



## wwPDB EM Validation Summary Report ⓘ

Nov 9, 2024 – 08:36 PM EST

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

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

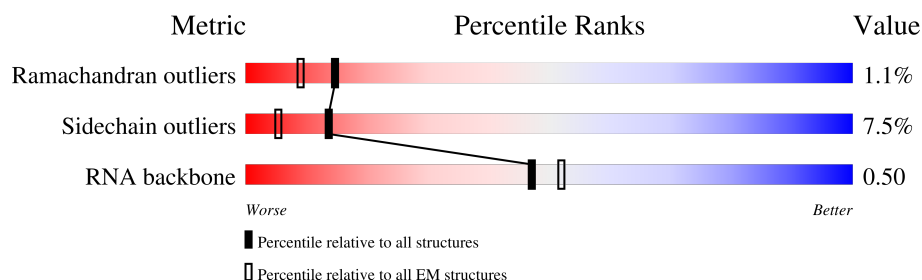
EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

# 1 Overall quality at a glance

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

The reported resolution of this entry is 4.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	103	
2	1	110	
3	2	100	
4	3	104	
5	4	94	
6	5	36	
7	6	36	
8	7	32	

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Mol	Chain	Length	Quality of chain
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AC	329	
12	AD	329	
13	AE	1407	
14	C	75	
15	D	1542	
16	E	87	
17	F	71	
18	G	241	
19	H	557	
20	I	233	
21	J	205	
22	K	167	
23	L	135	
24	M	151	
25	N	129	
26	O	127	
27	P	99	
28	Q	117	
29	R	123	
30	S	101	
31	T	89	

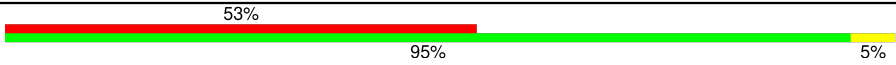
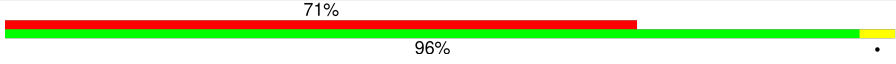
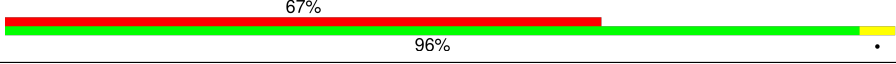
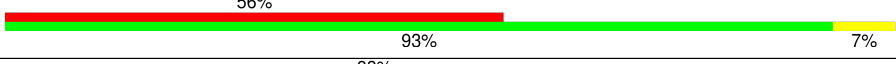
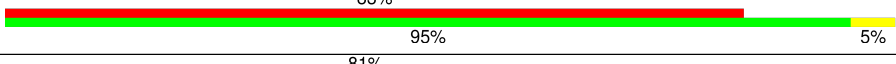
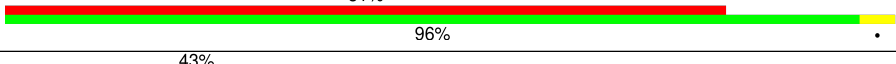
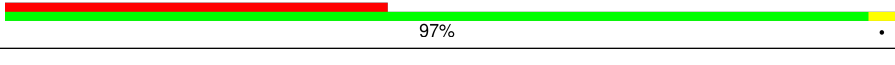
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Mol	Chain	Length	Quality of chain
32	U	82	
33	V	84	
34	W	83	
35	X	116	
36	Y	141	
37	Z	121	
38	a	2904	
39	b	76	
40	c	78	
41	d	120	
42	e	62	
43	f	58	
44	g	66	
45	h	271	
46	i	56	
47	j	209	
48	k	55	
49	l	201	
50	m	46	
51	n	177	
52	o	64	
53	p	175	
54	q	38	
55	r	149	
56	s	142	

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Mol	Chain	Length	Quality of chain
57	t	123	
58	u	144	
59	v	136	
60	w	119	
61	x	116	
62	y	114	
63	z	117	

## 2 Entry composition

There are 65 unique types of molecules in this entry. The entry contains 299095 atoms, of which 123940 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L21.

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

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

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

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

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

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

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

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

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

- Molecule 6 is a DNA chain called NT DNA.

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

- Molecule 7 is a DNA chain called T DNA.

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

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

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

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

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

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

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

There are 2 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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



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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 64 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

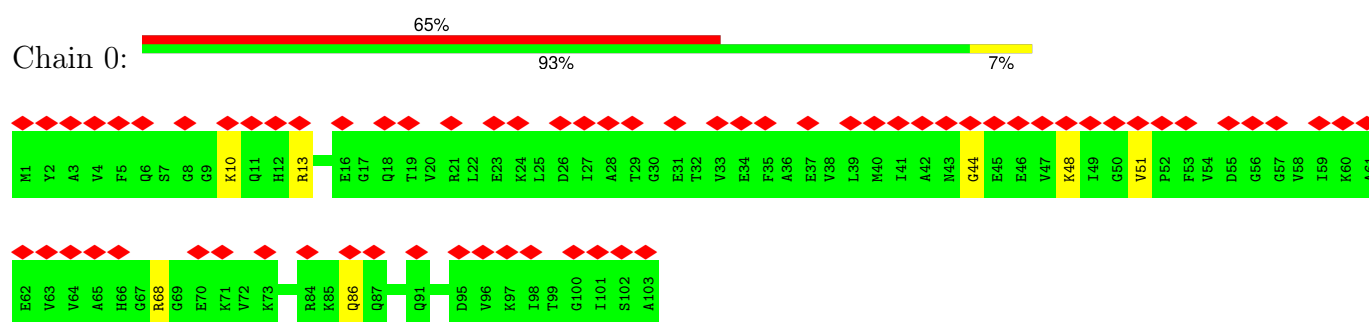
- Molecule 65 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

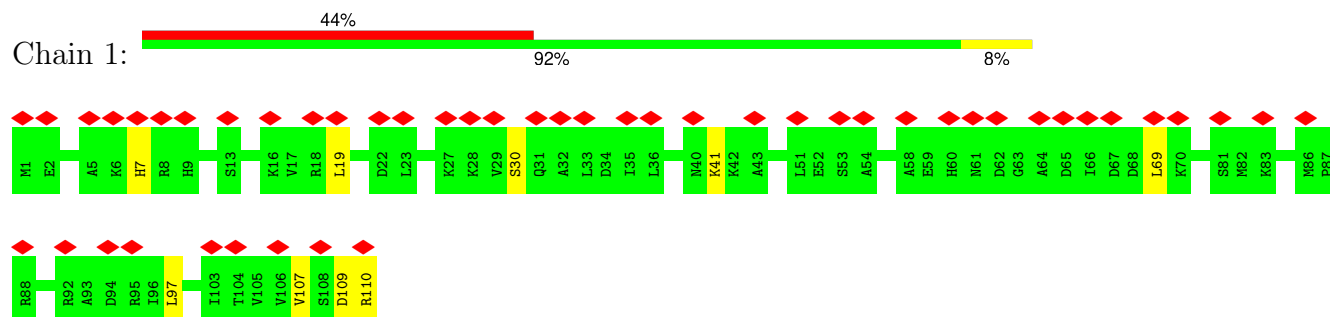
### 3 Residue-property plots [i](#)

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

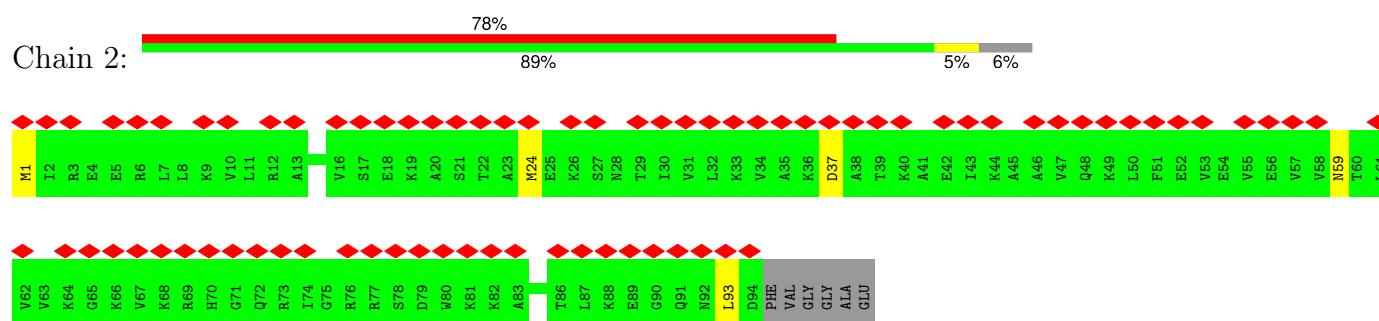
- Molecule 1: 50S ribosomal protein L21



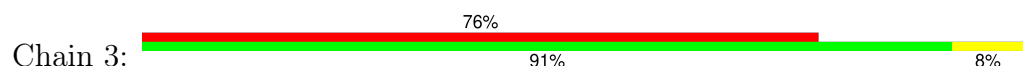
- Molecule 2: 50S ribosomal protein L22



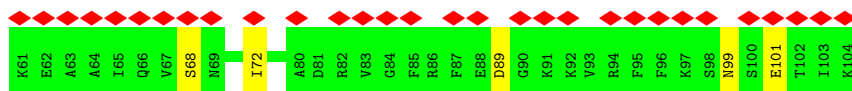
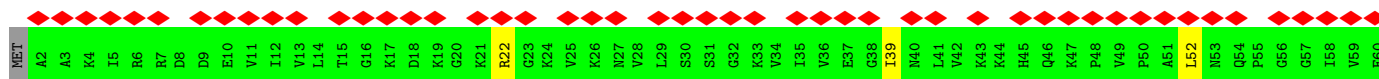
- Molecule 3: 50S ribosomal protein L23



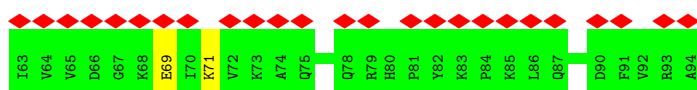
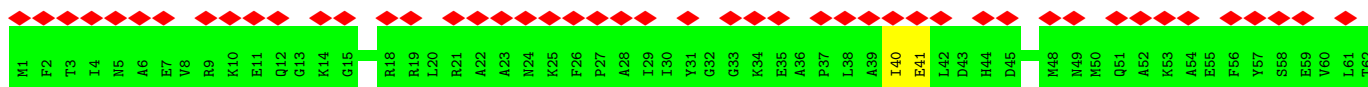
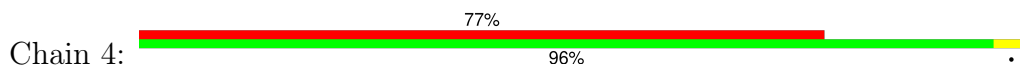
- Molecule 4: 50S ribosomal protein L24



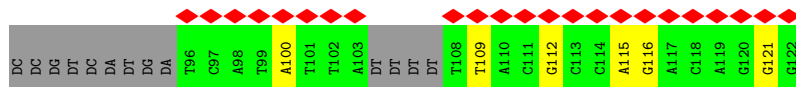




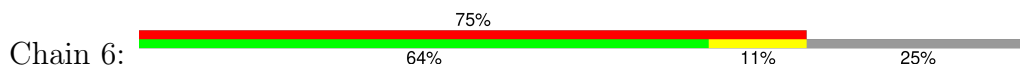
• Molecule 5: 50S ribosomal protein L25



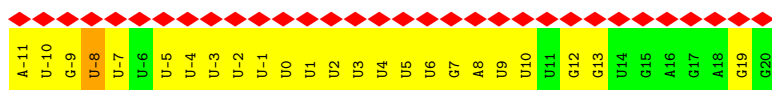
• Molecule 6: NT DNA



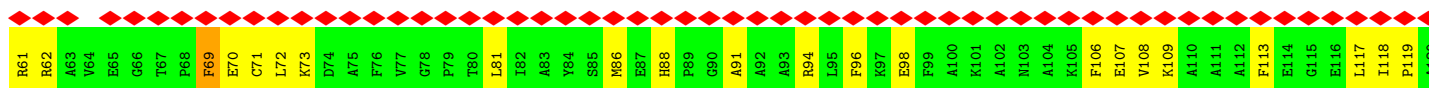
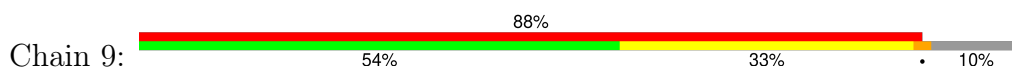
• Molecule 7: T DNA

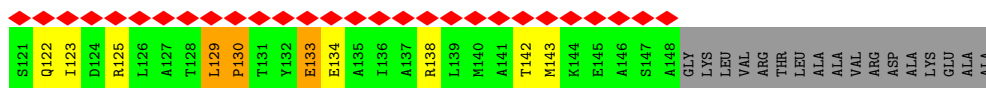


• Molecule 8: mRNA with 27 nt long spacer

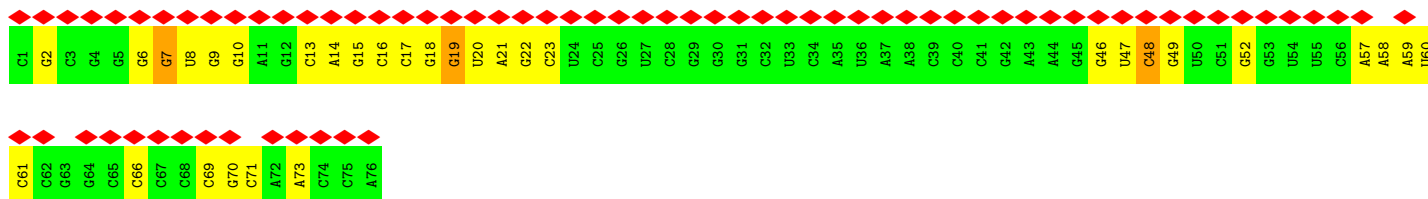


• Molecule 9: 50S ribosomal protein L10





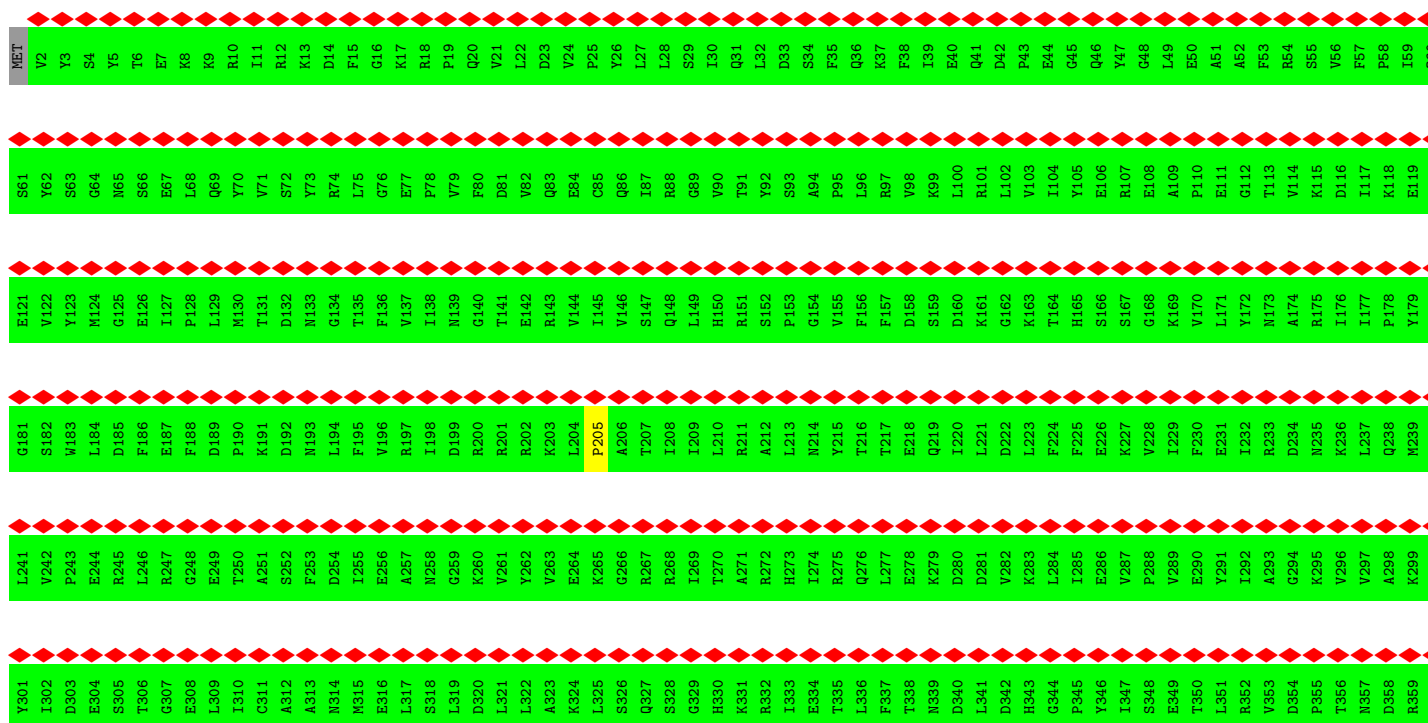
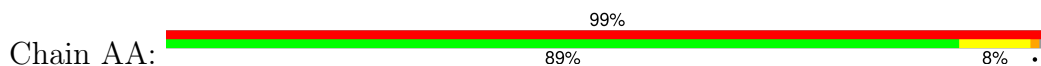
• Molecule 10: E-site and P-site tRNA (fMet)



