



wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Nov 3, 2019 – 08:02 PM EST

PDB ID : 6T34
EMDB ID: : EMD-10373
Title : Atomic model for Turnip mosaic virus (TuMV)
Authors : Valle, M.V.; Cuesta, R.
Deposited on : 2019-10-10
Resolution : 5.20 Å(reported)
Based on PDB ID : 5ODV

This is a wwPDB/EMDatabank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

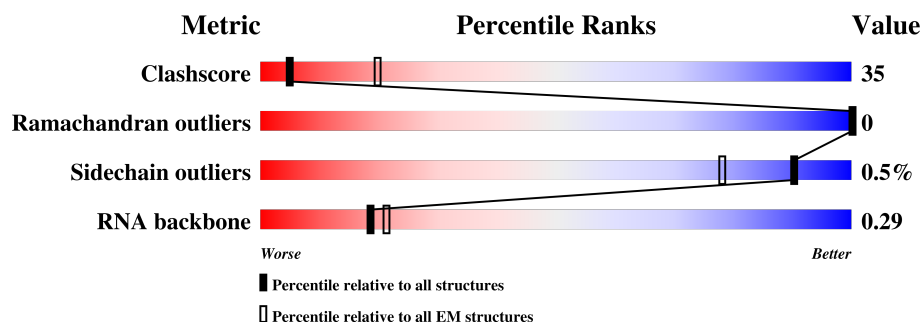
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.20 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.













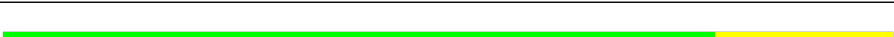


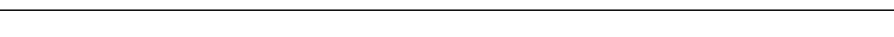
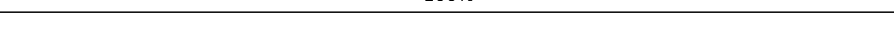
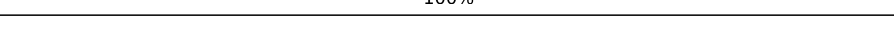
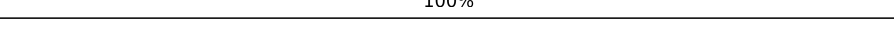
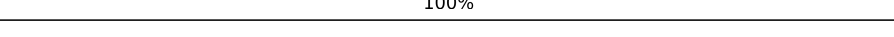
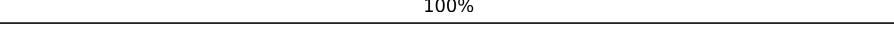
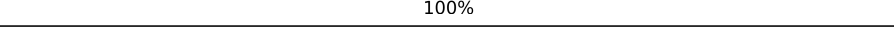
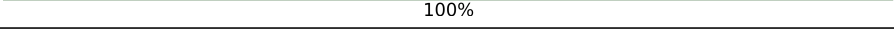
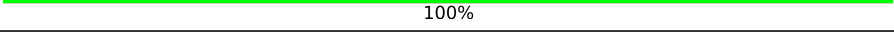
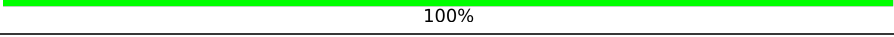
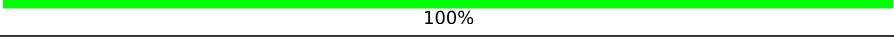
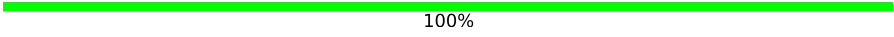
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531
RNA backbone	3747	458

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	207	78% 22%
1	B	207	72% 27%
1	C	207	73% 26%
1	D	207	73% 26%
1	E	207	74% 26%
1	F	207	73% 27%
1	G	207	73% 27%
1	H	207	73% 27%






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Mol	Chain	Length	Quality of chain
1	I	207	 71%29%
1	J	207	 70%29%
1	K	207	 71%29%
1	L	207	 74%25%
1	M	207	 74%25%
1	N	207	 74%26%
1	O	207	 75%24%
1	P	207	 75%24%
1	Q	207	 74%25%
1	R	207	 74%25%
1	S	207	 80%20%
2	a	5	 100%
2	b	5	 100%
2	c	5	 100%
2	d	5	 100%
2	e	5	 100%
2	f	5	 100%
2	g	5	 100%
2	h	5	 100%
2	i	5	 100%
2	j	5	 100%
2	k	5	 100%
2	l	5	 100%
2	m	5	 100%
2	n	5	 100%

