



wwPDB EM Validation Summary Report ⓘ

Mar 11, 2025 – 11:31 PM EDT

PDB ID : 7M5D
EMDB ID : EMD-23673
Title : Cryo-EM structure of a non-rotated E.coli 70S ribosome in complex with RF3-GTP, RF1 and P-tRNA (state I)
Authors : Zhang, J.
Deposited on : 2021-03-23
Resolution : 2.80 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev117
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

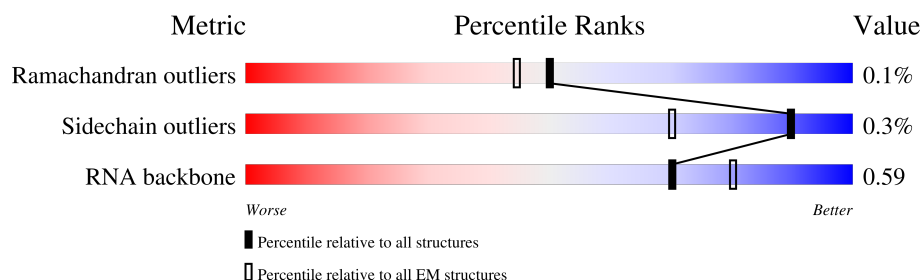
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.

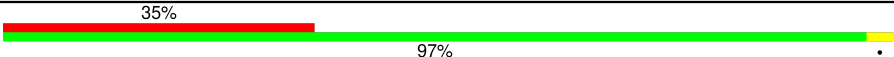
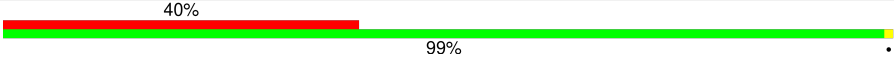
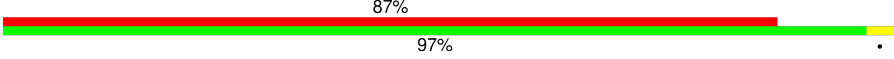
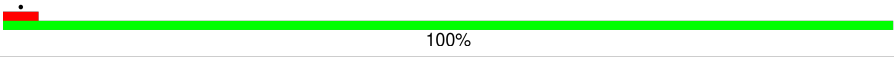
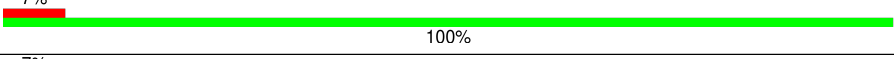
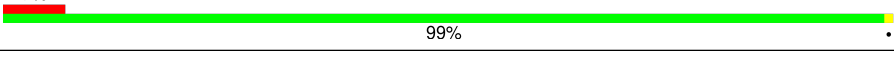
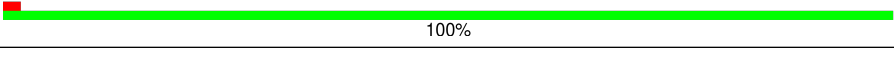
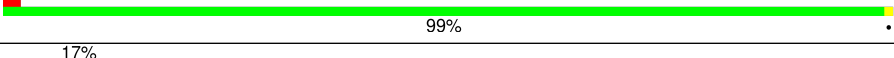
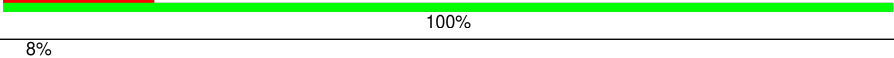
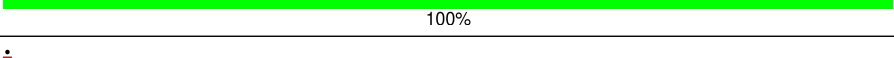
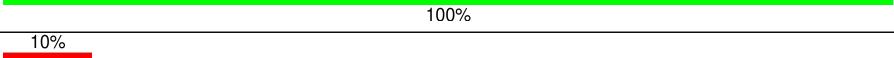
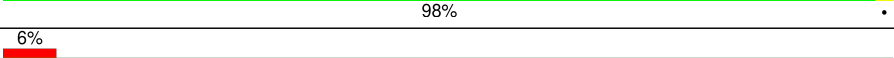
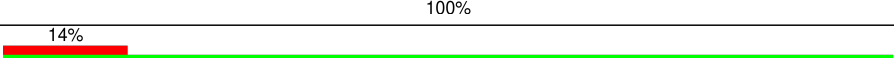
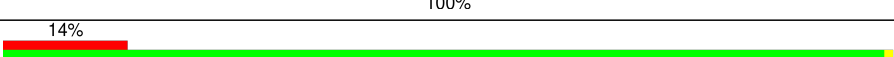
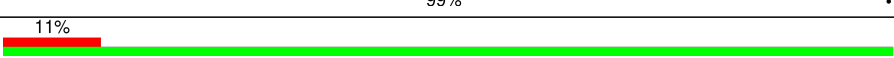
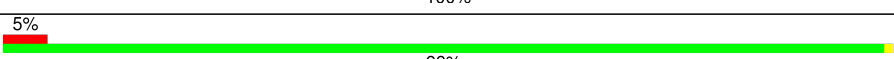
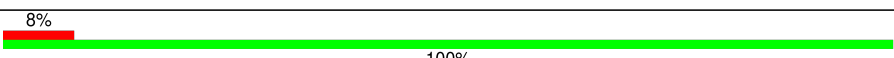
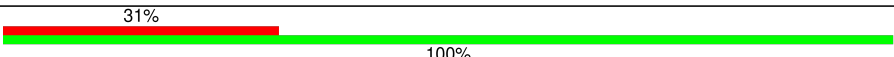
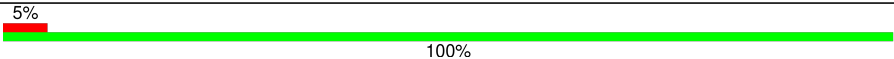

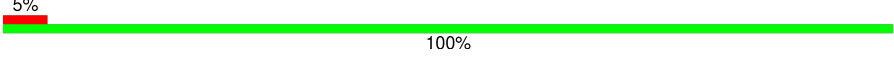
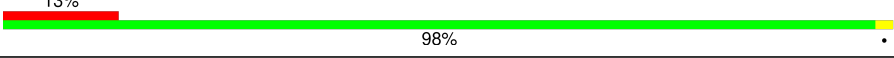
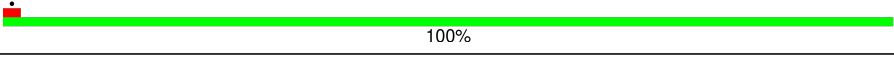
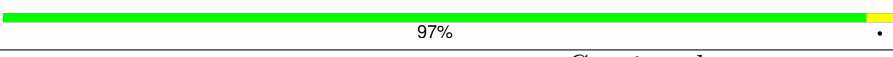



The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment 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	1	2903	<div> <div>10%</div> <div>65%</div> <div>30%</div> <div>.</div> </div>
2	2	1534	<div> <div>10%</div> <div>66%</div> <div>30%</div> <div>.</div> </div>
3	3	120	<div> <div>7%</div> <div>67%</div> <div>31%</div> <div>.</div> </div>
4	4	15	<div> <div>40%</div> <div>40%</div> <div>60%</div> </div>
5	5	76	<div> <div>11%</div> <div>58%</div> <div>36%</div> <div>7%</div> </div>
6	B	271	<div> <div>99%</div> <div>.</div> </div>
7	C	209	<div> <div>5%</div> <div>100%</div> </div>
8	D	201	<div> <div>10%</div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
9	E	177	
10	F	175	
11	G	149	
12	J	142	
13	K	123	
14	L	144	
15	M	136	
16	N	119	
17	O	116	
18	P	114	
19	Q	117	
20	R	103	
21	S	110	
22	T	94	
23	U	103	
24	V	94	
25	W	76	
26	X	77	
27	Y	62	
28	Z	58	
29	a	66	
30	b	56	
31	c	52	
32	d	46	
33	e	64	

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Mol	Chain	Length	Quality of chain
34	f	38	5% 100%
35	g	225	53% 97%
36	h	208	28% 98%
37	i	205	40% 100%
38	j	156	17% 99%
39	k	104	42% 98%
40	l	151	44% 99%
41	m	129	16% 100%
42	n	127	35% 97%
43	o	99	57% 96%
44	p	117	23% 98%
45	q	123	14% 98%
46	r	116	41% 98%
47	s	100	24% 98%
48	t	88	16% 99%
49	u	82	24% 98%
50	v	80	32% 99%
51	w	66	29% 100%
52	x	83	36% 100%
53	y	86	19% 99%
54	z	70	61% 97%
55	7	525	99% 96%
56	I	141	100% 97%
57	H	131	99% 93% 7%
58	A	360	43% 98%

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Mol	Chain	Length	Quality of chain
59	6	3	<div><div></div><div>100%</div></div>

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 153460 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 RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2903	Total	C	N	O	P	0	0
			62336	27816	11470	20147	2903		

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1534	Total	C	N	O	P	0	0
			32929	14693	6041	10661	1534		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	15	Total	C	N	O	P	0	0
			316	143	56	102	15		

- Molecule 5 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	5	76	Total	C	N	O	P	S	0	0
			1627	727	296	527	76	1		

- Molecule 6 is a protein called 50S ribosomal protein L2.

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

- Molecule 7 is a protein called 50S ribosomal protein L3.

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

- Molecule 8 is a protein called 50S ribosomal protein L4.

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

- Molecule 9 is a protein called 50S ribosomal protein L5.

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

- Molecule 10 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 11 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 12 is a protein called 50S ribosomal protein L13.

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

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 14 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 15 is a protein called 50S ribosomal protein L16.

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

- Molecule 16 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 17 is a protein called 50S ribosomal protein L18.

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

- Molecule 18 is a protein called 50S ribosomal protein L19.

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

- Molecule 19 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	117	Total	C	N	O	S	0	0
			947	604	192	151			

- Molecule 20 is a protein called 50S ribosomal protein L21.

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

- Molecule 21 is a protein called 50S ribosomal protein L22.

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

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	U	103	Total	C	N	O	0	0
			788	498	148	142		

- Molecule 24 is a protein called 50S ribosomal protein L25.

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

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 26 is a protein called 50S ribosomal protein L28.

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

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 28 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 29 is a protein called 50S ribosomal protein L31.

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

- Molecule 30 is a protein called 50S ribosomal protein L32.

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

- Molecule 31 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 32 is a protein called 50S ribosomal protein L34.

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

- Molecule 33 is a protein called 50S ribosomal protein L35.

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

- Molecule 34 is a protein called 50S ribosomal protein L36.

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

- Molecule 35 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 36 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 37 is a protein called 30S ribosomal protein S4.

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

- Molecule 38 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 39 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 40 is a protein called 30S ribosomal protein S7.

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

- Molecule 41 is a protein called 30S ribosomal protein S8.

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

- Molecule 42 is a protein called 30S ribosomal protein S9.

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

- Molecule 43 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 44 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 45 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 46 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	r	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 47 is a protein called 30S ribosomal protein S14.

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

- Molecule 48 is a protein called 30S ribosomal protein S15.

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

- Molecule 49 is a protein called 30S ribosomal protein S16.

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

- Molecule 50 is a protein called 30S ribosomal protein S17.

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

- Molecule 51 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	w	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 52 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	x	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 53 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	y	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 54 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	z	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 55 is a protein called Peptide chain release factor 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	7	525	Total	C	N	O	S	0	0
			4132	2607	721	782	22		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	151	GLY	PRO	conflict	UNP B7LEM0
7	295	GLY	LYS	conflict	UNP B7LEM0
7	296	GLY	PHE	conflict	UNP B7LEM0
7	297	GLY	THR	conflict	UNP B7LEM0
7	477	LYS	ALA	conflict	UNP B7LEM0
7	491	ALA	SER	conflict	UNP B7LEM0
7	492	ALA	GLN	conflict	UNP B7LEM0

- Molecule 56 is a protein called 50S ribosomal protein L11.

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

- Molecule 57 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	H	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 58 is a protein called Peptide chain release factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	A	360	Total	C	N	O	S	0	0
			2839	1735	526	563	15		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	SER	PRO	conflict	UNP A0A073V365
A	167	CYS	SER	conflict	UNP A0A073V365

- Molecule 59 is a protein called FME-PHE-PHE.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	6	3	Total	C	N	O	S	0	0
			32	24	3	4	1		

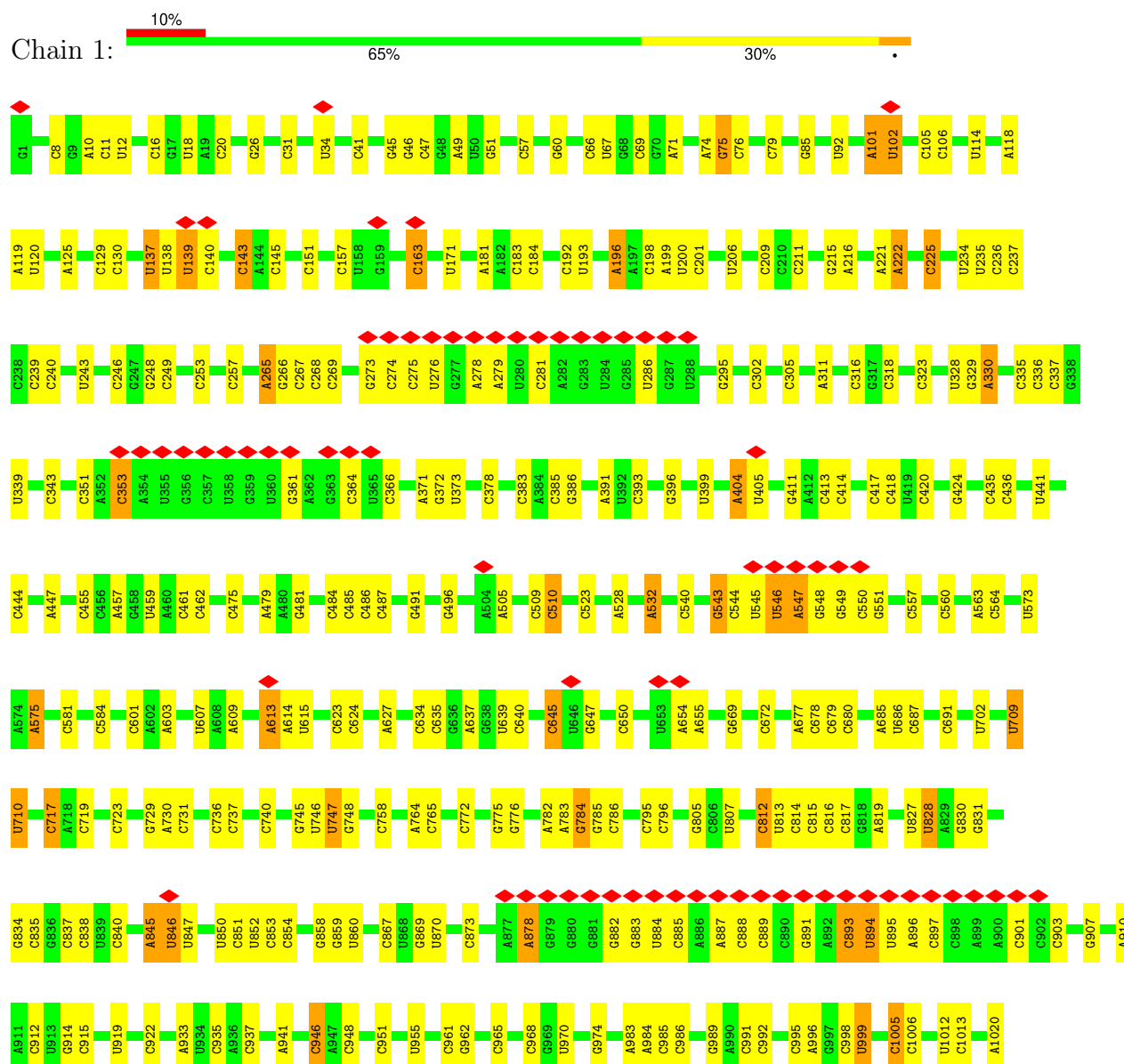
- Molecule 60 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
60	a	1	Total	Zn	0
			1	1	

