



## Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 01:13 PM UTC

PDB ID : 7MT2 / pdb\_00007mt2  
EMDB ID : EMD-23974  
Title : Mtb 70S initiation complex  
Authors : Cui, Z.; Zhang, J.  
Deposited on : 2021-05-12  
Resolution : 2.76 Å (reported)

This is a Full wwPDB EM Validation 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:

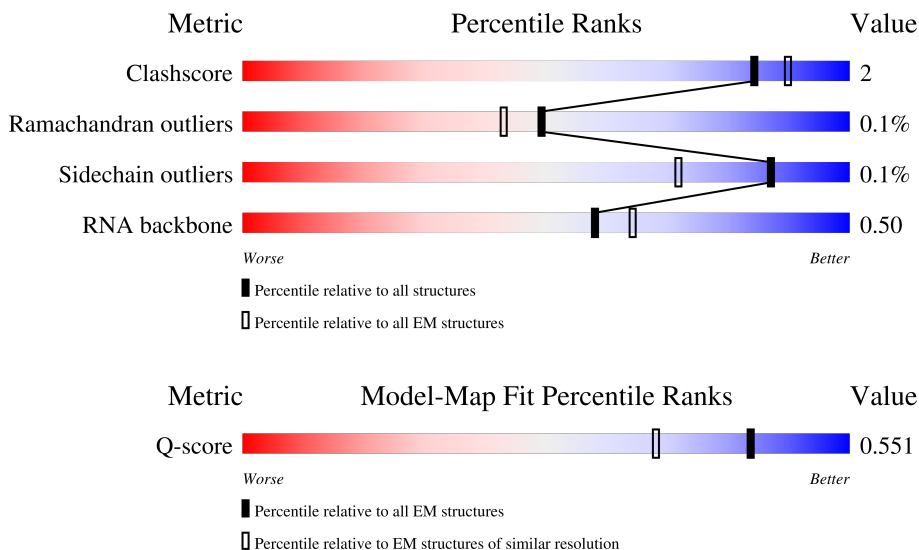
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ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

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

The reported resolution of this entry is 2.76 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.





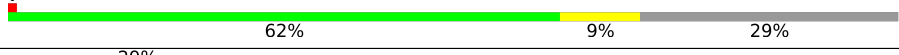




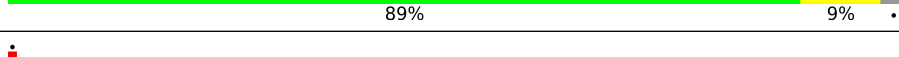
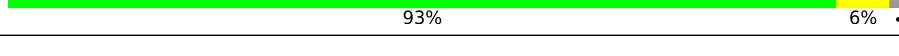

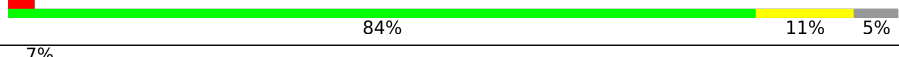
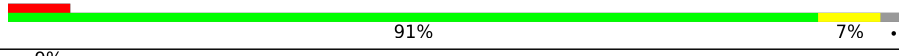


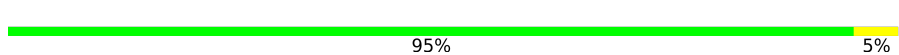

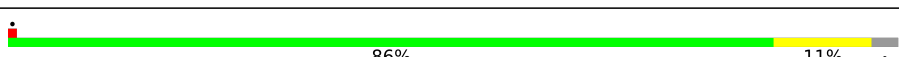
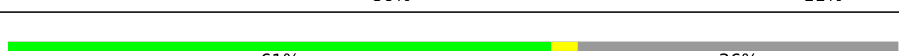
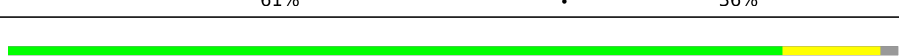

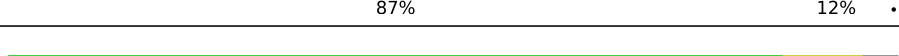
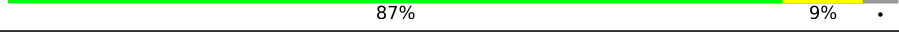


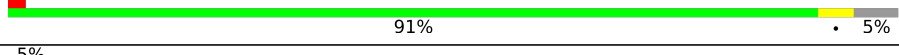
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10642 ( 2.26 - 3.26 )

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	
2	1	55	
3	2	47	

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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	
30	W	86	
31	X	64	
32	Y	77	
33	Z	65	
34	a	1537	
35	c	274	
36	d	201	
37	e	220	
38	f	96	
39	g	156	
40	h	132	
41	i	151	
42	j	101	
43	k	139	
44	l	124	
45	m	124	
46	n	61	
47	o	89	
48	p	162	
49	q	135	
50	r	84	
51	s	93	
52	t	86	
53	y	77	

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Mol	Chain	Length	Quality of chain
54	z	26	 12% 8% 77%

## 2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 148054 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
			66959	29848	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
			Total	C	N	O		
26	S	113	860	533	178	149	0	0

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

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

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

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

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

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

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

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

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

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

- 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 initiator tRNA (Met).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
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).

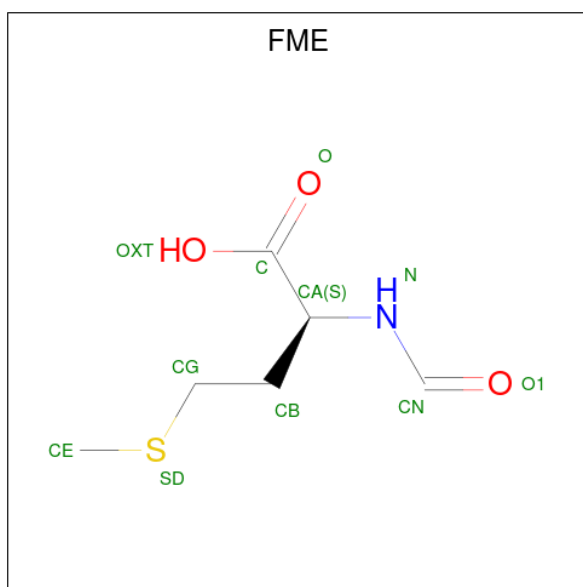
Mol	Chain	Residues	Atoms		AltConf
56	A	302	Total 302	Mg 302	0
56	B	5	Total 5	Mg 5	0
56	C	2	Total 2	Mg 2	0
56	D	1	Total 1	Mg 1	0
56	L	1	Total 1	Mg 1	0
56	a	128	Total 128	Mg 128	0
56	r	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
56	t	1	Total	Mg	0
			1	1	
56	y	1	Total	Mg	0
			1	1	
56	z	1	Total	Mg	0
			1	1	

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




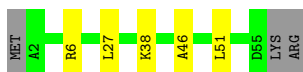
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
57	y	1	10	6	1	2	1	0

### 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:  86% 9% 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:  81% 16%

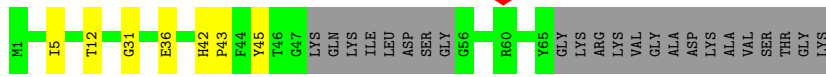


- Molecule 5: 50S ribosomal protein L36

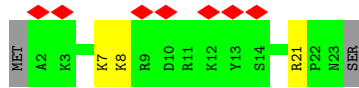
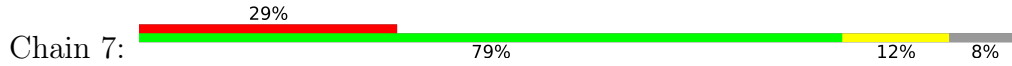
Chain 4:  76% 24%



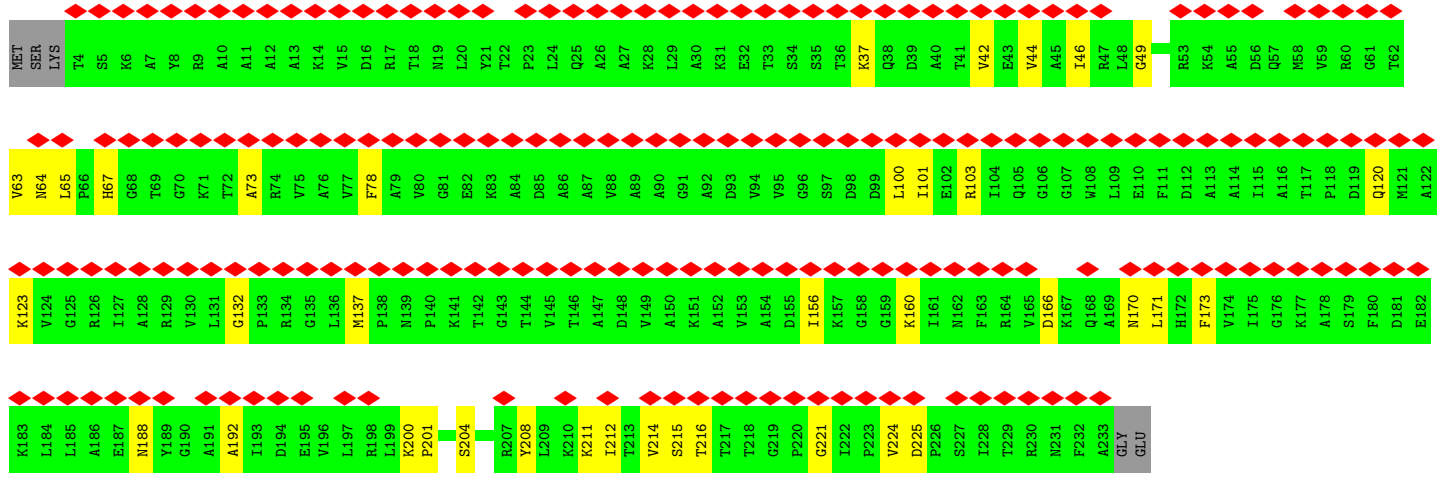
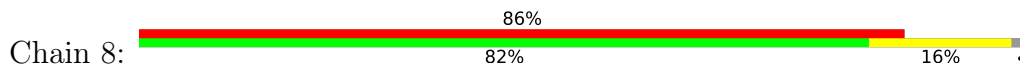
- Molecule 6: 50S ribosomal protein L31



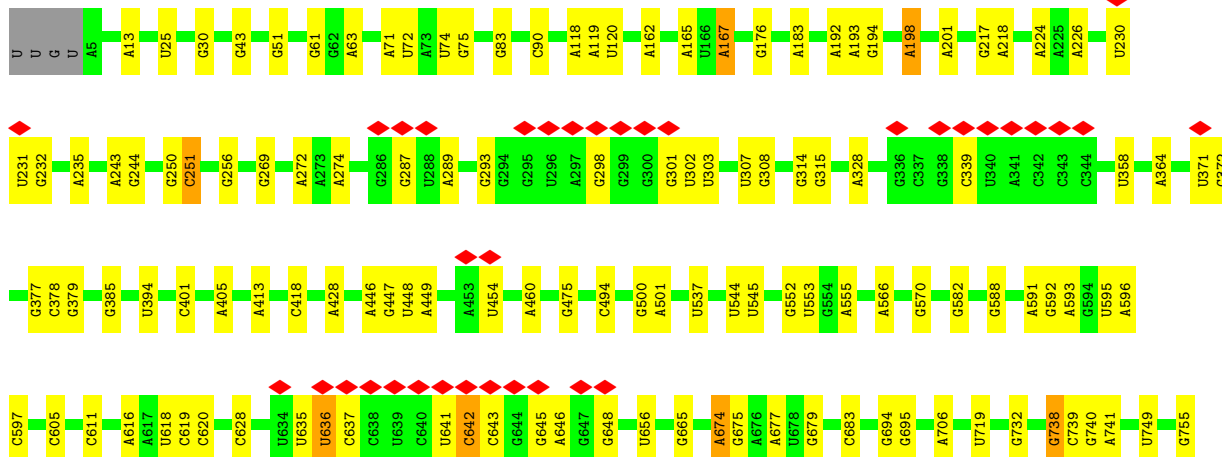
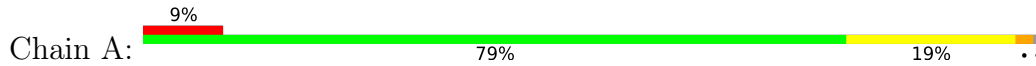
• Molecule 7: 50S ribosomal protein L37

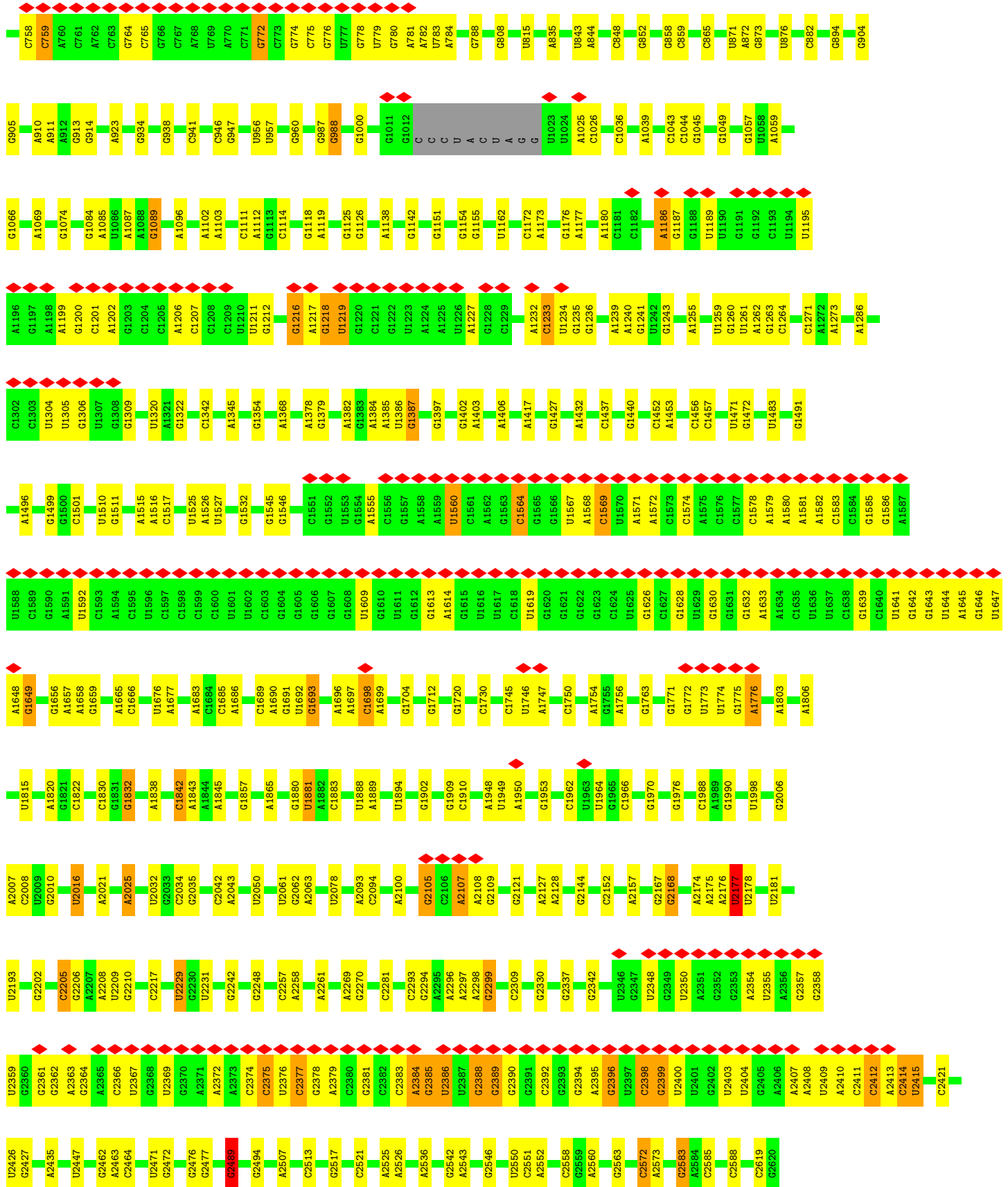


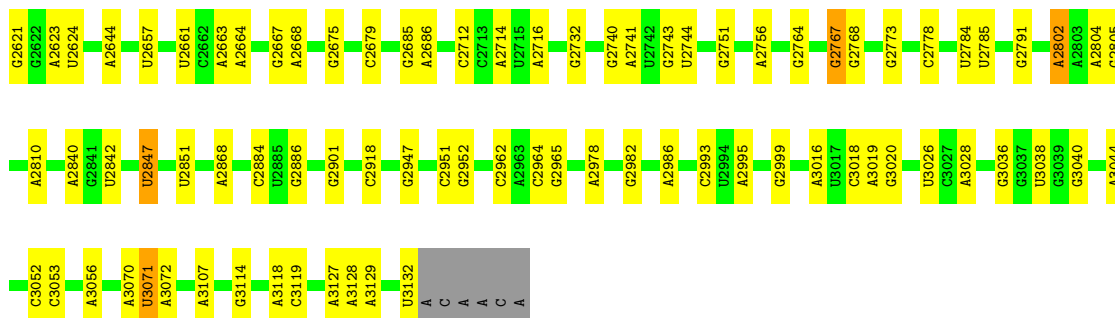
• Molecule 8: 50S ribosomal protein L1



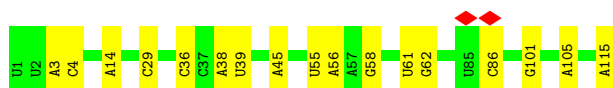
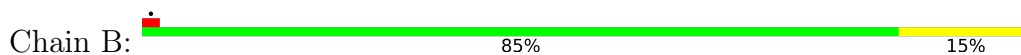
• Molecule 9: 23S rRNA



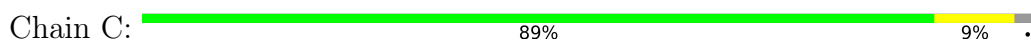




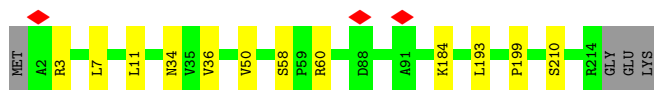
• Molecule 10: 5S rRNA



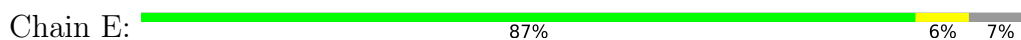
• Molecule 11: 50S ribosomal protein L2



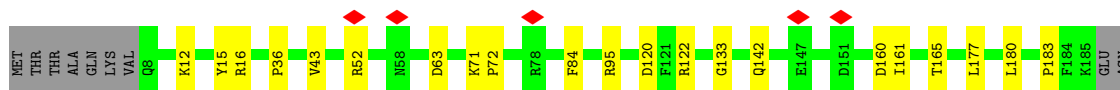
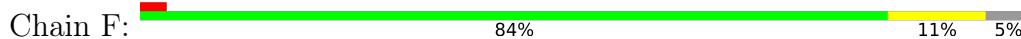
• Molecule 12: 50S ribosomal protein L3



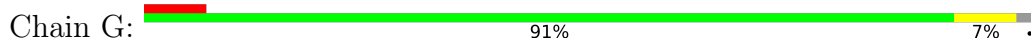
• Molecule 13: 50S ribosomal protein L4

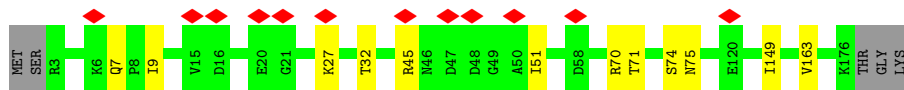


• Molecule 14: 50S ribosomal protein L5

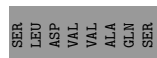
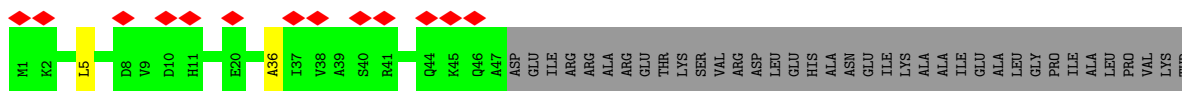


