



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 05:16 AM UTC

PDB ID : 8UQP / pdb_00008uqp
EMDB ID : EMD-42477
Title : Escherichia coli transcription-translation coupled complex class B (TTC-B) containing RfaH bound to ops signal, mRNA with a 24 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 : 2023-10-24
Resolution : 3.80 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

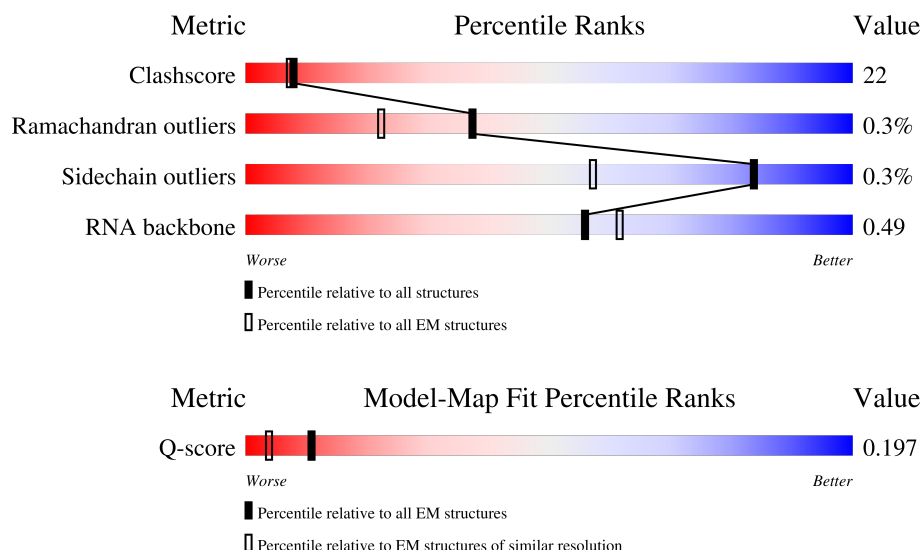
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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% 41%
2	1	110	59% 41%
3	2	100	51% 42% 6%

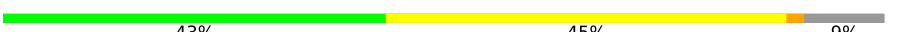
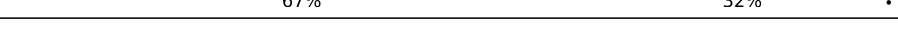
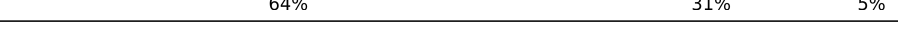
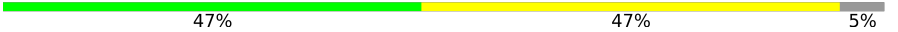
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	3	104	
5	4	94	
6	5	38	
7	6	38	
8	7	41	
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	C	75	
17	D	1542	
18	E	87	
19	F	71	
20	G	241	
21	H	557	
22	I	233	
23	J	206	
24	K	167	
25	L	135	
26	M	179	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
27	N	130	
28	O	130	
29	P	103	
30	Q	129	
31	R	124	
32	S	101	
33	T	89	
34	U	82	
35	V	84	
36	W	92	
37	X	118	
38	Y	142	
39	Z	121	
40	a	2904	
41	b	85	
42	c	78	
43	d	120	
44	e	63	
45	f	59	
46	g	70	
47	h	273	
48	i	57	
49	j	209	
50	k	55	
51	l	201	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
52	m	46	 57% 43%
53	n	179	 44% 54% ...
54	o	65	 58% 35% 5% .
55	p	177	 67% 32% .
56	q	38	 61% 39%
57	r	149	 9% 68% 32%
58	s	142	 55% 44% ..
59	t	123	 45% 54% .
60	u	144	 62% 37% .
61	v	136	 49% 49% .
62	w	127	 45% 46% . 6%
63	x	117	 63% 36% .
64	y	115	 62% 37% .
65	z	118	 57% 42% ..

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
67	ZN	AE	1502	-	-	X	-

2 Entry composition [i](#)

There are 67 unique types of molecules in this entry. The entry contains 276039 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
1	0	103	Total	C	H	N	O	S	0	0
			1655	516	839	153	145	2		

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 8 is a RNA chain called mRNA with 24 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		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AD	218	Total	C	N	O	S	0	0
			1677	1048	297	326	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 30S ribosomal protein S18.

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

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

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

- Molecule 18 is a protein called 30S ribosomal protein S20.

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

- Molecule 19 is a protein called 30S ribosomal protein S21.

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

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

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

- Molecule 21 is a protein called 30S ribosomal protein S1.

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

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

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

- Molecule 23 is a protein called 30S ribosomal protein S4.

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

- Molecule 24 is a protein called 30S ribosomal protein S5.

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

- Molecule 25 is a protein called 30S ribosomal protein S6.

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

- Molecule 26 is a protein called 30S ribosomal protein S7.

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

- Molecule 27 is a protein called 30S ribosomal protein S8.

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

- Molecule 28 is a protein called 30S ribosomal protein S9.

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

- Molecule 29 is a protein called 30S ribosomal protein S10.

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

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

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

- Molecule 31 is a protein called 30S ribosomal protein S12.

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

- Molecule 32 is a protein called 30S ribosomal protein S14.

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

- Molecule 33 is a protein called 30S ribosomal protein S15.

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

- Molecule 34 is a protein called 30S ribosomal protein S16.

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

- Molecule 35 is a protein called 30S ribosomal protein S17.

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

- Molecule 36 is a protein called 30S ribosomal protein S19.

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

- Molecule 37 is a protein called 30S ribosomal protein S13.

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

- Molecule 38 is a protein called 50S ribosomal protein L11.

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

- Molecule 39 is a protein called 50S ribosomal protein L7/L12.

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

- Molecule 40 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	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 41 is a protein called 50S ribosomal protein L27.

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

- Molecule 42 is a protein called 50S ribosomal protein L28.

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

- Molecule 43 is a RNA chain called 5S rRNA.

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

- Molecule 44 is a protein called 50S ribosomal protein L29.

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

- Molecule 45 is a protein called 50S ribosomal protein L30.

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

- Molecule 46 is a protein called 50S ribosomal protein L31.

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

- Molecule 47 is a protein called 50S ribosomal protein L2.

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

- Molecule 48 is a protein called 50S ribosomal protein L32.

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

- Molecule 49 is a protein called 50S ribosomal protein L3.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L4.

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

- Molecule 52 is a protein called 50S ribosomal protein L34.

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

- Molecule 53 is a protein called 50S ribosomal protein L5.

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

- Molecule 54 is a protein called 50S ribosomal protein L35.

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

- Molecule 55 is a protein called 50S ribosomal protein L6.

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

- Molecule 56 is a protein called 50S ribosomal protein L36.

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

- Molecule 57 is a protein called 50S ribosomal protein L9.

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

- Molecule 58 is a protein called 50S ribosomal protein L13.

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

- Molecule 59 is a protein called 50S ribosomal protein L14.

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

- Molecule 60 is a protein called 50S ribosomal protein L15.

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

- Molecule 61 is a protein called 50S ribosomal protein L16.

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

- Molecule 62 is a protein called 50S ribosomal protein L17.

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

- Molecule 63 is a protein called 50S ribosomal protein L18.

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

- Molecule 64 is a protein called 50S ribosomal protein L19.

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

- Molecule 65 is a protein called 50S ribosomal protein L20.

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

- Molecule 66 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

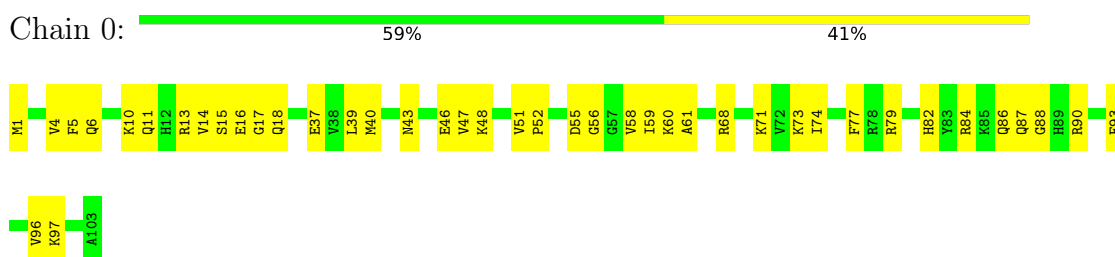
- Molecule 67 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

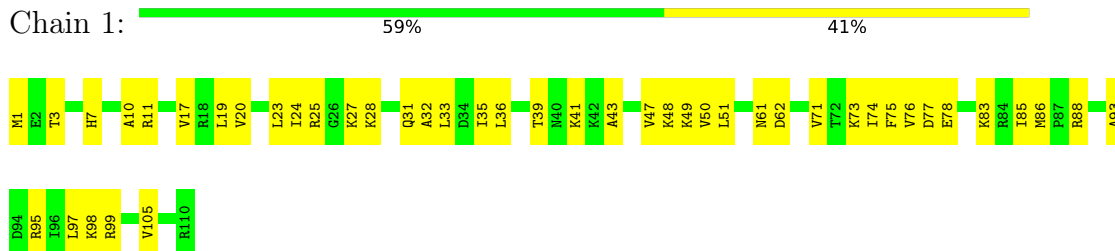
3 Residue-property plots [i](#)

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

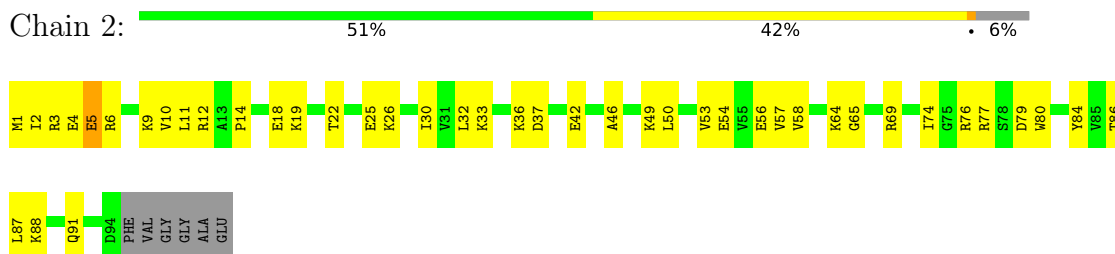
- Molecule 1: Ribosomal protein L21



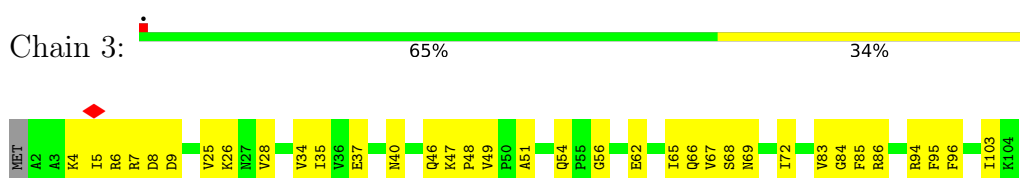
- Molecule 2: 50S ribosomal protein L22



- Molecule 3: 50S ribosomal protein L23

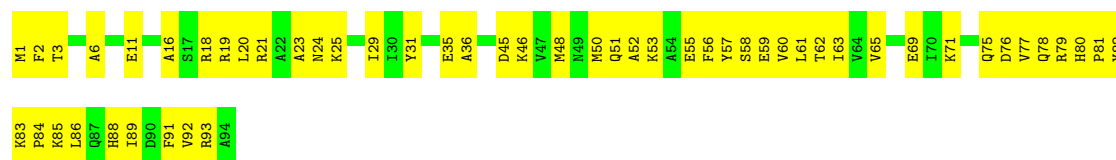


- Molecule 4: 50S ribosomal protein L24



- Molecule 5: 50S ribosomal protein L25

Chain 4: 



- Molecule 6: NT DNA ops

Chain 5: 



- Molecule 7: T DNA ops

Chain 6: 

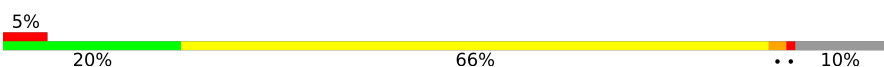


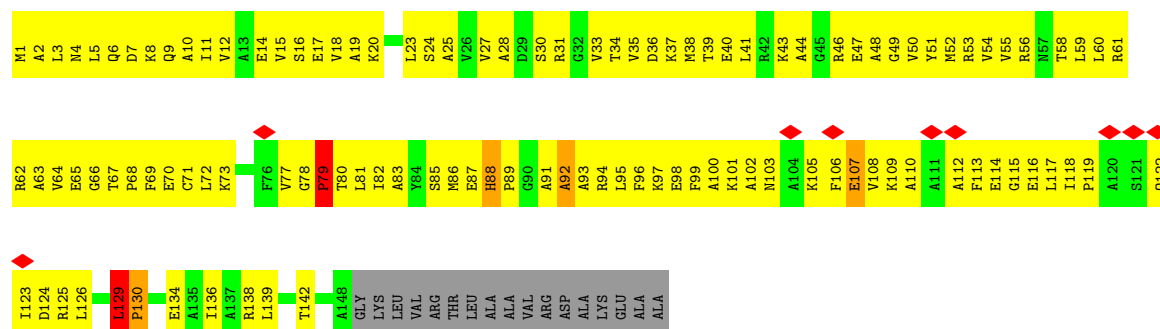
- Molecule 8: mRNA with 24 nt long spacer

Chain 7: 



- Molecule 9: 50S ribosomal protein L10

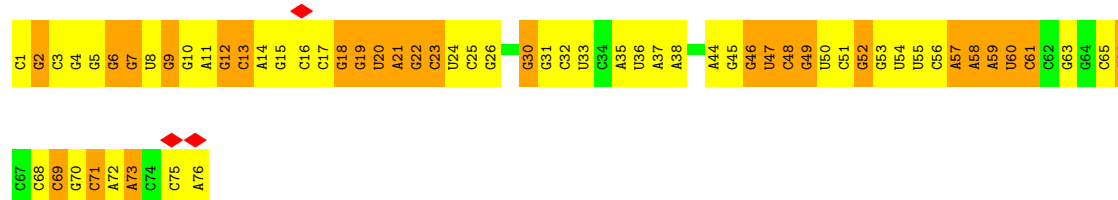
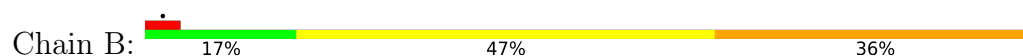
Chain 9: 



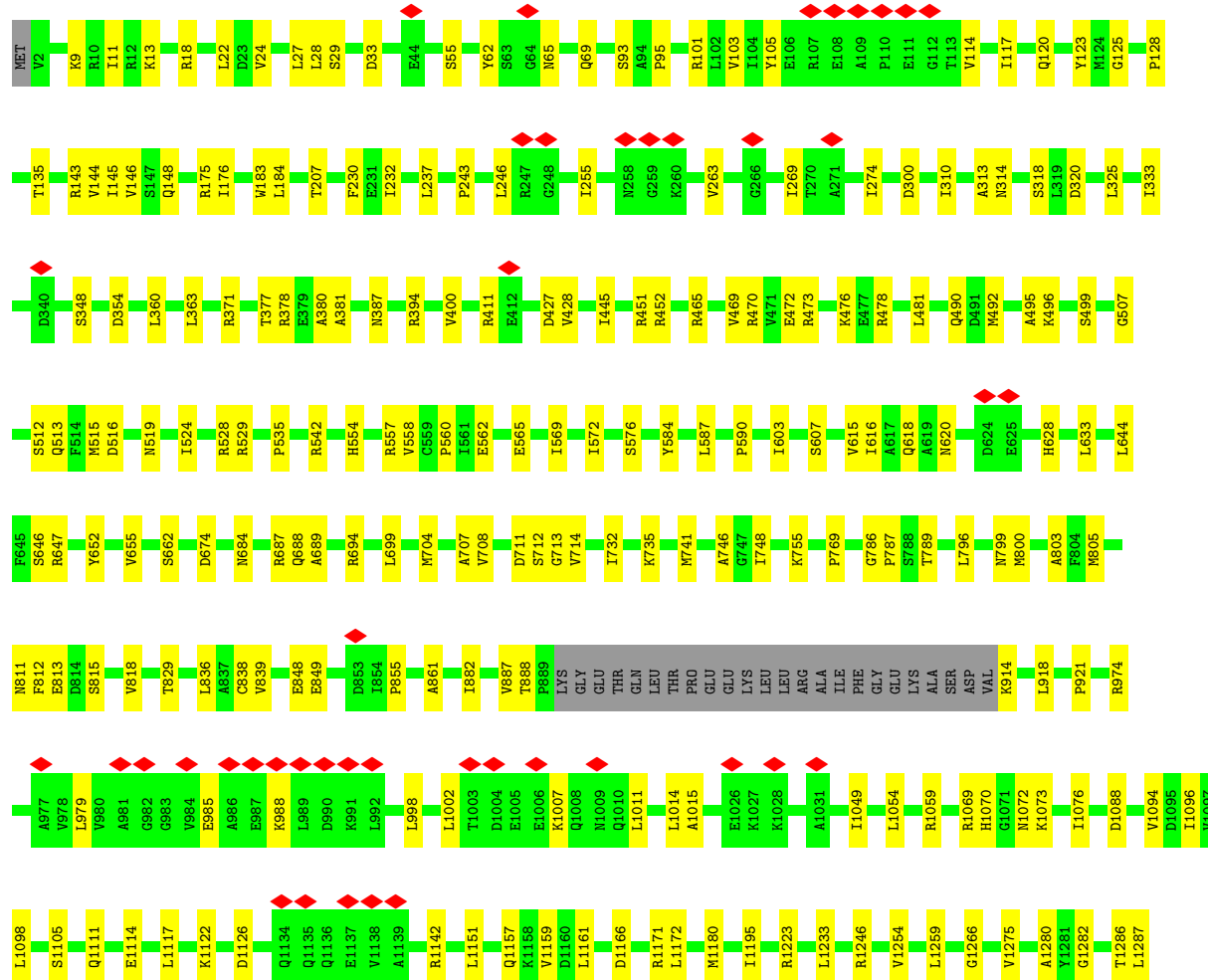
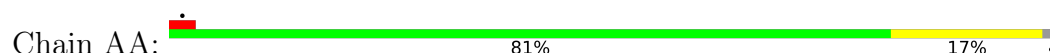
- Molecule 10: E-site and P-site fMet-tRNA

