



wwPDB EM Validation Summary Report ⓘ

Jun 27, 2026 – 04:21 PM EDT

PDB ID : 6VZ7 / pdb_00006vz7
EMDB ID : EMD-21486
Title : Escherichia coli transcription-translation complex C1 (TTC-C1) containing a 27 nt long mRNA spacer, NusG, and fMet-tRNAs at P-site and E-site
Authors : Molodtsov, V.; Wang, C.; Su, M.; Ebright, R.H.
Deposited on : 2020-02-27
Resolution : 7.00 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:

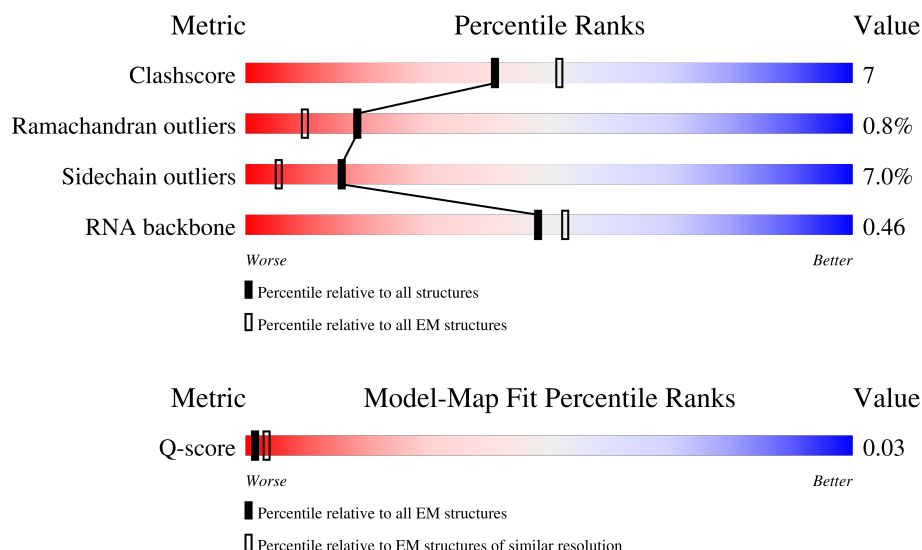
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 7.00 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	483 (6.50 - 7.50)

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	100% 84% 15% •
2	1	110	100% 75% 25%
3	2	94	100% 91% 6% •

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Mol	Chain	Length	Quality of chain
4	3	103	
5	4	94	
6	5	27	
7	6	27	
8	7	16	
9	A	76	
9	B	76	
10	AA	1341	
11	AB	112	
12	AC	230	
12	AD	230	
13	AE	1358	
14	AF	83	
15	C	66	
16	D	1542	
17	E	86	
18	F	70	
19	G	225	
20	H	557	
21	I	208	
22	J	205	
23	K	156	
24	L	104	
25	M	151	
26	N	129	

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Mol	Chain	Length	Quality of chain
27	O	127	
28	P	99	
29	Q	117	
30	R	123	
31	S	100	
32	T	88	
33	U	82	
34	V	80	
35	W	83	
36	X	116	
37	Y	3	
38	a	2903	
39	b	76	
40	c	77	
41	d	120	
42	e	62	
43	f	58	
44	g	66	
45	h	271	
46	i	56	
47	j	209	
48	k	52	
49	l	201	
50	m	46	
51	n	177	

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Mol	Chain	Length	Quality of chain
52	o	64	
53	p	175	
54	q	38	
55	r	149	
56	s	142	
57	t	123	
58	u	144	
59	v	136	
60	w	119	
61	x	116	
62	y	114	
63	z	117	

2 Entry composition

There are 65 unique types of molecules in this entry. The entry contains 299447 atoms, of which 125488 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
			848	259	306	89	167	27		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	16	Total	C	H	N	O	P	0	0
			515	154	168	62	115	16		

- Molecule 9 is a RNA chain called E-site and P-site tRNA (fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
9	A	76	Total	C	H	N	O	P	0	0
			2446	723	826	295	527	75		
9	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 1848954948
B	?	-	U	deletion	GB 1848954948

- Molecule 10 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	AA	1322	Total	C	H	N	O	S	0	0
			20852	6539	10427	1817	2026	43		

- Molecule 11 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	AB	98	Total	C	H	N	O	S	0	0
			1573	505	783	139	140	6		

- 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.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AE	1335	Total	C	H	N	O	S	0	0
			20999	6526	10611	1854	1958	50		

- Molecule 14 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AF	83	Total	C	H	N	O	S	0	0
			1318	399	663	123	132	1		

- Molecule 15 is a protein called 30S ribosomal protein S18.

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

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

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

- Molecule 17 is a protein called 30S ribosomal protein S20.

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

- Molecule 18 is a protein called 30S ribosomal protein S21.

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

- Molecule 19 is a protein called 30S ribosomal protein S2.

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

- Molecule 20 is a protein called 30S ribosomal protein S1.

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

- Molecule 21 is a protein called 30S ribosomal protein S3.

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

- Molecule 22 is a protein called 30S ribosomal protein S4.

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

- Molecule 23 is a protein called 30S ribosomal protein S5.

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

- Molecule 24 is a protein called 30S ribosomal protein S6.

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

- Molecule 25 is a protein called 30S ribosomal protein S7.

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

- Molecule 26 is a protein called 30S ribosomal protein S8.

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

- Molecule 27 is a protein called 30S ribosomal protein S9.

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

- Molecule 28 is a protein called 30S ribosomal protein S10.

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

- Molecule 29 is a protein called 30S ribosomal protein S11.

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

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

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

- Molecule 31 is a protein called 30S ribosomal protein S14.

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

- Molecule 32 is a protein called 30S ribosomal protein S15.

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

- Molecule 33 is a protein called 30S ribosomal protein S16.

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

- Molecule 34 is a protein called 30S ribosomal protein S17.

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

- Molecule 35 is a protein called 30S ribosomal protein S19.

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

- Molecule 36 is a protein called 30S ribosomal protein S13.

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

- Molecule 37 is a RNA chain called mRNA in the ribosomal RNA entrance pore.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	Y	3	Total	C	H	N	O	P	0	0
			90	27	30	6	24	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		

- 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	7	1	Total	Mg	0
			1	1	

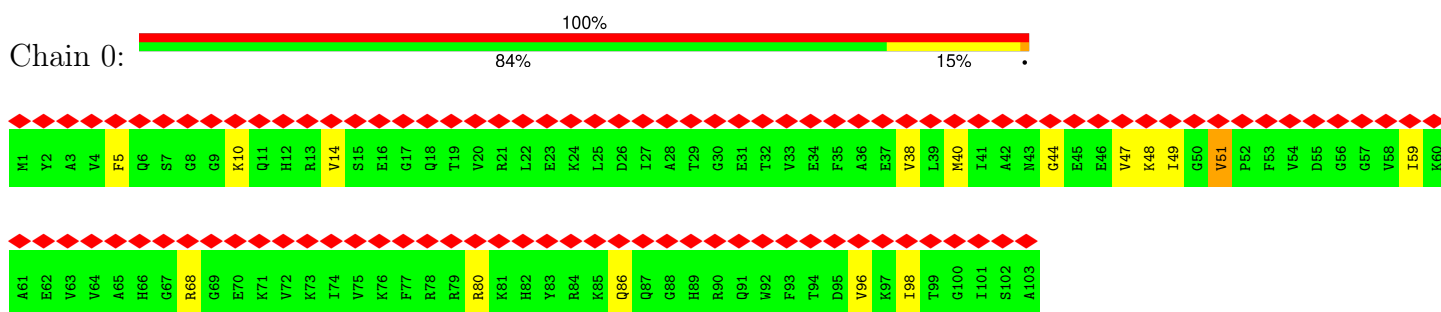
- Molecule 65 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

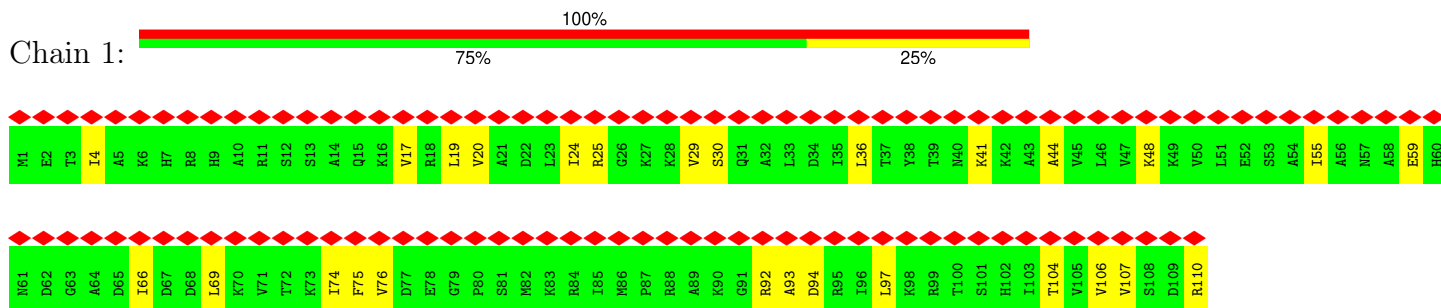
3 Residue-property plots

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

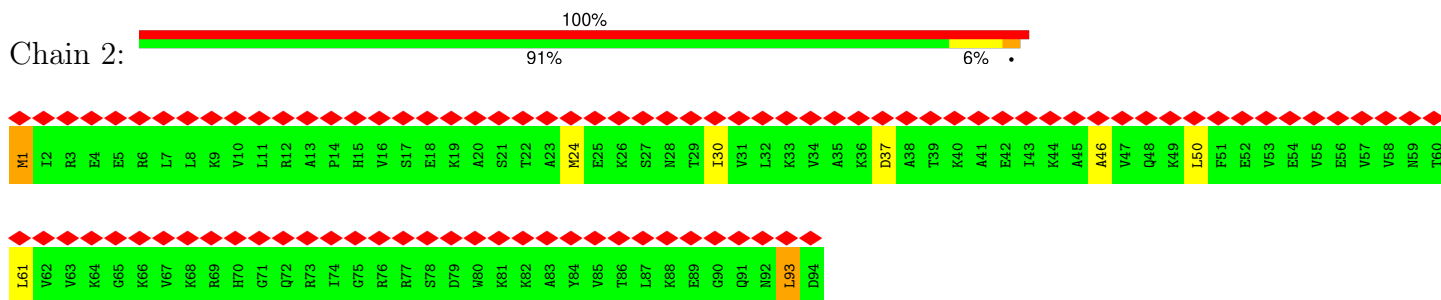
- Molecule 1: 50S ribosomal protein L21



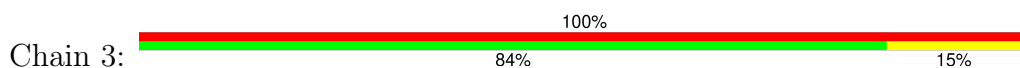
- Molecule 2: 50S ribosomal protein L22

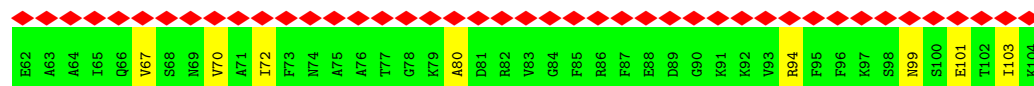


- Molecule 3: 50S ribosomal protein L23

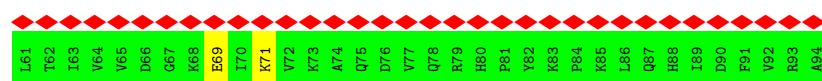
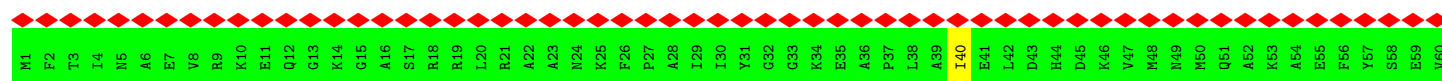


- Molecule 4: 50S ribosomal protein L24

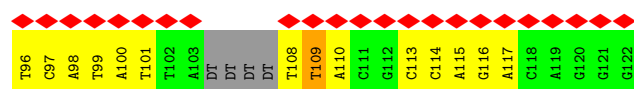
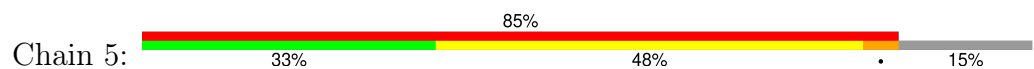




• Molecule 5: 50S ribosomal protein L25



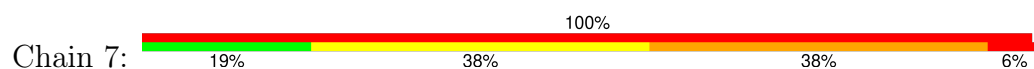
• Molecule 6: NT DNA



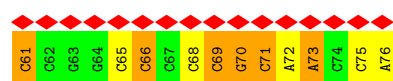
• Molecule 7: T DNA



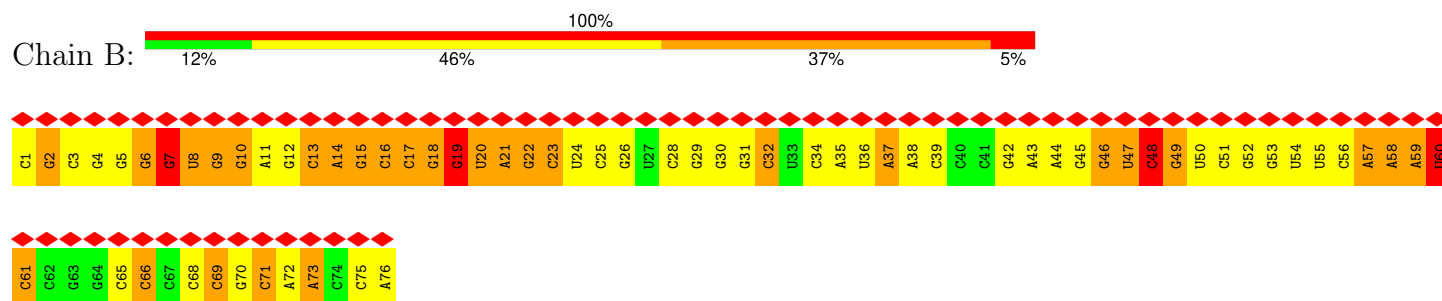
• Molecule 8: mRNA with 27 nt long spacer



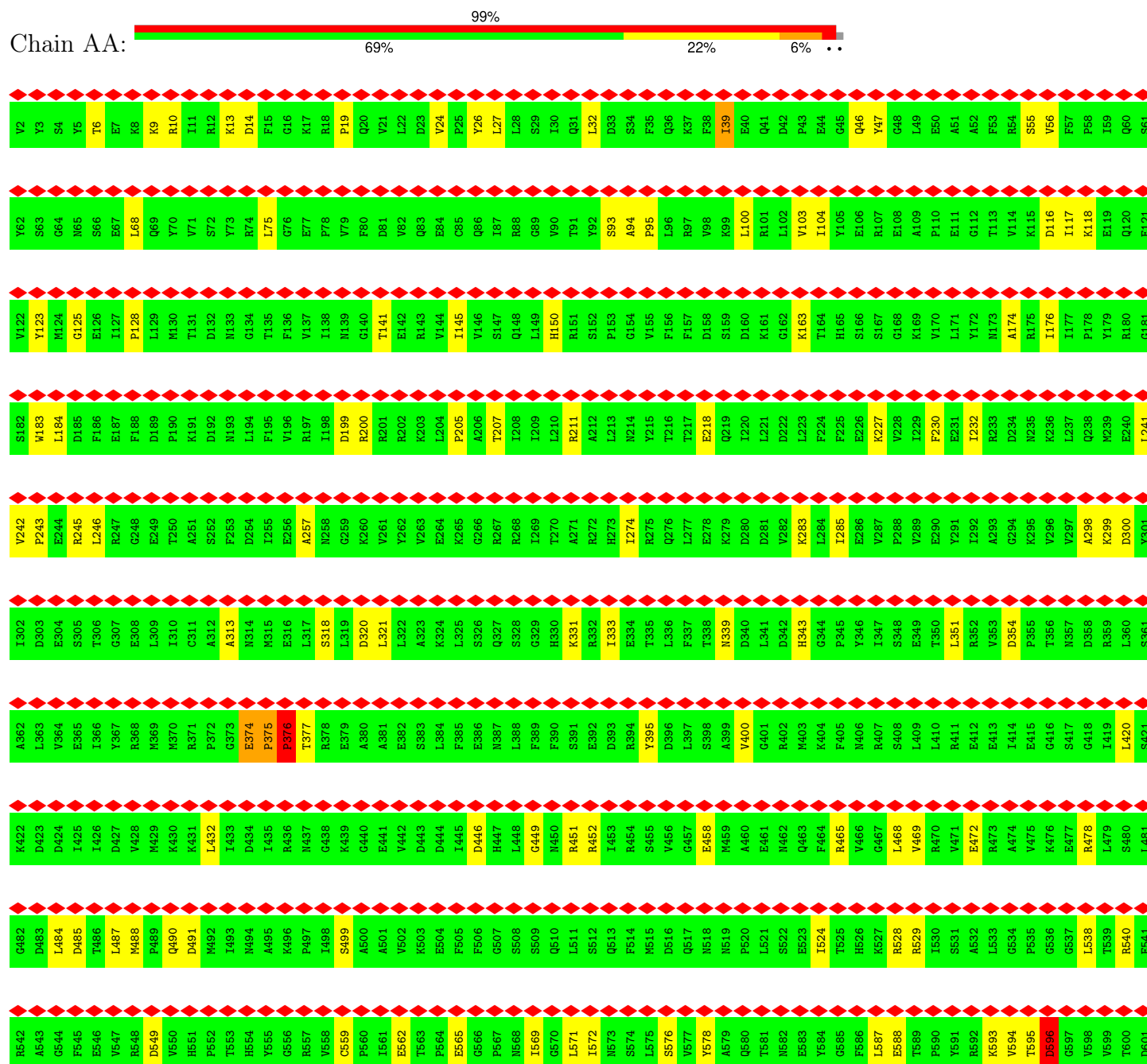
• Molecule 9: E-site and P-site tRNA (fMet)



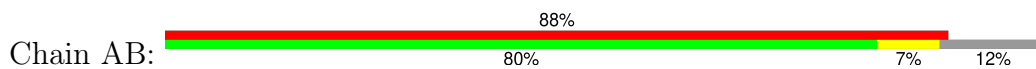
Chain B:



