



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:28 PM UTC

PDB ID : 8URI / pdb_00008uri
EMDB ID : EMD-42493
Title : Escherichia coli transcription-translation coupled complex class B (TTC-B) containing RfaH bound to ops signal, NusA, mRNA with a 27 nt long spacer, and fMet-tRNAs in E-site and P-site of the ribosome
Authors : Molodtsov, V.; Wang, C.; Ebright, R.H.
Deposited on : 2023-10-26
Resolution : 5.30 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

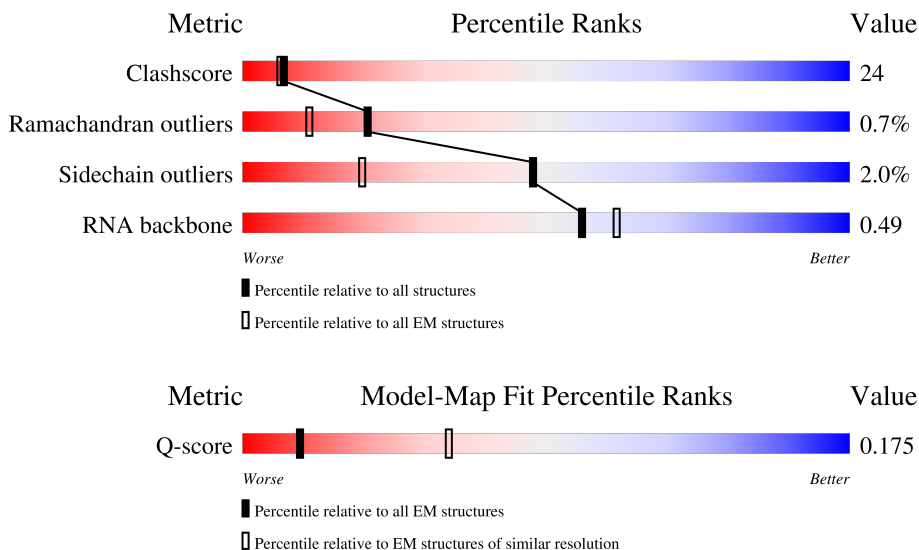
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 5.30 Å.

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







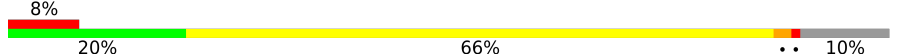
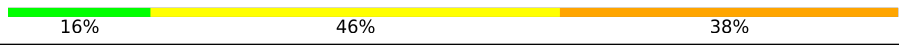
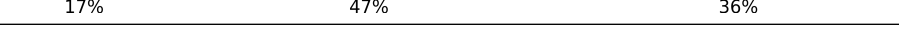
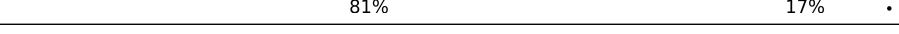
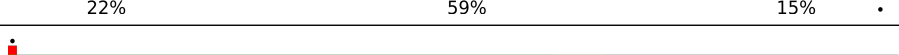
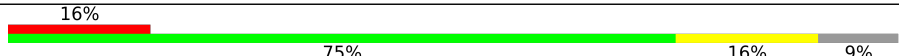
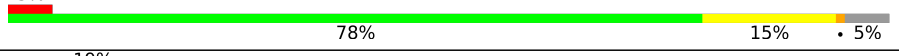
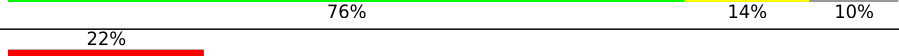
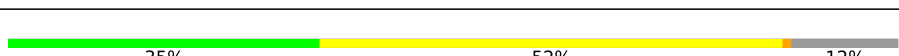





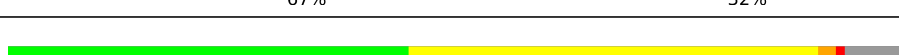
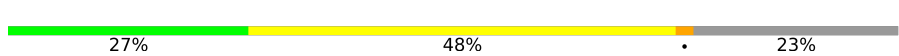



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	625 (4.80 - 5.80)

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

Mol	Chain	Length	Quality of chain
1	0	103	59% (green), 41% (yellow)
2	1	110	59% (green), 41% (yellow)
3	2	100	52% (green), 41% (yellow), 6% (grey)





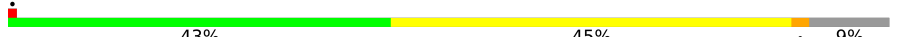


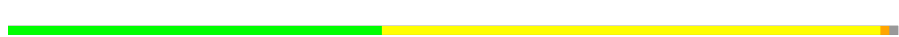

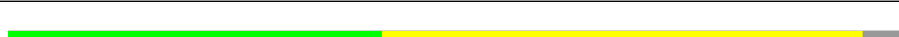



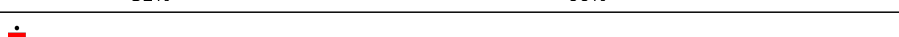
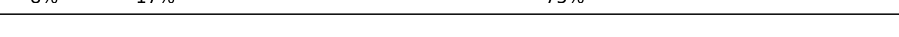










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Mol	Chain	Length	Quality of chain
4	3	104	
5	4	94	
6	5	38	
7	6	38	
8	7	44	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	162	
13	AC	329	
13	AD	329	
14	AE	1407	
15	AF	91	
16	AG	495	
17	C	75	
18	D	1542	
19	E	87	
20	F	71	
21	G	241	
22	H	557	
23	I	233	
24	J	206	
25	K	167	
26	L	135	

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

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

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

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

2 Entry composition [i](#)

There are 68 unique types of molecules in this entry. The entry contains 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 Ribosomal protein L21.

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 8 is a RNA chain called mRNA with 27 nt long spacer.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 18 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
18	D	1524	49126	14585	16423	6003	10591	1524	0	0

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
19	E	86	1388	414	719	138	114	3	0	0

- Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
20	F	70	1218	366	629	125	97	1	0	0

- Molecule 21 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
21	G	225	3545	1113	1785	316	323	8	0	0

- Molecule 22 is a protein called 30S ribosomal protein S1.

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

- Molecule 23 is a protein called 30S ribosomal protein S3.

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

- Molecule 24 is a protein called 30S ribosomal protein S4.

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

- Molecule 25 is a protein called 30S ribosomal protein S5.

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

- Molecule 26 is a protein called 30S ribosomal protein S6.

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

- Molecule 27 is a protein called 30S ribosomal protein S7.

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

- Molecule 28 is a protein called 30S ribosomal protein S8.

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

- Molecule 29 is a protein called 30S ribosomal protein S9.

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

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

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

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

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

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

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

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

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

- 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
			Total	C	H	N	O	P		
41	a	2880	92918	27587	31077	11398	19976	2880	0	0

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 42 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
42	b	76	1181	360	599	117	104	1	0	0

- Molecule 43 is a protein called 50S ribosomal protein L28.

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

- Molecule 44 is a RNA chain called 5S rRNA.

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

- Molecule 45 is a protein called 50S ribosomal protein L29.

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

- Molecule 46 is a protein called 50S ribosomal protein L30.

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

- Molecule 47 is a protein called 50S ribosomal protein L31.

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

- Molecule 48 is a protein called 50S ribosomal protein L2.

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

- Molecule 49 is a protein called 50S ribosomal protein L32.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L33.

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

- Molecule 52 is a protein called 50S ribosomal protein L4.

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

- Molecule 53 is a protein called 50S ribosomal protein L34.

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

- Molecule 54 is a protein called 50S ribosomal protein L5.

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

- Molecule 55 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace	
55	o	64	Total	C	H	N	O	S	0	0
			1076	323	572	105	74	2		

- Molecule 56 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace	
56	p	175	Total	C	H	N	O	S	0	0
			2671	826	1358	241	244	2		

- Molecule 57 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace	
57	q	38	Total	C	H	N	O	S	0	0
			645	185	343	65	48	4		

- Molecule 58 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace	
58	r	149	Total	C	H	N	O	S	0	0
			2259	699	1148	197	214	1		

- Molecule 59 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace	
59	s	142	Total	C	H	N	O	S	0	0
			2291	714	1162	212	199	4		

- Molecule 60 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace	
60	t	123	Total	C	H	N	O	S	0	0
			1969	593	1023	181	166	6		

- Molecule 61 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
61	u	144	2182	654	1129	207	190	2	0	0

- Molecule 62 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
62	v	136	2231	686	1157	205	177	6	0	0

- Molecule 63 is a protein called 50S ribosomal protein L17.

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

- Molecule 64 is a protein called 50S ribosomal protein L18.

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

- Molecule 65 is a protein called 50S ribosomal protein L19.

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

- Molecule 66 is a protein called 50S ribosomal protein L20.

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

- Molecule 67 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

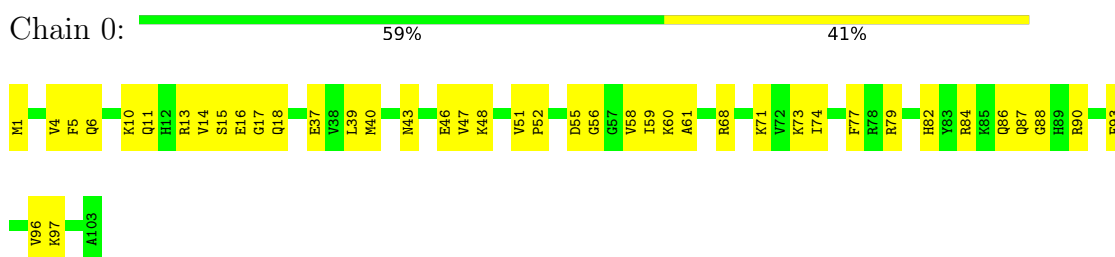
- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

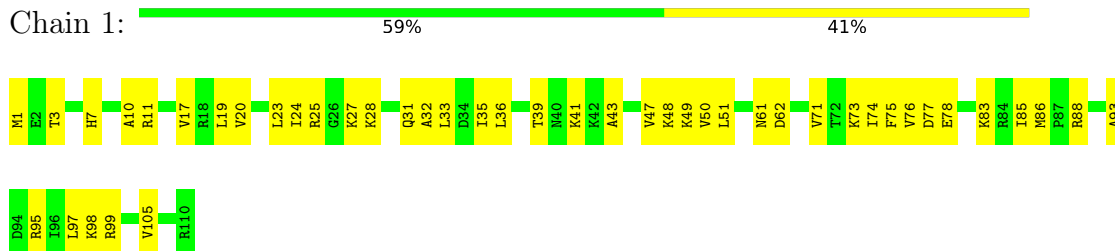
3 Residue-property plots [i](#)

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

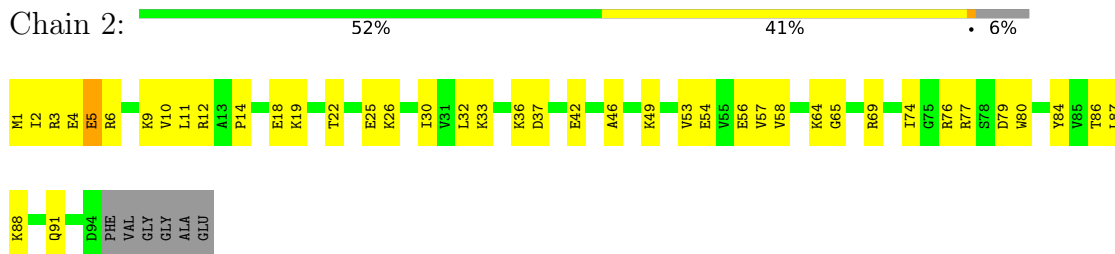
- Molecule 1: Ribosomal protein L21



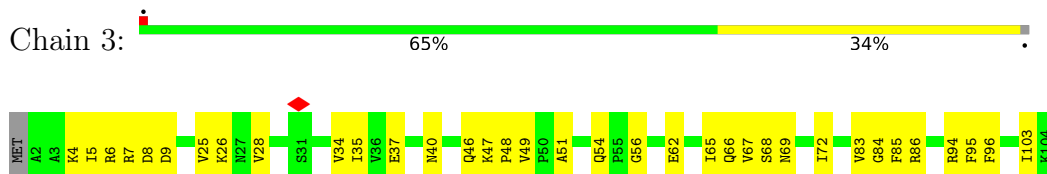
- Molecule 2: 50S ribosomal protein L22



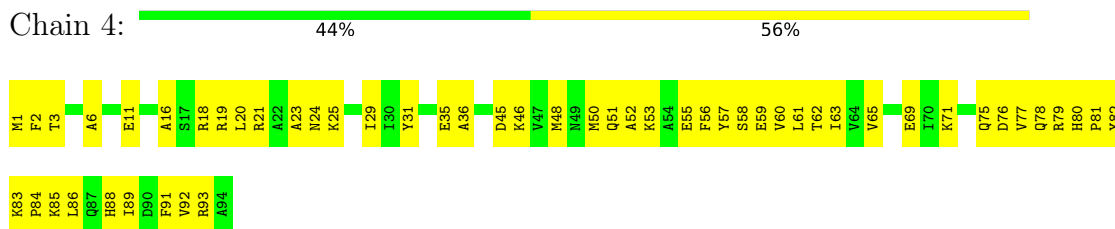
- Molecule 3: 50S ribosomal protein L23



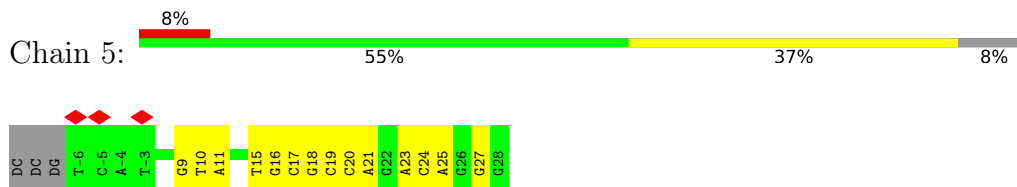
- Molecule 4: 50S ribosomal protein L24



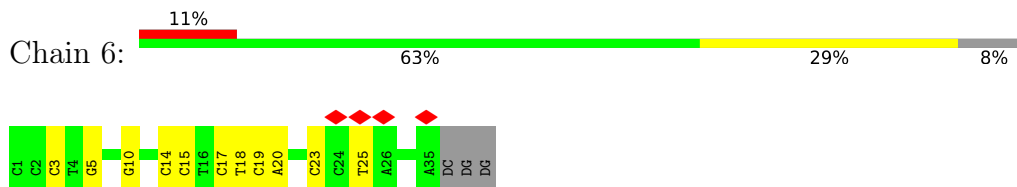
- Molecule 5: 50S ribosomal protein L25



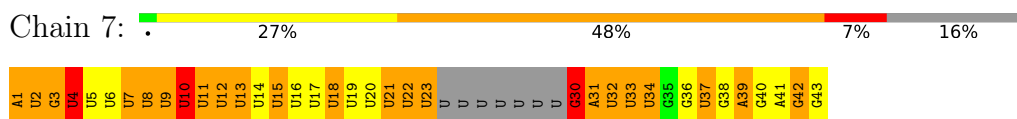
- Molecule 6: NT DNA ops



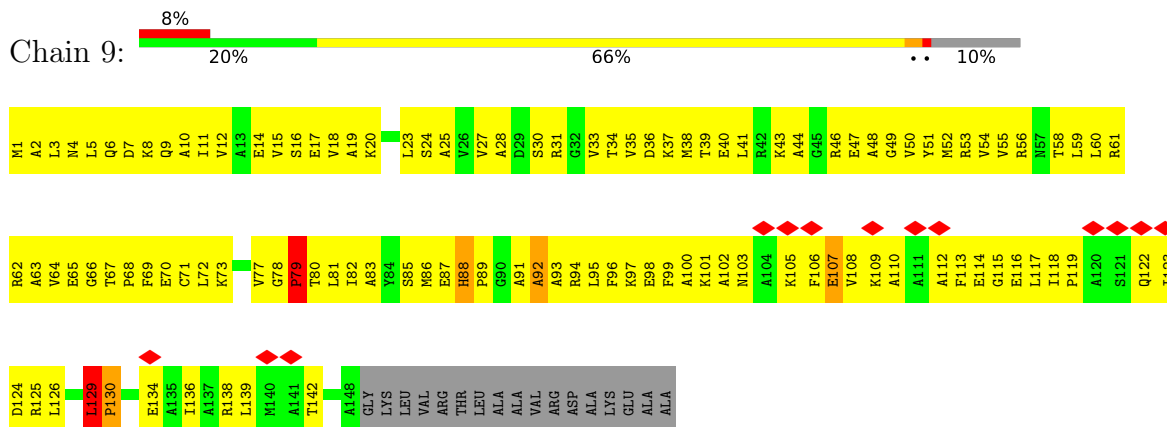
- Molecule 7: T DNA ops



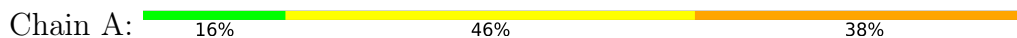
- Molecule 8: mRNA with 27 nt long spacer

