



wwPDB EM Validation Summary Report ⓘ

Oct 27, 2024 – 01:15 AM EDT

PDB ID : 6VYR
EMDB ID : EMD-21469
Title : Escherichia coli transcription-translation complex A1 (TTC-A1) containing an 18 nt long mRNA spacer, NusG, and fMet-tRNAs at E-site and P-site
Authors : Molodtsov, V.; Wang, C.; Su, M.; Ebright, R.H.
Deposited on : 2020-02-27
Resolution : 3.80 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:

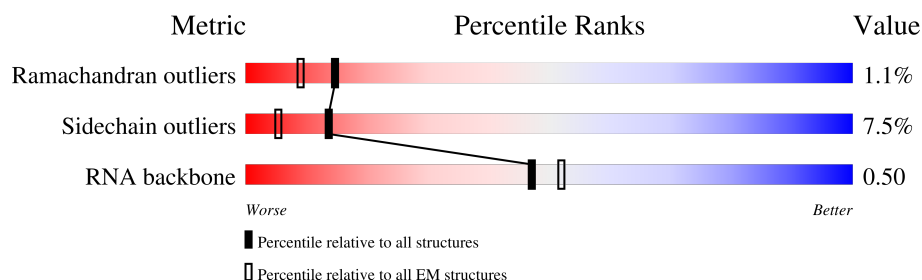
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 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 3.80 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	0	103	<div> <div>38%</div> <div>93%</div> <div>7%</div> </div>
2	1	110	<div> <div>19%</div> <div>92%</div> <div>8%</div> </div>
3	2	100	<div> <div>52%</div> <div>89%</div> <div>5%</div> <div>6%</div> </div>
4	3	104	<div> <div>54%</div> <div>91%</div> <div>8%</div> </div>
5	4	94	<div> <div>48%</div> <div>96%</div> </div>
6	5	36	<div> <div>64%</div> <div>47%</div> <div>17%</div> <div>36%</div> </div>
7	6	36	<div> <div>75%</div> <div>64%</div> <div>11%</div> <div>25%</div> </div>
8	7	35	<div> <div>97%</div> <div>26%</div> <div>71%</div> </div>

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Mol	Chain	Length	Quality of chain
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	C	75	
16	D	1542	
17	E	87	
18	F	71	
19	G	241	
20	H	557	
21	I	233	
22	J	206	
23	K	167	
24	L	135	
25	M	179	
26	N	130	
27	O	130	
28	P	103	
29	Q	129	
30	R	124	
31	S	101	

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Mol	Chain	Length	Quality of chain
32	T	89	
33	U	82	
34	V	84	
35	W	92	
36	X	118	
37	Y	142	
38	Z	121	
39	a	2904	
40	b	85	
41	c	78	
42	d	120	
43	e	63	
44	f	59	
45	g	70	
46	h	273	
47	i	57	
48	j	209	
49	k	55	
50	l	201	
51	m	46	
52	n	179	
53	o	65	
54	p	177	
55	q	38	
56	r	149	

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Mol	Chain	Length	Quality of chain
57	s	142	<div> <div>34%</div> <div>96%</div> <div>.</div> </div>
58	t	123	<div> <div>43%</div> <div>95%</div> <div>5%</div> </div>
59	u	144	<div> <div>48%</div> <div>96%</div> <div>.</div> </div>
60	v	136	<div> <div>43%</div> <div>96%</div> <div>.</div> </div>
61	w	127	<div> <div>28%</div> <div>87%</div> <div>6% • 6%</div> </div>
62	x	117	<div> <div>68%</div> <div>94%</div> <div>5% •</div> </div>
63	y	115	<div> <div>61%</div> <div>95%</div> <div>• •</div> </div>
64	z	118	<div> <div>27%</div> <div>96%</div> <div>• •</div> </div>

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 300728 atoms, of which 124723 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 18 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	35	Total	C	H	N	O	P	0	0
			829	327	97	106	264	35		

- 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		

- 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 Transcription termination/antitermination protein NusG.

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
13	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
13	AD	228	Total	C	H	N	O	S	0	0
			3556	1100	1789	312	349	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 30S ribosomal protein S18.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 37 is a protein called 50S ribosomal protein L11.

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

- Molecule 38 is a protein called 50S ribosomal protein L7/L12.

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

- Molecule 39 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	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 40 is a protein called 50S ribosomal protein L27.

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

- Molecule 41 is a protein called 50S ribosomal protein L28.

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

- Molecule 42 is a RNA chain called 5S rRNA.

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

- Molecule 43 is a protein called 50S ribosomal protein L29.

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

- Molecule 44 is a protein called 50S ribosomal protein L30.

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

- Molecule 45 is a protein called 50S ribosomal protein L31.

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

- Molecule 46 is a protein called 50S ribosomal protein L2.

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

- Molecule 47 is a protein called 50S ribosomal protein L32.

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

- Molecule 48 is a protein called 50S ribosomal protein L3.

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

- Molecule 49 is a protein called 50S ribosomal protein L33.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L34.

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

- Molecule 52 is a protein called 50S ribosomal protein L5.

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

- Molecule 53 is a protein called 50S ribosomal protein L35.

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

- Molecule 54 is a protein called 50S ribosomal protein L6.

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

- Molecule 55 is a protein called 50S ribosomal protein L36.

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

- Molecule 56 is a protein called 50S ribosomal protein L9.

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

- Molecule 57 is a protein called 50S ribosomal protein L13.

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

- Molecule 58 is a protein called 50S ribosomal protein L14.

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

- Molecule 59 is a protein called 50S ribosomal protein L15.

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

- Molecule 60 is a protein called 50S ribosomal protein L16.

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

- Molecule 61 is a protein called 50S ribosomal protein L17.

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

- Molecule 62 is a protein called 50S ribosomal protein L18.

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

- Molecule 63 is a protein called 50S ribosomal protein L19.

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

- Molecule 64 is a protein called 50S ribosomal protein L20.

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

- Molecule 65 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

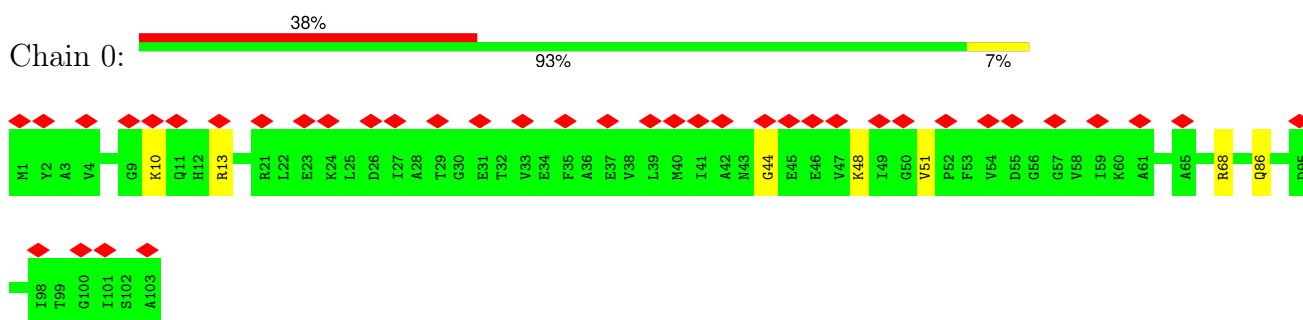
- Molecule 66 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

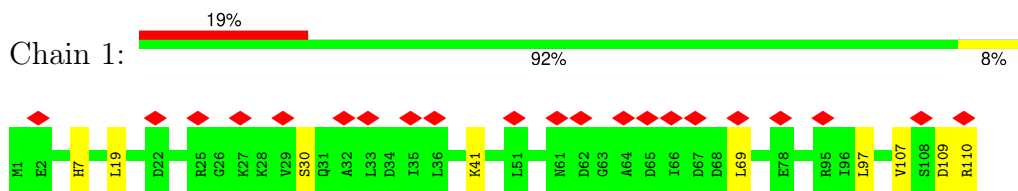
3 Residue-property plots [i](#)

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.

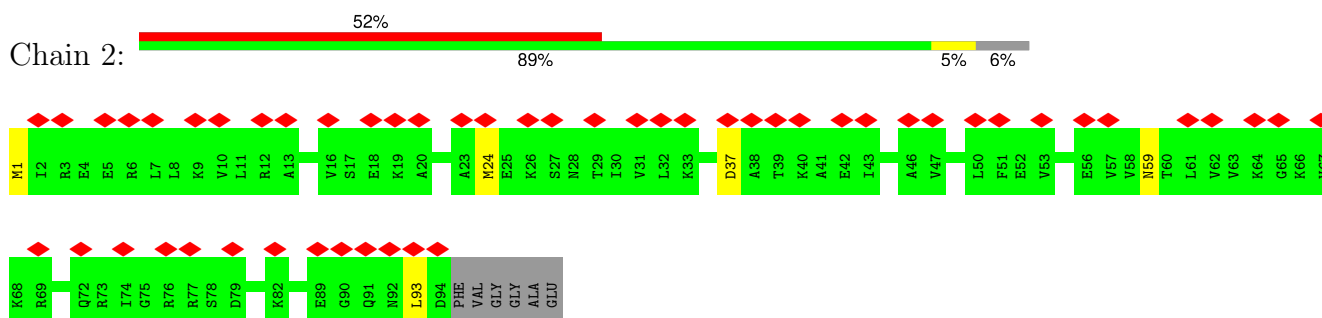
- Molecule 1: 50S ribosomal protein L21



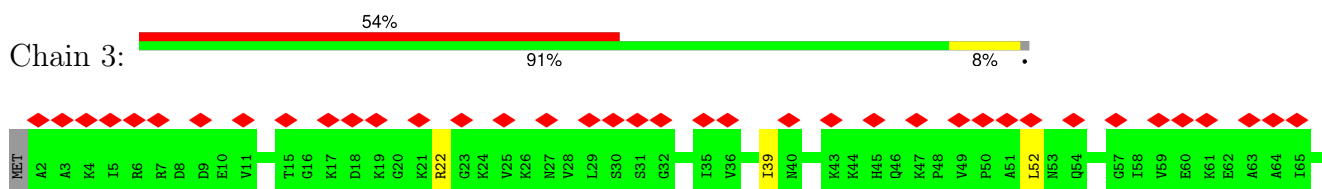
- Molecule 2: 50S ribosomal protein L22

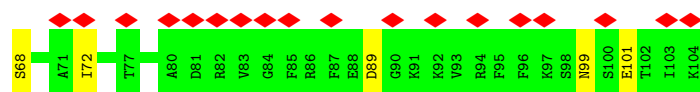


- Molecule 3: 50S ribosomal protein L23

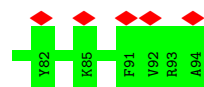
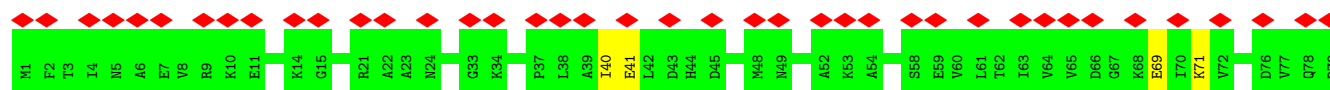


- Molecule 4: 50S ribosomal protein L24

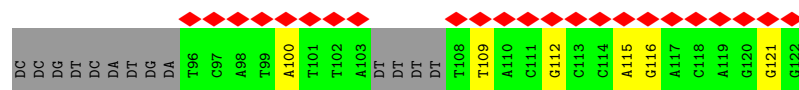




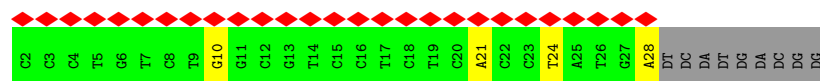
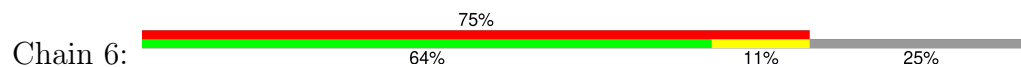
- Molecule 5: 50S ribosomal protein L25



- Molecule 6: NT DNA



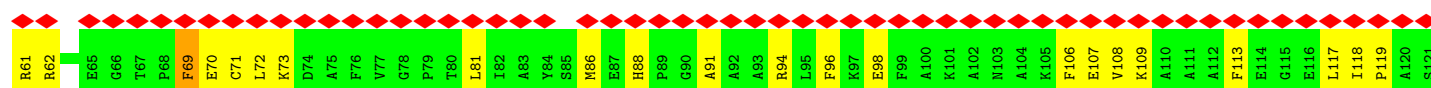
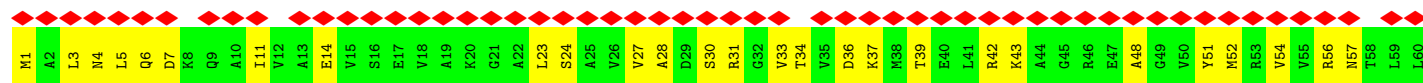
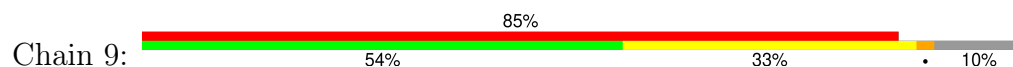
- Molecule 7: T DNA

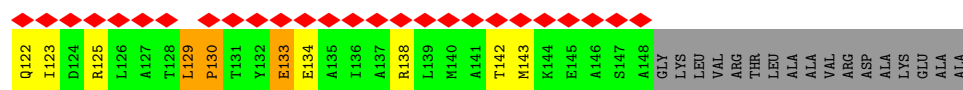


- Molecule 8: mRNA with 18 nt long spacer

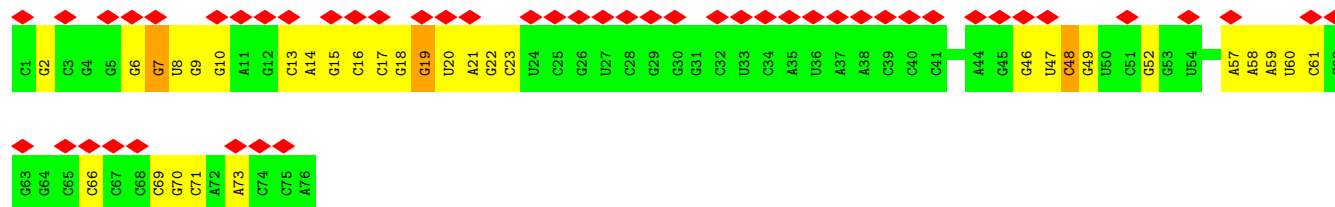


- Molecule 9: 50S ribosomal protein L10

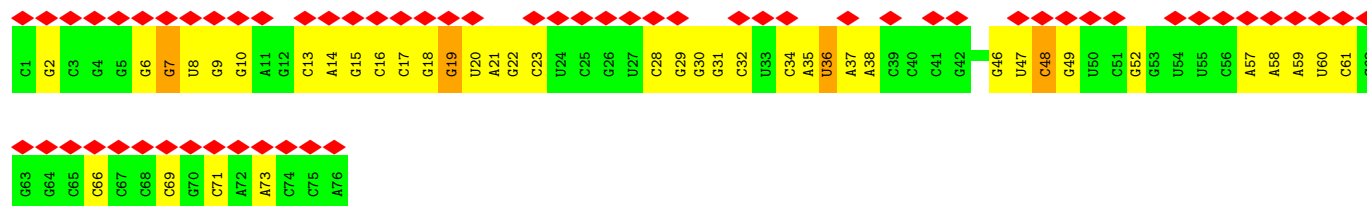
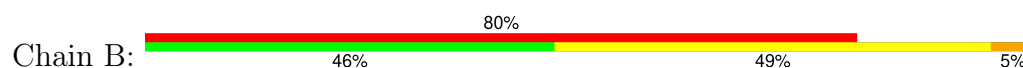




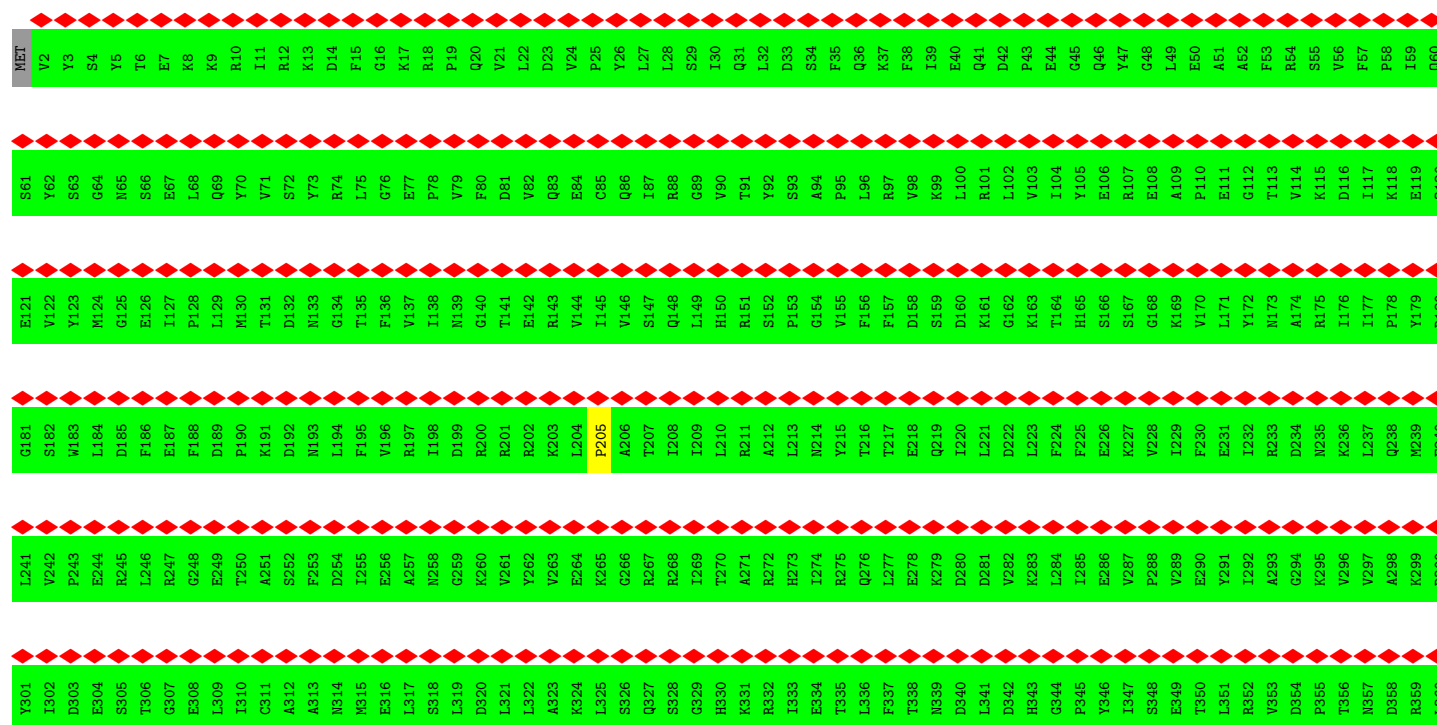
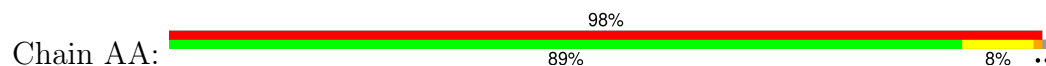
• Molecule 10: E-site and P-site tRNA (fMet)