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



• Molecule 11: DNA-directed RNA polymerase subunit beta

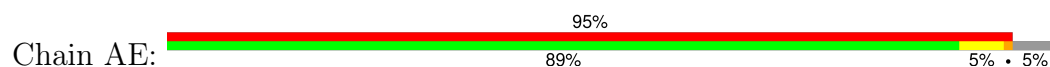


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E1083	H1023	E963	T843	L783	V723	V663	I603	A543	D483	D423	L363
D1084	E1024	L964	K844	A784	V724	G664	H604	G544	L484	D424	V364
M1085	F1025	Q965	L845	T785	Q725	A665	Y605	F445	D485	I425	E365
P1086	E1026	I966	G846	G786	Q726	S666	L606	E546	I486	I426	I366
Y1087	K1027	L967	P847	P787	V727	L667	S607	V547	L487	D427	Y367
D1088	K1028	E968	E848	S788	D728	I668	A608	R548	M488	V428	R368
E1089	A969	A969	E849	T789	A729	P669	I609	R549	M489	V429	M369
N1090	E1030	G970	T850	D790	S730	F670	E610	V550	Q490	K430	M370
G1091	A1031	L971	T851	L791	R731	L671	E611	H551	D491	K431	R371
T1092	K1032	F972	A852	G792	I732	E672	G612	P552	M492	L432	P372
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P1094	R1034	R974	T854	L794	I734	D674	Y614	H554	A494	D434	E374
D1095	K1035	I975	P855	A795	K735	D675	V615	Y555	A495	I435	P375
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N1099	G1039	L979	E859	M799	D739	A679	A619	C559	S499	K439	E379
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S1105	G1045	E985	L865	M605	E745	M685	E625	E565	F505	I445	F385
R1106	V1046	D986	D866	P906	A746	Q686	E626	G566	F506	D446	E386
M1107	L1047	E987	E867	M807	G747	R687	G627	P567	G507	H447	N387
N1108	K1048	L988	S868	N808	I748	Q688	H628	I568	S508	L448	L388
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T1115	A1055	D937	A875	S815	K755	A695	T635	L575	M515	S455	Y395
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K1133	K1073	Q955	THR	I633	L773	G713	M653	K593	L533	R473	E413
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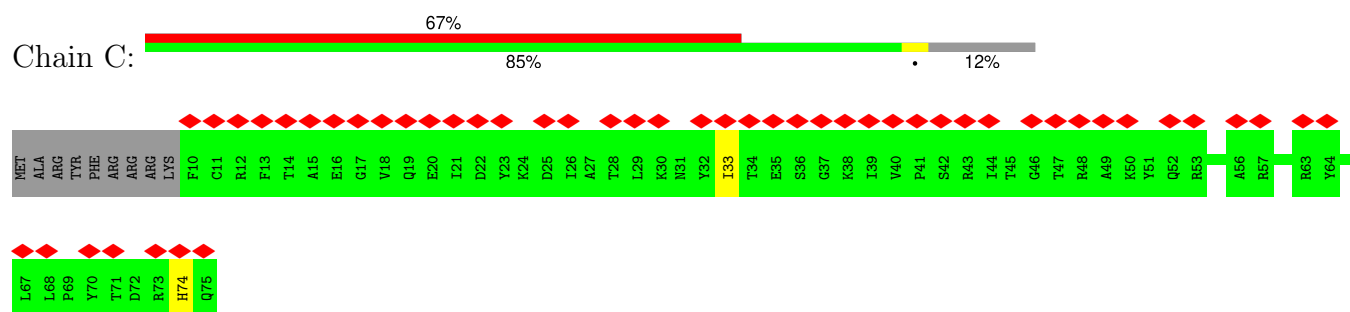
• Molecule 13: DNA-directed RNA polymerase subunit beta'



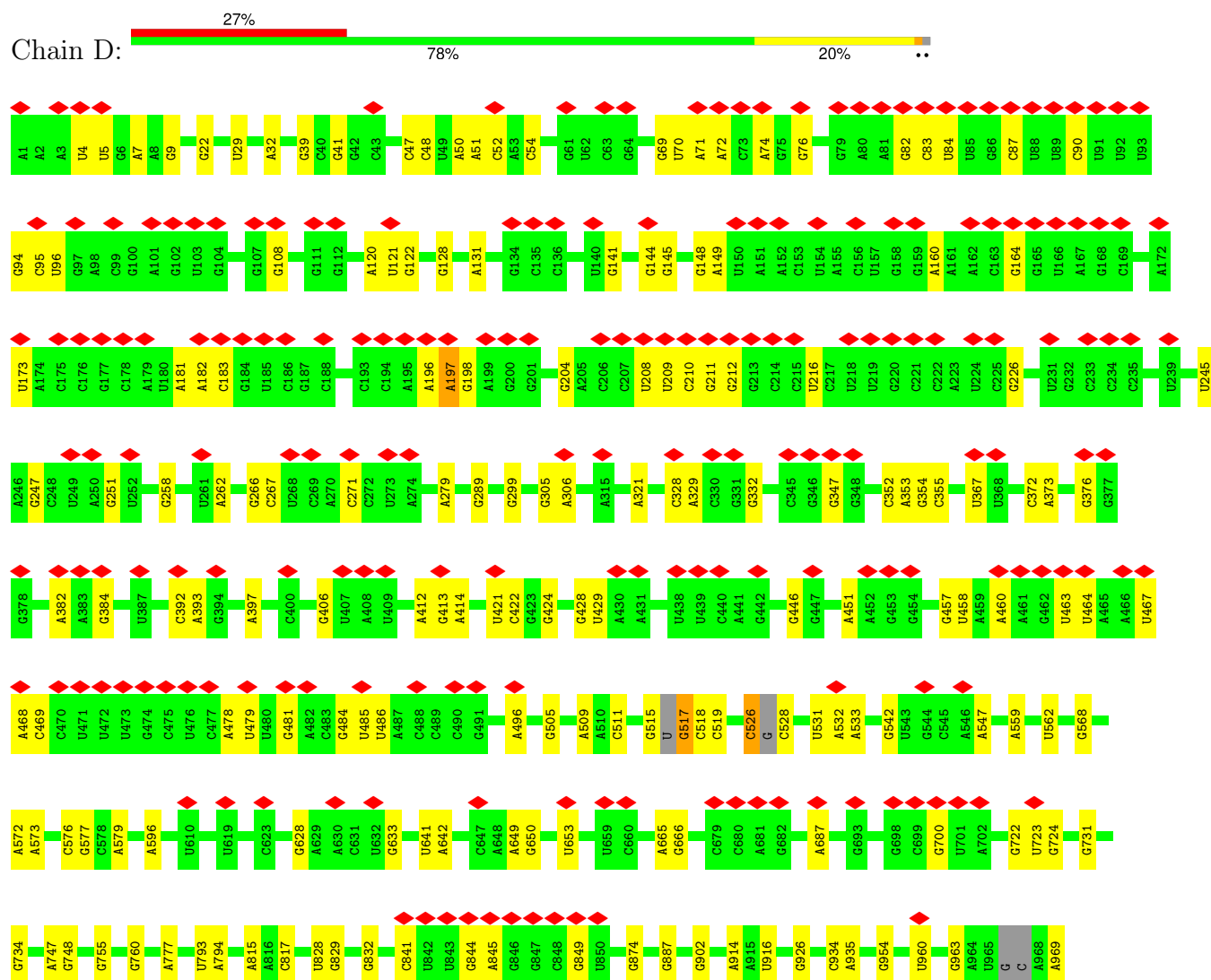
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LEU	I22	LEU
ALA	I23	LEU
GLN	A24	LEU
THR	L25	LEU
THR	L26	LEU
GLU	E16	LEU
LYS	F17	LEU
ASP	D18	LEU
LEU	A19	LEU
VAL	I20	LEU
PHE	K21	LEU
LEU	I22	LEU
ALA	I23	LEU
GLN	A24	LEU
THR	L25	LEU
THR	L26	LEU
GLU	E16	LEU
LYS	F17	LEU
ASP	D18	LEU
LEU	A19	LEU
VAL	I20	LEU
PHE	K21	LEU
LEU	I22	LEU
ALA	I23	LEU
GLN	A24	LEU
THR	L25	LEU
THR	L26	LEU
GLU	E16	LEU
LYS	F17	LEU
ASP	D18	LEU
LEU	A19	LEU
VAL	I20	LEU
PHE	K21	LEU
LEU	I22	LEU
ALA	I23	LEU
GLN	A24	LEU
THR	L25	LEU

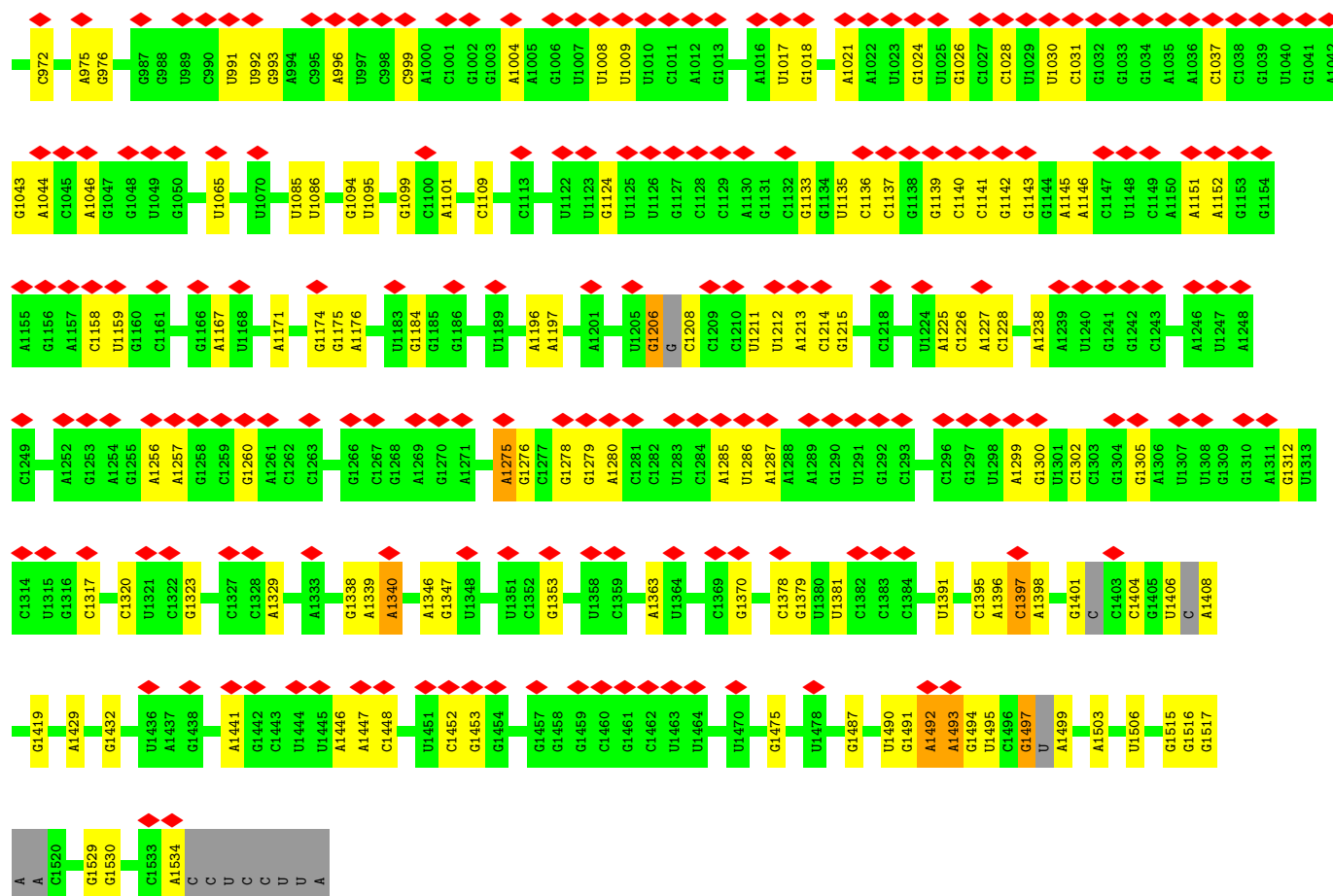
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A1264	V1204	L1144	Q1084	T1024	K964	A904	T844	A784	M724	I664	M604	L544
T1265	E1205	F1145	G1085	M1025	S965	R905	E845	D785	M725	Q665	L605	H545
L1266	R1206	E1146	N1086	P1026	V966	G906	E846	T786	A726	E666	N606	A546
V1267	G1207	A1147	D1087	V1027	V967	H907	E847	R787	D727	Q667	T607	R547
N1268	D1208	R1148	V1088	I1028	N968	I908	V848	L788	S728	F668	C608	V548
A1269	V1209	R1149	L1089	T1029	S969	I909	L849	K789	G729	Q669	Y609	K549
G1270	I1210	P1150	I1090	E1030	S970	N910	K850	T790	A730	S670	R610	V550
S1271	S1211	K1151	P1091	V1031	G971	K911	P851	A791	R731	I611	I611	R551
D1272	D1212	E1152	G1092	S1032	K972	G912	G852	N792	G732	L672	L612	I552
T1273	G1213	P1153	T1093	G1033	L974	E913	L853	S793	S733	V673	G613	T553
F1274	P1214	A1154	D1094	F1034	V974	A914	A854	G794	A734	T674	L614	E554
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G1277	P1217	A1157	A1097	F1037	S977	V917	L857	T797	I737	E677	T617	K557
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Q1279	D1219	I1159	Y1099	D1039	N979	A919	P859	R799	Q739	Y679	I619	A559
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N1295	N1235	L1175	I1115	G1055	Y995	PHE	N875	G815	I755	S635	G635	G575
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T1297	V1237	I1177	S1117	S1057	V997	ILE	V877	H817	T757	M697	A637	A577
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S1303	L1243	S1183	R1123	D1063	L1003	ALA	R883	T823	D643	T703	S583	V583
R1304	Q1244	D1184	I1124	S1064	A1004	GLU	S884	P824	R764	E704	M644	P584
D1305	G1245	P1185	P1125	A1065	K1005	S948	V885	V825	E765	T705	V645	K585
L1306	V1246	Y1186	Q1126	E1066	G1006	S949	V886	I826	G766	V706	I646	G586
L1307	K1247	E1187	GLU	R1067	D1007	I950	S887	E827	T767	I707	L647	L587
G1308	I1248	E1188	GLY	T1068	G1008	Q951	C888	G828	N768	N708	P648	P588
I1309	N1249	M1189	GLY	A1069	E1009	V952	D889	G829	V769	R709	K649	Y589
T1310	D1250	I1190	THR	G1070	Q1010	K953	T890	D830	L770	D710	K650	S590
K1311	K1251	P1191	LYS	K1071	V1011	N954	R891	V831	Q771	I651	H651	S590
A1312	H1252	K1192	ASP	D1072	A1012	K955	F892	K832	Y772	Q712	E652	V592
S1313	I1253	M1193	ILE	T1073	G1013	G956	G893	E833	F773	E713	I653	N593
L1314	E1254	R1194	G1136	L1074	G1014	S957	V894	P834	I774	E714	I654	Q594
A1315	V1255	L1195	G1137	R1075	E1015	I958	C895	L835	S775	K715	S655	A595
T1316	L1256	L1196	L1138	P1076	T1016	K959	A896	R836	T776	Q716	E656	L596
E1317	V1257	M1197	P1139	A1077	V1017	K959	H897	D837	H777	V717	E656	G597
S1318	R1258	V1198	R1140	L1078	A1018	L960	C998	R838	G778	S718	E658	K598
F1319	Q1259	F1200	R1140	K1079	N1019	L960	Y899	R838	A779	S719	E659	K599
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- Molecule 14: 30S ribosomal protein S18



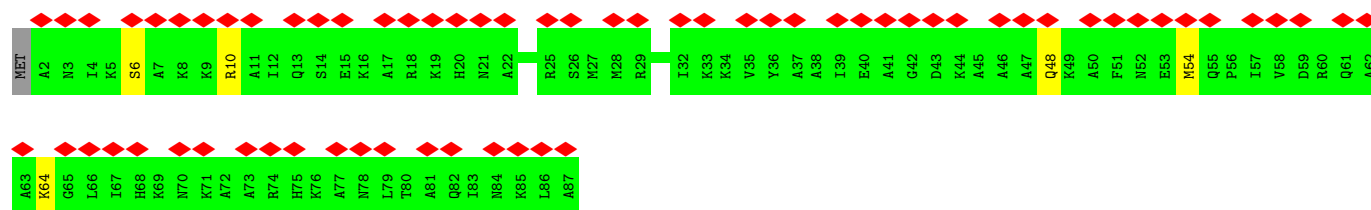
- Molecule 15: 16S rRNA





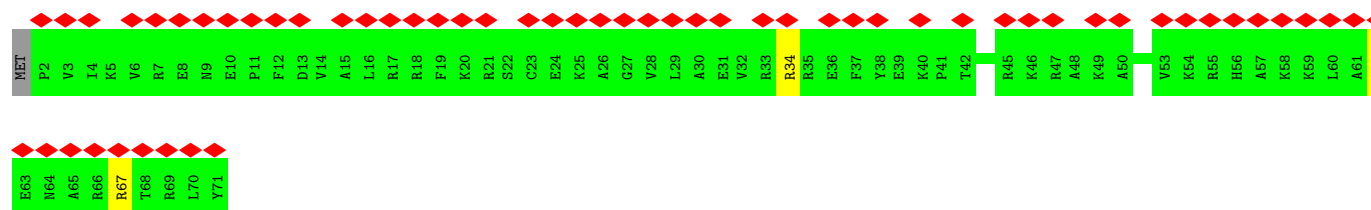
• Molecule 16: 30S ribosomal protein S20

Chain E: 76% 93% 6%



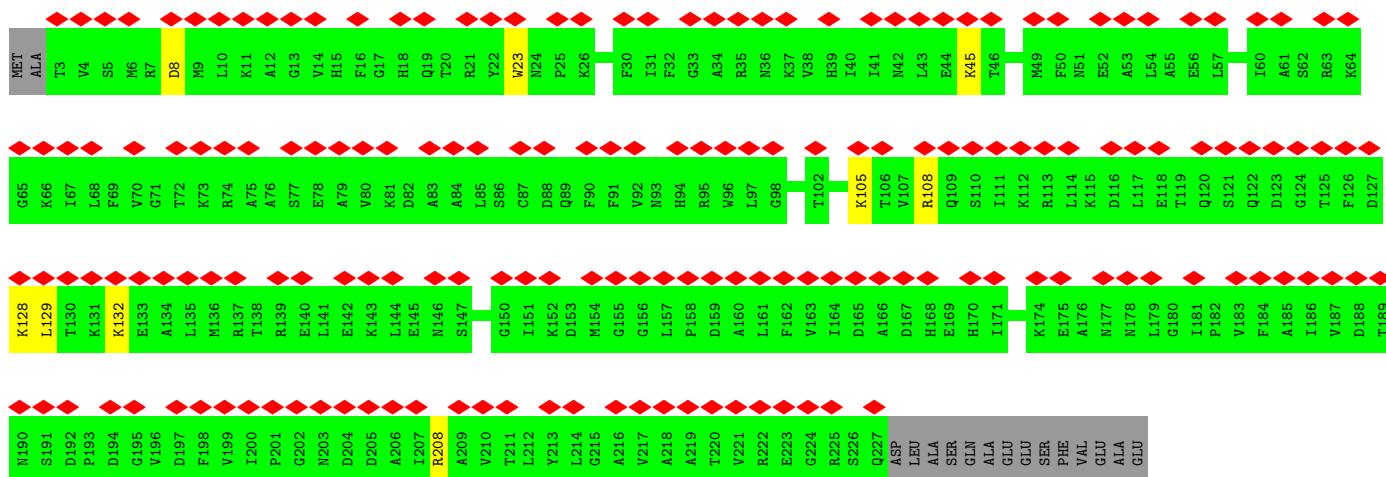
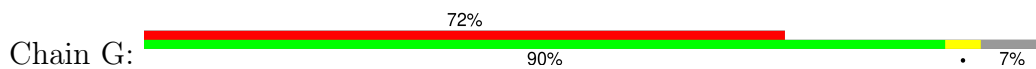
• Molecule 17: 30S ribosomal protein S21

