



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 10:22 PM UTC

PDB ID : 6VYR / pdb_00006vyr
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:

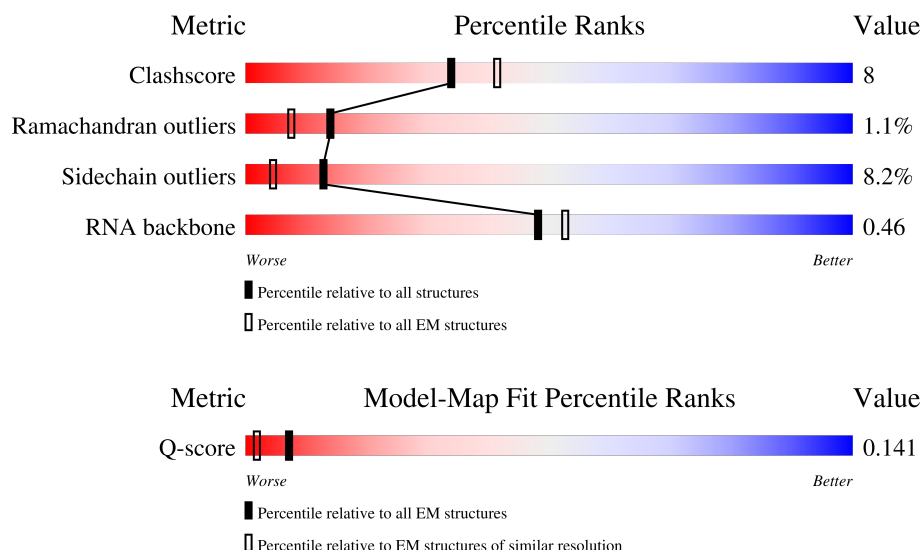
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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)	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	10198 (3.30 - 4.30)

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	38% 84% 15% .
2	1	110	19% 77% 23%
3	2	100	52% 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	35	
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	

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Mol	Chain	Length	Quality of chain
27	O	130	
28	P	103	
29	Q	129	
30	R	124	
31	S	101	
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	

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

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 (CCD ID: MG) (formula: Mg).

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

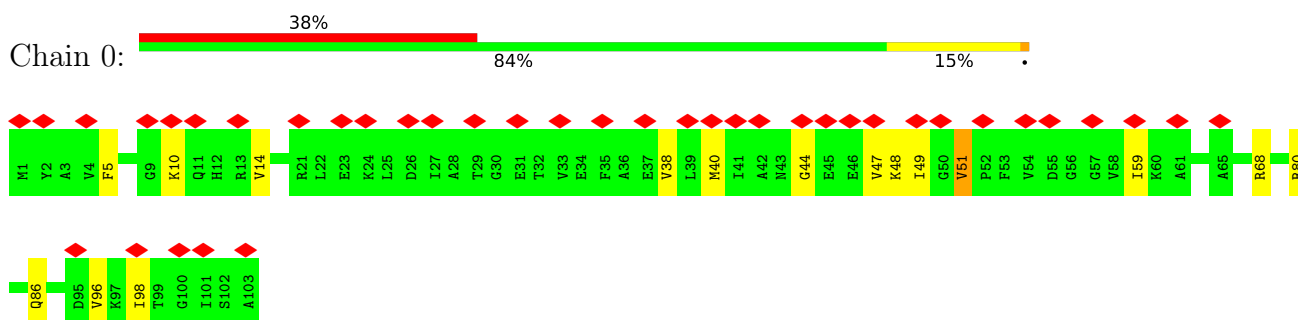
- Molecule 66 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

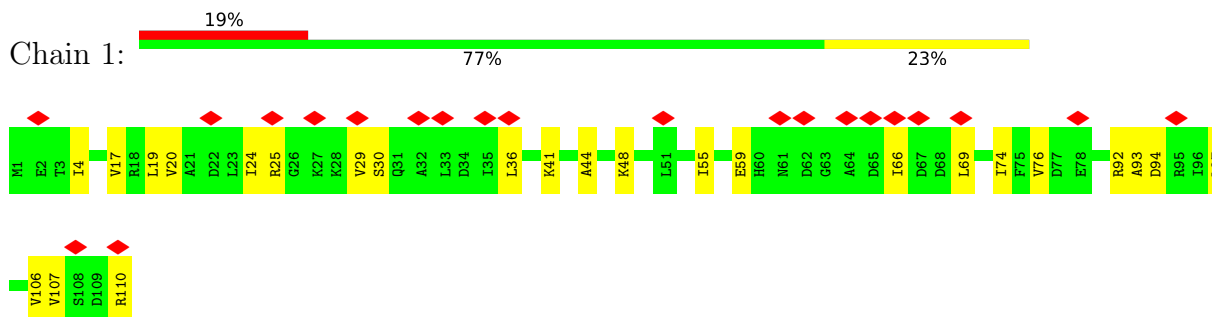
3 Residue-property plots [i](#)

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.

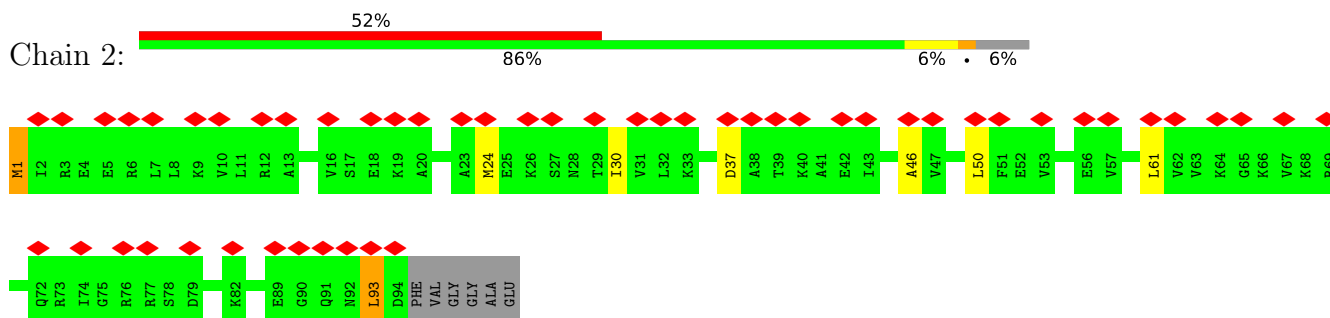
- Molecule 1: 50S ribosomal protein L21



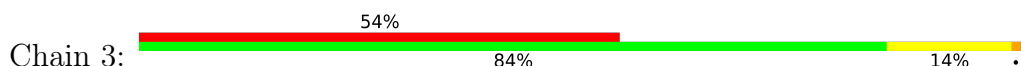
- Molecule 2: 50S ribosomal protein L22

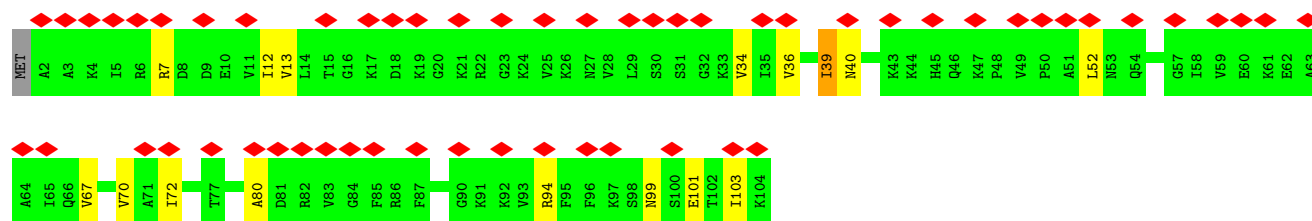


- Molecule 3: 50S ribosomal protein L23

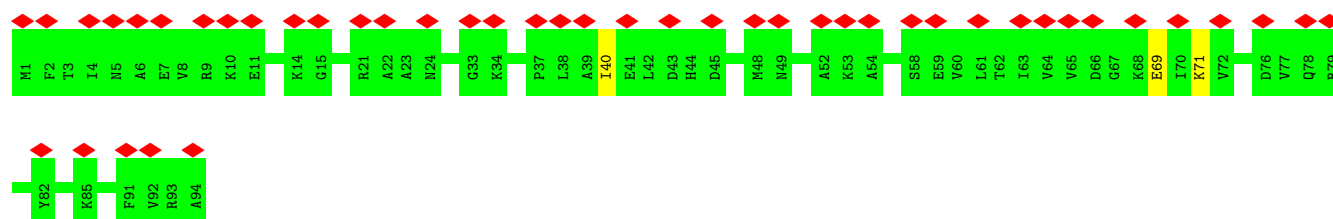


- Molecule 4: 50S ribosomal protein L24

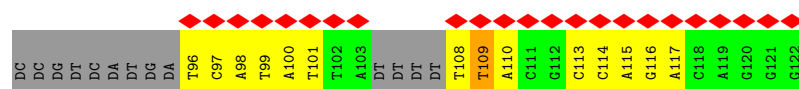
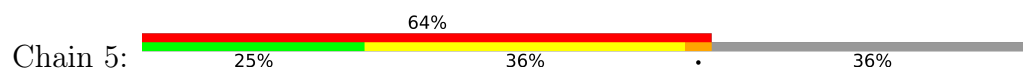




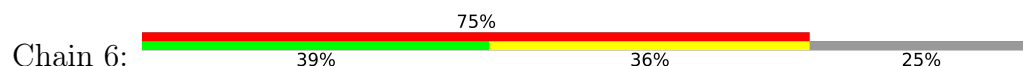
• Molecule 5: 50S ribosomal protein L25



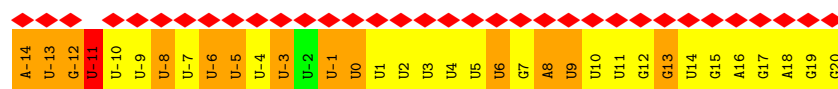
• Molecule 6: NT DNA



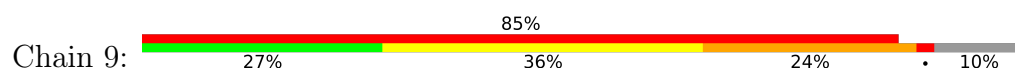
• Molecule 7: T DNA

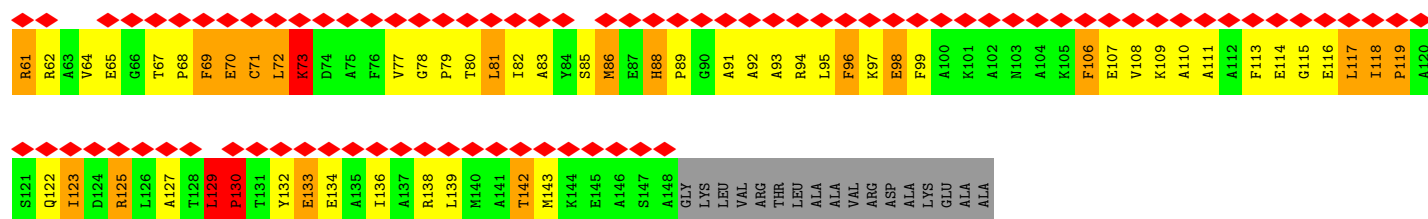


• Molecule 8: mRNA with 18 nt long spacer

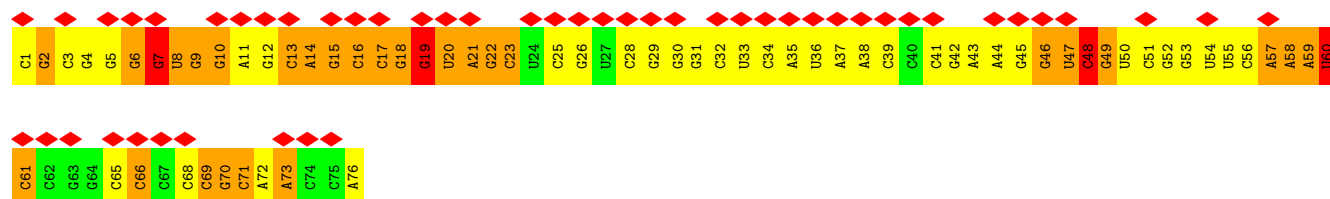


• Molecule 9: 50S ribosomal protein L10

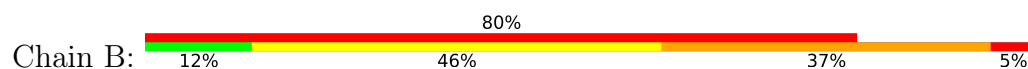




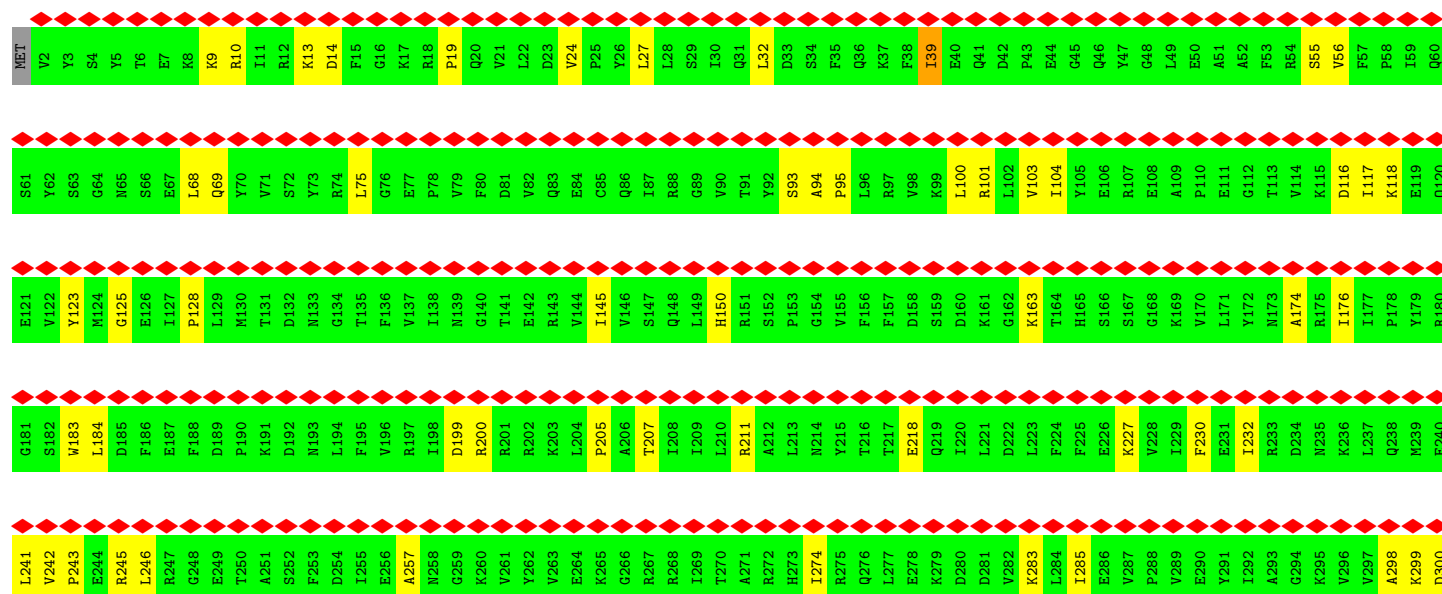
• Molecule 10: E-site and P-site tRNA (fMet)



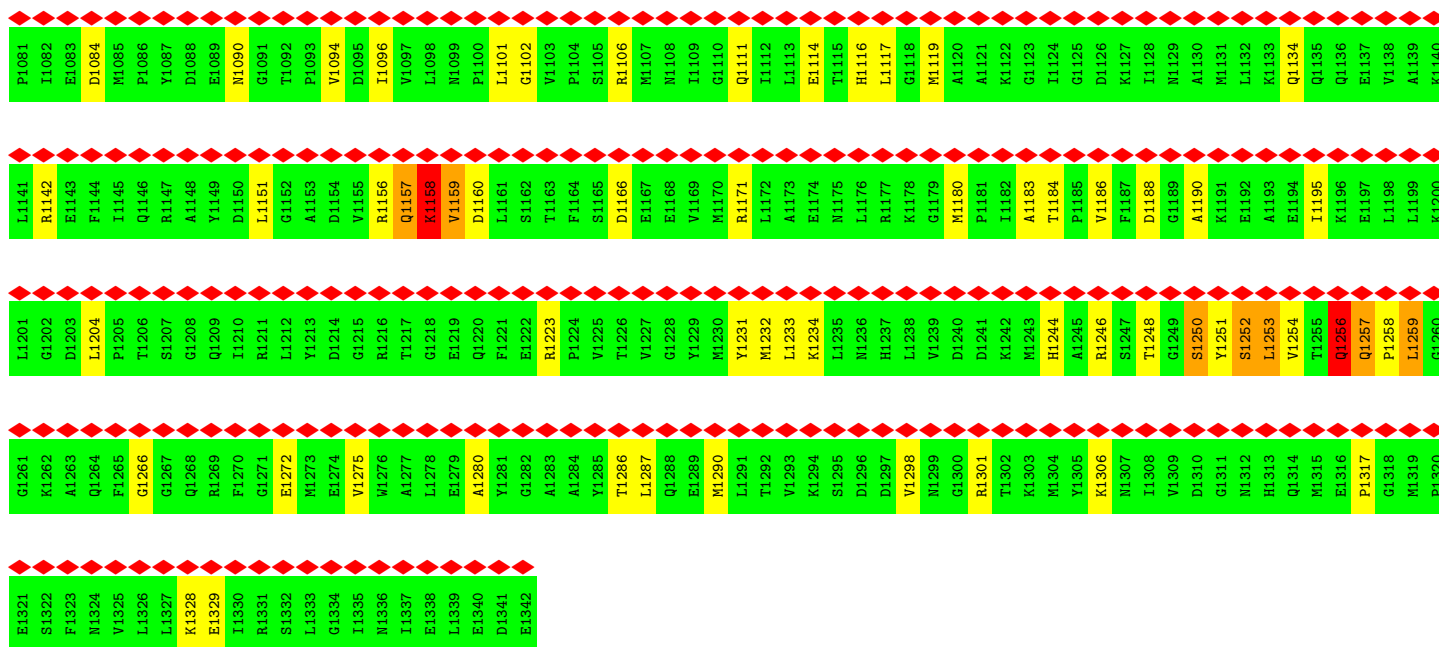
• Molecule 10: E-site and P-site tRNA (fMet)



