



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 10:39 AM UTC

PDB ID : 6OLG / pdb_00006olg
EMDB ID : EMD-0601
Title : Human ribosome nascent chain complex stalled by a drug-like small molecule
(CDH1_RNC with PP tRNA)
Authors : Li, W.; Cate, J.H.D.
Deposited on : 2019-04-16
Resolution : 3.40 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:

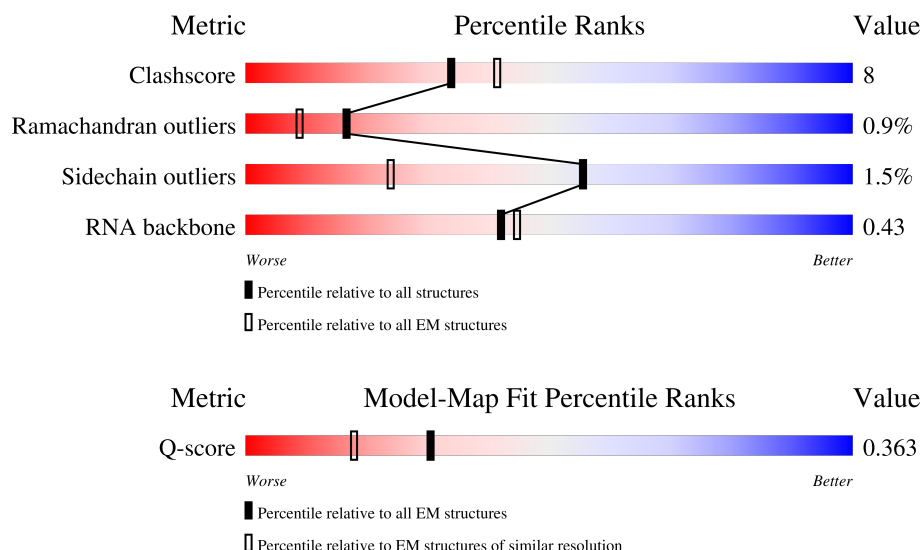
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	AA	257	
2	BA	215	
3	AB	394	

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Mol	Chain	Length	Quality of chain
4	BB	212	
5	AC	363	
6	BC	222	
7	A3	157	
8	A4	119	
9	AD	294	
10	AE	194	
11	AF	234	
12	AG	234	
13	AH	191	
14	AI	211	
15	AJ	169	
16	AK	109	
17	AL	205	
18	AM	139	
19	AN	203	
20	AO	195	
21	AP	153	
22	AQ	187	
23	AR	181	
24	AS	175	
25	AT	157	
26	AU	99	
27	AV	129	
28	AW	121	

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Mol	Chain	Length	Quality of chain
29	AX	117	
30	AY	127	
31	AZ	134	
32	Aa	147	
33	Ab	121	
34	Ac	103	
35	Ad	106	
36	Ae	129	
37	Af	109	
38	Ag	114	
39	Ah	122	
40	Ai	97	
41	Aj	84	
42	Ak	69	
43	Al	50	
44	Am	50	
45	An	25	
46	Ao	105	
47	Ap	91	
48	Aq	138	
49	At	122	
50	Au	217	
51	A2	3612	
52	B1	1708	
53	BD	220	

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Mol	Chain	Length	Quality of chain
54	BE	257	32% 79% 21%
55	BF	190	53% 77% 23%
56	BG	232	51% 80% 19%
57	BH	183	50% 80% 19%
58	BI	207	28% 77% 20%
59	BJ	179	36% 80% 18%
60	BK	98	71% 71% 28%
61	BL	153	30% 83% 16%
62	BM	120	99% 79% 21%
63	BN	149	24% 83% 17%
64	BO	136	30% 86% 13%
65	BP	120	61% 61% 29% 8%
66	BQ	139	52% 83% 17%
67	BR	125	55% 80% 18%
68	BS	139	58% 81% 17%
69	BT	143	53% 76% 23%
70	BU	97	59% 87% 13%
71	BV	81	41% 91% 9%
72	BW	129	15% 81% 18%
73	BX	139	20% 78% 22%
74	BY	125	38% 85% 15%
75	BZ	86	70% 87% 13%
76	Ba	97	25% 70% 30%
77	Bb	80	42% 90% 10%
78	Bc	62	53% 68% 31%

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Mol	Chain	Length	Quality of chain
79	Bd	51	
80	Be	55	
81	Bf	73	
82	Bg	314	
83	Bv	76	
84	Bx	16	
85	A	39	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 216796 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 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	252	Total	C	N	O	S	0	0
			1930	1209	395	320	6		

- Molecule 2 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	BA	215	Total	C	N	O	S	0	0
			1704	1083	298	315	8		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AB	394	Total	C	N	O	S	0	0
			3178	2024	596	544	14		

- Molecule 4 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	BB	212	Total	C	N	O	S	0	0
			1722	1093	308	307	14		

- Molecule 5 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AC	363	Total	C	N	O	S	0	0
			2888	1817	577	480	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	BC	222	Total	C	N	O	S	0	0
			1724	1114	296	304	10		

- Molecule 7 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A3	157	Total	C	N	O	P	0	0
			3337	1489	587	1104	157		

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A4	119	Total	C	N	O	P	0	0
			2541	1132	454	836	119		

- Molecule 9 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AD	294	Total	C	N	O	S	0	0
			2392	1510	436	432	14		

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AE	194	Total	C	N	O	S	0	0
			1571	1013	294	263	1		

- Molecule 11 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AF	234	Total	C	N	O	S	0	0
			1950	1252	376	313	9		

- Molecule 12 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AG	234	Total	C	N	O	S	0	0
			1880	1197	362	317	4		

- Molecule 13 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AH	191	Total	C	N	O	S	0	0
			1526	960	285	275	6		

- Molecule 14 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AI	208	Total	C	N	O	S	0	0
			1692	1074	327	278	13		

- Molecule 15 is a protein called 60S ribosomal protein L11.

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

- Molecule 16 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AK	109	Total	C	N	O	S	0	0
			872	554	159	151	8		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AL	205	Total	C	N	O	S	0	0
			1657	1036	344	273	4		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 19 is a protein called 60S ribosomal protein L15.

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

- Molecule 20 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AO	195	Total	C	N	O	S	0	0
			1606	1034	315	252	5		

- Molecule 21 is a protein called 60S ribosomal protein L17.

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

- Molecule 22 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 23 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AR	181	Total	C	N	O	S	0	0
			1517	938	329	241	9		

- Molecule 24 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AS	175	Total	C	N	O	S	0	0
			1449	921	283	234	11		

- Molecule 25 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AT	157	Total	C	N	O	S	0	0
			1284	815	250	214	5		

- Molecule 26 is a protein called 60S ribosomal protein L22.

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

- Molecule 27 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AV	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 28 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AW	121	Total	C	N	O	S	0	0
			989	617	202	167	3		

- Molecule 29 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AX	117	Total	C	N	O	S	0	0
			958	612	180	165	1		

- Molecule 30 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AY	127	Total	C	N	O	S	0	0
			1064	668	216	177	3		

- Molecule 31 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AZ	134	Total	C	N	O	S	0	0
			1103	712	207	181	3		

- Molecule 32 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Aa	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 33 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ab	68	Total	C	N	O	S	0	0
			559	344	122	90	3		

- Molecule 34 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ac	103	Total	C	N	O	S	0	0
			801	508	141	145	7		

- Molecule 35 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ad	106	Total	C	N	O	S	0	0
			879	555	170	152	2		

- Molecule 36 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ae	129	Total	C	N	O	S	0	0
			1064	673	220	166	5		

- Molecule 37 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Af	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 38 is a protein called 60S ribosomal protein L34.

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

- Molecule 39 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Ah	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 40 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ai	97	Total	C	N	O	S	0	0
			794	497	168	124	5		

- Molecule 41 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Aj	84	Total	C	N	O	S	0	0
			689	423	152	109	5		

- Molecule 42 is a protein called 60S ribosomal protein L38.

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

- Molecule 43 is a protein called 60S ribosomal protein L39.

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

- Molecule 44 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Am	50	Total	C	N	O	S	0	0
			411	254	87	64	6		

- Molecule 45 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	An	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 46 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ao	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 47 is a protein called 60S ribosomal protein L37a.

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

- Molecule 48 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Aq	138	Total	C	N	O	S	0	0
			1046	654	196	193	3		

- Molecule 49 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	At	122	Total	C	N	O	S	0	0
			980	607	204	165	4		

- Molecule 50 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Au	217	Total	C	N	O	S	0	0
			1744	1114	314	307	9		

- Molecule 51 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	A2	3612	Total	C	N	O	P	0	0
			77427	34482	14158	25175	3612		

- Molecule 52 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B1	1708	Total	C	N	O	P	0	0
			36456	16274	6546	11928	1708		

- Molecule 53 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BD	220	Total	C	N	O	S	0	0
			1709	1090	308	304	7		

- Molecule 54 is a protein called 40S ribosomal protein S4, Y isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BE	257	Total	C	N	O	S	0	0
			2031	1298	381	344	8		

- Molecule 55 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BF	190	Total	C	N	O	S	0	0
			1502	939	285	271	7		

- Molecule 56 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BG	232	Total	C	N	O	S	0	0
			1884	1176	379	322	7		

- Molecule 57 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BH	183	Total	C	N	O	S	0	0
			1479	941	272	265	1		

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BI	207	Total	C	N	O	S	0	0
			1696	1064	334	293	5		

- Molecule 59 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BJ	179	Total	C	N	O	S	0	0
			1495	953	299	241	2		

- Molecule 60 is a protein called 40S ribosomal protein S10.

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

- Molecule 61 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	BL	153	Total	C	N	O	S	0	0
			1258	804	235	213	6		

- Molecule 62 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	BM	120	Total	C	N	O	S	0	0
			931	584	164	174	9		

- Molecule 63 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	BN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 64 is a protein called 40S ribosomal protein S14.

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

- Molecule 65 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	BP	120	Total	C	N	O	S	0	0
			999	636	188	168	7		

- Molecule 66 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	BQ	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

- Molecule 67 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	BR	125	Total	C	N	O	S	0	0
			1011	634	187	186	4		

- Molecule 68 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	BS	139	Total	C	N	O	S	0	0
			1154	725	233	195	1		

- Molecule 69 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	BT	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 70 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	BU	97	Total	C	N	O	S	0	0
			769	483	144	138	4		

- Molecule 71 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	BV	81	Total	C	N	O	S	0	0
			617	380	114	118	5		

- Molecule 72 is a protein called 40S ribosomal protein S15a.

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

- Molecule 73 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	BX	139	Total	C	N	O	S	0	0
			1080	682	214	181	3		

- Molecule 74 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	BY	125	Total	C	N	O	S	0	0
			1015	642	199	169	5		

- Molecule 75 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	BZ	86	Total	C	N	O	S	0	0
			688	442	129	116	1		

- Molecule 76 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ba	97	Total	C	N	O	S	0	0
			774	481	160	128	5		

- Molecule 77 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Bb	80	Total	C	N	O	S	0	0
			625	391	116	111	7		

- Molecule 78 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bc	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 79 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Bd	51	Total	C	N	O	S	0	0
			427	269	87	66	5		

- Molecule 80 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Be	55	Total	C	N	O	S	0	0
			437	272	96	68	1		

- Molecule 81 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Bf	73	Total	C	N	O	S	0	0
			601	379	115	100	7		

- Molecule 82 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Bg	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

- Molecule 83 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Bv	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 84 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Bx	16	Total	C	N	O	P	0	0
			320	144	32	128	16		

- Molecule 85 is a protein called Cadherin-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
85	A	39	Total	C	N	O	0	0
			190	112	39	39		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	ALA	-	insertion	UNP P12830
A	10	GLU	VAL	conflict	UNP P12830

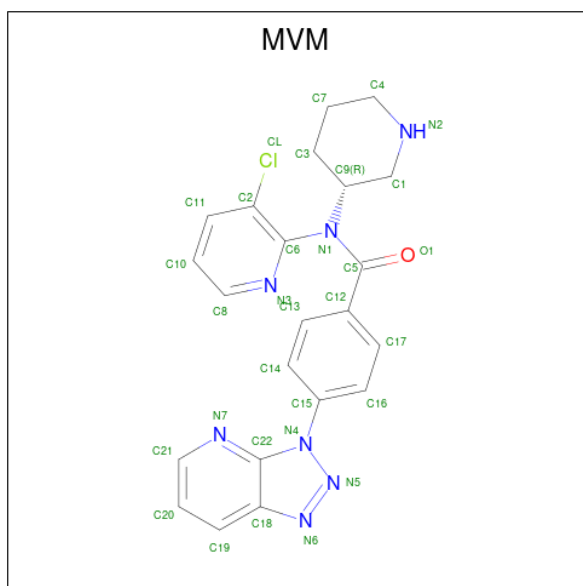
- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	AB	2	Total	Mg	0
			2	2	
86	A3	6	Total	Mg	0
			6	6	
86	A4	9	Total	Mg	0
			9	9	
86	AP	1	Total	Mg	0
			1	1	
86	AY	1	Total	Mg	0
			1	1	
86	Aa	1	Total	Mg	0
			1	1	
86	Ae	1	Total	Mg	0
			1	1	
86	A2	226	Total	Mg	0
			226	226	
86	B1	75	Total	Mg	0
			75	75	
86	BI	1	Total	Mg	0
			1	1	
86	Ba	1	Total	Mg	0
			1	1	
86	Bv	2	Total	Mg	0
			2	2	

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	Aj	1	Total	Zn	0
			1	1	
87	Ao	1	Total	Zn	0
			1	1	
87	Ap	1	Total	Zn	0
			1	1	
87	Ba	1	Total	Zn	0
			1	1	
87	Bd	1	Total	Zn	0
			1	1	

- Molecule 88 is N-(3-chloropyridin-2-yl)-N-[(3R)-piperidin-3-yl]-4-(3H-[1,2,3]triazolo[4,5-b]pyridin-3-yl)benzamide (CCD ID: MVM) (formula: C₂₂H₂₀ClN₇O).

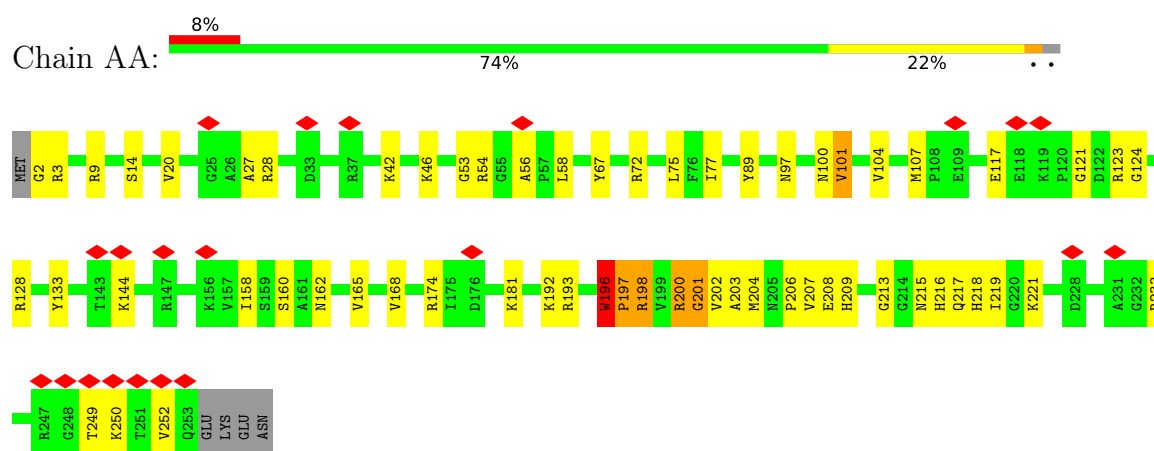


Mol	Chain	Residues	Atoms					AltConf
88	A2	1	Total	C	Cl	N	O	0
			31	22	1	7	1	

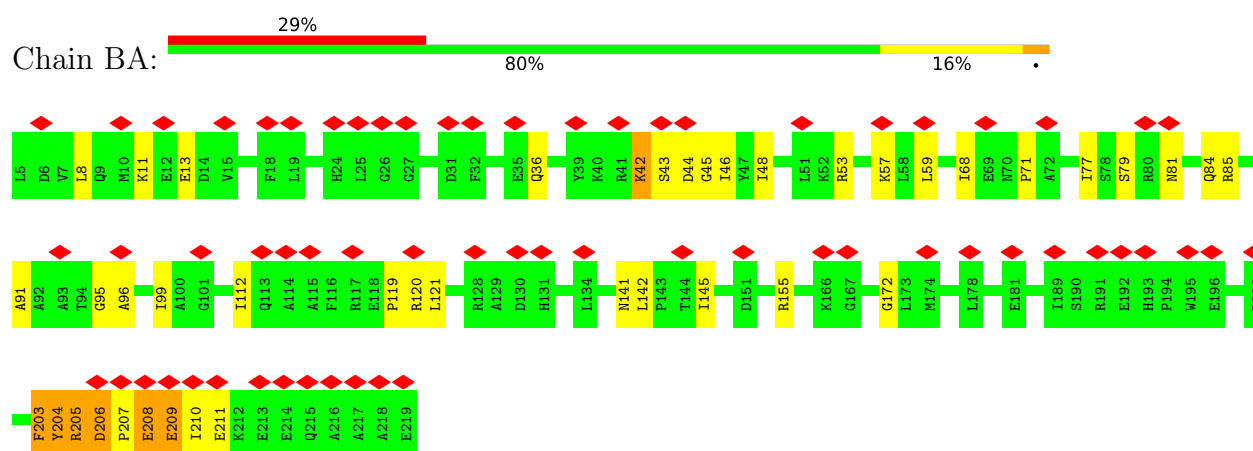
3 Residue-property plots

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.

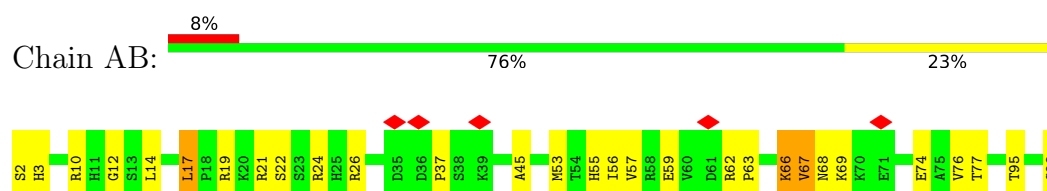
• Molecule 1: 60S ribosomal protein L8

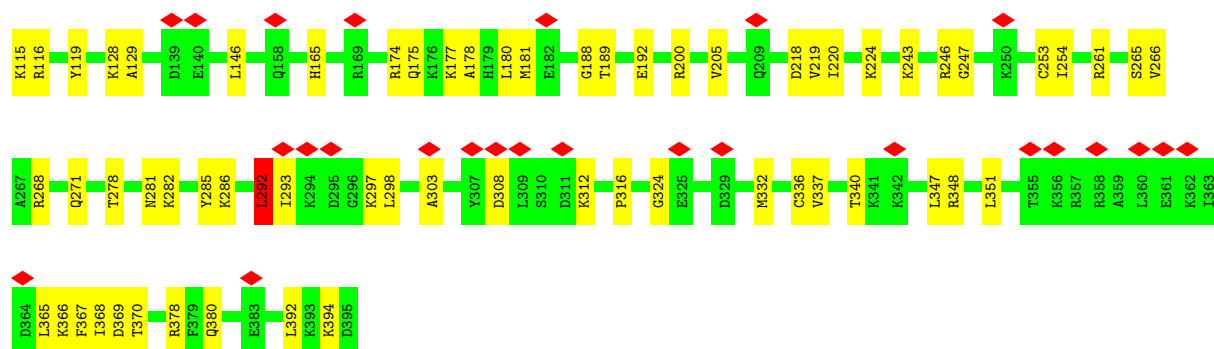


• Molecule 2: 40S ribosomal protein SA



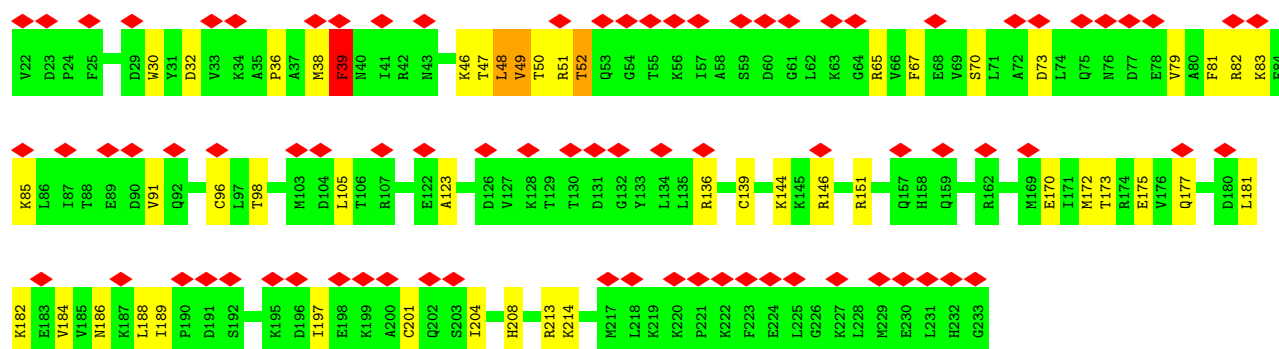
• Molecule 3: 60S ribosomal protein L3





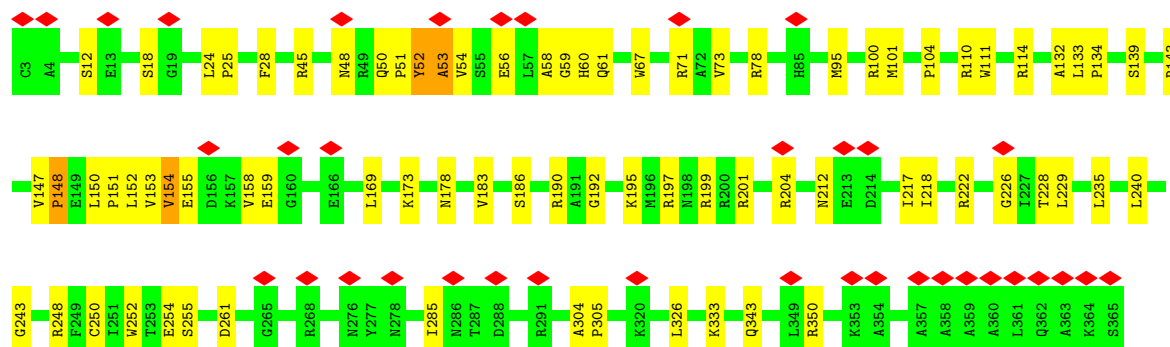
• Molecule 4: 40S ribosomal protein S3a

Chain BB: 38% 77% 21% .



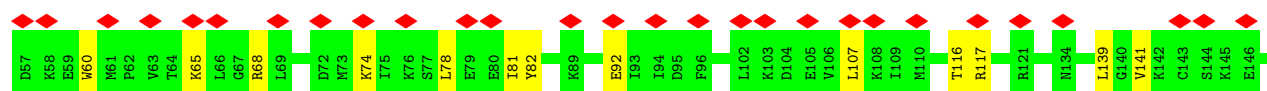
• Molecule 5: 60S ribosomal protein L4

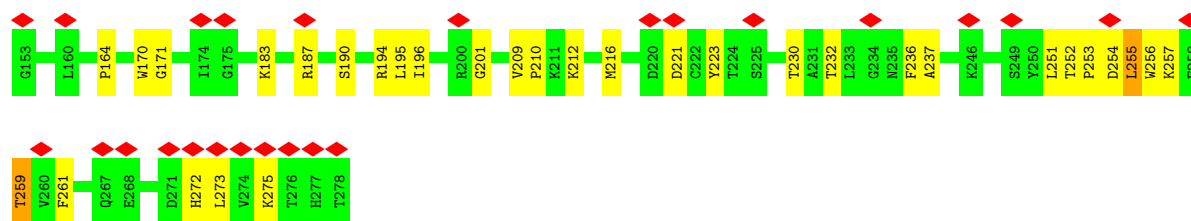
Chain AC: 10% 79% 20% .



