



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 08:48 PM UTC

PDB ID : 6GZ4 / pdb_00006gz4
EMDB ID : EMD-0099
Title : tRNA translocation by the eukaryotic 80S ribosome and the impact of GTP hydrolysis, Translocation-intermediate-POST-2 (TI-POST-2)
Authors : Flis, J.; Holm, M.; Rundlet, E.J.; Loerke, J.; Hilal, T.; Dabrowski, M.; Buerger, J.; Mielke, T.; Blanchard, S.C.; Spahn, C.M.T.; Budkevich, T.V.
Deposited on : 2018-07-03
Resolution : 3.60 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:

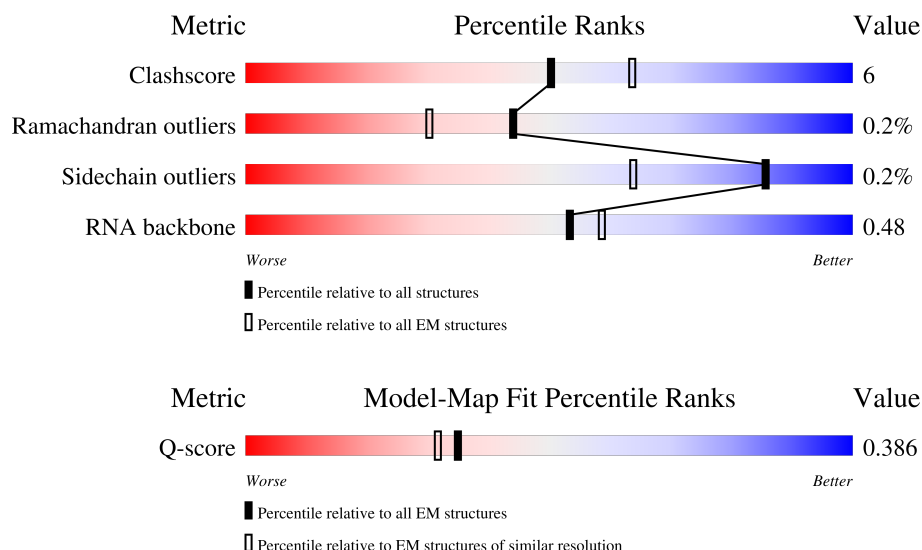
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.60 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	12797 (3.10 - 4.10)

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	252	 5% 75% 25%
2	BA	215	 30% 84% 16%
3	AB	394	 7% 77% 23%

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Mol	Chain	Length	Quality of chain
4	BB	212	
5	AC	363	
6	BC	222	
7	A2	3612	
8	Bv	76	
9	Bx	11	
10	Bw	76	
11	B1	1708	
12	BD	220	
13	BF	190	
14	BK	98	
15	BM	120	
16	BP	120	
17	BQ	139	
18	BR	125	
19	BS	139	
20	BT	143	
21	BU	97	
22	BZ	86	
23	Bc	62	
24	Bd	51	
25	Bf	73	
26	Bg	314	
27	BE	257	
28	BG	232	

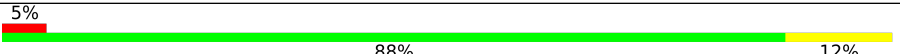
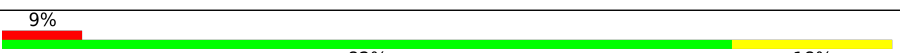
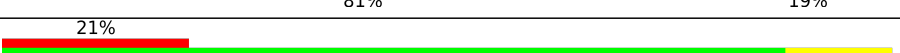
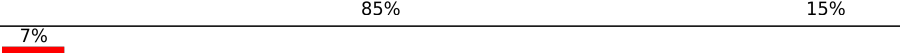
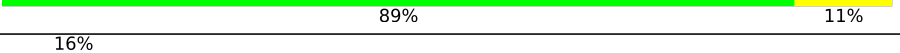
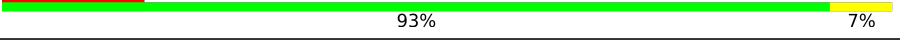
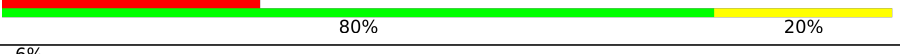
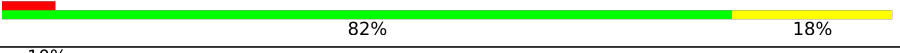
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Mol	Chain	Length	Quality of chain
29	BH	183	
30	BI	207	
31	BJ	179	
32	BL	153	
33	BN	149	
34	BO	136	
35	BV	81	
36	BW	129	
37	BX	141	
38	BY	125	
39	Ba	97	
40	Bb	80	
41	Be	55	
42	A3	157	
43	A4	119	
44	AD	294	
45	AE	194	
46	AF	234	
47	AG	234	
48	AH	191	
49	AI	208	
50	AJ	169	
51	AL	205	
52	AM	139	
53	AN	203	

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Mol	Chain	Length	Quality of chain
54	AO	195	
55	AP	153	
56	AQ	187	
57	AR	181	
58	AS	175	
59	AT	157	
60	AU	99	
61	AV	129	
62	AW	121	
63	AX	117	
64	AY	127	
65	AZ	134	
66	Aa	147	
67	Ab	68	
68	Ac	103	
69	Ad	106	
70	Ae	129	
71	Af	109	
72	Ag	114	
73	Ah	122	
74	Ai	97	
75	Aj	84	
76	Ak	69	
77	Al	50	
78	Am	50	

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Mol	Chain	Length	Quality of chain
79	An	25	
80	Ao	105	
81	Ap	91	
82	At	122	
83	Au	217	
84	Aq	151	
85	AK	202	
86	Ct	853	

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 225601 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 ribosomal protein uL2.

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 ribosomal protein uS2.

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 ribosomal protein uL3.

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 ribosomal protein eS1.

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 ribosomal protein uL4.

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 ribosomal protein eS28.

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 28S ribosomal RNA.

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

- Molecule 8 is a RNA chain called ap/P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Bv	76	Total	C	N	O	P	0	0
			1620	723	290	531	76		

- Molecule 9 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Bx	11	Total	C	N	O	P	0	0
			234	105	41	77	11		

- Molecule 10 is a RNA chain called pe/E-site-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Bw	76	Total	C	N	O	P	0	0
			1627	725	294	532	76		

- Molecule 11 is a RNA chain called 18S ribosomal RNA.

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

- Molecule 12 is a protein called ribosomal protein uS3.

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

- Molecule 13 is a protein called ribosomal protein uS7.

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

- Molecule 14 is a protein called ribosomal protein eS10.

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

- Molecule 15 is a protein called ribosomal protein eS12.

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

- Molecule 16 is a protein called ribosomal protein uS19.

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

- Molecule 17 is a protein called ribosomal protein uS9.

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

- Molecule 18 is a protein called ribosomal protein eS17.

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

- Molecule 19 is a protein called ribosomal protein uS13.

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

- Molecule 20 is a protein called ribosomal protein eS19.

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

- Molecule 21 is a protein called ribosomal protein uS10.

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

- Molecule 22 is a protein called ribosomal protein uS10.

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

- Molecule 23 is a protein called ribosomal protein eS28.

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

- Molecule 24 is a protein called ribosomal protein uS14.

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

- Molecule 25 is a protein called ribosomal protein eS31.

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

- Molecule 26 is a protein called ribosomal protein RACK 1.

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

- Molecule 27 is a protein called ribosomal protein eS4.

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

- Molecule 28 is a protein called ribosomal protein eS6.

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

- Molecule 29 is a protein called ribosomal protein eS7.

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

- Molecule 30 is a protein called ribosomal protein eS8.

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

- Molecule 31 is a protein called ribosomal protein uS4.

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

- Molecule 32 is a protein called ribosomal protein uS17.

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

- Molecule 33 is a protein called ribosomal protein uS15.

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

- Molecule 34 is a protein called ribosomal protein uS11.

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

- Molecule 35 is a protein called ribosomal protein eS21.

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

- Molecule 36 is a protein called ribosomal protein uS8.

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

- Molecule 37 is a protein called ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 38 is a protein called ribosomal protein eS24.

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

- Molecule 39 is a protein called ribosomal protein eS26.

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

- Molecule 40 is a protein called ribosomal protein eS27.

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

- Molecule 41 is a protein called ribosomal protein eS30.

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

- Molecule 42 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 43 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 44 is a protein called ribosomal protein uL18.

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

- Molecule 45 is a protein called ribosomal protein eL6.

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

- Molecule 46 is a protein called ribosomal protein uL30.

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

- Molecule 47 is a protein called ribosomal protein eL8.

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

- Molecule 48 is a protein called ribosomal protein uL6.

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

- Molecule 49 is a protein called ribosomal protein uL16.

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

- Molecule 50 is a protein called ribosomal protein uL5.

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

- Molecule 51 is a protein called ribosomal protein eL13.

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

- Molecule 52 is a protein called ribosomal protein eL14.

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

- Molecule 53 is a protein called ribosomal protein eL15.

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

- Molecule 54 is a protein called ribosomal protein uL13.

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

- Molecule 55 is a protein called ribosomal protein uL22.

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

- Molecule 56 is a protein called ribosomal protein eL18.

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

- Molecule 57 is a protein called ribosomal protein eL19.

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

- Molecule 58 is a protein called ribosomal protein eL20.

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

- Molecule 59 is a protein called ribosomal protein eL21.

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

- Molecule 60 is a protein called ribosomal protein eL22.

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

- Molecule 61 is a protein called ribosomal protein uL14.

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

- Molecule 62 is a protein called ribosomal protein eL24.

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

- Molecule 63 is a protein called ribosomal protein uL23.

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

- Molecule 64 is a protein called ribosomal protein uL24.

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

- Molecule 65 is a protein called ribosomal protein eL27.

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

- Molecule 66 is a protein called ribosomal protein uL15.

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

- Molecule 67 is a protein called ribosomal protein eL29.

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

- Molecule 68 is a protein called ribosomal protein eL30.

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

- Molecule 69 is a protein called ribosomal protein eL31.

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

- Molecule 70 is a protein called ribosomal protein eL32.

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

- Molecule 71 is a protein called ribosomal protein eL33.

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

- Molecule 72 is a protein called ribosomal protein eL34.

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

- Molecule 73 is a protein called ribosomal protein uL29.

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

- Molecule 74 is a protein called ribosomal protein eL36.

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

- Molecule 75 is a protein called ribosomal protein eL37.

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

- Molecule 76 is a protein called ribosomal protein eL38.

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

- Molecule 77 is a protein called ribosomal protein eL39.

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

- Molecule 78 is a protein called ribosomal protein eL40.

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

- Molecule 79 is a protein called ribosomal protein eL41.

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

- Molecule 80 is a protein called ribosomal protein eL42.

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

- Molecule 81 is a protein called ribosomal protein eL43.

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

- Molecule 82 is a protein called ribosomal protein eL28.

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

- Molecule 83 is a protein called ribosomal protein uL1.

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

- Molecule 84 is a protein called ribosomal protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Aq	151	Total	C	N	O	S	0	0
			1140	708	215	213	4		

- Molecule 85 is a protein called ribosomal protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	AK	202	Total	C	N	O	S	0	0
			1556	989	272	286	9		

- Molecule 86 is a protein called eukaryotic elongation factor 2 (eEF2).

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Ct	853	Total	C	N	O	S	0	0
			6659	4226	1146	1243	44		

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	AA	1	Total	Mg	0
			1	1	
87	A2	236	Total	Mg	0
			236	236	
87	Bx	1	Total	Mg	0
			1	1	
87	B1	67	Total	Mg	0
			67	67	
87	BD	2	Total	Mg	0
			2	2	
87	BS	2	Total	Mg	0
			2	2	
87	Bd	2	Total	Mg	0
			2	2	
87	Ba	1	Total	Mg	0
			1	1	
87	A3	4	Total	Mg	0
			4	4	
87	A4	8	Total	Mg	0
			8	8	
87	AL	1	Total	Mg	0
			1	1	
87	AY	1	Total	Mg	0
			1	1	

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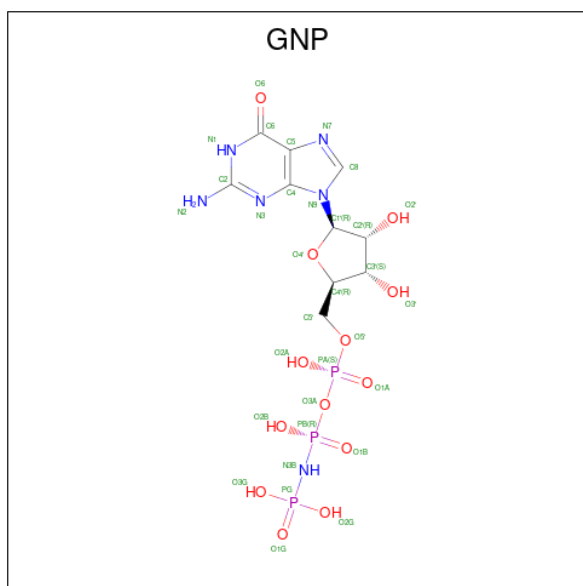
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
87	An	1	Total	Mg	0
			1	1	

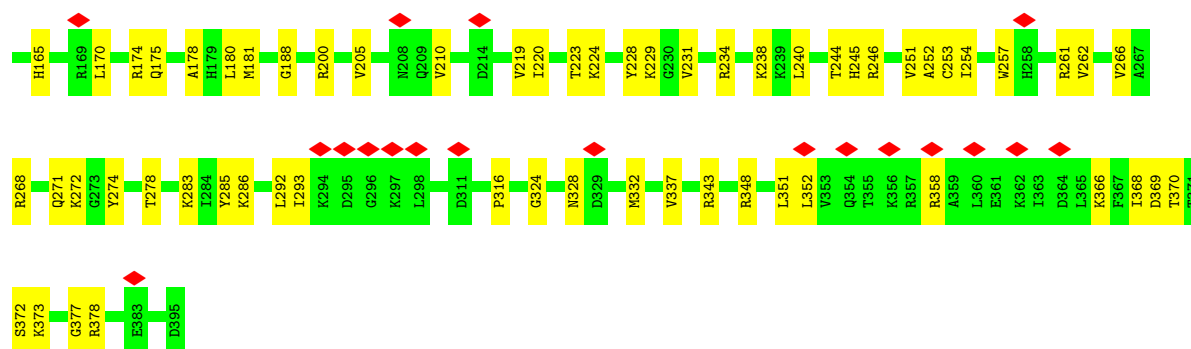
- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

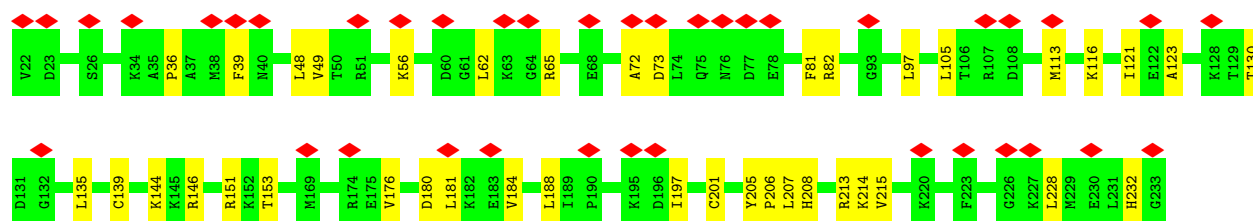
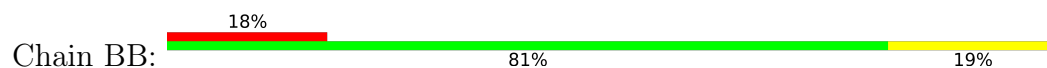
- Molecule 89 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: C₁₀H₁₇N₆O₁₃P₃).



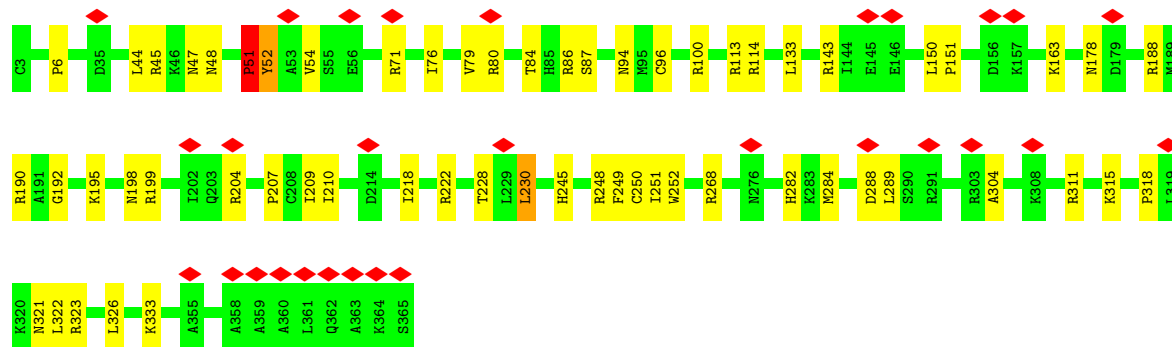
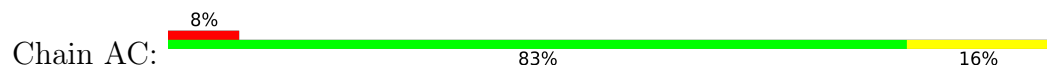
Mol	Chain	Residues	Atoms					AltConf
89	Ct	1	Total	C	N	O	P	0
			32	10	6	13	3	



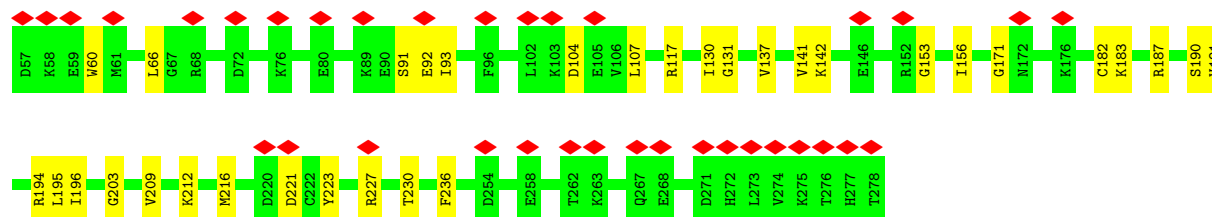
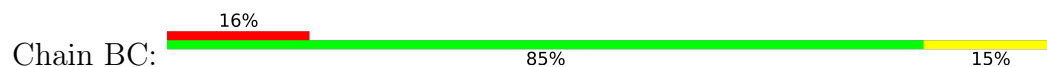
• Molecule 4: ribosomal protein eS1