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Mol	Chain	Length	Quality of chain
2	o	5	 100%
2	p	5	 100%
2	q	5	 100%
2	r	5	 100%
2	s	5	 100%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 65474 atoms, of which 31559 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 Coat protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	207	3335	1056	1650	301	315	13	0	0
1	B	207	3335	1056	1650	301	315	13	0	0
1	C	207	3335	1056	1650	301	315	13	0	0
1	D	207	3335	1056	1650	301	315	13	0	0
1	E	207	3335	1056	1650	301	315	13	0	0
1	F	207	3335	1056	1650	301	315	13	0	0
1	G	207	3335	1056	1650	301	315	13	0	0
1	H	207	3335	1056	1650	301	315	13	0	0
1	I	207	3335	1056	1650	301	315	13	0	0
1	J	207	3335	1056	1650	301	315	13	0	0
1	K	207	3335	1056	1650	301	315	13	0	0
1	L	207	3335	1056	1650	301	315	13	0	0
1	M	207	3335	1056	1650	301	315	13	0	0
1	N	207	3335	1056	1650	301	315	13	0	0
1	O	207	3335	1056	1650	301	315	13	0	0
1	P	207	3335	1056	1650	301	315	13	0	0
1	Q	207	3335	1056	1650	301	315	13	0	0

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	R	207	Total	C	H	N	O	S	0	0
			3335	1056	1650	301	315	13		
1	S	207	Total	C	H	N	O	S	0	0
			3335	1056	1650	301	315	13		

- Molecule 2 is a RNA chain called RNA (5'-R(P*UP*UP*UP*UP*U)-3').

Mol	Chain	Residues	Atoms						AltConf	Trace
2	a	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	b	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	c	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	d	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	e	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	f	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	g	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	h	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	i	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	j	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	k	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	l	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	m	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	n	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	o	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	p	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	q	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		

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Mol	Chain	Residues	Atoms						AltConf	Trace
2	r	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		
2	s	5	Total	C	H	N	O	P	0	0
			111	45	11	10	40	5		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

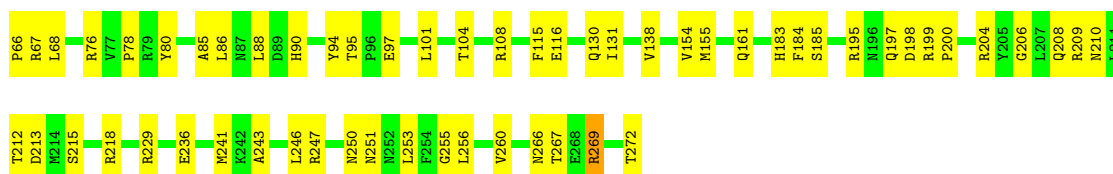
- Molecule 1: Coat protein

Chain A: 



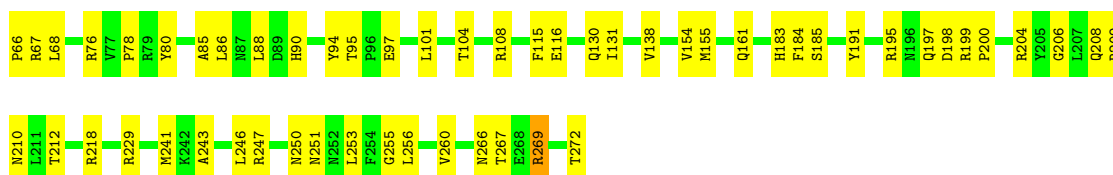
- Molecule 1: Coat protein

Chain B: 



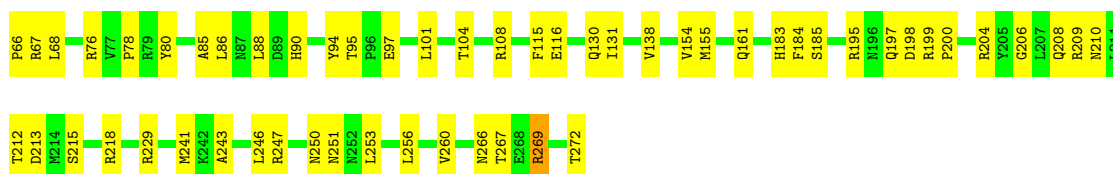
- Molecule 1: Coat protein

Chain C: 



