



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 02:50 AM UTC

PDB ID : 8YDG / pdb_00008ydg
EMDB ID : EMD-39170
Title : E.coli transcription translation coupling complex in TTC-B state 3 (subclass2) 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 : 5.10 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:

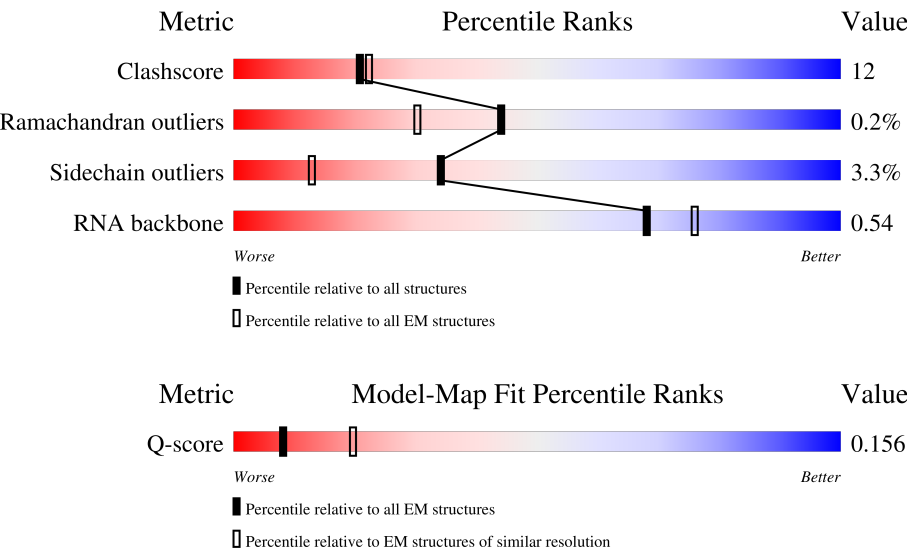
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 5.10 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.



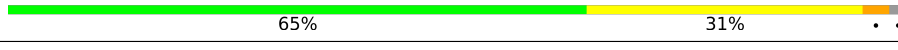
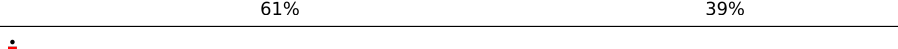
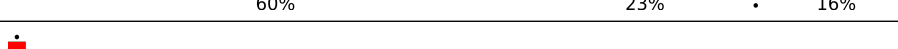
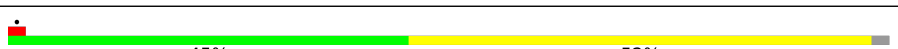
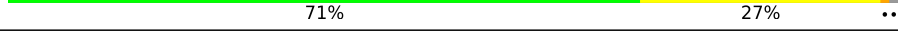
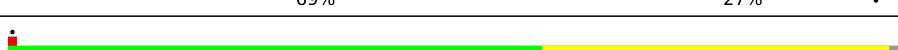
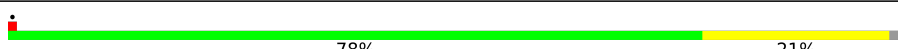
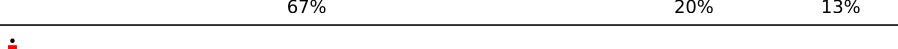
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	844 (4.60 - 5.60)

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	50% 16% 34%
2	B	57	67% 30% ••
3	C	55	53% 38% 9%

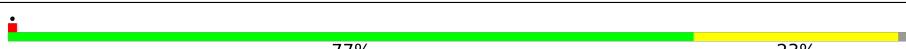
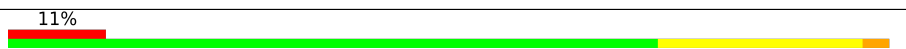
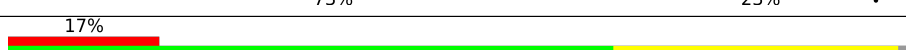
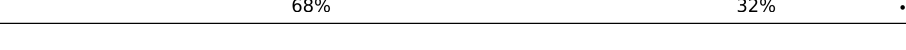
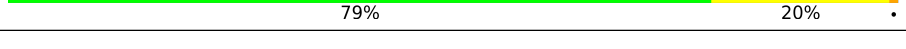
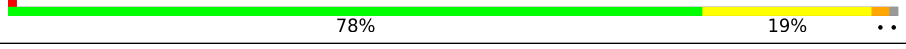
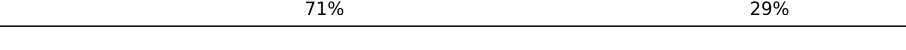
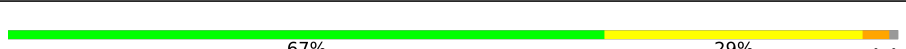
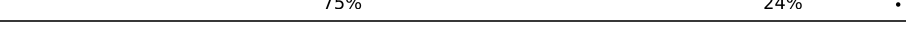
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Mol	Chain	Length	Quality of chain
4	D	46	
5	E	65	
6	F	38	
7	G	241	
8	H	233	
9	I	206	
10	J	167	
11	K	135	
12	L	179	
13	M	130	
14	N	130	
15	O	103	
16	P	129	
17	Q	124	
18	R	118	
19	S	101	
20	T	89	
21	U	82	
22	V	84	
23	W	75	
24	X	92	
25	Y	87	
26	Z	71	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

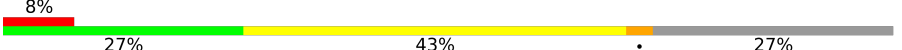
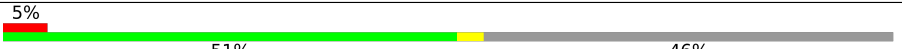
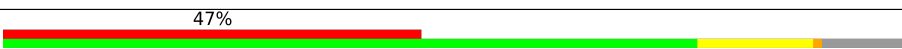
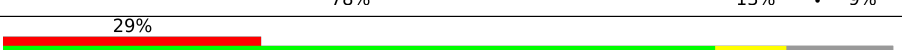
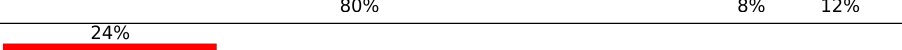
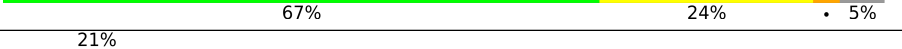
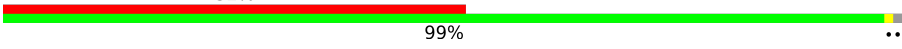
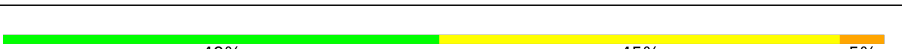
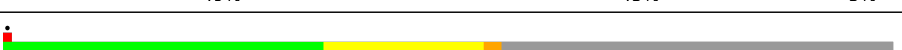
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Mol	Chain	Length	Quality of chain
29	d	201	
30	e	179	
31	f	177	
32	g	149	
33	i	142	
34	j	142	
35	k	123	
36	l	144	
37	m	136	
38	n	127	
39	o	117	
40	p	115	
41	q	118	
42	r	103	
43	s	110	
44	t	100	
45	u	104	
46	v	94	
47	w	85	
48	x	78	
49	y	63	
50	z	59	
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	
65	a	234	
66	0	716	
67	h	6	

2 Entry composition

There are 70 unique types of molecules in this entry. The entry contains 183439 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	46	Total	C	N	O	S	0	0
			355	221	62	66	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	149	Total	C	N	O	S	0	0
			1111	699	197	214	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	S	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	33	Total	C	N	O	P	0	0
			689	308	101	247	33		

- 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		

- Molecule 65 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	a	132	Total	C	N	O	S	0	0
			1013	638	183	190	2		

- Molecule 66 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	0	697	Total	C	N	O	S	0	0
			5399	3403	929	1042	25		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	705	GLY	-	expression tag	UNP P0A6M8
0	706	SER	-	expression tag	UNP P0A6M8
0	707	SER	-	expression tag	UNP P0A6M8
0	708	GLY	-	expression tag	UNP P0A6M8
0	709	HIS	-	expression tag	UNP P0A6M8
0	710	HIS	-	expression tag	UNP P0A6M8
0	711	HIS	-	expression tag	UNP P0A6M8
0	712	HIS	-	expression tag	UNP P0A6M8
0	713	HIS	-	expression tag	UNP P0A6M8
0	714	HIS	-	expression tag	UNP P0A6M8

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Chain	Residue	Modelled	Actual	Comment	Reference
0	715	HIS	-	expression tag	UNP P0A6M8
0	716	HIS	-	expression tag	UNP P0A6M8

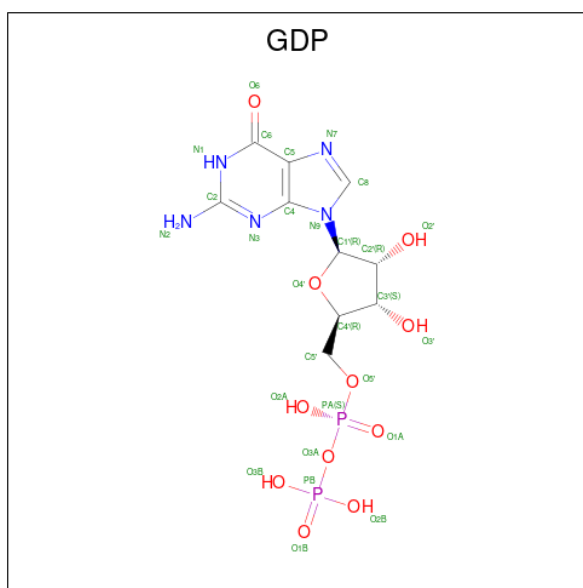
- Molecule 67 is a protein (with D amino acids) called Viomycin.

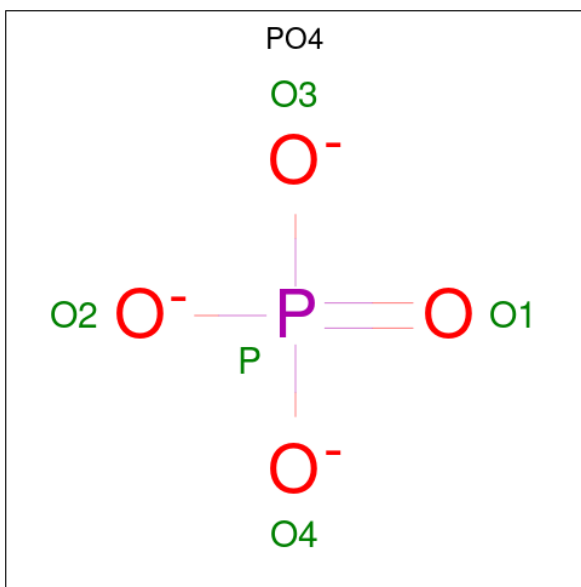
Mol	Chain	Residues	Atoms				AltConf	Trace
67	h	6	Total	C	N	O	0	0
			48	25	13	10		

- Molecule 68 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 69 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



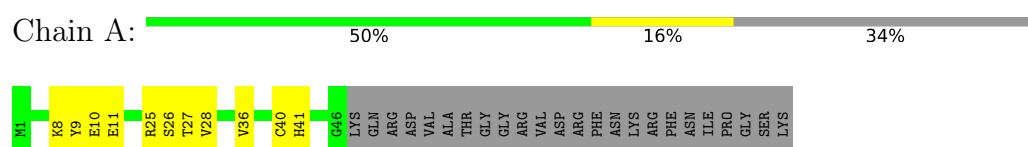


Mol	Chain	Residues	Atoms			AltConf
			Total	O	P	
70	0	1	5	4	1	0

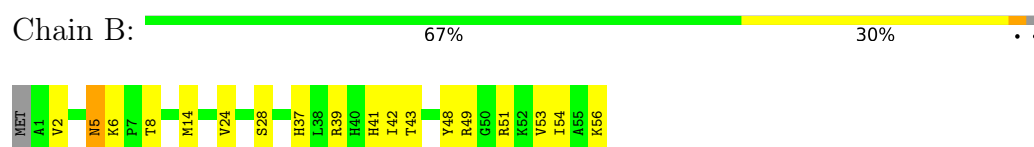
3 Residue-property plots [i](#)

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

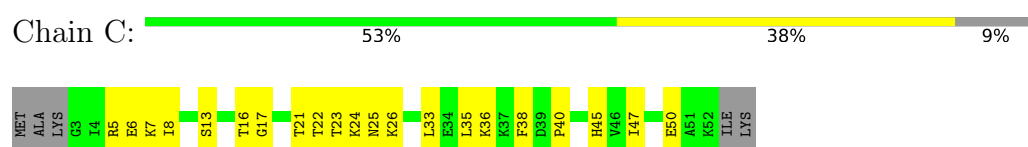
• Molecule 1: 50S ribosomal protein L31



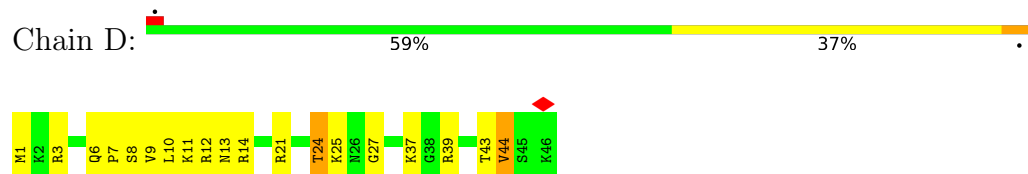
• Molecule 2: 50S ribosomal protein L32



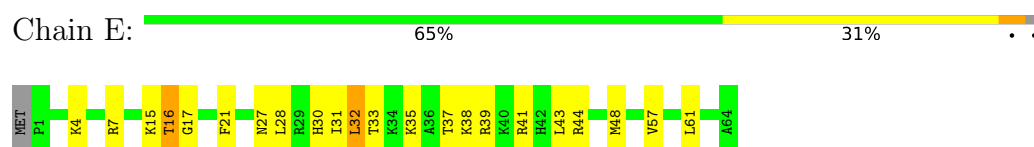
• Molecule 3: 50S ribosomal protein L33



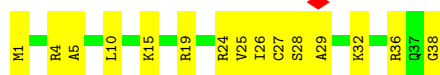
• Molecule 4: 50S ribosomal protein L34



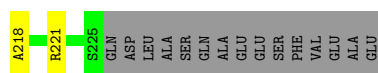
• Molecule 5: 50S ribosomal protein L35



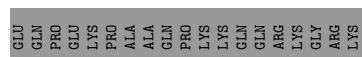
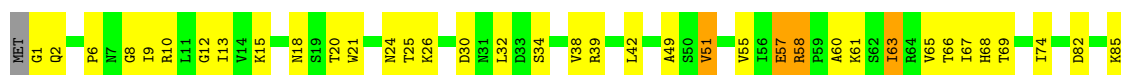
• Molecule 6: 50S ribosomal protein L36



• Molecule 7: 30S ribosomal protein S2



• Molecule 8: 30S ribosomal protein S3



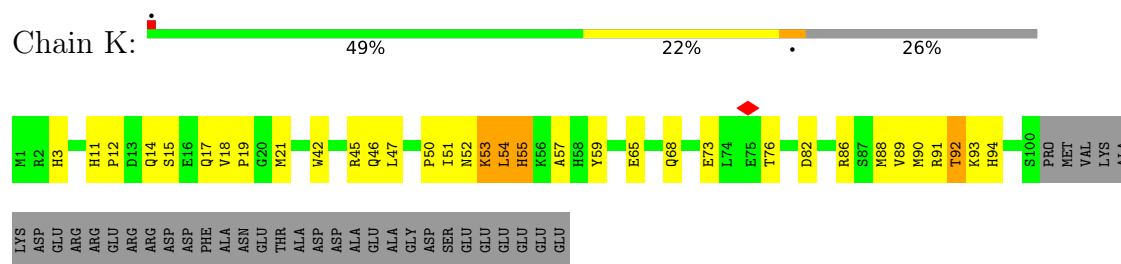
• Molecule 9: 30S ribosomal protein S4



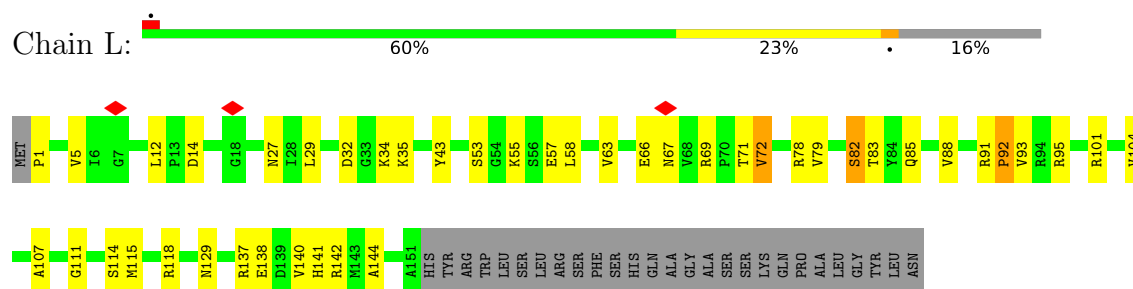
• Molecule 10: 30S ribosomal protein S5



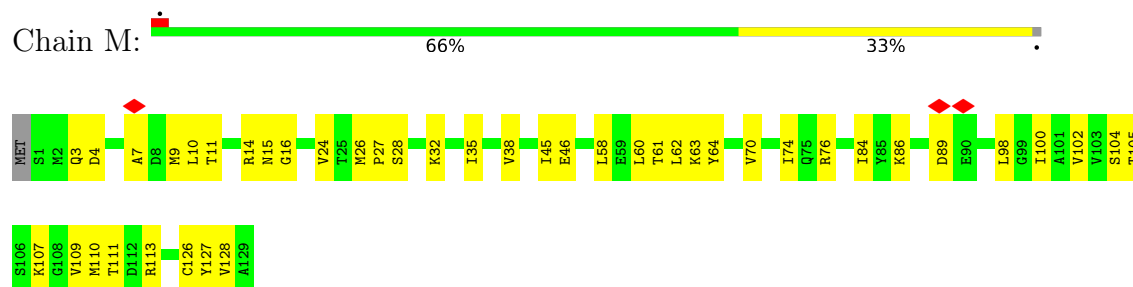
- Molecule 11: 30S ribosomal protein S6, fully modified isoform



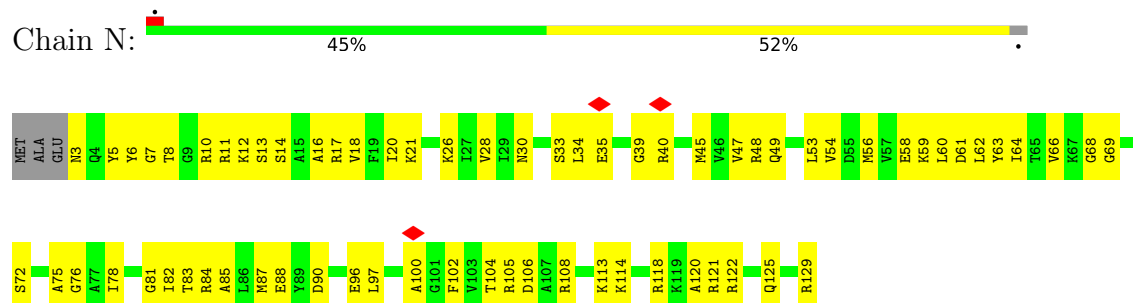
- Molecule 12: 30S ribosomal protein S7



- Molecule 13: 30S ribosomal protein S8



- Molecule 14: 30S ribosomal protein S9



Chain T:  78% 21% .



