



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 05:20 PM UTC

PDB ID : 8URY / pdb_00008ury
EMDB ID : EMD-42504
Title : Escherichia coli transcription-translation coupled complex class B (TTC-B) containing RfaH bound to ops signal, NusA, mRNA with a 30 nt long spacer, and fMet-tRNA in E-site and P-site of the ribosome
Authors : Molodtsov, V.; Wang, C.; Ebright, R.H.
Deposited on : 2023-10-27
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

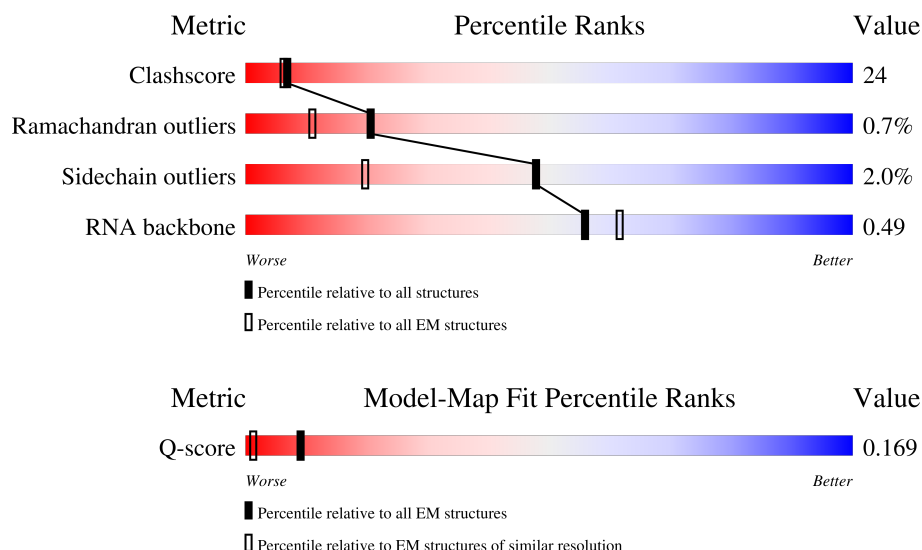
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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

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

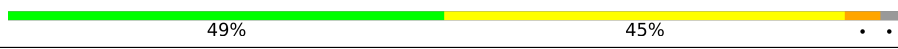
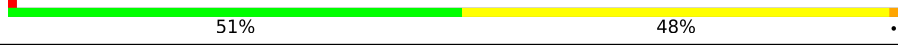
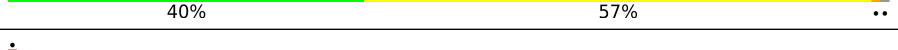
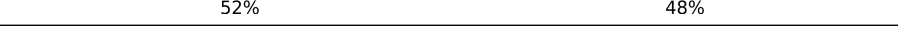
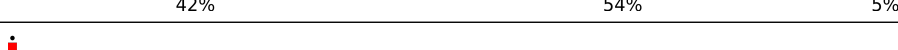
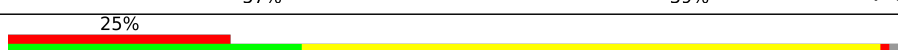
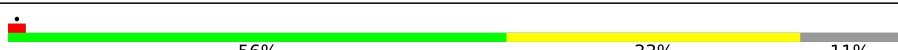
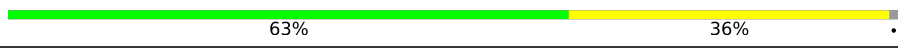
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Mol	Chain	Length	Quality of chain
4	3	104	
5	4	94	
6	5	38	
7	6	38	
8	7	47	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	162	
13	AC	329	
13	AD	329	
14	AE	1407	
15	AF	91	
16	AG	495	
17	C	75	
18	D	1542	
19	E	87	
20	F	71	
21	G	241	
22	H	557	
23	I	233	
24	J	206	
25	K	167	
26	L	104	

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Mol	Chain	Length	Quality of chain
27	M	179	
28	N	130	
29	O	130	
30	P	99	
31	Q	117	
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	62	
46	f	59	
47	g	70	
48	h	273	
49	i	57	
50	j	209	
51	k	55	

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

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

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

2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 280292 atoms, of which 98639 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

- 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 Large ribosomal subunit protein bL25.

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

- Molecule 6 is a DNA chain called NT DNA ops.

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

- Molecule 7 is a DNA chain called T DNA.

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

- Molecule 8 is a RNA chain called mRNA with 30 nt long spacer.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	37	Total	C	N	O	P	0	0
			772	345	110	280	37		

- 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 fMet-tRNA.

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AC	221	Total	C	N	O	S	0	0
			1698	1060	299	333	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	AD	299	Total	C	N	O	S	0	0
			2078	1287	378	407	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AE	1337	Total	C	N	O	S	0	0
			10404	6535	1856	1963	50		

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

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

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

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

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

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

- 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
			49126	14585	16423	6003	10591	1524	0

- 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
			1388	414	719	138	114	3	0

- 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 Small ribosomal subunit protein bS1.

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 Small ribosomal subunit protein uS10.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 42 is a protein called Large ribosomal subunit protein bL27.

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 Large ribosomal subunit protein uL29.

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 Large ribosomal subunit protein bL31.

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 Large ribosomal subunit protein bL35.

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 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 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 Large ribosomal subunit protein bL19.

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).

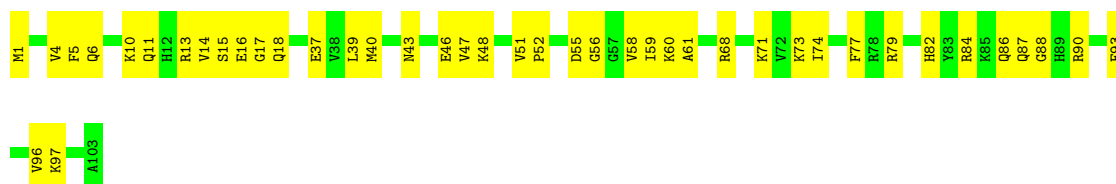
Mol	Chain	Residues	Atoms		AltConf
68	AE	2	Total	Zn	0
			2	2	

3 Residue-property plots

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

• Molecule 1: 50S ribosomal protein L21

Chain 0: 



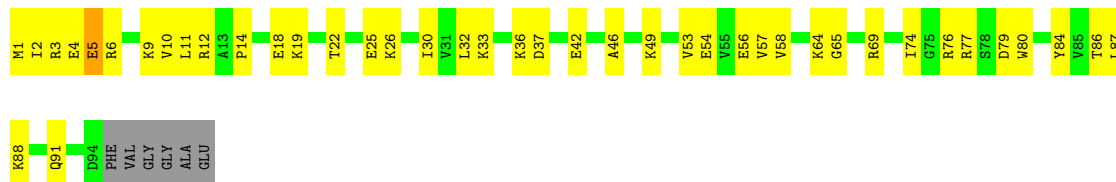
• Molecule 2: 50S ribosomal protein L22

Chain 1: 



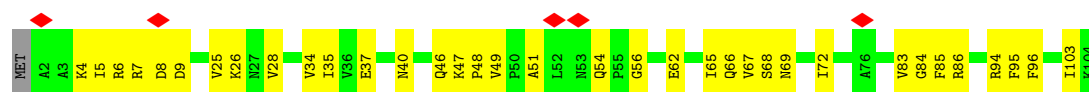
• Molecule 3: 50S ribosomal protein L23

Chain 2: 



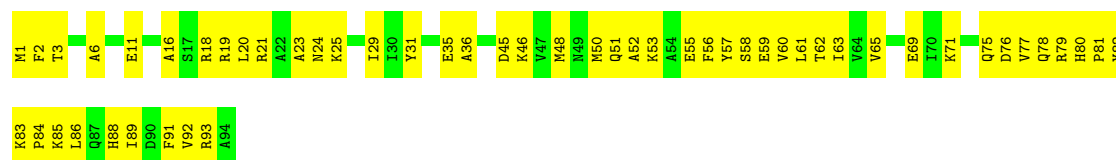
• Molecule 4: 50S ribosomal protein L24

Chain 3: 



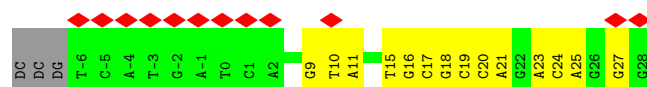
- Molecule 5: Large ribosomal subunit protein bL25

Chain 4: 44% 56%



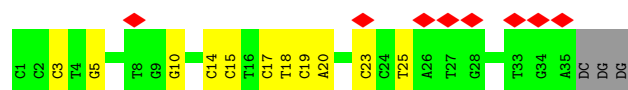
- Molecule 6: NT DNA ops

Chain 5: 32% 55% 37% 8%



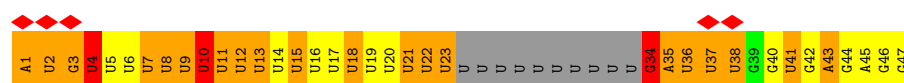
- Molecule 7: T DNA

Chain 6: 21% 63% 29% 8%



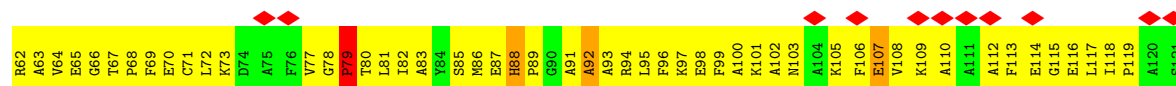
- Molecule 8: mRNA with 30 nt long spacer

Chain 7: 11% 28% 43% 6% 21%



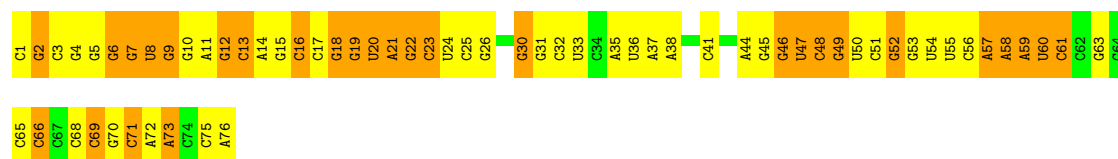
- Molecule 9: 50S ribosomal protein L10

Chain 9: 10% 20% 66% 10%

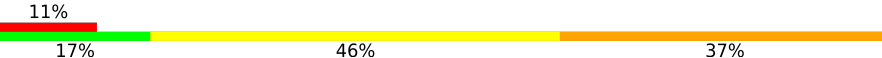


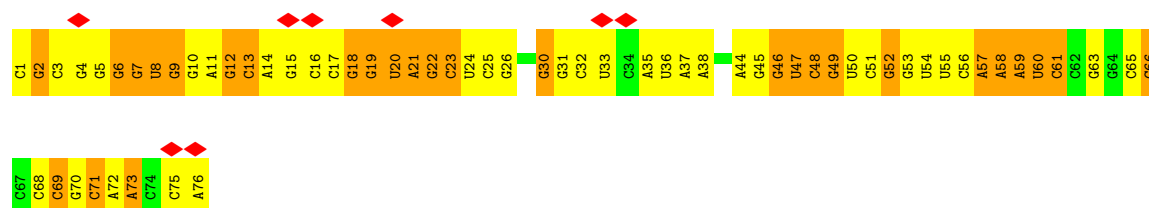
- Molecule 10: E-site and P-site fMet-tRNA

Chain A: 



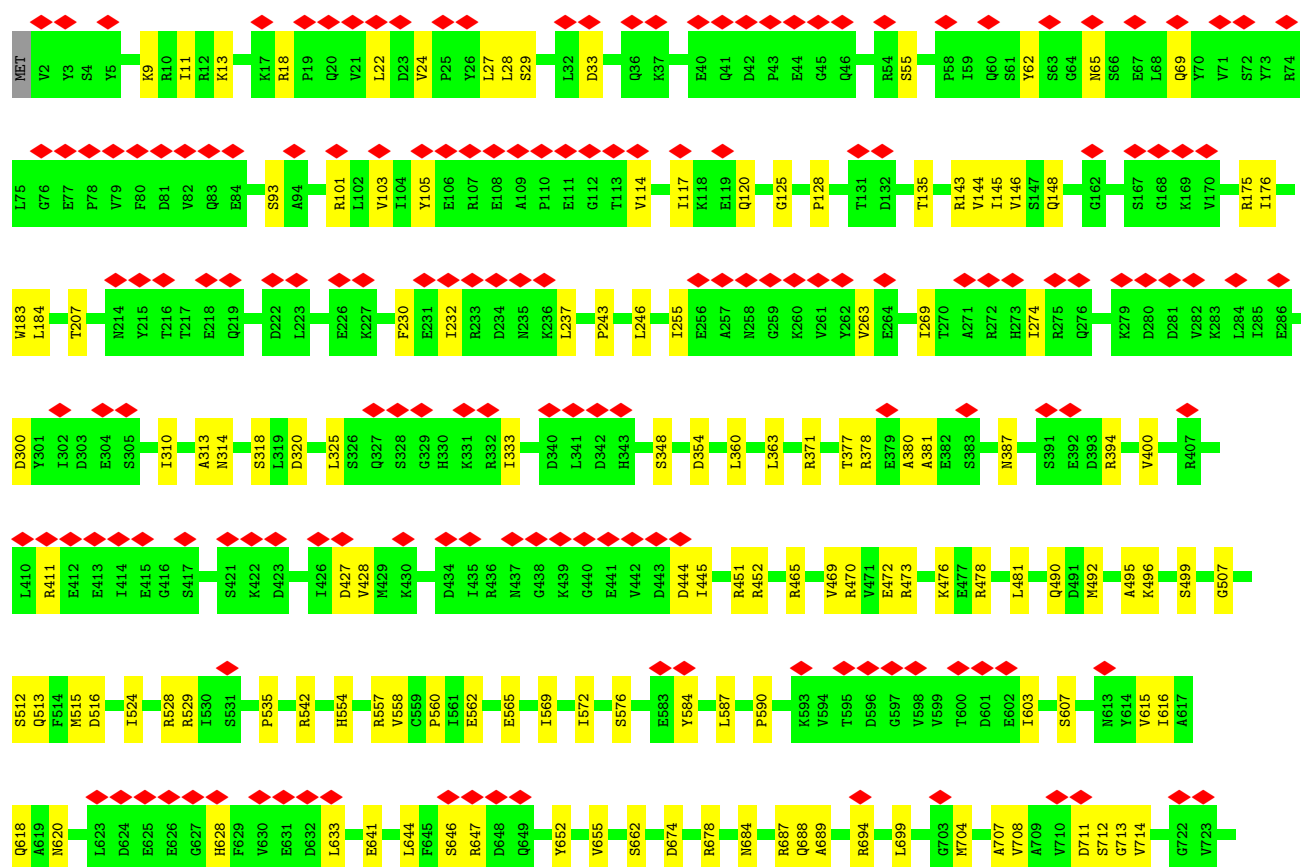
- Molecule 10: E-site and P-site fMet-tRNA

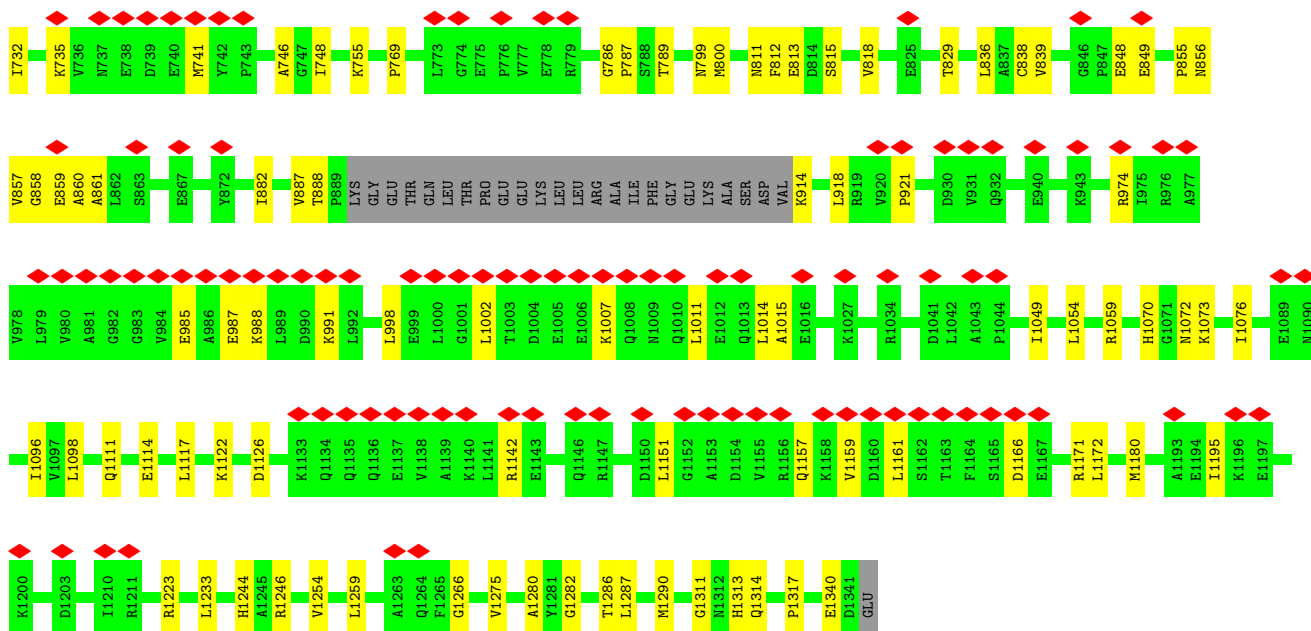
Chain B: 



