800	0	865	5	0
80	A6	4279	0	4232	80	0
81	X7	259	0	130	8	0
82	A3	1651	0	856	38	0
83	a2	1	0	0	0	0
83	b2	1	0	0	0	0
83	d2	1	0	0	0	0
83	f2	1	0	0	0	0
83	j5	1	0	0	0	0
83	m5	1	0	0	0	0
83	o5	1	0	0	0	0
83	p5	1	0	0	0	0
84	14	701	0	0	0	0
84	22	177	0	0	0	0
84	34	16	0	0	0	0
84	44	34	0	0	0	0
84	A3	6	0	0	0	0
84	A5	6	0	0	0	0
84	A6	2	0	0	0	0
84	B2	1	0	0	0	0
84	B5	5	0	0	0	0
84	C2	2	0	0	0	0
84	C5	8	0	0	0	0
84	D5	1	0	0	0	0
84	E2	2	0	0	0	0
84	E5	1	0	0	0	0
84	F2	2	0	0	0	0
84	F5	4	0	0	0	0
84	I2	2	0	0	0	0
84	I5	4	0	0	0	0
84	J2	1	0	0	0	0
84	J5	2	0	0	0	0
84	K5	5	0	0	0	0
84	L2	1	0	0	0	0
84	L5	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	M5	1	0	0	0	0
84	N2	2	0	0	0	0
84	N5	7	0	0	0	0
84	P5	7	0	0	0	0
84	Q2	1	0	0	0	0
84	Q5	4	0	0	0	0
84	R5	3	0	0	0	0
84	S2	4	0	0	0	0
84	S5	4	0	0	0	0
84	T2	1	0	0	0	0
84	T5	1	0	0	0	0
84	U2	1	0	0	0	0
84	V5	3	0	0	0	0
84	X2	3	0	0	0	0
84	Y2	1	0	0	0	0
84	Y5	2	0	0	0	0
84	a5	3	0	0	0	0
84	b5	1	0	0	0	0
84	d2	1	0	0	0	0
84	d5	3	0	0	0	0
84	e5	3	0	0	0	0
84	f5	1	0	0	0	0
84	j5	7	0	0	0	0
84	l5	1	0	0	0	0
84	m5	3	0	0	0	0
84	o5	3	0	0	0	0
85	A6	32	0	13	1	0
86	A3	14	0	0	3	0
87	A1	7	0	0	0	0
87	A6	6	0	0	0	0
All	All	212865	0	157835	1395	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 1395 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)
26:S2:4:VAL:CG1	33:Z2:42:LEU:HD22	1.12	1.52
56:J5:55:ARG:CD	82:A3:20:G:H22	1.25	1.47
12:F2:125:THR:N	33:Z2:58:ARG:NH2	1.64	1.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:S2:4:VAL:HG11	33:Z2:42:LEU:CD2	0.99	1.44
1:A1:218:PHE:CD2	80:A6:225:GLU:OE2	1.75	1.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A1	379/381 (100%)	352 (93%)	27 (7%)	0	100	100
2	A2	205/207 (99%)	185 (90%)	19 (9%)	1 (0%)	24	55
3	a2	96/98 (98%)	91 (95%)	5 (5%)	0	100	100
4	B2	212/214 (99%)	197 (93%)	15 (7%)	0	100	100
5	b2	79/81 (98%)	74 (94%)	5 (6%)	0	100	100
6	C2	215/217 (99%)	206 (96%)	9 (4%)	0	100	100
7	c2	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
8	D2	221/223 (99%)	210 (95%)	11 (5%)	0	100	100
9	d2	51/53 (96%)	49 (96%)	2 (4%)	0	100	100
10	E2	258/260 (99%)	233 (90%)	25 (10%)	0	100	100
11	e2	58/60 (97%)	55 (95%)	3 (5%)	0	100	100
12	F2	204/206 (99%)	182 (89%)	22 (11%)	0	100	100
13	G2	224/226 (99%)	204 (91%)	18 (8%)	2 (1%)	14	43
14	g2	316/318 (99%)	299 (95%)	17 (5%)	0	100	100
15	H2	182/184 (99%)	166 (91%)	16 (9%)	0	100	100
16	I2	184/199 (92%)	163 (89%)	21 (11%)	0	100	100
17	J2	183/185 (99%)	174 (95%)	9 (5%)	0	100	100
18	K2	94/96 (98%)	82 (87%)	12 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	L2	153/155 (99%)	140 (92%)	13 (8%)	0	100	100
20	M2	122/124 (98%)	95 (78%)	27 (22%)	0	100	100
21	N2	148/150 (99%)	140 (95%)	8 (5%)	0	100	100
22	O2	125/127 (98%)	114 (91%)	11 (9%)	0	100	100
23	P2	122/124 (98%)	113 (93%)	9 (7%)	0	100	100
24	Q2	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
25	R2	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
26	S2	143/145 (99%)	128 (90%)	14 (10%)	1 (1%)	18	49
27	T2	141/143 (99%)	135 (96%)	6 (4%)	0	100	100
28	U2	105/107 (98%)	99 (94%)	6 (6%)	0	100	100
29	V2	85/87 (98%)	72 (85%)	13 (15%)	0	100	100
30	W2	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
31	X2	142/144 (99%)	131 (92%)	11 (8%)	0	100	100
32	Y2	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
33	Z2	68/70 (97%)	68 (100%)	0	0	100	100
35	f2	69/71 (97%)	56 (81%)	13 (19%)	0	100	100
39	a5	146/148 (99%)	129 (88%)	16 (11%)	1 (1%)	18	49
40	A5	250/252 (99%)	235 (94%)	15 (6%)	0	100	100
41	b5	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
42	B5	384/386 (100%)	368 (96%)	16 (4%)	0	100	100
43	c5	95/97 (98%)	95 (100%)	0	0	100	100
44	C5	359/361 (99%)	330 (92%)	29 (8%)	0	100	100
45	D5	294/296 (99%)	281 (96%)	13 (4%)	0	100	100
46	d5	107/109 (98%)	99 (92%)	8 (8%)	0	100	100
47	e5	125/127 (98%)	118 (94%)	7 (6%)	0	100	100
48	f5	104/106 (98%)	99 (95%)	5 (5%)	0	100	100
49	F5	220/222 (99%)	211 (96%)	7 (3%)	2 (1%)	14	43
50	g5	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
51	G5	231/233 (99%)	219 (95%)	12 (5%)	0	100	100
52	h5	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
53	H5	189/191 (99%)	173 (92%)	16 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	i5	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
55	I5	207/220 (94%)	201 (97%)	6 (3%)	0	100	100
56	J5	167/169 (99%)	155 (93%)	12 (7%)	0	100	100
57	j5	85/87 (98%)	81 (95%)	4 (5%)	0	100	100
58	k5	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
59	l5	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
60	L5	191/193 (99%)	174 (91%)	15 (8%)	2 (1%)	12	40
61	m5	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
62	M5	134/136 (98%)	123 (92%)	11 (8%)	0	100	100
63	N5	201/203 (99%)	187 (93%)	14 (7%)	0	100	100
64	o5	103/105 (98%)	98 (95%)	5 (5%)	0	100	100
65	p5	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
66	P5	181/183 (99%)	175 (97%)	6 (3%)	0	100	100
67	Q5	183/185 (99%)	175 (96%)	8 (4%)	0	100	100
68	S5	170/172 (99%)	158 (93%)	12 (7%)	0	100	100
69	U5	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
70	V5	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
71	Z5	133/135 (98%)	123 (92%)	10 (8%)	0	100	100
72	K5	195/197 (99%)	191 (98%)	4 (2%)	0	100	100
73	n5	23/25 (92%)	23 (100%)	0	0	100	100
74	R5	186/188 (99%)	177 (95%)	9 (5%)	0	100	100
75	X5	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
76	Y5	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
77	T5	157/159 (99%)	147 (94%)	10 (6%)	0	100	100
78	E5	153/175 (87%)	144 (94%)	9 (6%)	0	100	100
79	W5	96/98 (98%)	83 (86%)	13 (14%)	0	100	100
80	A6	535/611 (88%)	496 (93%)	39 (7%)	0	100	100
All	All	11887/12157 (98%)	11117 (94%)	761 (6%)	9 (0%)	49	75

