



wwPDB EM Validation Summary Report ⓘ

Jun 15, 2026 – 06:44 PM EDT

PDB ID : 8VL1 / pdb_00008vl1
EMDB ID : EMD-43335
Title : Escherichia coli transcription-translation loosely coupled complex (TTC-LC) containing mRNA with a 36 nt long spacer, ops signal, RfaH, NusA, and fMet-tRNAs in E-site and P-site
Authors : Molodtsov, V.; Wang, C.; Ebright, R.H.
Deposited on : 2024-01-11
Resolution : 5.30 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

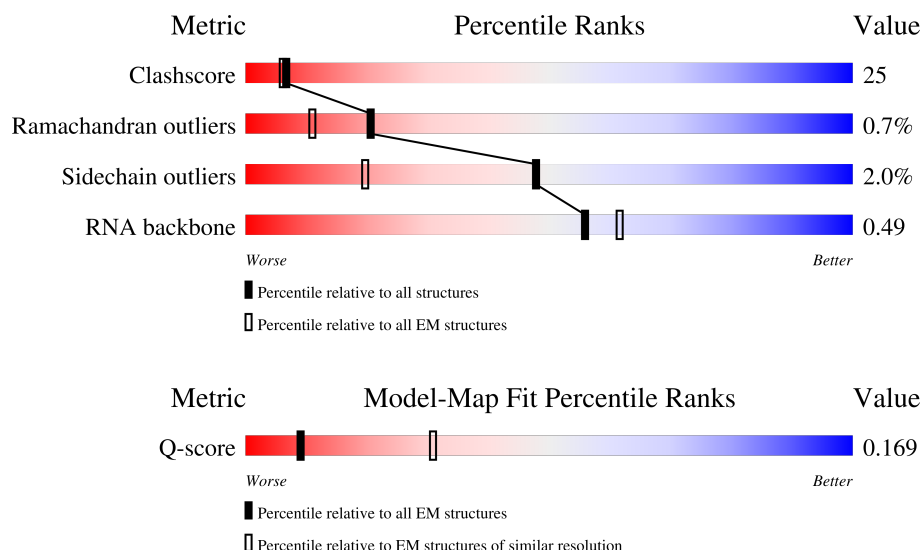
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.30 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.



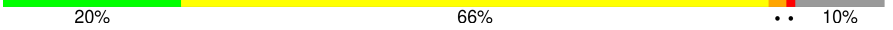
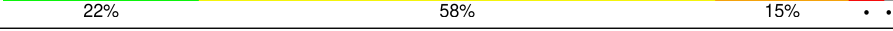
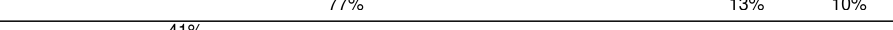
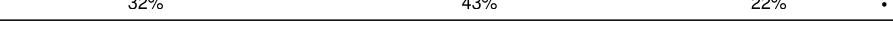
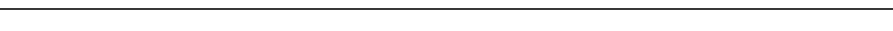
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	625 (4.80 - 5.80)

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	100	

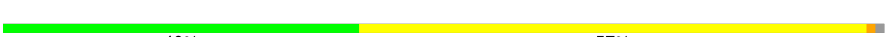
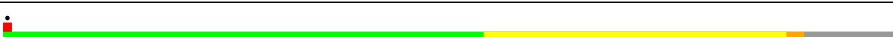
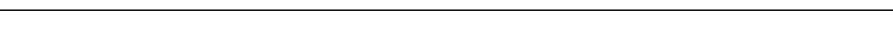
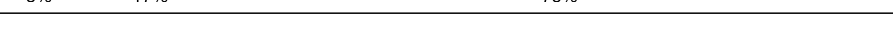
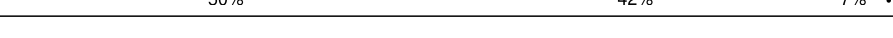
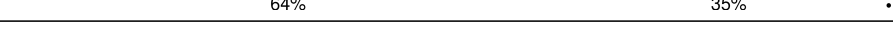
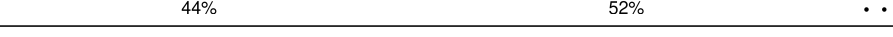
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Mol	Chain	Length	Quality of chain
4	3	104	
5	4	94	
6	5	38	
7	6	38	
8	7	53	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	162	
13	AC	329	
13	AD	329	
14	AE	1407	
15	AF	91	
16	AG	495	
17	C	75	
18	D	1542	
19	E	87	
20	F	71	
21	G	241	
22	H	557	
23	I	233	
24	J	206	
25	K	167	
26	L	135	

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

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

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
68	ZN	AE	1502	-	-	X	-

2 Entry composition [i](#)

There are 68 unique types of molecules in this entry. The entry contains 280046 atoms, of which 98638 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 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 ops.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	5	35	Total	C	N	O	P		0	0
			726	342	141	208	35			

- Molecule 7 is a DNA chain called T DNA ops.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	35	Total	C	N	O	P	0	0
			703	336	117	215	35		

- Molecule 8 is a RNA chain called mRNA with 36 nt long spacer.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	25	Total	C	N	O	P	0	0
			527	235	80	187	25		

- 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 2446	C 723	H 826	N 295	O 527	P 75	0	0
10	B	76	Total 2433	C 723	H 813	N 295	O 527	P 75	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AA	1316	Total	C	N	O	S	0	0
			10381	6514	1810	2014	43		

- Molecule 12 is a protein called Transcription antitermination protein RfaH.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AB	161	Total	C	N	O	S	0	0
			1286	828	222	232	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AC	221	Total	C	N	O	S	0	0
			1698	1060	299	333	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	1337	Total	C	N	O	S	0	0
			10404	6535	1856	1963	50		

- 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 Small ribosomal subunit protein uS15.

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	AE	1	Total	Mg	0
			1	1	

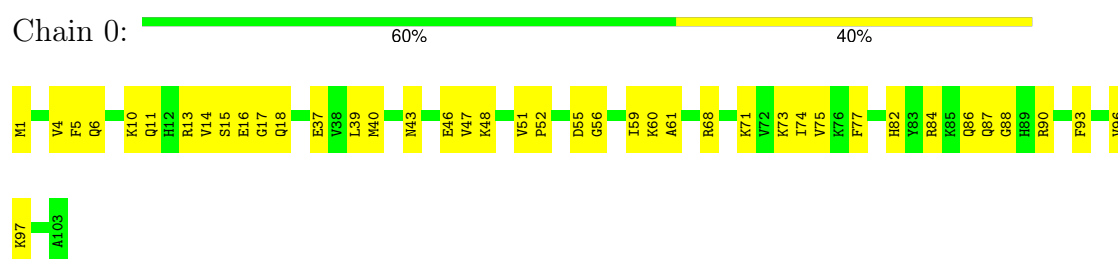
- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

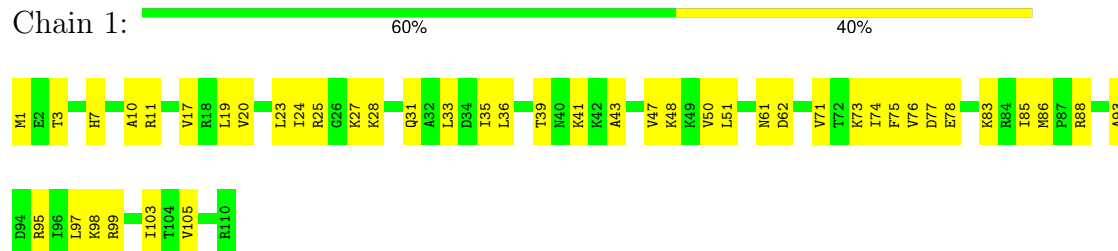
3 Residue-property plots [i](#)

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

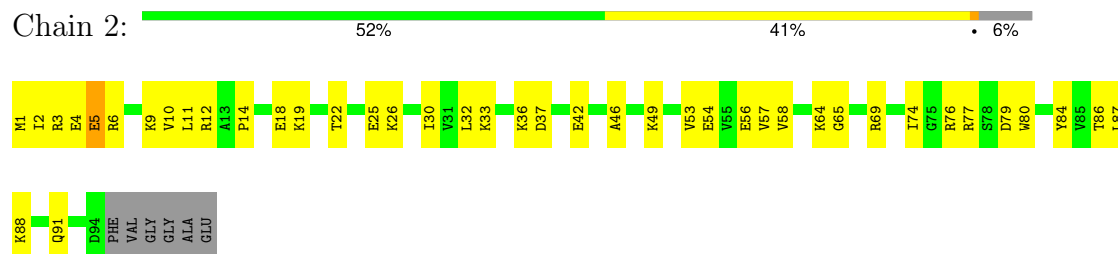
• Molecule 1: Ribosomal protein L21



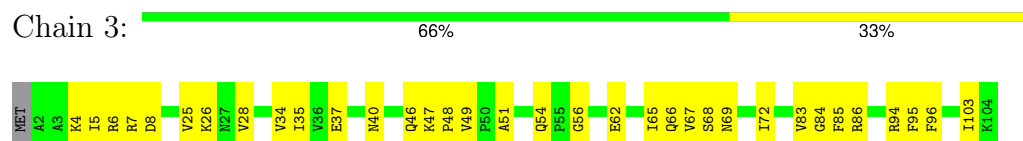
• Molecule 2: 50S ribosomal protein L22



• Molecule 3: 50S ribosomal protein L23



• Molecule 4: 50S ribosomal protein L24



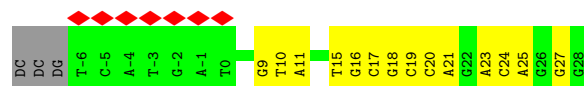
- Molecule 5: 50S ribosomal protein L25

Chain 4: 



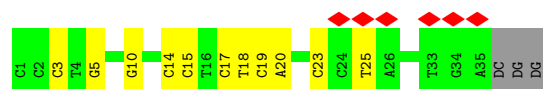
- Molecule 6: NT DNA ops

Chain 5: 



- Molecule 7: T DNA ops

Chain 6: 

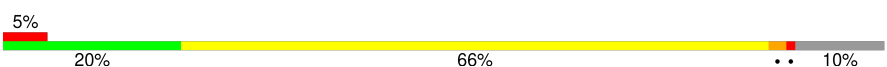


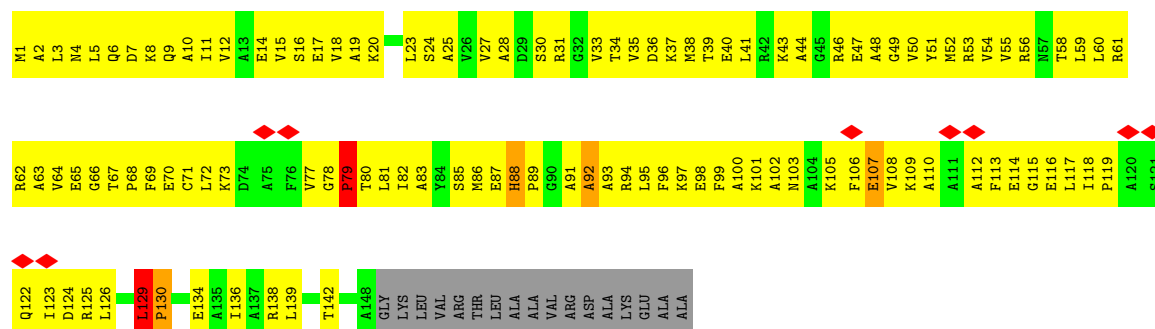
- Molecule 8: mRNA with 36 nt long spacer

Chain 7: 



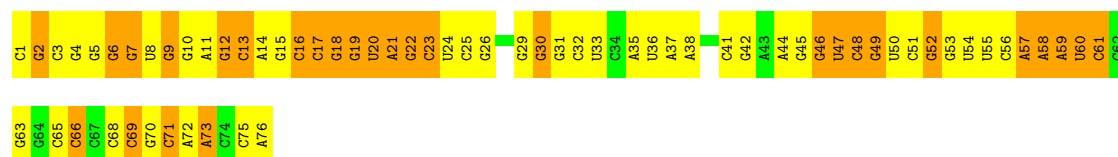
- Molecule 9: 50S ribosomal protein L10

Chain 9: 

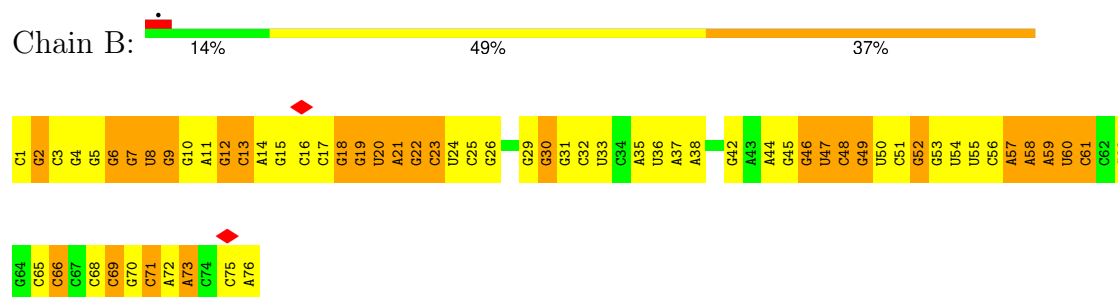


- Molecule 10: E-site and P-site tRNA (fMet)

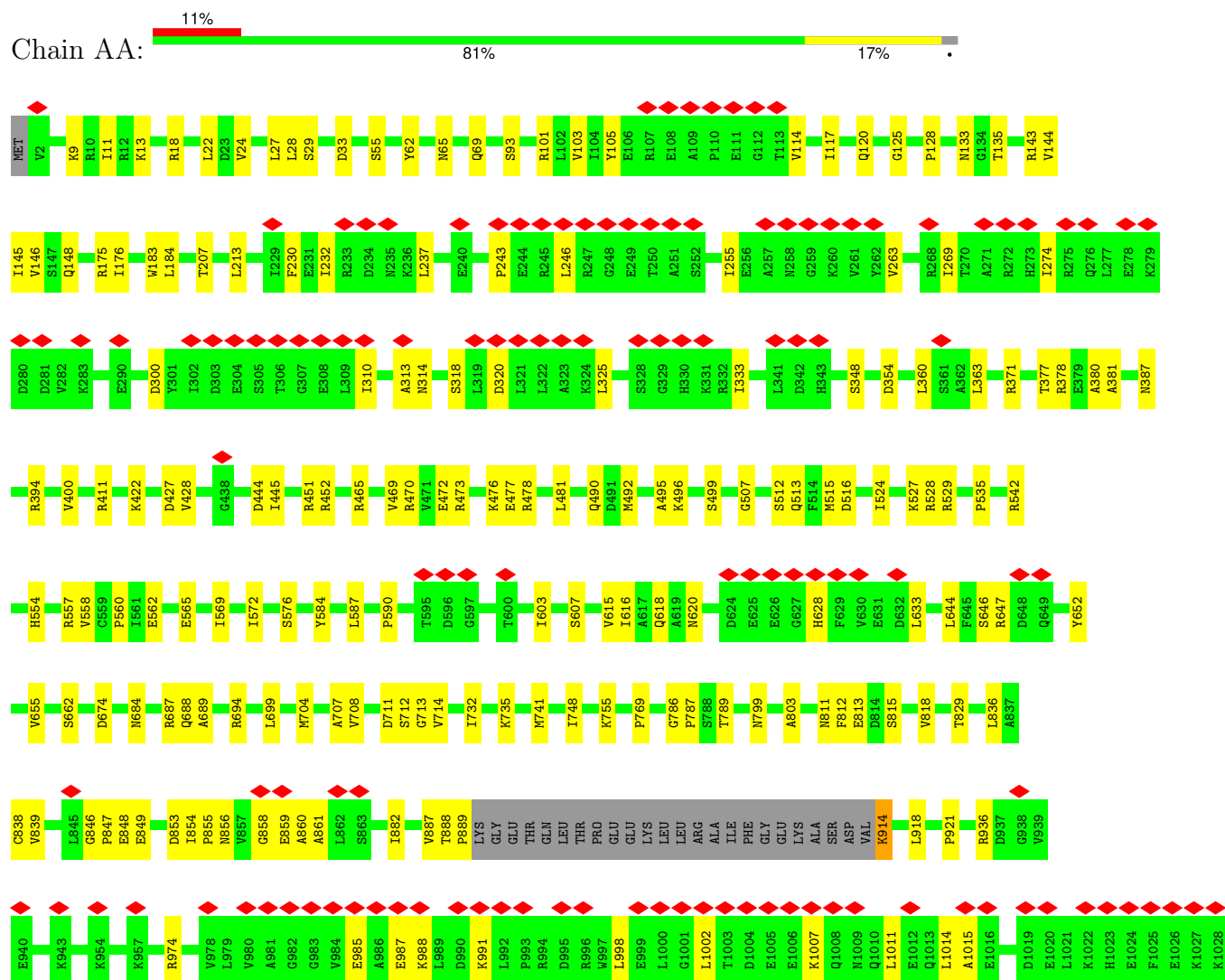
Chain A: 

