wwPDB EM Validation Summary Report

Sep 17, 2026 – 05:20 AM 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:

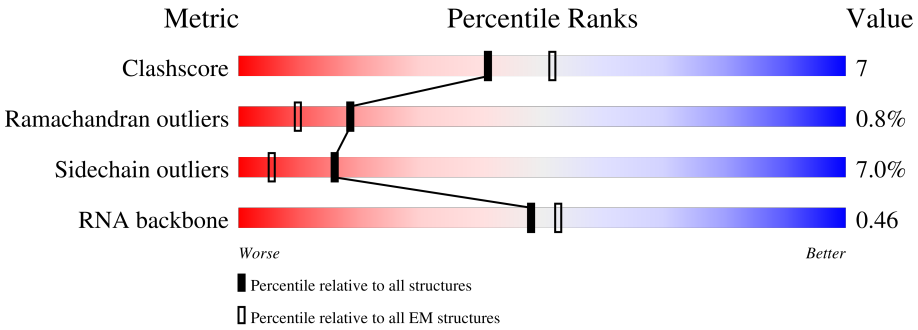
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

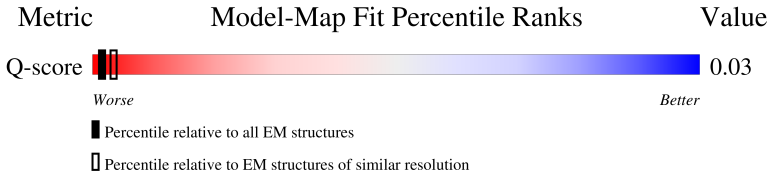
1 Overall quality at a glance (i)

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.





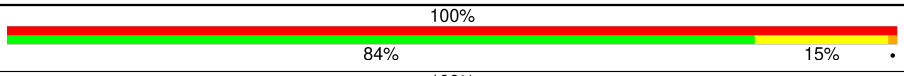
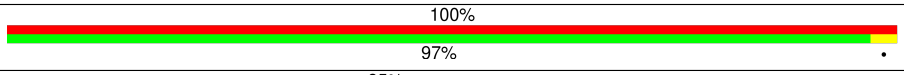
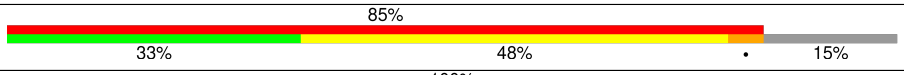
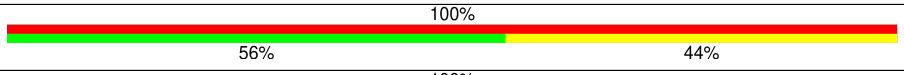
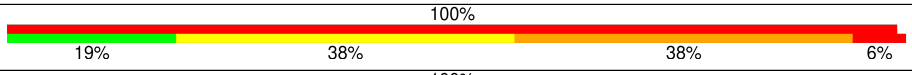
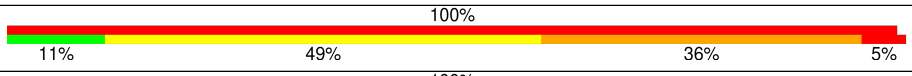
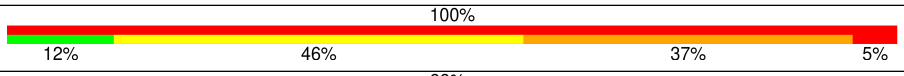
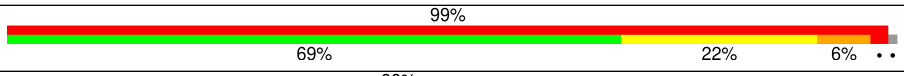
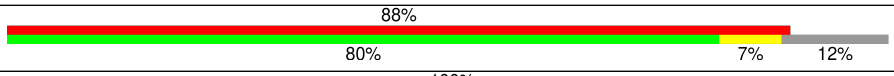
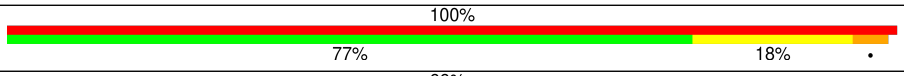
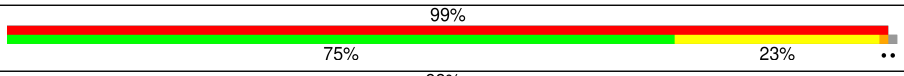
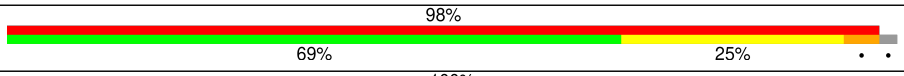
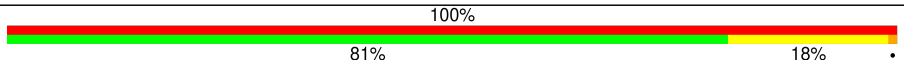
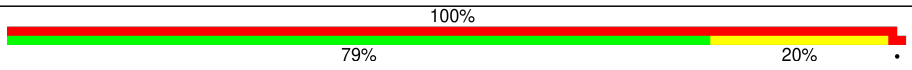
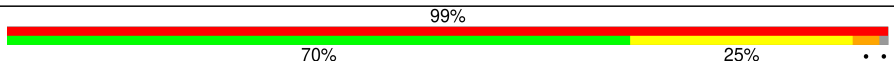
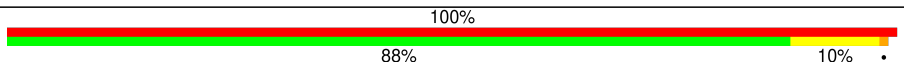
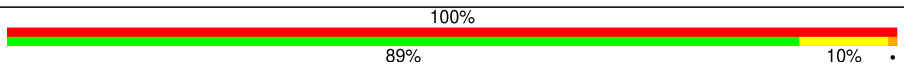
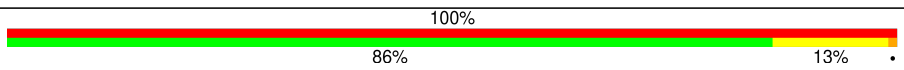
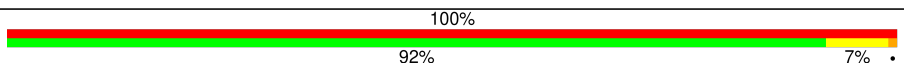
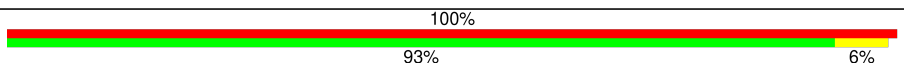
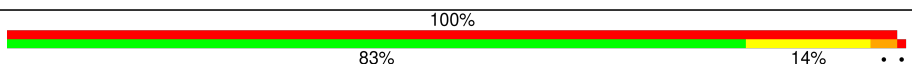
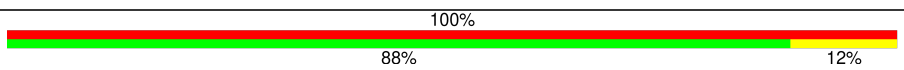
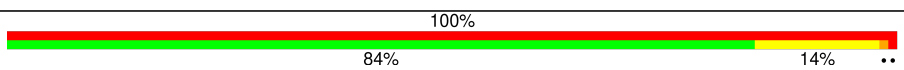
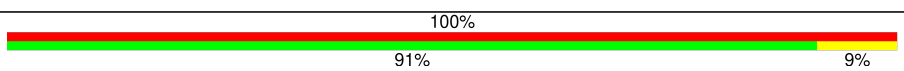
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	483 (6.50 - 7.50)

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 <=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%, •

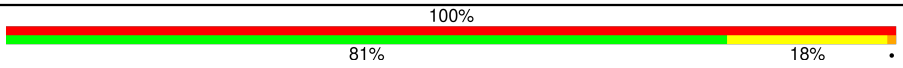
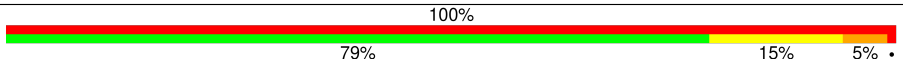
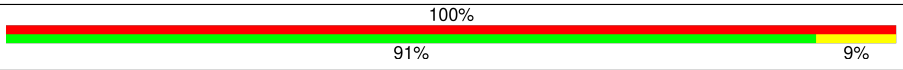
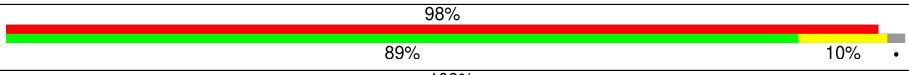
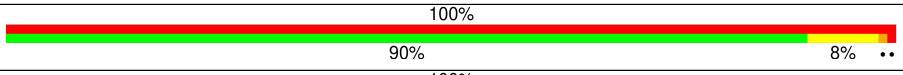
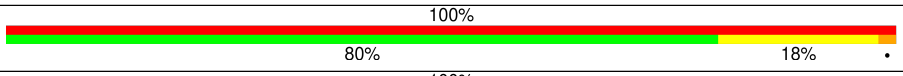
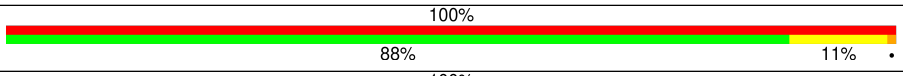
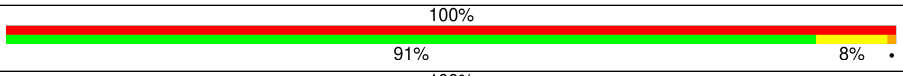
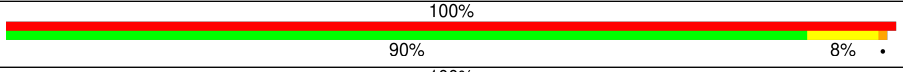
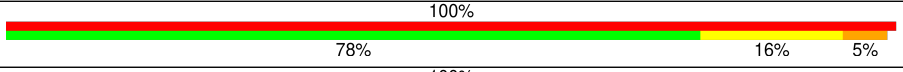
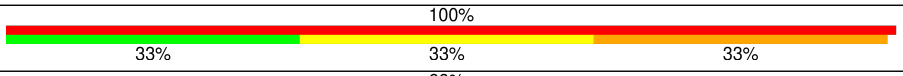
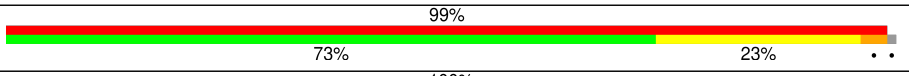
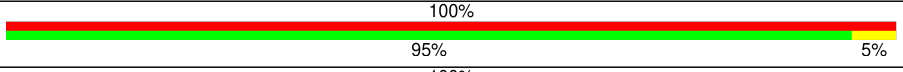
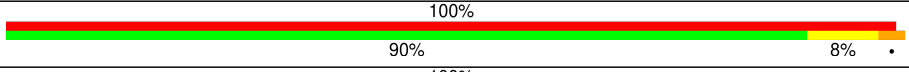
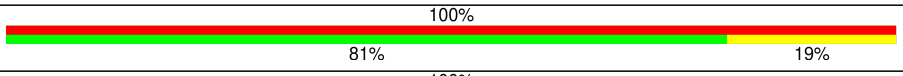
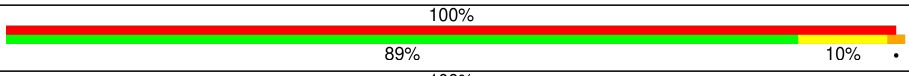
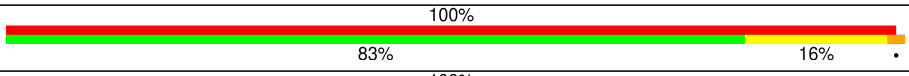
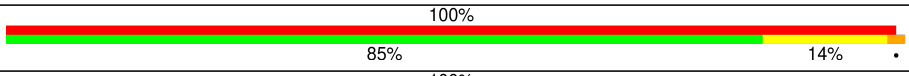
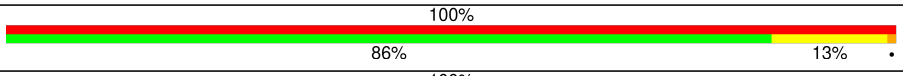
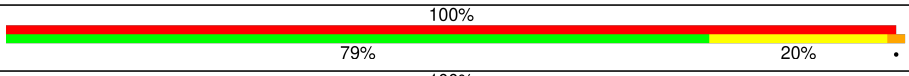
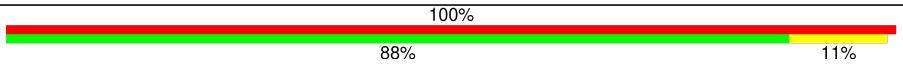
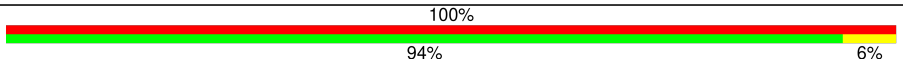
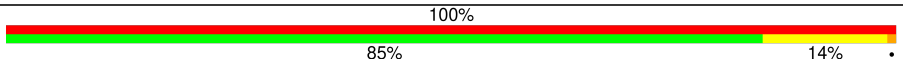
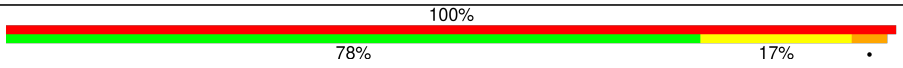
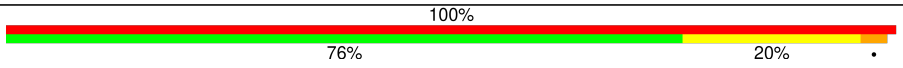
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Mol	Chain	Length	Quality of chain
4	3	103	
5	4	94	
6	5	27	
7	6	27	
8	7	16	
9	A	76	
9	B	76	
10	AA	1341	
11	AB	112	
12	AC	230	
12	AD	230	
13	AE	1358	
14	AF	83	
15	C	66	
16	D	1542	
17	E	86	
18	F	70	
19	G	225	
20	H	557	
21	I	208	
22	J	205	
23	K	156	
24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

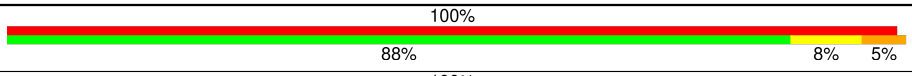
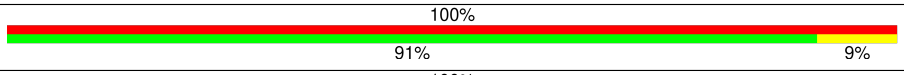
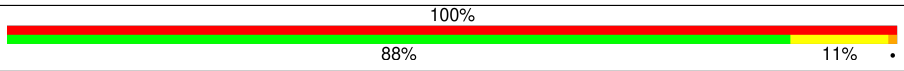
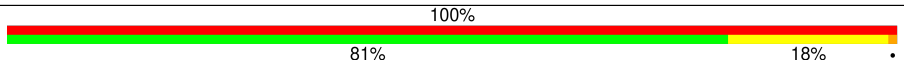
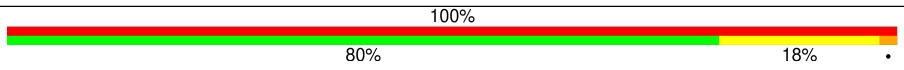
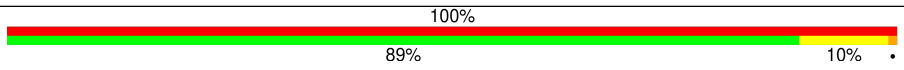
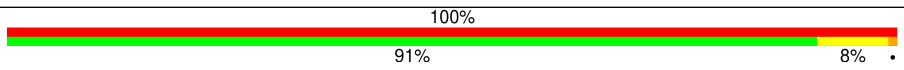
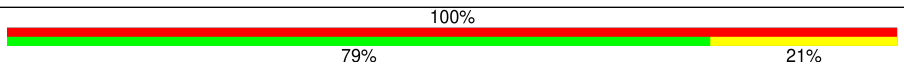
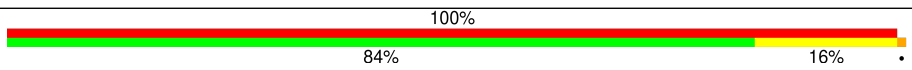
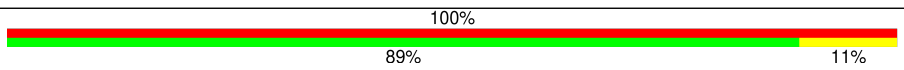
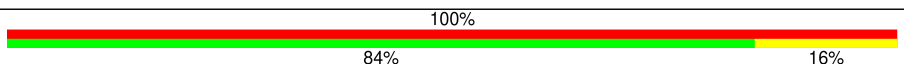
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Mol	Chain	Length	Quality of chain
27	O	127	
28	P	99	
29	Q	117	
30	R	123	
31	S	100	
32	T	88	
33	U	82	
34	V	80	
35	W	83	
36	X	116	
37	Y	3	
38	a	2903	
39	b	76	
40	c	77	
41	d	120	
42	e	62	
43	f	58	
44	g	66	
45	h	271	
46	i	56	
47	j	209	
48	k	52	
49	l	201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

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 (i)

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

• Molecule 1: 50S ribosomal protein L21

Chain 0:





• Molecule 2: 50S ribosomal protein L22

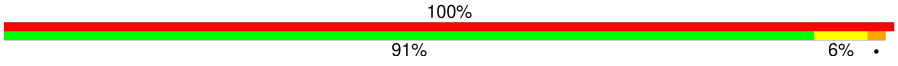
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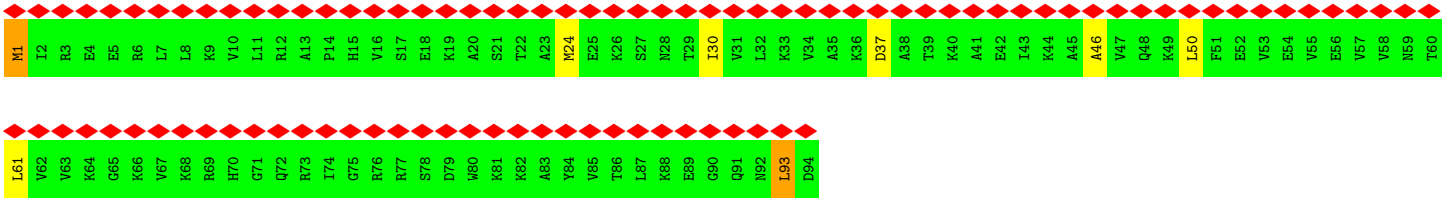




• Molecule 3: 50S ribosomal protein L23

Chain 2:





• Molecule 4: 50S ribosomal protein L24

Chain 3:



A2 A3 K4 I5 R6 R7 D8 D9 E10 V11 I12 V13 L14 T15 G16 K17 D18 K19 G20 K21 R22 G23 K24 V25 K26 N27 V28 L29 S30 S31 G32 K33 V34 I35 V36 E37 G38 T39 N40 L41 V42 K43 K44 H45 Q46 K47 P48 V49 P50 A51 L52 N53 Q54 P55 G56 G57 I58 V59 E60 K61