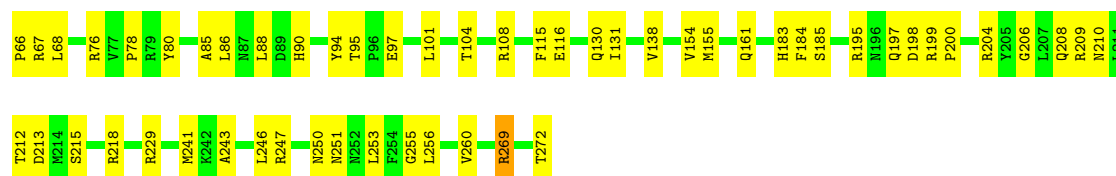
- Molecule 1: Coat protein

Chain D: 



- Molecule 1: Coat protein

Chain E:  74% 26%



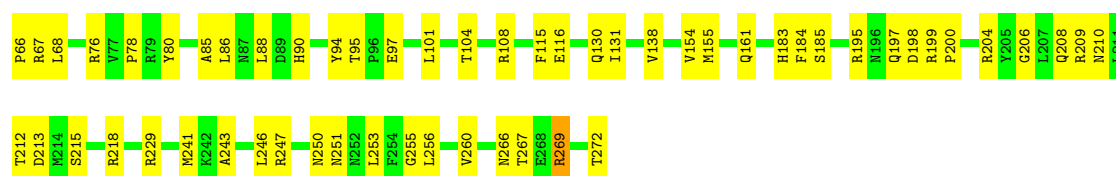
• Molecule 1: Coat protein

Chain F:  73% 27%



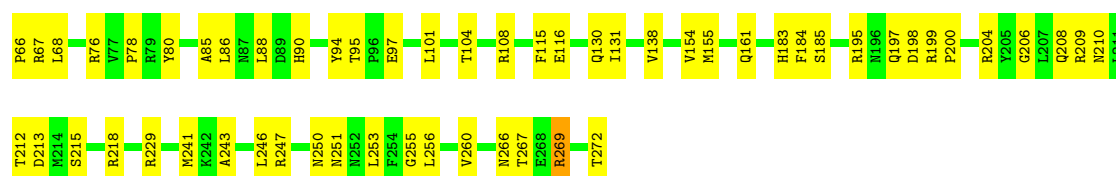
• Molecule 1: Coat protein

Chain G:  73% 27%



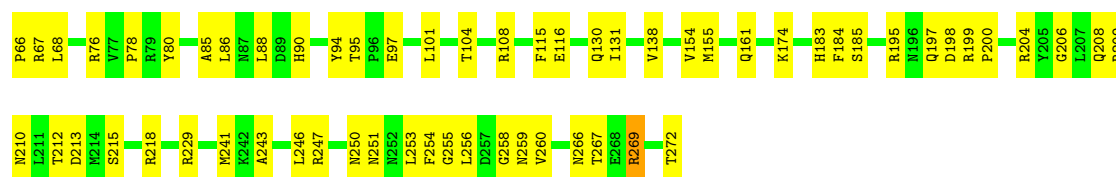
• Molecule 1: Coat protein

Chain H:  73% 27%



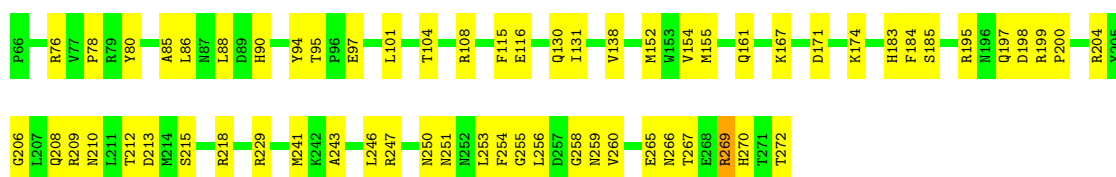
• Molecule 1: Coat protein

Chain I:  71% 29%



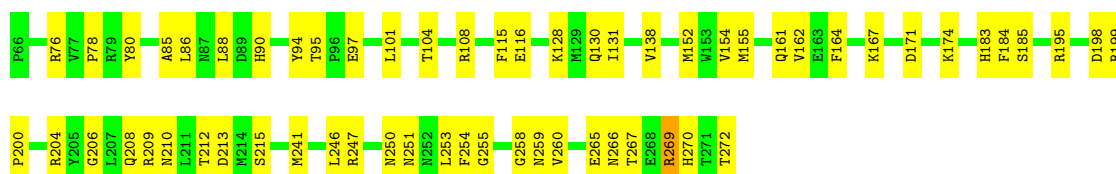
• Molecule 1: Coat protein

Chain J:  70% 29%



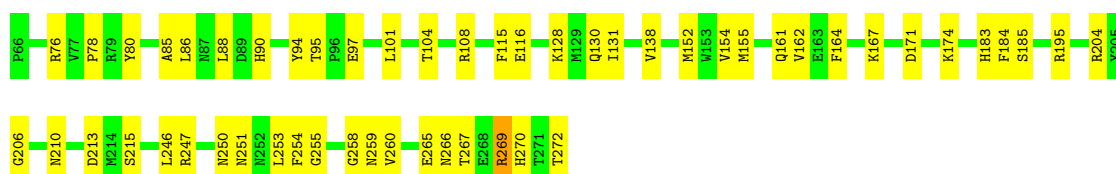
- Molecule 1: Coat protein

Chain K: 71% 29%



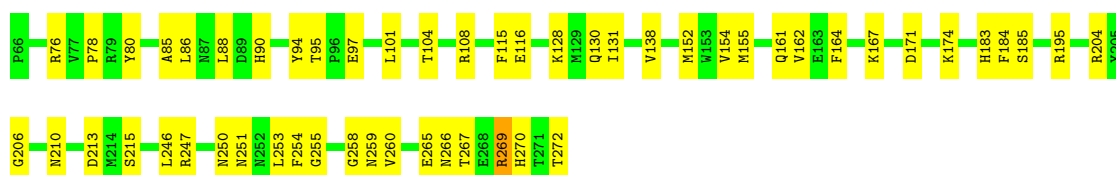
- Molecule 1: Coat protein

Chain L: 74% 25%



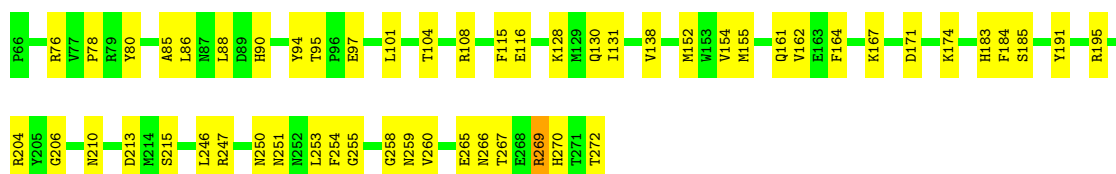
- Molecule 1: Coat protein

Chain M: 74% 25%



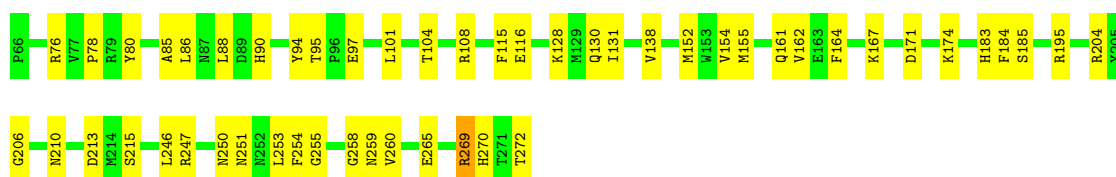
- Molecule 1: Coat protein

Chain N: 74% 26%



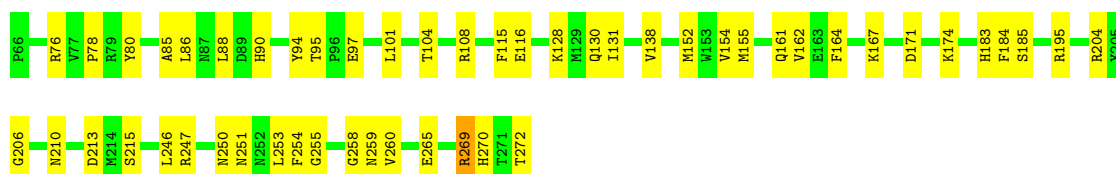
- Molecule 1: Coat protein

Chain O: 75% 24%



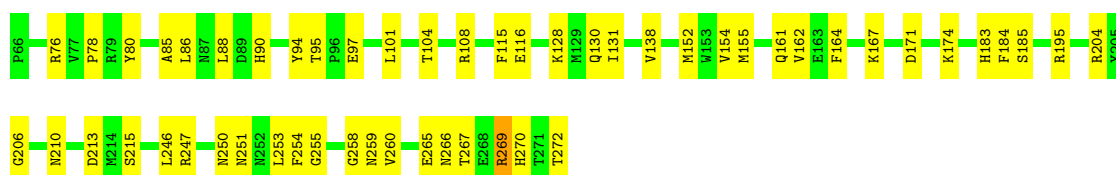
- Molecule 1: Coat protein

Chain P: 75% 24%



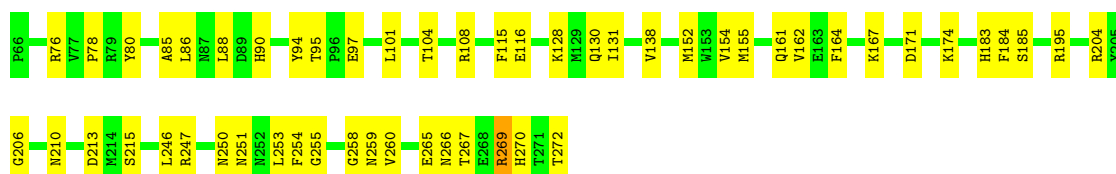
- Molecule 1: Coat protein

Chain Q: 74% 25%



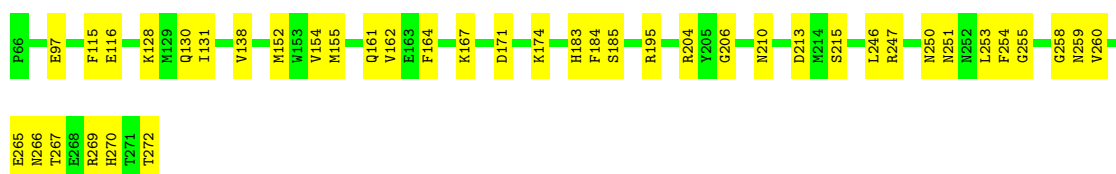