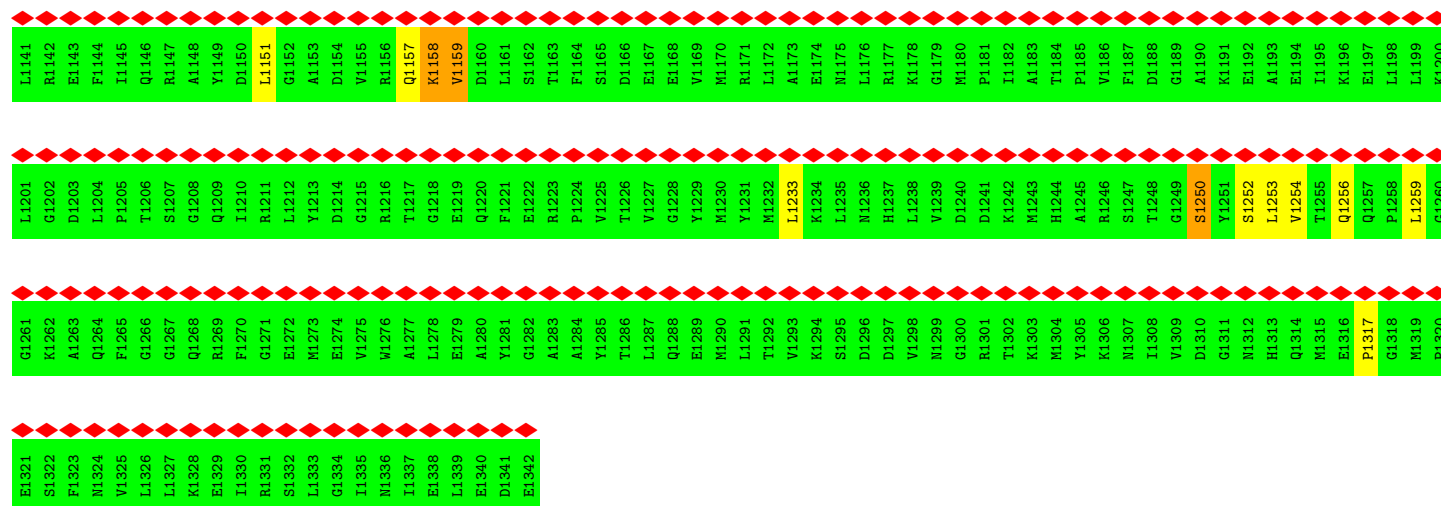
• Molecule 10: E-site and P-site tRNA (fMet)



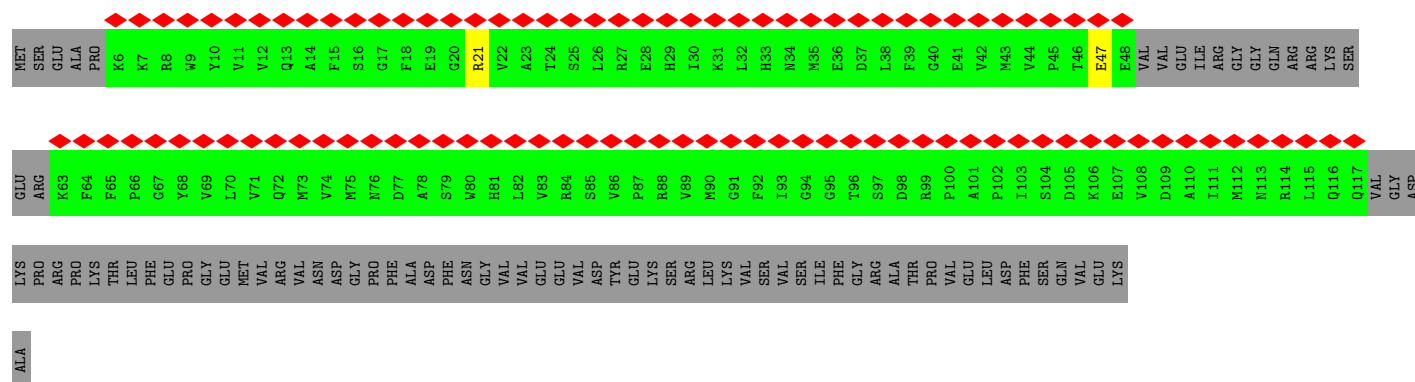
• Molecule 11: DNA-directed RNA polymerase subunit beta



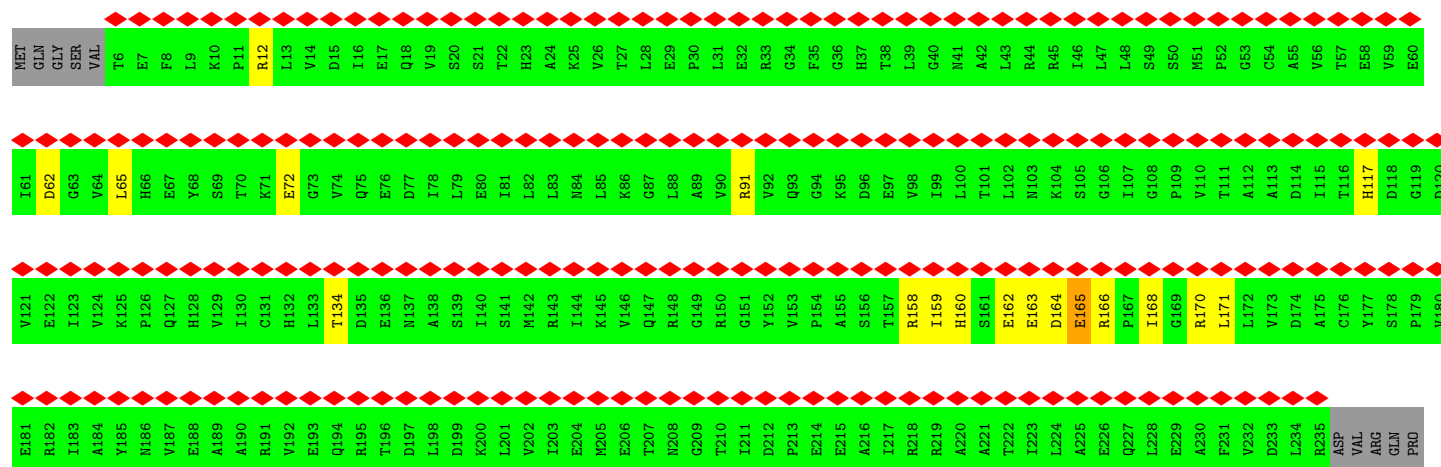
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L1021	K1022	H1023	E1024	F1025	E1026	K1027	K1028	L1029	E1030	A1031	K1032	R1033	I1034	K1035	I1036	T1037	G1038	G1039	D1040	D1041	L1042	A1043	P1044	G1045	I1046	L1047	K1048	I1049	I1050	K1051	Y1052	Y1053	L1054	A1055	V1056	K1057	R1058	R1059	I1060	Q1061	P1062	G1063	D1064	K1065	E1066	M1067	G1068	R1069	N1070	L1071	N1072	K1073	G1074	V1075	I1076	S1077	K1078	I1079	N1080
S961	E962	E963	L964	Q965	I966	L967	E968	A969	G970	L971	F972	S973	R974	I975	R976	A977	V978	L979	V980	A981	G982	G983	V984	E985	A986	E987	K988	L989	D990	K991	L992	P993	R994	D995	R996	W997	L998	E999	L1000	G1001	L1002	T1003	D1004	E1005	E1006	K1007	Q1008	N1009	Q1010	L1011	E1012	Q1013	L1014	A1015	E1016	Q1017	Y1018	D1019	E1020
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D601	E602	I603	H604	Y605	L606	S607	A608	I609	E610	E611	G612	N613	Y614	V615	I616	A617	Q618	A619	N620	S621	N622	L623	D624	E625	E626	G627	H628	F629	V630	E631	D632	L633	V634	T635	C636	R637	S638	K639	G640	E641	S642	S643	L644	F645	S646	R647	D648	Q649	V650	D651	Y652	M653	D654	V655	S656	T657	Q658	Q659	V660
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G721	G722	V723	V724	Q725	V726	V727	D728	A729	S730	R731	I732	V733	I734	K735	V736	M737	E738	D739	E740	M741	V742	F743	G744	E745	A746	G747	I748	D749	V750	N751	N752	L753	T754	K755	V756	T757	F758	S759	N760	Q761	N762	T763	G764	I765	N766	Q767	M768	P769	T770	D771	S772	L773	G774	E775	P776	V777	E778	R779	G780
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R841	D842	T843	K844	L845	G846	P847	E848	E849	T850	T851	A852	D853	T854	P855	N856	V857	G858	E859	A860	A861	L862	S863	K864	L865	D866	E867	S868	G869	T870	V871	H872	L873	G874	A875	E876	V877	T878	G879	C880	D881	L882	L883	V884	G885	K886	V887	T888	P889	K890	G891	GLU	THR	GLN	LEU	PRO	GLU	GLU	LYS	
LEU	LEU	ARG	ALA	ILE	PHE	GLY	GLU	LYS	ALA	S911	D912	V913	K914	D915	S916	S917	L918	R919	V920	P921	N922	G923	V924	S925	G926	T927	V928	I929	D930	V931	Q932	V933	F934	T935	R936	D937	G938	V939	E940	K941	D942	K943	R944	A945	L946	E947	I948	E949	E950	N951	Q952	L953	K954	Q955	A956	K957	K958	D959	L960
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P1081	I1082	E1083	I1084	P1085	M1086	Y1087	D1088	E1089	N1090	G1091	T1092	P1093	I1094	D1095	I1096	V1097	L1098	N1099	P1100	L1101	G1102	V1103	P1104	S1105	R1106	M1107	N1108	I1109	G1110	Q1111	I1112	L1113	E1114	T1115	H1116	L1117	G1118	M1119	A1120	I1121	K1122	G1123	I1124	G1125	D1126	K1127	I1128	N1129	A1130	M1131	L1132	K1133	Q1134	Q1135	Q1136	E1137	V1138	A1139	K1140



• Molecule 12: Transcription termination/antitermination protein NusG



• Molecule 13: DNA-directed RNA polymerase subunit alpha



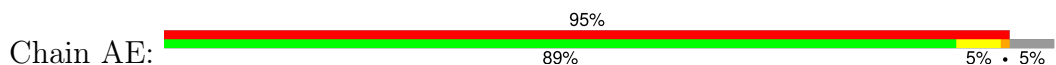
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THR	GLU	ILE	LYS	ASP	VAL	LEU	ALA	SER	GLY	ARG	GLY	LEU	LEU	SER	LEU	R12	L13	V14	D15	I16	E17	Q18	V19	S20	S21	T22	H23	A24	K25	V26	T27	L28	I29	P30	L31	E32	R33	Q34	F35	G36	H37	T38	L39	G40	M41	A42	L43	R44	R45	I46	L47	L48	S49	M51	P52	G53	C54	A55	V56	T57	E58	V59	E60						

• Molecule 13: DNA-directed RNA polymerase subunit alpha



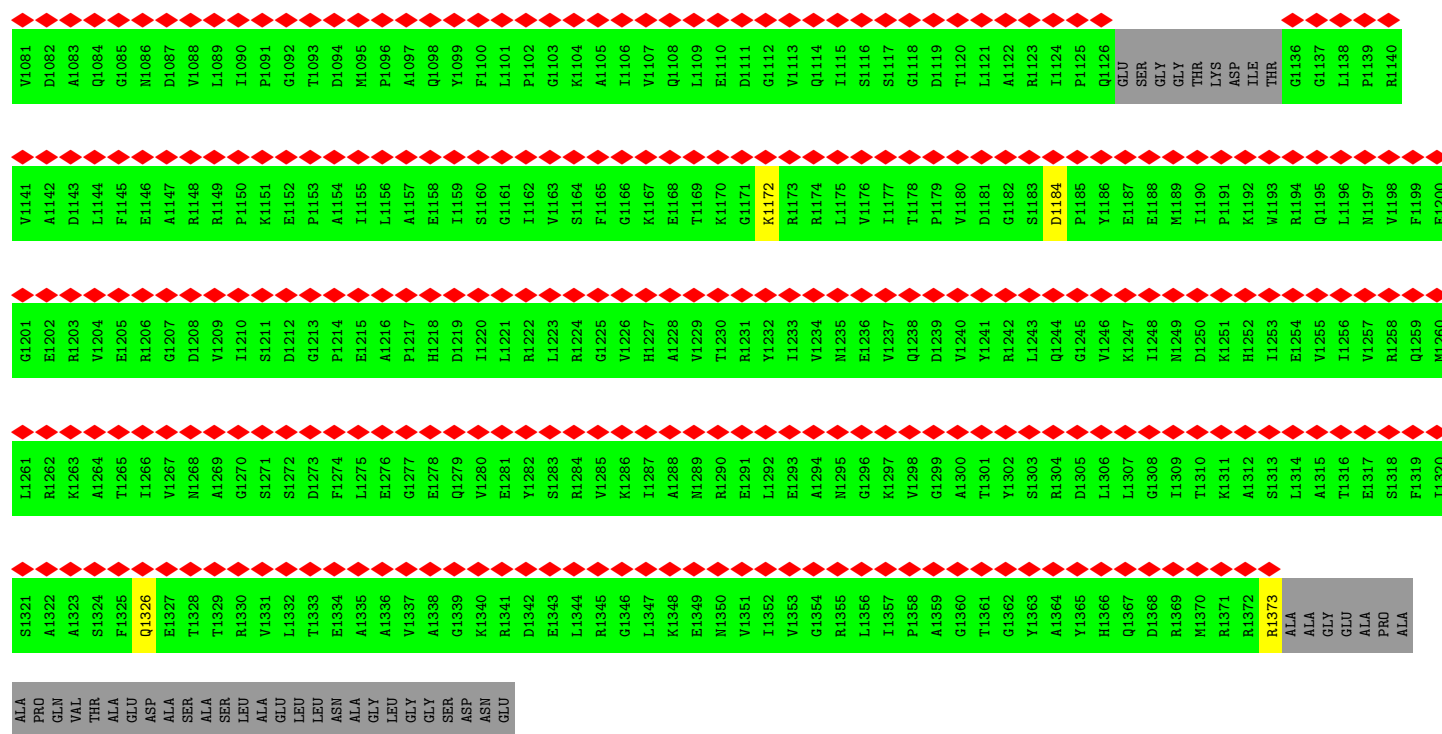
THR	GLU	ILE	LYS	ASP	VAL	LEU	ALA	SER	GLY	ARG	MET	PRO	VAL	ASP	ASP	ASN	TRP	PRO	PRO	THR	ALA	VAL	ARG	SER	ILE	ASP	GLU																																
GLU	VAL	LYS	GLU	GLU	PRO	GLU	PHE	ASP	PRO	ILE	LEU	LEU	LEU	ASP	ASP	LEU	TRP	PRO	PRO	THR	ALA	VAL	SER	ILE	ALA	ASP	GLU																																
E181	R182	I183	A184	N186	V187	E188	A189	A190	L191	V192	E193	Q194	R195	T196	D197	L198	D199	K200	L201	V202	I203	E204	M205	E206	T207	N208	G209	T210	I211	D212	P213	E214	E215	A216	I217	R218	R219	A220	A221	T222	I223	L224	A225	E226	Q227	L228	E229	A230	F231	V232	D233	LEU	ARG	ASP	VAL	ARG	GLN	PRO	
V121	E122	I123	V124	K125	P126	Q127	H128	V129	I130	C131	H132	L133	T134	D135	E136	N137	A138	S139	I140	S141	M142	R143	I144	K145	V146	Q147	R148	G149	R150	G151	V152	V153	P154	A155	S156	T157	R158	I159	H160	S161	E162	E163	D164	A165	R166	P167	I168	G169	R170	L171	L172	V173	D174	A175	C176	Y177	S178	P179	H180
I61	D62	G63	V64	L65	H66	E67	Y68	S69	T70	K71	E72	G73	V74	Q75	E76	D77	I78	L79	E80	I81	L82	L83	N84	K86	G87	L88	A89	V90	R91	V92	Q93	G94	K95	D96	E97	V98	I99	L100	T101	L102	M103	K104	S105	G106	I107	G108	P109	V110	T111	A112	A113	D114	I115	T116	H117	D118	G119	L120	
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• Molecule 14: DNA-directed RNA polymerase subunit beta'

