



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 04:28 AM UTC

PDB ID : 8YDE / pdb_00008yde
EMDB ID : EMD-39168
Title : E.coli transcription translation coupling complex in TTC-B state 1 (subclass 3) containing mRNA with 39-mer spacer, NusG, NusA, fMet-tRNA(iMet), Phe-tRNA(Phe), and viomycin
Authors : Zhang, J.; Lu, G.; Wang, C.; Lin, J.
Deposited on : 2024-02-20
Resolution : 5.00 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:

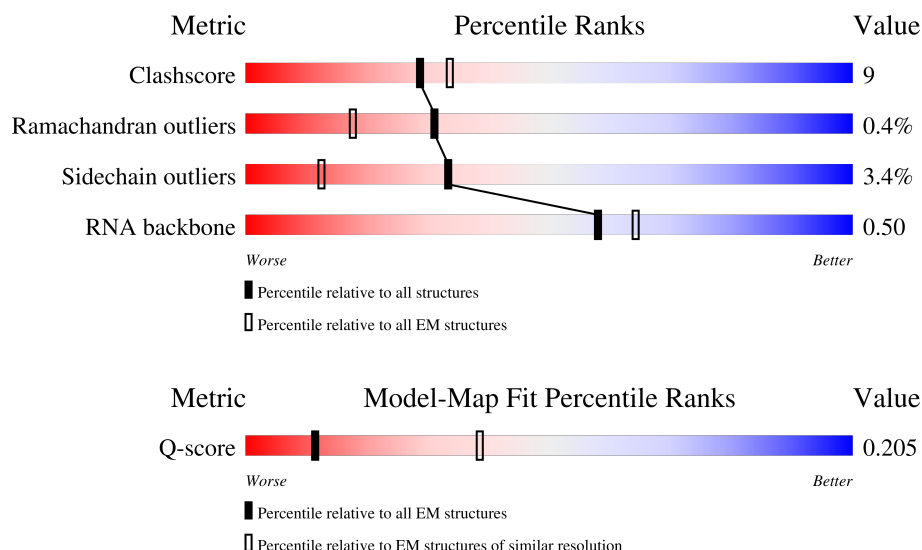
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 5.00 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.



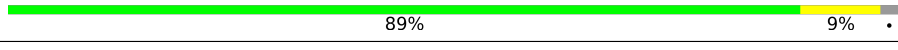
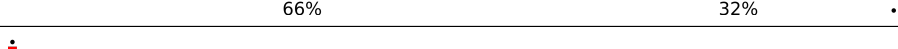
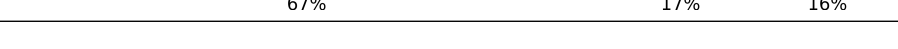
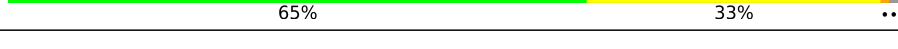
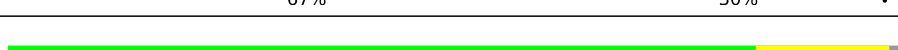
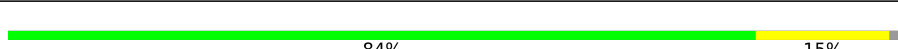
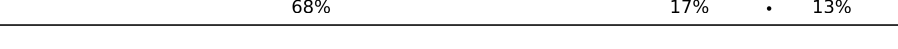
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1057 (4.50 - 5.50)

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	A	70	
2	B	57	
3	C	55	

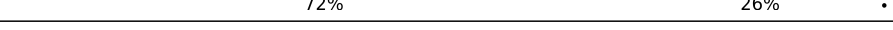
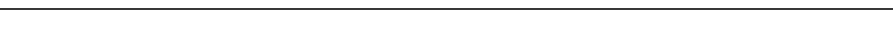
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Mol	Chain	Length	Quality of chain
4	D	46	
5	E	65	
6	F	38	
7	G	241	
8	H	233	
9	I	206	
10	J	167	
11	K	135	
12	L	179	
13	M	130	
14	N	130	
15	O	103	
16	P	129	
17	Q	124	
18	R	118	
19	S	101	
20	T	89	
21	U	82	
22	V	84	
23	W	75	
24	X	92	
25	Y	87	
26	Z	71	
27	b	273	
28	c	209	

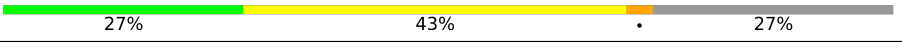
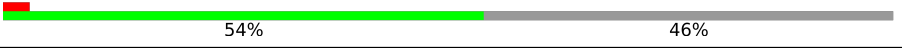
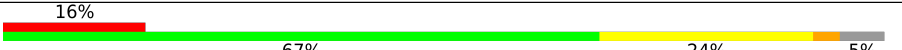
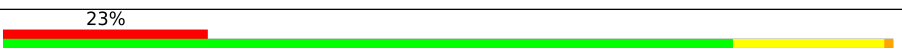
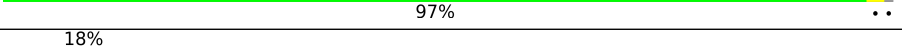
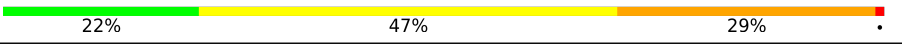
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Mol	Chain	Length	Quality of chain
29	d	201	
30	e	179	
31	f	177	
32	g	149	
33	i	142	
34	j	142	
35	k	123	
36	l	144	
37	m	136	
38	n	127	
39	o	117	
40	p	115	
41	q	118	
42	r	103	
43	s	110	
44	t	100	
45	u	104	
46	v	94	
47	w	85	
48	x	78	
49	y	63	
50	z	59	
51	1	2904	
52	2	120	
53	3	1542	

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Mol	Chain	Length	Quality of chain
54	4	56	
55	8	37	
56	9	37	
57	A1	329	
57	A2	329	
58	B1	1407	
59	B2	1342	
60	W0	91	
61	NA	495	
62	NG	181	
63	5	76	
64	6	77	
64	7	77	
65	h	6	

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
65	5OH	h	6	-	-	X	-

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 178130 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 2 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 3 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 4 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 5 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 6 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 7 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 8 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 9 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 10 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 11 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 12 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 13 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 14 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 15 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 16 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 17 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 18 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 19 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 20 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 21 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 22 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 23 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 24 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 25 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 26 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 28 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 29 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 30 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 31 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	52	Total	C	N	O	S	0	0
			400	256	73	70	1		

- Molecule 33 is a protein called 50S ribosomal protein L11.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	j	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 35 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	k	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 36 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	l	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 37 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	m	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 38 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	n	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 39 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	o	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 40 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	p	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 41 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 42 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 43 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 44 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 45 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	u	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 46 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	v	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 47 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 48 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	x	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 49 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 51 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1929590828

- Molecule 52 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	U	conflict	GB NR_103249

- Molecule 53 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	35	Total	C	N	O	P	0	0
			729	326	105	263	35		

- Molecule 55 is a DNA chain called templete DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	8	27	Total	C	N	O	P	0	0
			539	257	88	167	27		

- Molecule 56 is a DNA chain called non-templete DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	9	20	Total	C	N	O	P	0	0
			417	195	84	118	20		

- Molecule 57 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	A1	301	Total	C	N	O	S	0	0
			2088	1293	380	409	6		
57	A2	288	Total	C	N	O	S	0	0
			2029	1257	366	400	6		

- Molecule 58 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	B1	1335	Total	C	N	O	S	0	0
			10353	6509	1842	1955	47		

- Molecule 59 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	B2	1340	Total	C	N	O	S	0	0
			10546	6616	1839	2048	43		

- Molecule 60 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	W0	82	Total	C	N	O	S	0	0
			650	396	122	131	1		

- Molecule 61 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	NA	492	Total	C	N	O	0	0
			2432	1448	492	492		

- Molecule 62 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	NG	154	Total	C	N	O	0	0
			758	450	154	154		

- Molecule 63 is a RNA chain called tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
63	5	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		

- Molecule 64 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
64	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
64	7	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 65 is a protein (with D amino acids) called Viomycin.

Mol	Chain	Residues	Atoms				AltConf	Trace
65	h	6	Total	C	N	O	0	0
			48	25	13	10		

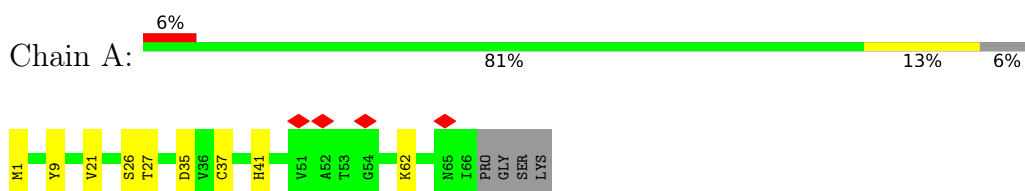
- Molecule 66 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
66	B1	1	Total	Mg	0
			1	1	

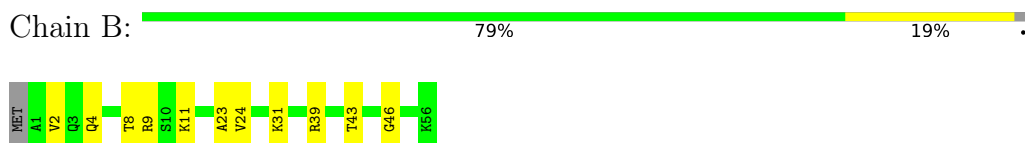
3 Residue-property plots [i](#)

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.

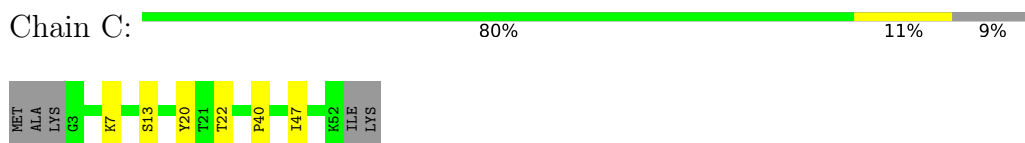
- Molecule 1: 50S ribosomal protein L31



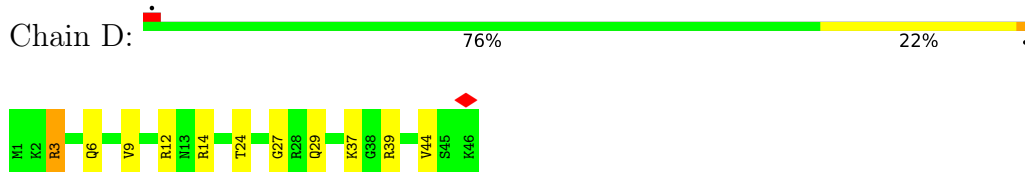
- Molecule 2: 50S ribosomal protein L32



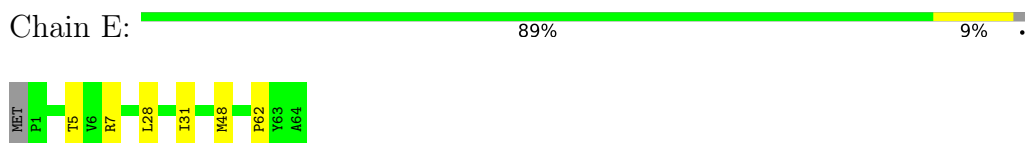
- Molecule 3: 50S ribosomal protein L33



- Molecule 4: 50S ribosomal protein L34



- Molecule 5: 50S ribosomal protein L35



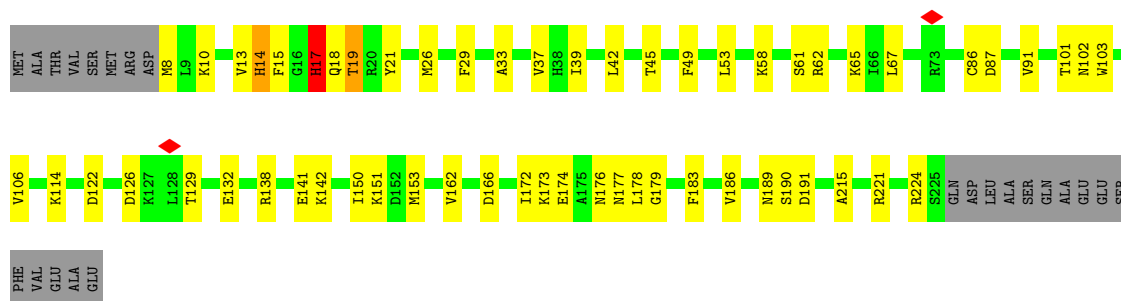
- Molecule 6: 50S ribosomal protein L36

Chain F:  66% 32% .



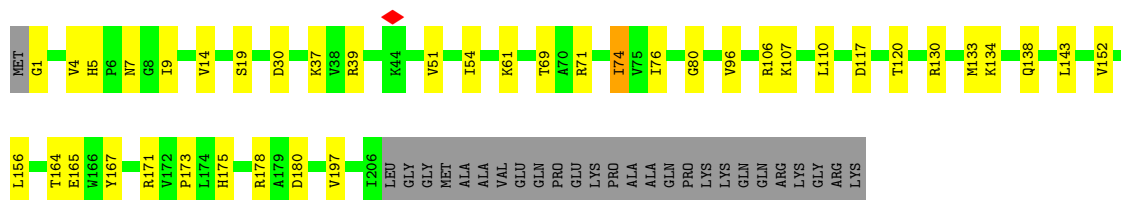
- Molecule 7: 30S ribosomal protein S2

Chain G:  66% 23% . 10%



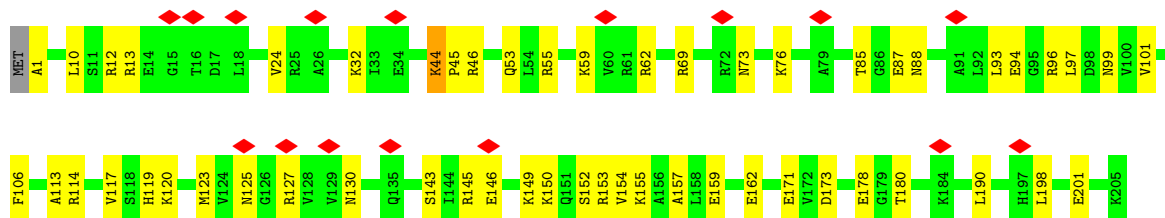
- Molecule 8: 30S ribosomal protein S3

Chain H:  71% 17% 12%



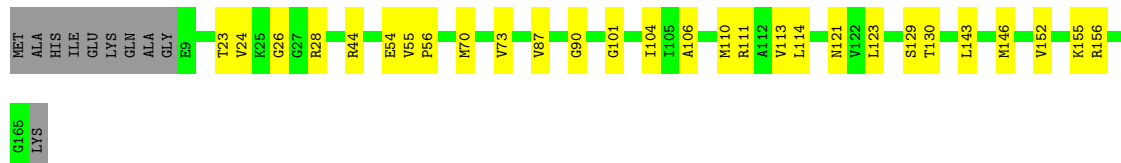
- Molecule 9: 30S ribosomal protein S4

Chain I:  8% 73% 26%

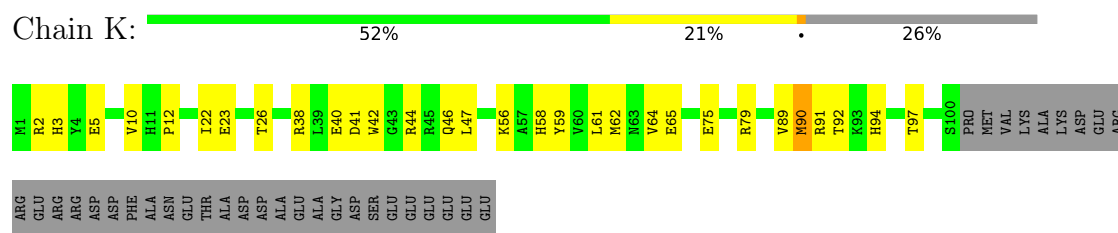


- Molecule 10: 30S ribosomal protein S5

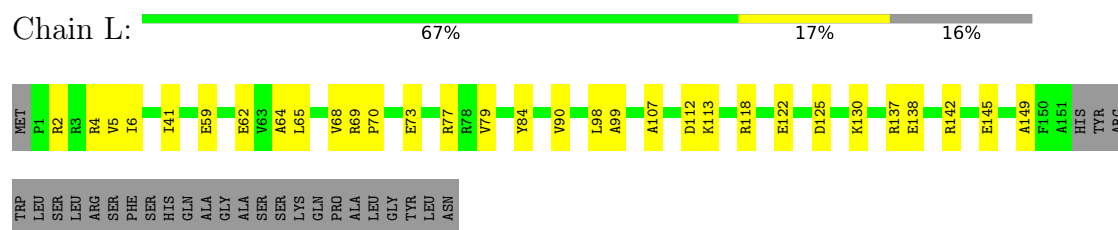
Chain J:  77% 17% 6%



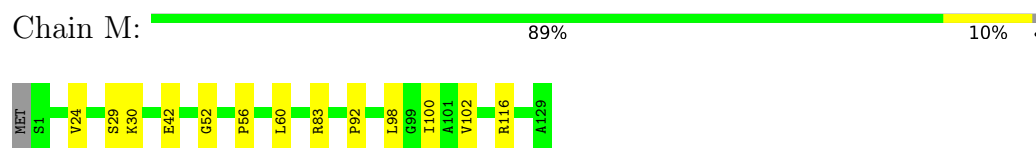
- Molecule 11: 30S ribosomal protein S6, fully modified isoform