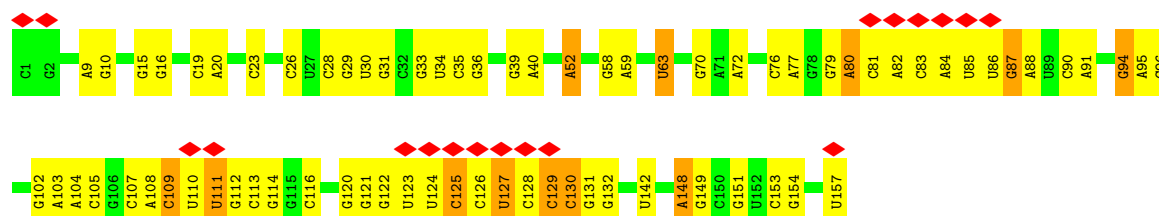
• Molecule 6: 40S ribosomal protein S2

Chain BC: 24% 80% 19% .

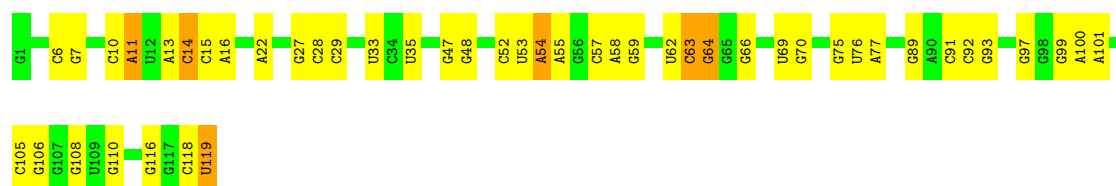




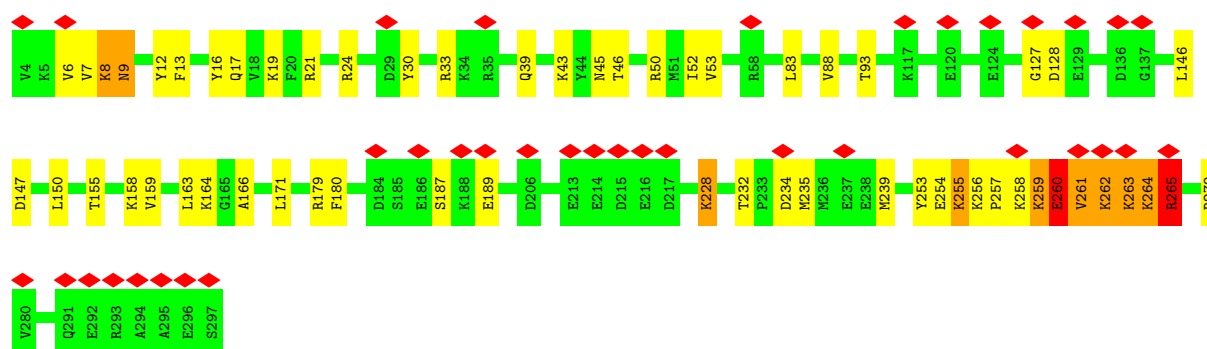
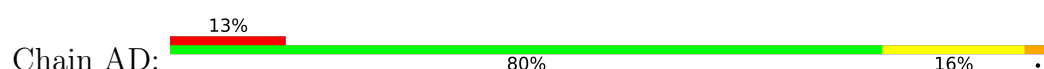
• Molecule 7: 5.8S ribosomal RNA



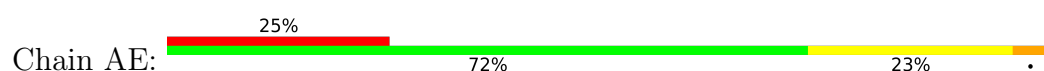
• Molecule 8: 5S ribosomal RNA

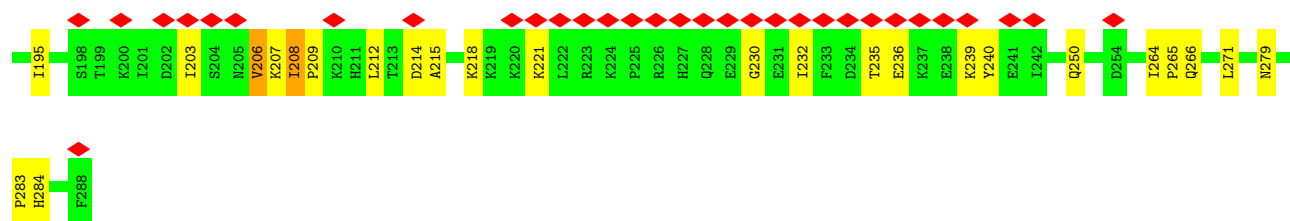


• Molecule 9: 60S ribosomal protein L5

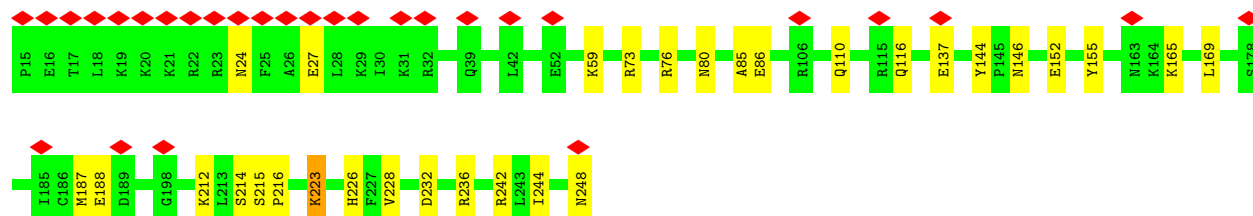
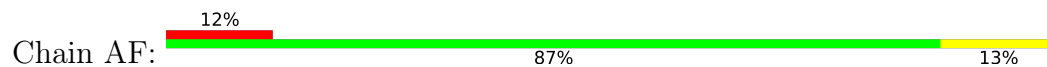


• Molecule 10: 60S ribosomal protein L6

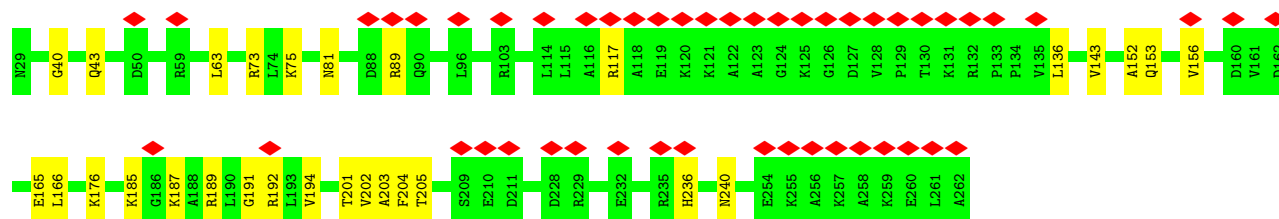
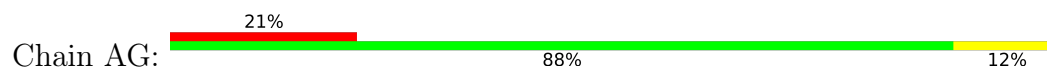




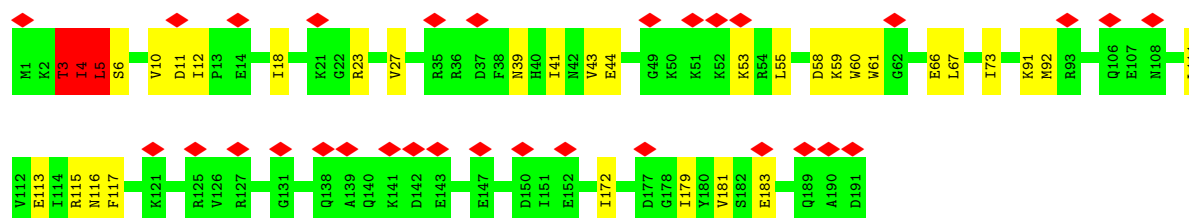
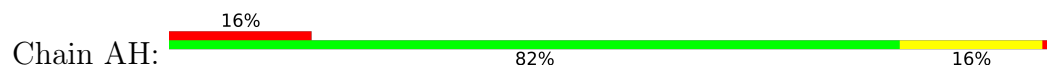
• Molecule 11: 60S ribosomal protein L7



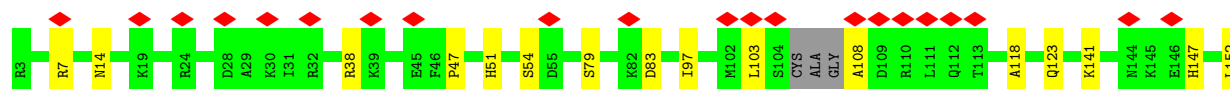
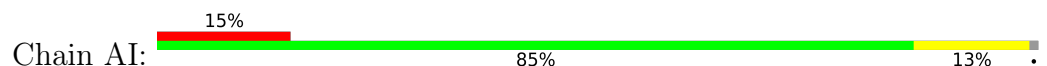
• Molecule 12: 60S ribosomal protein L7a



• Molecule 13: 60S ribosomal protein L9

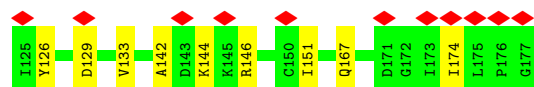
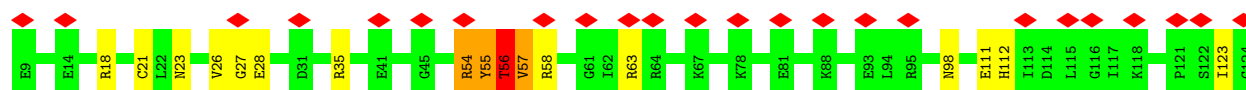
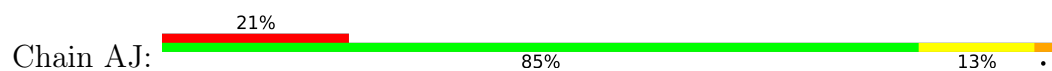


• Molecule 14: 60S ribosomal protein L10

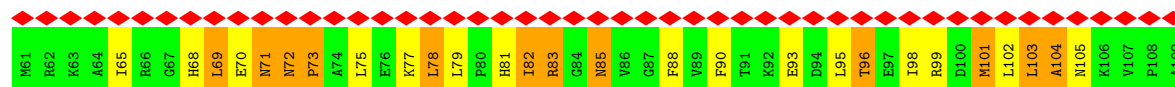
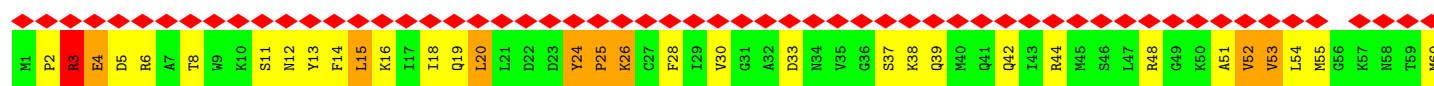




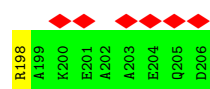
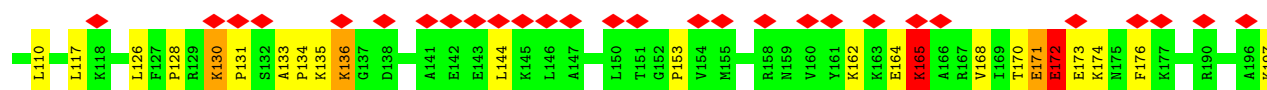
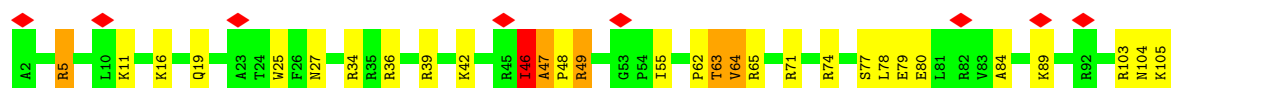
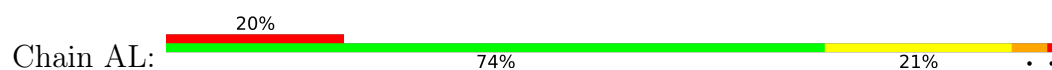
- Molecule 15: 60S ribosomal protein L11



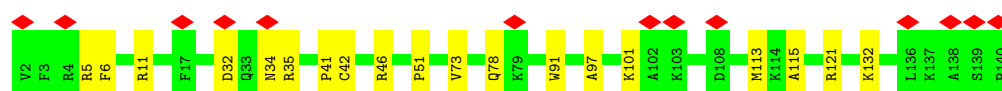
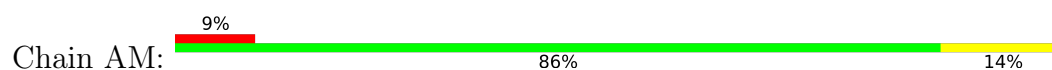
- Molecule 16: 60S acidic ribosomal protein P0



- Molecule 17: 60S ribosomal protein L13

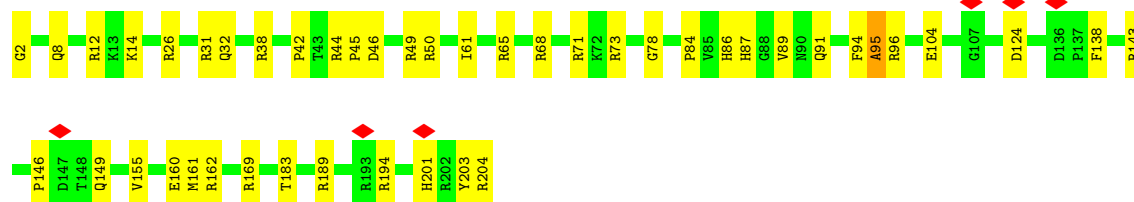


- Molecule 18: 60S ribosomal protein L14



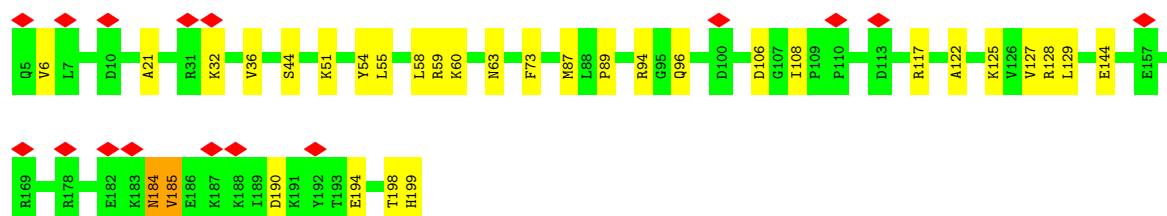
- Molecule 19: 60S ribosomal protein L15

Chain AN:  78% 22%



- Molecule 20: 60S ribosomal protein L13a

Chain AO:  8% 84% 15%



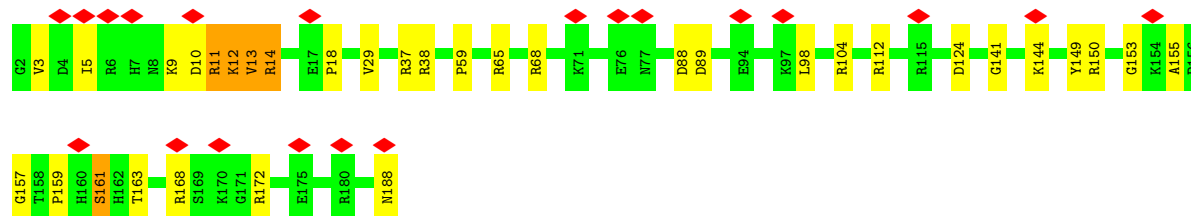
- Molecule 21: 60S ribosomal protein L17

Chain AP:  10% 88% 12%



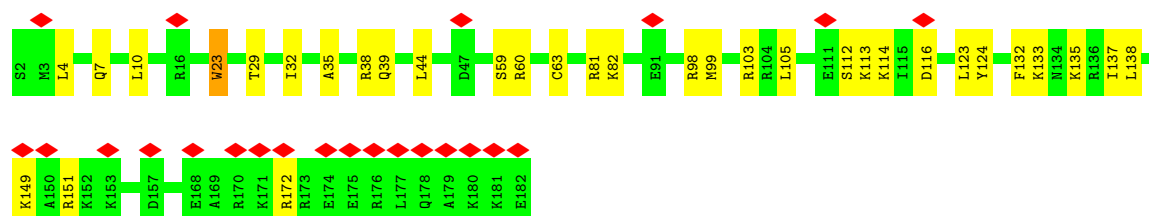
- Molecule 22: 60S ribosomal protein L18

Chain AQ:  11% 82% 16%

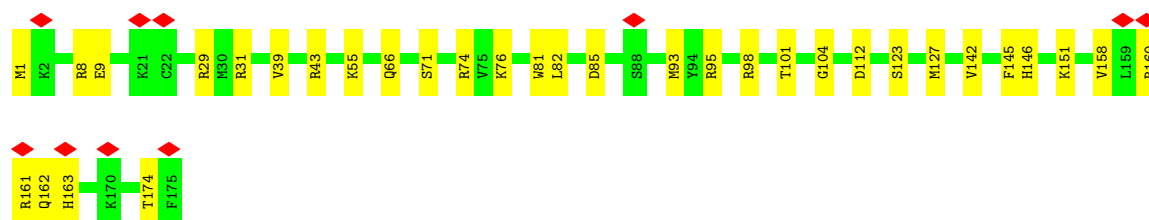
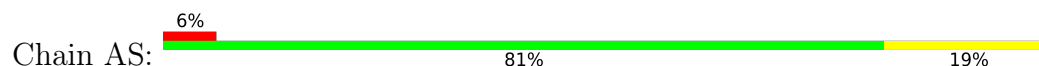


- Molecule 23: 60S ribosomal protein L19

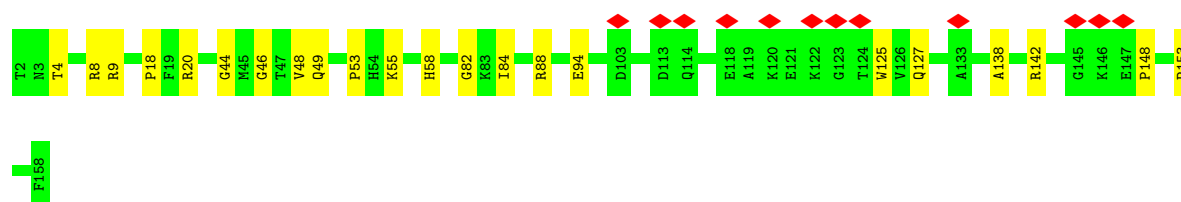
Chain AR:  13% 82% 18%



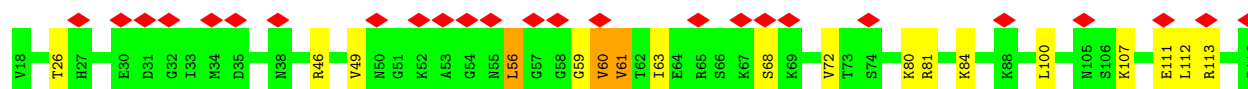
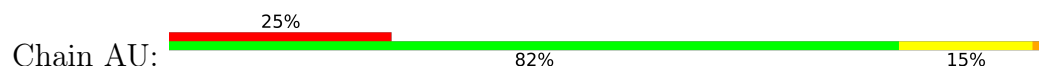
- Molecule 24: 60S ribosomal protein L18a



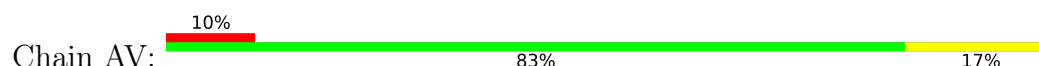
- Molecule 25: 60S ribosomal protein L21



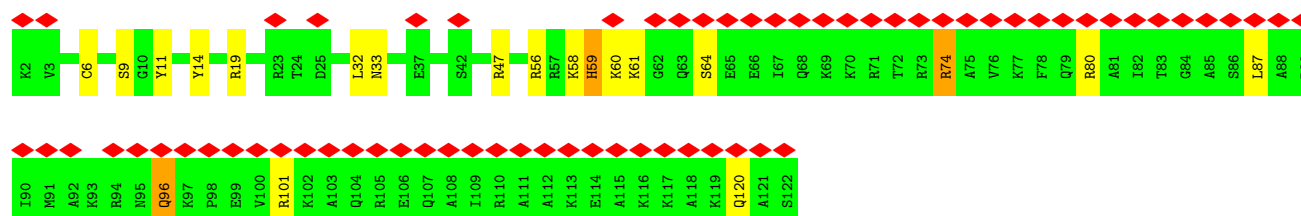
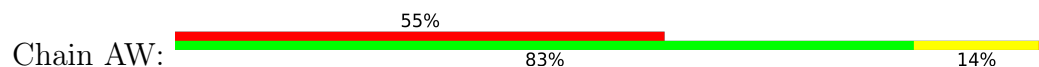
- Molecule 26: 60S ribosomal protein L22



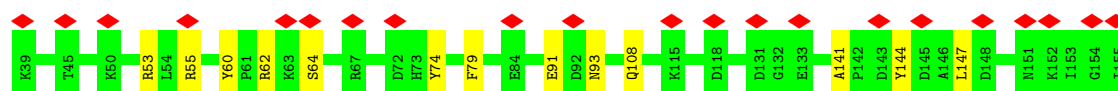
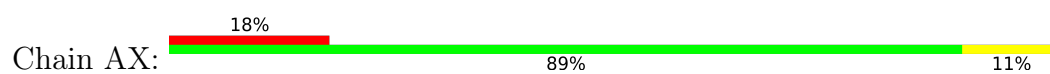
- Molecule 27: 60S ribosomal protein L23



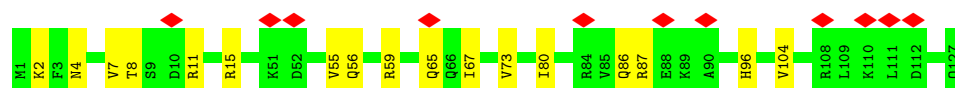
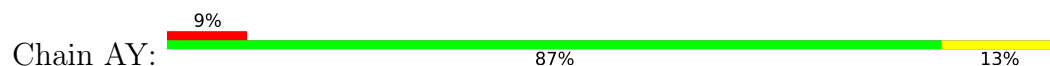
- Molecule 28: 60S ribosomal protein L24



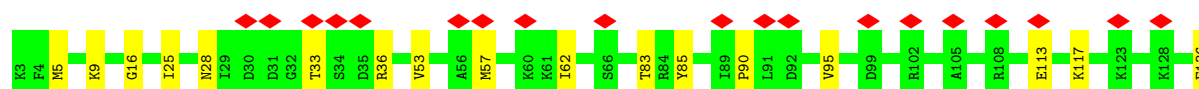
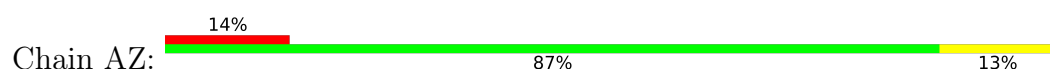
- Molecule 29: 60S ribosomal protein L23a



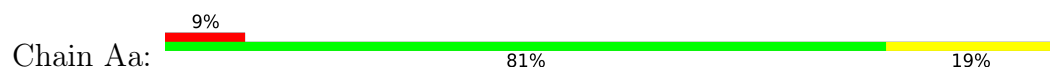
- Molecule 30: 60S ribosomal protein L26



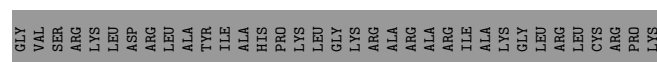
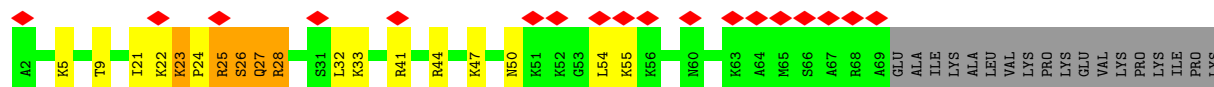
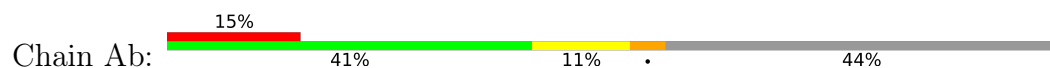
- Molecule 31: 60S ribosomal protein L27