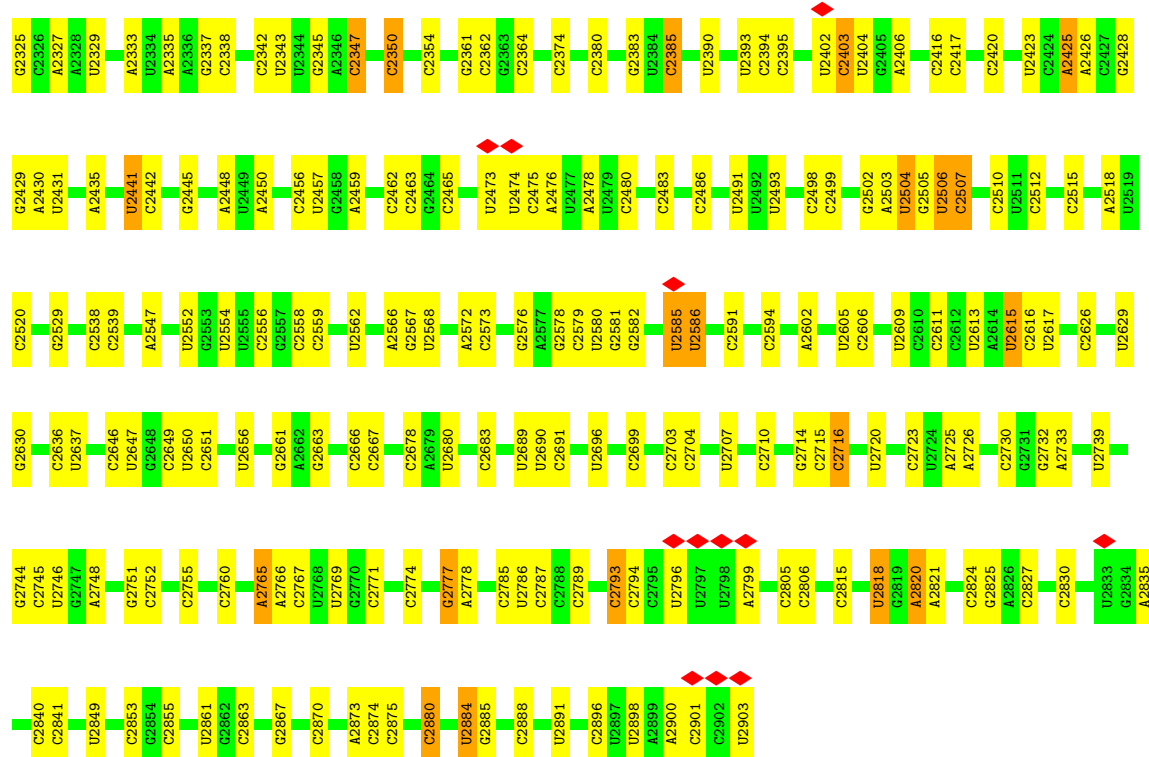
3 Residue-property plots

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

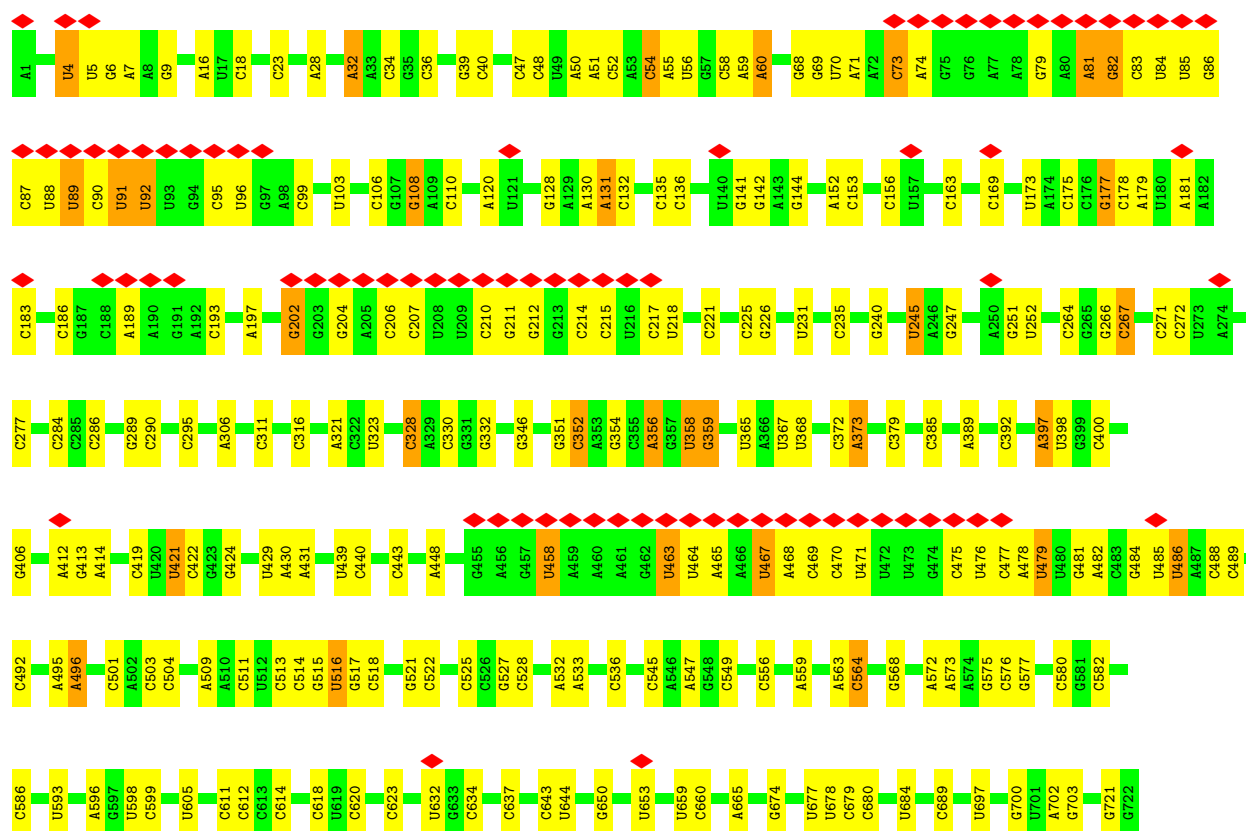
• Molecule 1: 23S ribosomal RNA

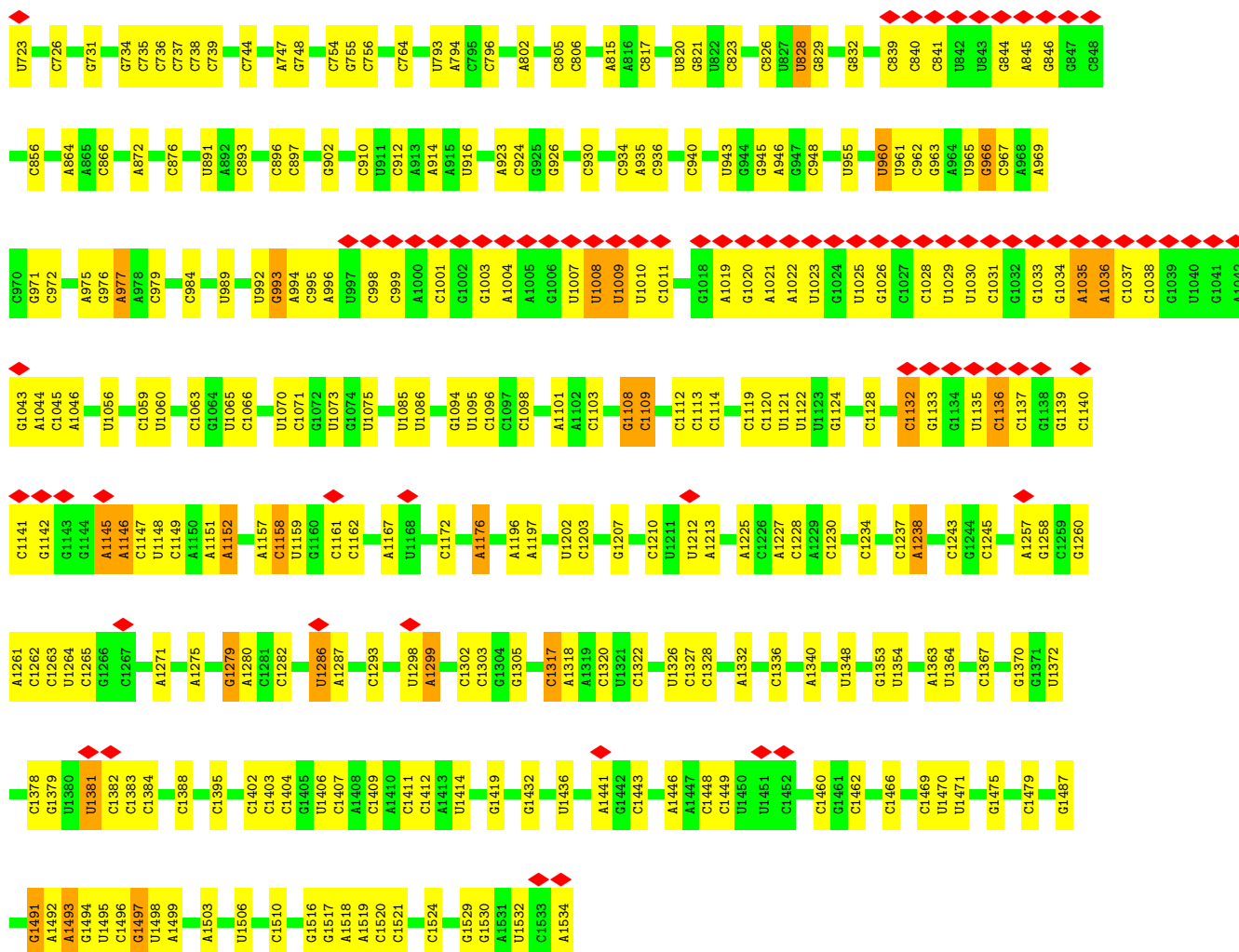




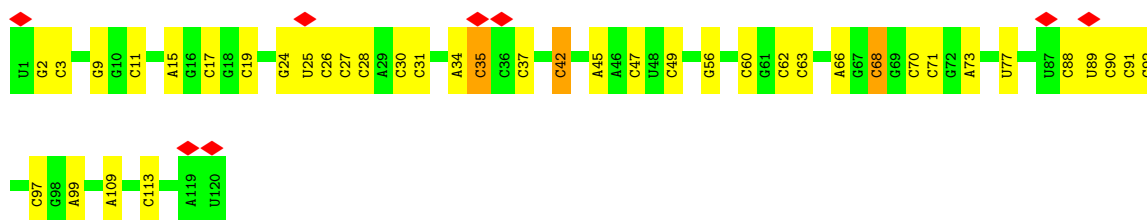


• Molecule 2: 16S ribosomal RNA

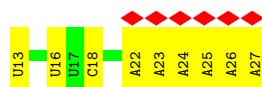




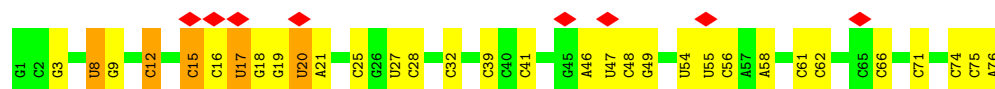
• Molecule 3: 5S ribosomal RNA



• Molecule 4: mRNA



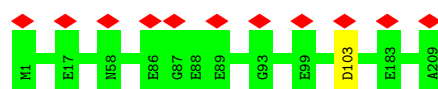
• Molecule 5: P-tRNA



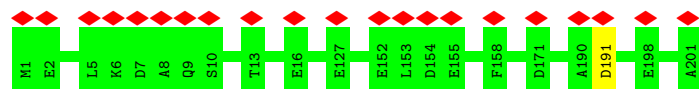
• Molecule 6: 50S ribosomal protein L2



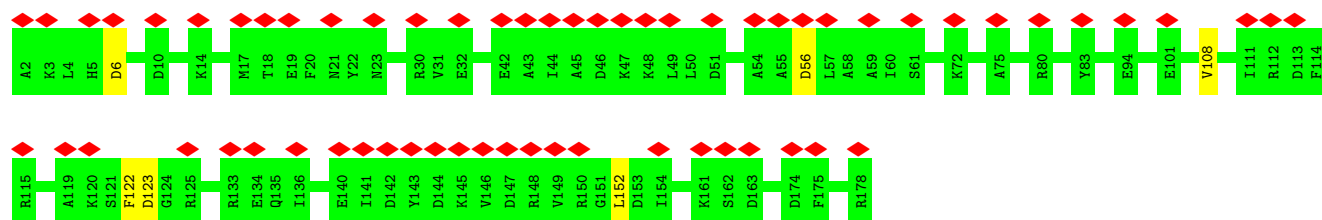
• Molecule 7: 50S ribosomal protein L3



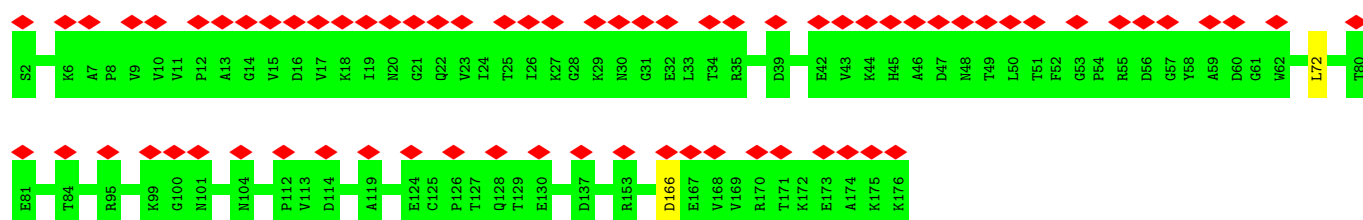
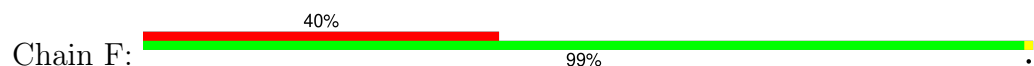
• Molecule 8: 50S ribosomal protein L4