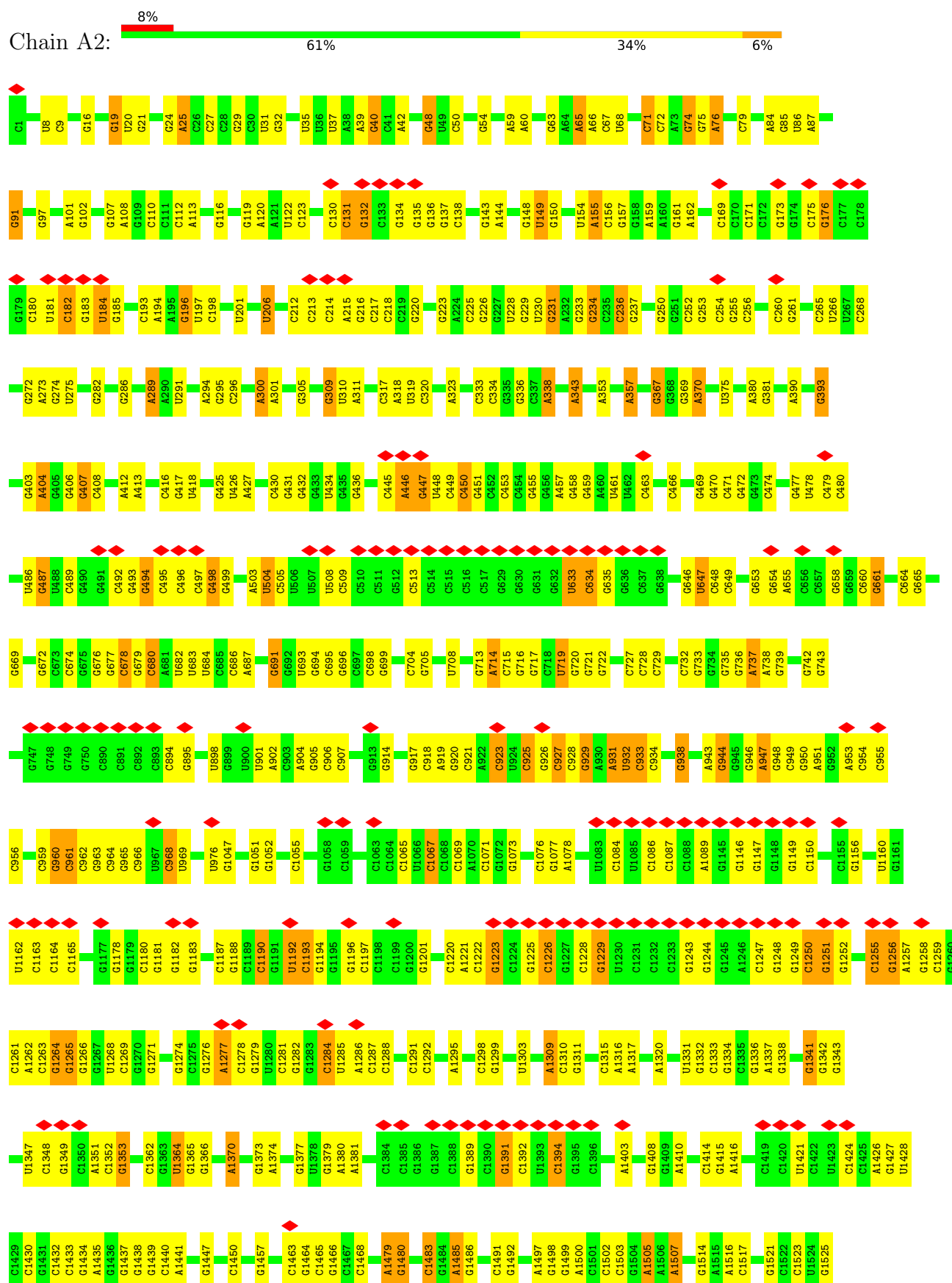
• Molecule 5: ribosomal protein uL4



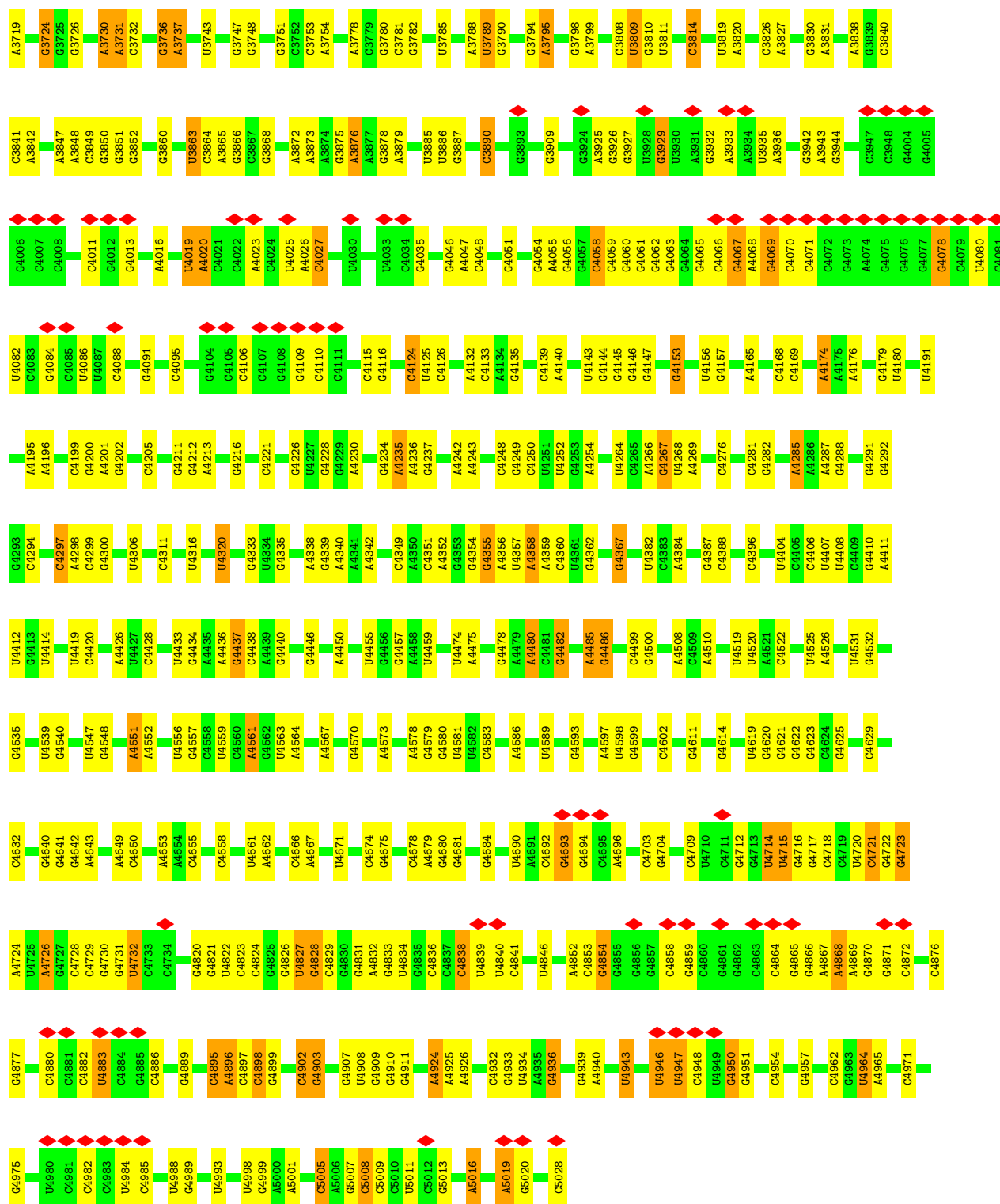
• Molecule 6: ribosomal protein eS28



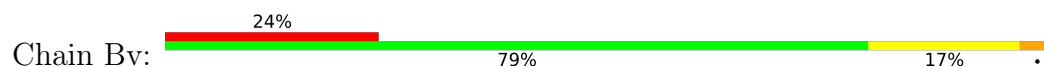
• Molecule 7: 28S ribosomal RNA

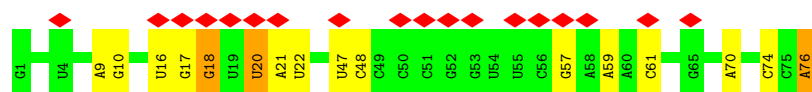




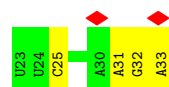


• Molecule 8: ap/P-site tRNA

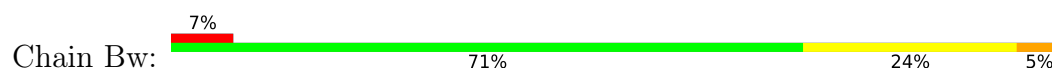




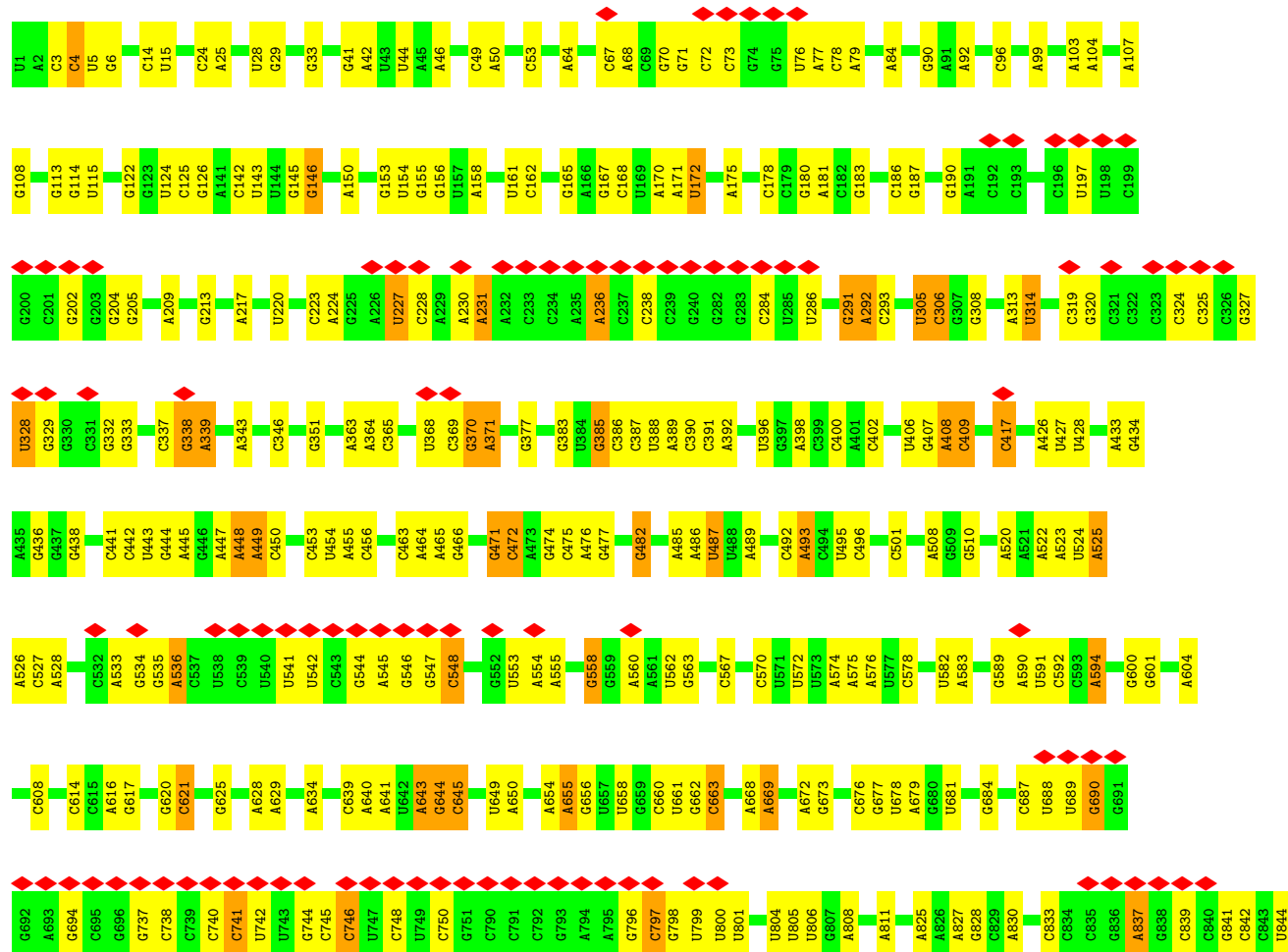
• Molecule 9: mRNA

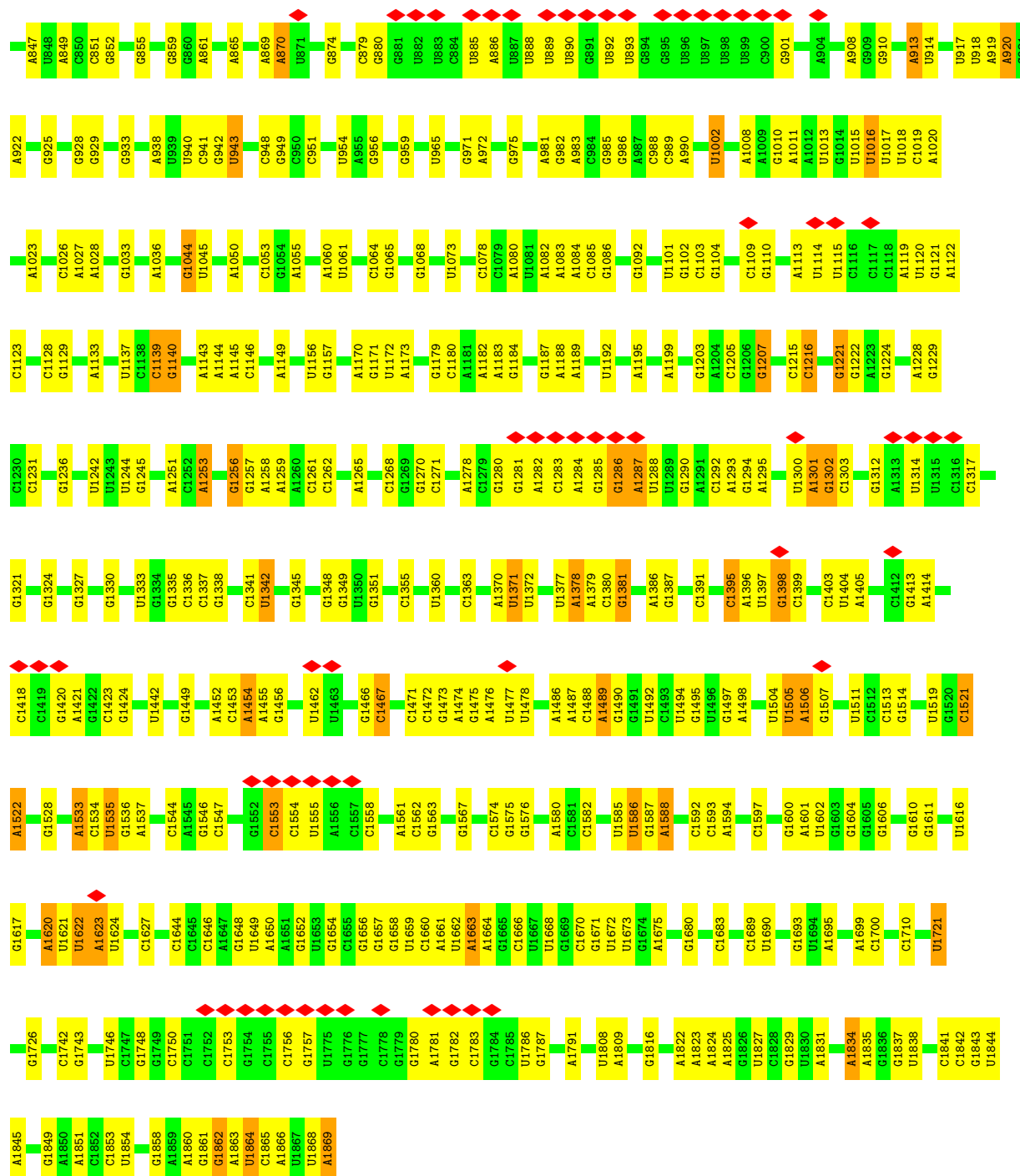


• Molecule 10: pe/E-site-tRNA

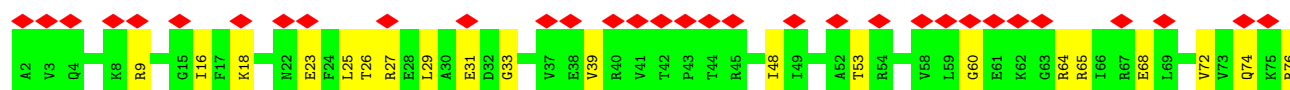
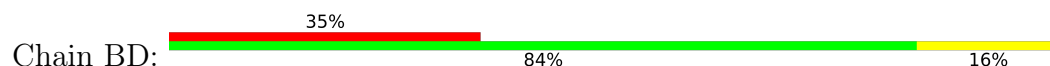


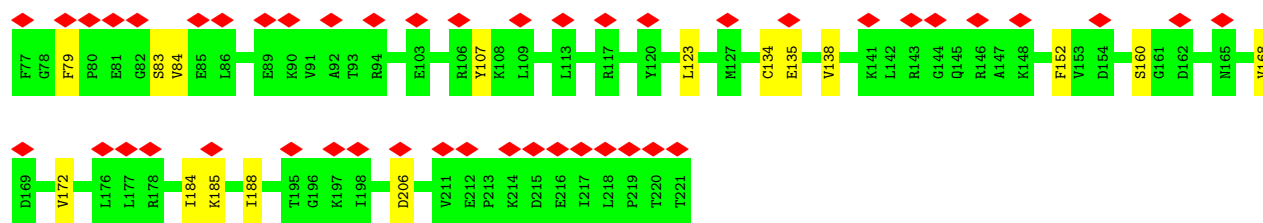
• Molecule 11: 18S ribosomal RNA



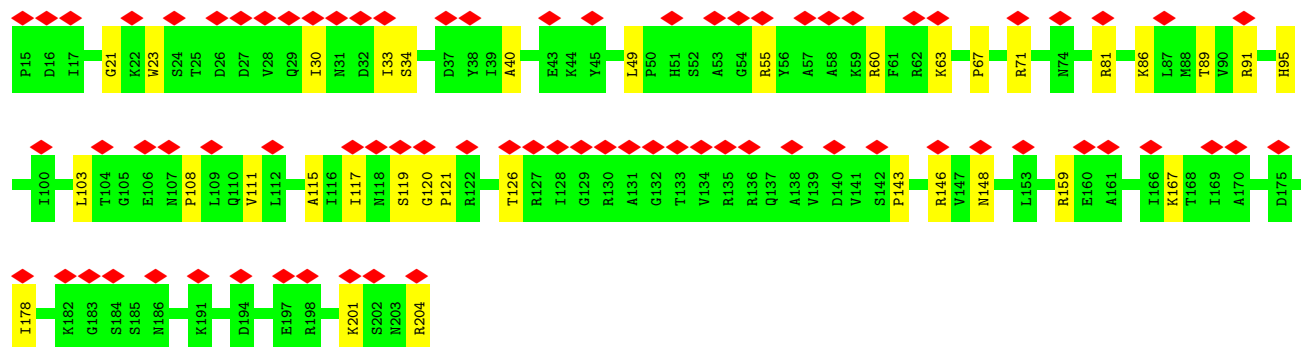
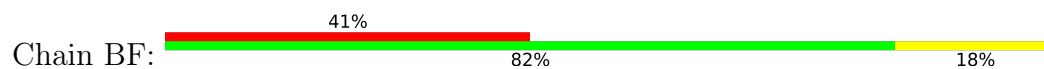


• Molecule 12: ribosomal protein uS3

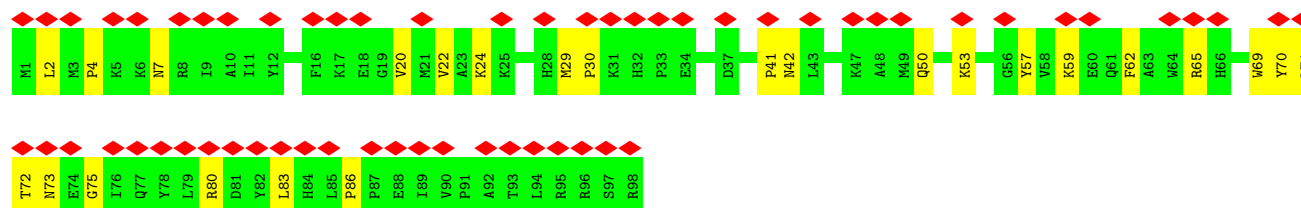
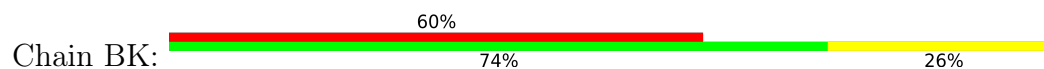




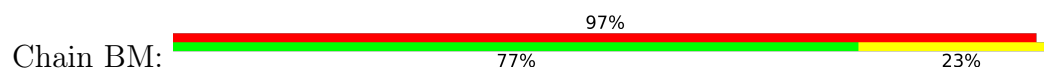
• Molecule 13: ribosomal protein uS7



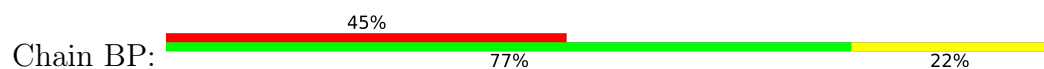
• Molecule 14: ribosomal protein eS10

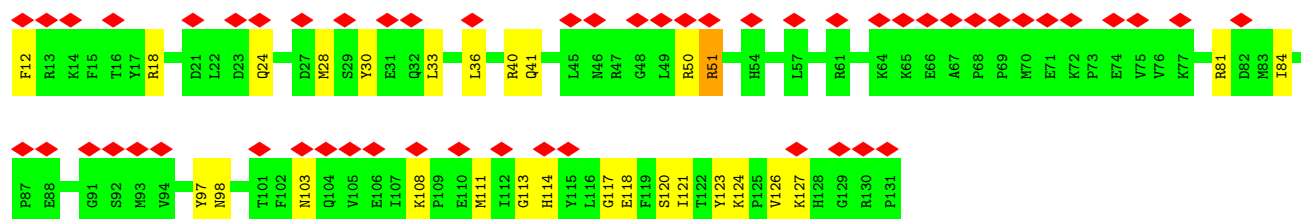


• Molecule 15: ribosomal protein eS12

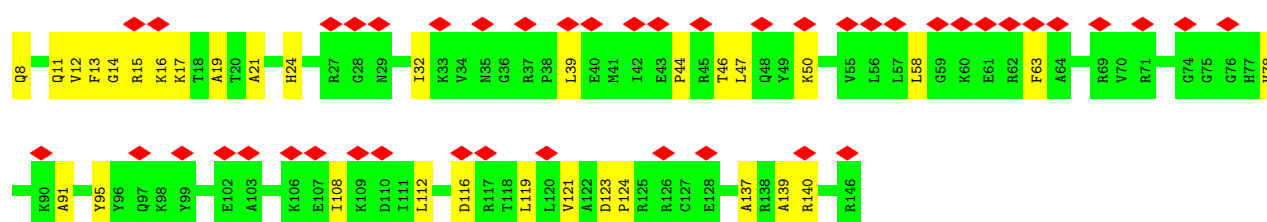
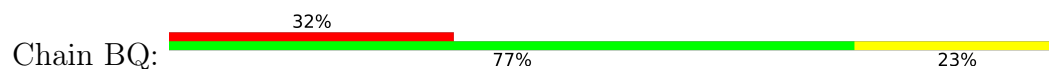


• Molecule 16: ribosomal protein uS19

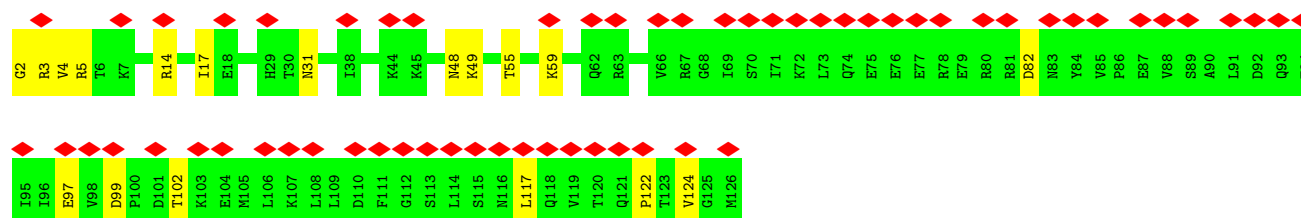




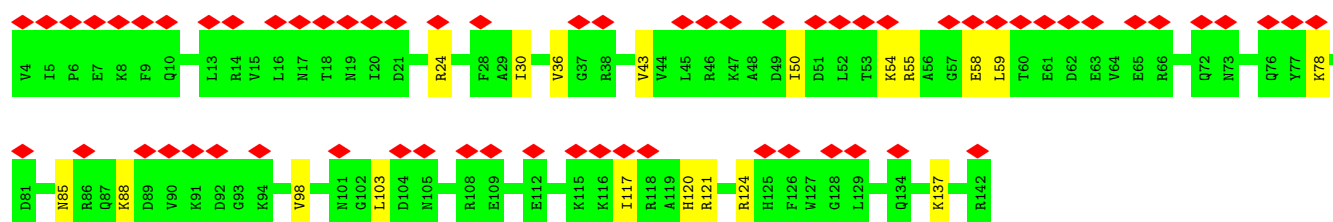
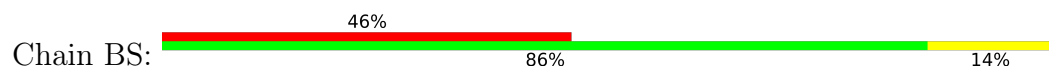
• Molecule 17: ribosomal protein uS9



