



## wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 04:45 AM UTC

PDB ID : 6TPQ / pdb\_00006tpq  
EMDB ID : EMD-10543  
Title : RNase M5 bound to 50S ribosome with precursor 5S rRNA  
Authors : Oerum, S.; Dendooven, T.; Gilet, L.; Catala, M.; Degut, C.; Trinquier, A.;  
Barraud, P.; Luisi, B.; Condon, C.; Tisne, C.  
Deposited on : 2019-12-13  
Resolution : 3.07 Å(reported)  
Based on initial model : 3J3V

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

---

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

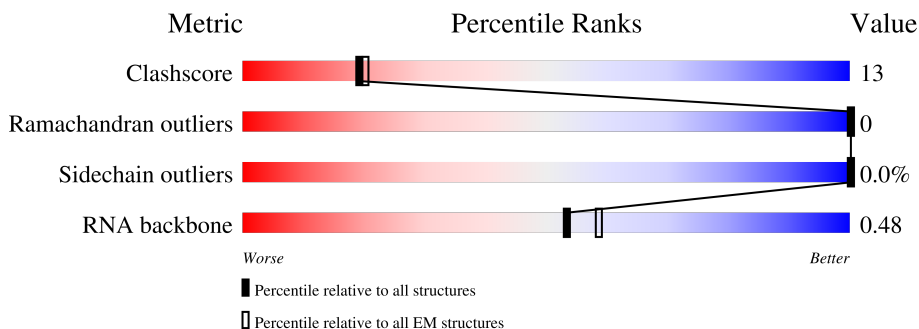
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : **NOT EXECUTED**  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.07 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.




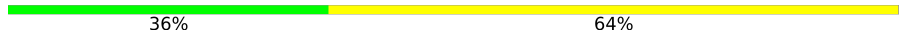











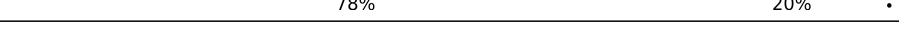







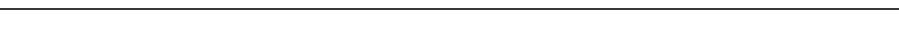


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	187	19% 18% 63%
1	B	187	52% 45% .
2	V	123	37% 49% 14%
3	b	166	23% 51% 26%
4	U	2924	53% 35% 11%
5	W	277	75% 24% .
6	X	209	80% 19% .

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
7	Y	207	 73% 26%
8	Z	179	 36% 64%
9	a	179	 64% 34%
10	c	145	 79% 19%
11	d	122	 72% 28%
12	e	146	 74% 26%
13	f	144	 72% 24%
14	g	120	 78% 22%
15	h	120	 72% 28%
16	i	115	 65% 34%
17	j	119	 69% 29%
18	k	102	 66% 33%
19	l	113	 86% 11%
20	m	95	 78% 20%
21	n	103	 60% 38%
22	o	94	 65% 22% 13%
23	p	59	 71% 20% 8%
24	q	49	 67% 31%
25	r	44	 77% 23%
26	s	66	 74% 23%
27	t	37	 68% 30%
28	u	62	 73% 21% 6%
29	v	66	 70% 29%
30	w	59	 71% 27%

## 2 Entry composition [i](#)

There are 32 unique types of molecules in this entry. The entry contains 91728 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 Ribonuclease M5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	183	1425	887	269	266	3	0	0
1	A	69	548	343	108	95	2	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	58	ALA	ASP	engineered mutation	UNP A0A087LGV4
A	58	ALA	ASP	engineered mutation	UNP A0A087LGV4

- Molecule 2 is a RNA chain called pre-5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	V	123	2628	1172	473	860	123	0	0

- Molecule 3 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	b	123	955	602	163	189	1	0	0

- Molecule 4 is a RNA chain called pre-23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	U	2924	62790	28012	11594	20260	2924	0	0

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	W	275	Total	C	N	O	S	0	0
			2111	1312	416	377	6		

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	X	207	Total	C	N	O	S	0	0
			1575	988	290	292	5		

- Molecule 7 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Y	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Z	178	Total	C	N	O	S	0	0
			1404	893	245	259	7		

