



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:23 AM UTC

PDB ID : 6VZJ / pdb_00006vzj
EMDB ID : EMD-21494
Title : Escherichia coli transcription-translation complex A1 (TTC-A1) containing mRNA with a 15 nt long spacer, fMet-tRNAs at E-site and P-site, and lacking transcription factor NusG
Authors : Molodtsov, V.; Wang, C.; Su, M.; Ebright, R.H.
Deposited on : 2020-02-28
Resolution : 4.10 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:

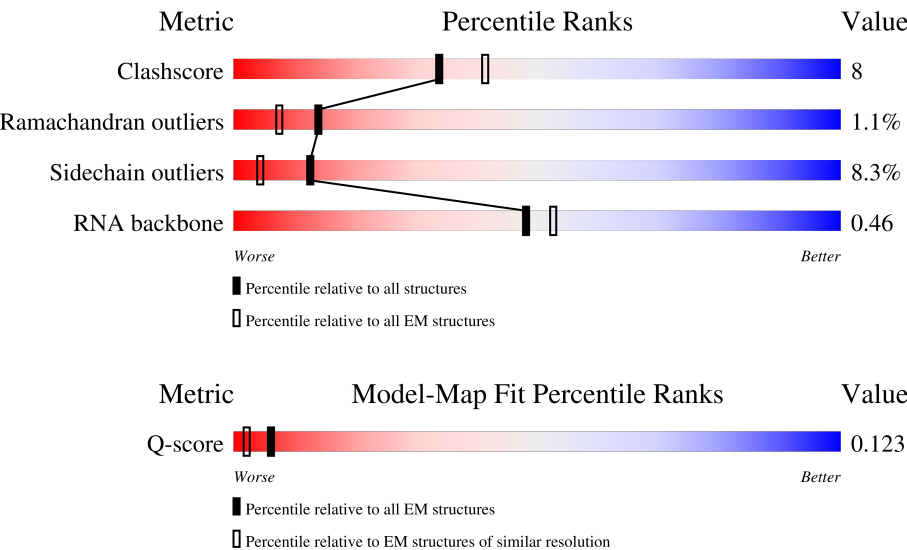
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.10 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	6458 (3.60 - 4.60)

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	0	103	65% 84% 15% .
2	1	110	44% 75% 25%
3	2	100	78% 86% 6% . 6%

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Mol	Chain	Length	Quality of chain
4	3	104	76% 84% 14% ..
5	4	94	77% 97% .
6	5	36	64% 25% 36% . 36%
7	6	36	75% 39% 36% 25%
8	7	32	100% 47% 47% .
9	9	165	88% 27% 36% 24% . 10%
10	A	76	95% 12% 47% 36% 5%
10	B	76	99% 12% 46% 37% 5%
11	AA	1342	99% 69% 22% 6% ..
12	AC	329	70% 50% 16% . 30%
12	AD	329	69% 52% 17% . 31%
13	AE	1407	95% 67% 24% . 5%
14	C	75	67% 72% 15% . 12%
15	D	1542	27% 71% 24% ..
16	E	87	76% 87% 11% .
17	F	71	82% 87% 10% ..
18	G	241	72% 79% 13% . 7%
19	H	557	46% 25% 16% . 54%
20	I	233	76% 79% 9% . 11%
21	J	205	84% 90% 9%
22	K	167	50% 76% 14% .. 7%
23	L	135	67% 67% 10% 23%
24	M	151	83% 84% 14% ..
25	N	129	69% 91% 9%
26	O	127	84% 81% 18% .

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Mol	Chain	Length	Quality of chain
27	P	99	90% 77% 16% 6% .
28	Q	117	83% 91% 9%
29	R	123	45% 88% 11% .
30	S	101	80% 89% 8% ...
31	T	89	66% 79% 18% ..
32	U	82	88% 88% 11% .
33	V	84	71% 87% 7% . 5%
34	W	83	94% 90% 8% .
35	X	116	89% 77% 18% 5%
36	Y	141	99% 38% 40% 19% .
37	Z	121	25% 7% 12% 6% . 75%
38	a	2904	25% 73% 23% ..
39	b	76	82% 93% 7%
40	c	78	74% 88% 8% ..
41	d	120	41% 81% 19%
42	e	62	74% 87% 11% .
43	f	58	69% 86% 12% .
44	g	66	95% 85% 14% .
45	h	271	71% 86% 13% .
46	i	56	48% 79% 20% .
47	j	209	54% 88% 11%
48	k	55	85% 89% 5% 5%
49	l	201	70% 85% 14% .
50	m	46	35% 78% 17% .
51	n	177	86% 76% 20% .

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Mol	Chain	Length	Quality of chain
52	o	64	81% 89% 6% 5%
53	p	175	87% 91% 9%
54	q	38	71% 87% 11%
55	r	149	95% 88% 9%
56	s	142	62% 81% 18%
57	t	123	53% 80% 18%
58	u	144	71% 88% 12%
59	v	136	67% 91% 8%
60	w	119	56% 82% 18%
61	x	116	83% 83% 16%
62	y	114	81% 89% 11%
63	z	117	43% 84% 15%

2 Entry composition

There are 65 unique types of molecules in this entry. The entry contains 299095 atoms, of which 123940 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 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	0	103	Total	C	H	N	O	S	0	0
			1655	516	839	153	145	2		

- Molecule 2 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1	110	Total	C	H	N	O	S	0	0
			1779	532	922	166	156	3		

- Molecule 3 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	2	94	Total	C	H	N	O	S	0	0
			1557	470	811	140	134	2		

- Molecule 4 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	3	103	Total	C	H	N	O		0	0
			1632	498	844	148	142			

- Molecule 5 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	4	94	Total	C	H	N	O	S	0	0
			1533	479	780	137	134	3		

- Molecule 6 is a DNA chain called NT DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	5	23	Total	C	H	N	O	P	0	0
			732	225	260	87	137	23		

- Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	6	27	Total	C	H	N	O	P	0	0
			847	259	305	89	167	27		

- Molecule 8 is a RNA chain called mRNA with 27 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	32	Total	C	H	N	O	P	0	0
			769	300	97	100	240	32		

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	148	Total	C	N	O	S	0	0
			1117	705	196	209	7		

- Molecule 10 is a RNA chain called E-site and P-site tRNA (fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
10	A	76	Total	C	H	N	O	P	0	0
			2446	723	826	295	527	75		
10	B	76	Total	C	H	N	O	P	0	0
			2433	723	813	295	527	75		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	U	deletion	GB 1848959854
B	?	-	U	deletion	GB 1848959854

- Molecule 11 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	AA	1322	Total	C	H	N	O	S	0	0
			20851	6539	10426	1817	2026	43		

- Molecule 12 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AC	230	Total	C	H	N	O	S	0	0
			3599	1112	1813	317	351	6		

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Mol	Chain	Residues	Atoms						AltConf	Trace
12	AD	228	Total	C	H	N	O	S	0	0
			3556	1100	1789	312	349	6		

- Molecule 13 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AE	1335	Total	C	H	N	O	S	0	0
			21000	6526	10612	1854	1958	50		

- Molecule 14 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	C	66	Total	C	H	N	O	S	0	0
			1103	344	559	102	97	1		

- Molecule 15 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	D	1524	Total	C	H	N	O	P	0	0
			49126	14585	16423	6003	10591	1524		

- Molecule 16 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	E	86	Total	C	H	N	O	S	0	0
			1388	414	719	138	114	3		

- Molecule 17 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	F	70	Total	C	H	N	O	S	0	0
			1218	366	629	125	97	1		

- Molecule 18 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	G	225	Total	C	H	N	O	S	0	0
			3545	1113	1785	316	323	8		

- Molecule 19 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	H	259	Total	C	H	N	O	S	0	0
			3184	1073	1454	305	349	3		

- Molecule 20 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	I	208	Total	C	H	N	O	S	0	0
			3346	1036	1710	307	290	3		

- Molecule 21 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	J	205	Total	C	H	N	O	S	0	0
			3350	1026	1707	315	298	4		

- Molecule 22 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	K	156	Total	C	H	N	O	S	0	0
			2348	717	1196	217	212	6		

- Molecule 23 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	L	104	Total	C	H	N	O	S	0	0
			1694	536	846	153	152	7		

- Molecule 24 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	M	151	Total	C	H	N	O	S	0	0
			2416	735	1235	227	215	4		

- Molecule 25 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	N	129	Total	C	H	N	O	S	0	0
			2010	616	1031	173	184	6		

- Molecule 26 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	O	127	Total	C	H	N	O	S	0	0
			2092	634	1070	206	179	3		

- Molecule 27 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	P	99	Total	C	H	N	O	S	0	0
			1621	495	831	151	143	1		

- Molecule 28 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	Q	117	Total	C	H	N	O	S	0	0
			1764	540	887	174	160	3		

- Molecule 29 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	R	121	Total	C	H	N	O	S	0	0
			1940	580	1001	194	161	4		

- Molecule 30 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	S	100	Total	C	H	N	O	S	0	0
			1649	499	844	164	139	3		

- Molecule 31 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	T	88	Total	C	H	N	O	S	0	0
			1448	439	734	144	130	1		

- Molecule 32 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	U	82	Total	C	H	N	O	S	0	0
			1315	406	666	128	114	1		

- Molecule 33 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	V	80	Total	C	H	N	O	S	0	0
			1339	411	691	121	113	3		

- Molecule 34 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	W	83	Total	C	H	N	O	S	0	0
			1351	424	688	126	111	2		

- Molecule 35 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	X	116	Total	C	H	N	O	S	0	0
			1864	558	964	181	158	3		

- Molecule 36 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Y	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 37 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Z	30	Total	C	N	O	S	0	0
			227	144	33	47	3		

- Molecule 38 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	a	2880	Total	C	H	N	O	P	0	0
			92918	27587	31077	11398	19976	2880		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	887	A	U	conflict	GB 937521852

- Molecule 39 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	b	76	Total	C	H	N	O	S	0	0
			1181	360	599	117	104	1		

- Molecule 40 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	c	77	Total	C	H	N	O	S	0	0
			1277	388	652	129	106	2		

- Molecule 41 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	d	120	Total	C	H	N	O	P	0	0
			3870	1144	1301	468	837	120		

- Molecule 42 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	e	62	Total	C	H	N	O	S	0	0
			1032	308	531	98	94	1		

- Molecule 43 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	f	58	Total	C	H	N	O	S	0	0
			936	281	488	87	78	2		

- Molecule 44 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	g	66	Total	C	H	N	O	S	0	0
			1042	323	520	99	94	6		

- Molecule 45 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	h	271	Total	C	H	N	O	S	0	0
			4236	1288	2154	423	364	7		

- Molecule 46 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	i	56	Total	C	H	N	O	S	0	0
			903	269	459	94	80	1		

- Molecule 47 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	j	209	Total	C	H	N	O	S	0	0
			3182	979	1617	288	294	4		

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	k	52	Total	C	H	N	O		0	0
			890	275	464	78	73			

- Molecule 49 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	l	201	Total	C	H	N	O	S	0	0
			3171	974	1619	283	290	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
50	m	46	Total	C	H	N	O	S	0	0
			795	228	418	90	57	2		

- Molecule 51 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	n	177	Total	C	H	N	O	S	0	0
			2853	899	1443	249	256	6		

- Molecule 52 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	o	64	Total	C	H	N	O	S	0	0
			1076	323	572	105	74	2		

- Molecule 53 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	p	175	Total	C	H	N	O	S	0	0
			2671	826	1358	241	244	2		

- Molecule 54 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	q	38	Total	C	H	N	O	S	0	0
			645	185	343	65	48	4		

- Molecule 55 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	r	149	Total	C	H	N	O	S	0	0
			2259	699	1148	197	214	1		

- Molecule 56 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	s	142	Total	C	H	N	O	S	0	0
			2291	714	1162	212	199	4		

- Molecule 57 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	t	123	Total	C	H	N	O	S	0	0
			1969	593	1023	181	166	6		

- Molecule 58 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	u	144	Total	C	H	N	O	S	0	0
			2182	654	1129	207	190	2		

- Molecule 59 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	v	136	Total	C	H	N	O	S	0	0
			2231	686	1157	205	177	6		

- Molecule 60 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	w	119	Total	C	H	N	O	S	0	0
			1945	588	994	195	163	5		

- Molecule 61 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	x	116	Total	C	H	N	O		0	0
			1815	552	923	178	162			

- Molecule 62 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	y	114	Total	C	H	N	O	S	0	0
			1879	574	962	179	163	1		

- Molecule 63 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	z	117	Total	C	H	N	O		0	0
			1967	604	1020	192	151			

- Molecule 64 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
64	AE	1	Total	Mg	0
			1	1	

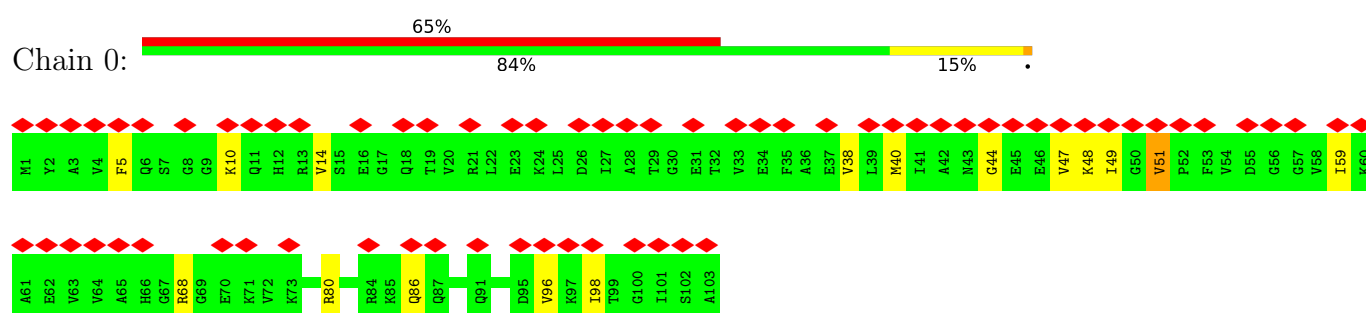
- Molecule 65 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
65	AE	2	Total	Zn	0
			2	2	

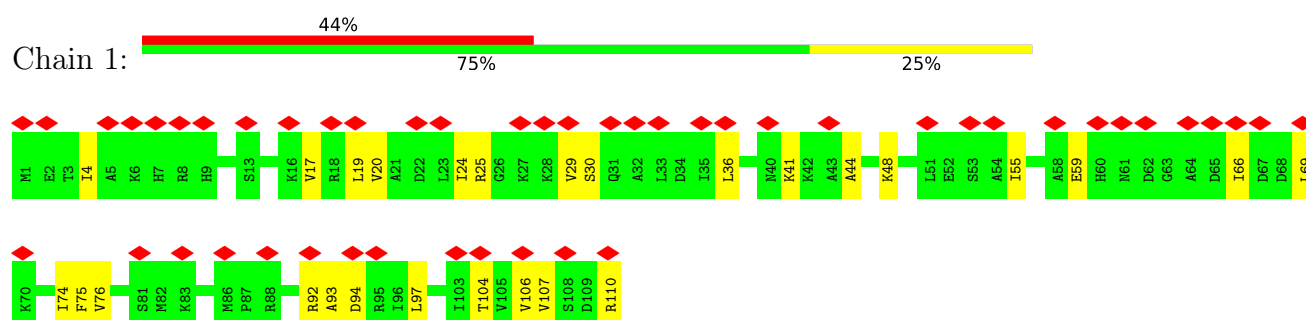
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

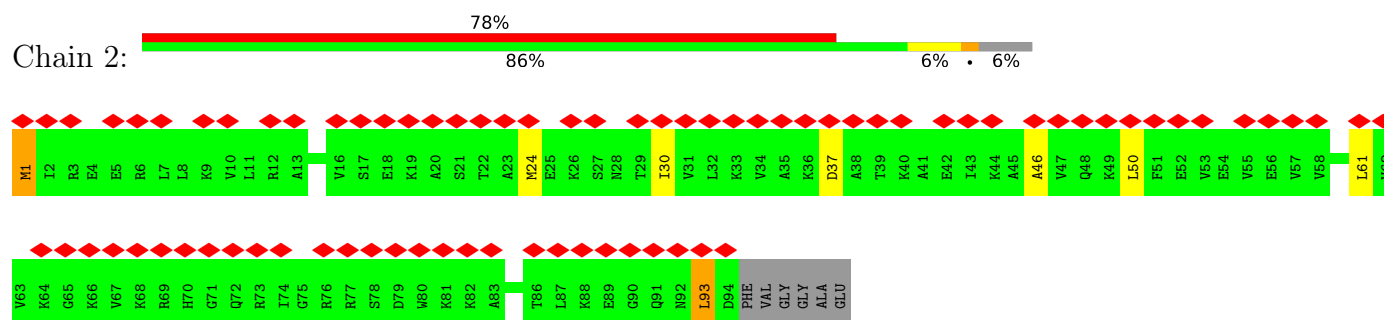
• Molecule 1: 50S ribosomal protein L21



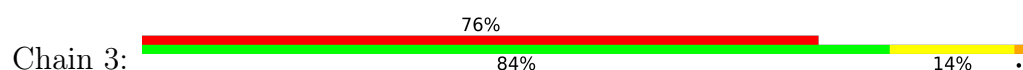
• Molecule 2: 50S ribosomal protein L22

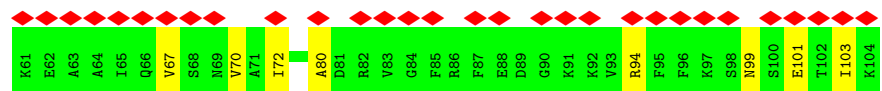


• Molecule 3: 50S ribosomal protein L23

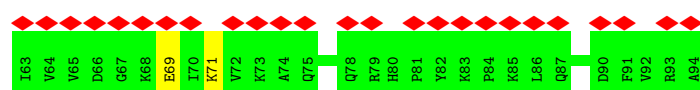
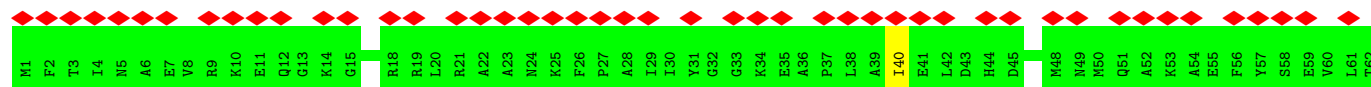
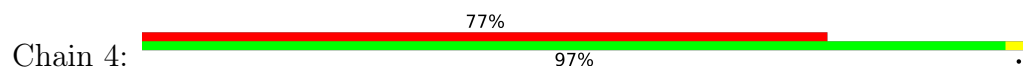


• Molecule 4: 50S ribosomal protein L24

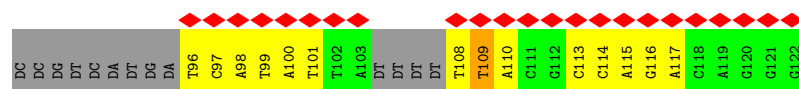
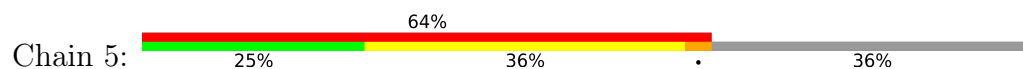