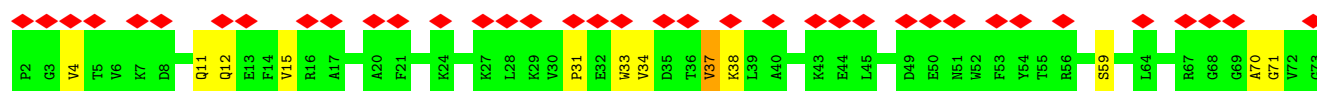
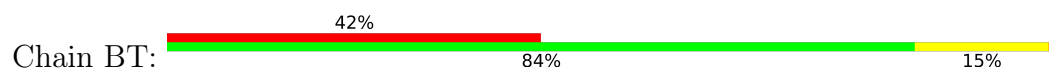
• Molecule 18: ribosomal protein eS17

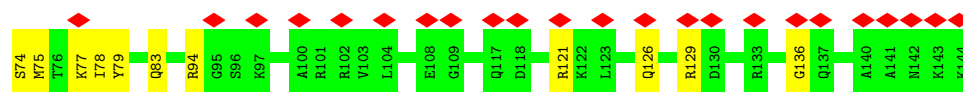


• Molecule 19: ribosomal protein uS13

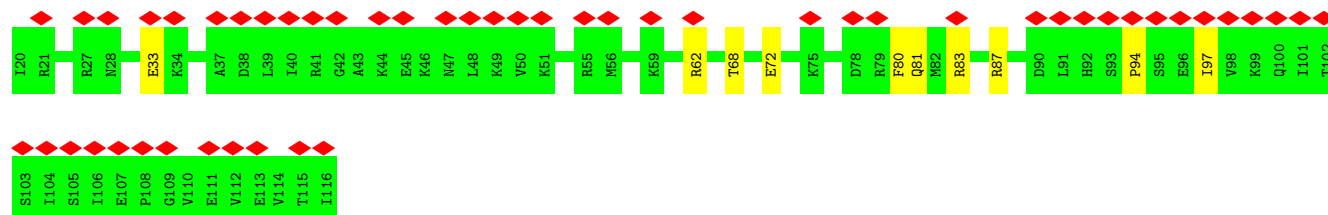
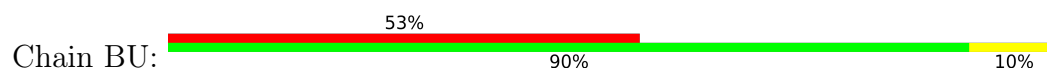


• Molecule 20: ribosomal protein eS19

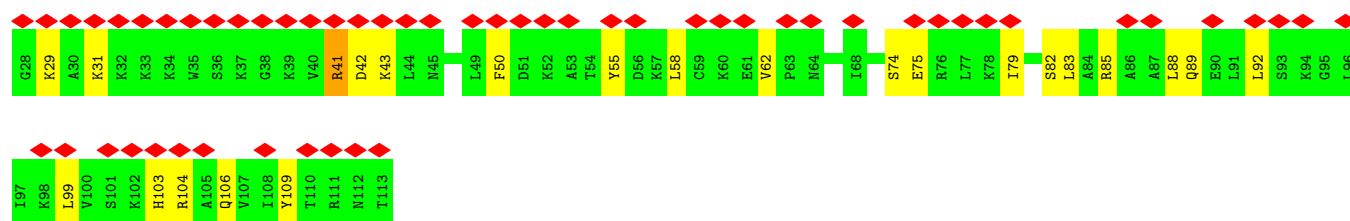
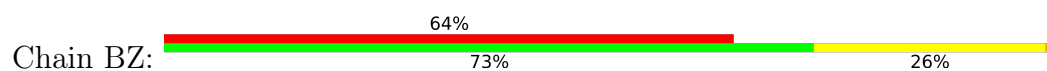




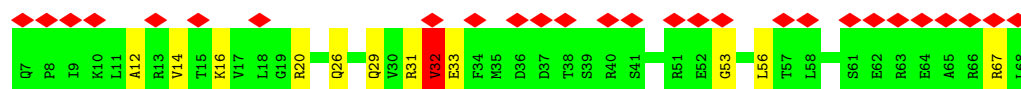
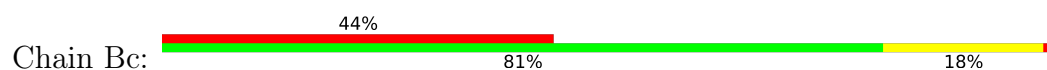
- Molecule 21: ribosomal protein uS10



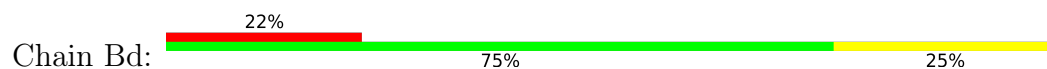
- Molecule 22: ribosomal protein uS10



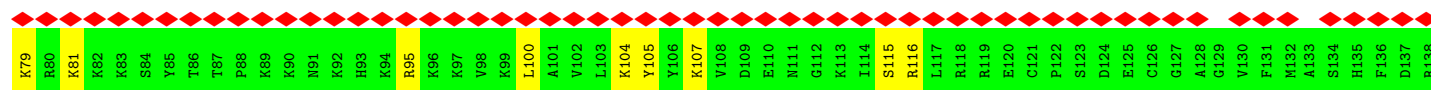
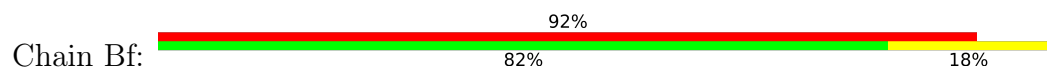
- Molecule 23: ribosomal protein eS28



- Molecule 24: ribosomal protein uS14

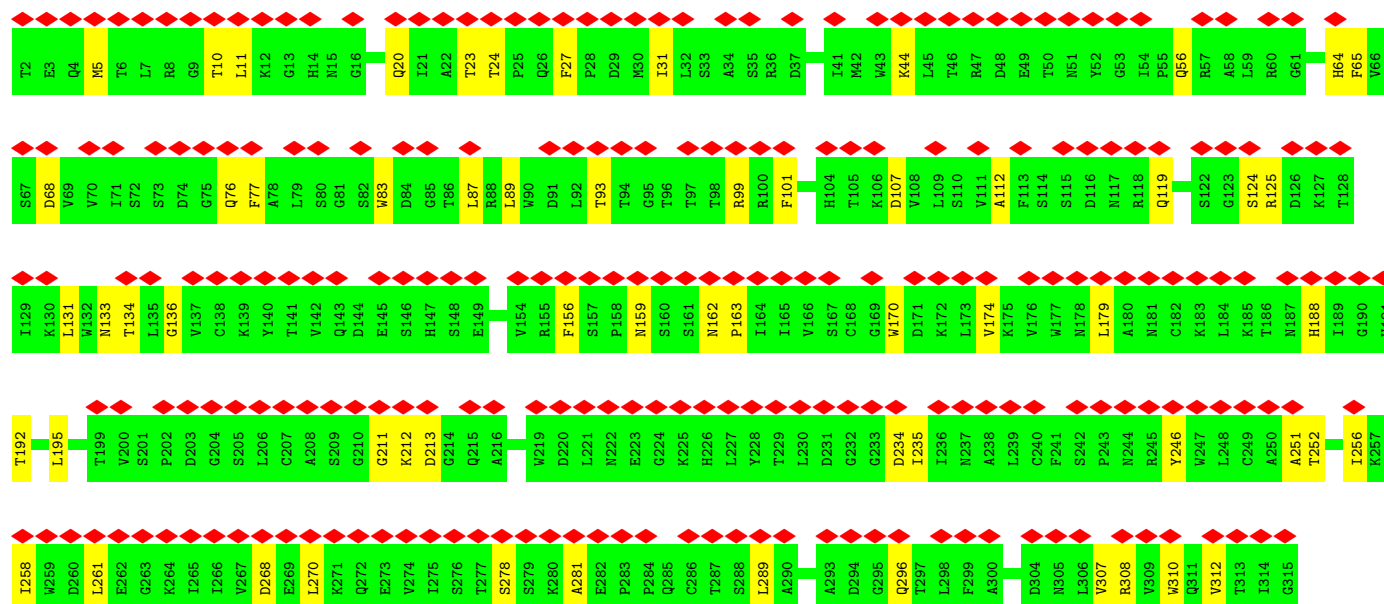
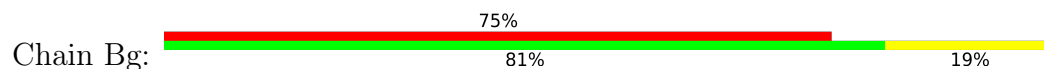


- Molecule 25: ribosomal protein eS31

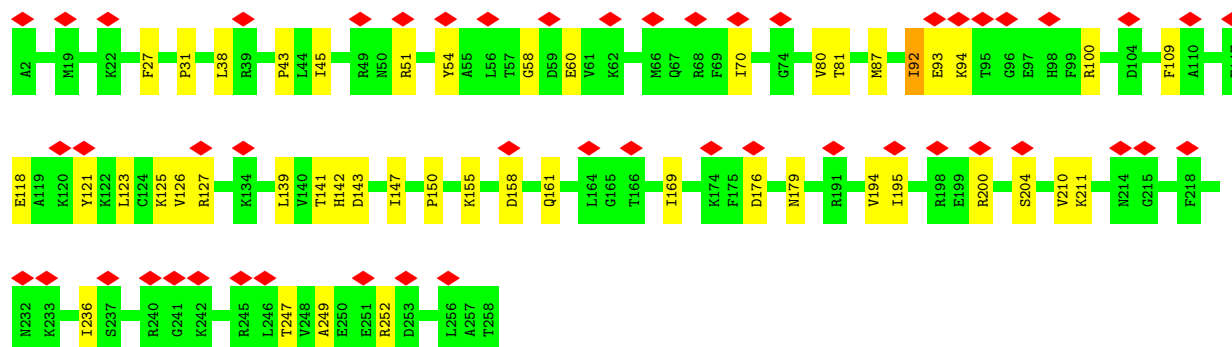
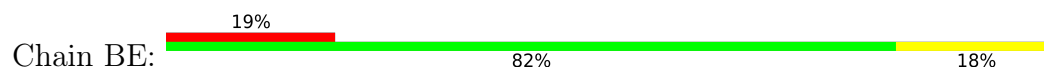




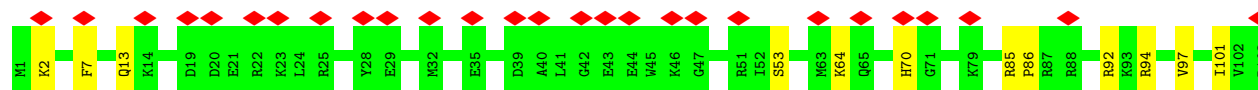
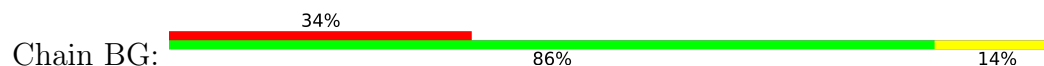
• Molecule 26: ribosomal protein RACK 1

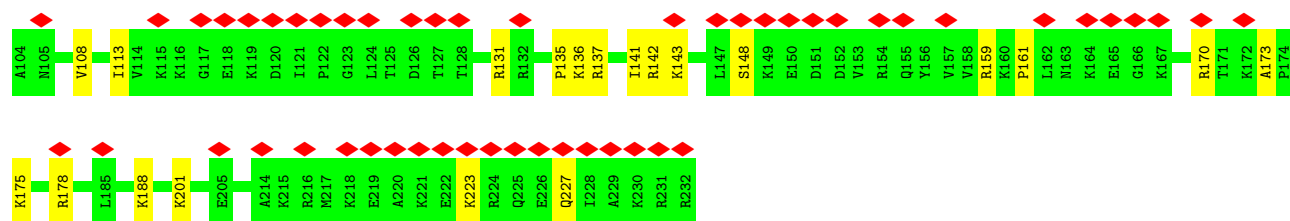


• Molecule 27: ribosomal protein eS4

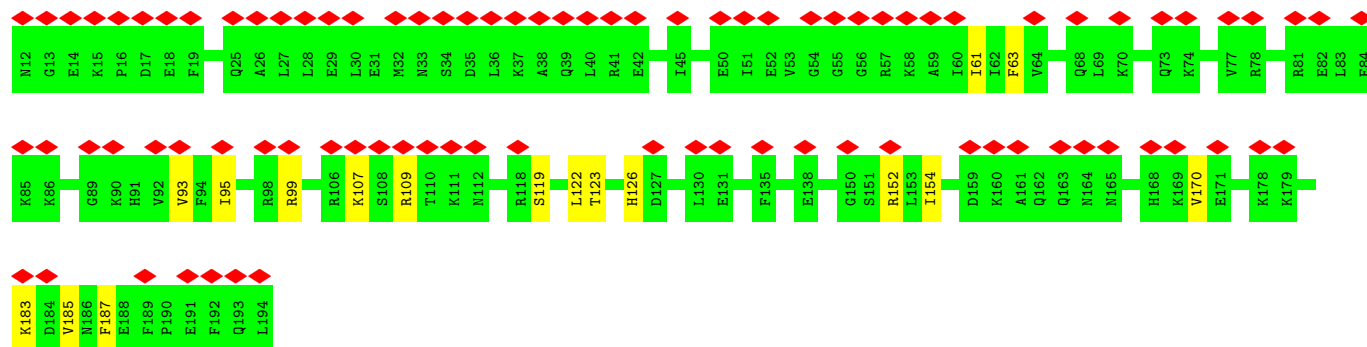
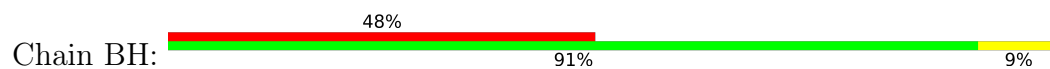


• Molecule 28: ribosomal protein eS6

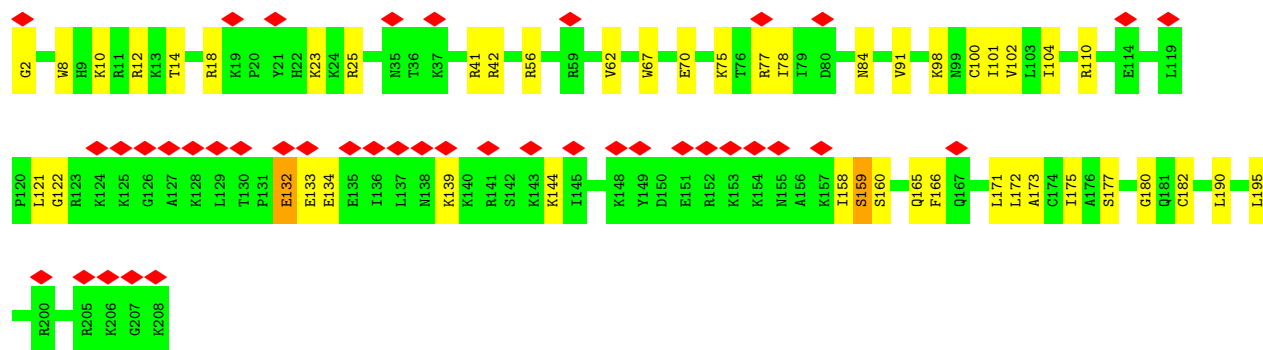
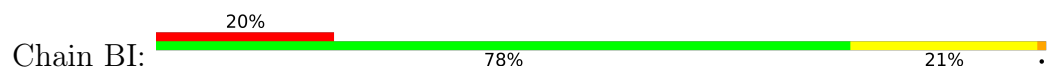




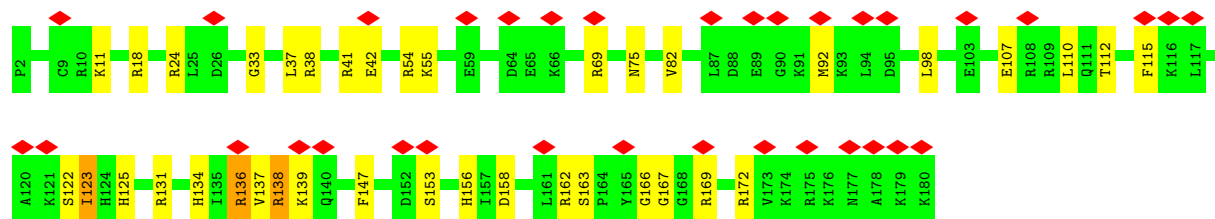
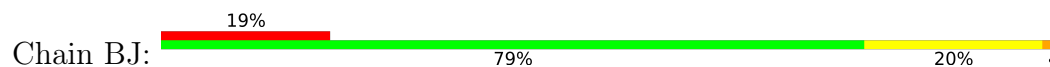
- Molecule 29: ribosomal protein eS7



