



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 03:40 PM UTC

PDB ID : 9NCK / pdb_00009nck
EMDB ID : EMD-49259
Title : Nanotube of computationally designed peptide assembly R3K (16 protofilament)
Authors : Das, A.; Conticello, V.
Deposited on : 2025-02-16
Resolution : 3.58 Å(reported)

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

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

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 : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

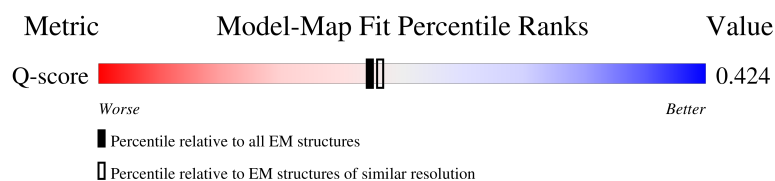
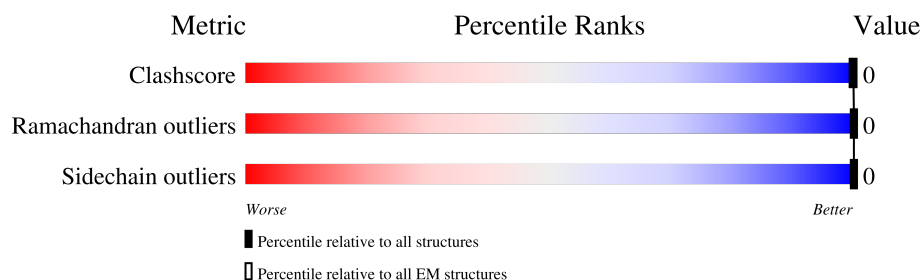
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.58 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



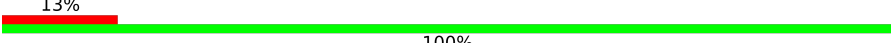
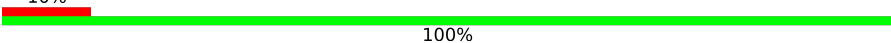
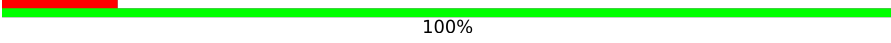
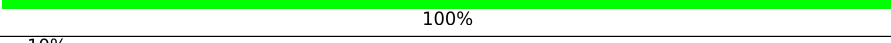
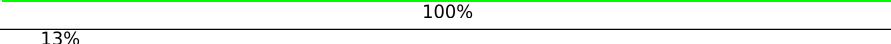
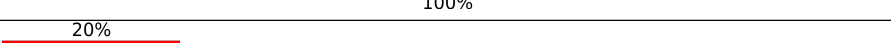
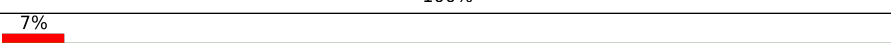

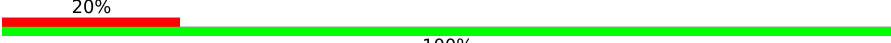
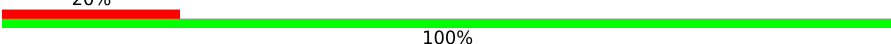
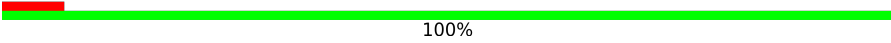
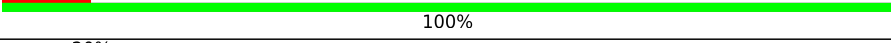
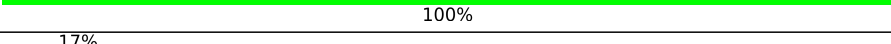
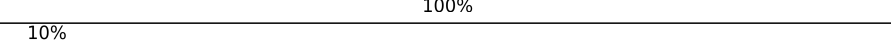
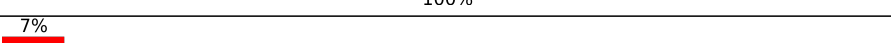


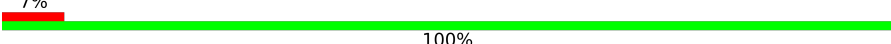
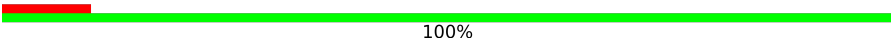
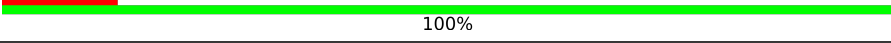
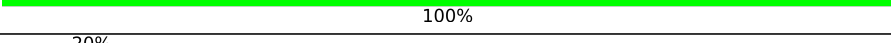
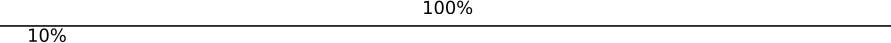
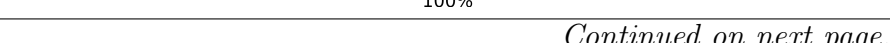


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12629 (3.08 - 4.08)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	30	<div> <div>20%</div> <div>100%</div> </div>
1	0A	30	<div> <div>7%</div> <div>100%</div> </div>
1	1	30	<div> <div>10%</div> <div>100%</div> </div>
1	1A	30	<div> <div>20%</div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
1	2	30	13% 
1	2A	30	10% 
1	3	30	13% 
1	3A	30	13% 
1	4	30	10% 
1	4A	30	13% 
1	5	30	20% 
1	5A	30	7% 
1	6	30	7% 
1	6A	30	20% 
1	7	30	20% 
1	7A	30	7% 
1	8	30	10% 
1	8A	30	20% 
1	9	30	17% 
1	9A	30	10% 
1	A	30	7% 
1	AA	30	13% 
1	AB	30	13% 
1	B	30	7% 
1	BA	30	10% 
1	BB	30	13% 
1	C	30	7% 
1	CA	30	20% 
1	CB	30	10% 

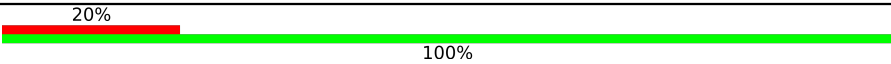
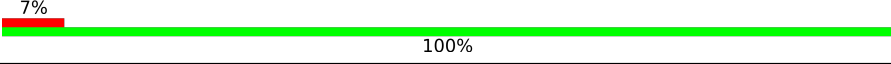
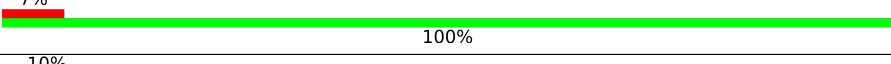
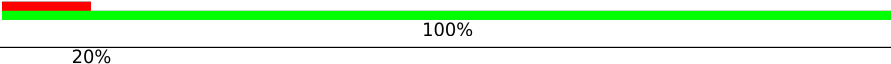
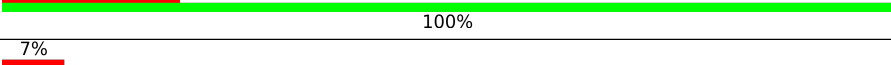
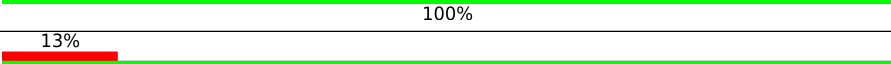
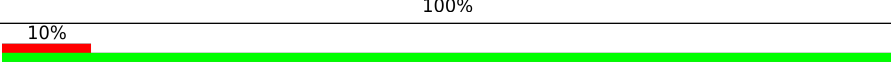
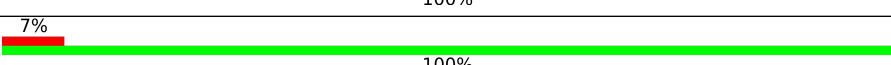
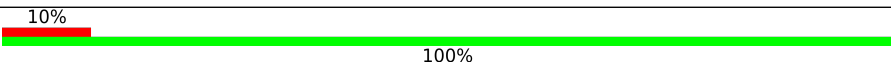
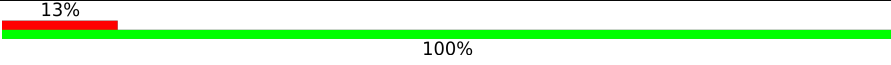
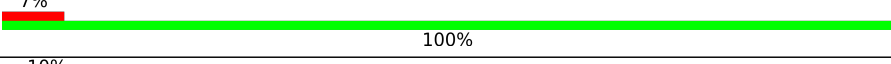
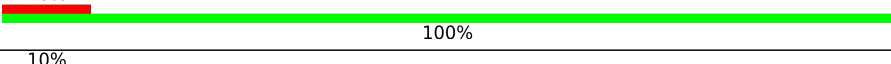
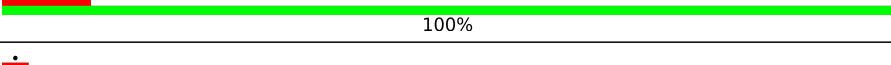
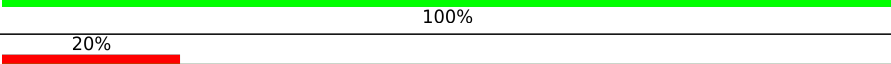
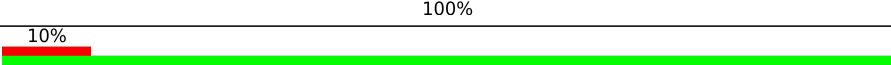
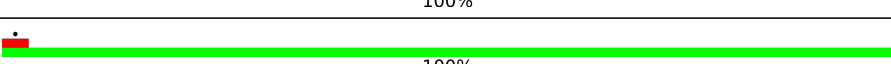
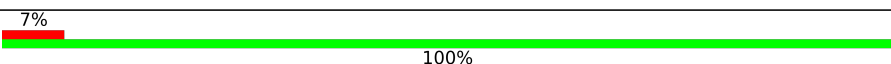
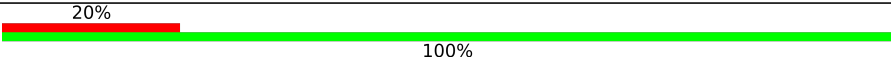
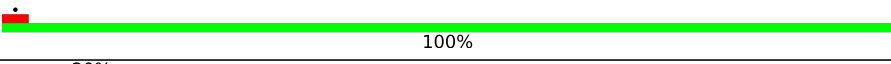
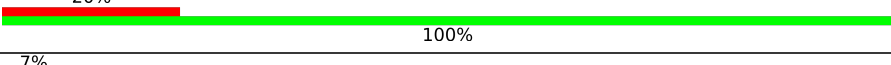
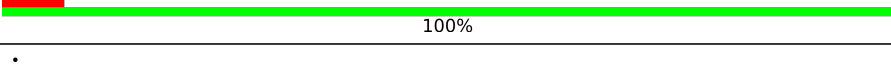
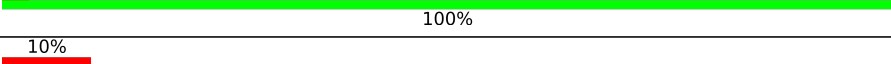
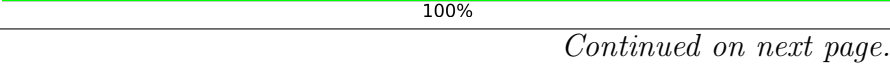


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Mol	Chain	Length	Quality of chain
1	D	30	7% 100%
1	DA	30	7% 100%
1	DB	30	20% 100%
1	E	30	7% 100%
1	EA	30	20% 100%
1	EB	30	7% 100%
1	F	30	7% 100%
1	FA	30	10% 100%
1	FB	30	20% 100%
1	G	30	7% 100%
1	GA	30	13% 100%
1	GB	30	10% 100%
1	H	30	7% 100%
1	HA	30	17% 100%
1	HB	30	13% 100%
1	I	30	7% 100%
1	IA	30	10% 100%
1	IB	30	10% 100%
1	J	30	7% 100%
1	JA	30	20% 100%
1	JB	30	7% 100%
1	K	30	7% 100%
1	KA	30	10% 100%
1	KB	30	20% 100%
1	L	30	7% 100%

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Mol	Chain	Length	Quality of chain
1	LA	30	
1	LB	30	
1	M	30	
1	MA	30	
1	MB	30	
1	N	30	
1	NA	30	
1	NB	30	
1	O	30	
1	OA	30	
1	OB	30	
1	P	30	
1	PA	30	
1	PB	30	
1	Q	30	
1	QA	30	
1	QB	30	
1	R	30	
1	RA	30	
1	RB	30	
1	S	30	
1	SA	30	
1	SB	30	
1	T	30	
1	TA	30	

