



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 05:11 AM UTC

PDB ID : 8URX / pdb_00008urx
EMDB ID : EMD-42503
Title : Escherichia coli transcription-translation coupled complex class B (TTC-B) containing RfaH bound to ops signal, mRNA with a 30 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 : 2023-10-27
Resolution : 6.60 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:

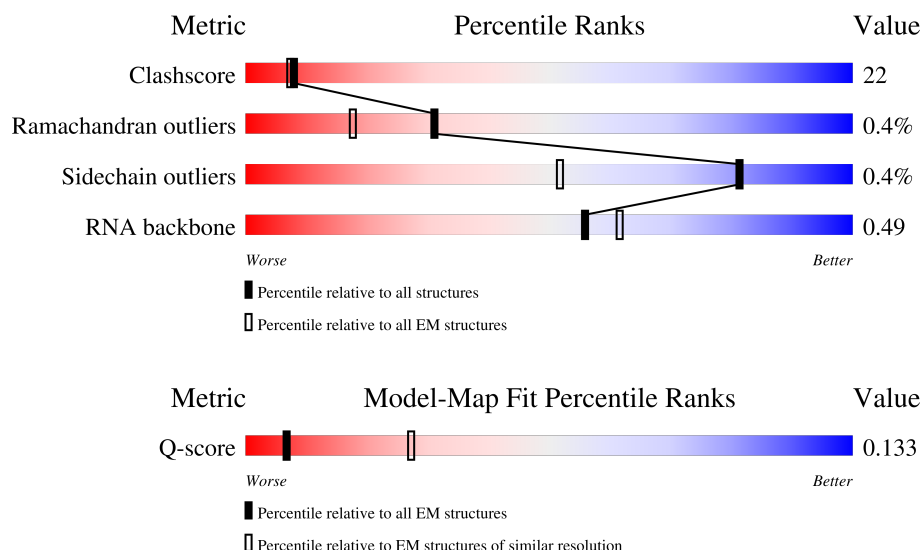
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 6.60 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	531 (6.10 - 7.10)

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

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

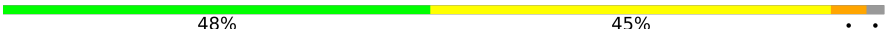
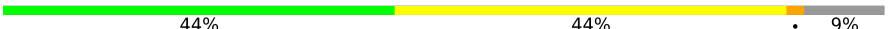
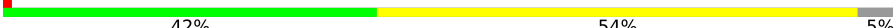
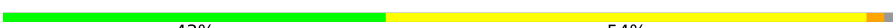
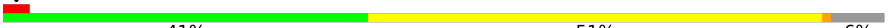
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Mol	Chain	Length	Quality of chain
4	3	104	
5	4	94	
6	5	38	
7	6	38	
8	7	47	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	162	
13	AC	329	
13	AD	329	
14	AE	1407	
15	AF	91	
16	C	75	
17	D	1542	
18	E	87	
19	F	71	
20	G	241	
21	H	557	
22	I	233	
23	J	206	
24	K	167	
25	L	135	
26	M	179	

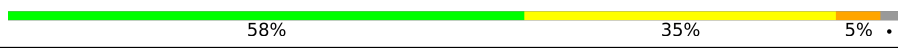
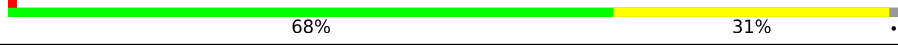
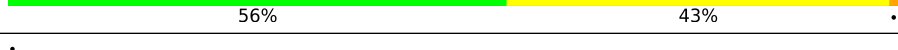
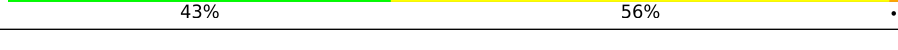
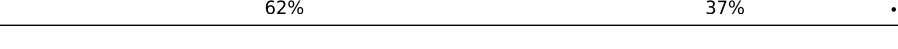
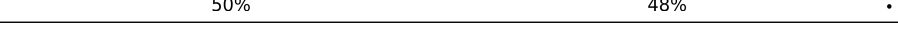
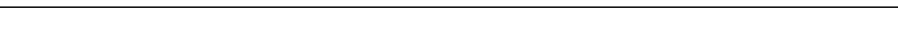
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Mol	Chain	Length	Quality of chain
27	N	130	
28	O	130	
29	P	103	
30	Q	129	
31	R	124	
32	S	101	
33	T	89	
34	U	82	
35	V	84	
36	W	92	
37	X	118	
38	Y	142	
39	Z	121	
40	a	2904	
41	b	85	
42	c	78	
43	d	120	
44	e	63	
45	f	59	
46	g	70	
47	h	273	
48	i	57	
49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

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

2 Entry composition [i](#)

There are 67 unique types of molecules in this entry. The entry contains 275954 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 30 nt long spacer.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	33	Total	C	N	O	P	0	0
			687	307	96	251	33		

- 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	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	

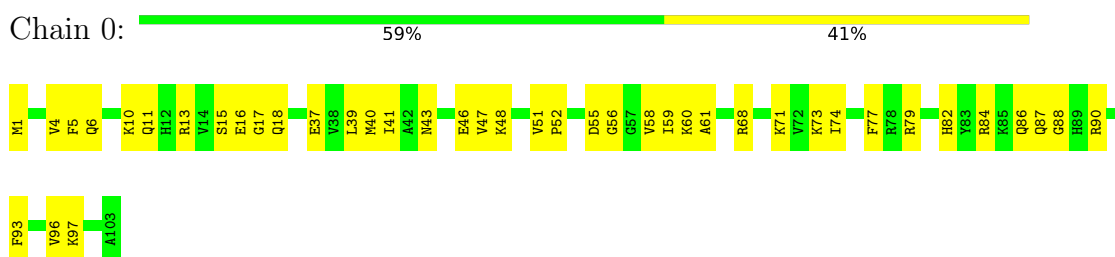
- Molecule 67 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

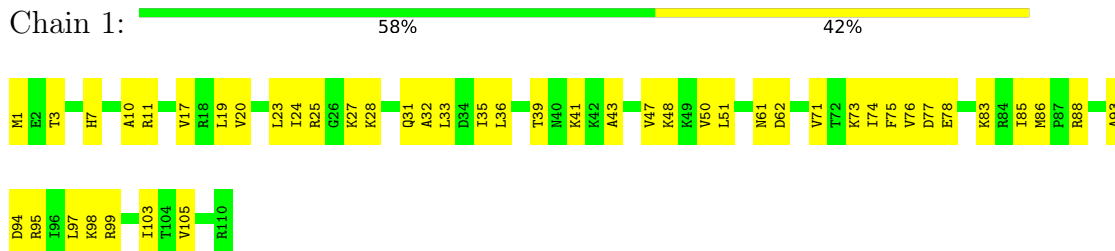
3 Residue-property plots [i](#)

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.

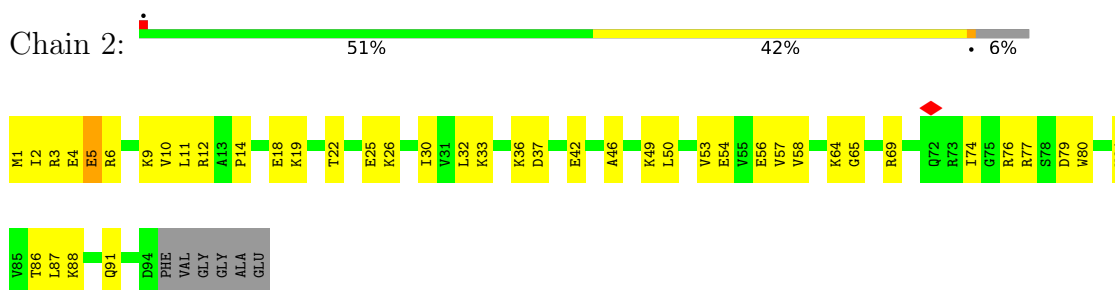
- Molecule 1: Ribosomal protein L21



- Molecule 2: 50S ribosomal protein L22



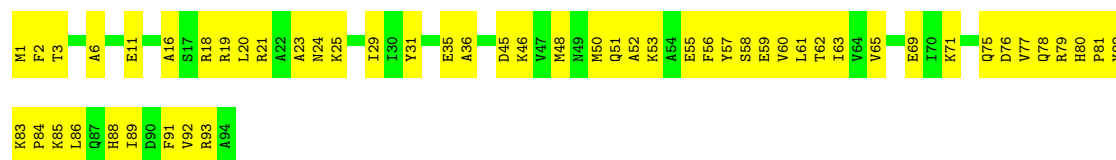
- Molecule 3: 50S ribosomal protein L23



- Molecule 4: 50S ribosomal protein L24



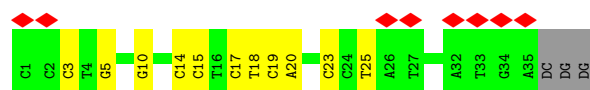
- Molecule 5: 50S ribosomal protein L25



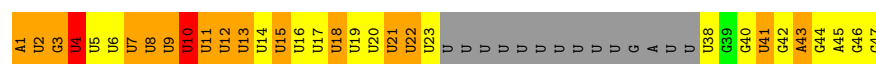
- Molecule 6: NT DNA ops



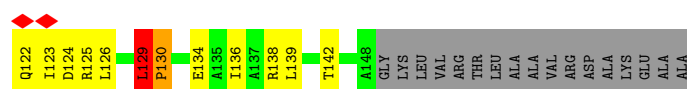
- Molecule 7: T DNA ops



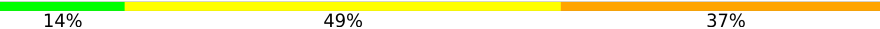
- Molecule 8: mRNA with 30 nt long spacer

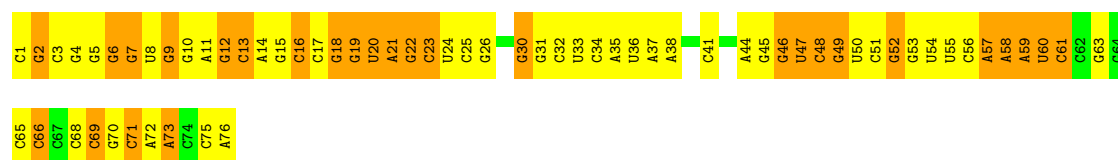


- Molecule 9: 50S ribosomal protein L10



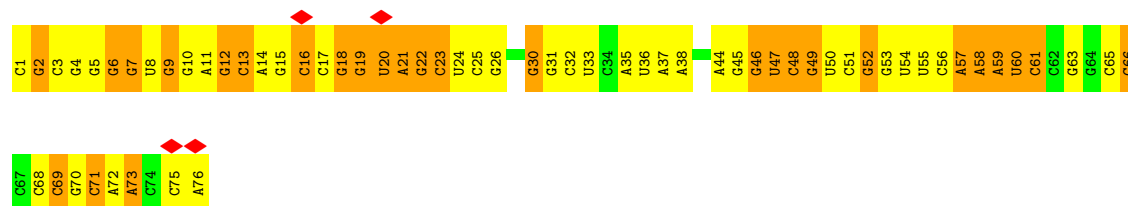
- Molecule 10: E-site and P-site fMet-tRNA

Chain A: 



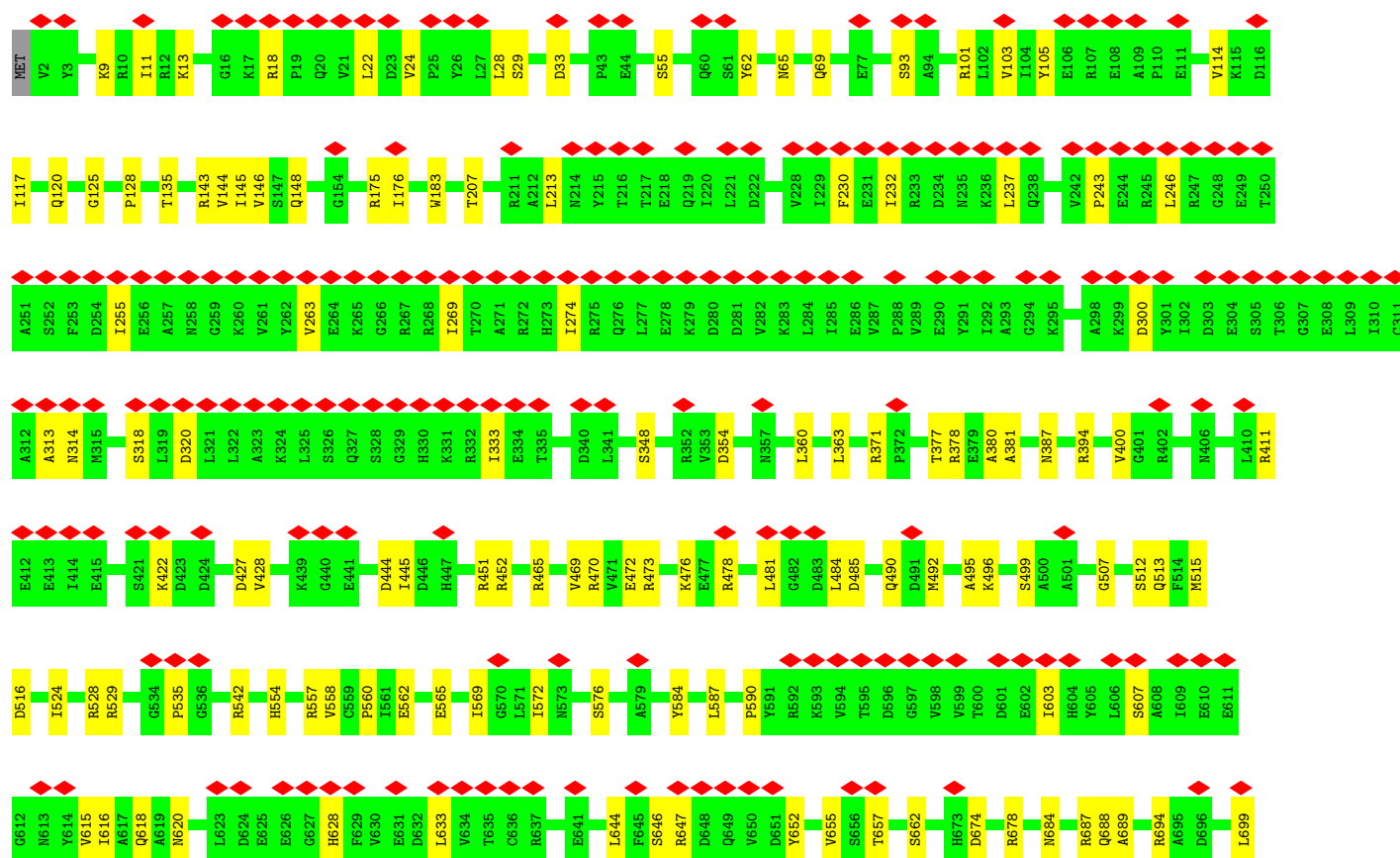
• Molecule 10: E-site and P-site fMet-tRNA

