



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:14 PM UTC

PDB ID : 8UQM / pdb_00008uqm
EMDB ID : EMD-42474
Title : Escherichia coli transcription-translation coupled complex class B (TTC-B) containing RfaH in loaded state, NusA, 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 : 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

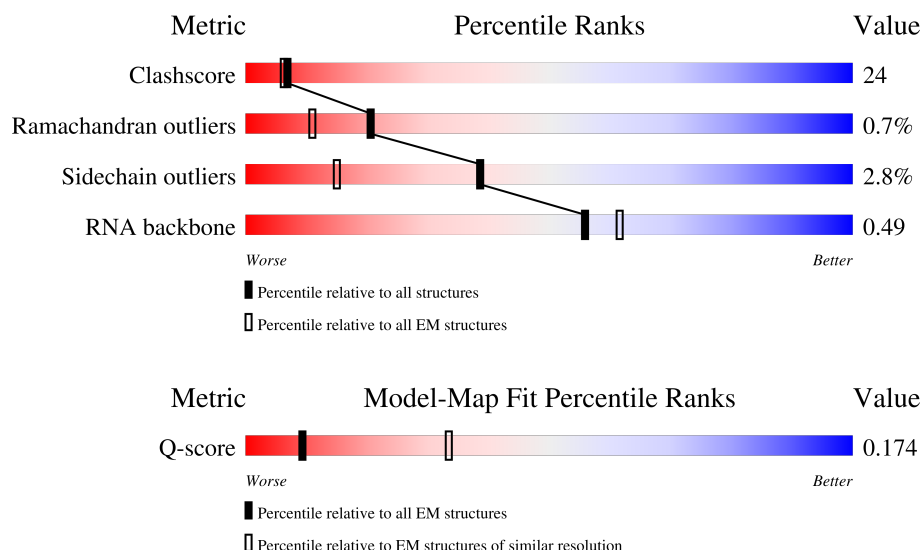
1 Overall quality at a glance i

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.



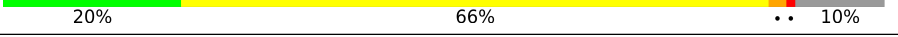
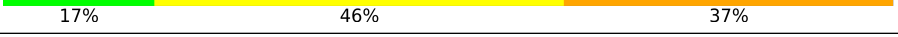
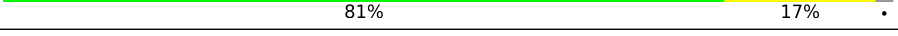
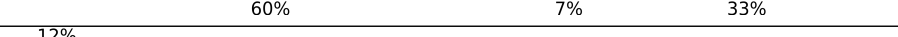
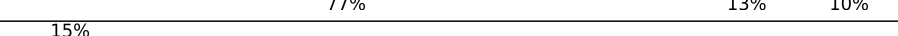
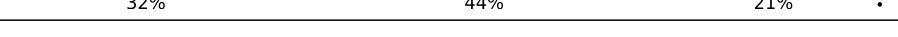
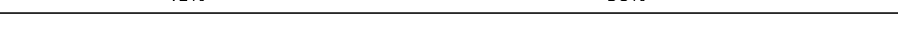
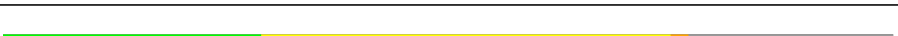
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	625 (4.80 - 5.80)

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	60% 40%
2	1	110	58% 42%
3	2	100	51% 42% 6%

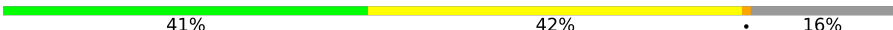
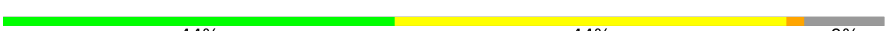
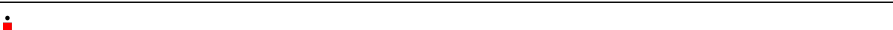
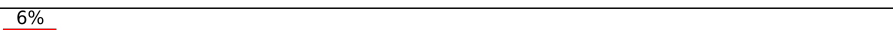
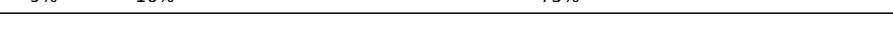
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Mol	Chain	Length	Quality of chain
4	3	104	
5	4	94	
6	5	36	
7	6	36	
8	7	41	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	162	
13	AC	329	
13	AD	329	
14	AE	1407	
15	AF	91	
16	AG	495	
17	C	75	
18	D	1542	
19	E	87	
20	F	71	
21	G	241	
22	H	557	
23	I	233	
24	J	206	
25	K	167	
26	L	135	

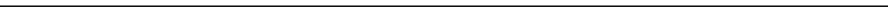
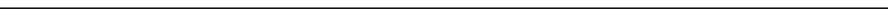
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Mol	Chain	Length	Quality of chain
27	M	179	
28	N	130	
29	O	130	
30	P	103	
31	Q	129	
32	R	124	
33	S	101	
34	T	89	
35	U	82	
36	V	84	
37	W	92	
38	X	118	
39	Y	142	
40	Z	121	
41	a	2904	
42	b	85	
43	c	78	
44	d	120	
45	e	63	
46	f	59	
47	g	70	
48	h	273	
49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

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Mol	Chain	Length	Quality of chain
52	l	201	 59% 40%
53	m	46	 57% 43%
54	n	179	 44% 54% ...
55	o	65	 58% 35% 5% .
56	p	177	 67% 32% .
57	q	38	 61% 39%
58	r	149	 68% 32%
59	s	142	 55% 44% ..
60	t	123	 46% 54% .
61	u	144	 63% 36% .
62	v	136	 49% 49% .
63	w	127	 43% 47% . 6%
64	x	117	 63% 36% .
65	y	115	 63% 37% .
66	z	118	 58% 41% ..

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 280205 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.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	5	31	Total	C	N	O	P		0	0
			636	303	117	185	31			

- Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	36	Total	C	N	O	P	0	0
			706	337	119	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		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

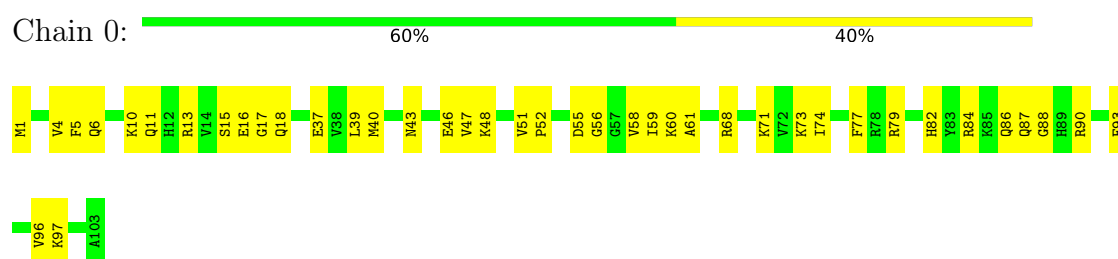
- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

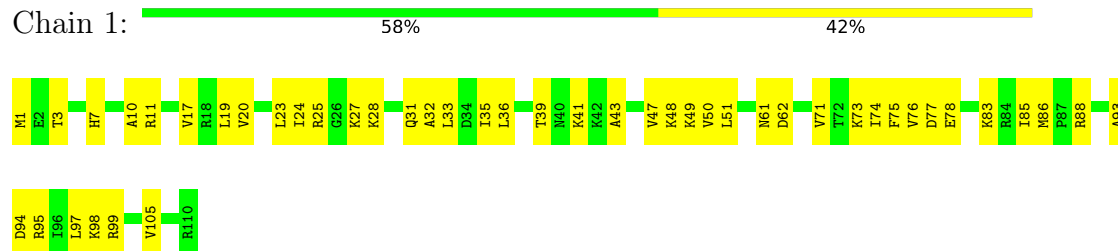
3 Residue-property plots

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.

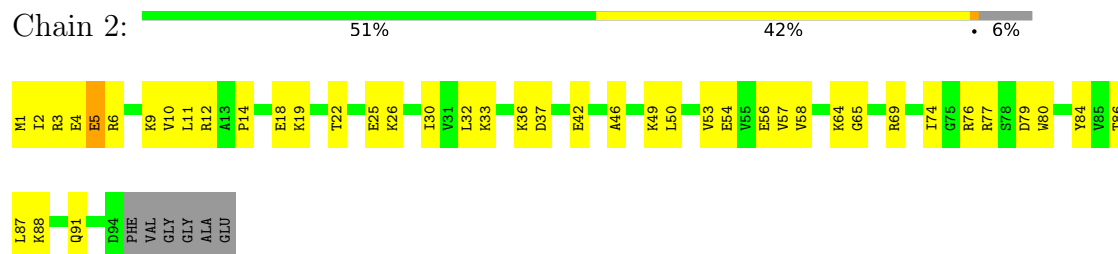
• Molecule 1: Ribosomal protein L21



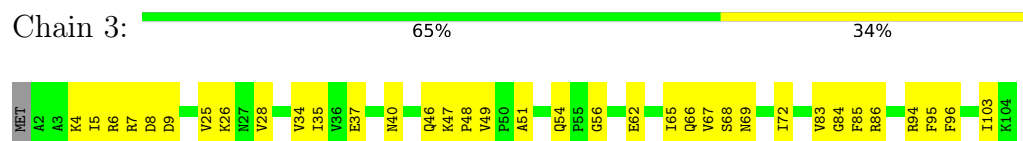
• Molecule 2: 50S ribosomal protein L22



• Molecule 3: 50S ribosomal protein L23

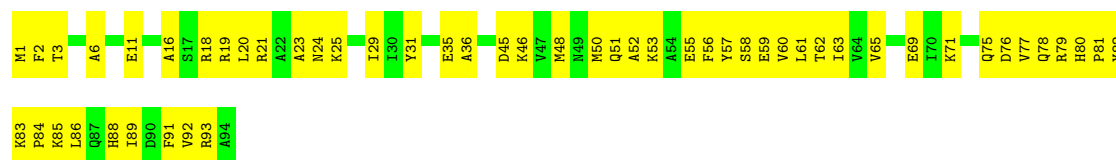


• Molecule 4: 50S ribosomal protein L24



- Molecule 5: 50S ribosomal protein L25

Chain 4: 



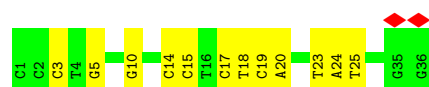
- Molecule 6: NT DNA

Chain 5: 



- Molecule 7: T DNA

Chain 6: 

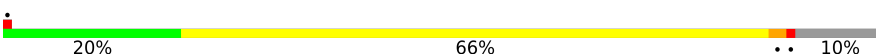


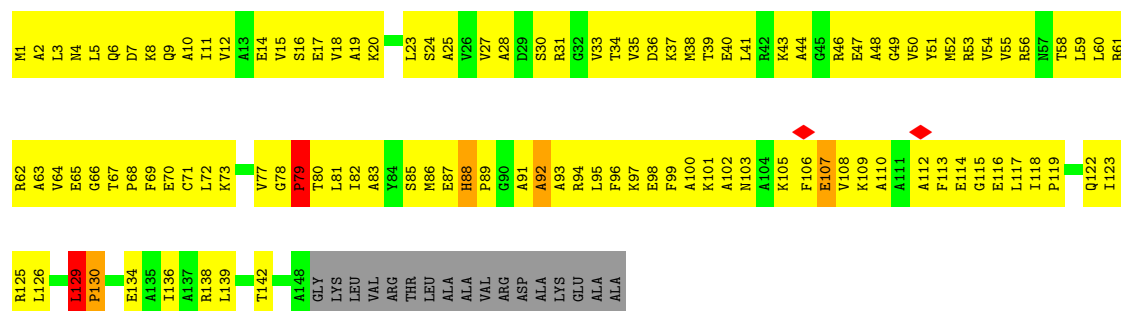
- Molecule 8: mRNA with 24 nt long spacer

Chain 7: 



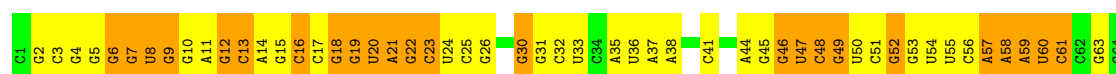
- Molecule 9: 50S ribosomal protein L10

Chain 9: 



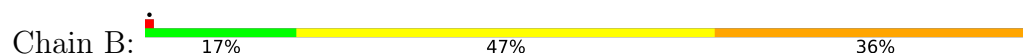
- Molecule 10: E-site and P-site fMet-tRNA

Chain A: 

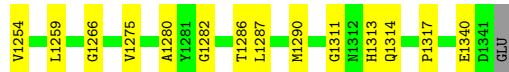
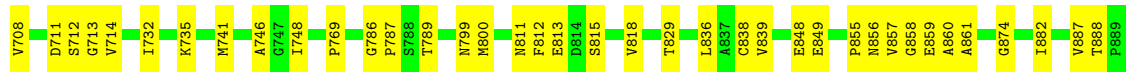
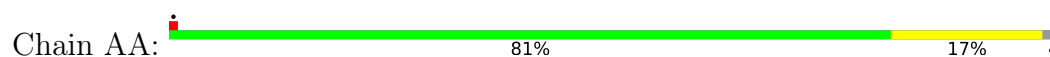




• Molecule 10: E-site and P-site fMet-tRNA

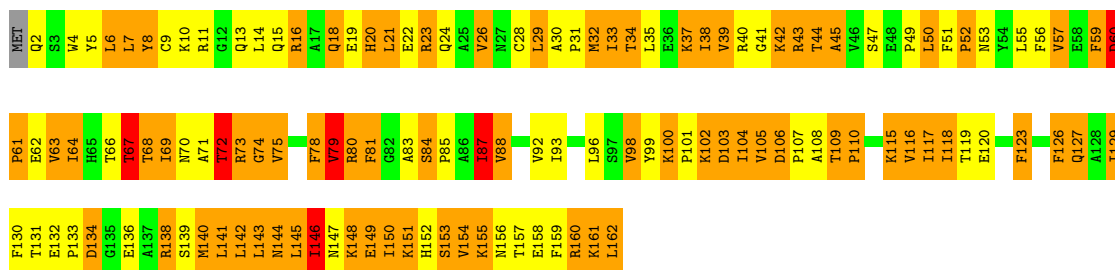


• Molecule 11: DNA-directed RNA polymerase subunit beta



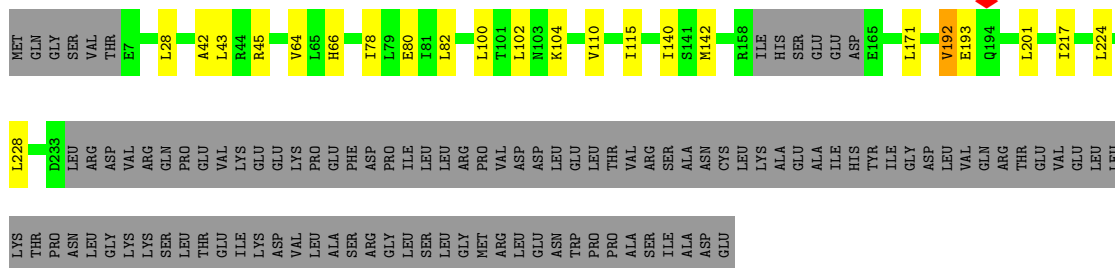
• Molecule 12: Transcription antitermination protein RfaH