E62 A63 A64 I65 Q66 V67 S68 N69 V70 A71 I72 F73 N74 A75 A76 T77 G78 K79 A80 D81 R82 V83 G84 F85 R86 F87 E88 D89 G90 K91 K92 V93 R94 F95 F96 K97 S98 N99 S100 E101 T102 I103 K104

- Molecule 5: 50S ribosomal protein L25

Chain 4:



M1 F2 T3 I4 N5 A6 E7 V8 R9 K10 E11 Q12 G13 K14 G15 A16 S17 R18 R19 L20 R21 A22 A23 N24 K25 F26 P27 A28 I29 I30 Y31 G32 G33 K34 E35 A36 P37 L38 A39 I40 E41 L42 D43 H44 D45 K46 V47 M48 N49 M50 Q51 A52 K53 A54 E55 F56 Y57 S58 E59 V60

L61 T62 I63 V64 V65 D66 G67 K68 E69 I70 K71 V72 K73 A74 Q75 D76 V77 Q78 R79 H80 P81 Y82 K83 P84 K85 L86 Q87 H88 I89 D90 F91 V92 R93 A94

- Molecule 6: NT DNA

Chain 5:



T96 C97 A98 T99 A100 T101 T102 A103 DT DT DT DT T108 T109 A110 C111 G112 C113 C114 A115 G116 A117 C118 A119 G120 G121 G122

- Molecule 7: T DNA

Chain 6:



C2 C3 C4 T5 G6 T7 C8 T9 G10 G11 C12 G13 T14 C15 C16 T17 C18 T19 C20 A21 C22 C23 T24 A25 T26 G27 A28

- Molecule 8: mRNA with 27 nt long spacer

Chain 7:



U55 U56 G57 A58 U59 U60 U61 G62 G63 U64 G65 A66 G67 A68 G69 G70

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

Chain A:

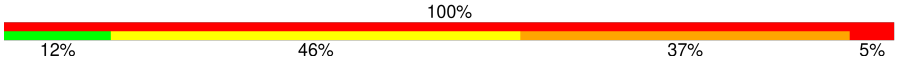


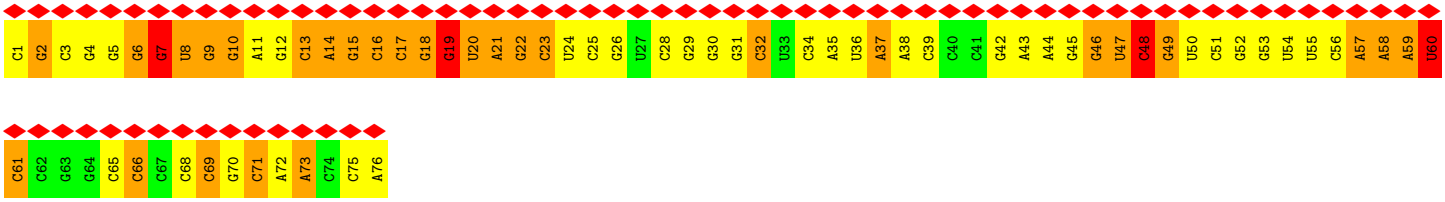
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C61 C62 G63 G64 C65 C66 C67 C68 G69 G70 C71 A72 A73 C74 C75 A76

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

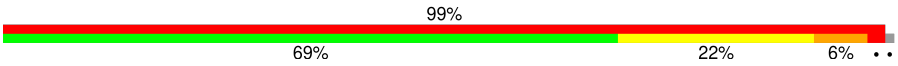
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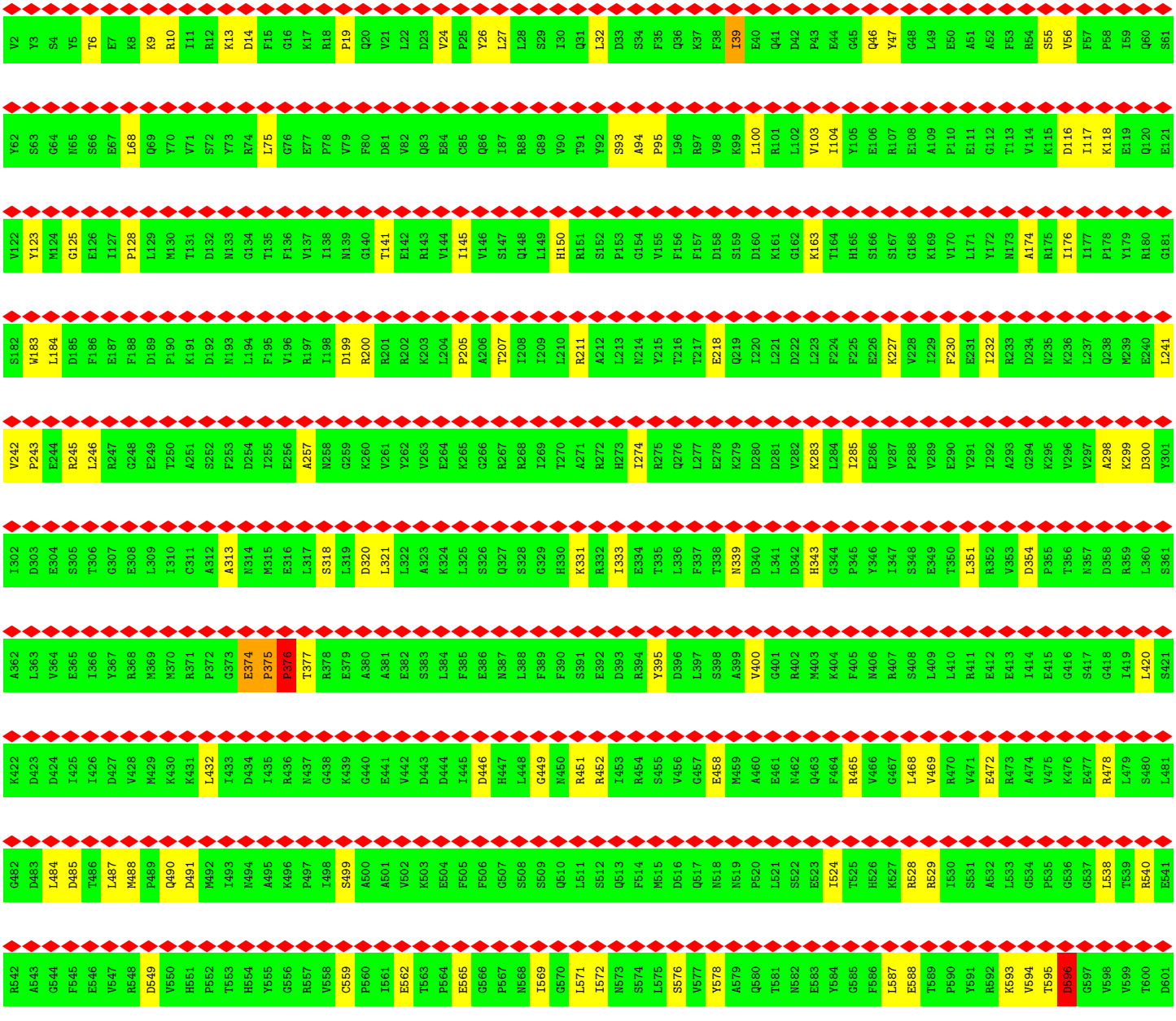


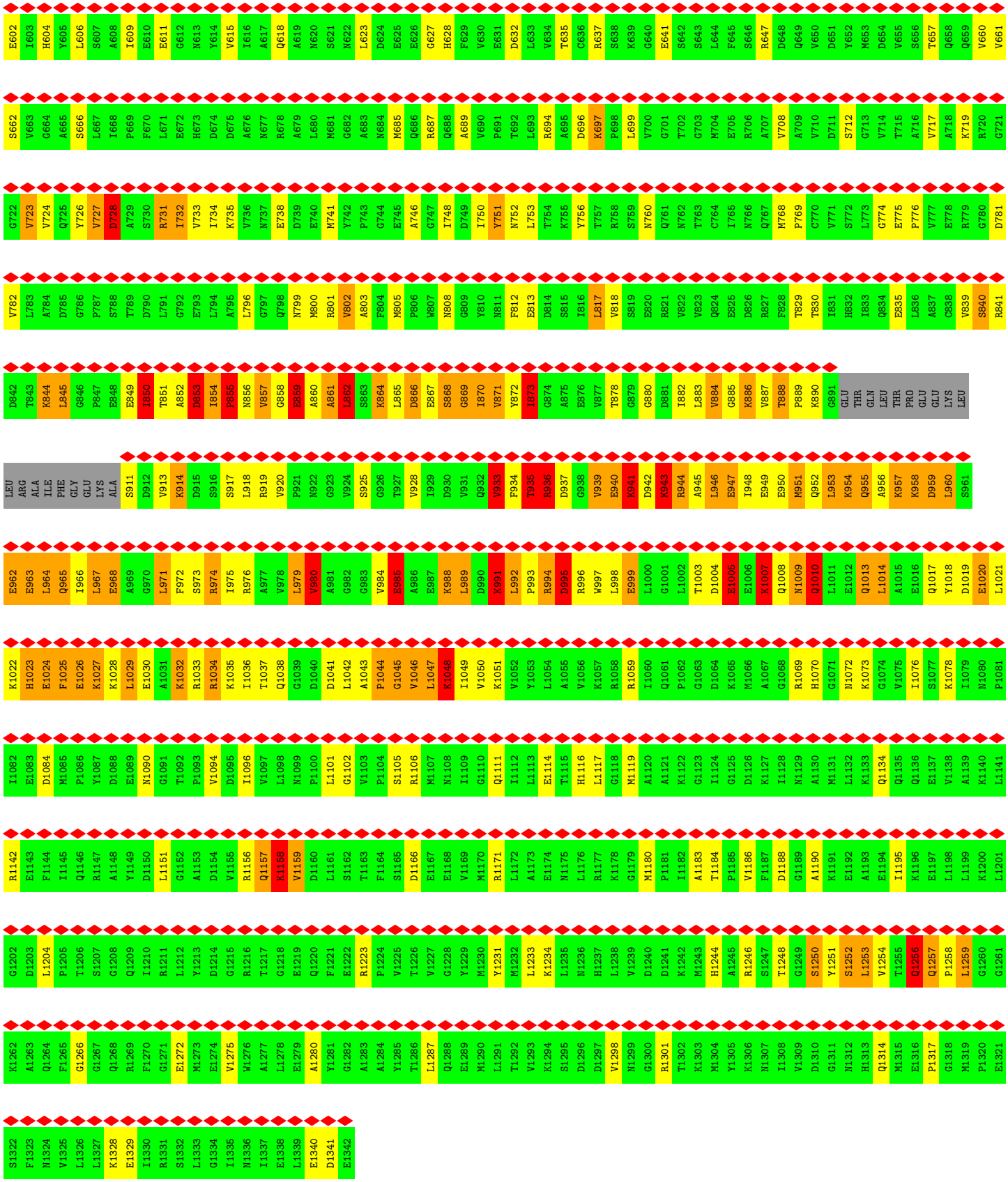


• Molecule 10: DNA-directed RNA polymerase subunit beta

Chain AA:

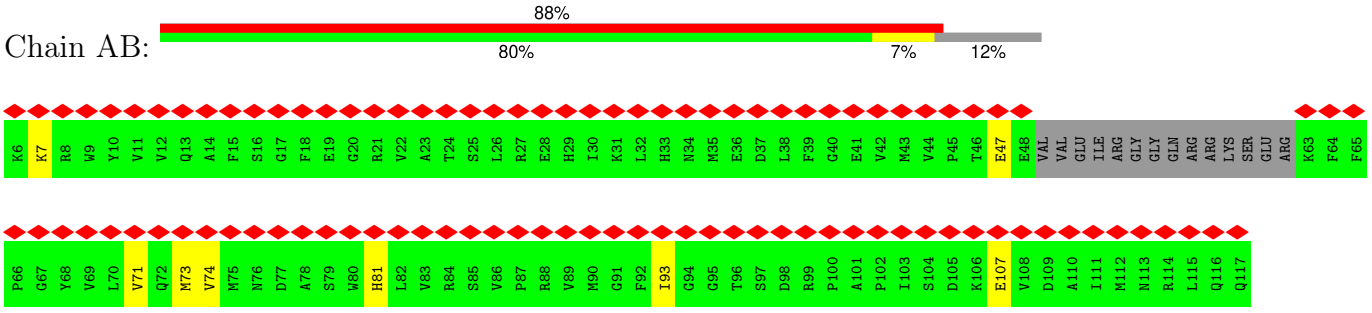






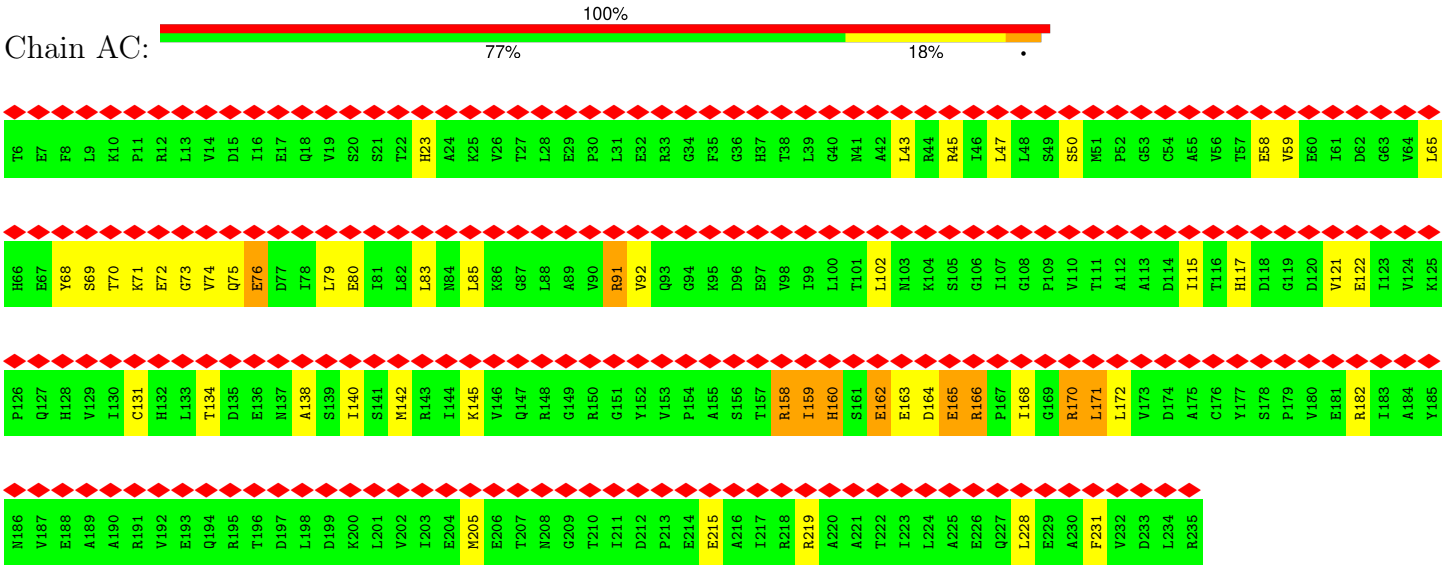
- Molecule 11: Transcription termination/antitermination protein NusG

Chain AB:



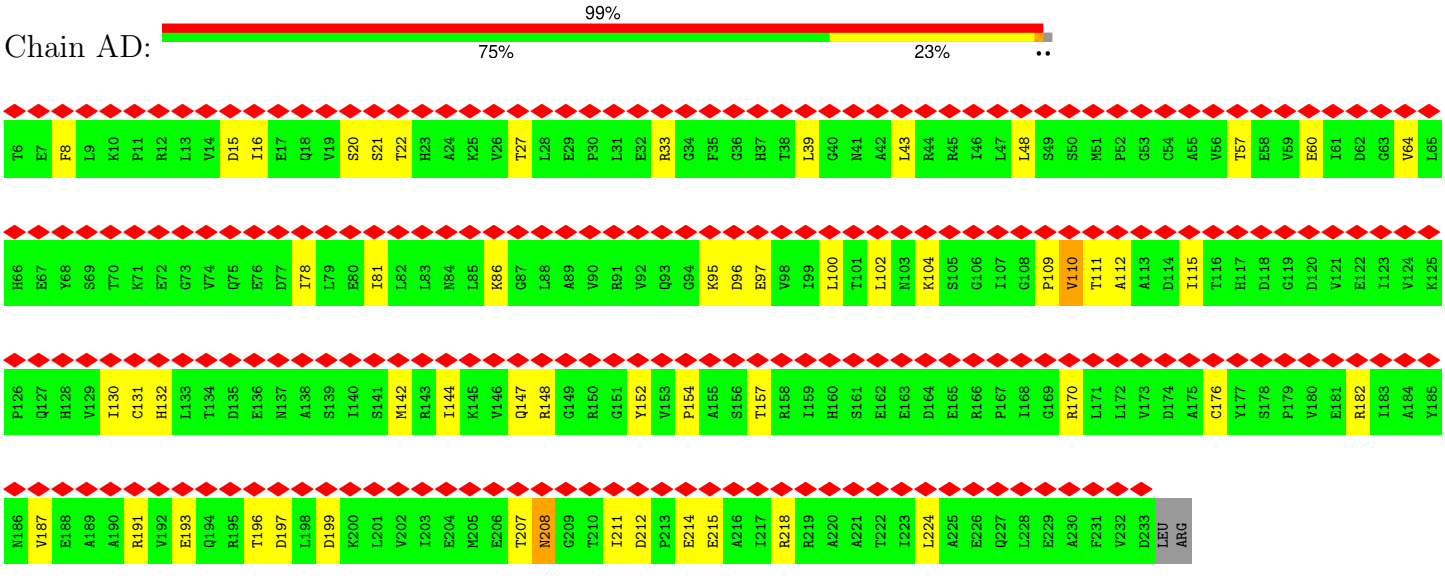
• Molecule 12: DNA-directed RNA polymerase subunit alpha

Chain AC:



