



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 11:54 AM UTC

PDB ID : 6X6T / pdb_00006x6t
EMDB ID : EMD-22082
Title : Cryo-EM structure of an Escherichia coli coupled transcription-translational complex B1 (TTC-B1) containing an mRNA with a 24 nt long spacer, transcription factors NusA and NusG, and fMet-tRNAs at P-site and E-site
Authors : Molodtsov, V.; Ebright, R.H.; Wang, C.; Su, M.
Deposited on : 2020-05-29
Resolution : 3.20 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:

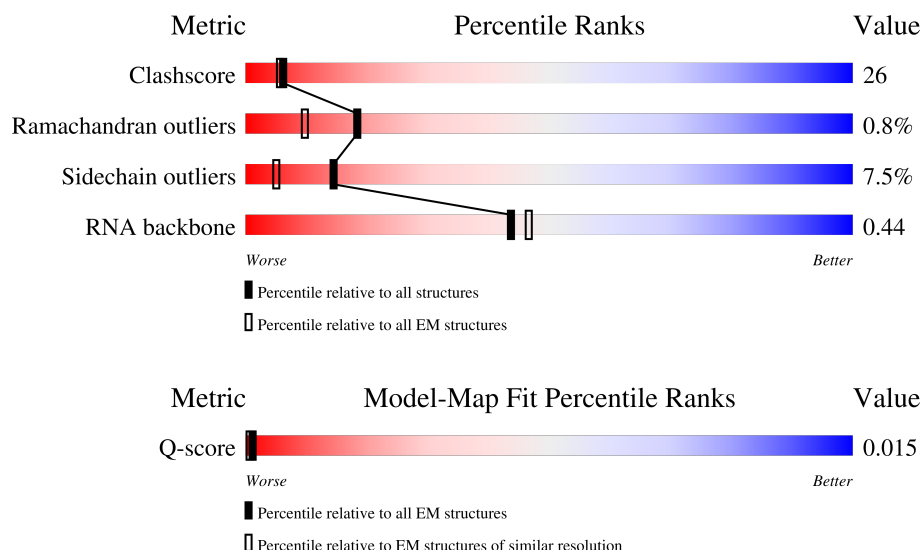
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.20 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	15020 (2.70 - 3.70)

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	68% 75% 25%
2	1	110	79% 70% 29% .
3	2	100	63% 76% 17% 6%

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

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

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Mol	Chain	Length	Quality of chain
52	l	201	69% 72% 25%
53	m	46	65% 65% 33%
54	n	179	68% 70% 26%
55	o	65	63% 74% 22%
56	p	177	76% 76% 21%
57	q	38	79% 79% 18%
58	r	149	72% 64% 32%
59	s	142	71% 70% 27%
60	t	123	67% 72% 27%
61	u	144	62% 78% 19%
62	v	136	72% 71% 29%
63	w	127	59% 60% 33% 6%
64	x	117	60% 74% 25%
65	y	115	62% 78% 18%
66	z	118	63% 73% 25%

2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 291628 atoms, of which 109913 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 6 is a DNA chain called NT DNA.

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

- Molecule 7 is a DNA chain called T DNA.

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

- Molecule 8 is a RNA chain called mRNA with 24 nt long spacer.

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AB	162	Total	C	H	N	O	S	0	0
			1283	816	1	222	237	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AC	301	Total	C	N	O	S	0	0
			2094	1296	379	413	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	AD	299	Total	C	N	O	S	0	0
			2078	1287	378	407	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	conflict	UNP A0A4S1NBU2

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms		AltConf
67	7	1	Total 1	Mg 1	0

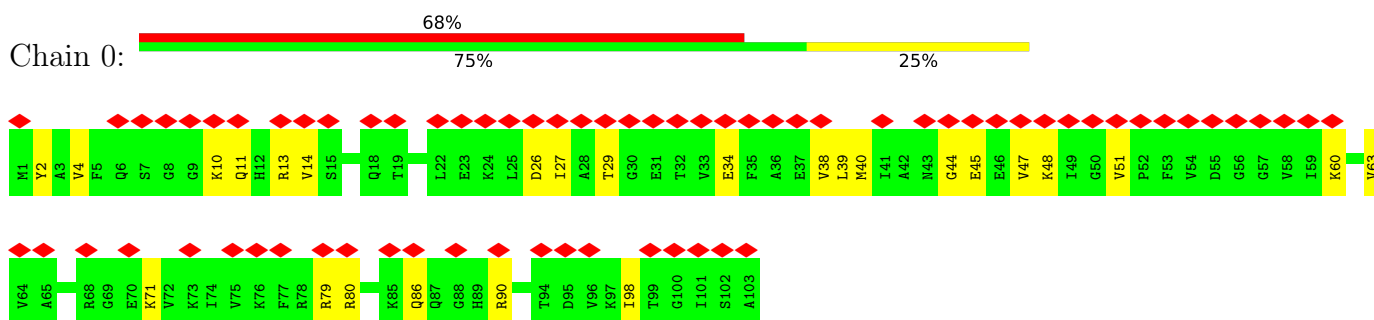
- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

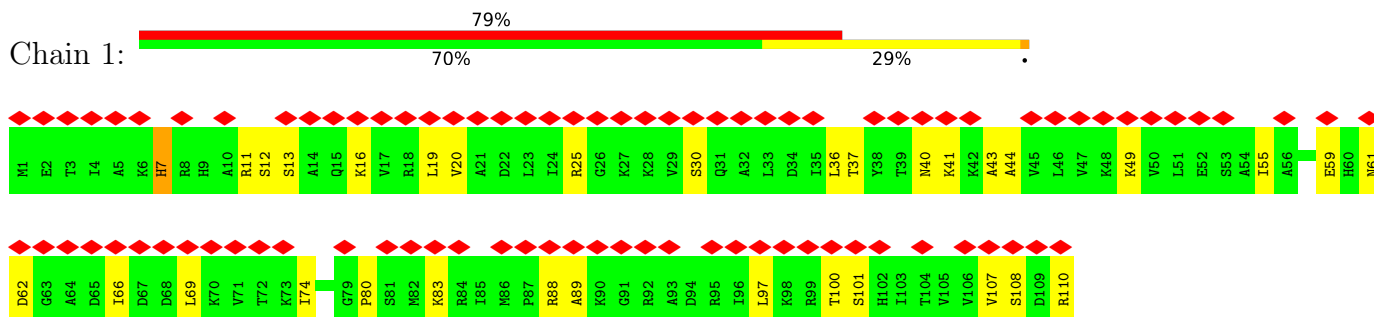
3 Residue-property plots [i](#)

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

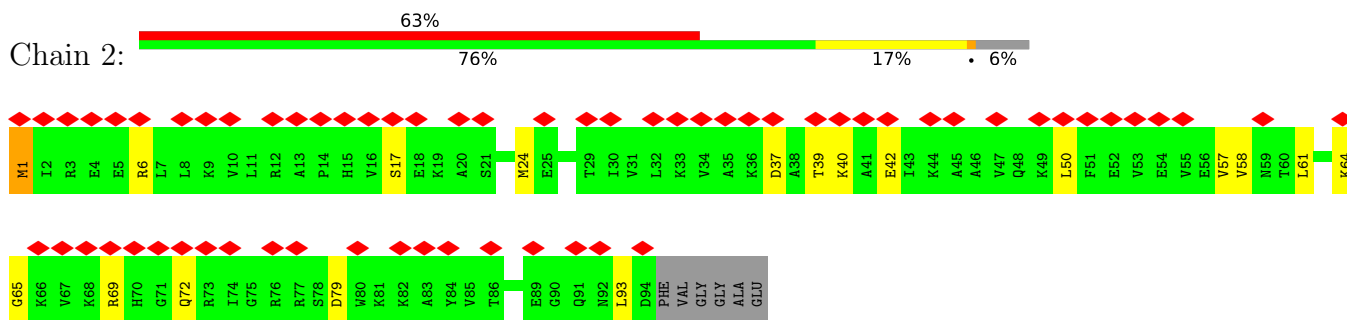
- Molecule 1: 50S ribosomal protein L21



- Molecule 2: 50S ribosomal protein L22

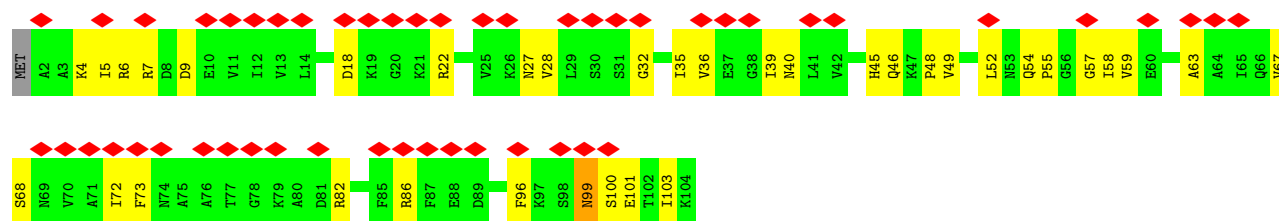


- Molecule 3: 50S ribosomal protein L23

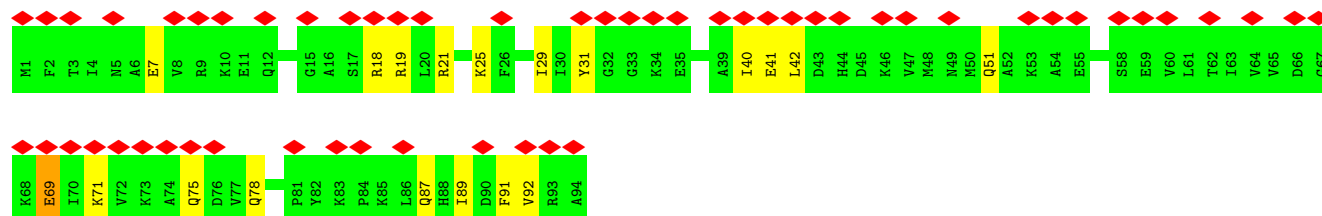
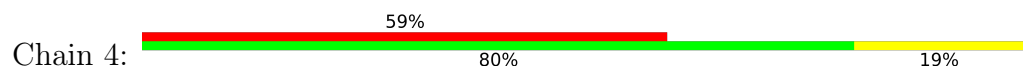


- Molecule 4: 50S ribosomal protein L24

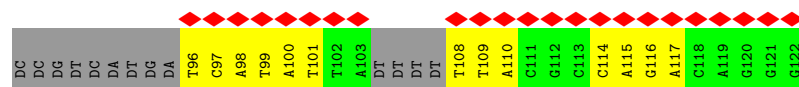




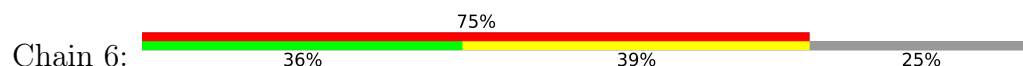
• Molecule 5: 50S ribosomal protein L25



• Molecule 6: NT DNA



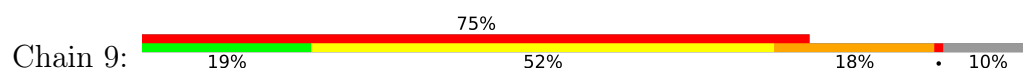
• Molecule 7: T DNA

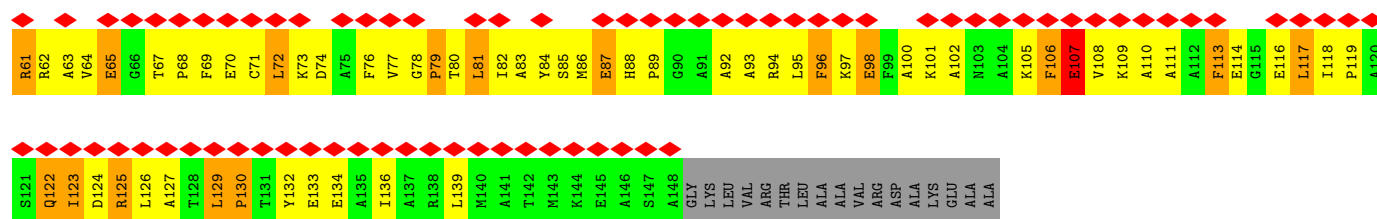


• Molecule 8: mRNA with 24 nt long spacer



• Molecule 9: 50S ribosomal protein L10





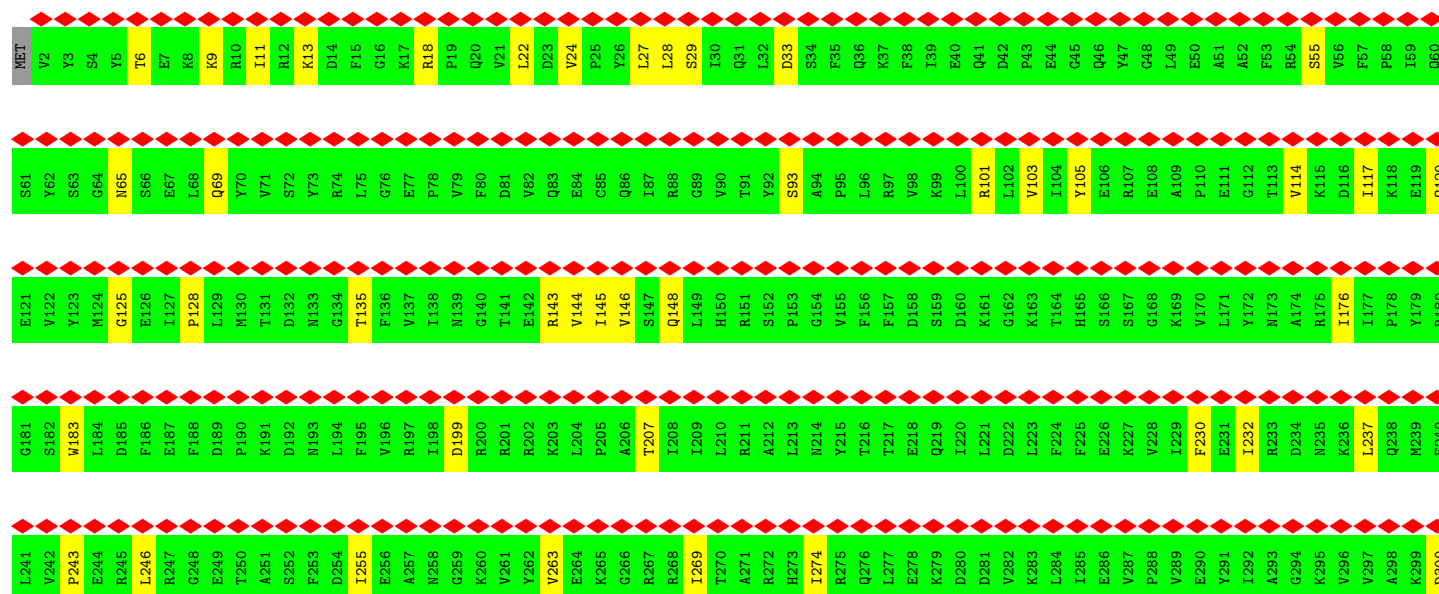
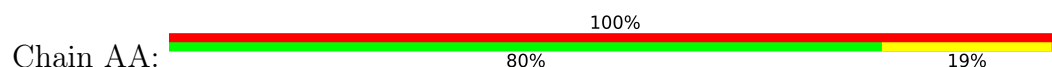
• Molecule 10: E-site and P-site tRNA (fMet)



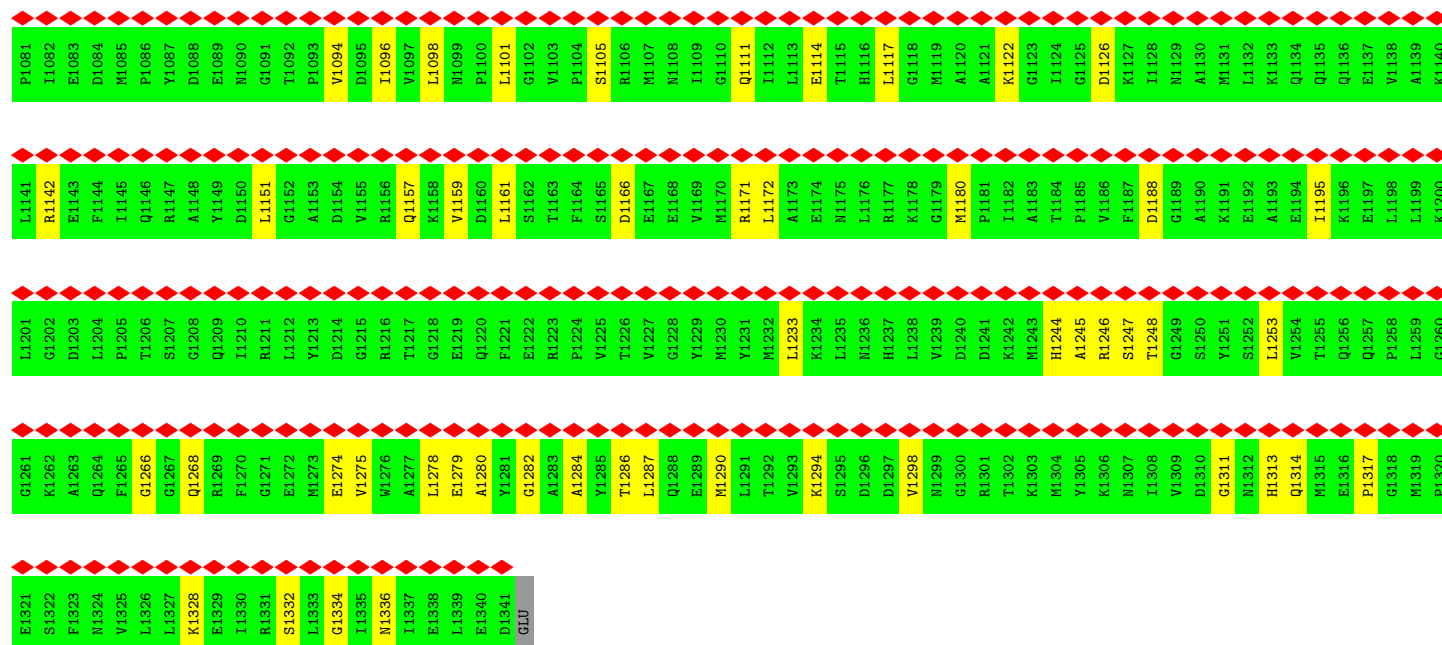
• Molecule 10: E-site and P-site tRNA (fMet)



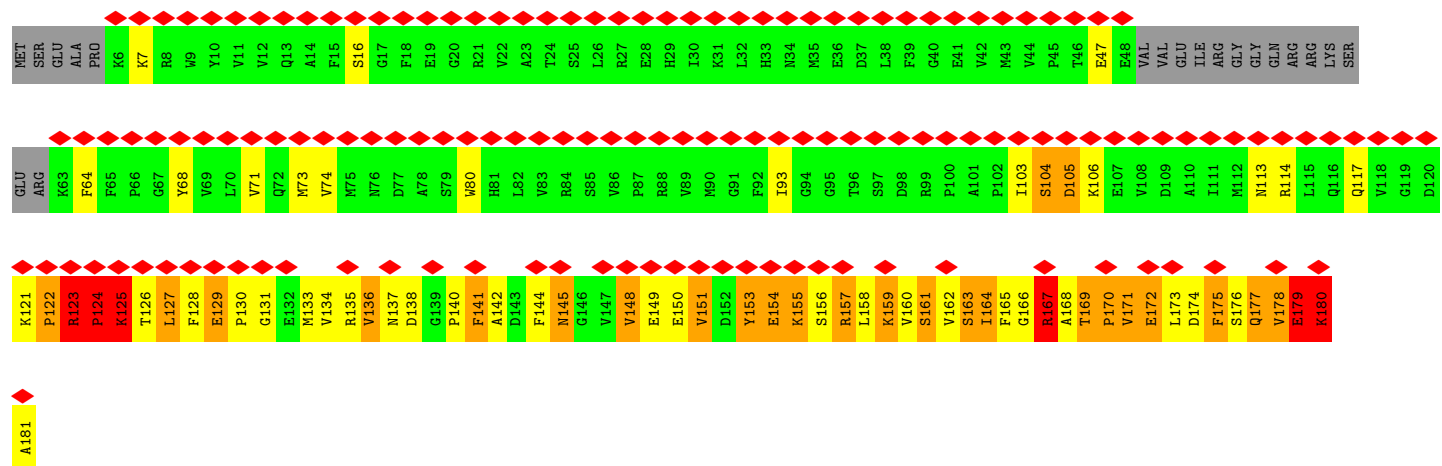
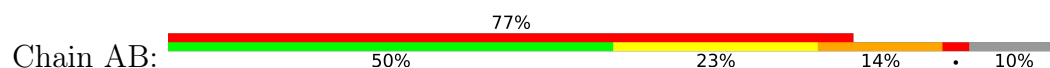
• Molecule 11: DNA-directed RNA polymerase subunit beta