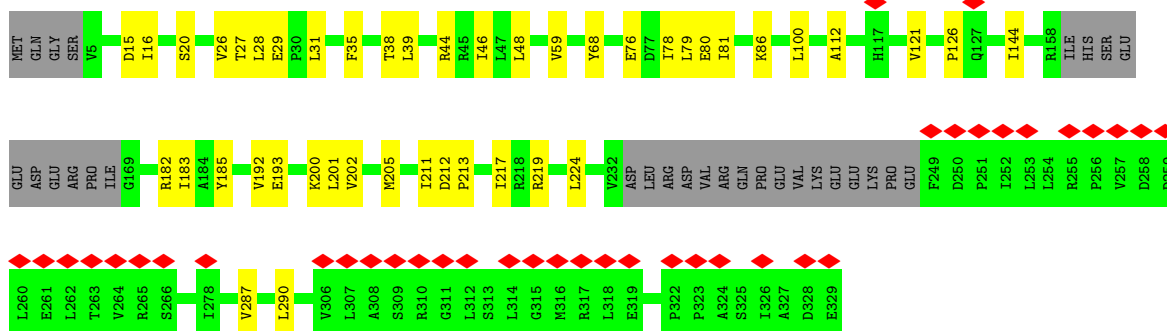
• Molecule 13: DNA-directed RNA polymerase subunit alpha

Chain AC: 60% 7% 33%



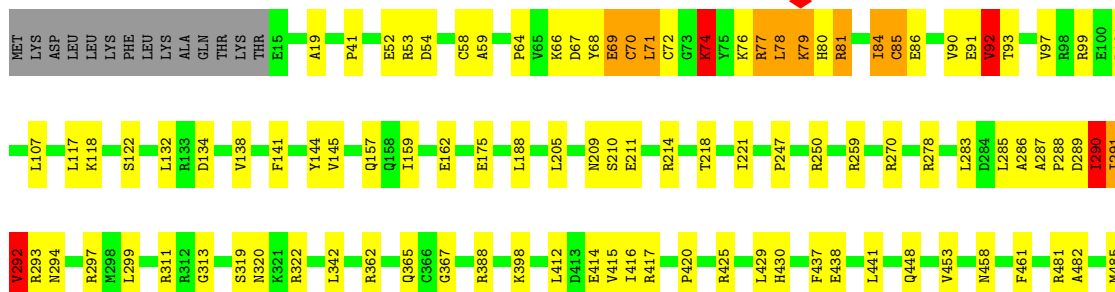
• Molecule 13: DNA-directed RNA polymerase subunit alpha

Chain AD: 12% 78% 13% 9%

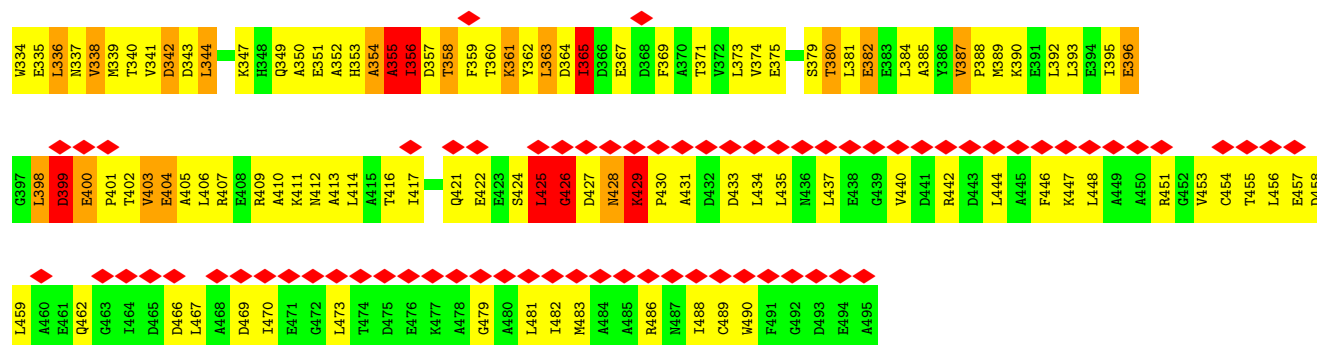


• Molecule 14: DNA-directed RNA polymerase subunit beta'

Chain AE: 78% 15% 5%

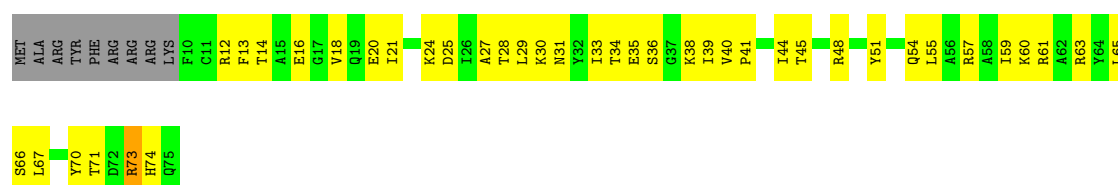






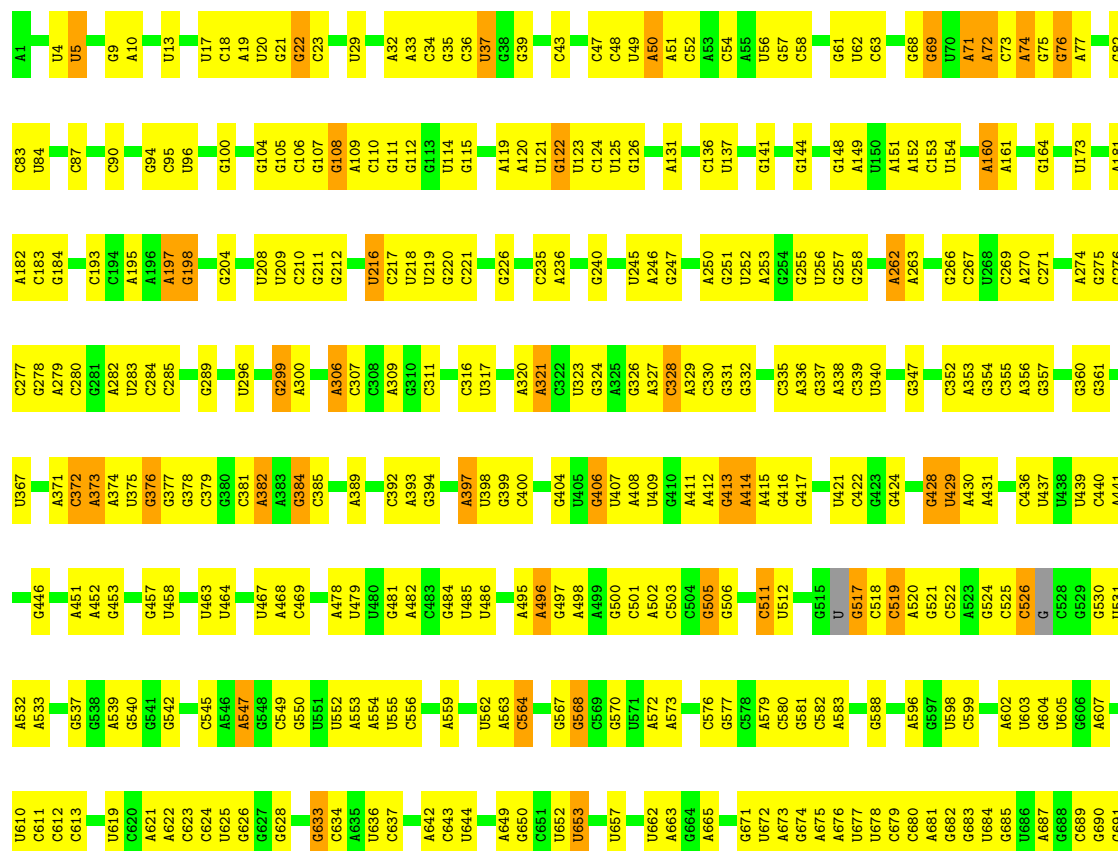
• Molecule 17: 30S ribosomal protein S18