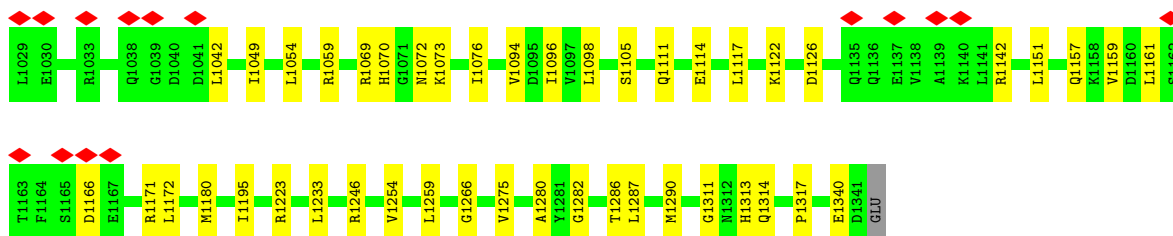


• Molecule 10: E-site and P-site tRNA (fMet)

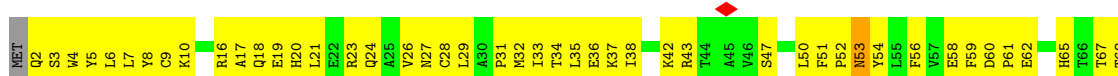


• Molecule 11: DNA-directed RNA polymerase subunit beta

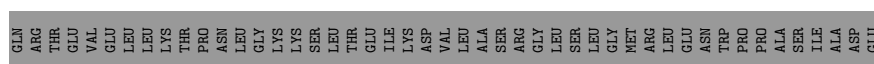
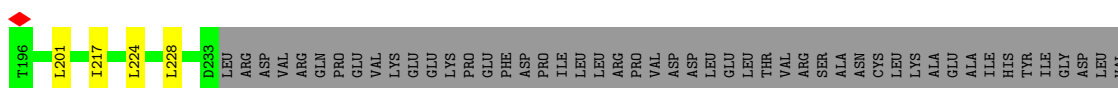




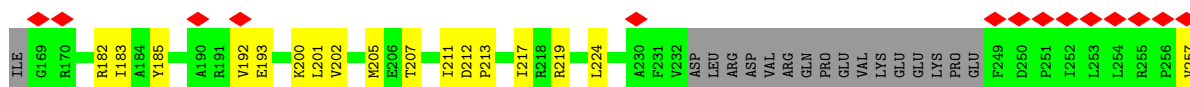
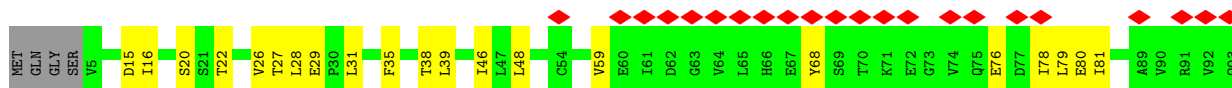
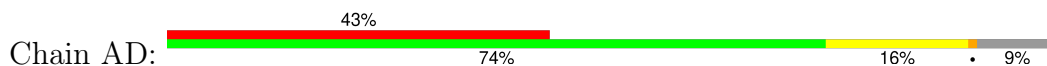
• Molecule 12: Transcription antitermination protein RfaH

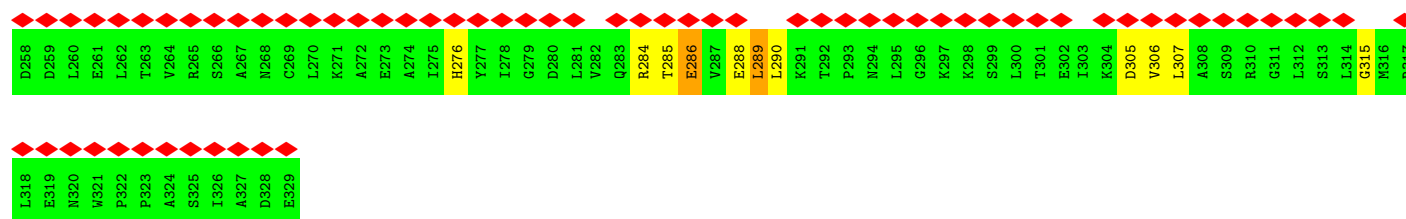


• Molecule 13: DNA-directed RNA polymerase subunit alpha

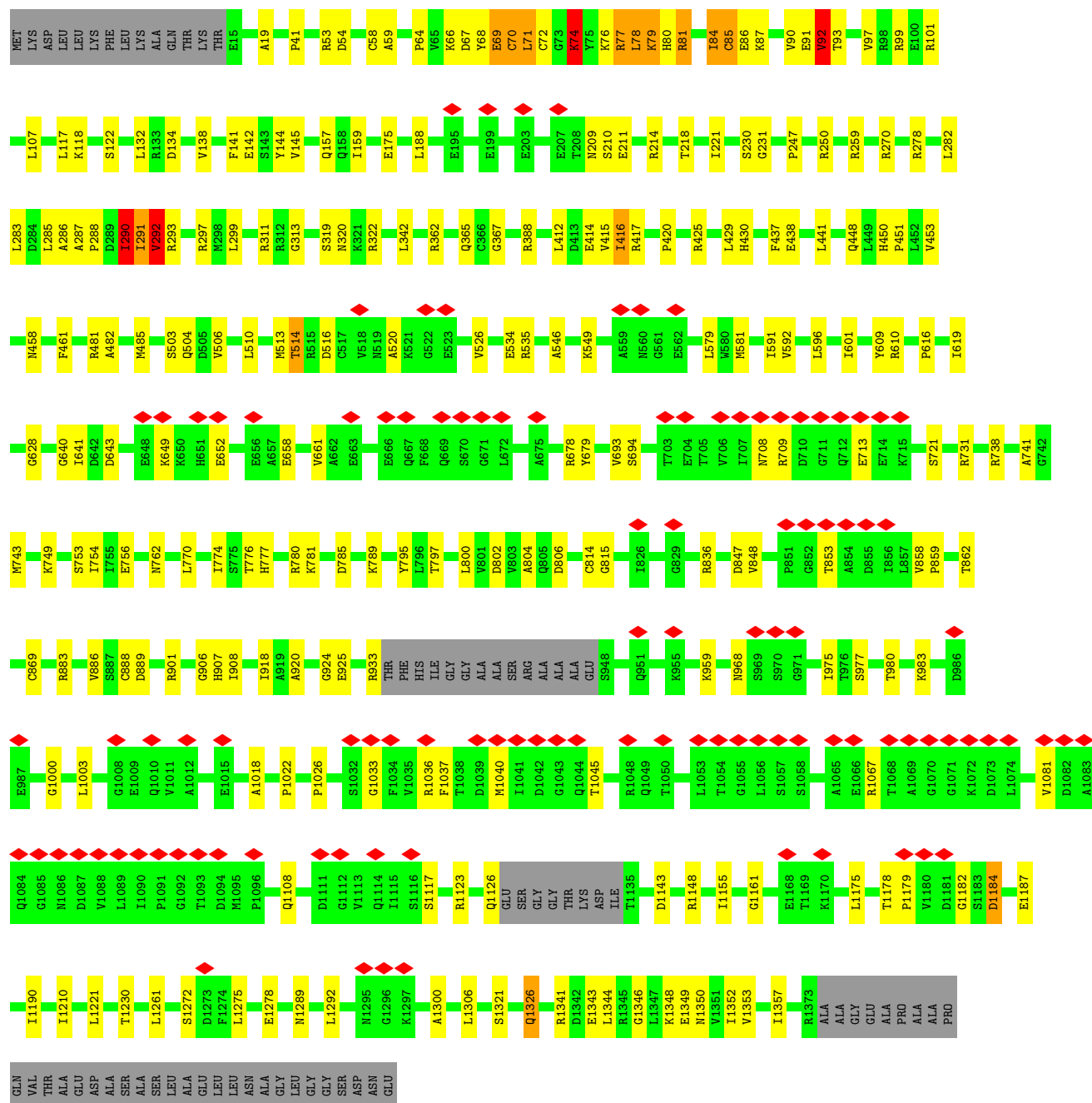
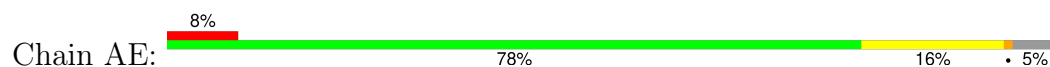


• Molecule 13: DNA-directed RNA polymerase subunit alpha

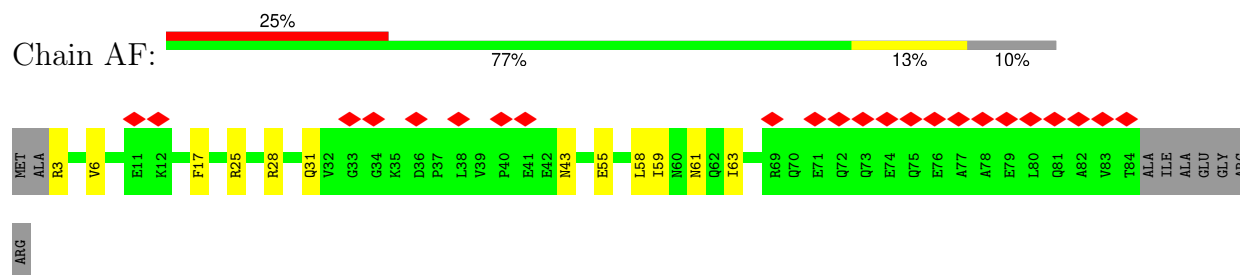




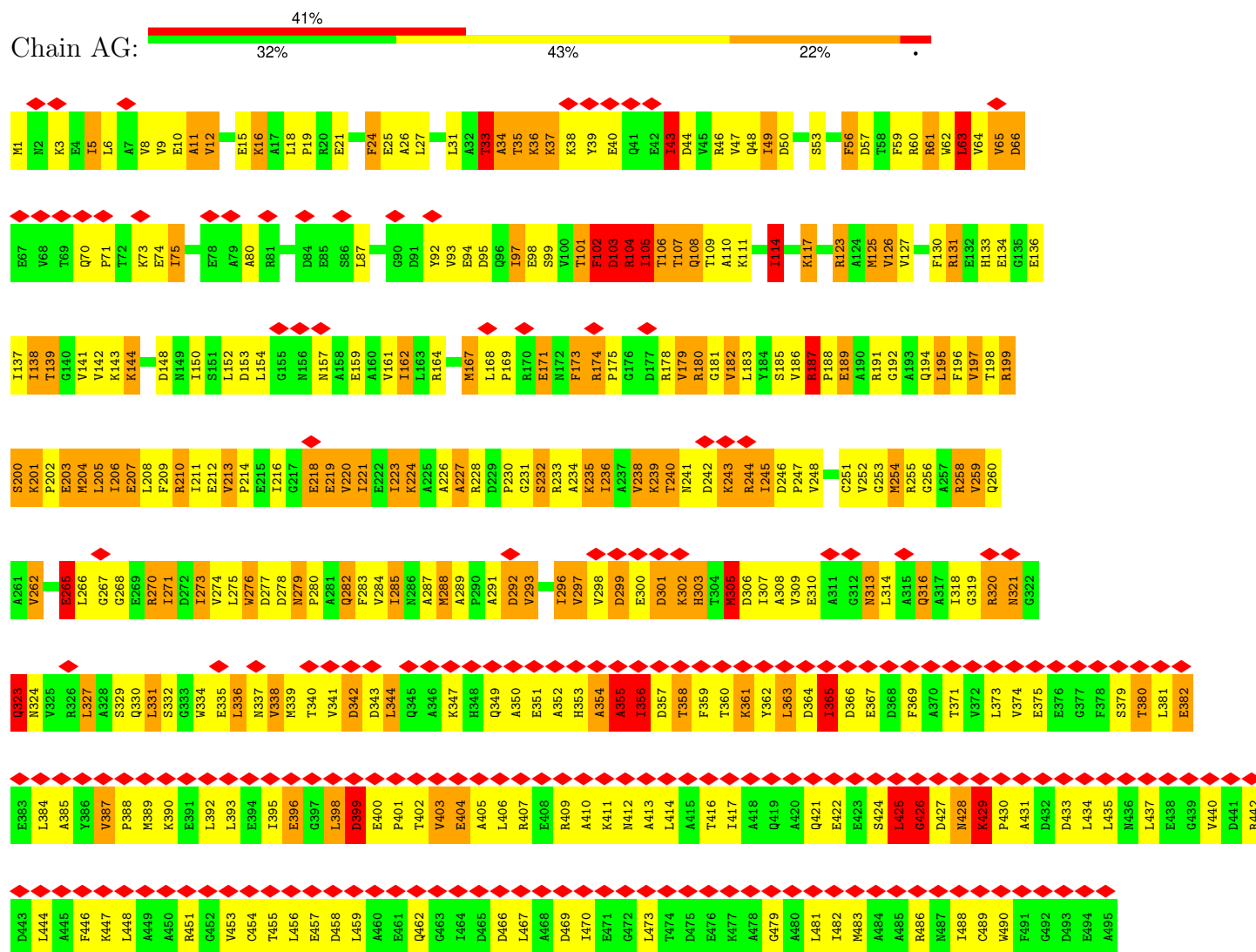
• Molecule 14: DNA-directed RNA polymerase subunit beta'



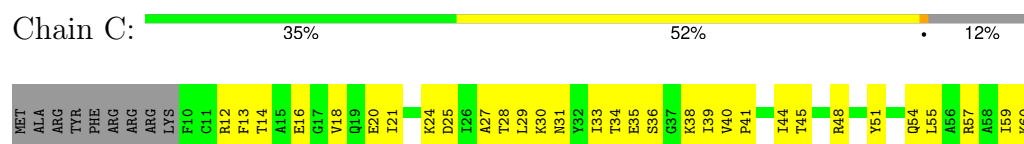
- Molecule 15: DNA-directed RNA polymerase subunit omega