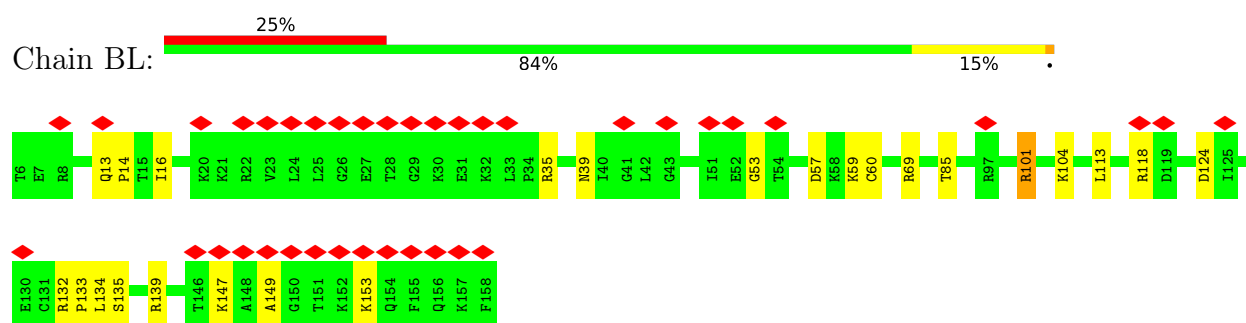
- Molecule 30: ribosomal protein eS8



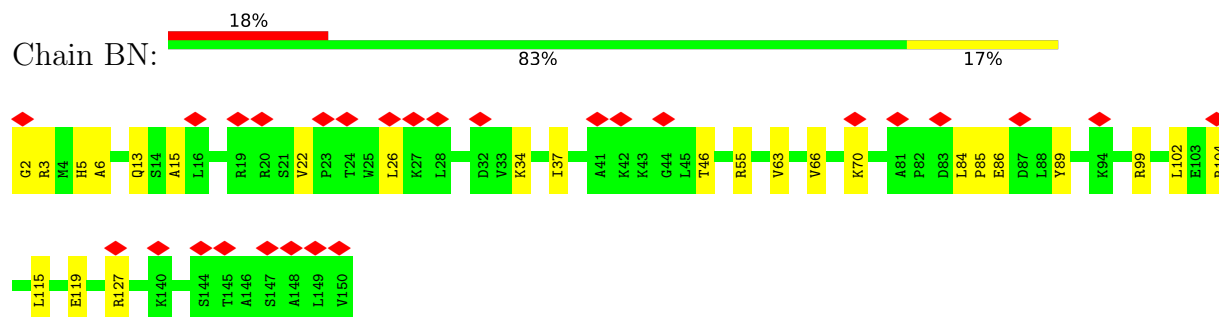
- Molecule 31: ribosomal protein uS4



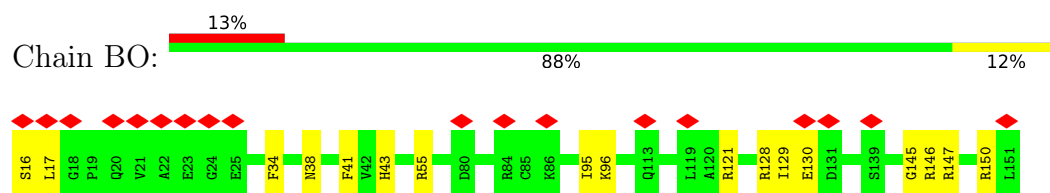
- Molecule 32: ribosomal protein uS17



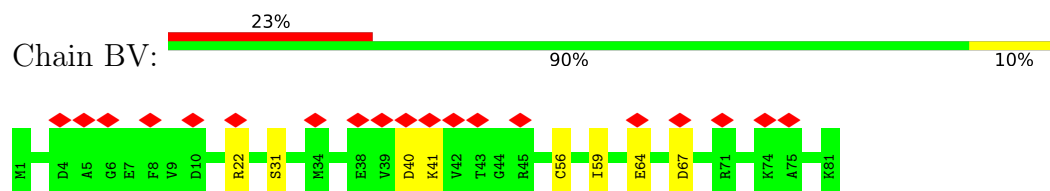
- Molecule 33: ribosomal protein uS15



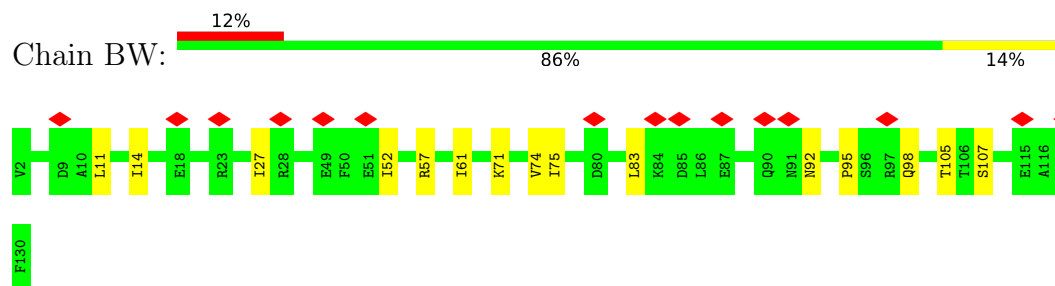
- Molecule 34: ribosomal protein uS11



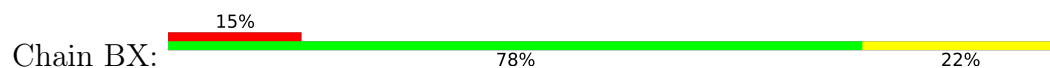
- Molecule 35: ribosomal protein eS21

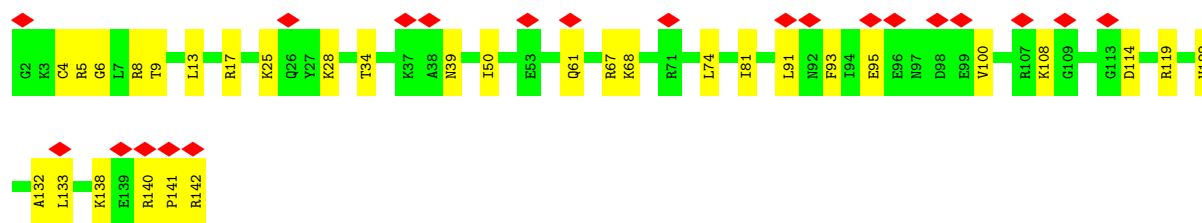


- Molecule 36: ribosomal protein uS8

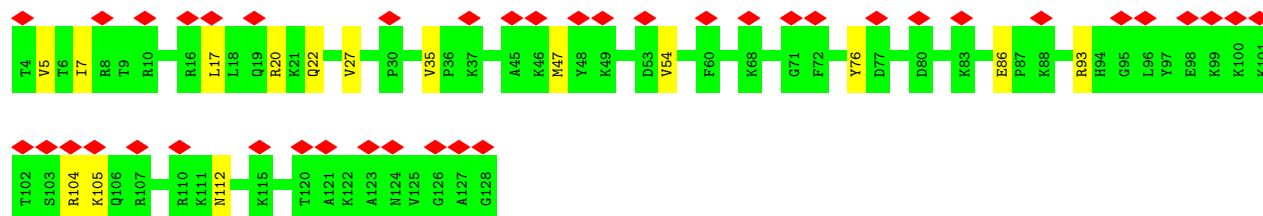
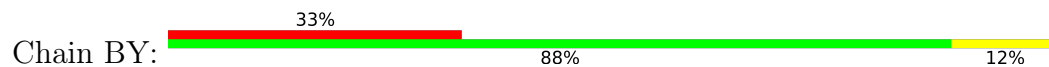


- Molecule 37: ribosomal protein uS12

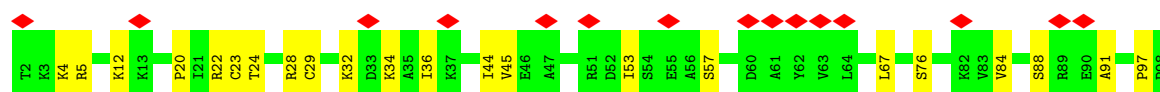
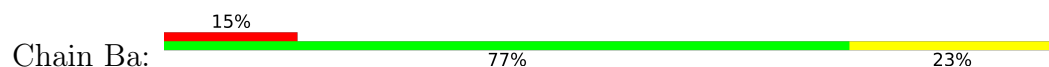




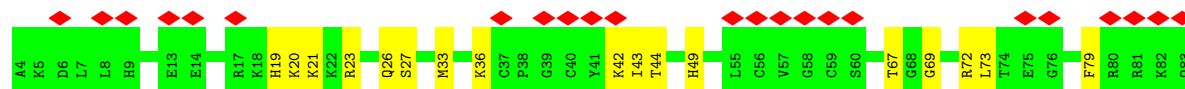
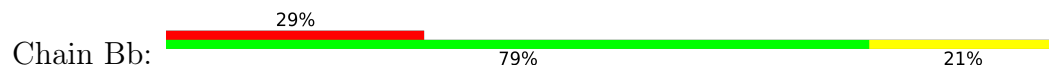
- Molecule 38: ribosomal protein eS24



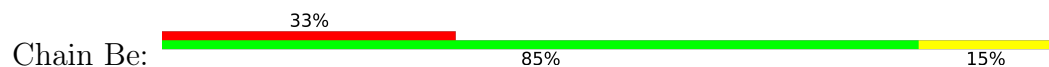
- Molecule 39: ribosomal protein eS26



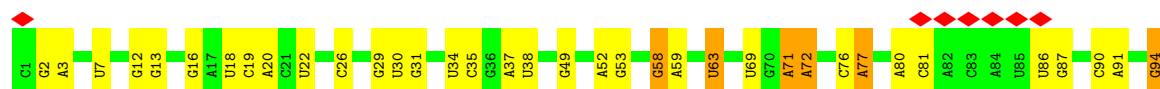
- Molecule 40: ribosomal protein eS27



- Molecule 41: ribosomal protein eS30



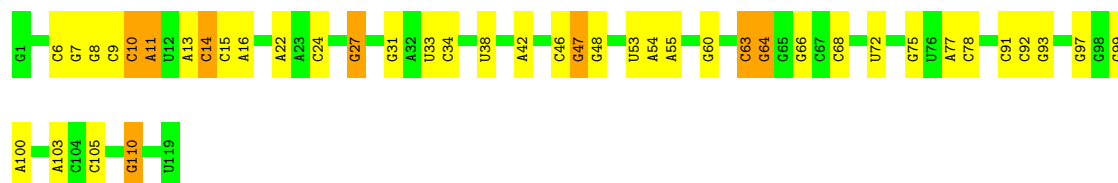
- Molecule 42: 5.8S ribosomal RNA





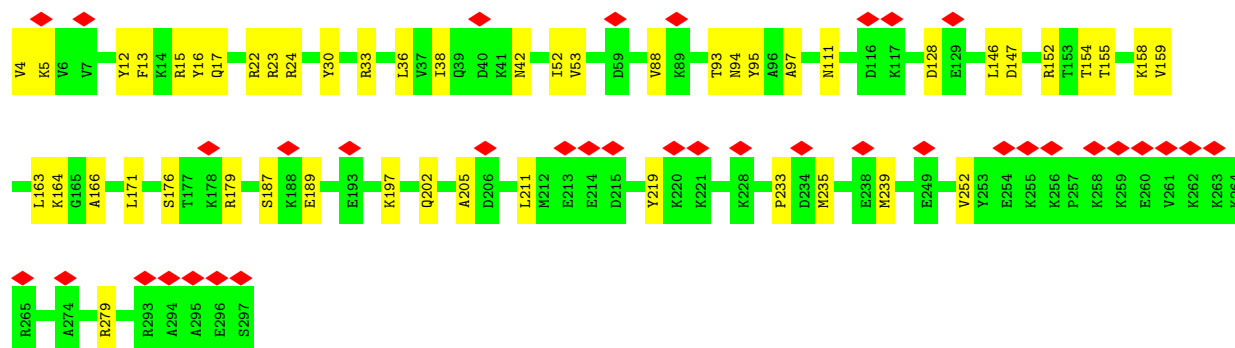
- Molecule 43: 5S ribosomal RNA

Chain A4: 65% 29% 7%



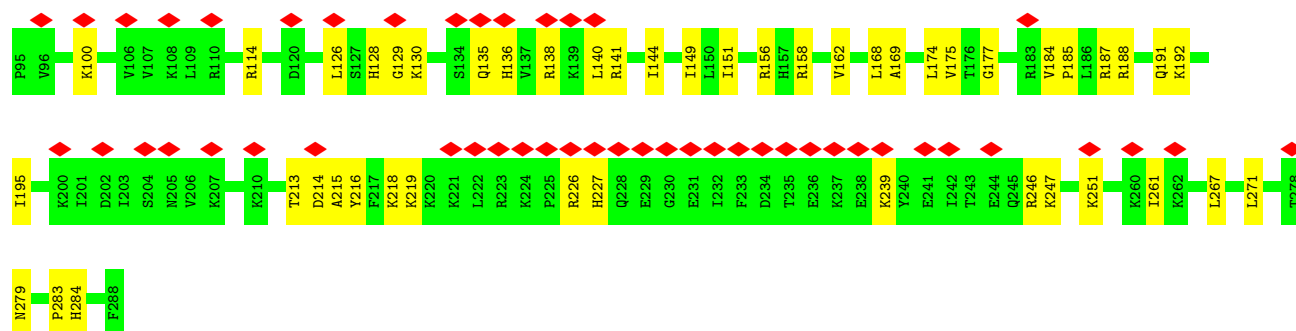
- Molecule 44: ribosomal protein uL18

Chain AD: 13% 83% 17%



- Molecule 45: ribosomal protein eL6

Chain AE: 25% 76% 24%



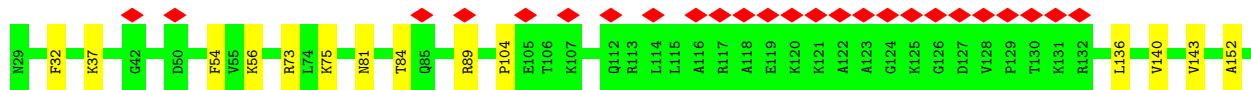
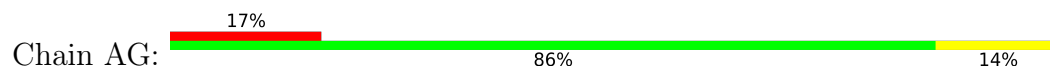
- Molecule 46: ribosomal protein uL30

Chain AF: 9% 85% 15%

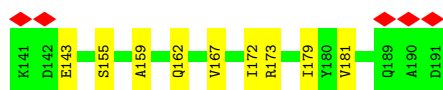
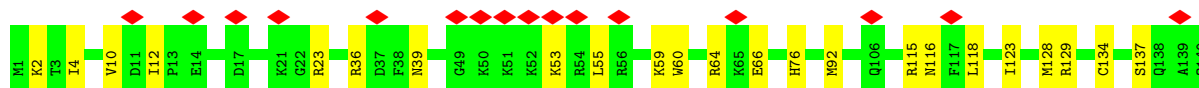
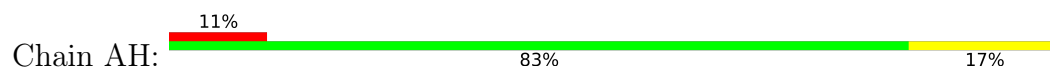




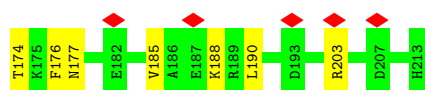
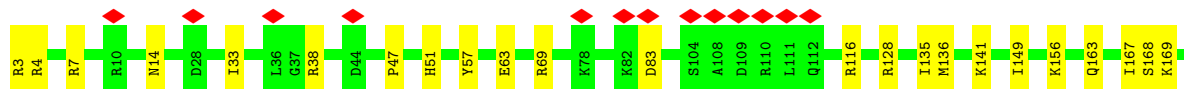
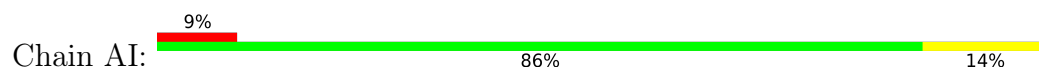
- Molecule 47: ribosomal protein eL8



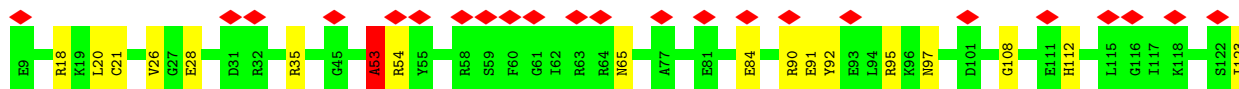
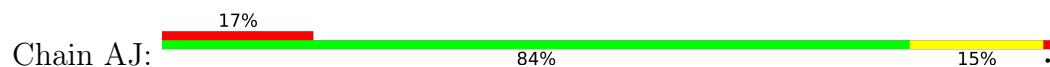
- Molecule 48: ribosomal protein uL6



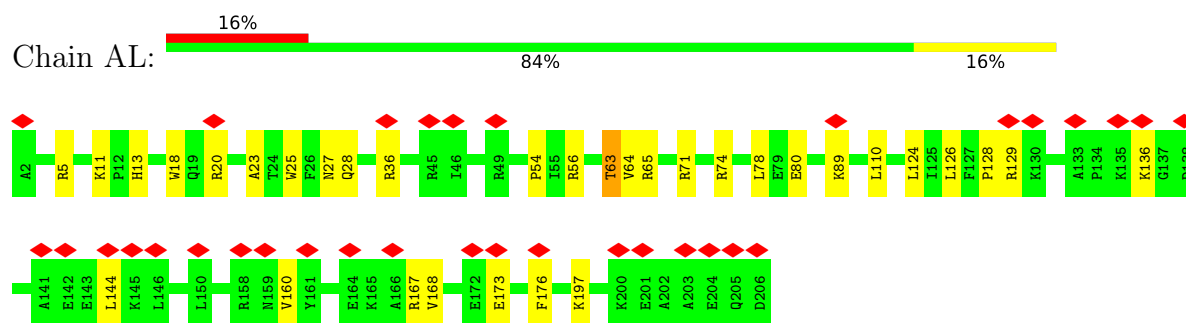
- Molecule 49: ribosomal protein uL16



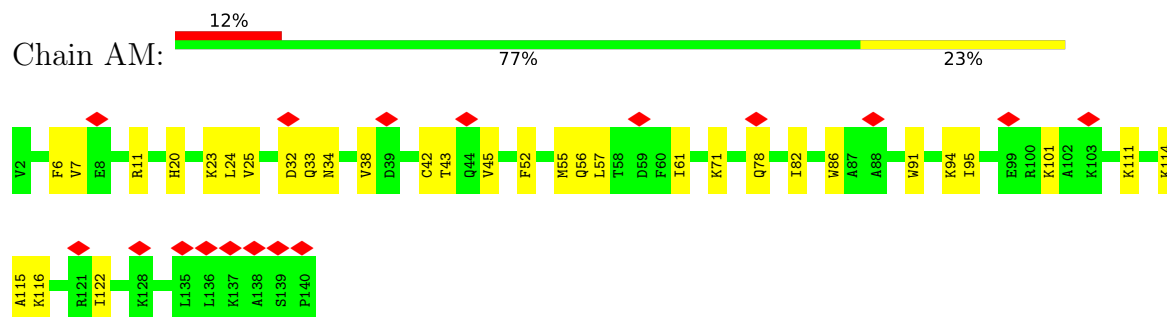
- Molecule 50: ribosomal protein uL5



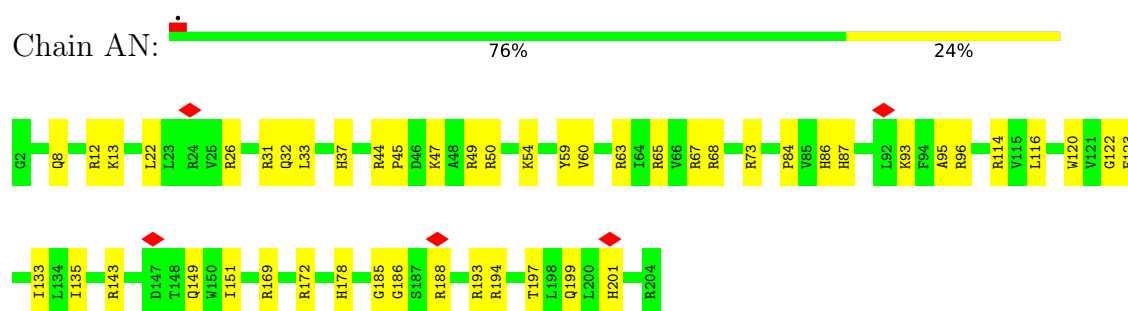
- Molecule 51: ribosomal protein eL13



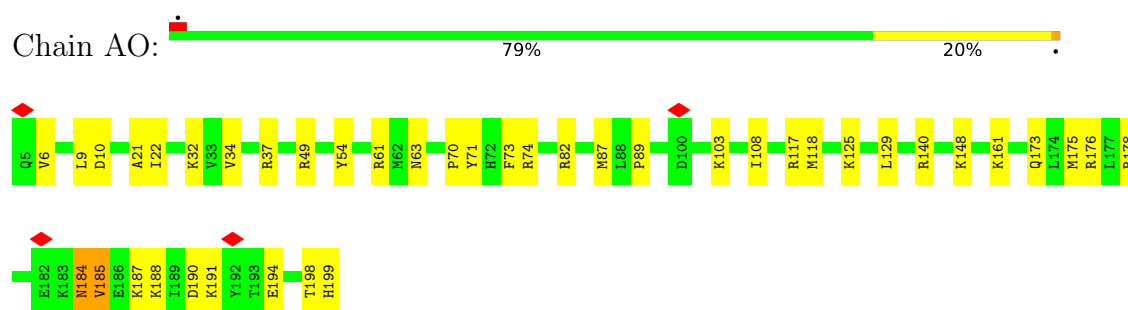
• Molecule 52: ribosomal protein eL14



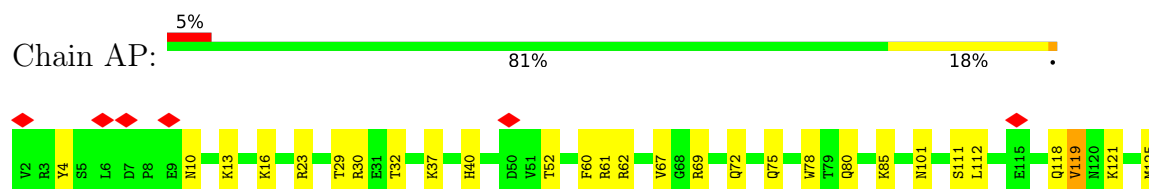
• Molecule 53: ribosomal protein eL15



• Molecule 54: ribosomal protein uL13



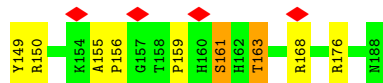
• Molecule 55: ribosomal protein uL22





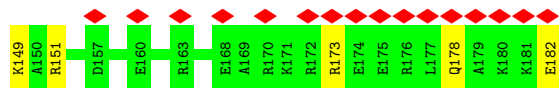
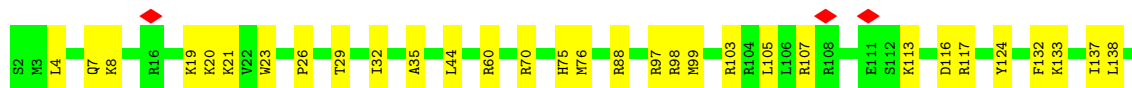
- Molecule 56: ribosomal protein eL18

Chain AQ: 9% 80% 18%



- Molecule 57: ribosomal protein eL19

Chain AR: 10% 80% 20%



- Molecule 58: ribosomal protein eL20

Chain AS: 5% 77% 23%



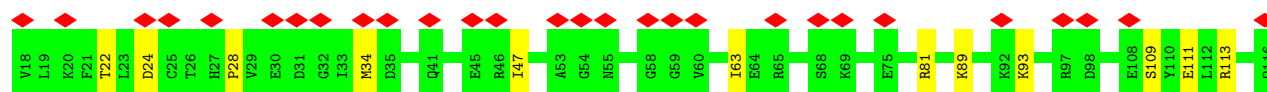
- Molecule 59: ribosomal protein eL21

Chain AT: 10% 89% 11%

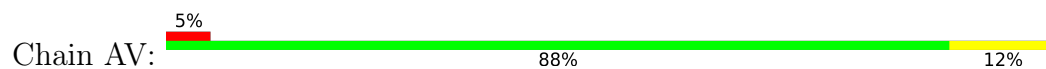


- Molecule 60: ribosomal protein eL22

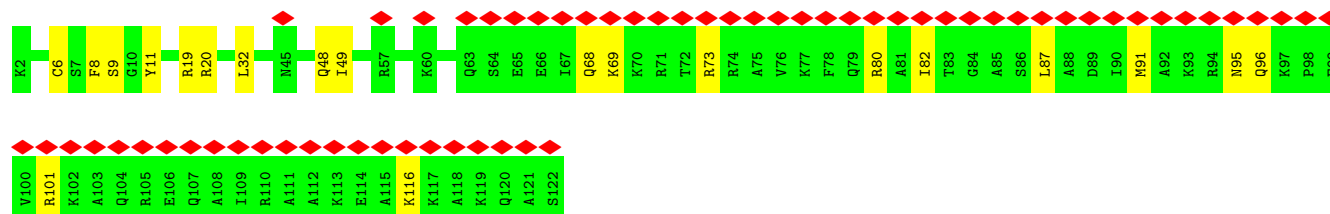
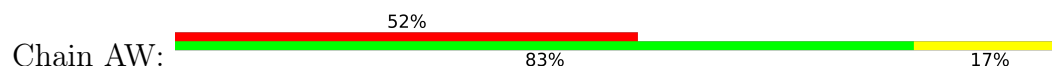
Chain AU: 28% 88% 12%