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	S2	14	ILE

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Mol	Chain	Res	Type
13	G2	149	LYS
60	L5	77	LEU
49	F5	234	GLU
39	a5	46	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A1	344/344 (100%)	344 (100%)	0	100	100
2	A2	174/174 (100%)	173 (99%)	1 (1%)	78	81
3	a2	84/84 (100%)	84 (100%)	0	100	100
4	B2	191/191 (100%)	191 (100%)	0	100	100
5	b2	70/70 (100%)	70 (100%)	0	100	100
6	C2	176/176 (100%)	176 (100%)	0	100	100
7	c2	56/56 (100%)	56 (100%)	0	100	100
8	D2	182/182 (100%)	182 (100%)	0	100	100
9	d2	47/47 (100%)	47 (100%)	0	100	100
10	E2	221/221 (100%)	221 (100%)	0	100	100
11	e2	51/51 (100%)	51 (100%)	0	100	100
12	F2	173/173 (100%)	173 (100%)	0	100	100
13	G2	193/193 (100%)	193 (100%)	0	100	100
14	g2	261/261 (100%)	261 (100%)	0	100	100
15	H2	165/165 (100%)	165 (100%)	0	100	100
16	I2	150/160 (94%)	150 (100%)	0	100	100
17	J2	158/158 (100%)	158 (100%)	0	100	100
18	K2	89/89 (100%)	89 (100%)	0	100	100
19	L2	136/136 (100%)	136 (100%)	0	100	100
20	M2	100/100 (100%)	100 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	N2	127/127 (100%)	127 (100%)	0	100	100
22	O2	96/96 (100%)	96 (100%)	0	100	100
23	P2	104/104 (100%)	104 (100%)	0	100	100
24	Q2	117/117 (100%)	117 (100%)	0	100	100
25	R2	113/113 (100%)	113 (100%)	0	100	100
26	S2	128/128 (100%)	128 (100%)	0	100	100
27	T2	115/115 (100%)	115 (100%)	0	100	100
28	U2	100/100 (100%)	99 (99%)	1 (1%)	68	76
29	V2	74/74 (100%)	74 (100%)	0	100	100
30	W2	110/110 (100%)	110 (100%)	0	100	100
31	X2	119/119 (100%)	119 (100%)	0	100	100
32	Y2	112/112 (100%)	111 (99%)	1 (1%)	70	78
33	Z2	61/61 (100%)	61 (100%)	0	100	100
35	f2	43/62 (69%)	43 (100%)	0	100	100
39	a5	118/118 (100%)	118 (100%)	0	100	100
40	A5	194/194 (100%)	194 (100%)	0	100	100
41	b5	46/46 (100%)	46 (100%)	0	100	100
42	B5	322/322 (100%)	322 (100%)	0	100	100
43	c5	81/81 (100%)	81 (100%)	0	100	100
44	C5	288/288 (100%)	288 (100%)	0	100	100
45	D5	244/244 (100%)	244 (100%)	0	100	100
46	d5	96/96 (100%)	96 (100%)	0	100	100
47	e5	109/109 (100%)	109 (100%)	0	100	100
48	f5	90/90 (100%)	90 (100%)	0	100	100
49	F5	186/186 (100%)	186 (100%)	0	100	100
50	g5	95/95 (100%)	95 (100%)	0	100	100
51	G5	191/191 (100%)	191 (100%)	0	100	100
52	h5	104/104 (100%)	104 (100%)	0	100	100
53	H5	171/171 (100%)	170 (99%)	1 (1%)	78	81
54	i5	81/81 (100%)	81 (100%)	0	100	100
55	I5	180/186 (97%)	180 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	J5	147/147 (100%)	146 (99%)	1 (1%)	76	80
57	j5	70/70 (100%)	70 (100%)	0	100	100
58	k5	68/68 (100%)	68 (100%)	0	100	100
59	l5	45/45 (100%)	45 (100%)	0	100	100
60	L5	154/154 (100%)	154 (100%)	0	100	100
61	m5	47/47 (100%)	47 (100%)	0	100	100
62	M5	107/107 (100%)	107 (100%)	0	100	100
63	N5	175/175 (100%)	175 (100%)	0	100	100
64	o5	90/90 (100%)	90 (100%)	0	100	100
65	p5	71/71 (100%)	71 (100%)	0	100	100
66	P5	145/145 (100%)	145 (100%)	0	100	100
67	Q5	150/150 (100%)	149 (99%)	1 (1%)	76	80
68	S5	156/156 (100%)	156 (100%)	0	100	100
69	U5	87/87 (100%)	87 (100%)	0	100	100
70	V5	104/104 (100%)	104 (100%)	0	100	100
71	Z5	115/115 (100%)	115 (100%)	0	100	100
72	K5	160/160 (100%)	160 (100%)	0	100	100
73	n5	23/23 (100%)	23 (100%)	0	100	100
74	R5	153/153 (100%)	153 (100%)	0	100	100
75	X5	105/105 (100%)	105 (100%)	0	100	100
76	Y5	109/109 (100%)	109 (100%)	0	100	100
77	T5	136/136 (100%)	136 (100%)	0	100	100
78	E5	135/152 (89%)	135 (100%)	0	100	100
79	W5	86/86 (100%)	86 (100%)	0	100	100
80	A6	478/538 (89%)	478 (100%)	0	100	100
All	All	10152/10264 (99%)	10146 (100%)	6 (0%)	87	90

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
53	H5	48	VAL
56	J5	171	VAL
67	Q5	98	LYS

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Mol	Chain	Res	Type
28	U2	20	ILE
2	A2	133	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 159 such sidechains are listed below:

Mol	Chain	Res	Type
59	I5	4	GLN
76	Y5	4	GLN
62	M5	126	GLN
68	S5	154	HIS
78	E5	157	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	22	1779/1798 (98%)	367 (20%)	42 (2%)
36	14	3292/3396 (96%)	562 (17%)	74 (2%)
37	34	120/121 (99%)	10 (8%)	0
38	44	157/158 (99%)	34 (21%)	0
81	X7	11/20 (55%)	6 (54%)	0
82	A3	75/76 (98%)	24 (32%)	2 (2%)
All	All	5434/5569 (97%)	1003 (18%)	118 (2%)

5 of 1003 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	22	2	A
34	22	3	U
34	22	25	C
34	22	26	A
34	22	27	U

5 of 118 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
36	14	1015	U
36	14	2705	A
36	14	1562	C
36	14	2593	A
36	14	2447	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