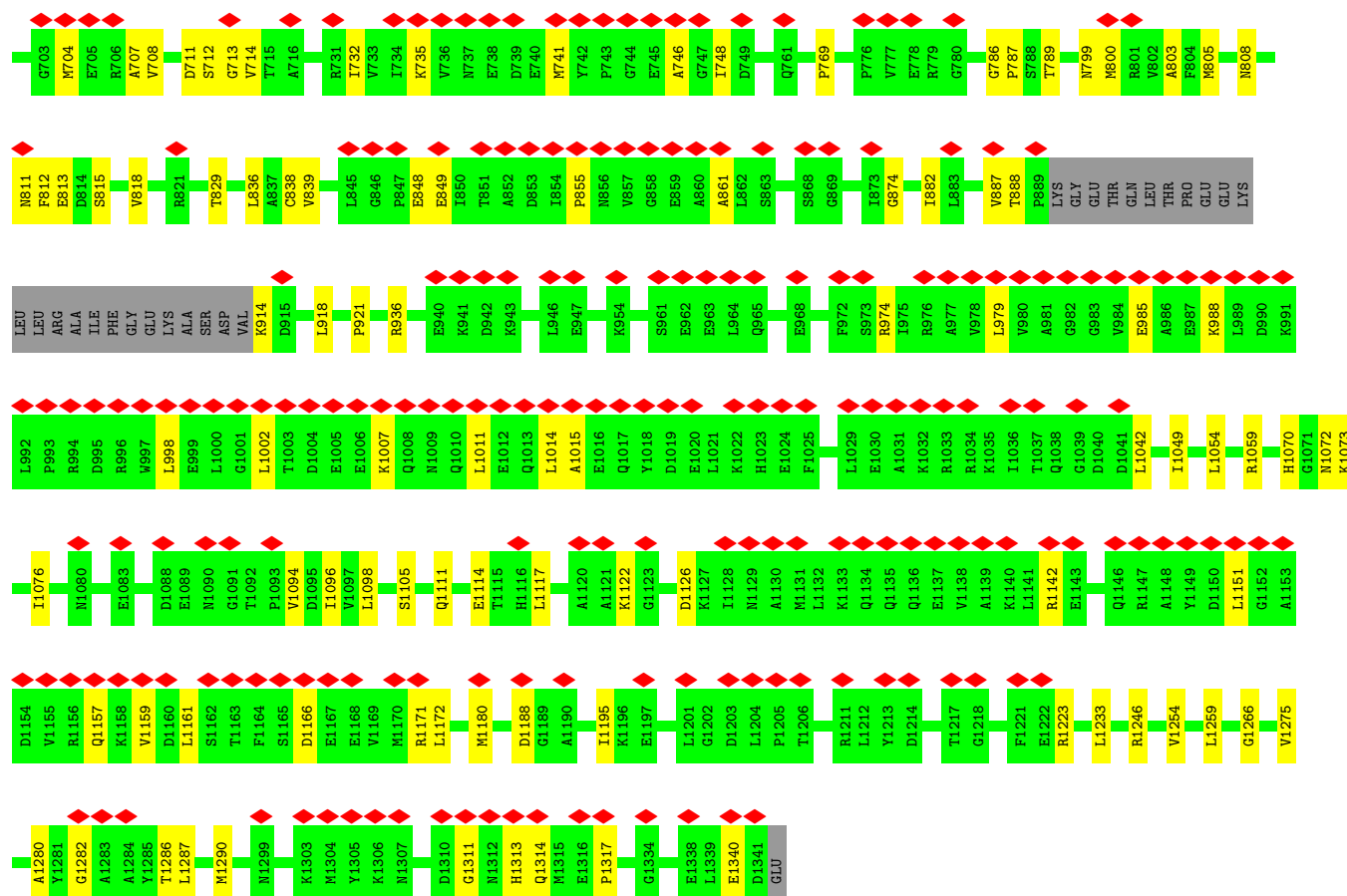
Chain B: 



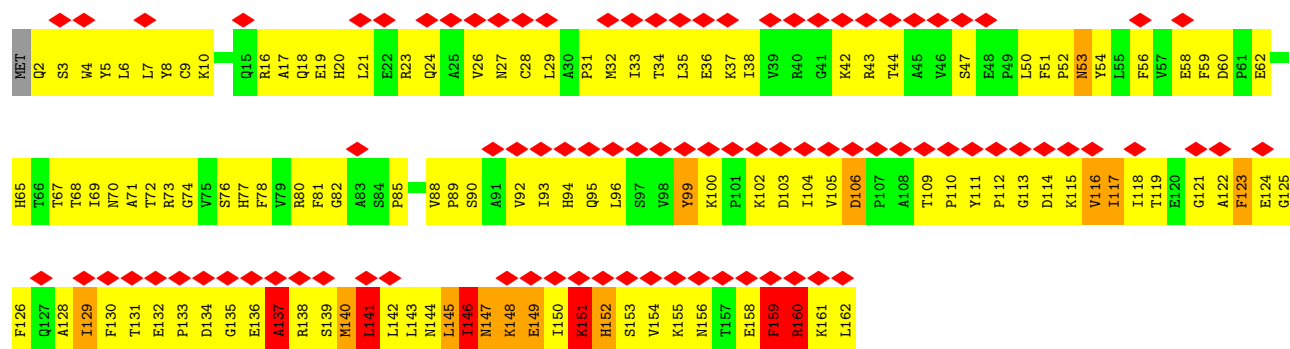
• Molecule 11: DNA-directed RNA polymerase subunit beta

Chain AA: 

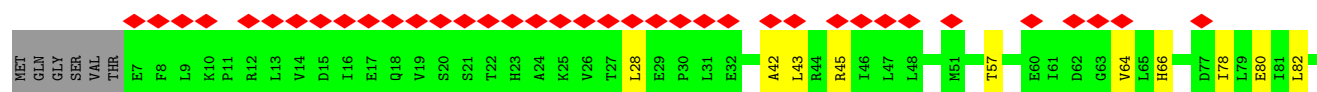


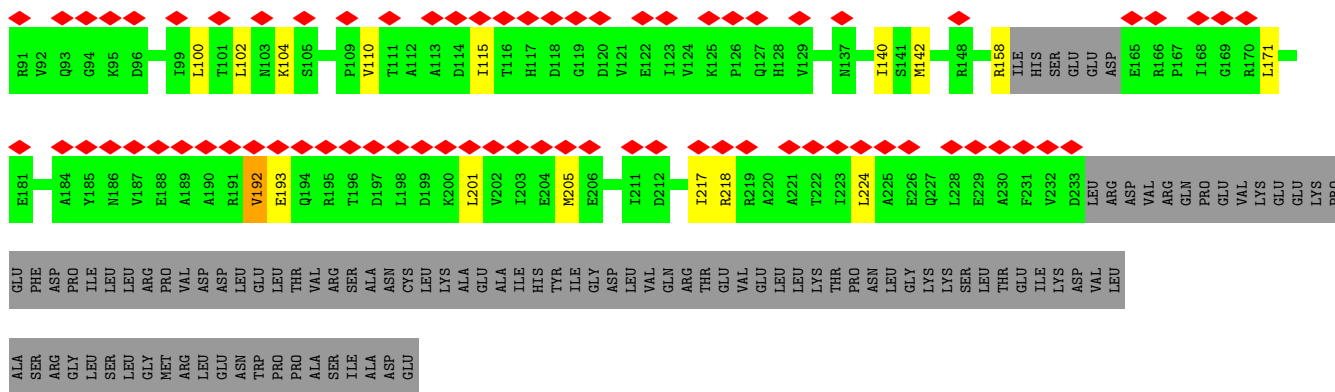


• Molecule 12: Transcription antitermination protein RfaH

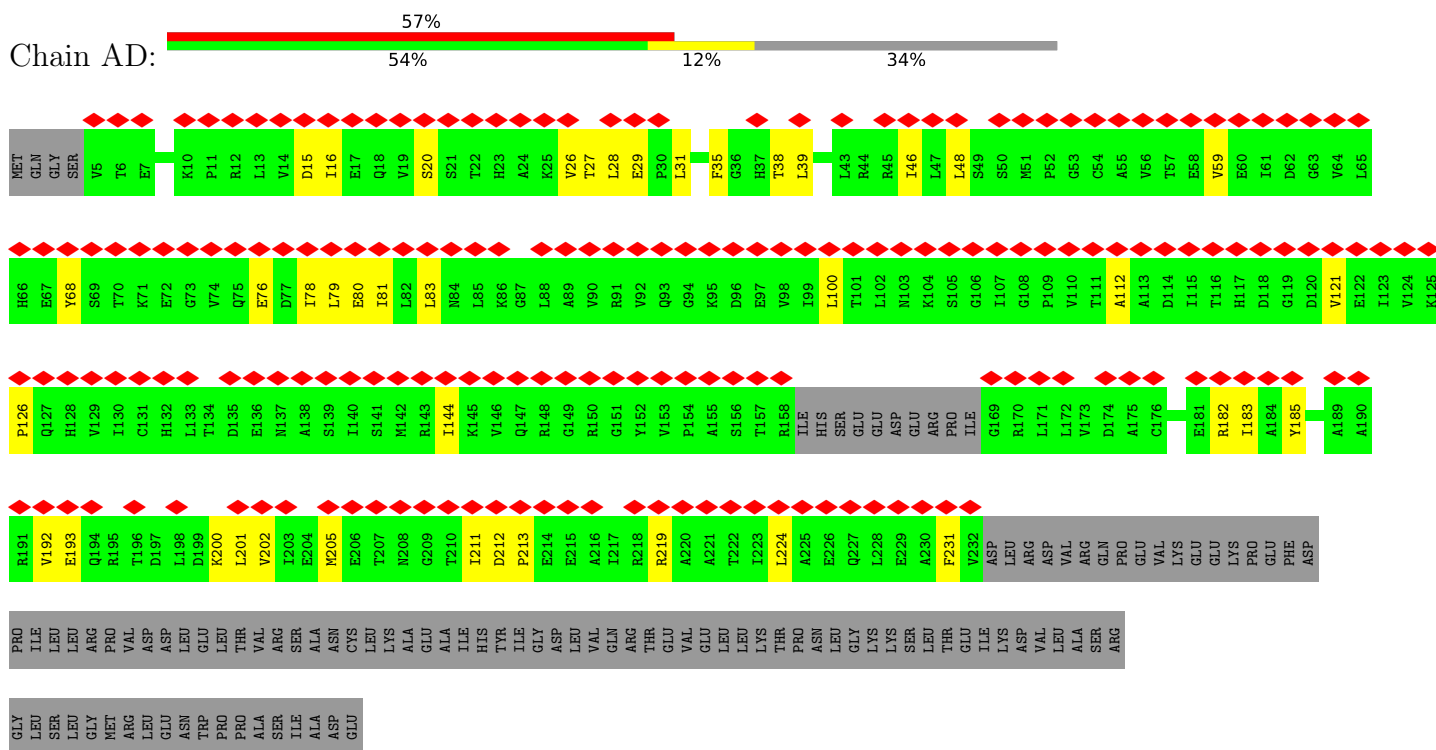


• Molecule 13: DNA-directed RNA polymerase subunit alpha

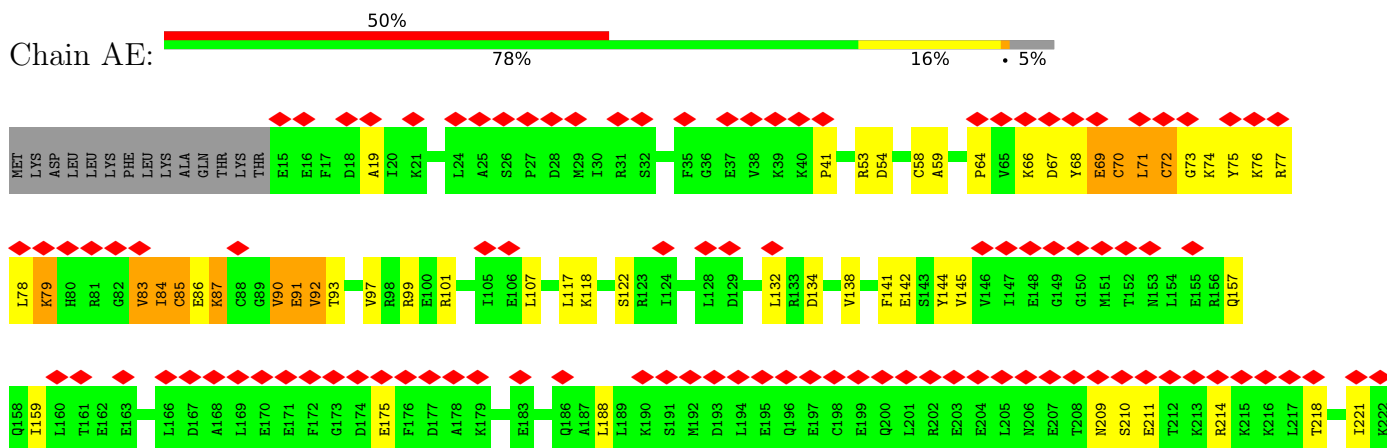




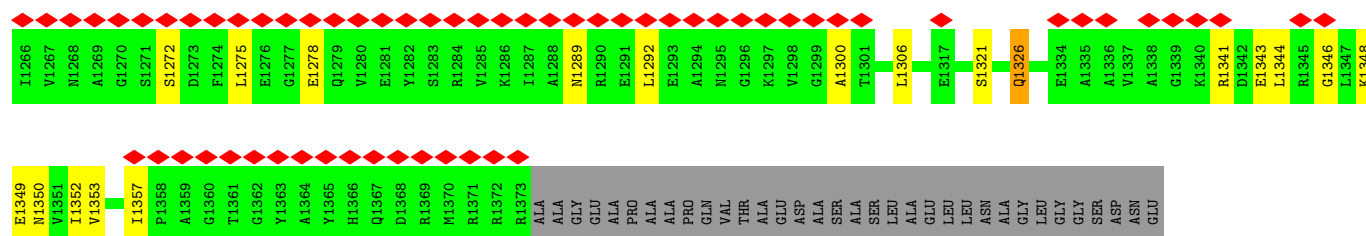
• Molecule 13: DNA-directed RNA polymerase subunit alpha



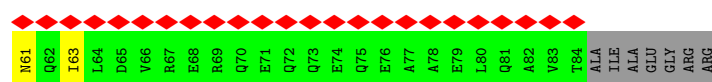
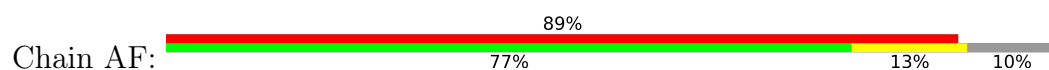
• Molecule 14: DNA-directed RNA polymerase subunit beta'







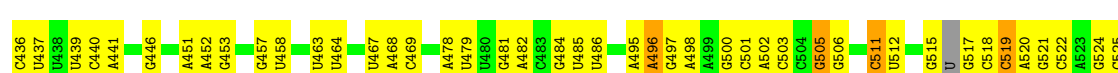
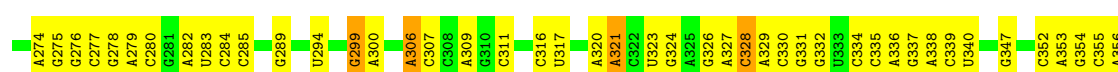
- Molecule 15: DNA-directed RNA polymerase subunit omega



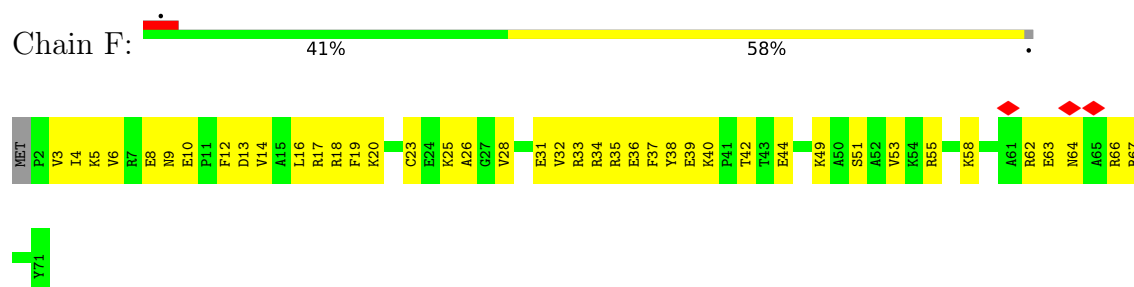
- Molecule 16: 30S ribosomal protein S18



