



wwPDB EM Validation Summary Report ⓘ

Nov 22, 2022 – 02:57 AM EST

PDB ID : 7U96
EMDB ID : EMD-26392
Title : SAAV pH 5.5 capsid structure
Authors : Mietzsch, M.; McKenna, R.
Deposited on : 2022-03-10
Resolution : 2.14 Å(reported)

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

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

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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

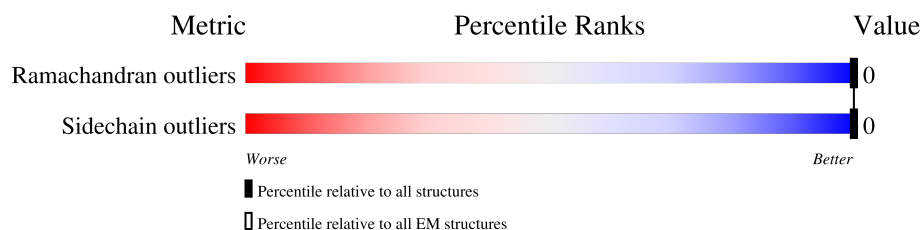
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY




The reported resolution of this entry is 2.14 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.


















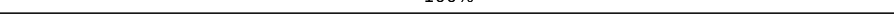
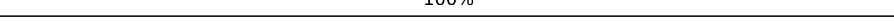
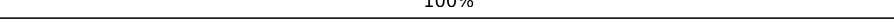
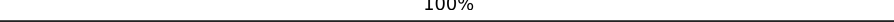
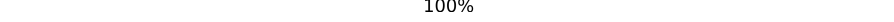
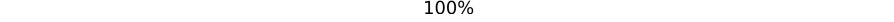
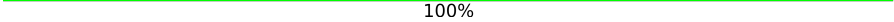
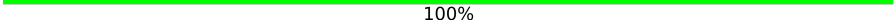

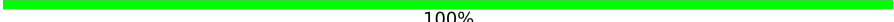
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 ≥ 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	1	513	 100%
1	2	513	 100%
1	3	513	 100%
1	4	513	 100%
1	5	513	 100%
1	6	513	 100%
1	7	513	 100%
1	8	513	 100%
1	A	513	 100%
1	B	513	 100%
















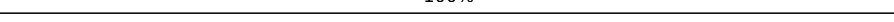
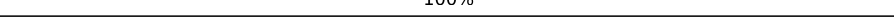
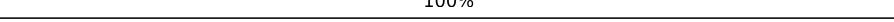
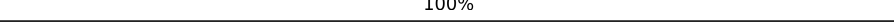
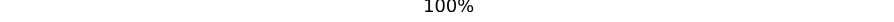
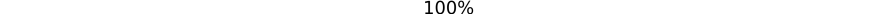
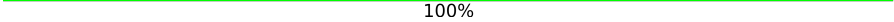
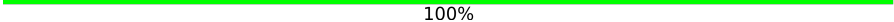

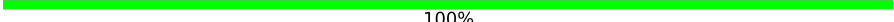
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Mol	Chain	Length	Quality of chain
1	C	513	 100%
1	D	513	 100%
1	E	513	 100%
1	F	513	 100%
1	G	513	 100%
1	H	513	 100%
1	I	513	 100%
1	J	513	 100%
1	K	513	 100%
1	L	513	 100%
1	M	513	 100%
1	N	513	 100%
1	O	513	 100%
1	P	513	 100%
1	Q	513	 100%
1	R	513	 100%
1	S	513	 100%
1	T	513	 100%
1	U	513	 100%
1	V	513	 100%
1	W	513	 100%
1	X	513	 100%
1	Y	513	 100%
1	Z	513	 100%
1	a	513	 100%

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Mol	Chain	Length	Quality of chain
1	b	513	 100%
1	c	513	 100%
1	d	513	 100%
1	e	513	 100%
1	f	513	 100%
1	g	513	 100%
1	h	513	 100%
1	i	513	 100%
1	j	513	 100%
1	k	513	 100%
1	l	513	 100%
1	m	513	 100%
1	n	513	 100%
1	o	513	 100%
1	p	513	 100%
1	q	513	 100%
1	r	513	 100%
1	s	513	 100%
1	t	513	 100%
1	u	513	 100%
1	v	513	 100%
1	w	513	 100%
1	x	513	 100%
1	y	513	 100%
1	z	513	 100%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 242520 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 Capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	B	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	C	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	D	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	E	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	F	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	G	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	H	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	I	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	J	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	K	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	L	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	M	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	N	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	O	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	P	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		
1	Q	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	S	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	T	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	U	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	V	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	W	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	X	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	Y	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	Z	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	a	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	b	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	c	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	d	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	e	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	f	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	g	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	h	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	i	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	j	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	k	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	l	513	Total 4042	C 2561	N 692	O 774	S 15	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	n	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	o	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	p	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	q	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	r	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	s	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	t	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	u	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	v	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	w	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	x	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	y	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	z	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	1	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	2	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	3	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	4	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	5	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	6	513	Total 4042	C 2561	N 692	O 774	S 15	0	0
1	7	513	Total 4042	C 2561	N 692	O 774	S 15	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	513	Total	C	N	O	S	0	0
			4042	2561	692	774	15		