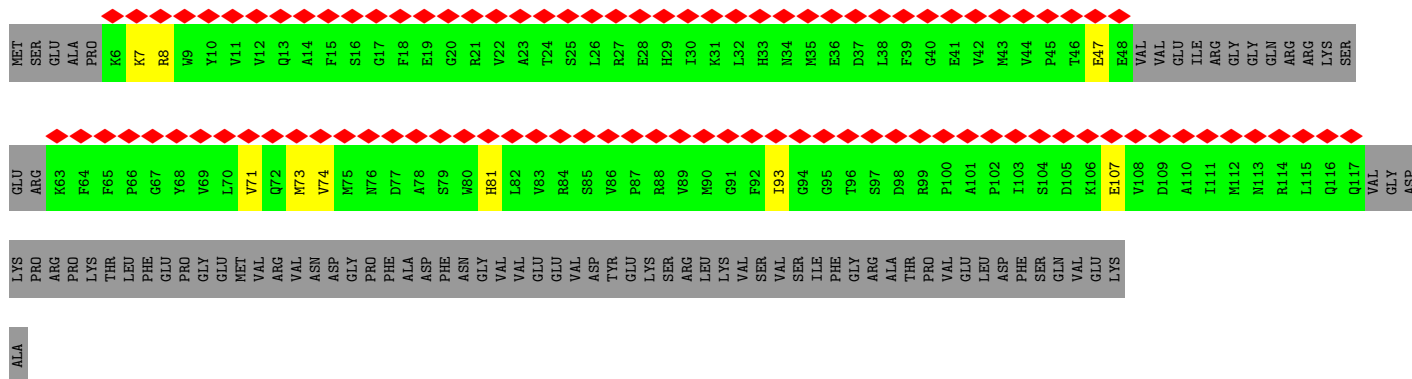
• Molecule 11: DNA-directed RNA polymerase subunit beta



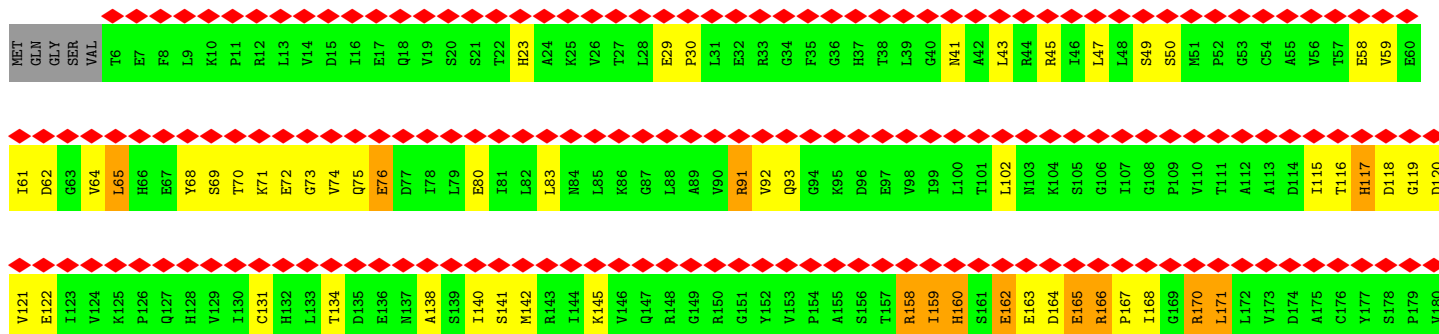
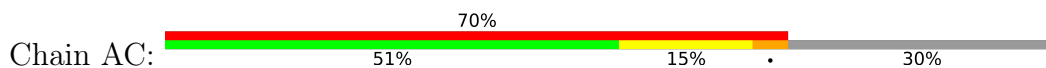
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S961	E962	E963	L964	Q965	L966	L967	E968	A969	G970	L971	F972	S973	R974	I975	R976	A977	V978	L979	V980	A981	G982	G983	V984	E985	A986	E987	K988	L989	D990	K991	L992	P993	R994	D995	R996	W997	L998	E999	L1000	G1001	L1002	T1003	D1004	E1005	E1006	K1007	Q1008	N1009	Q1010	L1011	E1012	Q1013	L1014	A956	K957	A1015	E1016	Q1017	I1018	D1019	E1020
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D781	V782	L783	A784	D785	G786	P787	S788	T789	D790	L791	I792	E793	L794	A795	L796	G797	Q798	N799	M800	R801	Y802	A803	F804	M805	P806	W807	N808	G809	Y810	N811	F812	E813	D814	S815	T816	L817	V818	S819	E820	R821	V822	V823	Q824	E825	D826	R827	F828	T829	T830	L831	H832	L833	Q834	E835	L836	A837	C838	V839	S840		
G721	G722	V723	V724	Q725	V726	V727	D728	A729	S730	R731	I732	V733	I734	K735	V736	N737	E738	D739	E740	Y741	Y742	P743	G744	E745	G746	G747	I748	D749	I750	Y751	N752	L753	T754	K755	Y756	T757	R758	S759	N760	Q761	N762	T763	C764	I765	N766	Q767	N768	P769	C770	V771	S772	L773	G774	E775	P776	V777	R778	R779	G780		
V661	S662	V663	G664	A665	S666	L667	T668	P669	F670	L671	H672	H673	D674	D675	A676	N677	R678	A679	L680	M681	G682	A683	N684	M685	Q686	R687	Q688	A689	V690	P691	T692	L693	R694	A695	D696	K697	P698	L699	V700	G701	T702	G703	M704	E705	R706	A707	V708	A709	V710	D651	Y652	G713	V714	T655	T656	A716	V717	K718	K719	R720	
D601	E602	I603	H604	Y605	L606	S607	A608	T609	E610	E611	G612	N613	Y614	V615	I616	A617	Q618	A619	N620	S621	E622	L623	D624	E625	Q626	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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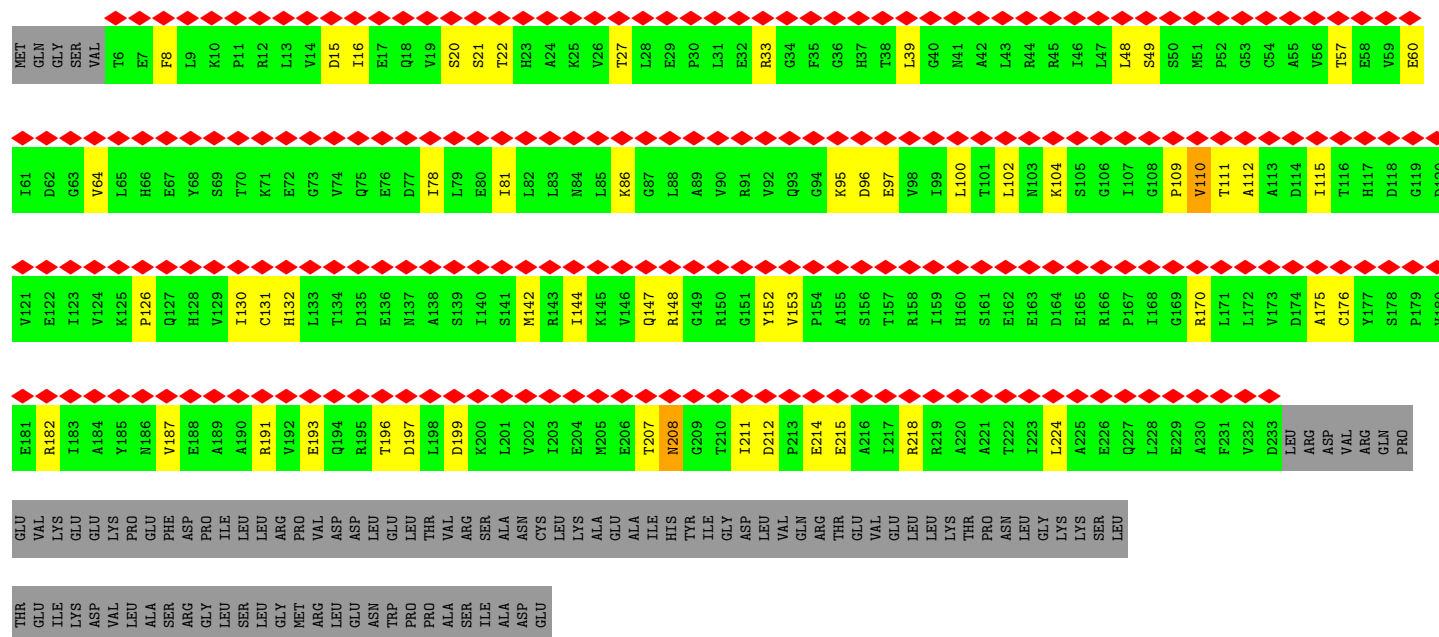
• Molecule 12: Transcription termination/antitermination protein NusG



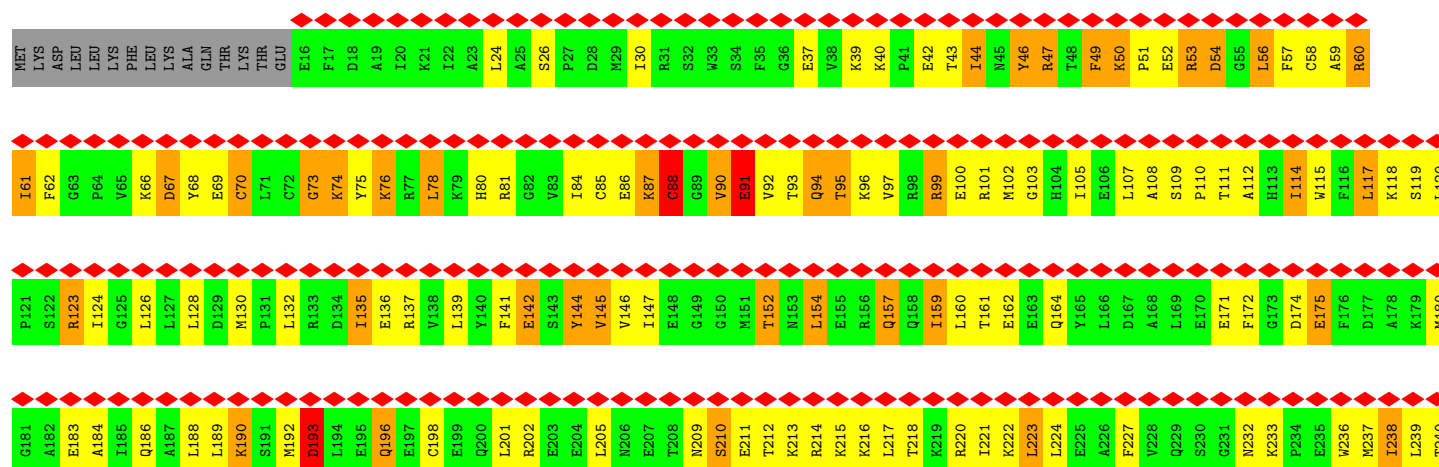
• Molecule 13: DNA-directed RNA polymerase subunit alpha



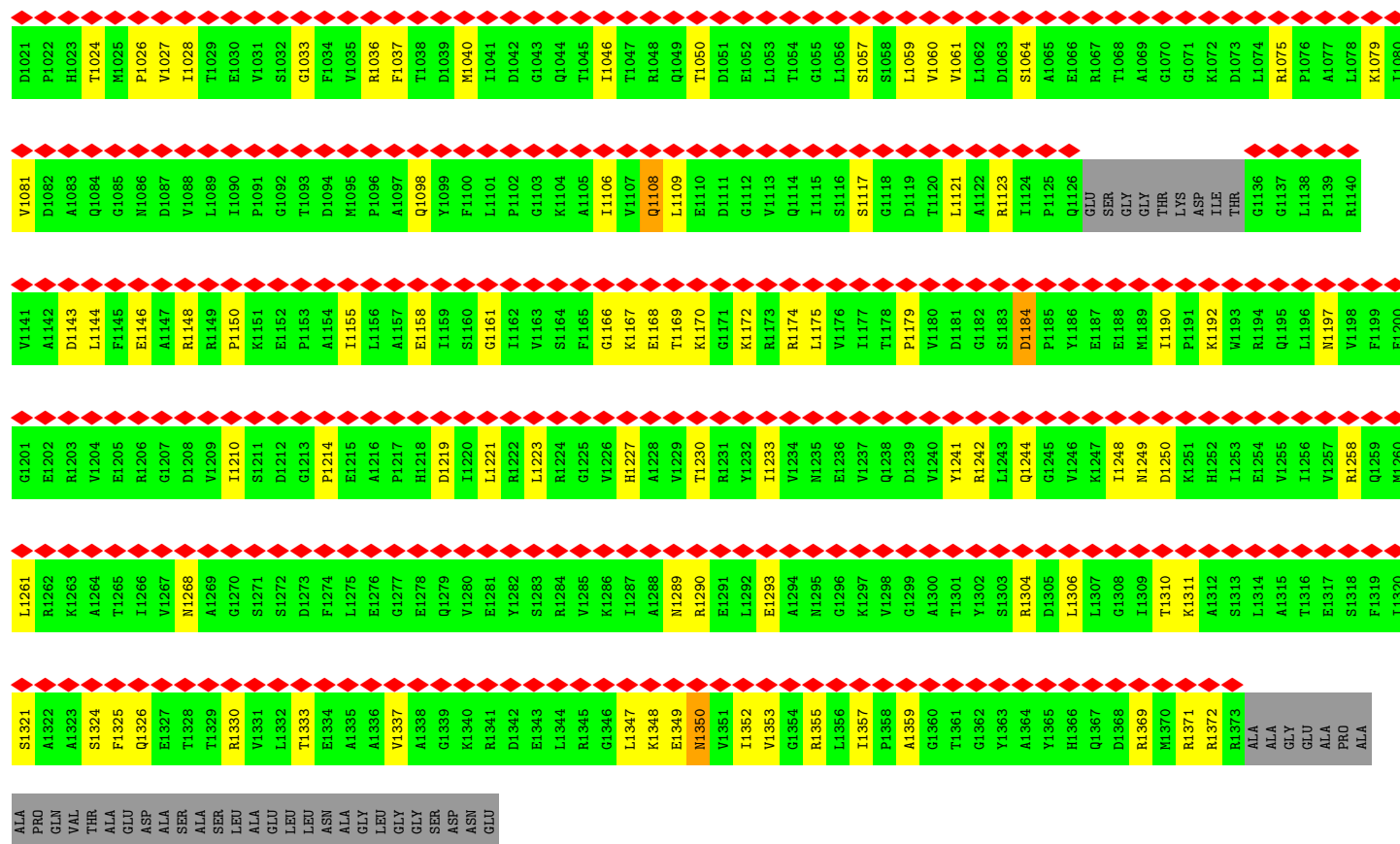
- Molecule 13: DNA-directed RNA polymerase subunit alpha



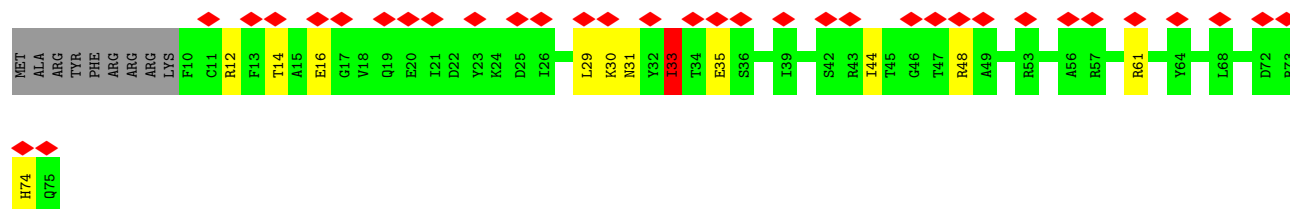
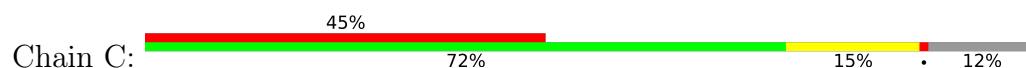
- Molecule 14: DNA-directed RNA polymerase subunit beta'



