



## wwPDB EM Validation Summary Report ⓘ

Feb 19, 2025 – 03:20 pm GMT

PDB ID : 7P1T  
EMDB ID : EMD-13164  
Title : Cryo-EM structure of encapsulin from Mycobacterium tuberculosis  
Authors : Lewis, C.J.; Berger, C.; Ravelli, R.B.G.  
Deposited on : 2021-07-02  
Resolution : 2.29 Å(reported)  
Based on initial model : 619G

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : **FAILED**  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.41

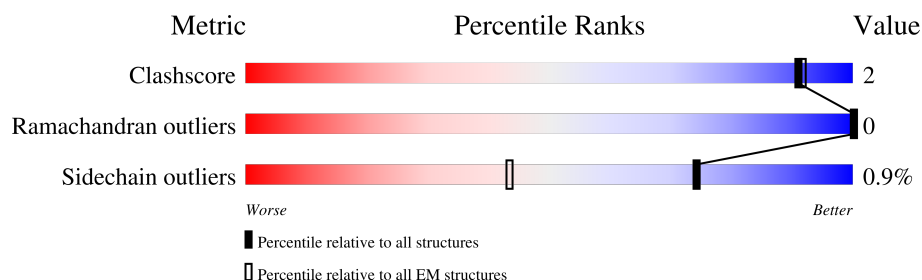
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.29 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	265	<div><div></div>95%5%</div>
1	AA	265	<div><div></div>94%6%</div>
1	AB	265	<div><div></div>95%5%</div>
1	B	265	<div><div></div>94%6%</div>
1	BA	265	<div><div></div>95%5%</div>
1	BB	265	<div><div></div>95%5%</div>
1	C	265	<div><div></div>95%5%</div>
1	CA	265	<div><div></div>95%5%</div>
1	CB	265	<div><div></div>95%5%</div>


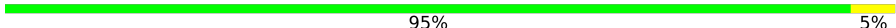
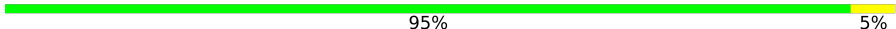
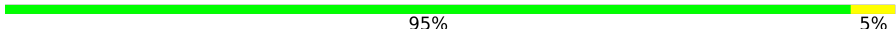
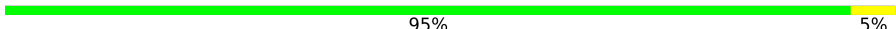





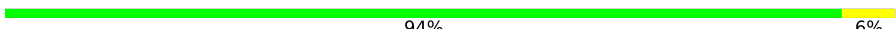
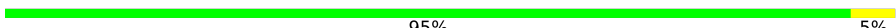
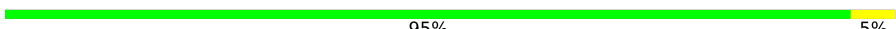
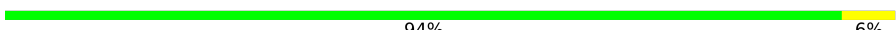
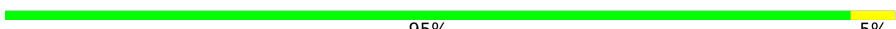
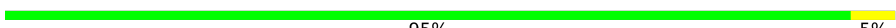
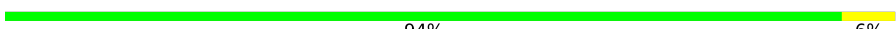
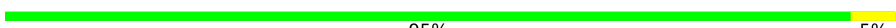
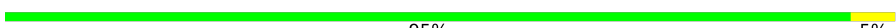
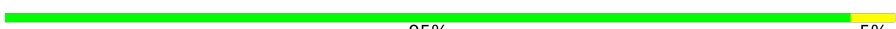
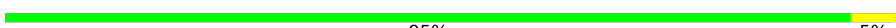