Chain A: 

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



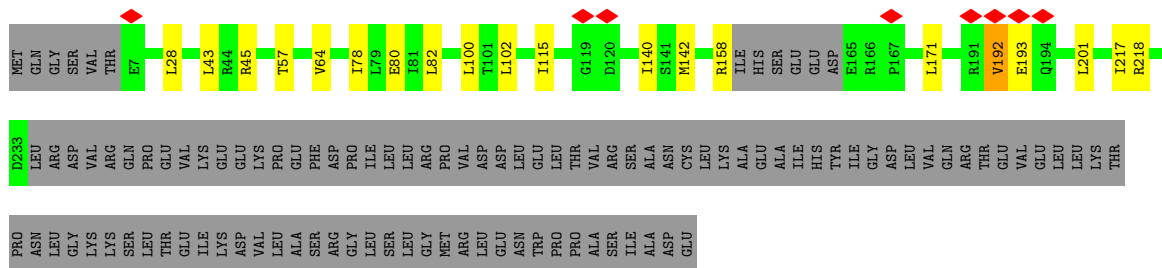
- Molecule 11: DNA-directed RNA polymerase subunit beta



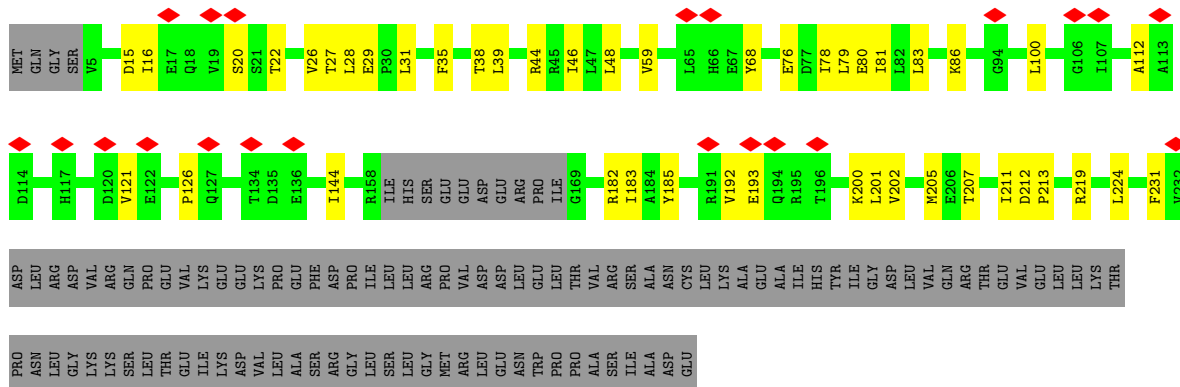
- Molecule 12: Transcription antitermination protein RfaH



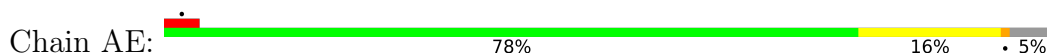
- Molecule 13: DNA-directed RNA polymerase subunit alpha

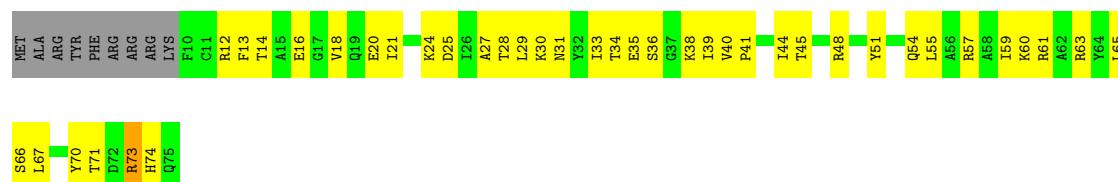


- Molecule 13: DNA-directed RNA polymerase subunit alpha



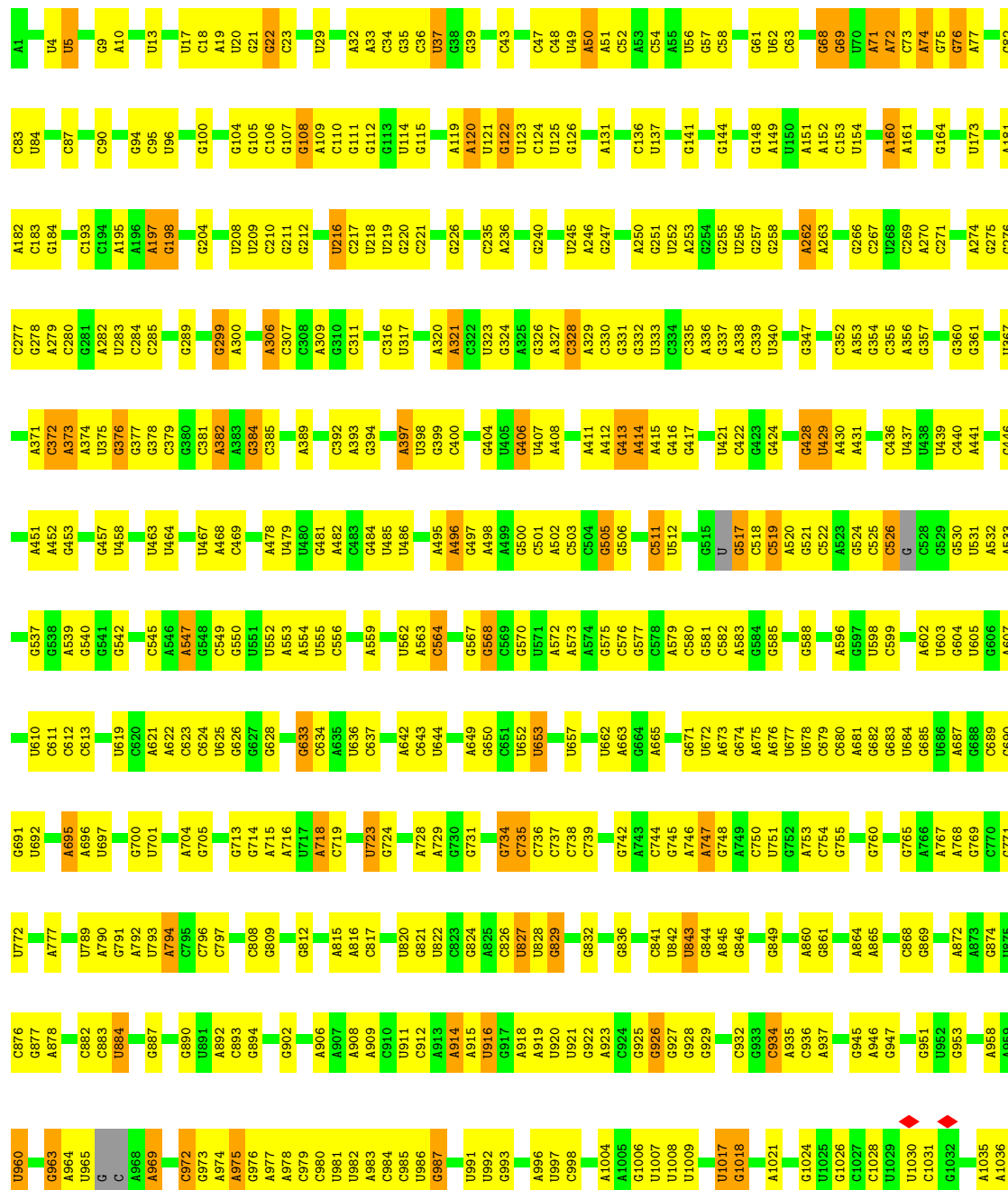
- Molecule 14: DNA-directed RNA polymerase subunit beta'

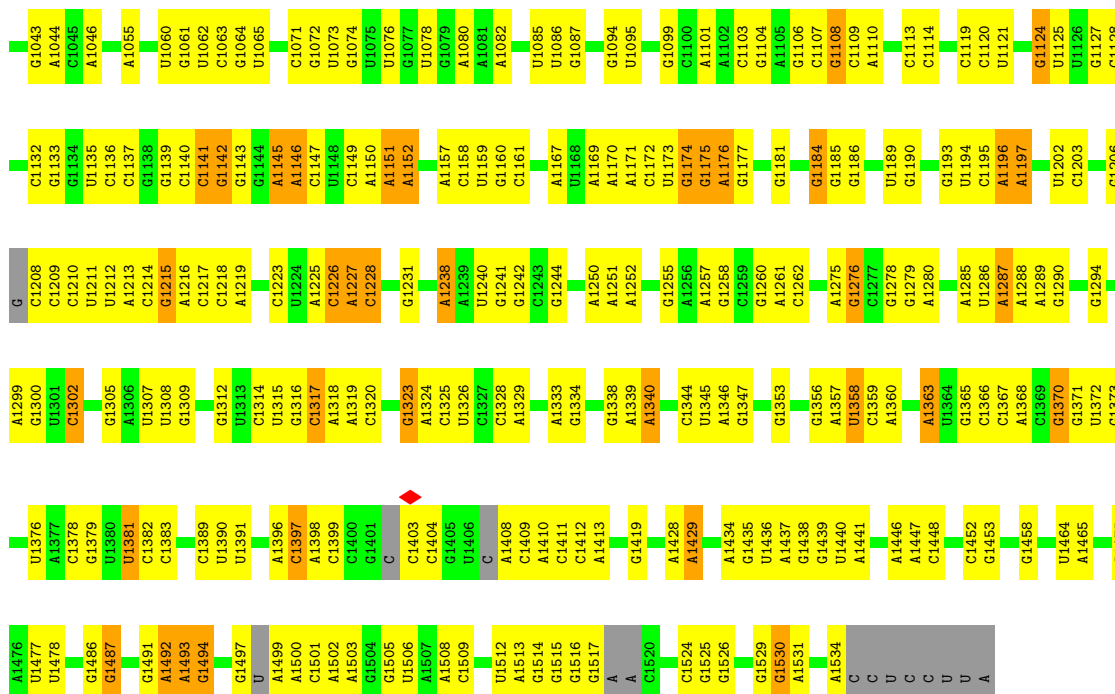




• Molecule 17: 16S rRNA

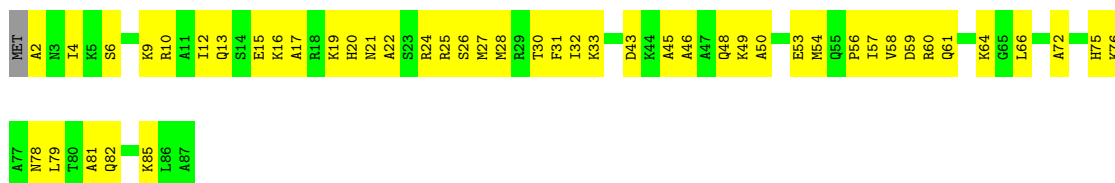
Chain D: 49% 43% 7%





• Molecule 18: 30S ribosomal protein S20

Chain E: 45% 54%



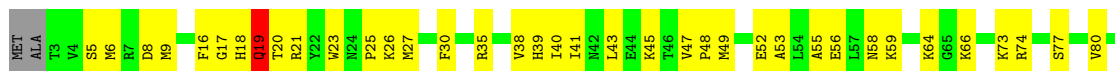
• Molecule 19: 30S ribosomal protein S21