- Molecule 32: 60S ribosomal protein L27a



- Molecule 33: 60S ribosomal protein L29

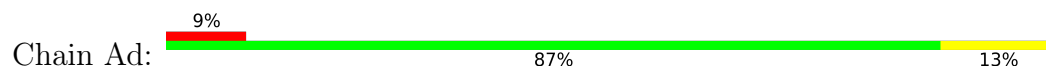


- Molecule 34: 60S ribosomal protein L30

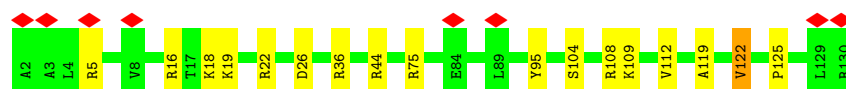




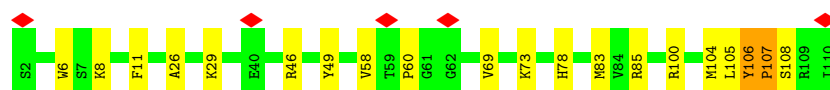
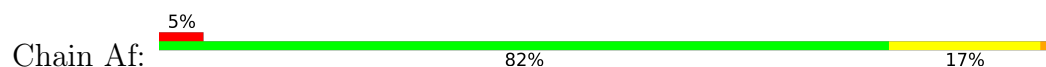
- Molecule 35: 60S ribosomal protein L31



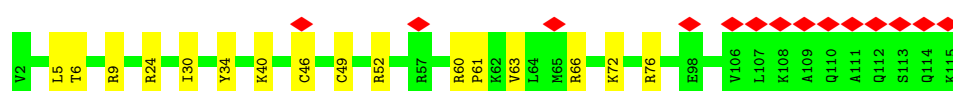
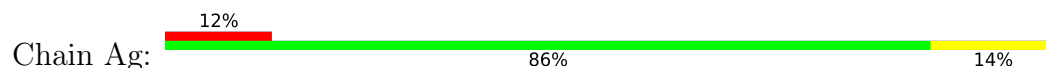
- Molecule 36: 60S ribosomal protein L32



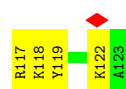
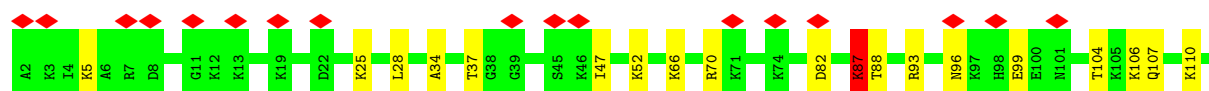
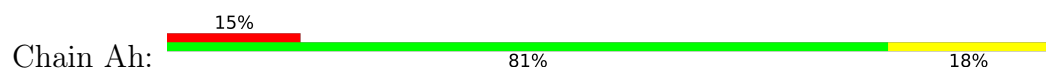
- Molecule 37: 60S ribosomal protein L35a



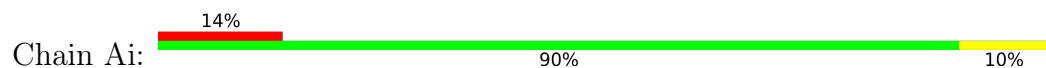
- Molecule 38: 60S ribosomal protein L34

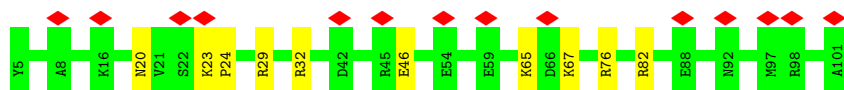


- Molecule 39: 60S ribosomal protein L35

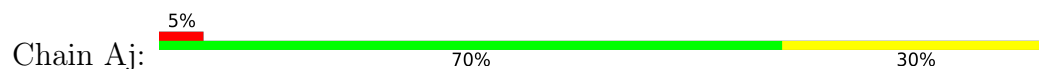


- Molecule 40: 60S ribosomal protein L36

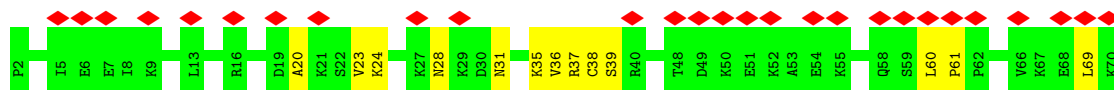
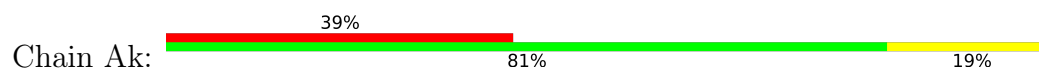




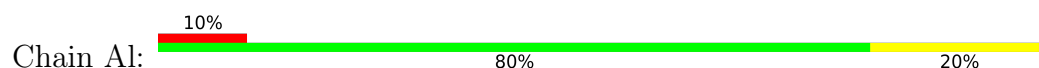
- Molecule 41: 60S ribosomal protein L37



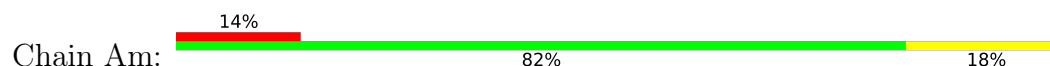
- Molecule 42: 60S ribosomal protein L38



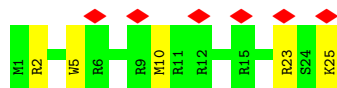
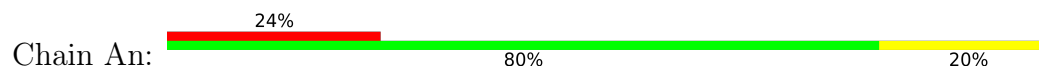
- Molecule 43: 60S ribosomal protein L39



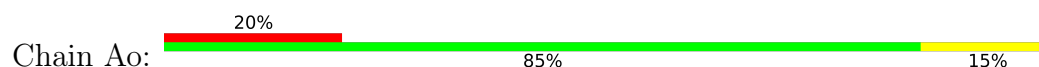
- Molecule 44: 60S ribosomal protein L40



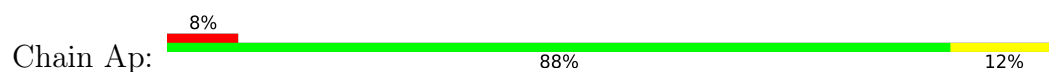
- Molecule 45: 60S ribosomal protein L41



- Molecule 46: 60S ribosomal protein L36a



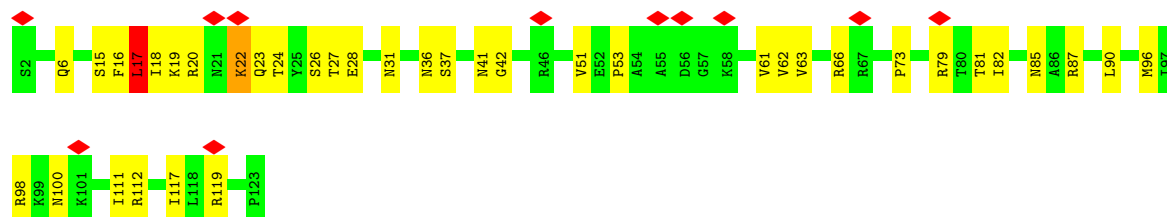
- Molecule 47: 60S ribosomal protein L37a



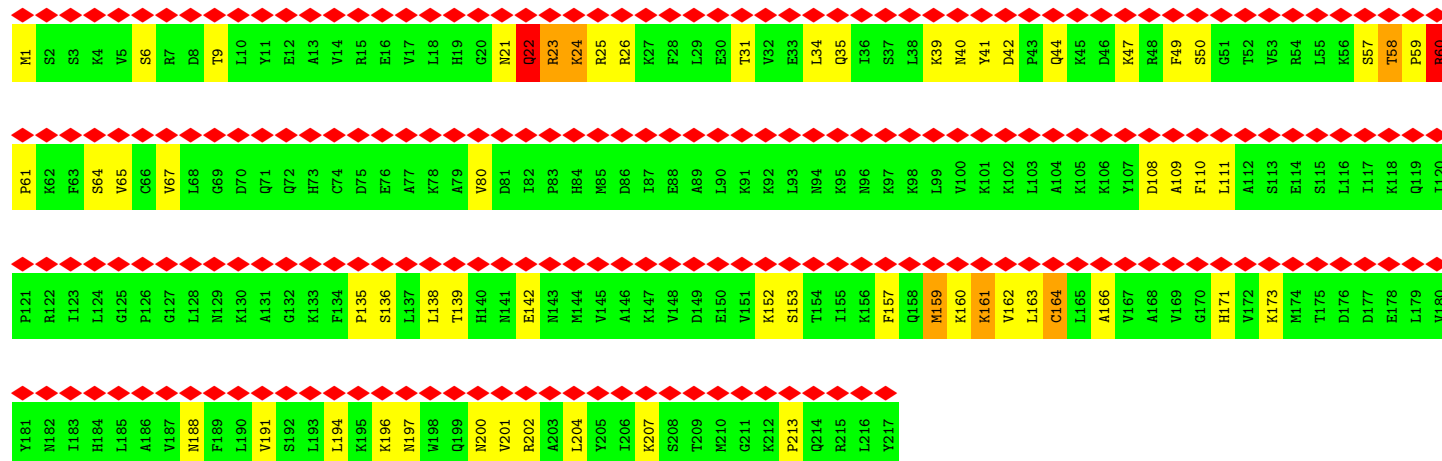
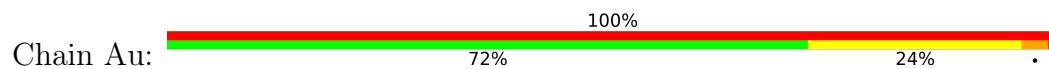
• Molecule 48: 60S ribosomal protein L12



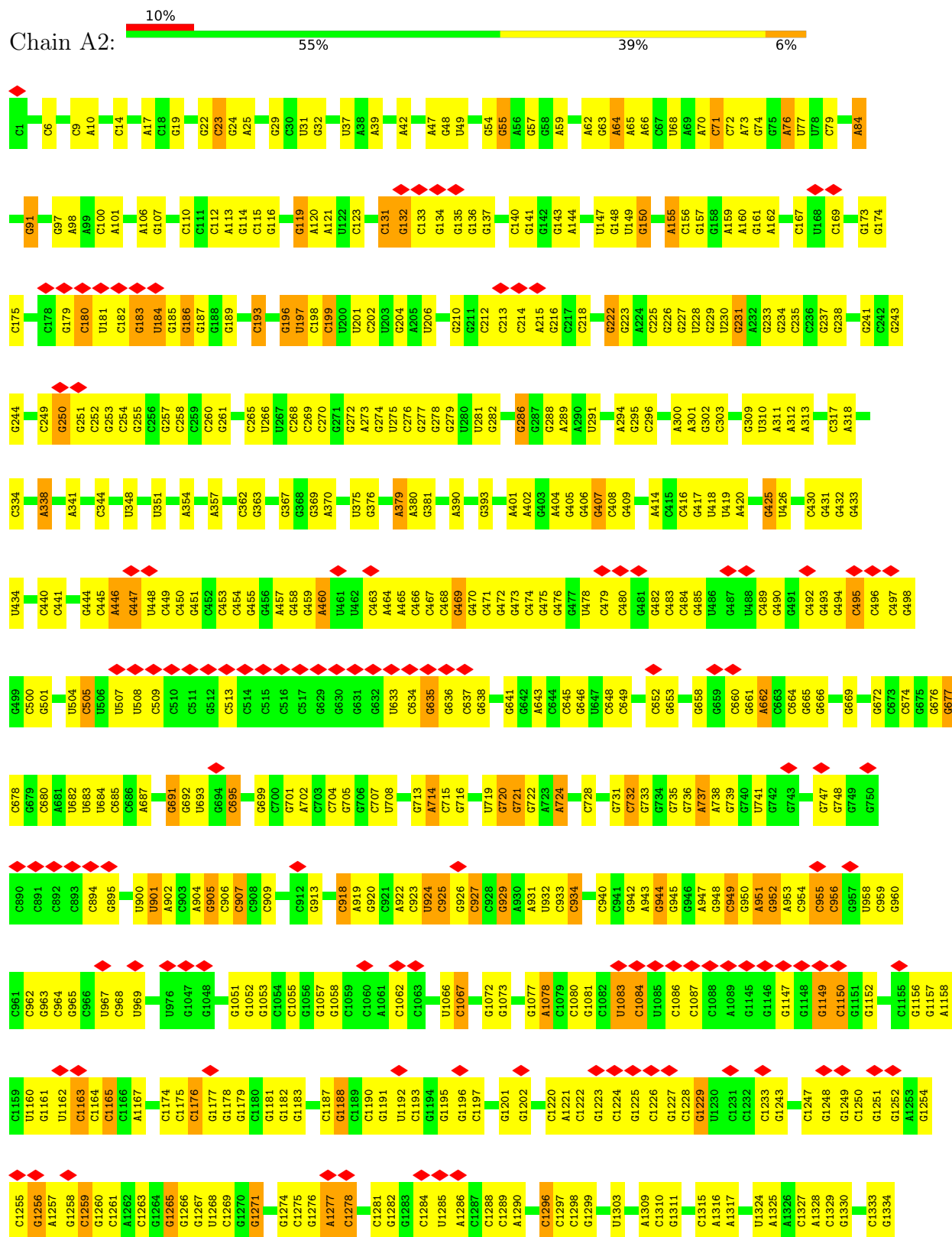
• Molecule 49: 60S ribosomal protein L28

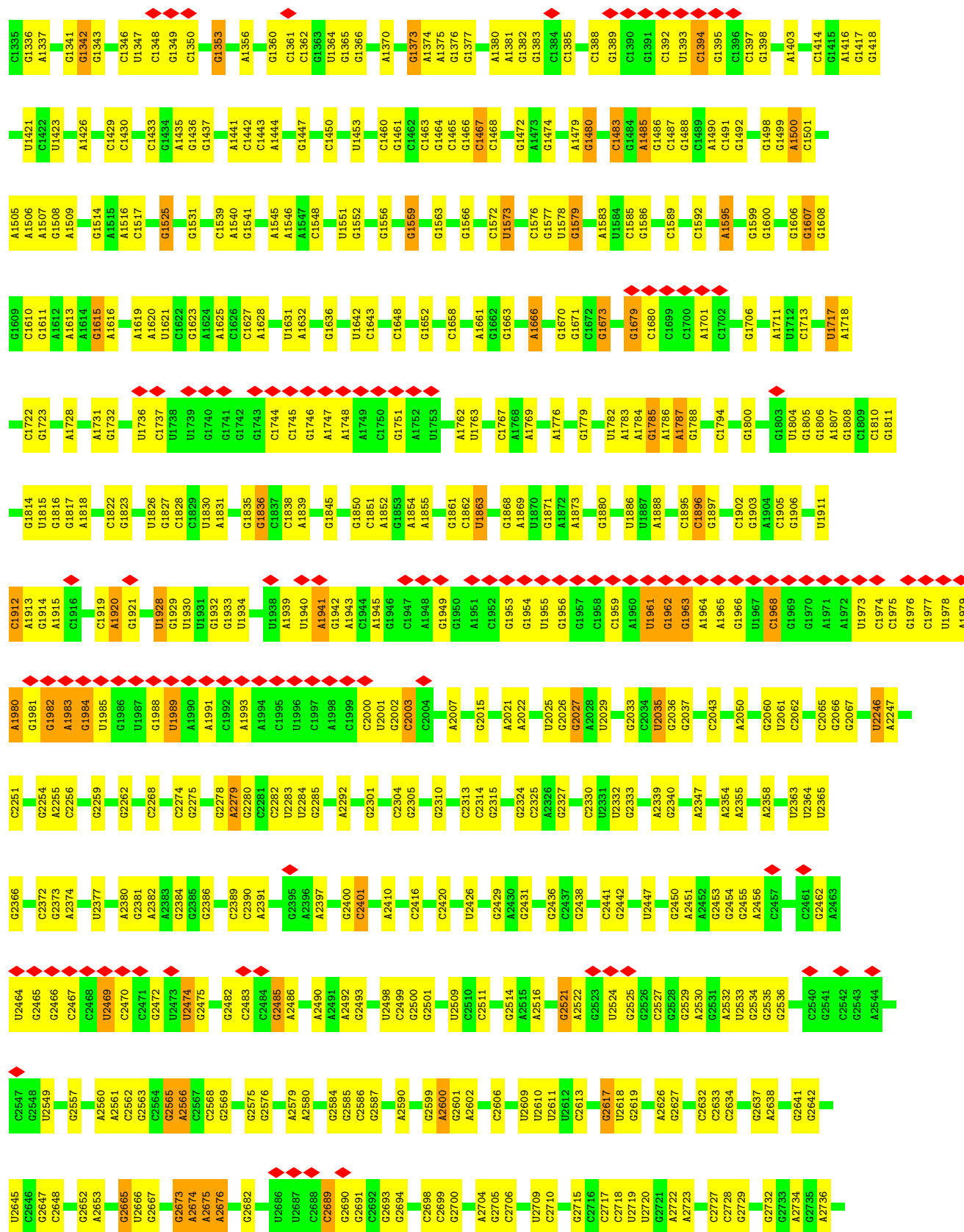


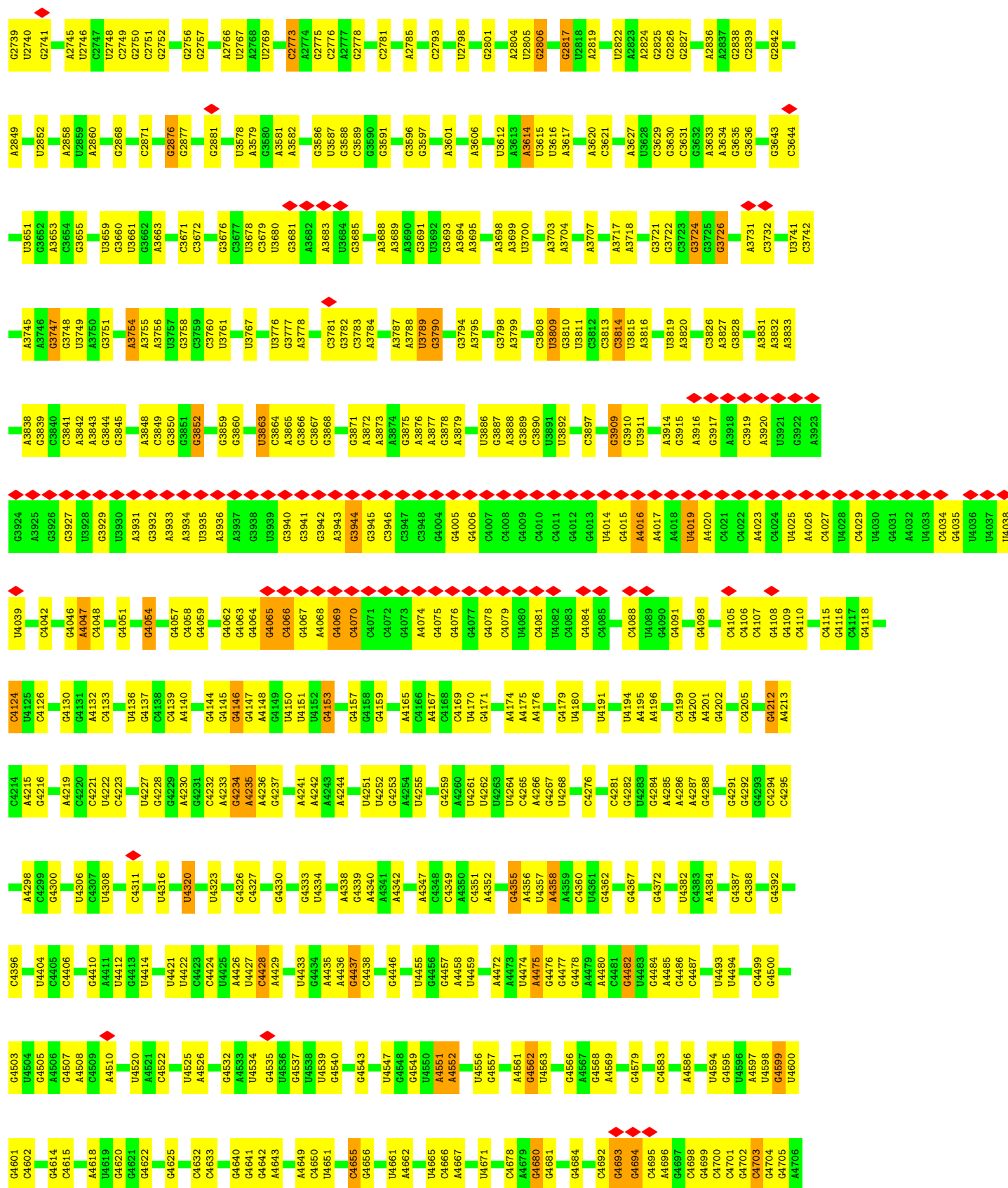
• Molecule 50: 60S ribosomal protein L10a