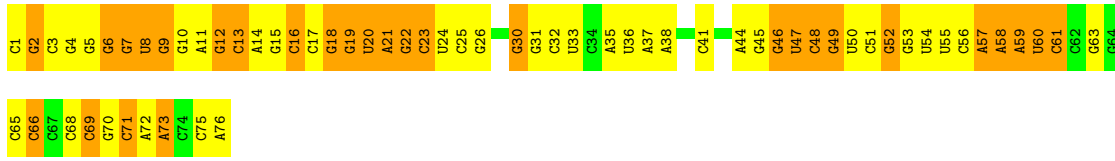


- Molecule 9: 50S ribosomal protein L10

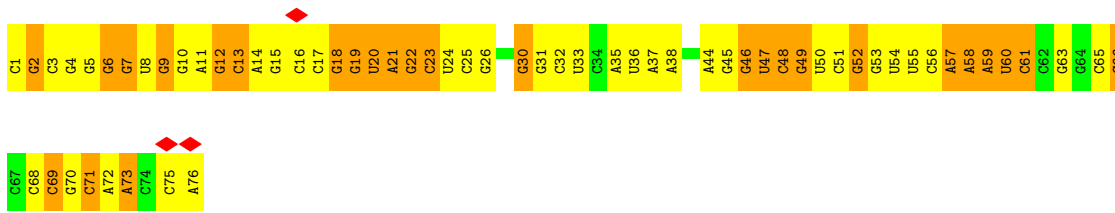
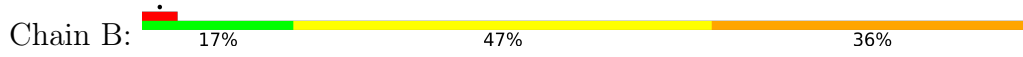


- Molecule 10: E-site and P-site fMet-tRNA

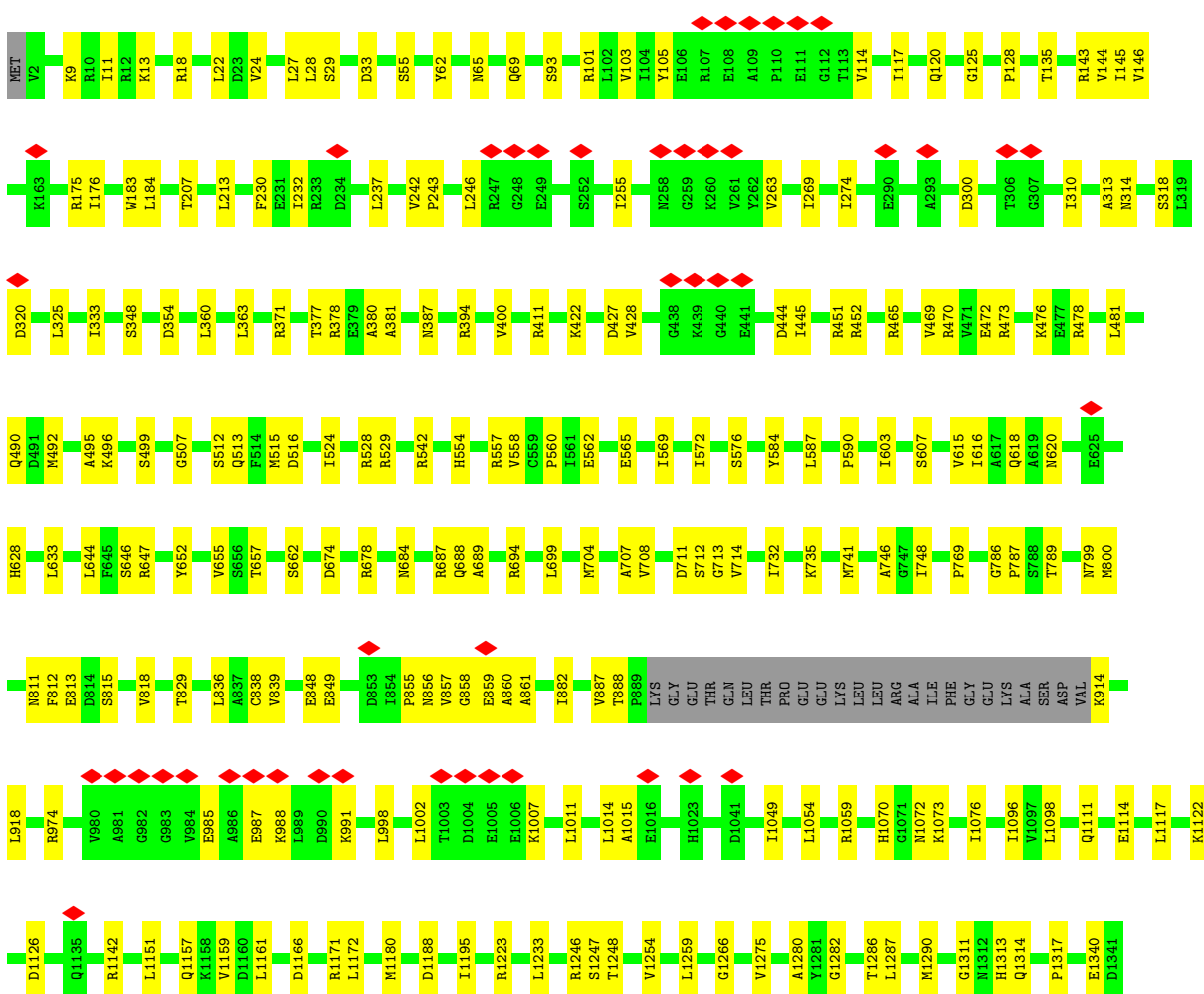
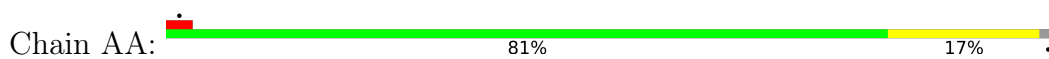




• Molecule 10: E-site and P-site fMet-tRNA

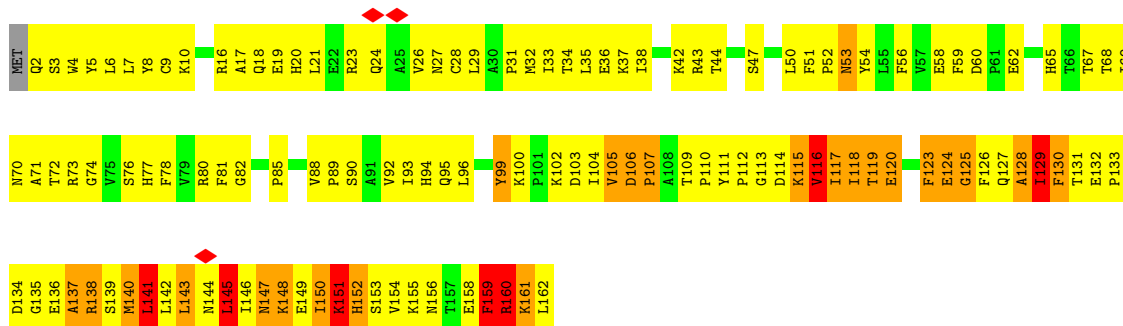


• Molecule 11: DNA-directed RNA polymerase subunit beta

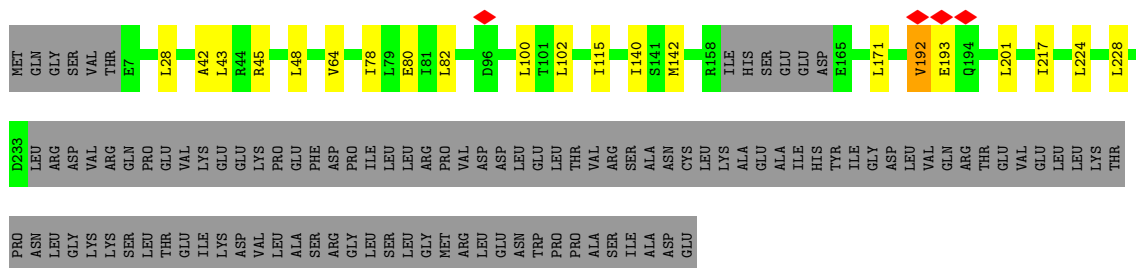


GLU

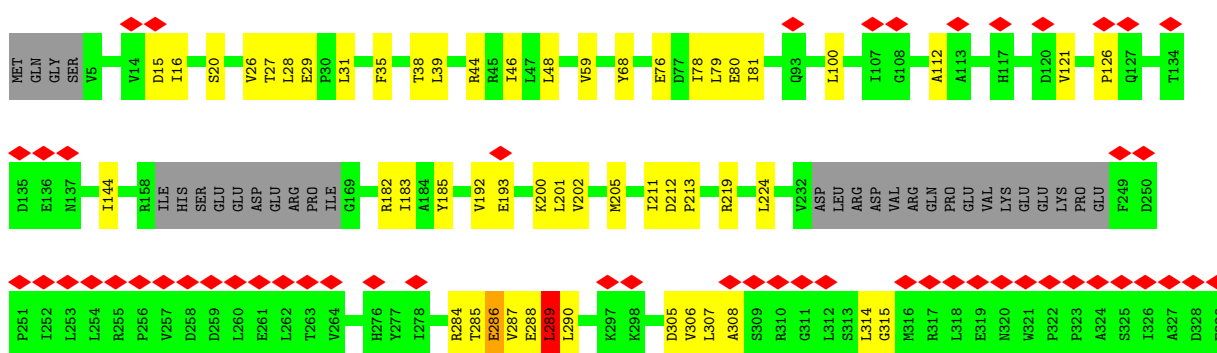
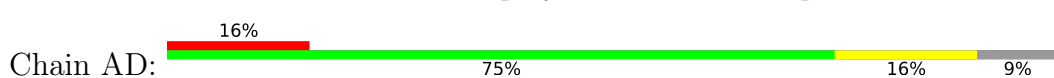
• Molecule 12: Transcription antitermination protein RfaH



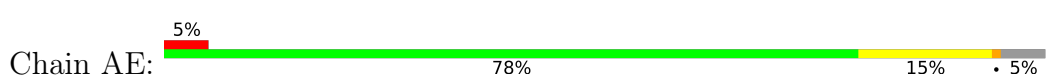
• Molecule 13: DNA-directed RNA polymerase subunit alpha

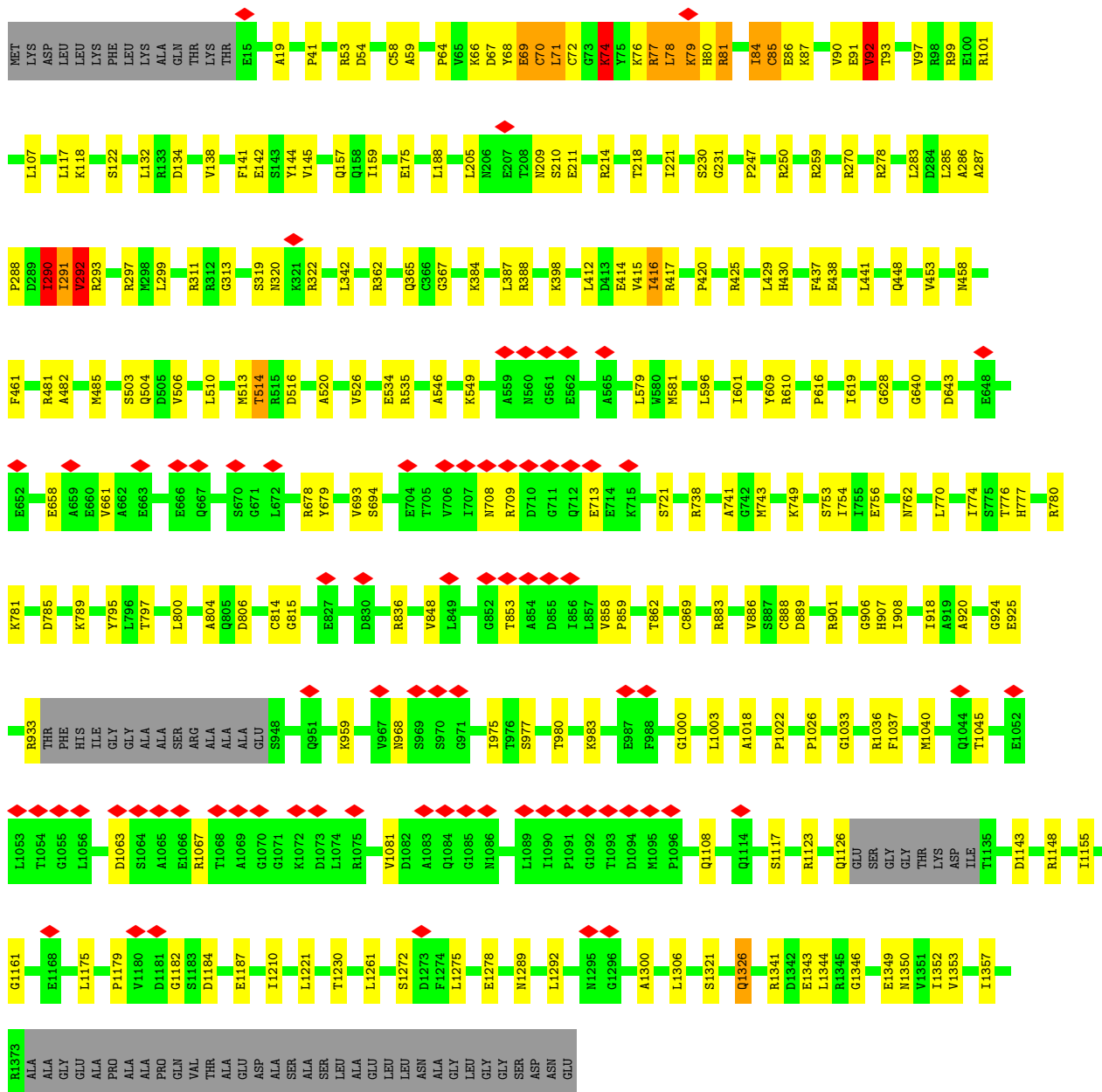


• Molecule 13: DNA-directed RNA polymerase subunit alpha

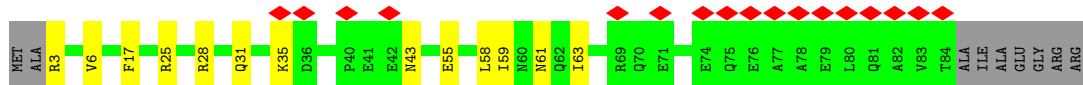
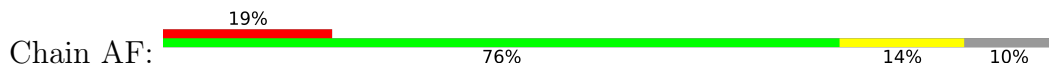


• Molecule 14: DNA-directed RNA polymerase subunit beta'