• Molecule 15: 50S ribosomal protein L6

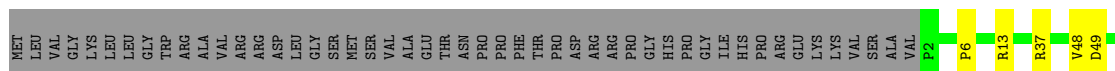




• Molecule 16: 50S ribosomal protein L9



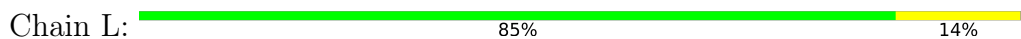
• Molecule 17: 50S ribosomal protein L13



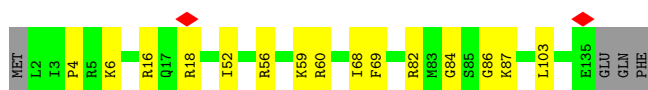
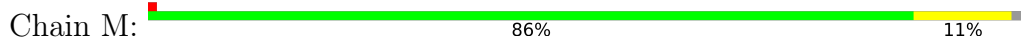
• Molecule 18: 50S ribosomal protein L14




• Molecule 19: 50S ribosomal protein L15

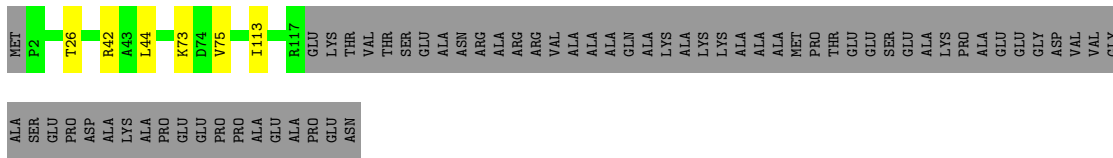


• Molecule 20: 50S ribosomal protein L16




• Molecule 21: 50S ribosomal protein L17

Chain N:  61% 36%




- Molecule 22: 50S ribosomal protein L18

Chain O:  87% 11%




- Molecule 23: 50S ribosomal protein L19

Chain P:  87% 12%




- Molecule 24: 50S ribosomal protein L20

Chain Q:  87% 9%



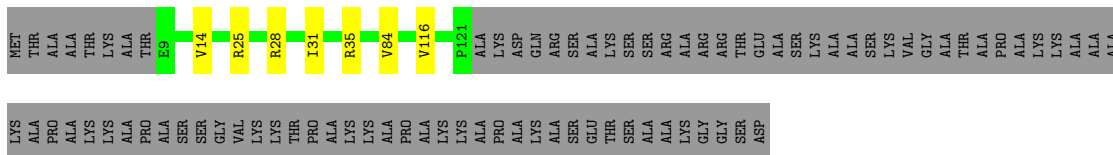
- Molecule 25: 50S ribosomal protein L21

Chain R:  87% 9%




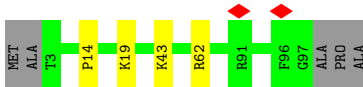
- Molecule 26: 50S ribosomal protein L22

Chain S:  54% 43%

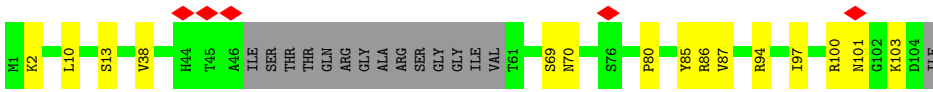
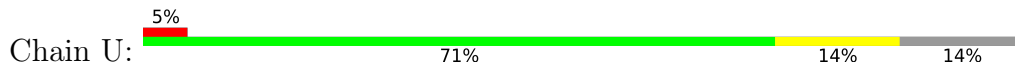


- Molecule 27: 50S ribosomal protein L23

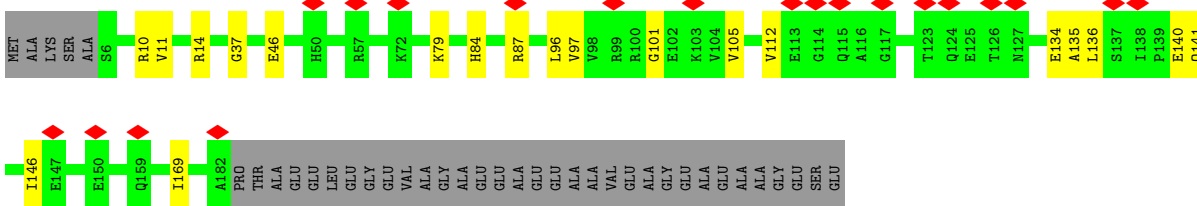
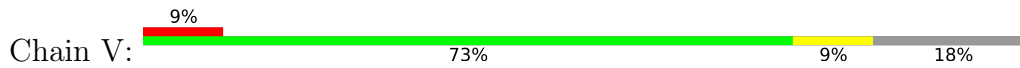
Chain T:  91% 5%



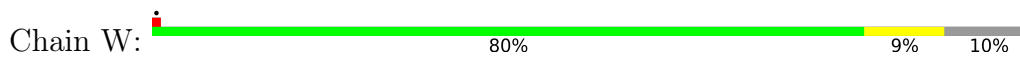
- Molecule 28: 50S ribosomal protein L24



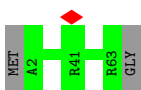
- Molecule 29: 50S ribosomal protein L25



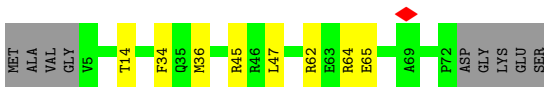
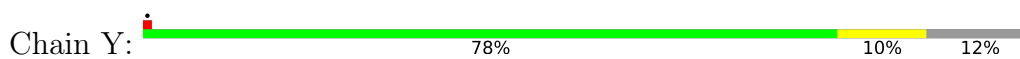
- Molecule 30: 50S ribosomal protein L27



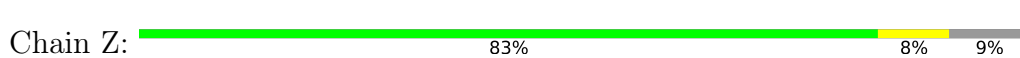
- Molecule 31: 50S ribosomal protein L28



- Molecule 32: 50S ribosomal protein L29

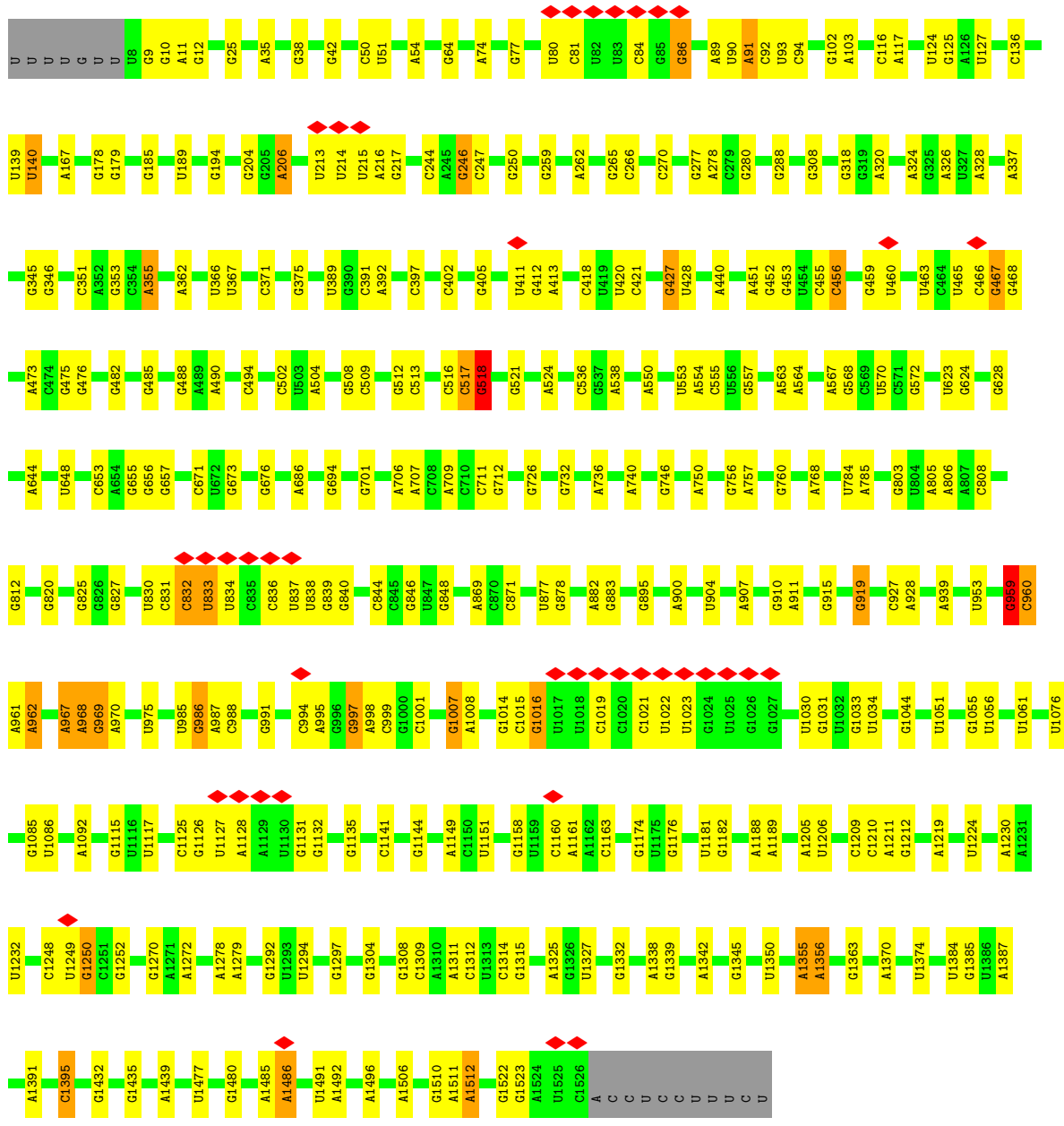
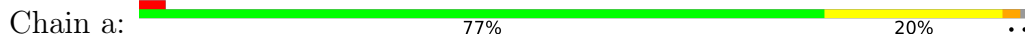


- Molecule 33: 50S ribosomal protein L30



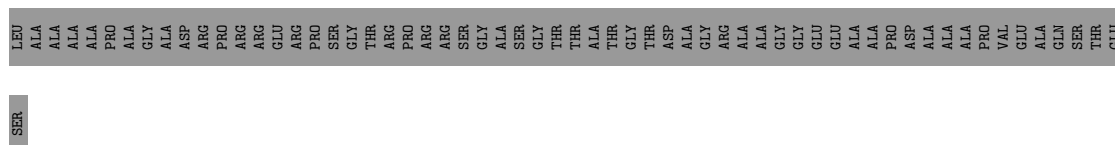


• Molecule 34: 16S rRNA



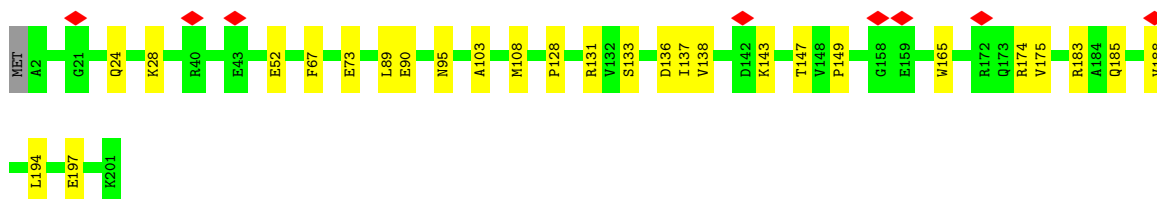
• Molecule 35: 30S ribosomal protein S3





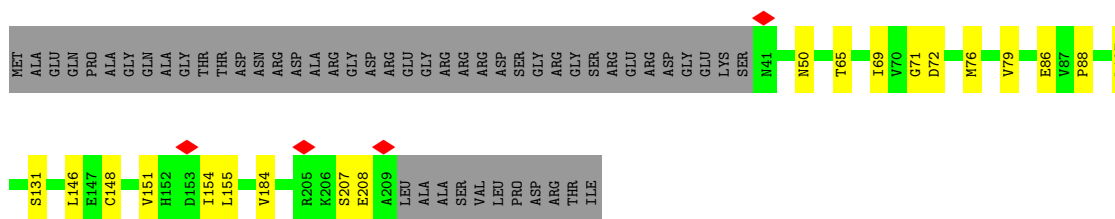
- Molecule 36: 30S ribosomal protein S4

Chain d: 86% 13%



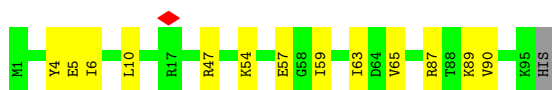
- Molecule 37: 30S ribosomal protein S5

Chain e: 68% 9% 23%



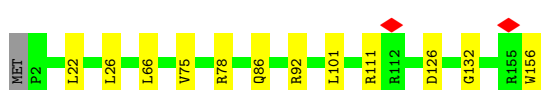
- Molecule 38: 30S ribosomal protein S6

Chain f: 85% 14%



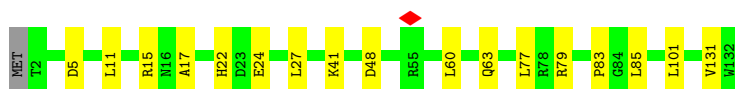
- Molecule 39: 30S ribosomal protein S7

Chain g: 92% 8%

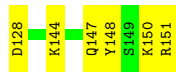
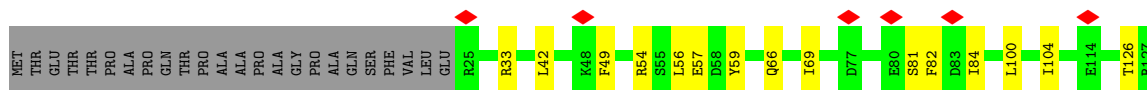


- Molecule 40: 30S ribosomal protein S8

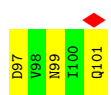
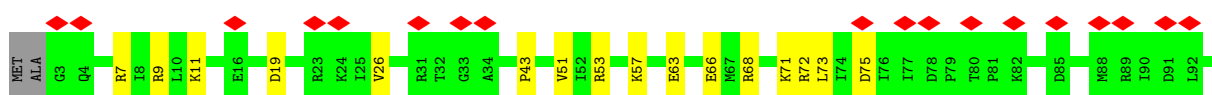
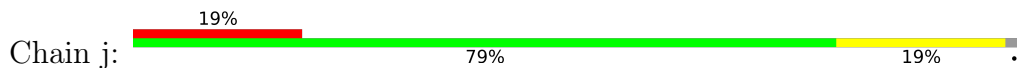
Chain h: 86% 13%



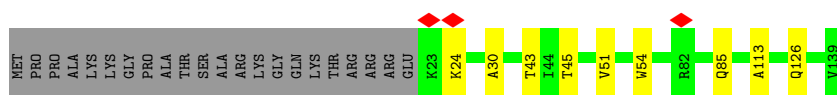
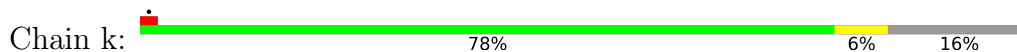
- Molecule 41: 30S ribosomal protein S9



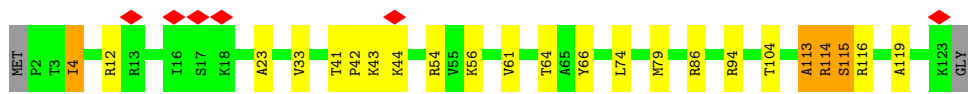
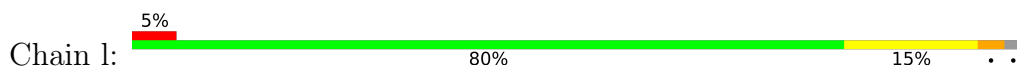
• Molecule 42: 30S ribosomal protein S10



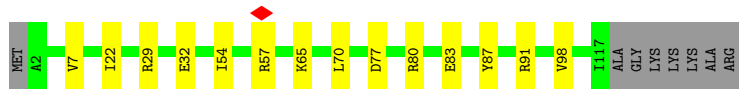
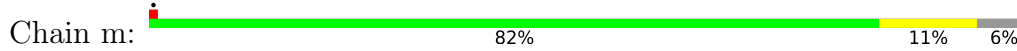
• Molecule 43: 30S ribosomal protein S11



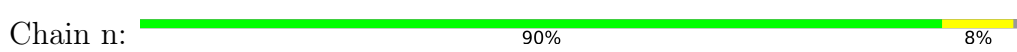
• Molecule 44: 30S ribosomal protein S12



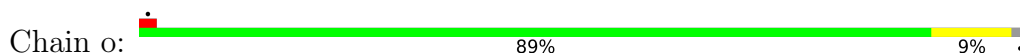
• Molecule 45: 30S ribosomal protein S13



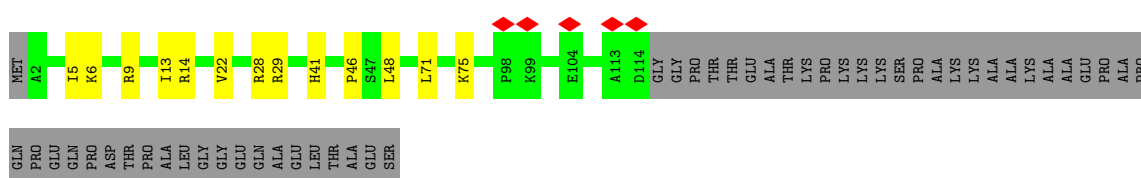
• Molecule 46: 30S ribosomal protein S14 type Z



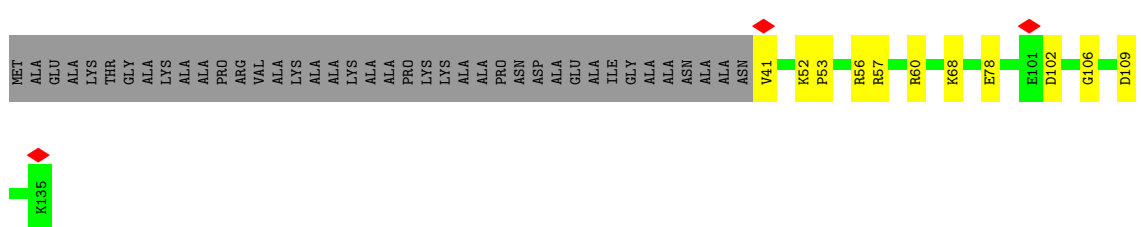
• Molecule 47: 30S ribosomal protein S15



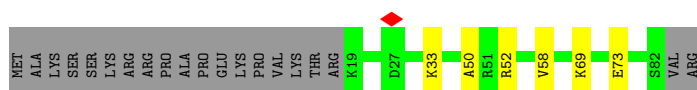
• Molecule 48: 30S ribosomal protein S16