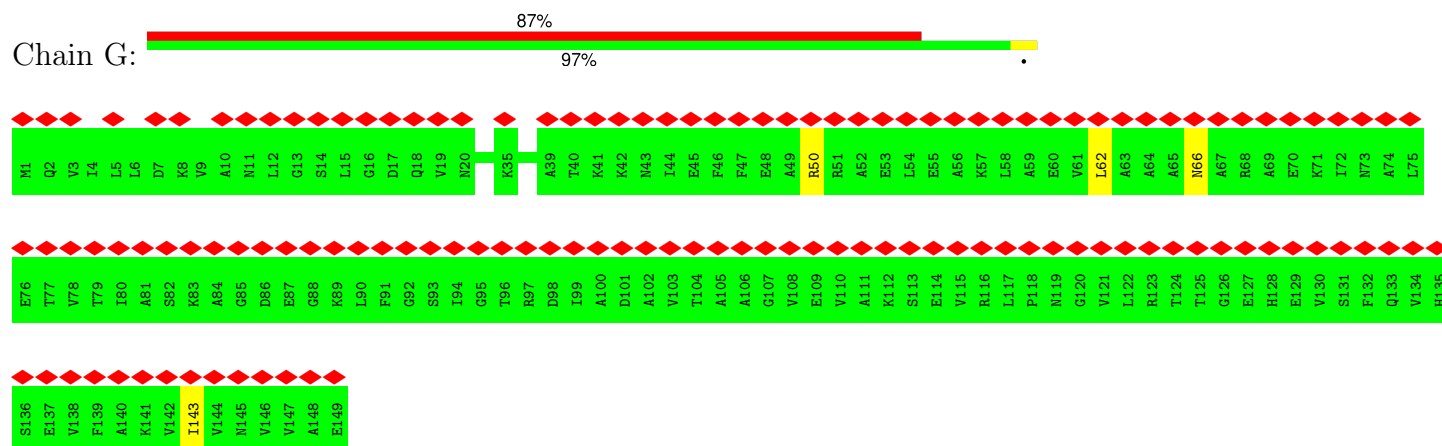
• Molecule 9: 50S ribosomal protein L5



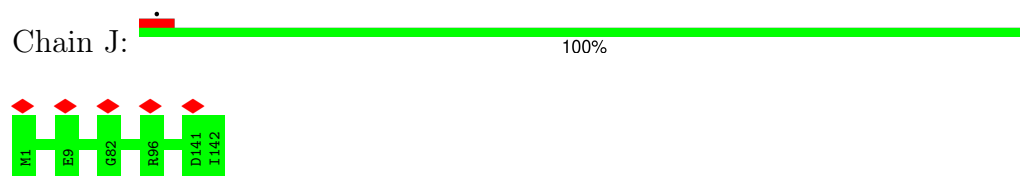
• Molecule 10: 50S ribosomal protein L6



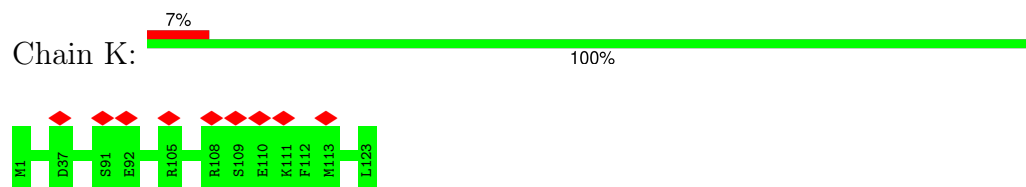
- Molecule 11: 50S ribosomal protein L9



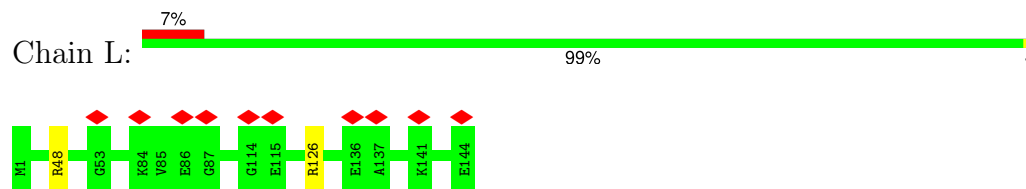
- Molecule 12: 50S ribosomal protein L13



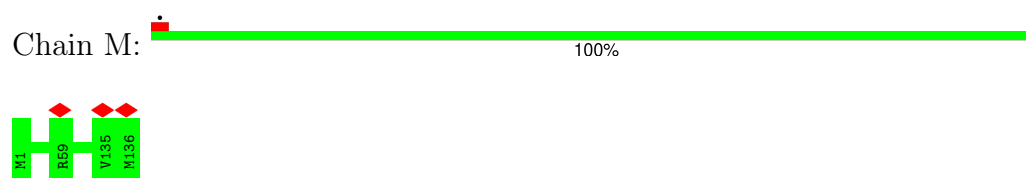
- Molecule 13: 50S ribosomal protein L14



- Molecule 14: 50S ribosomal protein L15

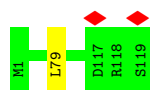


- Molecule 15: 50S ribosomal protein L16

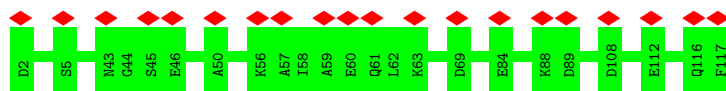


- Molecule 16: 50S ribosomal protein L17

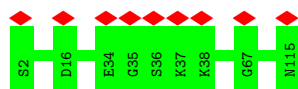




- Molecule 17: 50S ribosomal protein L18



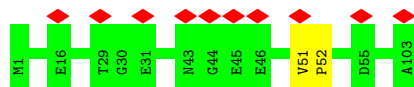
- Molecule 18: 50S ribosomal protein L19



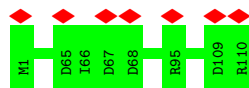
- Molecule 19: 50S ribosomal protein L20



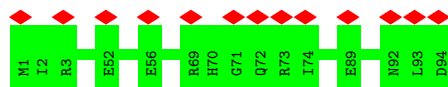
- Molecule 20: 50S ribosomal protein L21



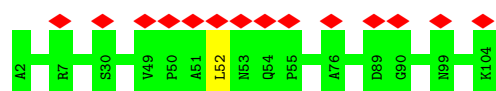
- Molecule 21: 50S ribosomal protein L22



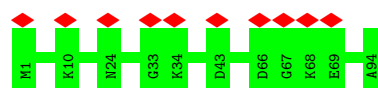
- Molecule 22: 50S ribosomal protein L23



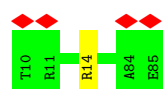
- Molecule 23: 50S ribosomal protein L24



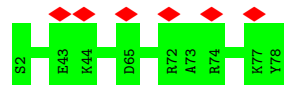
- Molecule 24: 50S ribosomal protein L25



- Molecule 25: 50S ribosomal protein L27



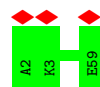
- Molecule 26: 50S ribosomal protein L28



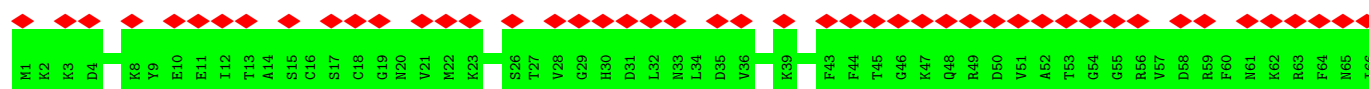
- Molecule 27: 50S ribosomal protein L29



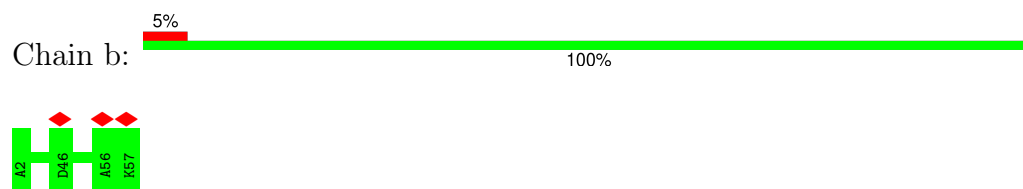
- Molecule 28: 50S ribosomal protein L30



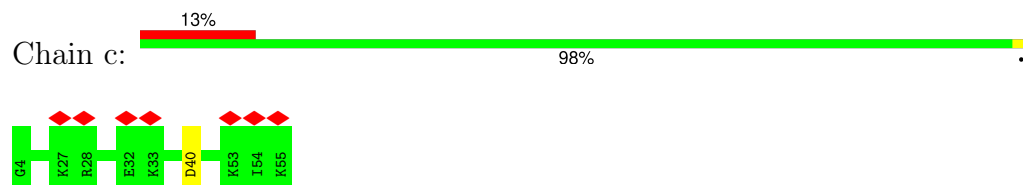
- Molecule 29: 50S ribosomal protein L31



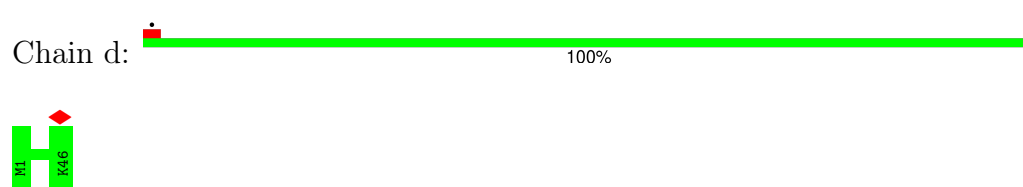
- Molecule 30: 50S ribosomal protein L32



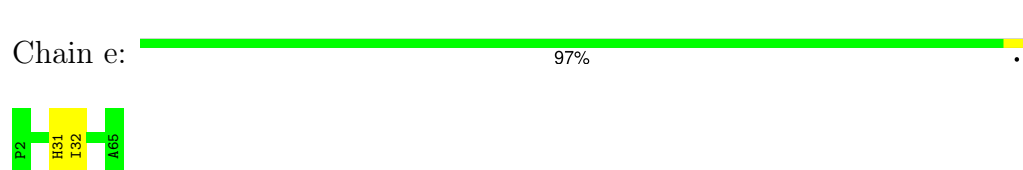
- Molecule 31: 50S ribosomal protein L33



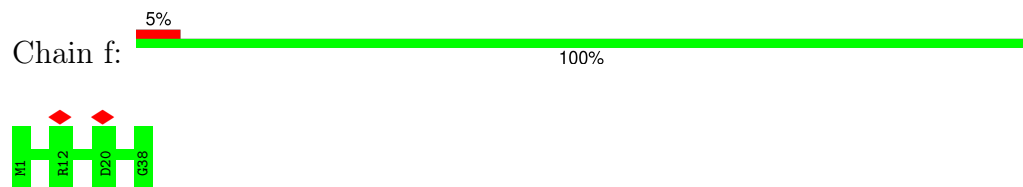
- Molecule 32: 50S ribosomal protein L34



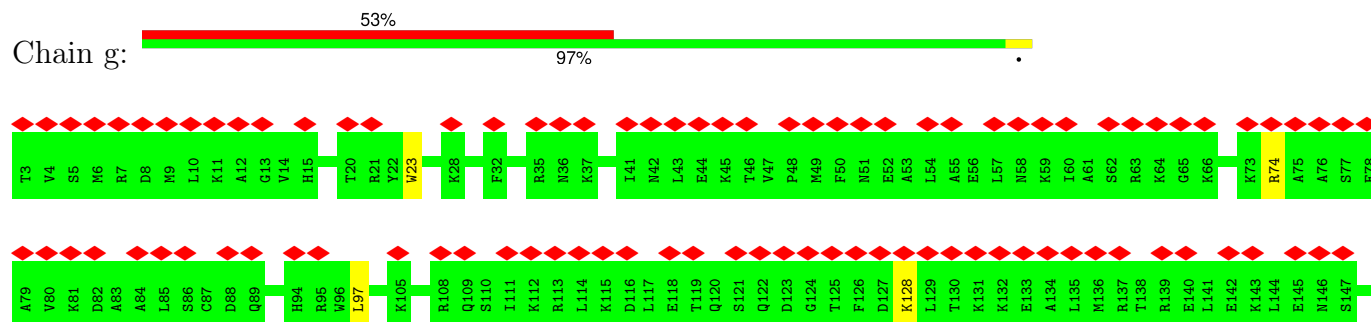
- Molecule 33: 50S ribosomal protein L35