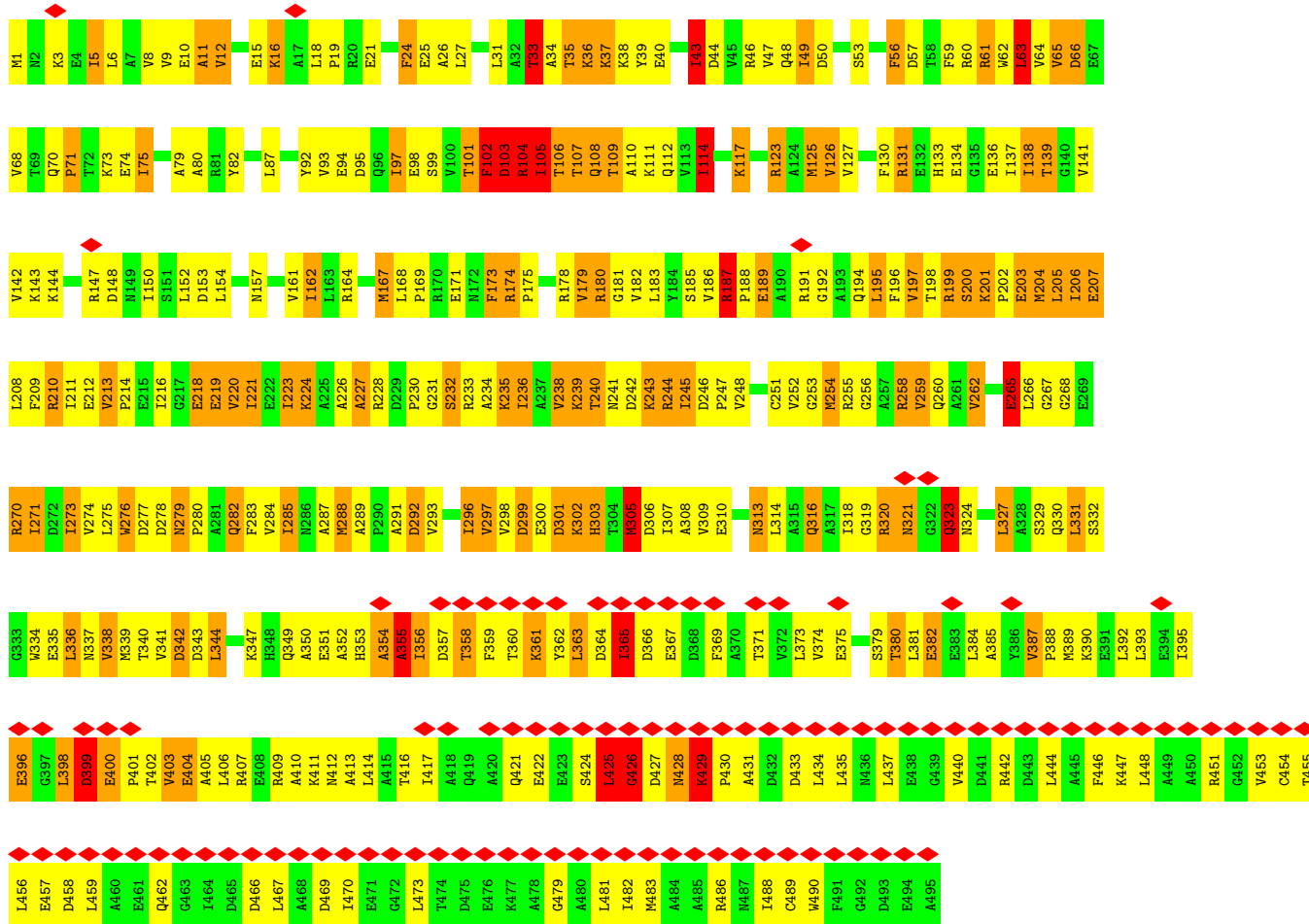


• Molecule 15: DNA-directed RNA polymerase subunit omega

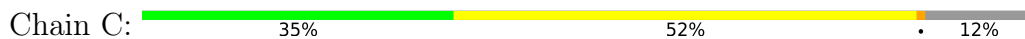


• Molecule 16: Transcription termination/antitermination protein NusA

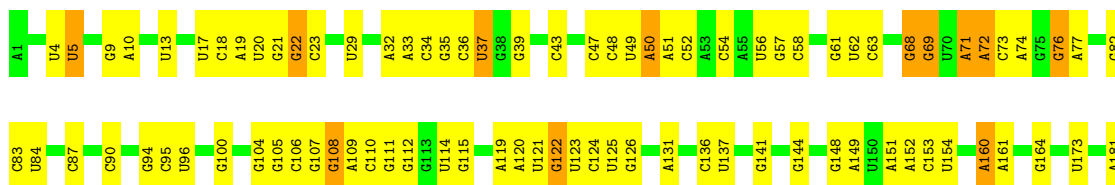




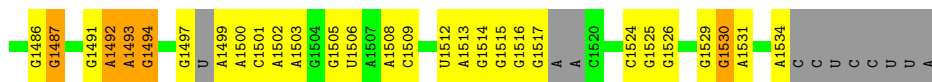
• Molecule 17: 30S ribosomal protein S18



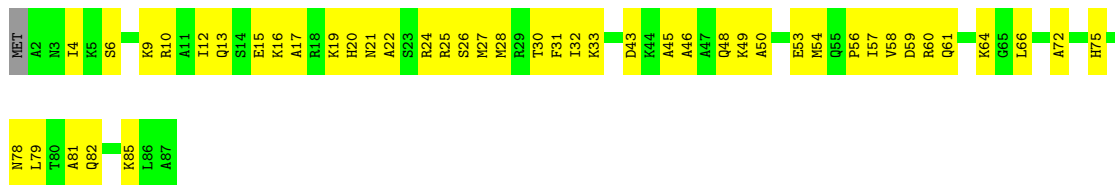
• Molecule 18: 16S rRNA



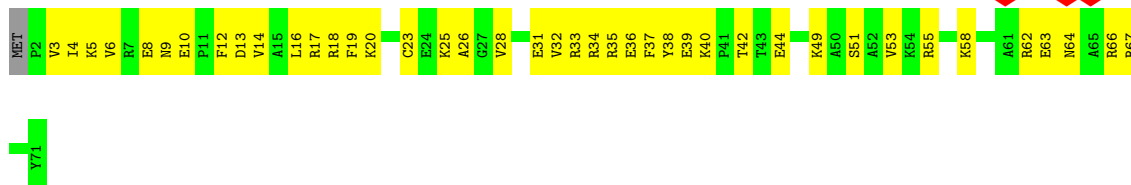
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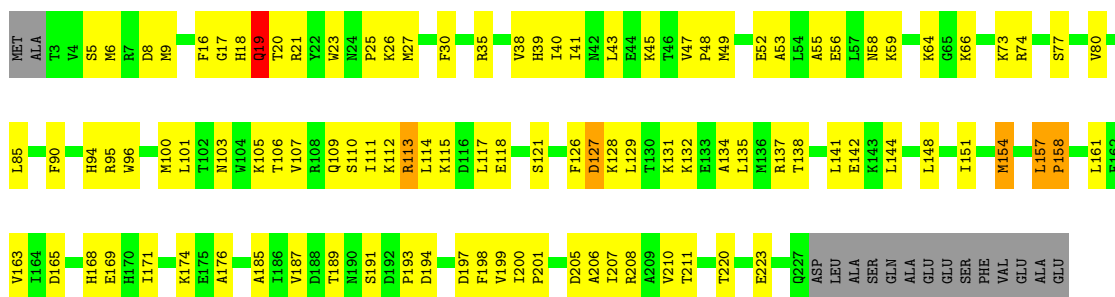
• Molecule 19: 30S ribosomal protein S20



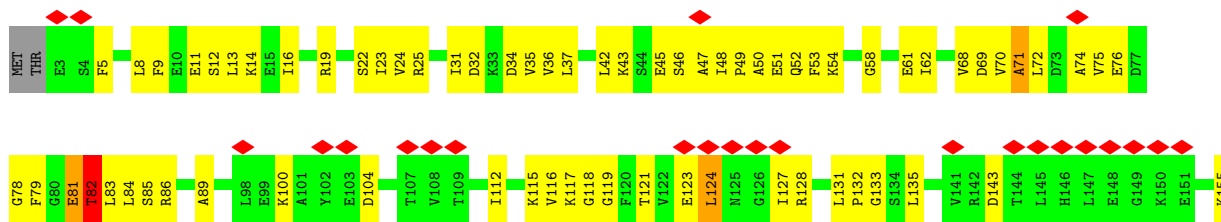
• Molecule 20: 30S ribosomal protein S21

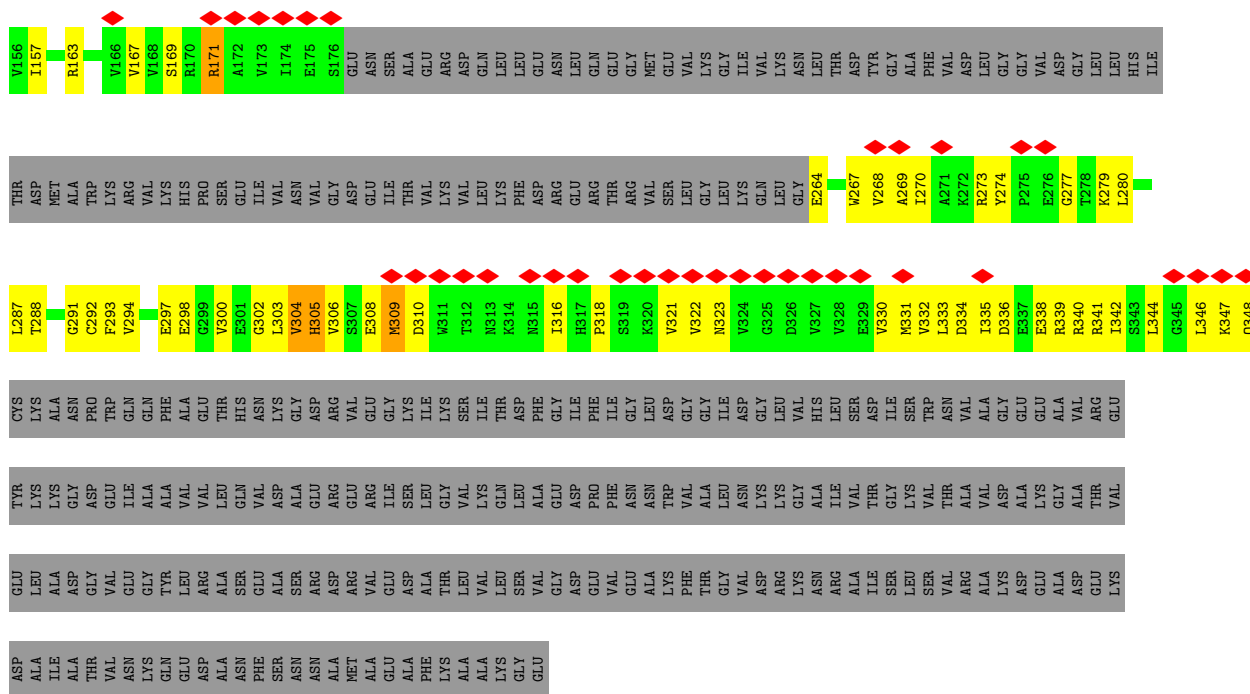


• Molecule 21: 30S ribosomal protein S2

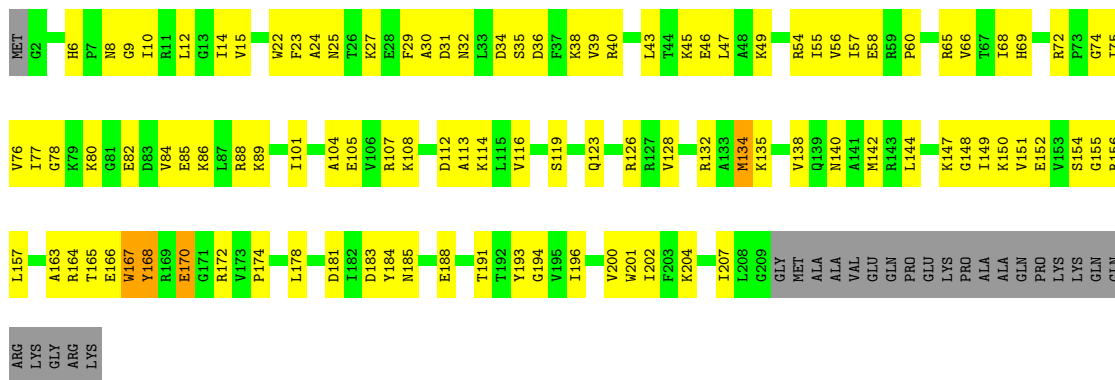


• Molecule 22: 30S ribosomal protein S1

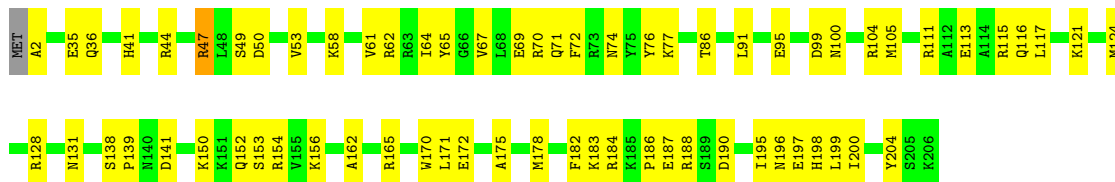




• Molecule 23: 30S ribosomal protein S3



• Molecule 24: 30S ribosomal protein S4

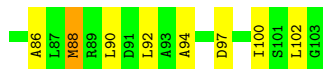


• Molecule 25: 30S ribosomal protein S5

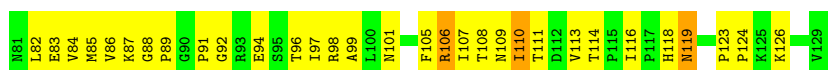
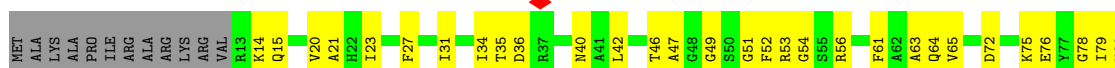




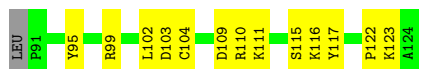
• Molecule 30: 30S ribosomal protein S10



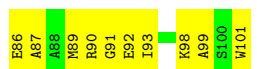
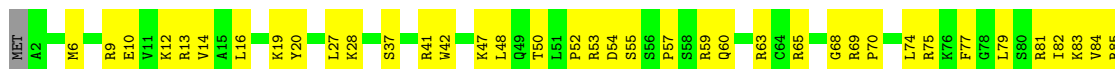
• Molecule 31: 30S ribosomal protein S11



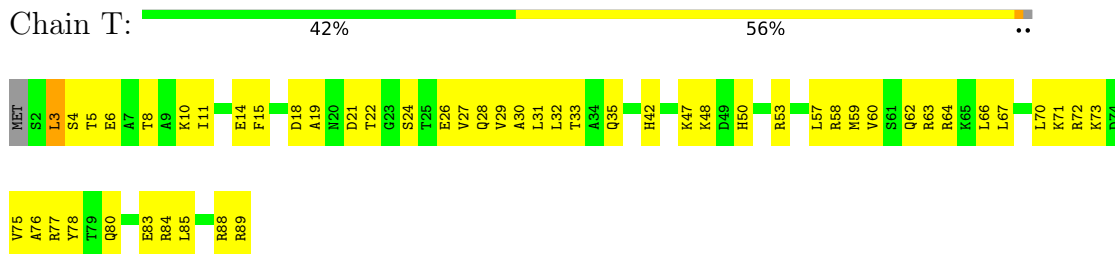
• Molecule 32: 30S ribosomal protein S12



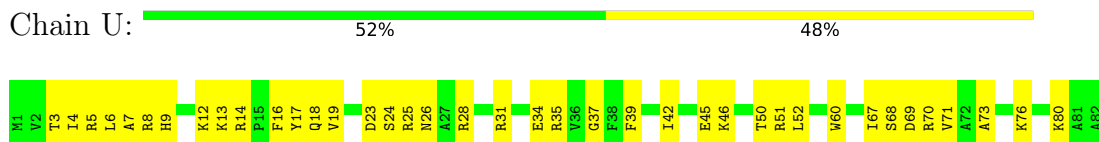
• Molecule 33: 30S ribosomal protein S14



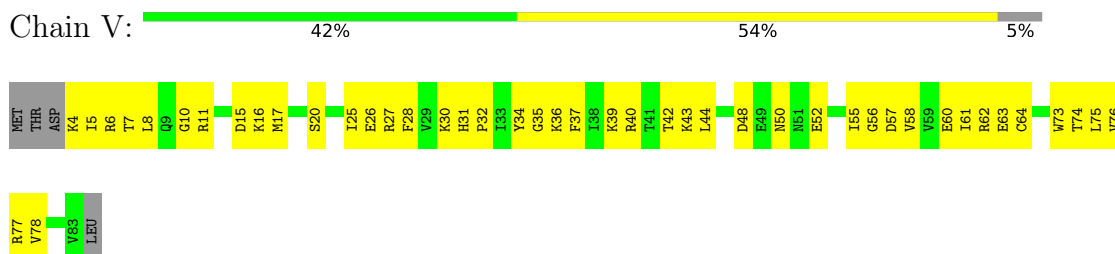
• Molecule 34: 30S ribosomal protein S15