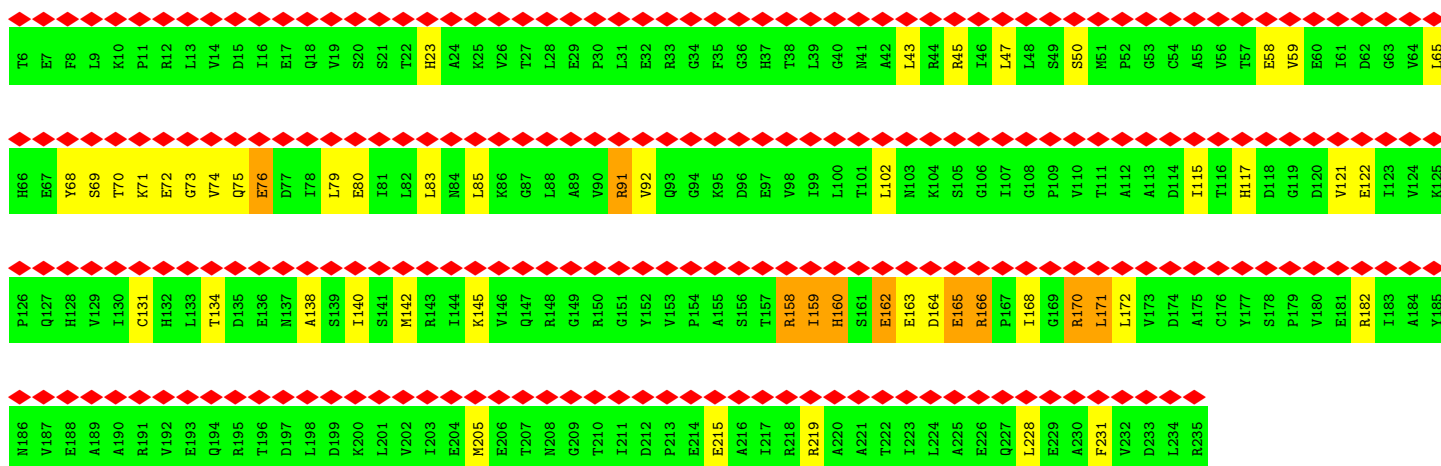
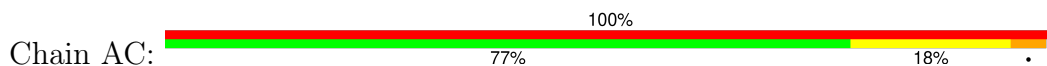
Chain AA:



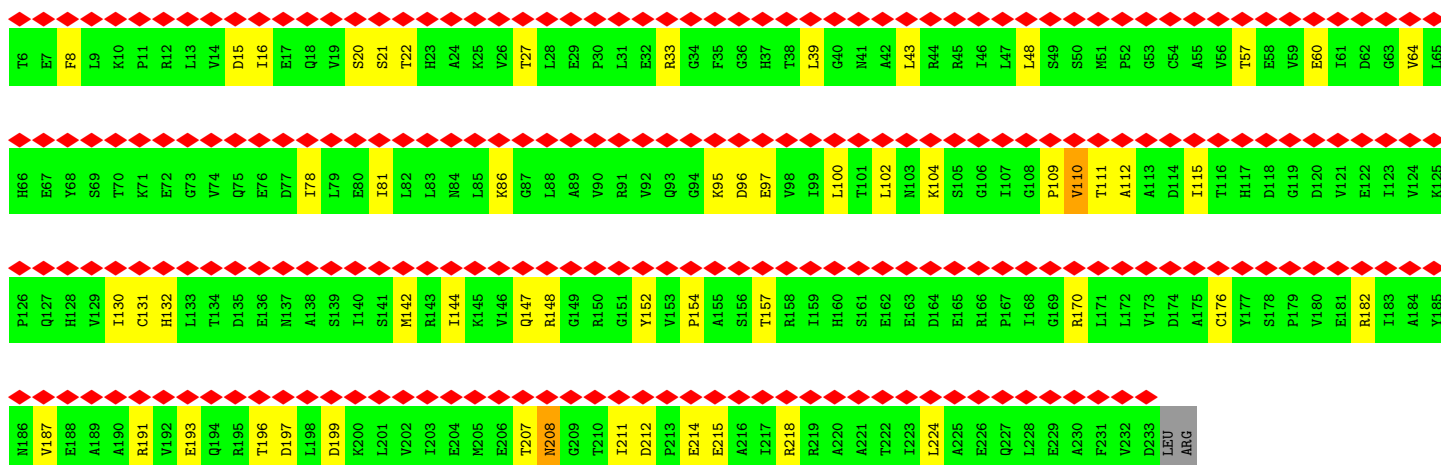
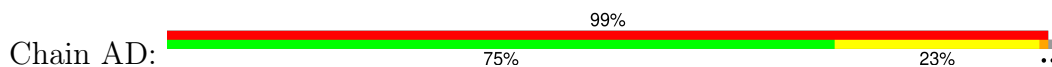
- Molecule 11: Transcription termination/antitermination protein NusG



• Molecule 12: DNA-directed RNA polymerase subunit alpha



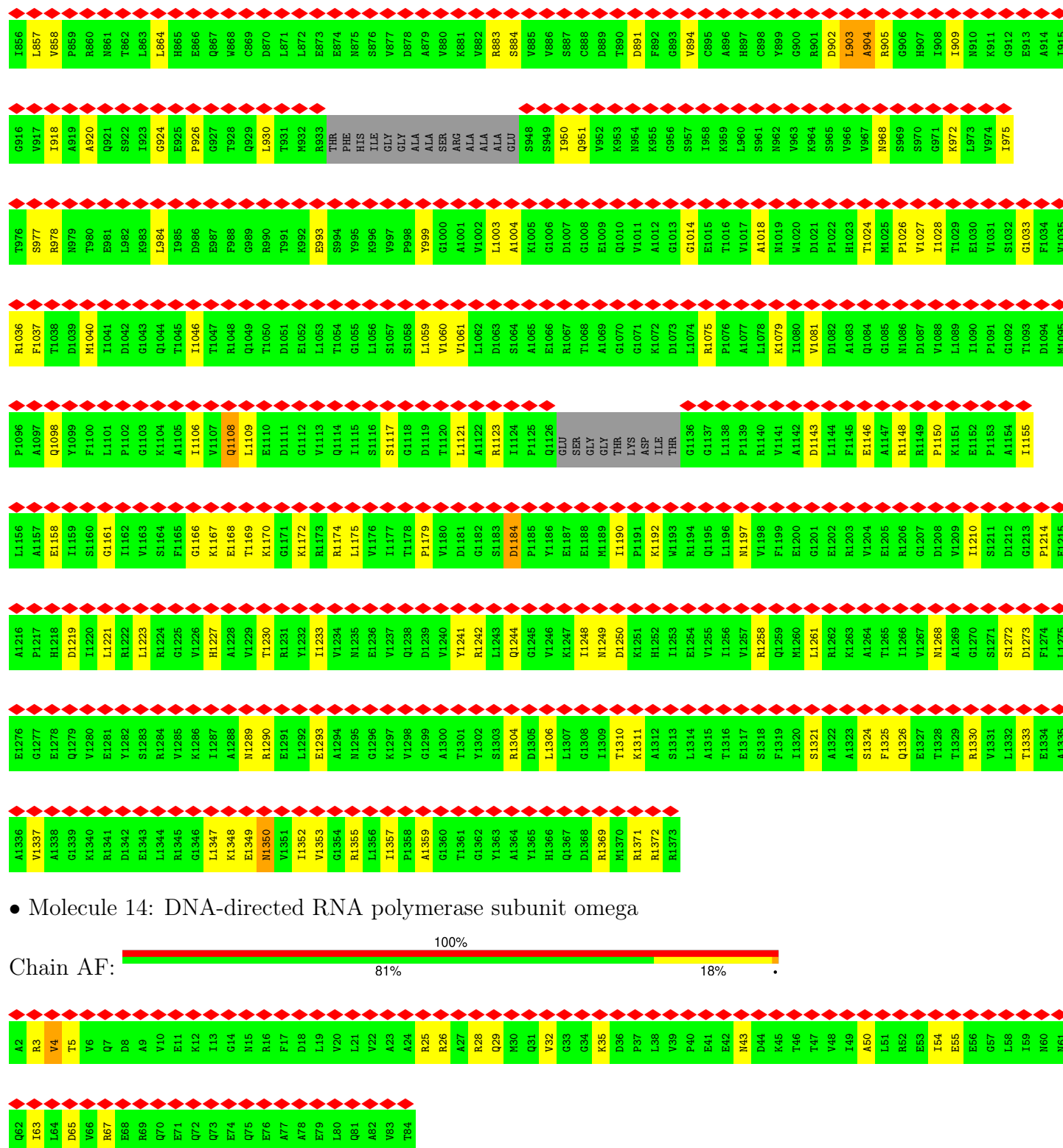
• Molecule 12: DNA-directed RNA polymerase subunit alpha



• Molecule 13: DNA-directed RNA polymerase subunit

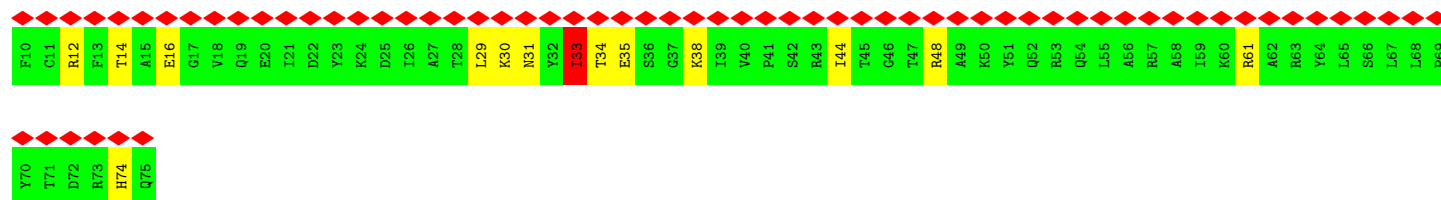


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Q736	I737	R738	Q739	L740	A741	G742	M743	R744	G745	L746	M747	A748	K749	P750	D751	G752	S753	I754	I755	E756	T757	P758	I759	T760	A761	N762	F763	R764	E765	G766	L767	N768	V769	L770	D771	Q772	F773	I774	S775	T776	H777	G778	A779	R780	L781	G782	L783	A784	D785	T786	A787	L788	K789	T790	A791	G792	T793	G794	A795		
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E556	K557	D558	A559	N560	G561	E562	L563	V564	A565	K566	T567	S568	L569	K570	D571	T572	T573	V574	G575	R576	A577	S578	L579	M580	I581	D582	V583	P584	K585	G586	L587	P588	G589	S590	I591	V592	Q593	Q594	A595	L596	G597	K598	S599	A600	I601	S602	K603	M604	L605	N606	T607	C608	Y609	R610	I611	L612	G613	L614	K615		
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I316	T317	G318	S319	N320	K321	R322	S323	L324	K325	S326	L327	A328	D329	N330	I331	K332	G333	K334	Q335	G336	R337	F338	R339	Q340	N341	L342	L343	G344	K345	R346	V347	D348	Y349	S350	G351	R352	S353	V354	I355	T356	V357	G358	P359	V360	L361	R362	L363	H364	Q365	C366	G367	L368	P369	K370	K371	N372	A373	L374	E375		
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Q196	E197	C198	E199	Q200	L201	R202	E203	E204	L205	N206	E207	T208	N209	S210	E211	T212	K213	R214	K215	K216	L217	T218	K219	R220	I221	K222	L223	L224	E225	A226	F227	Q228	Q229	S230	G231	N232	G233	P234	E235	W236	W237	I238	L239	T240	V241	L242	V244	L245	P246	P247	D248	L249	R250	P251	L252	V253	P254	L255			
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K76	R77	L78	K79	H80	R81	G82	V83	I84	C85	E86	K87	C88	G89	V90	E91	V92	T93	Q94	T95	K96	G97	R98	R99	E100	R101	M102	G103	H104	I105	E106	L107	A108	S109	P110	T111	A112	H113	I114	W115	F116	L117	K118	S119	L120	P121	S122	R123	I124	G125	L126	L127	V128	D129	M130	P131	L132	R133	D134	I135		
E16	F17	D18	A19	I20	K21	L22	A23	L24	A25	S26	P27	D28	N29	I30	R31	S32	V33	S34	F35	G36	E37	V38	K39	K40	P41	E42	T43	I44	N45	Y46	R47	T48	F49	K50	P51	E52	R53	D54	G55	L56	F57	C58	A59	R60	T61	F62	G63	P64	V65	K66	D67	V68	E69	C70	L71	G72	T73	K74	Y75		

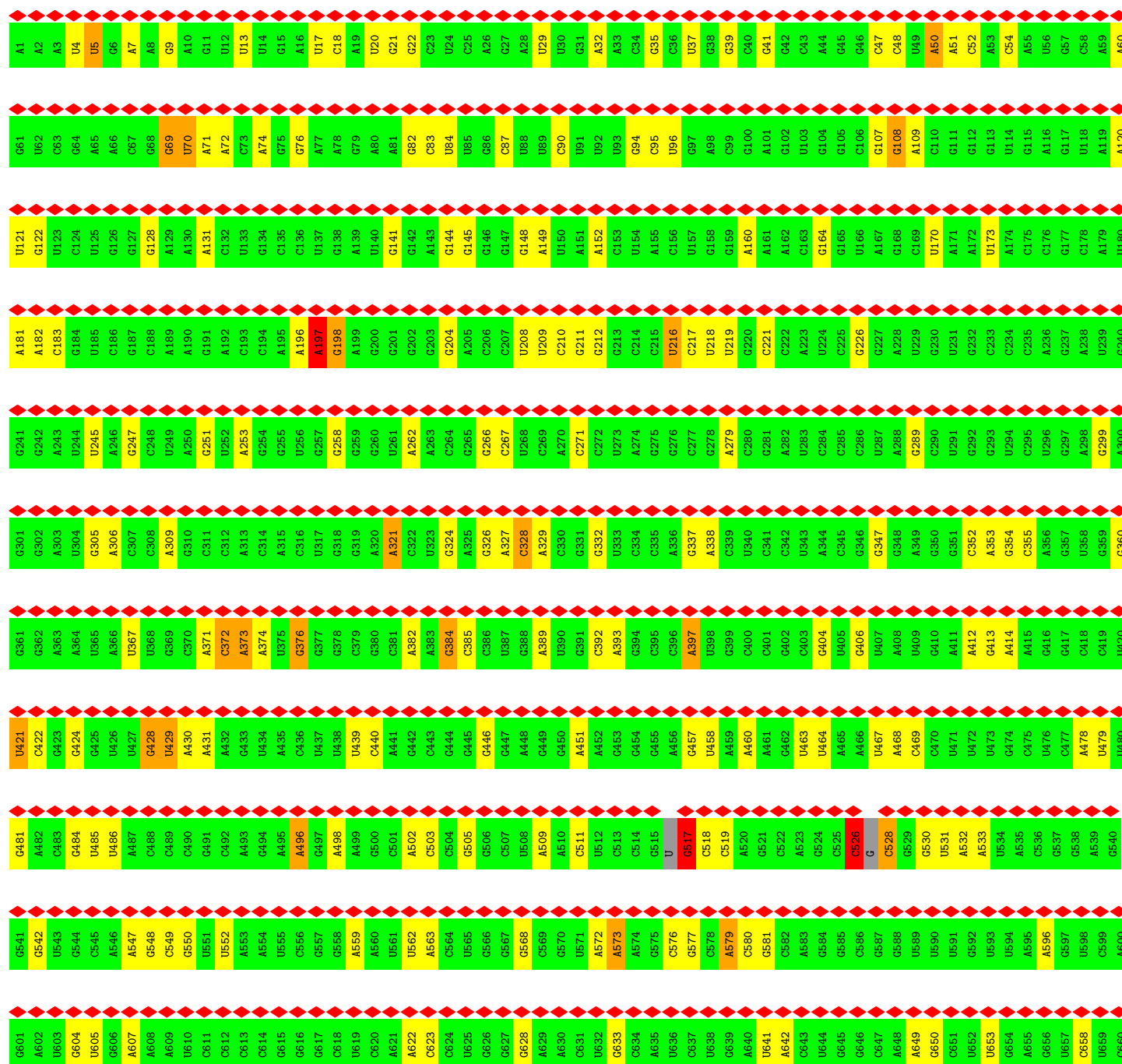


- Molecule 14: DNA-directed RNA polymerase subunit omega

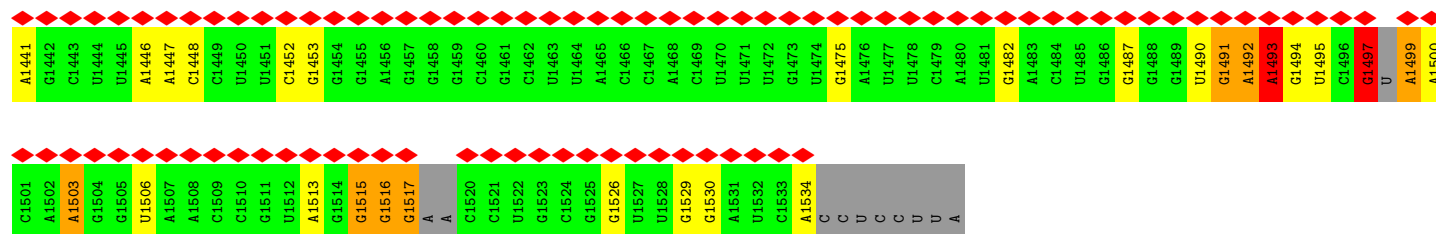
- Molecule 15: 30S ribosomal protein S18



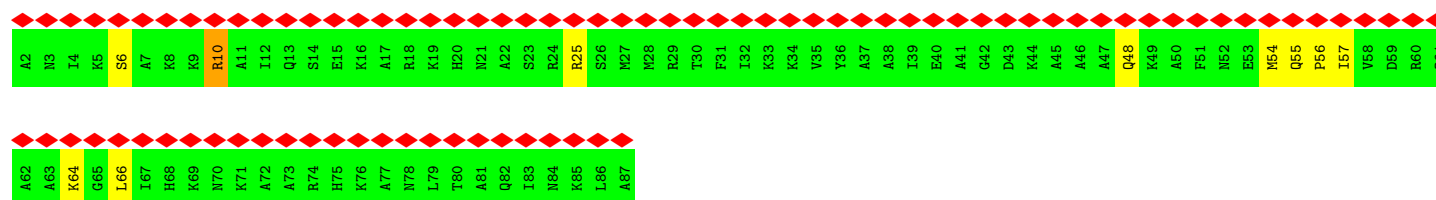
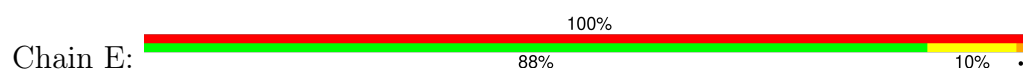
● Molecule 16: 16S rRNA



