



## wwPDB EM Validation Summary Report ⓘ

Mar 26, 2026 – 10:29 AM UTC

PDB ID : 7MT7 / pdb\_00007mt7  
EMDB ID : EMD-23976  
Title : Mtb 70S with P and E site tRNAs  
Authors : Cui, Z.; Zhang, J.  
Deposited on : 2021-05-13  
Resolution : 2.71 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](mailto: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>.

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

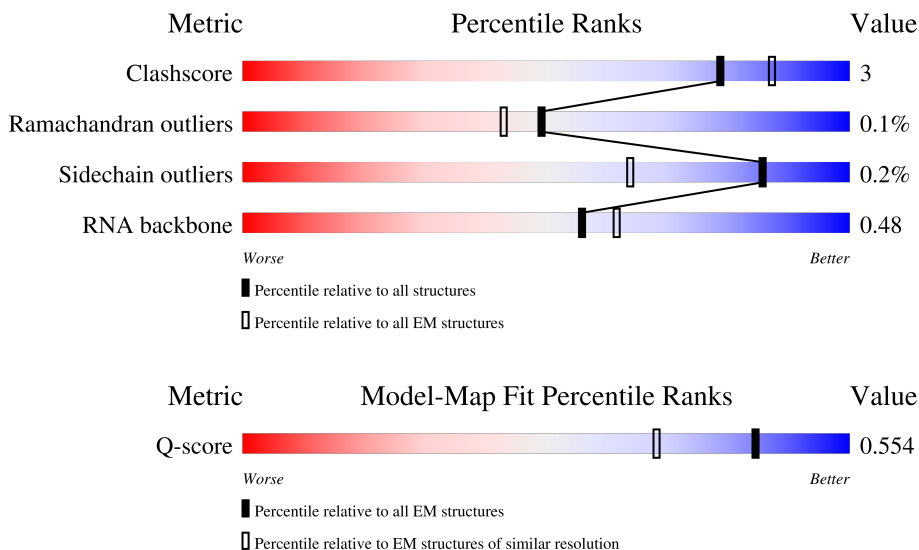
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 2.71 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.











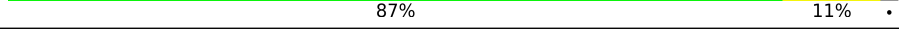
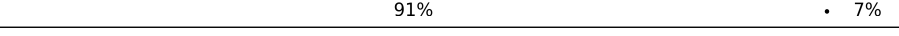
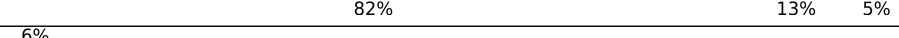
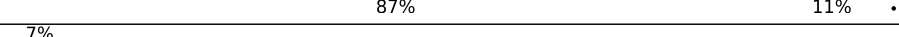

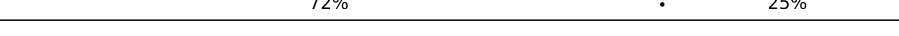

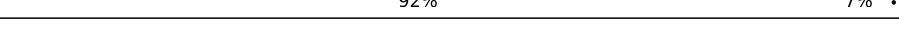
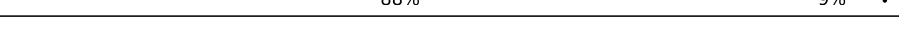

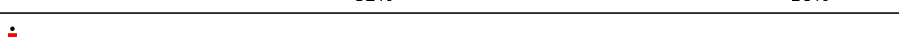






Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10297 ( 2.21 - 3.21 )

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	57	84% 11% 5%
2	1	55	80% 7% 13%
3	2	47	91% 6%

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Mol	Chain	Length	Quality of chain
4	3	64	
5	4	37	
6	6	80	
7	7	24	
8	8	235	
9	A	3138	
10	B	115	
11	C	280	
12	D	217	
13	E	223	
14	F	187	
15	G	179	
16	H	152	
17	J	195	
18	K	122	
19	L	146	
20	M	138	
21	N	180	
22	O	122	
23	P	113	
24	Q	129	
25	R	104	
26	S	197	
27	T	100	
28	U	105	

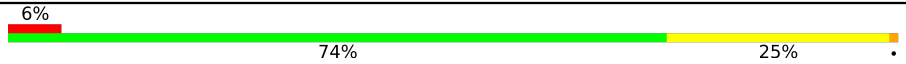

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Mol	Chain	Length	Quality of chain
29	V	215	67% 15% 18%
30	W	86	84% 6% 10%
31	X	64	89% 8%
32	Y	77	78% 10% 12%
33	Z	65	78% 12% 9%
34	a	1537	74% 22%
35	c	274	68% 7% 24%
36	d	201	84% 15%
37	e	220	68% 9% 23%
38	f	96	86% 12%
39	g	156	85% 14%
40	h	132	83% 16%
41	i	151	69% 15% 16%
42	j	101	15% 82% 16%
43	k	139	81% 16%
44	l	124	5% 84% 14%
45	m	124	75% 19% 6%
46	n	61	84% 15%
47	o	89	89% 9%
48	p	162	64% 6% 30%
49	q	135	59% 11% 30%
50	r	84	74% 24%
51	s	93	82% 8% 11%
52	t	86	93% 6%
53	x	77	5% 65% 34%

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Mol	Chain	Length	Quality of chain
53	y	77	
54	z	26	

## 2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 149696 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 L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	0	54	429	266	94	69	0	0

- Molecule 2 is a protein called 50S ribosomal protein L33 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	48	400	245	84	67	4	0	0

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	44	374	222	97	54	1	0	0

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	3	62	494	298	112	84	0	0

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	37	299	182	66	47	4	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	1	VAL	MET	conflict	UNP P9WH89

- Molecule 6 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	57	Total	C	N	O	S	0	0
			446	277	82	82	5		

- Molecule 7 is a protein called 50S ribosomal protein L37.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	7	22	Total	C	N	O	0	0
			186	111	47	28		

- Molecule 8 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	230	Total	C	N	O	S	0	0
			1704	1068	310	323	3		

- Molecule 9 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	3118	Total	C	N	O	P	0	0
			66958	29847	12340	21653	3118		

- Molecule 10 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	115	Total	C	N	O	P	0	0
			2458	1097	456	790	115		

- Molecule 11 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	272	Total	C	N	O	S	0	0
			2088	1277	437	369	5		

- Molecule 12 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	213	Total	C	N	O	S	0	0
			1590	985	307	292	6		

- Molecule 13 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	E	207	1552	958	303	289	2	0	0

- Molecule 14 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	F	178	1408	885	267	251	5	0	0

- Molecule 15 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	G	174	1330	836	249	244	1	0	0

- Molecule 16 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	H	47	350	220	64	65	1	0	0

- Molecule 17 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	J	146	1143	724	217	199	3	0	0

- Molecule 18 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	K	122	941	590	180	169	2	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	1	VAL	MET	conflict	UNP A0A045HTP7

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	L	144	1075	666	217	190	2	0	0

- Molecule 20 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	M	134	1072	679	215	177	1	0	0

- Molecule 21 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	N	116	908	574	175	158	1	0	0

- Molecule 22 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
22	O	119	905	552	191	162	0	0

- Molecule 23 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	P	112	907	573	174	159	1	0	0

- Molecule 24 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
24	Q	124	993	616	207	170	0	0

- Molecule 25 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
25	R	100	757	482	138	137	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	1	MET	-	insertion	UNP P9WHC3

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	S	113	Total	C	N	O	0	0
			860	533	178	149		

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	T	95	Total	C	N	O	0	0
			741	469	138	134		

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	U	90	Total	C	N	O	S	0	0
			699	430	138	129	2		

- Molecule 29 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	V	177	Total	C	N	O	0	0
			1319	822	243	254		

- Molecule 30 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	W	77	Total	C	N	O	0	0
			564	345	117	102		

- Molecule 31 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X	62	Total	C	N	O	S	0	0
			468	284	100	80	4		

- Molecule 32 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	68	Total	C	N	O	S	0	0
			560	343	109	107	1		

- Molecule 33 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Z	59	Total	C	N	O	0	0
			476	293	101	82		

- Molecule 34 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	1519	Total	C	N	O	P	0	0
			32620	14535	5961	10605	1519		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	c	207	Total	C	N	O	S	0	0
			1654	1030	322	298	4		

- Molecule 36 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	d	200	Total	C	N	O	S	0	0
			1650	1036	316	296	2		

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e	169	Total	C	N	O	S	0	0
			1222	770	231	218	3		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	95	Total	C	N	O	S	0	0
			757	480	133	141	3		

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	155	Total	C	N	O	S	0	0
			1230	768	241	219	2		

- Molecule 40 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	131	Total	C	N	O	S	0	0
			1006	631	188	186	1		

- Molecule 41 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	i	127	Total	C	N	O	0	0
			992	628	195	169		

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	99	Total	C	N	O	S	0	0
			789	496	146	144	3		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	k	117	Total	C	N	O	0	0
			873	540	175	158		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	122	Total	C	N	O	S	0	0
			959	594	197	166	2		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	m	116	Total	C	N	O	S	0	0
			945	578	196	168	3		

- Molecule 46 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	60	Total	C	N	O	S	0	0
			468	294	96	73	5		

- Molecule 47 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	o	87	Total	C	N	O	0	0
			718	449	144	125		

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	p	113	Total	C	N	O	0	0
			884	564	166	154		

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	95	Total	C	N	O	S	0	0
			770	482	152	133	3		

- Molecule 50 is a protein called 30S ribosomal protein S18 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r	64	Total	C	N	O	S	0	0
			506	315	98	90	3		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	83	Total	C	N	O	S	0	0
			672	432	125	114	1		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	t	85	Total	C	N	O	0	0
			652	394	141	117		

- Molecule 53 is a RNA chain called tRNA (Met).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
53	x	77	1643	732	297	537	77	0	0
53	y	77	1644	732	297	538	77	0	0

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
54	z	6	129	58	25	40	6	0	0

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	1	1	Total 1	Zn 1	0
55	4	1	Total 1	Zn 1	0
55	6	1	Total 1	Zn 1	0
55	X	1	Total 1	Zn 1	0
55	n	1	Total 1	Zn 1	0
55	r	1	Total 1	Zn 1	0

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

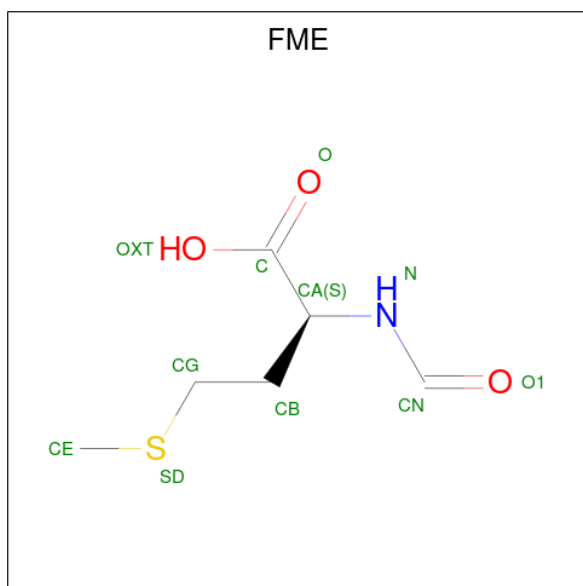
Mol	Chain	Residues	Atoms		AltConf
56	4	2	Total 2	Mg 2	0
56	A	297	Total 297	Mg 297	0
56	B	5	Total 5	Mg 5	0
56	C	2	Total 2	Mg 2	0
56	D	1	Total 1	Mg 1	0
56	E	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
56	L	1	Total	Mg	0
			1	1	
56	U	1	Total	Mg	0
			1	1	
56	a	129	Total	Mg	0
			129	129	
56	r	1	Total	Mg	0
			1	1	
56	t	1	Total	Mg	0
			1	1	
56	y	2	Total	Mg	0
			2	2	

- Molecule 57 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C<sub>6</sub>H<sub>11</sub>NO<sub>3</sub>S).




Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
57	y	1	10	6	1	2	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.