14 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
82	5MC	A3	49	82	19,22,23	0.97	1 (5%)	26,32,35	1.20	3 (11%)
82	5MU	A3	54	82	19,22,23	1.11	2 (10%)	27,32,35	1.39	4 (14%)
82	YYG	A3	37	82	38,42,43	1.63	10 (26%)	45,62,65	2.79	15 (33%)
82	PSU	A3	39	82	18,21,22	2.64	7 (38%)	21,30,33	1.75	5 (23%)
82	1MA	A3	58	82	21,25,26	1.19	3 (14%)	30,37,40	1.39	3 (10%)
82	7MG	A3	46	82	23,26,27	3.25	7 (30%)	27,39,42	2.23	8 (29%)
82	M2G	A3	26	84,82	24,27,28	1.28	2 (8%)	33,40,43	1.39	5 (15%)
82	H2U	A3	17	82	18,21,22	1.19	2 (11%)	19,30,33	1.20	3 (15%)
82	H2U	A3	16	82	18,21,22	1.22	2 (11%)	19,30,33	1.34	3 (15%)
82	5MC	A3	40	82	19,22,23	1.55	1 (5%)	26,32,35	1.21	4 (15%)
82	OMC	A3	32	82	19,22,23	1.57	3 (15%)	25,31,34	1.32	4 (16%)
82	OMG	A3	34	81,82	22,25,27	1.74	3 (13%)	32,37,41	1.78	7 (21%)
82	PSU	A3	55	82	18,21,22	2.71	7 (38%)	21,30,33	1.64	5 (23%)
82	2MG	A3	10	82	23,26,27	2.12	6 (26%)	33,38,41	2.06	8 (24%)

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
82	5MC	A3	49	82	-	2/7/25/26	0/2/2/2
82	5MU	A3	54	82	-	2/7/25/26	0/2/2/2
82	YYG	A3	37	82	-	7/24/42/43	0/4/4/4
82	PSU	A3	39	82	-	0/7/25/26	0/2/2/2
82	1MA	A3	58	82	-	2/7/25/26	0/3/3/3
82	7MG	A3	46	82	-	3/7/37/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
82	M2G	A3	26	84,82	-	2/11/29/30	0/3/3/3
82	H2U	A3	17	82	-	3/7/38/39	0/2/2/2
82	H2U	A3	16	82	-	5/7/38/39	0/2/2/2
82	5MC	A3	40	82	-	0/7/25/26	0/2/2/2
82	OMC	A3	32	82	-	0/9/27/28	0/2/2/2
82	OMG	A3	34	81,82	-	2/7/25/28	0/3/3/3
82	PSU	A3	55	82	-	4/7/25/26	0/2/2/2
82	2MG	A3	10	82	-	2/9/27/28	0/3/3/3

The worst 5 of 56 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	A3	46	7MG	C8-N9	9.18	1.51	1.45
82	A3	46	7MG	C5-N7	7.35	1.44	1.35
82	A3	10	2MG	C2-N2	6.43	1.46	1.33
82	A3	55	PSU	C1'-C5	6.10	1.64	1.50
82	A3	39	PSU	C1'-C5	5.91	1.63	1.50

The worst 5 of 77 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	A3	37	YYG	C1'-N9-C8	-7.48	105.47	126.73
82	A3	10	2MG	C2-N3-C4	7.35	121.20	112.00
82	A3	37	YYG	C10-C11-N2	-7.26	104.76	119.32
82	A3	37	YYG	O23-C21-N20	6.96	122.48	110.77
82	A3	37	YYG	C5-C4-N3	-6.87	118.41	123.99

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
82	A3	16	H2U	O4'-C4'-C5'-O5'
82	A3	16	H2U	C3'-C4'-C5'-O5'
82	A3	16	H2U	O4'-C1'-N1-C6
82	A3	17	H2U	O4'-C4'-C5'-O5'
82	A3	17	H2U	C3'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
82	A3	58	1MA	1	0
82	A3	34	OMG	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1068 ligands modelled in this entry, 1066 are monoatomic - leaving 2 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
86	5CR	A3	101	82	13,14,15	0.62	0	16,17,19	1.09	2 (12%)
85	GNP	A6	701	84	34,34,34	1.81	5 (14%)	47,54,54	1.32	5 (10%)

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
86	5CR	A3	101	82	-	0/9/10/12	0/1/1/1
85	GNP	A6	701	84	-	8/18/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	A6	701	GNP	PA-O3A	-6.40	1.52	1.59
85	A6	701	GNP	PB-O3A	-5.17	1.52	1.59
85	A6	701	GNP	PG-O1G	3.42	1.51	1.46
85	A6	701	GNP	PB-O2B	-3.21	1.48	1.56
85	A6	701	GNP	PG-O2G	-2.03	1.51	1.56

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	A6	701	GNP	O1G-PG-N3B	-4.37	105.34	111.77
85	A6	701	GNP	O2B-PB-O1B	4.07	118.59	109.87
85	A6	701	GNP	O1B-PB-N3B	-3.99	105.90	111.77
85	A6	701	GNP	O3G-PG-O1G	-3.34	105.08	113.45
85	A6	701	GNP	O2G-PG-O3G	2.95	115.51	107.59

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

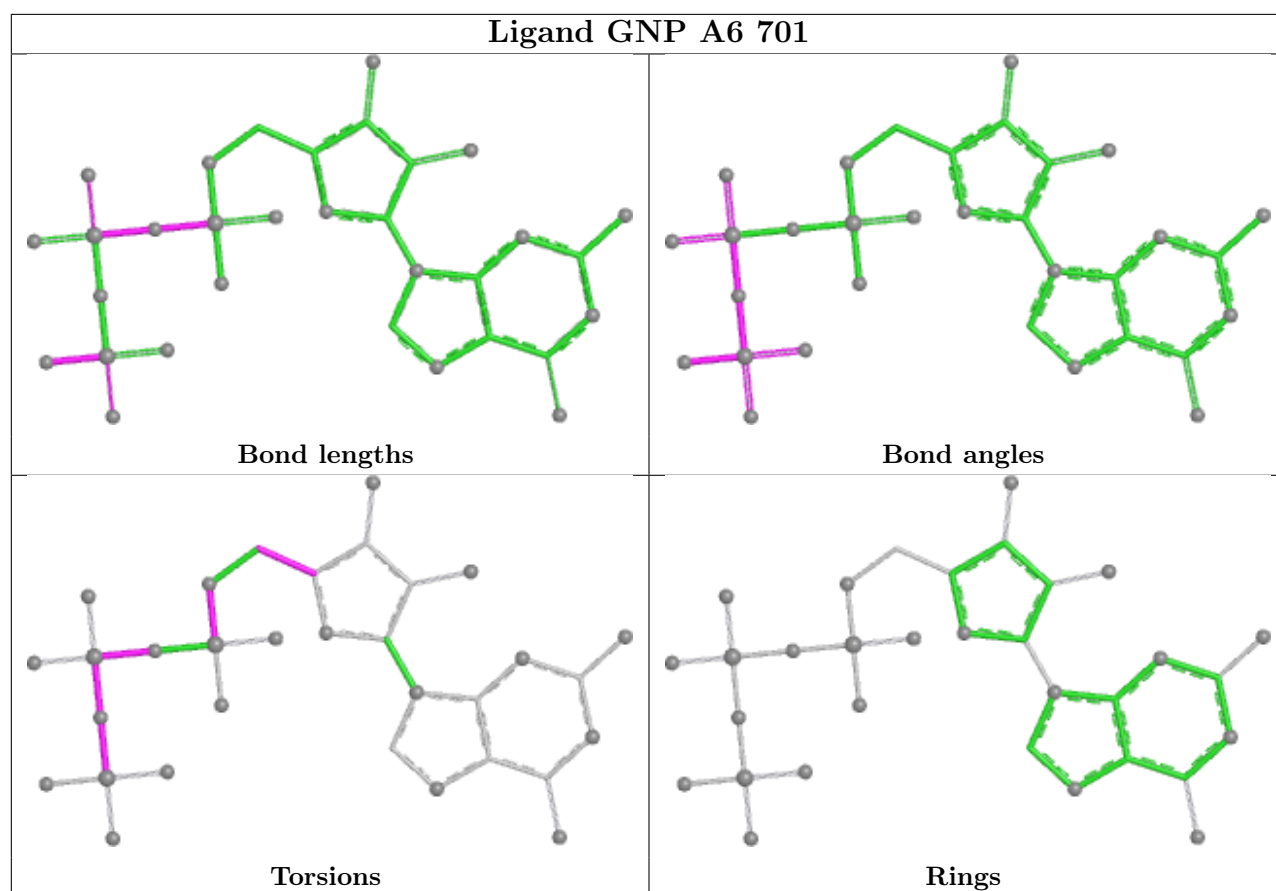
Mol	Chain	Res	Type	Atoms
85	A6	701	GNP	PB-N3B-PG-O1G
85	A6	701	GNP	PG-N3B-PB-O1B
85	A6	701	GNP	PG-N3B-PB-O3A
85	A6	701	GNP	PA-O3A-PB-O2B
85	A6	701	GNP	C5'-O5'-PA-O3A