Chain F: 82% 94% 2%

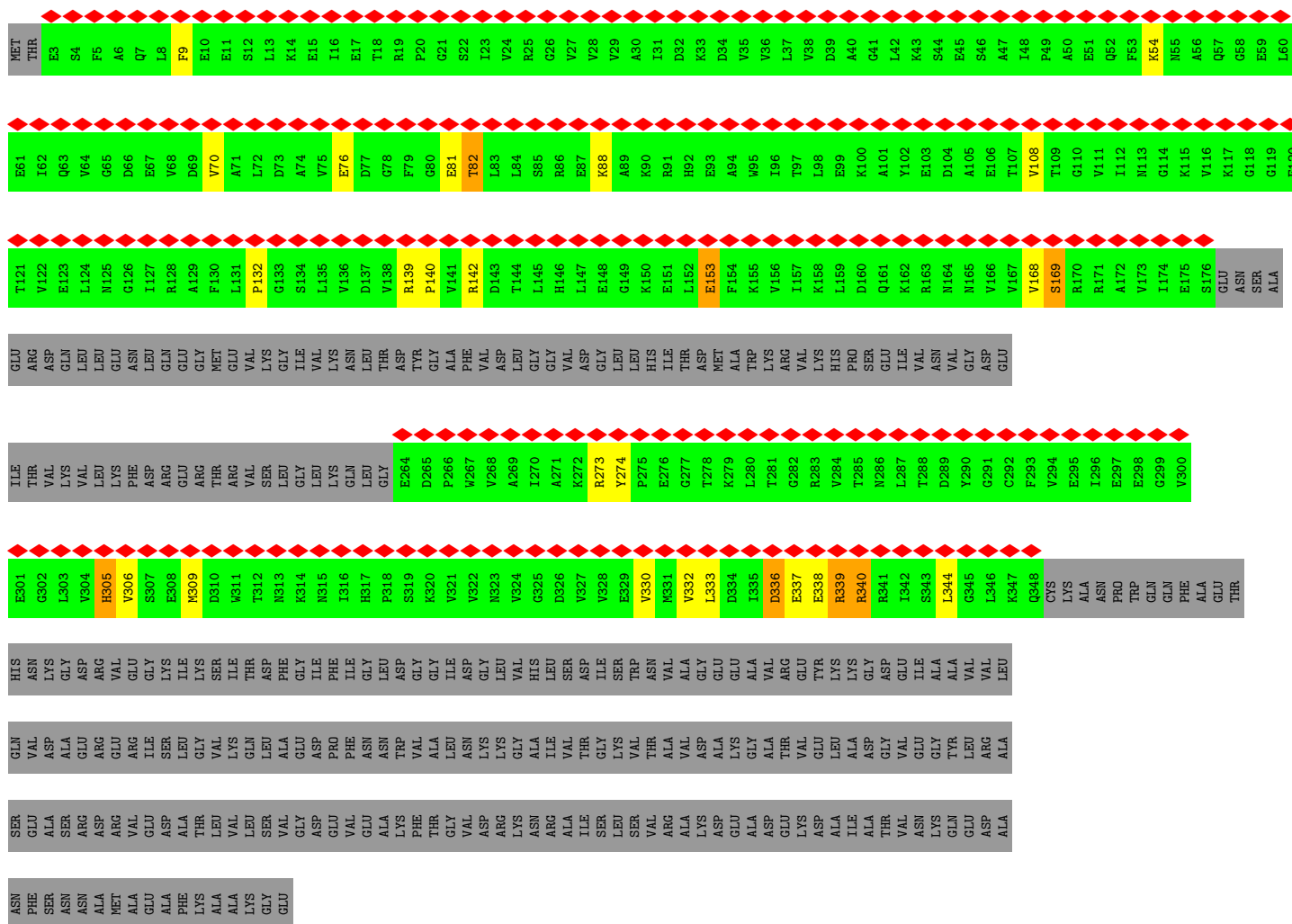
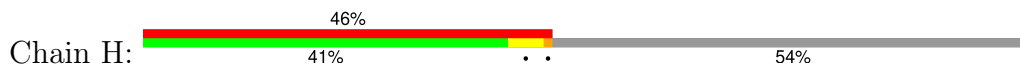


• Molecule 18: 30S ribosomal protein S2



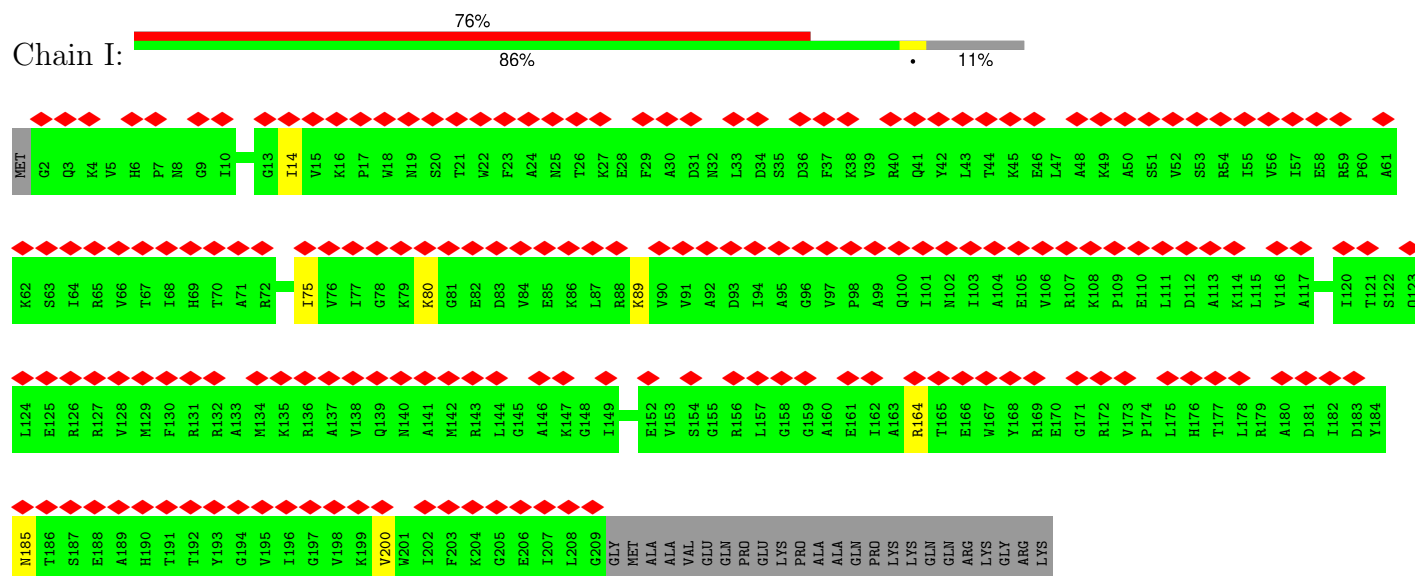


• Molecule 19: 30S ribosomal protein S1



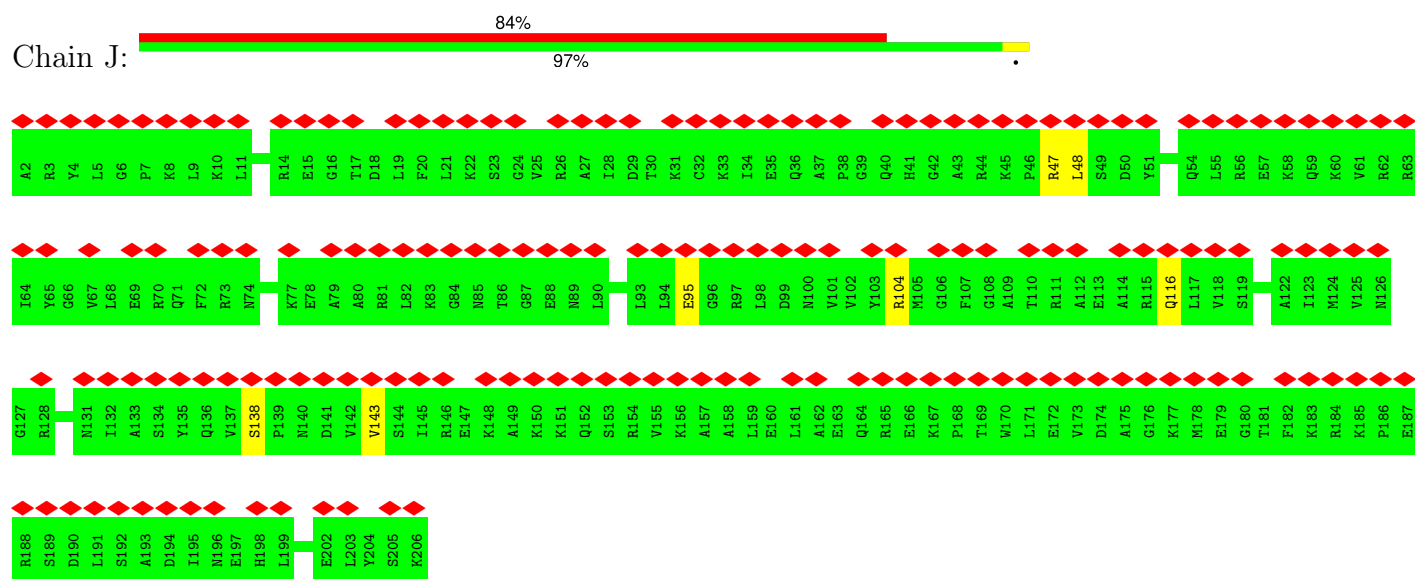
- Molecule 20: 30S ribosomal protein S3

Chain I:



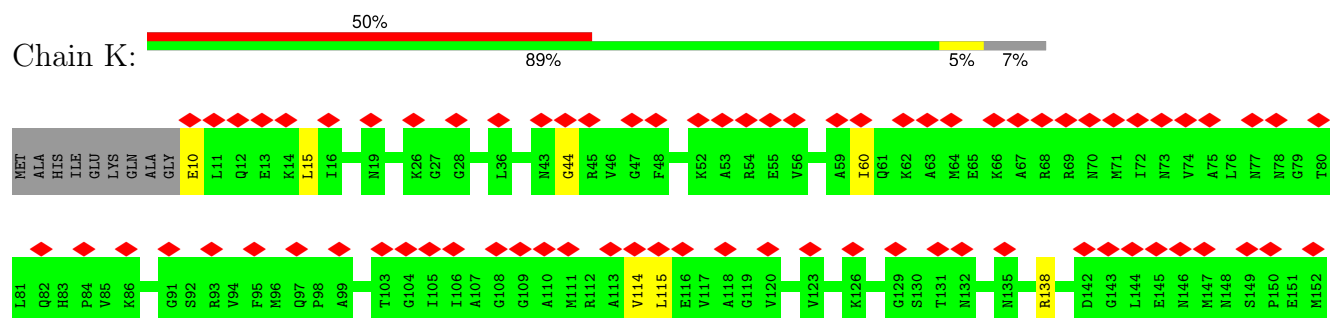
- Molecule 21: 30S ribosomal protein S4

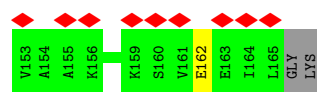
Chain J:



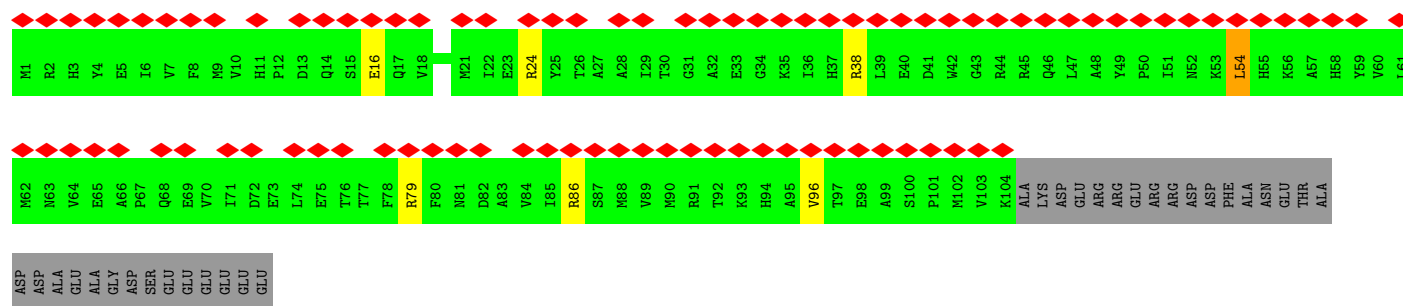
- Molecule 22: 30S ribosomal protein S5

Chain K:

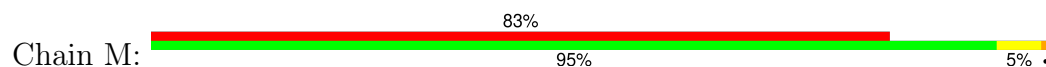




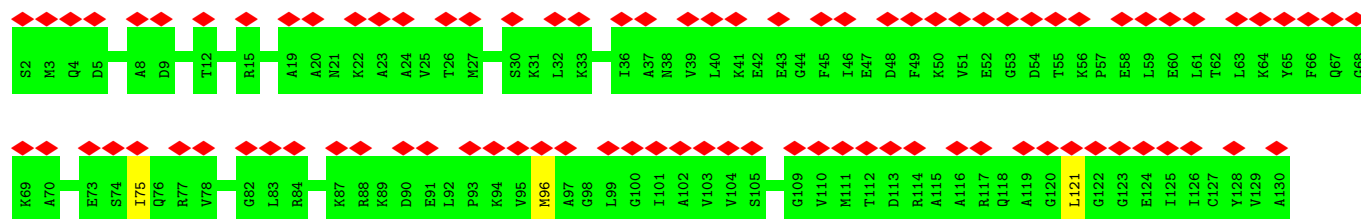
- Molecule 23: 30S ribosomal protein S6



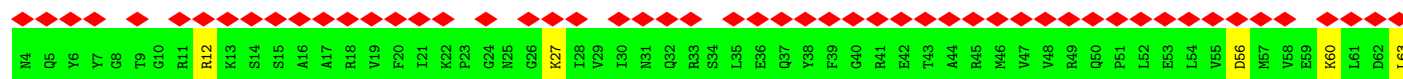
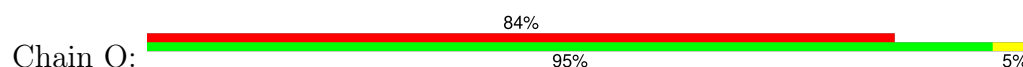
- Molecule 24: 30S ribosomal protein S7

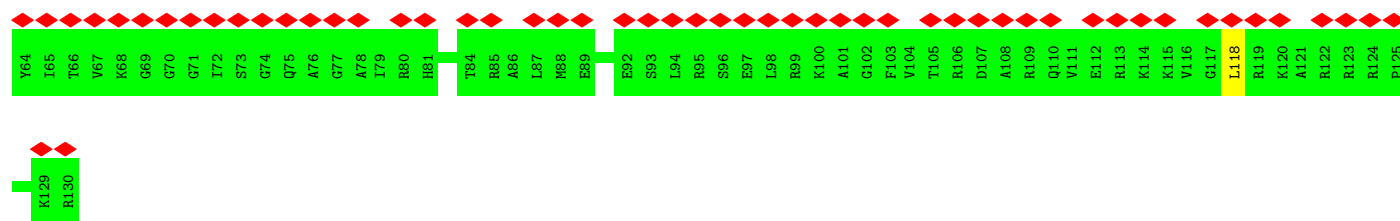


- Molecule 25: 30S ribosomal protein S8

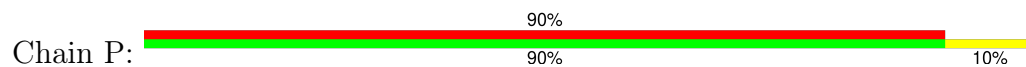


- Molecule 26: 30S ribosomal protein S9

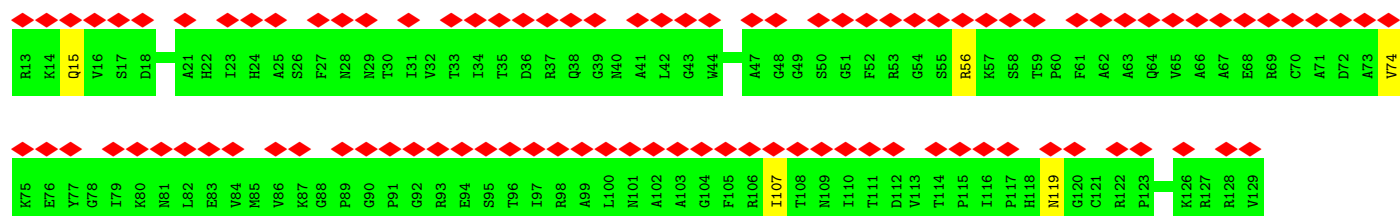
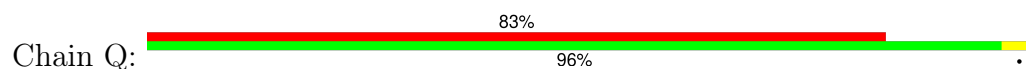