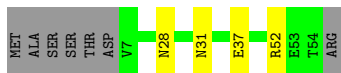
- Molecule 1: 50S ribosomal protein L32

Chain 0:  84% 11% 5%




- Molecule 2: 50S ribosomal protein L33 2

Chain 1:  80% 7% 13%




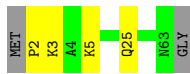
- Molecule 3: 50S ribosomal protein L34

Chain 2:  91% 6%




- Molecule 4: 50S ribosomal protein L35

Chain 3:  91% 6%

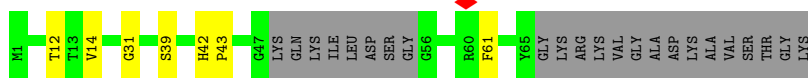


- Molecule 5: 50S ribosomal protein L36

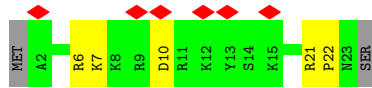
Chain 4:  84% 16%



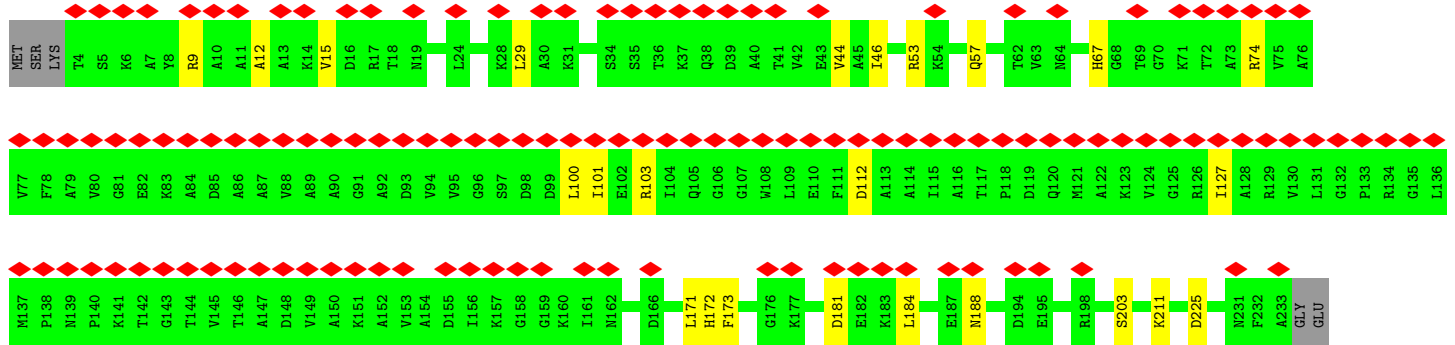
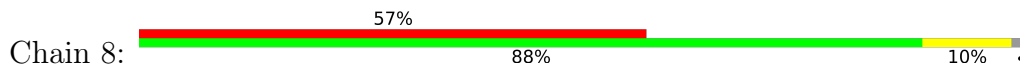
- Molecule 6: 50S ribosomal protein L31



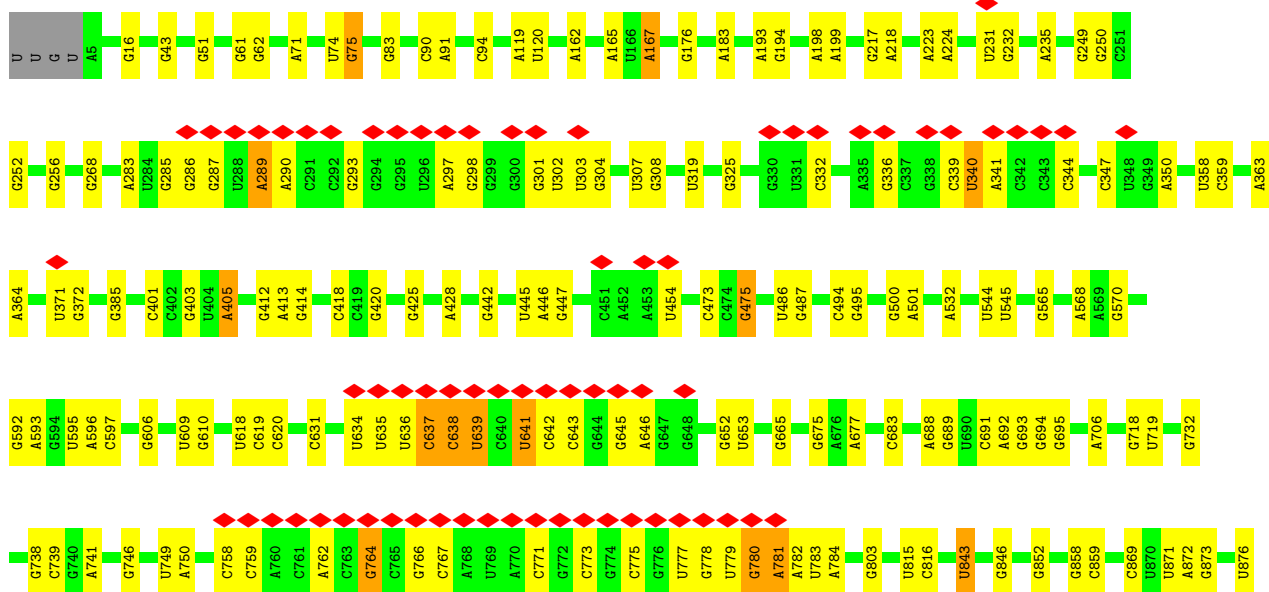
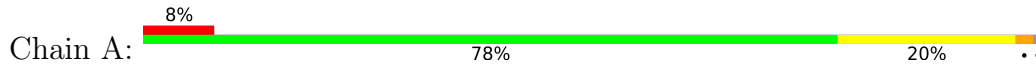
• Molecule 7: 50S ribosomal protein L37

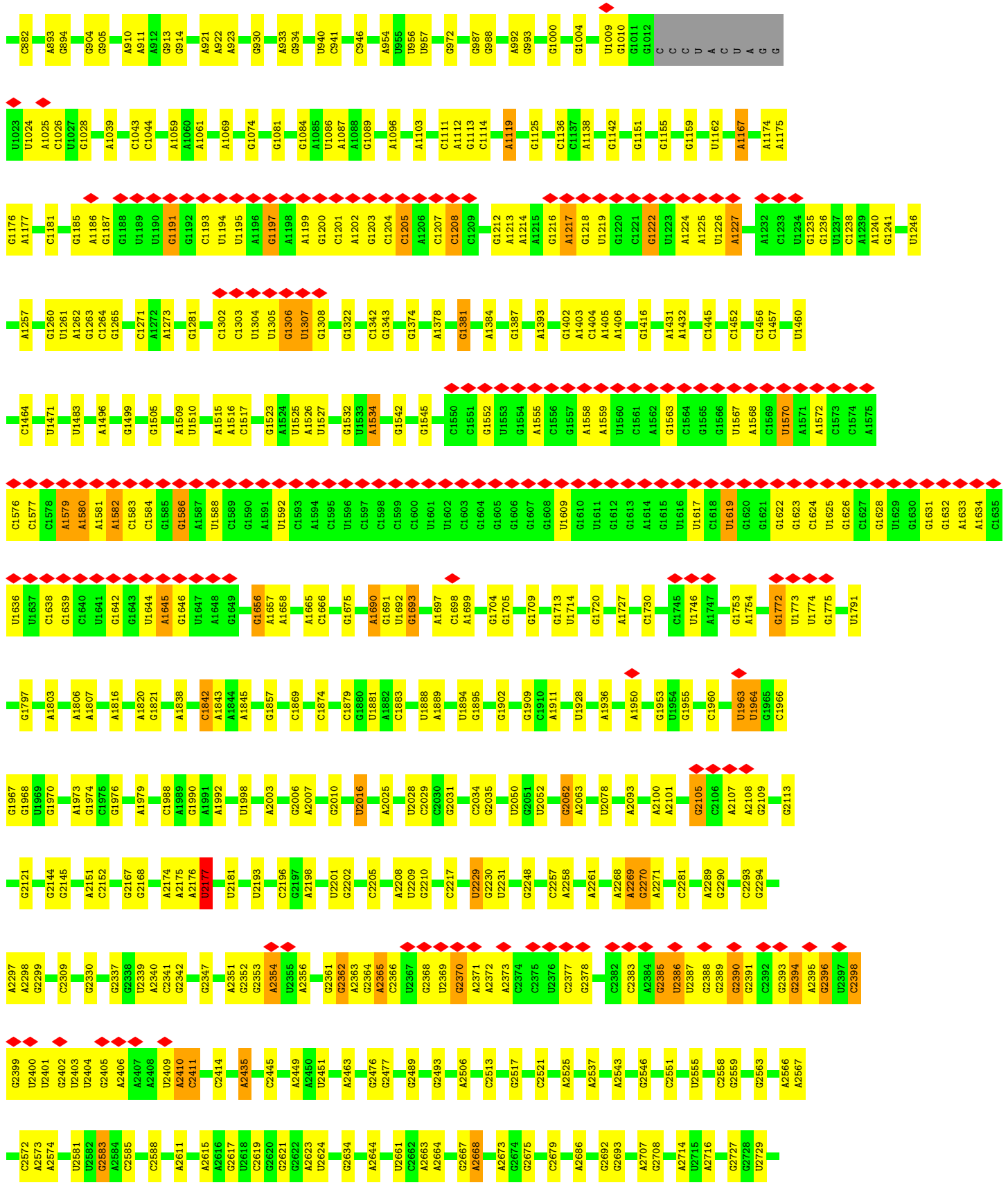


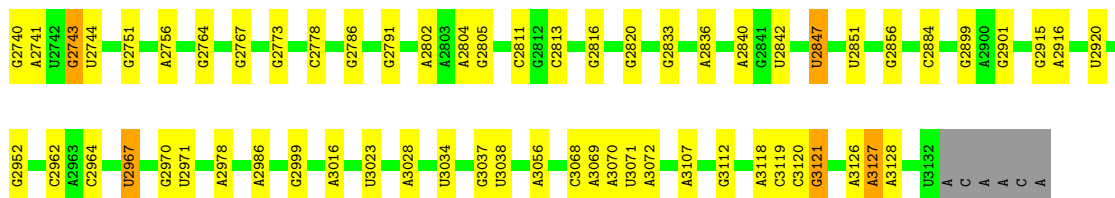
• Molecule 8: 50S ribosomal protein L1



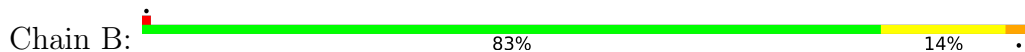
• Molecule 9: 23S rRNA



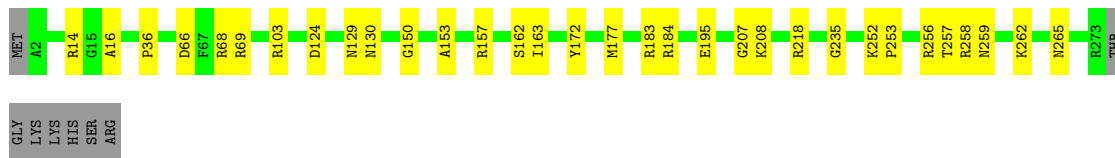
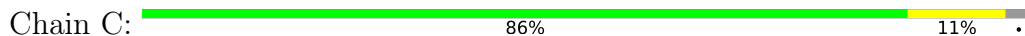




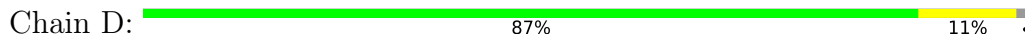
• Molecule 10: 5S rRNA



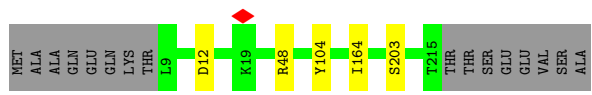
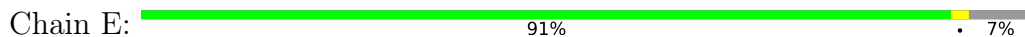
• Molecule 11: 50S ribosomal protein L2