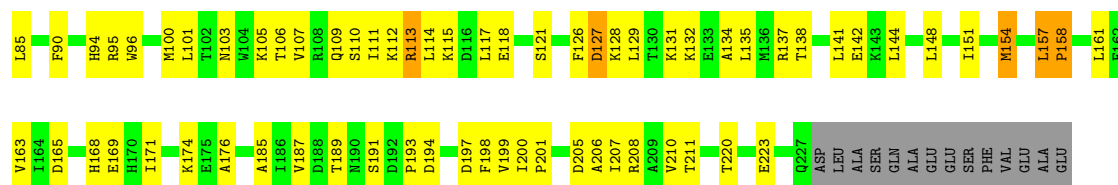
Chain F: 41% 58%



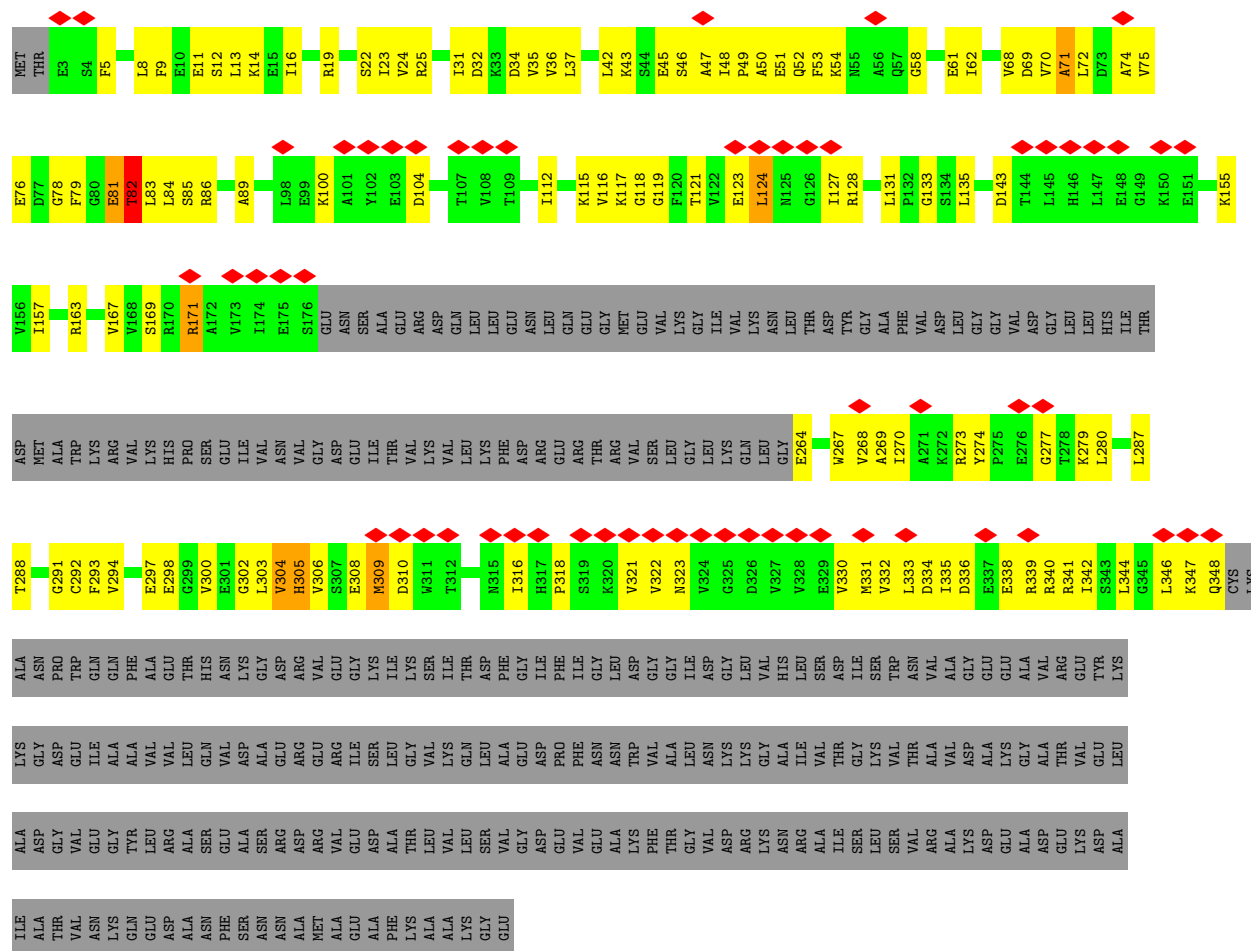
• Molecule 20: 30S ribosomal protein S2

Chain G: 51% 40% 7%

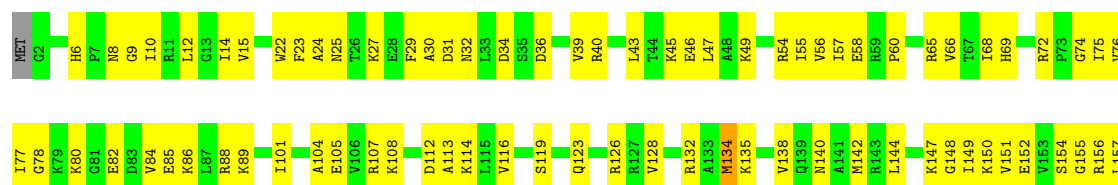


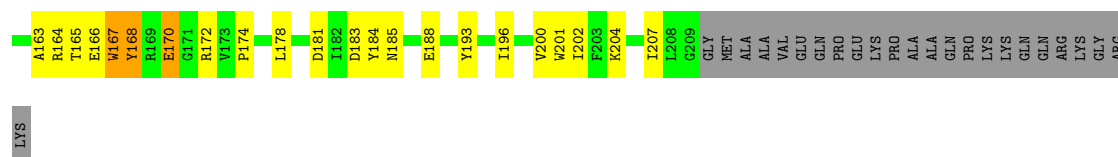


• Molecule 21: 30S ribosomal protein S1

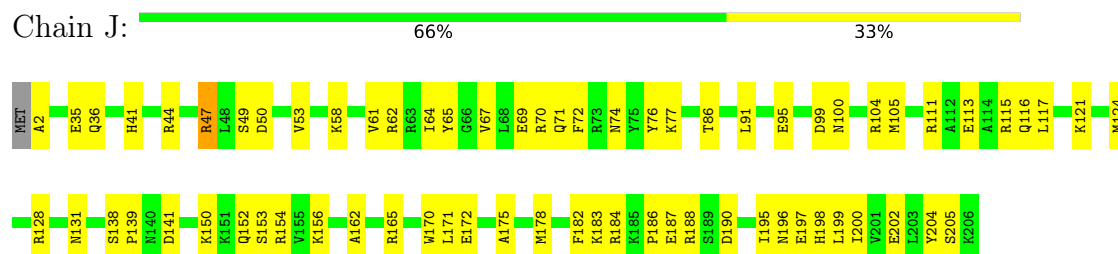


• Molecule 22: 30S ribosomal protein S3

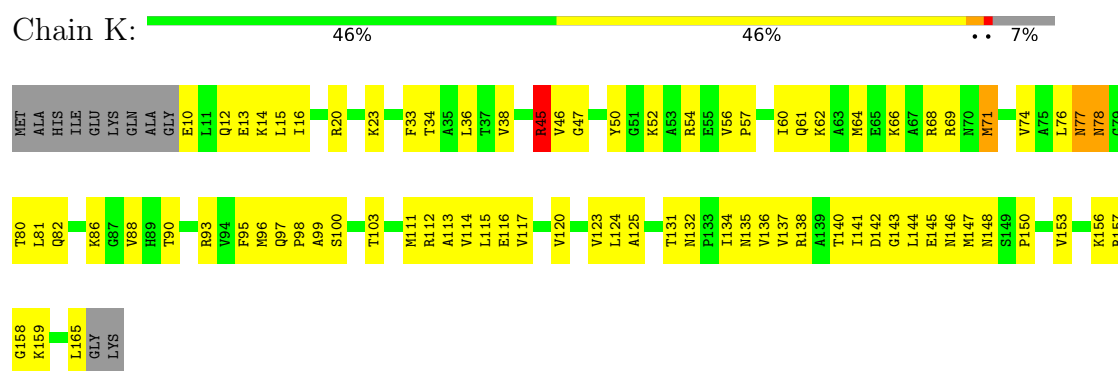




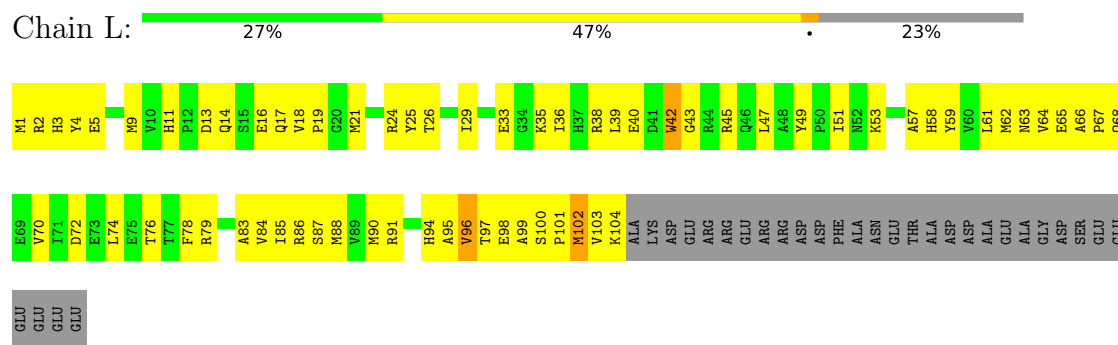
- Molecule 23: 30S ribosomal protein S4



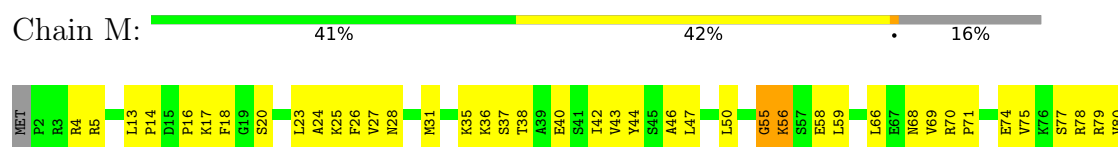
- Molecule 24: 30S ribosomal protein S5

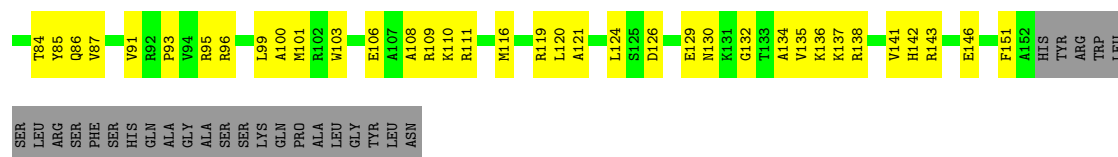


- Molecule 25: 30S ribosomal protein S6



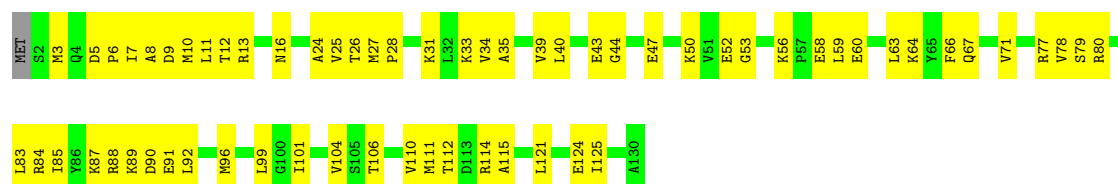
- Molecule 26: 30S ribosomal protein S7





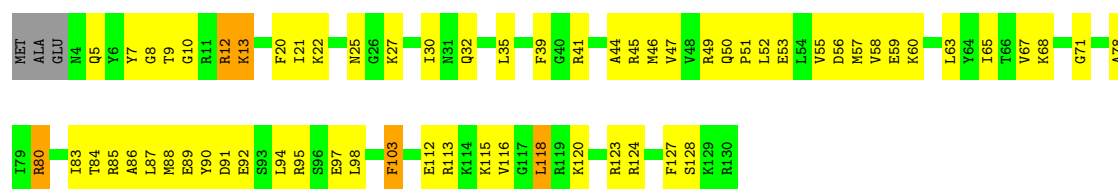
- Molecule 27: 30S ribosomal protein S8

Chain N: 51% 48%



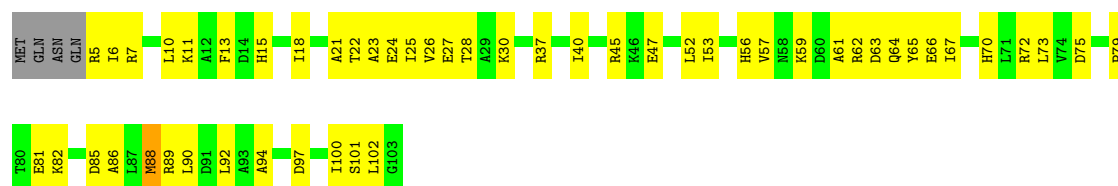
- Molecule 28: 30S ribosomal protein S9

Chain O: 48% 45%



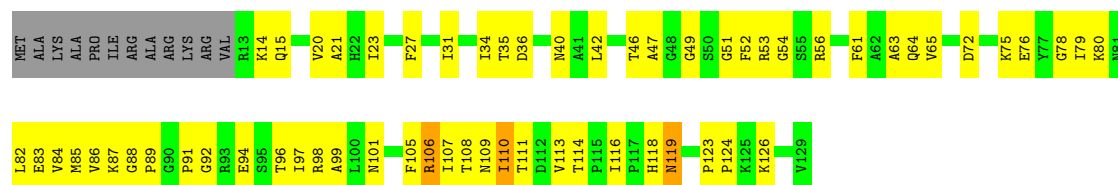
- Molecule 29: 30S ribosomal protein S10

Chain P: 47% 49%



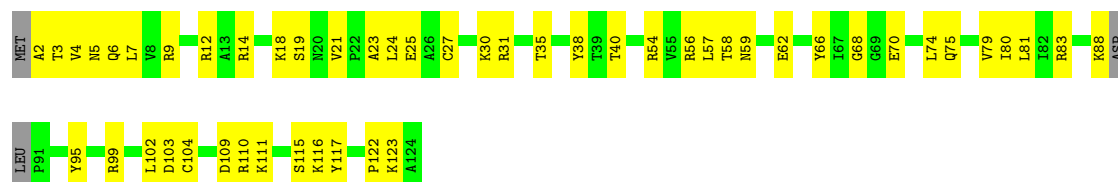
- Molecule 30: 30S ribosomal protein S11

Chain Q: 43% 45% 9%



- Molecule 31: 30S ribosomal protein S12

Chain R: 57% 40%



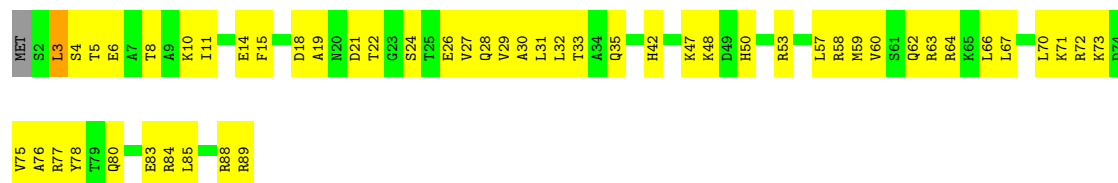
- Molecule 32: 30S ribosomal protein S14

Chain S: 51% 48%



- Molecule 33: 30S ribosomal protein S15

Chain T: 42% 56%



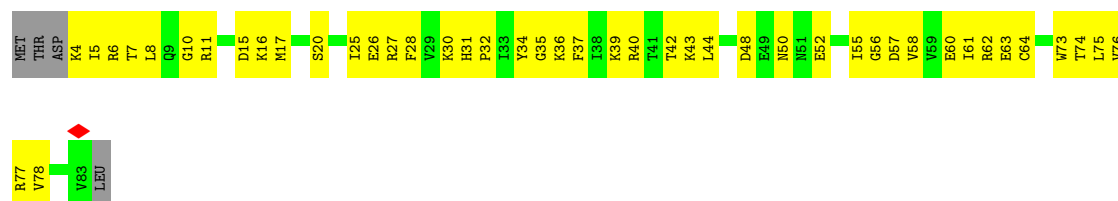
- Molecule 34: 30S ribosomal protein S16

Chain U: 51% 49%



- Molecule 35: 30S ribosomal protein S17

Chain V: 42% 54% 5%

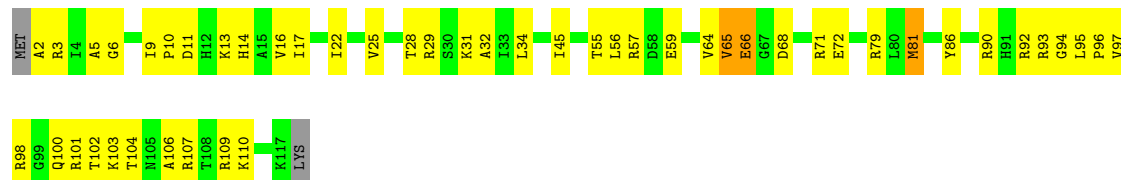


- Molecule 36: 30S ribosomal protein S19

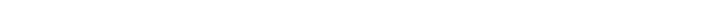
Chain W: 54% 34% 10%

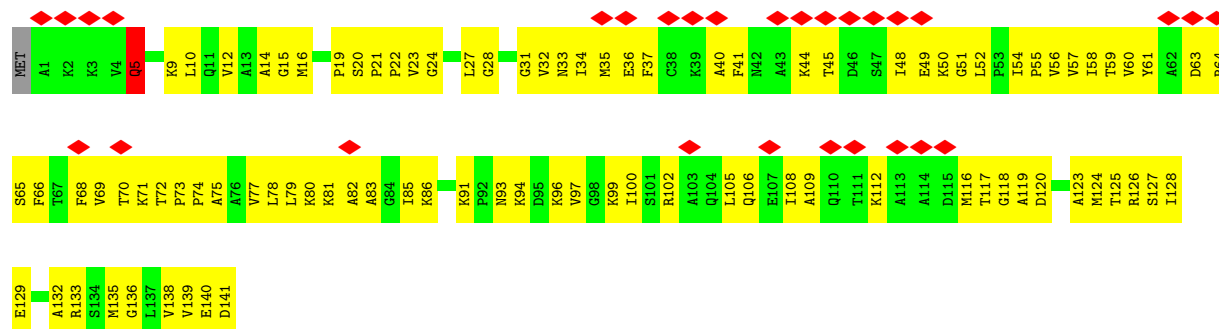
- Molecule 37: 30S ribosomal protein S13

Chain X: 57% 39% . .

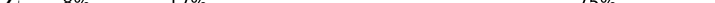


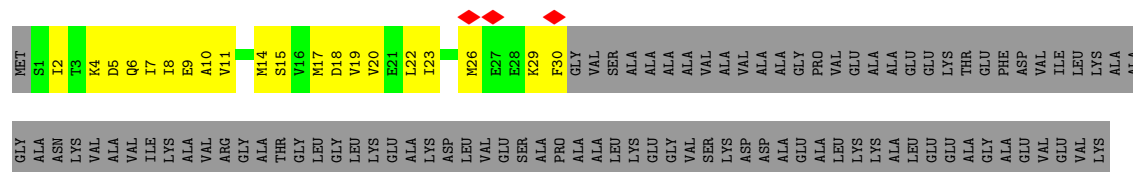
- Molecule 38: 50S ribosomal protein L11

Chain Y:  20% 34% 65%



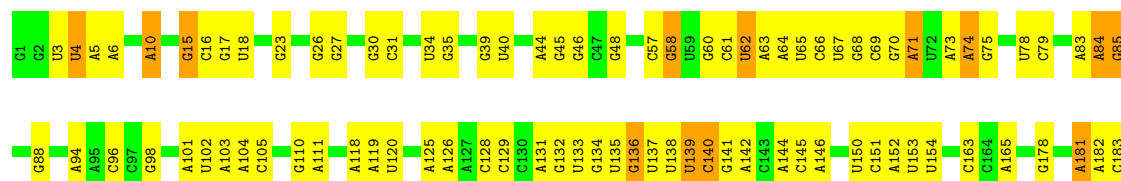
- Molecule 39: 50S ribosomal protein L7/L12

