



wwPDB EM Validation Summary Report ⓘ

Jun 15, 2026 – 04:44 PM EDT

PDB ID : 9Y79 / pdb_00009y79
EMDB ID : EMD-72646
Title : Escherichia coli transcription-translation loosely coupled complex (TTC-LC[^]walked) containing mRNA with a 39 nt long spacer, NusG, NusA, and fMet-tRNAs in E-site and P-site
Authors : Shandilya, S.; Wang, C.; Molodtsov, V.; Ebright, R.H.
Deposited on : 2025-09-09
Resolution : 3.20 Å (reported)
Based on initial model : 8VOQ

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

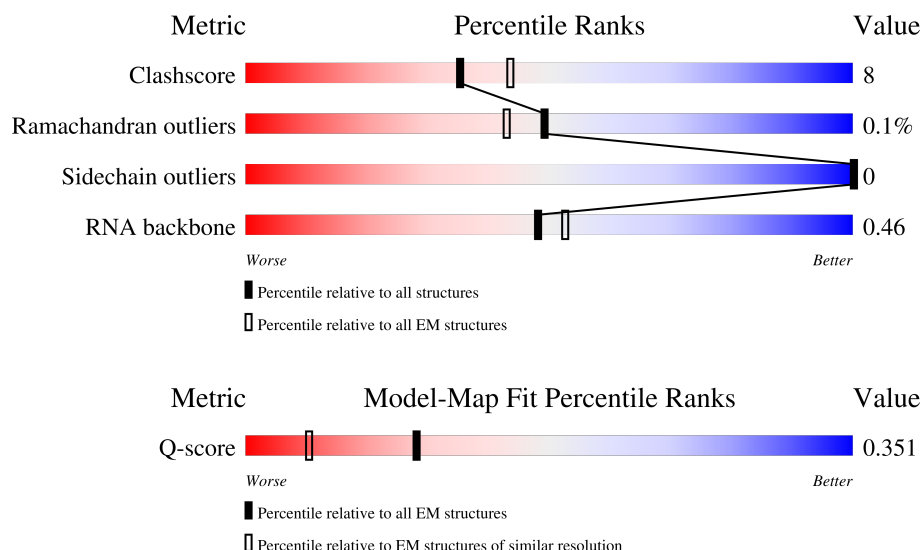
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

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






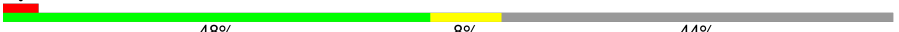


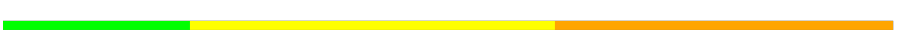





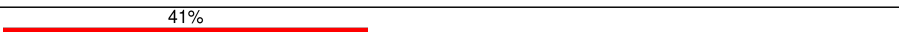

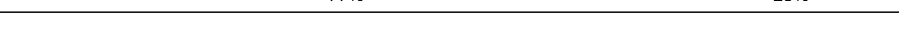

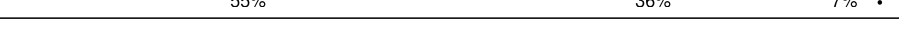
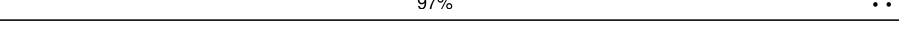







Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	103	
2	1	110	
3	2	100	













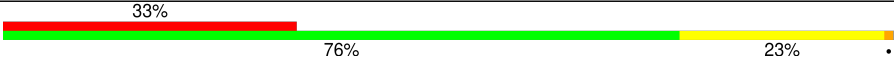






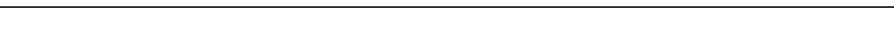
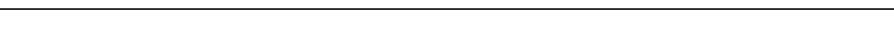


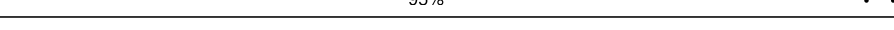
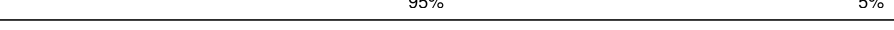
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Mol	Chain	Length	Quality of chain
4	3	104	
5	4	94	
6	5	50	
7	6	50	
8	7	56	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AC	329	
12	AD	329	
13	AE	1407	
14	AF	91	
15	AG	495	
16	C	75	
17	D	1542	
18	E	87	
19	F	71	
20	G	241	
21	H	557	
22	I	233	
23	J	206	
24	K	167	
25	L	135	
26	M	179	

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Mol	Chain	Length	Quality of chain
27	N	130	
28	NG	181	
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	 90% 10%
53	m	46	 98% .
54	n	179	 84% 15% .
55	o	65	 95% . .
56	p	177	 85% 14% .
57	q	38	 89% 11%
58	r	149	 6% 77% 23%
59	s	142	 87% 13%
60	t	123	 85% 15%
61	u	144	 94% 6%
62	v	136	 93% 7%
63	w	127	 90% . 6%
64	x	117	 84% 15% .
65	y	115	 90% 9% .
66	z	118	 92% 7% .

2 Entry composition [i](#)

There are 68 unique types of molecules in this entry. The entry contains 313173 atoms, of which 131874 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
			1633	498	845	148	142			

- Molecule 5 is a protein called Large ribosomal subunit protein bL25.

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
			734	225	260	84	142	23		

- Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	6	28	Total	C	H	N	O	P	0	0
			884	271	312	110	163	28		

- Molecule 8 is a RNA chain called mRNA with 39 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	31	Total	C	H	N	O	P	0	0
			955	285	318	82	239	31		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
9	9	148	Total	C	H	N	O	S	0	0
			2272	705	1155	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
			2445	723	825	295	527	75		
10	B	76	Total	C	H	N	O	P	0	0
			2445	723	825	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	H	N	O	S	0	0
			21153	6631	10586	1841	2052	43		

- Molecule 12 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AC	220	Total	C	H	N	O	S	0	0
			3406	1056	1716	298	330	6		
12	AD	298	Total	C	H	N	O	S	0	0
			3965	1284	1892	377	406	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AE	1335	Total	C	H	N	O	S	0	0
			21006	6526	10618	1854	1958	50		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AF	82	Total	C	H	N	O	S	0	0
			1309	396	659	122	131	1		

- Molecule 15 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	AG	495	Total	C	H	N	O	S	0	0
			7687	2396	3835	669	774	13		

- Molecule 16 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	C	66	Total	C	H	N	O	S	0	0
			1105	344	561	102	97	1		

- Molecule 17 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	D	1524	Total	C	H	N	O	P	0	0
			49154	14585	16451	6003	10591	1524		

- Molecule 18 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	E	86	Total	C	H	N	O	S	0	0
			1389	414	720	138	114	3		

- Molecule 19 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	F	70	Total	C	H	N	O	S	0	0
			1219	366	630	125	97	1		

- Molecule 20 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	G	225	Total	C	H	N	O	S	0	0
			3548	1113	1788	316	323	8		

- Molecule 21 is a protein called Small ribosomal subunit protein bS1.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	H	259	Total	C	H	N	O	S	0	0
			3187	1073	1457	305	349	3		

- Molecule 22 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	I	208	Total	C	H	N	O	S	0	0
			3347	1036	1711	307	290	3		

- Molecule 23 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	J	205	Total	C	H	N	O	S	0	0
			3351	1026	1708	315	298	4		

- Molecule 24 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	K	156	Total	C	H	N	O	S	0	0
			2349	717	1197	217	212	6		

- Molecule 25 is a protein called Small ribosomal subunit protein bS6.

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

- Molecule 26 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	M	151	Total	C	H	N	O	S	0	0
			2420	735	1239	227	215	4		

- Molecule 27 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	N	129	Total	C	H	N	O	S	0	0
			2011	616	1032	173	184	6		

- Molecule 28 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	NG	162	Total	C	H	N	O	S	0	0
			1752	824	459	223	239	7		

- Molecule 29 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	O	127	Total	C	H	N	O	S	0	0
			2093	634	1071	206	179	3		

- Molecule 30 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	P	99	Total	C	H	N	O	S	0	0
			1622	495	832	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
			1765	540	888	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
			1941	580	1002	194	161	4		

- Molecule 33 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	S	100	Total	C	H	N	O	S	0	0
			1650	499	845	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
			1449	439	735	144	130	1		

- Molecule 35 is a protein called Small ribosomal subunit protein bS16.

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 Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	V	80	Total	C	H	N	O	S	0	0
			1340	411	692	121	113	3		

- Molecule 37 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	W	83	Total	C	H	N	O	S	0	0
			1352	424	689	126	111	2		

- Molecule 38 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	X	116	Total	C	H	N	O	S	0	0
			1866	558	966	181	158	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
39	Y	141	Total	C	H	N	O	S	0	0
			2118	651	1086	179	196	6		

- Molecule 40 is a protein called Large ribosomal subunit protein bL12.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	Z	30	Total	C	H	N	O	S	0	0
			462	144	235	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
			92945	27587	31104	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
			1182	360	600	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
			1278	388	653	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
			3869	1144	1300	468	837	120		

- Molecule 45 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	e	62	Total	C	H	N	O	S	0	0
			1033	308	532	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
			937	281	489	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
			4237	1288	2155	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
			3181	979	1616	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
			891	275	465	78	73			

- Molecule 52 is a protein called Large ribosomal subunit protein uL4.

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 Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	n	177	Total	C	H	N	O	S	0	0
			2855	899	1445	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
			1077	323	573	105	74	2		

- Molecule 56 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	p	175	Total	C	H	N	O	S	0	0
			2672	826	1359	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 Large ribosomal subunit protein bL9.

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 Large ribosomal subunit protein uL13.

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 Large ribosomal subunit protein uL14.

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 Large ribosomal subunit protein uL15.

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 Large ribosomal subunit protein bL17.

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 Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	x	116	Total	C	H	N	O		0	0
			1816	552	924	178	162			

- Molecule 65 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	y	114	Total	C	H	N	O	S	0	0
			1880	574	963	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) (labeled as "Ligand of Interest" by depositor).

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


- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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:  85% 15%




- Molecule 2: 50S ribosomal protein L22

Chain 1:  95% 5%




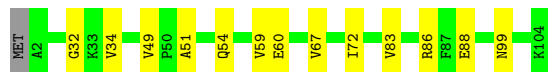
- Molecule 3: 50S ribosomal protein L23

Chain 2:  82% 12% 6%




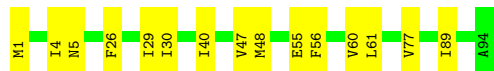
- Molecule 4: 50S ribosomal protein L24

Chain 3:  87% 12% .

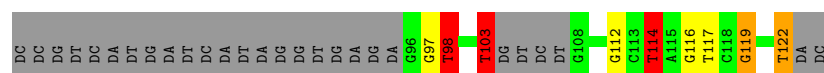


- Molecule 5: Large ribosomal subunit protein bL25

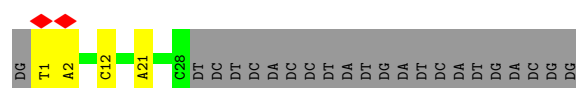
Chain 4:  84% 16%



- Molecule 6: NT DNA



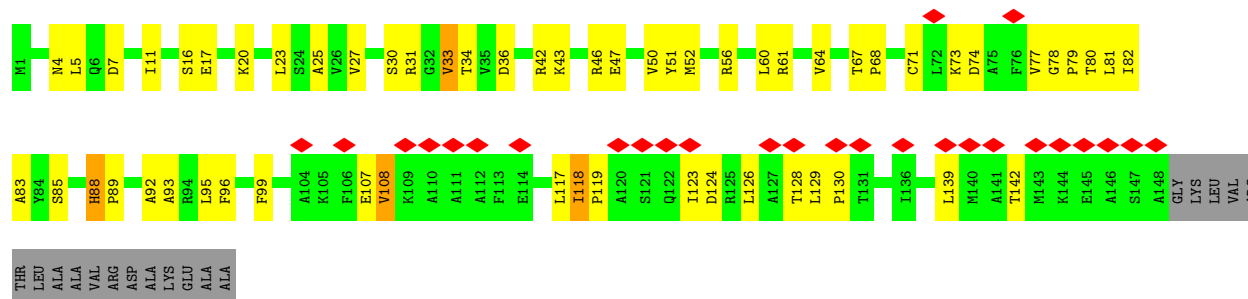
- Molecule 7: T DNA



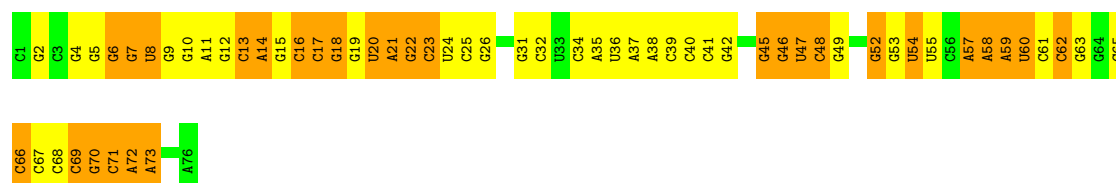
- Molecule 8: mRNA with 39 nt long spacer