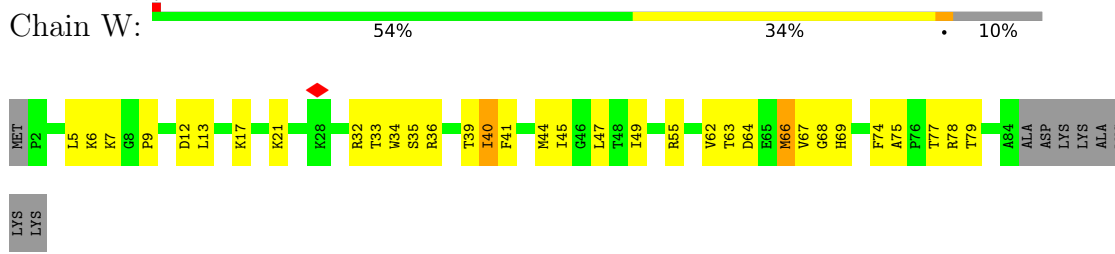
- Molecule 35: 30S ribosomal protein S16



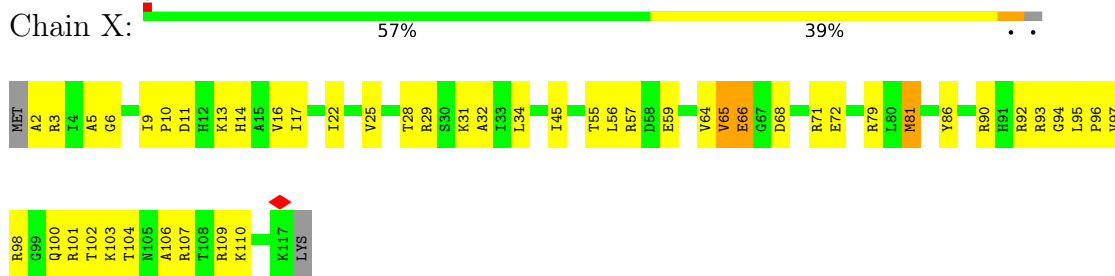
- Molecule 36: 30S ribosomal protein S17



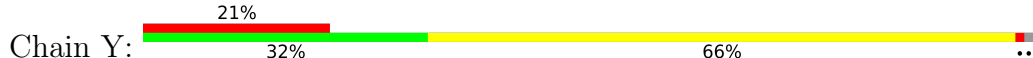
- Molecule 37: 30S ribosomal protein S19



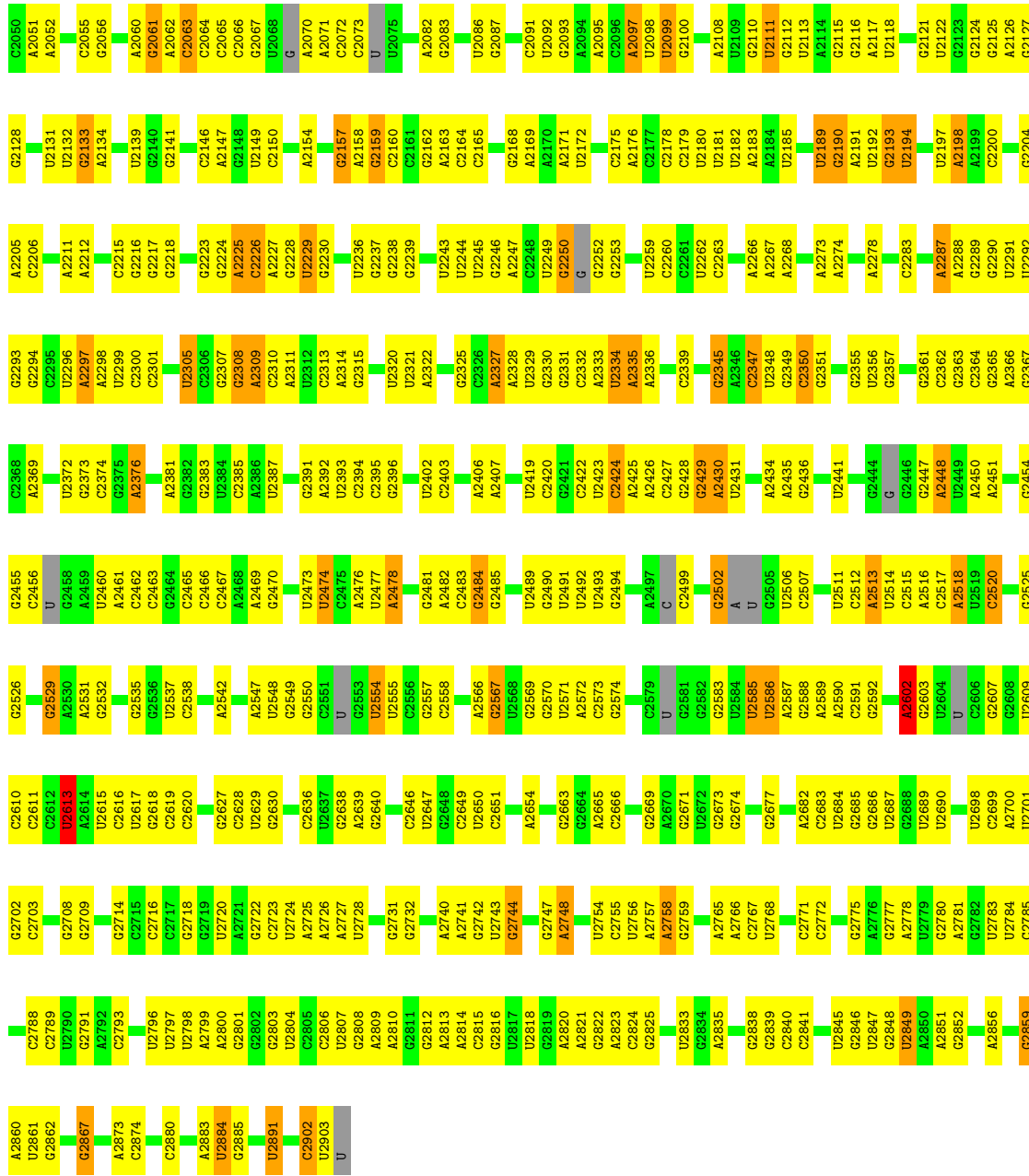
- Molecule 38: 30S ribosomal protein S13



- Molecule 39: 50S ribosomal protein L11



G1972	A1900	U1818	U1720	A1603	C1512	G1410	C1323	G1236	G1138	U1066	C994	G914	C837	U744
G1980	G1906	A1819	G1721	C1607	U1513	U4411	G1333	G1238	G1139	A1067	C995	C915	C838	G
G1982	G1907	U1820	U1729	A1608	A1515	U4412	G1334	G1238	U1140	G1068	A996	G916	U839	U
G1983	G1910	G1823	C1730	A1609	G1529	U4414	U1340	G1243	A1141	A1069	C997	A920	C840	U
A1987	U	U1825	G1731	A1610	U1554	U4415	G1341	G1243	A1142	A1070	C998	C921	U842	G748
U1991	A1912	G1826	G1738	G1613	U1554	U4416	A1342	A1246	A1144	A1071	C999	C922	A845	A750
G1992	A1913	U1827	A1754	A1614	A1535	G1417	G1343	A1247	C1145	G1074	C1005	A927	U846	A751
U1993	U	A1828	A1746	C1617	C1537	U4420	U1344	G1248	A1147	C1075	C1006	A928	A851	A752
C1996	A1916	C1830	U1747	A	G1542	G1421	C1345	U1249	G1154	C1076	C1007	U929	U852	A753
A1997	A1918	C1831	G1750	G1619	G1543	G1422	A1346	C1250	G1154	A1077	A1008	G930	U852	A754
A1998	A1919	C1832	G1753	G1622	G1546	A1427	C1348	G1252	G1160	U1078	A1009	U931	G856	A755
C1999	A1920	U1833	C1753	G1622	G1546	U4428	C1349	A1253	G1161	A1080	C1079	U931	G857	A756
G2002	G1921	G1836	A1755	U1647	C1547	G1429	C1350	G1256	G1162	U1081	U1012	G938	G858	A757
C2006	G1922	C1836	A1756	U1648	A1548	G1430	U1352	G1256	C1167	U1082	C1013	G939	G859	A761
U2007	U1923	G1839	A1757	A1650	A1549	U4431	A1353	C1257	A1168	U1083	A1014	G940	U861	A764
C2008	U1924	U1840	U1758	G1651	U1554	U4432	A1354	A1262	A1169	A1084	U1019	A941	G862	A765
A2009	C1925	G1841	C1764	A1652	C1558	G1441	G1360	G1266	C1171	A1085	A1020	A945	G869	U773
G2010	U1926	U1842	G1756	G1653	U1559	U4435	C1361	A1269	G1171	A1086	A1021	C946	U870	G774
U2011	A1927	C1843	A1757	A1654	G1560	U4436	C1362	A1270	C1172	G1087	G1022	A947	U871	G775
C2012	U1928	G1844	G1770	A1655	C1561	G1441	C1363	G1271	U1173	A1088	G1023	C948	U872	G776
A2013	G1929	U1845	A1773	C1656	U1562	U4442	G1364	G1272	A1174	A1090	G1024	G952	C873	
U2014	U1930	G1846	A1774	U1657	U1562	U4443	A1365	A1272	A1175	A1095	G1026	G953	G874	G780
A2015	C1931	U1847	C1774	G1658	C1564	U4444	G1366	A1273	G1177	A1096	A1027	G954	A878	A781
U2016	U1932	A1848	U1778	G1659	C1565	U4445	C1367	G1276	C1178	A1096	A1028	U	A879	A782
U2017	G1933	U1853	U1779	A1664	C1566	G1452	G1371	G1278	U1180	U1101	A1029	C957	G880	A783
A2020	A1936	A1854	U1783	A1666	G1567	U4452	G1378	G1279	U1181	C1102	U1033	U958	G881	G785
C2021	A1937	U1855	A1784	G1666	G1568	U4453	A1379	G1280	U1182	C1103	U1033	U959	G881	G786
U2022	U	G1856	U1785	G1667	A1569	U4454	U1379	G1281	G1186	G1106	G1036	A960	U885	G787
C2023	U1940	U1857	A1786	A1668	A1570	U4455	G1380	G1282	U1187	U1107	G1038	C961	G885	A788
C2024	U1944	U1858	A1786	G1674	A1571	U4456	A1383	G1283	U1188	U1108	A1039	G962	G885	A789
C2025	G1945	G1862	C1790	A1676	U1572	U4467	A1384	C1289	U1189	G1109	A1040	C964	G888	A800
U2026	U1946	U1863	G1791	A1677	U1578	U4468	A1385	C1290	A1189	A1111	G1041	C965	C890	G805
G2027	C1947	U1864	G1792	A1677	A1580	U4470	C1386	G1296	G1190	G1112	G1042	G966	G891	C806
U2028	A1953	G1869	C1793	G1681	G1581	U4477	A1387	G1296	U1196	C1114	C1044	C967	C892	U807
A	U1954	C1870	G1794	U1682	C1582	U4482	A1392	G1296	U1197	C1115	C1045	C969	U894	U811
G2031	U1955	A1871	C1795	U1683	U1584	U4488	A1393	G1296	U1198	U1119	A1046	U970	U895	C812
G2032	U1956	U1872	U1796	U1684	U1584	U4490	U1394	G1300	U1199	G1120	G1047	A973	A896	U813
U2033	C1957	G1873	U1798	G1684	C1585	U4497	A1395	A1301	C1200	C1121	C1048	G974	C897	U814
U2034	C1958	C1874	G1799	U1684	G1587	U4498	U1396	A1301	U1201	G1122	C1049	A975	C898	C815
G2035	G1959	U1875	C1800	G1695	U1588	G1500	U1397	G1310	A1204	G1125	C1053	A880	A899	G818
C2036	A1960	G1876	A1801	U1703	U1589	U1500	C1398	G1311	A1205	G1128	A1054	A900	C901	A819
A2037	C1961	C1879	A1802	G1703	A1591	G1503	C1399	U1312	G1206	G1128	G1056	A901	C901	A819
G2038	U	U1880	A1803	G1707	A1596	U1506	U1400	U1313	U1209	G1131	G1057	A901	G904	U826
U2039	U1963	C1881	A1808	U1708	A1597	U1507	A1403	C1314	G1212	U1131	U1058	A984	G907	U827
G2040	G1964	U1882	A1809	U1709	A1597	U1507	C1404	C1315	G1212	U1132	U1059	C985	G907	U828
U2041	C1965	G1883	A1810	G1710	U1599	U1508	U1405	U1318	G1223	A1133	U1060	C986	C908	
A2042	U1966	U1884	U1811	U1710	U1599	U1509	U1406	U1319	U1223	A1134	U1061	C987	A909	U832
C2043	C1967	A1885	G1811	U1714	C1600	U1509	U1406	C1320	U1224	C1135	A1061	A990	A911	A833
C2044	A1970	U1889	C1816	G1715	U1602	U1510	G1408	A1321	A1226	C1136	C1064	A990	C912	G834
G2049	U1971	A1890	G1817			G1511	U1409	A1322		G1137	U1065	G993	U913	



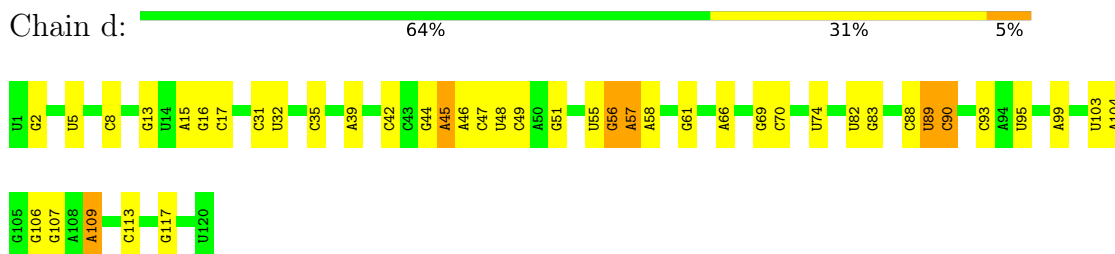
- Molecule 42: 50S ribosomal protein L27



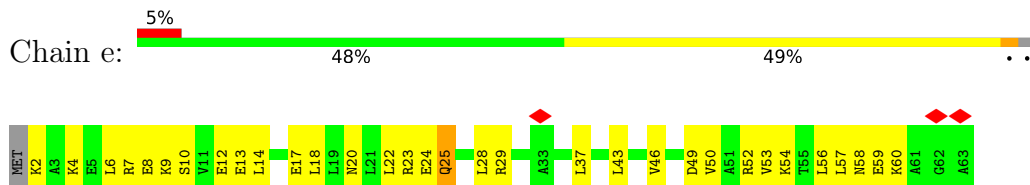
- Molecule 43: 50S ribosomal protein L28



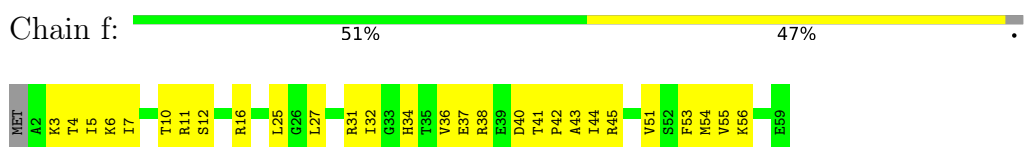
• Molecule 44: 5S rRNA



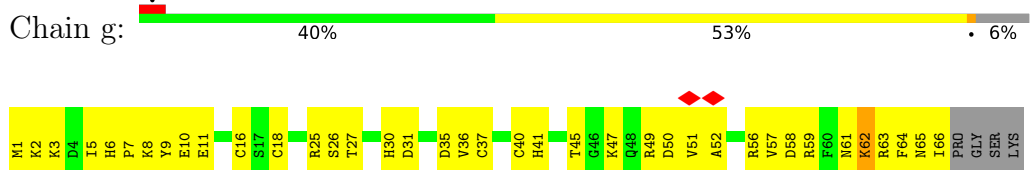
• Molecule 45: 50S ribosomal protein L29



