



wwPDB EM Validation Summary Report ⓘ

Nov 13, 2022 – 02:55 PM EST

PDB ID : 6VU3
EMDB ID : EMD-21386
Title : Cryo-EM structure of Escherichia coli transcription-translation complex A (TTC-A) containing mRNA with a 12 nt long spacer
Authors : Molodtsov, V.; Wang, C.; Su, M.; Ebright, R.
Deposited on : 2020-02-14
Resolution : 3.70 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:

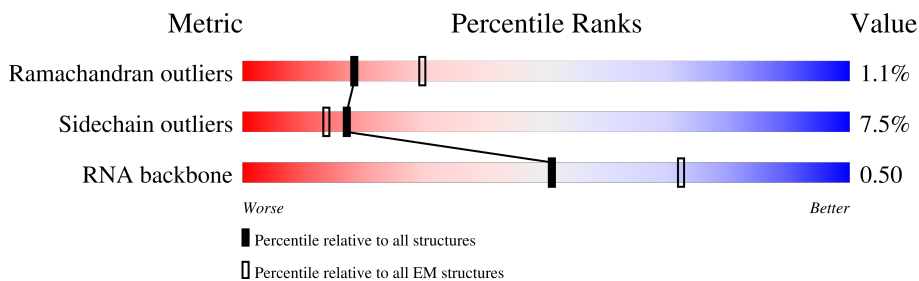
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 3.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	
2	1	110	
3	2	94	
4	3	103	
5	4	94	
6	5	36	
7	6	27	
8	7	29	

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Mol	Chain	Length	Quality of chain
9	9	148	98% 60% 37%
10	A	76	55% 58% 38%
10	B	76	30% 46% 49% 5%
11	AA	1342	86% 89% 8%
12	AB	181	53% 53% 46%
13	AC	230	63% 92% 7%
13	AD	230	89% 98%
14	AE	1407	75% 89% 5% 5%
15	C	66	23% 97%
16	D	1542	45% 78% 20%
17	E	86	76% 94% 6%
18	F	70	33% 96%
19	G	225	36% 96%
20	H	557	23% 41% 54%
21	I	208	25% 97%
22	J	205	20% 97%
23	K	156	37% 95% 5%
24	L	104	52% 93% 6%
25	M	151	70% 95% 5%
26	N	129	26% 98%
27	O	127	28% 95% 5%
28	P	99	43% 91% 9%
29	Q	117	71% 96%
30	R	124	83% 92% 6%
31	S	100	68% 96%

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Mol	Chain	Length	Quality of chain
32	T	88	78% 86% 14%
33	U	82	22% 93% 7%
34	V	80	42% 98% .
35	W	83	98% 95% 5%
36	X	116	46% 90% 10%
37	Y	141	67% 69% 28% .
38	Z	30	100% 50% 47% .
39	a	2904	43% 81% 18% .
40	b	76	39% 99% .
41	c	77	68% 95% 5%
42	d	120	73% 86% 14%
43	e	62	97% 98% .
44	f	58	66% 97% .
45	g	66	62% 91% 9%
46	h	271	38% 93% 7%
47	i	56	80% 89% 11%
48	j	209	64% 97% .
49	k	52	29% 94% 6%
50	l	201	72% 93% 7%
51	m	46	80% 93% 7%
52	n	177	36% 90% 10%
53	o	64	56% 92% 8%
54	p	175	99% 98% .
55	q	38	50% 95% 5%
56	r	149	56% 93% 7%

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Mol	Chain	Length	Quality of chain
57	s	142	
58	t	123	
59	u	144	
60	v	136	
61	w	119	
62	x	116	
63	y	114	
64	z	117	

2 Entry composition [i](#)

There are 66 unique types of molecules in this entry. The entry contains 300609 atoms, of which 124724 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	
			Total	C	H	N	O			S
1	0	103	1655	516	839	153	145	2	0	0

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

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

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

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

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

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

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

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

- Molecule 6 is a DNA chain called NT DNA.

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

- Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
7	6	27	848	259	306	89	167	27	0	0

- Molecule 8 is a RNA chain called mRNA with 12 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
8	7	29	709	273	97	94	216	29	0	0

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

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

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

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	U	deletion	GB 1845826323
B	?	-	U	deletion	GB 1845826323

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
13	AC	230	Total	C	H	N	O	S	0	0
			3599	1112	1813	317	351	6		
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	
			Total	C	H	N	O			S
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	
			Total	C	H	N	O			S
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	
			Total	C	H	N	O			P
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	
			Total	C	H	N	O			S
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	
			Total	C	H	N	O			S
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
			Total	C	H	N	O	S		
19	G	225	3545	1113	1785	316	323	8	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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	
			Total	C	H	N	O			S
40	b	76	1181	360	599	117	104	1	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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	
			Total	C	H	N	O			S
60	v	136	2231	686	1157	205	177	6	0	0

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

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

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

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

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

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

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

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

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

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

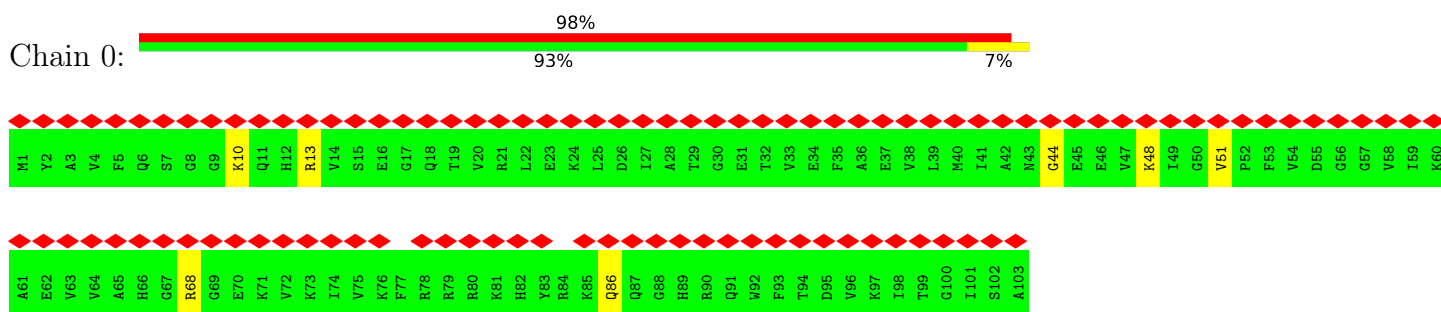
- Molecule 66 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

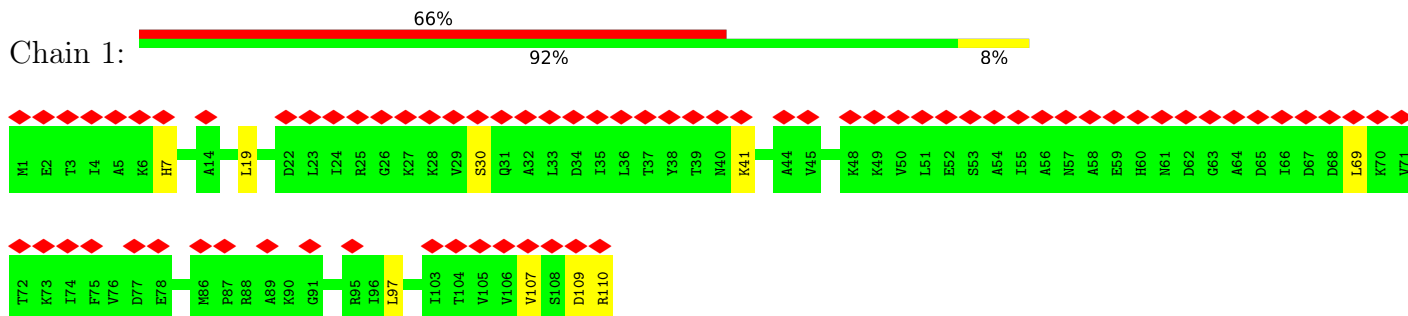
3 Residue-property plots

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.

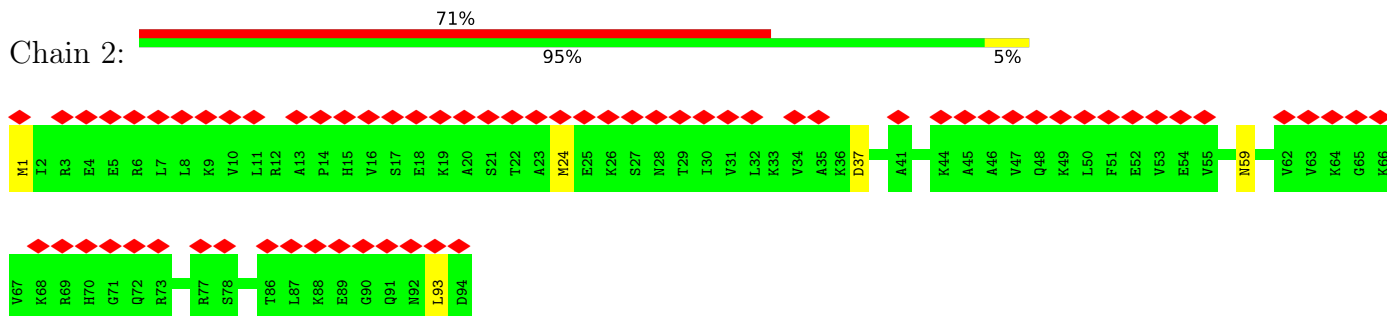
- Molecule 1: 50S ribosomal protein L21



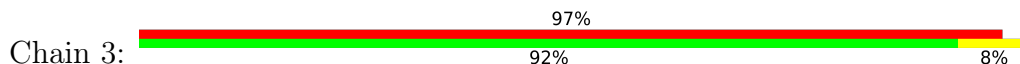
- Molecule 2: 50S ribosomal protein L22

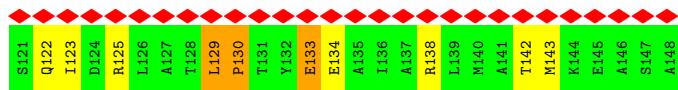


- Molecule 3: 50S ribosomal protein L23



- Molecule 4: 50S ribosomal protein L24

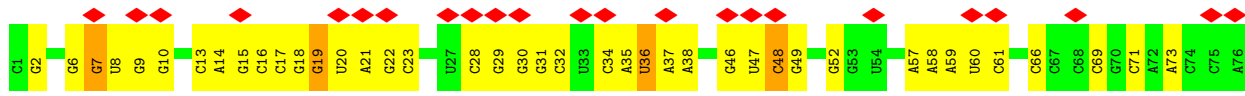




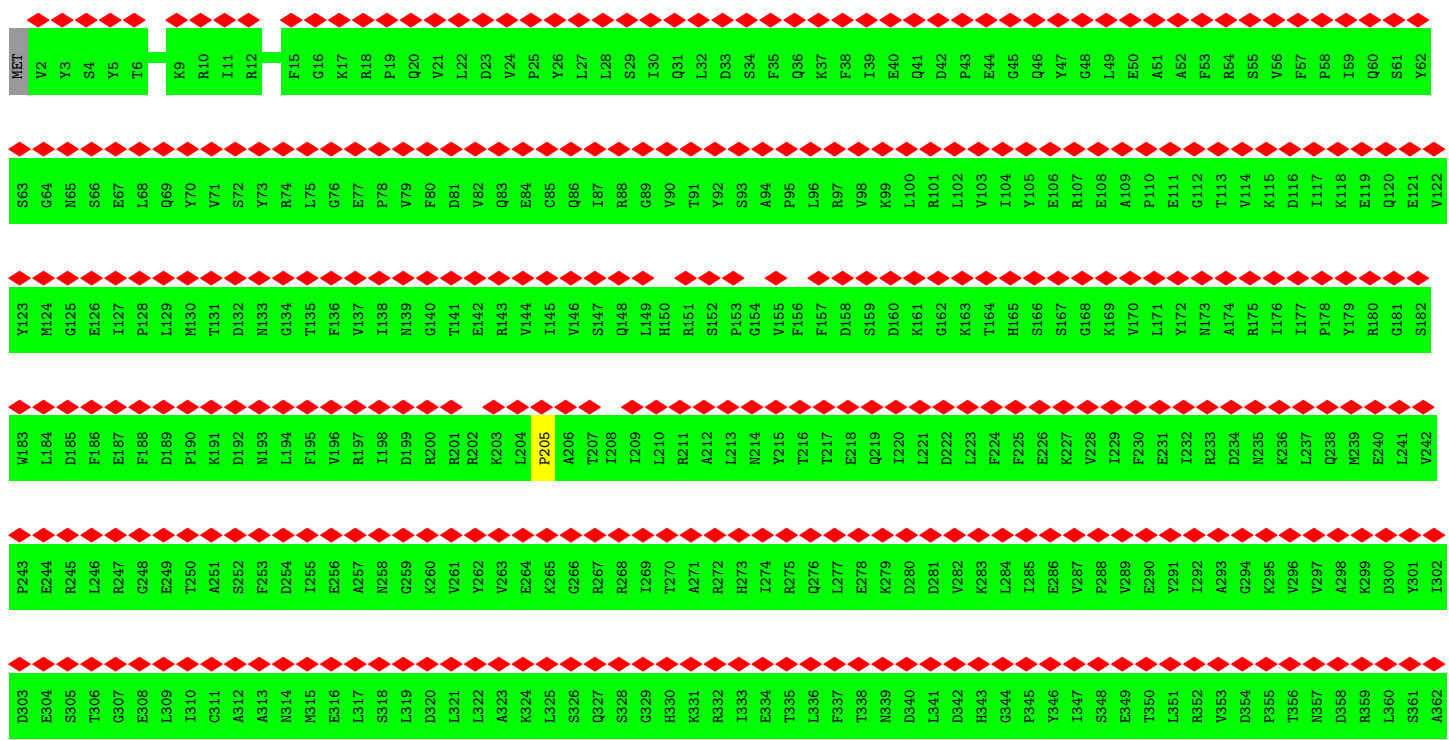
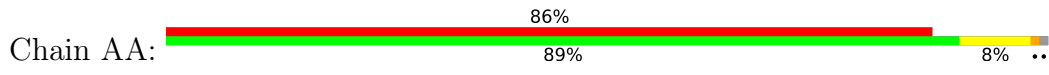
• Molecule 10: E-site and A-site tRNA (fMet)



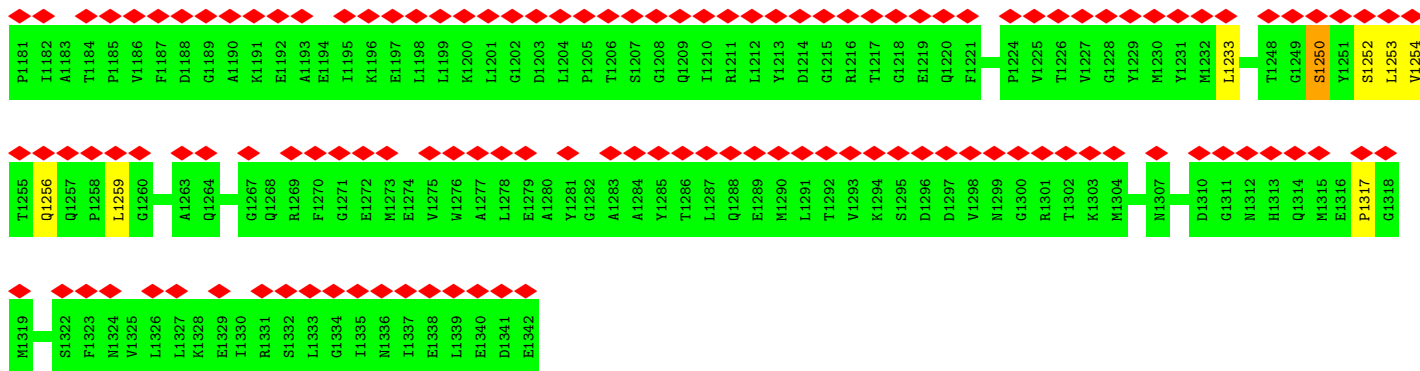
• Molecule 10: E-site and A-site tRNA (fMet)



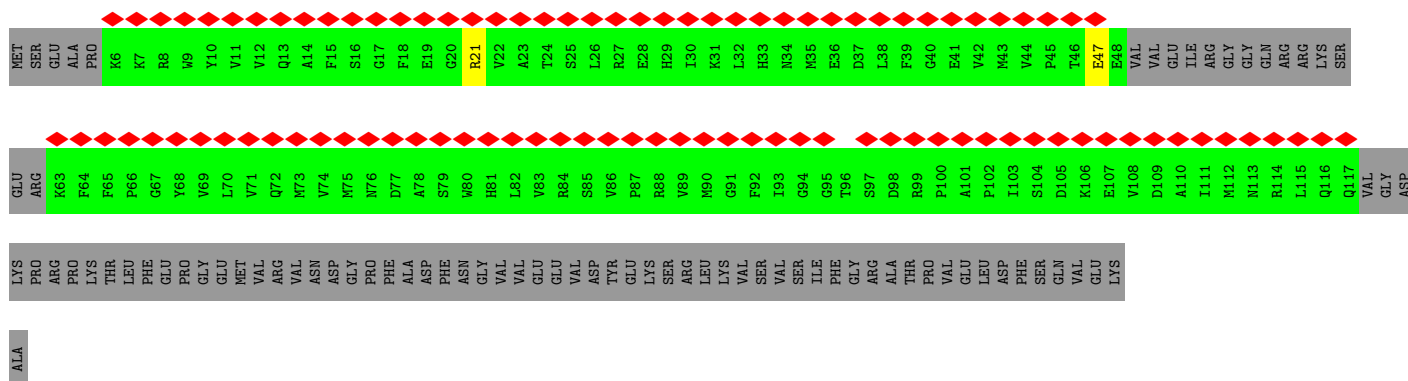
• Molecule 11: DNA-directed RNA polymerase subunit beta