- Molecule 9: 50S ribosomal protein L10



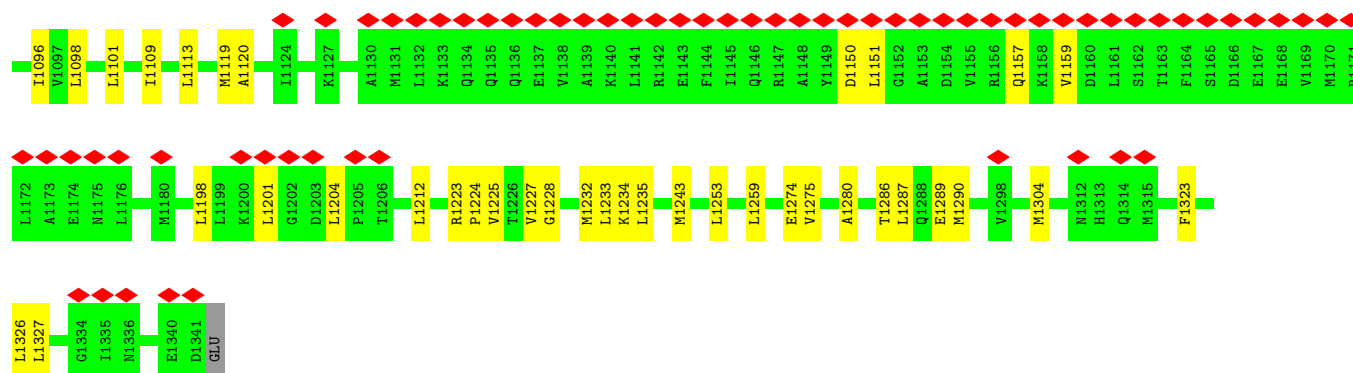
- Molecule 10: E-site and P-site tRNA (fMet)



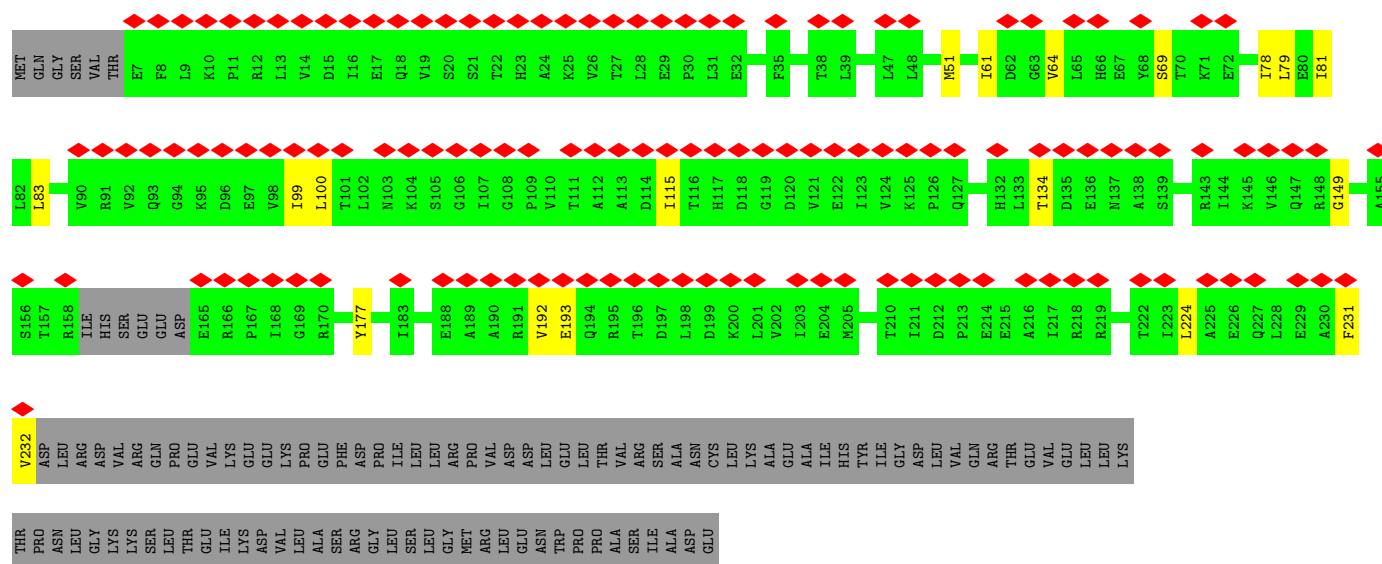
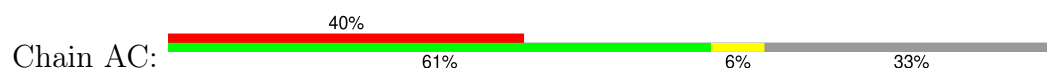
- Molecule 10: E-site and P-site tRNA (fMet)



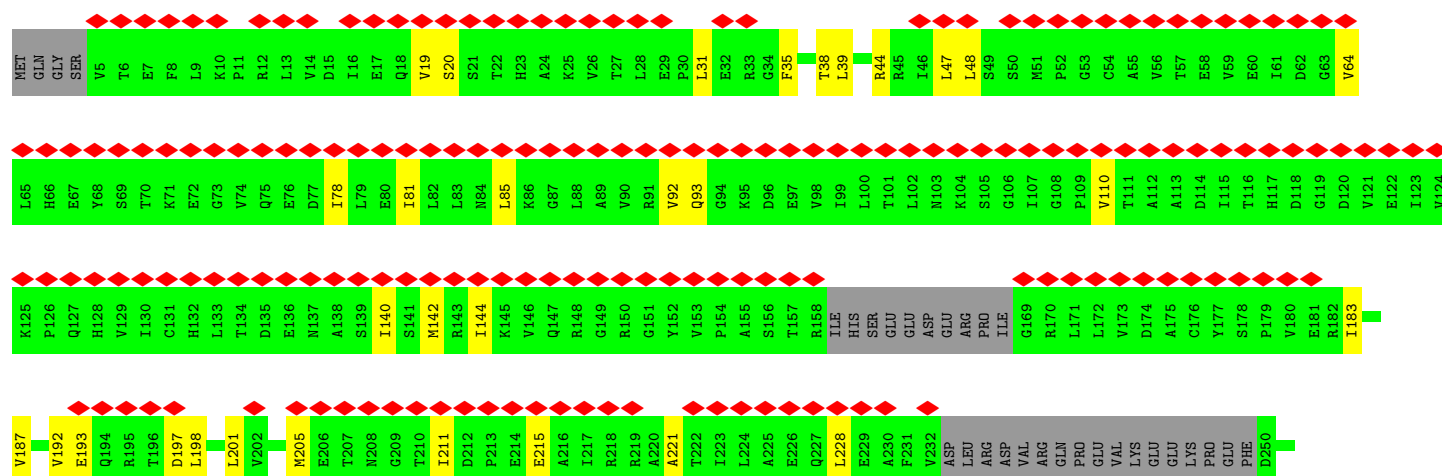
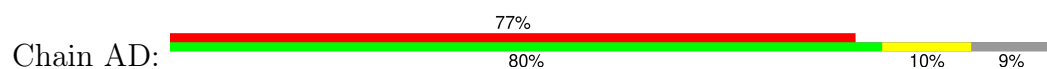


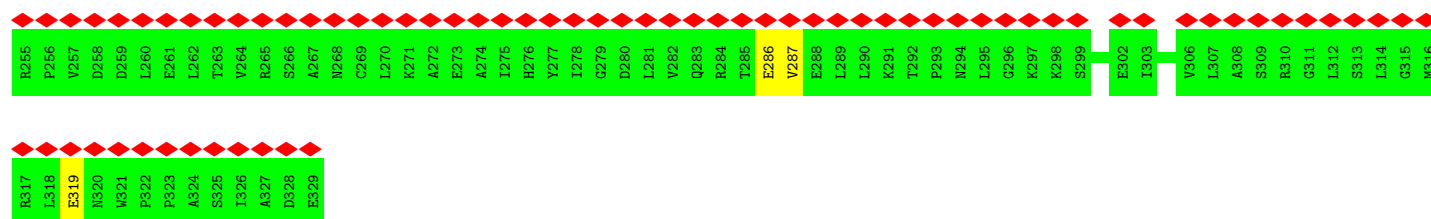


- Molecule 12: DNA-directed RNA polymerase subunit alpha

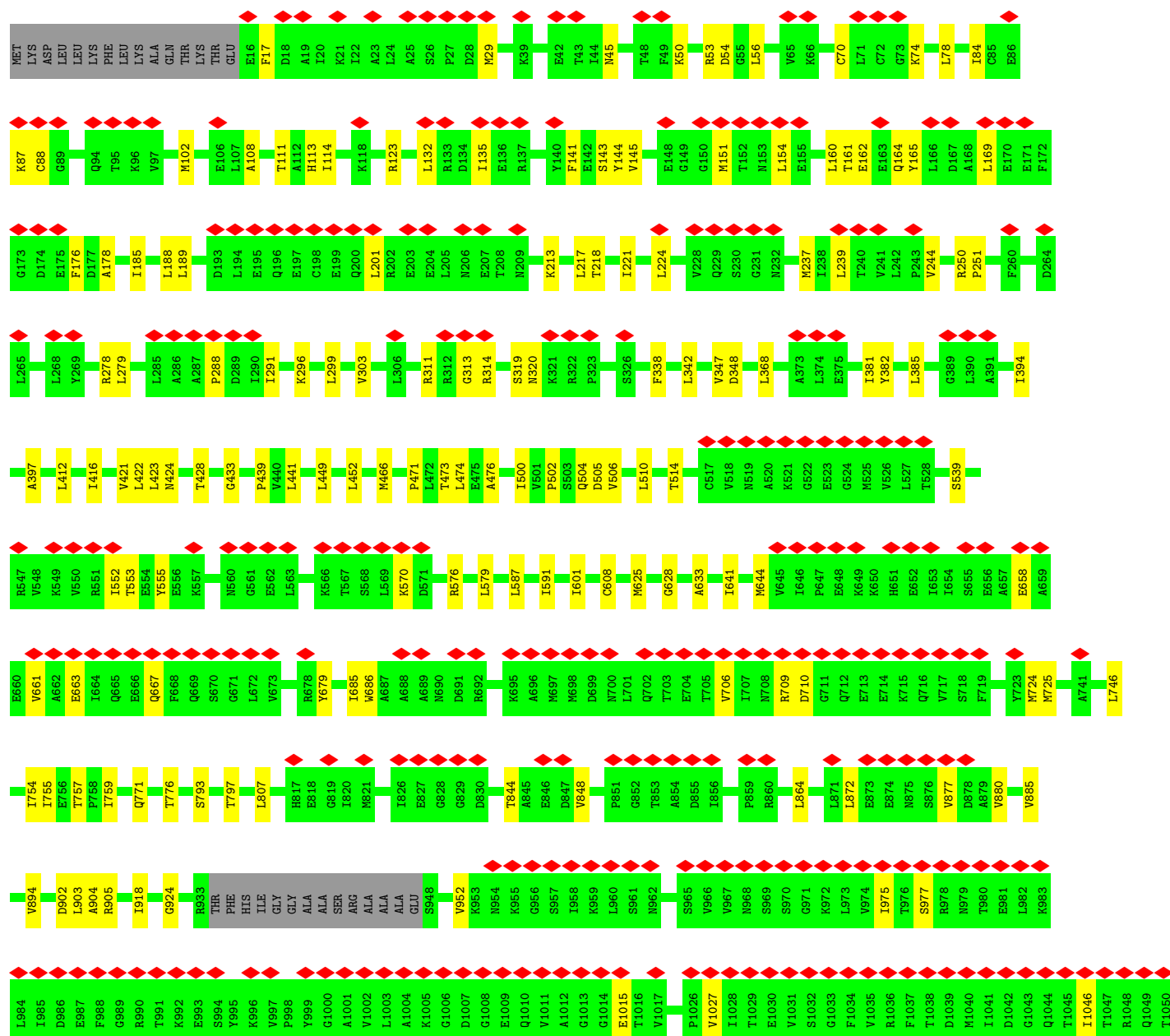
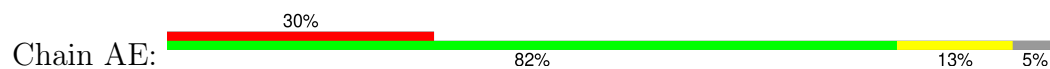