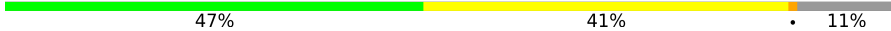
Chain C: 35% 52% 12%

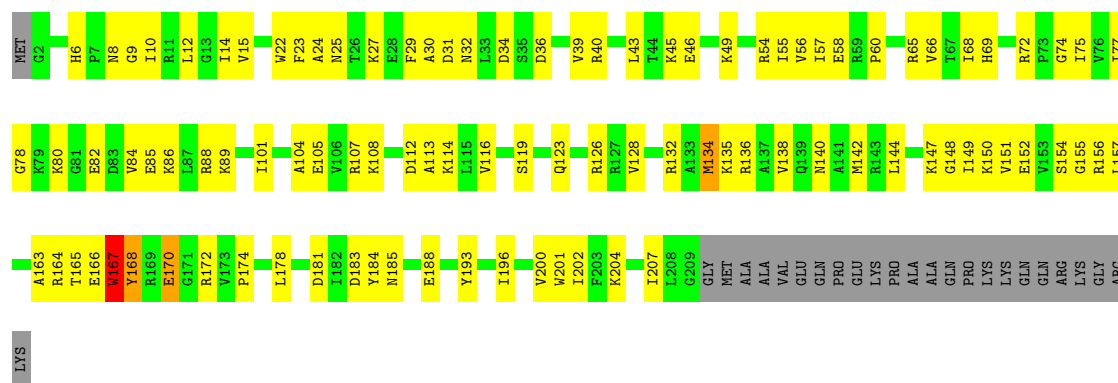


• Molecule 18: 16S rRNA

Chain D: 49% 43% 7%

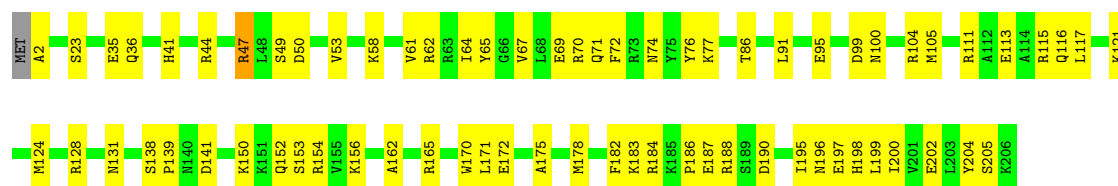


Chain I:  47% 41% 11%

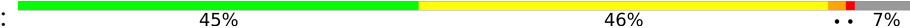


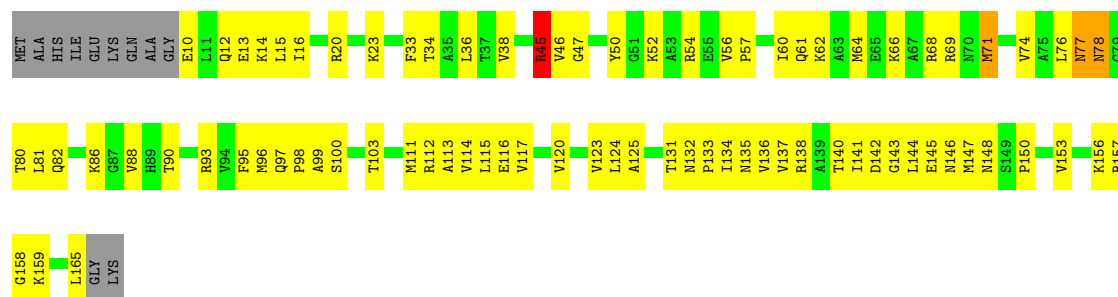
- Molecule 24: 30S ribosomal protein S4

Chain J:  66% 33%

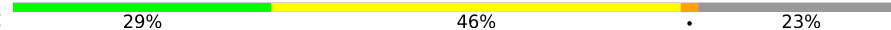


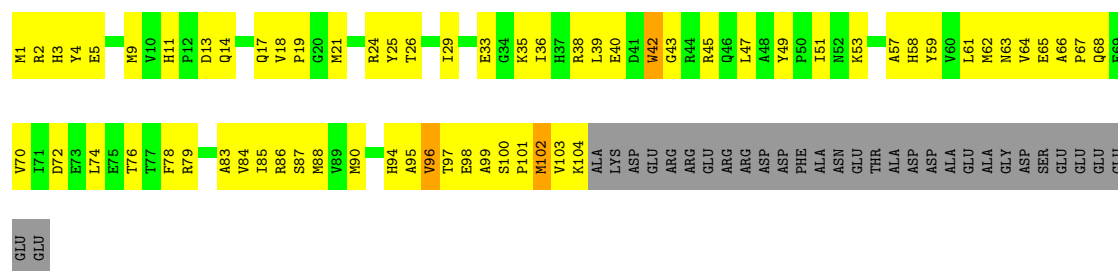
- Molecule 25: 30S ribosomal protein S5

Chain K:  45% 46% 7%

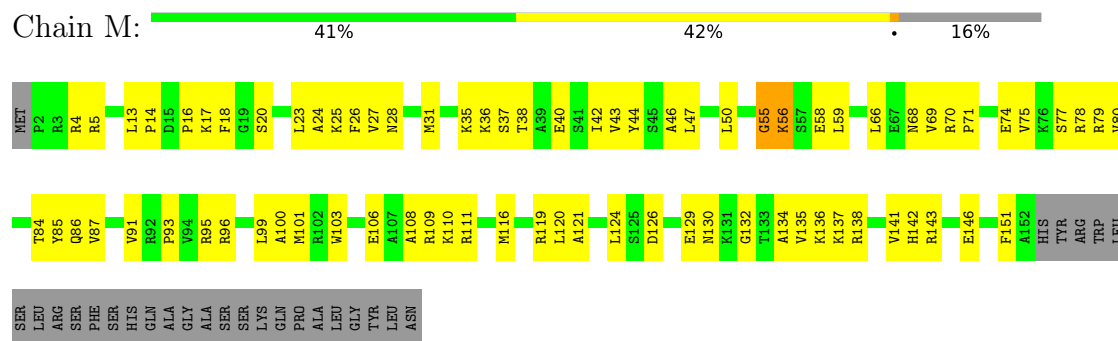


- Molecule 26: 30S ribosomal protein S6

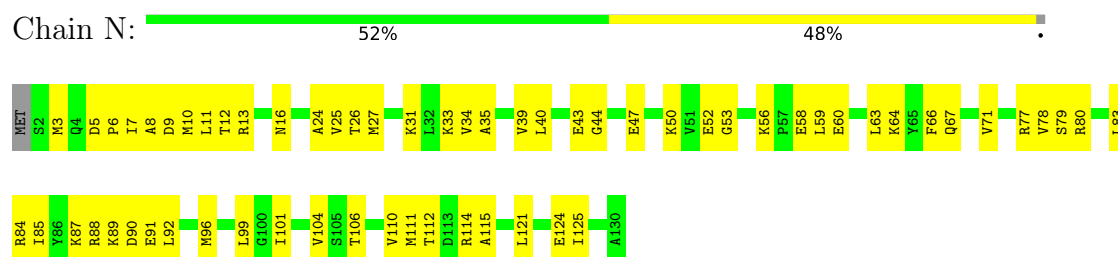
Chain L:  29% 46% 23%



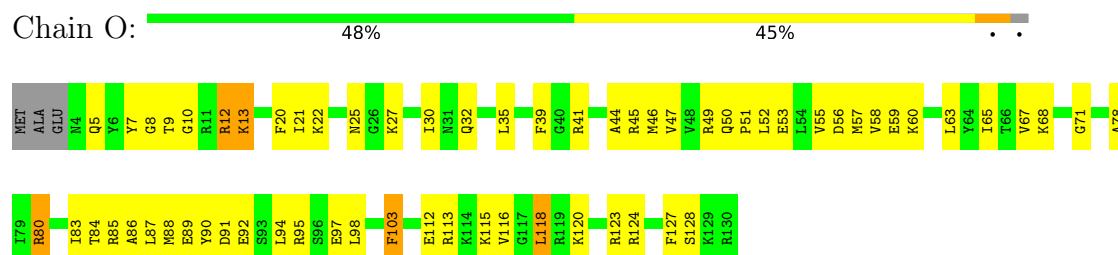
- Molecule 27: 30S ribosomal protein S7



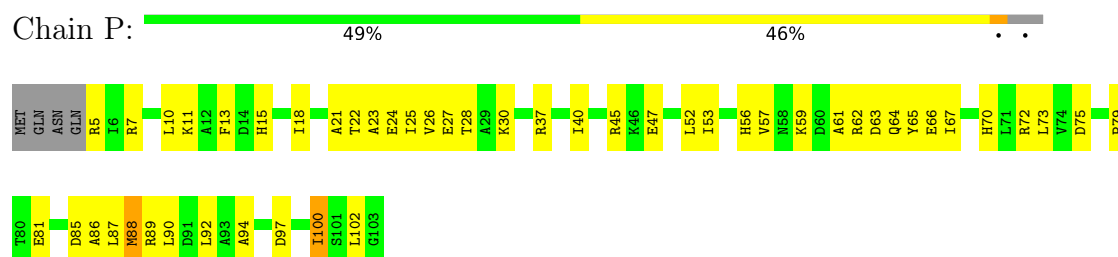
- Molecule 28: 30S ribosomal protein S8



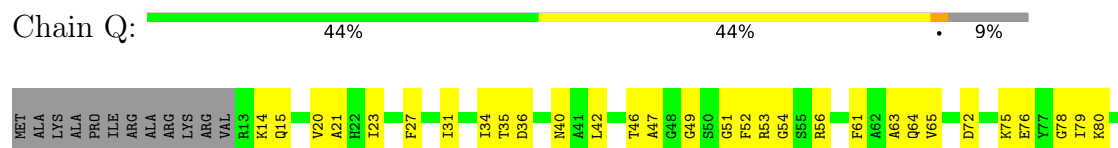
- Molecule 29: 30S ribosomal protein S9



- Molecule 30: 30S ribosomal protein S10



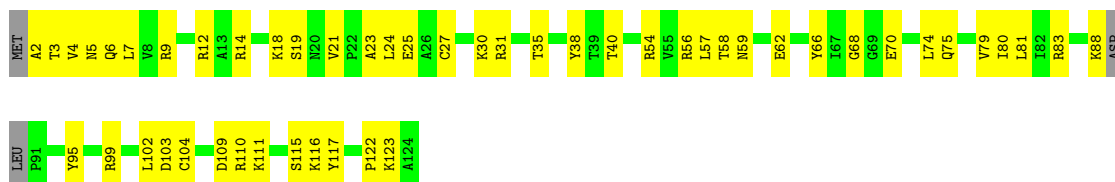
- Molecule 31: 30S ribosomal protein S11





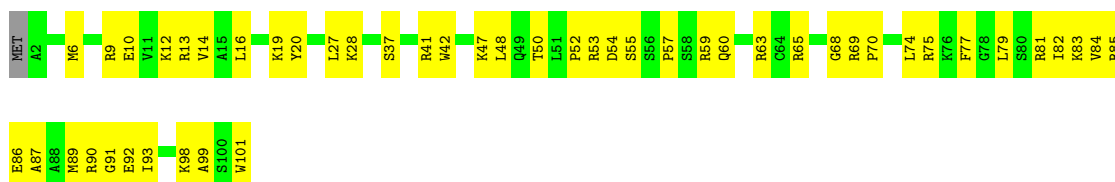
• Molecule 32: 30S ribosomal protein S12

Chain R: 57% 40%



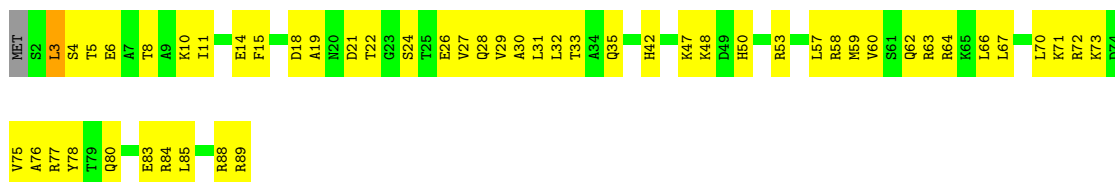
• Molecule 33: 30S ribosomal protein S14

Chain S: 51% 48%



• Molecule 34: 30S ribosomal protein S15

Chain T: 42% 56%



• Molecule 35: 30S ribosomal protein S16

Chain U: 51% 49%

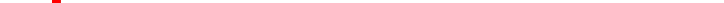


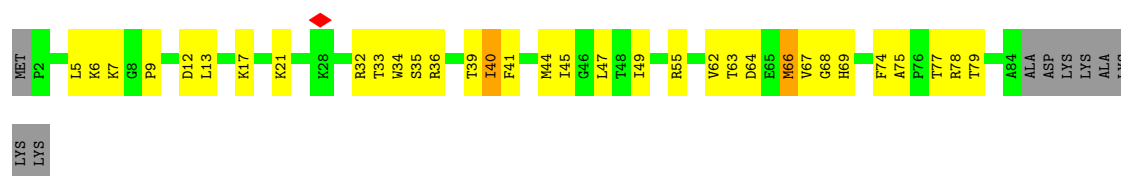
• Molecule 36: 30S ribosomal protein S17

Chain V: 42% 54% 5%



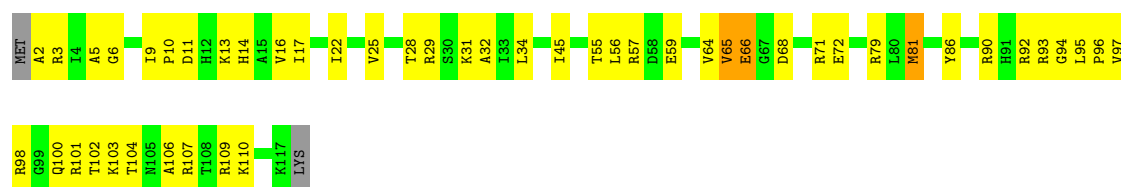
- Molecule 37: 30S ribosomal protein S19

Chain W:  54% 34% 10%

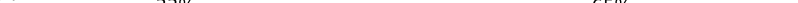


- Molecule 38: 30S ribosomal protein S13

Chain X: 57% 39% .



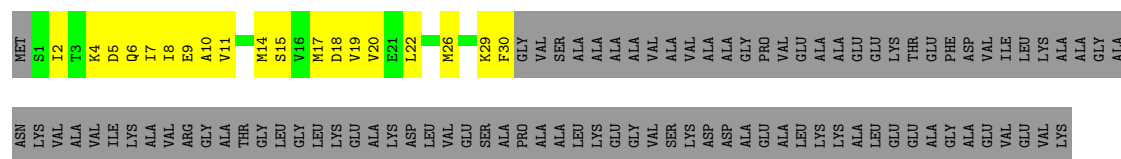
- Molecule 39: 50S ribosomal protein L11

Chain Y:  6% 33% 65% ..