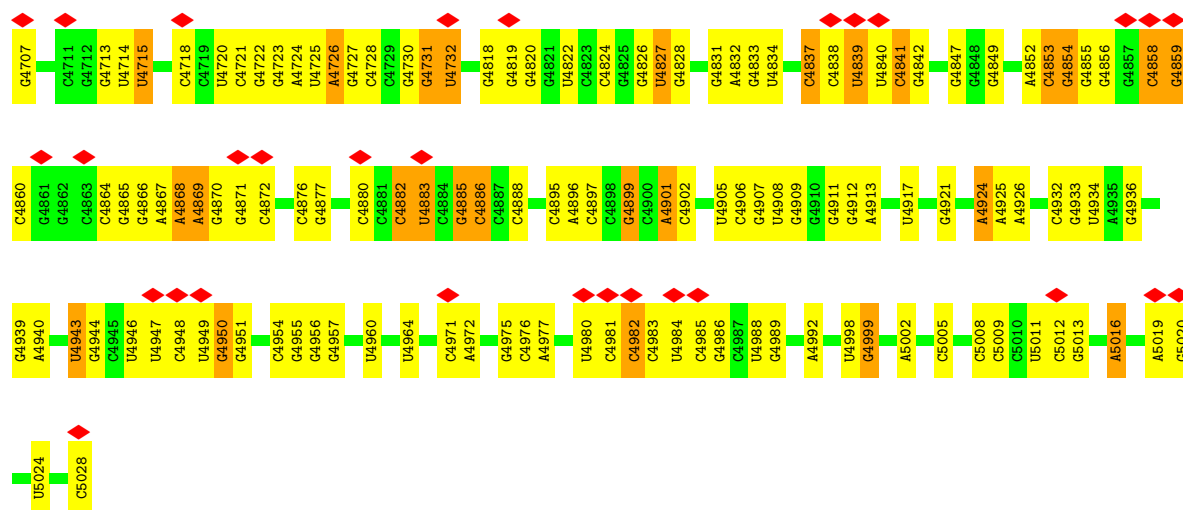


• Molecule 51: 28S ribosomal RNA

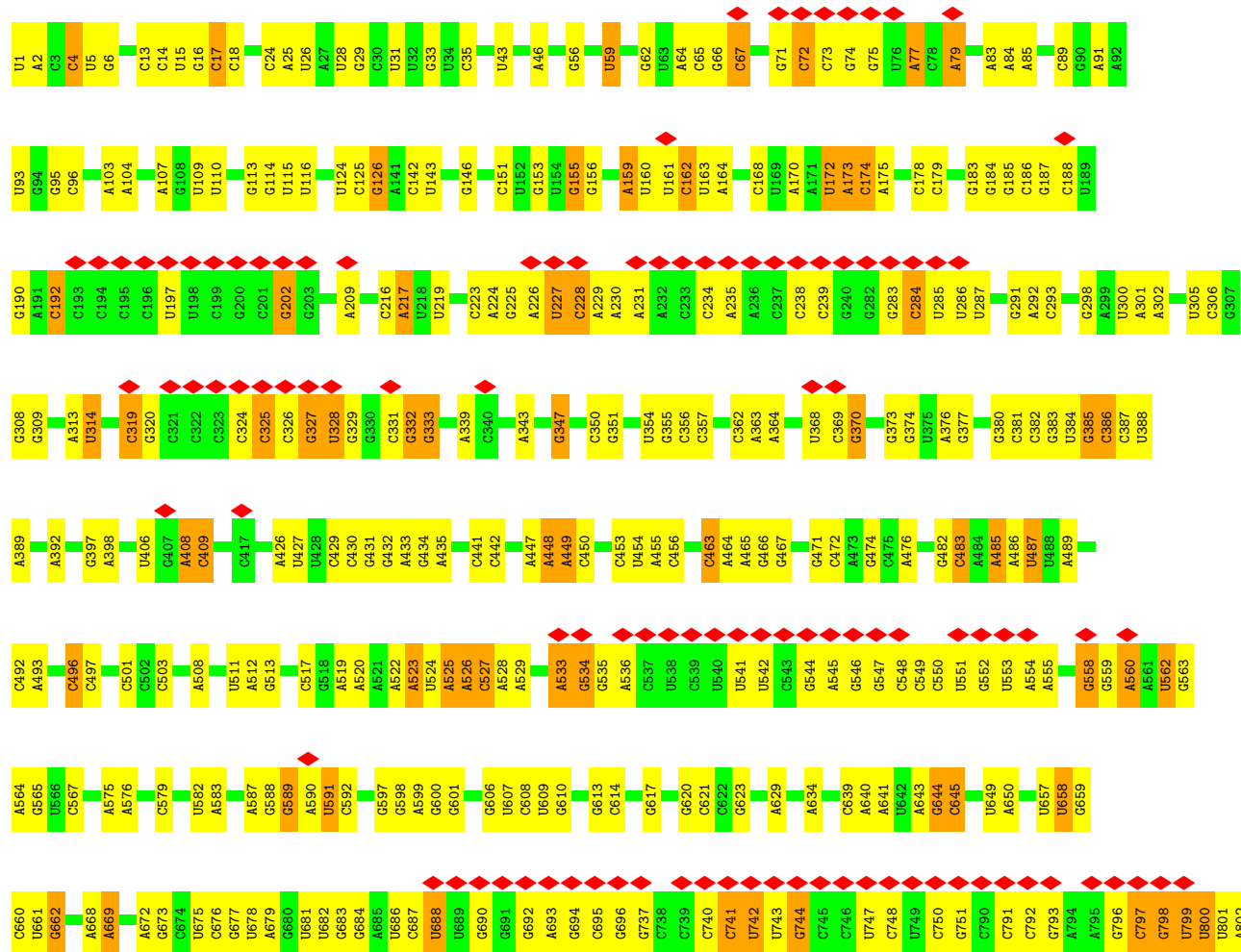




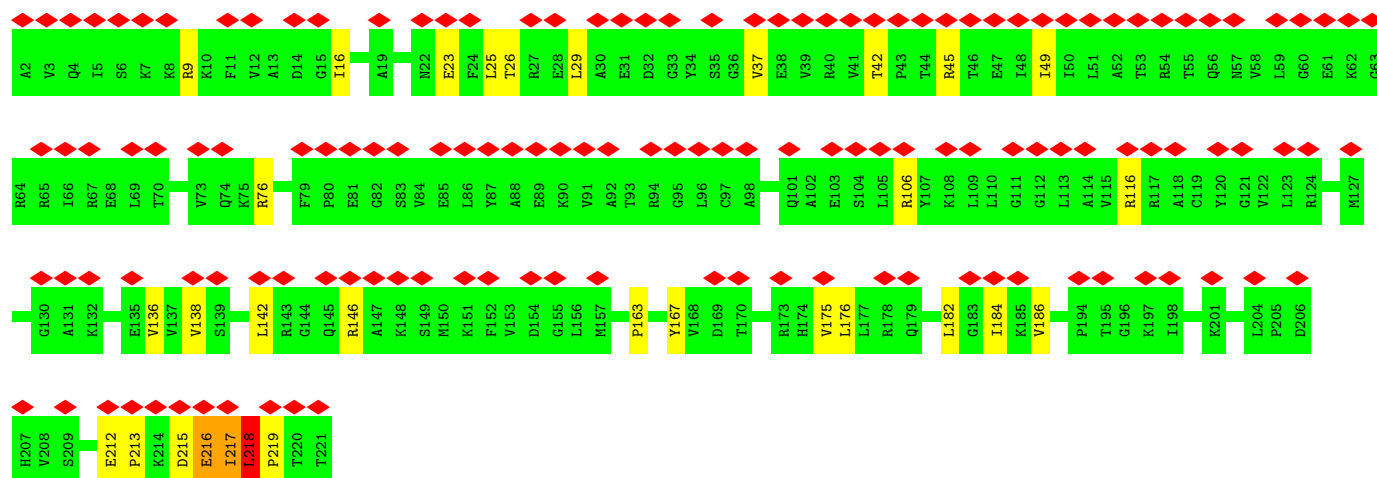




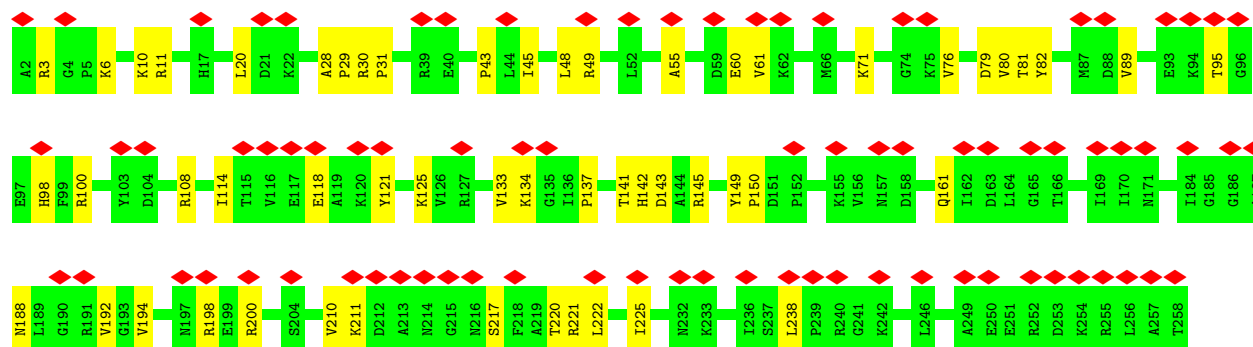
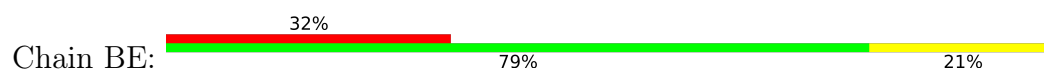
• Molecule 52: 18S ribosomal RNA



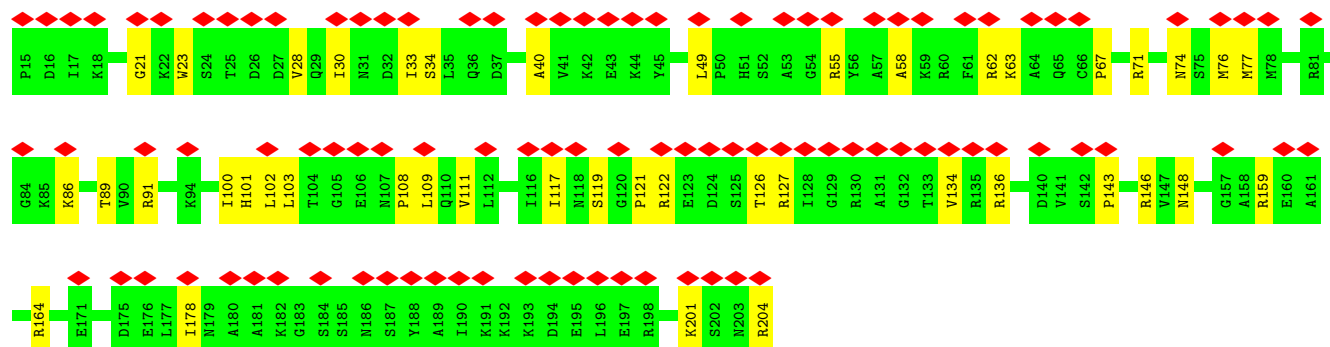
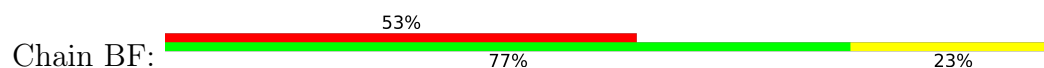




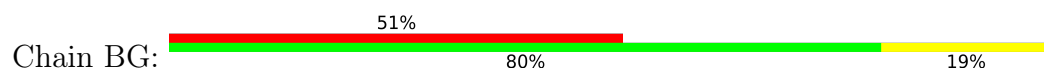
- Molecule 54: 40S ribosomal protein S4, Y isoform 1

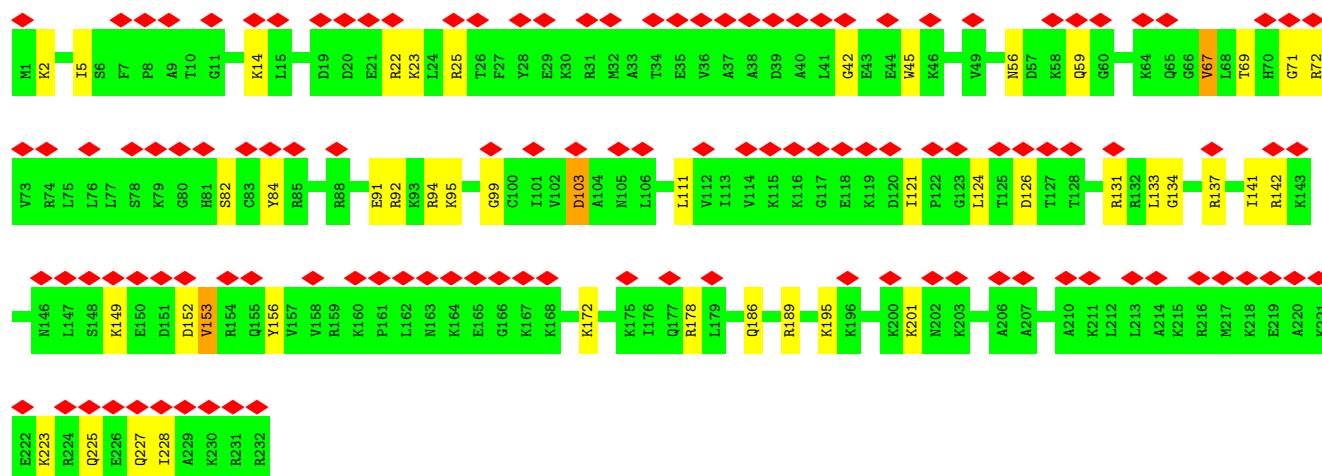


- Molecule 55: 40S ribosomal protein S5



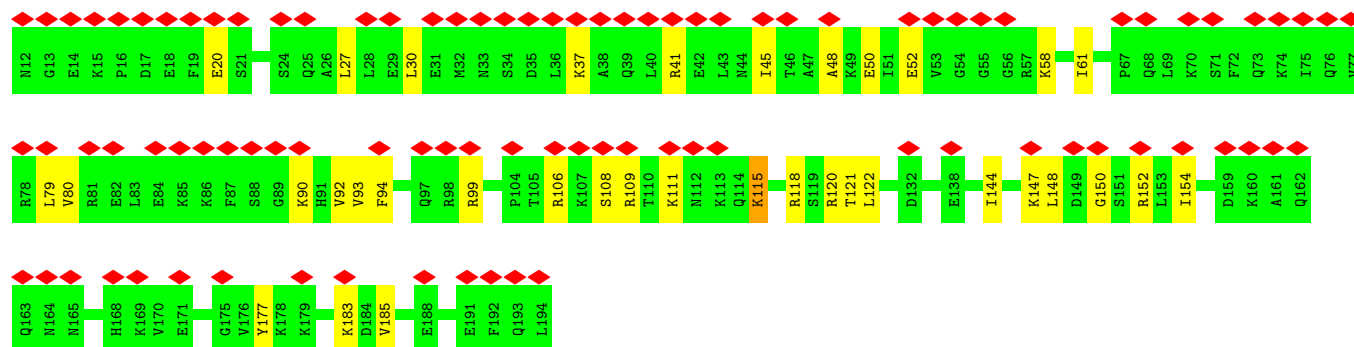
- Molecule 56: 40S ribosomal protein S6





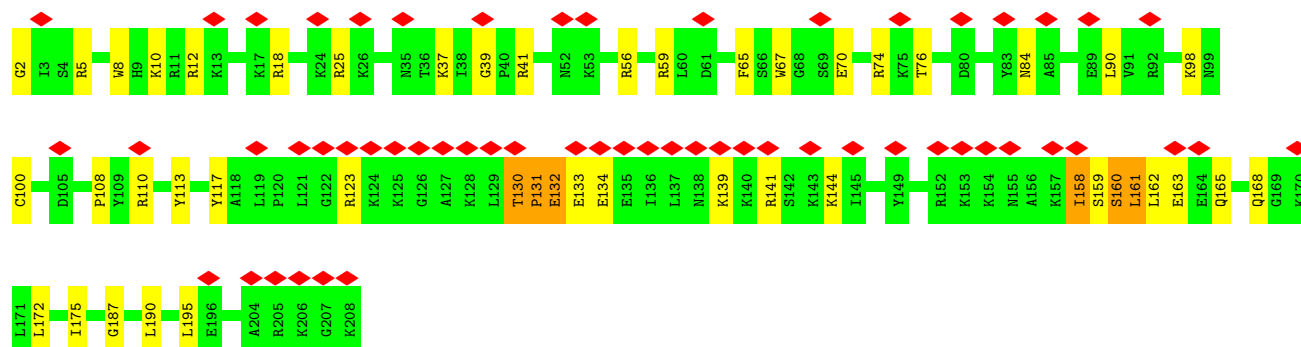
- Molecule 57: 40S ribosomal protein S7

Chain BH: 50% 80% 19% .



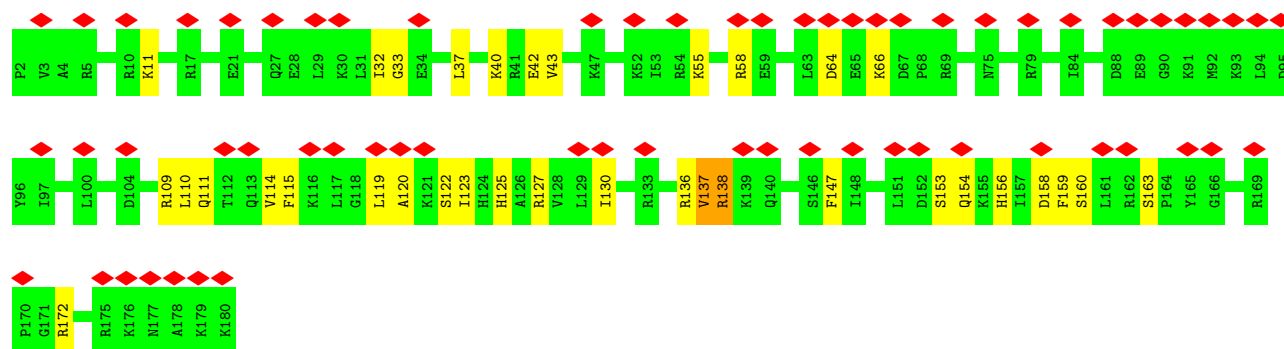
- Molecule 58: 40S ribosomal protein S8

Chain BI: 28% 77% 20% .

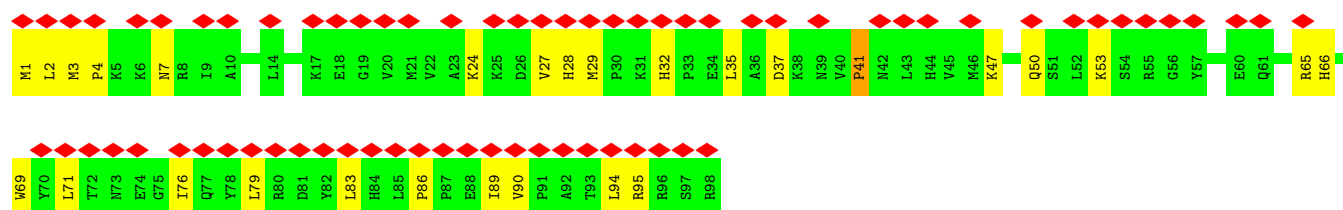
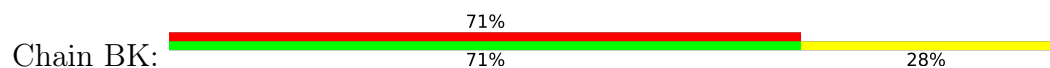


- Molecule 59: 40S ribosomal protein S9

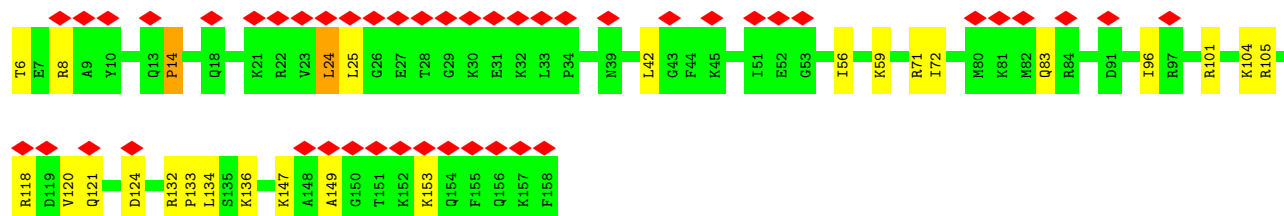
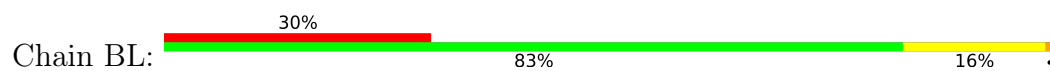
Chain BJ: 36% 80% 18% .



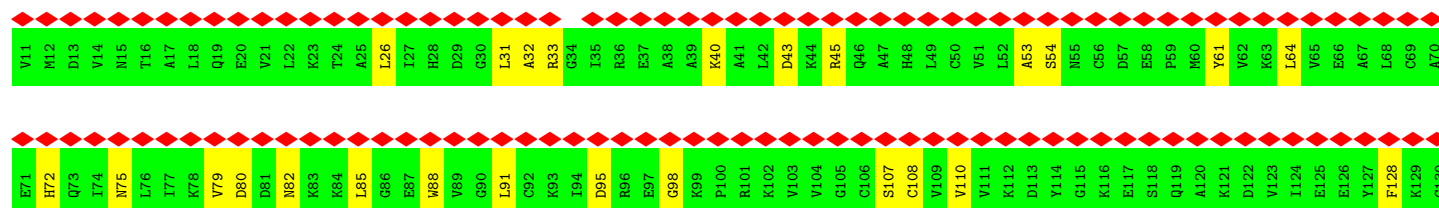
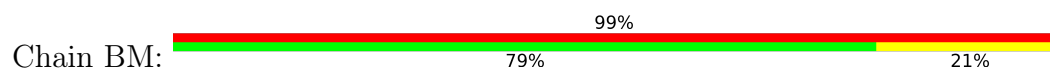
• Molecule 60: 40S ribosomal protein S10



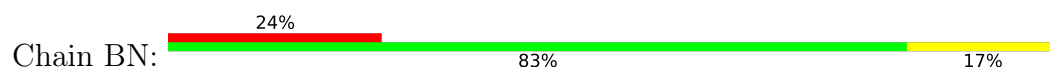
• Molecule 61: 40S ribosomal protein S11

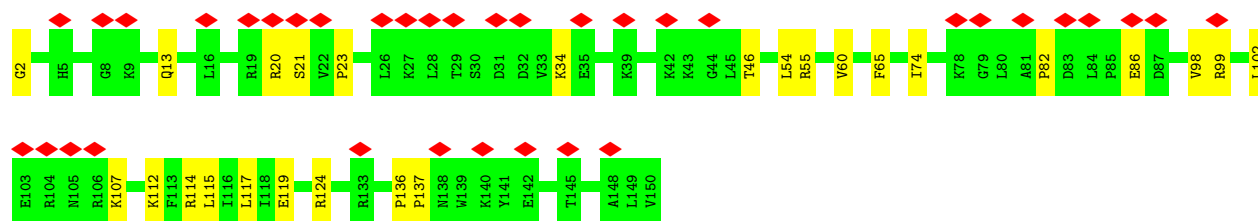


• Molecule 62: 40S ribosomal protein S12

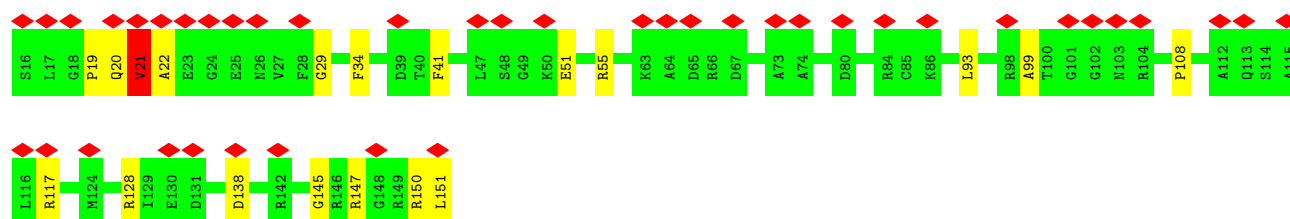
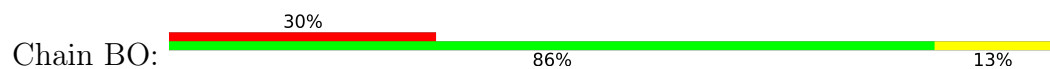


• Molecule 63: 40S ribosomal protein S13

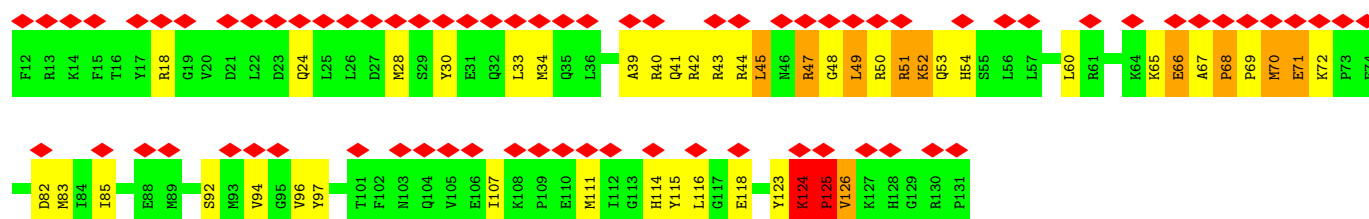




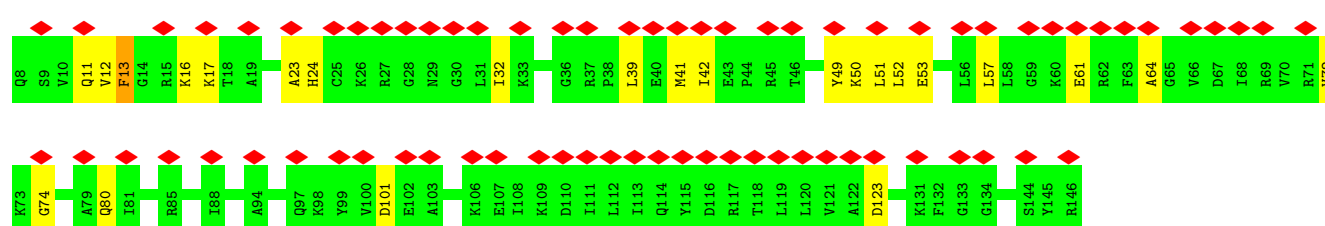
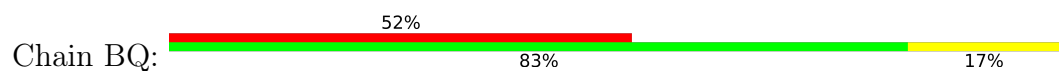
• Molecule 64: 40S ribosomal protein S14



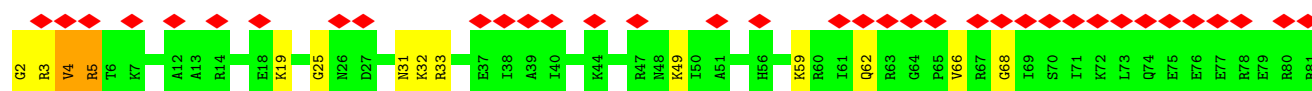
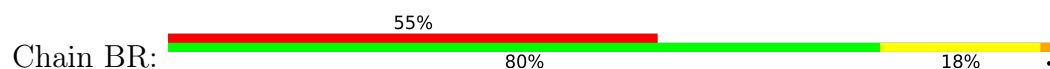
• Molecule 65: 40S ribosomal protein S15