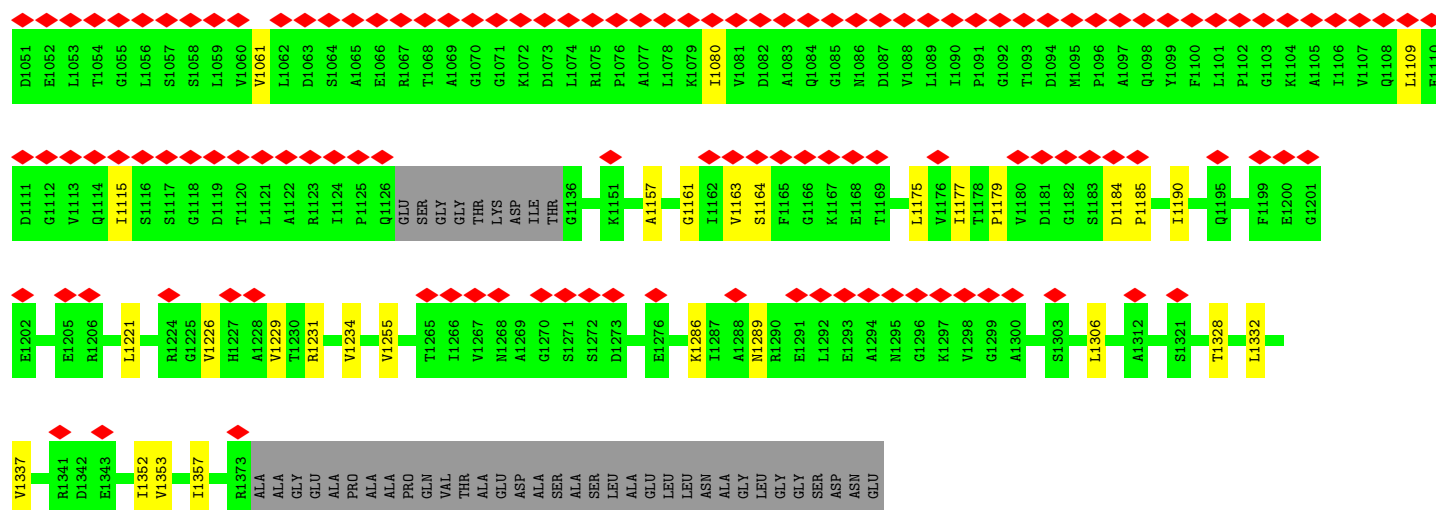
- Molecule 12: DNA-directed RNA polymerase subunit alpha



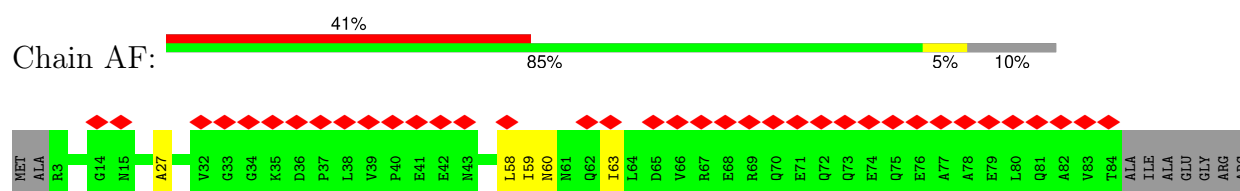


• Molecule 13: DNA-directed RNA polymerase subunit beta'

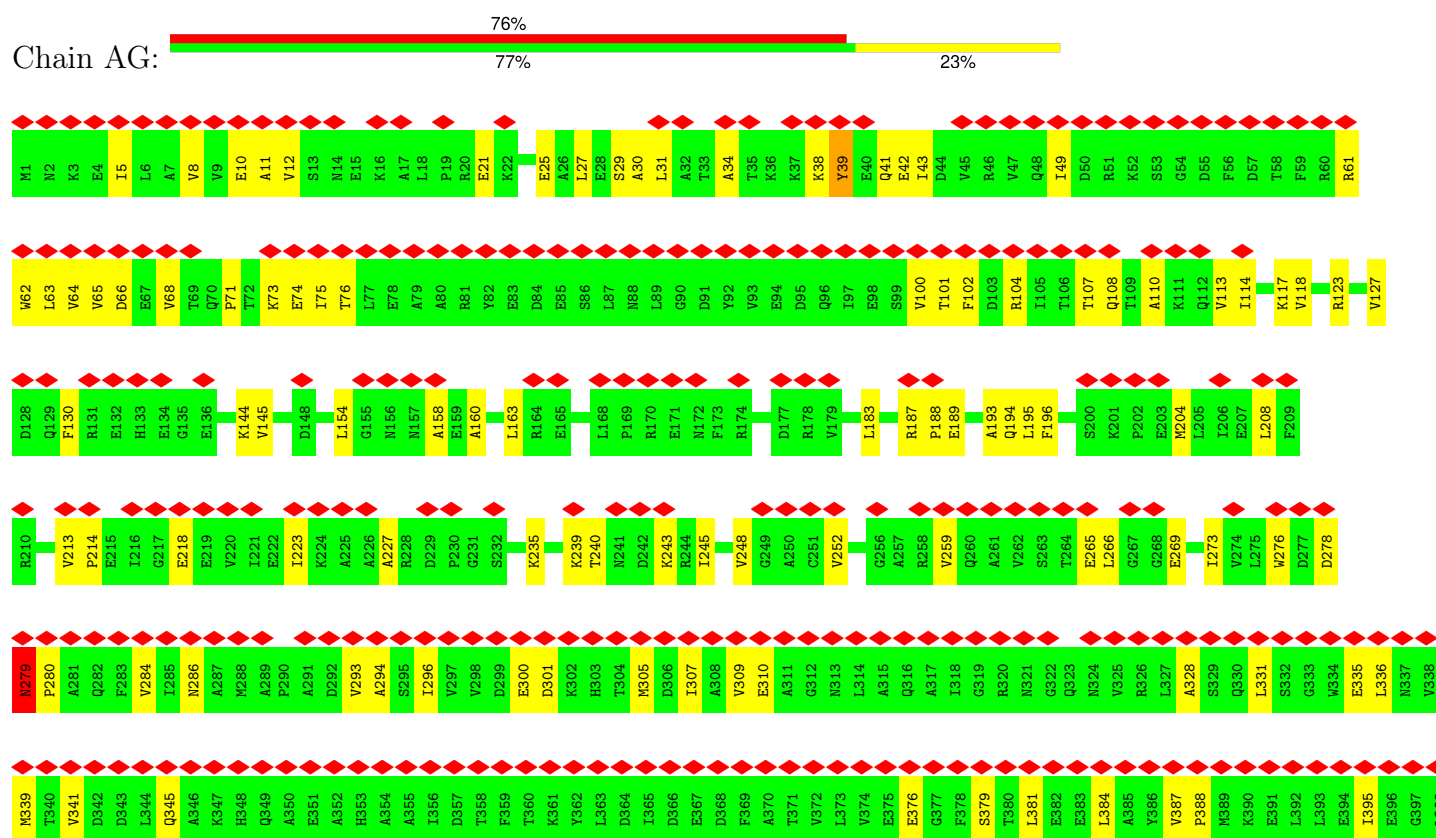




- Molecule 14: DNA-directed RNA polymerase subunit omega



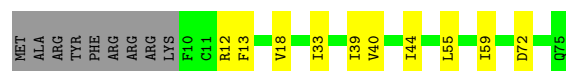
- Molecule 15: Transcription termination/antitermination protein NusA





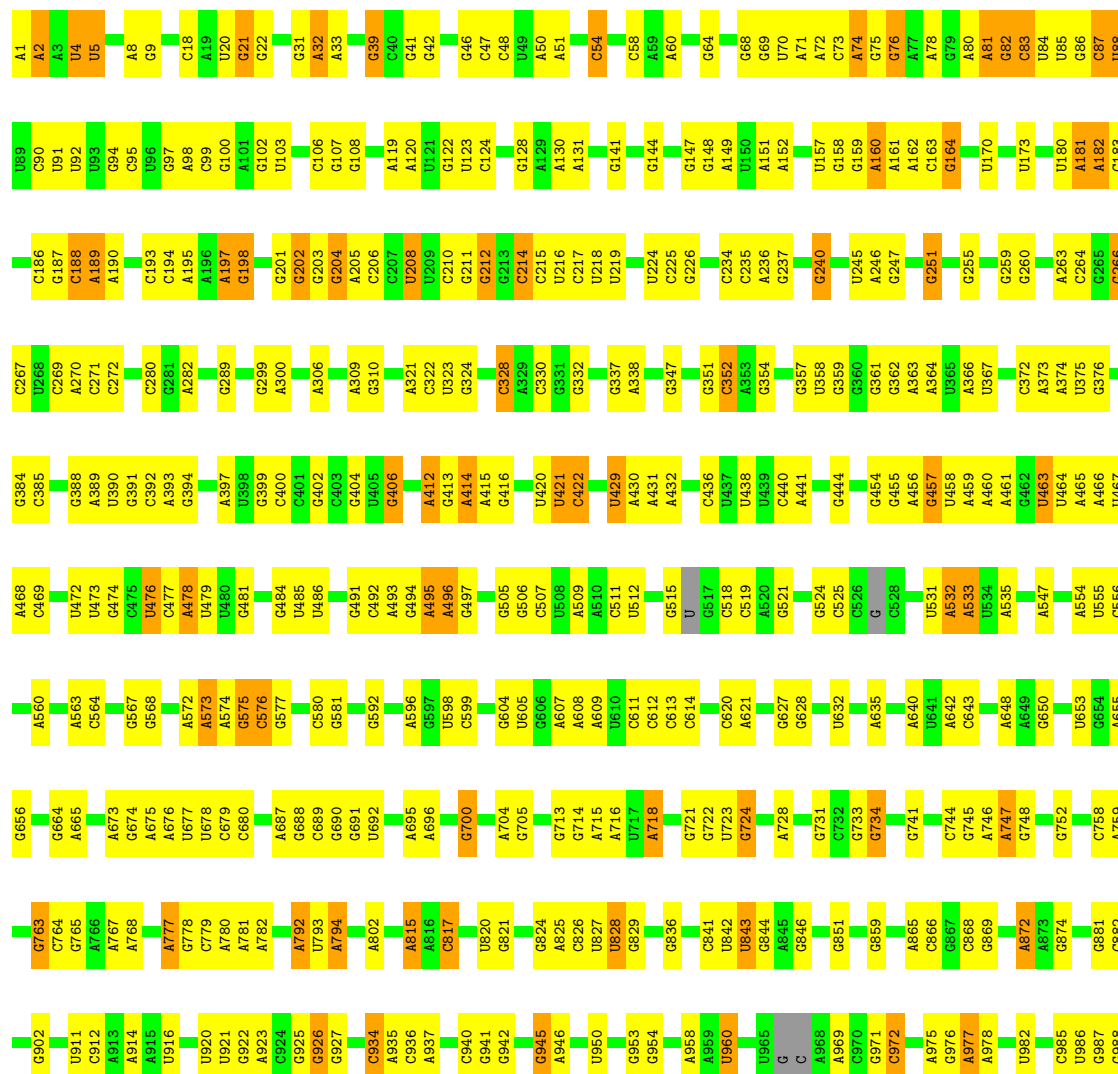
- Molecule 16: Small ribosomal subunit protein bS18

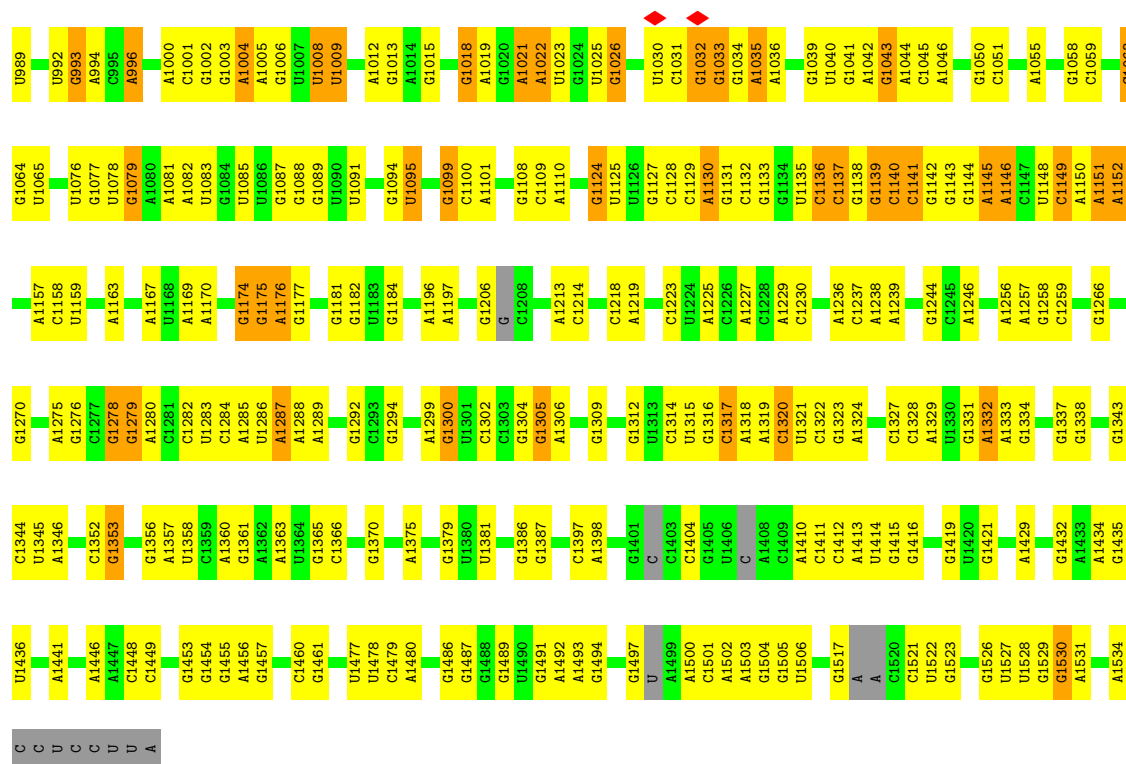
Chain C: 75% 13% 12%



- Molecule 17: 16S rRNA

Chain D: 55% 36% 7%





- Molecule 18: Small ribosomal subunit protein bS20

Chain E: 97%



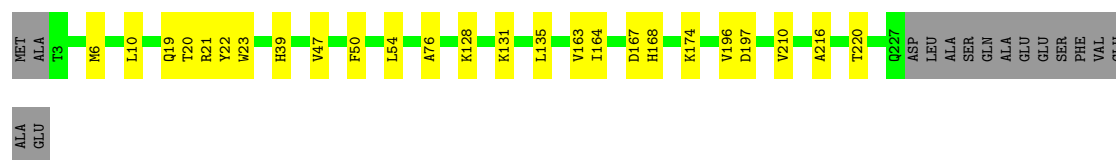
- Molecule 19: Small ribosomal subunit protein bS21