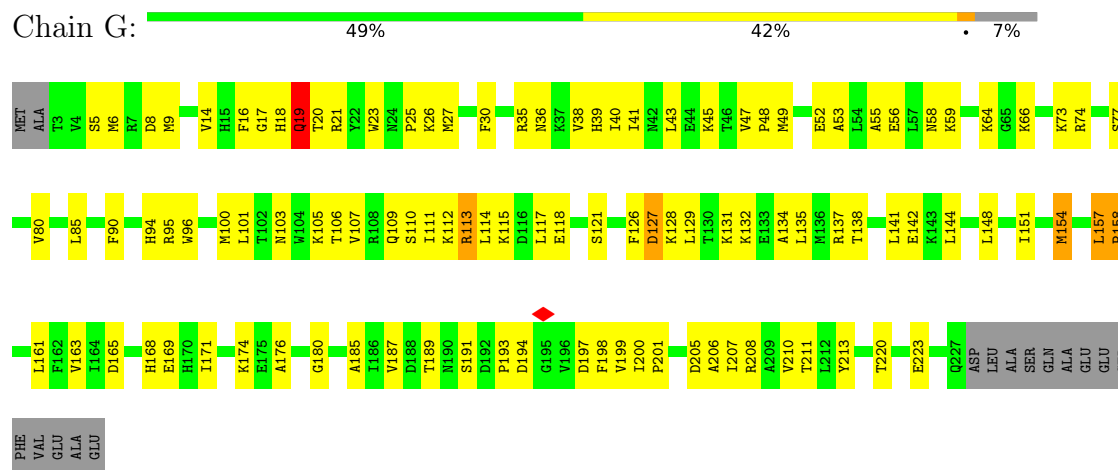
- Molecule 17: 16S rRNA



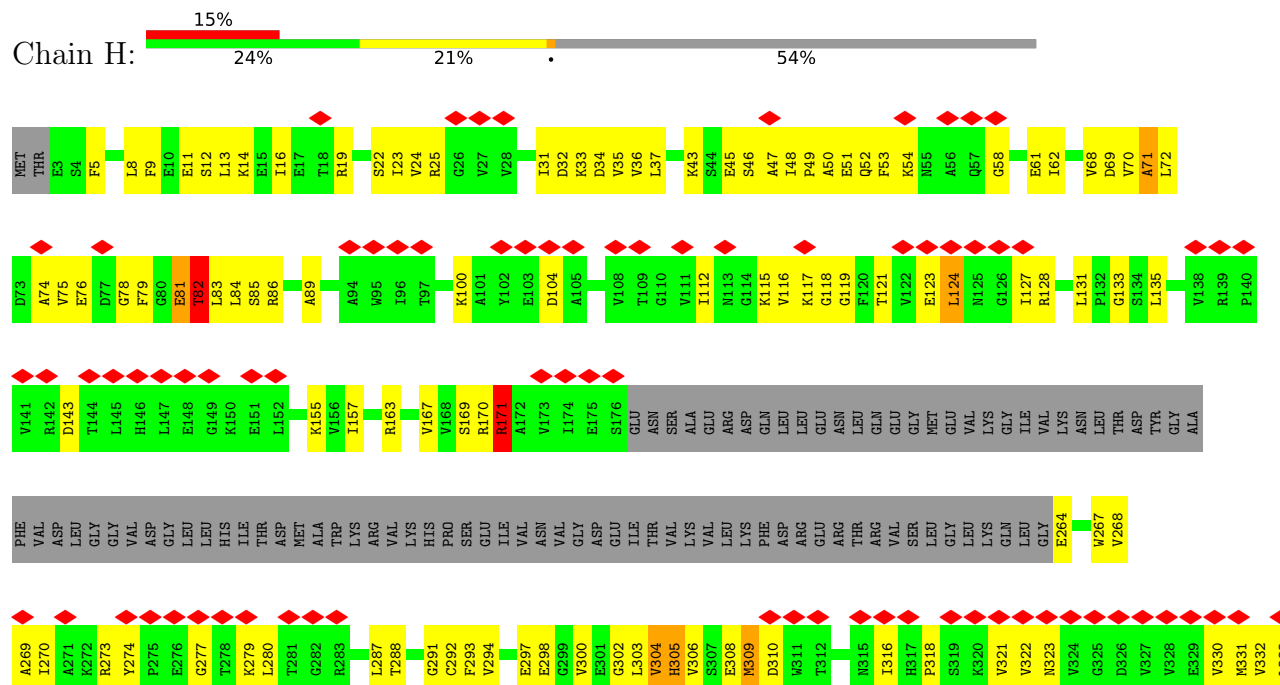
• Molecule 19: 30S ribosomal protein S21

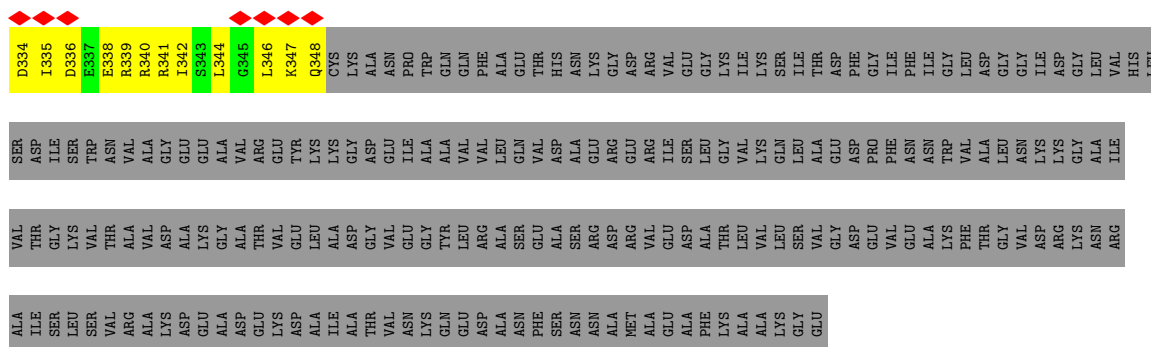


• Molecule 20: 30S ribosomal protein S2



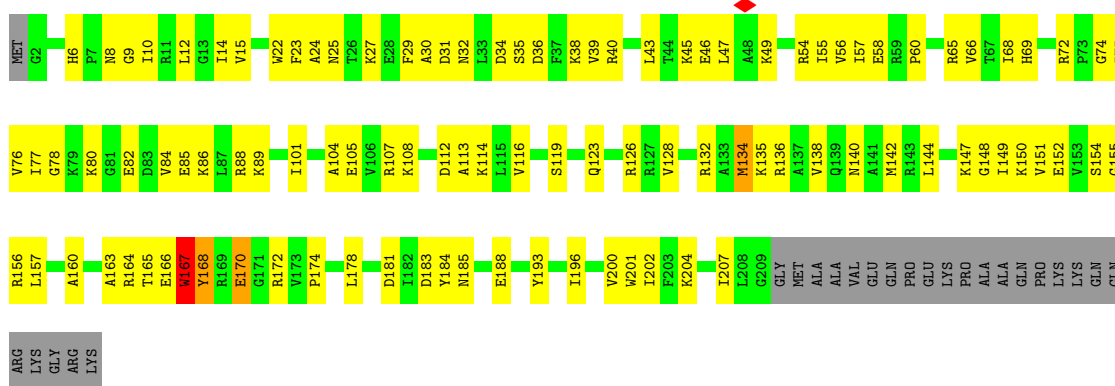
• Molecule 21: 30S ribosomal protein S1





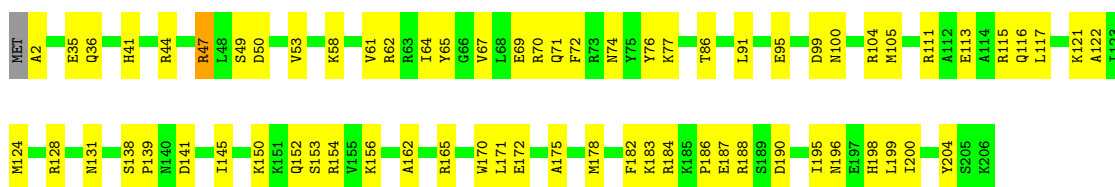
• Molecule 22: 30S ribosomal protein S3

Chain I: 45% 43% 11%



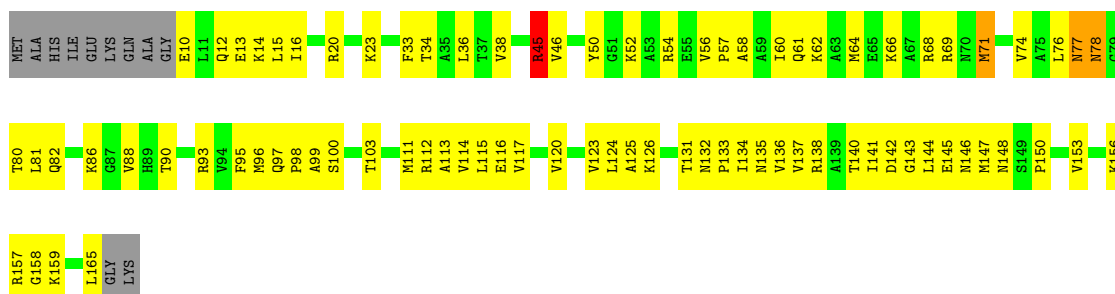
• Molecule 23: 30S ribosomal protein S4

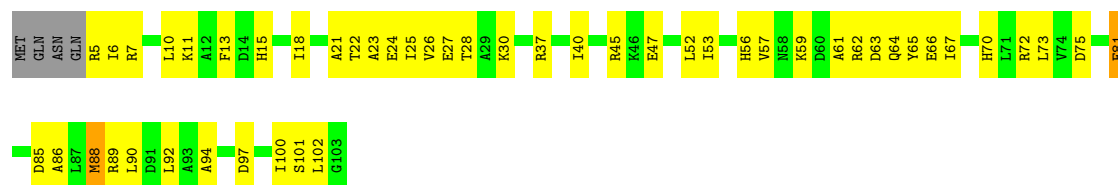
Chain J: 67% 33%



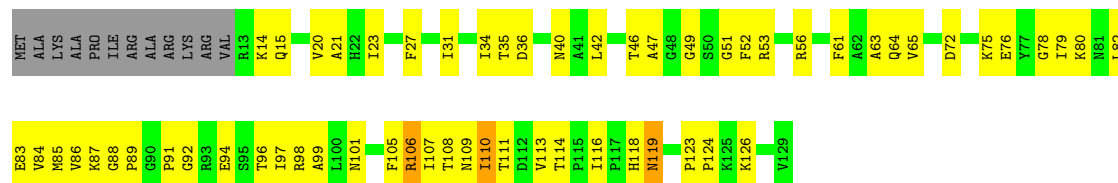
• Molecule 24: 30S ribosomal protein S5

Chain K: 44% 47% 7%

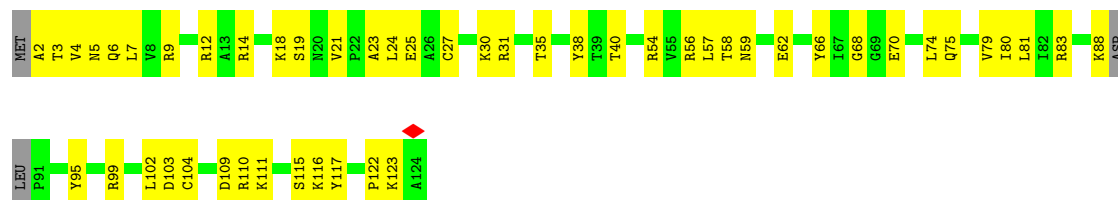




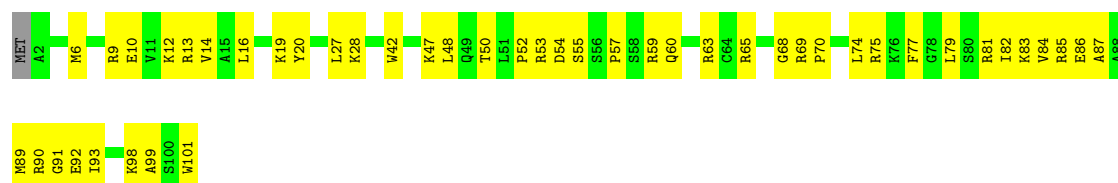
• Molecule 30: 30S ribosomal protein S11



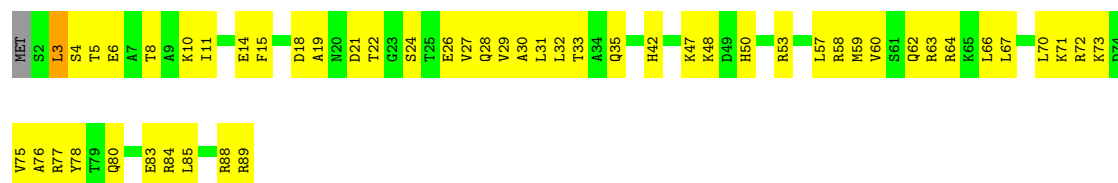
• Molecule 31: 30S ribosomal protein S12



• Molecule 32: 30S ribosomal protein S14



• Molecule 33: 30S ribosomal protein S15



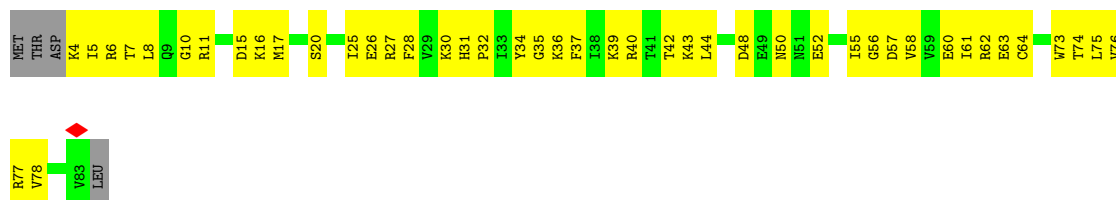
• Molecule 34: 30S ribosomal protein S16

Chain U:  54% 46%



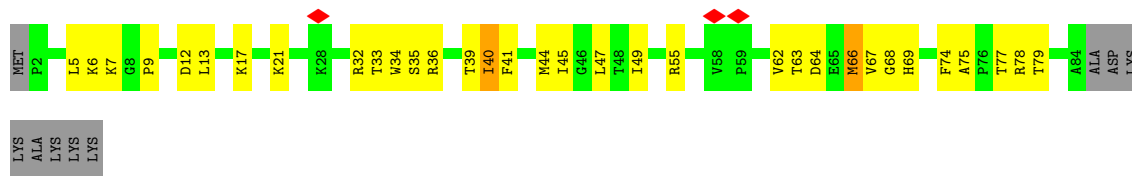
- Molecule 35: 30S ribosomal protein S17

Chain V:  42% 54% 5%



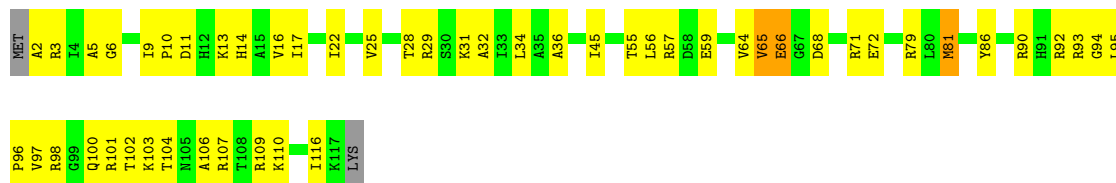
- Molecule 36: 30S ribosomal protein S19