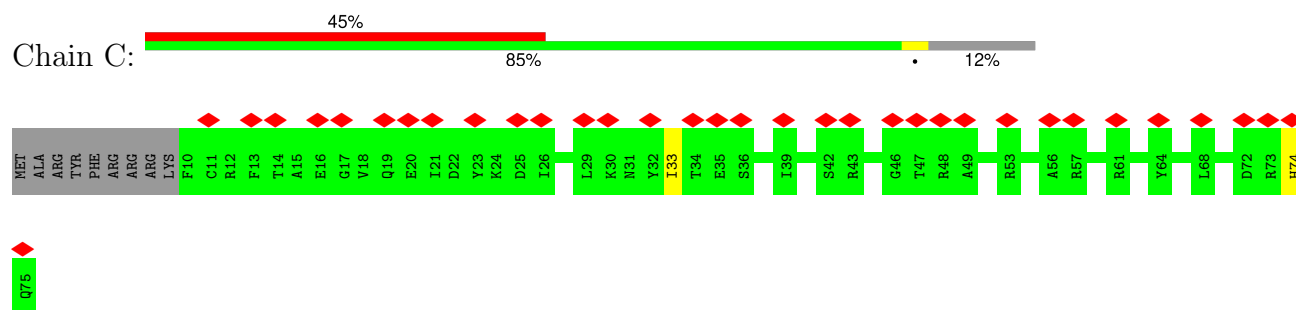


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I61	P121	G181	V241																																																							
F62	S122	A182	L242																																																							
G63	R123	E183	P243																																																							
P64	I124	A184	V244																																																							
V65	G125	I185	L245																																																							
K66	L126	Q186	P246																																																							
D67	L127	A187	P247																																																							
Y68	L128	L188	D248																																																							
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C70	M130	K190	R250																																																							
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G73	D133	D193	V253																																																							
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V83	S143	E203	S263																																																							
I84	Y144	E204	D264																																																							
C85	V145	L205	L265																																																							
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G89	G149	N209	Y269																																																							
V90	G150	S210	R270																																																							
E91	M151	E211	R271																																																							
V92	T152	T212	V272																																																							
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Q94	L154	R214	M274																																																							
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G103	E163	L223	L283																																																							
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L107	D167	F227	A287																																																							
A108	A168	V228	P288																																																							
S109	L169	Q229	D289																																																							
P110	E170	S230	I290																																																							
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I114	D174	P234	M294																																																							
W115	E175	E235	E295																																																							
F116	F176	W236	K296																																																							
L117	T177	M237	R297																																																							
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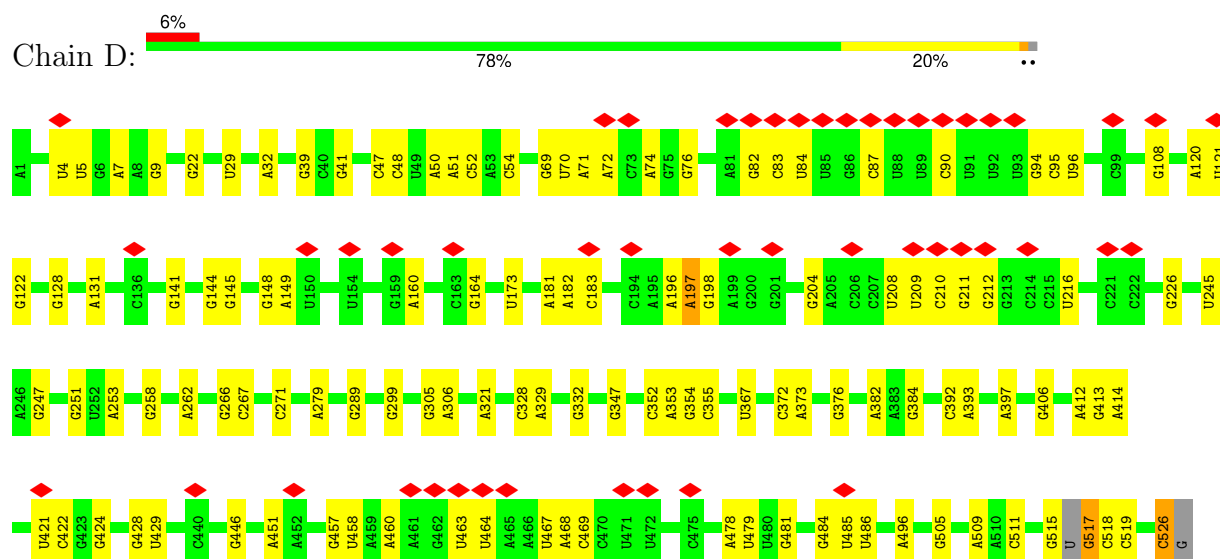
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H1023	V963	R843	L783	Y723	E663	K603	S543	L483	L423	L363	V303
T1024	K964	T844	A784	W724	T664	M604	L544	M484	N424	H364	D304
M1025	S965	A845	D785	W725	Q665	L605	H545	M485	Q425	Q365	A305
P1026	V966	E846	T786	A726	E666	M606	A546	S486	A426	C366	L306
V1027	H967	D847	A787	D727	Q667	T607	R547	T487	P427	G367	L307
I1028	N968	R848	L788	S728	F668	C608	V548	M488	T428	L368	D308
T1029	S969	L849	K789	G729	Q669	Y609	K549	M489	L429	P369	N309
E1030	H970	K850	T790	A730	Q670	R610	V550	I490	H430	K370	G310
V1031	K971	P851	A791	R731	G671	I611	R551	L491	R431	K371	R311
S1032	K972	G852	W792	S732	L672	L612	I552	S492	L432	M372	R312
G1033	L973	T853	S793	G733	V673	G613	T553	P493	G433	A373	G313
F1034	V974	A854	G794	A734	T674	L614	E554	A494	I434	L374	R314
V1035	I975	D855	Y795	A735	A675	K615	Y555	M495	Q435	E375	A315
R1036	T976	L856	L796	Q736	G676	P616	E556	G496	A436	L376	I316
F1037	S977	L857	T797	I737	E677	T617	K557	E497	F437	F377	T317
T1038	R978	R798	R798	R738	B678	V618	D558	P498	E438	K378	G318
D1039	P859	R799	R799	Q739	Y679	I619	A559	I499	P439	P379	S319
M1040	R860	L800	L800	L740	N680	F620	N560	I500	V440	F380	N320
I1041	R861	W801	A741	A741	K681	A621	G561	V501	L441	I381	K321
D1042	T862	D802	G742	G742	V682	D622	E562	P502	I442	Y382	R322
G1043	L863	W803	W743	W743	I683	Q623	L563	S503	E443	G383	P323
Q1044	L864	A804	R744	R744	D684	I624	V564	Q504	G444	K384	L324
I1045	E925	Q805	G745	G745	I685	M625	A565	D505	K445	K385	K325
T1046	R986	D806	L746	L746	V686	Y626	K566	V506	A446	E386	S326
T1047	Q927	L807	W747	W747	A687	T627	T567	V507	I447	L387	L327
R1048	W868	W808	A748	A748	A688	G628	S568	L508	Q448	R388	A328
Q1049	C869	R809	K749	K749	A689	F629	L569	G509	L449	G389	D329
T1050	D870	T810	P750	P750	N690	A630	K570	L510	H450	L390	M330
D1051	L871	E811	D751	D751	D691	Y631	D571	Y511	P451	A391	I331
E1052	L872	D812	G752	G752	R692	A632	T572	Y512	L452	T392	K332
L1053	E873	D813	S753	S753	V693	A633	T573	M513	V453	T393	G333
T1054	E874	C814	I754	I754	S694	R634	V574	T514	C454	I394	K334
G1055	N875	G815	I755	I755	K695	S635	G575	R515	A455	K395	Q335
L1056	K996	T816	E756	E756	A696	G636	R576	D516	A456	A396	G336
S1057	W877	H817	T757	T757	M697	A637	A577	C517	Y457	A397	R337
L1058	D878	E818	P758	P758	R698	S638	I578	V518	N458	K398	F338
V1059	A879	G819	I759	I759	D699	V639	L579	N519	A459	K399	R339
G1060	W880	T820	T760	T760	N700	G640	N580	A520	D460	M400	Q340
V1061	K881	M821	A761	A761	L701	I641	M581	K521	F461	V401	N341
L1062	H882	M822	W762	W762	Q702	D642	I582	G522	D462	E402	L342
D1063	R883	T823	F763	F763	T703	D643	V583	E523	G463	R403	L343
S1064	S884	P824	R764	R764	E704	M644	P584	G524	D464	E404	G344
A1065	W885	W825	E765	E765	T705	V645	K585	M525	Q465	E405	K345
E1066	R886	T826	G766	G766	V706	I646	G586	V526	A466	A406	R346
R1067	S887	E827	L767	L767	I707	P647	L587	L527	A467	V407	V347
T1068	C888	G828	W768	W768	W708	E648	P588	T528	V468	V408	D348
A1069	D889	G829	V769	V769	K649	G649	Y589	G529	H469	W409	V349
G1070	T890	D830	L770	L770	K650	R650	S590	P530	V470	D410	S350
V1071	D891	W831	Q771	Q771	H651	H651	I591	K531	P471	I411	G351
K1072	F892	K832	Y772	Y772	E652	I653	V592	E532	L472	L412	R352
D1073	G893	E833	F773	F773	E713	I653	N593	A533	T473	D413	S353
L1074	W894	P834	I774	I774	T654	I654	Q594	E534	L474	E414	V354
R1075	C895	L835	S775	S775	K715	S655	A595	R535	E475	V415	I355
P1076	A896	R836	T776	T776	Q716	E566	L596	L536	A476	I416	T356
A1077	H897	D837	H777	H777	V717	A657	G597	Y537	Q477	R417	V357
L1078	C898	R838	G778	G778	S718	E658	K598	R538	L478	E418	G358
K1079	W899	W839	A779	A779	F719	A659	K599	S539	E479	H419	P359
I1080	G900	L840	R780	R780	N720	E660	A600	G540	A480	P420	Y360

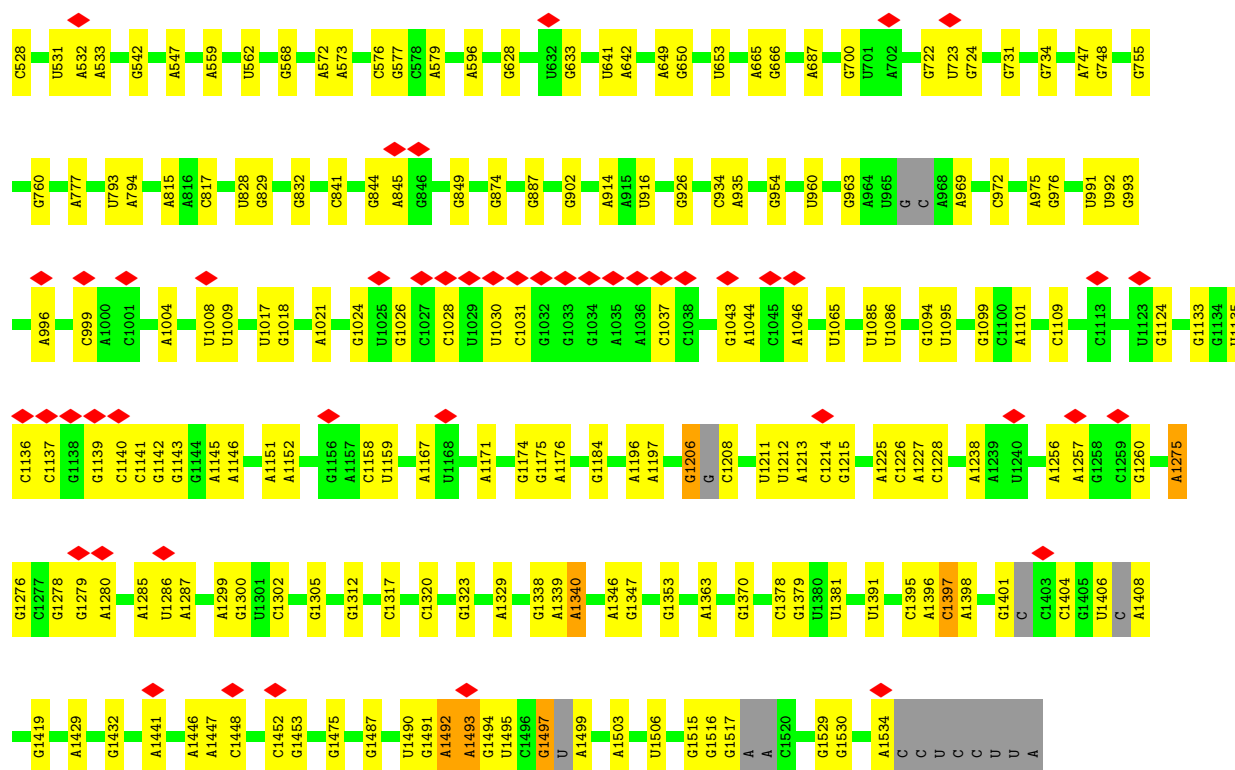


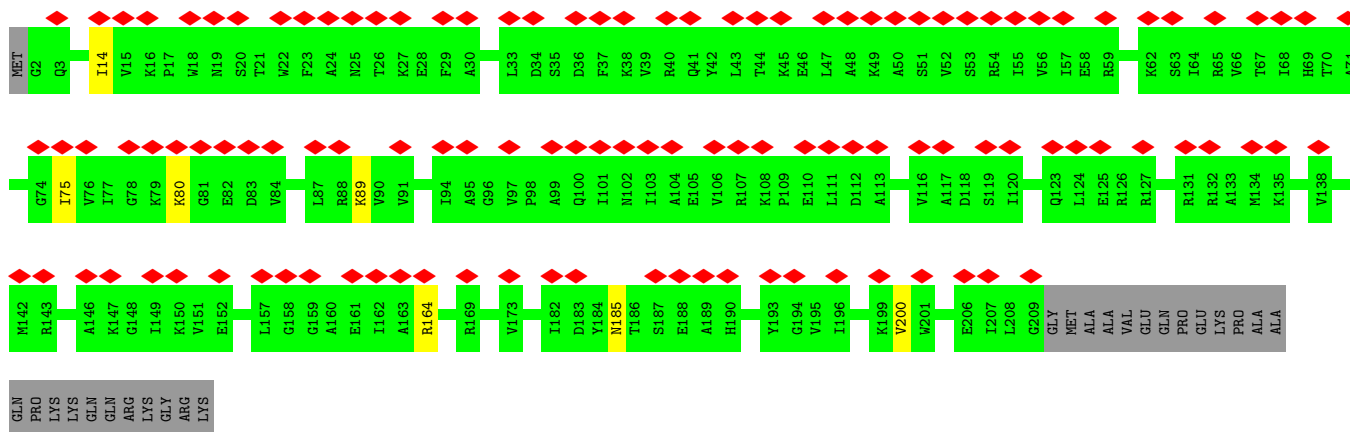
• Molecule 15: 30S ribosomal protein S18



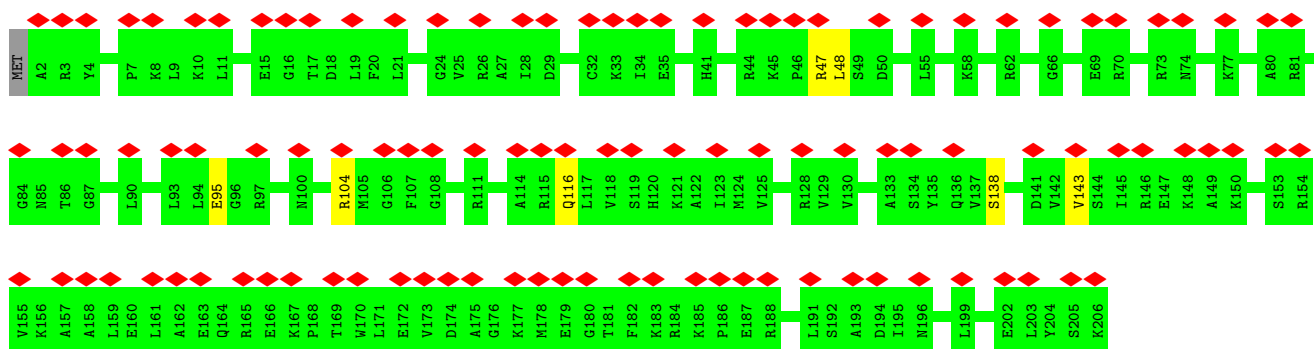
• Molecule 16: 16S rRNA



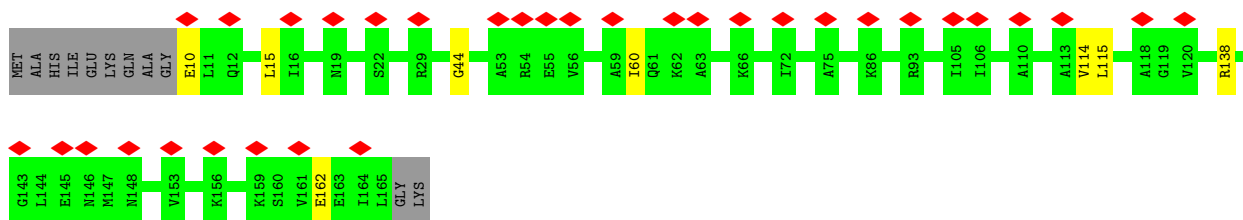
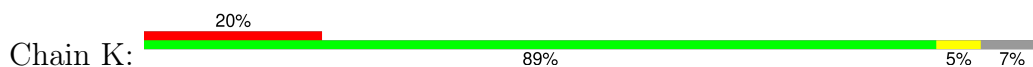