Chain F: 87% 11%



- Molecule 20: 30S ribosomal protein S2

Chain G: 83% 10% 7%

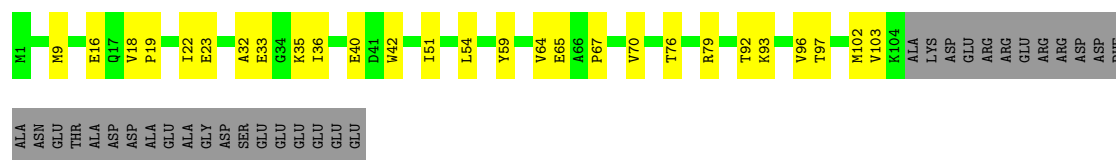


- Molecule 21: Small ribosomal subunit protein bS1


Chain H: 17% 35% 11% 54%



Chain L:  57% 20% 23%




- Molecule 26: Small ribosomal subunit protein uS7

Chain M:  77% 7% 16%



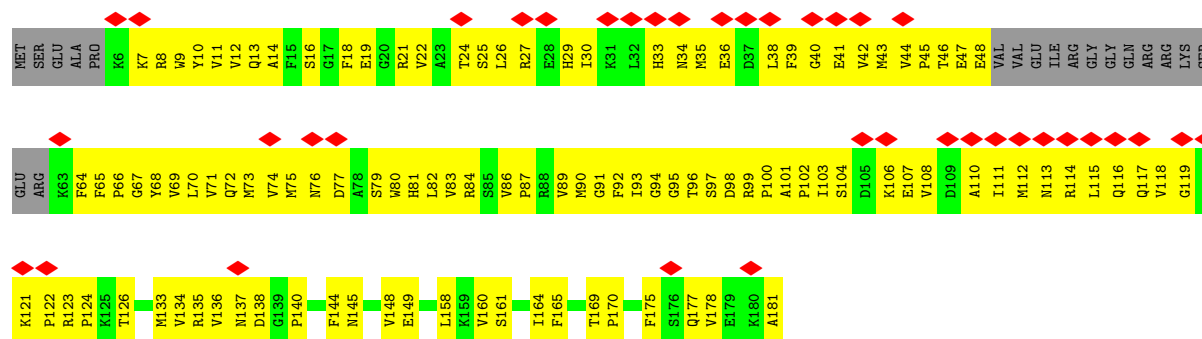
- Molecule 27: Small ribosomal subunit protein uS8

Chain N:  89% 10%




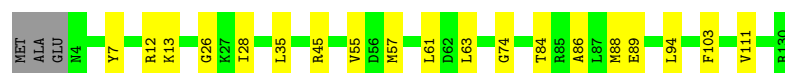
- Molecule 28: Transcription termination/antitermination protein NusG

Chain NG:  21% 28% 62% 10%



- Molecule 29: Small ribosomal subunit protein uS9

Chain O:  83% 15%




- Molecule 30: Small ribosomal subunit protein uS10

Chain P:  71% 24%



- Molecule 31: 30S ribosomal protein S11

Chain Q:  81% 10% 9%



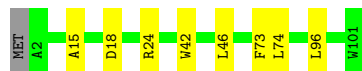
- Molecule 32: 30S ribosomal protein S12

Chain R:  92% 6%




- Molecule 33: Small ribosomal subunit protein uS14

Chain S:  91% 8%




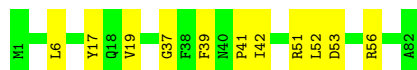
- Molecule 34: Small ribosomal subunit protein uS15

Chain T:  88% 11%




- Molecule 35: Small ribosomal subunit protein bS16

Chain U:  87% 13%



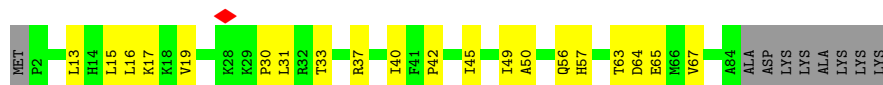
- Molecule 36: Small ribosomal subunit protein uS17

Chain V:  82% 13% 5%

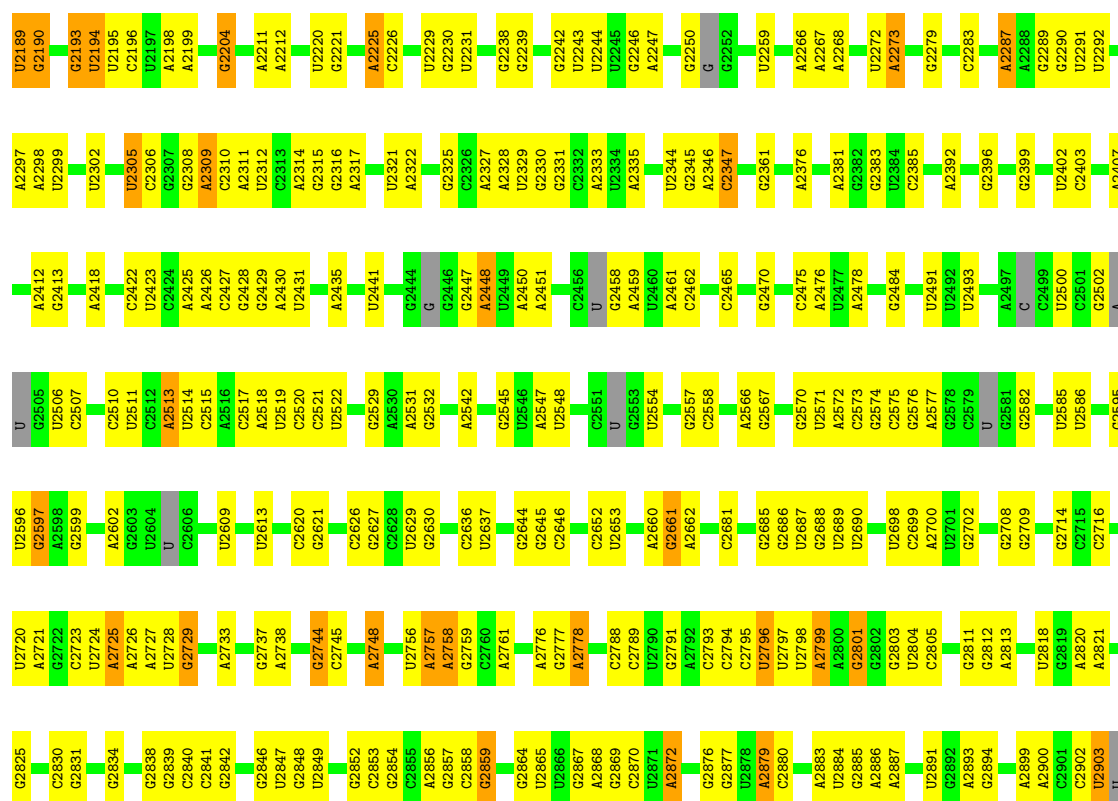


- Molecule 37: Small ribosomal subunit protein uS19

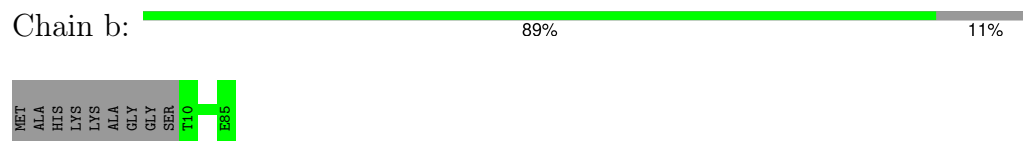
Chain W:  68% 22% 10%



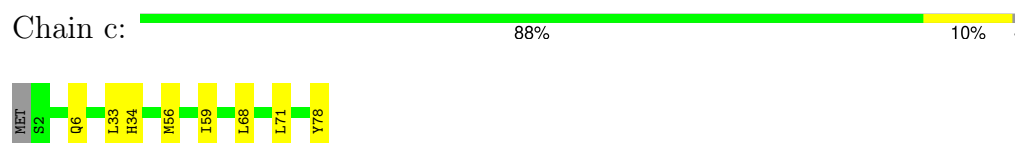
U2118	A2119	G2120	G2121	G2122	G2123	G2124	G2125	A2126	G2127	G2128	U2131	U2132	G2133	G2134	U2139	G2140	G2141	A2142	C2143	G2144	C2145	A2147	G2148	C2149	U2151	G2152	G2157	A2158	G2159	C2160	G2161	G2162	C2163	C2164	C2165	U2166	U2167	G2168	A2171	U2172	C2173	C2174	C2175	A2176	C2177	U2182	A2183	A2184	U2185	G2186	U2187	U2188	
U2022	C2023	G2027	U2028	G2029	A	A2031	G2032	A2033	G2038	U2039	G2040	C2043	G2048	G2049	A2052	C2055	G2056	A2060	G2061	A2062	U2068	G	A2070	A2071	C2072	C2073	U	U2075	G2093	A2097	U2098	U2099	G2100	A2101	G2102	C2103	C2104	G2107	A2108	U2109	G2110	U2111	G2112	U2113	A2114	U2115	G2116	U2117	U2118				
G1831	C1832	C1833	U1834	G	G1836	C1837	G1840	U1841	G1842	G1843	G1844	G1845	G1846	A1847	G1848	G1849	A1853	A1854	U1855	U1856	G1857	A1858	U1859	G1869	C1870	A1871	A1872	A1876	A1877	U1880	C1881	G1884	A1885	U1886	C1887	G1888	A1889	A1890	G1896	G1897	U1898	A1899	G1904	C1905	G1906	G1907	U1908	G1910	U	A1912			
A1913	C1914	U	A1916	U	A1918	G1921	G1922	U1923	C1924	C1925	G1929	G1930	A1936	A1937	A1938	U	U1940	C1941	C1942	G1945	U1946	C1947	G1948	U1955	G1959	A1960	C1961	U1963	G1964	C1967	A1970	U1971	G1972	G1973	C1974	G1975	A1987	U1991	G1992	U1993	C1996	G1997	U2008	G2011	U2012	U2013	G2018	A2019	A2020	C2021			
U1714	G1715	U1720	A1721	A1722	U1729	C1730	G1731	G1732	G1733	G1734	A1735	U1736	U1737	G1738	A1739	G1740	U1751	C1752	G1753	G1756	A1757	U1758	C1760	G1764	U1765	G1766	A1773	C1774	U1784	A1789	C1790	U1791	G1792	C1795	U1796	C1800	A1801	A1802	A1803	A1808	C1809	G1811	C1816	C1817	U1820	A1829	G1830						
U1509	A1510	G1511	A1515	G1516	G1517	C1518	G1519	U1520	G1521	G1524	A1528	G1529	A1532	C1533	U1534	A1535	C1536	G1537	G1538	U1539	G1540	C1541	U1542	A1544	A1551	A1552	A1553	U1554	G1560	C1561	U1562	U1563	C1564	C1565	A1566	A1569	C1575	U1576	C1577	U1578	A1579	A1580	G1581	C1582	U1583	U1584	C1585	A1586	G1587	U1588			
U1589	A1590	A1591	C1592	U1593	A1594	C1595	A1596	G1601	A1608	A1609	A1610	G1613	A1614	A1615	A1616	C1617	A	U1619	G1620	U1621	G1622	A1630	A1637	G1645	C1646	U1647	U1648	G1649	A1650	G1651	A1664	C1670	U1671	A1672	G1673	G1674	A1676	A1677	A1678	A1679	C1691	G1697	A1698	A1699	G1703	G1707							
U1405	U1406	G1407	A1408	G1409	G1410	U1411	U1412	A1413	A1414	U1415	G1416	C1417	G1418	A1419	A1420	G1421	G1422	A1427	C1428	G1432	A1433	A1434	U1443	G1444	G1452	A1453	C1454	G1459	U1460	A1461	C1462	C1463	G1473	U1474	G1482	U1485	A1490	G1491	G1492	C1493	U1497	A1503	A1504	U1505	U1506	C1507	A1508						
A1284	A1285	A1286	G1287	G1288	C1289	C1290	C1291	A1292	C1293	U1294	U1295	G1296	C1297	C1298	G1299	G1300	A1301	A1302	G1303	C1319	C1320	A1321	A1322	C1323	U1329	C1345	G1346	U1352	A1353	A1354	G1355	G1356	C1357	G1358	A1359	A1365	A1378	U1379	G1380	A1383	A1384	C1385	A1386	A1387	A1392	A1395	G1401						
U1173	U1174	A1175	U1176	G1177	C1178	G1179	U1180	U1183	U1184	U1185	G1186	G1187	U1188	A1189	G1190	G1191	C1196	G1197	U1198	U1199	C1200	G1212	G1223	G1227	G1235	G1236	A1237	G1238	G1248	U1249	G1250	C1251	G1252	A1253	G1256	C1257	U1258	G1259	G1266	U1267	A1268	A1269	C1270	G1271	A1272	U1273	C1278	G1279					
U1094	A1095	A1096	U1097	C1100	U1101	C1102	A1103	C1104	U1105	G1106	G1107	U1108	C1109	C1110	A1111	G1112	G1115	G1116	U1119	G1120	G1128	A1129	U1132	A1133	A1134	C1135	G1136	G1137	G1138	G1139	C1140	U1141	A1142	A1143	A1144	C1150	A1151	C1152	C1153	G1154	G1157	U1159	G1160	A1165	U1166	C1167	G1168	A1169	C1170	G1171			
A1028	A1029	U1033	G1034	U1035	G1036	A1039	A1040	G1041	G1042	C1043	C1044	C1045	A1046	G1047	A1048	C1049	A1050	G1051	C1052	C1053	A1054	G1055	G1056	G1059	U1060	U1061	G1062	G1063	U1064	U1065	U1066	A1067	G1068	A1069	A1070	G1071	C1072	A1073	G1074	C1075	C1076	A1077	A1080	U1081	U1082	U1083	A1084	A1085	A1086	U1087	A1088	A1089	A1090
C817	G818	A819	A825	U826	U827	U828	A833	A834	U839	A845	U846	U847	C848	A849	U850	G856	G857	G858	G859	U860	G862	U868	U870	G875	G876	A877	G878	G879	G880	G881	G882	U883	C884	C885	A886	A887	C888	C889	G890	A891	A892	C893	U894	A895	A896	C897							
A699	G707	G708	U709	U710	G711	U714	A715	U716	C717	A721	G728	G729	A730	G733	A734	G738	U744	G	U	U	G748	A752	U756	G757	U772	G760	A761	U767	G768	G775	G776	A782	A783	G784	C785	C786	C787	A788	A802	U803	A804	G805	C806	U807		C812							