Chain Z:  8% 17% 75%



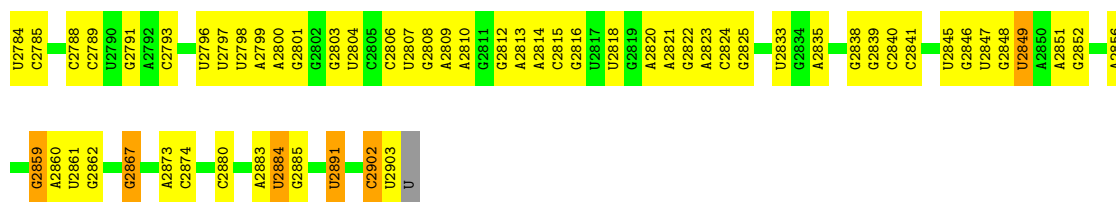
- Molecule 40: 23S rRNA

Chain a: 50% 42% 7%



G1416	C1417	G1418	A1419	G1420	G1421	G1422	A1427	C1428	G1429	G1430	A1431	G1432	A1433	A1434	G1435	G1441	U1442	U1443	G1444	G1445	G1452	A1453	C1454	U1460	U1467	U1468	A1469	A1470	U1477	G1482	A1490	A1494	A1495	A1496	U1497	C1498	G1499	G1500	A1503	U1506	C1507	A1508	A1509	G1510	G1511	U1512	G1513	G1514					
G1341	A1342	G1343	U1344	C1345	G1346	A1347	C1348	C1349	C1350	C1351	U1352	A1353	A1354	G1360	G1361	C1362	A1365	A1366	A1367	G1368	G1369	C1370	A1371	A1378	U1379	G1380	A1383	A1384	C1385	C1386	A1387	A1392	A1393	U1394	A1395	U1396	U1397	C1398	C1399	U1400	A1403	C1404	U1405	U1406	G1407	G1408	A1409	G1410	G1411	U1412	A1413	U1414	U1415
A1144	C1145	C1146	A1147	G1154	G1160	C1161	G1162	C1167	G1168	A1169	C1170	G1171	C1172	U1173	U1174	A1175	U1176	C1177	C1178	U1179	U1180	U1181	G1182	U1183	G1186	G1187	U1188	A1189	G1190	C1196	G1197	U1198	U1199	C1200	U1201	A1204	A1205	G1206	U1209	G1212	G1223	U1224	G1225	A1226	C1236	A1237	G1238	C1243					
A1246	A1247	G1248	U1249	G1250	C1251	G1252	A1253	G1256	C1257	A1262	G1266	A1269	C1270	G1271	A1272	U1273	A1276	G1277	U1278	G1279	U1280	G1281	U1282	G1283	C1289	C1289	C1289	A1289	C1290	U1294	C1295	G1296	G1300	A1301	G1310	G1311	U1312	C1313	C1314	C1315	U1318	C1319	C1320	A1321	A1322	C1323	G1333	G1334	U1340				
G1341	A1342	G1343	U1344	C1345	G1346	A1347	C1348	C1349	C1350	C1351	U1352	A1353	A1354	G1360	G1361	C1362	A1365	A1366	A1367	G1368	G1369	C1370	A1371	A1378	U1379	G1380	A1383	A1384	C1385	C1386	A1387	A1392	A1393	U1394	A1395	U1396	U1397	C1398	C1399	U1400	A1403	C1404	U1405	U1406	G1407	G1408	A1409	G1410	G1411	U1412	A1413	U1414	U1415
A1144	C1145	C1146	A1147	G1154	G1160	C1161	G1162	C1167	G1168	A1169	C1170	G1171	C1172	U1173	U1174	A1175	U1176	C1177	C1178	U1179	U1180	U1181	G1182	U1183	G1186	G1187	U1188	A1189	G1190	C1196	G1197	U1198	U1199	C1200	U1201	A1204	A1205	G1206	U1209	G1212	G1223	U1224	G1225	A1226	C1236	A1237	G1238	C1243					
A1246	A1247	G1248	U1249	G1250	C1251	G1252	A1253	G1256	C1257	A1262	G1266	A1269	C1270	G1271	A1272	U1273	A1276	G1277	U1278	G1279	U1280	G1281	U1282	G1283	C1289	C1289	C1289	A1289	C1290	U1294	C1295	G1296	G1300	A1301	G1310	G1311	U1312	C1313	C1314	C1315	U1318	C1319	C1320	A1321	A1322	C1323	G1333	G1334	U1340				
G1341	A1342	G1343	U1344	C1345	G1346	A1347	C1348	C1349	C1350	C1351	U1352	A1353	A1354	G1360	G1361	C1362	A1365	A1366	A1367	G1368	G1369	C1370	A1371	A1378	U1379	G1380	A1383	A1384	C1385	C1386	A1387	A1392	A1393	U1394	A1395	U1396	U1397	C1398	C1399	U1400	A1403	C1404	U1405	U1406	G1407	G1408	A1409	G1410	G1411	U1412	A1413	U1414	U1415
A1144	C1145	C1146	A1147	G1154	G1160	C1161	G1162	C1167	G1168	A1169	C1170	G1171	C1172	U1173	U1174	A1175	U1176	C1177	C1178	U1179	U1180	U1181	G1182	U1183	G1186	G1187	U1188	A1189	G1190	C1196	G1197	U1198	U1199	C1200	U1201	A1204	A1205	G1206	U1209	G1212	G1223	U1224	G1225	A1226	C1236	A1237	G1238	C1243					
A1246	A1247	G1248	U1249	G1250	C1251	G1252	A1253	G1256	C1257	A1262	G1266	A1269	C1270	G1271	A1272	U1273	A1276	G1277	U1278	G1279	U1280	G1281	U1282	G1283	C1289	C1289	C1289	A1289	C1290	U1294	C1295	G1296	G1300	A1301	G1310	G1311	U1312	C1313	C1314	C1315	U1318	C1319	C1320	A1321	A1322	C1323	G1333	G1334	U1340				
G1341	A1342	G1343	U1344	C1345	G1346	A1347	C1348	C1349	C1350	C1351	U1352	A1353	A1354	G1360	G1361	C1362	A1365	A1366	A1367	G1368	G1369	C1370	A1371	A1378	U1379	G1380	A1383	A1384	C1385	C1386	A1387	A1392	A1393	U1394	A1395	U1396	U1397	C1398	C1399	U1400	A1403	C1404	U1405	U1406	G1407	G1408	A1409	G1410	G1411	U1412	A1413	U1414	U1415
A1144	C1145	C1146	A1147	G1154	G1160	C1161	G1162	C1167	G1168	A1169	C1170	G1171	C1172	U1173	U1174	A1175	U1176	C1177	C1178	U1179	U1180	U1181	G1182	U1183	G1186	G1187	U1188	A1189	G1190	C1196	G1197	U1198	U1199	C1200	U1201	A1204	A1205	G1206	U1209	G1212	G1223	U1224	G1225	A1226	C1236	A1237	G1238	C1243					
A1246	A1247	G1248	U1249	G1250	C1251	G1252	A1253	G1256	C1257	A1262	G1266	A1269	C1270	G1271	A1272	U1273	A1276	G1277	U1278	G1279	U1280	G1281	U1282	G1283	C1289	C1289	C1289	A1289	C1290	U1294	C1295	G1296	G1300	A1301	G1310	G1311	U1312	C1313	C1314	C1315	U1318	C1319	C1320	A1321	A1322	C1323	G1333	G1334	U1340				
G1341	A1342	G1343	U1344	C1345	G1346	A1347	C1348	C1349	C1350	C1351	U1352	A1353	A1354	G1360	G1361	C1362	A1365	A1366	A1367	G1368	G1369	C1370	A1371	A1378	U1379	G1380	A1383	A1384	C1385	C1386	A1387	A1392	A1393	U1394	A1395	U1396	U1397	C1398	C1399	U1400	A1403	C1404	U1405	U1406	G1407	G1408	A1409	G1410	G1411	U1412	A1413	U1414	U1415
A1144	C1145	C1146	A1147	G1154	G1160	C1161	G1162	C1167	G1168	A1169	C1170	G1171	C1172	U1173	U1174	A1175	U1176	C1177	C1178	U1179	U1180	U1181	G1182	U1183	G1186	G1187	U1188	A1189	G1190	C1196	G1197	U1198	U1199	C1200	U1201	A1204	A1205	G1206	U1209	G1212	G1223	U1224	G1225	A1226	C1236	A1237	G1238	C1243					
A1246	A1247	G1248	U1249	G1250	C1251	G1252	A1253	G1256	C1257	A1262	G1266	A1269	C1270	G1271	A1272	U1273	A1276	G1277	U1278	G1279	U1280	G1281	U1282	G1283	C1289	C1289	C1289	A1289	C1290	U1294	C1295	G1296	G1300	A1301	G1310	G1311	U1312	C1313	C1314	C1315	U1318	C1319	C1320	A1321	A1322	C1323	G1333	G1334	U1340				
G1341	A1342	G1343	U1344	C1345	G1346	A1347	C1348	C1349	C1350	C1351	U1352	A1353	A1354	G1360	G1361	C1362	A1365	A1366	A1367	G1368	G1369	C1370	A1371	A1378	U1379	G1380	A1383	A1384	C1385	C1386	A1387	A1392	A1393	U1394	A1395	U1396	U1397	C1398	C1399	U1400	A1403	C1404	U1405	U1406	G1407	G1408	A1409	G1410	G1411	U1412	A1413	U1414	U1415
A1144	C1145	C1146	A1147	G1154	G1160	C1161	G1162	C1167	G1168	A1169	C1170	G1171	C1172	U1173	U1174	A1175	U1176	C1177	C1178	U1179	U1180	U1181	G1182	U1183	G1186	G1187	U1188	A1189	G1190	C1196	G1197	U1198	U1199	C1200	U1201	A1204	A1205	G1206	U1209	G1212	G1223	U1224	G1225	A1226	C1236	A1237	G1238	C1243					
A1246	A1247	G1248	U1249	G1250	C1251	G1252	A1253	G1256	C1257	A1262	G1266	A1269	C1270	G1271	A1272	U1273	A1276	G1277	U1278	G1279	U1280	G1281	U1282	G1283	C1289	C1289	C1289	A1289	C1290	U1294	C1295	G1296	G1300	A1301	G1310	G1311	U1312	C1313	C1314	C1315	U1318	C1319	C1320	A1321	A1322	C1323	G1333	G1334	U1340				
G1341	A1342	G1343	U1344	C1345	G1346	A1347	C1348	C1349	C1350	C1351	U1352	A1353	A1354	G1360	G1361	C1362	A1365	A1366	A1367	G1368	G1369	C1370	A1371	A1378	U1379	G1380	A1383	A1384	C1385	C1386	A1387	A1392	A1393	U1394	A1395	U1396	U1397	C1398	C1399	U1400	A1403	C1404	U1405	U1406	G1407	G1408	A1409	G1410	G1411	U1412	A1413	U1414	U1415
A1144	C1145	C1146	A1147	G1154	G1160	C1161	G1162	C1167	G1168	A1169	C1170	G1171	C1172	U1173	U1174	A1175	U1176	C1177	C1178	U1179	U1180	U1181	G1182	U1183	G1186	G1187	U1188	A1189	G1190	C1196	G1197	U1198	U1199	C1200	U1201	A1204	A1205	G1206	U1209	G1212	G1223	U1224	G1225	A1226	C1236	A1237	G1238	C1243					
A1246	A1247	G1248	U1249	G1250	C1251	G1252	A1253	G1256	C1257	A1262	G1266	A1269	C1270	G1271	A1272	U1273	A1276	G1277	U1278	G1279	U1280	G1281	U1282	G1283	C1289	C1289	C1289	A1289	C1290	U1294	C1295	G1296	G1300	A1301	G1310	G1311	U1312	C1313	C1314	C1315	U1318	C1319	C1320	A1321	A1322	C1323	G1333	G1334	U1340				
G1341	A1342	G1343	U1344	C1345	G1346	A1347	C1348	C1349	C1350	C1351	U1352	A1353	A1354	G1360	G1361	C1362	A1365	A1366	A1367	G1368	G1369	C1370	A1371	A1378	U1379	G1380	A1383	A1384	C1385	C1386	A1387	A1392	A1393	U1394	A1395	U1396	U1397	C1398	C1399	U1400	A1403	C1404	U1405	U1406	G1407	G1408	A1409	G1410	G1411	U1412	A1413	U1414	U1415
A1144	C1145	C1146	A1147	G1154	G1160	C1161	G1162	C1167	G1168	A1169	C1170	G1171	C1172	U1173	U1174	A1175	U1176	C1177	C1178	U1179	U1180	U1181	G1182	U1183	G1186	G1187	U1188	A1189	G1190	C1196	G1197	U1198	U1199	C1200	U1201	A1204	A1205	G1206	U1209	G1212	G1223	U1224	G1225	A1226	C1236	A1237	G1238	C1243					
A1246	A1247	G1248	U1249	G1250	C1251	G1252	A1253	G1256	C1257	A1262	G1266	A1269	C1270	G1271	A1272	U1273	A1276	G1277	U1278	G1279	U1280	G1281	U1282	G1283	C1289	C1289	C1289	A1289	C1290	U1294	C1295	G1296	G1300	A1301	G1310	G1311	U1312	C1313	C1314	C1315	U1318	C1319	C1320	A1321	A1322	C1323	G1333	G1334	U1340				
G1341	A1342	G1343	U1344	C1345	G1346	A1347	C1348	C1349	C1350	C1351	U1352	A1353	A1354	G1360	G1361	C1362	A1365	A1366	A1367	G1368	G1369	C1370	A1371	A1378	U1379	G1380	A1383	A1384	C1385	C1386	A1387	A1392	A1393	U1394	A1395	U1396	U1397	C1398	C1399	U1400	A1403	C1404	U1405	U1406	G1407	G1408	A1409	G1410	G1411	U1412	A1413	U1414	U1415
A1144	C1145	C1146	A1147	G11																																																	

C2699	U2609	G2595	G2455	A2369	G2293	A2205	G2128	C2050	U1971	A1890	G1817	U1720	A1608	A1515
A2700	C2610	G2526	C2456	U2372	G2294	C2206	U2131	A2051	G1972	A1900	U1818	G1721	A1609	G1529
G2702	C2611	G2529	U	U2373	C2295	A2211	U2132	A2052	G1980	G1906	U1820	U1729	A1610	U1534
C2703	C2612	A2530	G2458	G2373	U2296	A2212	C2133	C2055	U1981	G1907	G1823	C1730	A1613	A1535
G2708	C2613	A2531	U2450	G2374	A2297	C2215	A2134	G2056	U1982	G1910	G1824	G1731	A1614	C1536
G2709	U2615	G2532	A2461	A2376	U2299	G2216	U2139	A2060	G1983	U	U1825	C1732	A1617	G1537
G2714	C2616	G2535	C2462	A2377	C2300	G2217	G2140	G2061	A1987	G1912	G1826	G1738	A	U1542
G2715	G2536	U2537	G2464	U2381	C2301	G2218	G2141	C2062	U1991	A1913	U1827	U1747	G1619	U1543
G2716	C2617	G2538	C2465	G2382	U2305	G2223	C2146	C2064	U1992	A1914	G1828	A1746	G1622	G1546
G2717	U2630	A2542	C2466	U2383	G2306	G2224	A2147	C2065	U1993	U	C1830	U1747	G1622	G1546
G2718	G2627	U2548	A2468	C2385	G2308	A2225	G2148	C2066	U1996	A1916	U1831	G1750	U1647	G1547
G2719	C2628	A2547	U2469	A2386	A2309	C2226	U2149	G2067	C1997	U	G1832	G1750	U1648	C1548
U2720	C2619	U2537	G2470	U2387	C2310	A2227	C2150	U2068	C1998	A1918	C1833	G1757	G1649	A1549
G2721	G2630	G2538	U2471	U2387	A2311	G2228	A2154	G	C1999	A1919	U1834	G1753	A1650	U1554
G2722	U2630	A2542	U2473	G2391	U2312	U2229	A2154	A2070	C1999	G1920	G1836	G1753	G1651	U1554
G2723	C2636	U2548	U2474	A2392	C2313	G2230	G2157	A2071	G2002	G1921	C1836	G1755	A1652	U1554
U2724	U2637	C2551	C2475	U2393	G2314	C2236	C2158	C2072	U1992	G1922	G1839	G1756	G1653	C1558
A2725	G2638	U	A2476	U2394	A2315	U2237	A2159	C2073	C2006	U1923	G1840	G1757	A1654	U1559
A2726	A2639	G2553	U2477	C2395	G2316	G2238	C2160	U	U2007	C1924	U1841	U1758	A1655	G1560
A2727	G2640	U2554	A2478	G2396	U2320	G2239	C2161	U2075	C2007	C1925	G1842	C1764	C1656	C1561
U2728	U2646	U2555	G2481	U2402	U2321	G2239	C2162	A2082	G2010	U1926	G1843	U1778	U1657	U1562
G2731	U2647	G2557	A2482	C2403	A2322	U2243	A2163	G2083	U2011	A1938	C1844	G1770	C1658	C1564
G2732	G2648	C2558	C2483	A2406	G2325	U2244	C2164	G2083	G2012	U1937	G1845	U1770	C1659	C1564
A2740	C2649	U2566	G2484	A2407	C2326	U2245	C2165	U2086	G2013	A1938	G1846	A1773	A1664	C1566
A2741	U2650	A2567	G2485	U2407	A2327	G2246	C2166	G2087	A2014	U1931	U1847	C1774	A1665	G1567
G2742	C2651	G2567	U2489	U2419	A2328	A2247	G2168	C2091	A2015	G1932	A1848	U1778	G1667	G1568
U2743	A2654	U2568	U2490	C2420	U2329	U2248	C2169	U2092	U2016	G1933	C1853	U1779	A1668	A1570
G2744	U2657	G2570	U2491	G2421	G2331	G2250	A2171	G2093	A2020	A1936	A1854	A1784	G1674	A1571
G2747	G2663	U2571	U2492	C2422	C2332	G	U2172	A2094	C2021	U1937	U1855	A1784	C1675	A1572
A2748	A2665	C2573	G2494	U2423	A2333	G2252	C2175	C2096	U2022	U	G1857	A1786	A1676	U1578
U2754	C2666	G2574	U2497	A2425	U2334	G2253	A2176	C2097	C2023	U1940	U1858	A1789	A1677	A1579
G2755	G2669	U2579	C	A2426	A2335	U2259	C2177	U2098	G2024	U1944	U1859	A1789	A1677	A1580
U2756	A2670	U	C2427	C2428	C2339	C2260	C2178	U2099	C2025	G1945	G1862	C1790	G1681	G1581
A2757	G2671	G2581	G2429	G2429	G2345	U2261	C2179	G2100	U2026	U1946	G1863	A1791	C1582	C1582
U2758	U2672	G2582	U2502	A2430	A2346	C2262	U2180	G2111	G2027	U1946	U1683	G1792	A1583	G1583
G2759	G2673	U2583	A	U2431	C2347	C2263	U2181	A2108	U2028	C1957	U1684	C1793	U1584	U1584
A2765	C2674	U2584	U2505	U2434	U2348	A2266	A2183	U2109	G2029	A1963	G1869	A1794	C1585	C1585
G2766	G2677	U2585	U2506	A2435	G2349	A2267	A2184	G2110	A	G1954	C1870	C1795	A1586	A1586
U2768	U2680	G2586	C2507	G2436	C2350	A2268	U2185	G2112	A2031	U1955	A1871	U1796	G1587	G1587
C2771	U2681	G2588	U2511	U2441	G2355	A2273	U2189	A2114	U2034	U1956	A1872	G1797	U1588	U1588
C2772	A2682	A2590	C2512	U2444	U2356	A2274	A2191	G2115	A2033	C1957	G1873	G1799	A1590	A1590
G2775	C2683	C2591	A2513	G	G2357	A2278	U2192	G2116	C2036	G1959	G1874	C1800	A1591	A1591
G2776	U2684	G2592	U2514	G2446	G2361	C2283	G2193	A2117	A2037	A1960	G1875	A1801	A1700	A1596
G2777	G2685	A2602	C2515	G2447	C2362	A2287	U2194	U2118	U2038	C	C1879	A1802	G1703	A1597
U2778	G2686	A2516	A2518	A2448	G2363	A2288	U2197	G2121	U2039	U1963	U1880	A1803	G1703	A1597
A2778	U2687	C2517	A2518	U2449	G2364	A2289	A2198	U2122	G2040	G1964	C1881	A1808	G1707	U1599
U2779	G2688	U	A2518	A2449	C2364	G2289	A2199	G2123	U2041	U1965	U1882	G1811	G1708	C1600
U2780	U2689	U2519	A2450	A2450	G2365	G2289	A2199	G2124	C2043	A1966	G1884	G1811	G1710	G1601
U2781	C2690	C2520	A2451	A2451	A2366	G2290	C2200	G2125	C2044	C1967	A1885	G1814	U1714	A1603
U2783	U2698	C2521	G2454	G2454	G2368	U2292	G2204	G2127	G2049	A1970	A1889	C1816	G1715	C1607



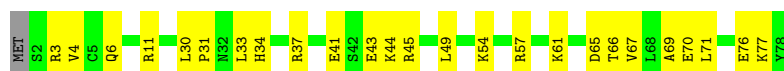
- Molecule 41: 50S ribosomal protein L27