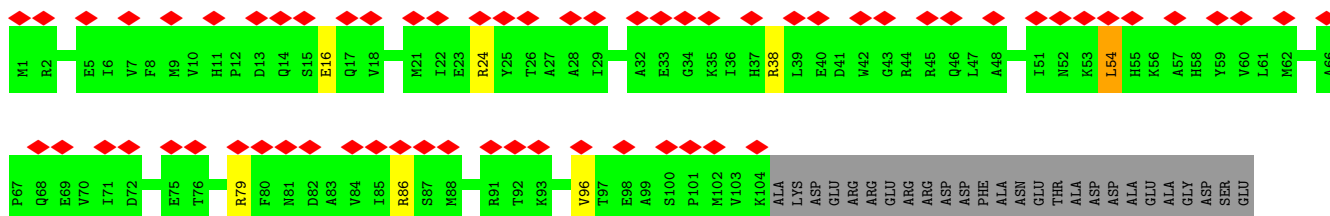
• Molecule 22: 30S ribosomal protein S4



• Molecule 23: 30S ribosomal protein S5

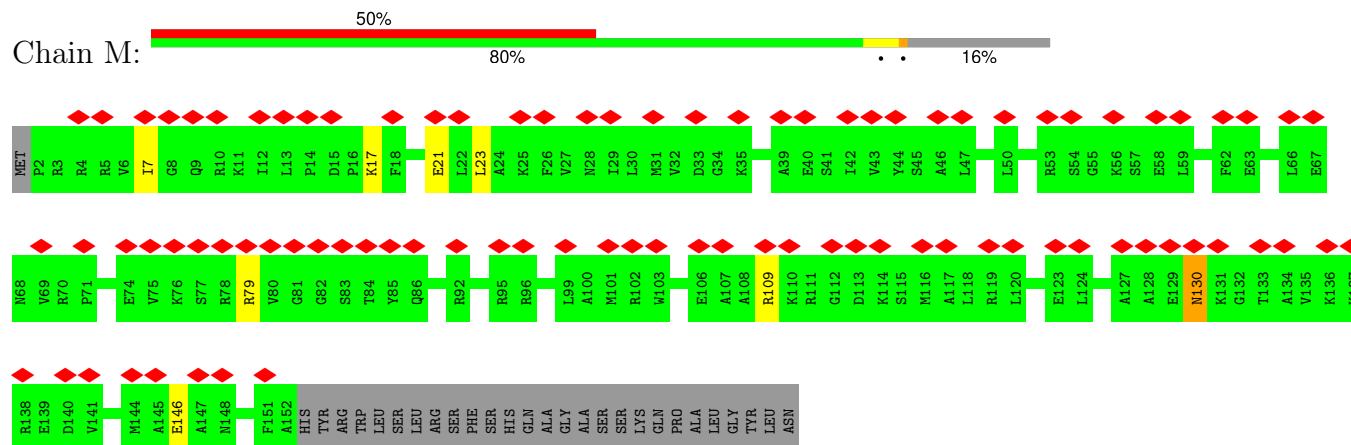


• Molecule 24: 30S ribosomal protein S6

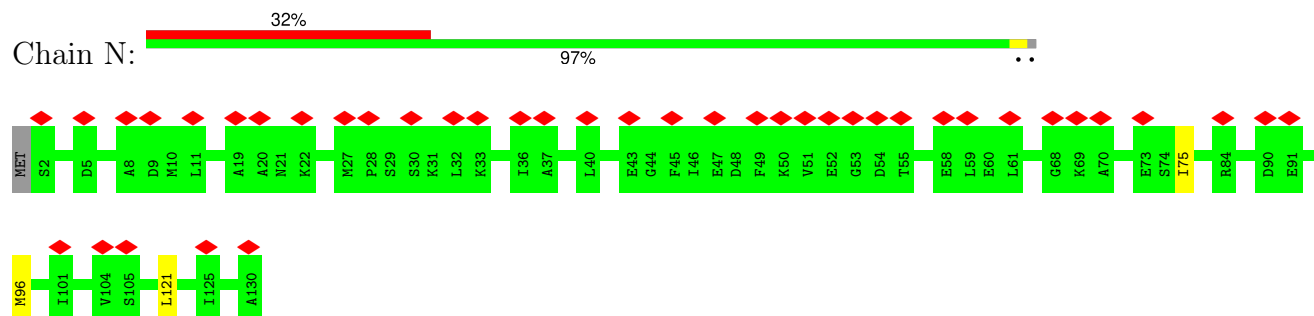


GLU
GLU
GLU
GLU

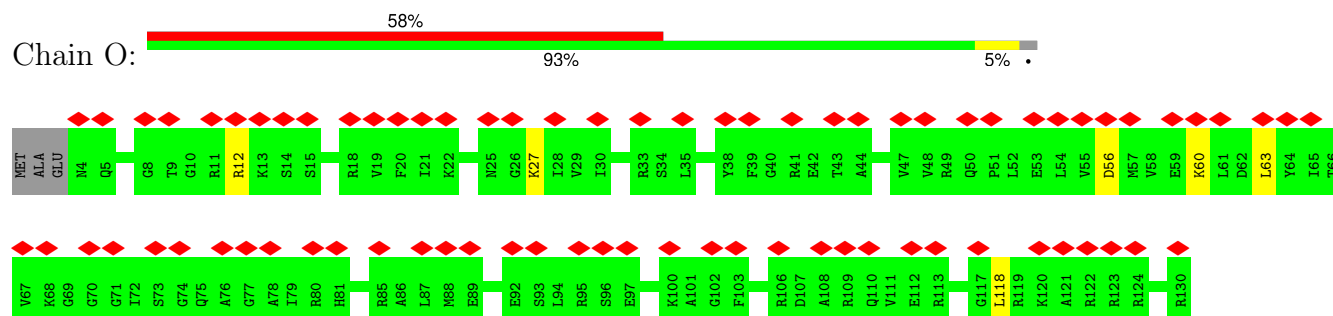
• Molecule 25: 30S ribosomal protein S7



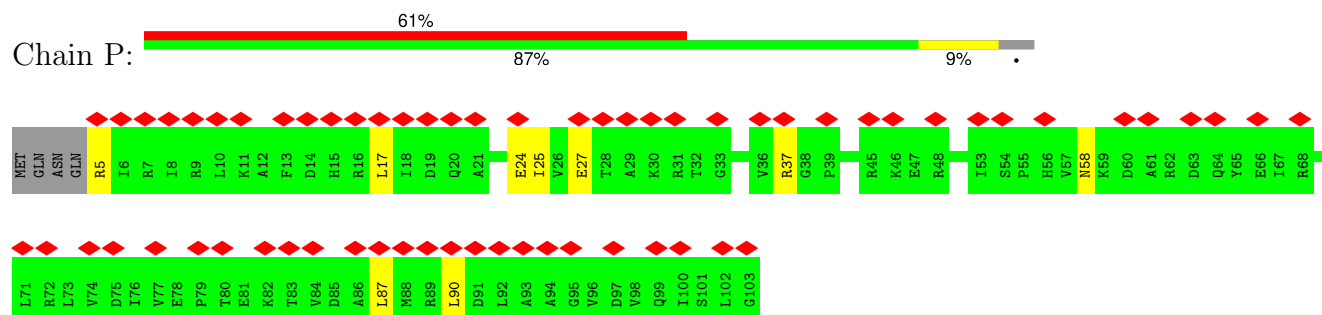
• Molecule 26: 30S ribosomal protein S8



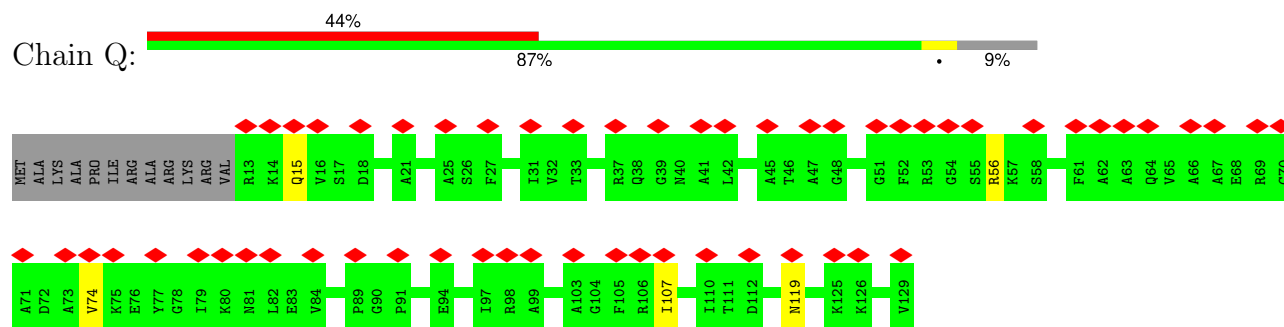
• Molecule 27: 30S ribosomal protein S9



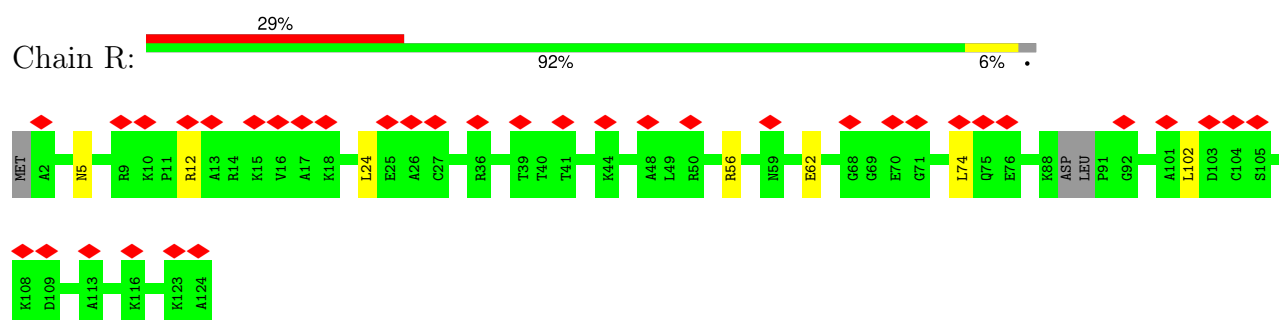
• Molecule 28: 30S ribosomal protein S10



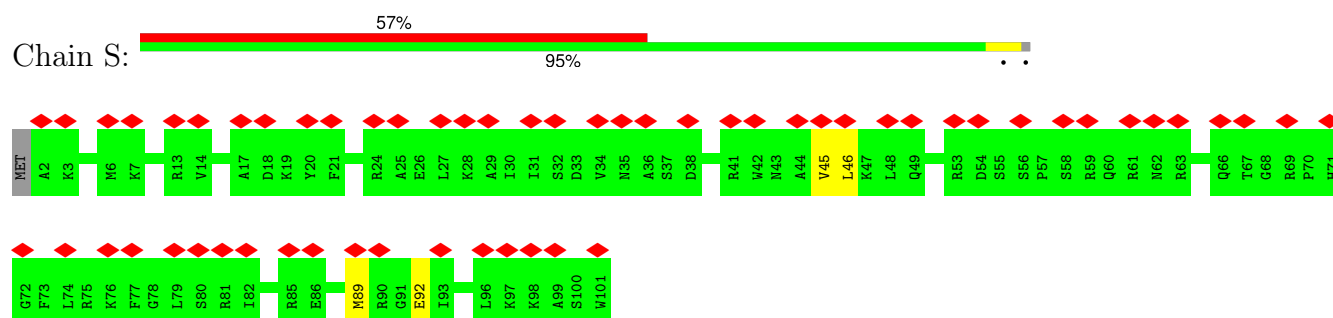
- Molecule 29: 30S ribosomal protein S11



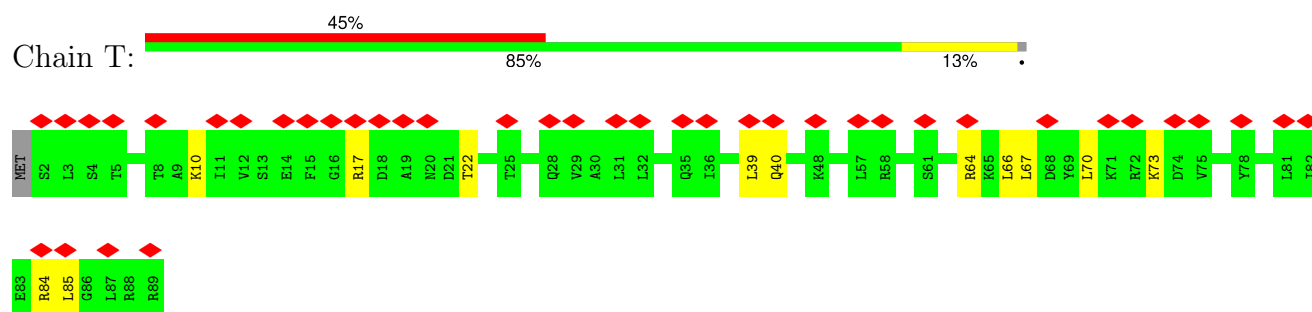
- Molecule 30: 30S ribosomal protein S12



- Molecule 31: 30S ribosomal protein S14

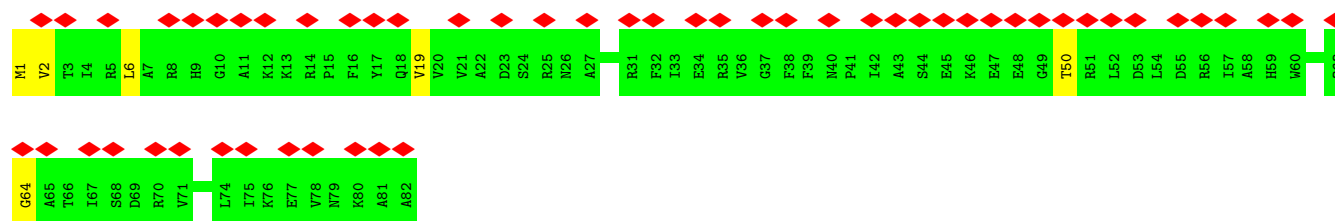


- Molecule 32: 30S ribosomal protein S15

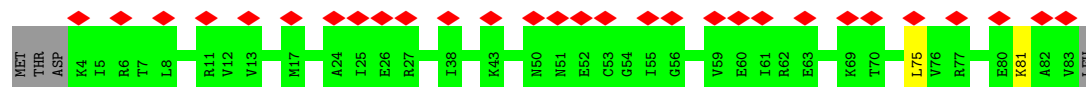


- Molecule 33: 30S ribosomal protein S16

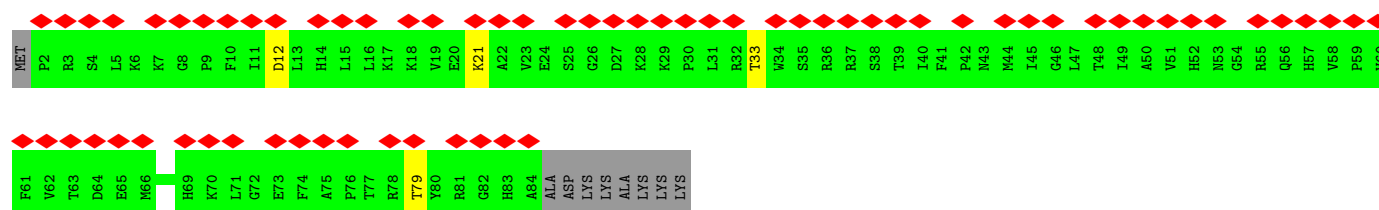
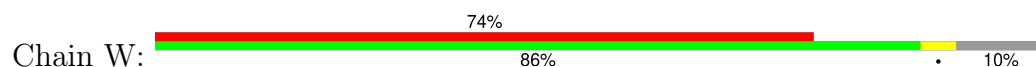




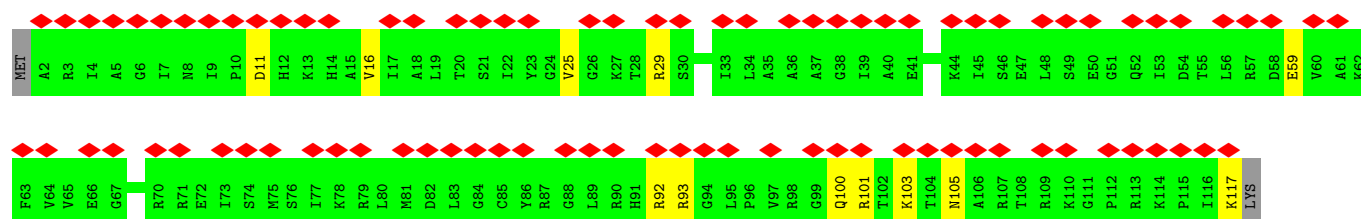
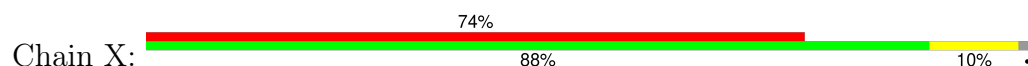
• Molecule 34: 30S ribosomal protein S17



• Molecule 35: 30S ribosomal protein S19

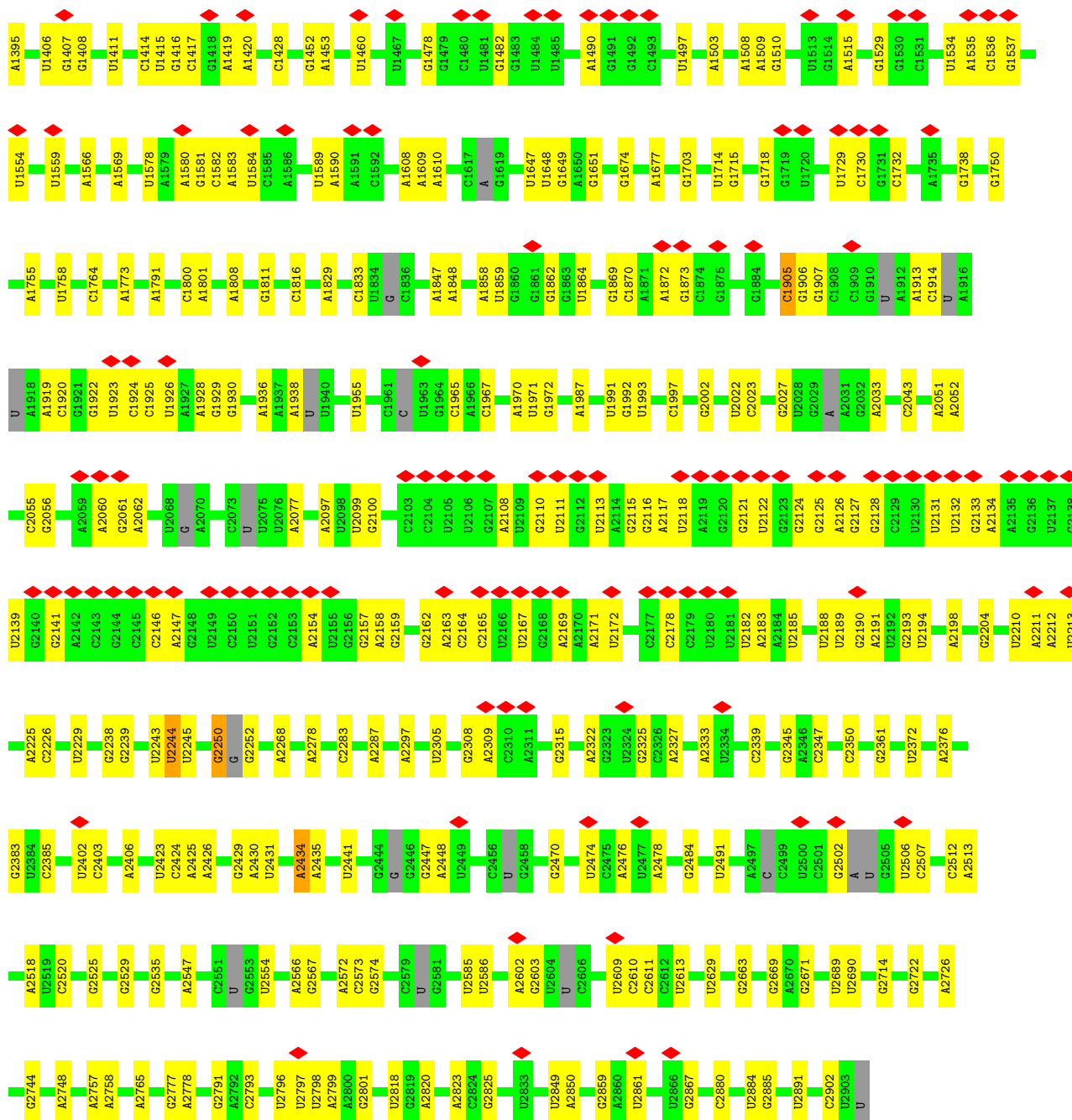


• Molecule 36: 30S ribosomal protein S13

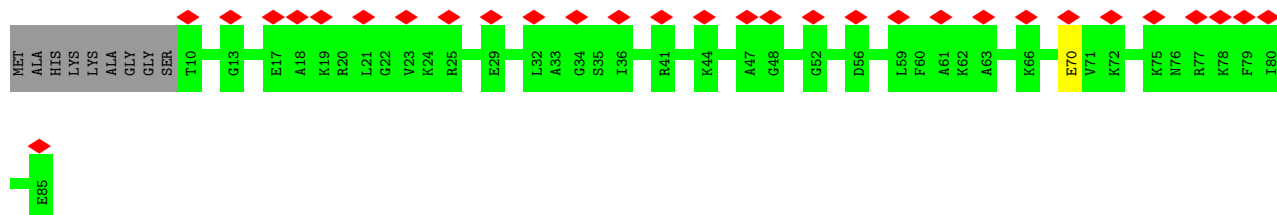
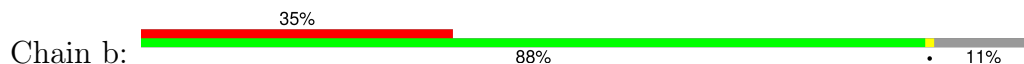