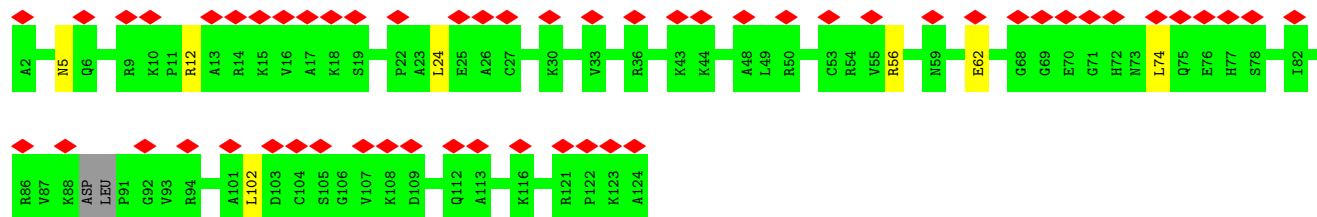
• Molecule 27: 30S ribosomal protein S10



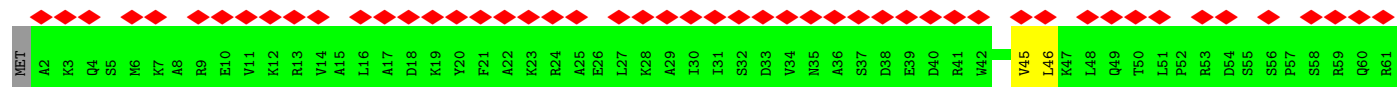
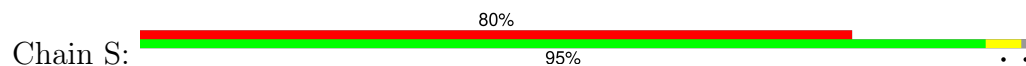
• Molecule 28: 30S ribosomal protein S11

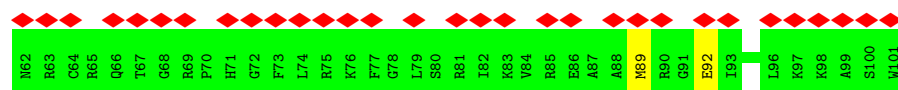


• Molecule 29: 30S ribosomal protein S12



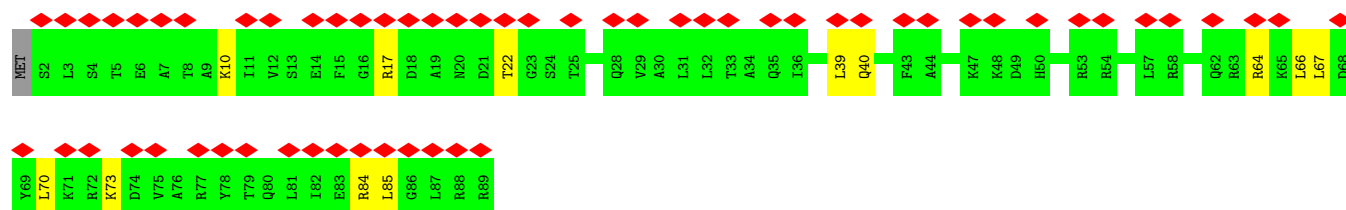
• Molecule 30: 30S ribosomal protein S14





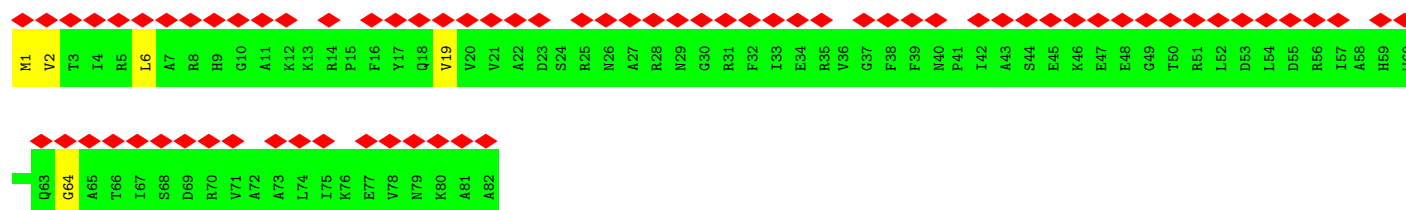
- Molecule 31: 30S ribosomal protein S15

Chain T:



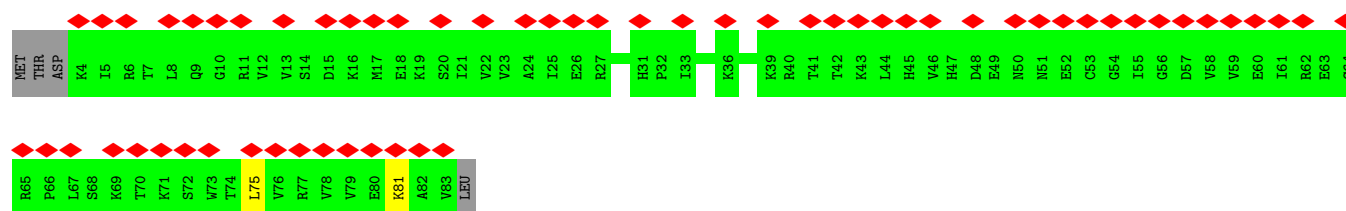
- Molecule 32: 30S ribosomal protein S16

Chain U:



- Molecule 33: 30S ribosomal protein S17

Chain V:



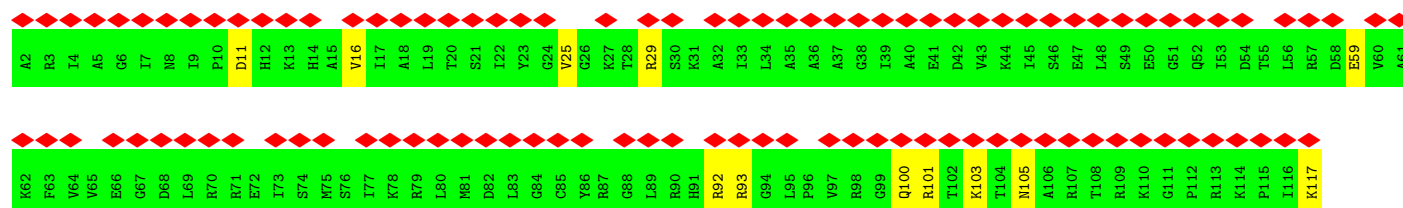
- Molecule 34: 30S ribosomal protein S19

Chain W:



- Molecule 35: 30S ribosomal protein S13

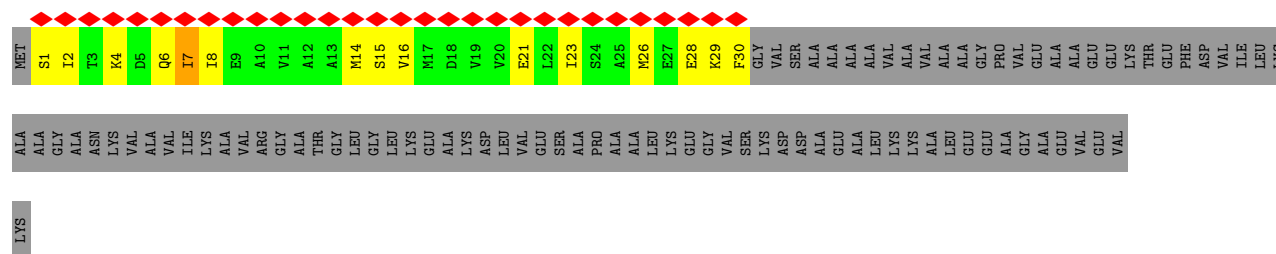
Chain X:



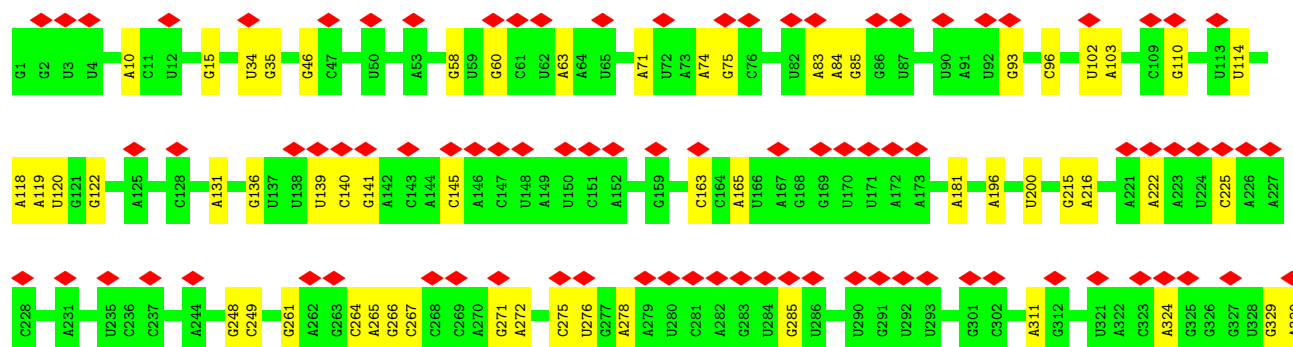
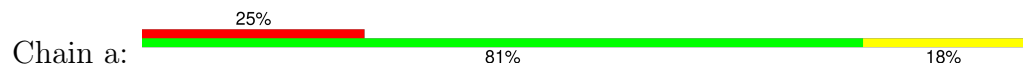
• Molecule 36: 50S ribosomal protein L11

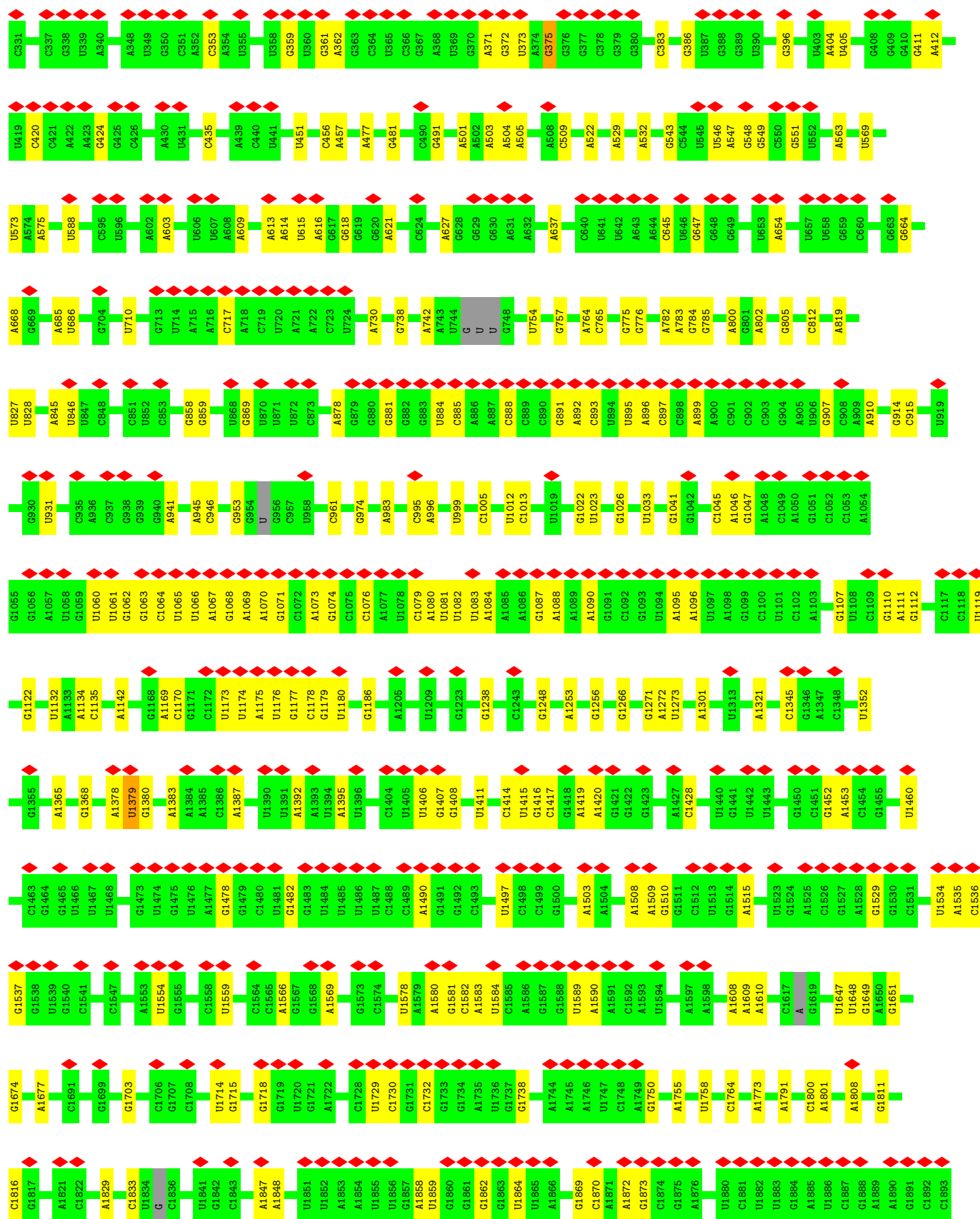


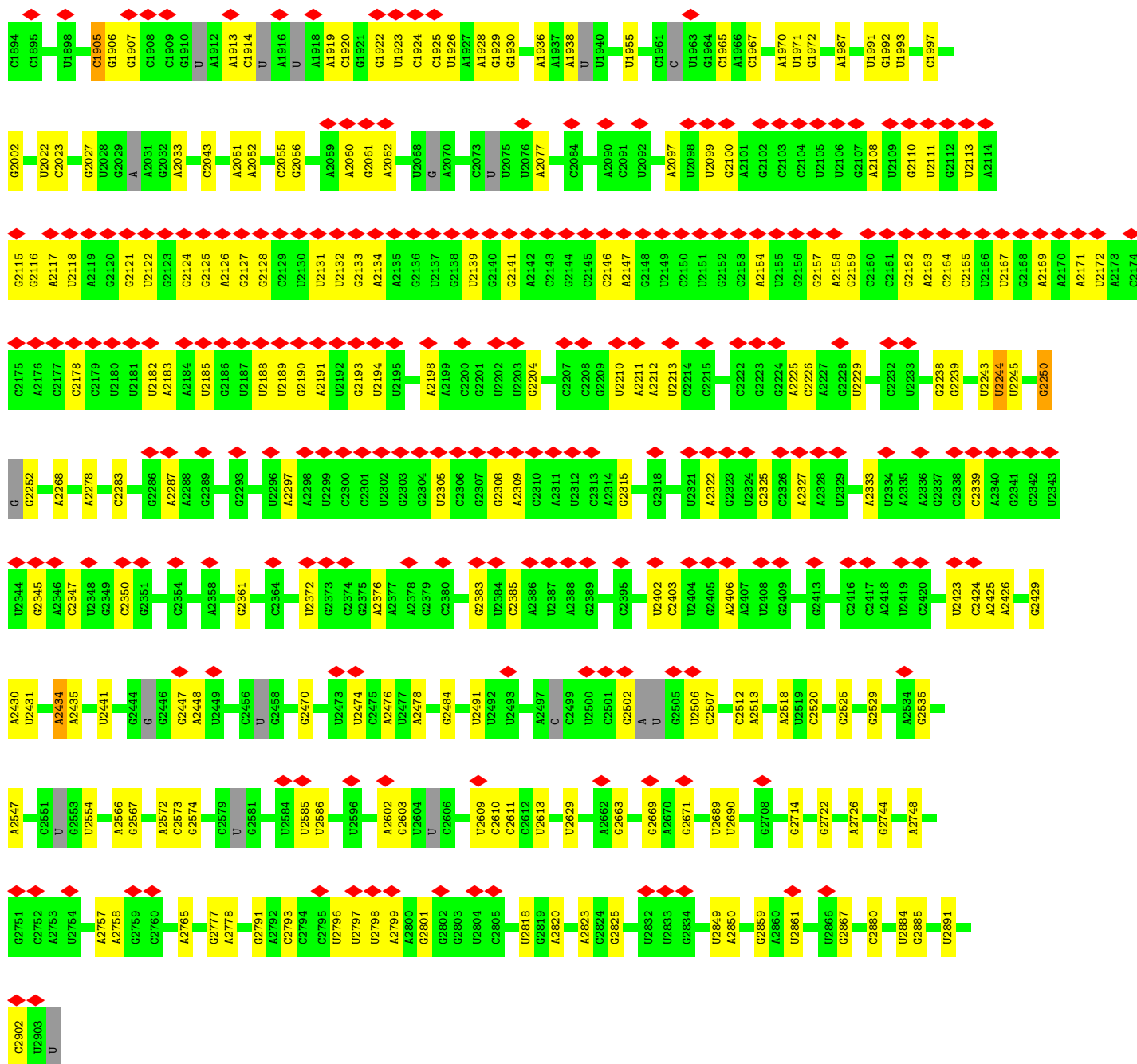
• Molecule 37: 50S ribosomal protein L7/L12



• Molecule 38: 23S rRNA

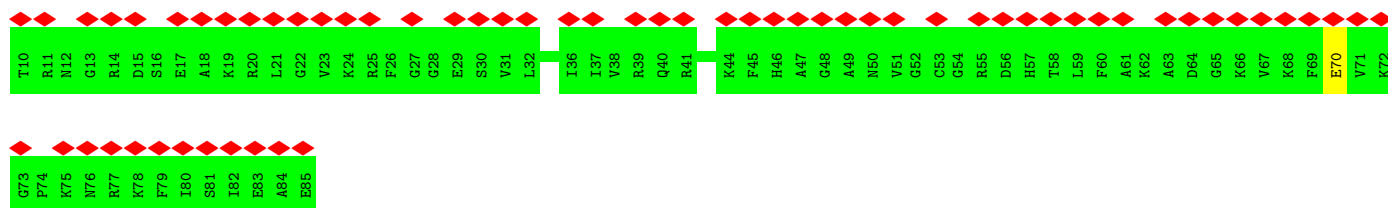






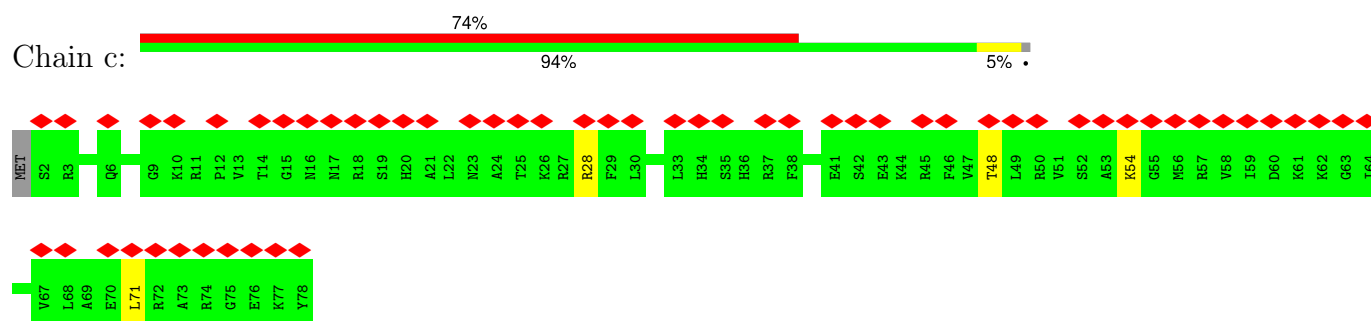
- Molecule 39: 50S ribosomal protein L27