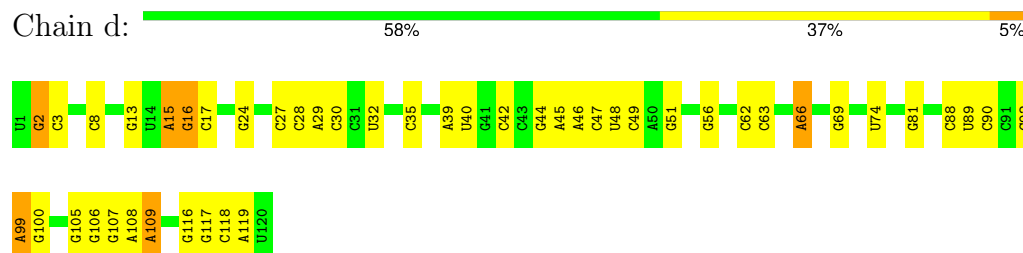
• Molecule 42: 50S ribosomal protein L27




• Molecule 43: 50S ribosomal protein L28

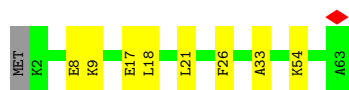


• Molecule 44: 5S rRNA




• Molecule 45: Large ribosomal subunit protein uL29

Chain e:  86% 13%



- Molecule 46: 50S ribosomal protein L30

Chain f:  80% 19%




- Molecule 47: 50S ribosomal protein L31

Chain g:  69% 26% 6%



- Molecule 48: 50S ribosomal protein L2

Chain h:  89% 10%



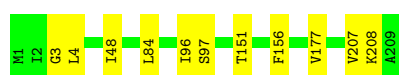
- Molecule 49: 50S ribosomal protein L32

Chain i:  95% 5%




- Molecule 50: 50S ribosomal protein L3

Chain j:  95% 5%




- Molecule 51: 50S ribosomal protein L33

Chain k:  82% 13% 5%



- Molecule 52: Large ribosomal subunit protein uL4

Chain l:  90% 10%




- Molecule 53: 50S ribosomal protein L34

Chain m:  98%



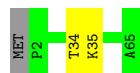
- Molecule 54: Large ribosomal subunit protein uL5

Chain n:  84% 15%




- Molecule 55: 50S ribosomal protein L35

Chain o:  95%




- Molecule 56: Large ribosomal subunit protein uL6

Chain p:  85% 14%




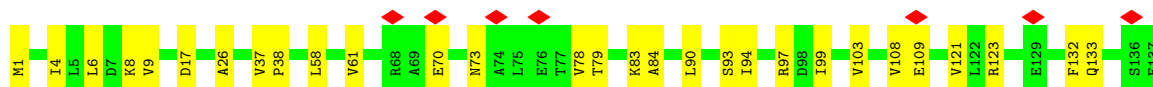
- Molecule 57: 50S ribosomal protein L36

Chain q:  89% 11%



- Molecule 58: Large ribosomal subunit protein bL9

Chain r:  6% 77% 23%





- Molecule 59: Large ribosomal subunit protein uL13

Chain s: 87% 13%



- Molecule 60: Large ribosomal subunit protein uL14

Chain t: 85% 15%



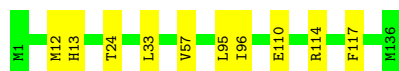
- Molecule 61: Large ribosomal subunit protein uL15

Chain u: 94% 6%



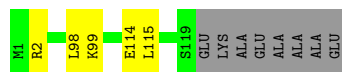
- Molecule 62: 50S ribosomal protein L16

Chain v: 93% 7%



- Molecule 63: Large ribosomal subunit protein bL17

Chain w: 90% 6%



- Molecule 64: Large ribosomal subunit protein uL18

Chain x: 84% 15%

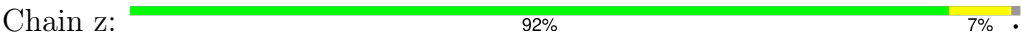


- Molecule 65: Large ribosomal subunit protein bL19

Chain y: 90% 9%



- 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	31000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.076	Depositor
Minimum map value	-0.092	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.044	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	666.624, 666.624, 666.624	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.302, 1.302, 1.302	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	0.30	0/829	0.37	0/1107
2	1	0.28	0/864	0.33	0/1156
3	2	0.27	0/752	0.32	0/1005
4	3	0.25	0/796	0.37	0/1062
5	4	0.24	0/766	0.33	0/1025
6	5	3.89	22/529 (4.2%)	3.65	39/813 (4.8%)
7	6	0.19	0/642	0.39	0/987
8	7	0.41	0/703	0.61	0/1086
9	9	0.20	0/1131	0.48	0/1524
10	A	0.19	0/1810	0.36	0/2821
10	B	0.22	0/1810	0.39	0/2821
11	AA	0.13	0/10736	0.31	0/14487
12	AC	0.12	0/1710	0.27	0/2317
12	AD	0.11	0/2091	0.29	0/2847
13	AE	0.12	0/10545	0.31	0/14236
14	AF	0.12	0/652	0.27	0/879
15	AG	0.15	0/3897	0.39	1/5273 (0.0%)
16	C	0.26	0/553	0.34	0/743
17	D	0.28	0/36610	0.29	0/57091
18	E	0.26	0/675	0.39	0/895
19	F	0.22	0/597	0.33	0/792
20	G	0.21	0/1791	0.35	0/2413
21	H	0.18	0/1746	0.47	0/2382
22	I	0.24	0/1663	0.34	0/2241
23	J	0.22	0/1665	0.30	0/2227
24	K	0.26	0/1165	0.35	0/1568
25	L	0.24	0/867	0.39	0/1171
26	M	0.20	0/1195	0.31	0/1602
27	N	0.26	0/989	0.31	0/1326
28	NG	0.24	0/1322	0.55	0/1782
29	O	0.22	0/1034	0.36	0/1375
30	P	0.25	0/800	0.42	0/1082

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	Q	0.25	0/893	0.31	0/1205
32	R	0.23	0/952	0.29	0/1274
33	S	0.22	0/817	0.31	0/1088
34	T	0.25	0/722	0.41	0/964
35	U	0.24	0/659	0.34	0/884
36	V	0.26	0/657	0.39	0/881
37	W	0.20	0/680	0.30	0/915
38	X	0.22	0/909	0.36	0/1215
39	Y	0.16	0/1046	0.39	0/1410
40	Z	0.17	0/227	0.47	0/304
41	a	0.32	0/69247	0.31	0/107985
42	b	0.28	0/589	0.32	0/779
43	c	0.30	0/635	0.33	0/848
44	d	0.28	0/2872	0.26	0/4478
45	e	0.26	0/502	0.32	0/667
46	f	0.31	0/452	0.39	0/605
47	g	0.20	0/531	0.39	0/709
48	h	0.29	0/2121	0.35	0/2852
49	i	0.28	0/450	0.30	0/599
50	j	0.29	0/1586	0.33	0/2134
51	k	0.27	0/433	0.29	0/576
52	l	0.26	0/1571	0.32	0/2113
53	m	0.29	0/380	0.33	0/498
54	n	0.22	0/1434	0.35	0/1926
55	o	0.28	0/513	0.32	0/676
56	p	0.22	0/1333	0.31	0/1805
57	q	0.26	0/303	0.33	0/397
58	r	0.18	0/1122	0.35	0/1515
59	s	0.31	0/1152	0.35	0/1551
60	t	0.28	0/955	0.35	0/1279
61	u	0.27	0/1062	0.35	0/1413
62	v	0.25	0/1093	0.32	0/1460
63	w	0.30	0/964	0.40	0/1289
64	x	0.25	0/902	0.32	0/1209
65	y	0.27	0/929	0.30	0/1242
66	z	0.33	0/960	0.36	0/1278
All	All	0.34	22/194588 (0.0%)	0.38	40/286159 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	5	0	5
12	AD	0	1
21	H	0	1
28	NG	0	1
30	P	0	1
All	All	0	9

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	5	114	DT	C4-C5	-38.15	0.68	1.44
6	5	122	DT	C4-C5	-35.41	0.73	1.44
6	5	98	DT	N1-C2	-34.02	0.70	1.38
6	5	103	DT	N1-C2	-33.99	0.70	1.38
6	5	119	DG	C5-C4	-29.97	0.78	1.38

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	5	103	DT	C2-N1-C1'	-32.82	70.12	119.35
6	5	98	DT	C2-N1-C1'	-32.68	70.34	119.35
6	5	122	DT	C4-C5-C7	-32.52	73.62	122.40
6	5	119	DG	C4-C5-N7	-31.16	64.06	110.80
6	5	114	DT	C4-C5-C6	-28.40	76.60	119.20

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	5	103	DT	Sidechain
6	5	114	DT	Sidechain
6	5	119	DG	Sidechain
6	5	122	DT	Sidechain
6	5	98	DT	Sidechain

