



## wwPDB EM Validation Summary Report ⓘ

Jul 15, 2025 – 11:54 AM EDT

PDB ID : 8VOR / pdb\_00008vor  
EMDB ID : EMD-43390  
Title : Escherichia coli transcription-translation loosely coupled complex (TTC-LC) containing mRNA with a 51 nt long spacer, NusG, NusA, and fMet-tRNAs in E-site and P-site  
Authors : Molodtsov, V.; Wang, C.; Ebright, R.H.  
Deposited on : 2024-01-15  
Resolution : 3.60 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev118  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.44

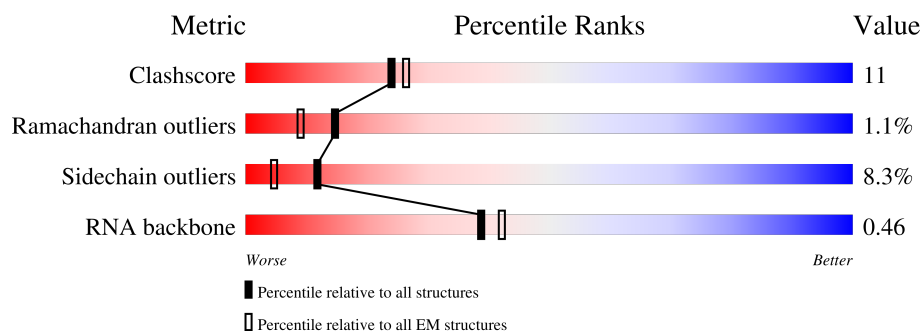
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.60 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	84% 15% .
2	1	110	75% 25%
3	2	100	86% 7% . 6%
4	3	104	84% 14% ..
5	4	94	97% .
6	5	36	6% 28% 36% 36%
7	6	36	36% 39% 25%









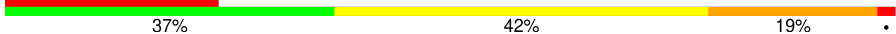
















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Mol	Chain	Length	Quality of chain
8	7	68	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	181	
13	AC	329	
13	AD	329	
14	AE	1407	
15	AF	91	
16	AG	495	
17	C	75	
18	D	1542	
19	E	87	
20	F	71	
21	G	241	
22	H	557	
23	I	233	
24	J	206	
25	K	167	
26	L	135	
27	M	179	
28	N	130	
29	O	130	
30	P	103	

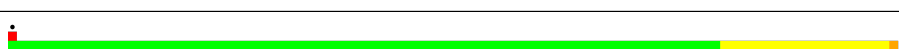

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Mol	Chain	Length	Quality of chain
31	Q	129	 82% 9% 9%
32	R	124	 86% 11% .
33	S	101	 89% 8% ...
34	T	89	 79% 18% ..
35	U	82	 88% 11% .
36	V	84	 87% 7% . 5%
37	W	92	 82% 8% . 10%
38	X	118	 76% 17% 5% .
39	Y	142	 24% 37% 42% 19% ..
40	Z	121	 7% 10% 7% . 75%
41	a	2904	 73% 23% ..
42	b	85	 84% 6% 11%
43	c	78	 88% 8% ..
44	d	120	 81% 19%
45	e	63	 86% 11% ..
46	f	59	 81% 15% ..
47	g	70	 81% 11% . 6%
48	h	273	 84% 14% ..
49	i	57	 77% 19% ..
50	j	209	 88% 11%
51	k	55	 89% 5% 5%
52	l	201	 85% 14% .
53	m	46	 78% 17% .
54	n	179	 75% 21% ..
55	o	65	 88% 6% 5% .

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Mol	Chain	Length	Quality of chain
56	p	177	 90% 8% .
57	q	38	 89% 8% .
58	r	149	 88% 9% .
59	s	142	 82% 16% .
60	t	123	 80% 19% .
61	u	144	 89% 10% .
62	v	136	 91% 8% .
63	w	127	 77% 17% 6%
64	x	117	 82% 16% ..
65	y	115	 89% 10% .
66	z	118	 84% 15% .

## 2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 291173 atoms, of which 109913 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ribosomal protein L21.

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

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

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

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

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

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

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

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

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

- Molecule 6 is a DNA chain called NT DNA.

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

- Molecule 7 is a DNA chain called T DNA.

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

- Molecule 8 is a RNA chain called mRNA with 51 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	31	Total	C	H	N	O	P	0	0
			744	289	97	92	235	31		

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

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
10	A	76	Total	C	H	N	O	P	0	0
			2446	723	826	295	527	75		
10	B	76	Total	C	H	N	O	P	0	0
			2434	723	814	295	527	75		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AB	161	Total	C	N	O	S	0	0
			1276	813	221	235	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AC	220	Total	C	N	O	S	0	0
			1690	1056	298	330	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	AD	298	Total	C	N	O	S	0	0
			2073	1284	377	406	6		

- Molecule 14 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AE	1335	Total	C	H	N	O	S	0	0
			21000	6526	10612	1854	1958	50		

- 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

Chain 0:  84% 15% .



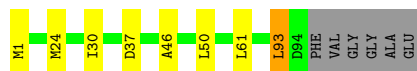
- Molecule 2: 50S ribosomal protein L22

Chain 1:  75% 25%




- Molecule 3: 50S ribosomal protein L23

Chain 2:  86% 7% . 6%



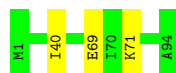
- Molecule 4: 50S ribosomal protein L24

Chain 3:  84% 14% ..

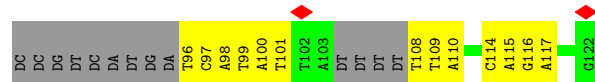
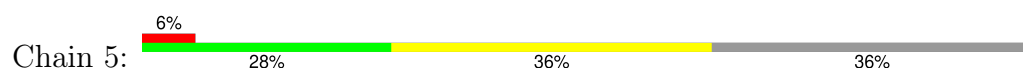


- Molecule 5: 50S ribosomal protein L25

Chain 4:  97% .



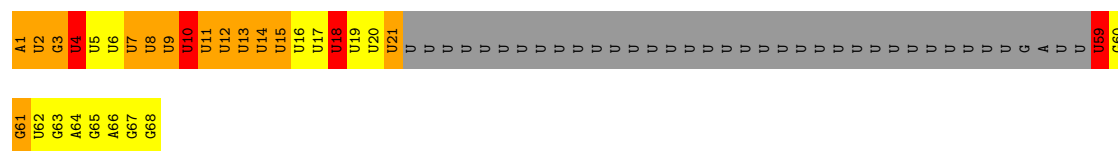
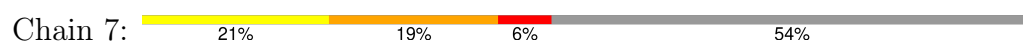
- Molecule 6: NT DNA



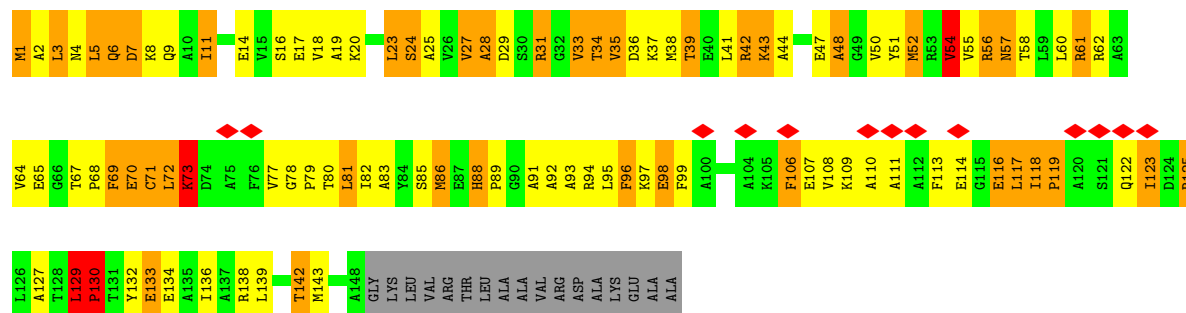
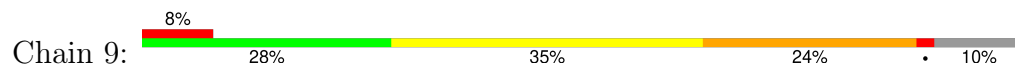
• Molecule 7: T DNA



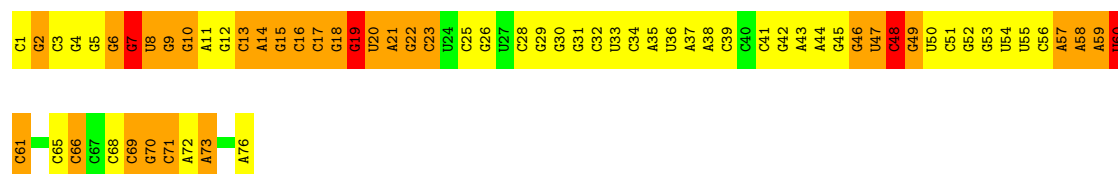
• Molecule 8: mRNA with 51 nt long spacer



• Molecule 9: 50S ribosomal protein L10

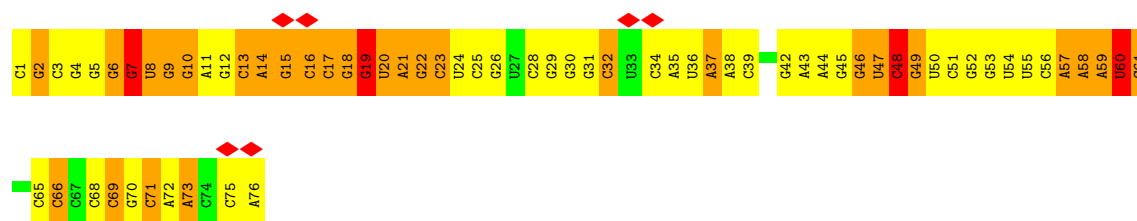


• Molecule 10: E-site and P-site tRNA (fMet)

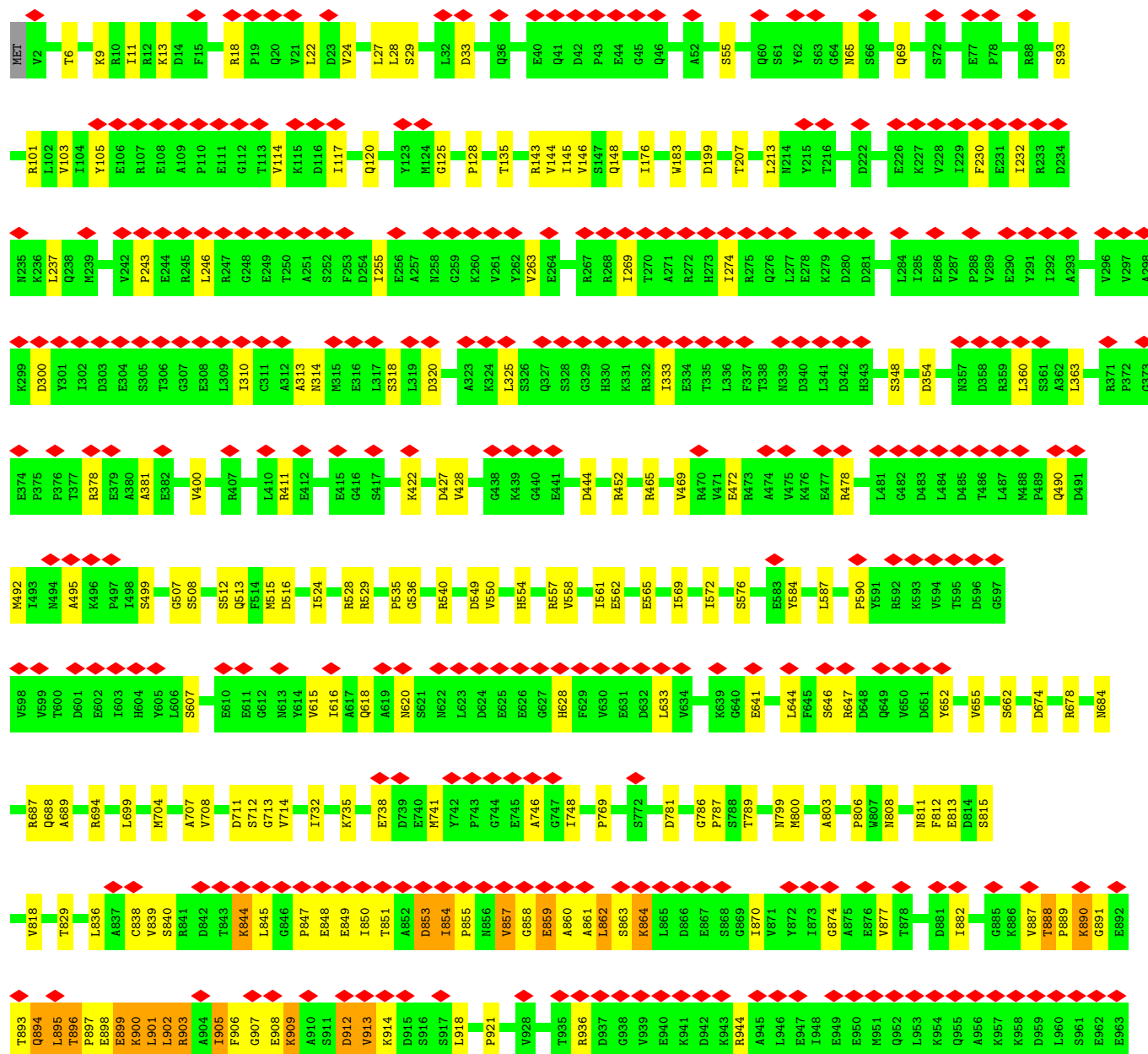
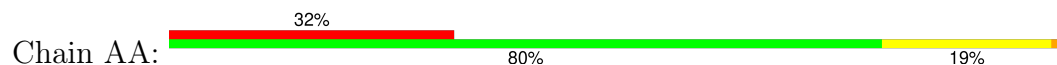