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	c	142	Total	C	N	O	S	0	0
			1124	710	206	203	5		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	d	122	Total	C	N	O	S	0	0
			921	571	173	173	4		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	e	146	Total	C	N	O	S	0	0
			1082	671	207	202	2		

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	f	138	Total	C	N	O	S	0	0
			1097	703	208	181	5		

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	g	119	Total	C	N	O	S	0	0
			954	583	186	181	4		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	h	120	Total	C	N	O	S	0	0
			913	564	176	172	1		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	i	114	Total	C	N	O	0	0
			937	595	184	158		

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	j	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	k	101	Total	C	N	O	0	0
			787	501	139	147		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	l	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	m	93	Total	C	N	O	S	0	0
			752	472	137	139	4		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	n	101	Total	C	N	O	S	0	0
			762	478	142	138	4		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	o	82	Total	C	N	O	0	0
			630	390	123	117		

- Molecule 23 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	p	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 24 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	q	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 25 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	r	44	Total	C	N	O	S	0	0
			368	222	89	55	2		

- Molecule 26 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	s	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 27 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	t	36	Total	C	N	O	S	0	0
			289	181	59	45	4		

- Molecule 28 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	u	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 29 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	v	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 30 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	w	58	Total	C	N	O	S	0	0
			456	281	89	85	1		

- Molecule 31 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
31	V	1	Total	Mg	0
			1	1	
31	U	214	Total	Mg	0
			214	214	
31	W	2	Total	Mg	0
			2	2	
31	e	1	Total	Mg	0
			1	1	
31	u	1	Total	Mg	0
			1	1	

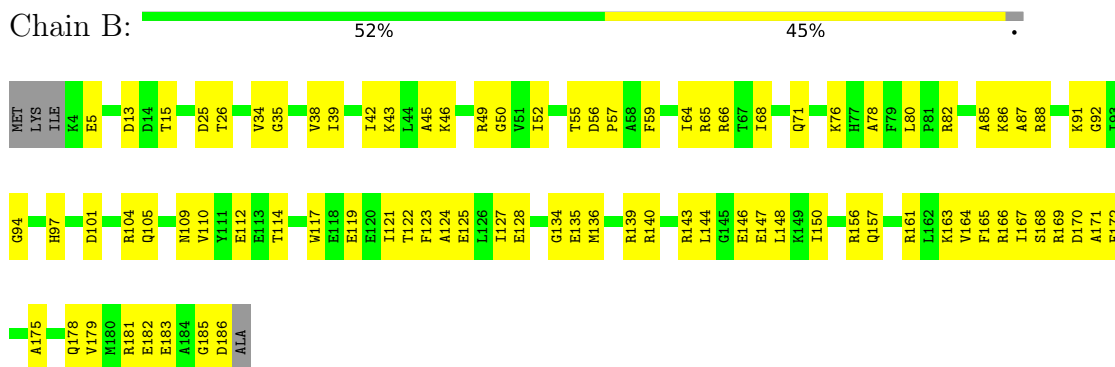
- Molecule 32 is ZINC ION (CCD ID: ZN) (formula: Zn).

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>AltConf</b>
32	p	1	Total 1	Zn 1	0
32	q	1	Total 1	Zn 1	0
32	t	1	Total 1	Zn 1	0

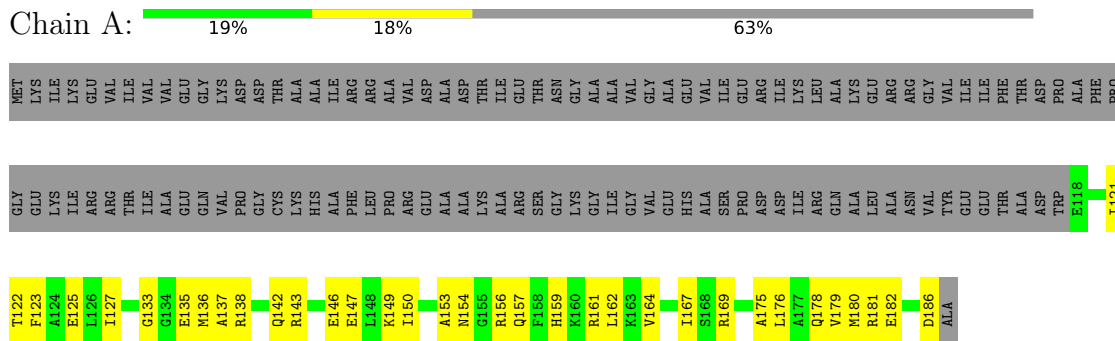
### 3 Residue-property plots [i](#)

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. 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. 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.