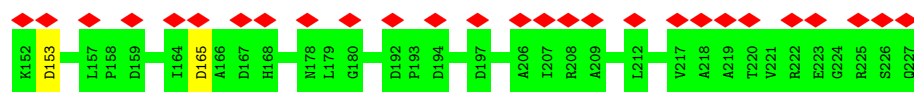


- Molecule 34: 50S ribosomal protein L36

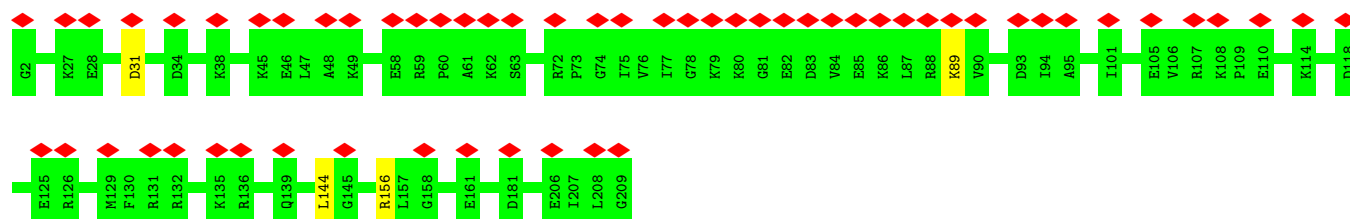


- Molecule 35: 30S ribosomal protein S2

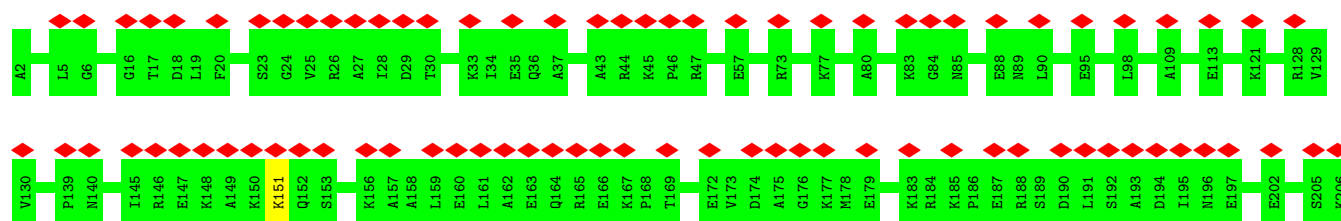
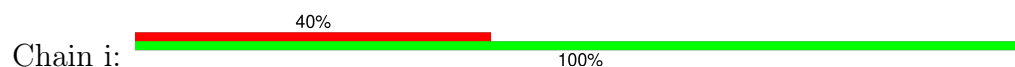




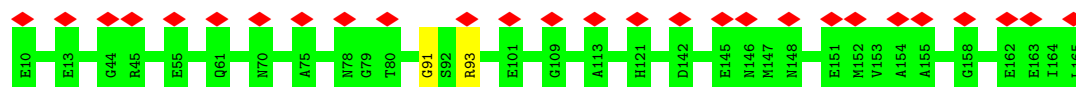
- Molecule 36: 30S ribosomal protein S3



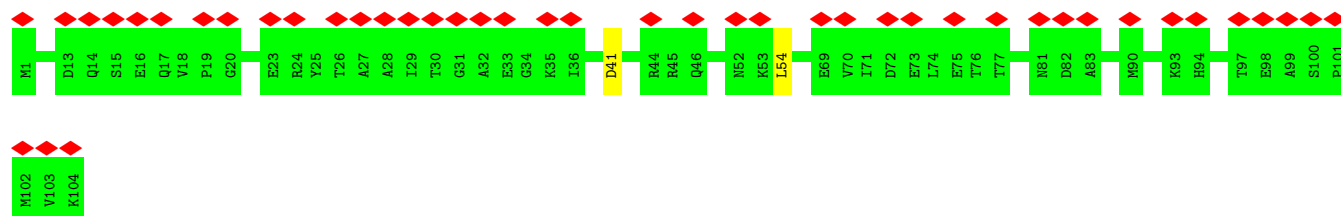
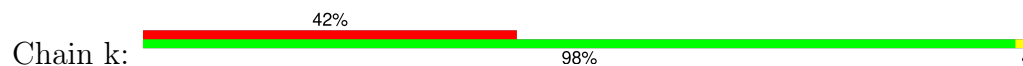
- Molecule 37: 30S ribosomal protein S4



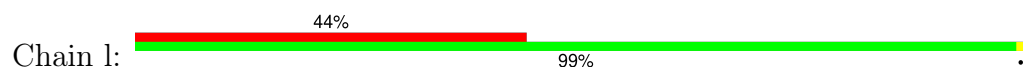
- Molecule 38: 30S ribosomal protein S5

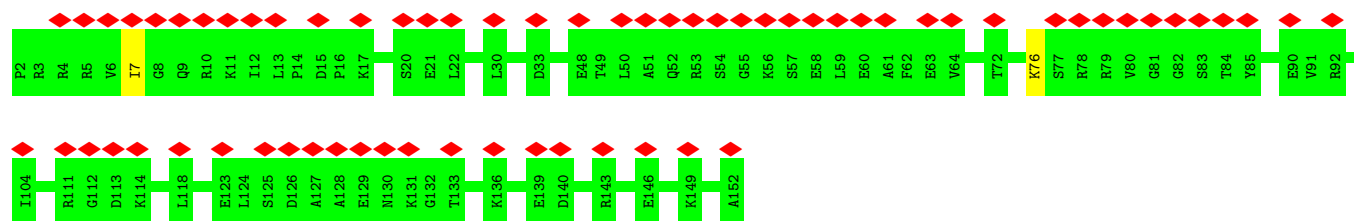


- Molecule 39: 30S ribosomal protein S6

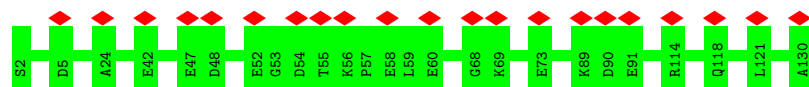


- Molecule 40: 30S ribosomal protein S7

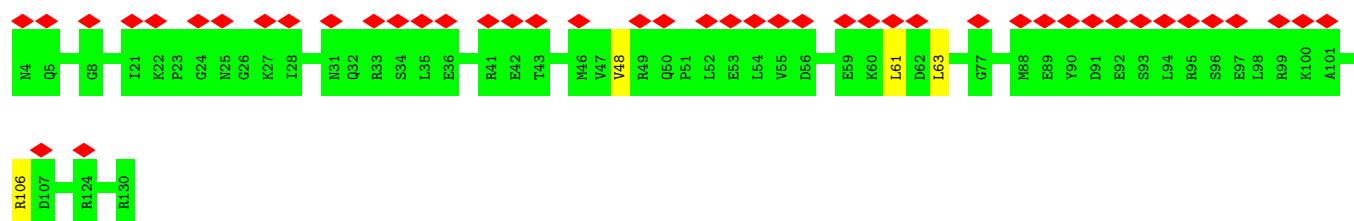




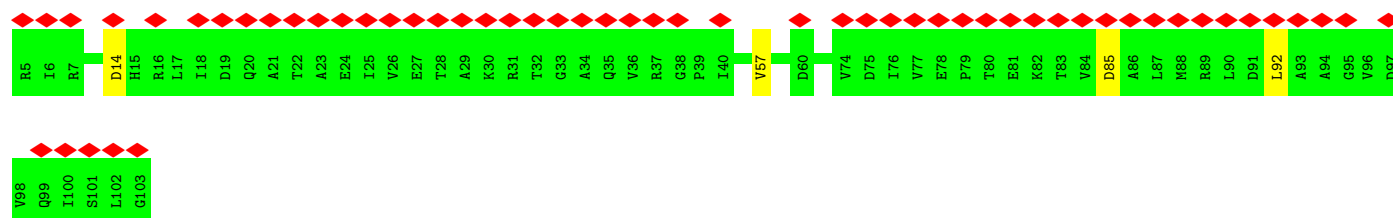
• Molecule 41: 30S ribosomal protein S8



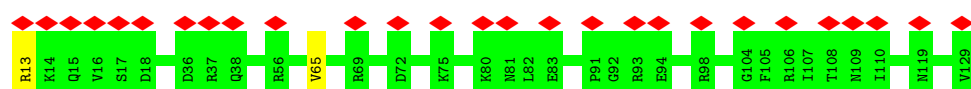
• Molecule 42: 30S ribosomal protein S9



• Molecule 43: 30S ribosomal protein S10

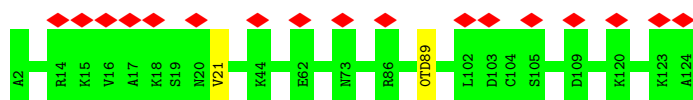


• Molecule 44: 30S ribosomal protein S11

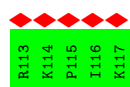
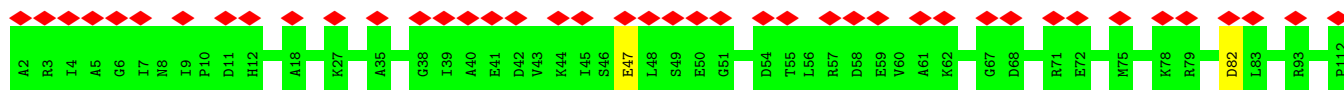


• Molecule 45: 30S ribosomal protein S12

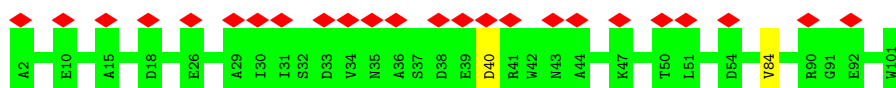




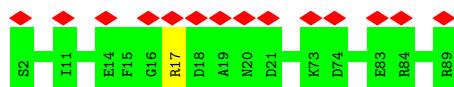
- Molecule 46: 30S ribosomal protein S13



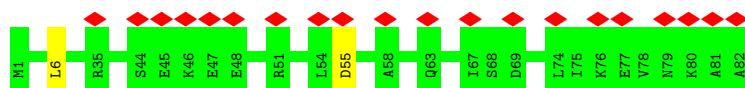
- Molecule 47: 30S ribosomal protein S14



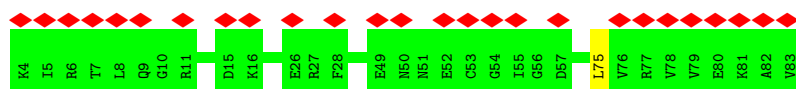
- Molecule 48: 30S ribosomal protein S15



- Molecule 49: 30S ribosomal protein S16

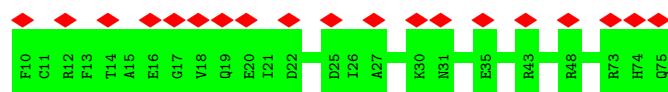


- Molecule 50: 30S ribosomal protein S17

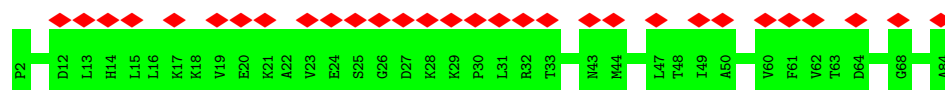


- Molecule 51: 30S ribosomal protein S18

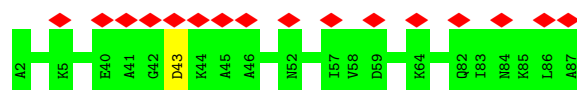




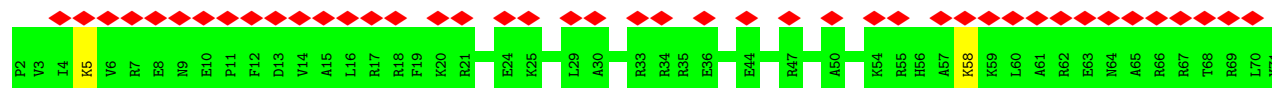
- Molecule 52: 30S ribosomal protein S19



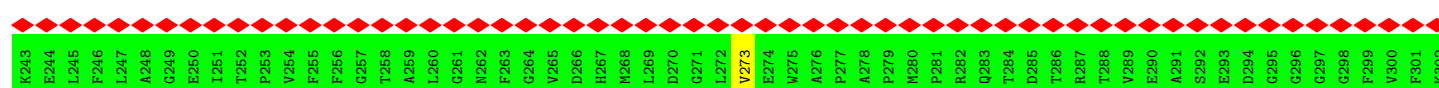
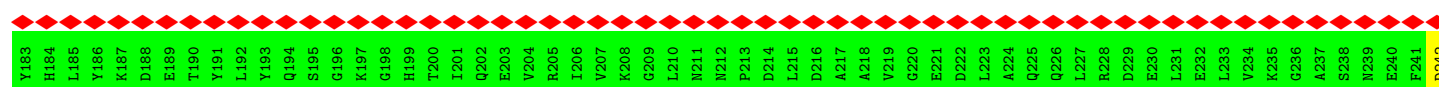
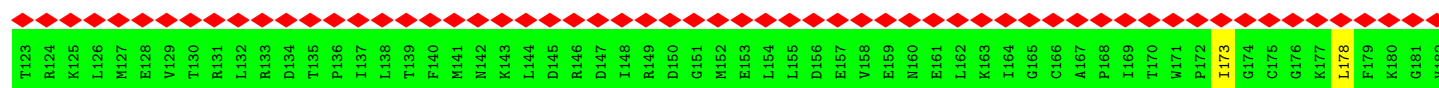
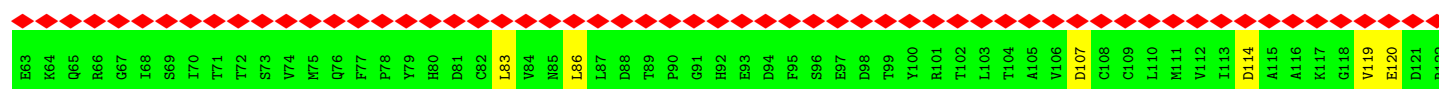
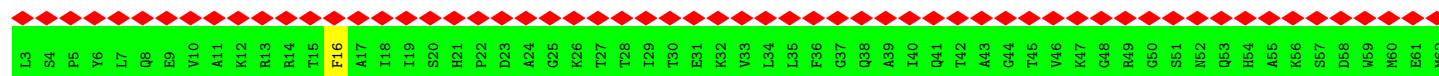
- Molecule 53: 30S ribosomal protein S20

