



wwPDB EM Validation Summary Report ⓘ

Mar 11, 2025 – 03:06 PM EDT

PDB ID : 6VZ7
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.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

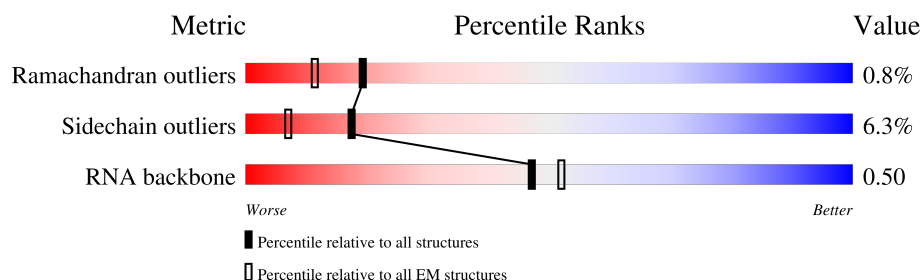
1 Overall quality at a glance

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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	<div> <div>100%</div> <div> <div>93%</div> <div>7%</div> </div> </div>
2	1	110	<div> <div>100%</div> <div> <div>92%</div> <div>8%</div> </div> </div>
3	2	94	<div> <div>100%</div> <div> <div>95%</div> <div>5%</div> </div> </div>
4	3	103	<div> <div>100%</div> <div> <div>92%</div> <div>8%</div> </div> </div>
5	4	94	<div> <div>100%</div> <div> <div>96%</div> <div>.</div> </div> </div>
6	5	27	<div> <div>85%</div> <div> <div>63%</div> <div>22%</div> <div>15%</div> </div> </div>
7	6	27	<div> <div>100%</div> <div> <div>85%</div> <div>15%</div> </div> </div>
8	7	16	<div> <div>100%</div> <div> <div>44%</div> <div>44%</div> <div>12%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
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	
27	O	127	
28	P	99	
29	Q	117	
30	R	123	
31	S	100	

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Mol	Chain	Length	Quality of chain
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	
52	o	64	
53	p	175	
54	q	38	
55	r	149	
56	s	142	

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Mol	Chain	Length	Quality of chain
57	t	123	<div><div></div><div>100%</div><div>95%</div><div>5%</div></div>
58	u	144	<div><div></div><div>100%</div><div>96%</div><div>•</div></div>
59	v	136	<div><div></div><div>100%</div><div>96%</div><div>•</div></div>
60	w	119	<div><div></div><div>100%</div><div>93%</div><div>7%</div></div>
61	x	116	<div><div></div><div>100%</div><div>95%</div><div>5%</div></div>
62	y	114	<div><div></div><div>100%</div><div>96%</div><div>•</div></div>
63	z	117	<div><div></div><div>100%</div><div>97%</div><div>•</div></div>

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 (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
64	7	1	Total	Mg	0
			1	1	

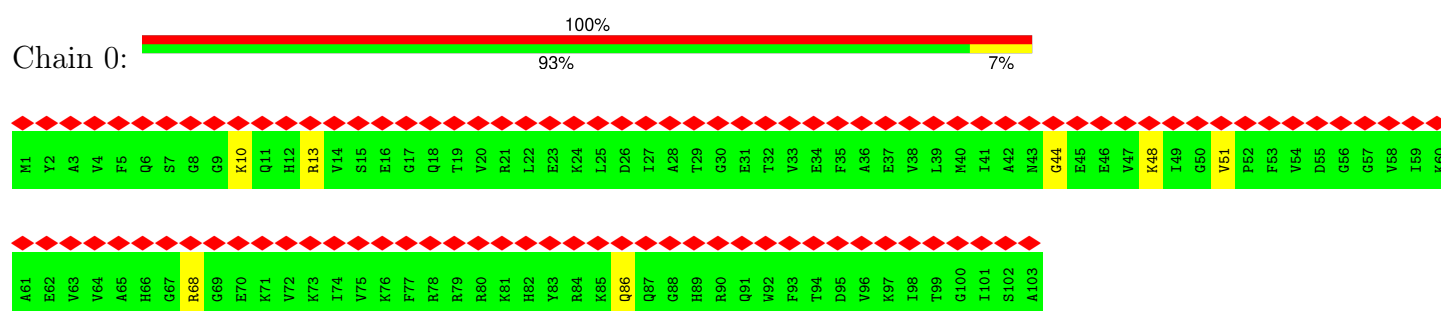
- Molecule 65 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

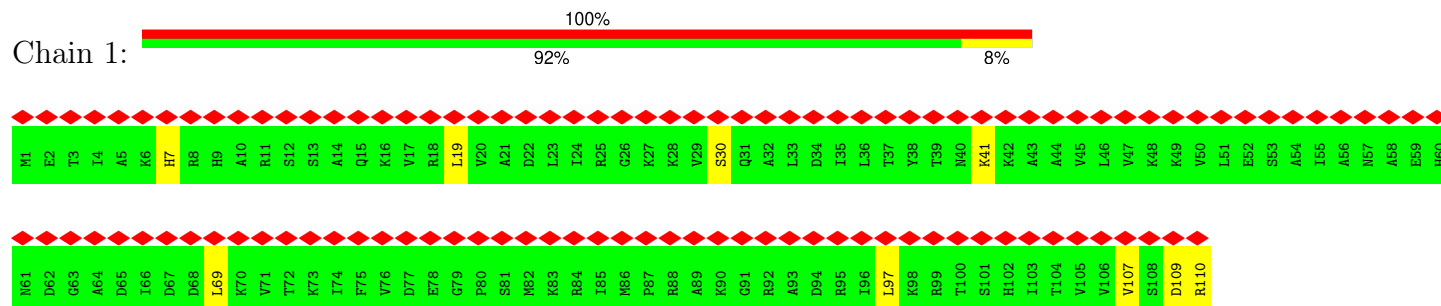
3 Residue-property plots

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.

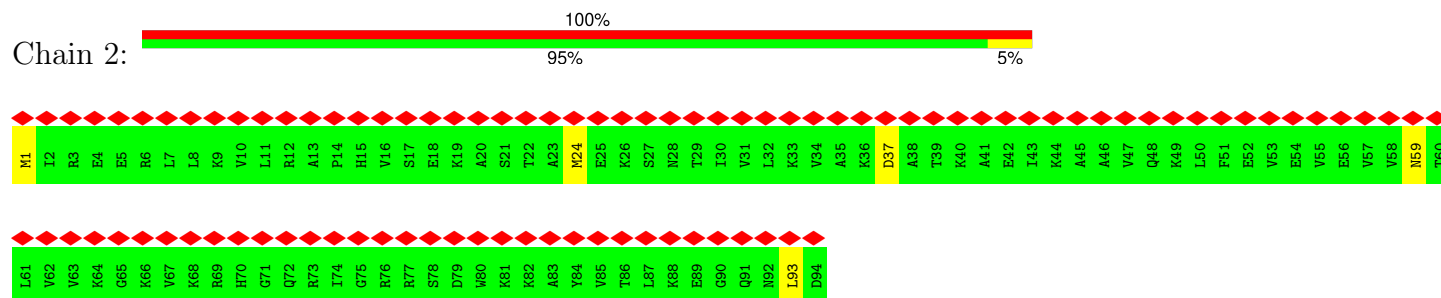
• Molecule 1: 50S ribosomal protein L21



• Molecule 2: 50S ribosomal protein L22

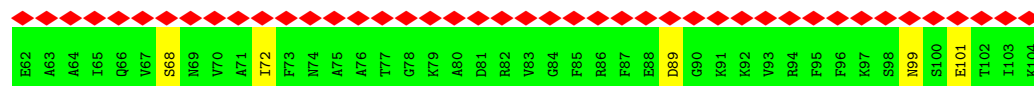


• Molecule 3: 50S ribosomal protein L23

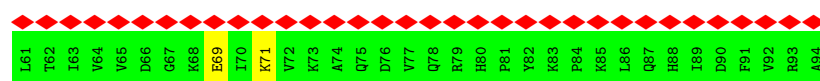
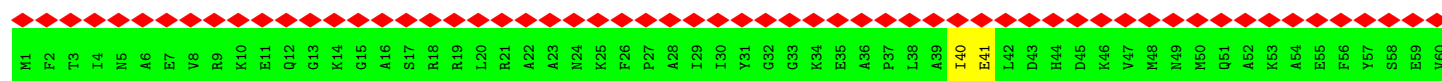


• Molecule 4: 50S ribosomal protein L24

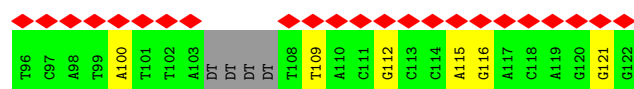
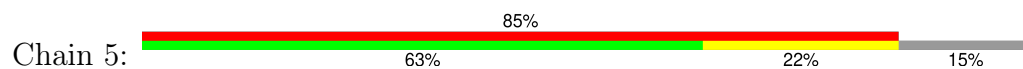




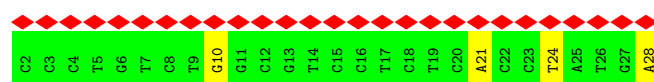
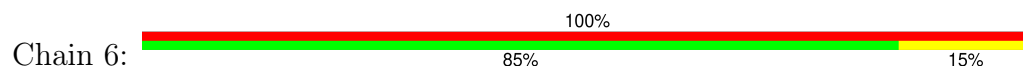
• Molecule 5: 50S ribosomal protein L25



• Molecule 6: NT DNA



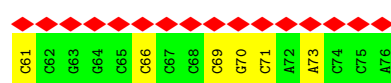
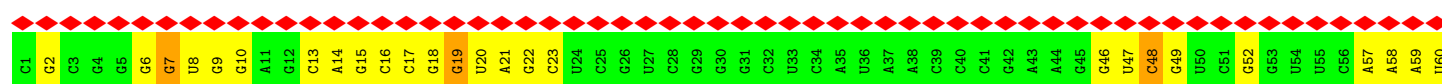
• Molecule 7: T DNA



• Molecule 8: mRNA with 27 nt long spacer



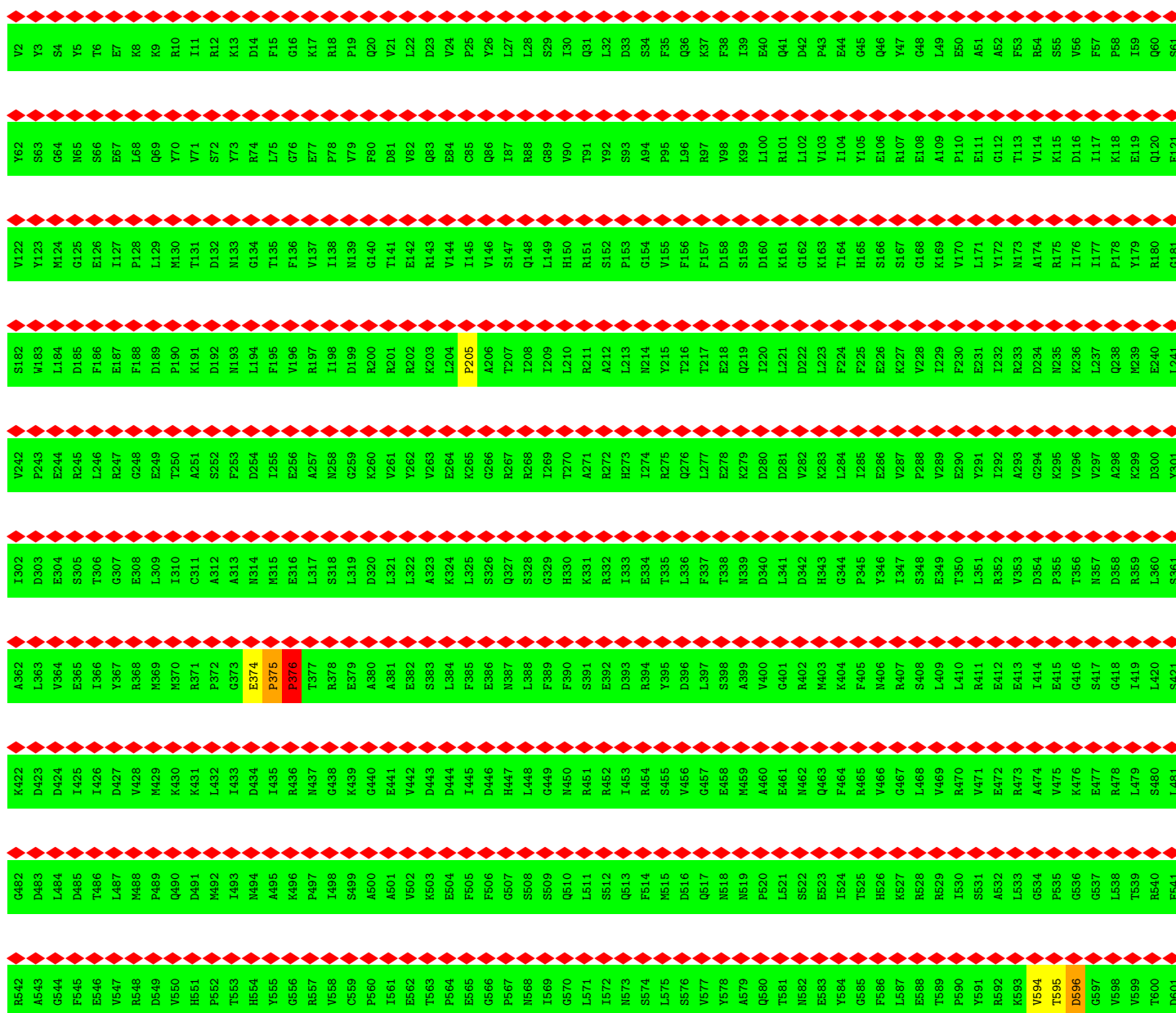
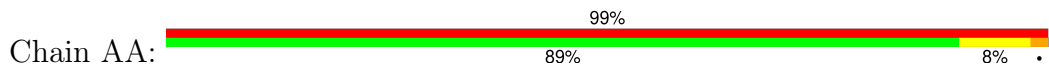
• Molecule 9: E-site and P-site tRNA (fMet)



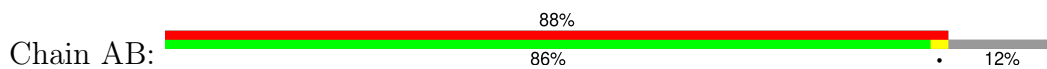
• Molecule 9: E-site and P-site tRNA (fMet)



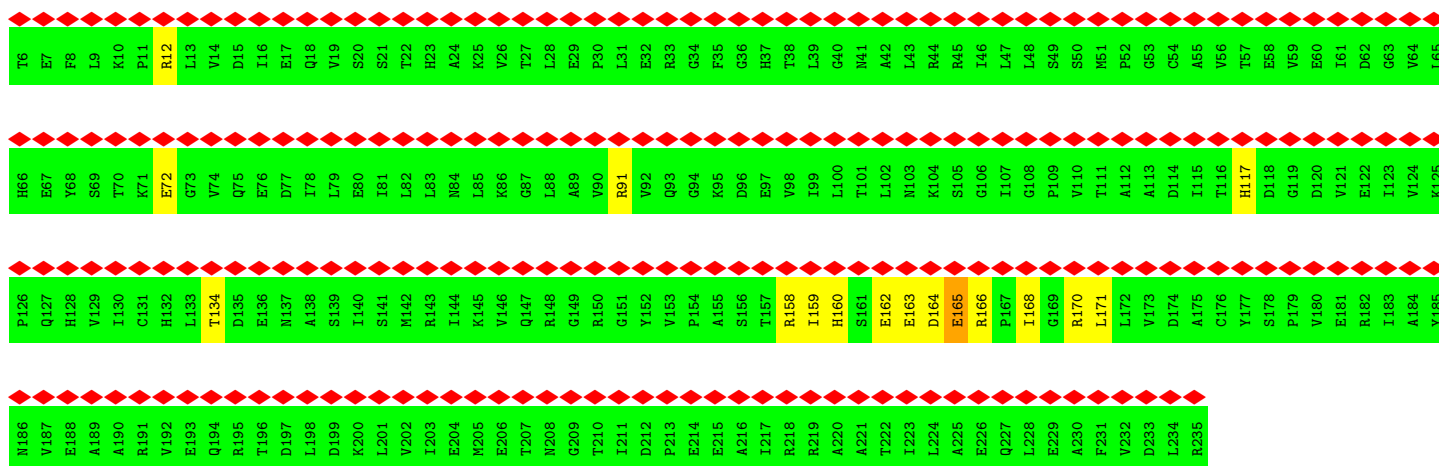
• Molecule 10: DNA-directed RNA polymerase subunit beta