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Mol	Chain	Length	Quality of chain
1	TB	30	20% 100%
1	U	30	13% 100%
1	UA	30	13% 100%
1	UB	30	10% 100%
1	V	30	7% 100%
1	VA	30	17% 100%
1	VB	30	13% 100%
1	W	30	20% 100%
1	WA	30	10% 100%
1	WB	30	13% 100%
1	X	30	10% 100%
1	XA	30	20% 100%
1	XB	30	10% 100%
1	Y	30	20% 100%
1	YA	30	10% 100%
1	YB	30	20% 100%
1	Z	30	10% 100%
1	ZA	30	20% 100%
1	ZB	30	7% 100%
1	a	30	13% 100%
1	aA	30	10% 100%
1	aB	30	20% 100%
1	b	30	17% 100%
1	bA	30	13% 100%
1	bB	30	10% 100%

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Mol	Chain	Length	Quality of chain
1	c	30	<div> <div>10%</div> <div>100%</div> </div>
1	cA	30	<div> <div>17%</div> <div>100%</div> </div>
1	cB	30	<div> <div>17%</div> <div>100%</div> </div>
1	d	30	<div> <div>20%</div> <div>100%</div> </div>
1	dA	30	<div> <div>10%</div> <div>100%</div> </div>
1	dB	30	<div> <div>10%</div> <div>100%</div> </div>
1	e	30	<div> <div>10%</div> <div>100%</div> </div>
1	eA	30	<div> <div>20%</div> <div>100%</div> </div>
1	eB	30	<div> <div>10%</div> <div>100%</div> </div>
1	f	30	<div> <div>20%</div> <div>100%</div> </div>
1	fA	30	<div> <div>7%</div> <div>100%</div> </div>
1	fB	30	<div> <div>20%</div> <div>100%</div> </div>
1	g	30	<div> <div>10%</div> <div>100%</div> </div>
1	gA	30	<div> <div>20%</div> <div>100%</div> </div>
1	gB	30	<div> <div>7%</div> <div>100%</div> </div>
1	h	30	<div> <div>13%</div> <div>100%</div> </div>
1	hA	30	<div> <div>10%</div> <div>100%</div> </div>
1	hB	30	<div> <div>20%</div> <div>100%</div> </div>
1	i	30	<div> <div>10%</div> <div>100%</div> </div>
1	iA	30	<div> <div>13%</div> <div>100%</div> </div>
1	iB	30	<div> <div>10%</div> <div>100%</div> </div>
1	j	30	<div> <div>10%</div> <div>100%</div> </div>
1	jA	30	<div> <div>13%</div> <div>100%</div> </div>
1	jB	30	<div> <div>13%</div> <div>100%</div> </div>
1	k	30	<div> <div>20%</div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
1	kA	30	<div> <div>10%</div> <div>100%</div> </div>
1	l	30	<div> <div>7%</div> <div>100%</div> </div>
1	lA	30	<div> <div>20%</div> <div>100%</div> </div>
1	m	30	<div> <div>20%</div> <div>100%</div> </div>
1	mA	30	<div> <div>10%</div> <div>100%</div> </div>
1	n	30	<div> <div>7%</div> <div>100%</div> </div>
1	nA	30	<div> <div>20%</div> <div>100%</div> </div>
1	o	30	<div> <div>17%</div> <div>100%</div> </div>
1	oA	30	<div> <div>10%</div> <div>100%</div> </div>
1	p	30	<div> <div>17%</div> <div>100%</div> </div>
1	pA	30	<div> <div>13%</div> <div>100%</div> </div>
1	q	30	<div> <div>7%</div> <div>100%</div> </div>
1	qA	30	<div> <div>17%</div> <div>100%</div> </div>
1	r	30	<div> <div>20%</div> <div>100%</div> </div>
1	rA	30	<div> <div>10%</div> <div>100%</div> </div>
1	s	30	<div> <div>7%</div> <div>100%</div> </div>
1	sA	30	<div> <div>20%</div> <div>100%</div> </div>
1	t	30	<div> <div>20%</div> <div>100%</div> </div>
1	tA	30	<div> <div>7%</div> <div>100%</div> </div>
1	u	30	<div> <div>7%</div> <div>100%</div> </div>
1	uA	30	<div> <div>20%</div> <div>100%</div> </div>
1	v	30	<div> <div>13%</div> <div>100%</div> </div>
1	vA	30	<div> <div>10%</div> <div>100%</div> </div>
1	w	30	<div> <div>13%</div> <div>100%</div> </div>
1	wA	30	<div> <div>13%</div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
1	x	30	<div><div>10%</div><div></div><div>100%</div></div>
1	xA	30	<div><div>13%</div><div></div><div>100%</div></div>
1	y	30	<div><div>20%</div><div></div><div>100%</div></div>
1	yA	30	<div><div>10%</div><div></div><div>100%</div></div>
1	z	30	<div><div>10%</div><div></div><div>100%</div></div>
1	zA	30	<div><div>20%</div><div></div><div>100%</div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 34880 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 Bundlemer nanotube.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	U	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	V	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	W	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	X	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	Y	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	Z	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	a	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	B	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	b	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	c	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	d	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	e	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	f	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	g	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	h	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	C	30	Total	C	N	O	S	0	1
			218	136	38	41	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	i	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	j	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	k	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	l	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	m	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	n	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	o	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	D	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	p	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	q	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	r	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	s	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	t	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	u	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	v	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	E	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	w	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	x	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	y	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	z	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	0	30	Total	C	N	O	S	0	1
			218	136	38	41	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	2	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	F	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	3	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	4	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	5	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	6	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	7	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	8	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	9	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	G	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	AA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	BA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	CA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	DA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	EA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	FA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	GA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	H	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	HA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	IA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	JA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	KA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	LA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	MA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	NA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	I	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	OA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	PA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	QA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	RA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	SA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	TA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	UA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	J	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	VA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	WA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	XA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	YA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	ZA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	aA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	bA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	K	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	cA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	dA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	eA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	fA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	gA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	hA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	iA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	L	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	jA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	kA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	lA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	mA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	nA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	oA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	pA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	M	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	qA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	rA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	sA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	tA	30	Total	C	N	O	S	0	1
			218	136	38	41	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	uA	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	vA	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	wA	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	N	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	xA	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	yA	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	zA	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	0A	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	1A	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	2A	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	3A	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	O	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	4A	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	5A	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	6A	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	7A	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	8A	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	9A	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	AB	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	P	30	Total 218	C 136	N 38	O 41	S 3	0	1
1	BB	30	Total 218	C 136	N 38	O 41	S 3	0	1

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	DB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	EB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	FB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	GB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	HB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	Q	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	IB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	JB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	KB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	LB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	MB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	NB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	OB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	R	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	PB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	QB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	RB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	SB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	TB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	UB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		

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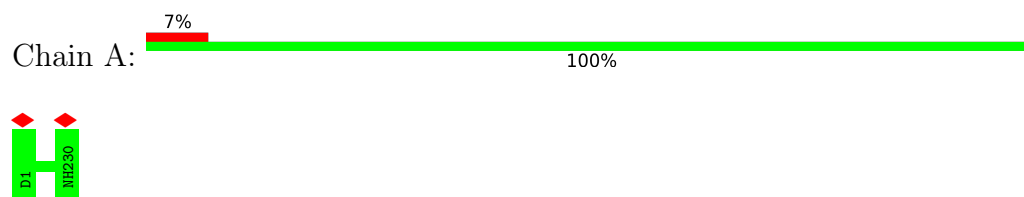
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Mol	Chain	Residues	Atoms					AltConf	Trace
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			218	136	38	41	3		
1	S	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	WB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	XB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	YB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	ZB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	aB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	bB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	cB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	T	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	dB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	eB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	fB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	gB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	hB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	iB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		
1	jB	30	Total	C	N	O	S	0	1
			218	136	38	41	3		

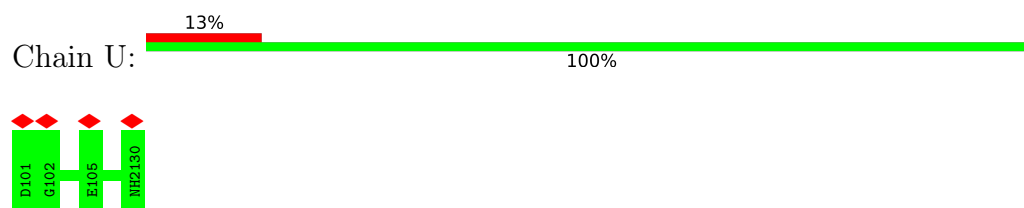
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

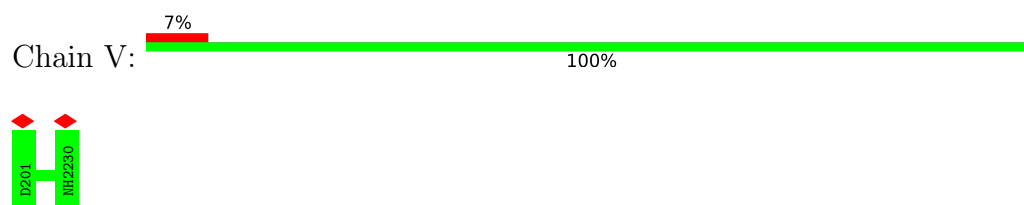
- Molecule 1: Bundlemer nanotube



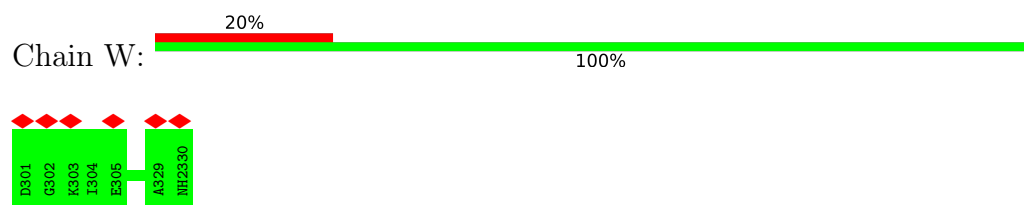
- Molecule 1: Bundlemer nanotube



- Molecule 1: Bundlemer nanotube

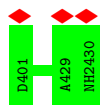


- Molecule 1: Bundlemer nanotube

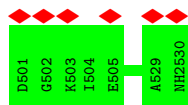


- Molecule 1: Bundlemer nanotube

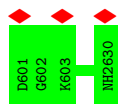




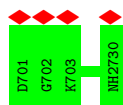
- Molecule 1: Bundlemer nanotube



- Molecule 1: Bundlemer nanotube



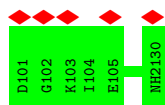
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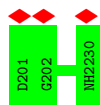
- Molecule 1: Bundlemer nanotube



- Molecule 1: Bundlemer nanotube

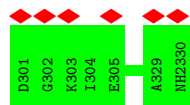


- Molecule 1: Bundlemer nanotube



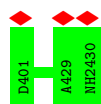
- Molecule 1: Bundlemer nanotube

Chain d:  20% 100%



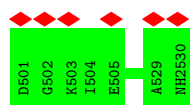
- Molecule 1: Bundlemer nanotube

Chain e:  10% 100%



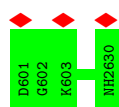
- Molecule 1: Bundlemer nanotube

Chain f:  20% 100%



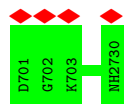
- Molecule 1: Bundlemer nanotube

Chain g:  10% 100%



- Molecule 1: Bundlemer nanotube

Chain h:  13% 100%



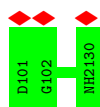
- Molecule 1: Bundlemer nanotube

Chain C:  7% 100%

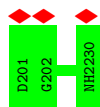


- Molecule 1: Bundlemer nanotube

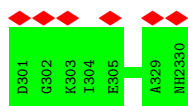
Chain i:  10% 100%



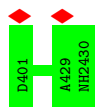
- Molecule 1: Bundlemer nanotube



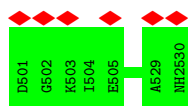
- Molecule 1: Bundlemer nanotube



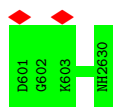
- Molecule 1: Bundlemer nanotube



- Molecule 1: Bundlemer nanotube

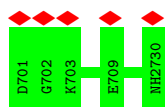


- Molecule 1: Bundlemer nanotube



- Molecule 1: Bundlemer nanotube

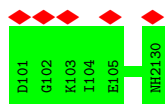




- Molecule 1: Bundlemer nanotube



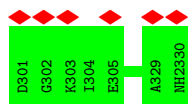
- Molecule 1: Bundlemer nanotube



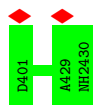
- Molecule 1: Bundlemer nanotube



- Molecule 1: Bundlemer nanotube

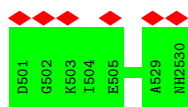


- Molecule 1: Bundlemer nanotube

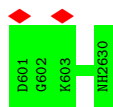


- Molecule 1: Bundlemer nanotube

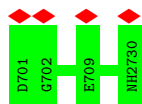




- Molecule 1: Bundlemer nanotube



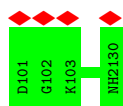
- Molecule 1: Bundlemer nanotube



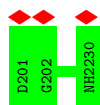
- Molecule 1: Bundlemer nanotube



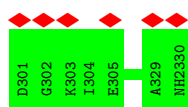
- Molecule 1: Bundlemer nanotube



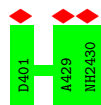
- Molecule 1: Bundlemer nanotube



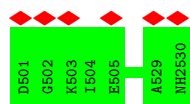
- Molecule 1: Bundlemer nanotube



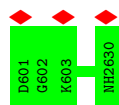
- Molecule 1: Bundlemer nanotube



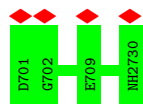
- Molecule 1: Bundlemer nanotube



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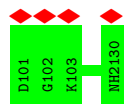
- Molecule 1: Bundlemer nanotube