Chain W:  54% 34% 10%



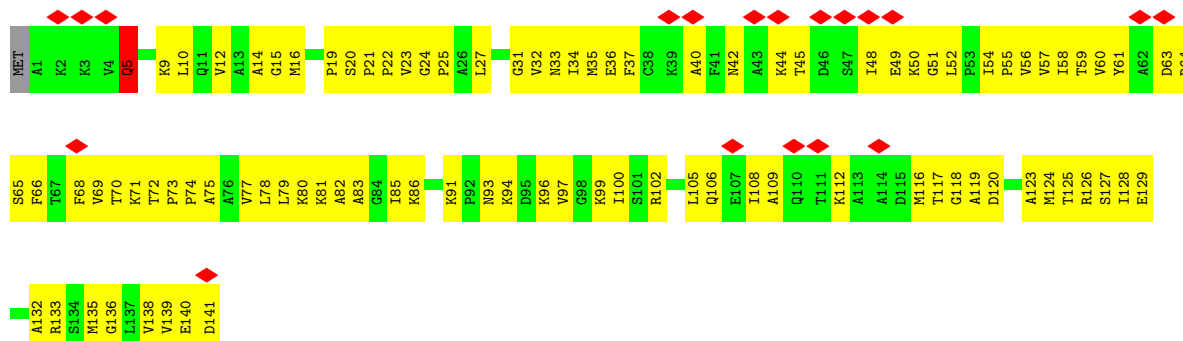
- Molecule 37: 30S ribosomal protein S13

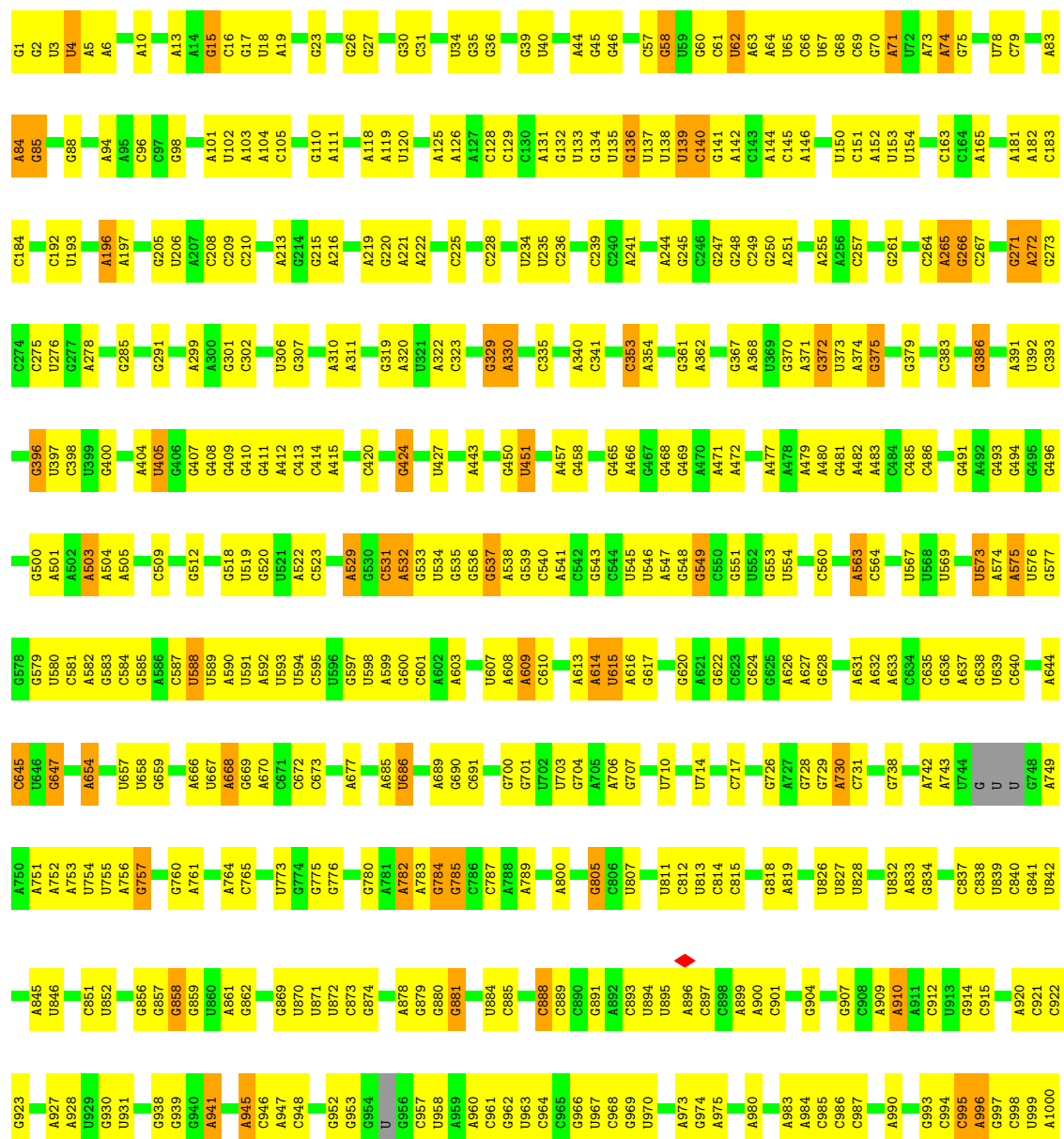
Chain X:  55% 41% 2%



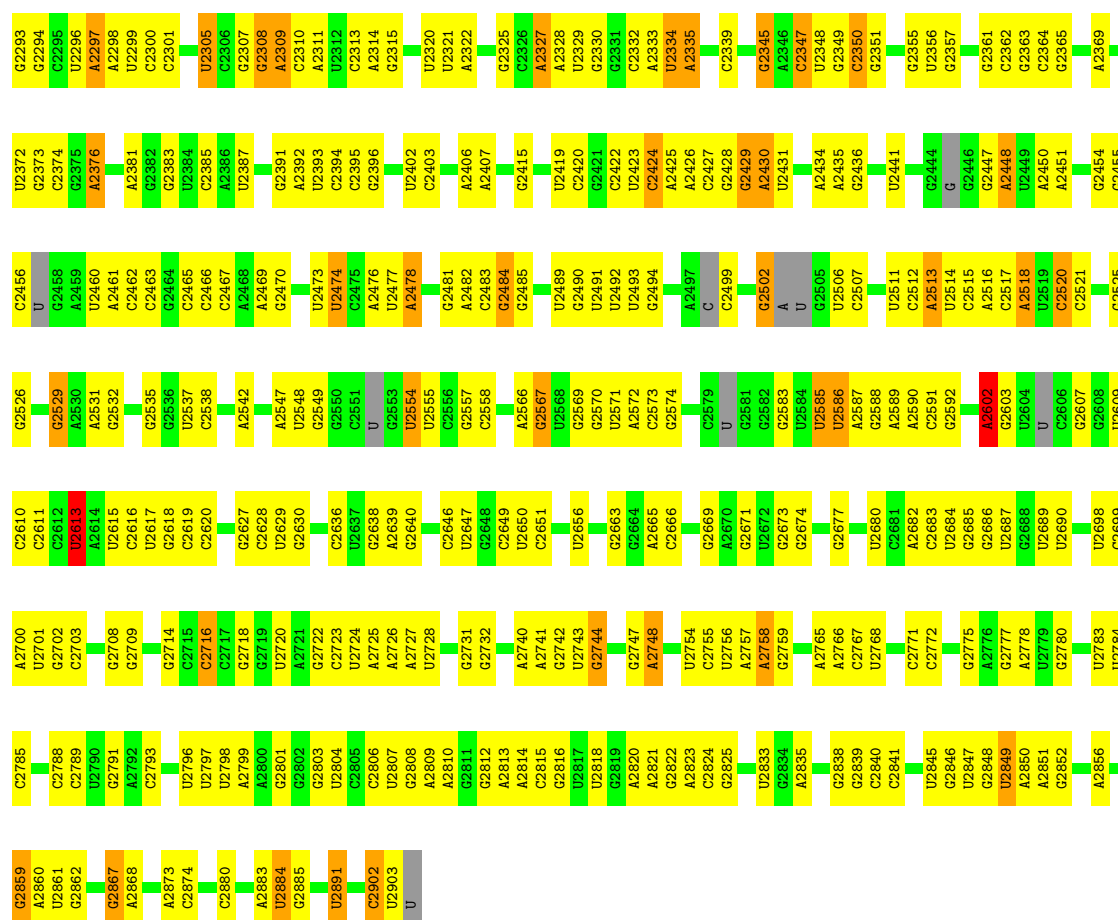
- Molecule 38: 50S ribosomal protein L11

Chain Y:  13% 34% 65% 2%





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C2206	U2210	U2131	A2051	A1981	U1820	U1750	G1613	G1529	U1415	G1341	C1243	C1146	A1074	A1005	
A2211	A2212	G2133	A2052	U1982	A1822	G1730	A1614	U1534	G1416	A1342	A1246	A1147	C1075	C1006	
C2215	C2216	A2134	G2055	G1983	G1823	C1732	G1617	C1536	G1417	U1343	A1247	C1153	C1076	C1007	
C2217	C2218	U2139	G2056	A1987	U1825	G1738	A1619	G1537	G1418	U1344	U1248	C1154	A1077	A1008	
C2224	A2225	U2140	A2060	U1991	G1826	U1746	G1619	U1542	G1421	G1346	U1249	G1160	C1079	A1009	
C2226	C2227	G2141	G2061	U1992	U1827	A1747	G1622	U1543	G1422	A1347	C1250	C1161	U1081	U1012	
C2228	U2229	U2142	A2062	U1993	G1828	U1747	G1622	G1543	G1423	C1349	C1251	G1162	U1082	U1013	
C2230	C2231	C2146	C2063	U1994	A1829	G1750	G1622	G1544	A1427	C1350	A1253	G1167	U1083	A1014	
C2232	C2233	A2147	G2064	C1995	C1830	G1750	U1647	G1546	G1428	C1351	G1256	C1168	U1084	U1019	
C2234	C2235	G2148	C2065	U1997	G1831	G1750	U1648	C1547	G1429	U1352	G1257	A1169	A1085	A1020	
C2236	C2237	U2149	C2066	A1998	C1832	G1753	G1649	A1548	G1430	A1353	C1257	C1170	A1086	A1021	
C2238	C2239	C2150	G2067	C1999	C1833	U1754	A1650	A1549	A1431	A1354	A1262	G1171	A1087	G1022	
C2240	C2241	U2150	U2068	C2000	U1834	A1755	G1651	G1554	G1432	G1355	A1262	C1172	A1088	U1023	
C2242	C2243	G2161	G	U	G	G1756	A1652	U1554	G1434	G1356	G1266	U1173	A1089	U1024	
C2244	C2245	A2154	A2070	G1922	C1836	A1757	G1653	U1559	A1434	G1360	A1269	U1174	A1090	G1025	
C2246	C2247	U2157	C2071	C1924	G1839	U1758	A1654	G1560	G1435	G1361	A1270	A1175	A1095	G1026	
C2248	C2249	C2158	C2072	U1925	G1840	G1764	A1655	G1561	G1441	C1362	C1270	U1176	A1096	A1027	
C2250	C2251	U2159	U	U	U1941	U1778	A1656	G1562	U1442	A1365	A1271	C1177	A1028	A1029	
C2252	C2253	C2160	A1927	A1928	G1842	G1770	C1658	U1563	U1443	U1378	A1272	C1178	U1101		
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C2256	C2257	A2163	U1931	G1945	G1845	C1774	A1664	A1566	G1445	G1380	A1276	U1181			
C2258	C2259	C2164	A1932	G1946	U1846	U1778	A1665	G1567	G1452	C1370	G1277	U1182	G1036	G1036	
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C2266	C2267	U2170	U	U	U1855	A1786	A1672	A1572	U1467	A1384	C1290	G1188	G1041	G1041	
C2268	C2269	C2175	U1944	G1945	U1856	A1789	G1673	A1580	A1469	A1385	C1295	G1189	G1042	G1042	
C2270	C2271	U2176	G1946	U1947	G1857	G1791	A1675	G1581	A1470	A1386	G1296	G1190	G1043	G1043	
C2272	C2273	U2181	U1947	U1948	U1858	G1792	A1677	C1582	A1477	A1387	G1295	U1198	A1046	A1046	
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C2276	C2277	U2183	U1955	U1956	U1863	U1794	G1682	U1584	U1490	U1393	G1300	U1201	A1048	A1048	
C2278	C2279	U2184	U1957	U1958	U1864	G1795	G1683	C1585	U1497	U1394	A1301	A1204	C1053	C1053	
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C2294	C2295	U2192	C1967	C1968	U1880	A1808	C1708	A1598	C1507	U1405	C1320	U1225	U1065	U1065	
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C2302	C2303	U2196	U1972	U1973	A1890	C1816	G1715	A1607	C1512	G1410	G1333	A1237	G1068	G1068	
C2304	C2305	U2197	U1974	U1975	A1891	C1817	U1720	C1607	U1513	U1411	G1334	G1238	A1069	A1069	
C2306	C2307	U2198	U1976	U1977	A1900	U1818	G1721	A1609	A1514	A1413		U1240	A1143	A1143	
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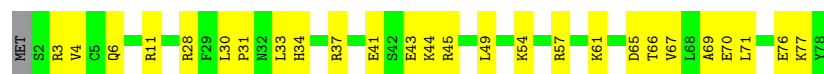
• Molecule 41: 50S ribosomal protein L27

Chain b: 56% 33% 11%



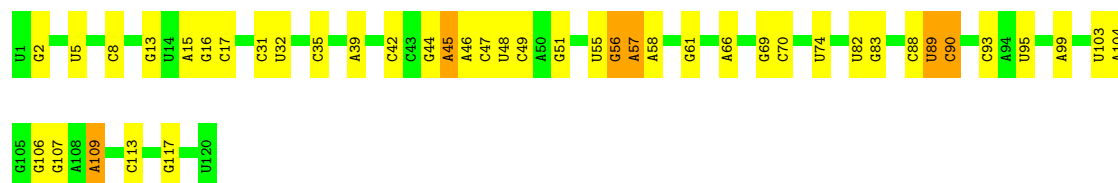
• Molecule 42: 50S ribosomal protein L28

Chain c: 65% 33%



• Molecule 43: 5S rRNA

Chain d: 64% 31% 5%



- Molecule 44: 50S ribosomal protein L29

Chain e: 



- Molecule 45: 50S ribosomal protein L30

Chain f: 



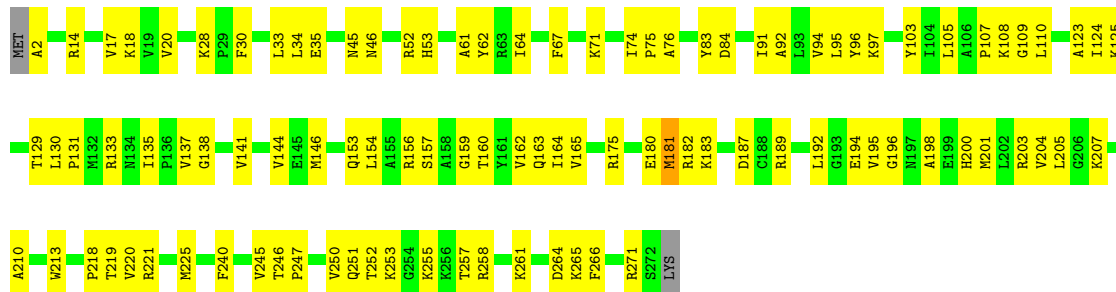
- Molecule 46: 50S ribosomal protein L31