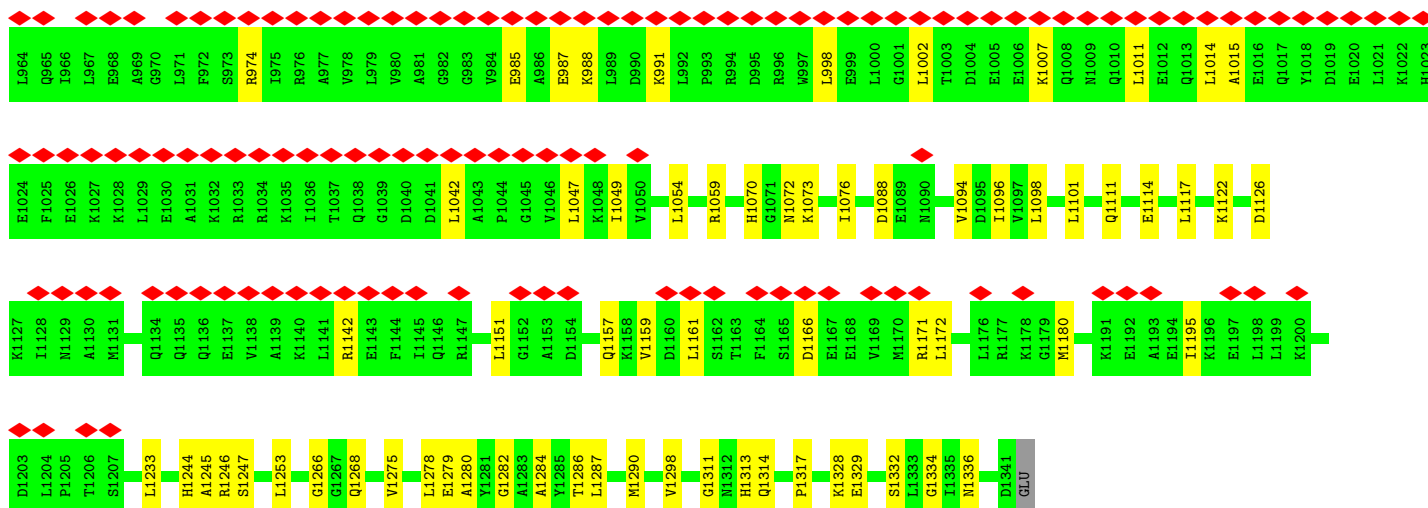
• Molecule 10: E-site and P-site tRNA (fMet)



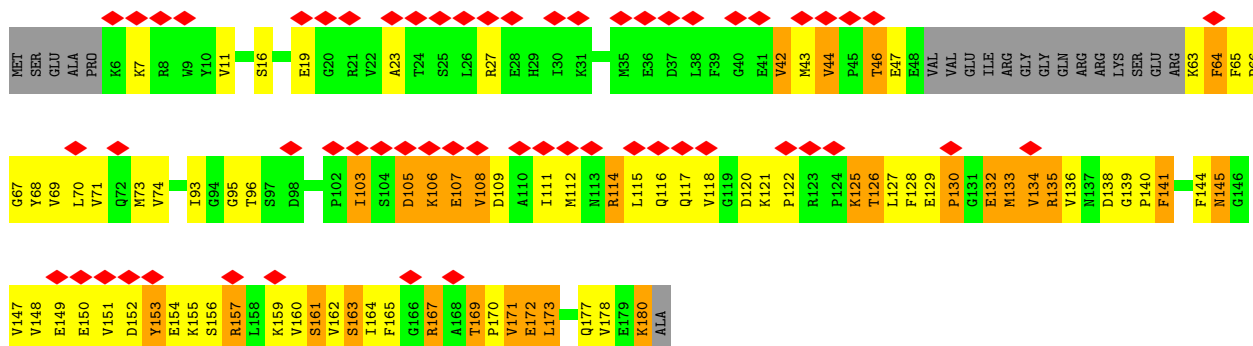
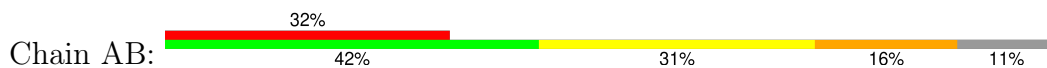


• Molecule 11: DNA-directed RNA polymerase subunit beta

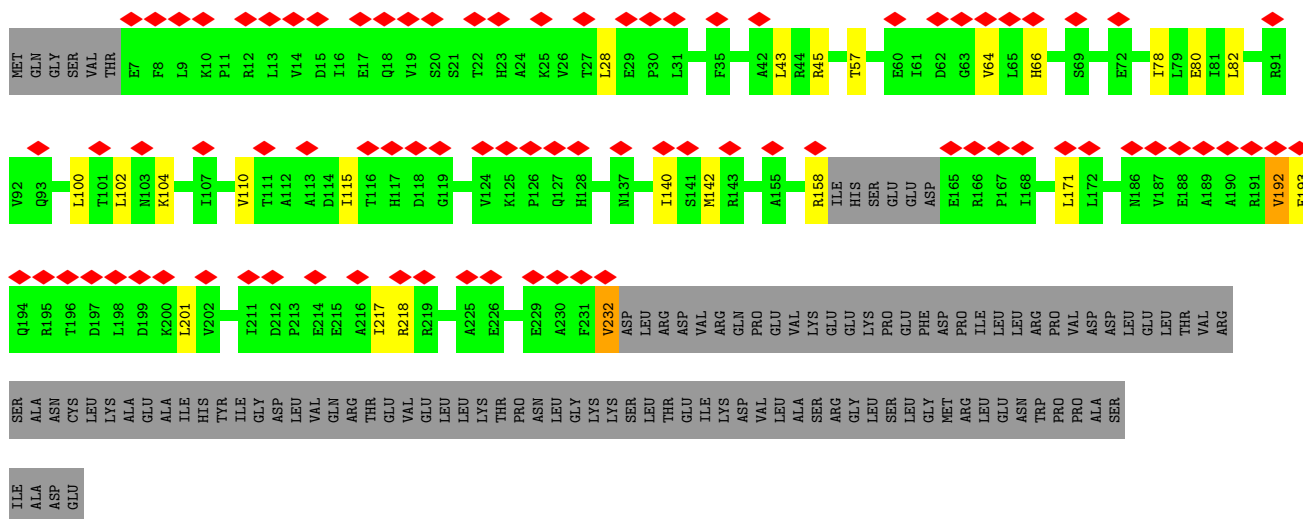




• Molecule 12: Transcription termination/antitermination protein NusG

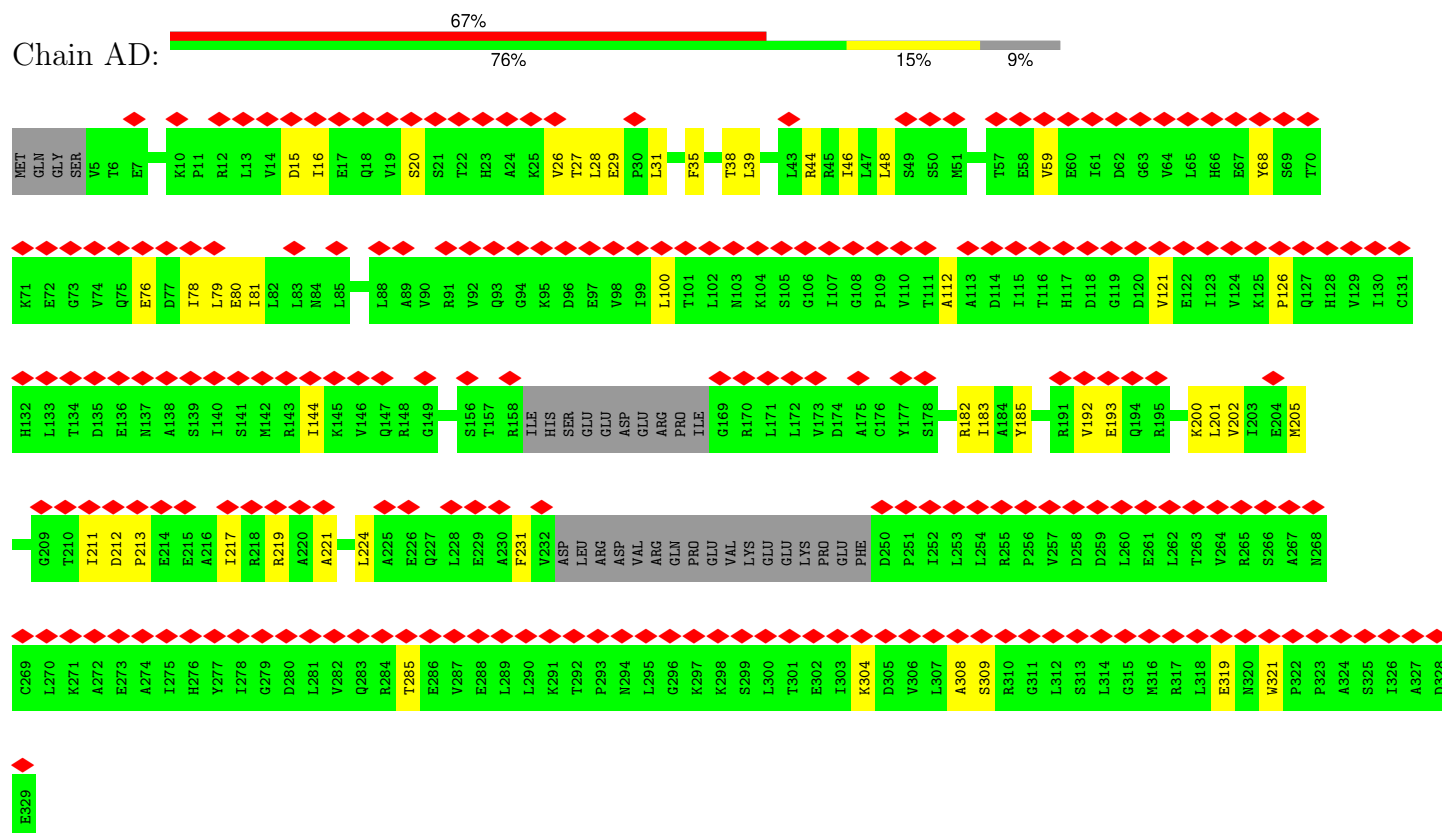


• Molecule 13: DNA-directed RNA polymerase subunit alpha



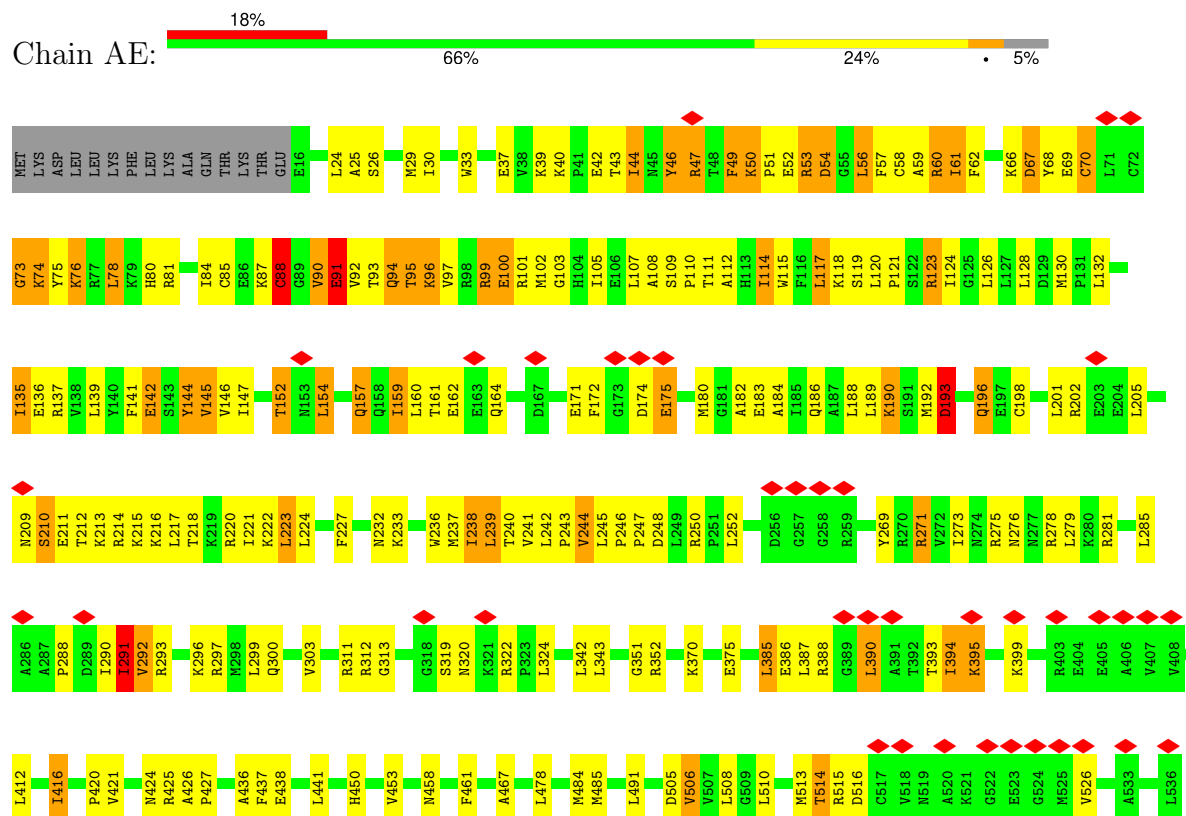
• Molecule 13: DNA-directed RNA polymerase subunit alpha

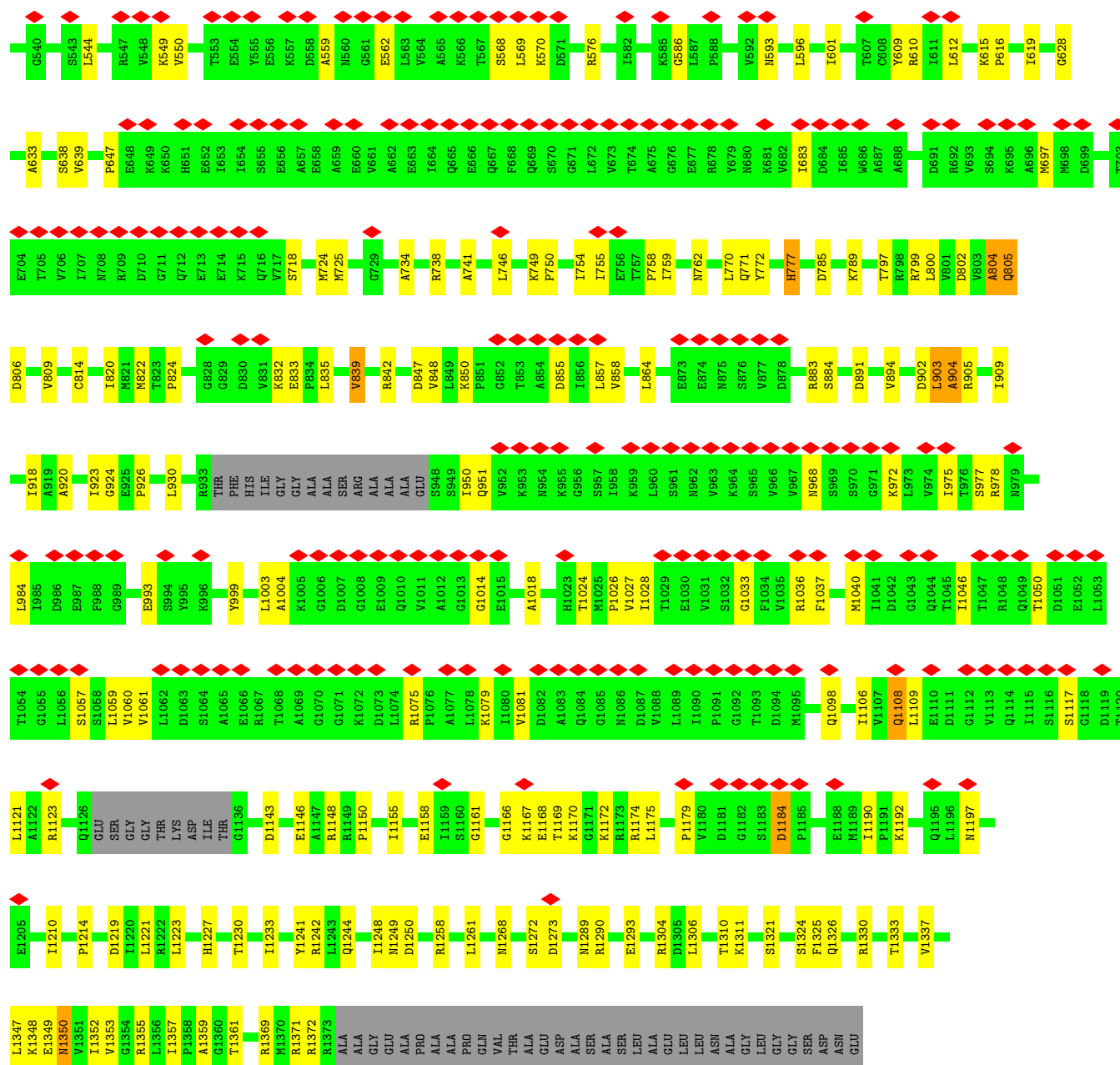
Chain AD:



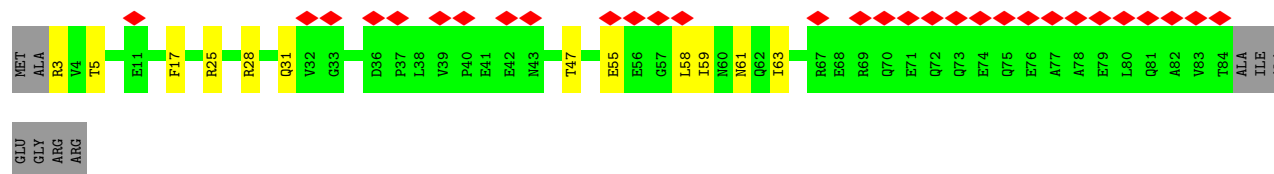
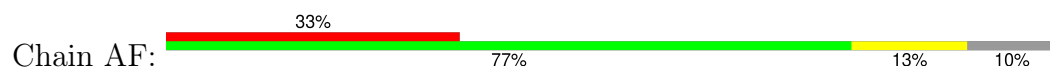
• Molecule 14: DNA-directed RNA polymerase subunit beta'

Chain AE:



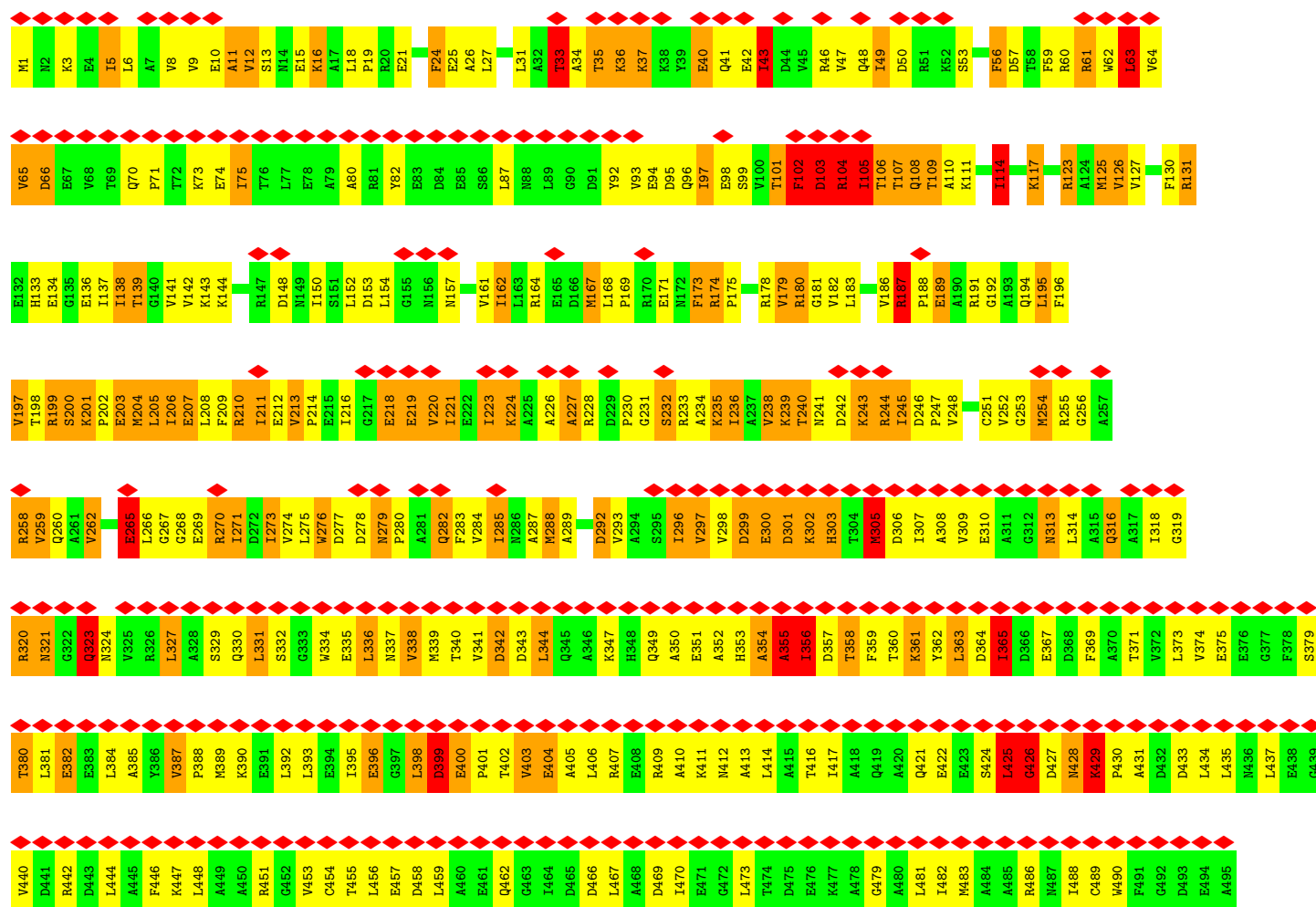


• Molecule 15: DNA-directed RNA polymerase subunit omega



• Molecule 16: Transcription termination/antitermination protein NusA





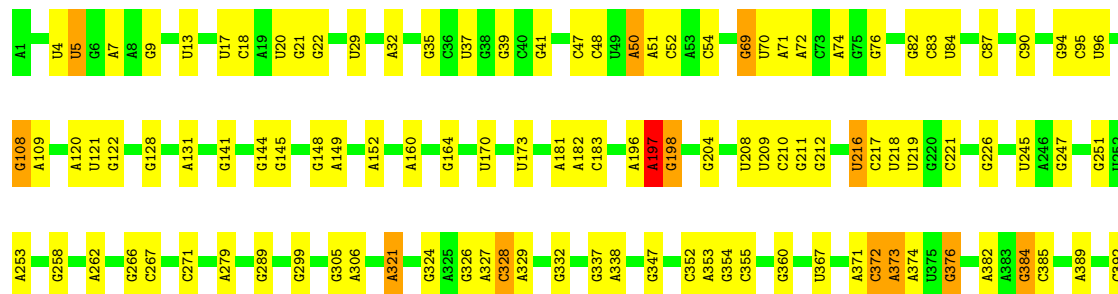
• Molecule 17: 30S ribosomal protein S18

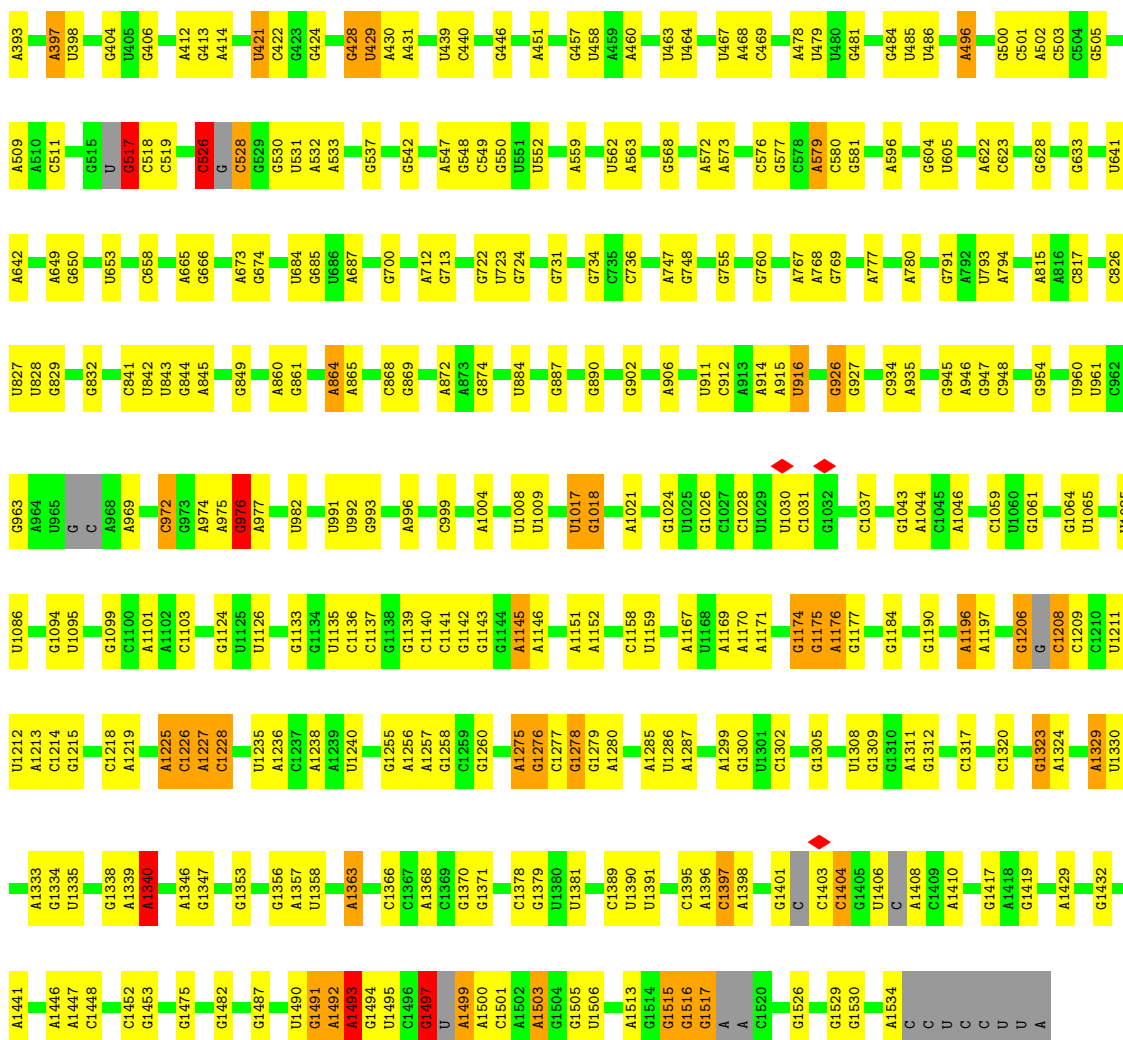
Chain C: 73% 13% 12%



• Molecule 18: 16S rRNA

Chain D: 70% 25%





• Molecule 19: 30S ribosomal protein S20

Chain E: 87% 11% •



• Molecule 20: 30S ribosomal protein S21

Chain F: 87% 10% ••

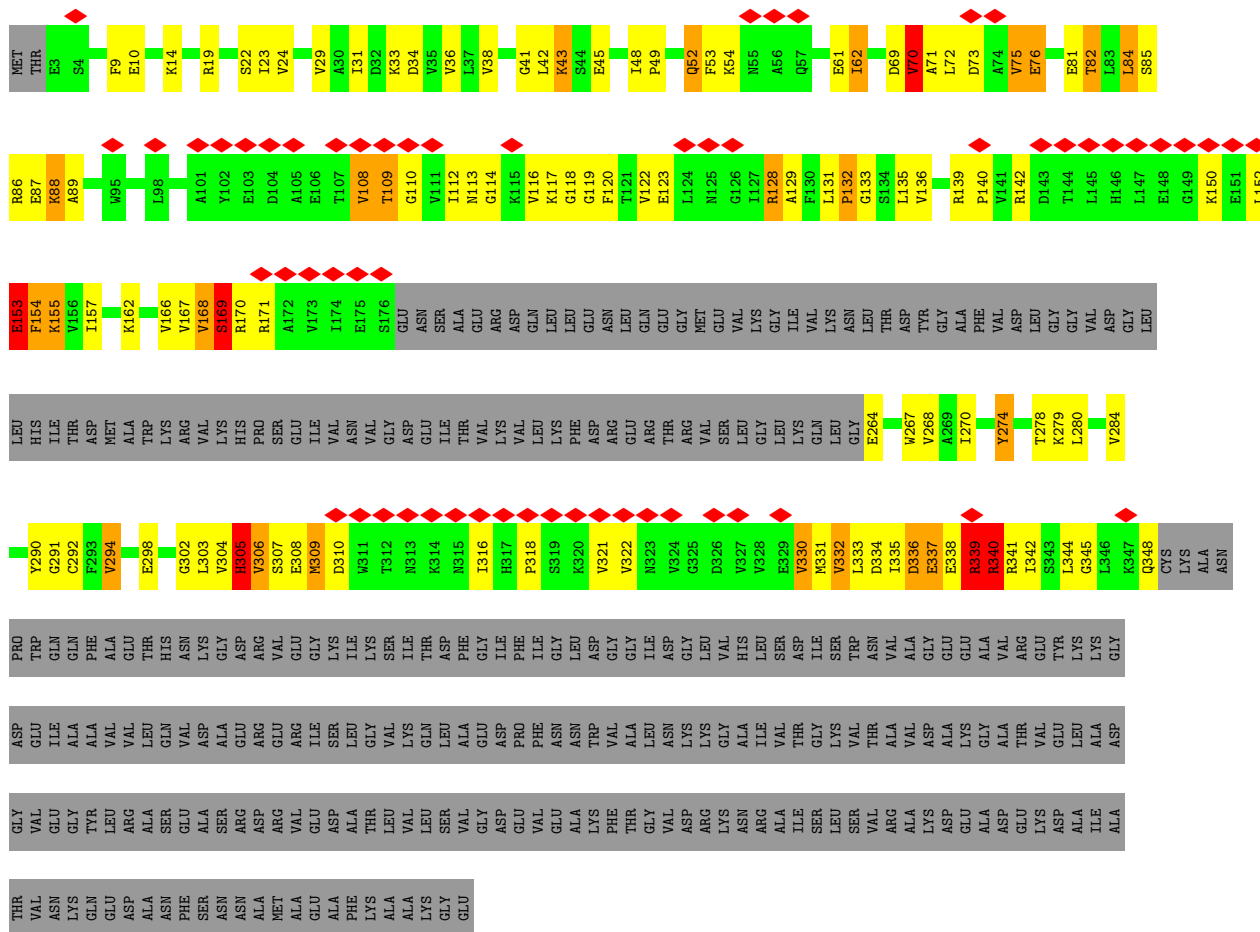


• Molecule 21: 30S ribosomal protein S2

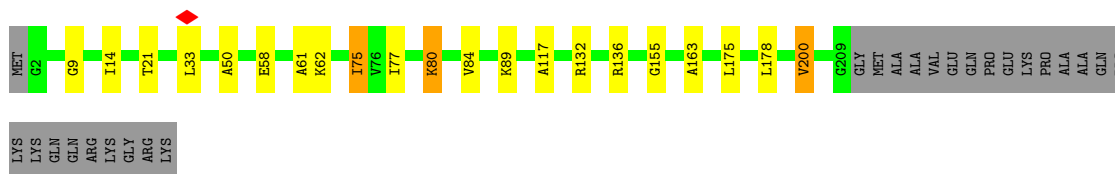
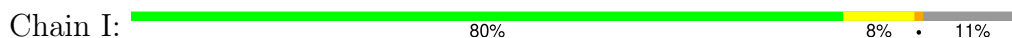
Chain G: 80% 12% • 7%