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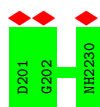


- Molecule 1: Bundlemer nanotube

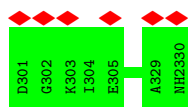


- Molecule 1: Bundlemer nanotube

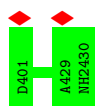




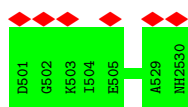
- Molecule 1: Bundlemer nanotube



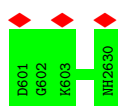
- Molecule 1: Bundlemer nanotube



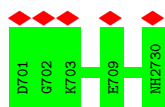
- Molecule 1: Bundlemer nanotube



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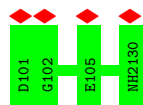


- Molecule 1: Bundlemer nanotube



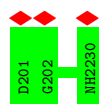
- Molecule 1: Bundlemer nanotube

Chain AA:  13% 100%



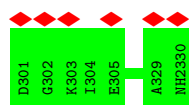
- Molecule 1: Bundlemer nanotube

Chain BA:  10% 100%



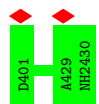
- Molecule 1: Bundlemer nanotube

Chain CA:  20% 100%



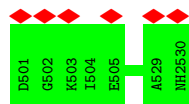
- Molecule 1: Bundlemer nanotube

Chain DA:  7% 100%



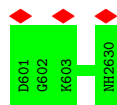
- Molecule 1: Bundlemer nanotube

Chain EA:  20% 100%



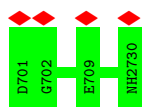
- Molecule 1: Bundlemer nanotube

Chain FA:  10% 100%



- Molecule 1: Bundlemer nanotube

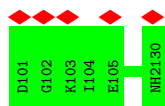
Chain GA:  13% 100%



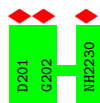
- Molecule 1: Bundlemer nanotube



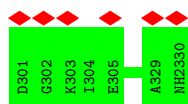
- Molecule 1: Bundlemer nanotube



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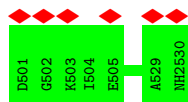
- Molecule 1: Bundlemer nanotube



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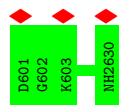


- Molecule 1: Bundlemer nanotube



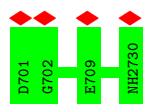
- Molecule 1: Bundlemer nanotube

Chain MA:  100%



- Molecule 1: Bundlemer nanotube

Chain NA:  100%



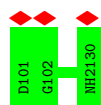
- Molecule 1: Bundlemer nanotube

Chain I:  100%



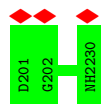
- Molecule 1: Bundlemer nanotube

Chain OA:  100%



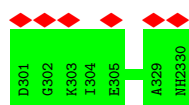
- Molecule 1: Bundlemer nanotube

Chain PA:  100%



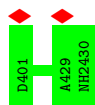
- Molecule 1: Bundlemer nanotube

Chain QA:  100%

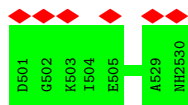


- Molecule 1: Bundlemer nanotube

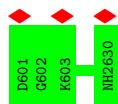
Chain RA:  100%



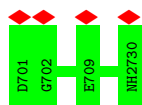
- Molecule 1: Bundlemer nanotube



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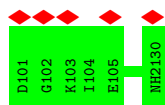
- Molecule 1: Bundlemer nanotube



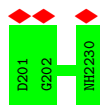
- Molecule 1: Bundlemer nanotube



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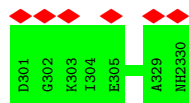


- Molecule 1: Bundlemer nanotube



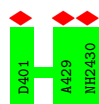
- Molecule 1: Bundlemer nanotube

Chain XA:  20% 100%



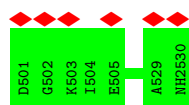
- Molecule 1: Bundlemer nanotube

Chain YA:  10% 100%



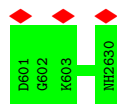
- Molecule 1: Bundlemer nanotube

Chain ZA:  20% 100%



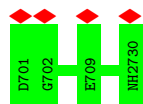
- Molecule 1: Bundlemer nanotube

Chain aA:  10% 100%



- Molecule 1: Bundlemer nanotube

Chain bA:  13% 100%



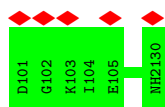
- Molecule 1: Bundlemer nanotube

Chain K:  7% 100%

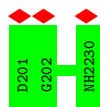


- Molecule 1: Bundlemer nanotube

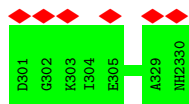
Chain cA:  17% 100%



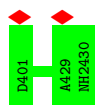
- Molecule 1: Bundlemer nanotube



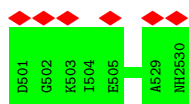
- Molecule 1: Bundlemer nanotube



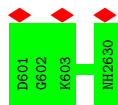
- Molecule 1: Bundlemer nanotube



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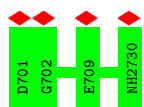


- Molecule 1: Bundlemer nanotube



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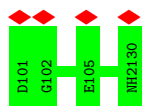




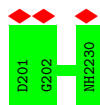
- Molecule 1: Bundlemer nanotube



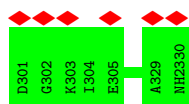
- Molecule 1: Bundlemer nanotube



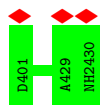
- Molecule 1: Bundlemer nanotube



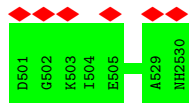
- Molecule 1: Bundlemer nanotube



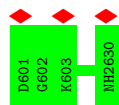
- Molecule 1: Bundlemer nanotube



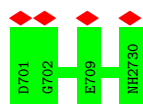
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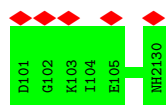
- Molecule 1: Bundlemer nanotube



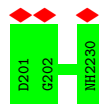
- Molecule 1: Bundlemer nanotube



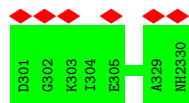
- Molecule 1: Bundlemer nanotube



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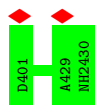


- Molecule 1: Bundlemer nanotube

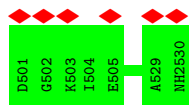


- Molecule 1: Bundlemer nanotube

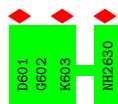




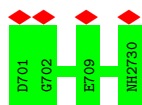
- Molecule 1: Bundlemer nanotube



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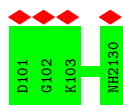
- Molecule 1: Bundlemer nanotube



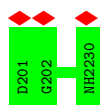
- Molecule 1: Bundlemer nanotube



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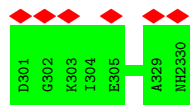


- Molecule 1: Bundlemer nanotube



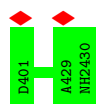
• Molecule 1: Bundlemer nanotube

Chain zA: 



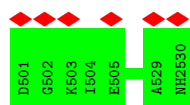
• Molecule 1: Bundlemer nanotube

Chain 0A: 



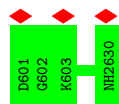
• Molecule 1: Bundlemer nanotube

Chain 1A: 



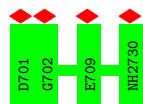
• Molecule 1: Bundlemer nanotube

Chain 2A: 



• Molecule 1: Bundlemer nanotube

Chain 3A: 



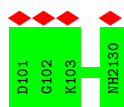
• Molecule 1: Bundlemer nanotube

Chain O: 

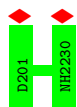


• Molecule 1: Bundlemer nanotube

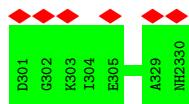
Chain 4A: 



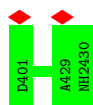
- Molecule 1: Bundlemer nanotube



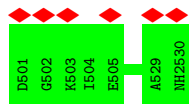
- Molecule 1: Bundlemer nanotube



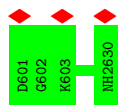
- Molecule 1: Bundlemer nanotube



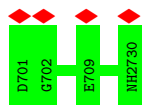
- Molecule 1: Bundlemer nanotube



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- Molecule 1: Bundlemer nanotube



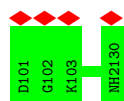
- Molecule 1: Bundlemer nanotube

Chain P:  7% 100%



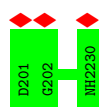
- Molecule 1: Bundlemer nanotube

Chain BB:  13% 100%



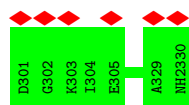
- Molecule 1: Bundlemer nanotube

Chain CB:  10% 100%



- Molecule 1: Bundlemer nanotube

Chain DB:  20% 100%



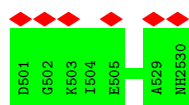
- Molecule 1: Bundlemer nanotube

Chain EB:  7% 100%



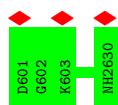
- Molecule 1: Bundlemer nanotube

Chain FB:  20% 100%

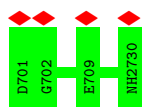


- Molecule 1: Bundlemer nanotube

Chain GB:  10% 100%



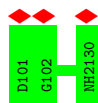
- Molecule 1: Bundlemer nanotube



- Molecule 1: Bundlemer nanotube



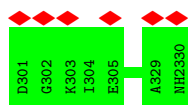
- Molecule 1: Bundlemer nanotube



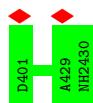
- Molecule 1: Bundlemer nanotube



- Molecule 1: Bundlemer nanotube

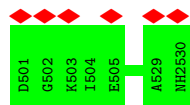


- Molecule 1: Bundlemer nanotube



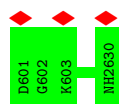
- Molecule 1: Bundlemer nanotube

Chain MB:  20% 100%



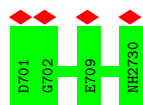
- Molecule 1: Bundlemer nanotube

Chain NB:  10% 100%



- Molecule 1: Bundlemer nanotube

Chain OB:  13% 100%



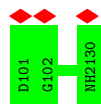
- Molecule 1: Bundlemer nanotube

Chain R:  100%



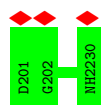
- Molecule 1: Bundlemer nanotube

Chain PB:  10% 100%



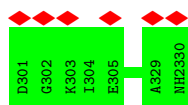
- Molecule 1: Bundlemer nanotube

Chain QB:  10% 100%

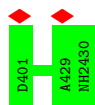


- Molecule 1: Bundlemer nanotube

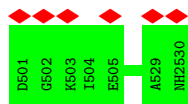
Chain RB:  20% 100%



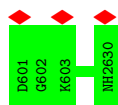
- Molecule 1: Bundlemer nanotube



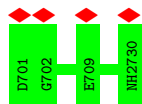
- Molecule 1: Bundlemer nanotube



- Molecule 1: Bundlemer nanotube



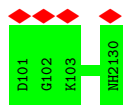
- Molecule 1: Bundlemer nanotube



- Molecule 1: Bundlemer nanotube

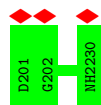


- Molecule 1: Bundlemer nanotube



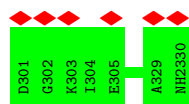
- Molecule 1: Bundlemer nanotube

Chain XB:  10% 100%



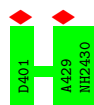
- Molecule 1: Bundlemer nanotube

Chain YB:  20% 100%



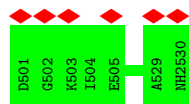
- Molecule 1: Bundlemer nanotube

Chain ZB:  7% 100%



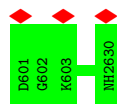
- Molecule 1: Bundlemer nanotube

Chain aB:  20% 100%



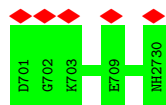
- Molecule 1: Bundlemer nanotube

Chain bB:  10% 100%



- Molecule 1: Bundlemer nanotube

Chain cB:  17% 100%

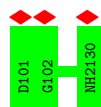


- Molecule 1: Bundlemer nanotube

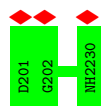
Chain T:  1% 100%



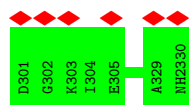
- Molecule 1: Bundlemer nanotube



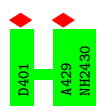
- Molecule 1: Bundlemer nanotube



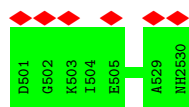
- Molecule 1: Bundlemer nanotube



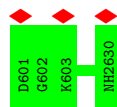
- Molecule 1: Bundlemer nanotube



- Molecule 1: Bundlemer nanotube

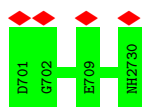


- Molecule 1: Bundlemer nanotube



- Molecule 1: Bundlemer nanotube

Chain jB:  13% 100%



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=22.830°, rise=4.155 Å, axial sym=C1	Depositor
Number of segments used	44140	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 ($e^-/\text{Å}^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	0.241	Depositor
Minimum map value	-0.086	Depositor
Average map value	0.015	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	211.14122, 211.14122, 628.37646	wwPDB
Map dimensions	251, 251, 747	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84120005, 0.84120005, 0.8412001	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NH2