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	A3	101	5CR	3	0
85	A6	701	GNP	1	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

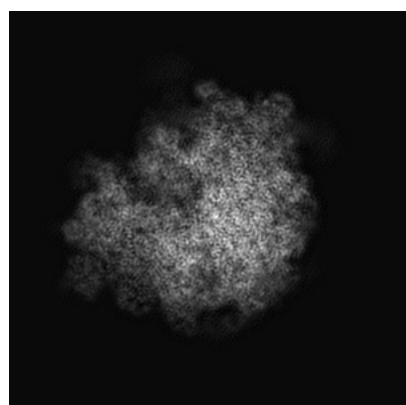
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4140. These allow visual inspection of the internal detail of the map and identification of artifacts.

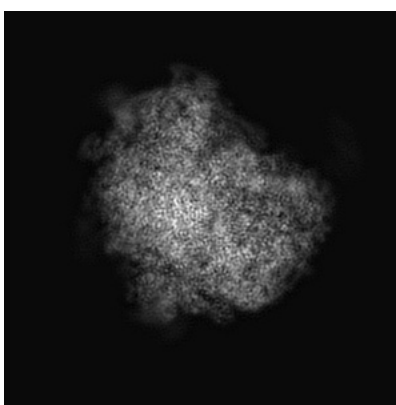
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

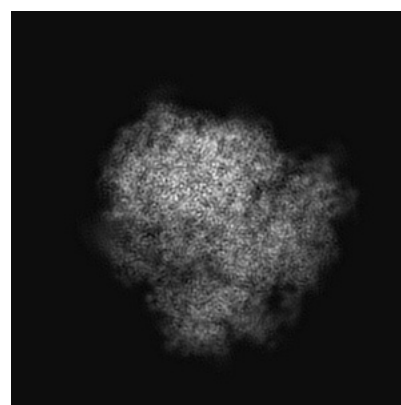
6.1.1 Primary map



X



Y

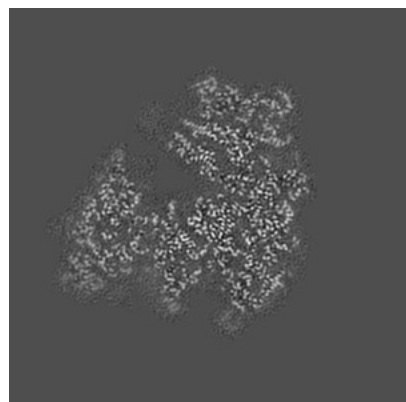


Z

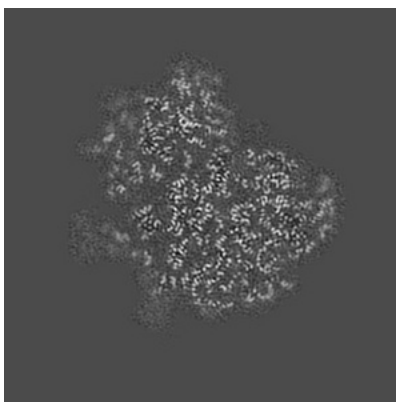
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

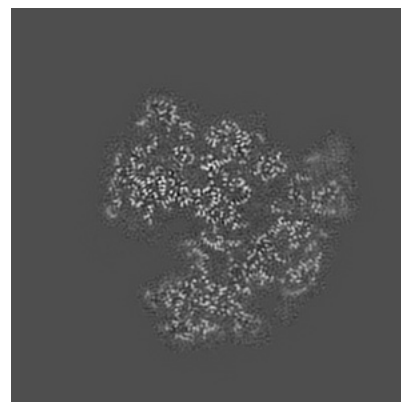
6.2.1 Primary map



X Index: 206



Y Index: 206

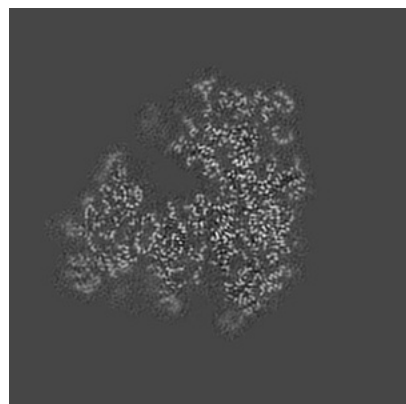


Z Index: 206

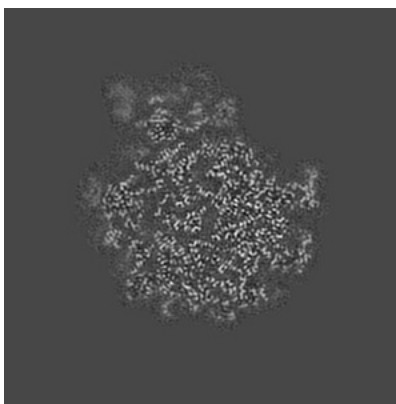
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

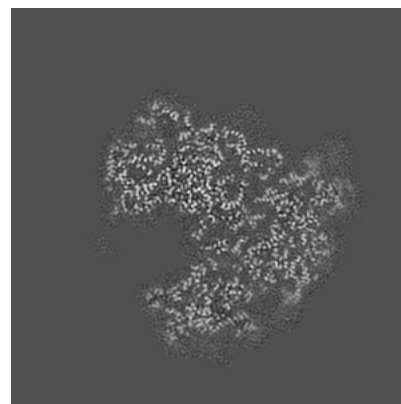
6.3.1 Primary map



X Index: 209



Y Index: 239

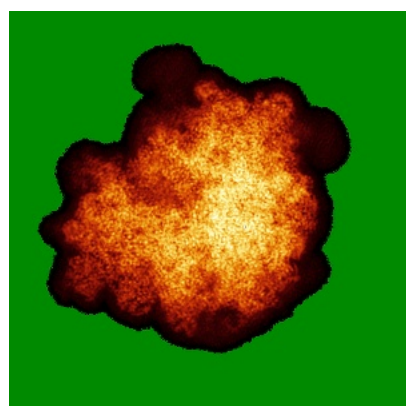


Z Index: 198

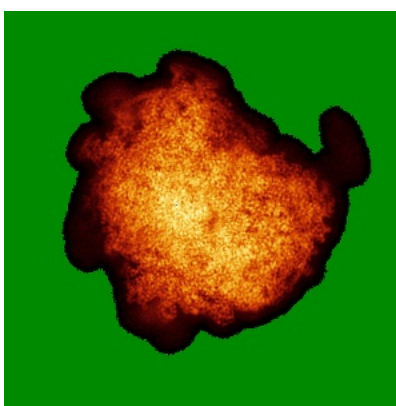
The images above show the largest variance slices of the map in three orthogonal directions.