• Molecule 12: DNA-directed RNA polymerase subunit alpha

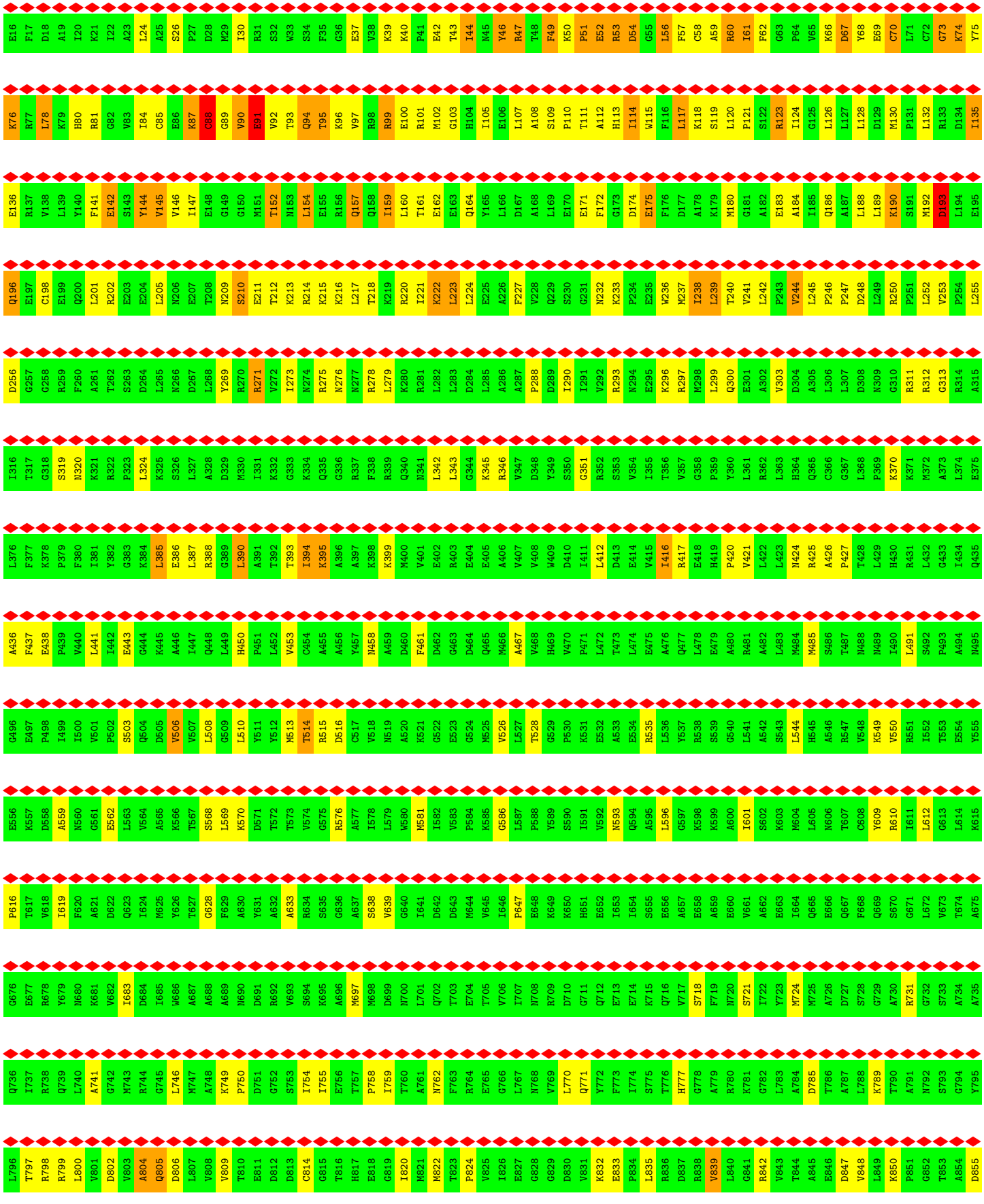
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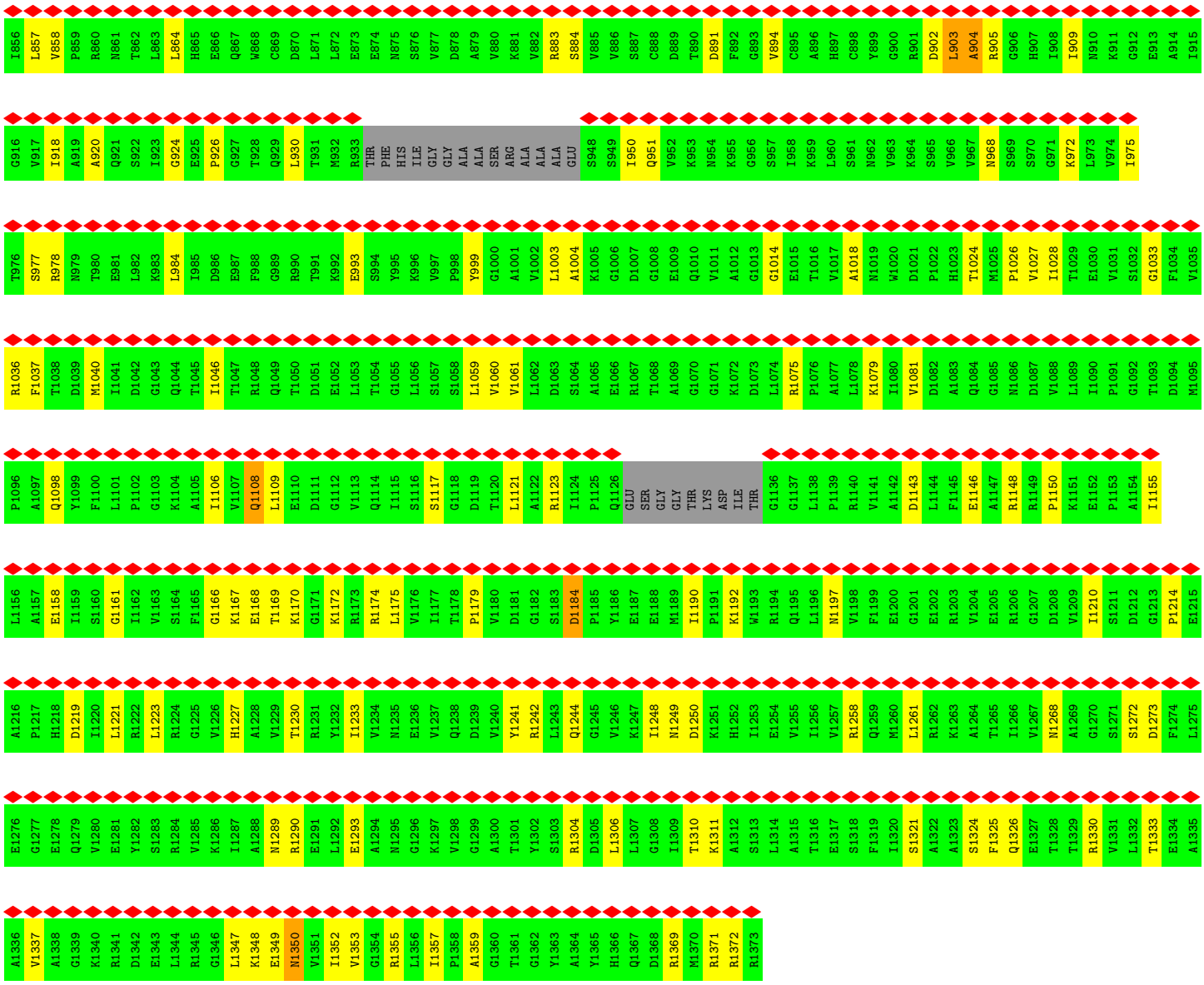


• Molecule 13: DNA-directed RNA polymerase subunit

Chain AE:



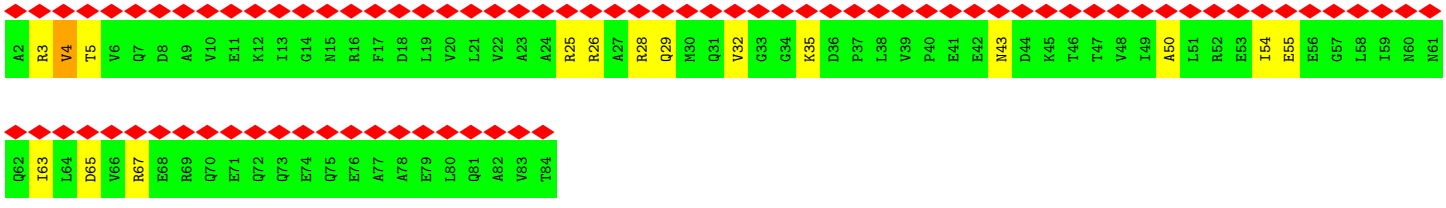

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K76 R77 L78 K79 H80 R81 G82 V83 I84 C85 E86 K87 C88 G89 V90 E91 V92 T93 Q94 T95 K96 V97 R98 R99 E100 R101 M102 G103 H104 I105 E106 L107 A108 S109 P110 T111 A112 H113 I114 W115 F116 L117 K118 S119 L120 P121 S122 R123 I124 G125 L126 L127 L128 D129 M130 P131 L132 R133 D134 I135
E136 R137 V138 L139 Y140 F141 E142 S143 Y144 V145 V146 I147 E148 G149 G150 M151 T152 N153 L154 E155 R156 Q157 Q158 I159 L160 T161 E162 E163 Q164 Y165 L166 D167 A168 L169 E170 E171 F172 G173 D174 E175 F176 D177 A178 K179 M180 G181 A182 E183 A184 I185 Q186 A187 L188 L189 K190 S191 M192 D193 L194 E195
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 V228 Q229 S230 G231 N232 K233 P234 E235 W236 M237 I238 L239 T240 V241 L242 P243 V244 L245 P246 P247 D248 L249 R250 P251 L252 V253 P254 L255
D256 G257 G258 R259 F260 A261 T262 S263 D264 L265 N266 D267 L268 Y269 R270 R271 V272 I273 N274 R275 N276 N277 R278 L279 K280 R281 L282 L283 D284 L285 A286 A287 P288 D289 I290 I291 V292 R293 N294 E295 K296 R297 M298 L299 Q300 E301 A302 V303 D304 A305 L306 L307 D308 N309 G310 R311 R312 G313 R314 A315
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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 E652 I653 I654 S655 E656 A657 E658 A659 E660 V661 A662 E663 I664 Q665 E666 Q667 F668 Q669 S670 G671 L672 V673 T674 A675
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L796 T797 R798 R799 L800 V801 D802 V803 A804 Q805 D806 L807 V808 V809 T810 E811 D812 D813 C814 G815 T816 H817 E818 G819 I820 M821 M822 T823 P824 V825 I826 E827 G828 G829 D830 V831 K832 E833 P834 L835 R836 D837 R838 V839 L840 G841 R842 V843 T844 A845 E846 D847 V848 L849 K850 P851 G852 T853 A854 D855



• Molecule 14: DNA-directed RNA polymerase subunit omega

Chain AF:

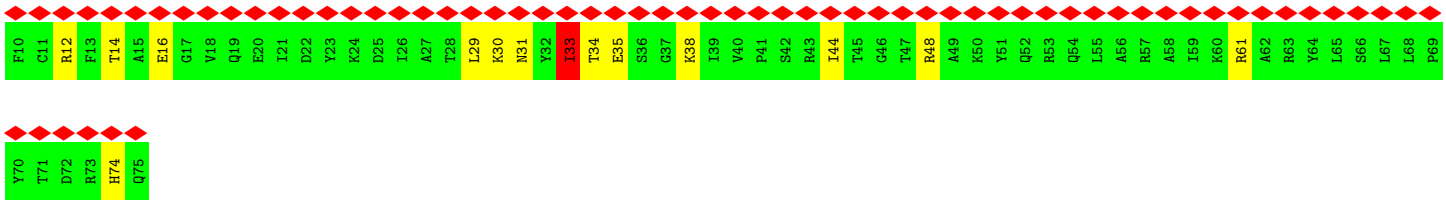




• Molecule 15: 30S ribosomal protein S18

Chain C:

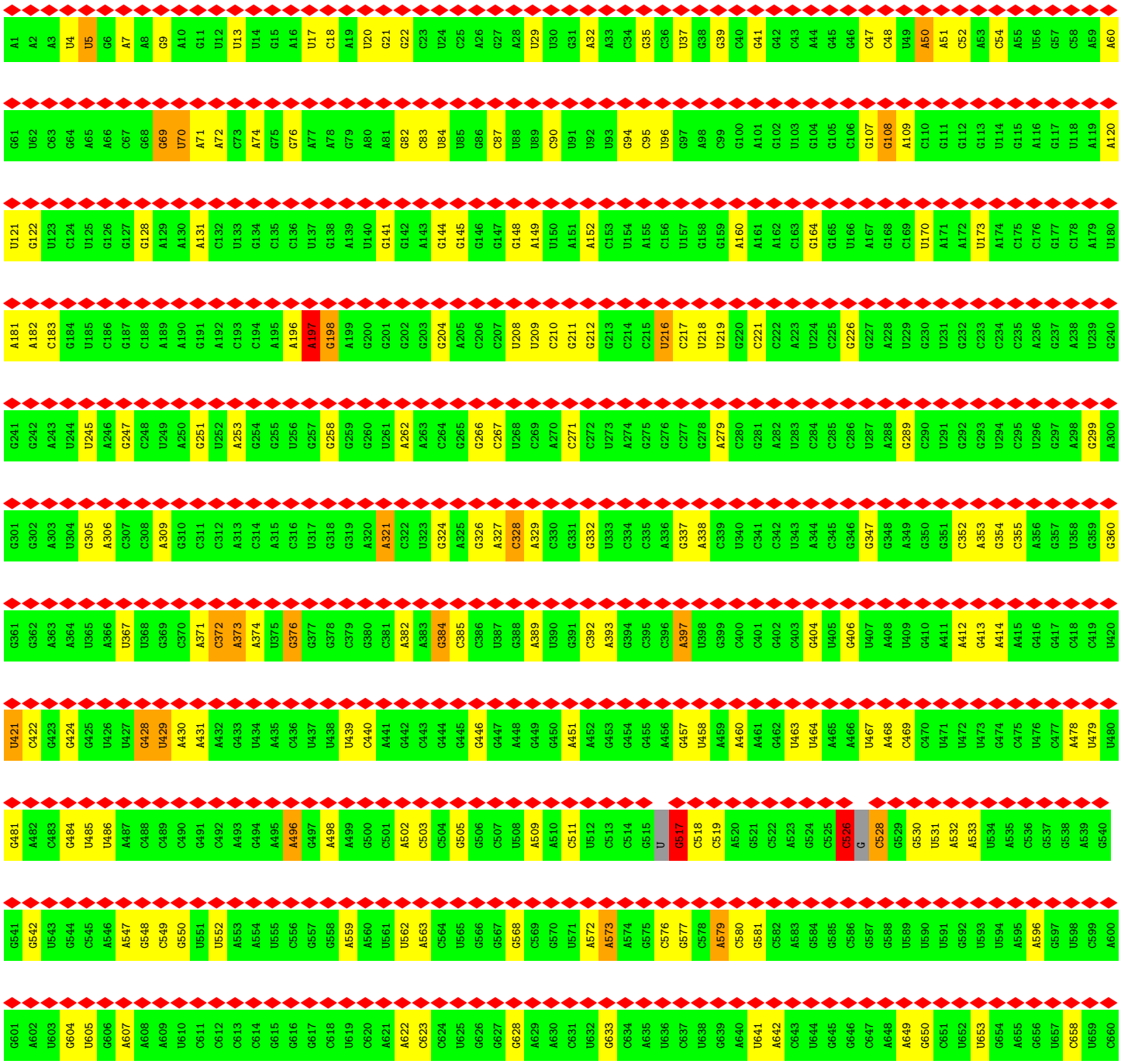


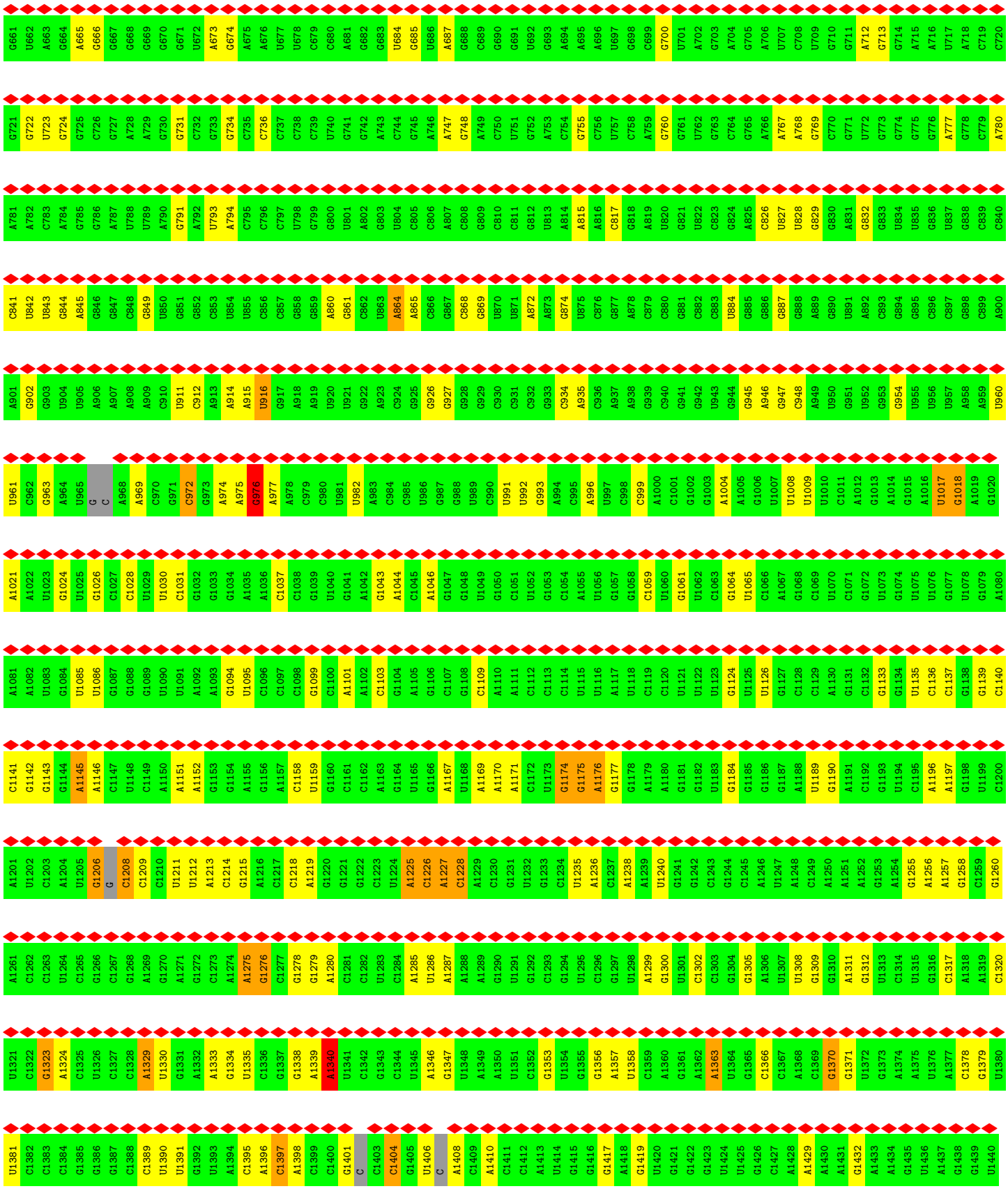


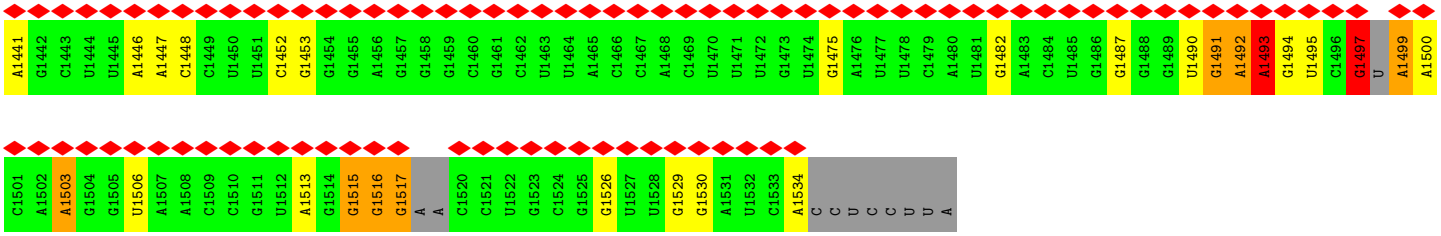
• Molecule 16: 16S rRNA

Chain D:



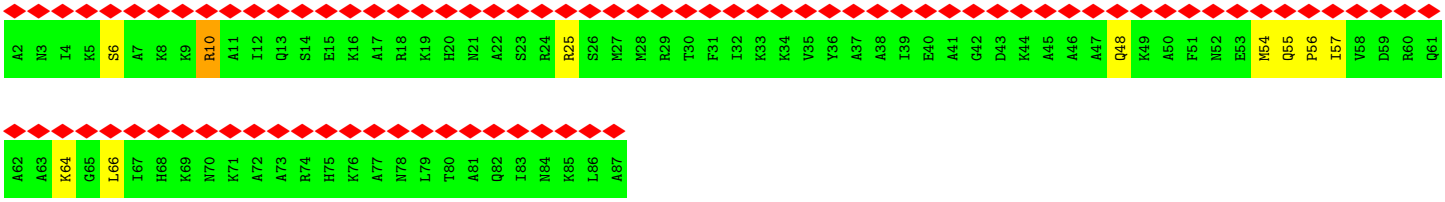



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G721 G722 U723 G724 G725 C726 G727 A728 A729 G730 G731 C732 G733 G734 C735 C736 C737 C738 C739 U740 G741 G742 A743 C744 G745 A746 A747 G748 A749 C750 U751 G752 A753 C754 G755 C756 U757 C758 A759 G760 G761 U762 G763 C764 G765 A766 A767 A768 G769 C770 G771 U772 G773 G774 G775 G776 A777 G778 C779 A780
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U961 C962 G963 A964 U965 G C A968 A969 C970 G971 C972 G973 A974 A975 G976 A977 A978 C979 C980 U981 U982 A983 C984 C985 U986 G987 G988 U989 C990 U991 U992 G993 A994 C995 A996 U997 C998 C999 A1000 C1001 G1002 G1003 A1004 A1005 G1006 U1007 U1008 U1009 U1010 C1011 A1012 G1013 A1014 C1015 A1016 U1017 G1018 A1019 G1020
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C1141 G1142 G1143 G1144 A1145 A1146 C1147 U1148 C1149 A1150 A1151 A1152 G1153 G1154 A1155 G1156 A1157 C1158 U1159 G1160 C1161 C1162 A1163 G1164 U1165 G1166 A1167 U1168 A1169 A1170 A1171 C1172 U1173 G1174 G1175 A1176 G1177 G1178 A1179 A1180 G1181 G1182 U1183 G1184 G1185 G1186 G1187 A1188 U1189 G1190 A1191 C1192 G1193 U1194 C1195 A1196 A1197 G1198 U1199 C1200
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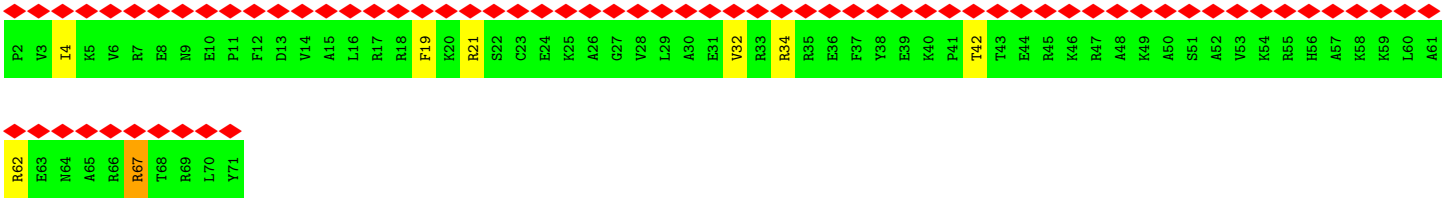
• Molecule 17: 30S ribosomal protein S20





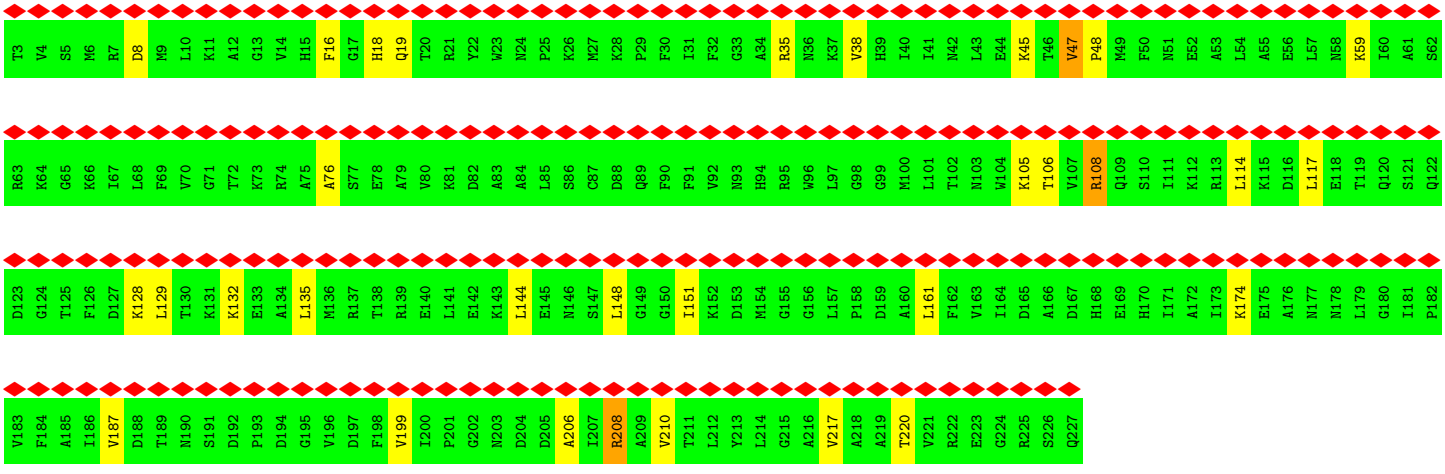
• Molecule 18: 30S ribosomal protein S21





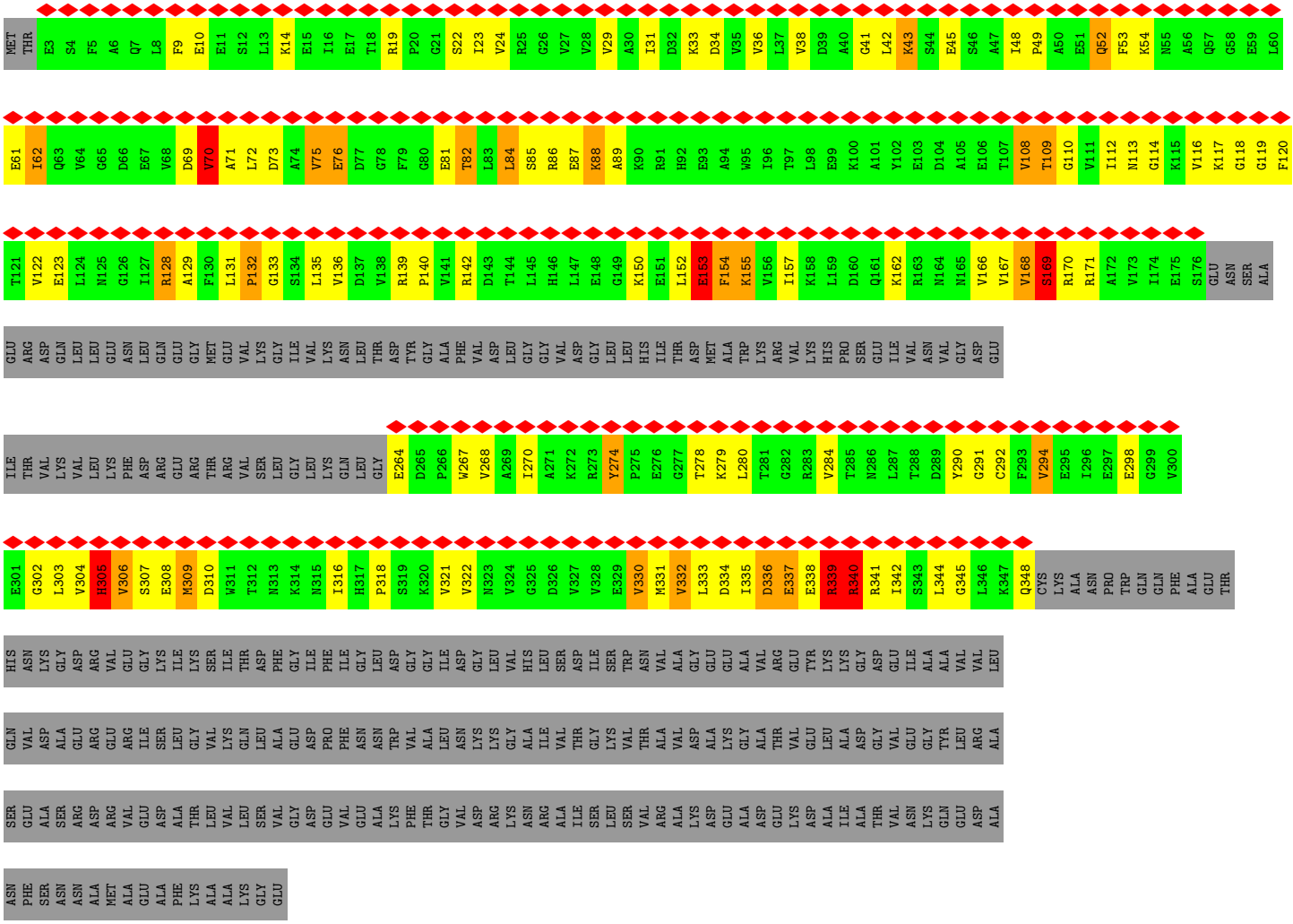
• Molecule 19: 30S ribosomal protein S2





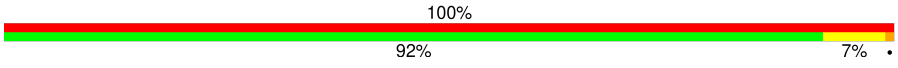
• Molecule 20: 30S ribosomal protein S1

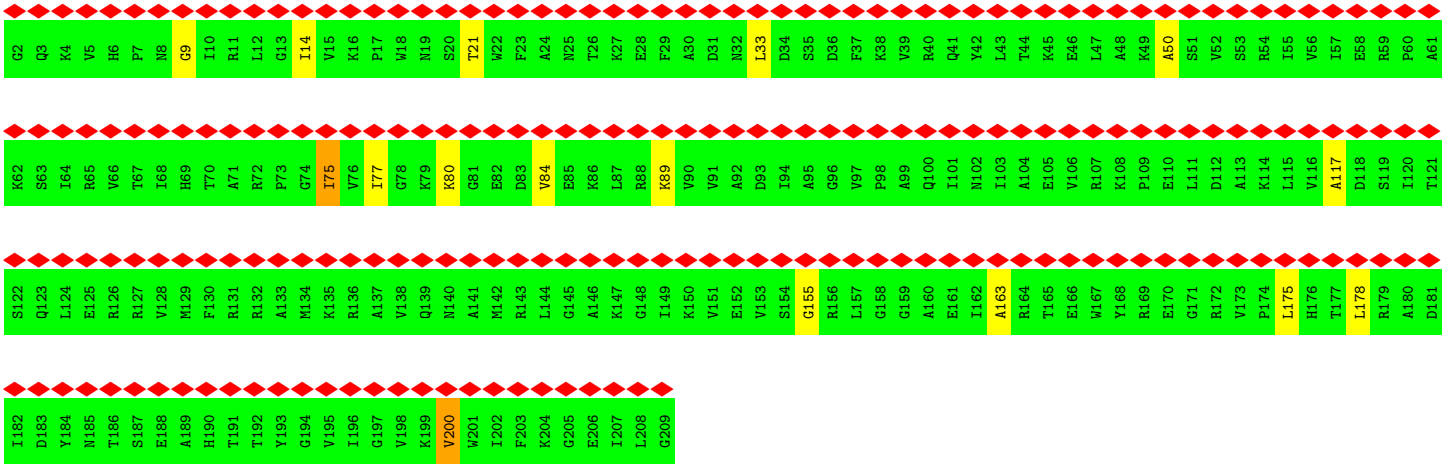




• Molecule 21: 30S ribosomal protein S3

Chain I:

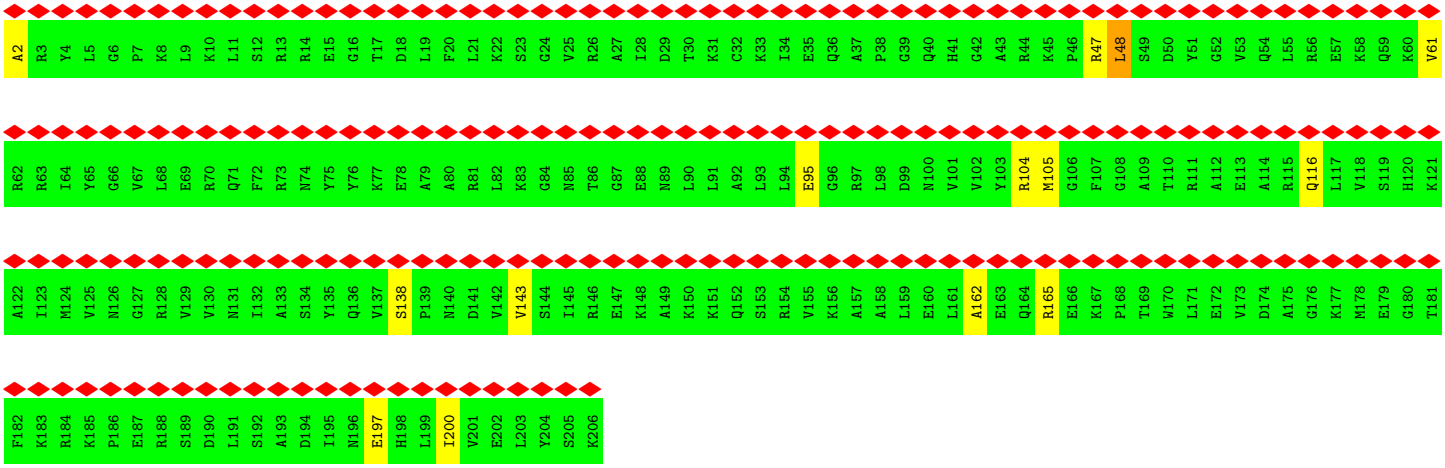




• Molecule 22: 30S ribosomal protein S4

Chain J:

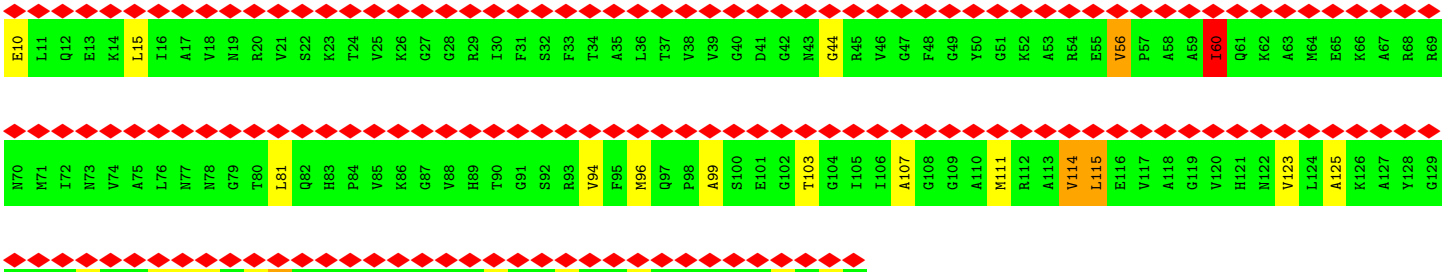




• Molecule 23: 30S ribosomal protein S5

Chain K:





• Molecule 24: 30S ribosomal protein S6

Chain L:

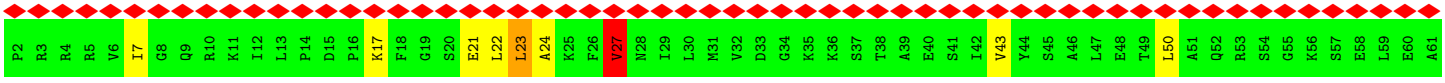




• Molecule 25: 30S ribosomal protein S7

Chain M:





F62 E63 V64 A65 L66 E67 N68 V69 R70 P71 T72 V73 E74 V75 K76 S77 R78 R79 V80 G81 G82 S83 T84 Y85 Q86 V87 P88 V89 E90 V91 R92 P93 V94 R95 R96 N97 A98 L99 A100 M101 R102 W103 I104 V105 E106 A107 A108 R109 K110 R111 G112 D113 K114 S115 M116 A117 L118 R119 L120 A121

N122 E123 L124 S125 D126 A127 A128 E129 N130 K131 G132 T133 A134 V135 K136 K137 R138 E139 D140 V141 H142 R143 M144 A145 E146 A147 N148 K149 A150 F151 A152

• Molecule 26: 30S ribosomal protein S8

Chain N:



S2 M3 Q4 D5 P6 I7 A8 D9 M10 L11 T12 R13 I14 R15 N16 G17 Q18 A19 A20 N21 K22 A23 A24 V25 T26 M27 P28 S29 S30 K31 L32 K33 V34 A35 I36 A37 N38 V39 L40 K41 E42 E43 G44 F45 I46 E47 D48 F49 K50 V51 E52 G53 D54 T55 K56 P57 E58 L59 E60 L61

T62 L63 K64 Y65 F66 Q67 G68 K69 A70 V71 V72 E73 S74 I75 Q76 R77 V78 S79 R80 P81 G82 L83 R84 I85 Y86 K87 R88 K89 D90 E91 L92 P93 K94 V95 M96 A97 G98 L99 G100 I101 A102 V103 V104 S105 T106 S107 K108 G109 V110 M111 T112 D113 R114 A115 A116 R117 Q118 A119 G120 L121

G122 G123 E124 I125 I126 C127 Y128 V129 A130

• Molecule 27: 30S ribosomal protein S9

Chain O:



N4 Q5 Y6 Y7 G8 T9 G10 R11 R12 K13 S14 S15 A16 A17 R18 V19 F20 I21 K22 P23 G24 N25 G26 K27 I28 V29 I30 N31 Q32 R33 S34 L35 E36 Q37 Y38 F39 G40 R41 E42 T43 A44 R45 M46 V47 V48 R49 Q50 P51 L52 E53 L54 V55 D56 M57 V58 E59 K60 L61 D62 L63

Y64 I65 T66 V67 K68 G69 G70 G71 I72 S73 G74 Q75 A76 G77 A78 I79 R80 H81 G82 I83 T84 R85 A86 L87 M88 E89 Y90 D91 E92 S93 L94 R95 S96 E97 L98 R99 K100 A101 G102 F103 V104 T105 R106 D107 A108 R109 Q110 V111 E112 R113 K114 K115 V116 G117 L118 R119 K120 A121 R122 R123