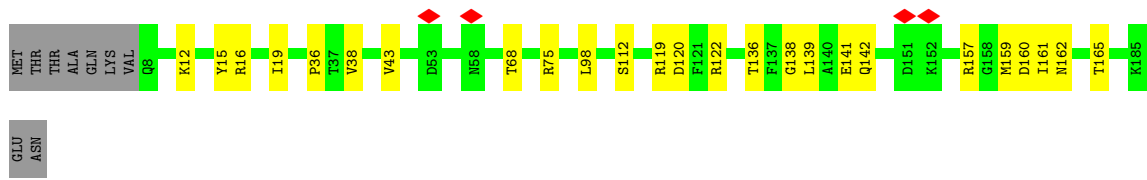
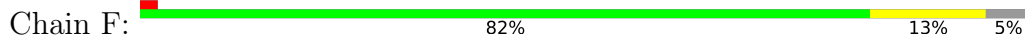
• Molecule 12: 50S ribosomal protein L3



• Molecule 13: 50S ribosomal protein L4

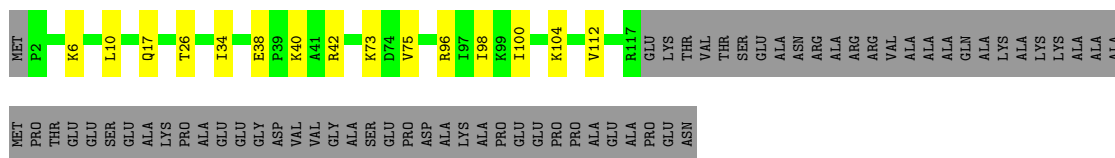


• Molecule 14: 50S ribosomal protein L5

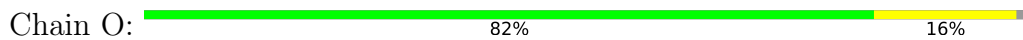


• Molecule 15: 50S ribosomal protein L6

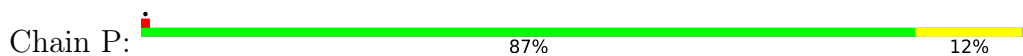




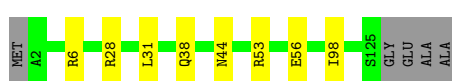
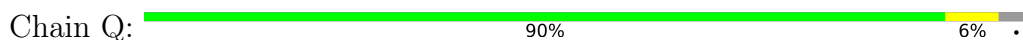
• Molecule 22: 50S ribosomal protein L18



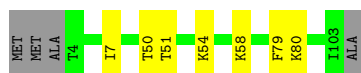
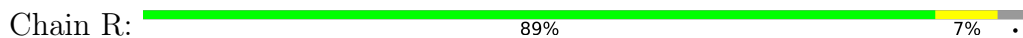
• Molecule 23: 50S ribosomal protein L19



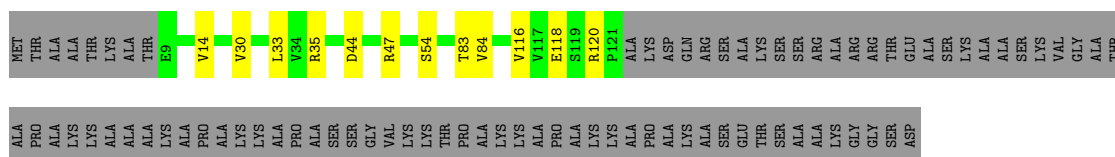
• Molecule 24: 50S ribosomal protein L20



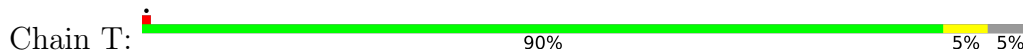
• Molecule 25: 50S ribosomal protein L21

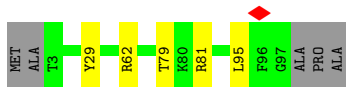


• Molecule 26: 50S ribosomal protein L22

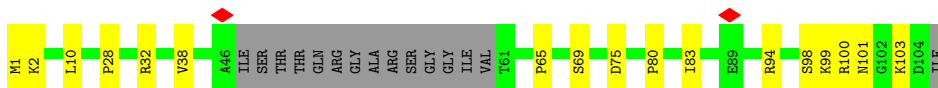


• Molecule 27: 50S ribosomal protein L23

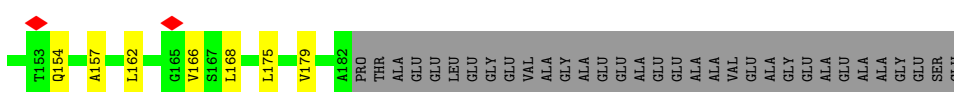




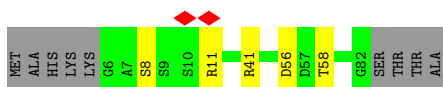
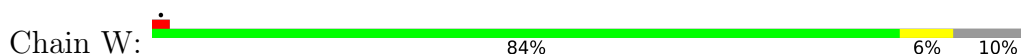
• Molecule 28: 50S ribosomal protein L24



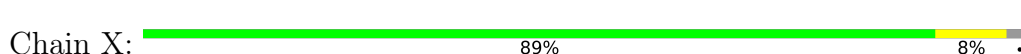
• Molecule 29: 50S ribosomal protein L25



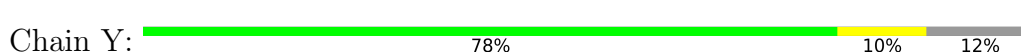
• Molecule 30: 50S ribosomal protein L27



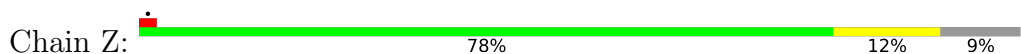
• Molecule 31: 50S ribosomal protein L28

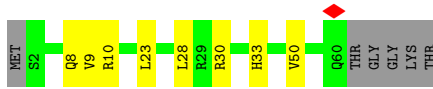


• Molecule 32: 50S ribosomal protein L29

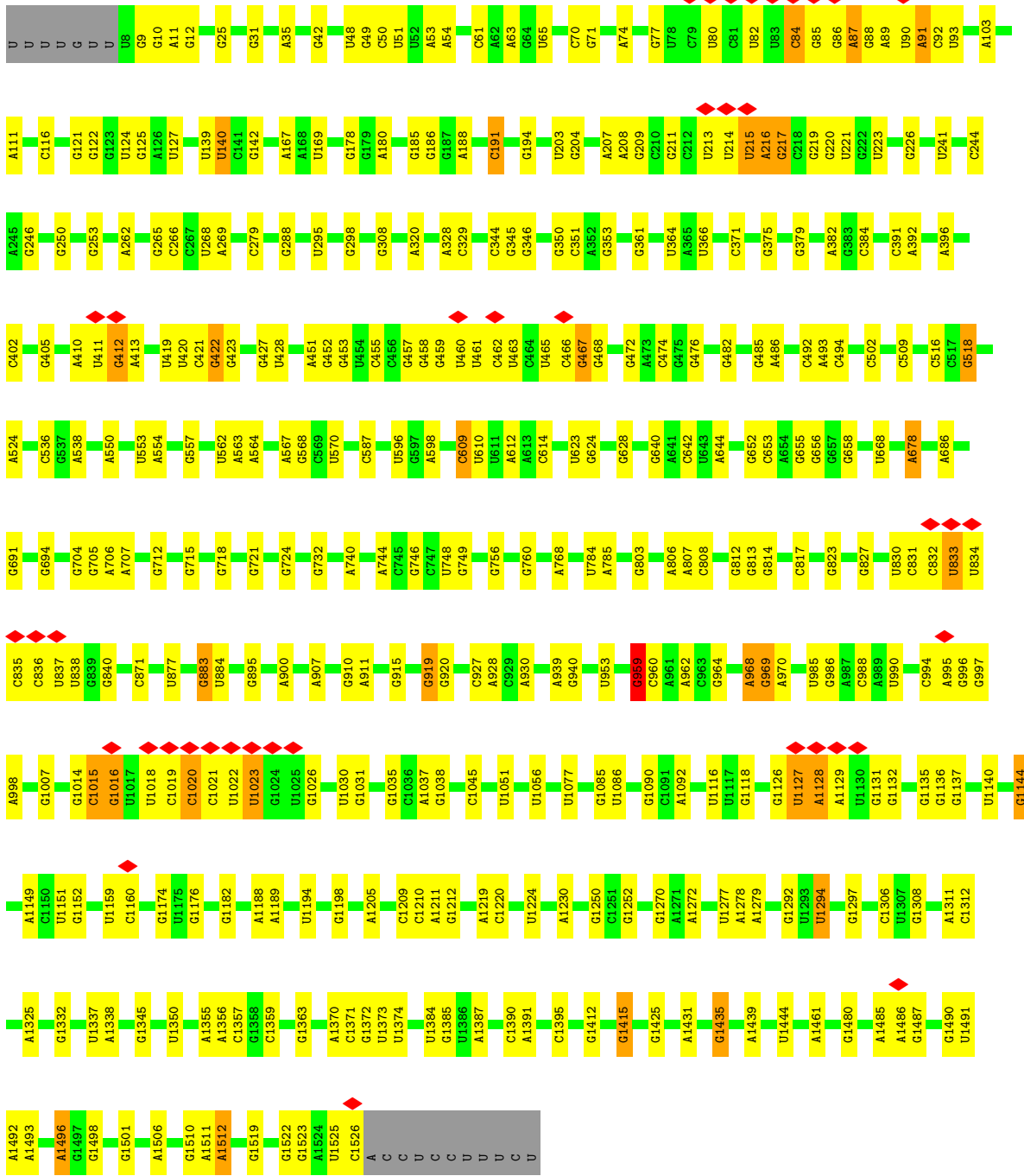


• Molecule 33: 50S ribosomal protein L30



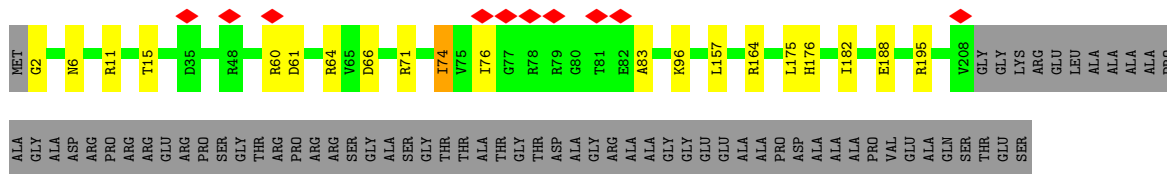


• Molecule 34: 16S rRNA

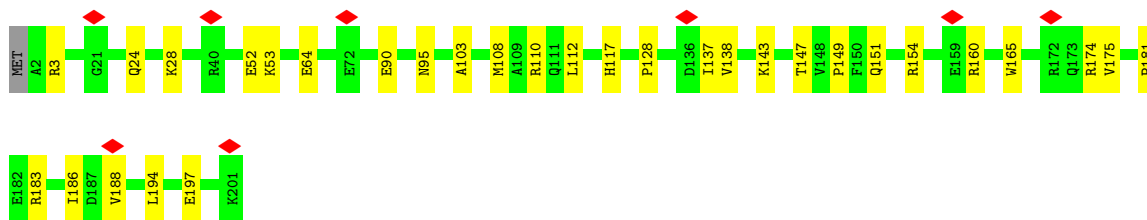
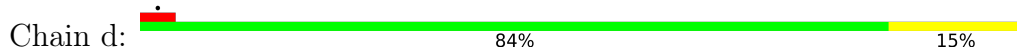