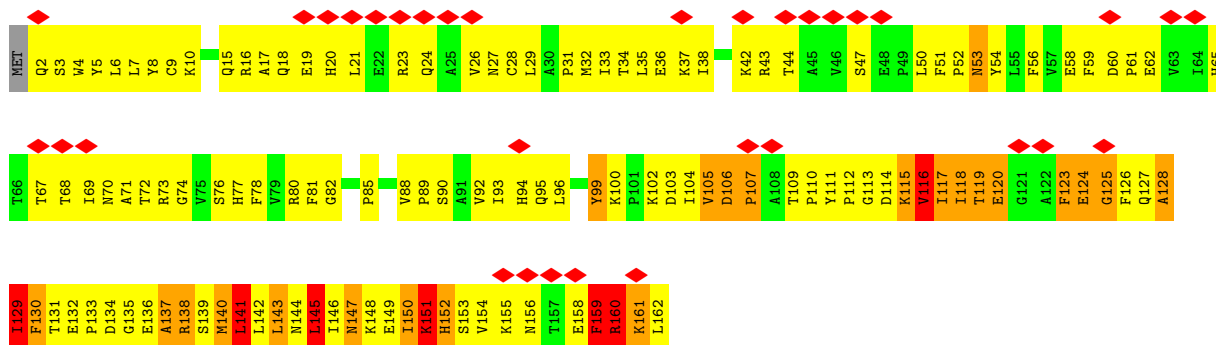
- Molecule 11: DNA-directed RNA polymerase subunit beta

Chain AA: 

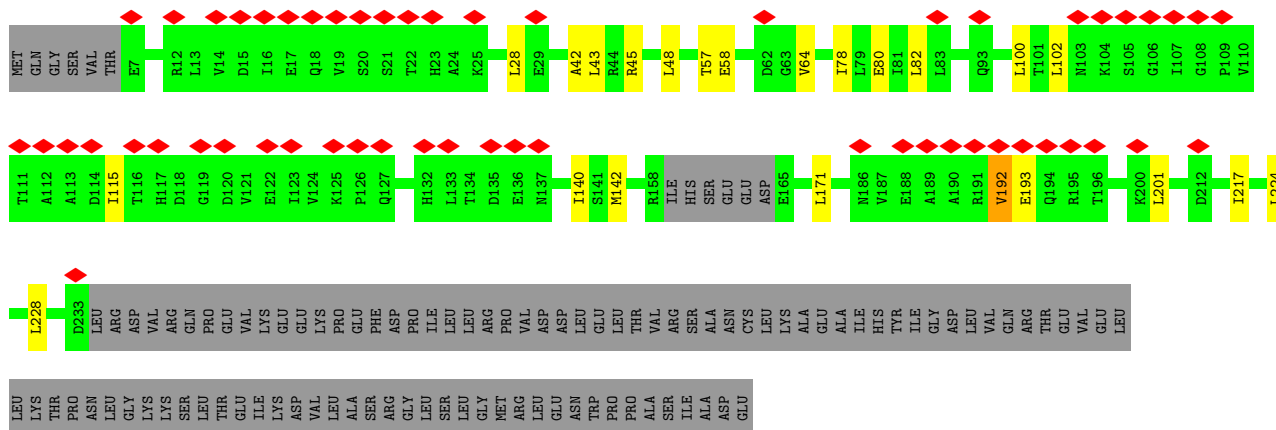




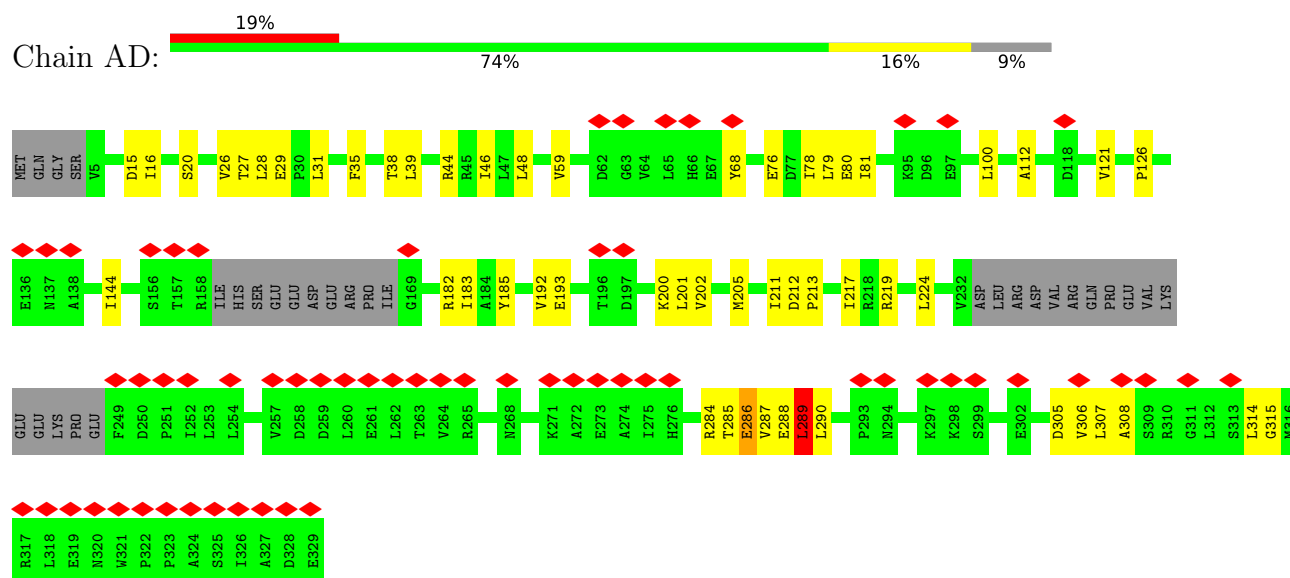
• Molecule 12: Transcription antitermination protein RfaH



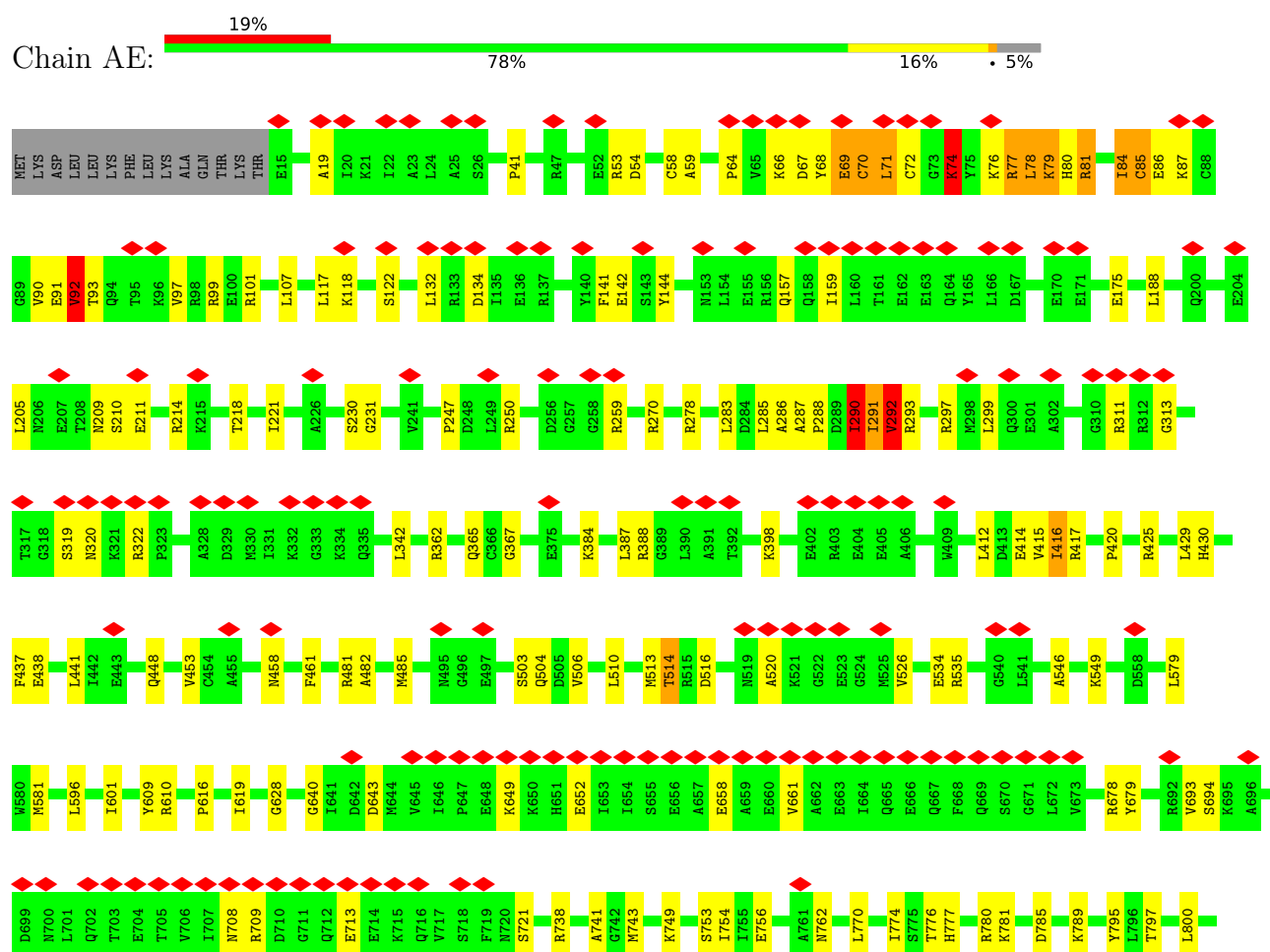
• Molecule 13: DNA-directed RNA polymerase subunit alpha

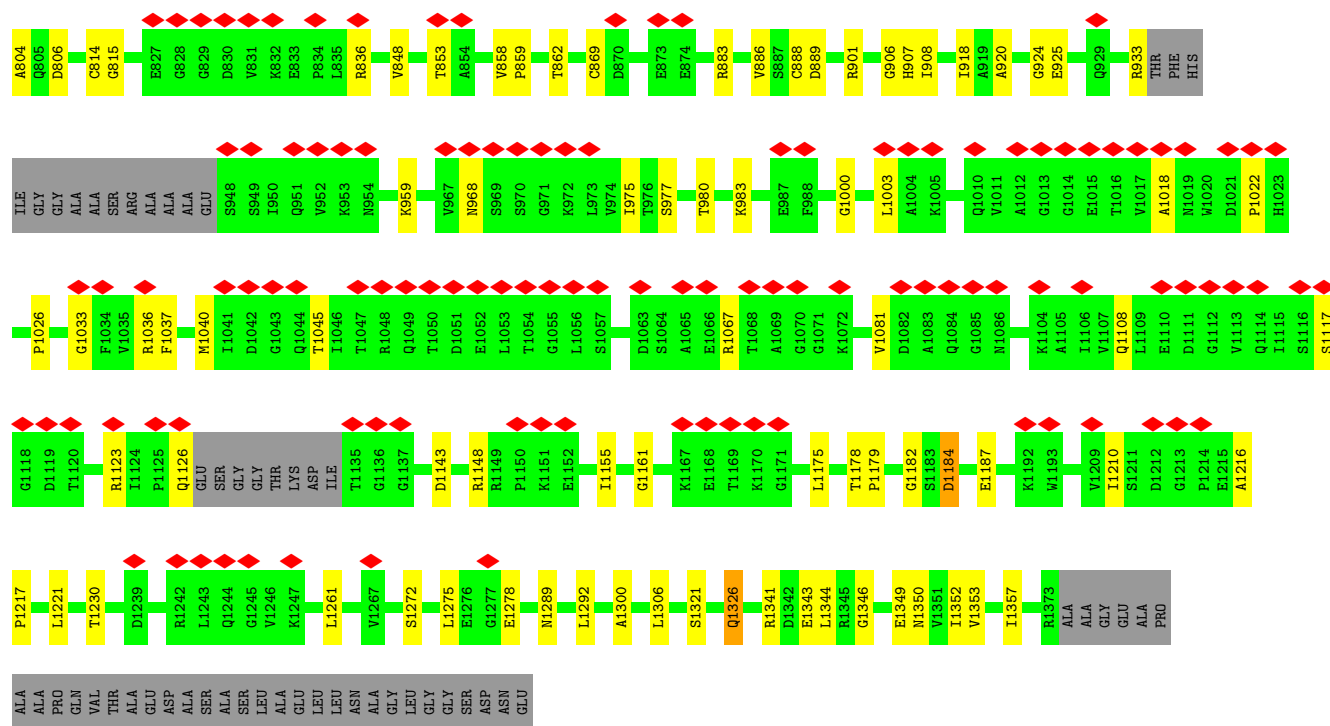


• Molecule 13: DNA-directed RNA polymerase subunit alpha

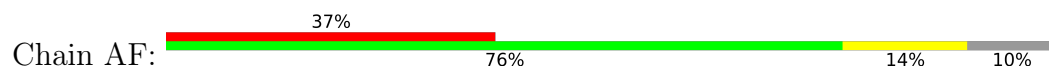


• Molecule 14: DNA-directed RNA polymerase subunit beta'

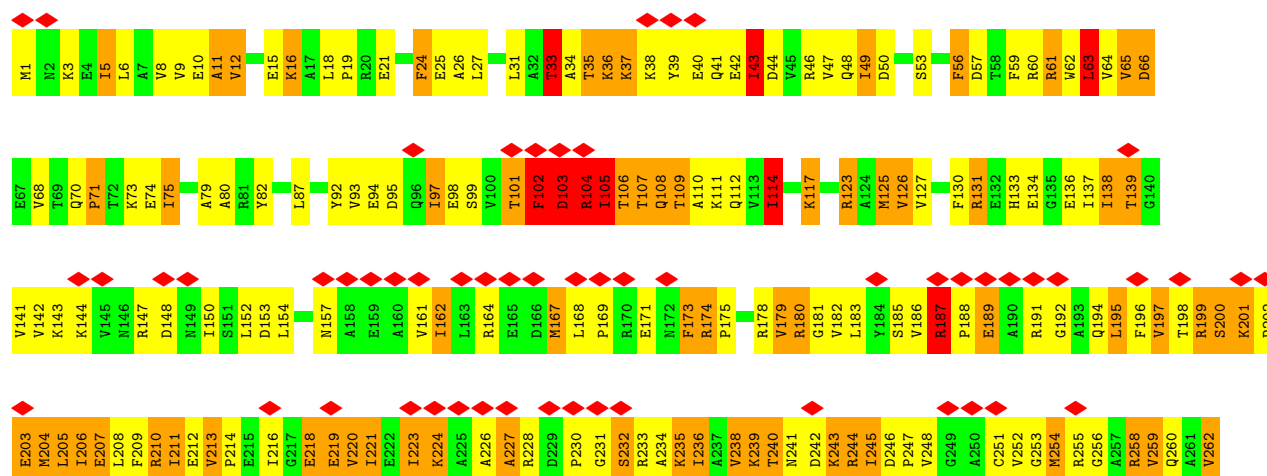


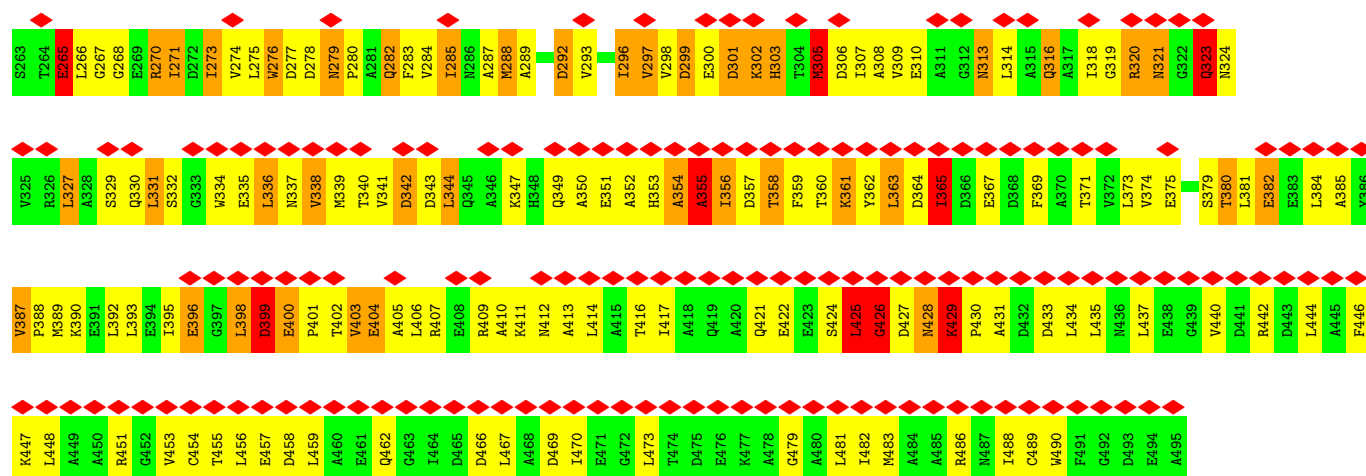


• Molecule 15: DNA-directed RNA polymerase subunit omega



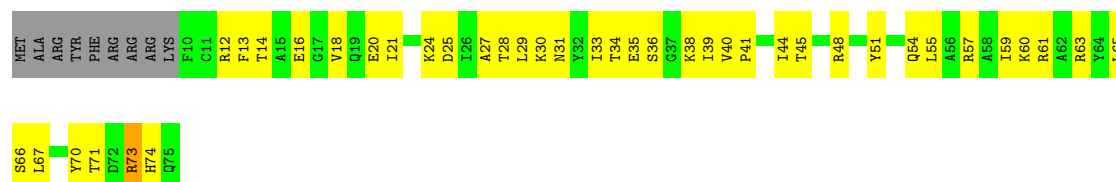
• Molecule 16: Transcription termination/antitermination protein NusA





