



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 01:44 PM UTC

PDB ID : 6X7F / pdb_00006x7f
EMDB ID : EMD-22084
Title : Cryo-EM structure of an Escherichia coli coupled transcription-translational complex B2 (TTC-B2) containing an mRNA with a 24 nt long spacer, transcription factors NusA and NusG, and fMet-tRNAs at P-site and E-site
Authors : Molodtsov, V.; Ebright, R.H.; Wang, C.; Su, M.
Deposited on : 2020-05-29
Resolution : 3.50 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

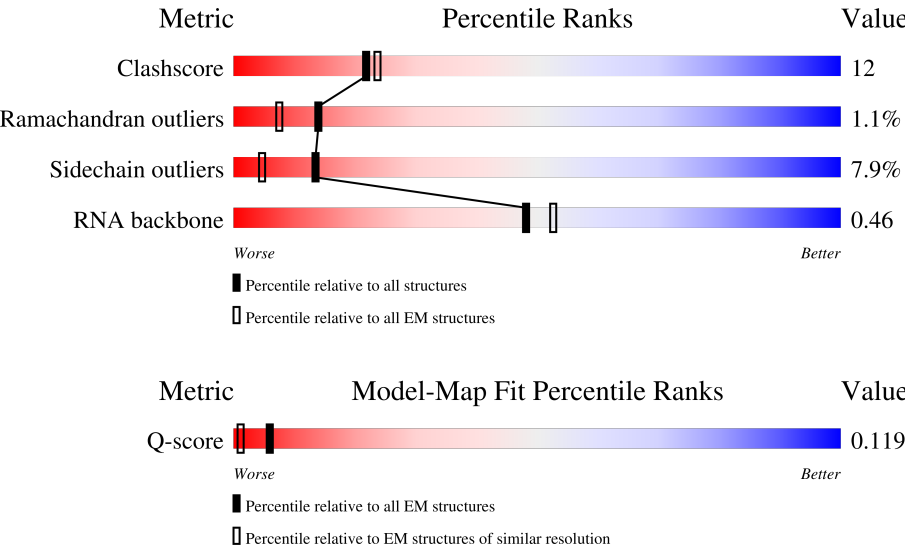
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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

Mol	Chain	Length	Quality of chain
1	0	103	42% 84% 15% .
2	1	110	41% 75% 25%
3	2	100	36% 86% 6% . 6%

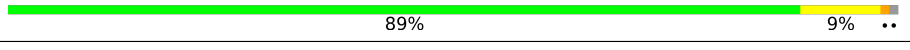
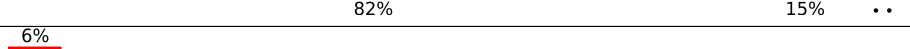
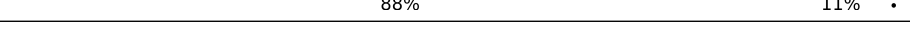
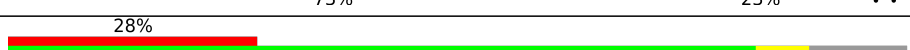
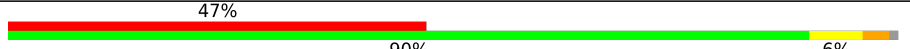
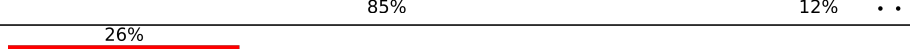
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Mol	Chain	Length	Quality of chain
4	3	104	
5	4	94	
6	5	36	
7	6	36	
8	7	41	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	181	
13	AC	329	
13	AD	329	
14	AE	1407	
15	AF	91	
16	AG	495	
17	C	75	
18	D	1542	
19	E	87	
20	F	71	
21	G	241	
22	H	557	
23	I	233	
24	J	206	
25	K	167	
26	L	135	

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Mol	Chain	Length	Quality of chain
27	M	179	
28	N	130	
29	O	130	
30	P	103	
31	Q	129	
32	R	124	
33	S	101	
34	T	89	
35	U	82	
36	V	84	
37	W	92	
38	X	118	
39	Y	142	
40	Z	121	
41	a	2904	
42	b	85	
43	c	78	
44	d	120	
45	e	63	
46	f	59	
47	g	70	
48	h	273	
49	i	57	
50	j	209	
51	k	55	

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Mol	Chain	Length	Quality of chain
52	l	201	
53	m	46	
54	n	179	
55	o	65	
56	p	177	
57	q	38	
58	r	149	
59	s	142	
60	t	123	
61	u	144	
62	v	136	
63	w	127	
64	x	117	
65	y	115	
66	z	118	

2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 291738 atoms, of which 109912 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 24 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	33	Total	C	H	N	O	P	0	0
			784	307	97	96	251	33		

- 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 1848954948
B	?	-	U	deletion	GB 1848954948

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AA	1340	Total	C	N	O	S	0	0
			10567	6631	1841	2052	43		

- Molecule 12 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AB	175	Total	C	N	O	S	0	0
			1403	889	250	257	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AC	301	Total	C	N	O	S	0	0
			2094	1296	379	413	6		
13	AD	297	Total	C	N	O	S	0	0
			2068	1281	376	405	6		

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	1384	VAL	MET	variant	UNP A0A4S1NBU2

- Molecule 15 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AF	82	Total	C	N	O	S	0	0
			650	396	122	131	1		

- Molecule 16 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AG	495	Total	C	N	O	S	0	0
			3852	2396	669	774	13		

- Molecule 17 is a protein called 30S ribosomal protein S18.

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

- Molecule 18 is a RNA chain called 16S rRNA.

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

- Molecule 19 is a protein called 30S ribosomal protein S20.

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

- Molecule 20 is a protein called 30S ribosomal protein S21.

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

- Molecule 21 is a protein called 30S ribosomal protein S2.

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

- Molecule 22 is a protein called 30S ribosomal protein S1.

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

- Molecule 23 is a protein called 30S ribosomal protein S3.

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

- Molecule 24 is a protein called 30S ribosomal protein S4.

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

- Molecule 25 is a protein called 30S ribosomal protein S5.

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

- Molecule 26 is a protein called 30S ribosomal protein S6.

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

- Molecule 27 is a protein called 30S ribosomal protein S7.

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

- Molecule 28 is a protein called 30S ribosomal protein S8.

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

- Molecule 29 is a protein called 30S ribosomal protein S9.

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

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

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

- Molecule 31 is a protein called 30S ribosomal protein S11.

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

- Molecule 32 is a protein called 30S ribosomal protein S12.

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

- Molecule 33 is a protein called 30S ribosomal protein S14.

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

- Molecule 34 is a protein called 30S ribosomal protein S15.

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

- Molecule 35 is a protein called 30S ribosomal protein S16.

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

- Molecule 36 is a protein called 30S ribosomal protein S17.

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

- Molecule 37 is a protein called 30S ribosomal protein S19.

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

- Molecule 38 is a protein called 30S ribosomal protein S13.

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

- Molecule 39 is a protein called 50S ribosomal protein L11.

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

- Molecule 40 is a protein called 50S ribosomal protein L7/L12.

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

- Molecule 41 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	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	variant	GB 937521852

- Molecule 42 is a protein called 50S ribosomal protein L27.

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

- Molecule 43 is a protein called 50S ribosomal protein L28.

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

- Molecule 44 is a RNA chain called 5S rRNA.

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

- Molecule 45 is a protein called 50S ribosomal protein L29.

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

- Molecule 46 is a protein called 50S ribosomal protein L30.

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

- Molecule 47 is a protein called 50S ribosomal protein L31.

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

- Molecule 48 is a protein called 50S ribosomal protein L2.

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

- Molecule 49 is a protein called 50S ribosomal protein L32.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L33.

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

- Molecule 52 is a protein called 50S ribosomal protein L4.

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

- Molecule 53 is a protein called 50S ribosomal protein L34.

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

- Molecule 54 is a protein called 50S ribosomal protein L5.

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

- Molecule 55 is a protein called 50S ribosomal protein L35.

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

- Molecule 56 is a protein called 50S ribosomal protein L6.

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

- Molecule 57 is a protein called 50S ribosomal protein L36.

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

- Molecule 58 is a protein called 50S ribosomal protein L9.

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

- Molecule 59 is a protein called 50S ribosomal protein L13.

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

- Molecule 60 is a protein called 50S ribosomal protein L14.

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

- Molecule 61 is a protein called 50S ribosomal protein L15.

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

- Molecule 62 is a protein called 50S ribosomal protein L16.

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

- Molecule 63 is a protein called 50S ribosomal protein L17.

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

- Molecule 64 is a protein called 50S ribosomal protein L18.

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

- Molecule 65 is a protein called 50S ribosomal protein L19.

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

- Molecule 66 is a protein called 50S ribosomal protein L20.

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

- Molecule 67 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

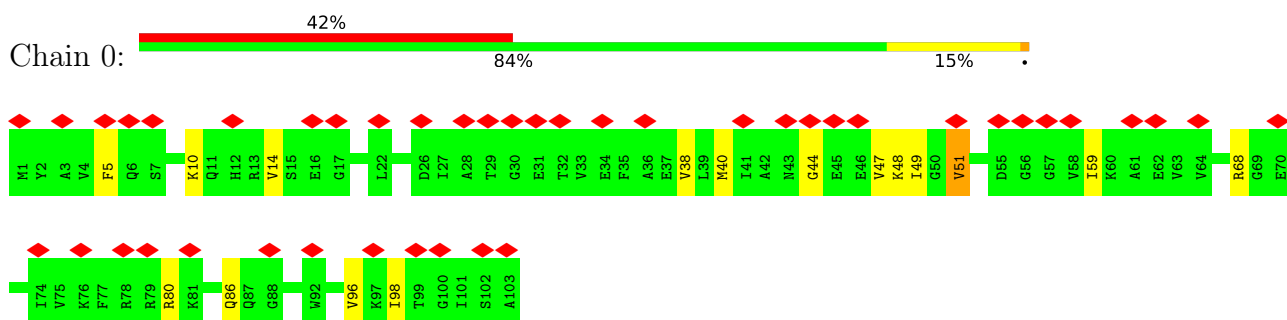
- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

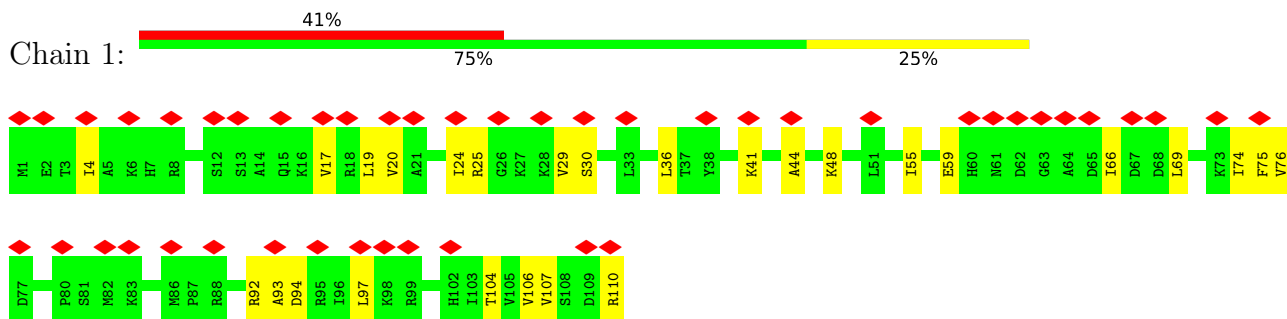
3 Residue-property plots [i](#)

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.

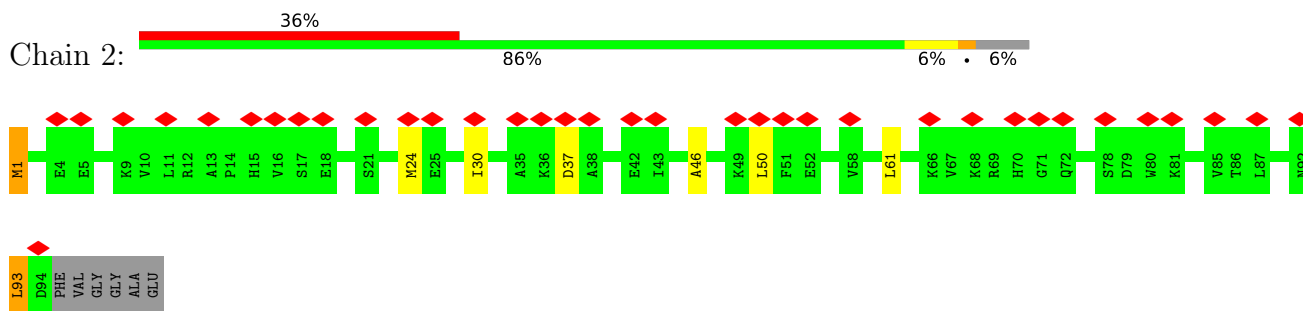
- Molecule 1: 50S ribosomal protein L21



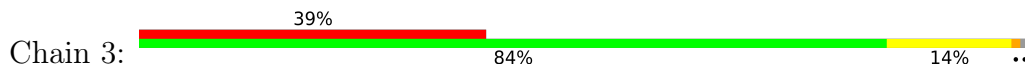
- Molecule 2: 50S ribosomal protein L22

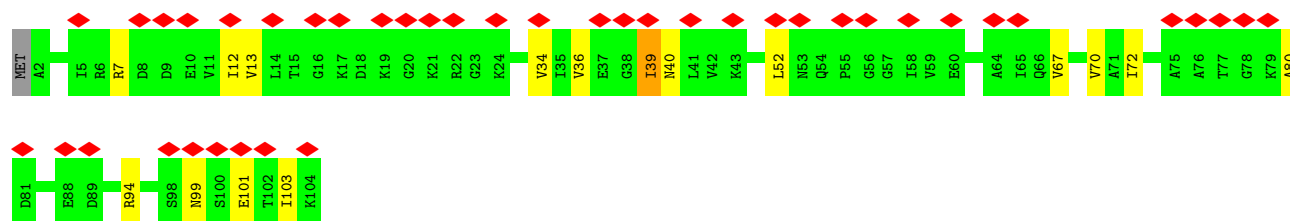


- Molecule 3: 50S ribosomal protein L23

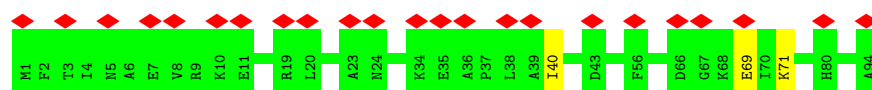


- Molecule 4: 50S ribosomal protein L24

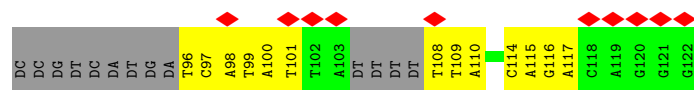
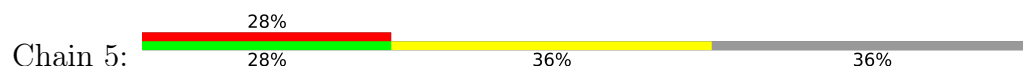




• Molecule 5: 50S ribosomal protein L25



• Molecule 6: NT DNA



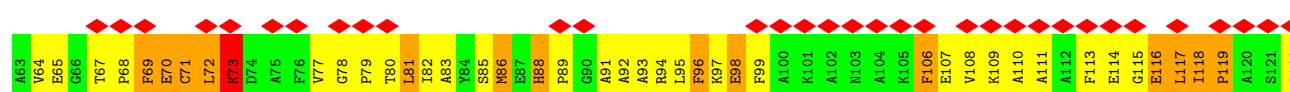
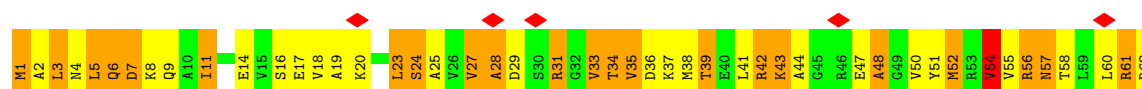
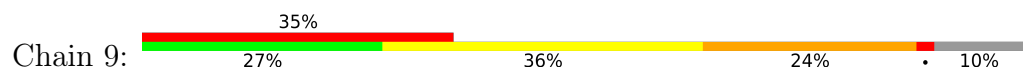
• Molecule 7: T DNA

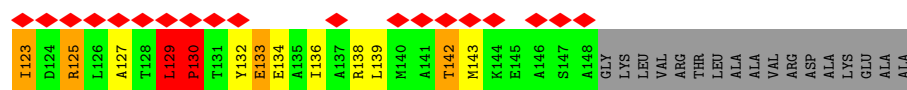


• Molecule 8: mRNA with 24 nt long spacer

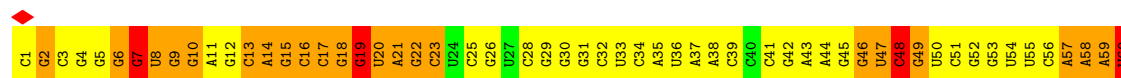


• Molecule 9: 50S ribosomal protein L10

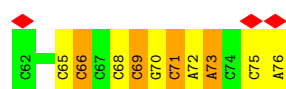
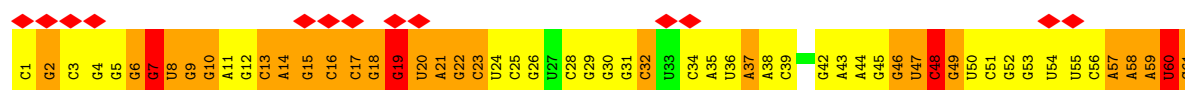