Chain b:

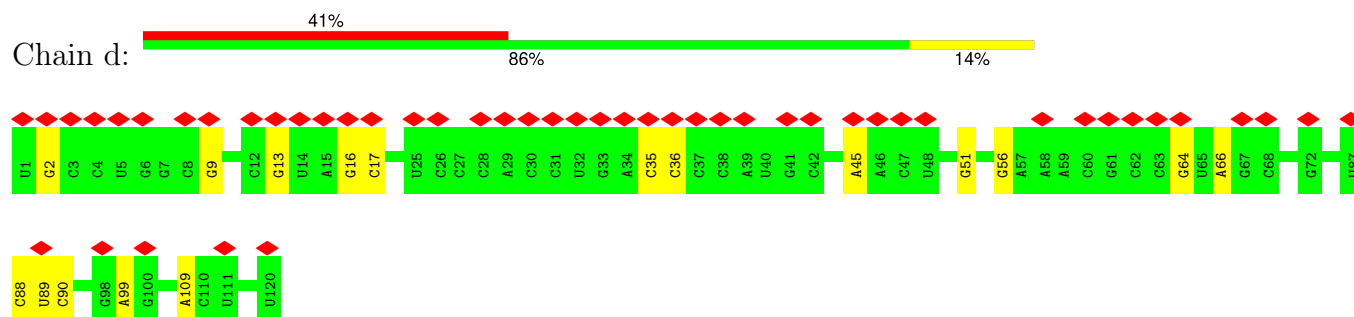


- Molecule 40: 50S ribosomal protein L28

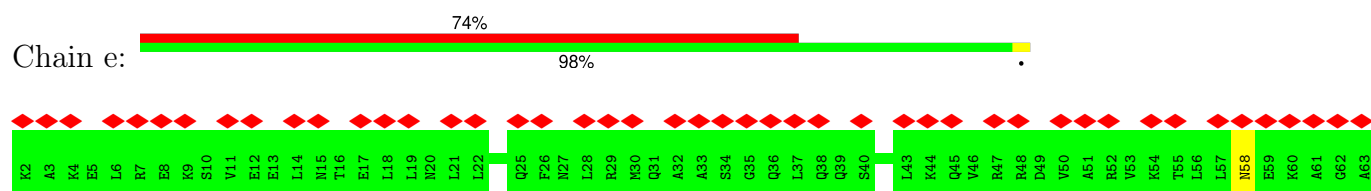




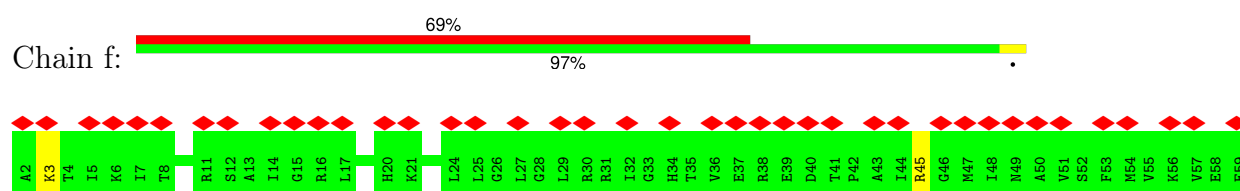
- Molecule 41: 5S rRNA



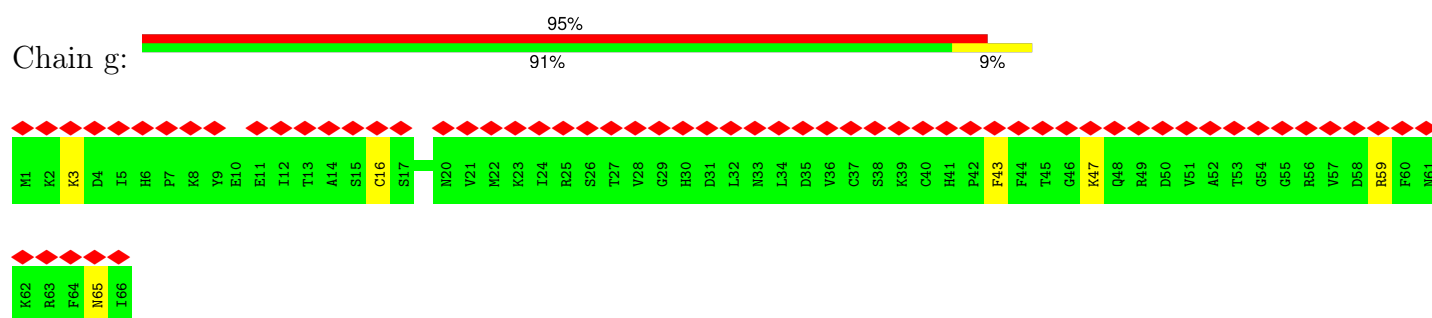
- Molecule 42: 50S ribosomal protein L29



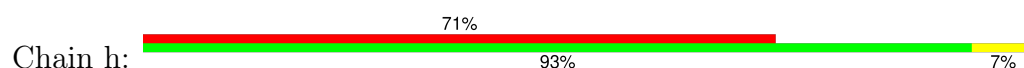
- Molecule 43: 50S ribosomal protein L30

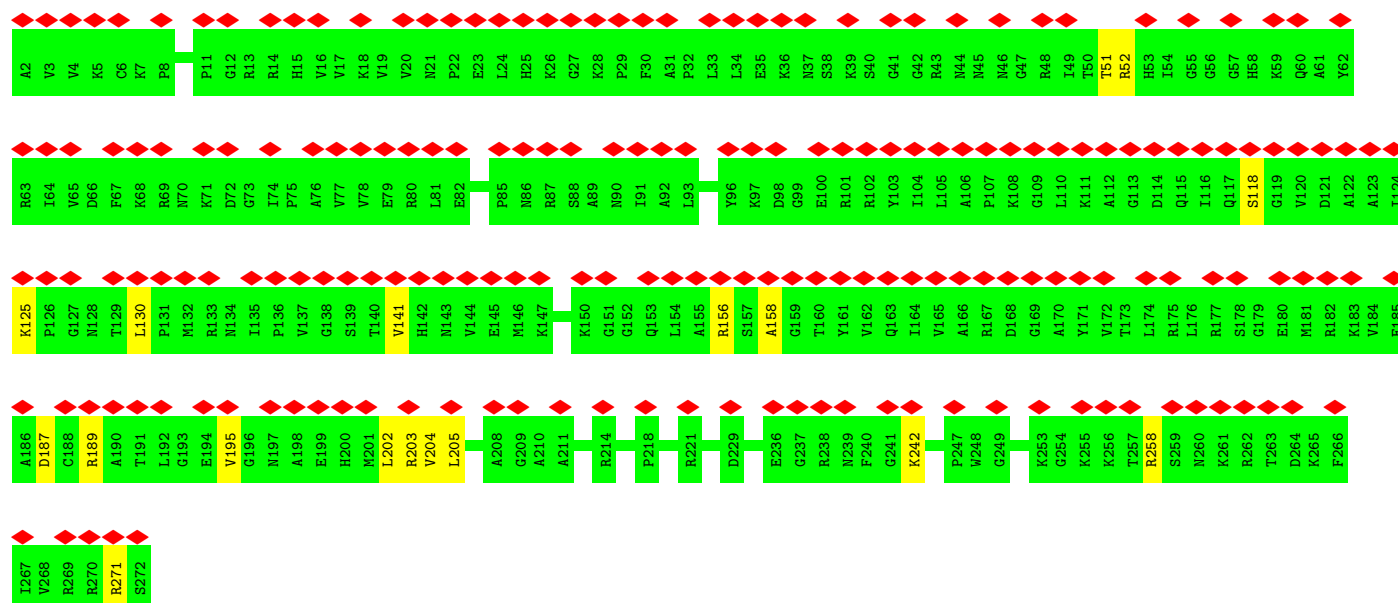


- Molecule 44: 50S ribosomal protein L31



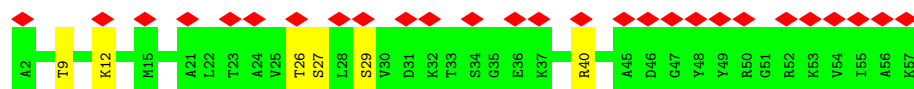
- Molecule 45: 50S ribosomal protein L2





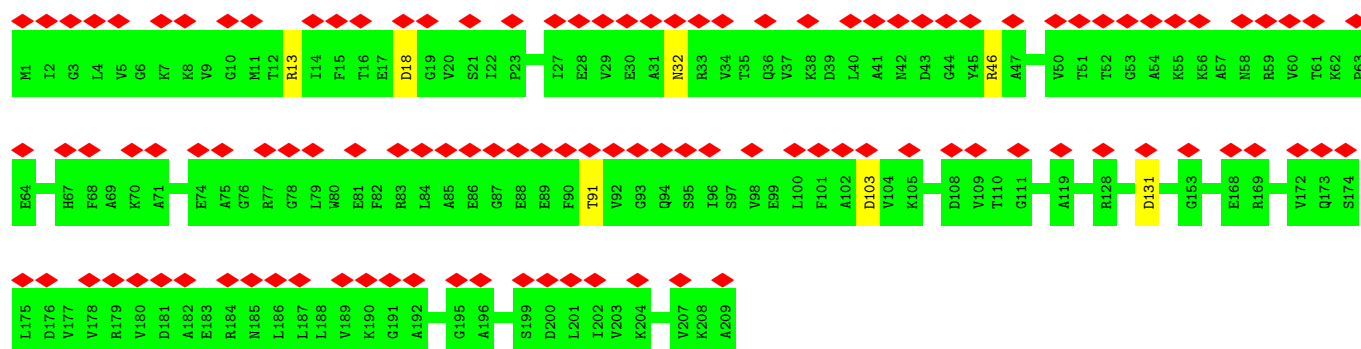
• Molecule 46: 50S ribosomal protein L32

Chain i:



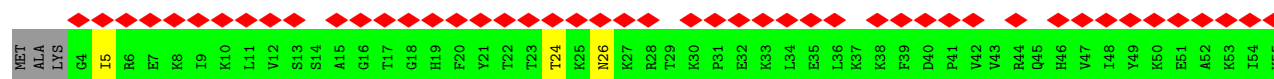
• Molecule 47: 50S ribosomal protein L3

Chain j:

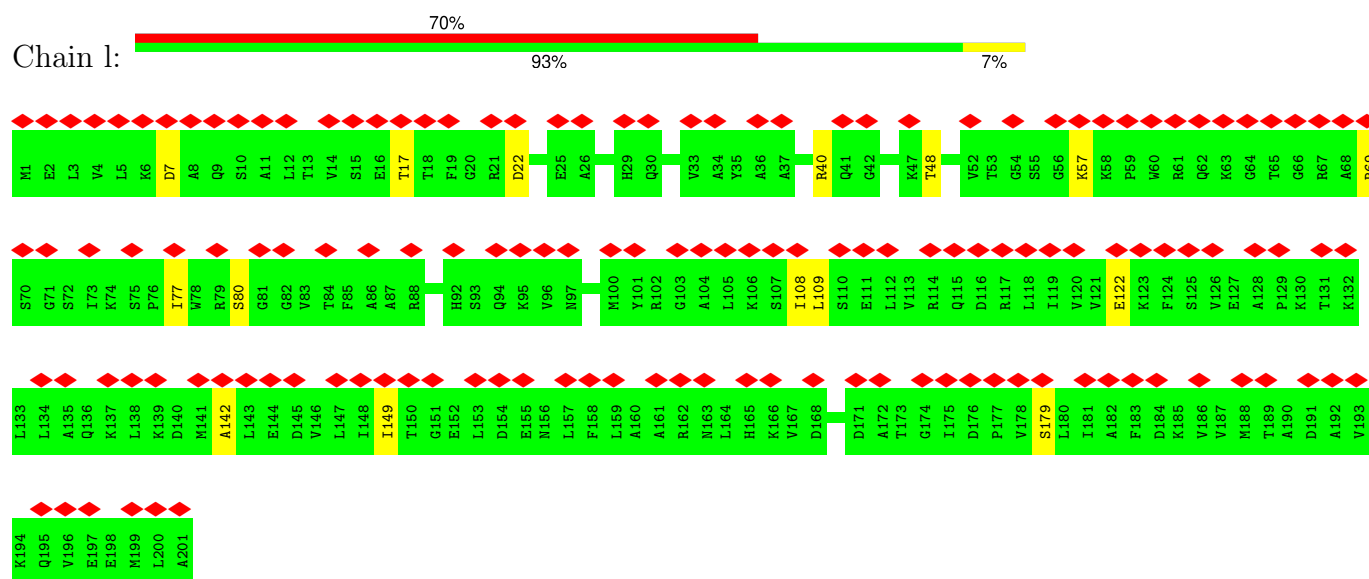


• Molecule 48: 50S ribosomal protein L33

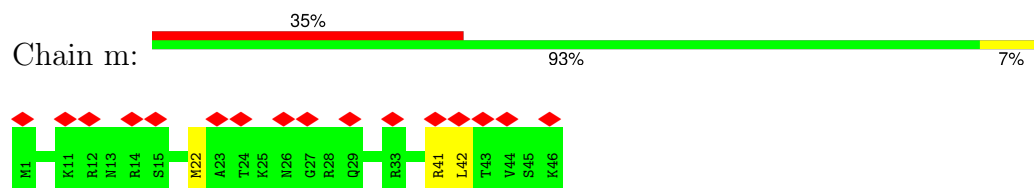
Chain k:



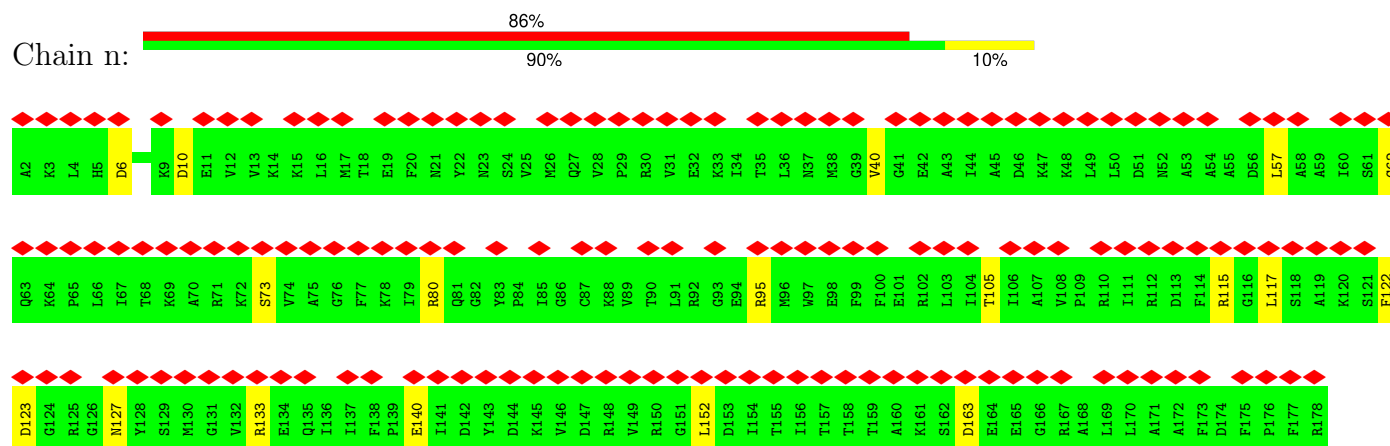
• Molecule 49: 50S ribosomal protein L4



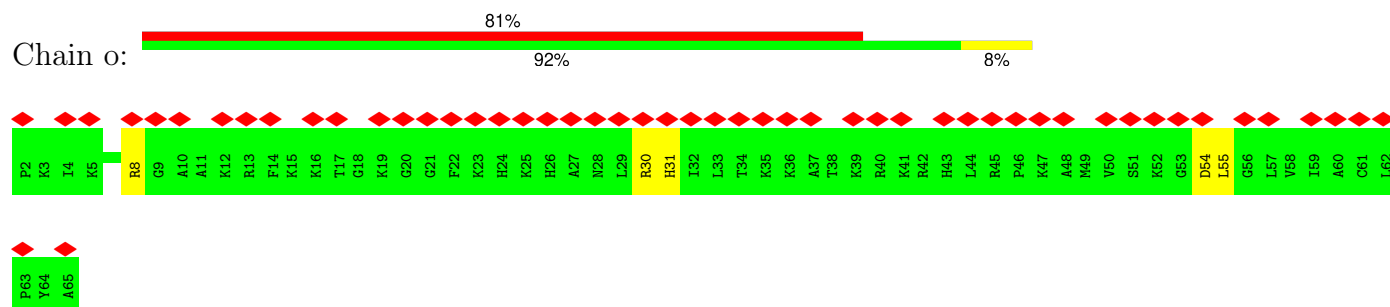
- Molecule 50: 50S ribosomal protein L34