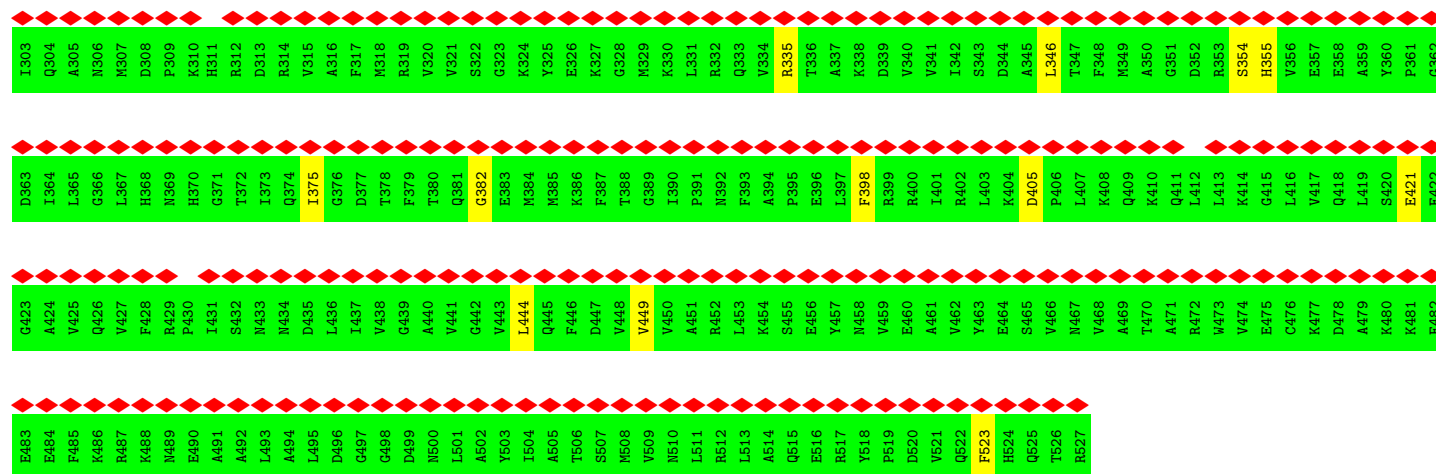


- Molecule 54: 30S ribosomal protein S21

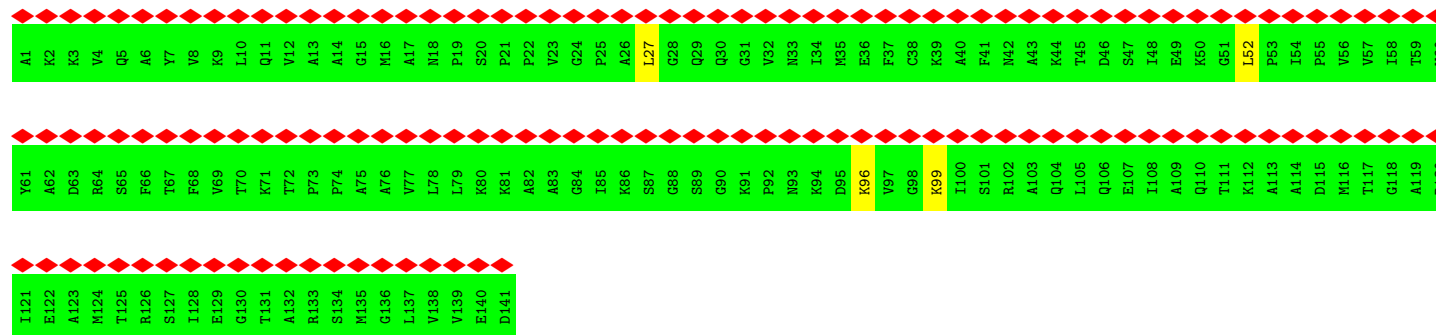


- Molecule 55: Peptide chain release factor 3

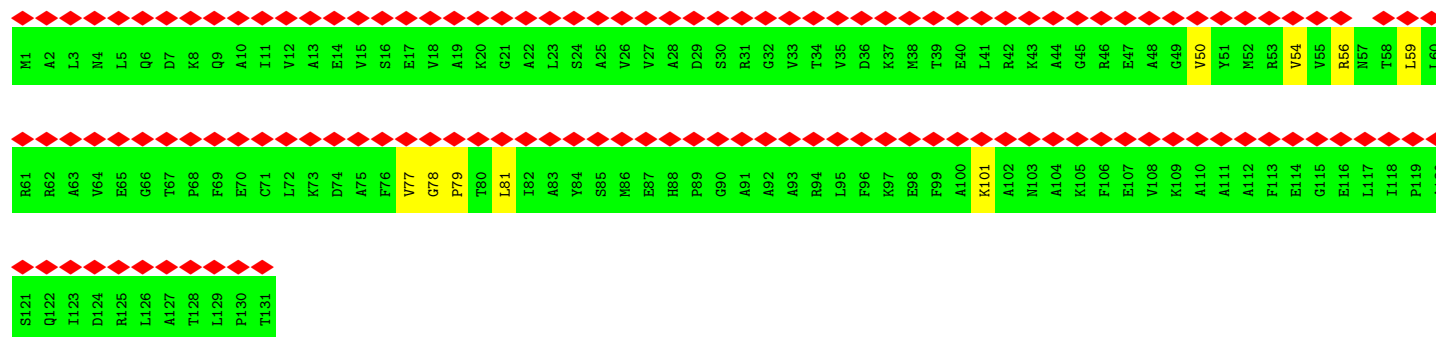
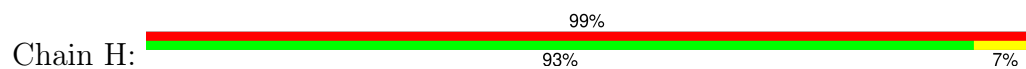




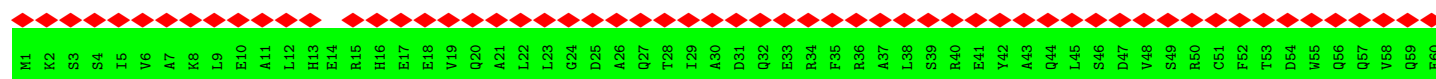
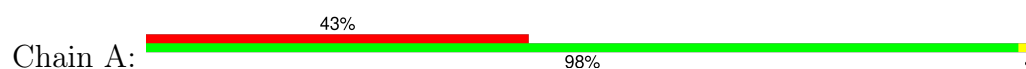
• Molecule 56: 50S ribosomal protein L11

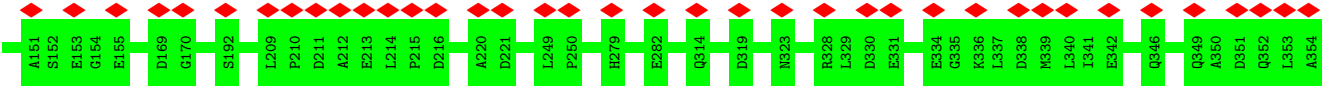
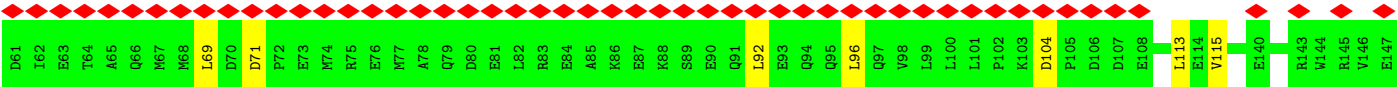


• Molecule 57: 50S ribosomal protein L10



• Molecule 58: Peptide chain release factor 1





• Molecule 59: FME-PHE-PHE



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	86478	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.261	Depositor
Minimum map value	-0.155	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	373.31998, 373.31998, 373.31998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.037, 1.037, 1.037	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MA6, UR3, 5MC, 5MU, 7MG, G7M, H2U, FME, OMC, 0TD, 4SU, PSU, 3TD, 6MZ, 1MG, ZN, OMG, 2MA, 2MG, 4OC, OMU

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	1	0.53	4/69286 (0.0%)	1.47	1274/108087 (1.2%)
2	2	0.52	5/36590 (0.0%)	1.46	641/57074 (1.1%)
3	3	0.52	0/2872	1.49	73/4478 (1.6%)
4	4	0.57	0/353	1.55	3/546 (0.5%)
5	5	0.51	0/1704	1.41	22/2654 (0.8%)
6	B	0.41	0/2121	0.79	3/2852 (0.1%)
7	C	0.39	0/1586	0.71	1/2134 (0.0%)
8	D	0.40	0/1571	0.70	1/2113 (0.0%)
9	E	0.44	0/1434	0.88	6/1926 (0.3%)
10	F	0.39	0/1333	0.73	2/1805 (0.1%)
11	G	0.50	0/1122	0.97	3/1515 (0.2%)
12	J	0.38	0/1152	0.68	0/1551
13	K	0.41	0/955	0.79	0/1279
14	L	0.36	0/1062	0.69	0/1413
15	M	0.38	0/1093	0.68	0/1460
16	N	0.40	0/964	0.67	1/1289 (0.1%)
17	O	0.40	0/902	0.67	0/1209
18	P	0.38	0/929	0.63	0/1242
19	Q	0.40	0/960	0.59	0/1278
20	R	0.42	0/829	0.73	0/1107
21	S	0.36	0/864	0.67	0/1156
22	T	0.38	0/752	0.66	0/1005
23	U	0.35	0/796	0.68	1/1062 (0.1%)
24	V	0.42	0/766	0.67	0/1025
25	W	0.35	0/589	0.62	0/779
26	X	0.35	0/635	0.61	0/848
27	Y	0.37	0/502	0.57	0/667
28	Z	0.37	0/452	0.63	0/605
29	a	0.41	0/531	0.74	0/709
30	b	0.33	0/450	0.62	0/599
31	c	0.37	0/433	0.70	1/576 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	d	0.32	0/380	0.59	0/498
33	e	0.39	0/513	0.75	1/676 (0.1%)
34	f	0.30	0/303	0.69	0/397
35	g	0.51	0/1791	0.90	5/2413 (0.2%)
36	h	0.41	0/1663	0.75	3/2241 (0.1%)
37	i	0.41	0/1665	0.70	0/2227
38	j	0.47	0/1165	0.78	0/1568
39	k	0.46	0/867	0.87	4/1171 (0.3%)
40	l	0.45	0/1195	0.75	1/1602 (0.1%)
41	m	0.41	0/989	0.70	0/1326
42	n	0.43	0/1034	0.83	3/1375 (0.2%)
43	o	0.41	0/800	0.86	4/1082 (0.4%)
44	p	0.36	0/893	0.65	1/1205 (0.1%)
45	q	0.44	0/960	0.83	1/1286 (0.1%)
46	r	0.40	0/909	0.78	2/1215 (0.2%)
47	s	0.40	0/817	0.66	2/1088 (0.2%)
48	t	0.39	0/722	0.61	0/964
49	u	0.39	0/659	0.79	2/884 (0.2%)
50	v	0.40	0/657	0.75	1/881 (0.1%)
51	w	0.42	0/553	0.67	0/743
52	x	0.40	0/680	0.69	0/915
53	y	0.44	0/675	0.65	1/895 (0.1%)
54	z	0.41	0/597	0.62	0/792
55	7	0.54	1/4207 (0.0%)	0.98	19/5680 (0.3%)
56	I	0.50	0/1046	0.88	2/1410 (0.1%)
57	H	0.57	1/1001 (0.1%)	1.06	6/1350 (0.4%)
58	A	0.45	0/2879	0.78	6/3877 (0.2%)
59	6	0.55	0/23	0.66	0/29
All	All	0.50	11/165231 (0.0%)	1.30	2096/245833 (0.9%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	2	0	1
20	R	0	1
All	All	0	2

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	7	421	GLU	CG-CD	6.62	1.61	1.51
2	2	496	A	N9-C4	6.60	1.41	1.37
1	1	984	A	N9-C4	6.50	1.41	1.37
1	1	783	A	N9-C4	6.50	1.41	1.37
1	1	1669	A	N9-C4	6.49	1.41	1.37

The worst 5 of 2096 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	60	A	C8-N9-C4	-16.21	99.31	105.80
2	2	328	C	N1-C2-O2	14.75	127.75	118.90
1	1	1313	U	N3-C2-O2	-14.73	111.89	122.20
2	2	328	C	C2-N1-C1'	13.87	134.05	118.80
2	2	58	C	C6-N1-C2	-13.59	114.86	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	2	60	A	Sidechain
20	R	51	VAL	Peptide

5.2 Too-close contacts ⓘ

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
6	B	269/271 (99%)	260 (97%)	9 (3%)	0	100	100
7	C	207/209 (99%)	202 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	D	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
9	E	175/177 (99%)	168 (96%)	7 (4%)	0	100	100
10	F	173/175 (99%)	167 (96%)	6 (4%)	0	100	100
11	G	147/149 (99%)	145 (99%)	2 (1%)	0	100	100
12	J	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
13	K	121/123 (98%)	120 (99%)	1 (1%)	0	100	100
14	L	142/144 (99%)	141 (99%)	1 (1%)	0	100	100
15	M	134/136 (98%)	134 (100%)	0	0	100	100
16	N	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
17	O	114/116 (98%)	112 (98%)	2 (2%)	0	100	100
18	P	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
19	Q	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
20	R	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	13	39
21	S	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
22	T	92/94 (98%)	92 (100%)	0	0	100	100
23	U	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
24	V	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
25	W	74/76 (97%)	73 (99%)	1 (1%)	0	100	100
26	X	75/77 (97%)	75 (100%)	0	0	100	100
27	Y	60/62 (97%)	60 (100%)	0	0	100	100
28	Z	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
29	a	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
30	b	54/56 (96%)	53 (98%)	1 (2%)	0	100	100
31	c	50/52 (96%)	50 (100%)	0	0	100	100
32	d	44/46 (96%)	44 (100%)	0	0	100	100
33	e	62/64 (97%)	59 (95%)	2 (3%)	1 (2%)	8	27
34	f	36/38 (95%)	36 (100%)	0	0	100	100
35	g	223/225 (99%)	215 (96%)	8 (4%)	0	100	100
36	h	206/208 (99%)	202 (98%)	4 (2%)	0	100	100
37	i	203/205 (99%)	202 (100%)	1 (0%)	0	100	100
38	j	154/156 (99%)	148 (96%)	5 (3%)	1 (1%)	22	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	k	102/104 (98%)	102 (100%)	0	0	100	100
40	l	149/151 (99%)	148 (99%)	1 (1%)	0	100	100
41	m	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
42	n	125/127 (98%)	122 (98%)	3 (2%)	0	100	100
43	o	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
44	p	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
45	q	120/123 (98%)	115 (96%)	5 (4%)	0	100	100
46	r	114/116 (98%)	112 (98%)	2 (2%)	0	100	100
47	s	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
48	t	86/88 (98%)	86 (100%)	0	0	100	100
49	u	80/82 (98%)	79 (99%)	1 (1%)	0	100	100
50	v	78/80 (98%)	76 (97%)	2 (3%)	0	100	100
51	w	64/66 (97%)	64 (100%)	0	0	100	100
52	x	81/83 (98%)	81 (100%)	0	0	100	100
53	y	84/86 (98%)	84 (100%)	0	0	100	100
54	z	68/70 (97%)	68 (100%)	0	0	100	100
55	7	523/525 (100%)	501 (96%)	19 (4%)	3 (1%)	22	51
56	I	139/141 (99%)	130 (94%)	9 (6%)	0	100	100
57	H	129/131 (98%)	114 (88%)	14 (11%)	1 (1%)	16	44
58	A	358/360 (99%)	350 (98%)	7 (2%)	1 (0%)	37	67
59	6	1/3 (33%)	1 (100%)	0	0	100	100
All	All	6758/6867 (98%)	6602 (98%)	148 (2%)	8 (0%)	50	77