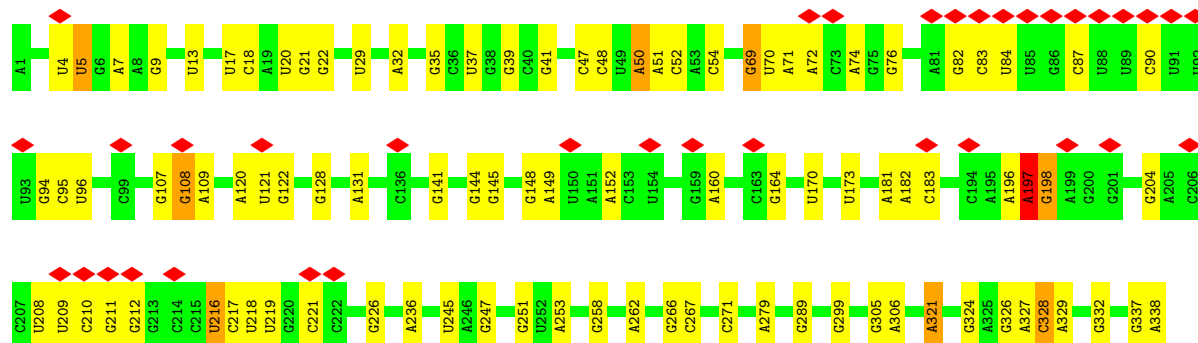
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P243	V303	L363	L423	L483	S543	K603	E663	Y723	L783	V843	L903	V963
V244	D304	H364	N424	M484	L544	M604	T664	M724	A784	T844	A904	K964
L245	A305	Q364	R425	M485	H545	L605	Q665	M725	D785	A845	R905	S965
P246	A306	Q365	A426	S486	A546	N606	Q666	A726	T786	E846	G906	V966
P247	L307	G367	P427	T487	R547	T607	Q667	D727	A787	D847	R907	V967
D248	D308	L368	T428	M488	V548	C608	F668	S728	L788	V848	I908	N968
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R250	G310	K370	H430	I490	V550	B610	S670	A730	T790	K850	N910	S970
P251	R311	K371	R431	L491	R551	I611	G671	R731	A791	P851	K911	G971
L252	R312	M372	L432	S492	I552	L612	L672	G732	N792	G852	G912	K972
V253	G313	A373	G433	P493	T553	G613	V673	S733	S793	T853	E913	L973
P254	R314	L374	I434	A494	E554	L614	T674	A734	G794	A854	A914	V974
L255	A315	E375	Q435	M495	Y555	K615	A675	A735	Y795	D855	I915	T975
D256	I316	L376	A436	G496	E556	P616	G676	Q736	L796	L856	G916	V976
G257	F377	F377	F437	E497	K557	T617	E677	I737	T797	L857	V917	S977
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R259	S319	P379	P439	I499	A559	I619	V679	Q739	R799	P859	A919	N979
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L265	K325	L385	K445	D505	A565	M625	I685	G745	Q805	R865	E925	R985
N266	S326	E386	A446	K506	K566	Y626	V686	L746	D806	E866	P926	D986
D267	L327	L387	I447	V507	T567	T627	A687	M747	L807	Q867	G927	E987
L268	A328	R388	Q448	L508	S568	G628	A688	A748	V808	V868	T928	F988
Y269	D329	G389	L449	G509	L569	F629	A689	K749	N809	C869	Q929	G989
R270	M330	L390	H450	L510	K570	A630	N690	P750	T810	D870	L930	R990
R271	I331	A391	P451	Y511	D571	Y631	D691	D751	E811	L871	T931	T991
V272	K332	T392	L452	Y512	T572	A632	R692	G752	D812	L872	Q932	K992
I273	G333	T393	V453	M513	T573	A633	V693	S753	D813	E873	R933	E993
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N276	G336	A396	A456	D516	R576	G636	A696	E756	T816	S876	HIS	K996
R277	R337	A397	Y457	C517	A577	A637	M697	T757	H817	V877	ILE	V997
R278	F338	K398	N458	V518	I578	S638	M698	P758	E818	D878	GLY	P998
L279	R339	K399	A459	N519	L579	V639	D699	I759	G819	A879	ALA	Y999
K280	Q340	M400	D460	K520	N580	G640	N700	T760	I820	V880	SER	G1000
R281	N341	V401	F461	A521	M581	I641	L701	A761	R821	K881	ARG	A1001
L282	L342	A402	D462	G522	I582	D643	Q702	R764	R822	V882	ALA	I1002
L283	L343	R403	G463	E523	V583	D643	T703	F763	T823	R883	ALA	L1003
D284	G344	A404	D464	G524	P584	M644	E704	R764	P824	S884	ALA	A1004
L285	K345	E405	Q465	M526	K585	V645	T705	E765	R825	V885	GLU	K1005
A286	R346	A406	M466	V526	G586	I646	V706	G766	T826	V886	S948	X1006
A287	V347	V407	A467	L527	L587	P647	I707	L767	E827	S887	I950	D1007
P288	D348	V408	V468	T528	P588	E648	N708	N768	R709	V888	Y951	G1008
D289	Y349	W409	H469	G529	Y589	K649	R709	V769	G829	C888	N952	E1009
I290	S350	D410	D470	P530	S590	K650	D710	L770	D830	T890	K953	Q1010
I291	G351	I411	P471	K531	I591	H651	G711	Q771	V831	D891	N954	V1011
V292	R352	L412	L472	E532	V592	E652	Q712	Y772	K832	F892	K955	I1012
R293	S353	D413	T473	A533	N593	I653	E713	F773	E833	G893	G956	G1013
E295	V354	N294	L474	E534	Q594	T654	E714	I774	P834	V894	S957	G1014
K296	I355	V415	E475	R535	A595	S655	K715	S775	L835	C895	I958	E1015
R297	T356	I416	A476	L536	L596	E656	Q716	T776	R836	A896	T1016	T1016
M298	V357	R417	Q477	Y537	G597	A657	V717	H777	D837	H897	L960	V1017
L299	P358	E418	L478	R538	K598	E658	V718	G778	R838	C898	A1018	N1019
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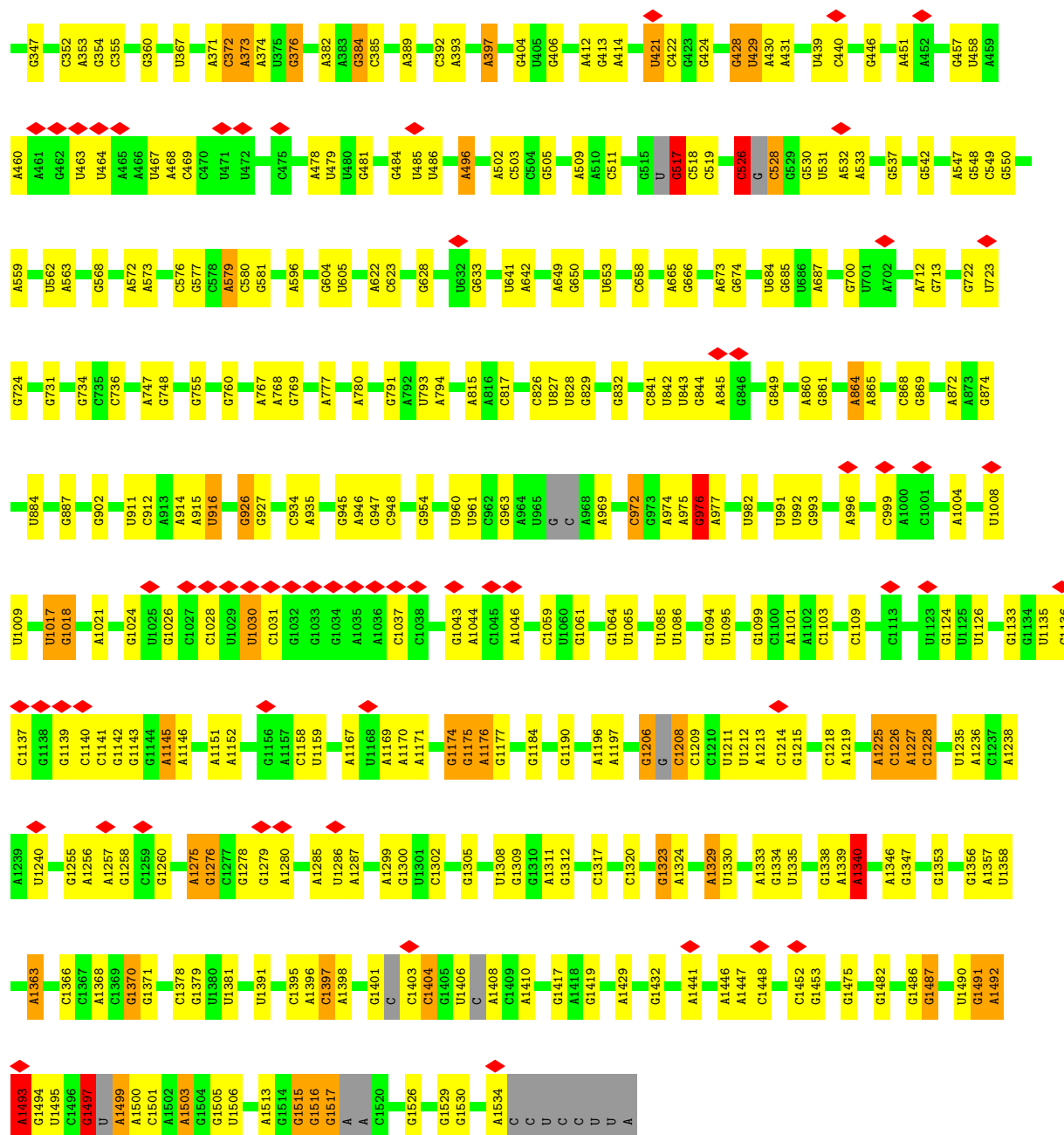


• Molecule 15: 30S ribosomal protein S18

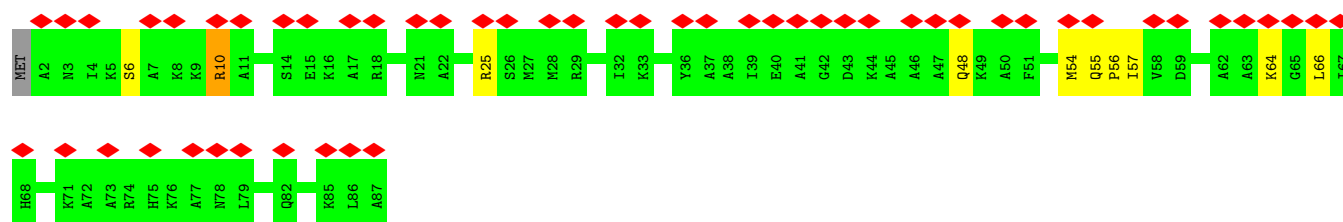
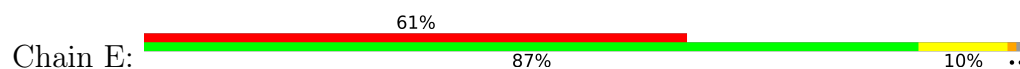


• Molecule 16: 16S rRNA

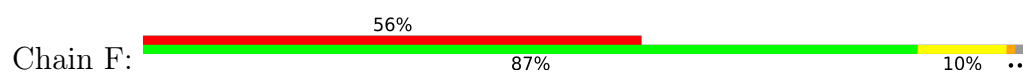




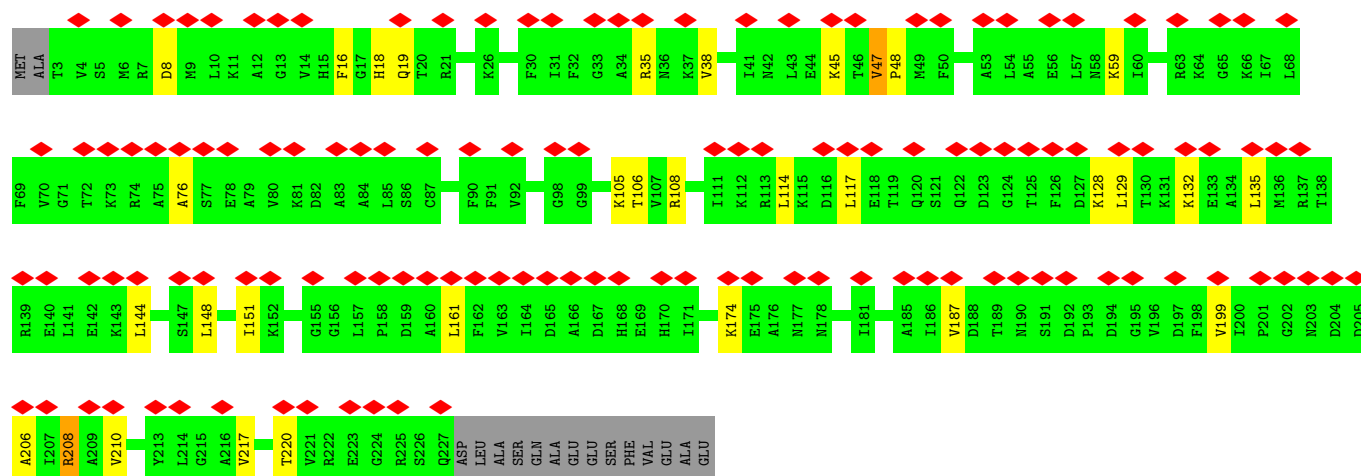
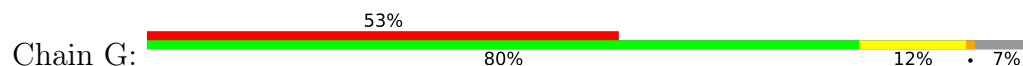
- Molecule 17: 30S ribosomal protein S20



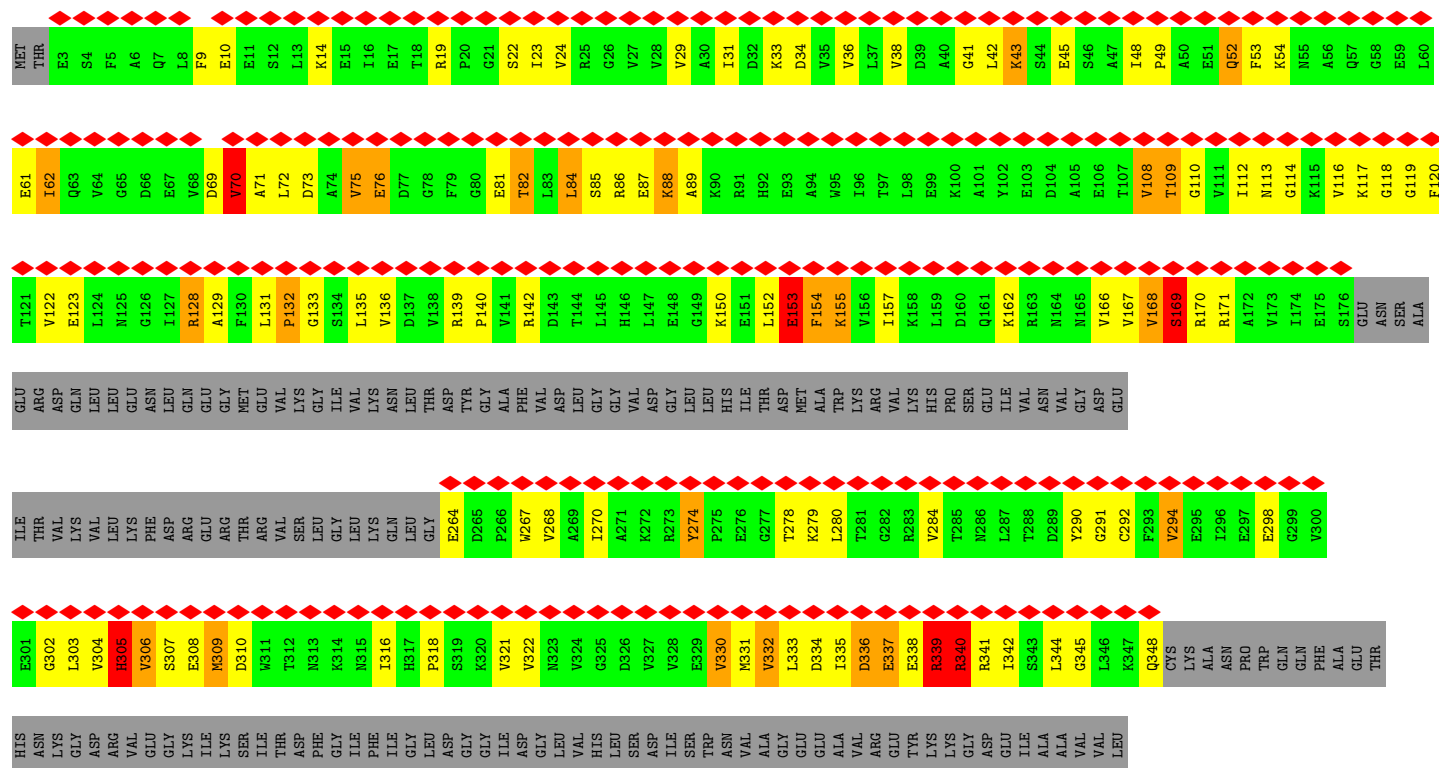
- Molecule 18: 30S ribosomal protein S21