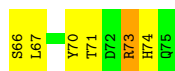


- Molecule 16: Transcription termination/antitermination protein NusA



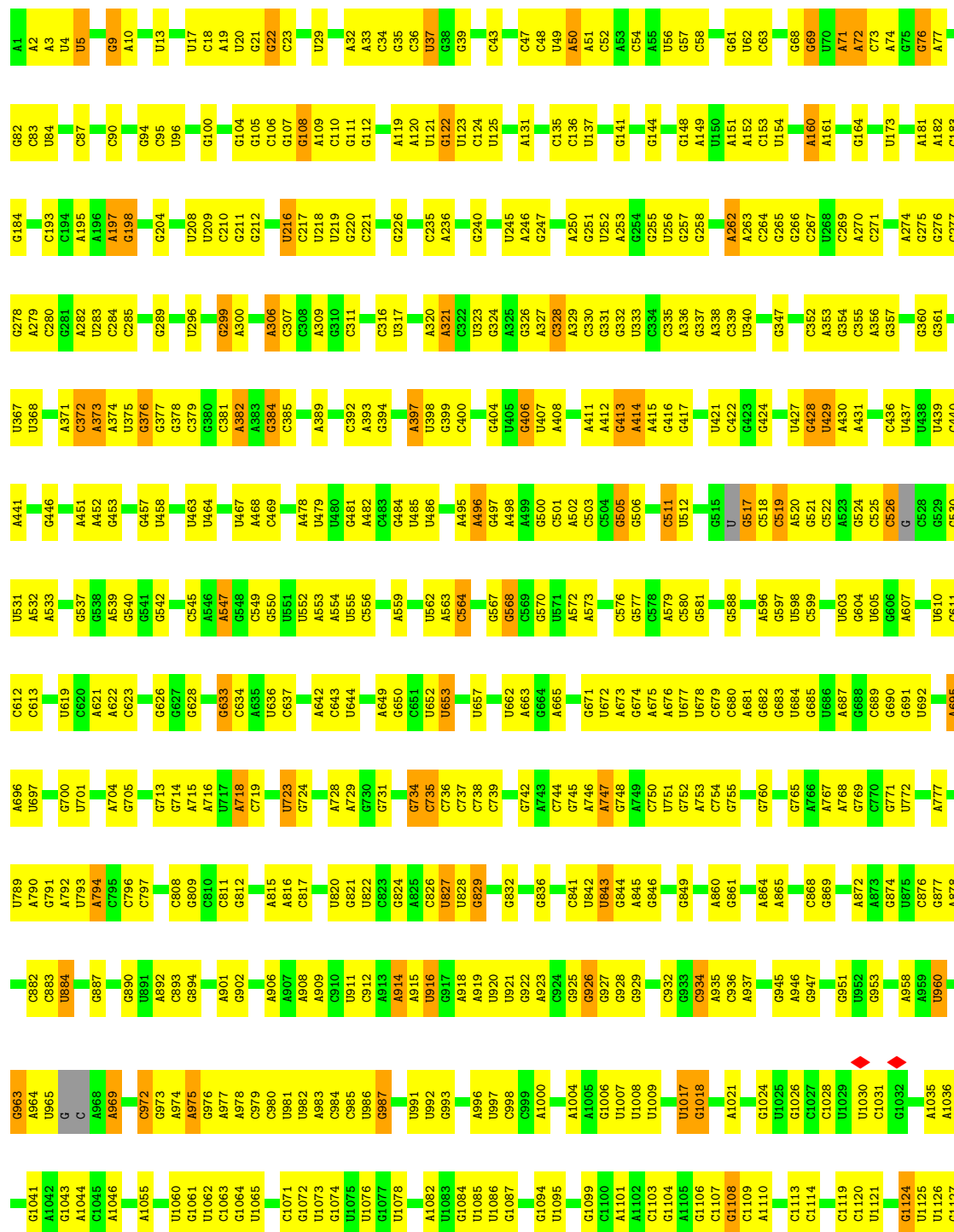
- Molecule 17: 30S ribosomal protein S18

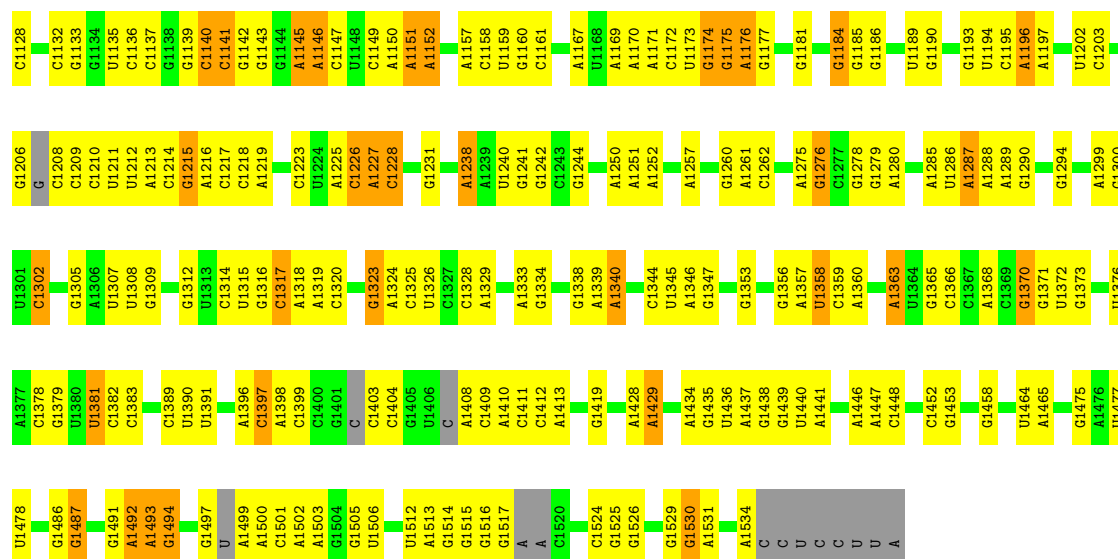




• Molecule 18: 16S rRNA

Chain D: 49% 43% 6%





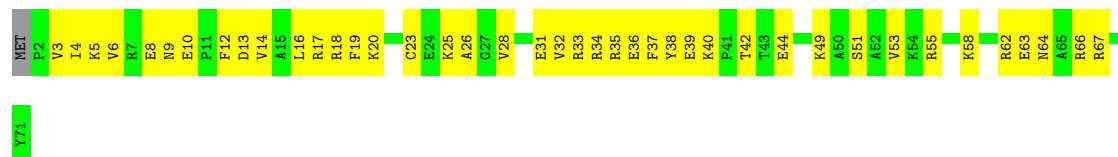
• Molecule 19: 30S ribosomal protein S20

Chain E: 47% 52%



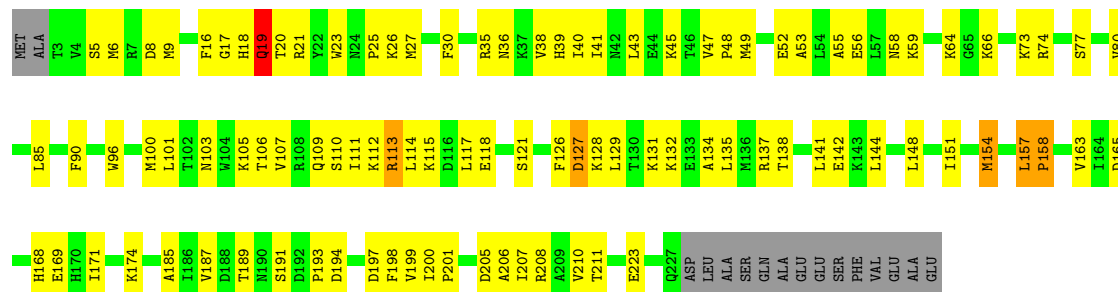
• Molecule 20: 30S ribosomal protein S21

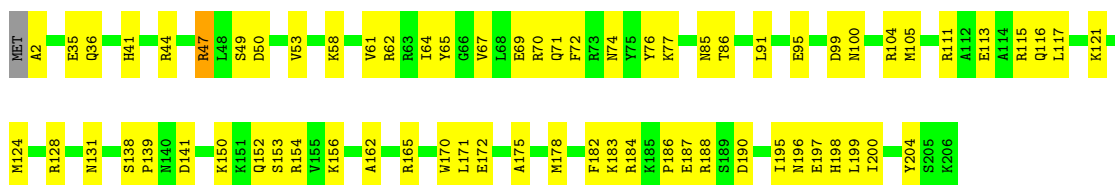
Chain F: 41% 58%



• Molecule 21: 30S ribosomal protein S2

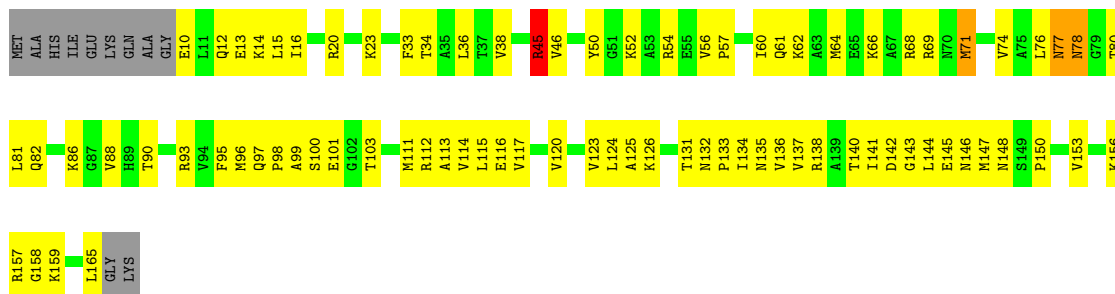
Chain G: 52% 39% 7%





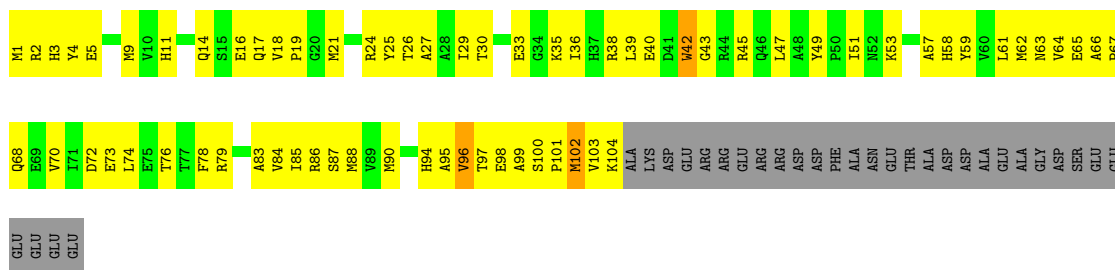
• Molecule 25: 30S ribosomal protein S5

Chain K: 44% 47% 7%



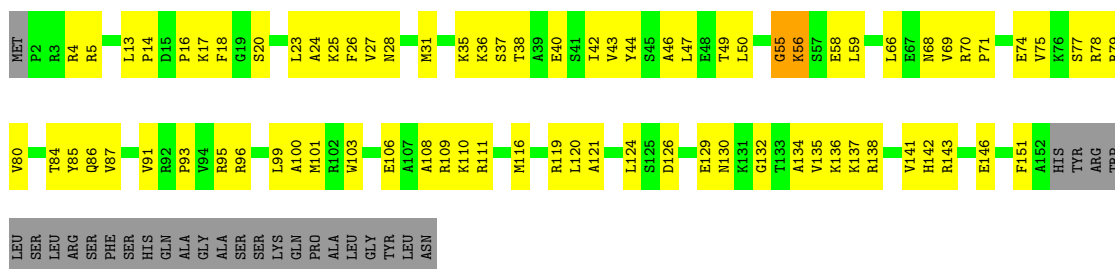
• Molecule 26: 30S ribosomal protein S6

Chain L: 27% 48% 23%



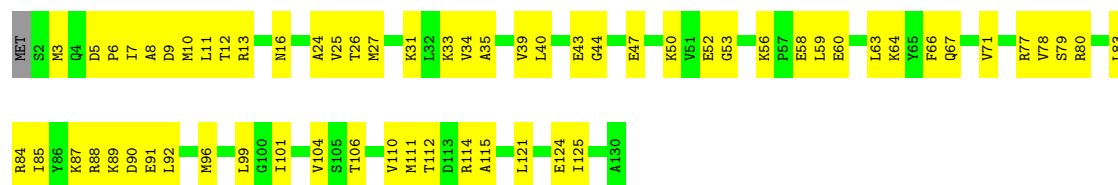
• Molecule 27: 30S ribosomal protein S7

Chain M: 41% 42% 16%



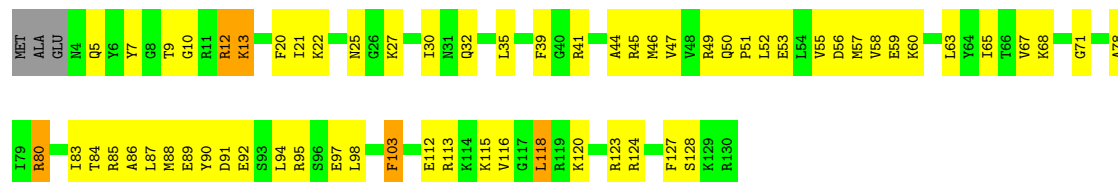
• Molecule 28: 30S ribosomal protein S8

Chain N: 52% 48%



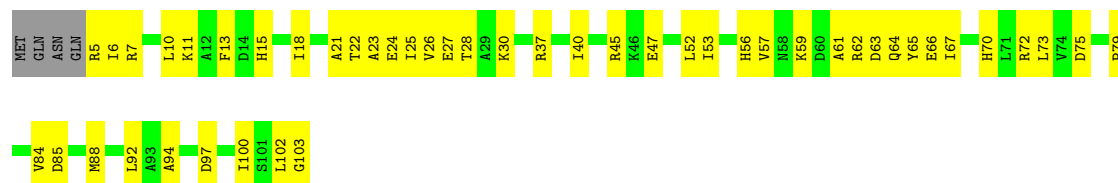
- Molecule 29: 30S ribosomal protein S9

Chain O: 49% 45%



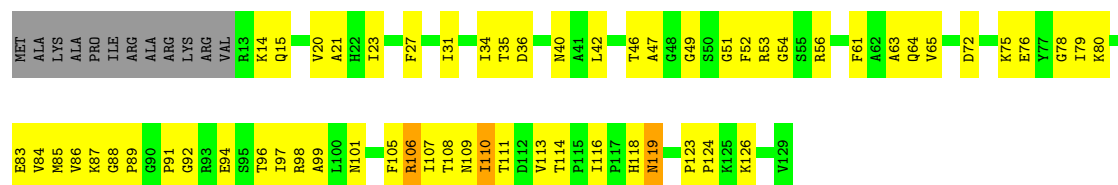
- Molecule 30: 30S ribosomal protein S10

Chain P: 50% 46%



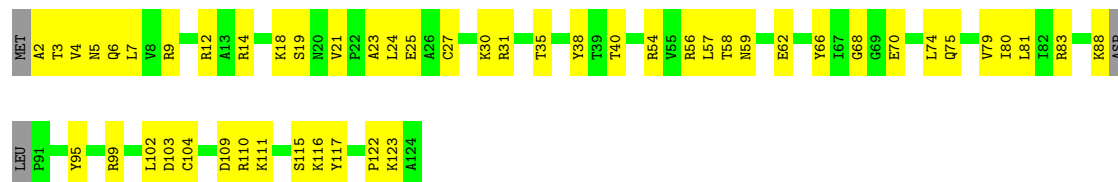
- Molecule 31: 30S ribosomal protein S11

Chain Q: 44% 44% 9%



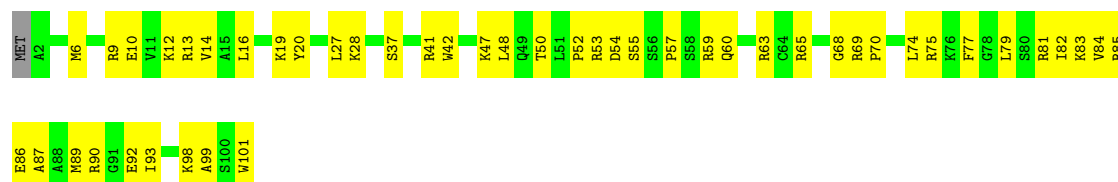
- Molecule 32: 30S ribosomal protein S12

Chain R: 57% 40%



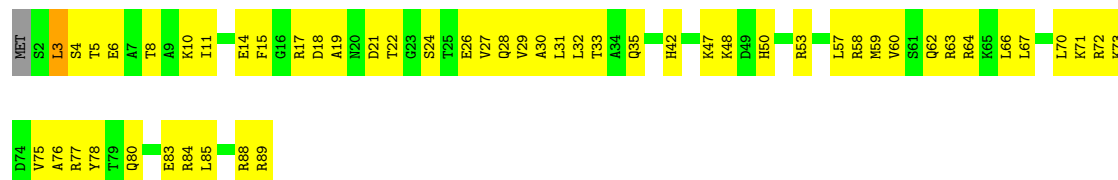
- Molecule 33: 30S ribosomal protein S14

Chain S: 52% 47%



- Molecule 34: Small ribosomal subunit protein uS15

Chain T: 40% 57% ..