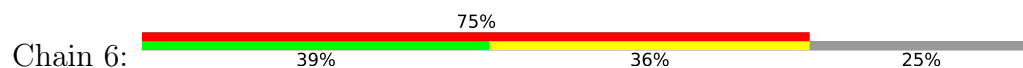
• Molecule 5: 50S ribosomal protein L25



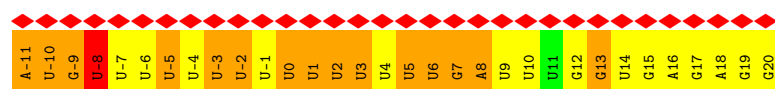
• Molecule 6: NT DNA



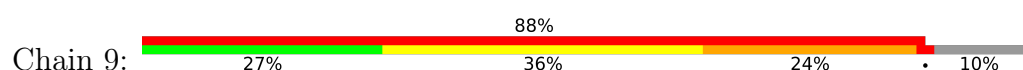
• Molecule 7: T DNA

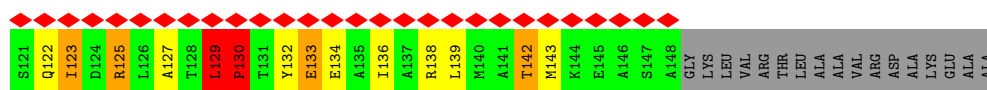


• Molecule 8: mRNA with 27 nt long spacer



• Molecule 9: 50S ribosomal protein L10





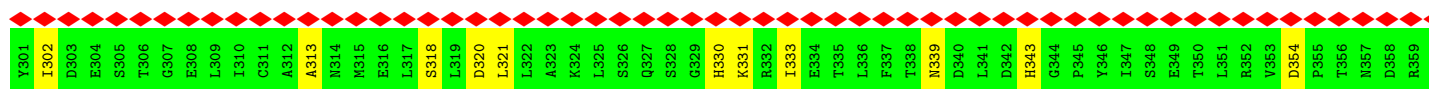
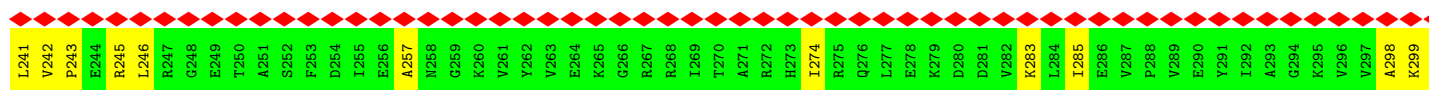
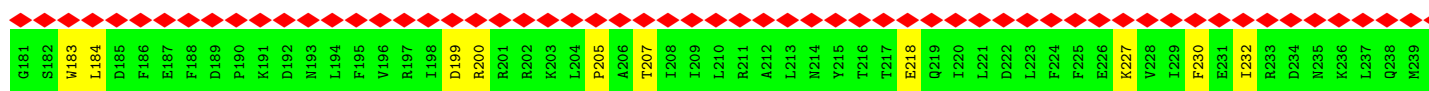
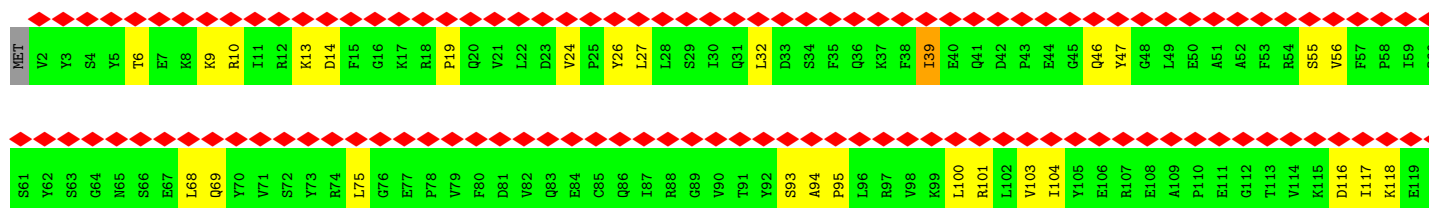
• Molecule 10: E-site and P-site tRNA (fMet)



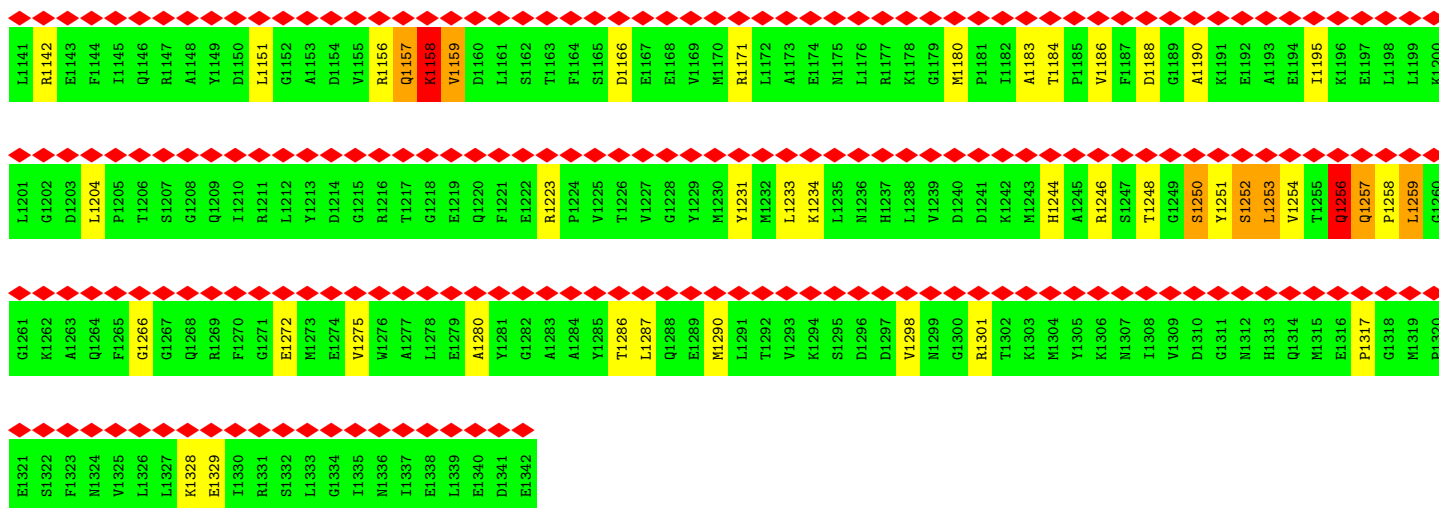
• Molecule 10: E-site and P-site tRNA (fMet)



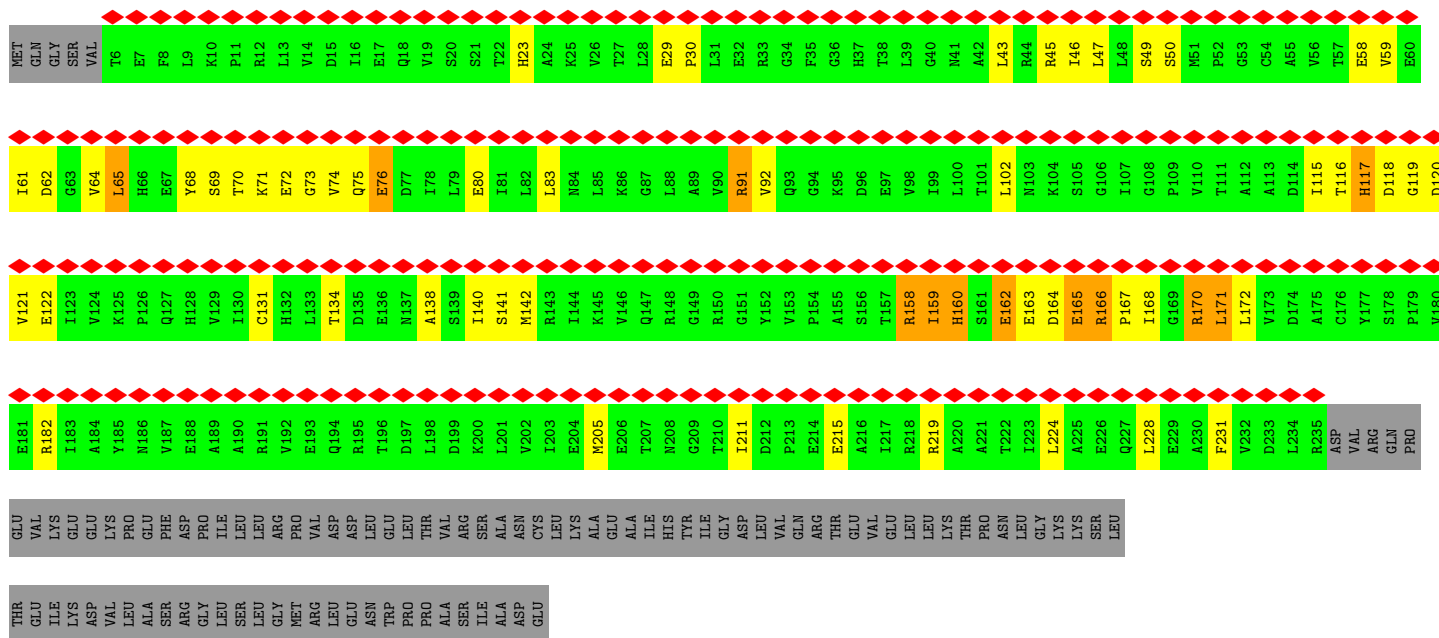
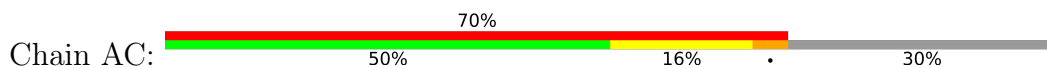
• Molecule 11: DNA-directed RNA polymerase subunit beta



P1081	L1021	S961	R841	D781	G721	V661	D601	E541	L481	S421	S361
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E1083	H1023	E963	T843	L783	V723	V663	I603	A543	D483	D423	L363
D1084	E1024	L964	K844	A784	V724	G664	H604	G544	L484	D424	V364
M1085	F1025	Q965	L845	D785	Q725	A665	Y605	F545	T485	I425	E365
P1086	E1026	I966	G846	G786	Q726	S666	L606	E546	T486	I426	I366
Y1087	K1027	L967	P847	P787	V727	L667	S607	V547	L487	D427	Y367
E1088	K1028	E968	E848	S788	D728	I668	A608	R548	M488	V428	R368
A1089	L1029	A969	E849	T789	A729	P669	I609	D549	P489	M429	M369
N1090	E1030	G970	T850	D790	S730	F670	E610	V550	Q490	K430	M370
G1091	A1031	L971	T851	L791	R731	L671	E611	H551	D491	K431	R371
T1092	K1032	A972	A852	G792	I732	E672	G612	P552	M492	I433	P372
P1093	R1033	D853	D853	E793	V733	H673	N613	T553	I493	I434	G373
V1094	R1034	T854	T854	L794	I734	D674	Y614	H554	A494	D434	E374
D1095	K1035	P855	P855	A795	K735	D675	V615	Y555	A495	I435	P375
I1096	I1036	R856	R856	L796	K736	A676	I616	G556	K496	R436	P376
Y1097	T1037	V857	V857	G797	M737	N677	A617	R557	P497	N437	T377
L1098	Q1038	G858	G858	Q798	E738	R678	Q618	V558	I498	G438	R378
N1099	G1039	E859	E859	N799	D739	A679	A619	C559	S499	K439	E379
P1100	D1040	A860	A860	M800	E740	L680	N620	P560	A500	G440	A380
L1101	D1041	A861	A861	R801	M741	M681	S621	I561	A501	E441	A381
V1102	L1042	L862	L862	V802	V742	G682	N622	E562	V502	V442	E382
V1103	A1043	S863	S863	A803	P743	A683	L623	T563	K503	D443	S383
P1104	P1044	K864	K864	F804	G744	N684	D624	P564	E504	E444	L384
S1105	G1045	L865	L865	M805	E745	M685	E625	E565	F505	I445	F385
R1106	G1046	D866	D866	P806	A746	Q686	E626	G566	F506	D446	F386
M1107	L1047	E867	E867	M807	G747	R687	G627	P567	G507	H447	N387
N1108	K1048	S868	S868	N808	I748	Q688	H628	N568	S508	L448	L388
I1109	I1049	G869	G869	G809	D749	A689	F629	I569	S509	G449	F389
G1110	V1050	D990	D990	Y810	I750	V690	V630	G570	Q510	N450	F390
Q1111	K1051	R991	R991	H811	Y751	P691	E631	L571	L511	R451	S391
I1112	V1052	L992	L992	F812	N752	T692	D632	I572	S512	R452	E392
L1113	Y1053	P993	P993	E813	L753	L693	L633	N573	Q513	I453	D393
E1114	L1054	R994	R994	D814	T754	G694	V634	S574	F514	R454	R394
T1115	A1055	D995	D995	S815	K755	A695	T635	L575	M515	S455	Y395
H1116	V1056	R996	R996	I816	Y756	D696	C636	S576	D516	V456	D396
L1117	K1057	E997	E997	L817	T757	K697	R637	V577	Q517	G457	L397
G1118	L1058	T878	T878	V818	R758	P698	S638	Y578	N518	E458	S398
M1119	R1059	G879	G879	S819	S759	L699	K639	A579	N519	M459	A399
A1120	I1060	C880	C880	E820	N760	V700	G640	Q580	P520	A460	V400
A1121	Q1061	D881	D881	R821	Q761	T701	E641	T581	L521	E461	G401
K1122	P1062	T882	T882	V822	N762	G702	S642	N582	S522	E462	R402
G1123	G1063	L883	L883	E823	T763	G703	S643	E583	E523	Q463	M403
I1124	D1064	V884	V884	Q824	G764	M704	L644	Y584	I524	F464	K404
G1125	K1065	G885	G885	E825	I765	E705	F645	G585	T525	R465	F405
D1126	M1066	X886	X886	D826	T766	R706	S646	F586	H526	V466	N406
K1127	A1067	V887	V887	R827	Q767	A707	R647	L587	K527	G467	R407
I1128	G1068	T888	T888	F828	M768	V708	D648	E588	R528	V468	S408
N1129	N1069	P889	P889	T829	P769	A709	Q649	T589	E529	V469	L409
A1130	H1070	K890	K890	T830	G770	V710	V650	I630	I330	R470	L410
M1131	G1071	G891	G891	L831	V771	D711	D651	Y591	S531	V471	R411
L1132	N1072	T892	T892	H832	S772	S712	Y652	R592	A532	E472	E412
K1133	K1073	G955	G955	I633	L773	G713	M653	K593	L533	R473	E413
Q1134	G1074	A956	A956	Q834	G774	V714	D654	V594	G534	A474	I414
Q1135	Y1075	X1015	X1015	E835	E775	T715	V655	T595	P535	V475	E415
Q1136	I1076	L836	L836	L836	P776	A716	S656	D596	G536	K476	E416
E1137	S1077	A837	A837	A837	P777	V717	T657	G597	G537	E477	S417
V1138	K1078	C838	C838	V839	E778	A718	Q658	V598	L538	R478	G418
A1139	I1079	V839	V839	S840	R779	K719	Q659	V599	T539	L479	I419
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• Molecule 12: DNA-directed RNA polymerase subunit alpha

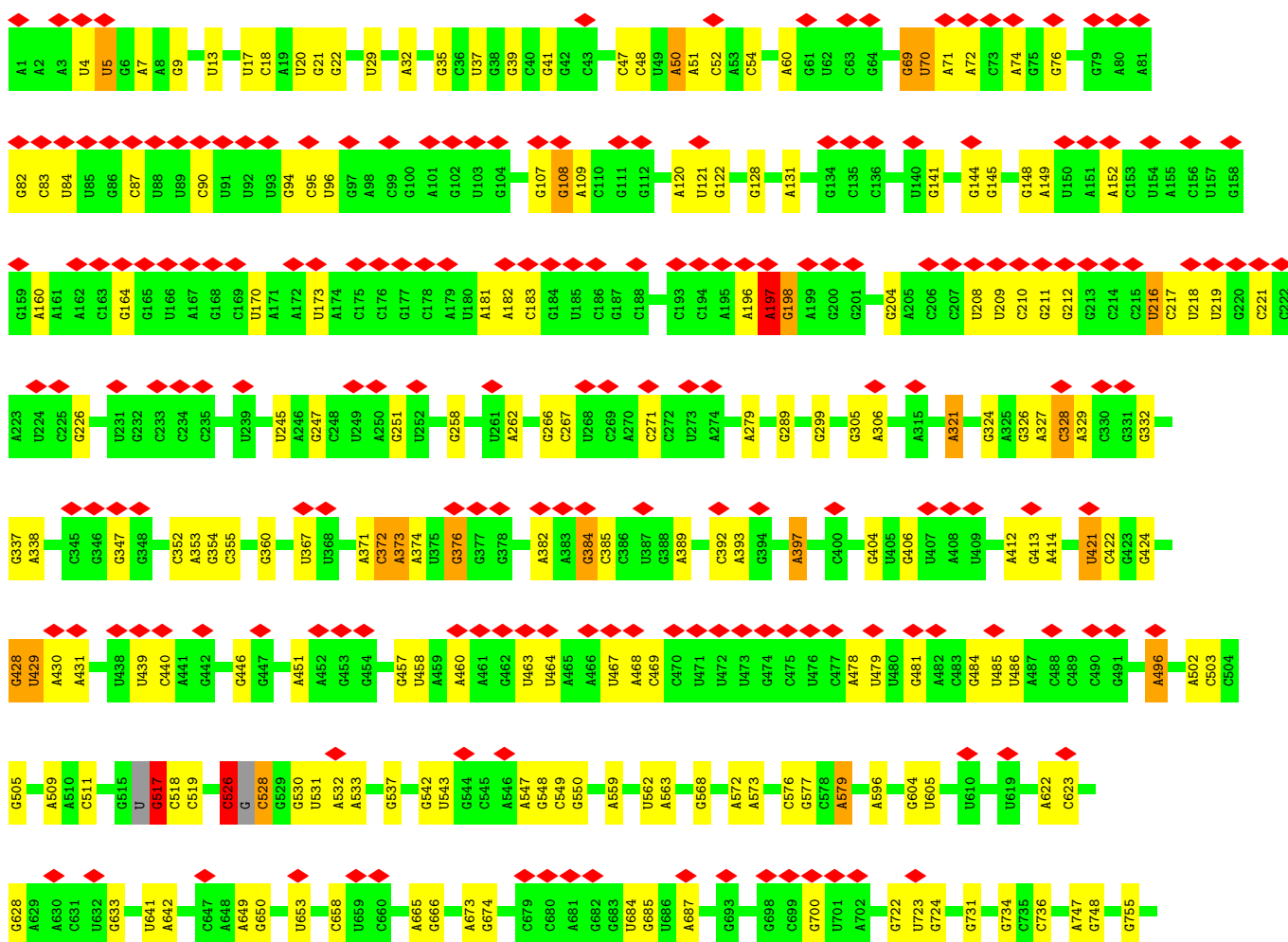


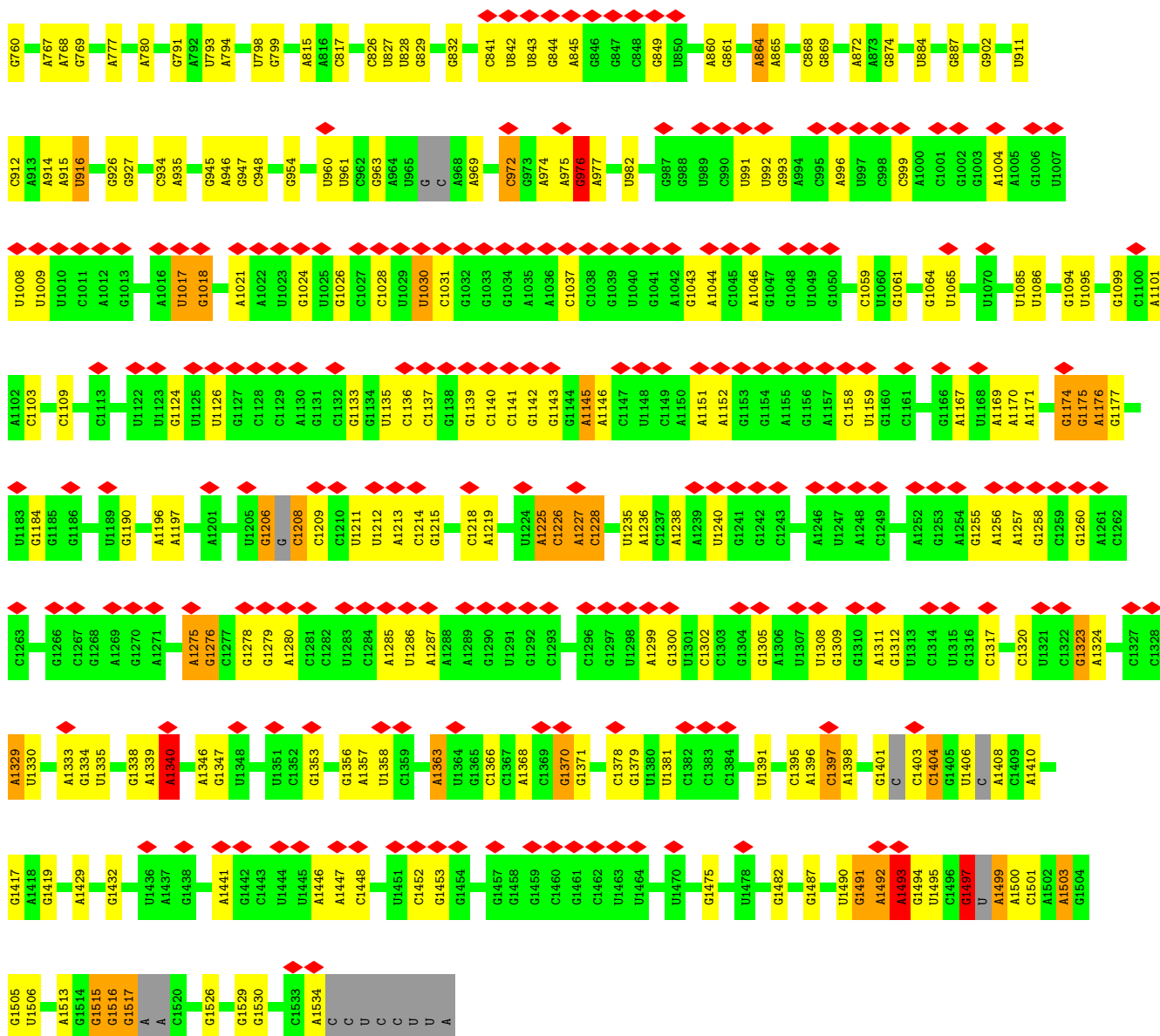
• Molecule 12: DNA-directed RNA polymerase subunit alpha