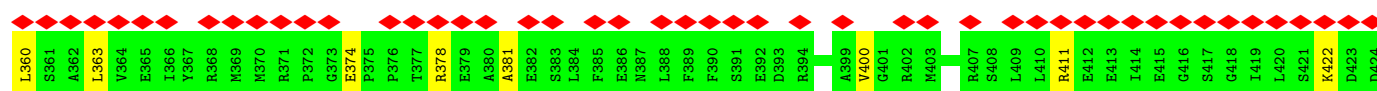
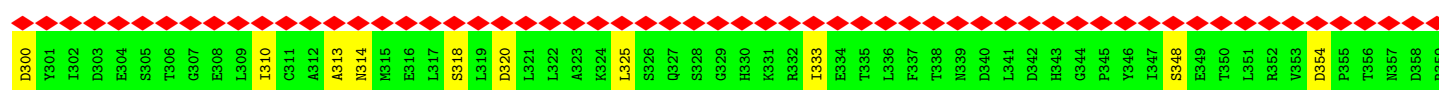
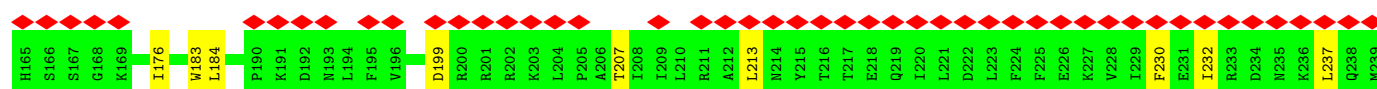
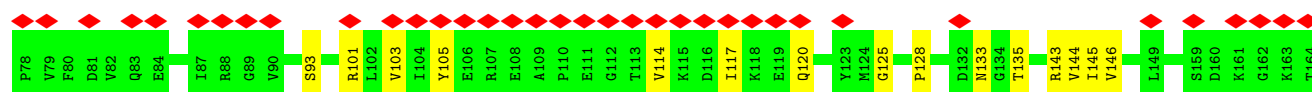
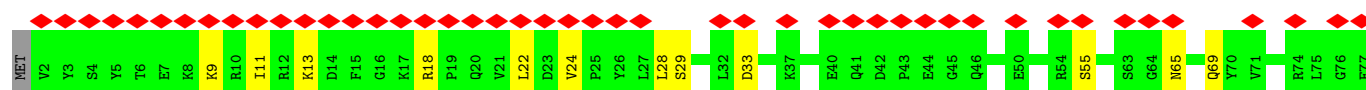
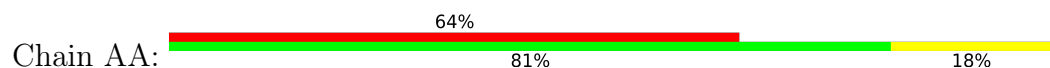
• Molecule 10: E-site and P-site tRNA (fMet)

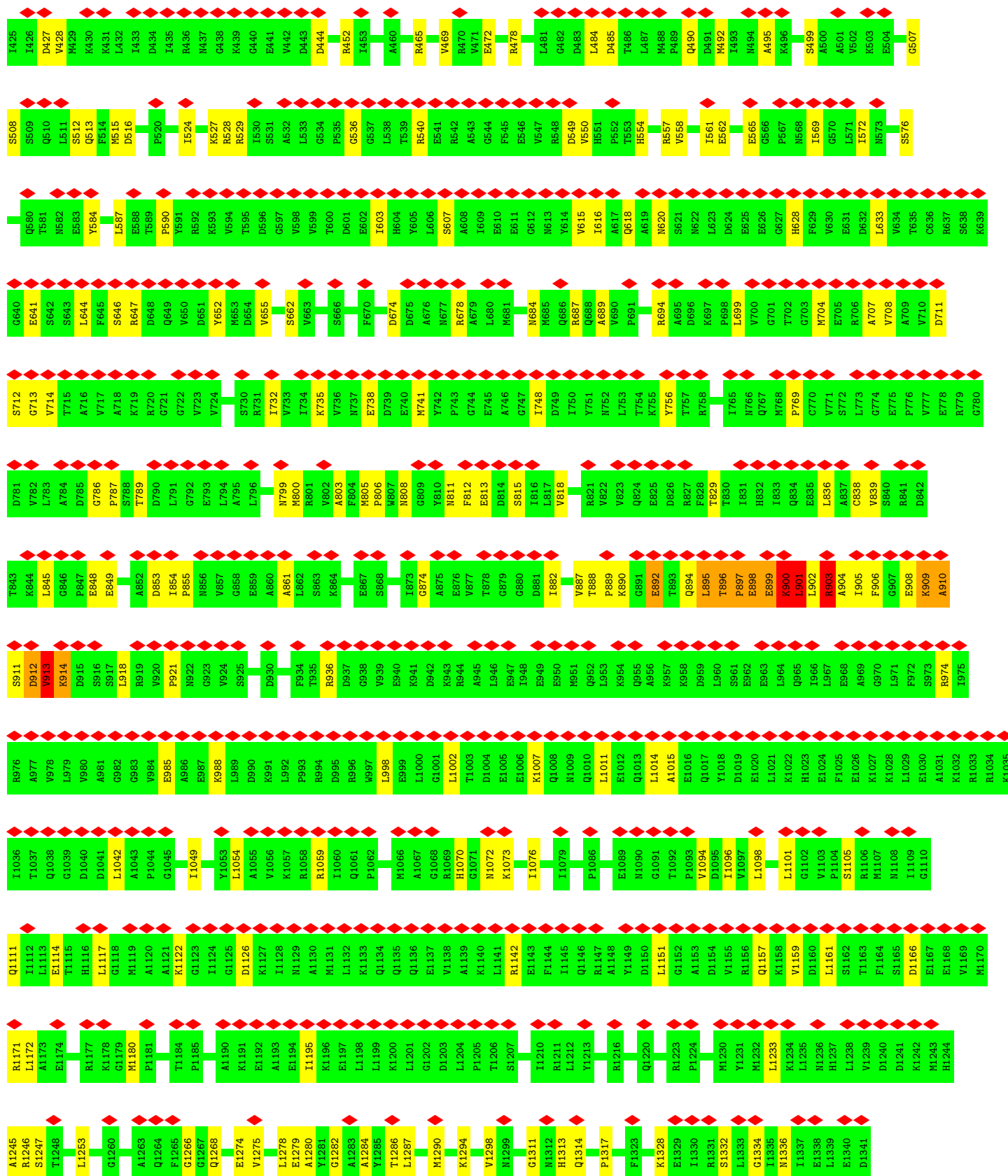


• Molecule 10: E-site and P-site tRNA (fMet)

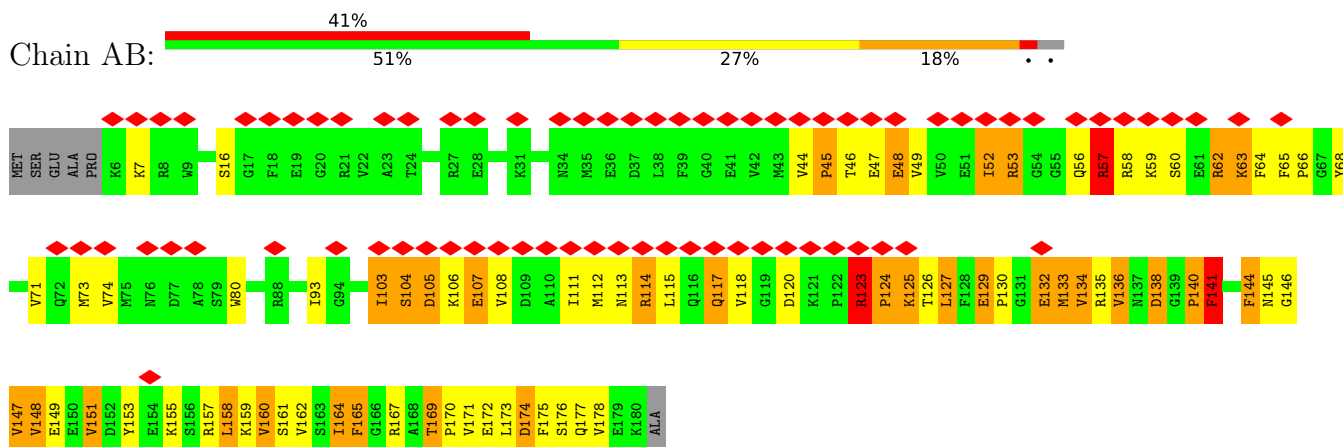


• Molecule 11: DNA-directed RNA polymerase subunit beta

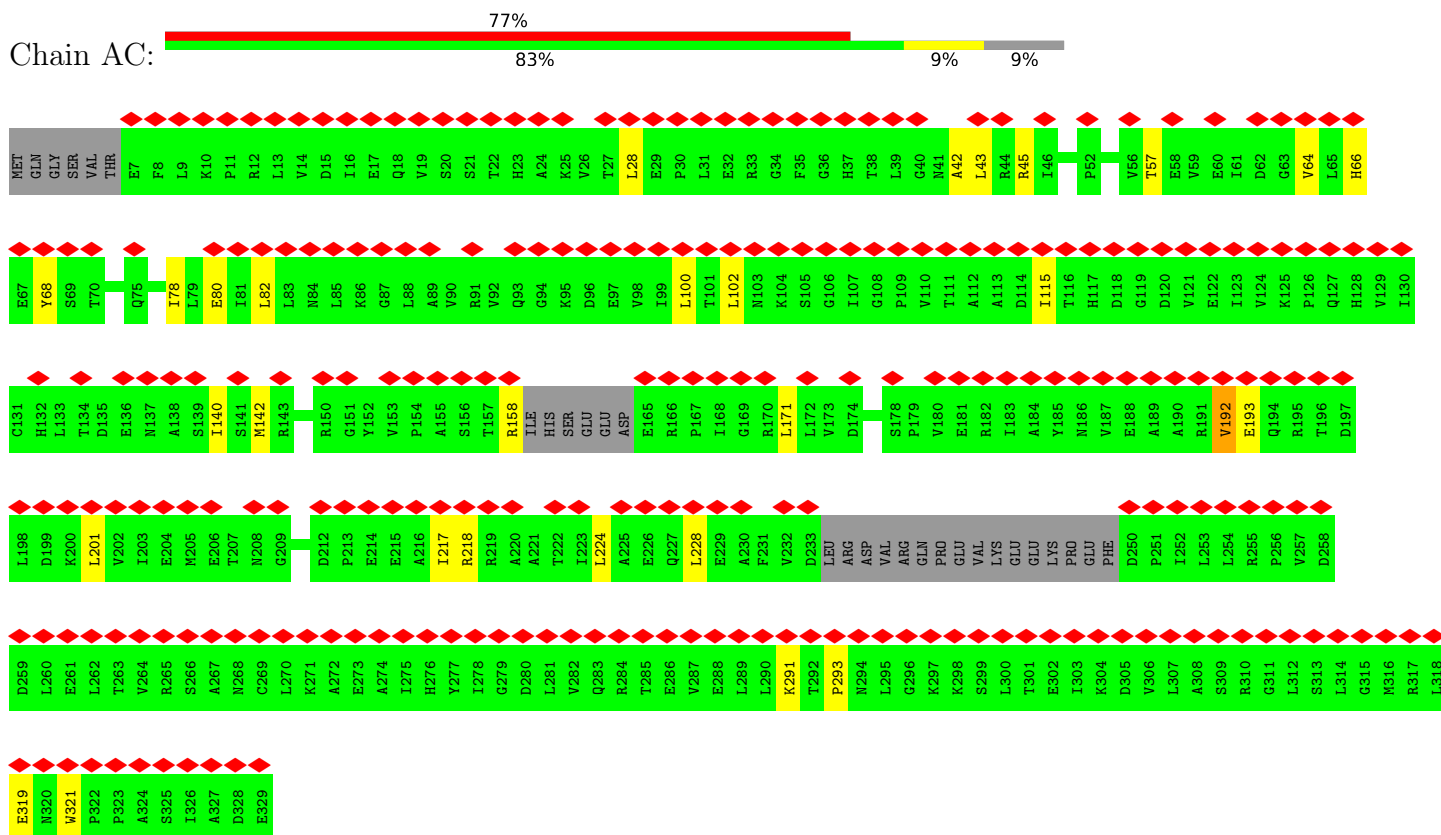




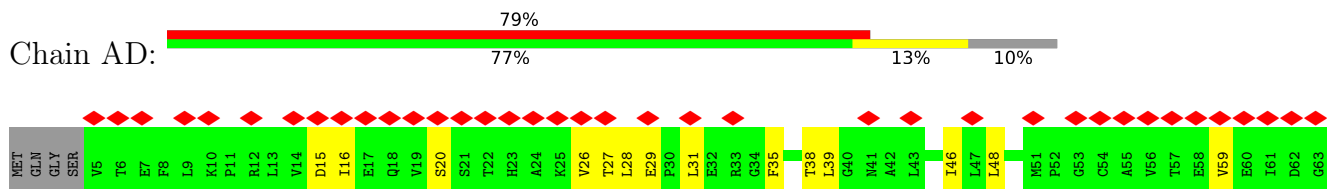
- Molecule 12: Transcription termination/antitermination protein NusG



- Molecule 13: DNA-directed RNA polymerase subunit alpha

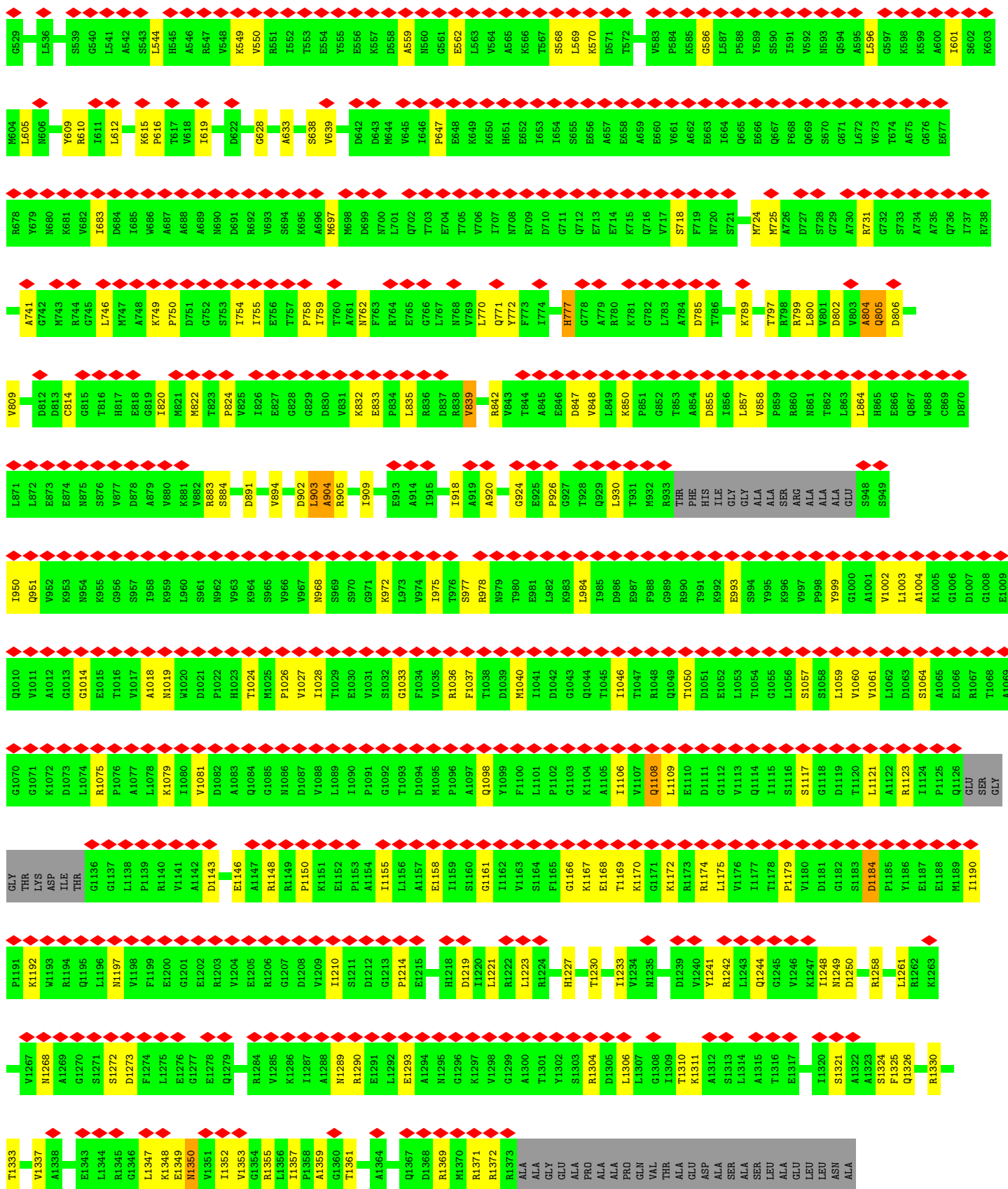


- Molecule 13: DNA-directed RNA polymerase subunit alpha





• Molecule 14: DNA-directed RNA polymerase subunit beta'



GLY
LEU
GLY
GLY
SER
ASP
ASN
GLU

• Molecule 15: DNA-directed RNA polymerase subunit omega

Chain AF: 86% 77% 13% 10%

Met Ala R3 R4 R5 R6 R7 R8 R9 R10 R11 R12 R13 R14 R15 R16 R17 R18 R19 R20 R21 R22 R23 R24 R25 R26 R27 R28 R29 R30 R31 R32 R33 R34 R35 R36 R37 R38 R39 R40 R41 R42 R43 R44 R45 R46 R47 R48 R49 R50 R51 R52 R53 R54 R55 R56 R57 R58 R59 R60

N61 Q62 I63 L64 V65 V66 R67 R68 R69 R70 R71 R72 R73 R74 R75 R76 R77 R78 R79 R80 R81 R82 R83 R84 R85 R86 R87 R88 R89 R90 R91 R92 R93 R94 R95 R96 R97 R98 R99 R100 R101 R102 R103 R104 R105 R106 R107 R108 R109 R110 R111 R112 R113 R114 R115 R116 R117 R118 R119 R120 R121 R122 R123 R124 R125 R126 R127 R128 R129 R130 R131 R132 R133 R134 R135 R136 R137 R138 R139 R140 R141 R142 R143 R144 R145 R146 R147 R148 R149 R150 R151 R152 R153 R154 R155 R156 R157 R158 R159 R160