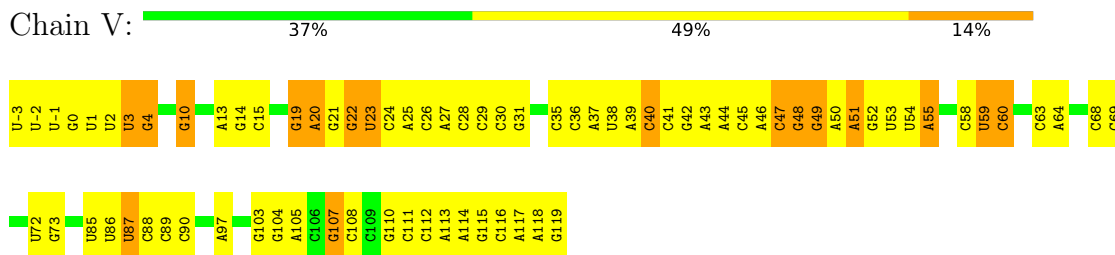
- Molecule 1: Ribonuclease M5



- Molecule 1: Ribonuclease M5



- Molecule 2: pre-5S rRNA

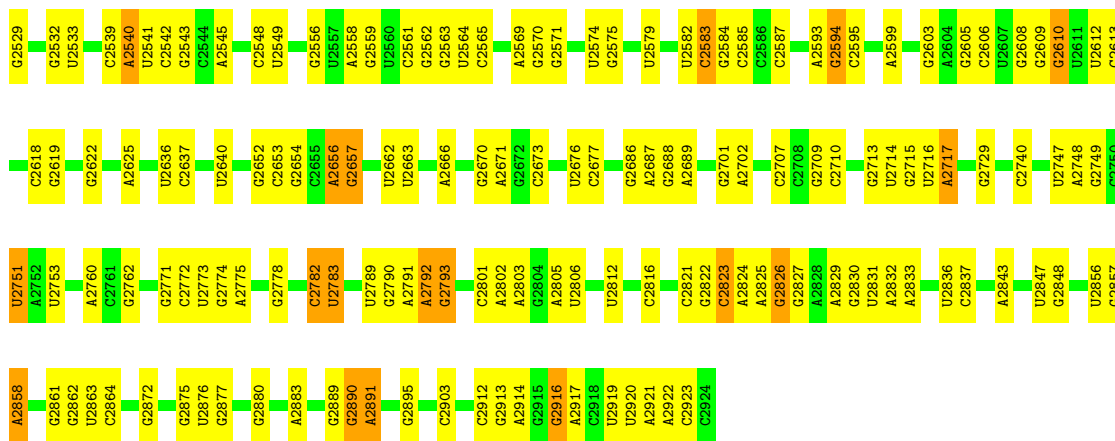


- Molecule 3: 50S ribosomal protein L10

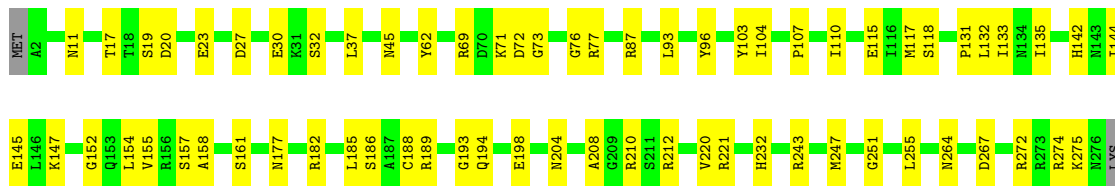
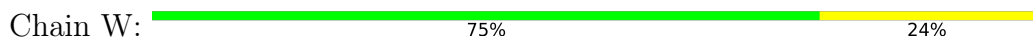