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	12	0
2	1	857	922	922	4	0
3	2	746	811	811	13	0
4	3	788	845	844	8	0
5	4	753	780	780	10	0
6	5	474	260	261	28	0
7	6	572	312	313	4	0
8	7	637	318	319	15	0
9	9	1117	1155	1155	65	0
10	A	1620	825	827	48	0
10	B	1620	825	827	58	0
11	AA	10567	10586	10585	168	0
12	AC	1690	1716	1714	14	0
12	AD	2073	1892	1889	26	0
13	AE	10388	10618	10610	137	0
14	AF	650	659	658	5	0
15	AG	3852	3835	3835	115	0
16	C	544	561	560	11	0
17	D	32703	16451	16460	380	0
18	E	669	720	719	1	0
19	F	589	630	629	8	0
20	G	1760	1788	1787	22	0
21	H	1730	1457	1455	60	0
22	I	1636	1711	1710	12	0
23	J	1643	1708	1707	9	0
24	K	1152	1197	1196	17	0
25	L	848	846	846	18	0
26	M	1181	1239	1238	9	0
27	N	979	1032	1031	9	0
28	NG	1293	459	1278	240	0
29	O	1022	1071	1070	15	0
30	P	790	832	831	27	0
31	Q	877	888	887	17	0
32	R	939	1002	1001	4	0
33	S	805	845	844	7	0
34	T	714	735	734	7	0
35	U	649	666	666	6	0
36	V	648	692	691	7	0
37	W	663	689	688	14	0
38	X	900	966	965	21	0
39	Y	1032	1086	1088	25	0
40	Z	227	235	237	7	0
41	a	61841	31104	31125	667	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	b	582	600	599	0	0
43	c	625	653	652	4	0
44	d	2569	1300	1301	31	0
45	e	501	532	531	7	0
46	f	448	489	488	8	0
47	g	522	520	520	23	0
48	h	2082	2155	2154	24	0
49	i	444	459	458	3	0
50	j	1565	1616	1616	8	0
51	k	426	465	464	4	0
52	l	1552	1619	1619	12	0
53	m	377	418	418	1	0
54	n	1410	1445	1444	18	0
55	o	504	573	572	1	0
56	p	1313	1359	1358	16	0
57	q	302	343	343	2	0
58	r	1111	1148	1148	26	0
59	s	1129	1162	1162	16	0
60	t	946	1023	1023	12	0
61	u	1053	1129	1129	7	0
62	v	1074	1157	1157	8	0
63	w	951	994	994	4	0
64	x	892	924	923	15	0
65	y	917	963	962	6	0
66	z	947	1020	1019	6	0
67	AE	1	0	0	0	0
68	AE	2	0	0	0	0
All	All	181299	131874	132686	2452	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 2452 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)
6:5:103:DT:C2	6:5:103:DT:C1'	1.84	1.59
6:5:98:DT:C2	6:5:98:DT:C1'	1.85	1.57
6:5:98:DT:C1'	6:5:98:DT:O2	1.68	1.36
6:5:103:DT:C1'	6:5:103:DT:O2	1.64	1.34
6:5:98:DT:C1'	6:5:98:DT:N3	1.91	1.31

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/100 (92%)	88 (96%)	4 (4%)	0	100	100
4	3	101/104 (97%)	95 (94%)	6 (6%)	0	100	100
5	4	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
9	9	146/165 (88%)	114 (78%)	28 (19%)	4 (3%)	4	25
11	AA	1338/1342 (100%)	1265 (94%)	73 (6%)	0	100	100
12	AC	216/329 (66%)	208 (96%)	8 (4%)	0	100	100
12	AD	292/329 (89%)	275 (94%)	17 (6%)	0	100	100
13	AE	1329/1407 (94%)	1259 (95%)	70 (5%)	0	100	100
14	AF	80/91 (88%)	78 (98%)	2 (2%)	0	100	100
15	AG	493/495 (100%)	432 (88%)	58 (12%)	3 (1%)	21	56
16	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
18	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
19	F	68/71 (96%)	67 (98%)	1 (2%)	0	100	100
20	G	223/241 (92%)	212 (95%)	11 (5%)	0	100	100
21	H	255/557 (46%)	201 (79%)	53 (21%)	1 (0%)	30	62
22	I	206/233 (88%)	196 (95%)	10 (5%)	0	100	100
23	J	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
24	K	154/167 (92%)	147 (96%)	7 (4%)	0	100	100
25	L	102/135 (76%)	98 (96%)	3 (3%)	1 (1%)	12	45
26	M	149/179 (83%)	143 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	N	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
28	NG	158/181 (87%)	141 (89%)	17 (11%)	0	100	100
29	O	125/130 (96%)	113 (90%)	12 (10%)	0	100	100
30	P	97/103 (94%)	86 (89%)	11 (11%)	0	100	100
31	Q	115/129 (89%)	109 (95%)	6 (5%)	0	100	100
32	R	117/124 (94%)	108 (92%)	9 (8%)	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%)	74 (92%)	6 (8%)	0	100	100
36	V	78/84 (93%)	70 (90%)	8 (10%)	0	100	100
37	W	81/92 (88%)	77 (95%)	4 (5%)	0	100	100
38	X	114/118 (97%)	104 (91%)	9 (8%)	1 (1%)	14	47
39	Y	139/142 (98%)	126 (91%)	12 (9%)	1 (1%)	18	52
40	Z	28/121 (23%)	25 (89%)	3 (11%)	0	100	100
42	b	74/85 (87%)	70 (95%)	4 (5%)	0	100	100
43	c	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
45	e	60/63 (95%)	59 (98%)	1 (2%)	0	100	100
46	f	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
47	g	64/70 (91%)	61 (95%)	3 (5%)	0	100	100
48	h	269/273 (98%)	248 (92%)	21 (8%)	0	100	100
49	i	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
50	j	207/209 (99%)	194 (94%)	13 (6%)	0	100	100
51	k	50/55 (91%)	47 (94%)	3 (6%)	0	100	100
52	l	199/201 (99%)	193 (97%)	6 (3%)	0	100	100
53	m	44/46 (96%)	44 (100%)	0	0	100	100
54	n	175/179 (98%)	162 (93%)	13 (7%)	0	100	100
55	o	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
56	p	173/177 (98%)	165 (95%)	8 (5%)	0	100	100
57	q	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
58	r	147/149 (99%)	138 (94%)	9 (6%)	0	100	100
59	s	140/142 (99%)	132 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
60	t	121/123 (98%)	108 (89%)	13 (11%)	0	100	100
61	u	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
62	v	134/136 (98%)	127 (95%)	7 (5%)	0	100	100
63	w	117/127 (92%)	107 (92%)	10 (8%)	0	100	100
64	x	114/117 (97%)	105 (92%)	9 (8%)	0	100	100
65	y	112/115 (97%)	106 (95%)	6 (5%)	0	100	100
66	z	115/118 (98%)	110 (96%)	5 (4%)	0	100	100
All	All	10079/11072 (91%)	9423 (94%)	645 (6%)	11 (0%)	49	79

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
15	AG	39	TYR
21	H	309	MET
38	X	103	LYS
9	9	33	VAL

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	1155/1157 (100%)	1155 (100%)	0	100	100
12	AC	185/286 (65%)	185 (100%)	0	100	100
12	AD	185/286 (65%)	185 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	AE	1120/1168 (96%)	1120 (100%)	0	100	100
14	AF	70/75 (93%)	70 (100%)	0	100	100
15	AG	409/409 (100%)	409 (100%)	0	100	100
16	C	57/65 (88%)	57 (100%)	0	100	100
18	E	65/66 (98%)	65 (100%)	0	100	100
19	F	60/61 (98%)	60 (100%)	0	100	100
20	G	187/199 (94%)	187 (100%)	0	100	100
21	H	137/461 (30%)	137 (100%)	0	100	100
22	I	171/190 (90%)	171 (100%)	0	100	100
23	J	172/173 (99%)	172 (100%)	0	100	100
24	K	119/126 (94%)	119 (100%)	0	100	100
25	L	91/116 (78%)	91 (100%)	0	100	100
26	M	124/147 (84%)	124 (100%)	0	100	100
27	N	104/105 (99%)	104 (100%)	0	100	100
28	NG	142/158 (90%)	142 (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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	8317/9148 (91%)	8317 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
24	K	121	HIS
65	y	52	ASN
36	V	47	HIS
64	x	19	GLN
56	p	73	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	34 (45%)	3 (4%)
10	B	75/76 (98%)	38 (50%)	5 (6%)
17	D	1513/1542 (98%)	268 (17%)	5 (0%)
41	a	2859/2904 (98%)	494 (17%)	0
44	d	119/120 (99%)	17 (14%)	0
8	7	30/56 (53%)	20 (66%)	3 (10%)
All	All	4671/4774 (97%)	871 (18%)	16 (0%)

5 of 871 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	3	G
8	7	4	U
8	7	5	U
8	7	6	U
8	7	7	U

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
17	D	1337	G
17	D	1145	A
10	B	22	G
17	D	758	C
10	B	21	A

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.

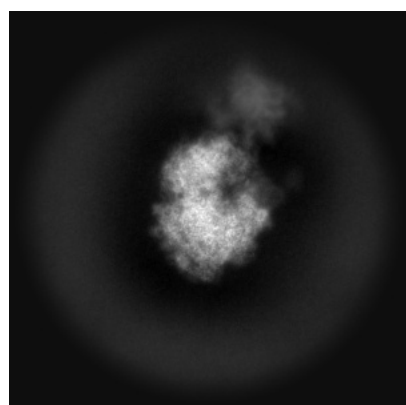
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72646. These allow visual inspection of the internal detail of the map and identification of artifacts.

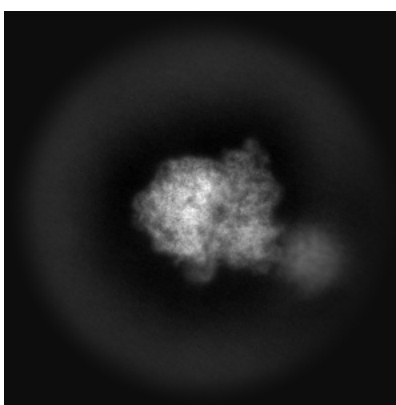
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

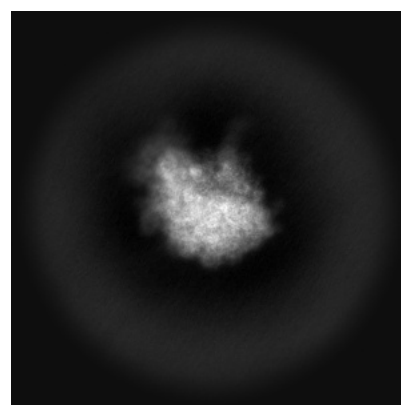
6.1.1 Primary map



X



Y

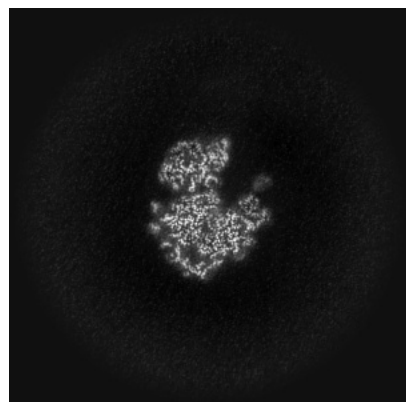


Z

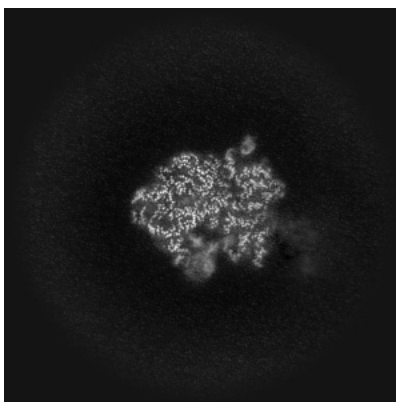
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

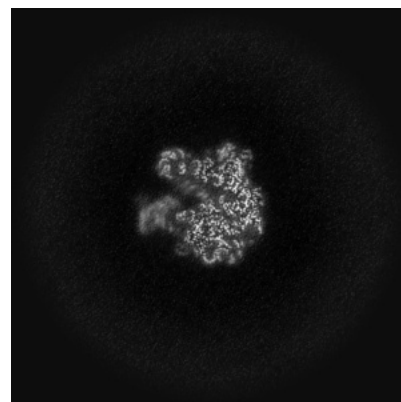
6.2.1 Primary map



X Index: 256



Y Index: 256

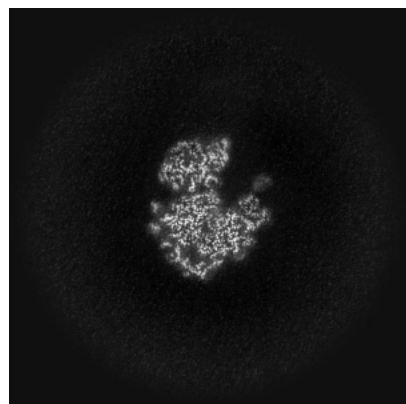


Z Index: 256

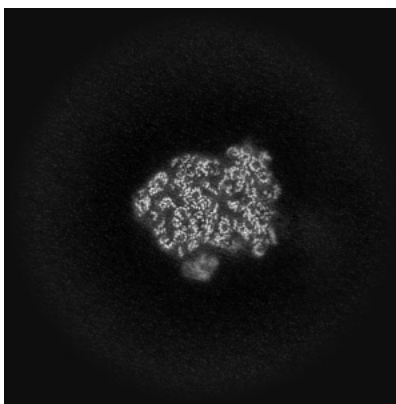
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

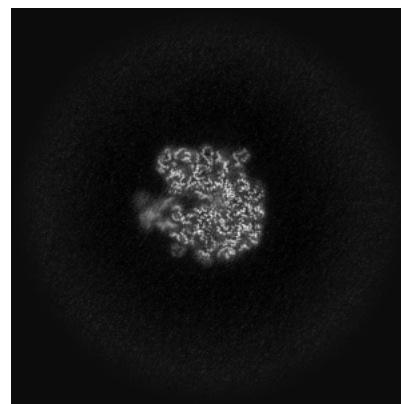
6.3.1 Primary map



X Index: 256



Y Index: 244

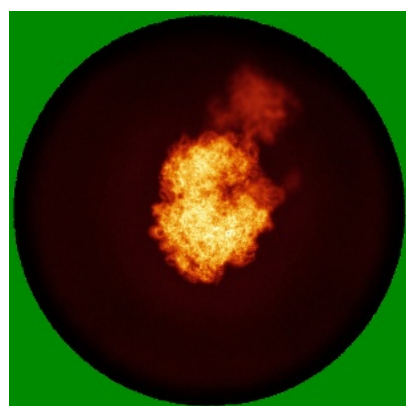


Z Index: 247

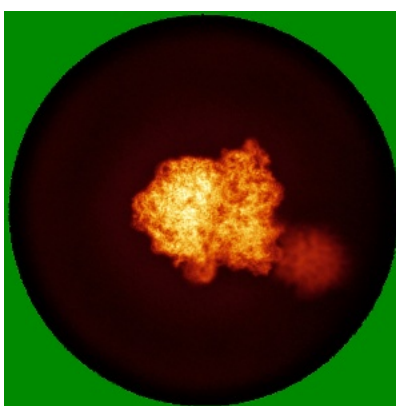
The images above show the largest variance slices of the map in three orthogonal directions.