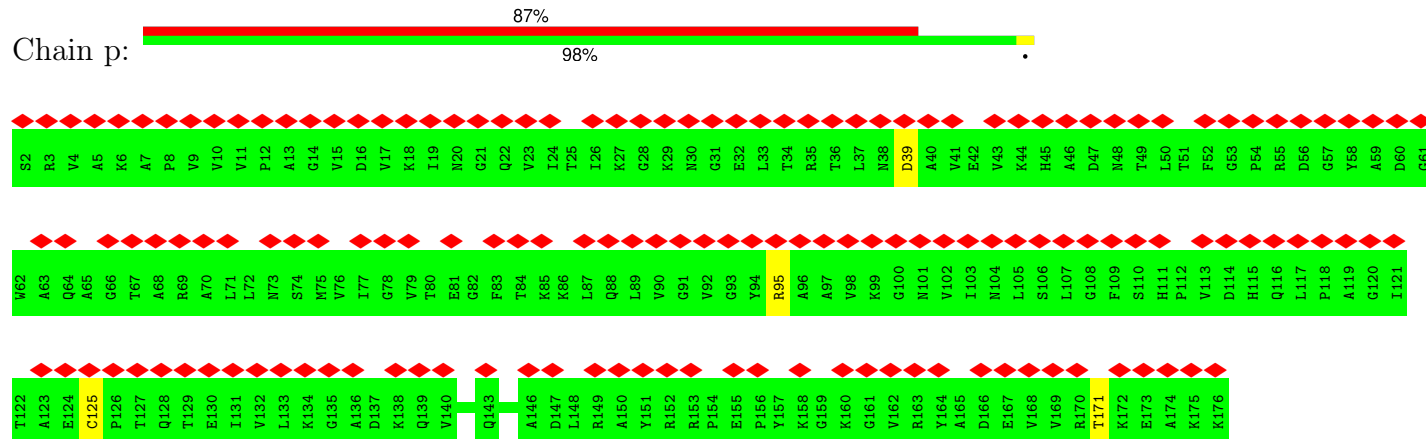
- Molecule 51: 50S ribosomal protein L5



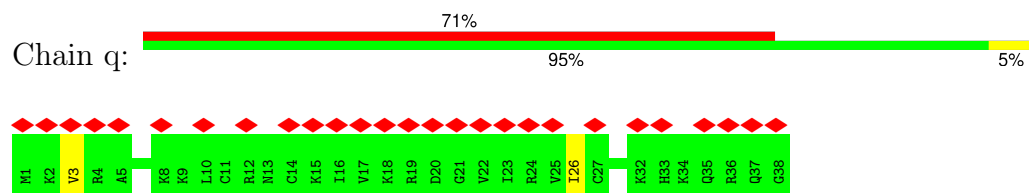
- Molecule 52: 50S ribosomal protein L35



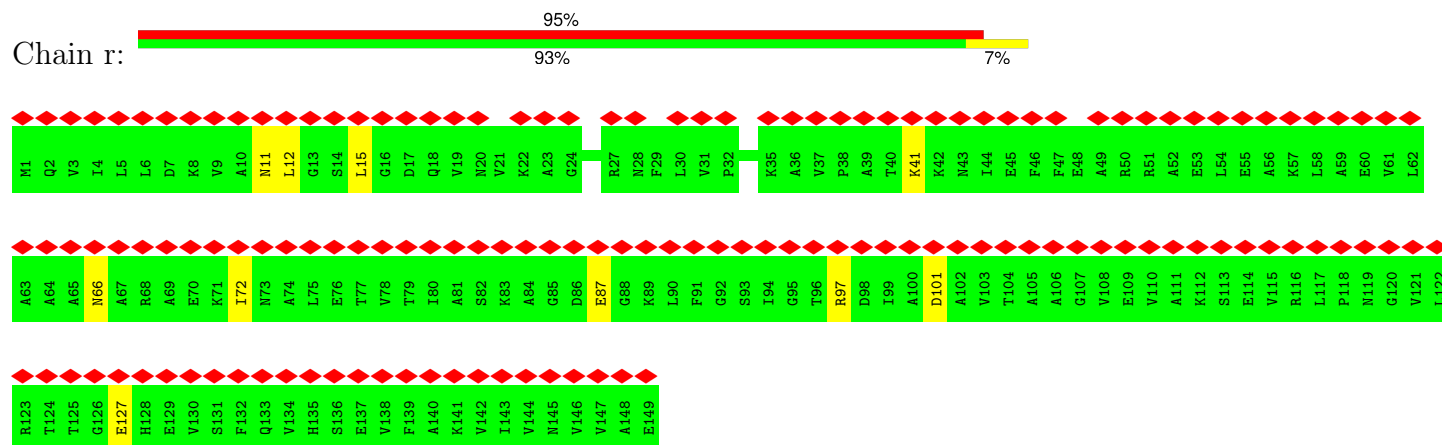
- Molecule 53: 50S ribosomal protein L6



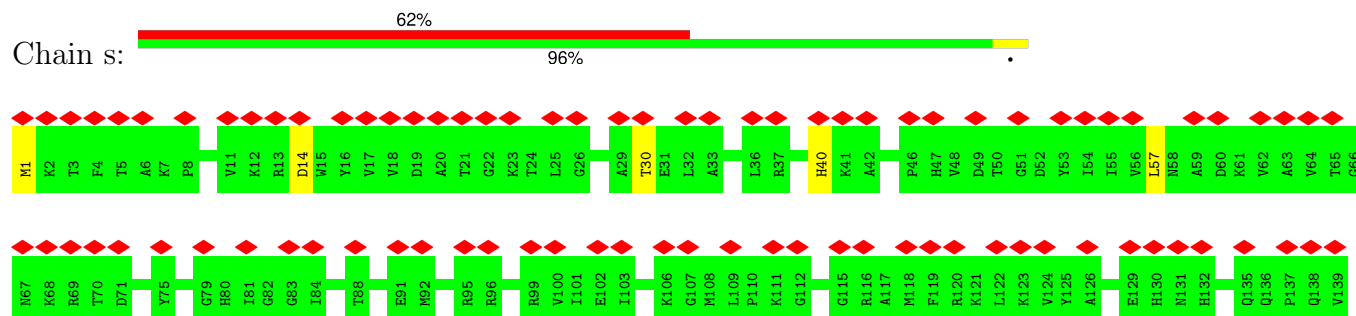
- Molecule 54: 50S ribosomal protein L36



- Molecule 55: 50S ribosomal protein L9

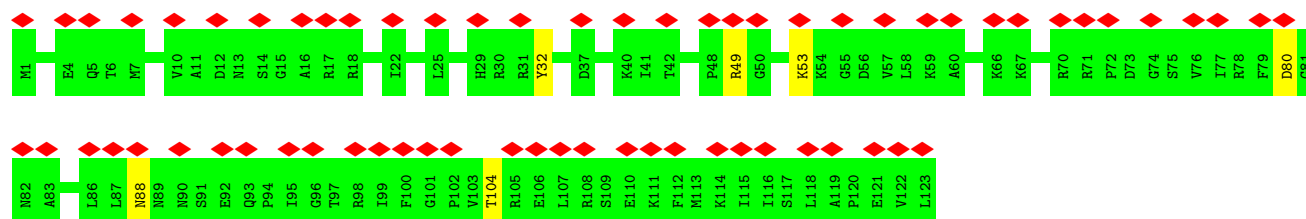


- Molecule 56: 50S ribosomal protein L13

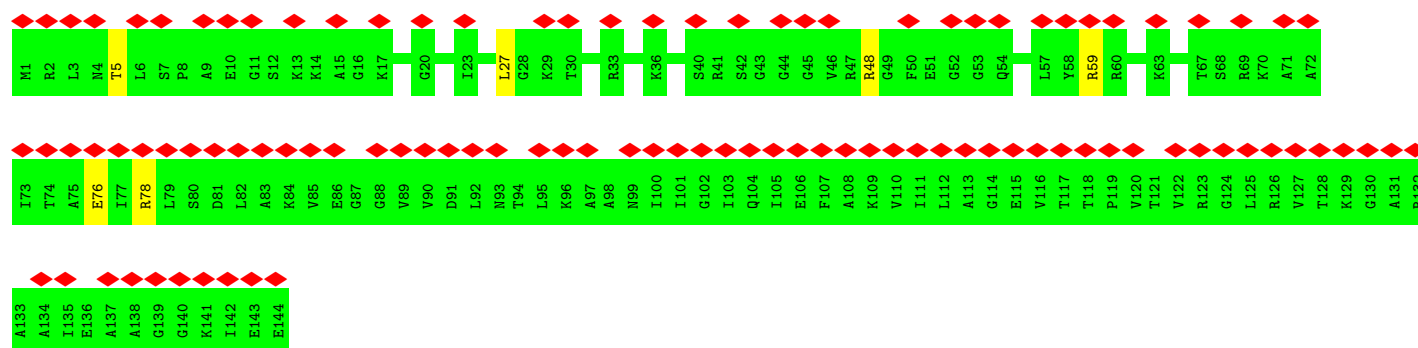




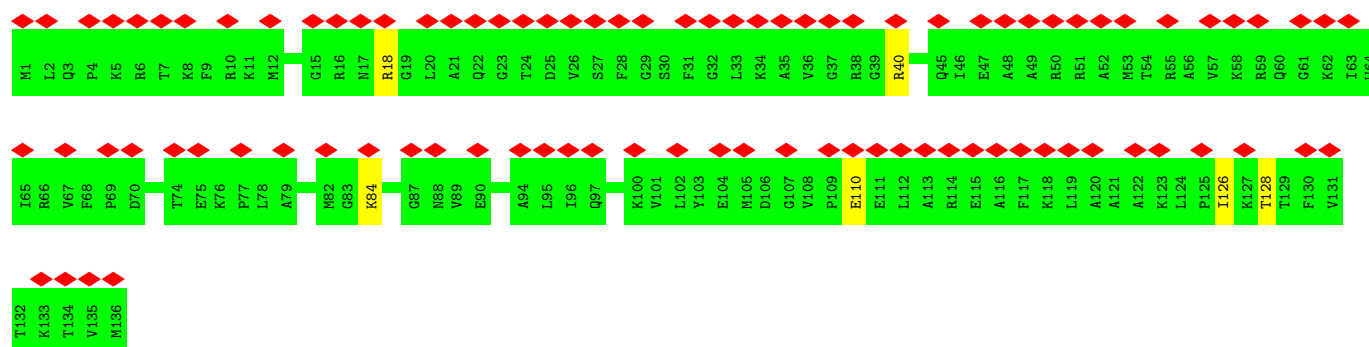
- Molecule 57: 50S ribosomal protein L14



- Molecule 58: 50S ribosomal protein L15

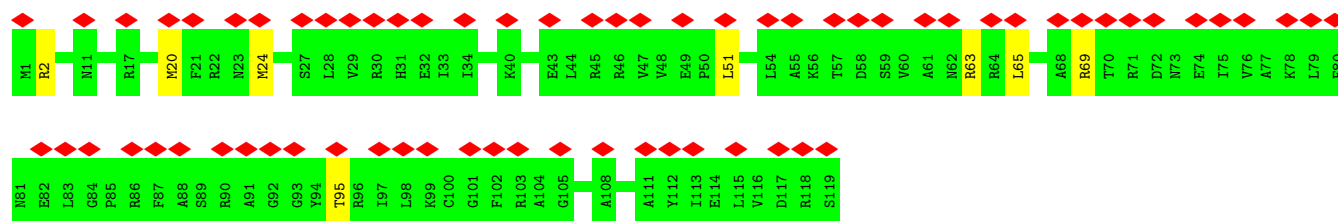


- Molecule 59: 50S ribosomal protein L16

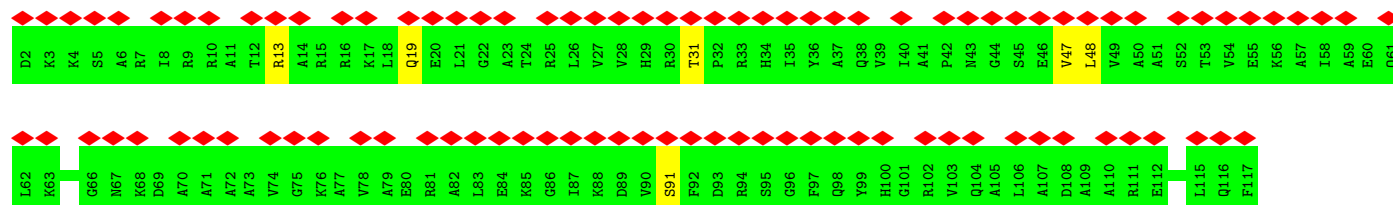
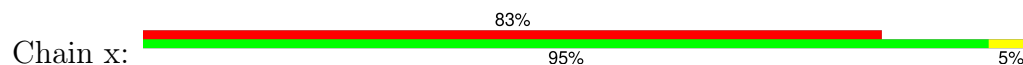


- Molecule 60: 50S ribosomal protein L17

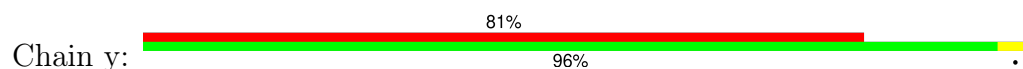




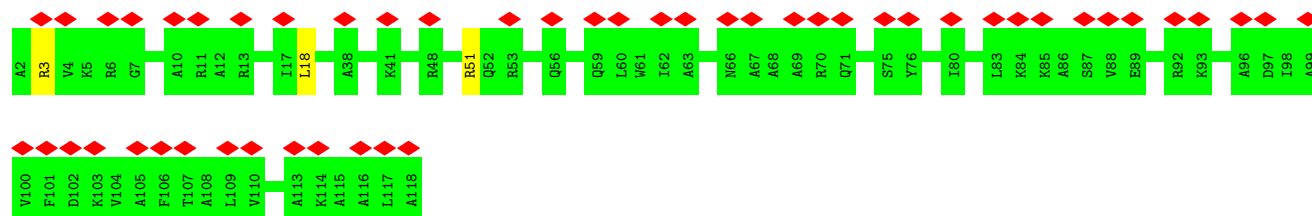
• Molecule 61: 50S ribosomal protein L18



• Molecule 62: 50S ribosomal protein L19



• Molecule 63: 50S ribosomal protein L20



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	27650	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.067	Depositor
Minimum map value	-0.032	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.017	Depositor
Map size ( $\text{\AA}$ )	532.48, 532.48, 532.48	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.04, 1.04, 1.04	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.38	0/829	0.67	0/1107
2	1	0.49	0/864	0.82	0/1156
3	2	0.41	0/752	0.71	0/1005
4	3	0.35	0/796	0.66	2/1062 (0.2%)
5	4	0.40	0/766	0.68	0/1025
6	5	1.13	6/528 (1.1%)	0.97	1/810 (0.1%)
7	6	1.11	4/603 (0.7%)	0.97	0/926
8	7	0.57	2/747 (0.3%)	0.88	3/1160 (0.3%)
9	9	0.79	2/1131 (0.2%)	0.64	1/1524 (0.1%)
10	A	0.38	0/1810	0.75	1/2821 (0.0%)
10	B	0.46	1/1810 (0.1%)	0.86	7/2821 (0.2%)
11	AA	0.58	2/10591 (0.0%)	0.75	15/14289 (0.1%)
12	AC	0.48	0/1808	0.62	1/2450 (0.0%)
12	AD	0.39	0/1789	0.57	0/2425
13	AE	0.52	4/10545 (0.0%)	0.66	5/14236 (0.0%)
14	C	0.48	0/553	0.83	0/743
15	D	0.34	10/36610 (0.0%)	0.74	30/57091 (0.1%)
16	E	0.57	0/675	0.85	0/895
17	F	0.56	0/597	0.87	0/792
18	G	0.49	0/1791	0.71	0/2413
19	H	0.54	1/1746 (0.1%)	1.03	13/2382 (0.5%)
20	I	0.43	0/1663	0.71	0/2241
21	J	0.47	0/1665	0.73	0/2227
22	K	0.45	0/1165	0.75	0/1568
23	L	0.43	0/867	0.75	1/1171 (0.1%)
24	M	0.50	0/1195	0.81	0/1602
25	N	0.41	0/989	0.69	0/1326
26	O	0.43	0/1034	0.75	0/1375
27	P	0.43	0/800	0.75	0/1082
28	Q	0.40	0/893	0.70	0/1205
29	R	0.35	0/952	0.74	0/1274
30	S	0.49	0/817	0.79	0/1088



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
31	T	0.53	0/722	0.86	0/964
32	U	0.44	0/659	0.78	0/884
33	V	0.34	0/657	0.62	0/881
34	W	0.38	0/680	0.62	0/915
35	X	0.49	0/909	0.86	0/1215
36	Y	0.67	0/1046	0.59	0/1410
37	Z	0.69	0/227	0.57	0/304
38	a	0.38	3/69247 (0.0%)	0.72	17/107985 (0.0%)
39	b	0.39	0/589	0.71	0/779
40	c	0.48	0/635	0.82	2/848 (0.2%)
41	d	0.29	0/2872	0.70	0/4478
42	e	0.53	0/502	0.83	0/667
43	f	0.45	0/452	0.78	0/605
44	g	0.43	0/531	0.68	0/709
45	h	0.39	0/2121	0.78	0/2852
46	i	0.40	0/450	0.79	0/599
47	j	0.44	0/1586	0.69	0/2134
48	k	0.35	0/433	0.64	0/576
49	l	0.46	0/1571	0.77	0/2113
50	m	0.53	0/380	0.99	0/498
51	n	0.49	0/1434	0.88	3/1926 (0.2%)
52	o	0.45	0/513	0.83	0/676
53	p	0.39	0/1333	0.67	0/1805
54	q	0.37	0/303	0.77	0/397
55	r	0.43	0/1122	0.69	0/1515
56	s	0.50	0/1152	0.75	0/1551
57	t	0.41	0/955	0.78	0/1279
58	u	0.40	0/1062	0.76	0/1413
59	v	0.47	0/1093	0.82	0/1460
60	w	0.52	0/964	0.87	0/1289
61	x	0.46	0/902	0.81	0/1209
62	y	0.41	0/929	0.73	1/1242 (0.1%)
63	z	0.60	0/960	0.91	0/1278
All	All	0.43	35/188372 (0.0%)	0.74	103/277748 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
10	A	0	2

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

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	13.73	1.70	1.47
15	D	1516	G	O3'-P	-13.42	1.45	1.61
15	D	1339	A	O3'-P	10.59	1.73	1.61
11	AA	374	GLU	C-N	10.44	1.54	1.34
13	AE	88	CYS	CB-SG	-10.14	1.65	1.82

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	D	1516	G	P-O3'-C3'	-18.99	96.91	119.70
15	D	1516	G	O3'-P-O5'	13.81	130.24	104.00
11	AA	1250	SER	C-N-CA	11.14	149.56	121.70
38	a	2252	G	N9-C1'-C2'	-10.93	99.80	114.00
15	D	1401	G	N9-C1'-C2'	-10.68	100.12	114.00