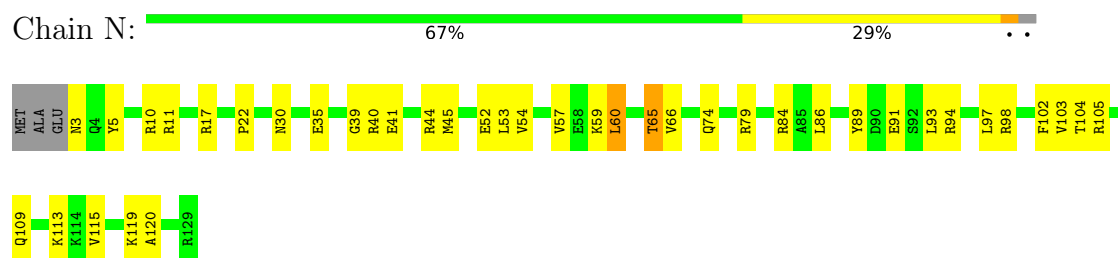
- Molecule 12: 30S ribosomal protein S7



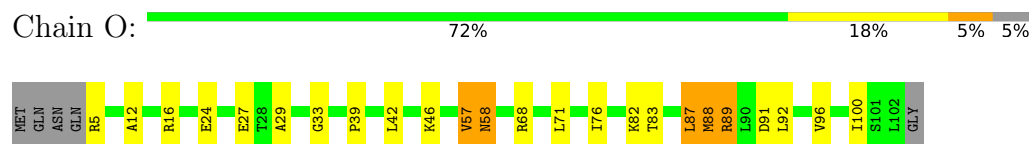
- Molecule 13: 30S ribosomal protein S8



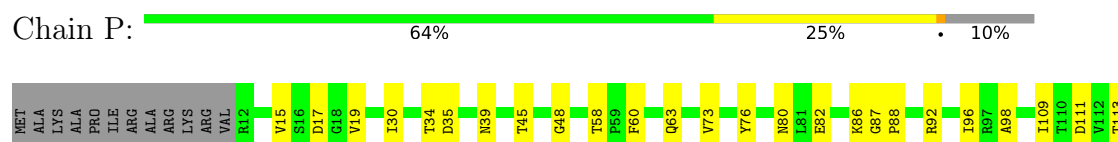
- Molecule 14: 30S ribosomal protein S9



- Molecule 15: 30S ribosomal protein S10



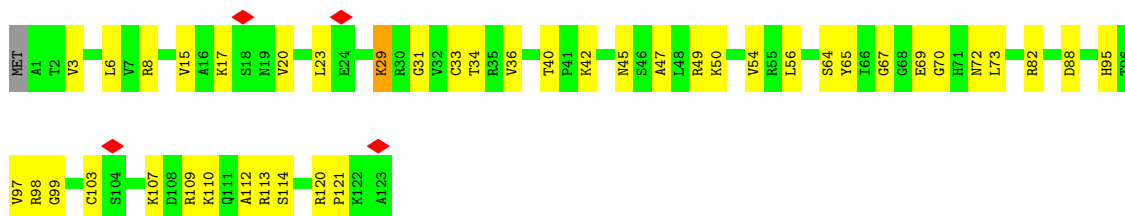
- Molecule 16: 30S ribosomal protein S11





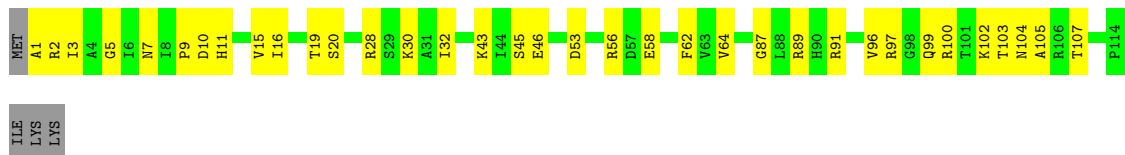
- Molecule 17: 30S ribosomal protein S12

Chain Q: 65% 33%



- Molecule 18: 30S ribosomal protein S13

Chain R: 67% 30%



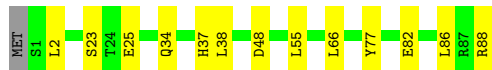
- Molecule 19: 30S ribosomal protein S14

Chain S: 84% 15%



- Molecule 20: 30S ribosomal protein S15

Chain T: 84% 15%



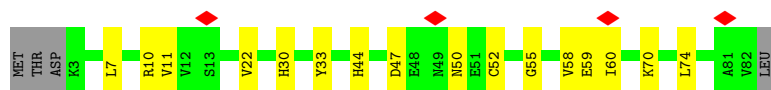
- Molecule 21: 30S ribosomal protein S16

Chain U: 7% 76% 23%



- Molecule 22: 30S ribosomal protein S17

Chain V: 5% 76% 19% 5%



- Molecule 23: 30S ribosomal protein S18

Chain W: 68% 17% 13%



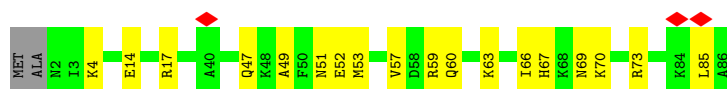
- Molecule 24: 30S ribosomal protein S19

Chain X: 74% 12% 14%



- Molecule 25: 30S ribosomal protein S20

Chain Y: 77% 21% 2%



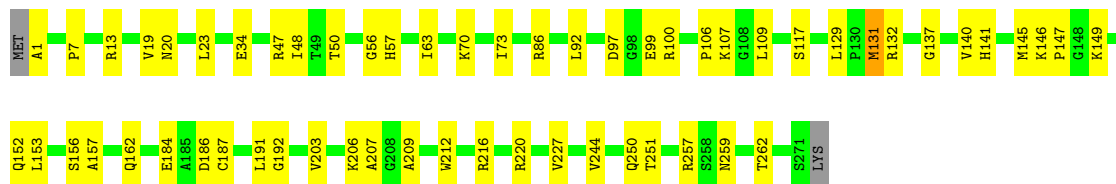
- Molecule 26: 30S ribosomal protein S21

Chain Z: 58% 31% 8%



- Molecule 27: 50S ribosomal protein L2

Chain b: 78% 21% 1%



- Molecule 28: 50S ribosomal protein L3

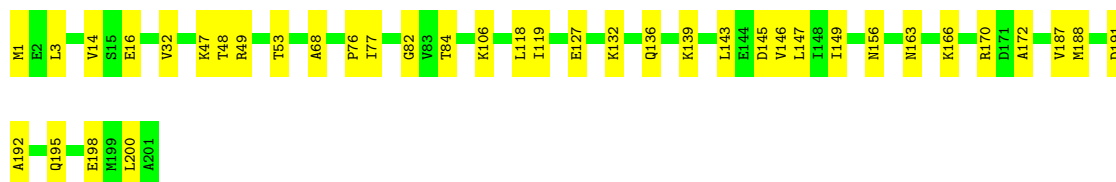
Chain c: 85% 15% 0%





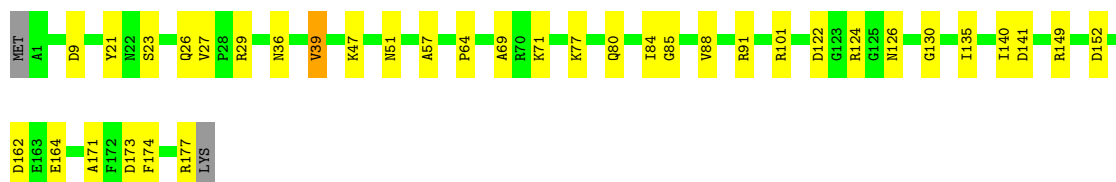
- Molecule 29: 50S ribosomal protein L4

Chain d: 81% 19%



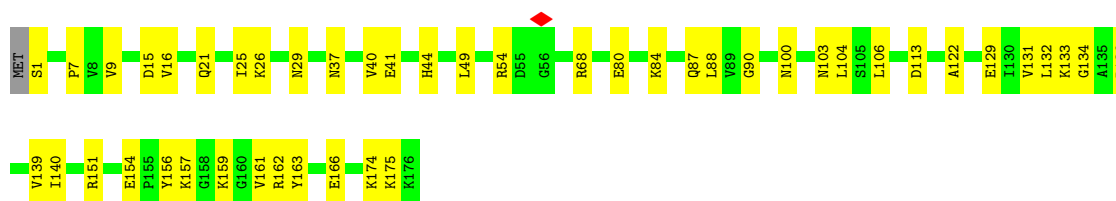
- Molecule 30: 50S ribosomal protein L5

Chain e: 79% 20% ..



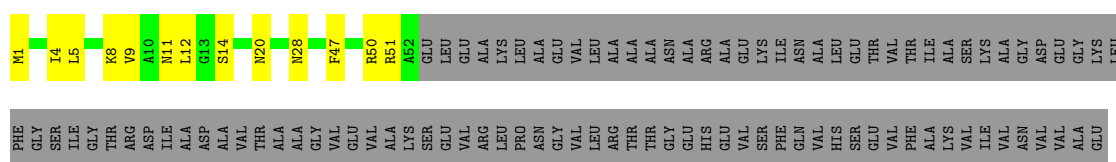
- Molecule 31: 50S ribosomal protein L6

Chain f: 73% 26% .



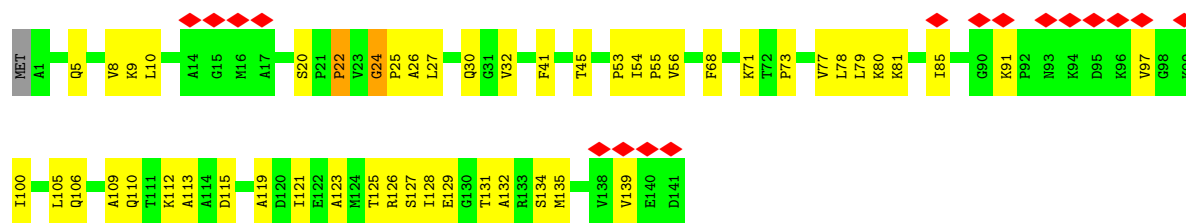
- Molecule 32: 50S ribosomal protein L9

Chain g: 26% 9% 65%

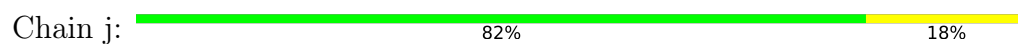


- Molecule 33: 50S ribosomal protein L11

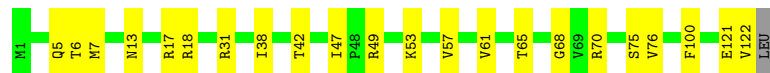
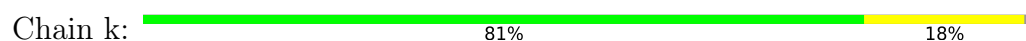
Chain i: 12% 64% 34% ..



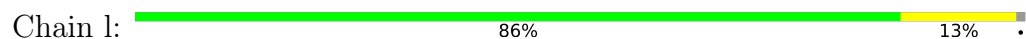
- Molecule 34: 50S ribosomal protein L13



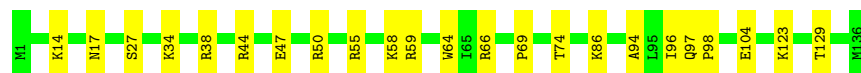
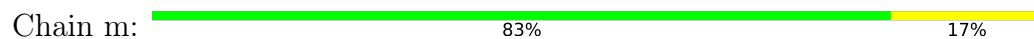
- Molecule 35: 50S ribosomal protein L14



- Molecule 36: 50S ribosomal protein L15



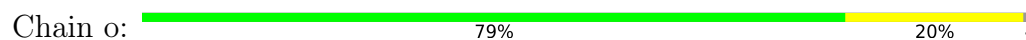
- Molecule 37: 50S ribosomal protein L16



- Molecule 38: 50S ribosomal protein L17



- Molecule 39: 50S ribosomal protein L18



- Molecule 40: 50S ribosomal protein L19

Chain p:  84% 15%



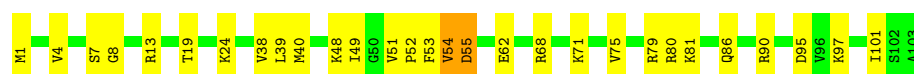
- Molecule 41: 50S ribosomal protein L20

Chain q:  84% 14%



- Molecule 42: 50S ribosomal protein L21

Chain r:  72% 26%



- Molecule 43: 50S ribosomal protein L22

Chain s:  85% 15%



- Molecule 44: 50S ribosomal protein L23

Chain t:  74% 19% 7%



- Molecule 45: 50S ribosomal protein L24

Chain u:  72% 26%



- Molecule 46: 50S ribosomal protein L25

Chain v:  85% 15%



- Molecule 47: 50S ribosomal protein L27

Chain w:  74% 14% 12%



- Molecule 48: 50S ribosomal protein L28

Chain x:  74% 23% ..



- Molecule 49: 50S ribosomal protein L29

Chain y:  76% 24%



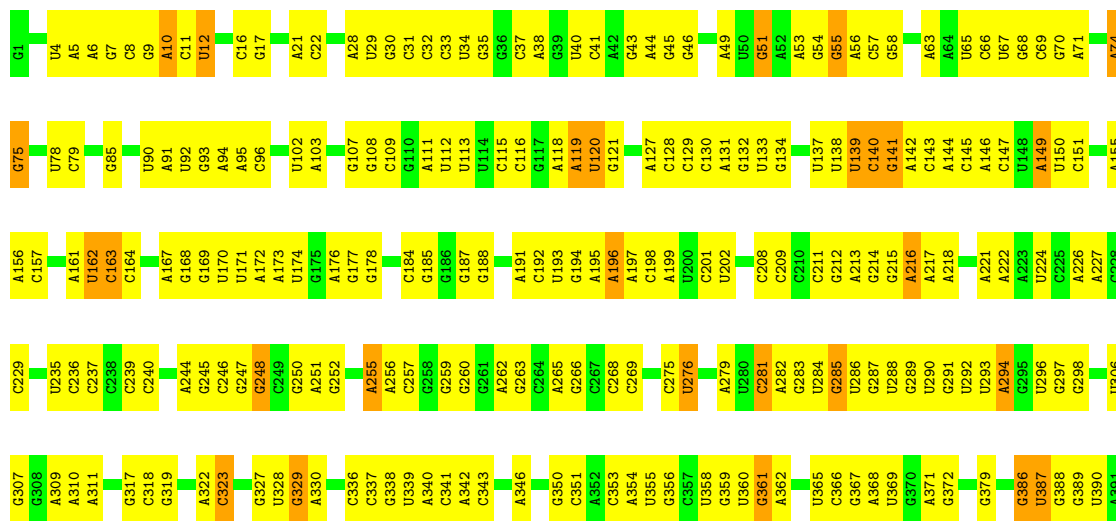
- Molecule 50: 50S ribosomal protein L30

Chain z:  76% 22% .