• Molecule 49: 30S ribosomal protein S17



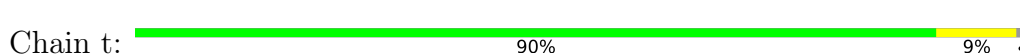
• Molecule 50: 30S ribosomal protein S18 1



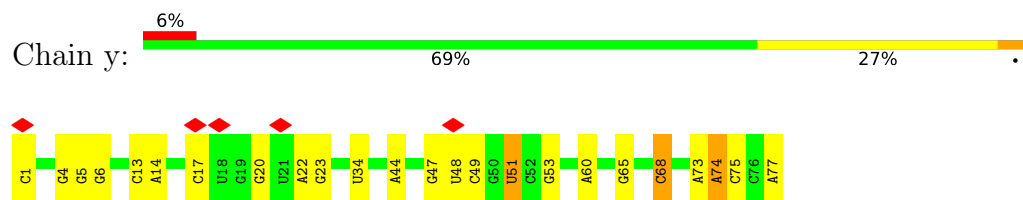
• Molecule 51: 30S ribosomal protein S19



• Molecule 52: 30S ribosomal protein S20



• Molecule 53: initiator 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	116035	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	0.426	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: MA6, ZN, MG, OMG, 2MG, UR3, G7M, 5MC, 4OC, FME, 5MU

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	0.38	0/435	0.52	0/581
2	1	0.32	0/407	0.49	0/543
3	2	0.42	0/377	0.58	0/494
4	3	0.35	0/499	0.49	0/664
5	4	0.33	0/303	0.56	0/402
6	6	0.25	0/455	0.63	0/611
7	7	0.20	0/188	0.49	0/243
8	8	0.17	0/1728	0.41	0/2339
9	A	0.37	0/74899	0.35	0/116863
10	B	0.29	0/2748	0.32	0/4280
11	C	0.40	0/2129	0.57	0/2861
12	D	0.37	0/1613	0.54	0/2174
13	E	0.36	0/1575	0.53	2/2129 (0.1%)
14	F	0.28	0/1429	0.50	0/1921
15	G	0.22	0/1351	0.49	0/1824
16	H	0.22	0/353	0.56	0/474
17	J	0.37	0/1170	0.45	0/1584
18	K	0.36	0/951	0.57	0/1278
19	L	0.37	0/1088	0.53	0/1453
20	M	0.29	0/1098	0.50	0/1481
21	N	0.37	0/925	0.49	0/1242
22	O	0.31	0/914	0.55	0/1228
23	P	0.36	0/922	0.53	0/1236
24	Q	0.44	0/1006	0.57	2/1349 (0.1%)
25	R	0.35	0/766	0.53	0/1030
26	S	0.36	0/874	0.54	0/1186
27	T	0.33	0/751	0.53	0/1012
28	U	0.31	0/705	0.71	2/941 (0.2%)
29	V	0.25	0/1336	0.55	0/1820
30	W	0.36	0/569	0.56	0/757
31	X	0.38	0/476	0.54	0/638
32	Y	0.30	0/564	0.49	0/756

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Z	0.34	0/480	0.53	0/645
34	a	0.31	0/36331	0.32	0/56686
35	c	0.26	0/1678	0.49	0/2254
36	d	0.25	0/1683	0.51	0/2269
37	e	0.28	0/1238	0.47	0/1673
38	f	0.26	0/767	0.45	0/1036
39	g	0.26	0/1250	0.52	0/1686
40	h	0.33	0/1021	0.50	0/1379
41	i	0.25	0/1010	0.53	0/1356
42	j	0.27	0/803	0.65	1/1086 (0.1%)
43	k	0.27	0/891	0.45	0/1204
44	l	0.32	0/970	0.73	0/1295
45	m	0.27	0/953	0.57	0/1274
46	n	0.32	0/477	0.53	0/634
47	o	0.30	0/727	0.53	0/973
48	p	0.27	0/901	0.58	0/1217
49	q	0.28	0/782	0.61	0/1045
50	r	0.30	0/511	0.55	0/685
51	s	0.25	0/690	0.50	0/928
52	t	0.27	0/654	0.47	0/867
53	y	0.24	0/1836	0.30	0/2859
54	z	0.38	0/144	0.72	0/222
All	All	0.34	0/160401	0.40	7/240667 (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	2
28	U	0	1
29	V	0	2
44	l	0	2
47	o	0	1
All	All	0	9

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	j	26	VAL	N-CA-C	-7.72	105.04	111.91
24	Q	72	ASN	CA-C-N	5.28	131.62	121.54
24	Q	72	ASN	C-N-CA	5.28	131.62	121.54
13	E	184	LEU	CA-C-N	5.05	131.79	121.48
13	E	184	LEU	C-N-CA	5.05	131.79	121.48
28	U	38	VAL	CA-C-N	5.03	131.14	121.54
28	U	38	VAL	C-N-CA	5.03	131.14	121.54

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	8	225	ASP	Mainchain
25	R	50	THR	Peptide
25	R	80	LYS	Peptide
28	U	101	ASN	Peptide
29	V	135	ALA	Peptide
29	V	136	LEU	Peptide
44	l	113	ALA	Peptide
44	l	115	SER	Peptide
47	o	44	LYS	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	3	0
2	1	400	0	409	2	0
3	2	374	0	410	1	0
4	3	494	0	533	7	0
5	4	299	0	323	5	0
6	6	446	0	431	4	0
7	7	186	0	202	3	0
8	8	1704	0	1767	20	0
9	A	66959	0	33725	164	0
10	B	2458	0	1254	4	0
11	C	2088	0	2123	15	0
12	D	1590	0	1633	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	E	1552	0	1593	7	0
14	F	1408	0	1449	12	0
15	G	1330	0	1390	6	0
16	H	350	0	367	1	0
17	J	1143	0	1173	5	0
18	K	941	0	1005	4	0
19	L	1075	0	1137	13	0
20	M	1072	0	1115	10	0
21	N	908	0	956	4	0
22	O	905	0	943	9	0
23	P	907	0	947	9	0
24	Q	993	0	1040	7	0
25	R	757	0	817	6	0
26	S	860	0	903	5	0
27	T	741	0	792	4	0
28	U	699	0	738	7	0
29	V	1319	0	1365	10	0
30	W	564	0	584	6	0
31	X	468	0	480	0	0
32	Y	560	0	570	5	0
33	Z	476	0	509	3	0
34	a	32620	0	16427	94	0
35	c	1654	0	1694	15	0
36	d	1650	0	1671	16	0
37	e	1222	0	1291	11	0
38	f	757	0	796	9	0
39	g	1230	0	1288	8	0
40	h	1006	0	1041	11	0
41	i	992	0	1052	15	0
42	j	789	0	821	13	0
43	k	873	0	887	6	0
44	l	959	0	1045	17	0
45	m	945	0	992	8	0
46	n	468	0	492	4	0
47	o	718	0	760	5	0
48	p	884	0	933	9	0
49	q	770	0	833	8	0
50	r	506	0	527	5	0
51	s	672	0	690	8	0
52	t	652	0	703	7	0
53	y	1644	0	835	5	0
54	z	129	0	66	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
55	r	1	0	0	0	0
56	A	302	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	L	1	0	0	0	0
56	a	128	0	0	0	0
56	r	1	0	0	0	0
56	t	1	0	0	0	0
56	y	1	0	0	0	0
56	z	1	0	0	0	0
57	y	10	0	10	1	0
All	All	148054	0	98002	524	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 2.