Chain b: 59% 31% 11%



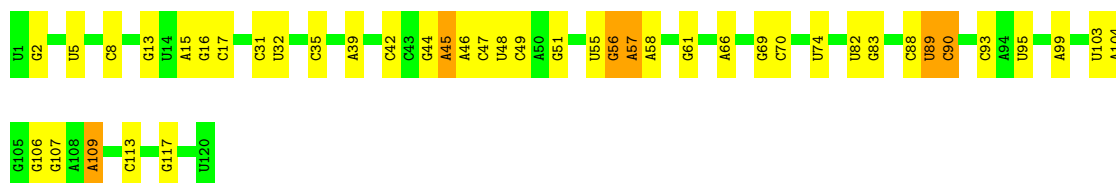
- Molecule 42: 50S ribosomal protein L28

Chain c: 67% 32%



- Molecule 43: 5S rRNA

Chain d: 64% 31% 5%



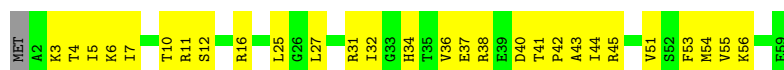
- Molecule 44: 50S ribosomal protein L29

Chain e: 46% 51% 3%



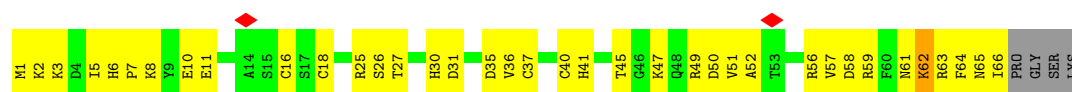
- Molecule 45: 50S ribosomal protein L30

Chain f: 51% 47%



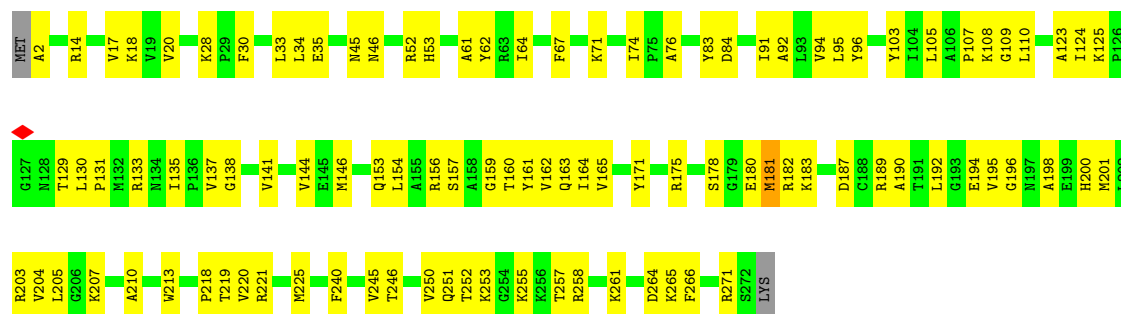
- Molecule 46: 50S ribosomal protein L31

Chain g: 41% 51% 6%



- Molecule 47: 50S ribosomal protein L2

Chain h: 62% 37%



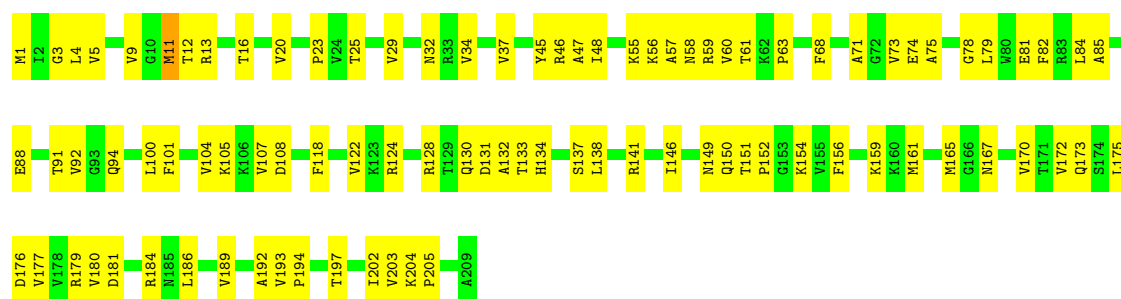
- Molecule 48: 50S ribosomal protein L32

Chain i: 54% 44%



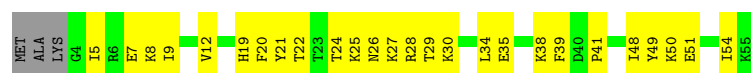
- Molecule 49: 50S ribosomal protein L3

Chain j: 56% 44%



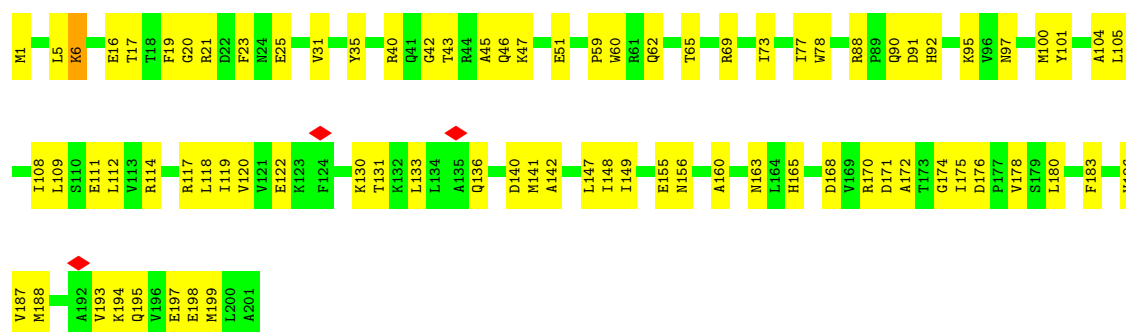
- Molecule 50: 50S ribosomal protein L33

Chain k: 47% 47% 5%



- Molecule 51: 50S ribosomal protein L4

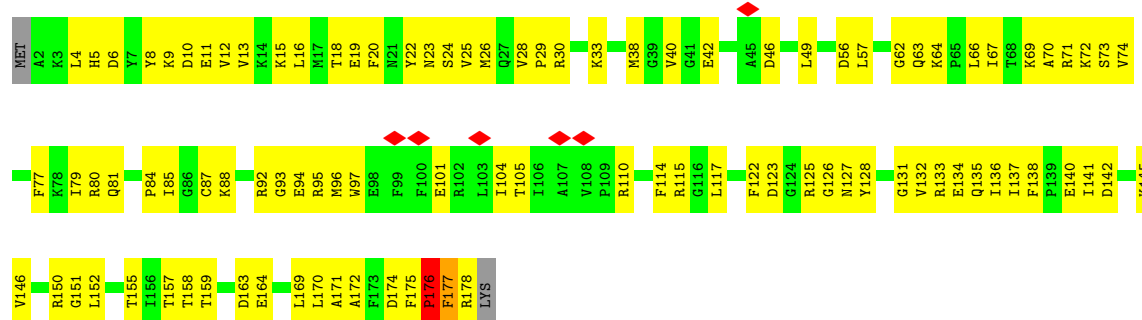
Chain l: 60% 40%



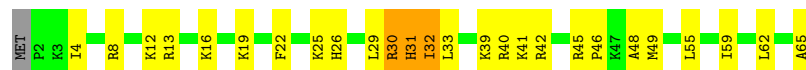
- Molecule 52: 50S ribosomal protein L34



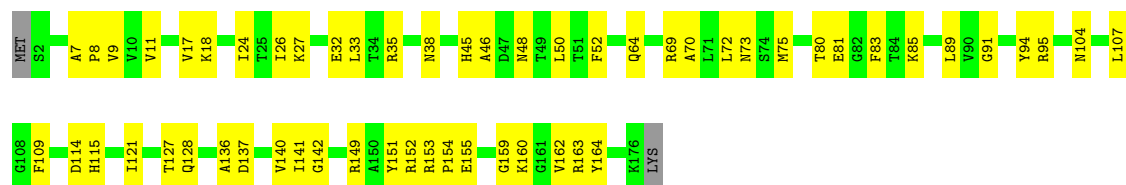
- Molecule 53: 50S ribosomal protein L5



- Molecule 54: 50S ribosomal protein L35



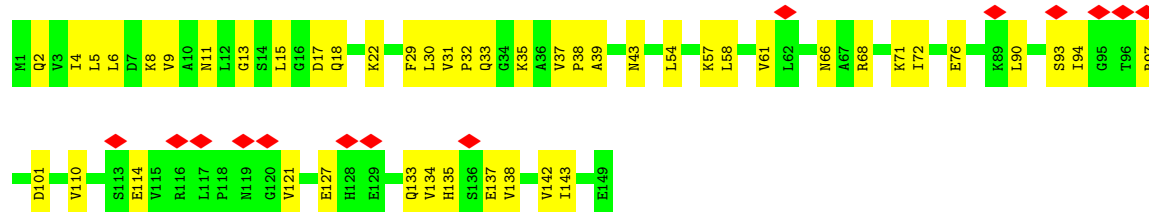
- Molecule 55: 50S ribosomal protein L6



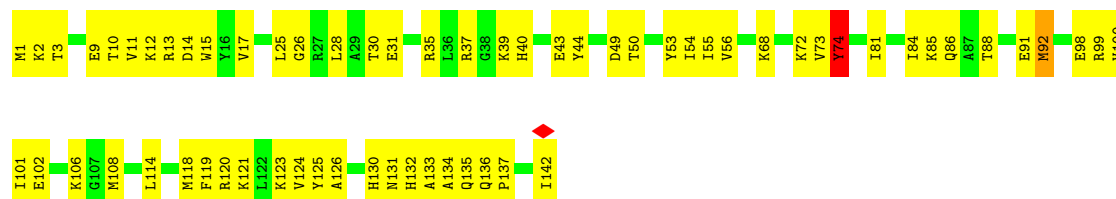
- Molecule 56: 50S ribosomal protein L36



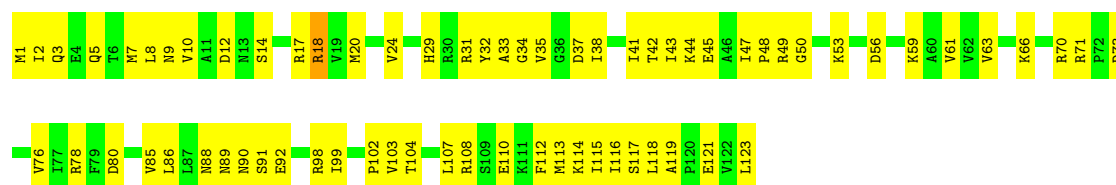
- Molecule 57: 50S ribosomal protein L9



- Molecule 58: 50S ribosomal protein L13



- Molecule 59: 50S ribosomal protein L14

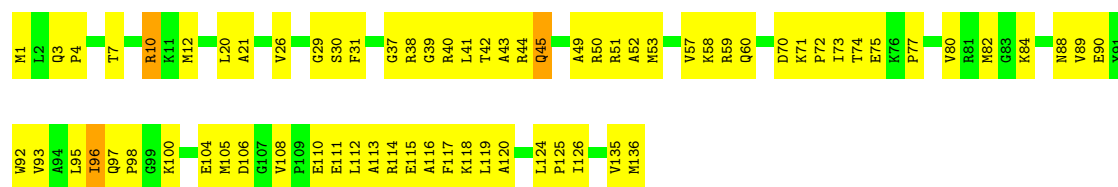


- Molecule 60: 50S ribosomal protein L15

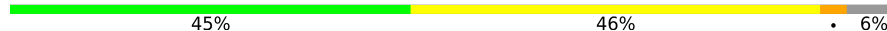


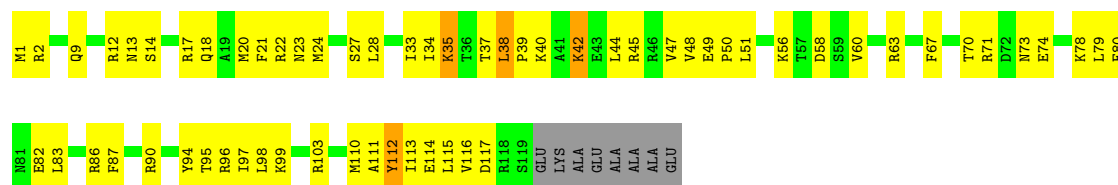
- Molecule 61: 50S ribosomal protein L16

Chain v: 



• Molecule 62: 50S ribosomal protein L17

Chain w: 



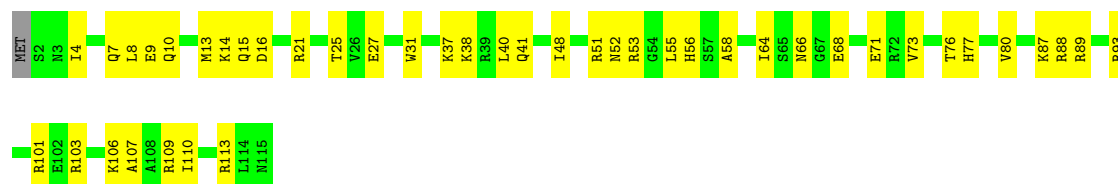
• Molecule 63: 50S ribosomal protein L18

Chain x: 



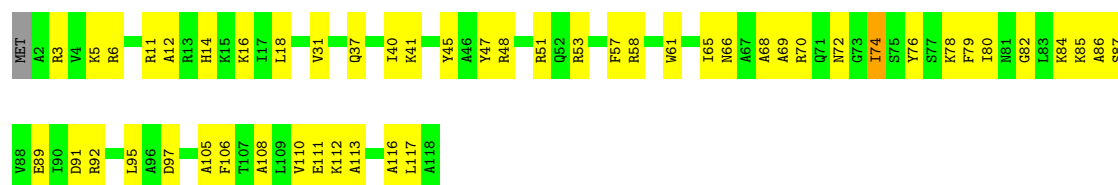
• Molecule 64: 50S ribosomal protein L19

Chain y: 



• Molecule 65: 50S ribosomal protein L20

Chain z: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	49622	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	0.034	Depositor
Minimum map value	-0.007	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0037	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 ⓘ

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	0.42	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	0.77	0/1259
7	6	0.56	0/783	0.78	0/1203
8	7	0.56	2/856 (0.2%)	0.88	4/1326 (0.3%)
9	9	0.36	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	0.37	0/10547	0.62	0/14232
12	AB	0.44	0/1317	1.10	9/1786 (0.5%)
13	AC	0.37	0/1718	0.61	0/2328
13	AD	0.32	0/1696	0.60	0/2298
14	AE	0.39	0/10561	0.64	5/14258 (0.0%)
15	AF	0.29	0/652	0.61	0/879
16	C	0.67	0/553	0.81	1/743 (0.1%)
17	D	0.29	0/36610	0.41	9/57091 (0.0%)
18	E	0.61	0/675	0.72	0/895
19	F	0.53	0/597	0.60	0/792
20	G	0.68	5/1791 (0.3%)	0.79	8/2413 (0.3%)
21	H	0.37	0/1746	0.81	0/2382
22	I	0.57	1/1663 (0.1%)	0.68	4/2241 (0.2%)
23	J	0.46	0/1665	0.58	0/2227
24	K	0.72	2/1165 (0.2%)	0.86	6/1568 (0.4%)
25	L	0.68	1/867 (0.1%)	0.79	1/1171 (0.1%)
26	M	0.56	0/1195	0.69	2/1602 (0.1%)
27	N	0.50	0/989	0.58	0/1326
28	O	0.65	3/1034 (0.3%)	0.79	3/1375 (0.2%)
29	P	0.49	0/800	0.65	1/1082 (0.1%)
30	Q	0.72	2/893 (0.2%)	0.76	2/1205 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	R	0.49	0/952	0.59	0/1274
32	S	0.52	0/817	0.61	0/1088
33	T	0.57	1/722 (0.1%)	0.68	0/964
34	U	0.41	0/659	0.53	0/884
35	V	0.48	0/657	0.63	0/881
36	W	0.55	1/680 (0.1%)	0.62	1/915 (0.1%)
37	X	0.45	0/909	0.72	1/1215 (0.1%)
38	Y	0.38	2/1046 (0.2%)	0.66	2/1410 (0.1%)
39	Z	0.12	0/227	0.40	0/304
40	a	0.30	0/69247	0.43	10/107985 (0.0%)
41	b	0.41	0/589	0.55	0/779
42	c	0.51	0/635	0.61	0/848
43	d	0.25	0/2872	0.37	0/4478
44	e	0.68	2/502 (0.4%)	0.65	1/667 (0.1%)
45	f	0.52	0/452	0.57	0/605
46	g	0.45	1/531 (0.2%)	0.64	0/709
47	h	0.49	1/2121 (0.0%)	0.58	0/2852
48	i	0.41	0/450	0.55	0/599
49	j	0.51	0/1586	0.57	1/2134 (0.0%)
50	k	0.45	0/433	0.62	0/576
51	l	0.51	1/1571 (0.1%)	0.62	0/2113
52	m	0.45	0/380	0.56	0/498
53	n	0.46	0/1434	0.66	1/1926 (0.1%)
54	o	0.51	0/513	0.71	1/676 (0.1%)
55	p	0.41	0/1333	0.62	2/1805 (0.1%)
56	q	0.45	0/303	0.64	0/397
57	r	0.28	0/1122	0.48	0/1515
58	s	0.70	2/1152 (0.2%)	0.73	2/1551 (0.1%)
59	t	0.52	0/955	0.75	3/1279 (0.2%)
60	u	0.43	0/1062	0.59	0/1413
61	v	0.60	1/1093 (0.1%)	0.77	3/1460 (0.2%)
62	w	0.83	3/964 (0.3%)	0.80	3/1289 (0.2%)
63	x	0.34	0/902	0.50	0/1209
64	y	0.41	0/929	0.54	0/1242
65	z	0.61	2/960 (0.2%)	0.62	0/1278
All	All	0.38	34/190707 (0.0%)	0.53	88/281021 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	9	0	3
12	AB	0	10
13	AC	0	1
13	AD	0	1
14	AE	0	4
20	G	0	1
21	H	0	5
22	I	0	1
24	K	0	2
28	O	0	1
37	X	0	1
38	Y	0	1
53	n	0	1
54	o	0	1
58	s	0	1
60	u	0	2
All	All	0	36

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	w	35	LYS	CE-NZ	-12.76	1.11	1.49
28	O	80	ARG	CD-NE	-10.48	1.31	1.46
62	w	42	LYS	CD-CE	-9.40	1.24	1.52
24	K	45	ARG	CG-CD	7.75	1.75	1.52
65	z	74	ILE	CG1-CD1	7.60	1.81	1.51

The worst 5 of 88 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	K	71	MET	CG-SD-CE	-11.33	75.98	100.90
20	G	158	PRO	N-CD-CG	-10.98	86.74	103.20
12	AB	141	LEU	CA-C-N	-10.58	106.29	122.16
12	AB	141	LEU	C-N-CA	-10.58	106.29	122.16
25	L	102	MET	CA-CB-CG	-9.61	94.88	114.10

There are no chirality outliers.