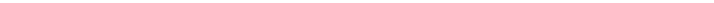


- Molecule 40: 50S ribosomal protein L7/L12

Chain Z: 9% 16% 75%



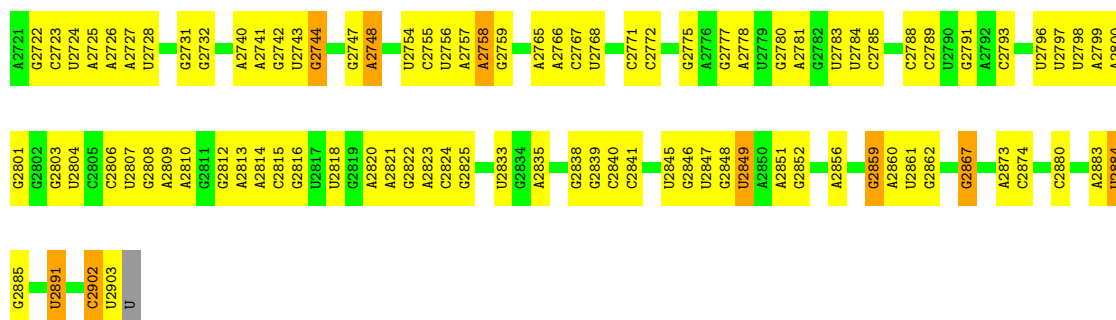
- Molecule 41: 23S rRNA

Chain a:  51% 41% 7%

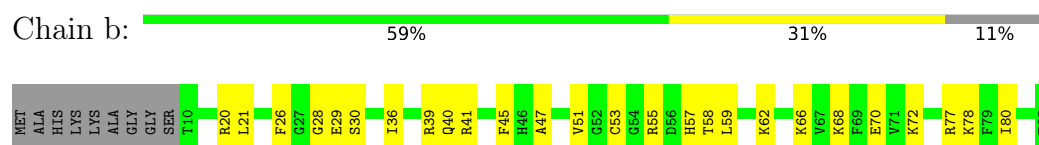


U1344	G1248	G1154	C1079	A1009	U931	G856	G757	A666	A586	A504	C398	G277	C184	G88
C1345	U1249	G1160	A1080	U1012	G938	G857	G760	A667	C587	A505	U399	A278	C192	A94
A1347	G1250	G1161	U1082	C1013	G858	G858	G761	A668	U589	C509	U589	G285	U193	A95
C1348	G1251	G1162	C1013	A1014	G859	G859	A764	G669	A590	G512	U405	G291	A196	C96
C1349	A1252	G1163	U1084	A941	A861	U860	C765	A670	A592	G407	G406	A197	A197	C97
C1350	G1253	G1164	U1085	A945	G862	G862	U773	C672	U593	U519	G407	A299	G205	G98
C1351	G1254	G1165	A1086	C946	G863	G863	U774	A675	U594	G520	G408	A300	G206	A101
U1352	C1257	G1166	G1087	A947	U870	U870	G775	A676	U595	U521	G301	A301	A207	U102
A1353	A1262	G1167	U1088	C948	U871	U871	G776	A677	U596	A522	G302	C302	A207	A103
A1354	G1266	G1168	G1089	G1024	U872	U872	G777	A678	U597	C523	A412	U306	C208	A104
G1360	G1267	U1172	G1025	G952	C873	C873	G780	A685	U598	G529	C413	G307	C210	C105
G1361	A1269	U1173	G953	G953	G874	G874	A781	U686	G600	C530	A415	A310	A213	G110
C1362	C1270	G1175	U	G954	A878	A878	A782	U687	C601	G531	C420	A311	A213	A111
A1365	G1271	U1176	G955	G956	G879	G879	A783	A689	A602	G532	G424	A312	G215	A118
A1366	A1272	G1177	G957	G958	G880	G880	G784	G690	A603	G533	A320	G319	G215	A119
A1367	U1273	U1103	U958	G959	G881	G881	G785	C691	U607	U534	G424	A320	A216	U120
G1368	A1276	G1180	A859	U960	U884	U884	G786	G700	A608	G535	U427	U321	A219	A125
G1369	G1277	U1181	A960	G961	C885	C885	C787	G701	A609	G536	A443	U322	G220	A126
C1370	C1278	U1182	C962	G962	C886	C886	A788	U702	C610	G537	A443	A323	A221	A125
G1371	G1279	U1183	U963	G963	C887	C887	A789	U703	G539	G538	A443	C323	A222	A126
A1378	G1280	G1186	C964	U970	C888	C888	A800	G704	A613	U451	U451	G329	A223	A127
U1379	G1281	U1187	G965	C965	C889	C889	A795	A795	A614	G543	A457	A330	U234	C128
G1380	U1282	U1188	G966	C966	C890	C890	A796	A796	U615	G544	A457	A330	U234	C128
A1383	G1283	U1189	A891	G967	C891	C891	G805	A797	U616	G545	A458	A335	U234	C129
A1384	C1289	G1190	A892	U967	C892	C892	C806	A798	G617	U546	G458	C335	U234	C130
A1385	C1290	U1191	C893	G968	A893	A893	U807	G708	G617	U547	G459	C335	U234	A131
C1386	C1291	G1192	U894	G969	C894	C894	U808	G709	G617	U548	G460	C335	U234	G132
A1387	U1294	U1193	U895	U970	U895	U895	U811	U710	G620	G549	G461	C335	U234	U133
C1392	C1295	U1194	A896	U971	A896	A896	C812	U711	G621	G550	G462	C335	U234	U134
A1393	G1296	U1195	C897	G974	C897	C897	U714	U714	G622	G551	G463	C335	U234	U135
U1394	G1300	U1201	A898	A975	A898	A898	C717	C717	G623	U552	A470	A354	U234	G136
A1395	A1301	U1202	A900	G975	A900	A900	G726	G726	G624	U553	A471	G361	U234	U137
U1396	G1310	A1204	C901	A980	C901	C901	A818	A818	G625	U554	A472	A362	U234	U138
U1397	G1311	A1205	G904	A981	G904	G904	A819	A819	G626	U555	A472	A362	U234	U139
C1398	U1312	G1206	A983	A984	A983	A983	U826	U826	G627	C560	A477	G367	U234	C140
C1399	U1313	U1209	C985	C985	A984	A984	U827	U827	G628	A563	A478	A368	U234	G141
U1400	C1314	U1212	C986	C986	A984	A984	U828	U828	G629	C564	A479	A369	U234	A142
A1403	C1315	G1213	C987	C987	A984	A984	U829	U829	G630	C565	A480	A370	U234	C143
C1404	U1318	A1214	C988	C988	A984	A984	U830	U830	G631	C566	A481	A371	U234	A144
U1405	C1319	G1215	A989	A989	A984	A984	U831	U831	G632	C567	A482	A372	U234	C145
U1406	C1320	U1223	C990	C990	A984	A984	U832	U832	G633	C568	A483	A373	U234	A146
G1407	A1321	G1224	A991	A991	A984	A984	U833	U833	G634	C569	A484	A374	U234	U150
G1408	C1322	G1225	A992	A992	A984	A984	U834	U834	G635	C570	A485	A375	U234	C151
U1409	A1323	A1226	A993	A993	A984	A984	U835	U835	G636	C571	A486	A376	U234	A152
U1410	C1324	G1227	A994	A994	A984	A984	U836	U836	G637	C572	A487	A377	U234	U153
U1411	G1333	G1228	C995	C995	A984	A984	U837	U837	G638	C573	A488	A378	U234	U154
U1412	G1334	U1229	A995	A995	A984	A984	U838	U838	G639	C574	A489	A379	U234	U155
A1413	U1340	G1230	A996	A996	A984	A984	U839	U839	G640	C575	A490	A380	U234	U156
C1414	G1341	G1231	A997	A997	A984	A984	U840	U840	G641	C576	A491	A381	U234	U157
U1415	G1342	G1232	C998	C998	A984	A984	U841	U841	G642	C577	A492	A382	U234	U158
G1416	G1343	G1233	A999	A999	A984	A984	U842	U842	G643	C578	A493	A383	U234	U159
A1417	U1344	G1234	A1000	A1000	A984	A984	U843	U843	G644	C579	A494	A384	U234	U160
U1418	G1345	G1235	A1001	A1001	A984	A984	U844	U844	G645	C580	A495	A385	U234	U161
U1419	G1346	G1236	A1002	A1002	A984	A984	U845	U845	G646	C581	A496	A386	U234	U162
U1420	G1347	G1237	A1003	A1003	A984	A984	U846	U846	G647	C582	A497	A387	U234	U163
U1421	G1348	G1238	A1004	A1004	A984	A984	U847	U847	G648	C583	A498	A388	U234	U164
U1422	G1349	G1239	A1005	A1005	A984	A984	U848	U848	G649	C584	A499	A389	U234	U165
U1423	G1350	G1240	A1006	A1006	A984	A984	U849	U849	G650	C585	A500	A390	U234	U166
U1424	G1351	G1241	A1007	A1007	A984	A984	U850	U850	G651	C586	A501	A391	U234	U167
U1425	G1352	G1242	A1008	A1008	A984	A984	U851	U851	G652	C587	A502	A392	U234	U168
U1426	G1353	G1243	A1009	A1009	A984	A984	U852	U852	G653	C588	A503	A393	U234	U169
U1427	G1354	G1244	A1010	A1010	A984	A984	U853	U853	G654	C589	A504	A394	U234	U170
U1428	G1355	G1245	A1011	A1011	A984	A984	U854	U854	G655	C590	A505	A395	U234	U171
U1429	G1356	G1246	A1012	A1012	A984	A984	U855	U855	G656	C591	A506	A396	U234	U172
U1430	G1357	G1247	A1013	A1013	A984	A984	U856	U856	G657	C592	A507	A397	U234	U173
U1431	G1358	G1248	A1014	A1014	A984	A984	U857	U857	G658	C593	A508	A398	U234	U174
U1432	G1359	G1249	A1015	A1015	A984	A984	U858	U858	G659	C594	A509	A399	U234	U175
U1433	G1360	G1250	A1016	A1016	A984	A984	U859	U859	G660	C595	A510	A400	U234	U176
U1434	G1361	G1251	A1017	A1017	A984	A984	U860	U860	G661	C596	A511	A401	U234	U177
U1435	G1362	G1252	A1018	A1018	A984	A984	U861	U861	G662	C597	A512	A402	U234	U178
U1436	G1363	G1253	A1019	A1019	A984	A984	U862	U862	G663	C598	A513	A403	U234	U179
U1437	G1364	G1254	A1020	A1020	A984	A984	U863	U863	G664	C599	A514	A404	U234	U180
U1438	G1365	G1255	A1021	A1021	A984	A984	U864	U864	G665	C600	A515	A405	U234	U181
U1439	G1366	G1256	A1022	A1022	A984	A984	U865	U865	G666	C601	A516	A406	U234	U182
U1440	G1367	G1257	A1023	A1023	A984	A984	U866	U866	G667	C602	A517	A407	U234	U183
U1441	G1368	G1258	A1024	A1024	A984	A984	U867	U867	G668	C603	A518	A408	U234	U184
U1442	G1369	G1259	A1025	A1025	A984	A984	U868	U868	G669	C604	A519	A409	U234	U185
U1443	G1370	G1260	A1026	A1026	A984	A984	U869	U869	G670	C605	A520	A410	U234	U186
U1444	G1371	G1261	A1027	A1027	A984	A984	U870	U870	G671	C606	A521	A411	U234	U187
U1445	G1372	G1262	A1028	A1028	A984	A984	U871	U871	G672	C607	A522	A412	U234	U188
U1446	G1373	G1263	A1029	A1029	A984	A984	U872	U872	G673	C608	A523	A413	U234	U189
U1447	G1374	G1264	A1030	A1030	A984	A984	U873	U873	G674	C609	A524	A414	U234	U190
U1448	G1375	G1265	A1031	A1031	A984	A984	U874	U874	G675	C610	A525	A415	U234	U191
U1449	G1376	G1266	A1032	A1032	A984	A984	U875	U875	G676	C611	A526	A416	U234	U192
U1450	G1377	G1267	A1033	A1033	A984	A984	U876	U876	G677	C612	A527	A417	U234	U193
U1451	G1378	G1268	A1034	A1034	A984	A984	U877	U877	G678	C613	A528	A418	U234	U194
U1452	G1379	G1269	A1035	A1035	A984	A984	U878	U878	G679	C614	A529	A419	U234	U195
U1453	G1380	G1270	A1036	A1036	A984	A984	U879	U879	G680	C615	A530	A420	U234	U196
U1454	G1381	G1271	A1037	A1037	A984	A984	U880	U880	G681	C616	A531	A421	U234	U197
U1455	G1382	G1272	A1038	A1038	A984	A984	U881	U881	G682	C617	A532	A422	U234	U198
U1456	G1383	G1273	A1039	A1039	A984	A984	U882	U882	G683	C618	A533	A423	U234	U199
U1457	G1384	G1274	A1040	A1040	A984	A984	U883	U883	G684	C619	A534	A424	U234	U200
U1458	G1385	G1275	A1041	A1041	A984	A984	U884	U88						

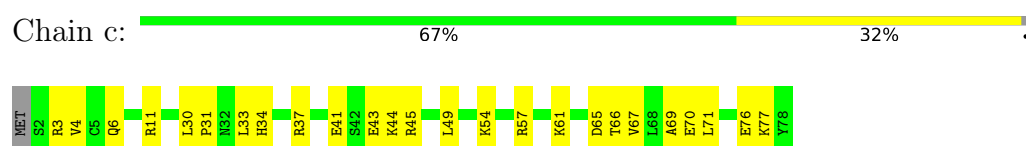
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A2468	A2469	G2470	G2391	U2473	U2474	U2475	A2476	U2554	U2477	G2481	G2482	C2483	C2484	U2489	U2490	U2491	U2492	U2493	G2494	C2497	C2499	C2502	A2505	U2507	U2511	C2512	A2513	U2514	C2515	C2516	C2517	U2518	C2519	C2520	G2525	G2526	C2529	A2530	U2531	U2532	U2533	U2534	U2535	U2536	U2537	U2538	U2539	U2540	U2541	U2542	U2543	U2544	U2545	U2546	U2547
G2308	A2309	C2310	C2311	U2312	U2313	U2314	G2315	U2320	U2321	A2322	C2325	C2326	C2327	U2328	U2329	U2330	U2331	C2332	A2333	U2334	A2335	C2338	C2345	C2346	C2347	U2348	C2349	C2350	C2351	G2355	U2356	C2357	G2361	C2362	C2363	C2364	C2365	C2366	C2367	U2369	C2372	C2373	C2374	U2375	A2376	U2377	U2378	U2379	U2380	U2381	U2382	U2383	C2385		
A2386	U2387	G2391	U2392	U2393	C2394	C2395	C2396	U2402	U2403	A2406	A2407	U2419	U2420	U2421	U2422	U2423	U2424	U2425	U2426	U2427	U2428	U2429	U2430	U2431	U2434	A2435	U2436	U2441	U2442	U2443	U2444	U2445	U2446	U2447	U2448	U2449	U2450	U2451	U2452	U2453	U2454	U2455	U2456	U2457	U2458	U2459	U2460	U2461	U2462	U2463	U2464	U2465	U2466	U2467	
A2468	A2469	G2470	U2473	U2474	U2475	U2476	A2478	G2481	G2482	C2483	C2484	U2489	U2490	U2491	U2492	U2493	G2494	C2497	C2499	C2502	A2505	U2507	U2511	C2512	A2513	U2514	C2515	C2516	C2517	U2518	C2519	C2520	G2525	G2526	C2529	A2530	U2531	U2532	U2533	U2534	U2535	U2536	U2537	U2538	U2539	U2540	U2541	U2542	U2543	U2544	U2545	U2546	U2547		
A2547	U2548	G2549	U2550	U2551	U2552	U2553	U2554	U2555	U2556	U2557	U2558	A2566	U2567	U2568	U2569	U2570	U2571	U2572	U2573	U2574	C2579	U2581	U2582	U2583	U2584	U2585	U2586	U2587	U2588	U2589	U2590	U2591	U2592	A2602	G2603	U2604	U2605	U2606	U2607	U2608	U2609	U2610	U2611	U2612	U2613	U2614	U2615	U2616	U2617	U2618	U2619	U2620	U2621		
A1419	A1420	G1421	G1422	A1427	C1428	G1429	G1430	A1431	G1432	A1433	A1434	G1435	G1441	U1442	U1443	G1444	G1445	G1452	A1453	C1454	U1460	U1467	U1468	U1469	A1470	A1477	G1482	G1483	G1484	A1490	A1497	C1498	U1499	G1500	A1503	U1506	C1507	U1508	A1509	G1510	G1511	U1512	U1513	A1514	A1515	G1519	U1524	A1535							



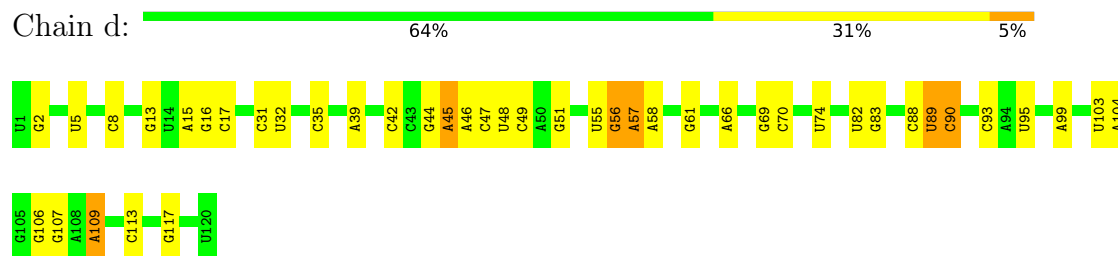
- Molecule 42: 50S ribosomal protein L27



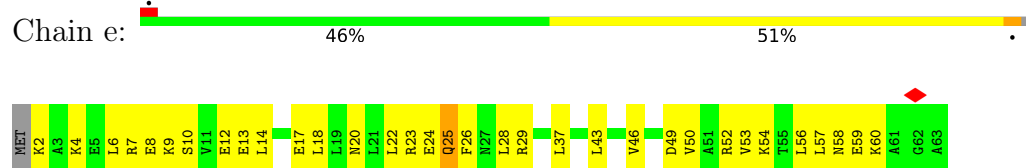
- Molecule 43: 50S ribosomal protein L28



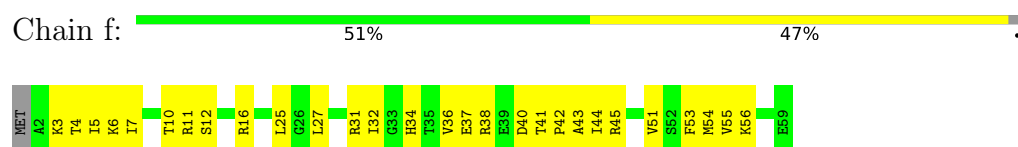
- Molecule 44: 5S rRNA



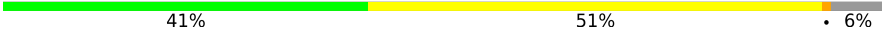
- Molecule 45: 50S ribosomal protein L29



- Molecule 46: 50S ribosomal protein L30



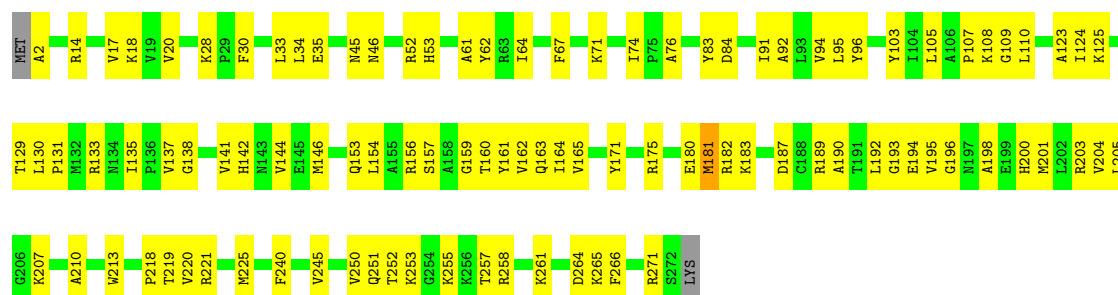
- Molecule 47: 50S ribosomal protein L31