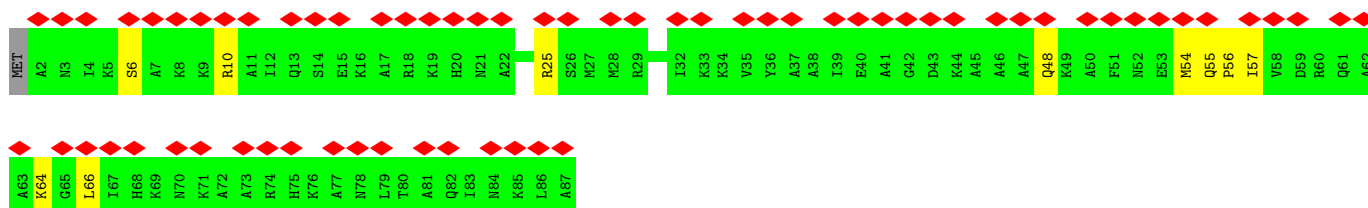
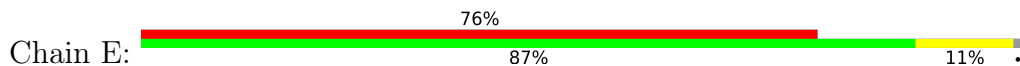


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K1263	R1203	A1083	H1023	V963	A903	T844	L783	L903	Y723	E663	K543	K543
A1264	V1204	Q1084	T1024	K964	A904	V844	A784	A904	M724	I664	M604	L544
T1265	E1205	G1085	M1025	S965	R905	A845	D785	R905	M725	Q665	L605	H545
L1266	R1206	N1086	P1026	V966	G906	E846	T786	G906	A726	E666	N606	A546
V1267	G1207	D1087	V1027	V967	H907	D847	A787	H907	D727	Q667	T607	R547
N1268	D1208	V1088	I1028	N968	I908	V848	L788	I908	S728	F668	C608	V548
A1269	V1209	L1089	T1029	S969	I909	L849	K789	I909	G729	Q669	Y609	K549
G1270	I1210	I1090	E1030	S970	N910	K850	T790	N910	A730	S670	R610	V550
S1271	S1211	P1091	V1031	G971	K911	P851	A791	K911	R731	G671	I611	R551
L1272	D1212	G1092	S1032	K972	G912	G852	N792	G912	G732	L672	L612	I552
D1273	G1213	T1093	G1033	L973	E913	T853	S793	E913	S733	V673	G613	T553
F1274	P1214	D1094	F1034	V974	A914	A854	G794	A914	A734	T674	L614	E554
E1215	L1215	I1155	V1035	I975	I915	D855	Y795	A735	A735	A675	K615	Y555
A1216	A1216	P1096	R1036	T976	G916	I856	L796	G916	Q736	G676	P616	E556
E1276	P1217	A1097	F1037	S977	V917	L857	T797	V917	I737	E677	T617	K557
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E1278	D1219	Y1099	D1039	N979	A919	P859	R799	A919	Q739	Y679	I619	A559
V1280	I1220	F1100	M1040	T980	A920	R860	L800	A920	L740	N680	F620	N560
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A1294	V1234	Q1114	T1054	S994	THR	E874	C814	THR	I754	S694	R634	V574
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K1297	V1237	S1117	S1057	V997	ILE	V877	H817	GLY	T577	M697	A637	A577
V1298	Q1238	G1118	S1058	P998	GLY	L1058	D878	GLY	P758	M698	S638	I578
G1299	D1239	D1119	L1059	Y999	ALA	L1059	G819	ALA	I759	D699	S639	L579
A1300	V1240	T1120	V1060	G1000	ALA	V880	I820	ALA	T760	N700	G640	W580
T1301	Y1241	L1121	V1061	I1061	ALA	K881	M821	ALA	A761	L701	I641	M581
Y1302	R1242	A1122	L1062	V1002	ALA	V882	M822	ALA	N762	Q702	D642	I582
S1303	L1243	R1123	D1063	L1003	ALA	R883	T823	ALA	F763	T703	D643	V583
R1304	Q1244	D1184	S1064	A1004	GLU	S884	P824	GLU	R764	E704	M644	P584
D1305	G1245	P1185	A1065	K1005	S948	V885	V825	S948	E765	T705	V645	K585
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L1307	K1247	E1187	R1067	D1007	I950	S887	E827	I950	L767	I707	P647	L587
G1308	L1248	E1188	T1068	G1008	Q951	C888	G828	Q951	N768	N708	E648	P588
I1309	N1249	M1189	A1069	E1009	V952	D889	G829	V952	V769	R709	K649	Y589
T1310	D1250	THR	G1070	Q1010	K953	T890	D830	K953	L770	D710	K650	S590
K1311	K1251	LYS	G1071	V1011	N954	D891	V831	N954	Q771	H651	I591	I591
A1312	H1252	ASP	K1072	A1012	K955	F892	K832	K955	Y772	Q712	E652	V592
S1313	I1253	ILE	D1073	G1013	G956	G893	E833	G956	F773	E713	I653	N593
L1314	E1254	G1136	L1074	G1014	S957	V894	P834	S957	I774	E714	I654	Q594
A1315	V1255	G1137	R1075	E1015	I958	C895	L835	I958	S775	K715	S655	A595
T1316	L1256	L1138	P1076	T1016	K959	A896	R836	K959	T776	Q716	E656	L596
E1317	V1257	P1139	A1077	V1017	L960	H897	D837	L960	H777	V717	A657	G597
S1318	R1258	R1140	L1078	A1018		C898	R838		G778	S718	E658	K598
F1319	Q1259	K1079	N1019	N1019		Y899	V839		A779	N719	A659	K599
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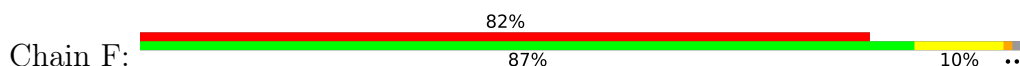




- Molecule 16: 30S ribosomal protein S20

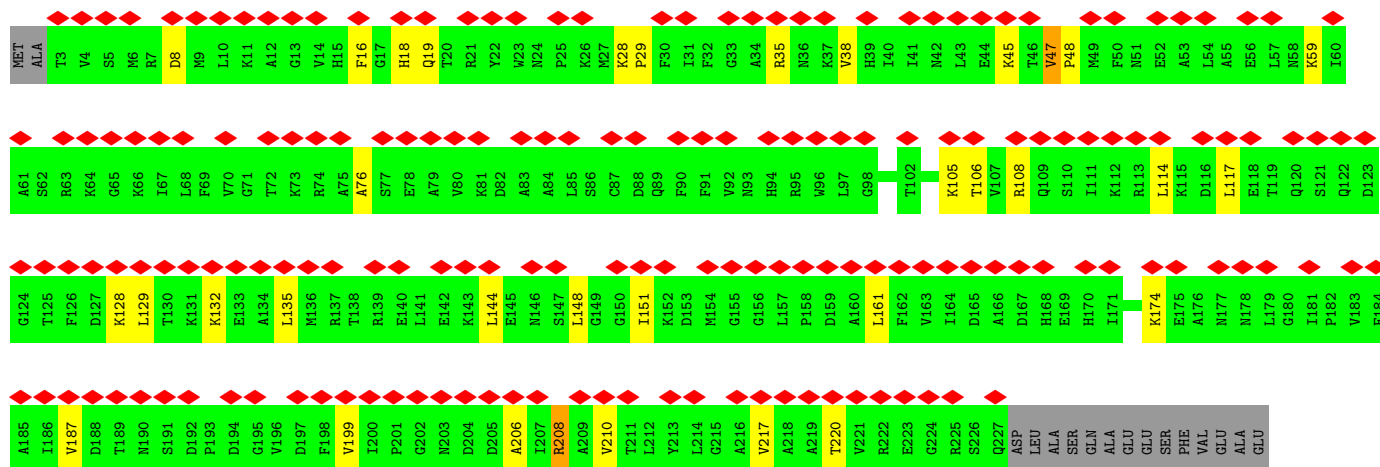
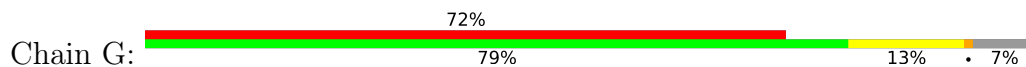


- Molecule 17: 30S ribosomal protein S21

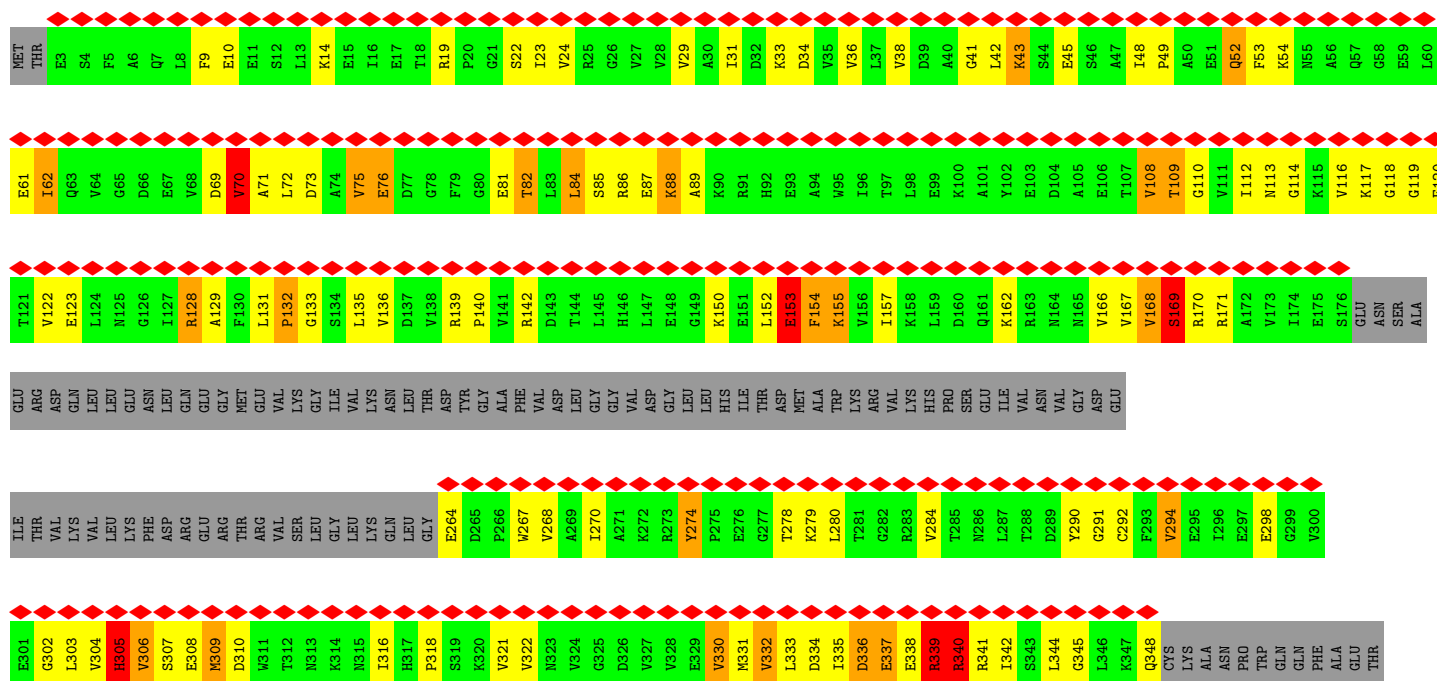
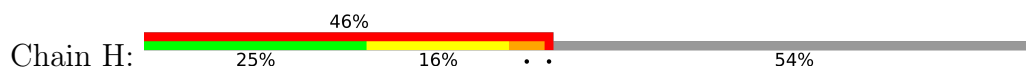