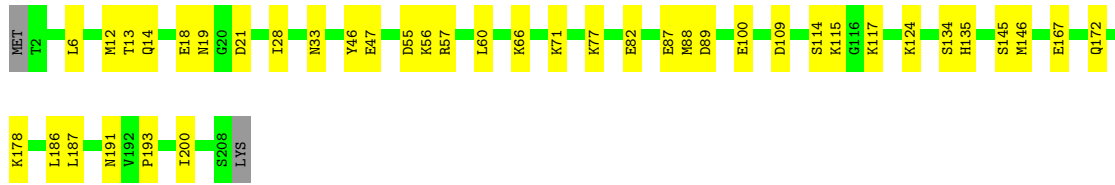
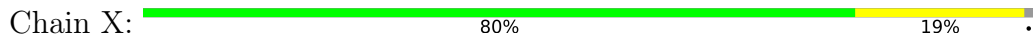




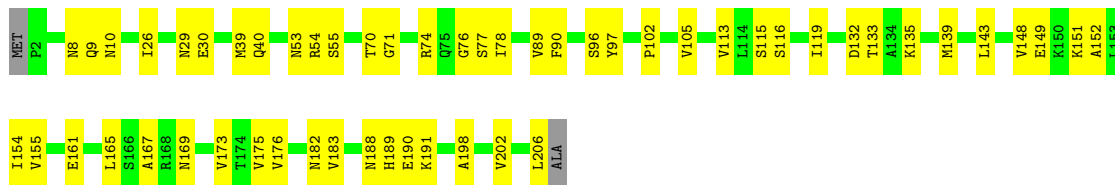
• Molecule 5: 50S ribosomal protein L2



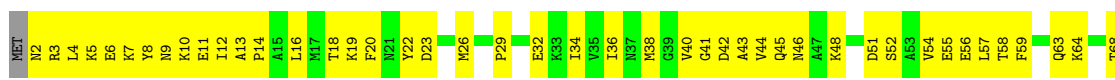
• Molecule 6: 50S ribosomal protein L3



• Molecule 7: 50S ribosomal protein L4



• Molecule 8: 50S ribosomal protein L5

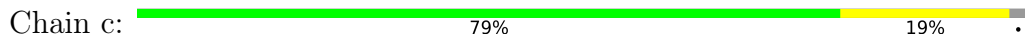




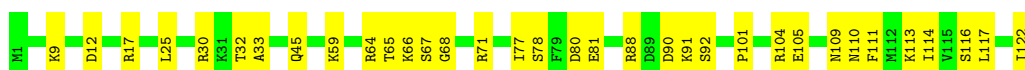
• Molecule 9: 50S ribosomal protein L6



• Molecule 10: 50S ribosomal protein L13



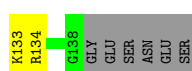
• Molecule 11: 50S ribosomal protein L14




• Molecule 12: 50S ribosomal protein L15

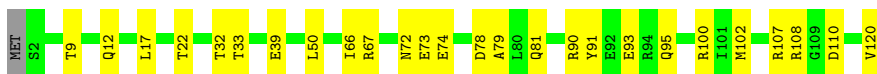


• Molecule 13: 50S ribosomal protein L16



- Molecule 14: 50S ribosomal protein L17

Chain g:  78% 22%



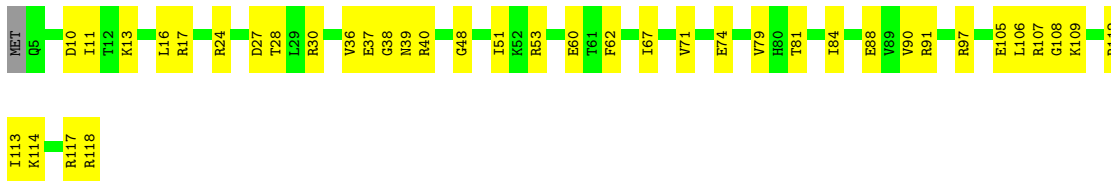
- Molecule 15: 50S ribosomal protein L18