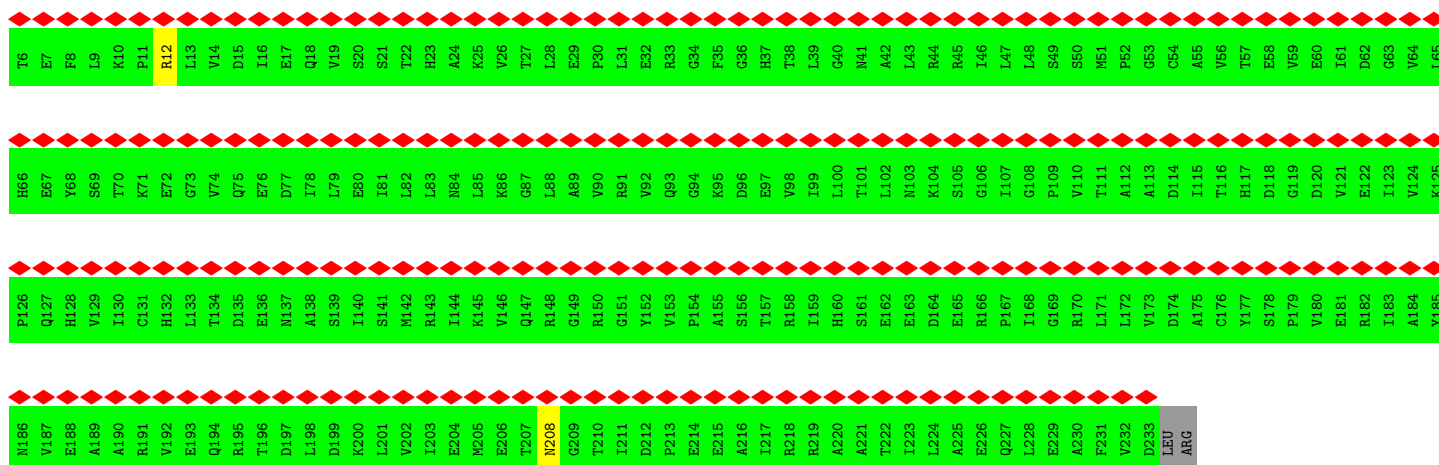
- Molecule 11: Transcription termination/antitermination protein NusG



- Molecule 12: DNA-directed RNA polymerase subunit alpha



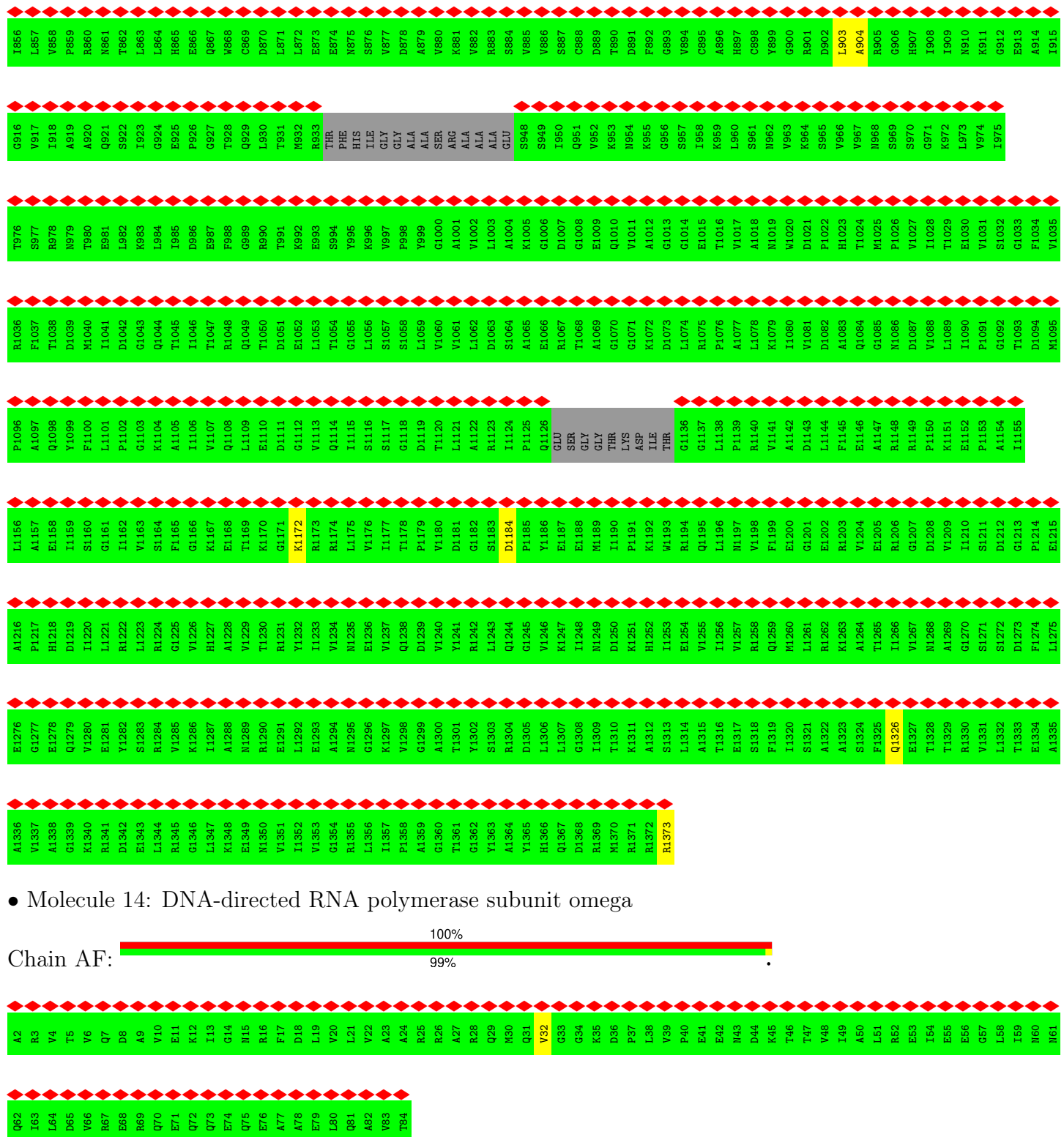
- Molecule 12: DNA-directed RNA polymerase subunit alpha

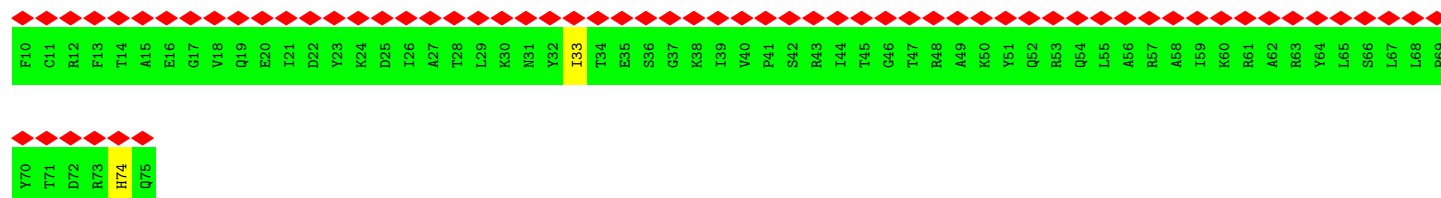


- Molecule 13: DNA-directed RNA polymerase subunit



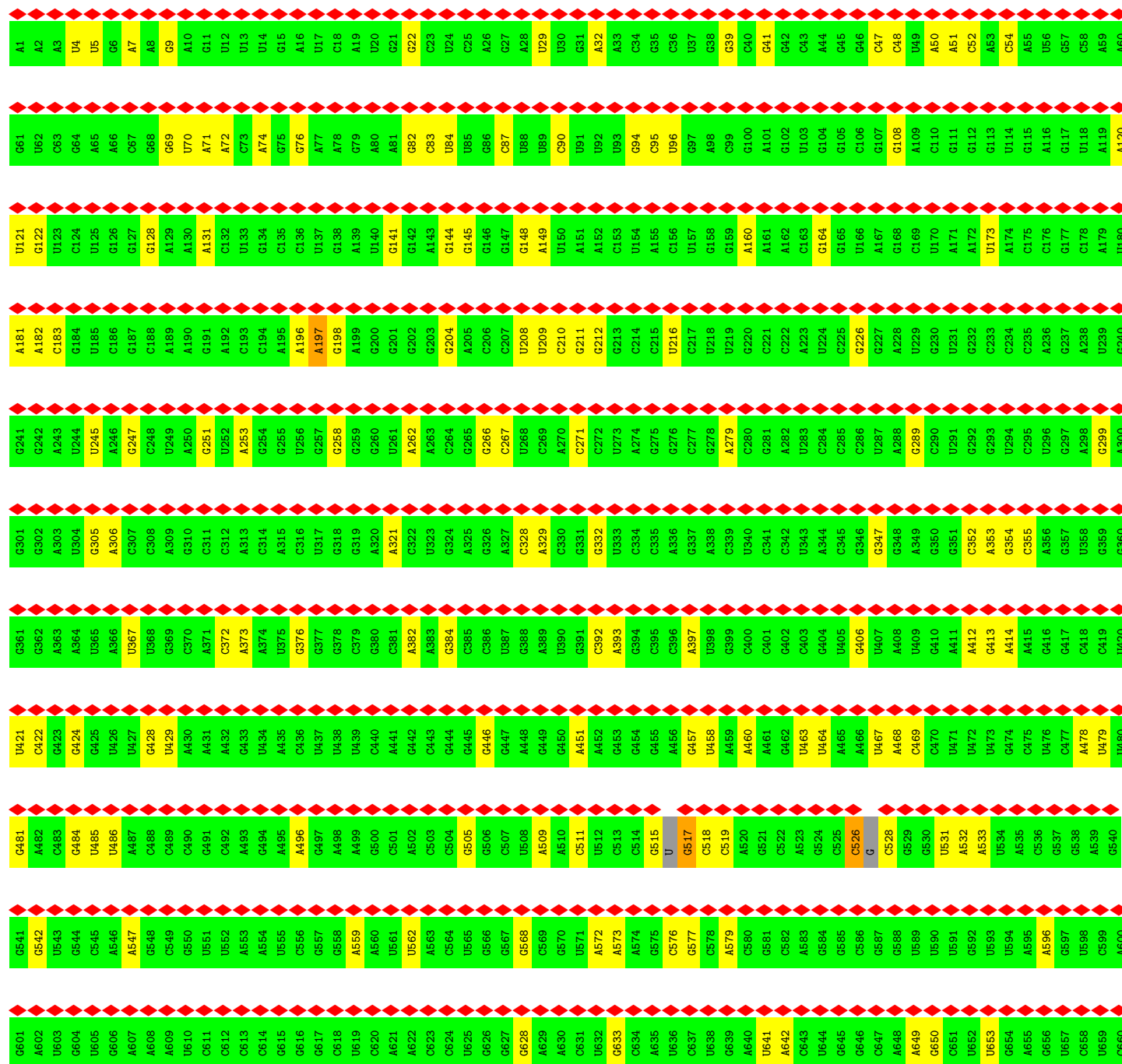
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Q736	I737	R738	Q739	L740	A741	G742	M743	R744	G745	L746	M747	A748	K749	P750	D751	G752	S753	I754	I755	E756	T757	P758	I759	T760	A761	N762	F763	R764	E765	G766	L767	N768	V769	L770	Q771	T772	F773	I774	S775	T776	D777	R778	G779	L780	K781	G782	L783	T844	D785	T786	A787	L788	K789	T790	A791	G792	T793	A794	D795	
G676	E677	D678	Y679	M680	K681	V682	I683	D684	I685	M686	A687	A688	A689	M690	D691	R692	V693	S694	K695	A696	M697	M698	D699	N700	L701	Q702	T703	E704	T705	V706	I707	N708	R709	D710	G711	Q712	F713	I714	S715	E596	L596	G597	K598	E599	A600	I601	S602	K603	M604	L605	N606	T607	C608	Y609	R610	I611	L612	T613	L614	K615
P616	T617	V618	I619	F620	A621	D622	Q623	I624	M625	Y626	T627	G628	F629	A630	Y631	A632	A633	R634	S635	G636	A637	S638	V639	G640	I641	D642	D643	M644	V645	I646	P647	E648	K649	K650	H651	E552	I553	I654	S655	E556	E557	E558	A659	E560	E561	A662	E663	I664	Q665	E566	F667	F668	Q669	S670	G671	L672	V673	T674	A675	
E556	K557	D558	A559	N560	G561	E562	L563	V564	A565	K566	T567	S568	L569	K570	D571	T572	T573	V574	G575	R576	A577	L578	L579	M580	I581	I582	V583	P584	K585	G586	L587	P588	E589	S590	I591	V592	N593	Q594	A595	L596	G597	K598	E599	A600	I601	S602	K603	M604	L605	N606	T607	C608	Y609	R610	I611	L612	T613	L614	K615	
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A436	F437	E438	P439	V440	L441	I442	F443	G444	A445	A446	I447	L448	L449	H450	P451	L452	V453	C454	A455	A456	Y457	M458	A459	D460	F461	D462	G463	D464	Q465	M466	A467	V468	H469	V470	P471	L472	L473	L474	E475	A476	A477	Q477	L478	E479	A480	L481	A482	L483	M484	M485	A486	T487	M488	N489	I490	L491	S492	P493	A494	N495
L376	F377	K378	P379	F380	I381	Y382	Q383	K384	E385	E386	L387	R388	G389	L390	A391	T392	T393	I394	K395	A396	A397	K398	K399	M400	V401	E402	R403	E404	E405	A406	V407	V408	W409	D410	I411	L412	D413	E414	V415	L416	R417	E418	H419	P420	V421	L422	L423	N424	R425	A426	T427	T428	L429	H430	R431	L432	Q433	I434	Q435	
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E136	R137	V138	L139	F140	E142	S143	I144	V145	V146	I147	E148	G149	G150	M151	T152	N153	L154	E155	R156	Q157	Q158	I159	L160	T161	E162	G163	Q164	Y165	L166	D167	A168	L169	E170	F171	F172	G173	D174	E175	F176	D177	A178	K179	M180	G181	A182	E183	T184	I185	Q186	A187	L188	L189	R190	S191	M192	D193	L194	E195		
Q196	E197	C198	E199	Q200	L201	R202	E203	D204	L205	N206	E207	T208	N209	S210	E211	T212	K213	R214	K215	K216	T217	T218	K219	R220	I221	K222	L223	L224	E225	A226	F227	V228	Q229	S230	G231	N232	K233	P234	E235	W236	W237	I238	L239	T240	V241	L242	V243	L244	P245	L246	L247	D248	L249	R250	P251	L252	V253	P254	L255	
K76	R77	L78	K79	H80	R81	G82	V83	I84	C85	E86	K87	C88	G89	V90	E91	V92	T93	Q94	T95	R96	V97	R98	R99	E100	R101	M102	G103	H104	I105	E106	L107	A108	S109	P110	T111	A112	H113	D114	W115	F116	L117	K118	S119	L120	P121	S122	R123	T124	G125	L126	L127	L128	D129	M130	P131	L132	R133	D134	T135	
E16	F17	D18	A19	I20	K21	I22	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	O55	L56	F57	C58	A59	R60	T61	P62	O63	P64	V65	K66	D67	V68	E69	C70	L71	C72	G73	K74	Y75	





● Molecule 16: 16S rRNA

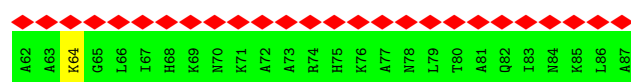
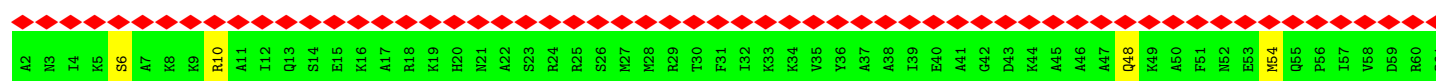
Chain D:



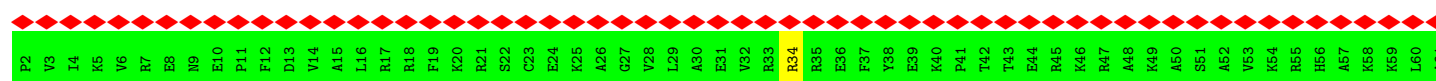
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C1382	U662	U842	G902	C962	A1022	A1082	G1142	U1202	C1262	C1322	C1402
C1383	A663	U843	G903	G963	U1023	U1083	G1143	C1203	C1263	G1323	C1403
C1384	G664	G844	U904	A964	G1024	G1084	G1144	U1204	U1264	A1324	C1404
G1385	A665	U845	U905	U965	U1025	U1085	A1145	U1205	G1265	C1325	G1405
G1386	G666	G846	A906	C	U1026	U1086	A1146	G	G1266	U1326	U1406
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C1388	G668	C948	A908	A969	C1028	G1088	U1148	C1209	G1268	C1328	A1408
C1389	G669	G849	A909	A970	U1029	G1089	C1149	C1210	A1269	A1329	C1409
U1390	G670	U890	C910	C970	U1030	U1090	A1150	U1210	U1270	U1330	A1410
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G1392	U672	A792	C912	C972	G1032	A1092	A1152	U1212	G1272	A1332	C1412
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A1394	G674	A794	A914	A974	G1034	G1094	G1154	C1214	A1274	G1334	U1414
C1395	A675	C795	U915	A975	A1035	U1095	A1155	G1215	A1275	U1335	G1415
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C1397	U677	C797	G917	A977	C1037	C1097	A1157	C1217	C1277	G1337	A1418
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C1399	C679	G799	A919	C979	G1039	G1099	U1159	A1219	G1279	A1339	U1420
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G1401	A681	G801	U921	U981	G1041	A1101	C1161	G1221	C1281	C1341	C1422
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C1403	G683	G803	A923	A983	G1043	C1103	A1163	C1223	U1283	G1343	A1424
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G1405	G685	C805	G925	C985	C1045	A1105	U1165	A1225	A1285	U1345	G1426
U1406	U686	C806	G926	U986	A1046	G1106	G1166	C1226	U1286	C1346	C1427
C	A687	A807	G927	U987	G1047	C1107	A1167	A1227	A1287	G1347	A1428
A1408	G688	C808	G928	U988	G1048	G1108	U1168	C1228	A1288	U1348	U1429
C1409	C689	G809	G929	U989	U1049	C1109	A1169	A1229	U1289	A1349	A1430
A1410	G690	C810	C930	C990	G1050	A1110	A1170	C1230	U1290	A1350	A1431
C1411	G691	U751	C931	U991	C1051	A1111	A1171	G1231	U1291	U1351	C1432
C1412	U692	G752	C932	U992	G1052	C1112	C1172	U1232	U1292	G1352	U1424
A1413	G693	A753	G933	G993	G1053	C1113	U1173	C1233	C1293	G1353	U1425
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G1415	G695	A815	A935	C995	A1055	U1115	G1175	U1235	U1295	G1355	C1427
G1416	A696	A816	C936	A996	U1056	U1116	A1176	A1236	C1296	G1356	A1428
A1418	U697	C817	A937	U997	G1056	C1117	G1177	C1237	G1297	U1357	U1429
U1419	G698	A759	G939	C999	G1058	U1118	G1178	A1238	U1298	U1358	A1430
U1420	C699	U760	G940	A1000	C1059	C1119	A1179	A1239	A1299	C1359	A1431
G1421	U701	G761	G941	C1001	U1060	C1120	A1180	U1240	U1300	A1360	C1432
C1422	G703	A762	G942	G1002	G1061	U1121	G1181	G1241	U1301	G1361	U1424
G1423	A704	G763	G943	G1003	U1062	U1122	G1182	G1242	C1302	A1362	U1425
U1424	G705	G764	U944	C1004	C1063	U1123	U1183	C1243	C1303	A1363	G1426
U1425	A706	C765	G945	A1005	G1064	G1124	G1184	G1244	G1304	U1364	C1427
G1426	U707	A766	G946	U1006	U1065	U1125	G1185	C1245	A1305	G1365	A1429
C1427	G707	A767	A947	G1007	C1066	U1126	G1186	U1246	G1306	C1366	U1430
A1428	C708	A768	C948	U1008	A1067	G1127	G1187	U1247	U1307	C1367	U1431
U1429	G709	G769	A949	U1009	G1068	C1128	A1188	C1248	U1308	U1368	C1432
A1430	U709	C770	G950	U1010	C1069	C1129	U1189	C1249	G1309	A1369	U1433
A1431	G711	G771	U951	C1011	U1070	A1130	G1190	U1250	C1310	G1370	A1434
G1432	A712	U772	U952	A1012	C1071	G1131	A1191	A1251	A1311	G1371	C1435
A1433	G713	U773	G953	U1013	G1072	C1132	C1192	G1252	G1312	U1372	U1436
A1434	G714	G774	C954	A1014	U1073	G1133	G1193	G1253	U1313	A1373	A1437
G1435	A715	G775	G955	G1015	G1074	G1134	U1194	U1254	C1314	A1374	C1438
U1436	U716	G776	U956	A1016	U1075	U1135	C1195	G1255	U1315	A1375	U1440
A1437	U717	A777	U957	U1017	U1076	C1136	A1196	A1256	G1316	U1376	
G1438	U718	G778	U958	U1018	G1077	C1137	A1197	A1257	C1317	A1377	
C1439	C719	C779	C959	A1019	U1078	G1138	G1198	G1258	A1318	C1378	
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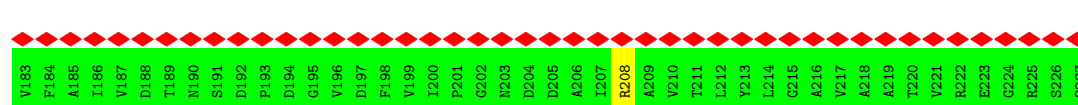
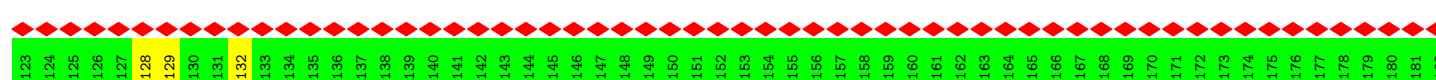
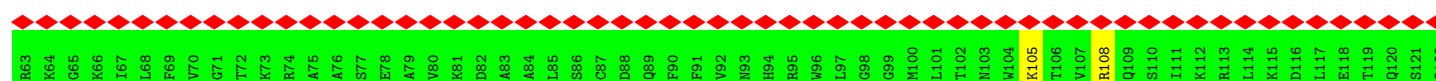
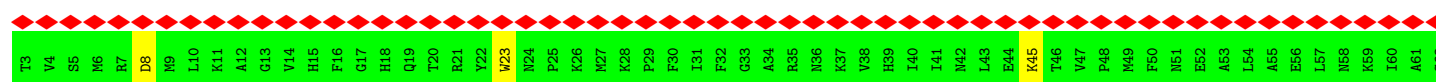
• Molecule 17: 30S ribosomal protein S20



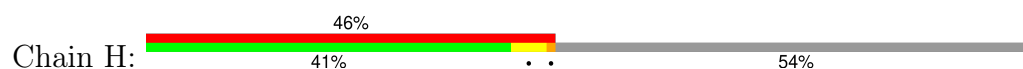
• Molecule 18: 30S ribosomal protein S21



• Molecule 19: 30S ribosomal protein S2

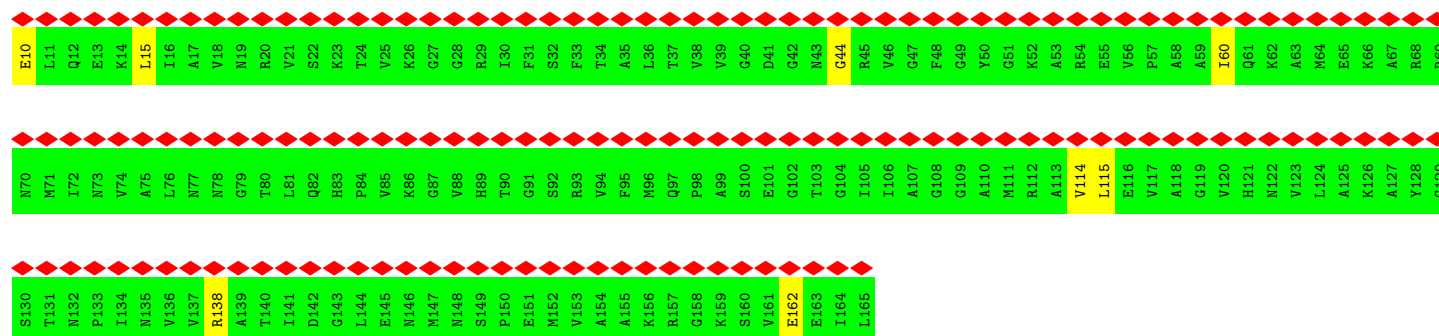


• Molecule 20: 30S ribosomal protein S1





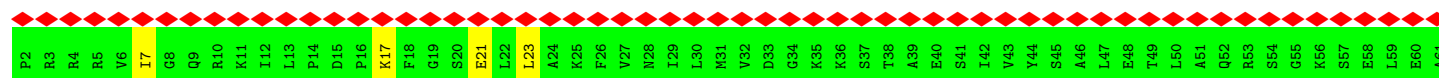
• Molecule 23: 30S ribosomal protein S5

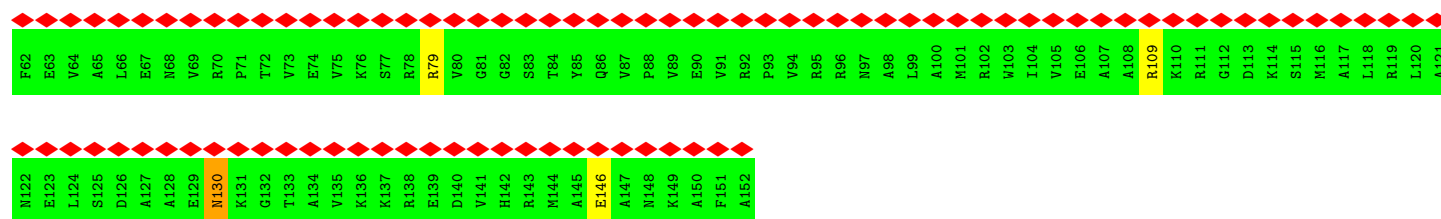


• Molecule 24: 30S ribosomal protein S6

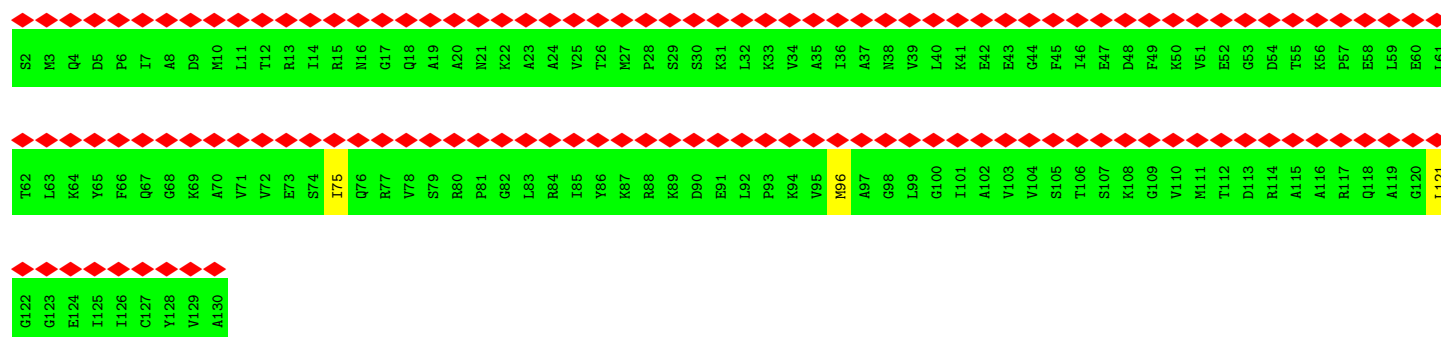


• Molecule 25: 30S ribosomal protein S7

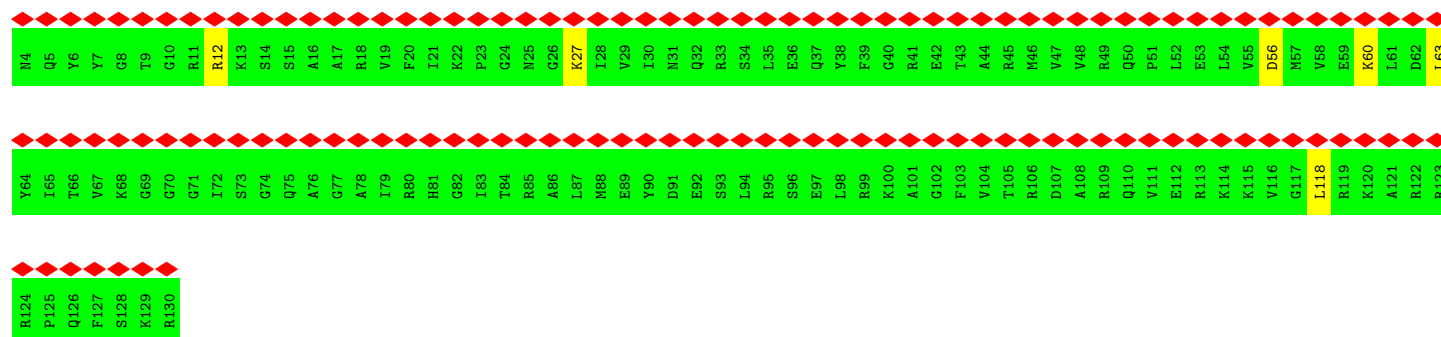




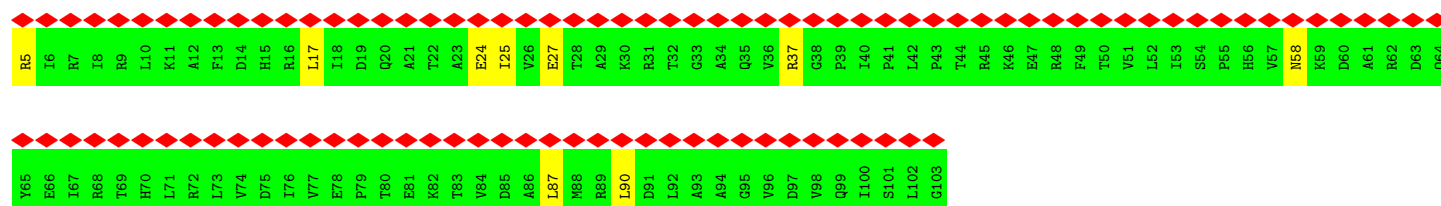
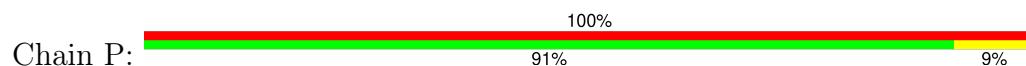
• Molecule 26: 30S ribosomal protein S8



• Molecule 27: 30S ribosomal protein S9



• Molecule 28: 30S ribosomal protein S10

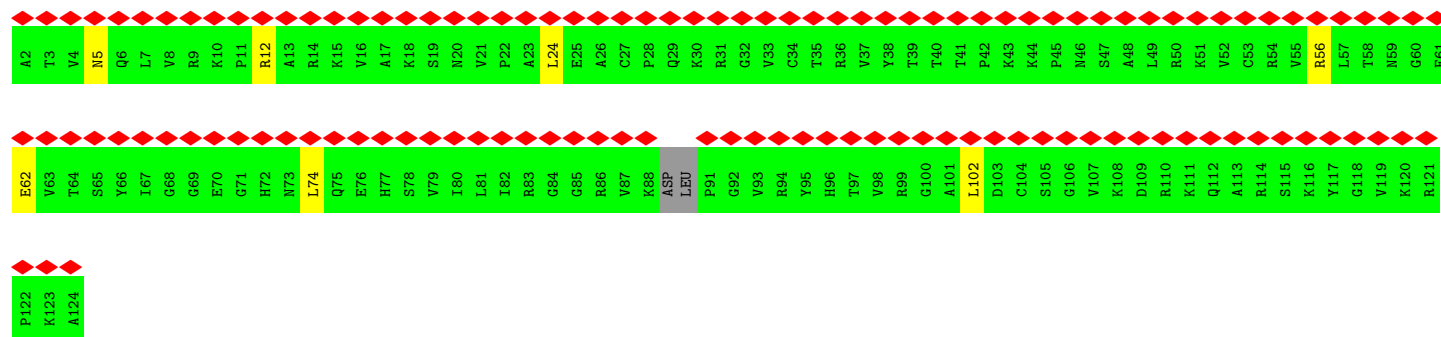


• Molecule 29: 30S ribosomal protein S11

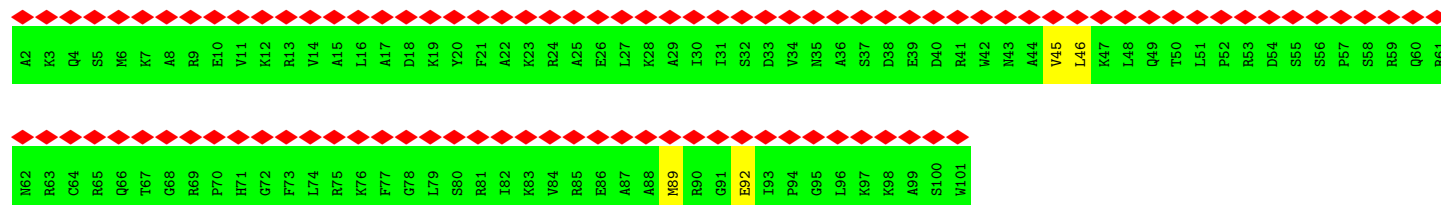




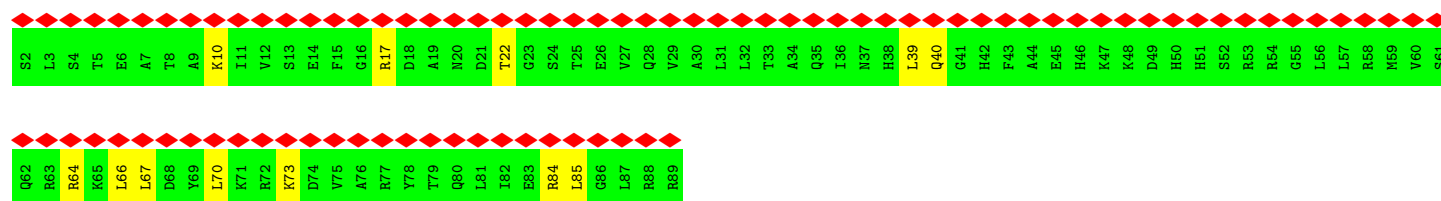
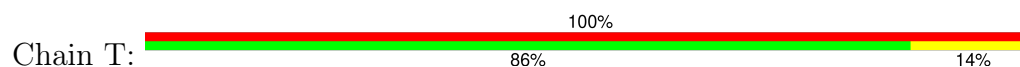
• Molecule 30: 30S ribosomal protein S12



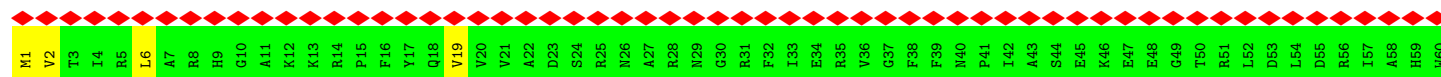
• Molecule 31: 30S ribosomal protein S14