• Molecule 35: 30S ribosomal protein S3

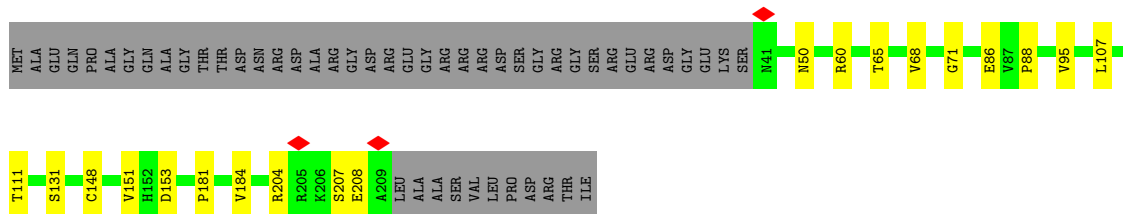




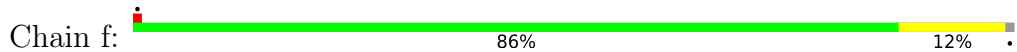
• Molecule 36: 30S ribosomal protein S4



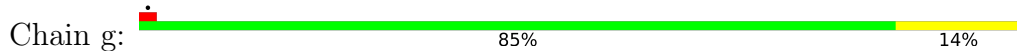
• Molecule 37: 30S ribosomal protein S5



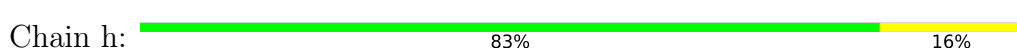
• Molecule 38: 30S ribosomal protein S6



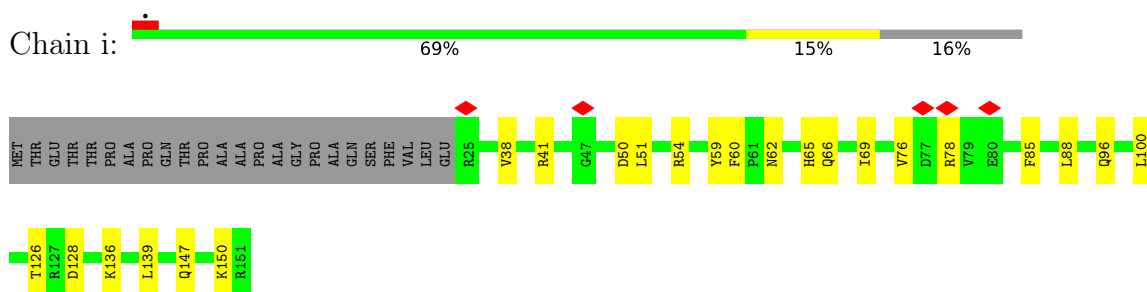
• Molecule 39: 30S ribosomal protein S7



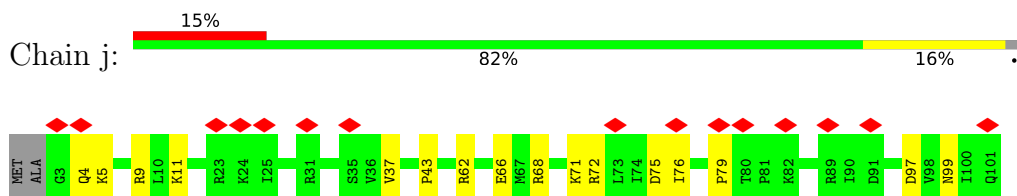
• Molecule 40: 30S ribosomal protein S8



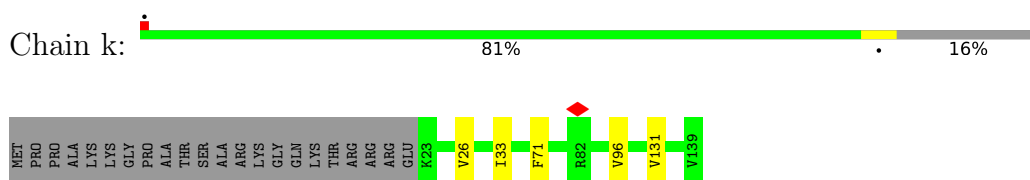
• Molecule 41: 30S ribosomal protein S9



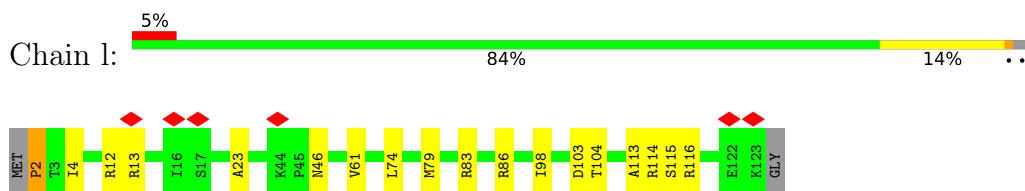
• Molecule 42: 30S ribosomal protein S10



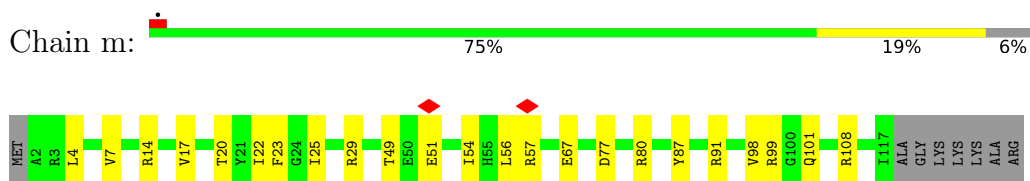
• Molecule 43: 30S ribosomal protein S11



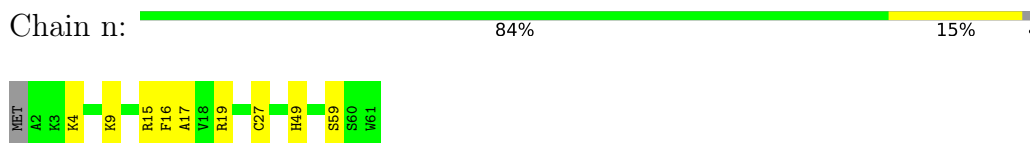
• Molecule 44: 30S ribosomal protein S12



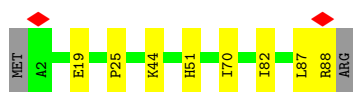
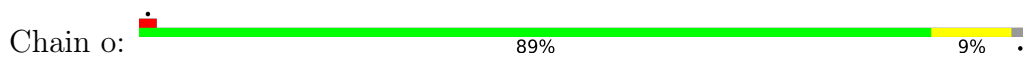
• Molecule 45: 30S ribosomal protein S13



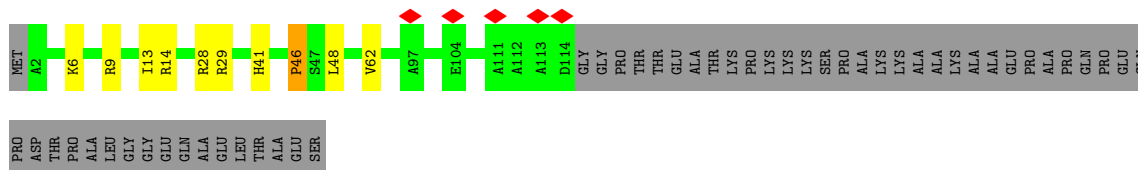
• Molecule 46: 30S ribosomal protein S14 type Z



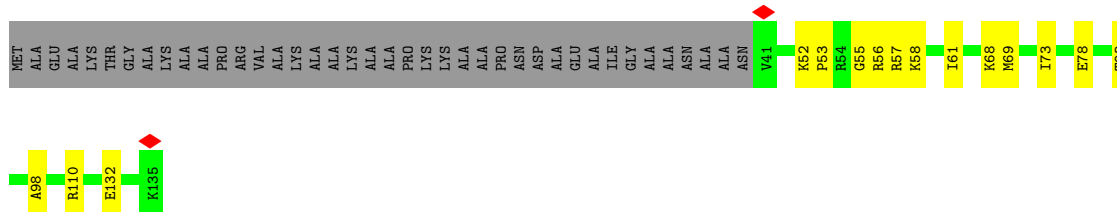
• Molecule 47: 30S ribosomal protein S15



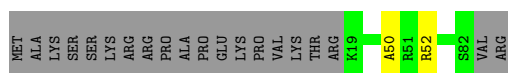
- Molecule 48: 30S ribosomal protein S16



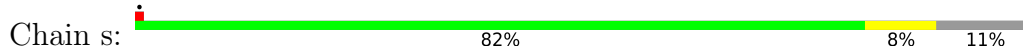
- Molecule 49: 30S ribosomal protein S17



- Molecule 50: 30S ribosomal protein S18 1



- Molecule 51: 30S ribosomal protein S19



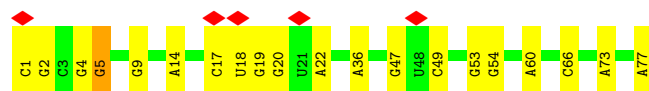
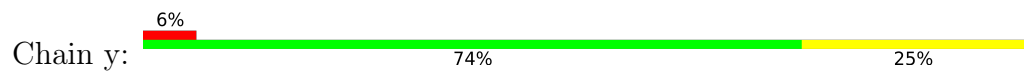
- Molecule 52: 30S ribosomal protein S20



- Molecule 53: tRNA (Met)



• Molecule 53: tRNA (Met)



• Molecule 54: mRNA



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	146018	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.410	Depositor
Minimum map value	-0.005	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.03	Depositor
Map size ( $\text{\AA}$ )	339.19998, 339.19998, 339.19998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.06, 1.06, 1.06	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 2MG, G7M, 4OC, FME, MG, MA6, UR3, OMG, 5MC, 5MU, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	0	0.40	0/435	0.53	0/581
2	1	0.35	0/407	0.51	0/543
3	2	0.46	0/377	0.62	0/494
4	3	0.38	0/499	0.55	0/664
5	4	0.35	0/303	0.59	0/402
6	6	0.27	0/455	0.65	0/611
7	7	0.22	0/188	0.53	0/243
8	8	0.22	0/1728	0.48	0/2339
9	A	0.39	0/74925	0.40	1/116904 (0.0%)
10	B	0.31	0/2749	0.33	0/4284
11	C	0.41	0/2129	0.61	0/2861
12	D	0.37	0/1613	0.57	0/2174
13	E	0.35	0/1575	0.55	0/2129
14	F	0.30	0/1429	0.54	0/1921
15	G	0.24	0/1351	0.53	0/1824
16	H	0.25	0/353	0.60	0/474
17	J	0.37	0/1170	0.47	0/1584
18	K	0.37	0/951	0.61	1/1278 (0.1%)
19	L	0.37	0/1088	0.55	0/1453
20	M	0.33	0/1098	0.57	0/1481
21	N	0.38	0/925	0.54	0/1242
22	O	0.33	0/914	0.59	0/1228
23	P	0.37	0/922	0.57	0/1236
24	Q	0.44	0/1006	0.61	0/1349
25	R	0.37	0/766	0.56	0/1030
26	S	0.37	0/874	0.55	0/1186
27	T	0.34	0/751	0.56	0/1012
28	U	0.33	0/705	0.77	4/941 (0.4%)
29	V	0.27	0/1336	0.59	0/1820
30	W	0.38	0/569	0.62	0/757
31	X	0.40	0/476	0.58	0/638
32	Y	0.31	0/564	0.53	0/756

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Z	0.35	0/480	0.58	0/645
34	a	0.33	0/36331	0.36	0/56686
35	c	0.27	0/1678	0.53	0/2254
36	d	0.28	0/1683	0.55	0/2269
37	e	0.31	0/1238	0.53	0/1673
38	f	0.27	0/767	0.47	0/1036
39	g	0.27	0/1250	0.54	0/1686
40	h	0.34	0/1021	0.52	0/1379
41	i	0.29	0/1010	0.57	0/1356
42	j	0.30	0/803	0.64	0/1086
43	k	0.29	0/891	0.49	0/1204
44	l	0.35	0/970	0.74	0/1295
45	m	0.30	0/953	0.62	0/1274
46	n	0.32	0/477	0.56	0/634
47	o	0.31	0/727	0.56	0/973
48	p	0.27	0/901	0.62	2/1217 (0.2%)
49	q	0.31	0/782	0.65	0/1045
50	r	0.33	0/511	0.61	0/685
51	s	0.28	0/690	0.52	0/928
52	t	0.29	0/654	0.48	0/867
53	x	0.18	0/1835	0.33	0/2859
53	y	0.28	0/1836	0.35	0/2859
54	z	0.39	0/144	0.79	1/222 (0.5%)
All	All	0.36	0/162263	0.44	9/243571 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
8	8	0	1
25	R	0	1
28	U	0	1
29	V	0	1
44	l	0	3
47	o	0	1
All	All	0	8