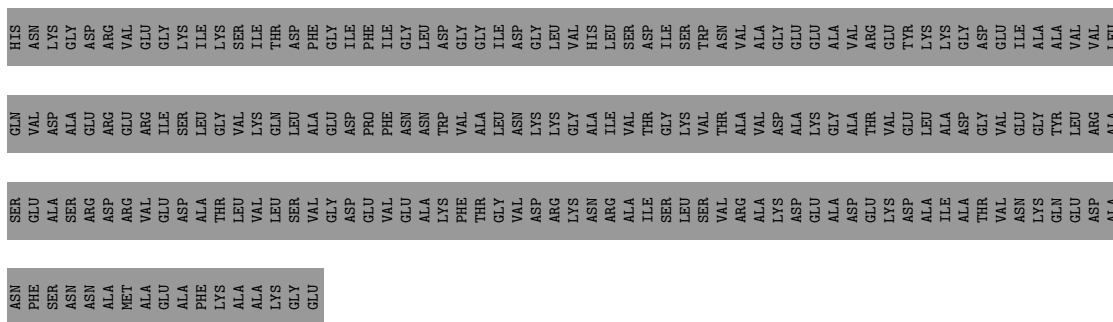


• Molecule 18: 30S ribosomal protein S2

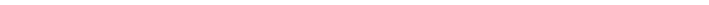


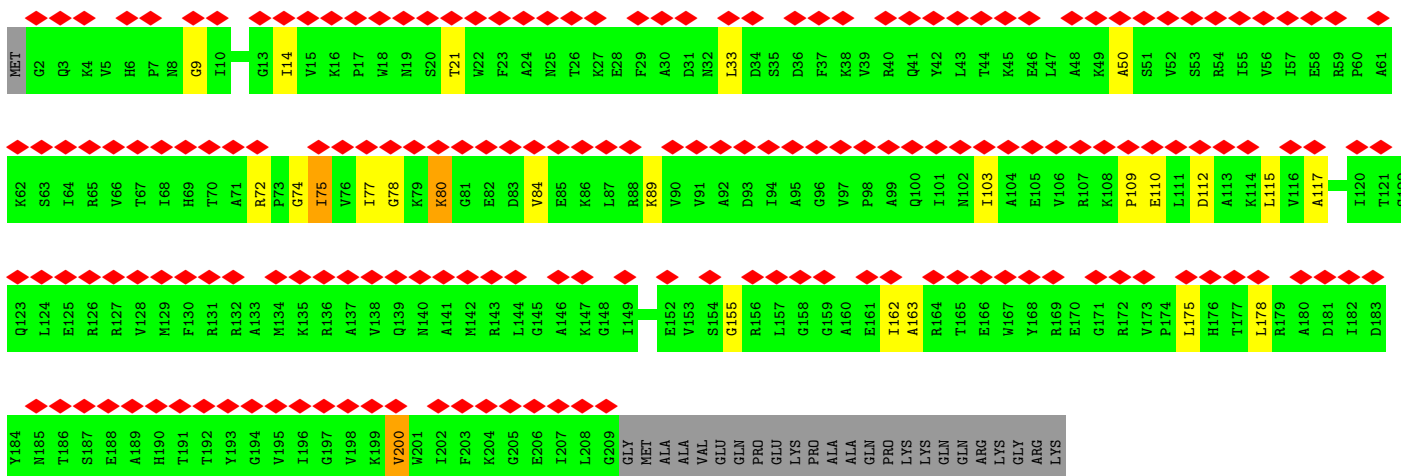
• Molecule 19: 30S ribosomal protein S1



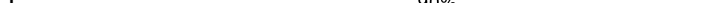


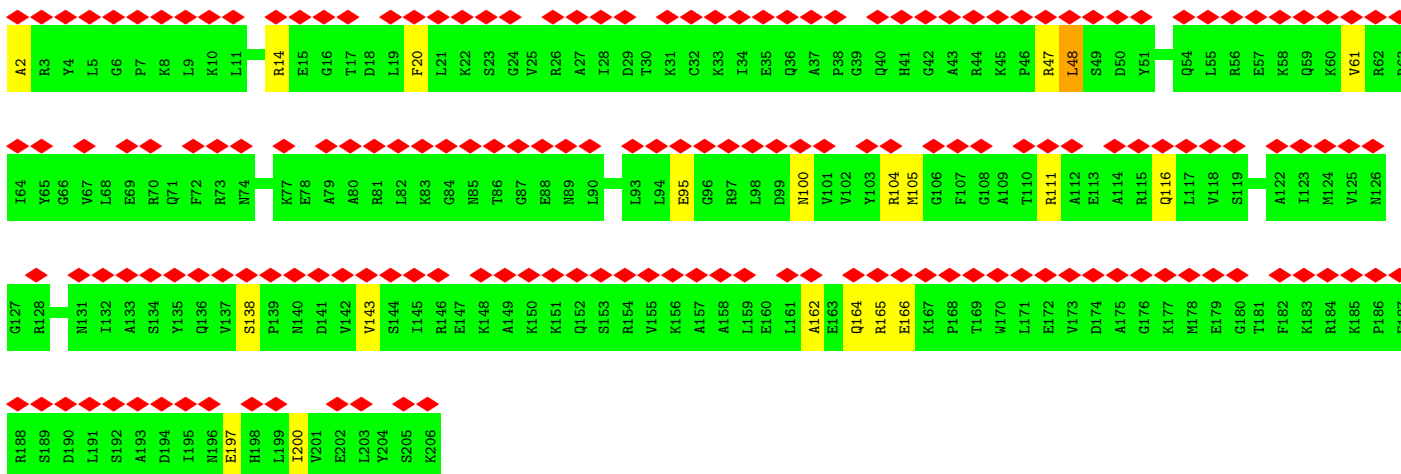
- Molecule 20: 30S ribosomal protein S3

Chain I:  76% 79% 9% 11%

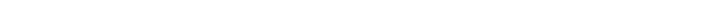


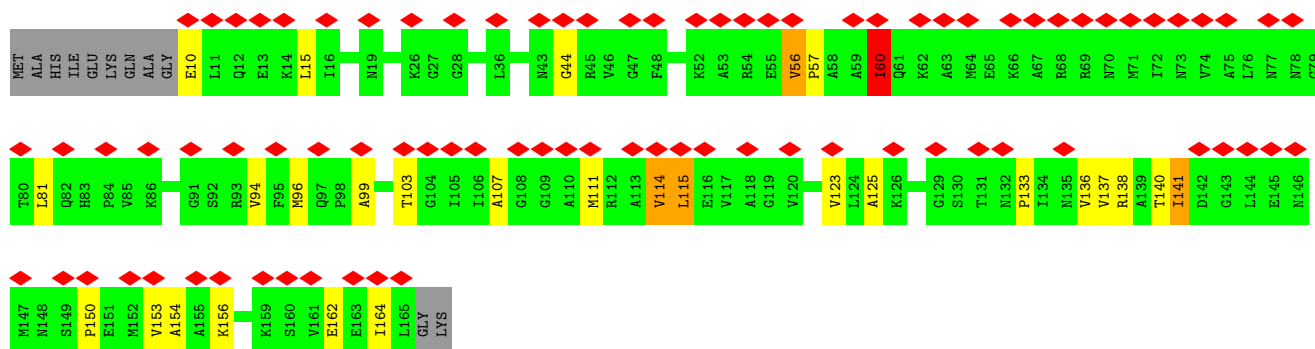
- Molecule 21: 30S ribosomal protein S4

Chain J:  84% 90% 9%

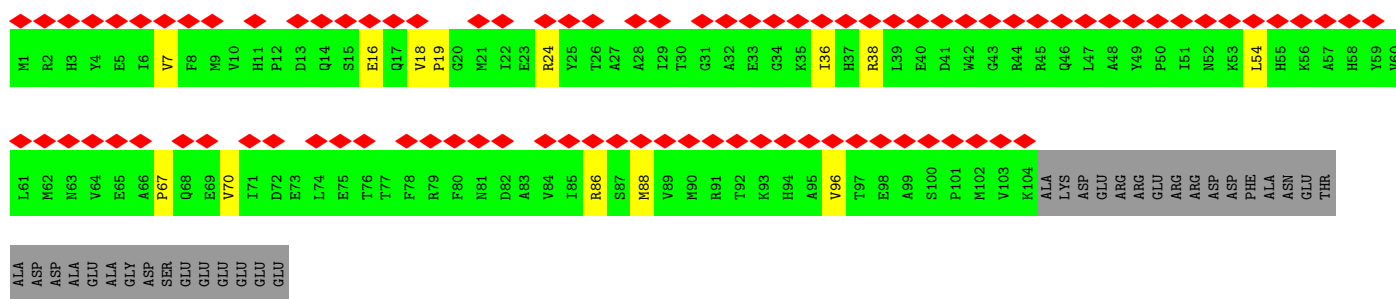


- Molecule 22: 30S ribosomal protein S5

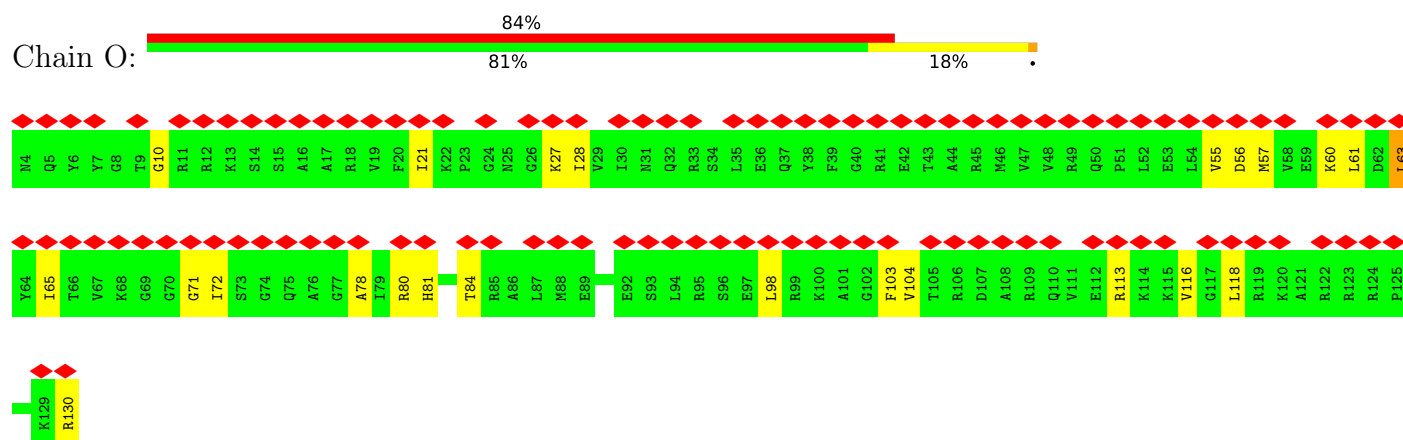
Chain K:  50% 76% 14% 7%



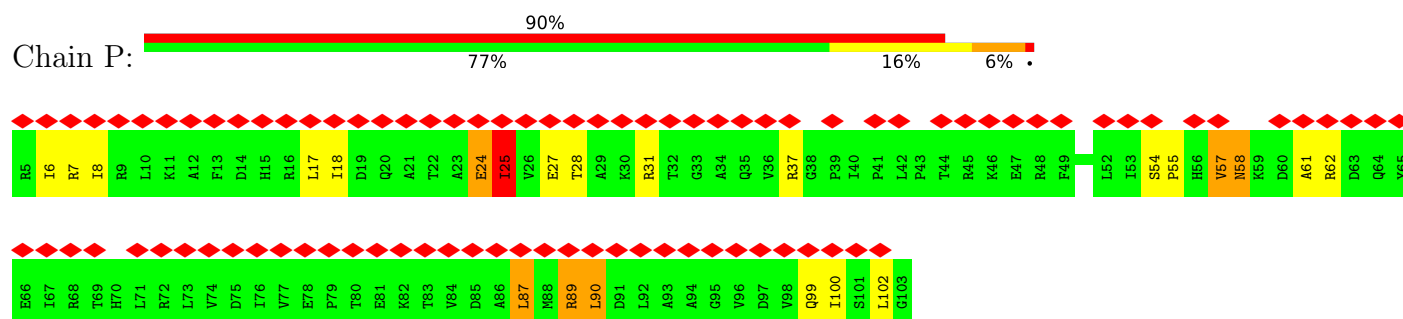
• Molecule 23: 30S ribosomal protein S6



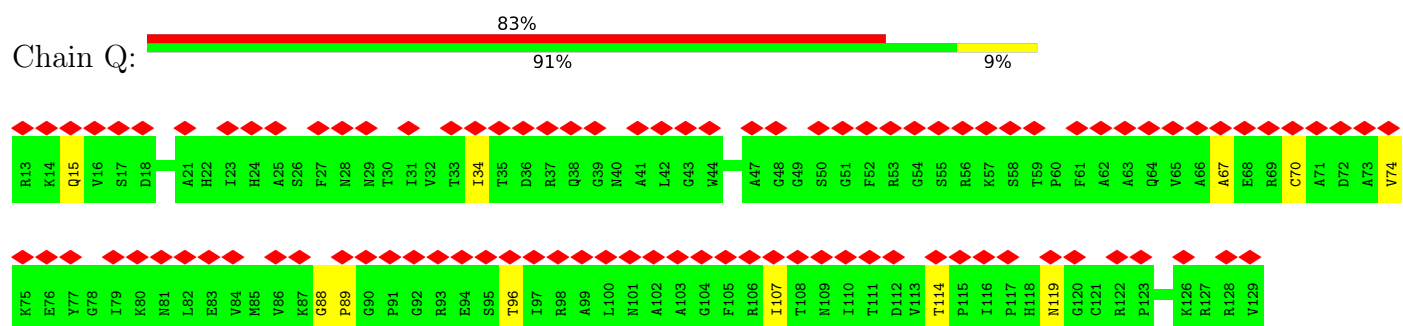
- Molecule 26: 30S ribosomal protein S9



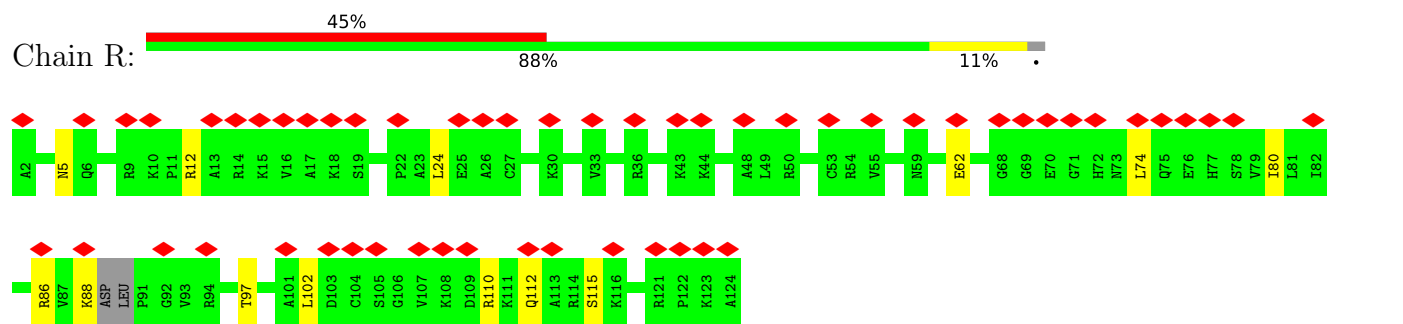
- Molecule 27: 30S ribosomal protein S10



- Molecule 28: 30S ribosomal protein S11

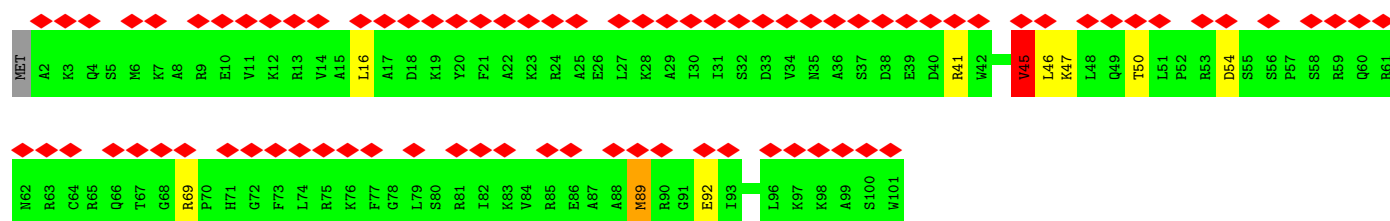


- Molecule 29: 30S ribosomal protein S12



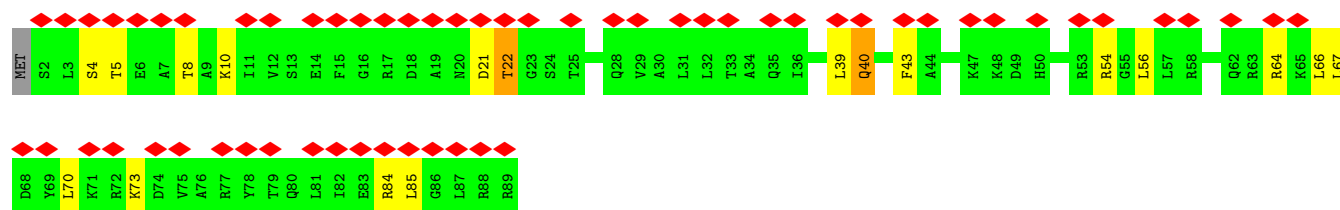
- Molecule 30: 30S ribosomal protein S14

Chain S: 



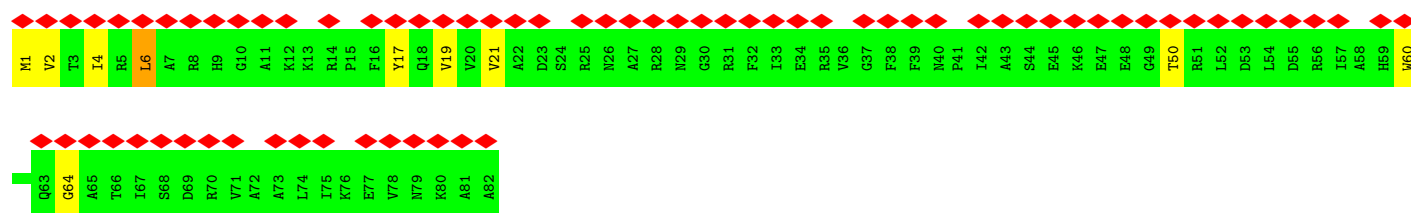
• Molecule 31: 30S ribosomal protein S15

Chain T: 



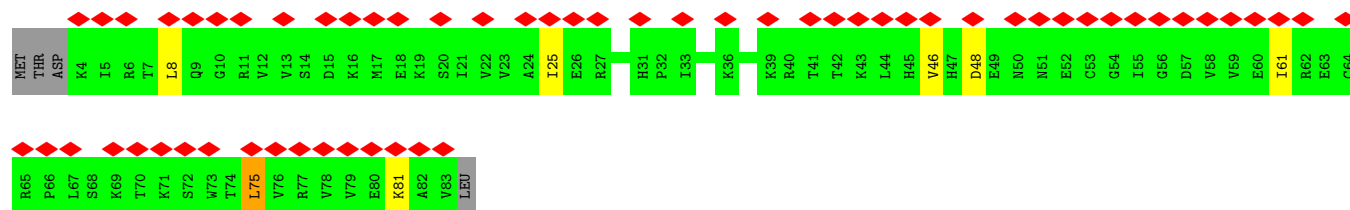
• Molecule 32: 30S ribosomal protein S16

Chain U: 

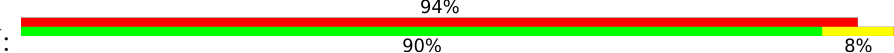


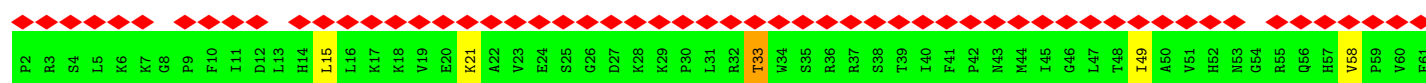
• Molecule 33: 30S ribosomal protein S17

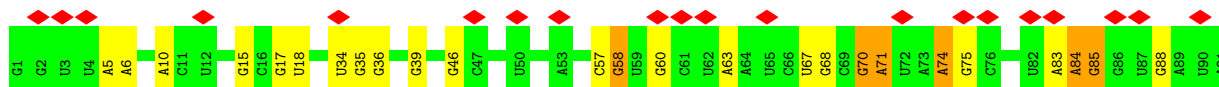
Chain V: 

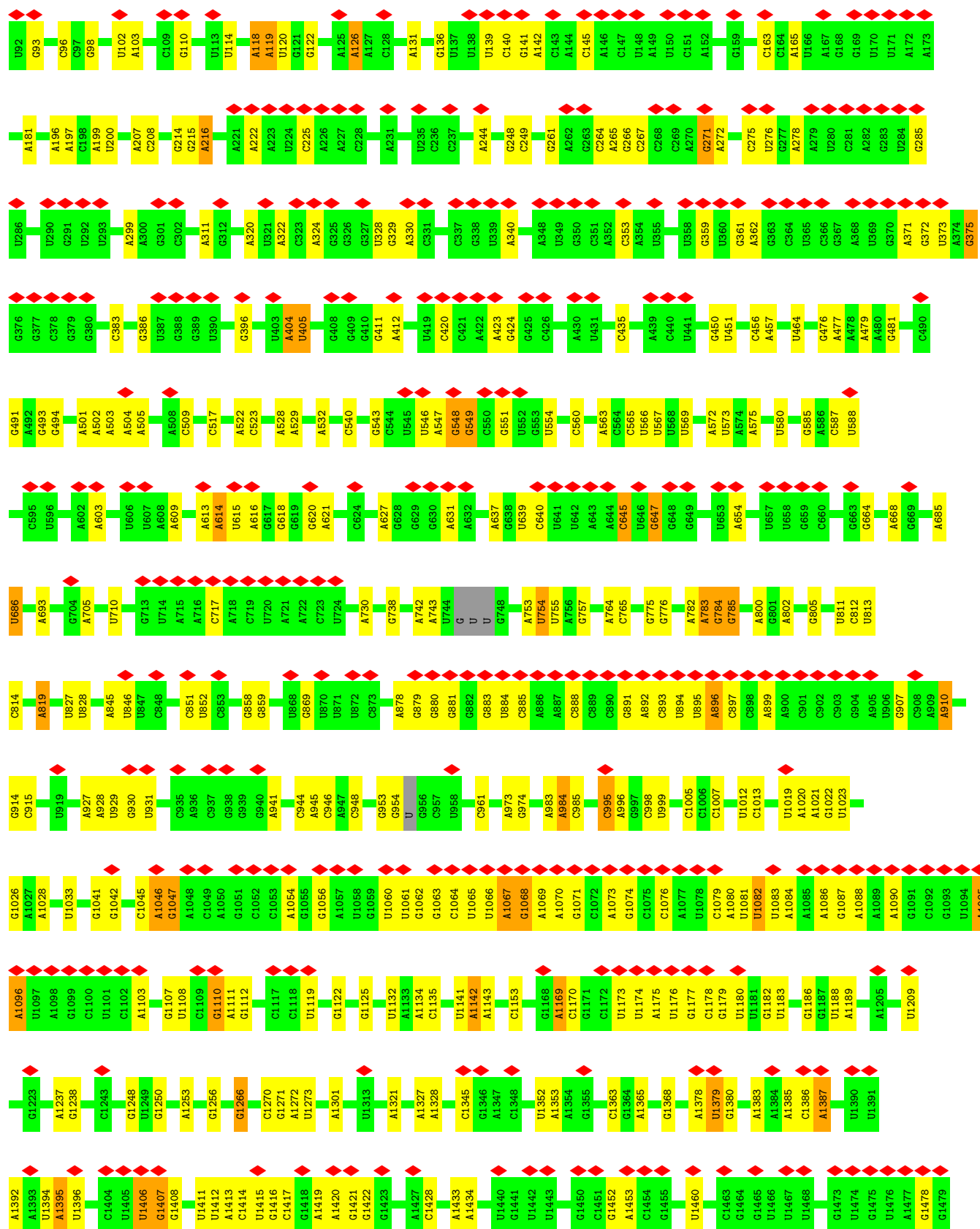


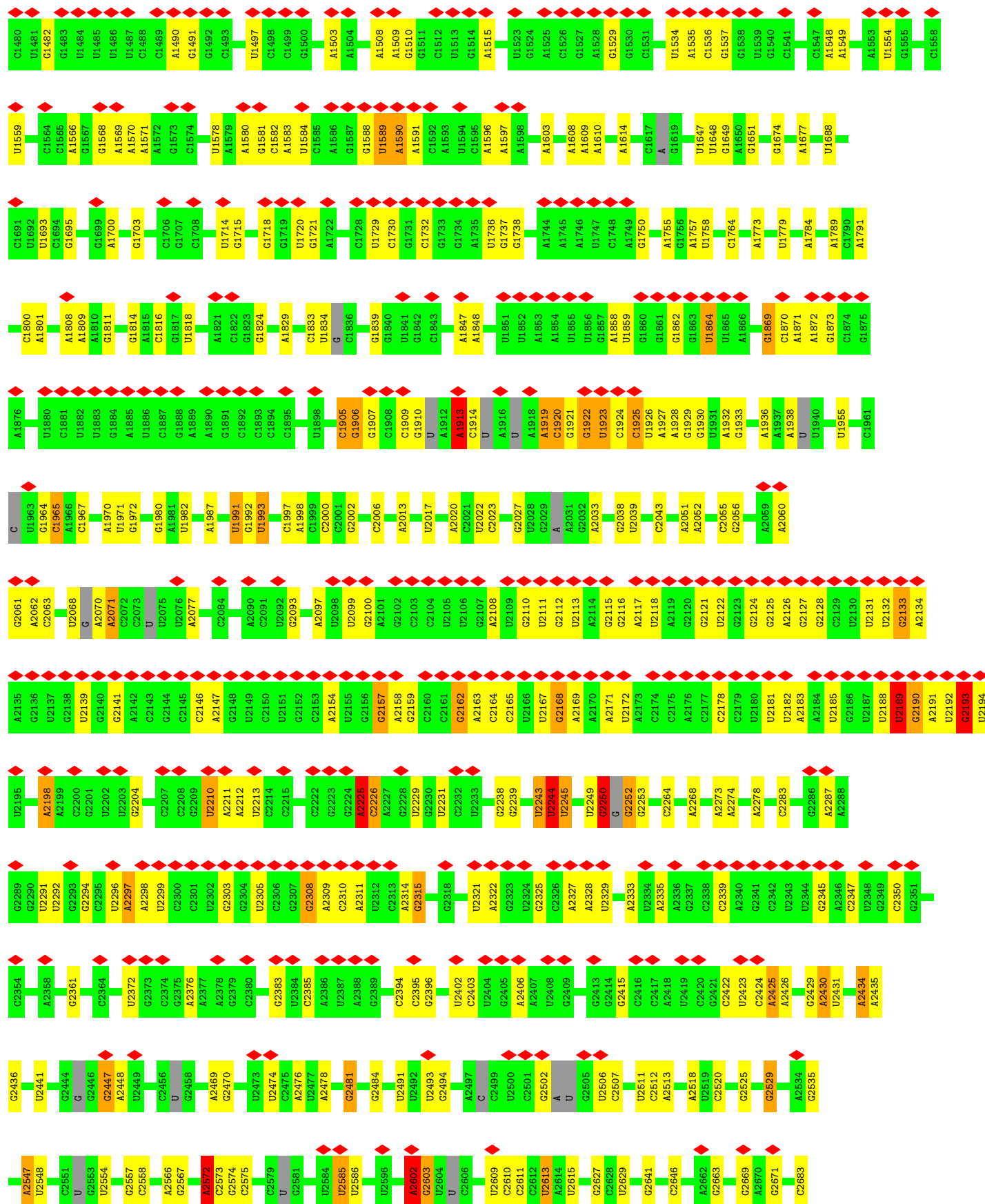
• Molecule 34: 30S ribosomal protein S19