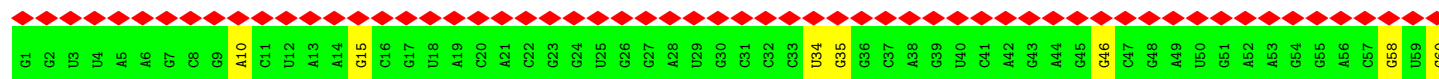


• Molecule 32: 30S ribosomal protein S15



• Molecule 33: 30S ribosomal protein S16





G841	U842	G843	A844	A845	U846	U847	C848	A849	U850	C851	U852	C853	C854	G855	G856	G857	G858	G859	U860	A861	G862	A863	G864	C865	C866	C867	U868	C869	U870	U871	U872	C873	C874	C875	C876	C877	A878	G879	C880	C881	C882	C883	U884	C885	A886	A887	C888	C889	C890	C891	A892	C893	U894	U895	A896	C897	C898	A899	A900
G121	U122	A123	G124	A125	G126	A127	G128	C129	G130	A131	U132	U133	G134	U135	G136	U137	U138	U139	C140	G141	A142	C143	A144	C145	G146	C147	U148	A149	C150	C151	A152	U153	U154	A155	A156	C157	G158	U159	A160	A161	U162	C163	A164	A165	U166	A167	G168	C169	U170	U171	A172	A173	U174	G175	A176	G177	A178	A179	U180
A181	A182	C183	C184	G185	G186	A187	G188	A189	A190	A191	C192	U193	G194	A195	A196	A197	C198	A199	U200	C201	U202	A203	A204	G205	U206	A207	C208	C209	C210	C211	G212	A213	G214	G215	A216	A217	A218	A219	G220	A221	A222	A223	U224	C225	A226	A227	C228	C229	U230	A231	G232	A233	U234	U235	C236	C237	C238	C239	C240
A241	G242	U243	A244	G245	C246	G247	G248	C249	G250	A251	G252	C253	G254	A255	A256	C257	G258	G259	G260	G261	A262	C263	C264	A265	G266	C267	C268	C269	A270	G271	A272	G273	C274	C275	U276	G277	A278	A279	U280	C281	A282	G283	U284	G285	U286	G287	U288	G289	U290	G291	U292	U293	A294	G295	U296	G297	U298	A299	A300
G301	C302	G303	U304	C305	U306	G307	G308	A309	A310	A311	G312	G313	C314	G315	C316	G317	C318	G319	A320	U321	A322	C323	A324	G325	G326	G327	U328	G329	A330	C331	A332	G333	C334	C335	C336	C337	G338	U339	A340	C341	A342	C343	A344	A345	A346	A347	A348	U349	G350	C351	A352	C353	A354	U355	G356	C357	U358	C359	U360
G361	A362	G363	C364	U365	C366	G367	A368	U369	G370	A371	G372	U373	A374	G375	G376	G377	C378	G379	G380	G381	A382	C383	A384	C385	G386	U387	G388	G389	U390	A391	A392	C393	C394	U395	G396	U397	G398	U399	G400	A401	A402	U403	A404	U405	A406	G407	G408	G409	G410	G411	A412	C413	C414	A415	U416	A417	C418	U419	C420
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	G450	U451	G452	A453	A454	C455	C456	A457	G458	U459	A460	C461	C462	G463	U464	G465	A466	G467	G468	A469	A470	A471	A472	G473	G474	C475	G476	A477	A478	A479	A480
G481	A482	A483	C484	C485	C486	C487	G488	G489	C490	A491	A492	G493	G494	G495	G496	A497	G498	U499	G500	A501	A502	A503	A504	A505	G506	A507	A508	C509	C510	U511	G512	A513	A514	A515	C516	C517	G518	U519	G520	U521	A522	C523	G524	U525	A526	C527	A528	A529	G530	C531	A532	G533	U534	G535	G536	G537	A538	G539	C540
A541	C542	G543	C544	U545	U546	A547	G548	G549	C550	G551	U552	G553	A554	G555	A556	C557	U558	G559	C560	G561	A562	A563	C564	C565	U566	U567	U568	U569	G570	U571	A572	U573	A574	A575	U576	G577	G578	G579	U580	C581	A582	G583	C584	G585	A586	C587	U588	U589	A590	U591	A592	U593	U594	C595	U596	G597	U598	A599	G600
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	C646	G647	G648	G649	C650	G651	U652	U653	A654	A655	G656	U657	U658	G659	C660
A661	G662	G663	G664	U665	A666	U667	A668	G669	A670	C671	C672	C673	G674	A675	A676	A677	C678	C679	C680	G681	G682	U683	G684	A685	U686	C687	U688	A689	G690	C691	C692	A693	U694	G695	G696	G697	C698	A699	G700	G701	U702	U703	G704	A705	A706	G707	G708	U709	U710	G711	G712	G713	U714	A715	A716	C717	A718	C719	U720
A721	A722	C723	U724	G725	G726	A727	G728	G729	A730	C731	C732	G733	A734	A735	C736	G737	G738	A739	C740	U741	A742	A743	U744	U745	U746	C747	A748	A749	A750	A751	A752	A753	U754	U755	A756	G757	C758	G759	G760	A761	U762	G763	A764	C765	U766	U767	G768	U769	G770	G771	C772	U773	G774	U775	G776	G777	G778	U779	G780
A781	A782	A783	G784	G785	C786	C787	A788	A789	U790	C791	U792	A793	A794	C795	C796	G797	G798	G799	A800	G801	A802	U803	A804	C805	C806	U807	C808	G809	U810	U811	C812	U813	C814	C815	C816	C817	C818	A819	A820	A821	C822	C823	U824	A825	U826	U827	U828	A829	C830	C831	U832	A833	C834	C835	C836	C837	C838	A839	C840
U841	U842	G843	A844	A845	U846	U847	C848	A849	U850	C851	U852	C853	C854	G855	G856	G857	G858	G859	U860	A861	G862	A863	G864	C865	C866	C867	U868	C869	U870	U871	U872	C873	C874	C875	C876	C877	A878	G879	C880	C881	C882	C883	U884	C885	A886	A887	C888	C889	C890	C891	A892	C893	U894	U895	A896	C897	C898	A899	A900

U1621	C1661	G1501	G1441	G1381	A1321	C1261	U1201	U1141	U1081	A1021	C961	C901
G1622	U1562	A1502	U1442	G1382	A1322	A1262	G1202	A1142	U1082	G1022	G962	C902
G1623	U1563	A1503	U1443	A1383	C1323	U1263	U1203	A1143	U1083	U1023	U963	C903
U1624	C1564	A1504	G1444	A1384	G1324	A1264	A1204	A1144	A1084	G1024	C964	G904
C1625	U1565	A1505	G1445	A1385	A1325	U1265	A1205	A1145	A1085	G1025	C965	A905
A1626	A1566	U1506	C1446	C1386	U1326	G1266	G1206	C1146	A1086	G1026	G966	U906
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	C908
U1629	A1569	G1509	G1449	G1389	U1329	A1269	U1209	U1149	A1089	A1029	G969	A909
A1630	A1570	G1510	G1450	U1390	C1330	C1270	G1210	C1150	A1090	C1030	U970	A910
G1631	A1571	G1511	C1451	U1391	G1331	G1271	C1211	A1151	G1091	G1031	G971	A911
A1632	A1572	C1512	G1452	A1392	A1332	A1272	G1212	C1152	C1092	A1032	A972	C912
G1633	G1573	U1513	A1453	A1393	G1333	U1273	A1213	G1153	G1093	U1033	A973	U913
A1634	C1574	G1514	C1454	U1394	G1334	A1274	A1214	G1154	U1094	G1034	G974	G914
A1635	C1575	A1515	G1455	A1395	C1335	A1275	G1215	A1155	A1095	U1035	A975	C915
U1636	U1576	G1516	G1456	U1396	A1336	A1276	G1216	A1156	A1096	G1036	G976	G916
A1637	U1577	C1517	U1457	U1397	G1337	G1277	U1217	G1157	U1097	G1037	G977	A917
U1578	U1578	C1518	U1458	C1398	G1338	C1278	G1218	C1158	A1098	G1038	G978	A918
A1579	G1579	G1519	G1459	C1399	G1339	G1279	U1219	U1159	G1099	A1039	A979	U919
A1640	A1580	U1520	U1460	U1400	U1340	G1280	G1220	G1160	C1100	A1040	A980	A920
A1641	G1581	G1521	C1461	G1401	G1341	G1281	C1221	G1161	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
C1646	A1586	C1526	U1466	U1406	G1346	A1286	A1226	G1166	G1106	A1046	C986	G926
U1647	G1587	G1527	U1467	G1407	A1347	A1287	G1227	C1167	G1107	G1047	C987	A927
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A1649	U1589	G1529	A1469	U1409	C1349	C1289	C1229	A1169	C1109	C1049	G989	U929
G1650	A1590	C1530	A1470	G1410	C1350	C1290	A1230	C1170	G1110	A1050	A990	G930
G1651	A1591	C1531	G1471	U1411	C1351	C1291	U1231	G1171	A1111	G1051	C991	U931
A1652	C1592	A1532	C1472	U1412	U1352	G1292	C1232	G1172	G1112	C1052	C992	U932
G1653	A1593	C1533	G1473	A1413	A1353	C1293	C1233	U1173	U1113	C1053	G993	A933
A1654	U1594	U1534	U1474	C1414	A1354	U1294	U1234	U1174	C1114	A1054	C994	U934
A1655	C1595	A1535	G1475	U1415	G1355	C1295	G1235	A1175	G1115	G1055	C995	C935
C1656	A1596	C1536	U1476	G1416	G1356	G1296	G1236	U1176	G1116	G1056	A996	A936
U1657	A1597	G1537	A1477	C1417	C1357	C1297	A1237	G1177	C1117	A1057	G997	C937
A1598	A1598	C1538	G1478	G1418	G1358	C1298	G1238	C1178	C1118	U1058	C998	G938
U1599	U1599	U1539	G1479	A1419	A1359	G1299	G1239	G1179	U1119	G1059	U999	G939
C1660	C1600	G1540	C1480	A1420	G1360	G1300	U1240	U1180	G1120	U1060	A1000	G940
G1661	G1601	C1541	U1481	G1421	G1361	A1301	A1241	U1181	C1121	U1061	A1001	A941
U1662	U1602	U1542	G1482	G1422	C1362	A1302	U1242	G1182	G1122	G1062	G1002	G942
G1663	A1603	G1543	G1483	G1423	C1363	G1303	C1243	U1183	C1123	G1063	G1003	A943
A1664	C1604	U1544	U1484	G1424	G1364	A1304	A1244	U1184	G1124	C1064	U1004	C944
A1665	U1605	A1545	U1485	G1425	A1365	C1305	G1245	G1185	G1125	U1065	C1005	A945
C1666	C1606	G1546	U1486	G1426	A1366	C1306	A1246	G1186	A1126	U1066	C1006	C946
G1667	C1607	C1547	U1487	A1427	A1367	A1307	A1247	G1187	A1127	A1067	C1007	A947
A1668	A1608	A1548	C1488	C1428	G1368	A1308	G1248	U1188	G1128	G1068	A1008	C948
A1669	A1609	U1549	C1489	G1429	G1369	G1309	U1249	A1189	U1129	A1069	A1009	G949
C1670	A1610	C1550	U1490	G1430	G1370	G1310	G1250	G1190	U1130	A1070	A1010	G950
U1671	C1611	A1551	G1491	A1431	G1371	G1311	C1251	G1191	G1131	G1071	G1011	C951
A1672	G1612	A1552	G1492	G1432	U1372	U1312	G1252	G1192	U1132	C1072	U1012	G952
G1673	G1613	A1553	C1493	A1433	A1373	U1313	A1253	G1193	A1133	G1073	C1013	G953
G1674	A1614	U1554	A1494	A1434	C1374	C1314	A1254	A1194	A1134	A1074	A1014	G954
C1675	C1615	G1555	A1495	G1435	U1375	C1315	U1255	G1195	C1135	C1075	U1015	PSU
A1676	A1616	C1556	A1496	G1436	G1376	U1316	G1256	C1196	G1136	C1076	G1016	G956
A1677	U1617	C1557	U1497	C1437	G1377	G1317	C1257	G1197	G1137	A1077	G1017	C957
A1678	6VZ	C1558	U1498	U1438	A1378	U1318	U1258	U1198	G1138	U1078	U1018	U958
A1679	G1619	U1559	C1499	A1439	U1379	C1319	G1259	U1199	G1139	C1079	U1019	A959
U1680	G1620	G1560	G1500	U1440	G1380	C1320	A1260	G1200	C1140	A1080	A1020	A960

U2401	U2402	C2403	U2404	G2405	A2406	A2407	U2408	G2409	G2410	A2411	A2412	G2413	G2414	G2415	U2416	C2417	A2418	U2419	C2420	G2421	C2422	U2423	C2424	A2425	A2426	C2427	G2428	G2429	A2430	U2431	A2432	A2433	A2434	A2435	G2436	G2437	U2438	A2439	C2440	U2441	C2442	G2443	C2444	2MG	G2446	G2447	A2448	U2449	U2450	A2451	C2452	A2453	G2454	G2455	C2456	PSU	G2458	A2459	U2460
A2281	G2282	C2283	A2284	C2285	G2286	A2287	A2288	G2289	G2290	U2291	U2292	G2293	G2294	C2295	U2296	A2297	A2298	U2299	C2300	C2301	U2302	G2303	G2304	U2305	C2306	G2307	G2308	A2309	C2310	A2311	U2312	G2313	A2314	G2315	G2316	A2317	G2318	G2319	U2320	U2321	A2322	G2323	U2324	G2325	C2326	A2327	A2328	U2329	G2330	G2331	C2332	A2333	U2334	A2335	A2336	G2337	C2338	C2339	A2340
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C2161	G2162	A2163	C2164	C2165	U2166	U2167	G2168	A2169	A2170	A2171	U2172	A2173	C2174	C2175	A2176	C2177	C2178	U2179	U2180	U2181	U2182	A2183	A2184	U2185	G2186	U2187	U2188	U2189	G2190	A2191	U2192	G2193	U2194	U2195	C2196	U2197	A2198	A2199	C2200	G2201	U2202	U2203	G2204	A2205	C2206	C2207	C2208	G2209	U2210	A2211	U2212	U2213	C2214	C2215	G2216	G2217	G2218	U2219	U2220
A2101	G2102	C2103	C2104	U2105	U2106	G2107	A2108	U2109	G2110	U2111	G2112	U2113	A2114	G2115	G2116	A2117	U2118	A2119	G2120	G2121	U2122	G2123	G2124	G2125	A2126	G2127	G2128	C2129	U2130	U2131	U2132	G2133	A2134	A2135	G2136	U2137	G2138	U2139	G2140	G2141	A2142	C2143	G2144	C2145	G2146	A2147	G2148	U2149	C2150	U2151	G2152	C2153	A2154	U2155	G2156	G2157	A2158	G2159	C2160
U2041	A2042	C2043	C2044	C2045	G2046	C2047	G2048	G2049	C2050	A2051	A2052	G2053	A2054	C2055	G2056	G2057	A2058	A2059	A2060	G2061	A2062	C2063	C2064	C2065	C2066	G2067	U2068	GTN	A2070	A2071	C2072	C2073	U	U2075	U2076	A2077	C2078	U2079	A2080	U2081	A2082	G2083	C2084	U2085	U2086	G2087	A2088	C2089	A2090	C2091	U2092	G2093	A2094	A2095	C2096	A2097	U2098	U2099	G2100
A1981	U1982	G1983	G1984	C1985	C1986	A1987	G1988	G1989	C1990	U1991	G1992	U1993	C1994	U1995	C1996	C1997	A1998	C1999	C2000	C2001	C2002	A2003	G2004	A2005	C2006	U2007	C2008	A2009	G2010	U2011	G2012	A2013	A2014	A2015	A2016	U2017	G2018	A2019	A2020	C2021	U2022	C2023	G2024	C2025	U2026	G2027	U2028	G2029	6MZ	A2031	A2032	A2033	U2034	G2035	C2036	A2037	G2038	U2039	G2040
G1921	G1922	U1923	C1924	C1925	U1926	A1927	A1928	G1929	G1930	U1931	A1932	G1933	C1934	G1935	A1936	A1937	A1938	5MU	U1940	C1941	C1942	U1943	U1944	G1945	U1946	C1947	G1948	G1949	G1950	U1951	A1952	A1953	G1954	U1955	U1956	C1957	G1958	G1959	A1960	C1961	5MC	U1963	G1964	C1965	A1966	C1967	G1968	A1969	A1970	U1971	G1972	G1973	C1974	G1975	U1976	A1977	A1978	U1979	G1980
G1861	G1862	G1863	U1864	U1865	A1866	G1867	C1868	G1869	C1870	A1871	A1872	G1873	C1874	G1875	A1876	A1877	G1878	C1879	U1880	C1881	U1882	U1883	G1884	A1885	U1886	C1887	G1888	A1889	G1890	G1891	C1892	C1893	C1894	C1895	G1896	G1897	C1898	A1899	A1900	A1901	C1902	G1903	G1904	C1905	G1906	G1907	C1908	C1909	G1910	PSU	A1912	A1913	C1914	3TD	A1916	PSU	A1918	A1919	C1920
A1801	A1802	U1803	C1804	A1805	C1806	G1807	A1808	A1809	A1810	G1811	U1812	G1813	G1814	A1815	C1816	G1817	U1818	A1819	U1820	C1821	C1822	G1823	G1824	U1825	G1826	U1827	G1828	A1829	C1830	G1831	C1832	C1833	U1834	2MG	C1836	C1837	C1838	G1839	G1840	U1841	G1842	C1843	C1844	G1845	G1846	A1847	A1848	G1849	G1850	U1851	U1852	A1853	A1854	U1855	U1856	G1857	A1858	U1859	G1860
C1741	U1742	G1743	A1744	A1745	A1746	U1747	C1748	A1749	G1750	U1751	C1752	G1753	A1754	A1755	G1756	A1757	U1758	A1759	C1760	C1761	A1762	G1763	C1764	U1765	G1766	G1767	C1768	U1769	U1770	C1771	A1772	A1773	C1774	U1775	G1776	C1777	C1778	U1779	A1780	G1721	U1782	G1723	A1784	U1785	A1786	A1787	C1788	A1789	C1790	A1791	G1792	G1793	A1794	C1795	U1796	G1797	U1798	A1799	C1800
G1681	G1682	U1683	G1684	C1685	C1686	G1687	U1688	A1689	A1690	U1691	U1692	G1693	C1694	G1695	G1696	G1697	A1698	A1699	A1700	A1701	A1762	G1703	C1704	A1705	C1706	G1707	C1708	U1709	G1710	A1711	U1712	A1713	U1714	G1715	U1716	U1717	U1718	G1719	U1720	G1721	A1722	G1723	G1724	U1725	C1726	G1727	C1728	U1729	C1730	G1731	C1732	G1733	G1734	A1735	U1736	G1737	U1738	A1739	G1740