- Molecule 21: 30S ribosomal protein S16

Chain U:  72% 28%



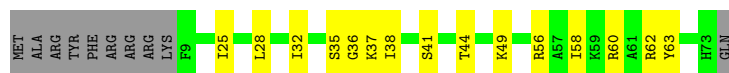
- Molecule 22: 30S ribosomal protein S17

Chain V:  65% 30% 5%



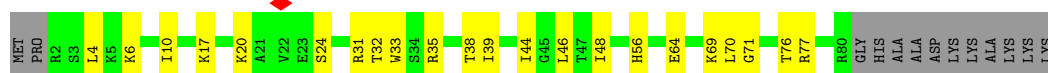
- Molecule 23: 30S ribosomal protein S18

Chain W:  67% 20% 13%



- Molecule 24: 30S ribosomal protein S19

Chain X:  62% 24% 14%



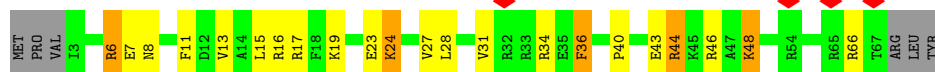
- Molecule 25: 30S ribosomal protein S20

Chain Y:  5% 64% 33%

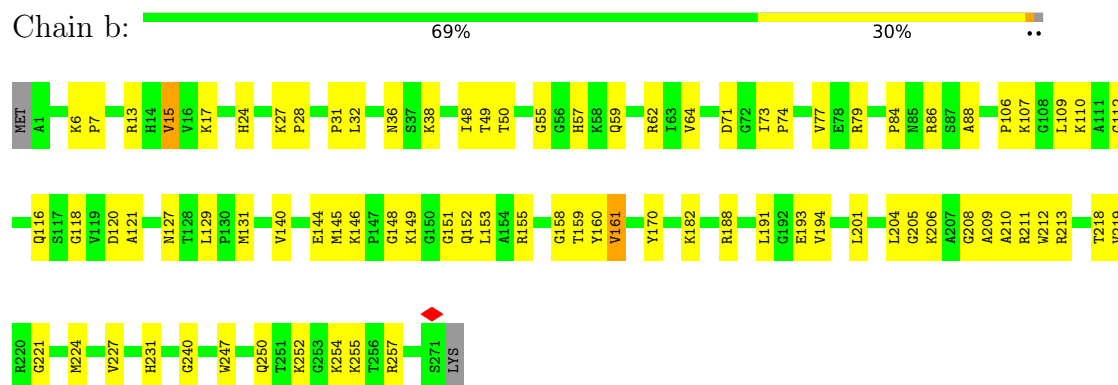


- Molecule 26: 30S ribosomal protein S21

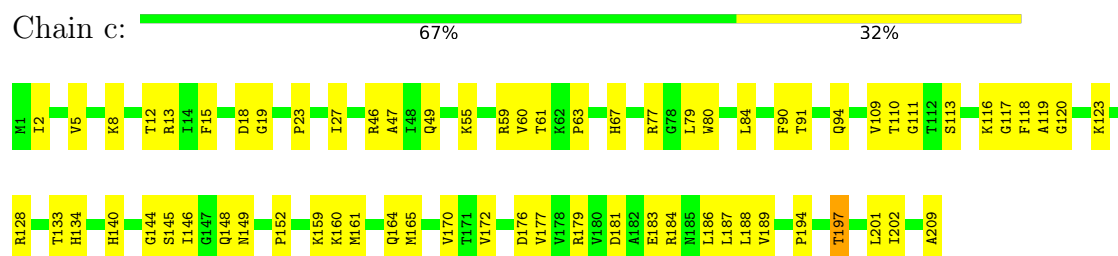
Chain Z:  6% 61% 24% 7% 8%



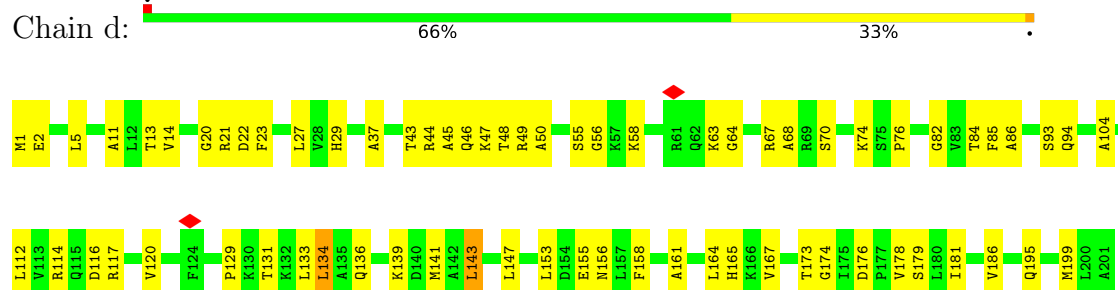
- Molecule 27: 50S ribosomal protein L2



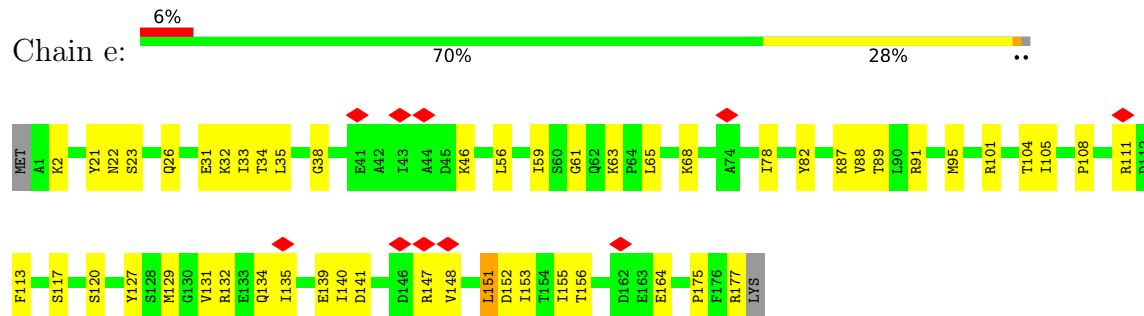
- Molecule 28: 50S ribosomal protein L3



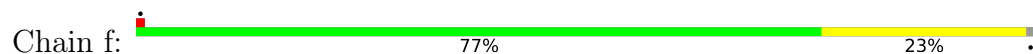
- Molecule 29: 50S ribosomal protein L4

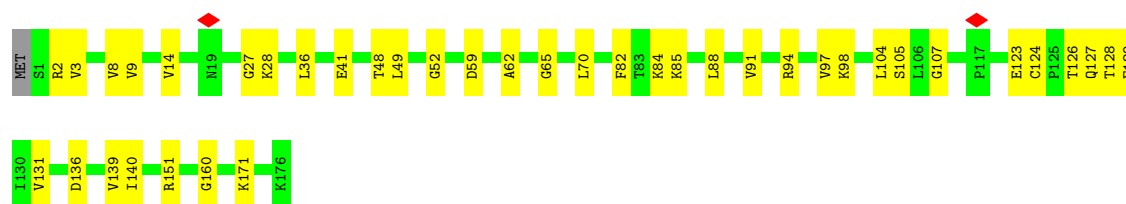


- Molecule 30: 50S ribosomal protein L5

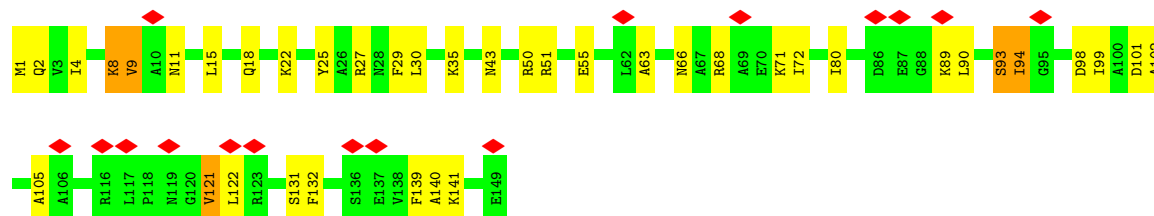
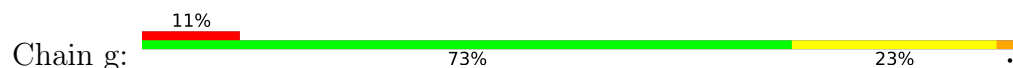


- Molecule 31: 50S ribosomal protein L6

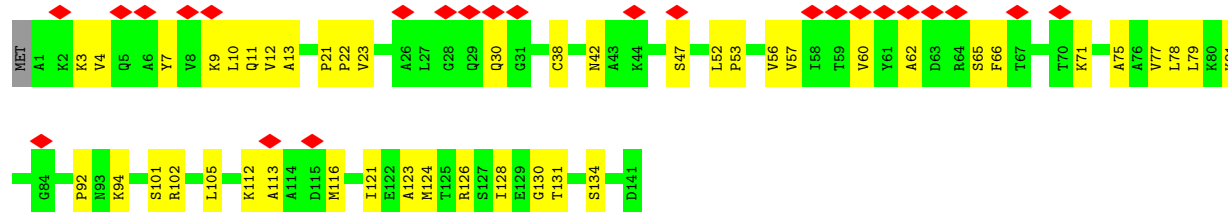




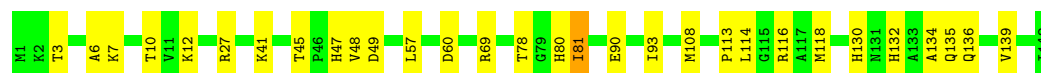
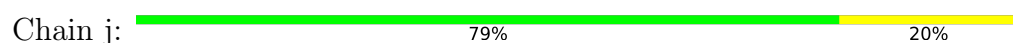
- Molecule 32: 50S ribosomal protein L9



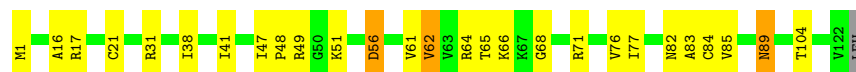
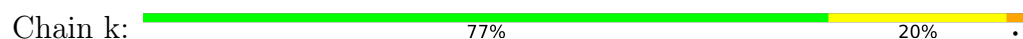
- Molecule 33: 50S ribosomal protein L11



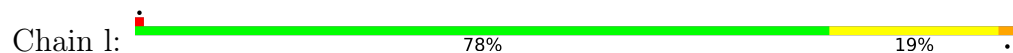
- Molecule 34: 50S ribosomal protein L13



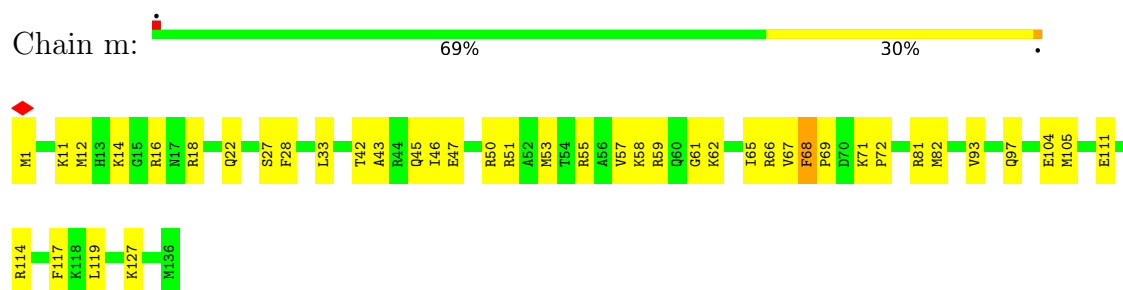
- Molecule 35: 50S ribosomal protein L14



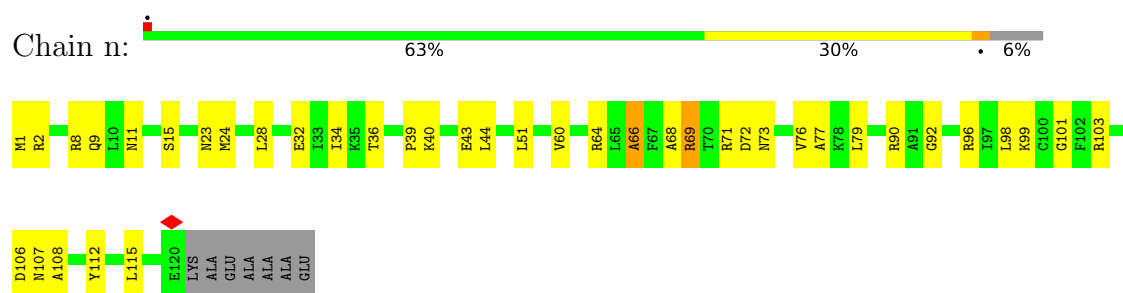
- Molecule 36: 50S ribosomal protein L15



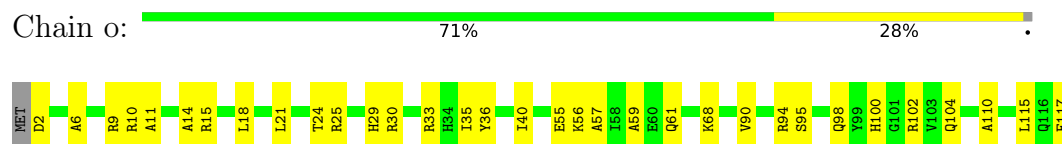
- Molecule 37: 50S ribosomal protein L16



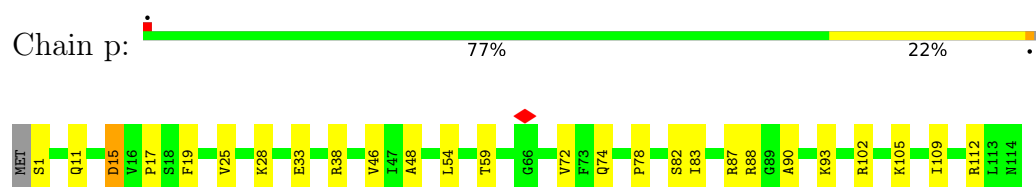
- Molecule 38: 50S ribosomal protein L17



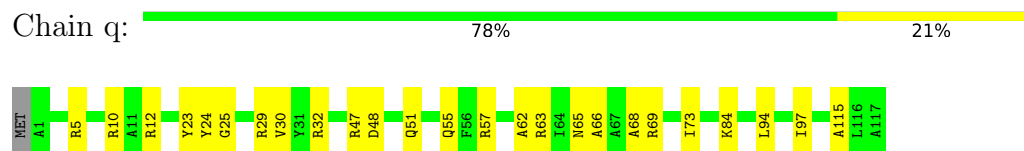
- Molecule 39: 50S ribosomal protein L18



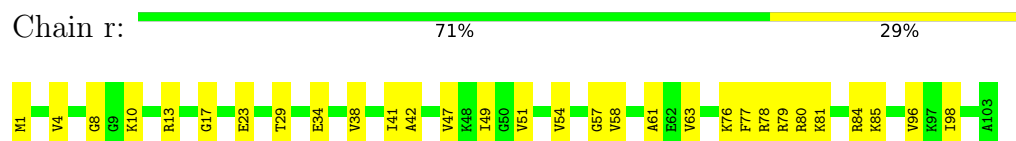
- Molecule 40: 50S ribosomal protein L19



- Molecule 41: 50S ribosomal protein L20



- Molecule 42: 50S ribosomal protein L21



- Molecule 43: 50S ribosomal protein L22

Chain s:  72% 28%



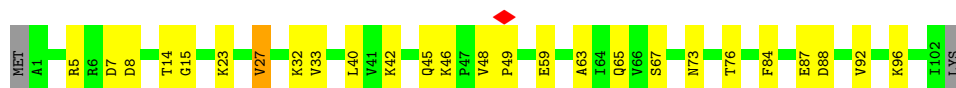
- Molecule 44: 50S ribosomal protein L23