• Molecule 37: 50S ribosomal protein L11

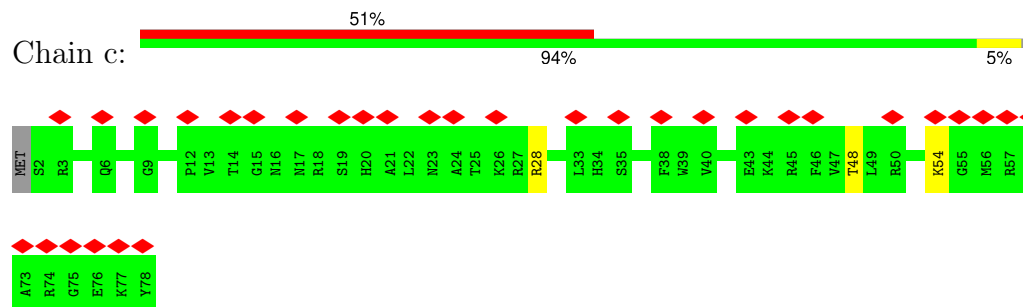




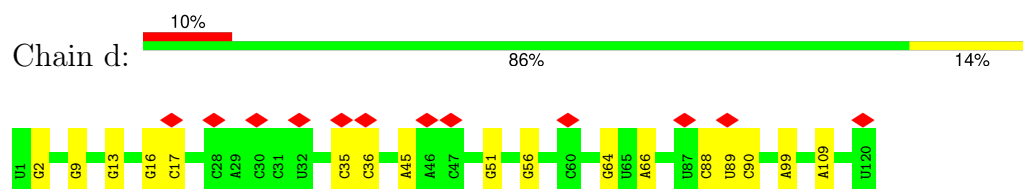
- Molecule 40: 50S ribosomal protein L27



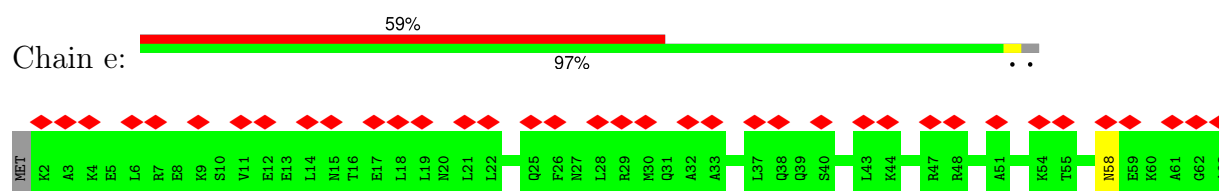
- Molecule 41: 50S ribosomal protein L28



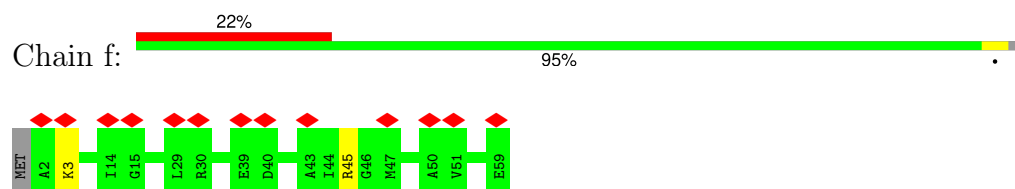
- Molecule 42: 5S rRNA



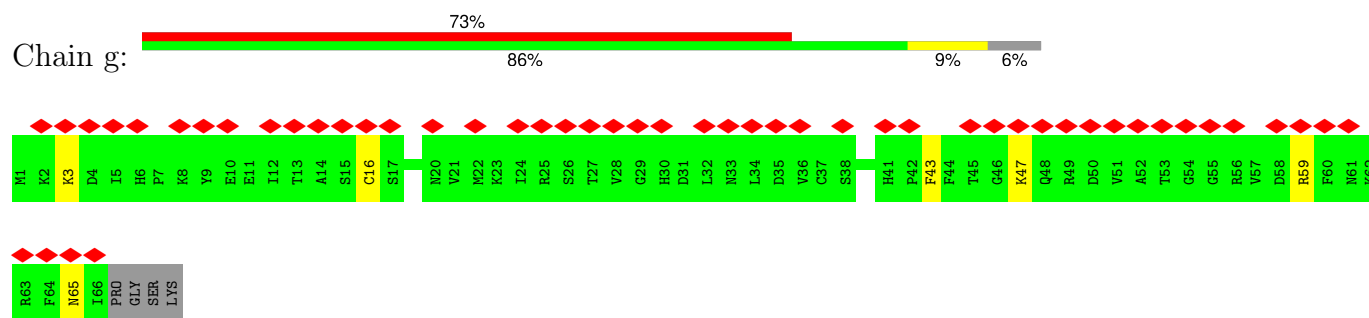
- Molecule 43: 50S ribosomal protein L29



- Molecule 44: 50S ribosomal protein L30

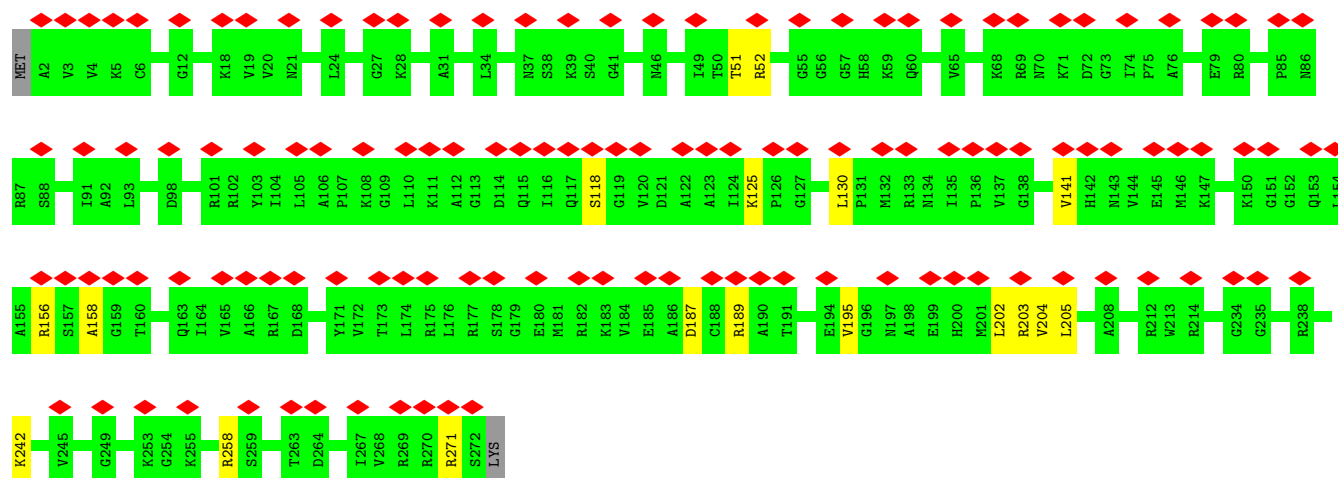


- Molecule 45: 50S ribosomal protein L31

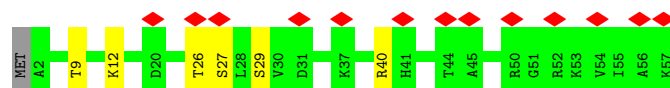
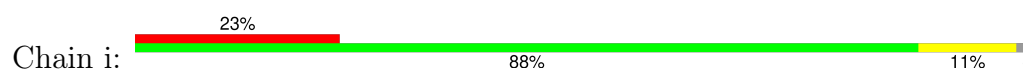


- Molecule 46: 50S ribosomal protein L2

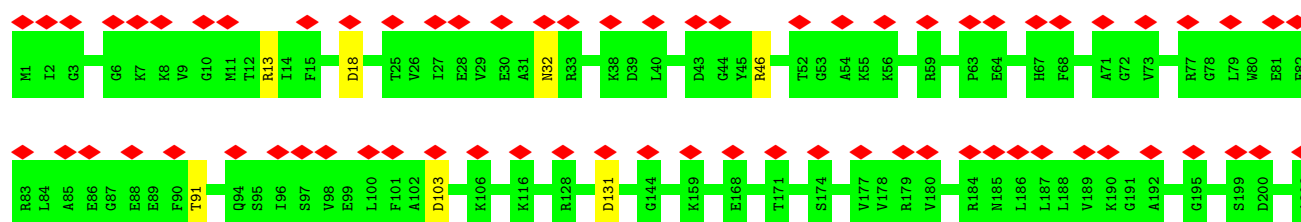




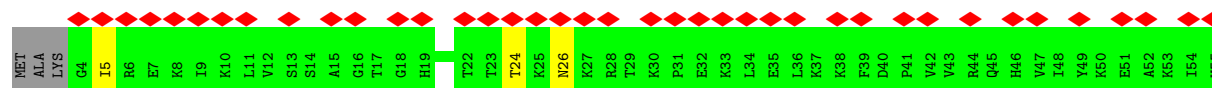
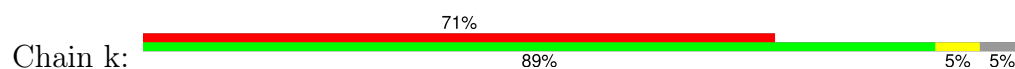
- Molecule 47: 50S ribosomal protein L32



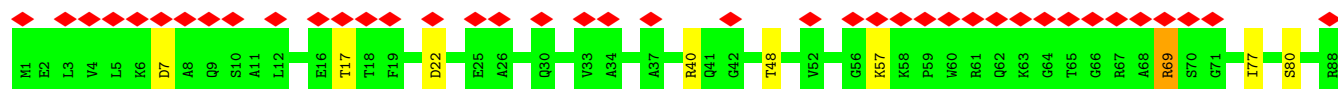
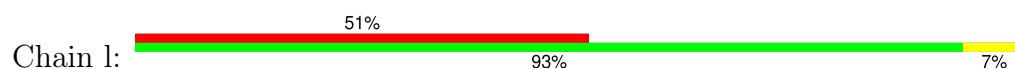
- Molecule 48: 50S ribosomal protein L3

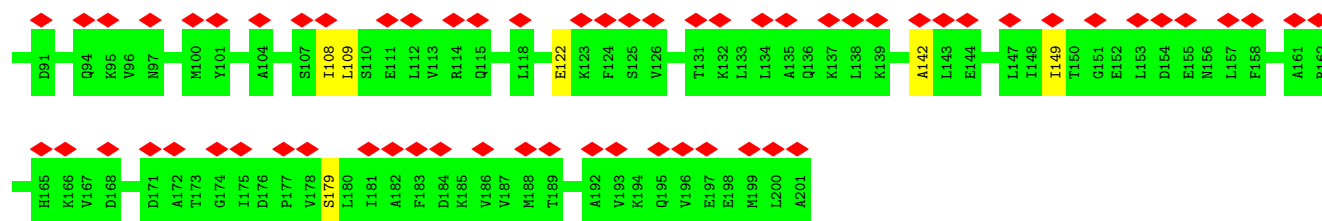


- Molecule 49: 50S ribosomal protein L33

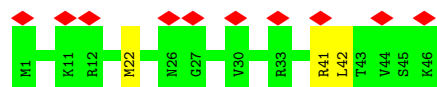


- Molecule 50: 50S ribosomal protein L4

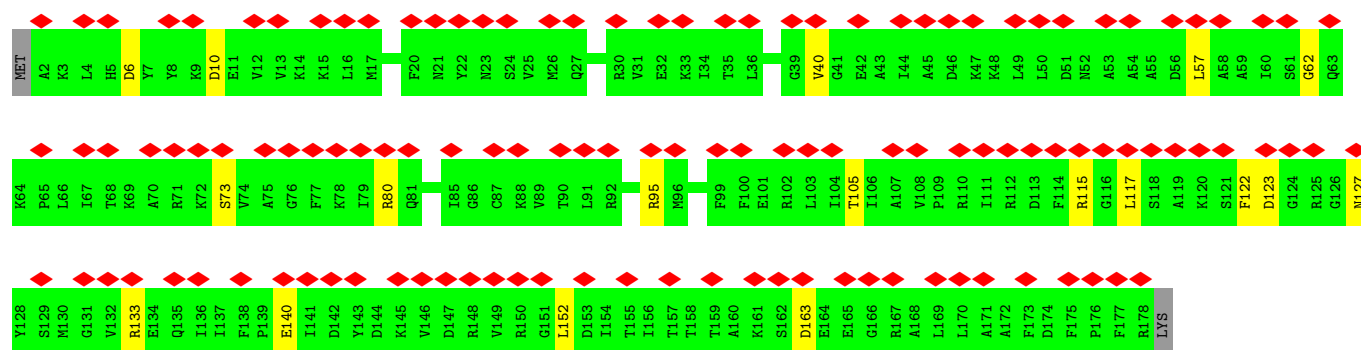
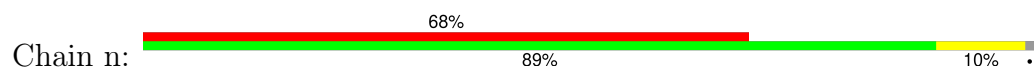




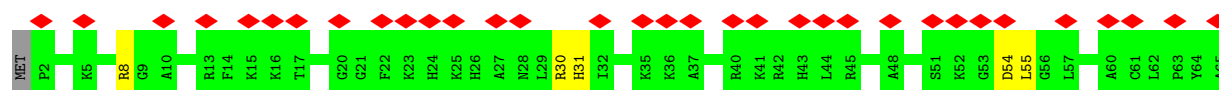
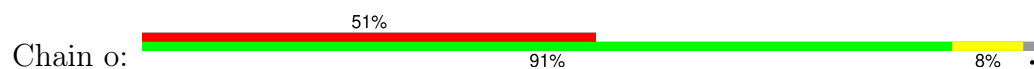
• Molecule 51: 50S ribosomal protein L34



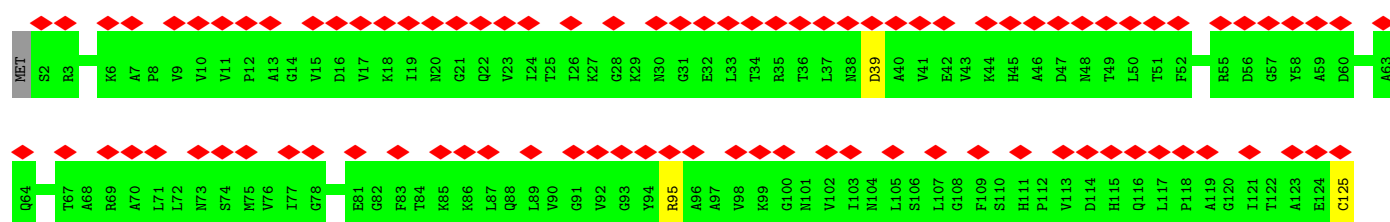
• Molecule 52: 50S ribosomal protein L5

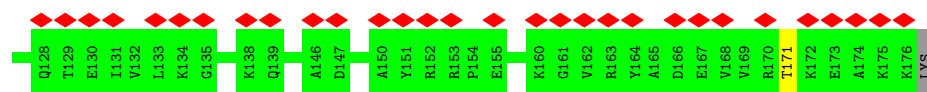


• Molecule 53: 50S ribosomal protein L35

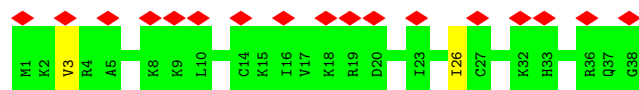
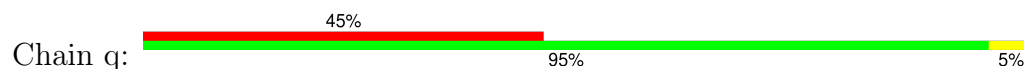