• Molecule 16: Transcription termination/antitermination protein NusA

Chain AG: 43% 31% 52% 17%

R1 R2 R3 R4 R5 R6 R7 R8 R9 R10 R11 R12 R13 R14 R15 R16 R17 R18 R19 R20 R21 R22 R23 R24 R25 R26 R27 R28 R29 R30 R31 R32 R33 R34 R35 R36 R37 R38 R39 R40 R41 R42 R43 R44 R45 R46 R47 R48 R49 R50 R51 R52 R53 R54 R55 R56 R57 R58 R59 R60

R61 R62 R63 R64 R65 R66 R67 R68 R69 R70 R71 R72 R73 R74 R75 R76 R77 R78 R79 R80 R81 R82 R83 R84 R85 R86 R87 R88 R89 R90 R91 R92 R93 R94 R95 R96 R97 R98 R99 R100 R101 R102 R103 R104 R105 R106 R107 R108 R109 R110 R111 R112 R113 R114 R115 R116 R117 R118 R119 R120

A121 E122 R123 R124 R125 R126 R127 R128 R129 R130 R131 R132 R133 R134 R135 R136 R137 R138 R139 R140 R141 R142 R143 R144 R145 R146 R147 R148 R149 R150 R151 R152 R153 R154 R155 R156 R157 R158 R159 R160 R161 R162 R163 R164 R165 R166 R167 R168 R169 R170 R171 R172 R173 R174 R175 R176 R177 R178 R179 R180 R181 R182 R183

R184 R185 R186 R187 R188 R189 R190 R191 R192 R193 R194 R195 R196 R197 R198 R199 R200 R201 R202 R203 R204 R205 R206 R207 R208 R209 R210 R211 R212 R213 R214 R215 R216 R217 R218 R219 R220 R221 R222 R223 R224 R225 R226 R227 R228 R229 R230 R231 R232 R233 R234 R235 R236 R237 R238 R239 R240 R241 R242 R243

R244 R245 R246 R247 R248 R249 R250 R251 R252 R253 R254 R255 R256 R257 R258 R259 R260 R261 R262 R263 R264 R265 R266 R267 R268 R269 R270 R271 R272 R273 R274 R275 R276 R277 R278 R279 R280 R281 R282 R283 R284 R285 R286 R287 R288 R289 R290 R291 R292 R293 R294 R295 R296 R297 R298 R299 R300 R301 R302 R303 R304 R305 R306 R307

R308 R309 R310 R311 R312 R313 R314 R315 R316 R317 R318 R319 R320 R321 R322 R323 R324 R325 R326 R327 R328 R329 R330 R331 R332 R333 R334 R335 R336 R337 R338 R339 R340 R341 R342 R343 R344 R345 R346 R347 R348 R349 R350 R351 R352 R353 R354 R355 R356 R357 R358 R359 R360 R361 R362 R363 R364 R365 R366 R367 R368 R369

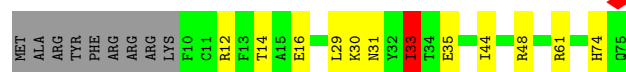
R370 R371 R372 R373 R374 R375 R376 R377 R378 R379 R380 R381 R382 R383 R384 R385 R386 R387 R388 R389 R390 R391 R392 R393 R394 R395 R396 R397 R398 R399 R400 R401 R402 R403 R404 R405 R406 R407 R408 R409 R410 R411 R412 R413 R414 R415 R416 R417 R418 R419 R420 R421 R422 R423 R424 R425 R426 R427 R428 R429

R430 R431 R432 R433 R434 R435 R436 R437 R438 R439 R440 R441 R442 R443 R444 R445 R446 R447 R448 R449 R450 R451 R452 R453 R454 R455 R456 R457 R458 R459 R460 R461 R462 R463 R464 R465 R466 R467 R468 R469 R470 R471 R472 R473 R474 R475 R476 R477 R478 R479 R480 R481 R482 R483 R484 R485 R486 R487 R488 R489

R490 R491 R492 R493 R494 R495

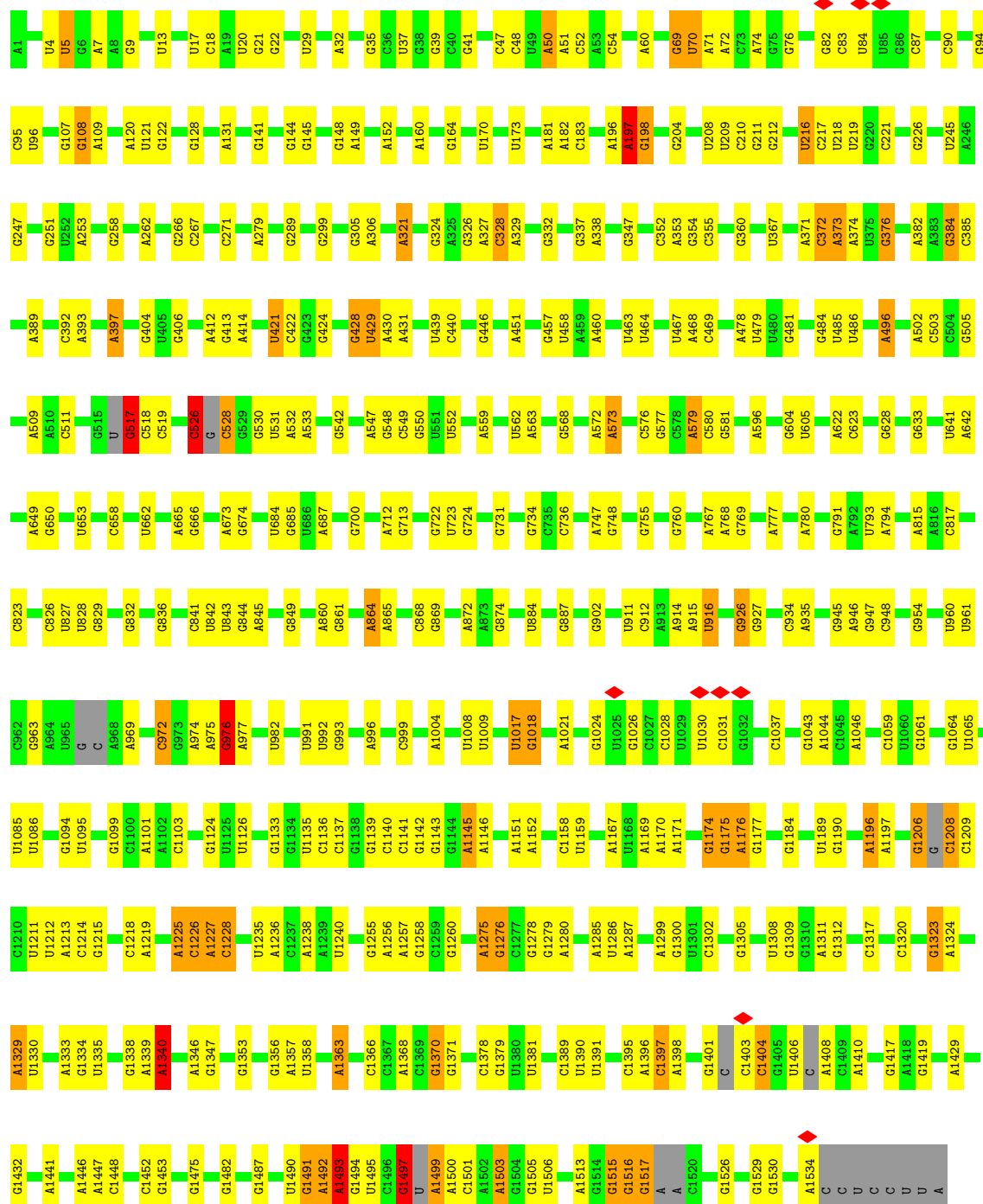
• Molecule 17: 30S ribosomal protein S18

Chain C:  72% 15% 12%

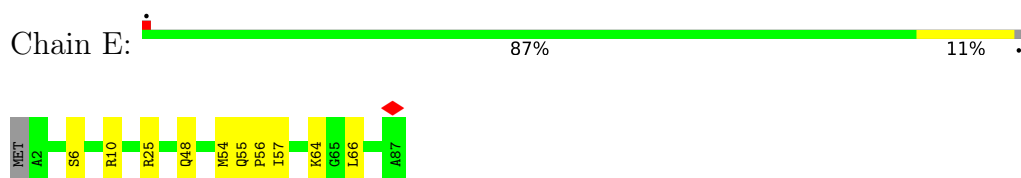


• Molecule 18: 16S rRNA

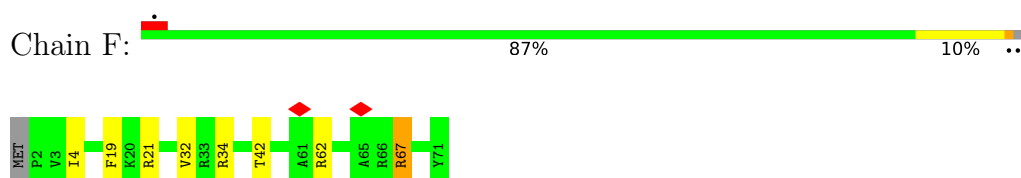
Chain D:  70% 25% 5%



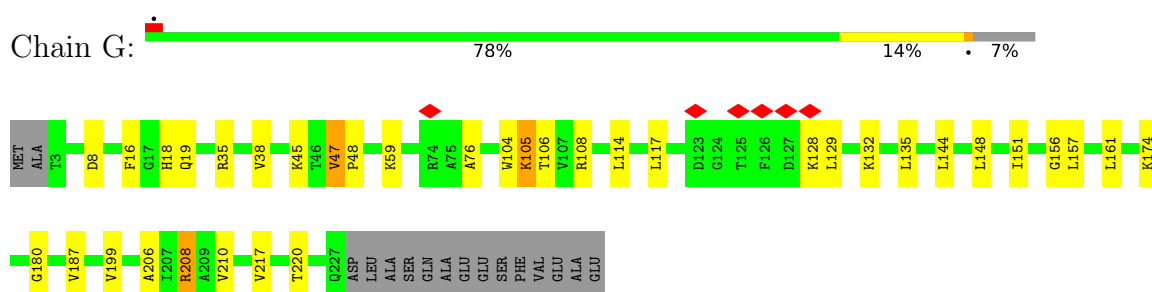
- Molecule 19: 30S ribosomal protein S20



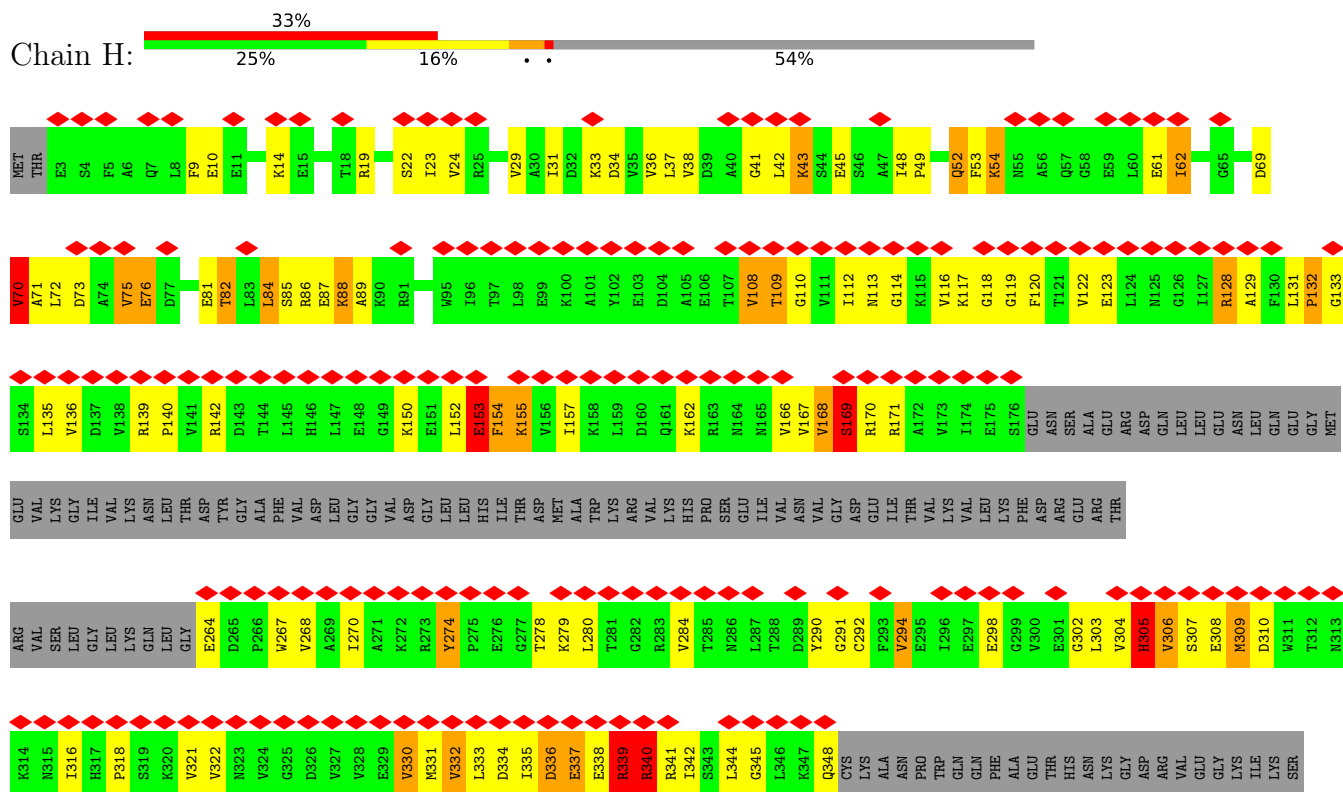
- Molecule 20: 30S ribosomal protein S21

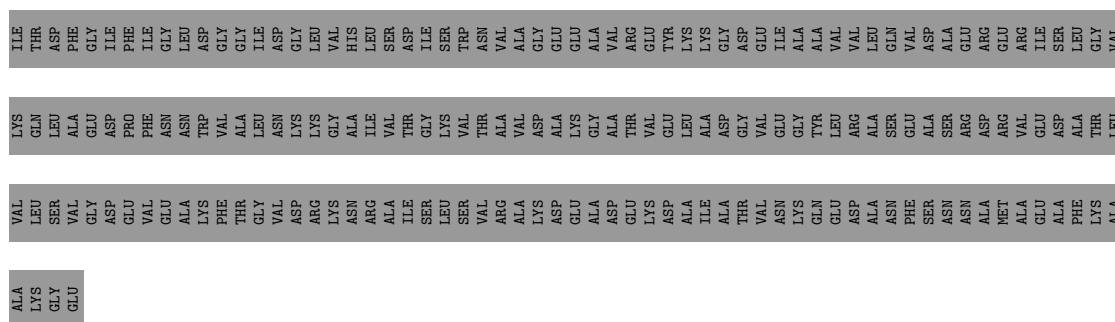


- Molecule 21: 30S ribosomal protein S2

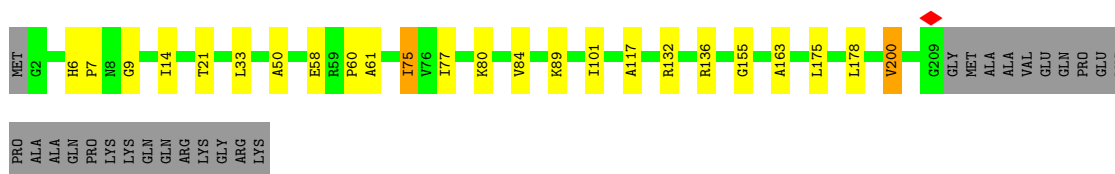
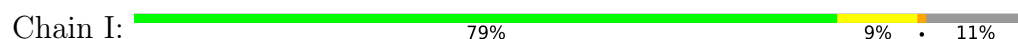


- Molecule 22: 30S ribosomal protein S1





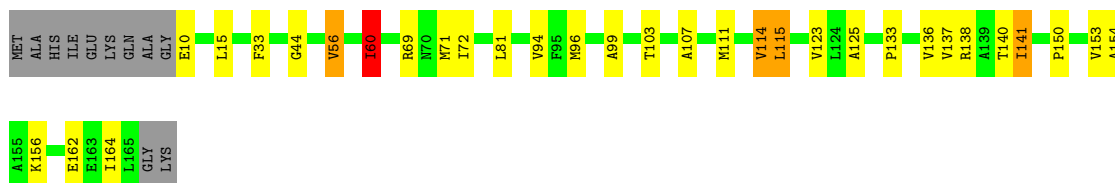
- Molecule 23: 30S ribosomal protein S3



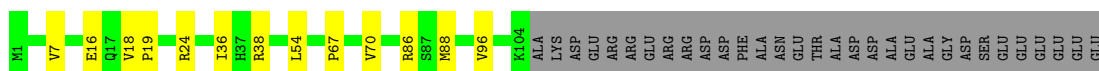
- Molecule 24: 30S ribosomal protein S4



- Molecule 25: 30S ribosomal protein S5

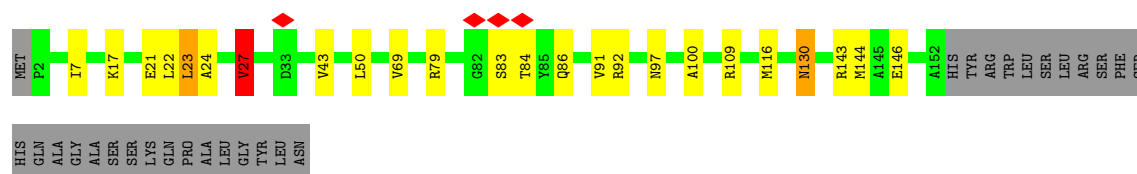


- Molecule 26: 30S ribosomal protein S6



- Molecule 27: 30S ribosomal protein S7





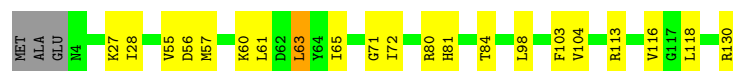
- Molecule 28: 30S ribosomal protein S8

Chain N: 89% 9% ..