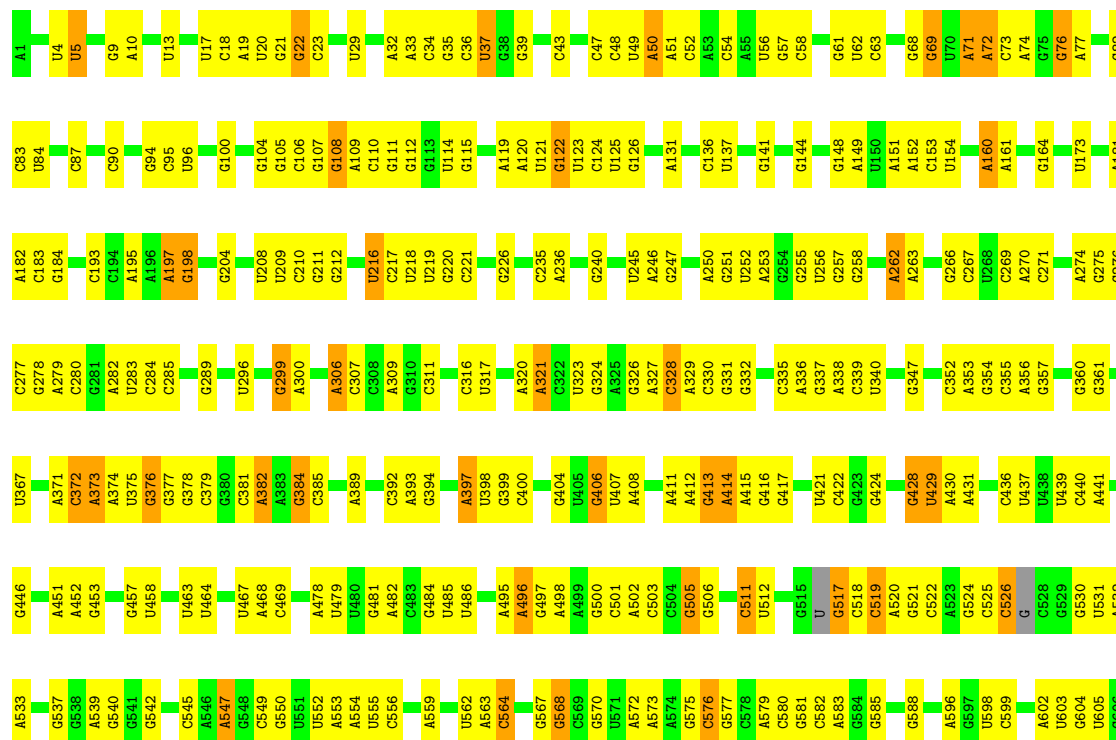
• Molecule 17: 30S ribosomal protein S18

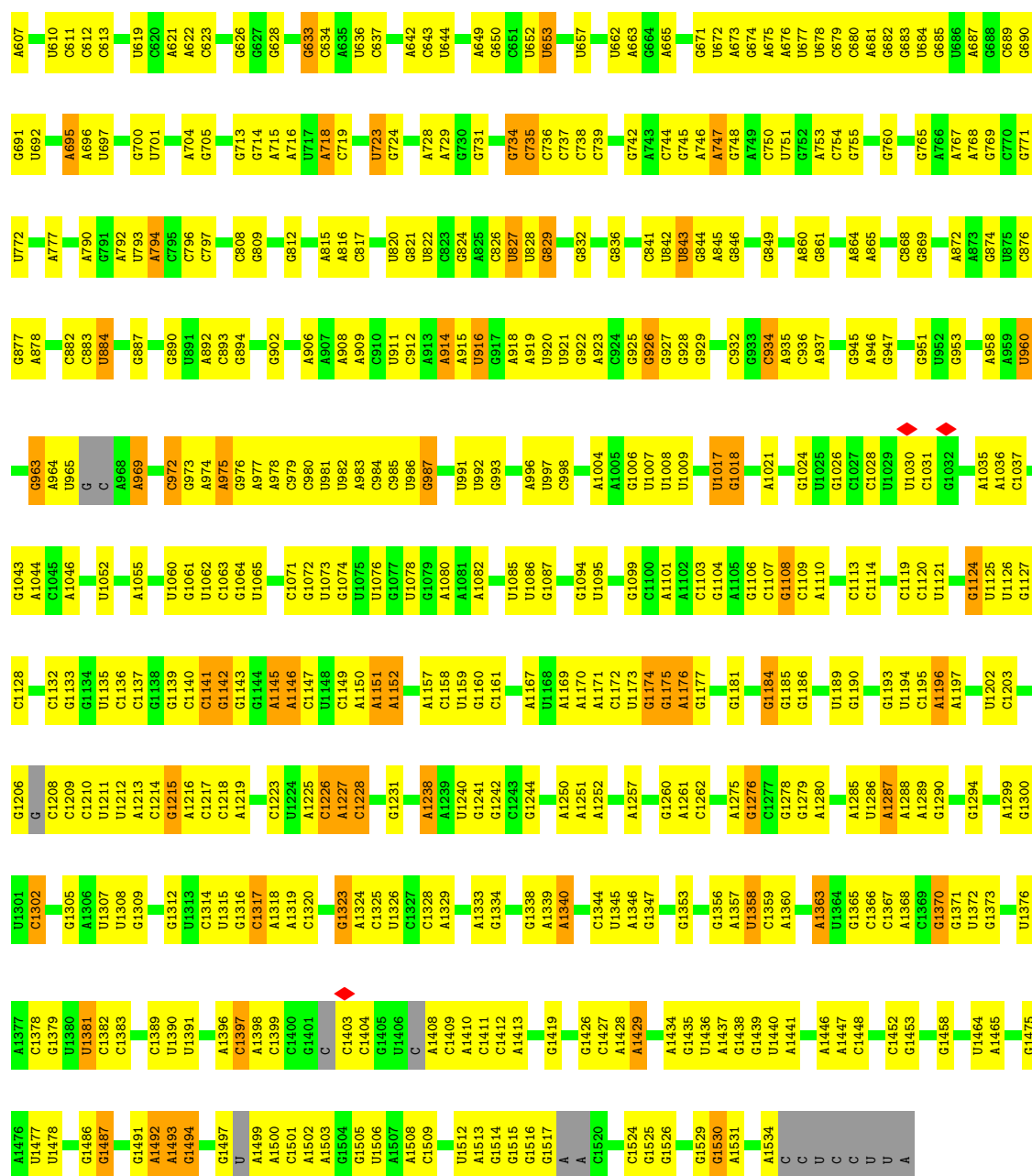
Chain C: 35% 52% 12%



• Molecule 18: 16S rRNA

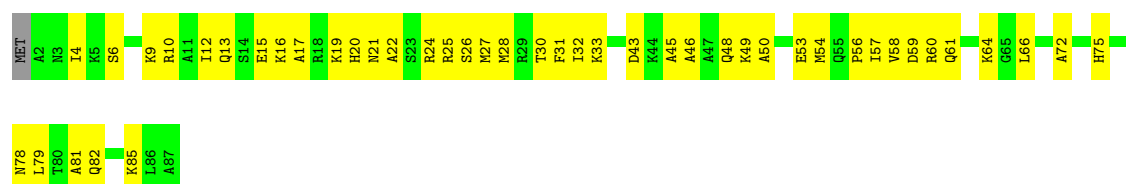
Chain D: 49% 43% 6%





- Molecule 19: 30S ribosomal protein S20

Chain E: 47% 52%

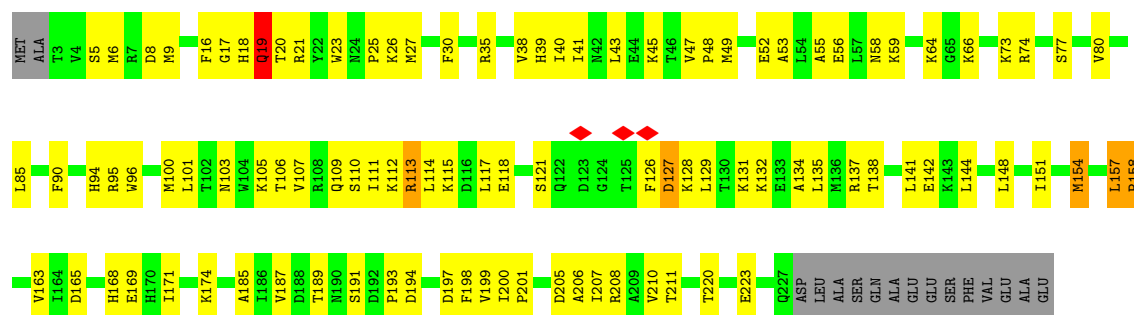


- Molecule 20: 30S ribosomal protein S21

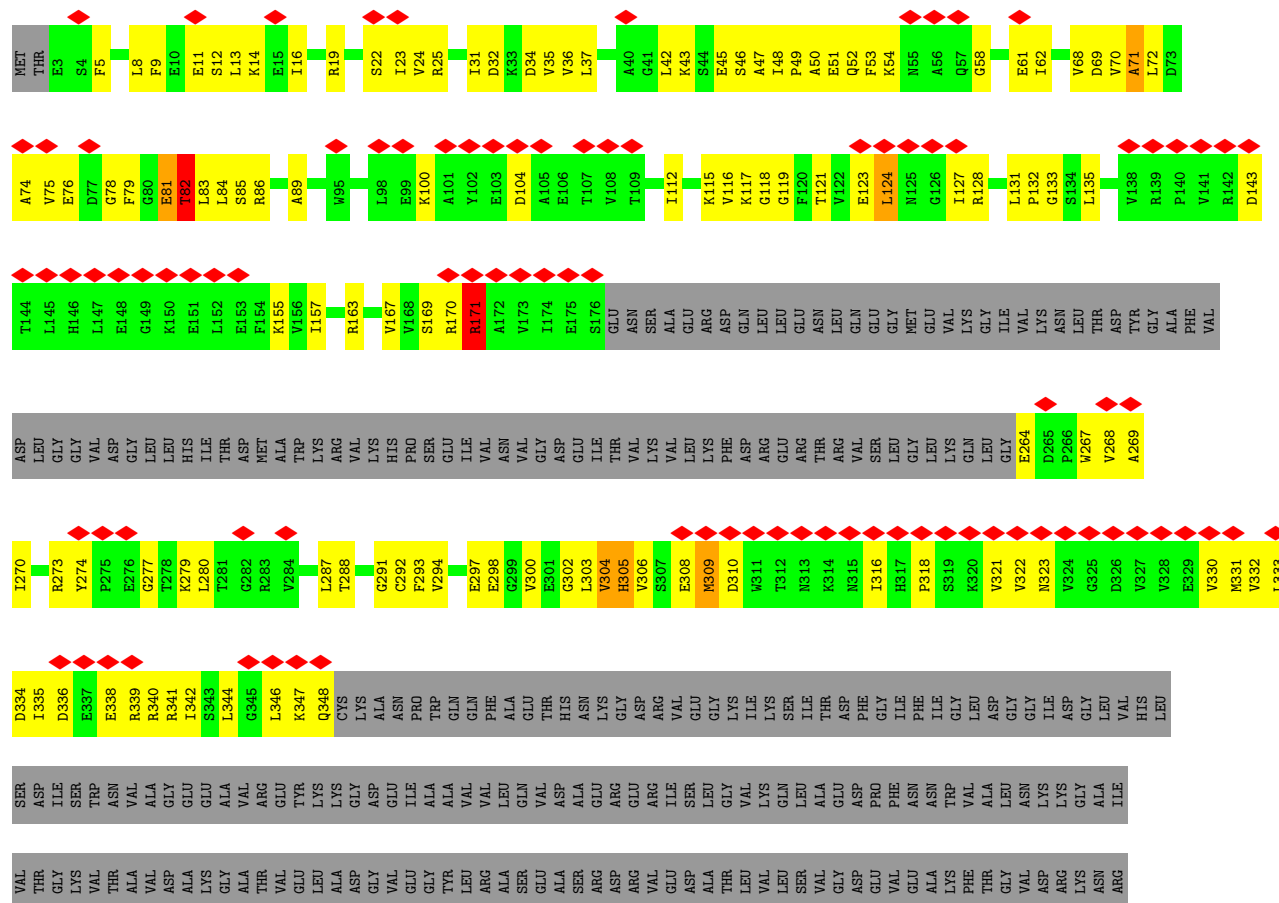
Chain F: 41% 58%



• Molecule 21: 30S ribosomal protein S2



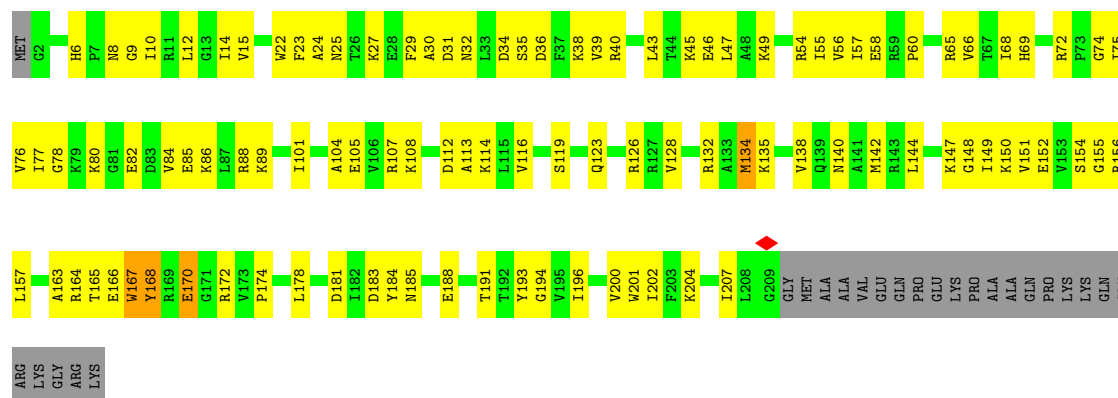
• Molecule 22: Small ribosomal subunit protein bS1



ALA
ILE
SER
LEU
VAL
SER
ARG
ALA
LYS
ASP
GLU
GLY
ASP
GLU
LYS
ASP
F23
ALA
TLE
N25
T96
ALA
THR
VAL
ASN
LYS
GLN
GLY
ASP
ALA
ASN
PHE
SER
ASN
ASN
MET
ALA
GLU
PHE
LYS
ALA
LYS
GLY
GLU

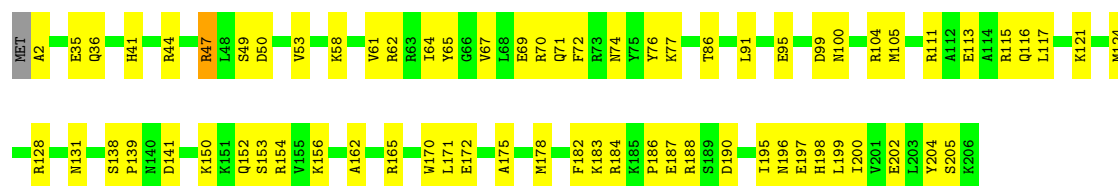
• Molecule 23: 30S ribosomal protein S3

Chain I: 45% 43% 11%



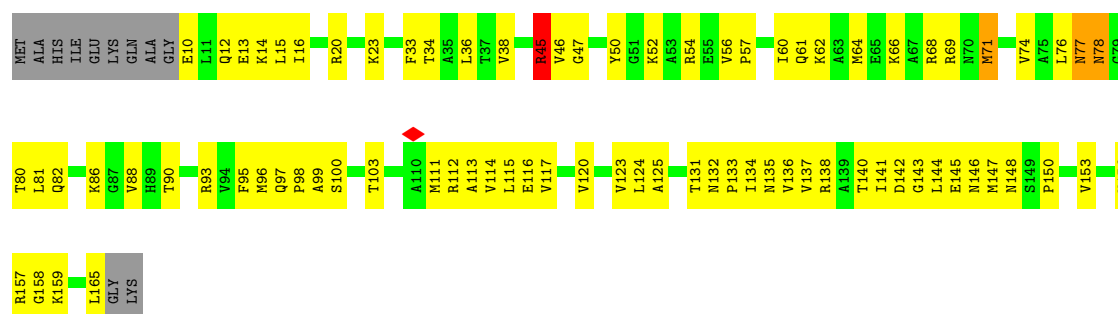
• Molecule 24: 30S ribosomal protein S4

Chain J: 66% 33%



• Molecule 25: 30S ribosomal protein S5

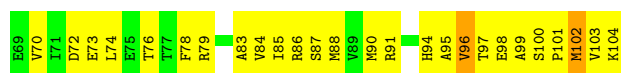
Chain K: 45% 46% 7%



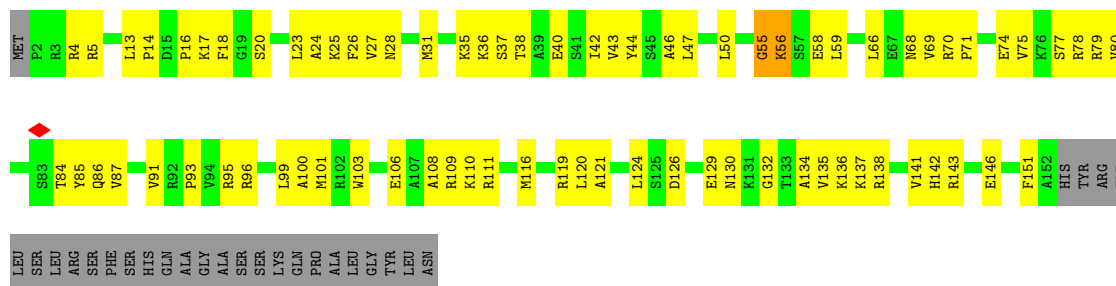
• Molecule 26: 30S ribosomal protein S6

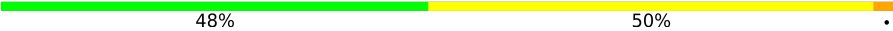
Chain L: 35% 62%





• Molecule 27: 30S ribosomal protein S7

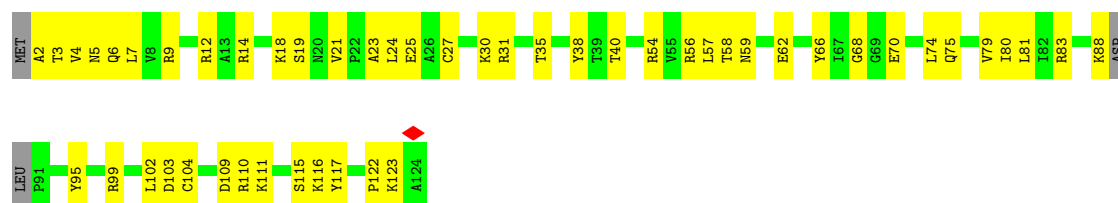


Chain Q:  48% 50%



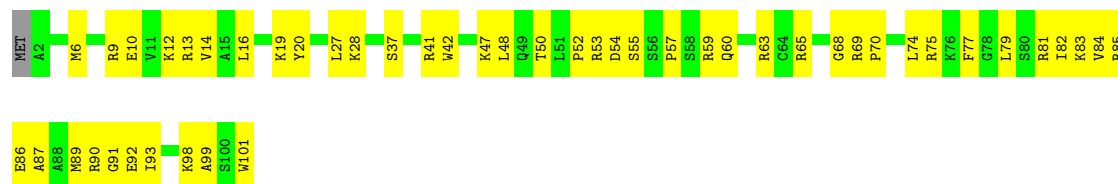
- Molecule 32: 30S ribosomal protein S12