• Molecule 54: 50S ribosomal protein L6

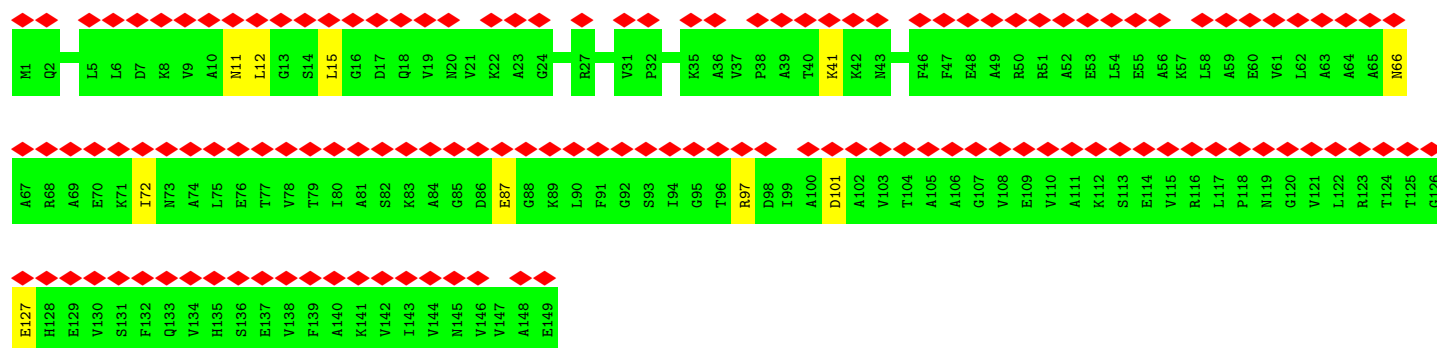
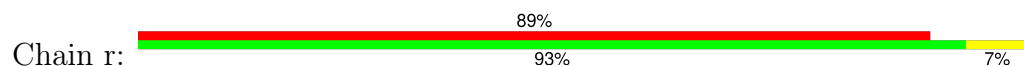




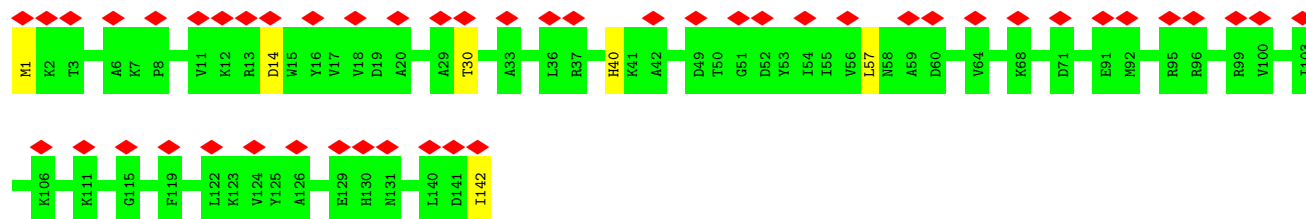
- Molecule 55: 50S ribosomal protein L36



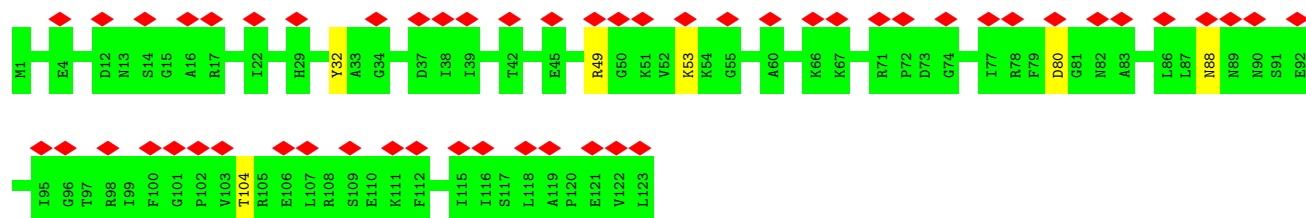
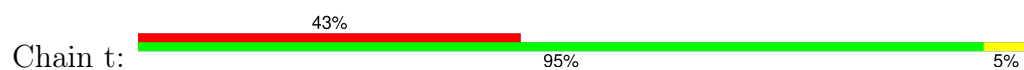
- Molecule 56: 50S ribosomal protein L9



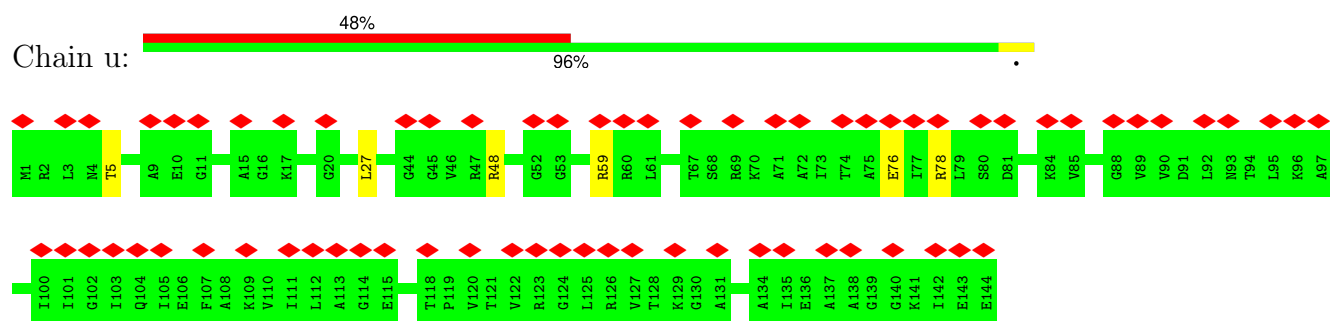
- Molecule 57: 50S ribosomal protein L13



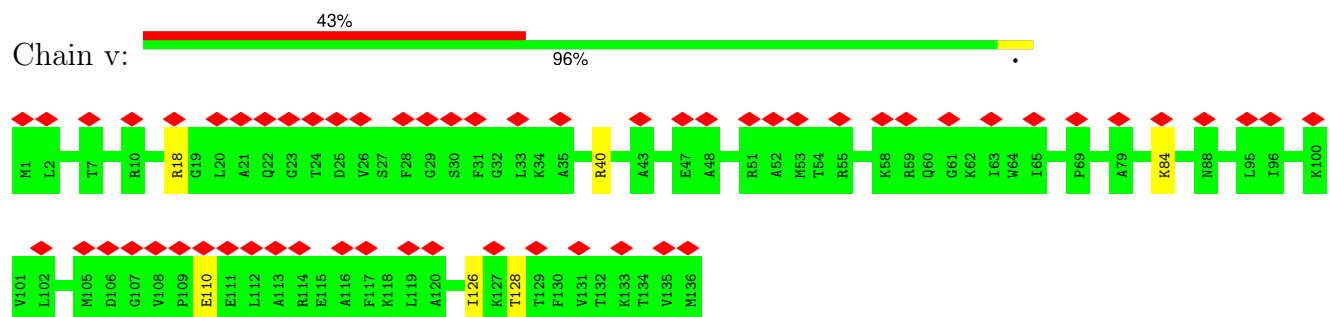
- Molecule 58: 50S ribosomal protein L14



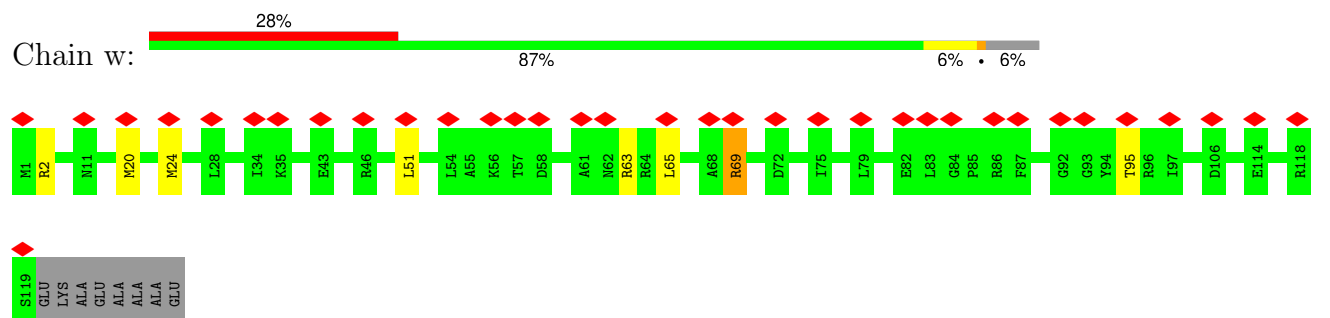
- Molecule 59: 50S ribosomal protein L15



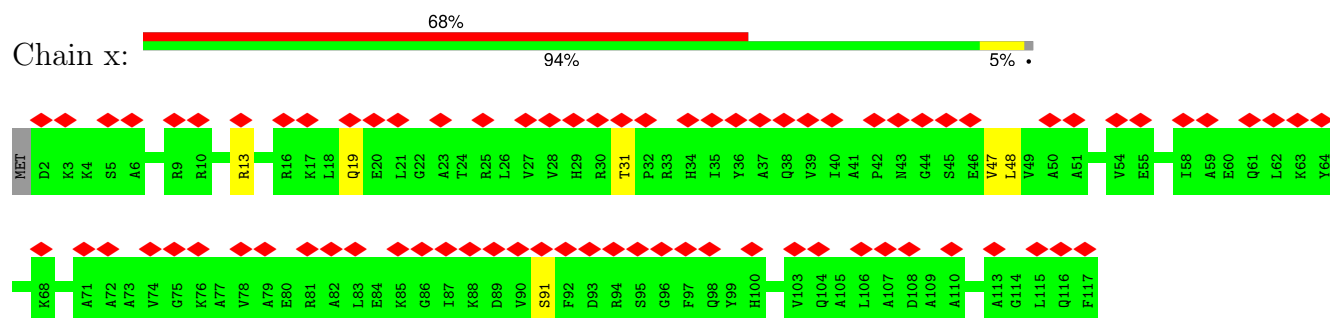
• Molecule 60: 50S ribosomal protein L16



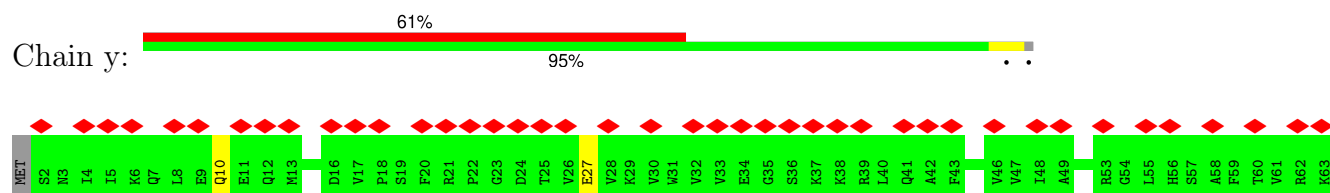
• Molecule 61: 50S ribosomal protein L17

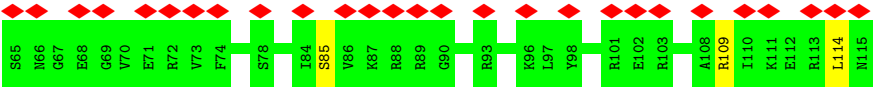


• Molecule 62: 50S ribosomal protein L18

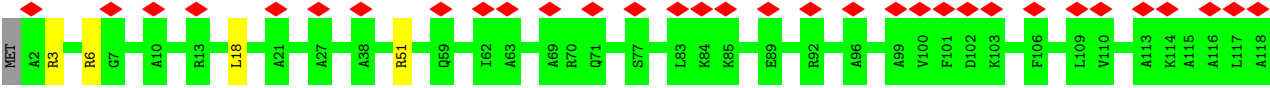


• Molecule 63: 50S ribosomal protein L19





• Molecule 64: 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	24582	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	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	0.069	Depositor
Minimum map value	-0.036	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	520.0, 520.0, 520.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	0.42	0/752	0.71	0/1005
4	3	0.35	0/796	0.66	2/1062 (0.2%)
5	4	0.40	0/766	0.68	0/1025
6	5	1.12	6/528 (1.1%)	0.97	1/810 (0.1%)
7	6	1.11	4/603 (0.7%)	0.97	0/926
8	7	0.55	2/813 (0.2%)	0.88	3/1262 (0.2%)
9	9	0.79	2/1131 (0.2%)	0.64	1/1524 (0.1%)
10	A	0.39	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	AB	0.43	0/808	0.60	0/1088
13	AC	0.48	0/1808	0.62	1/2450 (0.0%)
13	AD	0.39	0/1789	0.57	0/2425
14	AE	0.52	4/10545 (0.0%)	0.66	5/14236 (0.0%)
15	C	0.48	0/553	0.83	0/743
16	D	0.34	10/36610 (0.0%)	0.73	30/57091 (0.1%)
17	E	0.57	0/675	0.85	0/895
18	F	0.56	0/597	0.87	0/792
19	G	0.48	0/1791	0.71	0/2413
20	H	0.55	1/1746 (0.1%)	1.03	12/2382 (0.5%)
21	I	0.43	0/1663	0.71	0/2241
22	J	0.47	0/1665	0.73	0/2227
23	K	0.45	0/1165	0.75	0/1568
24	L	0.43	0/867	0.75	1/1171 (0.1%)
25	M	0.50	0/1195	0.81	0/1602
26	N	0.41	0/989	0.69	0/1326
27	O	0.43	0/1034	0.75	0/1375
28	P	0.43	0/800	0.75	0/1082
29	Q	0.40	0/893	0.70	0/1205
30	R	0.35	0/952	0.74	0/1274

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	S	0.49	0/817	0.79	0/1088
32	T	0.53	0/722	0.86	0/964
33	U	0.44	0/659	0.78	0/884
34	V	0.34	0/657	0.62	0/881
35	W	0.38	0/680	0.62	0/915
36	X	0.49	0/909	0.87	0/1215
37	Y	0.67	0/1046	0.58	0/1410
38	Z	0.69	0/227	0.57	0/304
39	a	0.38	3/69247 (0.0%)	0.72	19/107985 (0.0%)
40	b	0.39	0/589	0.71	0/779
41	c	0.48	0/635	0.82	1/848 (0.1%)
42	d	0.29	0/2872	0.70	0/4478
43	e	0.53	0/502	0.83	0/667
44	f	0.45	0/452	0.78	0/605
45	g	0.43	0/531	0.68	0/709
46	h	0.39	0/2121	0.78	0/2852
47	i	0.40	0/450	0.79	0/599
48	j	0.44	0/1586	0.69	0/2134
49	k	0.35	0/433	0.65	0/576
50	l	0.46	0/1571	0.77	1/2113 (0.0%)
51	m	0.53	0/380	0.99	0/498
52	n	0.49	0/1434	0.88	3/1926 (0.2%)
53	o	0.45	0/513	0.83	0/676
54	p	0.39	0/1333	0.67	0/1805
55	q	0.37	0/303	0.77	0/397
56	r	0.43	0/1122	0.69	0/1515
57	s	0.50	0/1152	0.75	0/1551
58	t	0.41	0/955	0.78	0/1279
59	u	0.40	0/1062	0.76	0/1413
60	v	0.47	0/1093	0.81	0/1460
61	w	0.52	0/964	0.87	1/1289 (0.1%)
62	x	0.46	0/902	0.81	0/1209
63	y	0.41	0/929	0.73	1/1242 (0.1%)
64	z	0.60	0/960	0.91	1/1278 (0.1%)
All	All	0.43	35/189246 (0.0%)	0.74	106/278938 (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
14	AE	0	5
20	H	0	3
36	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	13.81	1.70	1.47
16	D	1516	G	O3'-P	-13.35	1.45	1.61
16	D	1339	A	O3'-P	10.56	1.73	1.61
11	AA	374	GLU	C-N	10.36	1.53	1.34
14	AE	88	CYS	CB-SG	-10.20	1.65	1.82

The worst 5 of 106 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	D	1516	G	P-O3'-C3'	-19.01	96.89	119.70
16	D	1516	G	O3'-P-O5'	13.81	130.24	104.00
11	AA	1250	SER	C-N-CA	11.13	149.53	121.70
39	a	2252	G	N9-C1'-C2'	-10.94	99.78	114.00
16	D	1401	G	N9-C1'-C2'	-10.72	100.06	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	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%)	13	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	8
11	AA	1318/1342 (98%)	1149 (87%)	137 (10%)	32 (2%)	5	29
12	AB	94/181 (52%)	88 (94%)	6 (6%)	0	100	100
13	AC	228/329 (69%)	215 (94%)	11 (5%)	2 (1%)	14	45
13	AD	226/329 (69%)	212 (94%)	14 (6%)	0	100	100
14	AE	1329/1407 (94%)	1200 (90%)	120 (9%)	9 (1%)	19	52
15	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
17	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
18	F	68/71 (96%)	68 (100%)	0	0	100	100
19	G	223/241 (92%)	210 (94%)	13 (6%)	0	100	100
20	H	255/557 (46%)	188 (74%)	55 (22%)	12 (5%)	2	18
21	I	206/233 (88%)	196 (95%)	9 (4%)	1 (0%)	25	58
22	J	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
23	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	22	55
24	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	13	44
25	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	19	52
26	N	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16	49
27	O	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16	49
28	P	97/103 (94%)	88 (91%)	8 (8%)	1 (1%)	13	44
29	Q	115/129 (89%)	104 (90%)	9 (8%)	2 (2%)	7	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	R	117/124 (94%)	116 (99%)	1 (1%)	0	100	100
31	S	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
32	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
33	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	10	39
34	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
35	W	81/92 (88%)	78 (96%)	3 (4%)	0	100	100
36	X	114/118 (97%)	107 (94%)	5 (4%)	2 (2%)	7	34
37	Y	139/142 (98%)	102 (73%)	25 (18%)	12 (9%)	0	9
38	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	12
40	b	74/85 (87%)	69 (93%)	5 (7%)	0	100	100
41	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
43	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
44	f	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
45	g	64/70 (91%)	63 (98%)	1 (2%)	0	100	100
46	h	269/273 (98%)	259 (96%)	9 (3%)	1 (0%)	30	63
47	i	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
48	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
49	k	50/55 (91%)	50 (100%)	0	0	100	100
50	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	25	58
51	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
52	n	175/179 (98%)	162 (93%)	11 (6%)	2 (1%)	12	42
53	o	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
54	p	173/177 (98%)	161 (93%)	12 (7%)	0	100	100
55	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
56	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
57	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
58	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
59	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
60	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
61	w	117/127 (92%)	108 (92%)	9 (8%)	0	100	100
62	x	114/117 (97%)	108 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
64	z	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	14	45
All	All	9368/10486 (89%)	8606 (92%)	660 (7%)	102 (1%)	15	42