U2881	A2882	A2883	U2884	C2885	A2886	C2887	C2888	C2889	C2890	U2891	C2892	A2893	C2894	C2895	C2896	U2897	U2898	A2899	A2900	C2901	C2902	U2903																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
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• Molecule 39: 50S ribosomal protein L27



T10	R11	N12	G13	G14	D15	S16	E17	A18	K19	R20	L21	G22	V23	K24	R25	F26	G27	G28	E29	S30	V31	L32	A33	G34	S35	I36	I37	V38	R39	Q40	R41	G42	T43	K44	F45	H46	A47	G48	A49	N50	V51	G52	C53	G54	R55	D56	H57	T58	L59	F60	A61	K62	A63	D64	G65	K66	V67	K68	F69
E70	V71	K72	G73	P74	K75	N76	R77	K78	F79	I80	S81	I82	E83	A84	E85																																												

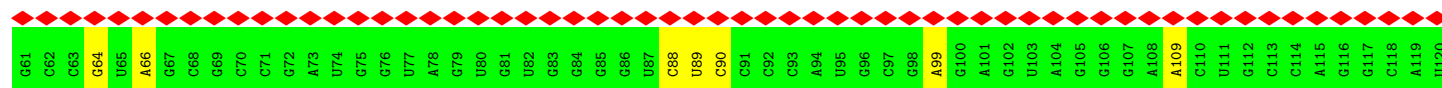
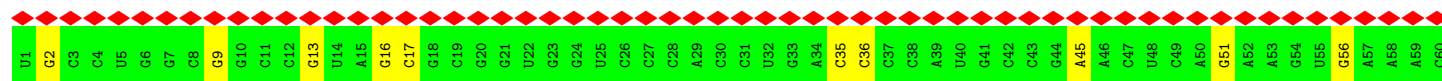
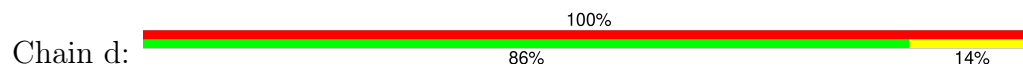
• Molecule 40: 50S ribosomal protein L28



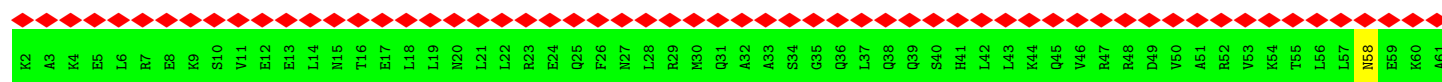
S2	R3	V4	C5	Q6	V7	T8	O9	K10	R11	P12	V13	T14	G15	M16	H17	R18	S19	H20	A21	L22	N23	A24	T25	K26	R27	R28	F29	L30	P31	R32	L33	H34	S35	H36	R37	F38	W39	V40	E41	S42	E43	K44	R45	F46	V47	T48	L49	R50	V51	S52	A53	K54	O55	M56	R57	V58	T59	D60	K61
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• Molecule 41: 5S rRNA



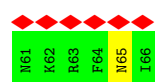
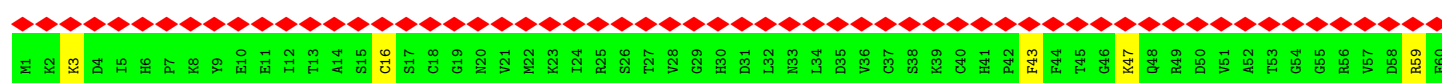
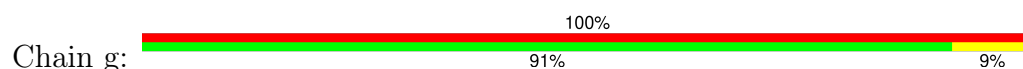
• Molecule 42: 50S ribosomal protein L29



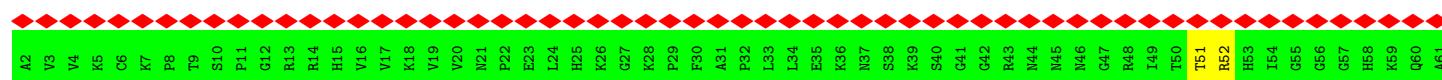
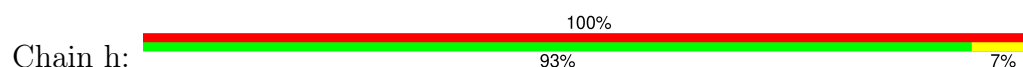
• Molecule 43: 50S ribosomal protein L30

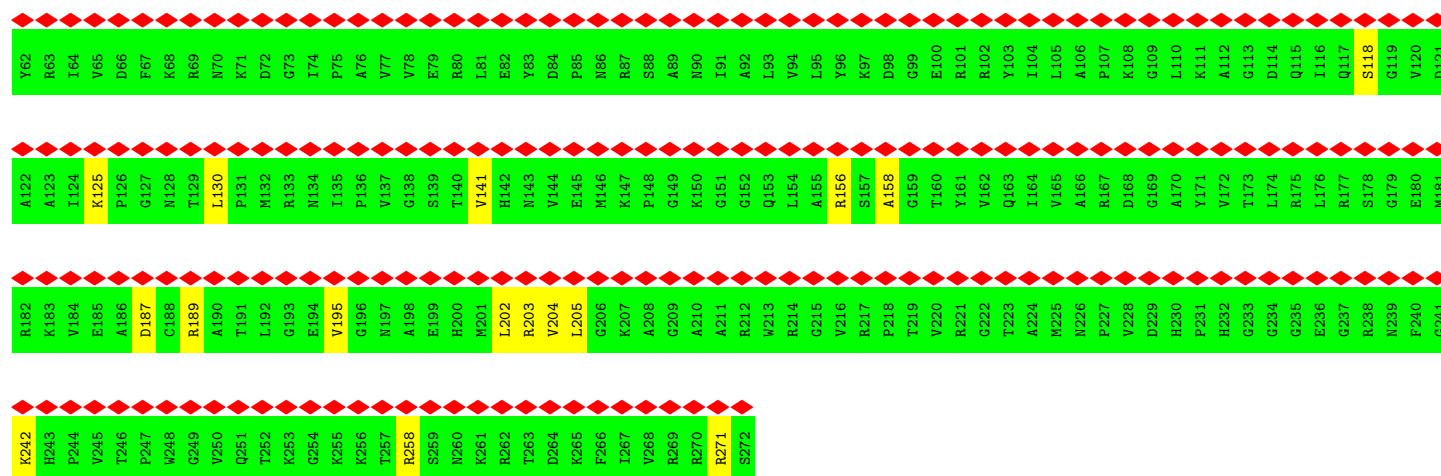


• Molecule 44: 50S ribosomal protein L31

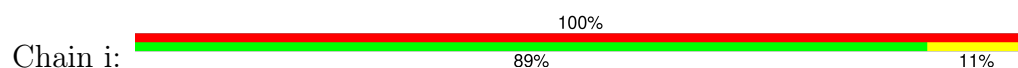


• Molecule 45: 50S ribosomal protein L2

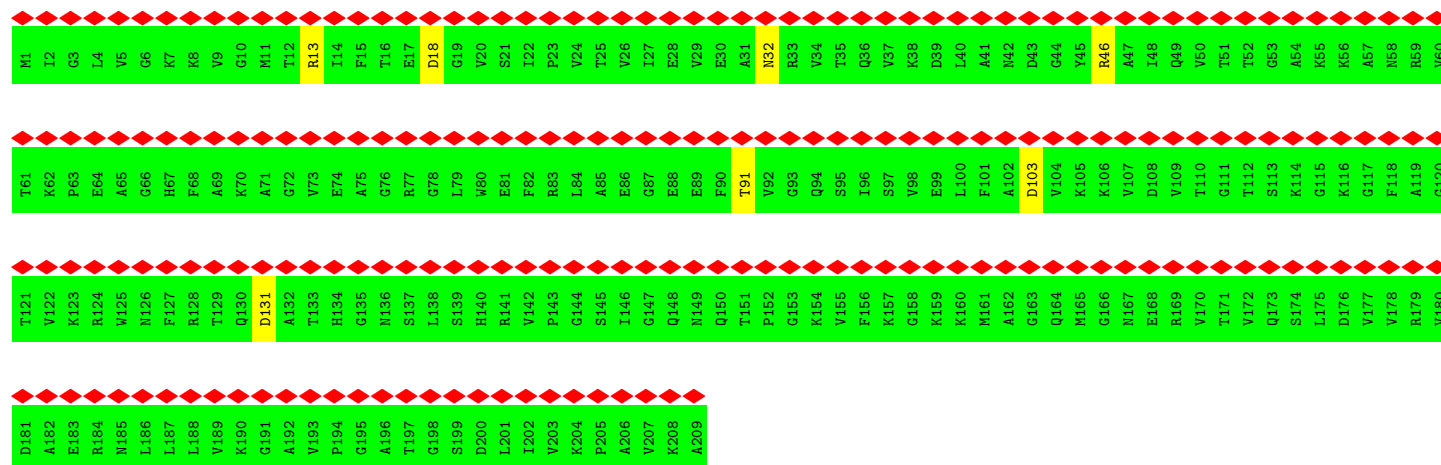




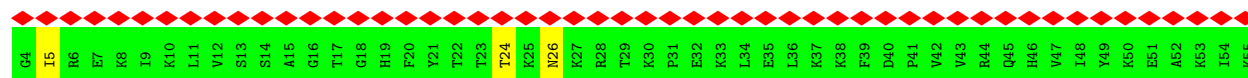
• Molecule 46: 50S ribosomal protein L32



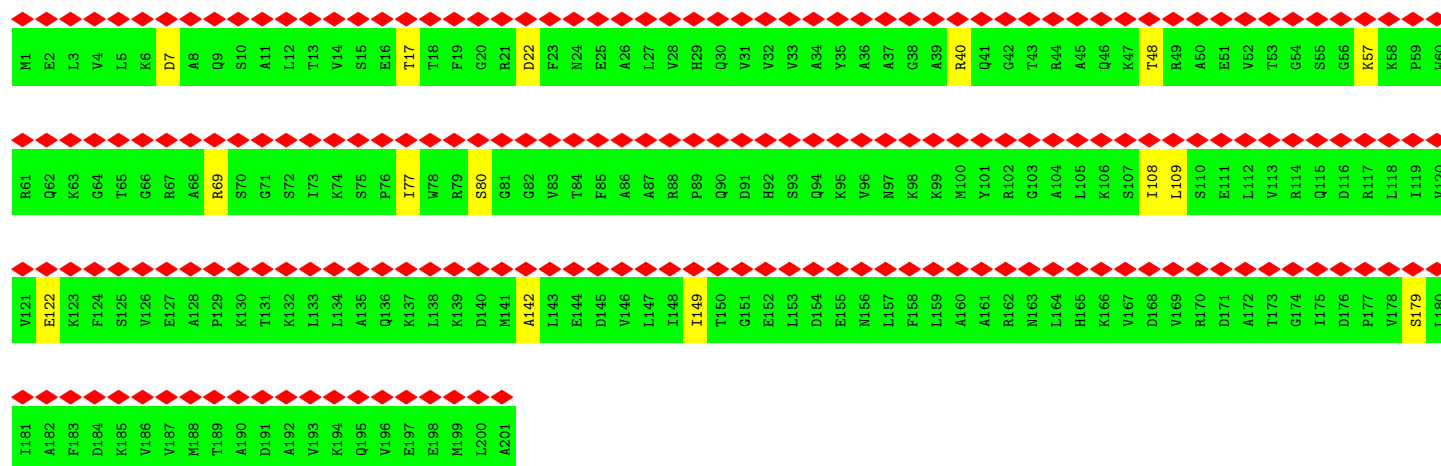
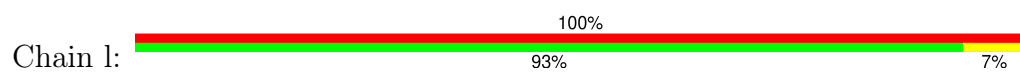
• Molecule 47: 50S ribosomal protein L3



• Molecule 48: 50S ribosomal protein L33



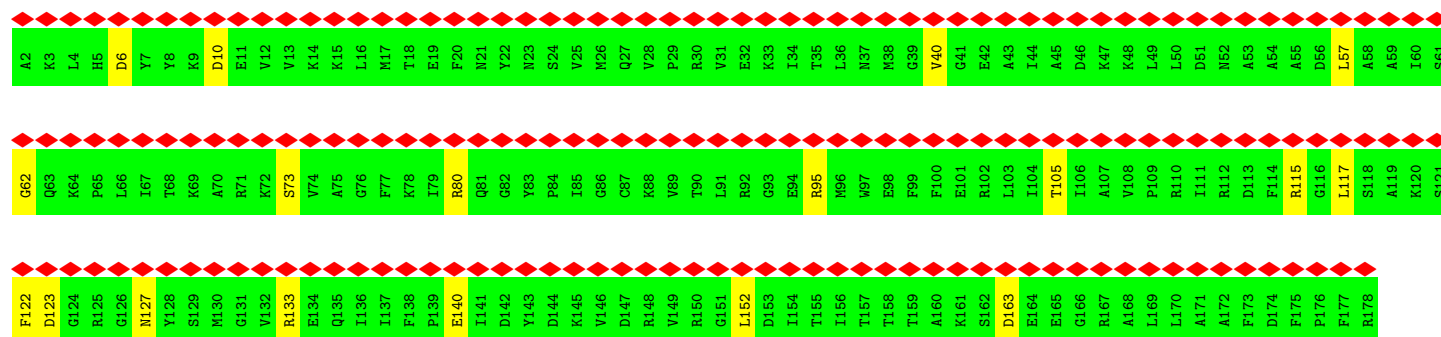
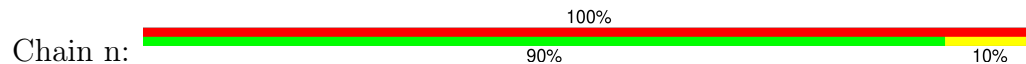
• Molecule 49: 50S ribosomal protein L4



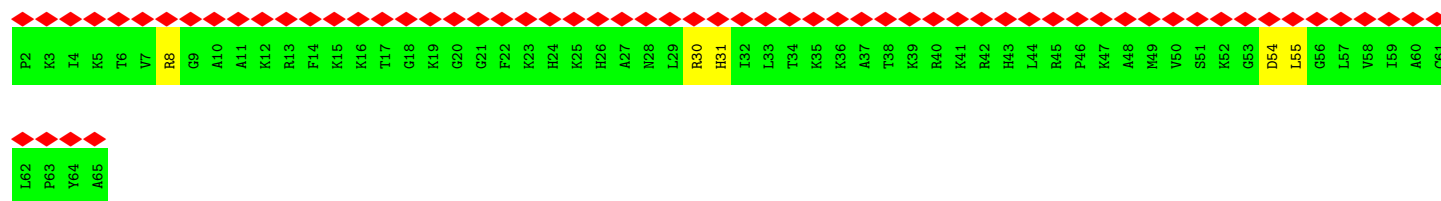
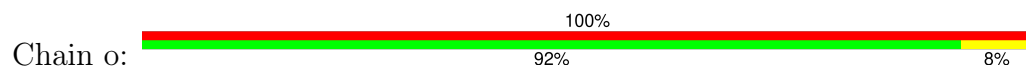
• Molecule 50: 50S ribosomal protein L34