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	e	32	ILE
55	7	120	GLU
57	H	79	PRO
55	7	355	HIS
20	R	52	PRO

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	
6	B	216/216 (100%)	216 (100%)	0	100	100
7	C	164/164 (100%)	164 (100%)	0	100	100
8	D	165/165 (100%)	165 (100%)	0	100	100
9	E	148/148 (100%)	148 (100%)	0	100	100
10	F	136/136 (100%)	136 (100%)	0	100	100
11	G	114/114 (100%)	113 (99%)	1 (1%)	75	92
12	J	116/116 (100%)	116 (100%)	0	100	100
13	K	104/104 (100%)	104 (100%)	0	100	100
14	L	103/103 (100%)	101 (98%)	2 (2%)	52	82
15	M	109/109 (100%)	109 (100%)	0	100	100
16	N	99/99 (100%)	99 (100%)	0	100	100
17	O	86/86 (100%)	86 (100%)	0	100	100
18	P	99/99 (100%)	99 (100%)	0	100	100
19	Q	89/89 (100%)	89 (100%)	0	100	100
20	R	84/84 (100%)	84 (100%)	0	100	100
21	S	93/93 (100%)	93 (100%)	0	100	100
22	T	81/81 (100%)	81 (100%)	0	100	100
23	U	84/84 (100%)	84 (100%)	0	100	100
24	V	78/78 (100%)	78 (100%)	0	100	100
25	W	58/58 (100%)	57 (98%)	1 (2%)	56	84
26	X	67/67 (100%)	67 (100%)	0	100	100
27	Y	54/54 (100%)	54 (100%)	0	100	100
28	Z	48/48 (100%)	48 (100%)	0	100	100
29	a	59/59 (100%)	59 (100%)	0	100	100
30	b	47/47 (100%)	47 (100%)	0	100	100
31	c	47/47 (100%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	d	38/38 (100%)	38 (100%)	0	100	100
33	e	51/51 (100%)	51 (100%)	0	100	100
34	f	34/34 (100%)	34 (100%)	0	100	100
35	g	187/187 (100%)	186 (100%)	1 (0%)	86	95
36	h	171/171 (100%)	170 (99%)	1 (1%)	84	95
37	i	172/172 (100%)	171 (99%)	1 (1%)	84	95
38	j	119/119 (100%)	118 (99%)	1 (1%)	79	93
39	k	91/91 (100%)	91 (100%)	0	100	100
40	l	124/124 (100%)	123 (99%)	1 (1%)	79	93
41	m	104/104 (100%)	104 (100%)	0	100	100
42	n	105/105 (100%)	104 (99%)	1 (1%)	73	91
43	o	86/86 (100%)	86 (100%)	0	100	100
44	p	90/90 (100%)	89 (99%)	1 (1%)	70	90
45	q	102/102 (100%)	102 (100%)	0	100	100
46	r	94/94 (100%)	94 (100%)	0	100	100
47	s	83/83 (100%)	83 (100%)	0	100	100
48	t	76/76 (100%)	75 (99%)	1 (1%)	65	88
49	u	65/65 (100%)	65 (100%)	0	100	100
50	v	74/74 (100%)	74 (100%)	0	100	100
51	w	57/57 (100%)	57 (100%)	0	100	100
52	x	72/72 (100%)	72 (100%)	0	100	100
53	y	65/65 (100%)	65 (100%)	0	100	100
54	z	60/60 (100%)	58 (97%)	2 (3%)	33	67
55	7	444/444 (100%)	444 (100%)	0	100	100
56	I	109/109 (100%)	107 (98%)	2 (2%)	54	83
57	H	100/100 (100%)	99 (99%)	1 (1%)	73	91
58	A	300/300 (100%)	300 (100%)	0	100	100
59	6	2/2 (100%)	2 (100%)	0	100	100
All	All	5623/5623 (100%)	5606 (100%)	17 (0%)	90	97

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	I	96	LYS
57	H	101	LYS
38	j	93	ARG
40	l	76	LYS
42	n	106	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
17	O	38	GLN
55	7	445	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2898/2903 (99%)	458 (15%)	11 (0%)
2	2	1529/1534 (99%)	237 (15%)	8 (0%)
3	3	119/120 (99%)	15 (12%)	0
4	4	14/15 (93%)	7 (50%)	1 (7%)
5	5	74/76 (97%)	18 (24%)	2 (2%)
All	All	4634/4648 (99%)	735 (15%)	22 (0%)

5 of 735 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	34	U
1	1	45	G
1	1	46	G
1	1	51	G

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	965	U
2	2	1491	G
2	2	1145	A
2	2	1492	A
1	1	1379	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

40 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$
1	PSU	1	2605	1	18,21,22	1.30	1 (5%)	21,30,33	1.82	4 (19%)
1	OMU	1	2552	1	19,22,23	3.19	8 (42%)	25,31,34	1.80	5 (20%)
5	5MU	5	54	5	19,22,23	5.00	7 (36%)	27,32,35	3.48	10 (37%)
45	0TD	q	89	45	8,9,10	1.51	1 (12%)	6,11,13	2.10	2 (33%)
2	UR3	2	1498	2	19,22,23	3.00	6 (31%)	26,32,35	1.62	4 (15%)
1	5MU	1	747	1	19,22,23	4.96	7 (36%)	27,32,35	3.73	10 (37%)
5	H2U	5	20	5	18,21,22	3.29	4 (22%)	19,30,33	1.48	3 (15%)
2	7MG	2	527	2	23,26,27	3.66	11 (47%)	27,39,42	2.19	9 (33%)
2	2MG	2	1516	2	18,26,27	2.63	6 (33%)	16,38,41	1.65	4 (25%)
1	OMG	1	2251	5,1	19,26,27	2.51	8 (42%)	21,38,41	1.50	4 (19%)
2	MA6	2	1518	2	19,26,27	1.64	3 (15%)	18,38,41	3.44	3 (16%)
2	MA6	2	1519	2	19,26,27	1.65	3 (15%)	18,38,41	3.36	3 (16%)
2	2MG	2	966	2	18,26,27	2.64	6 (33%)	16,38,41	1.67	4 (25%)
5	4SU	5	8	5	18,21,22	4.52	8 (44%)	25,30,33	2.29	5 (20%)
1	PSU	1	955	1	18,21,22	1.25	1 (5%)	21,30,33	1.74	4 (19%)
1	PSU	1	2457	1	18,21,22	1.01	1 (5%)	21,30,33	2.13	6 (28%)
59	FME	6	1	59	8,9,10	0.93	0	8,9,11	0.95	0
1	PSU	1	2504	1	18,21,22	1.38	1 (5%)	21,30,33	1.87	5 (23%)
1	PSU	1	1917	1	18,21,22	1.12	1 (5%)	21,30,33	1.74	4 (19%)
1	2MA	1	2503	1	18,25,26	3.67	6 (33%)	20,37,40	2.29	4 (20%)
1	PSU	1	746	1	18,21,22	1.24	1 (5%)	21,30,33	1.79	4 (19%)
1	G7M	1	2069	1	20,26,27	2.44	6 (30%)	16,39,42	1.48	2 (12%)
1	2MG	1	2445	1	18,26,27	2.58	6 (33%)	16,38,41	2.03	5 (31%)
1	PSU	1	2580	1	18,21,22	1.16	1 (5%)	21,30,33	1.90	4 (19%)
2	4OC	2	1402	2	20,23,24	3.29	8 (40%)	25,32,35	1.23	3 (12%)
2	2MG	2	1207	2	18,26,27	2.60	6 (33%)	16,38,41	1.60	4 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	1	1911	1	18,21,22	1.24	1 (5%)	21,30,33	1.84	4 (19%)
2	5MC	2	967	2	19,22,23	3.96	8 (42%)	26,32,35	0.97	1 (3%)
1	3TD	1	1915	1	19,22,23	4.34	8 (42%)	23,32,35	2.01	4 (17%)
2	PSU	2	516	2	18,21,22	1.19	1 (5%)	21,30,33	2.03	5 (23%)
1	5MC	1	1962	1	19,22,23	3.92	8 (42%)	26,32,35	1.08	2 (7%)
1	6MZ	1	2030	1	17,25,26	1.33	2 (11%)	15,36,39	3.83	4 (26%)
2	5MC	2	1407	2	19,22,23	3.99	8 (42%)	26,32,35	1.25	3 (11%)
1	2MG	1	1835	1	18,26,27	2.64	6 (33%)	16,38,41	1.63	4 (25%)
5	PSU	5	55	5	18,21,22	1.34	2 (11%)	21,30,33	1.82	4 (19%)
1	OMC	1	2498	1	19,22,23	3.05	8 (42%)	25,31,34	1.34	3 (12%)
1	1MG	1	745	1	19,26,27	3.37	6 (31%)	18,39,42	1.76	6 (33%)
5	4OC	5	32	5	20,23,24	3.31	8 (40%)	25,32,35	1.84	6 (24%)
1	6MZ	1	1618	1	17,25,26	1.40	2 (11%)	15,36,39	3.45	5 (33%)
1	5MU	1	1939	1	19,22,23	5.03	7 (36%)	27,32,35	3.61	10 (37%)

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
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	1/9/27/28	0/2/2/2
5	5MU	5	54	5	-	0/7/25/26	0/2/2/2
45	0TD	q	89	45	-	2/7/12/14	-
2	UR3	2	1498	2	-	1/7/25/26	0/2/2/2
1	5MU	1	747	1	-	1/7/25/26	0/2/2/2
5	H2U	5	20	5	-	4/7/38/39	0/2/2/2
2	7MG	2	527	2	-	2/7/37/38	0/3/3/3
2	2MG	2	1516	2	-	0/5/27/28	0/3/3/3
1	OMG	1	2251	5,1	-	0/5/27/28	0/3/3/3
2	MA6	2	1518	2	-	1/7/29/30	0/3/3/3
2	MA6	2	1519	2	-	4/7/29/30	0/3/3/3
2	2MG	2	966	2	-	0/5/27/28	0/3/3/3
5	4SU	5	8	5	-	2/7/25/26	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
59	FME	6	1	59	-	4/7/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	1	2504	1	-	0/7/25/26	0/2/2/2
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	2MA	1	2503	1	-	1/3/25/26	0/3/3/3
1	PSU	1	746	1	-	3/7/25/26	0/2/2/2
1	G7M	1	2069	1	-	2/3/25/26	0/3/3/3
1	2MG	1	2445	1	-	0/5/27/28	0/3/3/3
1	PSU	1	2580	1	-	1/7/25/26	0/2/2/2
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
2	2MG	2	1207	2	-	1/5/27/28	0/3/3/3
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
1	3TD	1	1915	1	-	2/7/25/26	0/2/2/2
2	PSU	2	516	2	-	3/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
1	6MZ	1	2030	1	-	4/5/27/28	0/3/3/3
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	2MG	1	1835	1	-	0/5/27/28	0/3/3/3
5	PSU	5	55	5	-	0/7/25/26	0/2/2/2
1	OMC	1	2498	1	-	0/9/27/28	0/2/2/2
1	1MG	1	745	1	-	0/3/25/26	0/3/3/3
5	4OC	5	32	5	-	2/9/29/30	0/2/2/2
1	6MZ	1	1618	1	-	4/5/27/28	0/3/3/3
1	5MU	1	1939	1	-	0/7/25/26	0/2/2/2

The worst 5 of 192 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	13.09	1.49	1.35
5	5	54	5MU	C2-N1	11.86	1.57	1.38
1	1	1939	5MU	C2-N1	11.78	1.56	1.38
1	1	747	5MU	C2-N1	11.31	1.56	1.38
1	1	1939	5MU	C6-N1	10.96	1.56	1.38

The worst 5 of 176 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2030	6MZ	C1'-N9-C4	-11.87	105.78	126.64
1	1	1939	5MU	C5-C4-N3	11.69	125.48	115.32
2	2	1519	MA6	N1-C6-N6	-11.52	103.52	116.83
5	5	54	5MU	C5-C4-N3	11.29	125.14	115.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	747	5MU	C5-C4-N3	11.21	125.07	115.32

There are no chirality outliers.

5 of 47 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
2	2	1402	4OC	O4'-C4'-C5'-O5'
2	2	1518	MA6	C5-C6-N6-C9
2	2	1519	MA6	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

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.

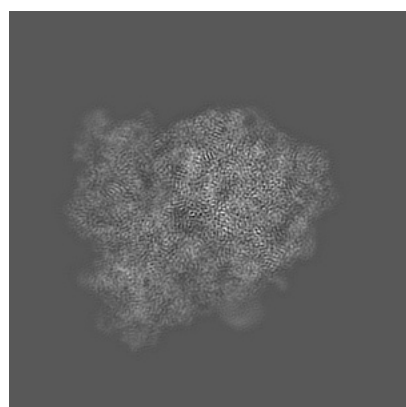
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23673. These allow visual inspection of the internal detail of the map and identification of artifacts.