L363	V364	E365	I366	R367	M368	M369	M370	R371	P372	G373	E374	P375	P376	T377	R378	E379	A380	A381	E382	S383	L384	F385	E386	N387	L388	F389	F390	S391	E392	D393	R394	Y395	D396	L397	S398	A399	V400	G401	R402	M403	K404	F405	N406	R407	S408	L409	L410	R411	E412	E413	I414	E415	G416	S417	G418	I419	L420	S421	K422	
D423	D424	I425	I426	D427	V428	M429	K430	K431	L432	I433	D434	I435	R436	N437	G438	K439	G440	E441	V442	D443	D444	I445	F446	H447	L448	G449	N450	R451	R452	I453	R454	S455	V456	G457	E458	M459	A460	E461	Q462	F464	R465	V466	G467	L468	V469	R470	V471	E472	R473	A474	V475	K476	E477	R478	L479	S480	L481	G482		
D483	L484	D485	T486	L487	M488	P489	Q490	D491	M492	I493	N494	A495	R496	P497	I498	S499	A500	A501	V502	K503	E504	F505	F506	G507	S508	S509	Q510	L511	S512	Q513	F514	M515	N518	N519	P520	L521	S522	E523	I524	T525	H526	K527	R528	R529	I530	S531	A532	L533	G534	P535	G536	G537	L538	T539	R540	E541	E542	L543		
G544	F545	E546	V547	R548	D549	V550	H551	P552	M553	H554	Y555	G556	R557	V558	C559	P560	I561	F564	E565	G566	P567	M568	I569	G570	L571	I572	N573	S574	L575	S576	V577	Y578	A579	Q580	T581	N582	E583	Y584	G585	F586	L587	E588	T589	P590	Y591	R592	K593	V594	T595	D596	G597	V598	V599	T600	D601	E602	I603	H604		
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S666	L667	I668	P669	F670	L671	E672	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	V709	V710	D711	T715	A716	A718	K719	R720	G722	V723	Y726	V727	D728	G792				
A729	S730	R731	I732	V733	I734	K735	V736	M737	E738	D739	E740	M741	F743	G744	E745	G747	I748	D749	I750	Y751	N752	L753	T754	K755	Y756	T757	R758	S759	M760	Q761	N762	T763	C764	I765	M766	Q767	M768	P769	C770	V771	P776	V777	E778	R779	G780	D781	V782	K783	A784	D785	G786	P787	T788	G792						
E793	L794	A795	L796	G797	Q798	M799	H800	A803	F804	H805	F806	M807	H808	G809	H810	H811	F812	E813	D814	S815	L816	L817	V818	S819	E820	R821	V822	G823	Q824	T830	R831	H832	L833	E835	L836	A837	S840	K844	L845	E849	T850	T851	A852	D853	L854	P855	H856	V857	G858	E859	L862	S863								
K864	L865	D866	E867	S868	G869	L870	V871	Y872	L873	G874	A875	E876	V877	T878	G879	G880	D881	Y884	G885	K886	K890	G891	GLU	THR	GLN	LEU	THR	PRO	GLU	GLU	LYS	LEU	LEU	ARG	ALA	ILE	PHE	GLY	LYS	ALA	S911	D912	V913	K914	D915	S916	S917	G970	L918	R919	T852	R921	R922	G923	V924	S925	G926			
T927	V928	I929	D930	V931	Q932	V933	F934	T935	R936	D937	G938	V939	E940	K941	K943	R944	A945	L946	E947	I948	E949	E950	K951	Q952	L953	K954	Q955	A956	K957	K958	D959	L960	S961	E962	E963	I964	Q965	I966	L967	E968	A969	G970	L971	F972	S973	R974	I975	R976	A977	V978	L979	V980	A981	G982	G983	V984	E985	A986		
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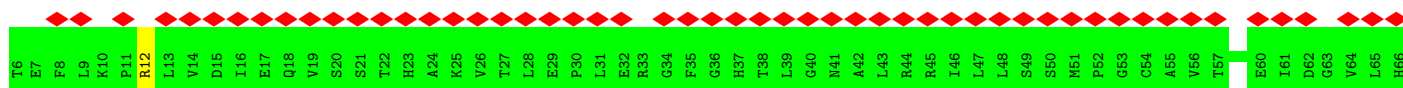
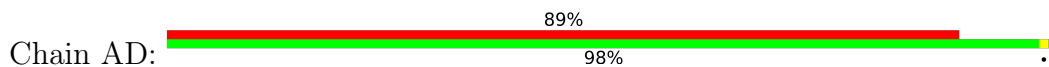
• Molecule 12: Transcription termination/antitermination protein NusG

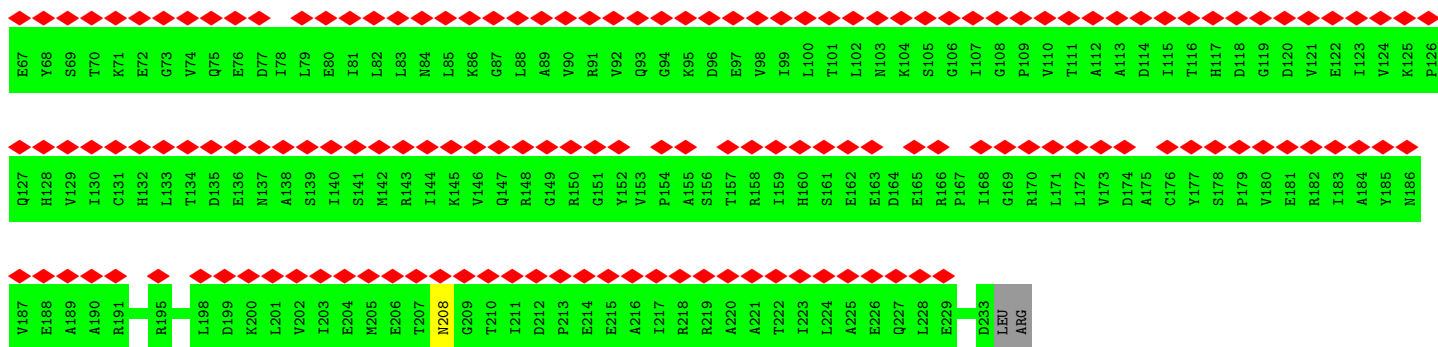


• Molecule 13: DNA-directed RNA polymerase subunit alpha



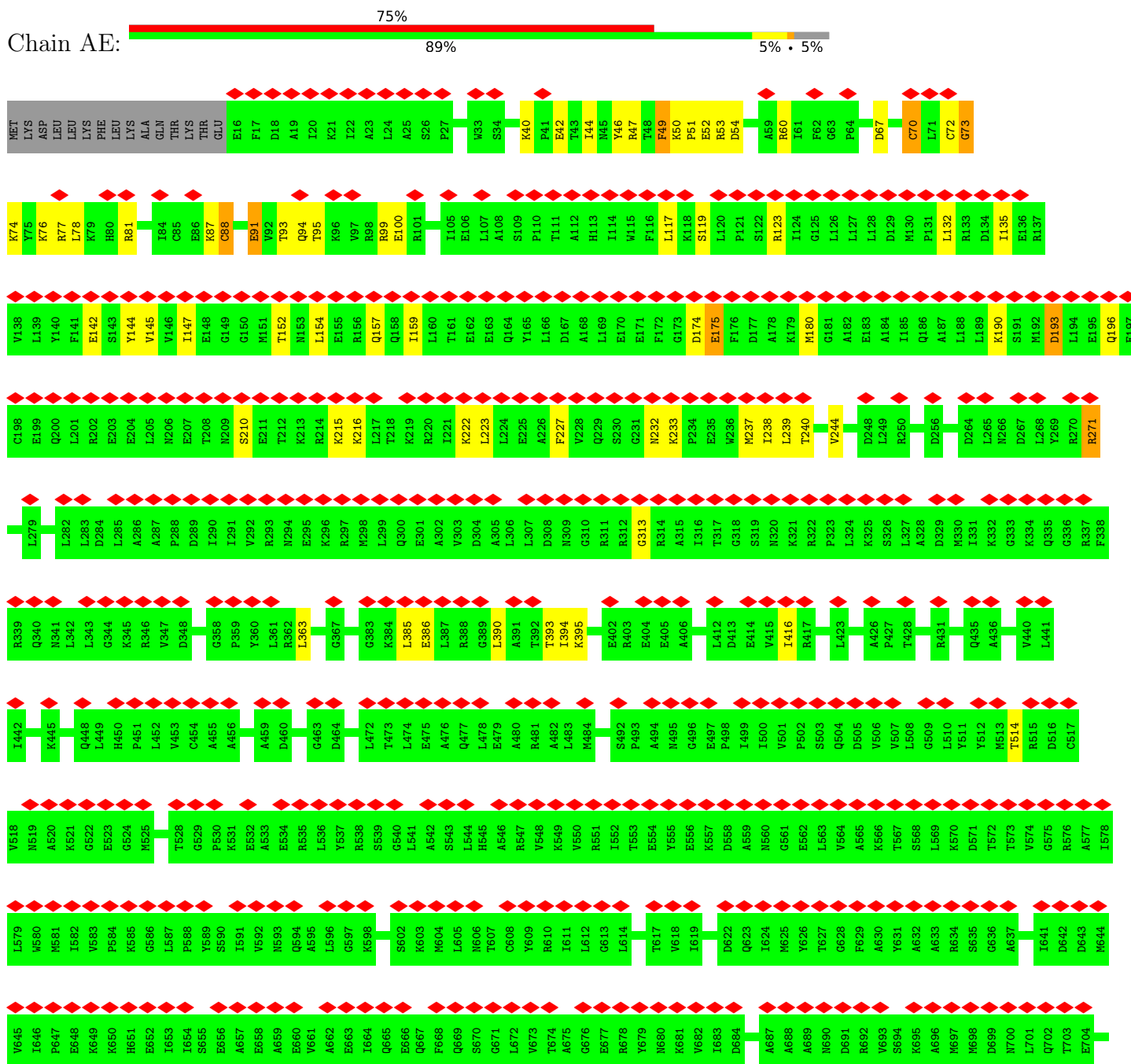
• Molecule 13: DNA-directed RNA polymerase subunit alpha

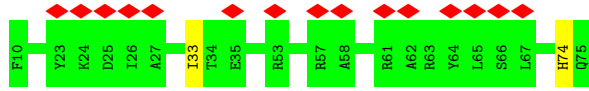




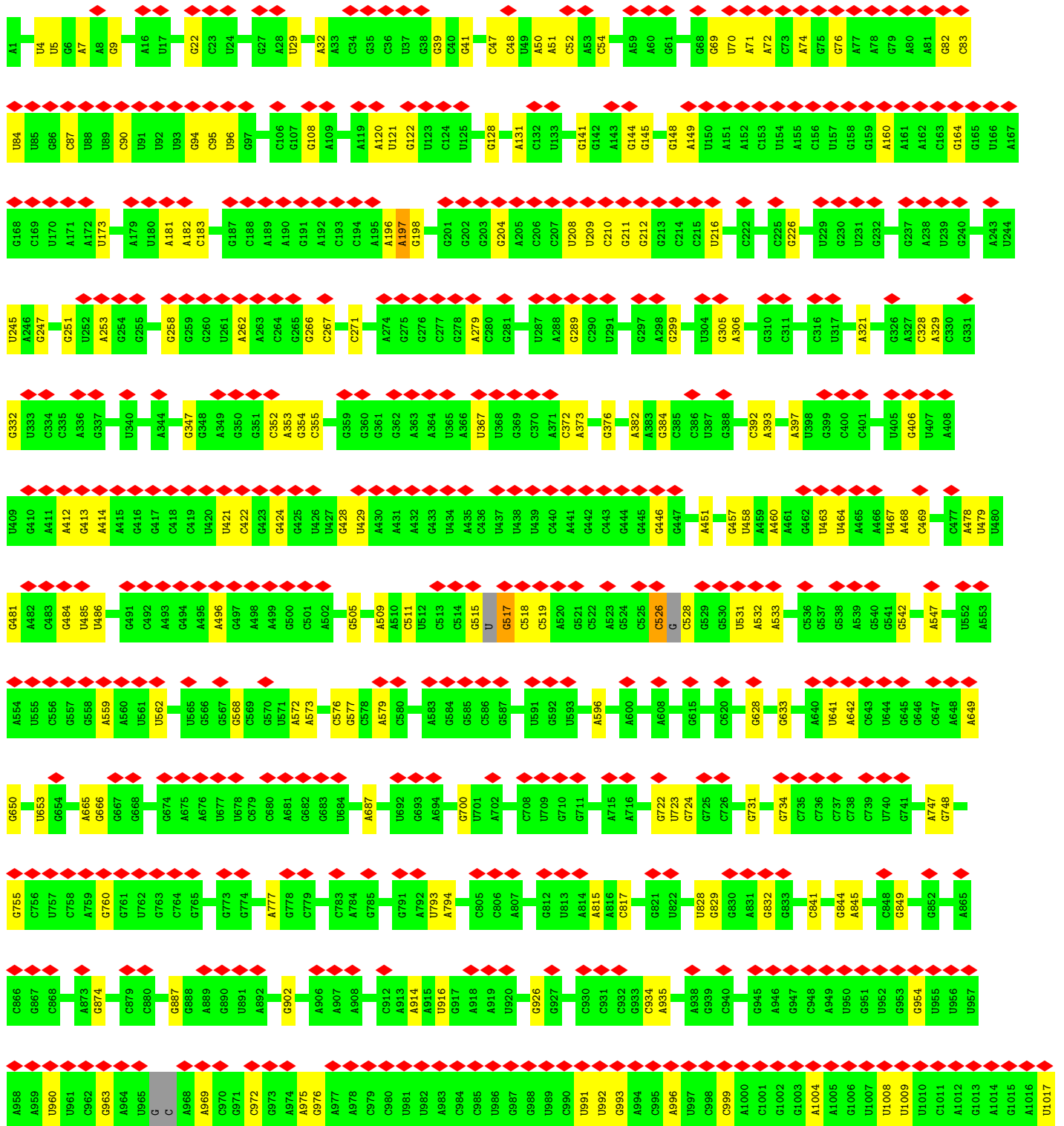
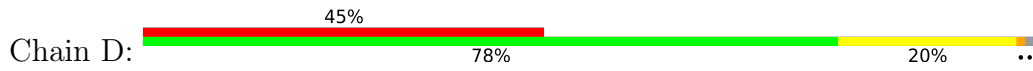
• Molecule 14: DNA-directed RNA polymerase subunit beta'

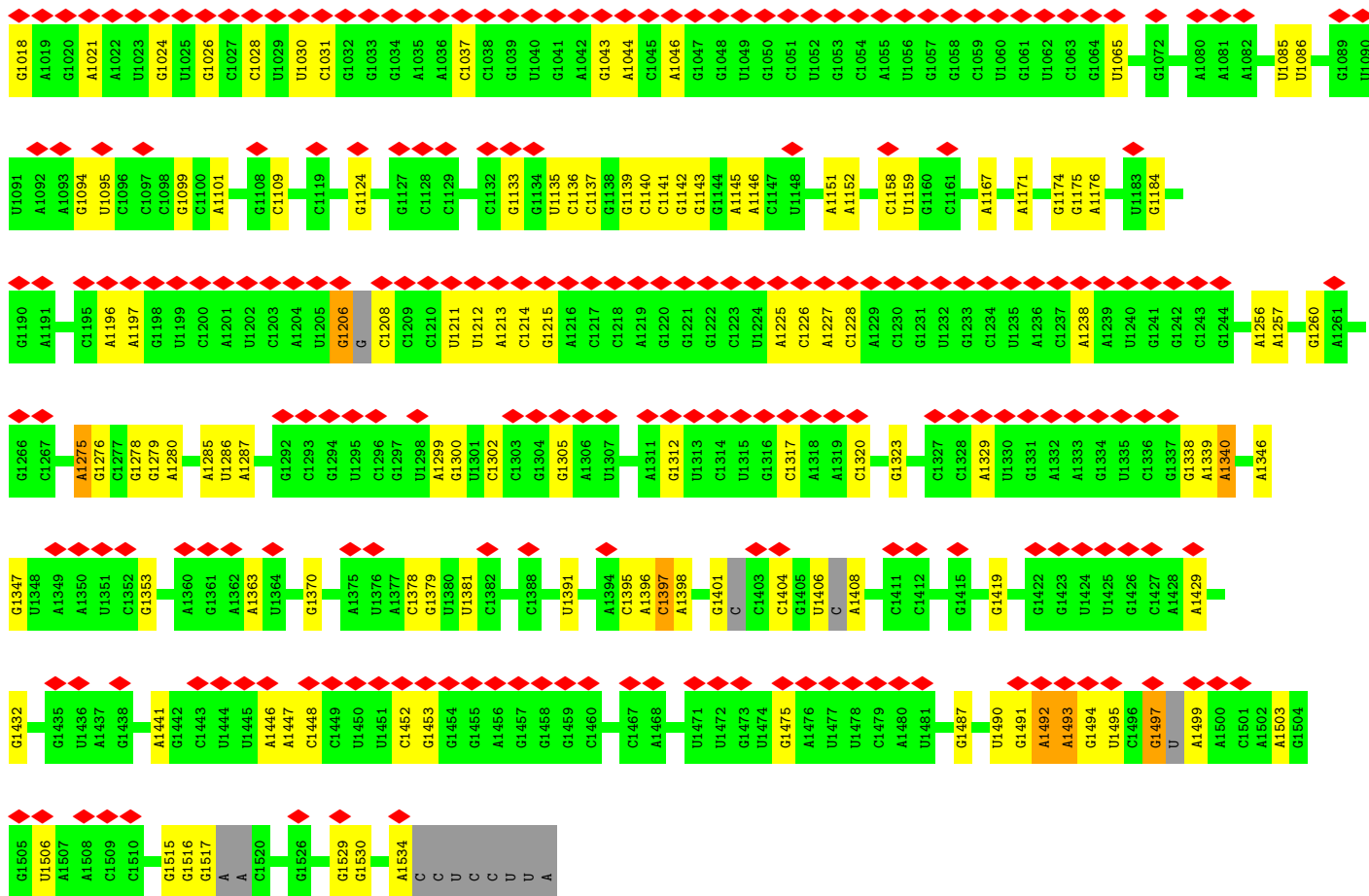
Chain AE:



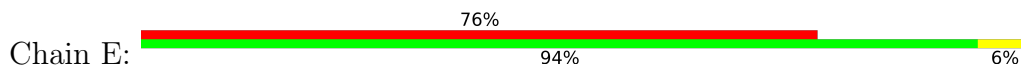


• Molecule 16: 16S rRNA

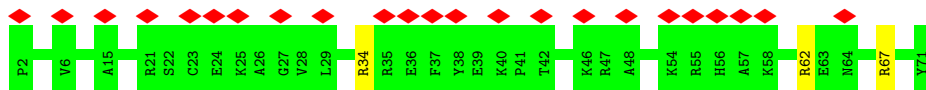




• Molecule 17: 30S ribosomal protein S20

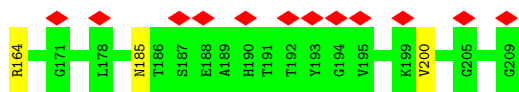


• Molecule 18: 30S ribosomal protein S21

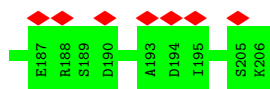
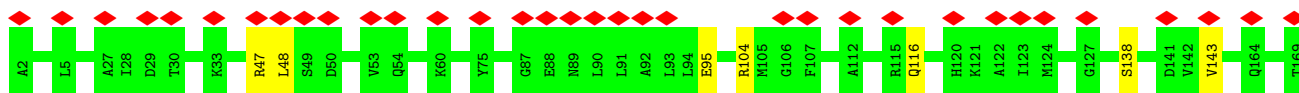


• Molecule 19: 30S ribosomal protein S2

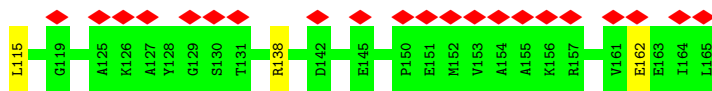
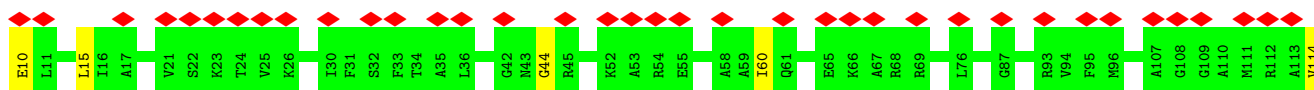




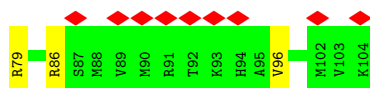
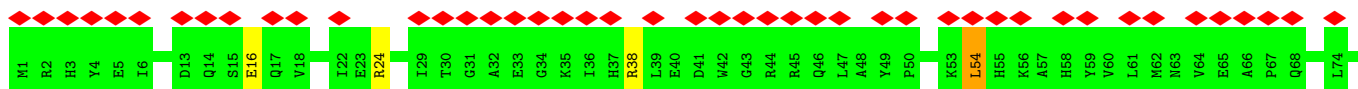
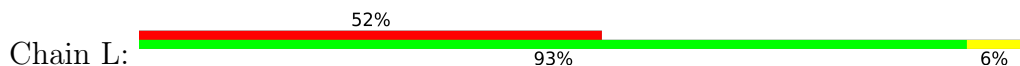
- Molecule 22: 30S ribosomal protein S4



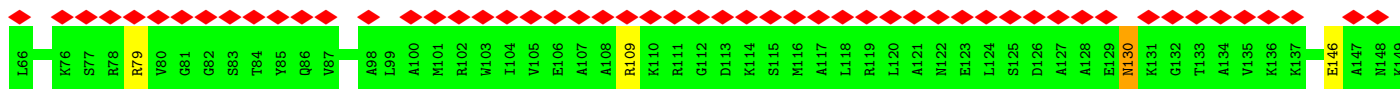
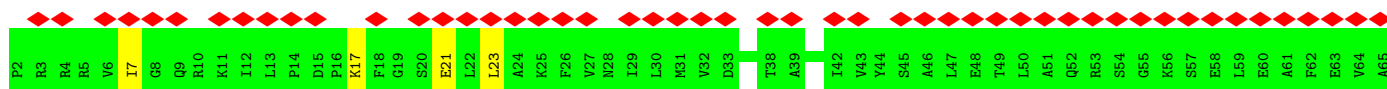
- Molecule 23: 30S ribosomal protein S5



- Molecule 24: 30S ribosomal protein S6

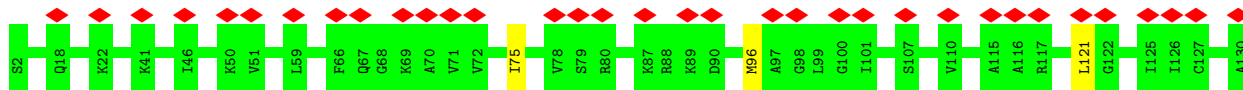


- Molecule 25: 30S ribosomal protein S7

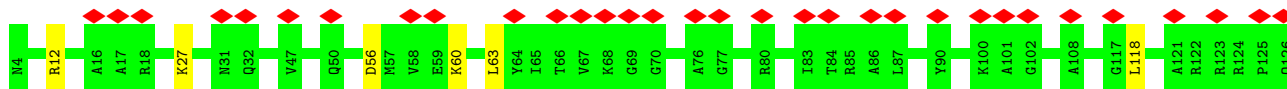




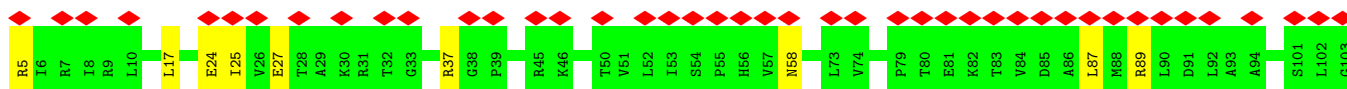
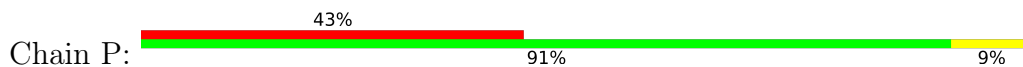
- Molecule 26: 30S ribosomal protein S8



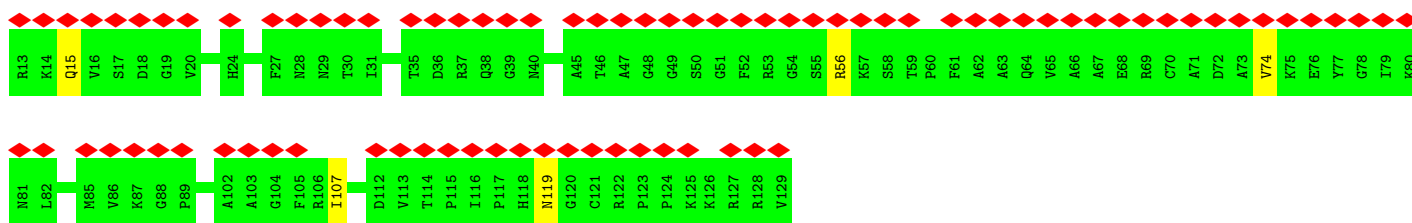
- Molecule 27: 30S ribosomal protein S9



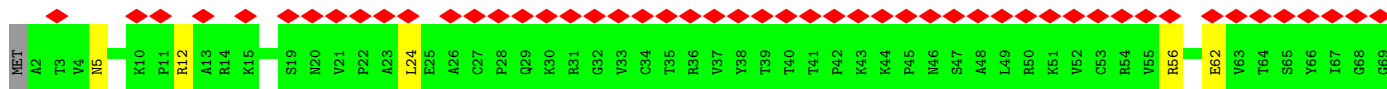
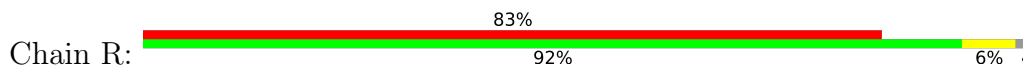
- Molecule 28: 30S ribosomal protein S10

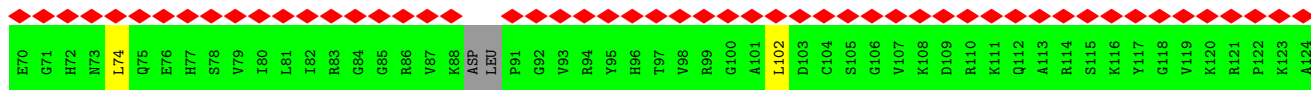


- Molecule 29: 30S ribosomal protein S11

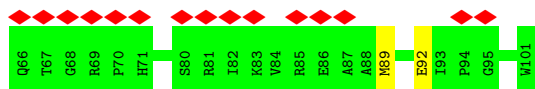
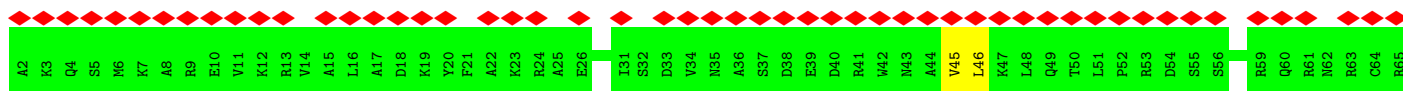
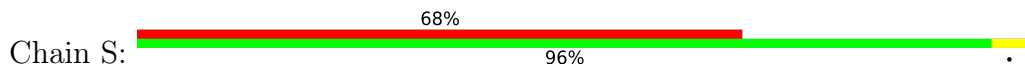


- Molecule 30: 30S ribosomal protein S12

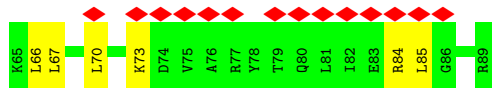
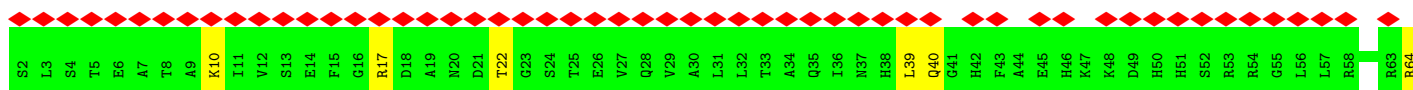
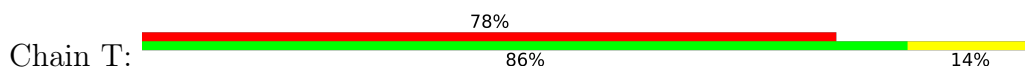




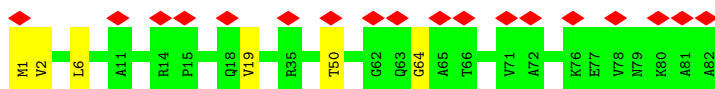
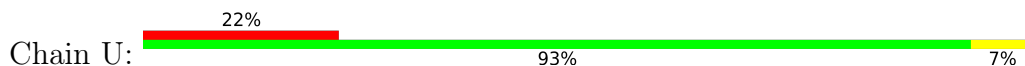
• Molecule 31: 30S ribosomal protein S14



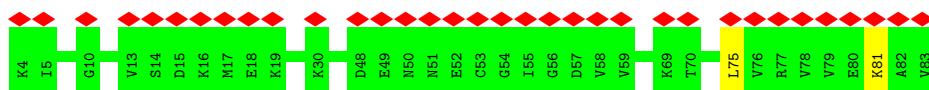
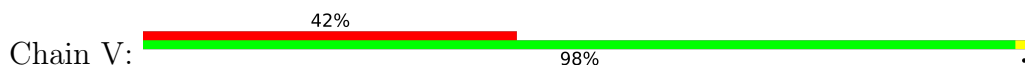
• Molecule 32: 30S ribosomal protein S15



• Molecule 33: 30S ribosomal protein S16

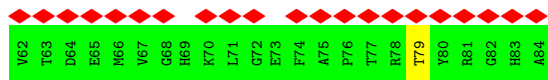


• Molecule 34: 30S ribosomal protein S17

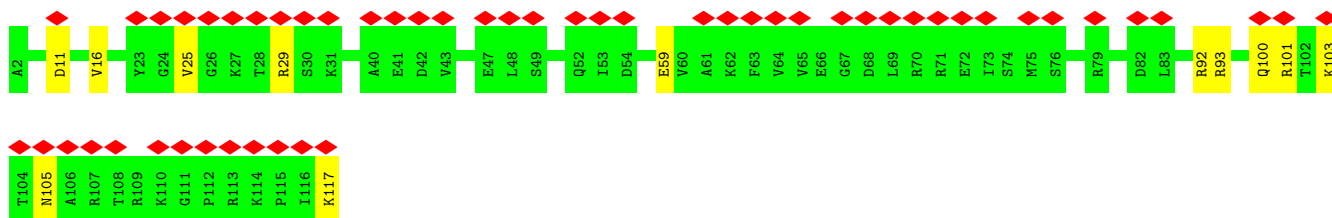
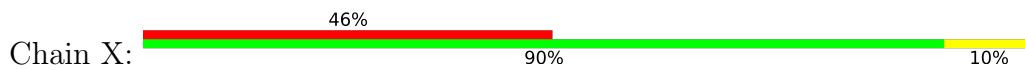


• Molecule 35: 30S ribosomal protein S19

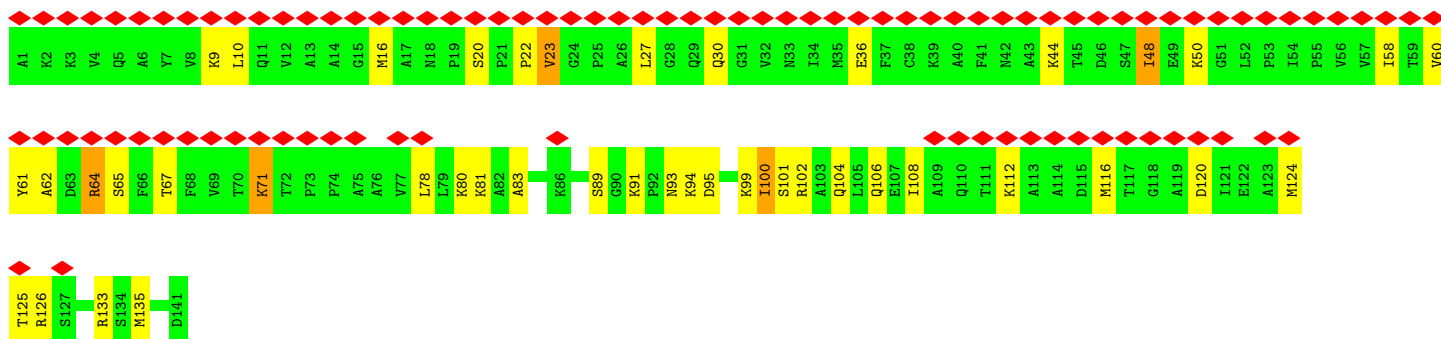




• Molecule 36: 30S ribosomal protein S13



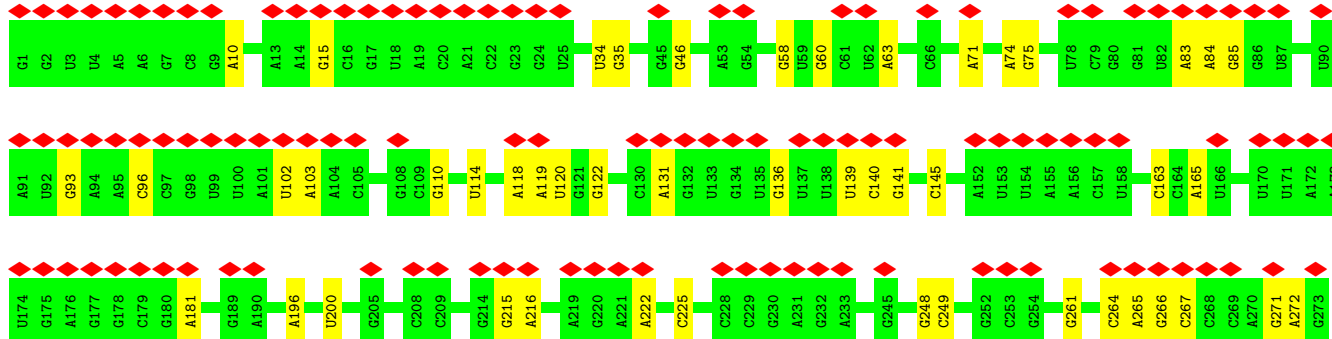
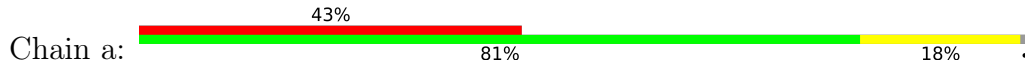
• Molecule 37: 50S ribosomal protein L11