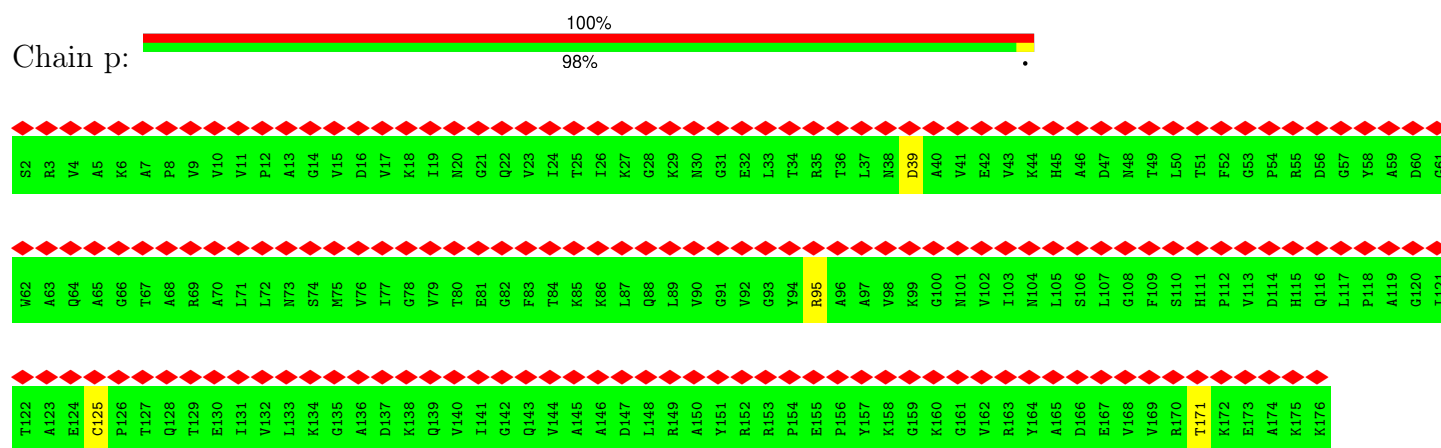
• Molecule 51: 50S ribosomal protein L5



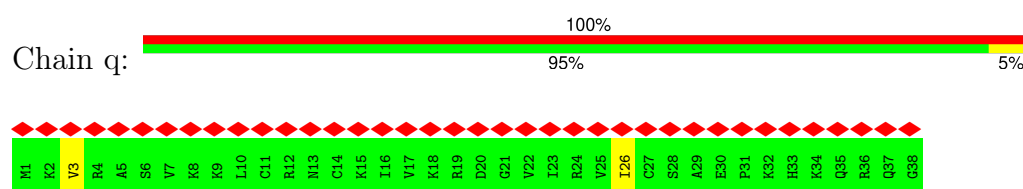
• Molecule 52: 50S ribosomal protein L35



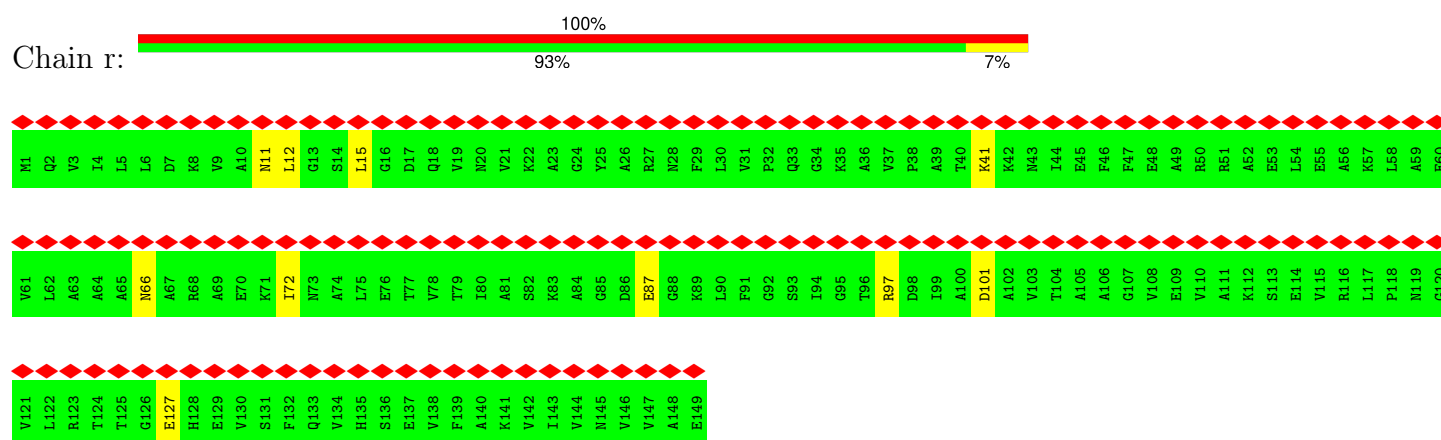
• Molecule 53: 50S ribosomal protein L6



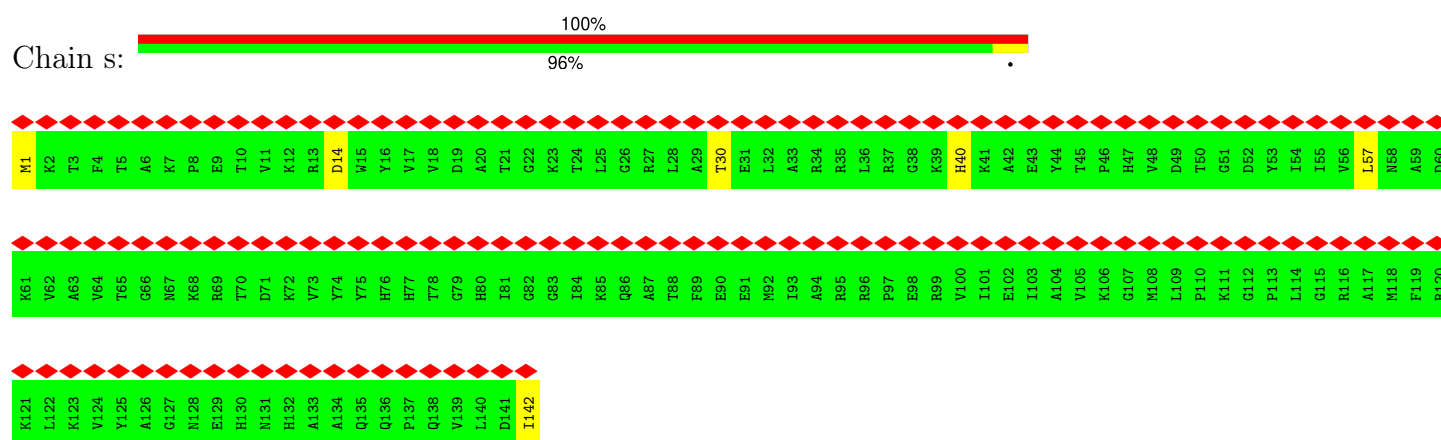
- Molecule 54: 50S ribosomal protein L36



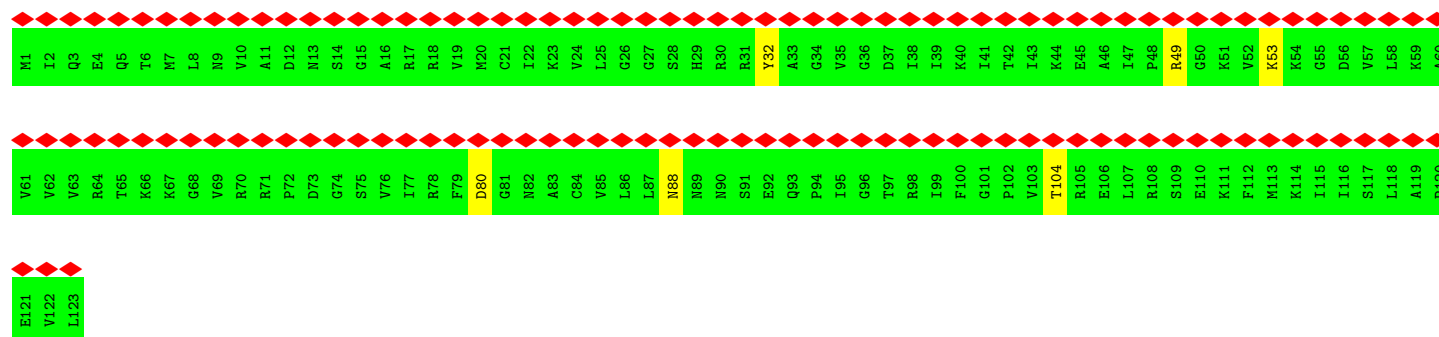
- Molecule 55: 50S ribosomal protein L9



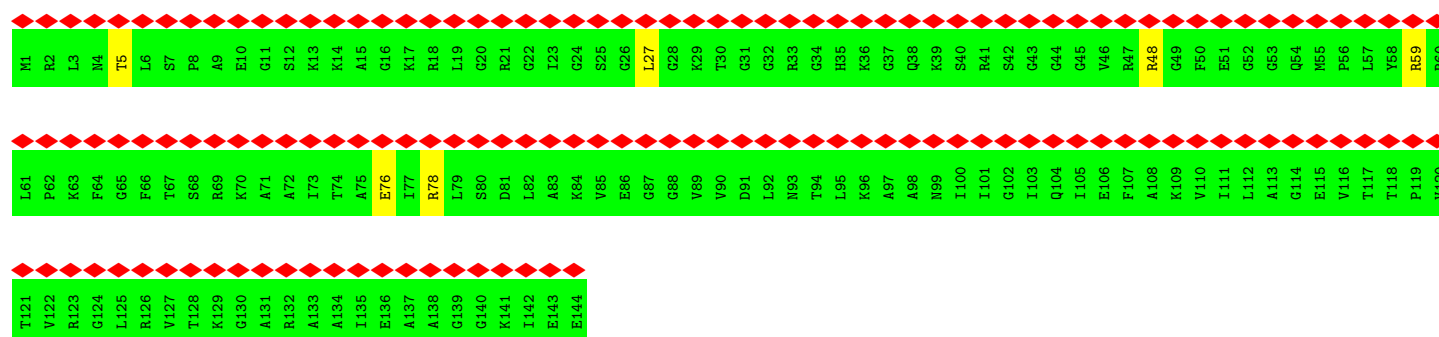
- Molecule 56: 50S ribosomal protein L13



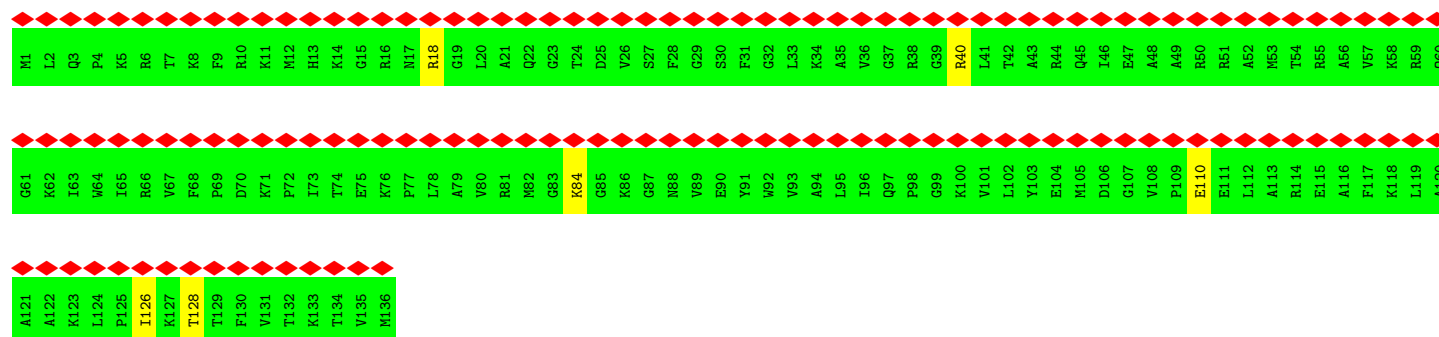
- Molecule 57: 50S ribosomal protein L14



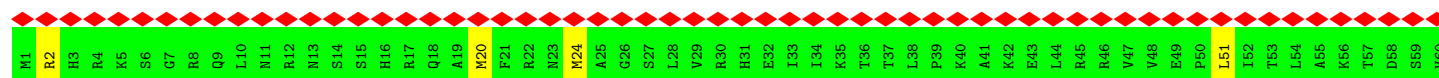
• Molecule 58: 50S ribosomal protein L15

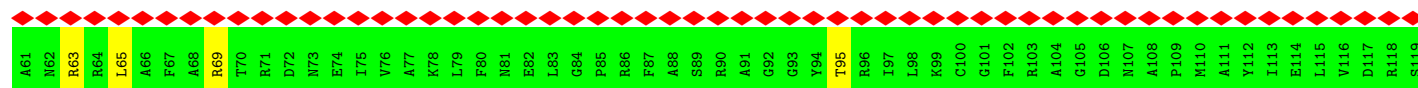


• Molecule 59: 50S ribosomal protein L16



• Molecule 60: 50S ribosomal protein L17

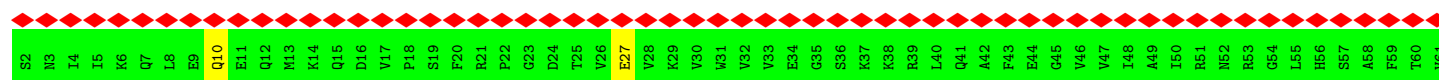




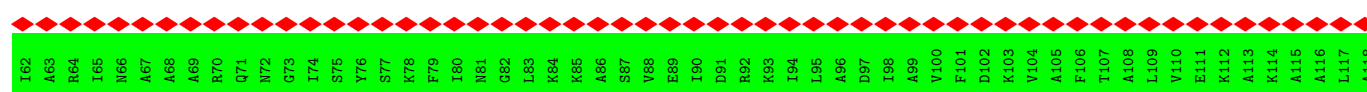
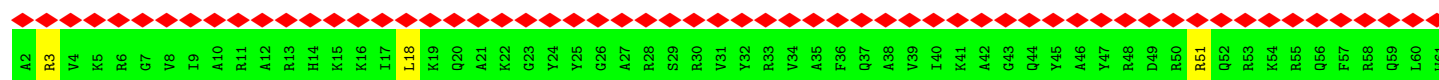
• Molecule 61: 50S ribosomal protein L18



• 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	0.38	0/829	0.67	0/1107
2	1	0.48	0/864	0.83	0/1156
3	2	0.42	0/752	0.71	0/1005
4	3	0.35	0/796	0.66	2/1062 (0.2%)
5	4	0.40	0/766	0.68	0/1025
6	5	1.13	6/528 (1.1%)	0.97	1/810 (0.1%)
7	6	1.11	4/603 (0.7%)	0.97	0/926
8	7	0.95	4/388 (1.0%)	1.04	0/604
9	A	0.39	0/1810	0.75	1/2821 (0.0%)
9	B	0.46	1/1810 (0.1%)	0.86	7/2821 (0.2%)
10	AA	0.58	2/10591 (0.0%)	0.77	19/14289 (0.1%)
11	AB	0.43	0/808	0.59	0/1088
12	AC	0.47	0/1808	0.61	1/2450 (0.0%)
12	AD	0.39	0/1789	0.56	0/2425
13	AE	0.52	3/10545 (0.0%)	0.66	5/14236 (0.0%)
14	AF	0.47	0/657	0.67	0/886
15	C	0.48	0/553	0.83	0/743
16	D	0.34	10/36610 (0.0%)	0.74	30/57091 (0.1%)
17	E	0.57	0/675	0.85	0/895
18	F	0.56	0/597	0.87	0/792
19	G	0.49	0/1791	0.71	0/2413
20	H	0.55	1/1746 (0.1%)	1.03	13/2382 (0.5%)
21	I	0.43	0/1663	0.71	0/2241
22	J	0.47	0/1665	0.73	0/2227
23	K	0.45	0/1165	0.75	0/1568
24	L	0.43	0/867	0.75	1/1171 (0.1%)
25	M	0.50	0/1195	0.81	0/1602
26	N	0.41	0/989	0.70	0/1326
27	O	0.43	0/1034	0.75	0/1375
28	P	0.43	0/800	0.75	0/1082
29	Q	0.40	0/893	0.70	0/1205
30	R	0.35	0/952	0.74	0/1274

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	S	0.49	0/817	0.79	0/1088
32	T	0.53	0/722	0.86	0/964
33	U	0.44	0/659	0.79	0/884
34	V	0.34	0/657	0.62	0/881
35	W	0.38	0/680	0.62	0/915
36	X	0.49	0/909	0.87	0/1215
37	Y	0.26	0/65	0.74	0/98
38	a	0.39	3/69247 (0.0%)	0.72	18/107985 (0.0%)
39	b	0.39	0/589	0.70	0/779
40	c	0.48	0/635	0.81	1/848 (0.1%)
41	d	0.30	0/2872	0.70	0/4478
42	e	0.54	0/502	0.83	0/667
43	f	0.45	0/452	0.78	0/605
44	g	0.43	0/531	0.68	0/709
45	h	0.39	0/2121	0.78	0/2852
46	i	0.40	0/450	0.79	0/599
47	j	0.44	0/1586	0.70	0/2134
48	k	0.35	0/433	0.65	0/576
49	l	0.46	0/1571	0.77	0/2113
50	m	0.53	0/380	0.99	0/498
51	n	0.49	0/1434	0.88	3/1926 (0.2%)
52	o	0.45	0/513	0.83	0/676
53	p	0.39	0/1333	0.67	0/1805
54	q	0.37	0/303	0.77	0/397
55	r	0.44	0/1122	0.69	0/1515
56	s	0.50	0/1152	0.75	0/1551
57	t	0.41	0/955	0.78	0/1279
58	u	0.40	0/1062	0.76	0/1413
59	v	0.47	0/1093	0.82	0/1460
60	w	0.52	0/964	0.87	0/1289
61	x	0.46	0/902	0.81	0/1209
62	y	0.41	0/929	0.72	1/1242 (0.1%)
63	z	0.60	0/960	0.91	0/1278
All	All	0.43	34/187139 (0.0%)	0.74	103/276026 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
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 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	D	1516	G	O3'-P	-13.47	1.45	1.61
16	D	1339	A	O3'-P	10.59	1.73	1.61
10	AA	374	GLU	C-N	10.38	1.53	1.34
13	AE	88	CYS	CB-SG	-10.14	1.65	1.82
6	5	109	DT	O3'-P	8.59	1.71	1.61