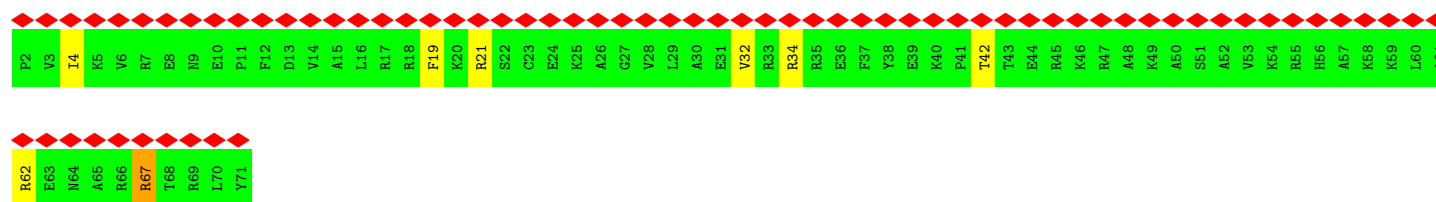
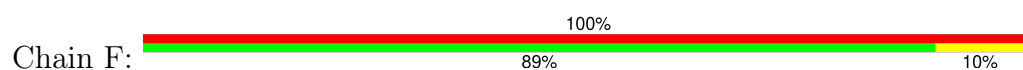
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U1321	C1322	C1383	A1324	C1325	U1326	C1327	C1328	A1329	U1330	U1331	G1331	A1271	C1272	U1393	A1274	A1275	G1276	C1277	G1278	G1279	A1280	U1341	C1342	U1383	C1344	U1345	A1346	U1347	U1348	A1349	A1350	U1351	C1352	G1353	U1354	G1355	G1356	A1357	U1358	C1359	A1360	G1361	C1362	A1363	U1364	G1365	C1366	C1367	A1368	C1369	G1370	G1371	U1372	G1373	A1374	U1375	U1376	A1377	C1378	G1379	U1380
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A901	C902	G903	U904	U905	A906	A907	A908	A909	C910	U911	C912	A913	A914	A915	U916	G917	A918	A919	U920	U921	G922	A923	C924	G925	G926	G927	G928	C929	C930	C931	C932	G933	C934	A935	C936	A937	A938	G939	C940	G941	C942	U943	C944	G945	A946	G947	C948	A949	U950	G951	U952	G953	C954	U955	U956	U957	A958	A959	U960		
C841	U842	U843	C844	A845	G846	G847	C848	C849	U850	C851	C852	C853	U854	U855	C856	C857	G858	G859	A860	C861	C862	U863	A864	A865	C866	G867	C868	U869	U870	U871	A872	G873	A874	U875	C876	G877	A878	C879	C880	G881	C882	C883	U884	G885	G886	C887	G888	A889	C890	U891	A892	C893	G894	G895	C896	C897	G898	C899	A900		
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G721	G722	U723	G724	G725	G726	G727	A728	A729	G730	G731	G732	G733	G734	C735	C736	C737	C738	C739	U740	G741	G742	A743	C744	G745	A746	A747	G748	A749	C750	U751	G752	A753	C754	G755	C756	U757	C758	A759	G760	G761	U762	G763	C764	G765	A766	A767	A768	G769	C770	G771	U772	G773	G774	G775	G776	A777	G778	C779	A780		
G661	U662	G663	A664	A665	G666	G667	G668	G669	G670	G671	U672	A673	G674	A675	A676	U677	U678	C679	C680	A681	G682	G683	U684	G685	U686	A687	G688	C689	G690	U691	U692	G693	A694	A695	A696	U697	G698	C699	G700	U701	A702	G703	A704	G705	A706	U707	C708	U709	G710	A711	G712	G713	A714	A715	A716	U717	A718	C719	C720		



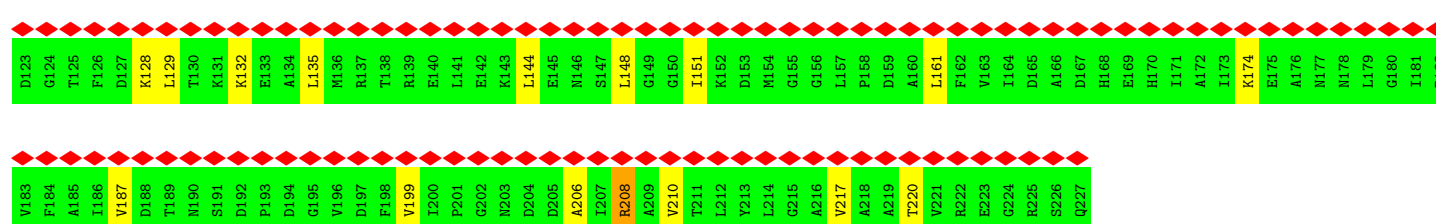
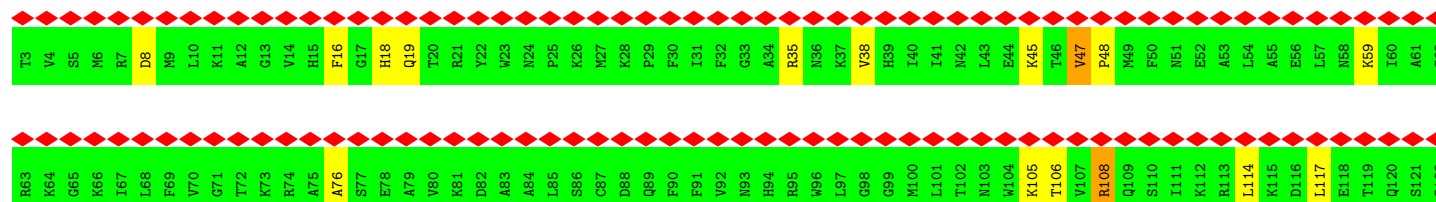
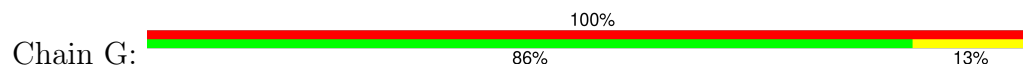
• Molecule 17: 30S ribosomal protein S20



• Molecule 18: 30S ribosomal protein S21



• Molecule 19: 30S ribosomal protein S2

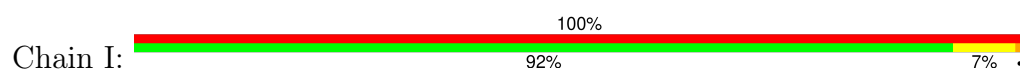


• Molecule 20: 30S ribosomal protein S1



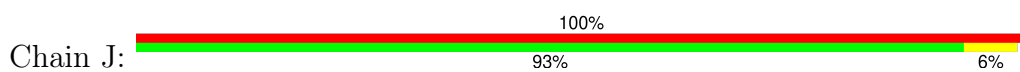
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E61	T62	Q63	V64	D66	E67	V68	D69	V70	A71	L72	D73	A74	V75	E76	D77	G78	F79	G80	E81	T82	L83	L84	S85	R86	E87	K88	A89	K90	R91	H92	E93	A94	W95	I96	T97	L98	E99	K100	A101	A102	E103	D104	A105	S106	T107	V108	T109	G110	V111	T112	N113	G114	K115	V116	K117	G118	G119	F120					
T121	V122	E123	L124	N125	G126	T127	R128	A129	F130	L131	P132	G133	S134	L135	V136	D137	V138	R139	P140	V141	R142	D143	T144	L145	H146	L147	E148	G149	K150	E151	L152	E153	F154	K155	V156	I157	K158	L159	D160	Q161	K162	R163	N164	N165	V166	V167	V168	S169	R170	R171	A172	T173	T174	E175	S176	GLU	ASN	ALA					
GLU	ARG	ASP	GLN	LEU	LEU	GLU	ASN	GLN	GLY	MET	GLU	VAL	LYS	GLY	ILE	VAL	ASN	LEU	THR	ASP	TYR	GLY	ALA	PHE	ASP	LEU	GLY	LEU	LEU	HIS	ILE	THR	ASP	MET	ALA	TRP	ARG	VAL	LYS	HIS	PRO	SER	GLU	ILE	K162	R163	ASN	VAL	GLY	ASP	GLU	V168	S169	R170	R171	A172	T173	T174	E175	S176	GLU	ASN	ALA
ILE	THR	VAL	LYS	VAL	LEU	LYS	PHE	ARG	GLU	THR	ARG	VAL	SER	LEU	GLY	LEU	LYS	GLN	LEU	GLY	E264	D265	P266	W267	V268	A269	I270	A271	K272	ASP	R273	Y274	P275	E276	G277	T278	K279	L280	T281	G282	R283	V284	T285	N286	L287	T288	D289	Y290	G291	C292	F293	V294	E295	I296	E297	Y298	G299	V300					
E301	G302	L303	V304	H305	V306	S307	E308	M309	D310	W311	T312	N313	K314	N315	I316	H317	P318	S319	K320	V321	V322	N323	V324	G325	D326	V327	V328	E329	V330	M331	V332	L333	D334	I335	D336	E337	E338	R339	R340	R341	I342	S343	L344	G345	L346	K347	Q348	CYS	LYS	ALA	ASN	PRO	TRP	GLN	PHE	ALA	GLU	THR					
HIS	ASN	LYS	GLY	ASP	ARG	VAL	GLU	GLY	ILE	LYS	SER	ILE	THR	THR	GLN	ASP	PHE	ILE	GLY	ASP	GLY	ILE	VAL	HIS	LEU	SER	ASP	ILE	SER	TRP	ASN	VAL	ALA	GLY	GLU	ALA	VAL	ARG	GLU	TYR	LYS	LYS	GLY	ASP	GLY	VAL	VAL	GLY	ALA	ALA	TRP	VAL	ARG	ALA									
GLN	VAL	ASP	ALA	ASP	ARG	GLU	ARG	ILE	SER	LEU	GLY	VAL	LYS	GLN	ALA	ASP	PRO	PHE	ILE	ASN	TRP	VAL	ALA	LEU	ASN	LYS	GLY	ALA	ILE	VAL	THR	GLY	LYS	VAL	THR	ASP	ALA	LEU	ALA	ASP	GLY	VAL	VAL	GLY	ASN	GLY	TRP	GLN	GLU	ASP	ARG	ALA											
SER	GLU	ALA	SER	ARG	ASP	ARG	VAL	GLU	ALA	THR	LEU	VAL	VAL	SER	LEU	VAL	GLY	GLU	GLU	ALA	PHE	THR	VAL	VAL	ARG	ASN	ARG	ILE	SER	LEU	SER	VAL	THR	ARG	LYS	ASP	ALA	ILE	ALA	ASP	GLY	THR	VAL	VAL	ASN	GLY	LYS	GLN	GLU	ASP	ARG	ALA											
ASN	PHE	SER	ASN	ASN	ALA	MET	ALA	GLU	ALA	LYS	ALA	GLY	GLU	GLY	GLY	GLY	GLY	TRP	VAL	THR	THR	GLY	VAL	ASP	ARG	LYS	ASN	ARG	ALA	VAL	LYS	ASP	GLU	ALA	ALA	ASP	GLU	ILE	ALA	ASP	GLY	VAL	VAL	ASN	GLY	LYS	GLN	GLU	ASP	ARG	ALA												

• Molecule 21: 30S ribosomal protein S3

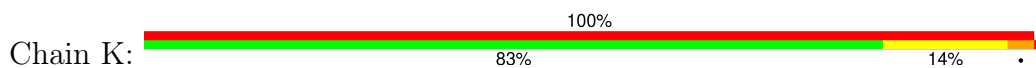


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S122	Q123	L124	E125	R126	T127	V128	M129	F130	R131	R132	A133	M134	K135	R136	A137	V138	Q139	N140	A141	M142	R143	L144	G145	A146	K147	G148	I149	K150	V151	E152	V153	S154	G155	R156	L157	G158	G159	A160	E161	I162	A163	R164	T165	E166	V167	Y168	R169	E170	G171	R172	V173	P174	L175	H176	T177	L178	R179	A180	D181			
K62	S63	I64	R65	V66	T67	I68	H69	T70	A71	R72	P73	G74	I75	V76	I77	G78	K79	K80	G81	E82	D83	V84	E85	K86	L87	R88	K89	V90	V91	A92	D93	I94	A95	G96	V97	P98	A99	Q100	I101	N102	I103	A104	E105	V106	R107	K108	P109	E110	L111	D112	A113	K114	L115	V116	A117	D118	S119	I120	T121			
G2	Q3	K4	V5	H6	P7	N8	G9	I10	R11	L12	G13	I14	V15	K16	P17	W18	N19	S20	T21	W22	F23	A24	N25	T26	K27	E28	F29	A30	D31	N32	L33	D34	S35	D36	F37	K38	V39	R40	Q41	Y42	L43	T44	K45	E46	L47	K48	P49	E50	S51	V52	S53	R54	I55	V56	I57	E58	P59	A60	T61			

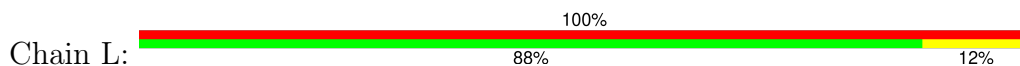
• Molecule 22: 30S ribosomal protein S4



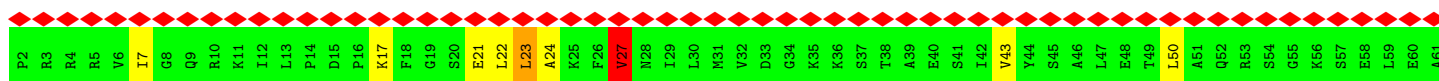
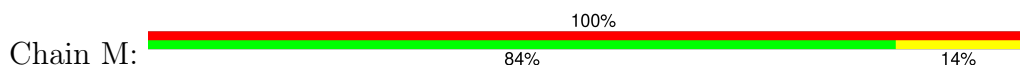
• Molecule 23: 30S ribosomal protein S5



• Molecule 24: 30S ribosomal protein S6

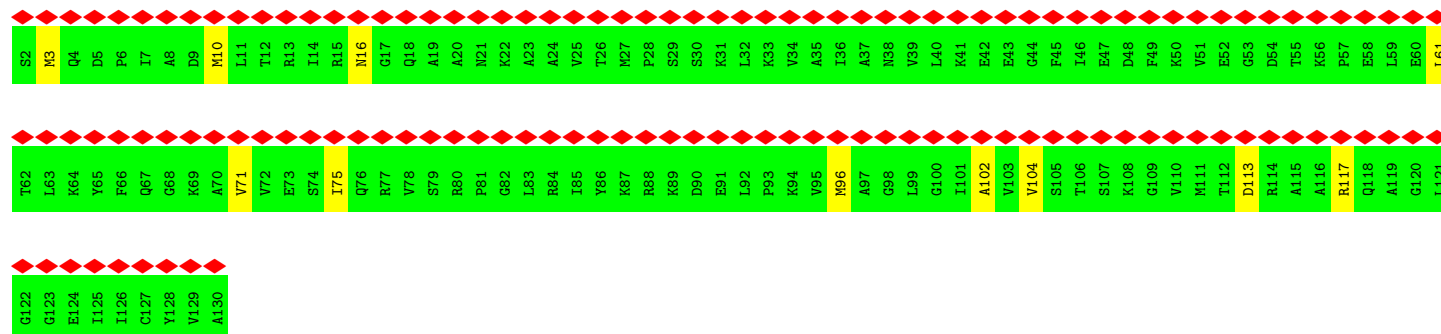
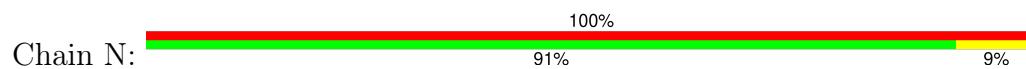


• Molecule 25: 30S ribosomal protein S7

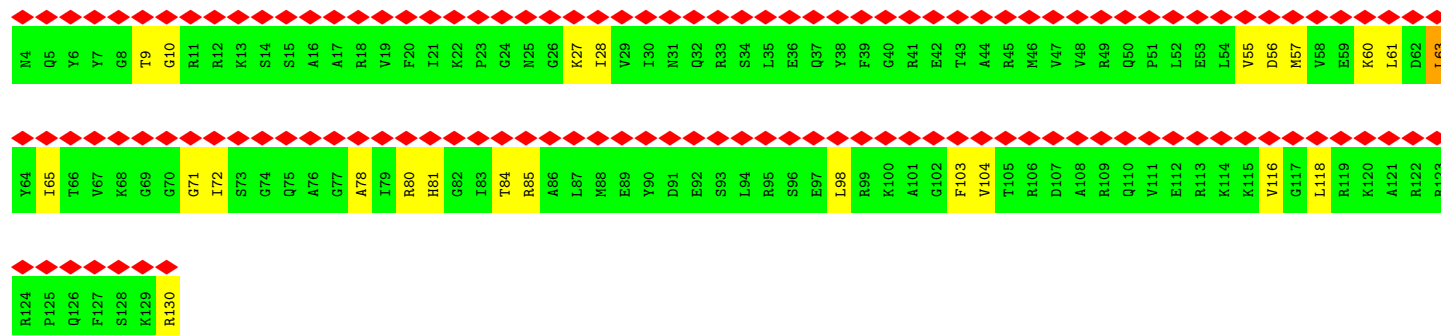
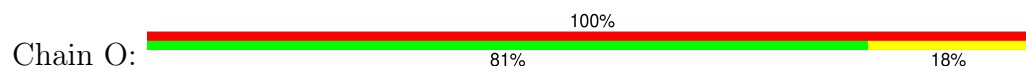




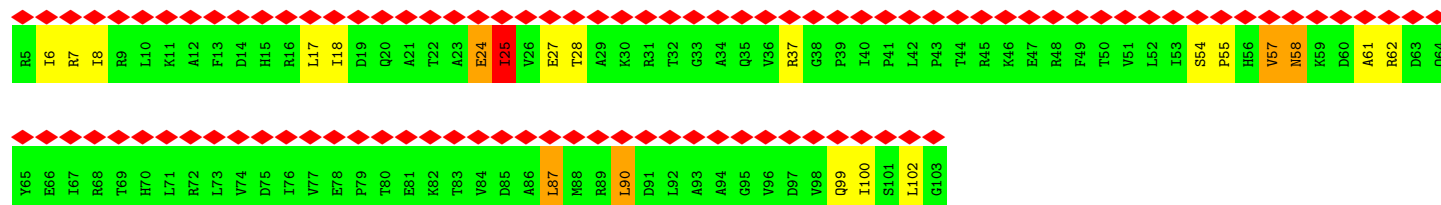
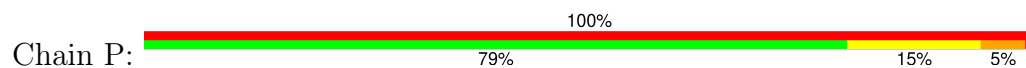
• Molecule 26: 30S ribosomal protein S8