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.68	0/219	1.04	0/290
1	0A	0.67	0/219	1.02	0/290
1	1	0.67	0/219	1.05	0/290
1	1A	0.67	0/219	1.03	0/290
1	2	0.66	0/219	1.07	0/290
1	2A	0.69	0/219	1.04	0/290
1	3	0.67	0/219	1.09	0/290
1	3A	0.66	0/219	1.04	0/290
1	4	0.65	0/219	1.05	0/290
1	4A	0.67	0/219	1.09	0/290
1	5	0.66	0/219	1.04	0/290
1	5A	0.63	0/219	1.03	0/290
1	6	0.66	0/219	1.02	0/290
1	6A	0.66	0/219	1.03	0/290
1	7	0.68	0/219	1.04	0/290
1	7A	0.67	0/219	1.03	0/290
1	8	0.70	0/219	1.07	0/290
1	8A	0.67	0/219	1.02	0/290
1	9	0.65	0/219	1.06	0/290
1	9A	0.69	0/219	1.05	0/290
1	A	0.67	0/219	1.02	0/290
1	AA	0.67	0/219	1.10	0/290
1	AB	0.66	0/219	1.06	0/290
1	B	0.67	0/219	1.02	0/290
1	BA	0.65	0/219	1.04	0/290
1	BB	0.67	0/219	1.09	0/290
1	C	0.66	0/219	1.01	0/290
1	CA	0.66	0/219	1.03	0/290
1	CB	0.64	0/219	1.05	0/290
1	D	0.66	0/219	1.03	0/290
1	DA	0.67	0/219	1.02	0/290
1	DB	0.66	0/219	1.04	0/290

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	E	0.66	0/219	1.02	0/290
1	EA	0.67	0/219	1.04	0/290
1	EB	0.66	0/219	1.02	0/290
1	F	0.67	0/219	1.05	0/290
1	FA	0.69	0/219	1.07	0/290
1	FB	0.68	0/219	1.04	0/290
1	G	0.67	0/219	1.02	0/290
1	GA	0.66	0/219	1.04	0/290
1	GB	0.69	0/219	1.05	0/290
1	H	0.66	0/219	1.03	0/290
1	HA	0.67	0/219	1.11	0/290
1	HB	0.66	0/219	1.10	0/290
1	I	0.66	0/219	1.01	0/290
1	IA	0.64	0/219	1.04	0/290
1	IB	0.67	0/219	1.07	0/290
1	J	0.66	0/219	1.02	0/290
1	JA	0.65	0/219	1.04	0/290
1	JB	0.65	0/219	1.04	0/290
1	K	0.66	0/219	1.00	0/290
1	KA	0.66	0/219	1.03	0/290
1	KB	0.66	0/219	1.02	0/290
1	L	0.67	0/219	1.02	0/290
1	LA	0.67	0/219	1.04	0/290
1	LB	0.66	0/219	1.02	0/290
1	M	0.67	0/219	1.04	0/290
1	MA	0.69	0/219	1.05	0/290
1	MB	0.67	0/219	1.06	0/290
1	N	0.67	0/219	1.02	0/290
1	NA	0.66	0/219	1.04	0/290
1	NB	0.69	0/219	1.05	0/290
1	O	0.67	0/219	1.03	0/290
1	OA	0.68	0/219	1.10	0/290
1	OB	0.65	0/219	1.09	0/290
1	P	0.66	0/219	1.02	0/290
1	PA	0.65	0/219	1.03	0/290
1	PB	0.68	0/219	1.04	0/290
1	Q	0.67	0/219	1.11	0/290
1	QA	0.66	0/219	1.03	0/290
1	QB	0.65	0/219	1.04	0/290
1	R	0.66	0/219	1.06	0/290
1	RA	0.68	0/219	1.03	0/290
1	RB	0.66	0/219	1.03	0/290
1	S	0.67	0/219	1.12	0/290

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	SA	0.66	0/219	1.01	0/290
1	SB	0.67	0/219	1.04	0/290
1	T	0.67	0/219	1.11	0/290
1	TA	0.68	0/219	1.06	0/290
1	TB	0.68	0/219	1.04	0/290
1	U	0.66	0/219	1.06	0/290
1	UA	0.66	0/219	1.06	0/290
1	UB	0.70	0/219	1.07	0/290
1	V	0.64	0/219	1.01	0/290
1	VA	0.69	0/219	1.11	0/290
1	VB	0.66	0/219	1.08	0/290
1	W	0.66	0/219	1.02	0/290
1	WA	0.66	0/219	1.03	0/290
1	WB	0.67	0/219	1.08	0/290
1	X	0.67	0/219	1.01	0/290
1	XA	0.66	0/219	1.01	0/290
1	XB	0.65	0/219	1.04	0/290
1	Y	0.68	0/219	1.07	0/290
1	YA	0.66	0/219	1.01	0/290
1	YB	0.65	0/219	1.03	0/290
1	Z	0.68	0/219	1.07	0/290
1	ZA	0.66	0/219	1.04	0/290
1	ZB	0.66	0/219	1.03	0/290
1	a	0.66	0/219	1.06	0/290
1	aA	0.68	0/219	1.05	0/290
1	aB	0.68	0/219	1.05	0/290
1	b	0.67	0/219	1.08	0/290
1	bA	0.66	0/219	1.05	0/290
1	bB	0.69	0/219	1.05	0/290
1	c	0.64	0/219	1.03	0/290
1	cA	0.65	0/219	1.05	0/290
1	cB	0.66	0/219	1.06	0/290
1	d	0.66	0/219	1.02	0/290
1	dA	0.65	0/219	1.05	0/290
1	dB	0.67	0/219	1.07	0/290
1	e	0.66	0/219	0.99	0/290
1	eA	0.65	0/219	1.08	0/290
1	eB	0.65	0/219	1.04	0/290
1	f	0.68	0/219	1.05	0/290
1	fA	0.67	0/219	1.03	0/290
1	fB	0.66	0/219	1.02	0/290
1	g	0.68	0/219	1.07	0/290
1	gA	0.67	0/219	1.08	0/290

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	gB	0.65	0/219	1.04	0/290
1	h	0.67	0/219	1.08	0/290
1	hA	0.68	0/219	1.04	0/290
1	hB	0.67	0/219	1.04	0/290
1	i	0.69	0/219	1.11	0/290
1	iA	0.66	0/219	1.07	0/290
1	iB	0.67	0/219	1.04	0/290
1	j	0.64	0/219	1.03	0/290
1	jA	0.66	0/219	1.09	0/290
1	jB	0.66	0/219	1.06	0/290
1	k	0.65	0/219	1.03	0/290
1	kA	0.63	0/219	1.05	0/290
1	l	0.67	0/219	1.02	0/290
1	lA	0.66	0/219	1.03	0/290
1	m	0.67	0/219	1.05	0/290
1	mA	0.67	0/219	1.02	0/290
1	n	0.69	0/219	1.09	0/290
1	nA	0.67	0/219	1.06	0/290
1	o	0.66	0/219	1.08	0/290
1	oA	0.69	0/219	1.05	0/290
1	p	0.67	0/219	1.10	0/290
1	pA	0.65	0/219	1.07	0/290
1	q	0.65	0/219	1.03	0/290
1	qA	0.68	0/219	1.10	0/290
1	r	0.65	0/219	1.02	0/290
1	rA	0.65	0/219	1.04	0/290
1	s	0.66	0/219	1.03	0/290
1	sA	0.66	0/219	1.02	0/290
1	t	0.67	0/219	1.06	0/290
1	tA	0.66	0/219	1.02	0/290
1	u	0.68	0/219	1.07	0/290
1	uA	0.67	0/219	1.04	0/290
1	v	0.66	0/219	1.08	0/290
1	vA	0.69	0/219	1.04	0/290
1	w	0.69	0/219	1.12	0/290
1	wA	0.65	0/219	1.04	0/290
1	x	0.64	0/219	1.04	0/290
1	xA	0.67	0/219	1.09	0/290
1	y	0.66	0/219	1.03	0/290
1	yA	0.65	0/219	1.06	0/290
1	z	0.67	0/219	1.00	0/290
1	zA	0.66	0/219	1.04	0/290
All	All	0.67	0/35040	1.05	0/46400