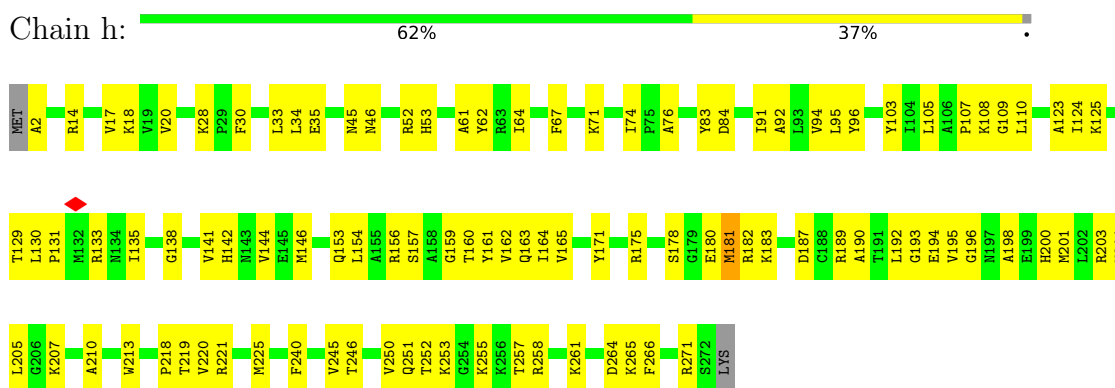
• Molecule 46: 50S ribosomal protein L30



• Molecule 47: 50S ribosomal protein L31

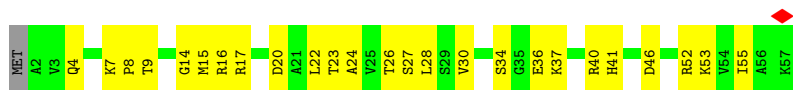


• Molecule 48: 50S ribosomal protein L2

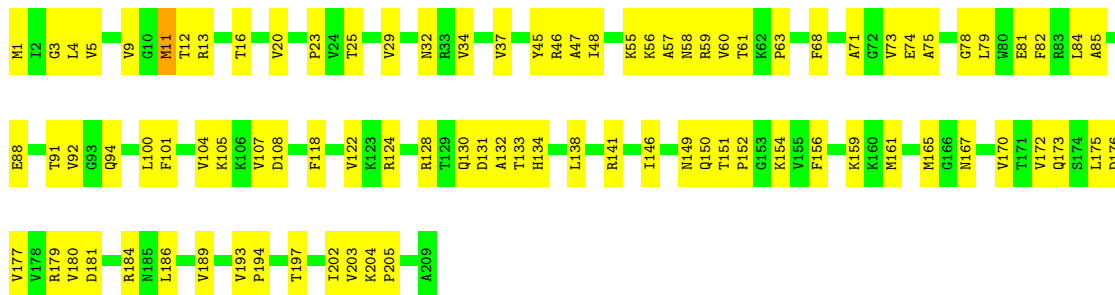
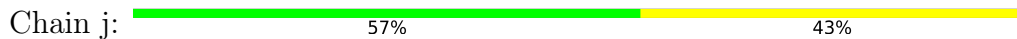


• Molecule 49: 50S ribosomal protein L32





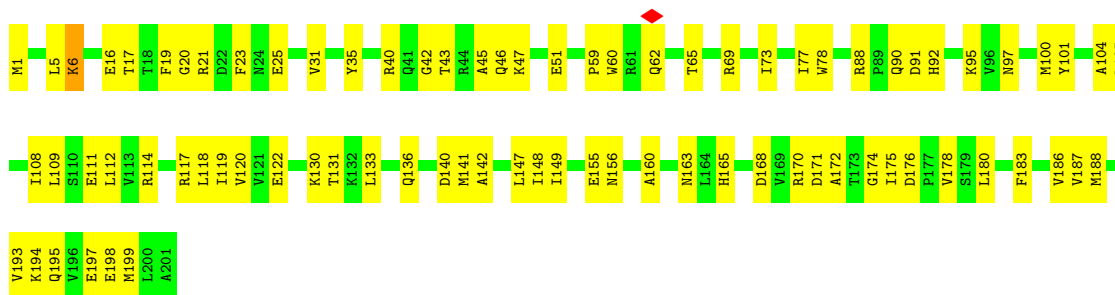
• Molecule 50: 50S ribosomal protein L3



• Molecule 51: 50S ribosomal protein L33



• Molecule 52: 50S ribosomal protein L4

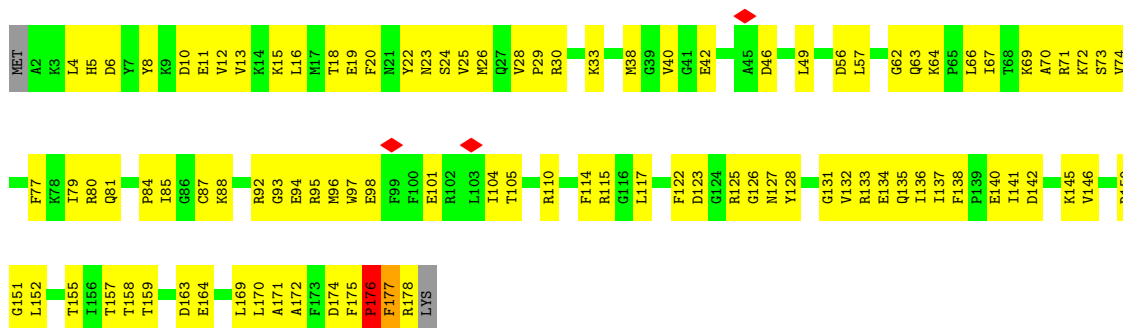


• Molecule 53: 50S ribosomal protein L34

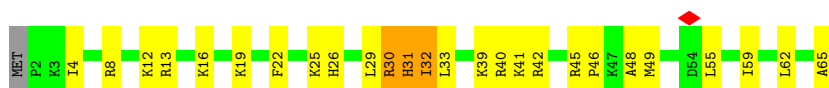


• Molecule 54: 50S ribosomal protein L5

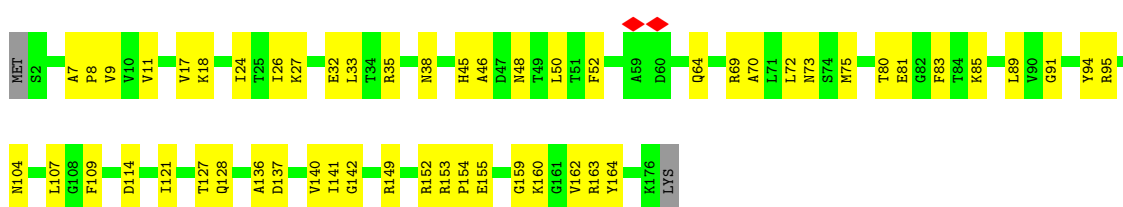




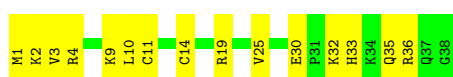
• Molecule 55: 50S ribosomal protein L35



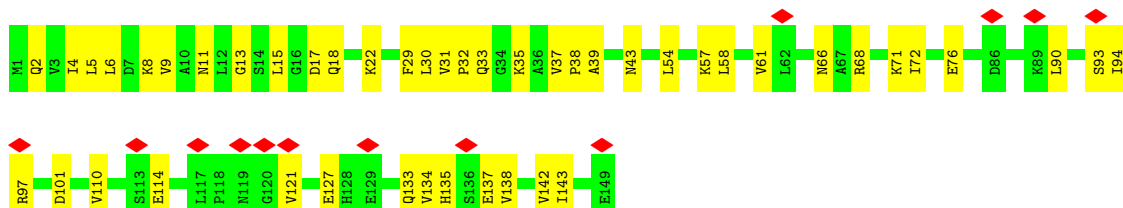
• Molecule 56: 50S ribosomal protein L6



• Molecule 57: 50S ribosomal protein L36

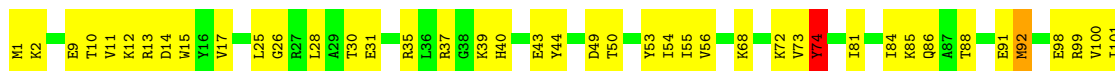


• Molecule 58: 50S ribosomal protein L9



• Molecule 59: 50S ribosomal protein L13

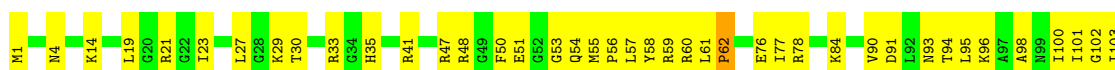




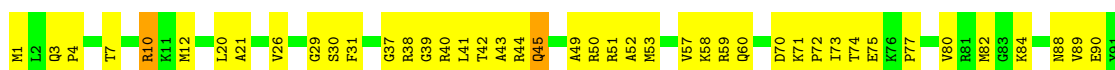
• Molecule 60: 50S ribosomal protein L14



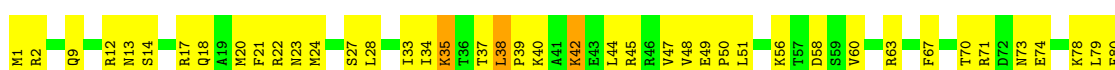
• Molecule 61: 50S ribosomal protein L15



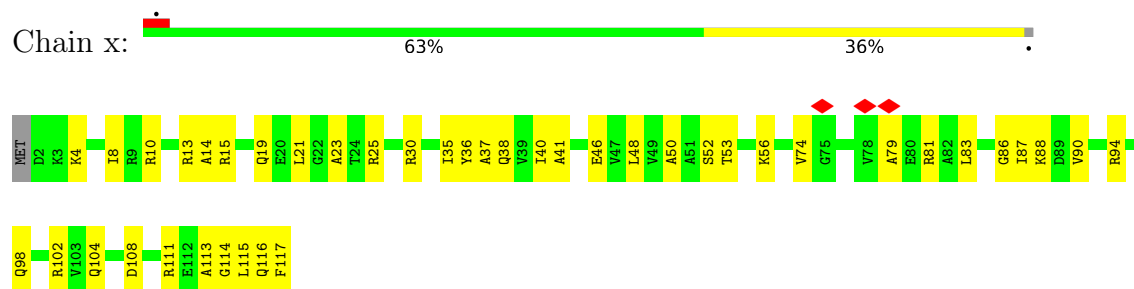
• Molecule 62: 50S ribosomal protein L16



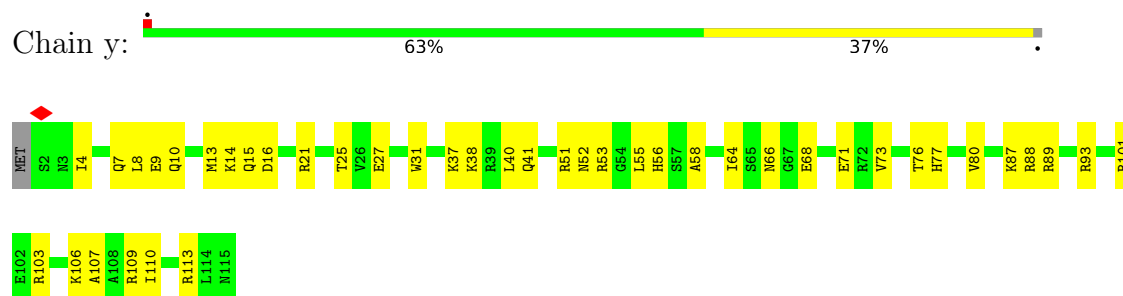
• Molecule 63: 50S ribosomal protein L17



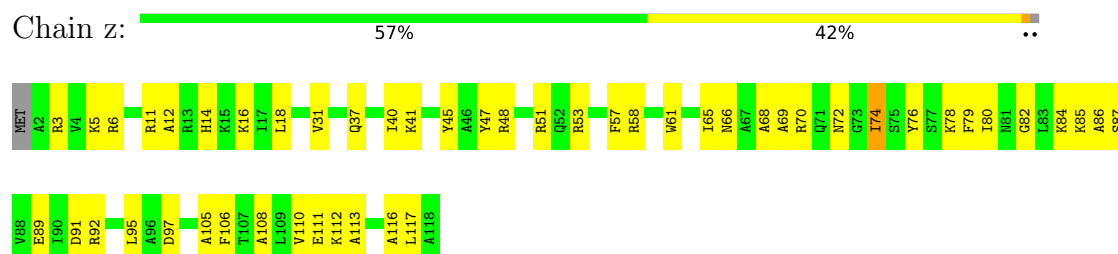
• Molecule 64: 50S ribosomal protein L18



- Molecule 65: 50S ribosomal protein L19



- Molecule 66: 50S ribosomal protein L20



4 Experimental information i

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18996	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	1250	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.035	Depositor
Minimum map value	-0.007	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0055	Depositor
Map size (Å)	531.968, 531.968, 531.968	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.039, 1.039, 1.039	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.43	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	0.49	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	0.61	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	47/5273 (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	0.37	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	0.65	3/1034 (0.3%)	0.79	3/1375 (0.2%)
30	P	0.48	0/800	0.66	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	0.48	0/657	0.63	0/881
37	W	0.56	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	0.40	0/304
41	a	0.30	0/69247	0.43	10/107985 (0.0%)
42	b	0.42	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	0.68	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	0.50	1/2121 (0.0%)	0.58	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	0.63	0/576
52	l	0.51	1/1571 (0.1%)	0.62	0/2113
53	m	0.45	0/380	0.56	0/498
54	n	0.46	0/1434	0.66	1/1926 (0.1%)
55	o	0.51	0/513	0.71	1/676 (0.1%)
56	p	0.41	0/1333	0.62	2/1805 (0.1%)
57	q	0.46	0/303	0.64	0/397
58	r	0.28	0/1122	0.48	0/1515
59	s	0.70	2/1152 (0.2%)	0.74	2/1551 (0.1%)
60	t	0.52	0/955	0.75	3/1279 (0.2%)
61	u	0.43	0/1062	0.59	0/1413
62	v	0.60	1/1093 (0.1%)	0.77	3/1460 (0.2%)
63	w	0.83	3/964 (0.3%)	0.80	3/1289 (0.2%)
64	x	0.34	0/902	0.50	0/1209
65	y	0.41	0/929	0.54	0/1242
66	z	0.62	2/960 (0.2%)	0.62	0/1278
All	All	0.41	39/195004 (0.0%)	0.56	146/286850 (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 39 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	-12.79	1.10	1.49
29	O	80	ARG	CD-NE	-10.47	1.31	1.46
63	w	42	LYS	CD-CE	-9.41	1.24	1.52
25	K	45	ARG	CG-CD	7.76	1.75	1.52

The worst 5 of 146 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	AG	104	ARG	CA-C-N	17.90	154.20	121.97
16	AG	104	ARG	C-N-CA	17.90	154.20	121.97
16	AG	246	ASP	CA-C-N	14.51	137.98	119.84
16	AG	246	ASP	C-N-CA	14.51	137.98	119.84
16	AG	354	ALA	O-C-N	-13.66	107.34	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 [i](#)