All (524) 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)
24:Q:44:ASN:HD21	25:R:79:PHE:HB3	1.53	0.73
9:A:1574:C:H42	9:A:1630:G:H1	1.39	0.67
34:a:919:G:N2	54:z:3:C:O2'	2.28	0.66
9:A:1564:C:H42	9:A:1639:G:H1	1.44	0.64
9:A:2362:G:H22	9:A:2409:U:H5''	1.64	0.62
22:O:31:PRO:HB2	22:O:46:LEU:HD22	1.80	0.62
36:d:147:THR:HG22	36:d:149:PRO:HD2	1.80	0.62
42:j:11:LYS:HG2	42:j:71:LYS:HG2	1.82	0.62
9:A:1772:G:HO2'	9:A:1775:G:H1	1.46	0.62
23:P:99:LEU:HD21	23:P:109:ILE:HD11	1.80	0.61
34:a:517:C:O2'	34:a:518:G7M:O4'	2.18	0.61
9:A:1517:C:H5	9:A:1532:G:H1	1.49	0.61
34:a:375:G:H5''	48:p:6:LYS:HB2	1.81	0.61
4:3:5:LYS:NZ	9:A:256:G:N7	2.48	0.61
34:a:830:U:H3	34:a:840:G:H1	1.47	0.61
9:A:1057:G:H4'	33:Z:37:ARG:HH22	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D:184:LYS:HB3	12:D:193:LEU:HD12	1.83	0.60
32:Y:36:MET:HG3	32:Y:47:LEU:HD11	1.83	0.60
34:a:1209:C:OP1	46:n:9:LYS:NZ	2.35	0.60
18:K:115:ILE:HG23	18:K:121:VAL:HG21	1.83	0.60
37:e:86:GLU:HG3	37:e:88:PRO:HD2	1.83	0.60
22:O:32:ARG:NH1	22:O:49:ASP:OD2	2.35	0.60
9:A:1585:G:H22	9:A:1619:U:H3	1.49	0.60
41:i:42:LEU:HD11	41:i:82:PHE:HB3	1.83	0.60
9:A:1692:U:O4	21:N:73:LYS:NZ	2.34	0.59
34:a:962:A:OP1	42:j:57:LYS:NZ	2.34	0.59
40:h:5:ASP:OD1	40:h:79:ARG:NH1	2.35	0.59
34:a:701:G:OP1	38:f:54:LYS:NZ	2.35	0.59
5:4:27:CYS:SG	5:4:28:SER:N	2.75	0.59
34:a:1224:U:H5''	41:i:147:GLN:HB2	1.85	0.59
8:8:64:ASN:HA	8:8:160:LYS:HG2	1.85	0.58
12:D:3:ARG:NH1	12:D:210:SER:O	2.36	0.58
9:A:679:G:O2'	9:A:1385:A:OP1	2.21	0.58
44:l:74:LEU:HD21	44:l:104:THR:HG22	1.85	0.58
15:G:7:GLN:OE1	15:G:70:ARG:NH2	2.36	0.58
6:6:42:HIS:ND1	6:6:43:PRO:O	2.36	0.58
32:Y:14:THR:O	32:Y:64:ARG:NH1	2.37	0.58
9:A:2918:C:H5'	12:D:199:PRO:HA	1.86	0.58
34:a:64:G:N7	52:t:6:SER:OG	2.36	0.58
9:A:1842:C:N4	9:A:1857:G:OP2	2.33	0.58
34:a:402:C:H5''	36:d:128:PRO:HD2	1.86	0.58
34:a:967:A:OP1	46:n:29:ARG:NH2	2.37	0.57
34:a:1339:G:O6	41:i:33:ARG:NH1	2.37	0.57
9:A:1771:G:H22	9:A:1776:A:H61	1.51	0.57
8:8:46:ILE:HB	8:8:171:LEU:HB2	1.87	0.57
18:K:107:ARG:HG3	18:K:112:MET:HE1	1.87	0.57
34:a:308:G:OP1	48:p:28:ARG:NH2	2.38	0.57
34:a:413:A:OP2	34:a:427:G:N2	2.38	0.57
9:A:2398:C:OP1	9:A:2399:G:N2	2.38	0.56
34:a:1007:G:N2	34:a:1211:A:N3	2.52	0.56
34:a:124:U:H5'	49:q:57:ARG:HH12	1.69	0.56
11:C:143:HIS:ND1	11:C:194:GLY:O	2.39	0.56
12:D:11:LEU:HD22	23:P:3:ARG:HD3	1.88	0.56
15:G:9:ILE:HD12	15:G:74:SER:HB3	1.88	0.56
9:A:2375:C:N4	9:A:2389:G:N7	2.53	0.56
9:A:1658:A:H61	9:A:1815:U:H3	1.53	0.56
9:A:2025:A:N6	9:A:2062:G:O2'	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2359:U:H3	9:A:2414:C:H42	1.54	0.56
34:a:655:G:H22	34:a:732:G:H1	1.54	0.56
44:l:33:VAL:HG12	44:l:56:LYS:HB3	1.86	0.56
34:a:516:C:OP1	44:l:86:ARG:NH1	2.38	0.56
9:A:2006:G:H1	9:A:2217:C:H5	1.54	0.56
9:A:2032:U:OP2	11:C:271:ARG:NH2	2.39	0.56
34:a:1001:C:H42	34:a:1014:G:H1	1.53	0.56
14:F:43:VAL:HG22	14:F:161:ILE:HG12	1.87	0.55
34:a:1432:G:OP2	52:t:33:ARG:NH2	2.39	0.55
9:A:1234:U:H2'	9:A:1235:G:H8	1.72	0.55
20:M:86:GLY:HA3	30:W:9:SER:HB3	1.88	0.55
9:A:764:G:N2	9:A:775:C:O2	2.39	0.55
9:A:1880:G:H5''	9:A:1881:U:H5'	1.88	0.55
35:c:188:GLU:HG2	35:c:195:ARG:HD2	1.88	0.55
9:A:2369:U:OP2	9:A:2396:G:N2	2.39	0.55
30:W:56:ASP:OD1	30:W:58:THR:OG1	2.25	0.55
9:A:1000:G:OP1	20:M:6:LYS:NZ	2.39	0.55
4:3:12:LYS:NZ	9:A:251:C:O2	2.40	0.55
11:C:66:ASP:OD2	11:C:103:ARG:NH1	2.39	0.55
11:C:270:ARG:NH2	34:a:671:C:O2'	2.40	0.54
29:V:10:ARG:NH1	29:V:11:VAL:O	2.40	0.54
9:A:835:A:O2'	11:C:4:ARG:NH1	2.40	0.54
26:S:35:ARG:NH1	26:S:84:VAL:O	2.41	0.54
40:h:24:GLU:OE1	40:h:63:GLN:NE2	2.41	0.54
41:i:69:ILE:HD12	41:i:100:LEU:HD23	1.89	0.54
45:m:87:TYR:OH	45:m:91:ARG:NH2	2.37	0.54
53:y:74:A:H5'	53:y:75:C:H5'	1.89	0.54
9:A:759:C:H41	9:A:772:G:H2'	1.71	0.54
9:A:2494:G:O2'	30:W:10:SER:OG	2.26	0.54
45:m:7:VAL:HG11	45:m:22:ILE:HG12	1.89	0.54
34:a:1342:A:OP1	41:i:144:LYS:NZ	2.41	0.54
50:r:50:ALA:HB1	50:r:52:ARG:HH11	1.72	0.54
37:e:71:GLY:HA3	37:e:148:CYS:HB3	1.90	0.54
45:m:77:ASP:OD1	45:m:80:ARG:NH1	2.40	0.54
36:d:73:GLU:OE2	36:d:131:ARG:NH1	2.41	0.54
9:A:2105:G:N2	9:A:2107:A:N3	2.55	0.53
34:a:456:C:O2	34:a:468:G:N2	2.41	0.53
24:Q:73:ASP:OD1	24:Q:114:ARG:NH2	2.41	0.53
34:a:1355:A:H5'	34:a:1356:A:H5''	1.90	0.53
40:h:11:LEU:HD22	40:h:77:LEU:HD22	1.90	0.53
15:G:71:THR:O	15:G:75:ASN:ND2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:V:14:ARG:HG2	29:V:46:GLU:HG2	1.90	0.53
35:c:57:GLU:OE2	35:c:64:ARG:NH1	2.36	0.53
6:6:12:THR:HG23	6:6:31:GLY:HA2	1.89	0.53
9:A:272:A:OP2	9:A:315:G:N1	2.39	0.53
34:a:482:G:OP2	36:d:143:LYS:NZ	2.38	0.53
34:a:757:A:OP2	34:a:803:G:N2	2.41	0.53
41:i:126:THR:HG22	41:i:128:ASP:H	1.74	0.53
24:Q:64:ARG:HD3	24:Q:100:ILE:HD11	1.90	0.53
9:A:2174:A:H2	9:A:2181:U:H3	1.57	0.53
19:L:103:VAL:HG21	19:L:109:VAL:HG12	1.91	0.52
23:P:52:GLY:O	23:P:55:ARG:NH1	2.42	0.52
42:j:66:GLU:OE2	42:j:68:ARG:NH1	2.42	0.52
9:A:1683:A:H5''	9:A:1698:C:H42	1.74	0.52
37:e:184:VAL:HG11	40:h:101:LEU:HD22	1.91	0.52
42:j:9:ARG:HB2	42:j:99:ASN:HB2	1.91	0.52
11:C:172:TYR:HB3	11:C:184:ARG:HG2	1.91	0.52
14:F:120:ASP:OD2	14:F:122:ARG:NH1	2.43	0.52
42:j:43:PRO:O	42:j:71:LYS:NZ	2.42	0.52
9:A:873:G:H1	9:A:882:C:H5	1.58	0.52
42:j:63:GLU:HG3	46:n:45:ARG:HE	1.73	0.52
47:o:25:PRO:HB2	47:o:70:ILE:HD12	1.91	0.52
9:A:2364:G:N3	9:A:2410:A:O2'	2.42	0.52
9:A:910:A:OP1	11:C:218:ARG:NH2	2.43	0.52
14:F:63:ASP:OD2	14:F:142:GLN:NE2	2.43	0.52
17:J:13:ARG:NH2	17:J:49:ASP:O	2.42	0.52
33:Z:2:SER:OG	33:Z:3:GLN:N	2.43	0.52
34:a:991:G:H1	34:a:1034:U:H3	1.56	0.52
8:8:201:PRO:HG2	8:8:204:SER:HB2	1.90	0.52
9:A:764:G:H1	9:A:774:G:H1	1.57	0.52
9:A:683:C:H5'	24:Q:31:LEU:HD22	1.91	0.52
9:A:1216:G:N2	9:A:1219:U:OP1	2.43	0.52
9:A:1560:U:H5	9:A:1643:G:H21	1.58	0.51
22:O:37:ARG:HH11	22:O:107:ARG:HH21	1.58	0.51
34:a:494:C:OP1	44:l:116:ARG:NH2	2.39	0.51
34:a:628:G:OP1	49:q:56:ARG:NH1	2.44	0.51
9:A:418:C:O2	28:U:69:SER:OG	2.28	0.51
9:A:1692:U:O2'	9:A:1693:G:N7	2.44	0.51
35:c:48:ARG:O	35:c:71:ARG:NH2	2.43	0.51
41:i:57:GLU:HG3	41:i:66:GLN:HE22	1.74	0.51
2:1:37:GLU:HG3	2:1:52:ARG:HG2	1.91	0.51
9:A:3026:U:O2'	9:A:3044:A:N3	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:S:28:ARG:HA	26:S:31:ILE:HG12	1.92	0.51
47:o:36:ILE:HG23	47:o:56:LEU:HD11	1.92	0.51
38:f:5:GLU:OE2	50:r:33:LYS:NZ	2.38	0.51
53:y:1:C:H42	53:y:73:A:H61	1.59	0.51
9:A:2357:G:O6	9:A:2415:U:N3	2.44	0.51
19:L:30:LYS:HG3	19:L:31:THR:HG23	1.93	0.51
53:y:51:U:H3	53:y:65:G:H1	1.59	0.51
35:c:60:ARG:NH2	42:j:97:ASP:OD1	2.43	0.51
9:A:1260:G:H4'	17:J:84:LEU:HD22	1.93	0.51
20:M:52:ILE:HD12	20:M:56:ARG:HH22	1.76	0.51
38:f:6:ILE:HG12	38:f:90:VAL:HG22	1.92	0.51
49:q:60:ARG:NH1	49:q:78:GLU:O	2.43	0.51
9:A:1516:A:O2'	9:A:1527:U:O2	2.29	0.51
34:a:392:A:OP1	48:p:14:ARG:NH2	2.43	0.51
8:8:101:ILE:HD11	8:8:123:LYS:HB3	1.92	0.50
9:A:1471:U:OP2	27:T:62:ARG:NH2	2.44	0.50
9:A:1206:A:N6	9:A:1218:G:OP1	2.43	0.50
34:a:1212:G:N2	51:s:54:GLY:O	2.44	0.50
39:g:78:ARG:HB2	39:g:156:TRP:HE1	1.76	0.50
8:8:215:SER:HB2	8:8:221:GLY:HA2	1.92	0.50
9:A:844:A:OP1	47:o:64:ARG:NH1	2.44	0.50
9:A:1427:G:OP1	9:A:2947:G:O2'	2.28	0.50
13:E:47:GLN:HE22	13:E:190:ASN:HB2	1.76	0.50
28:U:100:ARG:O	28:U:103:LYS:NZ	2.45	0.50
34:a:831:C:N3	34:a:832:C:N4	2.59	0.50
35:c:157:LEU:HD12	35:c:164:ARG:HG2	1.94	0.50
9:A:1555:A:N6	9:A:1649:G:O6	2.45	0.50
34:a:1158:G:N1	34:a:1161:A:OP2	2.45	0.50
8:8:211:LYS:NZ	9:A:2415:U:OP1	2.42	0.50
34:a:831:C:N4	34:a:833:U:O4	2.45	0.50
23:P:38:ARG:NH2	34:a:345:G:OP1	2.44	0.50
36:d:137:ILE:HG21	36:d:174:ARG:HH21	1.77	0.50
4:3:28:ASN:O	4:3:36:LYS:NZ	2.43	0.50
36:d:103:ALA:HB1	36:d:108:MET:HG3	1.94	0.50
9:A:765:C:O2	9:A:774:G:N2	2.45	0.49
36:d:183:ARG:HH22	36:d:188:VAL:HG22	1.77	0.49
42:j:19:ASP:HB3	42:j:72:ARG:HH12	1.76	0.49
9:A:1186:A:N6	9:A:1216:G:OP2	2.43	0.49
9:A:1382:A:OP1	24:Q:13:LYS:NZ	2.44	0.49
10:B:29:C:OP1	22:O:9:ARG:NH1	2.45	0.49
35:c:90:LEU:HD23	35:c:98:VAL:HG11	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:k:45:THR:HG22	43:k:51:VAL:HA	1.93	0.49
22:O:31:PRO:HD2	22:O:95:VAL:HG12	1.94	0.49
34:a:262:A:OP1	52:t:74:ASN:ND2	2.44	0.49
8:8:100:LEU:HA	8:8:103:ARG:HE	1.77	0.49
9:A:1902:G:O2'	9:A:2229:U:O4	2.29	0.49
34:a:968:A:H4'	34:a:969:G:H5''	1.95	0.49
36:d:133:SER:N	36:d:136:ASP:OD2	2.44	0.49
5:4:2:LYS:NZ	5:4:31:ARG:O	2.45	0.49
6:6:36:GLU:O	45:m:57:ARG:NH1	2.46	0.49
9:A:2381:G:O3'	9:A:2384:A:N6	2.46	0.49
14:F:15:TYR:OH	14:F:36:PRO:O	2.28	0.49
28:U:10:LEU:HD23	28:U:80:PRO:HG3	1.95	0.49
37:e:50:ASN:OD1	37:e:65:THR:OG1	2.31	0.49
41:i:84:ILE:HD13	41:i:104:ILE:HD11	1.94	0.49
9:A:2385:G:N2	9:A:2386:U:O4	2.40	0.49
8:8:73:ALA:HB1	8:8:156:ILE:HG22	1.95	0.48
9:A:162:A:OP2	9:A:167:A:N6	2.43	0.48
34:a:139:U:H5''	34:a:140:U:H5'	1.95	0.48
37:e:207:SER:OG	37:e:208:GLU:OE1	2.32	0.48
13:E:175:VAL:HG23	13:E:183:ILE:HD11	1.96	0.48
29:V:101:GLY:HA2	29:V:134:GLU:HB2	1.95	0.48
35:c:57:GLU:HG2	35:c:64:ARG:HB3	1.96	0.48
9:A:1322:G:H5''	19:L:33:GLY:HA2	1.95	0.48
34:a:389:U:H4'	48:p:29:ARG:HH21	1.79	0.48
44:l:54:ARG:NH1	44:l:64:THR:OG1	2.41	0.48
9:A:378:C:H2'	9:A:379:G:H8	1.79	0.48
9:A:588:G:N1	9:A:591:A:OP2	2.46	0.48
9:A:674:A:OP2	25:R:82:LYS:NZ	2.42	0.48
9:A:872:A:O2'	9:A:1894:U:OP1	2.26	0.48
9:A:2202:G:O2'	9:A:2205:C:OP1	2.27	0.48
34:a:1115:G:H1	34:a:1141:C:H42	1.61	0.48
48:p:5:ILE:HG12	48:p:22:VAL:HG22	1.95	0.48
48:p:41:HIS:HB2	48:p:48:LEU:HB3	1.94	0.48
49:q:68:LYS:H	49:q:68:LYS:HD2	1.78	0.48
51:s:2:PRO:HD2	51:s:7:LYS:HG3	1.95	0.48
7:7:7:LYS:NZ	9:A:1263:G:OP2	2.42	0.48
9:A:2342:G:N2	9:A:2421:C:O2	2.41	0.48
9:A:2426:U:H2'	9:A:2427:G:H8	1.78	0.48
34:a:355:A:N3	34:a:367:U:O2'	2.43	0.48
38:f:87:ARG:NH1	50:r:73:GLU:O	2.47	0.48
40:h:17:ALA:HB1	40:h:22:HIS:HB2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:O:99:ARG:NH1	22:O:102:TYR:O	2.46	0.48
34:a:871:C:H5'	40:h:83:PRO:HG2	1.96	0.48
45:m:29:ARG:NH1	45:m:32:GLU:OE2	2.43	0.48
5:4:1:VAL:N	9:A:2764:G:O2'	2.47	0.47
36:d:52:GLU:HG2	36:d:194:LEU:HB2	1.95	0.47
53:y:6:G:H1	53:y:68:C:H42	1.62	0.47
9:A:61:G:OP1	32:Y:45:ARG:NH2	2.47	0.47
14:F:177:LEU:HD23	14:F:180:LEU:HD12	1.95	0.47
29:V:112:VAL:HG13	29:V:146:ILE:HD13	1.96	0.47
34:a:259:G:OP1	52:t:75:LYS:NZ	2.47	0.47
6:6:45:TYR:HE1	14:F:183:PRO:HB3	1.79	0.47
15:G:45:ARG:HH21	15:G:51:ILE:HG13	1.77	0.47
19:L:122:ASP:OD1	19:L:142:SER:OG	2.32	0.47
8:8:65:LEU:HD21	8:8:173:PHE:HZ	1.78	0.47
11:C:263:SER:O	11:C:266:LYS:NZ	2.47	0.47
8:8:63:VAL:HG21	8:8:192:ALA:HA	1.96	0.47
8:8:166:ASP:OD1	8:8:170:ASN:N	2.44	0.47
9:A:2299:G:OP1	13:E:75:LYS:NZ	2.36	0.47
7:7:8:LYS:NZ	9:A:1089:G:O6	2.48	0.47
9:A:1457:C:O2'	9:A:2248:G:O2'	2.32	0.47
9:A:1471:U:OP1	27:T:19:LYS:NZ	2.40	0.47
9:A:2309:C:H5	9:A:2675:G:H1	1.62	0.47
9:A:3052:C:OP1	21:N:42:ARG:NH2	2.47	0.47
49:q:52:LYS:HD2	49:q:53:PRO:HD2	1.96	0.47
34:a:653:C:O2'	34:a:827:G:OP1	2.32	0.47
9:A:2358:G:N1	9:A:2415:U:O2	2.48	0.47
26:S:14:VAL:HG22	26:S:116:VAL:HG22	1.97	0.47
14:F:160:ASP:OD1	14:F:160:ASP:N	2.45	0.47
34:a:513:C:OP2	44:l:66:TYR:OH	2.31	0.47
9:A:946:C:H5	9:A:1322:G:H1	1.63	0.46
12:D:7:LEU:H	12:D:34:ASN:HD21	1.64	0.46
12:D:58:SER:OG	12:D:60:ARG:NH1	2.49	0.46
13:E:164:ILE:HG22	13:E:203:SER:HB2	1.98	0.46
30:W:53:ARG:HA	30:W:59:LEU:HD23	1.97	0.46
34:a:9:G:O6	37:e:131:SER:N	2.48	0.46
34:a:102:G:OP1	34:a:324:A:N6	2.47	0.46
52:t:46:LYS:HB3	52:t:50:LEU:HD13	1.96	0.46
8:8:78:PHE:HB3	8:8:120:GLN:HG3	1.96	0.46
9:A:1525:U:H4'	9:A:1838:A:H4'	1.98	0.46
9:A:1569:C:N4	9:A:1633:A:OP1	2.49	0.46
29:V:79:LYS:HB2	29:V:96:LEU:HD22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:d:24:GLN:O	36:d:28:LYS:NZ	2.41	0.46
51:s:50:ALA:HB1	51:s:57:HIS:HB3	1.98	0.46
17:J:6:PRO:HG2	17:J:48:VAL:HG21	1.98	0.46
36:d:137:ILE:HD13	36:d:174:ARG:HH21	1.80	0.46
43:k:43:THR:HA	43:k:54:TRP:HA	1.96	0.46
8:8:67:HIS:HB2	8:8:188:ASN:HD21	1.81	0.46
25:R:17:VAL:HG12	25:R:23:VAL:HG21	1.97	0.46
34:a:960:5MC:O2'	41:i:148:TYR:OH	2.31	0.46
4:3:16:ARG:HH22	4:3:59:THR:HG23	1.81	0.46
9:A:274:A:N7	9:A:314:G:N2	2.64	0.46
9:A:1172:C:H2'	9:A:1173:A:H8	1.81	0.46
42:j:7:ARG:HB3	42:j:101:GLN:HB2	1.98	0.46
9:A:3132:U:O2'	17:J:136:GLN:NE2	2.47	0.46
34:a:11:A:N6	36:d:197:GLU:O	2.49	0.46
41:i:54:ARG:HD2	41:i:59:TYR:HD1	1.81	0.46
48:p:9:ARG:HB3	48:p:29:ARG:NH1	2.31	0.46
11:C:68:ARG:NH1	11:C:150:GLY:O	2.49	0.46
34:a:136:C:OP1	49:q:41:VAL:N	2.49	0.46
34:a:986:G:H2'	34:a:988:C:H41	1.81	0.46
35:c:49:ALA:O	35:c:69:THR:OG1	2.34	0.46
37:e:146:LEU:HD13	37:e:154:ILE:HG21	1.97	0.46
39:g:111:ARG:NH2	39:g:126:ASP:OD2	2.49	0.46
9:A:2375:C:N4	9:A:2388:G:O2'	2.45	0.45
32:Y:62:ARG:NH1	32:Y:65:GLU:OE2	2.46	0.45
34:a:969:G:OP2	34:a:1350:U:O2'	2.33	0.45
48:p:13:ILE:HG12	48:p:14:ARG:HD2	1.98	0.45
9:A:2767:G:H5''	9:A:2768:G:H5''	1.97	0.45
9:A:3028:A:N6	9:A:3127:A:OP2	2.44	0.45
11:C:163:ILE:HG12	11:C:177:MET:HA	1.98	0.45
34:a:206:A:OP1	52:t:60:LYS:NZ	2.46	0.45
39:g:78:ARG:HD2	39:g:156:TRP:CD1	2.51	0.45
9:A:732:G:H1	9:A:739:C:H5	1.63	0.45
34:a:711:C:O2	50:r:69:LYS:NZ	2.44	0.45
39:g:22:LEU:HD21	39:g:66:LEU:HD12	1.98	0.45
40:h:85:LEU:HD12	44:l:4:ILE:HG21	1.97	0.45
9:A:871:U:H2'	9:A:872:A:C8	2.52	0.45
23:P:25:ILE:HD13	23:P:85:VAL:HA	1.98	0.45
23:P:51:GLY:HA2	23:P:56:GLU:HG3	1.97	0.45
34:a:81:C:H42	34:a:86:G:H1	1.63	0.45
34:a:756:G:N1	34:a:803:G:O2'	2.36	0.45
21:N:44:LEU:HD23	21:N:113:ILE:HD13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2078:U:H5''	11:C:256:ARG:HG2	1.99	0.45
34:a:38:G:O2'	44:l:115:SER:O	2.32	0.45
35:c:69:THR:HG22	35:c:102:ILE:HD11	1.98	0.45
34:a:676:G:OP1	43:k:24:LYS:NZ	2.43	0.45
34:a:1370:A:OP1	39:g:92:ARG:NH2	2.44	0.45
37:e:72:ASP:HB2	37:e:76:MET:HB2	1.98	0.45
45:m:54:ILE:HA	45:m:57:ARG:HG2	1.99	0.45
9:A:2489:OMG:OP2	20:M:82:ARG:NH1	2.50	0.45
41:i:81:SER:OG	41:i:82:PHE:N	2.49	0.45
42:j:51:VAL:HB	46:n:41:ARG:HB2	1.99	0.45
15:G:149:ILE:HG22	15:G:163:VAL:HG11	1.99	0.44
36:d:138:VAL:HB	36:d:175:VAL:HB	1.99	0.44
51:s:36:ARG:NH2	51:s:72:GLY:O	2.50	0.44
8:8:132:GLY:HA2	8:8:137:MET:HG2	1.98	0.44
9:A:2361:G:N2	9:A:2412:C:O2'	2.49	0.44
34:a:1008:A:HO2'	34:a:1210:C:HO2'	1.65	0.44
41:i:151:ARG:NH2	53:y:34:U:OP2	2.40	0.44
9:A:776:G:OP1	19:L:116:LYS:NZ	2.47	0.44
22:O:32:ARG:HE	22:O:34:VAL:HG22	1.83	0.44
51:s:19:VAL:HG21	51:s:44:PHE:HE1	1.81	0.44
9:A:193:A:H2'	9:A:194:G:C8	2.53	0.44
9:A:2624:U:O2'	30:W:41:ARG:NH1	2.50	0.44
11:C:162:SER:HB3	11:C:195:GLU:HG3	2.00	0.44
35:c:48:ARG:HH21	35:c:74:ILE:HG23	1.82	0.44
36:d:165:TRP:HD1	36:d:185:GLN:HG3	1.83	0.44
1:0:46:ALA:HB1	1:0:51:LEU:HB2	1.99	0.44
8:8:200:LYS:HZ3	8:8:208:TYR:HB2	1.82	0.44
17:J:37:ARG:HG2	17:J:118:ILE:HD13	1.97	0.44
28:U:86:ARG:HB2	28:U:97:ILE:HG12	1.99	0.44
45:m:65:LYS:HG3	45:m:70:LEU:HB2	1.98	0.44
34:a:904:U:OP2	44:l:94:ARG:NH2	2.47	0.44
19:L:86:PHE:HE1	19:L:100:LYS:HE3	1.83	0.44
21:N:26:THR:HG23	21:N:75:VAL:HG11	2.00	0.44
28:U:13:SER:OG	28:U:70:ASN:OD1	2.34	0.44
34:a:1210:C:H2'	34:a:1211:A:C8	2.52	0.44
9:A:1712:G:H21	9:A:1756:A:H62	1.64	0.44
14:F:133:GLY:O	14:F:165:THR:OG1	2.35	0.44
39:g:75:VAL:HG22	39:g:86:GLN:HB3	2.00	0.44
42:j:7:ARG:HD2	42:j:73:LEU:HD11	2.00	0.44
45:m:91:ARG:HG2	45:m:98:VAL:HA	2.00	0.44
9:A:636:U:O4	9:A:648:G:N1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:38:A:O2'	10:B:45:A:N1	2.51	0.43
51:s:45:ILE:HD12	51:s:64:GLU:HA	1.99	0.43
9:A:2471:U:H2'	9:A:2472:G:C8	2.52	0.43
18:K:97:ARG:NH2	34:a:337:A:OP1	2.40	0.43
38:f:47:ARG:NE	38:f:57:GLU:OE2	2.47	0.43
9:A:1354:G:OP2	25:R:92:ARG:NH1	2.52	0.43
8:8:212:ILE:HG23	8:8:224:VAL:HB	2.00	0.43
9:A:192:A:N3	9:A:808:G:O2'	2.46	0.43
9:A:605:C:O2'	26:S:28:ARG:NH2	2.52	0.43
9:A:641:U:OP2	9:A:642:C:N4	2.47	0.43
9:A:1232:A:H5''	9:A:1233:C:H5	1.84	0.43
9:A:1772:G:O2'	9:A:1775:G:N1	2.37	0.43
10:B:58:G:H4'	22:O:7:ALA:HB2	2.00	0.43
9:A:1613:G:H2'	9:A:1614:A:H8	1.83	0.43
9:A:2093:A:H2	9:A:2121:G:H21	1.65	0.43
18:K:122:LEU:HD22	23:P:69:VAL:HG11	1.98	0.43
34:a:760:G:H4'	34:a:1506:A:H4'	2.01	0.43
36:d:90:GLU:HA	36:d:95:ASN:HD22	1.83	0.43
41:i:49:PHE:HD2	41:i:56:LEU:HD22	1.83	0.43
43:k:30:ALA:N	43:k:45:THR:O	2.46	0.43
4:3:2:PRO:HB2	4:3:3:LYS:H	1.65	0.43
9:A:1049:G:N2	9:A:2507:A:OP2	2.52	0.43
9:A:2740:G:H5''	9:A:2741:A:H5''	1.99	0.43
20:M:59:LYS:HE2	20:M:60:ARG:HH12	1.84	0.43
34:a:736:A:OP1	34:a:844:C:O2'	2.34	0.43
36:d:67:PHE:HE1	36:d:89:LEU:HD11	1.83	0.43
44:l:33:VAL:HG23	44:l:79:MET:HE1	1.99	0.43
1:0:27:LEU:HD12	1:0:38:LYS:HB3	2.01	0.43
8:8:44:VAL:HG22	8:8:214:VAL:HG22	2.01	0.43
9:A:1641:U:H2'	9:A:1642:G:H8	1.83	0.43
28:U:2:LYS:HE3	28:U:85:TYR:HE2	1.84	0.43
34:a:726:G:O2'	38:f:89:LYS:NZ	2.41	0.43
44:l:114:ARG:HG3	44:l:119:ALA:HB3	2.01	0.43
49:q:106:GLY:N	49:q:109:ASP:OD2	2.51	0.43
8:8:37:LYS:NZ	9:A:2366:C:OP2	2.52	0.43
9:A:1647:U:H2'	9:A:1648:A:H8	1.83	0.43
9:A:2583:G:N3	9:A:2619:C:H2'	2.33	0.43
9:A:3071:U:H2'	9:A:3072:A:C8	2.53	0.43
12:D:7:LEU:H	12:D:34:ASN:ND2	2.17	0.43
7:7:21:ARG:NH2	9:A:1111:C:O2	2.51	0.43
9:A:611:C:O2	9:A:656:U:O2'	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1988:C:H5	23:P:93:ARG:HH21	1.66	0.43
23:P:47:ILE:HA	23:P:96:LEU:HD12	2.00	0.43
34:a:1248:C:H5'	34:a:1250:G:H1'	2.01	0.43
9:A:1953:G:H22	9:A:1976:G:H1	1.66	0.43
16:H:5:LEU:HA	16:H:36:ALA:HA	2.01	0.43
34:a:554:A:O2'	34:a:557:G:O2'	2.30	0.43
44:l:113:ALA:O	44:l:115:SER:N	2.38	0.43
9:A:552:G:N2	9:A:555:A:OP2	2.40	0.42
9:A:738:G:O6	19:L:71:ARG:NH2	2.46	0.42
34:a:77:G:H1	34:a:91:A:H2	1.67	0.42
34:a:103:A:N1	52:t:10:ARG:HG2	2.34	0.42
34:a:466:C:H3'	34:a:467:G:H8	1.83	0.42
51:s:2:PRO:HB2	51:s:7:LYS:HD2	2.00	0.42
9:A:1572:A:N1	9:A:1632:G:O2'	2.41	0.42
9:A:2802:A:OP1	9:A:2886:G:O2'	2.37	0.42
14:F:12:LYS:HE2	14:F:16:ARG:HH12	1.84	0.42
34:a:825:G:H5''	50:r:58:VAL:HG21	2.01	0.42
34:a:1182:G:H5'	35:c:176:HIS:CE1	2.54	0.42
35:c:175:LEU:HD23	35:c:182:ILE:HD13	2.00	0.42
9:A:1586:G:H22	9:A:1619:U:H1'	1.84	0.42
11:C:69:ARG:HE	11:C:130:ASN:HB2	1.84	0.42
19:L:67:ARG:NH1	19:L:68:ASN:O	2.52	0.42
5:4:9:PRO:HD3	5:4:16:LEU:HD12	2.00	0.42
9:A:947:G:N1	9:A:1320:U:OP2	2.41	0.42
13:E:41:HIS:HA	19:L:8:LEU:HD23	2.00	0.42
34:a:9:G:H2'	37:e:155:LEU:HD21	2.01	0.42
34:a:1055:G:O2'	34:a:1182:G:N2	2.52	0.42
34:a:1308:G:N1	34:a:1311:A:OP2	2.46	0.42
35:c:19:LYS:HE3	35:c:53:ASP:HB2	2.00	0.42
9:A:244:G:O2'	9:A:256:G:O6	2.32	0.42
29:V:37:GLY:HA3	29:V:97:VAL:HG22	2.01	0.42
34:a:1015:C:N4	34:a:1016:G:O6	2.53	0.42
34:a:1030:U:H2'	34:a:1031:G:H8	1.85	0.42
40:h:77:LEU:HD23	40:h:131:VAL:HA	2.00	0.42
51:s:12:ASP:OD2	51:s:35:SER:OG	2.34	0.42
9:A:2168:G:O2'	9:A:2206:G:O6	2.36	0.42
9:A:2354:A:N6	9:A:2383:C:N3	2.56	0.42
9:A:2513:C:O2'	20:M:84:GLY:O	2.37	0.42
9:A:2572:C:N4	30:W:75:ARG:HE	2.18	0.42
49:q:102:ASP:OD1	49:q:102:ASP:N	2.50	0.42
9:A:1546:G:H1	9:A:1822:C:H42	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2462:G:H4'	9:A:2464:C:C2	2.54	0.42
34:a:939:A:O2'	34:a:1325:A:N3	2.48	0.42
34:a:1051:U:OP2	35:c:2:GLY:N	2.52	0.42
39:g:26:LEU:HD13	39:g:101:LEU:HD22	2.02	0.42
24:Q:53:ARG:HA	24:Q:56:GLU:HB2	2.02	0.42
34:a:508:G:N2	34:a:521:G:OP1	2.50	0.42
4:3:19:THR:HG23	9:A:755:G:H5''	2.00	0.42
9:A:1119:A:N1	25:R:80:LYS:NZ	2.54	0.42
27:T:14:PRO:HD3	32:Y:34:PHE:CD1	2.55	0.42
34:a:997:G:H2'	34:a:998:A:C8	2.54	0.42
43:k:85:GLN:NE2	43:k:113:ALA:O	2.52	0.42
48:p:71:LEU:HG	48:p:75:LYS:HE2	2.02	0.42
8:8:49:GLY:N	8:8:208:TYR:O	2.48	0.42
9:A:2542:G:H22	9:A:2550:U:H3	1.68	0.42
9:A:2778:C:O2'	9:A:2978:A:N3	2.48	0.42
4:3:25:GLN:HG3	19:L:63:LEU:HD23	2.01	0.41
11:C:118:GLU:N	11:C:129:ASN:OD1	2.47	0.41
15:G:27:LYS:HD3	15:G:32:THR:HB	2.02	0.41
34:a:1181:U:H5''	35:c:5:ILE:HD13	2.01	0.41
38:f:6:ILE:HB	38:f:63:ILE:HB	2.02	0.41
44:l:43:LYS:HB3	44:l:44:LYS:H	1.76	0.41
9:A:988:G:O2'	9:A:1045:G:O6	2.31	0.41
9:A:1387:G:H21	13:E:89:GLN:HB2	1.85	0.41
9:A:2551:C:H5''	14:F:95:ARG:HD3	2.02	0.41
22:O:37:ARG:HA	22:O:42:ILE:HG22	2.02	0.41
24:Q:50:ARG:O	24:Q:54:LYS:NZ	2.52	0.41
34:a:648:U:O2'	47:o:22:THR:O	2.33	0.41
40:h:41:LYS:NZ	40:h:48:ASP:OD1	2.42	0.41
44:l:23:ALA:HB1	44:l:61:VAL:HG21	2.01	0.41
3:2:10:PRO:HG2	9:A:1440:G:H4'	2.02	0.41
9:A:1690:A:H5''	9:A:1691:G:H5''	2.01	0.41
9:A:1832:G:OP2	27:T:43:LYS:NZ	2.42	0.41
9:A:2551:C:H2'	9:A:2552:A:H8	1.85	0.41
12:D:36:VAL:HG13	12:D:50:VAL:HG23	2.02	0.41
34:a:706:A:H2'	34:a:707:A:C8	2.55	0.41
34:a:709:A:H1'	43:k:126:GLN:HE22	1.85	0.41
40:h:27:LEU:HD11	40:h:60:LEU:HD23	2.03	0.41
9:A:1235:G:H2'	9:A:1236:G:H8	1.86	0.41
9:A:2377:C:OP1	9:A:2381:G:N1	2.54	0.41
19:L:89:GLY:HA2	19:L:121:VAL:HG12	2.02	0.41
34:a:1486:A:OP1	44:l:44:LYS:NZ	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:307:U:H2'	9:A:308:G:H8	1.84	0.41
9:A:448:U:H2'	9:A:449:A:H8	1.85	0.41
9:A:960:G:N2	19:L:51:GLY:O	2.53	0.41
9:A:1084:G:OP2	20:M:87:LYS:NZ	2.53	0.41
37:e:107:LEU:HD21	37:e:151:VAL:HG22	2.01	0.41
39:g:126:ASP:O	39:g:132:GLY:N	2.54	0.41
9:A:1176:G:HO2'	9:A:1239:A:H61	1.61	0.41
9:A:1676:U:H2'	9:A:1677:A:H8	1.86	0.41
9:A:3019:A:H5''	9:A:3020:G:H5'	2.02	0.41
34:a:418:C:OP1	34:a:504:A:O2'	2.36	0.41
37:e:69:ILE:HD12	37:e:79:VAL:HG22	2.03	0.41
29:V:105:VAL:HG12	29:V:169:ILE:HD11	2.02	0.41
57:y:101:FME:HB2	57:y:101:FME:HE2	1.79	0.41
9:A:30:G:O2'	9:A:1345:A:N3	2.43	0.41
9:A:2377:C:O2'	9:A:2379:A:OP2	2.32	0.41
9:A:2551:C:H2'	9:A:2552:A:C8	2.56	0.41
10:B:61:U:H2'	10:B:62:G:H8	1.85	0.41
13:E:27:PRO:HG2	13:E:30:LEU:HB3	2.02	0.41
14:F:52:ARG:NH1	14:F:84:PHE:O	2.53	0.41
19:L:54:MET:HA	19:L:55:PRO:HD3	1.84	0.41
20:M:4:PRO:HG3	20:M:69:PHE:HE2	1.86	0.41
20:M:16:ARG:HH12	20:M:18:ARG:HH21	1.68	0.41
34:a:1384:U:H2'	34:a:1385:G:C8	2.56	0.41
41:i:49:PHE:HB2	41:i:56:LEU:HB2	2.03	0.41
44:l:41:THR:HA	44:l:42:PRO:HD3	1.89	0.41
8:8:42:VAL:HG13	8:8:216:THR:HB	2.03	0.41
9:A:1397:G:O5'	26:S:25:ARG:NH2	2.53	0.41
20:M:68:ILE:HG13	20:M:103:LEU:HD23	2.03	0.41
34:a:555:C:OP1	44:l:12:ARG:NH1	2.54	0.41
1:0:6:ARG:NE	9:A:2257:C:H41	2.19	0.40
2:1:15:CYS:SG	2:1:16:GLU:N	2.95	0.40
9:A:198:A:H62	9:A:960:G:H21	1.68	0.40
9:A:858:G:C6	11:C:208:LYS:HB2	2.56	0.40
9:A:2784:U:H5''	9:A:2785:U:H5'	2.02	0.40
14:F:71:LYS:HA	14:F:72:PRO:HD3	1.90	0.40
29:V:79:LYS:HE2	29:V:96:LEU:HD22	2.03	0.40
29:V:140:GLU:HG3	29:V:141:GLN:H	1.86	0.40
33:Z:30:ARG:HD2	33:Z:33:HIS:HB2	2.03	0.40
34:a:1181:U:OP1	42:j:53:ARG:NH2	2.54	0.40
9:A:1685:C:H2'	9:A:1686:A:C8	2.56	0.40
9:A:2127:A:H2'	9:A:2128:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:f:4:TYR:HB2	38:f:65:VAL:HG12	2.03	0.40
9:A:1578:C:H2'	9:A:1579:A:C8	2.57	0.40
9:A:2016:U:H1'	9:A:2847:U:H5''	2.04	0.40
28:U:87:VAL:HG22	28:U:94:ARG:HG2	2.03	0.40
34:a:869:A:H4'	40:h:15:ARG:HH22	1.86	0.40
5:4:22:ARG:NH1	5:4:36:GLN:O	2.54	0.40
9:A:2177:5MU:OP1	9:A:2842:U:O2'	2.39	0.40
25:R:27:LYS:NZ	25:R:29:GLU:OE2	2.54	0.40
34:a:246:G:O6	34:a:277:G:N1	2.54	0.40
34:a:959:2MG:O2'	41:i:150:LYS:O	2.33	0.40
38:f:10:LEU:HB2	38:f:59:ILE:HB	2.03	0.40
42:j:7:ARG:NE	42:j:75:ASP:OD1	2.43	0.40
47:o:64:ARG:HH11	47:o:64:ARG:HD3	1.77	0.40
9:A:1235:G:H2'	9:A:1236:G:C8	2.56	0.40
9:A:2364:G:N1	9:A:2400:U:O2'	2.55	0.40
29:V:84:HIS:CG	29:V:87:ARG:HE	2.40	0.40