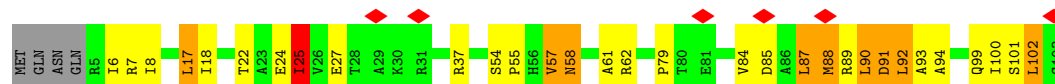
- Molecule 29: 30S ribosomal protein S9

Chain O: 82% 15% ..



- Molecule 30: 30S ribosomal protein S10

Chain P: 66% 20% 9% ..



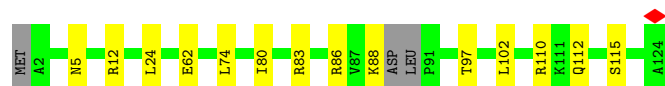
- Molecule 31: 30S ribosomal protein S11

Chain Q: 82% 9% 9% ..



- Molecule 32: 30S ribosomal protein S12

Chain R: 86% 11% ..



- Molecule 33: 30S ribosomal protein S14

Chain S: 88% 9% ...



- Molecule 34: 30S ribosomal protein S15

Chain T:  79% 18% ..



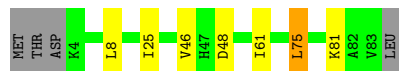
- Molecule 35: 30S ribosomal protein S16

Chain U:  88% 11% .



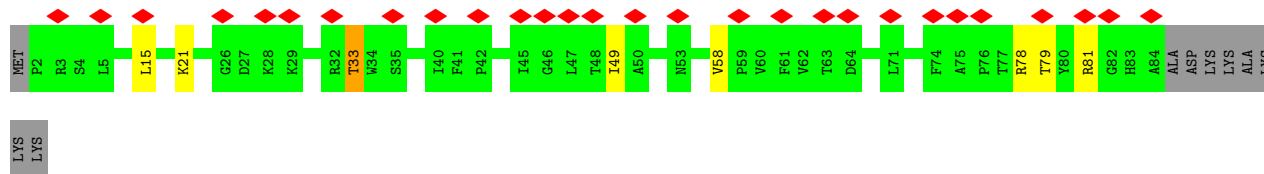
- Molecule 36: 30S ribosomal protein S17

Chain V:  87% 7% • 5%



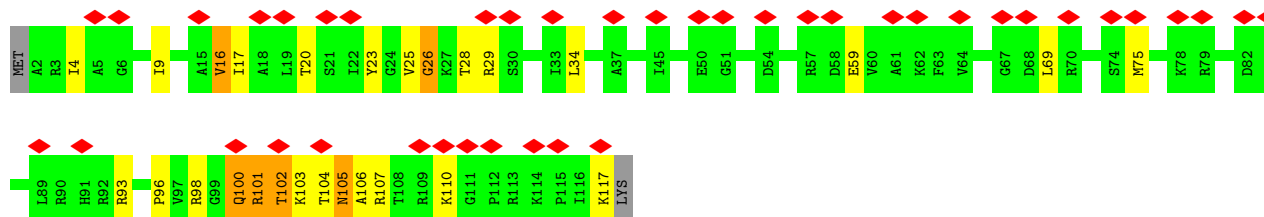
- Molecule 37: 30S ribosomal protein S19

Chain W:  30% 82% 8% • 10%



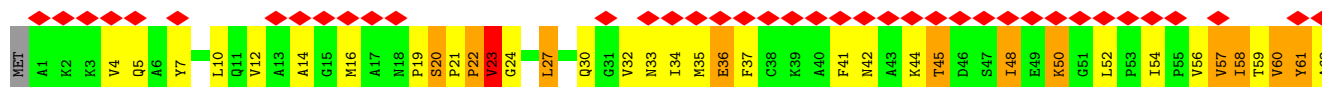
- Molecule 38: 30S ribosomal protein S13

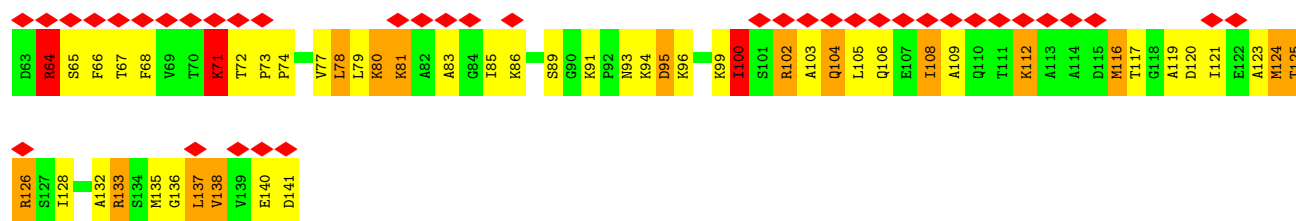
Chain X:  35% 75% 18% 5% .



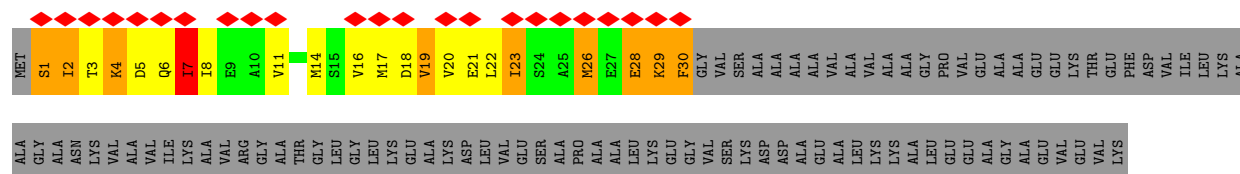
- Molecule 39: 50S ribosomal protein L11

Chain Y:  54% 38% 40% 18% ..

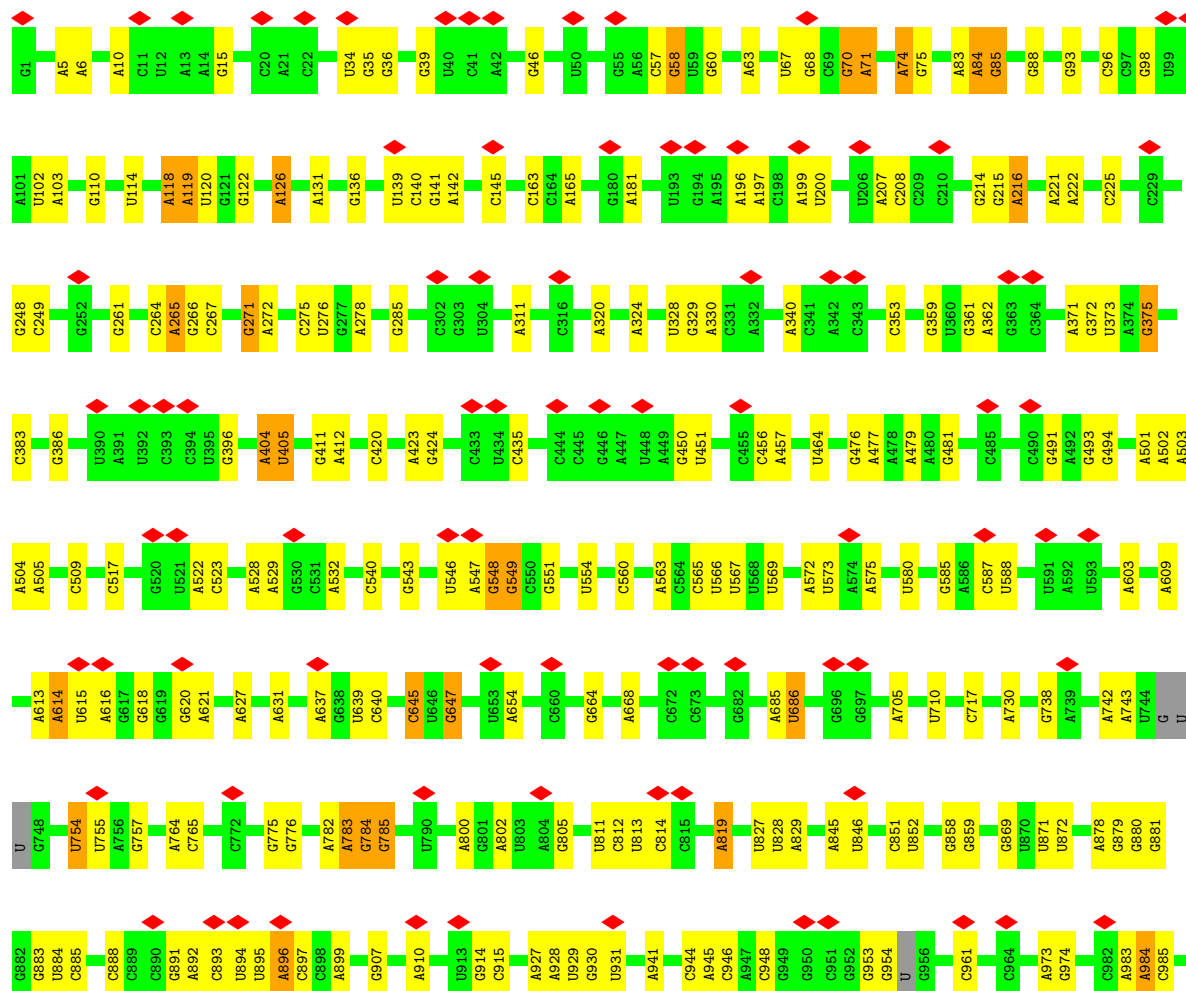
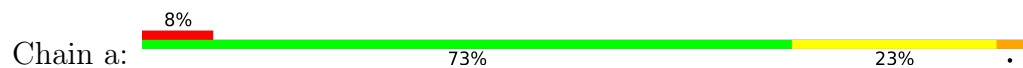


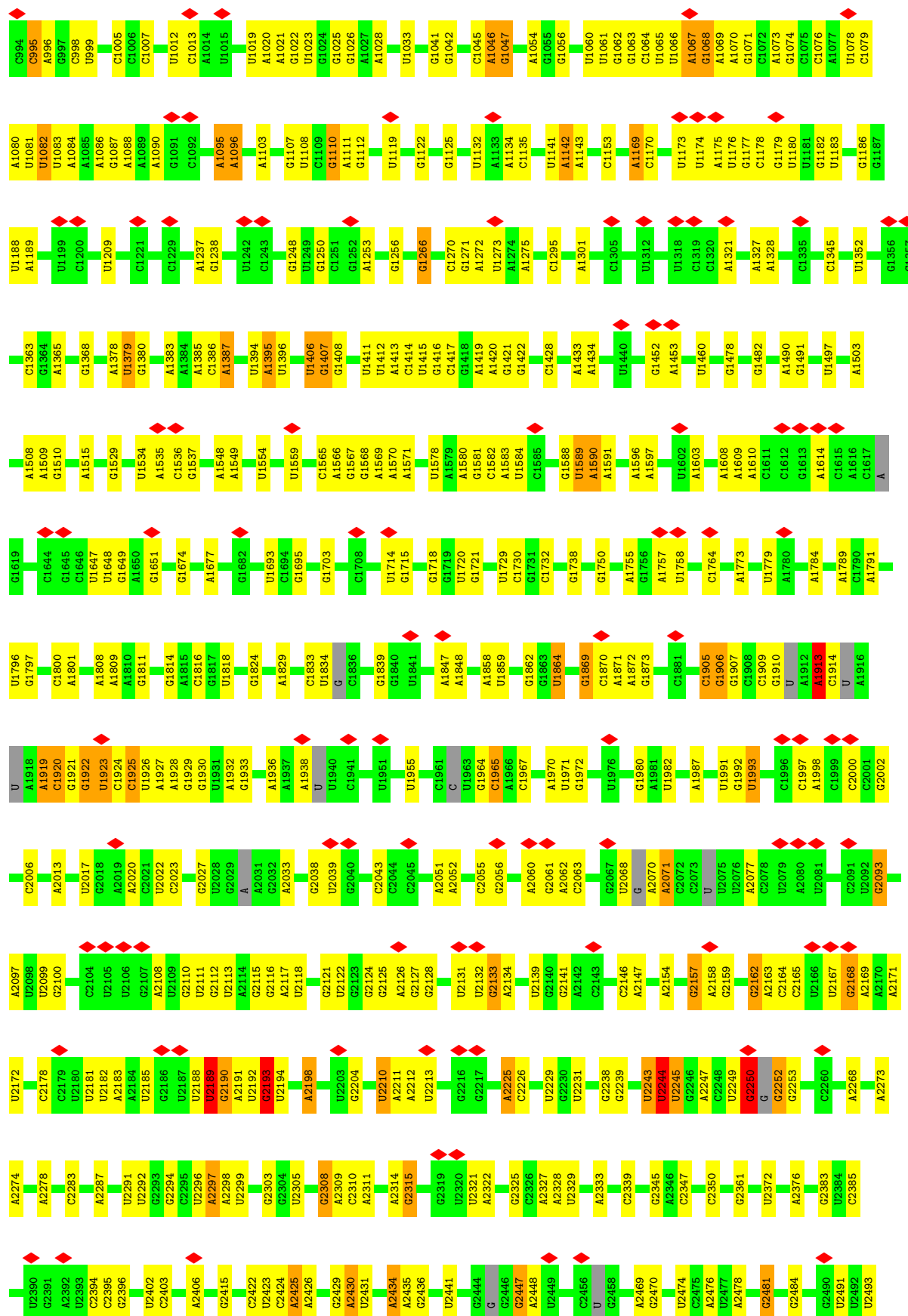


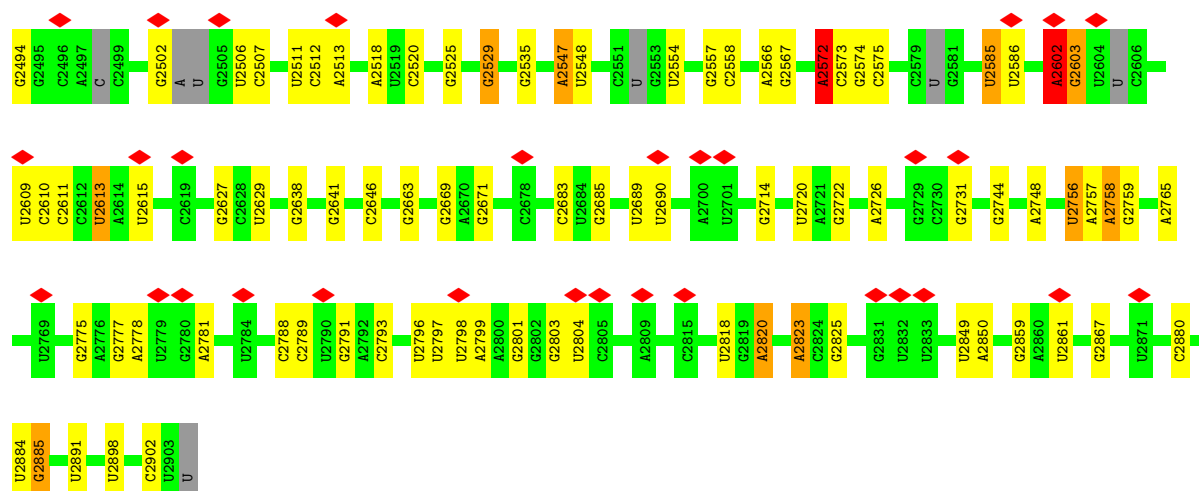
• Molecule 40: 50S ribosomal protein L7/L12



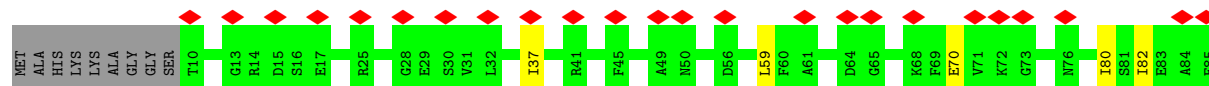
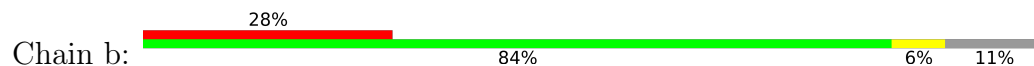
• Molecule 41: 23S rRNA



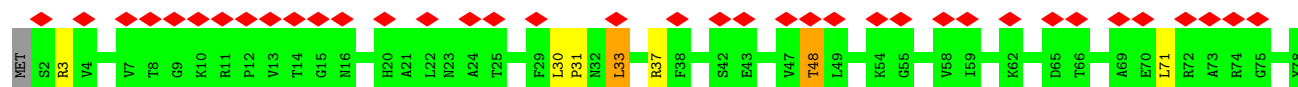
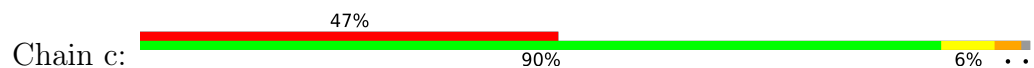




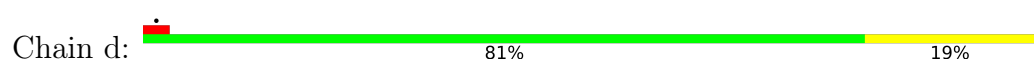
- Molecule 42: 50S ribosomal protein L27



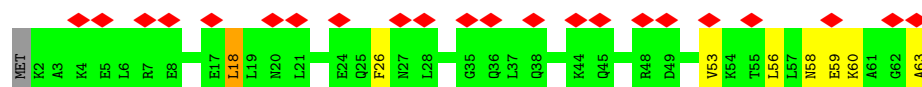
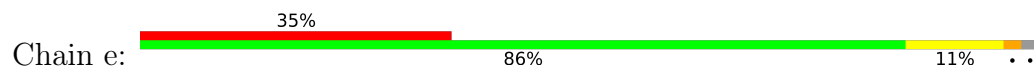
- Molecule 43: 50S ribosomal protein L28