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

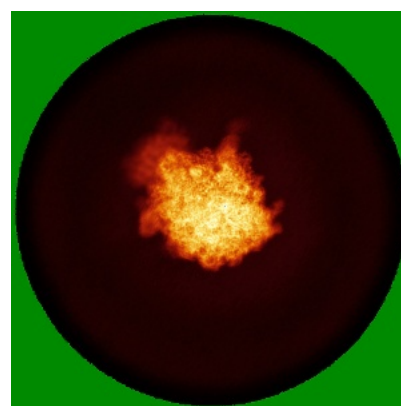
6.4.1 Primary map



X



Y

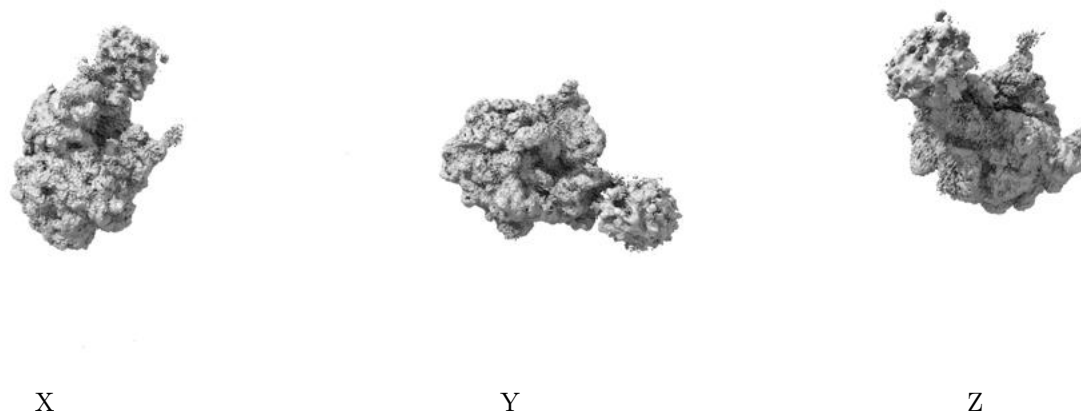


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

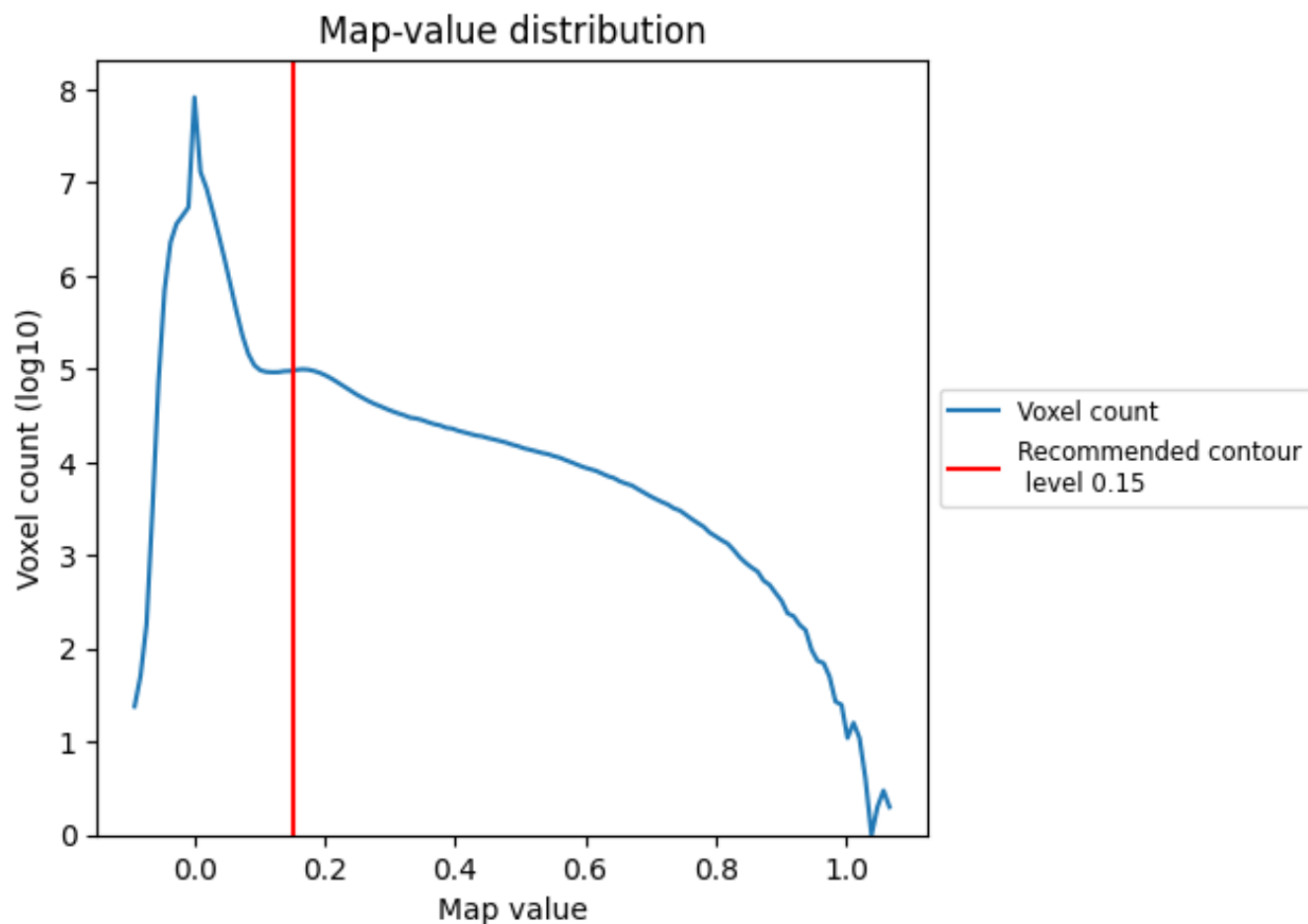
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

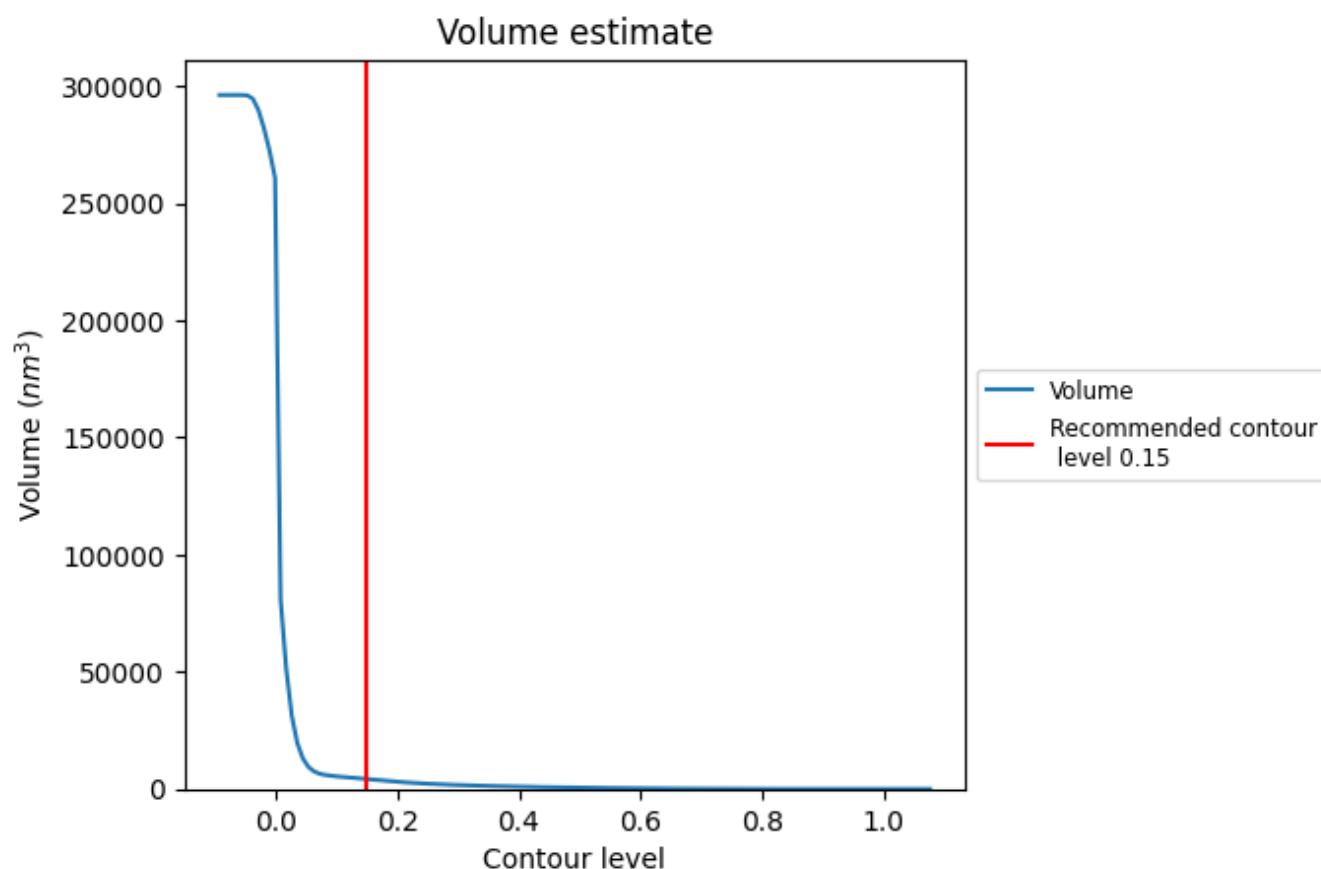
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

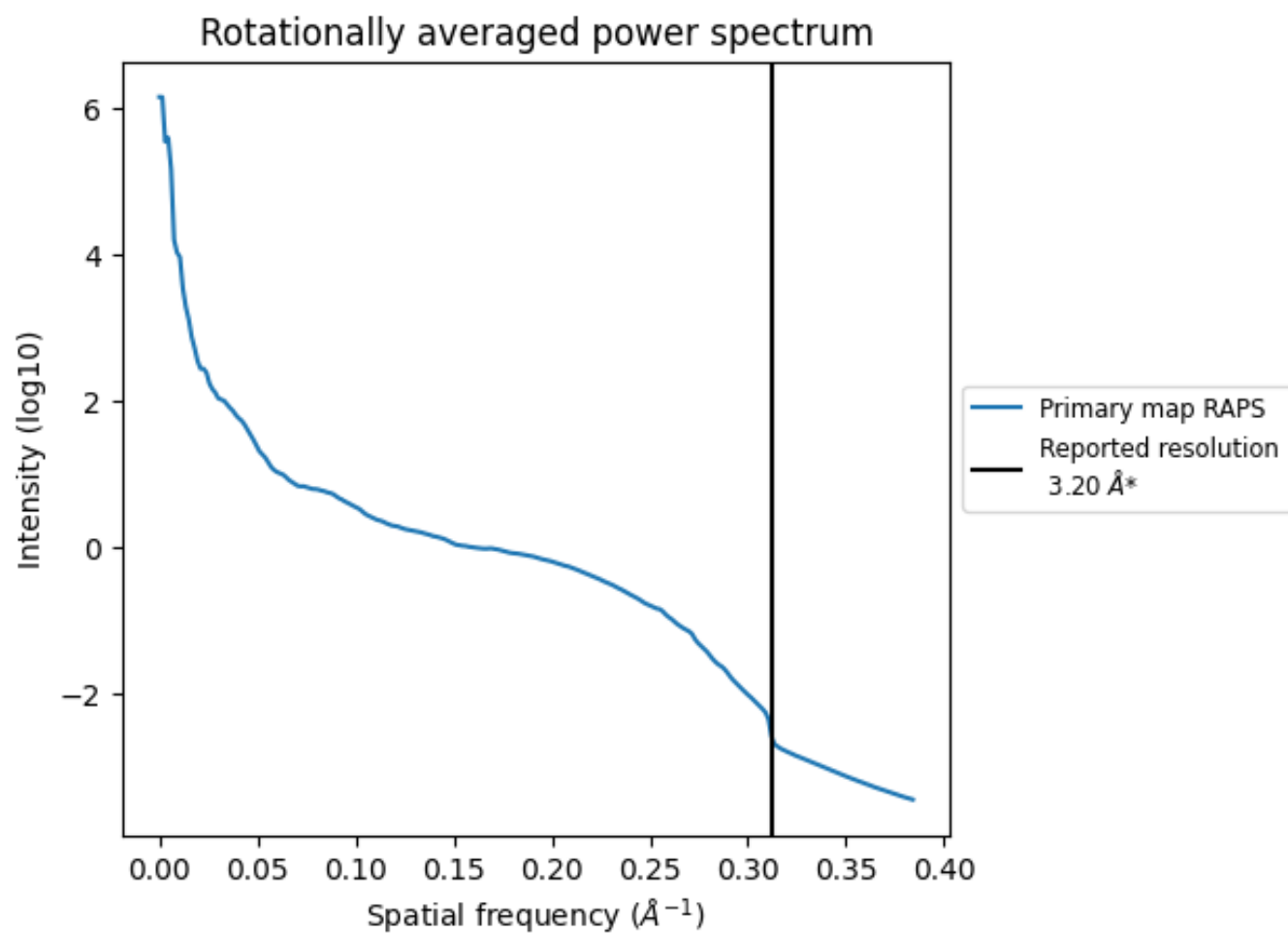
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4241 nm³; this corresponds to an approximate mass of 3831 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