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	0	218	0	215	0	0
1	0A	218	0	215	0	0
1	1	218	0	215	0	0
1	1A	218	0	215	0	0
1	2	218	0	215	0	0
1	2A	218	0	215	0	0
1	3	218	0	215	0	0
1	3A	218	0	215	0	0
1	4	218	0	215	0	0
1	4A	218	0	215	0	0
1	5	218	0	215	0	0
1	5A	218	0	215	0	0
1	6	218	0	215	0	0
1	6A	218	0	215	0	0
1	7	218	0	215	0	0
1	7A	218	0	215	0	0
1	8	218	0	215	0	0
1	8A	218	0	215	0	0
1	9	218	0	215	0	0
1	9A	218	0	215	0	0
1	A	218	0	218	0	0
1	AA	218	0	215	0	0
1	AB	218	0	215	0	0
1	B	218	0	218	0	0
1	BA	218	0	215	0	0
1	BB	218	0	215	0	0
1	C	218	0	218	0	0
1	CA	218	0	215	0	0
1	CB	218	0	215	0	0
1	D	218	0	218	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	DA	218	0	215	0	0
1	DB	218	0	215	0	0
1	E	218	0	218	0	0
1	EA	218	0	215	0	0
1	EB	218	0	215	0	0
1	F	218	0	218	0	0
1	FA	218	0	215	0	0
1	FB	218	0	215	0	0
1	G	218	0	218	0	0
1	GA	218	0	215	0	0
1	GB	218	0	215	0	0
1	H	218	0	218	0	0
1	HA	218	0	215	0	0
1	HB	218	0	215	0	0
1	I	218	0	218	0	0
1	IA	218	0	215	0	0
1	IB	218	0	215	0	0
1	J	218	0	218	0	0
1	JA	218	0	215	0	0
1	JB	218	0	215	0	0
1	K	218	0	218	0	0
1	KA	218	0	215	0	0
1	KB	218	0	215	0	0
1	L	218	0	218	0	0
1	LA	218	0	215	0	0
1	LB	218	0	215	0	0
1	M	218	0	218	0	0
1	MA	218	0	215	0	0
1	MB	218	0	215	0	0
1	N	218	0	218	0	0
1	NA	218	0	215	0	0
1	NB	218	0	215	0	0
1	O	218	0	218	0	0
1	OA	218	0	215	0	0
1	OB	218	0	215	0	0
1	P	218	0	218	0	0
1	PA	218	0	215	0	0
1	PB	218	0	215	0	0
1	Q	218	0	218	0	0
1	QA	218	0	215	0	0
1	QB	218	0	215	0	0
1	R	218	0	218	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	RA	218	0	215	0	0
1	RB	218	0	215	0	0
1	S	218	0	218	0	0
1	SA	218	0	215	0	0
1	SB	218	0	215	0	0
1	T	218	0	218	0	0
1	TA	218	0	215	0	0
1	TB	218	0	215	0	0
1	U	218	0	215	0	0
1	UA	218	0	215	0	0
1	UB	218	0	215	0	0
1	V	218	0	215	0	0
1	VA	218	0	215	0	0
1	VB	218	0	215	0	0
1	W	218	0	215	0	0
1	WA	218	0	215	0	0
1	WB	218	0	215	0	0
1	X	218	0	215	0	0
1	XA	218	0	215	0	0
1	XB	218	0	215	0	0
1	Y	218	0	215	0	0
1	YA	218	0	215	0	0
1	YB	218	0	215	0	0
1	Z	218	0	215	0	0
1	ZA	218	0	215	0	0
1	ZB	218	0	215	0	0
1	a	218	0	215	0	0
1	aA	218	0	215	0	0
1	aB	218	0	215	0	0
1	b	218	0	215	0	0
1	bA	218	0	215	0	0
1	bB	218	0	215	0	0
1	c	218	0	215	0	0
1	cA	218	0	215	0	0
1	cB	218	0	215	0	0
1	d	218	0	215	0	0
1	dA	218	0	215	0	0
1	dB	218	0	215	0	0
1	e	218	0	215	0	0
1	eA	218	0	215	0	0
1	eB	218	0	215	0	0
1	f	218	0	215	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	fA	218	0	215	0	0
1	fB	218	0	215	0	0
1	g	218	0	215	0	0
1	gA	218	0	215	0	0
1	gB	218	0	215	0	0
1	h	218	0	215	0	0
1	hA	218	0	215	0	0
1	hB	218	0	215	0	0
1	i	218	0	215	0	0
1	iA	218	0	215	0	0
1	iB	218	0	215	0	0
1	j	218	0	215	0	0
1	jA	218	0	215	0	0
1	jB	218	0	215	0	0
1	k	218	0	215	0	0
1	kA	218	0	215	0	0
1	l	218	0	215	0	0
1	lA	218	0	215	0	0
1	m	218	0	215	0	0
1	mA	218	0	215	0	0
1	n	218	0	215	0	0
1	nA	218	0	215	0	0
1	o	218	0	215	0	0
1	oA	218	0	215	0	0
1	p	218	0	215	0	0
1	pA	218	0	215	0	0
1	q	218	0	215	0	0
1	qA	218	0	215	0	0
1	r	218	0	215	0	0
1	rA	218	0	215	0	0
1	s	218	0	215	0	0
1	sA	218	0	215	0	0
1	t	218	0	215	0	0
1	tA	218	0	215	0	0
1	u	218	0	215	0	0
1	uA	218	0	215	0	0
1	v	218	0	215	0	0
1	vA	218	0	215	0	0
1	w	218	0	215	0	0
1	wA	218	0	215	0	0
1	x	218	0	215	0	0
1	xA	218	0	215	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	y	218	0	215	0	0
1	yA	218	0	215	0	0
1	z	218	0	215	0	0
1	zA	218	0	215	0	0
All	All	34880	0	34460	0	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 0.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	28/30 (93%)	28 (100%)	0	0	100	100
1	0A	28/30 (93%)	28 (100%)	0	0	100	100
1	1	28/30 (93%)	28 (100%)	0	0	100	100
1	1A	28/30 (93%)	28 (100%)	0	0	100	100
1	2	28/30 (93%)	28 (100%)	0	0	100	100
1	2A	28/30 (93%)	28 (100%)	0	0	100	100
1	3	28/30 (93%)	28 (100%)	0	0	100	100
1	3A	28/30 (93%)	28 (100%)	0	0	100	100
1	4	28/30 (93%)	28 (100%)	0	0	100	100
1	4A	28/30 (93%)	28 (100%)	0	0	100	100
1	5	28/30 (93%)	28 (100%)	0	0	100	100
1	5A	28/30 (93%)	28 (100%)	0	0	100	100
1	6	28/30 (93%)	28 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	6A	28/30 (93%)	28 (100%)	0	0	100	100
1	7	28/30 (93%)	28 (100%)	0	0	100	100
1	7A	28/30 (93%)	28 (100%)	0	0	100	100
1	8	28/30 (93%)	28 (100%)	0	0	100	100
1	8A	28/30 (93%)	28 (100%)	0	0	100	100
1	9	28/30 (93%)	28 (100%)	0	0	100	100
1	9A	28/30 (93%)	28 (100%)	0	0	100	100
1	A	28/30 (93%)	28 (100%)	0	0	100	100
1	AA	28/30 (93%)	28 (100%)	0	0	100	100
1	AB	28/30 (93%)	28 (100%)	0	0	100	100
1	B	28/30 (93%)	28 (100%)	0	0	100	100
1	BA	28/30 (93%)	28 (100%)	0	0	100	100
1	BB	28/30 (93%)	28 (100%)	0	0	100	100
1	C	28/30 (93%)	28 (100%)	0	0	100	100
1	CA	28/30 (93%)	28 (100%)	0	0	100	100
1	CB	28/30 (93%)	28 (100%)	0	0	100	100
1	D	28/30 (93%)	28 (100%)	0	0	100	100
1	DA	28/30 (93%)	28 (100%)	0	0	100	100
1	DB	28/30 (93%)	28 (100%)	0	0	100	100
1	E	28/30 (93%)	28 (100%)	0	0	100	100
1	EA	28/30 (93%)	28 (100%)	0	0	100	100
1	EB	28/30 (93%)	28 (100%)	0	0	100	100
1	F	28/30 (93%)	28 (100%)	0	0	100	100
1	FA	28/30 (93%)	28 (100%)	0	0	100	100
1	FB	28/30 (93%)	28 (100%)	0	0	100	100
1	G	28/30 (93%)	28 (100%)	0	0	100	100
1	GA	28/30 (93%)	28 (100%)	0	0	100	100
1	GB	28/30 (93%)	28 (100%)	0	0	100	100
1	H	28/30 (93%)	28 (100%)	0	0	100	100
1	HA	28/30 (93%)	28 (100%)	0	0	100	100
1	HB	28/30 (93%)	28 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	28/30 (93%)	28 (100%)	0	0	100	100
1	IA	28/30 (93%)	28 (100%)	0	0	100	100
1	IB	28/30 (93%)	28 (100%)	0	0	100	100
1	J	28/30 (93%)	28 (100%)	0	0	100	100
1	JA	28/30 (93%)	28 (100%)	0	0	100	100
1	JB	28/30 (93%)	28 (100%)	0	0	100	100
1	K	28/30 (93%)	28 (100%)	0	0	100	100
1	KA	28/30 (93%)	28 (100%)	0	0	100	100
1	KB	28/30 (93%)	28 (100%)	0	0	100	100
1	L	28/30 (93%)	28 (100%)	0	0	100	100
1	LA	28/30 (93%)	28 (100%)	0	0	100	100
1	LB	28/30 (93%)	28 (100%)	0	0	100	100
1	M	28/30 (93%)	28 (100%)	0	0	100	100
1	MA	28/30 (93%)	28 (100%)	0	0	100	100
1	MB	28/30 (93%)	28 (100%)	0	0	100	100
1	N	28/30 (93%)	28 (100%)	0	0	100	100
1	NA	28/30 (93%)	28 (100%)	0	0	100	100
1	NB	28/30 (93%)	28 (100%)	0	0	100	100
1	O	28/30 (93%)	28 (100%)	0	0	100	100
1	OA	28/30 (93%)	28 (100%)	0	0	100	100
1	OB	28/30 (93%)	28 (100%)	0	0	100	100
1	P	28/30 (93%)	28 (100%)	0	0	100	100
1	PA	28/30 (93%)	28 (100%)	0	0	100	100
1	PB	28/30 (93%)	28 (100%)	0	0	100	100
1	Q	28/30 (93%)	28 (100%)	0	0	100	100
1	QA	28/30 (93%)	28 (100%)	0	0	100	100
1	QB	28/30 (93%)	28 (100%)	0	0	100	100
1	R	28/30 (93%)	28 (100%)	0	0	100	100
1	RA	28/30 (93%)	28 (100%)	0	0	100	100
1	RB	28/30 (93%)	28 (100%)	0	0	100	100
1	S	28/30 (93%)	28 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	SA	28/30 (93%)	28 (100%)	0	0	100	100
1	SB	28/30 (93%)	28 (100%)	0	0	100	100
1	T	28/30 (93%)	28 (100%)	0	0	100	100
1	TA	28/30 (93%)	28 (100%)	0	0	100	100
1	TB	28/30 (93%)	28 (100%)	0	0	100	100
1	U	28/30 (93%)	28 (100%)	0	0	100	100
1	UA	28/30 (93%)	28 (100%)	0	0	100	100
1	UB	28/30 (93%)	28 (100%)	0	0	100	100
1	V	28/30 (93%)	28 (100%)	0	0	100	100
1	VA	28/30 (93%)	28 (100%)	0	0	100	100
1	VB	28/30 (93%)	28 (100%)	0	0	100	100
1	W	28/30 (93%)	28 (100%)	0	0	100	100
1	WA	28/30 (93%)	28 (100%)	0	0	100	100
1	WB	28/30 (93%)	28 (100%)	0	0	100	100
1	X	28/30 (93%)	28 (100%)	0	0	100	100
1	XA	28/30 (93%)	28 (100%)	0	0	100	100
1	XB	28/30 (93%)	28 (100%)	0	0	100	100
1	Y	28/30 (93%)	28 (100%)	0	0	100	100
1	YA	28/30 (93%)	28 (100%)	0	0	100	100
1	YB	28/30 (93%)	28 (100%)	0	0	100	100
1	Z	28/30 (93%)	28 (100%)	0	0	100	100
1	ZA	28/30 (93%)	28 (100%)	0	0	100	100
1	ZB	28/30 (93%)	28 (100%)	0	0	100	100
1	a	28/30 (93%)	28 (100%)	0	0	100	100
1	aA	28/30 (93%)	28 (100%)	0	0	100	100
1	aB	28/30 (93%)	28 (100%)	0	0	100	100
1	b	28/30 (93%)	28 (100%)	0	0	100	100
1	bA	28/30 (93%)	28 (100%)	0	0	100	100
1	bB	28/30 (93%)	28 (100%)	0	0	100	100
1	c	28/30 (93%)	28 (100%)	0	0	100	100
1	cA	28/30 (93%)	28 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	cB	28/30 (93%)	28 (100%)	0	0	100	100
1	d	28/30 (93%)	28 (100%)	0	0	100	100
1	dA	28/30 (93%)	28 (100%)	0	0	100	100
1	dB	28/30 (93%)	28 (100%)	0	0	100	100
1	e	28/30 (93%)	28 (100%)	0	0	100	100
1	eA	28/30 (93%)	28 (100%)	0	0	100	100
1	eB	28/30 (93%)	28 (100%)	0	0	100	100
1	f	28/30 (93%)	28 (100%)	0	0	100	100
1	fA	28/30 (93%)	28 (100%)	0	0	100	100
1	fB	28/30 (93%)	28 (100%)	0	0	100	100
1	g	28/30 (93%)	28 (100%)	0	0	100	100
1	gA	28/30 (93%)	28 (100%)	0	0	100	100
1	gB	28/30 (93%)	28 (100%)	0	0	100	100
1	h	28/30 (93%)	28 (100%)	0	0	100	100
1	hA	28/30 (93%)	28 (100%)	0	0	100	100
1	hB	28/30 (93%)	28 (100%)	0	0	100	100
1	i	28/30 (93%)	28 (100%)	0	0	100	100
1	iA	28/30 (93%)	28 (100%)	0	0	100	100
1	iB	28/30 (93%)	28 (100%)	0	0	100	100
1	j	28/30 (93%)	28 (100%)	0	0	100	100
1	jA	28/30 (93%)	28 (100%)	0	0	100	100
1	jB	28/30 (93%)	28 (100%)	0	0	100	100
1	k	28/30 (93%)	28 (100%)	0	0	100	100
1	kA	28/30 (93%)	28 (100%)	0	0	100	100
1	l	28/30 (93%)	28 (100%)	0	0	100	100
1	lA	28/30 (93%)	28 (100%)	0	0	100	100
1	m	28/30 (93%)	28 (100%)	0	0	100	100
1	mA	28/30 (93%)	28 (100%)	0	0	100	100
1	n	28/30 (93%)	28 (100%)	0	0	100	100
1	nA	28/30 (93%)	28 (100%)	0	0	100	100
1	o	28/30 (93%)	28 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	oA	28/30 (93%)	28 (100%)	0	0	100	100
1	p	28/30 (93%)	28 (100%)	0	0	100	100
1	pA	28/30 (93%)	28 (100%)	0	0	100	100
1	q	28/30 (93%)	28 (100%)	0	0	100	100
1	qA	28/30 (93%)	28 (100%)	0	0	100	100
1	r	28/30 (93%)	28 (100%)	0	0	100	100
1	rA	28/30 (93%)	28 (100%)	0	0	100	100
1	s	28/30 (93%)	28 (100%)	0	0	100	100
1	sA	28/30 (93%)	28 (100%)	0	0	100	100
1	t	28/30 (93%)	28 (100%)	0	0	100	100
1	tA	28/30 (93%)	28 (100%)	0	0	100	100
1	u	28/30 (93%)	28 (100%)	0	0	100	100
1	uA	28/30 (93%)	28 (100%)	0	0	100	100
1	v	28/30 (93%)	28 (100%)	0	0	100	100
1	vA	28/30 (93%)	28 (100%)	0	0	100	100
1	w	28/30 (93%)	28 (100%)	0	0	100	100
1	wA	28/30 (93%)	28 (100%)	0	0	100	100
1	x	28/30 (93%)	28 (100%)	0	0	100	100
1	xA	28/30 (93%)	28 (100%)	0	0	100	100
1	y	28/30 (93%)	28 (100%)	0	0	100	100
1	yA	28/30 (93%)	28 (100%)	0	0	100	100
1	z	28/30 (93%)	28 (100%)	0	0	100	100
1	zA	28/30 (93%)	28 (100%)	0	0	100	100
All	All	4480/4800 (93%)	4480 (100%)	0	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	0	19/19 (100%)	19 (100%)	0	100	100
1	0A	19/19 (100%)	19 (100%)	0	100	100
1	1	19/19 (100%)	19 (100%)	0	100	100
1	1A	19/19 (100%)	19 (100%)	0	100	100
1	2	19/19 (100%)	19 (100%)	0	100	100
1	2A	19/19 (100%)	19 (100%)	0	100	100
1	3	19/19 (100%)	19 (100%)	0	100	100
1	3A	19/19 (100%)	19 (100%)	0	100	100
1	4	19/19 (100%)	19 (100%)	0	100	100
1	4A	19/19 (100%)	19 (100%)	0	100	100
1	5	19/19 (100%)	19 (100%)	0	100	100
1	5A	19/19 (100%)	19 (100%)	0	100	100
1	6	19/19 (100%)	19 (100%)	0	100	100
1	6A	19/19 (100%)	19 (100%)	0	100	100
1	7	19/19 (100%)	19 (100%)	0	100	100
1	7A	19/19 (100%)	19 (100%)	0	100	100
1	8	19/19 (100%)	19 (100%)	0	100	100
1	8A	19/19 (100%)	19 (100%)	0	100	100
1	9	19/19 (100%)	19 (100%)	0	100	100
1	9A	19/19 (100%)	19 (100%)	0	100	100
1	A	19/19 (100%)	19 (100%)	0	100	100
1	AA	19/19 (100%)	19 (100%)	0	100	100
1	AB	19/19 (100%)	19 (100%)	0	100	100
1	B	19/19 (100%)	19 (100%)	0	100	100
1	BA	19/19 (100%)	19 (100%)	0	100	100
1	BB	19/19 (100%)	19 (100%)	0	100	100
1	C	19/19 (100%)	19 (100%)	0	100	100
1	CA	19/19 (100%)	19 (100%)	0	100	100
1	CB	19/19 (100%)	19 (100%)	0	100	100
1	D	19/19 (100%)	19 (100%)	0	100	100
1	DA	19/19 (100%)	19 (100%)	0	100	100
1	DB	19/19 (100%)	19 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	19/19 (100%)	19 (100%)	0	100	100
1	EA	19/19 (100%)	19 (100%)	0	100	100
1	EB	19/19 (100%)	19 (100%)	0	100	100
1	F	19/19 (100%)	19 (100%)	0	100	100
1	FA	19/19 (100%)	19 (100%)	0	100	100
1	FB	19/19 (100%)	19 (100%)	0	100	100
1	G	19/19 (100%)	19 (100%)	0	100	100
1	GA	19/19 (100%)	19 (100%)	0	100	100
1	GB	19/19 (100%)	19 (100%)	0	100	100
1	H	19/19 (100%)	19 (100%)	0	100	100
1	HA	19/19 (100%)	19 (100%)	0	100	100
1	HB	19/19 (100%)	19 (100%)	0	100	100
1	I	19/19 (100%)	19 (100%)	0	100	100
1	IA	19/19 (100%)	19 (100%)	0	100	100
1	IB	19/19 (100%)	19 (100%)	0	100	100
1	J	19/19 (100%)	19 (100%)	0	100	100
1	JA	19/19 (100%)	19 (100%)	0	100	100
1	JB	19/19 (100%)	19 (100%)	0	100	100
1	K	19/19 (100%)	19 (100%)	0	100	100
1	KA	19/19 (100%)	19 (100%)	0	100	100
1	KB	19/19 (100%)	19 (100%)	0	100	100
1	L	19/19 (100%)	19 (100%)	0	100	100
1	LA	19/19 (100%)	19 (100%)	0	100	100
1	LB	19/19 (100%)	19 (100%)	0	100	100
1	M	19/19 (100%)	19 (100%)	0	100	100
1	MA	19/19 (100%)	19 (100%)	0	100	100
1	MB	19/19 (100%)	19 (100%)	0	100	100
1	N	19/19 (100%)	19 (100%)	0	100	100
1	NA	19/19 (100%)	19 (100%)	0	100	100
1	NB	19/19 (100%)	19 (100%)	0	100	100
1	O	19/19 (100%)	19 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	OA	19/19 (100%)	19 (100%)	0	100	100
1	OB	19/19 (100%)	19 (100%)	0	100	100
1	P	19/19 (100%)	19 (100%)	0	100	100
1	PA	19/19 (100%)	19 (100%)	0	100	100
1	PB	19/19 (100%)	19 (100%)	0	100	100
1	Q	19/19 (100%)	19 (100%)	0	100	100
1	QA	19/19 (100%)	19 (100%)	0	100	100
1	QB	19/19 (100%)	19 (100%)	0	100	100
1	R	19/19 (100%)	19 (100%)	0	100	100
1	RA	19/19 (100%)	19 (100%)	0	100	100
1	RB	19/19 (100%)	19 (100%)	0	100	100
1	S	19/19 (100%)	19 (100%)	0	100	100
1	SA	19/19 (100%)	19 (100%)	0	100	100
1	SB	19/19 (100%)	19 (100%)	0	100	100
1	T	19/19 (100%)	19 (100%)	0	100	100
1	TA	19/19 (100%)	19 (100%)	0	100	100
1	TB	19/19 (100%)	19 (100%)	0	100	100
1	U	19/19 (100%)	19 (100%)	0	100	100
1	UA	19/19 (100%)	19 (100%)	0	100	100
1	UB	19/19 (100%)	19 (100%)	0	100	100
1	V	19/19 (100%)	19 (100%)	0	100	100
1	VA	19/19 (100%)	19 (100%)	0	100	100
1	VB	19/19 (100%)	19 (100%)	0	100	100
1	W	19/19 (100%)	19 (100%)	0	100	100
1	WA	19/19 (100%)	19 (100%)	0	100	100
1	WB	19/19 (100%)	19 (100%)	0	100	100
1	X	19/19 (100%)	19 (100%)	0	100	100
1	XA	19/19 (100%)	19 (100%)	0	100	100
1	XB	19/19 (100%)	19 (100%)	0	100	100
1	Y	19/19 (100%)	19 (100%)	0	100	100
1	YA	19/19 (100%)	19 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	YB	19/19 (100%)	19 (100%)	0	100	100
1	Z	19/19 (100%)	19 (100%)	0	100	100
1	ZA	19/19 (100%)	19 (100%)	0	100	100
1	ZB	19/19 (100%)	19 (100%)	0	100	100
1	a	19/19 (100%)	19 (100%)	0	100	100
1	aA	19/19 (100%)	19 (100%)	0	100	100
1	aB	19/19 (100%)	19 (100%)	0	100	100
1	b	19/19 (100%)	19 (100%)	0	100	100
1	bA	19/19 (100%)	19 (100%)	0	100	100
1	bB	19/19 (100%)	19 (100%)	0	100	100
1	c	19/19 (100%)	19 (100%)	0	100	100
1	cA	19/19 (100%)	19 (100%)	0	100	100
1	cB	19/19 (100%)	19 (100%)	0	100	100
1	d	19/19 (100%)	19 (100%)	0	100	100
1	dA	19/19 (100%)	19 (100%)	0	100	100
1	dB	19/19 (100%)	19 (100%)	0	100	100
1	e	19/19 (100%)	19 (100%)	0	100	100
1	eA	19/19 (100%)	19 (100%)	0	100	100
1	eB	19/19 (100%)	19 (100%)	0	100	100
1	f	19/19 (100%)	19 (100%)	0	100	100
1	fA	19/19 (100%)	19 (100%)	0	100	100
1	fB	19/19 (100%)	19 (100%)	0	100	100
1	g	19/19 (100%)	19 (100%)	0	100	100
1	gA	19/19 (100%)	19 (100%)	0	100	100
1	gB	19/19 (100%)	19 (100%)	0	100	100
1	h	19/19 (100%)	19 (100%)	0	100	100
1	hA	19/19 (100%)	19 (100%)	0	100	100
1	hB	19/19 (100%)	19 (100%)	0	100	100
1	i	19/19 (100%)	19 (100%)	0	100	100
1	iA	19/19 (100%)	19 (100%)	0	100	100
1	iB	19/19 (100%)	19 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	j	19/19 (100%)	19 (100%)	0	100	100
1	jA	19/19 (100%)	19 (100%)	0	100	100
1	jB	19/19 (100%)	19 (100%)	0	100	100
1	k	19/19 (100%)	19 (100%)	0	100	100
1	kA	19/19 (100%)	19 (100%)	0	100	100
1	l	19/19 (100%)	19 (100%)	0	100	100
1	lA	19/19 (100%)	19 (100%)	0	100	100
1	m	19/19 (100%)	19 (100%)	0	100	100
1	mA	19/19 (100%)	19 (100%)	0	100	100
1	n	19/19 (100%)	19 (100%)	0	100	100
1	nA	19/19 (100%)	19 (100%)	0	100	100
1	o	19/19 (100%)	19 (100%)	0	100	100
1	oA	19/19 (100%)	19 (100%)	0	100	100
1	p	19/19 (100%)	19 (100%)	0	100	100
1	pA	19/19 (100%)	19 (100%)	0	100	100
1	q	19/19 (100%)	19 (100%)	0	100	100
1	qA	19/19 (100%)	19 (100%)	0	100	100
1	r	19/19 (100%)	19 (100%)	0	100	100
1	rA	19/19 (100%)	19 (100%)	0	100	100
1	s	19/19 (100%)	19 (100%)	0	100	100
1	sA	19/19 (100%)	19 (100%)	0	100	100
1	t	19/19 (100%)	19 (100%)	0	100	100
1	tA	19/19 (100%)	19 (100%)	0	100	100
1	u	19/19 (100%)	19 (100%)	0	100	100
1	uA	19/19 (100%)	19 (100%)	0	100	100
1	v	19/19 (100%)	19 (100%)	0	100	100
1	vA	19/19 (100%)	19 (100%)	0	100	100
1	w	19/19 (100%)	19 (100%)	0	100	100
1	wA	19/19 (100%)	19 (100%)	0	100	100
1	x	19/19 (100%)	19 (100%)	0	100	100
1	xA	19/19 (100%)	19 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	y	19/19 (100%)	19 (100%)	0	100	100
1	yA	19/19 (100%)	19 (100%)	0	100	100
1	z	19/19 (100%)	19 (100%)	0	100	100
1	zA	19/19 (100%)	19 (100%)	0	100	100
All	All	3040/3040 (100%)	3040 (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. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	Z	617	ASN
1	c	217	ASN
1	j	217	ASN
1	q	217	ASN
1	x	217	ASN
1	BA	217	ASN
1	IA	217	ASN
1	WA	217	ASN
1	dA	217	ASN
1	hA	617	ASN
1	kA	217	ASN
1	oA	617	ASN
1	rA	217	ASN
1	yA	217	ASN
1	9A	617	ASN
1	CB	217	ASN
1	JB	217	ASN
1	NB	617	ASN
1	QB	217	ASN
1	XB	217	ASN
1	eB	217	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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](#)