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%)	52 (100%)	0	0	100	100
2	1	46/55 (84%)	46 (100%)	0	0	100	100
3	2	42/47 (89%)	41 (98%)	1 (2%)	0	100	100
4	3	60/64 (94%)	58 (97%)	2 (3%)	0	100	100
5	4	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
6	6	53/80 (66%)	47 (89%)	6 (11%)	0	100	100
7	7	20/24 (83%)	20 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	8	228/235 (97%)	220 (96%)	8 (4%)	0	100	100
11	C	270/280 (96%)	258 (96%)	12 (4%)	0	100	100
12	D	211/217 (97%)	194 (92%)	17 (8%)	0	100	100
13	E	205/223 (92%)	200 (98%)	5 (2%)	0	100	100
14	F	176/187 (94%)	161 (92%)	15 (8%)	0	100	100
15	G	172/179 (96%)	156 (91%)	16 (9%)	0	100	100
16	H	45/152 (30%)	41 (91%)	4 (9%)	0	100	100
17	J	144/195 (74%)	142 (99%)	2 (1%)	0	100	100
18	K	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
19	L	142/146 (97%)	136 (96%)	6 (4%)	0	100	100
20	M	132/138 (96%)	123 (93%)	9 (7%)	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%)	101 (92%)	9 (8%)	0	100	100
24	Q	122/129 (95%)	121 (99%)	1 (1%)	0	100	100
25	R	98/104 (94%)	92 (94%)	5 (5%)	1 (1%)	12	24
26	S	111/197 (56%)	109 (98%)	2 (2%)	0	100	100
27	T	93/100 (93%)	87 (94%)	6 (6%)	0	100	100
28	U	86/105 (82%)	75 (87%)	11 (13%)	0	100	100
29	V	175/215 (81%)	155 (89%)	20 (11%)	0	100	100
30	W	75/86 (87%)	66 (88%)	9 (12%)	0	100	100
31	X	60/64 (94%)	59 (98%)	1 (2%)	0	100	100
32	Y	66/77 (86%)	64 (97%)	2 (3%)	0	100	100
33	Z	57/65 (88%)	56 (98%)	1 (2%)	0	100	100
35	c	205/274 (75%)	186 (91%)	19 (9%)	0	100	100
36	d	198/201 (98%)	182 (92%)	16 (8%)	0	100	100
37	e	167/220 (76%)	156 (93%)	11 (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%)	121 (94%)	8 (6%)	0	100	100
41	i	125/151 (83%)	115 (92%)	10 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	j	97/101 (96%)	91 (94%)	6 (6%)	0	100	100
43	k	115/139 (83%)	104 (90%)	11 (10%)	0	100	100
44	l	120/124 (97%)	96 (80%)	22 (18%)	2 (2%)	7	14
45	m	114/124 (92%)	104 (91%)	10 (9%)	0	100	100
46	n	58/61 (95%)	55 (95%)	2 (3%)	1 (2%)	7	14
47	o	85/89 (96%)	78 (92%)	6 (7%)	1 (1%)	10	20
48	p	111/162 (68%)	100 (90%)	10 (9%)	1 (1%)	14	28
49	q	93/135 (69%)	76 (82%)	17 (18%)	0	100	100
50	r	62/84 (74%)	59 (95%)	3 (5%)	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%)	5170 (94%)	350 (6%)	6 (0%)	49	71

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	R	51	THR
44	l	114	ARG
46	n	17	ALA
48	p	46	PRO
47	o	19	GLU
44	l	4	ILE

### 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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	4	35/35 (100%)	35 (100%)	0	100	100
6	6	49/66 (74%)	48 (98%)	1 (2%)	48	69
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	88
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%)	94 (100%)	0	100	100
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%)	142 (100%)	0	100	100
30	W	55/62 (89%)	55 (100%)	0	100	100
31	X	51/52 (98%)	51 (100%)	0	100	100
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%)	170 (100%)	0	100	100
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	90 (100%)	0	100	100
44	l	104/105 (99%)	104 (100%)	0	100	100
45	m	99/104 (95%)	98 (99%)	1 (1%)	68	81
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%)	4581 (100%)	3 (0%)	87	95

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	6	5	ILE
13	E	104	TYR
45	m	83	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
4	3	28	ASN
8	8	57	GLN
8	8	172	HIS
8	8	231	ASN
11	C	135	ASN
11	C	203	ASN
11	C	227	ASN
12	D	130	HIS
12	D	183	HIS
13	E	47	GLN

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Mol	Chain	Res	Type
14	F	34	GLN
14	F	70	GLN
16	H	46	GLN
17	J	70	GLN
17	J	147	GLN
19	L	57	HIS
20	M	9	HIS
20	M	14	HIS
21	N	61	HIS
21	N	62	ASN
22	O	36	HIS
23	P	79	ASN
23	P	82	HIS
24	Q	44	ASN
27	T	58	ASN
29	V	82	HIS
29	V	91	GLN
29	V	127	ASN
29	V	154	GLN
31	X	45	ASN
35	c	122	GLN
35	c	176	HIS
36	d	115	HIS
37	e	163	ASN
41	i	65	HIS
41	i	66	GLN
41	i	147	GLN
42	j	99	ASN
42	j	101	GLN
43	k	28	HIS
43	k	126	GLN
43	k	128	HIS
44	l	75	GLN
45	m	101	GLN
47	o	50	HIS
47	o	51	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	114/115 (99%)	11 (9%)	1 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	a	1518/1537 (98%)	231 (15%)	0
53	y	76/77 (98%)	18 (23%)	0
54	z	5/26 (19%)	3 (60%)	0
9	A	3116/3138 (99%)	438 (14%)	4 (0%)
All	All	4829/4893 (98%)	701 (14%)	5 (0%)