• Molecule 19: 30S ribosomal protein S2

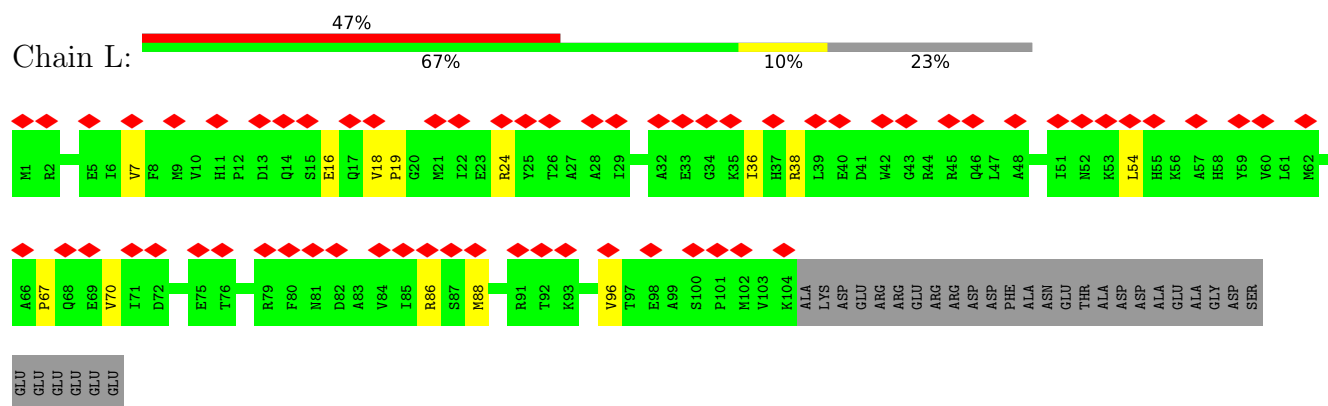


• Molecule 20: 30S ribosomal protein S1

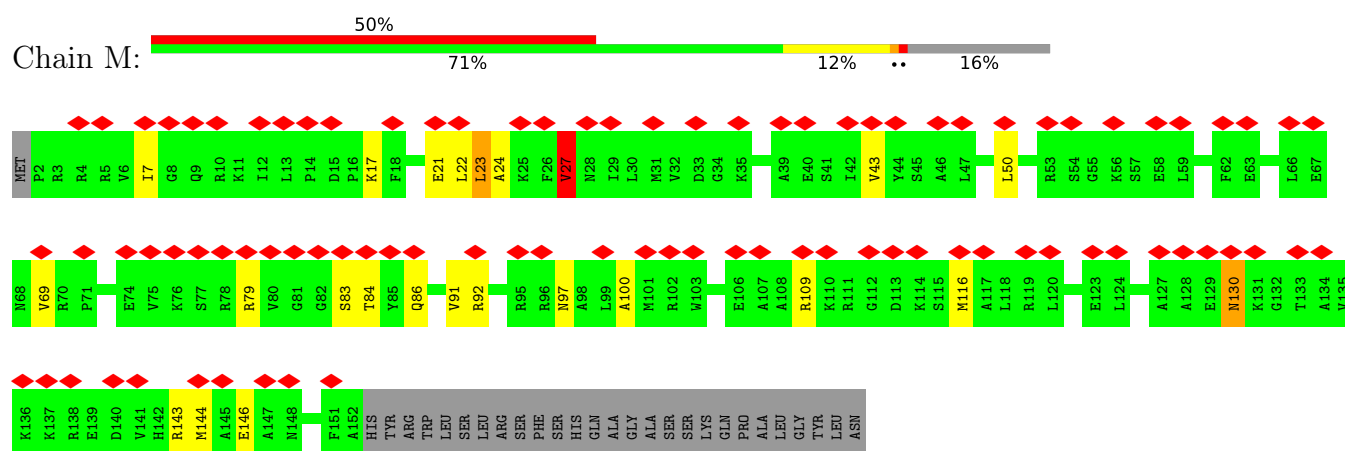




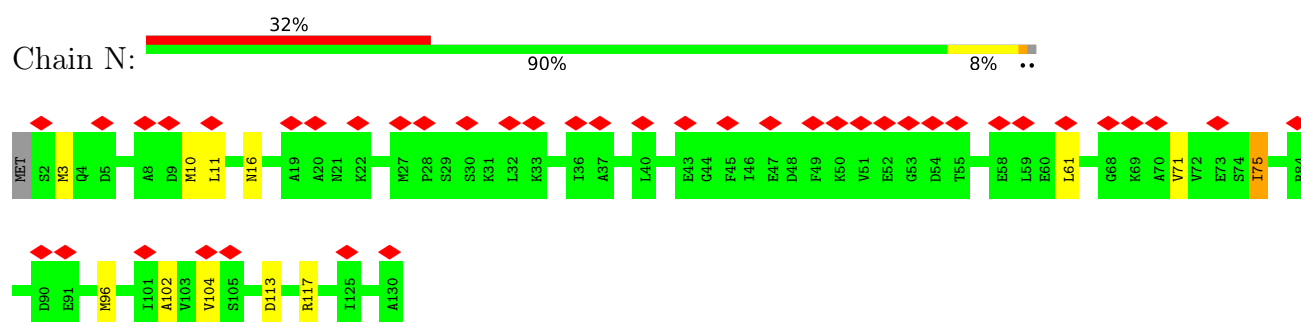
- Molecule 24: 30S ribosomal protein S6



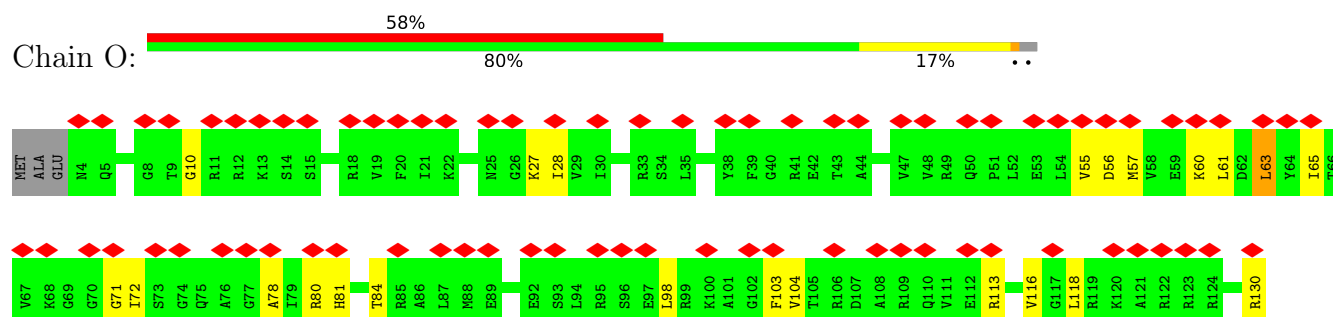
- Molecule 25: 30S ribosomal protein S7



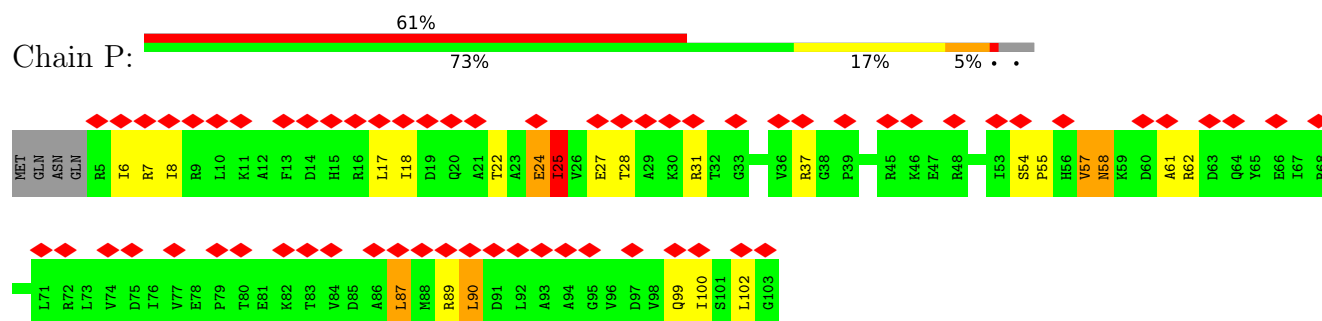
- Molecule 26: 30S ribosomal protein S8



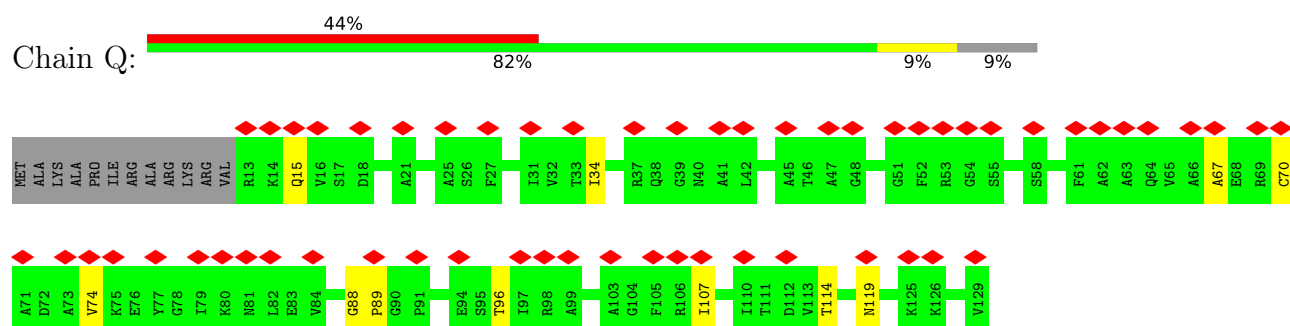
- Molecule 27: 30S ribosomal protein S9



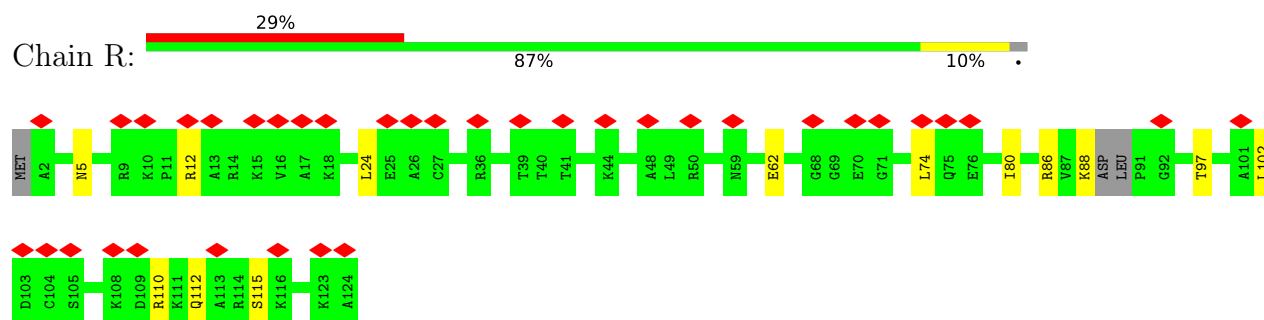
- Molecule 28: 30S ribosomal protein S10



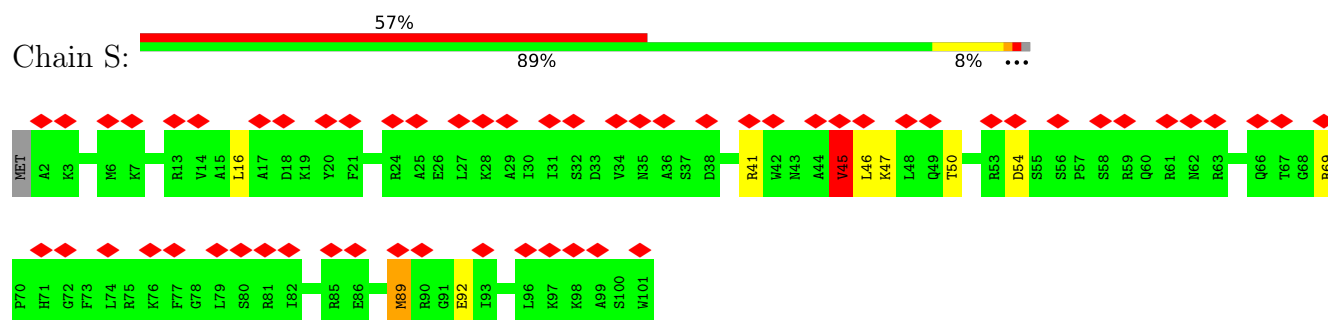
- Molecule 29: 30S ribosomal protein S11



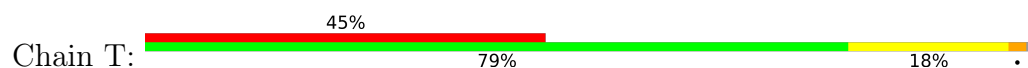
- Molecule 30: 30S ribosomal protein S12

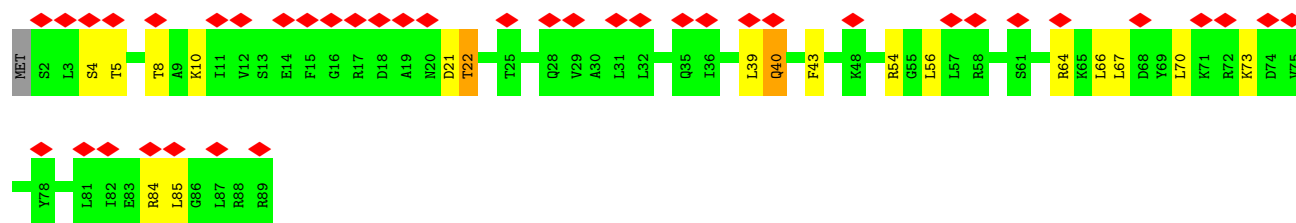


- Molecule 31: 30S ribosomal protein S14

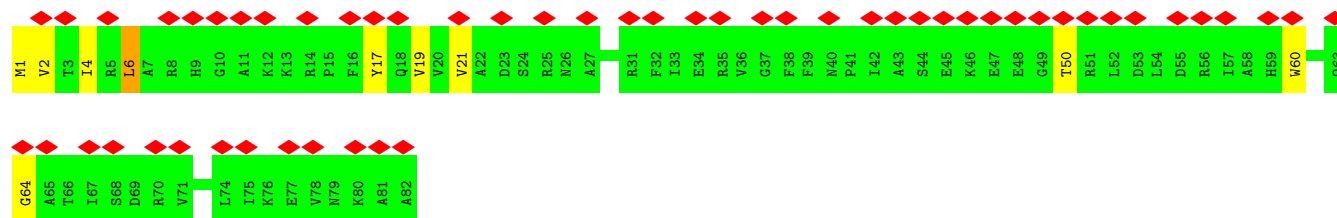
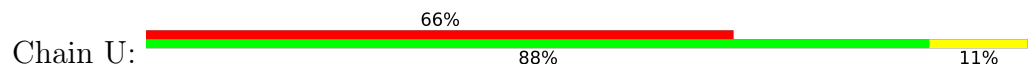


- Molecule 32: 30S ribosomal protein S15

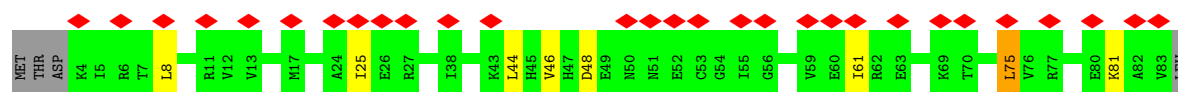
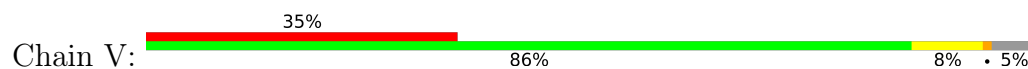




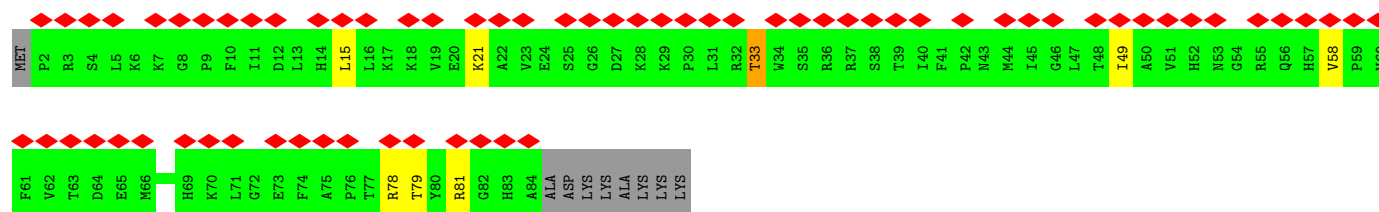
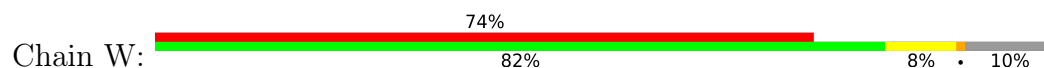
- Molecule 33: 30S ribosomal protein S16



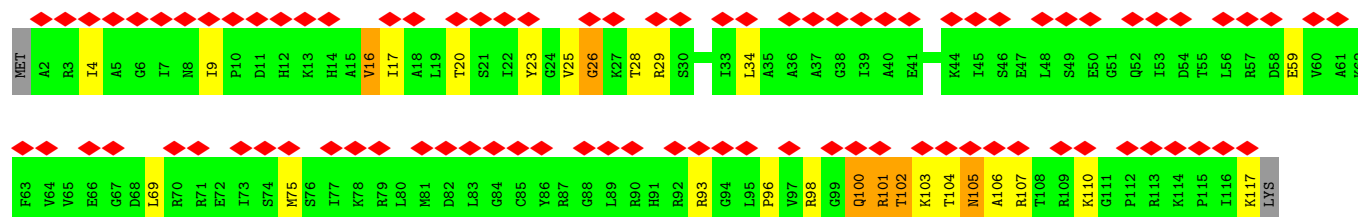
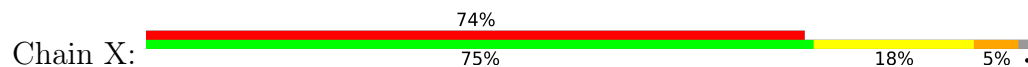
- Molecule 34: 30S ribosomal protein S17



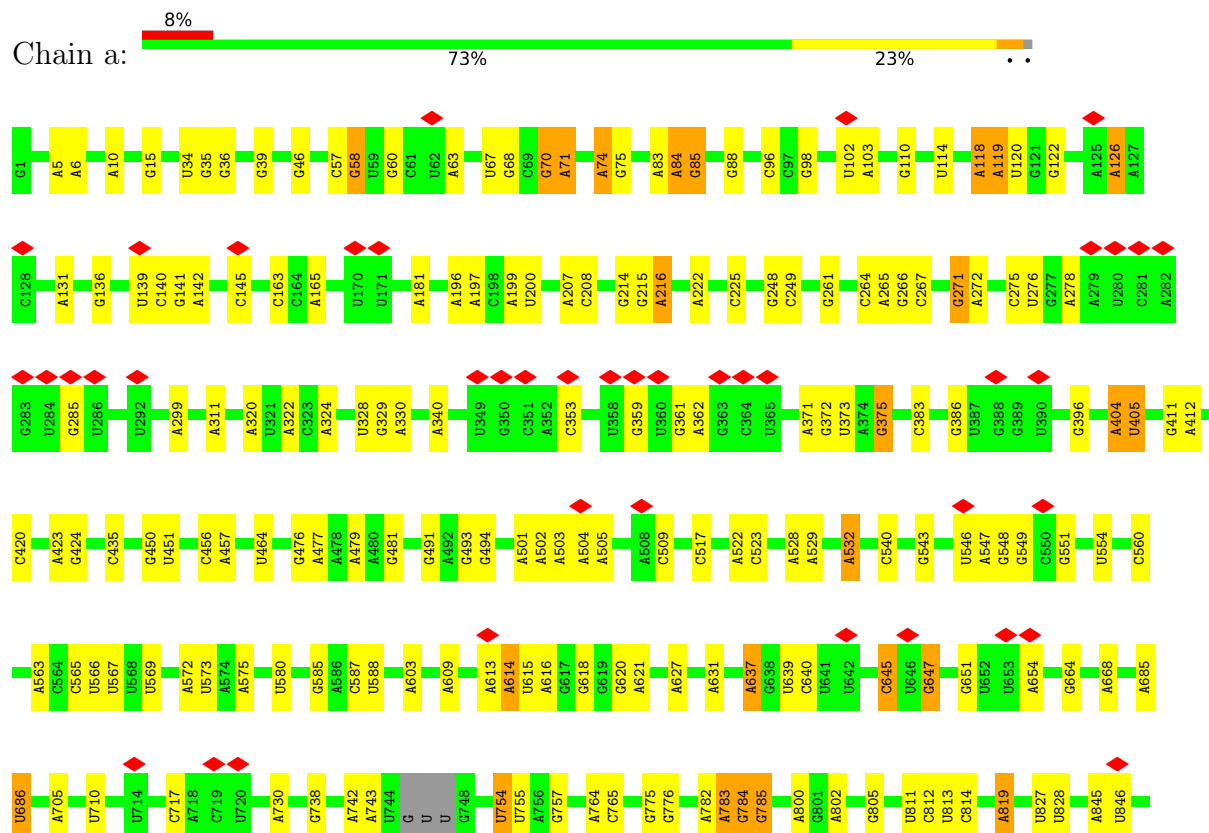
- Molecule 35: 30S ribosomal protein S19