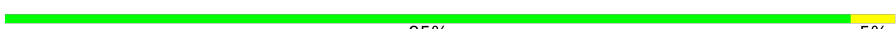


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Mol	Chain	Length	Quality of chain	
1	D	265	94%	6%
1	DA	265	95%	5%
1	DB	265	94%	6%
1	E	265	95%	5%
1	EA	265	95%	5%
1	EB	265	95%	5%
1	F	265	95%	5%
1	FA	265	95%	5%
1	FB	265	95%	5%
1	G	265	95%	5%
1	GA	265	94%	6%
1	GB	265	95%	5%
1	H	265	95%	5%
1	HA	265	95%	5%
1	HB	265	94%	6%
1	I	265	94%	6%
1	IA	265	95%	5%
1	J	265	95%	5%
1	JA	265	95%	5%
1	K	265	95%	5%
1	KA	265	95%	5%
1	L	265	95%	5%
1	LA	265	94%	6%
1	M	265	95%	5%
1	MA	265	95%	5%

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Mol	Chain	Length	Quality of chain
1	N	265	 94% 6%
1	NA	265	 95% 5%
1	O	265	 95% 5%
1	OA	265	 95% 5%
1	P	265	 95% 5%
1	PA	265	 94% 6%
1	Q	265	 94% 6%
1	QA	265	 95% 5%
1	R	265	 95% 5%
1	RA	265	 94% 6%
1	S	265	 94% 6%
1	SA	265	 95% 5%
1	T	265	 95% 5%
1	TA	265	 94% 6%
1	U	265	 95% 5%
1	UA	265	 95% 5%
1	V	265	 94% 6%
1	VA	265	 95% 5%
1	W	265	 95% 5%
1	WA	265	 95% 5%
1	X	265	 95% 5%
1	XA	265	 94% 6%
1	Y	265	 95% 5%
1	YA	265	 95% 5%
1	Z	265	 95% 5%

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Mol	Chain	Length	Quality of chain
1	ZA	265	<div><div></div><div>94%</div><div>6%</div></div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 122040 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 29 kDa antigen, Cfp29.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	B	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	C	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	D	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	E	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	F	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	G	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	H	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	I	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	J	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	K	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	L	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	M	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	N	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	O	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	P	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	Q	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	S	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	T	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	U	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	V	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	W	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	X	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	Y	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	Z	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	AA	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	BA	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	CA	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	DA	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	EA	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	FA	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	GA	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	HA	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	IA	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	JA	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	KA	265	Total 2034	C 1278	N 354	O 400	S 2	0	0
1	LA	265	Total 2034	C 1278	N 354	O 400	S 2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	MA	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	NA	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	OA	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	PA	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	QA	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	RA	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	SA	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	TA	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	UA	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	VA	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	WA	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	XA	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	YA	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	ZA	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	AB	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	BB	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	CB	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	DB	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	EB	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	FB	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		
1	GB	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	HB	265	Total	C	N	O	S	0	0
			2034	1278	354	400	2		

### 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: 29 kDa antigen, Cfp29

Chain A:  95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain B:  94% 6%



- Molecule 1: 29 kDa antigen, Cfp29

Chain C:  95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain D:  94% 6%



- Molecule 1: 29 kDa antigen, Cfp29

Chain E:  95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain F:  95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain G: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain H: 95% 5%



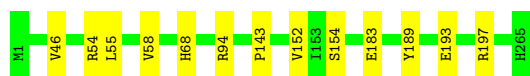
- Molecule 1: 29 kDa antigen, Cfp29

Chain I: 94% 6%



- Molecule 1: 29 kDa antigen, Cfp29

Chain J: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain K: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain L: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain M: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain N: 94% 6%