Chain t:  64% 28% 7%



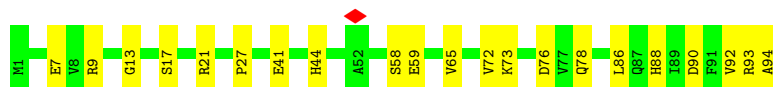
- Molecule 45: 50S ribosomal protein L24

Chain u:  73% 24%



- Molecule 46: 50S ribosomal protein L25

Chain v:  78% 22%



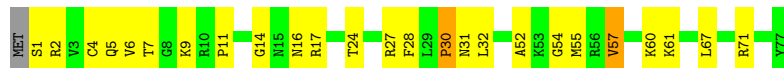
- Molecule 47: 50S ribosomal protein L27

Chain w:  64% 25% 12%



- Molecule 48: 50S ribosomal protein L28

Chain x:  67% 29%



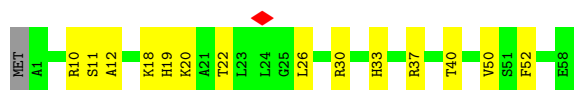
- Molecule 49: 50S ribosomal protein L29

Chain y:  78% 22%



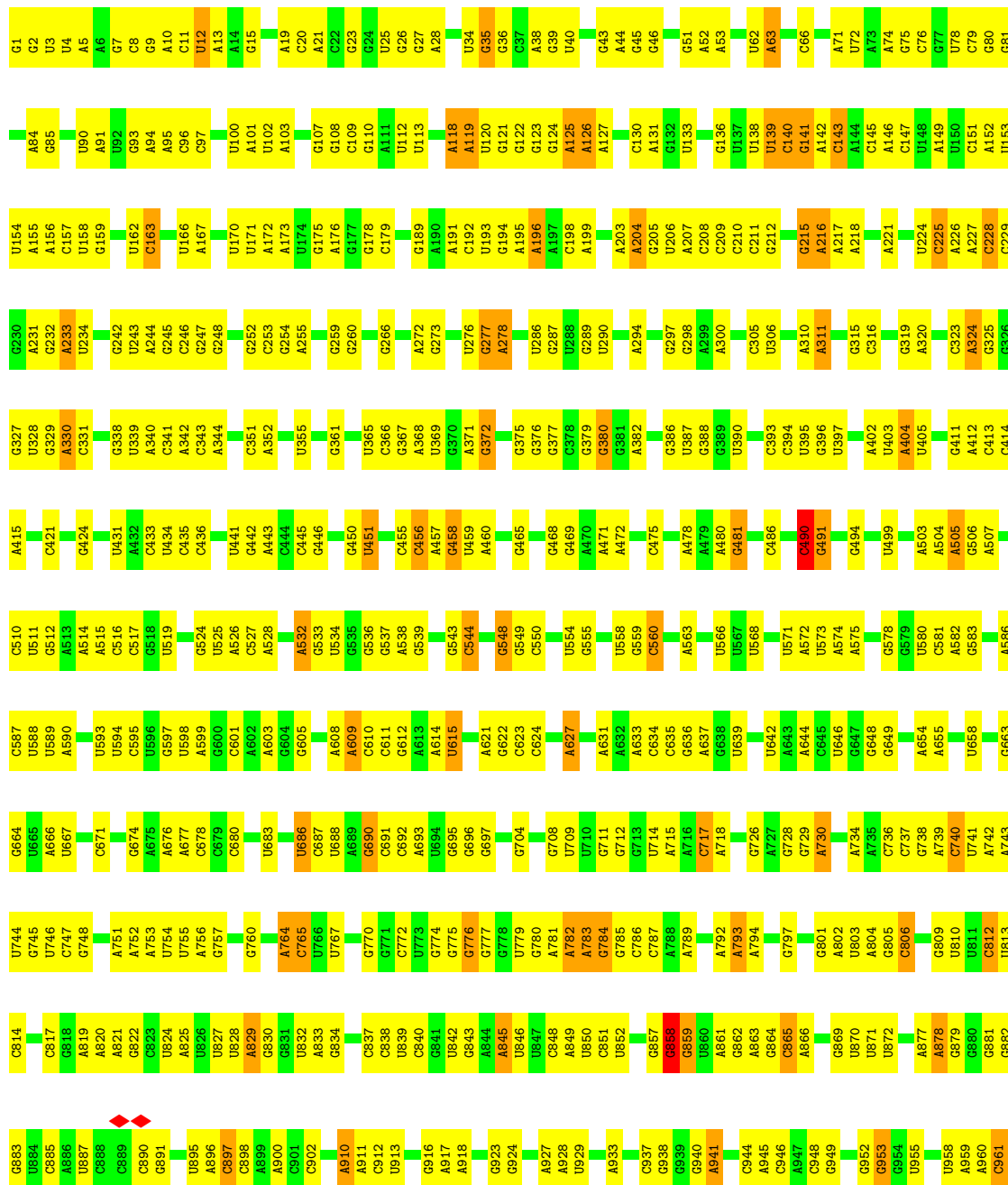
- Molecule 50: 50S ribosomal protein L30

Chain z: 

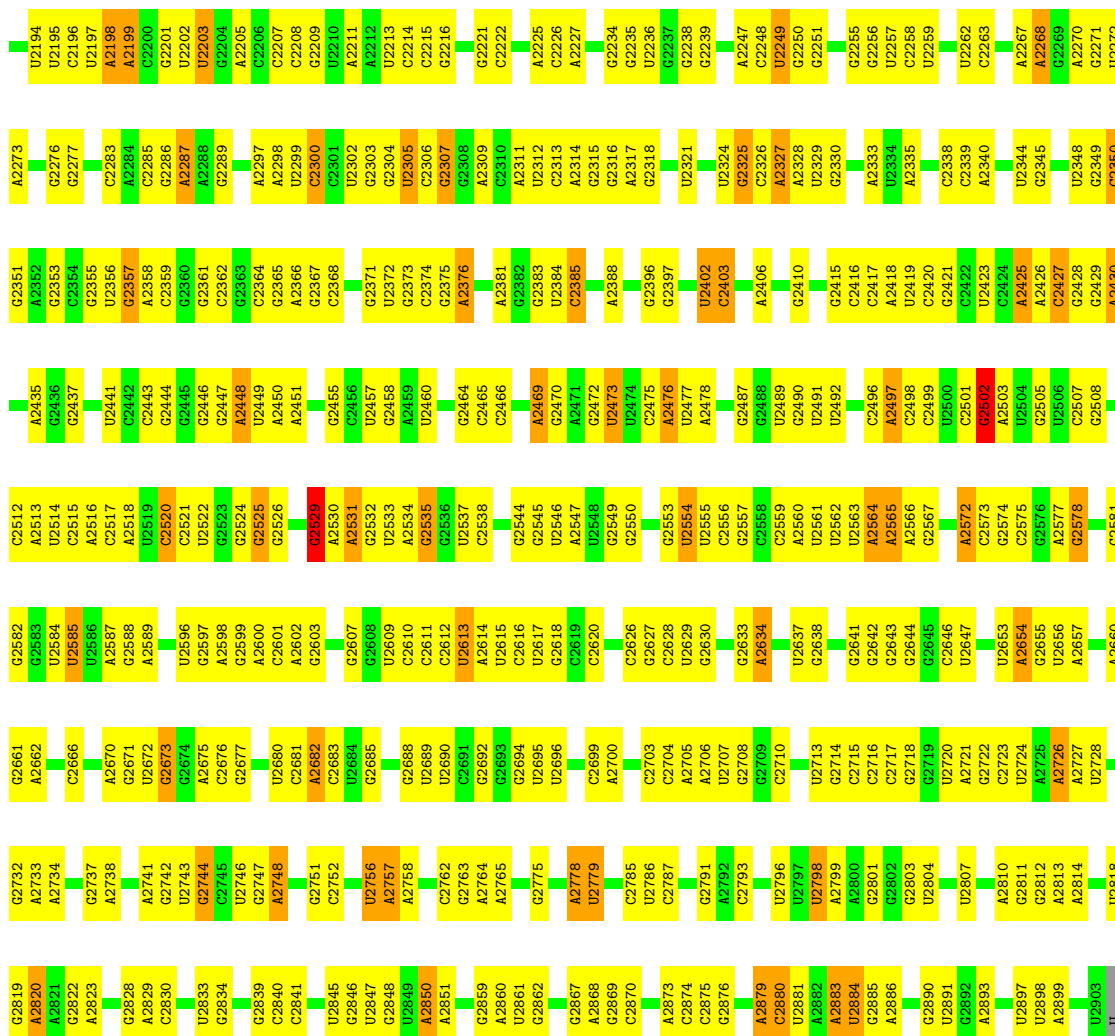


- Molecule 51: 23S rRNA

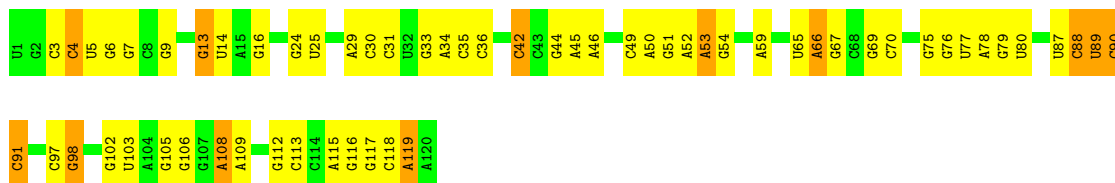
Chain 1: 



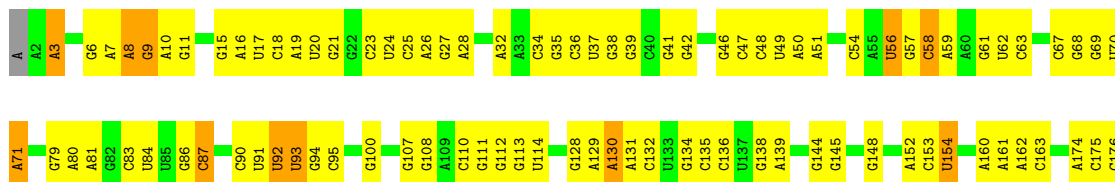




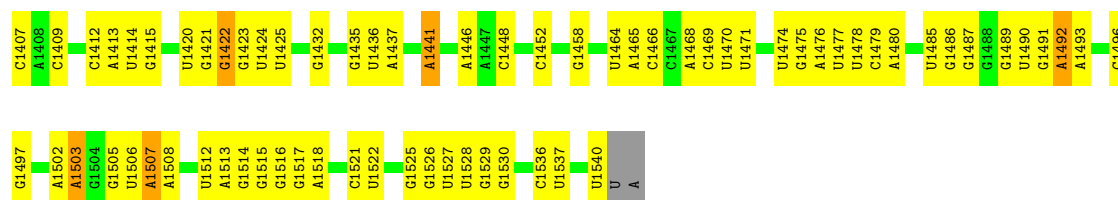
• Molecule 52: 5S rRNA



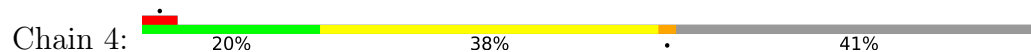
• Molecule 53: 16S rRNA



A1332	A1333	A1339	A1340	U1345	A1346	A1347	A1348	A1349	A1350	U1351	U1354	U1355	A1356	A1357	G1361	A1362	A1363	U1364	G1365	C1366	C1367	A1368	C1369	G1370	G1371	U1372	G1373	A1374	U1375	U1376	A1377	C1378	C1382	C1383	G1386	G1387	C1388	C1389	U1390	U1391	C1395	A1396	C1397	A1398	C1399	C1400	G1401	C1402	C1403	C1404	G1405	U1406		
A1257	G1182	U1183	G1184	G1187	A1188	C1192	U1193	U1194	C1195	A1196	A1197	G1198	U1199	C1200	A1201	C1210	U1211	C1212	A1213	C1214	G1215	A1216	C1217	C1218	A1219	G1220	G1221	C1222	A1225	C1226	A1229	C1230	G1231	U1232	G1233	C1234	U1235	A1236	C1237	A1238	A1239	U1240	G1241	G1242	C1243	G1244	C1245	A1250	A1251	C1252	G1253	A1254	U1256	
G1103	G1104	A1105	G1106	C1107	G1108	C1109	A1110	U1111	A1117	U1118	C1119	C1120	U1121	U1122	U1123	G1124	U1125	U1126	G1127	C1128	C1129	G1134	U1135	C1136	C1137	G1138	U1139	C1140	C1147	U1148	C1149	A1150	A1151	A1152	G1153	A1154	U1155	G1156	A1157	C1158	U1159	G1160	C1161	C1162	U1168	A1169	A1170	A1171	C1172	U1173	G1174	A1179	A1180	G1181
U1025	G1026	C1027	G1028	U1029	U1030	C1031	G1032	U1033	A1035	A1042	U1043	G1047	U1048	U1049	G1050	G1053	C1054	G1057	C1058	C1059	U1060	C1061	U1062	C1063	U1064	U1065	C1069	U1070	C1071	G993	U1072	U1073	G1074	C1077	U1078	G1079	A1004	A1005	G1006	U1007	U1008	U1091	U1092	A1093	U1094	U1095	C1096	C1097	C1098	G1099	C1100	A1102		
G947	U950	G951	U952	G953	G954	U955	U956	U957	U958	A959	U960	U961	C962	G963	A964	U965	G966	C967	A968	A969	C970	G971	C972	G973	A974	A975	G976	A977	A978	C979	C980	U981	U992	G993	A994	A1000	C1001	A1004	A1005	G1006	U1007	U1008	A1012	G1013	A1014	G1015	U1016	U1017	A938	G1018	A1019	A1022	U1023	G1024
G861	C862	U863	A864	A865	C866	G867	A872	A873	C874	U875	C876	G877	A878	G881	A882	C883	U884	A885	A886	A889	G894	G895	A900	A901	G902	G903	U904	U905	A906	A907	A908	A909	C910	A913	G917	A923	C924	G925	G926	G927	C934	A935	C936	A937	A938	G939	C940	G945	A946					
U684	G685	G690	G691	U697	A702	G703	A706	U707	A712	G713	A715	A718	C719	C720	G722	C723	G724	G725	A728	G731	C732	G733	G734	C735	C736	C737	C738	C739	G742	A743	A747	G748	A749	C750	U751	G752	G755	G756	U757	C758	G764	U765	A766	U767	A768	G769	C770							
G771	U772	G773	A777	G778	C779	A782	G792	U793	A794	C795	C796	G803	U804	C805	C806	A807	G812	U813	A814	A815	A816	C817	G818	A819	U820	C821	C826	C736	C827	A831	C832	U835	C836	U837	C840	C841	U842	U843	C844	A845	G846	U850	C851	U855	C856	C857	G858	A860						
G599	A600	A601	A602	A607	A608	C613	C620	A621	A622	C623	G624	A635	A639	U640	G642	C634	A635	U652	A653	A654	U655	C656	G639	U641	A642	C643	U644	G650	C651	C652	U652	U653	U657	C658	C660	G661	A665	G666	G667	G668	G669	A673	A675	A676	U677	A696	C679							
G515	U516	G517	C518	C519	A520	C528	G529	U530	U531	A532	A533	U534	A535	A539	U540	G541	C545	A546	A547	U552	A553	A554	U555	C556	G557	G558	A559	A560	U561	U562	A563	C564	U565	U566	C569	G570	U571	A572	A573	A574	G575	C576	G577	C578	A579	C580	G581	U593	U594	A595	A596	U597	U598	
U427	G428	U429	A430	A431	A432	G433	U434	U437	U438	U439	C440	G445	A448	G452	G453	G454	G455	U458	A459	A460	A461	G462	U467	U468	A478	U479	U480	C483	G484	U485	U486	C492	A493	G494	G497	A498	G499	C501	A502	G505	G506	U509	A510	C511	U512	G425	C514							
U273	G276	A279	C280	G281	C284	C285	G289	C290	U291	U296	G297	A298	G299	A300	G301	G302	A303	U304	G305	C308	A309	G310	C314	A315	C316	U317	C235	A236	U323	G324	A325	G326	A327	C328	G332	U333	C334	C335	A336	G337	A338	U343	A344	G347	G348	A349	C350	G351	C352	A353				
G354	C355	A356	G357	U358	G359	G362	A363	A366	U367	U368	G369	C372	G376	G377	G378	C379	G380	G384	C385	C386	U387	A389	U390	G391	C392	A393	A397	C401	G402	U405	G406	U407	A408	U409	G410	G413	A414	A415	G416	G417	C418	C419	U420	U421	G422	G423	G424	U426						



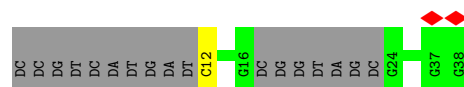
- Molecule 54: mRNA



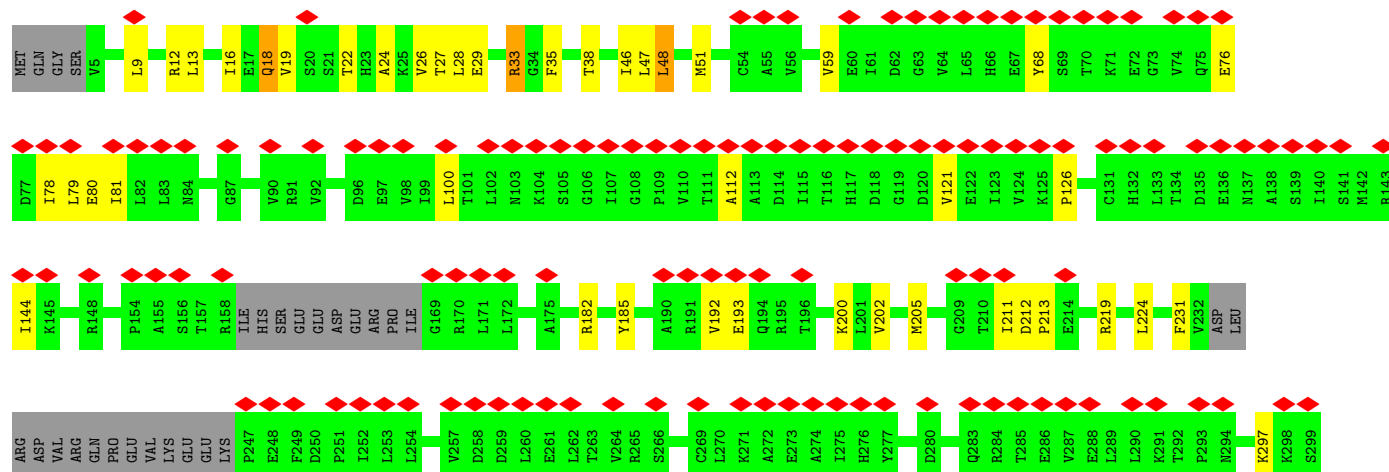
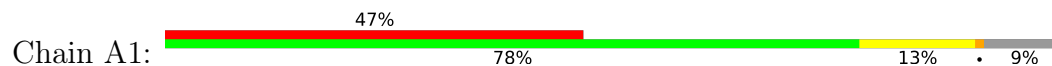
- Molecule 55: template DNA strand