Chain g:  41% 51% 6%



• Molecule 48: 50S ribosomal protein L2

Chain h:  62% 37%



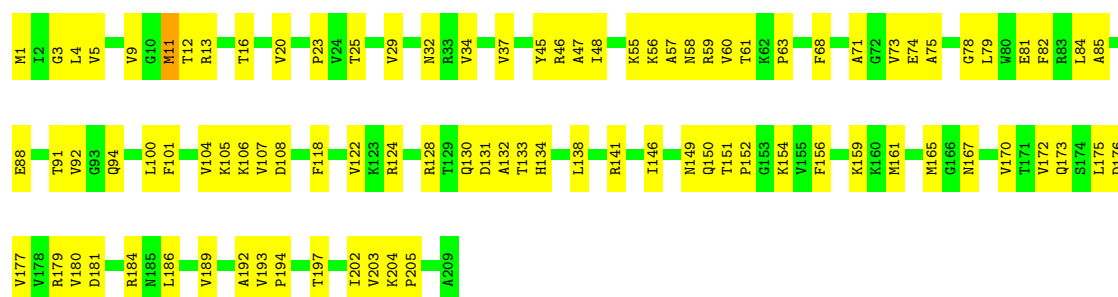
• Molecule 49: 50S ribosomal protein L32

Chain i:  54% 44%



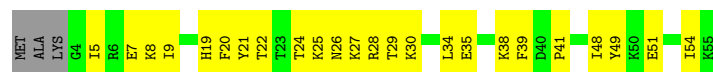
• Molecule 50: 50S ribosomal protein L3

Chain j:  56% 44%



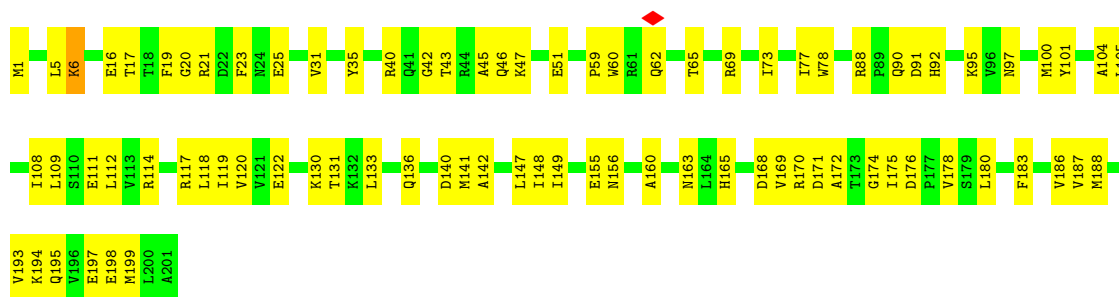
• Molecule 51: 50S ribosomal protein L33

Chain k:  51% 44% 5%



• Molecule 52: 50S ribosomal protein L4

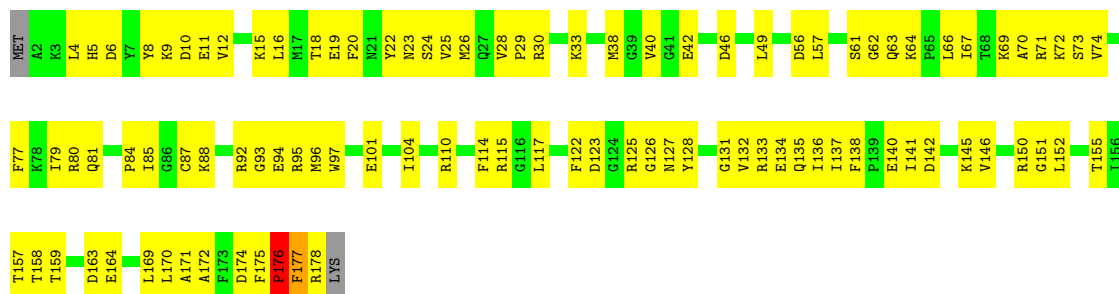
Chain l:  59% 40%



- Molecule 53: 50S ribosomal protein L34



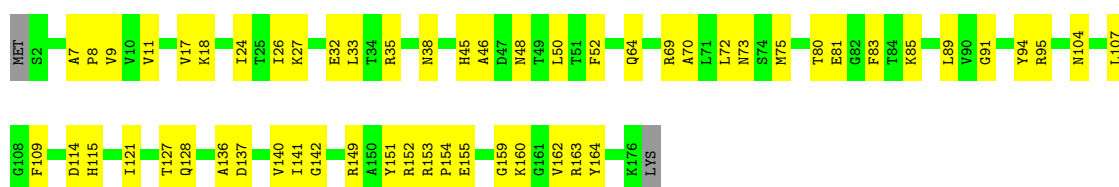
- Molecule 54: 50S ribosomal protein L5



- Molecule 55: 50S ribosomal protein L35



- Molecule 56: 50S ribosomal protein L6

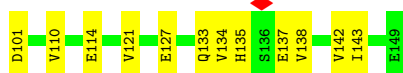


- Molecule 57: 50S ribosomal protein L36





- Molecule 58: 50S ribosomal protein L9



- Molecule 59: 50S ribosomal protein L13



- Molecule 60: 50S ribosomal protein L14

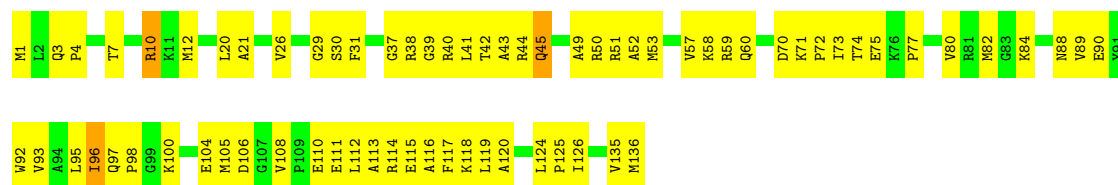


- Molecule 61: 50S ribosomal protein L15



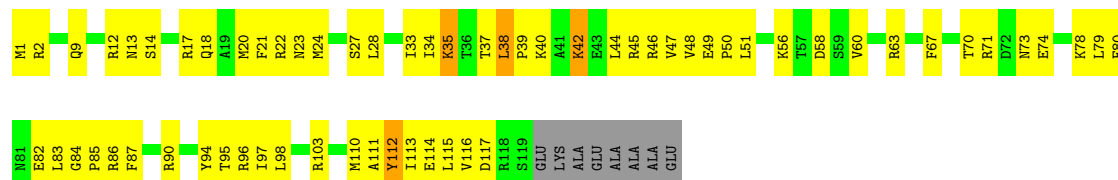
- Molecule 62: 50S ribosomal protein L16





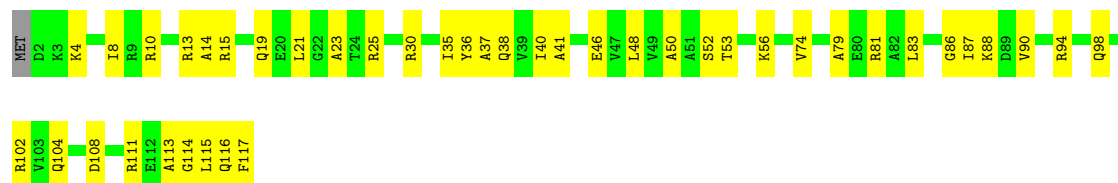
• Molecule 63: 50S ribosomal protein L17

Chain w: 43% 47% 6%



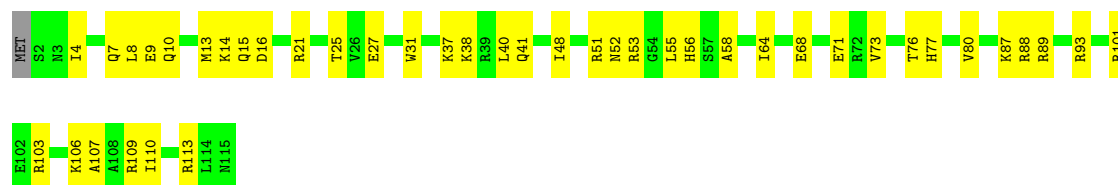
• Molecule 64: 50S ribosomal protein L18

Chain x: 63% 36%



• Molecule 65: 50S ribosomal protein L19

Chain y: 63% 37%



• Molecule 66: 50S ribosomal protein L20

Chain z: 58% 41%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19976	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	0.030	Depositor
Minimum map value	-0.008	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0019	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: 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	0.58	0/712	0.80	0/1094
7	6	0.57	0/786	0.80	0/1206
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	0.63	2/14232 (0.0%)
12	AB	0.98	0/1317	1.05	0/1786
13	AC	0.38	0/1718	0.62	0/2328
13	AD	0.30	0/2096	0.60	0/2854
14	AE	0.39	0/10561	0.64	5/14258 (0.0%)
15	AF	0.30	0/652	0.61	0/879
16	AG	0.94	5/3897 (0.1%)	1.26	28/5273 (0.5%)
17	C	0.68	0/553	0.81	1/743 (0.1%)
18	D	0.29	0/36610	0.41	9/57091 (0.0%)
19	E	0.61	0/675	0.72	0/895
20	F	0.53	0/597	0.60	0/792
21	G	0.68	5/1791 (0.3%)	0.79	8/2413 (0.3%)
22	H	0.38	0/1746	0.81	0/2382
23	I	0.57	1/1663 (0.1%)	0.68	5/2241 (0.2%)
24	J	0.46	0/1665	0.58	0/2227
25	K	0.72	2/1165 (0.2%)	0.86	6/1568 (0.4%)
26	L	0.68	1/867 (0.1%)	0.79	1/1171 (0.1%)
27	M	0.56	0/1195	0.69	2/1602 (0.1%)
28	N	0.50	0/989	0.58	0/1326
29	O	0.66	3/1034 (0.3%)	0.79	3/1375 (0.2%)
30	P	0.50	0/800	0.69	0/1082

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	Q	0.73	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	0.12	0/227	0.40	0/304
41	a	0.30	0/69247	0.43	10/107985 (0.0%)
42	b	0.42	0/589	0.56	0/779
43	c	0.51	0/635	0.61	0/848
44	d	0.25	0/2872	0.37	0/4478
45	e	0.69	2/502 (0.4%)	0.65	1/667 (0.1%)
46	f	0.52	0/452	0.57	0/605
47	g	0.45	1/531 (0.2%)	0.64	0/709
48	h	0.50	1/2121 (0.0%)	0.59	1/2852 (0.0%)
49	i	0.41	0/450	0.55	0/599
50	j	0.51	0/1586	0.57	1/2134 (0.0%)
51	k	0.46	0/433	0.62	0/576
52	l	0.51	1/1571 (0.1%)	0.62	0/2113
53	m	0.45	0/380	0.56	0/498
54	n	0.46	0/1434	0.66	1/1926 (0.1%)
55	o	0.51	0/513	0.71	1/676 (0.1%)
56	p	0.41	0/1333	0.62	2/1805 (0.1%)
57	q	0.46	0/303	0.64	0/397
58	r	0.28	0/1122	0.48	0/1515
59	s	0.70	2/1152 (0.2%)	0.73	2/1551 (0.1%)
60	t	0.52	0/955	0.75	3/1279 (0.2%)
61	u	0.43	0/1062	0.59	0/1413
62	v	0.60	1/1093 (0.1%)	0.77	3/1460 (0.2%)
63	w	0.83	2/964 (0.2%)	0.80	3/1289 (0.2%)
64	x	0.34	0/902	0.50	0/1209
65	y	0.41	0/929	0.54	0/1242
66	z	0.62	2/960 (0.2%)	0.62	0/1278
All	All	0.41	38/194903 (0.0%)	0.55	110/286688 (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
13	AC	0	1
13	AD	0	1
14	AE	0	4
16	AG	0	3
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	29

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	AG	429	LYS	C-N	13.79	1.50	1.33
63	w	35	LYS	CE-NZ	-12.79	1.10	1.49
29	O	80	ARG	CD-NE	-10.53	1.31	1.46
63	w	42	LYS	CD-CE	-9.37	1.24	1.52
25	K	45	ARG	CG-CD	7.74	1.75	1.52

The worst 5 of 110 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	AG	246	ASP	CA-C-N	14.54	138.02	119.84
16	AG	246	ASP	C-N-CA	14.54	138.02	119.84
16	AG	354	ALA	O-C-N	-13.68	107.32	122.09
16	AG	429	LYS	CA-C-N	11.45	132.17	119.92
16	AG	429	LYS	C-N-CA	11.45	132.17	119.92

There are no chirality outliers.

5 of 29 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
13	AC	192	VAL	Peptide
13	AD	20	SER	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	816	839	839	52	0
2	1	857	922	922	69	0
3	2	746	811	811	60	0
4	3	788	844	844	46	0
5	4	753	780	780	86	0
6	5	636	0	349	50	0
7	6	706	0	395	30	0
8	7	772	0	384	120	0
9	9	1117	0	1155	258	0
10	A	1620	826	827	107	0
10	B	1620	814	827	111	0
11	AA	10381	0	10390	299	0
12	AB	1286	0	1303	352	0
13	AC	1698	0	1718	13	0
13	AD	2078	0	1891	35	0
14	AE	10404	0	10626	230	0
15	AF	650	0	658	10	0
16	AG	3852	0	3828	846	0
17	C	544	559	560	106	0
18	D	32703	16423	16453	723	0
19	E	669	719	719	81	0
20	F	589	629	629	58	0
21	G	1760	1785	1787	192	0
22	H	1730	1454	1455	161	0
23	I	1636	1710	1710	153	0
24	J	1643	1707	1707	87	0
25	K	1152	1196	1196	130	0
26	L	848	846	846	102	0
27	M	1181	1235	1238	123	0
28	N	979	1031	1031	93	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	O	1022	1070	1070	90	0
30	P	790	831	831	152	0
31	Q	877	887	887	95	0
32	R	939	1001	1001	90	0
33	S	805	844	844	75	0
34	T	714	734	734	91	0
35	U	649	666	666	61	0
36	V	648	691	691	67	0
37	W	663	688	688	47	0
38	X	900	964	965	107	0
39	Y	1032	0	1088	212	0
40	Z	227	0	237	30	0
41	a	61841	31077	31120	1309	0
42	b	582	599	599	47	0
43	c	625	652	652	34	0
44	d	2569	1301	1301	43	0
45	e	501	531	531	44	0
46	f	448	488	488	38	0
47	g	522	520	520	66	0
48	h	2082	2154	2154	139	0
49	i	444	459	458	50	0
50	j	1565	1617	1616	121	0
51	k	426	464	464	42	0
52	l	1552	1619	1619	125	0
53	m	377	418	418	29	0
54	n	1410	1443	1444	156	0
55	o	504	572	572	52	0
56	p	1313	1358	1358	74	0
57	q	302	343	343	25	0
58	r	1111	1148	1148	53	0
59	s	1129	1162	1162	123	0
60	t	946	1023	1023	101	0
61	u	1053	1129	1129	78	0
62	v	1074	1157	1157	121	0
63	w	951	994	994	102	0
64	x	892	923	923	48	0
65	y	917	962	962	53	0
66	z	947	1020	1019	79	0
67	AE	1	0	0	0	0
68	AE	2	0	0	3	0
All	All	181566	98639	132754	7590	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 7590 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:145:LEU:CD2	30:P:88:MET:HB3	1.18	1.62
6:5:9:DA:H5''	11:AA:473:ARG:CB	1.29	1.62
25:K:45:ARG:CD	25:K:45:ARG:CG	1.75	1.61
16:AG:425:LEU:CD2	16:AG:429:LYS:HE2	1.21	1.61
12:AB:145:LEU:HD22	30:P:88:MET:CB	1.30	1.60