All (701) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	13	A
9	A	25	U
9	A	43	G
9	A	51	G
9	A	63	A
9	A	71	A
9	A	72	U
9	A	74	U
9	A	75	G
9	A	83	G
9	A	90	C
9	A	118	A
9	A	119	A
9	A	120	U
9	A	165	A
9	A	167	A
9	A	176	G
9	A	183	A
9	A	198	A
9	A	201	A
9	A	217	G
9	A	218	A
9	A	224	A
9	A	226	A
9	A	230	U
9	A	231	U
9	A	232	G
9	A	235	A
9	A	243	A
9	A	250	G
9	A	251	C
9	A	269	G
9	A	287	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
9	A	289	A
9	A	293	G
9	A	298	G
9	A	301	G
9	A	302	U
9	A	303	U
9	A	339	C
9	A	358	U
9	A	364	A
9	A	371	U
9	A	372	G
9	A	377	G
9	A	385	G
9	A	394	U
9	A	401	C
9	A	405	A
9	A	413	A
9	A	428	A
9	A	446	A
9	A	447	G
9	A	454	U
9	A	460	A
9	A	475	G
9	A	494	C
9	A	500	G
9	A	501	A
9	A	537	U
9	A	544	U
9	A	545	U
9	A	553	U
9	A	566	A
9	A	570	G
9	A	582	G
9	A	592	G
9	A	593	A
9	A	595	U
9	A	596	A
9	A	597	C
9	A	616	A
9	A	618	U
9	A	619	C
9	A	620	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
9	A	628	C
9	A	635	U
9	A	636	U
9	A	637	C
9	A	642	C
9	A	643	C
9	A	645	G
9	A	646	A
9	A	665	G
9	A	674	A
9	A	675	G
9	A	677	A
9	A	694	G
9	A	695	G
9	A	706	A
9	A	719	U
9	A	738	G
9	A	740	G
9	A	741	A
9	A	749	U
9	A	758	C
9	A	759	C
9	A	772	G
9	A	778	G
9	A	779	U
9	A	780	G
9	A	781	A
9	A	782	A
9	A	783	U
9	A	784	A
9	A	788	G
9	A	815	U
9	A	843	U
9	A	848	C
9	A	852	G
9	A	859	C
9	A	865	C
9	A	876	U
9	A	894	G
9	A	904	G
9	A	905	G
9	A	911	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
9	A	913	G
9	A	914	G
9	A	923	A
9	A	934	G
9	A	938	G
9	A	941	C
9	A	956	U
9	A	957	U
9	A	987	G
9	A	988	G
9	A	1025	A
9	A	1026	C
9	A	1036	C
9	A	1039	A
9	A	1043	C
9	A	1044	C
9	A	1059	A
9	A	1066	G
9	A	1069	A
9	A	1074	G
9	A	1085	A
9	A	1087	A
9	A	1089	G
9	A	1096	A
9	A	1102	A
9	A	1103	A
9	A	1112	A
9	A	1114	C
9	A	1118	G
9	A	1125	G
9	A	1126	G
9	A	1138	A
9	A	1142	G
9	A	1151	G
9	A	1154	G
9	A	1155	G
9	A	1162	U
9	A	1177	A
9	A	1180	A
9	A	1186	A
9	A	1187	G
9	A	1189	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
9	A	1195	U
9	A	1199	A
9	A	1200	G
9	A	1201	C
9	A	1202	A
9	A	1207	C
9	A	1211	U
9	A	1212	G
9	A	1216	G
9	A	1217	A
9	A	1218	G
9	A	1219	U
9	A	1227	A
9	A	1233	C
9	A	1240	A
9	A	1241	G
9	A	1243	G
9	A	1255	A
9	A	1259	U
9	A	1261	U
9	A	1262	A
9	A	1264	C
9	A	1271	C
9	A	1273	A
9	A	1286	A
9	A	1304	U
9	A	1305	U
9	A	1306	G
9	A	1309	G
9	A	1342	C
9	A	1368	A
9	A	1378	A
9	A	1379	G
9	A	1384	A
9	A	1386	U
9	A	1387	G
9	A	1402	G
9	A	1403	A
9	A	1406	A
9	A	1417	A
9	A	1432	A
9	A	1437	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
9	A	1452	C
9	A	1453	A
9	A	1456	C
9	A	1472	G
9	A	1483	U
9	A	1491	G
9	A	1496	A
9	A	1499	G
9	A	1501	C
9	A	1510	U
9	A	1511	G
9	A	1515	A
9	A	1526	A
9	A	1545	G
9	A	1560	U
9	A	1564	C
9	A	1567	U
9	A	1568	A
9	A	1569	C
9	A	1571	A
9	A	1580	A
9	A	1581	A
9	A	1582	A
9	A	1583	C
9	A	1592	U
9	A	1609	U
9	A	1626	G
9	A	1628	G
9	A	1644	U
9	A	1645	A
9	A	1646	G
9	A	1649	G
9	A	1656	G
9	A	1657	A
9	A	1659	G
9	A	1665	A
9	A	1666	C
9	A	1689	C
9	A	1693	G
9	A	1696	A
9	A	1697	A
9	A	1698	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
9	A	1699	A
9	A	1704	G
9	A	1720	G
9	A	1730	C
9	A	1745	C
9	A	1746	U
9	A	1747	A
9	A	1750	C
9	A	1754	A
9	A	1763	G
9	A	1773	U
9	A	1774	U
9	A	1776	A
9	A	1803	A
9	A	1806	A
9	A	1820	A
9	A	1830	C
9	A	1832	G
9	A	1842	C
9	A	1843	A
9	A	1845	A
9	A	1865	A
9	A	1881	U
9	A	1883	C
9	A	1888	U
9	A	1889	A
9	A	1909	G
9	A	1910	C
9	A	1948	A
9	A	1949	U
9	A	1950	A
9	A	1962	C
9	A	1964	U
9	A	1966	C
9	A	1970	G
9	A	1990	G
9	A	1998	U
9	A	2007	A
9	A	2008	C
9	A	2010	G
9	A	2016	U
9	A	2021	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
9	A	2025	A
9	A	2034	C
9	A	2035	G
9	A	2042	C
9	A	2043	A
9	A	2050	U
9	A	2061	U
9	A	2063	A
9	A	2094	C
9	A	2100	A
9	A	2105	G
9	A	2107	A
9	A	2108	A
9	A	2109	G
9	A	2144	G
9	A	2152	C
9	A	2157	A
9	A	2167	G
9	A	2168	G
9	A	2175	A
9	A	2176	A
9	A	2177	5MU
9	A	2178	U
9	A	2193	U
9	A	2205	C
9	A	2208	A
9	A	2209	U
9	A	2210	G
9	A	2229	U
9	A	2231	U
9	A	2242	G
9	A	2258	A
9	A	2261	A
9	A	2269	A
9	A	2270	G
9	A	2281	C
9	A	2293	C
9	A	2294	G
9	A	2296	A
9	A	2297	A
9	A	2298	A
9	A	2299	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
9	A	2330	G
9	A	2337	G
9	A	2348	U
9	A	2350	U
9	A	2355	U
9	A	2363	A
9	A	2367	U
9	A	2372	A
9	A	2374	C
9	A	2375	C
9	A	2376	U
9	A	2377	C
9	A	2378	G
9	A	2385	G
9	A	2386	U
9	A	2388	G
9	A	2389	G
9	A	2390	G
9	A	2392	C
9	A	2394	G
9	A	2395	A
9	A	2396	G
9	A	2398	C
9	A	2399	G
9	A	2403	U
9	A	2404	U
9	A	2407	A
9	A	2408	A
9	A	2411	C
9	A	2412	C
9	A	2413	A
9	A	2414	C
9	A	2415	U
9	A	2435	A
9	A	2447	U
9	A	2463	A
9	A	2476	G
9	A	2477	G
9	A	2489	OMG
9	A	2517	G
9	A	2521	C
9	A	2525	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
9	A	2526	A
9	A	2536	A
9	A	2543	A
9	A	2546	G
9	A	2558	C
9	A	2560	A
9	A	2563	G
9	A	2572	C
9	A	2573	A
9	A	2583	G
9	A	2585	C
9	A	2588	C
9	A	2621	G
9	A	2623	A
9	A	2644	A
9	A	2657	U
9	A	2661	U
9	A	2663	A
9	A	2664	A
9	A	2667	G
9	A	2668	A
9	A	2679	C
9	A	2685	G
9	A	2686	A
9	A	2712	C
9	A	2714	A
9	A	2716	A
9	A	2732	G
9	A	2743	G
9	A	2744	U
9	A	2751	G
9	A	2756	A
9	A	2767	G
9	A	2773	G
9	A	2802	A
9	A	2804	A
9	A	2805	G
9	A	2810	A
9	A	2840	A
9	A	2847	U
9	A	2851	U
9	A	2868	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
9	A	2884	C
9	A	2901	G
9	A	2951	C
9	A	2952	G
9	A	2962	C
9	A	2964	C
9	A	2965	G
9	A	2982	G
9	A	2986	A
9	A	2993	C
9	A	2995	A
9	A	2999	G
9	A	3016	A
9	A	3018	C
9	A	3036	G
9	A	3038	U
9	A	3040	G
9	A	3053	C
9	A	3056	A
9	A	3070	A
9	A	3071	U
9	A	3107	A
9	A	3114	G
9	A	3118	A
9	A	3119	C
9	A	3128	A
9	A	3129	A
10	B	3	A
10	B	4	C
10	B	14	A
10	B	36	C
10	B	39	U
10	B	55	U
10	B	56	A
10	B	86	C
10	B	101	G
10	B	105	A
10	B	115	A
34	a	10	G
34	a	12	G
34	a	25	G
34	a	35	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	42	G
34	a	50	C
34	a	51	U
34	a	54	A
34	a	74	A
34	a	80	U
34	a	84	C
34	a	86	G
34	a	89	A
34	a	90	U
34	a	91	A
34	a	92	C
34	a	93	U
34	a	94	C
34	a	116	C
34	a	117	A
34	a	125	G
34	a	127	U
34	a	140	U
34	a	167	A
34	a	178	G
34	a	179	G
34	a	185	G
34	a	189	U
34	a	194	G
34	a	204	G
34	a	206	A
34	a	213	U
34	a	214	U
34	a	215	U
34	a	216	A
34	a	217	G
34	a	244	C
34	a	246	G
34	a	247	C
34	a	250	G
34	a	265	G
34	a	266	C
34	a	270	C
34	a	278	A
34	a	280	G
34	a	288	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	318	G
34	a	320	A
34	a	326	A
34	a	328	A
34	a	346	G
34	a	351	C
34	a	353	G
34	a	355	A
34	a	362	A
34	a	366	U
34	a	371	C
34	a	391	C
34	a	397	C
34	a	405	G
34	a	411	U
34	a	412	G
34	a	420	U
34	a	421	C
34	a	427	G
34	a	428	U
34	a	440	A
34	a	451	A
34	a	452	G
34	a	453	G
34	a	455	C
34	a	456	C
34	a	459	G
34	a	460	U
34	a	463	U
34	a	465	U
34	a	467	G
34	a	473	A
34	a	475	G
34	a	476	G
34	a	485	G
34	a	488	G
34	a	490	A
34	a	502	C
34	a	509	C
34	a	512	G
34	a	517	C
34	a	518	G7M

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	524	A
34	a	536	C
34	a	538	A
34	a	550	A
34	a	553	U
34	a	563	A
34	a	564	A
34	a	567	A
34	a	568	G
34	a	570	U
34	a	572	G
34	a	623	U
34	a	624	G
34	a	644	A
34	a	656	G
34	a	657	G
34	a	673	G
34	a	686	A
34	a	694	G
34	a	712	G
34	a	740	A
34	a	746	G
34	a	750	A
34	a	768	A
34	a	784	U
34	a	785	A
34	a	805	A
34	a	806	A
34	a	808	C
34	a	812	G
34	a	820	G
34	a	832	C
34	a	833	U
34	a	834	U
34	a	836	C
34	a	837	U
34	a	838	U
34	a	839	G
34	a	846	G
34	a	848	G
34	a	877	U
34	a	878	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	882	A
34	a	883	G
34	a	895	G
34	a	900	A
34	a	907	A
34	a	910	G
34	a	911	A
34	a	915	G
34	a	919	G
34	a	927	C
34	a	928	A
34	a	953	U
34	a	959	2MG
34	a	961	A
34	a	962	A
34	a	967	A
34	a	968	A
34	a	969	G
34	a	970	A
34	a	975	U
34	a	985	U
34	a	986	G
34	a	987	A
34	a	994	C
34	a	995	A
34	a	997	G
34	a	999	C
34	a	1007	G
34	a	1016	G
34	a	1019	C
34	a	1021	C
34	a	1022	U
34	a	1023	U
34	a	1033	G
34	a	1044	G
34	a	1056	U
34	a	1061	U
34	a	1076	U
34	a	1085	G
34	a	1086	U
34	a	1092	A
34	a	1117	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	1125	C
34	a	1126	G
34	a	1127	U
34	a	1128	A
34	a	1131	G
34	a	1132	G
34	a	1135	G
34	a	1144	G
34	a	1149	A
34	a	1151	U
34	a	1160	C
34	a	1163	C
34	a	1174	G
34	a	1176	G
34	a	1188	A
34	a	1189	A
34	a	1205	A
34	a	1206	U
34	a	1219	A
34	a	1230	A
34	a	1232	U
34	a	1249	U
34	a	1250	G
34	a	1252	G
34	a	1270	G
34	a	1272	A
34	a	1278	A
34	a	1279	A
34	a	1292	G
34	a	1294	U
34	a	1297	G
34	a	1304	G
34	a	1309	C
34	a	1312	C
34	a	1314	C
34	a	1315	G
34	a	1327	U
34	a	1332	G
34	a	1338	A
34	a	1345	G
34	a	1355	A
34	a	1356	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
34	a	1363	G
34	a	1374	U
34	a	1387	A
34	a	1391	A
34	a	1395	4OC
34	a	1435	G
34	a	1439	A
34	a	1477	U
34	a	1480	G
34	a	1485	A
34	a	1486	A
34	a	1492	A
34	a	1496	A
34	a	1510	G
34	a	1512	MA6
34	a	1522	G
34	a	1523	G
53	y	4	G
53	y	5	G
53	y	13	C
53	y	14	A
53	y	17	C
53	y	20	G
53	y	22	A
53	y	23	G
53	y	44	A
53	y	47	G
53	y	48	U
53	y	49	C
53	y	51	U
53	y	53	G
53	y	60	A
53	y	68	C
53	y	74	A
53	y	77	A
54	z	2	A
54	z	3	C
54	z	4	A

All (5) RNA pucker outliers are listed below:

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Mol	Chain	Res	Type
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Mol	Chain	Res	Type
9	A	328	A
9	A	913	G
9	A	2177	5MU
9	A	2384	A
10	B	3	A

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

10 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$
9	OMG	A	2489	53,9	23,26,27	2.32	9 (39%)	32,38,41	1.89	8 (25%)
34	4OC	a	1395	34	20,23,24	3.04	8 (40%)	25,32,35	0.94	1 (4%)
34	UR3	a	1491	34	19,22,23	2.65	6 (31%)	26,32,35	1.60	4 (15%)
9	5MU	A	2177	9	19,22,23	4.77	7 (36%)	27,32,35	3.68	9 (33%)
34	MA6	a	1511	34	23,26,27	1.55	4 (17%)	33,38,41	3.07	12 (36%)
34	5MC	a	960	34	19,22,23	3.68	8 (42%)	26,32,35	1.03	2 (7%)
9	OMG	A	2791	9	23,26,27	2.32	9 (39%)	32,38,41	2.00	9 (28%)
34	MA6	a	1512	34	23,26,27	1.50	4 (17%)	33,38,41	3.30	13 (39%)
34	2MG	a	959	34	23,26,27	2.82	8 (34%)	33,38,41	2.45	10 (30%)
34	G7M	a	518	34	23,26,27	3.59	12 (52%)	34,39,42	1.73	7 (20%)

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
9	OMG	A	2489	53,9	-	2/9/27/28	0/3/3/3

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

All (75) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	2177	5MU	C2-N1	10.53	1.55	1.38
34	a	518	G7M	C8-N7	10.50	1.51	1.33
9	A	2177	5MU	C6-N1	10.45	1.55	1.38
9	A	2177	5MU	C4-C5	9.43	1.60	1.44
34	a	960	5MC	C6-C5	9.04	1.49	1.34
9	A	2177	5MU	C4-N3	-7.91	1.24	1.38
34	a	959	2MG	C2-N3	7.34	1.46	1.32
34	a	1395	4OC	C4-N3	6.76	1.44	1.32
34	a	959	2MG	C4-N3	6.73	1.49	1.34
34	a	960	5MC	C4-N3	6.57	1.44	1.34
34	a	1491	UR3	C6-C5	6.42	1.50	1.35
9	A	2177	5MU	C6-C5	6.24	1.44	1.34
9	A	2791	OMG	C4-N3	6.21	1.48	1.34
34	a	1395	4OC	C6-C5	6.15	1.49	1.35
34	a	1395	4OC	C2-N3	6.14	1.48	1.36
34	a	1491	UR3	C2-N1	6.14	1.47	1.38
9	A	2489	OMG	C4-N3	6.10	1.48	1.34
34	a	960	5MC	C2-N3	5.92	1.48	1.36
34	a	959	2MG	C2-N2	5.67	1.45	1.33
34	a	518	G7M	C2-N3	5.62	1.46	1.33
34	a	960	5MC	C5-C4	5.61	1.48	1.44
34	a	518	G7M	C8-N9	5.55	1.50	1.35
34	a	518	G7M	C4-N3	5.48	1.46	1.34
9	A	2791	OMG	C2-N3	5.38	1.46	1.33
9	A	2489	OMG	C2-N3	5.28	1.46	1.33
34	a	1491	UR3	C2-N3	5.07	1.49	1.39
34	a	518	G7M	C2-N2	4.85	1.45	1.34
34	a	1395	4OC	C4-N4	4.51	1.45	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	a	518	G7M	C5-N7	4.43	1.44	1.39
34	a	960	5MC	C6-N1	4.42	1.45	1.38
34	a	960	5MC	C4-N4	4.25	1.45	1.34
34	a	1511	MA6	C6-N6	4.22	1.48	1.36
34	a	959	2MG	C2-N1	4.21	1.43	1.36
34	a	960	5MC	C2-N1	4.13	1.48	1.40
9	A	2791	OMG	C2-N2	4.01	1.43	1.34
34	a	1512	MA6	C6-N6	3.95	1.47	1.36
34	a	1395	4OC	C2-N1	3.92	1.48	1.40
9	A	2489	OMG	C2-N2	3.89	1.43	1.34
34	a	518	G7M	C2-N1	3.50	1.46	1.37
34	a	1512	MA6	C5-C4	-3.42	1.33	1.39
34	a	1511	MA6	C5-C4	-3.39	1.33	1.39
9	A	2489	OMG	C5-N7	-3.33	1.32	1.39
34	a	518	G7M	C5-C6	3.21	1.52	1.43
34	a	959	2MG	C5-N7	-3.20	1.32	1.39
34	a	1395	4OC	C5-C4	3.20	1.48	1.41
9	A	2177	5MU	O4-C4	-3.16	1.17	1.23
9	A	2177	5MU	O2-C2	-3.08	1.17	1.23
34	a	1395	4OC	C6-N1	3.03	1.45	1.38
9	A	2489	OMG	O6-C6	-3.03	1.17	1.23
9	A	2791	OMG	C5-N7	-3.03	1.33	1.39
9	A	2791	OMG	O6-C6	-3.02	1.17	1.23
34	a	960	5MC	O2-C2	-2.96	1.18	1.23
34	a	1491	UR3	C6-N1	2.91	1.45	1.38
34	a	518	G7M	C6-N1	2.88	1.44	1.38
34	a	1511	MA6	C5-N7	-2.88	1.33	1.39
34	a	518	G7M	O6-C6	-2.86	1.18	1.23
34	a	959	2MG	O6-C6	-2.77	1.18	1.23
34	a	1512	MA6	C5-N7	-2.70	1.34	1.39
34	a	1511	MA6	C8-N9	-2.66	1.33	1.37
34	a	1395	4OC	O2-C2	-2.66	1.18	1.23
34	a	1512	MA6	C8-N9	-2.56	1.33	1.37
34	a	959	2MG	C5-C6	2.35	1.53	1.44
9	A	2489	OMG	C2-N1	2.28	1.43	1.37
9	A	2489	OMG	C4-N9	-2.28	1.32	1.38
34	a	518	G7M	C4-N9	2.25	1.43	1.38
9	A	2791	OMG	C2-N1	2.19	1.43	1.37
34	a	1491	UR3	O2-C2	-2.16	1.18	1.22
9	A	2791	OMG	C5-C6	2.15	1.52	1.44
9	A	2791	OMG	C6-N1	2.13	1.42	1.38
34	a	518	G7M	C5-C4	2.10	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	2791	OMG	C4-N9	-2.07	1.32	1.38
34	a	959	2MG	C6-N1	2.05	1.42	1.38
9	A	2489	OMG	C6-N1	2.05	1.42	1.38
9	A	2489	OMG	C5-C6	2.04	1.52	1.44
34	a	1491	UR3	C4-N3	2.01	1.44	1.40