Chain R:  57% 40%

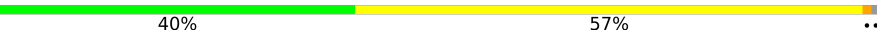


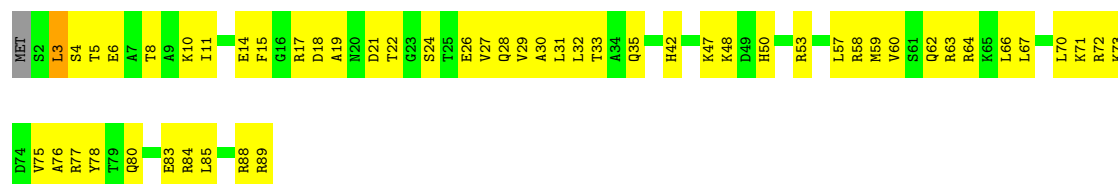
- Molecule 33: 30S ribosomal protein S14

Chain S:  51% 48%



- Molecule 34: 30S ribosomal protein S15

Chain T:  40% 57%

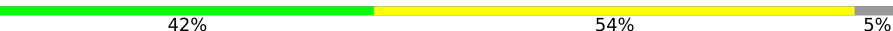


- Molecule 35: 30S ribosomal protein S16

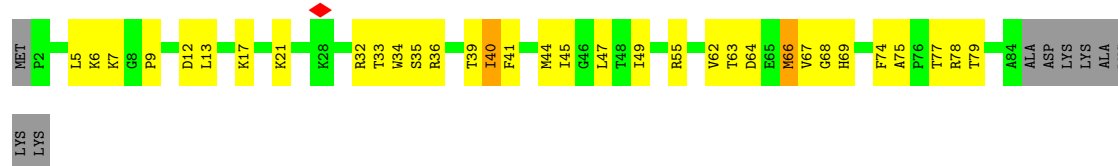
Chain U:  52% 48%



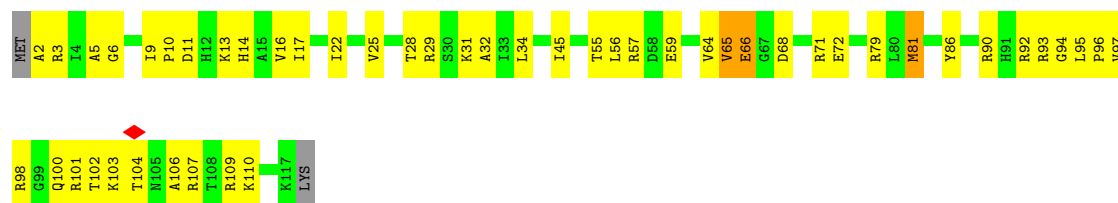
- Molecule 36: 30S ribosomal protein S17

Chain V:  42% 54% 5%

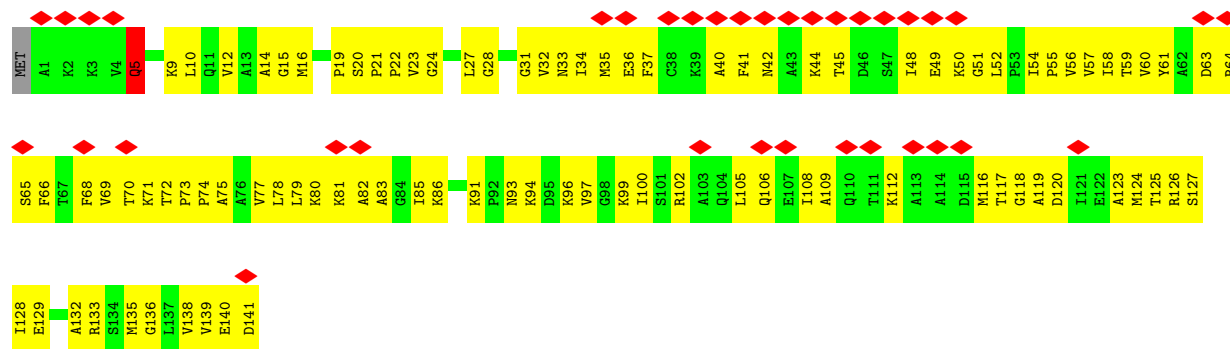
- Molecule 37: 30S ribosomal protein S19



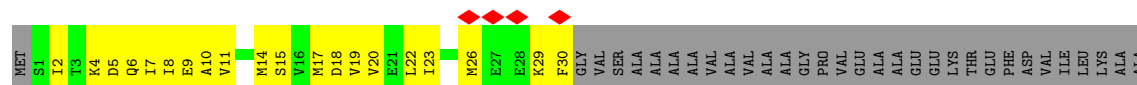
- Molecule 38: 30S ribosomal protein S13



- Molecule 39: 50S ribosomal protein L11



- Molecule 40: 50S ribosomal protein L7/L12



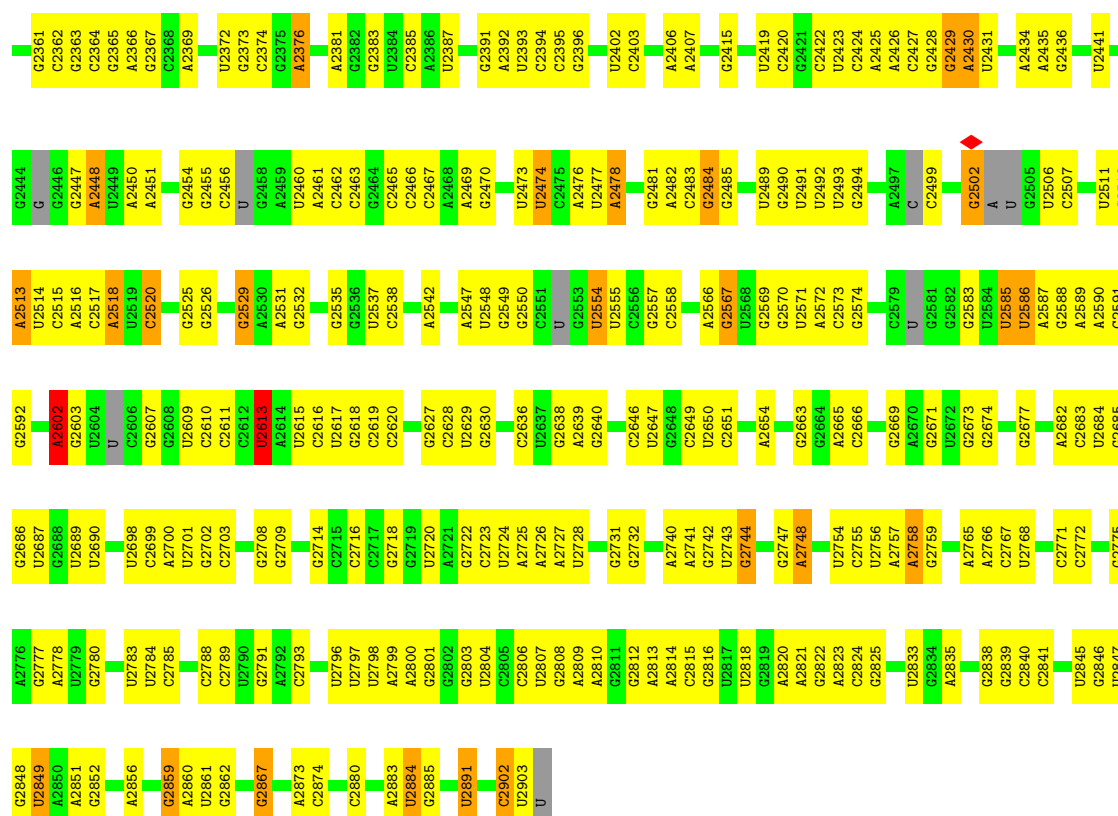
GLY
ALA
ASN
LYS
VAL
ALA
VAL
ILE
LYS
ALA
VAL
ARG
GLY
ALA
THR
GLY
LEU
GLY
LEU
LYS
GLU
ALA
LYS
ASP
LEU
VAL
GLU
SER
ALA
PRO
ALA
ALA
LEU
LYS
GLY
GLY
VAL
SER
LYS
ASP
ASP
ALA
ALA
GLU
ALA
LEU
LYS
LYS
ALA
LEU
GLU
GLU
ALA
GLY
VAL
GLU
LYS

• Molecule 41: 23S rRNA

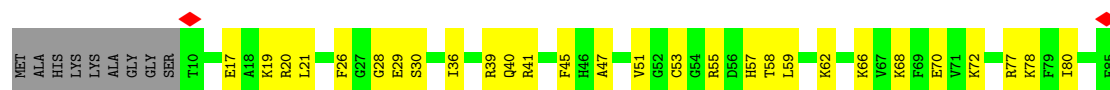
Chain a:  50% 42% 7%

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G834	C912	U913	G914	C915	G916	A920	C921	C922	G923	A927	A928	U929	G930	U931	G938	C939	G940	A941	A945	C946	A947	C948	G952	G953	G954	U	C956	C957	U958	A959	A960	C961	C962	U963	C964	C965	G966	U967	C968	G969	U970	A973	G974	A975	A980	A983	A984	C985	C986	C987	A909	A910	A900	
U744	G	U	U	U	G748	A749	A750	A751	A752	A753	U754	U755	A756	G757	G760	A761	A764	C765	U773	G774	G775	G776	G780	A781	A782	G783	G784	G785	C786	C787	A788	A789	A800	C805	C806	U807	U811	C812	U813	C814	C815	G818	A819	U826	U827	U828	A829	U832	A833					
U569	U573	A574	A575	U576	G577	G578	U580	C581	A582	G583	C584	G585	A586	C587	U588	U589	A590	A591	A592	U593	U594	C595	U596	U598	A599	G600	C601	A602	A603	U607	A608	A609	C610	A613	A614	U615	A616	U617	G620	A621	G622	C623	C624	G625	A626	A627	G628	A631	A632	A633	C634	C635		
G636	A637	G638	U639	C640	A644	G645	G646	A647	A654	U657	U658	G659	A666	U667	A668	G669	A670	C671	C672	A677	A685	U686	A689	C690	C691	G700	G701	U702	U703	G704	A705	A706	G707	G708	U709	U710	U714	G717	G726	A727	G728	G729	A730	C731	G738	A742								
A743	U744	G	U	U	G748	A749	A750	A751	A752	A753	U754	U755	A756	G757	G760	A761	A764	C765	U773	G774	G775	G776	G780	A781	A782	G783	G784	G785	C786	C787	A788	A789	A800	C805	C806	U807	U811	C812	U813	C814	C815	G818	A819	U826	U827	U828	A829	U832	A833					
G834	C912	U913	G914	C915	G916	A920	C921	C922	G923	A927	A928	U929	G930	U931	G938	C939	G940	A941	A945	C946	A947	C948	G952	G953	G954	U	C956	C957	U958	A959	A960	C961	C962	U963	C964	C965	G966	U967	C968	G969	U970	A973	G974	A975	A980	A983	A984	C985	C986	C987	A909	A910	A900	
G993	C994	C995	A996	G997	C998	U999	A1000	A1001	C1006	C1007	A1008	A1009	U1012	C1013	A1014	U1019	A1020	A1021	G1022	U1023	G1024	G1025	G1026	A1027	A1028	A1029	U1033	G1036	G1037	G1038	A1039	C1109	A1111	G1042	G1043	C1044	C1045	A1046	G1047	A1048	C1049	C1053	A1054	G1055	G1056	A1057	U1058	G1059	U1060	U1061	A1134			
A84	G85	G88	A94	A95	C96	C97	G98	A101	A102	A103	C105	G110	A111	A118	A119	U120	A125	A126	A127	C128	C129	C130	A131	G132	U133	G134	U135	G136	U137	U138	C139	G141	C140	G141	A142	C143	A144	C145	A146	U150	C151	A152	U153	U154	C163	C164	A165	G178	A181					
A182	C183	C184	C192	U193	A196	A197	G205	U206	A207	C208	C209	C210	A213	G214	G215	A216	A219	G220	A221	A222	A223	U224	C225	C228	U234	U235	C236	C239	C240	A241	A244	G245	C246	G247	G248	C249	G250	A251	A255	A256	C257	G261	C264	A265	C266	C267								
G271	A272	G273	C274	C275	U276	G277	A278	G285	G291	A299	A300	G301	C302	U306	G307	A310	G319	A320	U321	U324	C323	C325	C328	A329	A330	C335	A340	C341	C353	A354	G361	A362	G367	A368	A370	A371	A372	A377	U373	A374	G375	G379	C383	C386										
A391	U392	C393	G396	U397	C398	U399	G400	A404	U405	G406	G407	G408	G409	G410	G411	A412	C413	C414	A415	C420	G424	U427	A443	C444	C445	A449	G450	U451	A457	G458	G465	A466	G467	G468	G469	A470	A471	A472	A477	A478	A479	A480	G481	A482	A483	C484	C485	C486						
C491	A492	C493	C494	G495	G496	G500	U399	A501	A502	A503	A504	A505	C509	G512	A513	A514	U519	U520	U521	A522	C523	A529	U530	C531	A532	G533	U534	G535	G536	G537	A538	G539	C540	A541	C542	G543	C544	U545	U546	A547	G548	G549	C550	G551	U552	U553	U554	C560	A563	C564	U567			
U569	U573	A574	A575	U576	G577	G578	U580	C581	A582	G583	C584	G585	A586	C587	U588	U589	A590	A591	A592	U593	U594	C595	U596	U598	A599	G600	C601	A602	A603	U607	A608	A609	C610	A613	A614	U615	A616	U617	G620	A621	G622	C623	C624	G625	A626	A627	G628	A631	A632	A633	C634	C635		
G636	A637	G638	U639	C640	A644	G645	G646	A647	A654	U657	U658	G659	A666	U667	A668	G669	A670	C671	C672	A677	A685	U686	A689	C690	C691	G700	G701	U702	U703	G704	A705	A706	G707	G708	U709	U710	U714	G717	G726	A727	G728	G729	A730	C731	G738	A742								
A743	U744	G	U	U	G748	A749	A750	A751	A752	A753	U754	U755	A756	G757	G760	A761	A764	C765	U773	G774	G775	G776	G780	A781	A782	G783	G784	G785	C786	C787	A788	A789	A800	C805	C806	U807	U811	C812	U813	C814	C815	G818	A819	U826	U827	U828	A829	U832	A833					
G834	C912	U913	G914	C915	G916	A920	C921	C922	G923	A927	A928	U929	G930	U931	G938	C939	G940	A941	A945	C946	A947	C948	G952	G953	G954	U	C956	C957	U958	A959	A960	C961	C962	U963	C964	C965	G966	U967	C968	G969	U970	A973	G974	A975	A980	A983	A984	C985	C986	C987	A909	A910	A900	
G993	C994	C995	A996	G997	C998	U999	A1000	A1001	C1006	C1007	A1008	A1009	U1012	C1013	A1014	U1019	A1020	A1021	G1022	U1023	G1024	G1025	G1026	A1027	A1028	A1029	U1033	G1036	G1037	G1038	A1039	C1109	A1111	G1042	G1043	C1044	C1045	A1046	G1047	A1048	C1049	C1053	A1054	G1055	G1056	A1057	U1058	G1059	U1060	U1061	A1134			