- Molecule 22: 30S ribosomal protein S1



- Molecule 23: 30S ribosomal protein S3



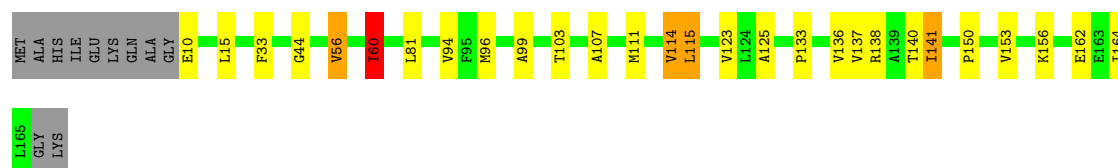
- Molecule 24: 30S ribosomal protein S4

Chain J:  92% 7%



- Molecule 25: 30S ribosomal protein S5

Chain K:  77% 14% 7%



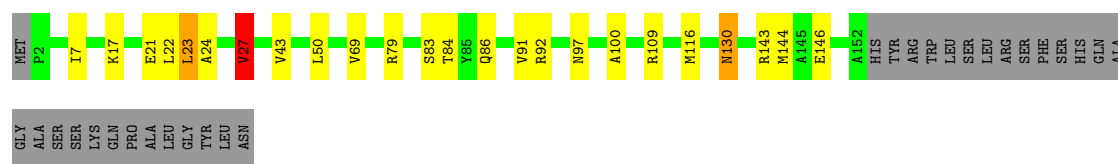
- Molecule 26: 30S ribosomal protein S6

Chain L:  67% 10% 23%



- Molecule 27: 30S ribosomal protein S7

Chain M:  71% 12% 16%




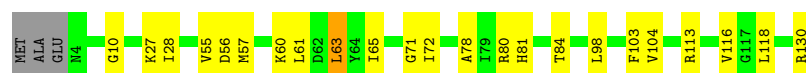
- Molecule 28: 30S ribosomal protein S8

Chain N:  90% 8%



- Molecule 29: 30S ribosomal protein S9

Chain O:  80% 17%

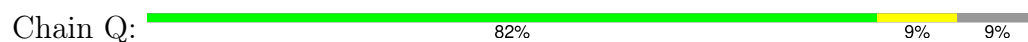


- Molecule 30: 30S ribosomal protein S10

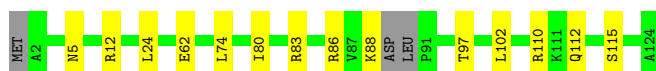
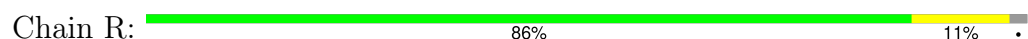
Chain P:  66% 21% 8%



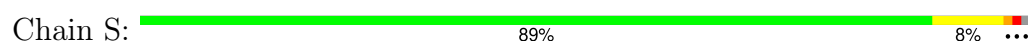
- Molecule 31: 30S ribosomal protein S11



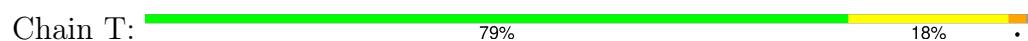
- Molecule 32: 30S ribosomal protein S12



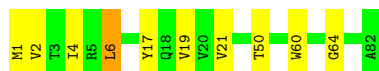
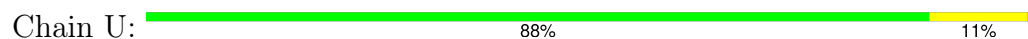
- Molecule 33: 30S ribosomal protein S14



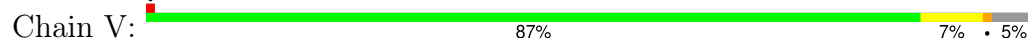
- Molecule 34: Small ribosomal subunit protein uS15



- Molecule 35: 30S ribosomal protein S16



- Molecule 36: 30S ribosomal protein S17

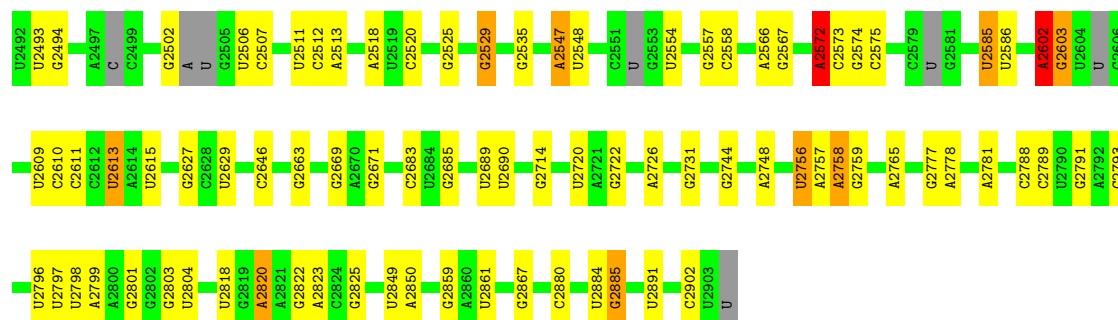


- Molecule 37: 30S ribosomal protein S19





G2372	A2376	G2383	U2384	C2385	C2394	C2395	G2396	U2402	C2403	A2406	G2415	C2422	U2423	C2424	A2425	A2426	G2429	A2430	U2431	A2434	A2435	A2436	U2441	G2444	G2446	G2447	A2448	C2456	U2458	A2469	G2470	U2474	C2475	A2476	U2477	A2478	G2481	G2484	U2491								
G2253	A2268	A2273	A2274	A2278	C2283	A2287	U2291	U2292	G2293	G2294	G2295	C2296	A2297	U2298	U2299	G2303	G2304	U2305	G2308	A2309	C2310	A2311	A2314	G2315	U2321	A2322	G2325	C2326	A2327	A2328	U2329	G2330	G2331	C2332	A2333	U2334	A2335	A2336	C2339	G2345	A2346	C2347	C2350	G2361			
G2157	A2158	G2159	G2162	A2163	C2164	C2165	U2167	G2168	A2169	U2170	A2171	U2172	C2178	U2181	A2182	U2183	U2185	U2188	G2189	A2190	A2191	U2192	C2193	A2194	A2198	G2204	U2210	A2211	U2212	U2213	A2225	C2226	U2229	G2230	U2231	G2238	G2239	U2243	U2244	U2245	U2249	G2250	G2252				
C2055	G2056	A2060	G2061	A2062	C2063	U2068	G2070	A2071	C2072	C2073	U2075	U2076	A2077	G2093	A2097	U2098	U2099	G2100	A2108	U2109	G2110	U2111	U2112	U2113	U2114	G2115	A2116	U2117	U2118	G2121	U2122	G2123	G2124	G2125	A2126	G2127	U2131	U2132	G2133	A2134	U2139	G2140	G2141	C2146	A2147	A2154	
A1938	U1940	U1955	C1961	U1963	C1964	C1965	A1966	C1967	A1970	U1971	G1972	G1980	A1981	U1982	A1987	U1991	G1992	U1993	C1997	G1998	C1999	C2000	C2001	G2002	A2013	U2017	A2020	C2021	U2022	C2023	G2027	U2028	G2029	A2031	C2032	A2033	U2038	U2039	C2043	A2051	A2052						
G1824	A1829	C1833	U1834	G1836	G1839	A1847	A1848	A1858	U1859	G1862	G1863	U1864	G1869	C1870	A1871	A1872	G1873	C1905	G1906	G1907	C1908	C1909	U1910	A1912	A1913	C1914	U1916	U1918	A1919	C1920	G1921	G1922	U1923	C1924	C1925	U1926	A1927	A1928	G1929	G1930	U1931	A1932	G1933	A1936	A1937		
A1509	G1510	A1515	G1529	U1534	A1535	G1537	U1548	A1549	U1554	U1559	C1565	A1566	G1567	G1568	A1569	A1570	A1571	U1578	A1579	A1580	G1581	C1582	U1583	U1584	G1588	U1589	A1590	A1591	A1596	A1597	A1603	A1608	A1609	A1610	A1614	C1617	A1619	U1647	U1648	G1649	A1650	G1651					
G1674	A1677	U1693	C1694	G1695	G1703	U1714	G1715	A1718	G1719	U1720	G1721	U1729	C1730	G1731	C1732	G1738	G1750	A1755	G1756	A1757	U1758	C1764	A1773	U1779	A1784	A1789	C1790	A1791	U1796	G1797	C1800	A1808	A1809	G1810	C1811	G1814	A1815	G1816	U1818								
U1352	C1363	G1364	A1365	G1368	A1378	U1379	G1380	A1383	A1384	C1386	A1387	U1394	A1395	U1396	U1406	G1407	G1408	U1411	A1412	A1413	C1414	U1415	G1416	A1418	A1419	A1420	C1428	A1433	A1434	G1452	A1453	U1460	G1478	G1482	A1490	G1491	U1497	A1503	A1508								
G1122	G1125	U1132	A1133	A1134	C1135	U1141	A1142	A1143	C1153	A1169	C1170	U1173	U1174	A1175	U1176	G1177	C1178	G1179	U1180	U1181	G1182	U1183	G1186	G1187	U1188	A1189	G1238	U1249	G1250	A1253	G1256	G1266	C1270	G1271	A1272	U1273	A1301	A1321	A1327	A1328	C1345						
A1028	U1033	G1041	A1042	C1045	A1046	G1047	U1054	G1055	U1060	U1061	G1062	C1063	C1064	U1065	U1066	A1067	G1068	A1069	A1070	C1071	C1072	A1073	C1075	C1076	C1079	A1080	U1081	U1082	A1084	U1085	A1086	G1087	A1088	U1089	A1090	A1095	A1096	A1103	G1107	U1108	C1109	G1110	A1111	G1112	U1119		
C997	C998	A999	G907	A910	G914	C915	A927	A928	U929	U931	A941	C944	A945	C946	A947	C948	G953	G954	U954	G956	A957	U946	G947	A954	G961	A973	G974	A983	A984	C985	C995	A996	G997	C998	U999	C1005	C1006	C1007	U1012	C1013	U1019	A1020	A1021	G1022	U1023	G1026	A1027
G757	A764	C765	G775	G776	A782	A783	G784	G785	A800	A802	G805	U811	C812	U813	C814	A819	U827	U828	A845	U846	C851	U852	G858	G859	G869	U870	U871	U872	A878	G879	G880	G881	G882	U884	C885	C888	G891	A892	C893	U894	U895	A896					
A609	A613	A614	U615	A616	G617	G618	G619	G620	A621	A627	A631	G637	G638	U639	C640	U641	U642	A643	A644	C645	G646	A654	G664	A668	A685	U686	A705	U710	U717	A730	G738	A742	A743	U744	G748	A753	U754	U755	A756	A603							



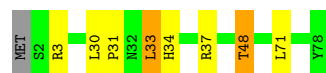
- Molecule 42: 50S ribosomal protein L27

Chain b: 84% 6% 11%



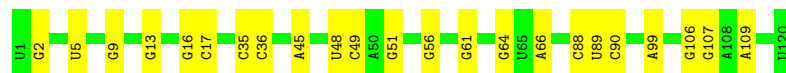
- Molecule 43: 50S ribosomal protein L28

Chain c: 88% 8% ..



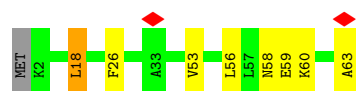
- Molecule 44: 5S rRNA

Chain d: 81% 19%



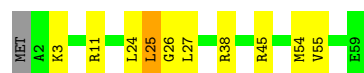
- Molecule 45: 50S ribosomal protein L29

Chain e: 86% 11% ..



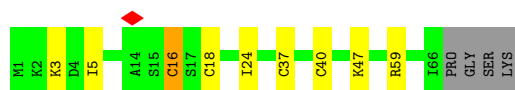
- Molecule 46: 50S ribosomal protein L30

Chain f: 81% 15% ..



- Molecule 47: 50S ribosomal protein L31

Chain g: 81% 11% 6%



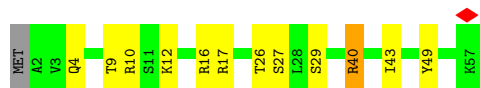
- Molecule 48: 50S ribosomal protein L2

Chain h: 84% 14% ..



- Molecule 49: 50S ribosomal protein L32

Chain i: 77% 19% ..



- Molecule 50: 50S ribosomal protein L3

Chain j: 88% 11%



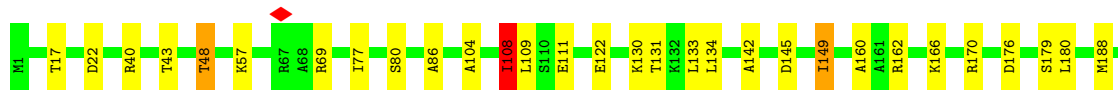
- Molecule 51: 50S ribosomal protein L33

Chain k: 89% 5% 5%



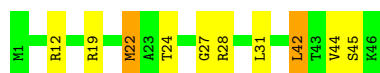
- Molecule 52: 50S ribosomal protein L4

Chain l: 85% 14% .



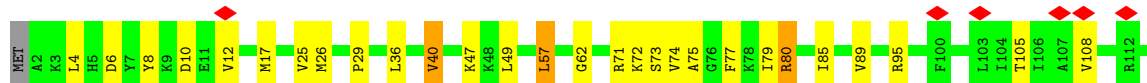
- Molecule 53: 50S ribosomal protein L34

Chain m: 78% 17% .



- Molecule 54: 50S ribosomal protein L5

Chain n: 75% 21% . .



- Molecule 55: 50S ribosomal protein L35

Chain o: 88% 6% 5% . .



- Molecule 56: 50S ribosomal protein L6

Chain p: 90% 8% . .



- Molecule 57: 50S ribosomal protein L36

Chain q: 89% 8% . .



- Molecule 58: 50S ribosomal protein L9

Chain r: 88% 9% . .