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%)	1195 (91%)	116 (9%)	1 (0%)	48	82
12	AB	159/162 (98%)	112 (70%)	30 (19%)	17 (11%)	0	6
13	AC	217/329 (66%)	203 (94%)	12 (6%)	2 (1%)	14	49
13	AD	293/329 (89%)	269 (92%)	24 (8%)	0	100	100
14	AE	1331/1407 (95%)	1213 (91%)	112 (8%)	6 (0%)	24	63
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
16	AG	493/495 (100%)	376 (76%)	88 (18%)	29 (6%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
50	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	k	50/55 (91%)	50 (100%)	0	0	100	100
52	l	199/201 (99%)	188 (94%)	11 (6%)	0	100	100
53	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
54	n	175/179 (98%)	160 (91%)	14 (8%)	1 (1%)	21	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%)	9187 (91%)	797 (8%)	74 (1%)	20	55

5 of 74 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	AB	52	PRO
12	AB	60	ASP
12	AB	87	ILE
12	AB	98	VAL
12	AB	109	THR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	84 (100%)	0	100	100
2	1	93/93 (100%)	93 (100%)	0	100	100
3	2	81/84 (96%)	81 (100%)	0	100	100
4	3	84/85 (99%)	84 (100%)	0	100	100
5	4	78/78 (100%)	78 (100%)	0	100	100
9	9	112/123 (91%)	112 (100%)	0	100	100
11	AA	1135/1157 (98%)	1129 (100%)	6 (0%)	81	82
12	AB	141/142 (99%)	64 (45%)	77 (55%)	0	0
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%)	285 (70%)	124 (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%)	84 (98%)	2 (2%)	44	63
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%)	8070 (97%)	229 (3%)	38	59

5 of 229 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	AG	63	LEU
16	AG	399	ASP
16	AG	189	GLU
16	AG	396	GLU
16	AG	321	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 120 such sidechains are listed below:

Mol	Chain	Res	Type
16	AG	428	ASN
62	v	97	GLN
24	J	36	GLN
62	v	45	GLN
66	z	72	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	8 (10%)
10	B	75/76 (98%)	29 (38%)	8 (10%)
18	D	1514/1542 (98%)	289 (19%)	20 (1%)
41	a	2859/2904 (98%)	512 (17%)	0
44	d	119/120 (99%)	15 (12%)	0
8	7	36/41 (87%)	26 (72%)	5 (13%)
All	All	4678/4759 (98%)	900 (19%)	41 (0%)

5 of 900 RNA backbone outliers are listed below:

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

5 of 41 RNA pucker outliers are listed below:

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

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

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

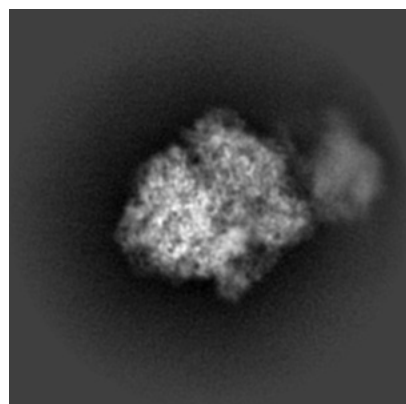
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42474. These allow visual inspection of the internal detail of the map and identification of artifacts.

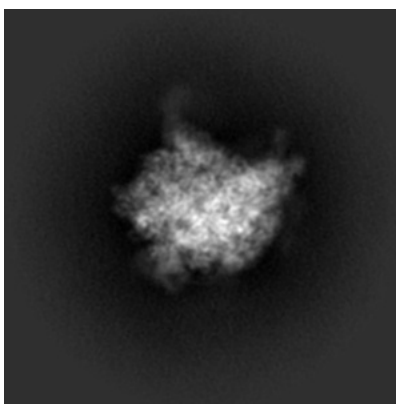
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

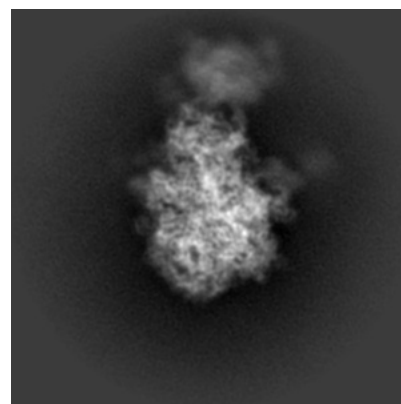
6.1.1 Primary map



X

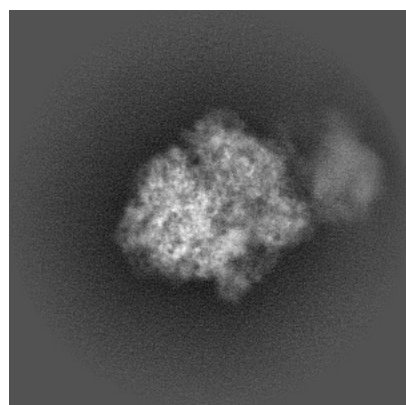


Y

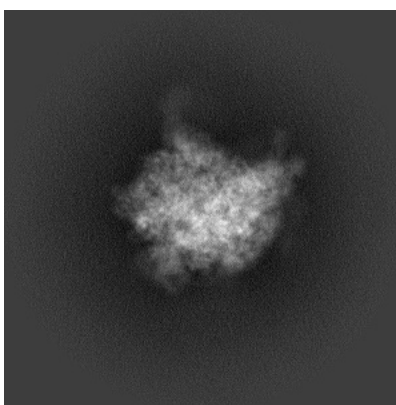


Z

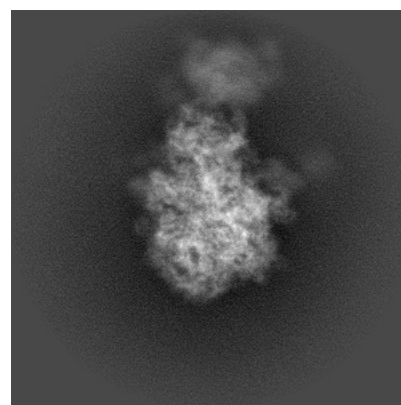
6.1.2 Raw map



X



Y

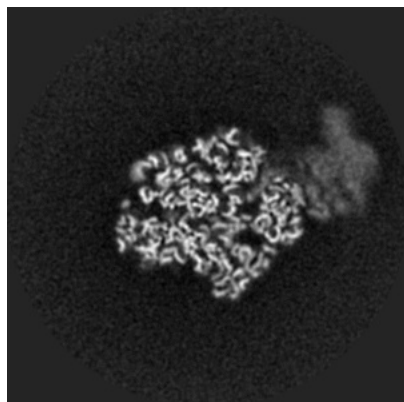


Z

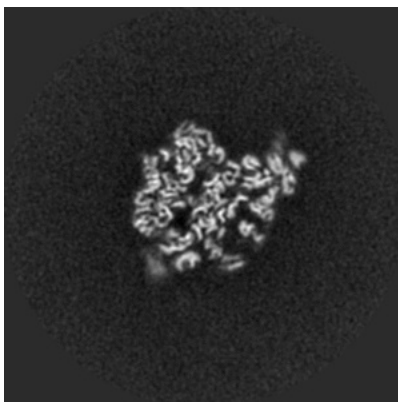
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

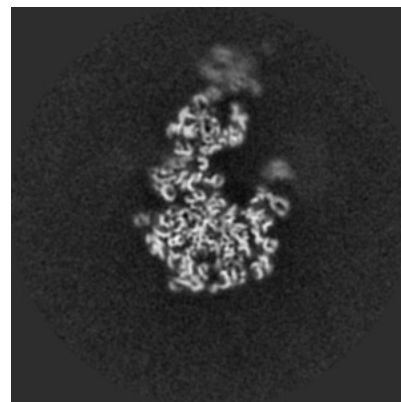
6.2.1 Primary map



X Index: 256

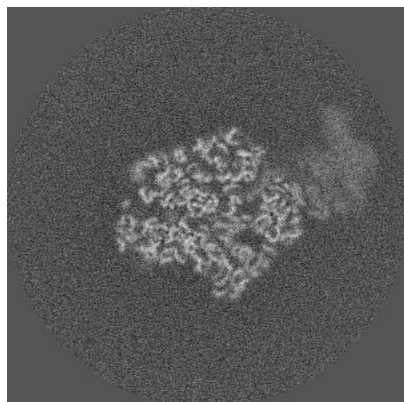


Y Index: 256

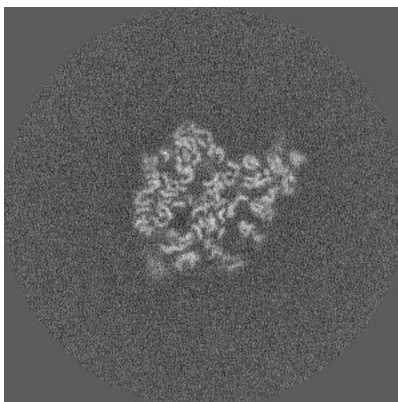


Z Index: 256

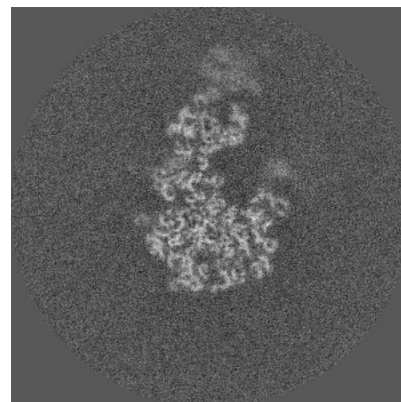
6.2.2 Raw map



X Index: 256



Y Index: 256

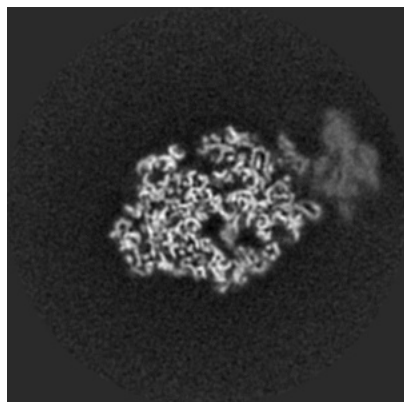


Z Index: 256

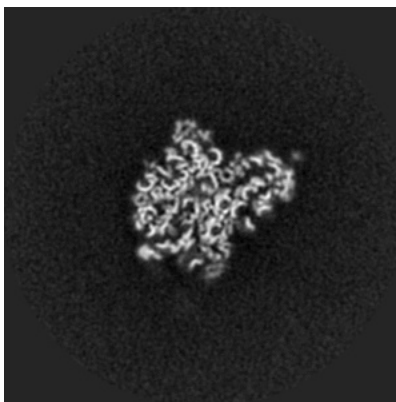
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

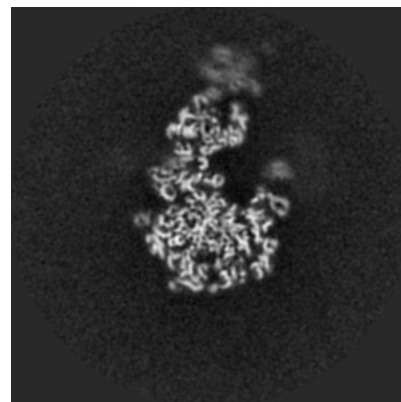
6.3.1 Primary map



X Index: 245

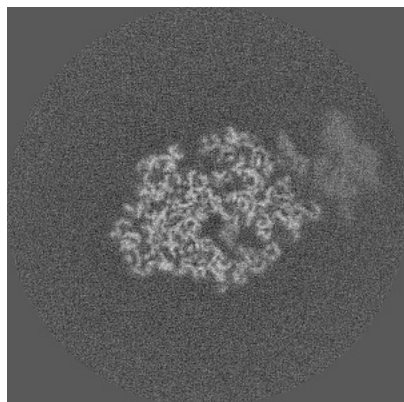


Y Index: 248

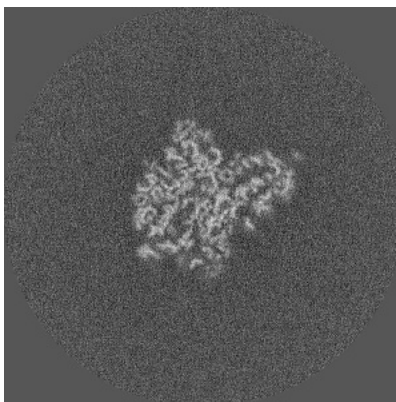


Z Index: 257

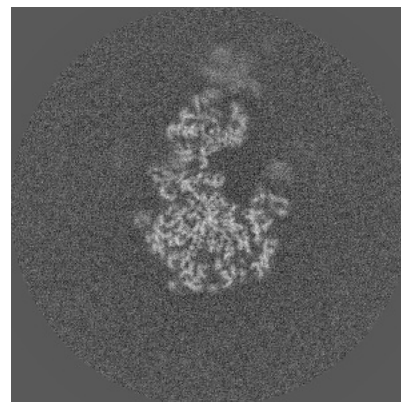
6.3.2 Raw map



X Index: 244



Y Index: 249



Z Index: 258

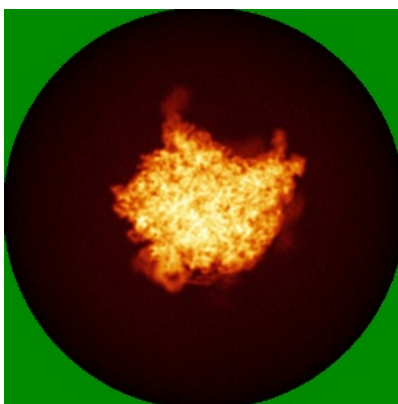
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