- Molecule 1: 29 kDa antigen, Cfp29

Chain O: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain P: 95% 5%



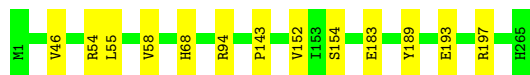
- Molecule 1: 29 kDa antigen, Cfp29

Chain Q: 94% 6%



- Molecule 1: 29 kDa antigen, Cfp29

Chain R: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain S: 94% 6%



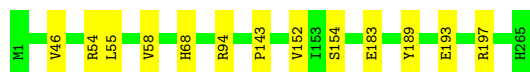
- Molecule 1: 29 kDa antigen, Cfp29

Chain T: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain U: 95% 5%



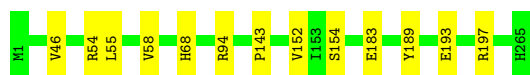
- Molecule 1: 29 kDa antigen, Cfp29

Chain V: 94% 6%



- Molecule 1: 29 kDa antigen, Cfp29

Chain W: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain X: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain Y: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain Z: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain AA: 94% 6%



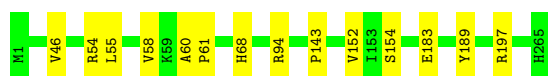
- Molecule 1: 29 kDa antigen, Cfp29

Chain BA: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain CA: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain DA: 95% 5%



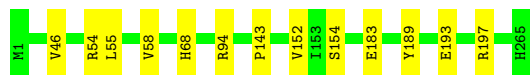
- Molecule 1: 29 kDa antigen, Cfp29

Chain EA: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain FA: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain GA: 94% 6%



- Molecule 1: 29 kDa antigen, Cfp29

Chain HA: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain IA: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain JA: 95% 5%



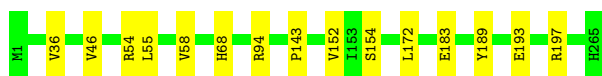
- Molecule 1: 29 kDa antigen, Cfp29

Chain KA: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain LA: 94% 6%



- Molecule 1: 29 kDa antigen, Cfp29

Chain MA: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain NA: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain OA: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain PA:  94% 6%



- Molecule 1: 29 kDa antigen, Cfp29

Chain QA:  95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain RA:  94% 6%



- Molecule 1: 29 kDa antigen, Cfp29

Chain SA:  95% 5%



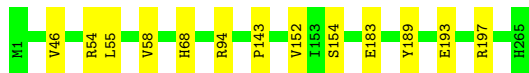
- Molecule 1: 29 kDa antigen, Cfp29

Chain TA:  94% 6%



- Molecule 1: 29 kDa antigen, Cfp29

Chain UA:  95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain VA:  95% 5%





- Molecule 1: 29 kDa antigen, Cfp29

Chain WA: 95% 5%



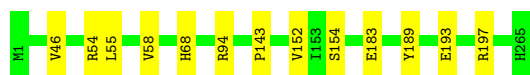
- Molecule 1: 29 kDa antigen, Cfp29

Chain XA: 94% 6%



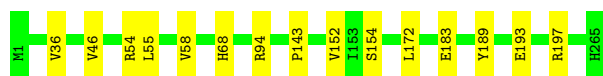
- Molecule 1: 29 kDa antigen, Cfp29

Chain YA: 95% 5%



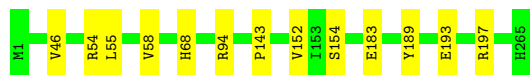
- Molecule 1: 29 kDa antigen, Cfp29

Chain ZA: 94% 6%



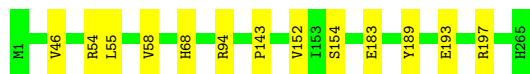
- Molecule 1: 29 kDa antigen, Cfp29

Chain AB: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain BB: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain CB: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain DB: 94% 6%



- Molecule 1: 29 kDa antigen, Cfp29

Chain EB: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain FB: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain GB: 95% 5%