R124 P125 Q126 F127 S128 K129 R130

• Molecule 28: 30S ribosomal protein S10

Chain P:

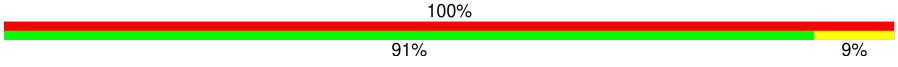


R5 I6 R7 I8 R9 L10 K11 A12 F13 D14 H15 R16 L17 I18 D19 Q20 A21 T22 A23 E24 I25 V26 E27 T28 A29 K30 R31 T32 G33 A34 Q35 V36 R37 G38 P39 I40 P41 L42 P43 T44 R45 K46 E47 R48 F49 T50 V51 L52 I53 S54 P55 H56 V57 N58 K59 D60 A61 R62 D63 Q64

Y65 E66 I67 R68 T69 H70 L71 R72 L73 V74 D75 I76 V77 E78 P79 T80 E81 K82 T83 V84 D85 A86 L87 M88 R89 L90 D91 L92 A93 A94 G95 V96 D97 V98 Q99 I100 S101 L102 G103

• Molecule 29: 30S ribosomal protein S11

Chain Q:

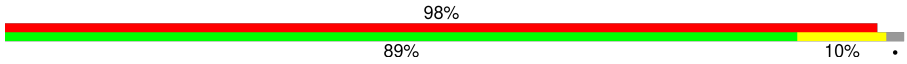


R13 K14 Q15 V16 S17 D18 G19 V20 A21 H22 I23 H24 A25 S26 F27 N28 N29 T30 I31 V32 T33 I34 T35 D36 R37 Q38 G39 N40 A41 L42 G43 W44 A45 T46 A47 G48 G49 S50 G51 F52 R53 G54 S55 R56 K57 S58 T59 P60 F61 A62 A63 Q64 V65 A66 A67 E68 R69 C70 A71 D72

A73 V74 K75 E76 Y77 G78 I79 K80 M81 L82 E83 V84 M85 V86 K87 G88 P89 G90 P91 G92 R93 E94 S95 T96 I97 R98 A99 L100 N101 A102 A103 G104 F105 R106 I107 T108 N109 I110 T111 D112 V113 T114 P115 I116 P117 H118 N119 G120 C121 R122 P123 P124 K125 K126 R127 R128 V129

- Molecule 30: 30S ribosomal protein S12

Chain R:



A2 T3 V4 N5 Q6 L7 V8 R9 K10 P11 R12 A13 R14 K15 V16 A17 K18 S19 N20 V21 P22 A23 L24 E25 A26 C27 P28 Q29 K30 R31 G32 V33 C34 T35 R36 V37 Y38 T39 T40 T41 P42 K43 K44 P45 N46 S47 A48 L49 R50 K51 V52 C53 R54 V55 R56 L57 T58 N59 G60 F61

E62 V63 T64 S65 Y66 I67 G68 G69 E70 G71 H72 N73 L74 Q75 E76 H77 S78 V79 I80 L81 I82 R83 G84 G85 R86 V87 K88 ASP LEU P91 G92 V93 R94 Y95 H96 T97 V98 R99 G100 A101 L102 D103 C104 S105 G106 V107 K108 D109 R110 K111 Q112 A113 R114 S115 K116 Y117 G118 V119 K120 R121

P122 K123 A124

- Molecule 31: 30S ribosomal protein S14

Chain S:



A2 K3 Q4 S5 M6 K7 A8 R9 E10 V11 K12 R13 V14 A15 L16 A17 D18 K19 Y20 F21 A22 K23 R24 A25 E26 L27 K28 A29 I30 I31 S32 D33 V34 N35 A36 S37 D38 E39 D40 R41 W42 N43 A44 V45 L46 K47 L48 Q49 T50 L51 P52 R53 D54 S55 S56 P57 S58 R59 Q60 R61

N62 R63 G64 R65 Q66 T67 G68 R69 P70 H71 G72 F73 L74 R75 K76 F77 G78 L79 S80 R81 I82 K83 V84 R85 E86 A87 A88 M89 R90 G91 E92 I93 P94 G95 L96 K97 K98 A99 S100 W101

- Molecule 32: 30S ribosomal protein S15

Chain T:



S2 L3 S4 T5 E6 A7 T8 A9 K10 I11 V12 S13 E14 F15 G16 R17 D18 A19 N20 D21 T22 G23 S24 T25 E26 V27 Q28 V29 A30 L31 L32 T33 A34 Q35 I36 N37 H38 L39 Q40 G41 H42 F43 A44 E45 H46 K47 K48 D49 H50 H51 S52 R53 R54 G55 L56 L57 R58 M59 V60 S61

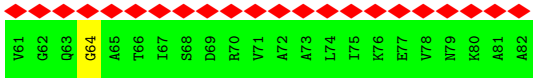
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- Molecule 33: 30S ribosomal protein S16

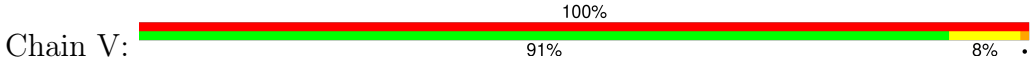
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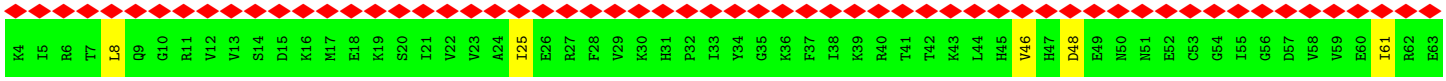


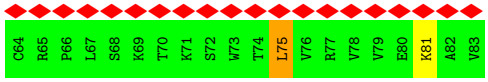
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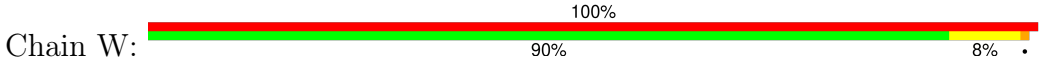
• Molecule 34: 30S ribosomal protein S17

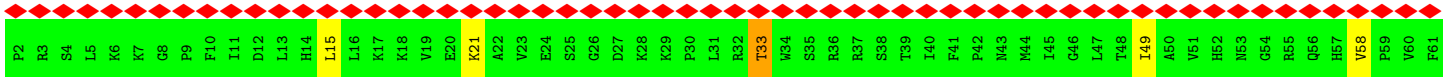


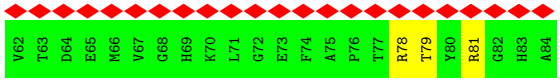




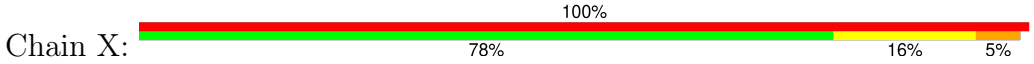
• Molecule 35: 30S ribosomal protein S19

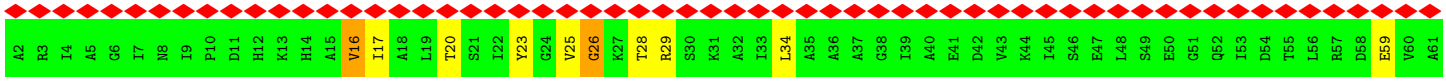


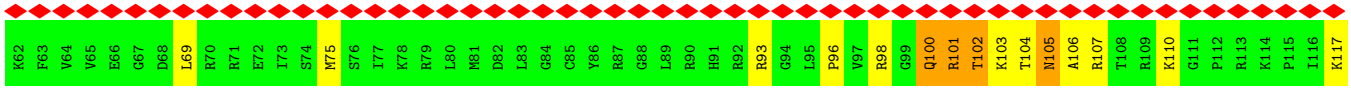




• Molecule 36: 30S ribosomal protein S13







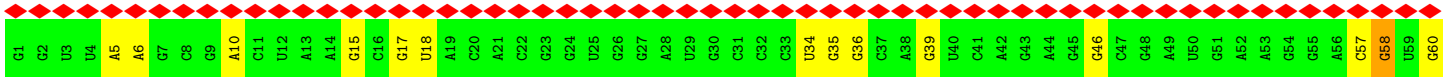
• Molecule 37: mRNA in the ribosomal RNA entrance pore

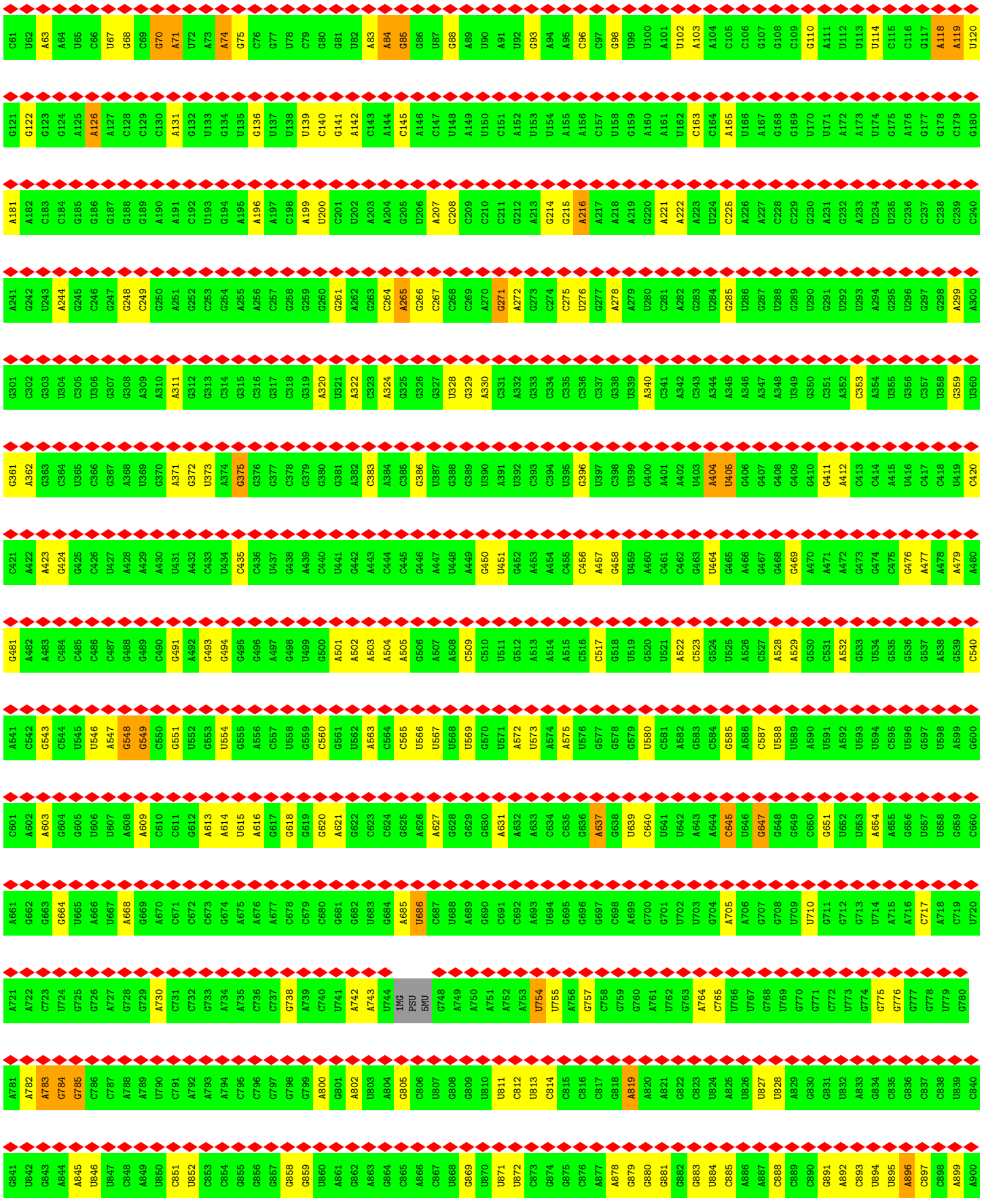




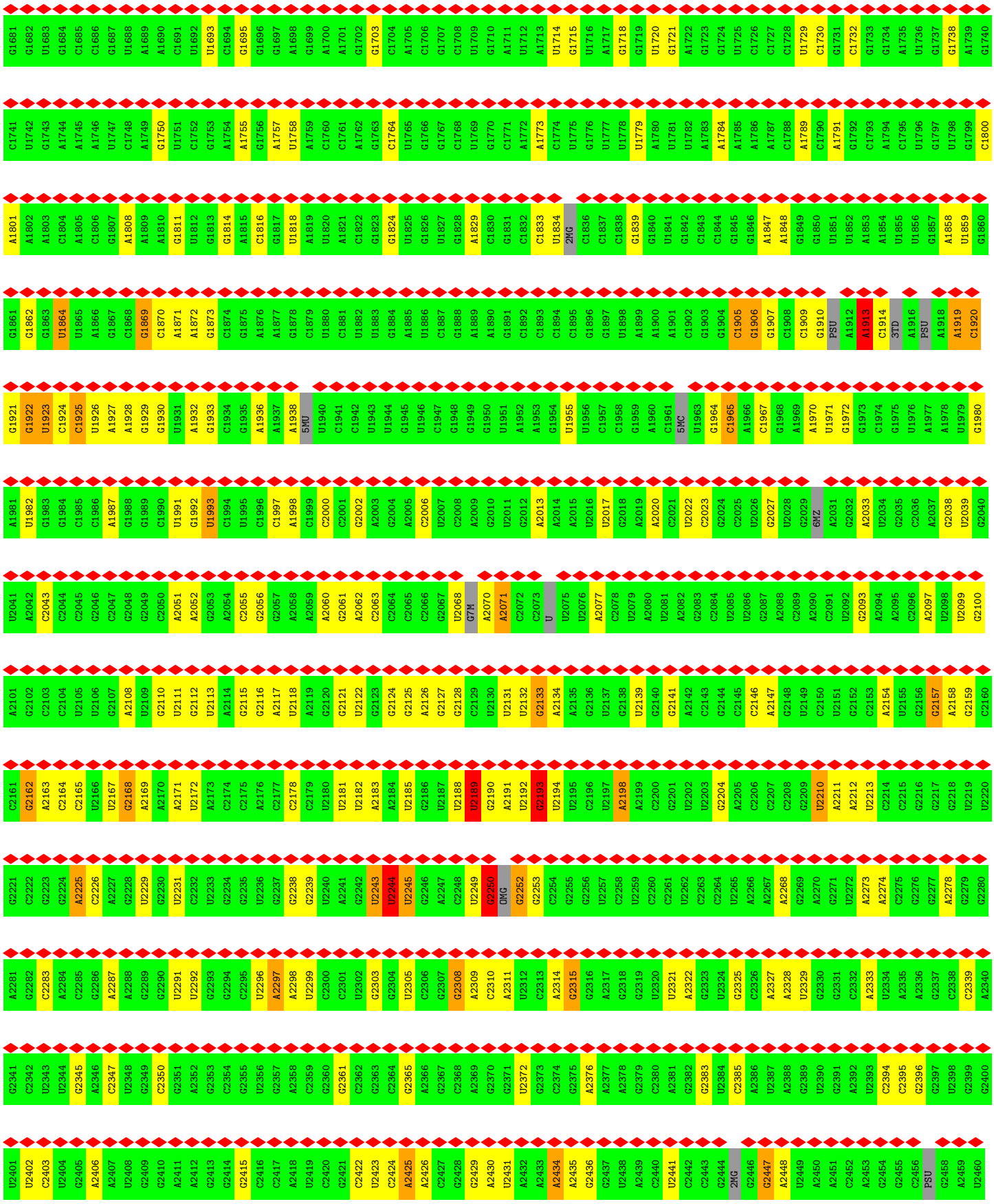
• Molecule 38: 23S rRNA

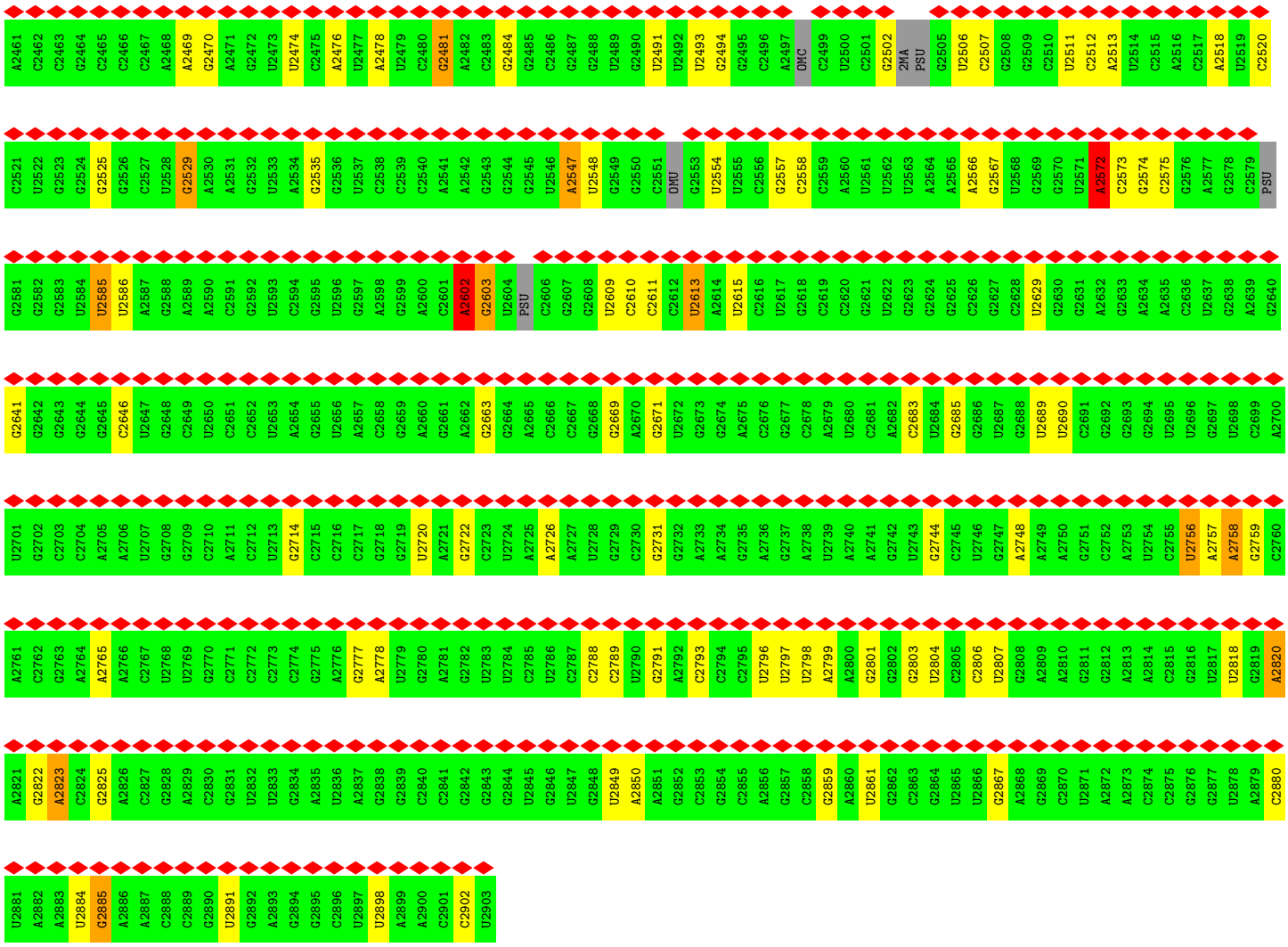





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A241 G242 U243 A244 G245 C246 G247 G248 C249 G250 A251 C252 C253 G254 A255 A256 C257 G258 C259 G260 C261 A262 G263 C264 A265 C266 C267 C268 C269 A270 G271 A272 G273 C274 C275 U276 G277 A278 A279 U280 C281 A282 C283 U284 G285 U286 G287 U288 G289 U290 G291 U292 U293 A294 G295 U296 G297 G298 A299 A300
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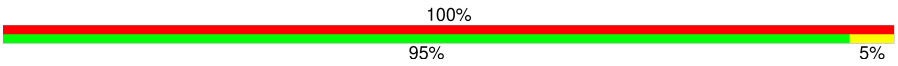
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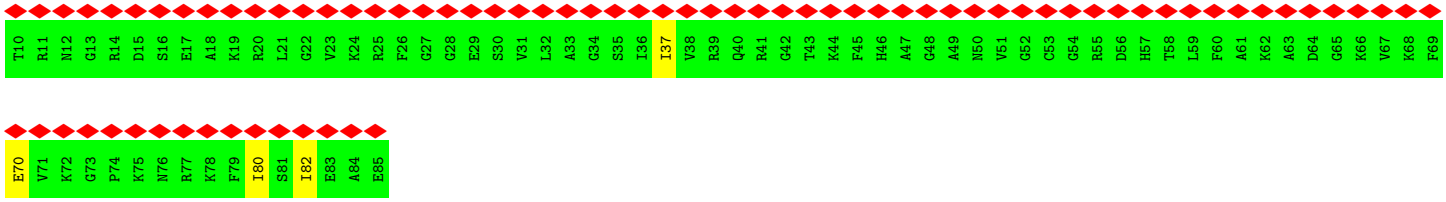