The worst 5 of 103 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	D	1516	G	P-O3'-C3'	-18.97	96.94	119.70
16	D	1516	G	O3'-P-O5'	13.77	130.17	104.00
10	AA	1007	LYS	O-C-N	-13.02	101.87	122.70
10	AA	1250	SER	C-N-CA	11.20	149.69	121.70
38	a	2252	G	N9-C1'-C2'	-10.97	99.74	114.00

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 [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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%)	13	49
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%)	13	49
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	52
12	AD	226/230 (98%)	212 (94%)	14 (6%)	0	100	100
13	AE	1329/1358 (98%)	1198 (90%)	122 (9%)	9 (1%)	19	57
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%)	25	64
22	J	203/205 (99%)	198 (98%)	5 (2%)	0	100	100
23	K	154/156 (99%)	146 (95%)	7 (4%)	1 (1%)	22	60
24	L	102/104 (98%)	97 (95%)	4 (4%)	1 (1%)	13	49
25	M	149/151 (99%)	144 (97%)	4 (3%)	1 (1%)	19	57
26	N	127/129 (98%)	121 (95%)	5 (4%)	1 (1%)	16	55
27	O	125/127 (98%)	115 (92%)	9 (7%)	1 (1%)	16	55
28	P	97/99 (98%)	88 (91%)	8 (8%)	1 (1%)	13	49
29	Q	115/117 (98%)	104 (90%)	9 (8%)	2 (2%)	7	37

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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%)	10	43
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%)	7	35
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	68
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%)	25	64
50	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
51	n	175/177 (99%)	162 (93%)	11 (6%)	2 (1%)	12	47
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	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	9136/9618 (95%)	8457 (93%)	604 (7%)	75 (1%)	19	55

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%)	78 (93%)	6 (7%)	12	32
2	1	93/93 (100%)	84 (90%)	9 (10%)	6	22
3	2	81/81 (100%)	76 (94%)	5 (6%)	15	36
4	3	84/84 (100%)	78 (93%)	6 (7%)	12	32
5	4	78/78 (100%)	74 (95%)	4 (5%)	20	41
10	AA	1140/1156 (99%)	1043 (92%)	97 (8%)	8	27
11	AB	86/98 (88%)	84 (98%)	2 (2%)	45	64
12	AC	198/198 (100%)	184 (93%)	14 (7%)	12	32
12	AD	196/198 (99%)	194 (99%)	2 (1%)	73	82
13	AE	1120/1134 (99%)	1051 (94%)	69 (6%)	15	36
14	AF	70/70 (100%)	70 (100%)	0	100	100
15	C	57/57 (100%)	55 (96%)	2 (4%)	31	51
17	E	65/65 (100%)	60 (92%)	5 (8%)	10	30
18	F	60/60 (100%)	57 (95%)	3 (5%)	20	41
19	G	187/187 (100%)	178 (95%)	9 (5%)	21	43
20	H	137/461 (30%)	128 (93%)	9 (7%)	14	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	I	171/171 (100%)	165 (96%)	6 (4%)	31	51
22	J	172/172 (100%)	165 (96%)	7 (4%)	26	47
23	K	119/119 (100%)	112 (94%)	7 (6%)	16	37
24	L	91/91 (100%)	85 (93%)	6 (7%)	14	34
25	M	124/124 (100%)	116 (94%)	8 (6%)	14	35
26	N	104/104 (100%)	102 (98%)	2 (2%)	52	69
27	O	105/105 (100%)	100 (95%)	5 (5%)	21	43
28	P	86/86 (100%)	78 (91%)	8 (9%)	7	23
29	Q	90/90 (100%)	87 (97%)	3 (3%)	33	52
30	R	101/103 (98%)	94 (93%)	7 (7%)	13	33
31	S	83/83 (100%)	79 (95%)	4 (5%)	21	43
32	T	76/76 (100%)	64 (84%)	12 (16%)	2	10
33	U	65/65 (100%)	61 (94%)	4 (6%)	15	36
34	V	74/74 (100%)	72 (97%)	2 (3%)	40	58
35	W	72/72 (100%)	68 (94%)	4 (6%)	17	38
36	X	94/94 (100%)	85 (90%)	9 (10%)	7	22
39	b	58/58 (100%)	57 (98%)	1 (2%)	56	72
40	c	67/67 (100%)	64 (96%)	3 (4%)	23	45
42	e	54/54 (100%)	53 (98%)	1 (2%)	52	69
43	f	48/48 (100%)	46 (96%)	2 (4%)	25	46
44	g	59/59 (100%)	53 (90%)	6 (10%)	6	20
45	h	216/216 (100%)	199 (92%)	17 (8%)	10	29
46	i	47/47 (100%)	41 (87%)	6 (13%)	3	14
47	j	164/164 (100%)	157 (96%)	7 (4%)	25	46
48	k	47/47 (100%)	44 (94%)	3 (6%)	14	35
49	l	165/165 (100%)	151 (92%)	14 (8%)	8	27
50	m	38/38 (100%)	35 (92%)	3 (8%)	10	29
51	n	148/148 (100%)	134 (90%)	14 (10%)	7	22
52	o	51/51 (100%)	46 (90%)	5 (10%)	6	21
53	p	136/136 (100%)	132 (97%)	4 (3%)	37	56
54	q	34/34 (100%)	32 (94%)	2 (6%)	16	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	r	114/114 (100%)	104 (91%)	10 (9%)	8	25
56	s	116/116 (100%)	110 (95%)	6 (5%)	19	40
57	t	104/104 (100%)	98 (94%)	6 (6%)	17	38
58	u	103/103 (100%)	97 (94%)	6 (6%)	17	38
59	v	109/109 (100%)	103 (94%)	6 (6%)	18	39
60	w	99/99 (100%)	91 (92%)	8 (8%)	9	28
61	x	86/86 (100%)	80 (93%)	6 (7%)	12	32
62	y	99/99 (100%)	95 (96%)	4 (4%)	27	47
63	z	89/89 (100%)	87 (98%)	2 (2%)	47	65
All	All	7614/7984 (95%)	7136 (94%)	478 (6%)	17	36

5 of 478 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	G	132	LYS
57	t	80	ASP
28	P	25	ILE
56	s	57	LEU
62	y	27	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
10	AA	1010	GLN
10	AA	1013	GLN
19	G	18	HIS
36	X	105	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	D	1515/1542 (98%)	289 (19%)	35 (2%)
37	Y	2/3 (66%)	2 (100%)	0
38	a	2859/2903 (98%)	531 (18%)	0
41	d	119/120 (99%)	17 (14%)	0
8	7	15/16 (93%)	7 (46%)	0
9	A	75/76 (98%)	29 (38%)	6 (8%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	B	75/76 (98%)	35 (46%)	6 (8%)
All	All	4660/4736 (98%)	910 (19%)	47 (1%)

5 of 910 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.

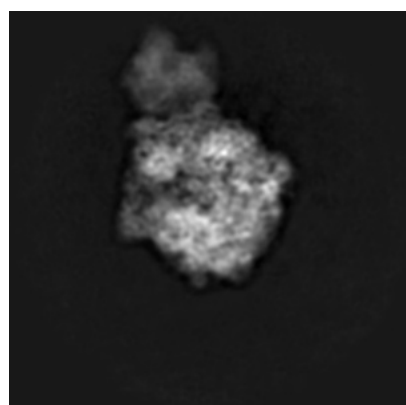
6 Map visualisation [i](#)

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.

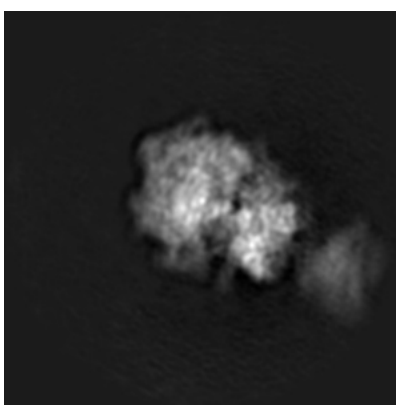
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

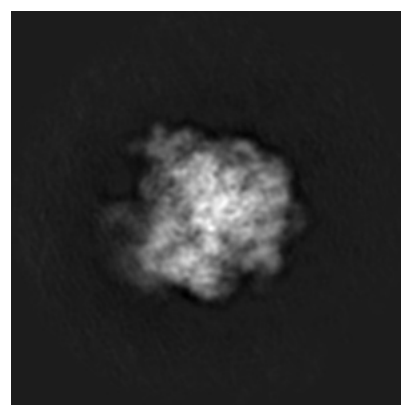
6.1.1 Primary map



X



Y

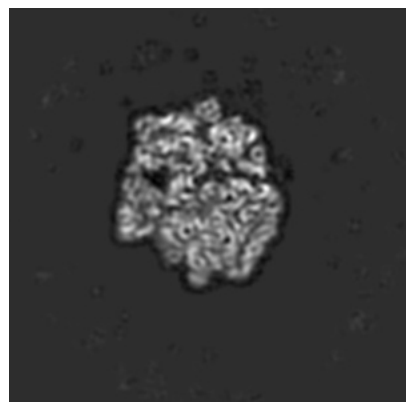


Z

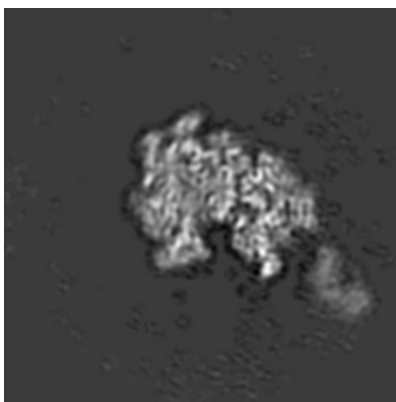
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

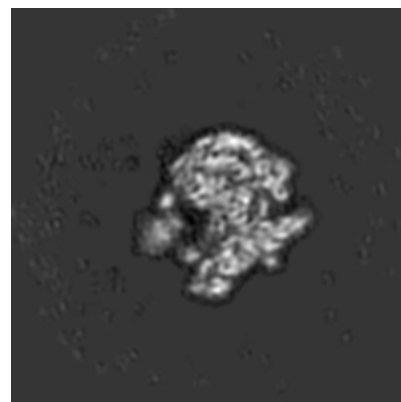
6.2.1 Primary map



X Index: 140



Y Index: 140

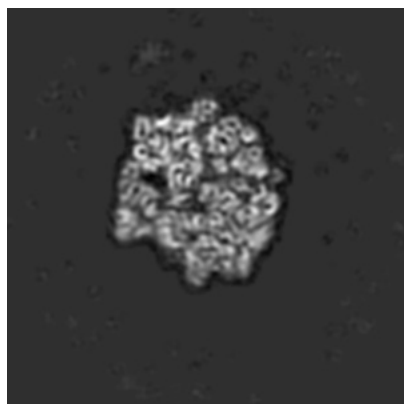


Z Index: 140

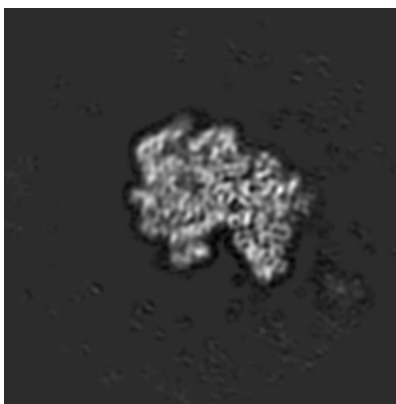
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

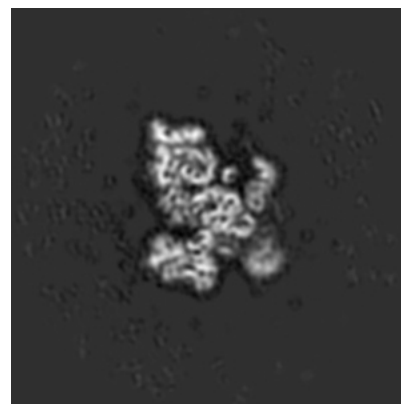
6.3.1 Primary map



X Index: 137



Y Index: 147

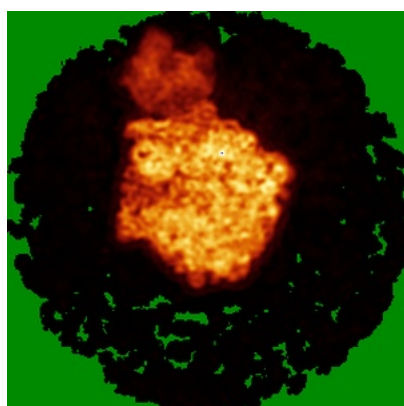


Z Index: 169

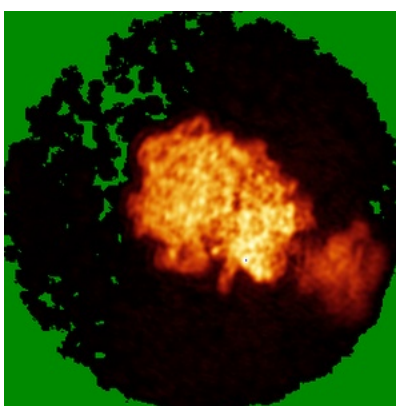
The images above show the largest variance slices of the map in three orthogonal directions.

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

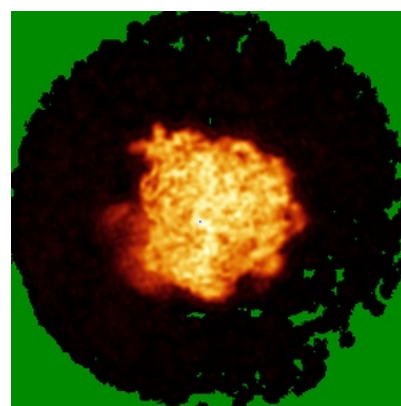
6.4.1 Primary map



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.