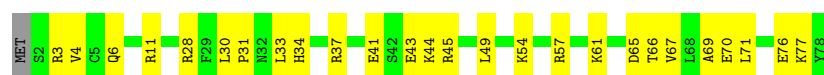
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A2288	A2198	G2123	U2041	C1964	G1884	G1709	G1601	G1510	U1411	G1137	G1236	G1137
G2289	A2199	G2124	C2042	C1965	A1885	G1710	U1602	G1511	U1412	A1237	G1238	G1138
G2290	C2200	G2125	C2043	C1966	A1889	U1714	A1603	G1512	G1413	G1139	G1238	G1139
U2291	G2200	A2126	C2044	C1967	G1816	G1715	C1607	U1513	G1414	C1140	C1243	C1140
U2292	G2204	G2127	G2049	A1890	G1817	G1716	A1608	G1514	U1415	U1340	U1243	U1141
G2293	A2205	G2128	C2050	U1971	U1818	U1720	A1609	A1515	G1416	G1341	A1246	A1142
G2294	C2206	A2051	A2051	G1972	U1820	G1721	A1610	G1529	U1417	A1342	A1247	A1143
C2295	U2131	U2131	A2052	G1906	G1816	U1729	G1613	U1534	G1418	G1343	G1248	C1145
U2297	G2132	G2133	C2055	G1907	G1823	C1730	G1614	A1535	A1419	G1344	U1249	C1146
A2297	G2133	A2134	G2056	G1910	U1825	G1730	A1614	C1536	G1420	G1345	G1250	A1147
A2298	A2134			U	G1826	G1732	A	G1537	G1422	A1347	G1251	A1147
U2299	U2139	U2139	A2060	A1912	U1827	G1738	G1619	U1542	A1427	C1348	A1252	G1154
G2300	G2140	G2141	G2061	A1913	G1828	U1738	G1619	U1543	G1428	C1350	A1253	G1160
C2301	G2141		A2062	C1914	A1829	A1746	G1622	U1543	G1429	G1351	G1256	G1161
U2305	C2146	C2146	C2063	U	C1830	U1747	G1622	G1546	G1430	U1352	C1257	G1162
G2306	A2147	C2064	C2064	U	G1831	G1750	U1647	C1547	A1431	A1353	A1262	C1167
G2308	A2225	C2065	C2065	U	C1833	G1750	U1648	A1548	A1433	G1360	G1266	G1168
A2309	G2148	C2066	C2066	A1918	C1833	G1750	G1649	A1549	A1434	G1361	A1269	A1169
A2309	U2149	G2067	C1996	A1919	U1834	G1750	G1650	A1549	G1435	C1362	C1270	C1170
C2310	G2067	U2068	C1997	G1920	G	G1753	A1650	U1554	G1441	A1365	G1271	C1172
A2311	U2068	G	C1997	G1921	G1835	A1754	G1651	U1554	U1442	A1366	G1272	U1173
U2312	A2070	A2070	C1999	G1922	G1835	A1755	A1652	C1558	U1443	A1367	A1272	U1174
C2313	A2071	A2071	G2002	U1923	G1839	G1756	A1653	U1559	G1444	A1368	U1273	A1175
A2314	C2072	C2072	G2002	U1924	U1840	A1757	A1654	U1560	G1445	G1369	A1276	G1177
G2315	C2073	C2073	C2006	C1925	U1841	U1758	A1655	G1567	G1452	C1370	C1277	C1178
U2320	U2075	U	C2006	C1926	G1842	G1764	G1656	G1568	U1453	A1378	C1278	G1179
U2321	U2075	U	U2007	A1927	C1843	C1764	U1657	U1569	G1454	U1379	G1279	U1180
A2322	G	A2082	G2010	U1928	C1844	G1770	G1658	A1570	U1460	G1380	G1280	U1181
G2325	A2082	G2083	U2011	G1930	G1845	C1771	G1659	A1571	U1467	A1383	G1281	U1182
A2326	C2072	C2072	U2012	U1931	A1847	A1773	A1665	A1572	U1468	A1384	C1289	G1186
A2327	C2073	C2073	A2013	G1932	G1847	C1774	G1666	A1578	A1469	A1385	C1290	U1187
A2328	U2086	U2087	A2014	A1933	U1853	U1778	G1667	A1579	A1470	A1386	U1294	A1189
U2329	C2091	C2091	U2016	A1936	A1854	U1779	A1668	A1580	G1482	A1387	C1295	G1190
G2330	U2092	U2092	U2017	A1937	U1855	U1779	A1668	A1581	G1482	A1392	G1296	C1196
C2331	G2093	G2093	A2017	U1938	U1856	A1783	G1674	C1571	A1490	A1393	G1300	G1197
A2332	U2172	U2172	A2020	U	G1857	A1784	C1675	A1572	A1491	U1394	U1198	U1198
A2333	G2252	G2253	C2021	U1940	A1858	A1785	A1676	A1579	A1494	A1395	U1199	U1199
U2334	G2253	G2253	C2022	U1941	U1859	A1786	A1677	A1580	A1495	U1396	C1200	C1200
A2335	A2097	A2097	U2023	U1944	G1869	C1793	U1688	A1581	A1496	U1397	G1310	U1201
A2336	U2097	U2097	C2023	U1945	C1870	G1794	U1688	A1582	A1497	C1398	G1311	A1204
C2339	U2098	U2098	C2024	G1945	A1871	U1795	U1688	C1582	U1497	A1399	G1312	A1205
G2345	U2109	U2109	G2025	U1946	U1872	U1796	U1688	C1583	C1498	U1399	U1313	G1206
A2346	G2110	G2110	C2026	C1947	U1864	G1792	G1684	U1584	G1500	A1403	C1315	G1206
U2348	U2111	U2111	U2027	U1951	G1869	C1793	U1688	A1585	A1495	C1404	G1315	G1212
G2349	G2112	G2112	G2031	U1952	C1870	G1794	U1688	A1586	A1496	U1405	U1318	G1212
A2268	U2185	U2185	G2032	A1953	A1871	U1795	U1688	C1587	U1497	U1406	C1319	G1223
C2350	U2185	U2185	G2033	G1954	U1872	U1796	U1688	C1588	C1498	U1406	C1320	U1224
G2351	U2113	U2113	U2034	U1955	G1874	G1797	G1693	U1589	C1499	A1403	U1318	G1223
U2189	U2114	U2114	U2034	U1956	C1874	U1798	G1695	A1590	G1500	C1404	U1318	G1223
G2190	G2115	G2115	G2035	C1957	G1875	C1800	A1700	A1591	A1503	U1405	C1319	G1223
A2191	G2116	G2116	C2036	C1958	C1879	A1801	A1596	A1597	U1506	U1406	C1320	U1224
U2192	A2117	A2117	U2037	A1960	U1880	A1802	G1703	A1598	C1507	G1408	A1321	G1225
G2193	G2193	G2193	G2038	C1961	C1881	A1803						



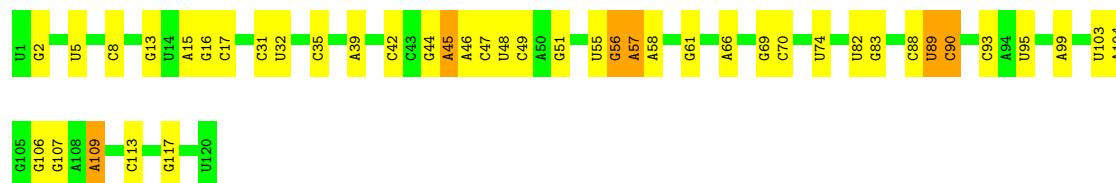
- Molecule 42: Large ribosomal subunit protein bL27



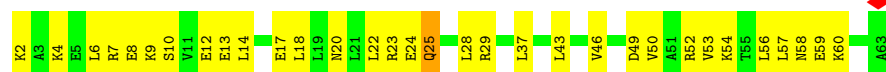
- Molecule 43: 50S ribosomal protein L28



- Molecule 44: 5S rRNA



- Molecule 45: Large ribosomal subunit protein uL29



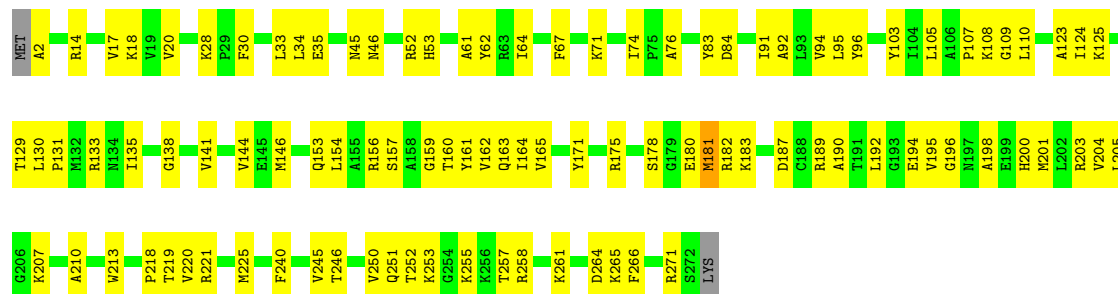
- Molecule 46: 50S ribosomal protein L30



- Molecule 47: Large ribosomal subunit protein bL31



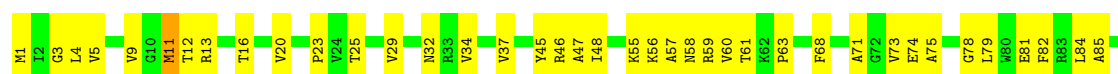
- Molecule 48: 50S ribosomal protein L2

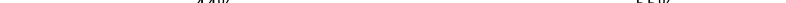


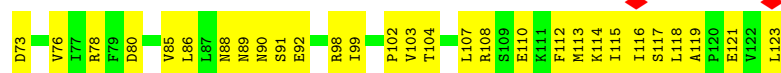
- Molecule 49: 50S ribosomal protein L32



- Molecule 50: 50S ribosomal protein L3



- Chain t:  44% 55%



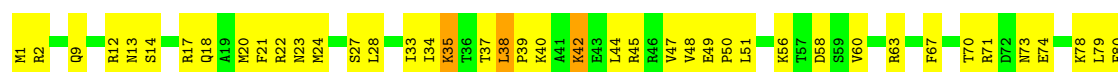
• Molecule 61: 50S ribosomal protein L15



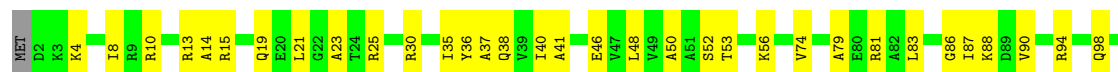
• Molecule 62: 50S ribosomal protein L16



• Molecule 63: 50S ribosomal protein L17



• Molecule 64: 50S ribosomal protein L18

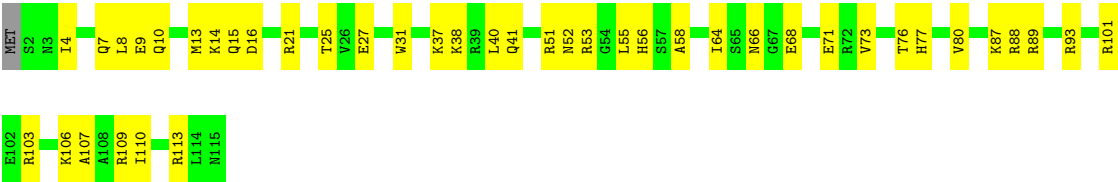


• Molecule 65: Large ribosomal subunit protein bL19

Chain y:

63%

37%

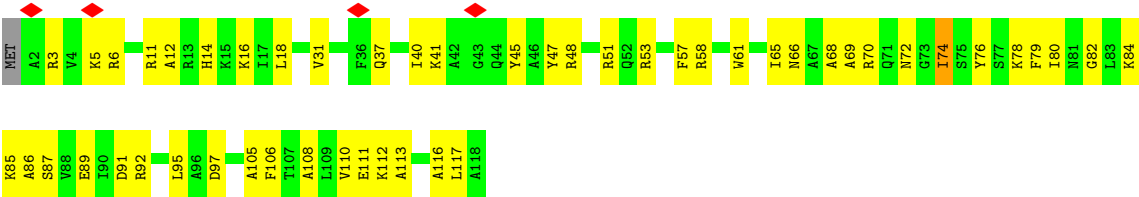


• Molecule 66: 50S ribosomal protein L20

Chain z:

57%

42%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12096	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.056	Depositor
Minimum map value	-0.015	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0048	Depositor
Map size (Å)	563.2, 563.2, 563.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	0	0.43	0/829	0.51	0/1107
2	1	0.60	0/864	0.63	0/1156
3	2	0.55	1/752 (0.1%)	0.67	0/1005
4	3	0.35	0/796	0.48	0/1062
5	4	0.57	0/766	0.63	0/1025
6	5	0.56	0/816	0.78	0/1259
7	6	0.57	0/783	0.78	0/1203
8	7	0.56	2/856 (0.2%)	0.88	4/1326 (0.3%)
9	9	0.37	0/1131	0.74	2/1524 (0.1%)
10	A	0.27	0/1810	0.58	0/2821
10	B	0.27	0/1810	0.58	0/2821
11	AA	0.38	0/10547	0.62	0/14232
12	AB	0.60	0/1317	1.22	18/1786 (1.0%)
13	AC	0.38	0/1718	0.62	0/2328
13	AD	0.36	0/2096	0.69	3/2854 (0.1%)
14	AE	0.39	0/10561	0.64	5/14258 (0.0%)
15	AF	0.30	0/652	0.61	0/879
16	AG	0.97	5/3897 (0.1%)	1.40	48/5273 (0.9%)
17	C	0.67	0/553	0.81	1/743 (0.1%)
18	D	0.29	0/36610	0.41	9/57091 (0.0%)
19	E	0.61	0/675	0.72	0/895
20	F	0.53	0/597	0.60	0/792
21	G	0.68	5/1791 (0.3%)	0.79	8/2413 (0.3%)
22	H	0.38	0/1746	0.81	0/2382
23	I	0.57	1/1663 (0.1%)	0.68	4/2241 (0.2%)
24	J	0.46	0/1665	0.58	0/2227
25	K	0.72	2/1165 (0.2%)	0.86	6/1568 (0.4%)
26	L	0.68	1/867 (0.1%)	0.79	1/1171 (0.1%)
27	M	0.56	0/1195	0.69	2/1602 (0.1%)
28	N	0.50	0/989	0.58	0/1326
29	O	0.66	3/1034 (0.3%)	0.79	3/1375 (0.2%)
30	P	0.51	0/800	0.69	0/1082

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	Q	0.72	2/893 (0.2%)	0.76	2/1205 (0.2%)
32	R	0.49	0/952	0.59	0/1274
33	S	0.52	0/817	0.61	0/1088
34	T	0.57	1/722 (0.1%)	0.68	0/964
35	U	0.41	0/659	0.53	0/884
36	V	0.49	0/657	0.62	0/881
37	W	0.55	1/680 (0.1%)	0.62	1/915 (0.1%)
38	X	0.45	0/909	0.72	1/1215 (0.1%)
39	Y	0.38	2/1046 (0.2%)	0.66	2/1410 (0.1%)
40	Z	0.13	0/227	0.41	0/304
41	a	0.30	0/69247	0.43	10/107985 (0.0%)
42	b	0.41	0/589	0.55	0/779
43	c	0.51	0/635	0.61	0/848
44	d	0.25	0/2872	0.37	0/4478
45	e	0.69	2/502 (0.4%)	0.65	1/667 (0.1%)
46	f	0.52	0/452	0.57	0/605
47	g	0.45	1/531 (0.2%)	0.64	0/709
48	h	0.49	1/2121 (0.0%)	0.59	0/2852
49	i	0.41	0/450	0.55	0/599
50	j	0.51	0/1586	0.57	1/2134 (0.0%)
51	k	0.45	0/433	0.62	0/576
52	l	0.51	1/1571 (0.1%)	0.62	0/2113
53	m	0.45	0/380	0.56	0/498
54	n	0.46	0/1434	0.66	1/1926 (0.1%)
55	o	0.51	0/513	0.71	1/676 (0.1%)
56	p	0.41	0/1333	0.62	2/1805 (0.1%)
57	q	0.46	0/303	0.64	0/397
58	r	0.28	0/1122	0.48	0/1515
59	s	0.70	2/1152 (0.2%)	0.73	2/1551 (0.1%)
60	t	0.52	0/955	0.75	3/1279 (0.2%)
61	u	0.43	0/1062	0.59	0/1413
62	v	0.60	1/1093 (0.1%)	0.77	3/1460 (0.2%)
63	w	0.83	2/964 (0.2%)	0.80	3/1289 (0.2%)
64	x	0.34	0/902	0.50	0/1209
65	y	0.41	0/929	0.54	0/1242
66	z	0.62	2/960 (0.2%)	0.62	0/1278
All	All	0.41	38/195004 (0.0%)	0.56	147/286850 (0.1%)

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

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

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	AG	429	LYS	C-N	13.86	1.51	1.33
63	w	35	LYS	CE-NZ	-12.74	1.11	1.49
29	O	80	ARG	CD-NE	-10.48	1.31	1.46
63	w	42	LYS	CD-CE	-9.39	1.24	1.52
25	K	45	ARG	CG-CD	7.73	1.75	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	AG	104	ARG	CA-C-N	17.91	154.21	121.97
16	AG	104	ARG	C-N-CA	17.91	154.21	121.97
16	AG	246	ASP	CA-C-N	14.47	137.93	119.84
16	AG	246	ASP	C-N-CA	14.47	137.93	119.84
16	AG	354	ALA	O-C-N	-13.72	107.27	122.09

There are no chirality outliers.