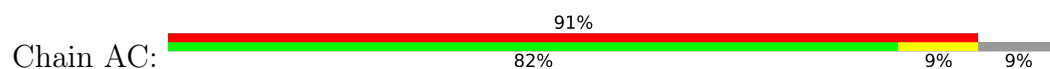
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H1023	E963	R903	T843	V723	V663	I603	A543	D483	D423	L363	D303
E1024	L964	A904	K844	V724	G664	H604	G544	L484	D424	V364	E304
F1025	Q965	T905	L845	Q725	A665	Y605	F545	L485	I425	E365	S305
E1026	L966	R906	G846	V726	S666	L606	E546	T486	I426	E366	T306
K1027	L967	G907	P847	V727	L667	S607	V547	L487	D427	Y367	G307
K1028	E968	E908	E848	D728	T668	A608	R548	M488	V428	R368	E308
L1029	A969	R909	E849	A729	P669	I609	D549	M489	M429	M369	L309
E1030	G970	A910	T850	S730	F670	E610	V550	Q490	K430	M370	I310
A1031	L971	S911	T851	R731	L671	E611	H551	D491	K431	R371	C311
K1032	F972	D912	A852	I732	E672	G612	P552	M492	L432	P372	A312
R1033	S973	Y913	D853	V733	H673	N613	T553	I493	I433	G373	A313
A1034	R974	K914	L794	I734	D674	Y614	H554	M494	D434	E374	N314
K1035	I975	D915	P855	K735	D675	V615	Y555	A495	I435	P375	M315
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L1039	L979	R919	E859	D739	A679	A619	C559	S499	K439	E379	L319
D1040	V980	Y920	A860	E740	L680	N620	P560	A500	G440	A380	D320
L1041	A981	P921	A861	N741	M681	S621	I561	A501	E441	A381	L321
A1043	G983	G923	S863	V742	A683	N622	E562	V502	V442	E382	L322
P1044	V984	Y924	K864	P743	L684	D624	T563	K503	D443	S383	A323
G1045	E985	S925	L865	E745	N685	E625	P564	E504	D444	L384	K324
V1046	G986	G926	D866	E746	M686	E626	E565	F505	I445	F385	L325
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K1048	X988	V928	S868	G747	R687	G627	P567	G507	H447	N387	Q327
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V1050	D990	D930	E869	D749	A689	F629	I569	S509	G449	F389	G329
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L1052	R992	Q932	T872	V751	P691	E631	L571	L511	R451	S391	K331
Y1053	P993	G933	E813	L753	L693	D632	I572	S512	R452	E392	R332
L1054	R994	F934	D814	T754	R694	L633	N573	Q513	I453	D393	I333
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V1056	R996	R936	T816	V756	D696	T635	L575	M515	S455	Y395	T335
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L1058	L998	G938	T877	T757	R697	R637	V577	Q517	G457	L397	F337
R1059	E999	Y939	G879	R758	P698	S638	V578	N518	E458	S398	T338
I1060	L1000	E940	C880	S759	L699	K639	A579	N519	M459	A399	N339
Q1061	G1001	K941	D881	N760	V700	G640	Q580	P520	A460	V400	D340
P1062	L1002	D942	R821	Q761	G701	E641	T581	L521	E461	G401	L341
T1063	K943	K943	R823	N762	T702	S642	N582	S522	R462	R402	D342
D1064	E945	R944	Q824	C764	G703	S643	E583	E523	Q463	M403	H343
K1065	E1005	A945	E825	T765	M704	L644	Y584	I524	F464	K404	G344
M1066	E1006	L946	D826	I766	E705	F645	G585	T525	R465	F405	P345
A1067	K1007	E947	R827	Q767	A707	R647	F586	H526	V466	N406	Y346
Q1068	Q1008	I948	T888	P768	V708	D648	E588	K527	G467	R407	I347
R1069	N1009	E949	F828	A769	A709	Q649	T589	R528	L468	S408	S348
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G1071	L1011	M951	T830	P770	V710	V650	P590	I530	R470	L410	T350
N1072	E1012	Q952	R831	V771	D711	D651	Y591	S531	V471	R411	L361
K1073	Q1013	L953	H832	T772	S712	Y652	R592	A532	E472	E412	R352
G1074	I1014	K954	T893	L773	G713	M653	K593	L533	R473	E413	V353
V1075	A1015	Q955	Q834	G774	V714	D654	V594	G534	A474	I414	D354
I1076	E1016	A956	E835	E775	T715	V655	T595	P535	V475	E415	P355
S1077	Q1017	K957	L836	P776	A716	S656	D596	G536	K476	G416	T356
K1078	E997	R957	A837	V777	V717	T657	G597	G537	E477	S417	N357
I1079	D1019	D959	C838	E778	A718	Q658	V598	L538	R478	G418	D358
N1080	E1020	L960	V839	R779	K719	Q659	V599	T539	L479	I419	R359
			R840	G780	R720	V660	T600	R540	S480	L420	L360



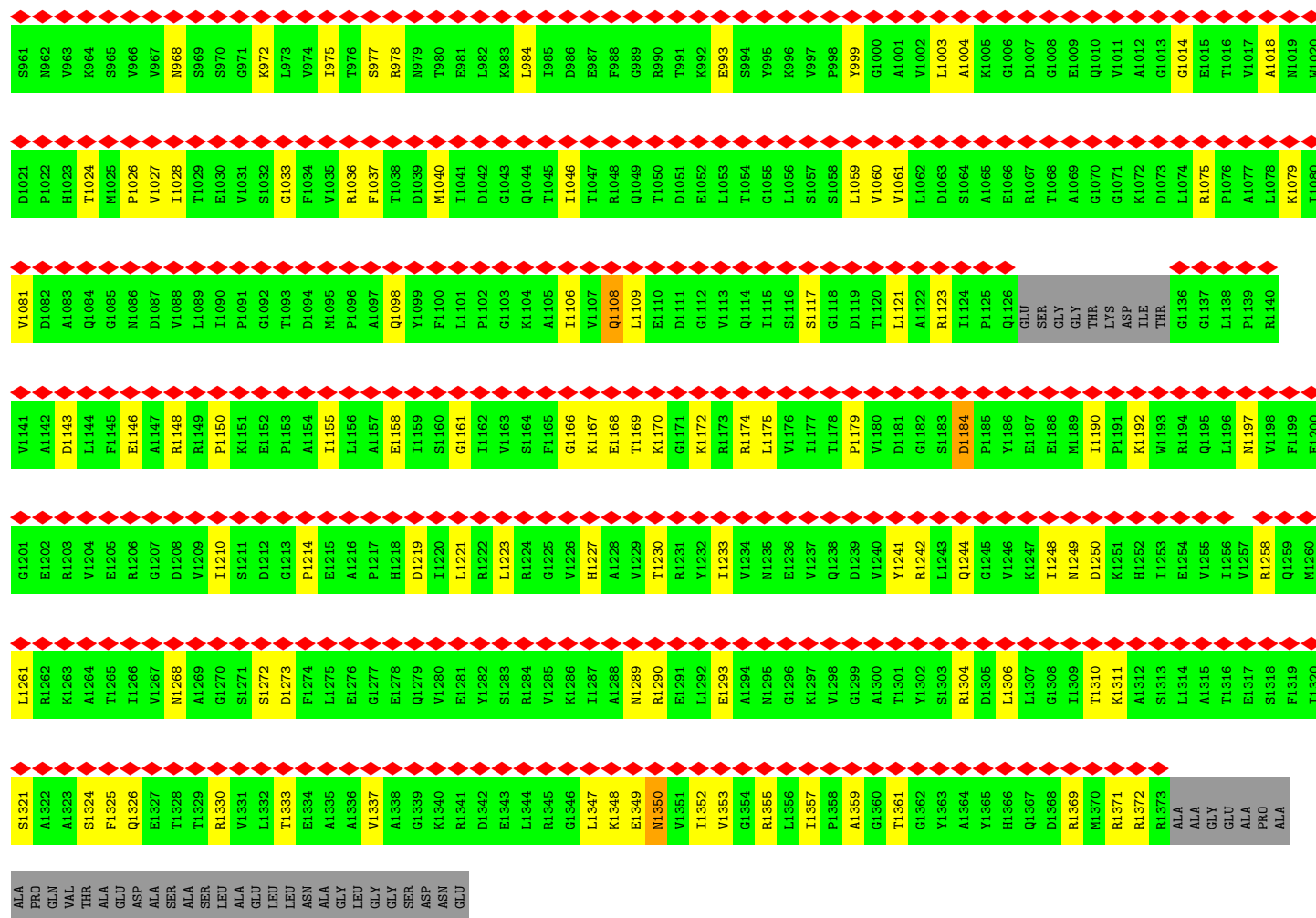
• Molecule 12: Transcription termination/antitermination protein NusG



• Molecule 13: DNA-directed RNA polymerase subunit alpha

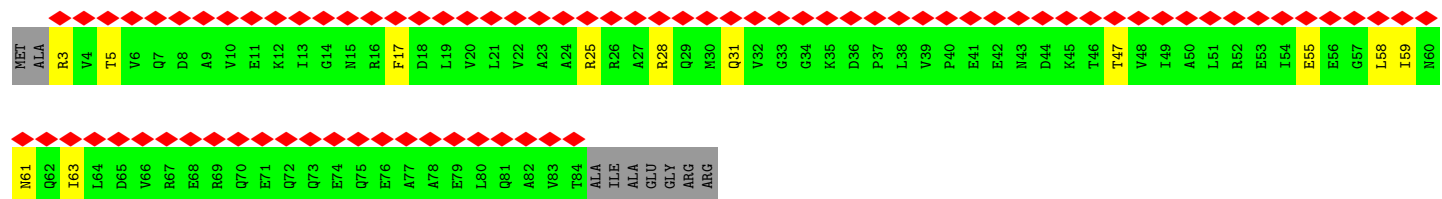




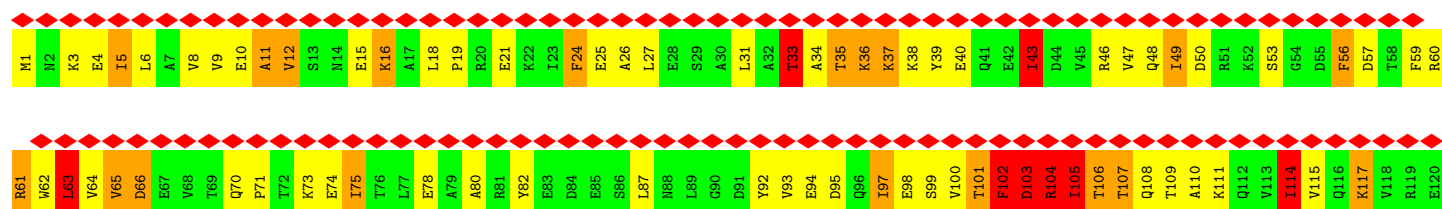
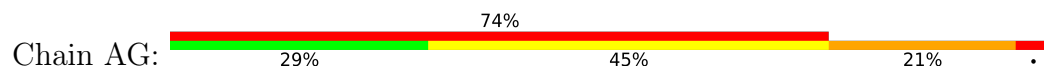


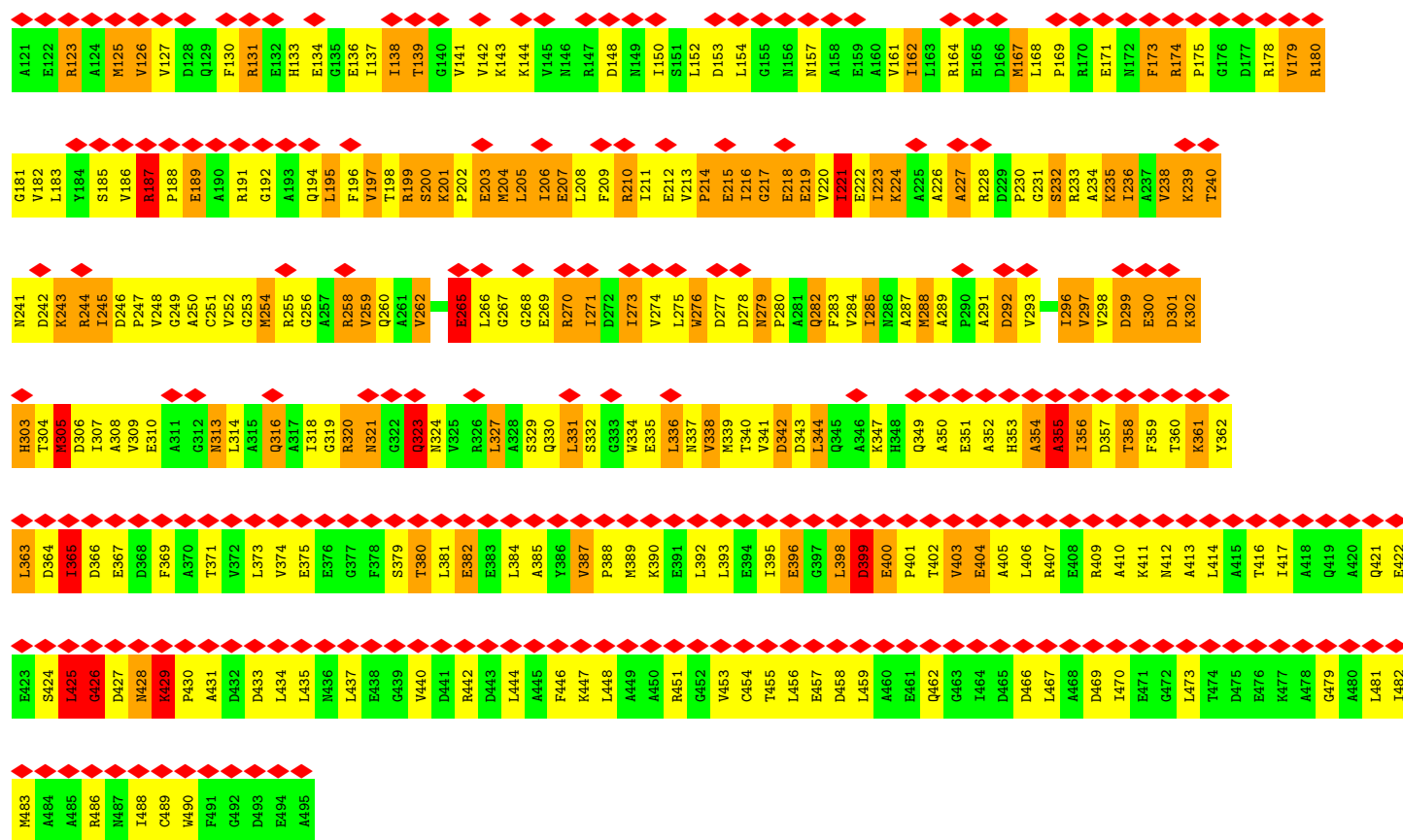
- Molecule 15: DNA-directed RNA polymerase subunit omega

Chain AF:

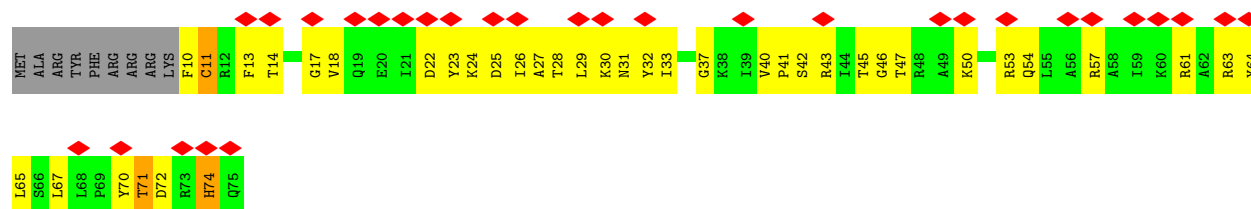


- Molecule 16: Transcription termination/antitermination protein NusA

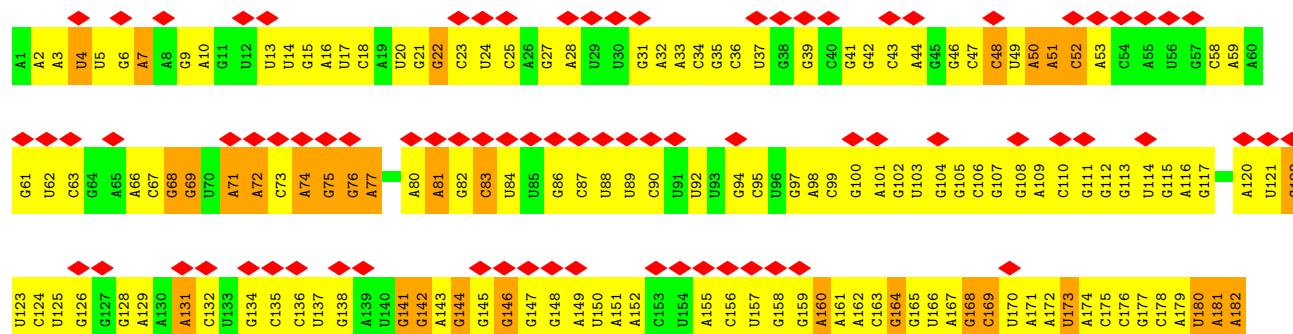


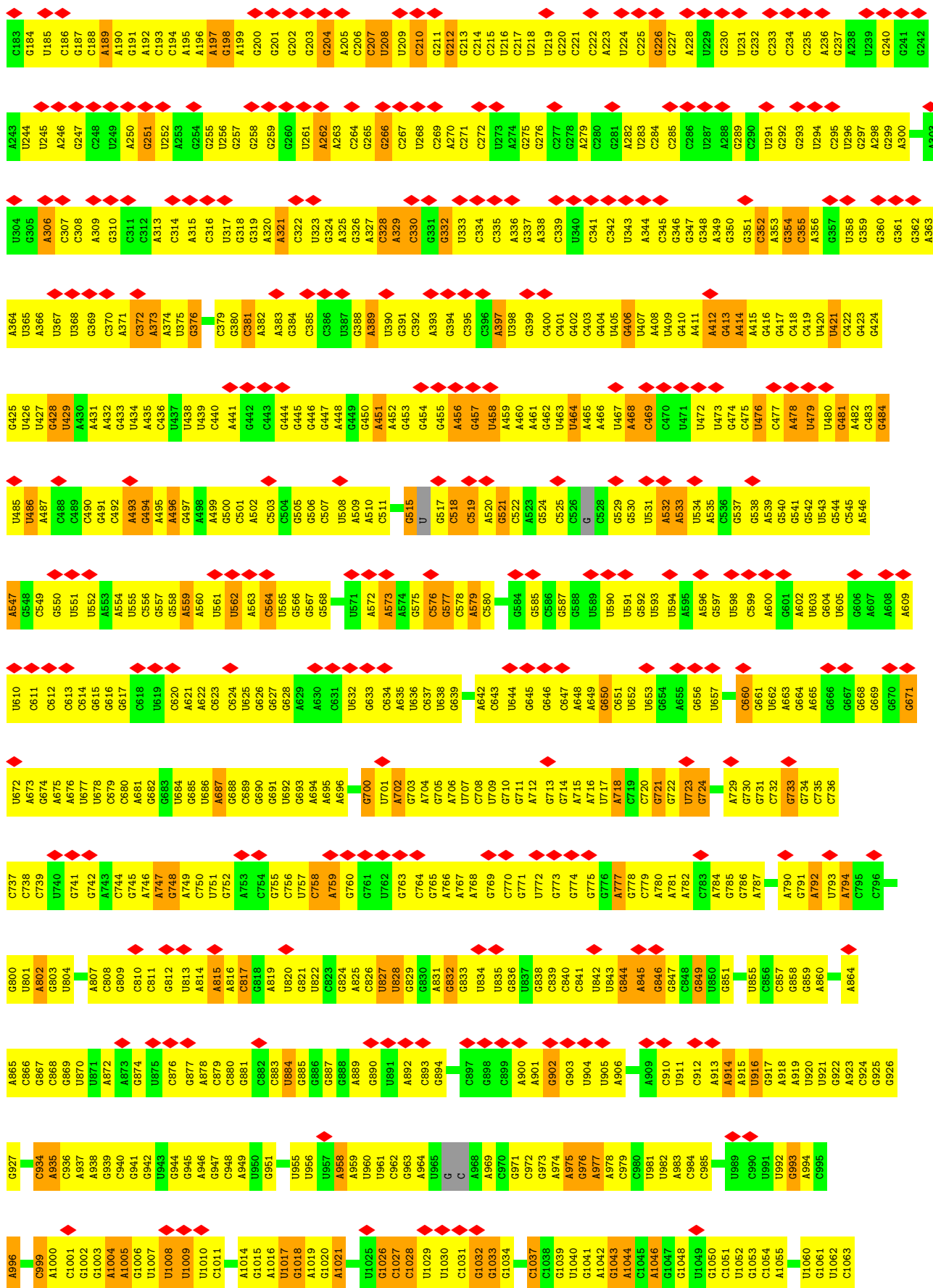


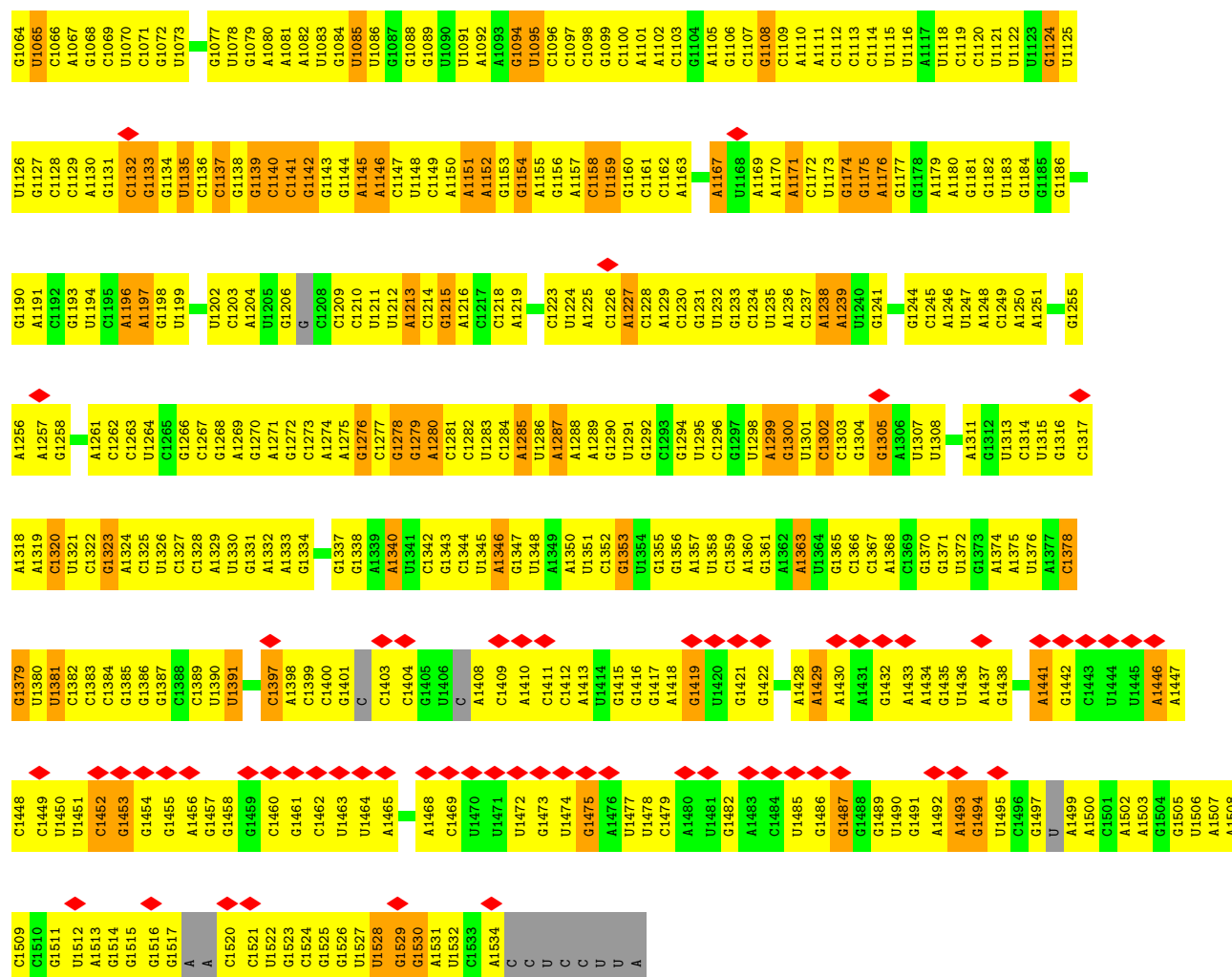
• Molecule 17: 30S ribosomal protein S18



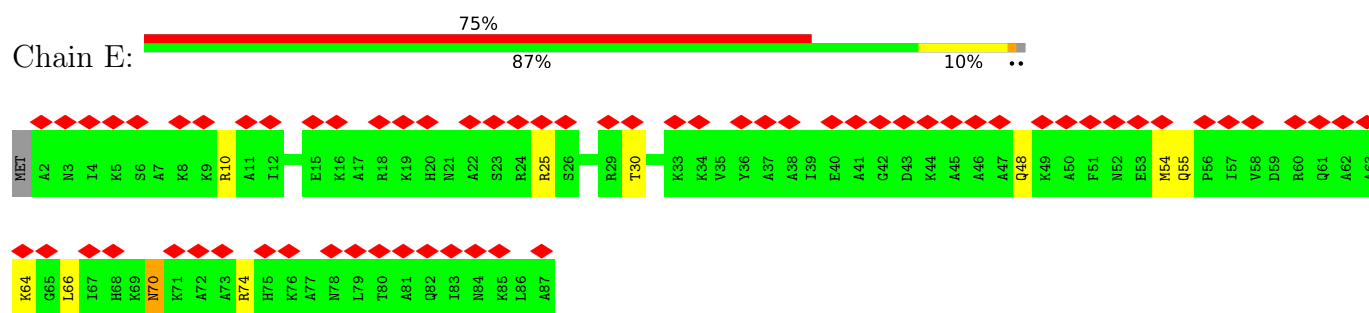
• Molecule 18: 16S rRNA



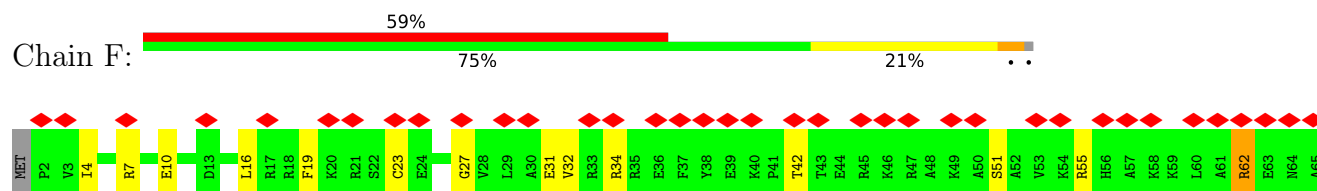




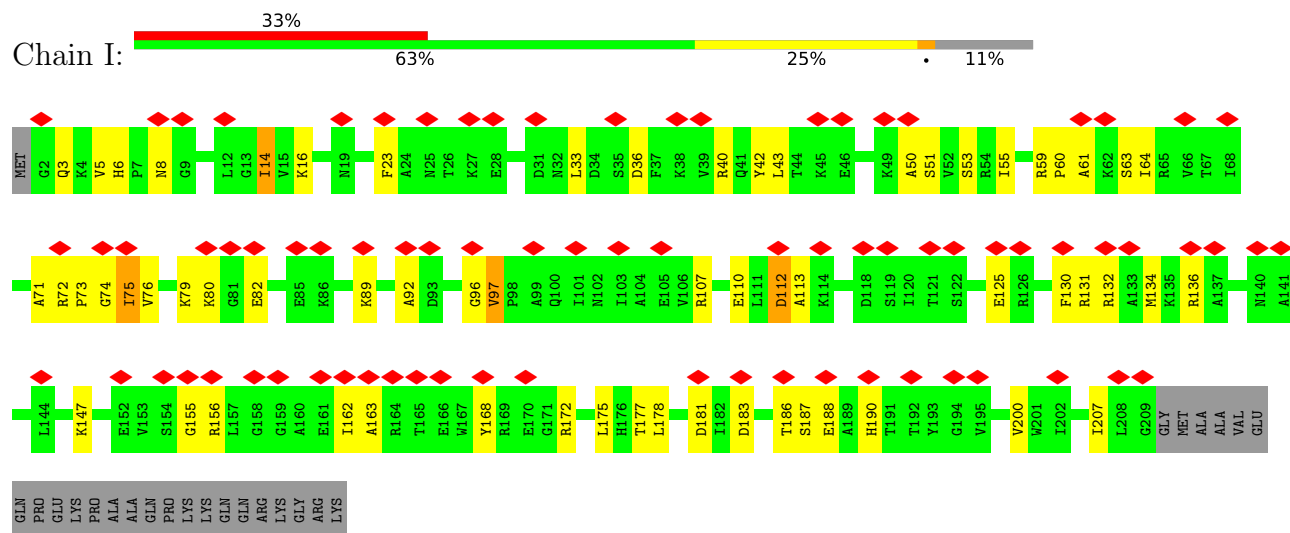
• Molecule 19: 30S ribosomal protein S20



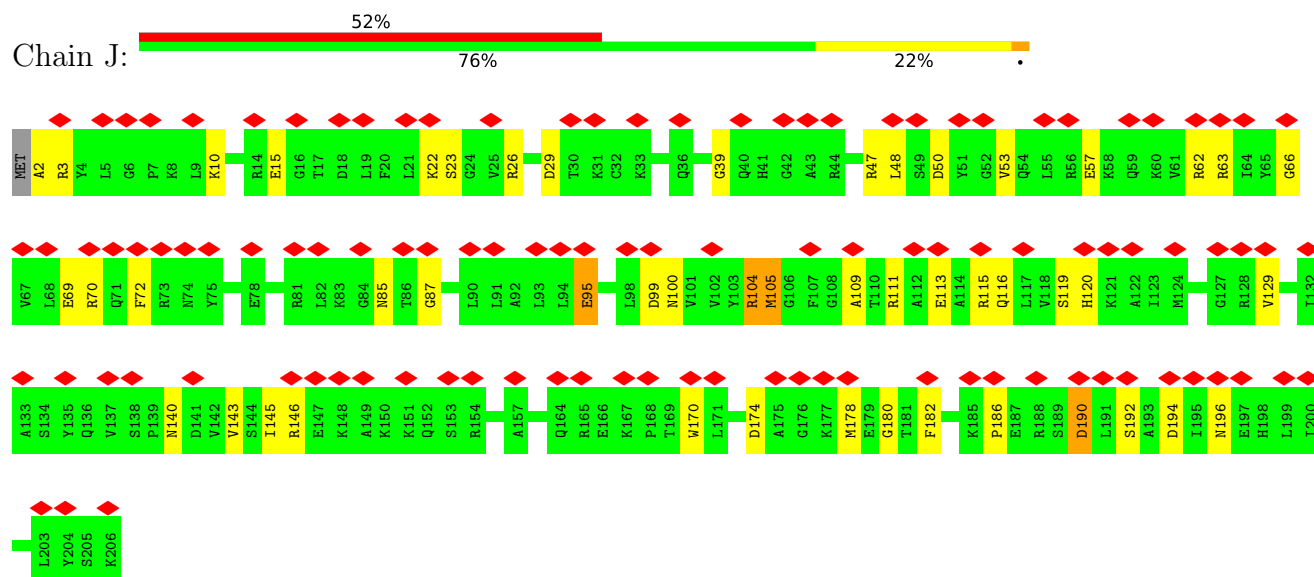
• Molecule 20: 30S ribosomal protein S21



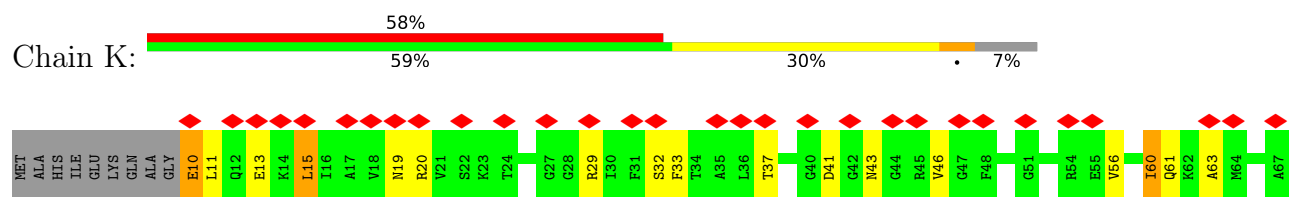
- Molecule 23: 30S ribosomal protein S3

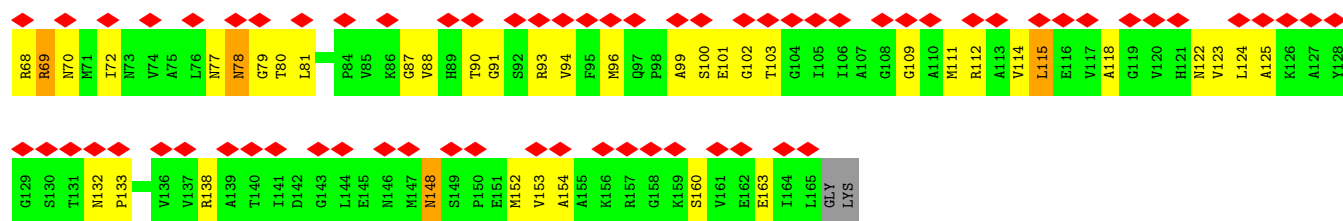


- Molecule 24: 30S ribosomal protein S4

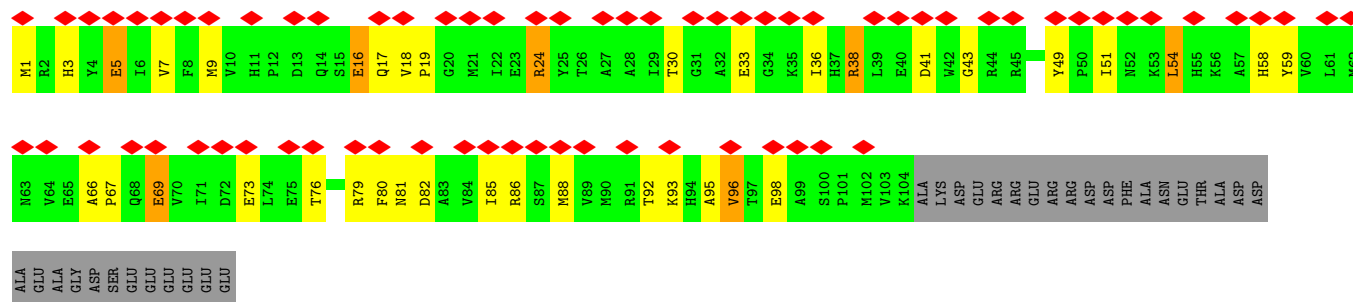


- Molecule 25: 30S ribosomal protein S5

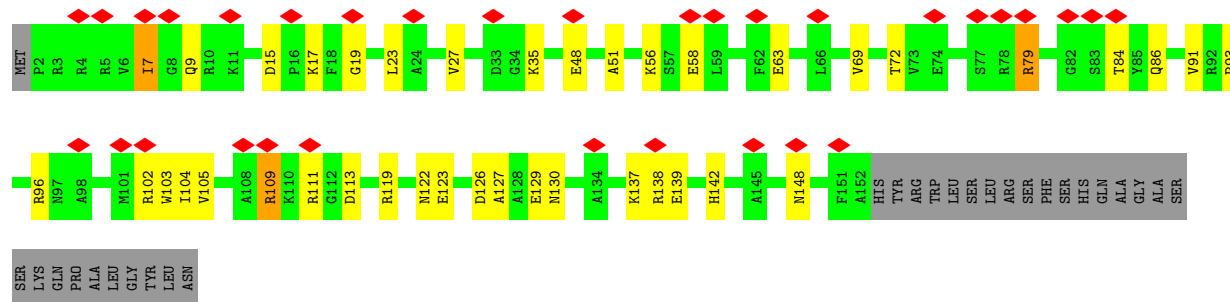




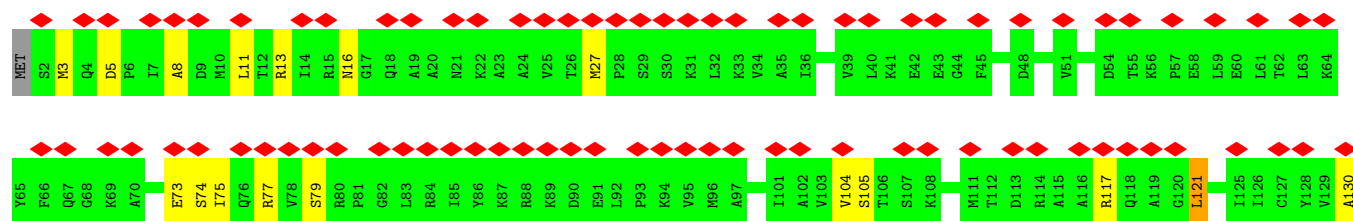
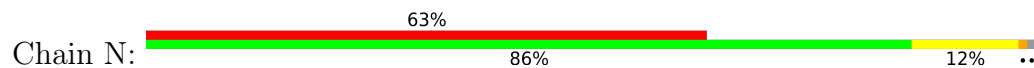
• Molecule 26: 30S ribosomal protein S6