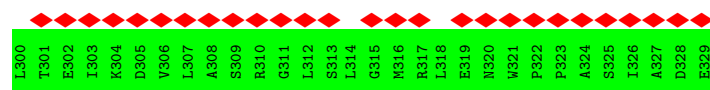


- Molecule 56: non-template DNA strand

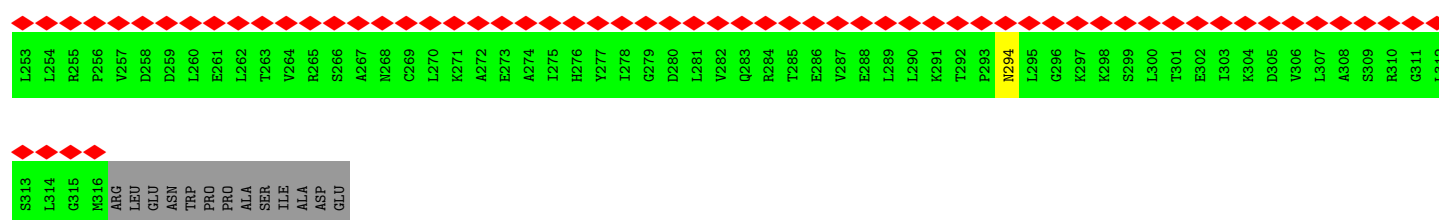
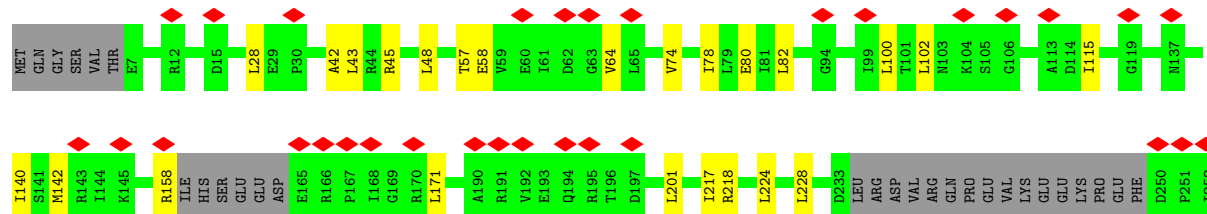
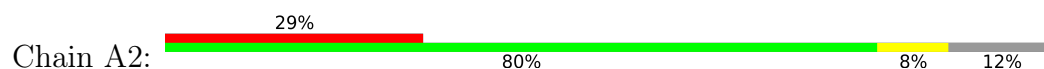


- Molecule 57: DNA-directed RNA polymerase subunit alpha

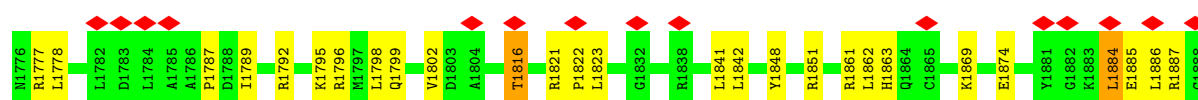
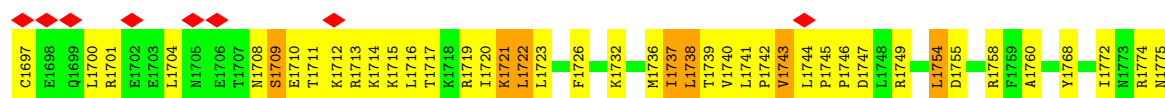
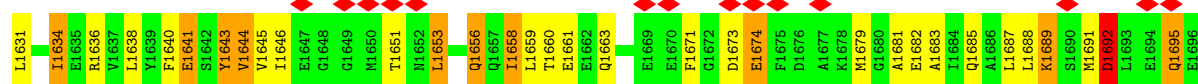
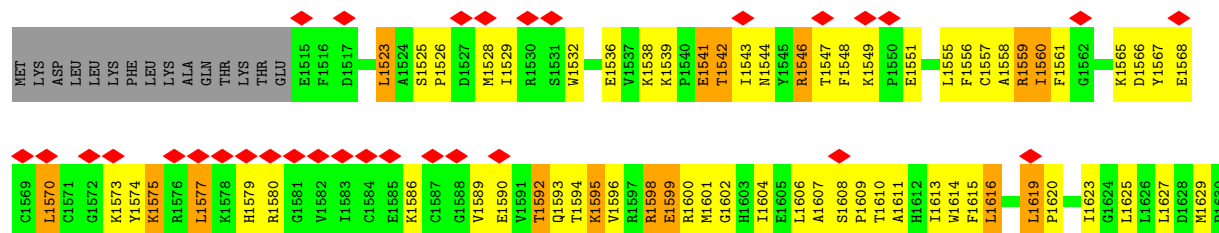


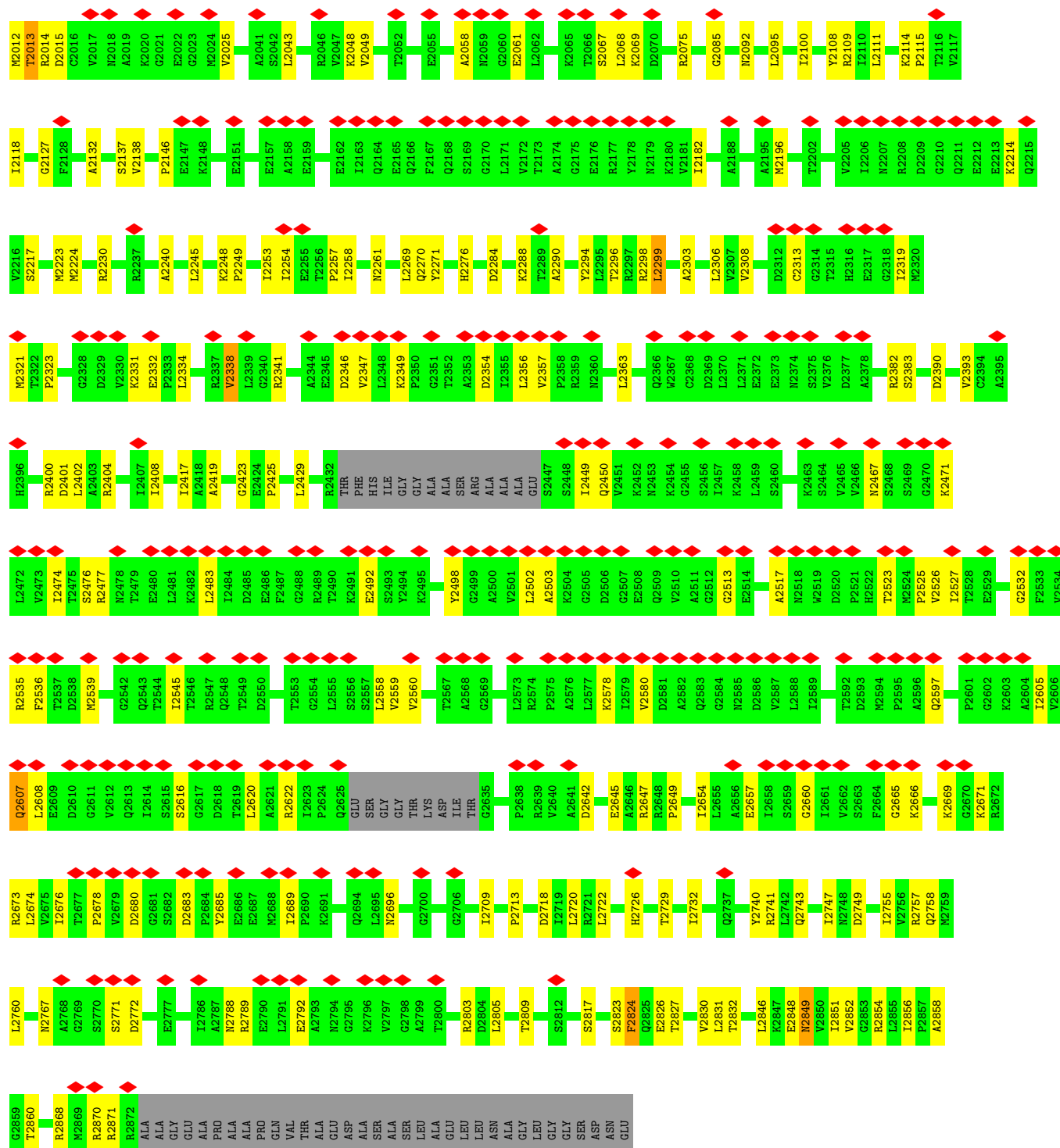


• Molecule 57: DNA-directed RNA polymerase subunit alpha

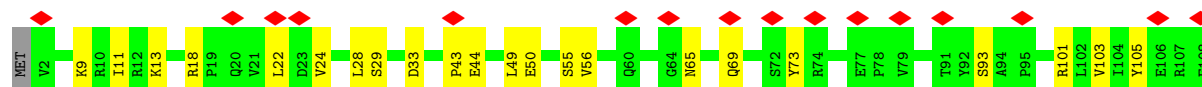
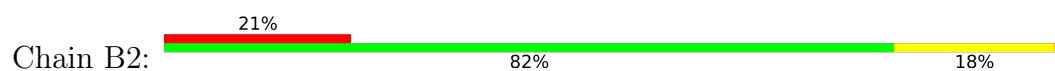


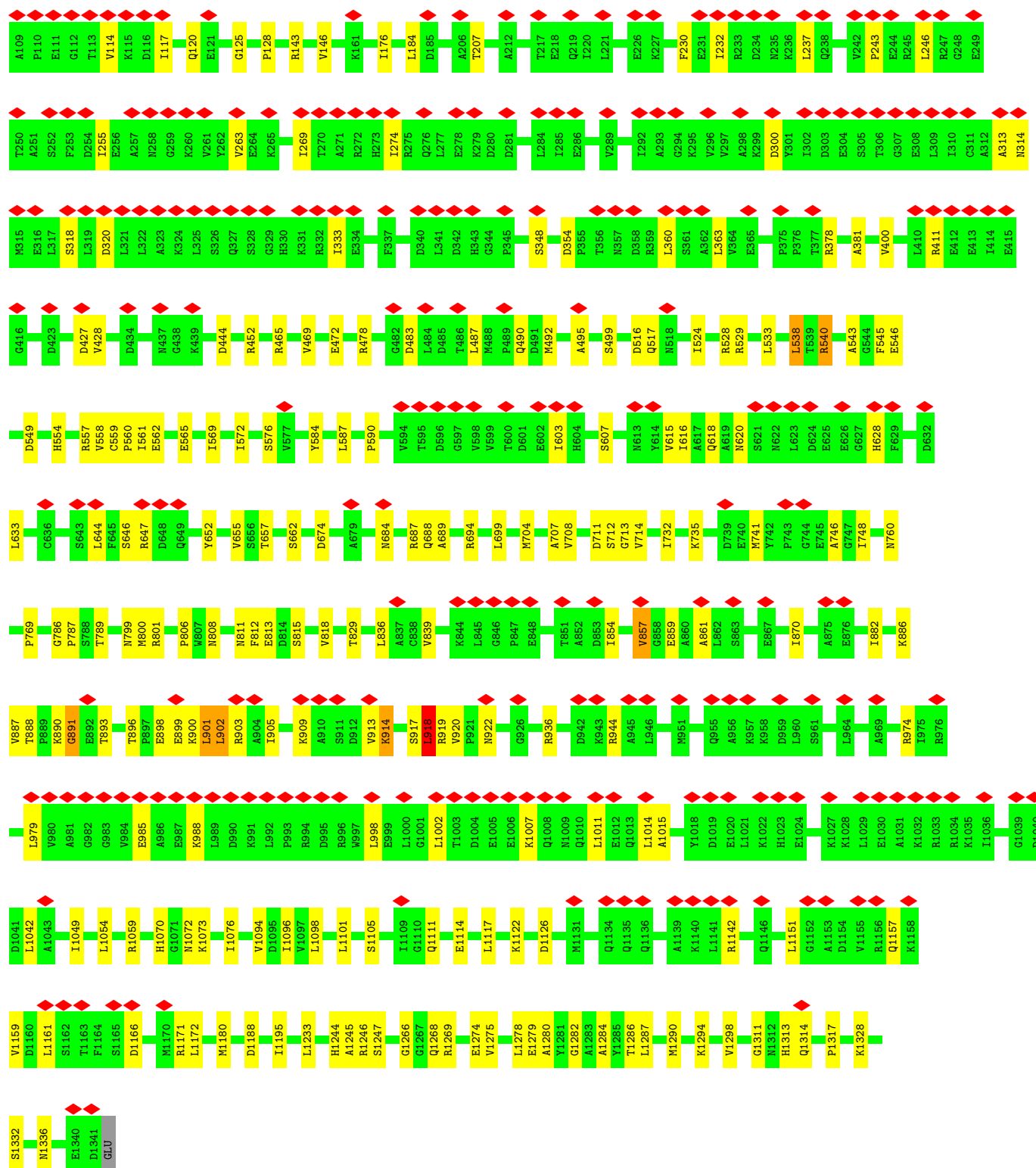
• Molecule 58: DNA-directed RNA polymerase subunit beta'



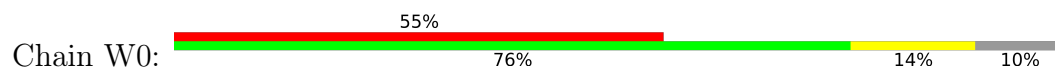


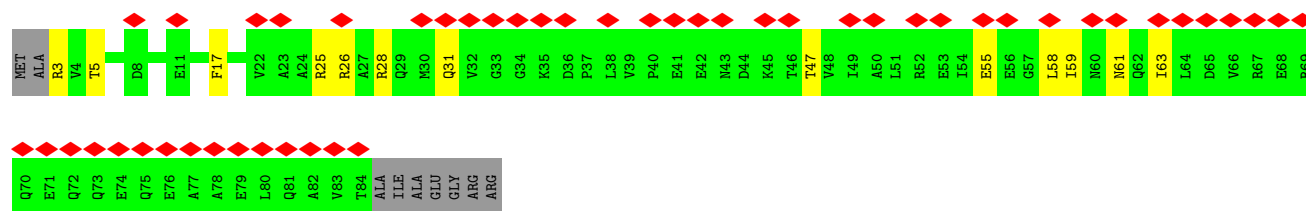
• Molecule 59: DNA-directed RNA polymerase subunit beta