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	36
2	1	93/93 (100%)	84 (90%)	9 (10%)	6	25
3	2	81/84 (96%)	76 (94%)	5 (6%)	15	40
4	3	84/85 (99%)	78 (93%)	6 (7%)	12	36
5	4	78/78 (100%)	74 (95%)	4 (5%)	20	45
9	9	112/123 (91%)	65 (58%)	47 (42%)	0	0
11	AA	1140/1157 (98%)	1039 (91%)	101 (9%)	8	29
12	AB	86/158 (54%)	84 (98%)	2 (2%)	45	63
13	AC	198/286 (69%)	182 (92%)	16 (8%)	9	32
13	AD	196/286 (68%)	194 (99%)	2 (1%)	73	80
14	AE	1120/1168 (96%)	1051 (94%)	69 (6%)	15	40
15	C	57/65 (88%)	55 (96%)	2 (4%)	31	54
17	E	65/66 (98%)	60 (92%)	5 (8%)	10	34
18	F	60/61 (98%)	57 (95%)	3 (5%)	20	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	G	187/199 (94%)	178 (95%)	9 (5%)	21	46
20	H	137/461 (30%)	128 (93%)	9 (7%)	14	38
21	I	171/190 (90%)	165 (96%)	6 (4%)	31	54
22	J	172/173 (99%)	165 (96%)	7 (4%)	26	50
23	K	119/126 (94%)	112 (94%)	7 (6%)	16	41
24	L	91/116 (78%)	85 (93%)	6 (7%)	14	38
25	M	124/147 (84%)	116 (94%)	8 (6%)	14	39
26	N	104/105 (99%)	102 (98%)	2 (2%)	52	69
27	O	105/107 (98%)	100 (95%)	5 (5%)	21	46
28	P	86/90 (96%)	78 (91%)	8 (9%)	7	27
29	Q	90/99 (91%)	87 (97%)	3 (3%)	33	56
30	R	101/104 (97%)	94 (93%)	7 (7%)	13	37
31	S	83/84 (99%)	79 (95%)	4 (5%)	21	46
32	T	76/77 (99%)	64 (84%)	12 (16%)	2	13
33	U	65/65 (100%)	60 (92%)	5 (8%)	10	34
34	V	74/78 (95%)	72 (97%)	2 (3%)	40	60
35	W	72/79 (91%)	68 (94%)	4 (6%)	17	43
36	X	94/96 (98%)	85 (90%)	9 (10%)	7	26
37	Y	109/110 (99%)	73 (67%)	36 (33%)	0	1
38	Z	26/85 (31%)	12 (46%)	14 (54%)	0	0
40	b	58/63 (92%)	57 (98%)	1 (2%)	56	72
41	c	67/68 (98%)	64 (96%)	3 (4%)	23	47
43	e	54/55 (98%)	53 (98%)	1 (2%)	52	69
44	f	48/49 (98%)	46 (96%)	2 (4%)	25	49
45	g	59/62 (95%)	53 (90%)	6 (10%)	6	24
46	h	216/218 (99%)	199 (92%)	17 (8%)	10	34
47	i	47/48 (98%)	41 (87%)	6 (13%)	3	18
48	j	164/164 (100%)	157 (96%)	7 (4%)	25	49
49	k	47/49 (96%)	44 (94%)	3 (6%)	14	39
50	l	165/165 (100%)	151 (92%)	14 (8%)	8	31
51	m	38/38 (100%)	35 (92%)	3 (8%)	10	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	n	148/150 (99%)	134 (90%)	14 (10%)	7	26
53	o	51/52 (98%)	46 (90%)	5 (10%)	6	25
54	p	136/138 (99%)	132 (97%)	4 (3%)	37	58
55	q	34/34 (100%)	32 (94%)	2 (6%)	16	41
56	r	114/114 (100%)	104 (91%)	10 (9%)	8	30
57	s	116/116 (100%)	110 (95%)	6 (5%)	19	44
58	t	104/104 (100%)	98 (94%)	6 (6%)	17	42
59	u	103/103 (100%)	97 (94%)	6 (6%)	17	42
60	v	109/109 (100%)	103 (94%)	6 (6%)	18	43
61	w	99/103 (96%)	91 (92%)	8 (8%)	9	32
62	x	86/87 (99%)	80 (93%)	6 (7%)	12	37
63	y	99/100 (99%)	95 (96%)	4 (4%)	27	50
64	z	89/90 (99%)	87 (98%)	2 (2%)	47	64
All	All	7791/8664 (90%)	7209 (92%)	582 (8%)	14	35

5 of 582 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	h	202	LEU
62	x	47	VAL
48	j	13	ARG
46	h	195	VAL
53	o	54	ASP

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

Mol	Chain	Res	Type
36	X	105	ASN
49	k	26	ASN
59	u	4	ASN
11	AA	69	GLN
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%)
16	D	1515/1542 (98%)	289 (19%)	35 (2%)
39	a	2859/2904 (98%)	531 (18%)	0
42	d	119/120 (99%)	17 (14%)	0
8	7	34/35 (97%)	23 (67%)	5 (14%)
All	All	4677/4753 (98%)	924 (19%)	52 (1%)

5 of 924 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-12	G
8	7	-11	U
8	7	-10	U
8	7	-8	U
8	7	-7	U

5 of 52 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	D	517	G
16	D	991	U
16	D	1491	G
16	D	531	U
16	D	641	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

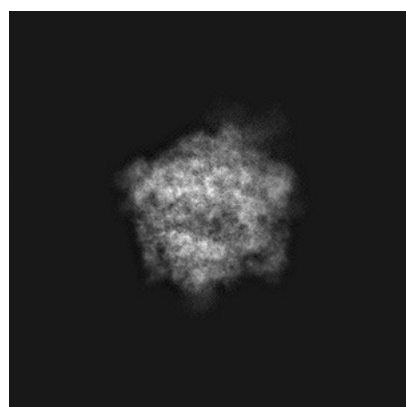
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21469. These allow visual inspection of the internal detail of the map and identification of artifacts.

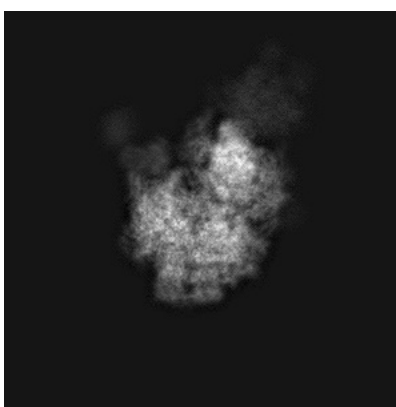
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

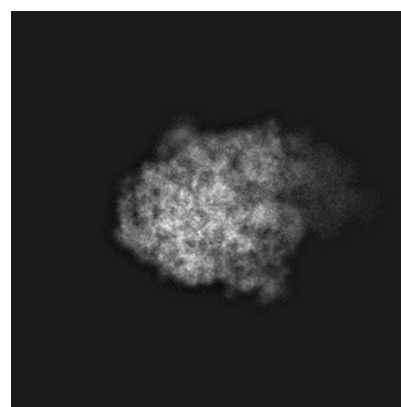
6.1.1 Primary map



X



Y

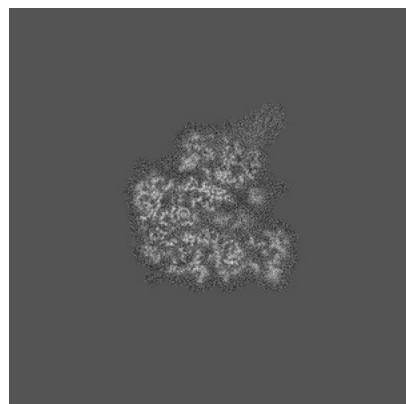


Z

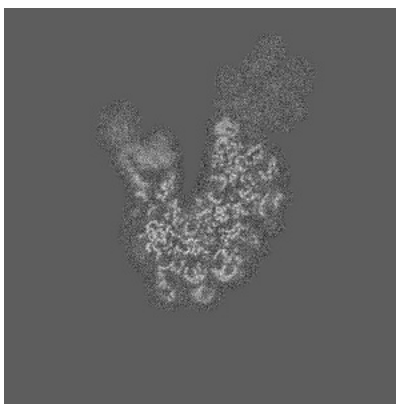
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

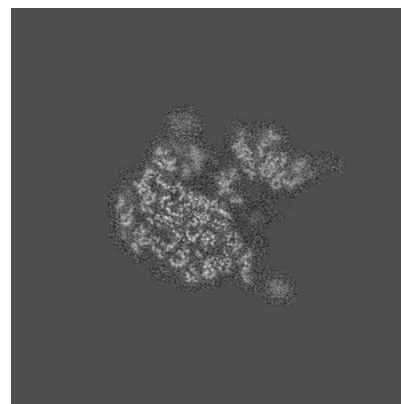
6.2.1 Primary map



X Index: 250



Y Index: 250

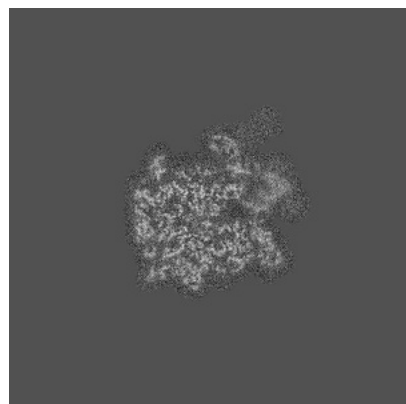


Z Index: 250

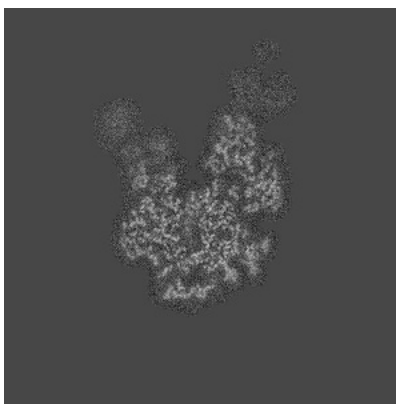
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

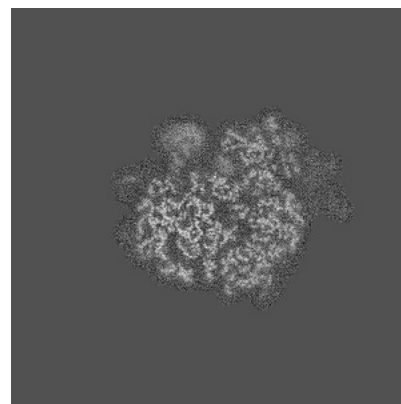
6.3.1 Primary map



X Index: 230



Y Index: 231

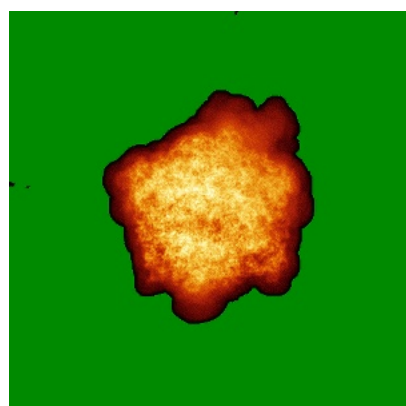


Z Index: 276

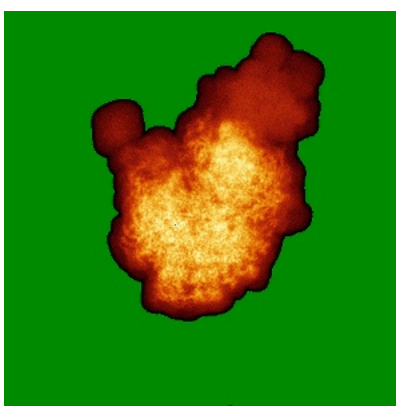
The images above show the largest variance slices of the map in three orthogonal directions.

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

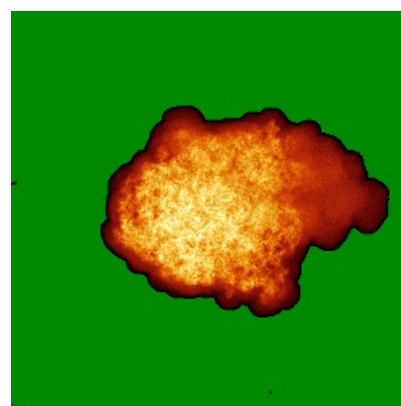
6.4.1 Primary map



X



Y

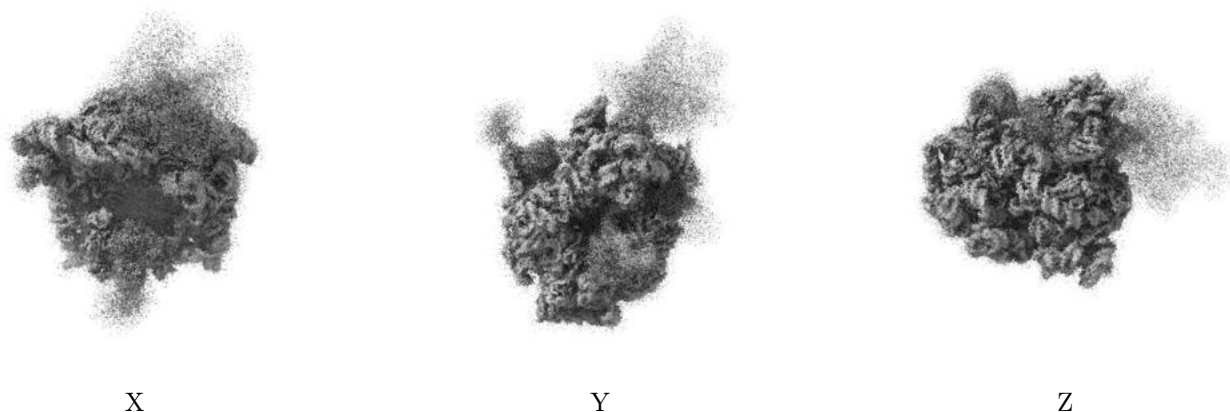


Z

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

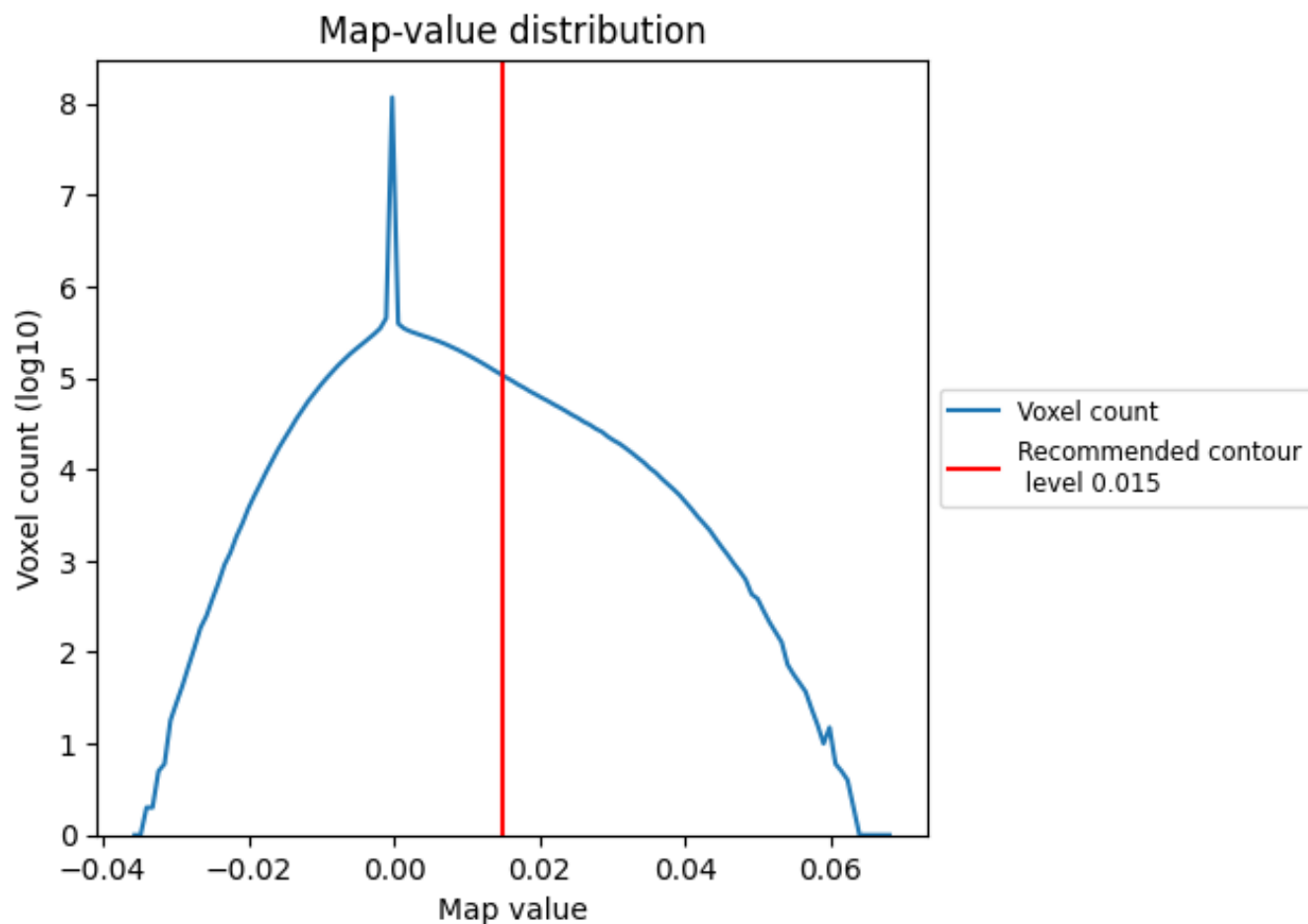
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