- Molecule 1: Coat protein

Chain R: 74% 25%



- Molecule 1: Coat protein

Chain S: 80% 20%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain a: 100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain b:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain c:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain d:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain e:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain f:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain g:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain h:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain i:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain j:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain k:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain l:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain m:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain n:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain o:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain p:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain q:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain r:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain s:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
Reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-40.8°, rise=4 Å, axial sym=C1	Depositor
Number of segments used	194432	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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 >2	RMSZ	# Z >2
1	A	0.49	0/1721	0.63	0/2326
1	B	0.49	0/1721	0.63	0/2326
1	C	0.49	0/1721	0.63	0/2326
1	D	0.49	0/1721	0.63	0/2326
1	E	0.49	0/1721	0.63	0/2326
1	F	0.49	0/1721	0.63	0/2326
1	G	0.49	0/1721	0.63	0/2326
1	H	0.49	0/1721	0.63	0/2326
1	I	0.49	0/1721	0.63	0/2326
1	J	0.49	0/1721	0.63	0/2326
1	K	0.49	0/1721	0.63	0/2326
1	L	0.49	0/1721	0.63	0/2326
1	M	0.49	0/1721	0.63	0/2326
1	N	0.49	0/1721	0.63	0/2326
1	O	0.49	0/1721	0.63	0/2326
1	P	0.49	0/1721	0.63	0/2326
1	Q	0.49	0/1721	0.63	0/2326
1	R	0.49	0/1721	0.63	0/2326
1	S	0.49	0/1721	0.63	0/2326
2	a	0.39	0/109	0.96	0/166
2	b	0.39	0/109	0.97	0/166
2	c	0.39	0/109	0.96	0/166
2	d	0.40	0/109	0.95	0/166
2	e	0.40	0/109	0.97	0/166
2	f	0.40	0/109	0.96	0/166
2	g	0.39	0/109	0.96	0/166
2	h	0.41	0/109	0.95	0/166
2	i	0.39	0/109	0.97	0/166
2	j	0.40	0/109	0.96	0/166
2	k	0.40	0/109	0.96	0/166
2	l	0.40	0/109	0.96	0/166
2	m	0.40	0/109	0.96	0/166
2	n	0.39	0/109	0.96	0/166
2	o	0.41	0/109	0.95	0/166