5 of 36 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	9	107	GLU	Peptide
9	9	79	PRO	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
9	9	92	ALA	Peptide
12	AB	106	ASP	Peptide
12	AB	116	VAL	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	55	0
2	1	857	922	922	68	0
3	2	746	811	811	61	0
4	3	788	844	844	45	0
5	4	753	780	780	87	0
6	5	726	0	392	110	0
7	6	703	0	396	34	0
8	7	772	0	383	122	0
9	9	1117	0	1155	258	0
10	A	1620	826	827	108	0
10	B	1620	814	827	112	0
11	AA	10381	0	10390	233	0
12	AB	1286	0	1302	337	0
13	AC	1698	0	1718	11	0
13	AD	1677	0	1713	29	0
14	AE	10404	0	10626	271	0
15	AF	650	0	658	15	0
16	C	544	559	560	106	0
17	D	32703	16423	16453	736	0
18	E	669	719	719	83	0
19	F	589	629	629	58	0
20	G	1760	1785	1787	154	0
21	H	1730	1454	1455	163	0
22	I	1636	1710	1710	153	0
23	J	1643	1707	1707	86	0
24	K	1152	1196	1196	116	0
25	L	848	846	846	104	0
26	M	1181	1235	1238	122	0
27	N	979	1031	1031	93	0
28	O	1022	1070	1070	91	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	P	790	831	831	133	0
30	Q	877	887	887	97	0
31	R	939	1001	1001	91	0
32	S	805	844	844	77	0
33	T	714	734	734	92	0
34	U	649	666	666	63	0
35	V	648	691	691	69	0
36	W	663	688	688	46	0
37	X	900	964	965	111	0
38	Y	1032	0	1088	212	0
39	Z	227	0	237	31	0
40	a	61841	31077	31120	1325	0
41	b	582	599	599	47	0
42	c	625	652	652	33	0
43	d	2569	1301	1301	42	0
44	e	501	531	531	45	0
45	f	448	488	488	38	0
46	g	522	520	520	66	0
47	h	2082	2154	2154	137	0
48	i	444	459	458	49	0
49	j	1565	1617	1616	123	0
50	k	426	464	464	41	0
51	l	1552	1619	1619	124	0
52	m	377	418	418	30	0
53	n	1410	1443	1444	157	0
54	o	504	572	572	51	0
55	p	1313	1358	1358	74	0
56	q	302	343	343	25	0
57	r	1111	1148	1148	54	0
58	s	1129	1162	1162	123	0
59	t	946	1023	1023	103	0
60	u	1053	1129	1129	79	0
61	v	1074	1157	1157	123	0
62	w	951	994	994	103	0
63	x	892	923	923	48	0
64	y	917	962	962	53	0
65	z	947	1020	1019	80	0
66	AE	1	0	0	0	0
67	AE	2	0	0	3	0
All	All	177400	98639	128790	6808	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 22.

The worst 5 of 6808 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)
12:AB:147:ASN:CB	29:P:100:ILE:HG23	1.21	1.65
6:5:10:DT:C7	11:AA:62:TYR:CD2	1.84	1.58
14:AE:79:LYS:HA	14:AE:81:ARG:CZ	1.26	1.58
24:K:45:ARG:CD	24:K:45:ARG:CG	1.75	1.58
6:5:9:DG:C5'	11:AA:473:ARG:HB3	1.34	1.56

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%)	101 (69%)	42 (29%)	3 (2%)	5	31
11	AA	1312/1342 (98%)	1198 (91%)	113 (9%)	1 (0%)	48	79
12	AB	159/162 (98%)	111 (70%)	43 (27%)	5 (3%)	3	25
13	AC	217/329 (66%)	203 (94%)	12 (6%)	2 (1%)	14	45
13	AD	214/329 (65%)	198 (92%)	16 (8%)	0	100	100
14	AE	1331/1407 (95%)	1213 (91%)	112 (8%)	6 (0%)	24	57
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
16	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
18	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	F	68/71 (96%)	68 (100%)	0	0	100	100
20	G	223/241 (92%)	212 (95%)	10 (4%)	1 (0%)	30	62
21	H	255/557 (46%)	182 (71%)	66 (26%)	7 (3%)	4	27
22	I	206/233 (88%)	193 (94%)	13 (6%)	0	100	100
23	J	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
24	K	154/167 (92%)	145 (94%)	8 (5%)	1 (1%)	21	54
25	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	43
26	M	149/179 (83%)	140 (94%)	8 (5%)	1 (1%)	18	51
27	N	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
28	O	125/130 (96%)	116 (93%)	8 (6%)	1 (1%)	16	48
29	P	97/103 (94%)	89 (92%)	8 (8%)	0	100	100
30	Q	115/129 (89%)	107 (93%)	8 (7%)	0	100	100
31	R	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
32	S	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
33	T	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
34	U	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
35	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
36	W	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
37	X	114/118 (97%)	103 (90%)	9 (8%)	2 (2%)	6	33
38	Y	139/142 (98%)	101 (73%)	38 (27%)	0	100	100
39	Z	28/121 (23%)	22 (79%)	6 (21%)	0	100	100
41	b	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
42	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
44	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
45	f	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
46	g	64/70 (91%)	62 (97%)	2 (3%)	0	100	100
47	h	269/273 (98%)	255 (95%)	14 (5%)	0	100	100
48	i	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
49	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
50	k	50/55 (91%)	50 (100%)	0	0	100	100
51	l	199/201 (99%)	188 (94%)	11 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
53	n	175/179 (98%)	161 (92%)	13 (7%)	1 (1%)	21	54
54	o	62/65 (95%)	57 (92%)	4 (6%)	1 (2%)	7	35
55	p	173/177 (98%)	162 (94%)	11 (6%)	0	100	100
56	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
57	r	147/149 (99%)	139 (95%)	8 (5%)	0	100	100
58	s	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
59	t	121/123 (98%)	114 (94%)	7 (6%)	0	100	100
60	u	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
61	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
62	w	117/127 (92%)	112 (96%)	5 (4%)	0	100	100
63	x	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
64	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
65	z	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
All	All	9486/10558 (90%)	8744 (92%)	709 (8%)	33 (0%)	37	67

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	AB	141	LEU
12	AB	152	HIS
20	G	127	ASP
21	H	304	VAL
26	M	56	LYS

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

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	140 (99%)	1 (1%)	76	77
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	68
15	AF	70/75 (93%)	69 (99%)	1 (1%)	59	70
16	C	57/65 (88%)	57 (100%)	0	100	100
18	E	65/66 (98%)	65 (100%)	0	100	100
19	F	60/61 (98%)	60 (100%)	0	100	100
20	G	187/199 (94%)	187 (100%)	0	100	100
21	H	137/461 (30%)	137 (100%)	0	100	100
22	I	171/190 (90%)	171 (100%)	0	100	100
23	J	172/173 (99%)	171 (99%)	1 (1%)	78	79
24	K	119/126 (94%)	119 (100%)	0	100	100
25	L	91/116 (78%)	91 (100%)	0	100	100
26	M	124/147 (84%)	124 (100%)	0	100	100
27	N	104/105 (99%)	104 (100%)	0	100	100
28	O	105/107 (98%)	105 (100%)	0	100	100
29	P	86/90 (96%)	86 (100%)	0	100	100
30	Q	90/99 (91%)	90 (100%)	0	100	100
31	R	101/104 (97%)	101 (100%)	0	100	100
32	S	83/84 (99%)	83 (100%)	0	100	100
33	T	76/77 (99%)	76 (100%)	0	100	100
34	U	65/65 (100%)	65 (100%)	0	100	100
35	V	74/78 (95%)	74 (100%)	0	100	100
36	W	72/79 (91%)	72 (100%)	0	100	100
37	X	94/96 (98%)	94 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	Y	109/110 (99%)	109 (100%)	0	100	100
39	Z	26/85 (31%)	26 (100%)	0	100	100
41	b	58/63 (92%)	58 (100%)	0	100	100
42	c	67/68 (98%)	67 (100%)	0	100	100
44	e	54/55 (98%)	54 (100%)	0	100	100
45	f	48/49 (98%)	48 (100%)	0	100	100
46	g	59/62 (95%)	59 (100%)	0	100	100
47	h	216/218 (99%)	216 (100%)	0	100	100
48	i	47/48 (98%)	47 (100%)	0	100	100
49	j	164/164 (100%)	164 (100%)	0	100	100
50	k	47/49 (96%)	47 (100%)	0	100	100
51	l	165/165 (100%)	165 (100%)	0	100	100
52	m	38/38 (100%)	38 (100%)	0	100	100
53	n	148/150 (99%)	148 (100%)	0	100	100
54	o	51/52 (98%)	51 (100%)	0	100	100
55	p	136/138 (99%)	136 (100%)	0	100	100
56	q	34/34 (100%)	34 (100%)	0	100	100
57	r	114/114 (100%)	114 (100%)	0	100	100
58	s	116/116 (100%)	116 (100%)	0	100	100
59	t	104/104 (100%)	104 (100%)	0	100	100
60	u	103/103 (100%)	103 (100%)	0	100	100
61	v	109/109 (100%)	109 (100%)	0	100	100
62	w	99/103 (96%)	99 (100%)	0	100	100
63	x	86/87 (99%)	86 (100%)	0	100	100
64	y	99/100 (99%)	99 (100%)	0	100	100
65	z	89/90 (99%)	89 (100%)	0	100	100
All	All	7890/8723 (90%)	7864 (100%)	26 (0%)	84	84

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	AE	81	ARG
14	AE	92	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
15	AF	63	ILE
14	AE	85	CYS
14	AE	93	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 111 such sidechains are listed below:

Mol	Chain	Res	Type
22	I	6	HIS
65	z	81	ASN
29	P	58	ASN
65	z	72	ASN
61	v	13	HIS

5.3.3 RNA ⓘ

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%)
17	D	1514/1542 (98%)	290 (19%)	20 (1%)
40	a	2859/2904 (98%)	510 (17%)	0
43	d	119/120 (99%)	15 (12%)	0
8	7	36/41 (87%)	26 (72%)	5 (13%)
All	All	4678/4759 (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
17	D	517	G
17	D	1213	A
17	D	991	U
17	D	1196	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
17	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.

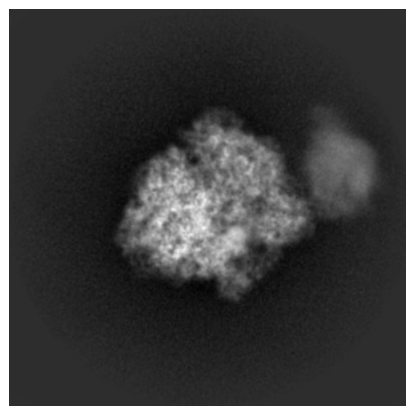
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42477. These allow visual inspection of the internal detail of the map and identification of artifacts.

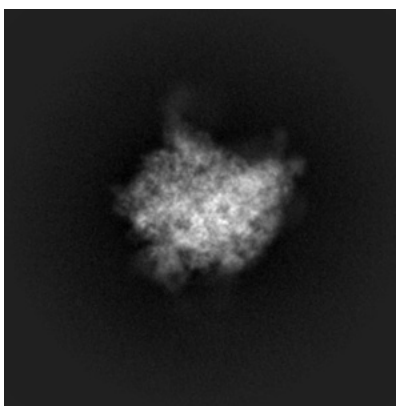
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

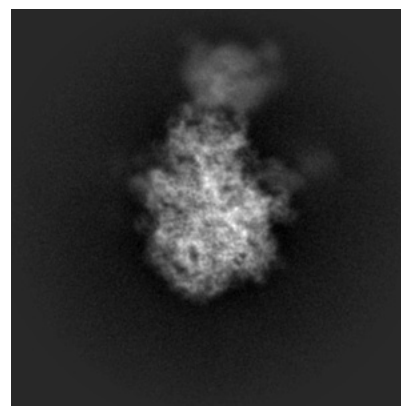
6.1.1 Primary map



X

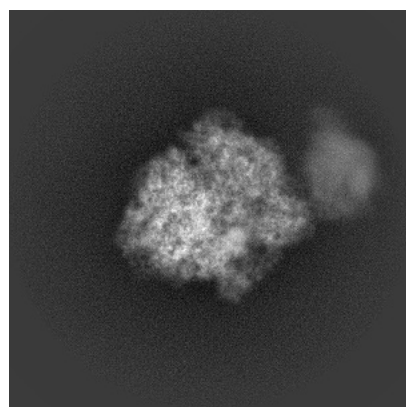


Y

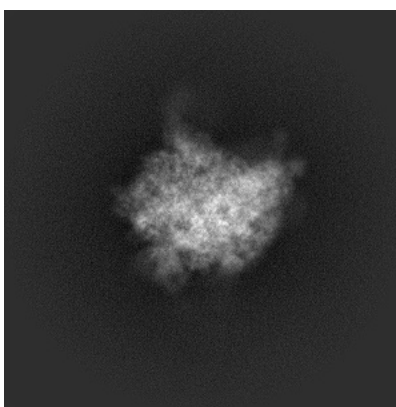


Z

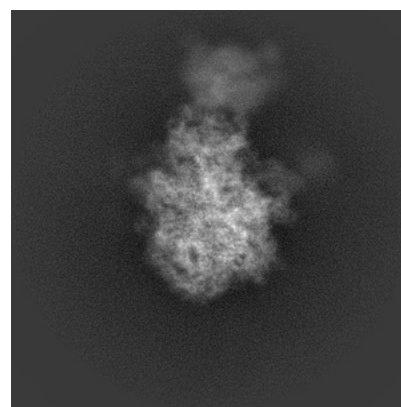
6.1.2 Raw map



X



Y

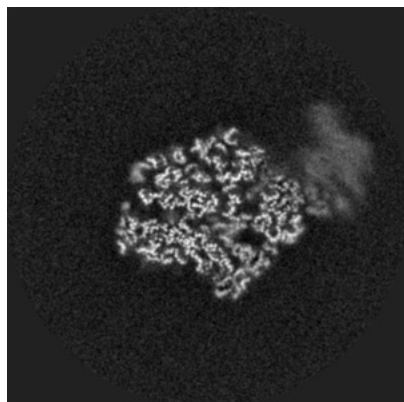


Z

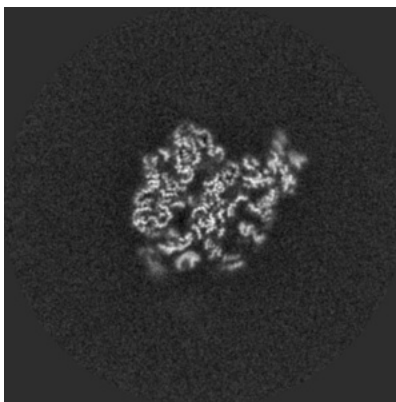
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

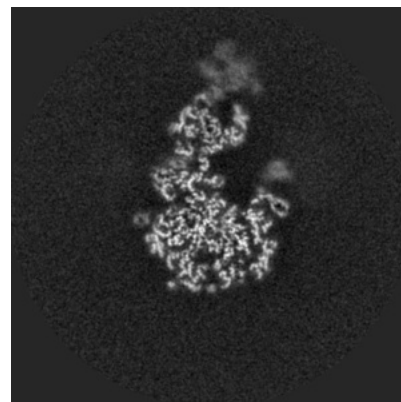
6.2.1 Primary map



X Index: 256

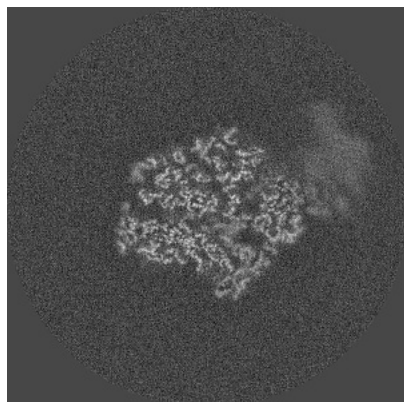


Y Index: 256

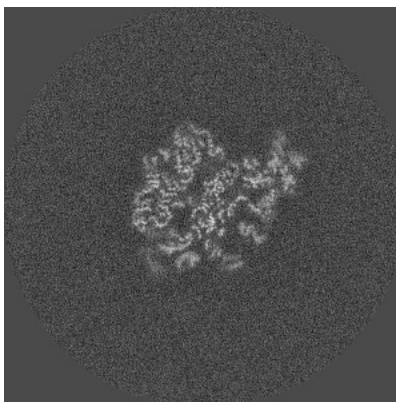


Z Index: 256

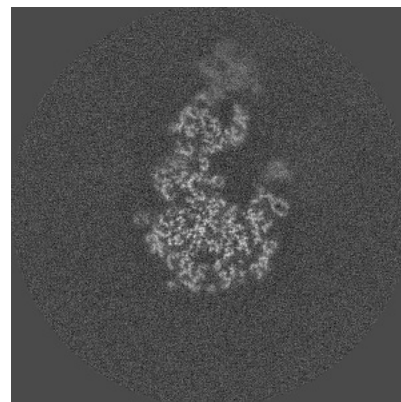
6.2.2 Raw map



X Index: 256



Y Index: 256

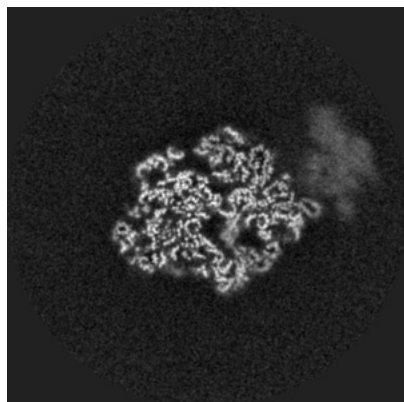


Z Index: 256

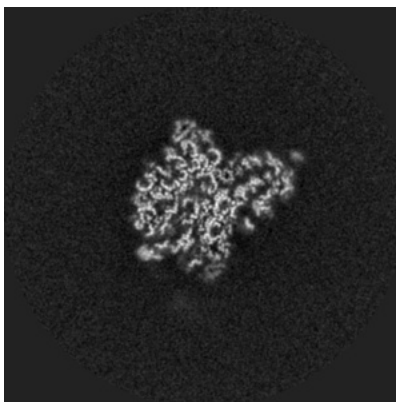
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