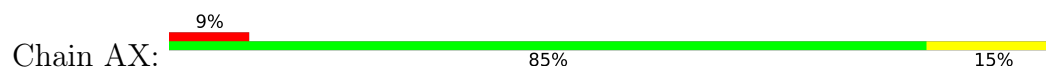
- Molecule 61: ribosomal protein uL14



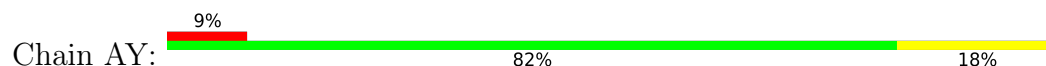
- Molecule 62: ribosomal protein eL24



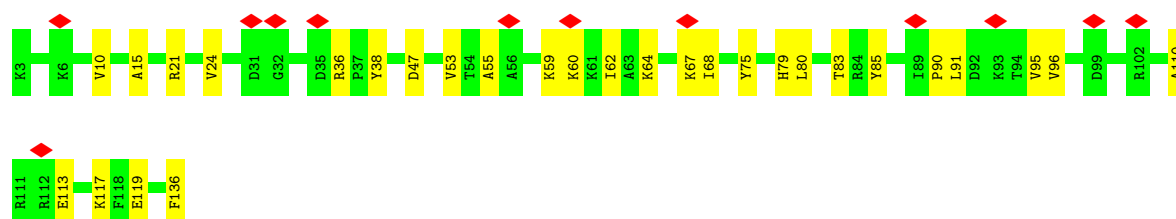
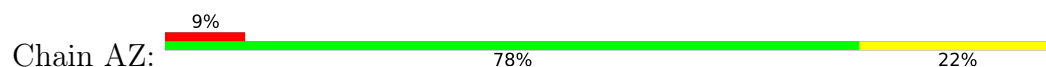
- Molecule 63: ribosomal protein uL23



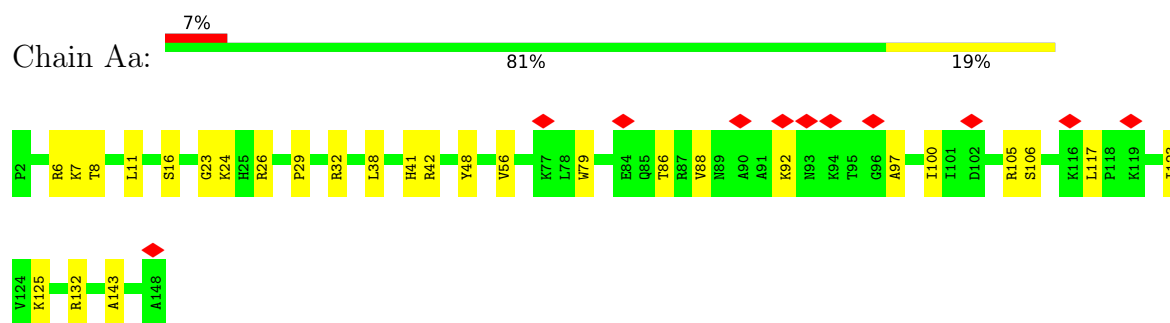
- Molecule 64: ribosomal protein uL24



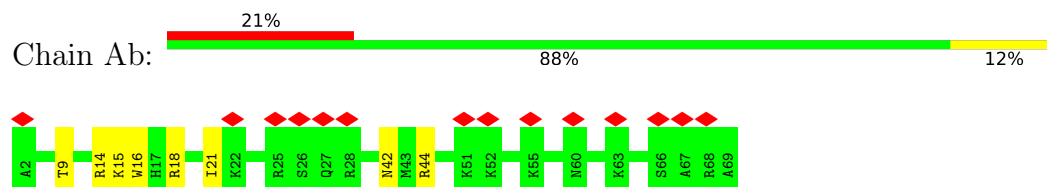
- Molecule 65: ribosomal protein eL27



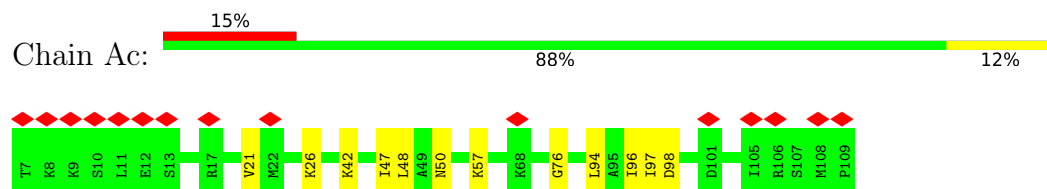
- Molecule 66: ribosomal protein uL15



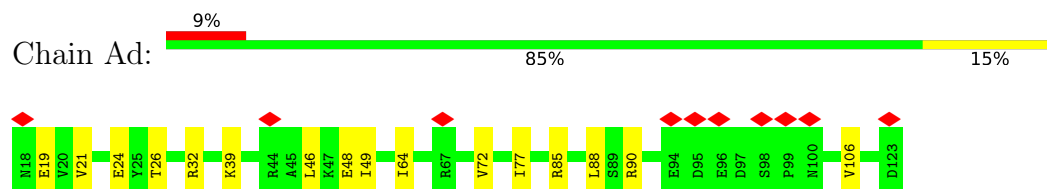
- Molecule 67: ribosomal protein eL29



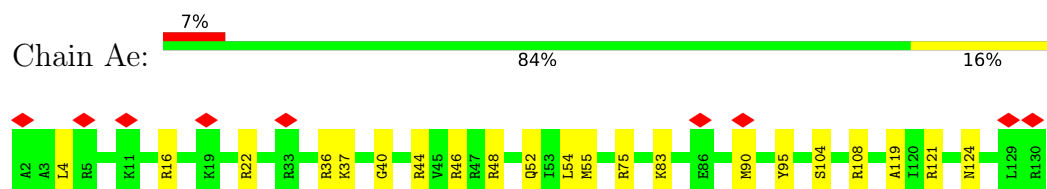
- Molecule 68: ribosomal protein eL30



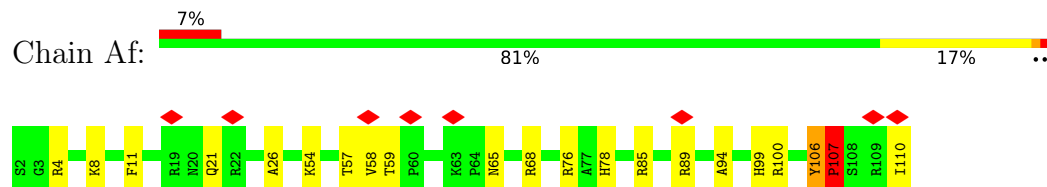
- Molecule 69: ribosomal protein eL31



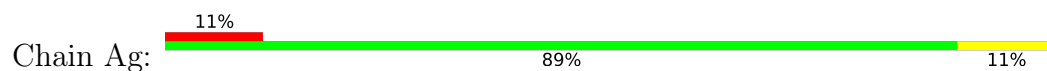
- Molecule 70: ribosomal protein eL32

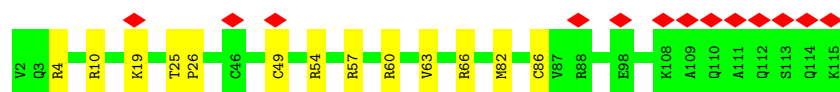


- Molecule 71: ribosomal protein eL33

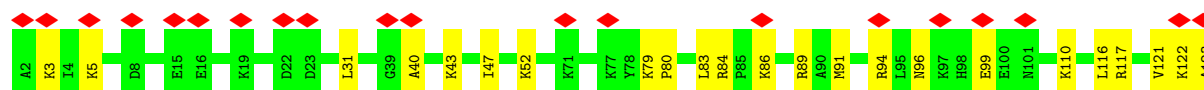
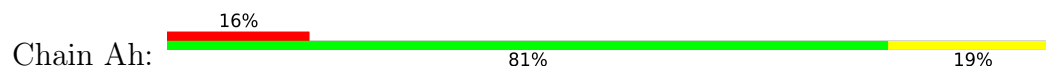


- Molecule 72: ribosomal protein eL34

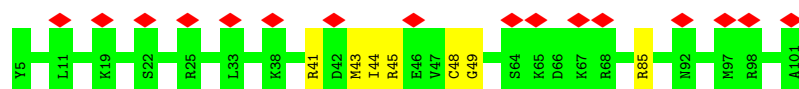




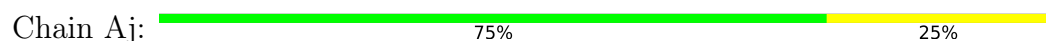
- Molecule 73: ribosomal protein uL29



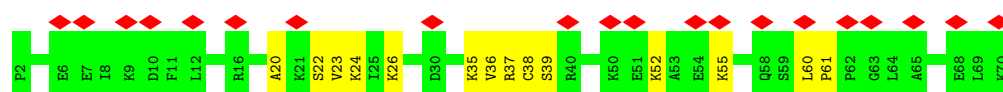
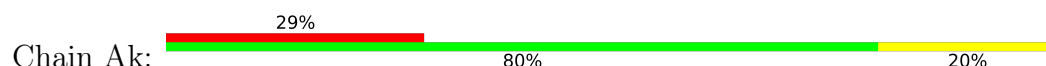
- Molecule 74: ribosomal protein eL36



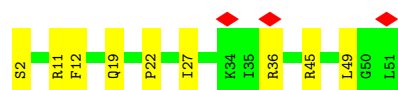
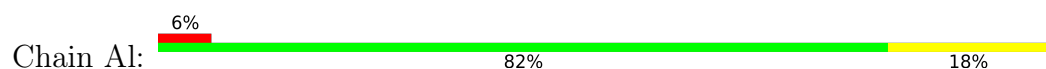
- Molecule 75: ribosomal protein eL37



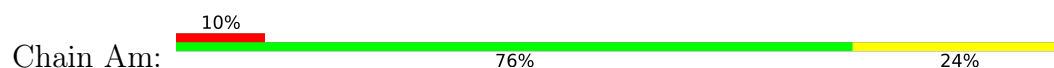
- Molecule 76: ribosomal protein eL38



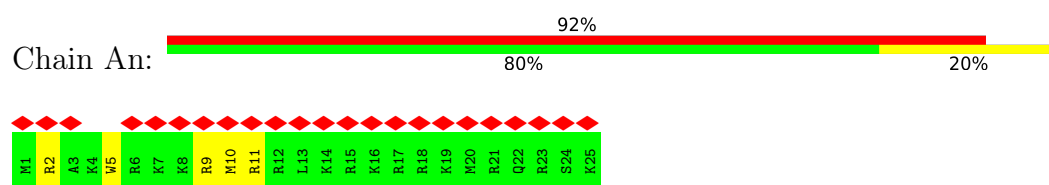
- Molecule 77: ribosomal protein eL39



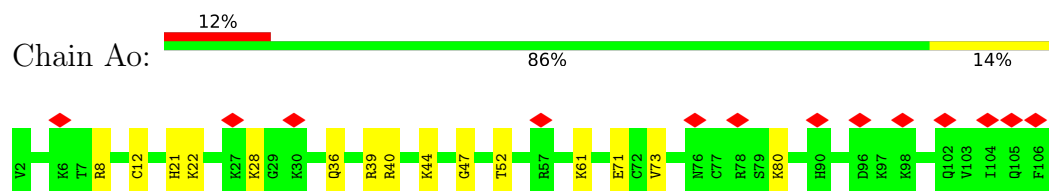
- Molecule 78: ribosomal protein eL40



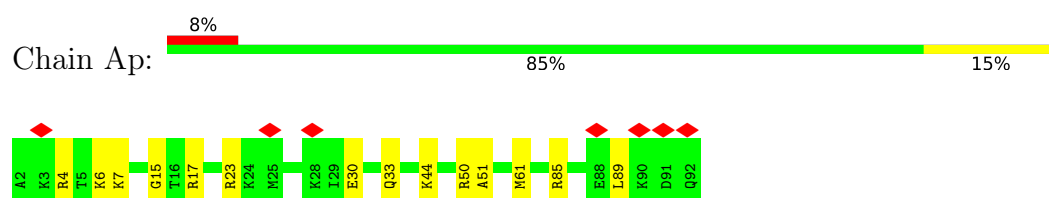
- Molecule 79: ribosomal protein eL41



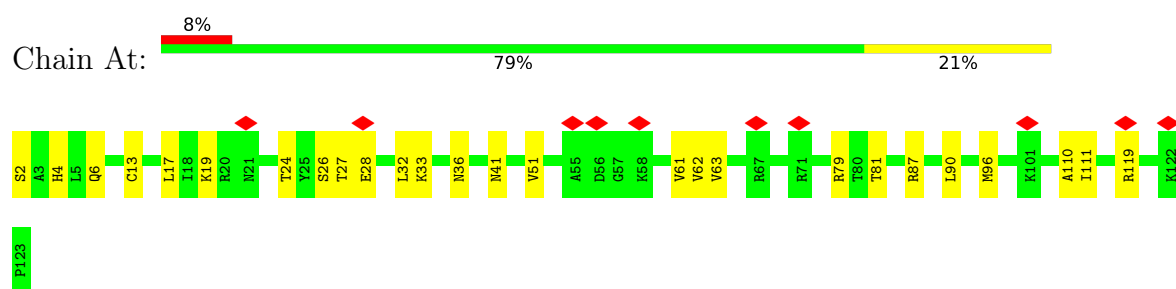
- Molecule 80: ribosomal protein eL42



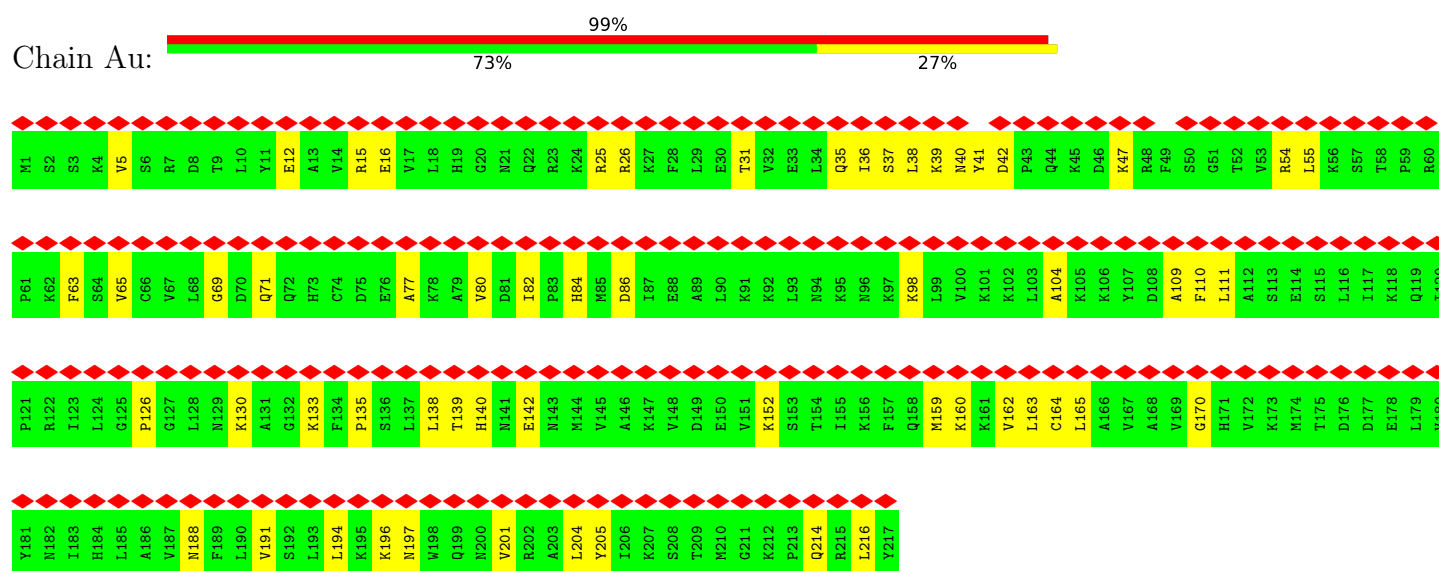
- Molecule 81: ribosomal protein eL43



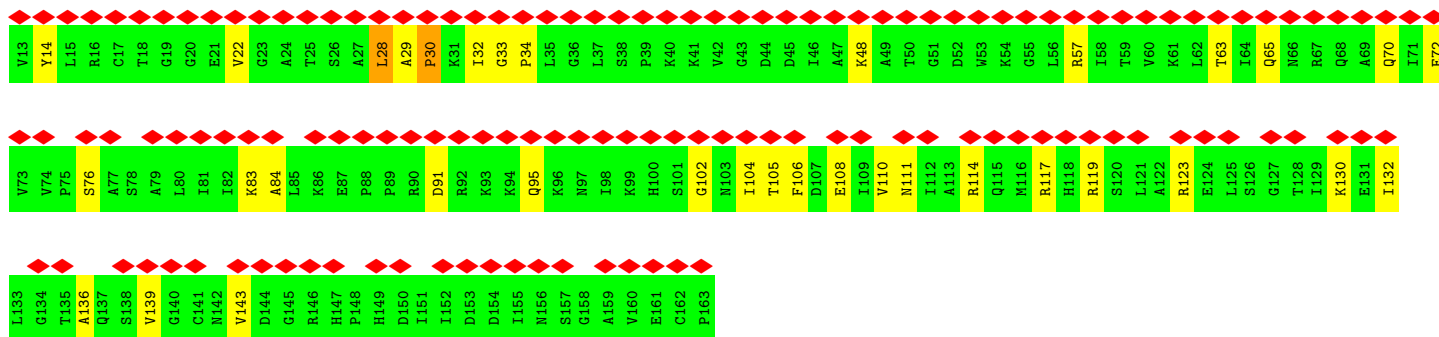
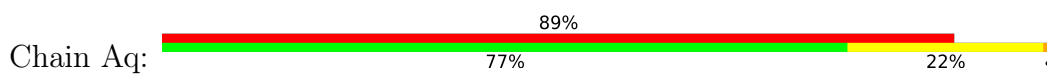
- Molecule 82: ribosomal protein eL28



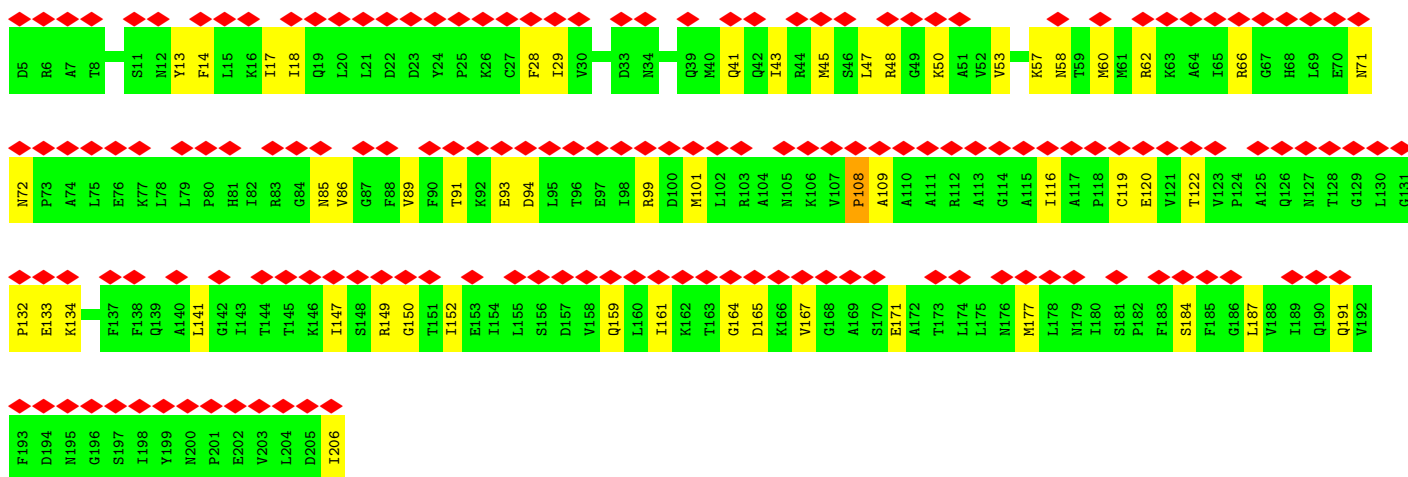
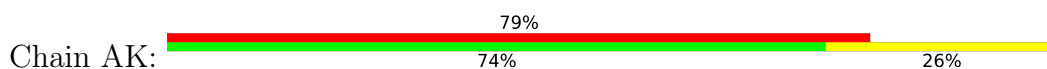
- Molecule 83: ribosomal protein uL1



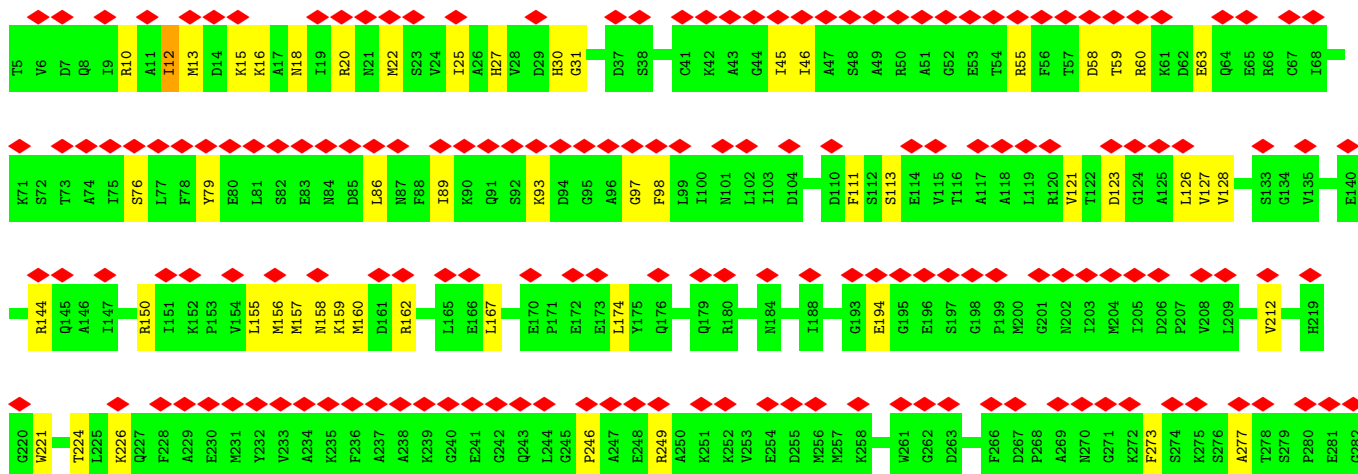
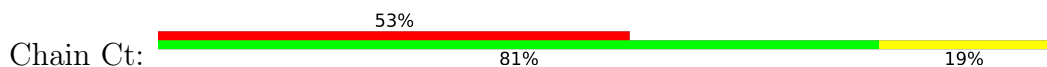
- Molecule 84: ribosomal protein uL11