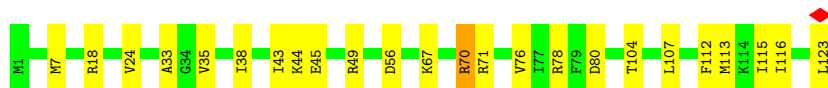
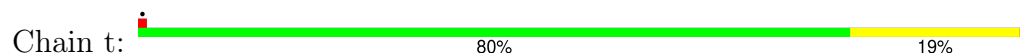
- Molecule 59: 50S ribosomal protein L13

Chain s: 82% 16% . .





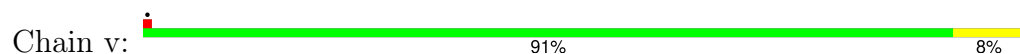
- Molecule 60: 50S ribosomal protein L14



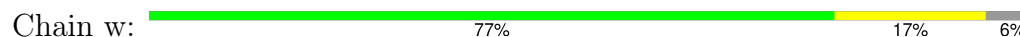
- Molecule 61: 50S ribosomal protein L15



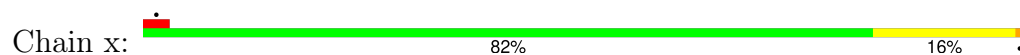
- Molecule 62: 50S ribosomal protein L16



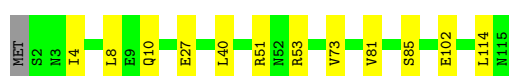
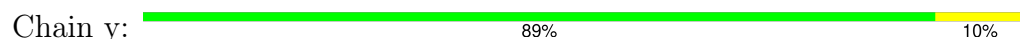
- Molecule 63: 50S ribosomal protein L17



- Molecule 64: 50S ribosomal protein L18



- Molecule 65: 50S ribosomal protein L19



- Molecule 66: 50S ribosomal protein L20

Chain z: 

84%

15%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24109	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	0.043	Depositor
Minimum map value	-0.011	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0039	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: MG, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	0	0.50	0/829	0.74	0/1107
2	1	0.67	0/864	1.08	0/1156
3	2	0.54	0/752	0.89	0/1005
4	3	0.47	0/796	0.77	0/1062
5	4	0.52	0/766	0.88	0/1025
6	5	0.64	1/528 (0.2%)	0.55	0/810
7	6	0.56	1/603 (0.2%)	0.56	0/926
8	7	0.62	3/717 (0.4%)	0.90	4/1110 (0.4%)
9	9	1.15	3/1131 (0.3%)	1.30	3/1524 (0.2%)
10	A	0.36	0/1810	0.72	2/2821 (0.1%)
10	B	0.44	0/1810	0.87	9/2821 (0.3%)
11	AA	0.38	0/10736	0.63	0/14487
12	AB	0.56	0/1304	0.82	2/1759 (0.1%)
13	AC	0.38	0/1710	0.61	0/2317
13	AD	0.30	0/2091	0.59	0/2847
14	AE	0.56	11/10545 (0.1%)	0.79	27/14236 (0.2%)
15	AF	0.30	0/652	0.61	0/879
16	AG	0.97	5/3897 (0.1%)	1.40	49/5273 (0.9%)
17	C	0.66	0/553	1.14	1/743 (0.1%)
18	D	0.40	9/36610 (0.0%)	0.75	38/57091 (0.1%)
19	E	0.76	0/675	1.32	0/895
20	F	0.72	0/597	1.20	0/792
21	G	0.65	0/1791	1.08	1/2413 (0.0%)
22	H	0.76	4/1746 (0.2%)	1.58	34/2382 (1.4%)
23	I	0.59	0/1663	0.99	0/2241
24	J	0.63	0/1665	1.08	0/2227
25	K	0.64	1/1165 (0.1%)	1.06	2/1568 (0.1%)
26	L	0.58	0/867	0.94	0/1171
27	M	0.68	0/1195	1.19	3/1602 (0.2%)
28	N	0.56	0/989	0.92	0/1326
29	O	0.59	0/1034	1.02	1/1375 (0.1%)
30	P	0.64	0/800	1.13	4/1082 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
31	Q	0.55	0/893	0.92	0/1205
32	R	0.50	0/952	0.81	0/1274
33	S	0.64	0/817	1.11	1/1088 (0.1%)
34	T	0.69	0/722	1.21	0/964
35	U	0.58	0/659	0.99	0/884
36	V	0.46	0/657	0.73	0/881
37	W	0.51	0/680	0.83	0/915
38	X	0.67	0/909	1.21	3/1215 (0.2%)
39	Y	1.04	0/1046	1.09	1/1410 (0.1%)
40	Z	1.02	0/227	1.12	0/304
41	a	0.41	3/69247 (0.0%)	0.75	54/107985 (0.1%)
42	b	0.51	0/589	0.76	0/779
43	c	0.63	0/635	0.97	0/848
44	d	0.37	0/2872	0.69	0/4478
45	e	0.69	0/502	1.19	0/667
46	f	0.62	0/452	1.02	0/605
47	g	0.56	0/531	0.99	1/709 (0.1%)
48	h	0.54	0/2121	0.85	0/2852
49	i	0.53	0/450	0.94	0/599
50	j	0.60	0/1586	0.87	0/2134
51	k	0.47	0/433	0.80	0/576
52	l	0.61	0/1571	1.03	1/2113 (0.0%)
53	m	0.69	0/380	1.22	0/498
54	n	0.63	0/1434	1.18	10/1926 (0.5%)
55	o	0.64	0/513	1.11	1/676 (0.1%)
56	p	0.58	0/1333	0.89	0/1805
57	q	0.51	0/303	0.88	0/397
58	r	0.63	0/1122	0.98	1/1515 (0.1%)
59	s	0.68	0/1152	1.02	2/1551 (0.1%)
60	t	0.57	0/955	0.88	0/1279
61	u	0.55	0/1062	0.95	1/1413 (0.1%)
62	v	0.60	0/1093	0.97	0/1460
63	w	0.68	0/964	1.13	0/1289
64	x	0.61	0/902	1.09	0/1209
65	y	0.53	0/929	0.79	0/1242
66	z	0.80	0/960	1.25	0/1278
All	All	0.50	41/194544 (0.0%)	0.84	256/286096 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
10	A	0	2
10	B	0	2
12	AB	0	1
13	AC	0	1
13	AD	0	3
14	AE	0	5
16	AG	0	6
22	H	0	3
38	X	0	1
All	All	0	24

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	18.20	1.70	1.47
16	AG	429	LYS	C-N	13.87	1.51	1.33
14	AE	93	THR	CA-C	12.12	1.69	1.52
22	H	169	SER	N-CA	11.79	1.61	1.46
14	AE	291	ILE	CA-C	11.49	1.67	1.52

The worst 5 of 256 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	AE	291	ILE	CA-C-N	20.30	158.51	121.97
14	AE	291	ILE	C-N-CA	20.30	158.51	121.97
16	AG	104	ARG	CA-C-N	17.90	154.18	121.97
16	AG	104	ARG	C-N-CA	17.90	154.18	121.97
18	D	1516	G	O3'-P-O5'	17.52	130.27	104.00

There are no chirality outliers.

5 of 24 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	A	19	G	Sidechain
10	A	7	G	Sidechain
12	AB	44	VAL	Mainchain
13	AC	192	VAL	Peptide
13	AD	20	SER	Peptide

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	816	839	839	8	0
2	1	857	922	922	14	0
3	2	746	811	811	5	0
4	3	788	844	844	10	0
5	4	753	780	780	0	0
6	5	472	260	260	26	0
7	6	542	305	306	23	0
8	7	647	97	321	97	0
9	9	1117	0	1153	167	0
10	A	1620	826	826	173	0
10	B	1620	814	827	139	0
11	AA	10567	0	10584	320	0
12	AB	1276	0	1244	273	0
13	AC	1690	0	1714	16	0
13	AD	2073	0	1889	46	0
14	AE	10388	10612	10610	394	0
15	AF	650	0	658	13	0
16	AG	3852	0	3826	802	0
17	C	544	559	560	23	0
18	D	32703	16423	16459	233	0
19	E	669	719	719	3	0
20	F	589	629	629	7	0
21	G	1760	1785	1785	44	0
22	H	1730	1454	1454	208	0
23	I	1636	1710	1710	32	0
24	J	1643	1707	1707	16	0
25	K	1152	1196	1196	22	0
26	L	848	846	846	3	0
27	M	1181	1235	1235	34	0
28	N	979	1031	1031	6	0
29	O	1022	1070	1070	12	0
30	P	790	831	831	112	0
31	Q	877	887	887	4	0
32	R	939	1001	1001	8	0
33	S	805	844	844	5	0
34	T	714	734	734	8	0
35	U	649	666	666	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	V	648	691	691	4	0
37	W	663	688	688	2	0
38	X	900	964	964	55	0
39	Y	1032	0	1088	83	0
40	Z	227	0	237	20	0
41	a	61841	31077	31123	296	0
42	b	582	599	599	3	0
43	c	625	652	652	4	0
44	d	2569	1301	1301	3	0
45	e	501	531	531	5	0
46	f	448	488	488	6	0
47	g	522	520	520	10	0
48	h	2082	2154	2154	20	0
49	i	444	459	458	6	0
50	j	1565	1617	1616	14	0
51	k	426	464	464	0	0
52	l	1552	1619	1619	13	0
53	m	377	418	418	10	0
54	n	1410	1443	1444	28	0
55	o	504	572	572	4	0
56	p	1313	1358	1358	7	0
57	q	302	343	343	1	0
58	r	1111	1148	1148	6	0
59	s	1129	1162	1162	12	0
60	t	946	1023	1023	12	0
61	u	1053	1129	1129	8	0
62	v	1074	1157	1157	5	0
63	w	951	994	994	8	0
64	x	892	923	923	9	0
65	y	917	962	962	4	0
66	z	947	1020	1019	12	0
67	AE	1	0	0	0	0
68	AE	2	0	0	0	0
All	All	181260	109913	132623	3318	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 11.

The worst 5 of 3318 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)
16:AG:425:LEU:CD2	16:AG:429:LYS:HE2	1.21	1.62
16:AG:287:ALA:CA	16:AG:331:LEU:HD12	1.19	1.62
11:AA:901:LEU:CD1	16:AG:8:VAL:HG13	1.31	1.60
22:H:131:LEU:CB	22:H:167:VAL:CA	1.78	1.57
17:C:12:ARG:HG3	22:H:264:GLU:CB	1.30	1.55

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%)	3 (3%)	1 (1%)	13	46
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/100 (92%)	90 (98%)	2 (2%)	0	100	100
4	3	101/104 (97%)	96 (95%)	4 (4%)	1 (1%)	13	46
5	4	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
9	9	146/165 (88%)	94 (64%)	38 (26%)	14 (10%)	0	6
11	AA	1338/1342 (100%)	1207 (90%)	127 (10%)	4 (0%)	37	67
12	AB	157/181 (87%)	130 (83%)	20 (13%)	7 (4%)	2	18
13	AC	216/329 (66%)	202 (94%)	12 (6%)	2 (1%)	14	48
13	AD	292/329 (89%)	269 (92%)	23 (8%)	0	100	100
14	AE	1329/1407 (94%)	1198 (90%)	120 (9%)	11 (1%)	16	51
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
16	AG	493/495 (100%)	376 (76%)	86 (17%)	31 (6%)	1	13
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	G	223/241 (92%)	210 (94%)	13 (6%)	0	100	100
22	H	255/557 (46%)	189 (74%)	54 (21%)	12 (5%)	2	18
23	I	206/233 (88%)	196 (95%)	9 (4%)	1 (0%)	25	59
24	J	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
25	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	22	55
26	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	13	46
27	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	19	53
28	N	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16	51
29	O	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16	51
30	P	97/103 (94%)	87 (90%)	8 (8%)	2 (2%)	5	33
31	Q	115/129 (89%)	104 (90%)	9 (8%)	2 (2%)	7	37
32	R	117/124 (94%)	116 (99%)	1 (1%)	0	100	100
33	S	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
34	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
35	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	10	41
36	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
37	W	81/92 (88%)	78 (96%)	3 (4%)	0	100	100
38	X	114/118 (97%)	107 (94%)	5 (4%)	2 (2%)	7	35
39	Y	139/142 (98%)	102 (73%)	25 (18%)	12 (9%)	0	7
40	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	11
42	b	74/85 (87%)	69 (93%)	5 (7%)	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%)	53 (95%)	3 (5%)	0	100	100
47	g	64/70 (91%)	63 (98%)	1 (2%)	0	100	100
48	h	269/273 (98%)	259 (96%)	9 (3%)	1 (0%)	30	63
49	i	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
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%)	190 (96%)	8 (4%)	1 (0%)	25	59
53	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	n	175/179 (98%)	162 (93%)	11 (6%)	2 (1%)	12	45
55	o	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
56	p	173/177 (98%)	161 (93%)	12 (7%)	0	100	100
57	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
58	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
59	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
60	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
61	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
62	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
63	w	117/127 (92%)	108 (92%)	9 (8%)	0	100	100
64	x	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
65	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
66	z	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	14	48
All	All	10078/11072 (91%)	9200 (91%)	763 (8%)	115 (1%)	15	45

5 of 115 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
12	AB	118	VAL
12	AB	121	LYS
14	AE	291	ILE
16	AG	34	ALA