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	p	46	PRO	CA-C-N	5.37	131.80	121.54
48	p	46	PRO	C-N-CA	5.37	131.80	121.54
18	K	110	ARG	CA-CB-CG	5.30	124.71	114.10
28	U	38	VAL	CA-C-N	5.18	131.43	121.54
28	U	38	VAL	C-N-CA	5.18	131.43	121.54

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	8	225	ASP	Mainchain
25	R	50	THR	Peptide
28	U	101	ASN	Peptide
29	V	62	ASN	Peptide
44	l	2	PRO	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	429	0	465	5	0
2	1	400	0	409	2	0
3	2	374	0	410	1	0
4	3	494	0	533	3	0
5	4	299	0	323	4	0
6	6	446	0	431	4	0
7	7	186	0	202	5	0
8	8	1704	0	1767	13	0
9	A	66958	0	33723	175	0
10	B	2458	0	1253	4	0
11	C	2088	0	2123	22	0
12	D	1590	0	1633	17	0
13	E	1552	0	1593	3	0
14	F	1408	0	1449	15	0
15	G	1330	0	1390	11	0
16	H	350	0	367	9	0
17	J	1143	0	1173	4	0
18	K	941	0	1005	12	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	L	1075	0	1137	7	0
20	M	1072	0	1115	9	0
21	N	908	0	956	9	0
22	O	905	0	943	12	0
23	P	907	0	947	11	0
24	Q	993	0	1040	6	0
25	R	757	0	817	4	0
26	S	860	0	903	7	0
27	T	741	0	792	3	0
28	U	699	0	738	9	0
29	V	1319	0	1365	17	0
30	W	564	0	584	4	0
31	X	468	0	480	3	0
32	Y	560	0	570	5	0
33	Z	476	0	509	4	0
34	a	32620	0	16427	110	0
35	c	1654	0	1694	13	0
36	d	1650	0	1671	20	0
37	e	1222	0	1291	11	0
38	f	757	0	796	8	0
39	g	1230	0	1288	14	0
40	h	1006	0	1041	12	0
41	i	992	0	1052	14	0
42	j	789	0	821	13	0
43	k	873	0	887	2	0
44	l	959	0	1045	11	0
45	m	945	0	992	13	0
46	n	468	0	492	7	0
47	o	718	0	760	5	0
48	p	884	0	933	7	0
49	q	770	0	833	12	0
50	r	506	0	527	1	0
51	s	672	0	690	5	0
52	t	652	0	703	4	0
53	x	1643	0	836	7	0
53	y	1644	0	835	4	0
54	z	129	0	66	2	0
55	1	1	0	0	0	0
55	4	1	0	0	0	0
55	6	1	0	0	0	0
55	X	1	0	0	0	0
55	n	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	r	1	0	0	0	0
56	4	2	0	0	0	0
56	A	297	0	0	0	0
56	B	5	0	0	0	0
56	C	2	0	0	0	0
56	D	1	0	0	0	0
56	E	1	0	0	0	0
56	L	1	0	0	0	0
56	U	1	0	0	0	0
56	a	129	0	0	0	0
56	r	1	0	0	0	0
56	t	1	0	0	0	0
56	y	2	0	0	0	0
57	y	10	0	10	0	0
All	All	149696	0	98835	587	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 3.

The worst 5 of 587 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:D:7:LEU:H	12:D:34:ASN:HD21	1.33	0.76
53:x:51:U:H3	53:x:65:G:H1	1.38	0.71
9:A:2581:U:HO2'	9:A:2611:A:HO2'	1.39	0.71
15:G:9:ILE:HB	15:G:51:ILE:HB	1.74	0.69
34:a:1118:G:H22	34:a:1137:G:H1	1.41	0.69

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	52/57 (91%)	51 (98%)	1 (2%)	0	100	100
2	1	46/55 (84%)	46 (100%)	0	0	100	100
3	2	42/47 (89%)	42 (100%)	0	0	100	100
4	3	60/64 (94%)	59 (98%)	1 (2%)	0	100	100
5	4	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
6	6	53/80 (66%)	47 (89%)	6 (11%)	0	100	100
7	7	20/24 (83%)	19 (95%)	1 (5%)	0	100	100
8	8	228/235 (97%)	214 (94%)	14 (6%)	0	100	100
11	C	270/280 (96%)	259 (96%)	11 (4%)	0	100	100
12	D	211/217 (97%)	195 (92%)	16 (8%)	0	100	100
13	E	205/223 (92%)	202 (98%)	3 (2%)	0	100	100
14	F	176/187 (94%)	162 (92%)	14 (8%)	0	100	100
15	G	172/179 (96%)	160 (93%)	12 (7%)	0	100	100
16	H	45/152 (30%)	36 (80%)	9 (20%)	0	100	100
17	J	144/195 (74%)	143 (99%)	1 (1%)	0	100	100
18	K	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
19	L	142/146 (97%)	133 (94%)	9 (6%)	0	100	100
20	M	132/138 (96%)	122 (92%)	10 (8%)	0	100	100
21	N	114/180 (63%)	110 (96%)	4 (4%)	0	100	100
22	O	117/122 (96%)	113 (97%)	4 (3%)	0	100	100
23	P	110/113 (97%)	99 (90%)	11 (10%)	0	100	100
24	Q	122/129 (95%)	121 (99%)	1 (1%)	0	100	100
25	R	98/104 (94%)	91 (93%)	6 (6%)	1 (1%)	12	30
26	S	111/197 (56%)	109 (98%)	2 (2%)	0	100	100
27	T	93/100 (93%)	89 (96%)	4 (4%)	0	100	100
28	U	86/105 (82%)	77 (90%)	9 (10%)	0	100	100
29	V	175/215 (81%)	154 (88%)	21 (12%)	0	100	100
30	W	75/86 (87%)	71 (95%)	4 (5%)	0	100	100
31	X	60/64 (94%)	60 (100%)	0	0	100	100
32	Y	66/77 (86%)	63 (96%)	3 (4%)	0	100	100
33	Z	57/65 (88%)	56 (98%)	1 (2%)	0	100	100
35	c	205/274 (75%)	188 (92%)	17 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	d	198/201 (98%)	182 (92%)	16 (8%)	0	100	100
37	e	167/220 (76%)	155 (93%)	12 (7%)	0	100	100
38	f	93/96 (97%)	90 (97%)	3 (3%)	0	100	100
39	g	153/156 (98%)	149 (97%)	4 (3%)	0	100	100
40	h	129/132 (98%)	122 (95%)	7 (5%)	0	100	100
41	i	125/151 (83%)	113 (90%)	12 (10%)	0	100	100
42	j	97/101 (96%)	86 (89%)	11 (11%)	0	100	100
43	k	115/139 (83%)	106 (92%)	9 (8%)	0	100	100
44	l	120/124 (97%)	98 (82%)	20 (17%)	2 (2%)	7	17
45	m	114/124 (92%)	104 (91%)	10 (9%)	0	100	100
46	n	58/61 (95%)	56 (97%)	1 (2%)	1 (2%)	7	17
47	o	85/89 (96%)	79 (93%)	5 (6%)	1 (1%)	10	25
48	p	111/162 (68%)	99 (89%)	11 (10%)	1 (1%)	14	33
49	q	93/135 (69%)	79 (85%)	14 (15%)	0	100	100
50	r	62/84 (74%)	60 (97%)	2 (3%)	0	100	100
51	s	81/93 (87%)	74 (91%)	7 (9%)	0	100	100
52	t	83/86 (96%)	82 (99%)	1 (1%)	0	100	100
All	All	5526/6423 (86%)	5172 (94%)	348 (6%)	6 (0%)	49	72

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	R	51	THR
44	l	114	ARG
46	n	17	ALA
47	o	19	GLU
48	p	46	PRO

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	44/47 (94%)	44 (100%)	0	100	100
2	1	45/51 (88%)	45 (100%)	0	100	100
3	2	38/40 (95%)	38 (100%)	0	100	100
4	3	53/54 (98%)	53 (100%)	0	100	100
5	4	35/35 (100%)	35 (100%)	0	100	100
6	6	49/66 (74%)	48 (98%)	1 (2%)	48	74
7	7	18/20 (90%)	18 (100%)	0	100	100
8	8	175/179 (98%)	175 (100%)	0	100	100
11	C	212/219 (97%)	212 (100%)	0	100	100
12	D	163/166 (98%)	163 (100%)	0	100	100
13	E	159/172 (92%)	158 (99%)	1 (1%)	78	90
14	F	147/155 (95%)	147 (100%)	0	100	100
15	G	143/147 (97%)	143 (100%)	0	100	100
16	H	36/121 (30%)	36 (100%)	0	100	100
17	J	120/161 (74%)	120 (100%)	0	100	100
18	K	101/101 (100%)	101 (100%)	0	100	100
19	L	108/110 (98%)	108 (100%)	0	100	100
20	M	110/114 (96%)	110 (100%)	0	100	100
21	N	94/139 (68%)	93 (99%)	1 (1%)	65	84
22	O	91/93 (98%)	91 (100%)	0	100	100
23	P	98/99 (99%)	98 (100%)	0	100	100
24	Q	97/99 (98%)	97 (100%)	0	100	100
25	R	81/83 (98%)	81 (100%)	0	100	100
26	S	87/140 (62%)	87 (100%)	0	100	100
27	T	81/83 (98%)	81 (100%)	0	100	100
28	U	77/88 (88%)	77 (100%)	0	100	100
29	V	142/164 (87%)	141 (99%)	1 (1%)	76	89
30	W	55/62 (89%)	55 (100%)	0	100	100
31	X	51/52 (98%)	50 (98%)	1 (2%)	48	74
32	Y	60/66 (91%)	60 (100%)	0	100	100
33	Z	51/55 (93%)	51 (100%)	0	100	100
35	c	170/210 (81%)	169 (99%)	1 (1%)	78	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	d	176/177 (99%)	176 (100%)	0	100	100
37	e	121/159 (76%)	121 (100%)	0	100	100
38	f	84/85 (99%)	84 (100%)	0	100	100
39	g	130/131 (99%)	130 (100%)	0	100	100
40	h	107/108 (99%)	107 (100%)	0	100	100
41	i	102/120 (85%)	102 (100%)	0	100	100
42	j	89/90 (99%)	89 (100%)	0	100	100
43	k	90/107 (84%)	88 (98%)	2 (2%)	45	72
44	l	104/105 (99%)	104 (100%)	0	100	100
45	m	99/104 (95%)	99 (100%)	0	100	100
46	n	46/47 (98%)	46 (100%)	0	100	100
47	o	77/79 (98%)	77 (100%)	0	100	100
48	p	90/125 (72%)	90 (100%)	0	100	100
49	q	85/105 (81%)	85 (100%)	0	100	100
50	r	54/72 (75%)	54 (100%)	0	100	100
51	s	75/85 (88%)	75 (100%)	0	100	100
52	t	64/65 (98%)	64 (100%)	0	100	100
All	All	4584/5155 (89%)	4576 (100%)	8 (0%)	85	95

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	k	131	VAL
43	k	26	VAL
31	X	14	PHE
29	V	146	ILE
35	c	74	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
24	Q	44	ASN
35	c	122	GLN
51	s	22	GLN
44	l	75	GLN

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Mol	Chain	Res	Type
24	Q	122	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	114/115 (99%)	16 (14%)	0
34	a	1518/1537 (98%)	239 (15%)	0
53	x	76/77 (98%)	15 (19%)	0
53	y	76/77 (98%)	16 (21%)	0
54	z	5/26 (19%)	2 (40%)	0
9	A	3116/3138 (99%)	486 (15%)	6 (0%)
All	All	4905/4970 (98%)	774 (15%)	6 (0%)

5 of 774 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	43	G
9	A	51	G
9	A	62	G
9	A	71	A
9	A	74	U

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	2365	A
9	A	2385	G
9	A	3127	A
9	A	913	G
9	A	893	A