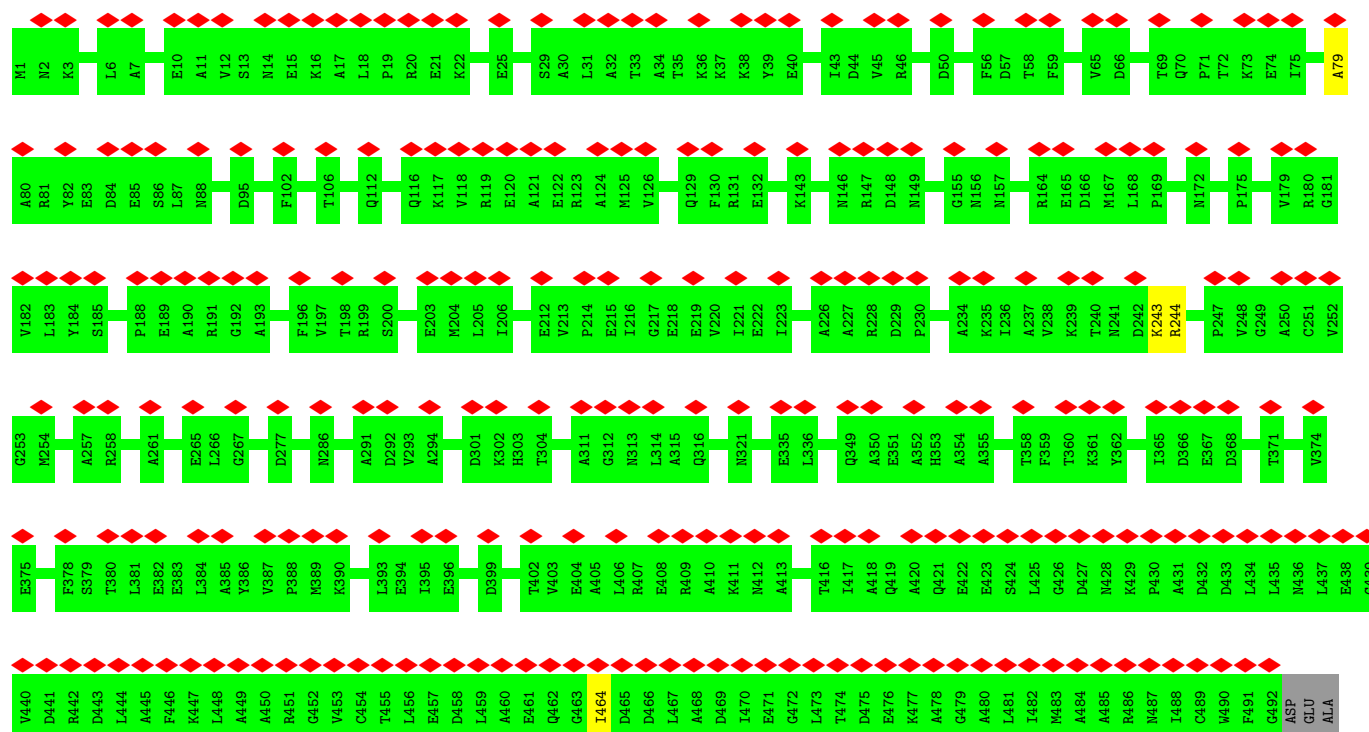


• Molecule 60: DNA-directed RNA polymerase subunit omega

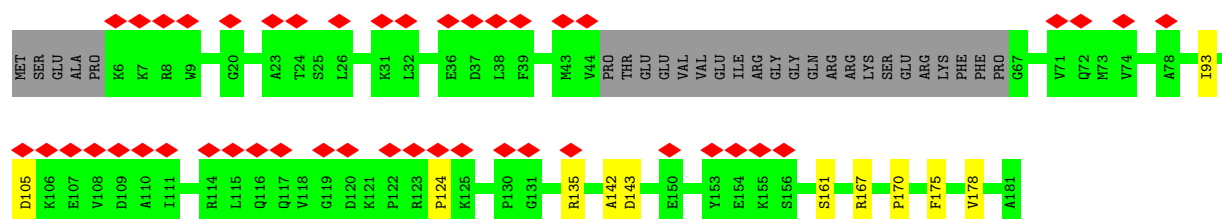
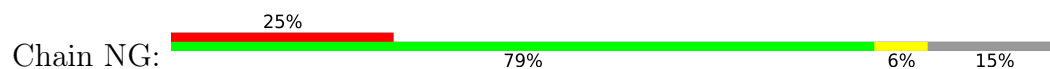




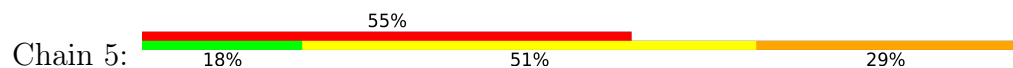
• Molecule 61: Transcription termination/antitermination protein NusA



• Molecule 62: Transcription termination/antitermination protein NusG

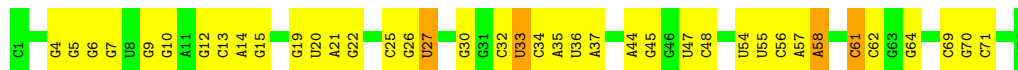


• Molecule 63: tRNA(Phe)

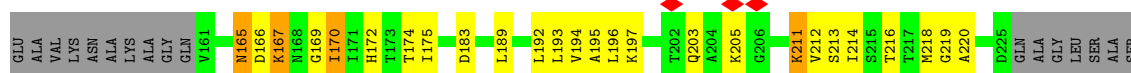
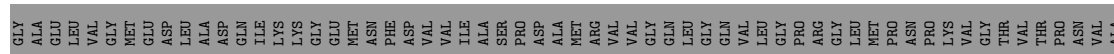
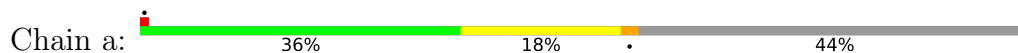




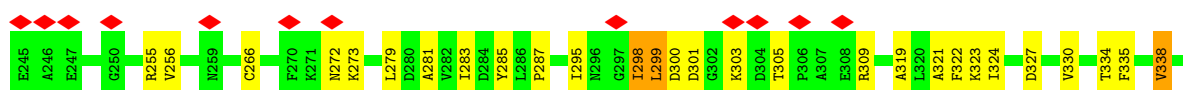
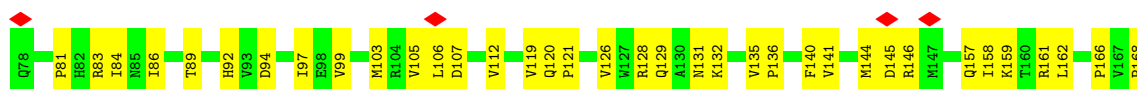
• Molecule 64: tRNA(fMet)

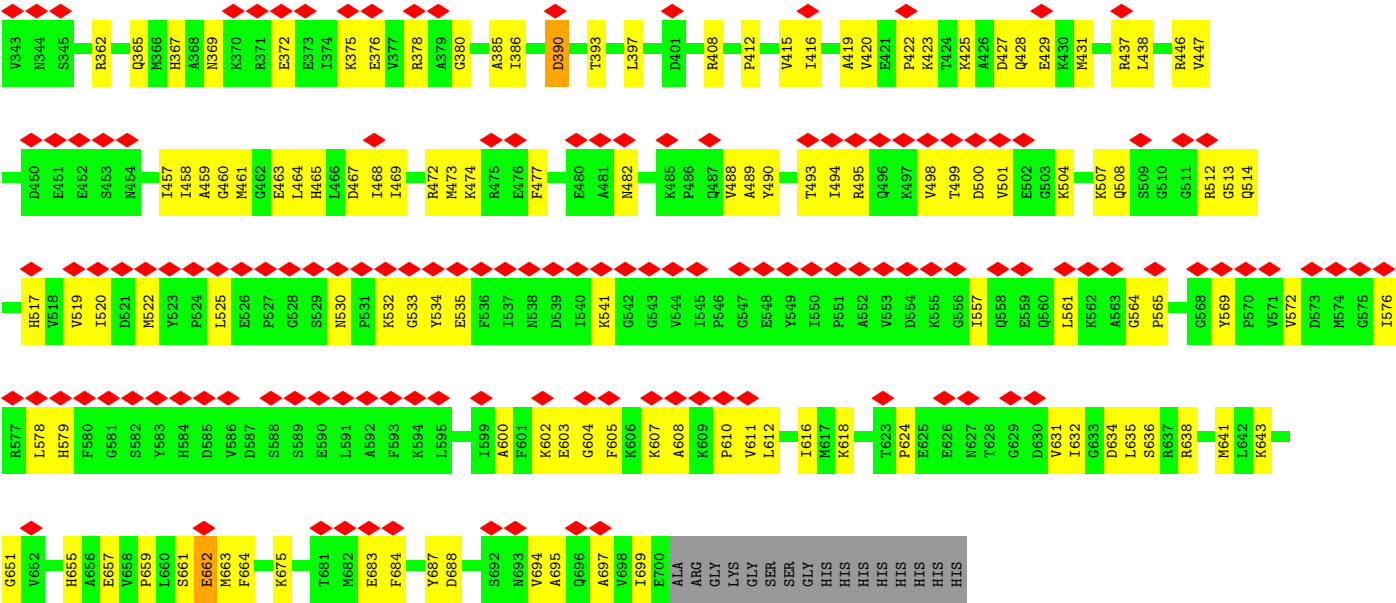


• Molecule 65: Large ribosomal subunit protein uL1

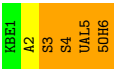


• Molecule 66: Elongation factor G





● Molecule 67: Viomycin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	569815	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	0.168	Depositor
Minimum map value	-0.079	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: GDP, KBE, 5OH, MG, DPP, UAL, PO4

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	0.25	0/362	0.73	0/485
2	B	0.37	0/450	0.80	2/599 (0.3%)
3	C	0.32	0/416	0.61	0/554
4	D	0.47	0/380	0.95	0/498
5	E	0.47	0/513	0.80	0/676
6	F	0.41	0/303	0.79	0/397
7	G	0.39	0/1735	0.82	0/2338
8	H	0.42	0/1651	0.80	0/2225
9	I	0.28	0/1665	0.76	1/2227 (0.0%)
10	J	0.46	0/1169	0.80	0/1573
11	K	0.41	0/835	0.90	3/1128 (0.3%)
12	L	0.42	0/1195	0.82	2/1602 (0.1%)
13	M	0.31	0/989	0.75	0/1326
14	N	0.29	0/1034	0.74	0/1375
15	O	0.56	0/796	0.81	0/1077
16	P	0.42	0/885	0.76	0/1195
17	Q	0.43	0/969	0.81	0/1300
18	R	0.28	0/892	0.70	0/1193
19	S	0.28	0/817	0.68	1/1088 (0.1%)
20	T	0.37	0/722	0.74	0/964
21	U	0.30	0/659	0.63	0/884
22	V	0.33	0/657	0.72	0/881
23	W	0.28	0/544	0.69	0/731
24	X	0.28	0/652	0.64	0/877
25	Y	0.26	0/671	0.64	2/888 (0.2%)
26	Z	0.56	0/550	1.09	1/728 (0.1%)
27	b	0.49	0/2121	0.82	0/2852
28	c	0.45	0/1586	0.77	0/2134
29	d	0.40	0/1571	0.80	3/2113 (0.1%)
30	e	0.30	0/1434	0.66	0/1926
31	f	0.29	0/1343	0.61	0/1816
32	g	0.34	0/1122	0.77	3/1515 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	0.39	0/1046	0.80	1/1410 (0.1%)
34	j	0.46	0/1152	0.72	0/1551
35	k	0.42	0/947	0.91	1/1268 (0.1%)
36	l	0.41	1/1054 (0.1%)	0.80	2/1403 (0.1%)
37	m	0.40	0/1093	0.81	2/1460 (0.1%)
38	n	0.54	1/973 (0.1%)	0.88	0/1301
39	o	0.32	0/902	0.68	0/1209
40	p	0.39	0/929	0.72	2/1242 (0.2%)
41	q	0.43	0/960	0.72	0/1278
42	r	0.38	0/829	0.78	1/1107 (0.1%)
43	s	0.52	0/864	0.83	0/1156
44	t	0.48	0/744	0.81	1/994 (0.1%)
45	u	0.33	0/787	0.74	2/1051 (0.2%)
46	v	0.35	0/766	0.66	0/1025
47	w	0.40	0/582	0.80	2/769 (0.3%)
48	x	0.62	0/635	1.16	5/848 (0.6%)
49	y	0.28	0/510	0.71	0/677
50	z	0.36	0/453	0.76	1/605 (0.2%)
51	1	0.59	0/69796	0.60	16/108888 (0.0%)
52	2	0.60	0/2872	0.55	1/4479 (0.0%)
53	3	0.60	0/36963	0.57	5/57662 (0.0%)
54	4	0.58	0/764	0.77	0/1183
55	8	0.56	0/599	0.70	1/919 (0.1%)
56	9	0.50	0/468	0.55	0/719
57	A1	0.55	0/2106	0.82	0/2868
57	A2	0.49	0/2048	0.75	0/2786
58	B1	0.56	5/10510 (0.0%)	0.74	8/14196 (0.1%)
59	B2	0.45	0/10714	0.66	0/14459
60	W0	0.30	0/652	0.61	0/879
61	NA	0.76	0/2431	1.22	0/3385
62	NG	1.15	0/756	1.04	0/1048
63	5	0.59	0/1812	0.90	3/2823 (0.1%)
64	6	0.60	0/1832	0.59	0/2855
65	a	0.47	0/1020	0.83	0/1370
66	0	0.39	0/5501	0.72	3/7446 (0.0%)
67	h	3.20	2/11 (18.2%)	0.74	0/13
All	All	0.54	9/196769 (0.0%)	0.67	75/289497 (0.0%)

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	h	3	SER	CA-C	-6.72	1.38	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	h	4	SER	CA-C	-6.31	1.39	1.52
38	n	66	ALA	CA-C	-6.09	1.43	1.52
58	B1	2849	ASN	CG-ND2	-5.31	1.22	1.33
58	B1	2607	GLN	CD-OE1	5.19	1.33	1.23

The worst 5 of 75 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	92	PRO	N-CA-C	-10.49	98.46	113.47
51	1	1020	A	C2'-C3'-O3'	7.34	120.51	109.50
48	x	11	PRO	N-CA-C	-7.32	99.55	111.77
51	1	2425	A	O3'-P-O5'	-6.89	93.66	104.00
12	L	82	SER	N-CA-C	6.89	116.41	108.49

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	355	0	353	10	0
2	B	444	0	461	15	0
3	C	409	0	440	17	0
4	D	377	0	418	17	0
5	E	504	0	574	16	0
6	F	302	0	341	14	0
7	G	1704	0	1732	46	0
8	H	1624	0	1699	45	0
9	I	1643	0	1710	41	0
10	J	1156	0	1199	38	0
11	K	817	0	808	26	0
12	L	1181	0	1240	46	0
13	M	979	0	1034	30	0
14	N	1022	0	1070	55	0
15	O	786	0	828	32	0
16	P	869	0	878	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	Q	955	0	1019	34	0
18	R	883	0	944	23	0
19	S	805	0	847	36	0
20	T	714	0	737	16	0
21	U	649	0	666	21	0
22	V	648	0	691	18	0
23	W	535	0	552	15	0
24	X	637	0	665	18	0
25	Y	665	0	714	21	0
26	Z	544	0	579	16	0
27	b	2082	0	2157	73	0
28	c	1565	0	1616	57	0
29	d	1552	0	1619	50	0
30	e	1410	0	1447	43	0
31	f	1323	0	1374	32	0
32	g	1111	0	1148	31	0
33	i	1032	0	1088	36	0
34	j	1129	0	1162	31	0
35	k	938	0	1012	20	0
36	l	1045	0	1117	29	0
37	m	1074	0	1157	31	0
38	n	960	0	1000	34	0
39	o	892	0	923	20	0
40	p	917	0	965	23	0
41	q	947	0	1022	22	0
42	r	816	0	839	22	0
43	s	857	0	922	19	0
44	t	738	0	807	15	0
45	u	779	0	834	22	0
46	v	753	0	780	14	0
47	w	575	0	592	21	0
48	x	625	0	655	22	0
49	y	509	0	543	9	0
50	z	449	0	491	10	0
51	1	62317	0	31346	1368	0
52	2	2568	0	1303	58	0
53	3	33012	0	16618	720	0
54	4	689	0	344	6	0
55	8	539	0	305	28	0
56	9	417	0	224	1	0
57	A1	2088	0	1895	25	0
57	A2	2029	0	1864	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	B1	10353	0	10548	322	0
59	B2	10546	0	10550	160	0
60	W0	650	0	658	11	0
61	NA	2432	0	1171	5	0
62	NG	758	0	334	10	0
63	5	1622	0	821	31	0
64	6	1640	0	837	27	0
65	a	1013	0	1081	41	0
66	0	5399	0	5363	152	0
67	h	48	0	40	5	0
68	B1	1	0	0	0	0
69	0	28	0	12	1	0
70	0	5	0	0	0	0
All	All	183439	0	132783	3774	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 12.

The worst 5 of 3774 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:92:PRO:HA	12:L:95:ARG:HE	1.12	1.13
53:3:112:G:H21	53:3:354:G:H5'	1.16	1.11
51:1:1060:U:H4'	51:1:1061:U:H5'	1.32	1.09
51:1:2061:G:H2'	51:1:2501:C:O2'	1.52	1.09
50:z:37:ARG:HH12	51:1:929:U:H5'	1.12	1.08

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	44/70 (63%)	38 (86%)	6 (14%)	0	100	100
2	B	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
3	C	48/55 (87%)	37 (77%)	11 (23%)	0	100	100
4	D	44/46 (96%)	35 (80%)	9 (20%)	0	100	100
5	E	62/65 (95%)	48 (77%)	13 (21%)	1 (2%)	7	36
6	F	36/38 (95%)	29 (81%)	7 (19%)	0	100	100
7	G	216/241 (90%)	182 (84%)	34 (16%)	0	100	100
8	H	204/233 (88%)	187 (92%)	17 (8%)	0	100	100
9	I	203/206 (98%)	170 (84%)	32 (16%)	1 (0%)	24	63
10	J	155/167 (93%)	129 (83%)	26 (17%)	0	100	100
11	K	98/135 (73%)	81 (83%)	17 (17%)	0	100	100
12	L	149/179 (83%)	130 (87%)	19 (13%)	0	100	100
13	M	127/130 (98%)	111 (87%)	16 (13%)	0	100	100
14	N	125/130 (96%)	110 (88%)	15 (12%)	0	100	100
15	O	96/103 (93%)	82 (85%)	14 (15%)	0	100	100
16	P	114/129 (88%)	104 (91%)	10 (9%)	0	100	100
17	Q	121/124 (98%)	97 (80%)	23 (19%)	1 (1%)	16	53
18	R	112/118 (95%)	99 (88%)	13 (12%)	0	100	100
19	S	98/101 (97%)	86 (88%)	12 (12%)	0	100	100
20	T	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
21	U	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
22	V	78/84 (93%)	69 (88%)	9 (12%)	0	100	100
23	W	63/75 (84%)	59 (94%)	4 (6%)	0	100	100
24	X	77/92 (84%)	70 (91%)	7 (9%)	0	100	100
25	Y	83/87 (95%)	77 (93%)	6 (7%)	0	100	100
26	Z	63/71 (89%)	47 (75%)	16 (25%)	0	100	100
27	b	269/273 (98%)	227 (84%)	42 (16%)	0	100	100
28	c	207/209 (99%)	177 (86%)	30 (14%)	0	100	100
29	d	199/201 (99%)	182 (92%)	17 (8%)	0	100	100
30	e	175/179 (98%)	165 (94%)	10 (6%)	0	100	100
31	f	174/177 (98%)	157 (90%)	17 (10%)	0	100	100
32	g	147/149 (99%)	124 (84%)	23 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	i	139/142 (98%)	124 (89%)	15 (11%)	0	100	100
34	j	140/142 (99%)	120 (86%)	20 (14%)	0	100	100
35	k	120/123 (98%)	98 (82%)	22 (18%)	0	100	100
36	l	141/144 (98%)	117 (83%)	24 (17%)	0	100	100
37	m	134/136 (98%)	116 (87%)	18 (13%)	0	100	100
38	n	118/127 (93%)	104 (88%)	14 (12%)	0	100	100
39	o	114/117 (97%)	103 (90%)	11 (10%)	0	100	100
40	p	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
41	q	115/118 (98%)	108 (94%)	7 (6%)	0	100	100
42	r	101/103 (98%)	88 (87%)	13 (13%)	0	100	100
43	s	108/110 (98%)	92 (85%)	16 (15%)	0	100	100
44	t	91/100 (91%)	77 (85%)	14 (15%)	0	100	100
45	u	100/104 (96%)	83 (83%)	17 (17%)	0	100	100
46	v	92/94 (98%)	79 (86%)	13 (14%)	0	100	100
47	w	73/85 (86%)	63 (86%)	10 (14%)	0	100	100
48	x	75/78 (96%)	66 (88%)	9 (12%)	0	100	100
49	y	61/63 (97%)	61 (100%)	0	0	100	100
50	z	56/59 (95%)	50 (89%)	6 (11%)	0	100	100
57	A1	295/329 (90%)	275 (93%)	20 (7%)	0	100	100
57	A2	282/329 (86%)	271 (96%)	11 (4%)	0	100	100
58	B1	1329/1407 (94%)	1207 (91%)	118 (9%)	4 (0%)	36	72
59	B2	1338/1342 (100%)	1208 (90%)	124 (9%)	6 (0%)	30	67
60	W0	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
61	NA	490/495 (99%)	476 (97%)	14 (3%)	0	100	100
62	NG	150/181 (83%)	134 (89%)	15 (10%)	1 (1%)	18	55
65	a	128/234 (55%)	105 (82%)	23 (18%)	0	100	100
66	0	695/716 (97%)	618 (89%)	72 (10%)	5 (1%)	18	55
67	h	2/6 (33%)	1 (50%)	1 (50%)	0	100	100
All	All	10486/11185 (94%)	9332 (89%)	1135 (11%)	19 (0%)	44	78