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	69	0
3	2	746	811	811	59	0
4	3	788	844	844	46	0
5	4	753	780	780	85	0
6	5	726	0	392	110	0
7	6	703	0	396	34	0
8	7	772	0	384	124	0
9	9	1117	0	1155	260	0
10	A	1620	826	827	109	0
10	B	1620	814	827	110	0
11	AA	10381	0	10389	266	0
12	AB	1286	0	1302	442	0
13	AC	1698	0	1718	12	0
13	AD	2078	0	1891	41	0
14	AE	10404	0	10626	263	0
15	AF	650	0	658	14	0
16	AG	3852	0	3827	775	0
17	C	544	559	560	106	0
18	D	32703	16423	16453	734	0
19	E	669	719	719	81	0
20	F	589	629	629	59	0
21	G	1760	1785	1787	154	0
22	H	1730	1454	1455	163	0
23	I	1636	1710	1710	154	0
24	J	1643	1707	1707	86	0
25	K	1152	1196	1195	127	0
26	L	848	846	846	105	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	92	0
30	P	790	831	831	111	0
31	Q	877	887	887	97	0
32	R	939	1001	1001	93	0
33	S	805	844	844	76	0
34	T	714	734	734	94	0
35	U	649	666	666	62	0
36	V	648	691	691	69	0
37	W	663	688	688	46	0
38	X	900	964	965	109	0
39	Y	1032	0	1088	214	0
40	Z	227	0	237	31	0
41	a	61841	31077	31120	1312	0
42	b	582	599	599	47	0
43	c	625	652	652	36	0
44	d	2569	1301	1301	41	0
45	e	501	531	531	43	0
46	f	448	488	488	38	0
47	g	522	520	520	68	0
48	h	2082	2154	2154	137	0
49	i	444	459	458	49	0
50	j	1565	1617	1616	120	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	155	0
55	o	504	572	572	51	0
56	p	1313	1358	1358	72	0
57	q	302	343	343	25	0
58	r	1111	1148	1148	53	0
59	s	1129	1162	1162	124	0
60	t	946	1023	1023	105	0
61	u	1053	1129	1129	77	0
62	v	1074	1157	1157	121	0
63	w	951	994	994	100	0
64	x	892	923	923	47	0
65	y	917	962	962	51	0
66	z	947	1020	1019	80	0
67	AE	1	0	0	0	0
68	AE	2	0	0	3	0
All	All	181653	98639	132794	7661	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 7661 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:425:LEU:CD2	16:AG:429:LYS:HE2	1.21	1.64
12:AB:145:LEU:HD23	30:P:88:MET:CA	1.24	1.59
6:5:11:DA:C5'	12:AB:67:THR:HG22	1.20	1.59
16:AG:287:ALA:CA	16:AG:331:LEU:HD12	1.18	1.58
12:AB:145:LEU:HG	30:P:88:MET:CG	1.28	1.58

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
2	1	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
3	2	92/100 (92%)	87 (95%)	5 (5%)	0	100	100
4	3	101/104 (97%)	98 (97%)	3 (3%)	0	100	100
5	4	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
9	9	146/165 (88%)	100 (68%)	43 (30%)	3 (2%)	5	28
11	AA	1312/1342 (98%)	1197 (91%)	114 (9%)	1 (0%)	48	82
12	AB	159/162 (98%)	106 (67%)	42 (26%)	11 (7%)	1	10
13	AC	217/329 (66%)	203 (94%)	12 (6%)	2 (1%)	14	49
13	AD	293/329 (89%)	263 (90%)	27 (9%)	3 (1%)	12	47
14	AE	1331/1407 (95%)	1212 (91%)	113 (8%)	6 (0%)	24	63
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	AG	493/495 (100%)	376 (76%)	86 (17%)	31 (6%)	1	12
17	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
19	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
20	F	68/71 (96%)	68 (100%)	0	0	100	100
21	G	223/241 (92%)	212 (95%)	10 (4%)	1 (0%)	30	67
22	H	255/557 (46%)	182 (71%)	66 (26%)	7 (3%)	4	24
23	I	206/233 (88%)	193 (94%)	13 (6%)	0	100	100
24	J	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
25	K	154/167 (92%)	145 (94%)	8 (5%)	1 (1%)	21	58
26	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	47
27	M	149/179 (83%)	140 (94%)	8 (5%)	1 (1%)	18	55
28	N	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
29	O	125/130 (96%)	116 (93%)	8 (6%)	1 (1%)	16	52
30	P	97/103 (94%)	89 (92%)	8 (8%)	0	100	100
31	Q	115/129 (89%)	107 (93%)	8 (7%)	0	100	100
32	R	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
33	S	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
34	T	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
35	U	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
36	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
37	W	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
38	X	114/118 (97%)	103 (90%)	9 (8%)	2 (2%)	6	32
39	Y	139/142 (98%)	101 (73%)	38 (27%)	0	100	100
40	Z	28/121 (23%)	22 (79%)	6 (21%)	0	100	100
42	b	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
43	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
45	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
46	f	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
47	g	64/70 (91%)	62 (97%)	2 (3%)	0	100	100
48	h	269/273 (98%)	255 (95%)	14 (5%)	0	100	100
49	i	54/57 (95%)	49 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
51	k	50/55 (91%)	50 (100%)	0	0	100	100
52	l	199/201 (99%)	188 (94%)	11 (6%)	0	100	100
53	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
54	n	175/179 (98%)	161 (92%)	13 (7%)	1 (1%)	21	58
55	o	62/65 (95%)	57 (92%)	4 (6%)	1 (2%)	7	36
56	p	173/177 (98%)	162 (94%)	11 (6%)	0	100	100
57	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
58	r	147/149 (99%)	139 (95%)	8 (5%)	0	100	100
59	s	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
60	t	121/123 (98%)	114 (94%)	7 (6%)	0	100	100
61	u	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
62	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
63	w	117/127 (92%)	112 (96%)	5 (4%)	0	100	100
64	x	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
65	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
66	z	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
All	All	10058/11053 (91%)	9177 (91%)	808 (8%)	73 (1%)	20	55

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 [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	84 (100%)	0	100	100
2	1	93/93 (100%)	93 (100%)	0	100	100
3	2	81/84 (96%)	81 (100%)	0	100	100
4	3	84/85 (99%)	84 (100%)	0	100	100
5	4	78/78 (100%)	78 (100%)	0	100	100
9	9	112/123 (91%)	112 (100%)	0	100	100
11	AA	1135/1157 (98%)	1130 (100%)	5 (0%)	84	83
12	AB	141/142 (99%)	122 (86%)	19 (14%)	4	15
13	AC	186/286 (65%)	186 (100%)	0	100	100
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1122/1168 (96%)	1104 (98%)	18 (2%)	55	69
15	AF	70/75 (93%)	69 (99%)	1 (1%)	59	71
16	AG	409/409 (100%)	288 (70%)	121 (30%)	0	2
17	C	57/65 (88%)	57 (100%)	0	100	100
19	E	65/66 (98%)	65 (100%)	0	100	100
20	F	60/61 (98%)	60 (100%)	0	100	100
21	G	187/199 (94%)	187 (100%)	0	100	100
22	H	137/461 (30%)	137 (100%)	0	100	100
23	I	171/190 (90%)	171 (100%)	0	100	100
24	J	172/173 (99%)	171 (99%)	1 (1%)	78	81
25	K	119/126 (94%)	119 (100%)	0	100	100
26	L	91/116 (78%)	91 (100%)	0	100	100
27	M	124/147 (84%)	124 (100%)	0	100	100
28	N	104/105 (99%)	104 (100%)	0	100	100
29	O	105/107 (98%)	105 (100%)	0	100	100
30	P	86/90 (96%)	85 (99%)	1 (1%)	63	74
31	Q	90/99 (91%)	90 (100%)	0	100	100
32	R	101/104 (97%)	101 (100%)	0	100	100
33	S	83/84 (99%)	83 (100%)	0	100	100
34	T	76/77 (99%)	76 (100%)	0	100	100
35	U	65/65 (100%)	65 (100%)	0	100	100
36	V	74/78 (95%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	W	72/79 (91%)	72 (100%)	0	100	100
38	X	94/96 (98%)	94 (100%)	0	100	100
39	Y	109/110 (99%)	109 (100%)	0	100	100
40	Z	26/85 (31%)	26 (100%)	0	100	100
42	b	58/63 (92%)	58 (100%)	0	100	100
43	c	67/68 (98%)	67 (100%)	0	100	100
45	e	54/55 (98%)	54 (100%)	0	100	100
46	f	48/49 (98%)	48 (100%)	0	100	100
47	g	59/62 (95%)	59 (100%)	0	100	100
48	h	216/218 (99%)	216 (100%)	0	100	100
49	i	47/48 (98%)	47 (100%)	0	100	100
50	j	164/164 (100%)	164 (100%)	0	100	100
51	k	47/49 (96%)	47 (100%)	0	100	100
52	l	165/165 (100%)	165 (100%)	0	100	100
53	m	38/38 (100%)	38 (100%)	0	100	100
54	n	148/150 (99%)	148 (100%)	0	100	100
55	o	51/52 (98%)	51 (100%)	0	100	100
56	p	136/138 (99%)	136 (100%)	0	100	100
57	q	34/34 (100%)	34 (100%)	0	100	100
58	r	114/114 (100%)	114 (100%)	0	100	100
59	s	116/116 (100%)	116 (100%)	0	100	100
60	t	104/104 (100%)	104 (100%)	0	100	100
61	u	103/103 (100%)	103 (100%)	0	100	100
62	v	109/109 (100%)	109 (100%)	0	100	100
63	w	99/103 (96%)	99 (100%)	0	100	100
64	x	86/87 (99%)	86 (100%)	0	100	100
65	y	99/100 (99%)	99 (100%)	0	100	100
66	z	89/90 (99%)	89 (100%)	0	100	100
All	All	8299/9132 (91%)	8133 (98%)	166 (2%)	48	65

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 114 such sidechains are listed below:

Mol	Chain	Res	Type
21	G	39	HIS
65	y	77	HIS
29	O	5	GLN
65	y	10	GLN
59	s	86	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	8 (10%)
10	B	75/76 (98%)	29 (38%)	8 (10%)
18	D	1514/1542 (98%)	290 (19%)	21 (1%)
41	a	2859/2904 (98%)	510 (17%)	0
44	d	119/120 (99%)	15 (12%)	0
8	7	36/44 (81%)	26 (72%)	5 (13%)
All	All	4678/4762 (98%)	899 (19%)	42 (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 42 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	D	517	G
18	D	1212	U
18	D	793	U

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Mol	Chain	Res	Type
18	D	1145	A
18	D	1214	C

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.

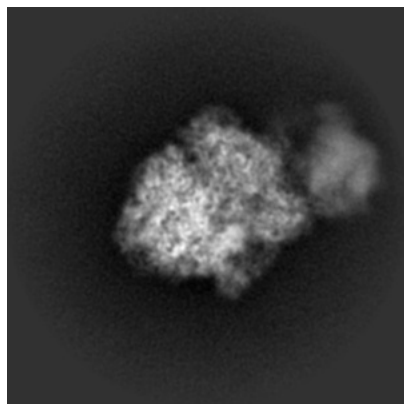
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42493. These allow visual inspection of the internal detail of the map and identification of artifacts.

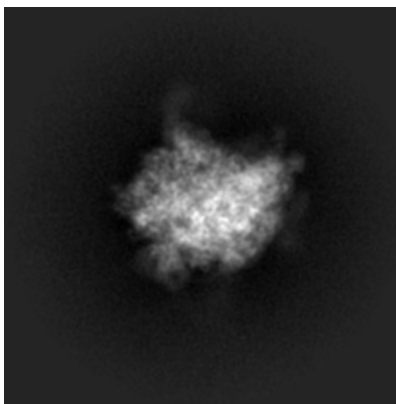
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

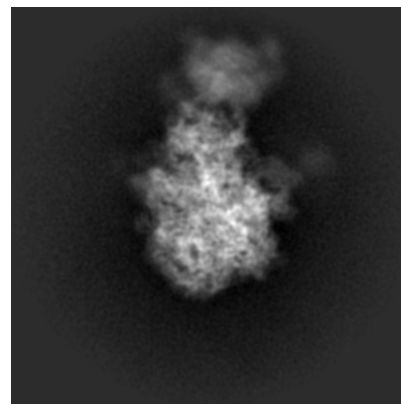
6.1.1 Primary map



X

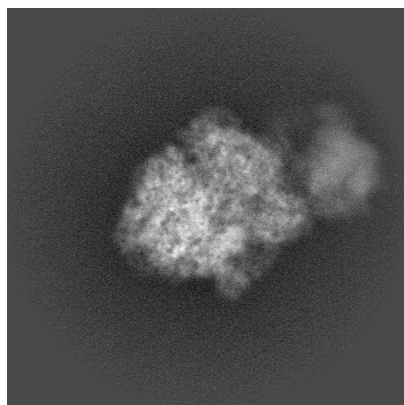


Y

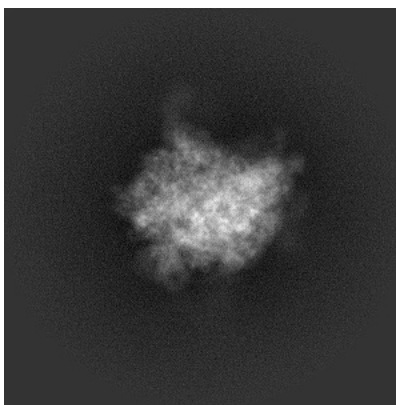


Z

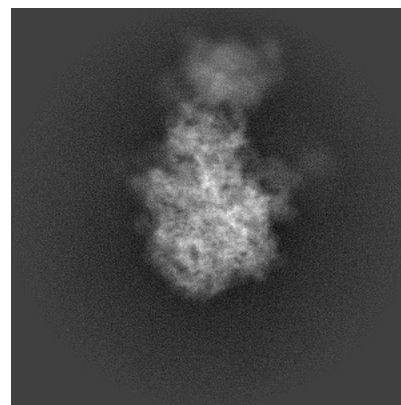
6.1.2 Raw map



X



Y

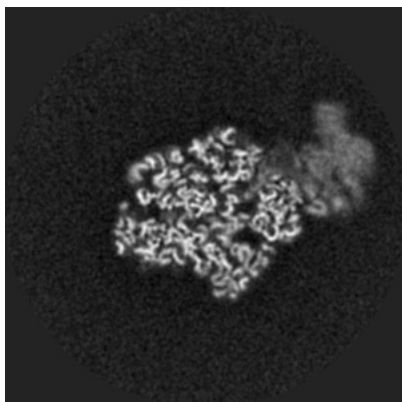


Z

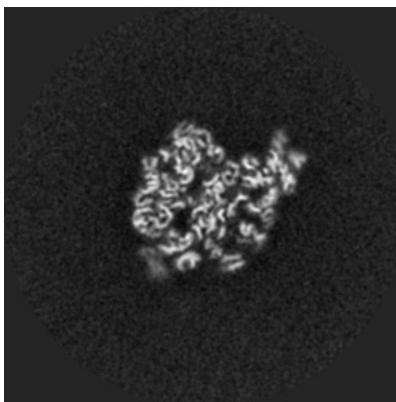
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

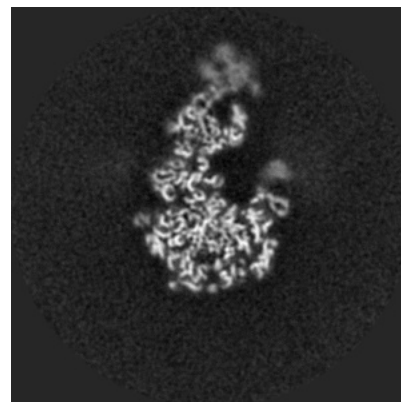
6.2.1 Primary map



X Index: 256

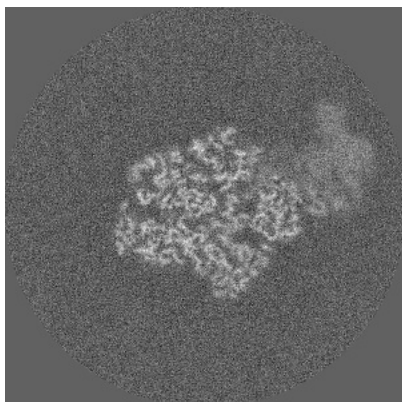


Y Index: 256

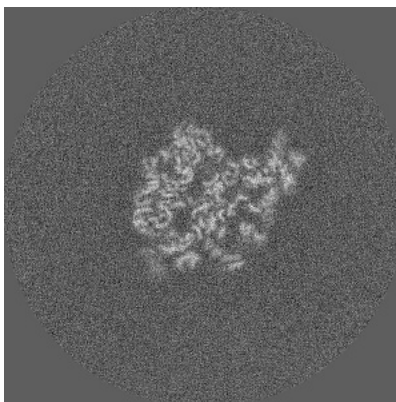


Z Index: 256

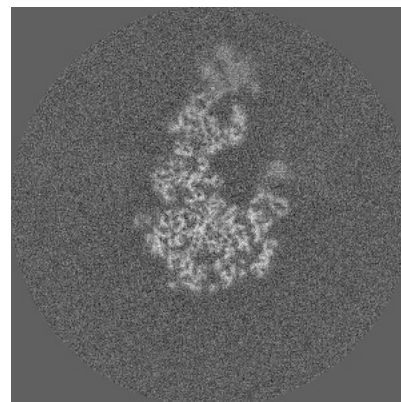
6.2.2 Raw map



X Index: 256



Y Index: 256

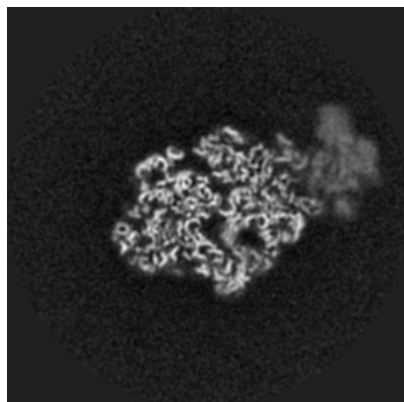


Z Index: 256

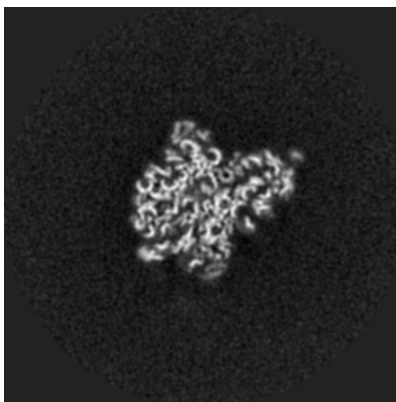
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