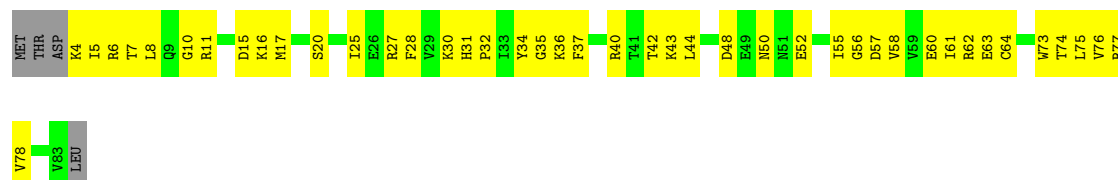
- Molecule 35: 30S ribosomal protein S16

Chain U: 54% 46%



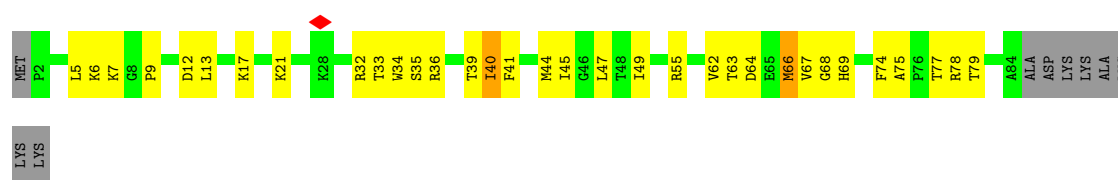
- Molecule 36: 30S ribosomal protein S17

Chain V: 44% 51% 5%



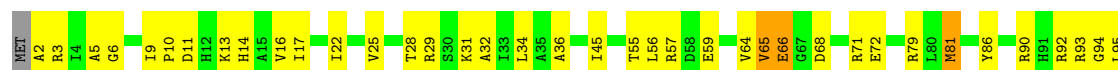
- Molecule 37: 30S ribosomal protein S19

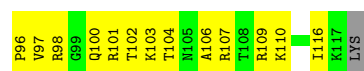
Chain W: 54% 34% 10%



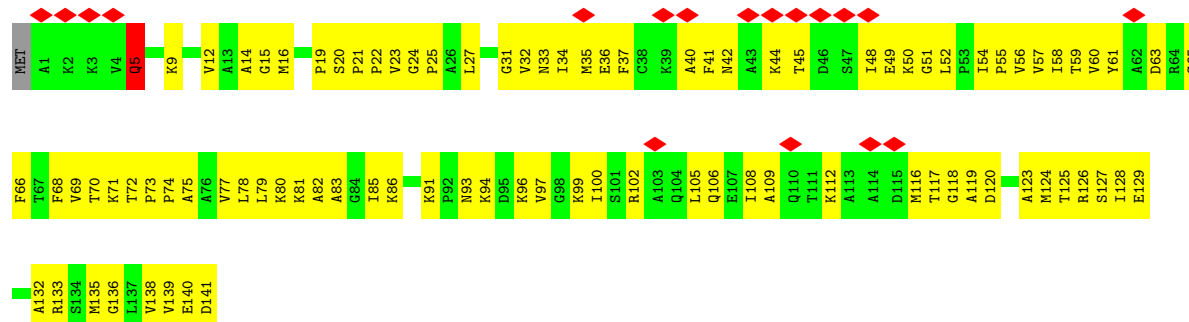
- Molecule 38: 30S ribosomal protein S13

Chain X: 55% 41%

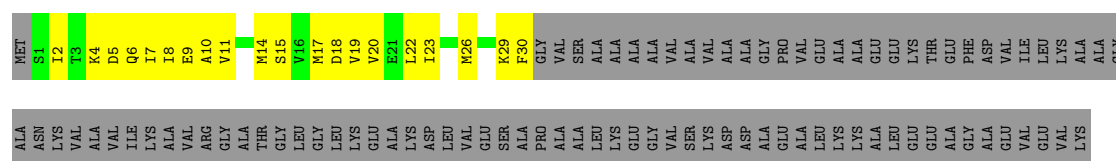




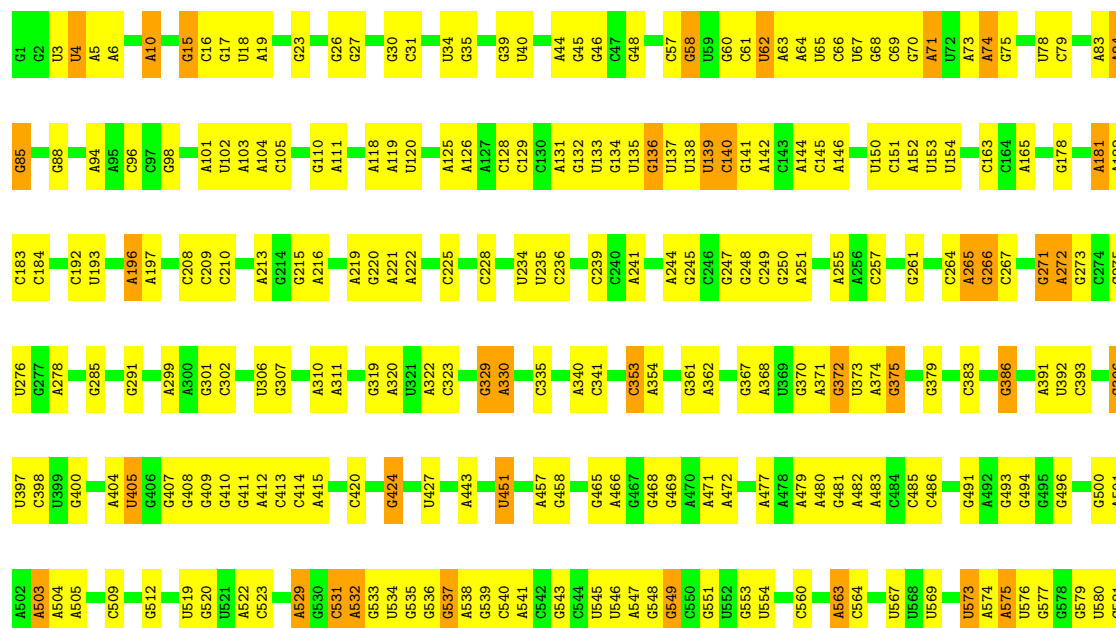
• Molecule 39: 50S ribosomal protein L11



• Molecule 40: 50S ribosomal protein L7/L12



• Molecule 41: 23S rRNA



G1811	G1710	C1607	G1514	U1415	A1342	C1146	G1074	C1005	U846	A752	U646	A582
G1816	U1714	A1608	A1515	G1416	G1343	A1147	C1075	C1006	C851	A753	G647	G583
U1818	G1715	A1610	U1520	G1417	U1344	C1153	C1076	C1007	U852	U754	A654	C584
A1819	U1720	G1613	G1521	G1418	C1345	G1154	U1077	A1008	G856	U755	A654	G585
U1820	G1721	A1614	U1529	A1420	A1419	C1154	C1078	A1009	G857	G756	U657	A586
A1821	U1729	C1617	U1534	G1421	A1347	G1160	A1080	U1012	G858	G760	U658	U588
G1822	C1730	A	C1428	G1422	C1348	G1161	U1081	C1013	G859	A761	G659	U589
G1823	C1730	A1535	U1536	G1427	C1349	G1162	U1082	C1013	G859	A761	A666	U591
U1825	C1732	G1619	G1537	C1428	C1350	C1161	U1083	A1014	U860	A764	U667	A592
G1826	G1738	G1622	U1542	G1429	U1352	C1167	A1084	A941	G861	C765	A668	U593
U1827	A1746	U1636	G1543	G1430	A1353	A1169	A1085	U1019	G862	U773	A670	U594
G1828	U1747	A1637	U1546	A1431	A1354	C1170	G1087	A1020	A776	G774	C671	C595
C1830	G1750	U1647	U1554	A1432	G1355	G1171	A1088	U1022	U870	G775	C672	U596
C1832	G1753	U1648	U1558	A1433	G1356	C1172	A1089	U1023	U871	G776	C672	U598
C1833	A1754	G1651	C1559	A1434	A1361	U1174	A1090	G1024	U872	G776	C672	U599
C1836	A1755	A1652	G1560	A1435	G1362	U1175	A1095	G1025	C873	G780	A677	G600
G1839	G1756	G1653	U1561	G1441	C1362	U1180	A1096	A1027	G874	A781	A685	C601
G1840	A1757	A1654	C1562	U1442	A1365	U1181	A1096	U1028	A878	A782	U686	A602
G1841	U1758	A1655	U1563	U1443	A1366	C1177	U1101	A1029	G879	A783	U686	A603
U1842	A1759	U1657	C1564	G1444	A1367	G1178	C1102	U1033	G880	G784	A689	G601
C1843	C1764	C1658	A1566	G1445	A1368	C1179	C1103	U1033	G881	G785	G690	G600
G1844	G1766	G1659	G1568	G1445	G1369	U1180	A1103	U1033	G881	C786	C691	U607
G1845	G1770	U1659	C1568	G1445	G1370	U1181	A1103	U1033	G881	C787	A609	A608
G1846	U1778	A1664	U1569	U1467	C1371	G1277	A1103	U1033	G881	C787	A609	A609
A1847	A1773	A1665	A1570	U1468	A1371	C1278	G1106	G1036	U884	C787	C610	C610
A1848	C1774	G1666	C1572	U1469	A1371	G1279	G1107	G1037	C885	A789	G700	A613
U1853	U1778	A1668	A1572	A1470	A1371	G1280	U1108	G1038	C885	A789	G701	A613
A1854	U1779	U1674	U1578	A1477	A1371	G1281	C1109	A1039	C888	A789	U702	A614
U1855	A1784	C1675	A1579	G1482	A1371	U1282	C1110	A1040	C889	A789	U703	A614
U1856	A1785	A1676	G1581	U1482	A1371	G1283	C1111	A1041	C890	A789	G704	U615
G1857	A1786	A1677	C1582	A1490	A1371	G1284	C1112	A1042	C891	A789	A705	A616
U1859	A1789	G1681	U1584	A1495	A1371	G1285	C1113	A1043	C892	A789	G707	G617
G1862	C1790	G1682	C1585	A1496	A1371	G1286	C1114	A1044	C893	A789	U710	G620
G1863	A1791	U1683	A1586	A1496	A1371	G1287	C1115	A1045	C894	A789	G622	A621
U1864	G1792	G1684	G1587	U1497	A1371	G1288	C1116	A1046	C895	A789	G623	C623
G1869	C1793	U1688	C1588	C1498	U1400	G1289	C1117	A1047	C896	A789	G624	C624
C1870	A1794	U1688	U1589	C1499	U1400	G1290	C1118	A1048	C897	A789	C717	G625
C1871	C1795	U1688	A1590	G1500	A1403	G1291	C1119	A1049	C898	A789	G726	A626
A1871	C1796	U1688	A1591	U1503	C1404	G1292	C1120	C1053	C899	A789	G727	A627
A1872	G1797	C1694	U1596	A1503	U1405	G1293	C1121	C1054	C900	A789	G728	G628
G1873	U1798	G1695	U1597	U1506	U1406	G1294	C1122	C1055	C901	A789	G729	G629
C1874	G1799	A1700	A1598	C1507	G1407	G1295	C1123	A1056	G907	A789	G731	G630
G1875	C1800	U1700	U1599	U1508	C1323	G1296	C1124	A1057	C908	A789	A631	A632
A1801	A1801	G1703	U1600	U1509	U1408	G1297	C1125	U1058	C909	A789	A633	A633
A1803	A1803	G1703	U1601	U1510	U1409	G1298	C1126	U1059	C910	A789	G738	C634
C1879	U1880	G1707	U1602	U1511	U1410	G1299	C1127	U1060	C911	A789	A635	C635
C1881	U1882	U1708	U1603	U1512	U1411	G1300	C1128	U1061	C912	A789	A636	C636
U1883	U1883	U1709	U1604	U1513	C1414	G1301	C1129	U1062	C913	A789	A637	A637

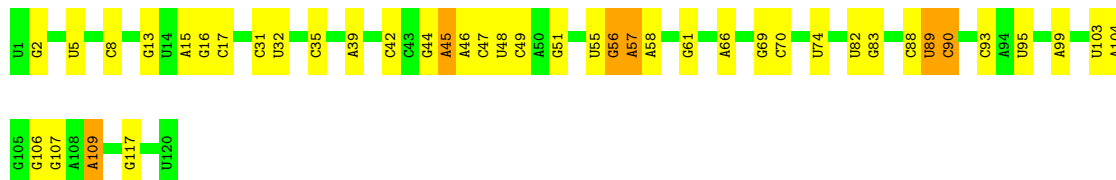
- Molecule 43: 50S ribosomal protein L28

Chain c: 



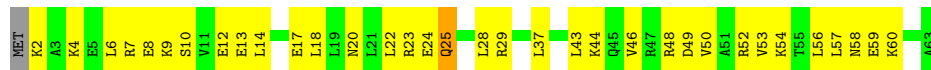
- Molecule 44: 5S rRNA

Chain d: 



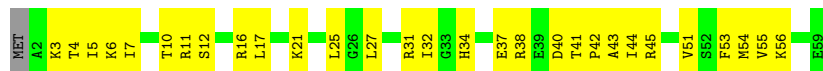
- Molecule 45: 50S ribosomal protein L29

Chain e: 

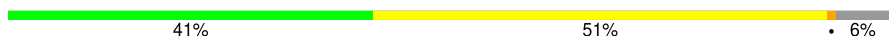


- Molecule 46: 50S ribosomal protein L30

Chain f: 



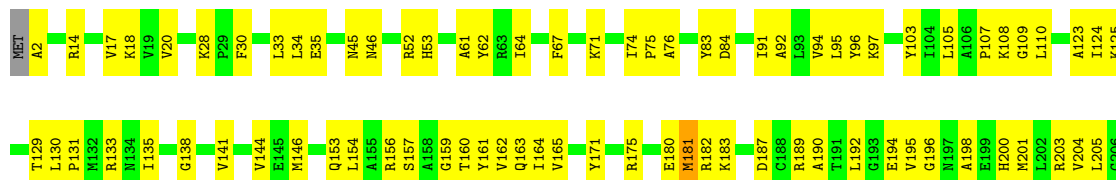
- Molecule 47: 50S ribosomal protein L31

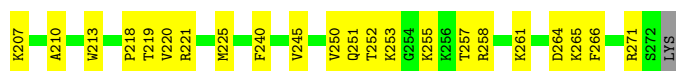
Chain g: 



- Molecule 48: 50S ribosomal protein L2

Chain h: 

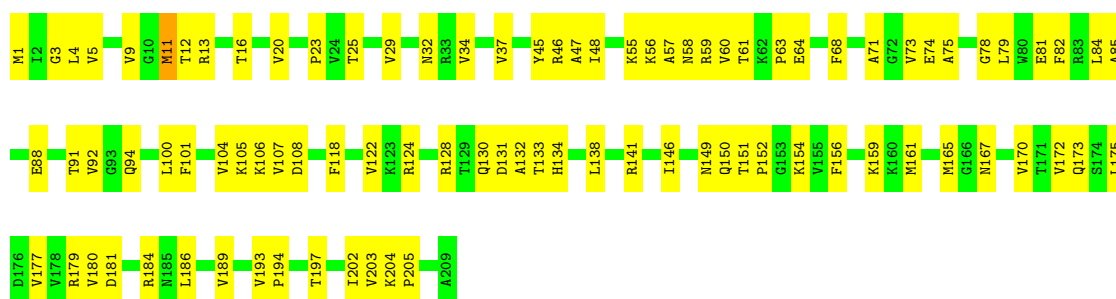




- Molecule 49: 50S ribosomal protein L32



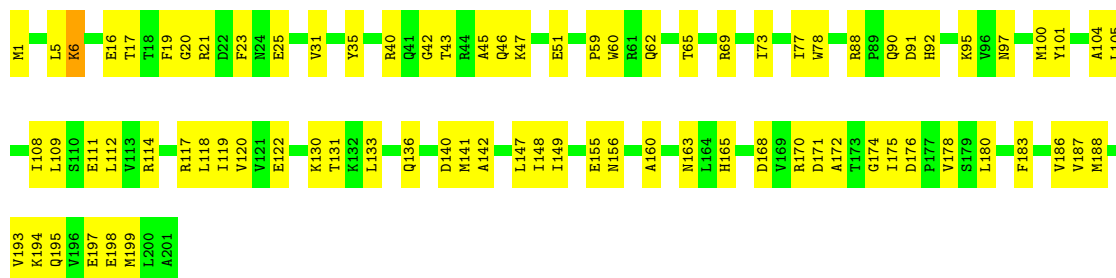
- Molecule 50: 50S ribosomal protein L3



- Molecule 51: 50S ribosomal protein L33



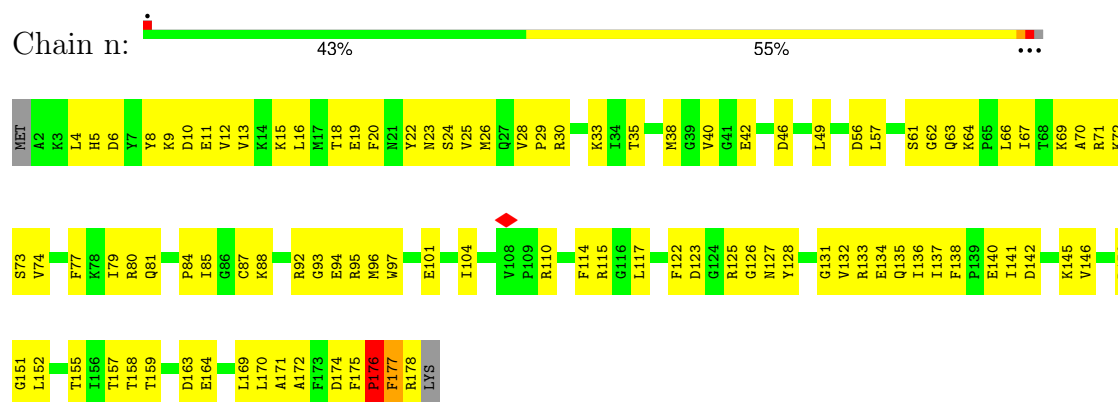
- Molecule 52: 50S ribosomal protein L4



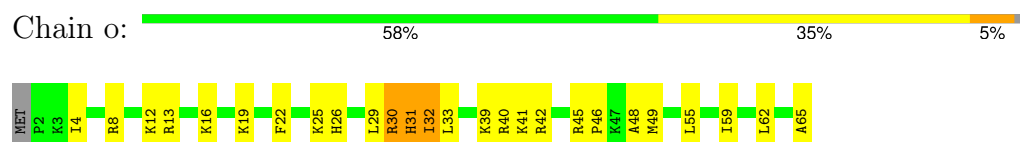
- Molecule 53: 50S ribosomal protein L34