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.

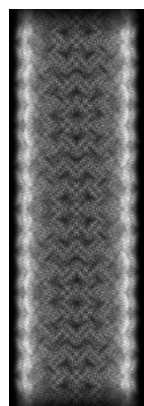
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49259. These allow visual inspection of the internal detail of the map and identification of artifacts.

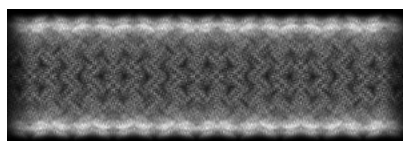
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

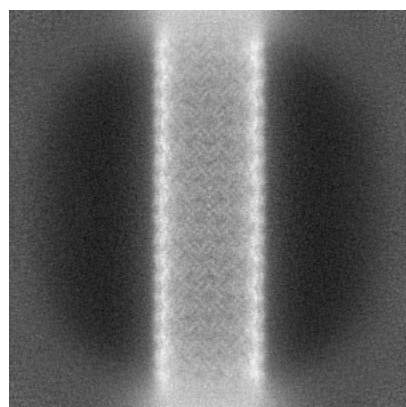


Y

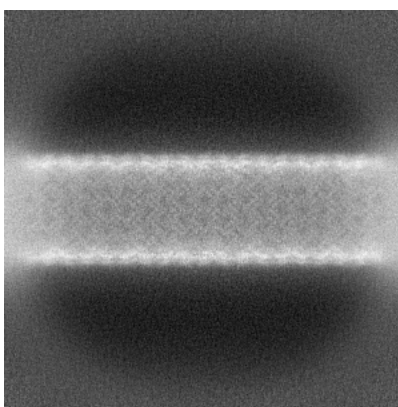


Z

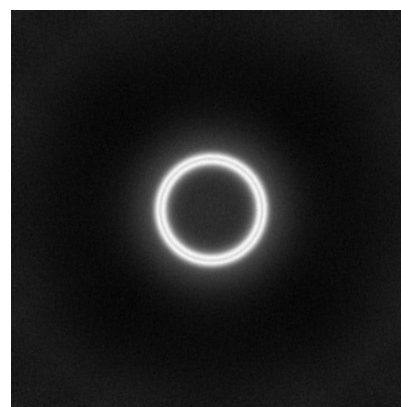
6.1.2 Raw map



X



Y



Z

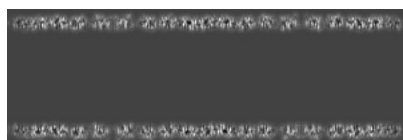
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