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A1801 A1802 A1803 C1804 A1805 C1806 G1807 A1808 A1809 A1810 G1811 U1812 G1813 G1814 A1815 C1816 G1817 U1818 A1819 U1820 A1821 C1822 G1823 G1824 U1825 G1826 U1827 G1828 A1829 C1830 G1831 C1832 C1833 U1834 2MG C1836 C1837 C1838 G1839 G1840 U1841 G1842 C1843 C1844 G1845 G1846 A1847 A1848 G1849 G1850 U1851 U1852 A1853 A1854 U1855 U1856 G1857 A1858 U1859 G1860
G1861 G1862 G1863 U1864 U1865 A1866 G1867 C1868 G1869 C1870 A1871 A1872 G1873 C1874 G1875 A1876 A1877 G1878 C1879 A1880 C1881 U1882 U1883 G1884 A1885 U1886 C1887 G1888 A1889 A1890 G1891 C1892 C1893 C1894 C1895 G1896 G1897 U1898 A1899 A1900 A1901 C1902 G1903 G1904 C1905 G1906 G1907 C1908 C1909 G1910 PSU A1912 A1913 C1914 3TD A1916 PSU A1918 A1919 C1920
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 C1958 G1959 A1960 C1961 5MC U1963 G1964 C1965 A1966 C1967 G1968 A1969 A1970 U1971 G1972 G1973 C1974 G1975 U1976 A1977 A1978 U1979 G1980
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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 G7M 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
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C2161 G2162 A2163 C2164 C2165 U2166 U2167 G2168 A2169 A2170 A2171 U2172 A2173 C2174 C2175 A2176 C2177 C2178 C2179 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 A2212 U2213 C2214 C2215 G2216 G2217 G2218 U2219 U2220
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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 C2313 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
G2341 C2342 U2343 U2344 G2345 A2346 C2347 U2348 G2349 C2350 G2351 A2352 G2353 C2354 G2355 U2356 G2357 A2358 C2359 G2360 G2361 C2362 G2363 C2364 G2365 A2366 G2367 C2368 A2369 G2370 G2371 U2372 G2373 C2374 G2375 A2376 A2377 A2378 G2379 C2380 A2381 G2382 G2383 U2384 C2385 A2386 U2387 A2388 G2389 U2390 G2391 A2392 U2393 C2394 C2395 G2396 G2397 U2398 G2399 G2400
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• Molecule 39: 50S ribosomal protein L27

Chain b:

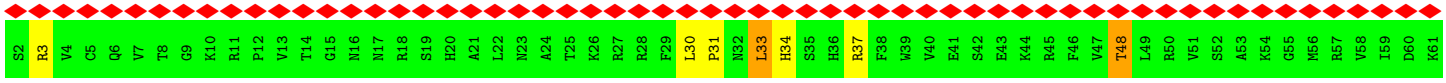




• Molecule 40: 50S ribosomal protein L28

Chain c:





K62 G63 I64 D65 T66 V67 L68 A69 E70 L71 R72 A73 R74 G75 E76 K77 Y78

• Molecule 41: 5S rRNA

Chain d:



U1 G2 C3 C4 U5 G6 G7 C8 G9 G10 C11 C12 G13 U14 A15 G16 C17 G18 C19 G20 G21 U22 G23 G24 U25 C26 C27 C28 A29 C30 C31 U32 G33 A34 C35 C36 C37 C38 A39 U40 G41 C42 C43 G44 A45 A46 C47 U48 C49 A50 G51 A52 A53 G54 U55 G56 A57 A58 A59 C60

G61 C62 C63 G64 U65 A66 G67 C68 G69 C70 C71 G72 A73 U74 G75 G76 U77 A78 G79 U80 G81 U82 G83 G84 G85 G86 U87 C88 U89 C90 C91 C92 C93 A94 U95 G96 C97 G98 A99 G100 A101 G102 U103 A104 G105 G106 G107 A108 A109 C110 U111 G112 C113 C114 A115 G116 G117 C118 A119 U120

• Molecule 42: 50S ribosomal protein L29

Chain e:



K2 A3 K4 E5 L6 R7 E8 K9 S10 V11 E12 E13 L14 N15 T16 E17 L18 L19 N20 L21 L22 R23 E24 Q25 F26 N27 L28 R29 M30 Q31 A32 A33 S34 G35 Q36 L37 Q38 Q39 S40 H41 L42 L43 K44 Q45 V46 R47 R48 D49 V50 A51 R52 V53 K54 T55 L56 L57 N58 E59 K60 A61

G62 A63

• Molecule 43: 50S ribosomal protein L30

Chain f:



A2 K3 T4 I5 K6 I7 T8 Q9 T10 R11 S12 A13 I14 G15 R16 L17 P18 K19 H20 K21 A22 T23 L24 L25 G26 L27 G28 L29 R30 R31 I32 G33 H34 T35 V36 E37 R38 E39 D40 T41 P42 A43 I44 R45 G46 M47 I48 N49 A50 V51 S52 F53 M54 V55 K56 V57 E58 E59

• Molecule 44: 50S ribosomal protein L31

Chain g:



M1 K2 K3 D4 I5 H6 P7 K8 Y9 E10 E11 I12 T13 A14 S15 C16 S17 C18 G19 N20 V21 M22 K23 I24 R25 S26 T27 V28 G29 H30 D31 L32 N33 L34 D35 V36 C37 S38 K39 C40 H41 P42 F43 F44 T45 G46 K47 Q48 R49 D50 V51 A52 T53 G54 G55 R56 V57 D58 R59 F60

N61 K62 R63 F64 N65 I66

• Molecule 45: 50S ribosomal protein L2

Chain h:



A2 V3 V4 K5 C6 K7 P8 T9 S10 P11 G12 R13 R14 H15 V16 V17 K18 V19 V20 N21 P22 E23 L24 H25 K26 G27 K28 P29 F30 A31 P32 L33 L34 E35 K36 N37 S38 K39 S40 G41 G42 R43 M44 N45 N46 G47 R48 I49 T50 T51 R52 H53 I54 G55 G56 G57 H58 K59 Q60 A61

Y62 R63 I64 V65 D66 F67 K68 R69 N70 K71 D72 G73 I74 P75 A76 V77 V78 E79 R80 L81 E82 Y83 D84 P85 N86 R87 S88 A89 N90 I91 A92 L93 V94 L95 Y96 K97 D98 G99 E100 R101 R102 Y103 I104 L105 A106 P107 K108 G109 L110 K111 A112 G113 D114 Q115 I116 Q117 S118 G119 V120 D121

A122 A123 I124 K125 P126 G127 N128 T129 L130 P131 M132 R133 N134 I135 P136 V137 G138 S139 T140 V141 H142 N143 V144 E145 M146 K147 P148 G149 K150 G151 G152 Q153 L154 A155 R156 S157 A158 G159 T160 Y161 V162 Q163 I164 V165 A166 R167 D168 G169 A170 Y171 V172 T173 L174 R175 L176 R177 S178 G179 E180 M181

R182 K183 V184 E185 A186 D187 C188 R189 A190 T191 L192 G193 E194 V195 G196 N197 A198 E199 H200 M201 L202 R203 V204 L205 G206 K207 A208 G209 A210 A211 R212 W213 R214 G215 V216 R217 P218 T219 V220 R221 G222 T223 A224 M225 N226 P227 V228 D229 H230 P231 H232 G233 G234 G235 E236 G237 R238 N239 F240 G241

K242 H243 P244 V245 T246 P247 W248 G249 V250 Q251 T252 K253 G254 K255 K256 T257 R258 S259 N260 K261 R262 T263 D264 K265 F266 I267 V268 R269 R270 R271 S272

- Molecule 46: 50S ribosomal protein L32

Chain i:



A2 V3 Q4 Q5 N6 K7 P8 T9 R10 S11 K12 R13 G14 M15 R16 R17 S18 H19 D20 A21 L22 T23 A24 V25 T26 S27 L28 S29 V30 D31 K32 T33 S34 G35 E36 K37 H38 L39 R40 H41 H42 I43 T44 A45 D46 G47 Y48 Y49 R50 G51 R52 K53 V54 I55 A56 K57

- Molecule 47: 50S ribosomal protein L3

Chain j:



M1 I2 G3 I4 V5 G6 K7 K8 V9 G10 M11 T12 R13 I14 F15 T16 E17 D18 G19 V20 S21 I22 P23 V24 T25 V26 I27 E28 V29 E30 A31 N32 R33 V34 T35 Q36 V37 K38 D39 L40 A41 N42 D43 G44 Y45 R46 A47 I48 Q49 V50 T51 T52 G53 A54 K55 K56 A57 N58 R59 V60

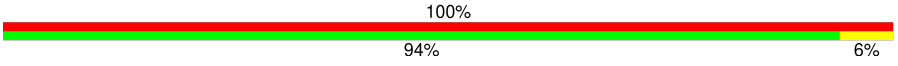
T61 K62 P63 E64 A65 G66 H67 F68 A69 K70 A71 G72 V73 E74 A75 G76 R77 G78 L79 W80 E81 F82 R83 L84 A85 E86 G87 E88 E89 F90 T91 V92 G93 Q94 S95 I96 S97 V98 E99 L100 F101 A102 D103 V104 K105 K106 V107 D108 V109 T110 G111 T112 S113 K114 G115 K116 G117 F118 A119 G120

T121 V122 K123 R124 W125 N126 F127 R128 T129 Q130 D131 A132 T133 H134 G135 N136 S137 L138 S139 H140 R141 V142 P143 G144 S145 I146 G147 Q148 N149 Q150 T151 P152 G153 K154 V155 F156 K157 G158 K159 K160 M161 A162 G163 Q164 M165 G166 N167 E168 R169 V170 T171 V172 Q173 S174 L175 D176 V177 V178 R179 V180

D181 A182 E183 R184 N185 L186 L187 L188 V189 K190 G191 A192 V193 P194 G195 A196 T197 G198 S199 D200 L201 I202 V203 K204 P205 A206 V207 K208 A209

- Molecule 48: 50S ribosomal protein L33

Chain k:



G4 I5 R6 E7 K8 I9 K10 L11 V12 S13 S14 A15 G16 T17 G18 H19 F20 Y21 T22 T23 T24 K25 N26 K27 R28 T29 K30 P31 E32 K33 L34 E35 L36 K37 K38 F39 D40 P41 V42 V43 R44 Q45 H46 V47 I48 Y49 K50 E51 A52 K53 I54 K55

- Molecule 49: 50S ribosomal protein L4

Chain l:

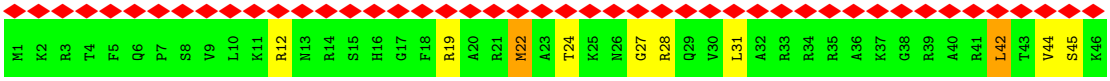




• Molecule 50: 50S ribosomal protein L34

Chain m:

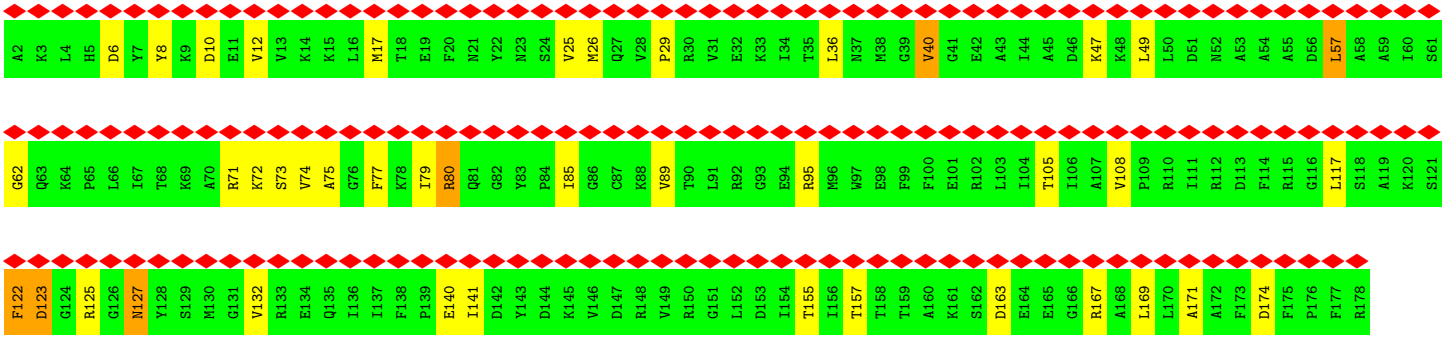




• Molecule 51: 50S ribosomal protein L5

Chain n:

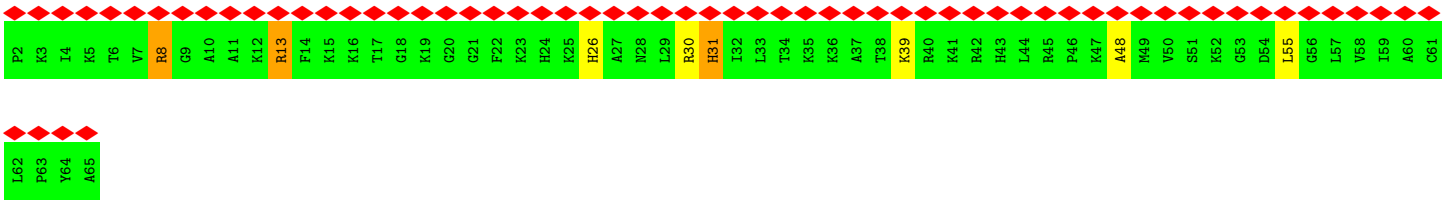




• Molecule 52: 50S ribosomal protein L35

Chain o:

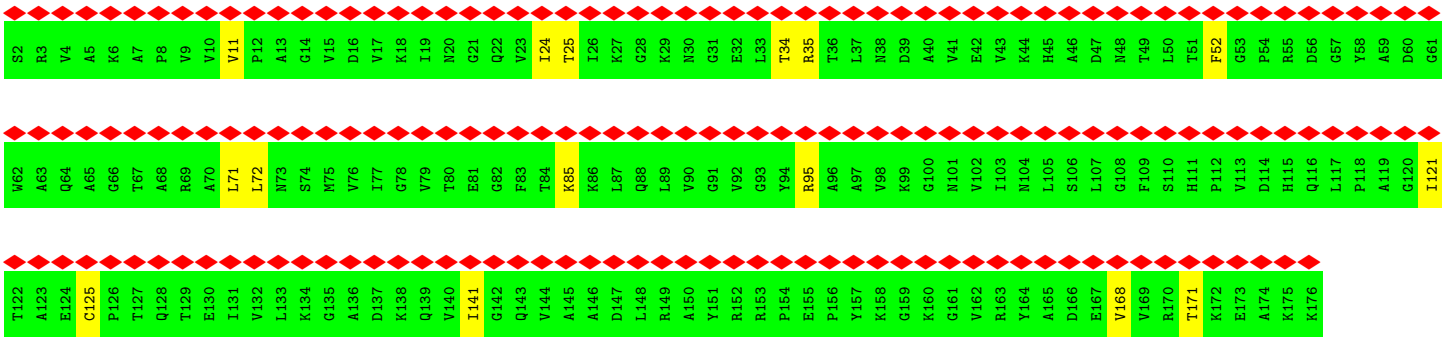




• Molecule 53: 50S ribosomal protein L6

Chain p:

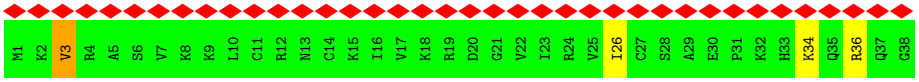




• Molecule 54: 50S ribosomal protein L36

Chain q:

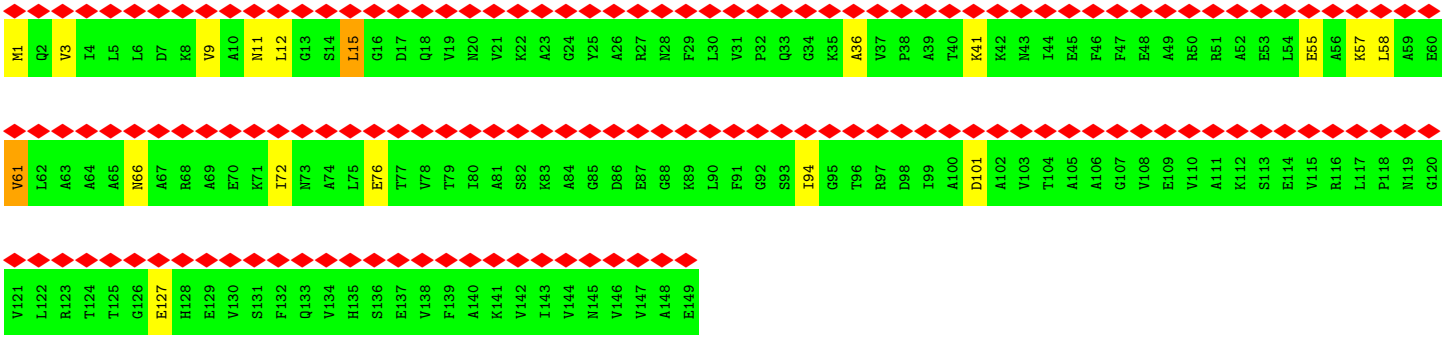




• Molecule 55: 50S ribosomal protein L9

Chain r:

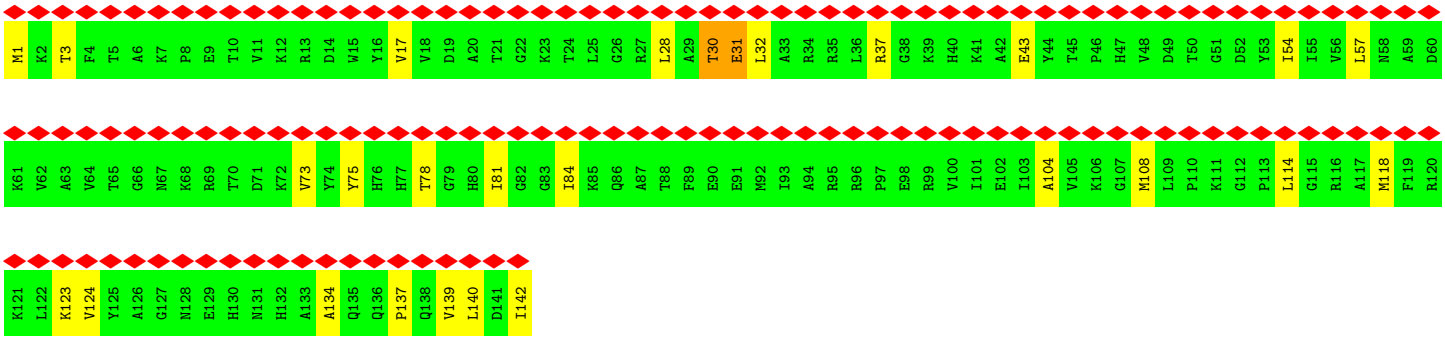




• Molecule 56: 50S ribosomal protein L13

Chain s:

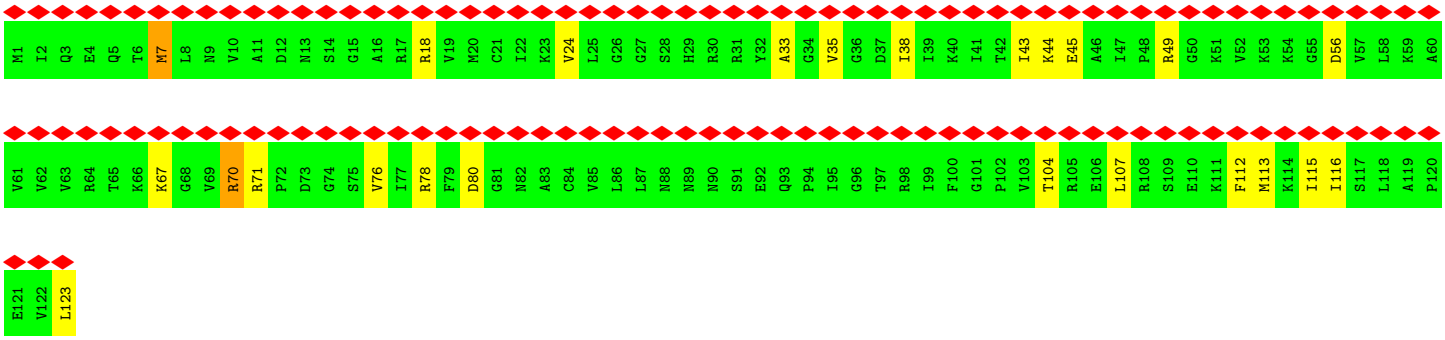




• Molecule 57: 50S ribosomal protein L14

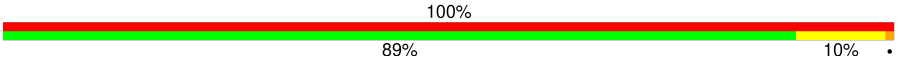
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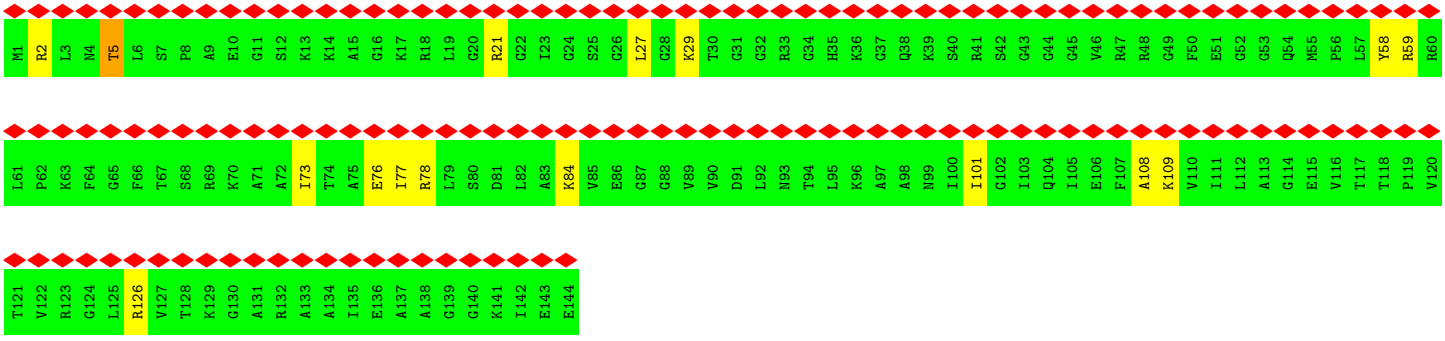




• Molecule 58: 50S ribosomal protein L15

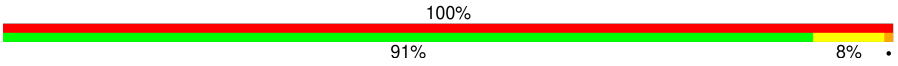
Chain u:

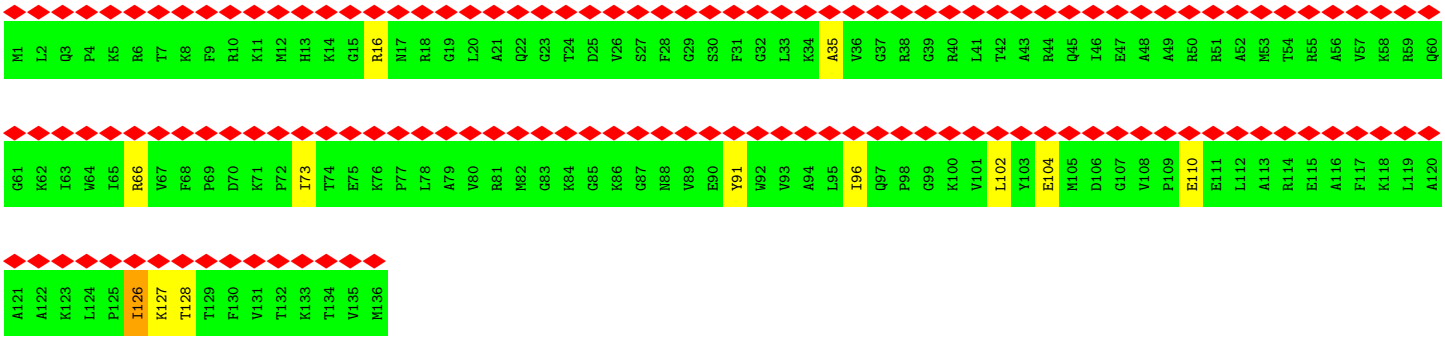




• Molecule 59: 50S ribosomal protein L16

Chain v:

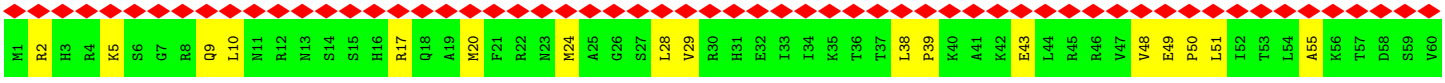




• Molecule 60: 50S ribosomal protein L17

Chain w:





A61 N62 R63 R64 L65 A66 F67 A68 R69 T70 R71 D72 N73 E74 I75 V76 A77 K78 L79 F80 N81 E82 L83 G84 P85 R86 F87 A88 S89 R90 A91 G92 G93 Y94 T95 R96 I97 L98 K99 C100 G101 F102 R103 A104 G105 D106 N107 A108 P109 M110 A111 Y112 I113 E114 L115 V116 D117 R118 S119

- Molecule 61: 50S ribosomal protein L18

Chain x:



D2 K3 K4 S5 A6 R7 I8 R9 R10 A11 T12 R13 A14 R15 R16 K17 L18 Q19 E20 L21 G22 A23 T24 R25 L26 V27 V28 H29 R30 T31 P32 R33 H34 I35 Y36 A37 Q38 V39 I40 A41 P42 N43 G44 S45 E46 V47 L48 V49 A50 A51 S52 T53 V54 E55 K56 A57 I58 A59 E60 Q61

L62 K63 Y64 T65 G66 N67 K68 D69 A70 A71 A72 A73 V74 G75 K76 A77 V78 A79 E80 R81 A82 L83 E84 K85 G86 I87 K88 D89 V90 S91 F92 D93 R94 S95 G96 F97 Q98 Y99 H100 G101 R102 V103 Q104 A105 L106 A107 D108 A109 A110 R111 E112 A113 G114 L115 Q116 F117

- Molecule 62: 50S ribosomal protein L19

Chain y:



S2 N3 I4 I5 K6 Q7 L8 E9 Q10 E11 Q12 M13 K14 Q15 D16 V17 P18 S19 F20 R21 P22 G23 D24 T25 V26 E27 V28 K29 V30 W31 V32 V33 E34 G35 S36 K37 K38 R39 L40 Q41 A42 F43 E44 G45 V46 V47 I48 A49 I50 R51 N52 R53 G54 L55 H56 S57 A58 F59 T60 V61

R62 K63 I64 S65 N66 G67 E68 G69 V70 E71 R72 V73 F74 Q75 T76 H77 S78 P79 V80 V81 D82 S83 I84 S85 V86 K87 R88 R89 G90 A91 V92 R93 K94 A95 K96 L97 Y98 Y99 L100 R101 E102 R103 T104 G105 K106 A107 A108 R109 I110 K111 E112 R113 L114 N115

- Molecule 63: 50S ribosomal protein L20

Chain z:



A2 R3 V4 K5 R6 G7 V8 I9 A10 R11 A12 R13 H14 K15 K16 I17 L18 K19 Q20 A21 K22 G23 Y24 Y25 G26 A27 R28 S29 R30 V31 Y32 R33 V34 A35 F36 Q37 A38 V39 I40 K41 A42 G43 Q44 Y45 A46 Y47 R48 D49 R50 R51 Q52 R53 K54 R55 Q56 F57 R58 Q59 L60 W61

I62 A63 R64 I65 N66 A67 A68 A69 R70 Q71 N72 G73 I74 S75 Y76 S77 K78 F79 I80 N81 G82 L83 K84 K85 A86 S87 V88 E89 I90 D91 R92 K93 I94 L95 A96 D97 I98 A99 V100 F101 D102 K103 V104 A105 F106 T107 A108 L109 V110 E111 K112 A113 K114 A115 A116 L117 A118

4 Experimental information (i)

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 ($e^-/Å^2$)	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 (i)

5.1 Standard geometry (i)

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

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(^{o})	Ideal(^{o})
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 (i)

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	816	839	839	8	0
2	1	857	922	922	14	0
3	2	746	811	811	6	0
4	3	788	844	844	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 (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	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 (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	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 (i)

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.

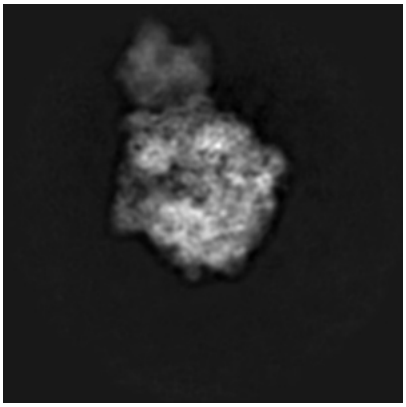
6 Map visualisation

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.

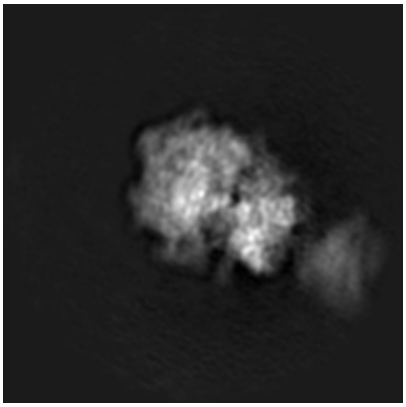
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

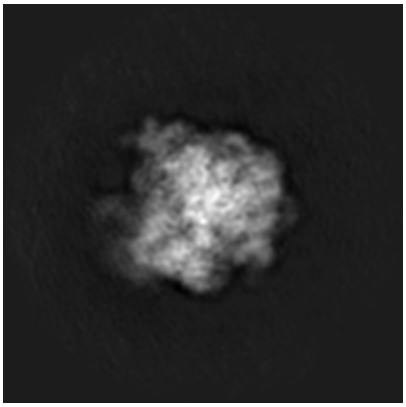
6.1.1 Primary map



X



Y

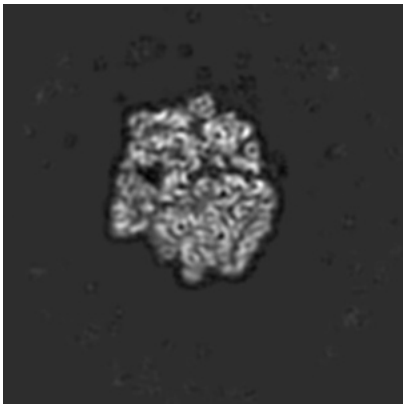


Z

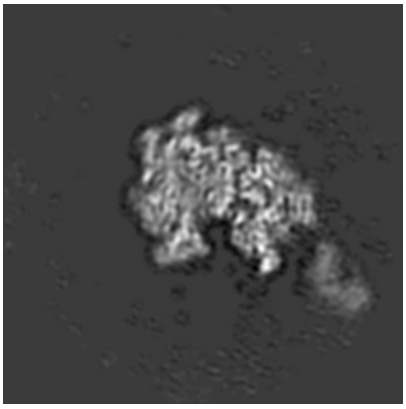
The images above show the map projected in three orthogonal directions.

6.2 Central slices

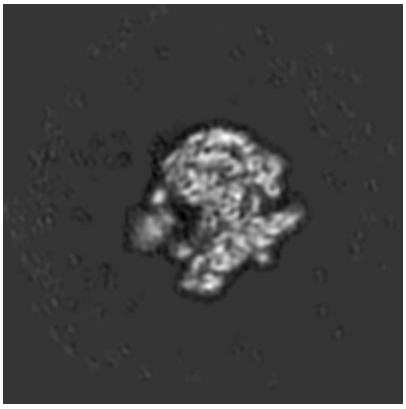
6.2.1 Primary map



X Index: 140



Y Index: 140

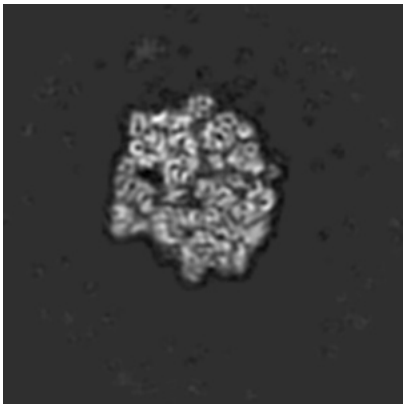


Z Index: 140

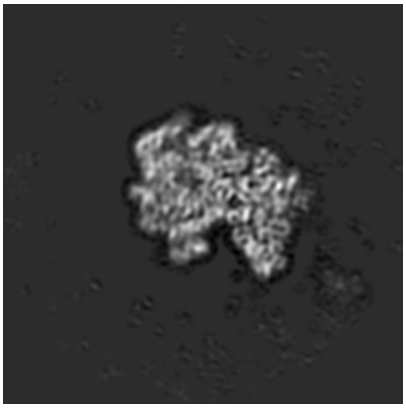
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

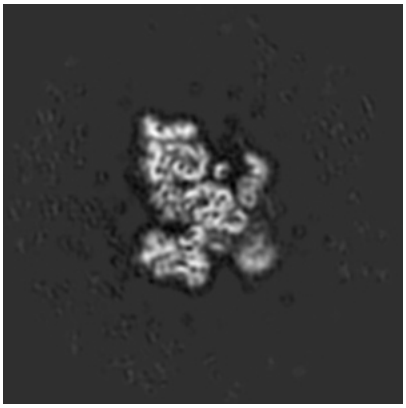
6.3.1 Primary map



X Index: 137



Y Index: 147

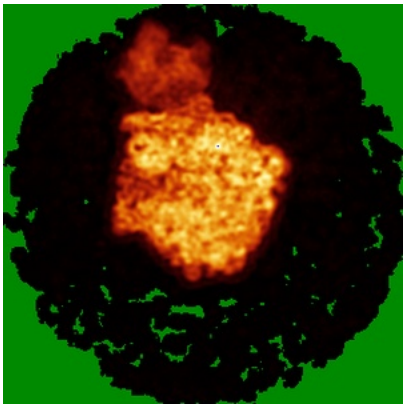


Z Index: 169

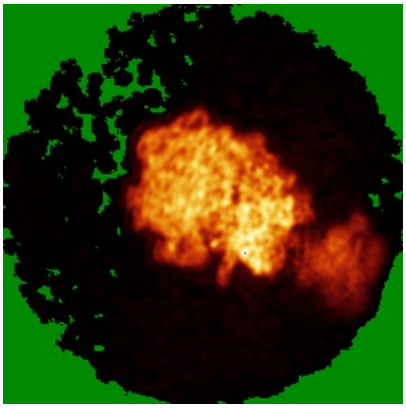
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

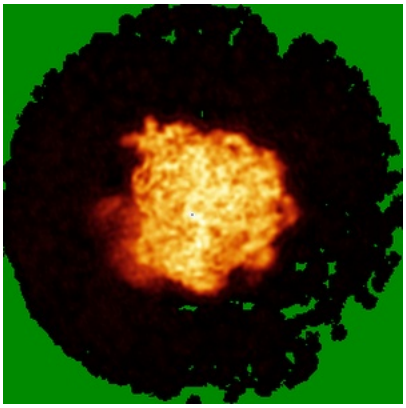
6.4.1 Primary map



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 (i)

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.