Chain g: 



- Molecule 47: 50S ribosomal protein L2

Chain h: 



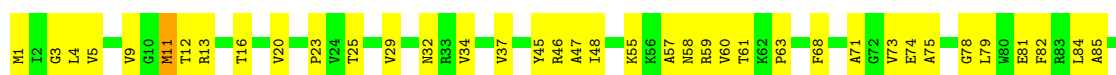
- Molecule 48: 50S ribosomal protein L32

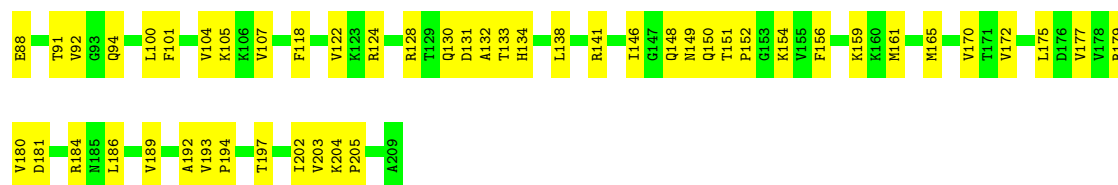
Chain i: 



- Molecule 49: 50S ribosomal protein L3

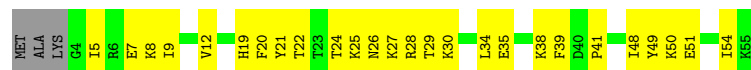
Chain j: 





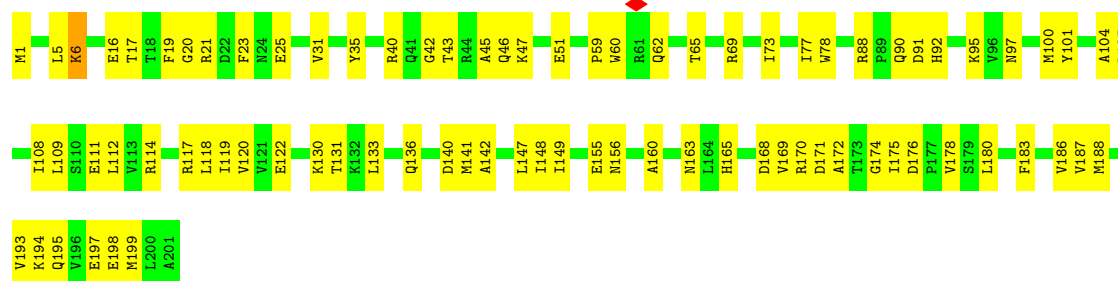
- Molecule 50: 50S ribosomal protein L33

Chain k: 47% 47% 5%



- Molecule 51: 50S ribosomal protein L4

Chain l: 59% 40%



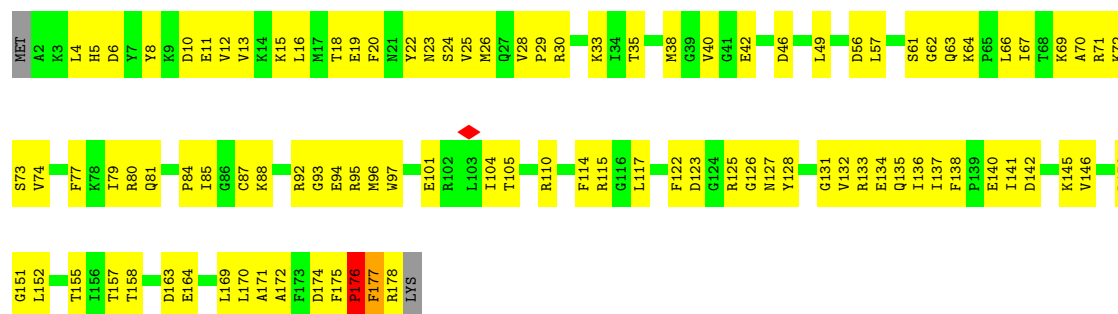
- Molecule 52: 50S ribosomal protein L34

Chain m: 57% 43%



- Molecule 53: 50S ribosomal protein L5

Chain n: 44% 54%



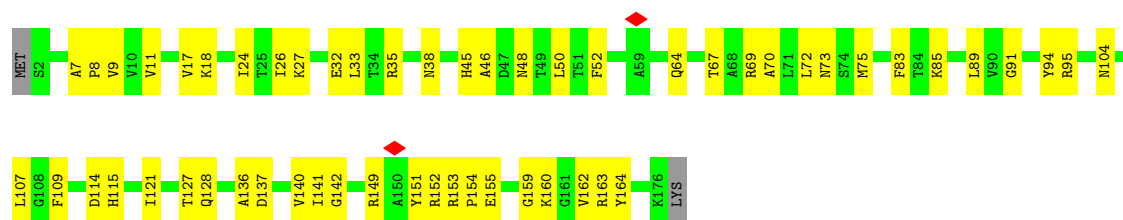
- Molecule 54: 50S ribosomal protein L35

Chain o:  58% 35% 5%



- Molecule 55: 50S ribosomal protein L6

Chain p:  68% 31%



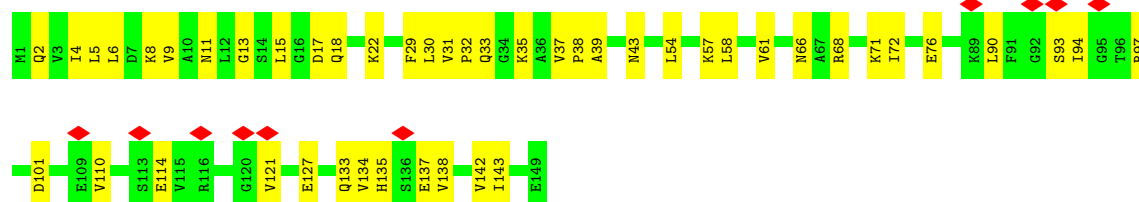
- Molecule 56: 50S ribosomal protein L36

Chain q:  55% 45%



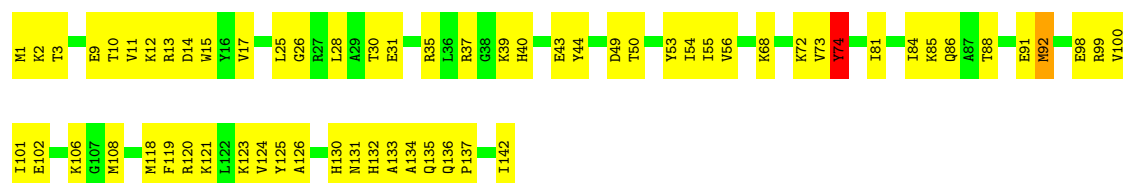
- Molecule 57: 50S ribosomal protein L9

Chain r:  7% 68% 32%



- Molecule 58: 50S ribosomal protein L13

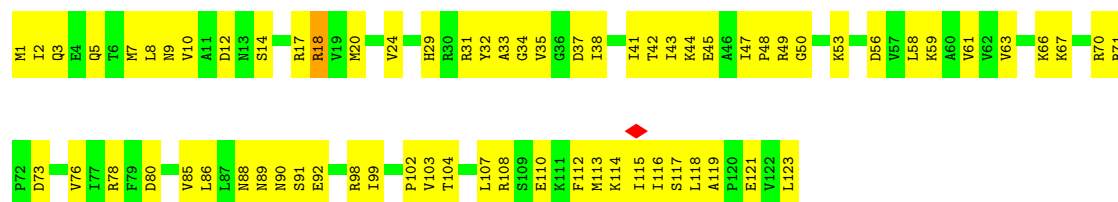
Chain s:  56% 43%



- Molecule 59: 50S ribosomal protein L14

Chain t:  43% 56%





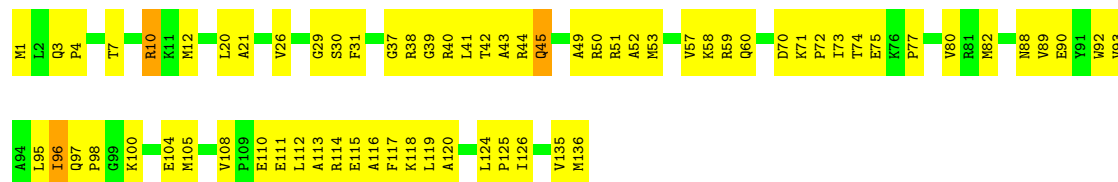
• Molecule 60: 50S ribosomal protein L15

Chain u: 62% 37%



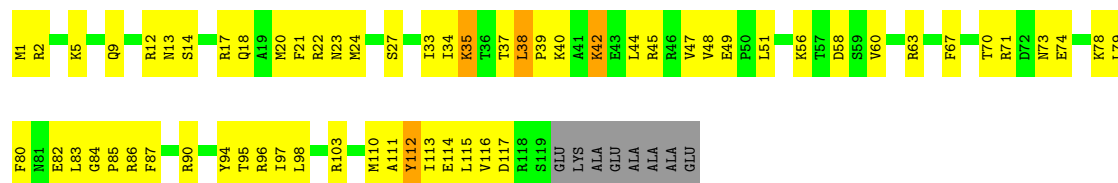
• Molecule 61: 50S ribosomal protein L16

Chain v: 50% 48%



• Molecule 62: 50S ribosomal protein L17

Chain w: 45% 46% 6%

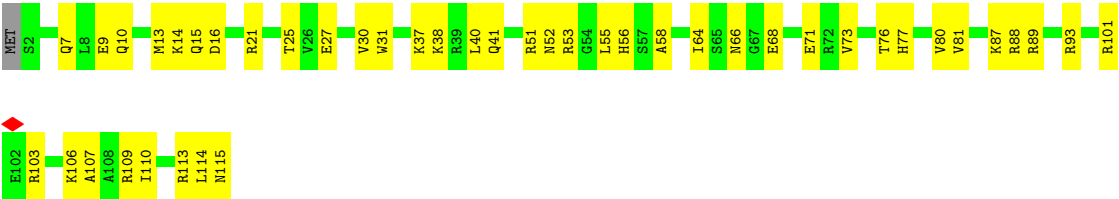


• Molecule 63: 50S ribosomal protein L18

Chain x: 63% 36%



• Molecule 64: 50S ribosomal protein L19



• Molecule 65: 50S ribosomal protein L20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	2632	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	0.027	Depositor
Minimum map value	-0.016	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0039	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	0.56	0/816	0.77	0/1259
7	6	0.56	0/783	0.78	0/1203
8	7	0.57	2/761 (0.3%)	0.88	3/1178 (0.3%)
9	9	0.37	0/1131	0.74	2/1524 (0.1%)
10	A	0.27	0/1810	0.58	0/2821
10	B	0.27	0/1810	0.58	0/2821
11	AA	0.38	0/10547	0.62	0/14232
12	AB	0.43	0/1317	1.11	10/1786 (0.6%)
13	AC	0.37	0/1718	0.61	0/2328
13	AD	0.32	0/1696	0.60	0/2298
14	AE	0.37	0/10561	0.64	5/14258 (0.0%)
15	AF	0.29	0/652	0.61	0/879
16	C	0.67	0/553	0.80	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	0.38	0/1746	0.81	0/2382
22	I	0.57	1/1663 (0.1%)	0.68	5/2241 (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	0.66	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	0.53	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	0.56	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	0.41	0/304
40	a	0.30	0/69247	0.43	10/107985 (0.0%)
41	b	0.41	0/589	0.56	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	1/2852 (0.0%)
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	0.46	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	0.62	2/960 (0.2%)	0.62	0/1278
All	All	0.38	34/190612 (0.0%)	0.53	90/280873 (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	9
13	AC	0	1
13	AD	0	1
14	AE	0	5
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	-12.79	1.10	1.49
28	O	80	ARG	CD-NE	-10.46	1.31	1.46
62	w	42	LYS	CD-CE	-9.39	1.24	1.52
24	K	45	ARG	CG-CD	7.72	1.75	1.52
8	7	46	G	C1'-N9	-7.60	1.36	1.48

The worst 5 of 90 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	K	71	MET	CG-SD-CE	-11.30	76.03	100.90
20	G	158	PRO	N-CD-CG	-10.98	86.72	103.20
12	AB	141	LEU	CA-C-N	-10.57	106.30	122.16
12	AB	141	LEU	C-N-CA	-10.57	106.30	122.16
12	AB	123	PHE	N-CA-C	-9.74	93.47	108.96

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

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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

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	73	0
3	2	746	811	811	59	0
4	3	788	844	844	45	0
5	4	753	780	780	87	0
6	5	726	0	392	111	0
7	6	703	0	396	35	0
8	7	687	0	342	110	0
9	9	1117	0	1155	258	0
10	A	1620	826	827	111	0
10	B	1620	814	827	111	0
11	AA	10381	0	10390	233	0
12	AB	1286	0	1302	340	0
13	AC	1698	0	1718	15	0
13	AD	1677	0	1713	26	0
14	AE	10404	0	10624	286	0
15	AF	650	0	658	10	0
16	C	544	559	560	111	0
17	D	32703	16423	16453	736	0
18	E	669	719	719	78	0
19	F	589	629	629	62	0
20	G	1760	1785	1787	158	0
21	H	1730	1454	1455	166	0
22	I	1636	1710	1710	154	0
23	J	1643	1707	1707	82	0
24	K	1152	1196	1196	120	0
25	L	848	846	846	106	0
26	M	1181	1235	1238	122	0
27	N	979	1031	1031	94	0
28	O	1022	1070	1070	92	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	P	790	831	831	122	0
30	Q	877	887	887	94	0
31	R	939	1001	1001	93	0
32	S	805	844	844	72	0
33	T	714	734	734	89	0
34	U	649	666	666	63	0
35	V	648	691	691	71	0
36	W	663	688	688	47	0
37	X	900	964	965	111	0
38	Y	1032	0	1088	212	0
39	Z	227	0	237	30	0
40	a	61841	31077	31120	1312	0
41	b	582	599	599	45	0
42	c	625	652	652	35	0
43	d	2569	1301	1301	44	0
44	e	501	531	531	45	0
45	f	448	488	488	39	0
46	g	522	520	520	62	0
47	h	2082	2154	2154	136	0
48	i	444	459	458	48	0
49	j	1565	1617	1616	116	0
50	k	426	464	464	43	0
51	l	1552	1619	1619	126	0
52	m	377	418	418	32	0
53	n	1410	1443	1444	155	0
54	o	504	572	572	52	0
55	p	1313	1358	1358	75	0
56	q	302	343	343	27	0
57	r	1111	1148	1148	52	0
58	s	1129	1162	1162	126	0
59	t	946	1023	1023	107	0
60	u	1053	1129	1129	78	0
61	v	1074	1157	1157	119	0
62	w	951	994	994	102	0
63	x	892	923	923	46	0
64	y	917	962	962	53	0
65	z	947	1020	1019	79	0
66	AE	1	0	0	0	0
67	AE	2	0	0	1	0
All	All	177315	98639	128747	6798	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 6798 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:11:DA:C5'	12:AB:67:THR:HG22	1.20	1.65
6:5:10:DT:C7	11:AA:62:TYR:CD2	1.84	1.57
24:K:45:ARG:CD	24:K:45:ARG:CG	1.75	1.56
6:5:10:DT:C5	11:AA:62:TYR:CD2	1.95	1.54
6:5:9:DG:C5'	11:AA:473:ARG:HB3	1.34	1.53