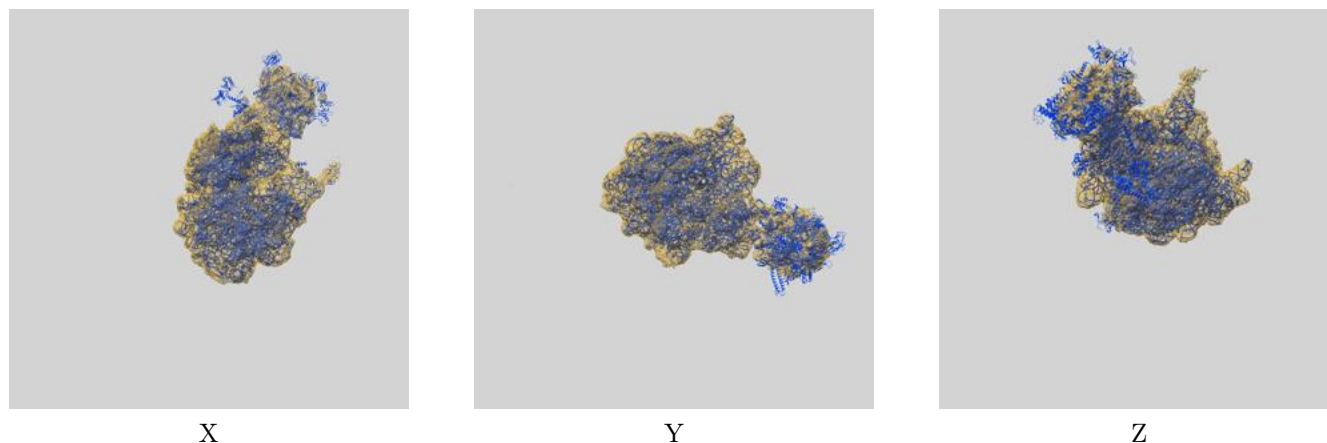
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

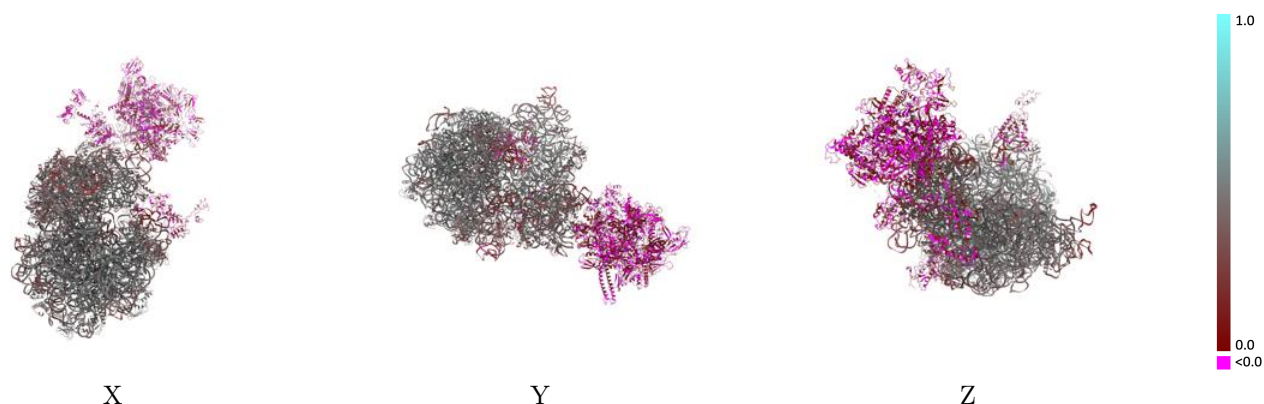
This section contains information regarding the fit between EMDB map EMD-72646 and PDB model 9Y79. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



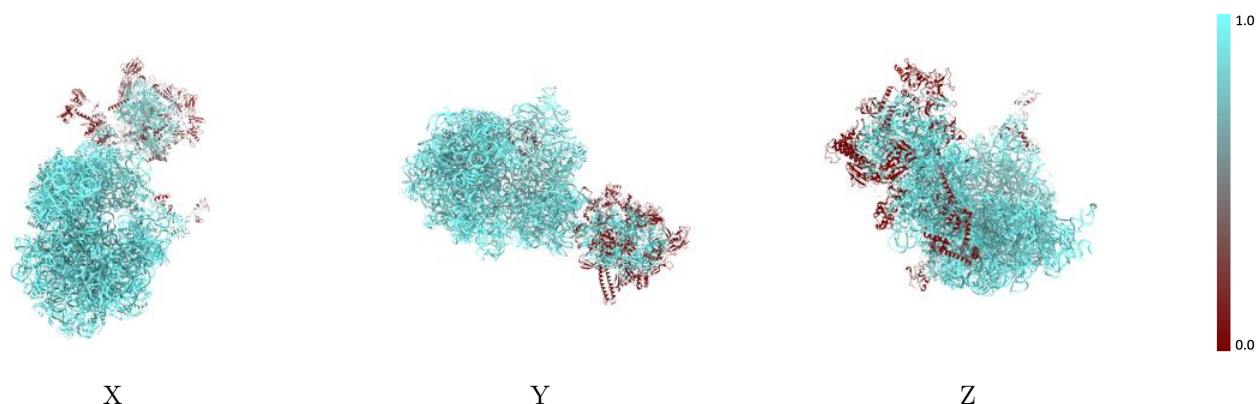
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



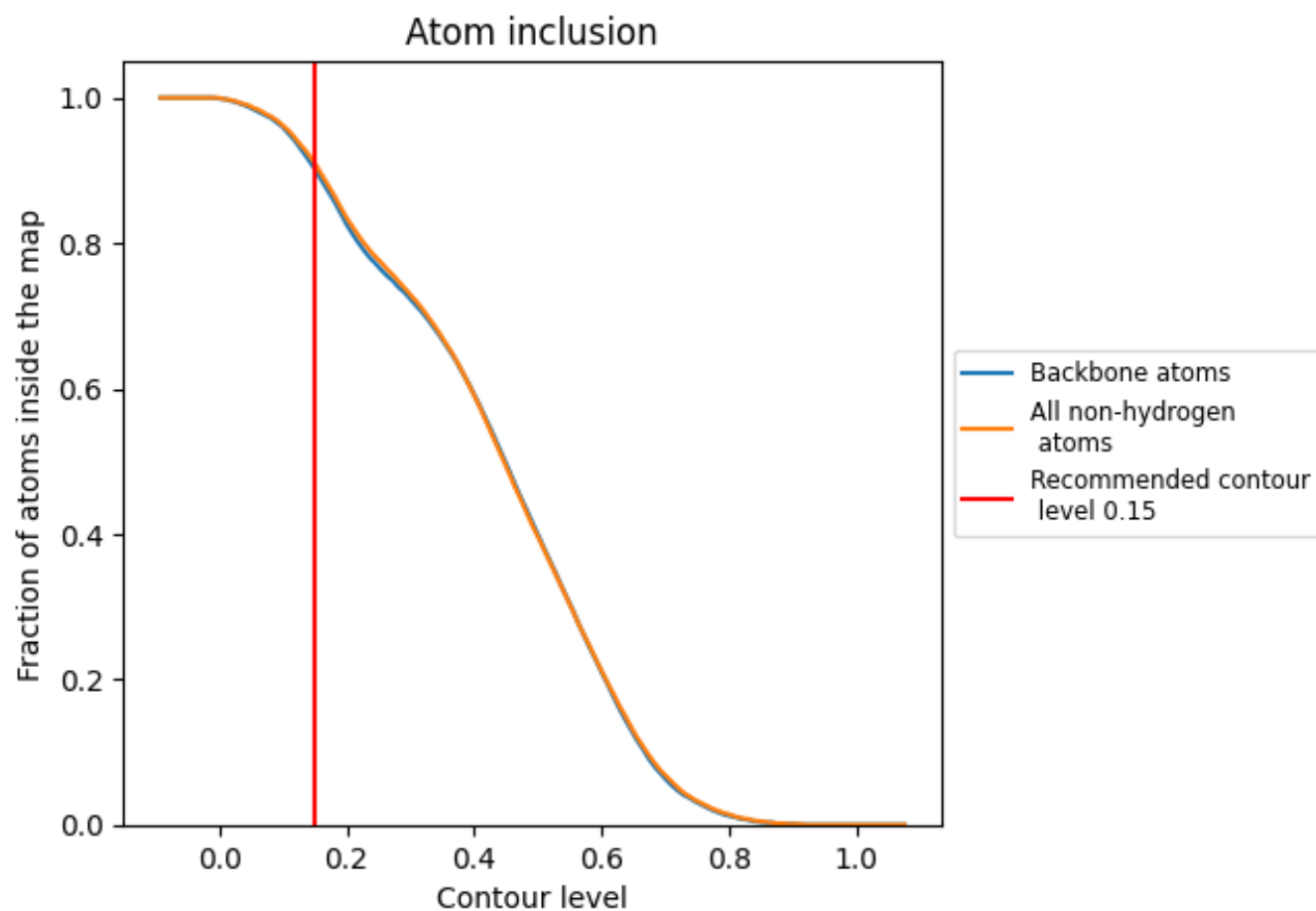
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 90% of all backbone atoms, 91% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9100	 0.3510
0	 0.9940	 0.4760
1	 0.9960	 0.4760
2	 0.9990	 0.4540
3	 0.9870	 0.4520
4	 0.9820	 0.4400
5	 0.9620	 0.1240
6	 0.9110	 0.0990
7	 0.9480	 0.0990
9	 0.7720	 0.1230
A	 0.9990	 0.2240
AA	 0.5500	 0.0360
AC	 0.3630	 0.0540
AD	 0.1610	 0.0300
AE	 0.6610	 0.0470
AF	 0.5270	 0.0500
AG	 0.2180	 0.0360
B	 0.9830	 0.2330
C	 0.9980	 0.4200
D	 0.9970	 0.4220
E	 0.9990	 0.3870
F	 0.9890	 0.3560
G	 0.9690	 0.3750
H	 0.6330	 0.1120
I	 0.9870	 0.4170
J	 0.9910	 0.4180
K	 0.9990	 0.4420
L	 0.9950	 0.4120
M	 0.9860	 0.3740
N	 0.9950	 0.4440
NG	 0.6940	 0.1100
O	 0.9850	 0.3940
P	 0.9920	 0.3670
Q	 0.9980	 0.4360
R	 0.9910	 0.4490



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Chain	Atom inclusion	Q-score
S	 0.9960	 0.4110
T	 0.9970	 0.3980
U	 0.9870	 0.4490
V	 0.9920	 0.4180
W	 0.9740	 0.3660
X	 0.9990	 0.3560
Y	 0.6020	 0.0990
Z	 0.2470	 0.1670
a	 0.9990	 0.4340
b	 0.9970	 0.4770
c	 1.0000	 0.4650
d	 1.0000	 0.4240
e	 0.9760	 0.3950
f	 0.9930	 0.4680
g	 0.9550	 0.2960
h	 1.0000	 0.4820
i	 0.9910	 0.4730
j	 0.9940	 0.4850
k	 1.0000	 0.4550
l	 0.9840	 0.4360
m	 1.0000	 0.4820
n	 0.9930	 0.3640
o	 0.9980	 0.4970
p	 0.9890	 0.4010
q	 1.0000	 0.4660
r	 0.8360	 0.2660
s	 0.9960	 0.4750
t	 0.9990	 0.4650
u	 0.9900	 0.4680
v	 1.0000	 0.4650
w	 1.0000	 0.4810
x	 0.9950	 0.4130
y	 0.9980	 0.4780
z	 0.9990	 0.4730