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	76 (90%)	8 (10%)	7	30
2	1	93/93 (100%)	86 (92%)	7 (8%)	11	37
3	2	81/84 (96%)	77 (95%)	4 (5%)	21	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3	84/85 (99%)	79 (94%)	5 (6%)	16	45
5	4	78/78 (100%)	75 (96%)	3 (4%)	28	57
9	9	112/123 (91%)	63 (56%)	49 (44%)	0	0
11	AA	1155/1157 (100%)	1130 (98%)	25 (2%)	47	69
12	AB	138/158 (87%)	108 (78%)	30 (22%)	1	5
13	AC	185/286 (65%)	184 (100%)	1 (0%)	86	93
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1120/1168 (96%)	1046 (93%)	74 (7%)	14	42
15	AF	70/75 (93%)	69 (99%)	1 (1%)	62	79
16	AG	409/409 (100%)	288 (70%)	121 (30%)	0	2
17	C	57/65 (88%)	55 (96%)	2 (4%)	31	60
19	E	65/66 (98%)	61 (94%)	4 (6%)	15	44
20	F	60/61 (98%)	57 (95%)	3 (5%)	20	49
21	G	187/199 (94%)	174 (93%)	13 (7%)	12	40
22	H	137/461 (30%)	124 (90%)	13 (10%)	7	30
23	I	171/190 (90%)	163 (95%)	8 (5%)	22	51
24	J	172/173 (99%)	164 (95%)	8 (5%)	22	51
25	K	119/126 (94%)	111 (93%)	8 (7%)	13	41
26	L	91/116 (78%)	84 (92%)	7 (8%)	10	36
27	M	124/147 (84%)	113 (91%)	11 (9%)	8	32
28	N	104/105 (99%)	101 (97%)	3 (3%)	37	63
29	O	105/107 (98%)	99 (94%)	6 (6%)	17	46
30	P	86/90 (96%)	73 (85%)	13 (15%)	2	15
31	Q	90/99 (91%)	88 (98%)	2 (2%)	47	69
32	R	101/104 (97%)	95 (94%)	6 (6%)	16	45
33	S	83/84 (99%)	79 (95%)	4 (5%)	21	51
34	T	76/77 (99%)	65 (86%)	11 (14%)	2	16
35	U	65/65 (100%)	60 (92%)	5 (8%)	10	36
36	V	74/78 (95%)	71 (96%)	3 (4%)	26	55
37	W	72/79 (91%)	66 (92%)	6 (8%)	9	34
38	X	94/96 (98%)	87 (93%)	7 (7%)	11	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	Y	109/110 (99%)	69 (63%)	40 (37%)	0	1
40	Z	26/85 (31%)	10 (38%)	16 (62%)	0	0
42	b	58/63 (92%)	57 (98%)	1 (2%)	56	75
43	c	67/68 (98%)	64 (96%)	3 (4%)	23	53
45	e	54/55 (98%)	51 (94%)	3 (6%)	17	47
46	f	48/49 (98%)	43 (90%)	5 (10%)	5	26
47	g	59/62 (95%)	55 (93%)	4 (7%)	13	41
48	h	216/218 (99%)	199 (92%)	17 (8%)	10	35
49	i	47/48 (98%)	41 (87%)	6 (13%)	3	19
50	j	164/164 (100%)	156 (95%)	8 (5%)	21	50
51	k	47/49 (96%)	44 (94%)	3 (6%)	14	43
52	l	165/165 (100%)	151 (92%)	14 (8%)	8	33
53	m	38/38 (100%)	36 (95%)	2 (5%)	19	48
54	n	148/150 (99%)	130 (88%)	18 (12%)	4	21
55	o	51/52 (98%)	47 (92%)	4 (8%)	10	36
56	p	136/138 (99%)	130 (96%)	6 (4%)	24	53
57	q	34/34 (100%)	31 (91%)	3 (9%)	8	32
58	r	114/114 (100%)	102 (90%)	12 (10%)	5	26
59	s	116/116 (100%)	106 (91%)	10 (9%)	8	33
60	t	104/104 (100%)	98 (94%)	6 (6%)	17	46
61	u	103/103 (100%)	96 (93%)	7 (7%)	13	41
62	v	109/109 (100%)	105 (96%)	4 (4%)	29	58
63	w	99/103 (96%)	91 (92%)	8 (8%)	9	35
64	x	86/87 (99%)	80 (93%)	6 (7%)	12	40
65	y	99/100 (99%)	91 (92%)	8 (8%)	9	35
66	z	89/90 (99%)	85 (96%)	4 (4%)	23	53
All	All	8313/9148 (91%)	7624 (92%)	689 (8%)	12	34

5 of 689 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	W	81	ARG
50	j	193	VAL

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Mol	Chain	Res	Type
39	Y	30	GLN
37	W	79	THR
40	Z	17	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 85 such sidechains are listed below:

Mol	Chain	Res	Type
26	L	11	HIS
38	X	105	ASN
26	L	94	HIS
31	Q	15	GLN
51	k	26	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	6 (8%)
10	B	75/76 (98%)	35 (46%)	6 (8%)
18	D	1514/1542 (98%)	291 (19%)	34 (2%)
41	a	2859/2904 (98%)	539 (18%)	0
44	d	119/120 (99%)	17 (14%)	0
8	7	30/68 (44%)	18 (60%)	4 (13%)
All	All	4672/4786 (97%)	929 (19%)	50 (1%)

5 of 929 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 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	D	531	U
18	D	992	U
18	D	1493	A
18	D	532	A

*Continued on next page...*

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Mol	Chain	Res	Type
18	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

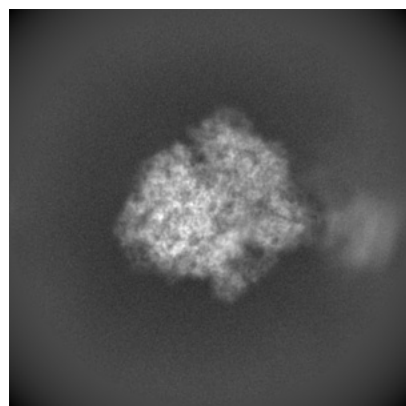
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43390. These allow visual inspection of the internal detail of the map and identification of artifacts.

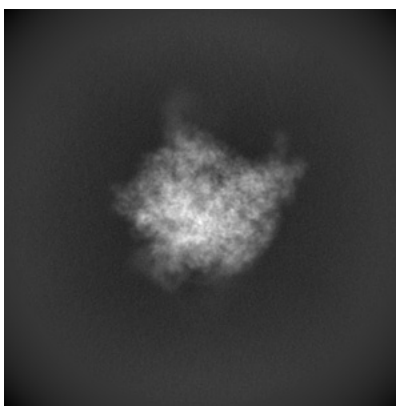
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

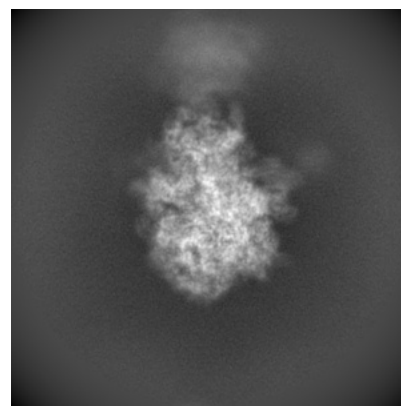
#### 6.1.1 Primary map



X

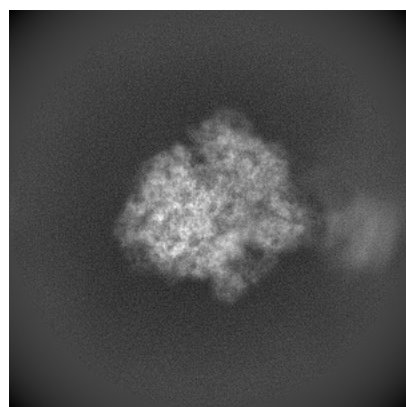


Y

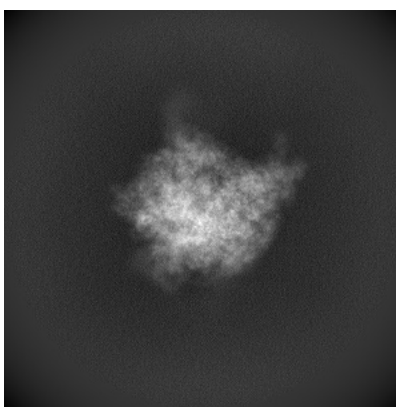


Z

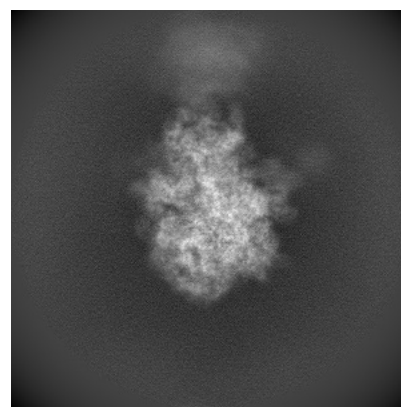
#### 6.1.2 Raw map



X



Y



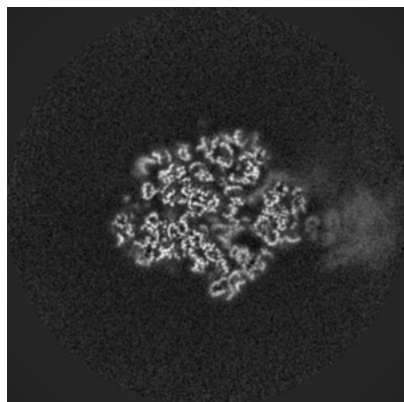
Z

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

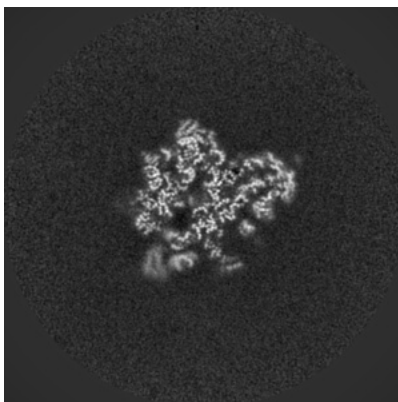


## 6.2 Central slices [i](#)

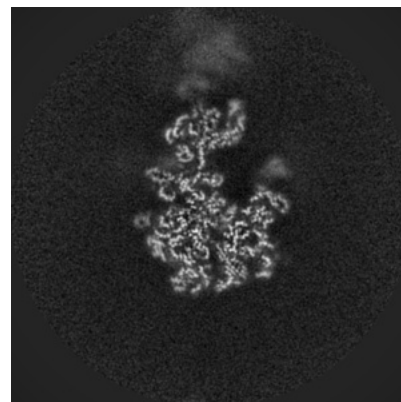
### 6.2.1 Primary map



X Index: 256

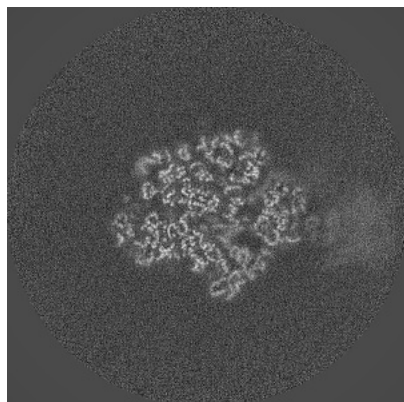


Y Index: 256

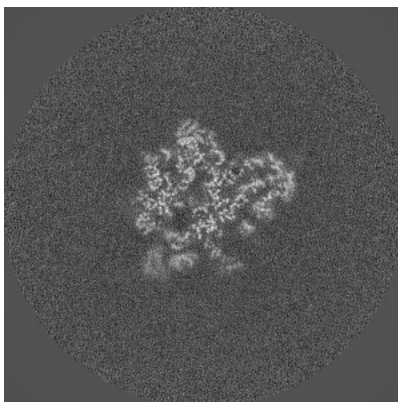


Z Index: 256

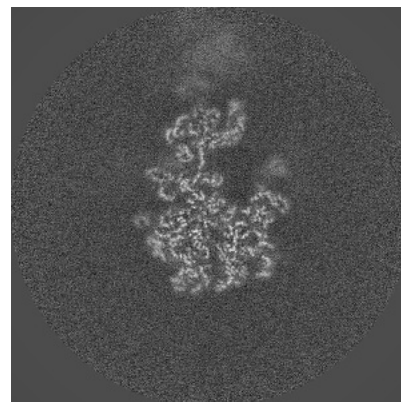
### 6.2.2 Raw map



X Index: 256



Y Index: 256

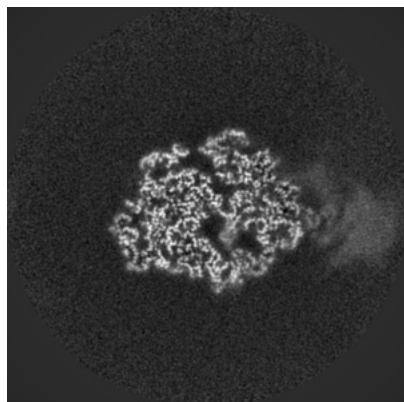


Z Index: 256

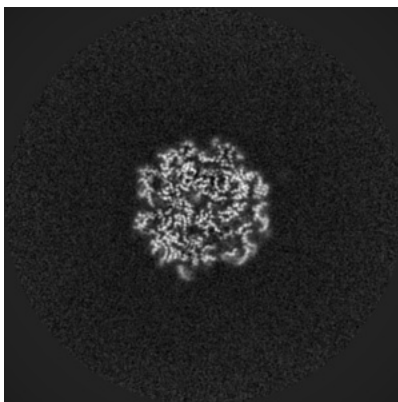
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

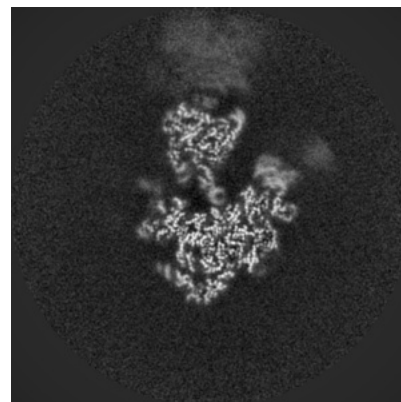
### 6.3.1 Primary map



X Index: 247

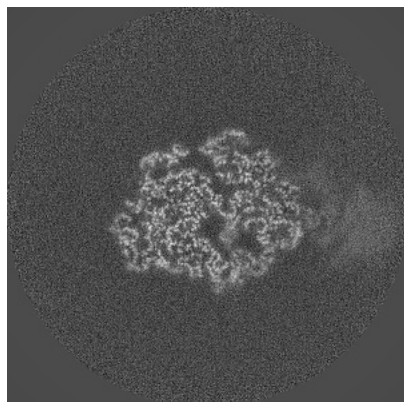


Y Index: 221

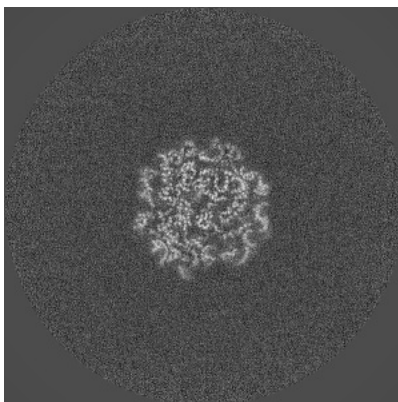


Z Index: 231

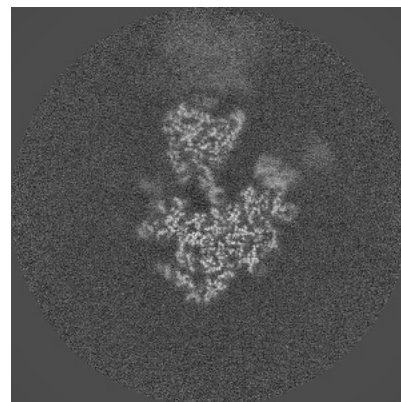
### 6.3.2 Raw map



X Index: 247



Y Index: 220



Z Index: 231

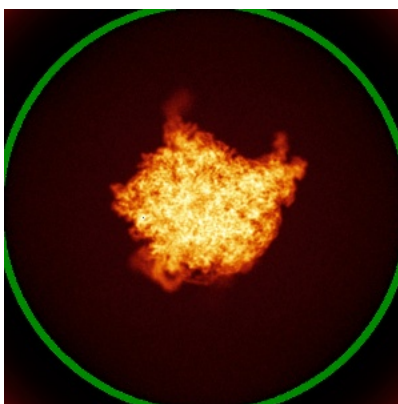
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