5 of 35 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	9	107	GLU	Peptide

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Mol	Chain	Res	Type	Group
9	9	79	PRO	Peptide
9	9	92	ALA	Peptide
12	AB	140	MET	Peptide
12	AB	151	LYS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	816	839	839	54	0
2	1	857	922	922	67	0
3	2	746	811	811	60	0
4	3	788	844	844	46	0
5	4	753	780	780	87	0
6	5	726	0	392	111	0
7	6	703	0	396	34	0
8	7	772	0	384	128	0
9	9	1117	0	1155	260	0
10	A	1620	826	827	110	0
10	B	1620	814	827	109	0
11	AA	10381	0	10389	268	0
12	AB	1286	0	1302	418	0
13	AC	1698	0	1718	13	0
13	AD	2078	0	1891	42	0
14	AE	10404	0	10626	271	0
15	AF	650	0	658	14	0
16	AG	3852	0	3827	772	0
17	C	544	559	560	107	0
18	D	32703	16423	16453	733	0
19	E	669	719	719	81	0
20	F	589	629	629	58	0
21	G	1760	1785	1787	153	0
22	H	1730	1454	1455	165	0
23	I	1636	1710	1710	153	0
24	J	1643	1707	1707	88	0
25	K	1152	1196	1196	117	0
26	L	848	846	846	106	0
27	M	1181	1235	1238	122	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	N	979	1031	1031	93	0
29	O	1022	1070	1070	91	0
30	P	790	831	831	85	0
31	Q	877	887	887	99	0
32	R	939	1001	1001	92	0
33	S	805	844	844	75	0
34	T	714	734	734	94	0
35	U	649	666	666	61	0
36	V	648	691	691	69	0
37	W	663	688	688	47	0
38	X	900	964	965	108	0
39	Y	1032	0	1088	214	0
40	Z	227	0	237	30	0
41	a	61841	31077	31120	1310	0
42	b	582	599	599	46	0
43	c	625	652	652	35	0
44	d	2569	1301	1301	41	0
45	e	501	531	531	44	0
46	f	448	488	488	38	0
47	g	522	520	520	67	0
48	h	2082	2154	2154	136	0
49	i	444	459	458	49	0
50	j	1565	1617	1616	119	0
51	k	426	464	464	43	0
52	l	1552	1619	1619	125	0
53	m	377	418	418	32	0
54	n	1410	1443	1444	152	0
55	o	504	572	572	51	0
56	p	1313	1358	1358	74	0
57	q	302	343	343	26	0
58	r	1111	1148	1148	53	0
59	s	1129	1162	1162	125	0
60	t	946	1023	1023	106	0
61	u	1053	1129	1129	78	0
62	v	1074	1157	1157	121	0
63	w	951	994	994	101	0
64	x	892	923	923	47	0
65	y	917	962	962	51	0
66	z	947	1020	1019	79	0
67	AE	1	0	0	0	0
68	AE	2	0	0	3	0
All	All	181653	98639	132795	7642	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 24.

The worst 5 of 7642 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)
6:5:11:DA:C5'	12:AB:67:THR:HG22	1.20	1.62
16:AG:425:LEU:CD2	16:AG:429:LYS:HE2	1.21	1.62
14:AE:79:LYS:HA	14:AE:81:ARG:CZ	1.26	1.61
25:K:45:ARG:CD	25:K:45:ARG:CG	1.75	1.58
6:5:9:DG:C5'	11:AA:473:ARG:HB3	1.34	1.57

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
2	1	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
3	2	92/100 (92%)	87 (95%)	5 (5%)	0	100	100
4	3	101/104 (97%)	98 (97%)	3 (3%)	0	100	100
5	4	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
9	9	146/165 (88%)	100 (68%)	43 (30%)	3 (2%)	5	25
11	AA	1312/1342 (98%)	1198 (91%)	113 (9%)	1 (0%)	48	78
12	AB	159/162 (98%)	105 (66%)	43 (27%)	11 (7%)	1	5
13	AC	217/329 (66%)	203 (94%)	12 (6%)	2 (1%)	14	44
13	AD	293/329 (89%)	263 (90%)	27 (9%)	3 (1%)	12	41
14	AE	1331/1407 (95%)	1212 (91%)	113 (8%)	6 (0%)	24	57
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	AG	493/495 (100%)	375 (76%)	87 (18%)	31 (6%)	1	6
17	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
19	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
20	F	68/71 (96%)	68 (100%)	0	0	100	100
21	G	223/241 (92%)	212 (95%)	10 (4%)	1 (0%)	30	61
22	H	255/557 (46%)	182 (71%)	66 (26%)	7 (3%)	4	20
23	I	206/233 (88%)	193 (94%)	13 (6%)	0	100	100
24	J	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
25	K	154/167 (92%)	145 (94%)	8 (5%)	1 (1%)	21	52
26	L	102/104 (98%)	97 (95%)	4 (4%)	1 (1%)	12	41
27	M	149/179 (83%)	140 (94%)	8 (5%)	1 (1%)	18	49
28	N	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
29	O	125/130 (96%)	116 (93%)	8 (6%)	1 (1%)	16	47
30	P	97/99 (98%)	88 (91%)	9 (9%)	0	100	100
31	Q	115/117 (98%)	107 (93%)	8 (7%)	0	100	100
32	R	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
33	S	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
34	T	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
35	U	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
36	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
37	W	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
38	X	114/118 (97%)	103 (90%)	9 (8%)	2 (2%)	6	28
39	Y	139/142 (98%)	101 (73%)	38 (27%)	0	100	100
40	Z	28/121 (23%)	22 (79%)	6 (21%)	0	100	100
42	b	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
43	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
45	e	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
46	f	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
47	g	64/70 (91%)	62 (97%)	2 (3%)	0	100	100
48	h	269/273 (98%)	255 (95%)	14 (5%)	0	100	100
49	i	54/57 (95%)	49 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
51	k	50/55 (91%)	50 (100%)	0	0	100	100
52	l	199/201 (99%)	188 (94%)	11 (6%)	0	100	100
53	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
54	n	175/179 (98%)	160 (91%)	14 (8%)	1 (1%)	21	52
55	o	62/64 (97%)	57 (92%)	4 (6%)	1 (2%)	7	30
56	p	173/177 (98%)	162 (94%)	11 (6%)	0	100	100
57	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
58	r	147/149 (99%)	139 (95%)	8 (5%)	0	100	100
59	s	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
60	t	121/123 (98%)	114 (94%)	7 (6%)	0	100	100
61	u	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
62	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
63	w	117/127 (92%)	112 (96%)	5 (4%)	0	100	100
64	x	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
65	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
66	z	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
All	All	10058/11004 (91%)	9174 (91%)	811 (8%)	73 (1%)	20	49

5 of 73 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	84 (100%)	0	100	100
2	1	93/93 (100%)	93 (100%)	0	100	100
3	2	81/84 (96%)	81 (100%)	0	100	100
4	3	84/85 (99%)	84 (100%)	0	100	100
5	4	78/78 (100%)	78 (100%)	0	100	100
9	9	112/123 (91%)	112 (100%)	0	100	100
11	AA	1135/1157 (98%)	1130 (100%)	5 (0%)	84	86
12	AB	141/142 (99%)	122 (86%)	19 (14%)	4	16
13	AC	186/286 (65%)	186 (100%)	0	100	100
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1122/1168 (96%)	1104 (98%)	18 (2%)	55	75
15	AF	70/75 (93%)	69 (99%)	1 (1%)	59	76
16	AG	409/409 (100%)	288 (70%)	121 (30%)	0	1
17	C	57/65 (88%)	57 (100%)	0	100	100
19	E	65/66 (98%)	65 (100%)	0	100	100
20	F	60/61 (98%)	60 (100%)	0	100	100
21	G	187/199 (94%)	187 (100%)	0	100	100
22	H	137/461 (30%)	137 (100%)	0	100	100
23	I	171/190 (90%)	171 (100%)	0	100	100
24	J	172/173 (99%)	171 (99%)	1 (1%)	78	83
25	K	119/126 (94%)	119 (100%)	0	100	100
26	L	91/91 (100%)	91 (100%)	0	100	100
27	M	124/147 (84%)	124 (100%)	0	100	100
28	N	104/105 (99%)	104 (100%)	0	100	100
29	O	105/107 (98%)	105 (100%)	0	100	100
30	P	86/86 (100%)	85 (99%)	1 (1%)	63	78
31	Q	90/90 (100%)	90 (100%)	0	100	100
32	R	101/104 (97%)	101 (100%)	0	100	100
33	S	83/84 (99%)	83 (100%)	0	100	100
34	T	76/77 (99%)	76 (100%)	0	100	100
35	U	65/65 (100%)	65 (100%)	0	100	100
36	V	74/78 (95%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	W	72/79 (91%)	72 (100%)	0	100	100
38	X	94/96 (98%)	94 (100%)	0	100	100
39	Y	109/110 (99%)	109 (100%)	0	100	100
40	Z	26/85 (31%)	26 (100%)	0	100	100
42	b	58/63 (92%)	58 (100%)	0	100	100
43	c	67/68 (98%)	67 (100%)	0	100	100
45	e	54/54 (100%)	54 (100%)	0	100	100
46	f	48/49 (98%)	48 (100%)	0	100	100
47	g	59/62 (95%)	59 (100%)	0	100	100
48	h	216/218 (99%)	216 (100%)	0	100	100
49	i	47/48 (98%)	47 (100%)	0	100	100
50	j	164/164 (100%)	164 (100%)	0	100	100
51	k	47/49 (96%)	47 (100%)	0	100	100
52	l	165/165 (100%)	165 (100%)	0	100	100
53	m	38/38 (100%)	38 (100%)	0	100	100
54	n	148/150 (99%)	148 (100%)	0	100	100
55	o	51/51 (100%)	51 (100%)	0	100	100
56	p	136/138 (99%)	136 (100%)	0	100	100
57	q	34/34 (100%)	34 (100%)	0	100	100
58	r	114/114 (100%)	114 (100%)	0	100	100
59	s	116/116 (100%)	116 (100%)	0	100	100
60	t	104/104 (100%)	104 (100%)	0	100	100
61	u	103/103 (100%)	103 (100%)	0	100	100
62	v	109/109 (100%)	109 (100%)	0	100	100
63	w	99/103 (96%)	99 (100%)	0	100	100
64	x	86/87 (99%)	86 (100%)	0	100	100
65	y	99/100 (99%)	99 (100%)	0	100	100
66	z	89/90 (99%)	89 (100%)	0	100	100
All	All	8299/9092 (91%)	8133 (98%)	166 (2%)	48	72

5 of 166 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	AG	270	ARG
16	AG	337	ASN
16	AG	276	TRP
16	AG	303	HIS
16	AG	358	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 116 such sidechains are listed below:

Mol	Chain	Res	Type
21	G	36	ASN
64	x	38	GLN
27	M	86	GLN
64	x	29	HIS
57	q	13	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	8 (10%)
10	B	75/76 (98%)	29 (38%)	8 (10%)
18	D	1514/1542 (98%)	289 (19%)	20 (1%)
41	a	2859/2904 (98%)	511 (17%)	0
44	d	119/120 (99%)	15 (12%)	0
8	7	36/47 (76%)	26 (72%)	5 (13%)
All	All	4678/4765 (98%)	899 (19%)	41 (0%)

5 of 899 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 41 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	D	517	G
18	D	1213	A
18	D	991	U

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Mol	Chain	Res	Type
18	D	1196	A
18	D	1447	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.

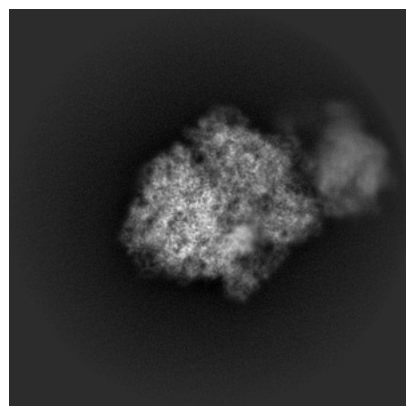
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42504. These allow visual inspection of the internal detail of the map and identification of artifacts.

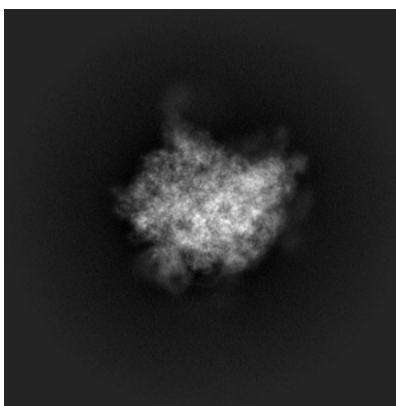
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

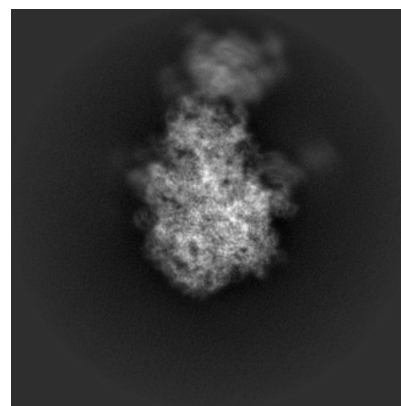
6.1.1 Primary map



X

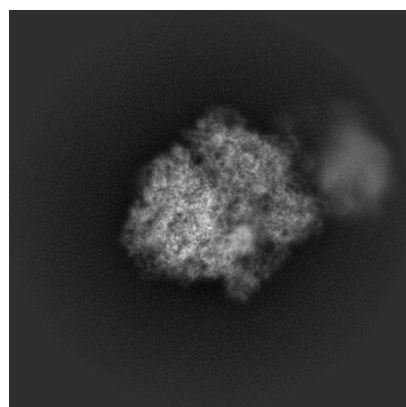


Y

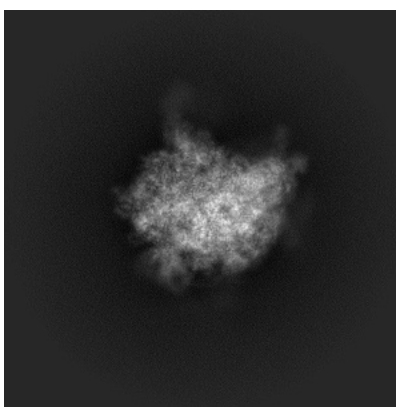


Z

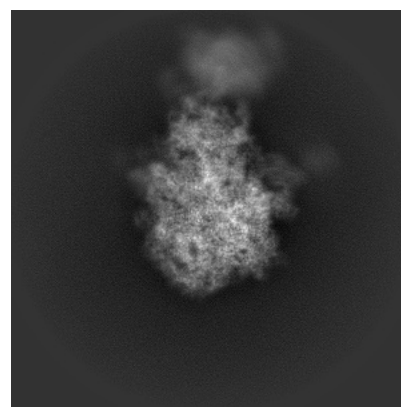
6.1.2 Raw map



X



Y

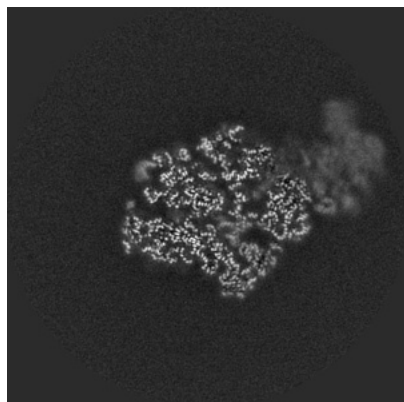


Z

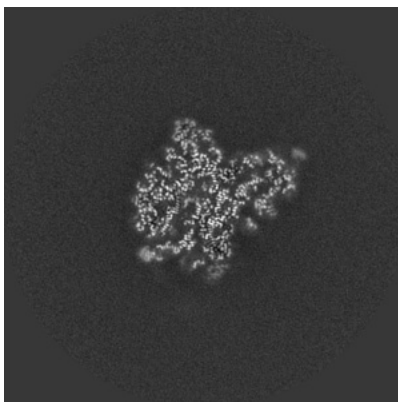
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

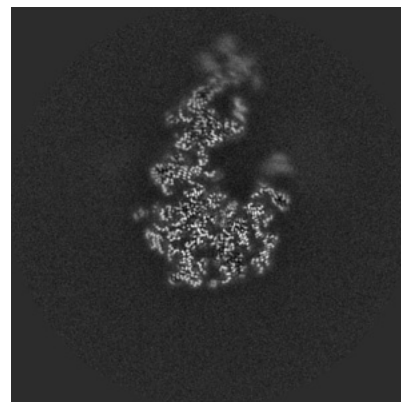
6.2.1 Primary map



X Index: 256

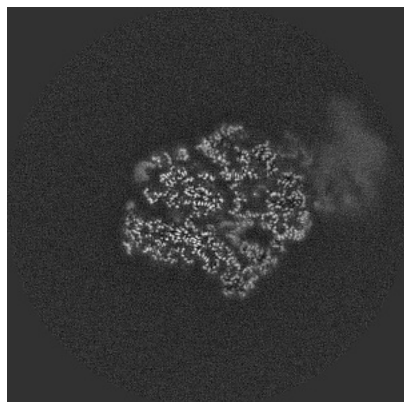


Y Index: 256

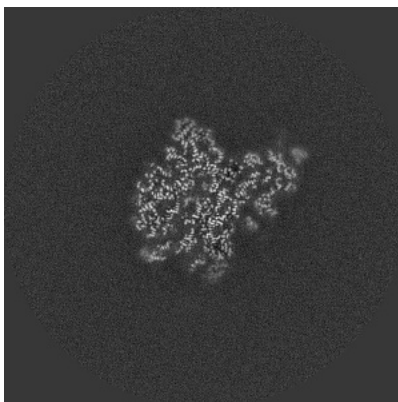


Z Index: 256

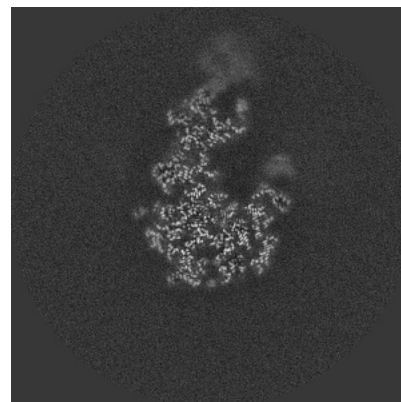
6.2.2 Raw map



X Index: 256



Y Index: 256

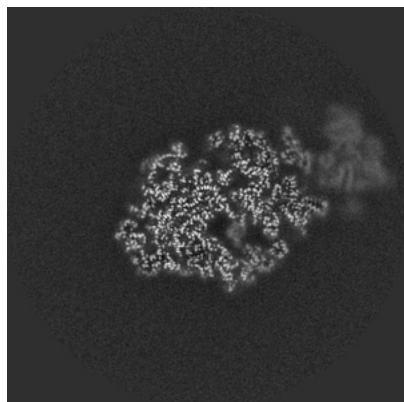


Z Index: 256

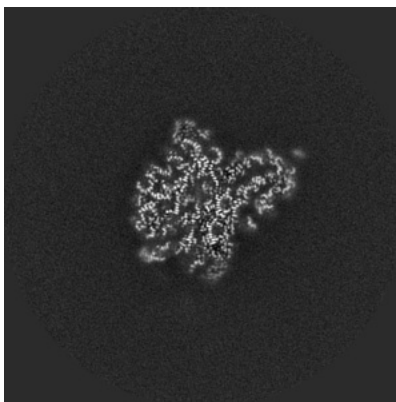
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