- Molecule 1: 29 kDa antigen, Cfp29

Chain HB: 94% 6%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	57805	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	163000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.37	0/2074	0.57	0/2828
1	AA	0.37	0/2074	0.57	0/2828
1	AB	0.37	0/2074	0.57	0/2828
1	B	0.37	0/2074	0.57	0/2828
1	BA	0.37	0/2074	0.57	0/2828
1	BB	0.37	0/2074	0.57	0/2828
1	C	0.37	0/2074	0.57	0/2828
1	CA	0.37	0/2074	0.57	0/2828
1	CB	0.37	0/2074	0.56	0/2828
1	D	0.37	0/2074	0.57	0/2828
1	DA	0.37	0/2074	0.57	0/2828
1	DB	0.37	0/2074	0.57	0/2828
1	E	0.37	0/2074	0.57	0/2828
1	EA	0.37	0/2074	0.57	0/2828
1	EB	0.37	0/2074	0.57	0/2828
1	F	0.37	0/2074	0.57	0/2828
1	FA	0.37	0/2074	0.57	0/2828
1	FB	0.37	0/2074	0.57	0/2828
1	G	0.37	0/2074	0.57	0/2828
1	GA	0.37	0/2074	0.57	0/2828
1	GB	0.37	0/2074	0.57	0/2828
1	H	0.37	0/2074	0.57	0/2828
1	HA	0.37	0/2074	0.57	0/2828
1	HB	0.37	0/2074	0.57	0/2828
1	I	0.37	0/2074	0.57	0/2828
1	IA	0.37	0/2074	0.57	0/2828
1	J	0.37	0/2074	0.57	0/2828
1	JA	0.37	0/2074	0.57	0/2828
1	K	0.37	0/2074	0.57	0/2828
1	KA	0.37	0/2074	0.57	0/2828
1	L	0.37	0/2074	0.57	0/2828
1	LA	0.37	0/2074	0.57	0/2828
1	M	0.37	0/2074	0.57	0/2828
1	MA	0.37	0/2074	0.57	0/2828

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	N	0.37	0/2074	0.57	0/2828
1	NA	0.37	0/2074	0.57	0/2828
1	O	0.37	0/2074	0.57	0/2828
1	OA	0.37	0/2074	0.57	0/2828
1	P	0.37	0/2074	0.57	0/2828
1	PA	0.37	0/2074	0.57	0/2828
1	Q	0.37	0/2074	0.57	0/2828
1	QA	0.37	0/2074	0.57	0/2828
1	R	0.37	0/2074	0.57	0/2828
1	RA	0.37	0/2074	0.57	0/2828
1	S	0.37	0/2074	0.57	0/2828
1	SA	0.37	0/2074	0.57	0/2828
1	T	0.37	0/2074	0.57	0/2828
1	TA	0.37	0/2074	0.57	0/2828
1	U	0.37	0/2074	0.57	0/2828
1	UA	0.37	0/2074	0.57	0/2828
1	V	0.37	0/2074	0.57	0/2828
1	VA	0.37	0/2074	0.57	0/2828
1	W	0.37	0/2074	0.57	0/2828
1	WA	0.37	0/2074	0.57	0/2828
1	X	0.37	0/2074	0.57	0/2828
1	XA	0.37	0/2074	0.57	0/2828
1	Y	0.37	0/2074	0.57	0/2828
1	YA	0.37	0/2074	0.57	0/2828
1	Z	0.37	0/2074	0.57	0/2828
1	ZA	0.37	0/2074	0.57	0/2828
All	All	0.37	0/124440	0.57	0/169680