Chain h:  72% 28%



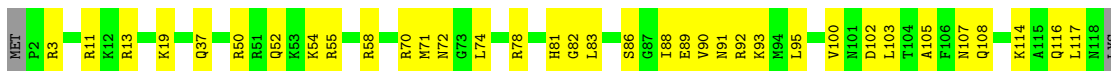
- Molecule 16: 50S ribosomal protein L19

Chain i:  65% 34%



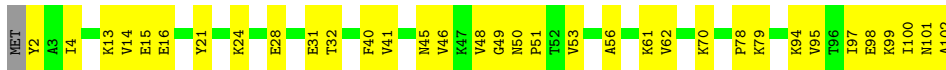
- Molecule 17: 50S ribosomal protein L20

Chain j:  69% 29%




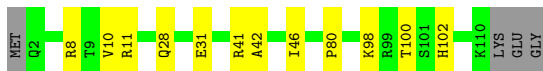
- Molecule 18: 50S ribosomal protein L21

Chain k:  66% 33%




- Molecule 19: 50S ribosomal protein L22

Chain l:  86% 11%

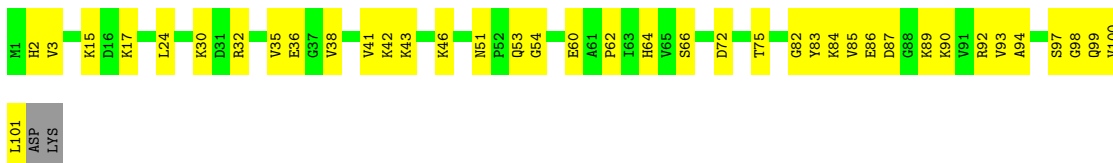


- Molecule 20: 50S ribosomal protein L23

Chain m:  78% 20%



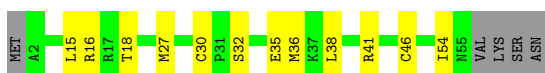
- Molecule 21: 50S ribosomal protein L24



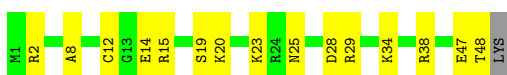
- Molecule 22: 50S ribosomal protein L27



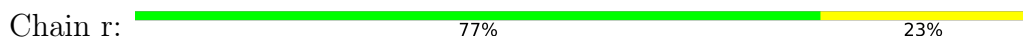
- Molecule 23: 50S ribosomal protein L32



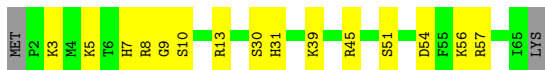
- Molecule 24: 50S ribosomal protein L33 1



- Molecule 25: 50S ribosomal protein L34



- Molecule 26: 50S ribosomal protein L35



- Molecule 27: 50S ribosomal protein L36

Chain t:  68% 30%



- Molecule 28: 50S ribosomal protein L28

Chain u:  73% 21% 6%



- Molecule 29: 50S ribosomal protein L29

Chain v:  70% 29%



- Molecule 30: 50S ribosomal protein L30

Chain w:  71% 27%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	92799	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	23.94	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	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: ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.19	0/554	0.40	0/736
1	B	0.16	0/1444	0.39	0/1939
2	V	0.29	0/2938	0.31	0/4579
3	b	0.17	0/963	0.48	1/1298 (0.1%)
4	U	0.41	0/70333	0.35	0/109728
5	W	0.38	0/2148	0.41	0/2881
6	X	0.39	0/1597	0.40	0/2140
7	Y	0.38	0/1580	0.42	0/2132
8	Z	0.22	0/1423	0.45	0/1910
9	a	0.25	0/1360	0.37	0/1832
10	c	0.43	0/1147	0.45	0/1542
11	d	0.38	0/928	0.43	0/1245
12	e	0.39	0/1094	0.47	0/1457
13	f	0.35	0/1120	0.40	0/1496
14	g	0.39	0/961	0.43	0/1284
15	h	0.27	0/922	0.40	0/1236
16	i	0.37	0/950	0.43	0/1269
17	j	0.49	0/952	0.49	0/1266
18	k	0.40	0/798	0.44	0/1070
19	l	0.42	0/851	0.41	0/1146
20	m	0.38	0/759	0.40	0/1011
21	n	0.33	0/772	0.41	0/1032
22	o	0.40	0/638	0.45	0/847
23	p	0.41	0/433	0.42	0/574
24	q	0.33	0/406	0.39	0/540
25	r	0.47	0/371	0.53	0/483
26	s	0.39	0/519	0.41	0/680
27	t	0.35	0/292	0.34	0/383
28	u	0.32	0/448	0.39	0/596
29	v	0.32	0/531	0.42	0/707
30	w	0.39	0/458	0.41	0/613
All	All	0.39	0/99690	0.36	1/149652 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
3	b	50	VAL	N-CA-C	-5.13	108.27	113.20