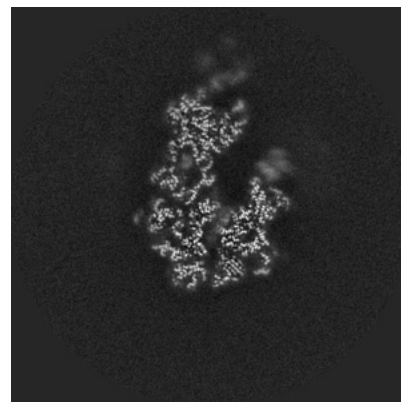
6.3.1 Primary map



X Index: 243

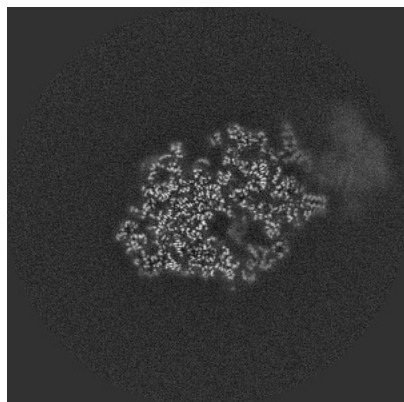


Y Index: 254

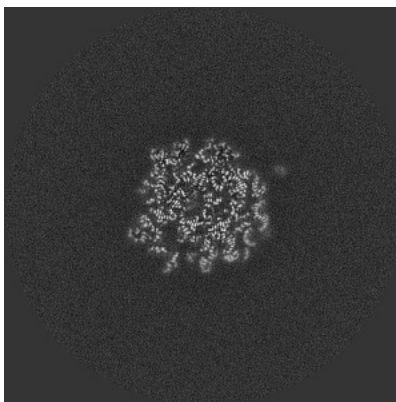


Z Index: 247

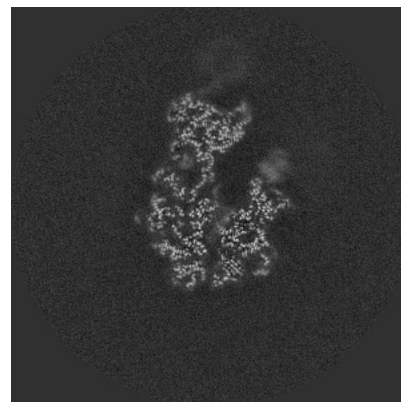
6.3.2 Raw map



X Index: 242



Y Index: 220



Z Index: 246

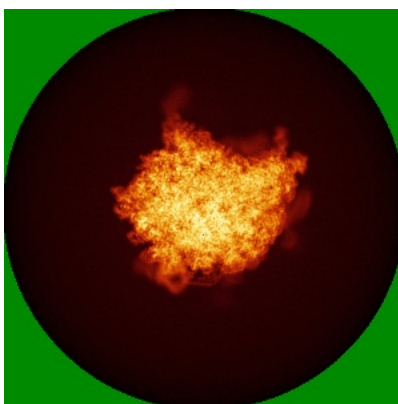
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

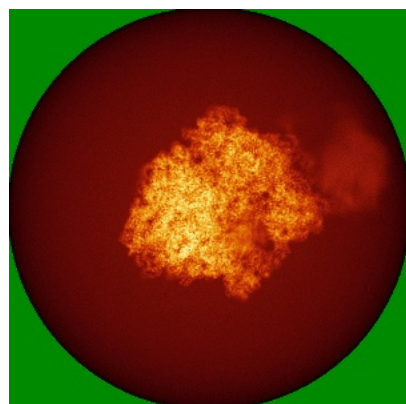


Y

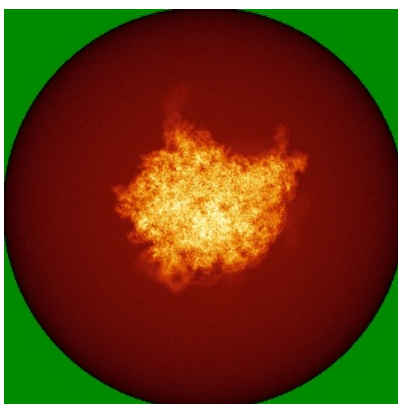


Z

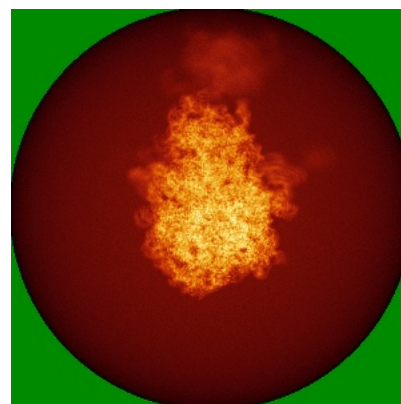
6.4.2 Raw map



X



Y

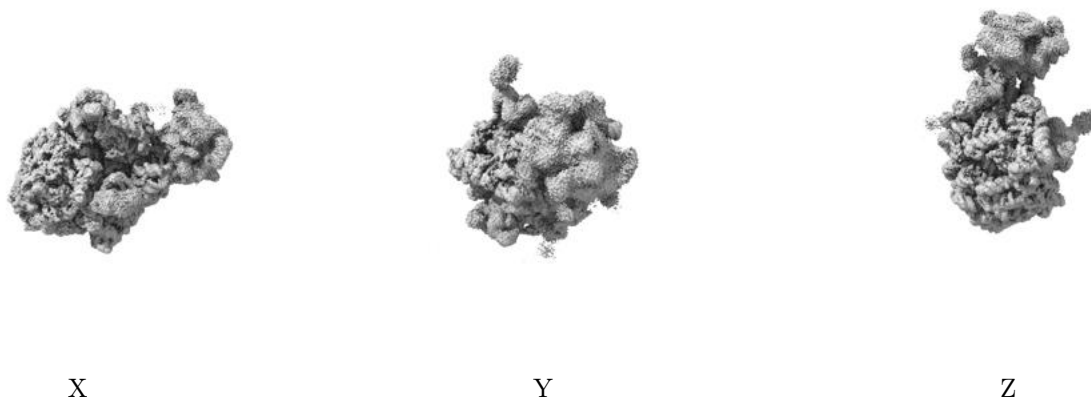


Z

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.

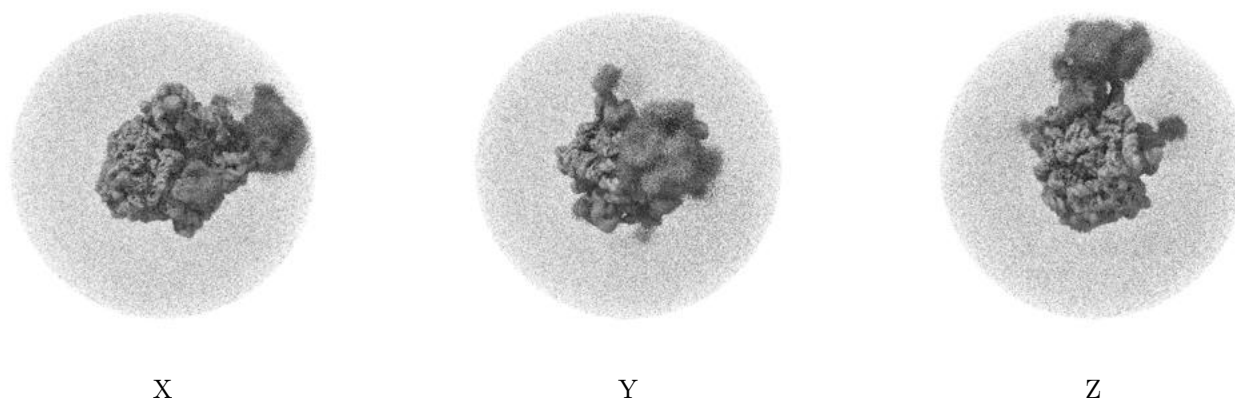
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0048. 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.

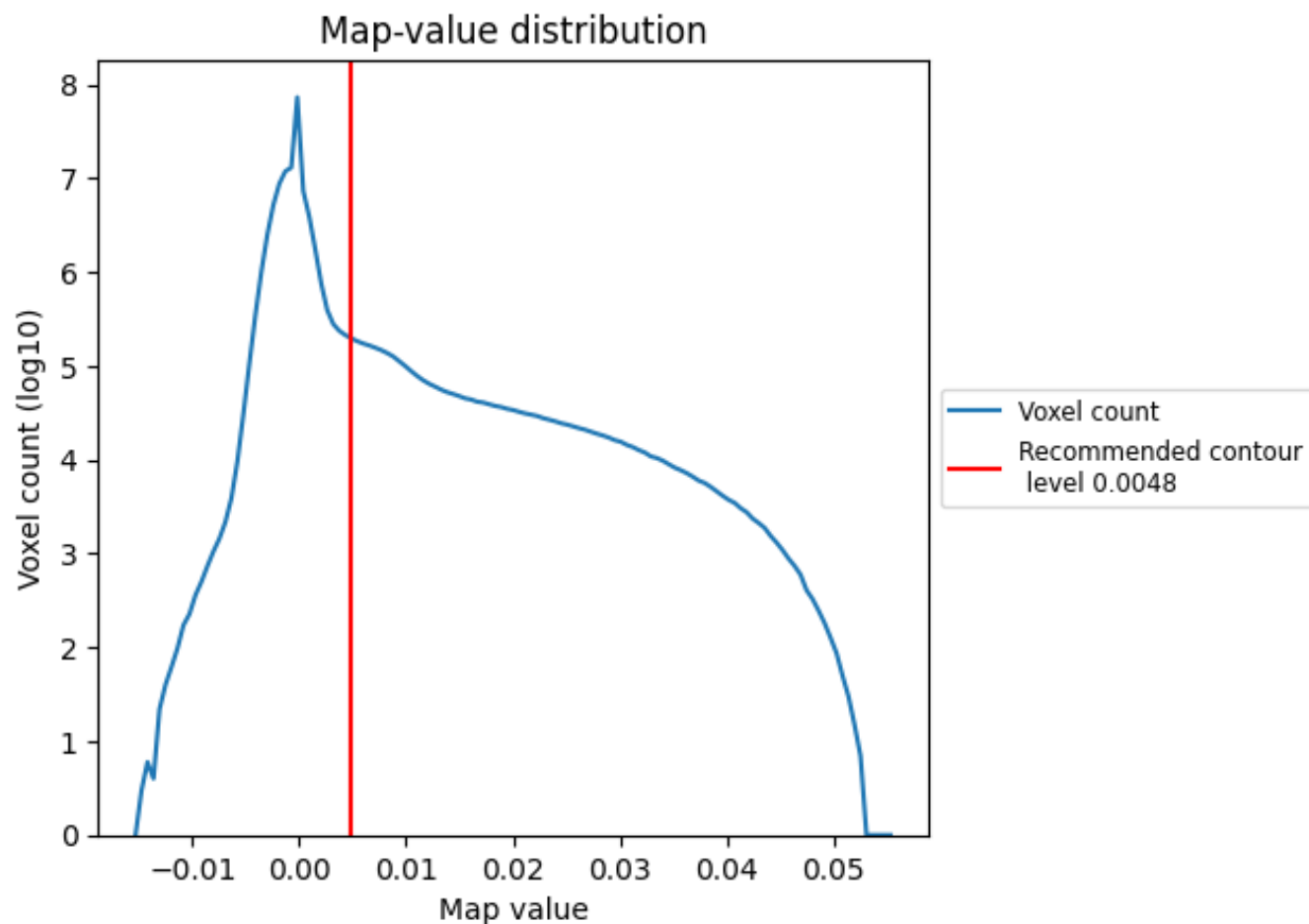
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

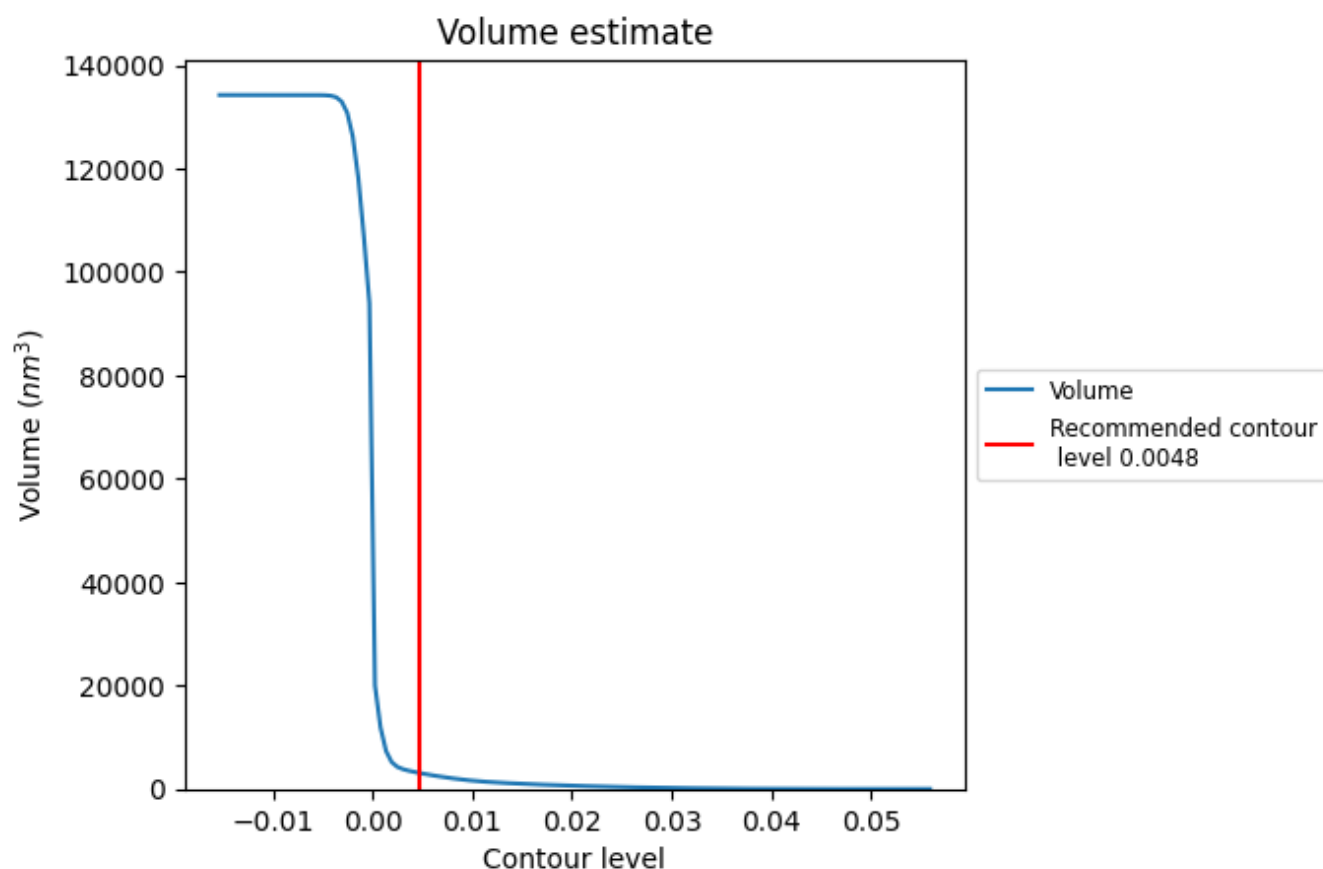
This section contains the results of statistical analysis of the map.

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.