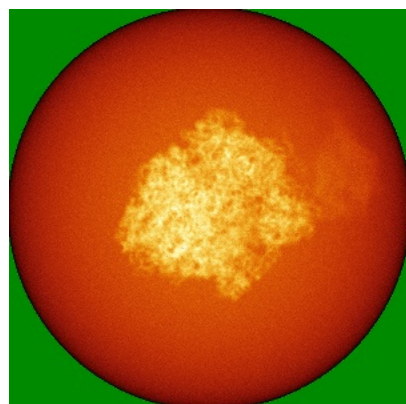


Y

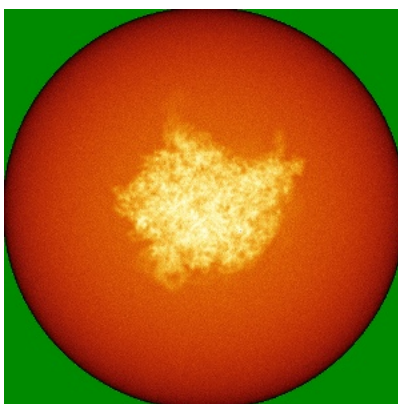


Z

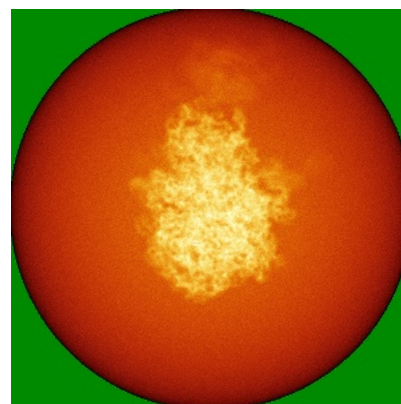
6.4.2 Raw map



X



Y

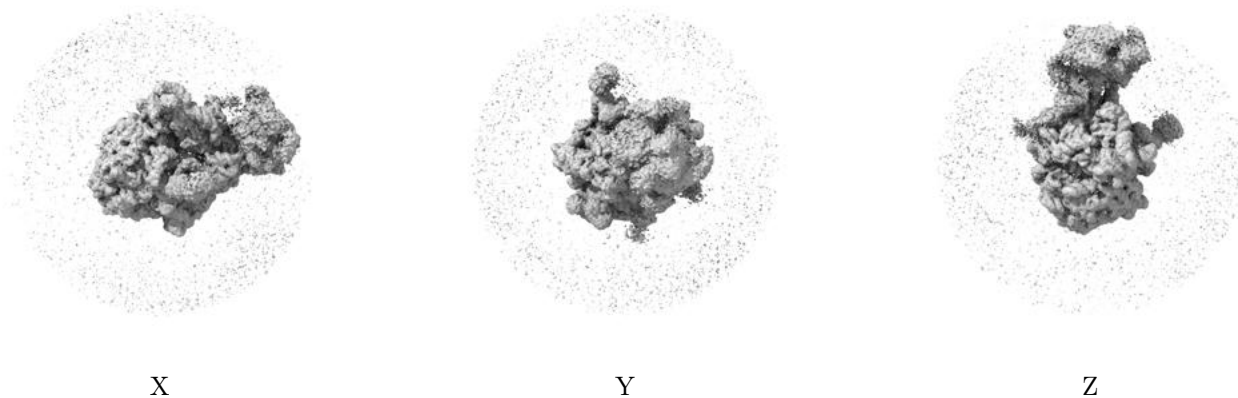


Z

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.

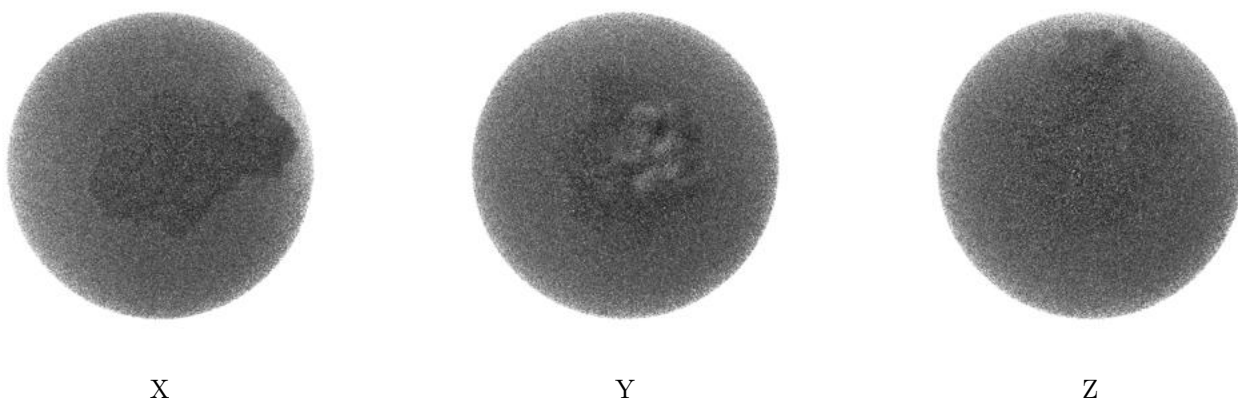
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0019. 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.

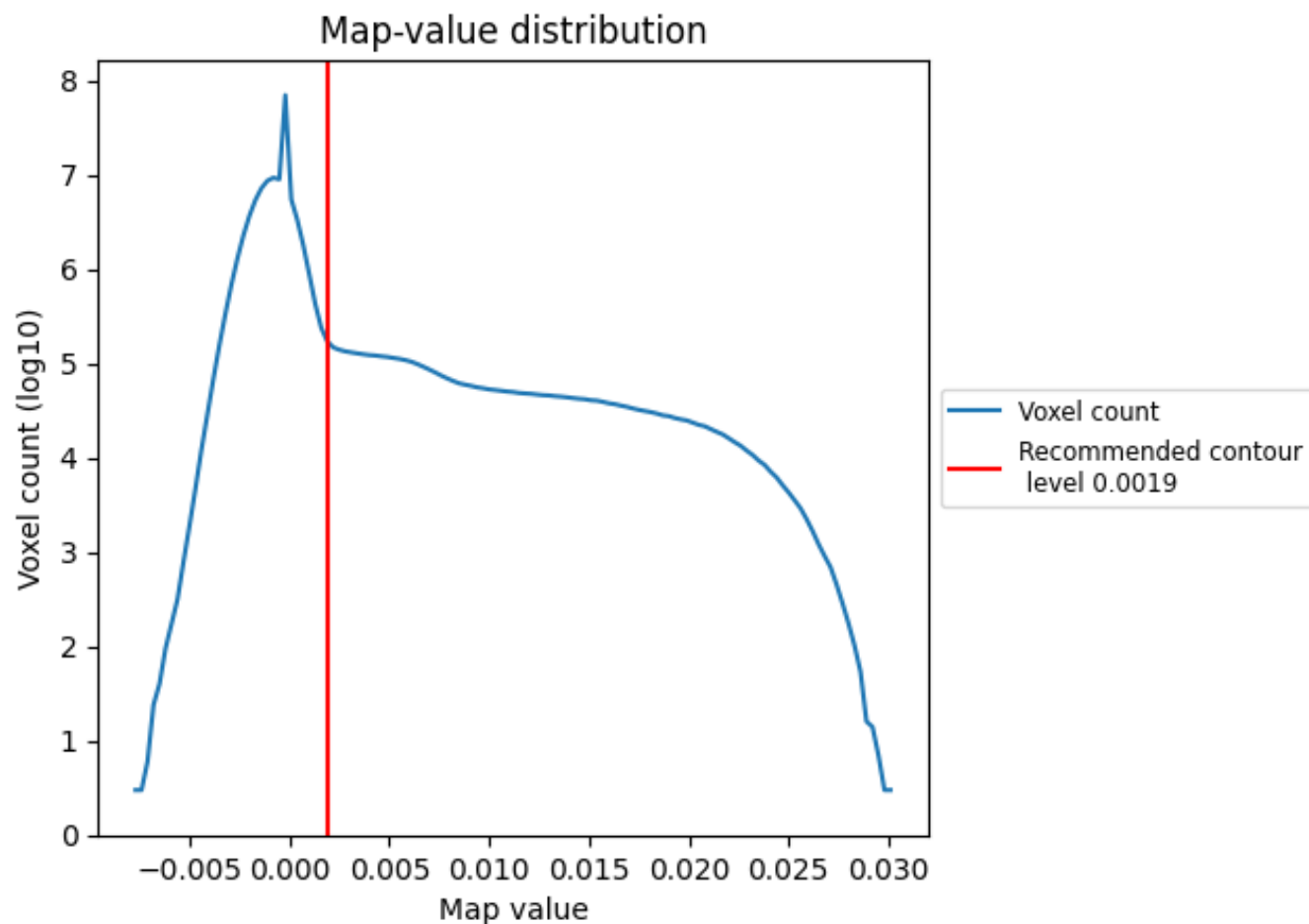
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

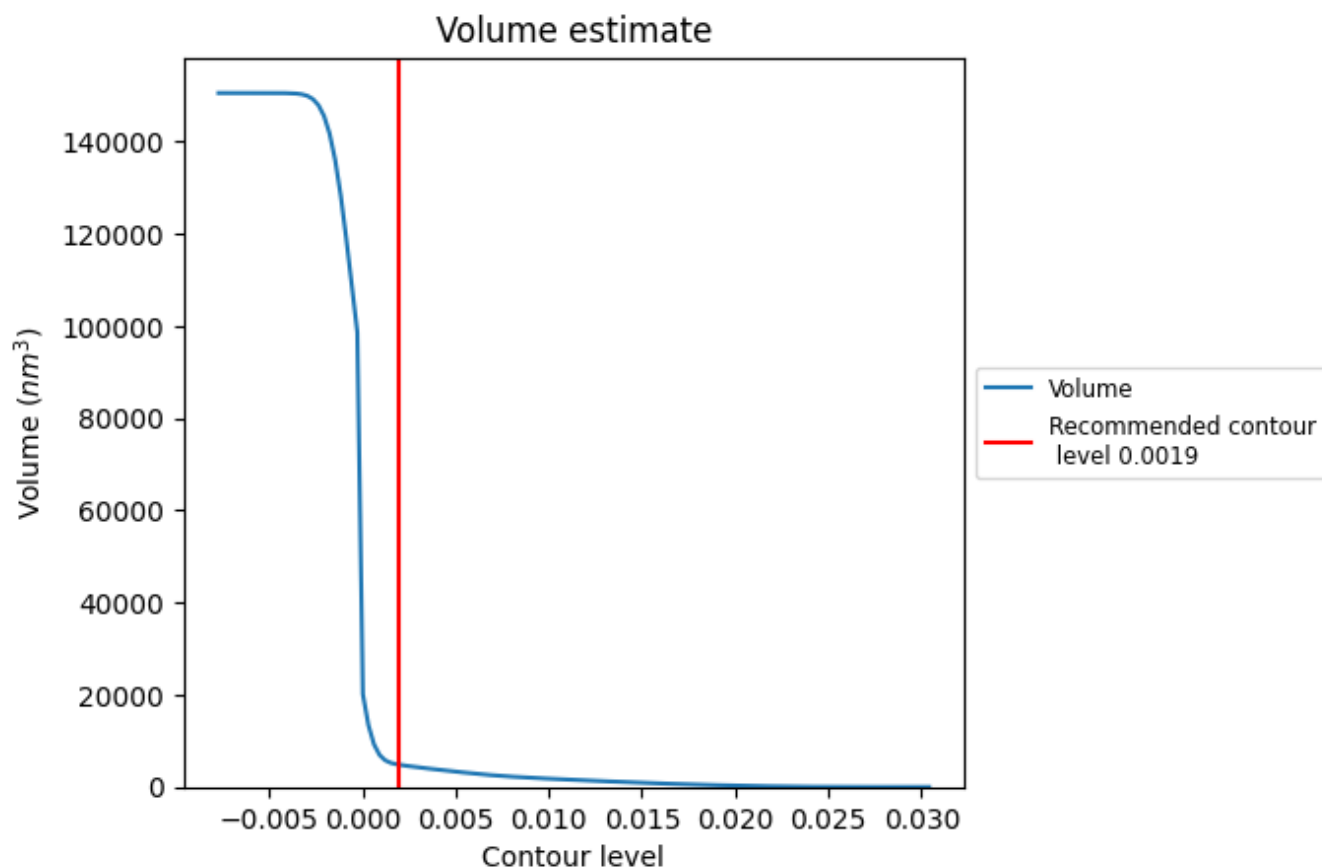
This section contains the results of statistical analysis of the map.

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.

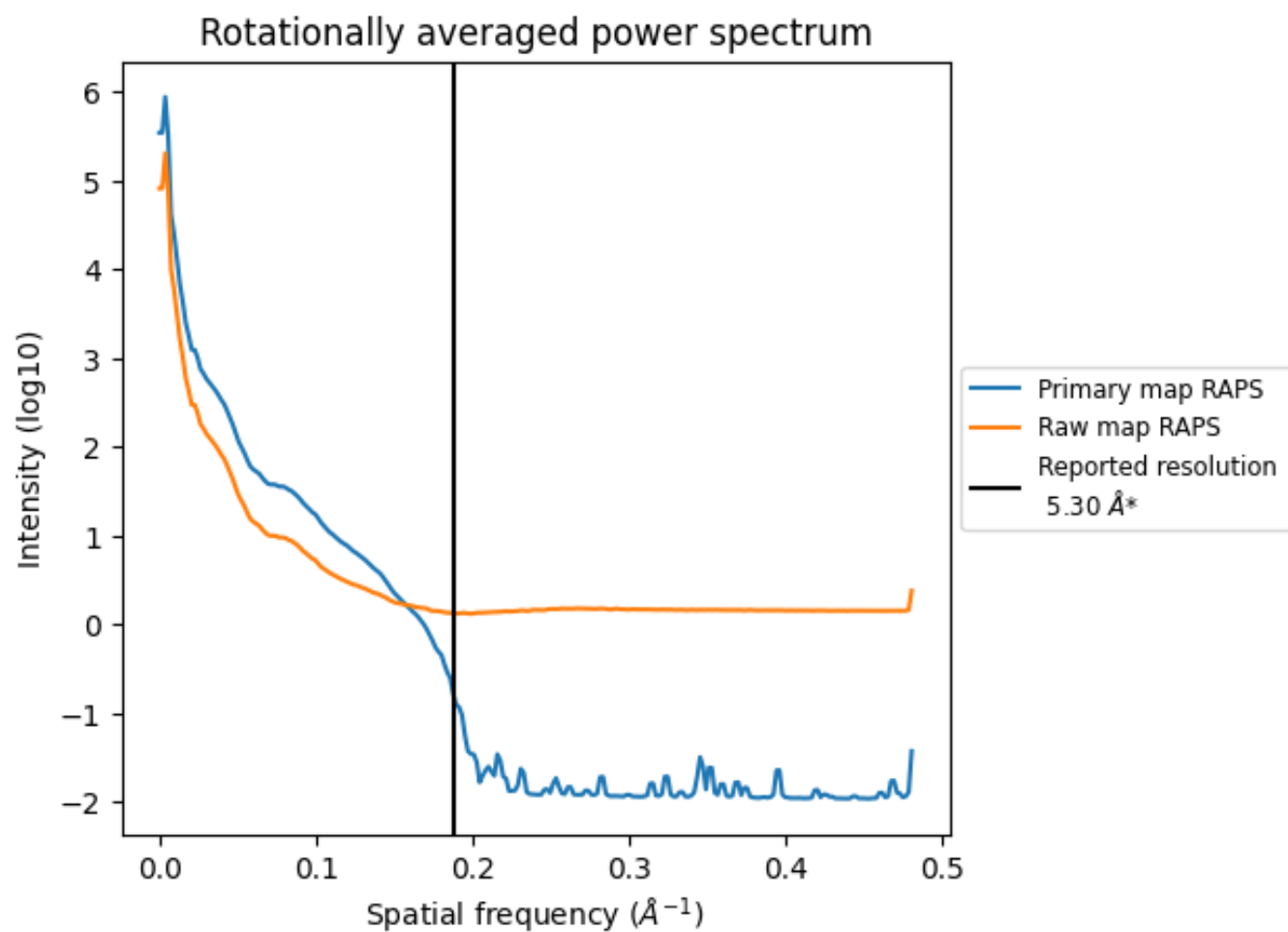
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4878 nm^3 ; this corresponds to an approximate mass of 4406 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 ⓘ