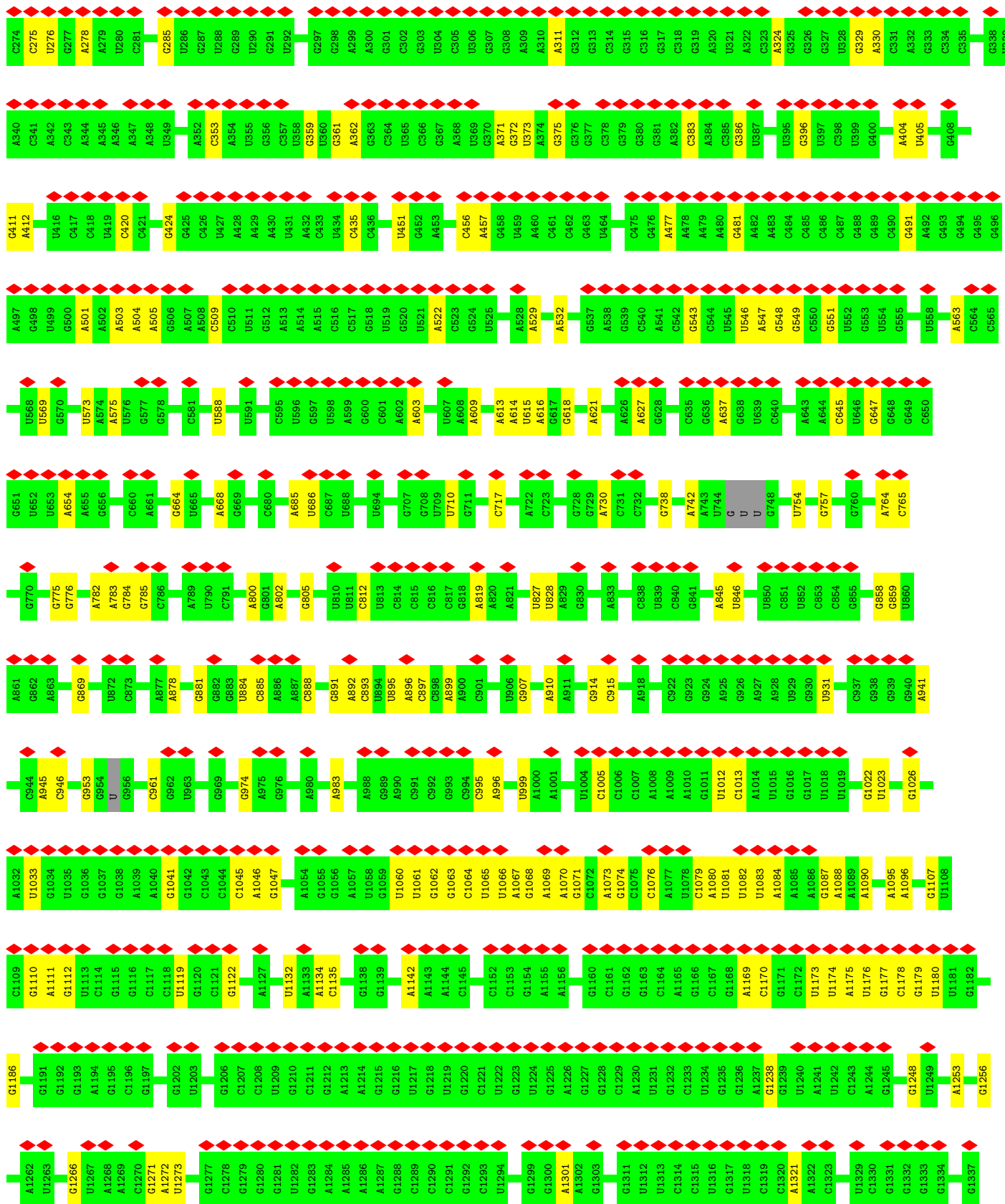


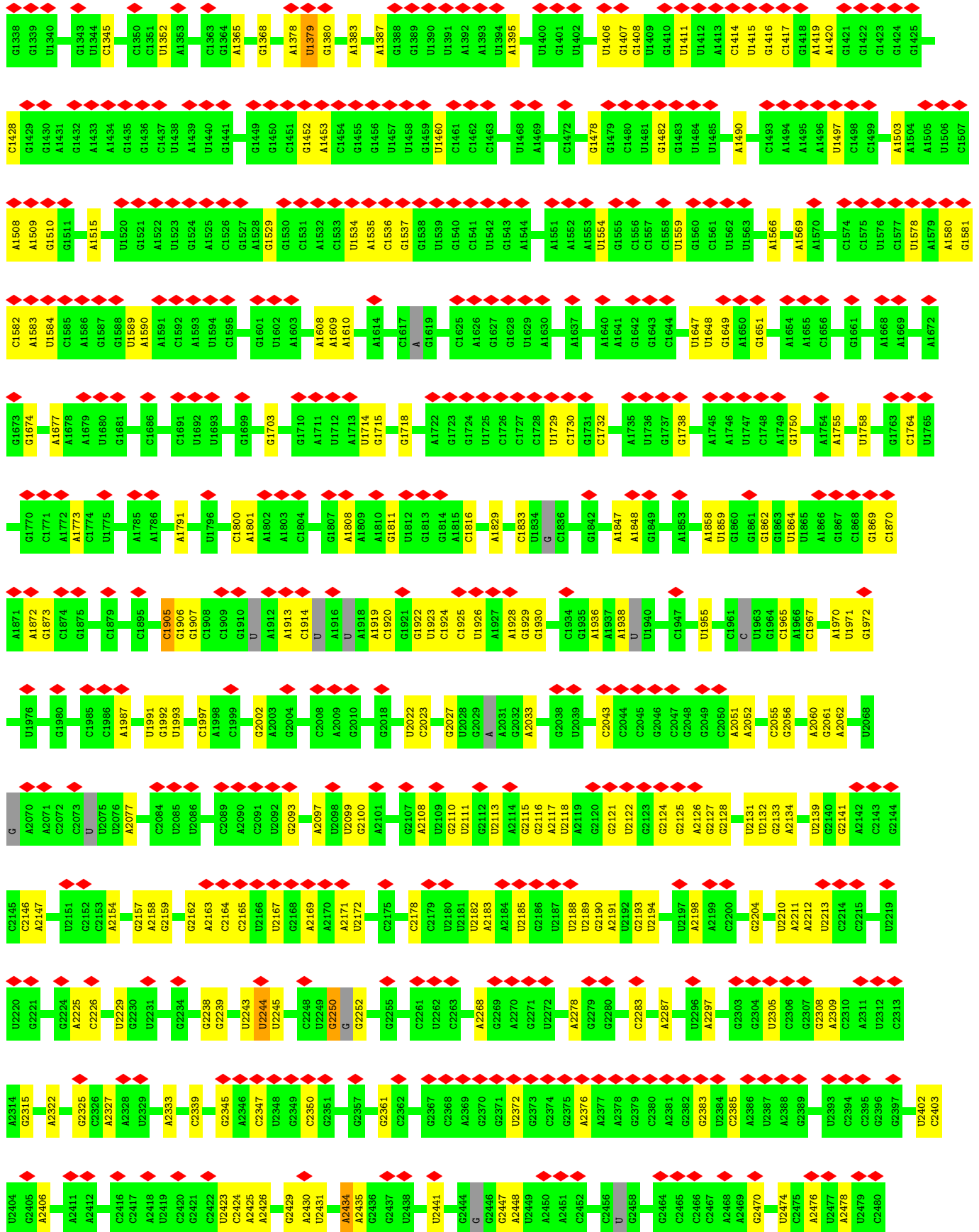
• Molecule 38: 50S ribosomal protein L7/L12

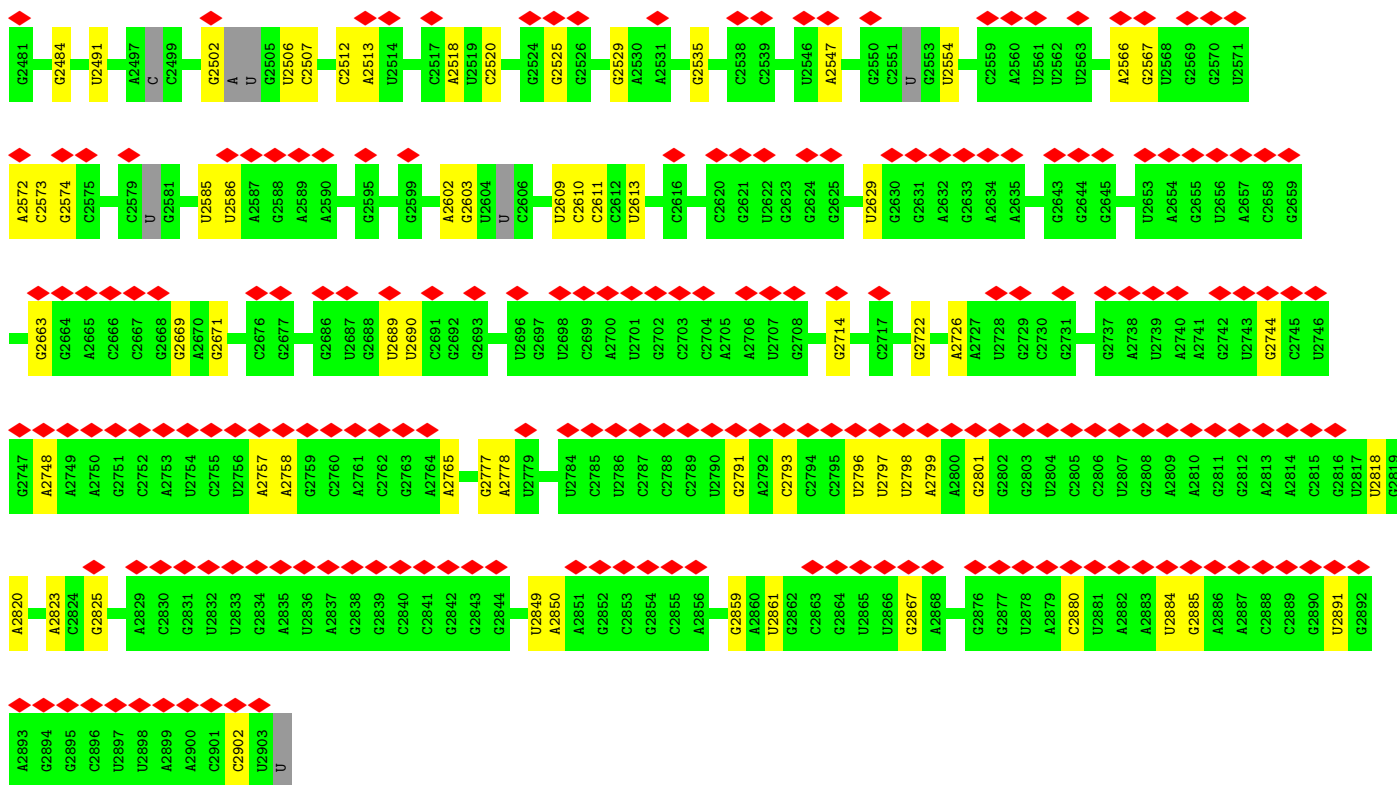


• Molecule 39: 23S rRNA

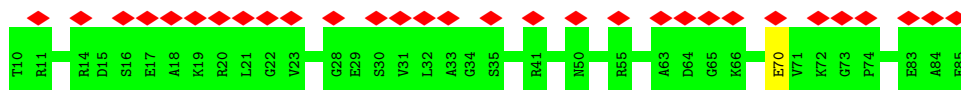
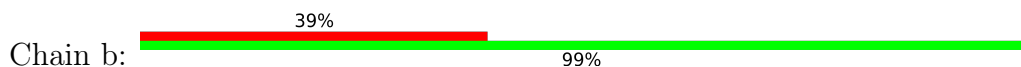




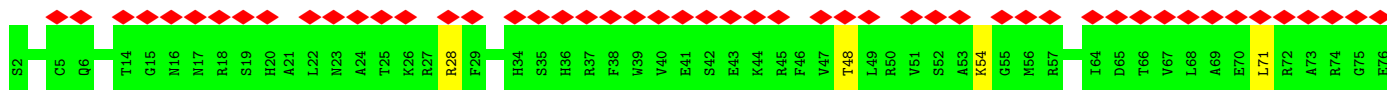




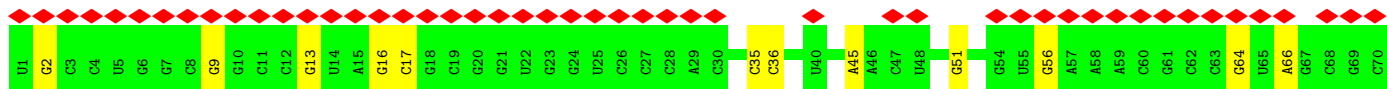
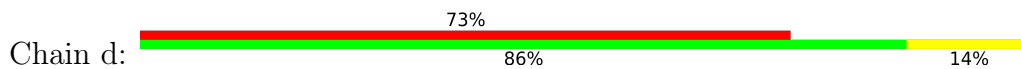
• Molecule 40: 50S ribosomal protein L27

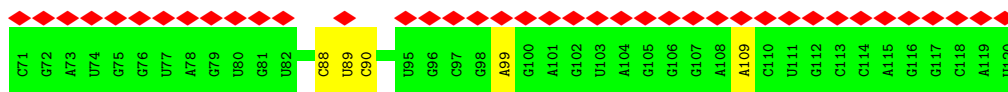


• Molecule 41: 50S ribosomal protein L28

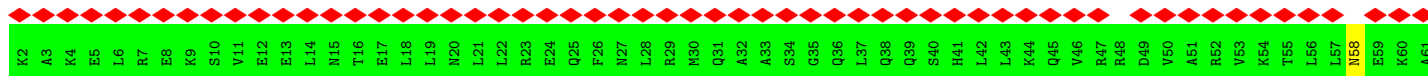


• Molecule 42: 5S rRNA

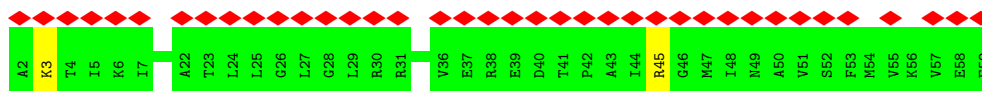




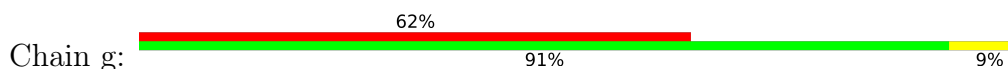
- Molecule 43: 50S ribosomal protein L29



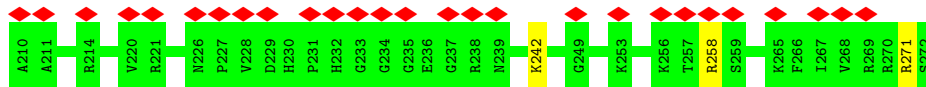
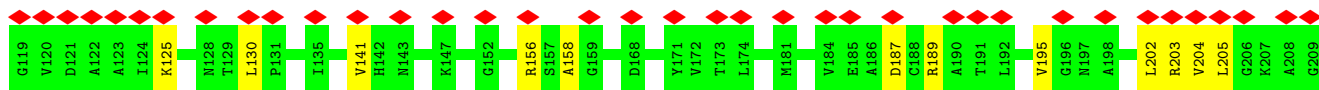
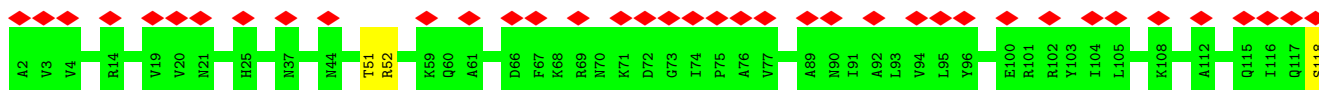
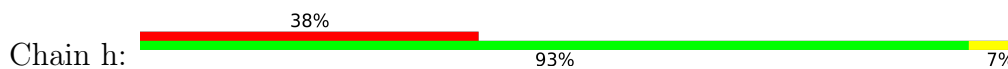
- Molecule 44: 50S ribosomal protein L30