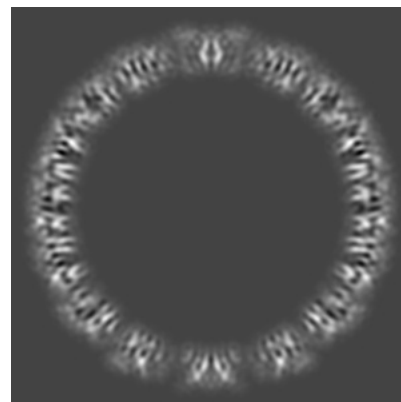
6.2.1 Primary map



X Index:
125

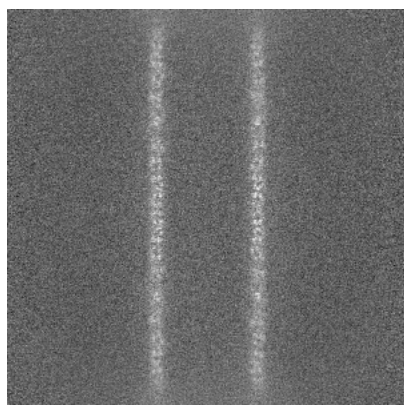


Y Index: 125

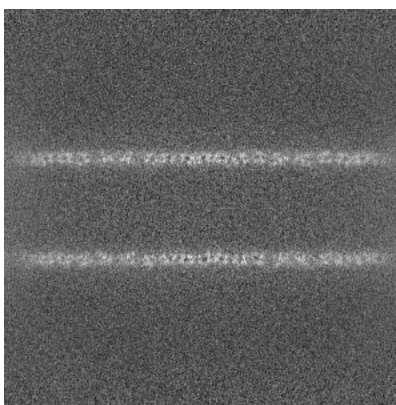


Z Index: 373

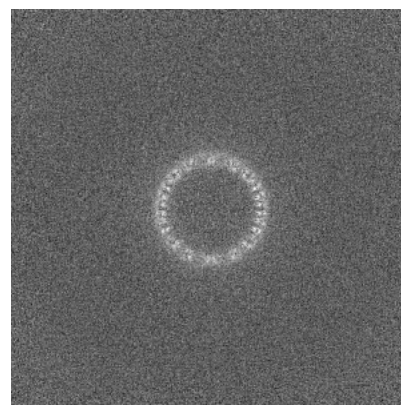
6.2.2 Raw map



X Index: 400



Y Index: 400

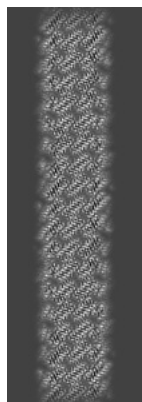


Z Index: 400

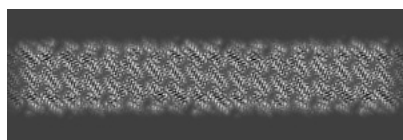
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

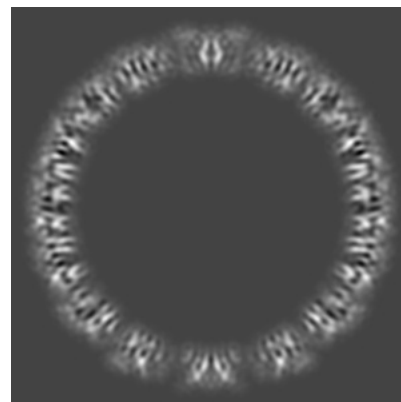
6.3.1 Primary map



X Index:
219

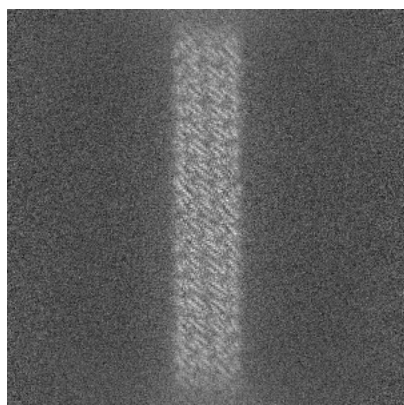


Y Index: 219

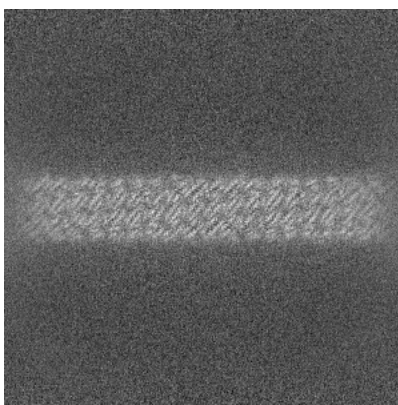


Z Index: 373

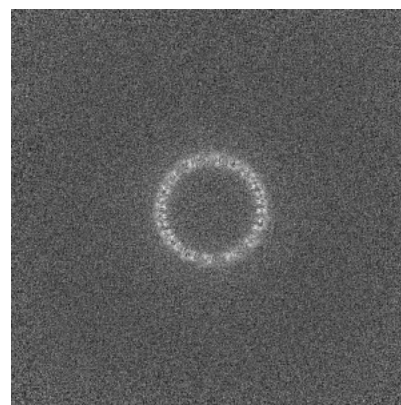
6.3.2 Raw map



X Index: 307



Y Index: 306

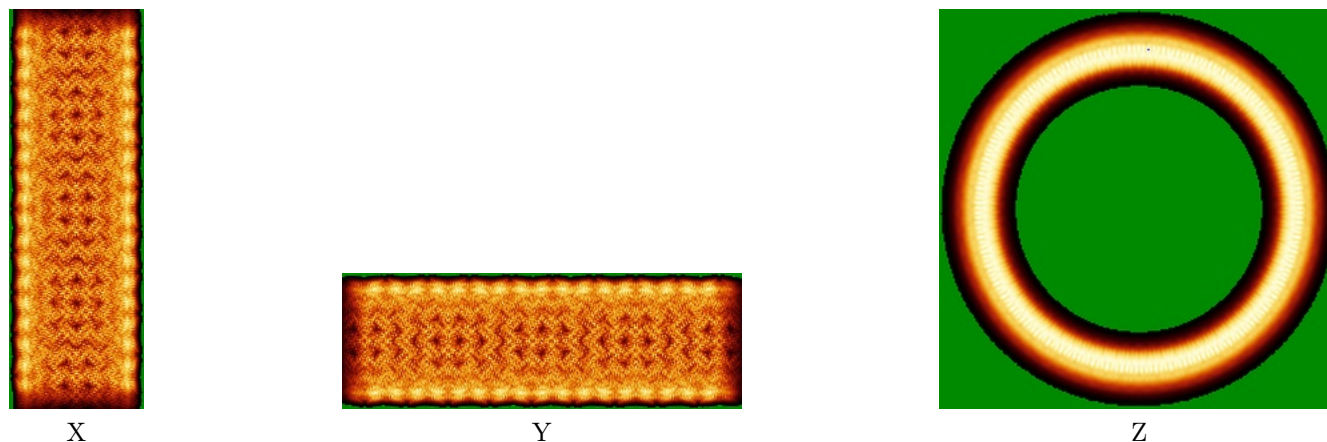


Z Index: 404

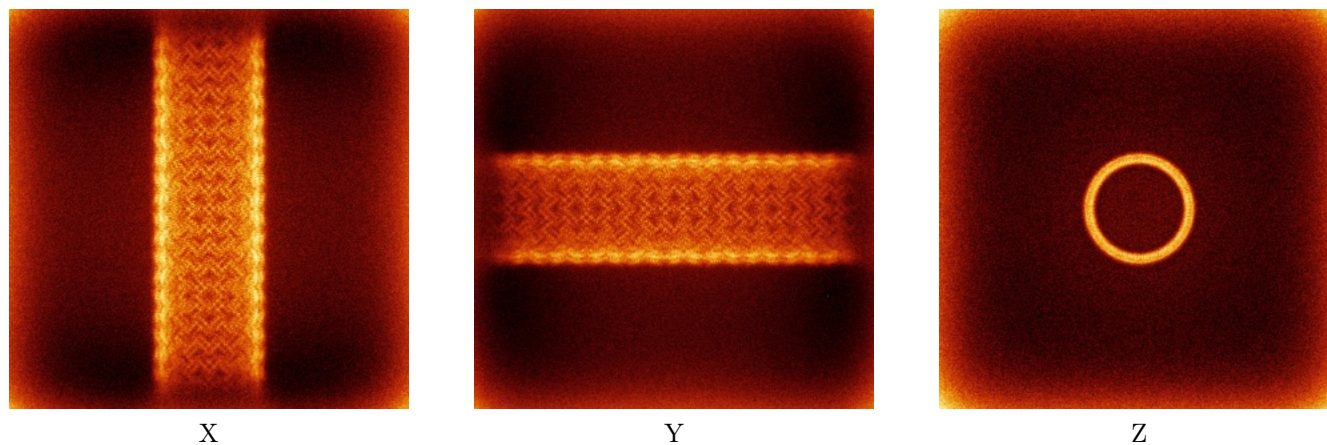
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



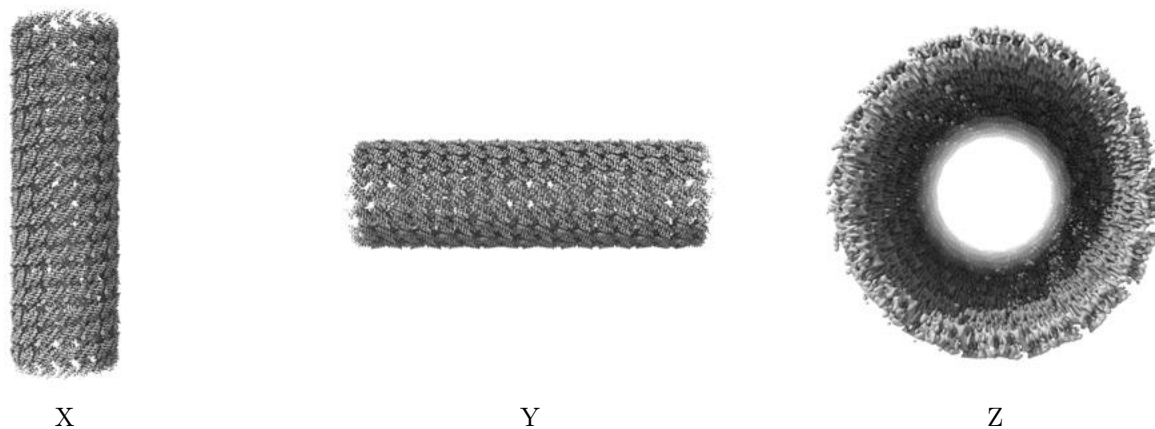
6.4.2 Raw map



The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

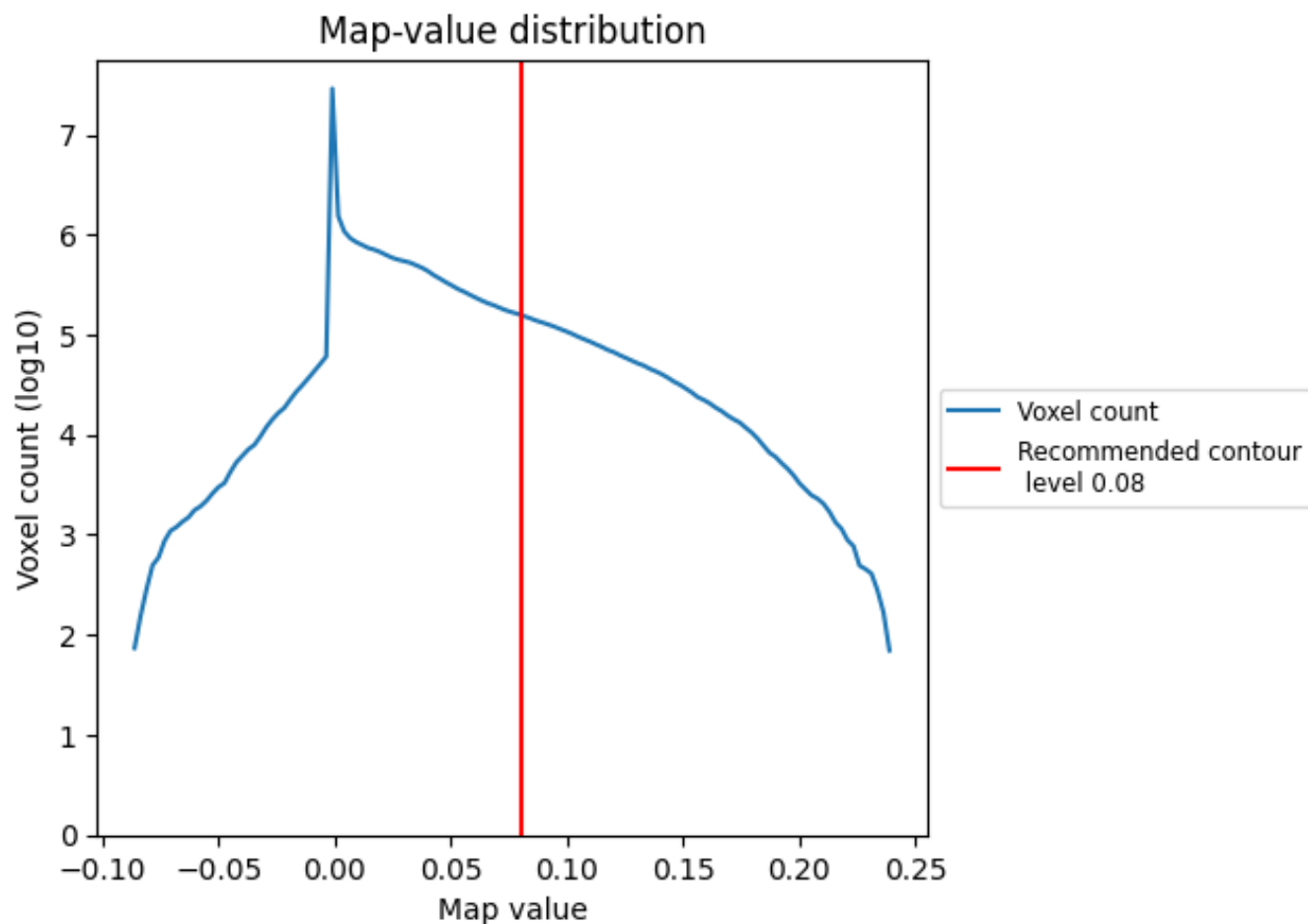
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