• Molecule 27: 30S ribosomal protein S7

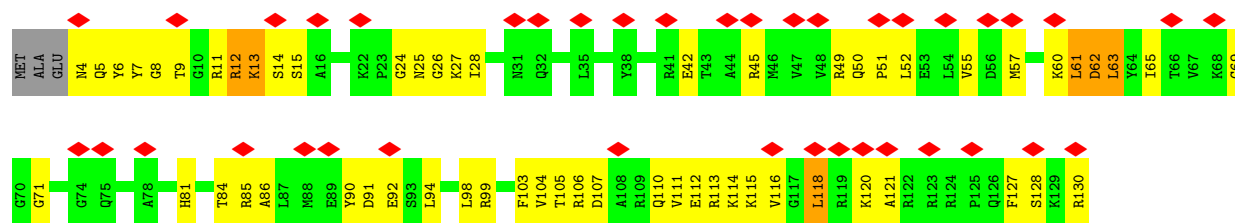


• Molecule 28: 30S ribosomal protein S8

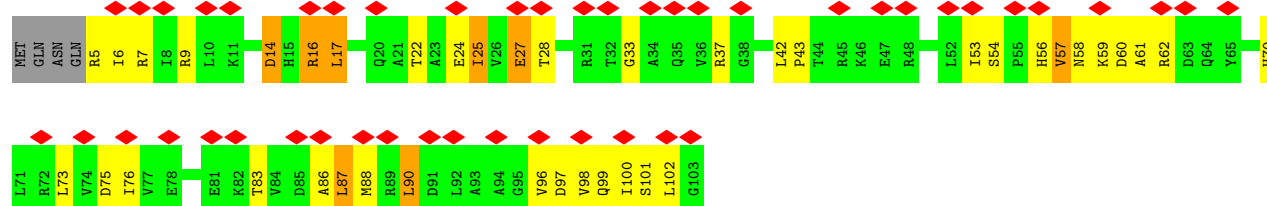
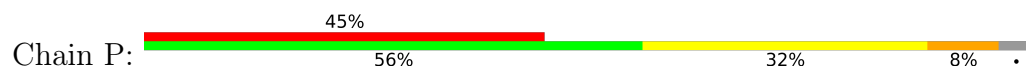


• Molecule 29: 30S ribosomal protein S9

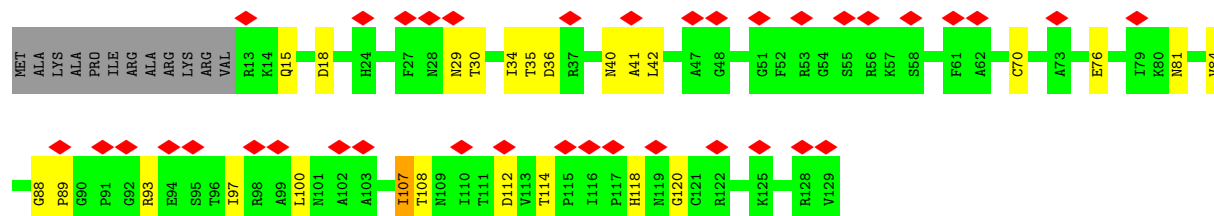




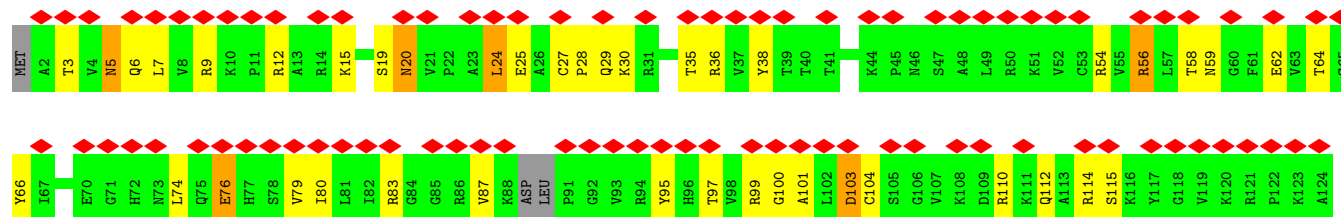
- Molecule 30: 30S ribosomal protein S10



- Molecule 31: 30S ribosomal protein S11

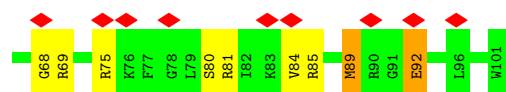


- Molecule 32: 30S ribosomal protein S12

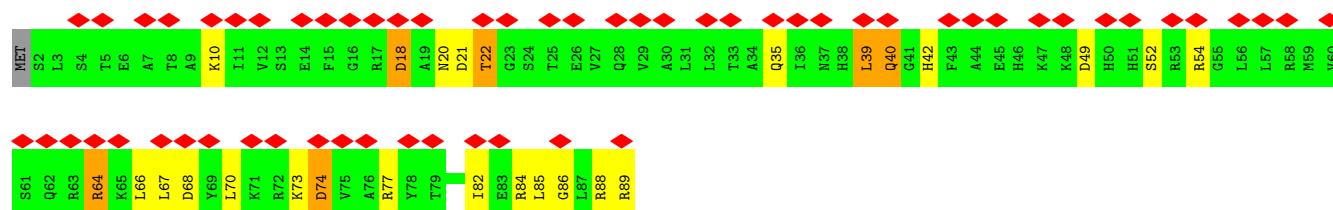


- Molecule 33: 30S ribosomal protein S14

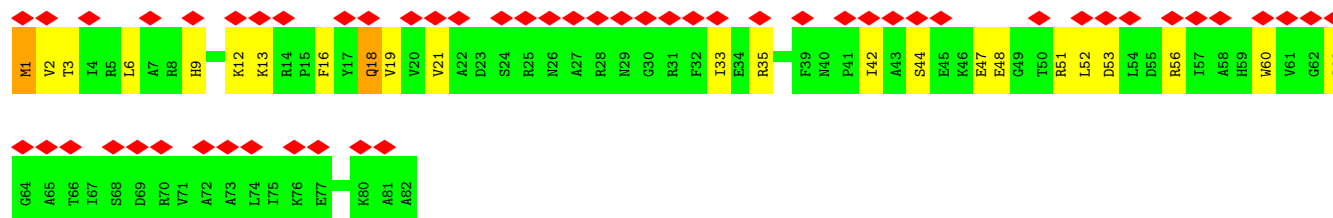
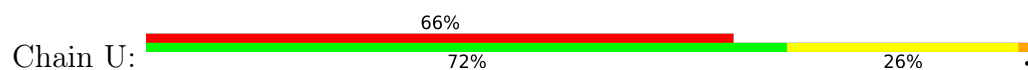




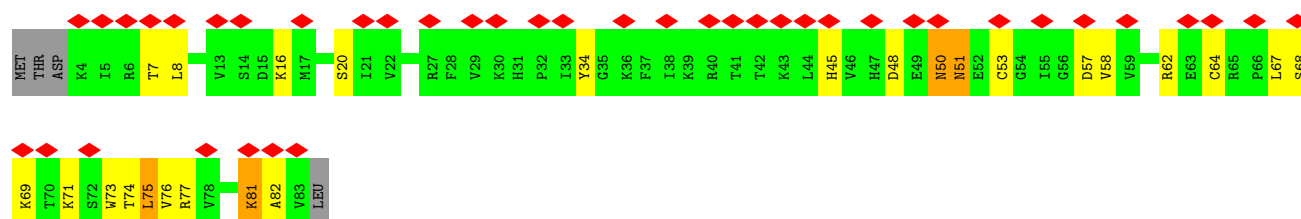
- Molecule 34: 30S ribosomal protein S15



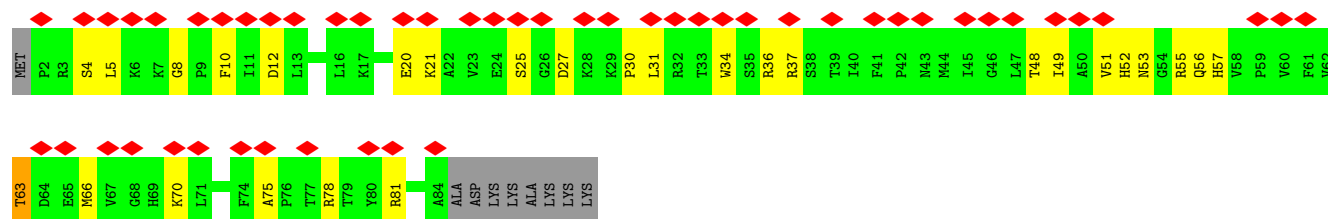
- Molecule 35: 30S ribosomal protein S16



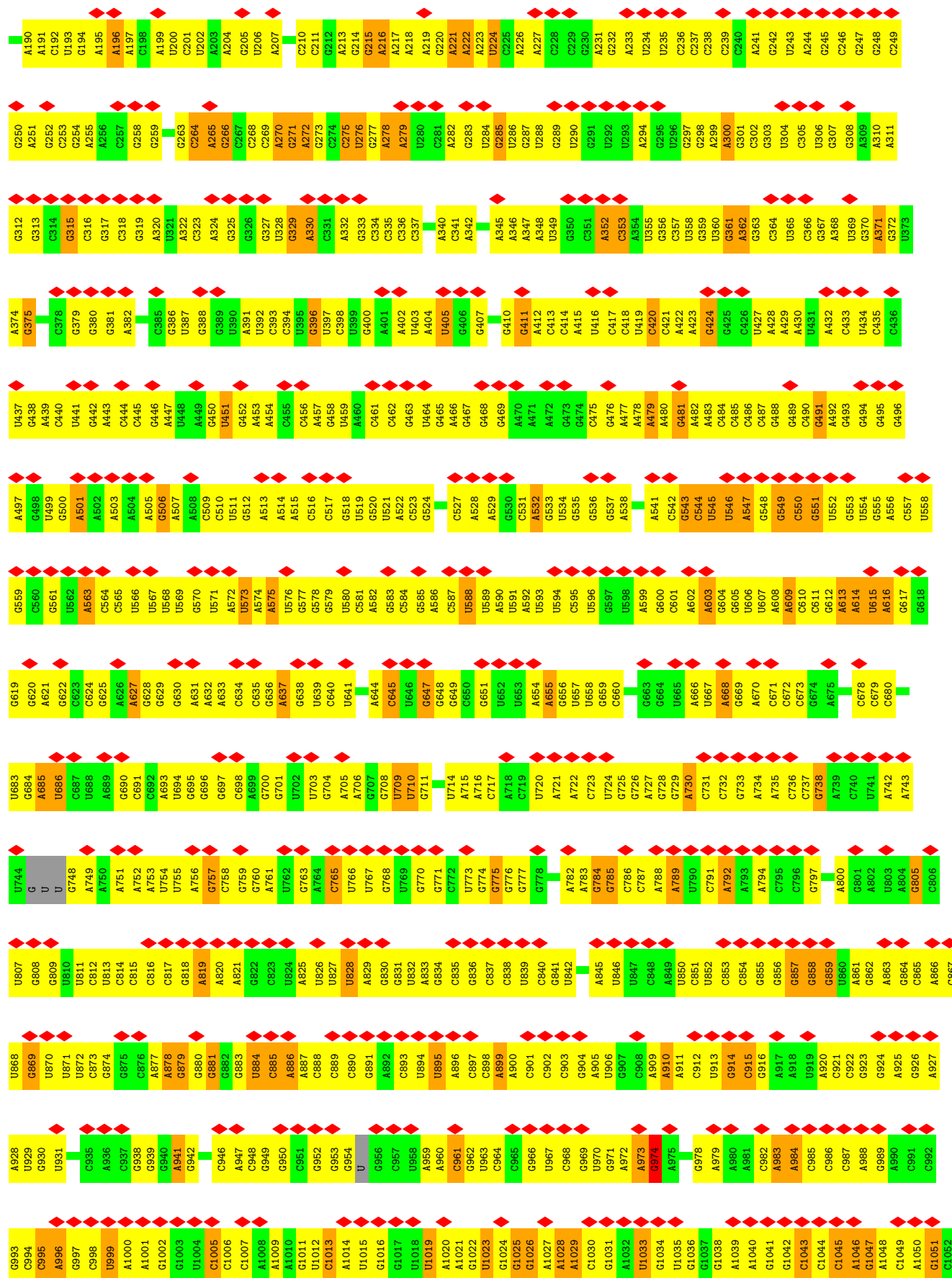
- Molecule 36: 30S ribosomal protein S17



- Molecule 37: 30S ribosomal protein S19

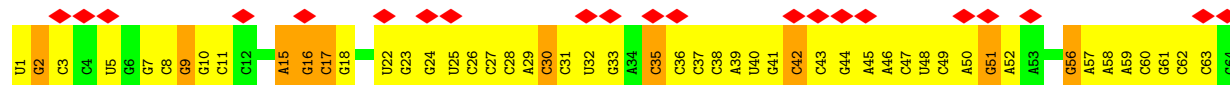


- Molecule 38: 30S ribosomal protein S13



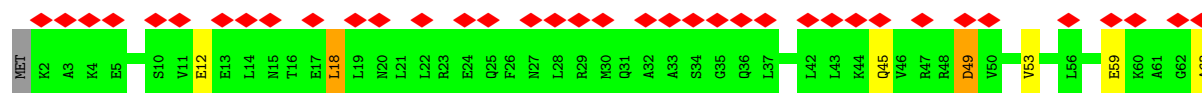
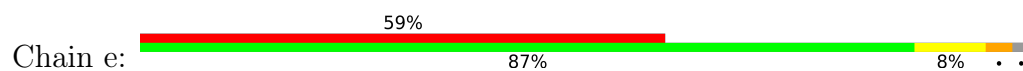
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C1791	C1730	A1665	C1604	G1543	A1483	G1421	G1360	C1298	G1238	C1178	C1117	G1055
G1792	G1731	G1666	C1605	A1544	U1484	G1422	G1361	G1299	G1239	G1179	C1118	G1056
C1793	G1732	G1667	C1606	A1545	U1485	G1423	C1362	G1300	U1240	U1180	U1119	G1059
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G1799	G1737	A1672	C1612	A1551	A1490	C1428	G1368	C1305	G1245	G1186	G1125	U1067
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A1803	C1741	A1676	A1616	G1555	A1494	G1432	A1368	U1309	G1250	A1129	G1129	A1069
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A1805	G1743	A1678	A	C1557	U1496	A1434	G1376	G1311	C1251	U1191	G1131	G1071
C1806	U1744	A1679	G1619	C1558	U1497	G1435	G1377	U1312	G1252	G1192	U1132	C1072
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U1812	G1750	G1687	C1626	C1565	A1505	G1442	A1384	C1319	C1260	U1199	C1140	C1079
C1813	C1751	U1688	A1626	A1566	U1506	U1443	A1385	C1320	C1261	U1201	U1141	A1080
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G1761	C1761	U1701	G1636	U1578	A1516	G1452	A1395	U1332	A1272	C1211	C1152	G1091
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C1826	G1763	G1703	C1638	A1579	C1518	G1454	U1397	G1333	A1274	A1213	G1154	G1093
U1827	C1764	A1705	C1639	A1580	G1519	G1455	U1398	C1334	A1275	G1214	A1155	A1094
C1828	U1765	G1706	A1640	G1581	U1520	G1456	C1399	C1335	A1276	G1215	A1156	A1095
A1829	G1766	G1707	A1641	C1582	A1521	U1457	U1457	G1336	G1277	U1097	U1157	A1096
C1830	C1767	C1708	G1642	U1583	G1522	G1460	U1400	A1336	A1278	G1216	G1158	U1097
G1831	G1768	U1709	G1643	U1584	A1523	C1461	G1401	G1337	G1279	U1217	C1158	A1098
C1832	C1768	U1710	C1644	C1585	A1525	C1462	A1403	U1340	C1278	U1217	G1159	A1098
A1833	U1769	G1710	G1645	A1586	G1526	C1463	C1404	G1341	C1278	G1218	U1159	C1100
C1834	C1770	U1711	C1646	G1587	C1527	G1464	U1405	A1342	G1280	U1219	G1159	C1100
G	G1771	U1712	U1647	G1587	G1527	C1465	U1406	A1343	G1281	G1220	G1160	U1101
C1836	A1772	A1713	U1648	U1588	A1528	G1465	G1407	U1344	G1282	C1221	C1161	C1102
C1837	C1773	G1714	U1649	G1589	G1529	U1466	G1408	C1345	G1283	U1222	G1162	A1103
C1838	C1774	U1715	A1650	A1590	G1530	U1467	U1409	G1346	U1284	U1224	G1163	U1104
G1839	U1775	U1716	G1651	A1591	C1531	U1468	U1409	A1285	A1284	U1224	C1164	U1105
C1840	U1778	U1717	A1652	A1592	C1532	A1469	G1410	A1347	A1285	G1225	A1165	G1106
U1841	U1779	G1719	G1653	A1593	C1533	A1470	U1411	C1348	A1286	G1226	G1107	U1108
C1842	A1780	U1720	U1654	U1594	U1534	G1471	U1412	U1349	G1287	A1266	G1167	U1108
G1843	C1781	A1721	A1655	G1595	A1535	C1472	A1413	C1350	G1288	G1228	C1167	C1109
C1844	U1782	A1722	A1656	A1596	A1536	G1473	U1414	C1351	A1298	C1229	G1168	G1110
G1845	U1783	G1723	C1657	A1597	G1537	U1474	U1415	U1352	C1299	C1229	A1169	A1111
U1846	A1784	U1724	U1658	A1598	G1538	G1475	C1416	U1353	C1291	A1230	G1112	A1111
A1847	A1785	U1725	C1659	U1599	U1539	U1476	C1417	A1354	G1292	U1231	G1171	U1113
C1848	A1786	C1726	G1659	C1600	U1539	A1477	G1418	A1354	G1292	G1232	C1172	C1114
G1849	A1787	C1727	G1660	G1601	G1540	G1478	G1479	G1356	C1295	U1234	U1173	
					</							