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

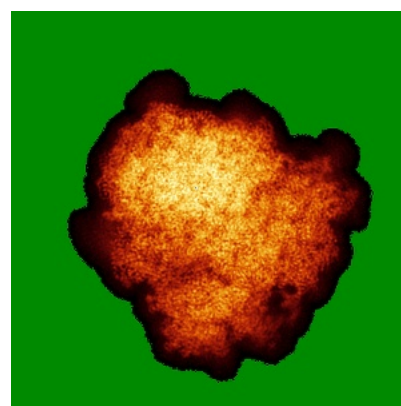
6.4.1 Primary map



X



Y

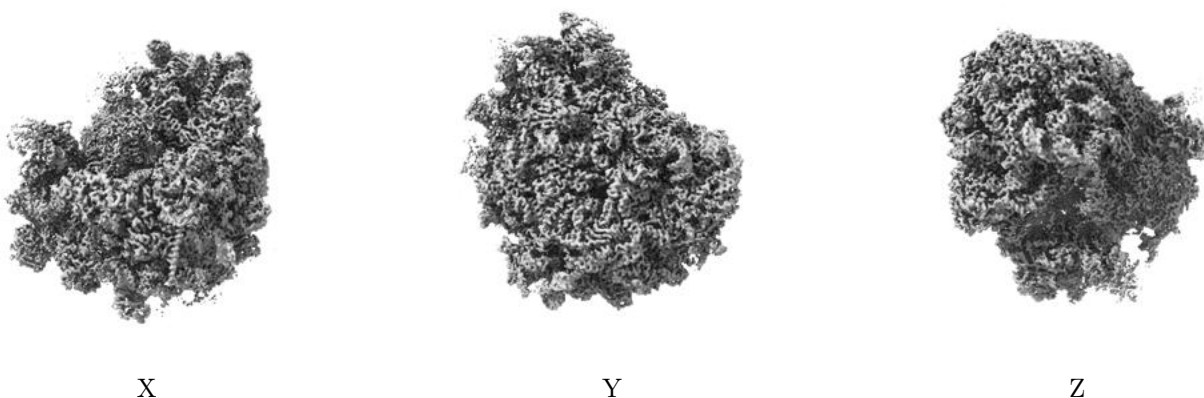


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

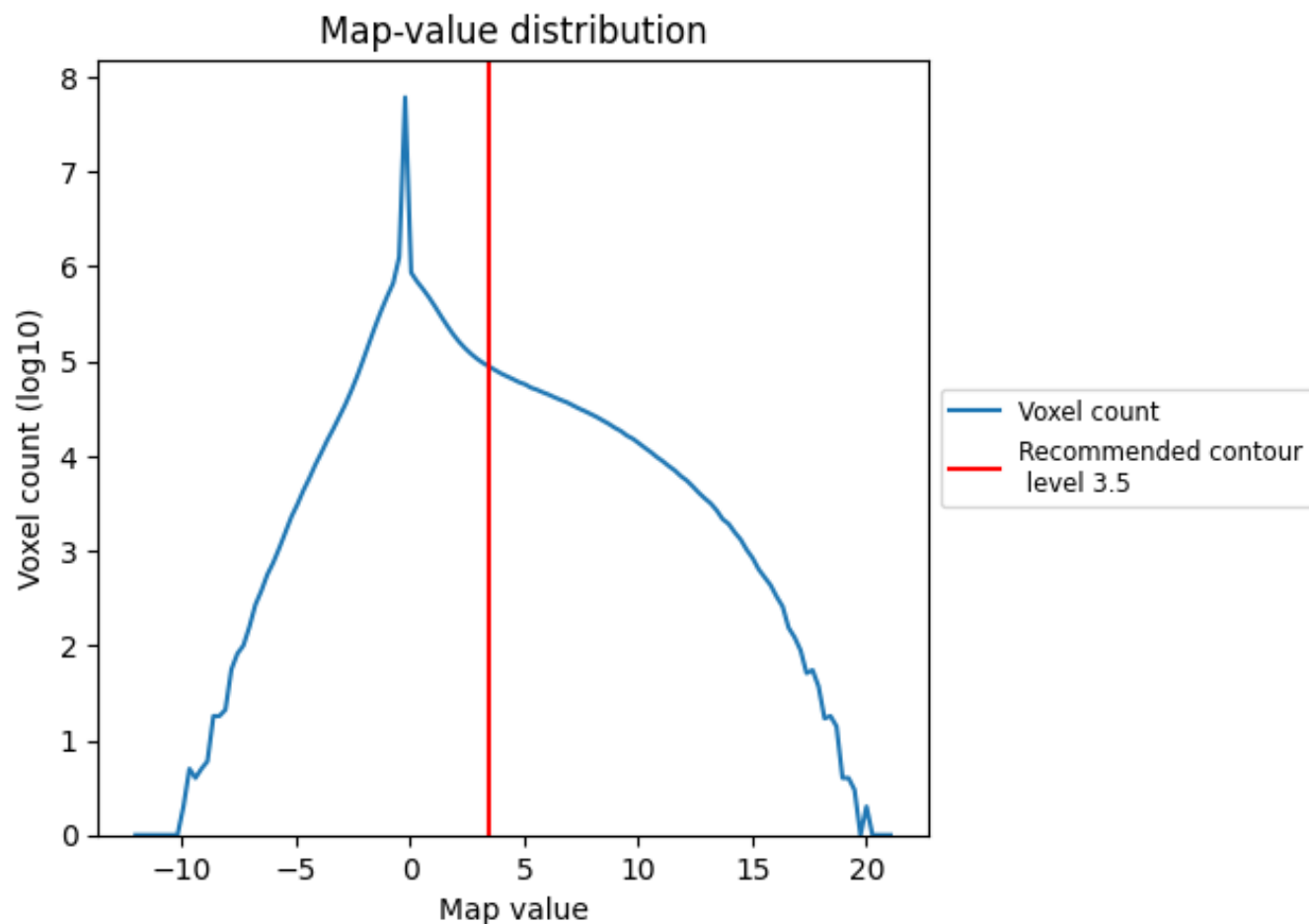
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