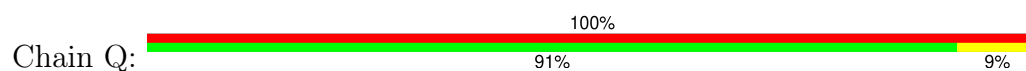
• Molecule 27: 30S ribosomal protein S9

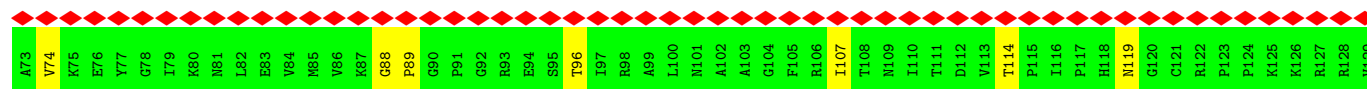


• Molecule 28: 30S ribosomal protein S10

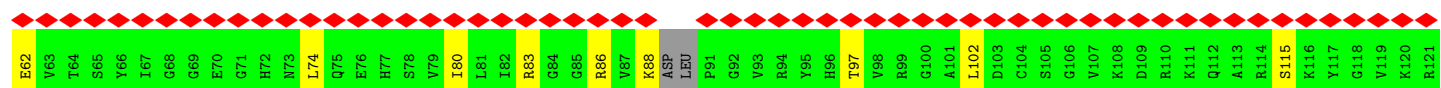
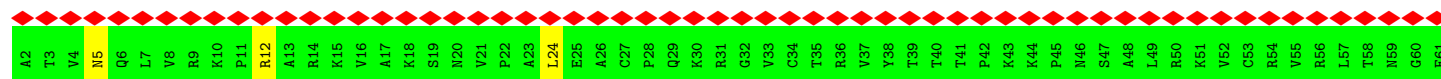
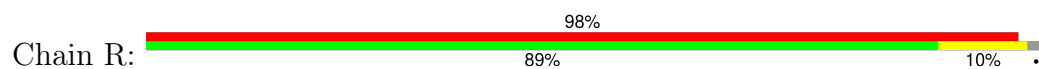


• Molecule 29: 30S ribosomal protein S11

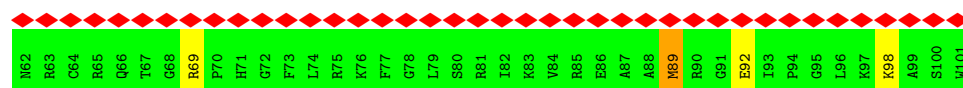
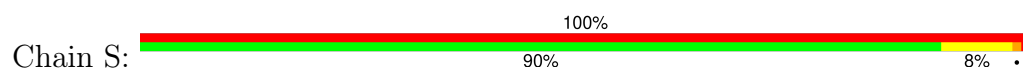




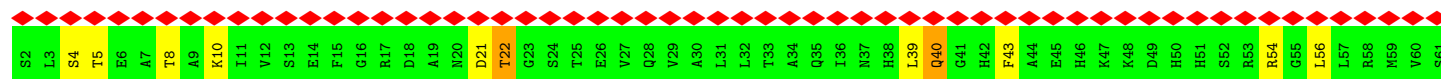
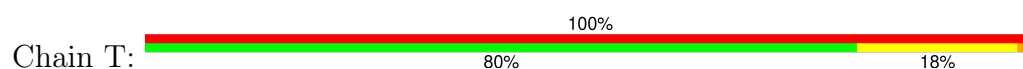
• Molecule 30: 30S ribosomal protein S12



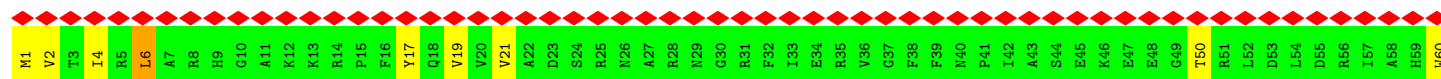
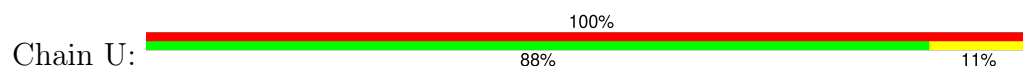
• Molecule 31: 30S ribosomal protein S14



• Molecule 32: 30S ribosomal protein S15

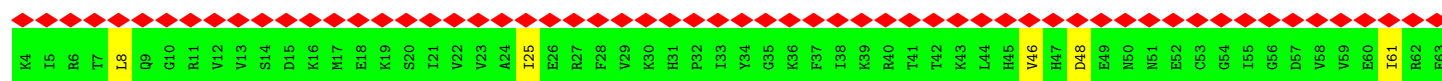
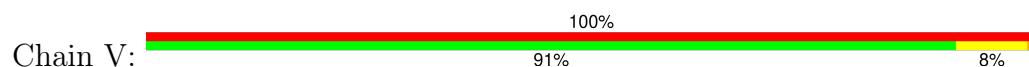


• Molecule 33: 30S ribosomal protein S16

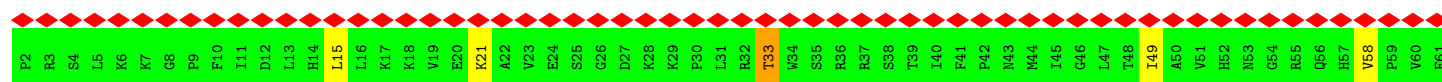
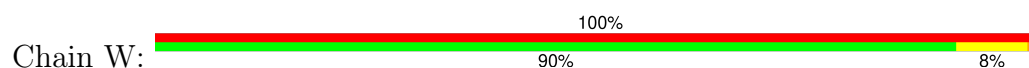




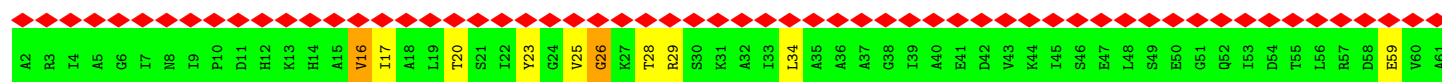
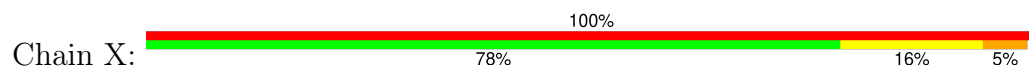
• Molecule 34: 30S ribosomal protein S17



• Molecule 35: 30S ribosomal protein S19



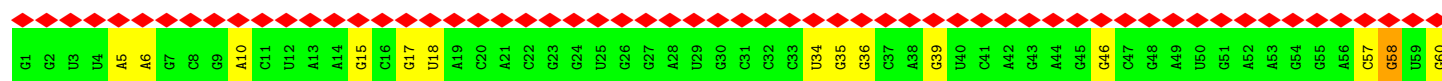
• Molecule 36: 30S ribosomal protein S13



• Molecule 37: mRNA in the ribosomal RNA entrance pore



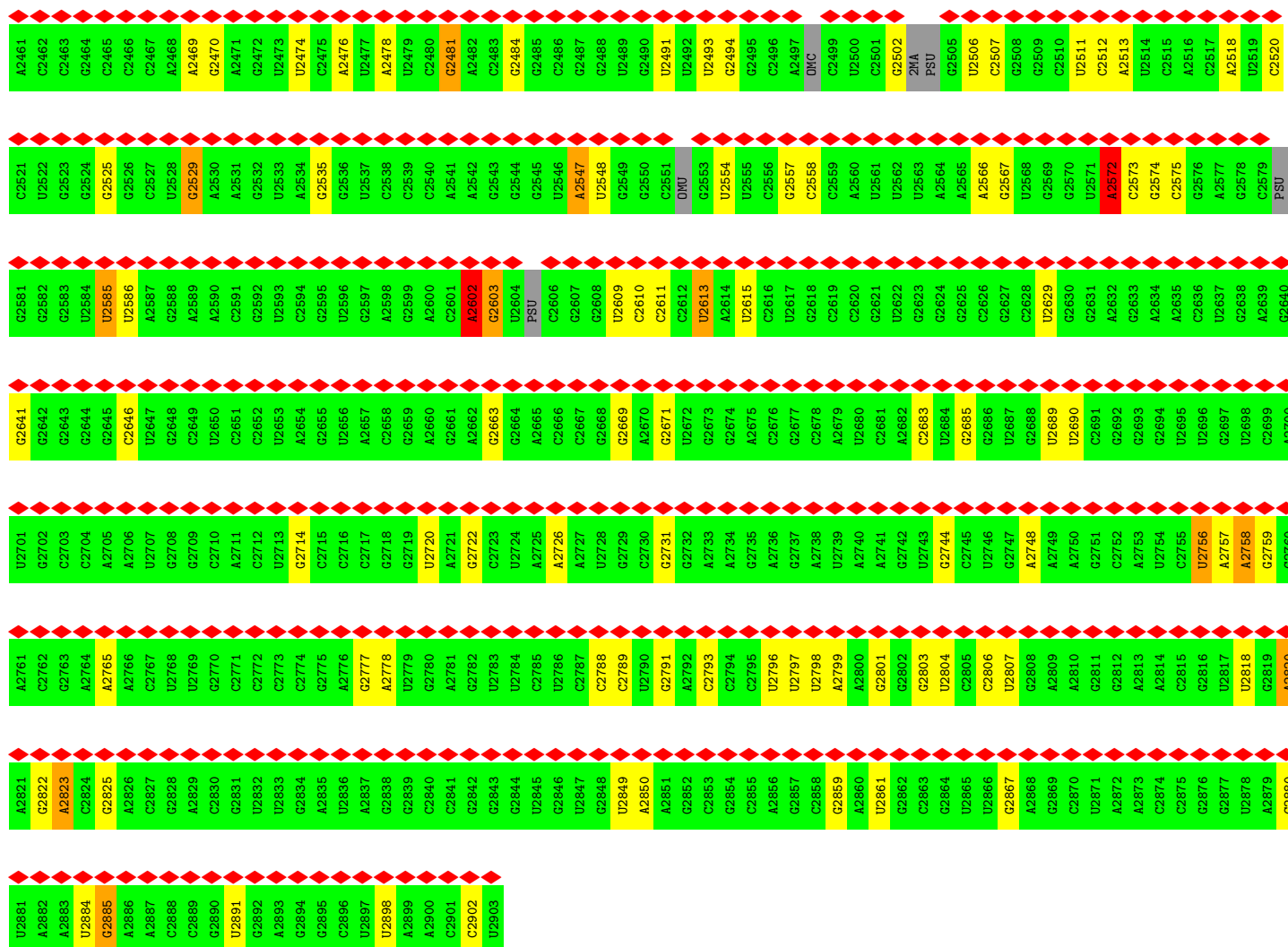
• Molecule 38: 23S rRNA



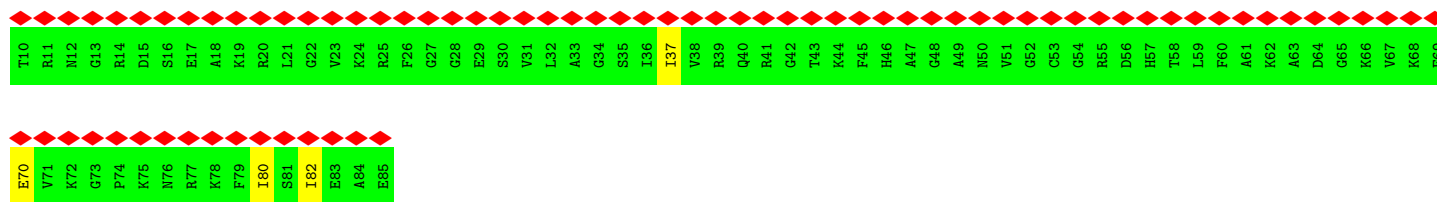
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A781	A782	A783	G784	G785	G786	G787	A788	A789	U790	C791	C792	A793	A794	C795	C796	G797	G798	G799	U800	A801	A802	A803	A804	C805	C806	U807	G808	G809	U810	U811	C812	U813	C814	C815	C816	C817	C818	A819	A820	A821	C822	C823	U824	U825	A826	U827	U828	U829	G830	G831	U832	U833	G834	C835	C836	C837	C838	U839	U840		
A721	A722	C723	U724	G725	G726	A727	G728	A729	U730	C731	C732	C733	A734	A735	C736	G737	G738	A739	C740	U741	A742	A743	U744	1MG	PSU	5MU	G748	A749	A750	A751	U811	A752	U753	U754	U755	A756	G757	C758	G759	U760	A761	U762	G763	A764	C765	U766	U767	G768	U769	G770	G771	G811	C772	U773	G774	G775	G776	G777	G778	U779	G780
A661	G662	G663	G664	U665	A666	U667	A668	G669	U670	C671	C672	C673	A674	A675	A676	A677	C678	C679	C680	G681	G682	U683	G684	A685	U686	C687	U688	A689	G690	C691	C692	A693	U694	G695	G696	G697	A698	U699	G700	G701	U702	G703	A644	A705	A706	G707	G708	U709	U710	G711	G712	U713	U714	A715	A716	C717	A718	C719	U720		
C601	A602	A603	G604	G605	U606	U607	A608	A609	C610	C611	G612	A613	A614	U615	A616	G617	G618	G619	G620	A621	G622	C623	C624	G625	A626	A627	G628	G629	G630	A631	A632	A633	C634	C635	G636	A637	G638	U639	C640	U641	U642	A643	A644	C645	U646	U647	G648	U649	U650	G651	U652	U653	A654	A655	G656	U657	U658	G659	C660		
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C421	A422	A423	G424	G425	C426	U427	A428	A429	A430	U431	A432	C433	U434	C435	C436	U437	G438	A439	C440	U441	G442	A443	C444	C445	G446	A447	U448	A449	C450	U451	G452	A453	A454	C455	C456	A457	G458	U459	A460	A461	C462	G463	U464	G465	A466	G467	G468	G469	A470	A471	A472	G473	C474	C475	G476	A477	A478	A479	A480		
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G121	G122	G123	G124	A125	A126	A127	C128	C129	C130	A131	G132	U133	G134	U135	G136	U137	U138	U139	C140	G141	A142	C143	A144	C145	A146	C147	U148	A149	U150	C151	A152	U153	U154	A155	A156	C157	G158	G159	A160	A161	U162	C163	C164	A165	U166	A167	G168	G169	U170	U171	A172	U173	U174	G175	A176	G177	C178	C179	G180		
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G1623	U1563	A1503	U1443	A1383	C1323	U1263	U1203	A1143	U1083	U1023	U963	C903
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G1627	G1567	C1507	C1447	A1387	A1327	U1267	C1207	A1147	G1087	A1027	U967	G907
G1628	G1568	A1508	G1448	G1388	A1328	A1268	C1208	U1148	A1088	A1028	C968	A908
U1629	A1569	G1509	G1449	G1389	A1269	A1269	U1209	U1149	A1089	A1029	G969	A909
A1630	U1570	G1510	G1450	U1390	C1330	C1270	G1210	C1150	A1090	C1030	U970	A910
G1631	A1571	G1511	C1451	U1391	G1331	G1271	C1211	A1151	G1091	G1031	G971	A911
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A1637	G1577	C1517	U1457	U1397	G1337	G1277	U1217	G1157	U1097	G1037	G977	A917
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A1640	U1580	U1520	U1460	U1400	U1340	G1280	G1220	G1160	C1100	A1040	A980	A920
A1641	G1581	G1521	C1461	G1401	G1341	U1281	C1221	C1161	U1101	G1041	A981	C921
A1642	A1582	A1522	C1462	U1402	U1342	U1282	U1222	G1162	C1102	G1042	C982	C922
G1643	A1583	U1523	C1463	A1403	G1343	G1283	G1223	G1163	A1103	C1043	A983	G923
A1644	U1584	G1524	G1464	C1404	U1344	A1284	U1224	C1164	U1104	C1044	A984	G924
G1645	C1585	A1525	G1465	U1405	C1345	A1285	G1225	A1165	U1105	C1045	C985	A925
A1646	A1586	C1526	U1466	U1406	A1346	A1286	A1226	G1166	G1106	A1046	C986	G926
U1647	G1587	G1527	U1467	G1407	A1347	A1287	G1227	C1167	G1107	G1047	C987	A927
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G1651	A1591	C1531	G1471	U1411	C1351	C1291	U1231	G1171	A1111	G1051	C991	U931
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G1658	A1598	C1538	G1478	G1418	G1358	C1298	G1238	G1178	C1118	U1058	C998	G938
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C1675	C1615	G1555	A1495	G1435	U1375	C1315	U1255	G1195	C1135	C1075	U1015	PSD
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A1677	G1617	C1557	U1497	C1437	G1377	G1317	C1257	G1197	U1137	A1077	G1017	C957
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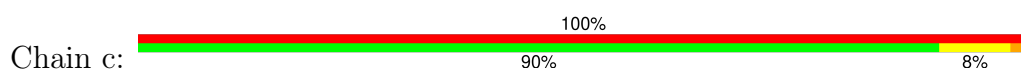
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G2345	G2405	C2225	C2285	A2225	C2165	U2105	C2045	C1985	C1925	U1865	A1805	A1745	C1685
A2346	A2406	C2226	G2286	C2226	U2166	U2106	G2046	C1986	U1926	A1866	C1806	A1746	C1686
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C2350	G2410	G2230	G2290	G2230	A2170	G2110	C2050	C1990	G1930	C1870	A1810	G1750	A1690
G2351	A2411	U2231	A2291	U2231	A2171	U2111	A2051	U1991	U1931	A1871	G1751	U1751	C1691
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C2354	G2414	G2234	G2294	G2234	C2174	A2114	A2054	C1994	C1934	C1874	G1814	A1754	C1694
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G2357	C2417	A2237	A2297	G2237	C2177	A2117	G2057	C1997	A1937	A1877	G1817	A1757	G1697
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G2367	G2427	U2247	G2307	G2247	U2187	G2127	G2067	U2007	C1947	C1887	U1827	G1767	G1707
C2368	G2428	C2248	G2308	C2248	U2188	G2128	U2068	C2008	G1948	G1888	G1828	C1768	C1708
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A2430	A2430	G2250	C2310	G2250	G2190	U2130	A2070	G2010	U1950	A1890	C1830	G1770	G1710
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A2432	A2432	G2252	U2312	G2252	U2192	U2132	C2072	G2012	A1952	G1892	C1832	A1772	U1712
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U2384	U2444	U2324	G2324	C2264	G2204	G2144	C2084	C2024	G1964	G1904	C1844	A1784	G1724
G2385	G2385	G2325	G2325	U2265	A2205	C2145	U2085	G2025	C1965	C1905	G1845	A1785	U1725
A2386	G2446	C2326	G2326	A2266	C2206	C2146	U2086	C2026	A1966	G1906	G1846	A1786	C1726
U2387	G2447	A2327	C2327	A2267	C2207	A2147	G2087	U2027	C1967	G1907	A1847	U1787	C1727
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G2389	U2449	U2329	G2329	G2269	C2209	U2149	C2089	G2029	A1969	C1909	G1849	U1789	U1729
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A2391	A2451	G2331	G2331	G2271	A2211	U2151	C2091	A2031	U1971	PSU	U1851	A1791	G1731
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• Molecule 39: 50S ribosomal protein L27