X

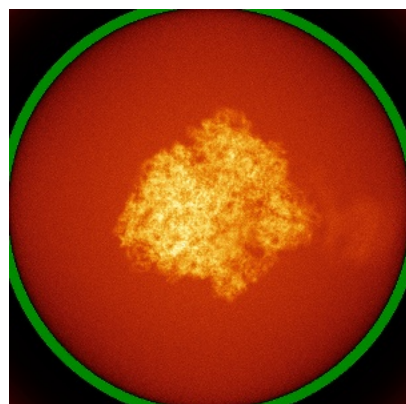


Y

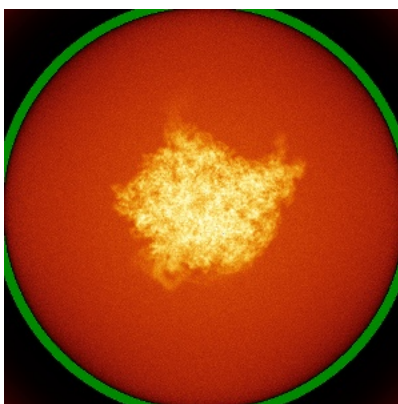


Z

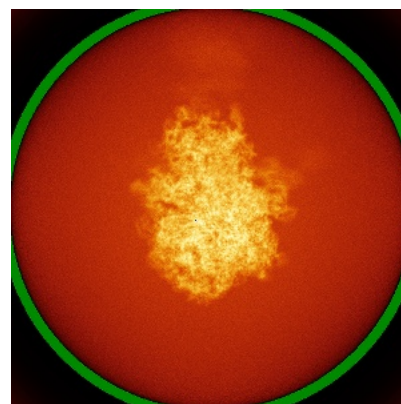
### 6.4.2 Raw map



X



Y



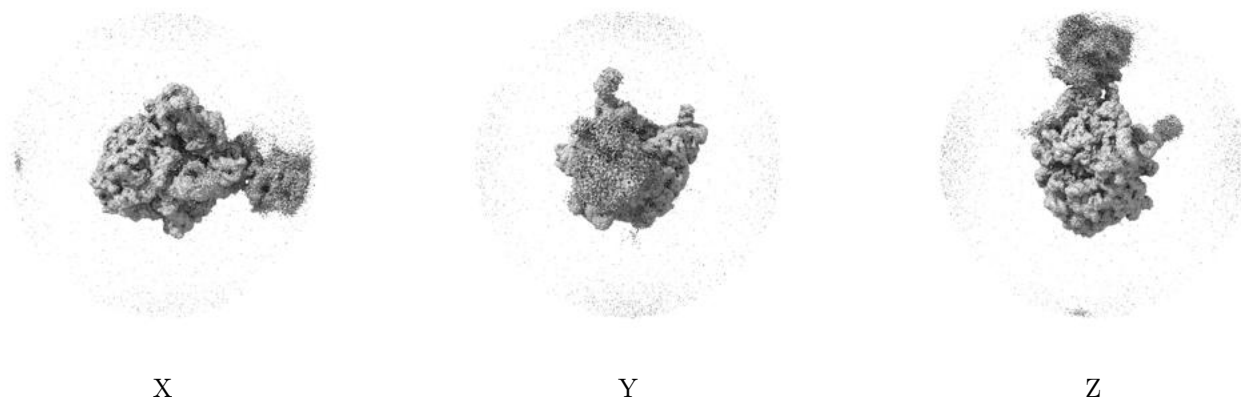
Z

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.



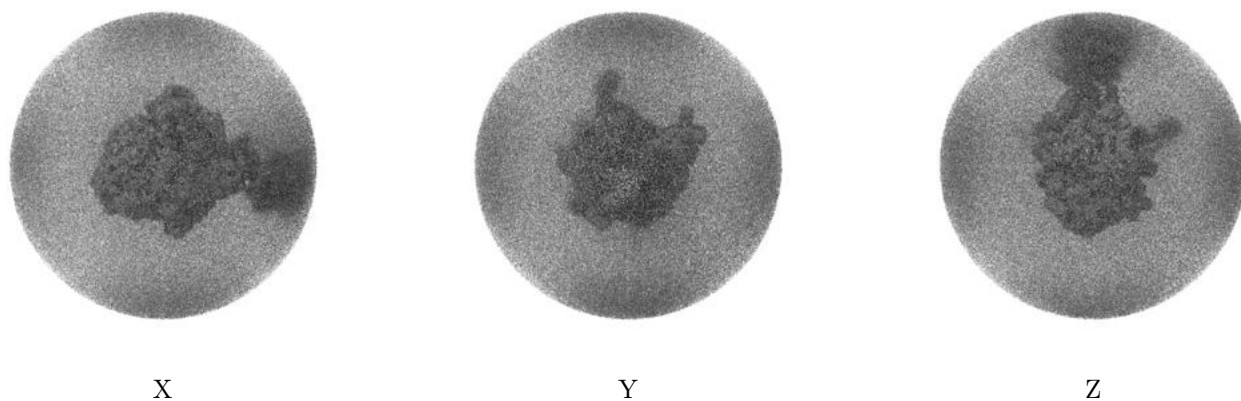
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0039. 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



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.

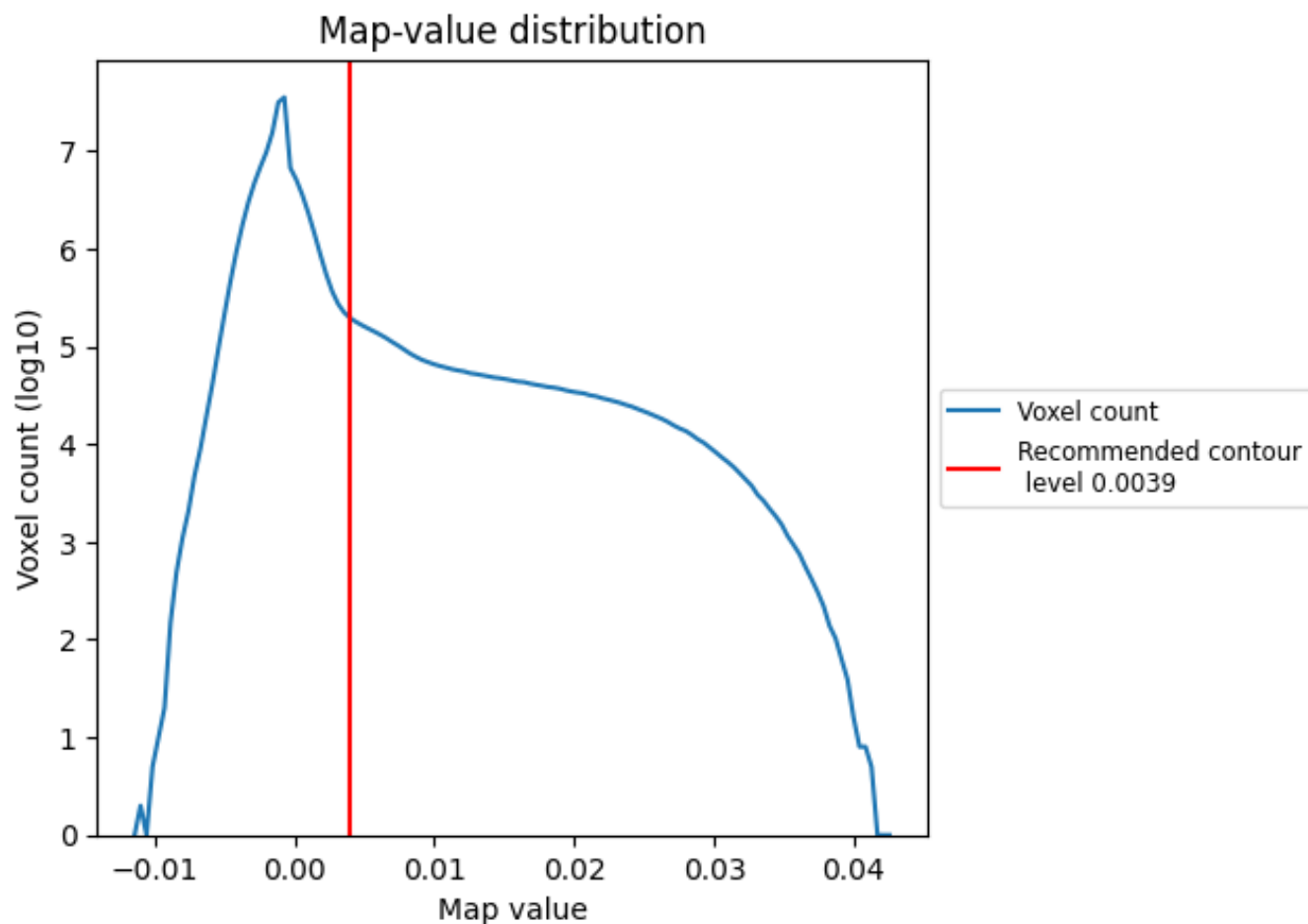
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

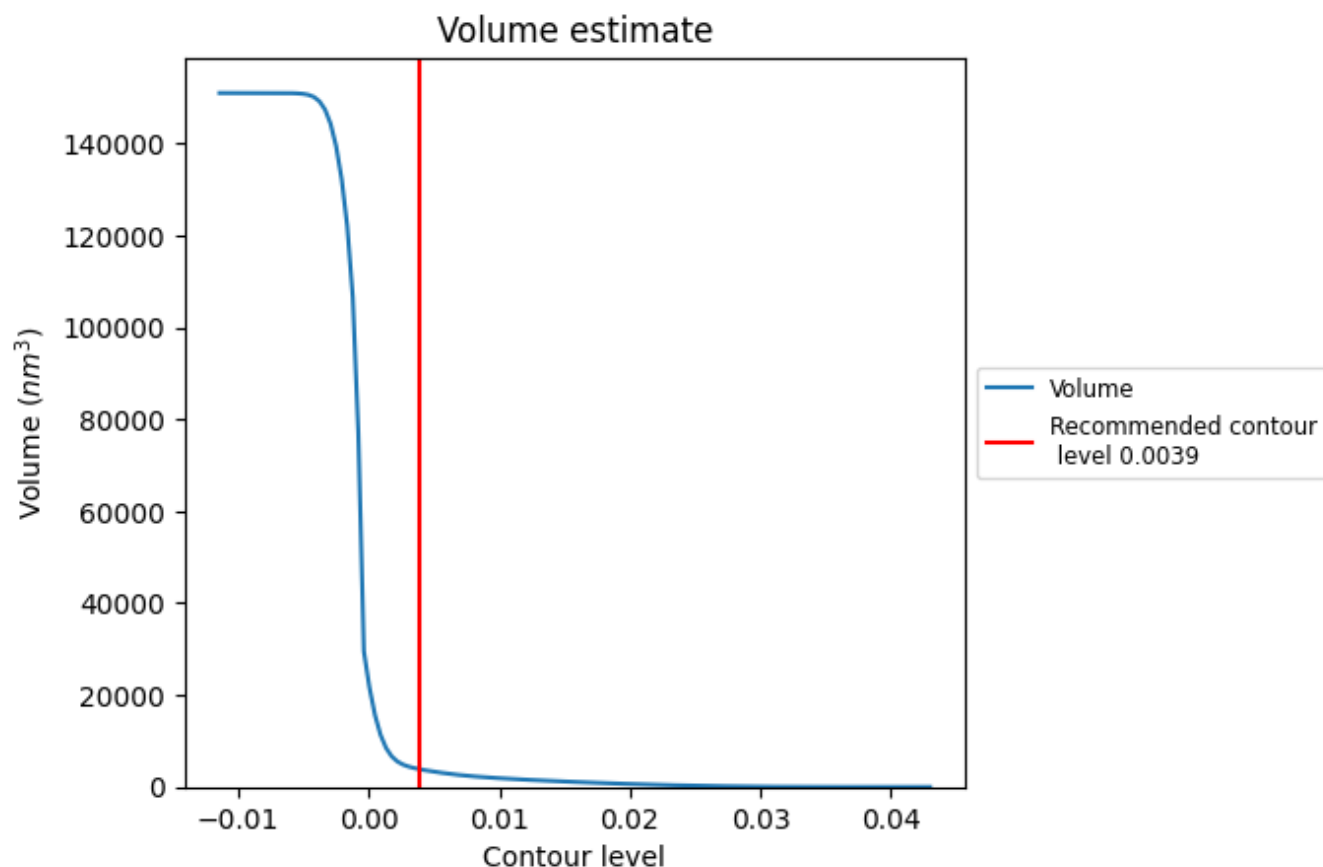
This section contains the results of statistical analysis of the map.

### 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.

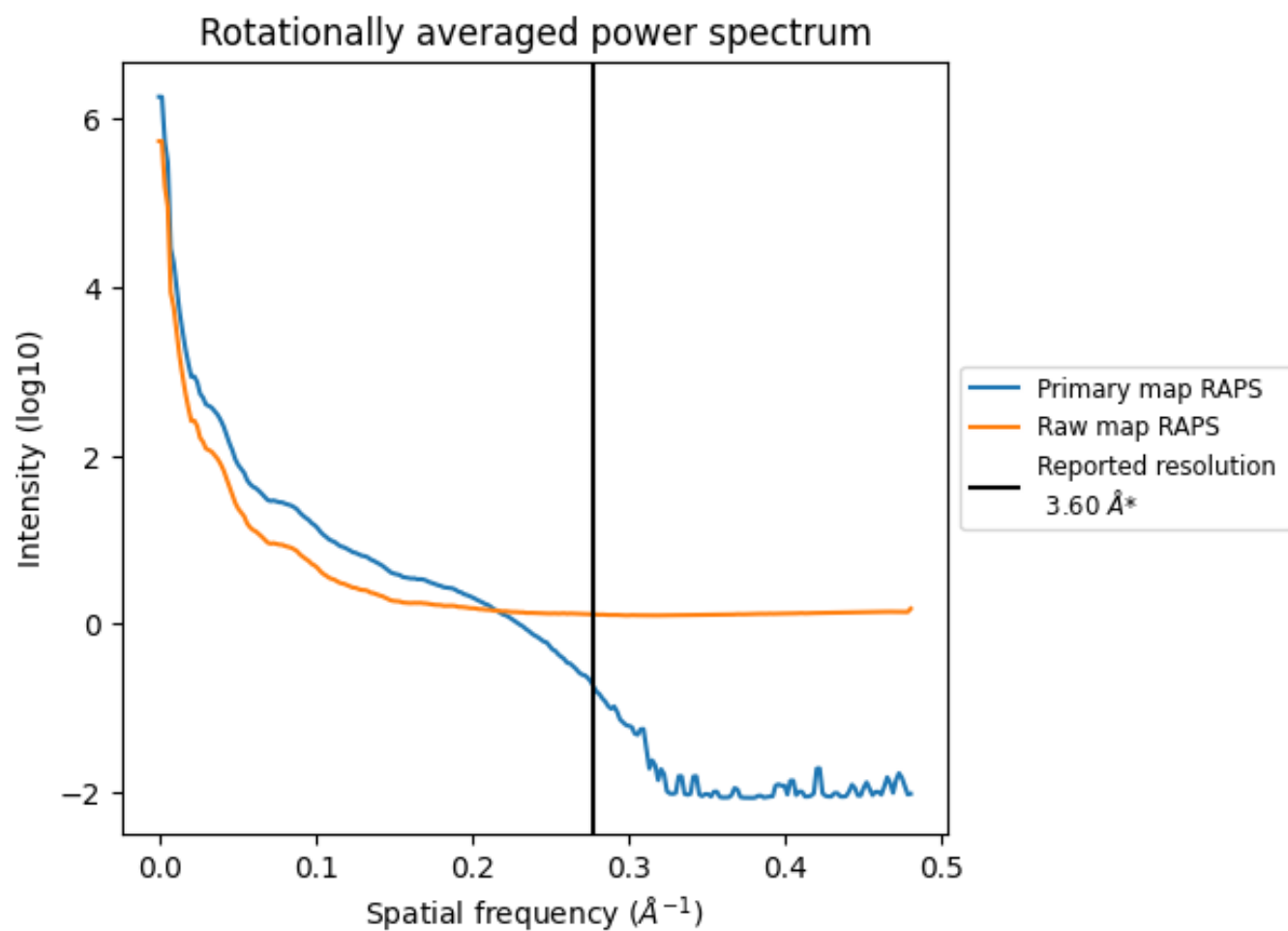
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is  $3859 \text{ nm}^3$ ; this corresponds to an approximate mass of 3486 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ