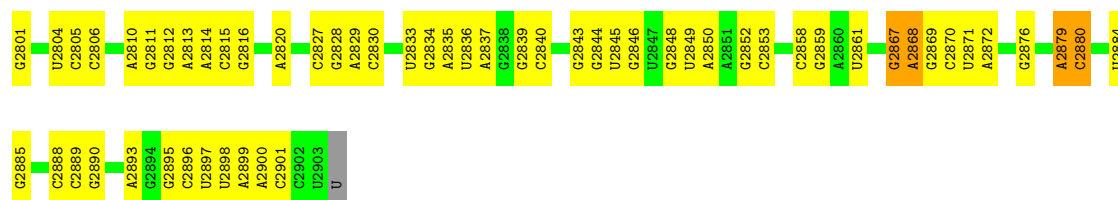
- Molecule 51: 23S rRNA

Chain 1:  42% 51% 7%



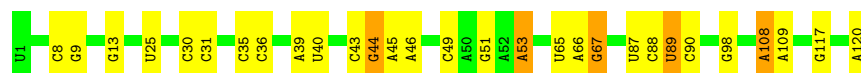
C1507	G1426	G1334	G1266	U1173	G1106	G1044	U958	A877	A800	G707	C624	U546	A472	U392
A1508	A1427	C1335	U1267	U1174	G1107	C1045	A959	A878	G801	G708	C627	A547	G473	C393
A1509	C1428	A1336	G1287	A1175	U1108	A1046	A960	G879	G805	U709	A627	G548	G474	C394
G1510	G1429	G1337	G1270	U1176	C1109	G1047	C961	G885	G809	G712	G628	G550	G475	U395
C1511	G1430	G1338	C1271	G1177	G1110	A1048	C968	C886	U810	G713	G629	C551	G476	G396
C1512	A1431	G1339	A1272	C1178	A1111	A1049	C968	U887	G815	G713	G630	U552	G481	U397
	G1432	G1343	U1273	G1179	G1112	A1050	A972	C888	U811	A718	A633	U553	A482	A402
A1515	A1433	U1180	A1274	U1180	C1113	A1054	A973	C889	G812	C719	C634	U554	A403	A403
G1516	A1434	U1181	U1275	U1182	G1115	G1055	A975	C890	U813	U720	C635	U555	C485	A404
G1517	G1435	U1182	A1276	U1183	G1116	G1056	A975	C891	C814	A721	C636	A556	U405	U405
C1518	G1436	G1346	G1278	U1184	C1117	A1057	A979	A892	C815	A722	A637	C557	G487	G406
G1519	G1437	A1347	C1279	U1185	C1118	U1058	A979	C893	A819	C723	G638	U558	G488	G409
U1520	C1438	C1348	G1280	G1186	U1119	G1059	A980	U894	A821	U724	U639	U562	G489	G410
G1521	A1439	G1349	U1187	G1187	G1120	U1060	A981	U895	A822	G725	U641	A563	C490	G411
A1522	U1440	U1352	U1282	U1188	C1121	U1061	C982	A896	A821	A727	U644	U566	A491	A492
U1523	U1441	G1283	G1283	G1193	G1123	G1062	A984	C897	A825	G728	A644	U567	G492	C414
G1524	U1442	A1284	A1284	G1194	G1124	C1064	C985	C898	U826	G729	C645	U568	G493	A415
A1525	G1448	A1285	A1285	G1195	G1130	U1066	G989	A899	U827	A730	U646	U569	G494	U416
C1526	G1449	A1286	G1286	G1196	U1131	U1067	G993	A900	U828	C736	G647	U570	G498	U419
G1527	G1450	A1287	G1287	G1197	G1132	A1068	G994	C901	U829	G745	G648	U571	U499	C421
A1528	G1451	G1288	G1288	U1198	U1133	A1069	C995	G902	G830	U746	U652	U572	G500	A422
G1529	G1452	C1289	C1289	U1199	A1134	A1070	C996	G903	U831	A747	U653	U573	A501	A503
C1530	A1453	G1292	G1292	C1200	C1135	G1071	A996	U906	A833	C747	A654	A574	A504	G424
	G1454	C1293	C1293	U1209	G1136	A1072	C1005	G907	C834	A752	G656	U580	A505	G425
G1533	C1455	U1294	U1294	A1204	U1137	C1073	A1009	G908	G836	G757	G662	A586	G506	C426
U1534	C1461	G1295	G1295	U1205	G1138	A1074	A1010	G909	C837	G758	G669	U590	C510	U431
A1535	C1462	G1296	G1296	A1206	U1139	C1075	A1011	G914	C840	G759	U670	U591	U511	A432
C1536	G1463	C1297	C1297	U1210	G1140	G1076	G1011	C915	U842	G760	A671	A592	U512	C433
G1537	G1464	G1298	G1298	G1211	U1141	U1077	G1012	G916	U843	U762	C671	U593	G518	U434
U1539	G1465	C1299	C1299	G1212	A1142	U1078	C1013	G917	A845	G763	C672	U594	U519	C435
C1540	U1466	G1300	G1300	U1219	A1143	A1080	U1014	G918	U846	A764	C673	U595	G520	C436
G1541	U1467	A1301	A1301	G1220	A1144	U1081	U1015	U919	U847	C765	G674	C596	U521	U437
U1542	U1468	C1306	C1306	U1221	C1145	U1082	U1016	G923	C848	G774	A677	U596	A522	G438
G1543	A1469	G1309	G1309	G1225	U1146	U1083	A1020	G924	A849	G775	C678	G597	A526	A439
A1544	A1470	U1310	U1310	U1226	G1148	A1084	A1021	A925	U850	U779	C679	A599	C527	C440
G1545	C1480	G1311	G1311	A1230	C1150	A1085	G1022	G926	U851	U780	C680	A603	A528	U441
C1546	U1481	C1314	C1314	U1231	A1151	A1086	U1023	A927	U852	G781	G681	G603	G529	C442
	G1482	U1403	U1403	G1232	C1152	G1087	G1024	A928	C853	U782	U683	U607	G530	C445
A1551	U1483	C1315	C1315	C1233	C1153	A1088	G1025	U929	C854	A783	G682	C531	A532	G446
C1552	U1484	U1316	U1316	U1237	G1155	A1089	G1026	U932	G855	G785	U684	A609	U534	U451
U1554	U1485	G1317	G1317	U1240	A1156	A1090	A1027	U933	G858	G786	U685	C610	G535	C452
G1555	U1486	C1318	C1318	U1241	U1157	C1091	U1027	G938	U859	A788	U686	C611	G536	A457
	U1487	U1319	U1319	G1238	A1158	C1092	G1031	G939	U860	A789	G687	A612	G537	C461
C1558	C1488	C1320	C1320	G1239	U1159	G1093	U1033	G940	G864	U790	G688	A613	G538	C462
U1559	U1489	A1321	A1321	U1242	G1160	U1094	U1034	A941	C865	C791	G689	A614	G539	C463
G1560	A1490	U1322	U1322	A1246	C1161	A1095	G1035	G942	U870	U792	G690	A615	C540	C464
C1561	G1491	G1323	G1323	U1247	U1162	A1096	U1036	G943	U871	A793	G691	A616	C541	G465
G1562	G1492	U1324	U1324	A1248	G1163	U1097	G1037	G944	U872	A794	G692	A617	C542	A466
	U1497	A1325	A1325	A1253	C1164	A1098	G1038	G945	U873	C796	U703	A618	G543	G467
A1566	G1500	U1326	U1326	U1254	A1165	G1099	G1039	A947	U874	A795	G704	G620	G544	C468
G1567	G1501	A1327	A1327	U1255	G1166	U1100	A1040	U955	U875	C796	A706	A621	G545	
C1568	C1502	U1328	U1328	U1256	U1167	C1101	G1041	G956	U876			G622	U546	
A1569	A1503	U1329	U1329	G1257	C1170	C1102	U1042	C957				A622		
A1570	A1504	C1330	C1330	U1258	G1171	A1103	G1043					A623		
C1571	U1505	G1333	G1333	G1259	C1172	C1104	C1043							
A1572	U1506					U1105								

	A2726		G2641		A2565		A2468		C2385		G2224		G2157		C2091		C1909		U1751		U1671		G1573
			G2642		A2566		A2469		A2386		A2225		A2158		G2092		G1910		C1752		A1672		C1574
	G2729		G2643		U2567		G2470		U2387		C2226		G2159		G2093		U1911		G1753		G1673		C1575
	G2730		G2644		U2568		A2471		G2388		A2227		C2160		A2094		A1912		A1754		G1674		
	G2731		G2645		G2569				G2389				C2161		A2096		A1913		A1755		A1675		U1578
	G2732		G2646		U2571		A2476		G2391		G2230		C2162		A2097		G1914		U1756		A1676		U1579
	A2733				A2572		A2482		A2392		U2233		A2163		A2098		U1915		U1758		A1677		A1580
	A2734		G2648		C2573		C2483		U2393		G2234		C2164		U2099		U1916		C1761		A1678		C1581
	G2735		G2649		G2574				C2394		G2235		C2165		G2100		U1917		A1679		C1582		A1583
	A2736		U2650		C2395		G2488		G2396		U2236		U2166		G2101		A1918		G1762		U1680		
	G2737		C2651		G2396		U2489		G2396		G2237		U2167		G2102		G1919		A1763		G1681		
			C2652				G2490				G2238		C2170		C2103		G1920		C1764				
					G2577						G2239		A2171		G2104		G1921		U1765				U1588
	A2741				G2578		U2491		U2402		G2240		U2172		U2105		G1922		G1766		G1695		U1589
	G2742		C2658		C2579		U2492		C2403		U2241		U2173		U2106		U1923		C1767		G1696		A1590
	U2743		G2659		U2580				A2404		A2242		C2174		U2107		C1924		C1768		G1697		A1591
	G2744				G2581		C2496		G2405		G2243								U1769		G1698		C1592
			G2661		G2582		A2497		A2406		U2244								A1772		G1702		U1594
	G2747		A2662		A2497		C2498		A2407		G2245								A1773		G1703		C1595
	A2748		G2663		U2584		C2499				A2247								C1774				U1594
					U2585						C2248								C1775				C1596
	G2749		A2670		U2586		G2502		A2411		G2249		U2182		G2112		G1930		C1776		G1710		A1597
	G2751		U2672		A2587				A2412		G2250		A2183		U2113		U1931				A1711		U1598
							G2505		C2420				U2185		G2115		G1935		A1780				C1600
	U2754				U2583		U2506		A2421		U2257		U2186				A1936		U1781		G1715		G1601
	C2755				C2584		C2507		G2422		C2258		U2187		U2118		A1937		U1782		U1716		U1602
	U2756				G2585				A2423		C2259		U2188		A2119		U1938		A1783		A1717		A1603
	A2757		A2679		U2580		C2510		G2424		C2260		U2189		G2122		U1939		A1784		G1718		C1604
	G2758		U2680		G2589		U2511		A2425		C2261		U2190		U2123		G1940		A1785		G1719		C1605
			C2681		G2599				A2426		A2267		A2191		G2123		U1941		A1786		U1720		C1606
	C2760		A2682		G2600		A2516		A2427		A2268		U2192		G2124		U1942		A1787		G1721		C1607
	A2761		G2683		G2601		G2428		G2428				C2193		G2125		U1943		C1788		A1722		A1608
	C2762		U2684		A2602		A2518		G2429		G2271		U2194		G2126		G1948		C1789		G1723		
	G2763								A2430		C2275		U2195		G2127		A1952		C1790				A1614
	A2764		U2687		U2609		G2525		G2431				U2196		G2128		A1953		A1794		G1724		A1615
	A2765		G2688		C2610		G2526		A2432		C2276		C2196		U2129		G1954		C1795		C1726		A1616
			U2689		C2611		C2527		G2433		G2277		A2199		U2130		G1955		C1796		C1727		
	U2768		U2690		C2612		U2528		A2434		G2278		C2200		U2131		U1956		U1797		C1728		C1625
					U2613		G2529		A2435		G2279		G2201		G2132		U1957		G1798		U1729		A1626
			G2697		A2614		A2530		G2436		A2281		U2202		G2133		U1958		C1799				
					U2615				G2437		C2282		U2203		A2134		U1963		C1800		G1731		A1634
	A2776		A2700		C2616		U2533		C2440		C2283		G2204		G2137		G1964		C1801		G1732		G1642
	G2777		U2701		U2617		A2534		U2441		C2284		A2205		U2138		G1965		A1802		G1733		G1643
	A2778		G2702		C2618						C2285				G2139		C1967		A1803		G1734		C1644
	U2779				C2619		C2539				G2286		C2208		G2141		G1968		A1804		A1735		
							G2545		G2446		A2287		G2209		G2142		G1969		G1807		U1736		G1645
	G2782		G2708		G2625		U2546		G2447		A2288		G2210		G2143		A1969		A1808		G1737		C1646
	U2783		G2709		C2626		U2547		G2448		G2289		U2211		U2144		A1970		A1809		G1738		U1647
	U2784		C2710		G2627		A2547		A2448		G2290		A2212		C2145		U1971		A1809		A1739		U1648
			A2711		C2628						U2291		G2213		G2146		G1972		U1812		G1740		
			G2712		U2629		G2455				U2292		U2214		A2147				G1813		C1741		G1651
	C2787		U2713		G2630		C2456		G2456		G2293		C2215		G2148		G1975		C1816		U1742		
	C2788		G2714		U2631		U2457		G2457		G2294		G2216		U2149		U1976		G1817		U1743		U1662
	C2789				A2632		G2458		G2458		C2295		G2217		C2150		A1977		C1817		A1744		G1663
			C2717		G2633		G2557				U2296		G2218		U2151		A1978		A1819		A1745		G1664
	A2792		G2718		A2634				C2462		U2297				C2152				A1819		A1746		
	C2793		G2719		A2635		U2561		C2463		A2298				C2153		G1983		U1820		U1747		G1667
			U2720		G2636		U2562		G2464		U2299		G2221		A2154		G1984		U1821		G1748		A1668
	U2798				U2637		U2563				U2300		G2222		U2155		C1985		A1822		A1749		A1669
	A2800		C2723		G2638		A2564		C2467		U2302		G2223		G2156		C1986		G1823		G1750		C1670