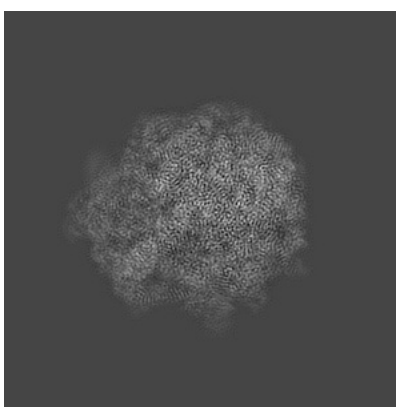
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

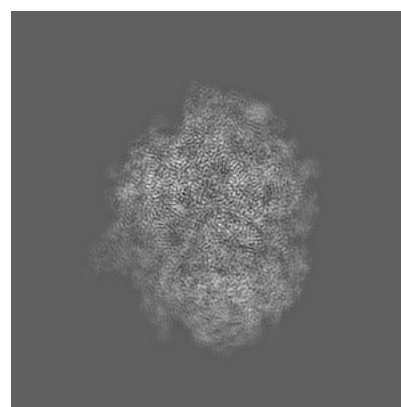
6.1.1 Primary map



X



Y

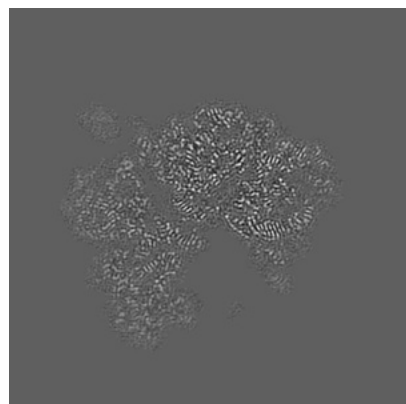


Z

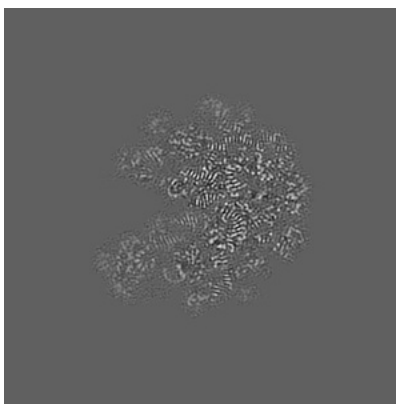
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

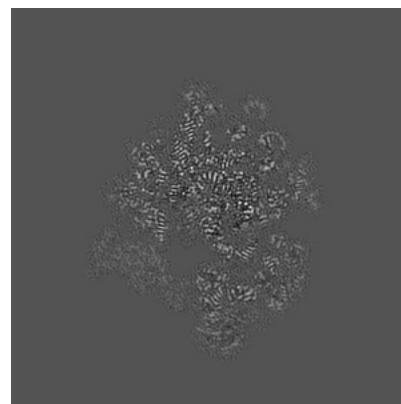
6.2.1 Primary map



X Index: 180



Y Index: 180

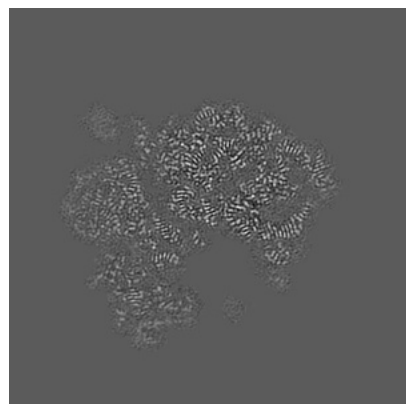


Z Index: 180

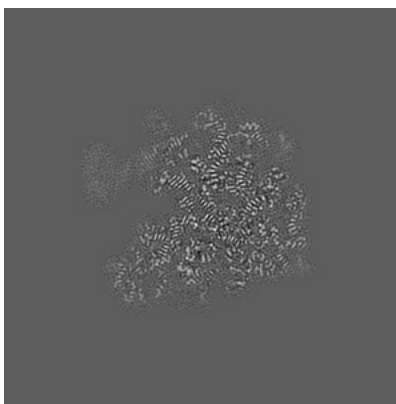
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

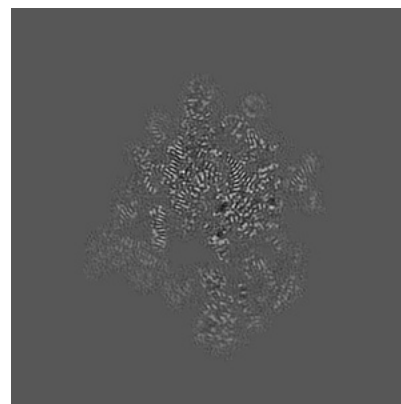
6.3.1 Primary map



X Index: 183



Y Index: 205

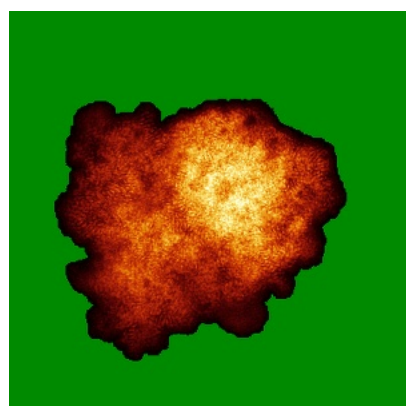


Z Index: 187

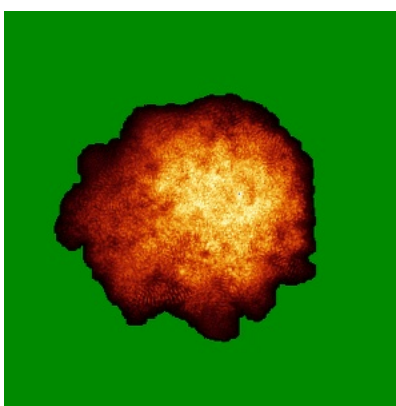
The images above show the largest variance slices of the map in three orthogonal directions.

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

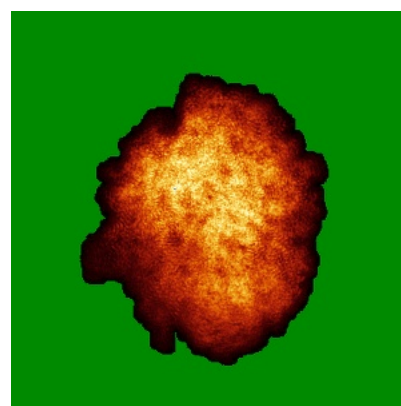
6.4.1 Primary map



X



Y

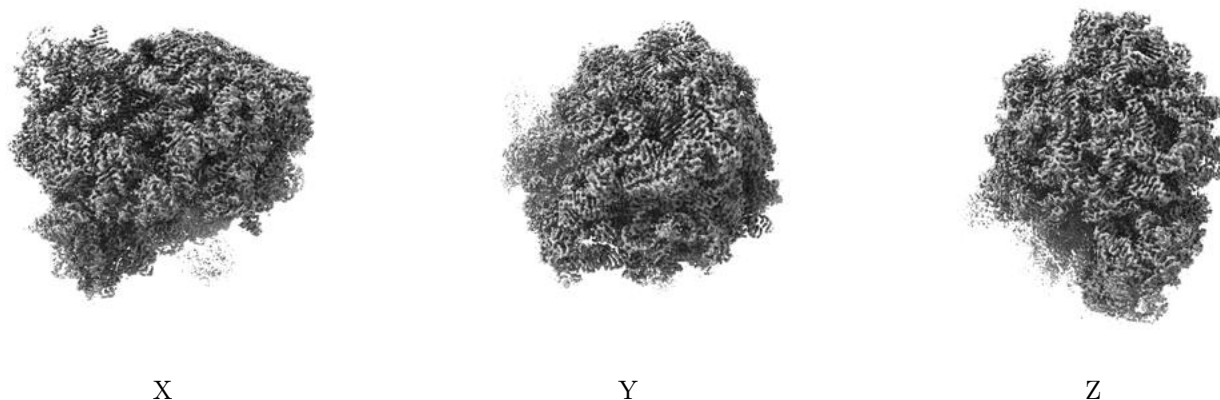


Z

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 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

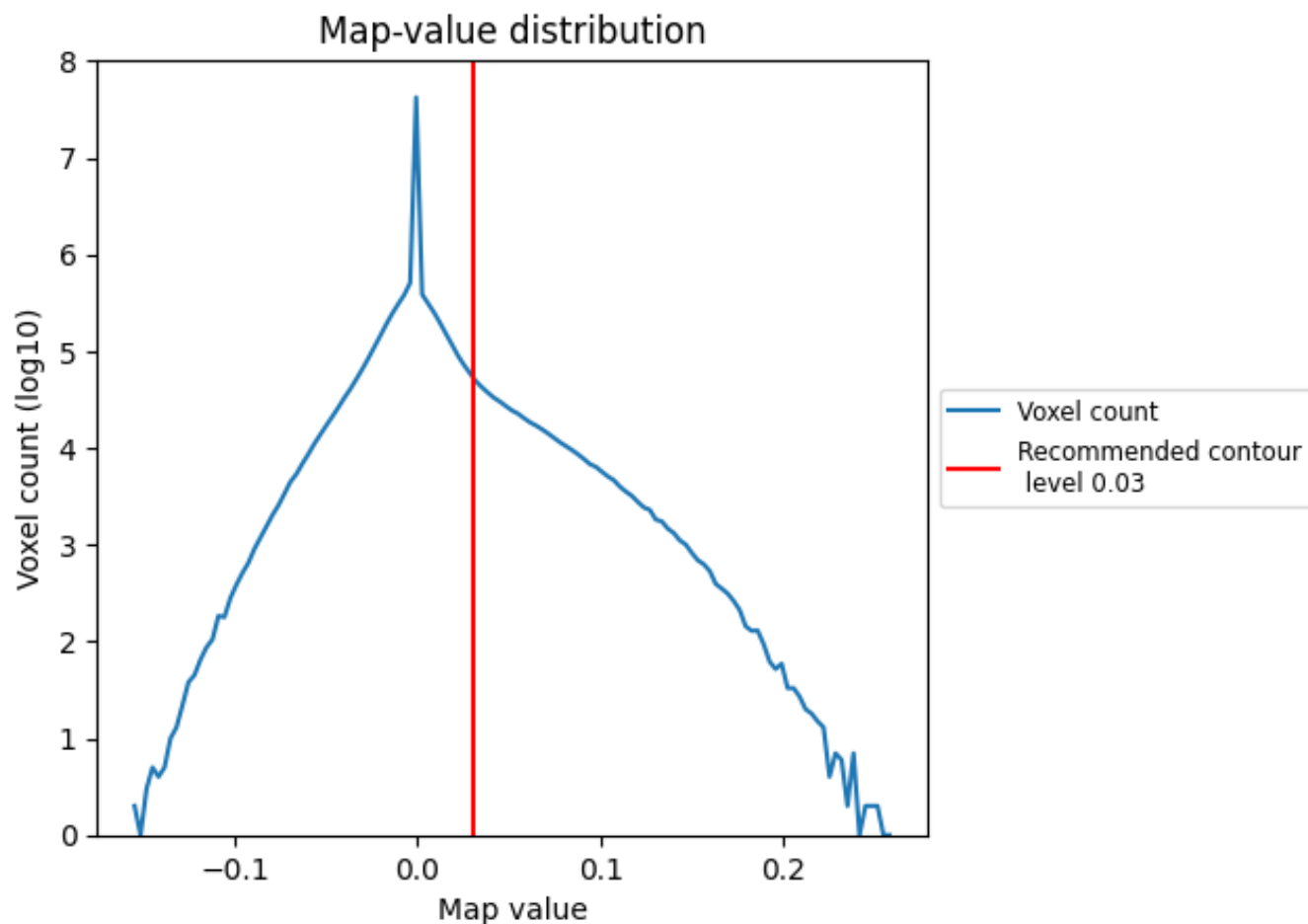
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

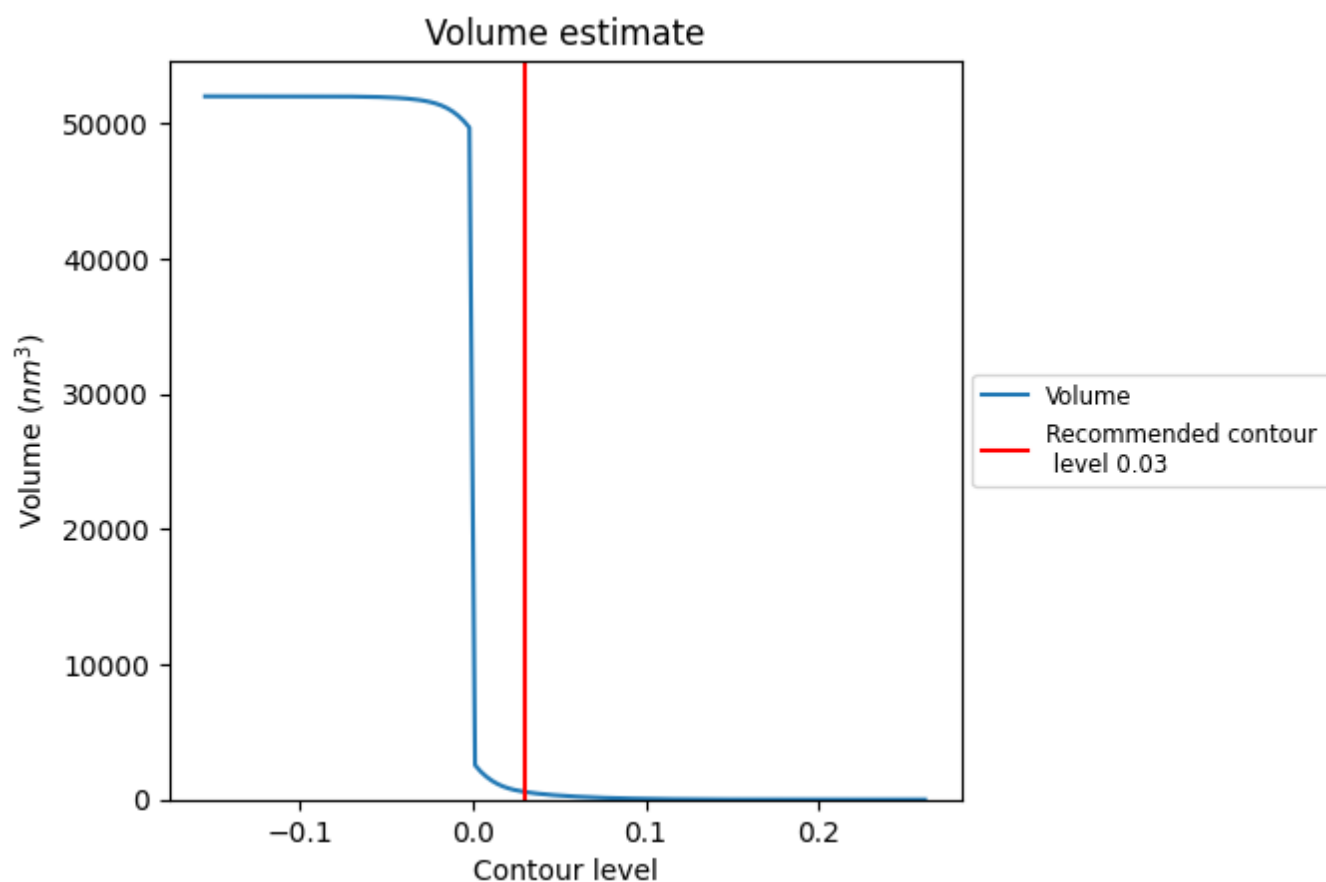
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