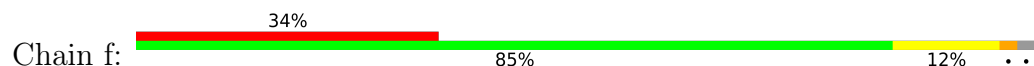
- Molecule 44: 5S rRNA

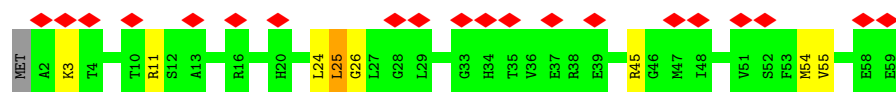


- Molecule 45: 50S ribosomal protein L29

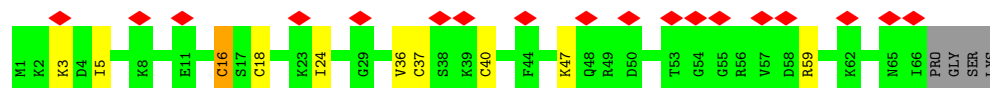
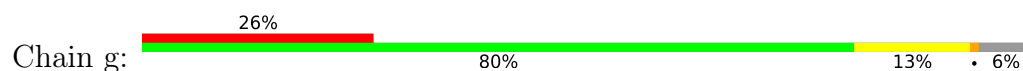


- Molecule 46: 50S ribosomal protein L30

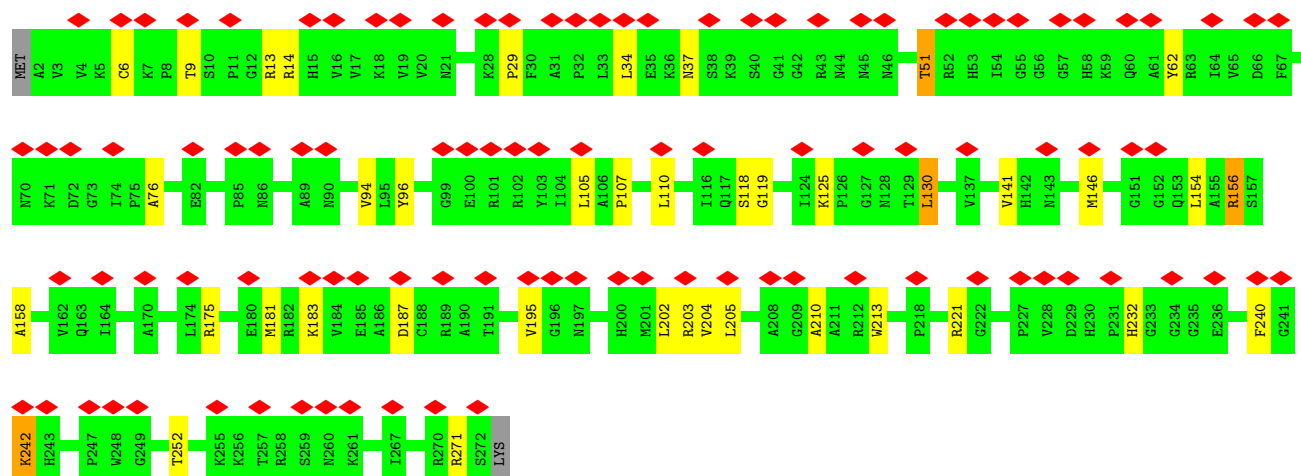
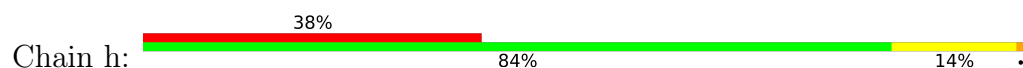




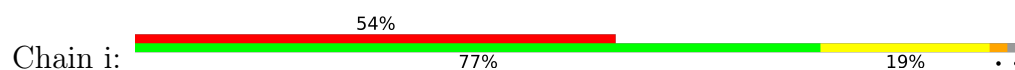
- Molecule 47: 50S ribosomal protein L31



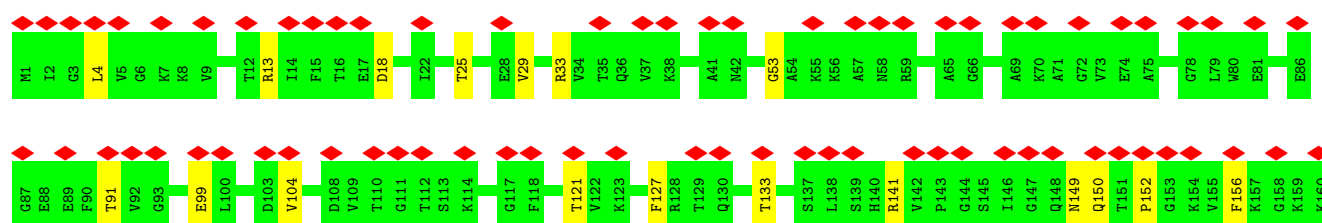
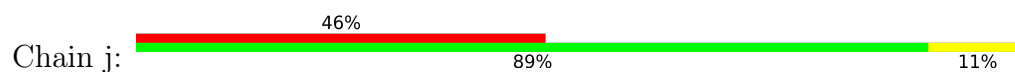
- Molecule 48: 50S ribosomal protein L2

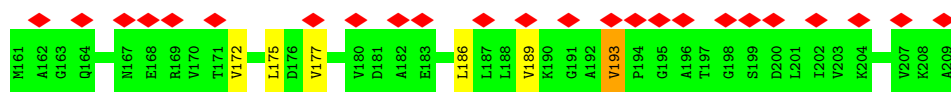


- Molecule 49: 50S ribosomal protein L32

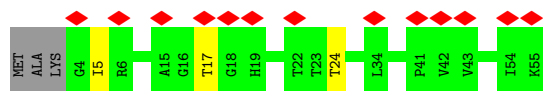
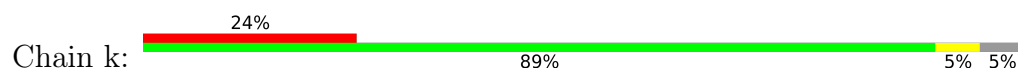


- Molecule 50: 50S ribosomal protein L3

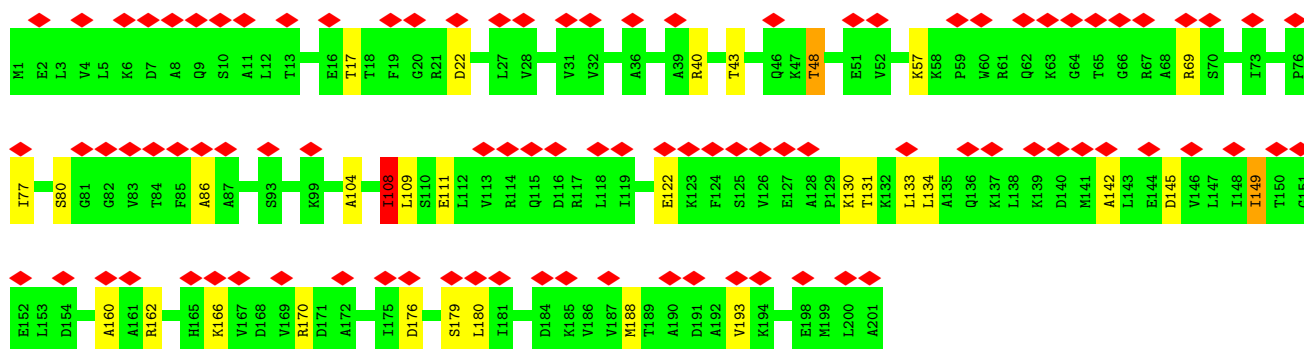
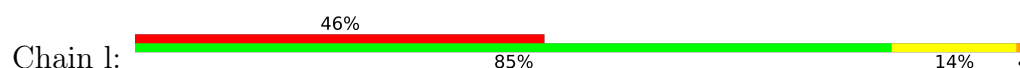




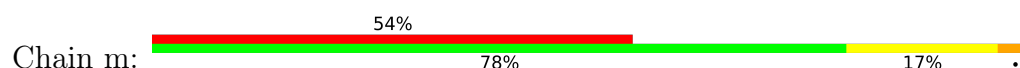
- Molecule 51: 50S ribosomal protein L33



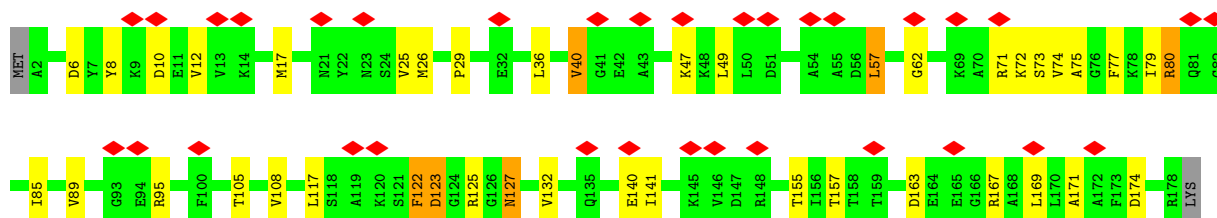
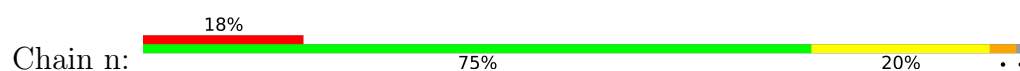
- Molecule 52: 50S ribosomal protein L4



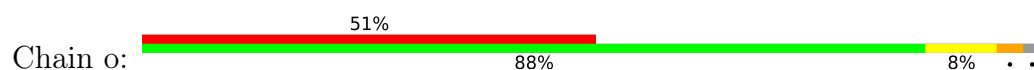
- Molecule 53: 50S ribosomal protein L34

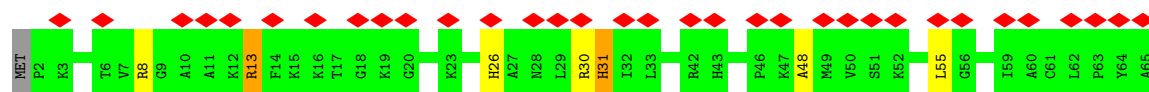


- Molecule 54: 50S ribosomal protein L5

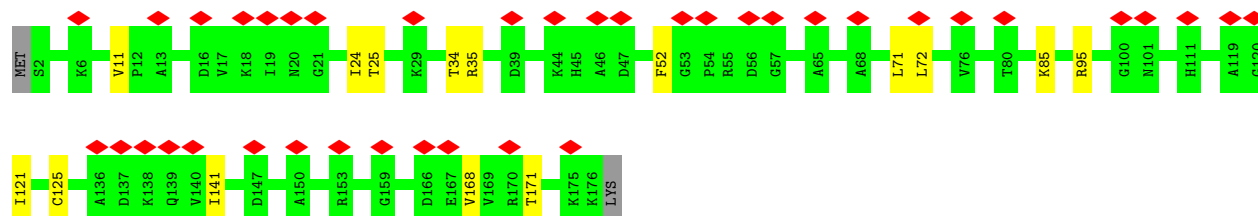
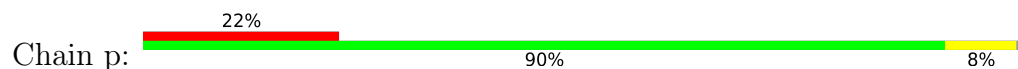


- Molecule 55: 50S ribosomal protein L35

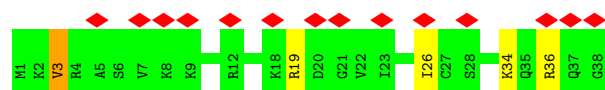
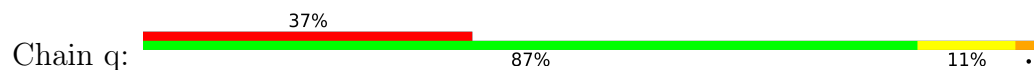




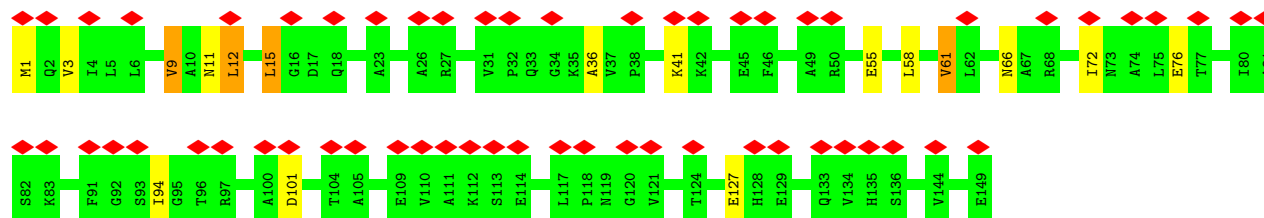
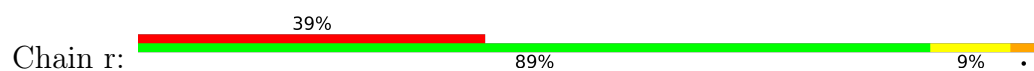
- Molecule 56: 50S ribosomal protein L6



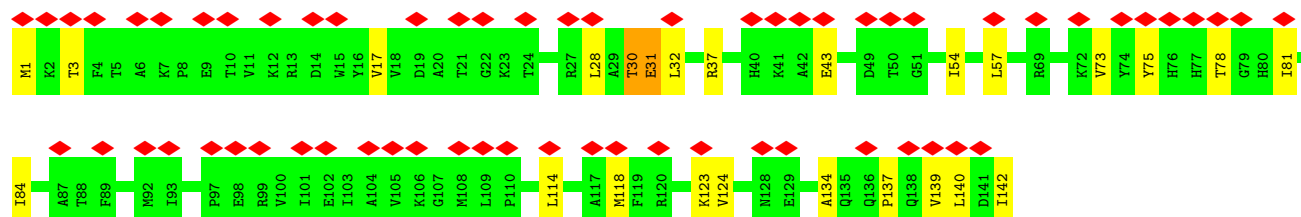
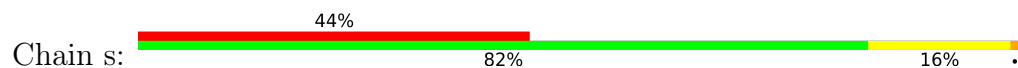
- Molecule 57: 50S ribosomal protein L36



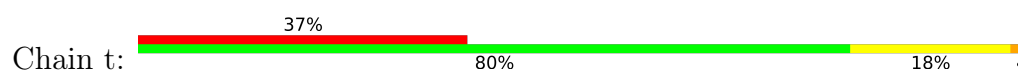
- Molecule 58: 50S ribosomal protein L9

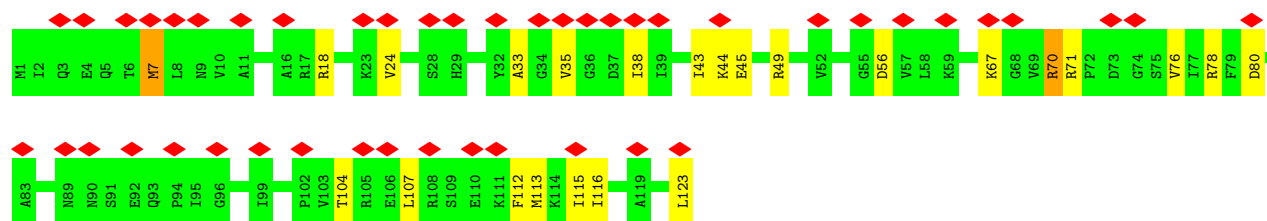


- Molecule 59: 50S ribosomal protein L13

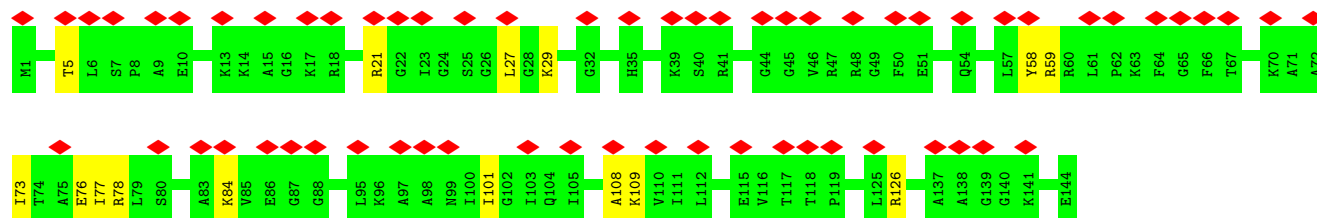
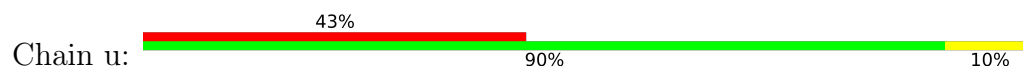


- Molecule 60: 50S ribosomal protein L14

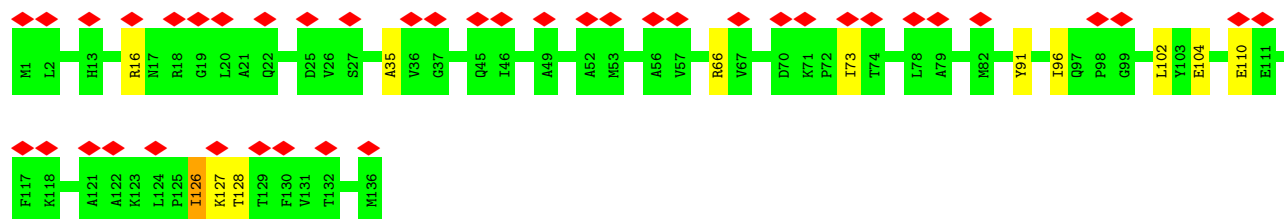
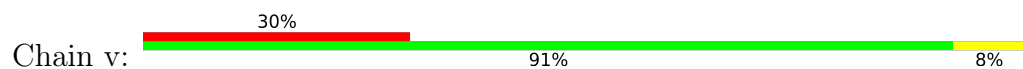