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	30
11	AA	1312/1342 (98%)	1197 (91%)	114 (9%)	1 (0%)	48	83
12	AB	159/162 (98%)	108 (68%)	43 (27%)	8 (5%)	1	16
13	AC	217/329 (66%)	203 (94%)	12 (6%)	2 (1%)	14	51
13	AD	214/329 (65%)	198 (92%)	16 (8%)	0	100	100
14	AE	1331/1407 (95%)	1208 (91%)	117 (9%)	6 (0%)	24	63
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

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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	67
21	H	255/557 (46%)	182 (71%)	66 (26%)	7 (3%)	4	25
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	59
25	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	48
26	M	149/179 (83%)	140 (94%)	8 (5%)	1 (1%)	18	56
27	N	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
28	O	125/130 (96%)	116 (93%)	8 (6%)	1 (1%)	16	54
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	34
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

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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	59
54	o	62/65 (95%)	57 (92%)	4 (6%)	1 (2%)	7	38
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%)	8735 (92%)	715 (8%)	36 (0%)	31	67

5 of 36 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

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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	84
12	AB	141/142 (99%)	138 (98%)	3 (2%)	47	65
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%)	1103 (98%)	19 (2%)	53	69
15	AF	70/75 (93%)	69 (99%)	1 (1%)	59	72
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	83
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%)	85 (99%)	1 (1%)	63	75
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

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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%)	7860 (100%)	30 (0%)	81	84

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	AE	78	LEU
15	AF	63	ILE

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Mol	Chain	Res	Type
14	AE	84	ILE
29	P	81	GLU
14	AE	292	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 107 such sidechains are listed below:

Mol	Chain	Res	Type
25	L	68	GLN
44	e	25	GLN
63	x	29	HIS
26	M	86	GLN
32	S	4	GLN

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	1515/1542 (98%)	290 (19%)	22 (1%)
40	a	2859/2904 (98%)	511 (17%)	0
43	d	119/120 (99%)	15 (12%)	0
8	7	31/47 (65%)	22 (70%)	4 (12%)
All	All	4674/4765 (98%)	896 (19%)	42 (0%)

5 of 896 RNA backbone outliers are listed below:

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

5 of 42 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
17	D	793	U
17	D	1212	U
17	D	991	U
17	D	1145	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
17	D	1214	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

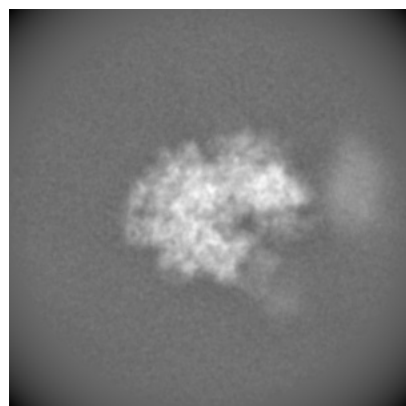
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42503. These allow visual inspection of the internal detail of the map and identification of artifacts.

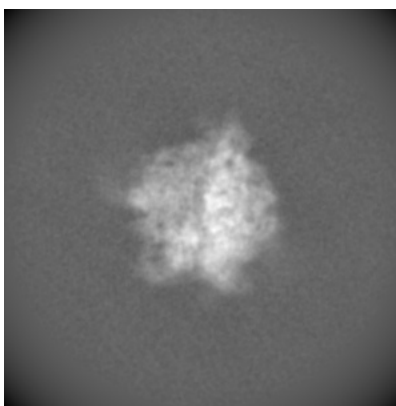
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

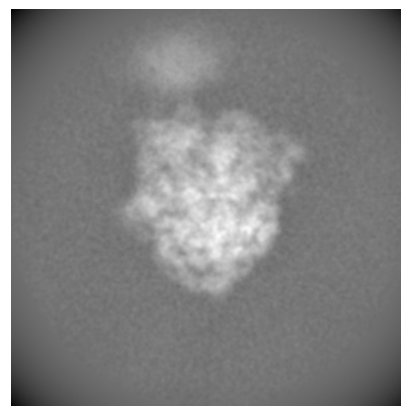
6.1.1 Primary map



X

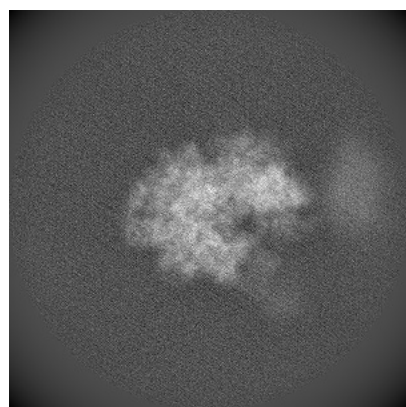


Y

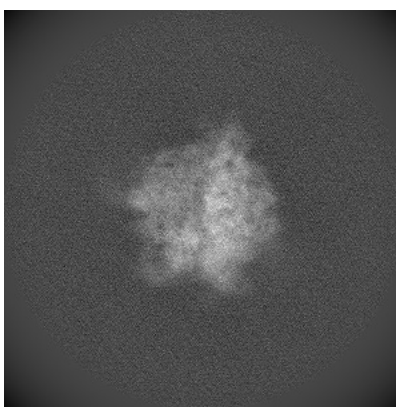


Z

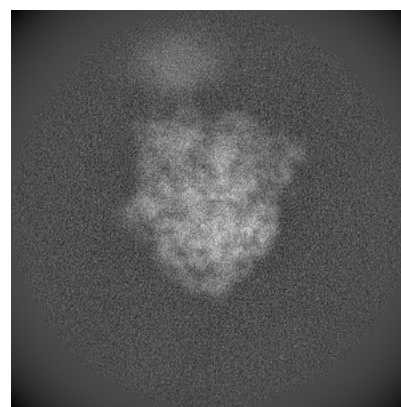
6.1.2 Raw map



X



Y

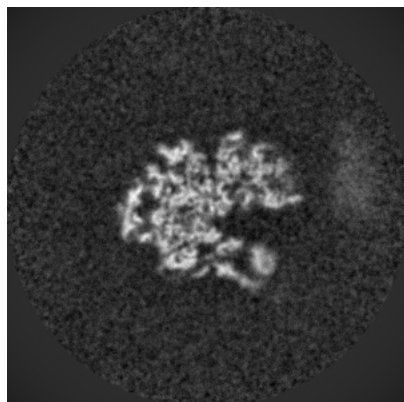


Z

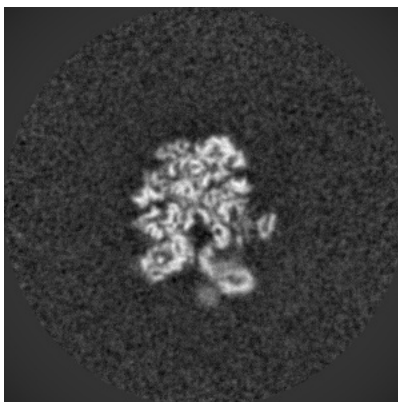
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

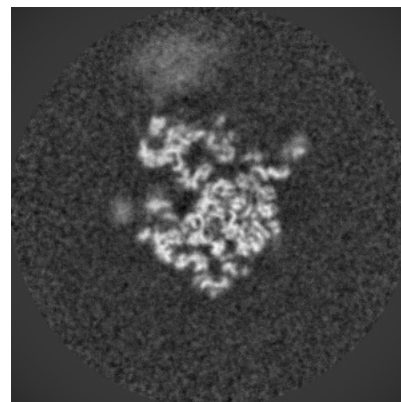
6.2.1 Primary map



X Index: 256

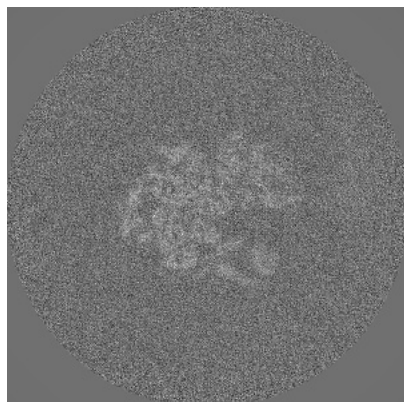


Y Index: 256

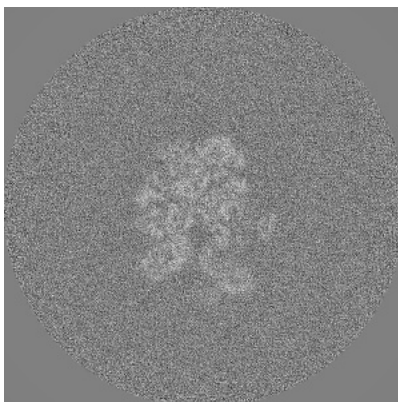


Z Index: 256

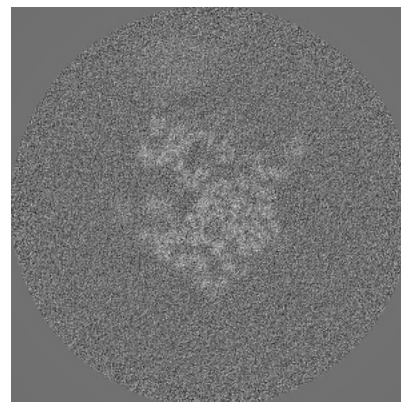
6.2.2 Raw map



X Index: 256



Y Index: 256

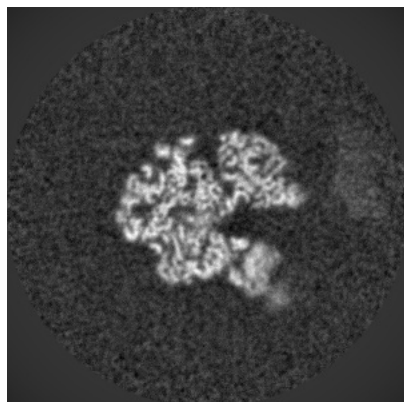


Z Index: 256

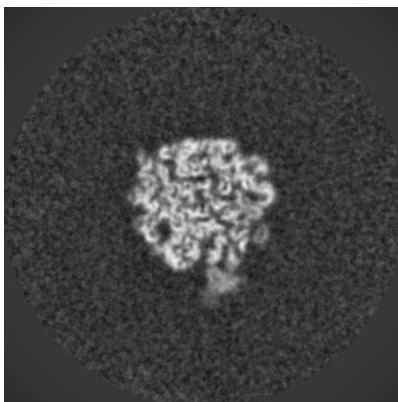
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

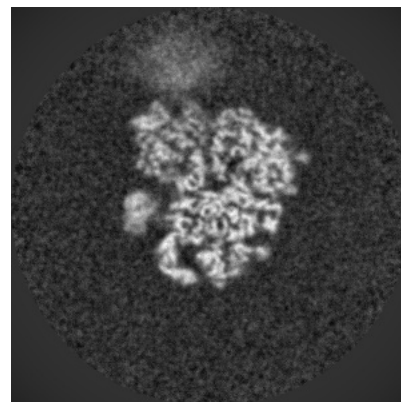
6.3.1 Primary map



X Index: 266

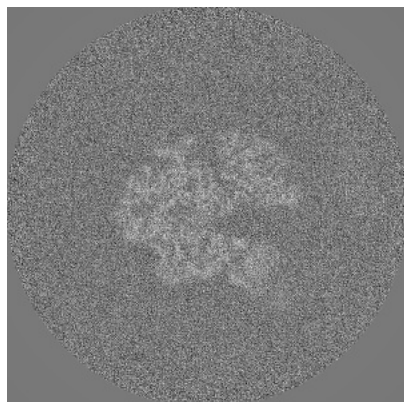


Y Index: 235

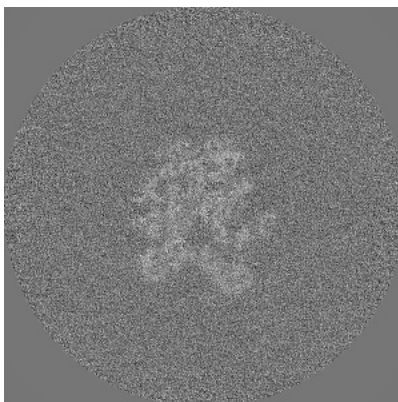


Z Index: 281

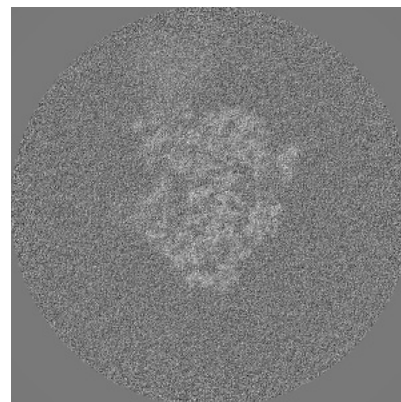
6.3.2 Raw map



X Index: 265



Y Index: 260

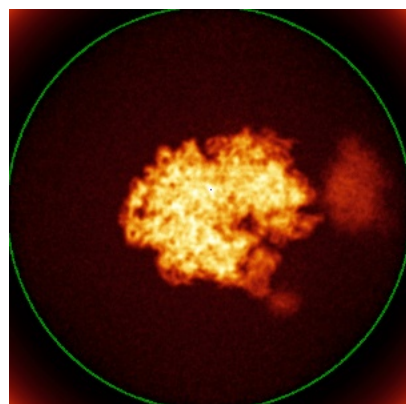


Z Index: 267

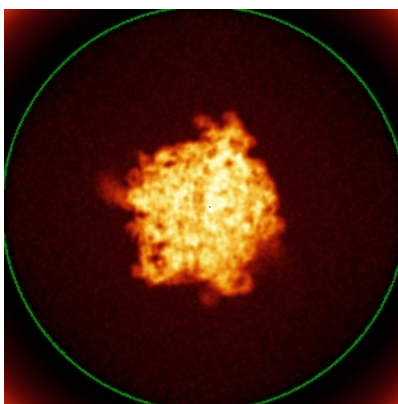
The images above show the largest variance slices of the map in three orthogonal directions.