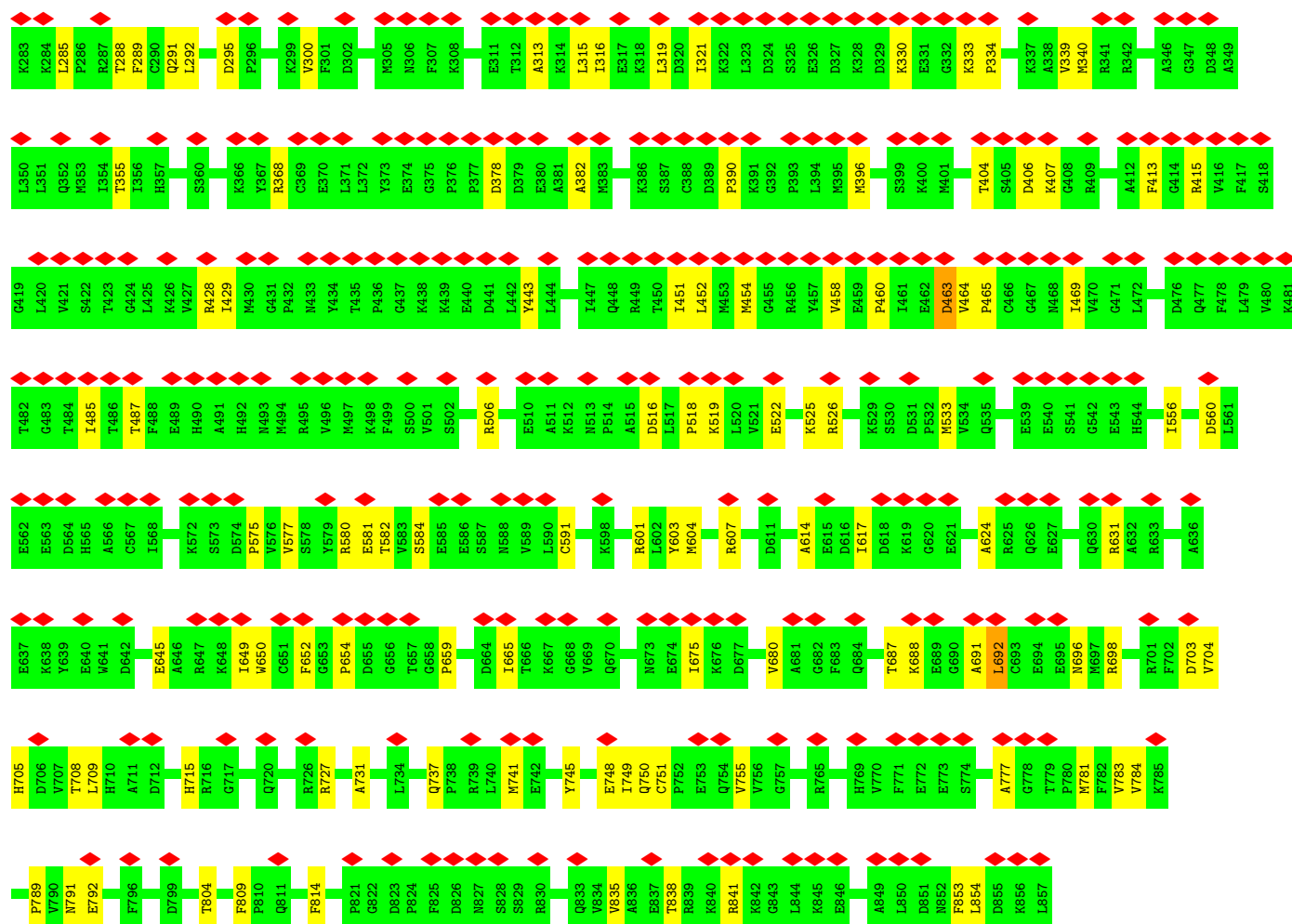


• Molecule 85: ribosomal protein uL10



• Molecule 86: eukaryotic elongation factor 2 (eEF2)





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	37941	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 ($e^-/\text{\AA}^2$)	30	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	12.587	Depositor
Minimum map value	-3.981	Depositor
Average map value	0.345	Depositor
Map value standard deviation	0.672	Depositor
Recommended contour level	2.5	Depositor
Map size ($\text{\AA}$)	394.875, 394.875, 394.875	wwPDB
Map dimensions	405, 405, 405	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.975, 0.975, 0.975	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.22	0/1968	0.51	0/2639
2	BA	0.21	0/1741	0.51	1/2366 (0.0%)
3	AB	0.21	0/3246	0.52	0/4345
4	BB	0.22	0/1749	0.62	0/2340
5	AC	0.21	0/2942	0.55	2/3951 (0.1%)
6	BC	0.21	0/1761	0.52	0/2379
7	A2	0.19	0/86612	0.34	0/135104
8	Bv	0.15	0/1810	0.29	0/2817
9	Bx	0.14	0/261	0.31	0/404
10	Bw	0.15	0/1819	0.29	0/2833
11	B1	0.17	0/40767	0.34	2/63536 (0.0%)
12	BD	0.18	0/1736	0.47	0/2338
13	BF	0.21	0/1524	0.58	0/2048
14	BK	0.22	0/851	0.57	0/1147
15	BM	0.18	0/941	0.52	0/1264
16	BP	0.24	0/1019	0.64	3/1361 (0.2%)
17	BQ	0.20	0/1126	0.55	0/1506
18	BR	0.18	0/1023	0.51	0/1373
19	BS	0.20	0/1172	0.55	0/1570
20	BT	0.20	0/1131	0.52	0/1515
21	BU	0.17	0/778	0.50	0/1045
22	BZ	0.21	0/696	0.56	0/929
23	Bc	0.19	0/490	0.58	2/656 (0.3%)
24	Bd	0.21	0/437	0.65	2/580 (0.3%)
25	Bf	0.15	0/613	0.44	0/811
26	Bg	0.16	0/2497	0.42	0/3399
27	BE	0.20	0/2072	0.55	0/2793
28	BG	0.18	0/1907	0.47	0/2538
29	BH	0.17	0/1501	0.48	0/2009
30	BI	0.22	0/1725	0.63	3/2298 (0.1%)
31	BJ	0.21	0/1520	0.57	0/2030
32	BL	0.20	0/1281	0.52	0/1710

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BN	0.20	0/1226	0.51	0/1649
34	BO	0.18	0/1029	0.49	0/1380
35	BV	0.18	0/623	0.50	0/833
36	BW	0.21	0/1051	0.54	0/1406
37	BX	0.21	0/1116	0.53	0/1490
38	BY	0.18	0/1032	0.52	0/1371
39	Ba	0.21	0/786	0.52	0/1053
40	Bb	0.17	0/637	0.46	0/854
41	Be	0.20	0/443	0.60	0/583
42	A3	0.18	0/3726	0.33	0/5804
43	A4	0.19	0/2839	0.35	0/4425
44	AD	0.21	0/2437	0.54	0/3262
45	AE	0.22	0/1603	0.61	0/2153
46	AF	0.21	0/1986	0.54	0/2644
47	AG	0.24	0/1913	0.57	0/2576
48	AH	0.21	0/1545	0.61	0/2077
49	AI	0.18	0/1730	0.50	0/2311
50	AJ	0.19	0/1376	0.57	2/1841 (0.1%)
51	AL	0.23	0/1688	0.61	0/2260
52	AM	0.23	0/1161	0.51	0/1554
53	AN	0.21	0/1746	0.56	1/2338 (0.0%)
54	AO	0.23	0/1638	0.51	0/2191
55	AP	0.20	0/1268	0.48	0/1701
56	AQ	0.21	0/1537	0.62	2/2052 (0.1%)
57	AR	0.20	0/1533	0.53	0/2025
58	AS	0.20	0/1488	0.49	0/1997
59	AT	0.18	0/1312	0.43	0/1753
60	AU	0.17	0/822	0.44	0/1103
61	AV	0.17	0/983	0.44	0/1319
62	AW	0.18	0/1004	0.50	0/1332
63	AX	0.17	0/975	0.46	0/1312
64	AY	0.18	0/1081	0.45	0/1439
65	AZ	0.19	0/1126	0.53	0/1502
66	Aa	0.21	0/1191	0.50	0/1591
67	Ab	0.23	0/569	0.67	0/750
68	Ac	0.19	0/812	0.48	0/1089
69	Ad	0.19	0/894	0.50	0/1204
70	Ae	0.21	0/1082	0.59	0/1443
71	Af	0.22	0/895	0.58	1/1198 (0.1%)
72	Ag	0.21	0/916	0.58	0/1220
73	Ah	0.20	0/1023	0.54	0/1351
74	Ai	0.18	0/805	0.51	0/1065
75	Aj	0.23	0/703	0.58	0/929

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Ak	0.18	0/575	0.47	0/761
77	Al	0.20	0/454	0.53	0/599
78	Am	0.19	0/417	0.51	0/553
79	An	0.18	0/241	0.56	0/305
80	Ao	0.22	0/877	0.54	0/1156
81	Ap	0.22	0/718	0.58	0/953
82	At	0.27	0/995	0.71	2/1334 (0.1%)
83	Au	0.21	0/1772	0.48	0/2375
84	Aq	0.26	0/1155	0.76	0/1558
85	AK	0.21	0/1580	0.65	4/2133 (0.2%)
86	Ct	0.21	0/6767	0.57	5/9139 (0.1%)
All	All	0.19	0/241617	0.43	32/353930 (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
2	BA	0	1
5	AC	0	3
17	BQ	0	1
22	BZ	0	1
23	Bc	0	1
27	BE	0	1
30	BI	0	1
31	BJ	0	2
45	AE	0	3
48	AH	0	3
49	AI	0	1
50	AJ	0	1
56	AQ	0	2
57	AR	0	1
71	Af	0	1
73	Ah	0	1
82	At	0	1
84	Aq	0	2
85	AK	0	2
86	Ct	0	3
All	All	0	32

There are no bond length outliers.

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	AJ	53	ALA	CA-C-N	6.98	134.87	121.54
50	AJ	53	ALA	C-N-CA	6.98	134.87	121.54
85	AK	94	ASP	CA-C-N	6.89	134.11	121.70
85	AK	94	ASP	C-N-CA	6.89	134.11	121.70
30	BI	132	GLU	CA-C-N	6.43	131.81	122.36

There are no chirality outliers.

5 of 32 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	AC	150	LEU	Peptide
5	AC	51	PRO	Peptide
5	AC	71	ARG	Peptide
2	BA	207	PRO	Peptide
17	BQ	13	PHE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	1930	0	2030	50	0
2	BA	1704	0	1704	22	0
3	AB	3178	0	3314	65	0
4	BB	1722	0	1794	28	0
5	AC	2888	0	3064	54	0
6	BC	1724	0	1808	20	0
7	A2	77427	0	39115	741	0
8	Bv	1620	0	821	4	0
9	Bx	234	0	118	1	0
10	Bw	1627	0	821	8	0
11	B1	36456	0	18411	362	0
12	BD	1709	0	1803	23	0
13	BF	1502	0	1557	30	0
14	BK	827	0	854	17	0
15	BM	931	0	961	16	0
16	BP	999	0	1046	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	BQ	1109	0	1174	22	0
18	BR	1011	0	1063	15	0
19	BS	1154	0	1210	15	0
20	BT	1112	0	1146	15	0
21	BU	769	0	837	7	0
22	BZ	688	0	766	17	0
23	Bc	488	0	514	6	0
24	Bd	427	0	428	13	0
25	Bf	601	0	623	8	0
26	Bg	2440	0	2396	32	0
27	BE	2031	0	2138	30	0
28	BG	1884	0	2044	25	0
29	BH	1479	0	1564	12	0
30	BI	1696	0	1785	30	0
31	BJ	1495	0	1615	26	0
32	BL	1258	0	1334	18	0
33	BN	1202	0	1289	16	0
34	BO	1016	0	1039	12	0
35	BV	617	0	622	6	0
36	BW	1034	0	1080	14	0
37	BX	1098	0	1167	24	0
38	BY	1015	0	1086	12	0
39	Ba	774	0	821	18	0
40	Bb	625	0	646	12	0
41	Be	437	0	483	6	0
42	A3	3337	0	1692	36	0
43	A4	2541	0	1285	25	0
44	AD	2392	0	2425	35	0
45	AE	1571	0	1701	33	0
46	AF	1950	0	2093	29	0
47	AG	1880	0	2018	22	0
48	AH	1526	0	1605	21	0
49	AI	1692	0	1744	18	0
50	AJ	1353	0	1386	18	0
51	AL	1657	0	1764	29	0
52	AM	1138	0	1204	27	0
53	AN	1701	0	1749	42	0
54	AO	1606	0	1745	30	0
55	AP	1242	0	1269	19	0
56	AQ	1513	0	1628	27	0
57	AR	1517	0	1670	25	0
58	AS	1449	0	1493	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	AT	1284	0	1352	16	0
60	AU	808	0	831	7	0
61	AV	969	0	1031	10	0
62	AW	989	0	1041	17	0
63	AX	958	0	1029	10	0
64	AY	1064	0	1145	21	0
65	AZ	1103	0	1179	18	0
66	Aa	1162	0	1213	22	0
67	Ab	559	0	590	6	0
68	Ac	801	0	845	6	0
69	Ad	879	0	924	12	0
70	Ae	1064	0	1160	15	0
71	Af	876	0	912	17	0
72	Ag	906	0	1002	12	0
73	Ah	1015	0	1148	17	0
74	Ai	794	0	870	6	0
75	Aj	689	0	717	19	0
76	Ak	569	0	637	11	0
77	Al	444	0	483	8	0
78	Am	411	0	443	10	0
79	An	240	0	289	4	0
80	Ao	863	0	931	13	0
81	Ap	708	0	758	10	0
82	At	980	0	1041	20	0
83	Au	1744	0	1859	32	0
84	Aq	1140	0	1191	22	0
85	AK	1556	0	1612	29	0
86	Ct	6659	0	6746	101	0
87	A2	236	0	0	0	0
87	A3	4	0	0	0	0
87	A4	8	0	0	0	0
87	AA	1	0	0	0	0
87	AL	1	0	0	0	0
87	AY	1	0	0	0	0
87	An	1	0	0	0	0
87	B1	67	0	0	0	0
87	BD	2	0	0	0	0
87	BS	2	0	0	0	0
87	Ba	1	0	0	0	0
87	Bd	2	0	0	0	0
87	Bx	1	0	0	0	0
88	Aj	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
88	Ao	1	0	0	0	0
88	Ap	1	0	0	0	0
88	Ba	1	0	0	0	0
88	Bd	1	0	0	0	0
89	Ct	32	0	13	2	0
All	All	225601	0	169554	2221	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 6.

The worst 5 of 2221 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)
11:B1:1656:G:H1	11:B1:1668:U:H3	1.06	1.02
7:A2:1871:G:H1	7:A2:1920:A:N6	1.57	1.01
11:B1:442:C:H42	11:B1:449:A:H62	1.05	1.00
7:A2:499:G:H1	7:A2:647:U:H3	1.03	0.97
7:A2:708:U:H3	7:A2:938:G:H1	1.02	0.96

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	250/252 (99%)	230 (92%)	20 (8%)	0	100	100
2	BA	213/215 (99%)	197 (92%)	16 (8%)	0	100	100
3	AB	392/394 (100%)	354 (90%)	38 (10%)	0	100	100
4	BB	210/212 (99%)	181 (86%)	29 (14%)	0	100	100
5	AC	361/363 (99%)	325 (90%)	33 (9%)	3 (1%)	16	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	BC	220/222 (99%)	207 (94%)	13 (6%)	0	100	100
12	BD	218/220 (99%)	205 (94%)	13 (6%)	0	100	100
13	BF	188/190 (99%)	172 (92%)	16 (8%)	0	100	100
14	BK	96/98 (98%)	80 (83%)	15 (16%)	1 (1%)	12	45
15	BM	118/120 (98%)	110 (93%)	8 (7%)	0	100	100
16	BP	118/120 (98%)	102 (86%)	15 (13%)	1 (1%)	16	49
17	BQ	137/139 (99%)	128 (93%)	9 (7%)	0	100	100
18	BR	123/125 (98%)	111 (90%)	12 (10%)	0	100	100
19	BS	137/139 (99%)	122 (89%)	15 (11%)	0	100	100
20	BT	141/143 (99%)	127 (90%)	13 (9%)	1 (1%)	18	51
21	BU	95/97 (98%)	91 (96%)	4 (4%)	0	100	100
22	BZ	84/86 (98%)	73 (87%)	11 (13%)	0	100	100
23	Bc	60/62 (97%)	53 (88%)	5 (8%)	2 (3%)	3	24
24	Bd	49/51 (96%)	45 (92%)	4 (8%)	0	100	100
25	Bf	71/73 (97%)	63 (89%)	8 (11%)	0	100	100
26	Bg	312/314 (99%)	283 (91%)	29 (9%)	0	100	100
27	BE	255/257 (99%)	237 (93%)	16 (6%)	2 (1%)	16	49
28	BG	230/232 (99%)	215 (94%)	15 (6%)	0	100	100
29	BH	181/183 (99%)	166 (92%)	15 (8%)	0	100	100
30	BI	205/207 (99%)	176 (86%)	27 (13%)	2 (1%)	12	45
31	BJ	177/179 (99%)	154 (87%)	21 (12%)	2 (1%)	11	43
32	BL	151/153 (99%)	136 (90%)	14 (9%)	1 (1%)	18	51
33	BN	147/149 (99%)	133 (90%)	14 (10%)	0	100	100
34	BO	134/136 (98%)	122 (91%)	12 (9%)	0	100	100
35	BV	79/81 (98%)	75 (95%)	4 (5%)	0	100	100
36	BW	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
37	BX	139/141 (99%)	124 (89%)	15 (11%)	0	100	100
38	BY	123/125 (98%)	109 (89%)	14 (11%)	0	100	100
39	Ba	95/97 (98%)	89 (94%)	6 (6%)	0	100	100
40	Bb	78/80 (98%)	71 (91%)	7 (9%)	0	100	100
41	Be	53/55 (96%)	49 (92%)	4 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	AD	292/294 (99%)	270 (92%)	22 (8%)	0	100	100
45	AE	192/194 (99%)	159 (83%)	32 (17%)	1 (0%)	24	57
46	AF	232/234 (99%)	215 (93%)	17 (7%)	0	100	100
47	AG	232/234 (99%)	217 (94%)	15 (6%)	0	100	100
48	AH	189/191 (99%)	175 (93%)	14 (7%)	0	100	100
49	AI	204/208 (98%)	187 (92%)	17 (8%)	0	100	100
50	AJ	167/169 (99%)	149 (89%)	16 (10%)	2 (1%)	10	41
51	AL	203/205 (99%)	170 (84%)	32 (16%)	1 (0%)	24	57
52	AM	137/139 (99%)	127 (93%)	10 (7%)	0	100	100
53	AN	201/203 (99%)	184 (92%)	16 (8%)	1 (0%)	24	57
54	AO	193/195 (99%)	185 (96%)	8 (4%)	0	100	100
55	AP	151/153 (99%)	146 (97%)	5 (3%)	0	100	100
56	AQ	185/187 (99%)	160 (86%)	23 (12%)	2 (1%)	11	43
57	AR	179/181 (99%)	167 (93%)	12 (7%)	0	100	100
58	AS	173/175 (99%)	162 (94%)	11 (6%)	0	100	100
59	AT	155/157 (99%)	139 (90%)	14 (9%)	2 (1%)	9	39
60	AU	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
61	AV	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
62	AW	119/121 (98%)	105 (88%)	14 (12%)	0	100	100
63	AX	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
64	AY	125/127 (98%)	120 (96%)	5 (4%)	0	100	100
65	AZ	132/134 (98%)	117 (89%)	15 (11%)	0	100	100
66	Aa	145/147 (99%)	128 (88%)	17 (12%)	0	100	100
67	Ab	66/68 (97%)	55 (83%)	11 (17%)	0	100	100
68	Ac	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
69	Ad	104/106 (98%)	99 (95%)	5 (5%)	0	100	100
70	Ae	127/129 (98%)	115 (91%)	12 (9%)	0	100	100
71	Af	107/109 (98%)	93 (87%)	12 (11%)	2 (2%)	6	33
72	Ag	112/114 (98%)	101 (90%)	11 (10%)	0	100	100
73	Ah	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
74	Ai	95/97 (98%)	87 (92%)	8 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
75	Aj	82/84 (98%)	75 (92%)	7 (8%)	0	100	100
76	Ak	67/69 (97%)	63 (94%)	4 (6%)	0	100	100
77	Al	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
78	Am	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
79	An	23/25 (92%)	23 (100%)	0	0	100	100
80	Ao	103/105 (98%)	95 (92%)	8 (8%)	0	100	100
81	Ap	89/91 (98%)	81 (91%)	8 (9%)	0	100	100
82	At	120/122 (98%)	106 (88%)	14 (12%)	0	100	100
83	Au	215/217 (99%)	194 (90%)	21 (10%)	0	100	100
84	Aq	149/151 (99%)	119 (80%)	30 (20%)	0	100	100
85	AK	200/202 (99%)	178 (89%)	21 (10%)	1 (0%)	24	57
86	Ct	850/853 (100%)	762 (90%)	87 (10%)	1 (0%)	48	79
All	All	12538/12699 (99%)	11394 (91%)	1116 (9%)	28 (0%)	44	72