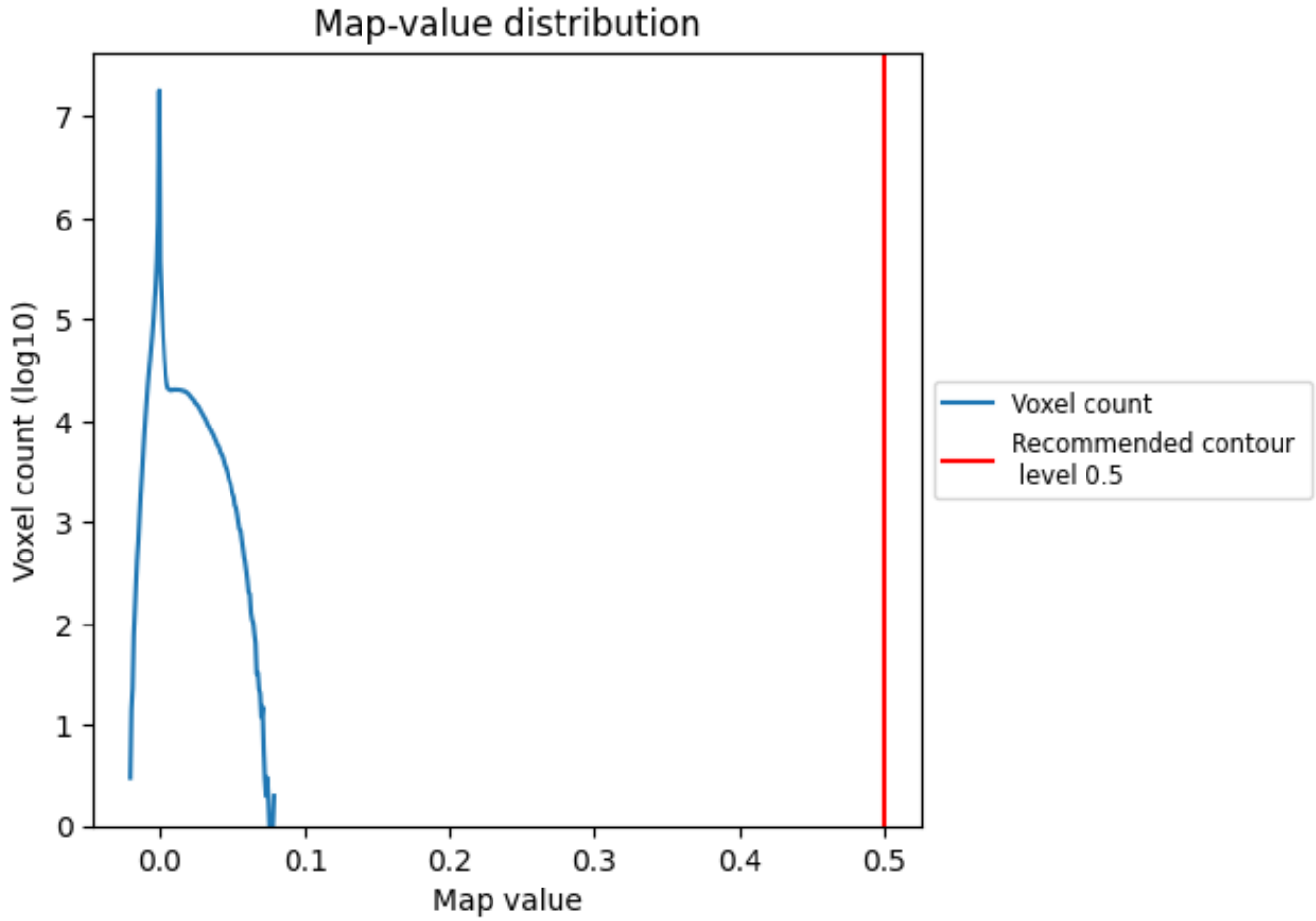
6.6 Mask visualisation (i)

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

7 Map analysis

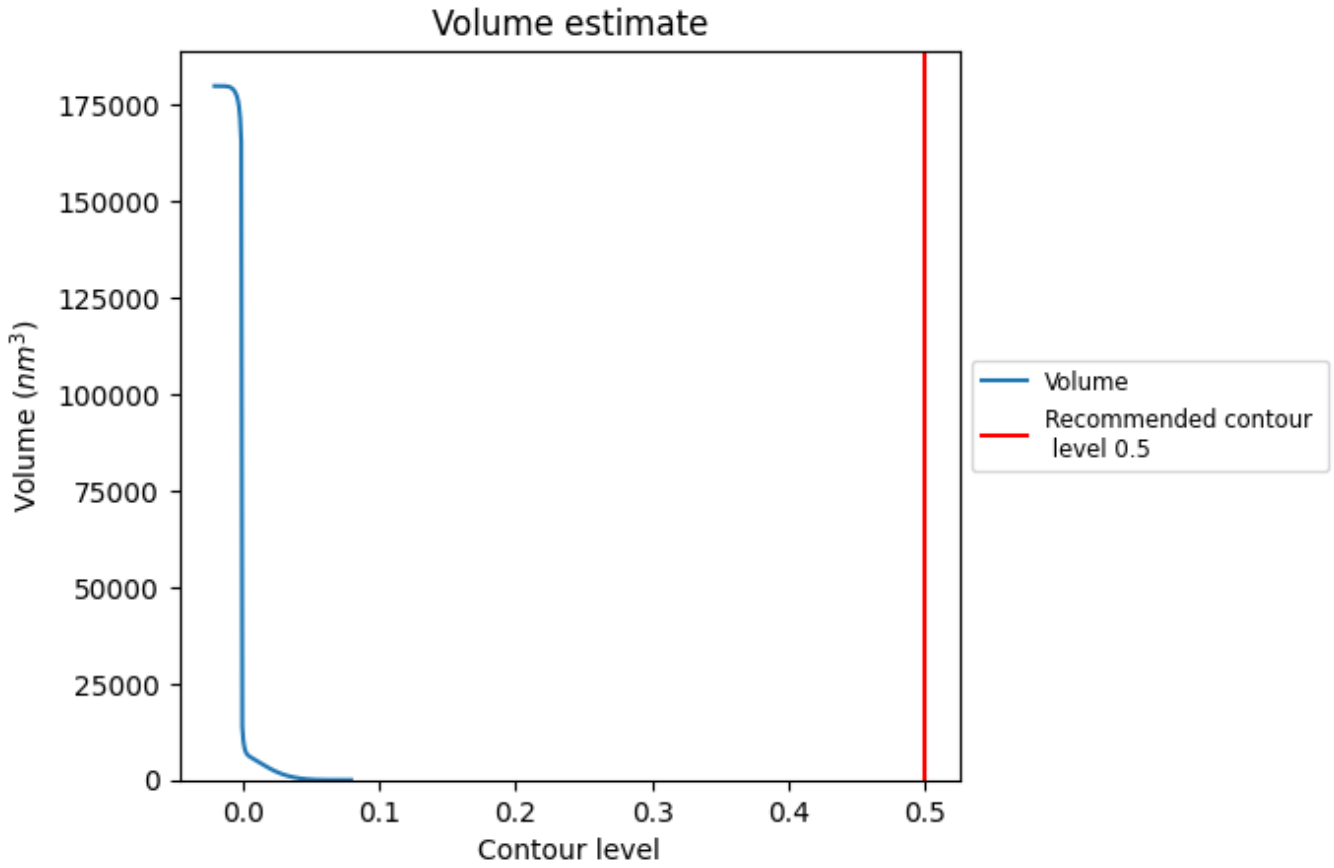
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



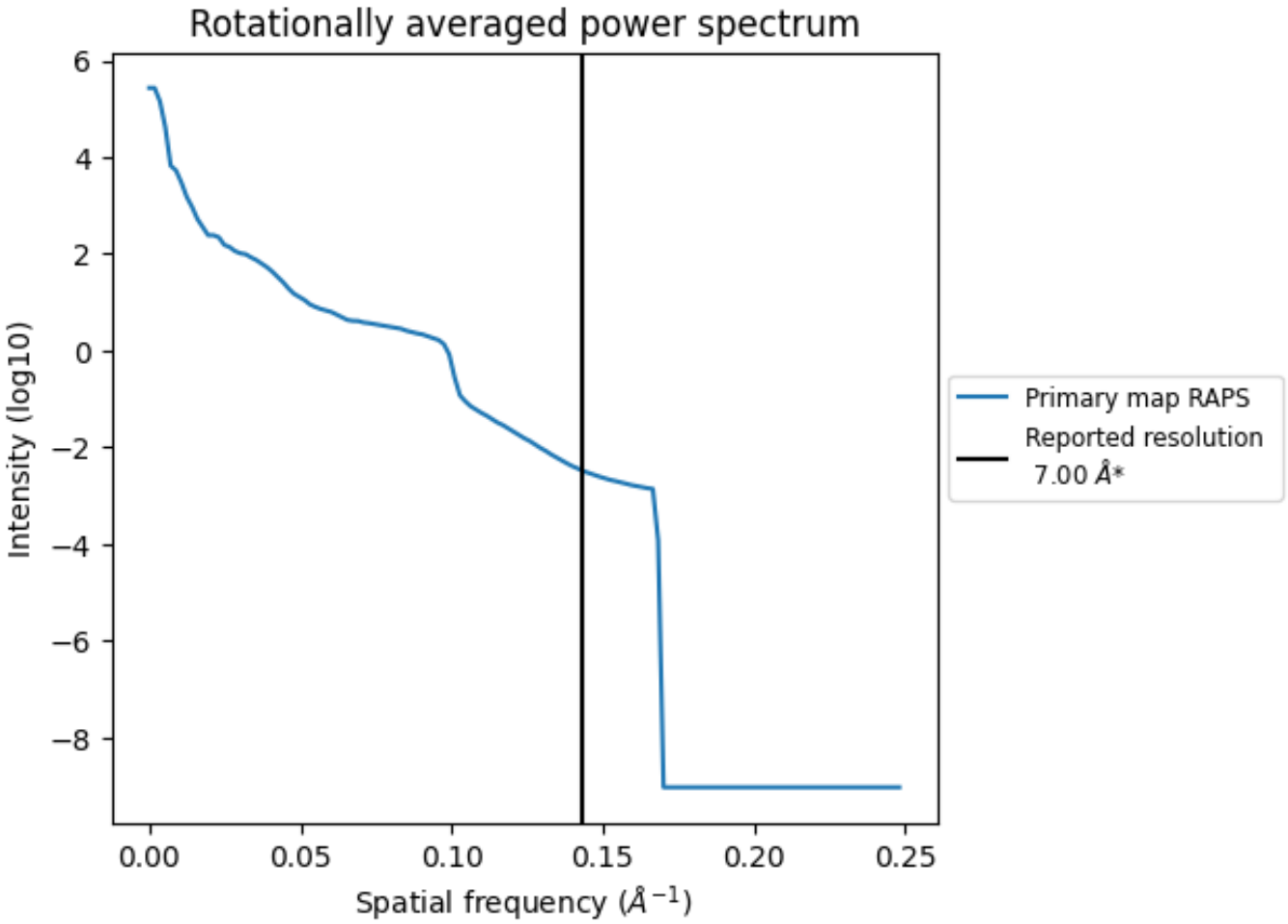
The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

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 (i)



*Reported resolution corresponds to spatial frequency of 0.143 Å^{-1}

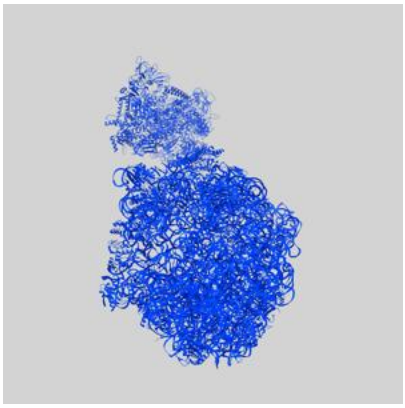
8 Fourier-Shell correlation (i)

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

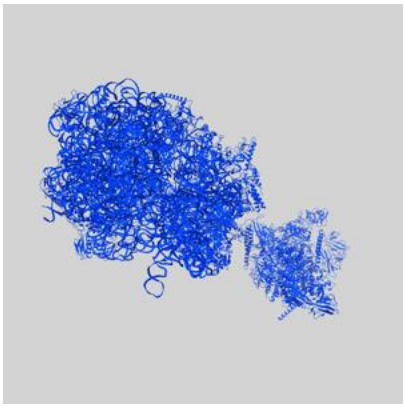
9 Map-model fit

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.

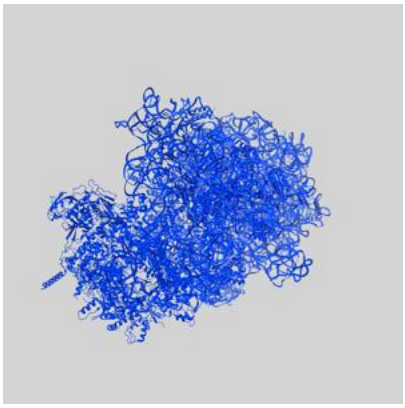
9.1 Map-model overlay



X



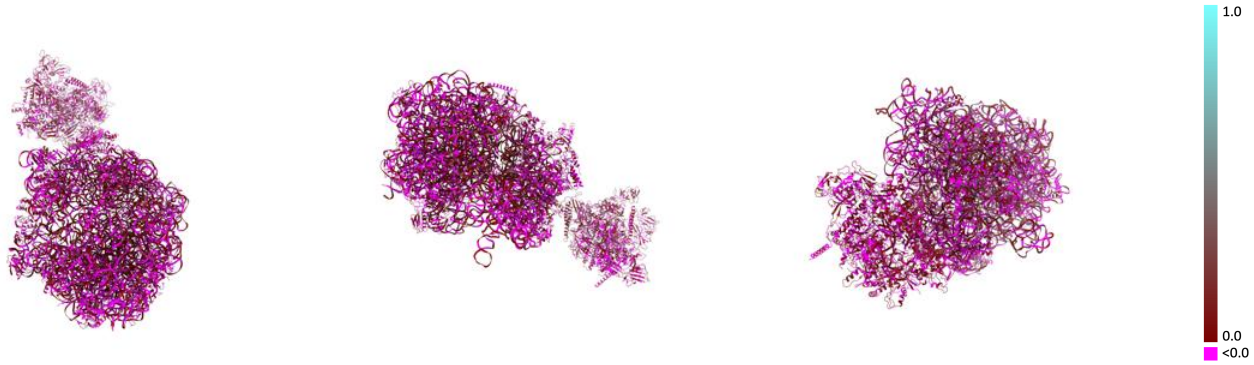
Y



Z

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.

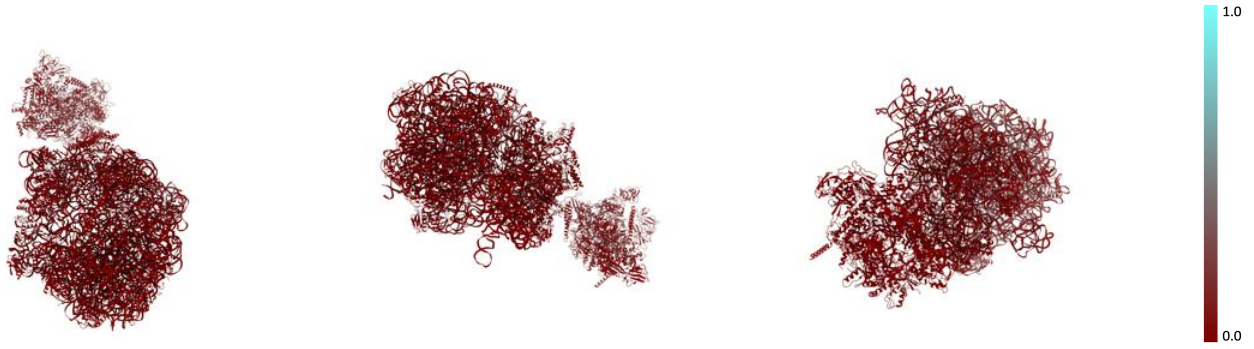
9.2 Q-score mapped to coordinate model



X Y Z

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.

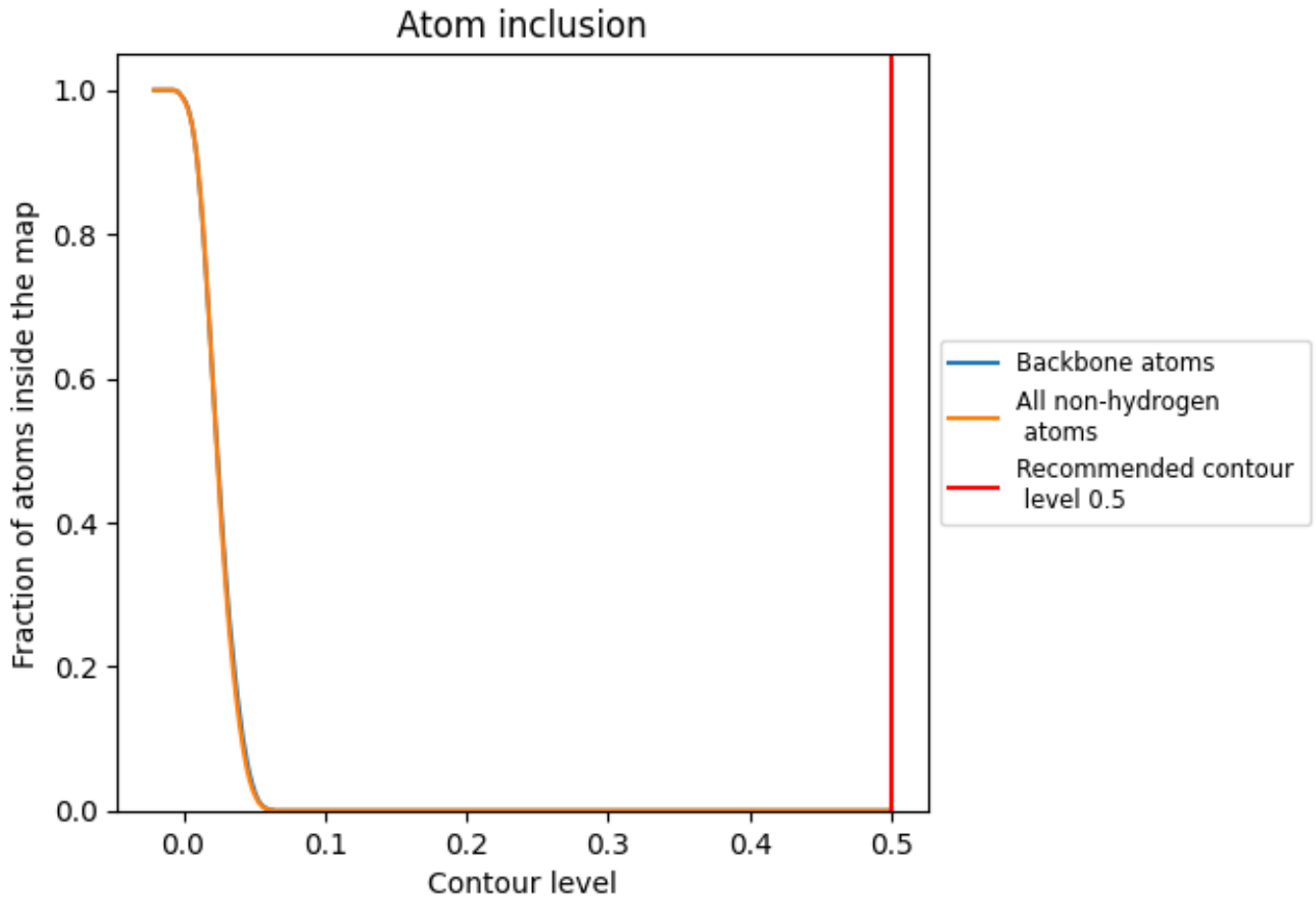
9.3 Atom inclusion mapped to coordinate model



X Y Z

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