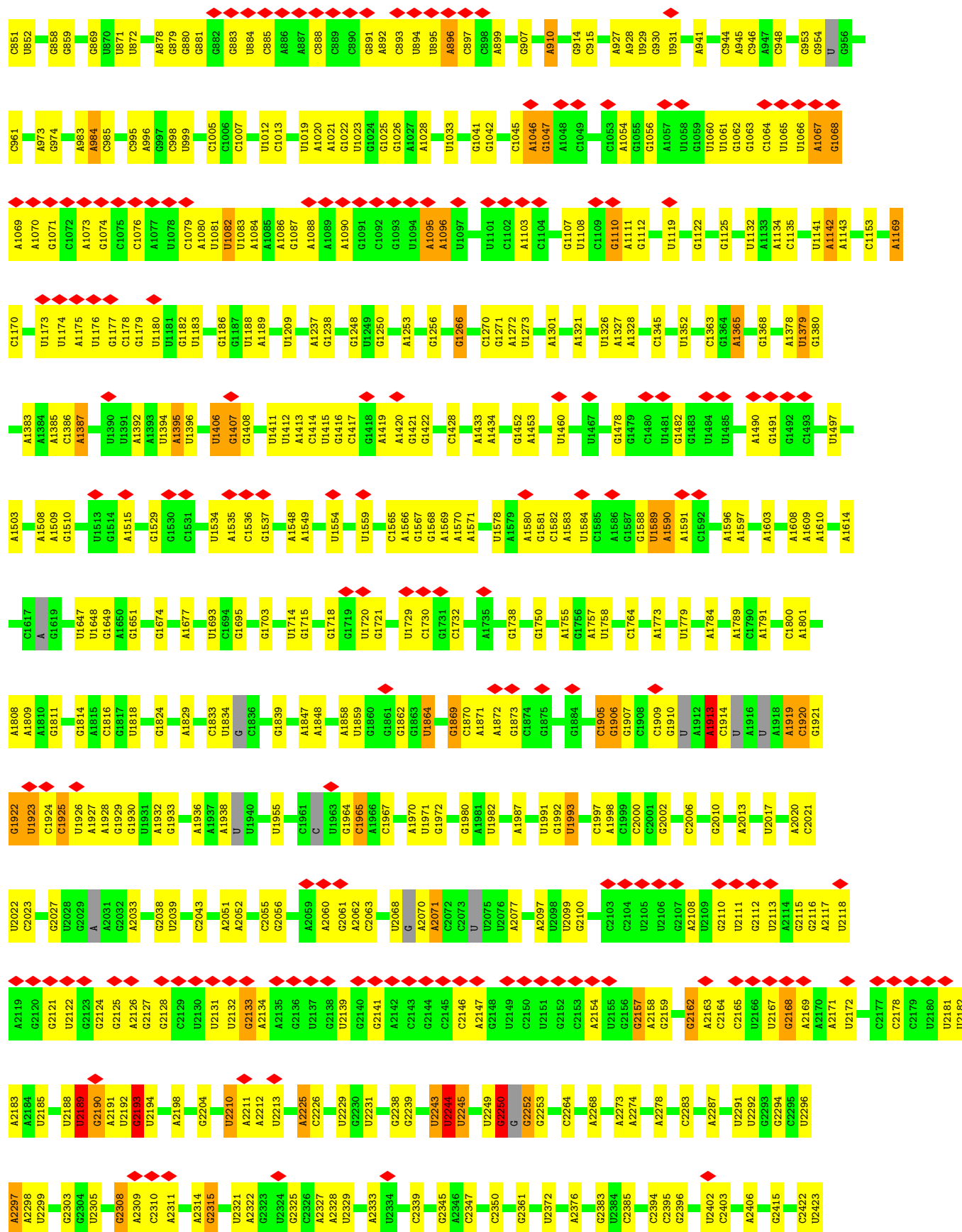


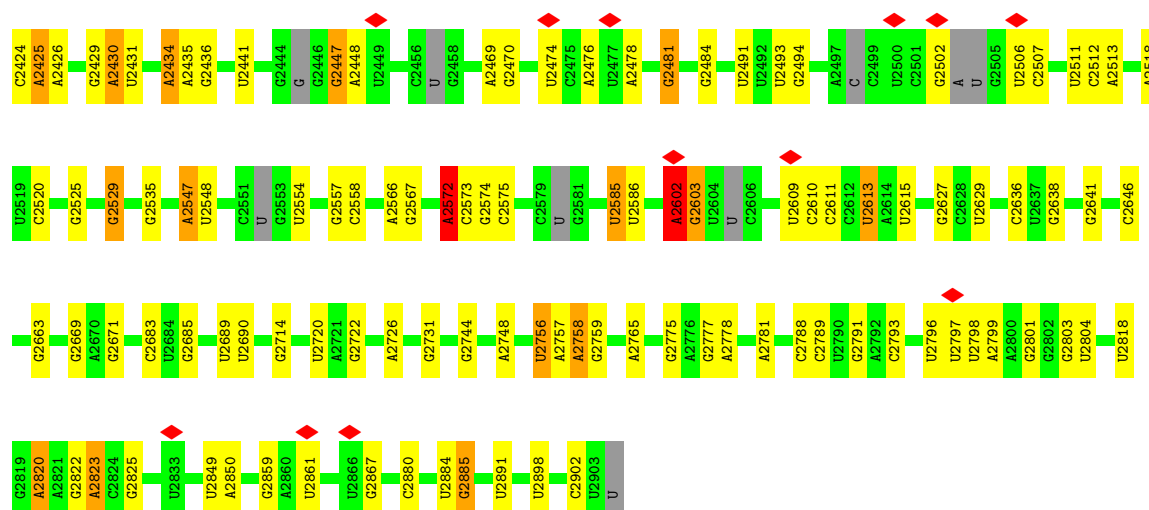
- Molecule 36: 30S ribosomal protein S13



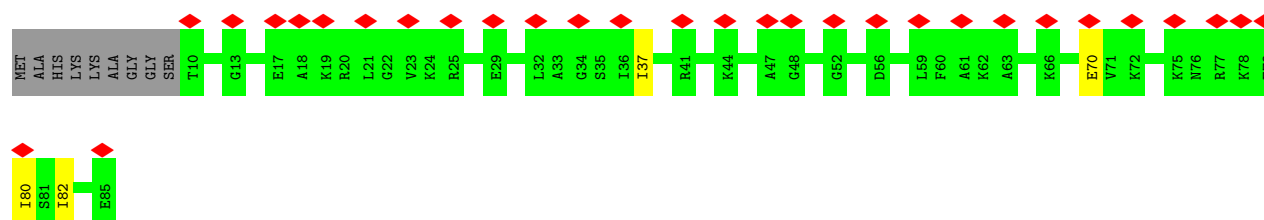
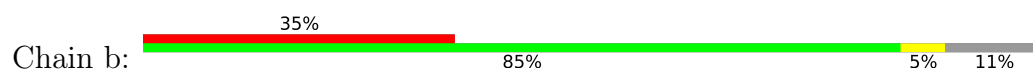
- Molecule 37: 50S ribosomal protein L11



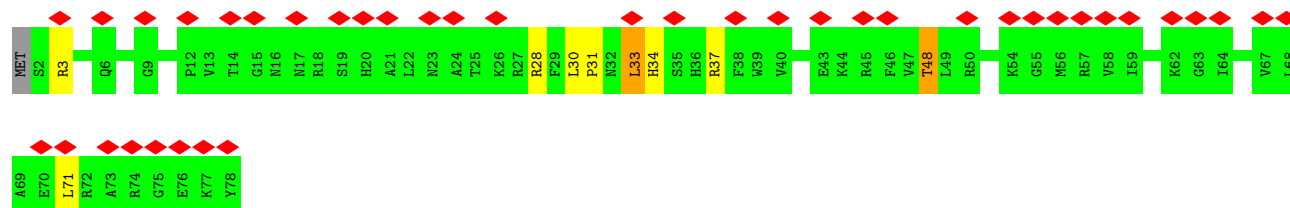
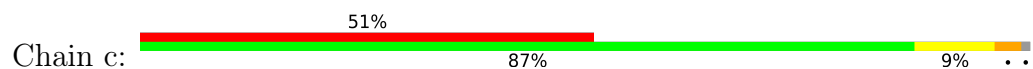




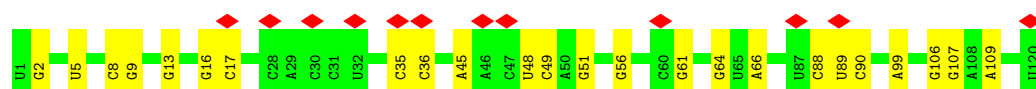
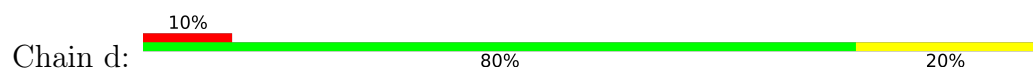
• Molecule 40: 50S ribosomal protein L27



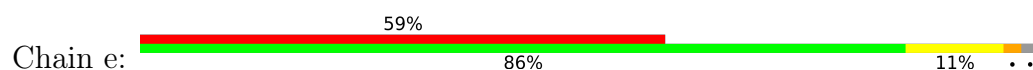
• Molecule 41: 50S ribosomal protein L28

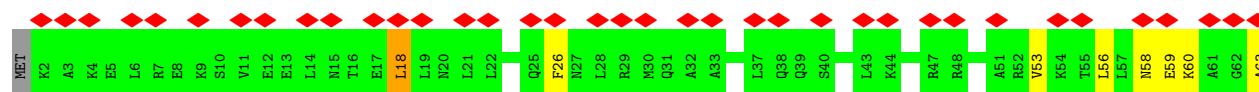


• Molecule 42: 5S rRNA

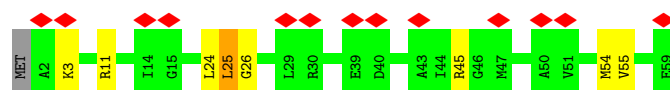
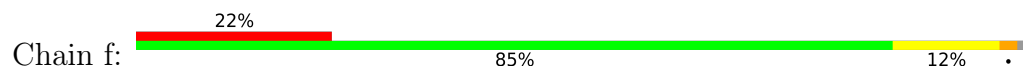


• Molecule 43: 50S ribosomal protein L29

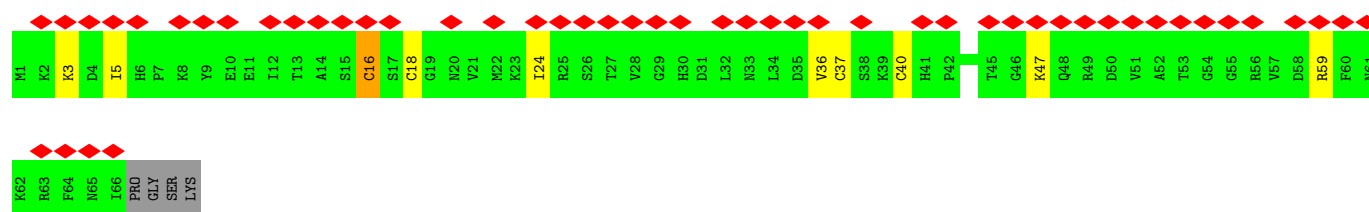
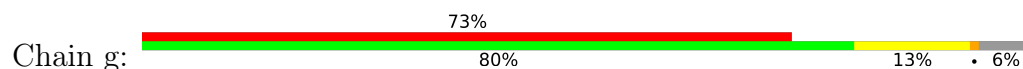




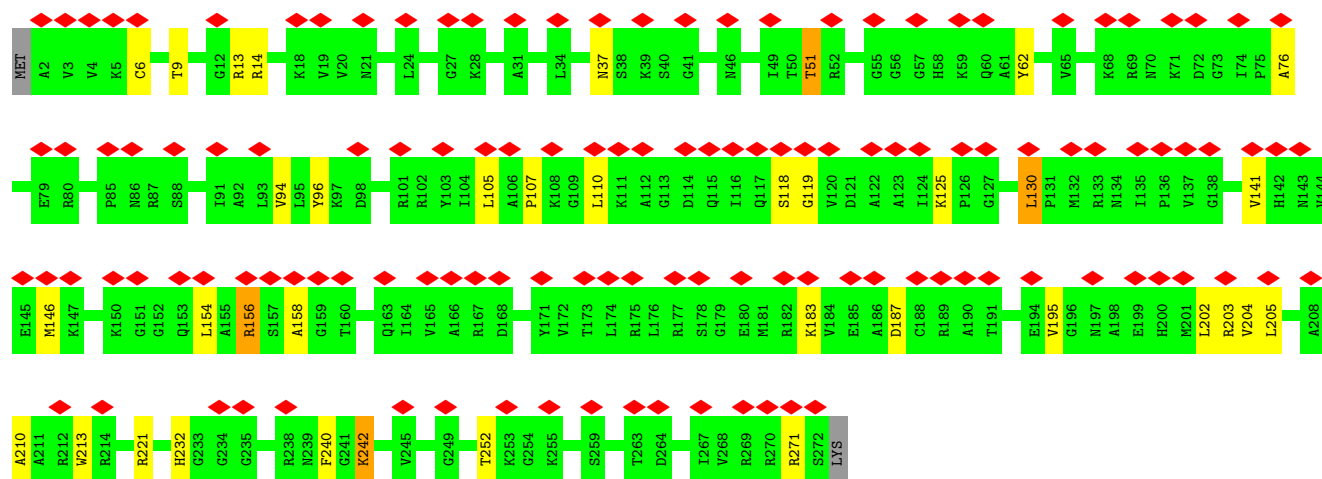
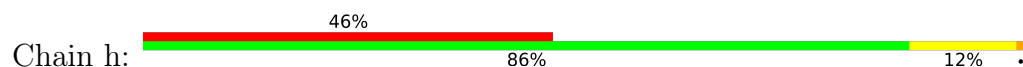
- Molecule 44: 50S ribosomal protein L30



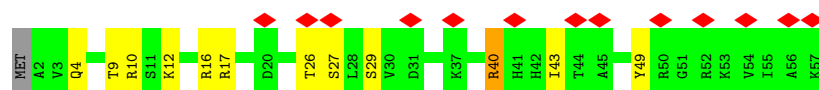
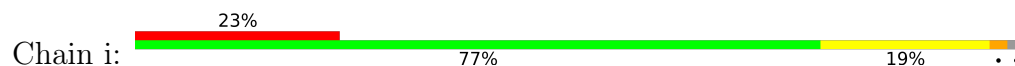
- Molecule 45: 50S ribosomal protein L31



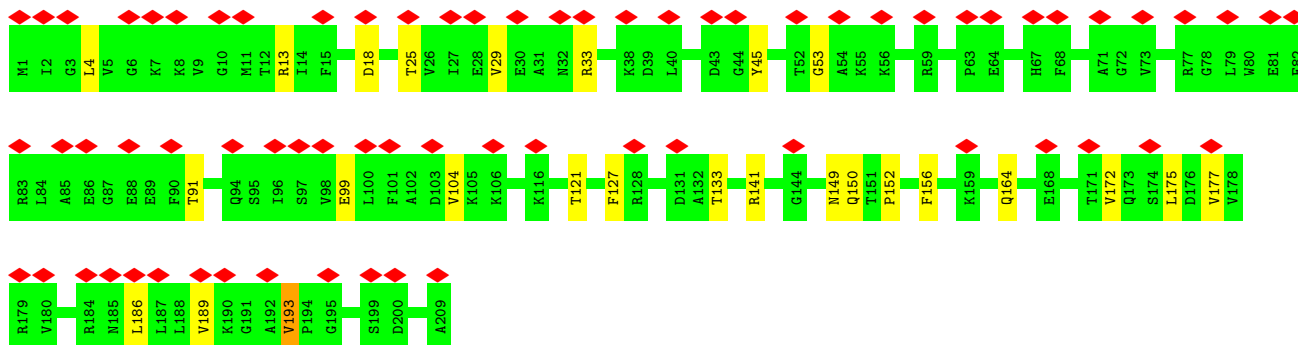
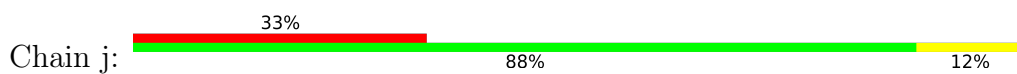
- Molecule 46: 50S ribosomal protein L2



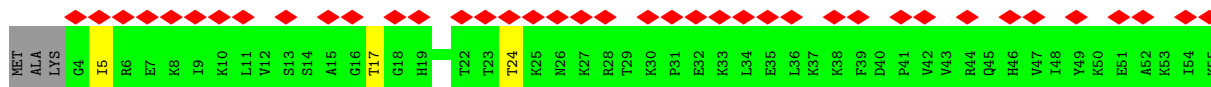
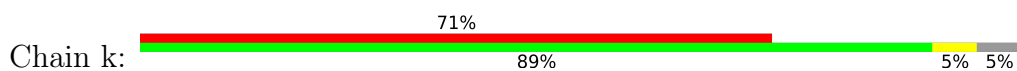
- Molecule 47: 50S ribosomal protein L32



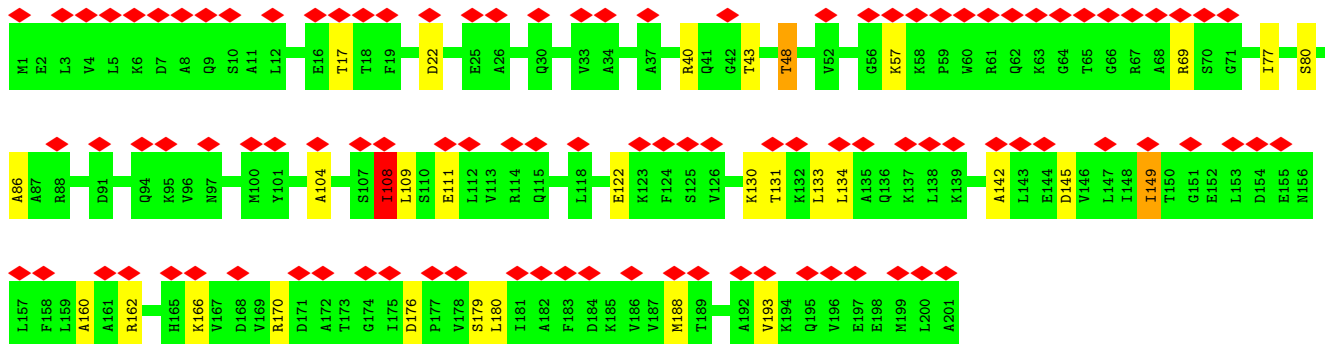
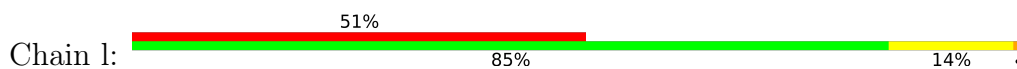
- Molecule 48: 50S ribosomal protein L3



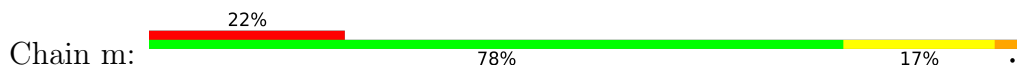
• Molecule 49: 50S ribosomal protein L33



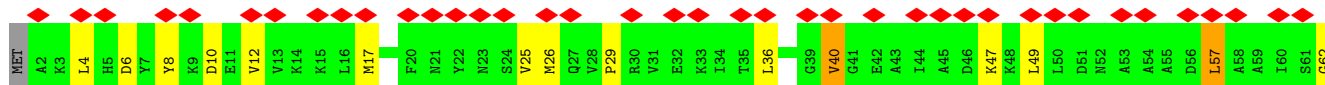
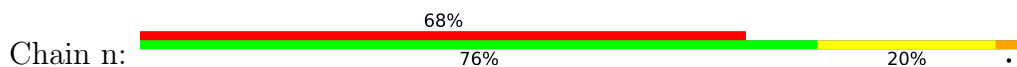
• Molecule 50: 50S ribosomal protein L4

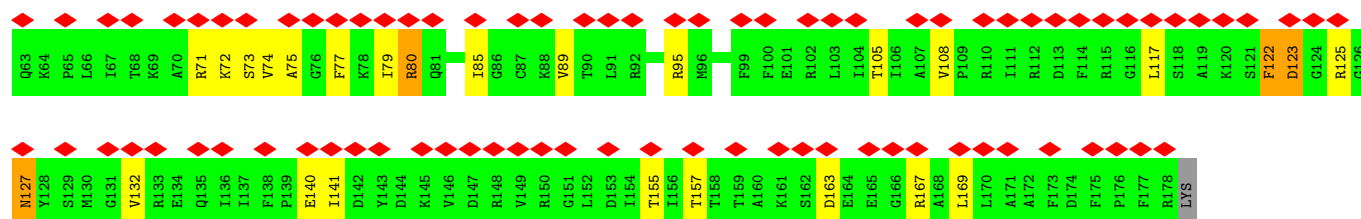


• Molecule 51: 50S ribosomal protein L34

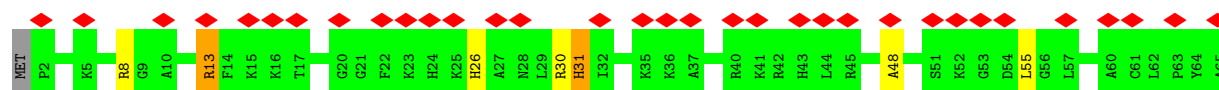
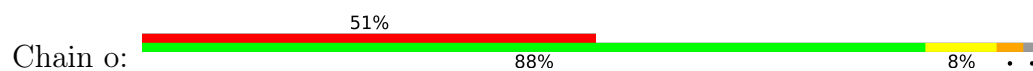