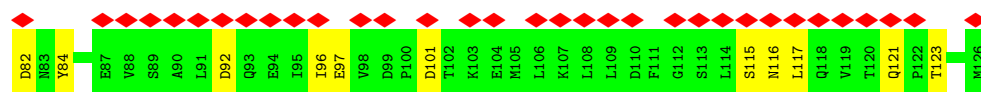


• Molecule 66: 40S ribosomal protein S16

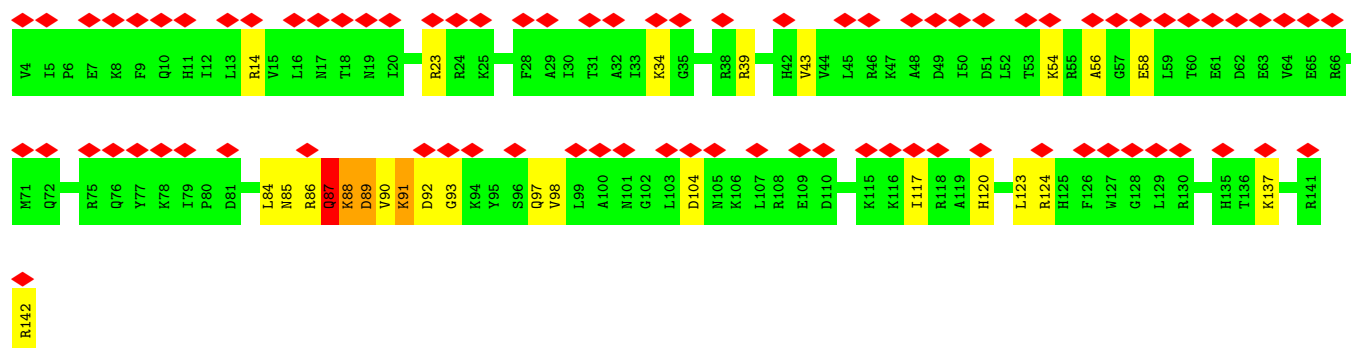
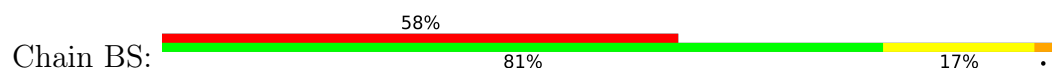


• Molecule 67: 40S ribosomal protein S17

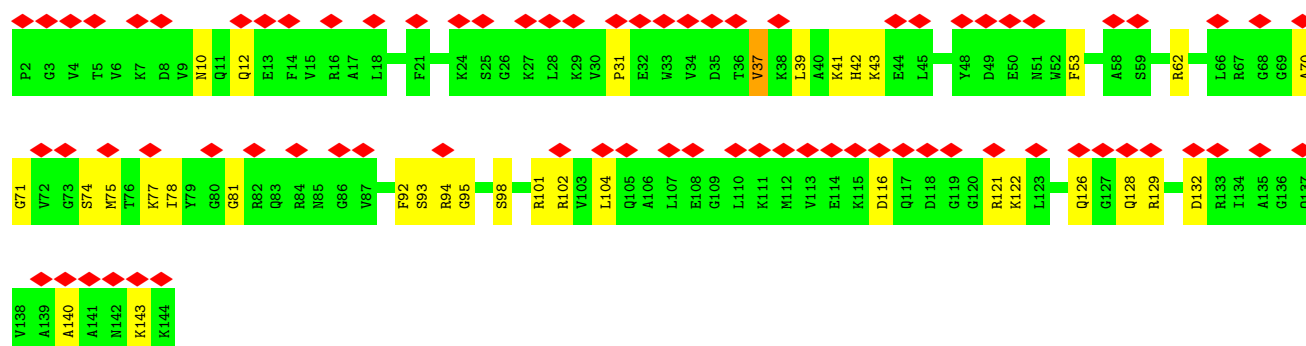
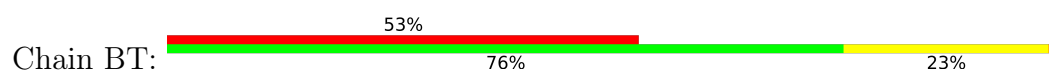




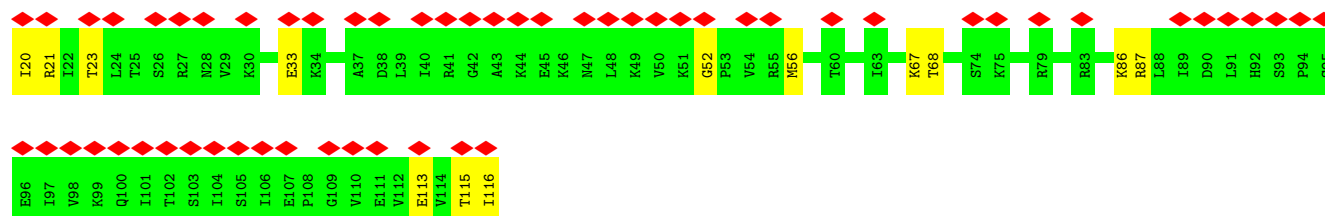
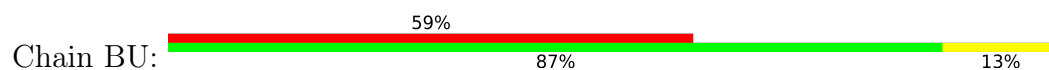
• Molecule 68: 40S ribosomal protein S18



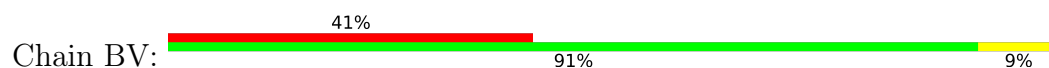
• Molecule 69: 40S ribosomal protein S19

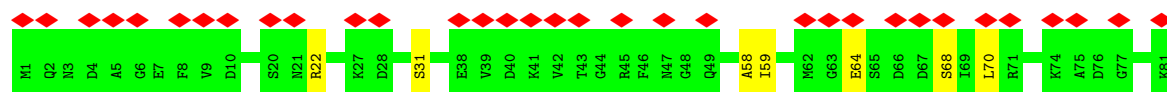


• Molecule 70: 40S ribosomal protein S20

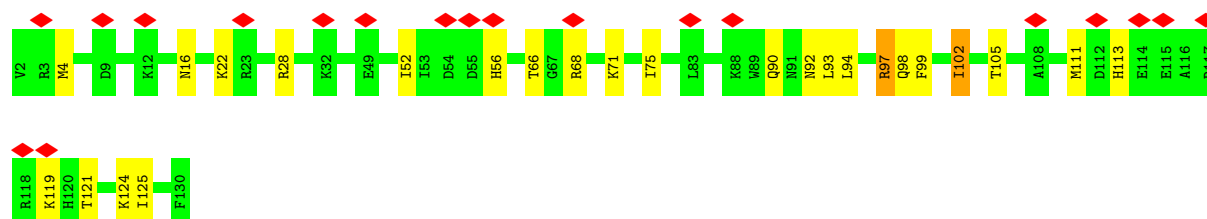
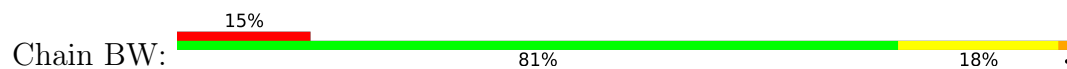


• Molecule 71: 40S ribosomal protein S21

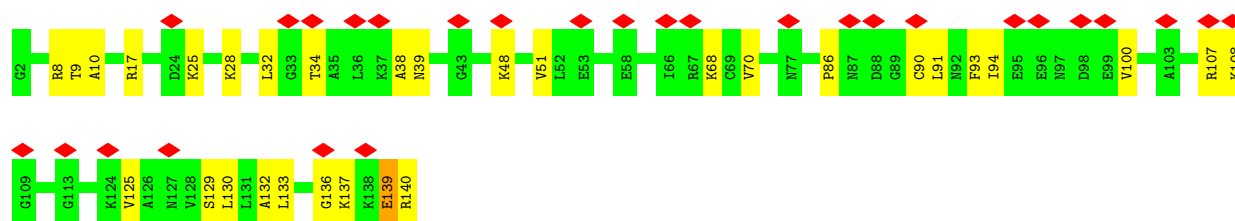
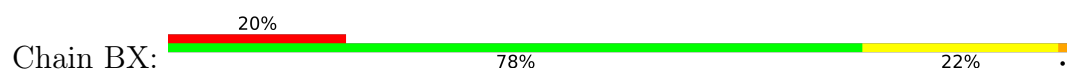




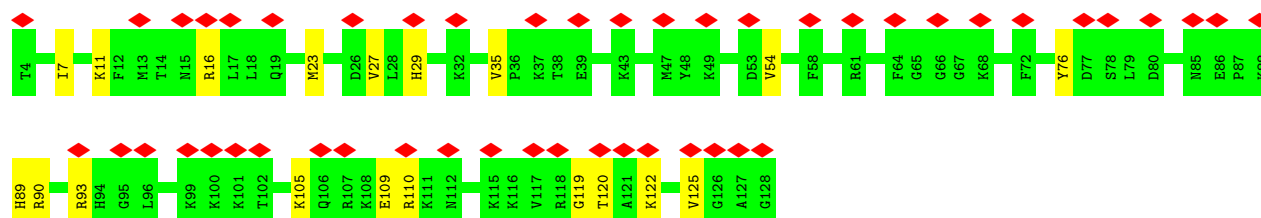
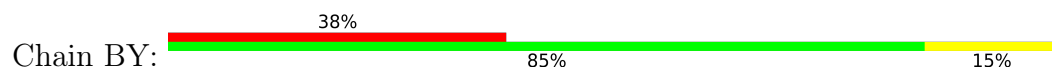
- Molecule 72: 40S ribosomal protein S15a



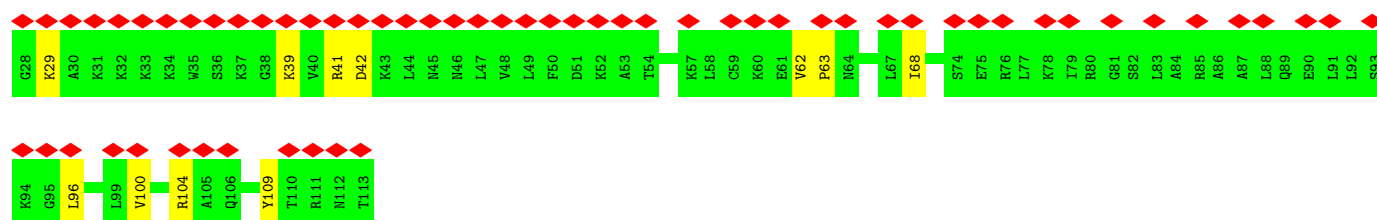
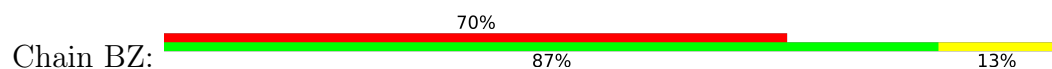
- Molecule 73: 40S ribosomal protein S23



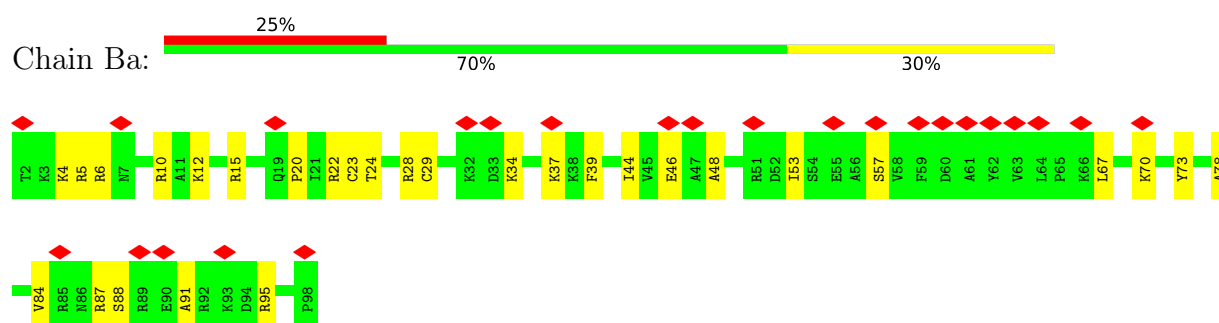
- Molecule 74: 40S ribosomal protein S24



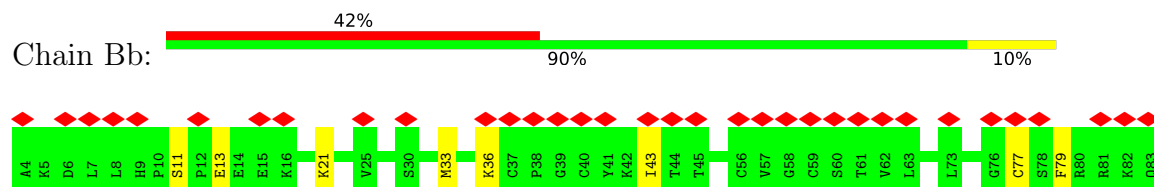
- Molecule 75: 40S ribosomal protein S25



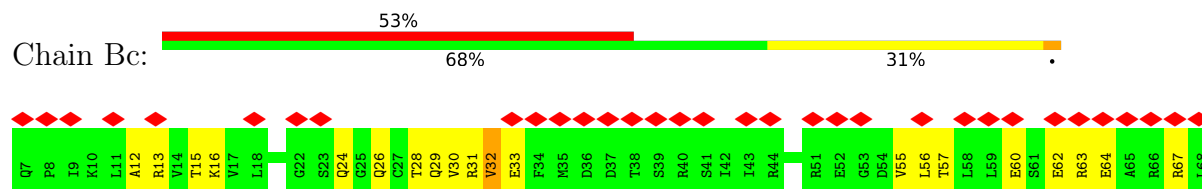
- Molecule 76: 40S ribosomal protein S26



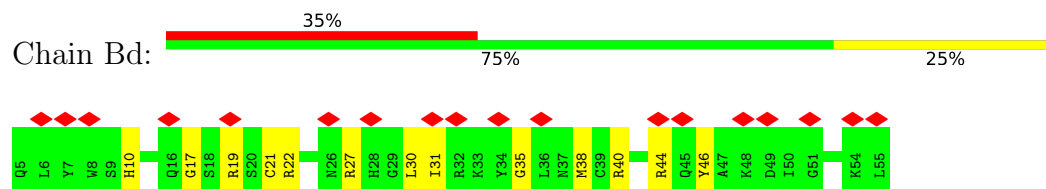
- Molecule 77: 40S ribosomal protein S27



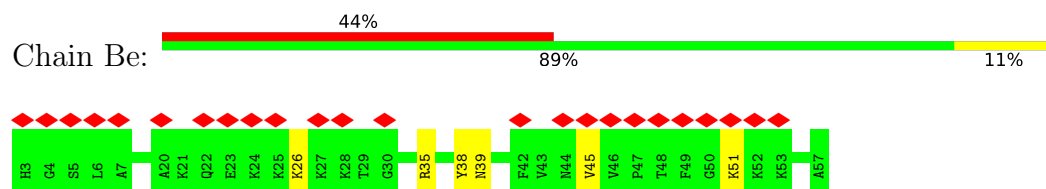
- Molecule 78: 40S ribosomal protein S28



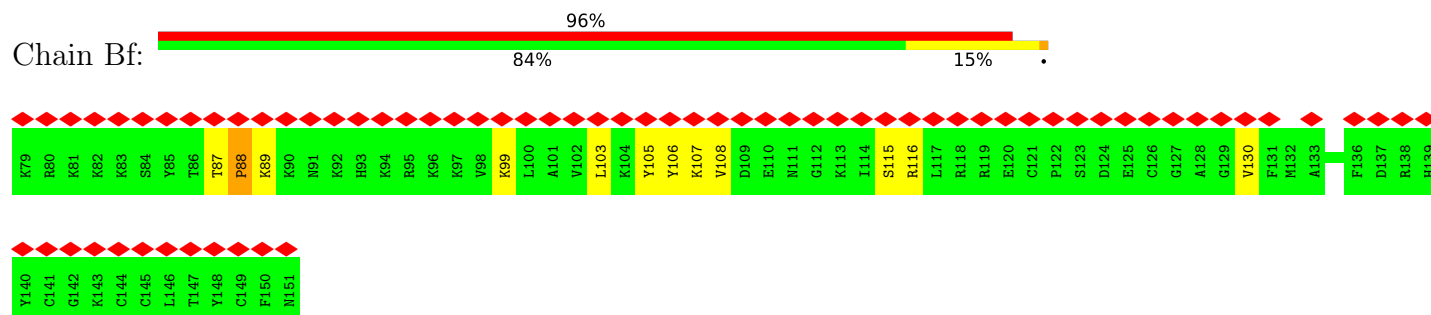
- Molecule 79: 40S ribosomal protein S29



- Molecule 80: 40S ribosomal protein S30

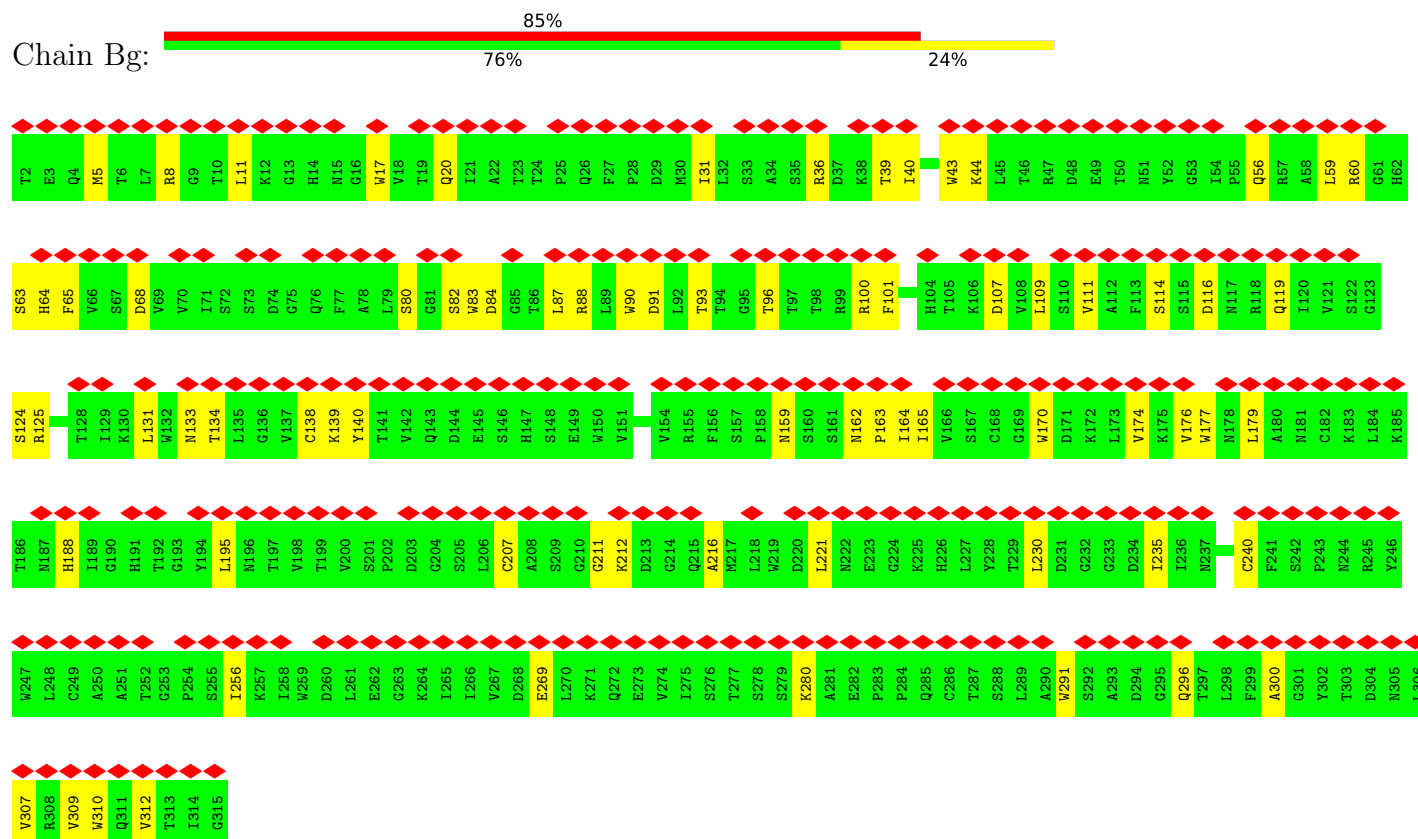


- Molecule 81: 40S ribosomal protein S27a



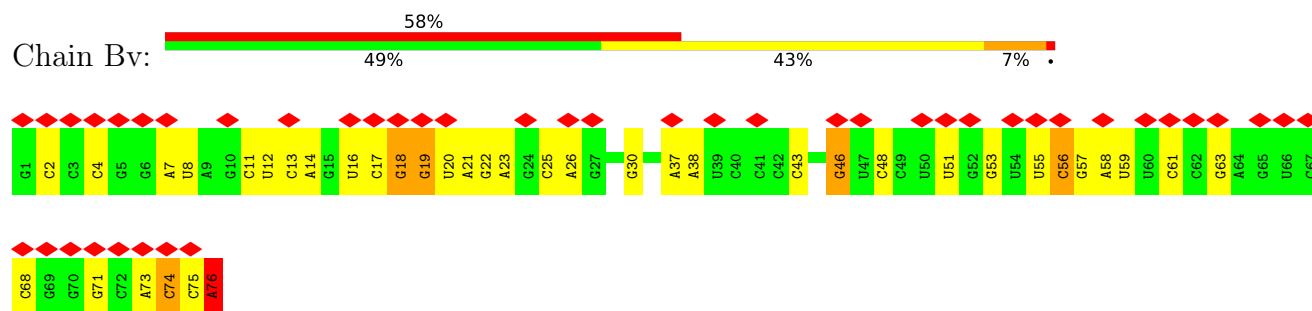
- Molecule 82: Receptor of activated protein C kinase 1

Chain Bg:



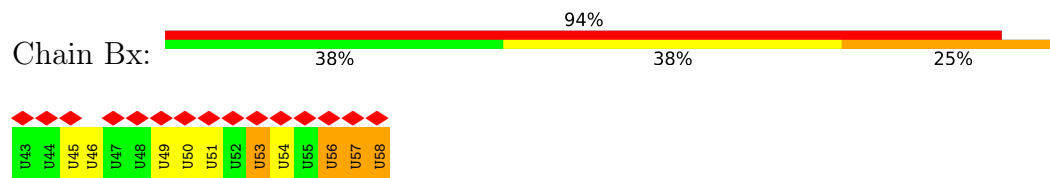
- Molecule 83: tRNA

Chain Bv:



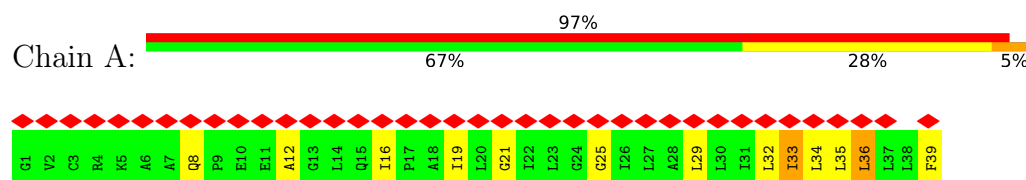
- Molecule 84: mRNA

Chain Bx:



- Molecule 85: Cadherin-1

Chain A:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16594	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.107	Depositor
Minimum map value	-0.054	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	471.5, 471.5, 471.5	wwPDB
Map dimensions	410, 410, 410	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.15, 1.15, 1.15	Depositor