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	BE	93	GLU
31	BJ	138	ARG
71	Af	107	PRO
5	AC	51	PRO
16	BP	51	ARG

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	AA	194/194 (100%)	192 (99%)	2 (1%)	68	75
2	BA	180/180 (100%)	180 (100%)	0	100	100
3	AB	343/343 (100%)	343 (100%)	0	100	100
4	BB	193/193 (100%)	192 (100%)	1 (0%)	81	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	AC	302/302 (100%)	301 (100%)	1 (0%)	86	83
6	BC	188/188 (100%)	187 (100%)	1 (0%)	81	80
12	BD	183/183 (100%)	183 (100%)	0	100	100
13	BF	160/160 (100%)	160 (100%)	0	100	100
14	BK	89/89 (100%)	89 (100%)	0	100	100
15	BM	102/102 (100%)	102 (100%)	0	100	100
16	BP	109/109 (100%)	108 (99%)	1 (1%)	70	76
17	BQ	115/115 (100%)	115 (100%)	0	100	100
18	BR	113/113 (100%)	113 (100%)	0	100	100
19	BS	121/121 (100%)	120 (99%)	1 (1%)	73	77
20	BT	113/113 (100%)	112 (99%)	1 (1%)	70	76
21	BU	90/90 (100%)	90 (100%)	0	100	100
22	BZ	75/75 (100%)	75 (100%)	0	100	100
23	Bc	55/55 (100%)	55 (100%)	0	100	100
24	Bd	45/45 (100%)	45 (100%)	0	100	100
25	Bf	66/66 (100%)	66 (100%)	0	100	100
26	Bg	272/272 (100%)	272 (100%)	0	100	100
27	BE	220/220 (100%)	220 (100%)	0	100	100
28	BG	202/202 (100%)	202 (100%)	0	100	100
29	BH	164/164 (100%)	164 (100%)	0	100	100
30	BI	179/179 (100%)	179 (100%)	0	100	100
31	BJ	160/160 (100%)	160 (100%)	0	100	100
32	BL	138/138 (100%)	137 (99%)	1 (1%)	76	78
33	BN	130/130 (100%)	129 (99%)	1 (1%)	73	77
34	BO	106/106 (100%)	106 (100%)	0	100	100
35	BV	65/65 (100%)	65 (100%)	0	100	100
36	BW	112/112 (100%)	112 (100%)	0	100	100
37	BX	113/113 (100%)	113 (100%)	0	100	100
38	BY	107/107 (100%)	107 (100%)	0	100	100
39	Ba	84/84 (100%)	84 (100%)	0	100	100
40	Bb	72/72 (100%)	72 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	Be	44/44 (100%)	44 (100%)	0	100	100
44	AD	248/248 (100%)	248 (100%)	0	100	100
45	AE	174/174 (100%)	174 (100%)	0	100	100
46	AF	203/203 (100%)	202 (100%)	1 (0%)	81	80
47	AG	199/199 (100%)	198 (100%)	1 (0%)	81	80
48	AH	170/170 (100%)	170 (100%)	0	100	100
49	AI	178/178 (100%)	178 (100%)	0	100	100
50	AJ	142/142 (100%)	142 (100%)	0	100	100
51	AL	171/171 (100%)	170 (99%)	1 (1%)	78	79
52	AM	118/118 (100%)	117 (99%)	1 (1%)	73	77
53	AN	171/171 (100%)	171 (100%)	0	100	100
54	AO	168/168 (100%)	166 (99%)	2 (1%)	63	73
55	AP	134/134 (100%)	133 (99%)	1 (1%)	76	78
56	AQ	164/164 (100%)	164 (100%)	0	100	100
57	AR	160/160 (100%)	160 (100%)	0	100	100
58	AS	156/156 (100%)	156 (100%)	0	100	100
59	AT	138/138 (100%)	138 (100%)	0	100	100
60	AU	89/89 (100%)	89 (100%)	0	100	100
61	AV	100/100 (100%)	100 (100%)	0	100	100
62	AW	100/100 (100%)	100 (100%)	0	100	100
63	AX	105/105 (100%)	105 (100%)	0	100	100
64	AY	119/119 (100%)	119 (100%)	0	100	100
65	AZ	117/117 (100%)	117 (100%)	0	100	100
66	Aa	120/120 (100%)	120 (100%)	0	100	100
67	Ab	58/58 (100%)	58 (100%)	0	100	100
68	Ac	88/88 (100%)	88 (100%)	0	100	100
69	Ad	97/97 (100%)	97 (100%)	0	100	100
70	Ae	115/115 (100%)	115 (100%)	0	100	100
71	Af	88/88 (100%)	88 (100%)	0	100	100
72	Ag	98/98 (100%)	98 (100%)	0	100	100
73	Ah	109/109 (100%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
74	Ai	83/83 (100%)	83 (100%)	0	100	100
75	Aj	71/71 (100%)	70 (99%)	1 (1%)	59	71
76	Ak	64/64 (100%)	64 (100%)	0	100	100
77	Al	47/47 (100%)	47 (100%)	0	100	100
78	Am	46/46 (100%)	46 (100%)	0	100	100
79	An	24/24 (100%)	24 (100%)	0	100	100
80	Ao	93/93 (100%)	93 (100%)	0	100	100
81	Ap	74/74 (100%)	74 (100%)	0	100	100
82	At	106/106 (100%)	106 (100%)	0	100	100
83	Au	196/196 (100%)	194 (99%)	2 (1%)	68	75
84	Aq	124/124 (100%)	123 (99%)	1 (1%)	73	77
85	AK	170/170 (100%)	170 (100%)	0	100	100
86	Ct	725/725 (100%)	722 (100%)	3 (0%)	84	81
All	All	10924/10924 (100%)	10900 (100%)	24 (0%)	85	85

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
54	AO	184	ASN
75	Aj	67	LEU
55	AP	119	VAL
83	Au	80	VAL
19	BS	78	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 191 such sidechains are listed below:

Mol	Chain	Res	Type
52	AM	33	GLN
62	AW	63	GLN
53	AN	37	HIS
55	AP	118	GLN
65	AZ	40	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	Bw	75/76 (98%)	12 (16%)	0
11	B1	1701/1708 (99%)	339 (19%)	3 (0%)
42	A3	156/157 (99%)	35 (22%)	0
43	A4	118/119 (99%)	18 (15%)	0
7	A2	3600/3612 (99%)	720 (20%)	7 (0%)
8	Bv	75/76 (98%)	12 (16%)	0
9	Bx	10/11 (90%)	3 (30%)	0
All	All	5735/5759 (99%)	1139 (19%)	10 (0%)

5 of 1139 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A2	8	U
7	A2	9	C
7	A2	19	G
7	A2	25	A
7	A2	32	G

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	B1	227	U
11	B1	797	C
11	B1	1689	C
7	A2	959	C
7	A2	4661	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
86	DDE	Ct	715	86	18,20,21	1.01	1 (5%)	17,28,30	0.94	1 (5%)

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	DDE	Ct	715	86	-	7/20/21/23	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	Ct	715	DDE	CD2-CG	2.54	1.41	1.36

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	Ct	715	DDE	CAU-CBW-CBI	-2.94	105.47	111.22

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	Ct	715	DDE	NAD-CBI-CBW-NCB
86	Ct	715	DDE	CE1-CAT-CAU-CBW
86	Ct	715	DDE	CA-CB-CG-ND1
86	Ct	715	DDE	CA-CB-CG-CD2
86	Ct	715	DDE	OAG-CBI-CBW-CAU

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 333 ligands modelled in this entry, 332 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
89	GNP	Ct	901	-	34,34,34	1.30	5 (14%)	47,54,54	0.70	2 (4%)

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
89	GNP	Ct	901	-	-	4/18/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	Ct	901	GNP	PB-O3A	4.46	1.64	1.59
89	Ct	901	GNP	PB-O1B	3.11	1.50	1.46
89	Ct	901	GNP	PG-N3B	2.87	1.70	1.63
89	Ct	901	GNP	PG-O1G	2.78	1.50	1.46
89	Ct	901	GNP	PB-O2B	-2.30	1.50	1.56

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	Ct	901	GNP	O1B-PB-N3B	-2.31	108.36	111.77
89	Ct	901	GNP	O2A-PA-O3A	2.00	112.69	107.27

There are no chirality outliers.

All (4) torsion outliers are listed below:

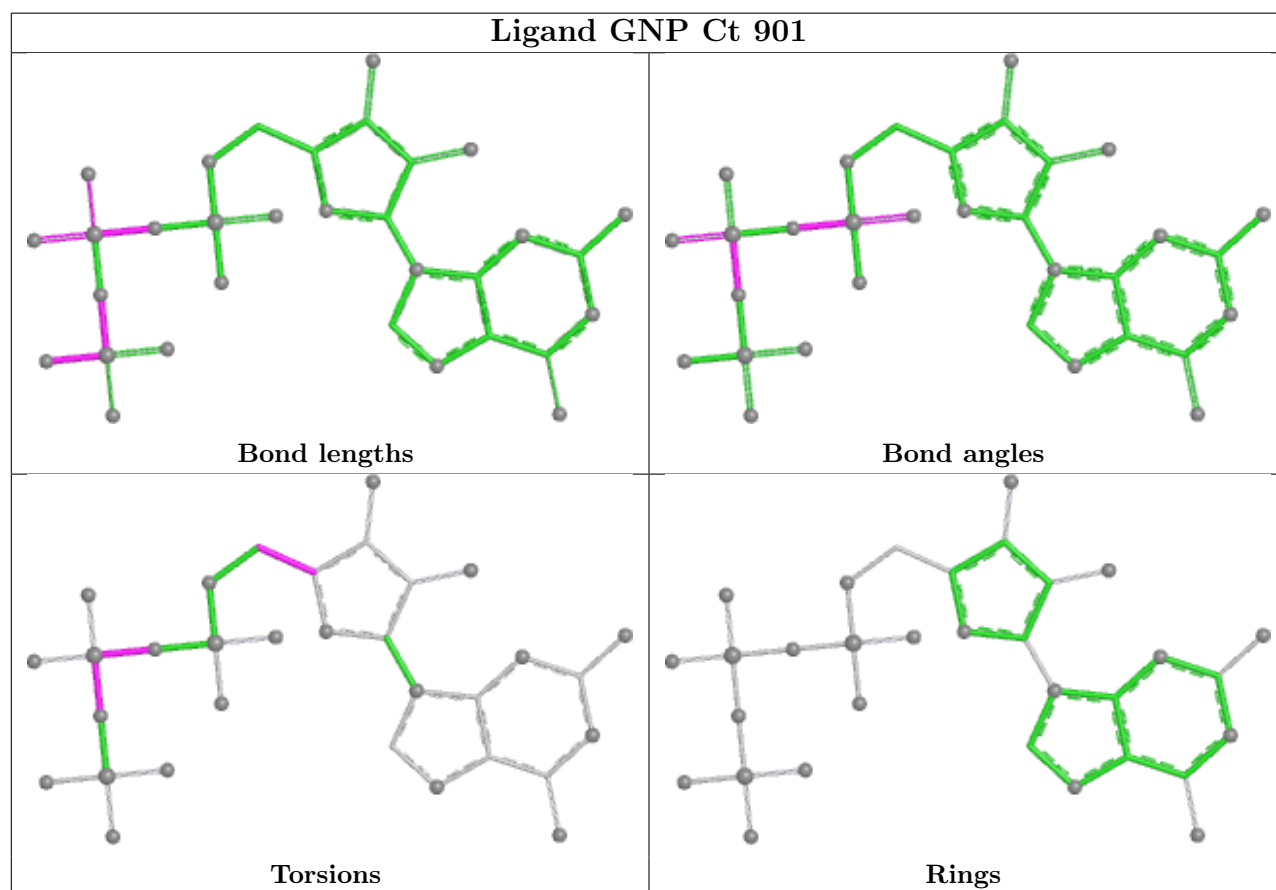
Mol	Chain	Res	Type	Atoms
89	Ct	901	GNP	PG-N3B-PB-O1B
89	Ct	901	GNP	C3'-C4'-C5'-O5'
89	Ct	901	GNP	PA-O3A-PB-O1B
89	Ct	901	GNP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
89	Ct	901	GNP	2	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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
7	A2	12
11	B1	6
49	AI	1

The worst 5 of 19 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	22.39
1	B1	751:G	O3'	790:C	P	19.97
1	A2	517:C	O3'	629:G	P	18.43
1	B1	696:G	O3'	737:G	P	17.82
1	A2	4734:C	O3'	4818:G	P	17.68

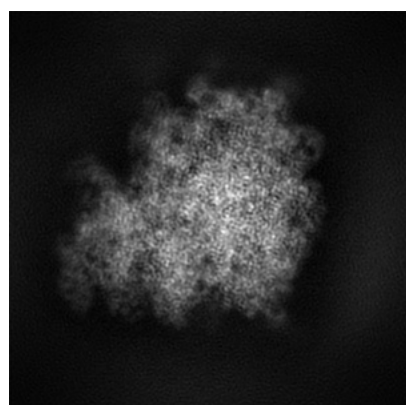
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0099. These allow visual inspection of the internal detail of the map and identification of artifacts.

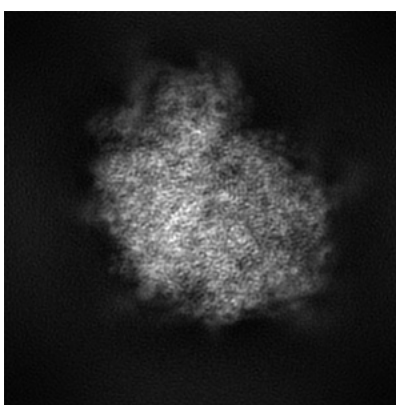
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

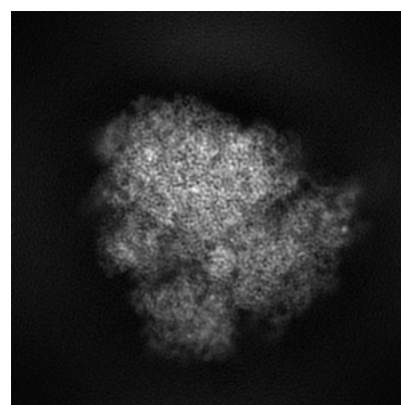
6.1.1 Primary map



X



Y

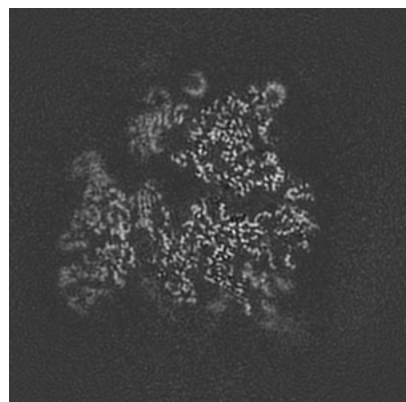


Z

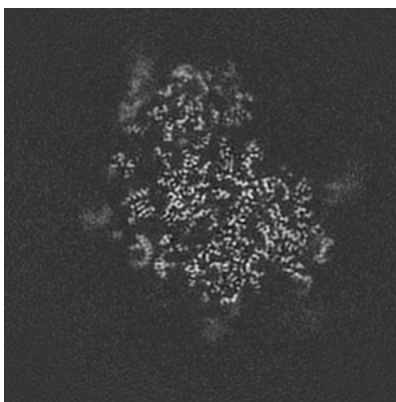
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

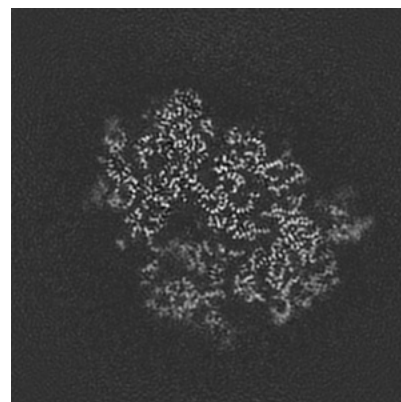
6.2.1 Primary map



X Index: 202



Y Index: 202

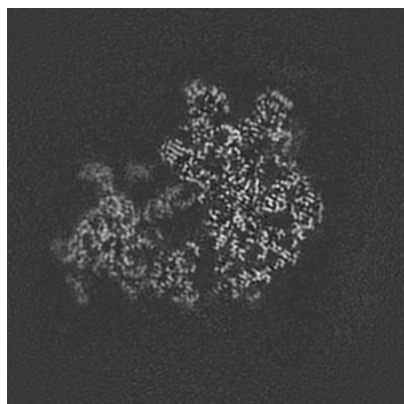


Z Index: 202

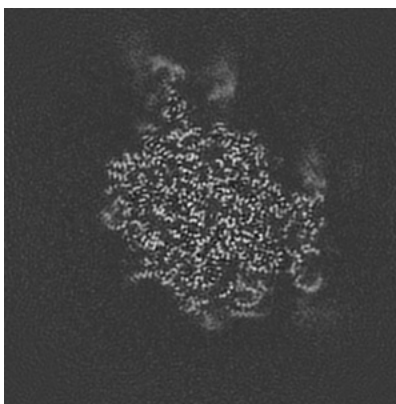
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

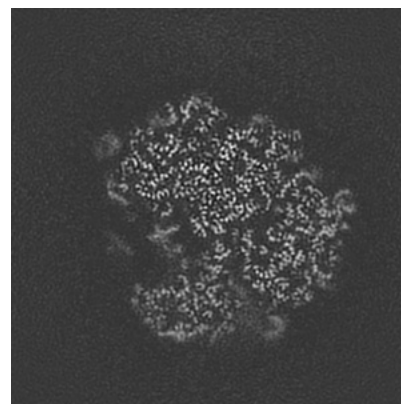
6.3.1 Primary map



X Index: 179



Y Index: 220

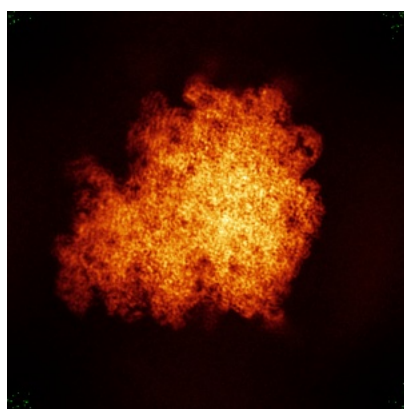


Z Index: 182

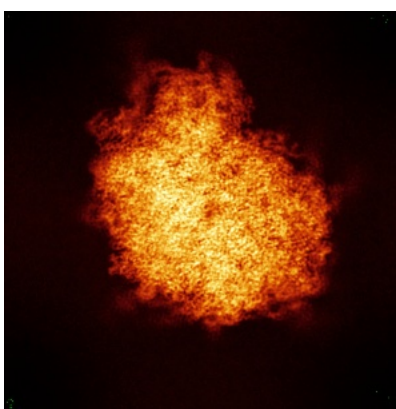
The images above show the largest variance slices of the map in three orthogonal directions.

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

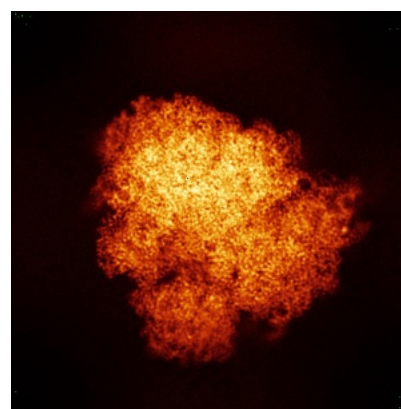
6.4.1 Primary map



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

This section was not generated.