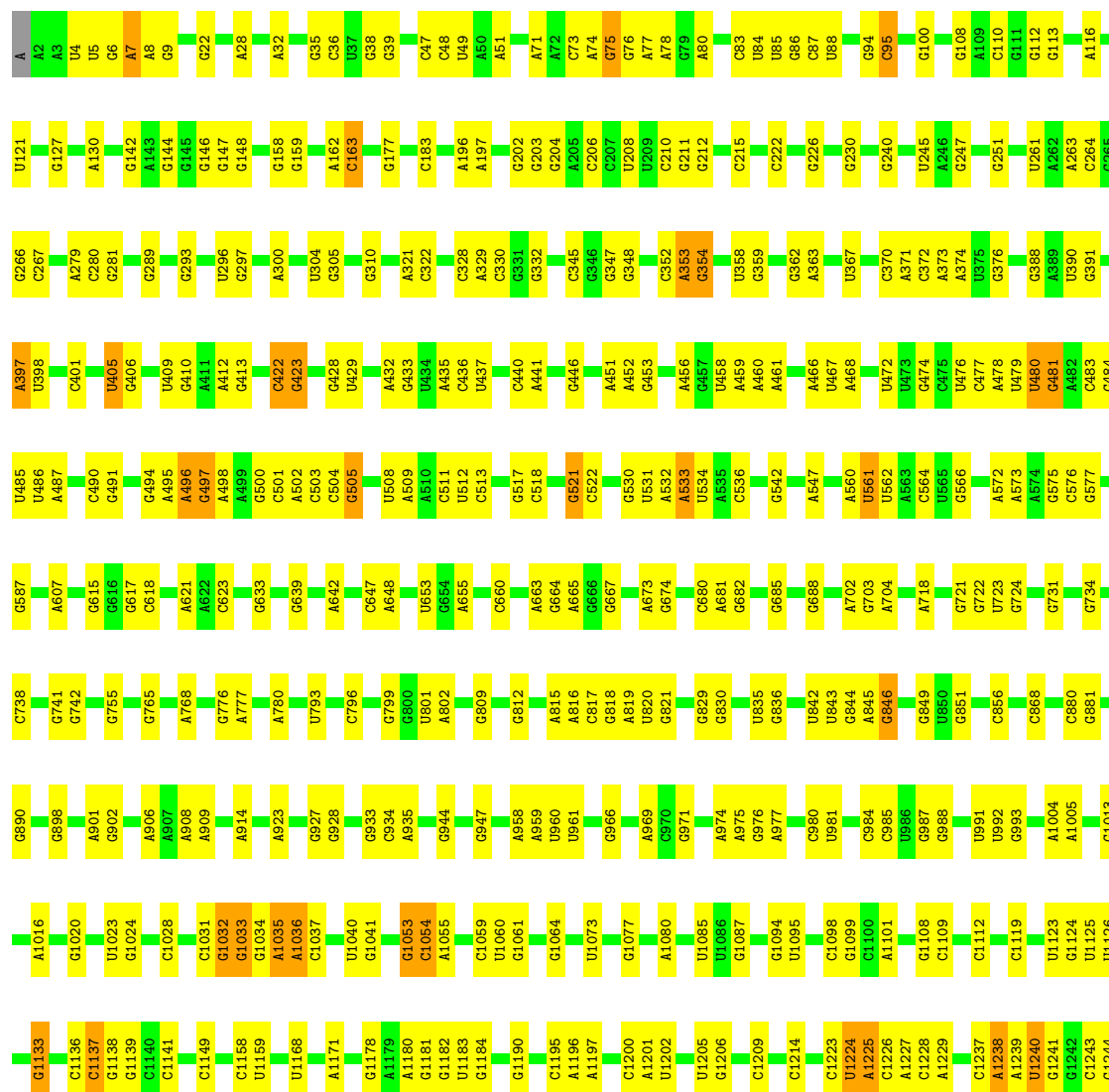
• Molecule 52: 5S rRNA

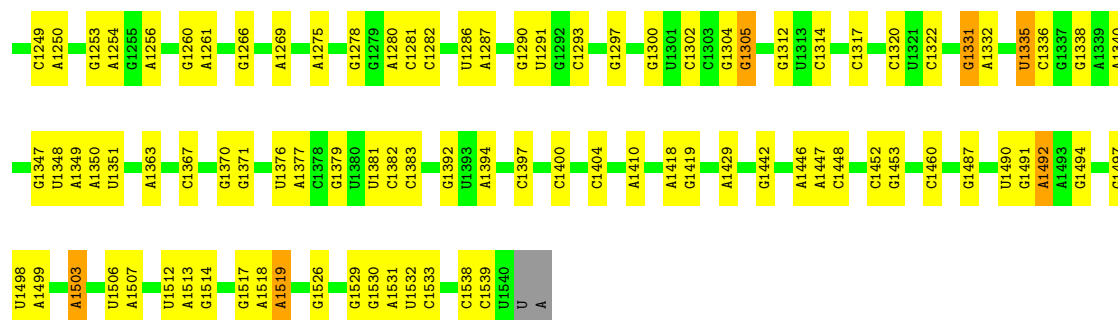
Chain 2: 76% 20%



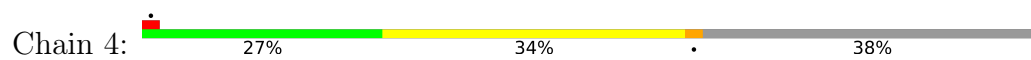
• Molecule 53: 16S rRNA

Chain 3: 68% 29%

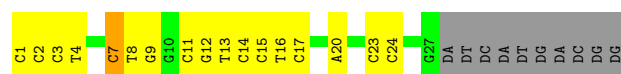




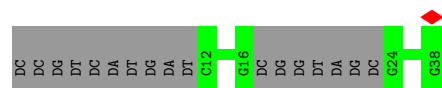
• Molecule 54: mRNA



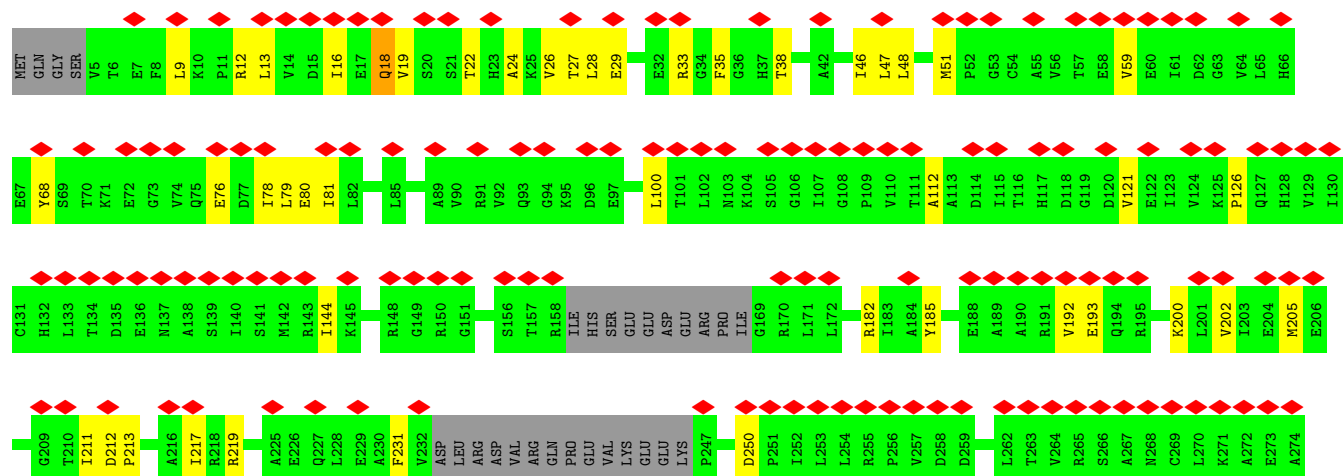
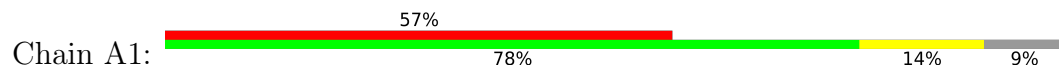
• Molecule 55: template DNA strand

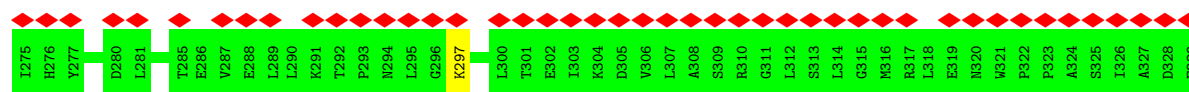


• Molecule 56: non-template DNA strand

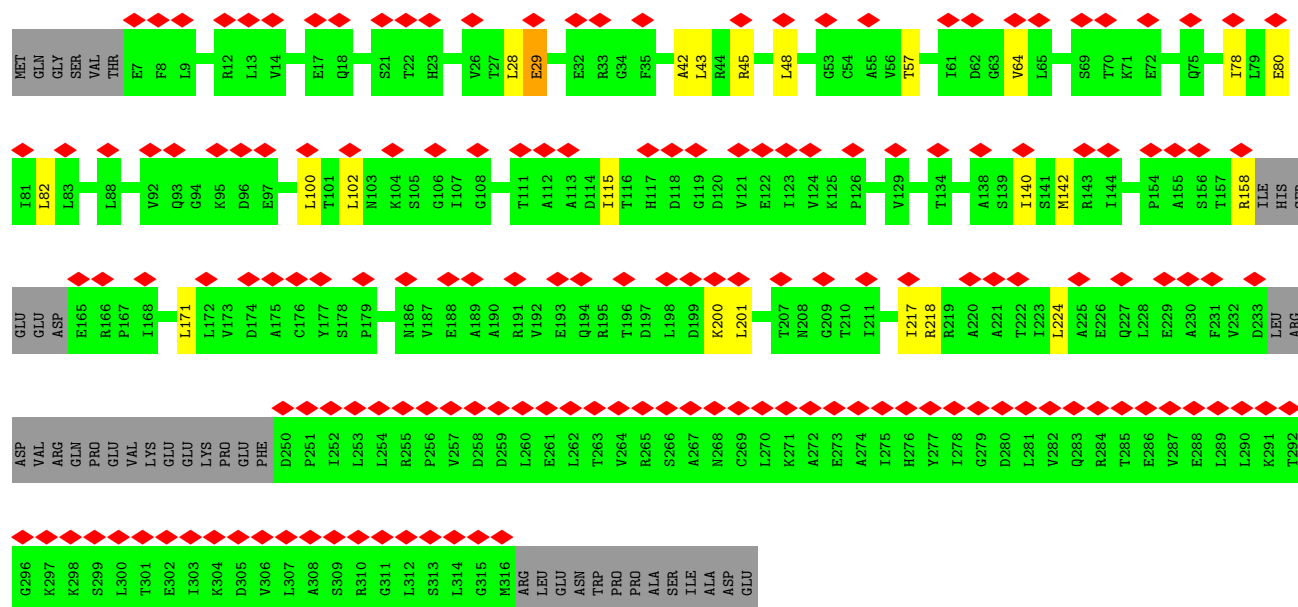
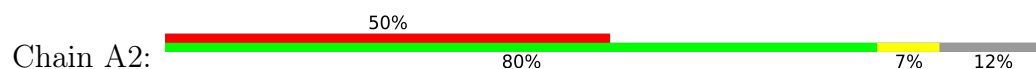


• Molecule 57: DNA-directed RNA polymerase subunit alpha

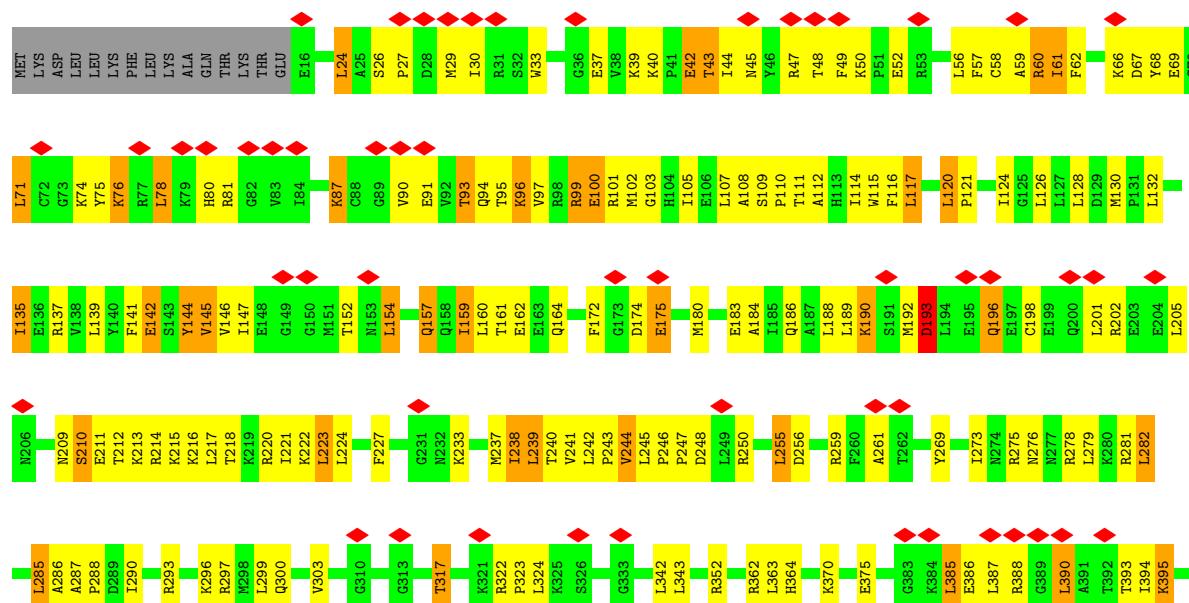


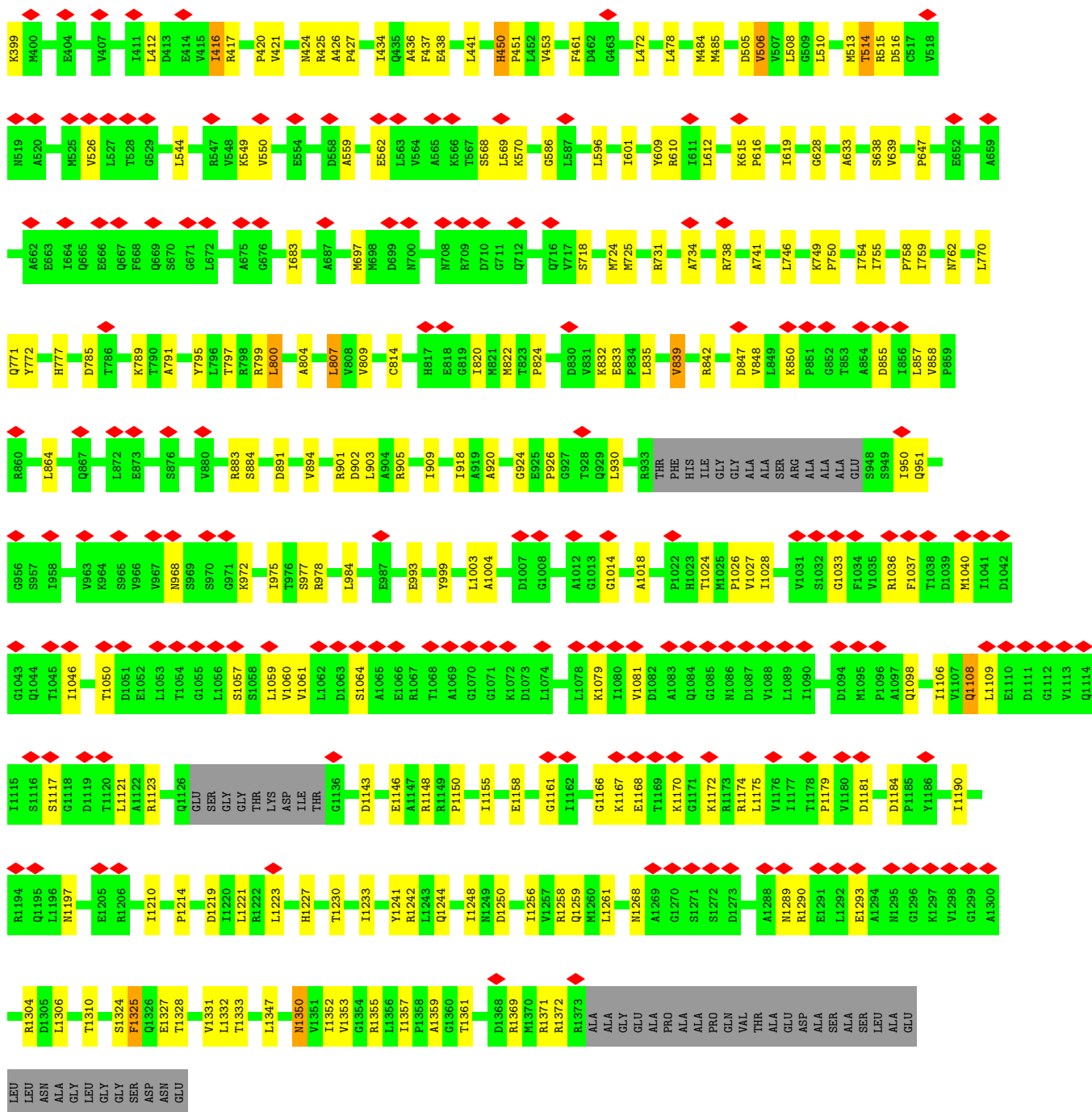


• Molecule 57: DNA-directed RNA polymerase subunit alpha

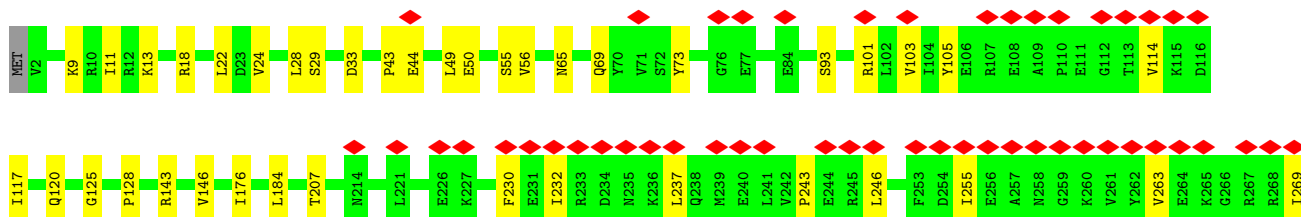
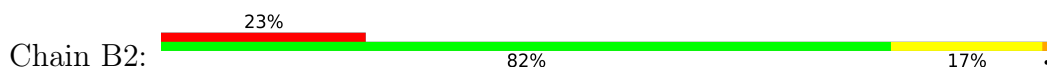


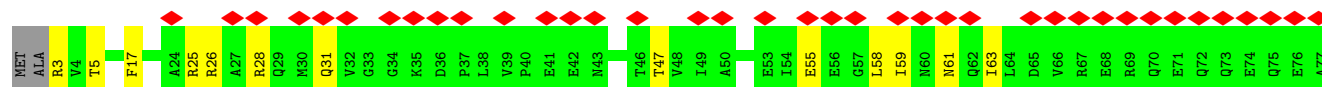
• Molecule 58: DNA-directed RNA polymerase subunit beta'