5 Model quality

5.1 Standard geometry

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

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	AA	0.36	0/1968	0.72	3/2639 (0.1%)
2	BA	0.33	0/1741	0.67	0/2366
3	AB	0.37	0/3246	0.72	1/4345 (0.0%)
4	BB	0.31	0/1749	0.76	2/2340 (0.1%)
5	AC	0.34	0/2942	0.73	2/3951 (0.1%)
6	BC	0.31	0/1761	0.67	0/2379
7	A3	0.32	0/3726	0.44	0/5804
8	A4	0.31	0/2839	0.43	0/4425
9	AD	0.31	0/2437	0.68	2/3262 (0.1%)
10	AE	0.31	0/1603	0.81	3/2153 (0.1%)
11	AF	0.35	0/1986	0.72	1/2644 (0.0%)
12	AG	0.31	0/1913	0.70	0/2576
13	AH	0.31	0/1545	0.72	2/2077 (0.1%)
14	AI	0.32	0/1730	0.72	0/2311
15	AJ	0.30	0/1376	0.70	0/1841
16	AK	0.36	0/886	1.20	6/1188 (0.5%)
17	AL	0.35	0/1688	0.80	0/2260
18	AM	0.34	0/1161	0.69	0/1554
19	AN	0.39	0/1746	0.70	0/2338
20	AO	0.36	0/1638	0.70	1/2191 (0.0%)
21	AP	0.35	0/1268	0.63	0/1701
22	AQ	0.36	0/1537	0.83	3/2052 (0.1%)
23	AR	0.32	0/1533	0.74	1/2025 (0.0%)
24	AS	0.35	0/1488	0.65	0/1997
25	AT	0.34	0/1312	0.62	0/1753
26	AU	0.29	0/822	0.61	0/1103
27	AV	0.33	0/983	0.62	0/1319
28	AW	0.34	0/1004	0.85	6/1332 (0.5%)
29	AX	0.30	0/975	0.63	0/1312
30	AY	0.32	0/1081	0.63	0/1439
31	AZ	0.30	0/1126	0.70	0/1502
32	Aa	0.38	0/1191	0.70	0/1591

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ab	0.31	0/569	0.75	0/750
34	Ac	0.30	0/812	0.65	0/1089
35	Ad	0.32	0/894	0.67	0/1204
36	Ae	0.33	0/1082	0.72	1/1443 (0.1%)
37	Af	0.39	0/895	0.82	3/1198 (0.3%)
38	Ag	0.34	0/916	0.71	0/1220
39	Ah	0.29	0/1023	0.65	0/1351
40	Ai	0.31	0/805	0.73	0/1065
41	Aj	0.37	0/703	0.87	0/929
42	Ak	0.27	0/575	0.74	0/761
43	Al	0.31	0/454	0.64	0/599
44	Am	0.33	0/417	0.82	0/553
45	An	0.31	0/241	0.72	0/305
46	Ao	0.32	0/877	0.73	0/1156
47	Ap	0.36	0/718	0.75	0/953
48	Aq	0.34	0/1058	1.08	6/1424 (0.4%)
49	At	0.38	0/995	0.94	5/1334 (0.4%)
50	Au	0.28	0/1772	0.75	3/2375 (0.1%)
51	A2	0.32	0/86613	0.44	0/135108
52	B1	0.27	0/40767	0.44	4/63536 (0.0%)
53	BD	0.29	1/1736 (0.1%)	0.63	0/2338
54	BE	0.30	0/2072	0.71	2/2793 (0.1%)
55	BF	0.29	0/1524	0.70	0/2048
56	BG	0.26	0/1907	0.69	1/2538 (0.0%)
57	BH	0.27	0/1501	0.67	0/2009
58	BI	0.32	0/1725	0.79	2/2298 (0.1%)
59	BJ	0.31	0/1520	0.75	0/2030
60	BK	0.30	0/851	0.78	0/1147
61	BL	0.32	0/1281	0.76	4/1710 (0.2%)
62	BM	0.23	0/941	0.67	0/1264
63	BN	0.31	0/1226	0.74	2/1649 (0.1%)
64	BO	0.31	0/1029	0.76	0/1380
65	BP	0.30	0/1019	0.93	3/1361 (0.2%)
66	BQ	0.29	0/1126	0.75	1/1506 (0.1%)
67	BR	0.27	0/1023	0.78	2/1373 (0.1%)
68	BS	0.25	0/1172	0.69	0/1570
69	BT	0.28	0/1131	0.70	0/1515
70	BU	0.26	0/778	0.61	0/1045
71	BV	0.28	0/623	0.70	0/833
72	BW	0.32	0/1051	0.68	0/1406
73	BX	0.31	0/1097	0.73	0/1464
74	BY	0.30	0/1032	0.73	0/1371
75	BZ	0.29	0/696	0.80	0/929

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Ba	0.33	0/786	0.75	0/1053
77	Bb	0.26	0/637	0.64	0/854
78	Bc	0.27	0/490	0.67	0/656
79	Bd	0.35	0/437	0.81	0/580
80	Be	0.29	0/443	0.77	1/583 (0.2%)
81	Bf	0.23	0/613	0.72	0/811
82	Bg	0.25	0/2497	0.60	0/3399
83	Bv	0.34	1/1813 (0.1%)	0.50	3/2823 (0.1%)
84	Bx	0.23	0/351	0.48	0/540
85	A	0.50	1/189 (0.5%)	1.04	2/260 (0.8%)
All	All	0.31	3/232504 (0.0%)	0.57	78/341259 (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	BB	0	1
9	AD	0	1
13	AH	0	1
29	AX	0	1
All	All	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	Bv	73	A	O3'-P	11.22	1.77	1.61
85	A	16	ILE	C-N	5.56	1.38	1.33
53	BD	212	GLU	C-N	5.07	1.40	1.33

The worst 5 of 78 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	BP	124	LYS	CA-C-N	12.33	135.25	119.84
65	BP	124	LYS	C-N-CA	12.33	135.25	119.84
16	AK	24	TYR	CA-C-N	10.66	133.17	119.84
16	AK	24	TYR	C-N-CA	10.66	133.17	119.84
16	AK	24	TYR	N-CA-C	9.62	120.52	108.11

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	AD	228	LYS	Peptide
13	AH	116	ASN	Peptide
29	AX	79	PHE	Peptide
4	BB	39	PHE	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	AA	1930	0	2030	67	0
2	BA	1704	0	1703	61	0
3	AB	3178	0	3314	82	0
4	BB	1722	0	1794	64	0
5	AC	2888	0	3064	92	0
6	BC	1724	0	1808	57	0
7	A3	3337	0	1692	38	0
8	A4	2541	0	1285	30	0
9	AD	2392	0	2425	76	0
10	AE	1571	0	1700	49	0
11	AF	1950	0	2093	23	0
12	AG	1880	0	2018	21	0
13	AH	1526	0	1605	29	0
14	AI	1692	0	1744	18	0
15	AJ	1353	0	1386	29	0
16	AK	872	0	916	79	0
17	AL	1657	0	1764	93	0
18	AM	1138	0	1204	14	0
19	AN	1701	0	1749	44	0
20	AO	1606	0	1745	25	0
21	AP	1242	0	1269	12	0
22	AQ	1513	0	1628	30	0
23	AR	1517	0	1670	23	0
24	AS	1449	0	1493	26	0
25	AT	1284	0	1352	21	0
26	AU	808	0	831	21	0
27	AV	969	0	1031	27	0
28	AW	989	0	1041	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	AX	958	0	1029	10	0
30	AY	1064	0	1145	13	0
31	AZ	1103	0	1179	10	0
32	Aa	1162	0	1212	21	0
33	Ab	559	0	590	31	0
34	Ac	801	0	845	33	0
35	Ad	879	0	924	9	0
36	Ae	1064	0	1160	13	0
37	Af	876	0	912	21	0
38	Ag	906	0	1002	12	0
39	Ah	1015	0	1148	33	0
40	Ai	794	0	870	8	0
41	Aj	689	0	717	32	0
42	Ak	569	0	637	9	0
43	Al	444	0	483	8	0
44	Am	411	0	443	7	0
45	An	240	0	289	6	0
46	Ao	863	0	929	11	0
47	Ap	708	0	757	7	0
48	Aq	1046	0	1116	60	0
49	At	980	0	1041	33	0
50	Au	1744	0	1859	59	0
51	A2	77427	0	39116	858	0
52	B1	36456	0	18411	403	0
53	BD	1709	0	1803	27	0
54	BE	2031	0	2138	32	0
55	BF	1502	0	1556	31	0
56	BG	1884	0	2044	34	0
57	BH	1479	0	1564	25	0
58	BI	1696	0	1784	43	0
59	BJ	1495	0	1615	52	0
60	BK	827	0	854	19	0
61	BL	1258	0	1334	17	0
62	BM	931	0	961	14	0
63	BN	1202	0	1289	16	0
64	BO	1016	0	1039	22	0
65	BP	999	0	1046	79	0
66	BQ	1109	0	1174	16	0
67	BR	1011	0	1063	20	0
68	BS	1154	0	1209	34	0
69	BT	1112	0	1146	25	0
70	BU	769	0	837	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
71	BV	617	0	622	6	0
72	BW	1034	0	1080	51	0
73	BX	1080	0	1147	37	0
74	BY	1015	0	1086	12	0
75	BZ	688	0	766	7	0
76	Ba	774	0	822	20	0
77	Bb	625	0	646	4	0
78	Bc	488	0	514	28	0
79	Bd	427	0	428	12	0
80	Be	437	0	483	7	0
81	Bf	601	0	623	10	0
82	Bg	2440	0	2396	43	0
83	Bv	1623	0	821	16	0
84	Bx	320	0	161	10	0
85	A	190	0	98	14	0
86	A2	226	0	0	0	0
86	A3	6	0	0	0	0
86	A4	9	0	0	0	0
86	AB	2	0	0	0	0
86	AP	1	0	0	0	0
86	AY	1	0	0	0	0
86	Aa	1	0	0	0	0
86	Ae	1	0	0	0	0
86	B1	75	0	0	0	0
86	BI	1	0	0	0	0
86	Ba	1	0	0	0	0
86	Bv	2	0	0	0	0
87	Aj	1	0	0	0	0
87	Ao	1	0	0	0	0
87	Ap	1	0	0	0	0
87	Ba	1	0	0	0	0
87	Bd	1	0	0	0	0
88	A2	31	0	0	7	0
All	All	216796	0	161317	3005	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 8.

The worst 5 of 3005 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)
34:Ac:17:ARG:CB	34:Ac:104:ILE:HD11	1.27	1.53
17:AL:165:LYS:CE	51:A2:505:C:H5'	1.34	1.53
4:BB:30:TRP:CH2	4:BB:48:LEU:HD21	1.42	1.53
17:AL:165:LYS:HE3	51:A2:505:C:C5'	1.37	1.50
17:AL:133:ALA:HB2	17:AL:136:LYS:CE	1.43	1.49

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	AA	250/257 (97%)	223 (89%)	24 (10%)	3 (1%)	10	35
2	BA	213/215 (99%)	196 (92%)	13 (6%)	4 (2%)	6	26
3	AB	392/394 (100%)	363 (93%)	29 (7%)	0	100	100
4	BB	210/212 (99%)	181 (86%)	27 (13%)	2 (1%)	12	40
5	AC	361/363 (99%)	333 (92%)	26 (7%)	2 (1%)	21	50
6	BC	220/222 (99%)	205 (93%)	15 (7%)	0	100	100
9	AD	292/294 (99%)	261 (89%)	27 (9%)	4 (1%)	9	31
10	AE	192/194 (99%)	159 (83%)	29 (15%)	4 (2%)	5	24
11	AF	232/234 (99%)	211 (91%)	20 (9%)	1 (0%)	30	59
12	AG	232/234 (99%)	211 (91%)	21 (9%)	0	100	100
13	AH	189/191 (99%)	178 (94%)	9 (5%)	2 (1%)	11	38
14	AI	204/211 (97%)	182 (89%)	22 (11%)	0	100	100
15	AJ	167/169 (99%)	153 (92%)	12 (7%)	2 (1%)	10	35
16	AK	107/109 (98%)	59 (55%)	35 (33%)	13 (12%)	0	1
17	AL	203/205 (99%)	166 (82%)	28 (14%)	9 (4%)	2	13
18	AM	137/139 (99%)	125 (91%)	12 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	AN	201/203 (99%)	184 (92%)	16 (8%)	1 (0%)	24	54
20	AO	193/195 (99%)	180 (93%)	13 (7%)	0	100	100
21	AP	151/153 (99%)	147 (97%)	4 (3%)	0	100	100
22	AQ	185/187 (99%)	159 (86%)	25 (14%)	1 (0%)	24	54
23	AR	179/181 (99%)	169 (94%)	9 (5%)	1 (1%)	21	50
24	AS	173/175 (99%)	162 (94%)	11 (6%)	0	100	100
25	AT	155/157 (99%)	140 (90%)	13 (8%)	2 (1%)	9	33
26	AU	97/99 (98%)	87 (90%)	8 (8%)	2 (2%)	5	24
27	AV	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
28	AW	119/121 (98%)	105 (88%)	13 (11%)	1 (1%)	16	44
29	AX	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
30	AY	125/127 (98%)	118 (94%)	7 (6%)	0	100	100
31	AZ	132/134 (98%)	117 (89%)	15 (11%)	0	100	100
32	Aa	145/147 (99%)	128 (88%)	17 (12%)	0	100	100
33	Ab	66/121 (54%)	56 (85%)	9 (14%)	1 (2%)	8	30
34	Ac	101/103 (98%)	96 (95%)	3 (3%)	2 (2%)	6	25
35	Ad	104/106 (98%)	99 (95%)	5 (5%)	0	100	100
36	Ae	127/129 (98%)	113 (89%)	14 (11%)	0	100	100
37	Af	107/109 (98%)	95 (89%)	9 (8%)	3 (3%)	4	19
38	Ag	112/114 (98%)	101 (90%)	11 (10%)	0	100	100
39	Ah	120/122 (98%)	111 (92%)	8 (7%)	1 (1%)	16	44
40	Ai	95/97 (98%)	86 (90%)	9 (10%)	0	100	100
41	Aj	82/84 (98%)	75 (92%)	7 (8%)	0	100	100
42	Ak	67/69 (97%)	63 (94%)	4 (6%)	0	100	100
43	Al	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
44	Am	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
45	An	23/25 (92%)	23 (100%)	0	0	100	100
46	Ao	103/105 (98%)	93 (90%)	10 (10%)	0	100	100
47	Ap	89/91 (98%)	80 (90%)	9 (10%)	0	100	100
48	Aq	136/138 (99%)	94 (69%)	38 (28%)	4 (3%)	3	19
49	At	120/122 (98%)	102 (85%)	16 (13%)	2 (2%)	7	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	Au	215/217 (99%)	193 (90%)	18 (8%)	4 (2%)	6	26
53	BD	218/220 (99%)	202 (93%)	15 (7%)	1 (0%)	24	54
54	BE	255/257 (99%)	235 (92%)	19 (8%)	1 (0%)	30	59
55	BF	188/190 (99%)	171 (91%)	17 (9%)	0	100	100
56	BG	230/232 (99%)	208 (90%)	21 (9%)	1 (0%)	30	59
57	BH	181/183 (99%)	166 (92%)	14 (8%)	1 (1%)	21	50
58	BI	205/207 (99%)	175 (85%)	26 (13%)	4 (2%)	6	25
59	BJ	177/179 (99%)	151 (85%)	25 (14%)	1 (1%)	21	50
60	BK	96/98 (98%)	82 (85%)	12 (12%)	2 (2%)	5	24
61	BL	151/153 (99%)	132 (87%)	18 (12%)	1 (1%)	18	47
62	BM	118/120 (98%)	112 (95%)	6 (5%)	0	100	100
63	BN	147/149 (99%)	129 (88%)	17 (12%)	1 (1%)	18	47
64	BO	134/136 (98%)	119 (89%)	13 (10%)	2 (2%)	8	30
65	BP	118/120 (98%)	101 (86%)	12 (10%)	5 (4%)	2	14
66	BQ	137/139 (99%)	127 (93%)	10 (7%)	0	100	100
67	BR	123/125 (98%)	105 (85%)	16 (13%)	2 (2%)	7	29
68	BS	137/139 (99%)	118 (86%)	16 (12%)	3 (2%)	5	24
69	BT	141/143 (99%)	129 (92%)	11 (8%)	1 (1%)	18	47
70	BU	95/97 (98%)	91 (96%)	4 (4%)	0	100	100
71	BV	79/81 (98%)	75 (95%)	4 (5%)	0	100	100
72	BW	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
73	BX	137/139 (99%)	124 (90%)	11 (8%)	2 (2%)	8	30
74	BY	123/125 (98%)	108 (88%)	15 (12%)	0	100	100
75	BZ	84/86 (98%)	74 (88%)	10 (12%)	0	100	100
76	Ba	95/97 (98%)	87 (92%)	8 (8%)	0	100	100
77	Bb	78/80 (98%)	71 (91%)	7 (9%)	0	100	100
78	Bc	60/62 (97%)	55 (92%)	5 (8%)	0	100	100
79	Bd	49/51 (96%)	43 (88%)	6 (12%)	0	100	100
80	Be	53/55 (96%)	51 (96%)	2 (4%)	0	100	100
81	Bf	71/73 (97%)	64 (90%)	6 (8%)	1 (1%)	9	31
82	Bg	312/314 (99%)	281 (90%)	31 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
85	A	37/39 (95%)	20 (54%)	14 (38%)	3 (8%)	1	4
All	All	11617/11838 (98%)	10430 (90%)	1084 (9%)	103 (1%)	16	42

5 of 103 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AA	196	TRP
1	AA	197	PRO
1	AA	201	GLY
2	BA	206	ASP
5	AC	148	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	194/199 (98%)	191 (98%)	3 (2%)	57	69
2	BA	180/180 (100%)	177 (98%)	3 (2%)	53	67
3	AB	343/343 (100%)	338 (98%)	5 (2%)	57	69
4	BB	193/193 (100%)	190 (98%)	3 (2%)	55	68
5	AC	302/302 (100%)	298 (99%)	4 (1%)	61	71
6	BC	188/188 (100%)	184 (98%)	4 (2%)	47	64
9	AD	248/248 (100%)	236 (95%)	12 (5%)	23	50
10	AE	174/174 (100%)	164 (94%)	10 (6%)	18	45
11	AF	203/203 (100%)	202 (100%)	1 (0%)	81	81
12	AG	199/199 (100%)	199 (100%)	0	100	100
13	AH	170/170 (100%)	166 (98%)	4 (2%)	43	62
14	AI	178/179 (99%)	178 (100%)	0	100	100
15	AJ	142/142 (100%)	139 (98%)	3 (2%)	47	64
16	AK	95/95 (100%)	86 (90%)	9 (10%)	8	29
17	AL	171/171 (100%)	163 (95%)	8 (5%)	23	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	AM	118/118 (100%)	117 (99%)	1 (1%)	73	77
19	AN	171/171 (100%)	170 (99%)	1 (1%)	78	80
20	AO	168/168 (100%)	166 (99%)	2 (1%)	63	72
21	AP	134/134 (100%)	134 (100%)	0	100	100
22	AQ	164/164 (100%)	159 (97%)	5 (3%)	36	59
23	AR	160/160 (100%)	158 (99%)	2 (1%)	61	71
24	AS	156/156 (100%)	156 (100%)	0	100	100
25	AT	138/138 (100%)	138 (100%)	0	100	100
26	AU	89/89 (100%)	88 (99%)	1 (1%)	65	74
27	AV	100/100 (100%)	100 (100%)	0	100	100
28	AW	100/100 (100%)	100 (100%)	0	100	100
29	AX	105/105 (100%)	105 (100%)	0	100	100
30	AY	119/119 (100%)	119 (100%)	0	100	100
31	AZ	117/117 (100%)	116 (99%)	1 (1%)	70	76
32	Aa	120/120 (100%)	120 (100%)	0	100	100
33	Ab	58/101 (57%)	52 (90%)	6 (10%)	7	24
34	Ac	88/88 (100%)	84 (96%)	4 (4%)	24	51
35	Ad	97/97 (100%)	97 (100%)	0	100	100
36	Ae	115/115 (100%)	114 (99%)	1 (1%)	70	76
37	Af	88/88 (100%)	87 (99%)	1 (1%)	65	74
38	Ag	98/98 (100%)	98 (100%)	0	100	100
39	Ah	109/109 (100%)	108 (99%)	1 (1%)	70	76
40	Ai	83/83 (100%)	83 (100%)	0	100	100
41	Aj	71/71 (100%)	70 (99%)	1 (1%)	59	70
42	Ak	64/64 (100%)	64 (100%)	0	100	100
43	Al	47/47 (100%)	47 (100%)	0	100	100
44	Am	46/46 (100%)	46 (100%)	0	100	100
45	An	24/24 (100%)	24 (100%)	0	100	100
46	Ao	93/93 (100%)	93 (100%)	0	100	100
47	Ap	74/74 (100%)	74 (100%)	0	100	100
48	Aq	114/114 (100%)	109 (96%)	5 (4%)	25	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	At	106/106 (100%)	104 (98%)	2 (2%)	50	66
50	Au	196/196 (100%)	187 (95%)	9 (5%)	24	50
53	BD	183/183 (100%)	180 (98%)	3 (2%)	55	68
54	BE	220/220 (100%)	220 (100%)	0	100	100
55	BF	160/160 (100%)	159 (99%)	1 (1%)	78	80
56	BG	202/202 (100%)	200 (99%)	2 (1%)	68	75
57	BH	164/164 (100%)	164 (100%)	0	100	100
58	BI	179/179 (100%)	176 (98%)	3 (2%)	53	67
59	BJ	160/160 (100%)	158 (99%)	2 (1%)	61	71
60	BK	89/89 (100%)	89 (100%)	0	100	100
61	BL	138/138 (100%)	137 (99%)	1 (1%)	76	78
62	BM	102/102 (100%)	102 (100%)	0	100	100
63	BN	130/130 (100%)	130 (100%)	0	100	100
64	BO	106/106 (100%)	105 (99%)	1 (1%)	70	76
65	BP	109/109 (100%)	99 (91%)	10 (9%)	8	29
66	BQ	115/115 (100%)	113 (98%)	2 (2%)	53	67
67	BR	113/113 (100%)	113 (100%)	0	100	100
68	BS	121/121 (100%)	118 (98%)	3 (2%)	42	62
69	BT	113/113 (100%)	112 (99%)	1 (1%)	70	76
70	BU	90/90 (100%)	90 (100%)	0	100	100
71	BV	65/65 (100%)	65 (100%)	0	100	100
72	BW	112/112 (100%)	110 (98%)	2 (2%)	51	67
73	BX	111/111 (100%)	110 (99%)	1 (1%)	70	76
74	BY	107/107 (100%)	107 (100%)	0	100	100
75	BZ	75/75 (100%)	74 (99%)	1 (1%)	61	71
76	Ba	84/84 (100%)	83 (99%)	1 (1%)	63	72
77	Bb	72/72 (100%)	71 (99%)	1 (1%)	59	70
78	Bc	55/55 (100%)	54 (98%)	1 (2%)	51	67
79	Bd	45/45 (100%)	45 (100%)	0	100	100
80	Be	44/44 (100%)	44 (100%)	0	100	100
81	Bf	66/66 (100%)	66 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
82	Bg	272/272 (100%)	270 (99%)	2 (1%)	76	78
All	All	10112/10161 (100%)	9962 (98%)	150 (2%)	55	69

5 of 150 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
55	BF	119	SER
73	BX	139	GLU
58	BI	158	ILE
65	BP	66	GLU
13	AH	111	LEU

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

Mol	Chain	Res	Type
46	Ao	36	GLN
56	BG	227	GLN
48	Aq	103	ASN
50	Au	197	ASN
61	BL	83	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	A2	3600/3612 (99%)	865 (24%)	15 (0%)
52	B1	1701/1708 (99%)	408 (23%)	10 (0%)
7	A3	156/157 (99%)	41 (26%)	3 (1%)
8	A4	118/119 (99%)	22 (18%)	0
83	Bv	75/76 (98%)	23 (30%)	0
84	Bx	15/16 (93%)	10 (66%)	0
All	All	5665/5688 (99%)	1369 (24%)	28 (0%)

5 of 1369 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A3	16	G
7	A3	23	C
7	A3	33	G
7	A3	34	U
7	A3	35	C

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	A2	4865	G
52	B1	1756	C
51	A2	4946	U
52	B1	1139	C
51	A2	4907	G

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 332 ligands modelled in this entry, 331 are monoatomic - leaving 1 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	MVM	A2	5327	-	35,35,35	1.95	4 (11%)	44,49,49	2.75	17 (38%)

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	MVM	A2	5327	-	-	2/20/28/28	0/5/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	A2	5327	MVM	N4-N5	-7.18	1.30	1.38
88	A2	5327	MVM	C5-N1	6.30	1.46	1.37
88	A2	5327	MVM	C6-N1	2.58	1.45	1.39
88	A2	5327	MVM	C12-C5	2.39	1.54	1.50

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	A2	5327	MVM	N7-C22-N4	7.36	134.16	125.88
88	A2	5327	MVM	C15-N4-C22	-7.23	124.12	130.55
88	A2	5327	MVM	C15-N4-N5	6.43	125.04	119.25
88	A2	5327	MVM	C7-C3-C9	4.54	119.43	110.81
88	A2	5327	MVM	C18-C22-N7	-4.37	121.17	127.18

There are no chirality outliers.