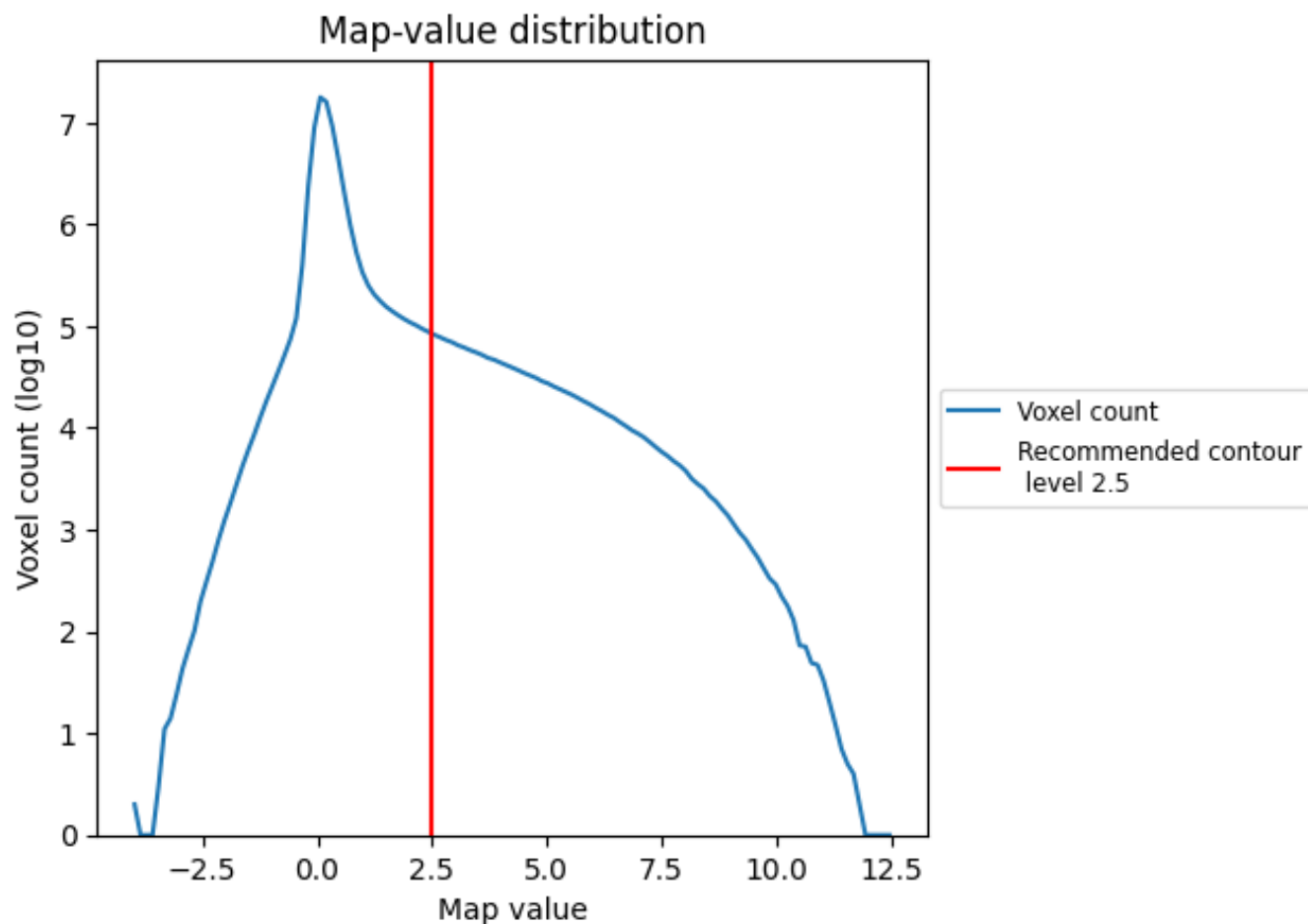
6.6 Mask visualisation

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

7 Map analysis [i](#)

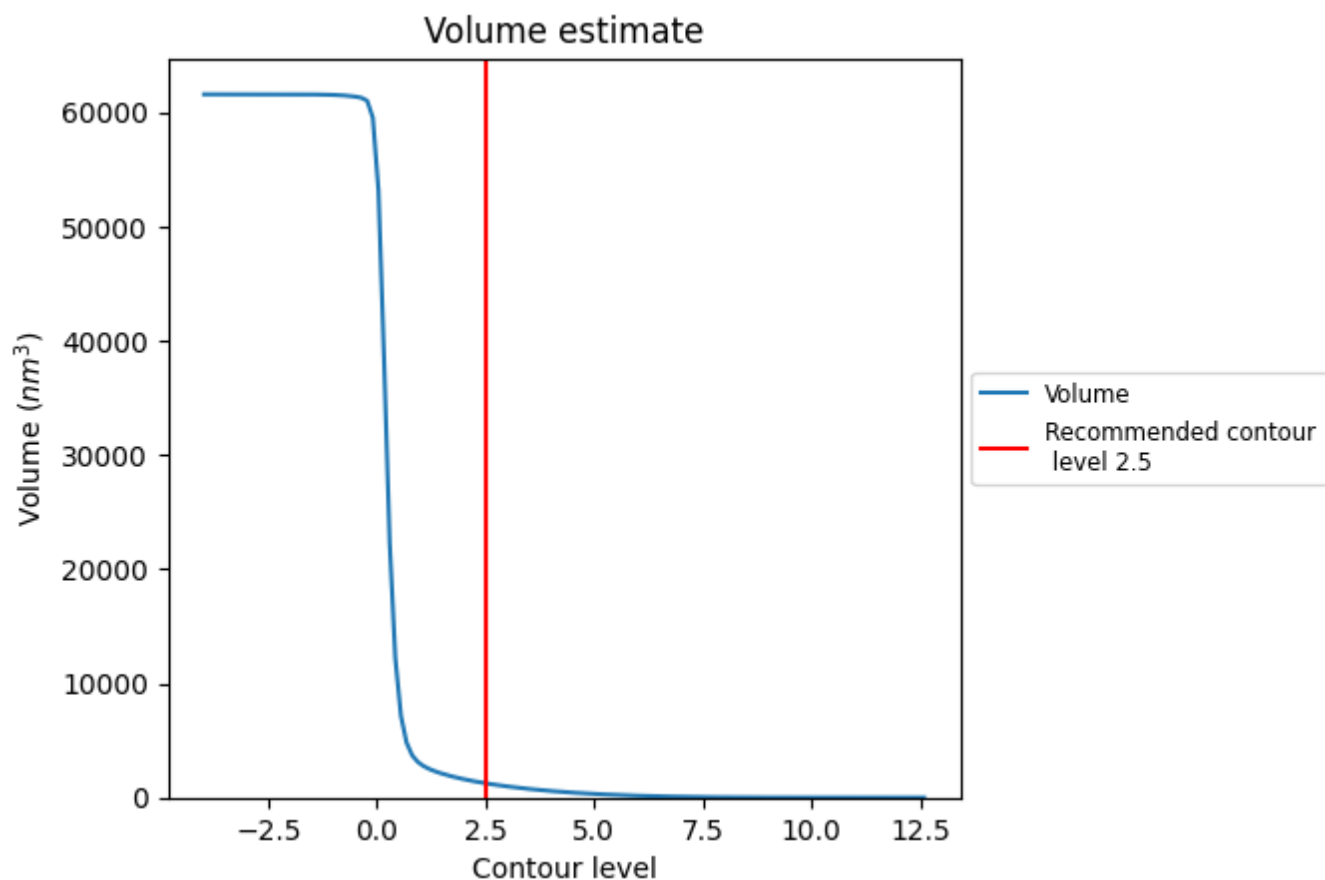
This section contains the results of statistical analysis of the map.

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.

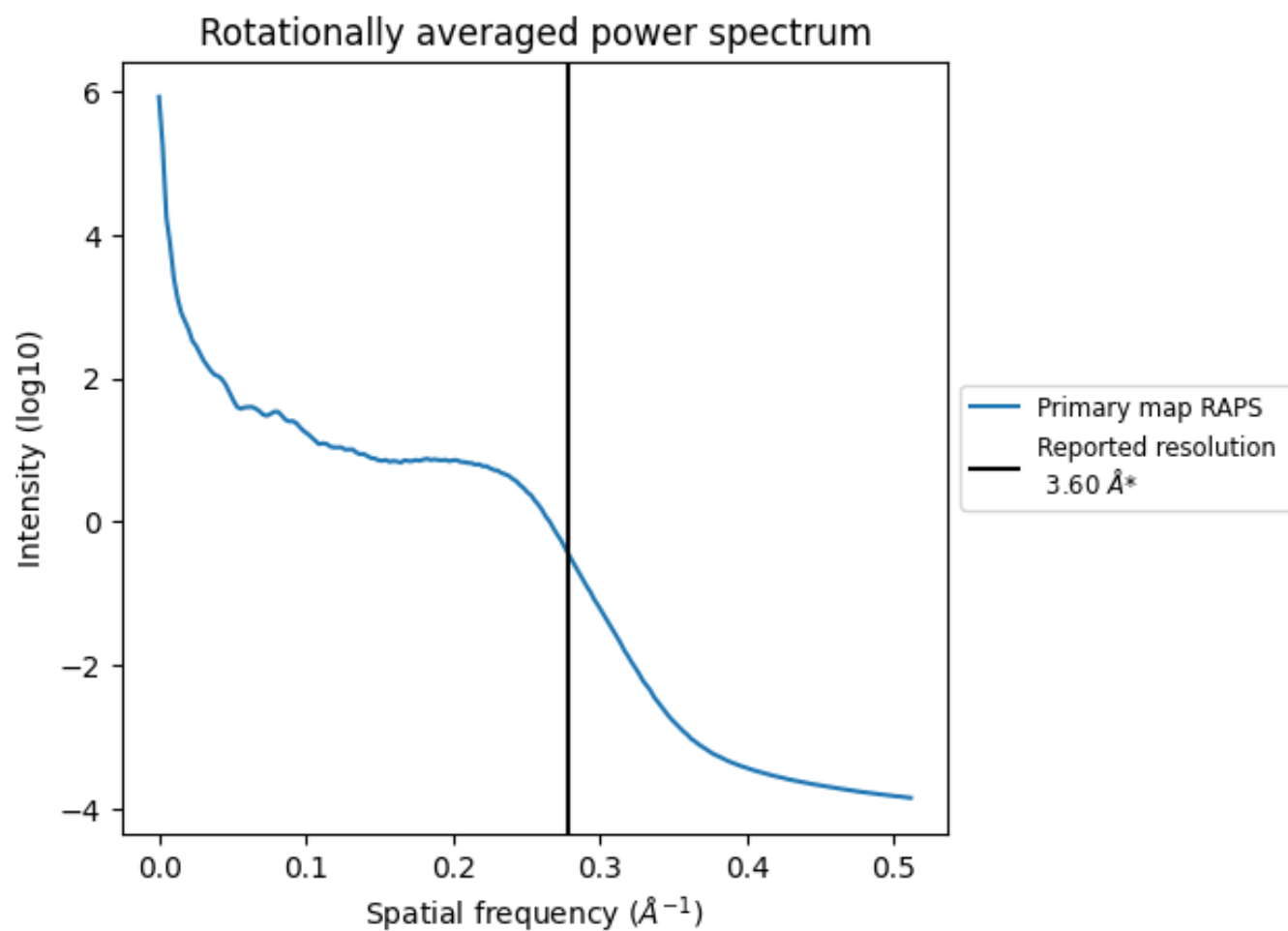
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1249 nm³; this corresponds to an approximate mass of 1128 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 0.278 Å⁻¹

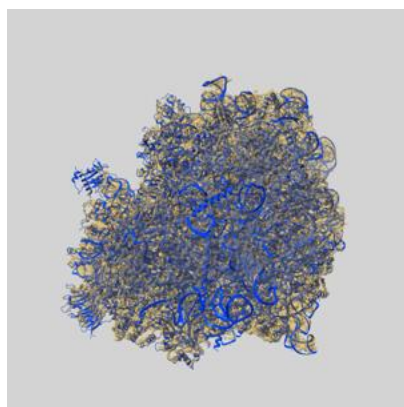
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

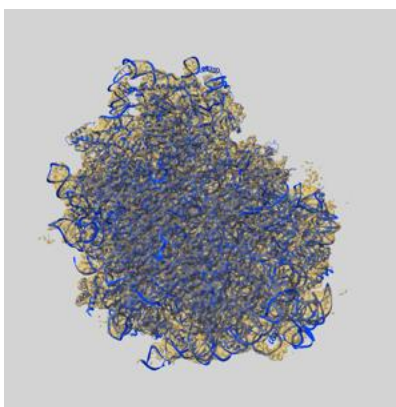
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0099 and PDB model 6GZ4. Per-residue inclusion information can be found in section [3](#) on page [21](#).

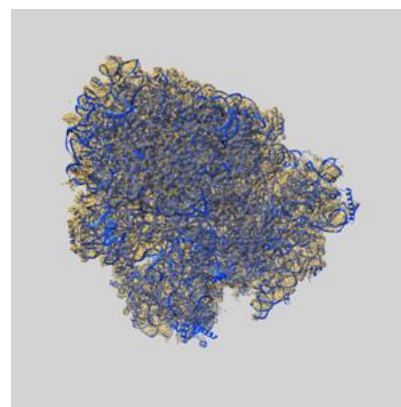
9.1 Map-model overlay [i](#)



X



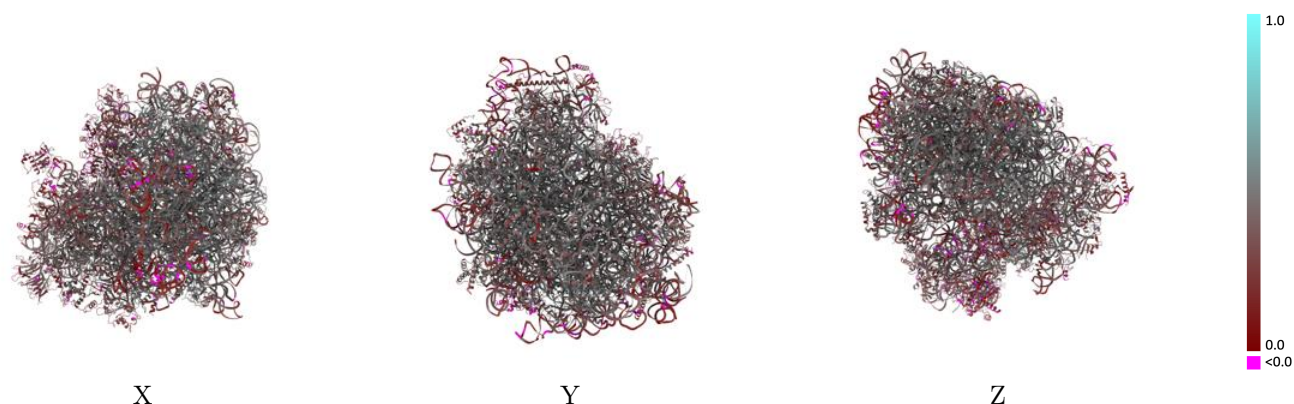
Y



Z

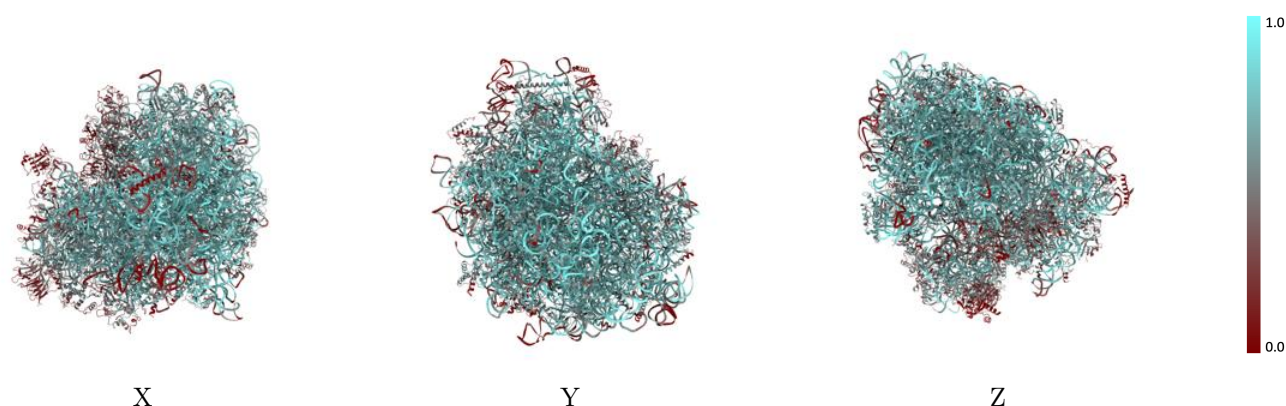
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



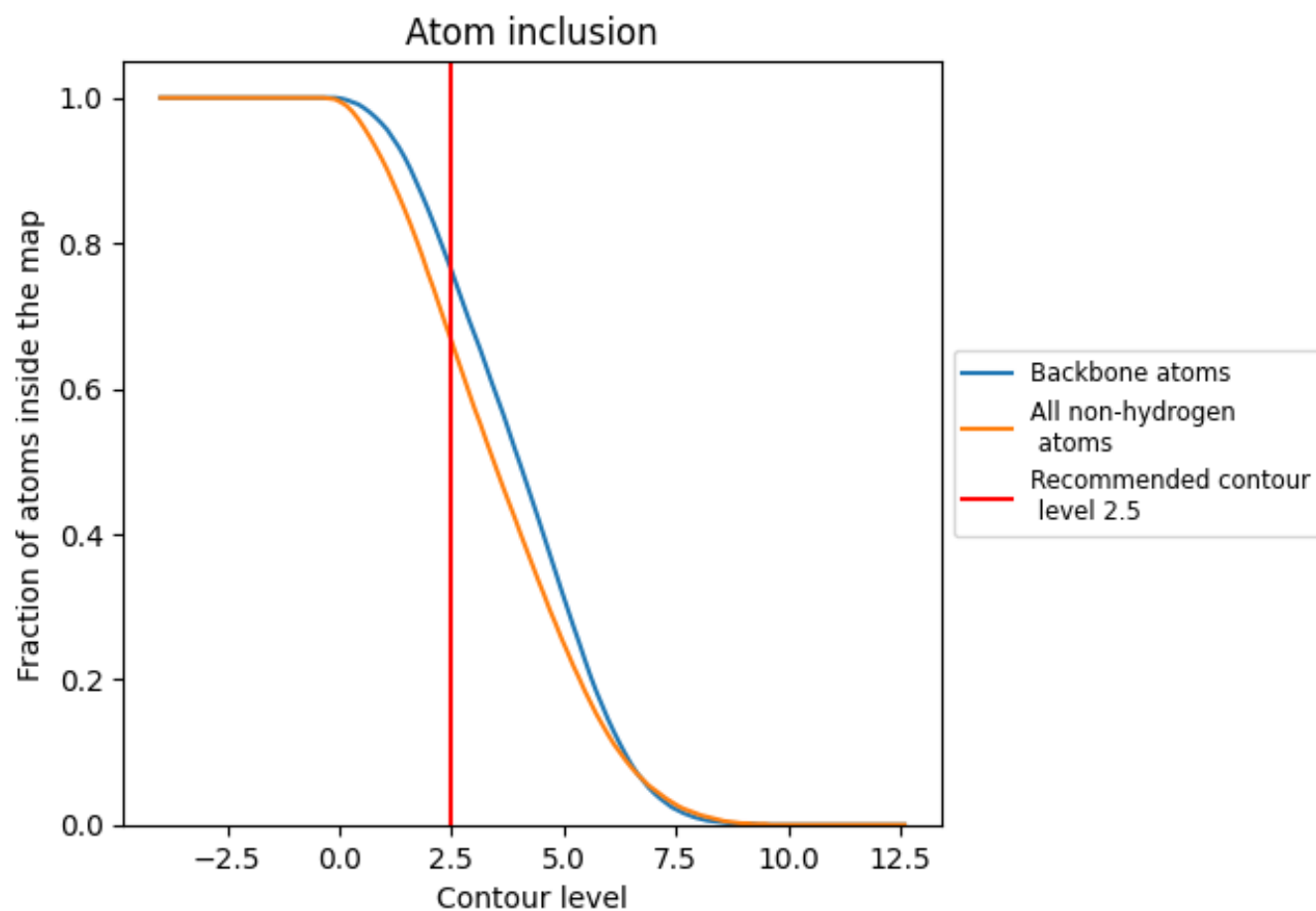
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 66% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6650	 0.3860
A2	 0.7820	 0.4100
A3	 0.7900	 0.4190
A4	 0.8630	 0.4490
AA	 0.6880	 0.4630
AB	 0.6570	 0.4340
AC	 0.6740	 0.4340
AD	 0.6340	 0.3880
AE	 0.5280	 0.3260
AF	 0.6320	 0.4100
AG	 0.5730	 0.3930
AH	 0.6070	 0.4210
AI	 0.6550	 0.4250
AJ	 0.6010	 0.3900
AK	 0.2480	 0.2370
AL	 0.6050	 0.3740
AM	 0.6140	 0.4000
AN	 0.7320	 0.4520
AO	 0.6640	 0.4130
AP	 0.6920	 0.4520
AQ	 0.6640	 0.4310
AR	 0.6220	 0.3990
AS	 0.6760	 0.4420
AT	 0.6600	 0.4300
AU	 0.5370	 0.3720
AV	 0.6620	 0.4620
AW	 0.3550	 0.3030
AX	 0.6440	 0.4420
AY	 0.6540	 0.4280
AZ	 0.6510	 0.4100
Aa	 0.7020	 0.4390
Ab	 0.5840	 0.3540
Ac	 0.6060	 0.3980
Ad	 0.6600	 0.4430
Ae	 0.6670	 0.4480



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Chain	Atom inclusion	Q-score
Af	 0.6770	 0.4320
Ag	 0.6470	 0.4200
Ah	 0.6100	 0.3900
Ai	 0.6140	 0.3880
Aj	 0.7470	 0.4610
Ak	 0.5190	 0.3710
Al	 0.6480	 0.4330
Am	 0.6350	 0.4240
An	 0.2450	 0.3570
Ao	 0.6410	 0.4450
Ap	 0.6530	 0.4300
Aq	 0.1210	 0.1330
At	 0.6900	 0.4130
Au	 0.0300	 0.0570
B1	 0.7520	 0.3930
BA	 0.4960	 0.3610
BB	 0.5650	 0.3730
BC	 0.5750	 0.4010
BD	 0.4530	 0.3430
BE	 0.5620	 0.3850
BF	 0.4470	 0.3250
BG	 0.4670	 0.2890
BH	 0.4040	 0.3090
BI	 0.5660	 0.3760
BJ	 0.5620	 0.3310
BK	 0.3390	 0.2280
BL	 0.5750	 0.3830
BM	 0.0640	 0.1660
BN	 0.5900	 0.3920
BO	 0.5970	 0.4020
BP	 0.4140	 0.2900
BQ	 0.4930	 0.3250
BR	 0.3800	 0.2720
BS	 0.4360	 0.2830
BT	 0.4180	 0.2680
BU	 0.3640	 0.3050
BV	 0.5390	 0.3810
BW	 0.5990	 0.4110
BX	 0.5970	 0.4180
BY	 0.4810	 0.3040
BZ	 0.2960	 0.2300
Ba	 0.6130	 0.4020

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Chain	Atom inclusion	Q-score
Bb	 0.5090	 0.3830
Bc	 0.4110	 0.3370
Bd	 0.5480	 0.3380
Be	 0.5140	 0.3820
Bf	 0.0750	 0.1500
Bg	 0.2470	 0.2730
Bv	 0.5430	 0.3230
Bw	 0.6770	 0.3650
Bx	 0.5870	 0.3640
Ct	 0.3730	 0.2930