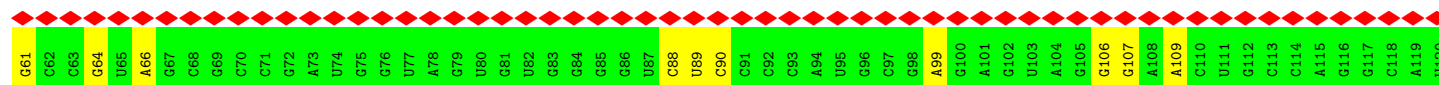
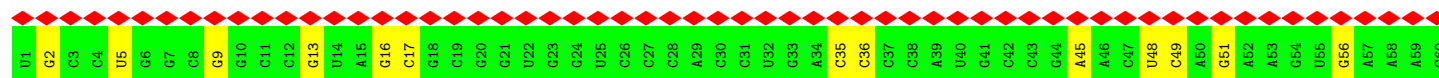
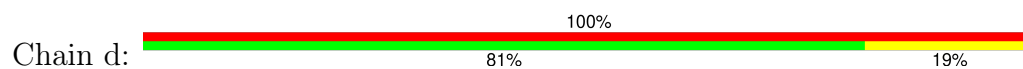


• Molecule 40: 50S ribosomal protein L28

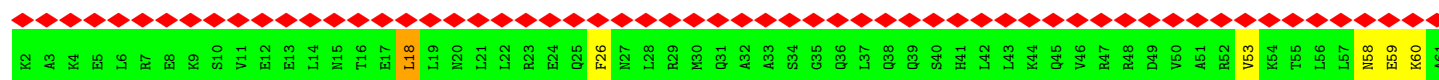
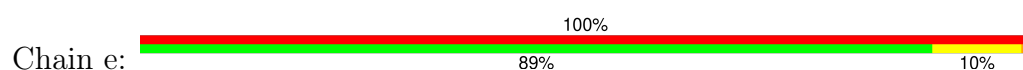




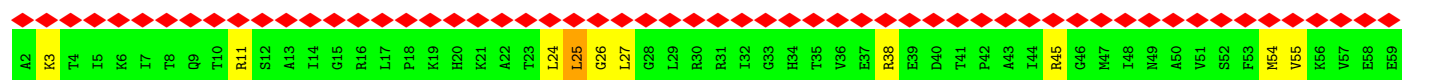
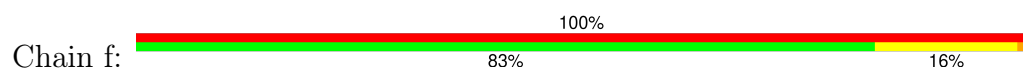
• Molecule 41: 5S rRNA



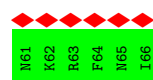
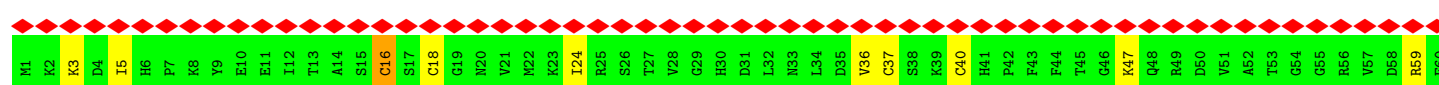
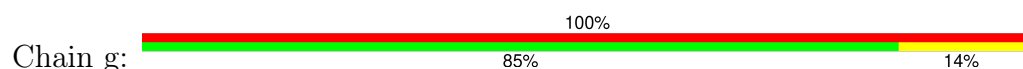
• Molecule 42: 50S ribosomal protein L29



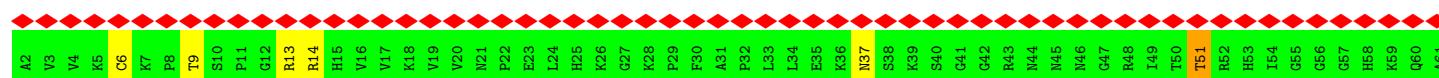
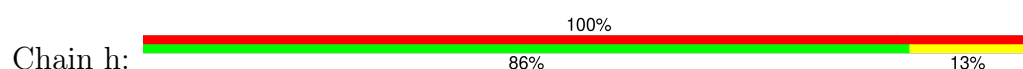
• Molecule 43: 50S ribosomal protein L30

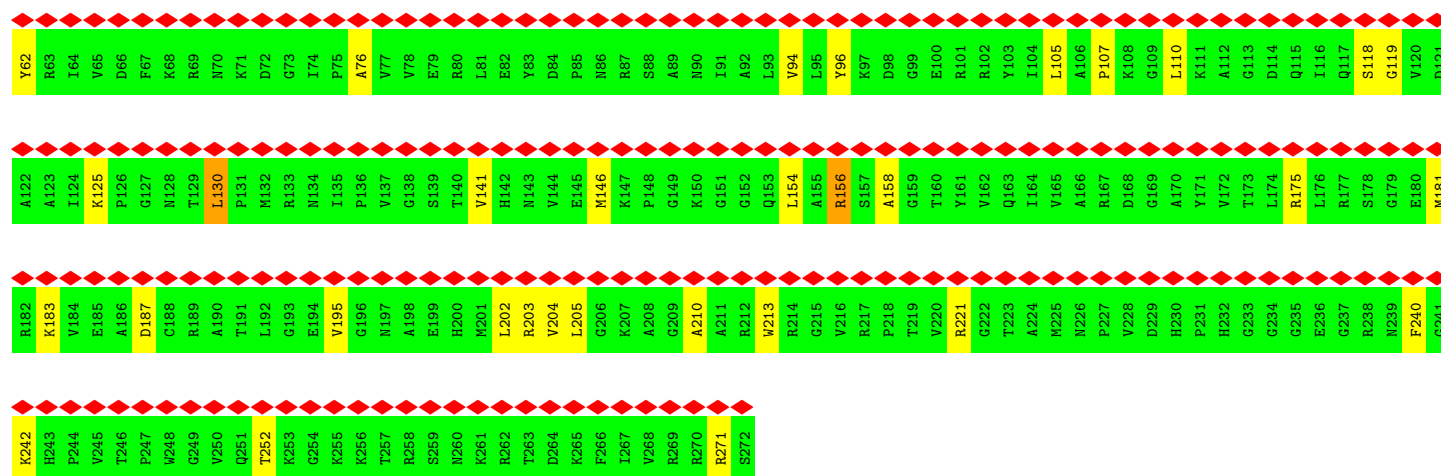


• Molecule 44: 50S ribosomal protein L31

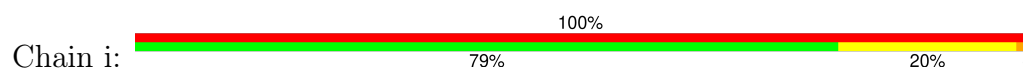


• Molecule 45: 50S ribosomal protein L2

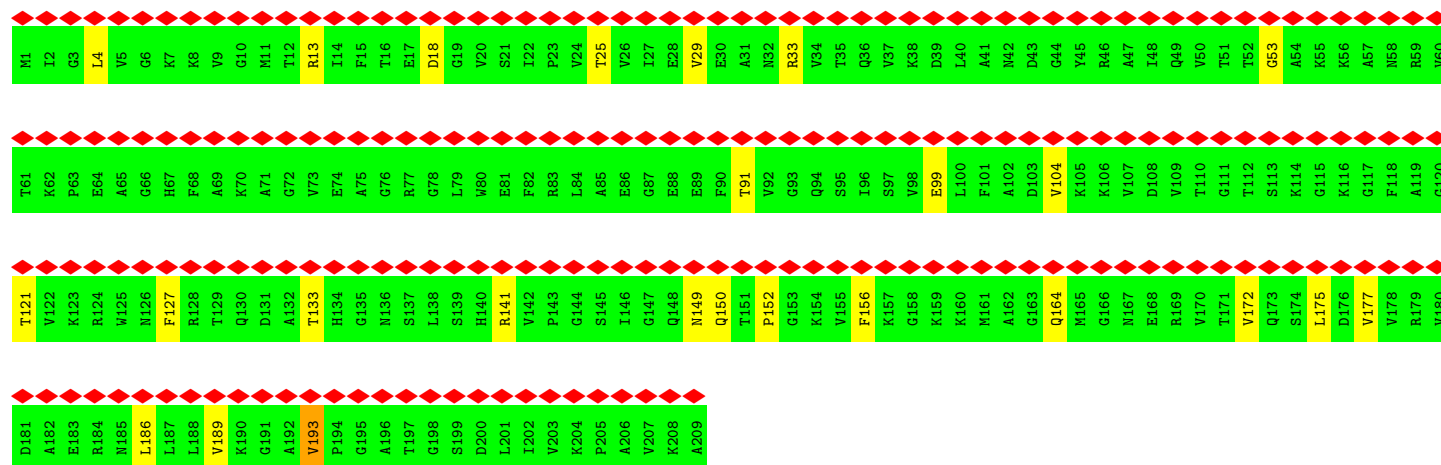
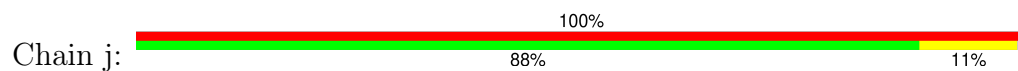




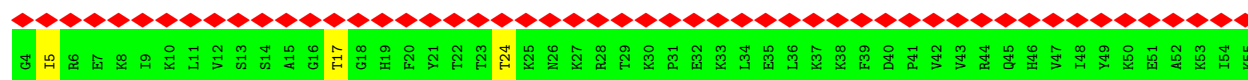
• Molecule 46: 50S ribosomal protein L32



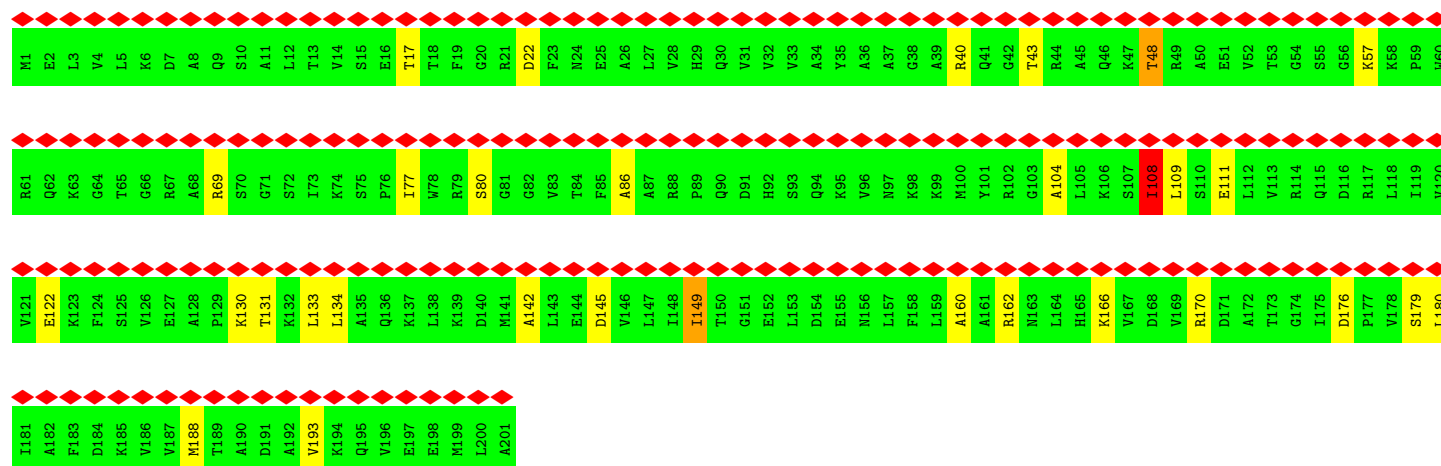
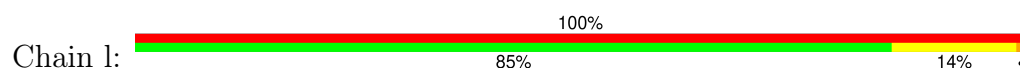
• Molecule 47: 50S ribosomal protein L3



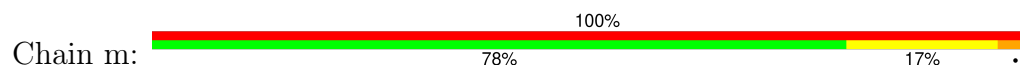
• Molecule 48: 50S ribosomal protein L33



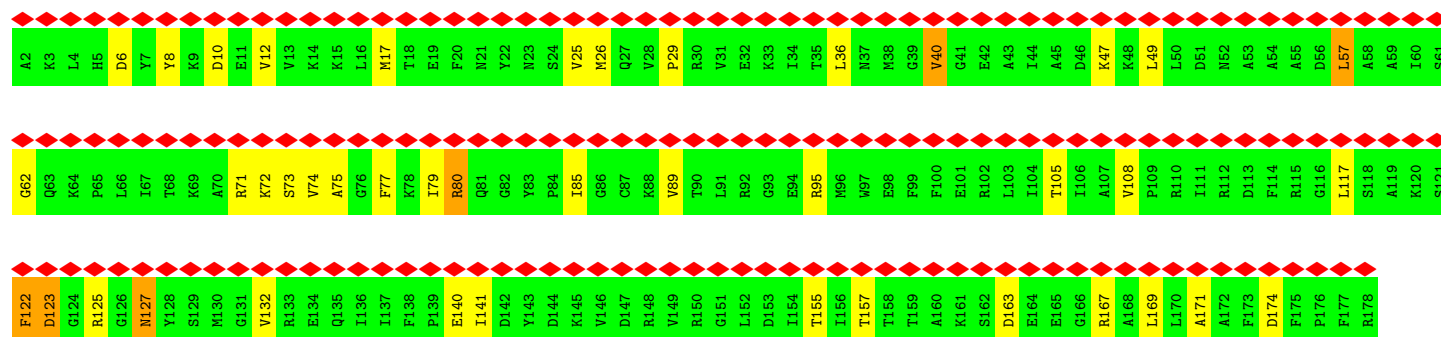
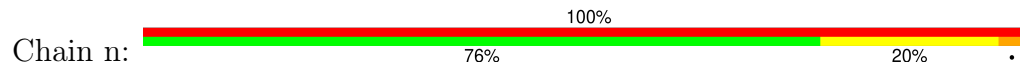
• Molecule 49: 50S ribosomal protein L4



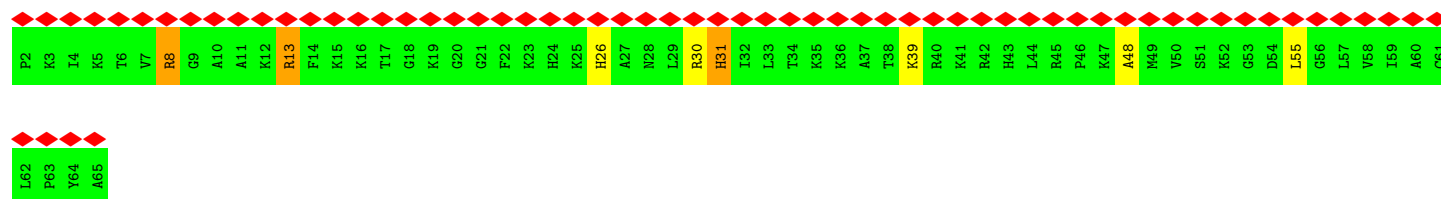
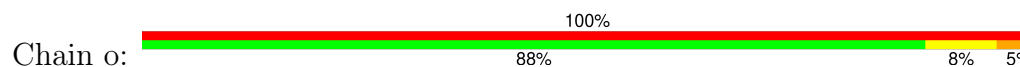
• Molecule 50: 50S ribosomal protein L34



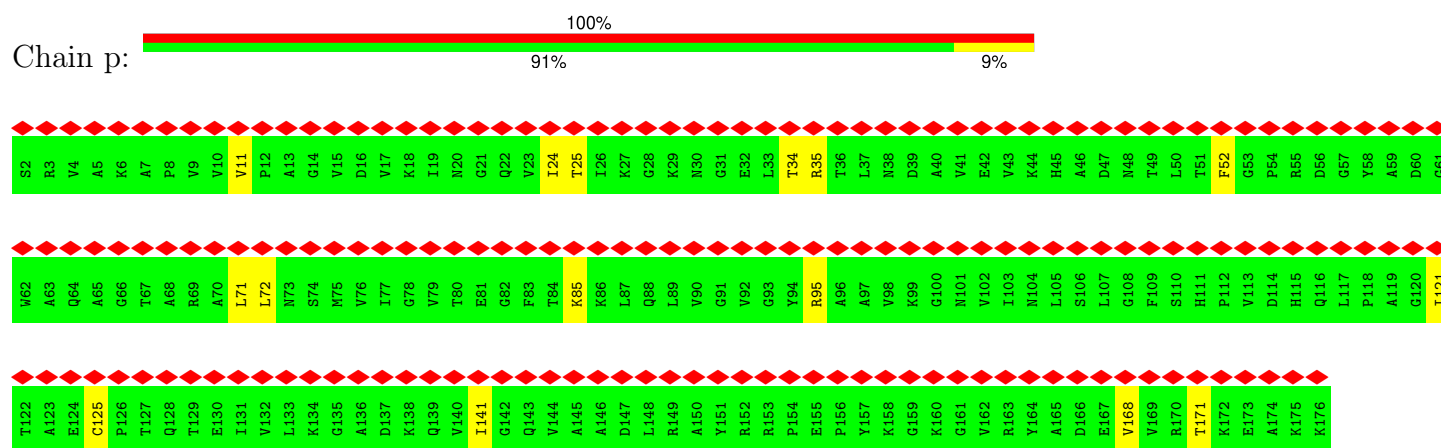
• Molecule 51: 50S ribosomal protein L5



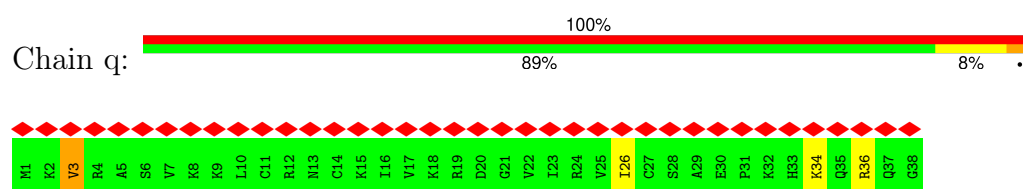
• Molecule 52: 50S ribosomal protein L35