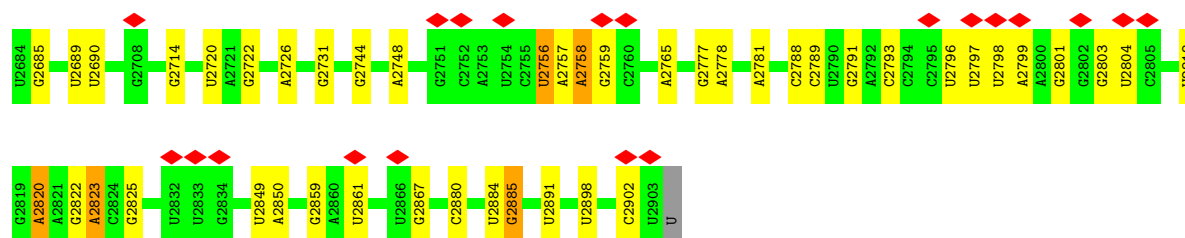
Chain W: 



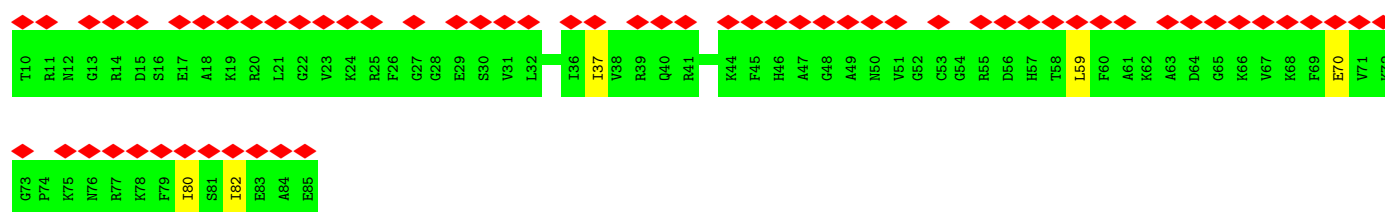
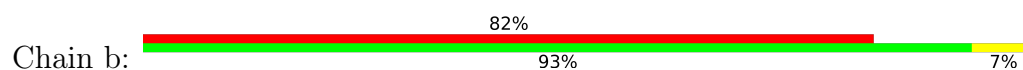




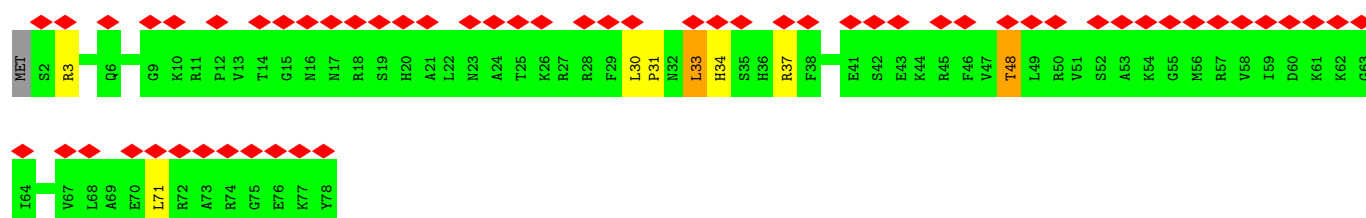
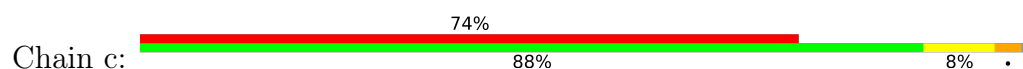




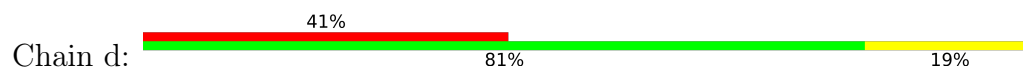
- Molecule 39: 50S ribosomal protein L27



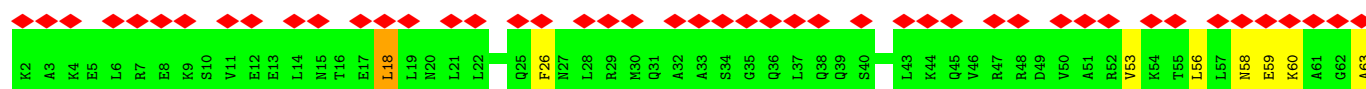
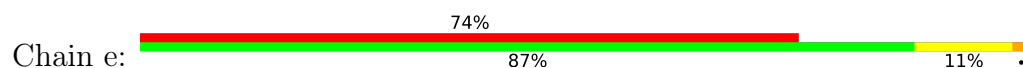
- Molecule 40: 50S ribosomal protein L28



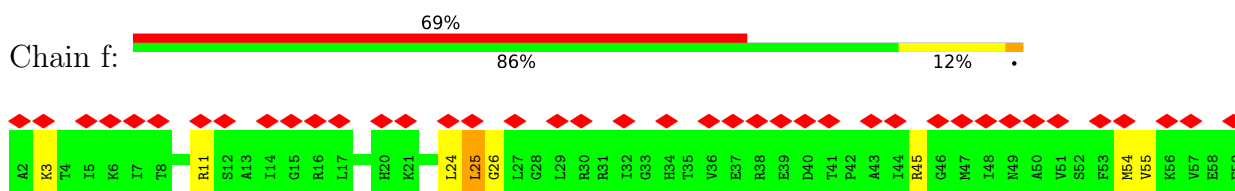
- Molecule 41: 5S rRNA



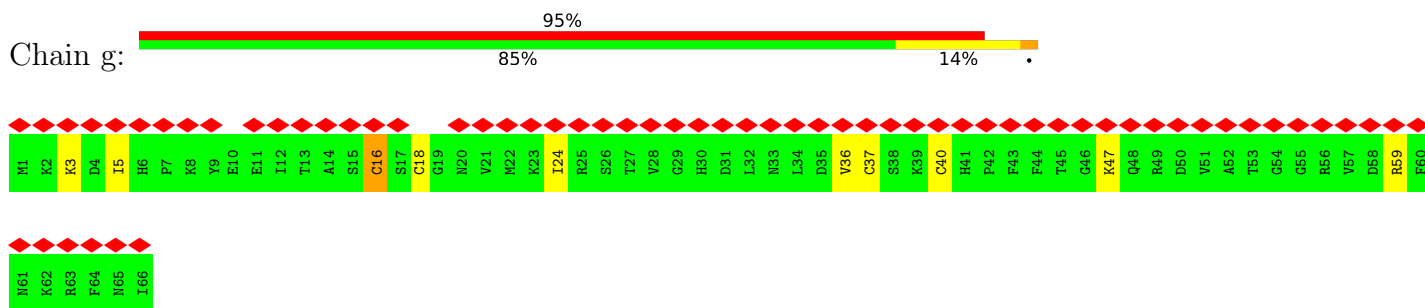
- Molecule 42: 50S ribosomal protein L29



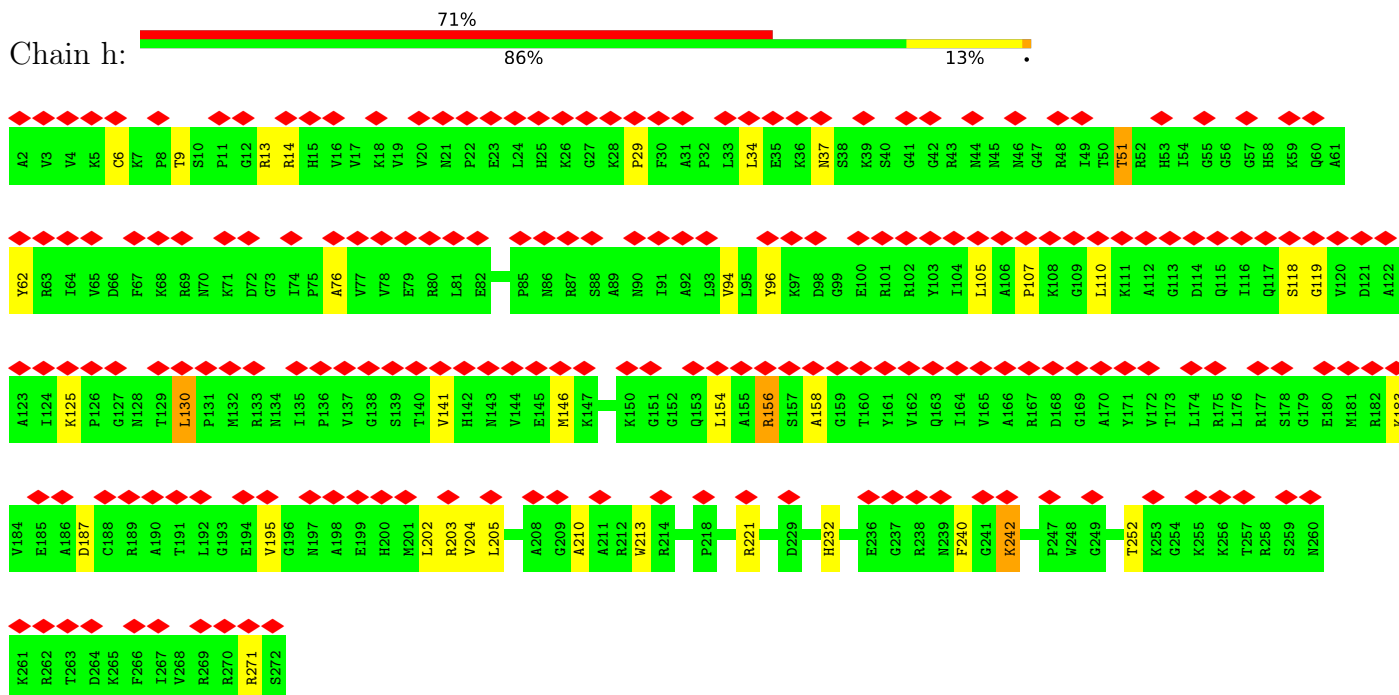
- Molecule 43: 50S ribosomal protein L30



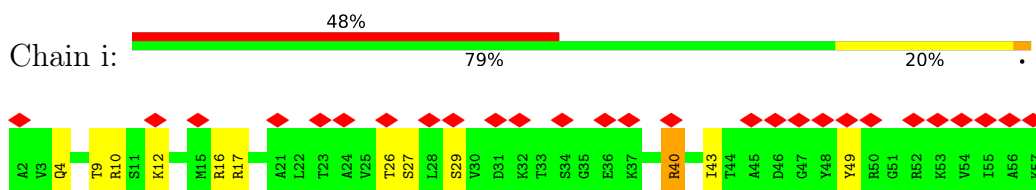
• Molecule 44: 50S ribosomal protein L31



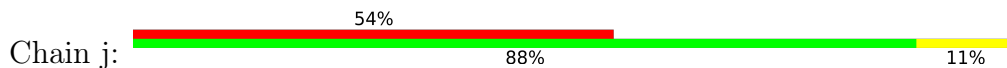
• Molecule 45: 50S ribosomal protein L2

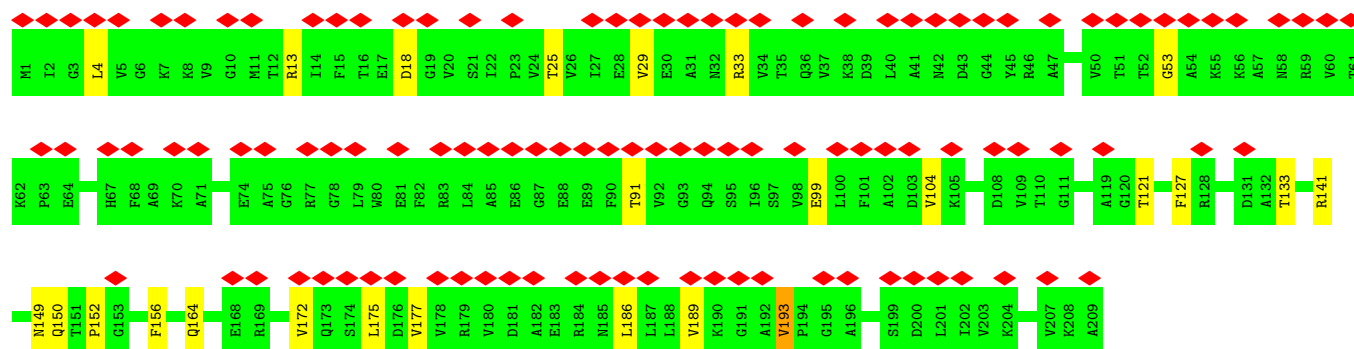


• Molecule 46: 50S ribosomal protein L32

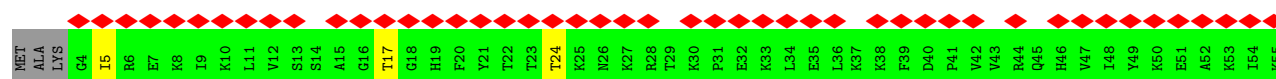
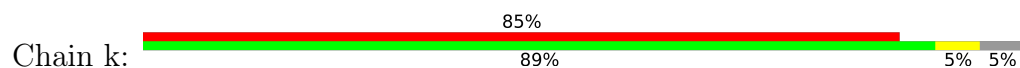


• Molecule 47: 50S ribosomal protein L3

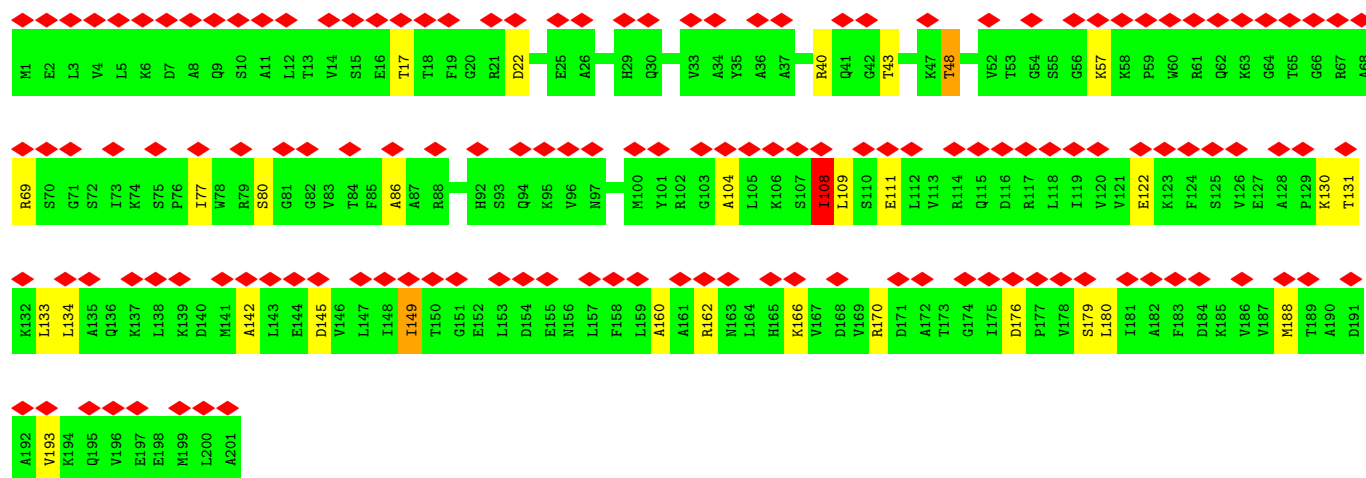
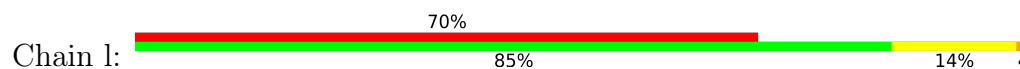




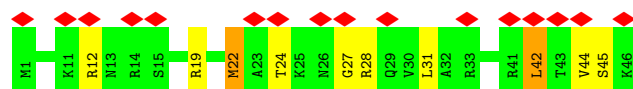
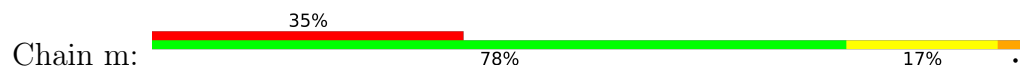
• Molecule 48: 50S ribosomal protein L33



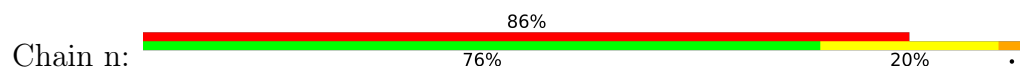
• Molecule 49: 50S ribosomal protein L4

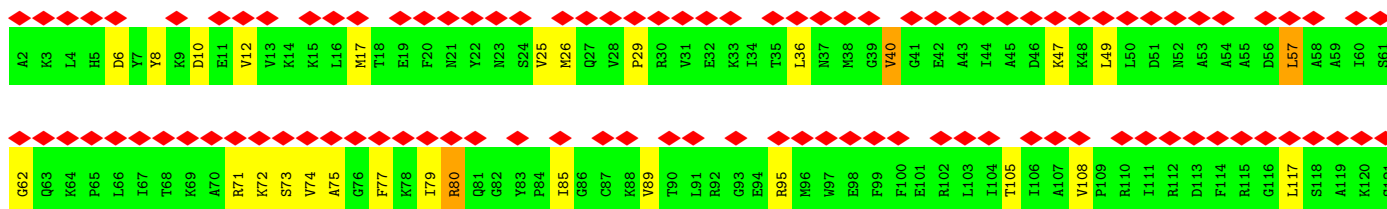


• Molecule 50: 50S ribosomal protein L34

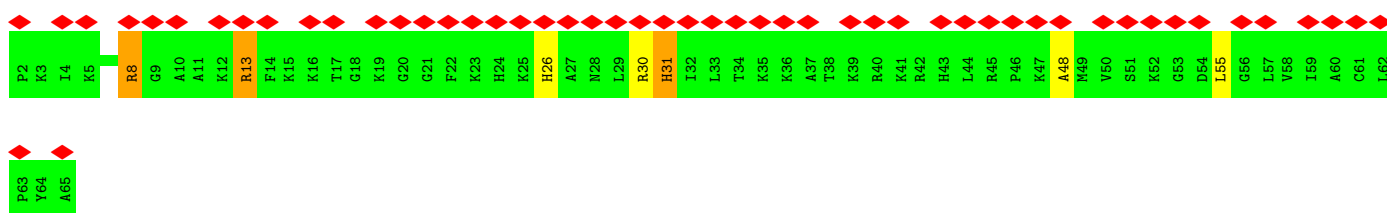
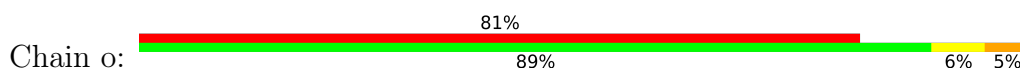