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

9 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
34	2MG	a	959	34	23,26,27	2.79	8 (34%)	33,38,41	2.42	10 (30%)
34	MA6	a	1512	34	23,26,27	1.48	4 (17%)	33,38,41	3.36	12 (36%)
9	5MU	A	2177	9	19,22,23	4.84	7 (36%)	27,32,35	3.63	9 (33%)
34	5MC	a	960	34	19,22,23	3.73	8 (42%)	26,32,35	0.88	1 (3%)
34	G7M	a	518	34	23,26,27	3.61	12 (52%)	34,39,42	1.73	9 (26%)
9	OMG	A	2791	9	23,26,27	2.30	8 (34%)	32,38,41	1.91	9 (28%)
34	UR3	a	1491	34	19,22,23	2.70	7 (36%)	26,32,35	1.62	3 (11%)
34	MA6	a	1511	34	23,26,27	1.57	4 (17%)	33,38,41	3.03	11 (33%)
34	4OC	a	1395	34	20,23,24	2.99	8 (40%)	25,32,35	1.17	2 (8%)

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
34	2MG	a	959	34	-	2/9/27/28	0/3/3/3
34	MA6	a	1512	34	-	3/11/29/30	0/3/3/3
9	5MU	A	2177	9	-	2/7/25/26	0/2/2/2
34	5MC	a	960	34	-	0/7/25/26	0/2/2/2
34	G7M	a	518	34	-	2/7/25/26	0/3/3/3
9	OMG	A	2791	9	-	0/9/27/28	0/3/3/3
34	UR3	a	1491	34	-	0/7/25/26	0/2/2/2
34	MA6	a	1511	34	-	1/11/29/30	0/3/3/3
34	4OC	a	1395	34	-	1/9/29/30	0/2/2/2

The worst 5 of 66 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	2177	5MU	C2-N1	10.98	1.55	1.38
34	a	518	G7M	C8-N7	10.55	1.51	1.33
9	A	2177	5MU	C6-N1	10.39	1.55	1.38
9	A	2177	5MU	C4-C5	9.35	1.60	1.44
34	a	960	5MC	C6-C5	9.06	1.49	1.34

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	2177	5MU	C5-C4-N3	12.10	125.84	115.32
34	a	1512	MA6	N1-C6-N6	-11.88	102.38	116.86
34	a	1511	MA6	N1-C6-N6	-10.01	104.66	116.86
9	A	2177	5MU	C5-C6-N1	-9.42	113.08	123.31
34	a	1512	MA6	C5-C6-N6	8.26	138.41	125.33

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	a	1512	MA6	O4'-C4'-C5'-O5'
34	a	959	2MG	O4'-C4'-C5'-O5'
34	a	1512	MA6	C3'-C4'-C5'-O5'
9	A	2177	5MU	O4'-C4'-C5'-O5'
34	a	959	2MG	C3'-C4'-C5'-O5'

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	a	959	2MG	1	0
9	A	2177	5MU	1	0
34	a	518	G7M	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 450 ligands modelled in this entry, 449 are monoatomic - leaving 1 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
57	FME	y	101	53	8,9,10	1.00	0	8,9,11	0.91	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
57	FME	y	101	53	-	6/7/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	y	101	FME	O1-CN-N-CA
57	y	101	FME	CB-CA-N-CN
57	y	101	FME	O-C-CA-CB
57	y	101	FME	CA-CB-CG-SD
57	y	101	FME	CB-CG-SD-CE

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.

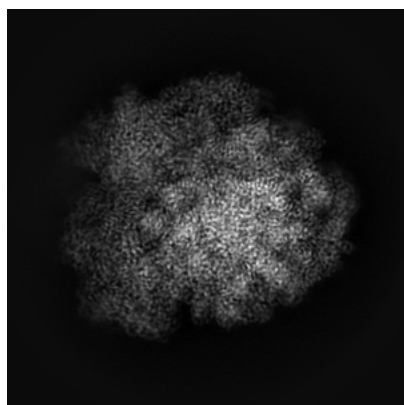
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23976. These allow visual inspection of the internal detail of the map and identification of artifacts.

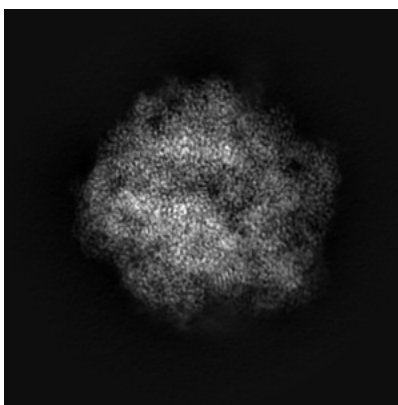
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

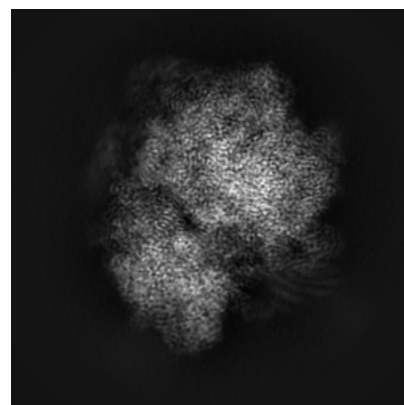
#### 6.1.1 Primary map



X



Y

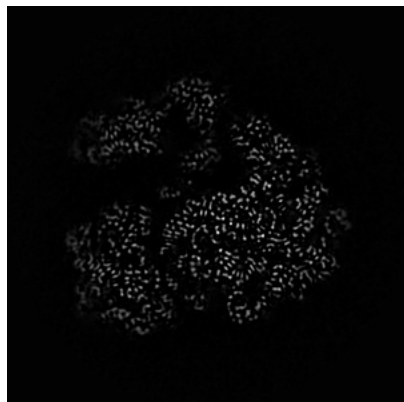


Z

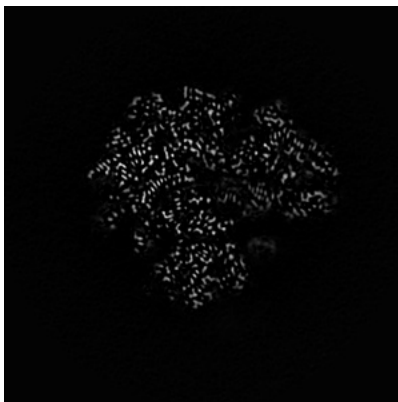
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

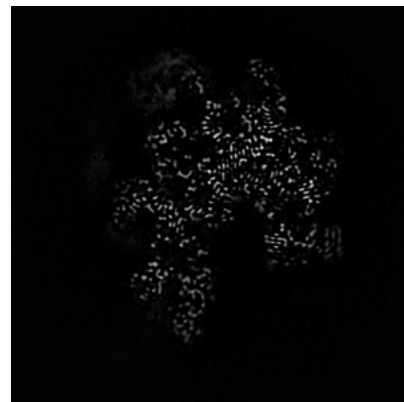
#### 6.2.1 Primary map



X Index: 160



Y Index: 160

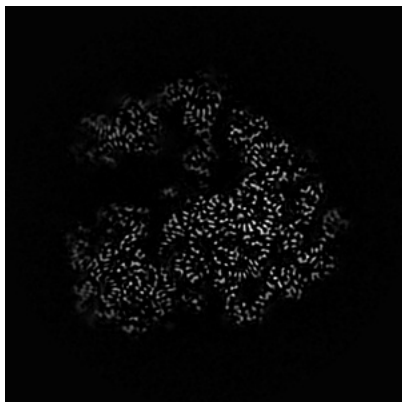


Z Index: 160

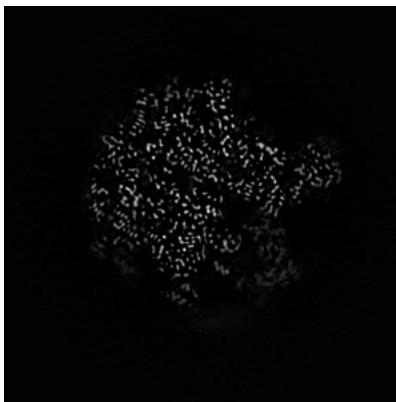
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

### 6.3.1 Primary map



X Index: 162



Y Index: 184

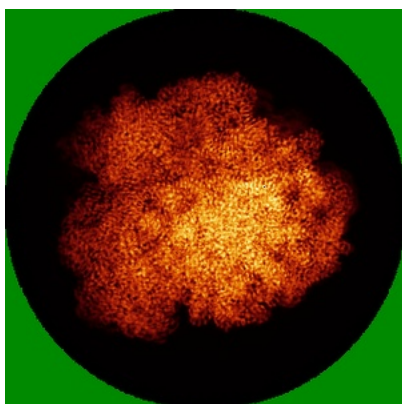


Z Index: 144

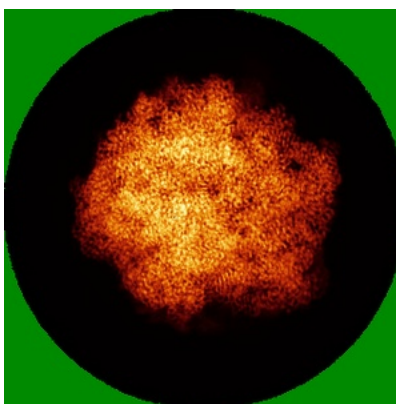
The images above show the largest variance slices of the map in three orthogonal directions.

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

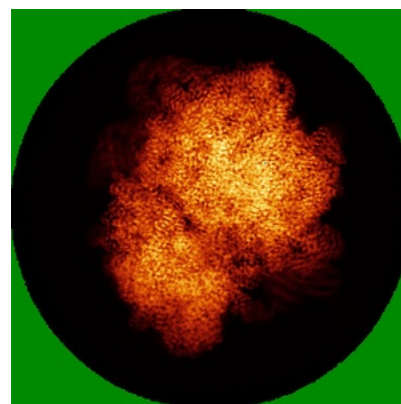
### 6.4.1 Primary map



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



X



Y



Z

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.

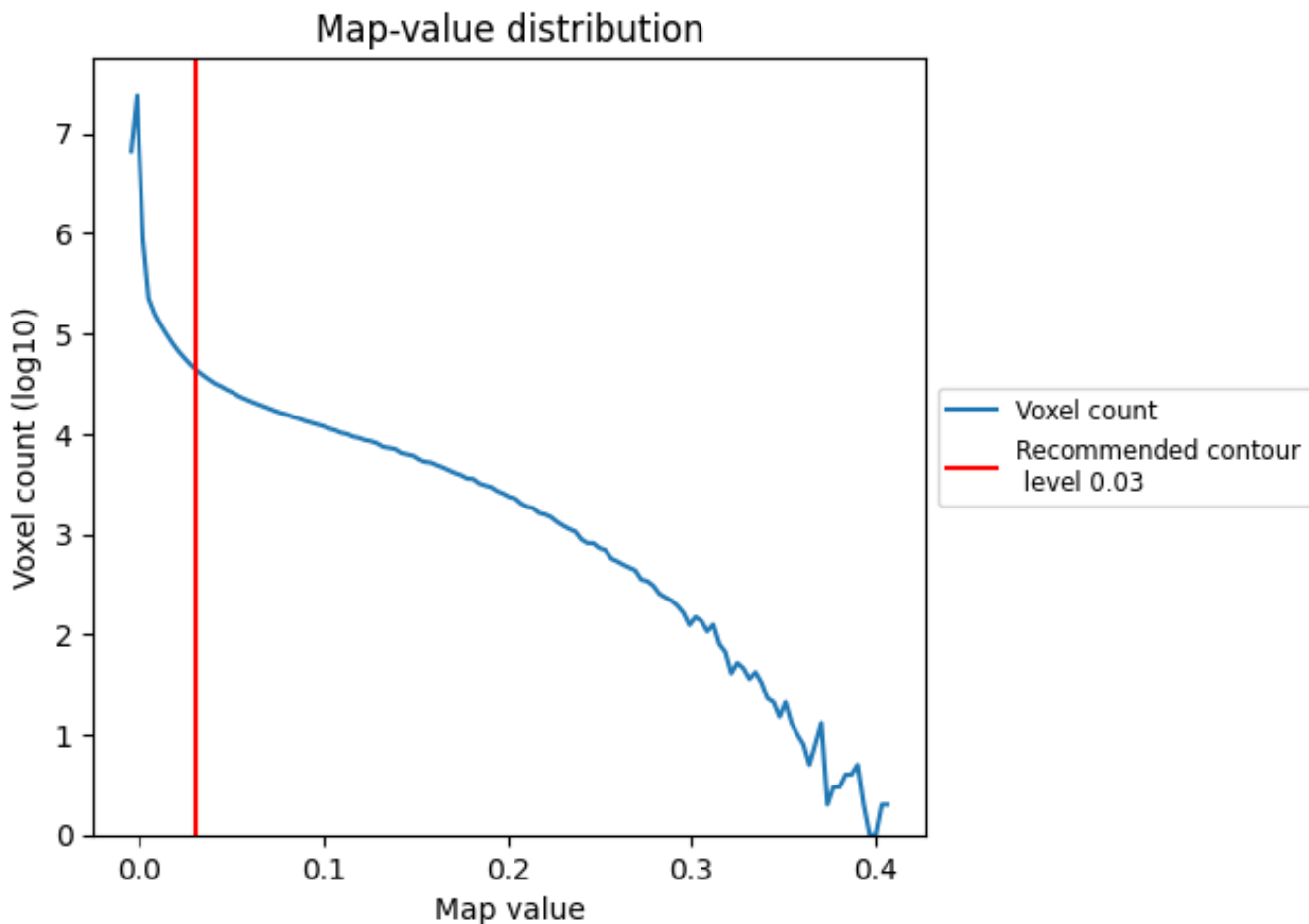
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