• Molecule 52: 50S ribosomal protein L5

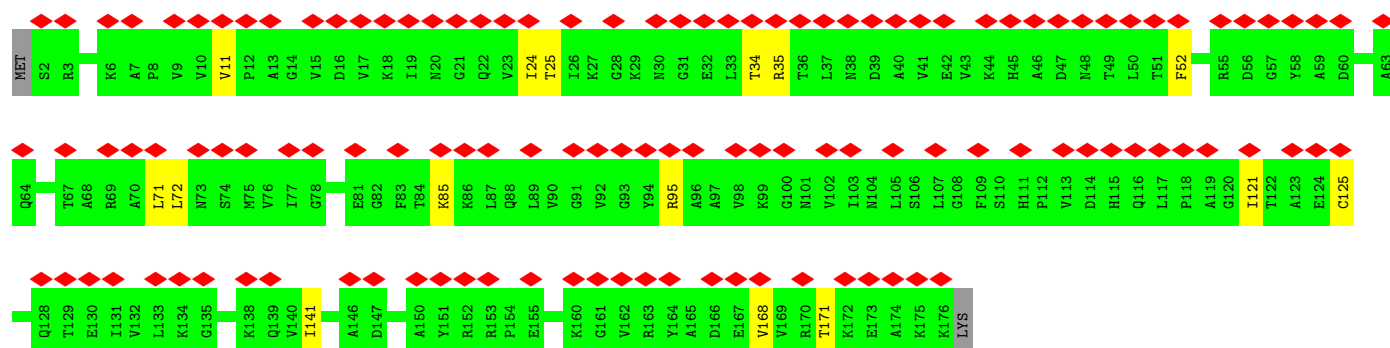
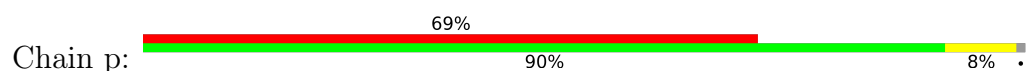




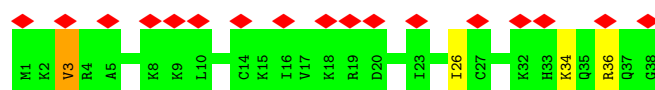
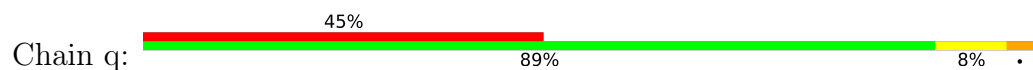
• Molecule 53: 50S ribosomal protein L35



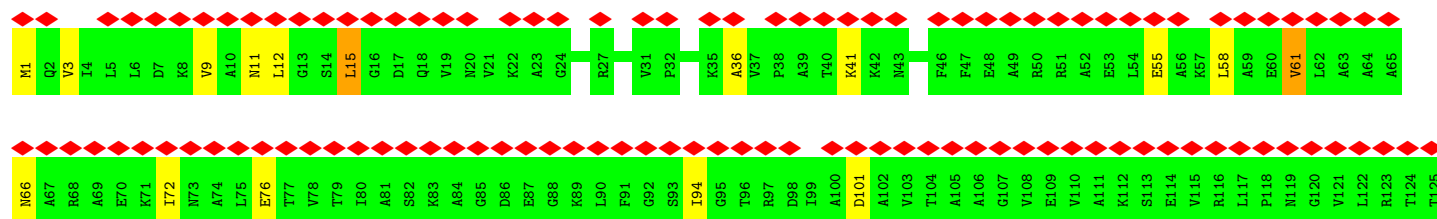
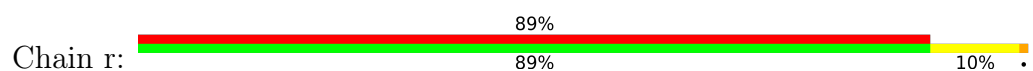
• Molecule 54: 50S ribosomal protein L6

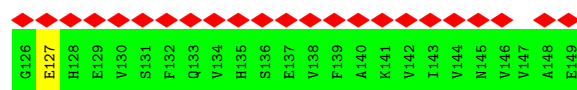


• Molecule 55: 50S ribosomal protein L36

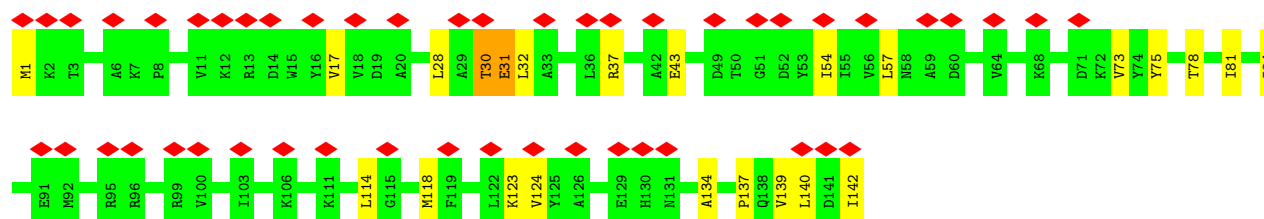
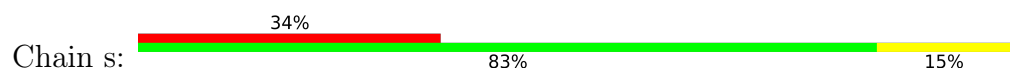


• Molecule 56: 50S ribosomal protein L9

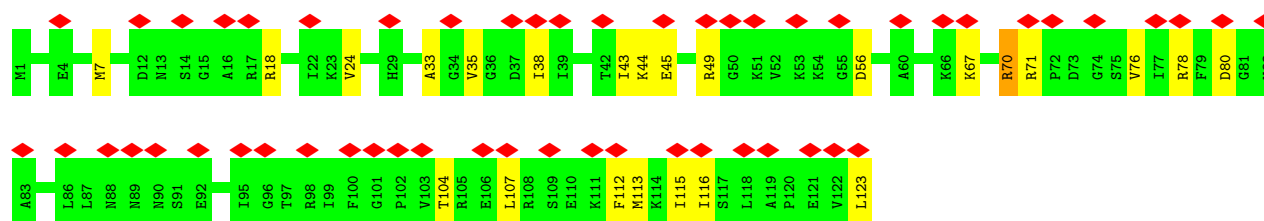
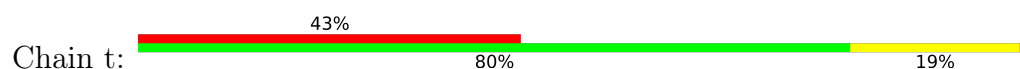




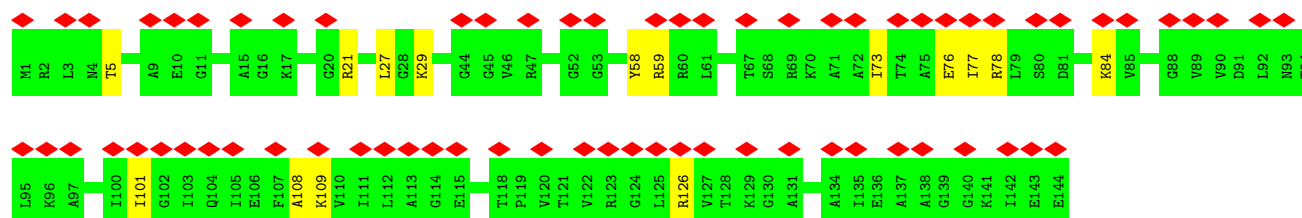
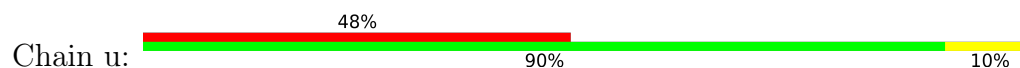
• Molecule 57: 50S ribosomal protein L13



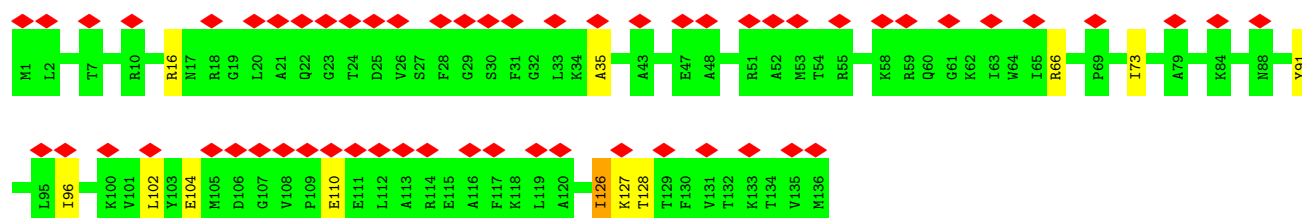
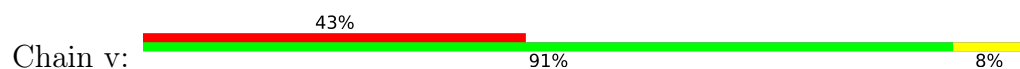
• Molecule 58: 50S ribosomal protein L14



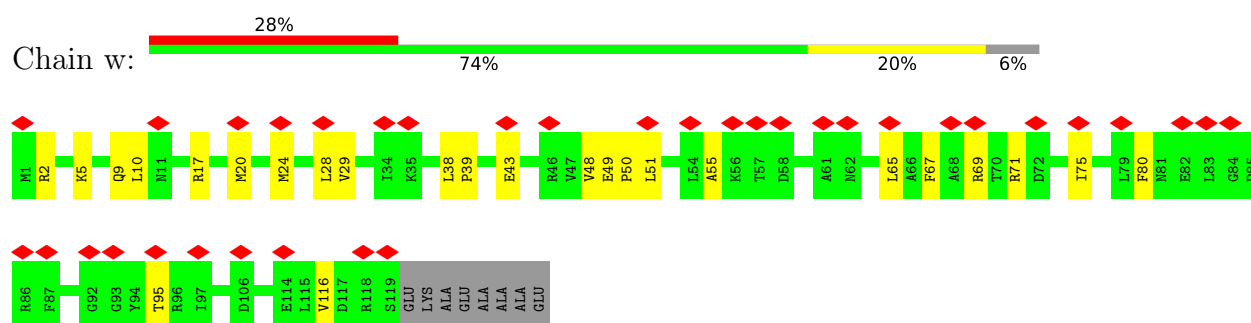
• Molecule 59: 50S ribosomal protein L15



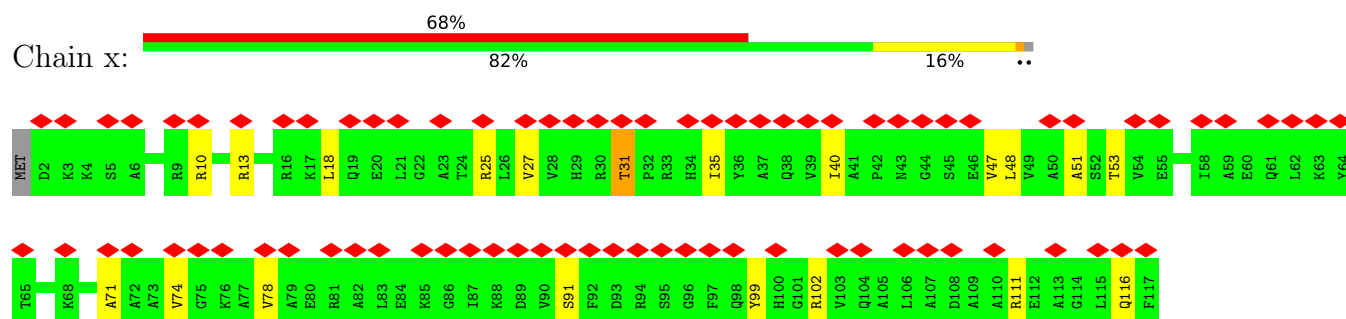
• Molecule 60: 50S ribosomal protein L16



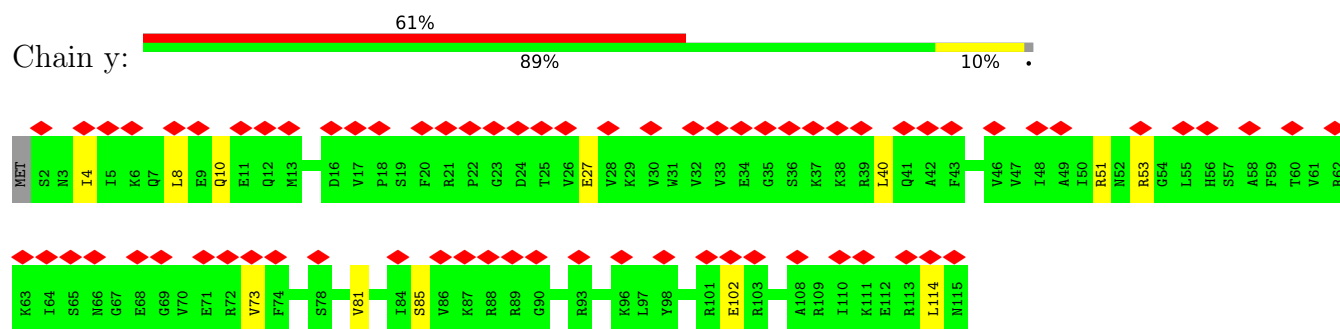
• Molecule 61: 50S ribosomal protein L17



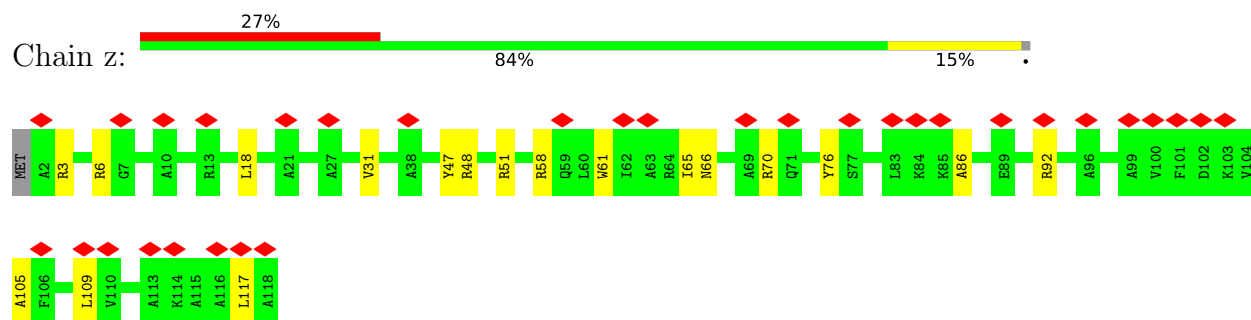
• Molecule 62: 50S ribosomal protein L18



• 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	0.49	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	0.77	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	0.56	2/813 (0.2%)	0.80	2/1262 (0.2%)
9	9	1.15	2/1131 (0.2%)	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	0.67	12/10591 (0.1%)	0.96	54/14289 (0.4%)
12	AB	0.43	1/808 (0.1%)	0.70	2/1088 (0.2%)
13	AC	0.60	4/1808 (0.2%)	0.73	9/2450 (0.4%)
13	AD	0.39	0/1789	0.55	0/2425
14	AE	0.54	9/10545 (0.1%)	0.74	23/14236 (0.2%)
15	C	0.66	0/553	1.14	2/743 (0.3%)
16	D	0.40	9/36610 (0.0%)	0.75	38/57091 (0.1%)
17	E	0.76	0/675	1.32	0/895
18	F	0.72	0/597	1.20	0/792
19	G	0.65	0/1791	1.08	1/2413 (0.0%)
20	H	0.76	4/1746 (0.2%)	1.58	34/2382 (1.4%)
21	I	0.58	0/1663	0.97	0/2241
22	J	0.63	0/1665	1.08	0/2227
23	K	0.64	1/1165 (0.1%)	1.06	2/1568 (0.1%)
24	L	0.58	0/867	0.94	0/1171
25	M	0.68	0/1195	1.19	3/1602 (0.2%)
26	N	0.55	0/989	0.91	0/1326
27	O	0.58	0/1034	1.02	1/1375 (0.1%)
28	P	0.60	0/800	1.10	4/1082 (0.4%)
29	Q	0.55	0/893	0.91	0/1205
30	R	0.49	0/952	0.81	0/1274

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	S	0.64	0/817	1.11	1/1088 (0.1%)
32	T	0.68	0/722	1.21	0/964
33	U	0.57	0/659	0.99	0/884
34	V	0.46	0/657	0.73	0/881
35	W	0.51	0/680	0.83	0/915
36	X	0.67	0/909	1.21	3/1215 (0.2%)
37	Y	1.04	0/1046	1.09	1/1410 (0.1%)
38	Z	1.02	0/227	1.13	0/304
39	a	0.40	3/69247 (0.0%)	0.75	56/107985 (0.1%)
40	b	0.51	0/589	0.76	0/779
41	c	0.63	0/635	0.97	0/848
42	d	0.37	0/2872	0.69	0/4478
43	e	0.69	0/502	1.19	0/667
44	f	0.62	0/452	1.02	0/605
45	g	0.55	0/531	0.99	1/709 (0.1%)
46	h	0.54	0/2121	0.85	0/2852
47	i	0.52	0/450	0.94	0/599
48	j	0.60	0/1586	0.87	0/2134
49	k	0.47	0/433	0.80	0/576
50	l	0.61	0/1571	1.03	1/2113 (0.0%)
51	m	0.68	0/380	1.22	0/498
52	n	0.62	0/1434	1.18	10/1926 (0.5%)
53	o	0.64	0/513	1.10	1/676 (0.1%)
54	p	0.58	0/1333	0.89	0/1805
55	q	0.50	0/303	0.88	0/397
56	r	0.63	0/1122	0.97	1/1515 (0.1%)
57	s	0.68	0/1152	1.02	2/1551 (0.1%)
58	t	0.57	0/955	0.88	0/1279
59	u	0.55	0/1062	0.96	1/1413 (0.1%)
60	v	0.59	0/1093	0.97	0/1460
61	w	0.67	0/964	1.13	0/1289
62	x	0.61	0/902	1.09	0/1209
63	y	0.52	0/929	0.79	0/1242
64	z	0.80	0/960	1.25	0/1278
All	All	0.50	49/189246 (0.0%)	0.84	268/278938 (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

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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 49 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	18.29	1.70	1.47
11	AA	374	GLU	C-N	17.43	1.53	1.33
11	AA	850	ILE	N-CA	-13.12	1.29	1.46
14	AE	93	THR	CA-C	12.23	1.69	1.52
20	H	169	SER	N-CA	11.82	1.61	1.46

The worst 5 of 268 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	D	1516	G	O3'-P-O5'	17.49	130.24	104.00
11	AA	727	VAL	N-CA-C	-17.18	95.10	110.74
20	H	88	LYS	CA-C-N	16.94	143.58	120.38
20	H	88	LYS	C-N-CA	16.94	143.58	120.38
10	B	29	G	C3'-C2'-O2'	15.97	134.66	110.70

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

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	13	0
3	2	746	811	811	6	0
4	3	788	844	844	10	0
5	4	753	780	780	0	0
6	5	472	260	261	24	0
7	6	542	305	306	23	0
8	7	732	97	362	85	0
9	9	1117	0	1153	163	0
10	A	1620	826	826	173	0
10	B	1620	813	827	139	0
11	AA	10425	10426	10428	398	0
12	AB	790	783	783	8	0
13	AC	1786	1813	1813	90	0
13	AD	1767	1789	1789	47	0
14	AE	10388	10612	10611	368	0
15	C	544	559	560	23	0
16	D	32703	16423	16459	222	0
17	E	669	719	719	4	0
18	F	589	629	629	8	0
19	G	1760	1785	1785	47	0
20	H	1730	1454	1454	212	0
21	I	1636	1710	1710	53	0
22	J	1643	1707	1707	31	0
23	K	1152	1196	1196	32	0
24	L	848	846	846	3	0
25	M	1181	1235	1235	32	0
26	N	979	1031	1031	6	0
27	O	1022	1070	1070	11	0
28	P	790	831	831	52	0
29	Q	877	887	887	4	0
30	R	939	1001	1001	7	0
31	S	805	844	844	5	0
32	T	714	734	734	8	0
33	U	649	666	666	3	0
34	V	648	691	691	5	0
35	W	663	688	688	2	0
36	X	900	964	964	58	0
37	Y	1032	0	1088	81	0
38	Z	227	0	237	19	0
39	a	61841	31077	31123	301	0
40	b	582	599	599	2	0
41	c	625	652	652	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	d	2569	1301	1301	4	0
43	e	501	531	531	5	0
44	f	448	488	488	5	0
45	g	522	520	520	11	0
46	h	2082	2154	2154	19	0
47	i	444	459	458	6	0
48	j	1565	1617	1616	16	0
49	k	426	464	464	0	0
50	l	1552	1619	1619	14	0
51	m	377	418	418	9	0
52	n	1410	1443	1444	28	0
53	o	504	572	572	3	0
54	p	1313	1358	1358	7	0
55	q	302	343	343	1	0
56	r	1111	1148	1148	4	0
57	s	1129	1162	1162	13	0
58	t	946	1023	1023	12	0
59	u	1053	1129	1129	7	0
60	v	1074	1157	1157	5	0
61	w	951	994	994	10	0
62	x	892	923	923	10	0
63	y	917	962	962	4	0
64	z	947	1020	1019	12	0
65	AE	1	0	0	0	0
66	AE	2	0	0	0	0
All	All	176005	124723	127564	2459	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 8.