• Molecule 51: 50S ribosomal protein L5

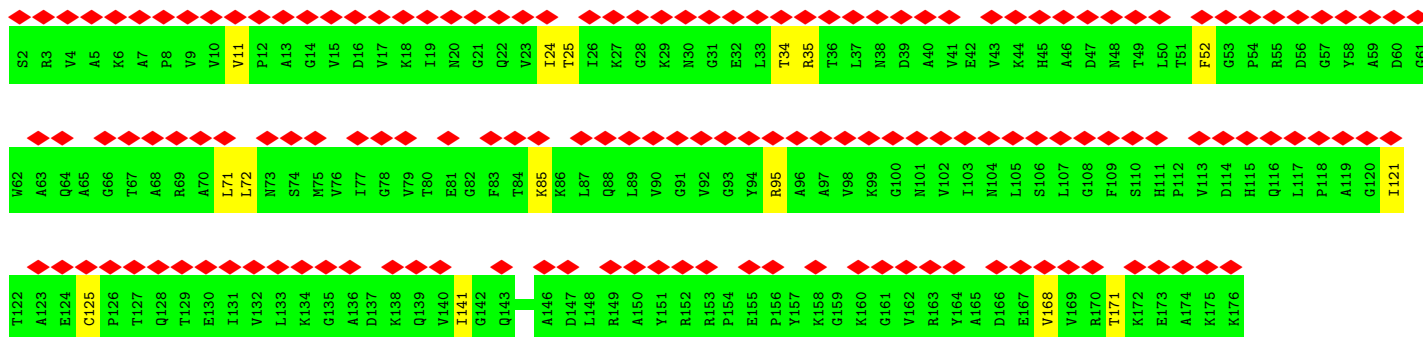
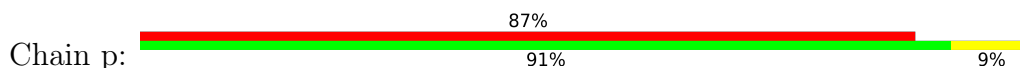




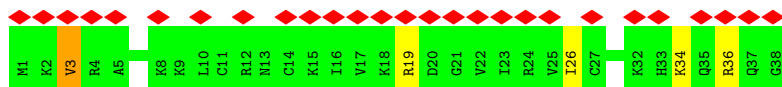
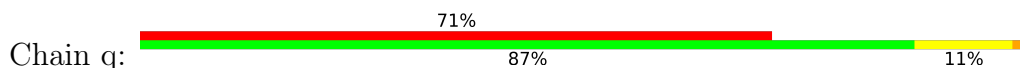
• Molecule 52: 50S ribosomal protein L35



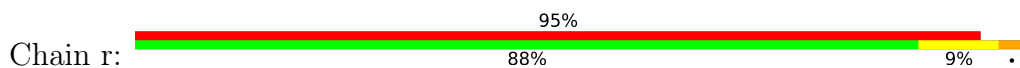
• Molecule 53: 50S ribosomal protein L6

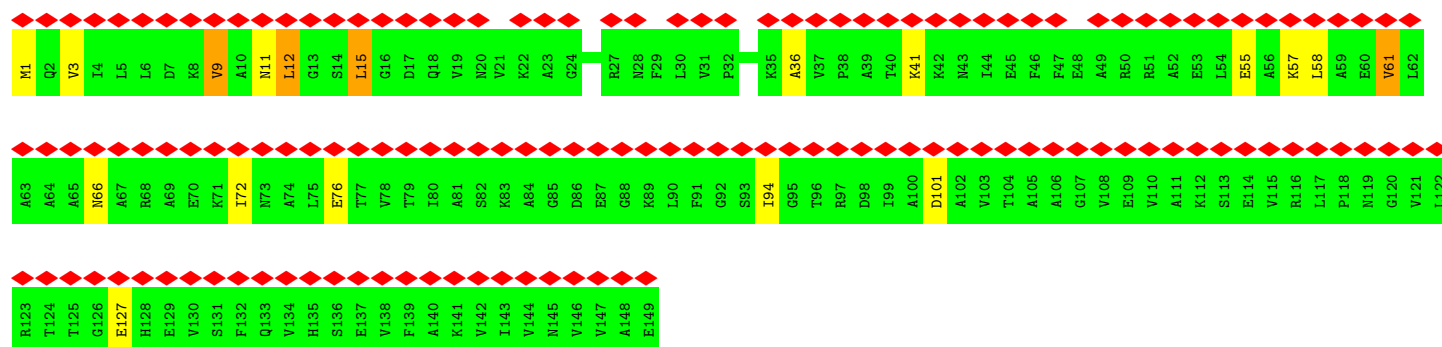


• Molecule 54: 50S ribosomal protein L36

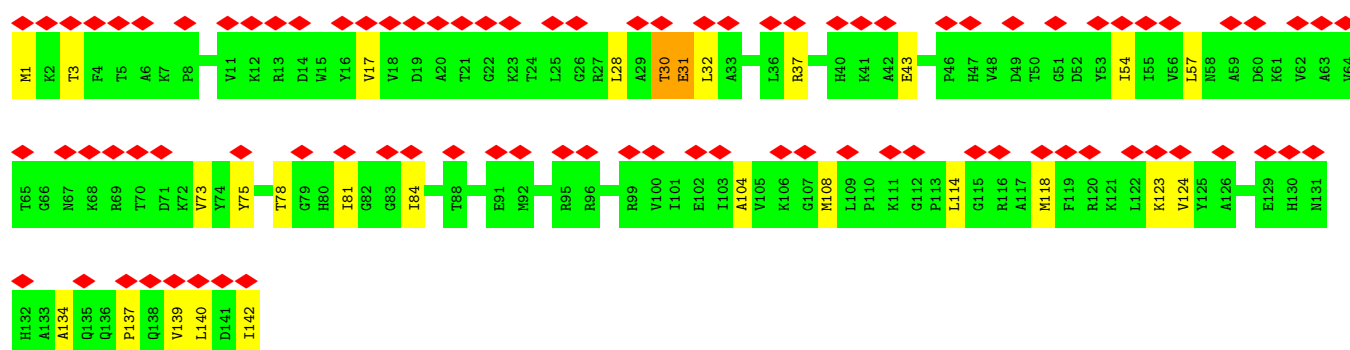
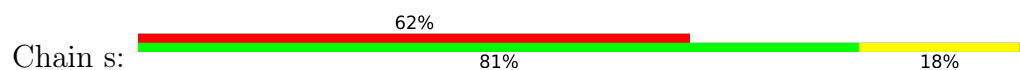


• Molecule 55: 50S ribosomal protein L9

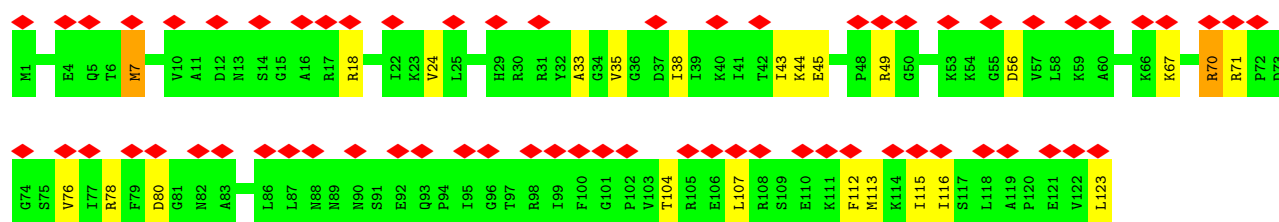
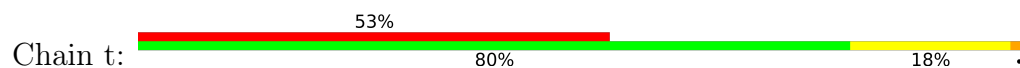




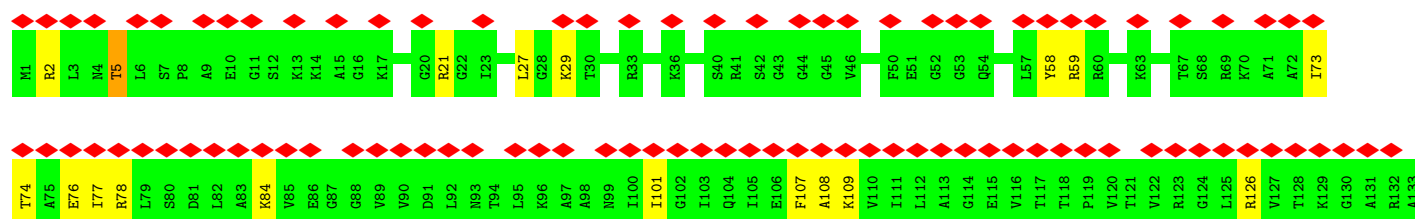
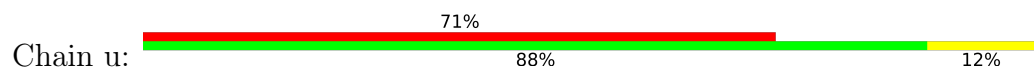
• Molecule 56: 50S ribosomal protein L13

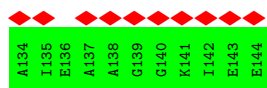


• Molecule 57: 50S ribosomal protein L14

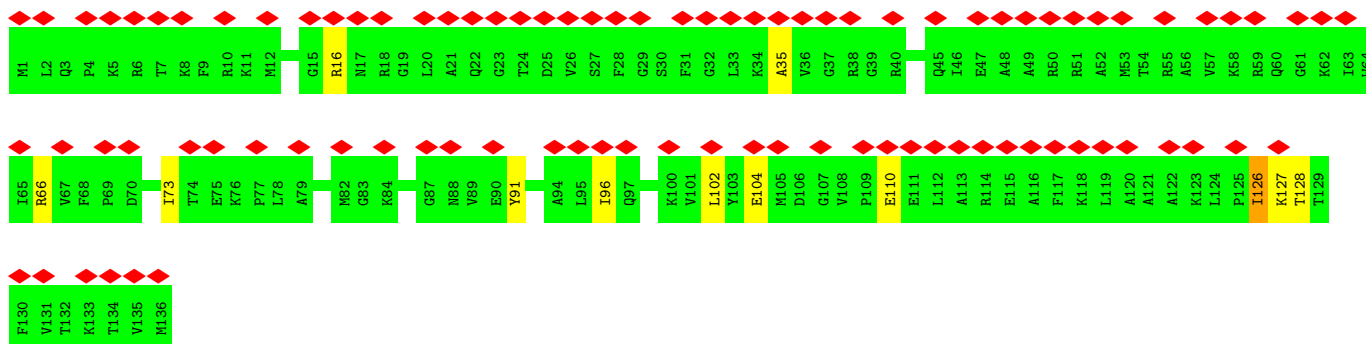
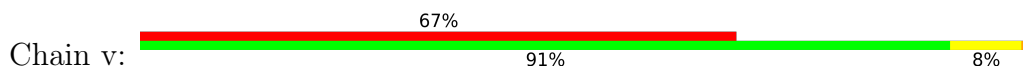


• Molecule 58: 50S ribosomal protein L15

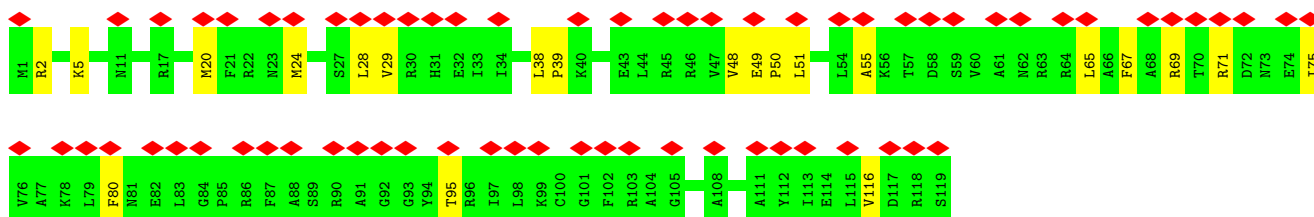
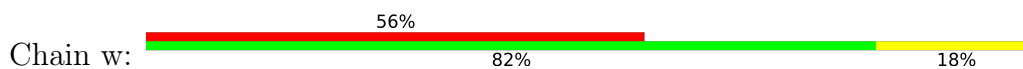




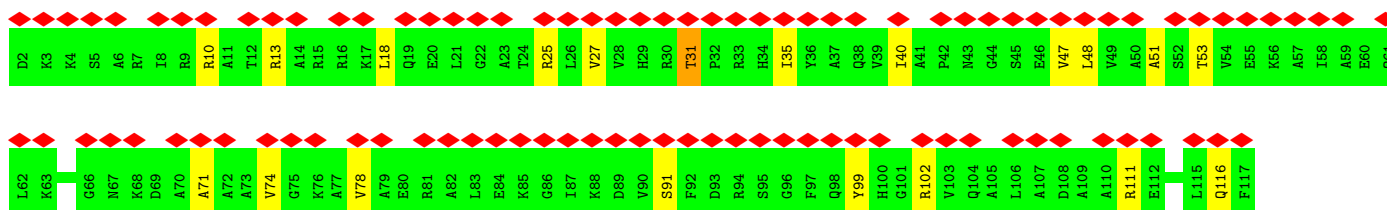
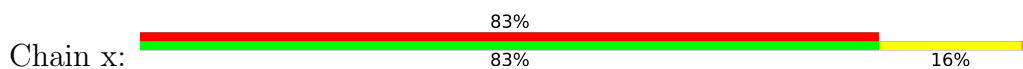
• Molecule 59: 50S ribosomal protein L16



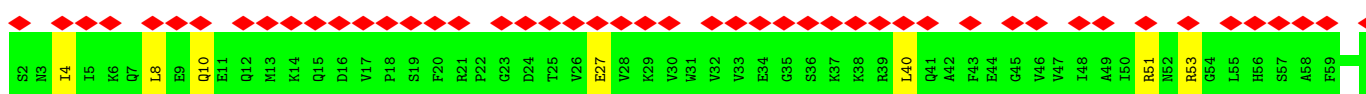
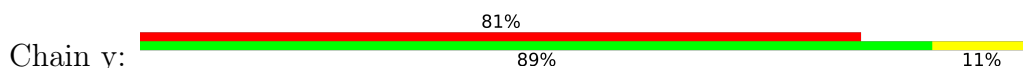
• Molecule 60: 50S ribosomal protein L17

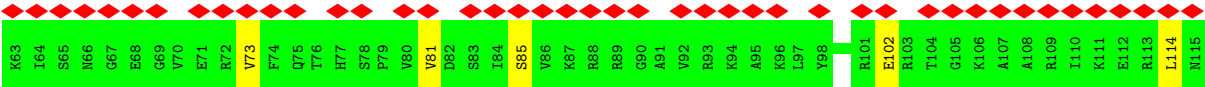


• Molecule 61: 50S ribosomal protein L18

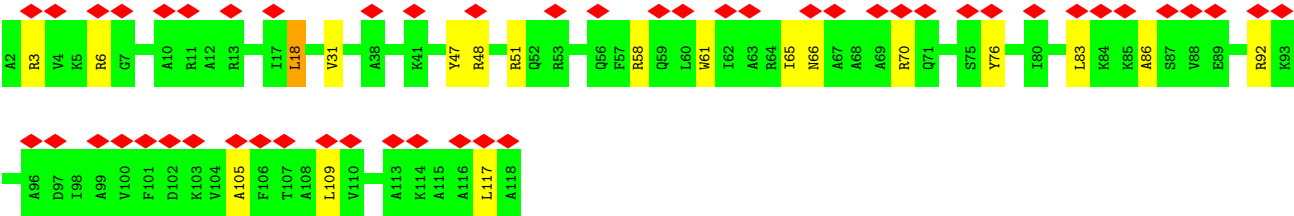
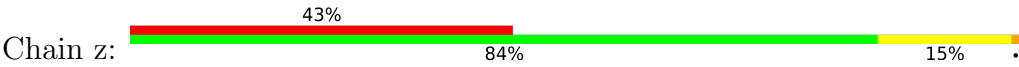


• Molecule 62: 50S ribosomal protein L19





• Molecule 63: 50S ribosomal protein L20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	27650	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	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	0.067	Depositor
Minimum map value	-0.032	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.017	Depositor
Map size ($\text{\AA}$)	532.48, 532.48, 532.48	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.04, 1.04, 1.04	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

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	0	0.49	0/829	0.74	0/1107
2	1	0.67	0/864	1.08	0/1156
3	2	0.54	0/752	0.89	0/1005
4	3	0.47	0/796	0.77	0/1062
5	4	0.52	0/766	0.88	0/1025
6	5	0.63	1/528 (0.2%)	0.55	0/810
7	6	0.55	1/603 (0.2%)	0.56	0/926
8	7	0.56	2/747 (0.3%)	0.81	2/1160 (0.2%)
9	9	1.15	3/1131 (0.3%)	1.30	4/1524 (0.3%)
10	A	0.36	0/1810	0.72	2/2821 (0.1%)
10	B	0.43	0/1810	0.87	9/2821 (0.3%)
11	AA	0.67	12/10591 (0.1%)	0.96	54/14289 (0.4%)
12	AC	0.60	3/1808 (0.2%)	0.73	9/2450 (0.4%)
12	AD	0.39	0/1789	0.56	0/2425
13	AE	0.54	9/10545 (0.1%)	0.74	23/14236 (0.2%)
14	C	0.66	0/553	1.15	2/743 (0.3%)
15	D	0.40	9/36610 (0.0%)	0.75	39/57091 (0.1%)
16	E	0.76	0/675	1.32	0/895
17	F	0.71	0/597	1.20	0/792
18	G	0.65	0/1791	1.08	1/2413 (0.0%)
19	H	0.76	4/1746 (0.2%)	1.58	34/2382 (1.4%)
20	I	0.58	0/1663	0.98	0/2241
21	J	0.63	0/1665	1.08	0/2227
22	K	0.63	1/1165 (0.1%)	1.06	2/1568 (0.1%)
23	L	0.58	0/867	0.94	0/1171
24	M	0.68	0/1195	1.19	3/1602 (0.2%)
25	N	0.55	0/989	0.91	0/1326
26	O	0.58	0/1034	1.02	1/1375 (0.1%)
27	P	0.60	0/800	1.11	4/1082 (0.4%)
28	Q	0.55	0/893	0.91	0/1205
29	R	0.49	0/952	0.81	0/1274
30	S	0.64	0/817	1.11	1/1088 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	T	0.69	0/722	1.21	0/964
32	U	0.58	0/659	0.99	0/884
33	V	0.46	0/657	0.73	0/881
34	W	0.51	0/680	0.83	0/915
35	X	0.67	0/909	1.21	3/1215 (0.2%)
36	Y	1.03	0/1046	1.08	0/1410
37	Z	1.03	0/227	1.13	0/304
38	a	0.40	3/69247 (0.0%)	0.75	57/107985 (0.1%)
39	b	0.50	0/589	0.76	0/779
40	c	0.63	0/635	0.97	0/848
41	d	0.37	0/2872	0.69	0/4478
42	e	0.69	0/502	1.19	0/667
43	f	0.62	0/452	1.02	0/605
44	g	0.55	0/531	0.99	1/709 (0.1%)
45	h	0.54	0/2121	0.85	0/2852
46	i	0.52	0/450	0.94	0/599
47	j	0.59	0/1586	0.87	0/2134
48	k	0.47	0/433	0.80	0/576
49	l	0.61	0/1571	1.03	1/2113 (0.0%)
50	m	0.68	0/380	1.22	0/498
51	n	0.62	0/1434	1.18	10/1926 (0.5%)
52	o	0.63	0/513	1.10	1/676 (0.1%)
53	p	0.58	0/1333	0.89	0/1805
54	q	0.50	0/303	0.88	0/397
55	r	0.63	0/1122	0.97	1/1515 (0.1%)
56	s	0.68	0/1152	1.02	2/1551 (0.1%)
57	t	0.57	0/955	0.88	0/1279
58	u	0.54	0/1062	0.95	1/1413 (0.1%)
59	v	0.59	0/1093	0.97	0/1460
60	w	0.67	0/964	1.13	0/1289
61	x	0.61	0/902	1.09	0/1209
62	y	0.52	0/929	0.79	0/1242
63	z	0.80	0/960	1.25	0/1278
All	All	0.50	48/188372 (0.0%)	0.84	267/277748 (0.1%)