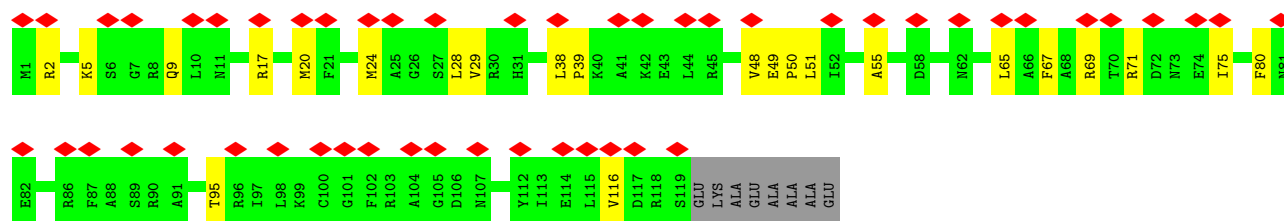
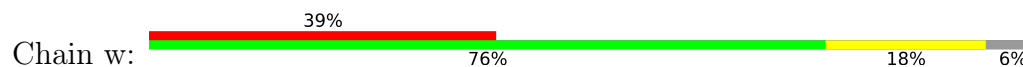
• Molecule 61: 50S ribosomal protein L15



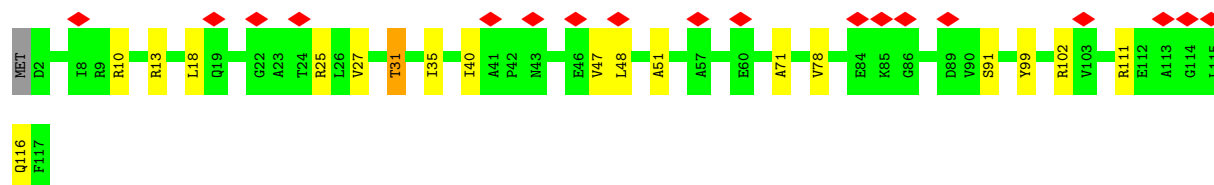
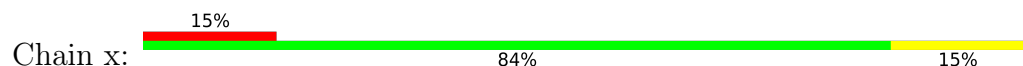
• Molecule 62: 50S ribosomal protein L16



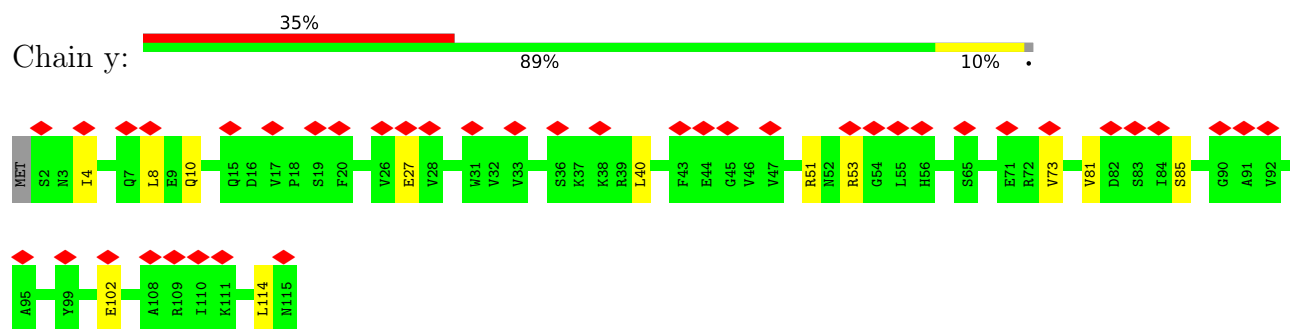
• Molecule 63: 50S ribosomal protein L17



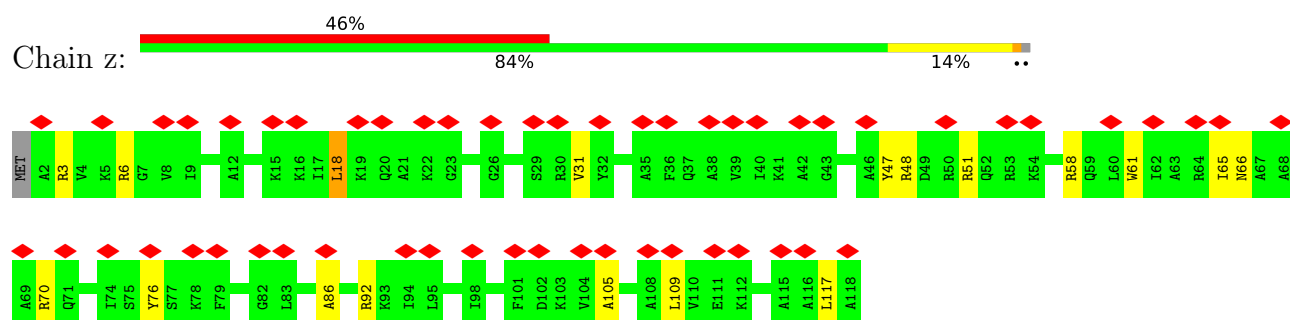
• Molecule 64: 50S ribosomal protein L18



- Molecule 65: 50S ribosomal protein L19



- Molecule 66: 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	45450	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	0.061	Depositor
Minimum map value	-0.027	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.00868	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	0.49	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	0.61	3/761 (0.4%)	0.89	4/1178 (0.3%)
9	9	1.15	3/1131 (0.3%)	1.30	4/1524 (0.3%)
10	A	0.36	0/1810	0.72	2/2821 (0.1%)
10	B	0.43	0/1810	0.87	9/2821 (0.3%)
11	AA	0.39	0/10736	0.66	7/14487 (0.0%)
12	AB	1.01	4/1433 (0.3%)	1.18	6/1930 (0.3%)
13	AC	0.35	0/2113	0.59	0/2877
13	AD	0.29	0/2086	0.59	0/2840
14	AE	0.54	9/10545 (0.1%)	0.74	23/14236 (0.2%)
15	AF	0.29	0/652	0.61	0/879
16	AG	0.86	1/3897 (0.0%)	1.14	18/5273 (0.3%)
17	C	0.66	0/553	1.14	2/743 (0.3%)
18	D	0.40	9/36610 (0.0%)	0.75	40/57091 (0.1%)
19	E	0.76	0/675	1.32	0/895
20	F	0.71	0/597	1.20	0/792
21	G	0.65	0/1791	1.08	1/2413 (0.0%)
22	H	0.76	4/1746 (0.2%)	1.58	34/2382 (1.4%)
23	I	0.58	0/1663	0.98	0/2241
24	J	0.63	0/1665	1.08	0/2227
25	K	0.64	1/1165 (0.1%)	1.06	2/1568 (0.1%)
26	L	0.58	0/867	0.94	0/1171
27	M	0.68	0/1195	1.19	3/1602 (0.2%)
28	N	0.55	0/989	0.91	0/1326
29	O	0.58	0/1034	1.02	1/1375 (0.1%)
30	P	0.64	0/800	1.13	4/1082 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	Q	0.55	0/893	0.92	0/1205
32	R	0.49	0/952	0.81	0/1274
33	S	0.64	0/817	1.11	1/1088 (0.1%)
34	T	0.68	0/722	1.21	0/964
35	U	0.57	0/659	0.99	0/884
36	V	0.45	0/657	0.73	0/881
37	W	0.51	0/680	0.83	0/915
38	X	0.67	0/909	1.21	3/1215 (0.2%)
39	Y	1.04	0/1046	1.09	1/1410 (0.1%)
40	Z	1.02	0/227	1.12	0/304
41	a	0.40	3/69247 (0.0%)	0.75	57/107985 (0.1%)
42	b	0.51	0/589	0.76	0/779
43	c	0.63	0/635	0.97	0/848
44	d	0.37	0/2872	0.69	0/4478
45	e	0.69	0/502	1.19	0/667
46	f	0.62	0/452	1.02	0/605
47	g	0.55	0/531	0.99	1/709 (0.1%)
48	h	0.54	0/2121	0.85	0/2852
49	i	0.52	0/450	0.94	0/599
50	j	0.60	0/1586	0.87	0/2134
51	k	0.46	0/433	0.80	0/576
52	l	0.61	0/1571	1.03	1/2113 (0.0%)
53	m	0.68	0/380	1.22	0/498
54	n	0.62	0/1434	1.18	10/1926 (0.5%)
55	o	0.63	0/513	1.10	1/676 (0.1%)
56	p	0.58	0/1333	0.89	0/1805
57	q	0.50	0/303	0.88	0/397
58	r	0.63	0/1122	0.97	1/1515 (0.1%)
59	s	0.68	0/1152	1.02	2/1551 (0.1%)
60	t	0.57	0/955	0.88	0/1279
61	u	0.54	0/1062	0.95	1/1413 (0.1%)
62	v	0.59	0/1093	0.97	0/1460
63	w	0.67	0/964	1.13	0/1289
64	x	0.61	0/902	1.09	0/1209
65	y	0.52	0/929	0.79	0/1242
66	z	0.80	0/960	1.25	0/1278
All	All	0.50	39/195115 (0.0%)	0.83	239/286888 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
10	A	0	2
10	B	0	2
11	AA	0	2
12	AB	0	1
13	AC	0	3
13	AD	0	3
14	AE	0	5
16	AG	0	5
22	H	0	3
38	X	0	1
All	All	0	27

The worst 5 of 39 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	18.21	1.70	1.47
12	AB	45	PRO	N-CA	18.12	1.70	1.47
16	AG	174	ARG	C-N	16.39	1.50	1.33
14	AE	93	THR	CA-C	12.18	1.69	1.52
22	H	169	SER	N-CA	11.83	1.61	1.46

The worst 5 of 239 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	D	1516	G	O3'-P-O5'	17.47	130.20	104.00
12	AB	44	VAL	CA-C-N	16.97	139.66	119.98
12	AB	44	VAL	C-N-CA	16.97	139.66	119.98
22	H	88	LYS	CA-C-N	16.94	143.59	120.38
22	H	88	LYS	C-N-CA	16.94	143.59	120.38

There are no chirality outliers.

5 of 27 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	A	19	G	Sidechain
10	A	7	G	Sidechain
11	AA	900	LYS	Mainchain
11	AA	910	ALA	Peptide
12	AB	104	SER	Mainchain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	816	839	839	8	0
2	1	857	922	922	14	0
3	2	746	811	811	6	0
4	3	788	844	844	11	0
5	4	753	780	780	0	0
6	5	472	260	260	31	0
7	6	542	305	306	24	0
8	7	687	97	341	98	0
9	9	1117	0	1153	165	0
10	A	1620	826	826	169	0
10	B	1620	813	827	141	0
11	AA	10567	0	10583	385	0
12	AB	1403	0	1397	244	0
13	AC	2094	0	1894	25	0
13	AD	2068	0	1888	35	0
14	AE	10388	10612	10611	381	0
15	AF	650	0	658	10	0
16	AG	3852	0	3825	1174	0
17	C	544	559	560	23	0
18	D	32703	16423	16459	222	0
19	E	669	719	719	3	0
20	F	589	629	629	8	0
21	G	1760	1785	1785	97	0
22	H	1730	1454	1454	210	0
23	I	1636	1710	1710	25	0
24	J	1643	1707	1707	16	0
25	K	1152	1196	1196	46	0
26	L	848	846	846	3	0
27	M	1181	1235	1235	33	0
28	N	979	1031	1031	7	0
29	O	1022	1070	1070	11	0
30	P	790	831	831	145	0
31	Q	877	887	887	4	0
32	R	939	1001	1001	7	0
33	S	805	844	844	6	0
34	T	714	734	734	8	0
35	U	649	666	666	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	V	648	691	691	4	0
37	W	663	688	688	2	0
38	X	900	964	964	57	0
39	Y	1032	0	1088	82	0
40	Z	227	0	237	20	0
41	a	61841	31077	31123	300	0
42	b	582	599	599	3	0
43	c	625	652	652	3	0
44	d	2569	1301	1301	3	0
45	e	501	531	531	5	0
46	f	448	488	488	5	0
47	g	522	520	520	11	0
48	h	2082	2154	2154	20	0
49	i	444	459	458	6	0
50	j	1565	1617	1616	14	0
51	k	426	464	464	0	0
52	l	1552	1619	1619	14	0
53	m	377	418	418	10	0
54	n	1410	1443	1444	27	0
55	o	504	572	572	3	0
56	p	1313	1358	1358	7	0
57	q	302	343	343	2	0
58	r	1111	1148	1148	5	0
59	s	1129	1162	1162	13	0
60	t	946	1023	1023	12	0
61	u	1053	1129	1129	7	0
62	v	1074	1157	1157	5	0
63	w	951	994	994	9	0
64	x	892	923	923	8	0
65	y	917	962	962	4	0
66	z	947	1020	1019	13	0
67	AE	1	0	0	0	0
68	AE	2	0	0	0	0
All	All	181826	109912	132974	3650	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 12.

The worst 5 of 3650 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)
12:AB:127:LEU:CD1	12:AB:153:TYR:CZ	1.75	1.66
16:AG:373:LEU:HB2	16:AG:378:PHE:CD1	1.14	1.64
16:AG:36:LYS:HB2	16:AG:45:VAL:CG2	1.24	1.63
12:AB:127:LEU:HD13	12:AB:153:TYR:CE1	1.16	1.62
12:AB:127:LEU:HD13	12:AB:153:TYR:CZ	1.28	1.61

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	44
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/100 (92%)	90 (98%)	2 (2%)	0	100	100
4	3	101/104 (97%)	96 (95%)	4 (4%)	1 (1%)	12	44
5	4	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
9	9	146/165 (88%)	95 (65%)	37 (25%)	14 (10%)	0	6
11	AA	1338/1342 (100%)	1215 (91%)	120 (9%)	3 (0%)	43	74
12	AB	173/181 (96%)	136 (79%)	26 (15%)	11 (6%)	1	11
13	AC	295/329 (90%)	274 (93%)	19 (6%)	2 (1%)	18	51
13	AD	291/329 (88%)	268 (92%)	23 (8%)	0	100	100
14	AE	1329/1407 (94%)	1199 (90%)	121 (9%)	9 (1%)	18	51
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
16	AG	493/495 (100%)	413 (84%)	56 (11%)	24 (5%)	1	16
17	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
19	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
20	F	68/71 (96%)	68 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	G	223/241 (92%)	210 (94%)	13 (6%)	0	100	100
22	H	255/557 (46%)	188 (74%)	55 (22%)	12 (5%)	2	17
23	I	206/233 (88%)	196 (95%)	9 (4%)	1 (0%)	24	57
24	J	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
25	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	21	54
26	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	44
27	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	18	51
28	N	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16	49
29	O	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16	49
30	P	97/103 (94%)	87 (90%)	8 (8%)	2 (2%)	5	31
31	Q	115/129 (89%)	104 (90%)	9 (8%)	2 (2%)	7	35
32	R	117/124 (94%)	116 (99%)	1 (1%)	0	100	100
33	S	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
34	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
35	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	9	39
36	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
37	W	81/92 (88%)	78 (96%)	3 (4%)	0	100	100
38	X	114/118 (97%)	107 (94%)	5 (4%)	2 (2%)	6	34
39	Y	139/142 (98%)	102 (73%)	25 (18%)	12 (9%)	0	7
40	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	10
42	b	74/85 (87%)	69 (93%)	5 (7%)	0	100	100
43	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
45	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
46	f	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
47	g	64/70 (91%)	63 (98%)	1 (2%)	0	100	100
48	h	269/273 (98%)	259 (96%)	9 (3%)	1 (0%)	30	62
49	i	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
50	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
51	k	50/55 (91%)	50 (100%)	0	0	100	100
52	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	24	57
53	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	n	175/179 (98%)	162 (93%)	11 (6%)	2 (1%)	11	43
55	o	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
56	p	173/177 (98%)	161 (93%)	12 (7%)	0	100	100
57	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
58	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
59	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
60	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
61	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
62	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
63	w	117/127 (92%)	108 (92%)	9 (8%)	0	100	100
64	x	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
65	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
66	z	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	14	47
All	All	10172/11072 (92%)	9323 (92%)	740 (7%)	109 (1%)	14	43