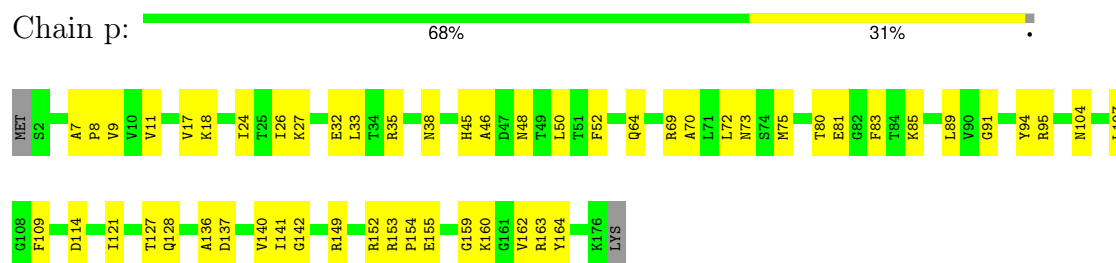
- Molecule 54: 50S ribosomal protein L5



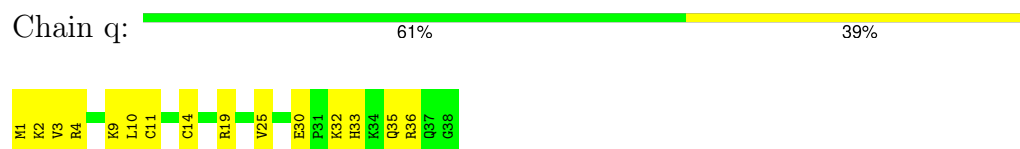
- Molecule 55: 50S ribosomal protein L35



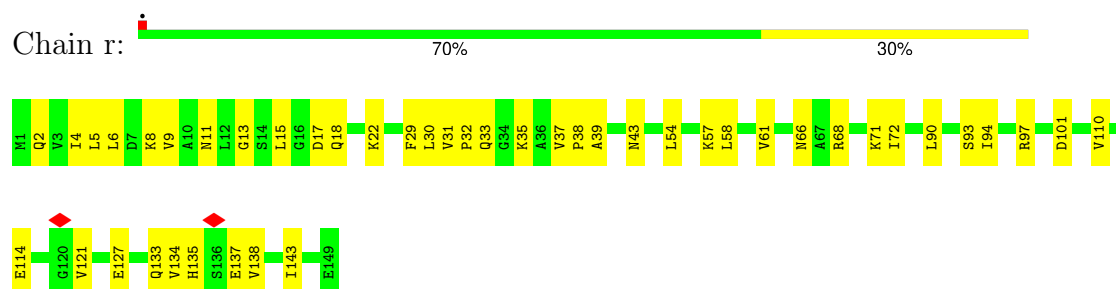
- Molecule 56: 50S ribosomal protein L6



- Molecule 57: 50S ribosomal protein L36



- Molecule 58: 50S ribosomal protein L9



- Molecule 59: 50S ribosomal protein L13

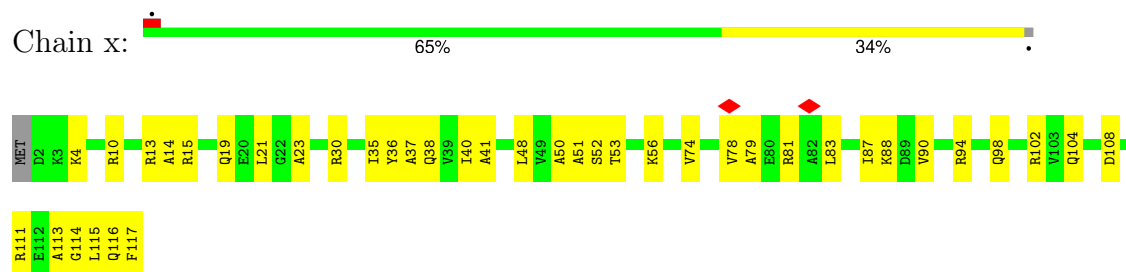
- Molecule 60: 50S ribosomal protein L14

- Molecule 61: 50S ribosomal protein L15

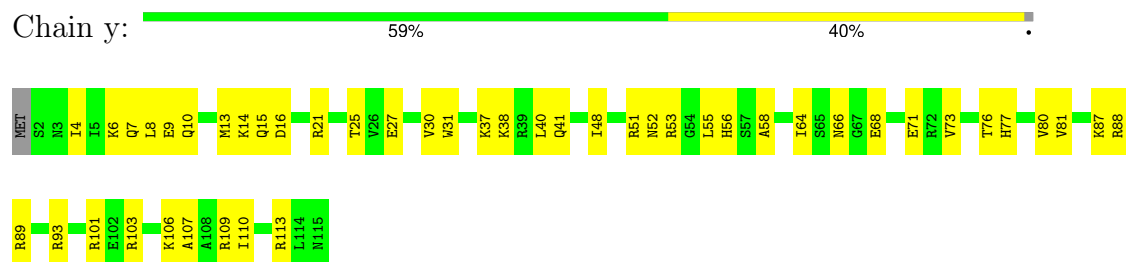
- Molecule 62: 50S ribosomal protein L16

- Molecule 63: 50S ribosomal protein L17

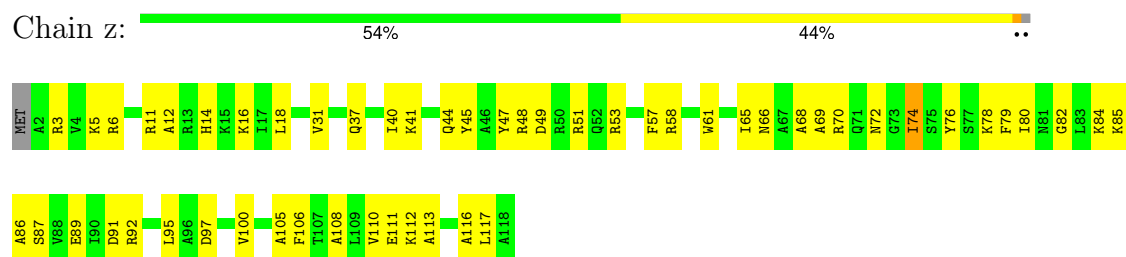
- Molecule 64: 50S ribosomal protein L18



- 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	20048	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1250	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.035	Depositor
Minimum map value	-0.007	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0032	Depositor
Map size ($\text{\AA}$)	532.48, 532.48, 532.48	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.04, 1.04, 1.04	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.43	0/829	0.51	0/1107
2	1	0.60	0/864	0.63	0/1156
3	2	0.55	1/752 (0.1%)	0.67	0/1005
4	3	0.35	0/796	0.48	0/1062
5	4	0.57	0/766	0.63	0/1025
6	5	0.57	0/816	0.78	0/1259
7	6	0.57	0/783	0.78	0/1203
8	7	0.61	2/585 (0.3%)	0.91	3/906 (0.3%)
9	9	0.37	0/1131	0.73	2/1524 (0.1%)
10	A	0.27	0/1810	0.58	0/2821
10	B	0.27	0/1810	0.58	0/2821
11	AA	0.38	0/10547	0.62	0/14232
12	AB	0.60	0/1317	1.21	17/1786 (1.0%)
13	AC	0.38	0/1718	0.62	0/2328
13	AD	0.37	0/2096	0.69	3/2854 (0.1%)
14	AE	0.39	0/10561	0.64	5/14258 (0.0%)
15	AF	0.30	0/652	0.61	0/879
16	AG	0.97	6/3897 (0.2%)	1.40	49/5273 (0.9%)
17	C	0.68	0/553	0.81	1/743 (0.1%)
18	D	0.29	0/36610	0.41	9/57091 (0.0%)
19	E	0.61	0/675	0.72	0/895
20	F	0.53	0/597	0.61	0/792
21	G	0.68	5/1791 (0.3%)	0.79	8/2413 (0.3%)
22	H	0.38	0/1746	0.81	0/2382
23	I	0.57	1/1663 (0.1%)	0.68	4/2241 (0.2%)
24	J	0.46	0/1665	0.58	0/2227
25	K	0.72	2/1165 (0.2%)	0.86	6/1568 (0.4%)
26	L	0.68	1/867 (0.1%)	0.79	1/1171 (0.1%)
27	M	0.56	0/1195	0.69	2/1602 (0.1%)
28	N	0.50	0/989	0.58	0/1326
29	O	0.66	3/1034 (0.3%)	0.79	3/1375 (0.2%)
30	P	0.51	0/800	0.73	0/1082

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	Q	0.72	2/893 (0.2%)	0.76	2/1205 (0.2%)
32	R	0.49	0/952	0.59	0/1274
33	S	0.52	0/817	0.61	0/1088
34	T	0.57	1/722 (0.1%)	0.68	0/964
35	U	0.41	0/659	0.53	0/884
36	V	0.49	0/657	0.62	0/881
37	W	0.55	1/680 (0.1%)	0.62	1/915 (0.1%)
38	X	0.45	0/909	0.72	1/1215 (0.1%)
39	Y	0.38	2/1046 (0.2%)	0.66	2/1410 (0.1%)
40	Z	0.13	0/227	0.41	0/304
41	a	0.30	0/69247	0.43	10/107985 (0.0%)
42	b	0.41	0/589	0.55	0/779
43	c	0.51	0/635	0.61	0/848
44	d	0.25	0/2872	0.37	0/4478
45	e	0.69	2/502 (0.4%)	0.65	1/667 (0.1%)
46	f	0.52	0/452	0.57	0/605
47	g	0.45	1/531 (0.2%)	0.64	0/709
48	h	0.49	1/2121 (0.0%)	0.59	1/2852 (0.0%)
49	i	0.41	0/450	0.55	0/599
50	j	0.51	0/1586	0.57	1/2134 (0.0%)
51	k	0.45	0/433	0.63	0/576
52	l	0.51	1/1571 (0.1%)	0.62	0/2113
53	m	0.45	0/380	0.56	0/498
54	n	0.46	0/1434	0.66	1/1926 (0.1%)
55	o	0.51	0/513	0.71	1/676 (0.1%)
56	p	0.41	0/1333	0.62	2/1805 (0.1%)
57	q	0.45	0/303	0.64	0/397
58	r	0.28	0/1122	0.48	0/1515
59	s	0.70	2/1152 (0.2%)	0.74	2/1551 (0.1%)
60	t	0.52	0/955	0.75	3/1279 (0.2%)
61	u	0.43	0/1062	0.59	0/1413
62	v	0.60	1/1093 (0.1%)	0.77	3/1460 (0.2%)
63	w	0.83	2/964 (0.2%)	0.80	3/1289 (0.2%)
64	x	0.34	0/902	0.50	0/1209
65	y	0.41	0/929	0.54	0/1242
66	z	0.62	2/960 (0.2%)	0.62	0/1278
All	All	0.41	39/194733 (0.0%)	0.56	147/286430 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	9	0	3
12	AB	0	2
13	AC	0	1
13	AD	0	2
14	AE	0	4
16	AG	0	6
21	G	0	1
22	H	0	5
23	I	0	1
25	K	0	2
29	O	0	1
38	X	0	1
39	Y	0	1
54	n	0	1
55	o	0	1
59	s	0	1
61	u	0	2
All	All	0	35

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	AG	429	LYS	C-N	13.90	1.51	1.33
63	w	35	LYS	CE-NZ	-12.73	1.11	1.49
29	O	80	ARG	CD-NE	-10.50	1.31	1.46
63	w	42	LYS	CD-CE	-9.41	1.24	1.52
25	K	45	ARG	CG-CD	7.73	1.75	1.52

The worst 5 of 147 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	AG	104	ARG	CA-C-N	17.96	154.29	121.97
16	AG	104	ARG	C-N-CA	17.96	154.29	121.97
16	AG	246	ASP	CA-C-N	14.50	137.97	119.84
16	AG	246	ASP	C-N-CA	14.50	137.97	119.84
16	AG	354	ALA	O-C-N	-13.70	107.29	122.09

There are no chirality outliers.

5 of 35 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	9	107	GLU	Peptide

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Mol	Chain	Res	Type	Group
9	9	79	PRO	Peptide
9	9	92	ALA	Peptide
12	AB	140	MET	Peptide
12	AB	151	LYS	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	54	0
2	1	857	922	922	68	0
3	2	746	811	811	59	0
4	3	788	844	844	43	0
5	4	753	780	780	88	0
6	5	726	0	392	112	0
7	6	703	0	396	34	0
8	7	527	0	262	83	0
9	9	1117	0	1155	258	0
10	A	1620	826	827	108	0
10	B	1620	813	827	112	0
11	AA	10381	0	10388	386	0
12	AB	1286	0	1300	437	0
13	AC	1698	0	1718	13	0
13	AD	2078	0	1891	37	0
14	AE	10404	0	10625	278	0
15	AF	650	0	658	10	0
16	AG	3852	0	3828	900	0
17	C	544	559	560	106	0
18	D	32703	16423	16453	734	0
19	E	669	719	719	78	0
20	F	589	629	629	58	0
21	G	1760	1785	1787	155	0
22	H	1730	1454	1455	168	0
23	I	1636	1710	1710	130	0
24	J	1643	1707	1707	85	0
25	K	1152	1196	1196	122	0
26	L	848	846	846	105	0
27	M	1181	1235	1238	124	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	N	979	1031	1031	94	0
29	O	1022	1070	1070	88	0
30	P	790	831	831	103	0
31	Q	877	887	887	96	0
32	R	939	1001	1001	92	0
33	S	805	844	844	73	0
34	T	714	734	734	91	0
35	U	649	666	666	58	0
36	V	648	691	691	68	0
37	W	663	688	688	48	0
38	X	900	964	965	113	0
39	Y	1032	0	1088	211	0
40	Z	227	0	237	31	0
41	a	61841	31077	31120	1317	0
42	b	582	599	599	46	0
43	c	625	652	652	35	0
44	d	2569	1301	1301	40	0
45	e	501	531	531	46	0
46	f	448	488	488	37	0
47	g	522	520	520	64	0
48	h	2082	2154	2154	138	0
49	i	444	459	458	49	0
50	j	1565	1617	1616	121	0
51	k	426	464	464	46	0
52	l	1552	1619	1619	125	0
53	m	377	418	418	30	0
54	n	1410	1443	1444	157	0
55	o	504	572	572	53	0
56	p	1313	1358	1358	74	0
57	q	302	343	343	25	0
58	r	1111	1148	1148	49	0
59	s	1129	1162	1162	127	0
60	t	946	1023	1023	104	0
61	u	1053	1129	1129	77	0
62	v	1074	1157	1157	122	0
63	w	951	994	994	103	0
64	x	892	923	923	44	0
65	y	917	962	962	56	0
66	z	947	1020	1019	84	0
67	AE	1	0	0	0	0
68	AE	2	0	0	3	0
All	All	181408	98638	132670	7742	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 25.