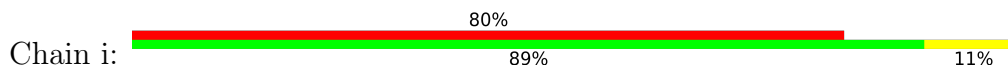
- Molecule 45: 50S ribosomal protein L31

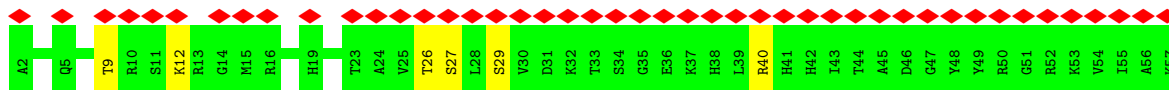


- Molecule 46: 50S ribosomal protein L2

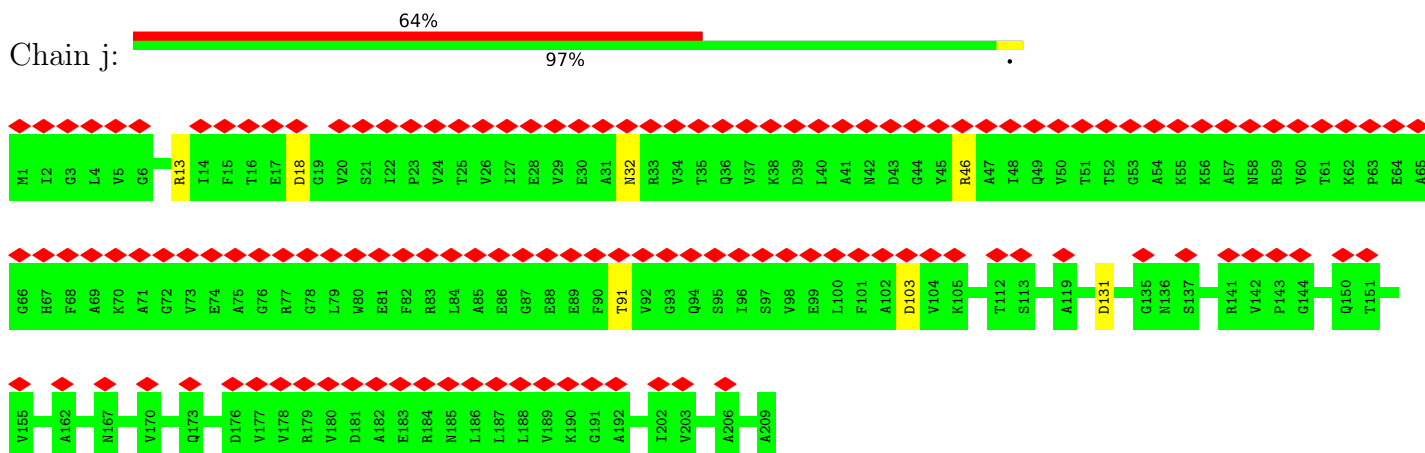


- Molecule 47: 50S ribosomal protein L32

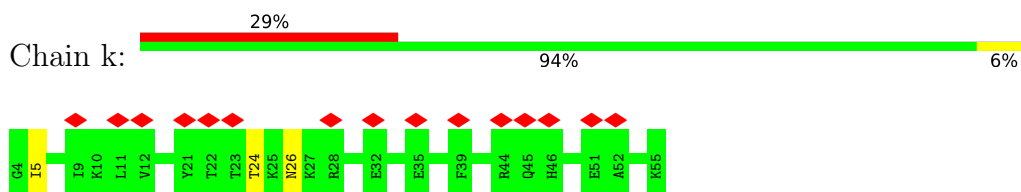




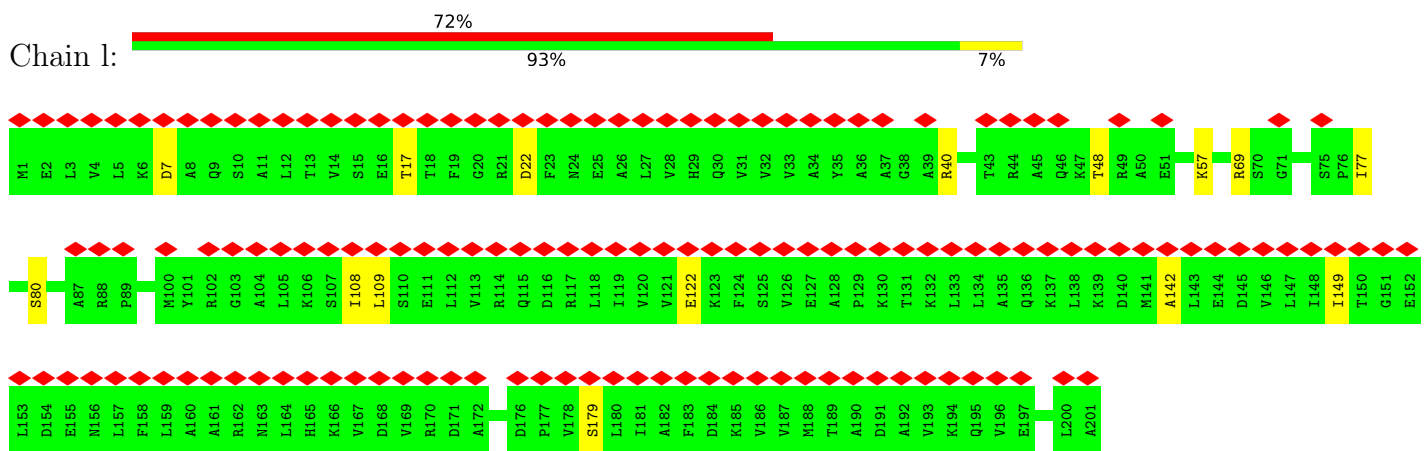
• Molecule 48: 50S ribosomal protein L3



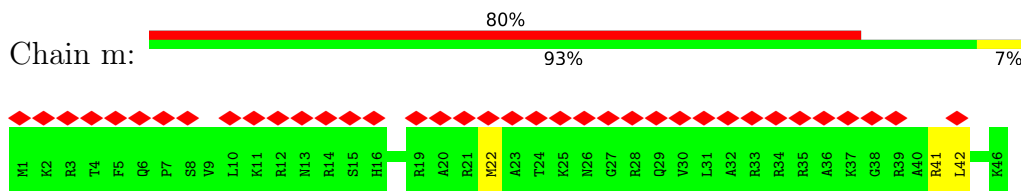
• Molecule 49: 50S ribosomal protein L33



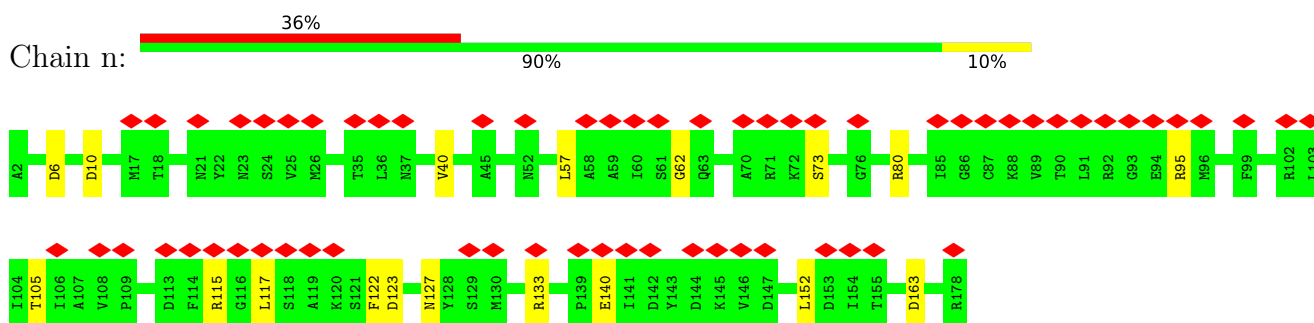
• Molecule 50: 50S ribosomal protein L4



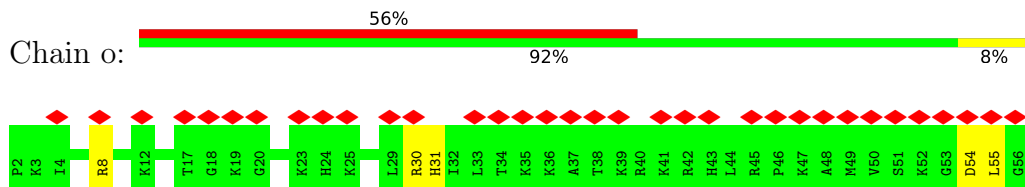
• Molecule 51: 50S ribosomal protein L34



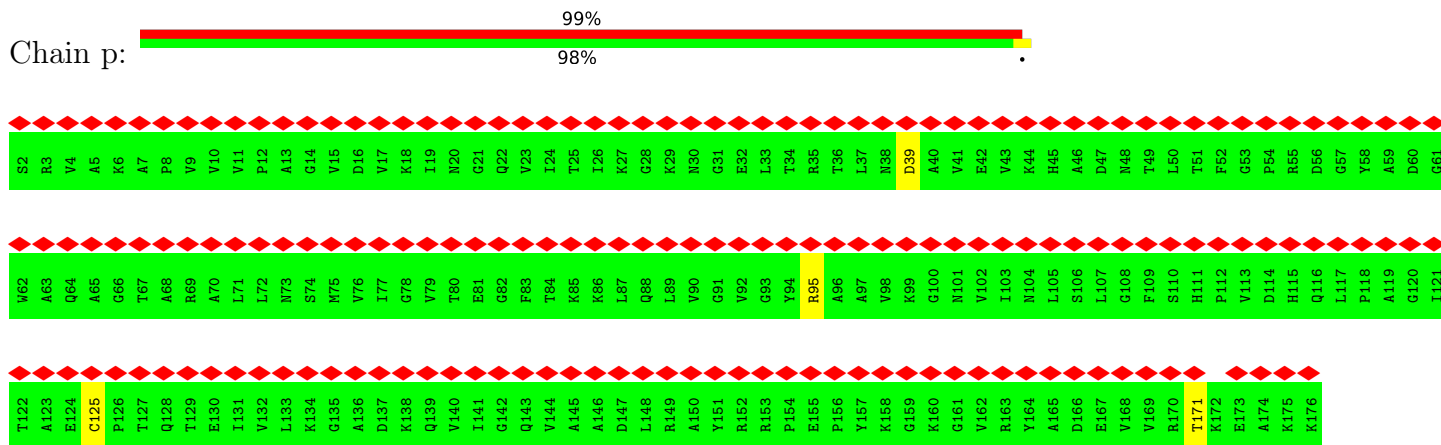
• Molecule 52: 50S ribosomal protein L5



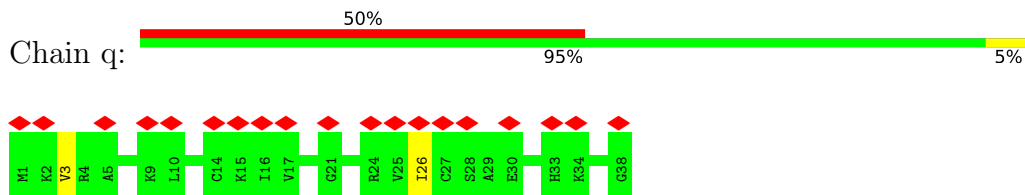
- Molecule 53: 50S ribosomal protein L35



- Molecule 54: 50S ribosomal protein L6



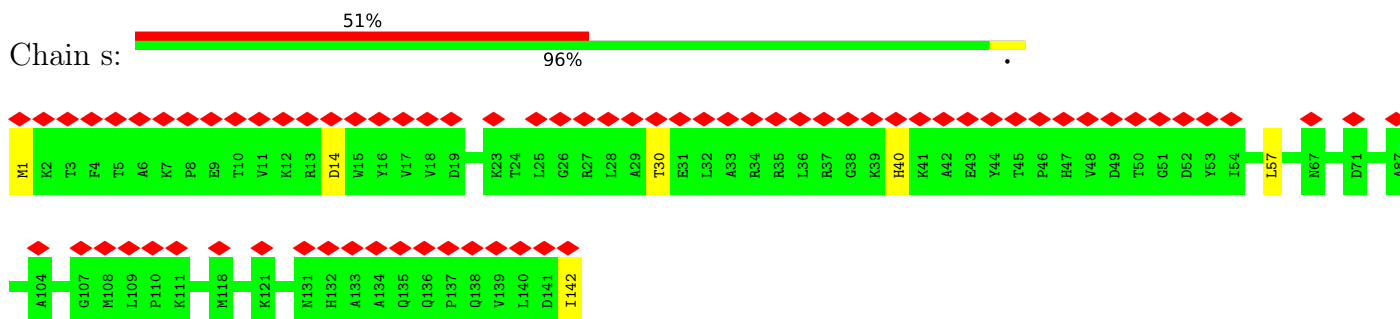
- Molecule 55: 50S ribosomal protein L36



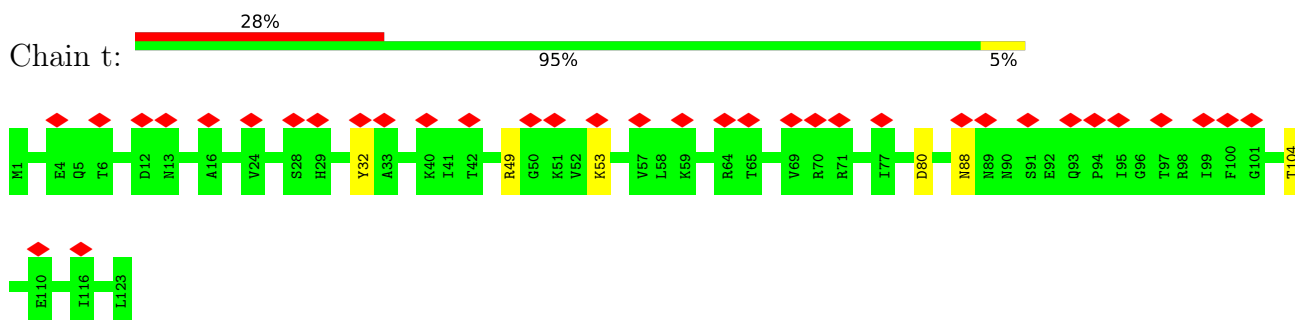
- Molecule 56: 50S ribosomal protein L9



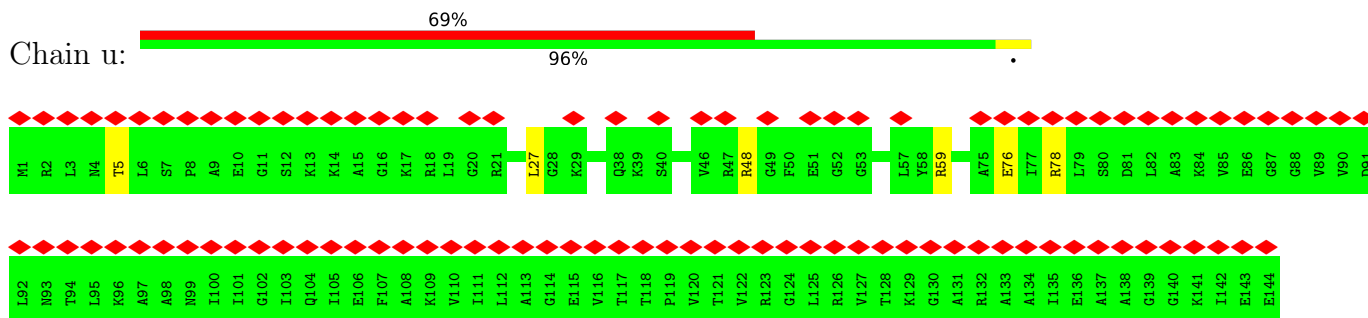
- Molecule 57: 50S ribosomal protein L13



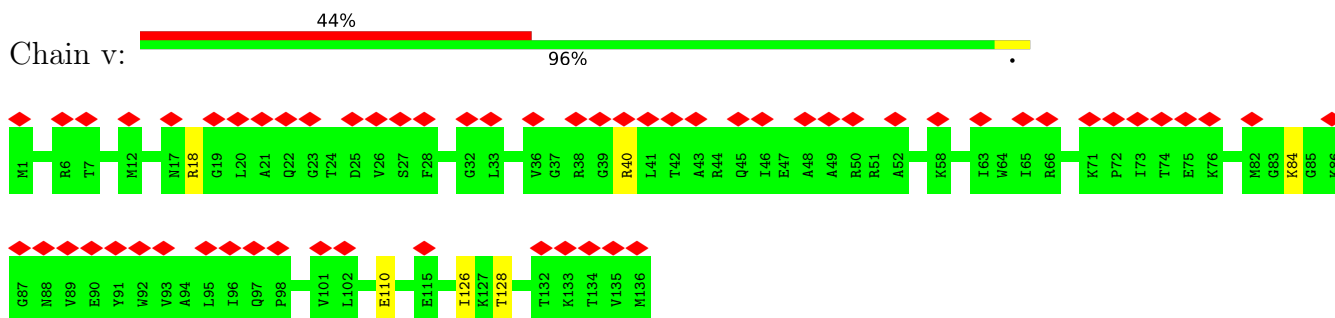
- Molecule 58: 50S ribosomal protein L14