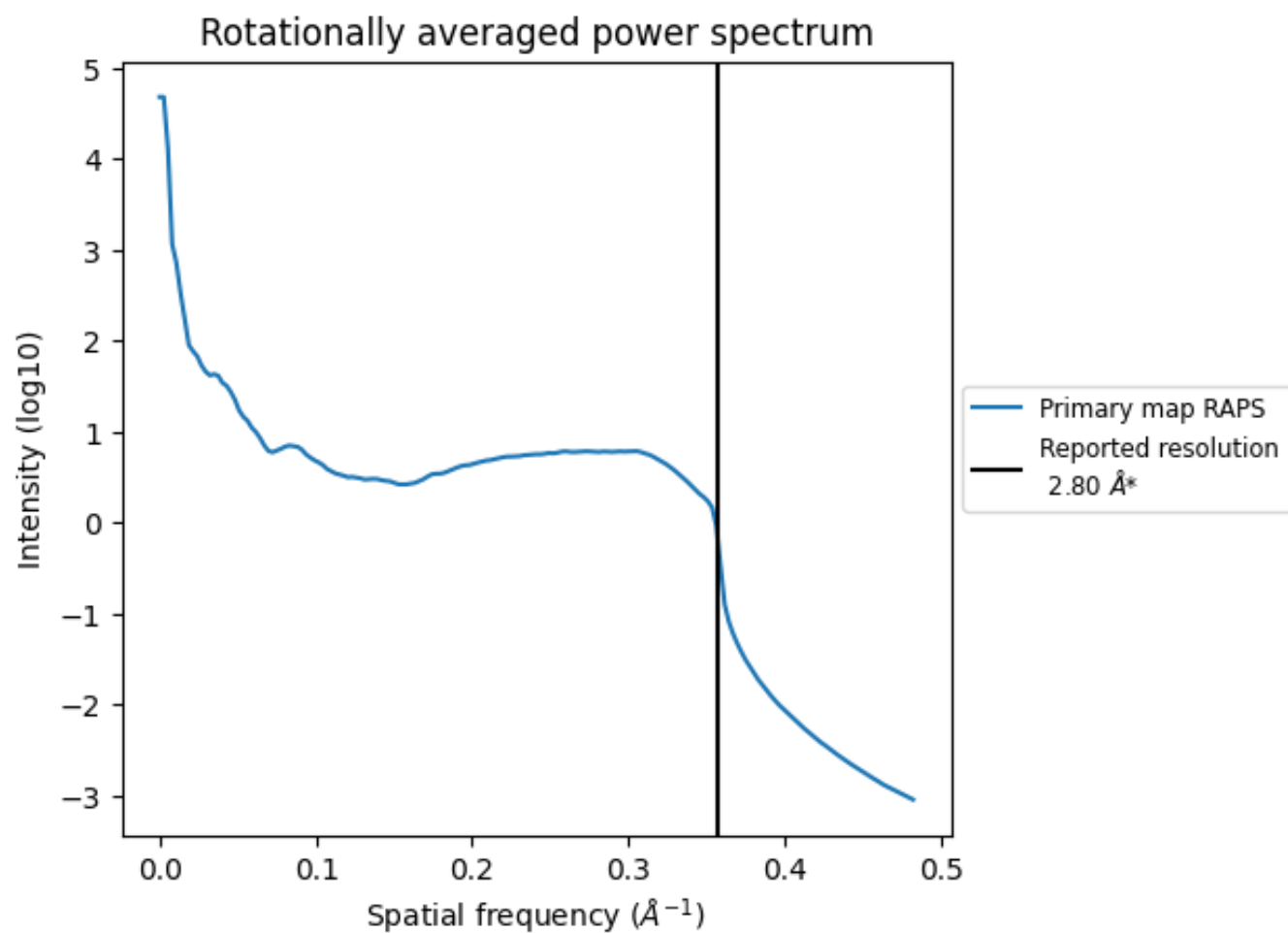
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 569 nm³; this corresponds to an approximate mass of 514 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 0.357 Å⁻¹

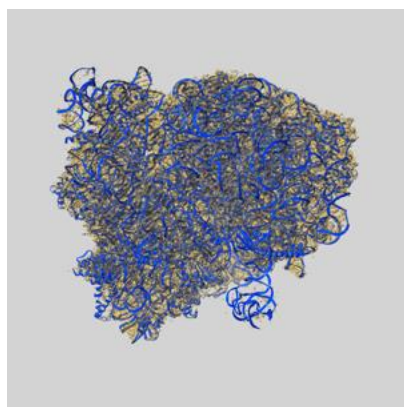
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

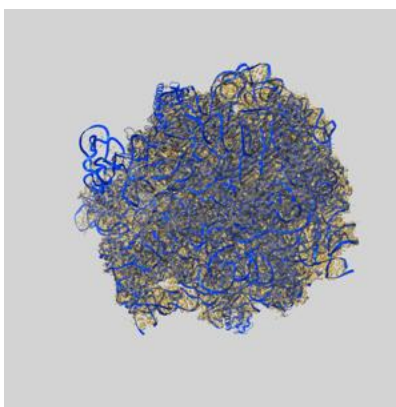
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23673 and PDB model 7M5D. Per-residue inclusion information can be found in section [3](#) on page [16](#).

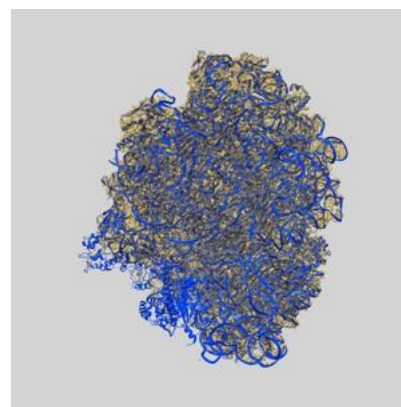
9.1 Map-model overlay [i](#)



X



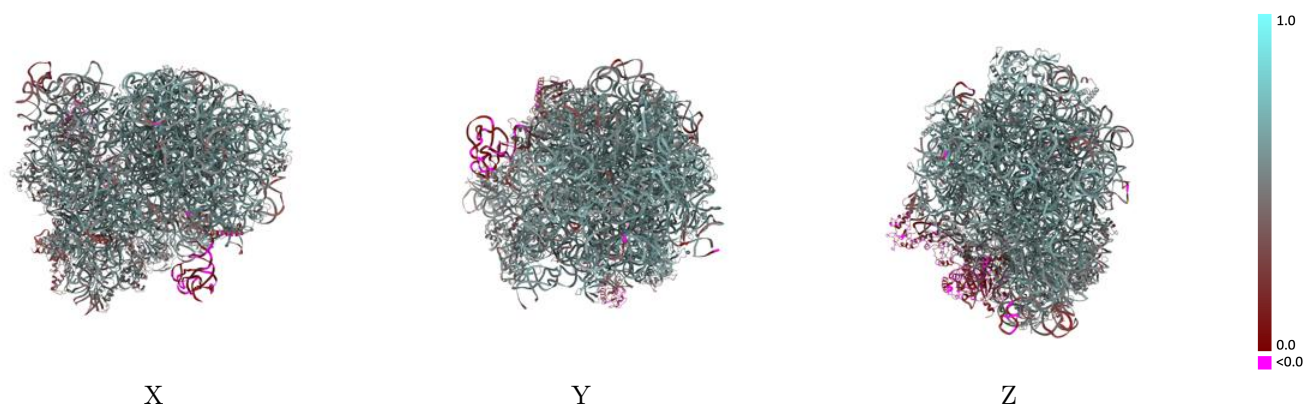
Y



Z

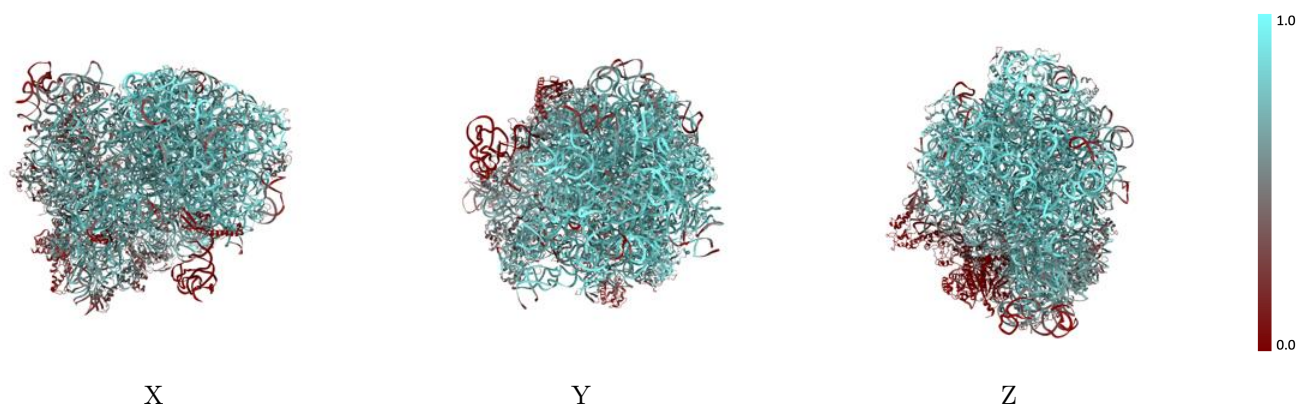
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



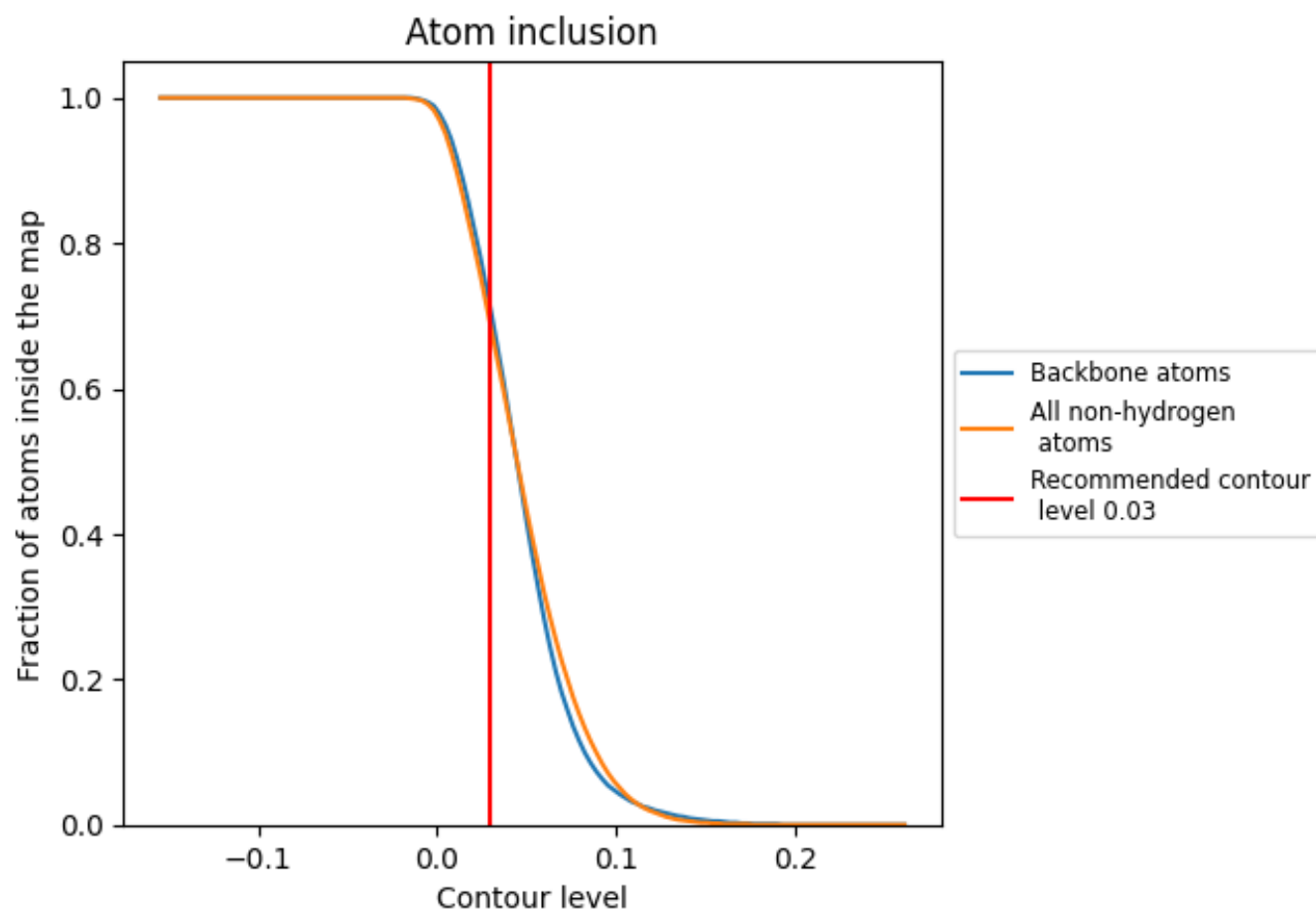
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 69% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6860	 0.5260
1	 0.7940	 0.5580
2	 0.7160	 0.5410
3	 0.7680	 0.5580
4	 0.4590	 0.4210
5	 0.6100	 0.5090
6	 0.0310	 0.2610
7	 0.0290	 0.1630
A	 0.4410	 0.4450
B	 0.8040	 0.5940
C	 0.7910	 0.5850
D	 0.7110	 0.5570
E	 0.5050	 0.4910
F	 0.4820	 0.4870
G	 0.1410	 0.3210
H	 0.0300	 0.0960
I	 0.0140	 0.1080
J	 0.7820	 0.5940
K	 0.7570	 0.5750
L	 0.7360	 0.5560
M	 0.7910	 0.5880
N	 0.8290	 0.6010
O	 0.6410	 0.5390
P	 0.7570	 0.5830
Q	 0.8140	 0.5940
R	 0.7530	 0.5690
S	 0.7580	 0.5730
T	 0.6820	 0.5630
U	 0.6790	 0.5360
V	 0.6920	 0.5710
W	 0.7770	 0.5820
X	 0.7590	 0.5970
Y	 0.5890	 0.5200
Z	 0.7890	 0.5780
a	 0.3030	 0.4070



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Chain	Atom inclusion	Q-score
b	 0.7830	 0.5870
c	 0.6750	 0.5520
d	 0.8590	 0.6170
e	 0.8410	 0.5990
f	 0.7840	 0.5940
g	 0.4010	 0.4420
h	 0.5460	 0.4990
i	 0.4470	 0.4890
j	 0.6280	 0.5300
k	 0.4720	 0.4750
l	 0.4410	 0.4670
m	 0.6300	 0.5470
n	 0.4860	 0.4860
o	 0.3950	 0.4540
p	 0.5990	 0.5310
q	 0.6580	 0.5420
r	 0.4800	 0.4780
s	 0.5610	 0.5290
t	 0.6260	 0.5300
u	 0.5420	 0.5100
v	 0.4980	 0.4920
w	 0.5580	 0.5190
x	 0.4820	 0.5010
y	 0.5770	 0.5410
z	 0.3610	 0.4230