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
58	B1	1620	PRO
59	B2	43	PRO
59	B2	918	LEU
66	0	199	GLY
59	B2	888	THR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	42/62 (68%)	42 (100%)	0	100	100
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%)	35 (92%)	3 (8%)	11	32
5	E	51/52 (98%)	46 (90%)	5 (10%)	7	24
6	F	34/34 (100%)	33 (97%)	1 (3%)	37	58
7	G	180/199 (90%)	172 (96%)	8 (4%)	25	46
8	H	170/190 (90%)	162 (95%)	8 (5%)	23	45
9	I	172/173 (99%)	170 (99%)	2 (1%)	63	74
10	J	119/126 (94%)	113 (95%)	6 (5%)	22	43
11	K	87/116 (75%)	83 (95%)	4 (5%)	24	45
12	L	124/147 (84%)	121 (98%)	3 (2%)	43	63
13	M	104/105 (99%)	102 (98%)	2 (2%)	50	66
14	N	105/107 (98%)	105 (100%)	0	100	100
15	O	86/90 (96%)	78 (91%)	8 (9%)	8	26
16	P	89/99 (90%)	88 (99%)	1 (1%)	65	74
17	Q	103/104 (99%)	101 (98%)	2 (2%)	50	66
18	R	92/96 (96%)	91 (99%)	1 (1%)	65	74
19	S	83/84 (99%)	82 (99%)	1 (1%)	63	74
20	T	76/77 (99%)	76 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	U	65/65 (100%)	65 (100%)	0	100	100
22	V	74/78 (95%)	74 (100%)	0	100	100
23	W	56/65 (86%)	56 (100%)	0	100	100
24	X	70/79 (89%)	70 (100%)	0	100	100
25	Y	65/66 (98%)	65 (100%)	0	100	100
26	Z	55/61 (90%)	46 (84%)	9 (16%)	2	11
27	b	216/218 (99%)	212 (98%)	4 (2%)	50	66
28	c	164/164 (100%)	163 (99%)	1 (1%)	78	82
29	d	165/165 (100%)	160 (97%)	5 (3%)	36	57
30	e	148/150 (99%)	146 (99%)	2 (1%)	59	72
31	f	137/138 (99%)	136 (99%)	1 (1%)	76	80
32	g	114/114 (100%)	111 (97%)	3 (3%)	40	61
33	i	109/110 (99%)	109 (100%)	0	100	100
34	j	116/116 (100%)	113 (97%)	3 (3%)	40	61
35	k	103/104 (99%)	100 (97%)	3 (3%)	37	58
36	l	102/103 (99%)	100 (98%)	2 (2%)	48	66
37	m	109/109 (100%)	108 (99%)	1 (1%)	70	77
38	n	100/103 (97%)	98 (98%)	2 (2%)	48	66
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%)	89 (100%)	0	100	100
42	r	84/84 (100%)	84 (100%)	0	100	100
43	s	93/93 (100%)	87 (94%)	6 (6%)	15	37
44	t	80/84 (95%)	77 (96%)	3 (4%)	29	50
45	u	83/85 (98%)	82 (99%)	1 (1%)	63	74
46	v	78/78 (100%)	77 (99%)	1 (1%)	61	73
47	w	57/63 (90%)	57 (100%)	0	100	100
48	x	67/68 (98%)	65 (97%)	2 (3%)	36	57
49	y	55/55 (100%)	55 (100%)	0	100	100
50	z	48/49 (98%)	47 (98%)	1 (2%)	47	65
57	A1	185/286 (65%)	174 (94%)	11 (6%)	18	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	A2	186/286 (65%)	185 (100%)	1 (0%)	81	82
58	B1	1110/1168 (95%)	1021 (92%)	89 (8%)	11	31
59	B2	1150/1157 (99%)	1119 (97%)	31 (3%)	39	60
60	W0	70/75 (93%)	69 (99%)	1 (1%)	59	72
65	a	109/181 (60%)	98 (90%)	11 (10%)	7	23
66	0	574/588 (98%)	554 (96%)	20 (4%)	32	53
67	h	2/2 (100%)	2 (100%)	0	100	100
All	All	8120/8683 (94%)	7850 (97%)	270 (3%)	34	55

5 of 270 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
59	B2	909	LYS
60	W0	63	ILE
66	0	504	LYS
43	s	97	LEU
43	s	67	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 150 such sidechains are listed below:

Mol	Chain	Res	Type
58	B1	1968	HIS
66	0	276	GLN
58	B1	2737	GLN
59	B2	1268	GLN
22	V	46	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	1	2902/2904 (99%)	439 (15%)	6 (0%)
52	2	119/120 (99%)	18 (15%)	0
53	3	1538/1542 (99%)	193 (12%)	1 (0%)
54	4	31/56 (55%)	18 (58%)	4 (12%)
63	5	75/76 (98%)	45 (60%)	10 (13%)
64	6	76/77 (98%)	14 (18%)	0
All	All	4741/4775 (99%)	727 (15%)	21 (0%)

5 of 727 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	1	10	A
51	1	12	U
51	1	23	G
51	1	34	U
51	1	35	G

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
63	5	35	A
63	5	57	G
63	5	75	C
63	5	60	U
63	5	48	C

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	$\# Z > 2$
67	UAL	h	5	67	6,8,9	2.35	2 (33%)	4,9,11	1.88	1 (25%)
67	5OH	h	6	67	7,12,13	0.76	0	4,16,18	1.33	1 (25%)
67	KBE	h	1	67	8,8,9	0.59	0	6,8,10	1.19	0
67	DPP	h	2	67	4,5,6	0.50	0	1,5,7	0.05	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
67	UAL	h	5	67	-	0/3/7/9	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
67	5OH	h	6	67	-	0/2/18/20	0/1/1/1
67	KBE	h	1	67	-	0/7/7/8	-
67	DPP	h	2	67	-	0/2/4/6	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	h	5	UAL	C1-N1	-4.90	1.32	1.40
67	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(°)
67	h	5	UAL	O-C-CA	-3.31	121.25	125.39
67	h	6	5OH	CR-CB-CA	-2.38	110.09	112.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
67	h	5	UAL	1	0
67	h	6	5OH	3	0
67	h	2	DPP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
70	PO4	0	802	-	4,4,4	1.00	0	6,6,6	0.50	0
69	GDP	0	801	-	29,30,30	1.16	2 (6%)	45,47,47	1.88	8 (17%)

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
69	GDP	0	801	-	-	2/16/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
69	0	801	GDP	C5-C4	2.79	1.46	1.38
69	0	801	GDP	C6-N1	-2.53	1.34	1.38

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
69	0	801	GDP	C5-C4-N3	-5.99	118.85	128.39
69	0	801	GDP	C2-N3-C4	5.05	121.00	112.30
69	0	801	GDP	N9-C4-N3	4.47	134.88	125.95
69	0	801	GDP	C6-C5-N7	3.59	136.83	130.29
69	0	801	GDP	C4-C5-N7	-2.78	106.27	110.67

There are no chirality outliers.

All (2) torsion outliers are listed below:

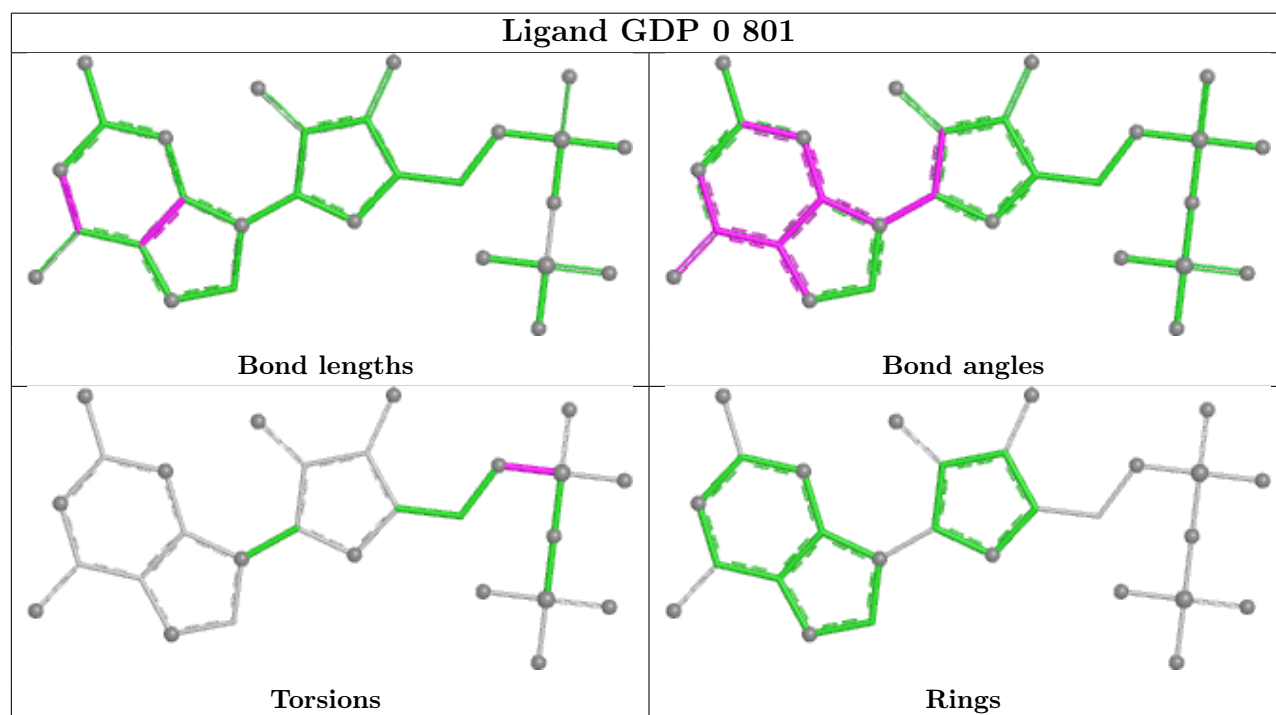
Mol	Chain	Res	Type	Atoms
69	0	801	GDP	C5'-O5'-PA-O3A
69	0	801	GDP	C5'-O5'-PA-O1A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
69	0	801	GDP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

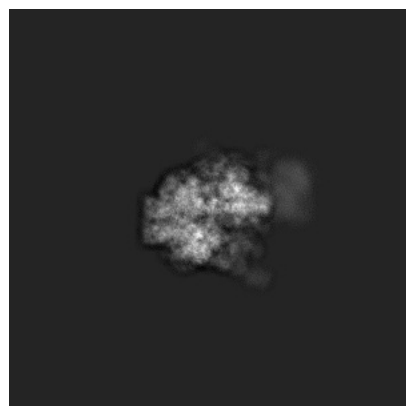
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39170. These allow visual inspection of the internal detail of the map and identification of artifacts.

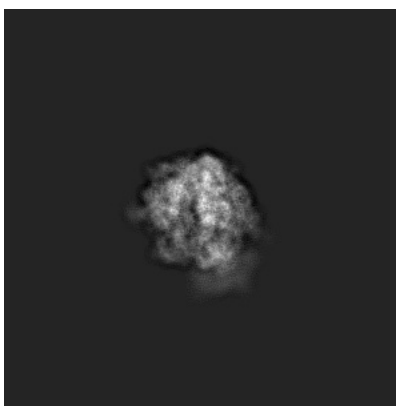
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

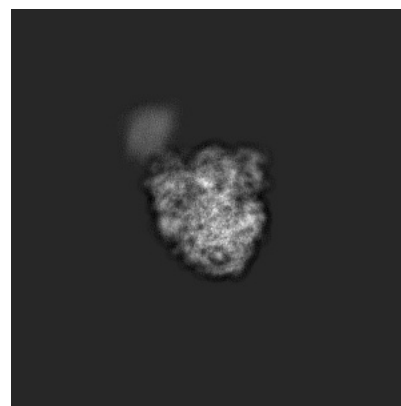
6.1.1 Primary map



X

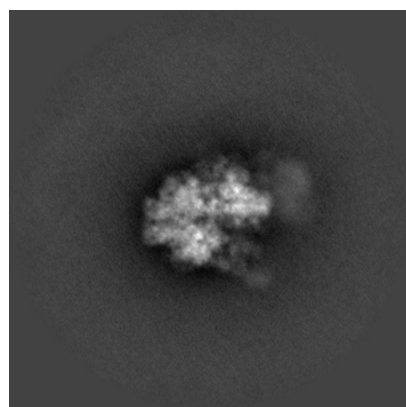


Y

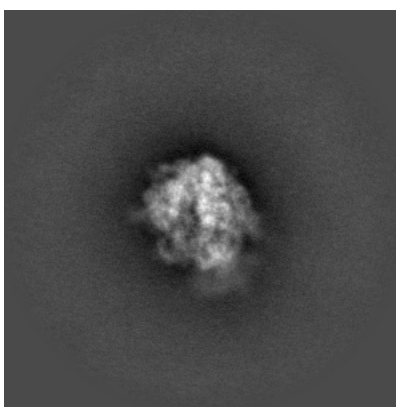


Z

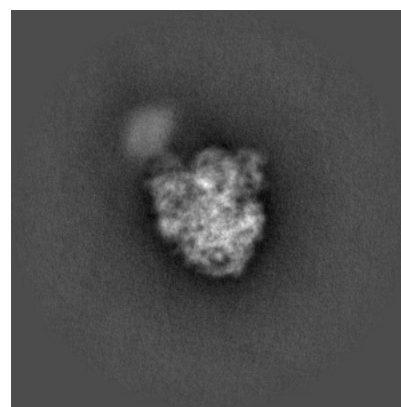
6.1.2 Raw map



X



Y

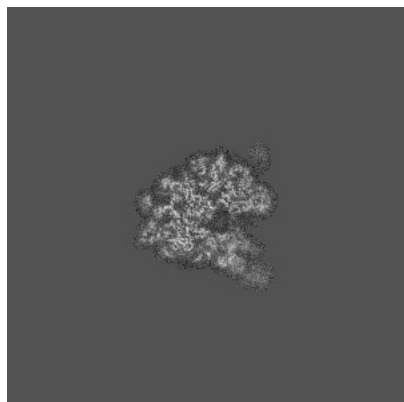


Z

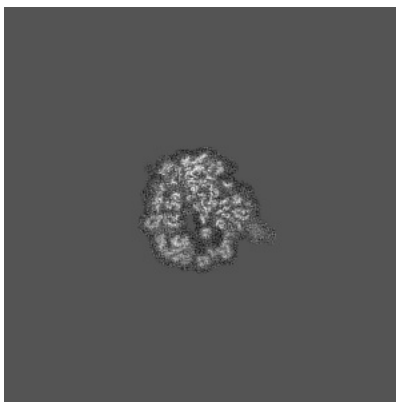
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