A2587	G2527	G2464	A2340	G2280	G2218	A2158	C2096	A2033	G1973	G1910	G1850
G2588	U2528	C2465	G2341	A2281	U2219	G2159	A2097	U2034	C1974	U	U1851
A2589	G2529	C2466	C2342	G2283	G2223	C2160	U2098	G2035	G1975	A1912	U1852
C2591	A2530	C2467	U2343	A2284	G2224	C2161	U2099	C2036	U1976	A1913	A1853
G2592	A2531	U2468	U2344	G2285	G2225	G2162	G2100	A2037	U1977	C1914	U1854
U2593	G2532	A2469	G2345	C2286	C2226	C2163	A2101	G2038	A1978	U	U1855
C2594	U2533	G2470	A2346	A2287	A2227	C2165	G2102	U2039	U1979	A1916	U1856
U2595	G2534	G2471	C2347	A2288	G2228	U2166	C2103	G2040	U1980	U	G1857
G2596	G2535	A2410	U2348	G2289	U2229	U2167	C2104	A2042	A1981	U	A1858
U2597	U2536	G2412	G2349	G2290	G2230	U2168	U2105	C2043	A1919	A1918	U1859
A2598	U2537	G2413	C2350	U2291	U2231	A2169	U2106	C2044	C1920	A1919	G1860
G2599	C2538	G2414	G2351	U2292	C2232	U2170	A2107	G2045	G1921	C1920	G1861
U2600	U2539	G2415	A2352	G2293	C2233	U2171	A2108	C2046	G1922	G1922	G1862
A2601	C2540	C2416	G2353	G2294	U2234	U2172	U2109	G2047	C1923	U1923	G1863
G2602	U2541	G2417	U2354	G2295	G2235	C2173	G2110	G2048	C1924	C1924	U1864
A2603	A2542	A2418	G2355	U2296	U2236	U2174	G2111	G2049	C1925	U1925	U1865
G2604	G2543	G2419	U2356	A2297	U2237	A2175	G2112	C2050	U1926	U1926	A1866
U	U2544	C2420	C2357	G2298	G2238	C2176	G1988	A2051	A1927	A1927	G1867
C2606	U2545	C2421	G2360	A2299	G2239	C2177	U1991	G2052	G1989	G1928	G1868
G2607	G2546	G2484	C2361	U2299	U2240	C2178	G1992	A2053	C1870	G1929	G1869
U2608	U2547	C2424	C2362	C2300	U2241	C2179	U1993	G2054	G1930	G1930	A1871
G2609	U2548	A2425	C2363	U2301	A2241	U2180	U1992	C2055	U1931	U1931	A1872
U2610	G2549	A2426	G2364	U2302	G2242	U2181	G1993	G2056	G1932	G1932	A1873
C2611	G2550	C2427	G2365	G2303	U2243	U2182	C1994	G2057	G1933	G1933	C1874
G2612	U2551	G2428	A2366	G2304	U2244	A2183	U1995	G2058	G1934	G1934	G1875
U2613	U	G2429	G2367	U2305	U2245	U2185	C1996	A2059	G1935	G1935	A1876
A2614	G2553	G2430	C2368	C2306	G2246	U2186	C1997	G2060	A1936	A1936	A1877
U2615	U2554	U2431	C2369	G2307	A2247	U2187	A1998	G2061	A1937	A1937	G1878
G2616	G2555	G2432	G2370	G2308	C2248	U2188	C1999	G2062	U	U	U1880
U2617	U2556	A2433	G2371	U2309	U2249	U2189	C2000	C2063	U1940	U1940	C1881
G2618	C2557	A2434	U2372	C2310	G2250	G2190	C2001	G2064	C1941	C1941	C1882
C2619	U2558	A2435	G2373	A2311	U2251	G2191	G2002	C2065	C1942	C1942	U1883
G2620	A2560	G2436	G2375	G2312	G2252	U2192	G2003	C2066	U1943	U1943	G1884
U2621	U2561	G2437	A2376	G2313	G2253	G2193	A2005	G2067	U1944	U1944	A1885
G2622	U2562	U2438	A2377	G2314	C2254	U2195	C2006	U2068	U1945	U1945	A1886
A2623	U2563	A2439	G2378	G2315	G2255	C2196	G2007	G	U1946	U1946	G1887
G2624	A2565	A2440	C2379	G2316	G2256	U2197	C2008	A2070	C1947	C1947	G1888
U2625	U2566	U2441	C2380	A2317	U2257	A2198	C2009	A2071	G1948	G1948	A1889
G2626	U2567	C2442	G2381	G2318	C2258	A2199	C2010	C2072	U1949	U1949	G1890
U2627	G2568	G2443	G2382	U2320	U2259	G2200	U2011	C2073	G1950	G1950	C1891
C2628	U2569	G2444	U2383	U2321	C2260	G2201	G2012	U	C	C	C1892
G2629	G2570	G	C2384	A2322	C2261	U2202	A2013	U2075	U1955	U1955	C1893
U2630	U2571	G2446	C2385	G2323	U2262	U2203	A2014	U2076	U1956	U1956	C1894
G2631	U2572	G2447	A2386	U2324	C2263	G2204	A2015	A2077	C1957	C1957	G1895
A2632	U2573	A2448	G2387	G2325	C2264	A2205	U2016	C2078	C1958	C1958	G1896
G2633	U2574	U2449	U2389	C2326	U2265	C2206	U2017	U2079	G1959	G1959	U1897
U2634	G2575	A2450	G2391	A2327	A2266	C2207	U2018	C2083	A1960	A1960	A1898
A2635	U2576	A2451	G2392	U2328	A2267	C2208	A2019	C2084	C1961	C1961	U1899
C2636	G2577	C2452	U2393	G2329	A2268	G2209	A2020	U2085	U1962	U1962	A1900
U2637	U2578	A2453	C2394	U2330	G2269	U2210	C2021	U2086	G1963	G1963	G1901
G2638	U2579	G2455	C2395	G2331	A2270	A2211	U2022	C2089	C1964	C1964	C1902
A2639	U	U	G2396	A2332	G2271	U2213	U2023	A2090	C1965	C1965	G1903
G2640	G2581	G2458	U2397	U2334	U2272	C2214	G2024	C2091	A1966	A1966	G1904
U2641	U2582	A2459	G2398	A2335	A2273	C2215	C2025	U2092	G1967	G1967	G1905
G2642	G2583	U2460	G2399	A2336	C2274	G2216	G2026	A2094	U1968	U1968	C1906
C2643	U2584	A2461	G2400	G2337	C2275	G2217	G2027	G2093	A1969	A1969	G1907
U2644	U2585	C2462	U2401	C2338	G2276	G2217	U2028	A2095	U1971	U1971	C1908
G2645	G2586	G2526	G2526	G2339	A2277	G2217	G2029	A	G1972	G1972	C1909
C2646					G2279		G2032				

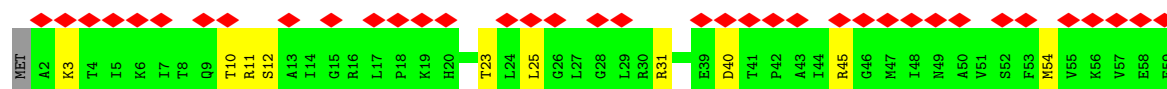
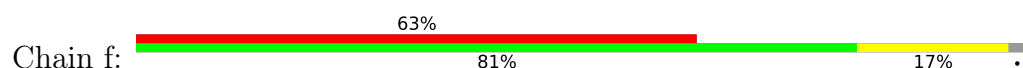




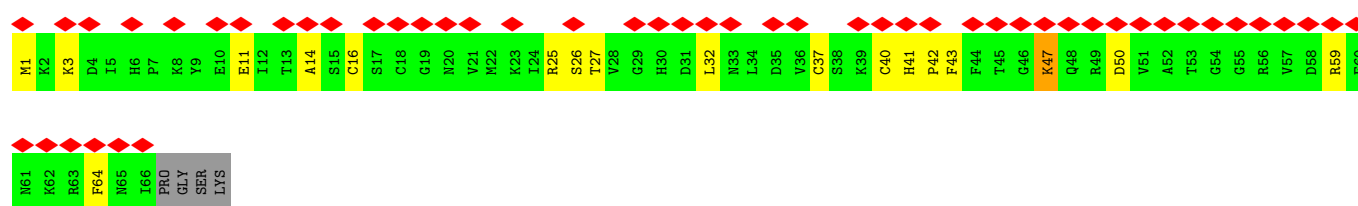
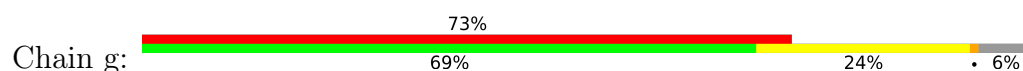
- Molecule 45: 50S ribosomal protein L29



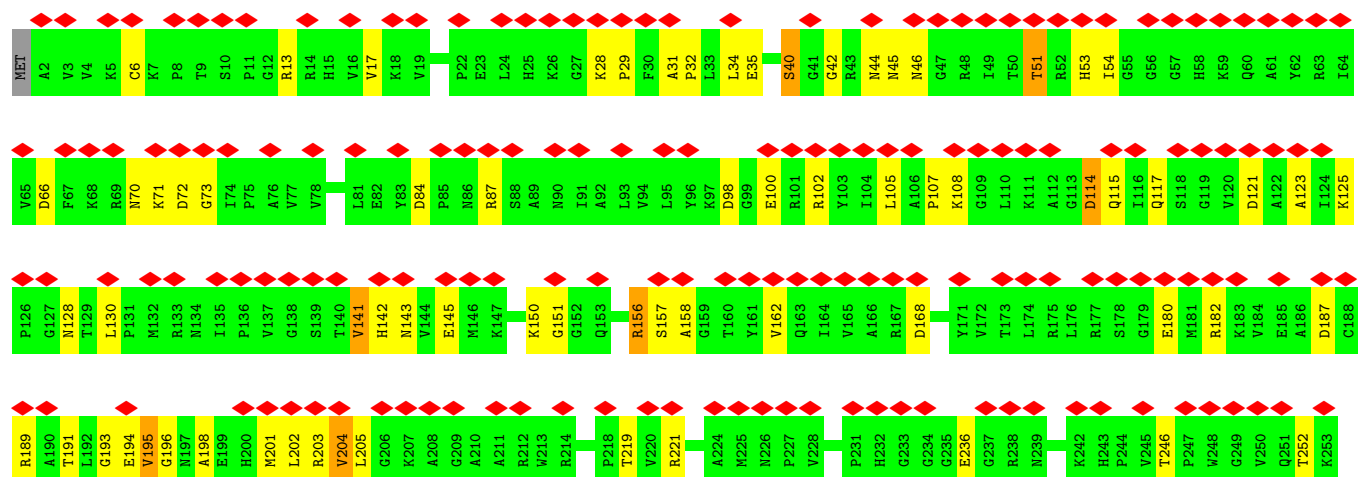
- Molecule 46: 50S ribosomal protein L30

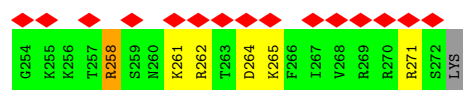


- Molecule 47: 50S ribosomal protein L31



- Molecule 48: 50S ribosomal protein L2

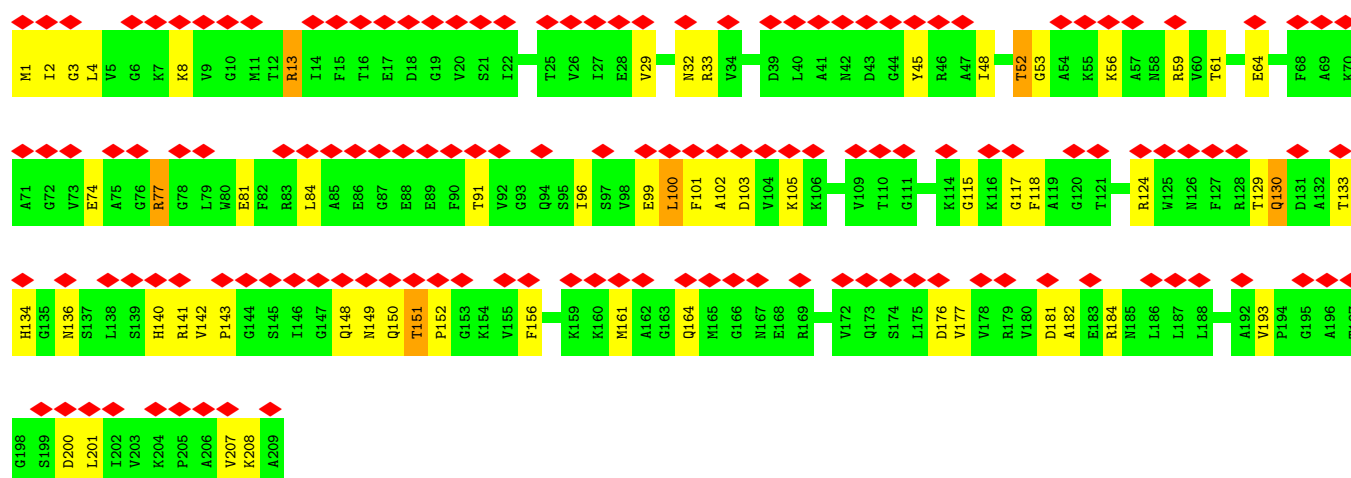




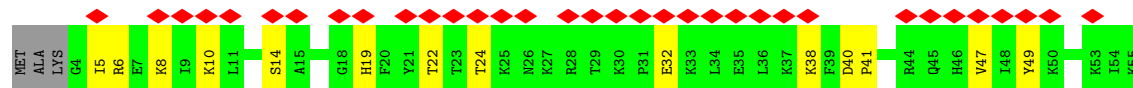
• Molecule 49: 50S ribosomal protein L32



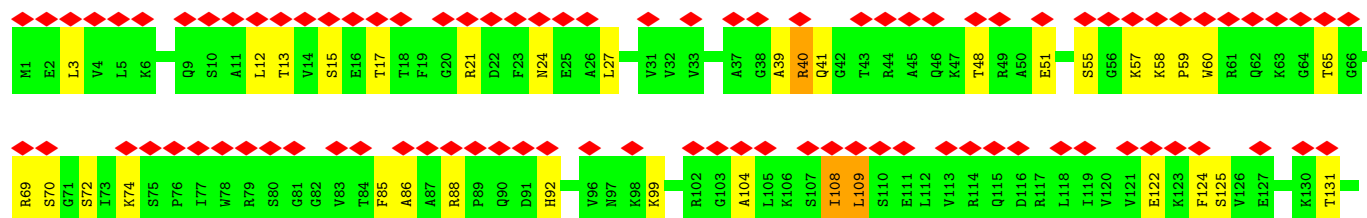
• Molecule 50: 50S ribosomal protein L3

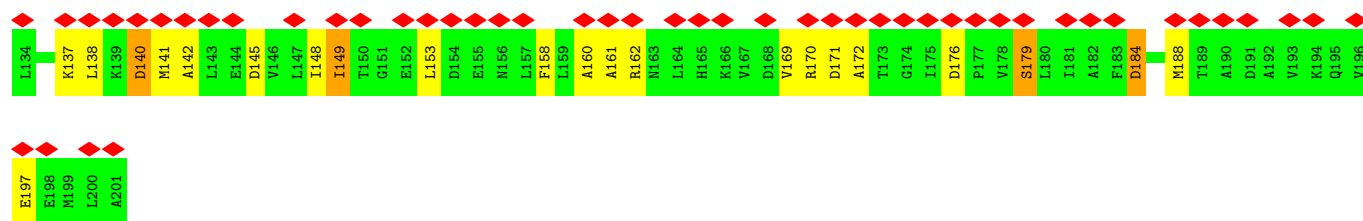


• Molecule 51: 50S ribosomal protein L33



• Molecule 52: 50S ribosomal protein L4

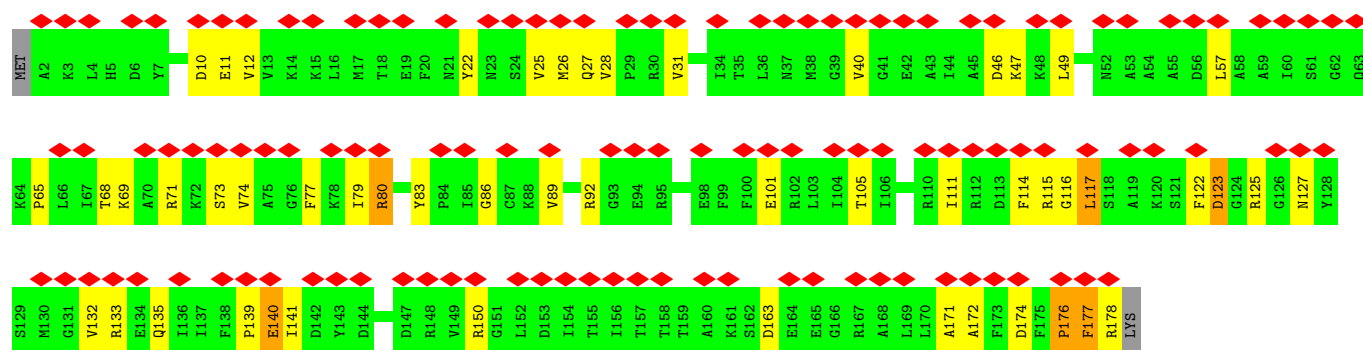




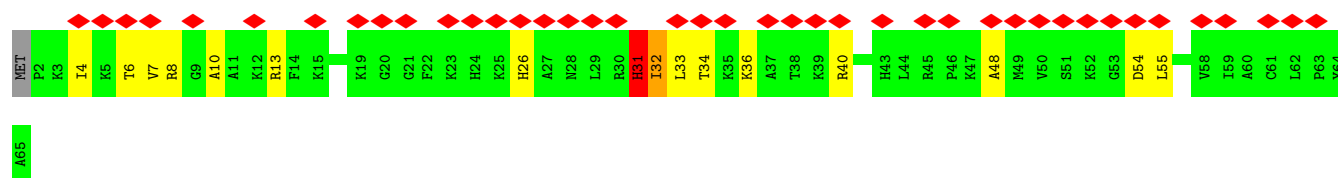
• Molecule 53: 50S ribosomal protein L34



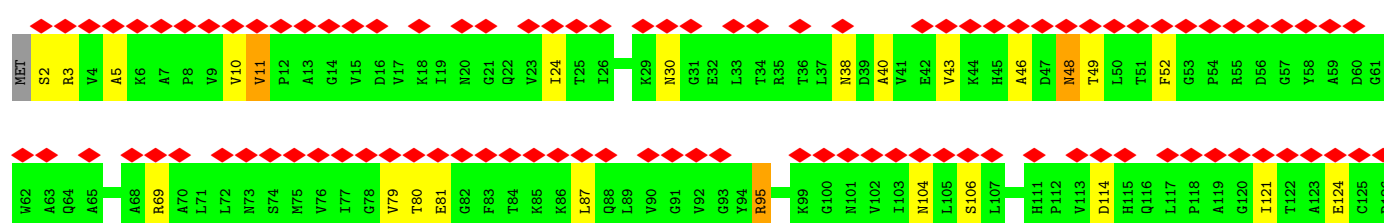
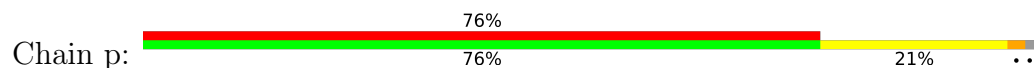
• Molecule 54: 50S ribosomal protein L5



• Molecule 55: 50S ribosomal protein L35

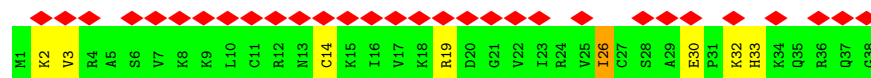
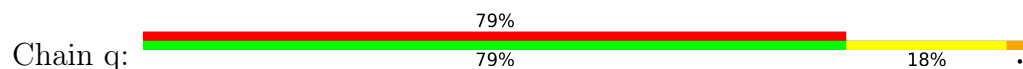


• Molecule 56: 50S ribosomal protein L6

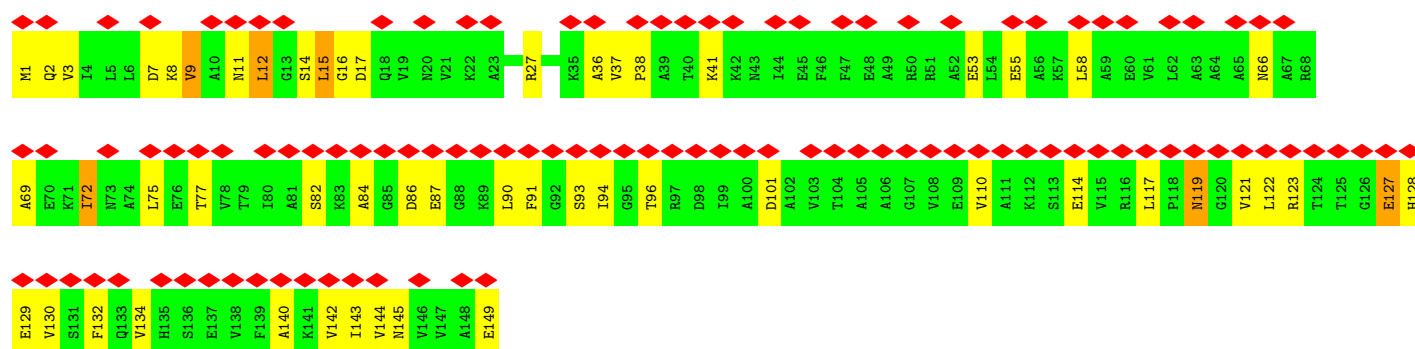




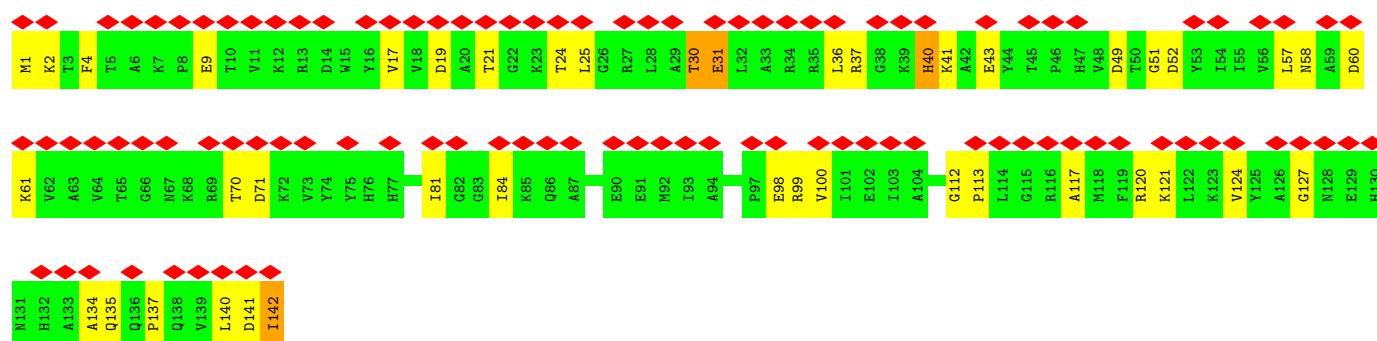
- Molecule 57: 50S ribosomal protein L36