All (75) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	2177	5MU	C5-C4-N3	12.04	125.79	115.32
34	a	1512	MA6	N1-C6-N6	-11.33	103.05	116.86
34	a	1511	MA6	N1-C6-N6	-10.30	104.31	116.86
9	A	2177	5MU	C5-C6-N1	-9.74	112.73	123.31
34	a	1512	MA6	C5-C6-N6	7.87	137.80	125.33
34	a	959	2MG	C2-N3-C4	7.71	121.65	112.00
34	a	1511	MA6	C5-C6-N6	7.40	137.05	125.33
34	a	959	2MG	C5-C4-N3	-6.56	117.95	128.39
34	a	1512	MA6	N1-C2-N3	-6.13	119.31	128.58
34	a	1511	MA6	N1-C2-N3	-5.77	119.85	128.58
9	A	2791	OMG	C5-C4-N3	-5.57	119.53	128.39
34	a	1491	UR3	C4-N3-C2	-5.37	120.26	124.58
9	A	2489	OMG	C5-C4-N3	-5.21	120.10	128.39
9	A	2177	5MU	C4-N3-C2	-4.99	120.80	127.34
34	a	1512	MA6	C5-C4-N3	-4.94	119.91	126.72
9	A	2177	5MU	O4-C4-C5	-4.88	119.34	124.92
9	A	2791	OMG	C2-N3-C4	4.87	120.69	112.30
9	A	2177	5MU	N3-C2-N1	4.86	121.22	114.89
34	a	959	2MG	C2-N1-C6	-4.80	118.75	124.55
34	a	518	G7M	C2-N3-C4	4.70	120.40	112.30
34	a	1512	MA6	N9-C8-N7	-4.48	107.58	113.94
34	a	1511	MA6	N9-C8-N7	-4.39	107.71	113.94
9	A	2489	OMG	C2-N3-C4	4.38	119.85	112.30
34	a	1511	MA6	C5-C4-N3	-4.37	120.70	126.72
34	a	959	2MG	N9-C4-N3	4.33	134.61	125.95
34	a	1511	MA6	C4-C5-C6	4.32	120.38	115.91
34	a	518	G7M	C5-C4-N3	-4.14	120.33	128.15
34	a	518	G7M	C5-C6-N1	4.05	120.21	111.84
34	a	1512	MA6	C4-C5-C6	4.01	120.05	115.91
34	a	1511	MA6	C2-N1-C6	3.75	120.98	111.83
34	a	1491	UR3	C5-C4-N3	3.71	119.92	115.04
9	A	2177	5MU	C5M-C5-C6	-3.70	117.84	122.85
34	a	1512	MA6	C2-N1-C6	3.69	120.84	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	1512	MA6	C2-N3-C4	3.65	120.74	111.83
9	A	2177	5MU	C5M-C5-C4	3.59	122.62	118.78
34	a	959	2MG	N1-C2-N2	3.47	120.11	116.56
9	A	2489	OMG	N9-C4-N3	3.41	132.77	125.95
9	A	2791	OMG	N9-C4-N3	3.34	132.62	125.95
34	a	1512	MA6	C5-N7-C8	3.28	108.61	103.45
9	A	2791	OMG	C2-N1-C6	-3.24	119.23	125.11
9	A	2489	OMG	C2-N1-C6	-3.18	119.35	125.11
34	a	1511	MA6	C2-N3-C4	3.11	119.44	111.83
34	a	1512	MA6	C4-C5-N7	-3.01	107.14	110.58
9	A	2489	OMG	N9-C8-N7	-2.98	107.88	113.40
9	A	2791	OMG	N9-C8-N7	-2.97	107.90	113.40
34	a	959	2MG	C5-C6-N1	2.96	120.79	113.25
34	a	1511	MA6	C5-N7-C8	2.92	108.04	103.45
34	a	518	G7M	C2-N1-C6	-2.91	119.83	125.11
9	A	2177	5MU	O2-C2-N1	-2.89	119.04	122.80
34	a	518	G7M	O6-C6-C5	-2.86	121.64	128.01
9	A	2791	OMG	C5-C6-N1	2.83	120.46	113.25
9	A	2177	5MU	O4-C4-N3	-2.79	114.87	120.11
34	a	1512	MA6	C5-C4-N9	2.76	108.82	105.81
34	a	1511	MA6	N3-C4-N9	2.74	131.82	127.17
9	A	2489	OMG	C5-C6-N1	2.67	120.05	113.25
34	a	1511	MA6	C4-N9-C8	2.66	108.53	105.74
34	a	959	2MG	O6-C6-C5	-2.63	119.59	126.53
9	A	2489	OMG	O6-C6-C5	-2.62	119.62	126.53
9	A	2791	OMG	O6-C6-C5	-2.59	119.70	126.53
34	a	959	2MG	N9-C8-N7	-2.59	108.60	113.40
34	a	1512	MA6	N3-C4-N9	2.41	131.26	127.17
34	a	960	5MC	C5-C6-N1	-2.36	120.75	123.31
9	A	2791	OMG	C1'-N9-C8	-2.35	120.06	126.73
34	a	518	G7M	C5-C4-N9	2.27	110.72	105.88
34	a	1395	4OC	C6-C5-C4	2.23	119.69	117.00
34	a	959	2MG	N1-C2-N3	-2.20	119.97	123.68
34	a	518	G7M	N9-C8-N7	-2.19	107.16	112.48
34	a	960	5MC	O2-C2-N3	-2.16	118.92	122.33
34	a	1491	UR3	C6-N1-C2	-2.15	120.04	121.80
9	A	2489	OMG	C1'-N9-C8	-2.10	120.75	126.73
34	a	1491	UR3	C1'-N1-C2	2.08	120.44	117.04
34	a	1511	MA6	C4-C5-N7	-2.04	108.25	110.58
9	A	2791	OMG	C8-N7-C5	2.02	107.87	104.26
34	a	959	2MG	C8-N7-C5	2.01	107.83	104.26
34	a	1512	MA6	C4-N9-C8	2.00	107.84	105.74

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	2177	5MU	C3'-C4'-C5'-O5'
9	A	2177	5MU	O4'-C4'-C5'-O5'
9	A	2489	OMG	O4'-C4'-C5'-O5'
34	a	1395	4OC	O4'-C4'-C5'-O5'
34	a	1512	MA6	O4'-C4'-C5'-O5'
9	A	2489	OMG	C3'-C4'-C5'-O5'
34	a	959	2MG	O4'-C4'-C5'-O5'
34	a	959	2MG	C3'-C4'-C5'-O5'
34	a	1512	MA6	C3'-C4'-C5'-O5'
34	a	1395	4OC	C3'-C4'-C5'-O5'
34	a	1512	MA6	C4'-C5'-O5'-P

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	2489	OMG	1	0
9	A	2177	5MU	1	0
34	a	960	5MC	1	0
34	a	959	2MG	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	0.90	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	-	3/7/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

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

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	y	101	FME	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
10	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	76:U	O3'	77:A	P	3.16

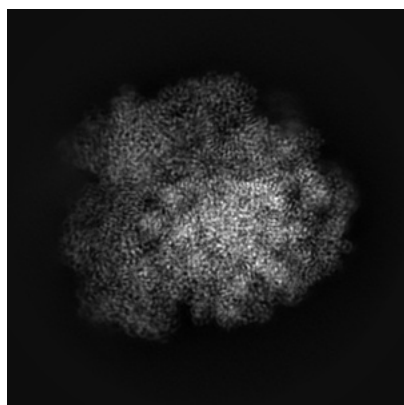
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23974. These allow visual inspection of the internal detail of the map and identification of artifacts.

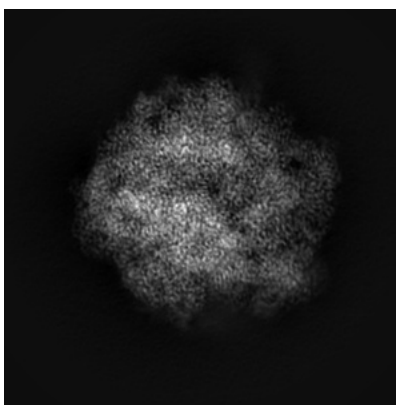
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

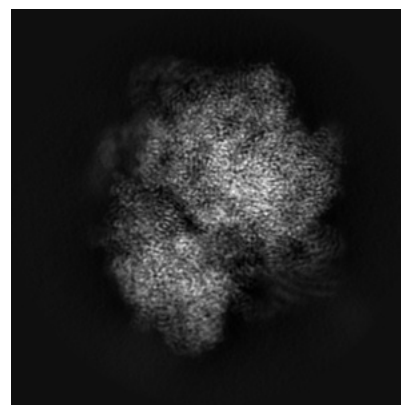
#### 6.1.1 Primary map



X



Y

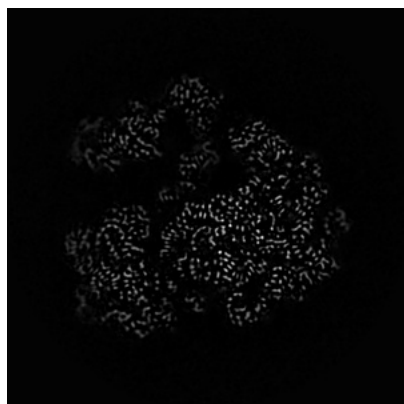


Z

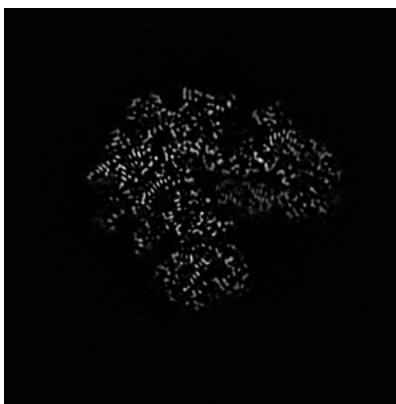
The images above show the map projected in three orthogonal directions.

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

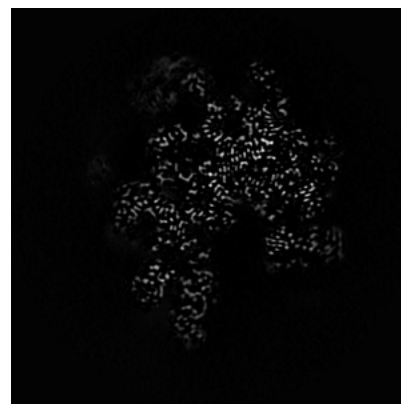
#### 6.2.1 Primary map



X Index: 160



Y Index: 160

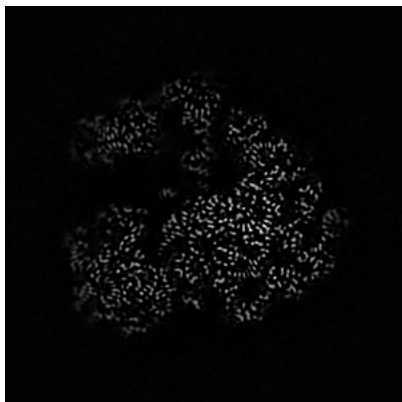


Z Index: 160

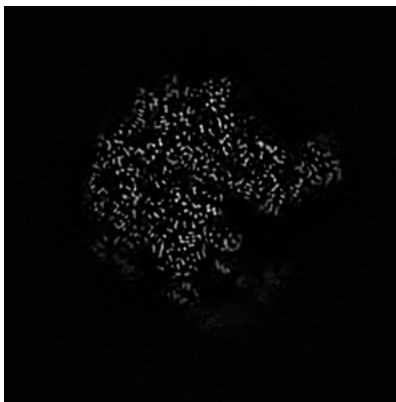
The images above show central slices of the map in three orthogonal directions.

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

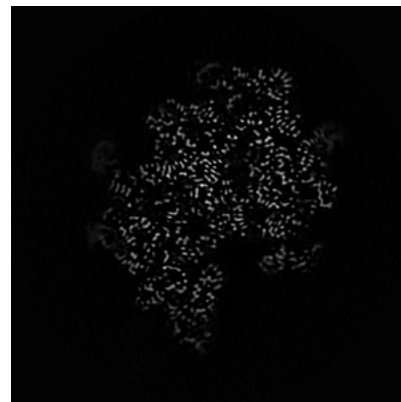
### 6.3.1 Primary map



X Index: 163



Y Index: 183

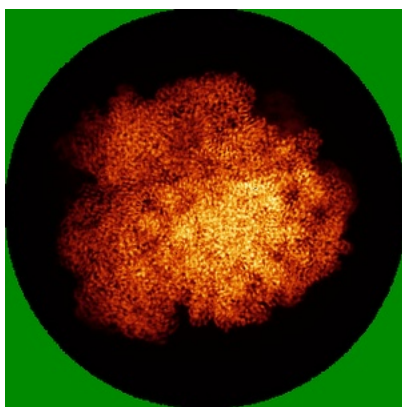


Z Index: 144

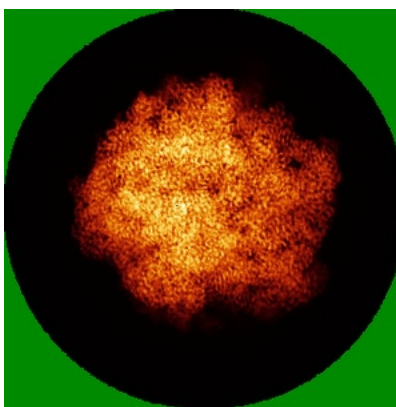
The images above show the largest variance slices of the map in three orthogonal directions.

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

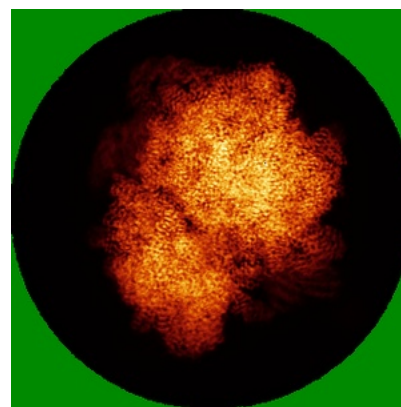
### 6.4.1 Primary map



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.

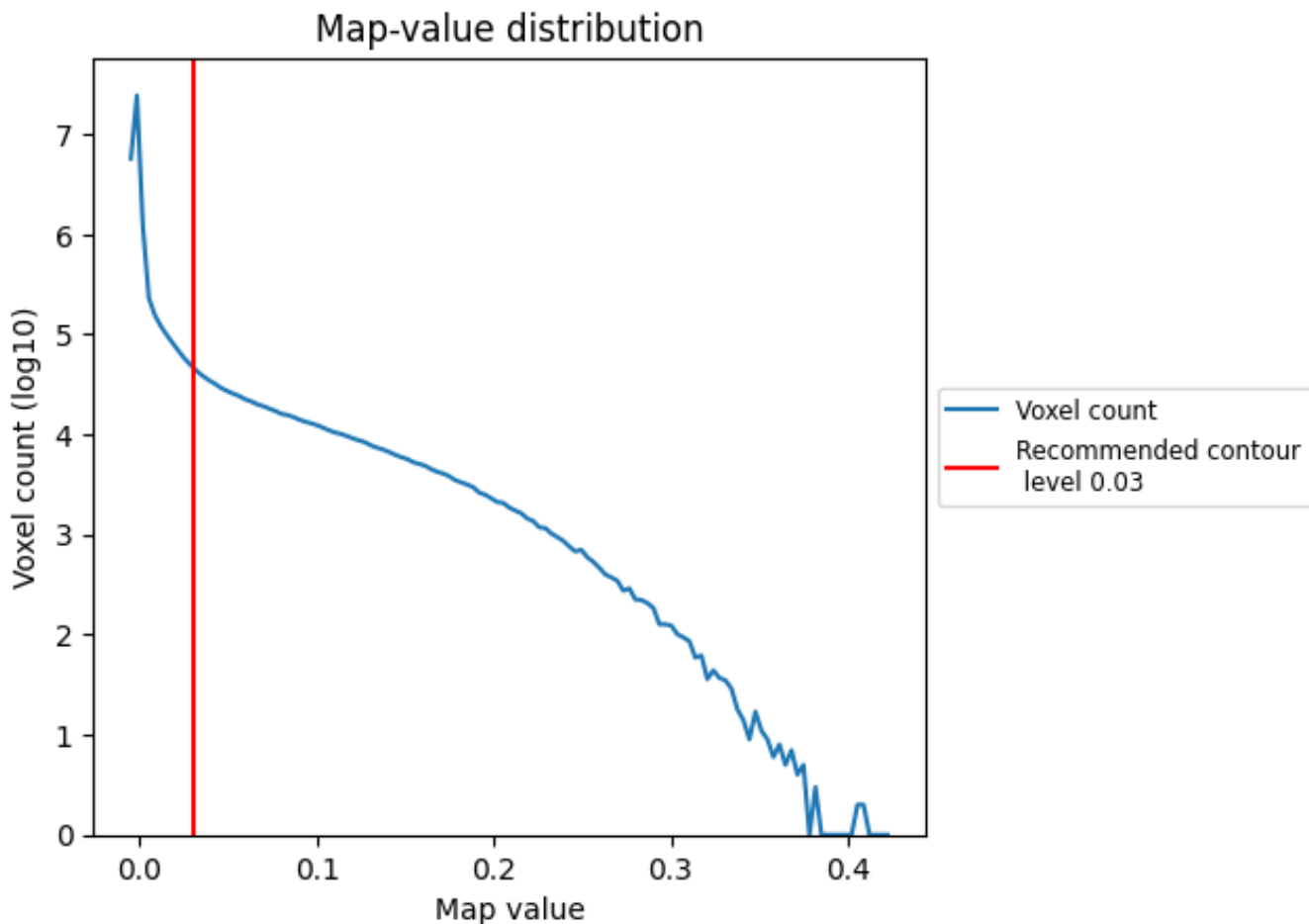
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

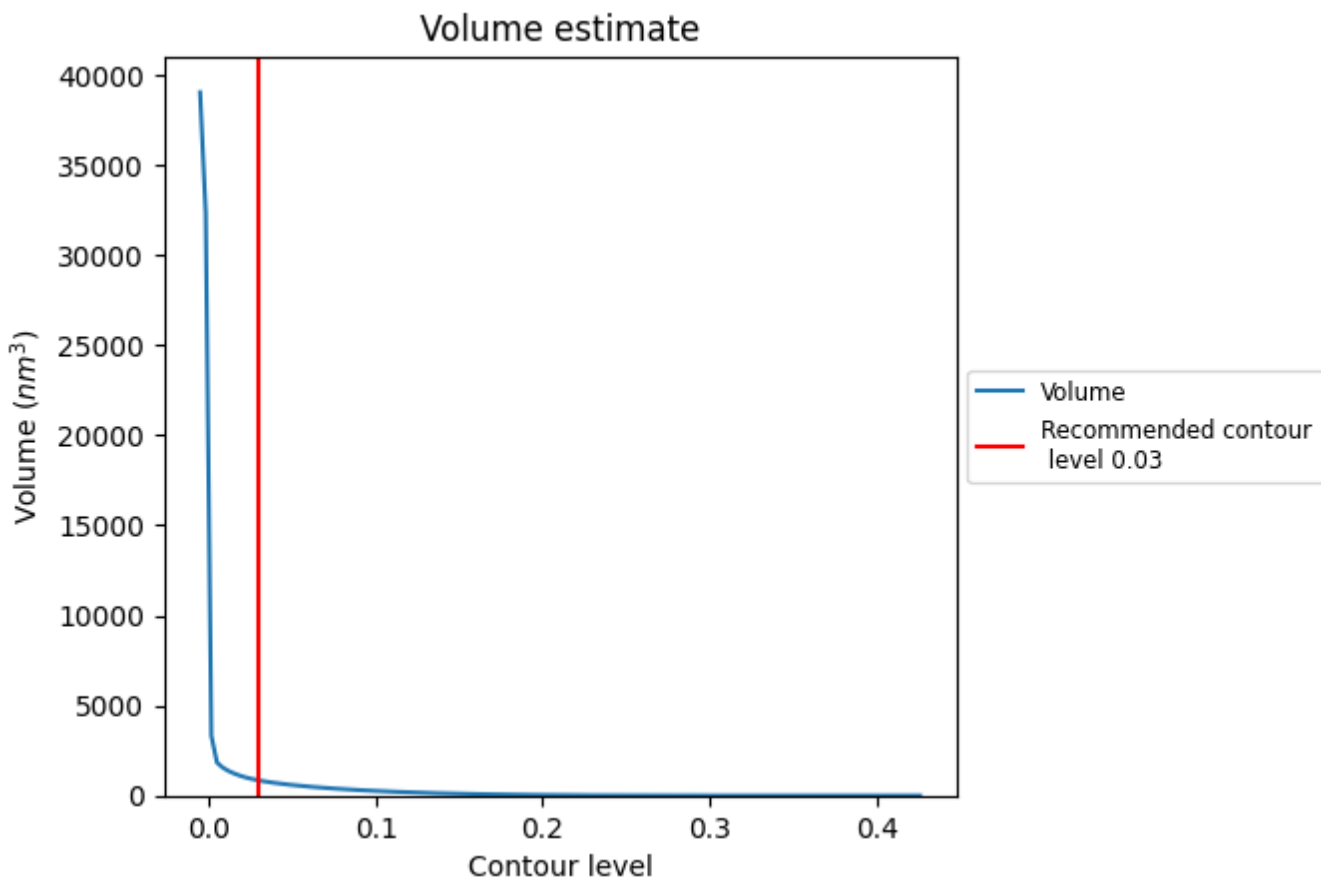
This section contains the results of statistical analysis of the map.