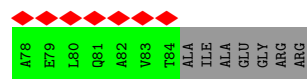




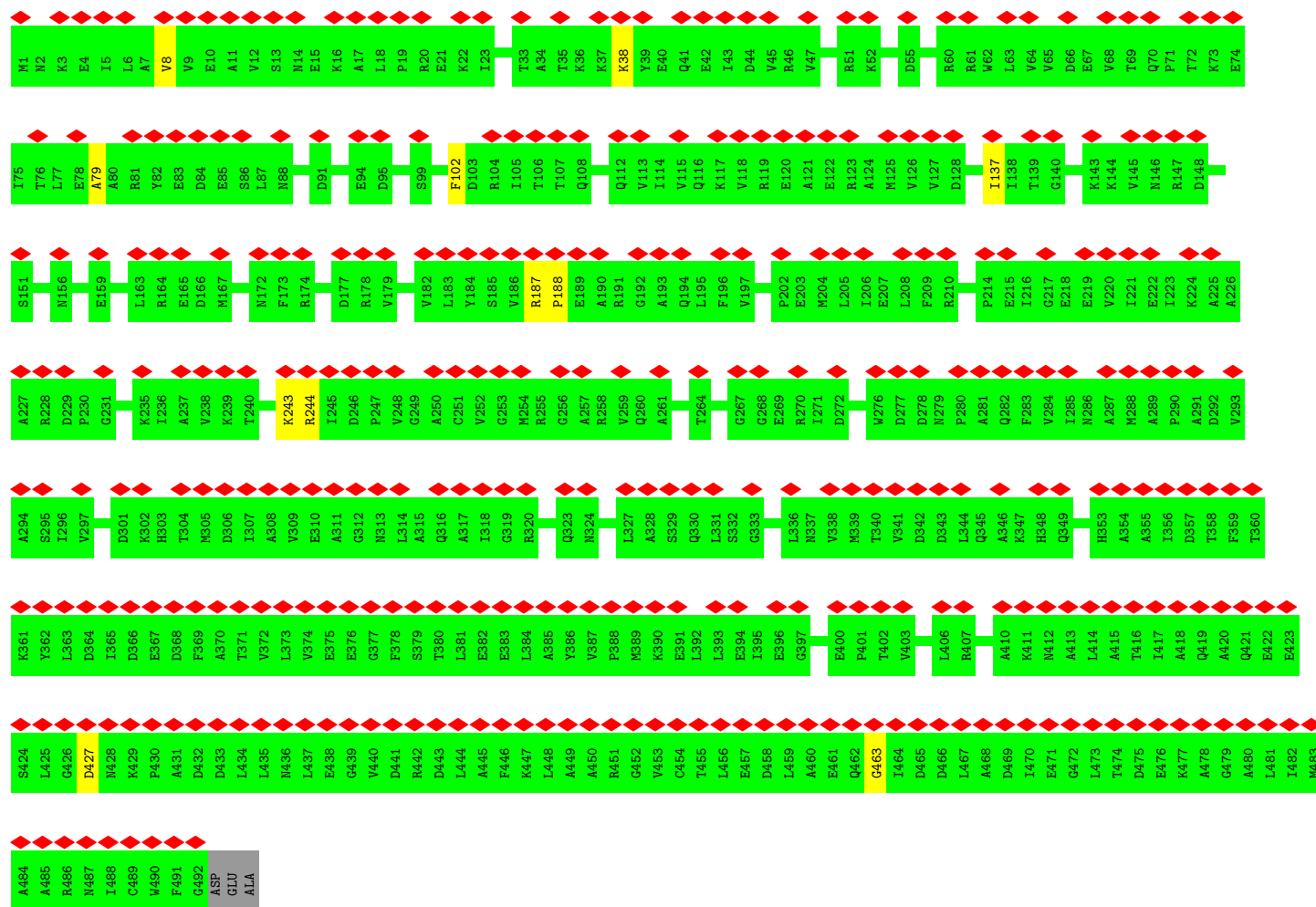
• Molecule 59: DNA-directed RNA polymerase subunit beta



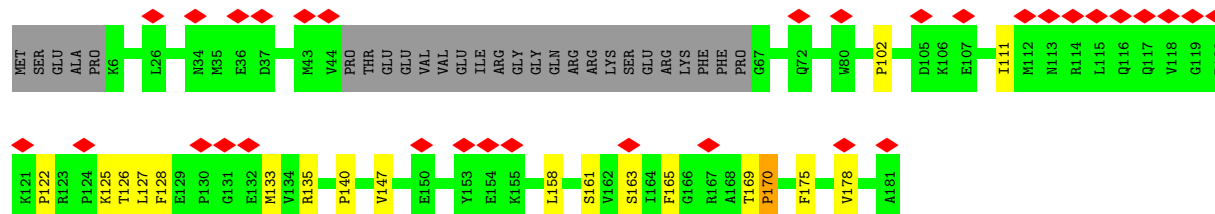
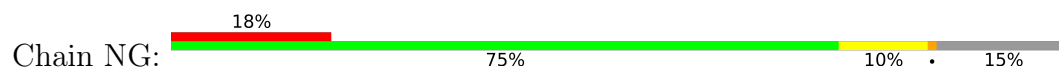




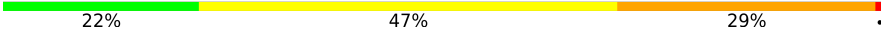
• Molecule 61: Transcription termination/antitermination protein NusA

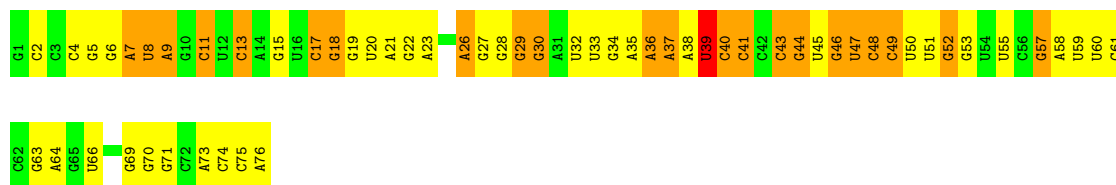


• Molecule 62: Transcription termination/antitermination protein NusG



• Molecule 63: tRNA(Phe)

Chain 5:  22% 47% 29% .



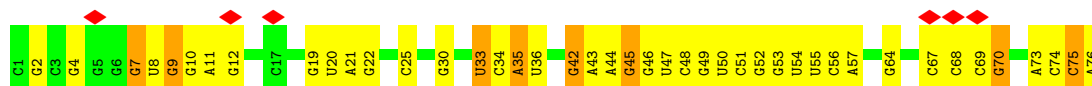
• Molecule 64: tRNA(fMet)

Chain 6:  77% 19% .



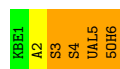
• Molecule 64: tRNA(fMet)

Chain 7:  8% 44% 45% 10%



• Molecule 65: Viomycin

Chain h:  17% 17% 67%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24010	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.175	Depositor
Minimum map value	-0.080	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.011	Depositor
Map size ($\text{\AA}$)	753.60004, 753.60004, 753.60004	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.57, 1.57, 1.57	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5OH, MG, UAL, KBE, DPP

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	A	0.27	0/531	0.54	0/709
2	B	0.40	0/450	0.60	0/599
3	C	0.28	0/416	0.52	0/554
4	D	0.47	0/380	0.76	2/498 (0.4%)
5	E	0.53	0/513	0.60	0/676
6	F	0.57	0/303	0.65	0/397
7	G	0.37	0/1735	0.64	0/2338
8	H	0.34	0/1651	0.55	0/2225
9	I	0.35	0/1665	0.71	0/2227
10	J	0.38	0/1169	0.68	2/1573 (0.1%)
11	K	0.46	0/835	0.77	0/1128
12	L	0.30	0/1195	0.67	3/1602 (0.2%)
13	M	0.35	0/989	0.52	0/1326
14	N	0.41	0/1034	0.77	0/1375
15	O	0.50	0/796	0.78	2/1077 (0.2%)
16	P	0.45	0/885	0.64	1/1195 (0.1%)
17	Q	0.50	0/969	0.86	2/1300 (0.2%)
18	R	0.33	0/892	0.73	2/1193 (0.2%)
19	S	0.32	0/817	0.61	0/1088
20	T	0.49	0/722	0.64	0/964
21	U	0.30	0/659	0.71	2/884 (0.2%)
22	V	0.44	0/657	0.71	0/881
23	W	0.54	0/544	0.74	1/731 (0.1%)
24	X	0.28	0/652	0.55	0/877
25	Y	0.28	0/671	0.52	0/888
26	Z	0.66	0/550	1.01	2/728 (0.3%)
27	b	0.49	0/2121	0.65	0/2852
28	c	0.42	0/1586	0.59	2/2134 (0.1%)
29	d	0.43	0/1571	0.62	0/2113
30	e	0.38	0/1434	0.60	2/1926 (0.1%)
31	f	0.29	0/1343	0.55	0/1816
32	g	0.32	0/405	0.74	0/544

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	0.31	0/1046	0.77	3/1410 (0.2%)
34	j	0.41	0/1152	0.55	1/1551 (0.1%)
35	k	0.45	0/947	0.66	0/1268
36	l	0.40	0/1054	0.63	0/1403
37	m	0.56	0/1093	0.74	0/1460
38	n	0.46	0/973	0.72	1/1301 (0.1%)
39	o	0.32	0/902	0.51	0/1209
40	p	0.42	0/929	0.61	0/1242
41	q	0.52	0/960	0.62	1/1278 (0.1%)
42	r	0.43	0/829	0.69	0/1107
43	s	0.44	0/864	0.58	0/1156
44	t	0.33	0/744	0.52	0/994
45	u	0.45	0/787	0.75	0/1051
46	v	0.34	0/766	0.51	0/1025
47	w	0.40	0/582	0.52	0/769
48	x	0.43	0/635	0.63	1/848 (0.1%)
49	y	0.29	0/510	0.64	0/677
50	z	0.41	0/453	0.53	0/605
51	1	0.51	0/69796	0.62	22/108888 (0.0%)
52	2	0.43	0/2872	0.46	0/4479
53	3	0.42	0/36963	0.43	0/57662
54	4	0.52	0/808	0.65	0/1251
55	8	0.56	0/599	0.70	1/919 (0.1%)
56	9	0.49	0/468	0.56	0/719
57	A1	0.55	0/2106	0.81	0/2868
57	A2	0.49	0/2048	0.75	0/2786
58	B1	0.57	4/10510 (0.0%)	0.75	8/14196 (0.1%)
59	B2	0.46	0/10714	0.67	1/14459 (0.0%)
60	W0	0.30	0/652	0.61	0/879
61	NA	0.76	0/2431	1.22	1/3385 (0.0%)
62	NG	1.10	0/756	1.06	0/1048
63	5	0.57	0/1812	0.86	3/2823 (0.1%)
64	6	0.40	0/1832	0.48	0/2855
64	7	0.39	0/1832	0.57	1/2855 (0.0%)
65	h	3.16	2/11 (18.2%)	0.75	0/13
All	All	0.48	6/191576 (0.0%)	0.62	67/282857 (0.0%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	h	3	SER	CA-C	-6.71	1.38	1.52
65	h	4	SER	CA-C	-6.16	1.40	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	B1	1350	ASN	CG-ND2	-5.36	1.22	1.33
58	B1	424	ASN	CG-ND2	-5.17	1.22	1.33
58	B1	1108	GLN	CD-OE1	5.11	1.33	1.23

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	P	73	VAL	N-CA-C	-9.03	104.53	113.20
41	q	33	VAL	N-CA-C	-8.80	104.72	112.12
12	L	64	ALA	N-CA-C	-7.70	105.05	114.75
51	1	1130	U	C2'-C3'-O3'	7.58	120.88	109.50
64	7	33	U	C2'-C3'-O3'	7.28	120.42	109.50

There are no chirality outliers.

There are no planarity outliers.

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	A	522	0	524	7	0
2	B	444	0	461	9	0
3	C	409	0	440	4	0
4	D	377	0	418	9	0
5	E	504	0	574	3	0
6	F	302	0	343	7	0
7	G	1704	0	1732	36	0
8	H	1624	0	1699	26	0
9	I	1643	0	1710	34	0
10	J	1156	0	1199	18	0
11	K	817	0	808	16	0
12	L	1181	0	1240	19	0
13	M	979	0	1034	8	0
14	N	1022	0	1070	23	0
15	O	786	0	828	15	0
16	P	869	0	878	21	0
17	Q	955	0	1019	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	R	883	0	944	20	0
19	S	805	0	847	10	0
20	T	714	0	737	6	0
21	U	649	0	666	15	0
22	V	648	0	691	8	0
23	W	535	0	552	8	0
24	X	637	0	665	7	0
25	Y	665	0	714	11	0
26	Z	544	0	579	12	0
27	b	2082	0	2157	46	0
28	c	1565	0	1616	28	0
29	d	1552	0	1619	27	0
30	e	1410	0	1447	23	0
31	f	1323	0	1374	31	0
32	g	400	0	423	7	0
33	i	1032	0	1088	41	0
34	j	1129	0	1162	22	0
35	k	938	0	1012	17	0
36	l	1045	0	1117	17	0
37	m	1074	0	1157	13	0
38	n	960	0	1000	19	0
39	o	892	0	923	16	0
40	p	917	0	965	17	0
41	q	947	0	1022	9	0
42	r	816	0	839	19	0
43	s	857	0	922	11	0
44	t	738	0	807	10	0
45	u	779	0	834	13	0
46	v	753	0	780	9	0
47	w	575	0	592	8	0
48	x	625	0	655	12	0
49	y	509	0	543	12	0
50	z	449	0	491	9	0
51	1	62317	0	31346	1462	0
52	2	2568	0	1303	15	0
53	3	33012	0	16618	188	0
54	4	729	0	364	5	0
55	8	539	0	305	29	0
56	9	417	0	224	0	0
57	A1	2088	0	1895	22	0
57	A2	2029	0	1864	17	0
58	B1	10353	0	10548	317	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	B2	10546	0	10550	167	0
60	W0	650	0	658	11	0
61	NA	2432	0	1171	10	0
62	NG	758	0	334	14	0
63	5	1622	0	821	26	0
64	6	1640	0	837	7	0
64	7	1640	0	837	21	0
65	h	48	0	40	9	0
66	B1	1	0	0	0	0
All	All	178130	0	126632	2811	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 9.

The worst 5 of 2811 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)
40:p:52:ARG:HH21	51:1:2720:U:H5''	0.95	1.09
51:1:275:C:H2'	51:1:276:U:H4'	1.37	1.07
51:1:1666:G:H2'	51:1:1667:G:H5'	1.41	1.03
51:1:2713:U:H3'	51:1:2714:G:H5'	1.41	1.03
51:1:1672:A:C2	51:1:2582:G:H5'	1.95	1.02

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	A	64/70 (91%)	59 (92%)	5 (8%)	0	100	100
2	B	54/57 (95%)	48 (89%)	4 (7%)	2 (4%)	2	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	48/55 (87%)	41 (85%)	7 (15%)	0	100	100
4	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
5	E	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
6	F	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	4	24
7	G	216/241 (90%)	187 (87%)	27 (12%)	2 (1%)	14	50
8	H	204/233 (88%)	194 (95%)	10 (5%)	0	100	100
9	I	203/206 (98%)	173 (85%)	29 (14%)	1 (0%)	24	63
10	J	155/167 (93%)	138 (89%)	17 (11%)	0	100	100
11	K	98/135 (73%)	85 (87%)	13 (13%)	0	100	100
12	L	149/179 (83%)	129 (87%)	20 (13%)	0	100	100
13	M	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
14	N	125/130 (96%)	104 (83%)	21 (17%)	0	100	100
15	O	96/103 (93%)	87 (91%)	8 (8%)	1 (1%)	12	47
16	P	114/129 (88%)	100 (88%)	13 (11%)	1 (1%)	14	50
17	Q	121/124 (98%)	94 (78%)	27 (22%)	0	100	100
18	R	112/118 (95%)	99 (88%)	12 (11%)	1 (1%)	14	50
19	S	98/101 (97%)	83 (85%)	15 (15%)	0	100	100
20	T	86/89 (97%)	75 (87%)	11 (13%)	0	100	100
21	U	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
22	V	78/84 (93%)	69 (88%)	8 (10%)	1 (1%)	9	40
23	W	63/75 (84%)	56 (89%)	5 (8%)	2 (3%)	3	20
24	X	77/92 (84%)	71 (92%)	6 (8%)	0	100	100
25	Y	83/87 (95%)	78 (94%)	5 (6%)	0	100	100
26	Z	63/71 (89%)	44 (70%)	18 (29%)	1 (2%)	7	36
27	b	269/273 (98%)	244 (91%)	25 (9%)	0	100	100
28	c	207/209 (99%)	189 (91%)	18 (9%)	0	100	100
29	d	199/201 (99%)	186 (94%)	13 (6%)	0	100	100
30	e	175/179 (98%)	157 (90%)	18 (10%)	0	100	100
31	f	174/177 (98%)	159 (91%)	15 (9%)	0	100	100
32	g	50/149 (34%)	44 (88%)	5 (10%)	1 (2%)	6	30
33	i	139/142 (98%)	116 (84%)	23 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	j	140/142 (99%)	128 (91%)	12 (9%)	0	100	100
35	k	120/123 (98%)	106 (88%)	14 (12%)	0	100	100
36	l	141/144 (98%)	129 (92%)	12 (8%)	0	100	100
37	m	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
38	n	118/127 (93%)	103 (87%)	15 (13%)	0	100	100
39	o	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
40	p	112/115 (97%)	103 (92%)	9 (8%)	0	100	100
41	q	115/118 (98%)	110 (96%)	3 (3%)	2 (2%)	7	34
42	r	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	12	47
43	s	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
44	t	91/100 (91%)	82 (90%)	9 (10%)	0	100	100
45	u	100/104 (96%)	84 (84%)	15 (15%)	1 (1%)	12	47
46	v	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
47	w	73/85 (86%)	67 (92%)	6 (8%)	0	100	100
48	x	75/78 (96%)	72 (96%)	2 (3%)	1 (1%)	9	40
49	y	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
50	z	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
57	A1	295/329 (90%)	273 (92%)	21 (7%)	1 (0%)	36	72
57	A2	282/329 (86%)	271 (96%)	11 (4%)	0	100	100
58	B1	1329/1407 (94%)	1202 (90%)	123 (9%)	4 (0%)	36	72
59	B2	1338/1342 (100%)	1201 (90%)	131 (10%)	6 (0%)	30	67
60	W0	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
61	NA	490/495 (99%)	472 (96%)	15 (3%)	3 (1%)	21	58
62	NG	150/181 (83%)	132 (88%)	12 (8%)	6 (4%)	2	17
65	h	2/6 (33%)	1 (50%)	1 (50%)	0	100	100
All	All	9586/10235 (94%)	8662 (90%)	885 (9%)	39 (0%)	31	67