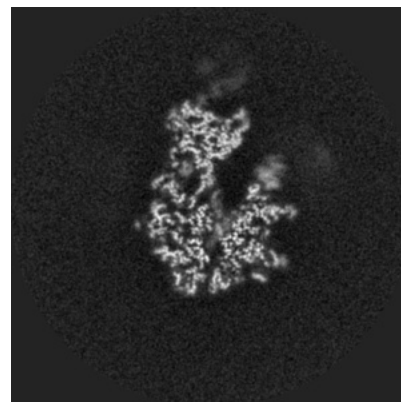
6.3.1 Primary map



X Index: 248

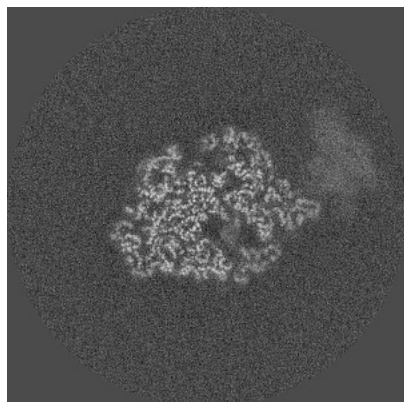


Y Index: 248

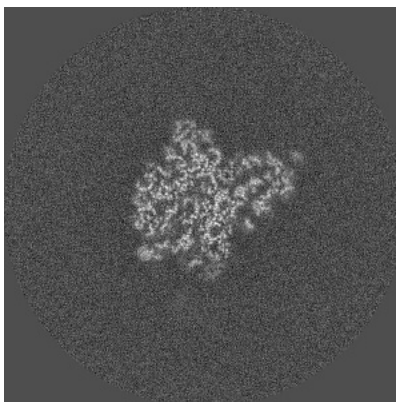


Z Index: 242

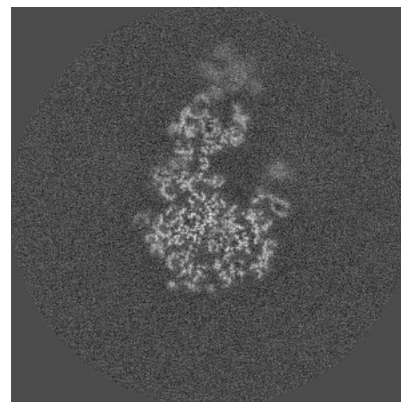
6.3.2 Raw map



X Index: 242



Y Index: 248



Z Index: 257

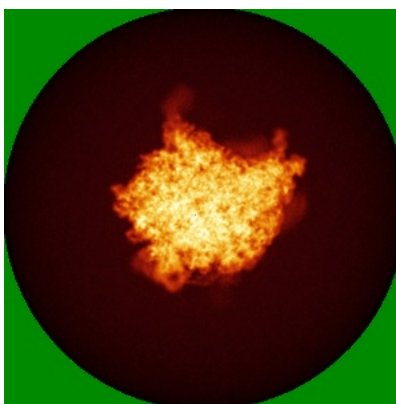
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

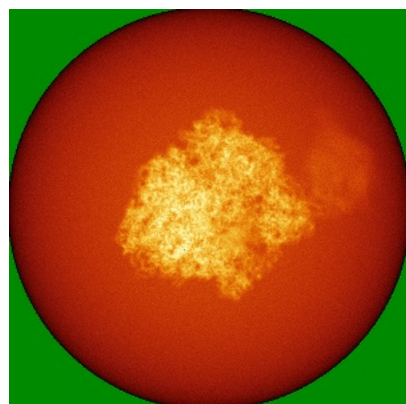


Y

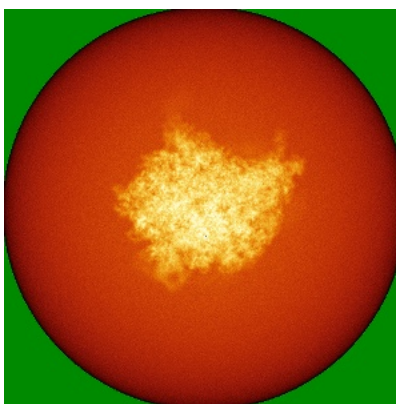


Z

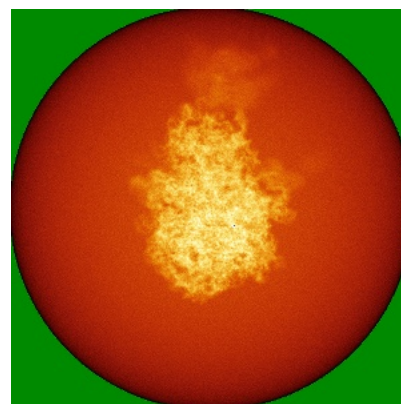
6.4.2 Raw map



X



Y

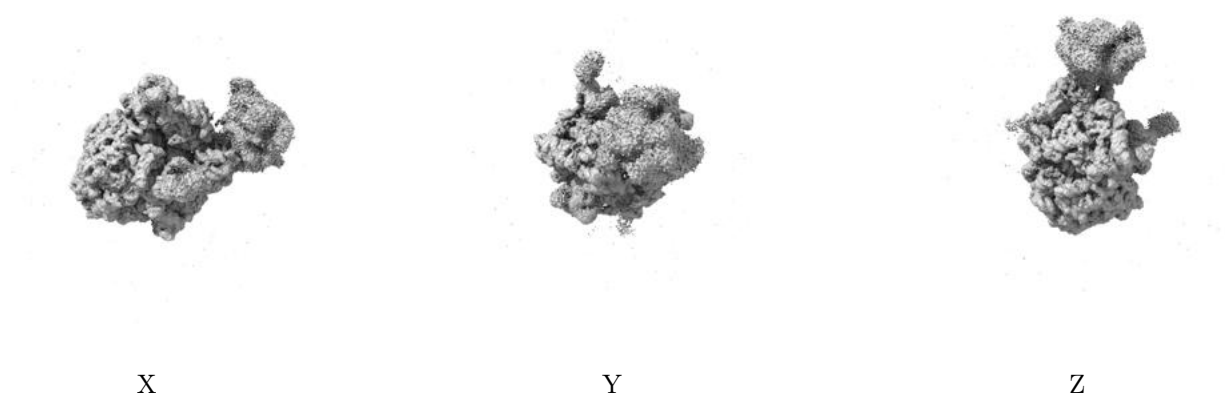


Z

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.

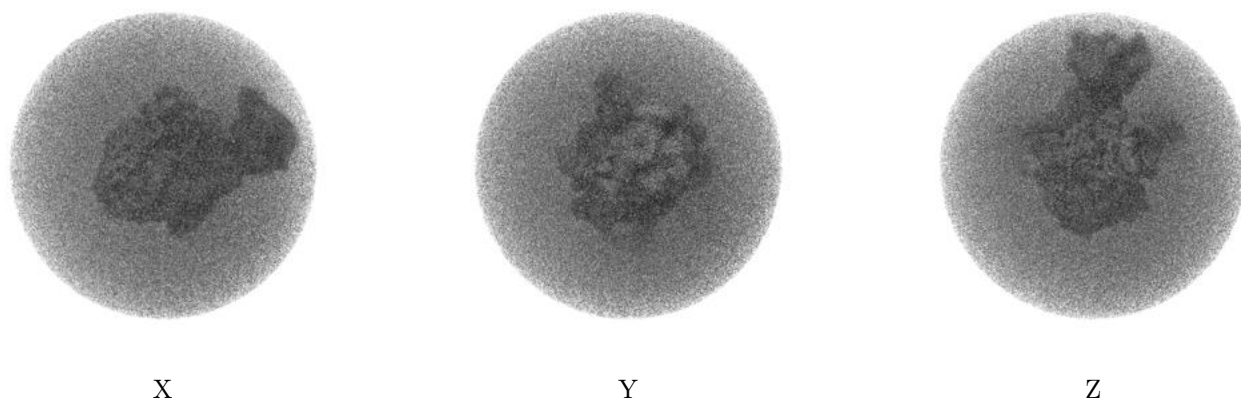
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0037. 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.

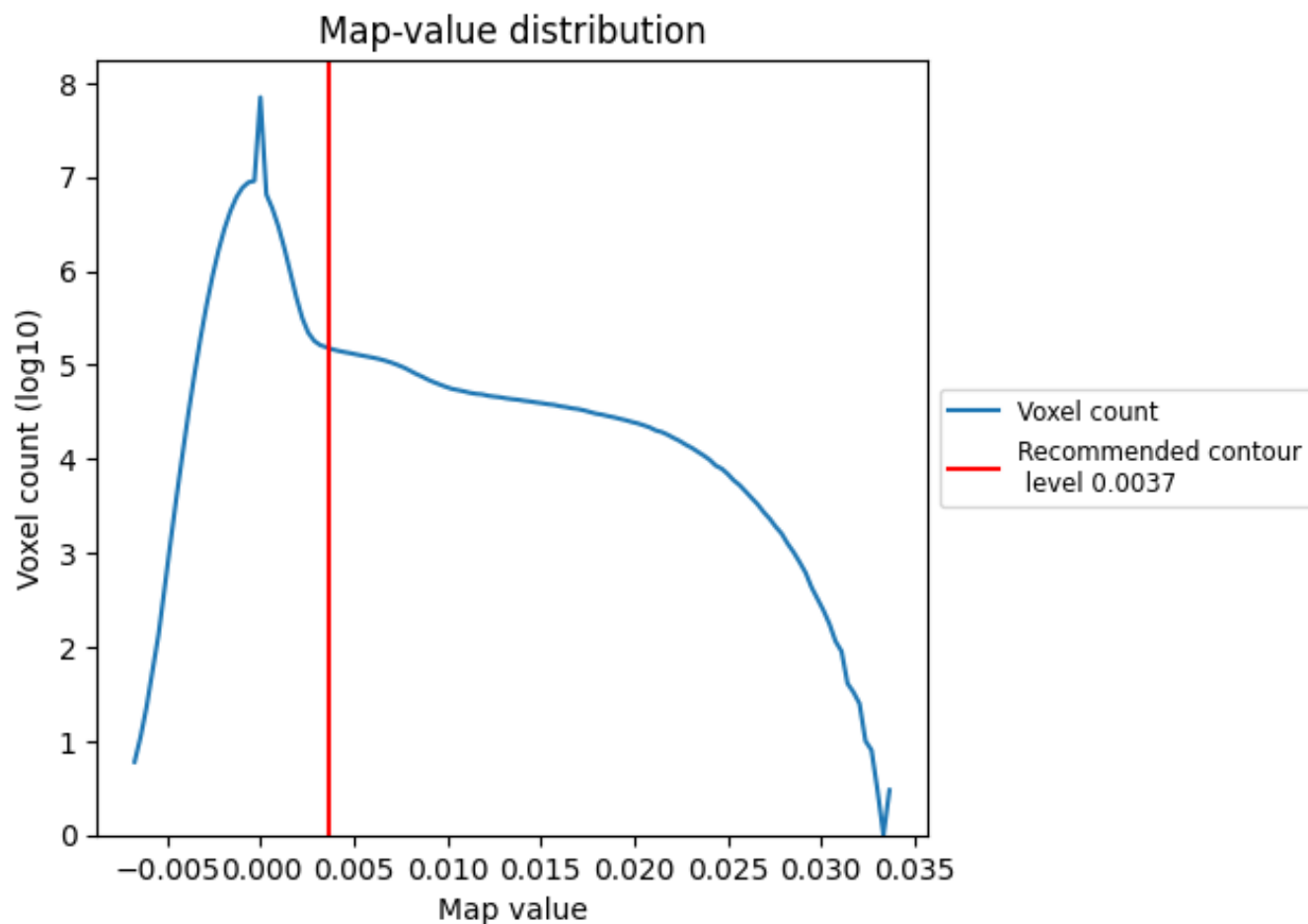
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

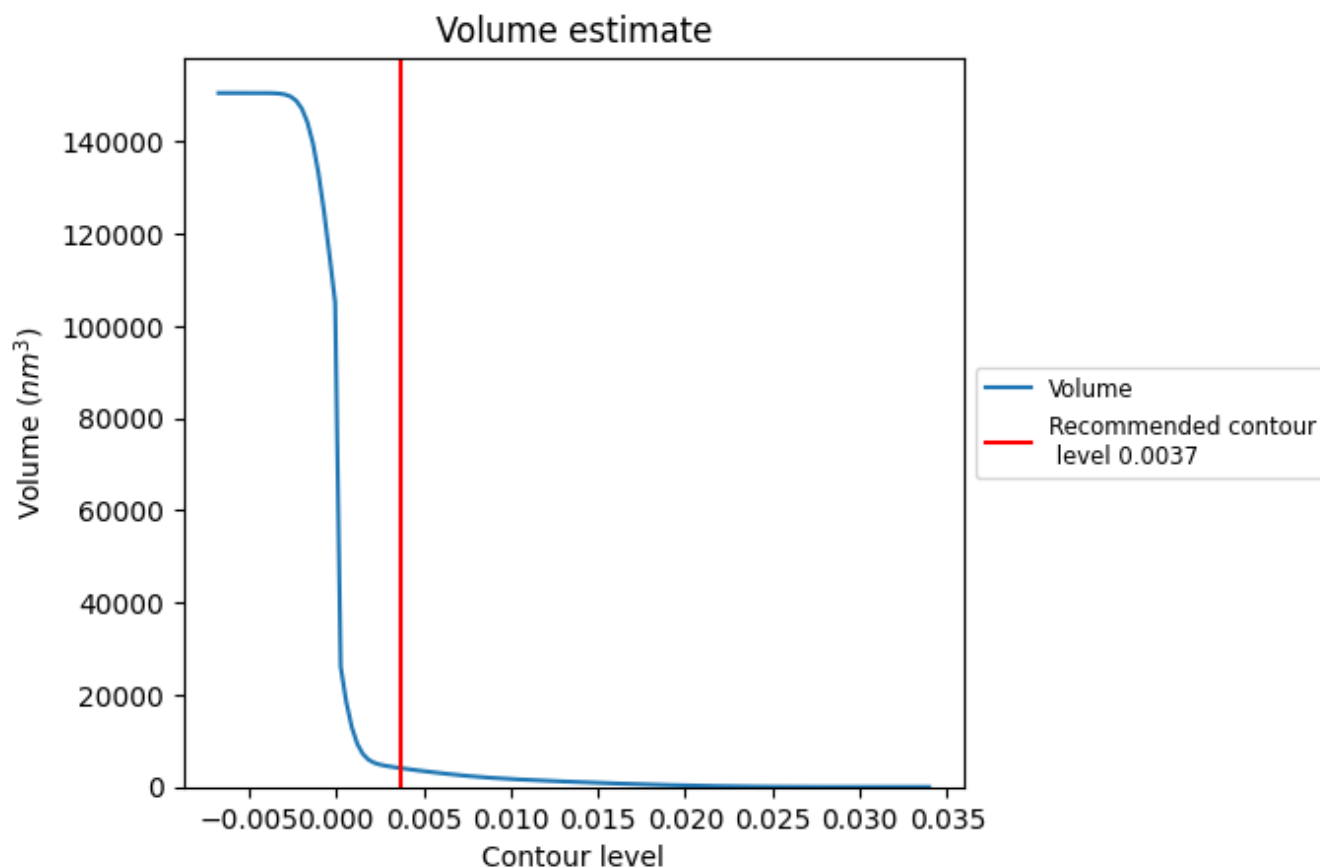
This section contains the results of statistical analysis of the map.

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.