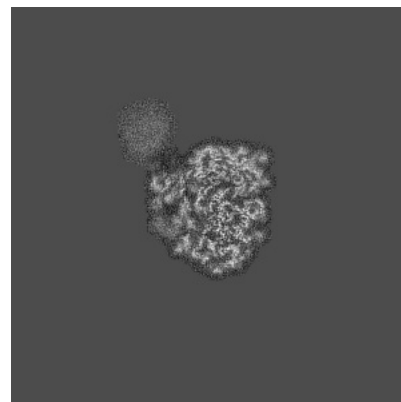
6.2.1 Primary map



X Index: 240

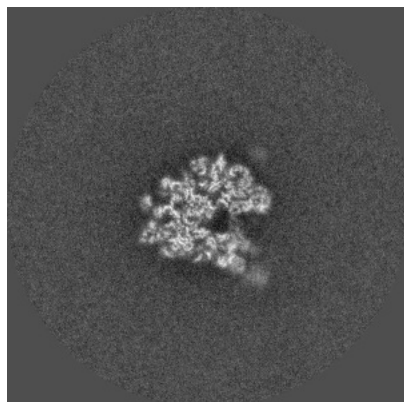


Y Index: 240

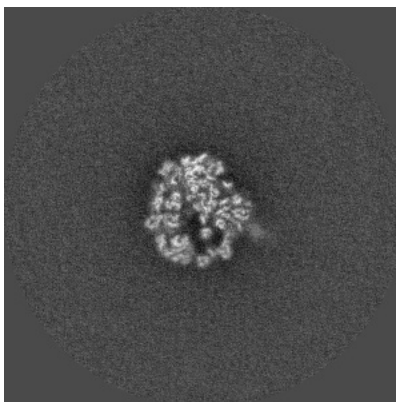


Z Index: 240

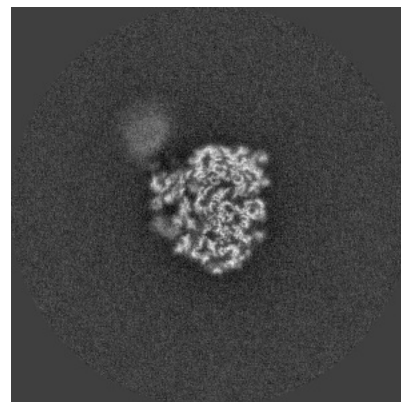
6.2.2 Raw map



X Index: 240



Y Index: 240

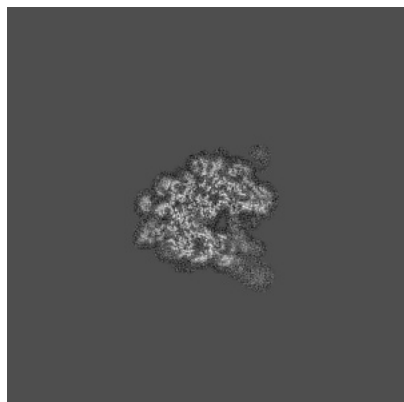


Z Index: 240

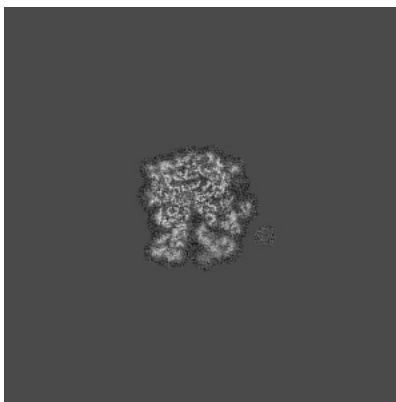
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

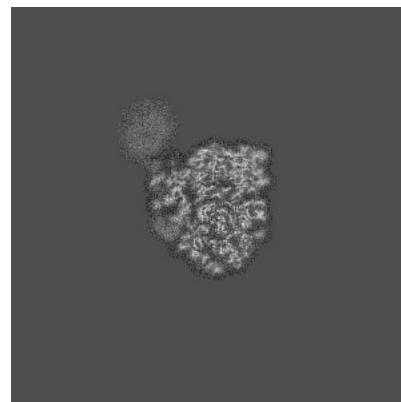
6.3.1 Primary map



X Index: 243

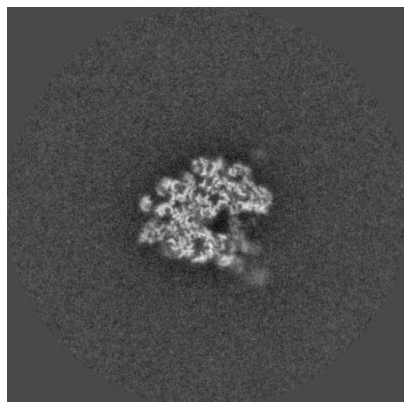


Y Index: 224

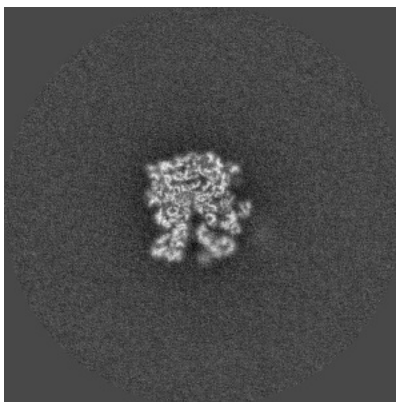


Z Index: 243

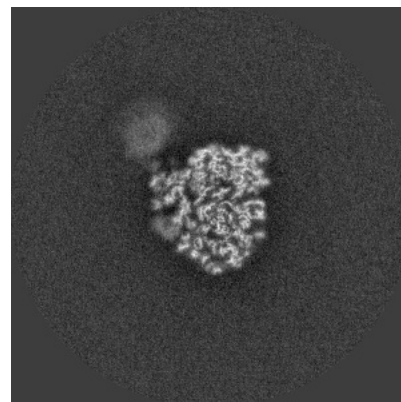
6.3.2 Raw map



X Index: 243



Y Index: 224

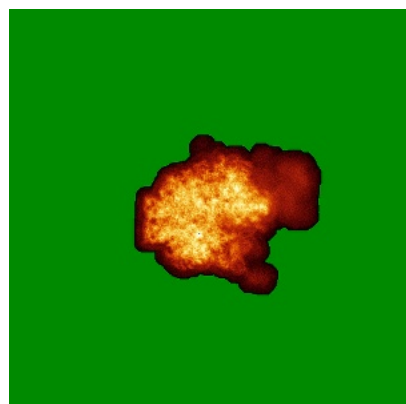


Z Index: 242

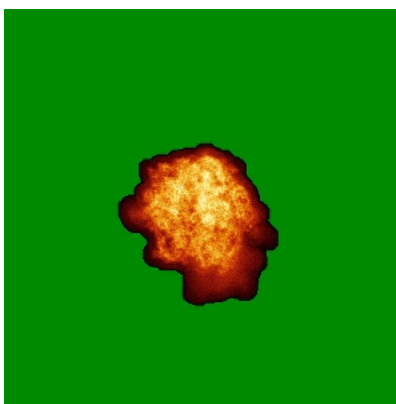
The images above show the largest variance slices of the map in three orthogonal directions.

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

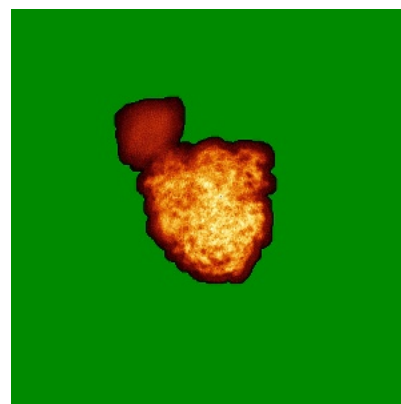
6.4.1 Primary map



X

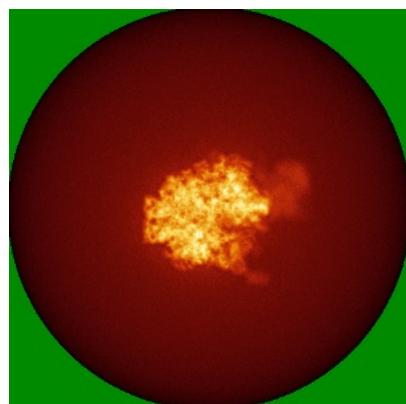


Y

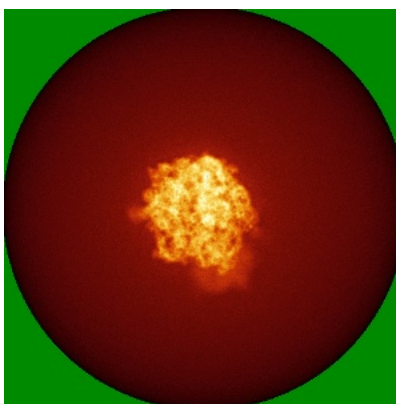


Z

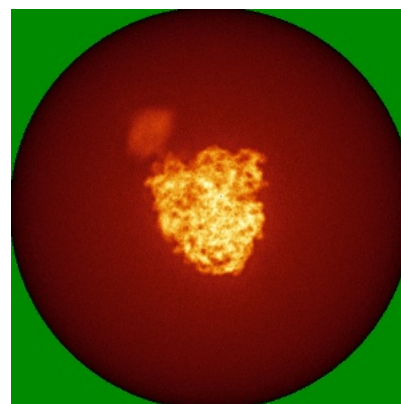
6.4.2 Raw map



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](#)

This section was not generated.

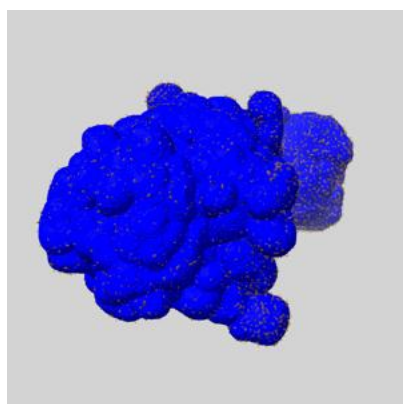
6.6 Mask visualisation [i](#)

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

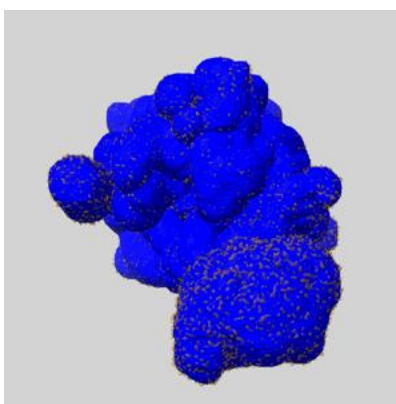
A mask typically either:

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

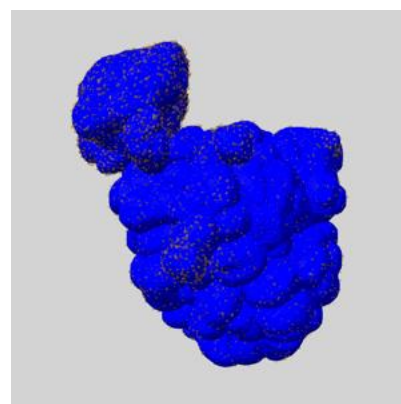
6.6.1 emd_39170_msk_1.map [i](#)



X



Y

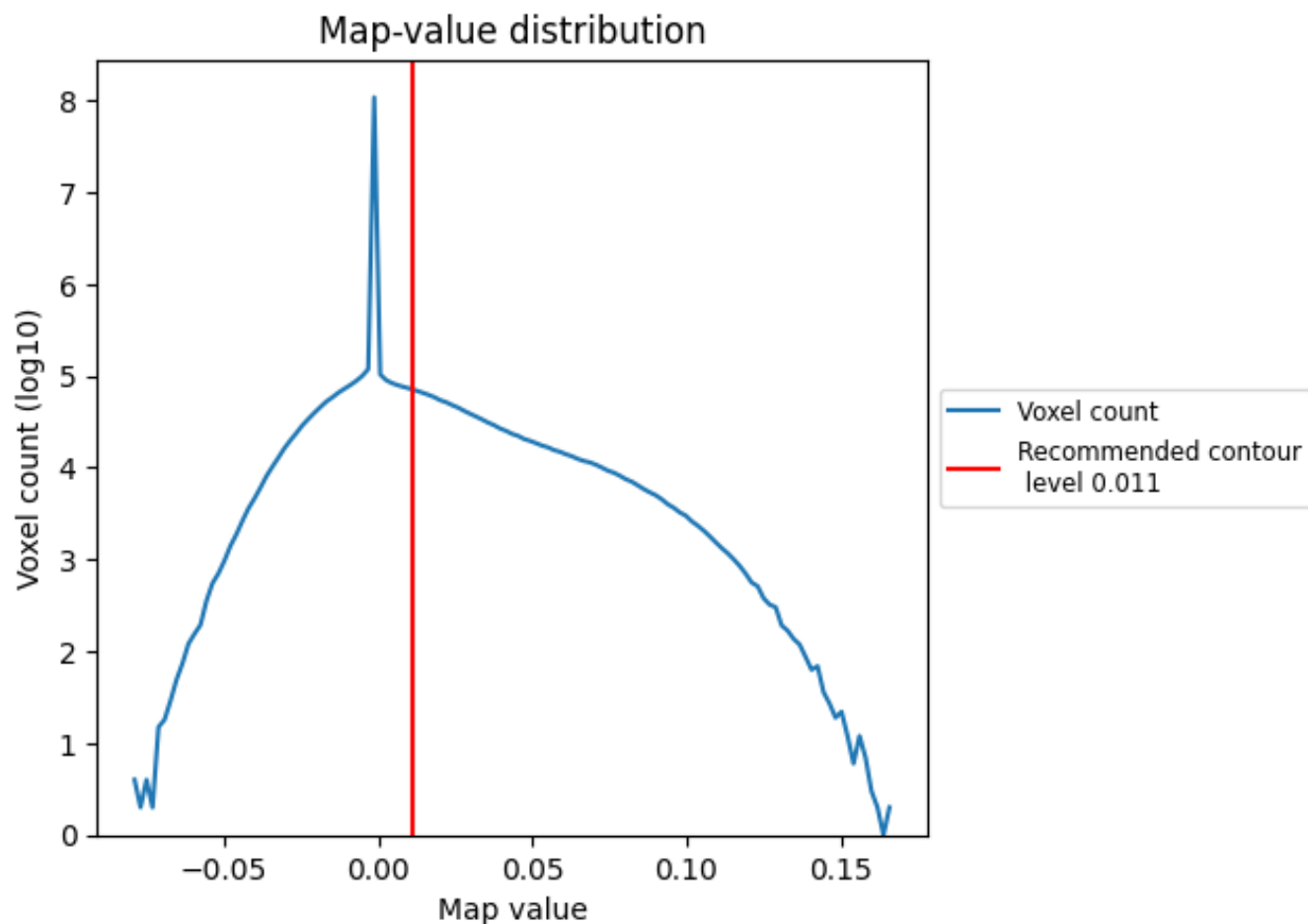


Z

7 Map analysis [i](#)

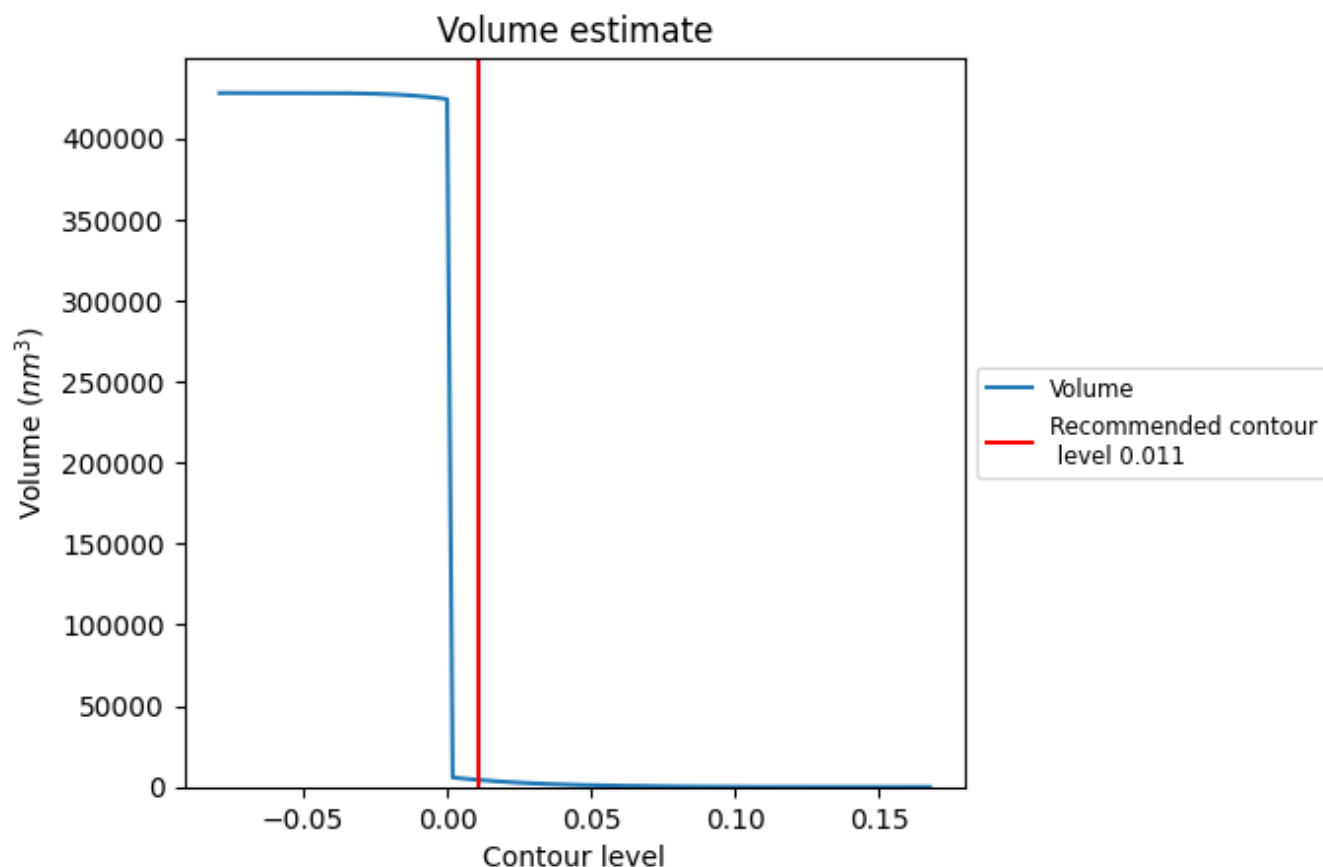
This section contains the results of statistical analysis of the map.