There are no chirality outliers.

There are no planarity outliers.

## 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	A	548	0	550	24	0
1	B	1425	0	1435	70	0
2	V	2628	0	1328	74	0
3	b	955	0	990	90	0
4	U	62790	0	31595	1120	0
5	W	2111	0	2200	51	0
6	X	1575	0	1642	30	0
7	Y	1561	0	1647	39	0
8	Z	1404	0	1467	119	0
9	a	1342	0	1388	39	0
10	c	1124	0	1162	22	0
11	d	921	0	977	25	0
12	e	1082	0	1132	29	0
13	f	1097	0	1165	28	0
14	g	954	0	983	20	0
15	h	913	0	947	25	0
16	i	937	0	1008	29	0
17	j	940	0	1005	35	0
18	k	787	0	826	25	0
19	l	842	0	899	9	0
20	m	752	0	802	14	0
21	n	762	0	821	30	0
22	o	630	0	644	18	0
23	p	426	0	442	9	0
24	q	401	0	410	11	0
25	r	368	0	410	8	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	s	512	0	564	14	0
27	t	289	0	327	9	0
28	u	444	0	487	9	0
29	v	530	0	568	17	0
30	w	456	0	491	13	0
31	U	214	0	0	0	0
31	V	1	0	0	0	0
31	W	2	0	0	0	0
31	e	1	0	0	0	0
31	u	1	0	0	0	0
32	p	1	0	0	0	0
32	q	1	0	0	0	0
32	t	1	0	0	0	0
All	All	91728	0	60312	1892	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 13.

The worst 5 of 1892 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)
4:U:1137:G:H21	4:U:1142:A:N6	1.26	1.32
4:U:1137:G:N2	4:U:1142:A:H62	1.32	1.25
4:U:970:U:HO2'	4:U:971:G:H8	1.12	0.95
4:U:325:G:H1	4:U:398:U:H3	0.98	0.93
14:g:120:VAL:HG13	14:g:120:VAL:OXT	1.67	0.92

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	67/187 (36%)	63 (94%)	4 (6%)	0	100	100
1	B	181/187 (97%)	169 (93%)	12 (7%)	0	100	100
3	b	121/166 (73%)	97 (80%)	24 (20%)	0	100	100
5	W	273/277 (99%)	242 (89%)	31 (11%)	0	100	100
6	X	205/209 (98%)	183 (89%)	22 (11%)	0	100	100
7	Y	203/207 (98%)	178 (88%)	25 (12%)	0	100	100
8	Z	176/179 (98%)	149 (85%)	27 (15%)	0	100	100
9	a	173/179 (97%)	151 (87%)	22 (13%)	0	100	100
10	c	140/145 (97%)	131 (94%)	9 (6%)	0	100	100
11	d	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
12	e	144/146 (99%)	129 (90%)	15 (10%)	0	100	100
13	f	136/144 (94%)	129 (95%)	7 (5%)	0	100	100
14	g	117/120 (98%)	105 (90%)	12 (10%)	0	100	100
15	h	118/120 (98%)	108 (92%)	10 (8%)	0	100	100
16	i	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
17	j	115/119 (97%)	109 (95%)	6 (5%)	0	100	100
18	k	99/102 (97%)	83 (84%)	16 (16%)	0	100	100
19	l	107/113 (95%)	105 (98%)	2 (2%)	0	100	100
20	m	91/95 (96%)	84 (92%)	7 (8%)	0	100	100
21	n	99/103 (96%)	90 (91%)	9 (9%)	0	100	100
22	o	80/94 (85%)	73 (91%)	7 (9%)	0	100	100
23	p	52/59 (88%)	47 (90%)	5 (10%)	0	100	100
24	q	46/49 (94%)	42 (91%)	4 (9%)	0	100	100
25	r	42/44 (96%)	40 (95%)	2 (5%)	0	100	100
26	s	62/66 (94%)	58 (94%)	4 (6%)	0	100	100
27	t	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
28	u	56/62 (90%)	50 (89%)	6 (11%)	0	100	100
29	v	63/66 (96%)	56 (89%)	7 (11%)	0	100	100
30	w	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
All	All	3288/3571 (92%)	2974 (90%)	314 (10%)	0	100	100