5 of 39 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
42	r	54	VAL
48	x	25	LYS
58	B1	121	PRO

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Mol	Chain	Res	Type
59	B2	897	PRO
61	NA	187	ARG

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	A	59/62 (95%)	58 (98%)	1 (2%)	53	68
2	B	47/48 (98%)	47 (100%)	0	100	100
3	C	45/49 (92%)	44 (98%)	1 (2%)	45	64
4	D	38/38 (100%)	37 (97%)	1 (3%)	40	61
5	E	51/52 (98%)	49 (96%)	2 (4%)	28	50
6	F	34/34 (100%)	30 (88%)	4 (12%)	5	19
7	G	180/199 (90%)	174 (97%)	6 (3%)	33	55
8	H	170/190 (90%)	167 (98%)	3 (2%)	51	67
9	I	172/173 (99%)	168 (98%)	4 (2%)	44	63
10	J	119/126 (94%)	117 (98%)	2 (2%)	53	68
11	K	87/116 (75%)	82 (94%)	5 (6%)	18	40
12	L	124/147 (84%)	124 (100%)	0	100	100
13	M	104/105 (99%)	103 (99%)	1 (1%)	68	76
14	N	105/107 (98%)	98 (93%)	7 (7%)	15	37
15	O	86/90 (96%)	78 (91%)	8 (9%)	8	26
16	P	89/99 (90%)	86 (97%)	3 (3%)	32	54
17	Q	103/104 (99%)	98 (95%)	5 (5%)	22	44
18	R	92/96 (96%)	91 (99%)	1 (1%)	65	74
19	S	83/84 (99%)	83 (100%)	0	100	100
20	T	76/77 (99%)	73 (96%)	3 (4%)	28	50
21	U	65/65 (100%)	64 (98%)	1 (2%)	57	71
22	V	74/78 (95%)	72 (97%)	2 (3%)	39	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	W	56/65 (86%)	52 (93%)	4 (7%)	13	35
24	X	70/79 (89%)	70 (100%)	0	100	100
25	Y	65/66 (98%)	64 (98%)	1 (2%)	57	71
26	Z	55/61 (90%)	47 (86%)	8 (14%)	3	14
27	b	216/218 (99%)	212 (98%)	4 (2%)	50	66
28	c	164/164 (100%)	164 (100%)	0	100	100
29	d	165/165 (100%)	162 (98%)	3 (2%)	51	67
30	e	148/150 (99%)	145 (98%)	3 (2%)	48	66
31	f	137/138 (99%)	135 (98%)	2 (2%)	57	71
32	g	41/114 (36%)	38 (93%)	3 (7%)	13	34
33	i	109/110 (99%)	108 (99%)	1 (1%)	70	77
34	j	116/116 (100%)	116 (100%)	0	100	100
35	k	103/104 (99%)	103 (100%)	0	100	100
36	l	102/103 (99%)	101 (99%)	1 (1%)	68	76
37	m	109/109 (100%)	103 (94%)	6 (6%)	19	42
38	n	100/103 (97%)	99 (99%)	1 (1%)	68	76
39	o	86/87 (99%)	86 (100%)	0	100	100
40	p	99/100 (99%)	99 (100%)	0	100	100
41	q	89/90 (99%)	86 (97%)	3 (3%)	32	54
42	r	84/84 (100%)	82 (98%)	2 (2%)	43	63
43	s	93/93 (100%)	92 (99%)	1 (1%)	65	74
44	t	80/84 (95%)	80 (100%)	0	100	100
45	u	83/85 (98%)	79 (95%)	4 (5%)	23	45
46	v	78/78 (100%)	77 (99%)	1 (1%)	61	72
47	w	57/63 (90%)	57 (100%)	0	100	100
48	x	67/68 (98%)	67 (100%)	0	100	100
49	y	55/55 (100%)	55 (100%)	0	100	100
50	z	48/49 (98%)	46 (96%)	2 (4%)	26	48
57	A1	185/286 (65%)	174 (94%)	11 (6%)	18	40
57	A2	186/286 (65%)	185 (100%)	1 (0%)	81	82
58	B1	1110/1168 (95%)	1017 (92%)	93 (8%)	10	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	B2	1150/1157 (99%)	1117 (97%)	33 (3%)	37	58
60	W0	70/75 (93%)	69 (99%)	1 (1%)	59	72
65	h	2/2 (100%)	2 (100%)	0	100	100
All	All	7381/7914 (93%)	7132 (97%)	249 (3%)	33	54

5 of 249 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	A1	22	THR
59	B2	516	ASP
58	B1	96	LYS
59	B2	483	ASP
59	B2	902	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 127 such sidechains are listed below:

Mol	Chain	Res	Type
29	d	90	GLN
58	B1	1238	GLN
36	l	104	GLN
58	B1	1195	GLN
59	B2	688	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	1	2902/2904 (99%)	399 (13%)	16 (0%)
52	2	119/120 (99%)	17 (14%)	1 (0%)
53	3	1538/1542 (99%)	253 (16%)	4 (0%)
54	4	33/56 (58%)	16 (48%)	2 (6%)
63	5	75/76 (98%)	43 (57%)	7 (9%)
64	6	76/77 (98%)	10 (13%)	0
64	7	76/77 (98%)	27 (35%)	2 (2%)
All	All	4819/4852 (99%)	765 (15%)	32 (0%)

5 of 765 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	1	10	A

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Mol	Chain	Res	Type
51	1	12	U
51	1	34	U
51	1	35	G
51	1	46	G

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
63	5	57	G
63	5	60	U
51	1	1930	G
51	1	1801	A
64	7	33	U

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
65	DPP	h	2	65	4,5,6	0.50	0	1,5,7	0.08	0
65	5OH	h	6	65	7,12,13	0.70	0	4,16,18	1.35	1 (25%)
65	UAL	h	5	65	6,8,9	2.38	2 (33%)	4,9,11	1.87	1 (25%)
65	KBE	h	1	65	8,8,9	0.58	0	6,8,10	1.19	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
65	DPP	h	2	65	-	0/2/4/6	-
65	5OH	h	6	65	-	0/2/18/20	0/1/1/1
65	UAL	h	5	65	-	0/3/7/9	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
65	KBE	h	1	65	-	0/7/7/8	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	h	5	UAL	C1-N1	-4.99	1.32	1.40
65	h	5	UAL	C-CA	-2.84	1.40	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	h	5	UAL	O-C-CA	-3.28	121.28	125.39
65	h	6	5OH	CR-CB-CA	-2.42	110.04	112.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
65	h	2	DPP	2	0
65	h	6	5OH	6	0
65	h	5	UAL	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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.

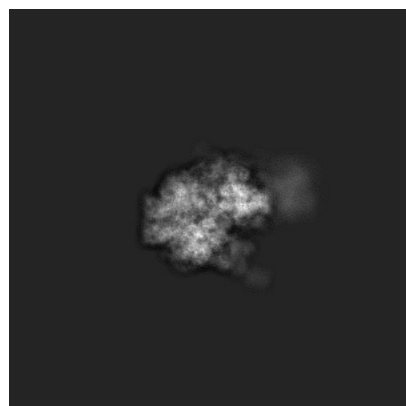
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39168. These allow visual inspection of the internal detail of the map and identification of artifacts.

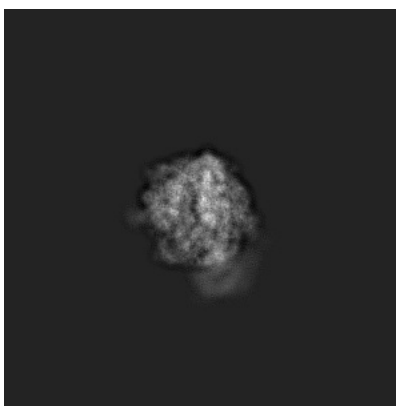
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

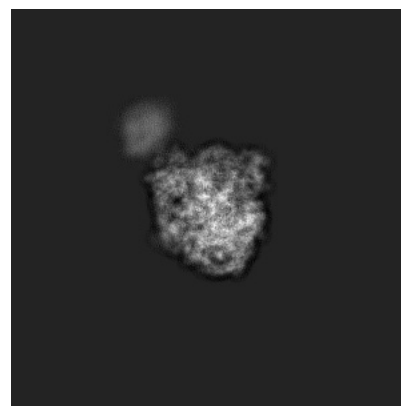
6.1.1 Primary map



X

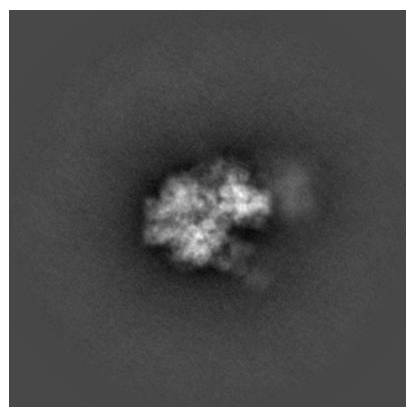


Y

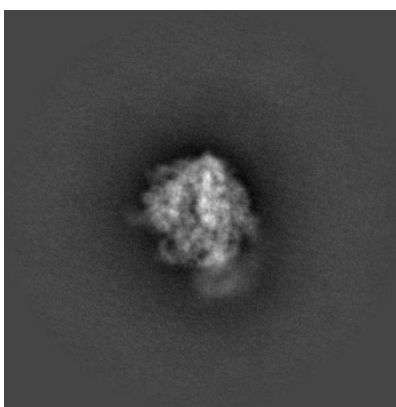


Z

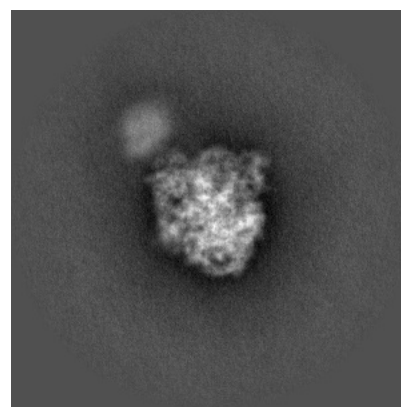
6.1.2 Raw map



X



Y

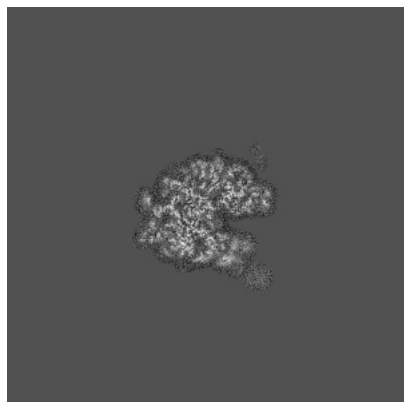


Z

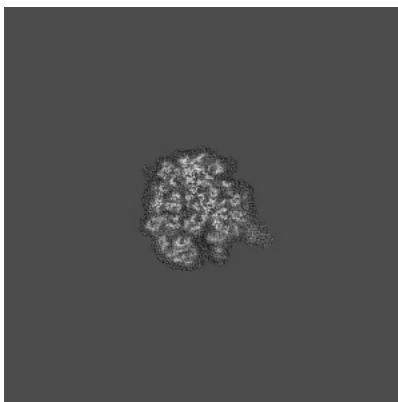
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

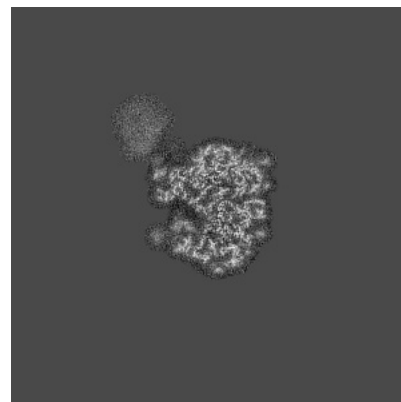
6.2.1 Primary map



X Index: 240

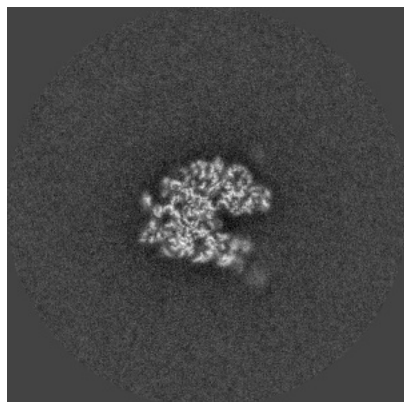


Y Index: 240

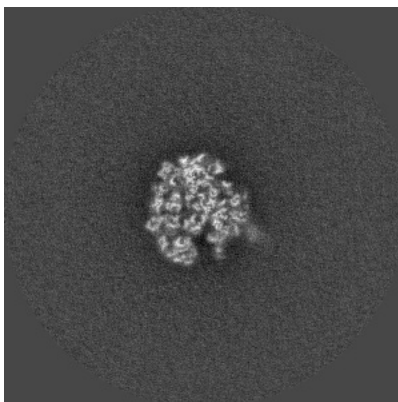


Z Index: 240

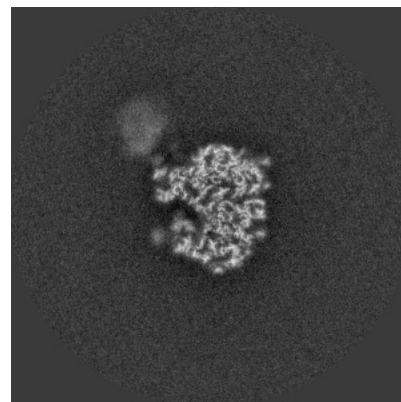
6.2.2 Raw map



X Index: 240



Y Index: 240

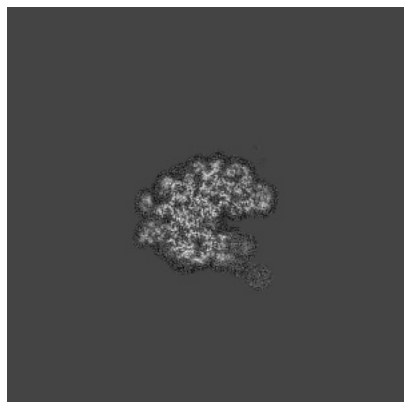


Z Index: 240

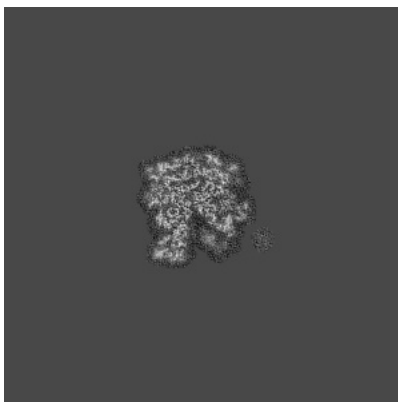
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

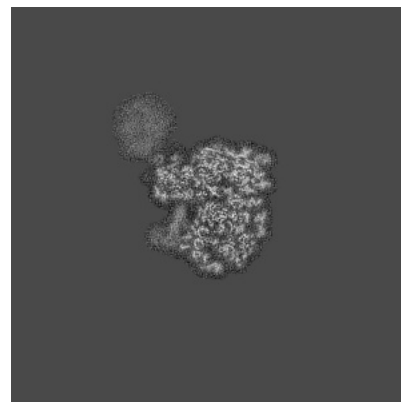
6.3.1 Primary map



X Index: 243

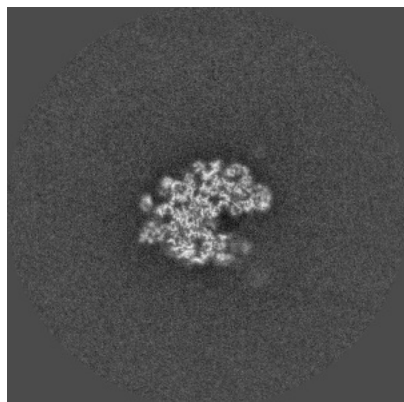


Y Index: 224

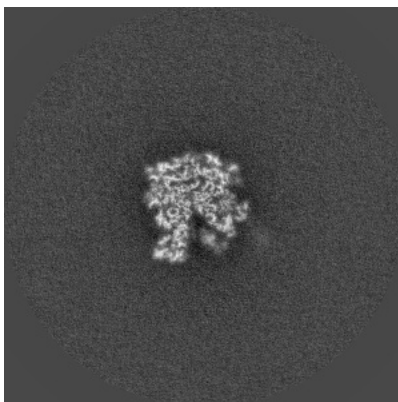


Z Index: 245

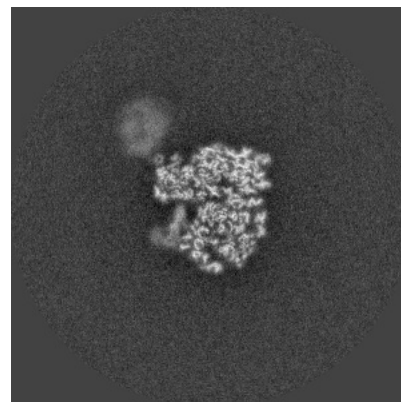
6.3.2 Raw map



X Index: 243



Y Index: 224

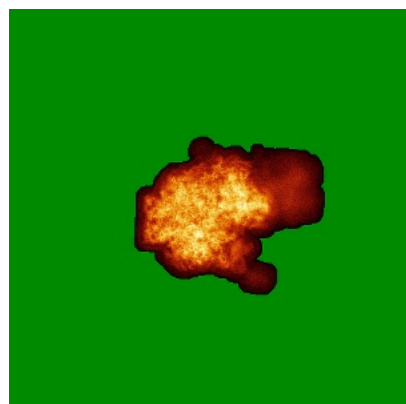


Z Index: 245

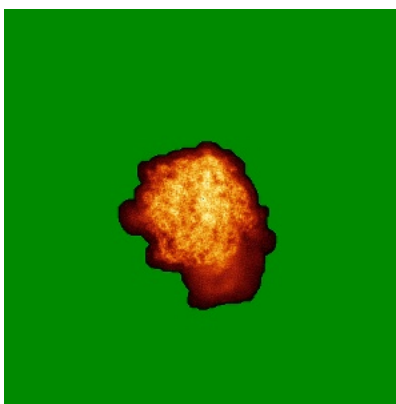
The images above show the largest variance slices of the map in three orthogonal directions.