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

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

## 5.2 Too-close contacts

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

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	13	48
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/100 (92%)	90 (98%)	2 (2%)	0	100	100
4	3	101/104 (97%)	96 (95%)	4 (4%)	1 (1%)	13	48
5	4	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
9	9	146/165 (88%)	95 (65%)	37 (25%)	14 (10%)	0	9
11	AA	1318/1342 (98%)	1150 (87%)	136 (10%)	32 (2%)	5	30
12	AC	228/329 (69%)	215 (94%)	11 (5%)	2 (1%)	14	50
12	AD	226/329 (69%)	212 (94%)	14 (6%)	0	100	100
13	AE	1329/1407 (94%)	1200 (90%)	120 (9%)	9 (1%)	19	56
14	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
16	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
17	F	68/71 (96%)	68 (100%)	0	0	100	100
18	G	223/241 (92%)	210 (94%)	13 (6%)	0	100	100
19	H	255/557 (46%)	188 (74%)	55 (22%)	12 (5%)	2	19
20	I	206/233 (88%)	197 (96%)	8 (4%)	1 (0%)	25	62
21	J	203/205 (99%)	198 (98%)	5 (2%)	0	100	100
22	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	22	59
23	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	13	48
24	M	149/151 (99%)	144 (97%)	4 (3%)	1 (1%)	19	56
25	N	127/129 (98%)	121 (95%)	5 (4%)	1 (1%)	16	53
26	O	125/127 (98%)	115 (92%)	9 (7%)	1 (1%)	16	53
27	P	97/99 (98%)	88 (91%)	8 (8%)	1 (1%)	13	48
28	Q	115/117 (98%)	104 (90%)	9 (8%)	2 (2%)	7	37
29	R	117/123 (95%)	116 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	S	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
31	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
32	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	10	42
33	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
34	W	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
35	X	114/116 (98%)	107 (94%)	5 (4%)	2 (2%)	7	36
36	Y	139/141 (99%)	102 (73%)	25 (18%)	12 (9%)	0	10
37	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	13
39	b	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
40	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
42	e	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
43	f	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
44	g	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
45	h	269/271 (99%)	259 (96%)	9 (3%)	1 (0%)	30	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	50/55 (91%)	50 (100%)	0	0	100	100
49	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	25	62
50	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
51	n	175/177 (99%)	162 (93%)	11 (6%)	2 (1%)	12	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	z	115/117 (98%)	110 (96%)	4 (4%)	1 (1%)	14	50
All	All	9274/10209 (91%)	8519 (92%)	653 (7%)	102 (1%)	15	46

5 of 102 Ramachandran outliers are listed below:

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

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	78 (93%)	6 (7%)	12	34
2	1	93/93 (100%)	84 (90%)	9 (10%)	6	23
3	2	81/84 (96%)	76 (94%)	5 (6%)	15	38
4	3	84/85 (99%)	78 (93%)	6 (7%)	12	34
5	4	78/78 (100%)	74 (95%)	4 (5%)	20	43
9	9	112/123 (91%)	65 (58%)	47 (42%)	0	0
11	AA	1140/1157 (98%)	1039 (91%)	101 (9%)	8	27
12	AC	198/286 (69%)	182 (92%)	16 (8%)	9	31
12	AD	196/286 (68%)	194 (99%)	2 (1%)	73	81
13	AE	1120/1168 (96%)	1051 (94%)	69 (6%)	15	38
14	C	57/65 (88%)	55 (96%)	2 (4%)	31	53
16	E	65/66 (98%)	60 (92%)	5 (8%)	10	32
17	F	60/61 (98%)	57 (95%)	3 (5%)	20	44
18	G	187/199 (94%)	178 (95%)	9 (5%)	21	45
19	H	137/461 (30%)	128 (93%)	9 (7%)	14	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	I	171/190 (90%)	165 (96%)	6 (4%)	31	53
21	J	172/172 (100%)	165 (96%)	7 (4%)	26	49
22	K	119/126 (94%)	112 (94%)	7 (6%)	16	40
23	L	91/116 (78%)	85 (93%)	6 (7%)	14	36
24	M	124/124 (100%)	116 (94%)	8 (6%)	14	37
25	N	104/104 (100%)	102 (98%)	2 (2%)	52	69
26	O	105/105 (100%)	100 (95%)	5 (5%)	21	45
27	P	86/86 (100%)	77 (90%)	9 (10%)	5	21
28	Q	90/90 (100%)	87 (97%)	3 (3%)	33	55
29	R	101/103 (98%)	94 (93%)	7 (7%)	13	35
30	S	83/84 (99%)	79 (95%)	4 (5%)	21	45
31	T	76/77 (99%)	64 (84%)	12 (16%)	2	13
32	U	65/65 (100%)	61 (94%)	4 (6%)	15	38
33	V	74/78 (95%)	72 (97%)	2 (3%)	40	61
34	W	72/72 (100%)	68 (94%)	4 (6%)	17	41
35	X	94/94 (100%)	85 (90%)	9 (10%)	7	24
36	Y	109/109 (100%)	72 (66%)	37 (34%)	0	1
37	Z	26/85 (31%)	12 (46%)	14 (54%)	0	0
39	b	58/58 (100%)	57 (98%)	1 (2%)	56	72
40	c	67/68 (98%)	64 (96%)	3 (4%)	23	47
42	e	54/54 (100%)	53 (98%)	1 (2%)	52	69
43	f	48/48 (100%)	46 (96%)	2 (4%)	25	49
44	g	59/59 (100%)	53 (90%)	6 (10%)	6	22
45	h	216/216 (100%)	199 (92%)	17 (8%)	10	32
46	i	47/47 (100%)	41 (87%)	6 (13%)	3	17
47	j	164/164 (100%)	157 (96%)	7 (4%)	25	48
48	k	47/49 (96%)	44 (94%)	3 (6%)	14	37
49	l	165/165 (100%)	151 (92%)	14 (8%)	8	30
50	m	38/38 (100%)	35 (92%)	3 (8%)	10	32
51	n	148/148 (100%)	134 (90%)	14 (10%)	7	24
52	o	51/51 (100%)	46 (90%)	5 (10%)	6	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
53	p	136/136 (100%)	132 (97%)	4 (3%)	37 58
54	q	34/34 (100%)	32 (94%)	2 (6%)	16 40
55	r	114/114 (100%)	104 (91%)	10 (9%)	8 28
56	s	116/116 (100%)	110 (95%)	6 (5%)	19 43
57	t	104/104 (100%)	98 (94%)	6 (6%)	17 40
58	u	103/103 (100%)	97 (94%)	6 (6%)	17 40
59	v	109/109 (100%)	103 (94%)	6 (6%)	18 42
60	w	99/99 (100%)	91 (92%)	8 (8%)	9 31
61	x	86/86 (100%)	80 (93%)	6 (7%)	12 35
62	y	99/99 (100%)	95 (96%)	4 (4%)	27 50
63	z	89/89 (100%)	87 (98%)	2 (2%)	47 65
All	All	7705/8430 (91%)	7124 (92%)	581 (8%)	14 33

5 of 581 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	h	203	ARG
61	x	48	LEU
47	j	18	ASP
45	h	202	LEU
52	o	55	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
22	K	70	ASN
35	X	105	ASN
58	u	4	ASN
11	AA	1236	ASN
9	9	103	ASN

### 5.3.3 RNA ⓘ

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

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	D	1515/1542 (98%)	288 (19%)	35 (2%)
38	a	2859/2904 (98%)	532 (18%)	0
41	d	119/120 (99%)	17 (14%)	0
8	7	31/32 (96%)	21 (67%)	3 (9%)
All	All	4674/4750 (98%)	922 (19%)	50 (1%)

5 of 922 RNA backbone outliers are listed below:

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

5 of 50 RNA pucker outliers are listed below:

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

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.



There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

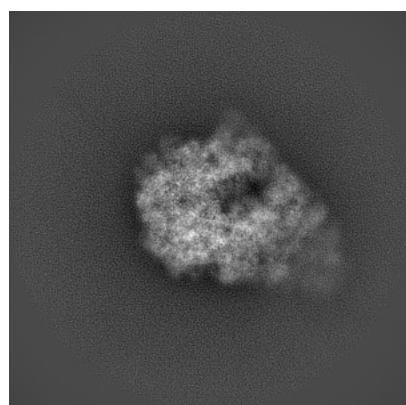
## 6 Map visualisation [i](#)

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

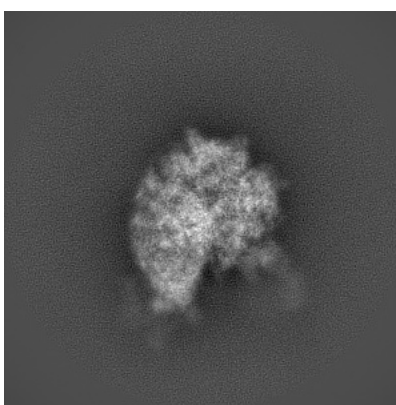
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

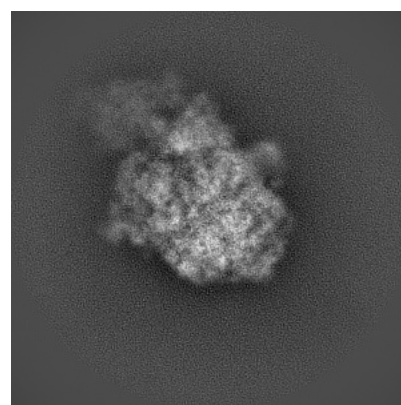
#### 6.1.1 Primary map



X



Y

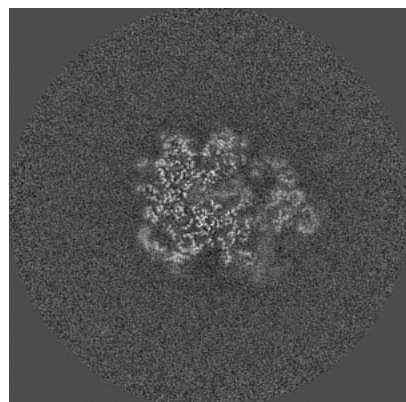


Z

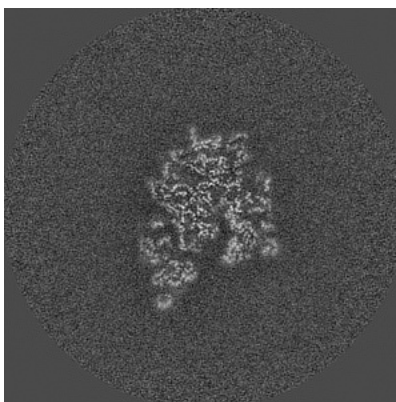
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

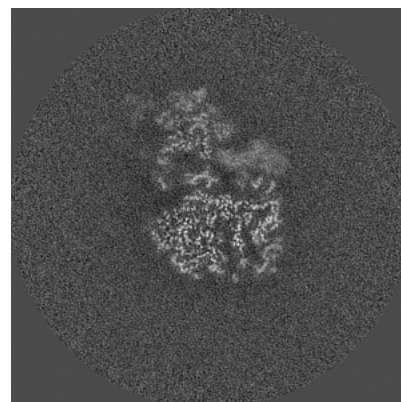
#### 6.2.1 Primary map



X Index: 256



Y Index: 256

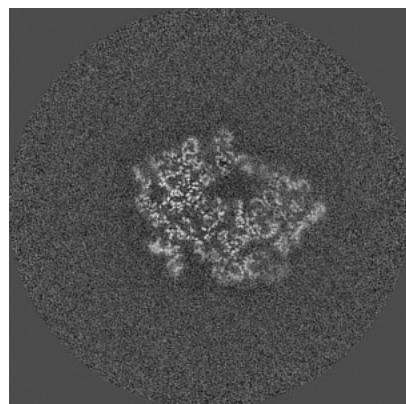


Z Index: 256

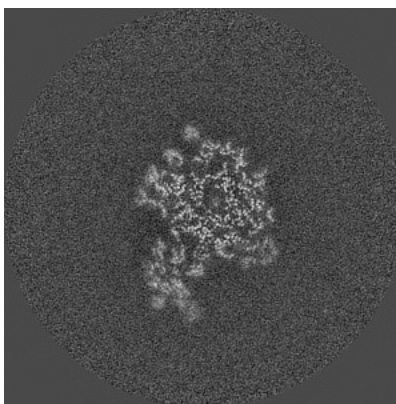
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

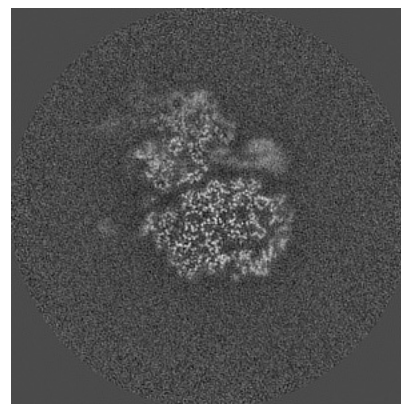
### 6.3.1 Primary map



X Index: 240



Y Index: 231

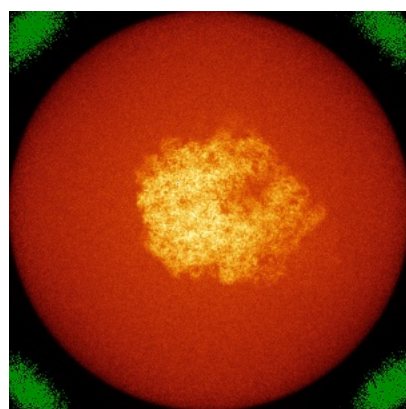


Z Index: 248

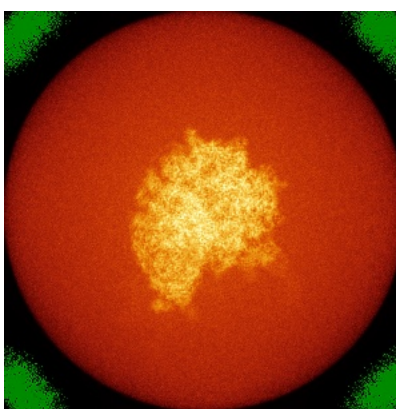
The images above show the largest variance slices of the map in three orthogonal directions.

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

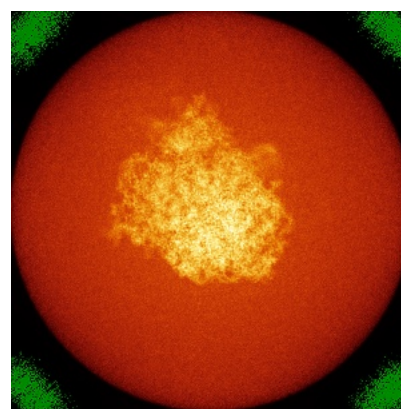
### 6.4.1 Primary map



X



Y

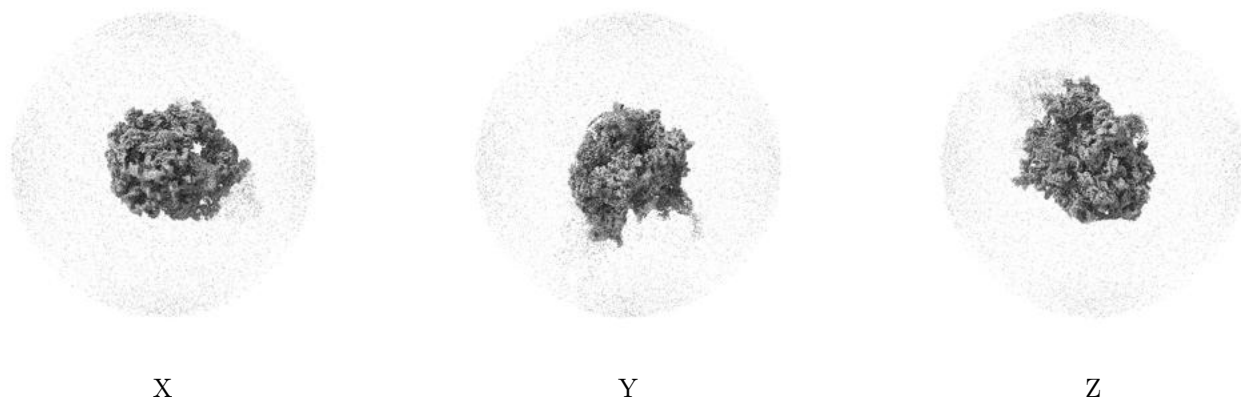


Z

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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



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

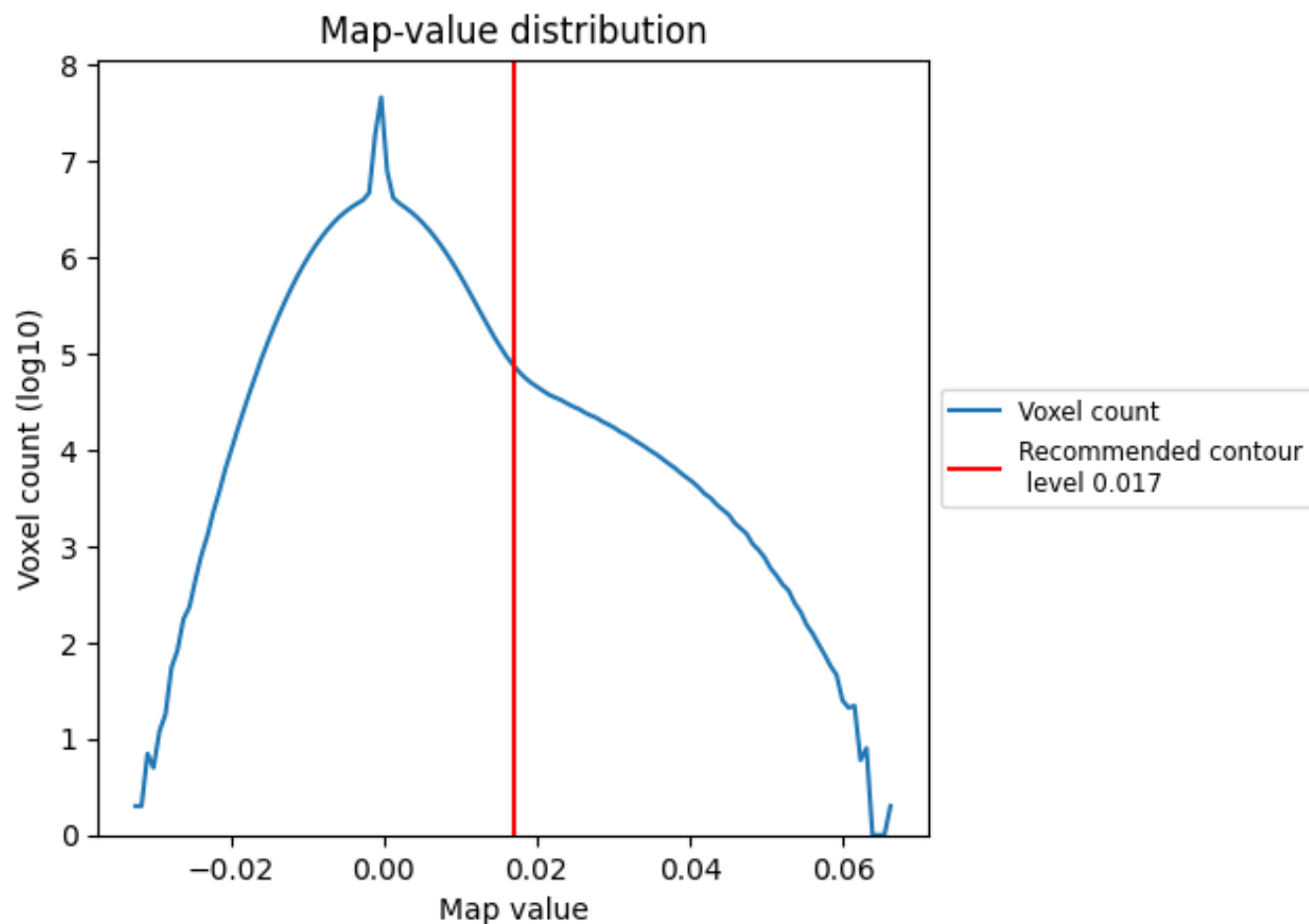
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