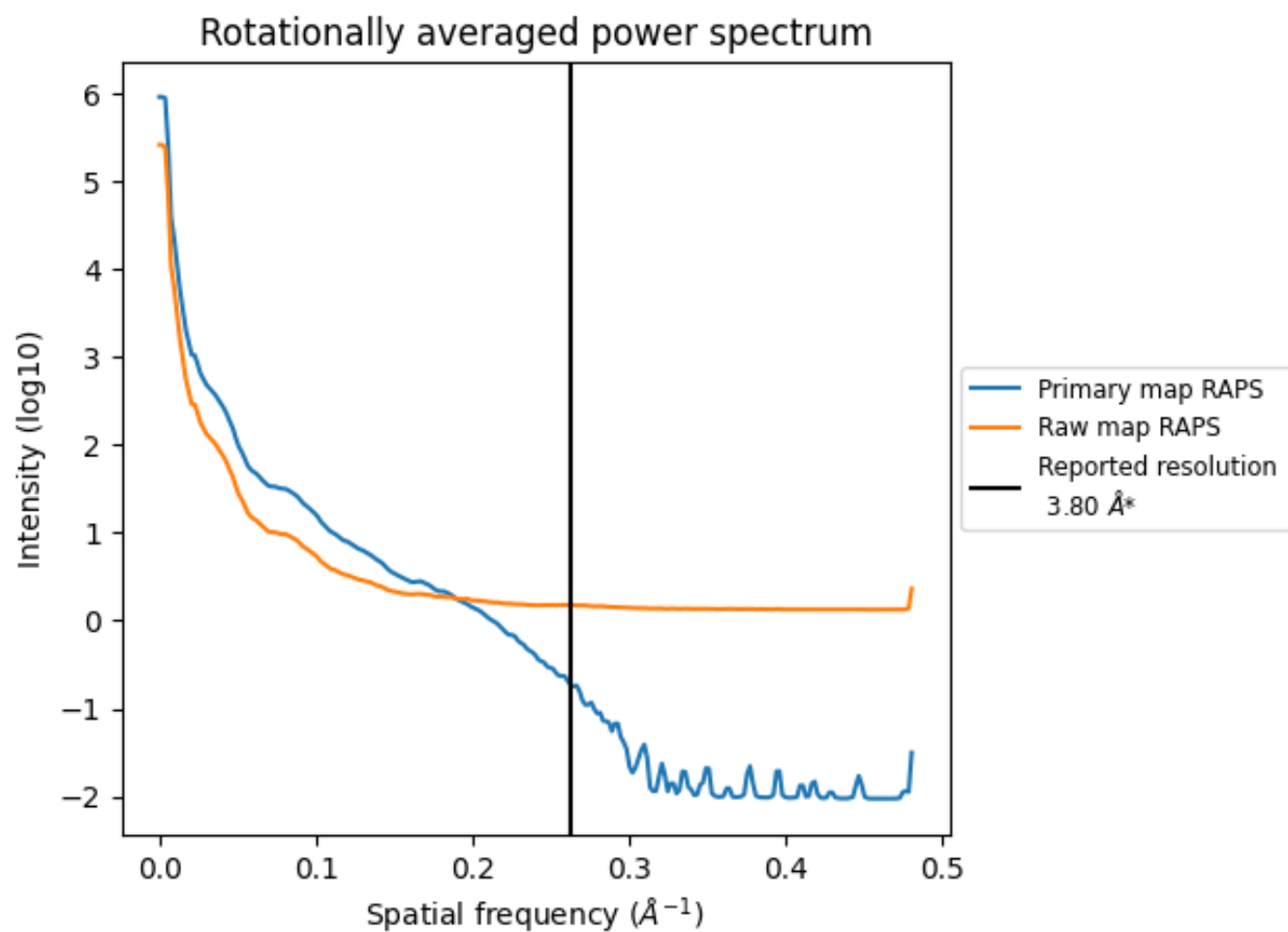
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4079 nm^3 ; this corresponds to an approximate mass of 3685 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 ⓘ

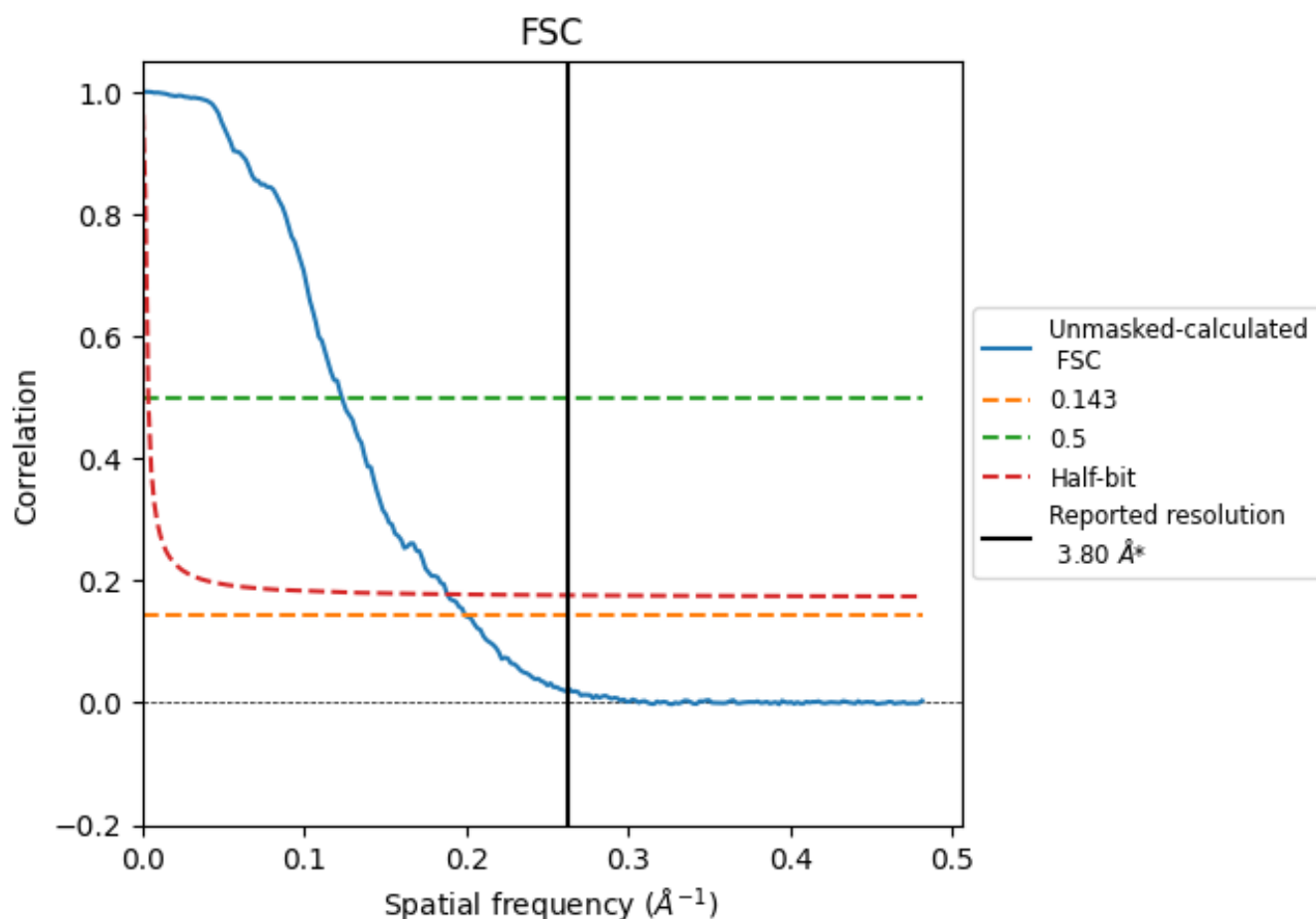


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

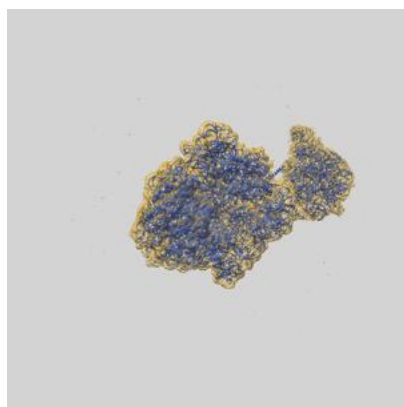
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.02	8.12	5.31

*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 5.02 differs from the reported value 3.8 by more than 10 %

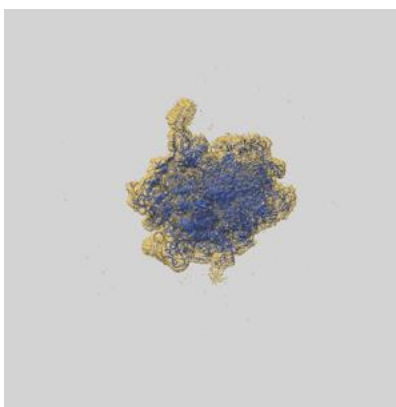
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-42477 and PDB model 8UQP. Per-residue inclusion information can be found in section [3](#) on page [16](#).

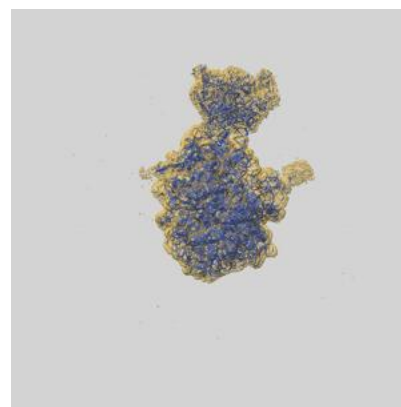
9.1 Map-model overlay [i](#)



X



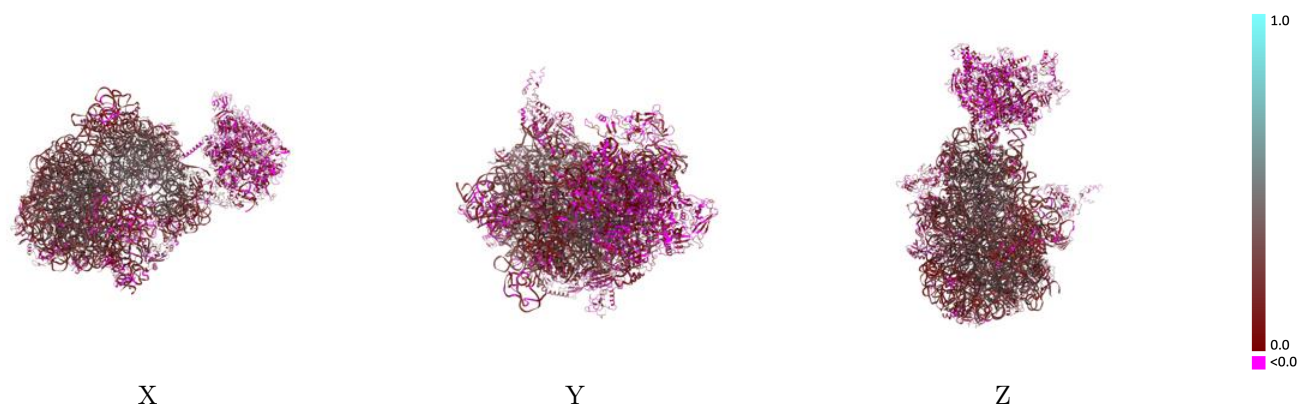
Y



Z

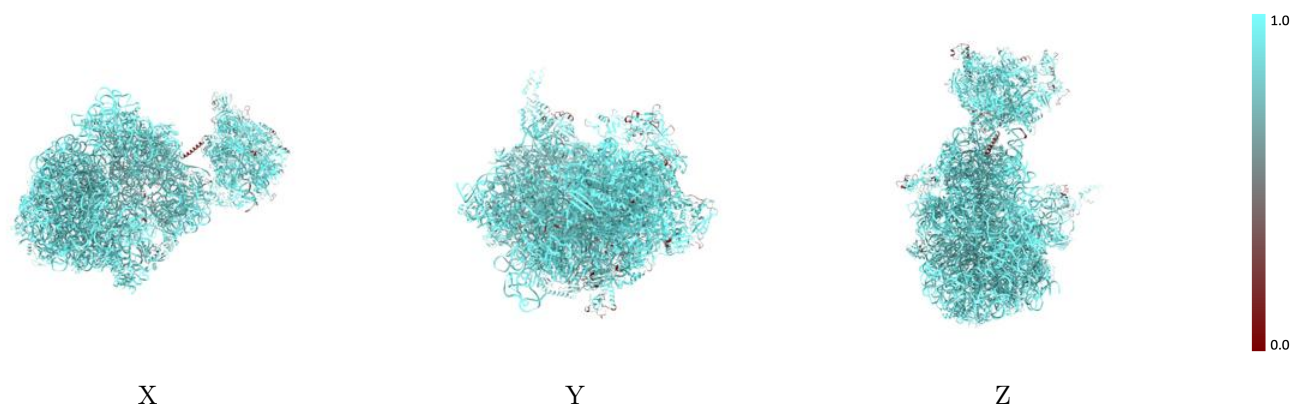
The images above show the 3D surface view of the map at the recommended contour level 0.0037 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



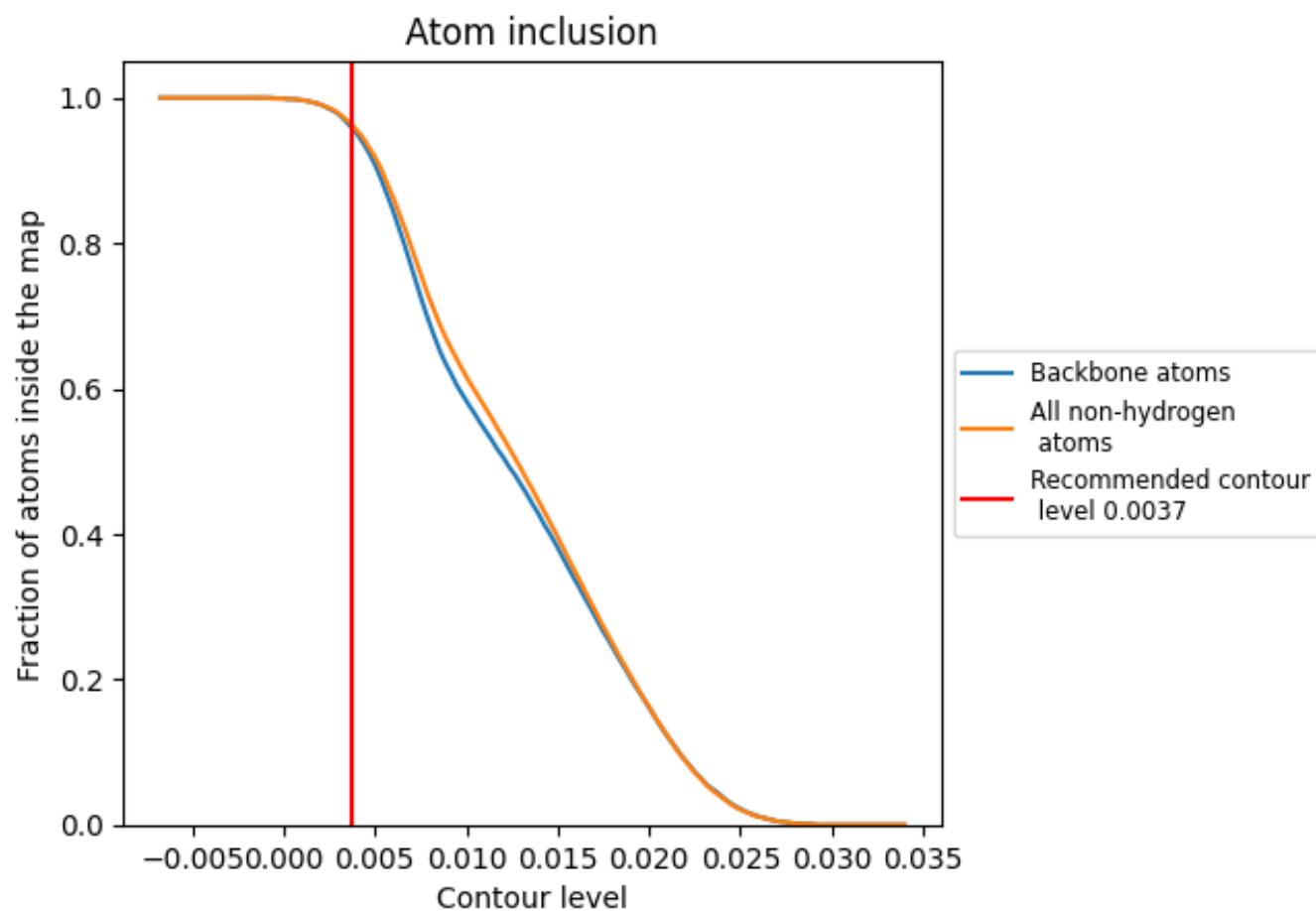
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0037).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.0037) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9640	 0.1970
0	 0.9620	 0.1700
1	 0.9580	 0.2760
2	 0.9490	 0.1540
3	 0.9550	 0.1090
4	 0.9730	 0.1470
5	 0.9020	 0.0740
6	 0.8790	 0.1000
7	 0.9260	 0.1100
9	 0.9120	 0.0720
A	 0.9880	 0.1760
AA	 0.9380	 0.0470
AB	 0.9750	 0.1520
AC	 0.9330	 0.0440
AD	 0.8380	 0.0120
AE	 0.9330	 0.0610
AF	 0.5600	 0.0210
B	 0.9200	 0.0920
C	 0.9730	 0.1770
D	 0.9940	 0.2680
E	 0.9790	 0.1620
F	 0.9590	 0.2180
G	 0.9560	 0.2080
H	 0.7420	 0.0610
I	 0.9620	 0.2700
J	 0.9800	 0.2420
K	 0.9830	 0.3380
L	 0.9540	 0.1120
M	 0.9650	 0.1790
N	 0.9710	 0.2650
O	 0.9720	 0.1620
P	 0.9600	 0.2040
Q	 0.9580	 0.1750
R	 0.9890	 0.3460
S	 0.9730	 0.1960



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
T	 0.9710	 0.2030
U	 0.9670	 0.1880
V	 0.9650	 0.2250
W	 0.9120	 0.1020
X	 0.9370	 0.1280
Y	 0.7780	 0.0690
Z	 0.8850	 0.0720
a	 0.9920	 0.2390
b	 0.9470	 0.1440
c	 0.9530	 0.1960
d	 0.9860	 0.1490
e	 0.9450	 0.1240
f	 0.9660	 0.1780
g	 0.9370	 0.0700
h	 0.9680	 0.2090
i	 0.9700	 0.2910
j	 0.9770	 0.2520
k	 0.9710	 0.1310
l	 0.9260	 0.1280
m	 0.9800	 0.2970
n	 0.9310	 0.1110
o	 0.9470	 0.1670
p	 0.9680	 0.1270
q	 0.9560	 0.1680
r	 0.8130	 0.0960
s	 0.9670	 0.2210
t	 0.9590	 0.2830
u	 0.9530	 0.1440
v	 0.9710	 0.2290
w	 0.9720	 0.2430
x	 0.9490	 0.0410
y	 0.9620	 0.2170
z	 0.9710	 0.2310