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
2	p	0.39	0/109	0.97	0/166
2	q	0.39	0/109	0.96	0/166
2	r	0.39	0/109	0.96	0/166
2	s	0.40	0/109	0.96	0/166
All	All	0.49	0/34770	0.66	0/47348

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1685	1650	1652	159	0
1	B	1685	1650	1648	230	0
1	C	1685	1650	1648	223	0
1	D	1685	1650	1648	223	0
1	E	1685	1650	1648	226	0
1	F	1685	1650	1648	227	0
1	G	1685	1650	1648	226	0
1	H	1685	1650	1648	224	0
1	I	1685	1650	1646	250	0
1	J	1685	1650	1647	261	0
1	K	1685	1650	1646	251	0
1	L	1685	1650	1646	222	0
1	M	1685	1650	1646	224	0
1	N	1685	1650	1646	227	0
1	O	1685	1650	1646	226	0
1	P	1685	1650	1646	222	0
1	Q	1685	1650	1646	222	0
1	R	1685	1650	1647	228	0
1	S	1685	1650	1647	157	0
2	a	100	11	51	0	0
2	b	100	11	51	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	c	100	11	51	0	0
2	d	100	11	51	0	0
2	e	100	11	51	0	0
2	f	100	11	51	0	0
2	g	100	11	51	0	0
2	h	100	11	51	0	0
2	i	100	11	51	0	0
2	j	100	11	51	0	0
2	k	100	11	51	0	0
2	l	100	11	51	0	0
2	m	100	11	51	0	0
2	n	100	11	51	0	0
2	o	100	11	51	0	0
2	p	100	11	51	0	0
2	q	100	11	51	0	0
2	r	100	11	51	0	0
2	s	100	11	51	0	0
All	All	33915	31559	32266	2188	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 35.

The worst 5 of 2188 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)
1:M:95:THR:CG2	1:N:195:ARG:HD3	1.29	1.63
1:R:95:THR:CG2	1:S:195:ARG:HD3	1.29	1.63
1:A:95:THR:CG2	1:B:195:ARG:HD3	1.29	1.63
1:N:95:THR:CG2	1:O:195:ARG:HD3	1.29	1.62
1:L:95:THR:CG2	1:M:195:ARG:HD3	1.29	1.61

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	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	B	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	C	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	D	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	E	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	F	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	G	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	H	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	I	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	J	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	K	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	L	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	M	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	N	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	O	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	P	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	Q	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	R	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
1	S	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
All	All	3895/3933 (99%)	3230 (83%)	665 (17%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	B	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	C	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	D	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	E	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	F	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	G	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	H	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	I	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	J	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	K	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	L	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	M	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	N	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	O	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	P	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	Q	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	R	183/183 (100%)	182 (100%)	1 (0%)	90	94
1	S	183/183 (100%)	182 (100%)	1 (0%)	90	94
All	All	3477/3477 (100%)	3458 (100%)	19 (0%)	90	94

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	269	ARG
1	K	269	ARG
1	P	269	ARG
1	H	269	ARG
1	Q	269	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	197	GLN
1	I	90	HIS

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Mol	Chain	Res	Type
1	Q	87	ASN
1	G	210	ASN
1	H	130	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	a	4/5 (80%)	0	0
2	b	4/5 (80%)	0	0
2	c	4/5 (80%)	0	0
2	d	4/5 (80%)	0	0
2	e	4/5 (80%)	0	0
2	f	4/5 (80%)	0	0
2	g	4/5 (80%)	0	0
2	h	4/5 (80%)	0	0
2	i	4/5 (80%)	0	0
2	j	4/5 (80%)	0	0
2	k	4/5 (80%)	0	0
2	l	4/5 (80%)	0	0
2	m	4/5 (80%)	0	0
2	n	4/5 (80%)	0	0
2	o	4/5 (80%)	0	0
2	p	4/5 (80%)	0	0
2	q	4/5 (80%)	0	0
2	r	4/5 (80%)	0	0
2	s	4/5 (80%)	0	0
All	All	76/95 (80%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.