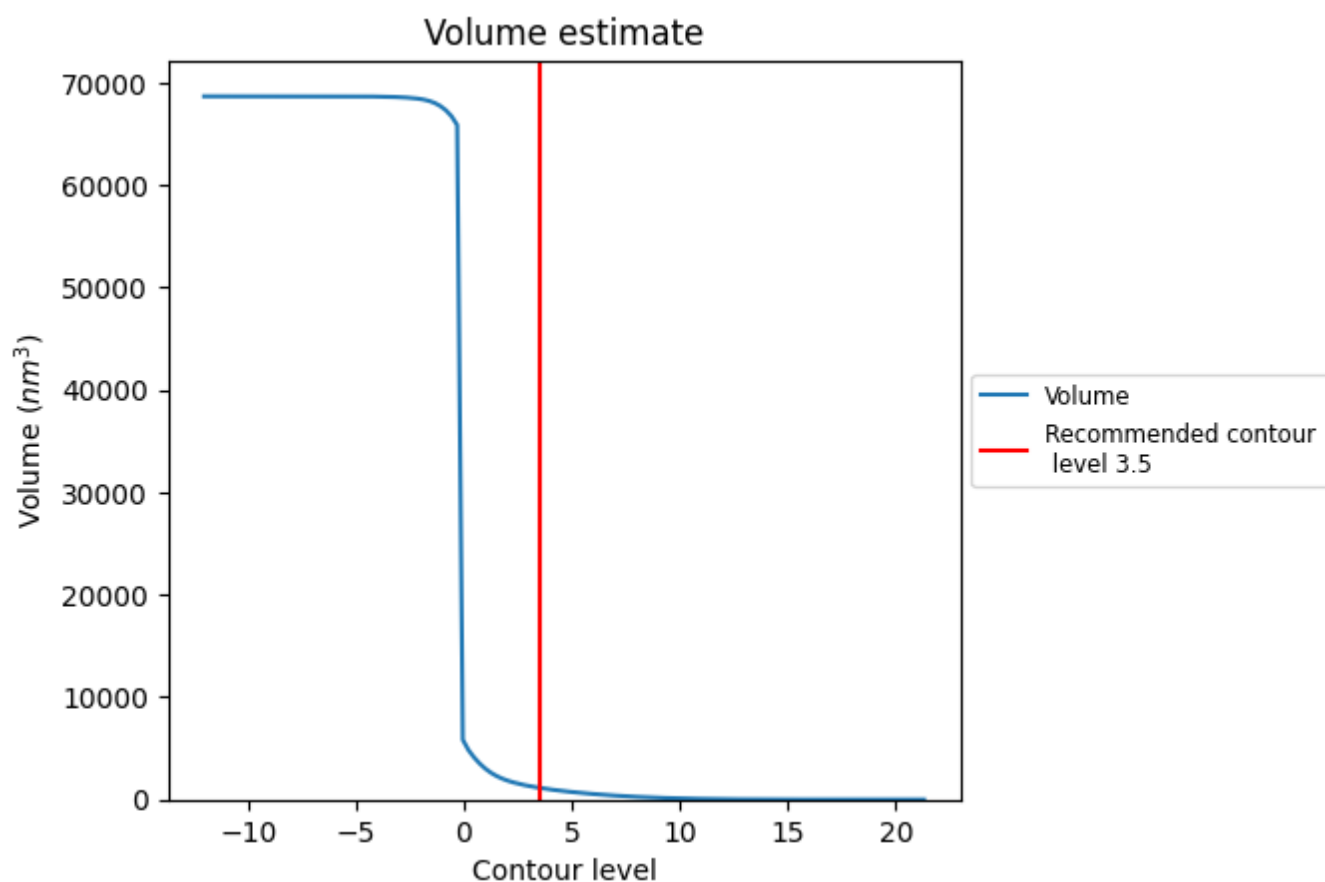
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

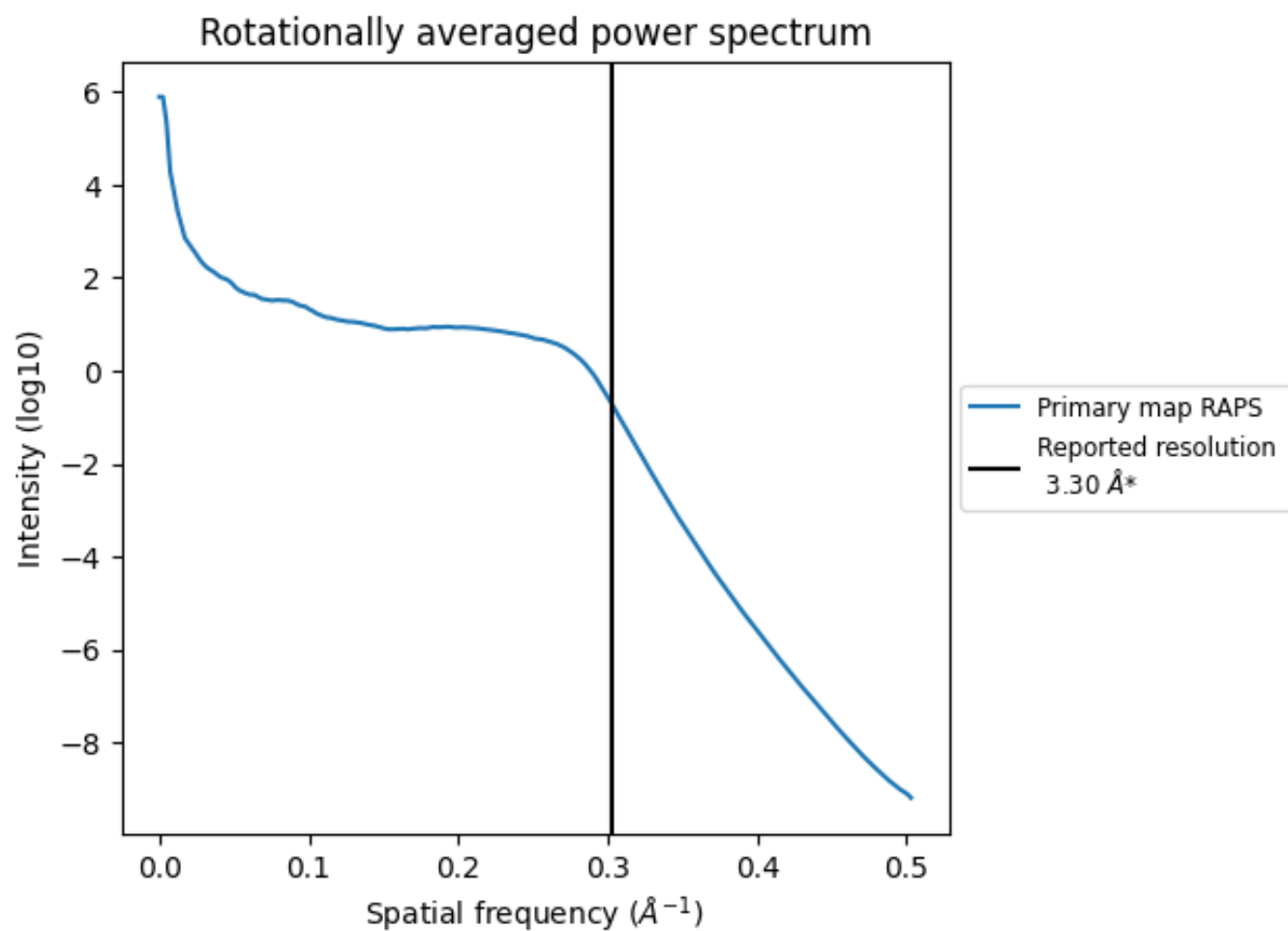
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1149 nm³; this corresponds to an approximate mass of 1038 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 ⓘ