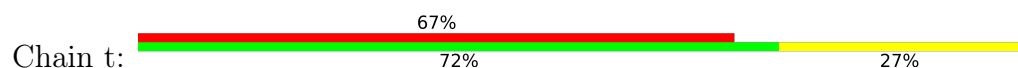
- Molecule 58: 50S ribosomal protein L9

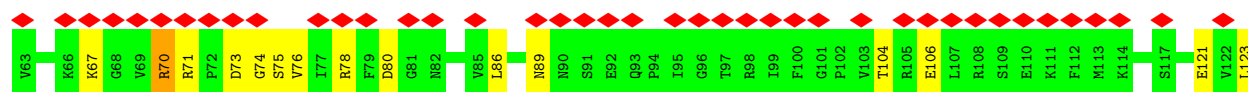


- Molecule 59: 50S ribosomal protein L13

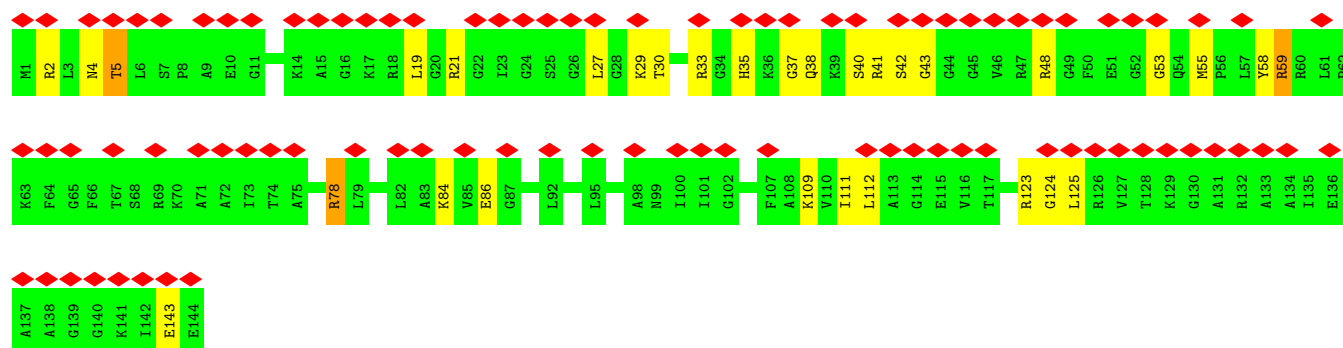
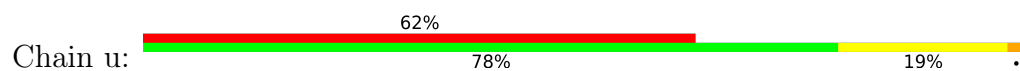


- Molecule 60: 50S ribosomal protein L14

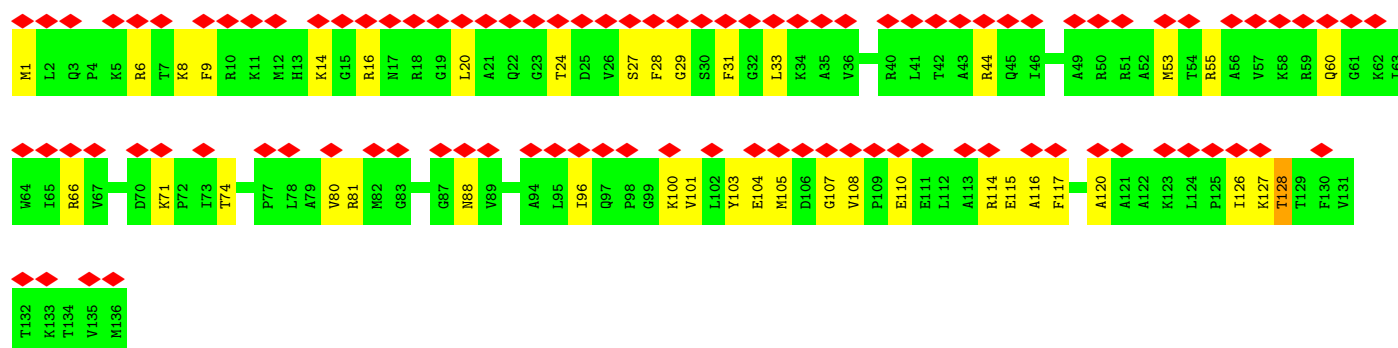




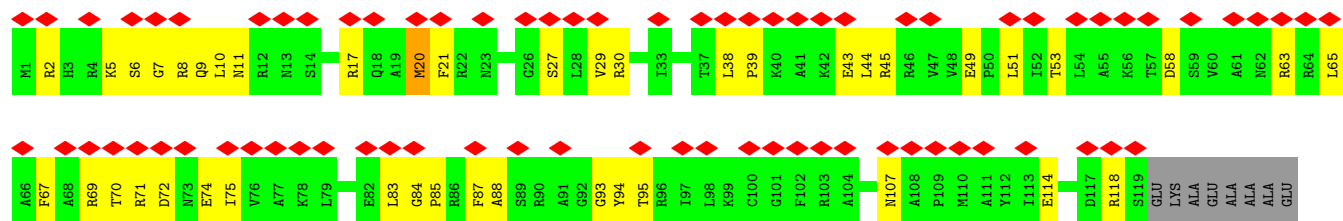
• Molecule 61: 50S ribosomal protein L15



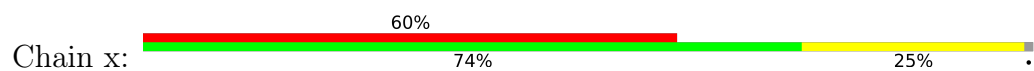
• Molecule 62: 50S ribosomal protein L16

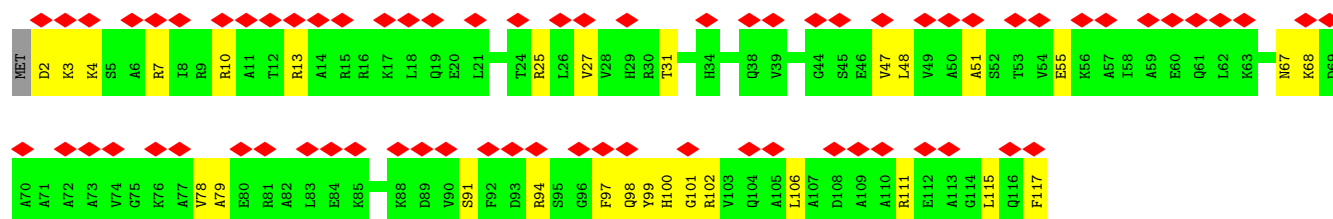


• Molecule 63: 50S ribosomal protein L17

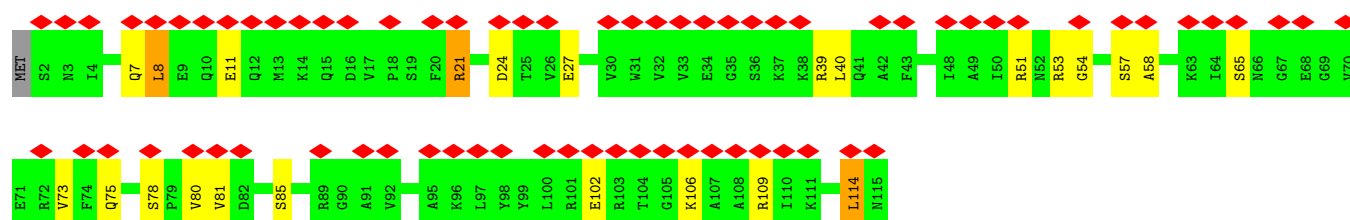
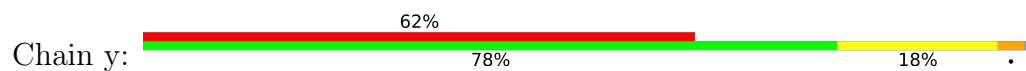


• Molecule 64: 50S ribosomal protein L18

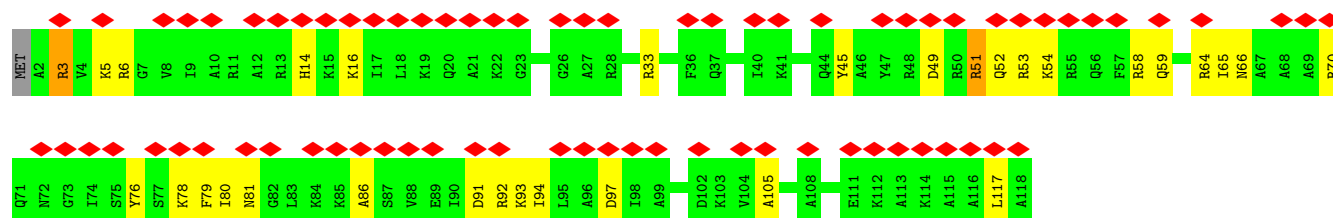
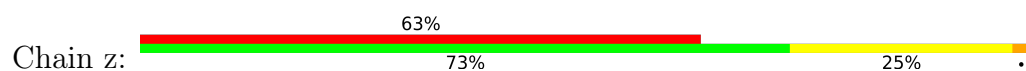




• Molecule 65: 50S ribosomal protein L19



• Molecule 66: 50S ribosomal protein L20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38957	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.065	Depositor
Minimum map value	-0.026	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.014	Depositor
Map size (Å)	532.48, 532.48, 532.48	wwPDB
Map dimensions	512, 512, 512	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: MG, ZN

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	0.56	0/829	0.51	0/1107
2	1	0.62	0/864	0.54	0/1156
3	2	0.55	0/752	0.52	0/1005
4	3	0.49	0/796	0.50	0/1062
5	4	0.50	0/766	0.49	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	0.51	1/761 (0.1%)	0.94	6/1178 (0.5%)
9	9	0.33	0/1131	0.74	0/1524
10	A	0.35	0/1810	0.57	0/2821
10	B	0.47	0/1810	0.72	2/2821 (0.1%)
11	AA	0.40	1/10736 (0.0%)	0.66	2/14487 (0.0%)
12	AB	0.87	2/1310 (0.2%)	1.08	4/1766 (0.2%)
13	AC	0.34	0/2113	0.60	0/2877
13	AD	0.30	0/2096	0.60	0/2854
14	AE	0.53	9/10545 (0.1%)	0.74	23/14236 (0.2%)
15	AF	0.29	0/652	0.61	0/879
16	AG	0.96	4/3897 (0.1%)	1.38	45/5273 (0.9%)
17	C	0.56	0/553	0.63	0/743
18	D	0.64	0/36610	0.47	9/57091 (0.0%)
19	E	0.51	0/675	0.48	0/895
20	F	0.47	0/597	0.49	0/792
21	G	0.69	1/1791 (0.1%)	0.69	3/2413 (0.1%)
22	H	0.28	0/1746	0.67	0/2382
23	I	0.52	0/1663	0.50	0/2241
24	J	0.51	0/1665	0.48	0/2227
25	K	0.61	0/1165	0.57	0/1568
26	L	0.50	0/867	0.48	0/1171
27	M	0.48	0/1195	0.56	0/1602
28	N	0.57	0/989	0.50	0/1326
29	O	0.48	0/1034	0.56	0/1375
30	P	0.45	0/800	0.56	0/1082

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	Q	0.53	0/893	0.50	0/1205
32	R	0.57	0/952	0.52	0/1274
33	S	0.53	0/817	0.52	0/1088
34	T	0.57	0/722	0.52	0/964
35	U	0.53	0/659	0.53	0/884
36	V	0.50	0/657	0.47	0/881
37	W	0.44	0/680	0.50	0/915
38	X	0.49	0/909	0.54	0/1215
39	Y	0.72	2/1046 (0.2%)	0.74	2/1410 (0.1%)
40	Z	0.14	0/227	0.41	0/304
41	a	0.68	0/69247	0.48	9/107985 (0.0%)
42	b	0.57	0/589	0.53	0/779
43	c	0.60	0/635	0.63	0/848
44	d	0.58	0/2872	0.41	0/4478
45	e	0.55	0/502	0.53	0/667
46	f	0.56	0/452	0.51	0/605
47	g	0.34	0/531	0.50	0/709
48	h	0.63	0/2121	0.51	0/2852
49	i	0.59	0/450	0.58	0/599
50	j	0.63	0/1586	0.50	0/2134
51	k	0.55	0/433	0.49	0/576
52	l	0.55	0/1571	0.49	0/2113
53	m	0.68	0/380	0.59	0/498
54	n	0.45	0/1434	0.50	0/1926
55	o	0.60	0/513	0.56	0/676
56	p	0.46	0/1333	0.47	0/1805
57	q	0.58	0/303	0.54	0/397
58	r	0.36	0/1122	0.47	0/1515
59	s	0.61	0/1152	0.52	0/1551
60	t	0.62	0/955	0.48	0/1279
61	u	0.57	0/1062	0.56	0/1413
62	v	0.58	0/1093	0.50	0/1460
63	w	0.63	0/964	0.54	0/1289
64	x	0.48	0/902	0.49	0/1209
65	y	0.59	0/929	0.49	0/1242
66	z	0.66	0/960	0.56	0/1278
All	All	0.61	22/195002 (0.0%)	0.56	105/286738 (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
9	9	0	3
13	AC	0	3
13	AD	0	1
14	AE	0	5
16	AG	0	7
21	G	0	2
22	H	0	5
29	O	0	1
54	n	0	1
55	o	0	1
All	All	0	29

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	Y	5	GLN	CA-C	17.51	1.70	1.52
12	AB	124	PRO	N-CA	17.39	1.69	1.47
21	G	157	LEU	C-N	17.12	1.54	1.33
16	AG	429	LYS	C-N	13.80	1.51	1.33
14	AE	93	THR	CA-C	12.21	1.69	1.52

The worst 5 of 105 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	AG	104	ARG	CA-C-N	17.91	154.21	121.97
16	AG	104	ARG	C-N-CA	17.91	154.21	121.97
12	AB	123	ARG	CA-C-N	17.03	141.12	119.84
12	AB	123	ARG	C-N-CA	17.03	141.12	119.84
11	AA	920	VAL	CA-C-N	15.70	139.47	119.84

There are no chirality outliers.

5 of 29 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	9	107	GLU	Peptide
9	9	117	LEU	Peptide
9	9	49	GLY	Peptide
13	AC	192	VAL	Peptide
13	AC	319	GLU	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	19	0
2	1	857	922	922	19	0
3	2	746	811	811	13	0
4	3	788	844	844	26	0
5	4	753	780	780	12	0
6	5	472	260	260	21	0
7	6	542	305	306	26	0
8	7	687	97	341	104	0
9	9	1117	0	1155	262	0
10	A	1620	826	827	128	0
10	B	1620	813	827	173	0
11	AA	10567	0	10584	277	0
12	AB	1282	1	1251	278	0
13	AC	2094	0	1894	25	0
13	AD	2078	0	1891	32	0
14	AE	10388	10612	10611	366	0
15	AF	650	0	658	10	0
16	AG	3852	0	3826	966	0
17	C	544	559	560	44	0
18	D	32703	16423	16456	1585	0
19	E	669	719	719	7	0
20	F	589	629	629	13	0
21	G	1760	1785	1787	199	0
22	H	1730	1454	1455	93	0
23	I	1636	1710	1710	53	0
24	J	1643	1707	1707	33	0
25	K	1152	1196	1196	43	0
26	L	848	846	846	27	0
27	M	1181	1235	1238	31	0
28	N	979	1031	1031	13	0
29	O	1022	1070	1070	50	0
30	P	790	831	830	86	0
31	Q	877	887	887	21	0
32	R	939	1001	1001	38	0
33	S	805	844	844	22	0
34	T	714	734	734	20	0
35	U	649	666	666	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	V	648	691	691	22	0
37	W	663	688	688	18	0
38	X	900	964	965	34	0
39	Y	1032	0	1088	187	0
40	Z	227	0	237	21	0
41	a	61841	31077	31119	2738	0
42	b	582	599	599	8	0
43	c	625	652	652	14	0
44	d	2569	1301	1301	99	0
45	e	501	531	531	5	0
46	f	448	488	488	8	0
47	g	522	520	520	12	0
48	h	2082	2154	2154	56	0
49	i	444	459	458	18	0
50	j	1565	1617	1616	54	0
51	k	426	464	464	9	0
52	l	1552	1619	1619	36	0
53	m	377	418	418	14	0
54	n	1410	1443	1444	34	0
55	o	504	572	572	19	0
56	p	1313	1358	1358	25	0
57	q	302	343	343	6	0
58	r	1111	1148	1148	39	0
59	s	1129	1162	1162	29	0
60	t	946	1023	1023	23	0
61	u	1053	1129	1129	25	0
62	v	1074	1157	1157	25	0
63	w	951	994	994	26	0
64	x	892	923	923	19	0
65	y	917	962	962	16	0
66	z	947	1020	1019	31	0
67	7	1	0	0	0	0
68	AA	2	0	0	0	0
All	All	181715	109913	132835	8055	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 26.