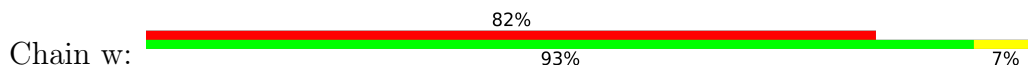
- Molecule 59: 50S ribosomal protein L15

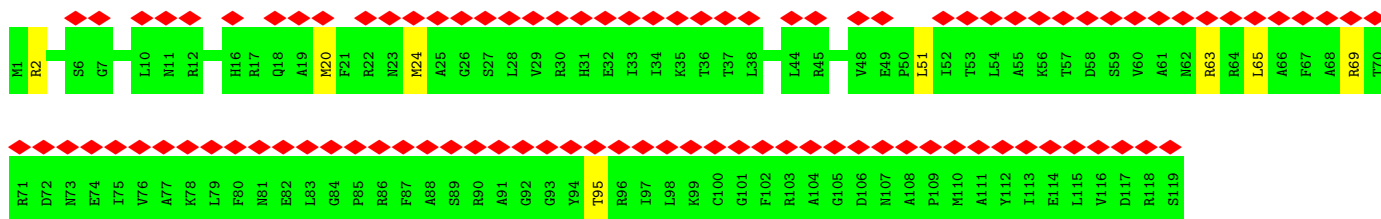


- Molecule 60: 50S ribosomal protein L16

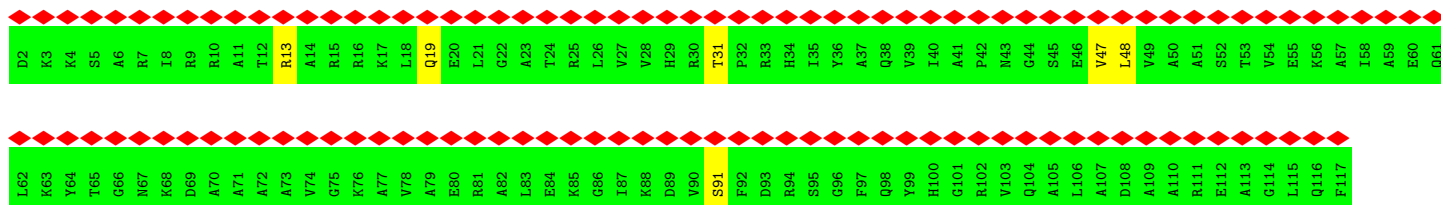


- Molecule 61: 50S ribosomal protein L17

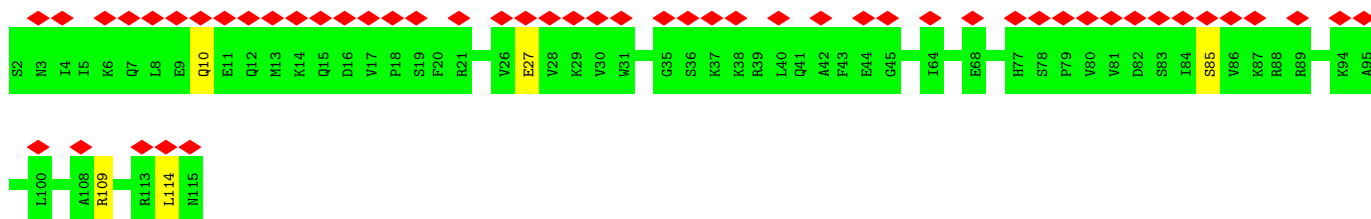




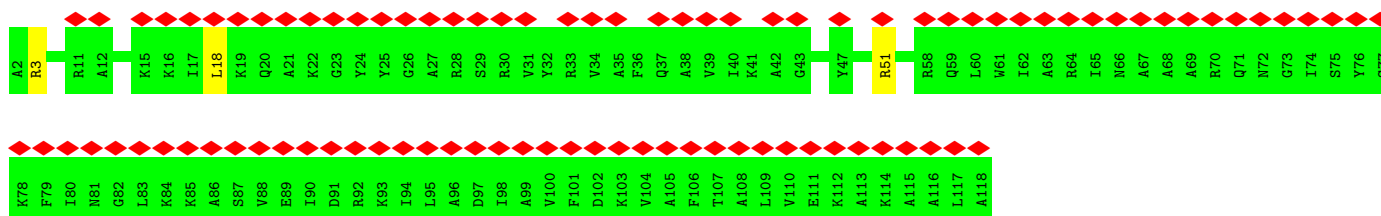
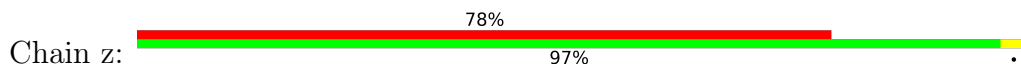
• Molecule 62: 50S ribosomal protein L18



• 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	24959	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	0.093	Depositor
Minimum map value	-0.039	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.007	Depositor
Map size (Å)	548.05, 548.05, 548.05	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0961, 1.0961, 1.0961	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.38	0/829	0.67	0/1107
2	1	0.49	0/864	0.82	0/1156
3	2	0.42	0/752	0.71	0/1005
4	3	0.35	0/796	0.66	2/1062 (0.2%)
5	4	0.40	0/766	0.68	0/1025
6	5	1.13	6/528 (1.1%)	0.97	1/810 (0.1%)
7	6	1.11	4/603 (0.7%)	0.97	0/926
8	7	0.60	2/681 (0.3%)	0.92	3/1058 (0.3%)
9	9	0.79	2/1131 (0.2%)	0.64	1/1524 (0.1%)
10	A	0.38	0/1810	0.75	1/2821 (0.0%)
10	B	0.46	1/1810 (0.1%)	0.86	7/2821 (0.2%)
11	AA	0.58	2/10591 (0.0%)	0.75	15/14289 (0.1%)
12	AB	0.43	0/808	0.59	0/1088
13	AC	0.48	0/1808	0.62	1/2450 (0.0%)
13	AD	0.39	0/1789	0.56	0/2425
14	AE	0.51	4/10545 (0.0%)	0.66	5/14236 (0.0%)
15	C	0.48	0/553	0.83	0/743
16	D	0.34	10/36610 (0.0%)	0.74	30/57091 (0.1%)
17	E	0.57	0/675	0.85	0/895
18	F	0.56	0/597	0.87	0/792
19	G	0.48	0/1791	0.71	0/2413
20	H	0.54	1/1746 (0.1%)	1.03	13/2382 (0.5%)
21	I	0.43	0/1663	0.71	0/2241
22	J	0.47	0/1665	0.73	0/2227
23	K	0.45	0/1165	0.75	0/1568
24	L	0.43	0/867	0.75	1/1171 (0.1%)
25	M	0.50	0/1195	0.81	0/1602
26	N	0.41	0/989	0.69	0/1326
27	O	0.43	0/1034	0.75	0/1375
28	P	0.43	0/800	0.75	0/1082
29	Q	0.40	0/893	0.70	0/1205
30	R	0.35	0/952	0.74	0/1274

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	S	0.49	0/817	0.78	0/1088
32	T	0.53	0/722	0.86	0/964
33	U	0.44	0/659	0.78	0/884
34	V	0.34	0/657	0.61	0/881
35	W	0.38	0/680	0.62	0/915
36	X	0.49	0/909	0.87	0/1215
37	Y	0.67	0/1046	0.59	0/1410
38	Z	0.69	0/227	0.57	0/304
39	a	0.38	3/69247 (0.0%)	0.72	17/107985 (0.0%)
40	b	0.39	0/589	0.71	0/779
41	c	0.48	0/635	0.81	1/848 (0.1%)
42	d	0.29	0/2872	0.70	0/4478
43	e	0.54	0/502	0.83	0/667
44	f	0.45	0/452	0.78	0/605
45	g	0.43	0/531	0.68	0/709
46	h	0.39	0/2121	0.78	0/2852
47	i	0.40	0/450	0.79	0/599
48	j	0.44	0/1586	0.70	0/2134
49	k	0.35	0/433	0.65	0/576
50	l	0.46	0/1571	0.77	0/2113
51	m	0.53	0/380	0.99	0/498
52	n	0.49	0/1434	0.88	3/1926 (0.2%)
53	o	0.45	0/513	0.83	0/676
54	p	0.39	0/1333	0.67	0/1805
55	q	0.37	0/303	0.77	0/397
56	r	0.44	0/1122	0.69	0/1515
57	s	0.50	0/1152	0.75	0/1551
58	t	0.41	0/955	0.78	0/1279
59	u	0.40	0/1062	0.76	0/1413
60	v	0.47	0/1093	0.81	0/1460
61	w	0.52	0/964	0.87	0/1289
62	x	0.46	0/902	0.81	0/1209
63	y	0.41	0/929	0.73	1/1242 (0.1%)
64	z	0.60	0/960	0.91	0/1278
All	All	0.43	35/189114 (0.0%)	0.74	102/278734 (0.0%)

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

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

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	B	0	2
11	AA	0	10
14	AE	0	5
20	H	0	3
36	X	0	1
All	All	0	23

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	13.77	1.70	1.47
16	D	1516	G	O3'-P	-13.35	1.45	1.61
16	D	1339	A	O3'-P	10.56	1.73	1.61
11	AA	374	GLU	C-N	10.40	1.54	1.34
14	AE	88	CYS	CB-SG	-10.19	1.65	1.82

The worst 5 of 102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	D	1516	G	P-O3'-C3'	-19.02	96.88	119.70
16	D	1516	G	O3'-P-O5'	13.81	130.24	104.00
11	AA	1250	SER	C-N-CA	11.16	149.59	121.70
39	a	2252	G	N9-C1'-C2'	-10.93	99.80	114.00
16	D	1401	G	N9-C1'-C2'	-10.69	100.10	114.00

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

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

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [\(i\)](#)

5.3.1 Protein backbone [\(i\)](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	15	51
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
4	3	101/103 (98%)	96 (95%)	4 (4%)	1 (1%)	15	51
5	4	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
9	9	146/148 (99%)	95 (65%)	37 (25%)	14 (10%)	0	8
11	AA	1318/1342 (98%)	1148 (87%)	138 (10%)	32 (2%)	6	35
12	AB	94/181 (52%)	88 (94%)	6 (6%)	0	100	100
13	AC	228/230 (99%)	215 (94%)	11 (5%)	2 (1%)	17	54
13	AD	226/230 (98%)	212 (94%)	14 (6%)	0	100	100
14	AE	1329/1407 (94%)	1199 (90%)	121 (9%)	9 (1%)	22	59
15	C	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
17	E	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
18	F	68/70 (97%)	68 (100%)	0	0	100	100
19	G	223/225 (99%)	210 (94%)	13 (6%)	0	100	100
20	H	255/557 (46%)	188 (74%)	55 (22%)	12 (5%)	2	23
21	I	206/208 (99%)	196 (95%)	9 (4%)	1 (0%)	29	66
22	J	203/205 (99%)	198 (98%)	5 (2%)	0	100	100
23	K	154/156 (99%)	146 (95%)	7 (4%)	1 (1%)	25	62
24	L	102/104 (98%)	97 (95%)	4 (4%)	1 (1%)	15	51
25	M	149/151 (99%)	144 (97%)	4 (3%)	1 (1%)	22	59
26	N	127/129 (98%)	121 (95%)	5 (4%)	1 (1%)	19	56
27	O	125/127 (98%)	115 (92%)	9 (7%)	1 (1%)	19	56
28	P	97/99 (98%)	88 (91%)	8 (8%)	1 (1%)	15	51
29	Q	115/117 (98%)	104 (90%)	9 (8%)	2 (2%)	9	42

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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	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
32	T	86/88 (98%)	82 (95%)	4 (5%)	0	100	100
33	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	12	47
34	V	78/80 (98%)	74 (95%)	4 (5%)	0	100	100
35	W	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
36	X	114/116 (98%)	107 (94%)	5 (4%)	2 (2%)	8	41
37	Y	139/141 (99%)	102 (73%)	25 (18%)	12 (9%)	1	10
38	Z	28/30 (93%)	19 (68%)	7 (25%)	2 (7%)	1	15
40	b	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
41	c	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
43	e	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
44	f	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
45	g	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
46	h	269/271 (99%)	259 (96%)	9 (3%)	1 (0%)	34	69
47	i	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
48	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
49	k	50/52 (96%)	50 (100%)	0	0	100	100
50	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	29	66
51	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
52	n	175/177 (99%)	162 (93%)	11 (6%)	2 (1%)	14	50
53	o	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
54	p	173/175 (99%)	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	117/119 (98%)	107 (92%)	10 (8%)	0	100	100
62	x	114/116 (98%)	108 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	y	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
64	z	115/117 (98%)	110 (96%)	4 (4%)	1 (1%)	17	54
All	All	9368/9974 (94%)	8603 (92%)	663 (7%)	102 (1%)	18	50

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 [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	78 (93%)	6 (7%)	14	45
2	1	93/93 (100%)	84 (90%)	9 (10%)	8	33
3	2	81/81 (100%)	76 (94%)	5 (6%)	18	49
4	3	84/84 (100%)	78 (93%)	6 (7%)	14	45
5	4	78/78 (100%)	74 (95%)	4 (5%)	24	55
9	9	112/112 (100%)	65 (58%)	47 (42%)	0	0
11	AA	1140/1157 (98%)	1039 (91%)	101 (9%)	9	37
12	AB	86/158 (54%)	84 (98%)	2 (2%)	50	71
13	AC	198/198 (100%)	182 (92%)	16 (8%)	11	41
13	AD	196/198 (99%)	194 (99%)	2 (1%)	76	86
14	AE	1120/1168 (96%)	1051 (94%)	69 (6%)	18	49
15	C	57/57 (100%)	55 (96%)	2 (4%)	36	63
17	E	65/65 (100%)	60 (92%)	5 (8%)	13	43
18	F	60/60 (100%)	57 (95%)	3 (5%)	24	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	G	187/187 (100%)	178 (95%)	9 (5%)	25	56
20	H	137/461 (30%)	128 (93%)	9 (7%)	16	48
21	I	171/171 (100%)	165 (96%)	6 (4%)	36	63
22	J	172/172 (100%)	165 (96%)	7 (4%)	30	59
23	K	119/119 (100%)	112 (94%)	7 (6%)	19	51
24	L	91/91 (100%)	85 (93%)	6 (7%)	16	48
25	M	124/124 (100%)	116 (94%)	8 (6%)	17	48
26	N	104/104 (100%)	102 (98%)	2 (2%)	57	76
27	O	105/105 (100%)	100 (95%)	5 (5%)	25	56
28	P	86/86 (100%)	78 (91%)	8 (9%)	9	35
29	Q	90/90 (100%)	87 (97%)	3 (3%)	38	64
30	R	101/104 (97%)	94 (93%)	7 (7%)	15	46
31	S	83/83 (100%)	79 (95%)	4 (5%)	25	56
32	T	76/76 (100%)	64 (84%)	12 (16%)	2	16
33	U	65/65 (100%)	60 (92%)	5 (8%)	13	43
34	V	74/74 (100%)	72 (97%)	2 (3%)	44	68
35	W	72/72 (100%)	68 (94%)	4 (6%)	21	53
36	X	94/94 (100%)	85 (90%)	9 (10%)	8	34
37	Y	109/109 (100%)	72 (66%)	37 (34%)	0	1
38	Z	26/26 (100%)	12 (46%)	14 (54%)	0	0
40	b	58/58 (100%)	57 (98%)	1 (2%)	60	79
41	c	67/67 (100%)	64 (96%)	3 (4%)	27	57
43	e	54/54 (100%)	53 (98%)	1 (2%)	57	76
44	f	48/48 (100%)	46 (96%)	2 (4%)	30	59
45	g	59/59 (100%)	53 (90%)	6 (10%)	7	31
46	h	216/216 (100%)	199 (92%)	17 (8%)	12	42
47	i	47/47 (100%)	41 (87%)	6 (13%)	4	23
48	j	164/164 (100%)	157 (96%)	7 (4%)	29	58
49	k	47/47 (100%)	44 (94%)	3 (6%)	17	48
50	l	165/165 (100%)	151 (92%)	14 (8%)	10	40
51	m	38/38 (100%)	35 (92%)	3 (8%)	12	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	n	148/148 (100%)	134 (90%)	14 (10%)	8	34
53	o	51/51 (100%)	46 (90%)	5 (10%)	8	33
54	p	136/136 (100%)	132 (97%)	4 (3%)	42	66
55	q	34/34 (100%)	32 (94%)	2 (6%)	19	51
56	r	114/114 (100%)	104 (91%)	10 (9%)	10	38
57	s	116/116 (100%)	110 (95%)	6 (5%)	23	55
58	t	104/104 (100%)	98 (94%)	6 (6%)	20	52
59	u	103/103 (100%)	97 (94%)	6 (6%)	20	52
60	v	109/109 (100%)	103 (94%)	6 (6%)	21	53
61	w	99/99 (100%)	91 (92%)	8 (8%)	11	41
62	x	86/86 (100%)	80 (93%)	6 (7%)	15	45
63	y	99/99 (100%)	95 (96%)	4 (4%)	31	60
64	z	89/89 (100%)	87 (98%)	2 (2%)	52	72
All	All	7791/8257 (94%)	7208 (92%)	583 (8%)	17	43

5 of 583 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	h	195	VAL
62	x	31	THR
47	i	40	ARG
46	h	189	ARG
53	o	31	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
9	9	103	ASN
19	G	18	HIS
36	X	105	ASN

5.3.3 RNA [i](#)

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

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	75/76 (98%)	35 (46%)	6 (8%)
16	D	1515/1542 (98%)	289 (19%)	35 (2%)
39	a	2859/2904 (98%)	532 (18%)	0
42	d	119/120 (99%)	17 (14%)	0
8	7	28/29 (96%)	18 (64%)	4 (14%)
All	All	4671/4747 (98%)	920 (19%)	51 (1%)

5 of 920 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-6	G
8	7	-5	U
8	7	-4	U
8	7	-2	U
8	7	-1	U

5 of 51 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	D	531	U
16	D	992	U
16	D	1492	A
16	D	532	A
16	D	722	G

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides 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.