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

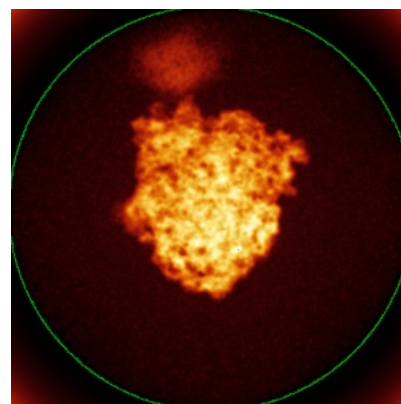
6.4.1 Primary map



X

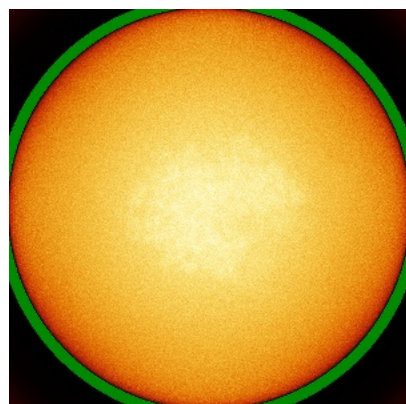


Y

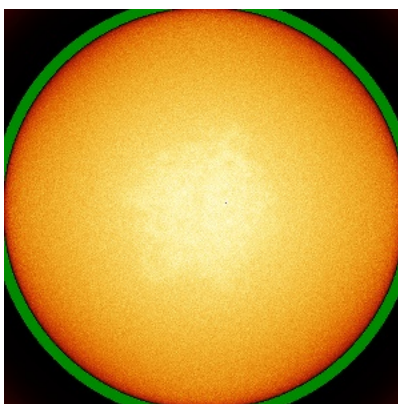


Z

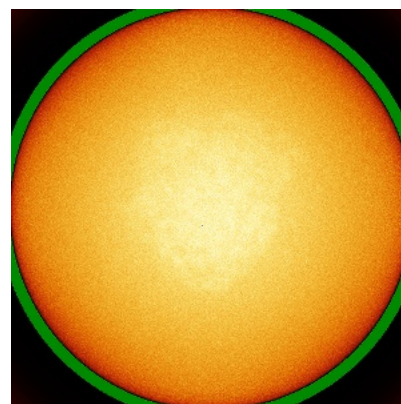
6.4.2 Raw map



X



Y

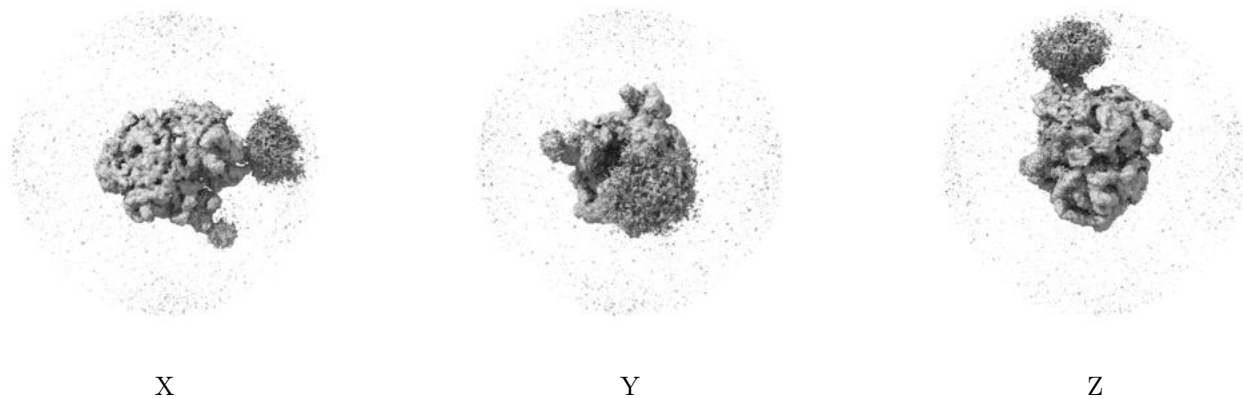


Z

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.

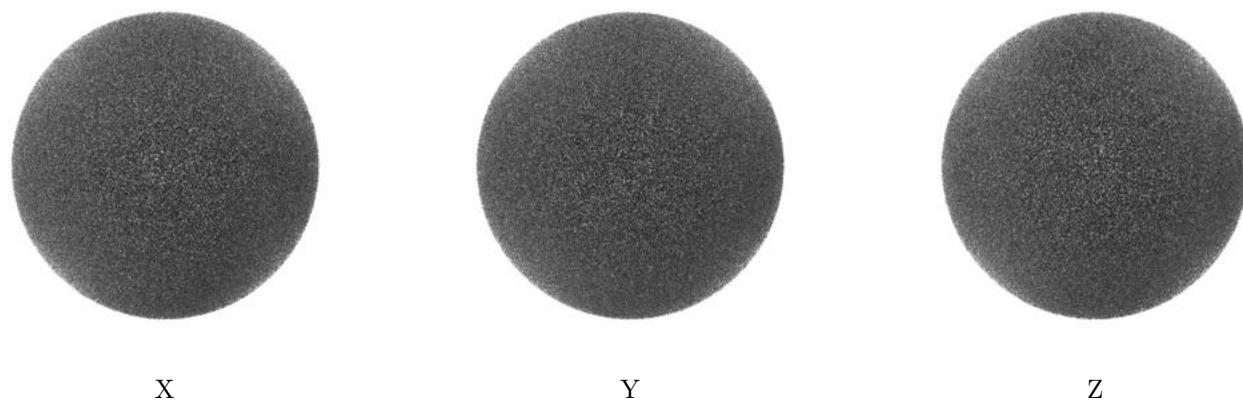
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0039. 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.

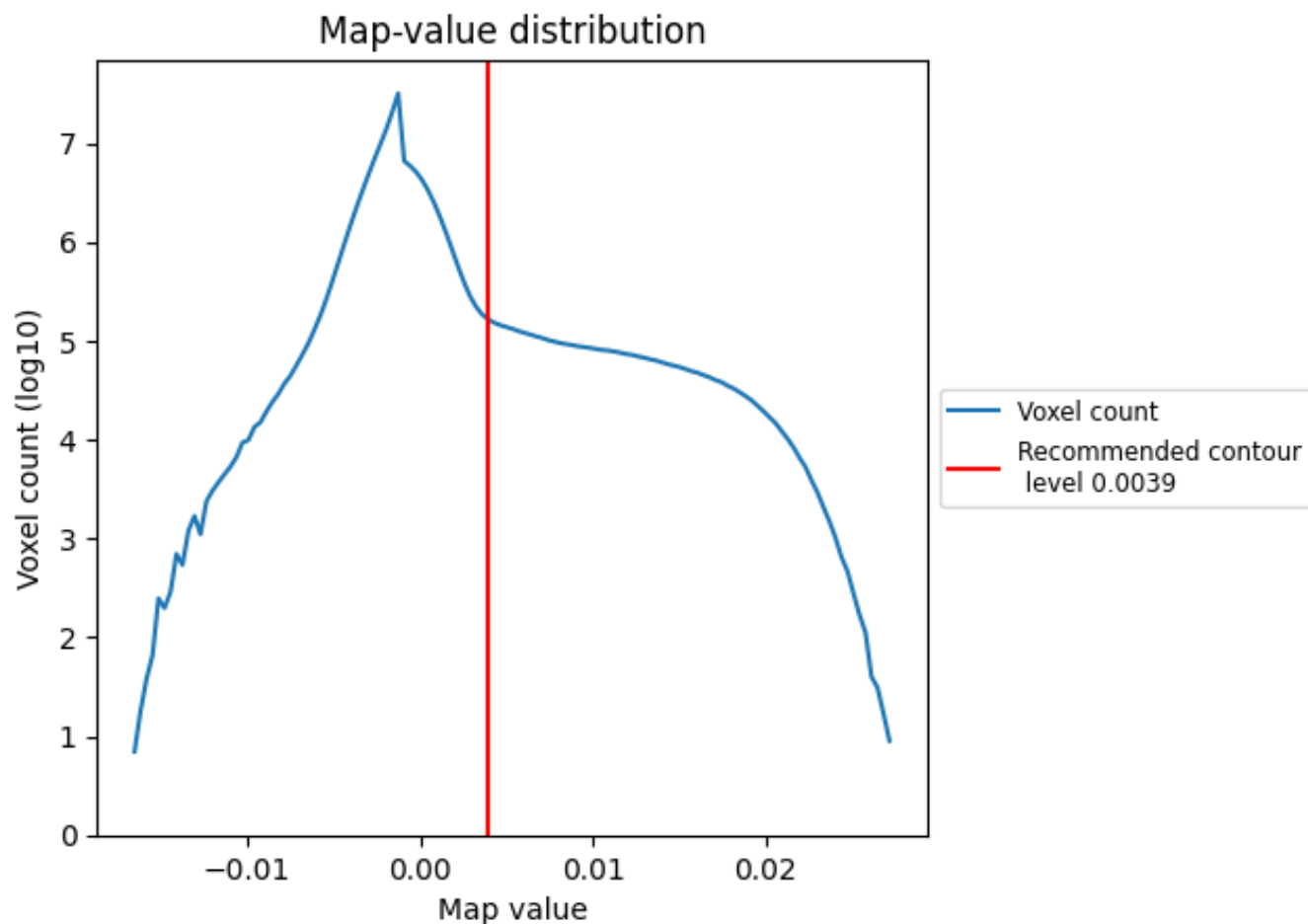
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

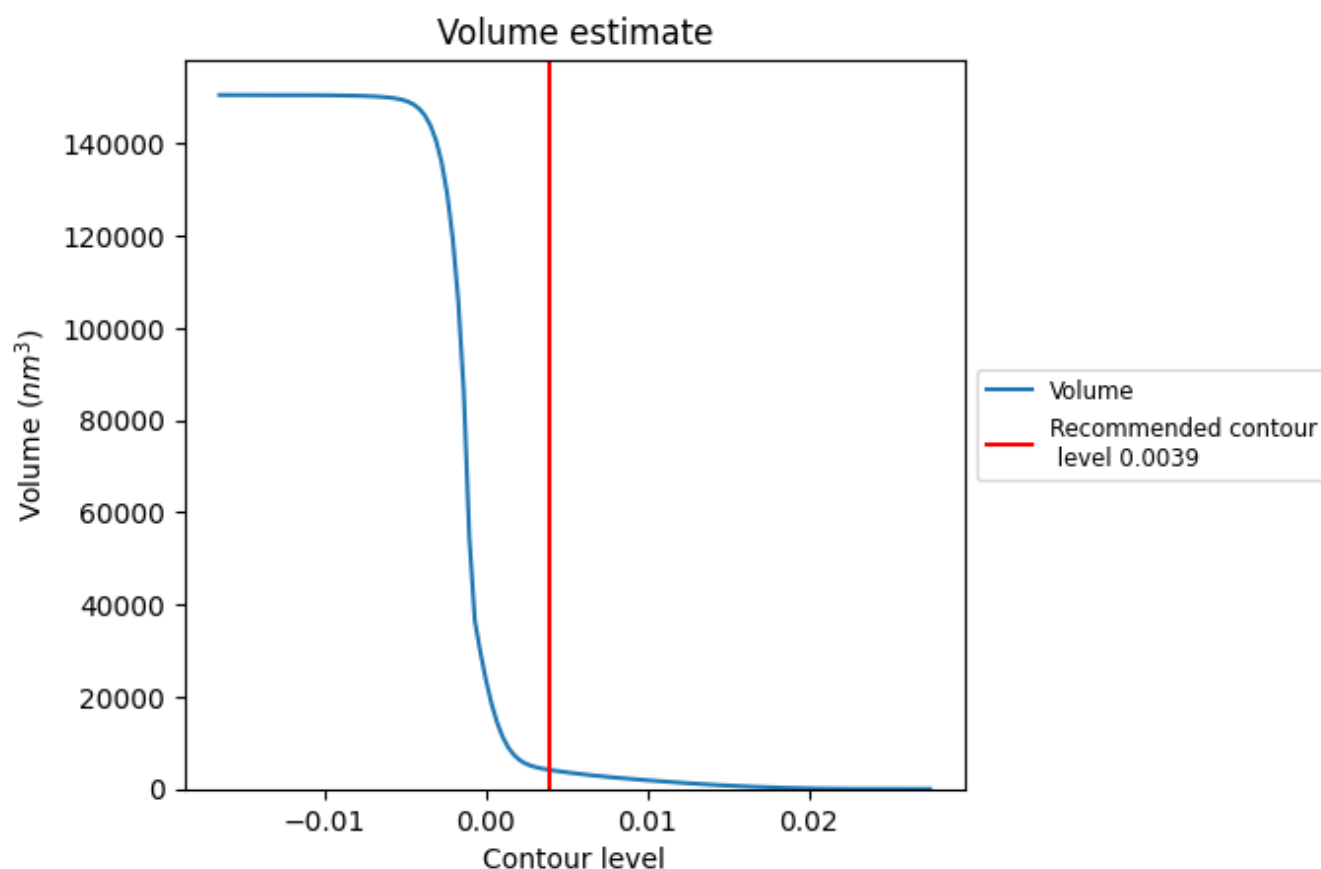
This section contains the results of statistical analysis of the map.

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.

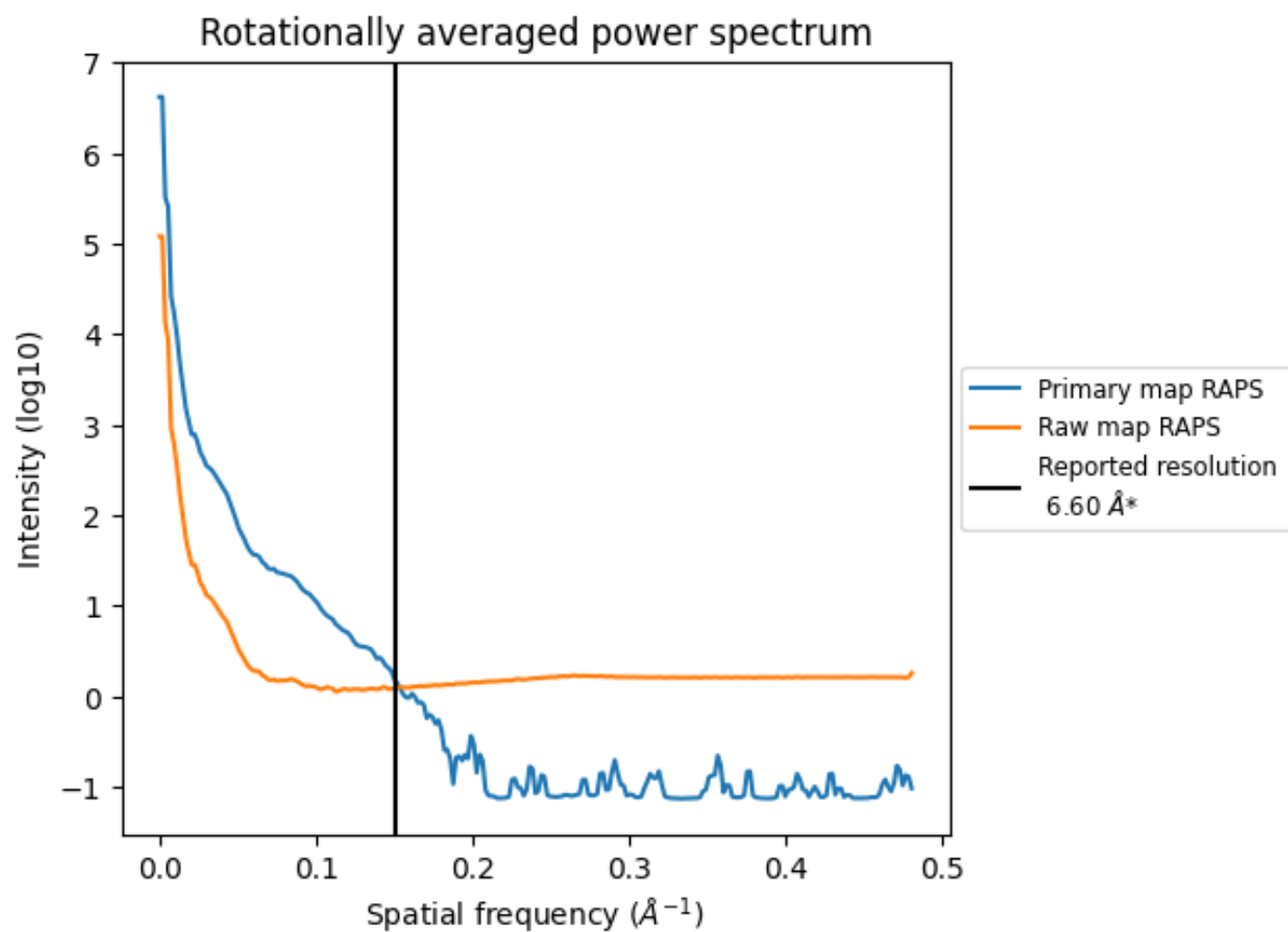
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4154 nm³; this corresponds to an approximate mass of 3752 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 ⓘ