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
10	A	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	B	0	2
11	AA	0	10
13	AE	0	5
19	H	0	3
35	X	0	1
All	All	0	23

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	18.18	1.70	1.47
11	AA	374	GLU	C-N	17.55	1.54	1.33
11	AA	850	ILE	N-CA	-13.11	1.29	1.46
13	AE	93	THR	CA-C	12.23	1.69	1.52
19	H	169	SER	N-CA	11.75	1.61	1.46

The worst 5 of 267 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	D	1516	G	O3'-P-O5'	17.49	130.24	104.00
11	AA	727	VAL	N-CA-C	-17.26	95.03	110.74
19	H	88	LYS	CA-C-N	16.90	143.53	120.38
19	H	88	LYS	C-N-CA	16.90	143.53	120.38
10	B	29	G	C3'-C2'-O2'	15.98	134.67	110.70

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	A	19	G	Sidechain
10	A	7	G	Sidechain
11	AA	205	PRO	Peptide
11	AA	594	VAL	Peptide
11	AA	595	THR	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	0	816	839	839	8	0
2	1	857	922	922	14	0
3	2	746	811	811	6	0
4	3	788	844	844	11	0
5	4	753	780	780	0	0
6	5	472	260	261	24	0
7	6	542	305	306	26	0
8	7	672	97	332	80	0
9	9	1117	0	1153	164	0
10	A	1620	826	826	175	0
10	B	1620	813	827	137	0
11	AA	10425	10426	10428	390	0
12	AC	1786	1813	1813	87	0
12	AD	1767	1789	1789	48	0
13	AE	10388	10612	10611	364	0
14	C	544	559	560	23	0
15	D	32703	16423	16459	225	0
16	E	669	719	719	3	0
17	F	589	629	629	8	0
18	G	1760	1785	1785	47	0
19	H	1730	1454	1454	211	0
20	I	1636	1710	1710	41	0
21	J	1643	1707	1707	30	0
22	K	1152	1196	1196	22	0
23	L	848	846	846	3	0
24	M	1181	1235	1235	34	0
25	N	979	1031	1031	5	0
26	O	1022	1070	1070	13	0
27	P	790	831	831	45	0
28	Q	877	887	887	4	0
29	R	939	1001	1001	7	0
30	S	805	844	844	5	0
31	T	714	734	734	8	0
32	U	649	666	666	3	0
33	V	648	691	691	4	0
34	W	663	688	688	2	0
35	X	900	964	964	57	0
36	Y	1032	0	1088	85	0
37	Z	227	0	237	18	0
38	a	61841	31077	31123	302	0
39	b	582	599	599	3	0
40	c	625	652	652	4	0
41	d	2569	1301	1301	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	e	501	531	531	5	0
43	f	448	488	488	5	0
44	g	522	520	520	11	0
45	h	2082	2154	2154	19	0
46	i	444	459	458	6	0
47	j	1565	1617	1616	15	0
48	k	426	464	464	0	0
49	l	1552	1619	1619	14	0
50	m	377	418	418	10	0
51	n	1410	1443	1444	28	0
52	o	504	572	572	4	0
53	p	1313	1358	1358	7	0
54	q	302	343	343	2	0
55	r	1111	1148	1148	6	0
56	s	1129	1162	1162	15	0
57	t	946	1023	1023	12	0
58	u	1053	1129	1129	9	0
59	v	1074	1157	1157	5	0
60	w	951	994	994	8	0
61	x	892	923	923	9	0
62	y	917	962	962	4	0
63	z	947	1020	1019	14	0
64	AE	1	0	0	0	0
65	AE	2	0	0	0	0
All	All	175155	123940	126751	2450	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 2450 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)
14:C:12:ARG:HG3	19:H:264:GLU:CB	1.30	1.58
19:H:131:LEU:CB	19:H:167:VAL:CA	1.78	1.57
19:H:131:LEU:CB	19:H:167:VAL:HA	1.03	1.48
12:AC:117:HIS:O	27:P:89:ARG:CB	1.64	1.46
9:9:31:ARG:NE	38:a:1054:A:H5'	1.31	1.43

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	0	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	12	46
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/100 (92%)	90 (98%)	2 (2%)	0	100	100
4	3	101/104 (97%)	96 (95%)	4 (4%)	1 (1%)	12	46
5	4	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
9	9	146/165 (88%)	95 (65%)	37 (25%)	14 (10%)	0	8
11	AA	1318/1342 (98%)	1150 (87%)	136 (10%)	32 (2%)	4	30
12	AC	228/329 (69%)	215 (94%)	11 (5%)	2 (1%)	14	49
12	AD	226/329 (69%)	212 (94%)	14 (6%)	0	100	100
13	AE	1329/1407 (94%)	1200 (90%)	120 (9%)	9 (1%)	18	55
14	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
16	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
17	F	68/71 (96%)	68 (100%)	0	0	100	100
18	G	223/241 (92%)	210 (94%)	13 (6%)	0	100	100
19	H	255/557 (46%)	188 (74%)	55 (22%)	12 (5%)	2	19
20	I	206/233 (88%)	197 (96%)	8 (4%)	1 (0%)	24	61
21	J	203/205 (99%)	198 (98%)	5 (2%)	0	100	100
22	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	21	58
23	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	46
24	M	149/151 (99%)	144 (97%)	4 (3%)	1 (1%)	18	55
25	N	127/129 (98%)	121 (95%)	5 (4%)	1 (1%)	16	52
26	O	125/127 (98%)	115 (92%)	9 (7%)	1 (1%)	16	52
27	P	97/99 (98%)	88 (91%)	8 (8%)	1 (1%)	12	46
28	Q	115/117 (98%)	104 (90%)	9 (8%)	2 (2%)	7	36
29	R	117/123 (95%)	116 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	S	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
31	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
32	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	9	41
33	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
34	W	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
35	X	114/116 (98%)	107 (94%)	5 (4%)	2 (2%)	6	35
36	Y	139/141 (99%)	102 (73%)	25 (18%)	12 (9%)	0	10
37	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	13
39	b	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
40	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
42	e	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
43	f	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
44	g	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
45	h	269/271 (99%)	259 (96%)	9 (3%)	1 (0%)	30	65
46	i	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
47	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
48	k	50/55 (91%)	50 (100%)	0	0	100	100
49	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	24	61
50	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
51	n	175/177 (99%)	162 (93%)	11 (6%)	2 (1%)	11	44
52	o	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
53	p	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
54	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
55	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
56	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
57	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
58	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
59	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
60	w	117/119 (98%)	107 (92%)	10 (8%)	0	100	100
61	x	114/116 (98%)	108 (95%)	6 (5%)	0	100	100
62	y	112/114 (98%)	105 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	z	115/117 (98%)	110 (96%)	4 (4%)	1 (1%)	14	49
All	All	9274/10209 (91%)	8519 (92%)	653 (7%)	102 (1%)	14	44

5 of 102 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
11	AA	596	ASP
11	AA	853	ASP
11	AA	859	GLU
11	AA	862	LEU

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	0	84/84 (100%)	76 (90%)	8 (10%)	8	27
2	1	93/93 (100%)	86 (92%)	7 (8%)	12	35
3	2	81/84 (96%)	77 (95%)	4 (5%)	22	46
4	3	84/85 (99%)	79 (94%)	5 (6%)	17	42
5	4	78/78 (100%)	75 (96%)	3 (4%)	29	51
9	9	112/123 (91%)	63 (56%)	49 (44%)	0	0
11	AA	1140/1157 (98%)	1027 (90%)	113 (10%)	7	26
12	AC	198/286 (69%)	183 (92%)	15 (8%)	12	35
12	AD	196/286 (68%)	193 (98%)	3 (2%)	57	70
13	AE	1120/1168 (96%)	1046 (93%)	74 (7%)	15	39
14	C	57/65 (88%)	55 (96%)	2 (4%)	32	54
16	E	65/66 (98%)	61 (94%)	4 (6%)	16	41
17	F	60/61 (98%)	57 (95%)	3 (5%)	22	45
18	G	187/199 (94%)	174 (93%)	13 (7%)	14	38
19	H	137/461 (30%)	124 (90%)	13 (10%)	8	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	I	171/190 (90%)	163 (95%)	8 (5%)	23	47
21	J	172/172 (100%)	164 (95%)	8 (5%)	23	47
22	K	119/126 (94%)	111 (93%)	8 (7%)	15	39
23	L	91/116 (78%)	84 (92%)	7 (8%)	12	34
24	M	124/124 (100%)	113 (91%)	11 (9%)	9	30
25	N	104/104 (100%)	101 (97%)	3 (3%)	37	58
26	O	105/105 (100%)	99 (94%)	6 (6%)	18	43
27	P	86/86 (100%)	76 (88%)	10 (12%)	5	21
28	Q	90/90 (100%)	88 (98%)	2 (2%)	45	64
29	R	101/103 (98%)	95 (94%)	6 (6%)	18	42
30	S	83/84 (99%)	79 (95%)	4 (5%)	23	46
31	T	76/77 (99%)	65 (86%)	11 (14%)	3	16
32	U	65/65 (100%)	60 (92%)	5 (8%)	12	34
33	V	74/78 (95%)	71 (96%)	3 (4%)	27	50
34	W	72/72 (100%)	66 (92%)	6 (8%)	10	32
35	X	94/94 (100%)	87 (93%)	7 (7%)	13	35
36	Y	109/109 (100%)	69 (63%)	40 (37%)	0	1
37	Z	26/85 (31%)	10 (38%)	16 (62%)	0	0
39	b	58/58 (100%)	57 (98%)	1 (2%)	53	68
40	c	67/68 (98%)	64 (96%)	3 (4%)	24	48
42	e	54/54 (100%)	51 (94%)	3 (6%)	19	43
43	f	48/48 (100%)	43 (90%)	5 (10%)	7	24
44	g	59/59 (100%)	54 (92%)	5 (8%)	10	32
45	h	216/216 (100%)	199 (92%)	17 (8%)	11	34
46	i	47/47 (100%)	41 (87%)	6 (13%)	4	19
47	j	164/164 (100%)	156 (95%)	8 (5%)	22	46
48	k	47/49 (96%)	44 (94%)	3 (6%)	16	40
49	l	165/165 (100%)	151 (92%)	14 (8%)	10	32
50	m	38/38 (100%)	36 (95%)	2 (5%)	20	44
51	n	148/148 (100%)	130 (88%)	18 (12%)	5	20
52	o	51/51 (100%)	47 (92%)	4 (8%)	11	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	p	136/136 (100%)	130 (96%)	6 (4%)	25	48
54	q	34/34 (100%)	31 (91%)	3 (9%)	9	31
55	r	114/114 (100%)	102 (90%)	12 (10%)	6	24
56	s	116/116 (100%)	106 (91%)	10 (9%)	10	32
57	t	104/104 (100%)	97 (93%)	7 (7%)	15	39
58	u	103/103 (100%)	96 (93%)	7 (7%)	14	38
59	v	109/109 (100%)	105 (96%)	4 (4%)	30	52
60	w	99/99 (100%)	91 (92%)	8 (8%)	11	33
61	x	86/86 (100%)	80 (93%)	6 (7%)	14	38
62	y	99/99 (100%)	91 (92%)	8 (8%)	11	33
63	z	89/89 (100%)	85 (96%)	4 (4%)	24	48
All	All	7705/8430 (91%)	7064 (92%)	641 (8%)	12	32

5 of 641 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	Z	3	THR
54	q	26	ILE
37	Z	30	PHE
37	Z	2	ILE
47	j	99	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
16	E	55	GLN
53	p	88	GLN
21	J	36	GLN
52	o	28	ASN
57	t	88	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	6 (8%)
10	B	75/76 (98%)	35 (46%)	6 (8%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	D	1515/1542 (98%)	289 (19%)	35 (2%)
38	a	2859/2904 (98%)	541 (18%)	0
41	d	119/120 (99%)	17 (14%)	0
8	7	31/32 (96%)	21 (67%)	3 (9%)
All	All	4674/4750 (98%)	932 (19%)	50 (1%)

5 of 932 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-9	G
8	7	-8	U
8	7	-7	U
8	7	-5	U
8	7	-4	U

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
15	D	532	A
15	D	1109	C
15	D	1493	A
15	D	562	U
15	D	793	U

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

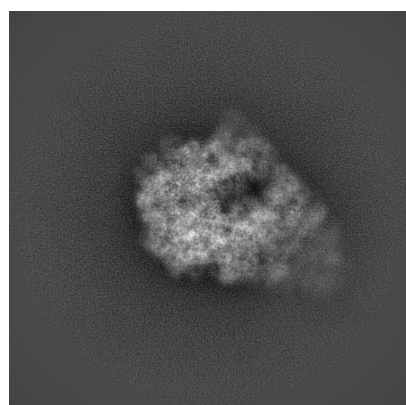
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21494. These allow visual inspection of the internal detail of the map and identification of artifacts.

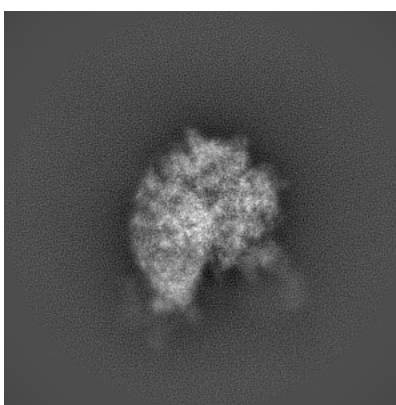
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

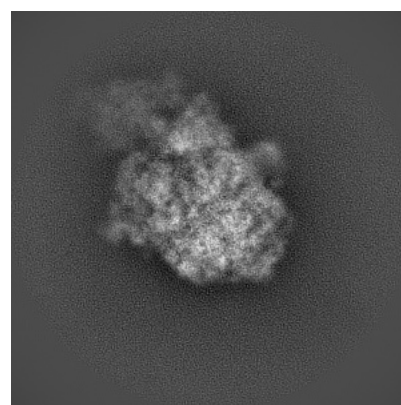
6.1.1 Primary map



X



Y

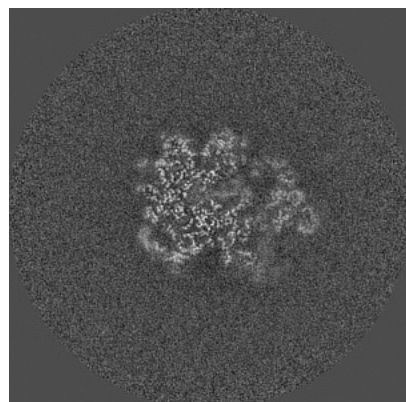


Z

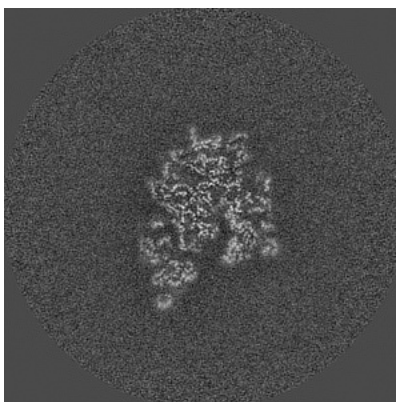
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

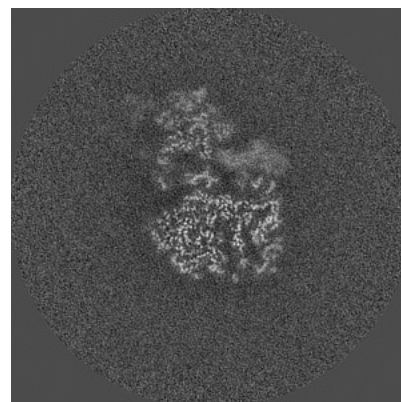
6.2.1 Primary map



X Index: 256



Y Index: 256

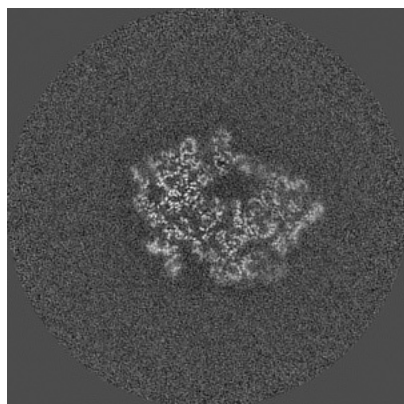


Z Index: 256

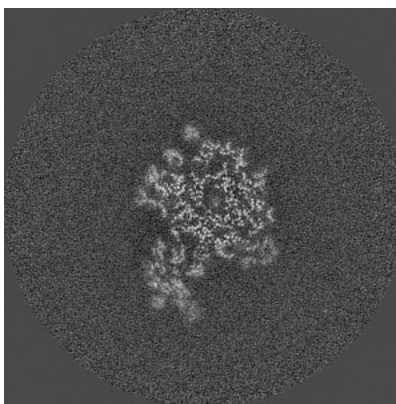
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

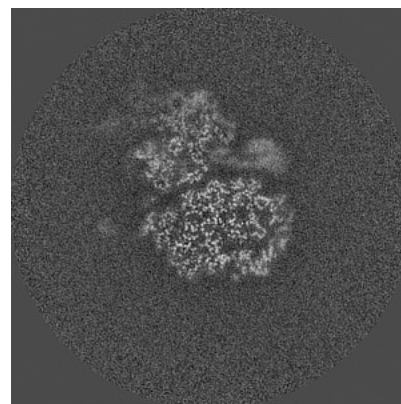
6.3.1 Primary map



X Index: 240



Y Index: 231

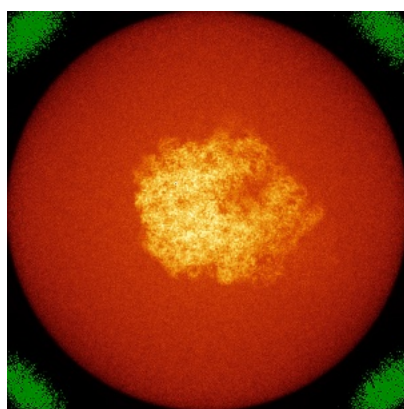


Z Index: 248

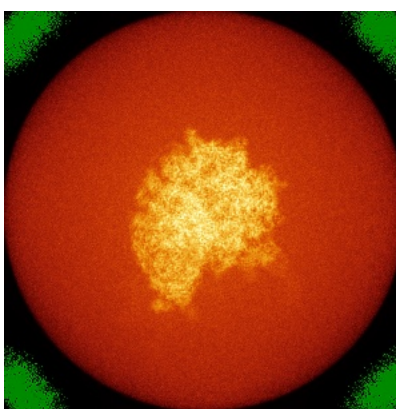
The images above show the largest variance slices of the map in three orthogonal directions.