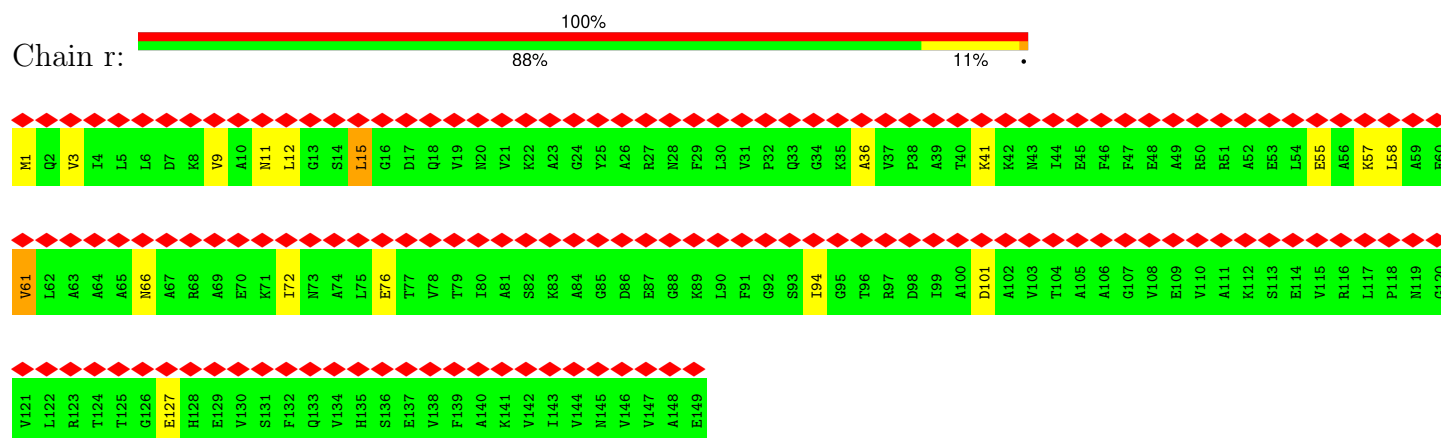
• Molecule 53: 50S ribosomal protein L6



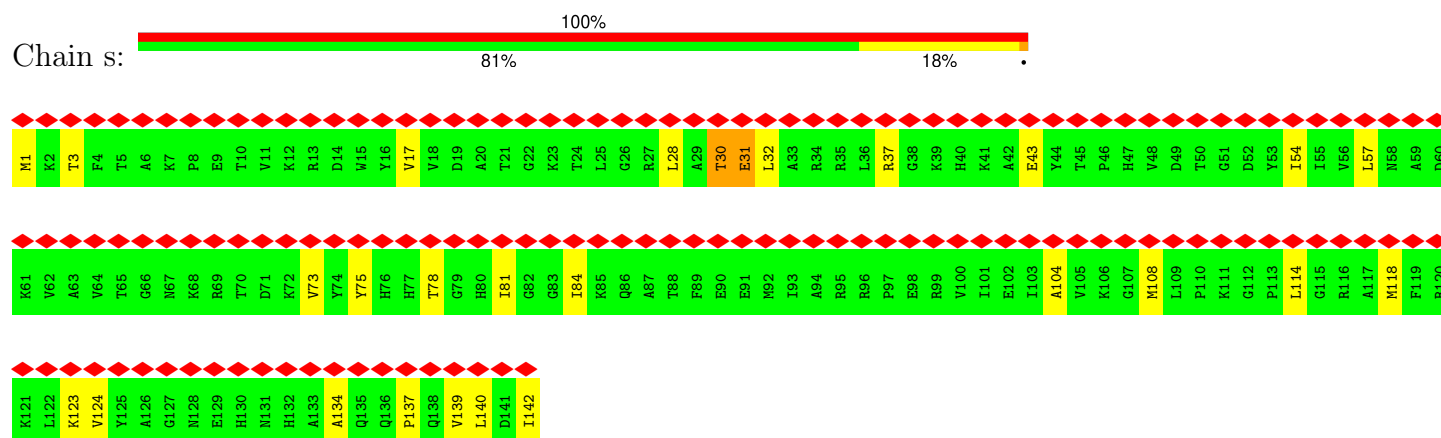
- Molecule 54: 50S ribosomal protein L36



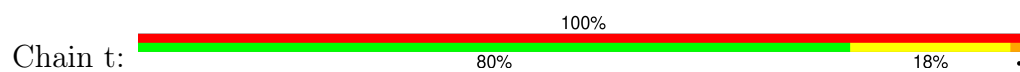
- Molecule 55: 50S ribosomal protein L9



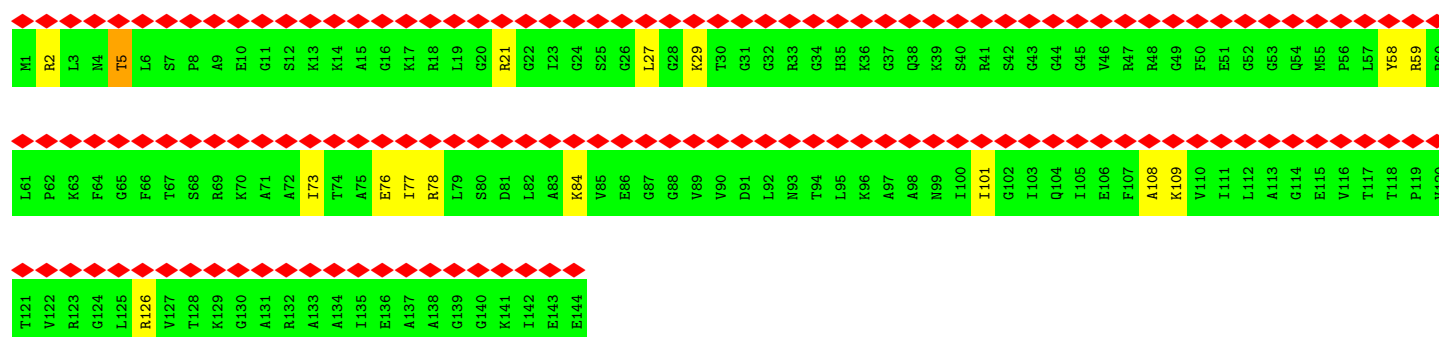
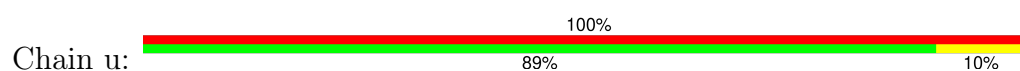
- Molecule 56: 50S ribosomal protein L13



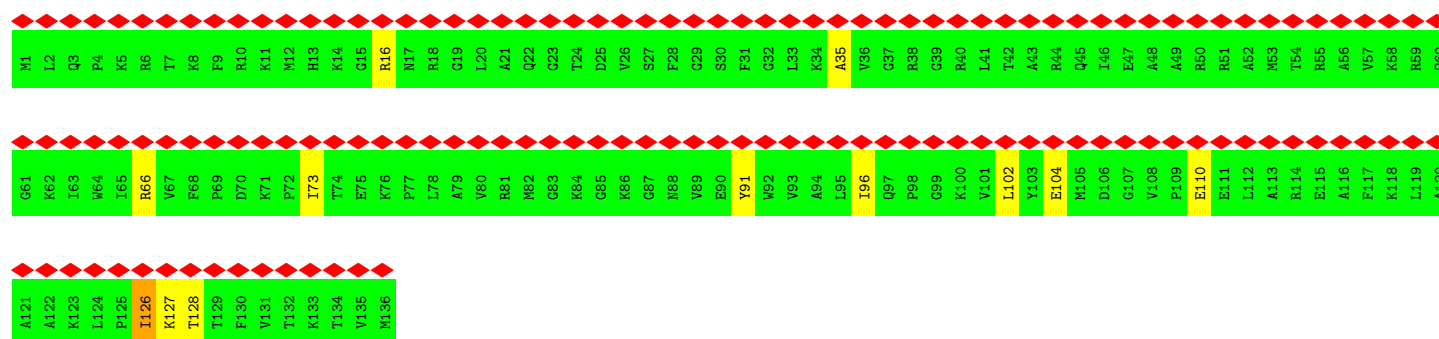
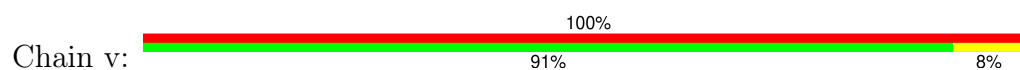
- Molecule 57: 50S ribosomal protein L14



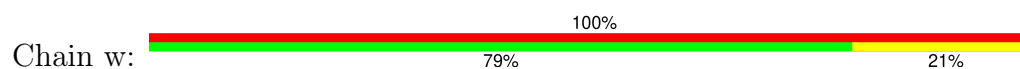
• Molecule 58: 50S ribosomal protein L15

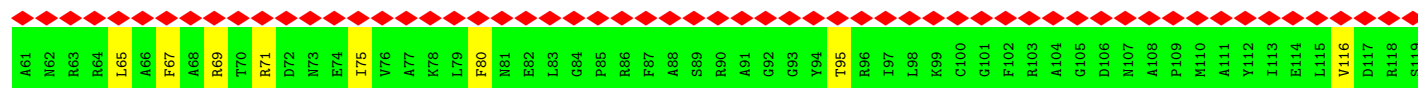


• Molecule 59: 50S ribosomal protein L16

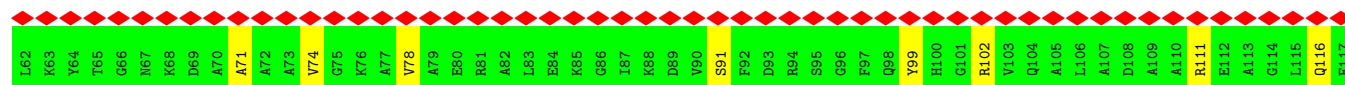
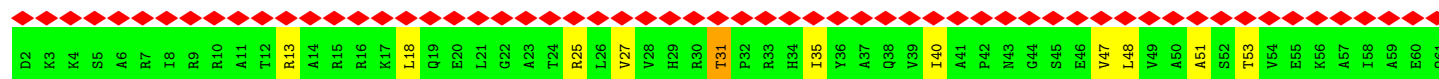
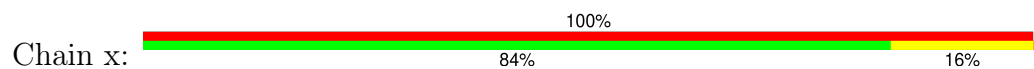


• Molecule 60: 50S ribosomal protein L17

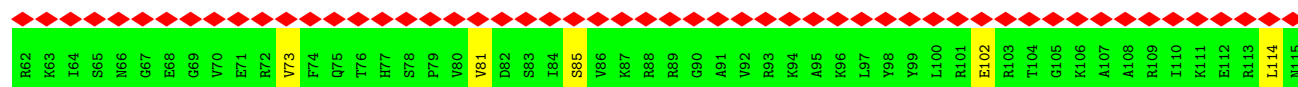
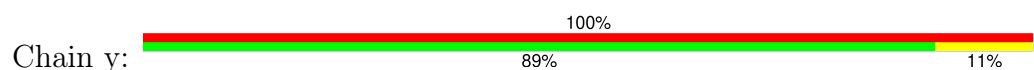




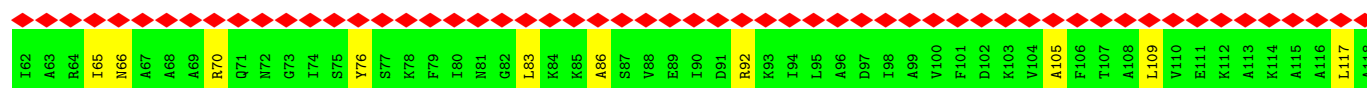
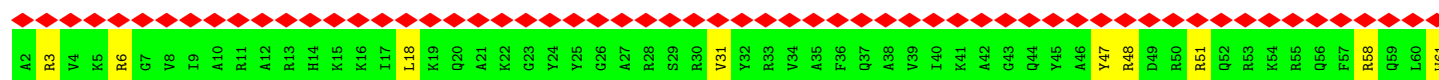
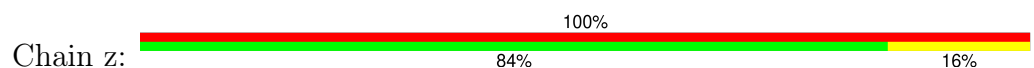
• Molecule 61: 50S ribosomal protein L18



• 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	5979	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	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	0.080	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	564.48, 564.48, 564.48	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.016, 2.016, 2.016	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	0.78	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	0.76	4/388 (1.0%)	0.55	0/604
9	A	0.36	0/1810	0.72	2/2821 (0.1%)
9	B	0.43	0/1810	0.87	9/2821 (0.3%)
10	AA	0.67	14/10591 (0.1%)	0.98	56/14289 (0.4%)
11	AB	0.42	0/808	0.70	2/1088 (0.2%)
12	AC	0.58	4/1808 (0.2%)	0.70	9/2450 (0.4%)
12	AD	0.39	0/1789	0.55	0/2425
13	AE	0.54	8/10545 (0.1%)	0.74	25/14236 (0.2%)
14	AF	0.47	0/657	0.73	0/886
15	C	0.66	0/553	1.14	2/743 (0.3%)
16	D	0.40	9/36610 (0.0%)	0.75	40/57091 (0.1%)
17	E	0.76	0/675	1.32	0/895
18	F	0.71	0/597	1.20	0/792
19	G	0.65	0/1791	1.08	1/2413 (0.0%)
20	H	0.76	4/1746 (0.2%)	1.58	34/2382 (1.4%)
21	I	0.58	0/1663	0.98	0/2241
22	J	0.63	0/1665	1.08	0/2227
23	K	0.64	0/1165	1.06	2/1568 (0.1%)
24	L	0.58	0/867	0.94	0/1171
25	M	0.68	0/1195	1.19	3/1602 (0.2%)
26	N	0.55	0/989	0.91	0/1326
27	O	0.58	0/1034	1.02	1/1375 (0.1%)
28	P	0.60	0/800	1.10	4/1082 (0.4%)
29	Q	0.55	0/893	0.91	0/1205
30	R	0.49	0/952	0.81	0/1274

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	S	0.64	0/817	1.11	1/1088 (0.1%)
32	T	0.69	0/722	1.21	0/964
33	U	0.57	0/659	0.99	0/884
34	V	0.46	0/657	0.73	0/881
35	W	0.51	0/680	0.83	0/915
36	X	0.67	0/909	1.21	3/1215 (0.2%)
37	Y	0.42	0/65	0.86	0/98
38	a	0.40	3/69247 (0.0%)	0.75	56/107985 (0.1%)
39	b	0.51	0/589	0.76	0/779
40	c	0.63	0/635	0.97	0/848
41	d	0.38	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	0.60	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	0.51	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	0.55	0/1062	0.95	1/1413 (0.1%)
59	v	0.60	0/1093	0.97	0/1460
60	w	0.68	0/964	1.13	0/1289
61	x	0.61	0/902	1.09	0/1209
62	y	0.53	0/929	0.79	0/1242
63	z	0.80	0/960	1.25	0/1278
All	All	0.49	48/187139 (0.0%)	0.83	267/276026 (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
9	A	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	B	0	2
10	AA	0	12
13	AE	0	5
14	AF	0	1
20	H	0	3
36	X	0	1
All	All	0	26

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	AA	374	GLU	C-N	17.47	1.53	1.33
10	AA	850	ILE	N-CA	-13.10	1.29	1.46
13	AE	93	THR	CA-C	12.26	1.69	1.52
20	H	169	SER	N-CA	11.74	1.61	1.46
16	D	1516	G	O3'-P	-10.78	1.45	1.61

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	D	1516	G	O3'-P-O5'	17.45	130.17	104.00
10	AA	1007	LYS	O-C-N	-17.26	101.87	122.58
10	AA	727	VAL	N-CA-C	-17.24	95.05	110.74
20	H	88	LYS	CA-C-N	16.93	143.58	120.38
20	H	88	LYS	C-N-CA	16.93	143.58	120.38

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	A	19	G	Sidechain
9	A	7	G	Sidechain
10	AA	205	PRO	Peptide
10	AA	594	VAL	Peptide
10	AA	595	THR	Peptide

5.2 Too-close contacts

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	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	10	0
5	4	753	780	780	0	0
6	5	472	260	261	23	0
7	6	542	306	306	15	0
8	7	347	168	169	16	0
9	A	1620	826	826	174	0
9	B	1620	813	827	139	0
10	AA	10425	10427	10430	354	0
11	AB	790	783	783	7	0
12	AC	1786	1813	1813	44	0
12	AD	1767	1789	1789	47	0
13	AE	10388	10611	10611	364	0
14	AF	655	663	663	14	0
15	C	544	559	560	24	0
16	D	32703	16423	16460	189	0
17	E	669	719	719	4	0
18	F	589	629	629	8	0
19	G	1760	1785	1785	47	0
20	H	1730	1454	1454	211	0
21	I	1636	1710	1710	7	0
22	J	1643	1707	1707	15	0
23	K	1152	1196	1196	16	0
24	L	848	846	846	3	0
25	M	1181	1235	1235	34	0
26	N	979	1031	1031	5	0
27	O	1022	1070	1070	11	0
28	P	790	831	831	22	0
29	Q	877	887	887	4	0
30	R	939	1001	1001	6	0
31	S	805	844	844	6	0
32	T	714	734	734	8	0
33	U	649	666	666	3	0
34	V	648	691	691	4	0
35	W	663	688	688	2	0
36	X	900	964	964	57	0
37	Y	60	30	31	2	0
38	a	61841	31077	31124	277	0
39	b	582	599	599	2	0
40	c	625	652	652	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
41	d	2569	1301	1301	3	0
42	e	501	531	531	4	0
43	f	448	488	488	6	0
44	g	522	520	520	11	0
45	h	2082	2154	2154	18	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	5	0
53	p	1313	1358	1358	7	0
54	q	302	343	343	1	0
55	r	1111	1148	1148	5	0
56	s	1129	1162	1162	15	0
57	t	946	1023	1023	12	0
58	u	1053	1129	1129	8	0
59	v	1074	1157	1157	5	0
60	w	951	994	994	10	0
61	x	892	923	923	8	0
62	y	917	962	962	4	0
63	z	947	1020	1019	13	0
64	7	1	0	0	0	0
65	AA	2	0	0	0	0
All	All	173959	125488	125591	2065	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 7.