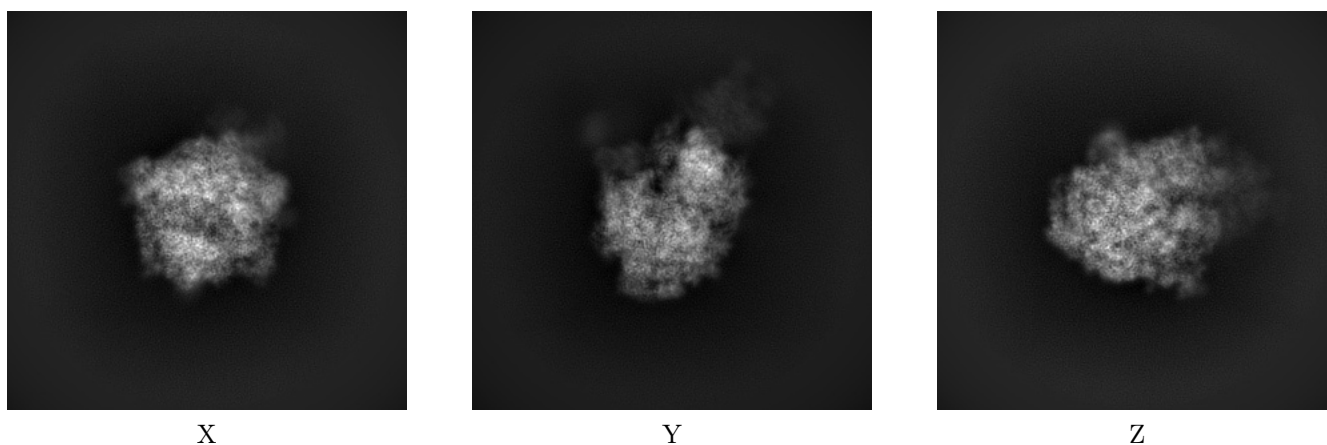
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21386. 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](#)

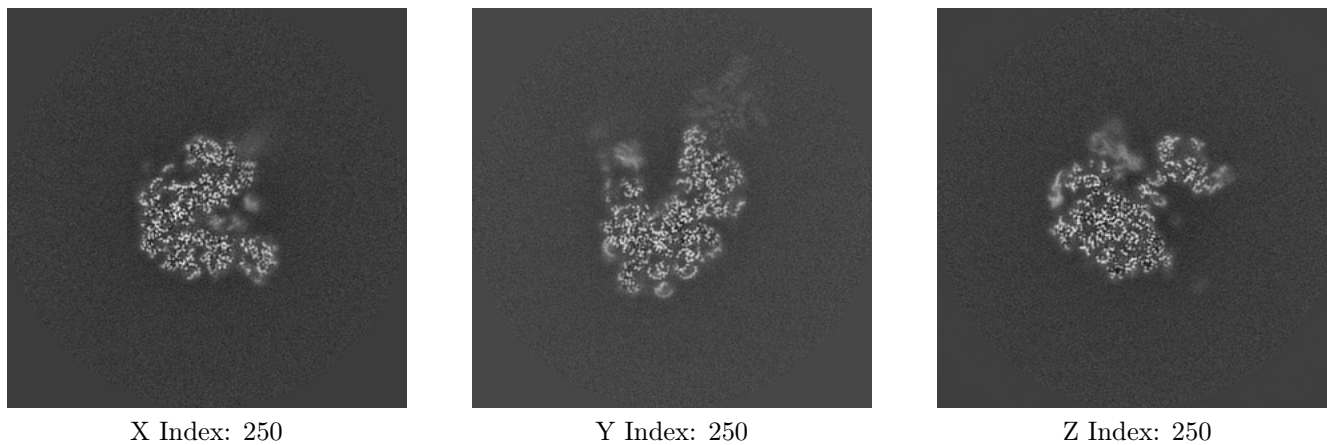
6.1.1 Primary map



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

6.2 Central slices [i](#)

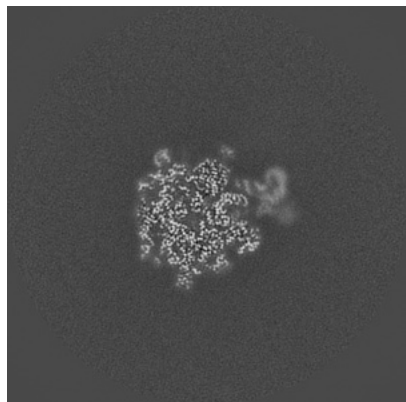
6.2.1 Primary map



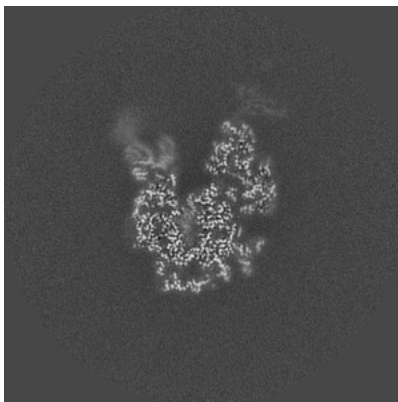
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

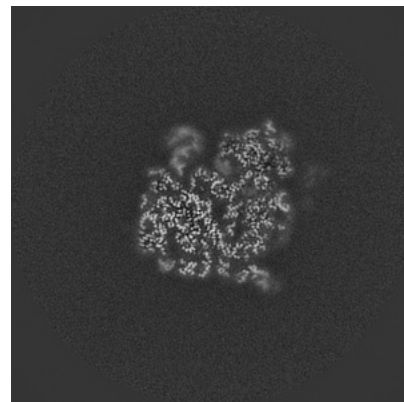
6.3.1 Primary map



X Index: 215



Y Index: 233

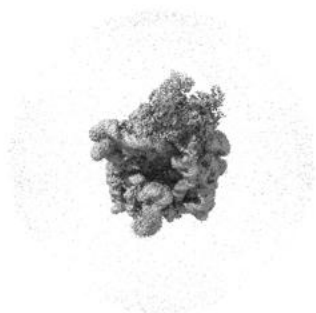


Z Index: 271

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

6.4 Orthogonal surface views [i](#)

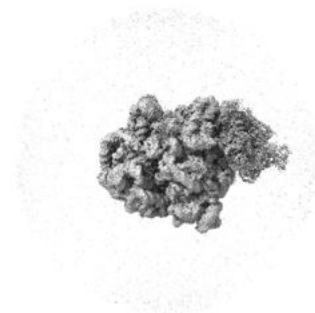
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.007. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

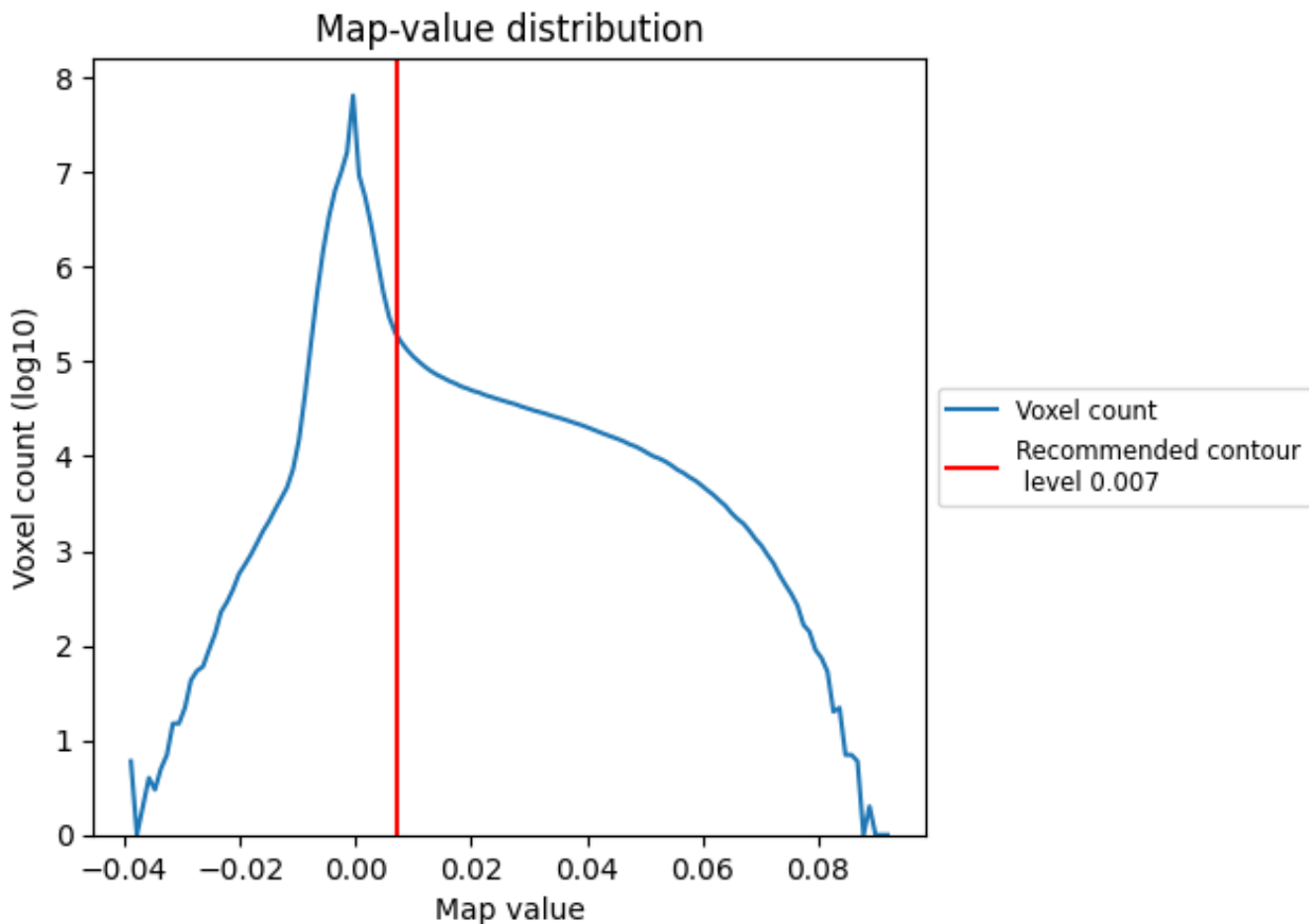
6.5 Mask visualisation

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

7 Map analysis [i](#)

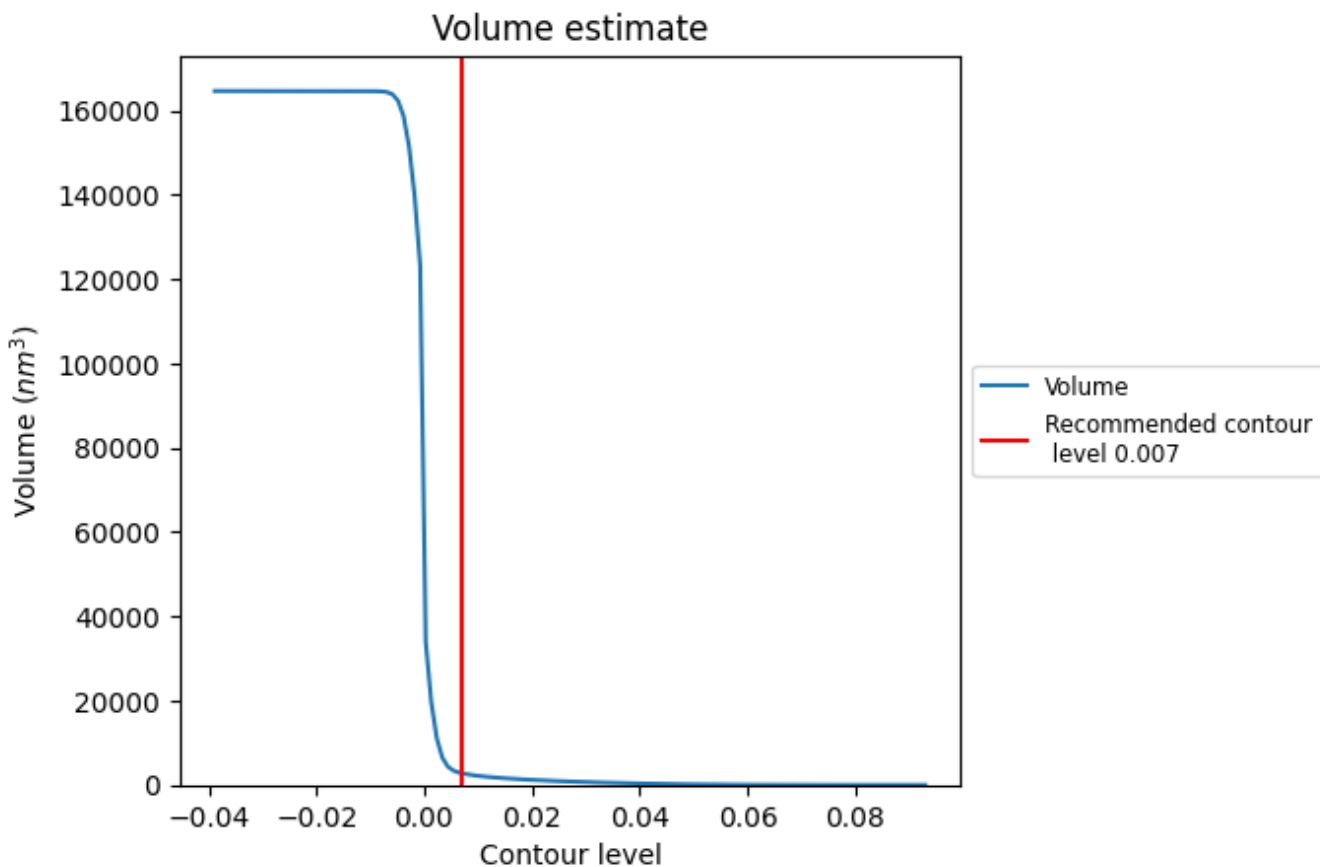
This section contains the results of statistical analysis of the map.

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.