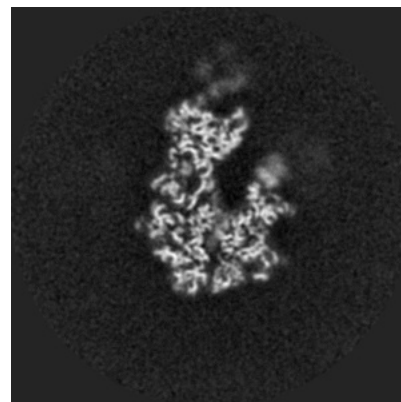
6.3.1 Primary map



X Index: 249

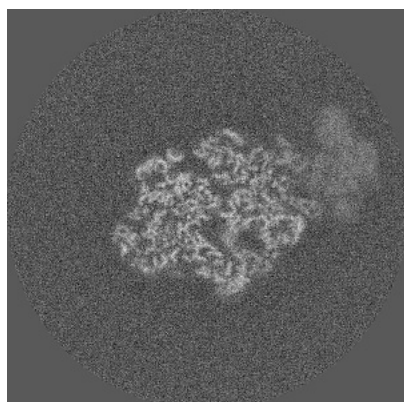


Y Index: 247

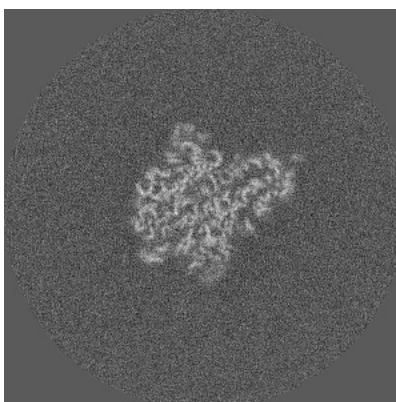


Z Index: 244

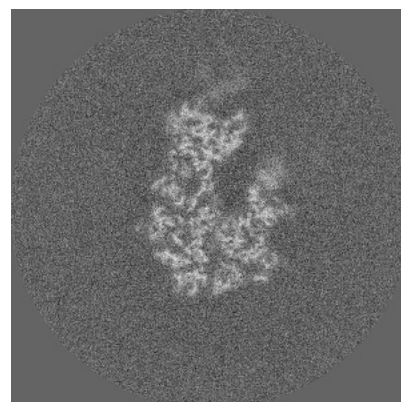
6.3.2 Raw map



X Index: 249



Y Index: 246



Z Index: 244

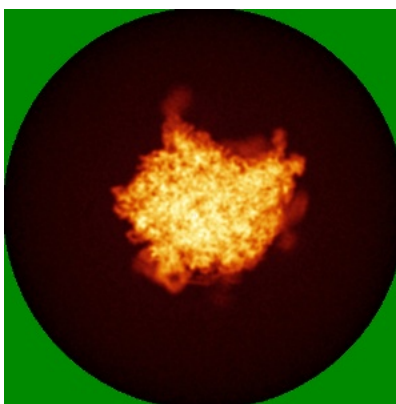
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

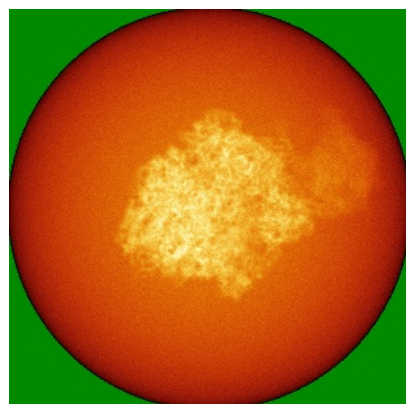


Y

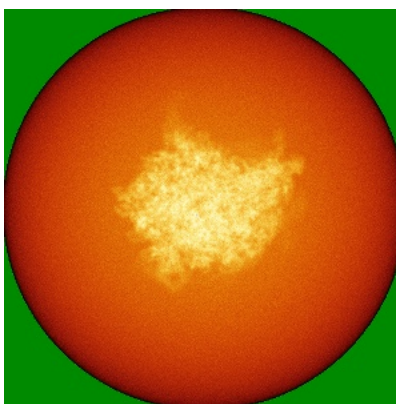


Z

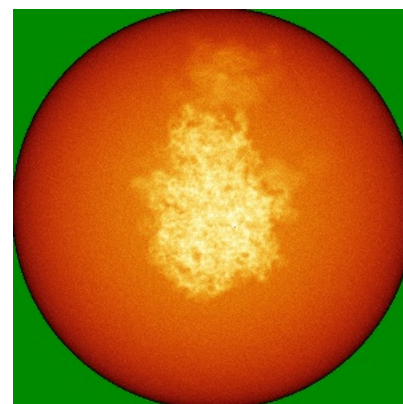
6.4.2 Raw map



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.

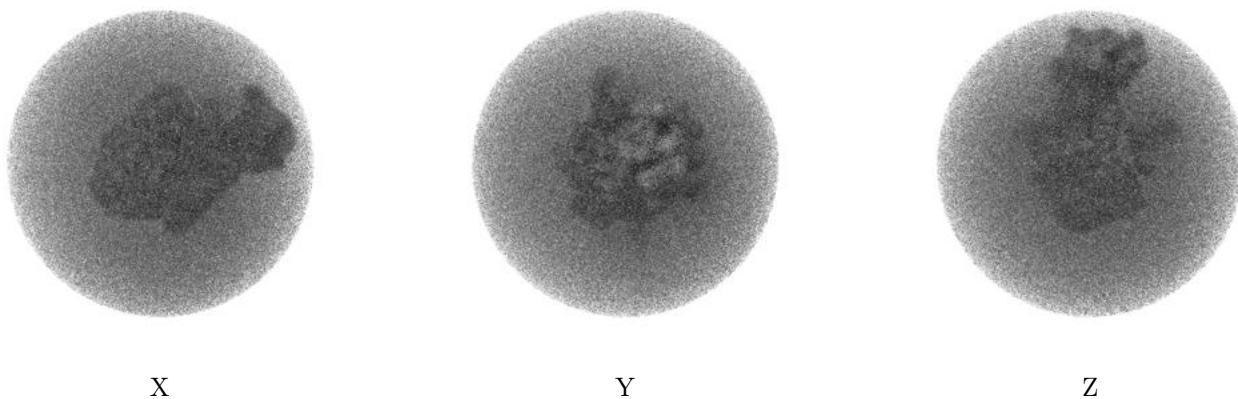
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0055. 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.

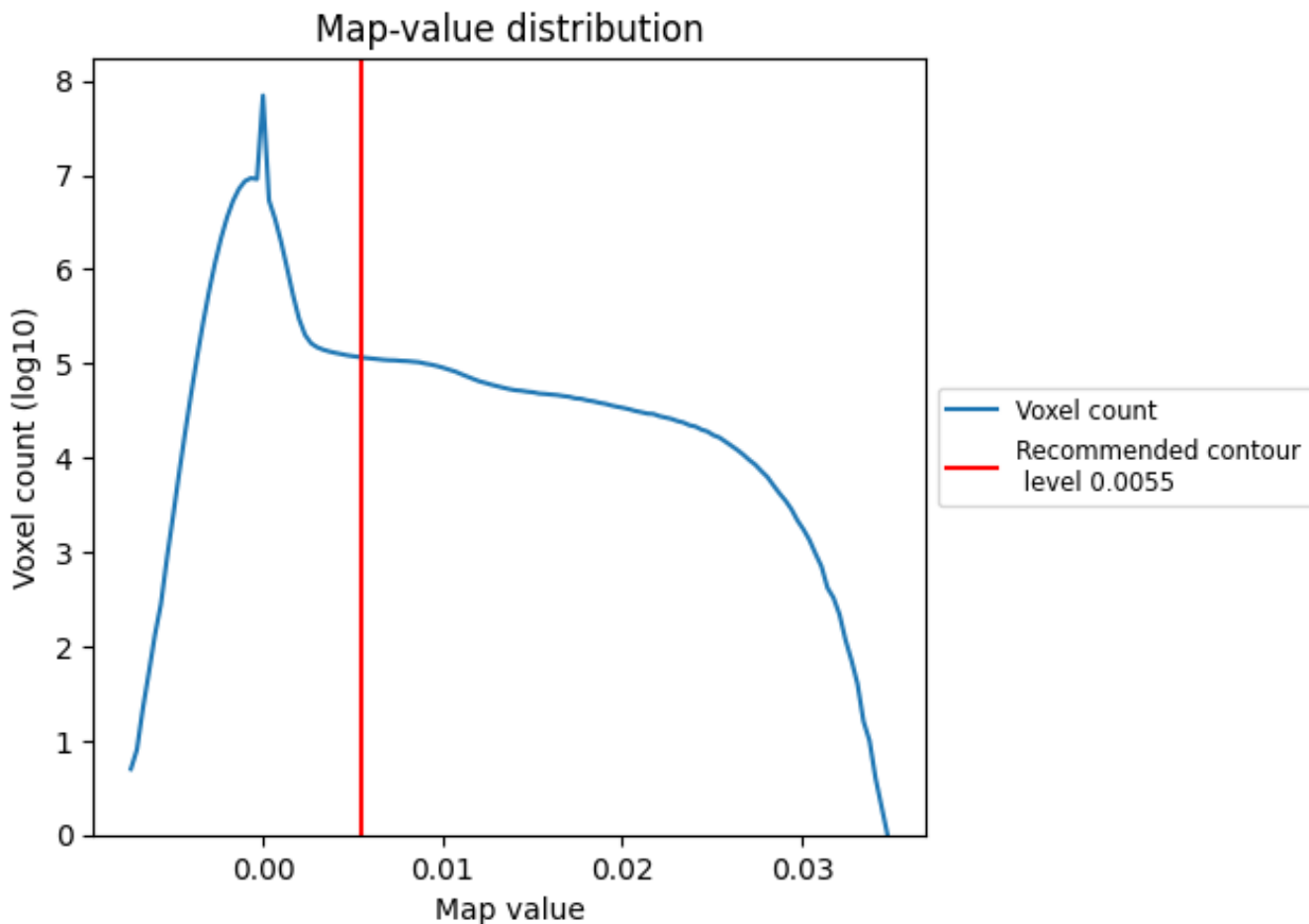
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

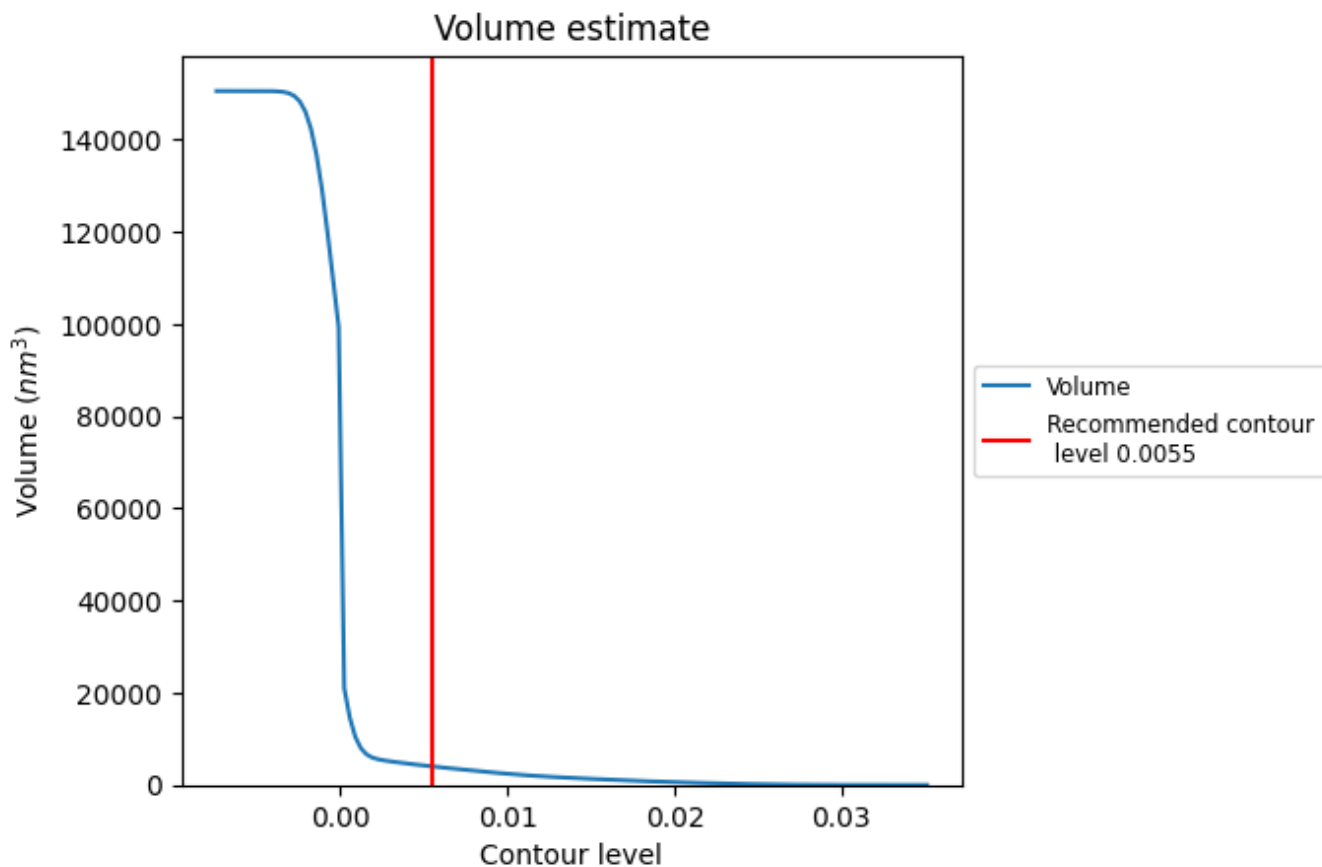
This section contains the results of statistical analysis of the map.

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.