The worst 5 of 8055 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:135:ARG:HB3	12:AB:181:ALA:CB	1.19	1.63
12:AB:128:PHE:CB	12:AB:175:PHE:CE1	1.81	1.61
16:AG:287:ALA:CA	16:AG:331:LEU:HD12	1.19	1.60
16:AG:210:ARG:HA	16:AG:216:ILE:CD1	1.28	1.57
16:AG:168:LEU:CD2	16:AG:231:GLY:HA3	1.34	1.57

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/100 (92%)	89 (97%)	3 (3%)	0	100	100
4	3	101/104 (97%)	97 (96%)	4 (4%)	0	100	100
5	4	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
9	9	146/165 (88%)	107 (73%)	37 (25%)	2 (1%)	9	39
11	AA	1338/1342 (100%)	1206 (90%)	126 (9%)	6 (0%)	30	62
12	AB	158/181 (87%)	119 (75%)	26 (16%)	13 (8%)	0	4
13	AC	295/329 (90%)	274 (93%)	19 (6%)	2 (1%)	18	52
13	AD	293/329 (89%)	269 (92%)	24 (8%)	0	100	100
14	AE	1329/1407 (94%)	1199 (90%)	121 (9%)	9 (1%)	18	52
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
16	AG	493/495 (100%)	377 (76%)	85 (17%)	31 (6%)	1	8
17	C	64/75 (85%)	61 (95%)	3 (5%)	0	100	100
19	E	84/87 (97%)	82 (98%)	2 (2%)	0	100	100
20	F	68/71 (96%)	67 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	G	223/241 (92%)	209 (94%)	13 (6%)	1 (0%)	30	62
22	H	255/557 (46%)	201 (79%)	45 (18%)	9 (4%)	3	20
23	I	206/233 (88%)	200 (97%)	6 (3%)	0	100	100
24	J	203/206 (98%)	199 (98%)	4 (2%)	0	100	100
25	K	154/167 (92%)	146 (95%)	6 (4%)	2 (1%)	9	40
26	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	45
27	M	149/179 (83%)	139 (93%)	9 (6%)	1 (1%)	18	52
28	N	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
29	O	125/130 (96%)	118 (94%)	6 (5%)	1 (1%)	16	50
30	P	97/103 (94%)	88 (91%)	8 (8%)	1 (1%)	12	45
31	Q	115/129 (89%)	105 (91%)	10 (9%)	0	100	100
32	R	117/124 (94%)	112 (96%)	4 (3%)	1 (1%)	14	47
33	S	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
34	T	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
35	U	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
36	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
37	W	81/92 (88%)	78 (96%)	3 (4%)	0	100	100
38	X	114/118 (97%)	104 (91%)	8 (7%)	2 (2%)	6	34
39	Y	139/142 (98%)	113 (81%)	25 (18%)	1 (1%)	18	52
40	Z	28/121 (23%)	24 (86%)	4 (14%)	0	100	100
42	b	74/85 (87%)	70 (95%)	4 (5%)	0	100	100
43	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
45	e	60/63 (95%)	59 (98%)	1 (2%)	0	100	100
46	f	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
47	g	64/70 (91%)	62 (97%)	2 (3%)	0	100	100
48	h	269/273 (98%)	254 (94%)	15 (6%)	0	100	100
49	i	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
50	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
51	k	50/55 (91%)	49 (98%)	1 (2%)	0	100	100
52	l	199/201 (99%)	192 (96%)	7 (4%)	0	100	100
53	m	44/46 (96%)	42 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	n	175/179 (98%)	168 (96%)	6 (3%)	1 (1%)	21	56
55	o	62/65 (95%)	56 (90%)	5 (8%)	1 (2%)	7	36
56	p	173/177 (98%)	165 (95%)	7 (4%)	1 (1%)	21	56
57	q	36/38 (95%)	36 (100%)	0	0	100	100
58	r	147/149 (99%)	137 (93%)	10 (7%)	0	100	100
59	s	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
60	t	121/123 (98%)	114 (94%)	7 (6%)	0	100	100
61	u	142/144 (99%)	133 (94%)	9 (6%)	0	100	100
62	v	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
63	w	117/127 (92%)	111 (95%)	6 (5%)	0	100	100
64	x	114/117 (97%)	113 (99%)	1 (1%)	0	100	100
65	y	112/115 (97%)	109 (97%)	3 (3%)	0	100	100
66	z	115/118 (98%)	110 (96%)	5 (4%)	0	100	100
All	All	10159/11072 (92%)	9310 (92%)	763 (8%)	86 (1%)	18	50

5 of 86 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	79	PRO
11	AA	888	THR
12	AB	121	LYS
12	AB	122	PRO
12	AB	123	ARG

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%)	79 (94%)	5 (6%)	17	50
2	1	93/93 (100%)	84 (90%)	9 (10%)	8	32
3	2	81/84 (96%)	77 (95%)	4 (5%)	22	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3	84/85 (99%)	78 (93%)	6 (7%)	13	44
5	4	78/78 (100%)	75 (96%)	3 (4%)	29	62
9	9	112/123 (91%)	80 (71%)	32 (29%)	0	2
11	AA	1155/1157 (100%)	1136 (98%)	19 (2%)	55	75
12	AB	138/158 (87%)	108 (78%)	30 (22%)	1	6
13	AC	186/286 (65%)	186 (100%)	0	100	100
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1120/1168 (96%)	1046 (93%)	74 (7%)	15	47
15	AF	70/75 (93%)	69 (99%)	1 (1%)	59	77
16	AG	409/409 (100%)	288 (70%)	121 (30%)	0	1
17	C	57/65 (88%)	54 (95%)	3 (5%)	20	53
19	E	65/66 (98%)	62 (95%)	3 (5%)	24	58
20	F	60/61 (98%)	57 (95%)	3 (5%)	22	55
21	G	187/199 (94%)	177 (95%)	10 (5%)	20	53
22	H	137/461 (30%)	124 (90%)	13 (10%)	8	32
23	I	171/190 (90%)	161 (94%)	10 (6%)	18	51
24	J	172/173 (99%)	164 (95%)	8 (5%)	23	57
25	K	119/126 (94%)	111 (93%)	8 (7%)	15	47
26	L	91/116 (78%)	81 (89%)	10 (11%)	6	26
27	M	124/147 (84%)	116 (94%)	8 (6%)	15	47
28	N	104/105 (99%)	100 (96%)	4 (4%)	29	62
29	O	105/107 (98%)	98 (93%)	7 (7%)	15	47
30	P	86/90 (96%)	76 (88%)	10 (12%)	5	24
31	Q	90/99 (91%)	87 (97%)	3 (3%)	33	65
32	R	101/104 (97%)	92 (91%)	9 (9%)	9	34
33	S	83/84 (99%)	76 (92%)	7 (8%)	10	38
34	T	76/77 (99%)	63 (83%)	13 (17%)	2	11
35	U	65/65 (100%)	59 (91%)	6 (9%)	8	33
36	V	74/78 (95%)	70 (95%)	4 (5%)	20	53
37	W	72/79 (91%)	69 (96%)	3 (4%)	26	60
38	X	94/96 (98%)	84 (89%)	10 (11%)	6	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	Y	109/110 (99%)	85 (78%)	24 (22%)	1	6
40	Z	26/85 (31%)	16 (62%)	10 (38%)	0	0
42	b	58/63 (92%)	58 (100%)	0	100	100
43	c	67/68 (98%)	63 (94%)	4 (6%)	17	50
45	e	54/55 (98%)	52 (96%)	2 (4%)	30	63
46	f	48/49 (98%)	46 (96%)	2 (4%)	26	60
47	g	59/62 (95%)	56 (95%)	3 (5%)	21	54
48	h	216/218 (99%)	202 (94%)	14 (6%)	15	47
49	i	47/48 (98%)	41 (87%)	6 (13%)	4	20
50	j	164/164 (100%)	156 (95%)	8 (5%)	22	55
51	k	47/49 (96%)	46 (98%)	1 (2%)	47	71
52	l	165/165 (100%)	153 (93%)	12 (7%)	13	43
53	m	38/38 (100%)	36 (95%)	2 (5%)	20	53
54	n	148/150 (99%)	134 (90%)	14 (10%)	8	32
55	o	51/52 (98%)	49 (96%)	2 (4%)	28	62
56	p	136/138 (99%)	131 (96%)	5 (4%)	30	63
57	q	34/34 (100%)	32 (94%)	2 (6%)	18	50
58	r	114/114 (100%)	103 (90%)	11 (10%)	8	32
59	s	116/116 (100%)	108 (93%)	8 (7%)	14	45
60	t	104/104 (100%)	95 (91%)	9 (9%)	9	36
61	u	103/103 (100%)	97 (94%)	6 (6%)	18	51
62	v	109/109 (100%)	105 (96%)	4 (4%)	30	63
63	w	99/103 (96%)	94 (95%)	5 (5%)	21	54
64	x	86/87 (99%)	81 (94%)	5 (6%)	18	51
65	y	99/100 (99%)	92 (93%)	7 (7%)	13	44
66	z	89/90 (99%)	86 (97%)	3 (3%)	32	64
All	All	8314/9148 (91%)	7689 (92%)	625 (8%)	14	42

5 of 625 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	Y	50	LYS
58	r	66	ASN

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Mol	Chain	Res	Type
39	Y	116	MET
39	Y	48	ILE
49	i	40	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 79 such sidechains are listed below:

Mol	Chain	Res	Type
30	P	58	ASN
58	r	18	GLN
38	X	14	HIS
51	k	26	ASN
63	w	3	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	76/76 (100%)	33 (43%)	10 (13%)
10	B	75/76 (98%)	41 (54%)	8 (10%)
18	D	1513/1542 (98%)	282 (18%)	8 (0%)
41	a	2859/2904 (98%)	534 (18%)	0
44	d	119/120 (99%)	18 (15%)	0
8	7	32/41 (78%)	19 (59%)	4 (12%)
All	All	4674/4759 (98%)	927 (19%)	30 (0%)

5 of 927 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-19	U
8	7	-17	U
8	7	-16	U
8	7	-15	U
8	7	-14	U

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	B	6	G
18	D	1145	A
10	B	21	A
18	D	1493	A

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Mol	Chain	Res	Type
18	D	428	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

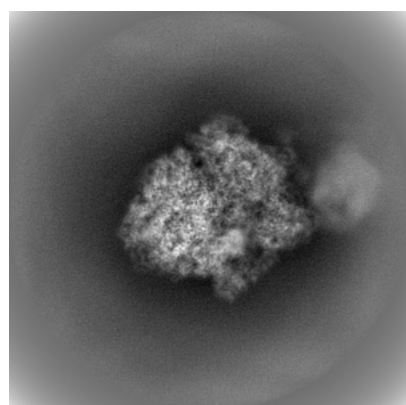
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22082. These allow visual inspection of the internal detail of the map and identification of artifacts.

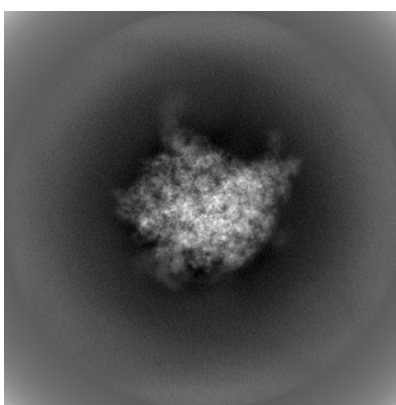
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

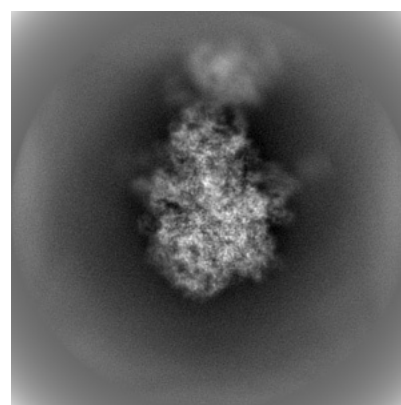
6.1.1 Primary map



X



Y

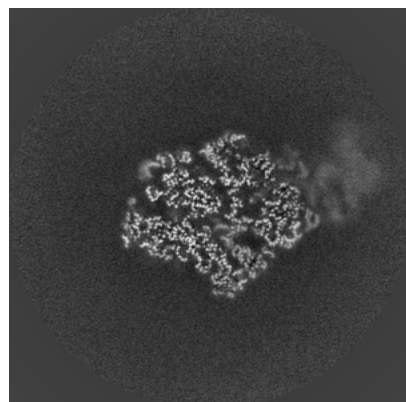


Z

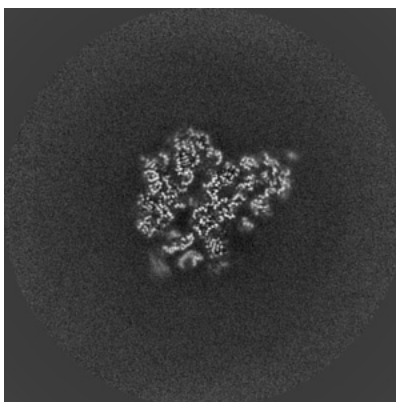
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

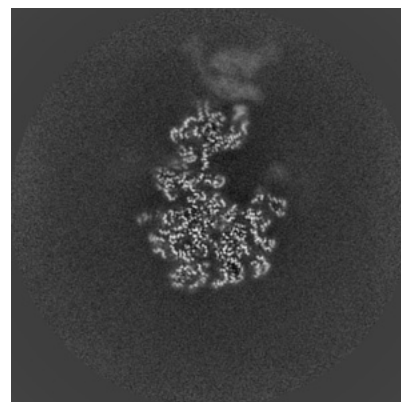
6.2.1 Primary map



X Index: 256



Y Index: 256

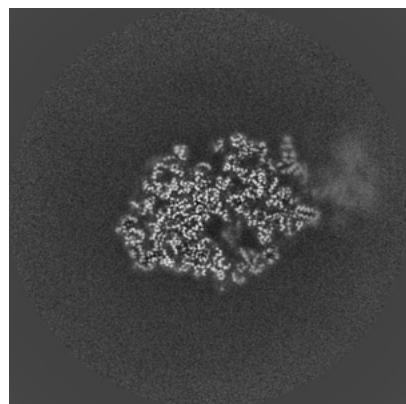


Z Index: 256

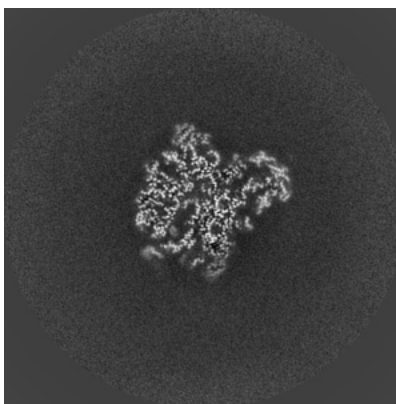
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

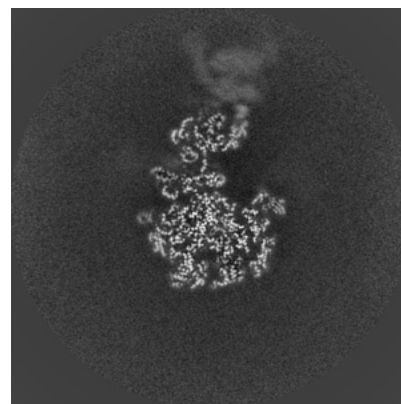
6.3.1 Primary map



X Index: 242



Y Index: 250

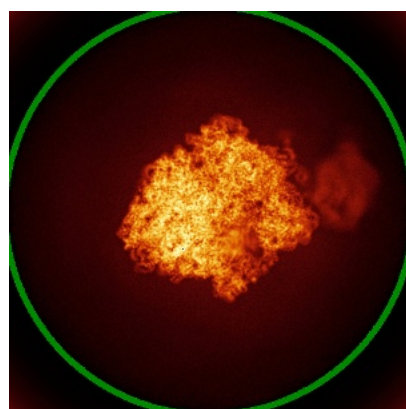


Z Index: 259

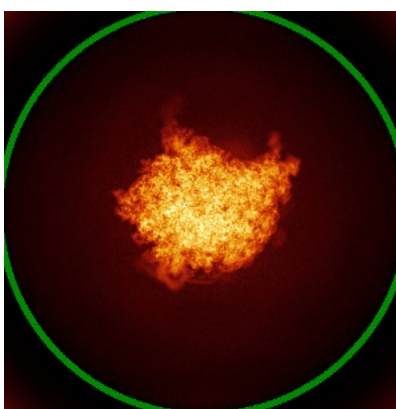
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

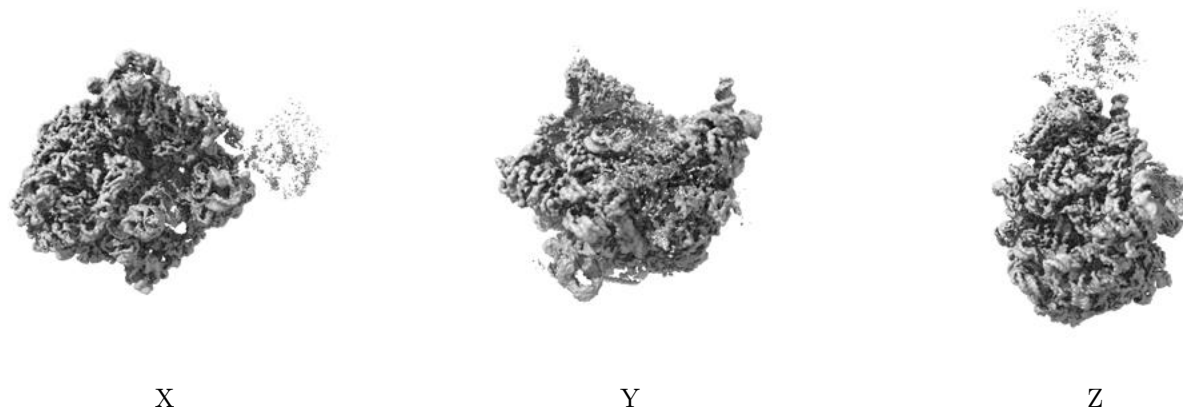


Z

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

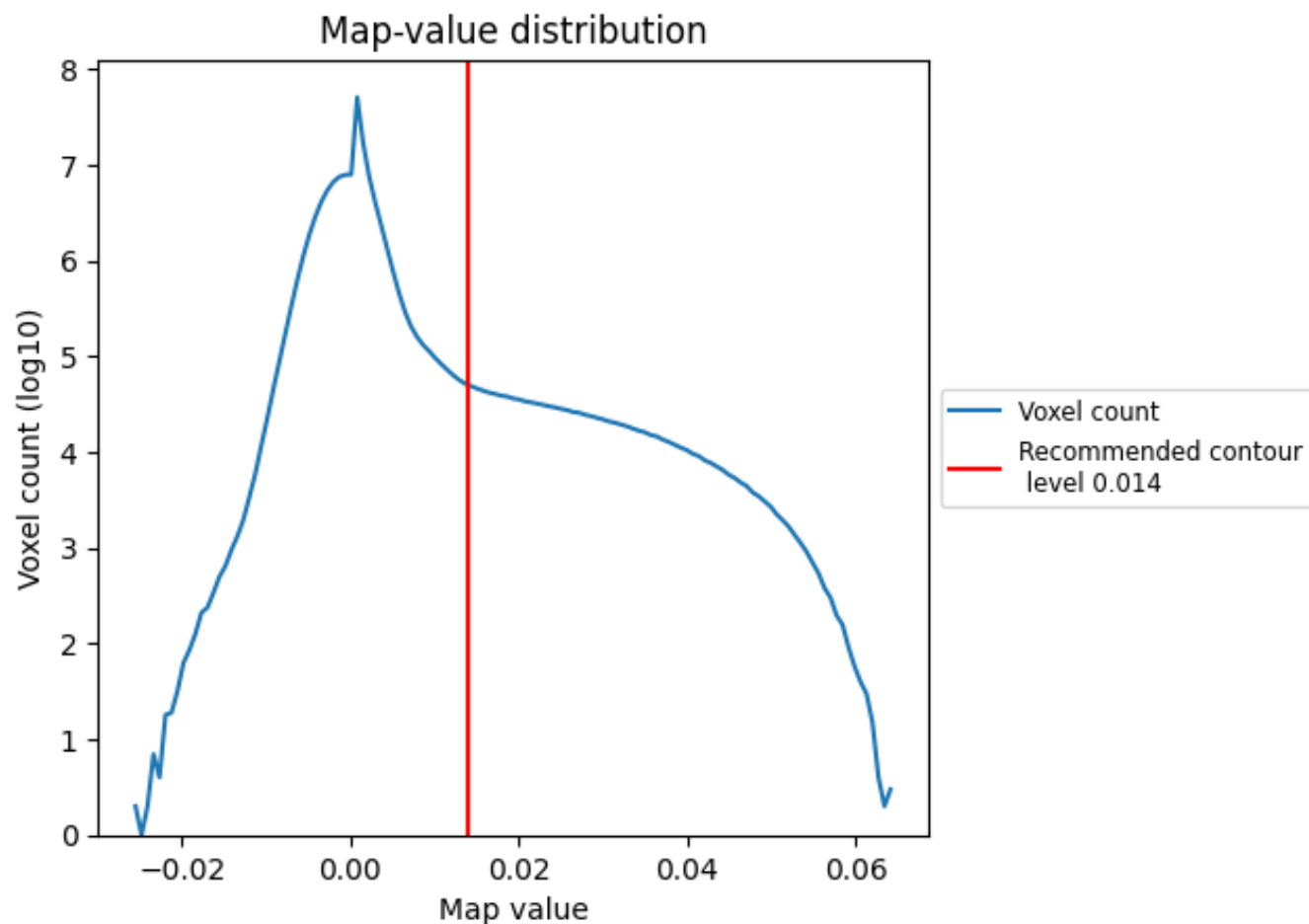
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