5 of 109 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
11	AA	913	VAL
12	AB	60	SER
12	AB	123	ARG
16	AG	3	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	76 (90%)	8 (10%)	8	31
2	1	93/93 (100%)	86 (92%)	7 (8%)	12	37
3	2	81/84 (96%)	77 (95%)	4 (5%)	22	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3	84/85 (99%)	79 (94%)	5 (6%)	17	44
5	4	78/78 (100%)	75 (96%)	3 (4%)	29	55
9	9	112/123 (91%)	63 (56%)	49 (44%)	0	0
11	AA	1155/1157 (100%)	1138 (98%)	17 (2%)	57	71
12	AB	154/158 (98%)	117 (76%)	37 (24%)	1	4
13	AC	186/286 (65%)	186 (100%)	0	100	100
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1120/1168 (96%)	1047 (94%)	73 (6%)	15	42
15	AF	70/75 (93%)	69 (99%)	1 (1%)	59	71
16	AG	409/409 (100%)	317 (78%)	92 (22%)	1	5
17	C	57/65 (88%)	55 (96%)	2 (4%)	32	57
19	E	65/66 (98%)	61 (94%)	4 (6%)	16	43
20	F	60/61 (98%)	57 (95%)	3 (5%)	22	48
21	G	187/199 (94%)	174 (93%)	13 (7%)	14	39
22	H	137/461 (30%)	124 (90%)	13 (10%)	8	31
23	I	171/190 (90%)	163 (95%)	8 (5%)	23	49
24	J	172/173 (99%)	164 (95%)	8 (5%)	23	49
25	K	119/126 (94%)	111 (93%)	8 (7%)	15	41
26	L	91/116 (78%)	84 (92%)	7 (8%)	12	37
27	M	124/147 (84%)	113 (91%)	11 (9%)	9	32
28	N	104/105 (99%)	101 (97%)	3 (3%)	37	60
29	O	105/107 (98%)	99 (94%)	6 (6%)	18	45
30	P	86/90 (96%)	73 (85%)	13 (15%)	3	16
31	Q	90/99 (91%)	88 (98%)	2 (2%)	45	65
32	R	101/104 (97%)	95 (94%)	6 (6%)	18	44
33	S	83/84 (99%)	79 (95%)	4 (5%)	23	49
34	T	76/77 (99%)	65 (86%)	11 (14%)	3	17
35	U	65/65 (100%)	60 (92%)	5 (8%)	12	37
36	V	74/78 (95%)	71 (96%)	3 (4%)	27	53
37	W	72/79 (91%)	66 (92%)	6 (8%)	10	34
38	X	94/96 (98%)	87 (93%)	7 (7%)	13	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	Y	109/110 (99%)	69 (63%)	40 (37%)	0	1
40	Z	26/85 (31%)	10 (38%)	16 (62%)	0	0
42	b	58/63 (92%)	57 (98%)	1 (2%)	53	70
43	c	67/68 (98%)	64 (96%)	3 (4%)	24	50
45	e	54/55 (98%)	51 (94%)	3 (6%)	19	46
46	f	48/49 (98%)	43 (90%)	5 (10%)	7	27
47	g	59/62 (95%)	54 (92%)	5 (8%)	10	34
48	h	216/218 (99%)	199 (92%)	17 (8%)	11	36
49	i	47/48 (98%)	41 (87%)	6 (13%)	4	21
50	j	164/164 (100%)	156 (95%)	8 (5%)	22	48
51	k	47/49 (96%)	44 (94%)	3 (6%)	16	42
52	l	165/165 (100%)	151 (92%)	14 (8%)	10	34
53	m	38/38 (100%)	36 (95%)	2 (5%)	20	47
54	n	148/150 (99%)	130 (88%)	18 (12%)	5	22
55	o	51/52 (98%)	47 (92%)	4 (8%)	11	36
56	p	136/138 (99%)	130 (96%)	6 (4%)	25	51
57	q	34/34 (100%)	31 (91%)	3 (9%)	9	32
58	r	114/114 (100%)	102 (90%)	12 (10%)	6	27
59	s	116/116 (100%)	106 (91%)	10 (9%)	10	33
60	t	104/104 (100%)	97 (93%)	7 (7%)	15	41
61	u	103/103 (100%)	96 (93%)	7 (7%)	14	40
62	v	109/109 (100%)	105 (96%)	4 (4%)	30	56
63	w	99/103 (96%)	91 (92%)	8 (8%)	11	35
64	x	86/87 (99%)	80 (93%)	6 (7%)	14	39
65	y	99/100 (99%)	91 (92%)	8 (8%)	11	35
66	z	89/90 (99%)	85 (96%)	4 (4%)	24	50
All	All	8330/9148 (91%)	7671 (92%)	659 (8%)	13	36

5 of 659 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	Y	94	LYS
54	n	117	LEU

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Mol	Chain	Res	Type
39	Y	135	MET
39	Y	91	LYS
48	h	183	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 88 such sidechains are listed below:

Mol	Chain	Res	Type
25	K	97	GLN
38	X	12	HIS
26	L	63	ASN
31	Q	15	GLN
48	h	25	HIS

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%)
18	D	1514/1542 (98%)	290 (19%)	34 (2%)
41	a	2859/2904 (98%)	541 (18%)	0
44	d	119/120 (99%)	17 (14%)	0
8	7	32/41 (78%)	17 (53%)	4 (12%)
All	All	4674/4759 (98%)	929 (19%)	50 (1%)

5 of 929 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-18	G
8	7	-17	U
8	7	-16	U
8	7	-14	U
8	7	-13	U

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	D	531	U
18	D	992	U
18	D	1493	A
18	D	532	A

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Mol	Chain	Res	Type
18	D	722	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

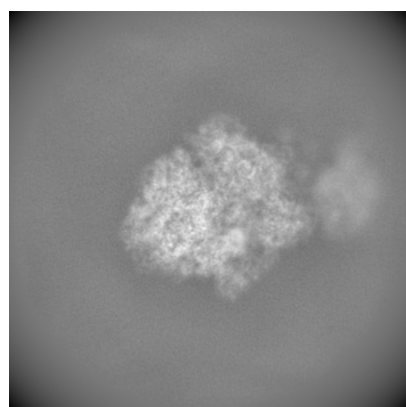
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22084. These allow visual inspection of the internal detail of the map and identification of artifacts.

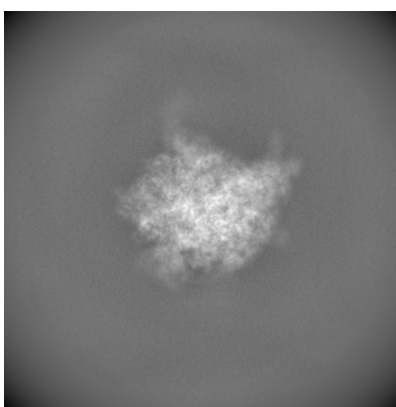
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

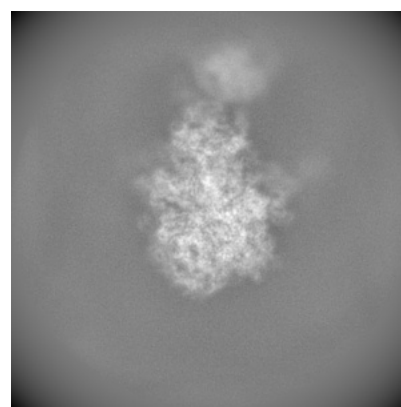
6.1.1 Primary map



X



Y

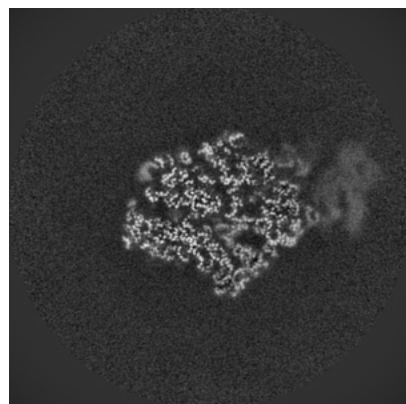


Z

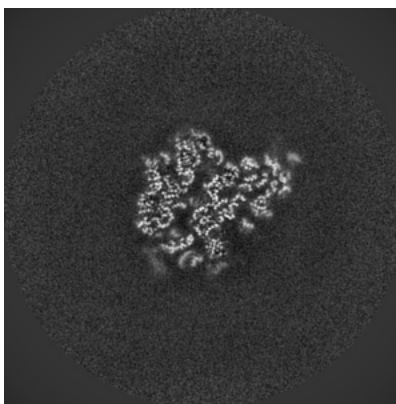
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

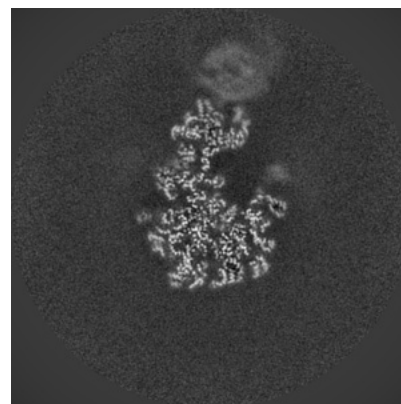
6.2.1 Primary map



X Index: 256



Y Index: 256

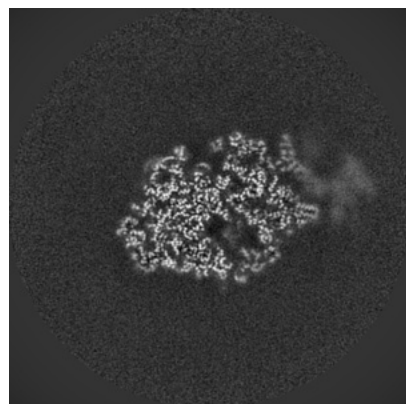


Z Index: 256

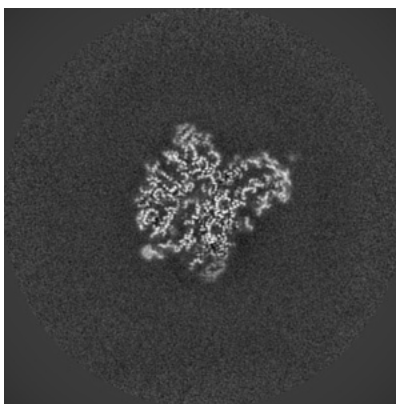
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

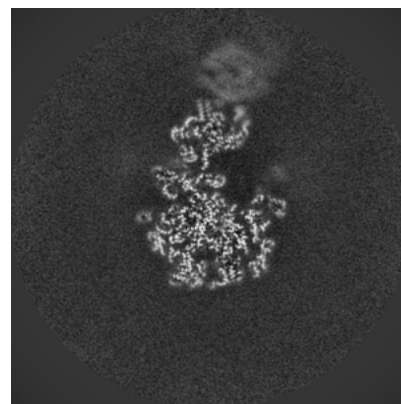
6.3.1 Primary map



X Index: 242



Y Index: 250

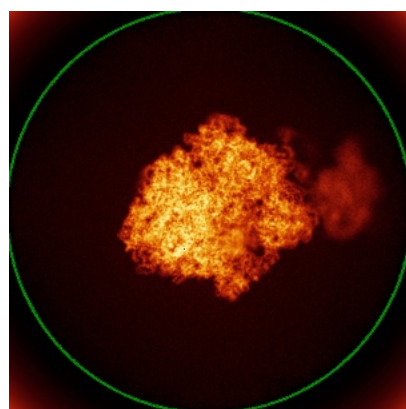


Z Index: 258

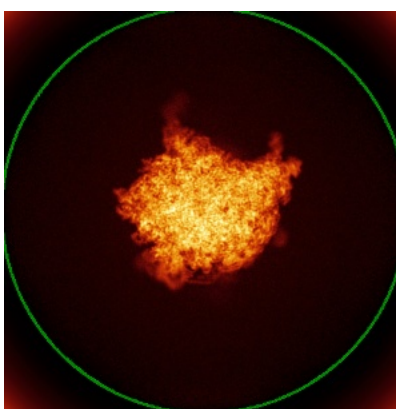
The images above show the largest variance slices of the map in three orthogonal directions.

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

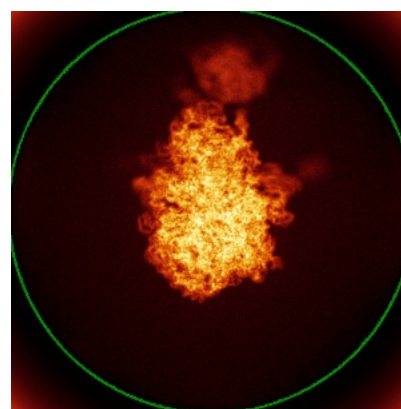
6.4.1 Primary map



X



Y

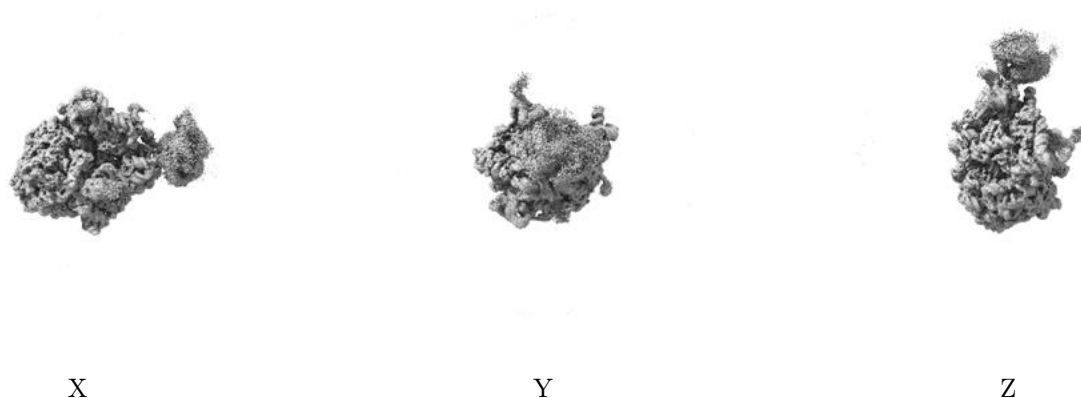


Z

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 0.00868. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

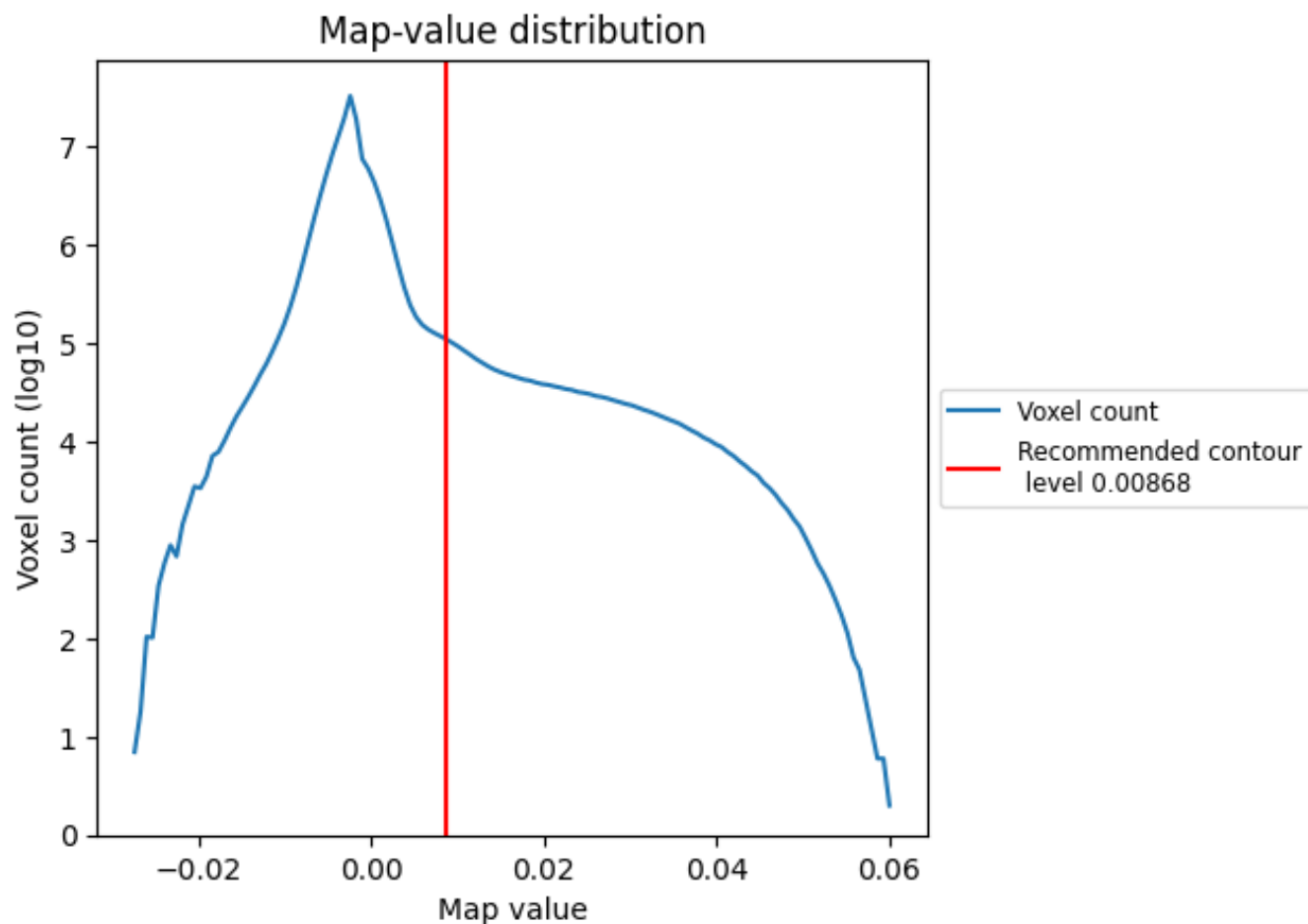
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

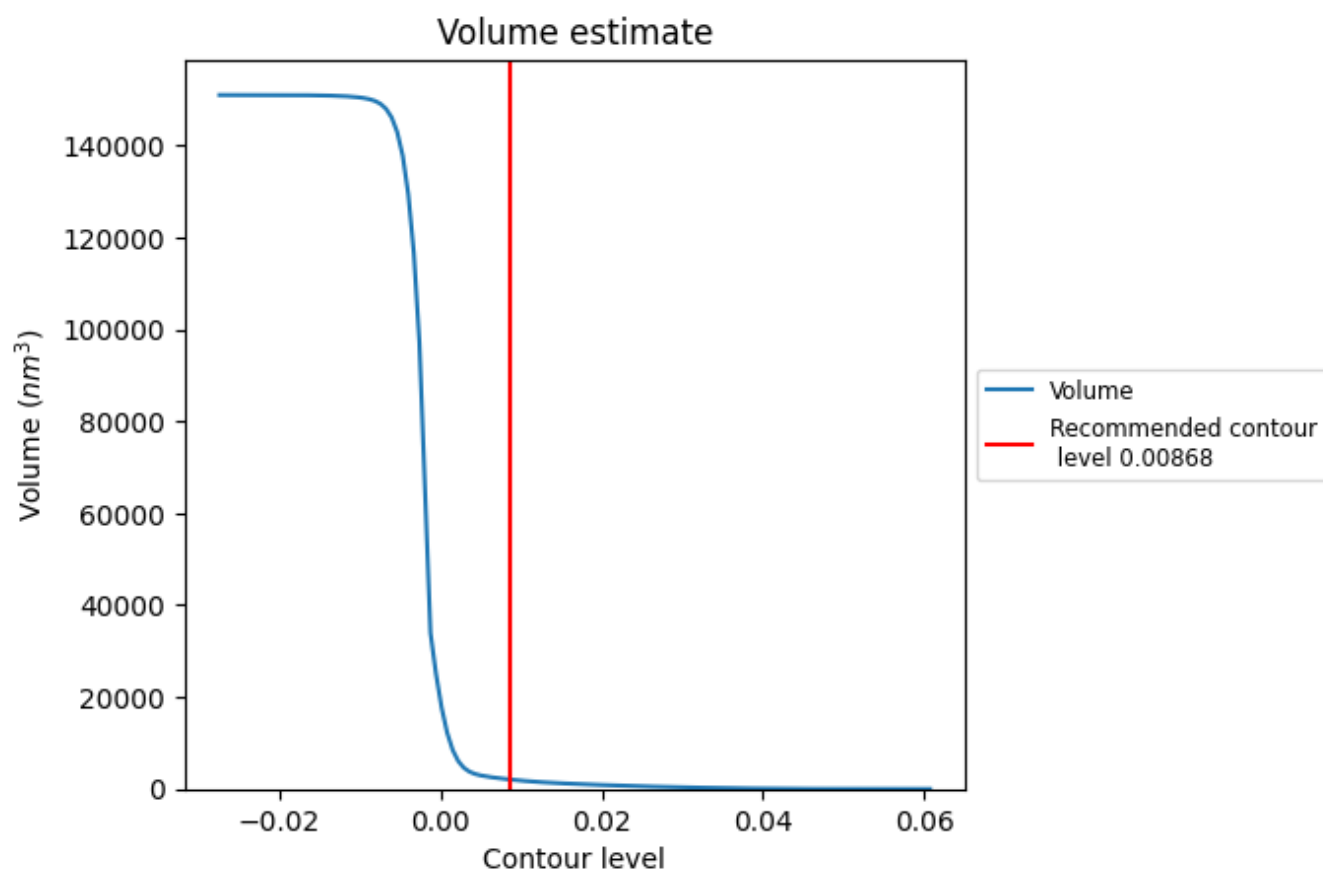
This section contains the results of statistical analysis of the map.