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

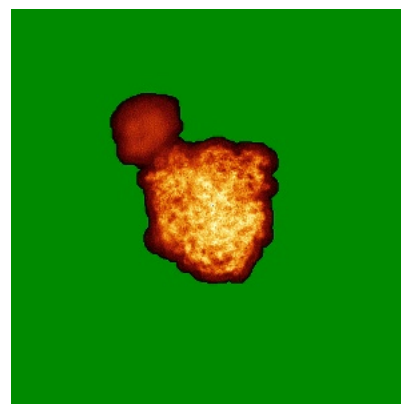
6.4.1 Primary map



X

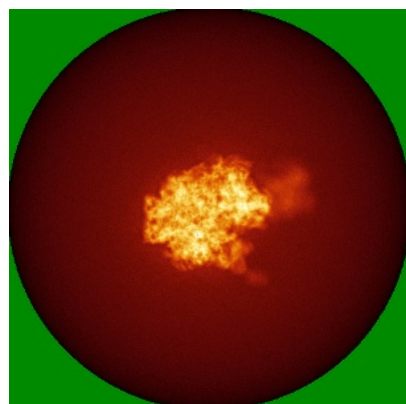


Y

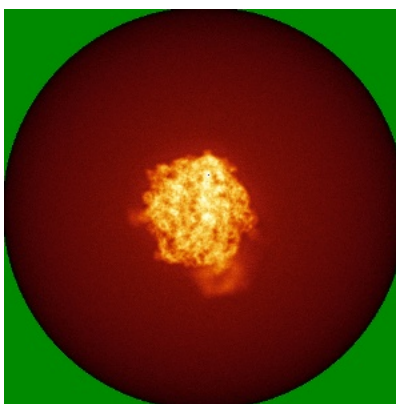


Z

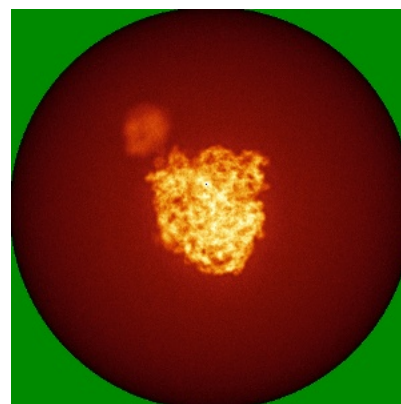
6.4.2 Raw map



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.

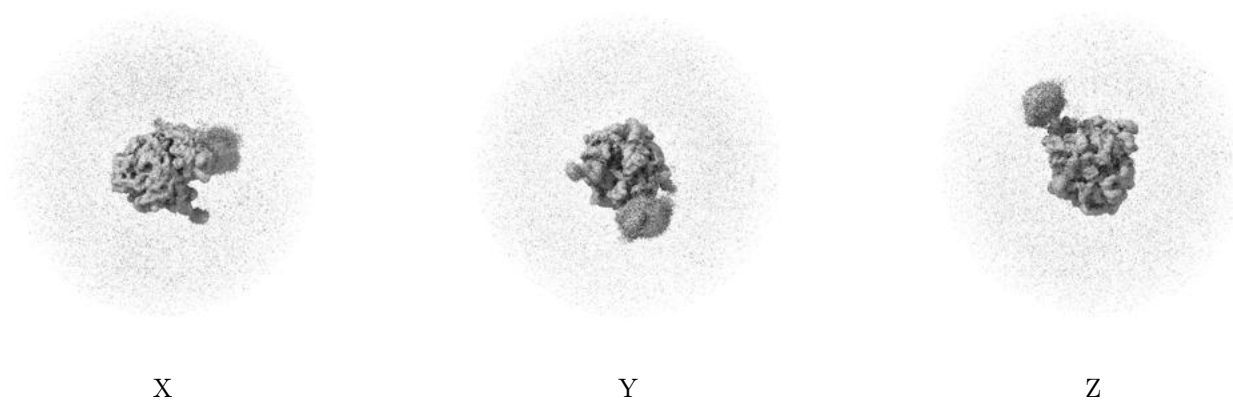
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.011. 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.

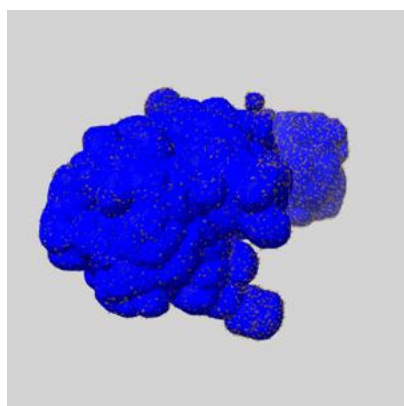
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

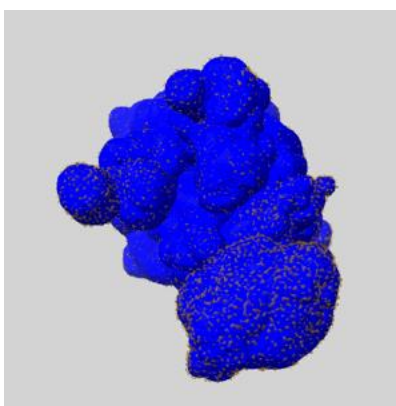
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

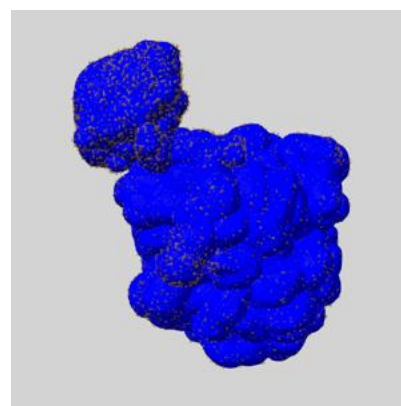
6.6.1 emd_39168_msk_1.map [i](#)



X



Y

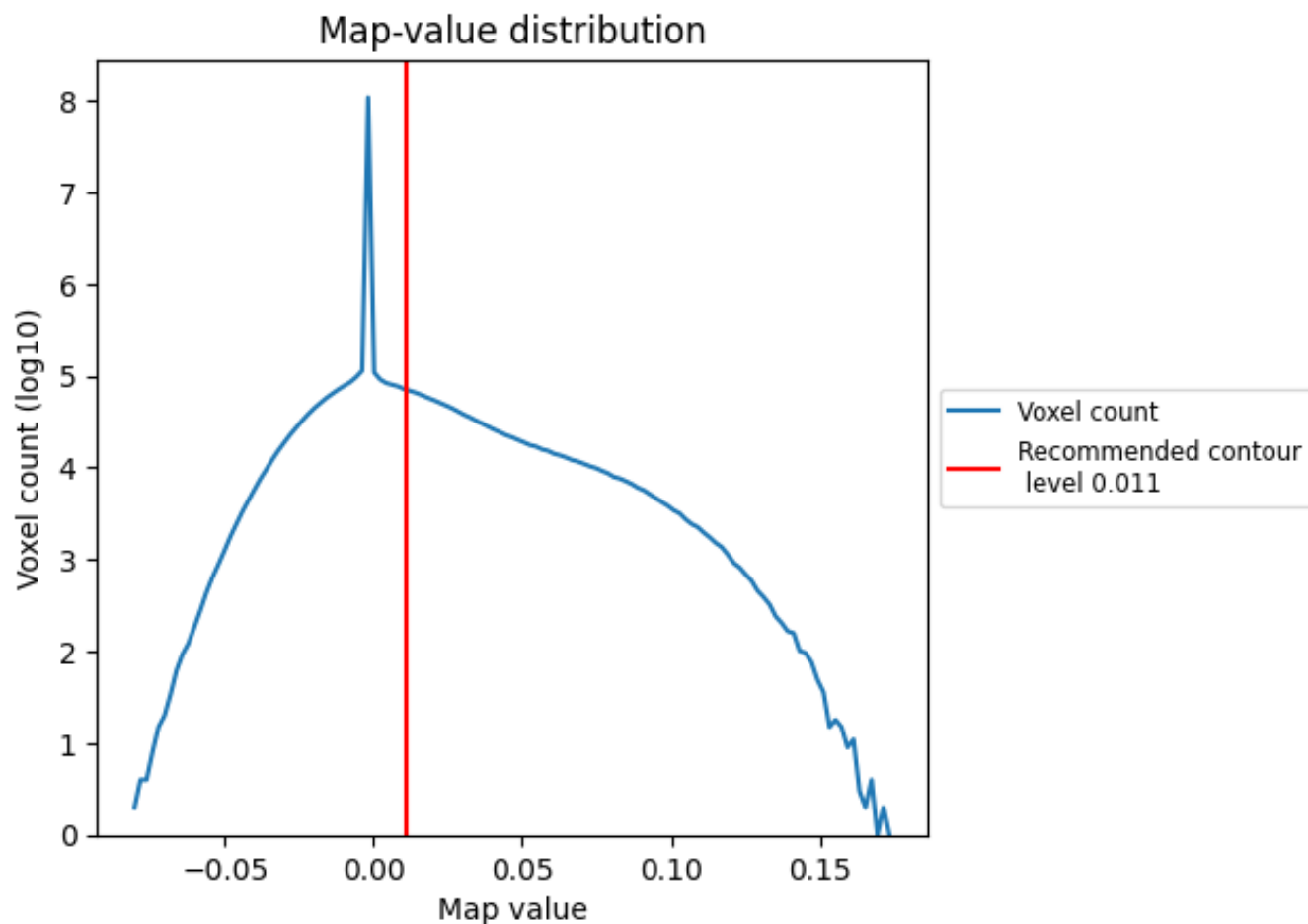


Z

7 Map analysis [i](#)

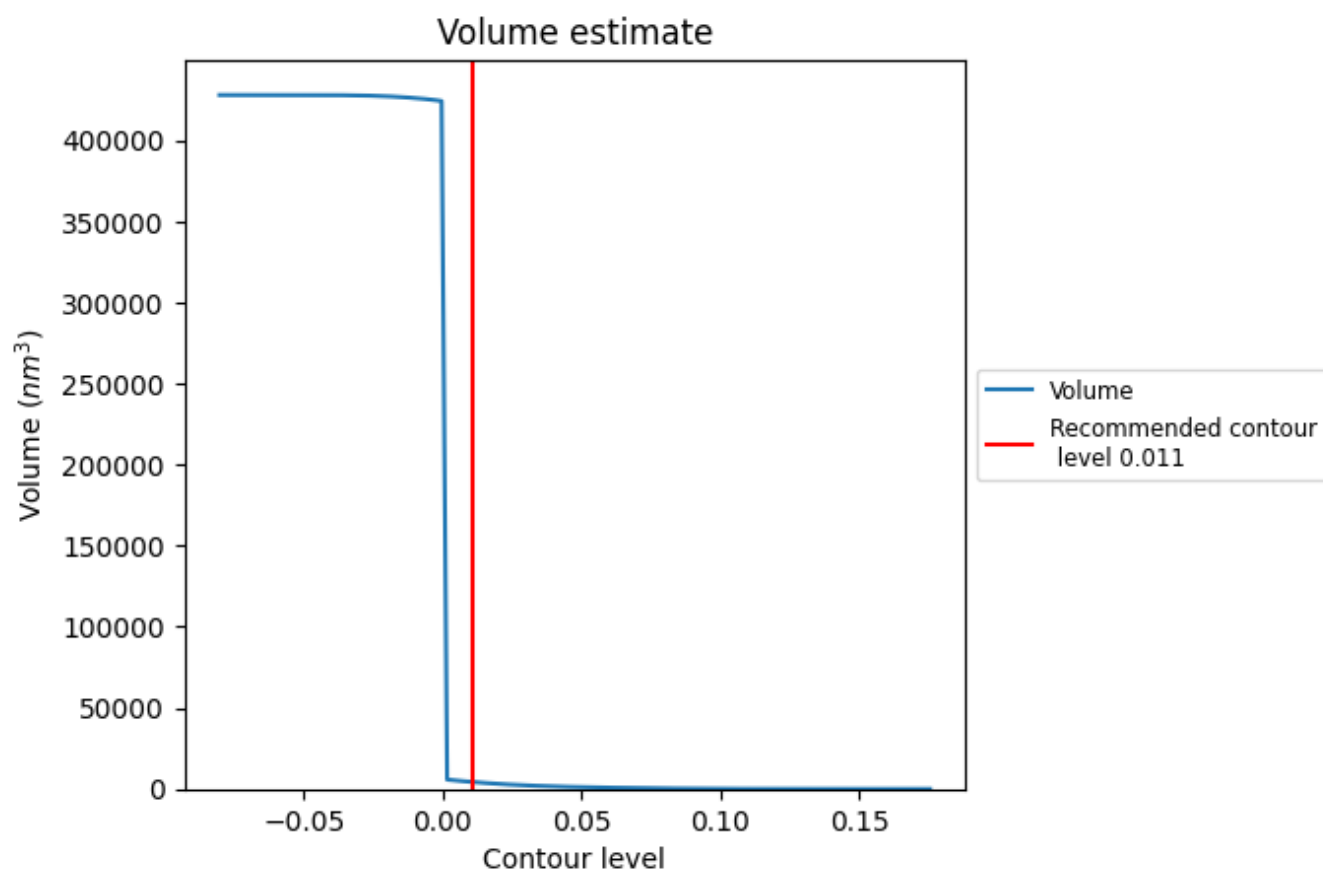
This section contains the results of statistical analysis of the map.

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.