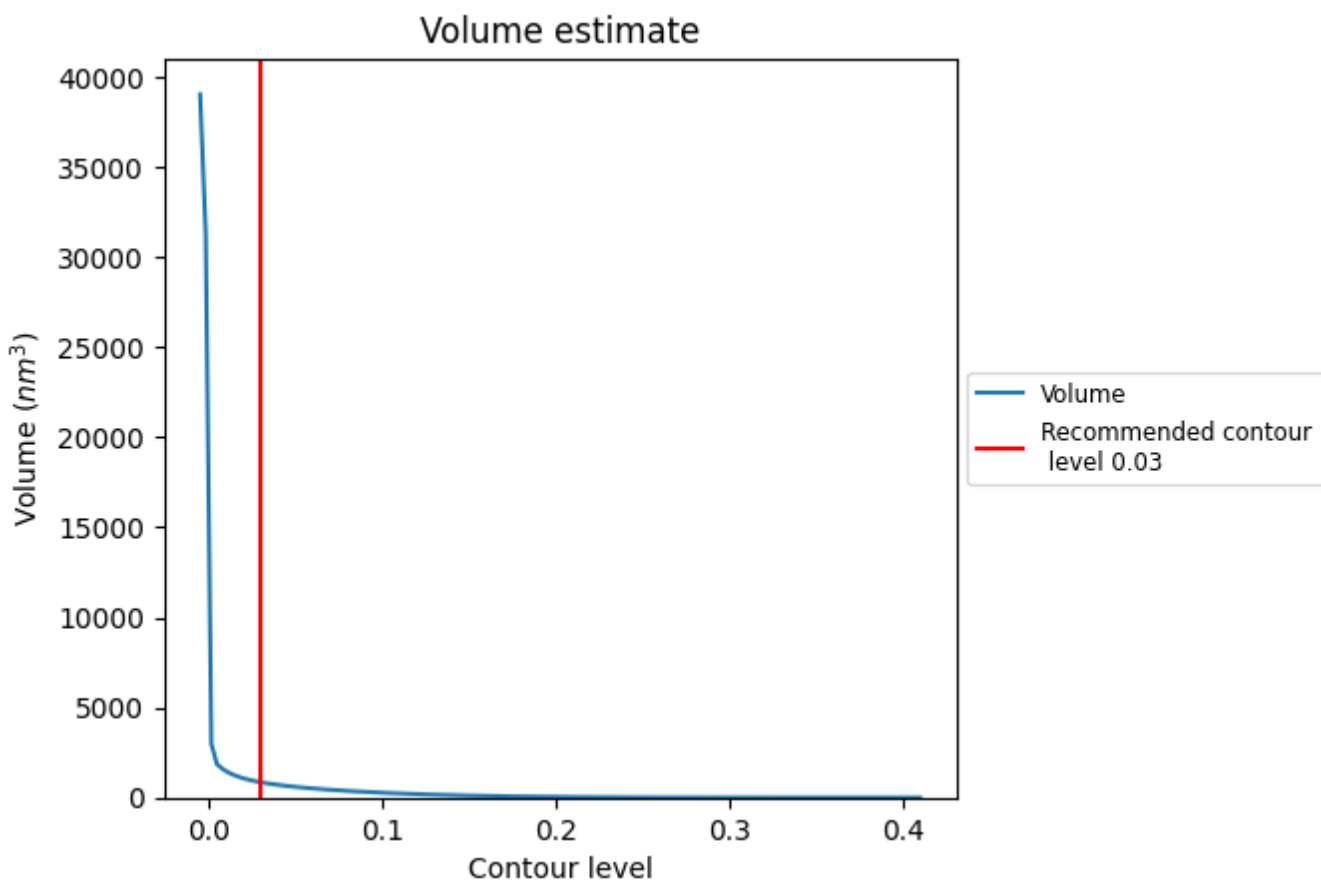
This section contains the results of statistical analysis of the map.

### 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.

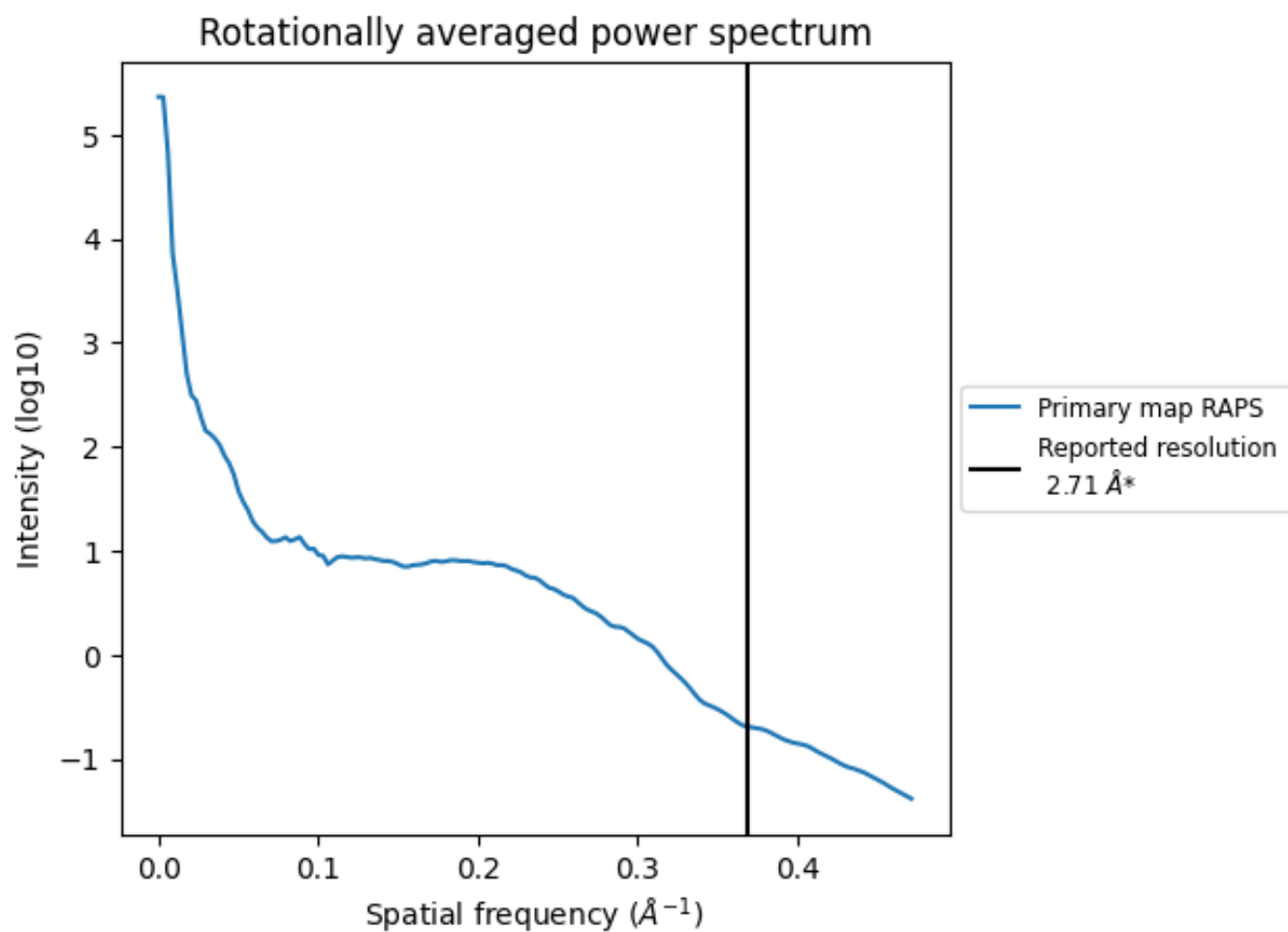
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 853 nm<sup>3</sup>; this corresponds to an approximate mass of 770 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 [i](#)