The worst 5 of 7742 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)
25:K:45:ARG:CD	25:K:45:ARG:CG	1.75	1.65
6:5:11:DA:C5'	12:AB:67:THR:HG22	1.20	1.60
6:5:10:DT:C7	11:AA:62:TYR:CD2	1.84	1.59
16:AG:425:LEU:CD2	16:AG:429:LYS:HE2	1.21	1.59
16:AG:287:ALA:CA	16:AG:331:LEU:HD12	1.19	1.59

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
2	1	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
3	2	92/100 (92%)	87 (95%)	5 (5%)	0	100	100
4	3	101/104 (97%)	98 (97%)	3 (3%)	0	100	100
5	4	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
9	9	146/165 (88%)	100 (68%)	43 (30%)	3 (2%)	5	28
11	AA	1312/1342 (98%)	1197 (91%)	114 (9%)	1 (0%)	48	82
12	AB	159/162 (98%)	107 (67%)	41 (26%)	11 (7%)	1	10
13	AC	217/329 (66%)	203 (94%)	12 (6%)	2 (1%)	14	49
13	AD	293/329 (89%)	263 (90%)	27 (9%)	3 (1%)	12	47
14	AE	1331/1407 (95%)	1211 (91%)	114 (9%)	6 (0%)	24	63
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	AG	493/495 (100%)	375 (76%)	86 (17%)	32 (6%)	1	12
17	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
19	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
20	F	68/71 (96%)	68 (100%)	0	0	100	100
21	G	223/241 (92%)	212 (95%)	10 (4%)	1 (0%)	30	67
22	H	255/557 (46%)	182 (71%)	66 (26%)	7 (3%)	4	24
23	I	206/233 (88%)	193 (94%)	13 (6%)	0	100	100
24	J	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
25	K	154/167 (92%)	145 (94%)	8 (5%)	1 (1%)	21	58
26	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	47
27	M	149/179 (83%)	140 (94%)	8 (5%)	1 (1%)	18	55
28	N	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
29	O	125/130 (96%)	116 (93%)	8 (6%)	1 (1%)	16	52
30	P	97/103 (94%)	89 (92%)	8 (8%)	0	100	100
31	Q	115/129 (89%)	107 (93%)	8 (7%)	0	100	100
32	R	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
33	S	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
34	T	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
35	U	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
36	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
37	W	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
38	X	114/118 (97%)	103 (90%)	9 (8%)	2 (2%)	6	32
39	Y	139/142 (98%)	101 (73%)	38 (27%)	0	100	100
40	Z	28/121 (23%)	22 (79%)	6 (21%)	0	100	100
42	b	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
43	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
45	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
46	f	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
47	g	64/70 (91%)	62 (97%)	2 (3%)	0	100	100
48	h	269/273 (98%)	255 (95%)	14 (5%)	0	100	100
49	i	54/57 (95%)	49 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
51	k	50/55 (91%)	50 (100%)	0	0	100	100
52	l	199/201 (99%)	188 (94%)	11 (6%)	0	100	100
53	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
54	n	175/179 (98%)	160 (91%)	14 (8%)	1 (1%)	21	58
55	o	62/65 (95%)	57 (92%)	4 (6%)	1 (2%)	7	36
56	p	173/177 (98%)	162 (94%)	11 (6%)	0	100	100
57	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
58	r	147/149 (99%)	139 (95%)	8 (5%)	0	100	100
59	s	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
60	t	121/123 (98%)	114 (94%)	7 (6%)	0	100	100
61	u	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
62	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
63	w	117/127 (92%)	112 (96%)	5 (4%)	0	100	100
64	x	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
65	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
66	z	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
All	All	10058/11053 (91%)	9175 (91%)	809 (8%)	74 (1%)	20	55

5 of 74 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	AB	107	PRO
12	AB	125	GLY
12	AB	130	PHE
12	AB	137	ALA
12	AB	141	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	84 (100%)	0	100	100
2	1	93/93 (100%)	93 (100%)	0	100	100
3	2	81/84 (96%)	81 (100%)	0	100	100
4	3	84/85 (99%)	84 (100%)	0	100	100
5	4	78/78 (100%)	78 (100%)	0	100	100
9	9	112/123 (91%)	112 (100%)	0	100	100
11	AA	1135/1157 (98%)	1130 (100%)	5 (0%)	84	83
12	AB	141/142 (99%)	124 (88%)	17 (12%)	5	17
13	AC	186/286 (65%)	186 (100%)	0	100	100
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1122/1168 (96%)	1104 (98%)	18 (2%)	55	69
15	AF	70/75 (93%)	69 (99%)	1 (1%)	59	71
16	AG	409/409 (100%)	288 (70%)	121 (30%)	0	2
17	C	57/65 (88%)	57 (100%)	0	100	100
19	E	65/66 (98%)	65 (100%)	0	100	100
20	F	60/61 (98%)	60 (100%)	0	100	100
21	G	187/199 (94%)	187 (100%)	0	100	100
22	H	137/461 (30%)	137 (100%)	0	100	100
23	I	171/190 (90%)	171 (100%)	0	100	100
24	J	172/173 (99%)	171 (99%)	1 (1%)	78	81
25	K	119/126 (94%)	119 (100%)	0	100	100
26	L	91/116 (78%)	91 (100%)	0	100	100
27	M	124/147 (84%)	124 (100%)	0	100	100
28	N	104/105 (99%)	104 (100%)	0	100	100
29	O	105/107 (98%)	105 (100%)	0	100	100
30	P	86/90 (96%)	86 (100%)	0	100	100
31	Q	90/99 (91%)	90 (100%)	0	100	100
32	R	101/104 (97%)	101 (100%)	0	100	100
33	S	83/84 (99%)	83 (100%)	0	100	100
34	T	76/77 (99%)	76 (100%)	0	100	100
35	U	65/65 (100%)	65 (100%)	0	100	100
36	V	74/78 (95%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	W	72/79 (91%)	72 (100%)	0	100	100
38	X	94/96 (98%)	94 (100%)	0	100	100
39	Y	109/110 (99%)	109 (100%)	0	100	100
40	Z	26/85 (31%)	26 (100%)	0	100	100
42	b	58/63 (92%)	58 (100%)	0	100	100
43	c	67/68 (98%)	67 (100%)	0	100	100
45	e	54/55 (98%)	54 (100%)	0	100	100
46	f	48/49 (98%)	48 (100%)	0	100	100
47	g	59/62 (95%)	59 (100%)	0	100	100
48	h	216/218 (99%)	216 (100%)	0	100	100
49	i	47/48 (98%)	47 (100%)	0	100	100
50	j	164/164 (100%)	164 (100%)	0	100	100
51	k	47/49 (96%)	47 (100%)	0	100	100
52	l	165/165 (100%)	165 (100%)	0	100	100
53	m	38/38 (100%)	38 (100%)	0	100	100
54	n	148/150 (99%)	148 (100%)	0	100	100
55	o	51/52 (98%)	51 (100%)	0	100	100
56	p	136/138 (99%)	136 (100%)	0	100	100
57	q	34/34 (100%)	34 (100%)	0	100	100
58	r	114/114 (100%)	114 (100%)	0	100	100
59	s	116/116 (100%)	116 (100%)	0	100	100
60	t	104/104 (100%)	104 (100%)	0	100	100
61	u	103/103 (100%)	103 (100%)	0	100	100
62	v	109/109 (100%)	109 (100%)	0	100	100
63	w	99/103 (96%)	99 (100%)	0	100	100
64	x	86/87 (99%)	86 (100%)	0	100	100
65	y	99/100 (99%)	99 (100%)	0	100	100
66	z	89/90 (99%)	89 (100%)	0	100	100
All	All	8299/9132 (91%)	8136 (98%)	163 (2%)	48	65

5 of 163 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	AG	273	ILE
16	AG	340	THR
16	AG	282	GLN
16	AG	309	VAL
16	AG	361	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 124 such sidechains are listed below:

Mol	Chain	Res	Type
16	AG	337	ASN
58	r	133	GLN
24	J	36	GLN
57	q	13	ASN
64	x	38	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	8 (10%)
10	B	75/76 (98%)	29 (38%)	8 (10%)
18	D	1514/1542 (98%)	289 (19%)	20 (1%)
41	a	2859/2904 (98%)	510 (17%)	0
44	d	119/120 (99%)	15 (12%)	0
8	7	23/53 (43%)	14 (60%)	3 (13%)
All	All	4665/4771 (97%)	886 (18%)	39 (0%)

5 of 886 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	3	G
8	7	4	U
8	7	5	U
8	7	7	U
8	7	8	U

5 of 39 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	D	992	U
18	D	1447	A
18	D	1145	A

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Mol	Chain	Res	Type
18	D	1212	U
18	D	1492	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

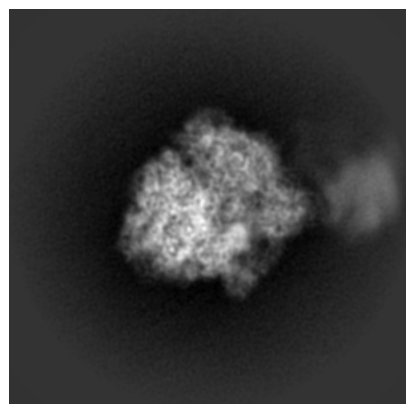
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43335. These allow visual inspection of the internal detail of the map and identification of artifacts.

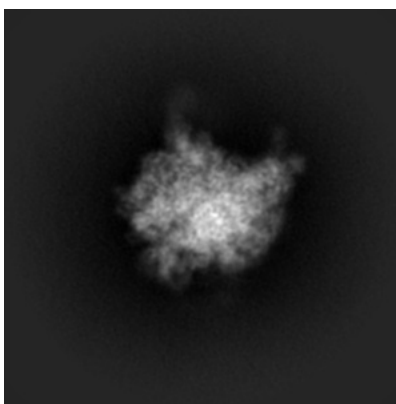
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

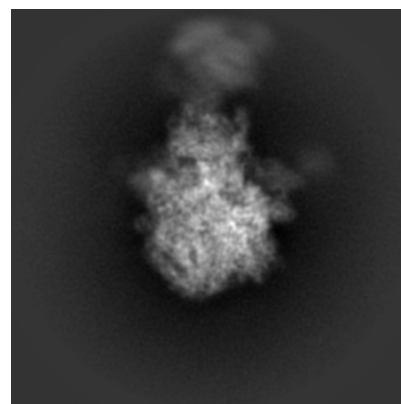
6.1.1 Primary map



X

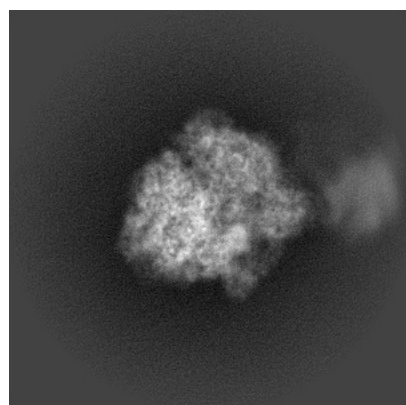


Y

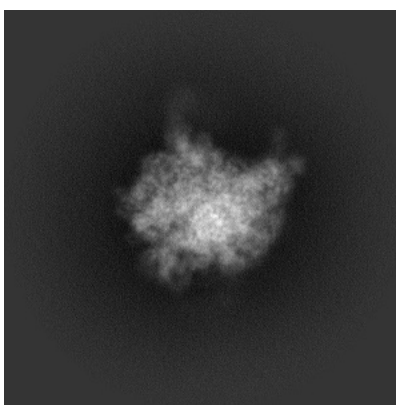


Z

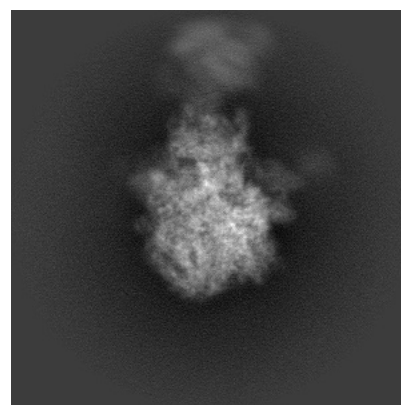
6.1.2 Raw map



X



Y

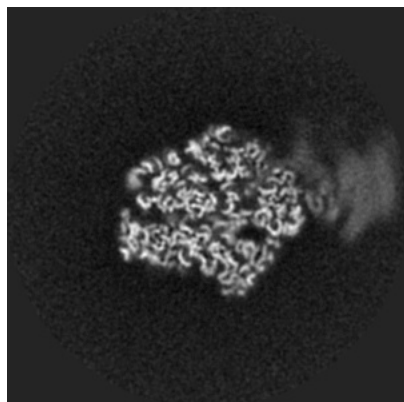


Z

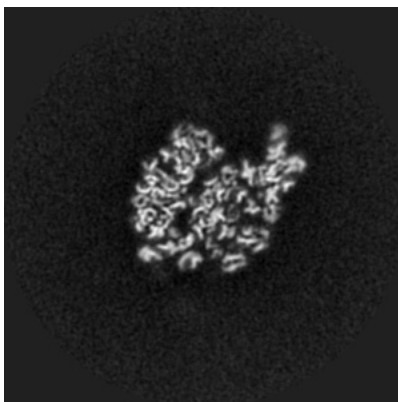
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

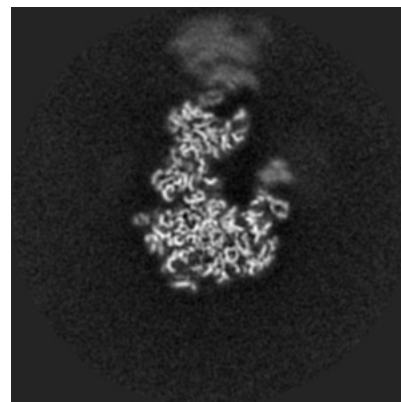
6.2.1 Primary map



X Index: 256

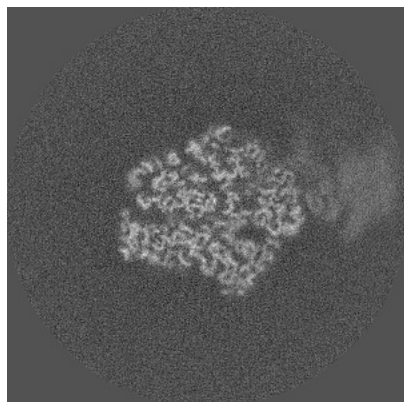


Y Index: 256

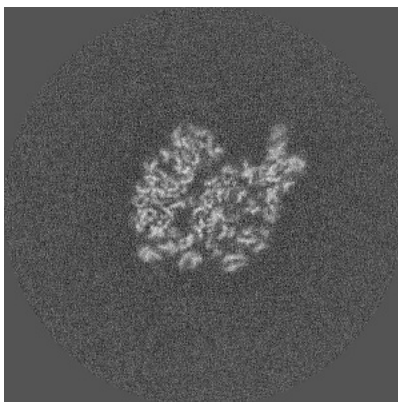


Z Index: 256

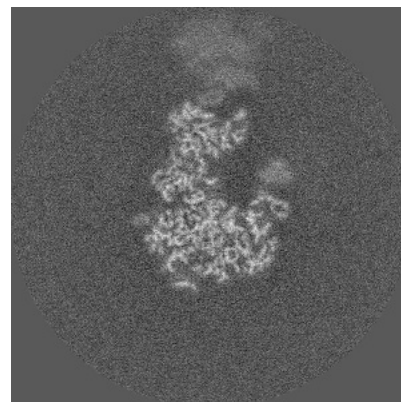
6.2.2 Raw map



X Index: 256



Y Index: 256

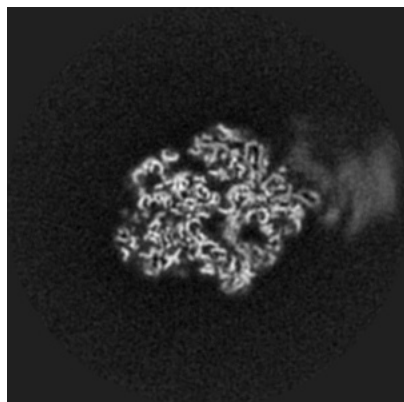


Z Index: 256

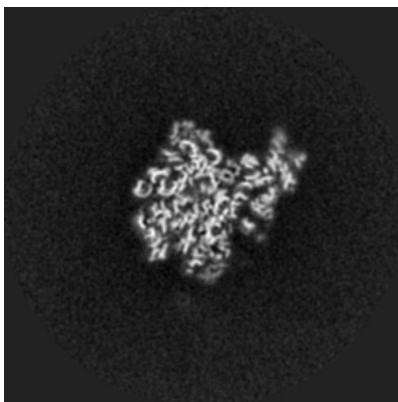
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