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

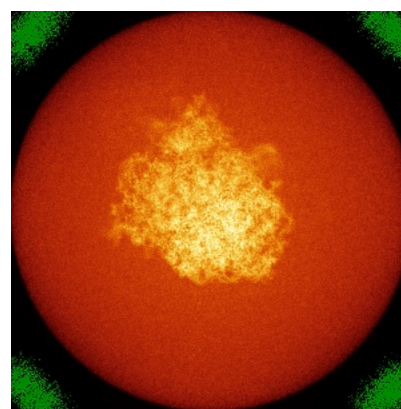
6.4.1 Primary map



X



Y

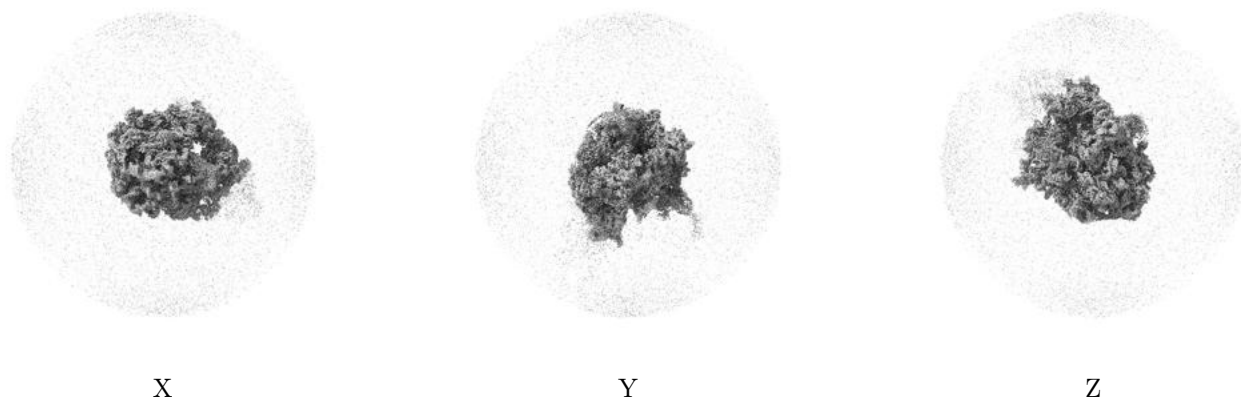


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.017. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

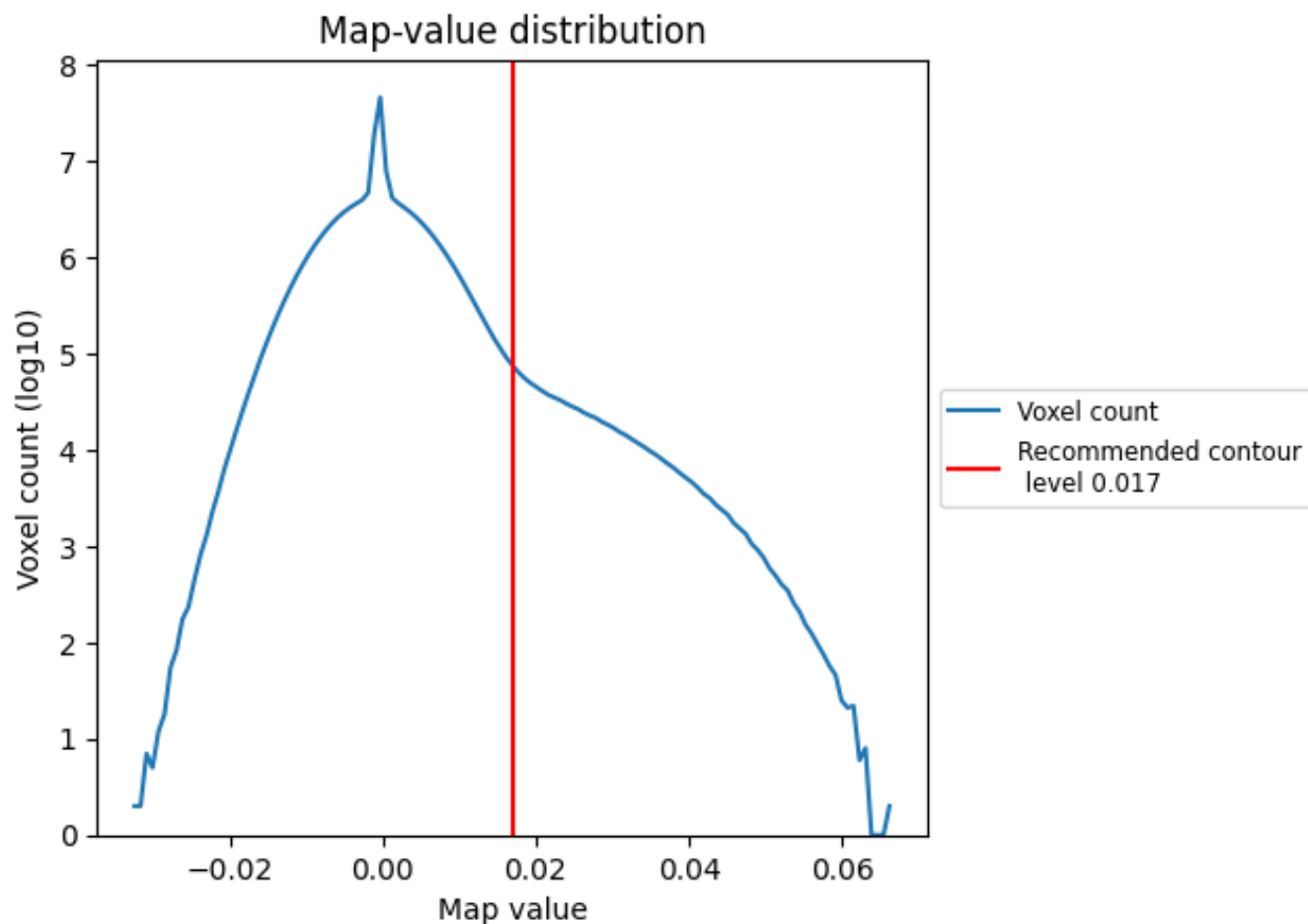
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

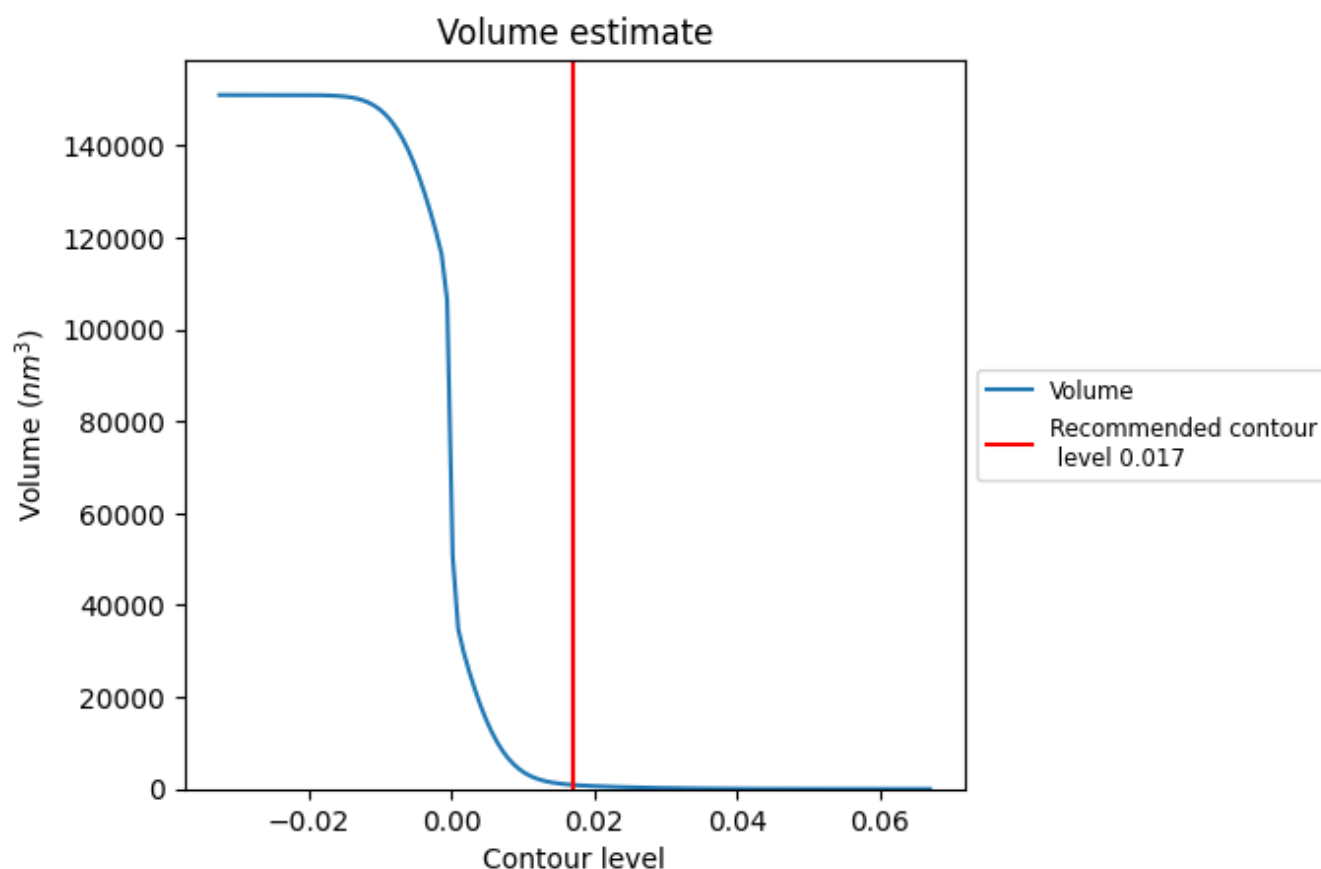
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

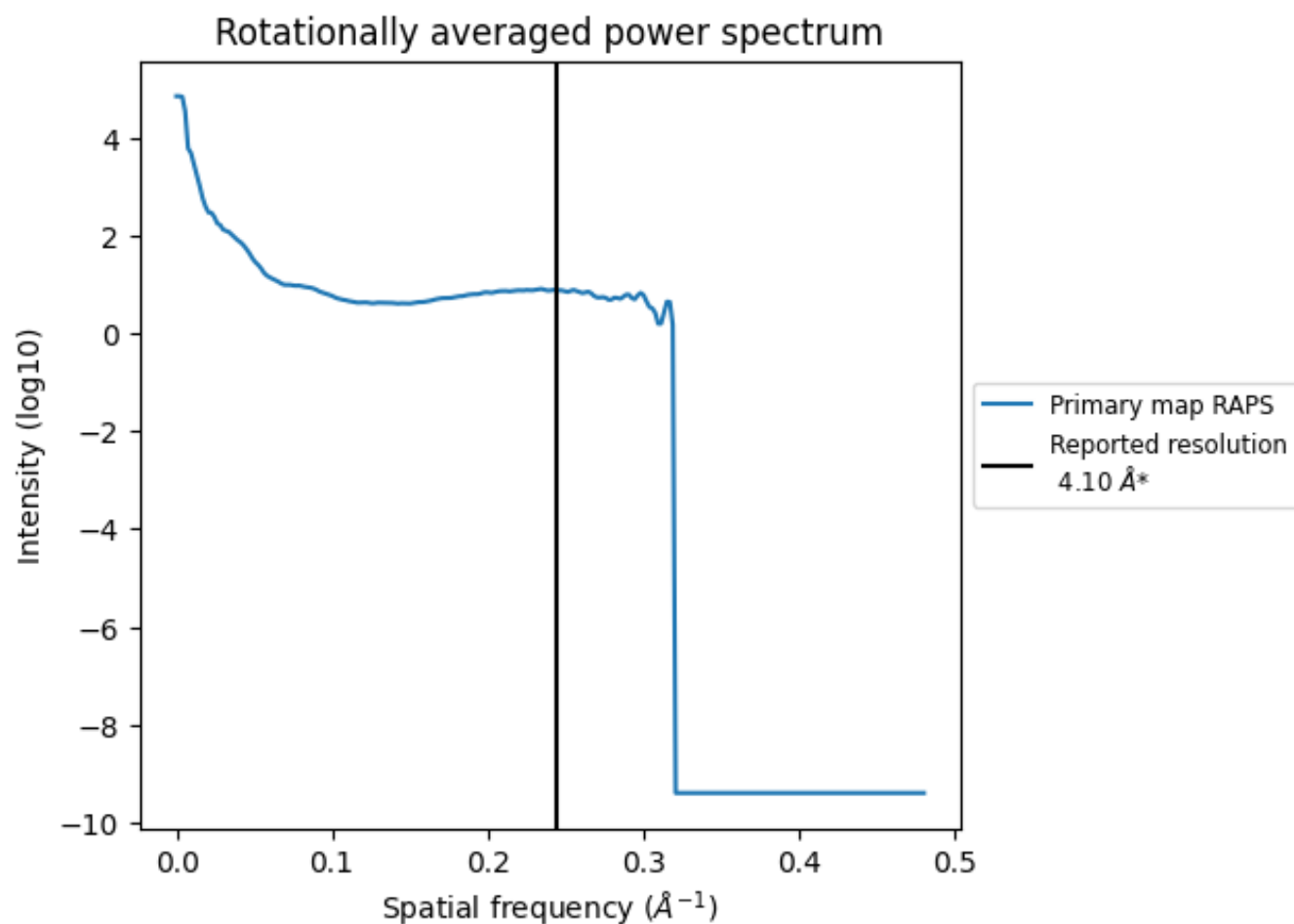
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 887 nm^3 ; this corresponds to an approximate mass of 801 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 0.244 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

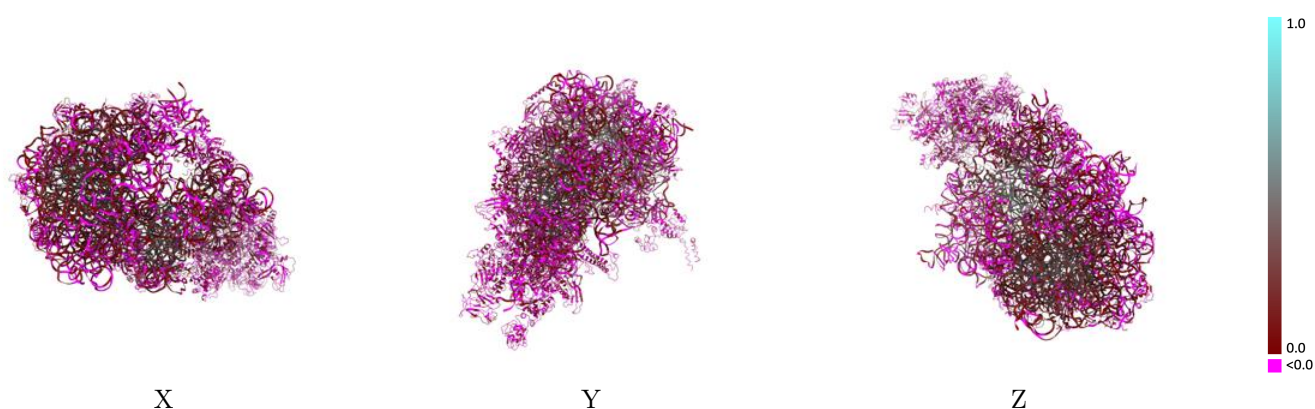
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21494 and PDB model 6VZJ. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)

This section was not generated.

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

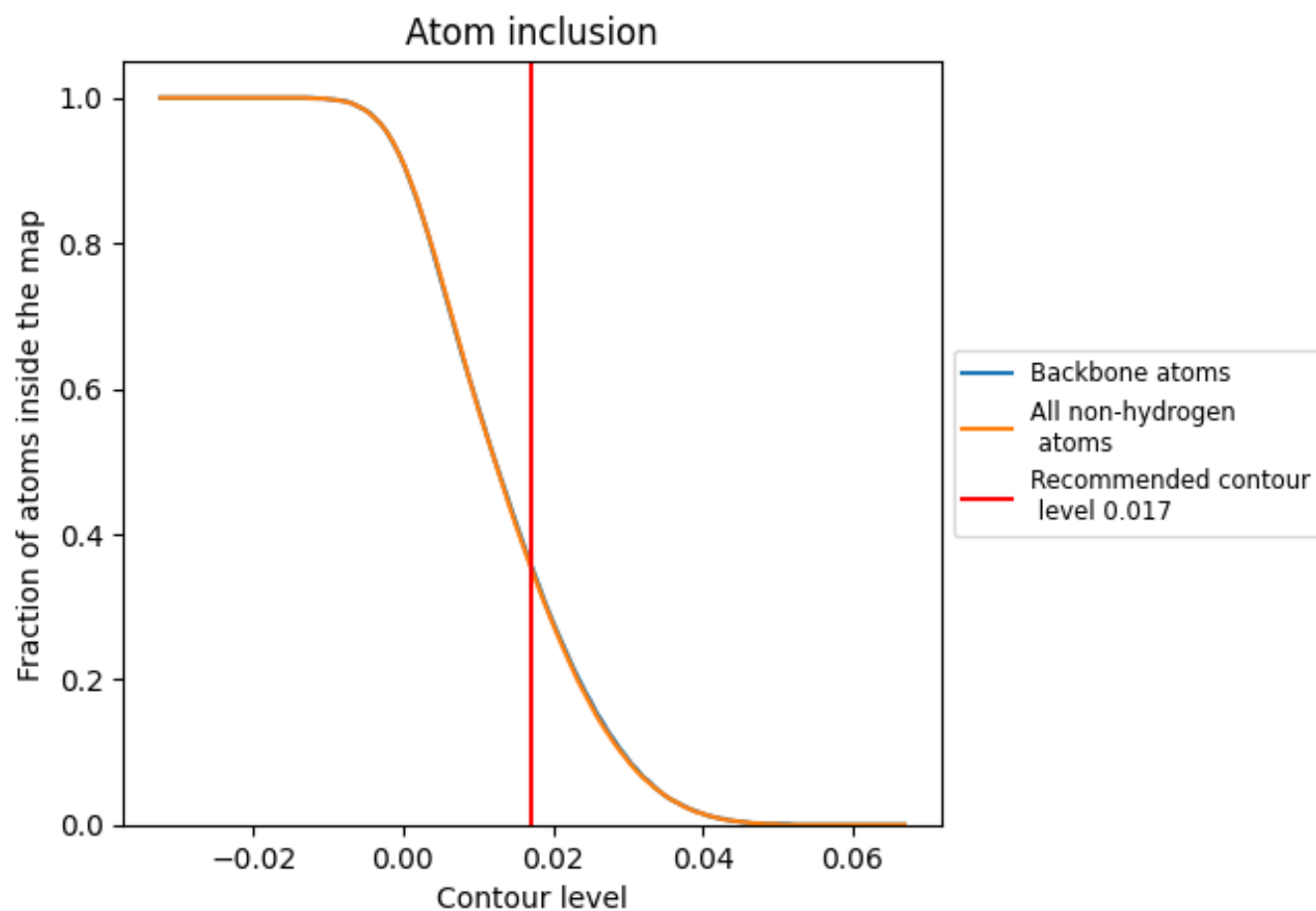


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 36% of all backbone atoms, 36% 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 (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3560	 0.1230
0	 0.3230	 0.1140
1	 0.4280	 0.2450
2	 0.2510	 0.0600
3	 0.2310	 0.0170
4	 0.2580	 0.0510
5	 0.0020	 -0.0050
6	 0.0050	 0.0520
7	 0.0130	 0.0190
9	 0.0700	 0.0020
A	 0.1760	 0.0960
AA	 0.0020	 0.0230
AC	 0.0020	 0.0180
AD	 0.0010	 0.0130
AE	 0.0020	 0.0180
B	 0.1270	 0.0350
C	 0.2410	 0.0790
D	 0.5260	 0.1880
E	 0.2120	 0.0040
F	 0.2200	 0.1780
G	 0.2310	 0.1020
H	 0.0080	 0.0140
I	 0.2080	 0.1290
J	 0.2270	 0.1030
K	 0.4110	 0.2670
L	 0.1620	 0.0260
M	 0.1900	 0.1040
N	 0.3250	 0.1810
O	 0.2000	 0.0480
P	 0.2030	 0.0890
Q	 0.2470	 0.1310
R	 0.4360	 0.3000
S	 0.2180	 0.0610
T	 0.3150	 0.1390
U	 0.1470	 -0.0110



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Chain	Atom inclusion	Q-score
V	 0.2770	 0.1500
W	 0.0910	 0.0010
X	 0.1420	 -0.0100
Y	 0.0440	 -0.0160
Z	 0.0130	 -0.0140
a	 0.5300	 0.1630
b	 0.2330	 0.0450
c	 0.2750	 0.0890
d	 0.4500	 0.0400
e	 0.2490	 0.0100
f	 0.3330	 0.1300
g	 0.0960	 -0.0160
h	 0.3070	 0.1140
i	 0.4580	 0.2290
j	 0.3760	 0.1720
k	 0.1790	 -0.0210
l	 0.2700	 0.0700
m	 0.4840	 0.2710
n	 0.1680	 0.0010
o	 0.2440	 0.0650
p	 0.1910	 0.0070
q	 0.3190	 0.1040
r	 0.0770	 -0.0010
s	 0.3690	 0.1680
t	 0.3700	 0.2120
u	 0.2880	 0.0750
v	 0.3430	 0.1570
w	 0.3980	 0.1670
x	 0.1890	 -0.0690
y	 0.2610	 0.1010
z	 0.4500	 0.2090