The worst 5 of 2459 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:H:131:LEU:CB	20:H:167:VAL:CA	1.78	1.62
15:C:12:ARG:HG3	20:H:264:GLU:CB	1.30	1.60
11:AA:1026:GLU:HG3	16:D:1030:U:C2	1.47	1.49
20:H:131:LEU:CB	20:H:167:VAL:HA	1.03	1.47
9:9:130:PRO:N	9:9:130:PRO:CA	1.70	1.45

There are no symmetry-related clashes.

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%)	12	43
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	43
5	4	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
9	9	146/165 (88%)	95 (65%)	37 (25%)	14 (10%)	0	7
11	AA	1318/1342 (98%)	1149 (87%)	137 (10%)	32 (2%)	4	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%)	18	51
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%)	24	57
22	J	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
23	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	21	54
24	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	43
25	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	18	51
26	N	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16	48
27	O	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16	48
28	P	97/103 (94%)	88 (91%)	8 (8%)	1 (1%)	12	43
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%)	9	38
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%)	6	33
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	62
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%)	24	57
51	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
52	n	175/179 (98%)	162 (93%)	11 (6%)	2 (1%)	11	41
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%)	14	41

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%)	76 (90%)	8 (10%)	8	30
2	1	93/93 (100%)	86 (92%)	7 (8%)	12	38
3	2	81/84 (96%)	77 (95%)	4 (5%)	22	47
4	3	84/85 (99%)	79 (94%)	5 (6%)	17	43
5	4	78/78 (100%)	75 (96%)	3 (4%)	29	53
9	9	112/123 (91%)	63 (56%)	49 (44%)	0	0
11	AA	1140/1157 (98%)	1027 (90%)	113 (10%)	7	28
12	AB	86/158 (54%)	85 (99%)	1 (1%)	63	72
13	AC	198/286 (69%)	183 (92%)	15 (8%)	12	37
13	AD	196/286 (68%)	193 (98%)	3 (2%)	57	69
14	AE	1120/1168 (96%)	1046 (93%)	74 (7%)	15	41
15	C	57/65 (88%)	55 (96%)	2 (4%)	32	54
17	E	65/66 (98%)	61 (94%)	4 (6%)	16	42
18	F	60/61 (98%)	57 (95%)	3 (5%)	22	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	G	187/199 (94%)	174 (93%)	13 (7%)	14	40
20	H	137/461 (30%)	124 (90%)	13 (10%)	8	30
21	I	171/190 (90%)	163 (95%)	8 (5%)	23	48
22	J	172/173 (99%)	164 (95%)	8 (5%)	23	48
23	K	119/126 (94%)	111 (93%)	8 (7%)	15	41
24	L	91/116 (78%)	84 (92%)	7 (8%)	12	37
25	M	124/147 (84%)	113 (91%)	11 (9%)	9	32
26	N	104/105 (99%)	101 (97%)	3 (3%)	37	58
27	O	105/107 (98%)	99 (94%)	6 (6%)	18	44
28	P	86/90 (96%)	77 (90%)	9 (10%)	6	26
29	Q	90/99 (91%)	88 (98%)	2 (2%)	45	63
30	R	101/104 (97%)	95 (94%)	6 (6%)	18	43
31	S	83/84 (99%)	79 (95%)	4 (5%)	23	47
32	T	76/77 (99%)	65 (86%)	11 (14%)	3	17
33	U	65/65 (100%)	60 (92%)	5 (8%)	12	37
34	V	74/78 (95%)	71 (96%)	3 (4%)	27	51
35	W	72/79 (91%)	66 (92%)	6 (8%)	10	34
36	X	94/96 (98%)	87 (93%)	7 (7%)	13	38
37	Y	109/110 (99%)	69 (63%)	40 (37%)	0	0
38	Z	26/85 (31%)	10 (38%)	16 (62%)	0	0
40	b	58/63 (92%)	57 (98%)	1 (2%)	53	67
41	c	67/68 (98%)	64 (96%)	3 (4%)	24	48
43	e	54/55 (98%)	51 (94%)	3 (6%)	19	45
44	f	48/49 (98%)	43 (90%)	5 (10%)	7	26
45	g	59/62 (95%)	54 (92%)	5 (8%)	10	33
46	h	216/218 (99%)	199 (92%)	17 (8%)	11	36
47	i	47/48 (98%)	41 (87%)	6 (13%)	4	21
48	j	164/164 (100%)	156 (95%)	8 (5%)	22	47
49	k	47/49 (96%)	44 (94%)	3 (6%)	16	42
50	l	165/165 (100%)	151 (92%)	14 (8%)	10	33
51	m	38/38 (100%)	36 (95%)	2 (5%)	20	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	n	148/150 (99%)	130 (88%)	18 (12%)	5	21
53	o	51/52 (98%)	47 (92%)	4 (8%)	11	36
54	p	136/138 (99%)	130 (96%)	6 (4%)	25	49
55	q	34/34 (100%)	31 (91%)	3 (9%)	9	33
56	r	114/114 (100%)	102 (90%)	12 (10%)	6	26
57	s	116/116 (100%)	106 (91%)	10 (9%)	10	33
58	t	104/104 (100%)	98 (94%)	6 (6%)	18	44
59	u	103/103 (100%)	96 (93%)	7 (7%)	14	40
60	v	109/109 (100%)	105 (96%)	4 (4%)	30	54
61	w	99/103 (96%)	91 (92%)	8 (8%)	11	35
62	x	86/87 (99%)	80 (93%)	6 (7%)	14	40
63	y	99/100 (99%)	91 (92%)	8 (8%)	11	35
64	z	89/90 (99%)	85 (96%)	4 (4%)	24	48
All	All	7791/8664 (90%)	7151 (92%)	640 (8%)	13	35

5 of 640 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	Z	3	THR
55	q	26	ILE
38	Z	30	PHE
38	Z	2	ILE
48	j	99	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 70 such sidechains are listed below:

Mol	Chain	Res	Type
45	g	33	ASN
46	h	25	HIS
55	q	35	GLN
14	AE	865	HIS
14	AE	817	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%)
16	D	1515/1542 (98%)	290 (19%)	35 (2%)
39	a	2859/2904 (98%)	540 (18%)	0
42	d	119/120 (99%)	17 (14%)	0
8	7	34/35 (97%)	23 (67%)	5 (14%)
All	All	4677/4753 (98%)	934 (19%)	52 (1%)

5 of 934 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.

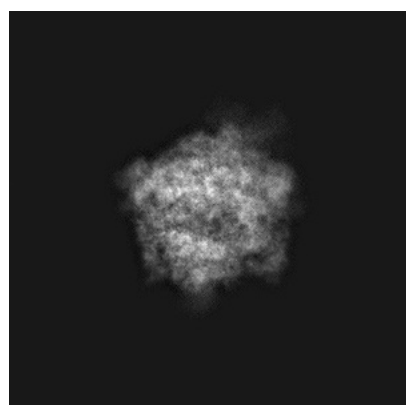
6 Map visualisation [i](#)

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.

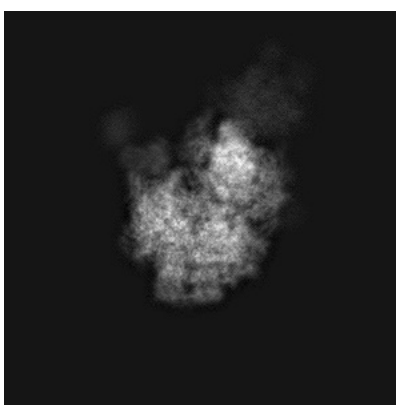
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

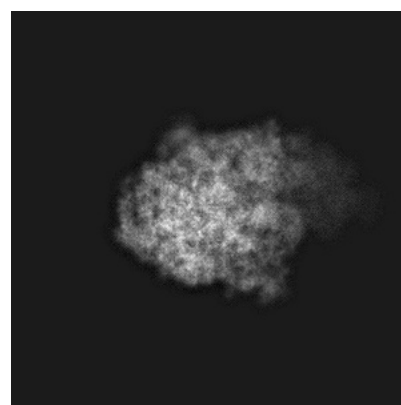
6.1.1 Primary map



X



Y

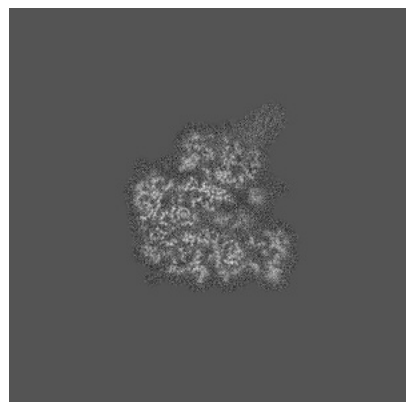


Z

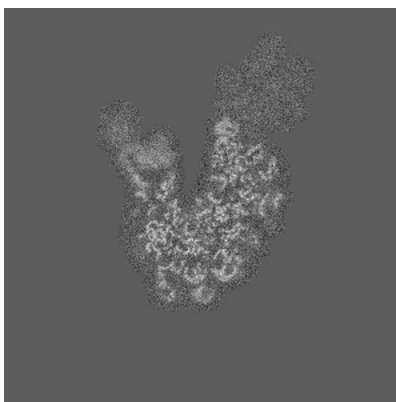
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

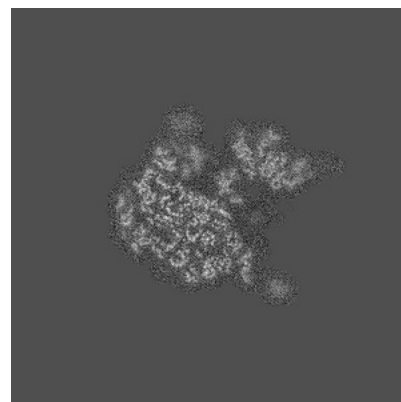
6.2.1 Primary map



X Index: 250



Y Index: 250

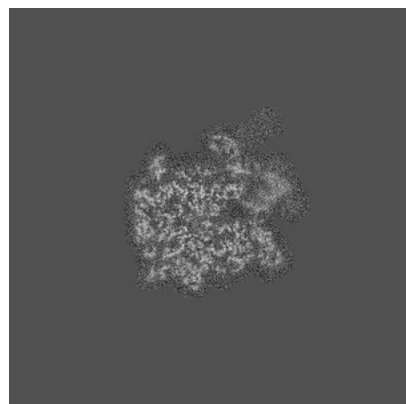


Z Index: 250

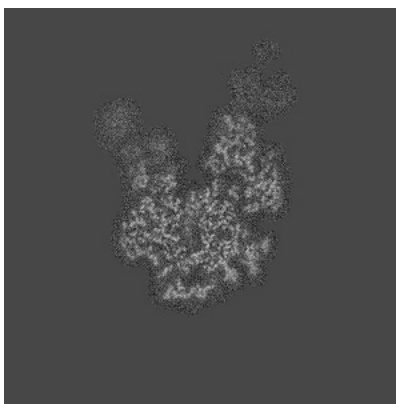
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

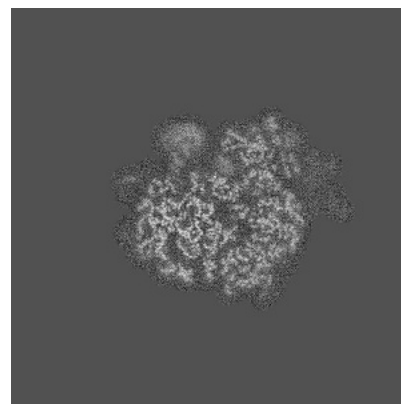
6.3.1 Primary map



X Index: 230



Y Index: 231

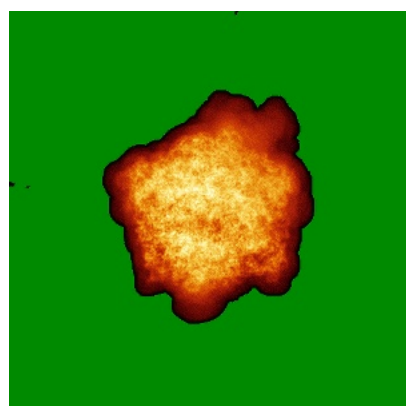


Z Index: 276

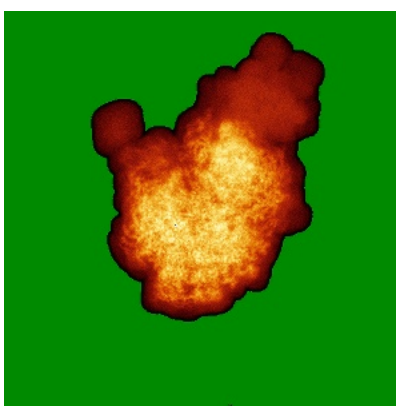
The images above show the largest variance slices of the map in three orthogonal directions.

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

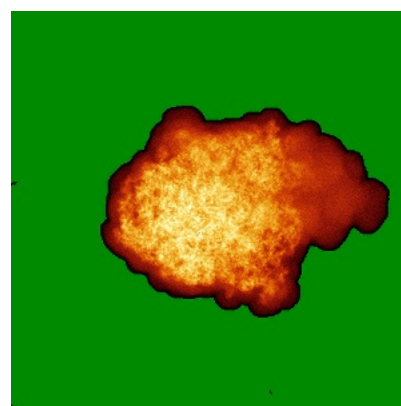
6.4.1 Primary map



X



Y

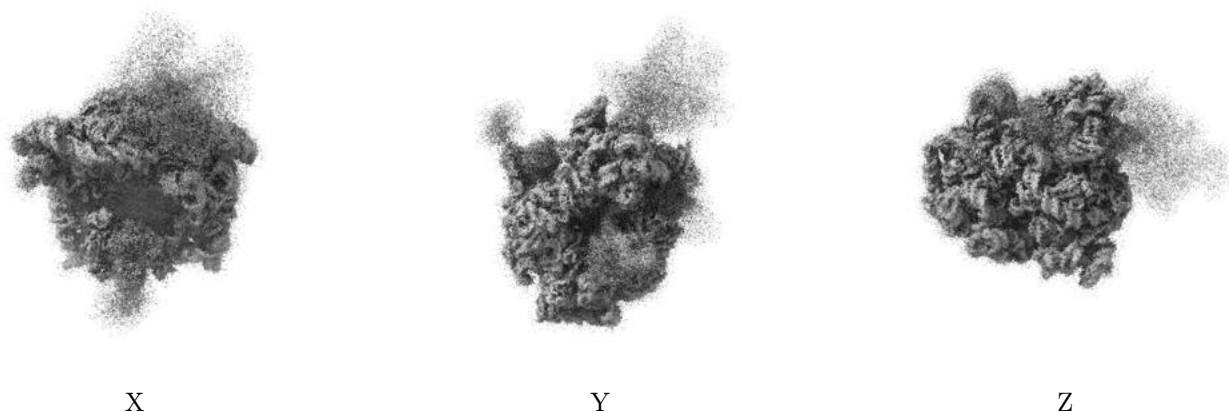


Z

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.