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.

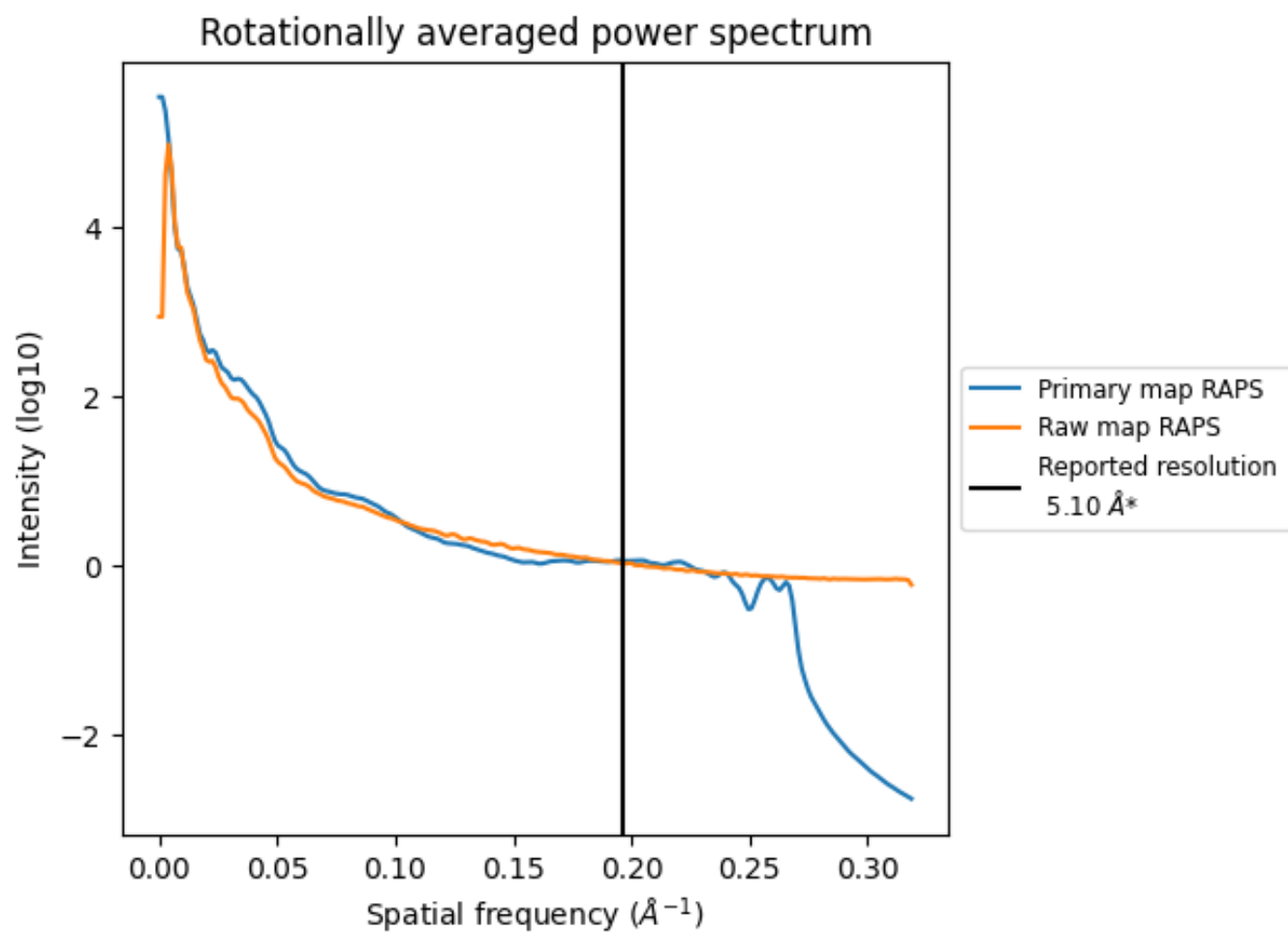
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4325 nm^3 ; this corresponds to an approximate mass of 3906 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 ⓘ

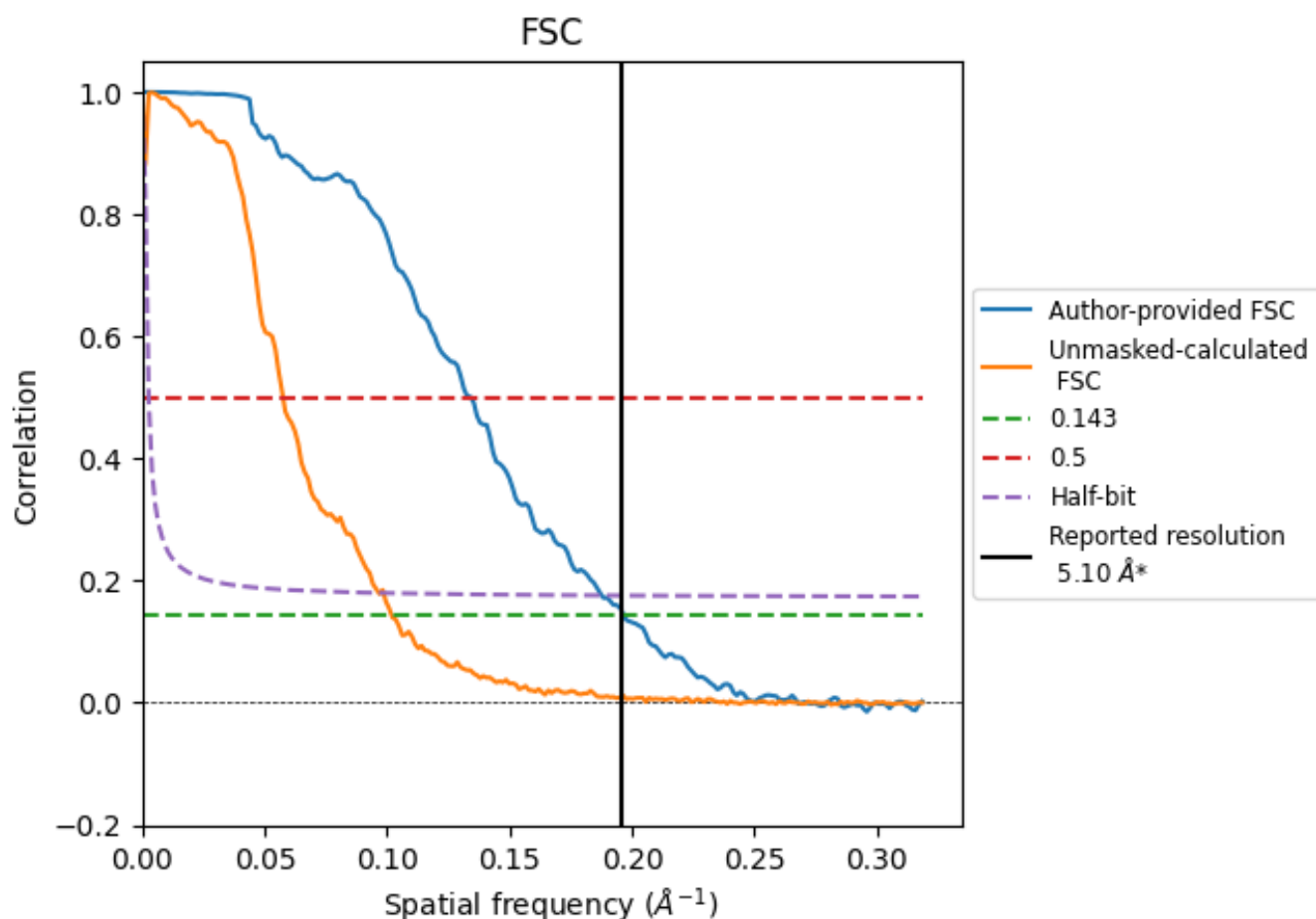


*Reported resolution corresponds to spatial frequency of 0.196 Å⁻¹

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 0.196 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.10	-	-
Author-provided FSC curve	5.08	7.45	5.33
Unmasked-calculated*	9.81	17.39	10.35

*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 9.81 differs from the reported value 5.1 by more than 10 %

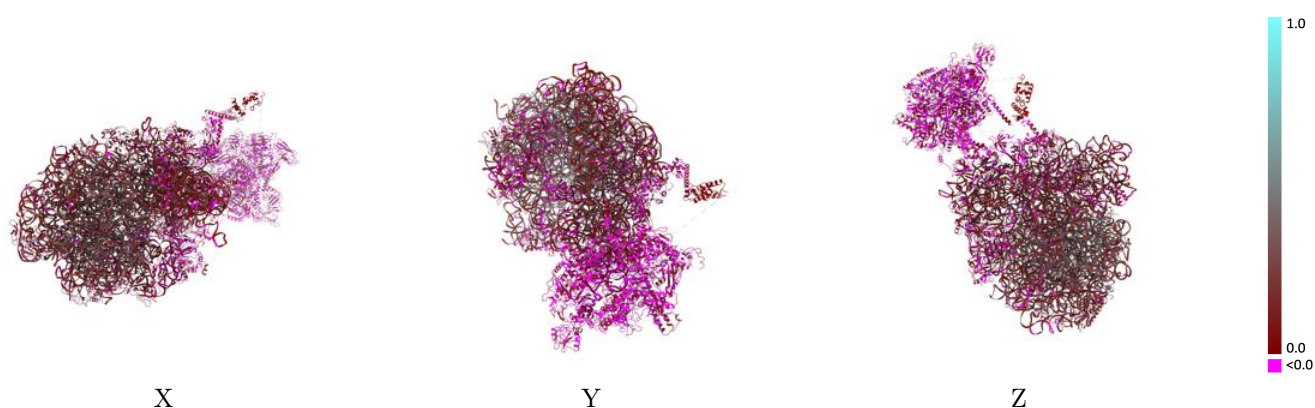
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-39170 and PDB model 8YDG. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)

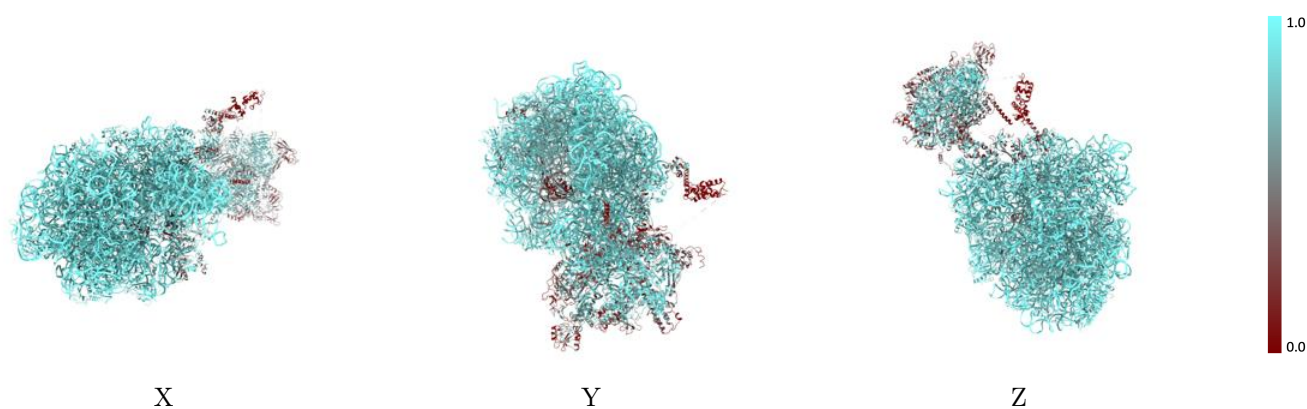
This section was not generated.

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



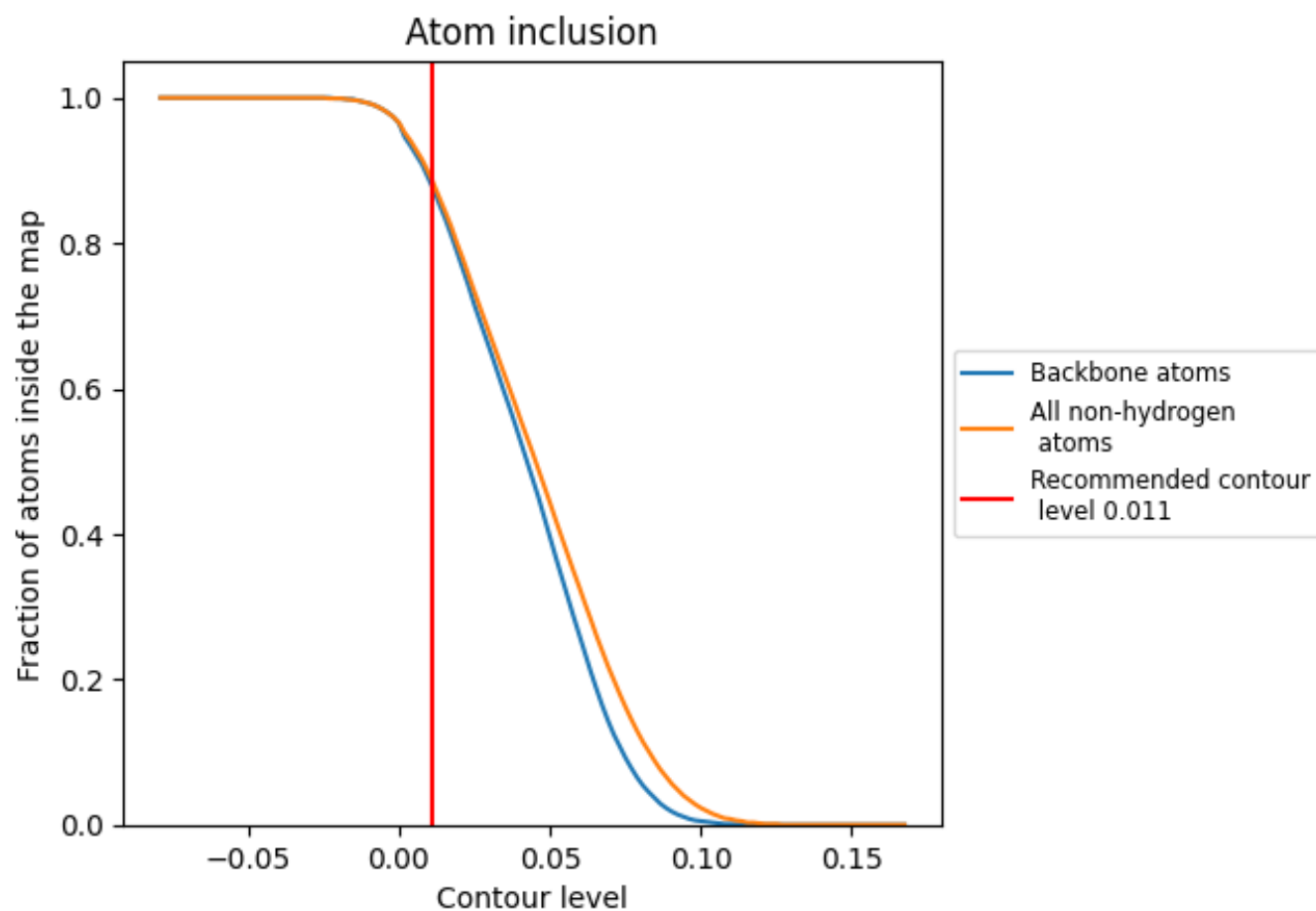
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 89% 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	 0.8870	 0.1560
0	 0.6070	 0.0450
1	 0.9840	 0.2390
2	 0.9710	 0.1000
3	 0.9780	 0.1870
4	 0.7850	 0.0670
5	 0.4280	 0.0330
6	 0.9550	 0.1580
8	 0.6810	 -0.0140
9	 0.7360	 -0.0020
A	 0.9060	 0.0170
A1	 0.4730	 -0.0040
A2	 0.6020	 0.0020
B	 0.9560	 0.2760
B1	 0.6400	 0.0040
B2	 0.6710	 -0.0030
C	 0.8750	 0.1090
D	 0.8840	 0.2500
E	 0.9020	 0.1820
F	 0.9420	 0.1670
G	 0.8950	 0.0980
H	 0.8830	 0.1170
I	 0.9110	 0.1280
J	 0.8820	 0.1200
K	 0.9420	 0.1390
L	 0.8820	 0.0870
M	 0.8820	 0.1210
N	 0.9000	 0.1030
NA	 0.4740	 0.0230
NG	 0.6540	 -0.0020
O	 0.9130	 0.0990
P	 0.9080	 0.1690
Q	 0.8750	 0.1790
R	 0.9050	 0.1250
S	 0.9110	 0.0900



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Chain	Atom inclusion	Q-score
T	 0.9300	 0.1750
U	 0.9090	 0.0880
V	 0.8970	 0.0760
W	 0.9480	 0.1620
W0	 0.3420	 -0.0220
X	 0.9030	 0.0820
Y	 0.9010	 0.0770
Z	 0.8080	 0.1150
a	 0.9140	 0.0330
b	 0.9100	 0.2580
c	 0.9420	 0.2500
d	 0.9120	 0.1440
e	 0.8640	 0.0450
f	 0.9070	 0.1010
g	 0.7650	 0.0760
h	 0.9580	 0.1870
i	 0.7690	 0.0220
j	 0.9230	 0.2090
k	 0.8890	 0.2590
l	 0.9030	 0.1370
m	 0.8780	 0.1670
n	 0.9440	 0.2600
o	 0.9590	 0.0520
p	 0.9220	 0.2160
q	 0.9440	 0.2380
r	 0.9540	 0.1830
s	 0.9090	 0.2450
t	 0.9180	 0.1720
u	 0.9530	 0.1550
v	 0.9320	 0.1060
w	 0.9250	 0.1310
x	 0.9300	 0.2100
y	 0.9480	 0.1440
z	 0.9060	 0.1510