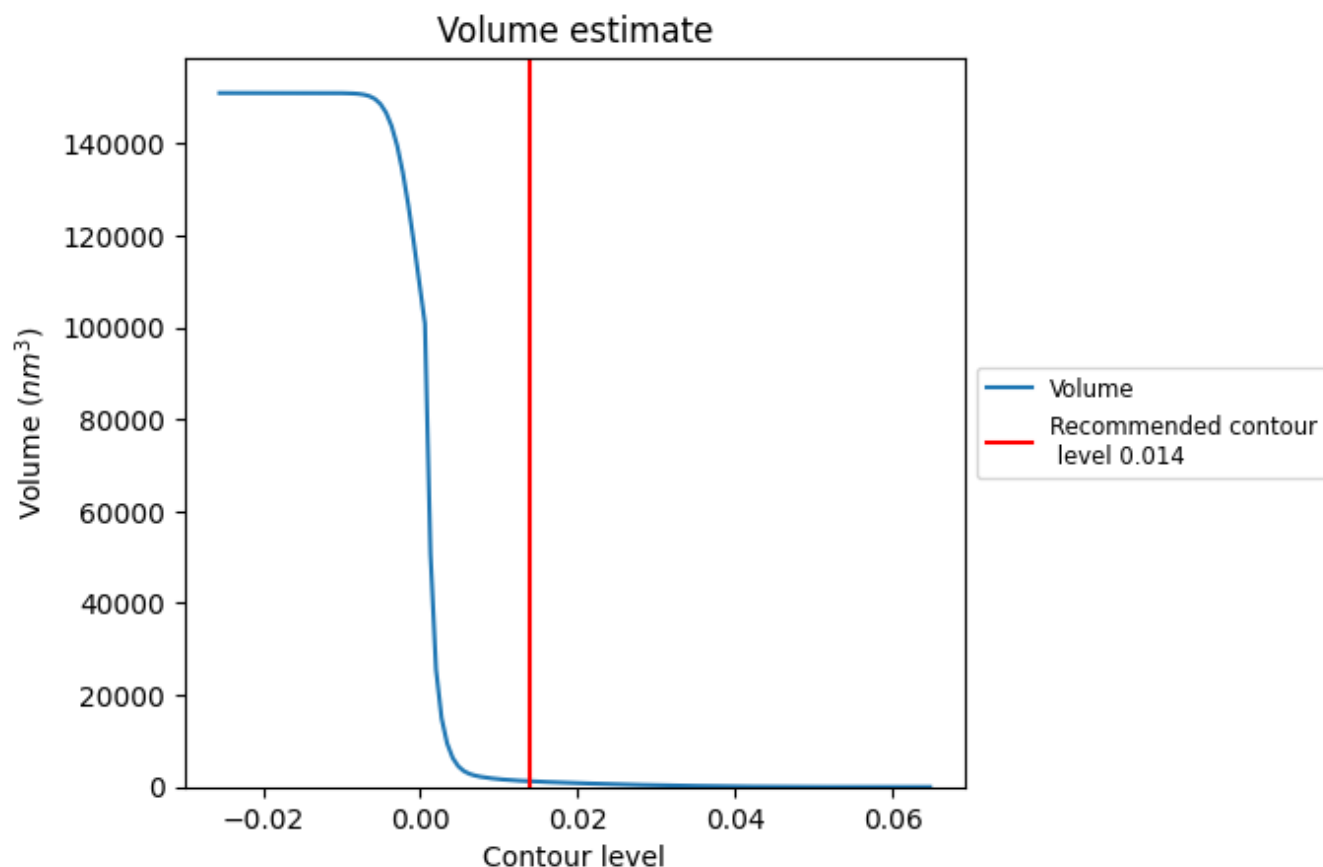
This section contains the results of statistical analysis of the map.

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.

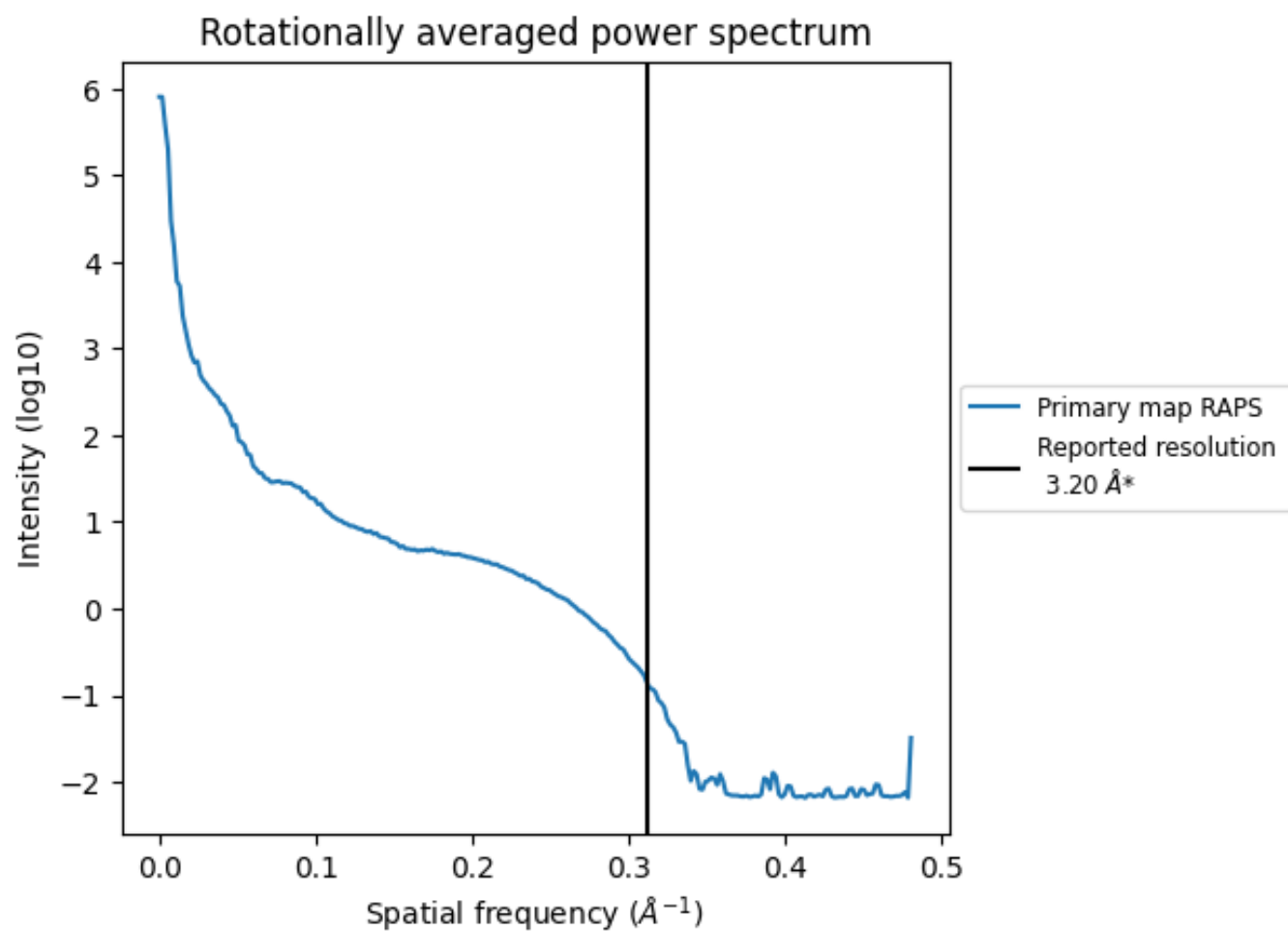
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1238 nm³; this corresponds to an approximate mass of 1118 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 0.312 Å⁻¹

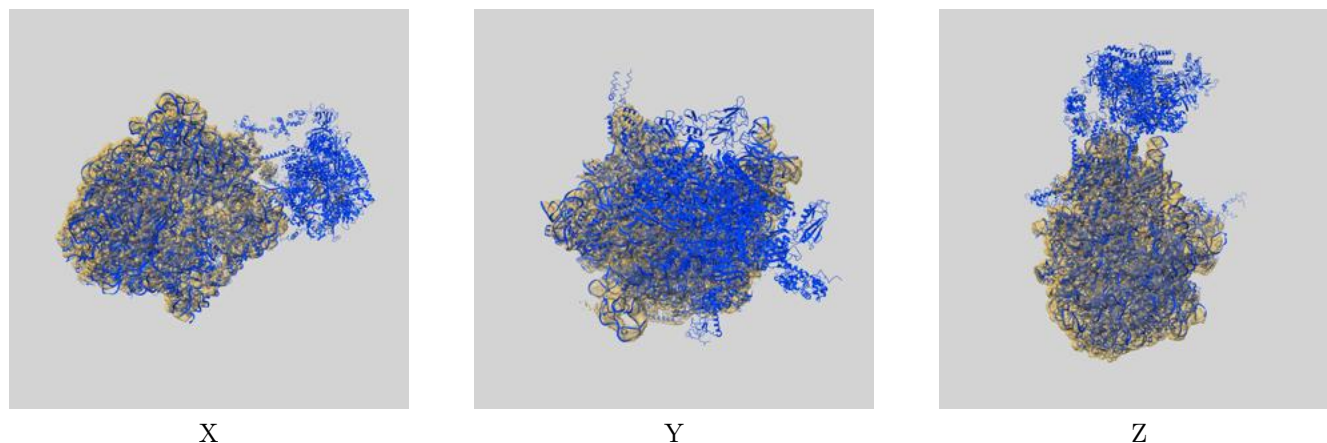
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

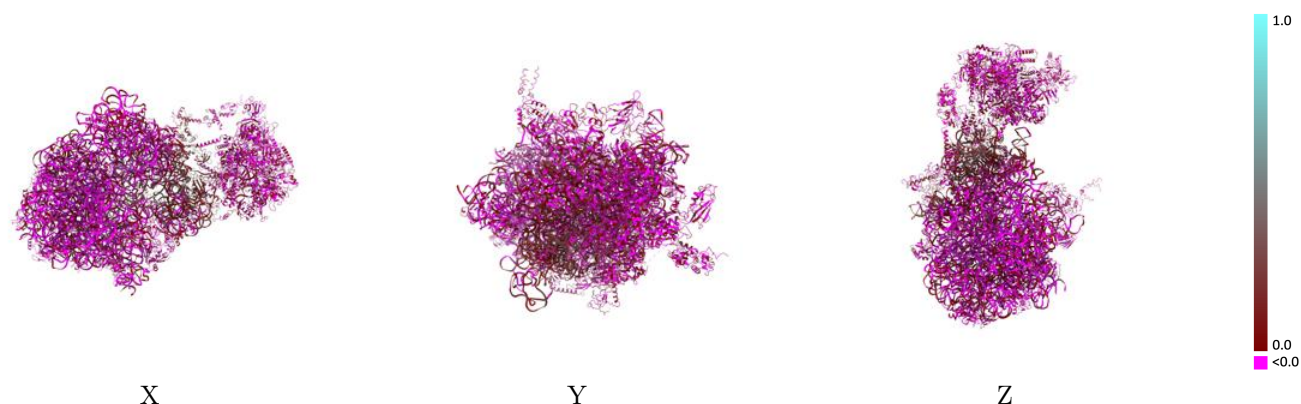
This section contains information regarding the fit between EMDB map EMD-22082 and PDB model 6X6T. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



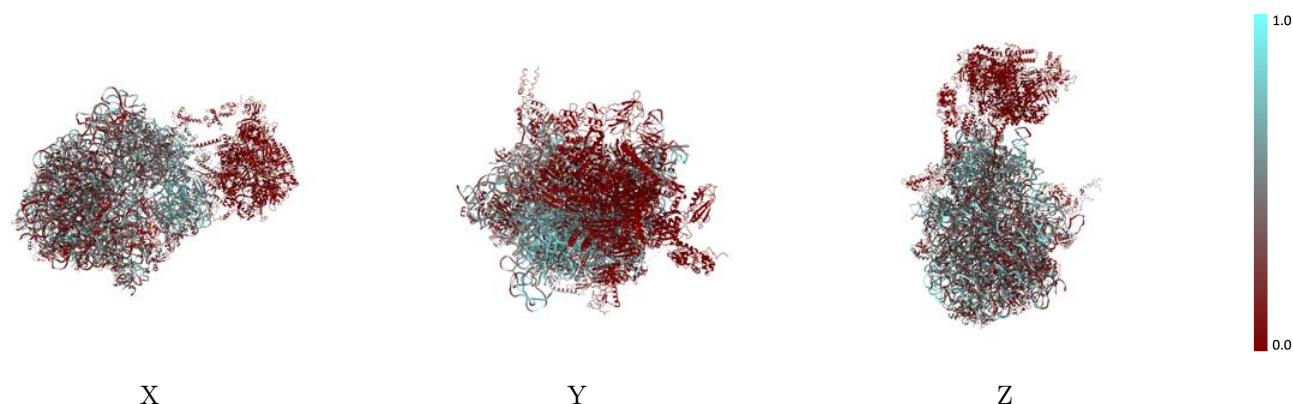
The images above show the 3D surface view of the map at the recommended contour level 0.014 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



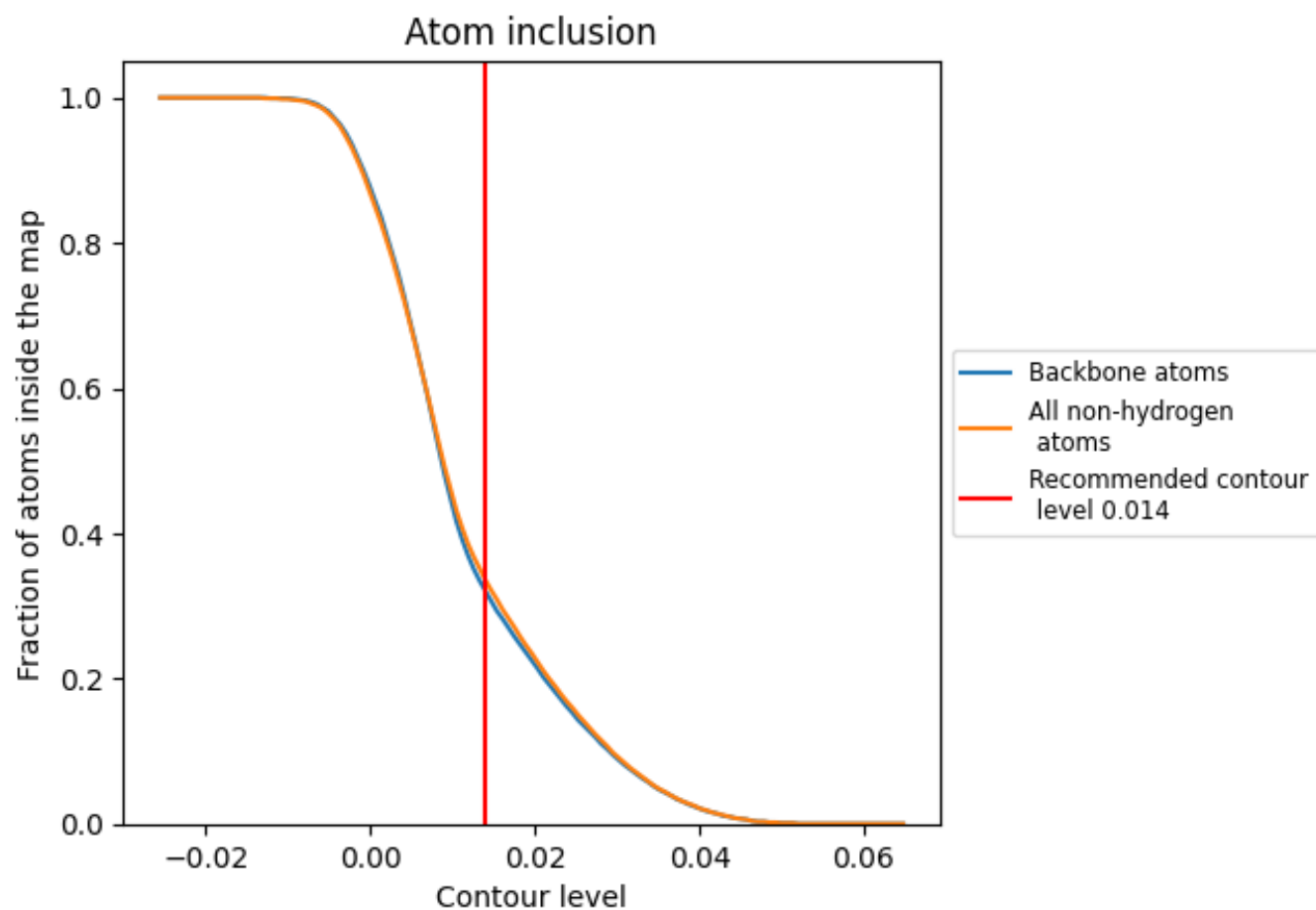
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.014).

9.4 Atom inclusion [i](#)



At the recommended contour level, 32% of all backbone atoms, 34% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3360	 0.0150
0	 0.2720	 -0.0410
1	 0.2300	 -0.0340
2	 0.2890	 0.0050
3	 0.4240	 0.0080
4	 0.3270	 0.0250
5	 0.0250	 0.0380
6	 0.0760	 0.0390
7	 0.1340	 0.0770
9	 0.1540	 0.0020
A	 0.4380	 0.0920
AA	 0.0070	 0.0250
AB	 0.1210	 0.1110
AC	 0.0010	 0.0090
AD	 0.0010	 0.0120
AE	 0.0030	 0.0160
AF	 0.0000	 0.0220
AG	 0.1970	 0.1380
B	 0.4330	 0.0350
C	 0.4020	 0.0440
D	 0.5580	 0.0510
E	 0.2630	 -0.0470
F	 0.3720	 0.1300
G	 0.4710	 0.1440
H	 0.0300	 0.0480
I	 0.5160	 0.2070
J	 0.4130	 0.0240
K	 0.3480	 0.0120
L	 0.3170	 -0.0540
M	 0.5520	 0.2370
N	 0.2880	 -0.0650
O	 0.5360	 0.1620
P	 0.4380	 0.1200
Q	 0.5270	 0.1840
R	 0.2590	 -0.0640



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Chain	Atom inclusion	Q-score
S	 0.4380	 0.1180
T	 0.3040	 -0.0380
U	 0.3090	 -0.0520
V	 0.3730	 -0.0230
W	 0.3460	 -0.0050
X	 0.3550	 0.0100
Y	 0.0340	 -0.0050
Z	 0.0000	 0.0130
a	 0.4330	 -0.0200
b	 0.2620	 -0.0670
c	 0.3560	 -0.0570
d	 0.4860	 -0.0050
e	 0.3520	 -0.0330
f	 0.2960	 0.0030
g	 0.2430	 0.0390
h	 0.2920	 -0.0770
i	 0.3530	 -0.0260
j	 0.2900	 -0.0160
k	 0.3090	 -0.0500
l	 0.2990	 -0.0110
m	 0.3380	 -0.0130
n	 0.2830	 -0.0430
o	 0.3180	 -0.0230
p	 0.2090	 -0.0260
q	 0.2330	 -0.0190
r	 0.2470	 0.0160
s	 0.2660	 -0.0210
t	 0.2770	 0.0020
u	 0.3100	 -0.0260
v	 0.2800	 -0.0150
w	 0.3380	 -0.0330
x	 0.3560	 -0.0420
y	 0.3130	 -0.0130
z	 0.3030	 -0.0140