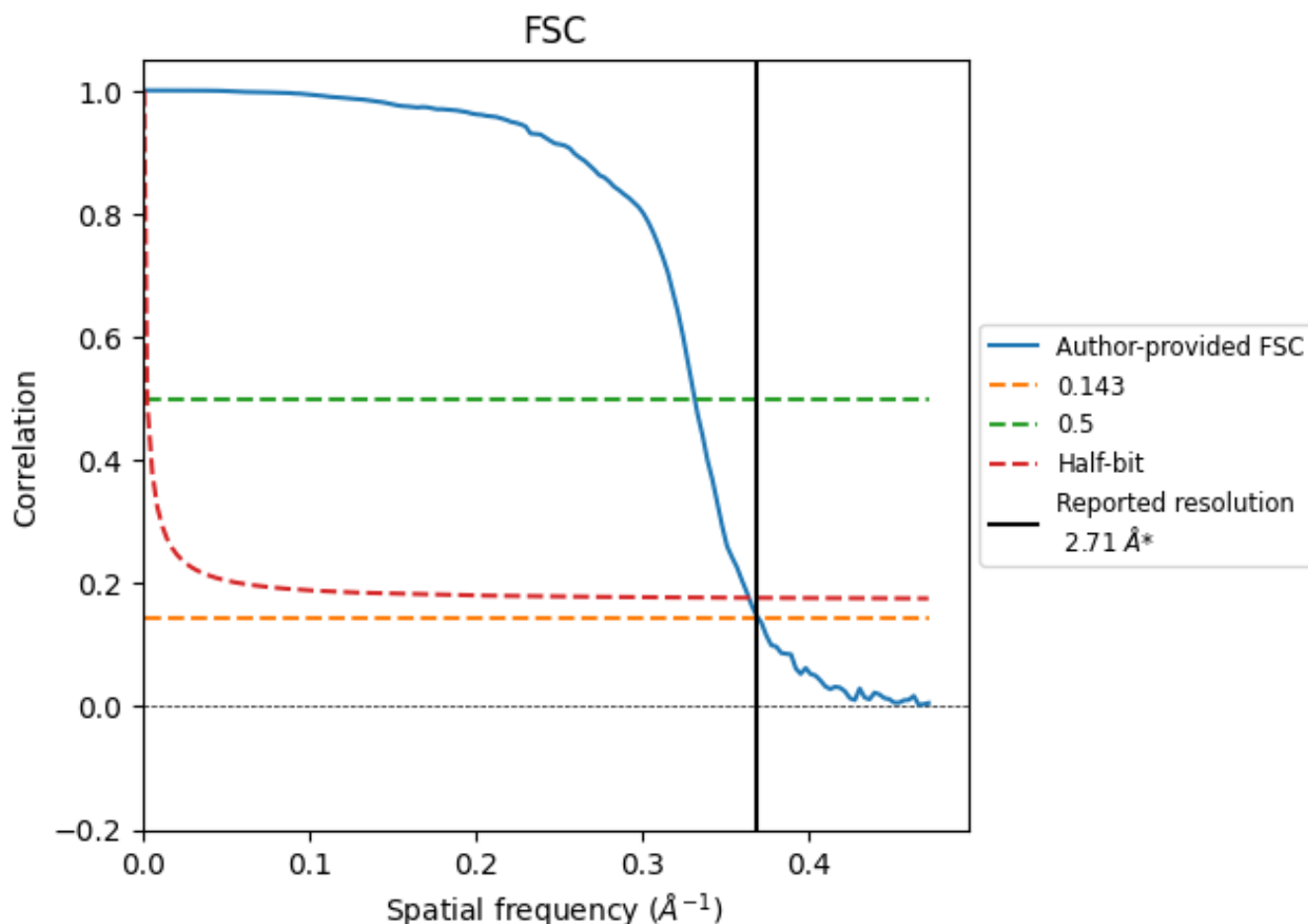


\*Reported resolution corresponds to spatial frequency of 0.369 Å<sup>-1</sup>

## 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 0.369 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

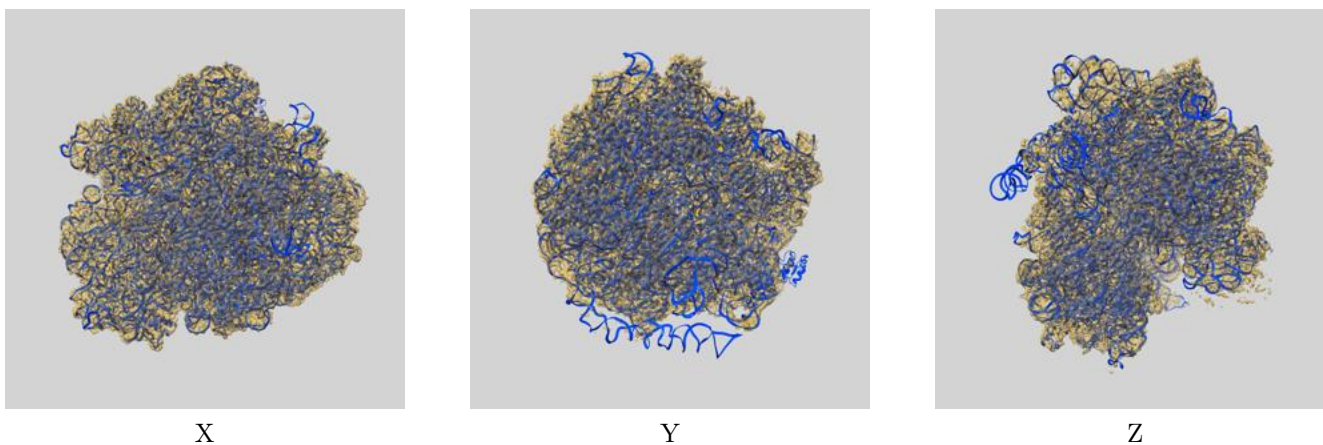
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.71	-	-
Author-provided FSC curve	2.70	3.02	2.75
Unmasked-calculated*	-	-	-

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

## 9 Map-model fit [i](#)

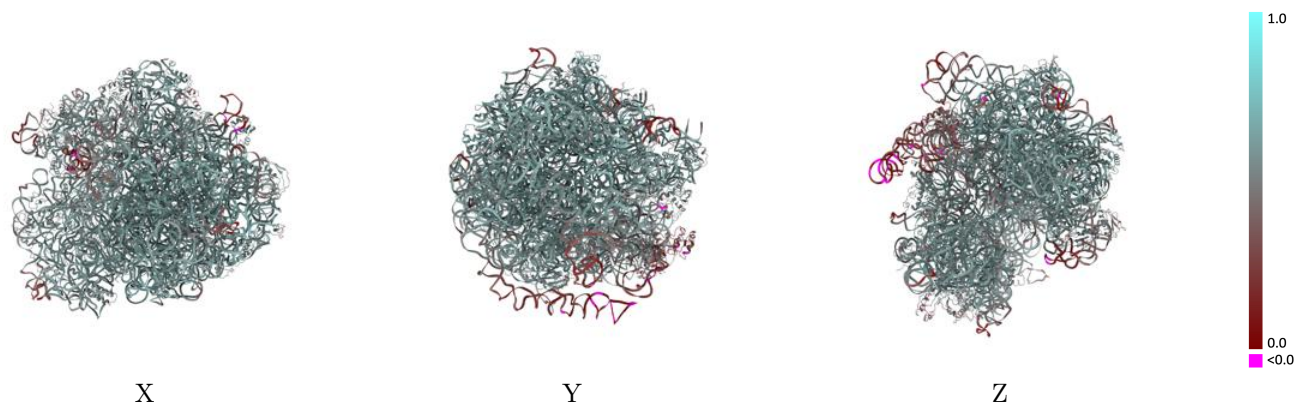
This section contains information regarding the fit between EMDB map EMD-23976 and PDB model 7MT7. Per-residue inclusion information can be found in section 3 on page 16.

### 9.1 Map-model overlay [i](#)



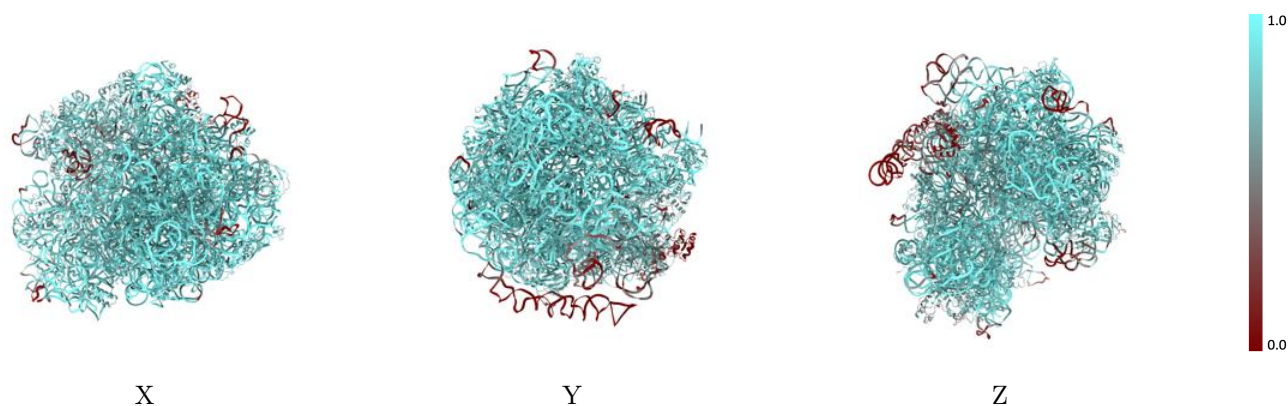
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



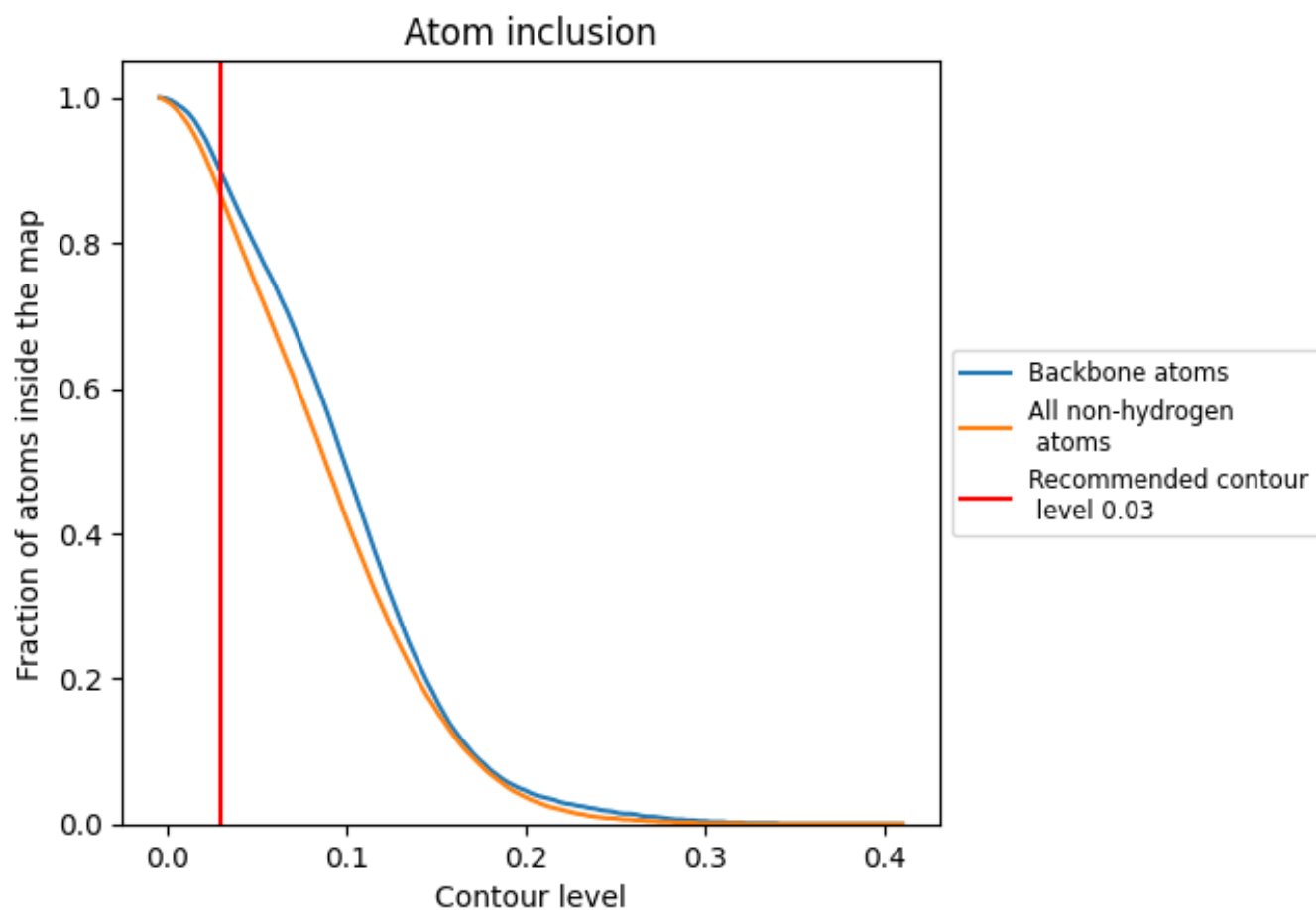
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 90% of all backbone atoms, 86% 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	 0.8620	 0.5540
0	 0.8830	 0.5810
1	 0.8840	 0.5660
2	 0.9450	 0.6070
3	 0.9240	 0.6070
4	 0.9070	 0.5770
6	 0.7720	 0.5030
7	 0.5710	 0.5370
8	 0.3220	 0.3340
A	 0.8740	 0.5580
B	 0.9350	 0.5810
C	 0.9110	 0.6000
D	 0.8850	 0.5820
E	 0.8790	 0.5770
F	 0.8030	 0.5260
G	 0.7310	 0.4810
H	 0.5950	 0.4840
J	 0.8730	 0.5790
K	 0.8750	 0.5750
L	 0.8850	 0.5830
M	 0.8680	 0.5710
N	 0.9070	 0.5920
O	 0.8340	 0.5580
P	 0.8610	 0.5680
Q	 0.8980	 0.5970
R	 0.8810	 0.5820
S	 0.8990	 0.5890
T	 0.8500	 0.5510
U	 0.8210	 0.5400
V	 0.7130	 0.4890
W	 0.9030	 0.5750
X	 0.9180	 0.5910
Y	 0.8210	 0.5470
Z	 0.8660	 0.5610
a	 0.9140	 0.5700



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Chain	Atom inclusion	Q-score
c	 0.7460	 0.5000
d	 0.7600	 0.5010
e	 0.8230	 0.5440
f	 0.7720	 0.5320
g	 0.7700	 0.5240
h	 0.8570	 0.5550
i	 0.7720	 0.5170
j	 0.6820	 0.4510
k	 0.8070	 0.5420
l	 0.8040	 0.5260
m	 0.7930	 0.5200
n	 0.8760	 0.5670
o	 0.8060	 0.5470
p	 0.7760	 0.5230
q	 0.8050	 0.5160
r	 0.8170	 0.5290
s	 0.8080	 0.5300
t	 0.7750	 0.5380
x	 0.6850	 0.4580
y	 0.8660	 0.5580
z	 0.7910	 0.4620