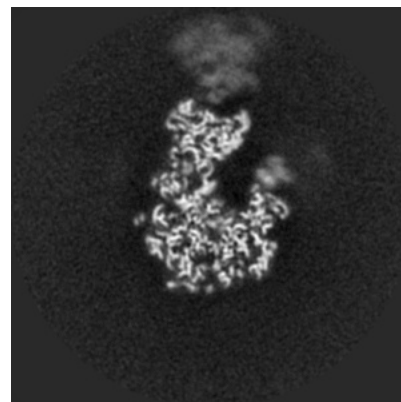
6.3.1 Primary map



X Index: 249

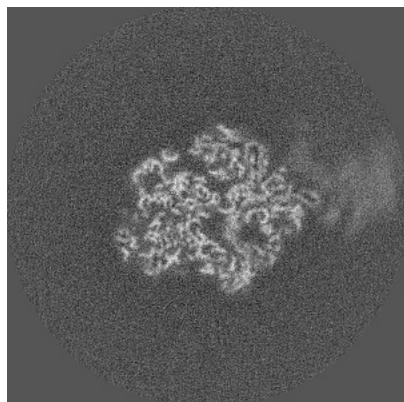


Y Index: 246

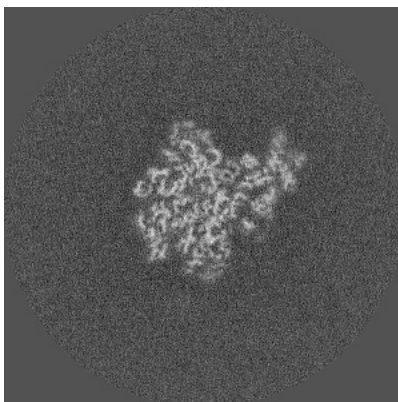


Z Index: 250

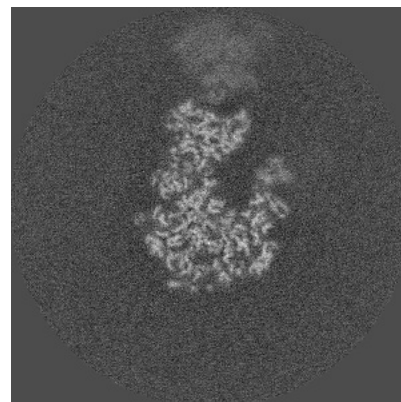
6.3.2 Raw map



X Index: 249



Y Index: 246



Z Index: 252

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

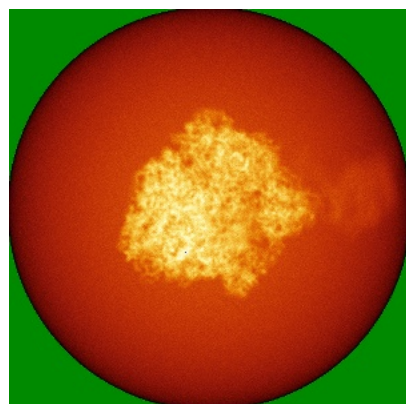


Y

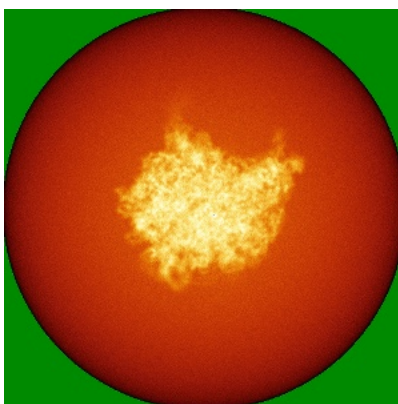


Z

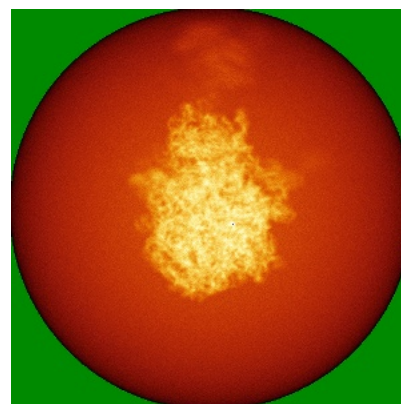
6.4.2 Raw map



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



X



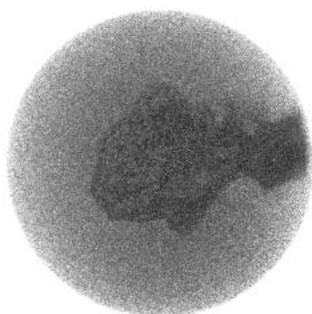
Y



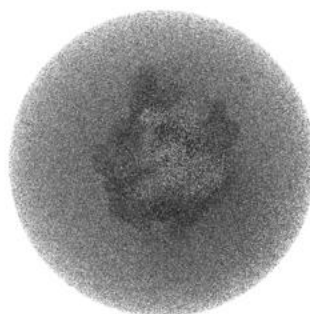
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0032. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

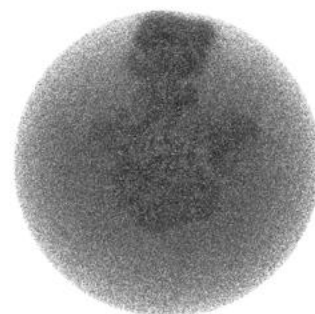
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

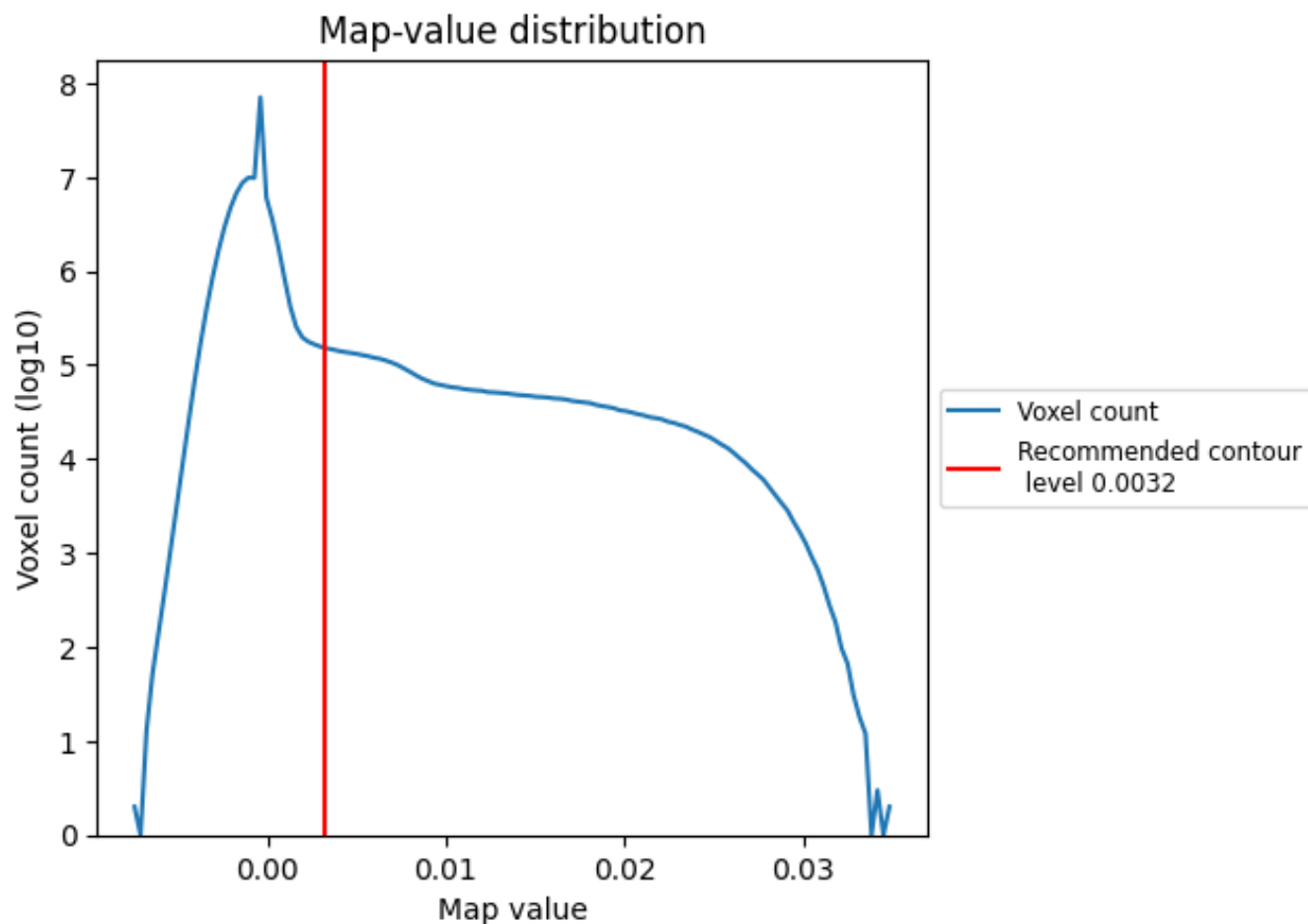
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

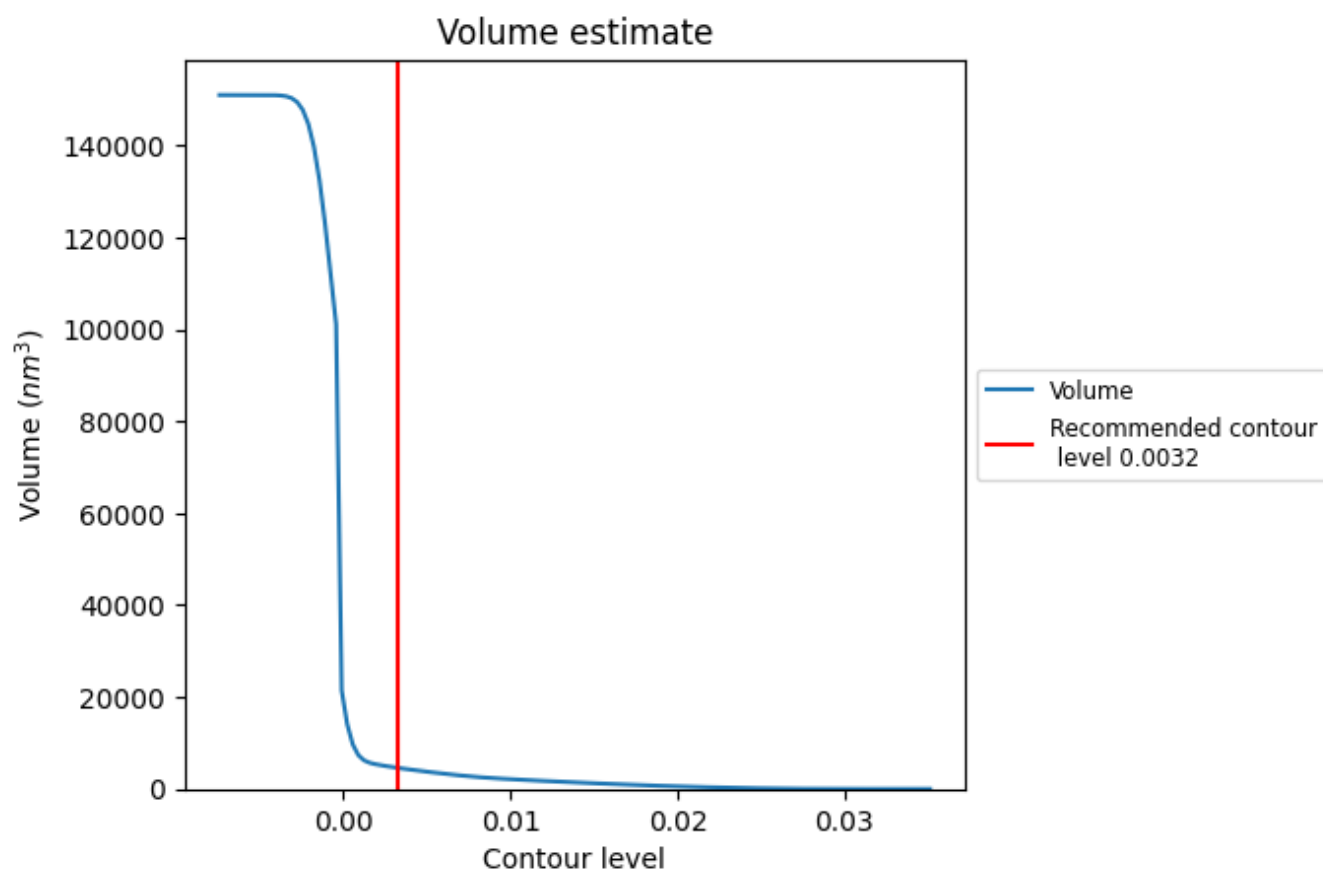
This section contains the results of statistical analysis of the map.

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.

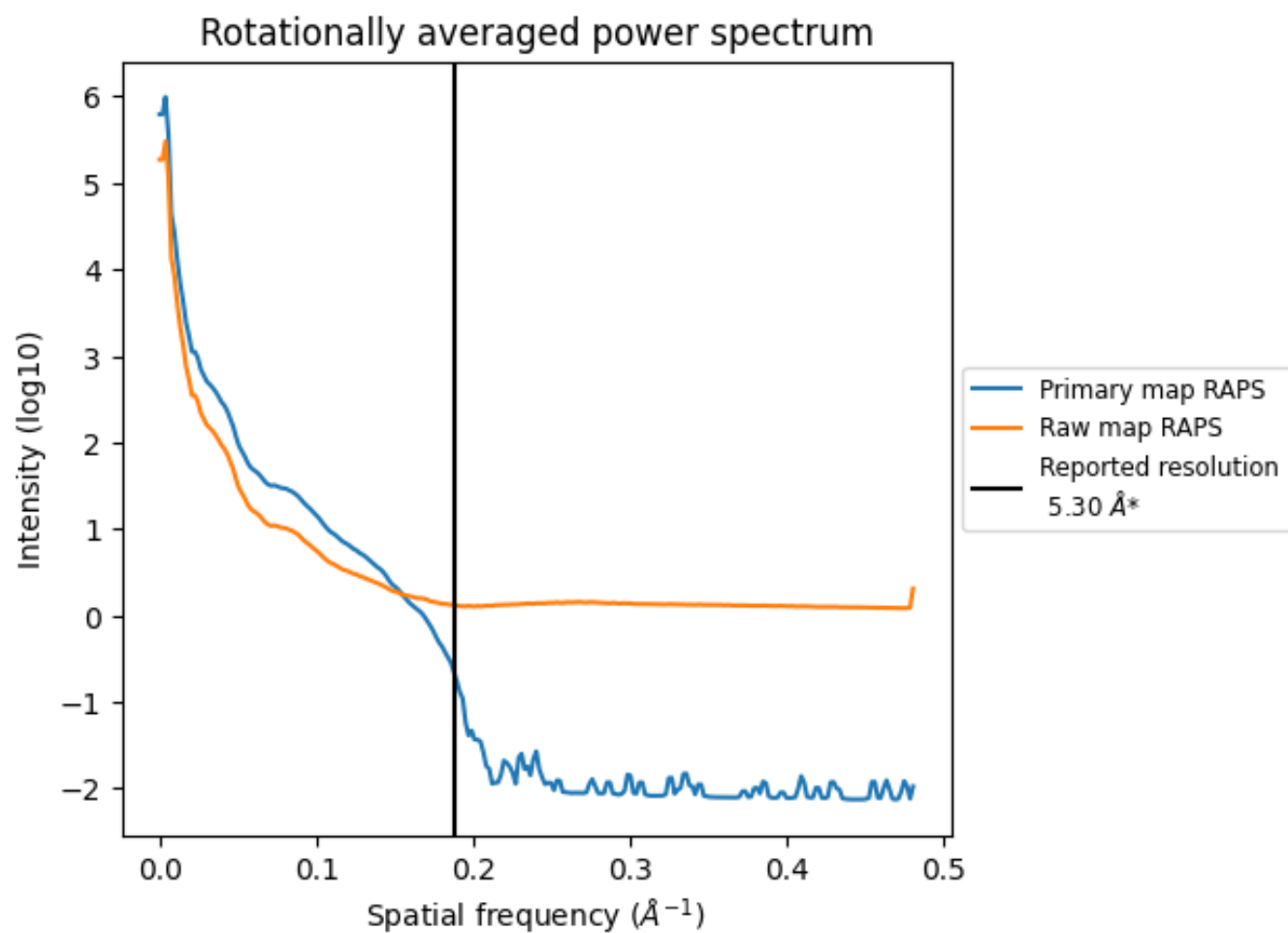
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4617 nm^3 ; this corresponds to an approximate mass of 4171 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](#)