3 Residue-property plots

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: Capsid protein

Chain A:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain B:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain C:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain D:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain E:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain F:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain G:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain H:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain I:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain J:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain K:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain L:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain M:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain N:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain O:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain P:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain Q:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain R:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain S:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain T:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain U:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain V:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain W:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain X:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain Y:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain Z:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain a:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain b:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain c:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain d:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain e:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain f:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain g:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain h:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain i:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain j:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain k:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain l:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain m:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain n:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain o:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain p:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain q:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain r:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain s:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain t:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain u:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain v:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain w:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain x:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain y:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain z:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain 1:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain 2:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain 3:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain 4:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain 5:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain 6:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain 7:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Capsid protein

Chain 8:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	402005	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 ($e^-/\text{\AA}^2$)	34	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	Not provided	
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	1	0.42	0/4167	0.53	0/5686
1	2	0.42	0/4167	0.53	0/5686
1	3	0.42	0/4167	0.53	0/5686
1	4	0.42	0/4167	0.53	0/5686
1	5	0.42	0/4167	0.53	0/5686
1	6	0.42	0/4167	0.53	0/5686
1	7	0.42	0/4167	0.53	0/5686
1	8	0.42	0/4167	0.53	0/5686
1	A	0.42	0/4167	0.53	0/5686
1	B	0.42	0/4167	0.53	0/5686
1	C	0.42	0/4167	0.53	0/5686
1	D	0.42	0/4167	0.53	0/5686
1	E	0.42	0/4167	0.53	0/5686
1	F	0.42	0/4167	0.53	0/5686
1	G	0.42	0/4167	0.53	0/5686
1	H	0.42	0/4167	0.53	0/5686
1	I	0.42	0/4167	0.53	0/5686
1	J	0.42	0/4167	0.53	0/5686
1	K	0.42	0/4167	0.53	0/5686
1	L	0.42	0/4167	0.53	0/5686
1	M	0.42	0/4167	0.53	0/5686
1	N	0.42	0/4167	0.53	0/5686
1	O	0.42	0/4167	0.53	0/5686
1	P	0.42	0/4167	0.53	0/5686
1	Q	0.42	0/4167	0.53	0/5686
1	R	0.42	0/4167	0.53	0/5686
1	S	0.42	0/4167	0.53	0/5686
1	T	0.42	0/4167	0.53	0/5686
1	U	0.42	0/4167	0.53	0/5686
1	V	0.42	0/4167	0.53	0/5686
1	W	0.42	0/4167	0.53	0/5686
1	X	0.42	0/4167	0.53	0/5686
1	Y	0.42	0/4167	0.53	0/5686
1	Z	0.42	0/4167	0.53	0/5686

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.42	0/4167	0.53	0/5686
1	b	0.42	0/4167	0.53	0/5686
1	c	0.42	0/4167	0.53	0/5686
1	d	0.42	0/4167	0.53	0/5686
1	e	0.42	0/4167	0.53	0/5686
1	f	0.42	0/4167	0.53	0/5686
1	g	0.42	0/4167	0.53	0/5686
1	h	0.42	0/4167	0.53	0/5686
1	i	0.42	0/4167	0.53	0/5686
1	j	0.42	0/4167	0.53	0/5686
1	k	0.42	0/4167	0.53	0/5686
1	l	0.42	0/4167	0.53	0/5686
1	m	0.42	0/4167	0.53	0/5686
1	n	0.42	0/4167	0.53	0/5686
1	o	0.42	0/4167	0.53	0/5686
1	p	0.42	0/4167	0.53	0/5686
1	q	0.42	0/4167	0.53	0/5686
1	r	0.42	0/4167	0.53	0/5686
1	s	0.42	0/4167	0.53	0/5686
1	t	0.42	0/4167	0.53	0/5686
1	u	0.42	0/4167	0.53	0/5686
1	v	0.42	0/4167	0.53	0/5686
1	w	0.42	0/4167	0.53	0/5686
1	x	0.42	0/4167	0.53	0/5686
1	y	0.42	0/4167	0.53	0/5686
1	z	0.42	0/4167	0.53	0/5686
All	All	0.42	0/250020	0.53	0/341160

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 [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles

5.3.1 Protein backbone

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	1	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	2	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	3	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	4	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	5	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	6	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	7	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	8	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	A	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	B	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	C	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	D	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	E	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	F	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	G	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	H	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	I	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	J	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	K	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	L	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	M	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	N	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	O	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	P	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	Q	511/513 (100%)	503 (98%)	8 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	S	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	T	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	U	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	V	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	W	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	X	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	Y	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	Z	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	a	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	b	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	c	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	d	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	e	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	f	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	g	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	h	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	i	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	j	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	k	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	l	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	m	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	n	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	o	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	p	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	q	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	r	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	s	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	t	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	u	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	v	511/513 (100%)	503 (98%)	8 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	w	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	x	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	y	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
1	z	511/513 (100%)	503 (98%)	8 (2%)	0	100	100
All	All	30660/30780 (100%)	30180 (98%)	480 (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	1	439/439 (100%)	439 (100%)	0	100	100
1	2	439/439 (100%)	439 (100%)	0	100	100
1	3	439/439 (100%)	439 (100%)	0	100	100
1	4	439/439 (100%)	439 (100%)	0	100	100
1	5	439/439 (100%)	439 (100%)	0	100	100
1	6	439/439 (100%)	439 (100%)	0	100	100
1	7	439/439 (100%)	439 (100%)	0	100	100
1	8	439/439 (100%)	439 (100%)	0	100	100
1	A	439/439 (100%)	439 (100%)	0	100	100
1	B	439/439 (100%)	439 (100%)	0	100	100
1	C	439/439 (100%)	439 (100%)	0	100	100
1	D	439/439 (100%)	439 (100%)	0	100	100
1	E	439/439 (100%)	439 (100%)	0	100	100
1	F	439/439 (100%)	439 (100%)	0	100	100
1	G	439/439 (100%)	439 (100%)	0	100	100
1	H	439/439 (100%)	439 (100%)	0	100	100
1	I	439/439 (100%)	439 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	439/439 (100%)	439 (100%)	0	100	100
1	K	439/439 (100%)	439 (100%)	0	100	100
1	L	439/439 (100%)	439 (100%)	0	100	100
1	M	439/439 (100%)	439 (100%)	0	100	100
1	N	439/439 (100%)	439 (100%)	0	100	100
1	O	439/439 (100%)	439 (100%)	0	100	100
1	P	439/439 (100%)	439 (100%)	0	100	100
1	Q	439/439 (100%)	439 (100%)	0	100	100
1	R	439/439 (100%)	439 (100%)	0	100	100
1	S	439/439 (100%)	439 (100%)	0	100	100
1	T	439/439 (100%)	439 (100%)	0	100	100
1	U	439/439 (100%)	439 (100%)	0	100	100
1	V	439/439 (100%)	439 (100%)	0	100	100
1	W	439/439 (100%)	439 (100%)	0	100	100
1	X	439/439 (100%)	439 (100%)	0	100	100
1	Y	439/439 (100%)	439 (100%)	0	100	100
1	Z	439/439 (100%)	439 (100%)	0	100	100
1	a	439/439 (100%)	439 (100%)	0	100	100
1	b	439/439 (100%)	439 (100%)	0	100	100
1	c	439/439 (100%)	439 (100%)	0	100	100
1	d	439/439 (100%)	439 (100%)	0	100	100
1	e	439/439 (100%)	439 (100%)	0	100	100
1	f	439/439 (100%)	439 (100%)	0	100	100
1	g	439/439 (100%)	439 (100%)	0	100	100
1	h	439/439 (100%)	439 (100%)	0	100	100
1	i	439/439 (100%)	439 (100%)	0	100	100
1	j	439/439 (100%)	439 (100%)	0	100	100
1	k	439/439 (100%)	439 (100%)	0	100	100
1	l	439/439 (100%)	439 (100%)	0	100	100
1	m	439/439 (100%)	439 (100%)	0	100	100
1	n	439/439 (100%)	439 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	o	439/439 (100%)	439 (100%)	0	100	100
1	p	439/439 (100%)	439 (100%)	0	100	100
1	q	439/439 (100%)	439 (100%)	0	100	100
1	r	439/439 (100%)	439 (100%)	0	100	100
1	s	439/439 (100%)	439 (100%)	0	100	100
1	t	439/439 (100%)	439 (100%)	0	100	100
1	u	439/439 (100%)	439 (100%)	0	100	100
1	v	439/439 (100%)	439 (100%)	0	100	100
1	w	439/439 (100%)	439 (100%)	0	100	100
1	x	439/439 (100%)	439 (100%)	0	100	100
1	y	439/439 (100%)	439 (100%)	0	100	100
1	z	439/439 (100%)	439 (100%)	0	100	100
All	All	26340/26340 (100%)	26340 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1155 such sidechains are listed below:

Mol	Chain	Res	Type
1	w	278	HIS
1	8	520	GLN
1	x	497	GLN
1	w	249	ASN
1	3	226	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-26392. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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 surface views

This section was not generated.

6.5 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.