The worst 5 of 2065 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)
20:H:131:LEU:CB	20:H:167:VAL:CA	1.78	1.56
15:C:12:ARG:HG3	20:H:264:GLU:CB	1.30	1.54
20:H:131:LEU:CB	20:H:167:VAL:HA	1.03	1.48
20:H:71:ALA:C	20:H:72:LEU:HD12	1.49	1.35
16:D:1358:U:O4	16:D:1363:A:N1	1.60	1.34

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	48
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
4	3	101/103 (98%)	96 (95%)	4 (4%)	1 (1%)	12	48
5	4	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
10	AA	1318/1341 (98%)	1145 (87%)	140 (11%)	33 (2%)	4	26
11	AB	94/112 (84%)	88 (94%)	6 (6%)	0	100	100
12	AC	228/230 (99%)	214 (94%)	12 (5%)	2 (1%)	14	51
12	AD	226/230 (98%)	212 (94%)	14 (6%)	0	100	100
13	AE	1329/1358 (98%)	1198 (90%)	122 (9%)	9 (1%)	18	56
14	AF	81/83 (98%)	74 (91%)	7 (9%)	0	100	100
15	C	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
17	E	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
18	F	68/70 (97%)	68 (100%)	0	0	100	100
19	G	223/225 (99%)	210 (94%)	13 (6%)	0	100	100
20	H	255/557 (46%)	189 (74%)	54 (21%)	12 (5%)	2	16
21	I	206/208 (99%)	196 (95%)	9 (4%)	1 (0%)	24	63
22	J	203/205 (99%)	198 (98%)	5 (2%)	0	100	100
23	K	154/156 (99%)	146 (95%)	7 (4%)	1 (1%)	21	59
24	L	102/104 (98%)	97 (95%)	4 (4%)	1 (1%)	12	48
25	M	149/151 (99%)	144 (97%)	4 (3%)	1 (1%)	18	56
26	N	127/129 (98%)	121 (95%)	5 (4%)	1 (1%)	16	54
27	O	125/127 (98%)	115 (92%)	9 (7%)	1 (1%)	16	54
28	P	97/99 (98%)	88 (91%)	8 (8%)	1 (1%)	12	48
29	Q	115/117 (98%)	104 (90%)	9 (8%)	2 (2%)	7	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	R	117/123 (95%)	116 (99%)	1 (1%)	0	100	100
31	S	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
32	T	86/88 (98%)	82 (95%)	4 (5%)	0	100	100
33	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	9	42
34	V	78/80 (98%)	74 (95%)	4 (5%)	0	100	100
35	W	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
36	X	114/116 (98%)	107 (94%)	5 (4%)	2 (2%)	6	34
39	b	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
40	c	75/77 (97%)	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	67
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	50/52 (96%)	50 (100%)	0	0	100	100
49	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	24	63
50	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
51	n	175/177 (99%)	162 (93%)	11 (6%)	2 (1%)	11	46
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
63	z	115/117 (98%)	110 (96%)	4 (4%)	1 (1%)	14	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	9136/9618 (95%)	8457 (93%)	604 (7%)	75 (1%)	18	54

5 of 75 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	AA	596	ASP
10	AA	853	ASP
10	AA	859	GLU
10	AA	862	LEU
10	AA	937	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	76 (90%)	8 (10%)	8	25
2	1	93/93 (100%)	86 (92%)	7 (8%)	12	33
3	2	81/81 (100%)	77 (95%)	4 (5%)	22	43
4	3	84/84 (100%)	79 (94%)	5 (6%)	17	39
5	4	78/78 (100%)	75 (96%)	3 (4%)	29	50
10	AA	1140/1156 (99%)	1027 (90%)	113 (10%)	7	24
11	AB	86/98 (88%)	85 (99%)	1 (1%)	63	75
12	AC	198/198 (100%)	185 (93%)	13 (7%)	15	37
12	AD	196/198 (99%)	193 (98%)	3 (2%)	57	72
13	AE	1120/1134 (99%)	1046 (93%)	74 (7%)	15	37
14	AF	70/70 (100%)	68 (97%)	2 (3%)	37	58
15	C	57/57 (100%)	55 (96%)	2 (4%)	32	53
17	E	65/65 (100%)	61 (94%)	4 (6%)	16	38
18	F	60/60 (100%)	57 (95%)	3 (5%)	22	43
19	G	187/187 (100%)	174 (93%)	13 (7%)	14	35
20	H	137/461 (30%)	124 (90%)	13 (10%)	8	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	I	171/171 (100%)	163 (95%)	8 (5%)	23	45
22	J	172/172 (100%)	164 (95%)	8 (5%)	23	45
23	K	119/119 (100%)	111 (93%)	8 (7%)	15	36
24	L	91/91 (100%)	84 (92%)	7 (8%)	12	32
25	M	124/124 (100%)	113 (91%)	11 (9%)	9	28
26	N	104/104 (100%)	101 (97%)	3 (3%)	37	58
27	O	105/105 (100%)	99 (94%)	6 (6%)	18	40
28	P	86/86 (100%)	77 (90%)	9 (10%)	6	21
29	Q	90/90 (100%)	88 (98%)	2 (2%)	45	64
30	R	101/103 (98%)	95 (94%)	6 (6%)	18	39
31	S	83/83 (100%)	79 (95%)	4 (5%)	23	44
32	T	76/76 (100%)	65 (86%)	11 (14%)	3	13
33	U	65/65 (100%)	60 (92%)	5 (8%)	12	32
34	V	74/74 (100%)	71 (96%)	3 (4%)	27	48
35	W	72/72 (100%)	66 (92%)	6 (8%)	10	30
36	X	94/94 (100%)	87 (93%)	7 (7%)	13	33
39	b	58/58 (100%)	57 (98%)	1 (2%)	53	69
40	c	67/67 (100%)	64 (96%)	3 (4%)	24	46
42	e	54/54 (100%)	51 (94%)	3 (6%)	19	40
43	f	48/48 (100%)	43 (90%)	5 (10%)	7	22
44	g	59/59 (100%)	54 (92%)	5 (8%)	10	29
45	h	216/216 (100%)	199 (92%)	17 (8%)	11	32
46	i	47/47 (100%)	41 (87%)	6 (13%)	4	15
47	j	164/164 (100%)	156 (95%)	8 (5%)	22	43
48	k	47/47 (100%)	44 (94%)	3 (6%)	16	37
49	l	165/165 (100%)	151 (92%)	14 (8%)	10	29
50	m	38/38 (100%)	36 (95%)	2 (5%)	20	41
51	n	148/148 (100%)	130 (88%)	18 (12%)	5	17
52	o	51/51 (100%)	47 (92%)	4 (8%)	11	32
53	p	136/136 (100%)	130 (96%)	6 (4%)	25	47
54	q	34/34 (100%)	31 (91%)	3 (9%)	9	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	r	114/114 (100%)	102 (90%)	12 (10%)	6	21
56	s	116/116 (100%)	106 (91%)	10 (9%)	10	29
57	t	104/104 (100%)	97 (93%)	7 (7%)	15	36
58	u	103/103 (100%)	96 (93%)	7 (7%)	14	36
59	v	109/109 (100%)	105 (96%)	4 (4%)	30	51
60	w	99/99 (100%)	91 (92%)	8 (8%)	11	31
61	x	86/86 (100%)	80 (93%)	6 (7%)	14	35
62	y	99/99 (100%)	91 (92%)	8 (8%)	11	31
63	z	89/89 (100%)	85 (96%)	4 (4%)	24	46
All	All	7614/7984 (95%)	7078 (93%)	536 (7%)	16	35

5 of 536 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
53	p	95	ARG
55	r	66	ASN
53	p	85	LYS
61	x	47	VAL
13	AE	146	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
52	o	28	ASN
54	q	35	GLN
13	AE	1238	GLN
13	AE	1195	GLN
55	r	11	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	D	1515/1542 (98%)	290 (19%)	35 (2%)
37	Y	2/3 (66%)	2 (100%)	0
38	a	2859/2903 (98%)	540 (18%)	0
41	d	119/120 (99%)	17 (14%)	0
8	7	15/16 (93%)	7 (46%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	A	75/76 (98%)	29 (38%)	6 (8%)
9	B	75/76 (98%)	35 (46%)	6 (8%)
All	All	4660/4736 (98%)	920 (19%)	47 (1%)

5 of 920 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	56	U
8	7	57	G
8	7	58	A
8	7	59	U
8	7	60	U

5 of 47 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	D	722	G
16	D	1211	U
16	D	793	U
16	D	1109	C
16	D	1213	A

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.

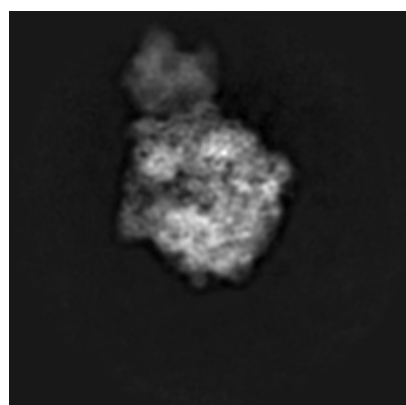
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21486. These allow visual inspection of the internal detail of the map and identification of artifacts.

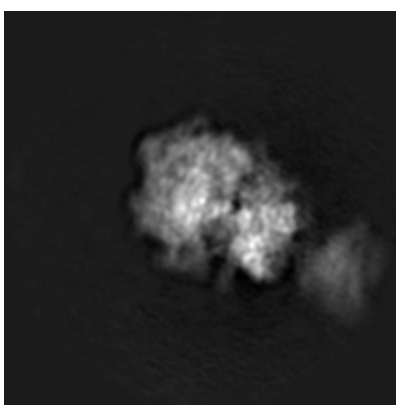
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

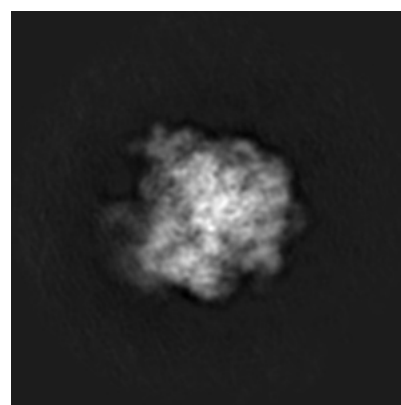
6.1.1 Primary map



X



Y

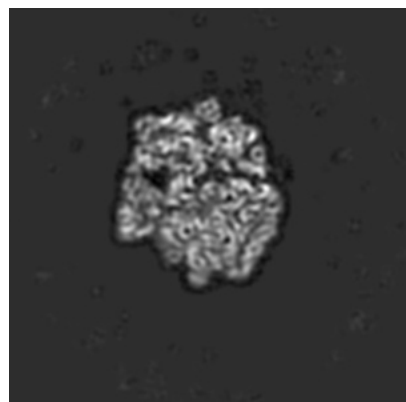


Z

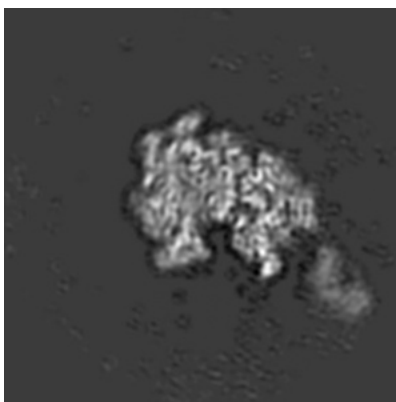
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

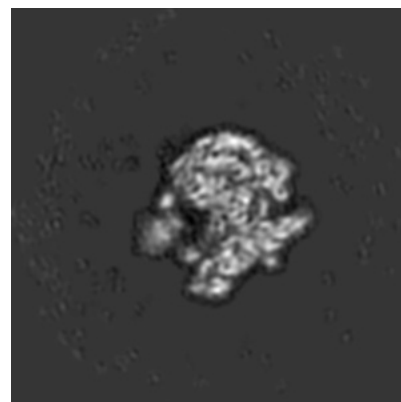
6.2.1 Primary map



X Index: 140



Y Index: 140

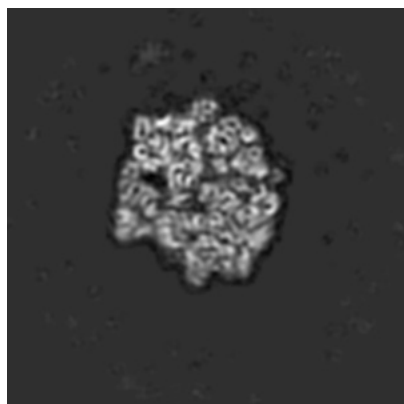


Z Index: 140

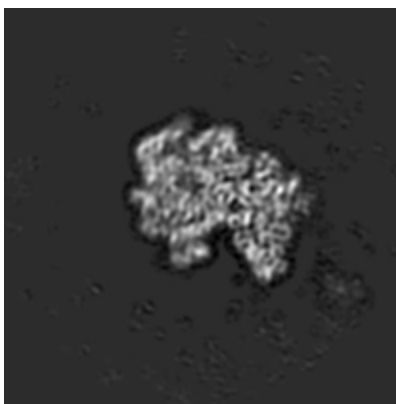
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

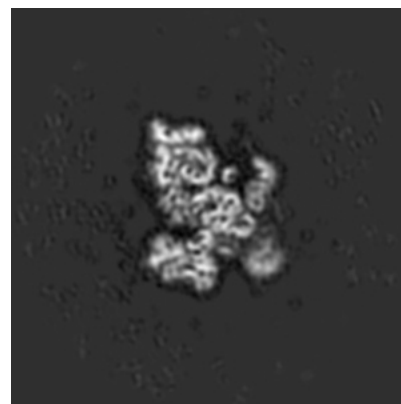
6.3.1 Primary map



X Index: 137



Y Index: 147

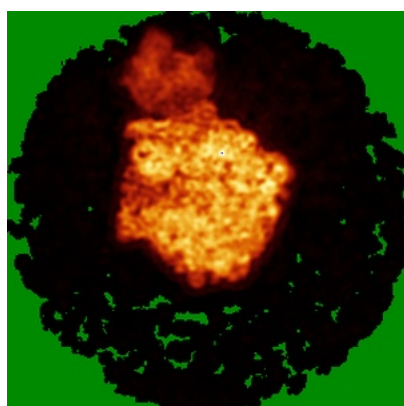


Z Index: 169

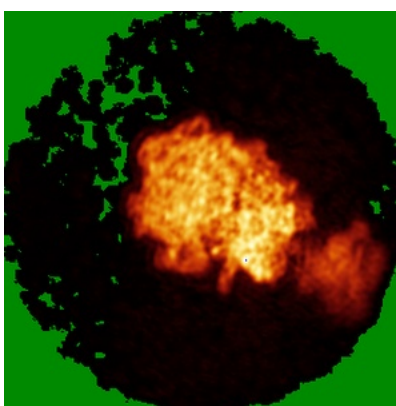
The images above show the largest variance slices of the map in three orthogonal directions.