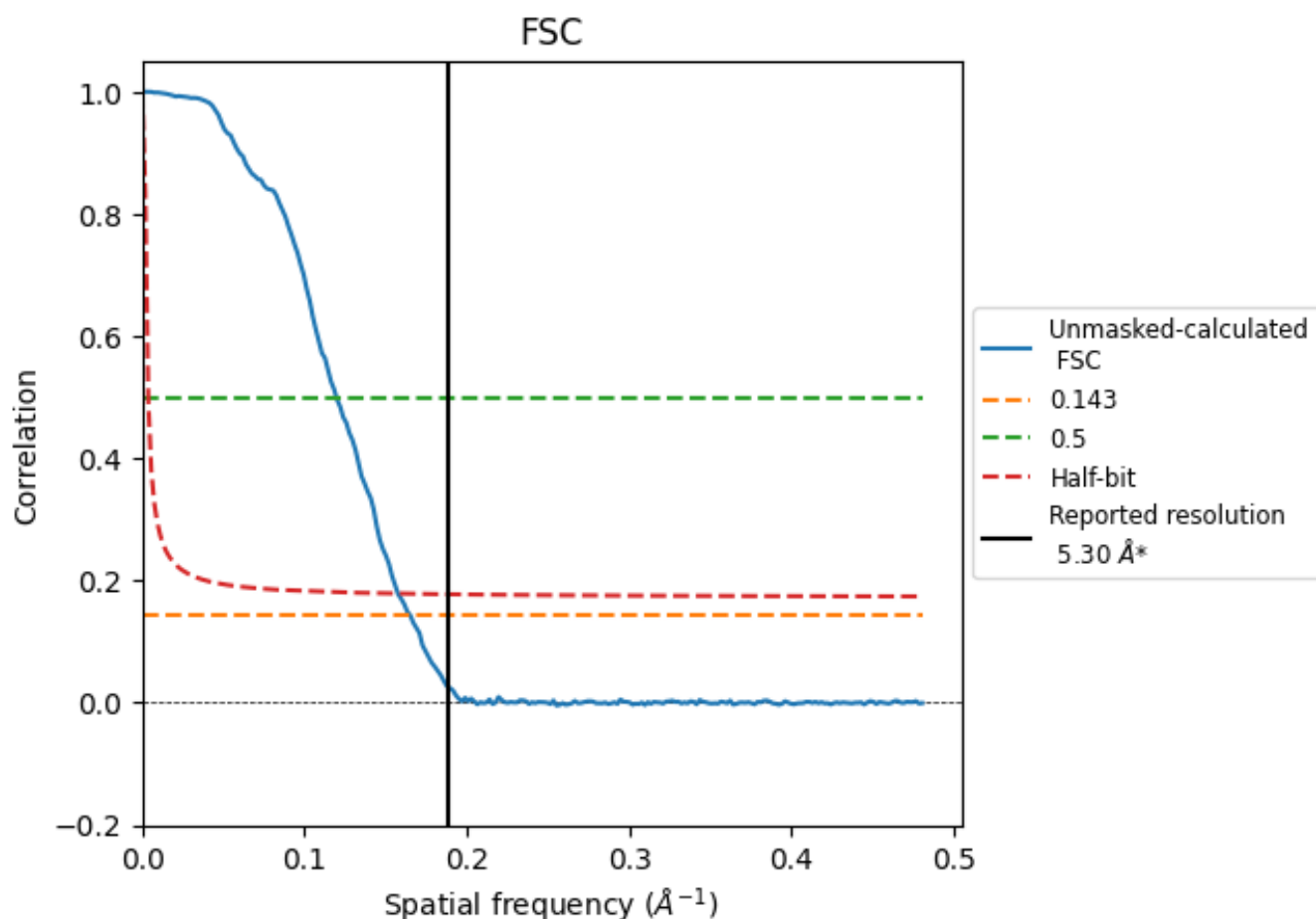


*Reported resolution corresponds to spatial frequency of 0.189 $\text{\AA}^{-1}$

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 0.189 Å⁻¹

8.2 Resolution estimates [i](#)

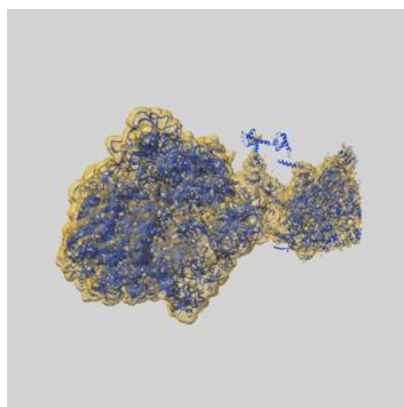
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.06	8.35	6.35

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.06 differs from the reported value 5.3 by more than 10 %

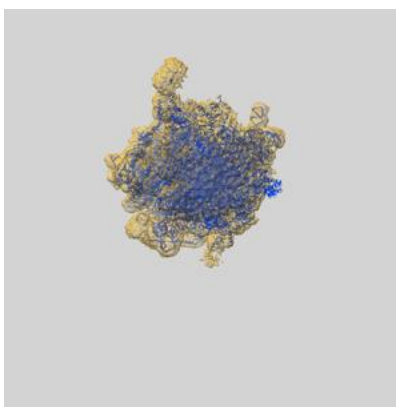
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43335 and PDB model 8VL1. Per-residue inclusion information can be found in section [3](#) on page [17](#).

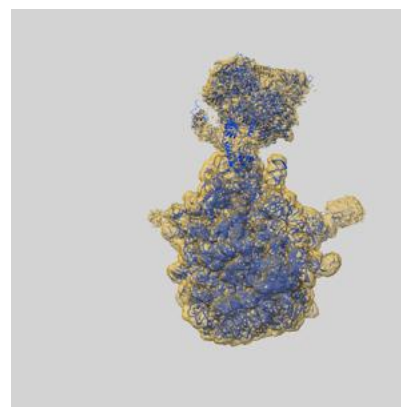
9.1 Map-model overlay [i](#)



X



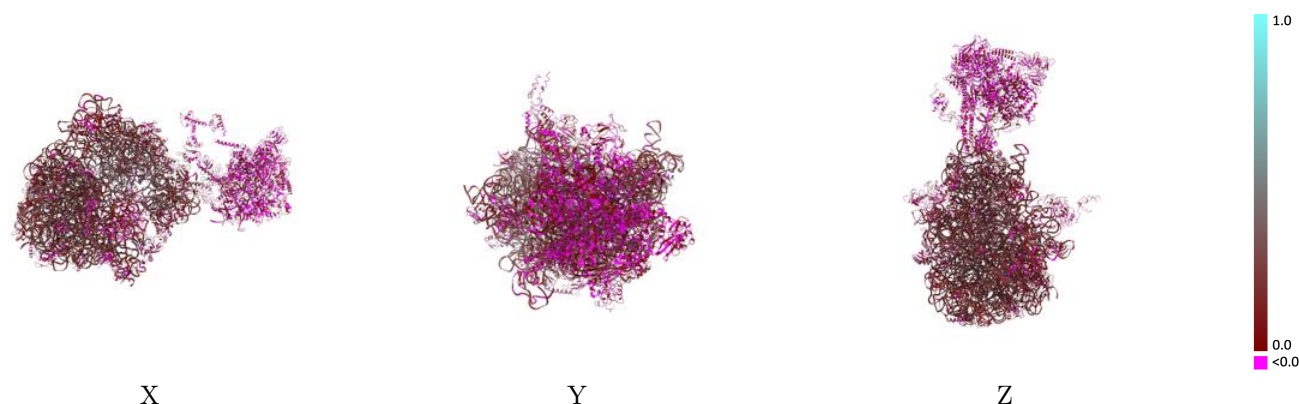
Y



Z

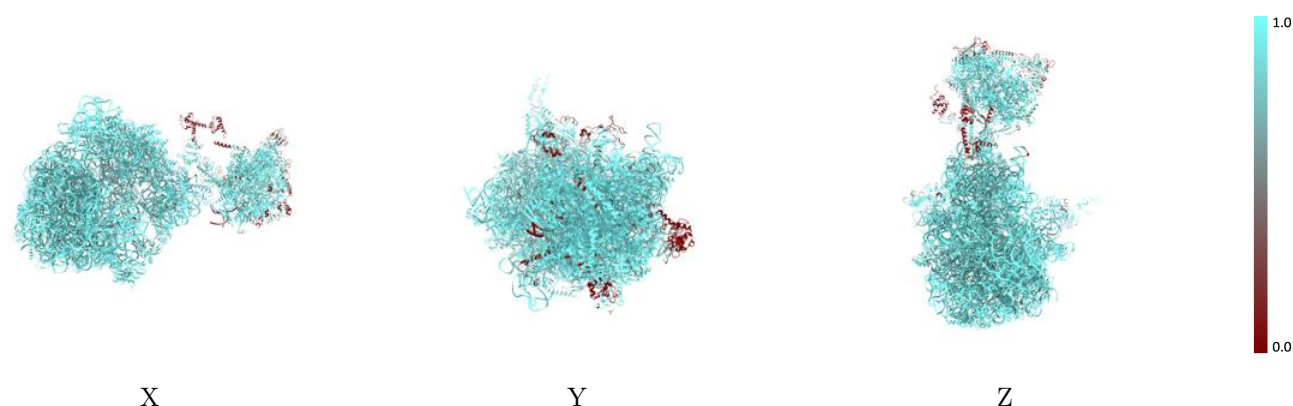
The images above show the 3D surface view of the map at the recommended contour level 0.0032 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



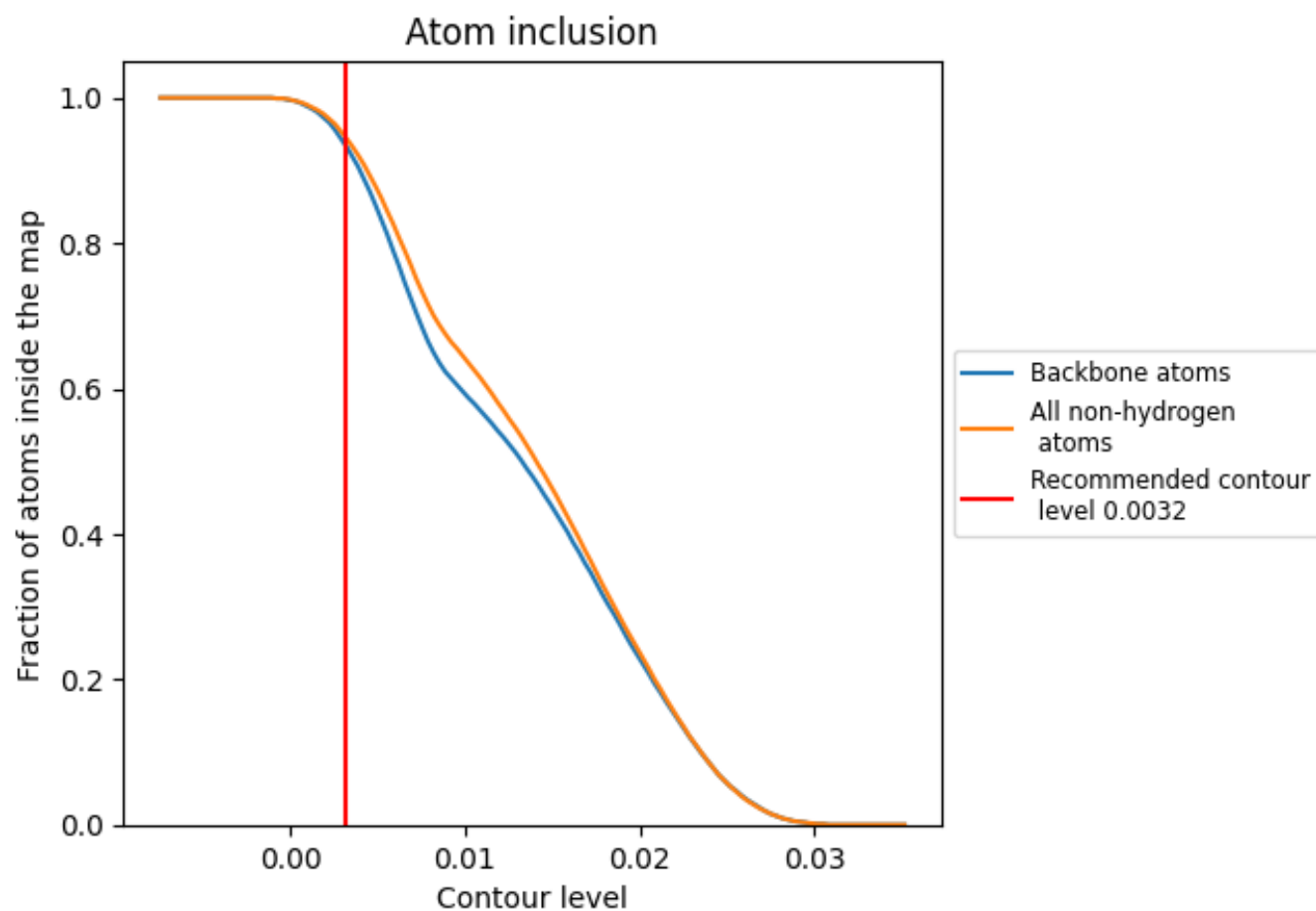
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0032).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 94% 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 (0.0032) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9450	 0.1690
0	 0.9860	 0.1640
1	 0.9800	 0.1890
2	 0.9740	 0.1670
3	 0.9850	 0.1450
4	 0.9820	 0.1480
5	 0.7960	 0.0610
6	 0.8010	 0.0410
7	 0.9830	 0.0840
9	 0.9400	 0.0720
A	 0.9990	 0.1890
AA	 0.8670	 0.0310
AB	 0.8960	 0.0830
AC	 0.9080	 0.0330
AD	 0.5300	 0.0270
AE	 0.8970	 0.0400
AF	 0.6910	 0.0140
AG	 0.5570	 0.0550
B	 0.9490	 0.1000
C	 0.9940	 0.1750
D	 0.9970	 0.2270
E	 0.9880	 0.1450
F	 0.9820	 0.1930
G	 0.9750	 0.1590
H	 0.8660	 0.0740
I	 0.9710	 0.1820
J	 0.9860	 0.1610
K	 0.9890	 0.2160
L	 0.9880	 0.1690
M	 0.9840	 0.1640
N	 0.9760	 0.1830
O	 0.9810	 0.1480
P	 0.9740	 0.1640
Q	 0.9870	 0.1760
R	 0.9910	 0.2180



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Chain	Atom inclusion	Q-score
S	 0.9830	 0.1590
T	 0.9860	 0.1650
U	 0.9860	 0.1450
V	 0.9780	 0.1870
W	 0.9290	 0.1100
X	 0.9680	 0.1290
Y	 0.8430	 0.0730
Z	 0.9340	 0.0500
a	 0.9980	 0.2190
b	 0.9750	 0.1500
c	 0.9820	 0.1810
d	 0.9980	 0.1840
e	 0.9900	 0.1330
f	 0.9860	 0.1770
g	 0.9770	 0.0970
h	 0.9860	 0.1680
i	 0.9740	 0.2050
j	 0.9810	 0.1510
k	 0.9900	 0.1420
l	 0.9740	 0.1510
m	 0.9890	 0.1910
n	 0.9690	 0.1210
o	 0.9820	 0.1500
p	 0.9840	 0.1350
q	 0.9830	 0.1490
r	 0.9170	 0.1190
s	 0.9780	 0.1690
t	 0.9590	 0.1590
u	 0.9870	 0.1610
v	 0.9870	 0.1810
w	 0.9770	 0.1650
x	 0.9700	 0.0960
y	 0.9760	 0.1460
z	 0.9870	 0.1550