### 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.

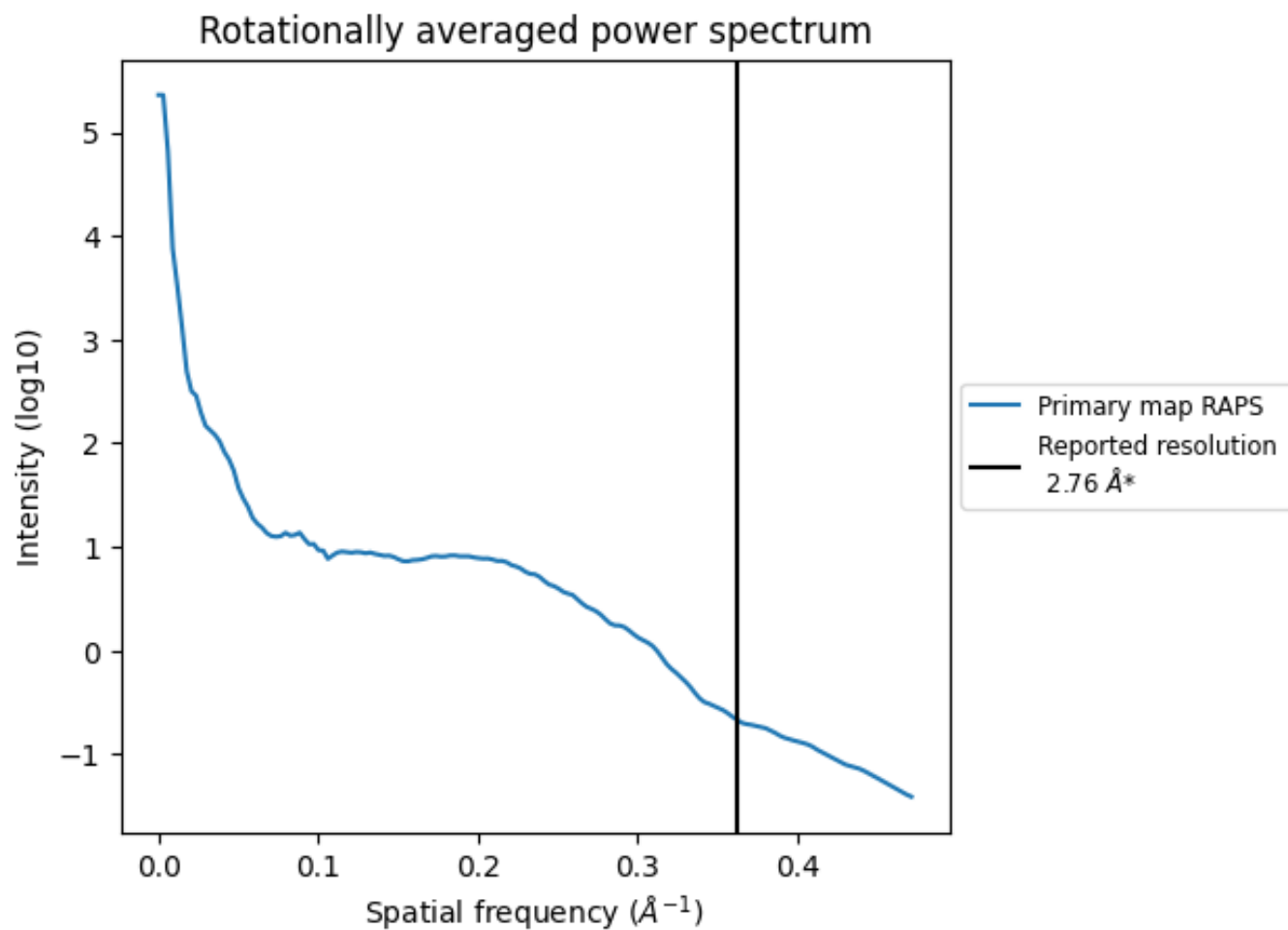
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 844  $\text{nm}^3$ ; this corresponds to an approximate mass of 762 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](#)

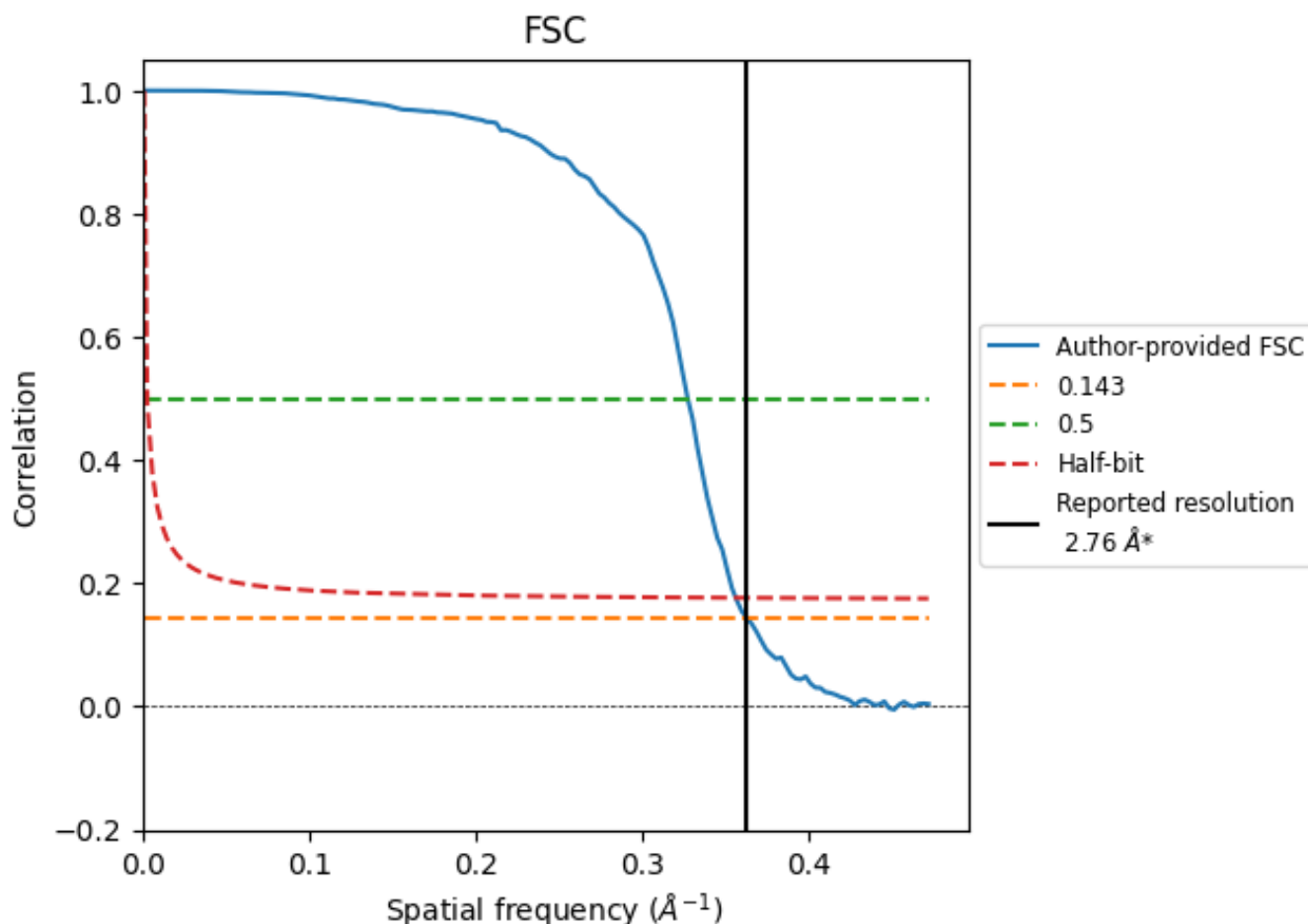


\*Reported resolution corresponds to spatial frequency of 0.362 Å<sup>-1</sup>

## 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 0.362 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

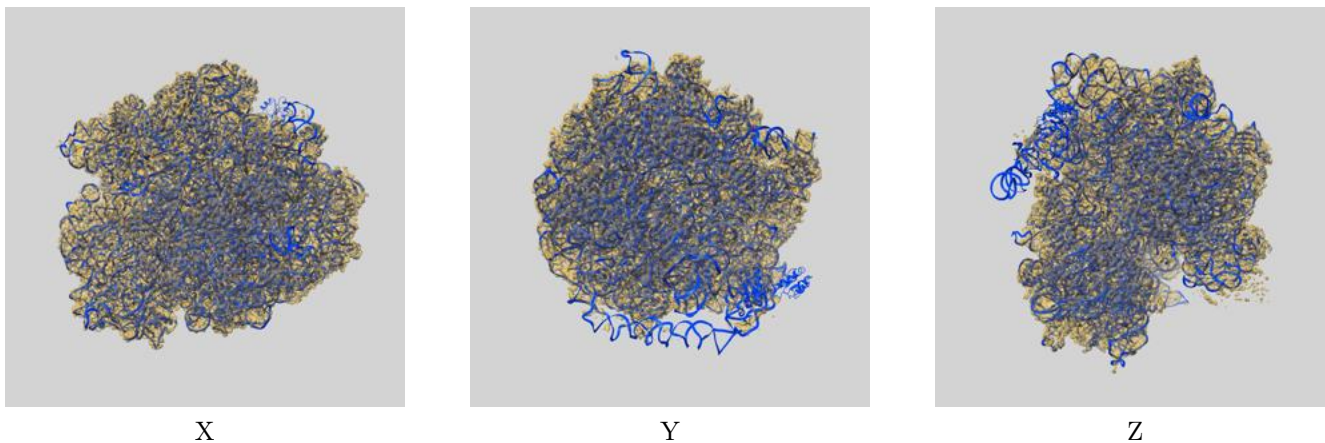
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.76	-	-
Author-provided FSC curve	2.75	3.06	2.81
Unmasked-calculated*	-	-	-

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

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

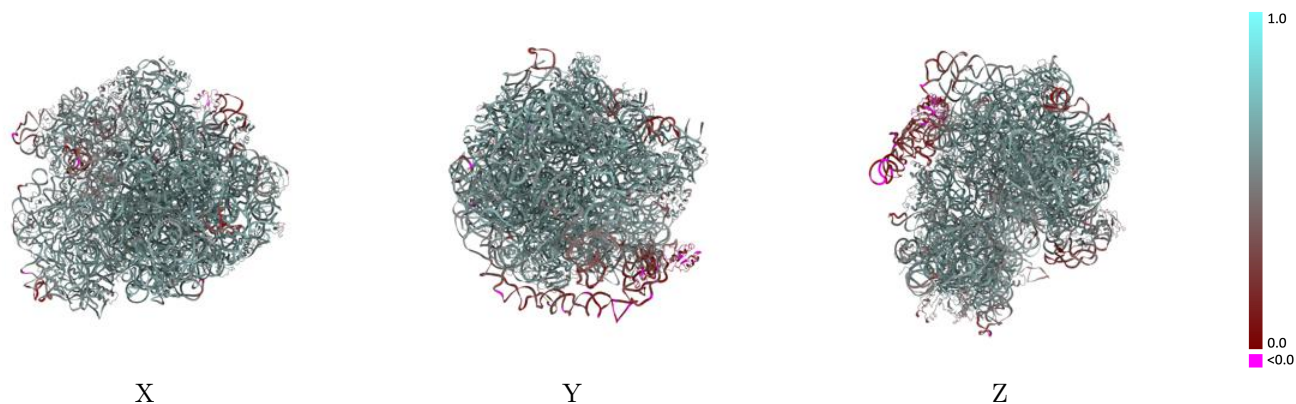
This section contains information regarding the fit between EMDB map EMD-23974 and PDB model 7MT2. Per-residue inclusion information can be found in section 3 on page 16.

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



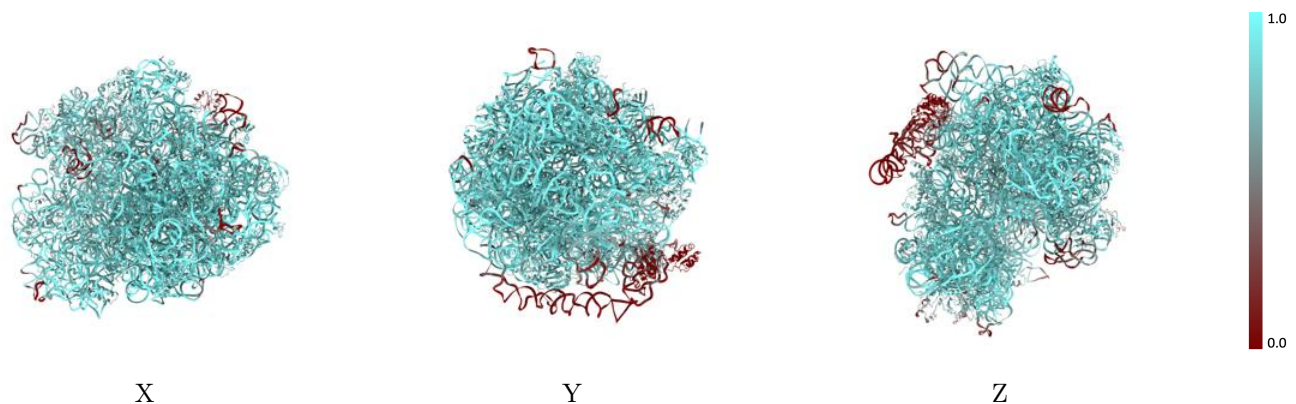
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



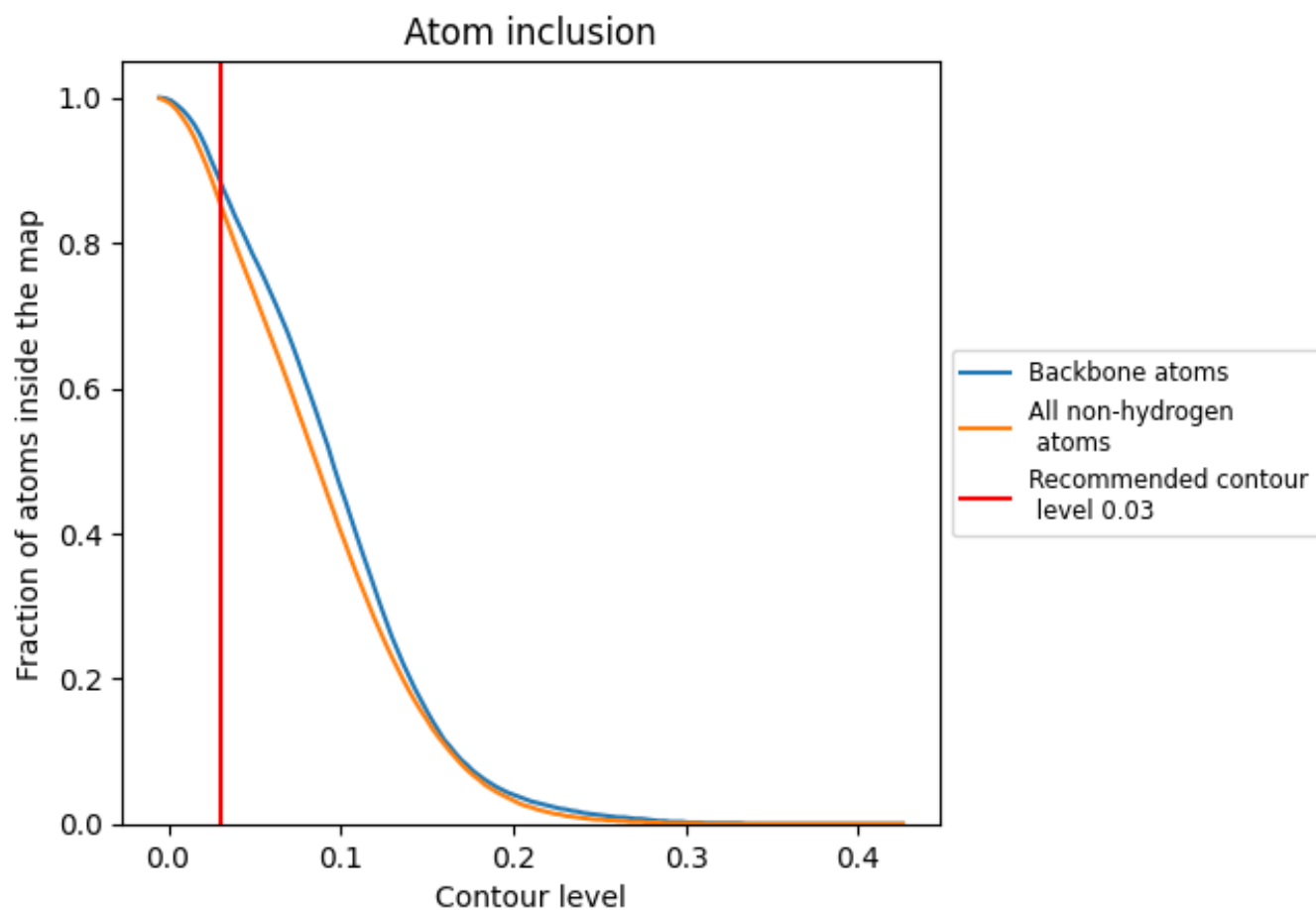
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 89% 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	 0.8550	 0.5510
0	 0.8370	 0.5770
1	 0.8510	 0.5660
2	 0.9160	 0.6070
3	 0.8900	 0.6050
4	 0.8820	 0.5750
6	 0.7830	 0.4930
7	 0.5140	 0.5390
8	 0.1140	 0.2250
A	 0.8670	 0.5560
B	 0.9250	 0.5730
C	 0.8990	 0.5980
D	 0.8820	 0.5820
E	 0.8810	 0.5770
F	 0.7990	 0.5230
G	 0.7150	 0.4790
H	 0.5360	 0.4640
J	 0.8640	 0.5720
K	 0.8740	 0.5740
L	 0.8780	 0.5810
M	 0.8310	 0.5670
N	 0.8900	 0.5910
O	 0.8450	 0.5550
P	 0.8360	 0.5620
Q	 0.8850	 0.5930
R	 0.8610	 0.5770
S	 0.8970	 0.5890
T	 0.8440	 0.5560
U	 0.8240	 0.5280
V	 0.6650	 0.4740
W	 0.9170	 0.5740
X	 0.9140	 0.5870
Y	 0.8250	 0.5420
Z	 0.8730	 0.5670
a	 0.9140	 0.5670



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Chain	Atom inclusion	Q-score
c	 0.7460	 0.5030
d	 0.7370	 0.5030
e	 0.8080	 0.5390
f	 0.7630	 0.5250
g	 0.7810	 0.5290
h	 0.8470	 0.5570
i	 0.7530	 0.5040
j	 0.6480	 0.4480
k	 0.8130	 0.5400
l	 0.7830	 0.5220
m	 0.7960	 0.5130
n	 0.8730	 0.5620
o	 0.8050	 0.5450
p	 0.7680	 0.5170
q	 0.7940	 0.5160
r	 0.8050	 0.5310
s	 0.8120	 0.5320
t	 0.7980	 0.5390
y	 0.8700	 0.5630
z	 0.8000	 0.4810