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

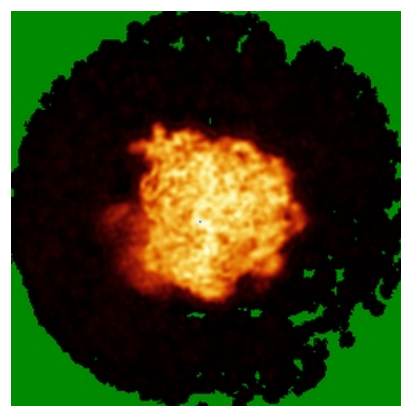
6.4.1 Primary map



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

6.5.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

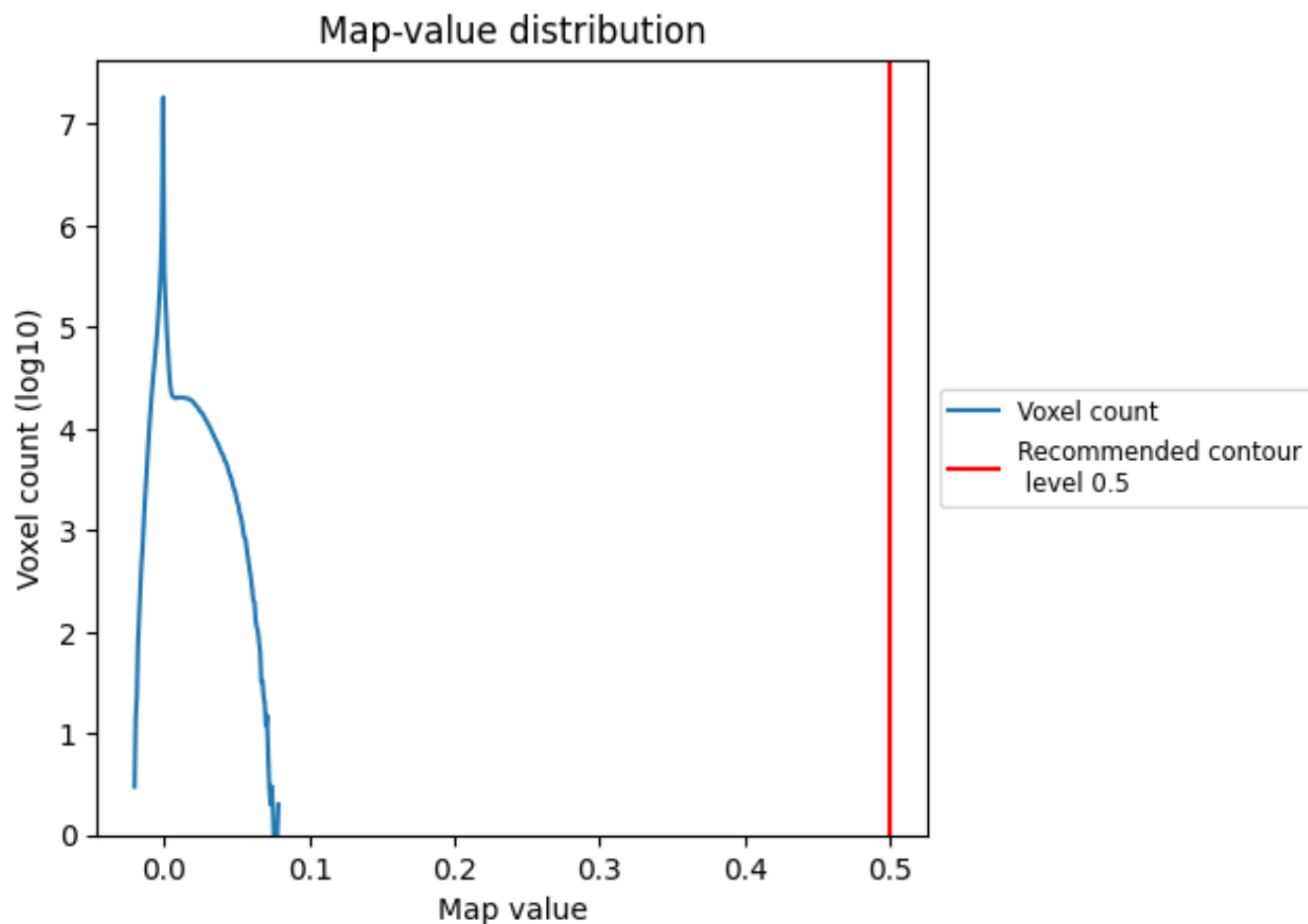
6.6 Mask visualisation

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

7 Map analysis [i](#)

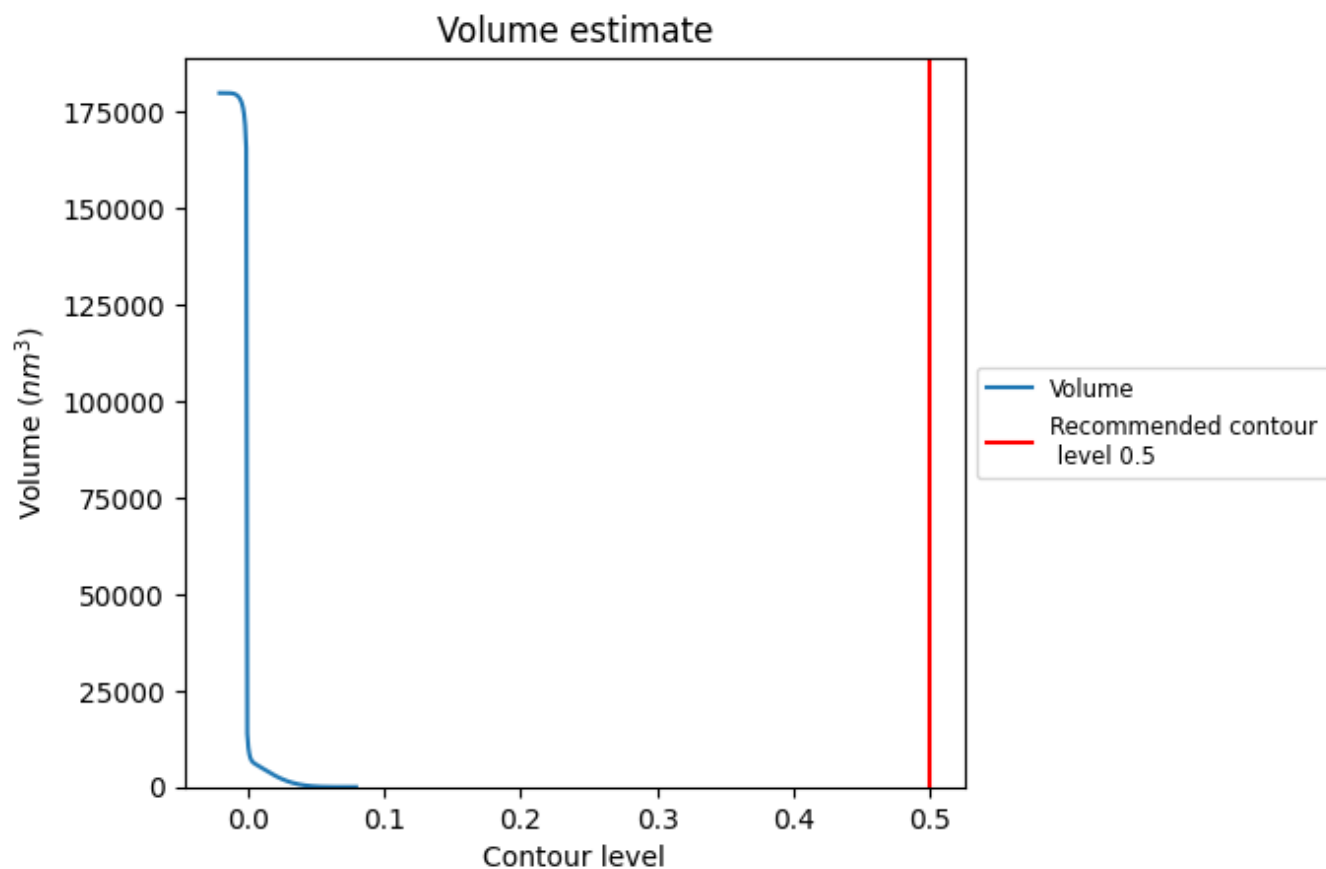
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



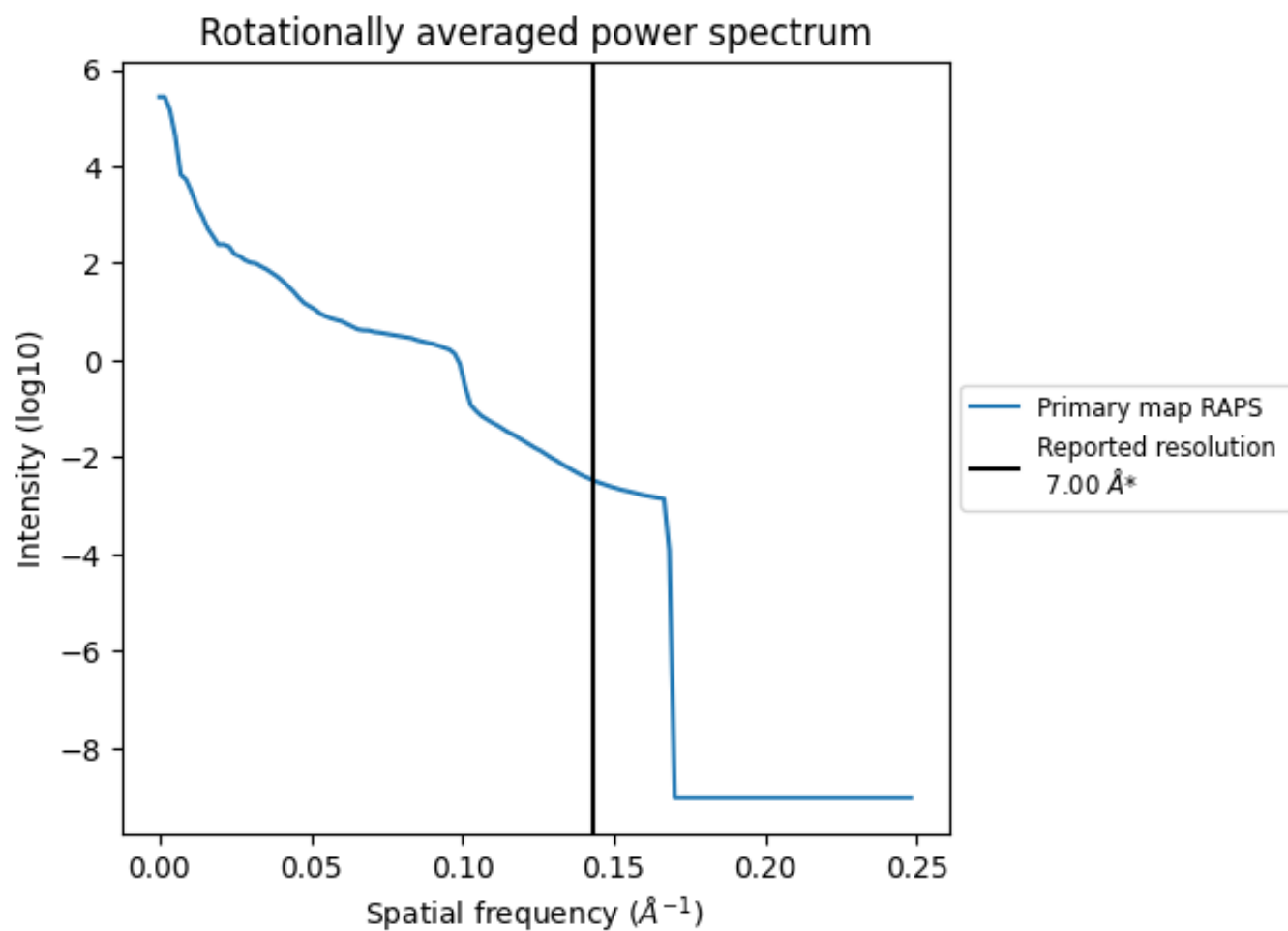
The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2 Volume estimate [i](#)



The volume 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 0.143 Å⁻¹

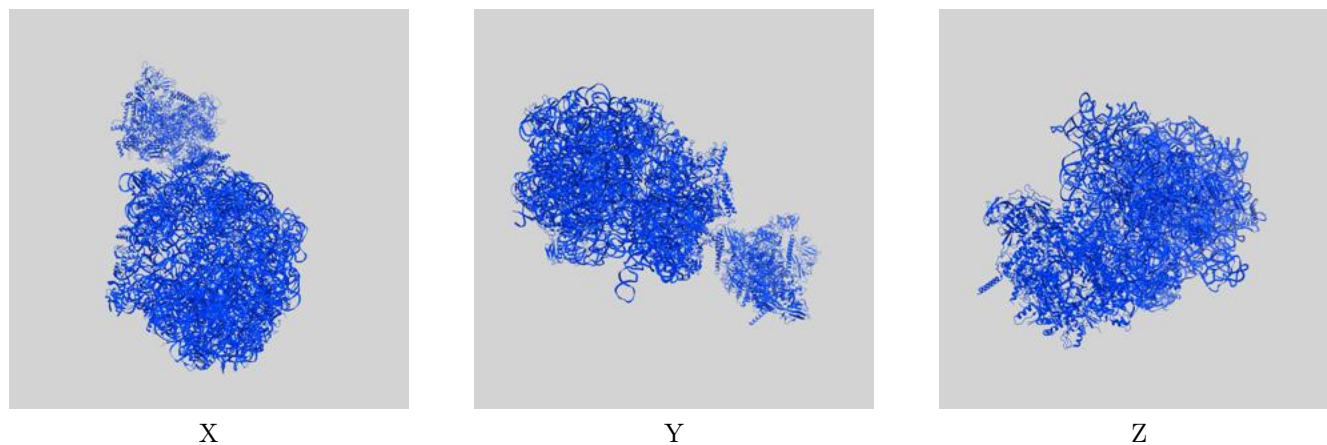
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

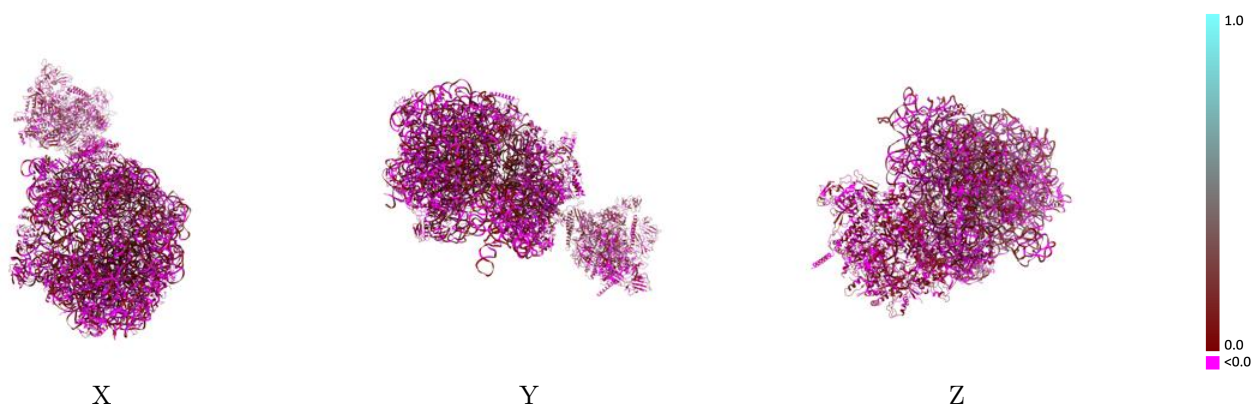
This section contains information regarding the fit between EMDB map EMD-21486 and PDB model 6VZ7. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



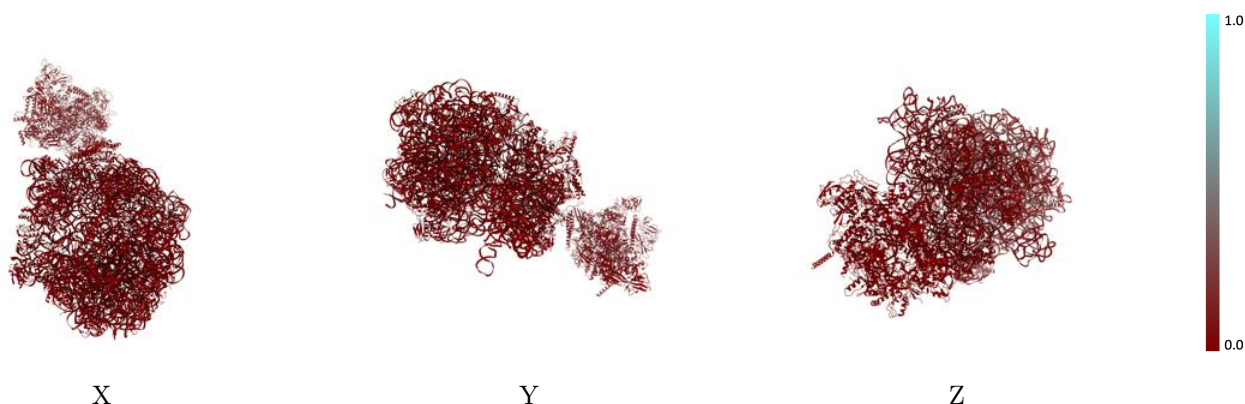
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



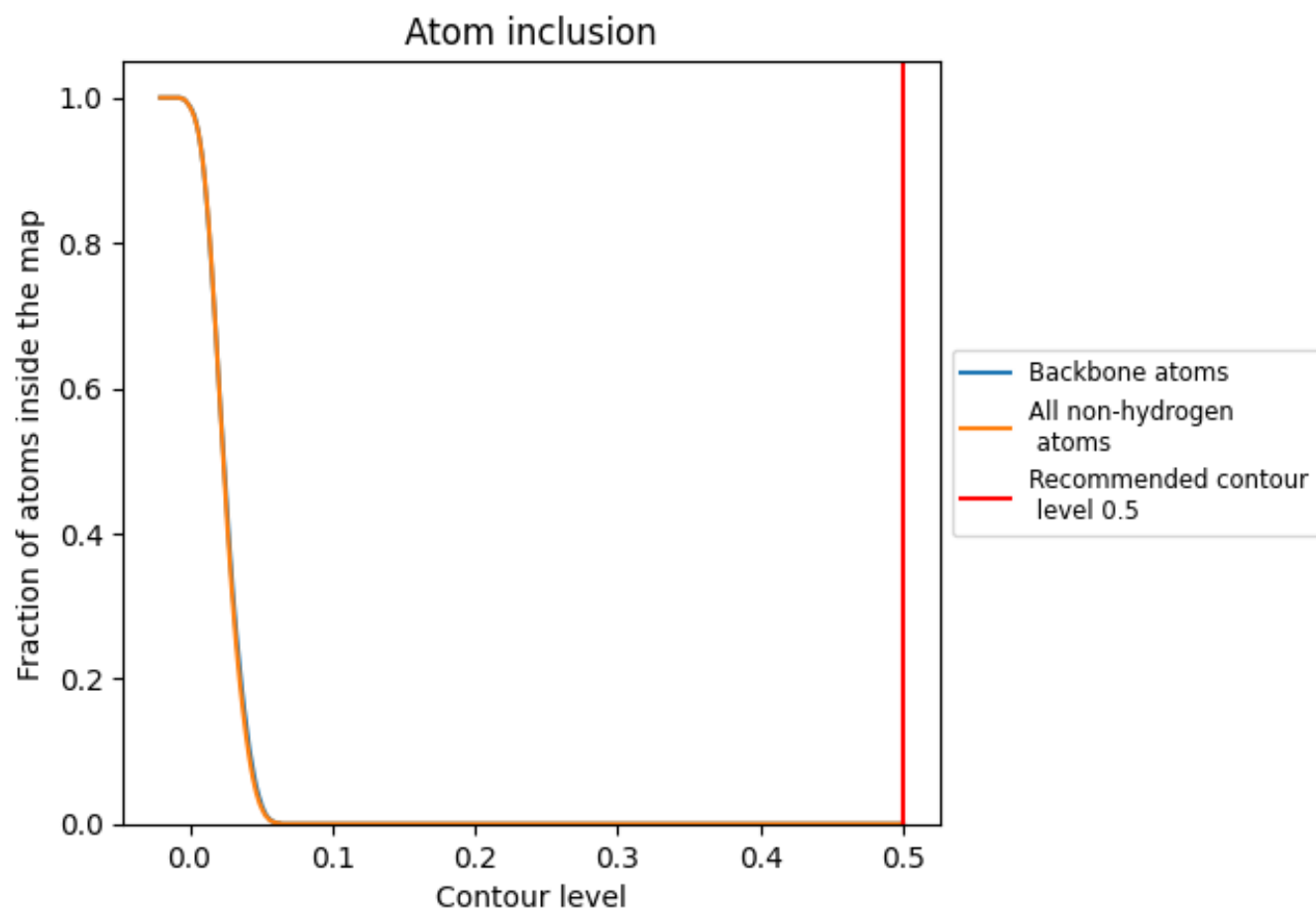
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 0% of all backbone atoms, 0% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.0000	0.0300
0	0.0000	0.0020
1	0.0000	0.0080
2	0.0000	-0.0330
3	0.0000	-0.0130
4	0.0000	-0.0030
5	0.0000	0.0950
6	0.0000	0.0900
7	0.0000	0.0580
A	0.0000	0.0900
AA	0.0000	0.0590
AB	0.0000	-0.0250
AC	0.0000	0.0180
AD	0.0000	-0.0080
AE	0.0000	0.0240
AF	0.0000	0.0100
B	0.0000	0.0390
C	0.0000	-0.0340
D	0.0000	0.0480
E	0.0000	-0.0150
F	0.0000	0.0690
G	0.0000	-0.0150
H	0.0000	0.0120
I	0.0000	-0.0090
J	0.0000	-0.0300
K	0.0000	0.0230
L	0.0000	0.0250
M	0.0000	-0.0080
N	0.0000	-0.0380
O	0.0000	-0.0220
P	0.0000	0.0170
Q	0.0000	0.0100
R	0.0000	0.0630
S	0.0000	-0.0070
T	0.0000	0.0160



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Chain	Atom inclusion	Q-score
U	 0.0000	 -0.0240
V	 0.0000	 0.0350
W	 0.0000	 -0.0100
X	 0.0000	 -0.0140
Y	 0.0000	 0.1350
a	 0.0000	 0.0430
b	 0.0000	 -0.0530
c	 0.0000	 0.0060
d	 0.0000	 0.0100
e	 0.0000	 -0.0190
f	 0.0000	 -0.0020
g	 0.0000	 0.0100
h	 0.0000	 0.0360
i	 0.0000	 -0.0340
j	 0.0000	 -0.0180
k	 0.0000	 -0.0000
l	 0.0000	 -0.0020
m	 0.0000	 -0.0210
n	 0.0000	 0.0070
o	 0.0000	 -0.0420
p	 0.0000	 0.0130
q	 0.0000	 -0.0130
r	 0.0000	 -0.0370
s	 0.0000	 -0.0310
t	 0.0000	 0.0190
u	 0.0000	 -0.0080
v	 0.0000	 0.0330
w	 0.0000	 -0.0340
x	 0.0000	 -0.0130
y	 0.0000	 -0.0280
z	 0.0000	 -0.0350