All (2) torsion outliers are listed below:

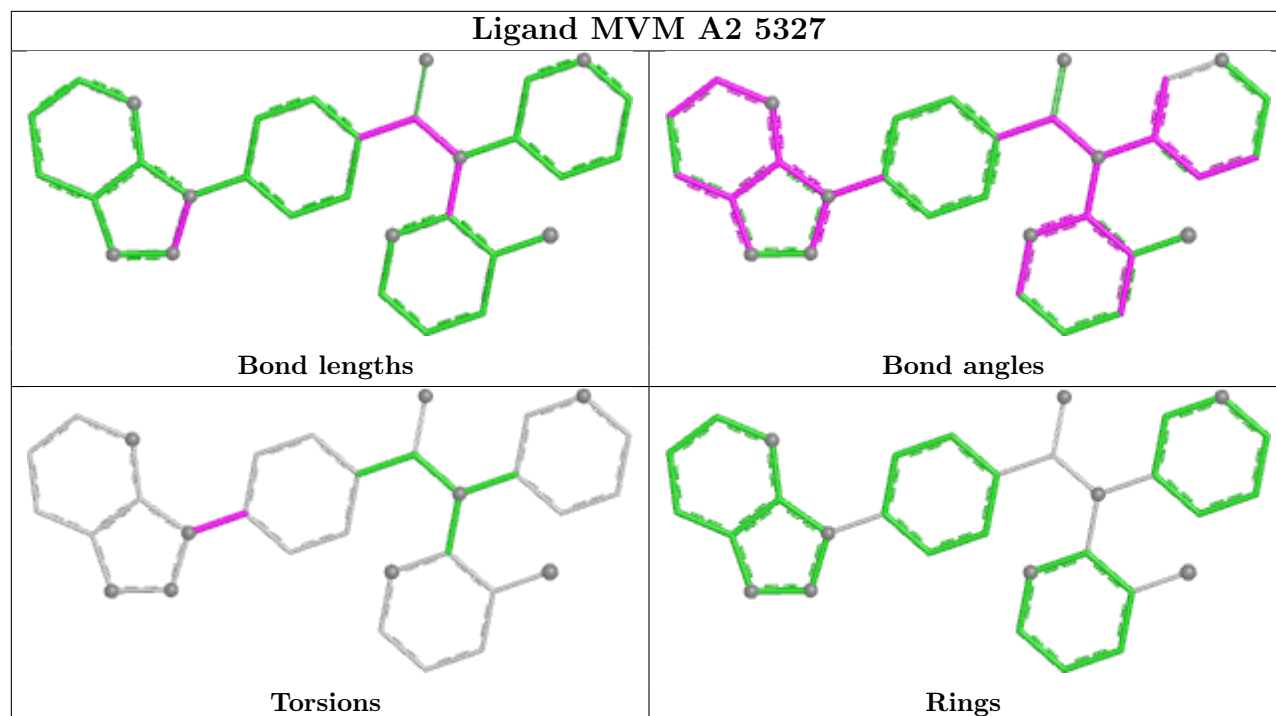
Mol	Chain	Res	Type	Atoms
88	A2	5327	MVM	C16-C15-N4-C22
88	A2	5327	MVM	C14-C15-N4-C22

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	A2	5327	MVM	7	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
51	A2	11
52	B1	6
83	Bv	1

The worst 5 of 18 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B1	126:G	O3'	141:A	P	20.56
1	B1	1757:G	O3'	1775:U	P	18.28
1	A2	3948:C	O3'	4004:G	P	18.11
1	B1	751:G	O3'	790:C	P	17.98
1	A2	4734:C	O3'	4818:G	P	17.83

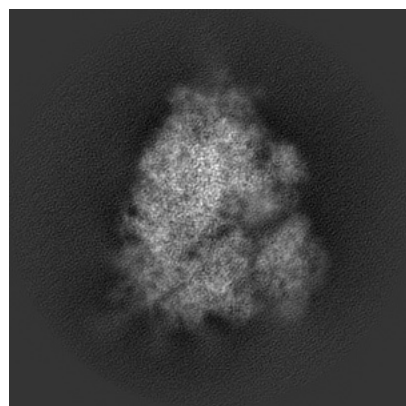
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0601. These allow visual inspection of the internal detail of the map and identification of artifacts.

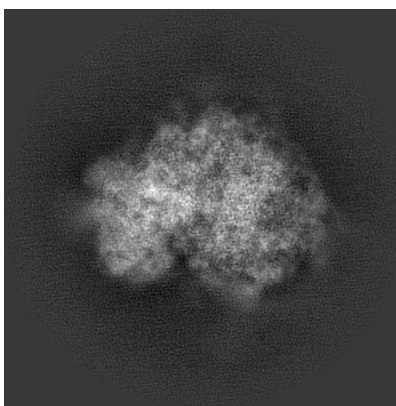
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

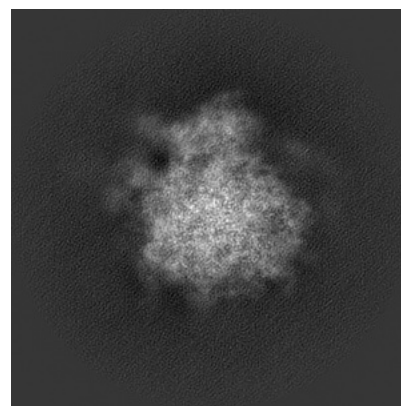
6.1.1 Primary map



X

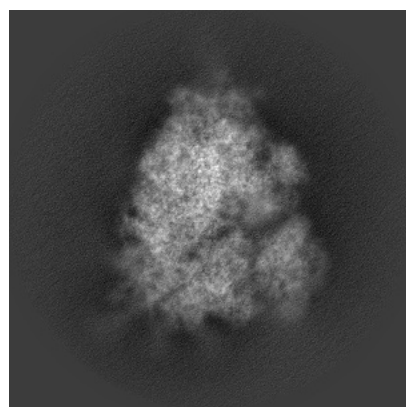


Y

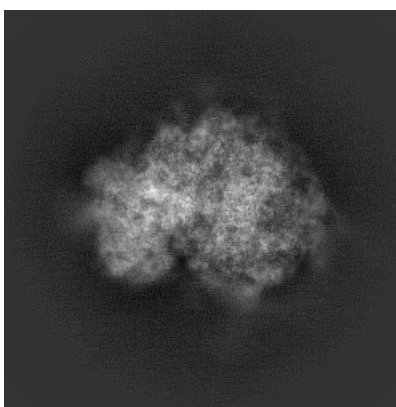


Z

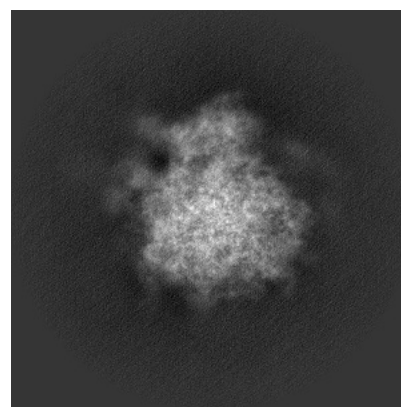
6.1.2 Raw map



X



Y

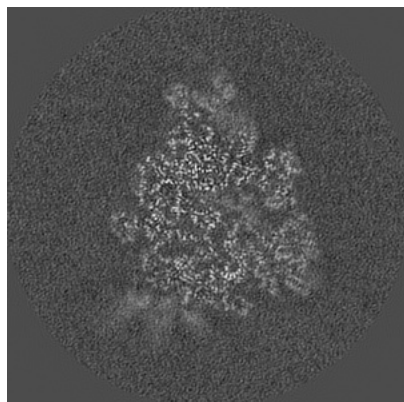


Z

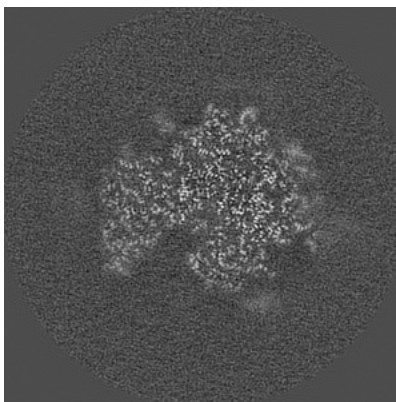
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

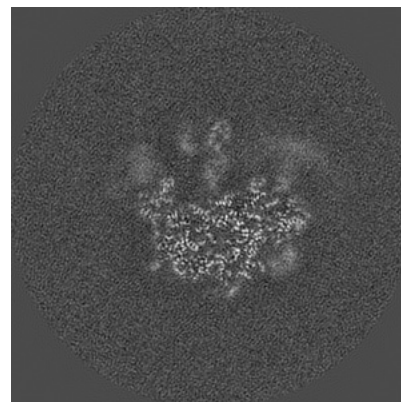
6.2.1 Primary map



X Index: 205

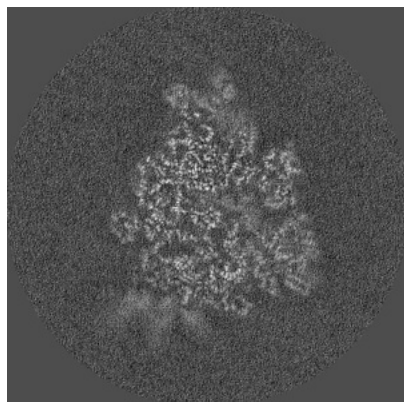


Y Index: 205

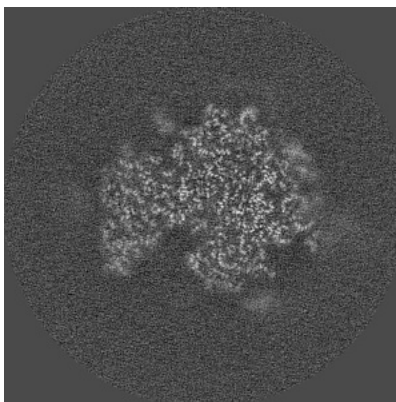


Z Index: 205

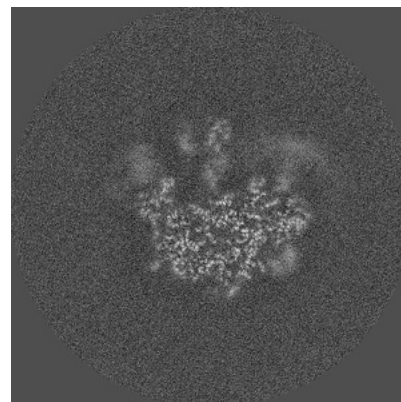
6.2.2 Raw map



X Index: 205



Y Index: 205

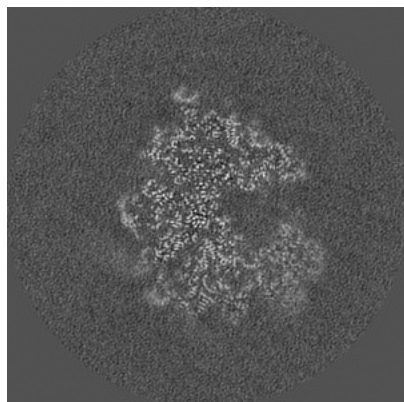


Z Index: 205

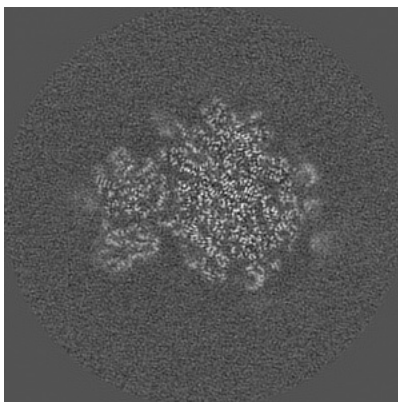
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

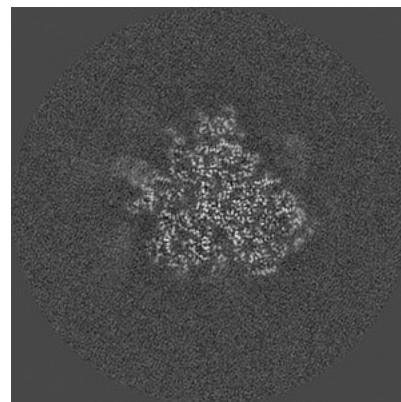
6.3.1 Primary map



X Index: 225

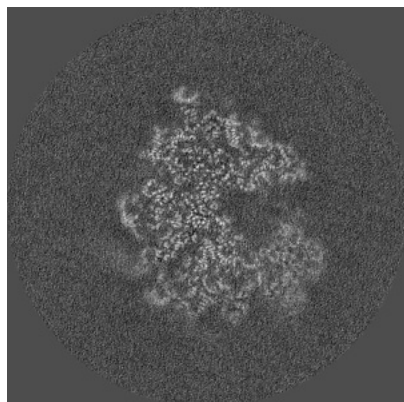


Y Index: 197

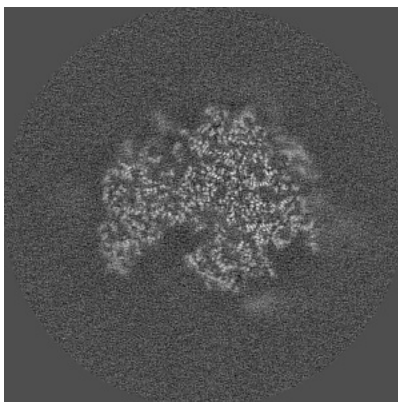


Z Index: 234

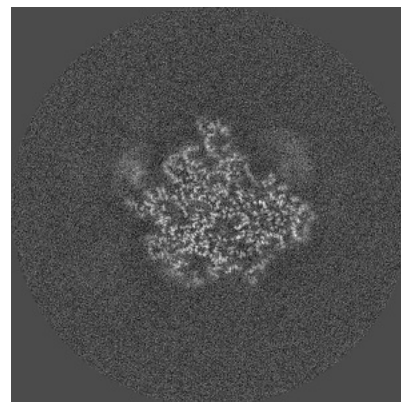
6.3.2 Raw map



X Index: 225



Y Index: 207

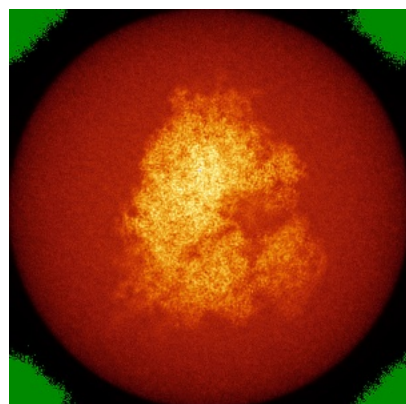


Z Index: 225

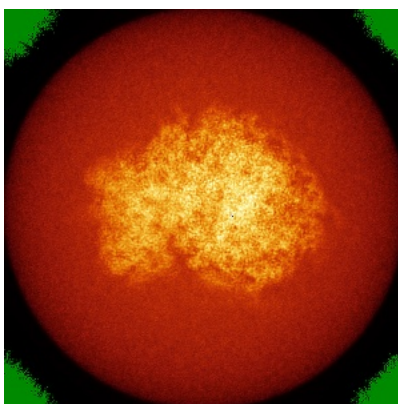
The images above show the largest variance slices of the map in three orthogonal directions.

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

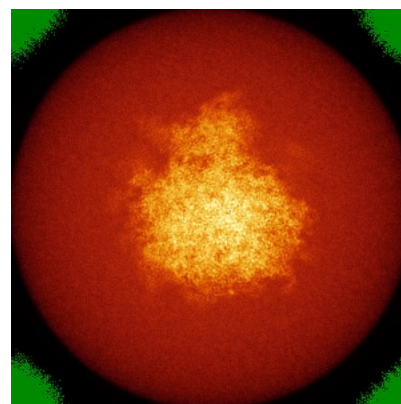
6.4.1 Primary map



X

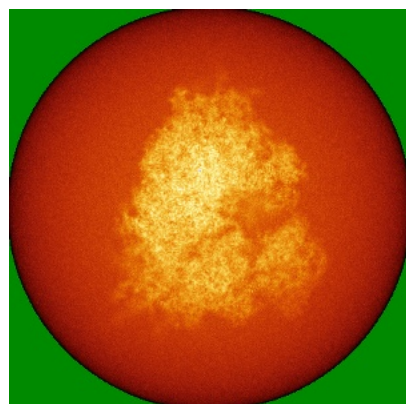


Y

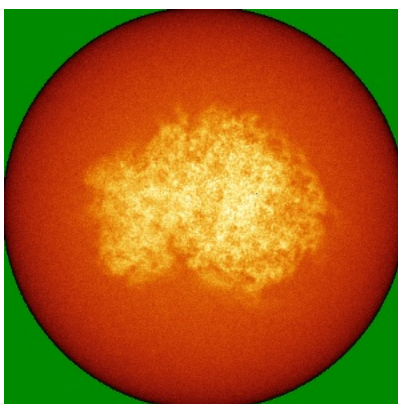


Z

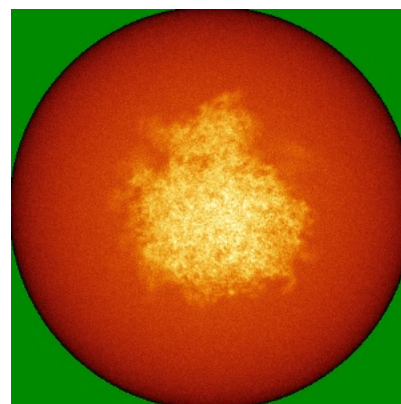
6.4.2 Raw map



X



Y

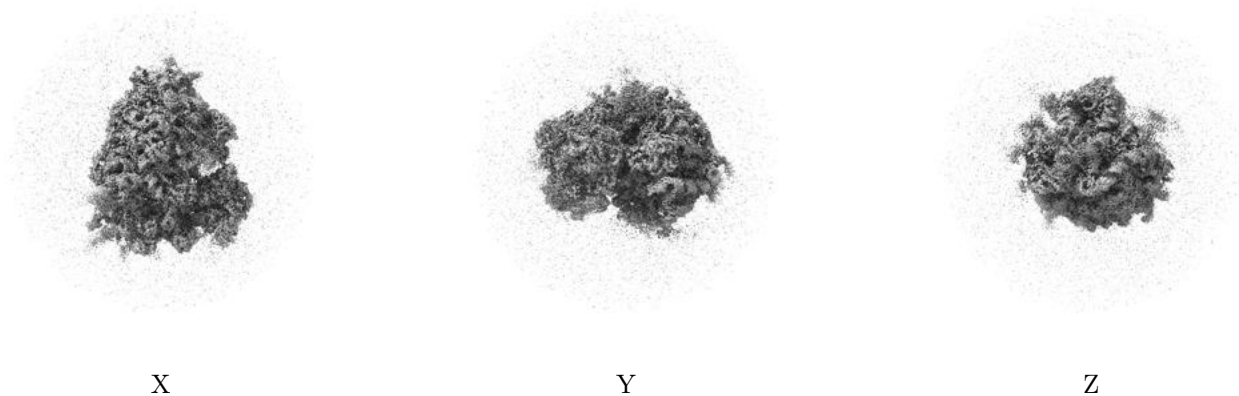


Z

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.

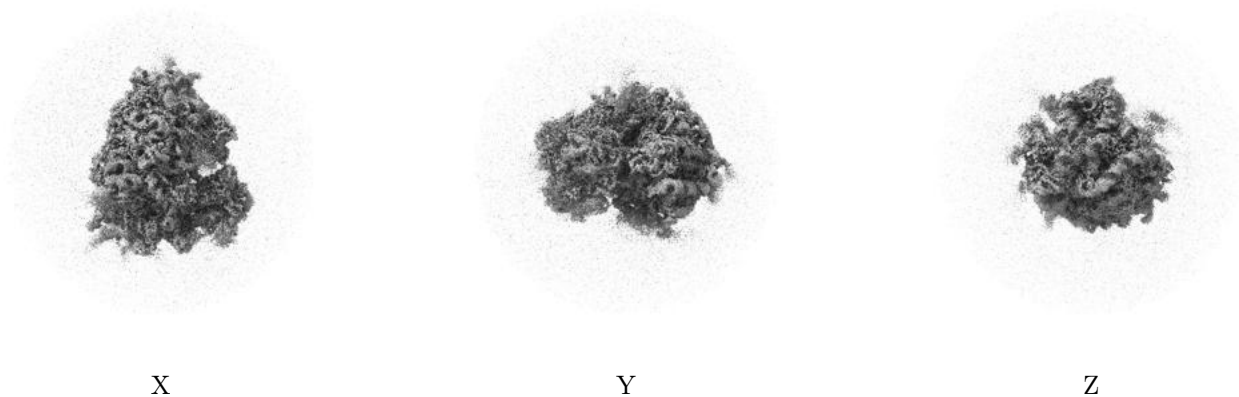
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

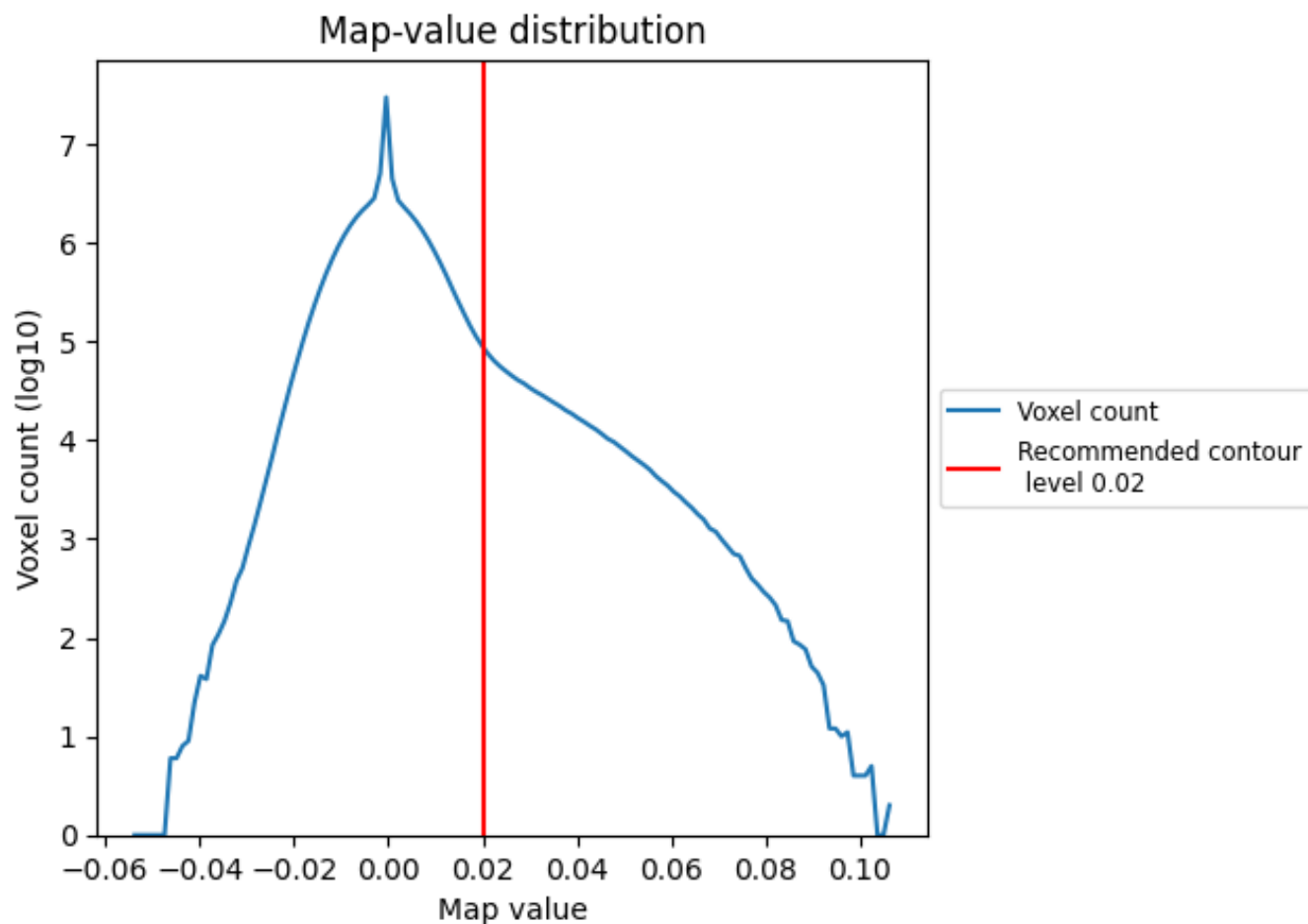
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