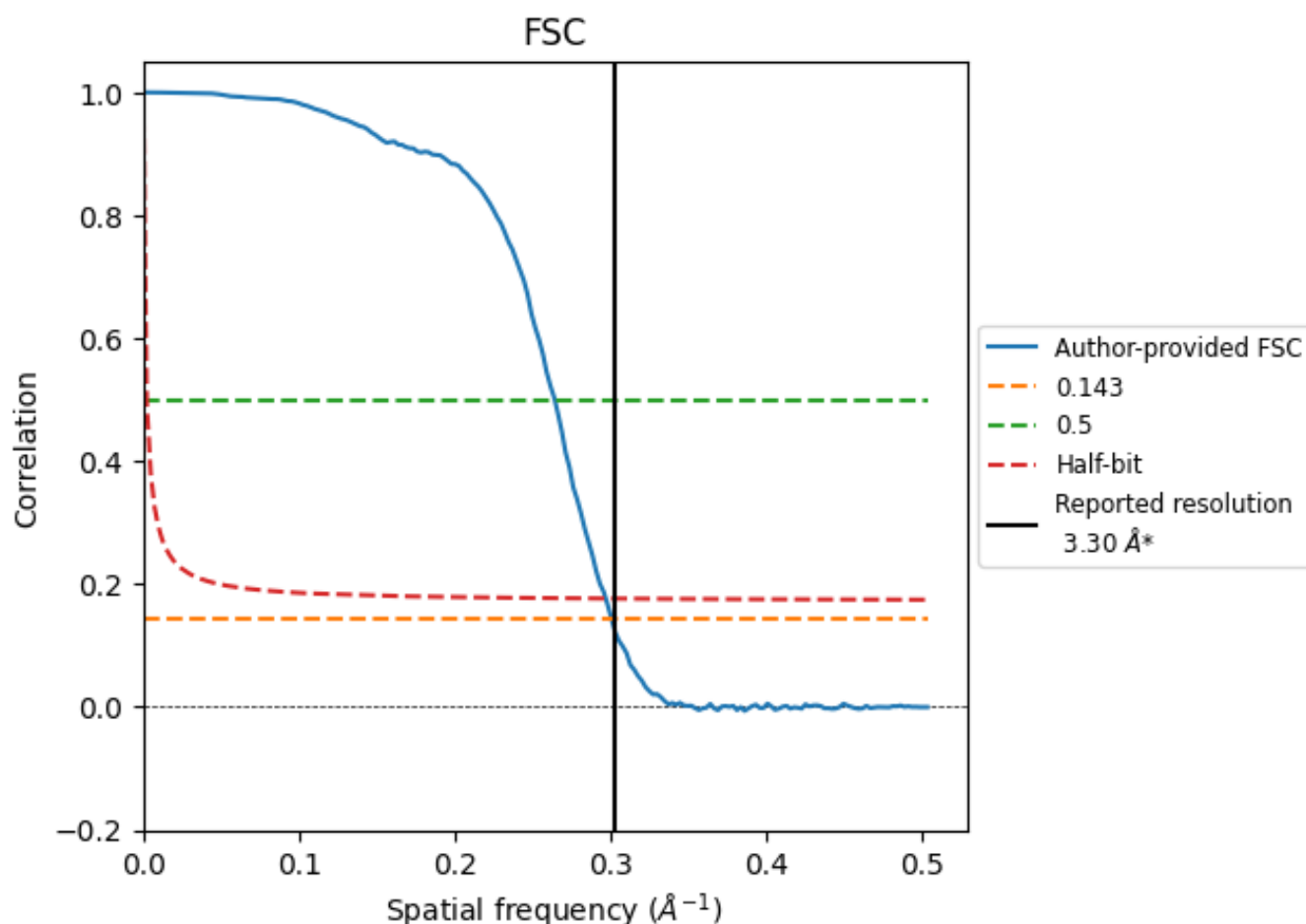


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

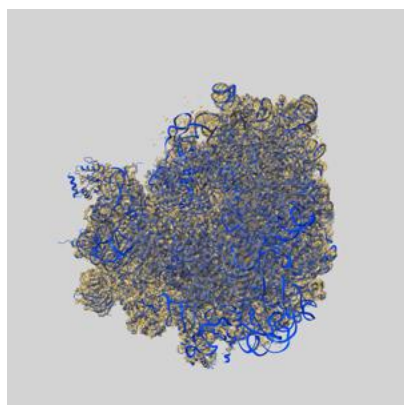
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.33	3.79	3.37
Unmasked-calculated*	-	-	-

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

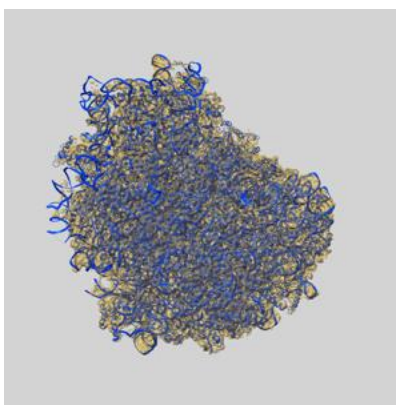
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4140 and PDB model 5M1J. Per-residue inclusion information can be found in [section 3](#) on [page 24](#).

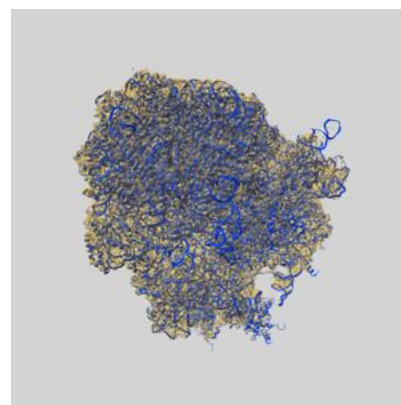
9.1 Map-model overlay [i](#)



X



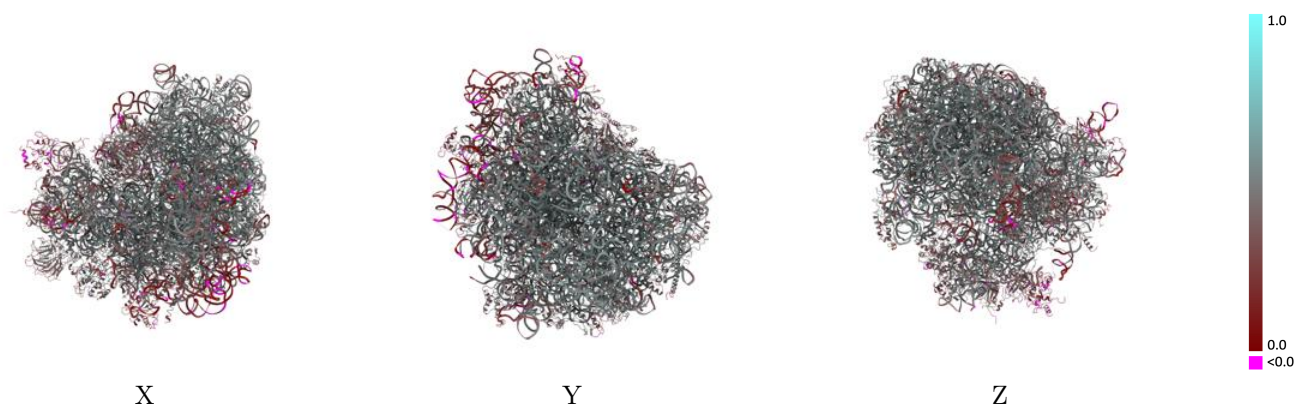
Y



Z

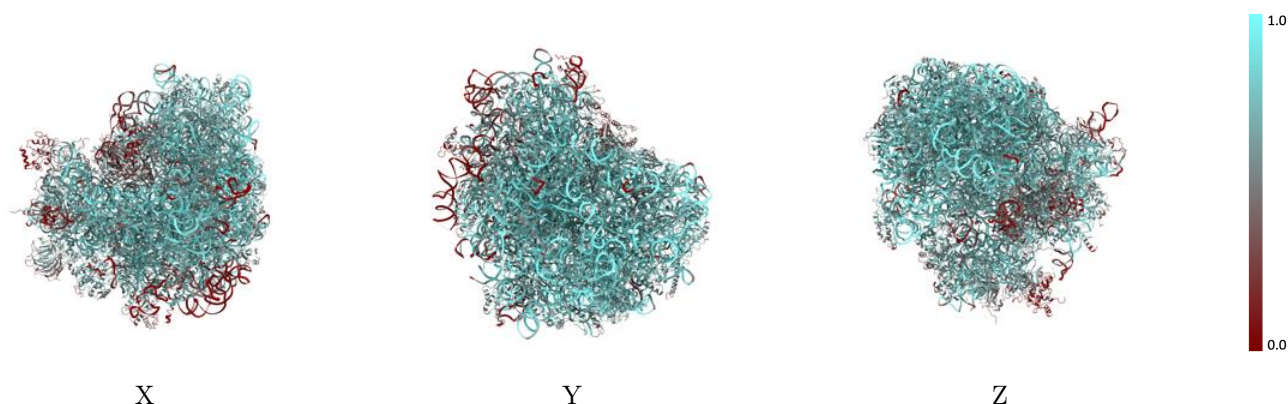
The images above show the 3D surface view of the map at the recommended contour level 3.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