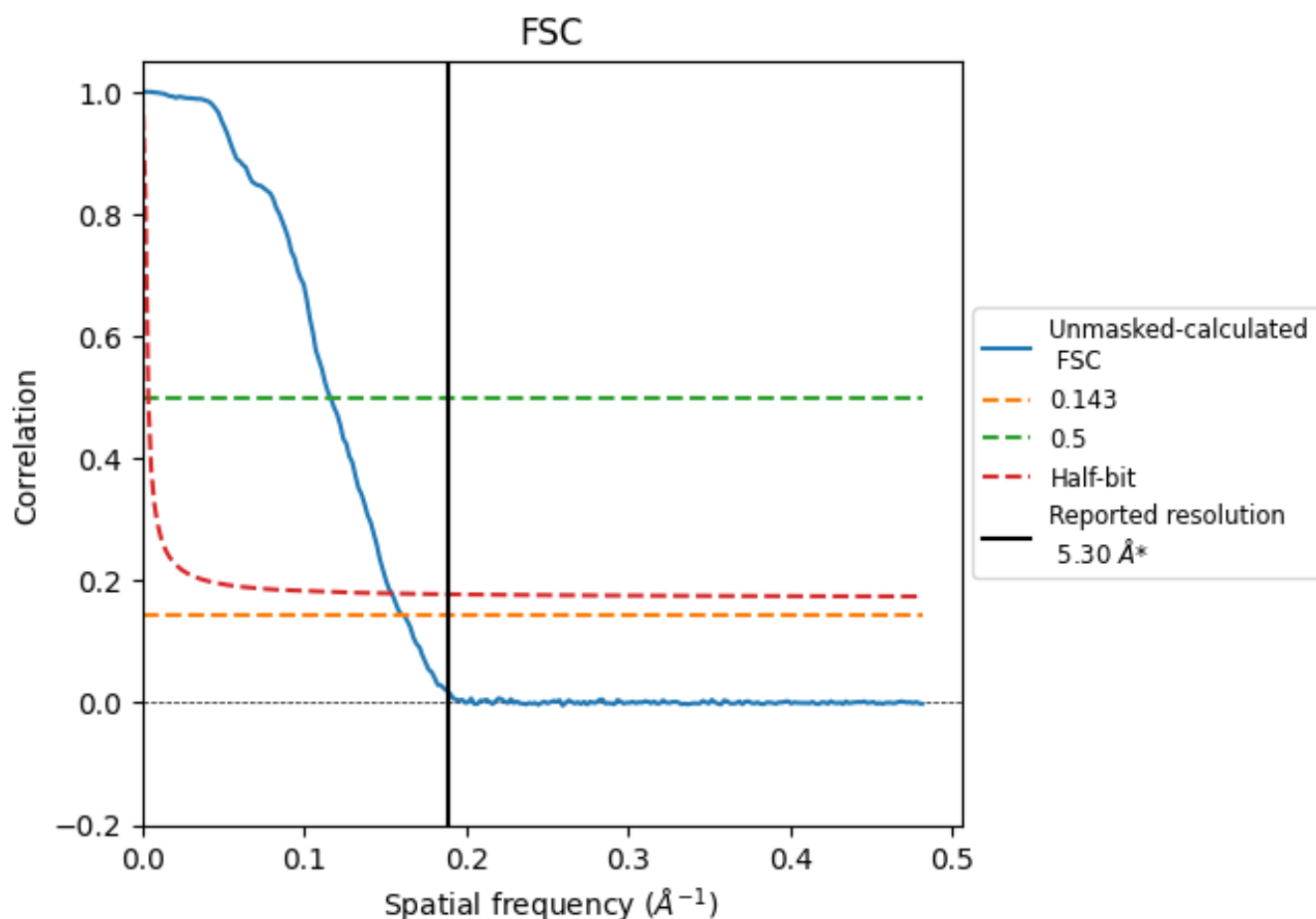


*Reported resolution corresponds to spatial frequency of 0.189 Å⁻¹

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](#)

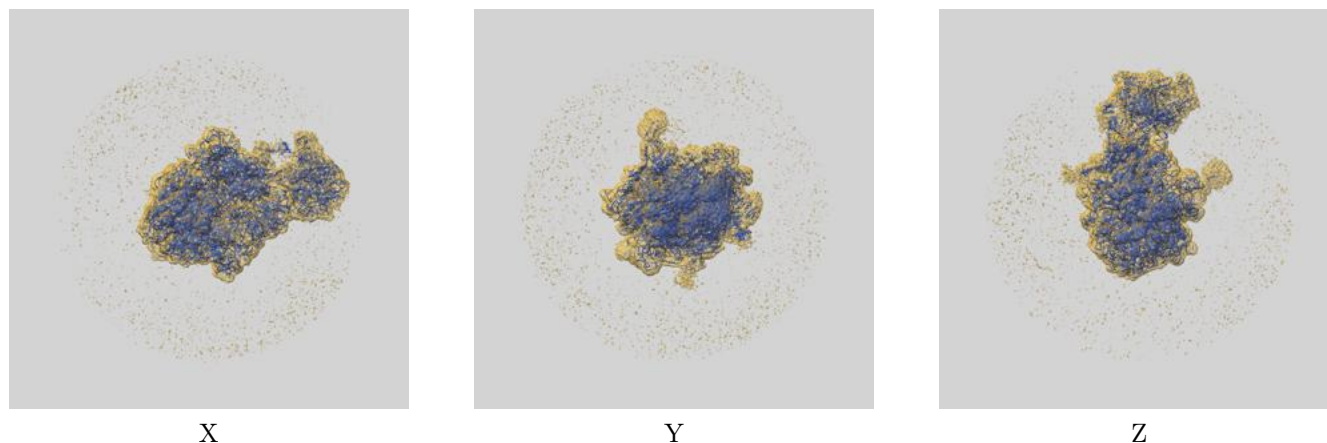
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.21	8.62	6.49

*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 6.21 differs from the reported value 5.3 by more than 10 %

9 Map-model fit [i](#)

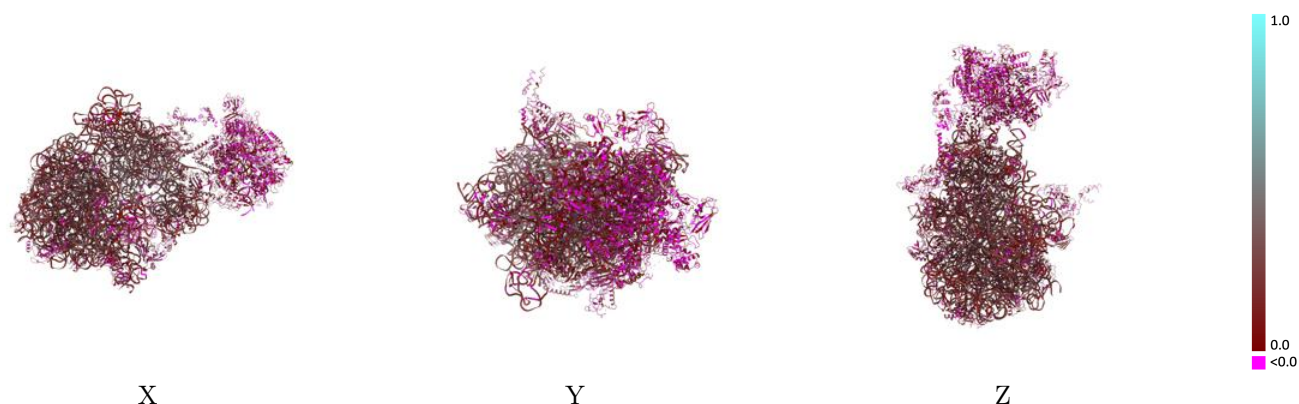
This section contains information regarding the fit between EMDB map EMD-42474 and PDB model 8UQM. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.0019 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

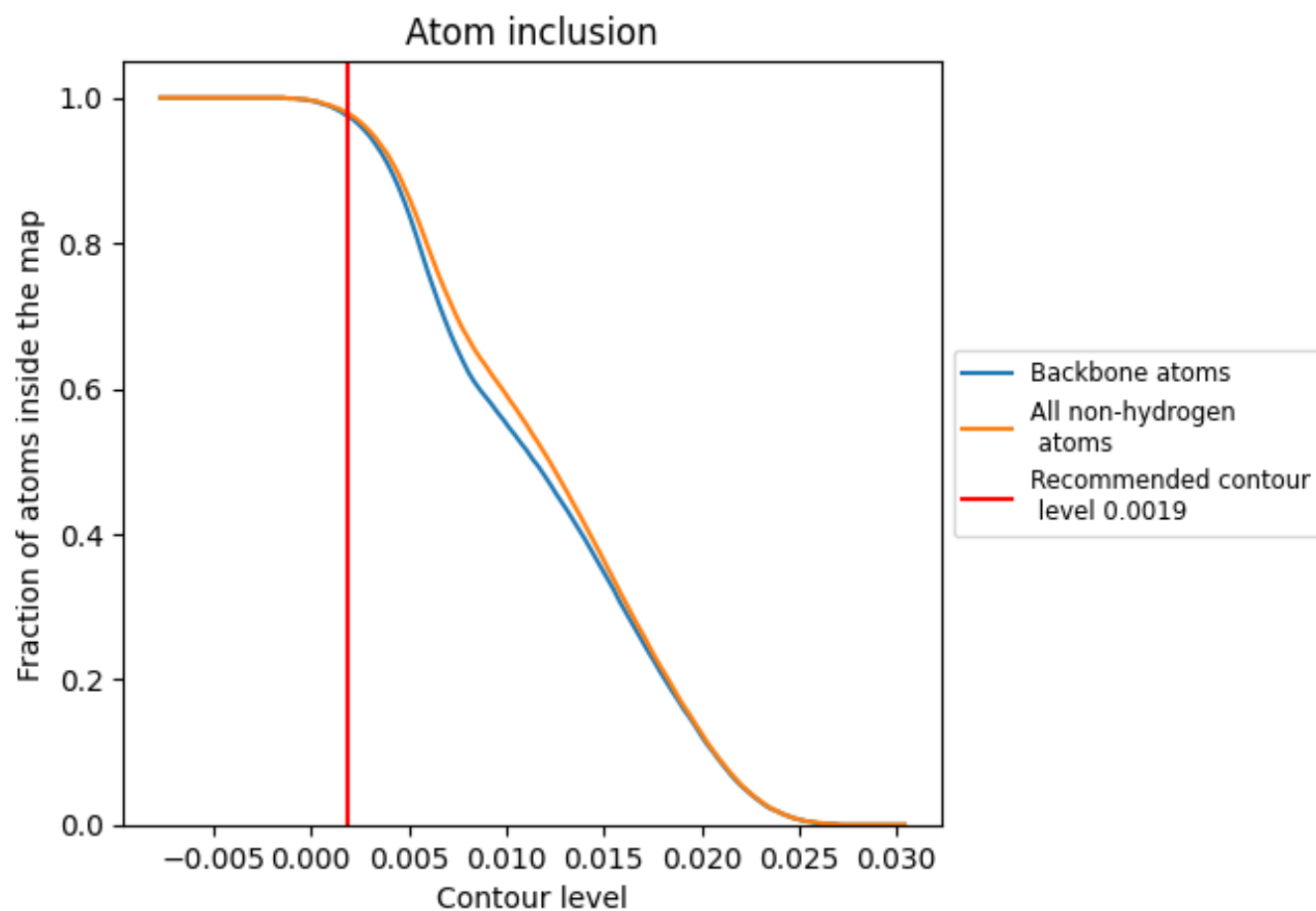


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 98% 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 (0.0019) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9780	 0.1740
0	 0.9810	 0.1530
1	 0.9800	 0.1790
2	 0.9780	 0.1490
3	 0.9850	 0.1330
4	 0.9890	 0.1570
5	 0.8930	 0.0610
6	 0.9290	 0.0700
7	 0.9720	 0.1090
9	 0.9790	 0.1000
A	 0.9990	 0.1900
AA	 0.9770	 0.0680
AB	 0.9910	 0.0890
AC	 0.9870	 0.0430
AD	 0.8800	 0.0530
AE	 0.9670	 0.0700
AF	 0.8310	 0.0770
AG	 0.8160	 0.1010
B	 0.9540	 0.1070
C	 0.9940	 0.1630
D	 0.9980	 0.2310
E	 0.9910	 0.1510
F	 0.9790	 0.1830
G	 0.9690	 0.1560
H	 0.8700	 0.0550
I	 0.9790	 0.1950
J	 0.9920	 0.1760
K	 0.9950	 0.2210
L	 0.9920	 0.1570
M	 0.9900	 0.1500
N	 0.9780	 0.1820
O	 0.9870	 0.1400
P	 0.9860	 0.1630
Q	 0.9920	 0.1620
R	 0.9970	 0.2230



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Chain	Atom inclusion	Q-score
S	 0.9880	 0.1630
T	 0.9840	 0.1590
U	 0.9890	 0.1670
V	 0.9810	 0.1740
W	 0.9550	 0.1120
X	 0.9800	 0.1400
Y	 0.9170	 0.0750
Z	 1.0000	 0.0220
a	 0.9970	 0.2170
b	 0.9820	 0.1350
c	 0.9770	 0.1630
d	 0.9990	 0.1810
e	 0.9800	 0.1280
f	 0.9860	 0.1660
g	 0.9820	 0.1030
h	 0.9840	 0.1620
i	 0.9770	 0.1880
j	 0.9920	 0.1680
k	 0.9950	 0.1450
l	 0.9700	 0.1340
m	 0.9890	 0.1710
n	 0.9730	 0.1220
o	 0.9700	 0.1310
p	 0.9930	 0.1540
q	 0.9900	 0.1570
r	 0.9410	 0.1140
s	 0.9810	 0.1790
t	 0.9770	 0.1910
u	 0.9880	 0.1440
v	 0.9840	 0.1890
w	 0.9780	 0.1670
x	 0.9760	 0.0960
y	 0.9800	 0.1750
z	 0.9860	 0.1440