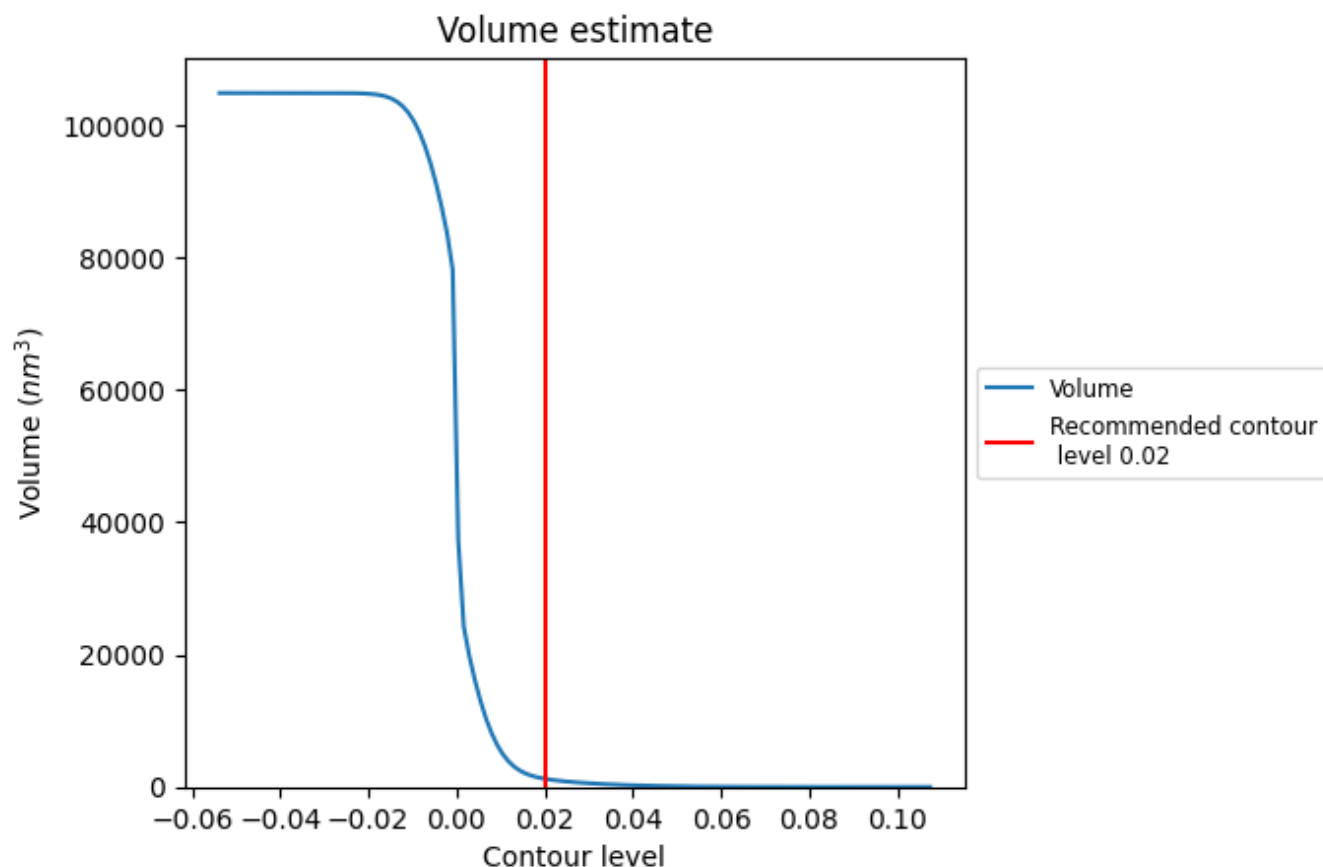
This section contains the results of statistical analysis of the map.

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.

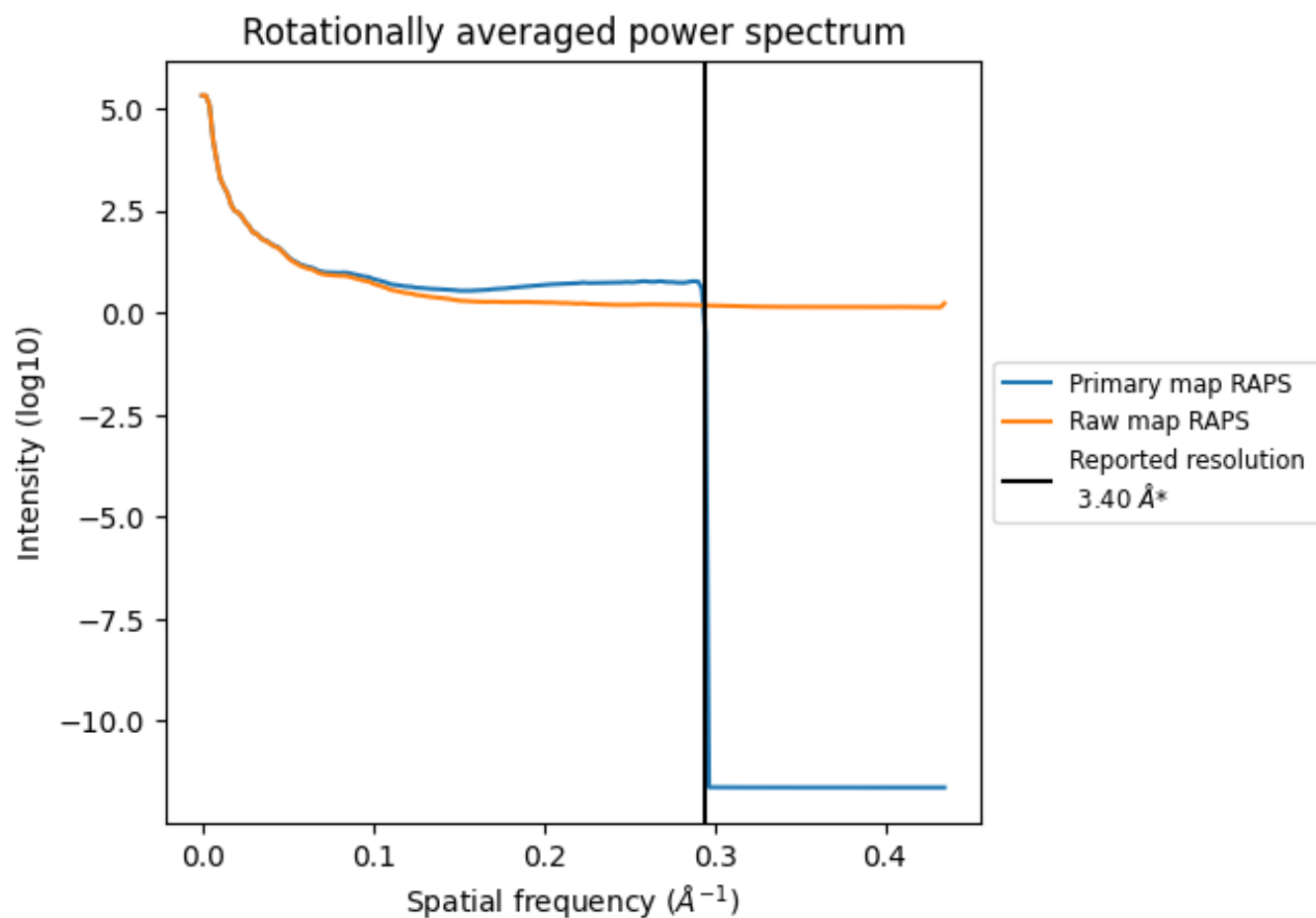
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1242 nm^3 ; this corresponds to an approximate mass of 1122 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 ⓘ

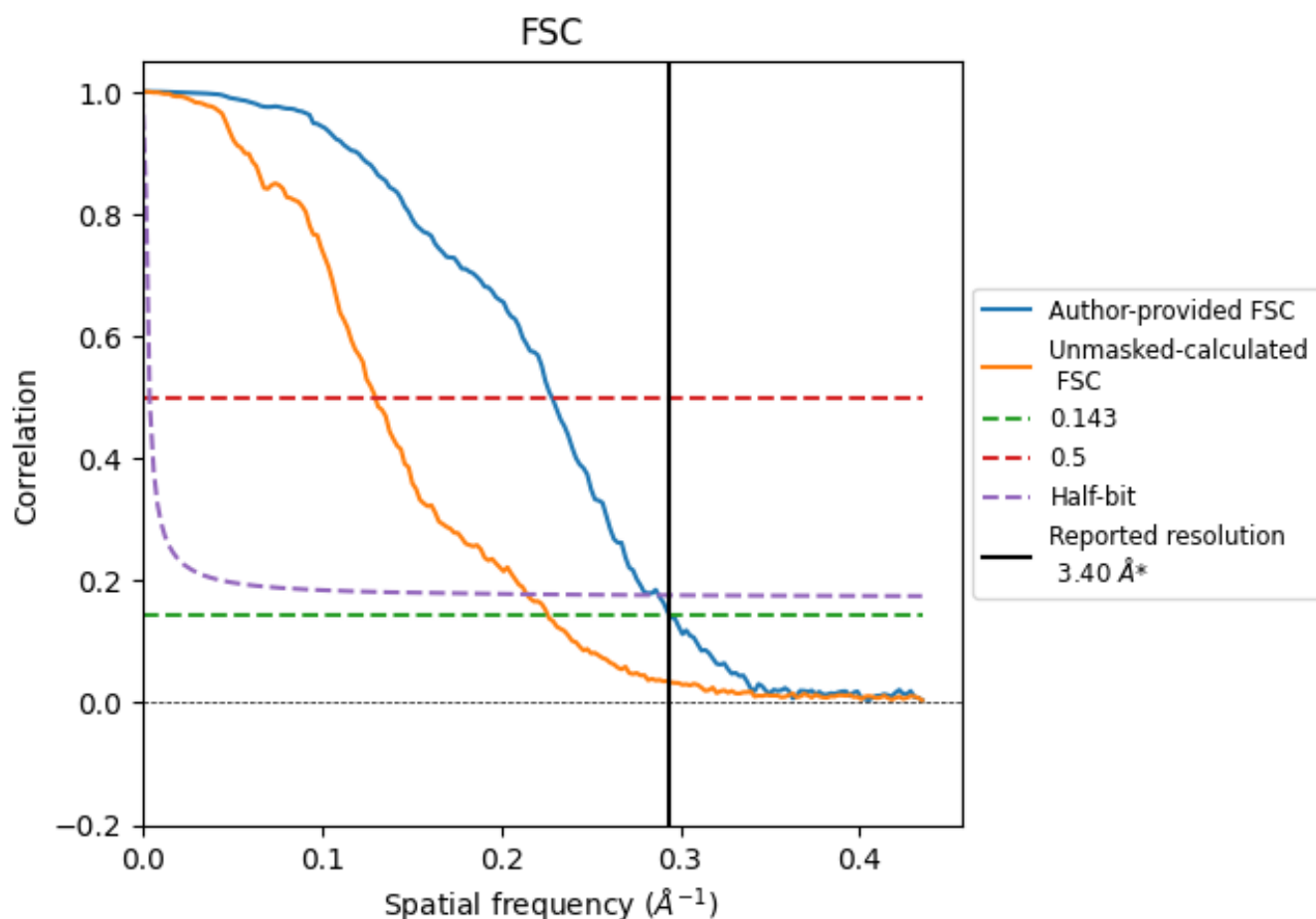


*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

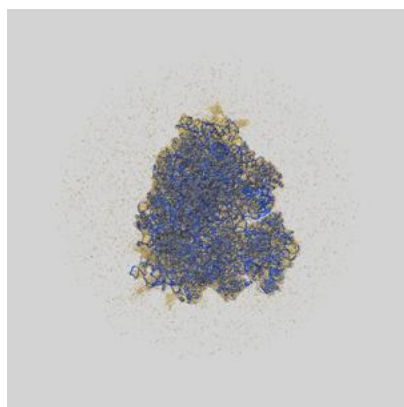
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.40	4.38	3.47
Unmasked-calculated*	4.42	7.70	4.67

*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 4.42 differs from the reported value 3.4 by more than 10 %

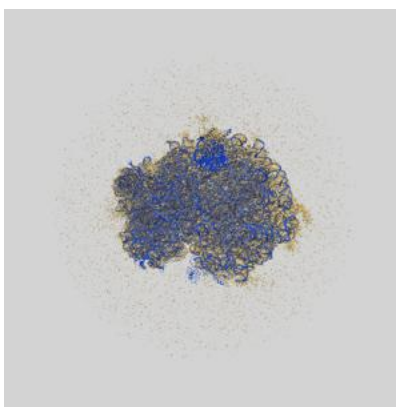
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0601 and PDB model 6OLG. Per-residue inclusion information can be found in section [3](#) on page [21](#).

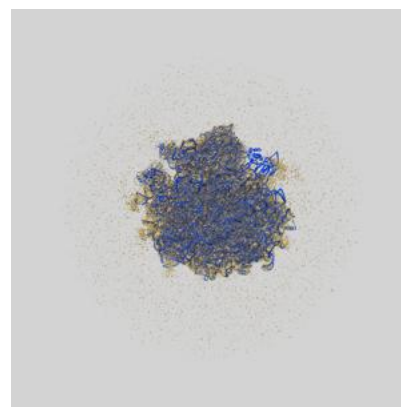
9.1 Map-model overlay [i](#)



X



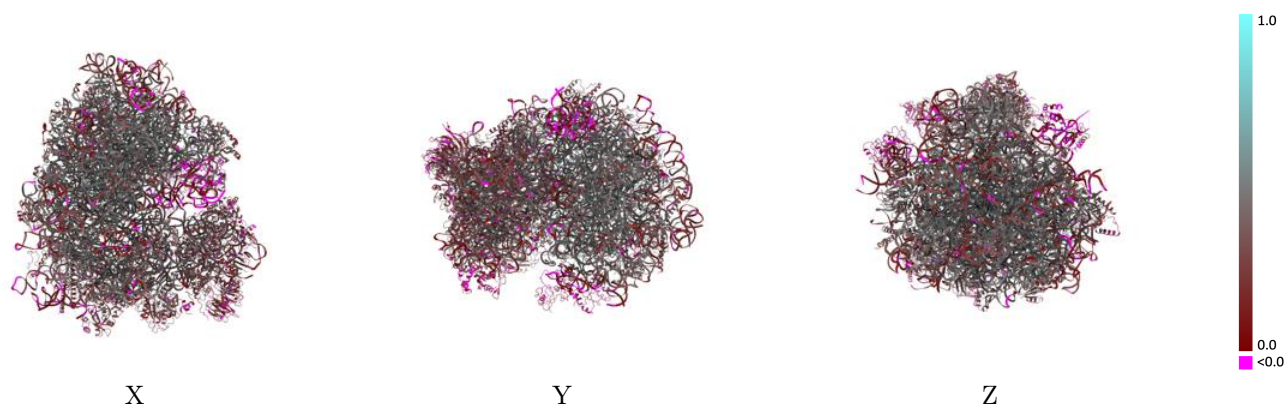
Y



Z

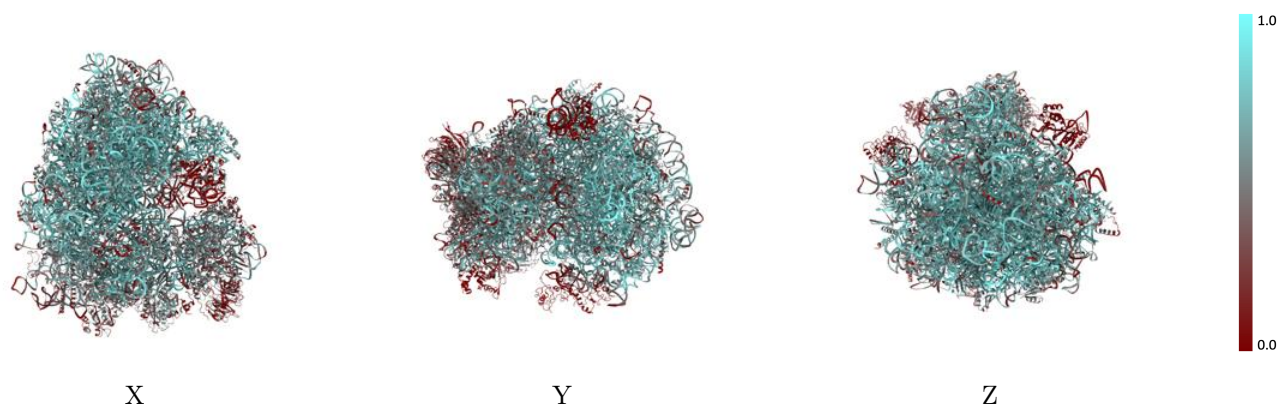
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



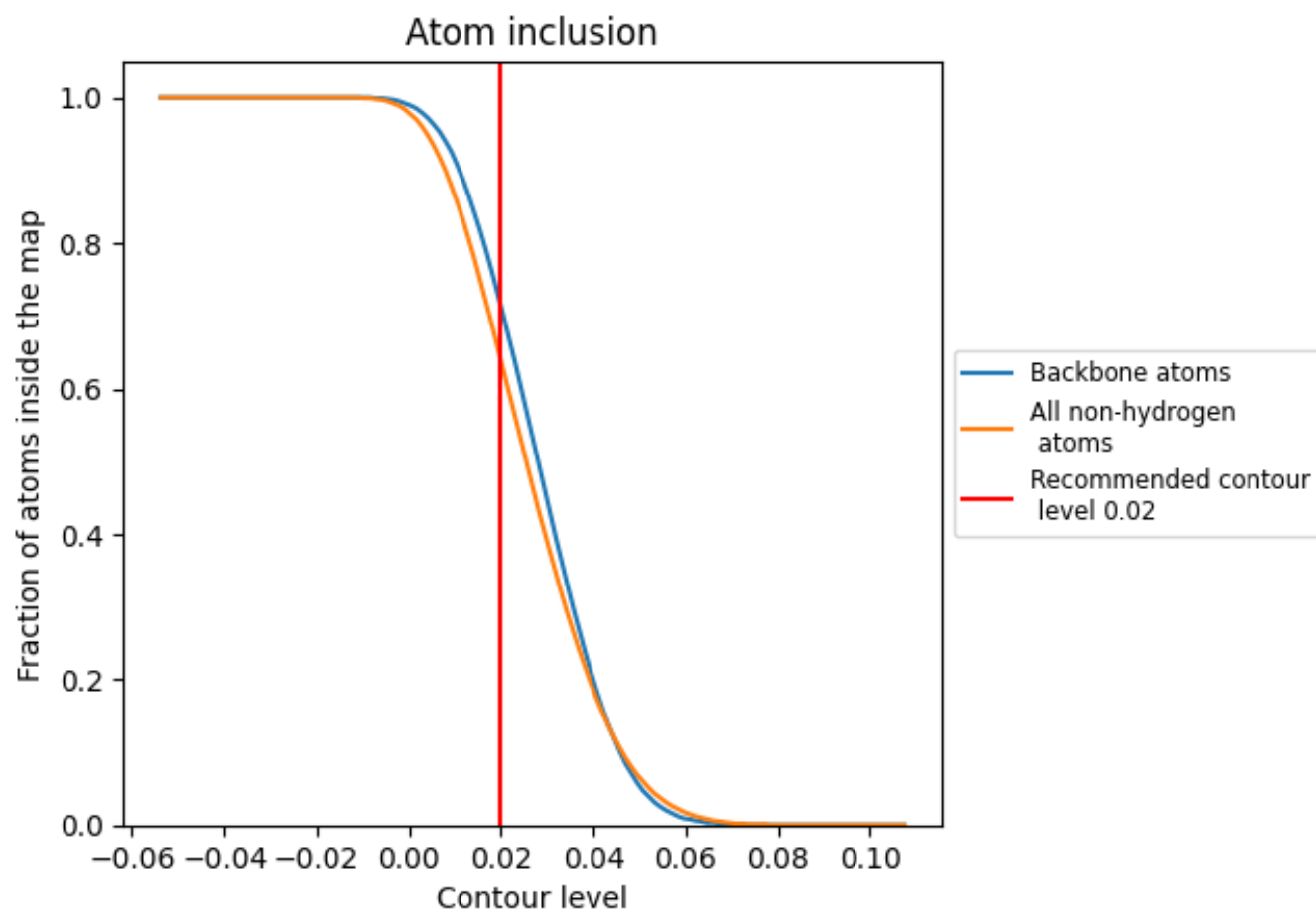
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 64% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6390	 0.3630
A	 0.0740	 0.0960
A2	 0.7520	 0.3930
A3	 0.7640	 0.4020
A4	 0.8630	 0.4520
AA	 0.6720	 0.4320
AB	 0.6500	 0.4280
AC	 0.6680	 0.4320
AD	 0.6230	 0.3830
AE	 0.5410	 0.3590
AF	 0.6380	 0.4090
AG	 0.5640	 0.3510
AH	 0.5730	 0.3930
AI	 0.6200	 0.4030
AJ	 0.5680	 0.3670
AK	 0.0390	 0.0470
AL	 0.5950	 0.3720
AM	 0.6480	 0.4040
AN	 0.7230	 0.4480
AO	 0.6530	 0.4190
AP	 0.6600	 0.4370
AQ	 0.6480	 0.4270
AR	 0.6270	 0.3870
AS	 0.6740	 0.4430
AT	 0.6590	 0.4100
AU	 0.5420	 0.3530
AV	 0.6480	 0.4400
AW	 0.3730	 0.2640
AX	 0.6000	 0.4040
AY	 0.6600	 0.4130
AZ	 0.6230	 0.3660
Aa	 0.6950	 0.4390
Ab	 0.5880	 0.3580
Ac	 0.5820	 0.3890
Ad	 0.6390	 0.4050



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Chain	Atom inclusion	Q-score
Ae	 0.6820	 0.4450
Af	 0.7040	 0.4620
Ag	 0.6200	 0.4080
Ah	 0.6070	 0.3720
Ai	 0.6190	 0.3560
Aj	 0.7170	 0.4510
Ak	 0.5040	 0.3110
Al	 0.6550	 0.4200
Am	 0.6450	 0.4080
An	 0.5520	 0.3670
Ao	 0.5720	 0.3850
Ap	 0.6530	 0.4230
Aq	 0.0210	 0.0630
At	 0.6650	 0.4220
Au	 0.0060	 0.0330
B1	 0.6890	 0.3570
BA	 0.5000	 0.3260
BB	 0.4860	 0.3100
BC	 0.5440	 0.3690
BD	 0.3340	 0.2720
BE	 0.5130	 0.3530
BF	 0.4070	 0.2760
BG	 0.3960	 0.2560
BH	 0.3740	 0.2540
BI	 0.5100	 0.3430
BJ	 0.5030	 0.3120
BK	 0.2780	 0.2000
BL	 0.5170	 0.3390
BM	 0.0410	 0.0730
BN	 0.5380	 0.3460
BO	 0.5330	 0.3590
BP	 0.3710	 0.2340
BQ	 0.4110	 0.2550
BR	 0.3540	 0.2520
BS	 0.3930	 0.2800
BT	 0.3690	 0.2290
BU	 0.3720	 0.2510
BV	 0.4860	 0.3190
BW	 0.5830	 0.3830
BX	 0.5610	 0.3700
BY	 0.4570	 0.2880
BZ	 0.3060	 0.2130

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Chain	Atom inclusion	Q-score
Ba	 0.5610	 0.3270
Bb	 0.4550	 0.3050
Bc	 0.3660	 0.2670
Bd	 0.4540	 0.3030
Be	 0.4120	 0.2940
Bf	 0.0920	 0.1090
Bg	 0.2130	 0.1920
Bv	 0.3690	 0.2530
Bx	 0.0910	 0.0900