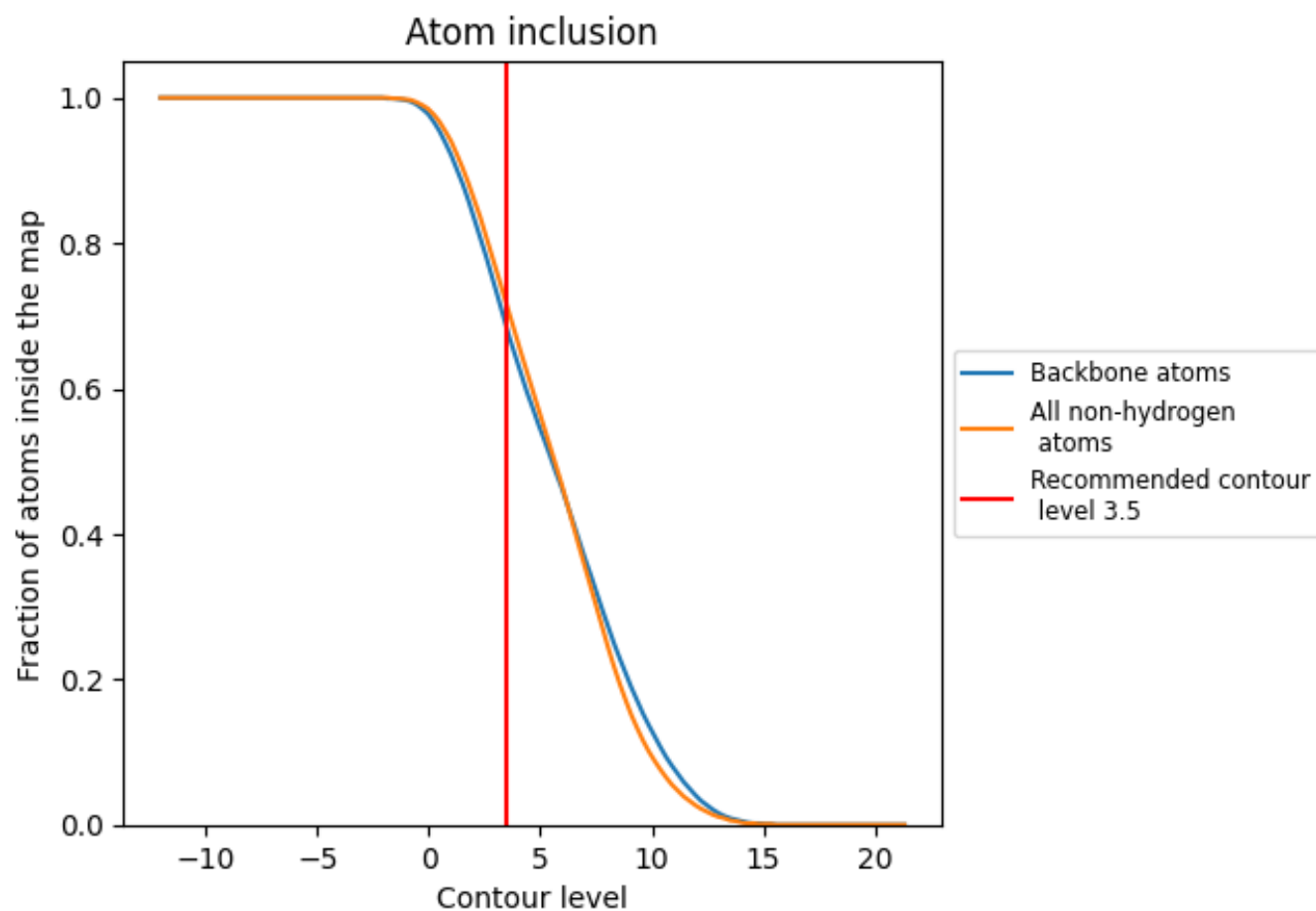
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 71% 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 (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7140	 0.4500
14	 0.8080	 0.4760
22	 0.7850	 0.4560
34	 0.8820	 0.5110
44	 0.8650	 0.5010
A1	 0.4290	 0.3930
A2	 0.6230	 0.4220
A3	 0.7560	 0.4830
A5	 0.7330	 0.4970
A6	 0.2620	 0.3170
B2	 0.6170	 0.4110
B5	 0.7060	 0.4680
C2	 0.6860	 0.4660
C5	 0.7070	 0.4570
D2	 0.5900	 0.4120
D5	 0.6310	 0.4150
E2	 0.6600	 0.4450
E5	 0.6230	 0.4440
F2	 0.5650	 0.3700
F5	 0.7110	 0.4720
G2	 0.5570	 0.3830
G5	 0.6170	 0.4160
H2	 0.4940	 0.3310
H5	 0.6450	 0.4520
I2	 0.6480	 0.4210
I5	 0.6570	 0.4460
J2	 0.6600	 0.4440
J5	 0.6080	 0.3880
K2	 0.5250	 0.3470
K5	 0.7200	 0.4870
L2	 0.6330	 0.4520
L5	 0.6820	 0.4510
M2	 0.0920	 0.1650
M5	 0.6520	 0.4380
N2	 0.6520	 0.4290



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Chain	Atom inclusion	Q-score
N5	 0.7620	 0.5020
O2	 0.6630	 0.4420
P2	 0.5150	 0.3600
P5	 0.6810	 0.4310
Q2	 0.6310	 0.4090
Q5	 0.7250	 0.4750
R2	 0.5770	 0.3890
R5	 0.6440	 0.4420
S2	 0.5540	 0.3540
S5	 0.6910	 0.4670
T2	 0.5810	 0.3910
T5	 0.7020	 0.4680
U2	 0.5100	 0.3610
U5	 0.5960	 0.4020
V2	 0.6040	 0.3960
V5	 0.6610	 0.4760
W2	 0.7090	 0.4780
W5	 0.4480	 0.3500
X2	 0.6680	 0.4740
X5	 0.6890	 0.4780
X7	 0.4980	 0.4460
Y2	 0.6000	 0.4010
Y5	 0.6760	 0.4690
Z2	 0.5890	 0.4250
Z5	 0.6390	 0.4170
a2	 0.6930	 0.4500
a5	 0.7020	 0.4470
b2	 0.6280	 0.4240
b5	 0.6620	 0.4330
c2	 0.6080	 0.4490
c5	 0.6520	 0.4460
d2	 0.7300	 0.4580
d5	 0.6650	 0.4500
e2	 0.5470	 0.4060
e5	 0.7140	 0.5000
f2	 0.2070	 0.2050
f5	 0.7460	 0.5180
g2	 0.5010	 0.3710
g5	 0.6840	 0.4650
h5	 0.6640	 0.4510
i5	 0.6040	 0.3940
j5	 0.7860	 0.5090

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Chain	Atom inclusion	Q-score
k5	 0.5940	 0.4010
l5	 0.7160	 0.4750
m5	 0.6780	 0.4670
n5	 0.7080	 0.4820
o5	 0.6510	 0.4710
p5	 0.6490	 0.4480