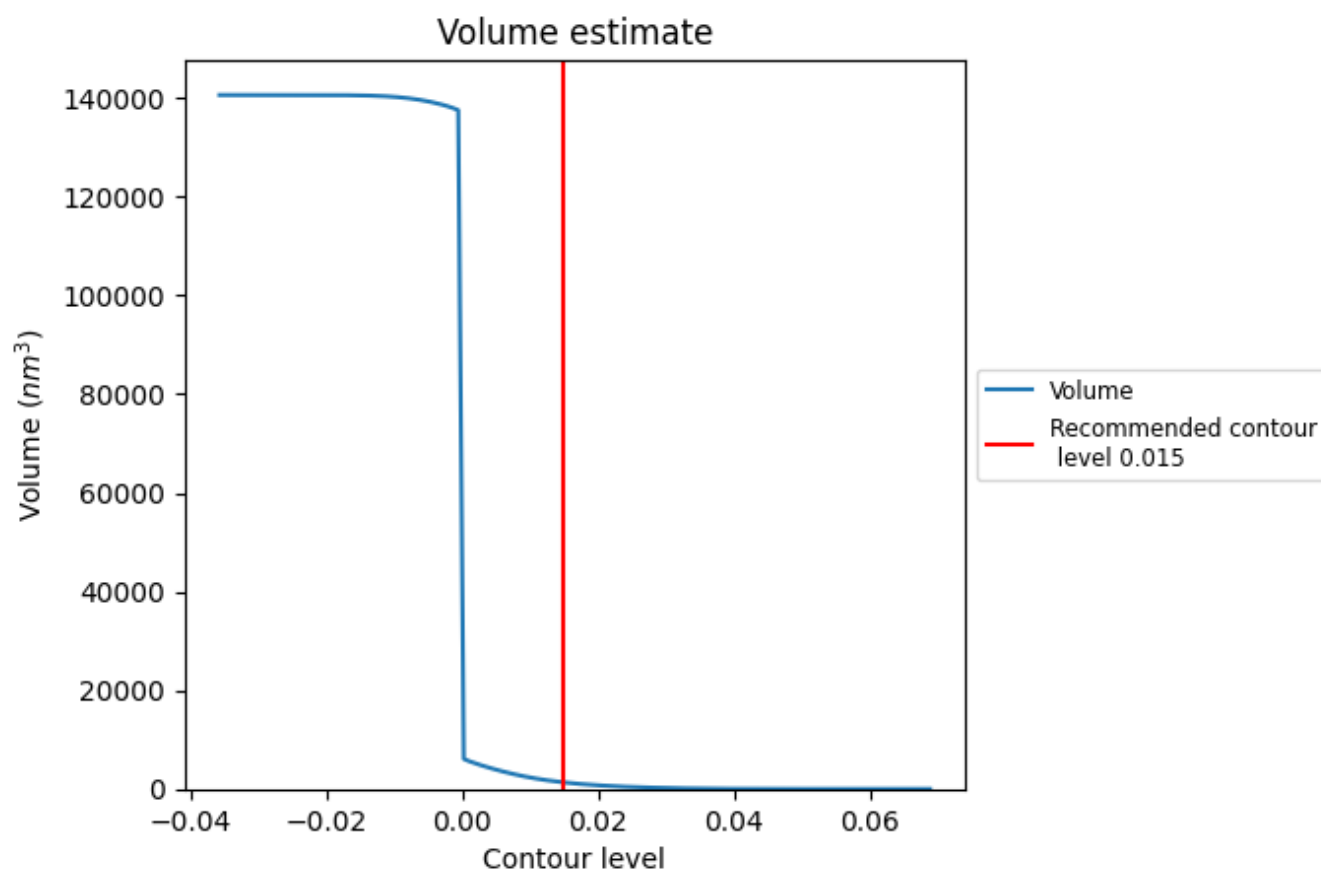
This section contains the results of statistical analysis of the map.

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.

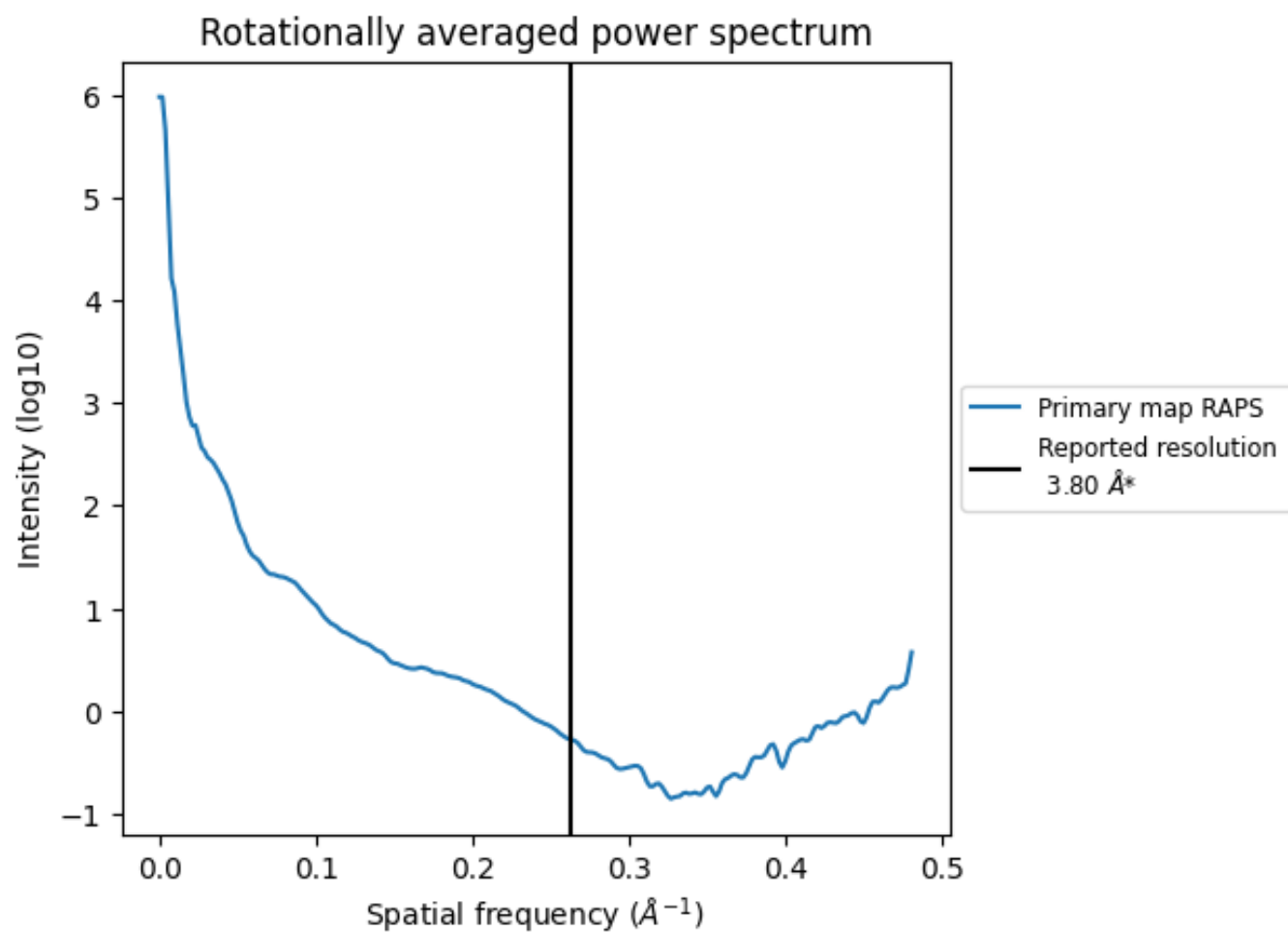
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1329 nm³; this corresponds to an approximate mass of 1201 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 0.263 Å⁻¹

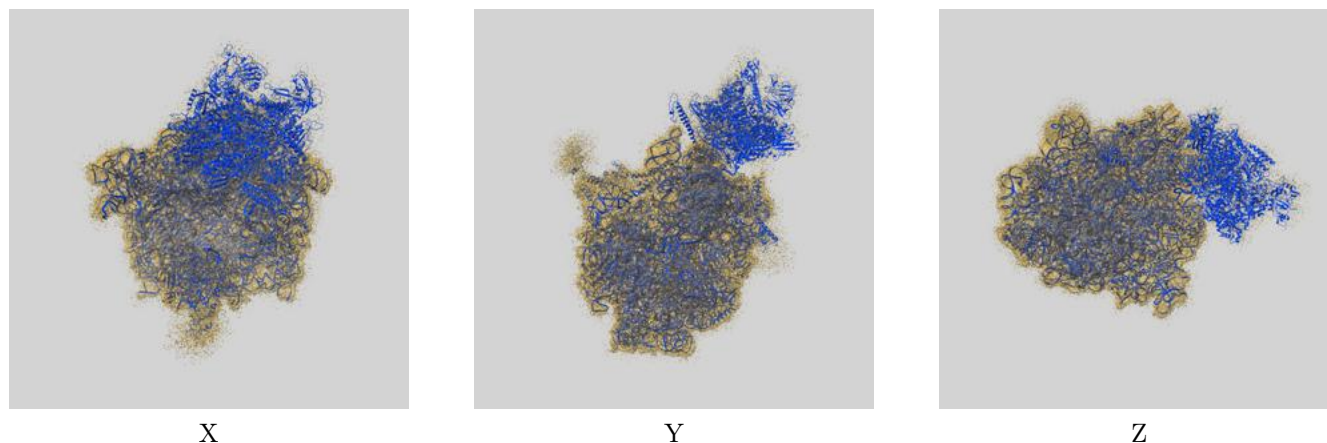
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

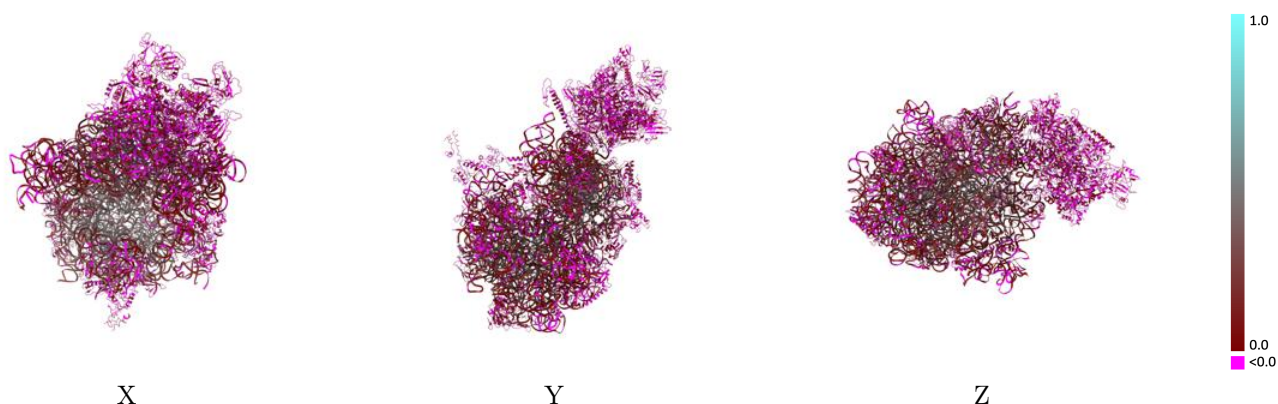
This section contains information regarding the fit between EMDB map EMD-21469 and PDB model 6VYR. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



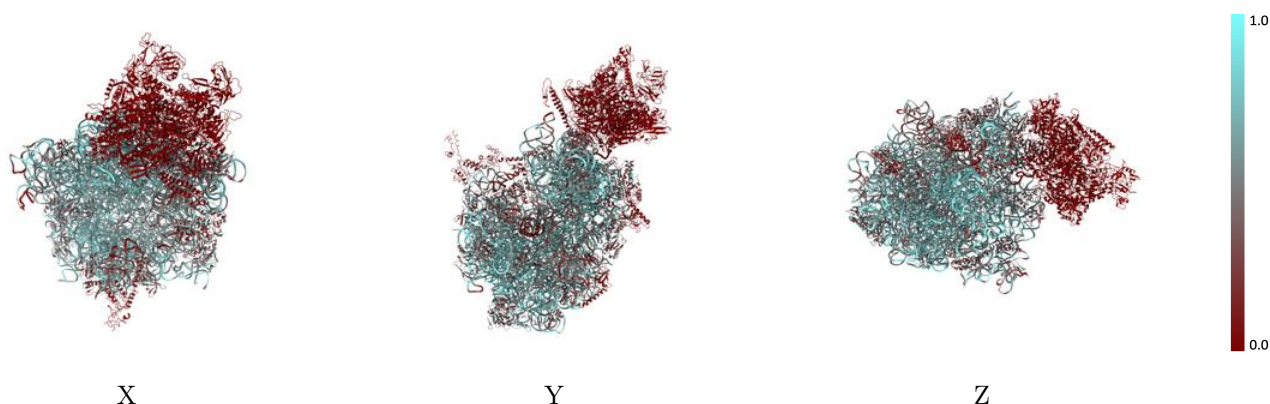
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



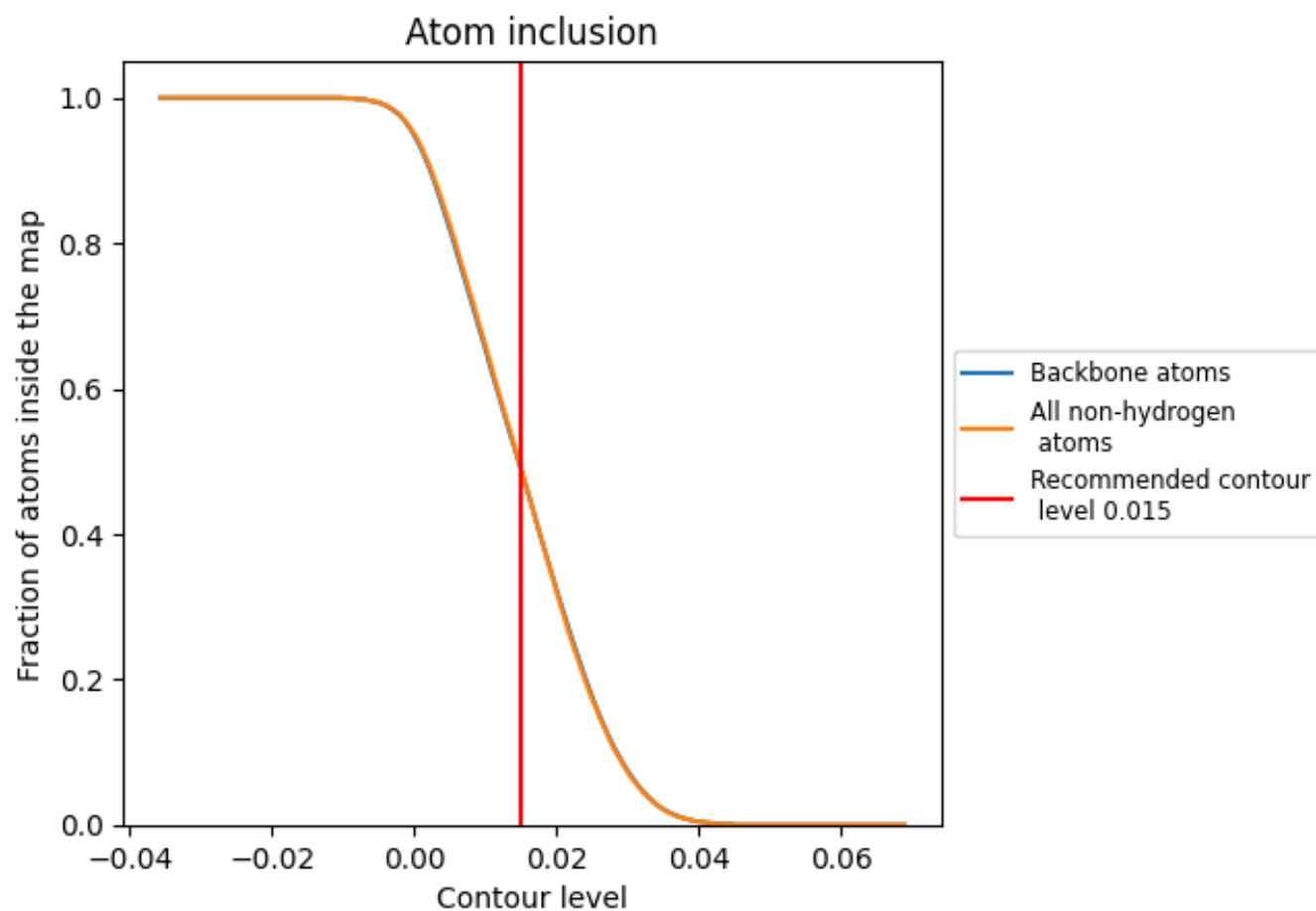
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 49% of all backbone atoms, 49% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4900	 0.1410
0	 0.5020	 0.1730
1	 0.5660	 0.2430
2	 0.3930	 0.0870
3	 0.3800	 0.0780
4	 0.4110	 0.1050
5	 0.0000	 0.0260
6	 0.0090	 0.0170
7	 0.0610	 0.0740
9	 0.1280	 0.0060
A	 0.3670	 0.0850
AA	 0.0070	 0.0150
AB	 0.0050	 0.0480
AC	 0.0120	 0.0270
AD	 0.0010	 0.0030
AE	 0.0050	 0.0200
B	 0.2700	 0.0430
C	 0.4300	 0.1360
D	 0.7020	 0.1970
E	 0.3500	 0.0310
F	 0.3850	 0.1720
G	 0.3910	 0.1200
H	 0.0280	 0.0060
I	 0.3870	 0.1470
J	 0.3990	 0.1330
K	 0.5800	 0.2670
L	 0.3550	 0.0730
M	 0.3640	 0.1160
N	 0.5370	 0.2170
O	 0.3820	 0.0940
P	 0.3430	 0.1050
Q	 0.4350	 0.1560
R	 0.5310	 0.2470
S	 0.3860	 0.0880
T	 0.4970	 0.1680



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Chain	Atom inclusion	Q-score
U	 0.3560	 0.0690
V	 0.4570	 0.1840
W	 0.2060	 0.0050
X	 0.2710	 0.0200
Y	 0.0800	 0.0180
Z	 0.0400	 0.0760
a	 0.6890	 0.1870
b	 0.4490	 0.1730
c	 0.4190	 0.1180
d	 0.6440	 0.1010
e	 0.3680	 0.0360
f	 0.5460	 0.2160
g	 0.2310	 0.0310
h	 0.4440	 0.1160
i	 0.5560	 0.2220
j	 0.4860	 0.1920
k	 0.3040	 0.0450
l	 0.4150	 0.1320
m	 0.5940	 0.2440
n	 0.3120	 0.0520
o	 0.4280	 0.1580
p	 0.3080	 0.0460
q	 0.4250	 0.1350
r	 0.1710	 0.0050
s	 0.5290	 0.2030
t	 0.4330	 0.1680
u	 0.4350	 0.1620
v	 0.4570	 0.1730
w	 0.5180	 0.1630
x	 0.3060	 -0.0030
y	 0.3810	 0.0940
z	 0.5930	 0.2570