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	2034	0	2013	9	0
1	AA	2034	0	2013	10	0
1	AB	2034	0	2013	9	0
1	B	2034	0	2013	10	0
1	BA	2034	0	2013	9	0
1	BB	2034	0	2013	9	0
1	C	2034	0	2013	9	0
1	CA	2034	0	2013	9	0
1	CB	2034	0	2013	9	0
1	D	2034	0	2013	10	0
1	DA	2034	0	2013	9	0
1	DB	2034	0	2013	11	0
1	E	2034	0	2013	8	0
1	EA	2034	0	2013	9	0
1	EB	2034	0	2013	8	0
1	F	2034	0	2013	8	0
1	FA	2034	0	2013	9	0
1	FB	2034	0	2013	9	0
1	G	2034	0	2013	10	0
1	GA	2034	0	2013	11	0
1	GB	2034	0	2013	8	0
1	H	2034	0	2013	9	0
1	HA	2034	0	2013	8	0
1	HB	2034	0	2013	10	0
1	I	2034	0	2013	11	0
1	IA	2034	0	2013	8	0
1	J	2034	0	2013	9	0
1	JA	2034	0	2013	9	0
1	K	2034	0	2013	8	0
1	KA	2034	0	2013	9	0
1	L	2034	0	2013	10	0
1	LA	2034	0	2013	10	0
1	M	2034	0	2013	8	0
1	MA	2034	0	2013	8	0
1	N	2034	0	2013	10	0
1	NA	2034	0	2013	8	0
1	O	2034	0	2013	9	0
1	OA	2034	0	2013	9	0
1	P	2034	0	2013	9	0
1	PA	2034	0	2013	10	0
1	Q	2034	0	2013	10	0
1	QA	2034	0	2013	9	0
1	R	2034	0	2013	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	RA	2034	0	2013	10	0
1	S	2034	0	2013	10	0
1	SA	2034	0	2013	9	0
1	T	2034	0	2013	8	0
1	TA	2034	0	2013	10	0
1	U	2034	0	2013	9	0
1	UA	2034	0	2013	9	0
1	V	2034	0	2013	11	0
1	VA	2034	0	2013	9	0
1	W	2034	0	2013	9	0
1	WA	2034	0	2013	8	0
1	X	2034	0	2013	9	0
1	XA	2034	0	2013	10	0
1	Y	2034	0	2013	9	0
1	YA	2034	0	2013	9	0
1	Z	2034	0	2013	9	0
1	ZA	2034	0	2013	10	0
All	All	122040	0	120780	371	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.

The worst 5 of 371 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:F:189:TYR:CE1	1:HA:197:ARG:HD3	2.48	0.49
1:K:189:TYR:CE1	1:MA:197:ARG:HD3	2.48	0.49
1:N:189:TYR:CE1	1:DA:197:ARG:HD3	2.48	0.49
1:EA:197:ARG:HD3	1:VA:189:TYR:CE1	2.48	0.49
1:IA:189:TYR:CE1	1:KA:197:ARG:HD3	2.48	0.49

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	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	AA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	AB	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	B	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	BA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	BB	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	C	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	CA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	CB	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	D	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	DA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	DB	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	E	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	EA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	EB	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	F	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	FA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	FB	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	G	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	GA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	GB	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	H	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	HA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	HB	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	I	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	IA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	J	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	JA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	K	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	KA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	LA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	M	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	MA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	N	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	NA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	O	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	OA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	P	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	PA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	Q	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	QA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	R	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	RA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	S	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	SA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	T	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	TA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	U	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	UA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	V	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	VA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	W	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	WA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	X	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	XA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	Y	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	YA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	Z	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
1	ZA	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
All	All	15780/15900 (99%)	15540 (98%)	240 (2%)	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	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	AA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	AB	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	B	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	BA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	BB	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	C	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	CA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	CB	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	D	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	DA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	DB	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	E	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	EA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	EB	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	F	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	FA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	FB	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	G	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	GA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	GB	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	H	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	HA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	HB	218/218 (100%)	216 (99%)	2 (1%)	75	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	IA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	J	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	JA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	K	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	KA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	L	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	LA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	M	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	MA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	N	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	NA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	O	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	OA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	P	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	PA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	Q	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	QA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	R	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	RA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	S	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	SA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	T	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	TA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	U	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	UA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	V	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	VA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	W	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	WA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	X	218/218 (100%)	216 (99%)	2 (1%)	75	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	XA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	Y	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	YA	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	Z	218/218 (100%)	216 (99%)	2 (1%)	75	87
1	ZA	218/218 (100%)	216 (99%)	2 (1%)	75	87
All	All	13080/13080 (100%)	12960 (99%)	120 (1%)	74	87

5 of 120 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	CA	58	VAL
1	DB	54	ARG
1	JA	58	VAL
1	CB	58	VAL
1	HB	54	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 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 oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

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.