There are no Ramachandran outliers to report.

### 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	A	50/143 (35%)	50 (100%)	0	100	100
1	B	139/143 (97%)	139 (100%)	0	100	100
3	b	105/138 (76%)	105 (100%)	0	100	100
5	W	223/225 (99%)	223 (100%)	0	100	100
6	X	168/170 (99%)	168 (100%)	0	100	100
7	Y	169/170 (99%)	168 (99%)	1 (1%)	78	81
8	Z	153/154 (99%)	153 (100%)	0	100	100
9	a	148/151 (98%)	148 (100%)	0	100	100
10	c	120/123 (98%)	120 (100%)	0	100	100
11	d	101/101 (100%)	101 (100%)	0	100	100
12	e	110/110 (100%)	110 (100%)	0	100	100
13	f	111/116 (96%)	111 (100%)	0	100	100
14	g	99/100 (99%)	99 (100%)	0	100	100
15	h	93/93 (100%)	93 (100%)	0	100	100
16	i	99/100 (99%)	99 (100%)	0	100	100
17	j	96/98 (98%)	96 (100%)	0	100	100
18	k	83/84 (99%)	83 (100%)	0	100	100
19	l	90/93 (97%)	90 (100%)	0	100	100
20	m	84/85 (99%)	84 (100%)	0	100	100
21	n	85/87 (98%)	85 (100%)	0	100	100
22	o	64/74 (86%)	64 (100%)	0	100	100
23	p	48/53 (91%)	48 (100%)	0	100	100
24	q	46/47 (98%)	46 (100%)	0	100	100
25	r	39/39 (100%)	39 (100%)	0	100	100
26	s	54/56 (96%)	54 (100%)	0	100	100
27	t	34/35 (97%)	34 (100%)	0	100	100

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	u	47/50 (94%)	47 (100%)	0	100	100
29	v	56/57 (98%)	56 (100%)	0	100	100
30	w	52/53 (98%)	52 (100%)	0	100	100
All	All	2766/2948 (94%)	2765 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	Y	206	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
17	j	37	GLN
20	m	55	ASN
30	w	40	ASN
17	j	72	ASN
17	j	118	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	V	122/123 (99%)	27 (22%)	4 (3%)
4	U	2923/2924 (99%)	607 (20%)	41 (1%)
All	All	3045/3047 (99%)	634 (20%)	45 (1%)

5 of 634 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	V	4	G
2	V	10	G
2	V	13	A
2	V	14	G
2	V	15	C

5 of 45 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	U	1337	A
4	U	1593	U
4	U	1349	U
4	U	1516	G
4	U	1689	A

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

There are no non-standard protein/DNA/RNA residues in this entry.

#### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

#### 5.6 Ligand geometry [i](#)

Of 222 ligands modelled in this entry, 222 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

#### 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-10543. 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

This section was not generated.

### 6.2 Central slices

This section was not generated.

### 6.3 Largest variance slices

This section was not generated.

### 6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

### 6.5 Orthogonal surface views

This section was not generated.

### 6.6 Mask visualisation

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

## 7 Map analysis

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

### 7.1 Map-value distribution

This section was not generated.

### 7.2 Volume estimate versus contour level

This section was not generated.

### 7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

## 8 Fourier-Shell correlation

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

## 9 Map-model fit

This section was not generated.