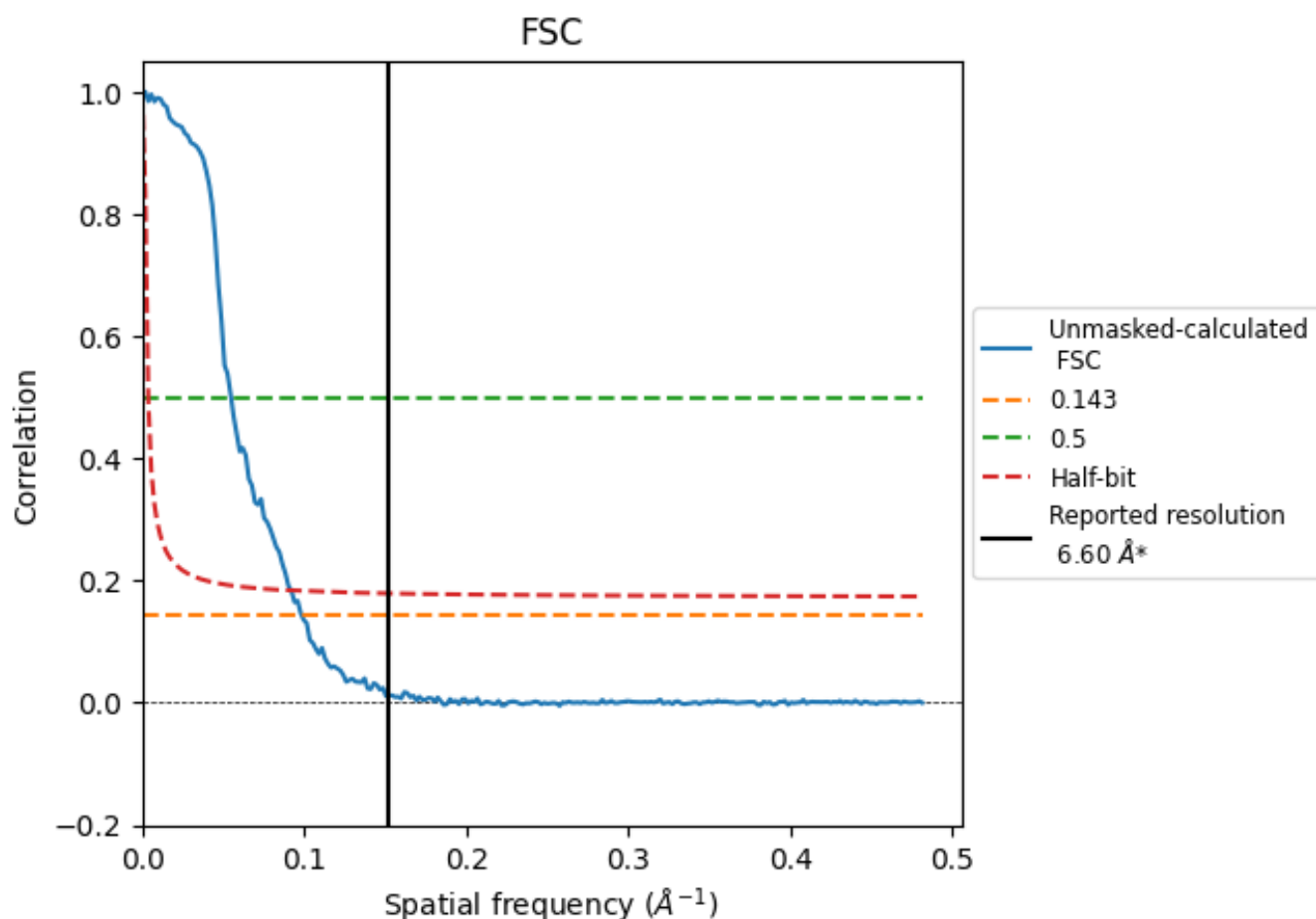


*Reported resolution corresponds to spatial frequency of 0.152 Å⁻¹

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 0.152 Å⁻¹

8.2 Resolution estimates [i](#)

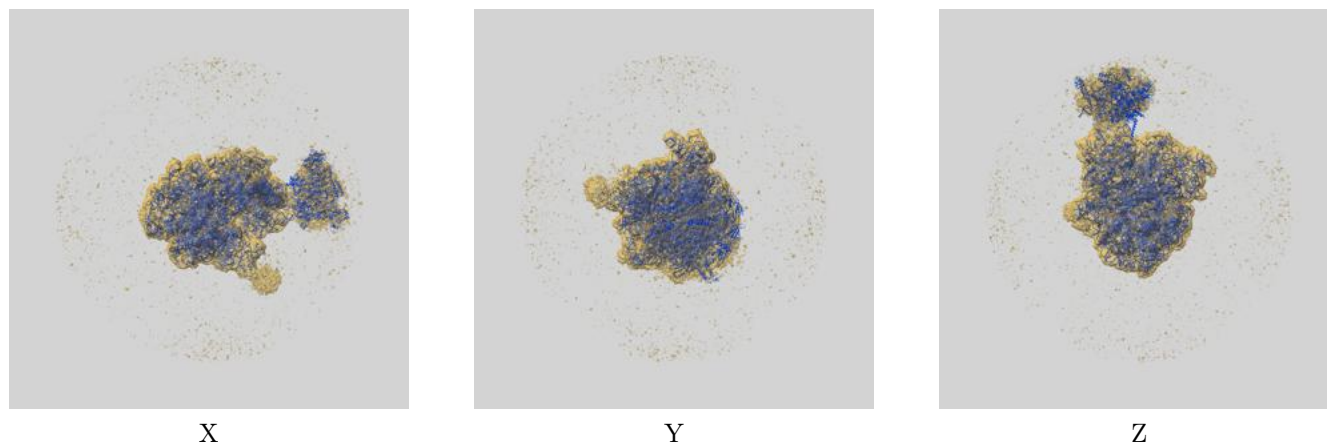
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	10.16	18.25	10.88

*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 10.16 differs from the reported value 6.6 by more than 10 %

9 Map-model fit [i](#)

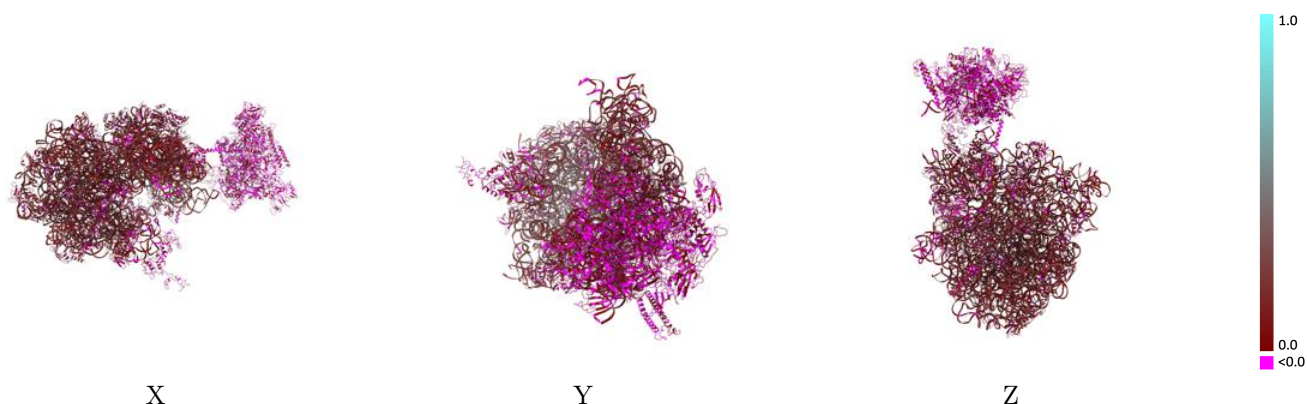
This section contains information regarding the fit between EMDB map EMD-42503 and PDB model 8URX. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



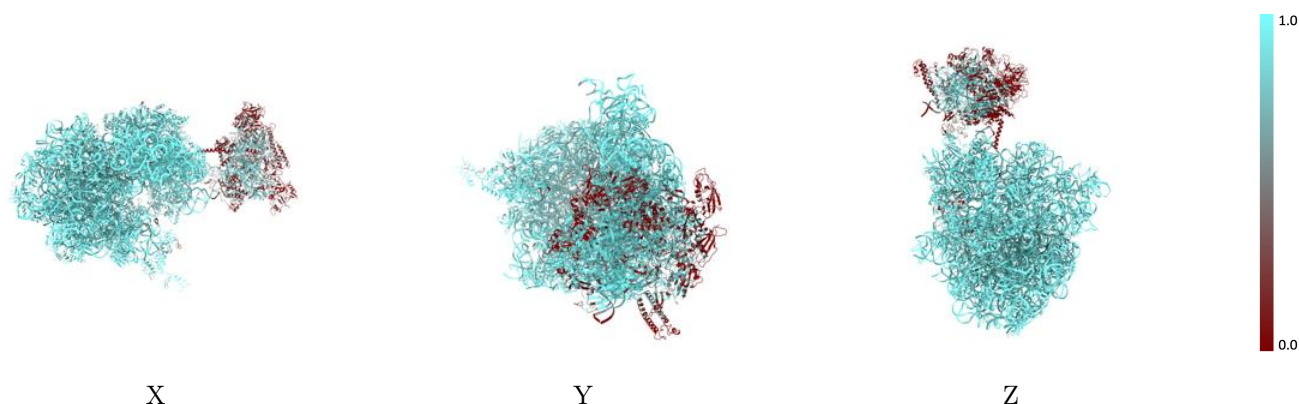
The images above show the 3D surface view of the map at the recommended contour level 0.0039 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



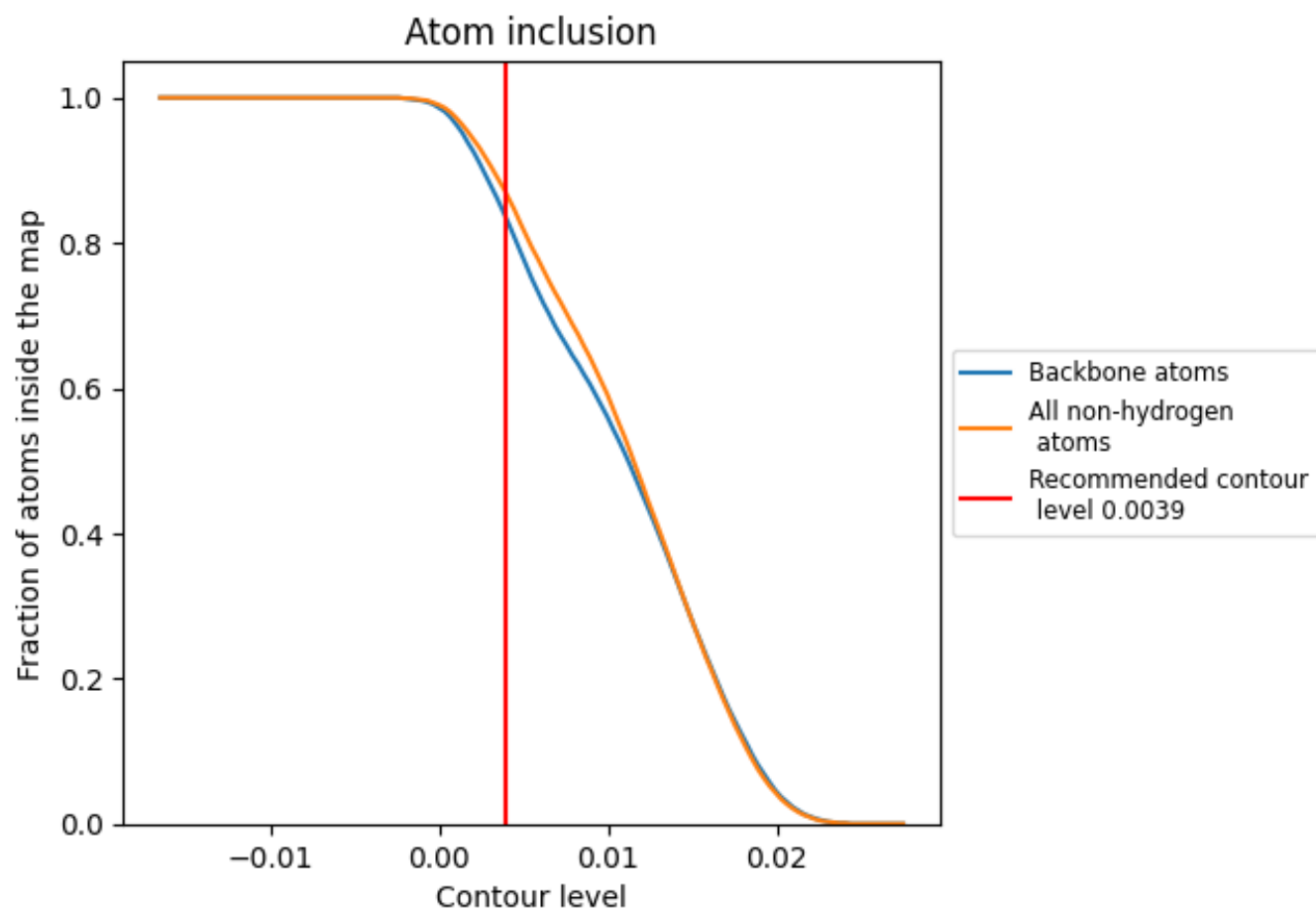
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.0039).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0039) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8720	 0.1330
0	 0.9860	 0.1440
1	 0.9740	 0.1480
2	 0.9800	 0.1350
3	 0.9860	 0.1210
4	 0.9760	 0.1330
5	 0.8030	 0.0160
6	 0.7170	 0.0410
7	 0.9200	 0.0370
9	 0.9320	 0.0410
A	 0.9890	 0.1430
AA	 0.6090	 0.0160
AB	 0.4120	 0.0120
AC	 0.4420	 0.0230
AD	 0.1390	 0.0110
AE	 0.4470	 0.0110
AF	 0.0190	 -0.0140
B	 0.8830	 0.0970
C	 0.9960	 0.1250
D	 0.9930	 0.1750
E	 0.9740	 0.1330
F	 0.9410	 0.1420
G	 0.9570	 0.1120
H	 0.6390	 0.0360
I	 0.9770	 0.1360
J	 0.9840	 0.1070
K	 0.9900	 0.1470
L	 0.9900	 0.1470
M	 0.9810	 0.1290
N	 0.9750	 0.1320
O	 0.9870	 0.1100
P	 0.9750	 0.1090
Q	 0.9920	 0.1340
R	 0.9770	 0.1490
S	 0.9880	 0.1340



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Chain	Atom inclusion	Q-score
T	 0.9990	 0.1430
U	 0.9810	 0.0920
V	 0.9570	 0.1270
W	 0.9070	 0.0790
X	 0.9620	 0.1250
Y	 0.8400	 0.0420
Z	 0.8900	 0.0320
a	 0.9940	 0.1770
b	 0.9770	 0.1050
c	 0.9800	 0.1360
d	 0.9990	 0.1690
e	 0.9960	 0.1530
f	 0.9890	 0.1580
g	 0.9430	 0.1100
h	 0.9880	 0.1100
i	 0.9740	 0.1380
j	 0.9850	 0.0990
k	 0.9900	 0.1230
l	 0.9760	 0.1360
m	 0.9800	 0.1390
n	 0.9700	 0.0870
o	 0.9800	 0.1350
p	 0.9700	 0.0980
q	 0.9830	 0.0930
r	 0.8760	 0.1020
s	 0.9870	 0.1350
t	 0.9580	 0.0950
u	 0.9940	 0.1220
v	 0.9760	 0.1290
w	 0.9850	 0.1310
x	 0.9880	 0.1020
y	 0.9580	 0.1080
z	 0.9900	 0.1270