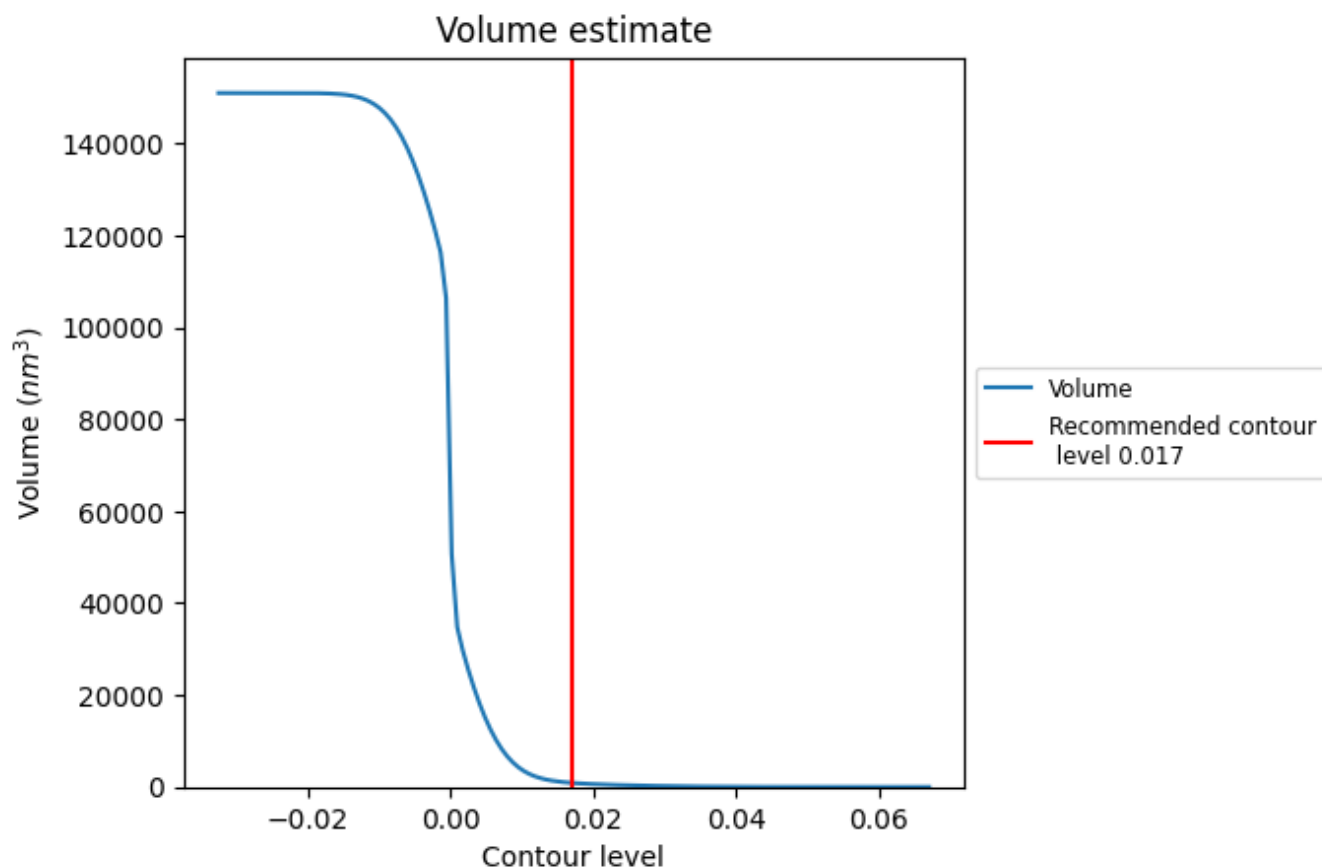
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

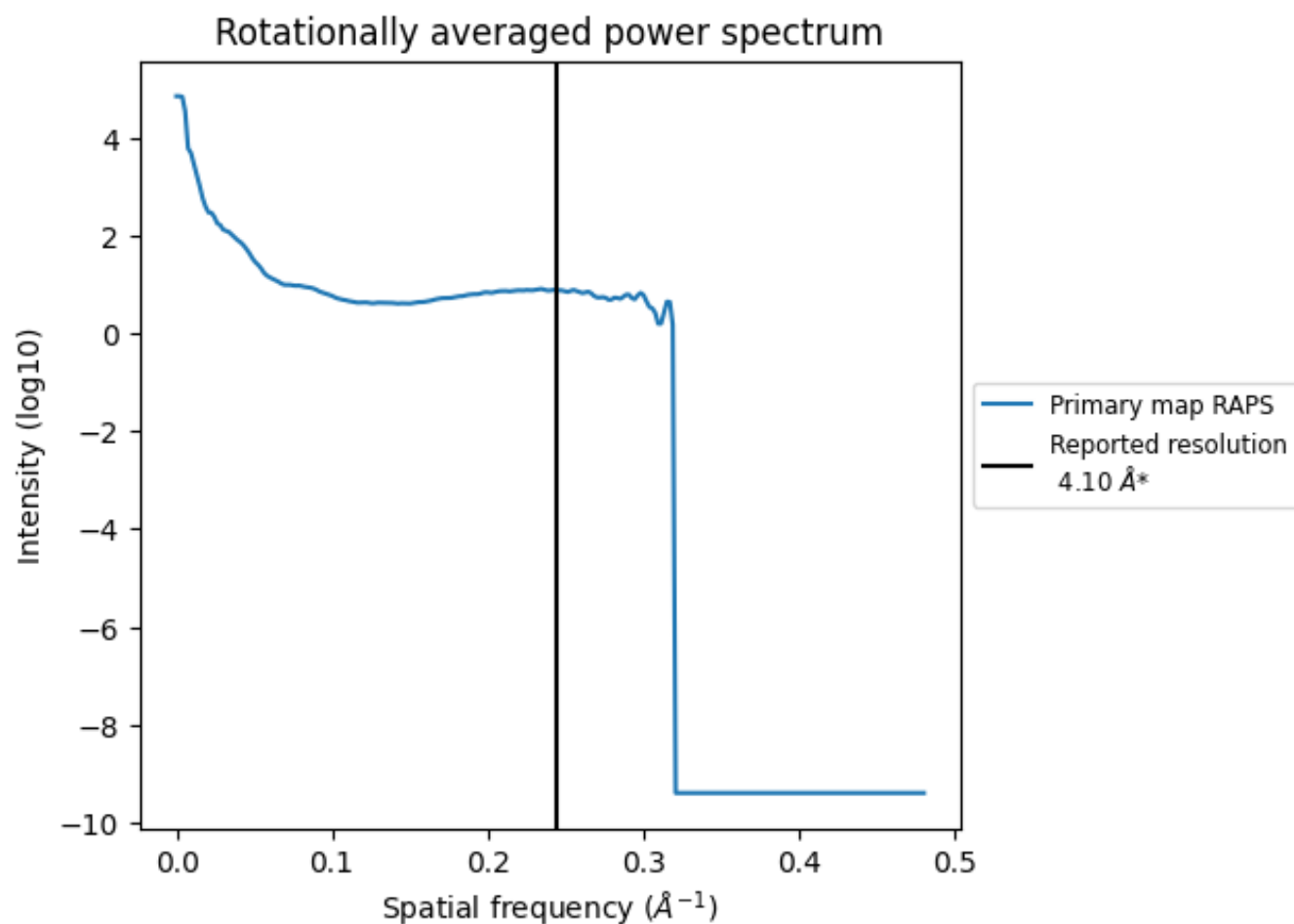
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 887 nm<sup>3</sup>; this corresponds to an approximate mass of 801 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ



\*Reported resolution corresponds to spatial frequency of 0.244  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation ⓘ

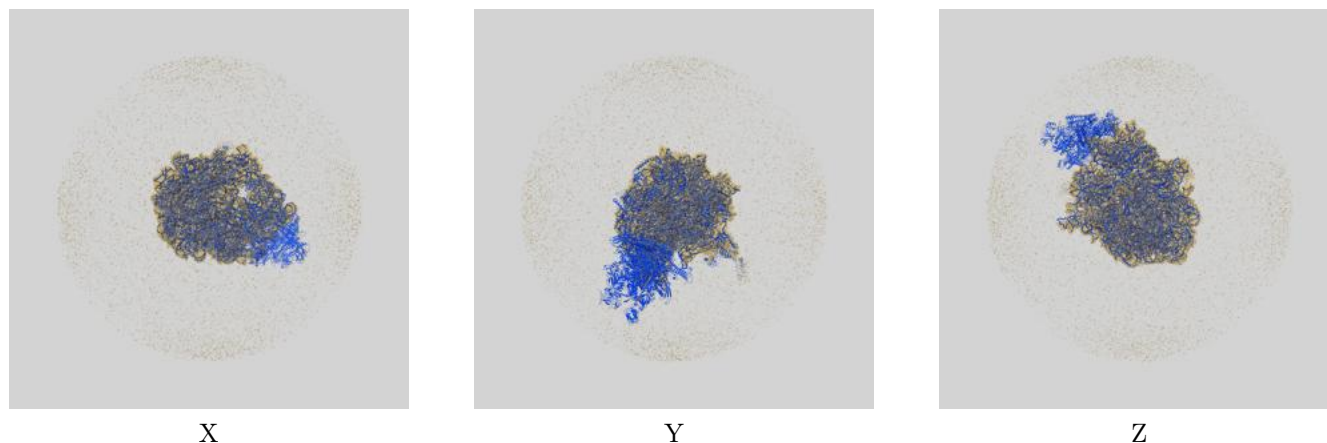
This section was not generated. No FSC curve or half-maps provided.



## 9 Map-model fit [i](#)

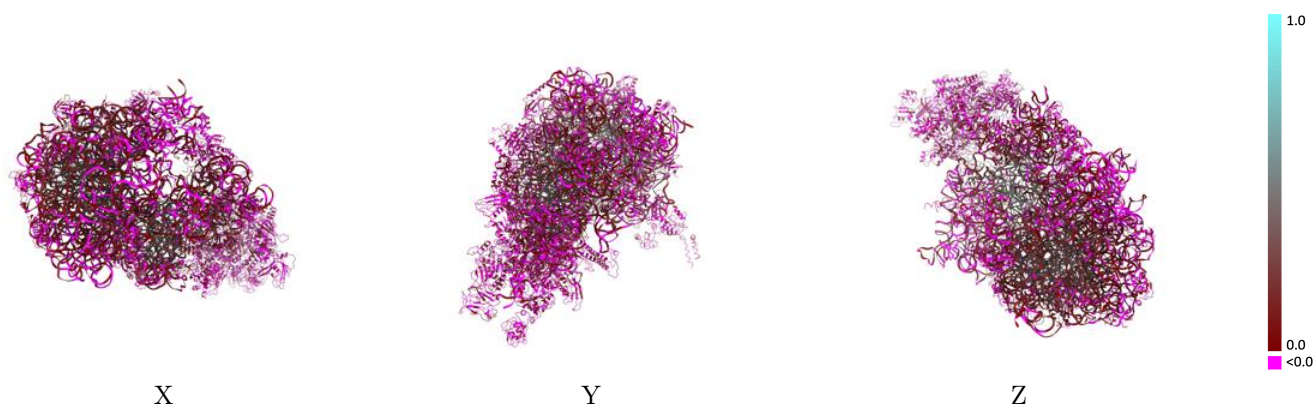
This section contains information regarding the fit between EMDB map EMD-21494 and PDB model 6VZJ. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

### 9.1 Map-model overlay [i](#)



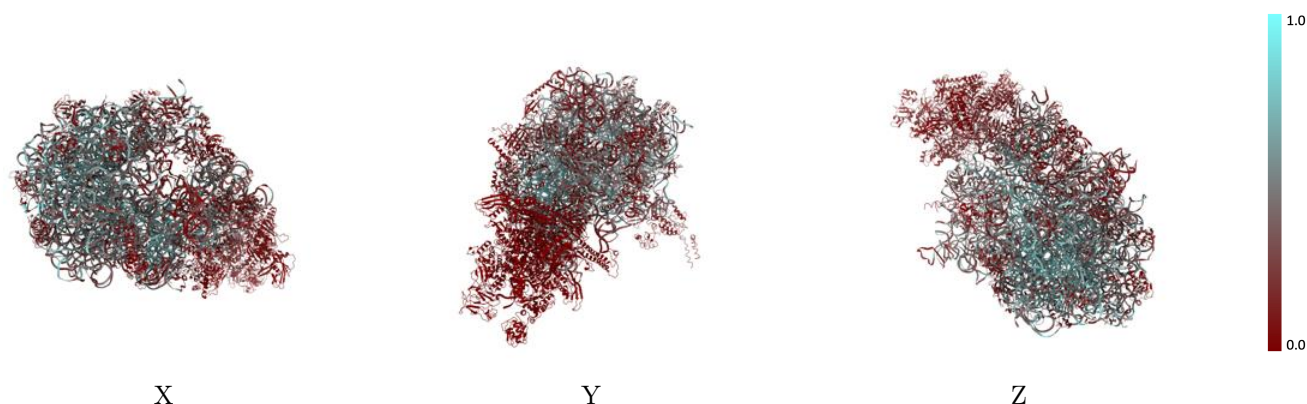
The images above show the 3D surface view of the map at the recommended contour level 0.017 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



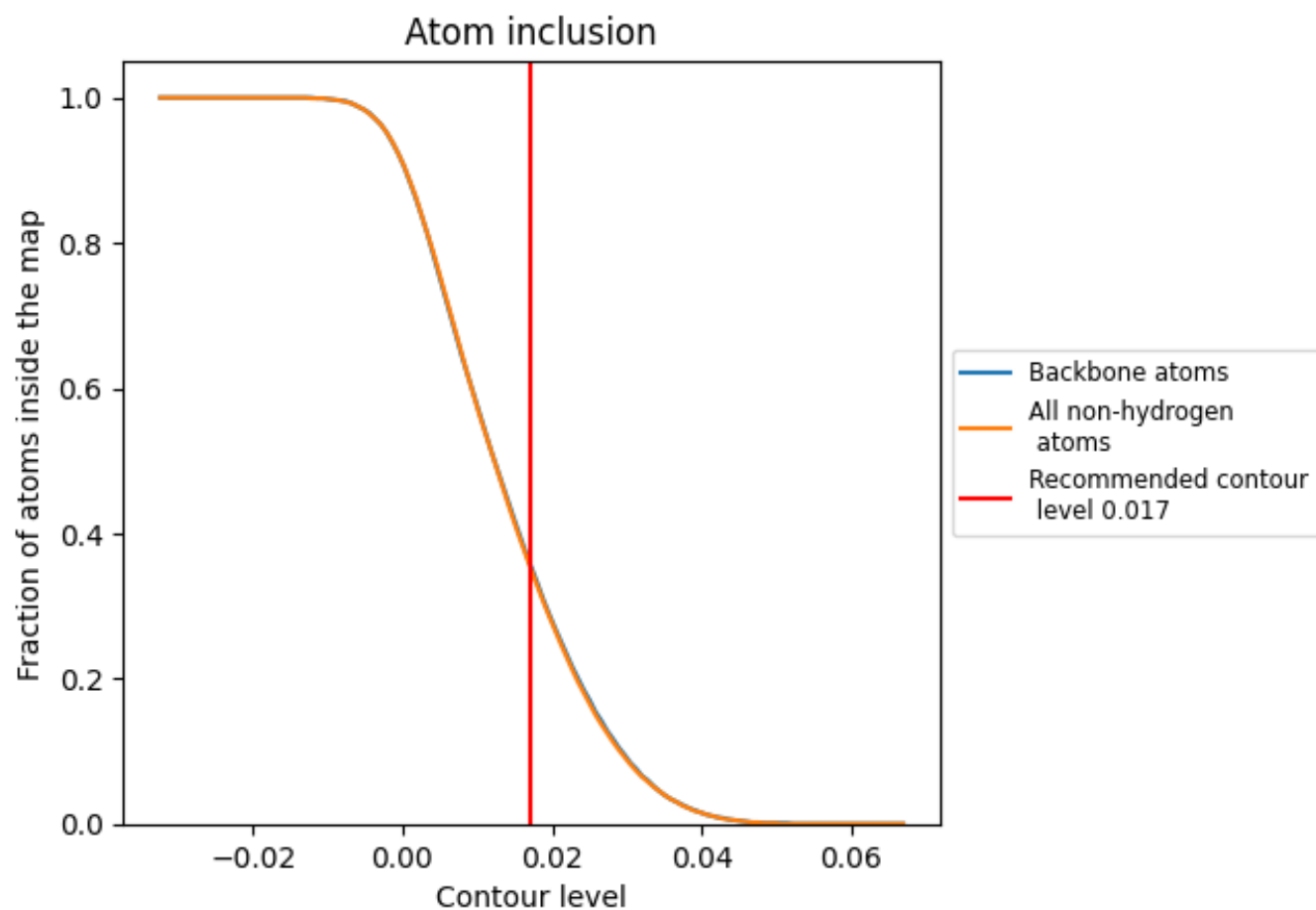
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.017).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 36% of all backbone atoms, 36% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ































































The table lists the average atom inclusion at the recommended contour level (0.017) and Q-score for the entire model and for each chain.

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



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