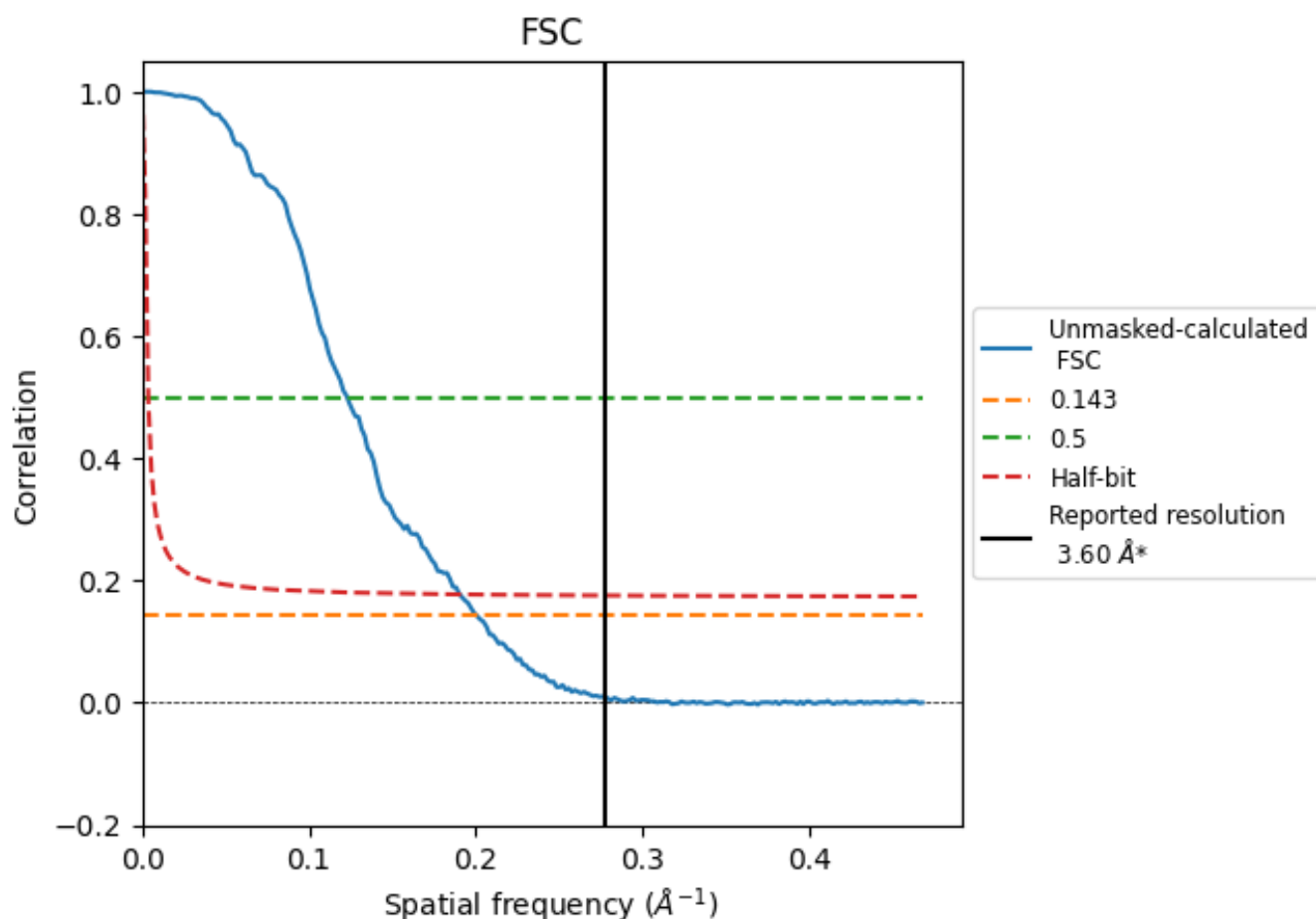


\*Reported resolution corresponds to spatial frequency of 0.278 Å<sup>-1</sup>

## 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 0.278 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

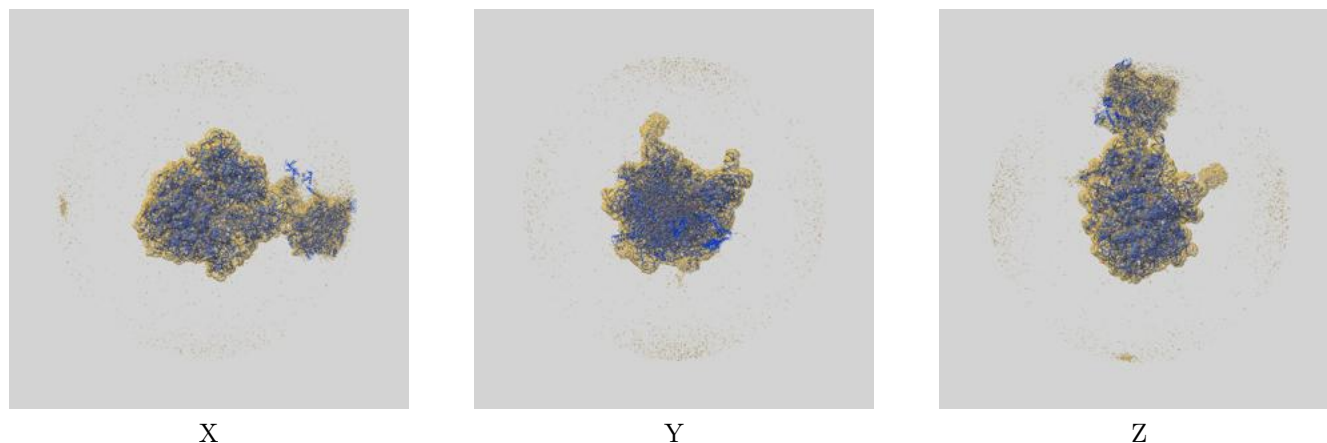
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.99	8.14	5.25

\*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 4.99 differs from the reported value 3.6 by more than 10 %

## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43390 and PDB model 8VOR. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

### 9.1 Map-model overlay [i](#)



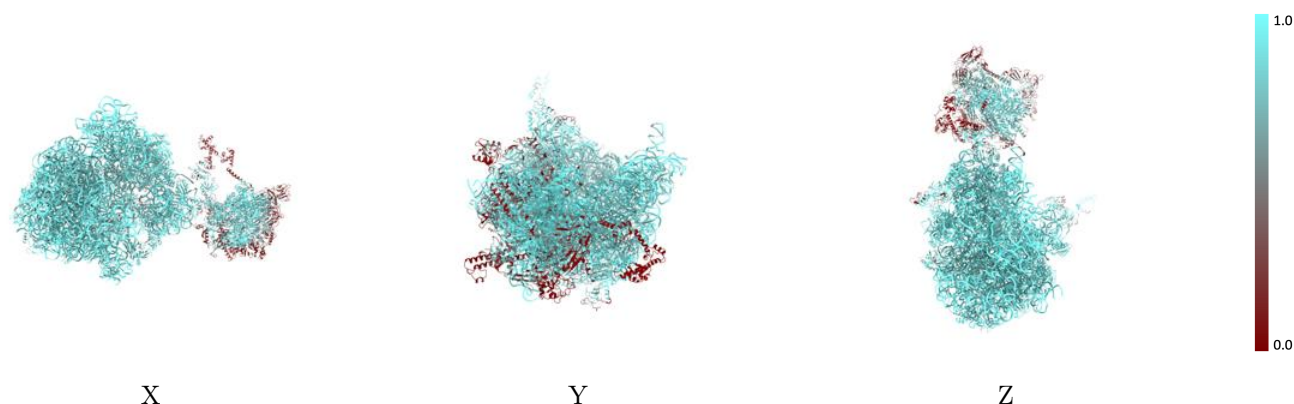
The images above show the 3D surface view of the map at the recommended contour level 0.0039 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



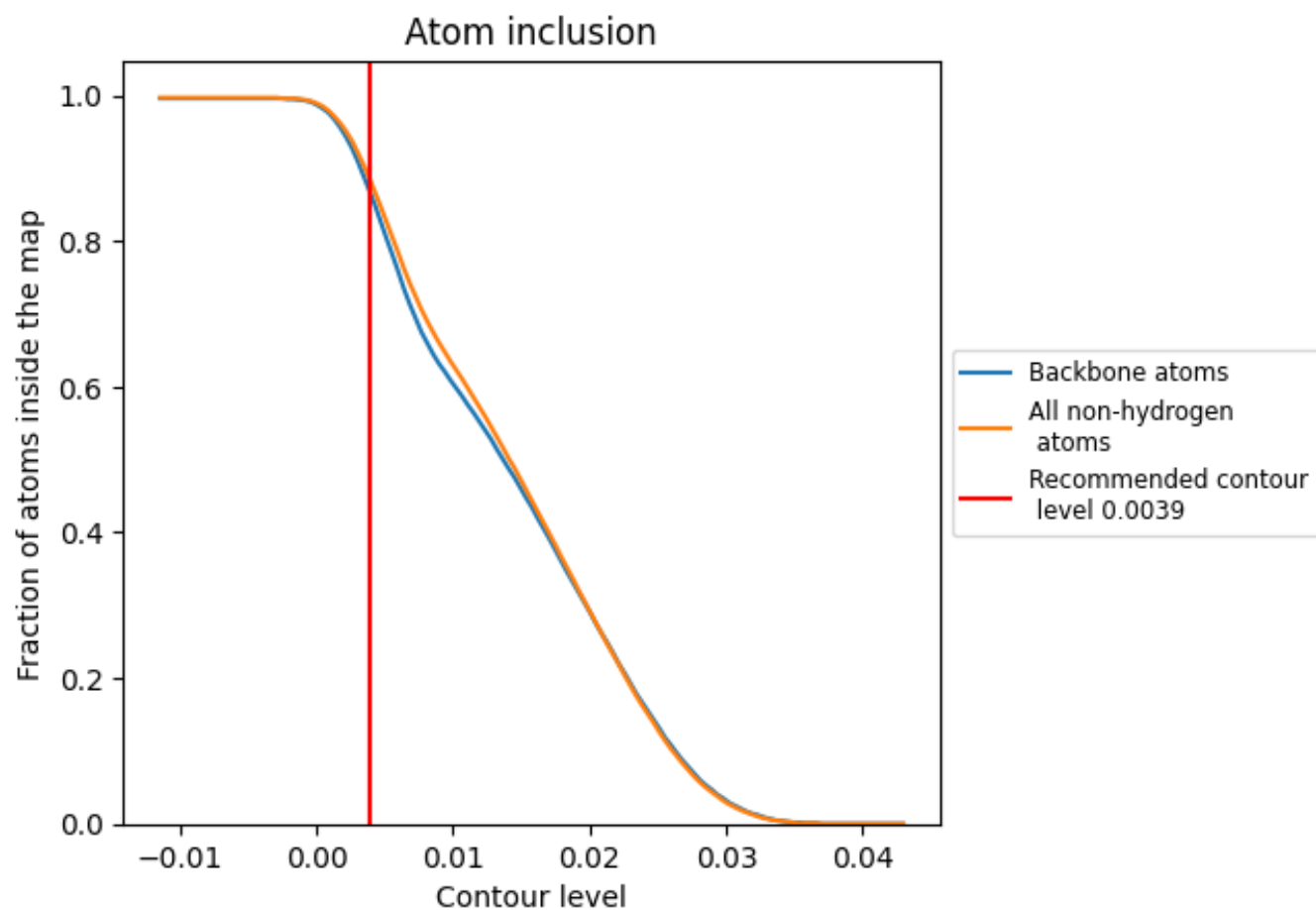
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0039).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 89% 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 (0.0039) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8860	 0.1710
0	 0.9440	 0.1900
1	 0.9400	 0.2830
2	 0.9100	 0.1350
3	 0.9370	 0.0970
4	 0.9500	 0.1260
5	 0.8620	 0.0410
6	 0.8670	 0.0330
7	 0.8900	 0.0820
9	 0.8700	 0.0380
A	 0.9910	 0.1860
AA	 0.6220	 0.0330
AB	 0.5790	 0.0520
AC	 0.5460	 0.0450
AD	 0.2720	 0.0170
AE	 0.7380	 0.0330
AF	 0.6070	 0.0160
AG	 0.3780	 0.0120
B	 0.8590	 0.0720
C	 0.9540	 0.1570
D	 0.9920	 0.2420
E	 0.9530	 0.0920
F	 0.9390	 0.2290
G	 0.9170	 0.1730
H	 0.7390	 0.0180
I	 0.9290	 0.1960
J	 0.9500	 0.1710
K	 0.9570	 0.2970
L	 0.9240	 0.0950
M	 0.9380	 0.1610
N	 0.9550	 0.2360
O	 0.9530	 0.1370
P	 0.8970	 0.1340
Q	 0.9450	 0.1870
R	 0.9640	 0.3070



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Chain	Atom inclusion	Q-score
S	 0.9440	 0.1420
T	 0.9510	 0.1990
U	 0.9570	 0.0840
V	 0.9540	 0.2130
W	 0.8580	 0.0380
X	 0.8780	 0.0700
Y	 0.7150	 0.0400
Z	 0.8240	 0.0420
a	 0.9900	 0.2290
b	 0.9200	 0.1270
c	 0.9130	 0.1820
d	 0.9810	 0.1250
e	 0.9220	 0.0860
f	 0.9520	 0.1860
g	 0.9430	 0.0580
h	 0.9330	 0.1930
i	 0.9420	 0.2460
j	 0.9350	 0.1650
k	 0.9020	 0.0770
l	 0.9290	 0.1590
m	 0.9660	 0.3090
n	 0.9040	 0.0540
o	 0.9210	 0.1680
p	 0.9250	 0.0450
q	 0.9280	 0.0890
r	 0.8600	 0.0470
s	 0.9370	 0.1750
t	 0.8950	 0.1730
u	 0.9450	 0.1540
v	 0.9230	 0.1860
w	 0.9390	 0.1770
x	 0.9330	 0.0070
y	 0.9120	 0.1120
z	 0.9580	 0.2350