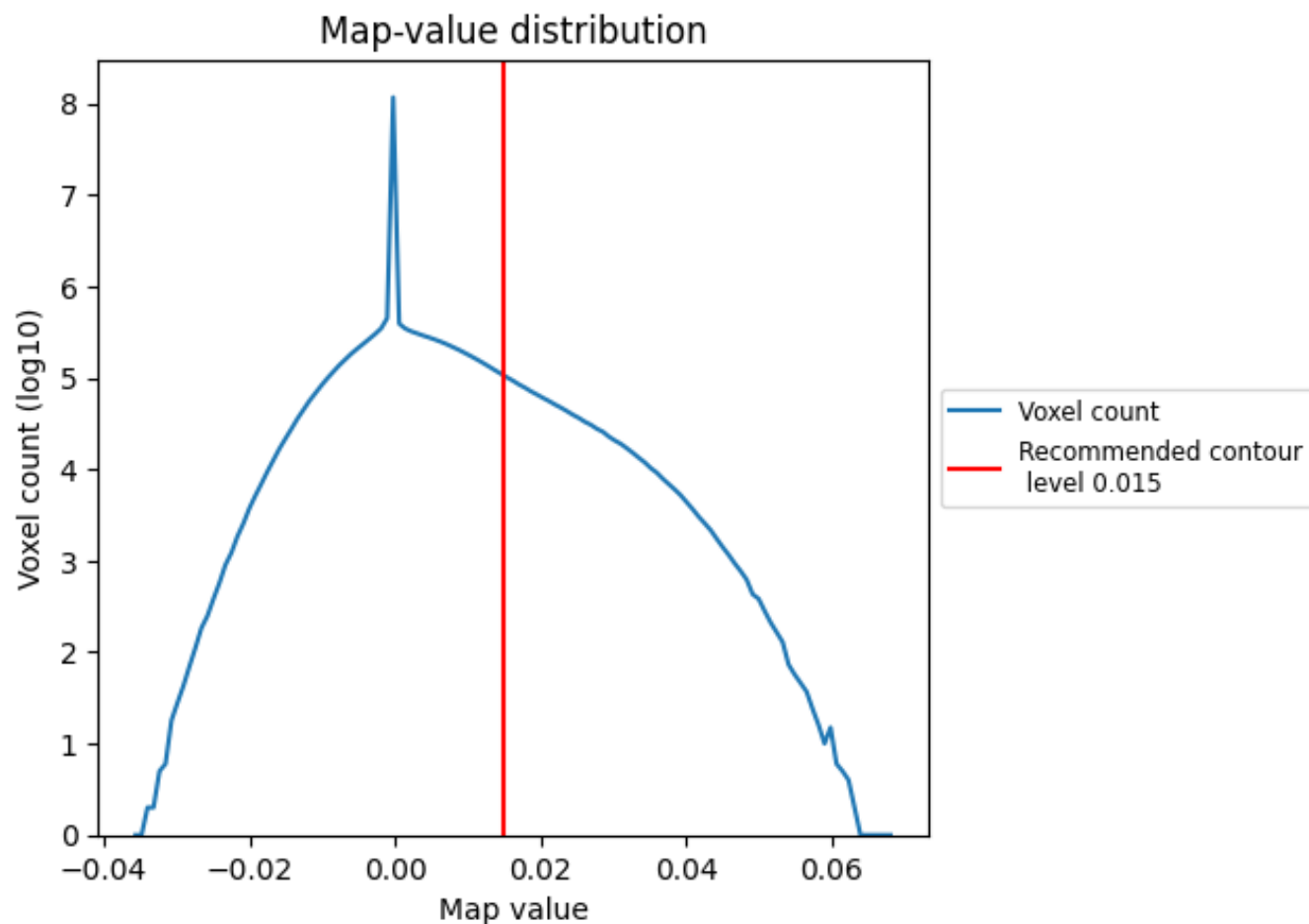
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

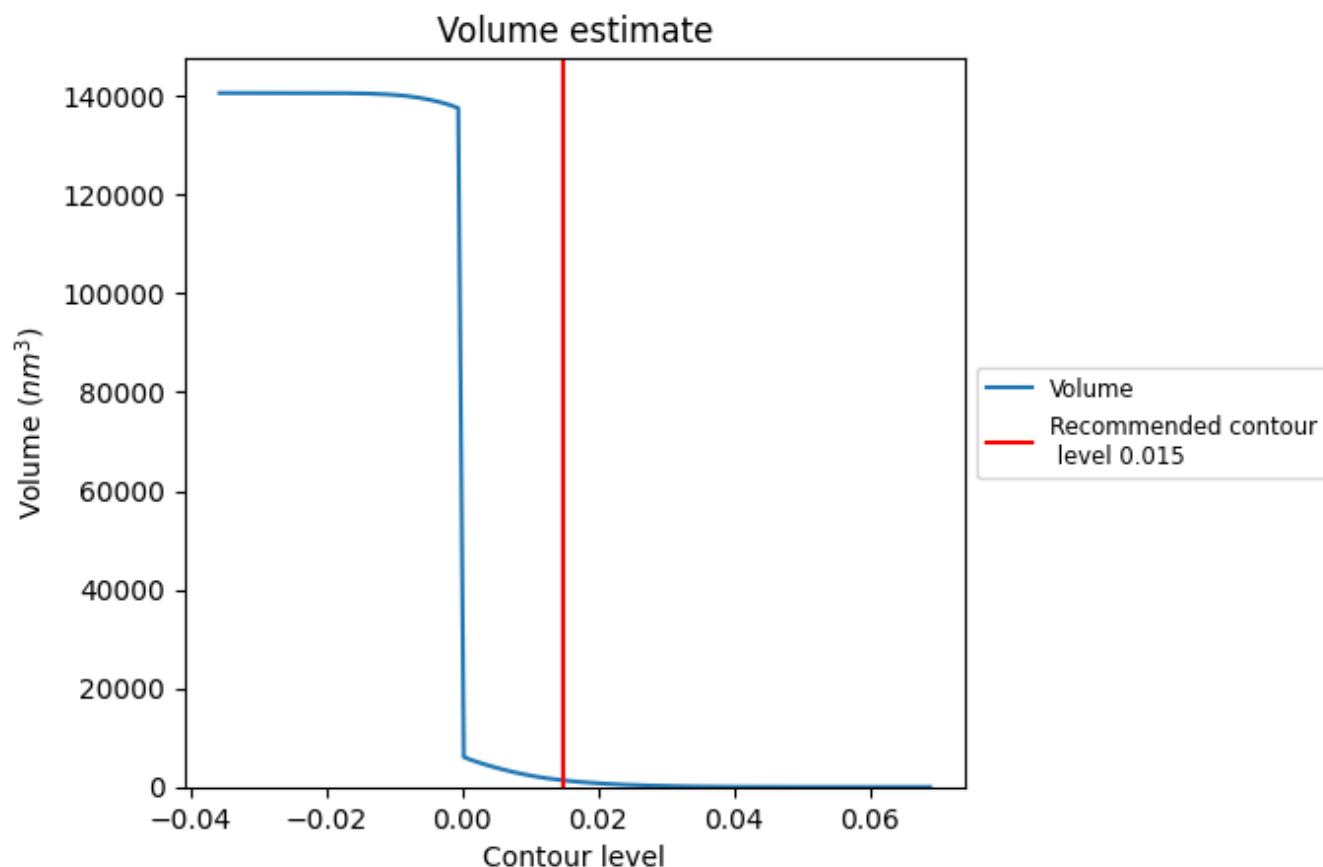
This section contains the results of statistical analysis of the map.

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.

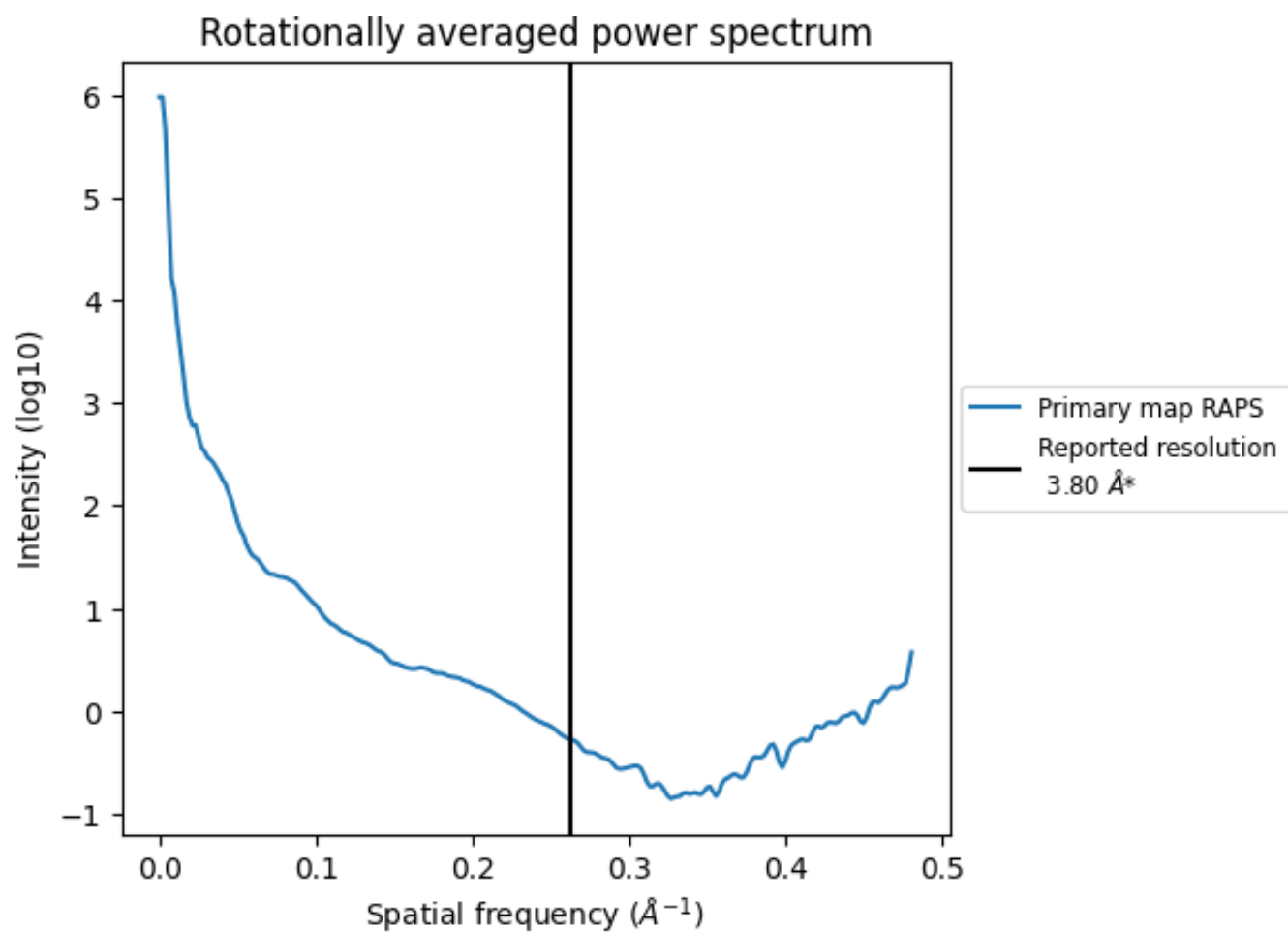
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1329 nm^3 ; 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

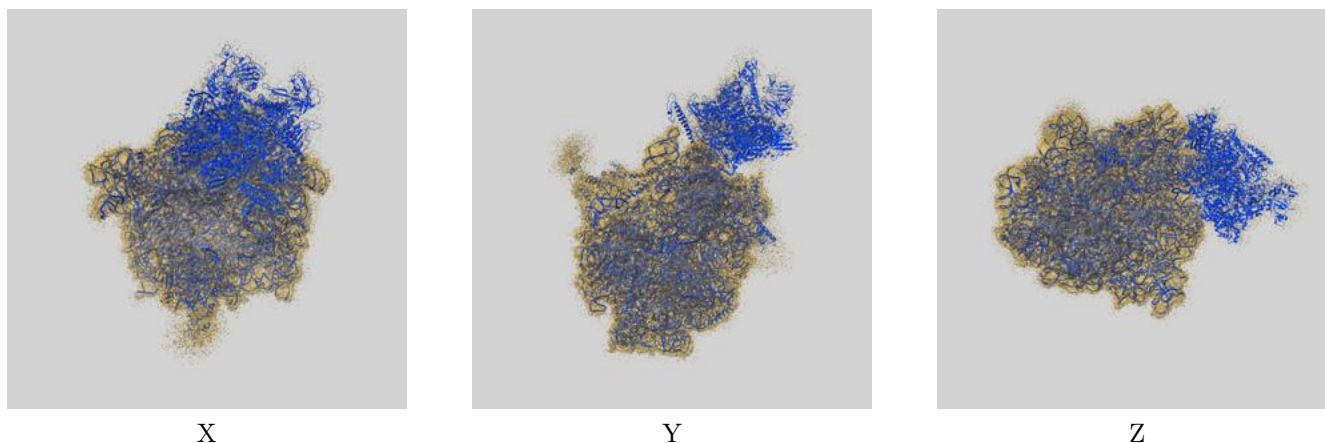
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

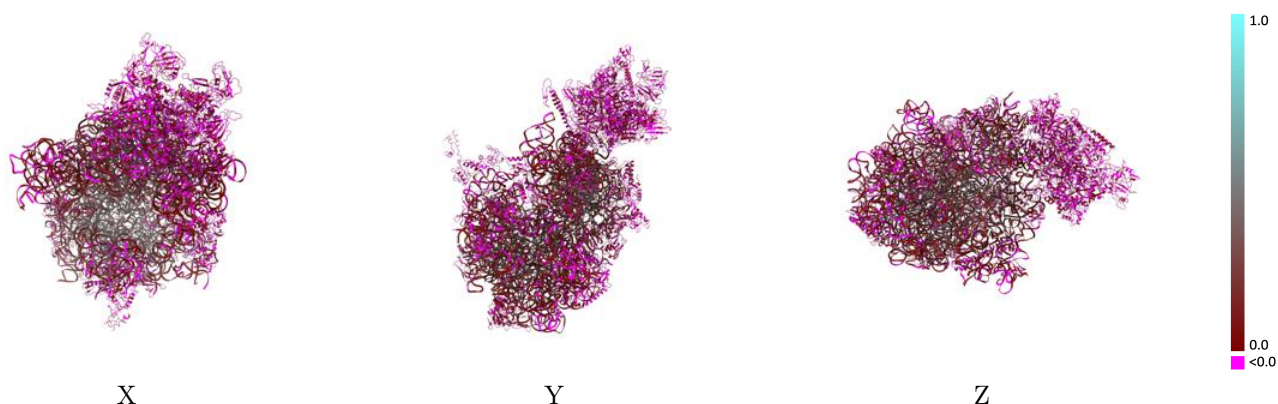
This section contains information regarding the fit between EMDB map EMD-21469 and PDB model 6VYR. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



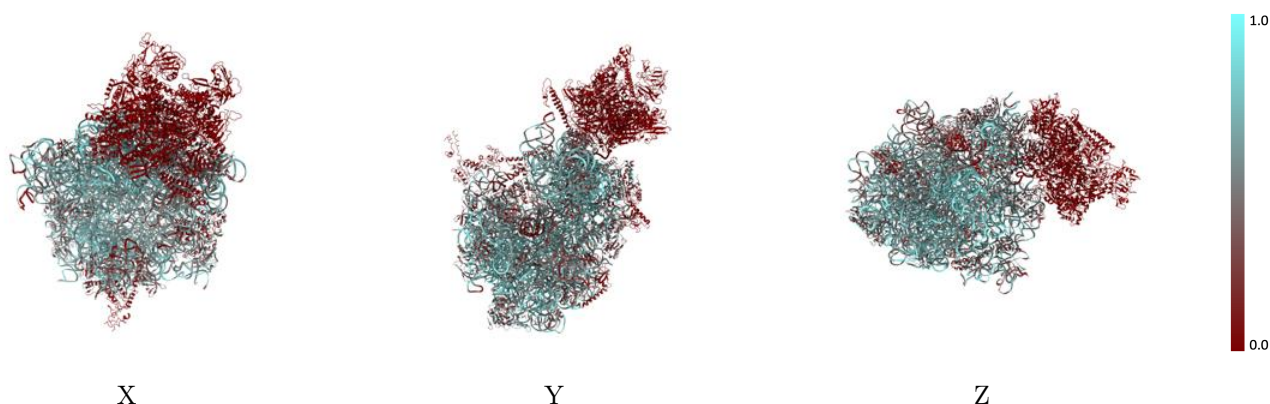
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



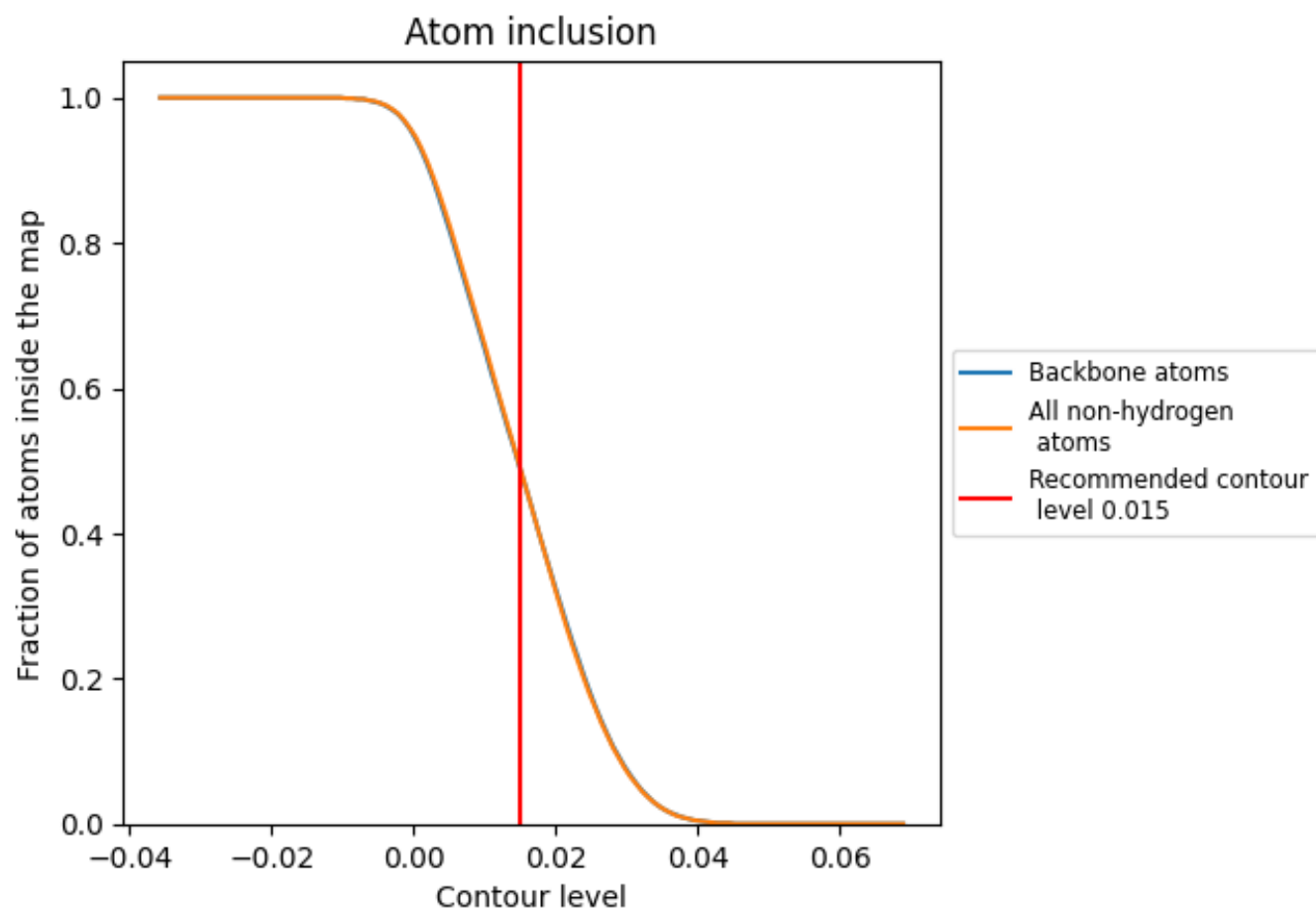
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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