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.

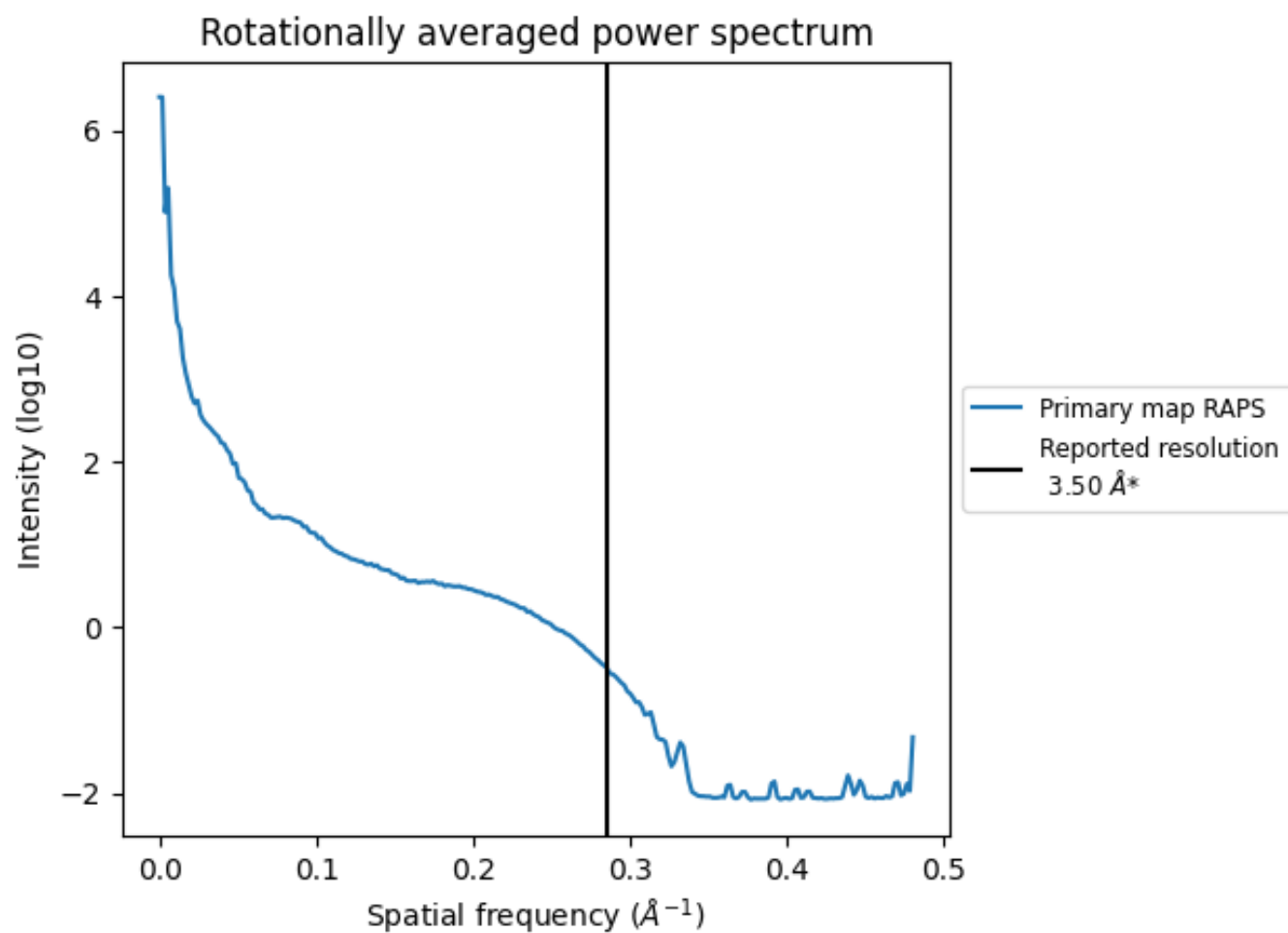
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2046 nm³; this corresponds to an approximate mass of 1848 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 0.286 Å⁻¹

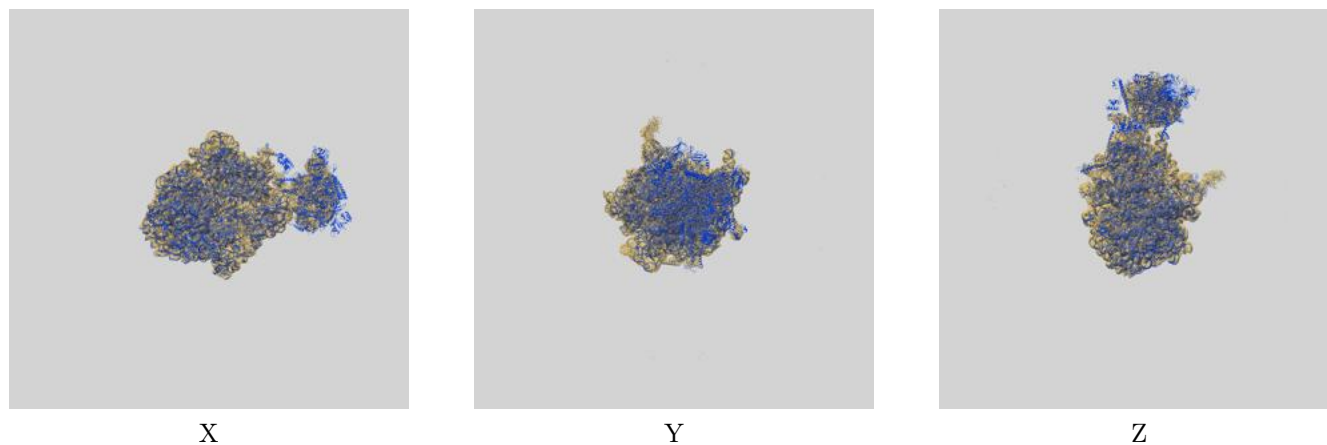
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

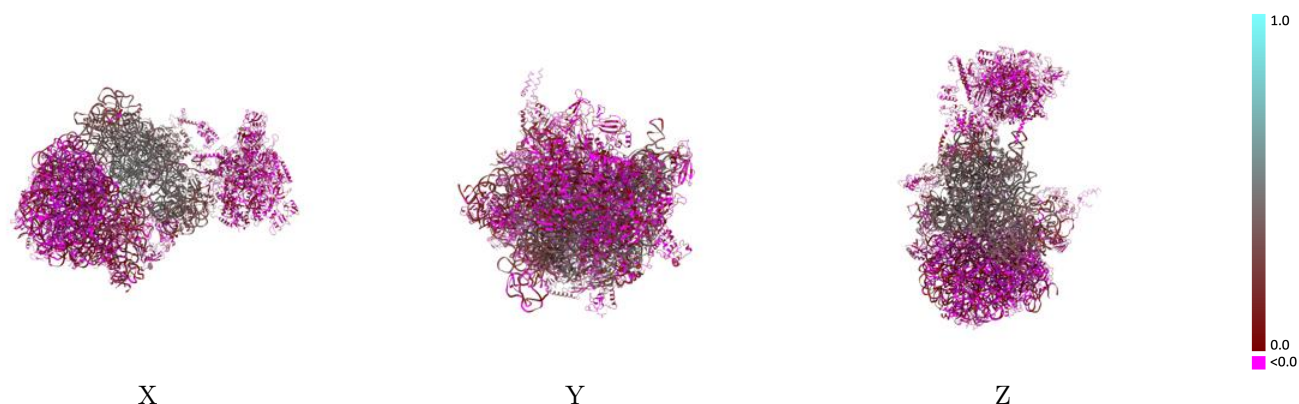
This section contains information regarding the fit between EMDB map EMD-22084 and PDB model 6X7F. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



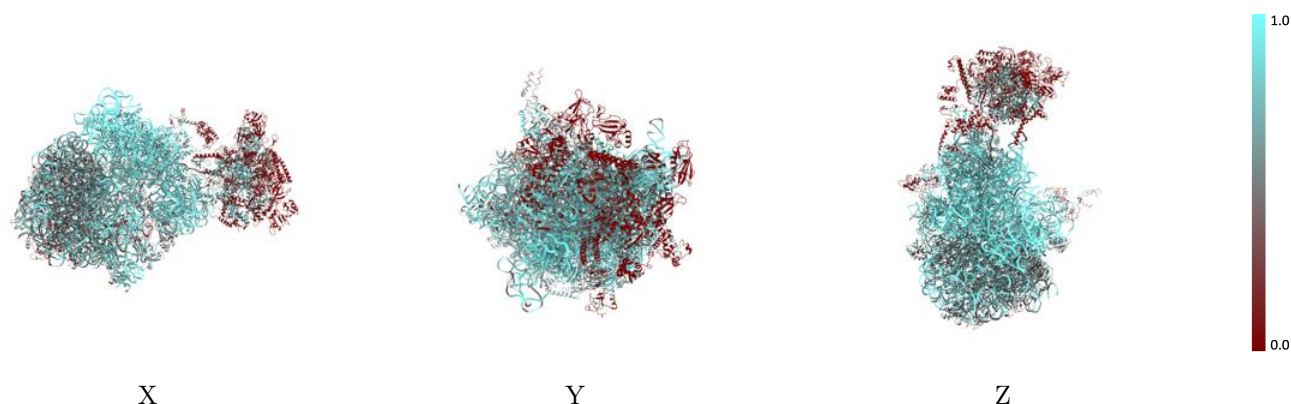
The images above show the 3D surface view of the map at the recommended contour level 0.00868 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



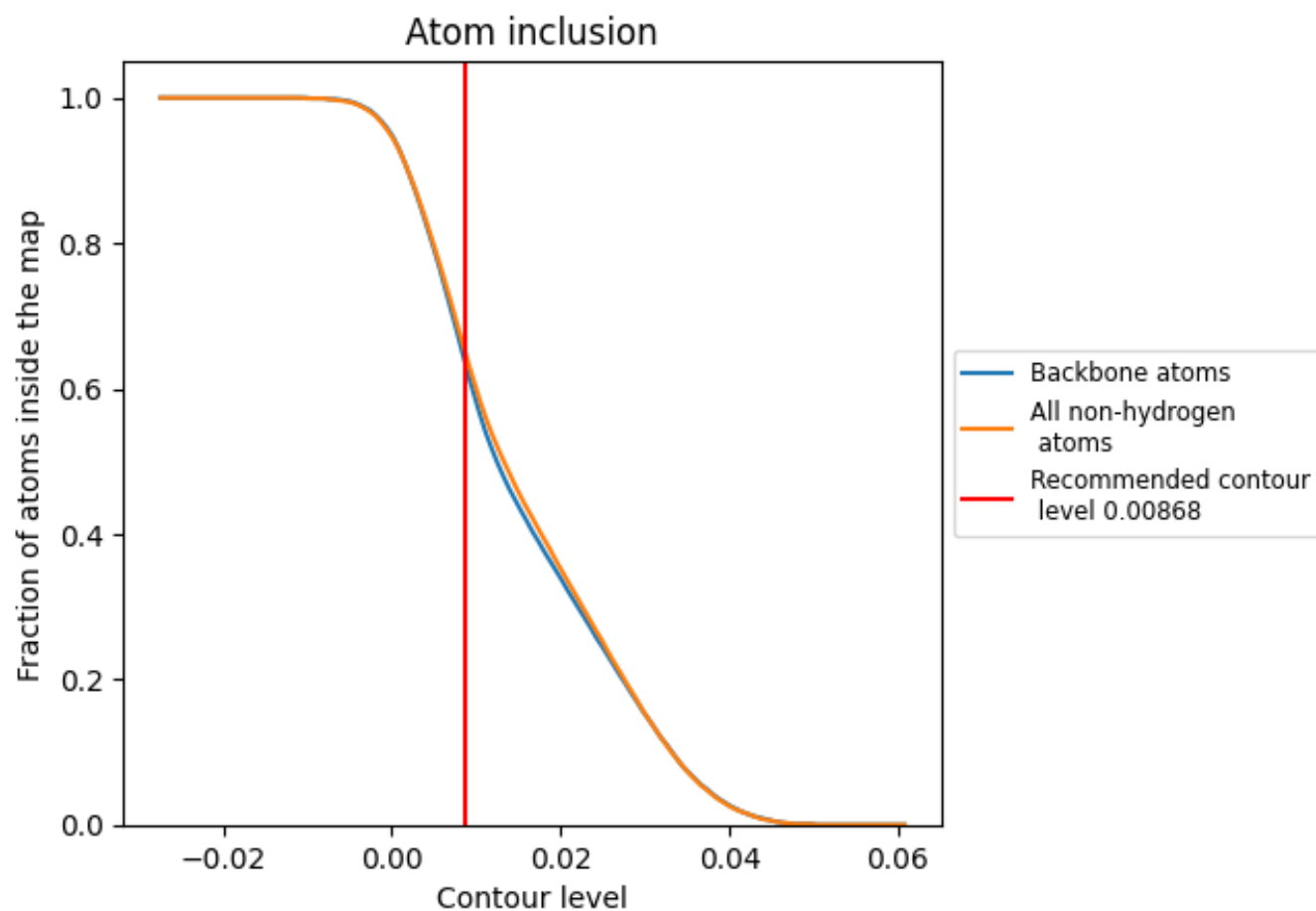
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00868).

9.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 65% 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 (0.00868) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6500	 0.1190
0	 0.5190	 -0.0330
1	 0.4900	 -0.0410
2	 0.5140	 -0.0410
3	 0.5220	 -0.0190
4	 0.5920	 0.0360
5	 0.4300	 0.0620
6	 0.6530	 0.0800
7	 0.5270	 0.0730
9	 0.5650	 0.0760
A	 0.8240	 0.1510
AA	 0.3150	 0.0280
AB	 0.4640	 0.1140
AC	 0.1880	 0.0250
AD	 0.1430	 0.0260
AE	 0.3140	 0.0260
AF	 0.0840	 0.0270
AG	 0.4770	 0.1020
B	 0.6850	 0.1050
C	 0.8240	 0.3760
D	 0.9800	 0.3900
E	 0.8610	 0.3190
F	 0.7750	 0.3290
G	 0.8290	 0.3410
H	 0.2740	 0.0500
I	 0.8350	 0.3790
J	 0.8560	 0.3850
K	 0.8670	 0.4210
L	 0.8310	 0.3460
M	 0.8030	 0.3120
N	 0.8720	 0.4070
O	 0.8510	 0.3080
P	 0.7670	 0.2900
Q	 0.8610	 0.3980
R	 0.8460	 0.4390



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Chain	Atom inclusion	Q-score
S	 0.8640	 0.3540
T	 0.8650	 0.3730
U	 0.8870	 0.3690
V	 0.8620	 0.3850
W	 0.5550	 0.0330
X	 0.5810	 0.0270
Y	 0.3890	 0.0680
Z	 0.1940	 -0.0110
a	 0.7050	 0.0100
b	 0.5880	 0.0210
c	 0.4290	 -0.0450
d	 0.8150	 0.0780
e	 0.5480	 0.0140
f	 0.5370	 -0.0350
g	 0.5910	 0.0400
h	 0.4970	 -0.0400
i	 0.4420	 -0.0600
j	 0.4780	 -0.0620
k	 0.5670	 -0.0250
l	 0.4910	 -0.0190
m	 0.4060	 -0.0810
n	 0.6490	 0.0580
o	 0.4440	 -0.0410
p	 0.6110	 0.0660
q	 0.5580	 -0.0130
r	 0.4850	 0.0680
s	 0.4870	 -0.0500
t	 0.4840	 -0.0350
u	 0.4770	 -0.0250
v	 0.5620	 0.0130
w	 0.4920	 -0.0820
x	 0.6510	 0.0400
y	 0.5170	 -0.0200
z	 0.4830	 -0.0540