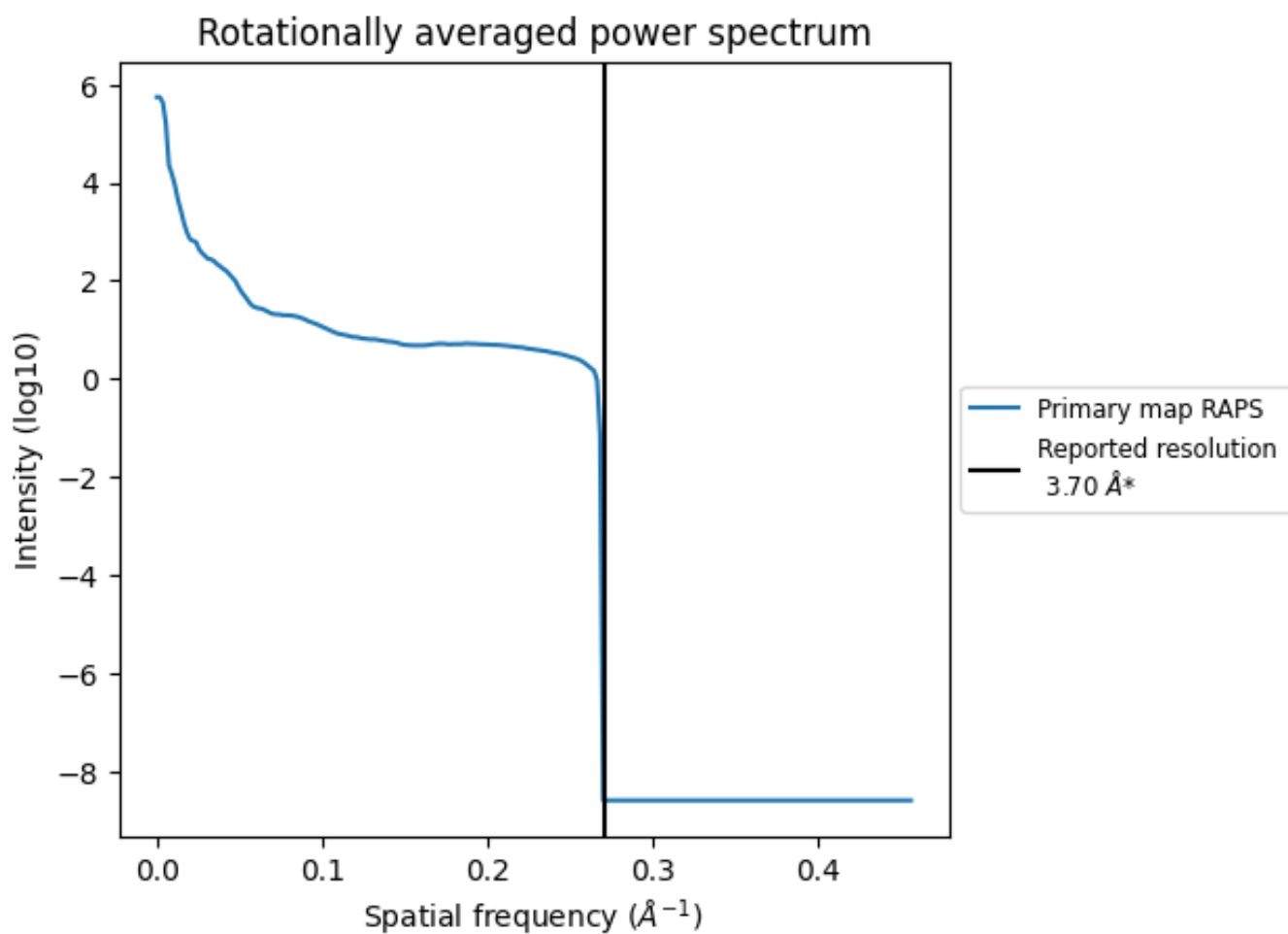
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2788 nm^3 ; this corresponds to an approximate mass of 2518 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 i

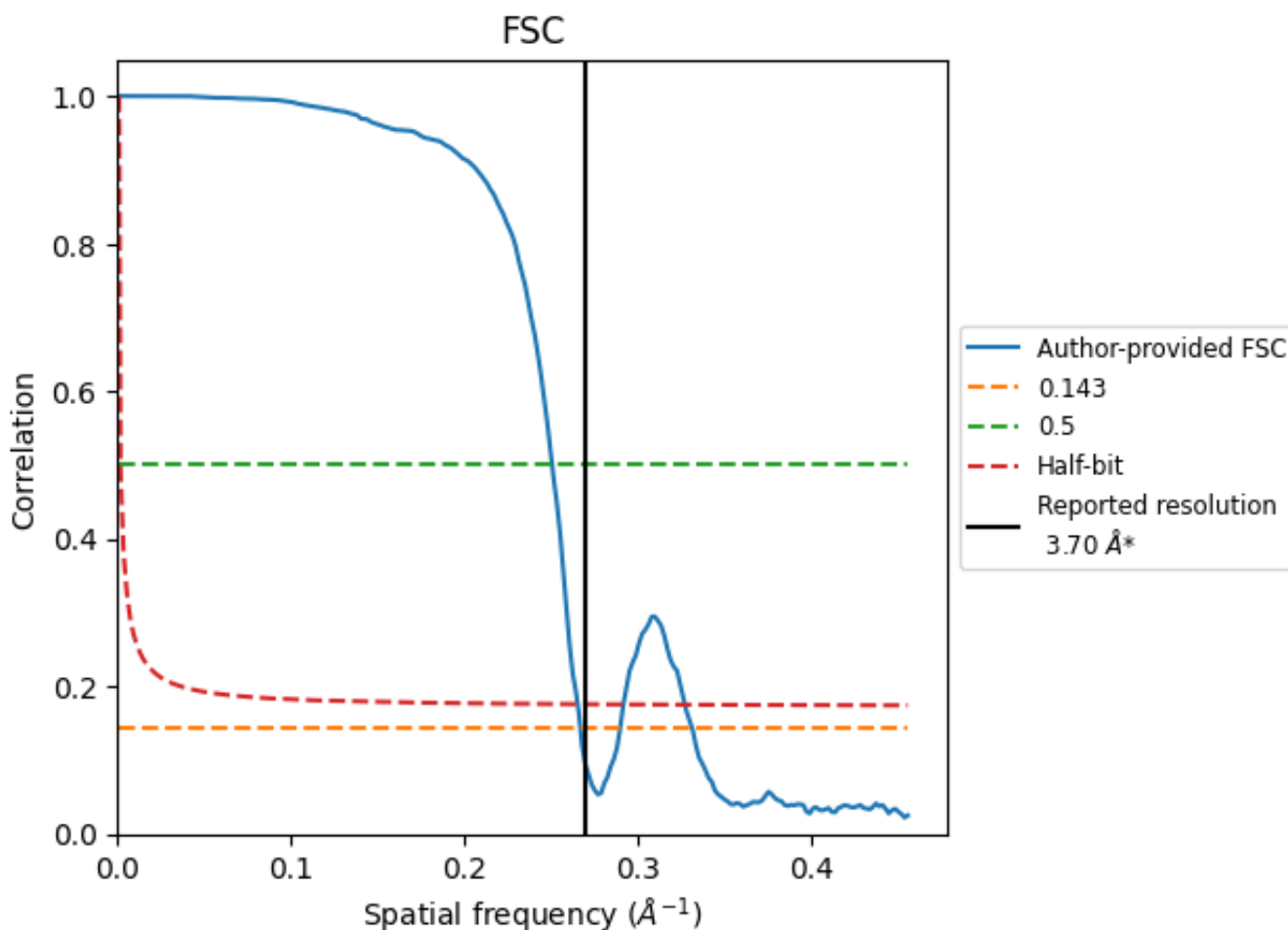


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [\(i\)](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

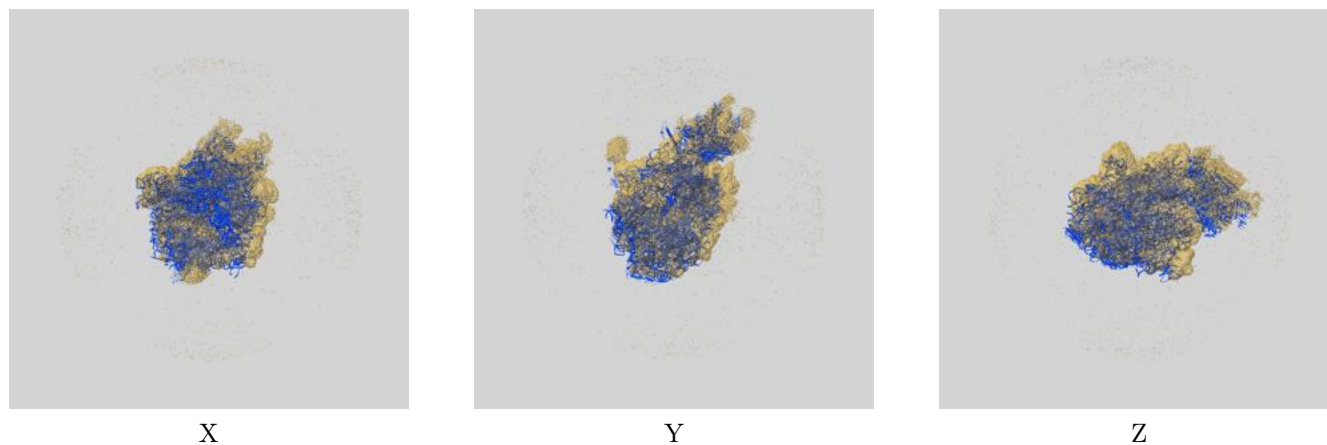
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.74	3.99	3.77
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

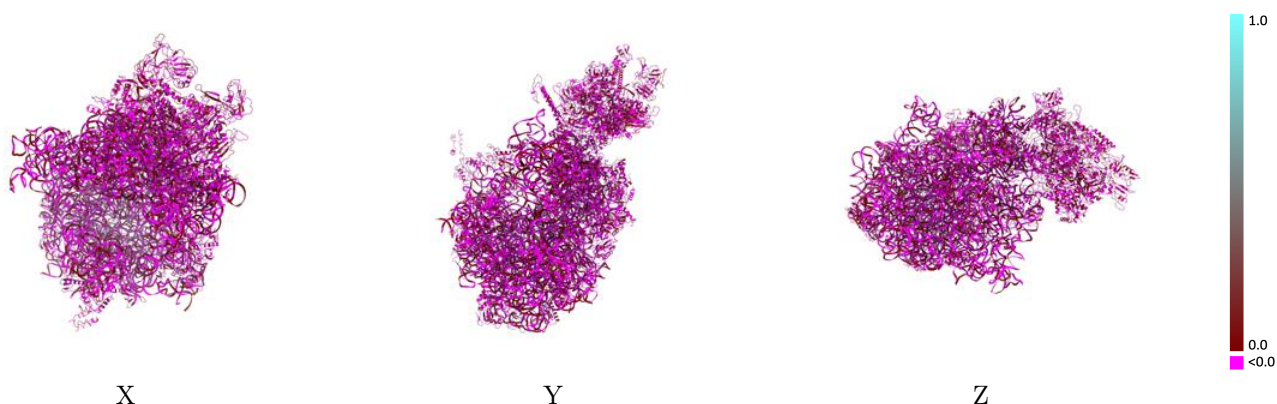
This section contains information regarding the fit between EMDB map EMD-21386 and PDB model 6VU3. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



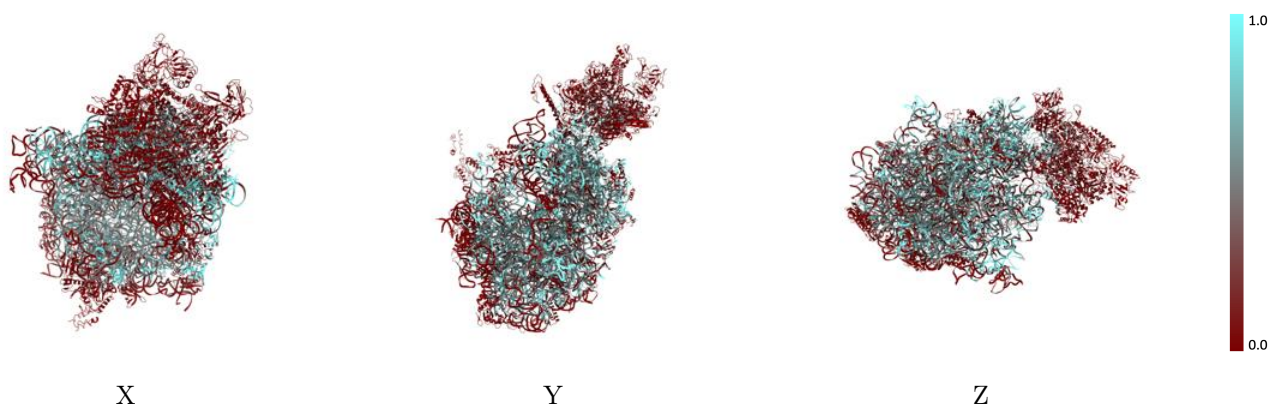
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



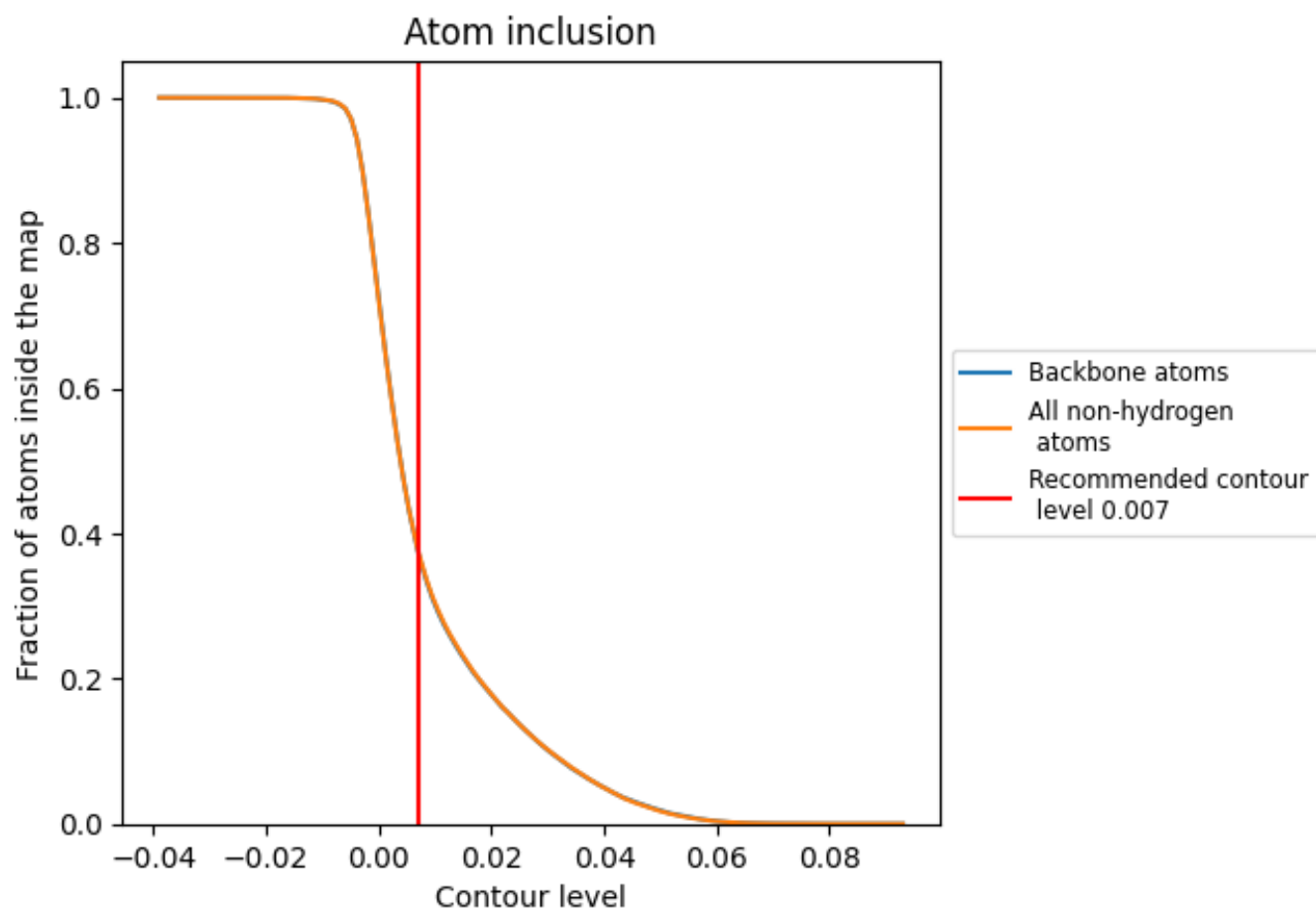
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 38% of all backbone atoms, 38% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3770	 -0.0190
0	 0.0402	 -0.0010
1	 0.2703	 -0.0400
2	 0.2507	 -0.0290
3	 0.0219	 0.0210
4	 0.0854	 -0.0290
5	 0.2288	 0.0200
6	 0.1882	 0.0230
7	 0.3562	 -0.0170
9	 0.0174	 0.0060
A	 0.3735	 -0.0160
AA	 0.1250	 -0.0120
AB	 0.0155	 0.0350
AC	 0.3221	 -0.0110
AD	 0.1005	 -0.0220
AE	 0.2033	 0.0040
B	 0.5858	 -0.0170
C	 0.6463	 -0.0020
D	 0.4430	 -0.0210
E	 0.2248	 -0.0240
F	 0.5599	 -0.0560
G	 0.5541	 -0.0250
H	 0.4679	 -0.0200
I	 0.6396	 -0.0300
J	 0.6956	 -0.0290
K	 0.5372	 -0.0390
L	 0.4256	 -0.0230
M	 0.2780	 -0.0410
N	 0.6052	 -0.0160
O	 0.6680	 -0.0130
P	 0.4980	 -0.0130
Q	 0.3013	 -0.0460
R	 0.1348	 -0.0380
S	 0.3230	 -0.0330
T	 0.2420	 -0.0080



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Chain	Atom inclusion	Q-score
U	 0.6715	 -0.0230
V	 0.5443	 0.0240
W	 0.0294	 -0.0160
X	 0.5127	 -0.0010
Y	 0.3033	 0.0010
Z	 0.0000	 0.0380
a	 0.4454	 -0.0240
b	 0.5583	 0.0030
c	 0.2712	 -0.0110
d	 0.2429	 -0.0060
e	 0.0286	 -0.0030
f	 0.2913	 -0.0150
g	 0.3386	 -0.0480
h	 0.5050	 -0.0350
i	 0.1939	 -0.0290
j	 0.3023	 -0.0270
k	 0.5837	 -0.0250
l	 0.2263	 -0.0100
m	 0.1944	 -0.0770
n	 0.5703	 0.0020
o	 0.3951	 -0.0820
p	 0.0078	 -0.0030
q	 0.4452	 -0.0050
r	 0.4224	 -0.0330
s	 0.4045	 -0.0170
t	 0.5820	 -0.0610
u	 0.2500	 -0.0590
v	 0.4741	 -0.0430
w	 0.1676	 -0.0150
x	 0.0081	 -0.0320
y	 0.4718	 0.0100
z	 0.2181	 -0.0050