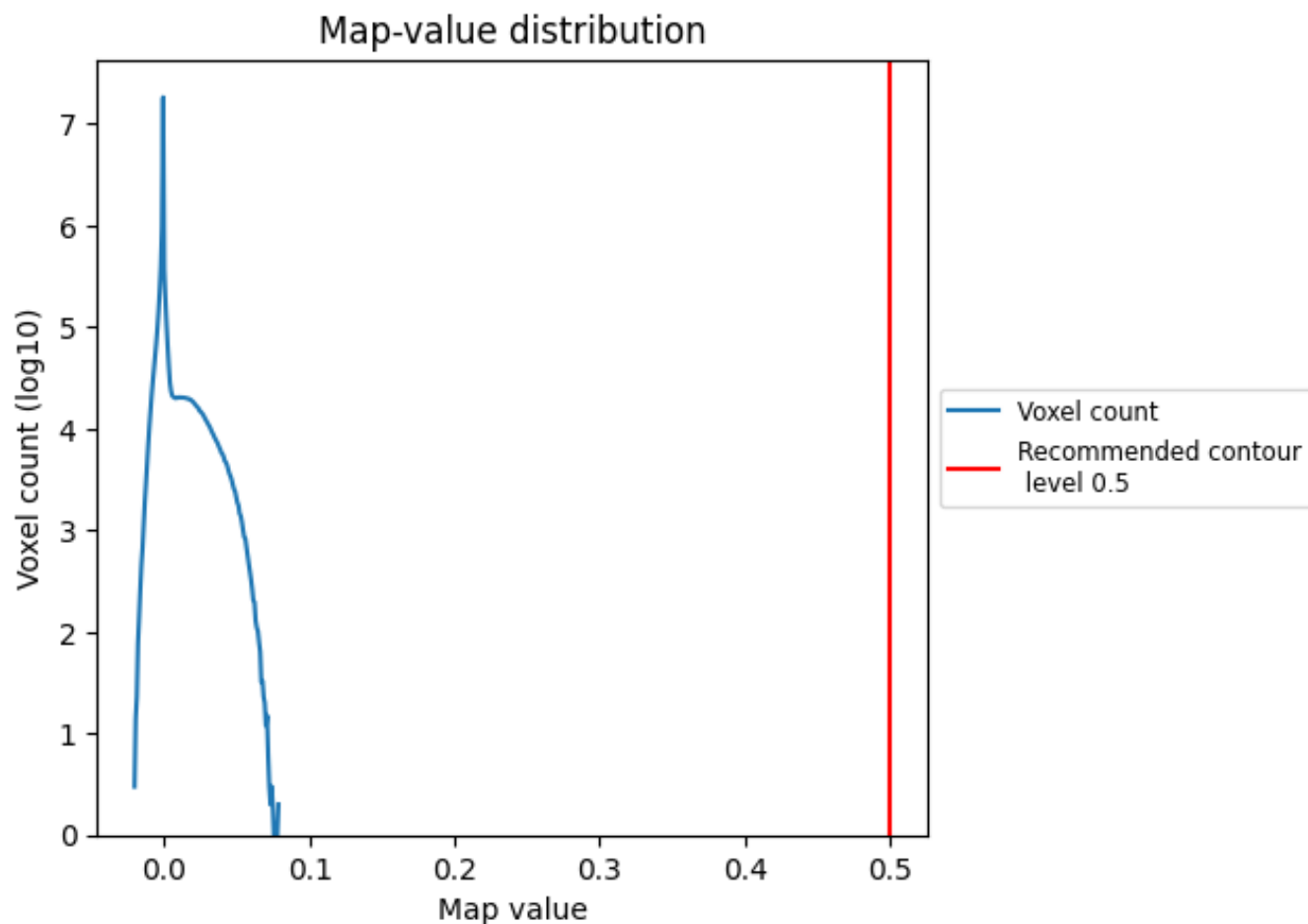
6.6 Mask visualisation

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

7 Map analysis [i](#)

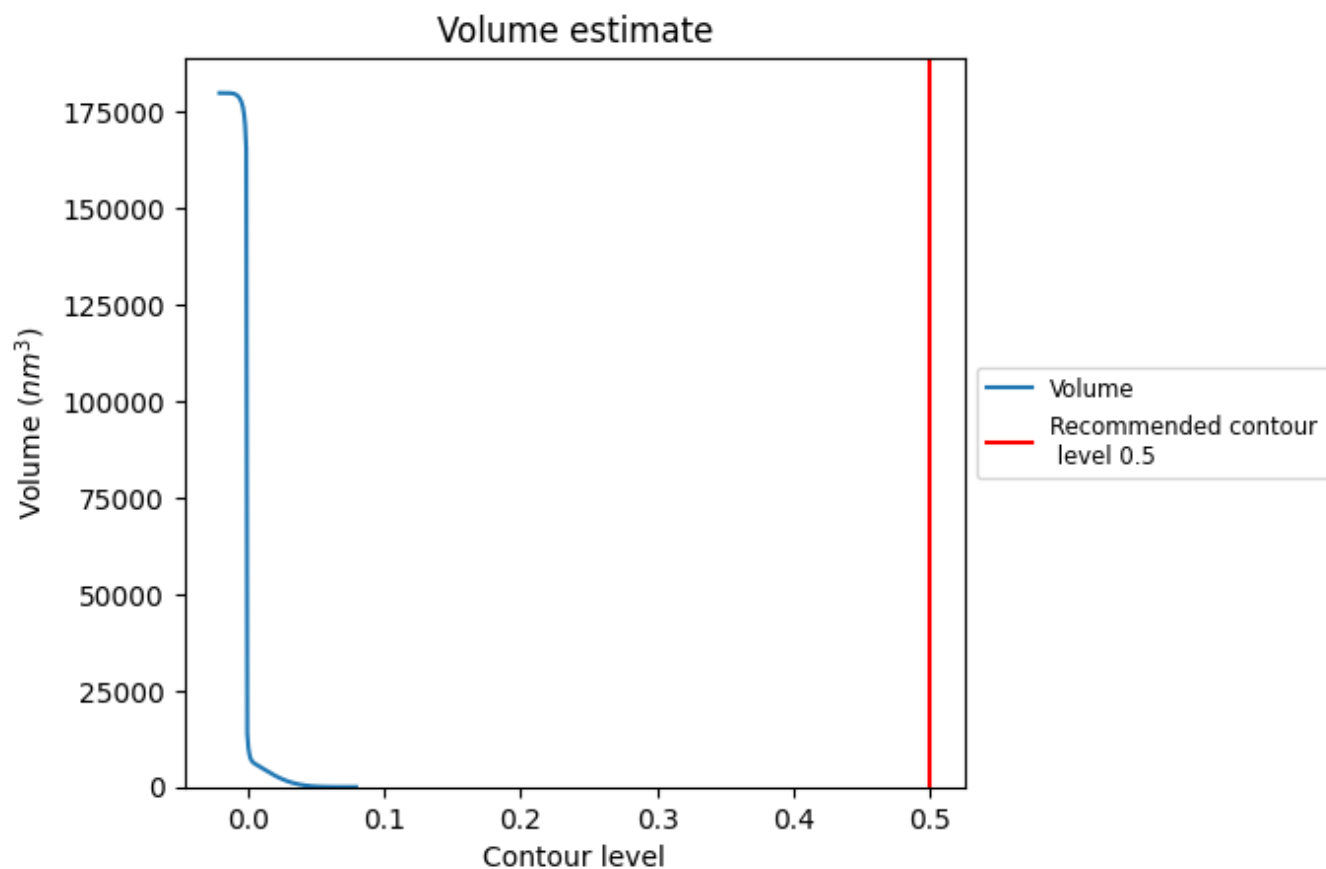
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



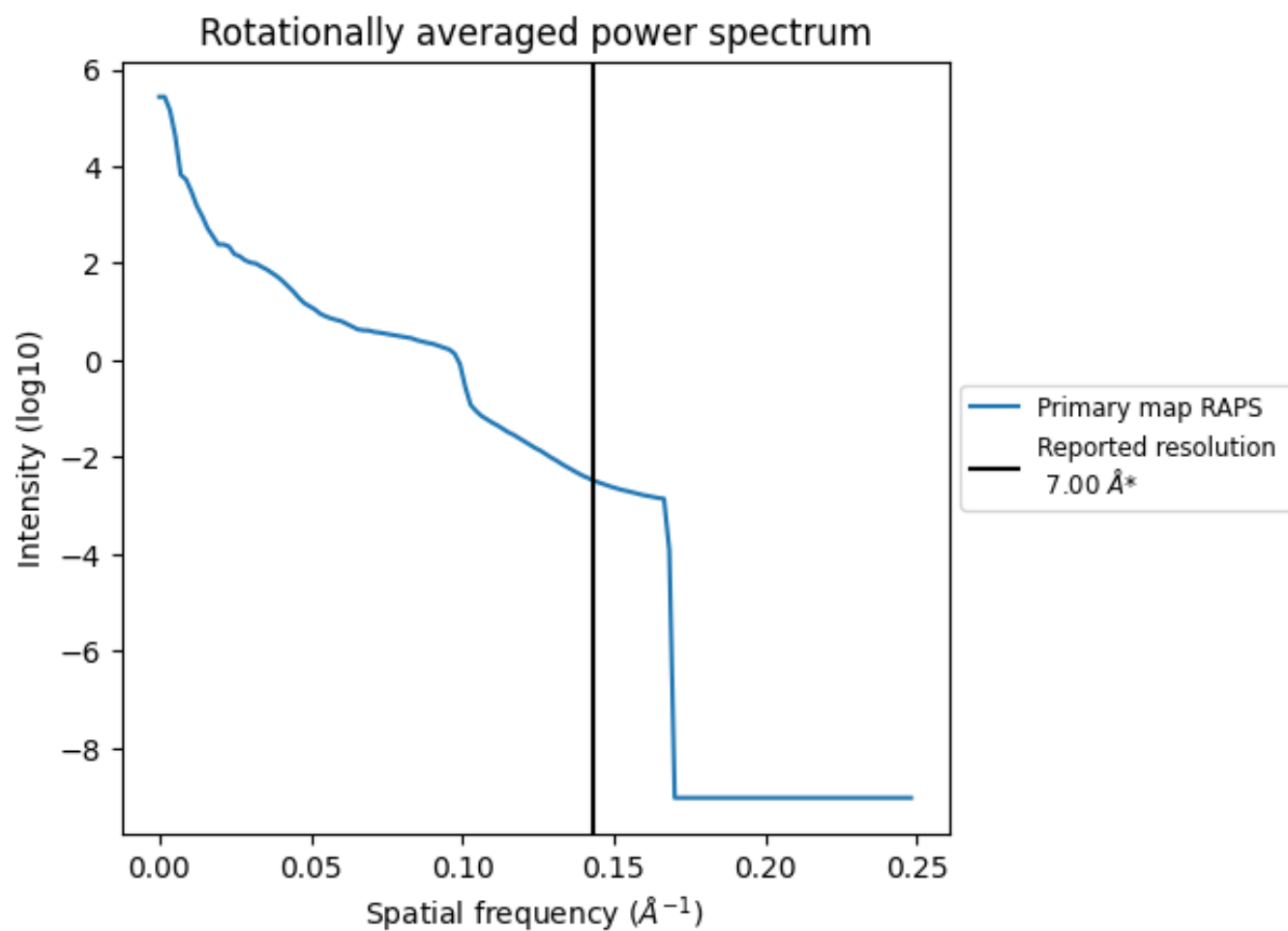
The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

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

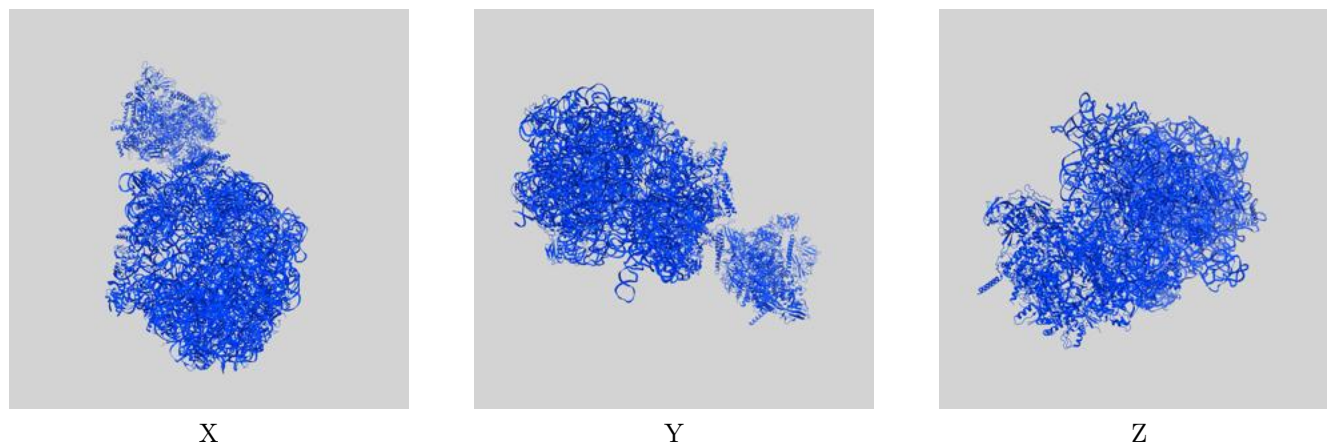
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

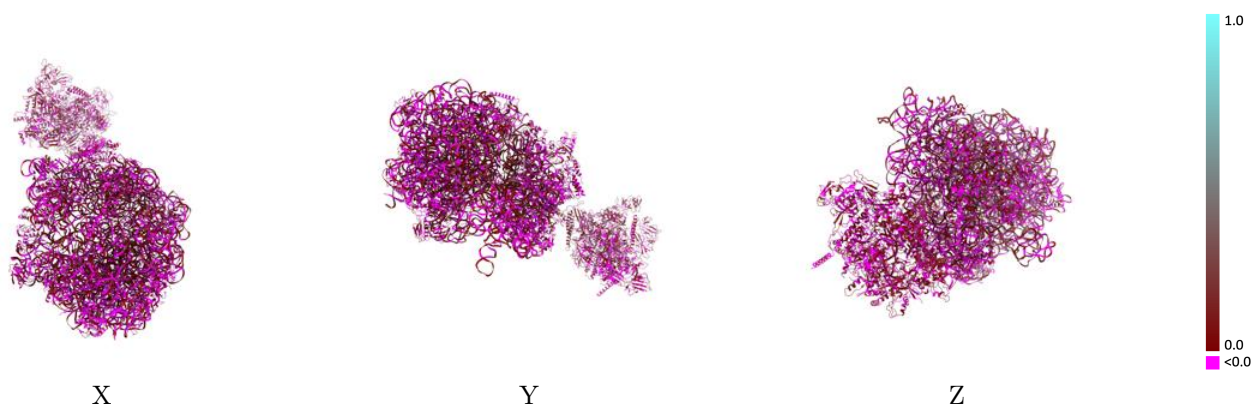
This section contains information regarding the fit between EMDB map EMD-21486 and PDB model 6VZ7. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



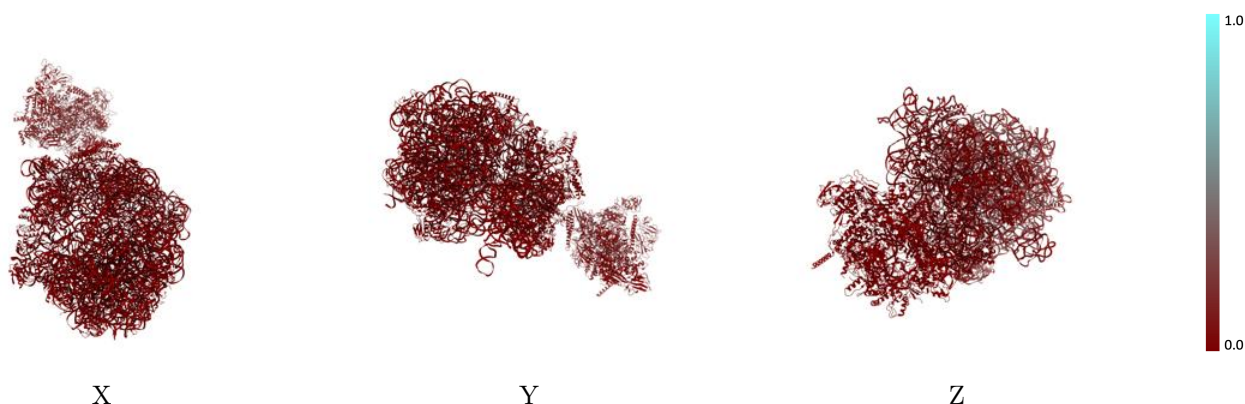
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



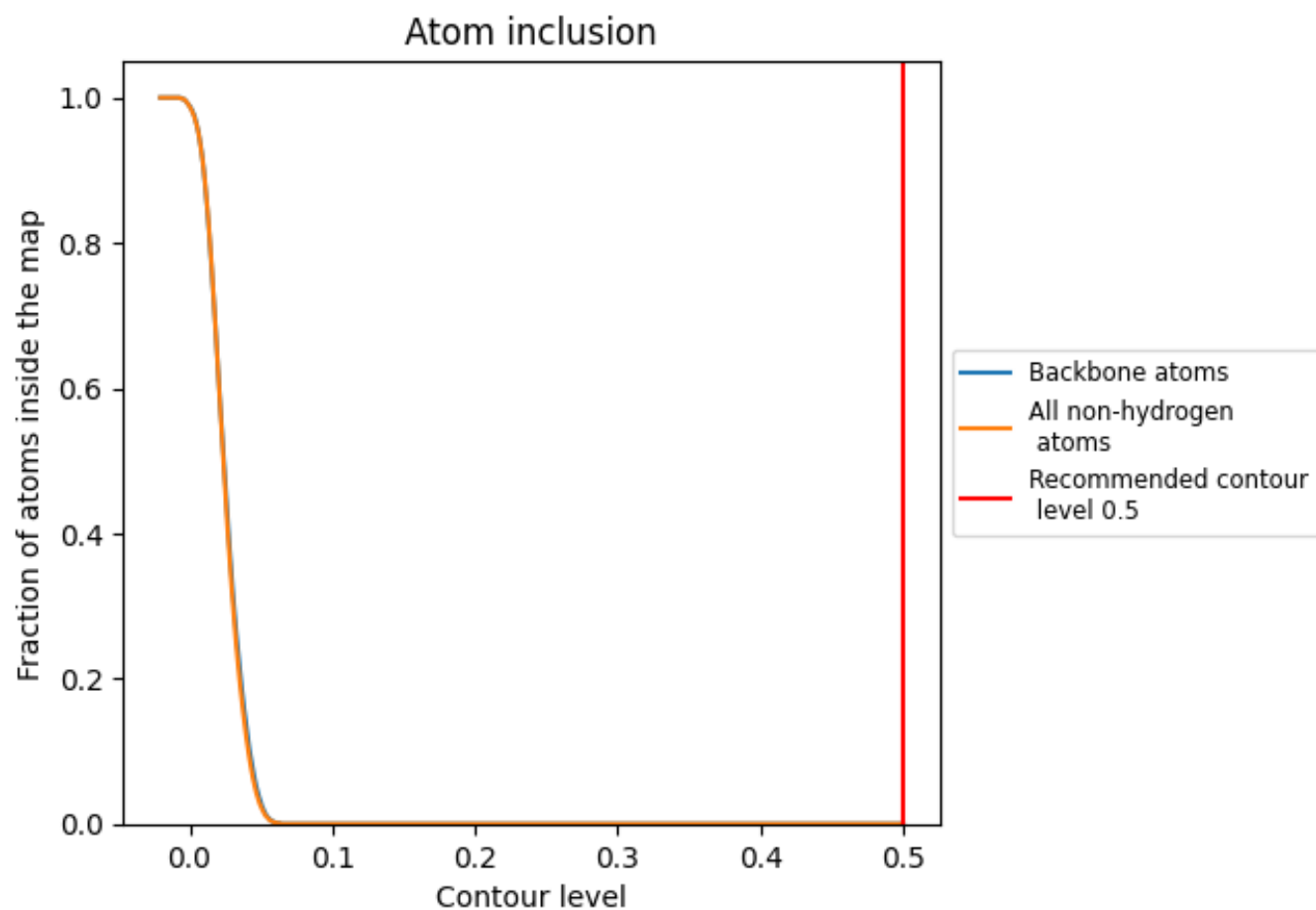
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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