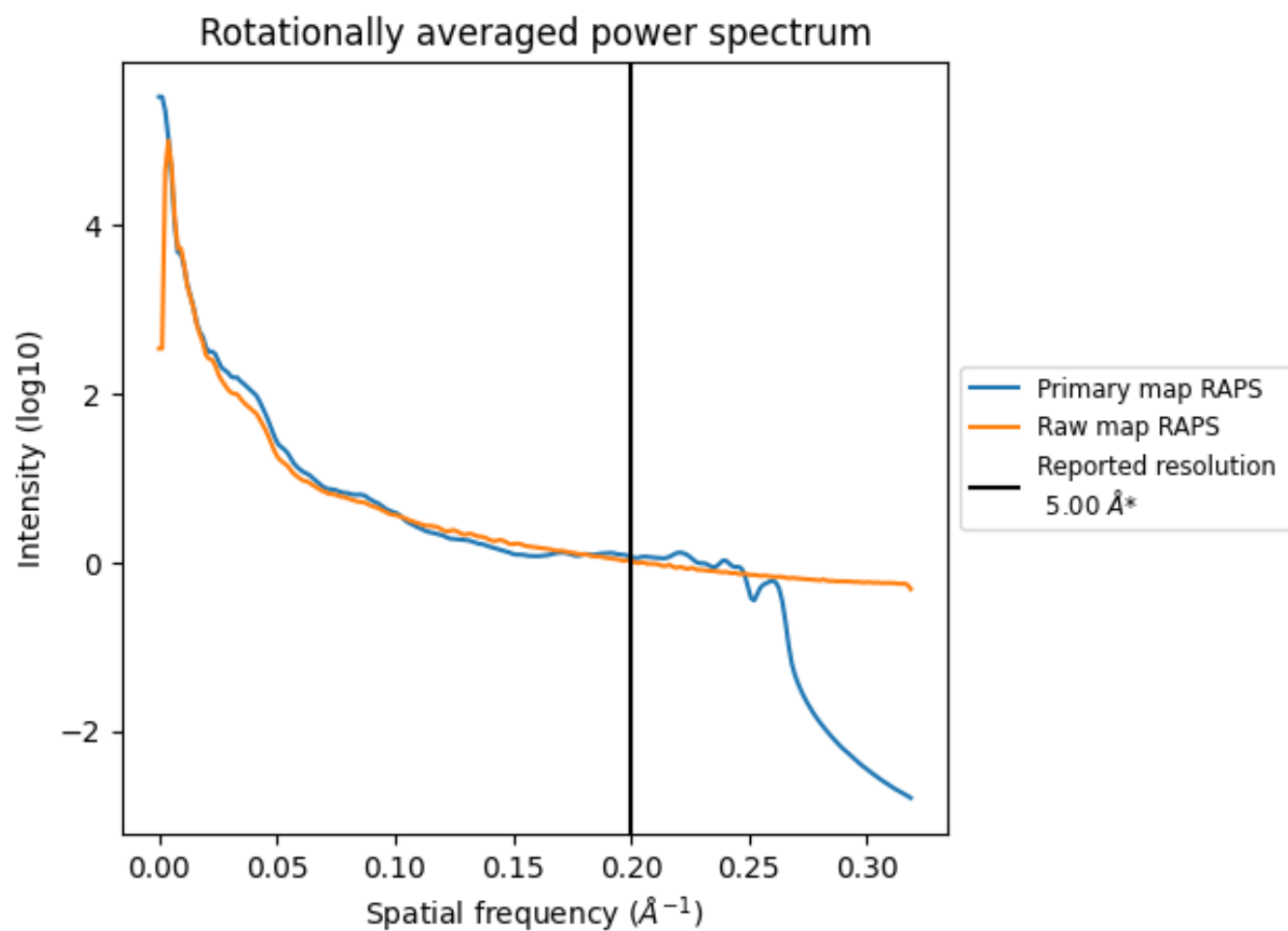
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4264 nm^3 ; this corresponds to an approximate mass of 3852 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 ⓘ

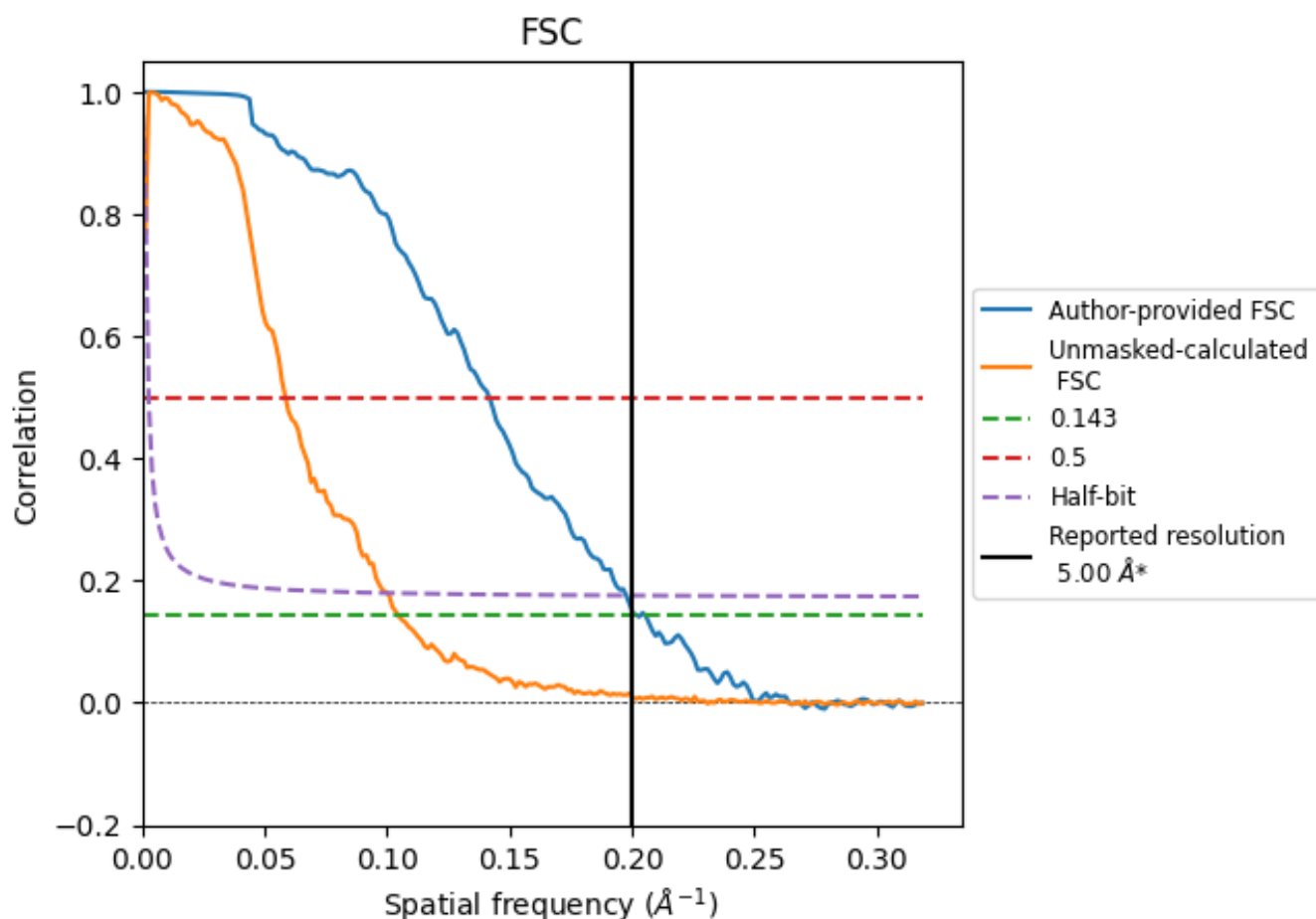


*Reported resolution corresponds to spatial frequency of 0.200 $\text{\AA}^{-1}$

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 0.200 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

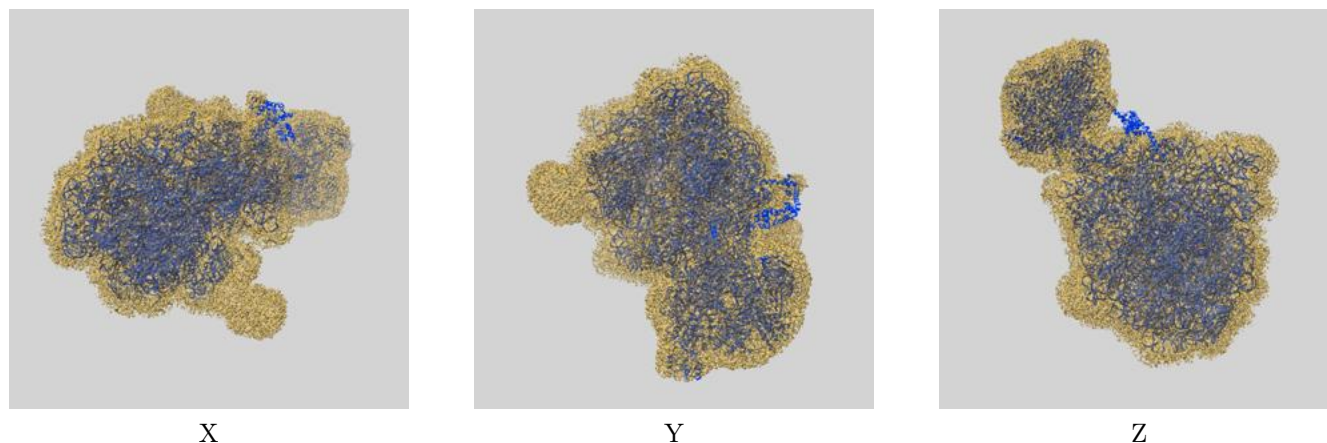
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.00	-	-
Author-provided FSC curve	4.95	7.06	5.06
Unmasked-calculated*	9.57	17.09	666.67

*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 9.57 differs from the reported value 5.0 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-39168 and PDB model 8YDE. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



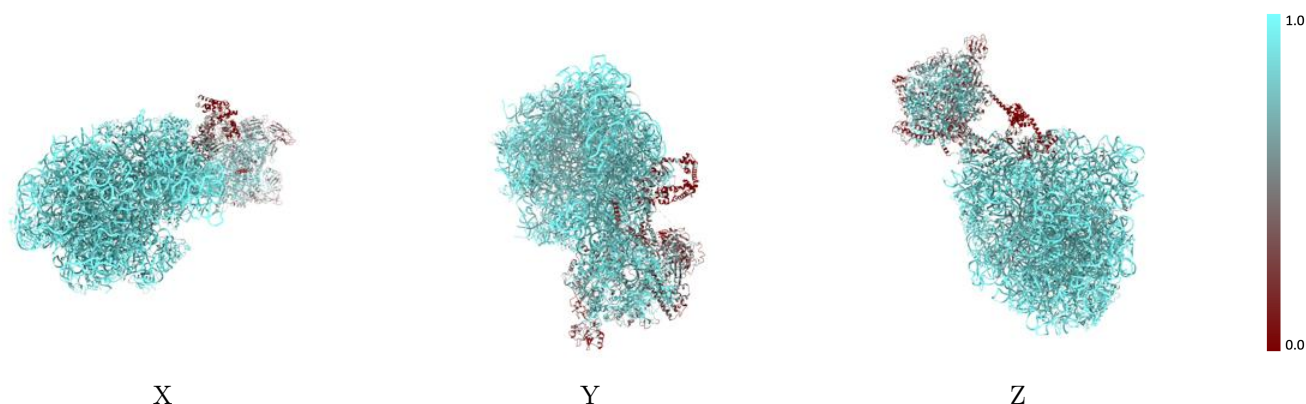
The images above show the 3D surface view of the map at the recommended contour level 0.011 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



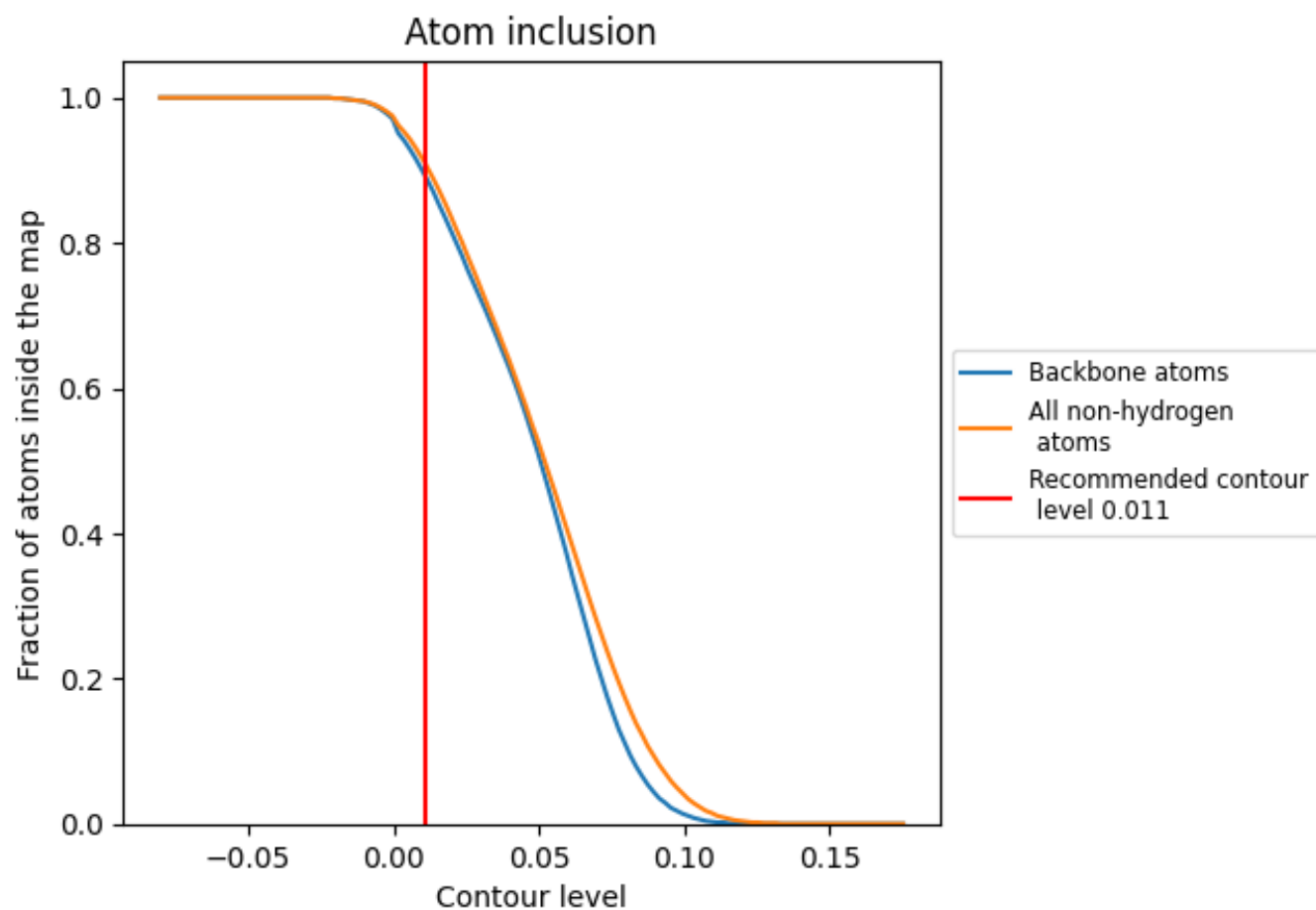
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.011).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 91% 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 (0.011) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9090	 0.2050
1	 0.9900	 0.2870
2	 0.9940	 0.2410
3	 0.9850	 0.2310
4	 0.7830	 0.0350
5	 0.9180	 0.0970
6	 0.9840	 0.2870
7	 0.7850	 0.0720
8	 0.8050	 0.0210
9	 0.7840	 0.0180
A	 0.8920	 0.1370
A1	 0.3580	 0.0100
A2	 0.3940	 0.0020
B	 0.9490	 0.2720
B1	 0.7120	 0.0000
B2	 0.6820	 -0.0070
C	 0.9350	 0.2470
D	 0.9410	 0.3120
E	 0.9450	 0.3080
F	 0.9490	 0.2430
G	 0.9190	 0.1650
H	 0.9080	 0.2190
I	 0.8090	 0.0590
J	 0.9300	 0.2570
K	 0.9350	 0.1620
L	 0.9340	 0.1930
M	 0.9450	 0.2460
N	 0.9640	 0.1760
NA	 0.3260	 0.0200
NG	 0.7490	 0.0140
O	 0.8940	 0.1390
P	 0.9390	 0.2150
Q	 0.8870	 0.1910
R	 0.9360	 0.1580
S	 0.9350	 0.2000



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Chain	Atom inclusion	Q-score
T	 0.9380	 0.2080
U	 0.8260	 0.0950
V	 0.8960	 0.1270
W	 0.9420	 0.1980
W0	 0.4180	 -0.0170
X	 0.9320	 0.1540
Y	 0.9030	 0.1380
Z	 0.8470	 0.1280
b	 0.9520	 0.3240
c	 0.9510	 0.2750
d	 0.9590	 0.2500
e	 0.9510	 0.2170
f	 0.9450	 0.1520
g	 0.9470	 0.1660
h	 0.9580	 0.2930
i	 0.8450	 0.0000
j	 0.9490	 0.2820
k	 0.8920	 0.2490
l	 0.9580	 0.2790
m	 0.9320	 0.2880
n	 0.9490	 0.2520
o	 0.9710	 0.2180
p	 0.9110	 0.1910
q	 0.9580	 0.2990
r	 0.9690	 0.2980
s	 0.9320	 0.2810
t	 0.9210	 0.1940
u	 0.9670	 0.2250
v	 0.9500	 0.2270
w	 0.9460	 0.2820
x	 0.9500	 0.3090
y	 0.9520	 0.1600
z	 0.9660	 0.2910