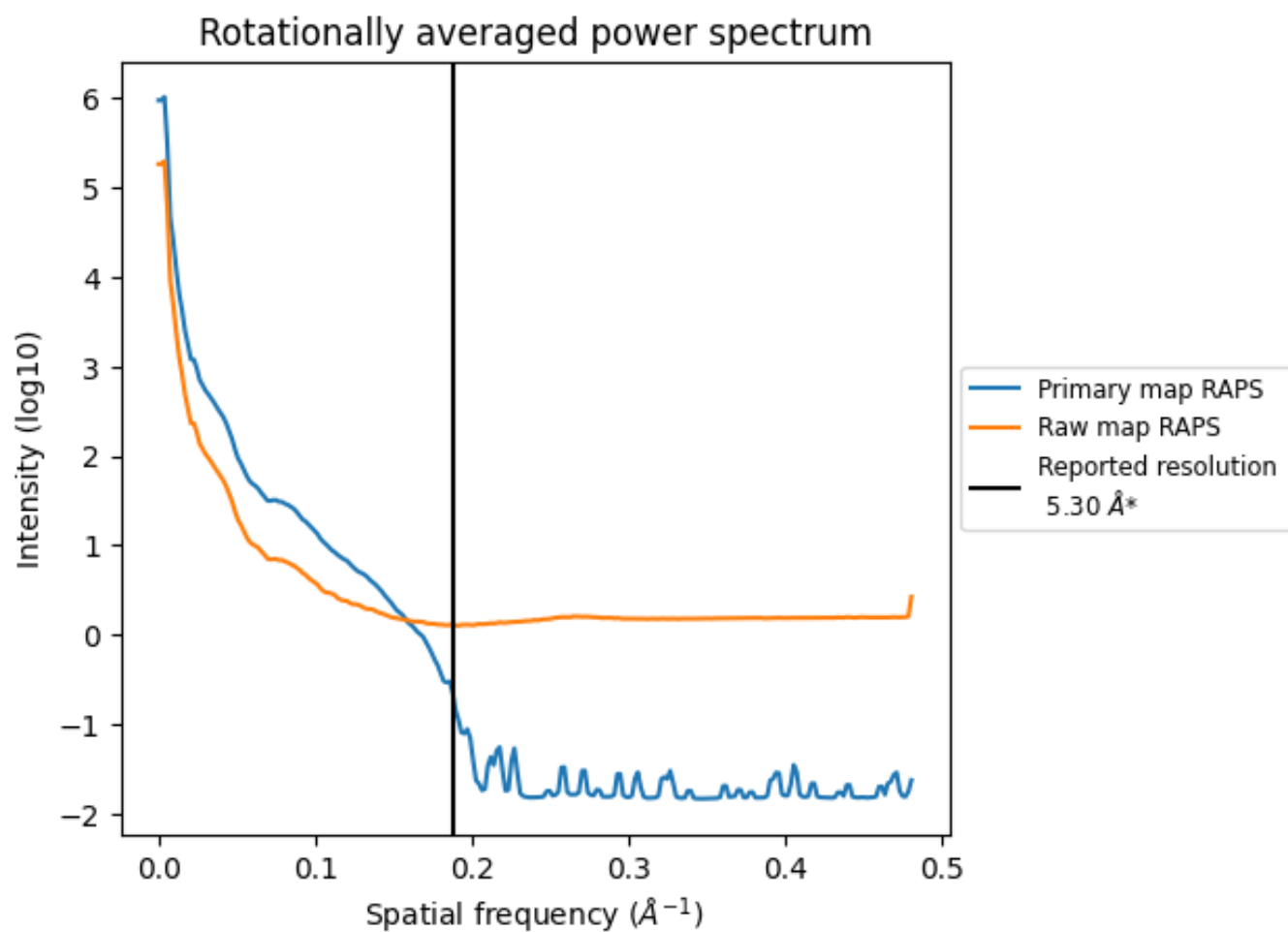
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 4028 nm^3 ; this corresponds to an approximate mass of 3638 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

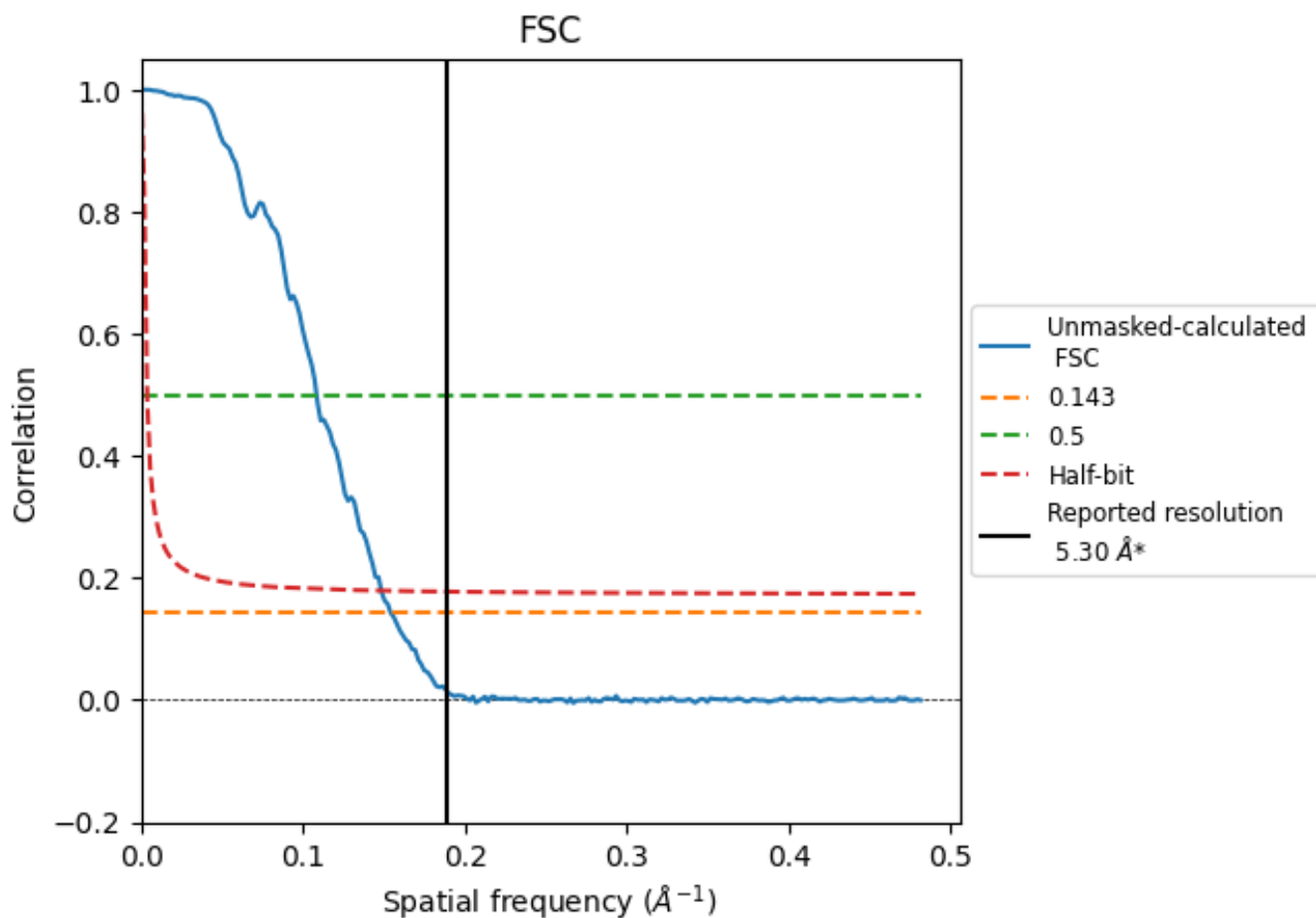


*Reported resolution corresponds to spatial frequency of 0.189 Å⁻¹

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 0.189 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.49	9.23	6.74

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.49 differs from the reported value 5.3 by more than 10 %

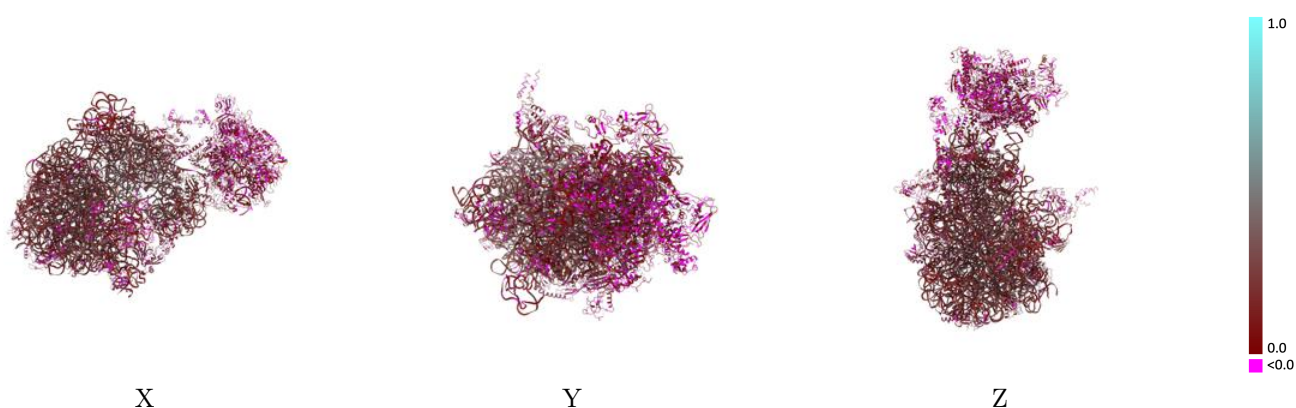
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-42493 and PDB model 8URI. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)

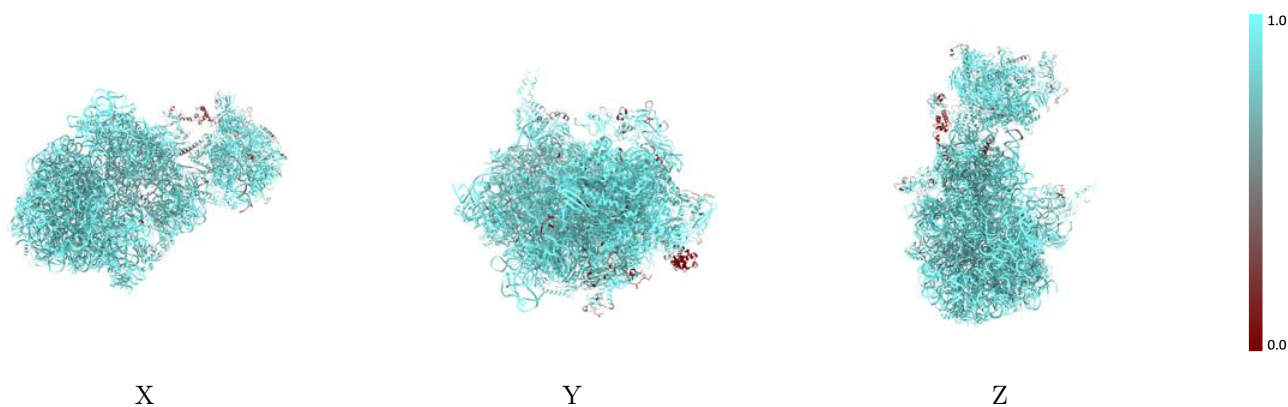
This section was not generated.

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



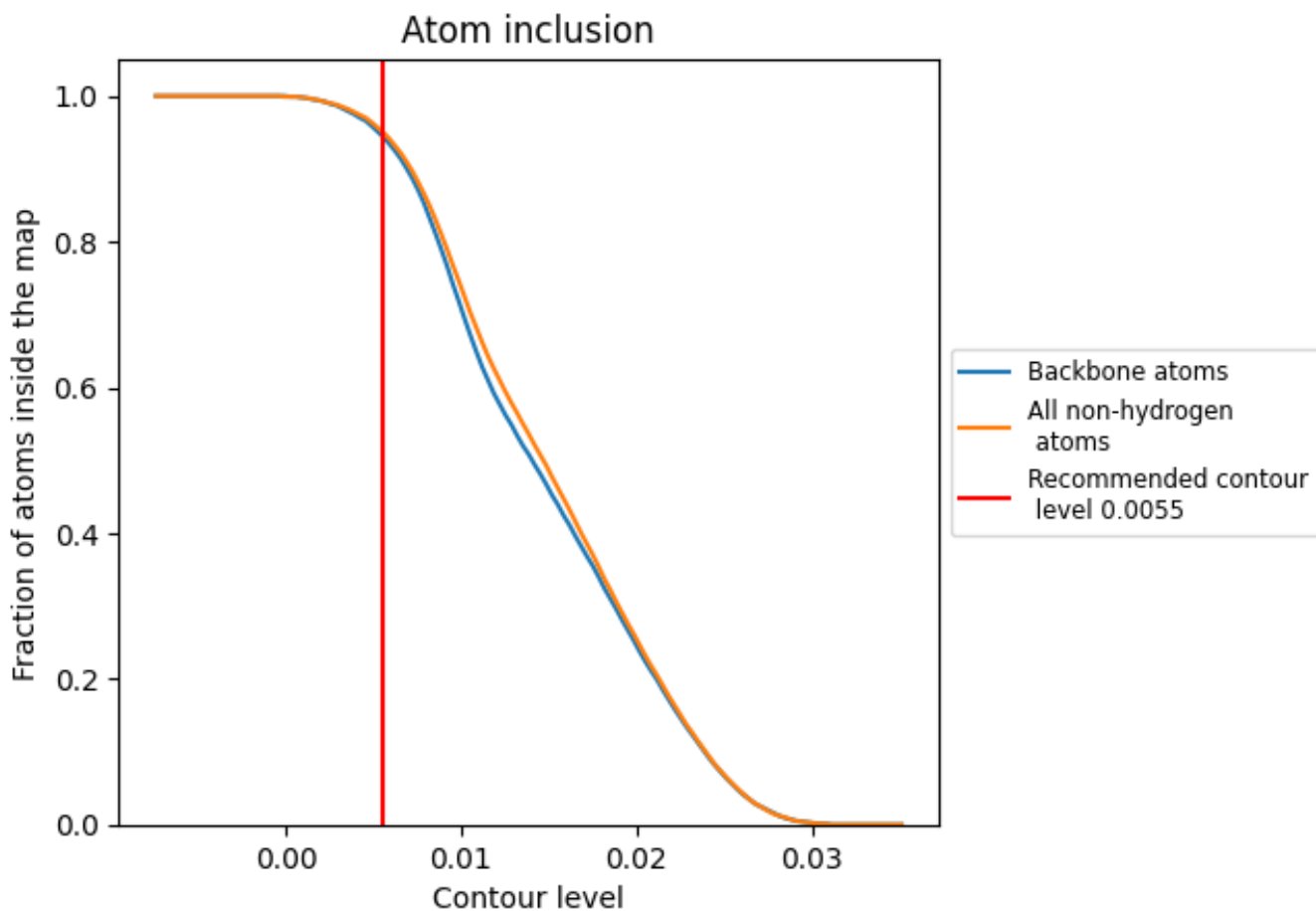
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0055).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 95% 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 (0.0055) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9510	 0.1750
0	 0.9510	 0.1540
1	 0.9380	 0.1820
2	 0.9370	 0.1440
3	 0.9550	 0.1320
4	 0.9650	 0.1620
5	 0.8790	 0.1300
6	 0.8610	 0.1270
7	 0.9300	 0.1380
9	 0.8980	 0.0990
A	 0.9790	 0.1710
AA	 0.9390	 0.0750
AB	 0.9590	 0.1230
AC	 0.9550	 0.0510
AD	 0.8040	 0.0560
AE	 0.9110	 0.0800
AF	 0.7100	 0.0880
AG	 0.7330	 0.0900
B	 0.9090	 0.1040
C	 0.9640	 0.1570
D	 0.9930	 0.2280
E	 0.9760	 0.1560
F	 0.9450	 0.1880
G	 0.9420	 0.1620
H	 0.7220	 0.0720
I	 0.9550	 0.2000
J	 0.9740	 0.1770
K	 0.9650	 0.2180
L	 0.9580	 0.1530
M	 0.9510	 0.1570
N	 0.9510	 0.1820
O	 0.9700	 0.1340
P	 0.9410	 0.1710
Q	 0.9540	 0.1570
R	 0.9830	 0.2250



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Chain	Atom inclusion	Q-score
S	 0.9660	 0.1690
T	 0.9540	 0.1570
U	 0.9590	 0.1560
V	 0.9530	 0.1690
W	 0.8960	 0.1200
X	 0.9290	 0.1440
Y	 0.7490	 0.0590
Z	 0.8720	 0.0610
a	 0.9920	 0.2160
b	 0.9510	 0.1240
c	 0.9500	 0.1670
d	 0.9890	 0.1820
e	 0.9370	 0.1270
f	 0.9680	 0.1740
g	 0.9310	 0.1180
h	 0.9520	 0.1600
i	 0.9420	 0.1980
j	 0.9680	 0.1680
k	 0.9620	 0.1350
l	 0.9260	 0.1330
m	 0.9660	 0.1790
n	 0.9410	 0.1230
o	 0.9350	 0.1260
p	 0.9640	 0.1530
q	 0.9560	 0.1570
r	 0.8380	 0.1190
s	 0.9570	 0.1790
t	 0.9350	 0.1810
u	 0.9580	 0.1390
v	 0.9740	 0.1890
w	 0.9490	 0.1640
x	 0.9500	 0.0930
y	 0.9440	 0.1650
z	 0.9730	 0.1540