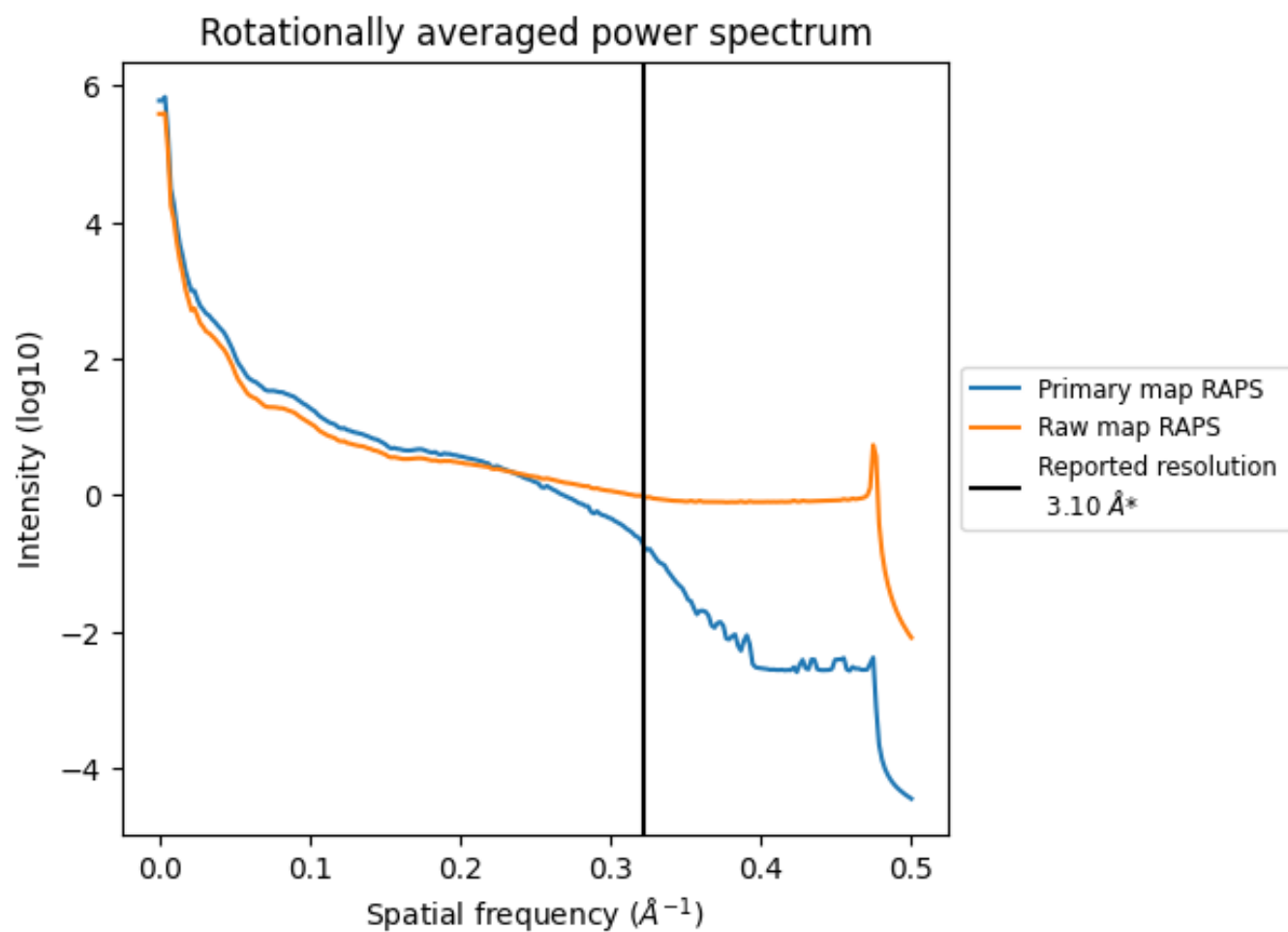
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3048 nm^3 ; this corresponds to an approximate mass of 2753 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 ⓘ

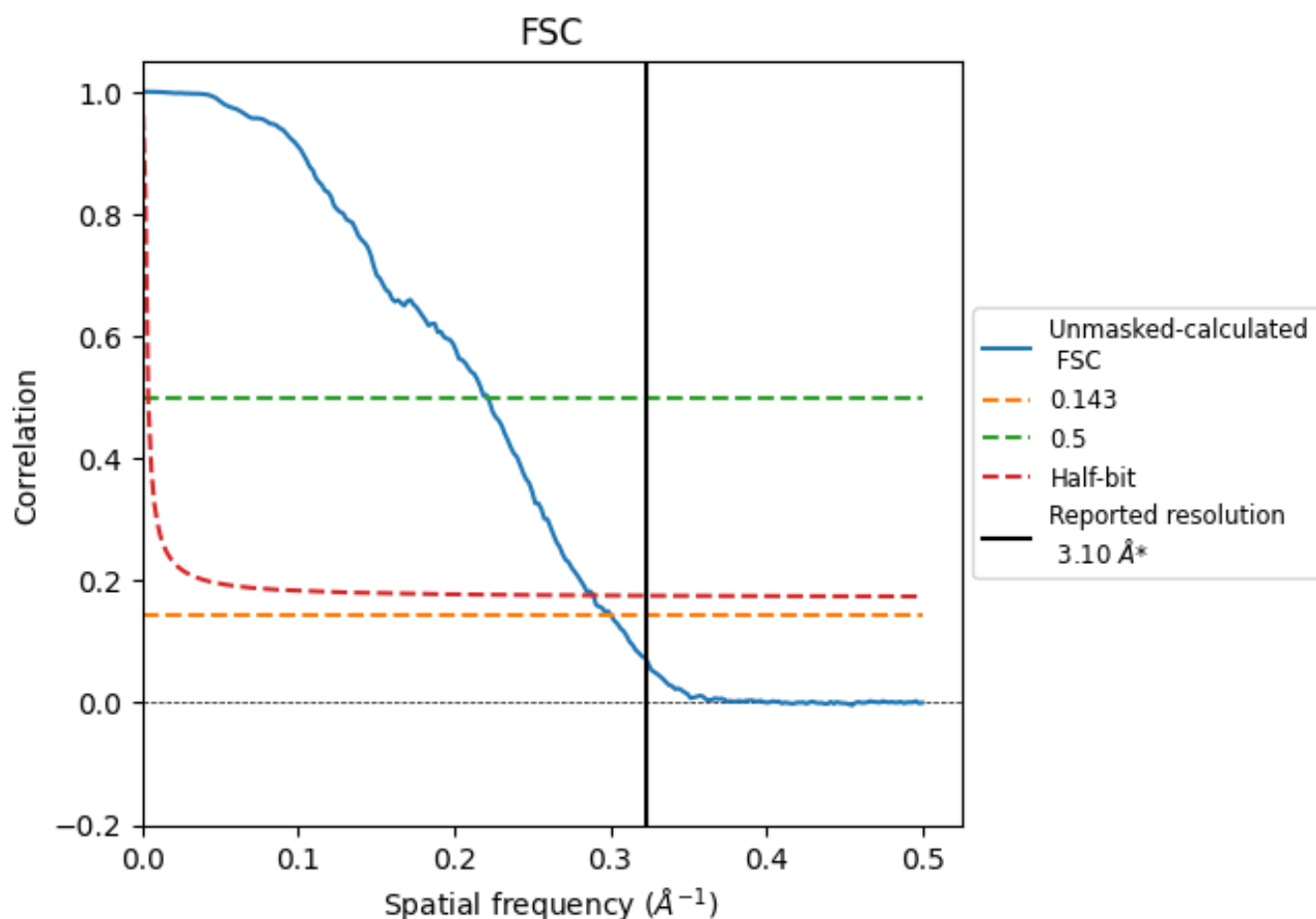


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

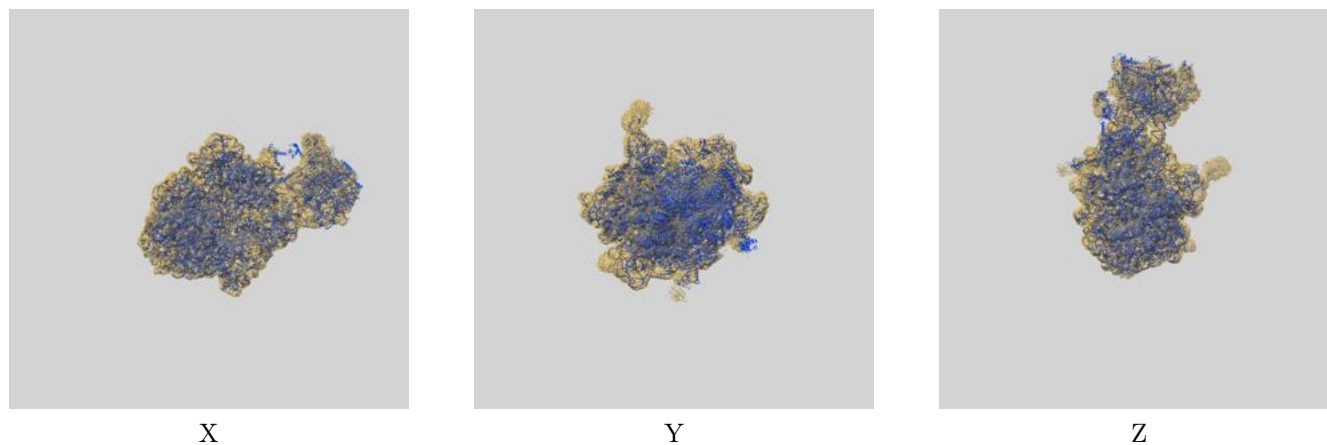
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.33	4.52	3.46

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

9 Map-model fit [i](#)

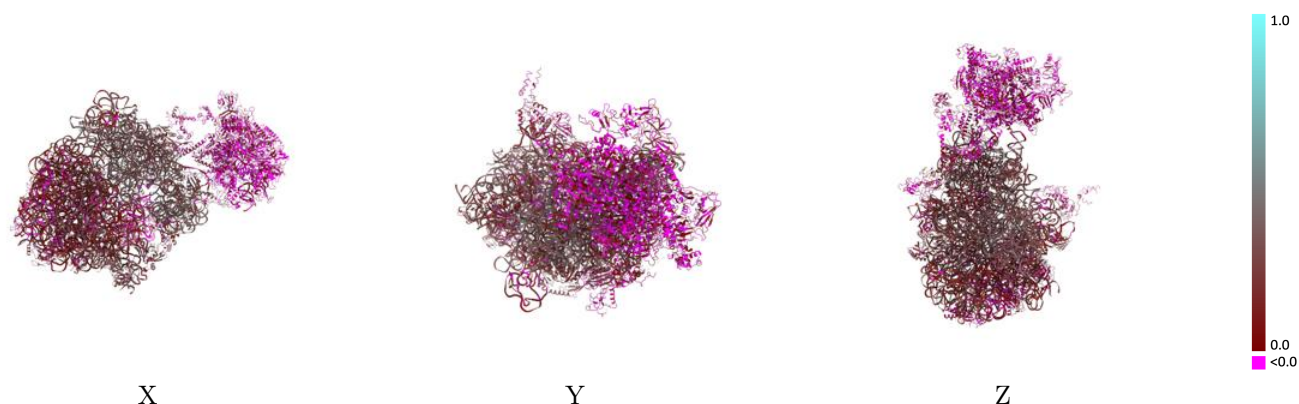
This section contains information regarding the fit between EMDB map EMD-42504 and PDB model 8URY. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



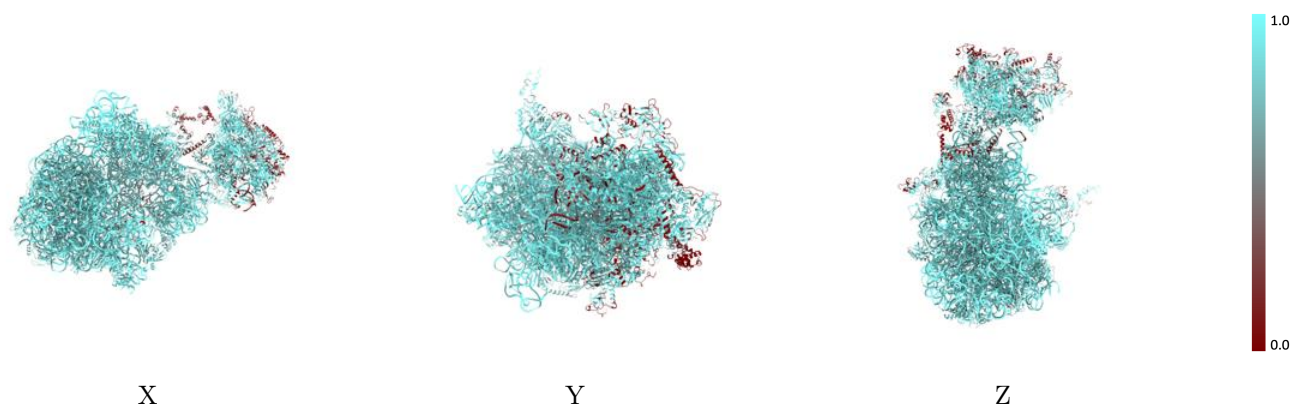
The images above show the 3D surface view of the map at the recommended contour level 0.0048 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



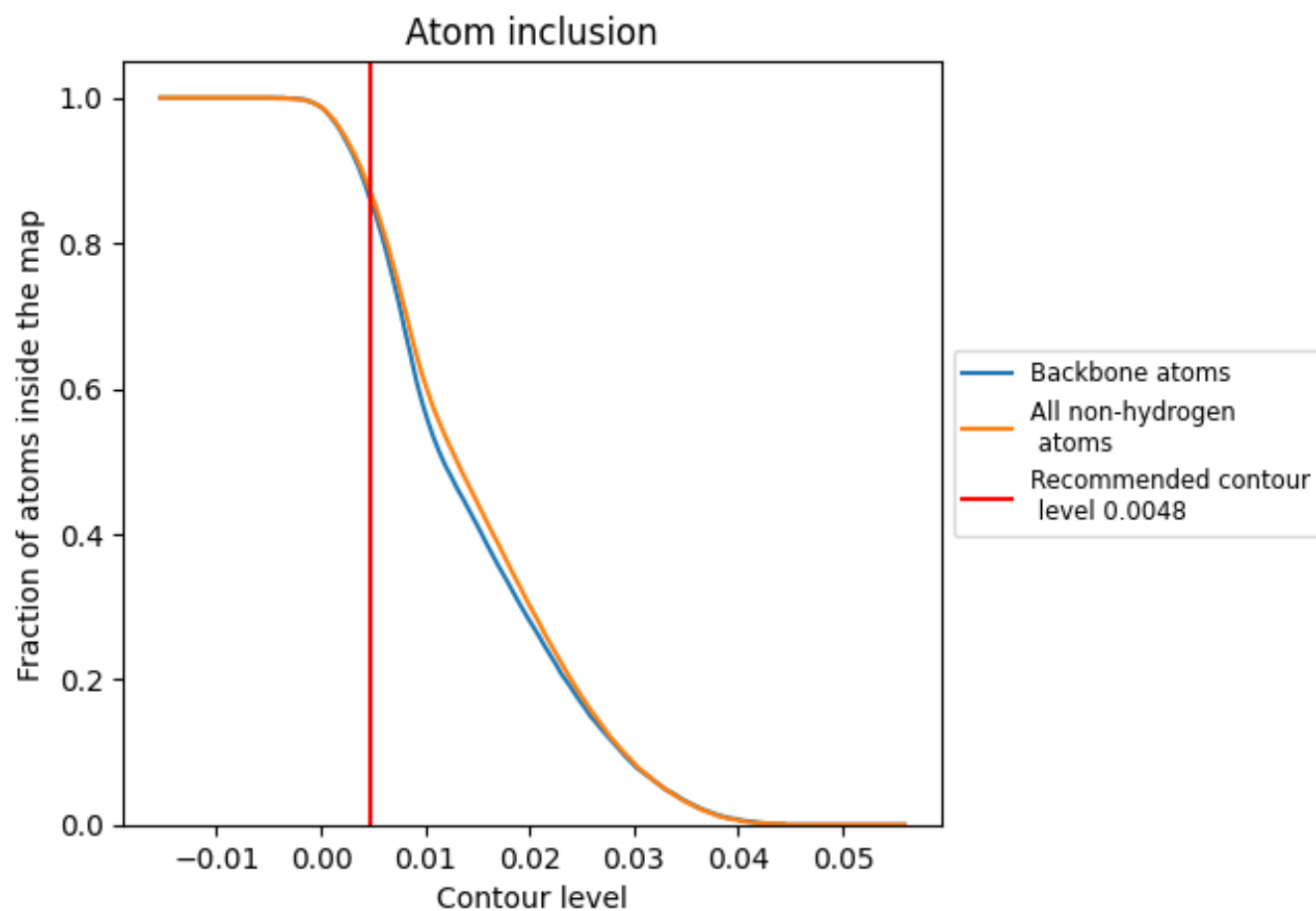
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0048).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 87% 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 (0.0048) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8690	 0.1690
0	 0.8390	 0.1200
1	 0.7740	 0.0580
2	 0.8160	 0.1040
3	 0.8240	 0.0530
4	 0.9230	 0.2810
5	 0.5950	 0.0250
6	 0.6810	 0.0070
7	 0.7860	 0.0090
9	 0.8650	 0.0920
A	 0.9580	 0.1850
AA	 0.7470	 0.0010
AB	 0.7460	 0.0140
AC	 0.7300	 0.0220
AD	 0.7870	 0.0640
AE	 0.7590	 0.0100
AF	 0.5270	 0.0320
AG	 0.5150	 0.0260
B	 0.8050	 0.0850
C	 0.8530	 0.1750
D	 0.9850	 0.3160
E	 0.9220	 0.2900
F	 0.8520	 0.1970
G	 0.8680	 0.2300
H	 0.5840	 0.0480
I	 0.8920	 0.2990
J	 0.8910	 0.2570
K	 0.8530	 0.2130
L	 0.8360	 0.1670
M	 0.9060	 0.2950
N	 0.8580	 0.2190
O	 0.9170	 0.2780
P	 0.8990	 0.2740
Q	 0.8990	 0.2380
R	 0.9250	 0.3070



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Chain	Atom inclusion	Q-score
S	 0.9200	 0.3230
T	 0.8770	 0.2350
U	 0.9070	 0.2980
V	 0.8910	 0.2580
W	 0.8980	 0.2080
X	 0.8870	 0.1690
Y	 0.6890	 0.0410
Z	 0.8060	 -0.0280
a	 0.9450	 0.1560
b	 0.8430	 0.1990
c	 0.8300	 0.1330
d	 0.9840	 0.2930
e	 0.8040	 0.1230
f	 0.8600	 0.1710
g	 0.8940	 0.2080
h	 0.8670	 0.2110
i	 0.8010	 0.1080
j	 0.8240	 0.1130
k	 0.8520	 0.1610
l	 0.7900	 0.1090
m	 0.7690	 0.1080
n	 0.8950	 0.1930
o	 0.8230	 0.1430
p	 0.9090	 0.1930
q	 0.8800	 0.2140
r	 0.8050	 0.1810
s	 0.8900	 0.2230
t	 0.8320	 0.1700
u	 0.8360	 0.1430
v	 0.8790	 0.1830
w	 0.8070	 0.0960
x	 0.9110	 0.2280
y	 0.8540	 0.1450
z	 0.7950	 0.1120