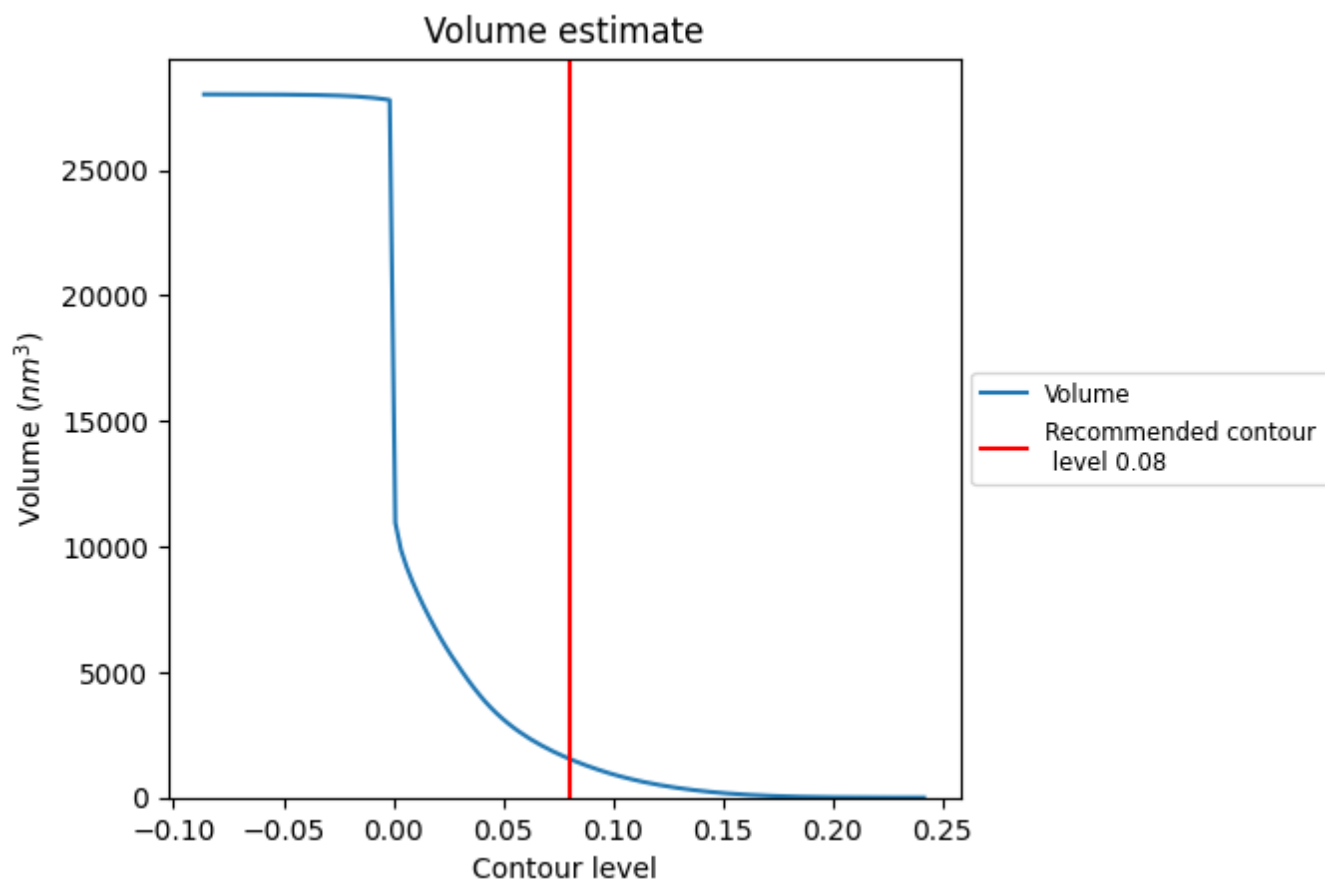
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1549 nm³; this corresponds to an approximate mass of 1400 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

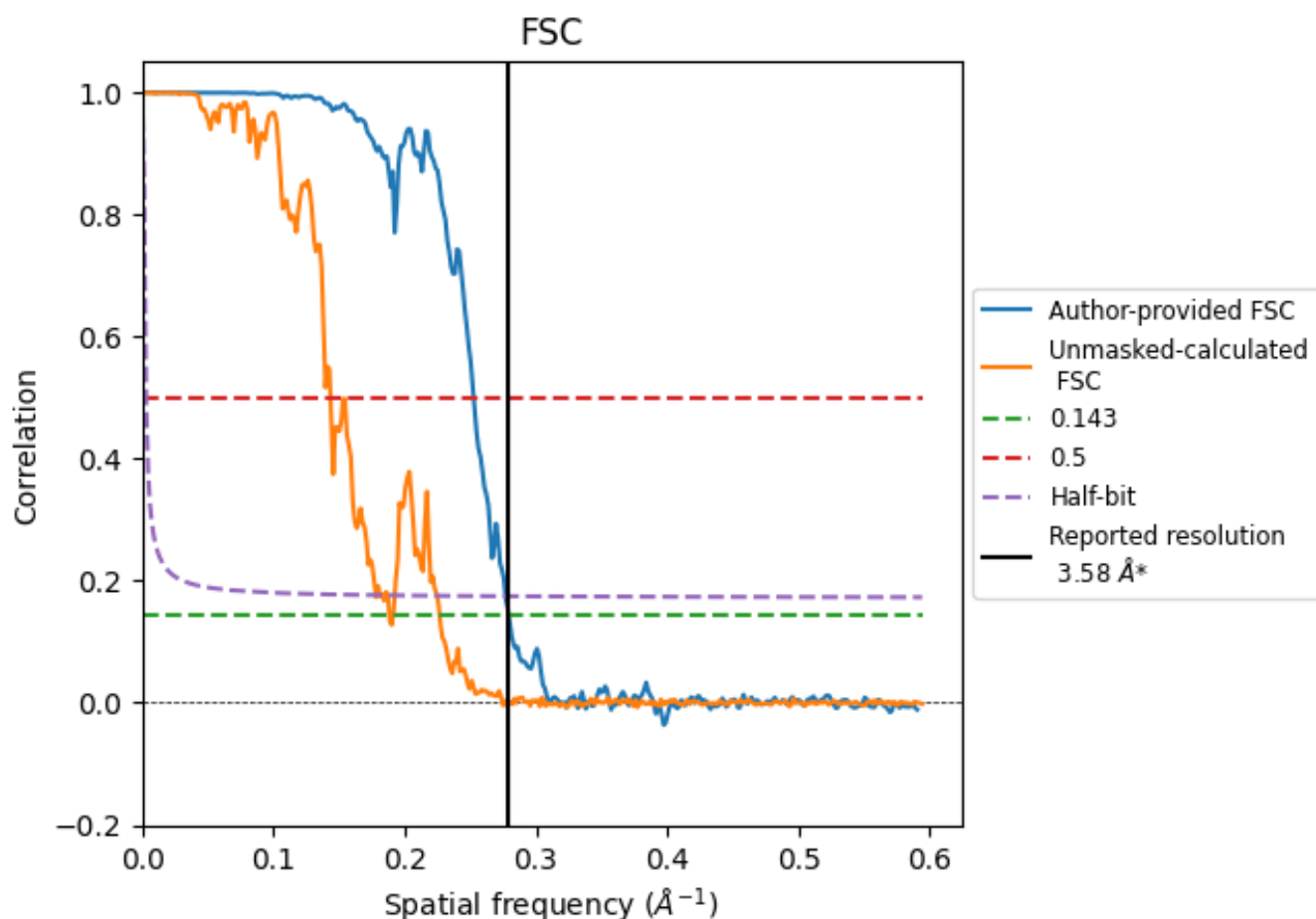
7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.279 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.58	-	-
Author-provided FSC curve	3.58	3.96	3.61
Unmasked-calculated*	5.31	6.97	5.61

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.31 differs from the reported value 3.58 by more than 10 %

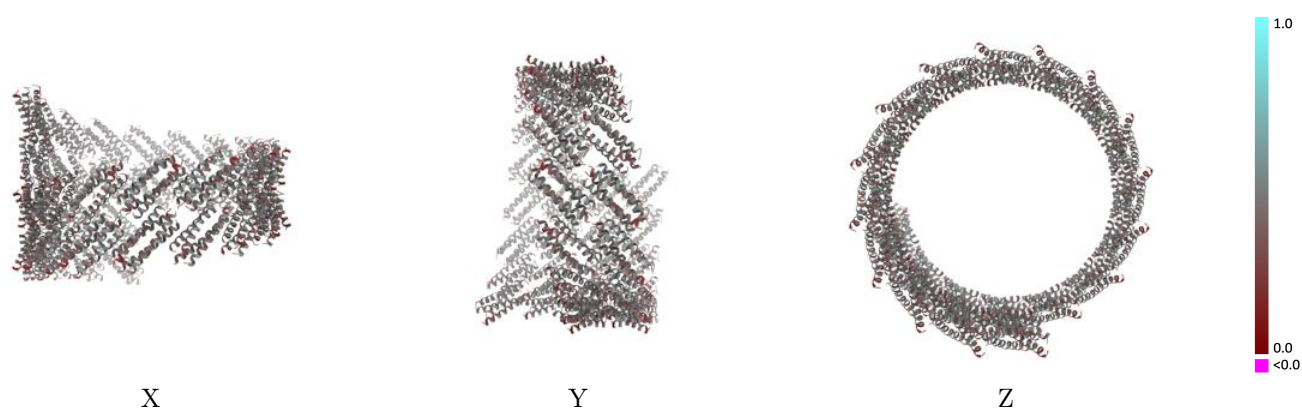
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-49259 and PDB model 9NCK. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)

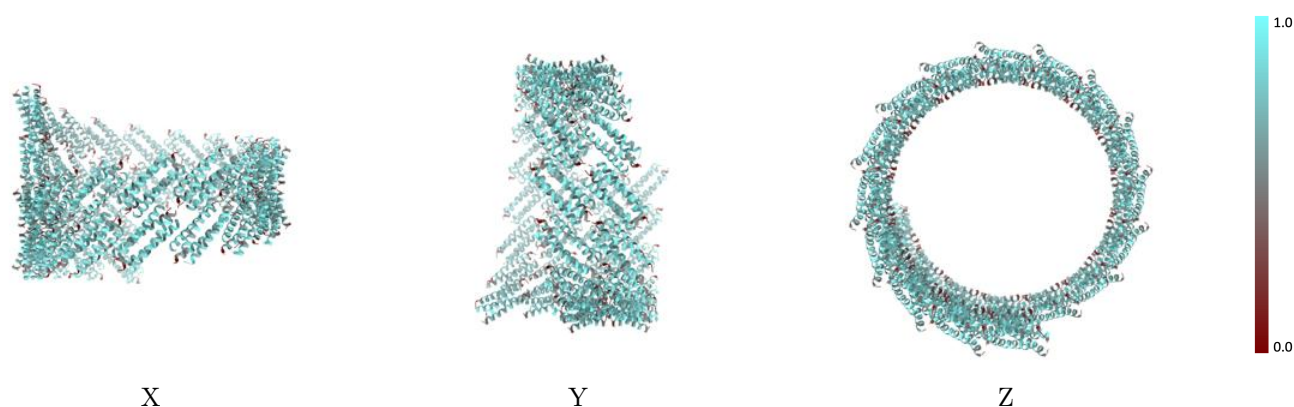
This section was not generated.

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



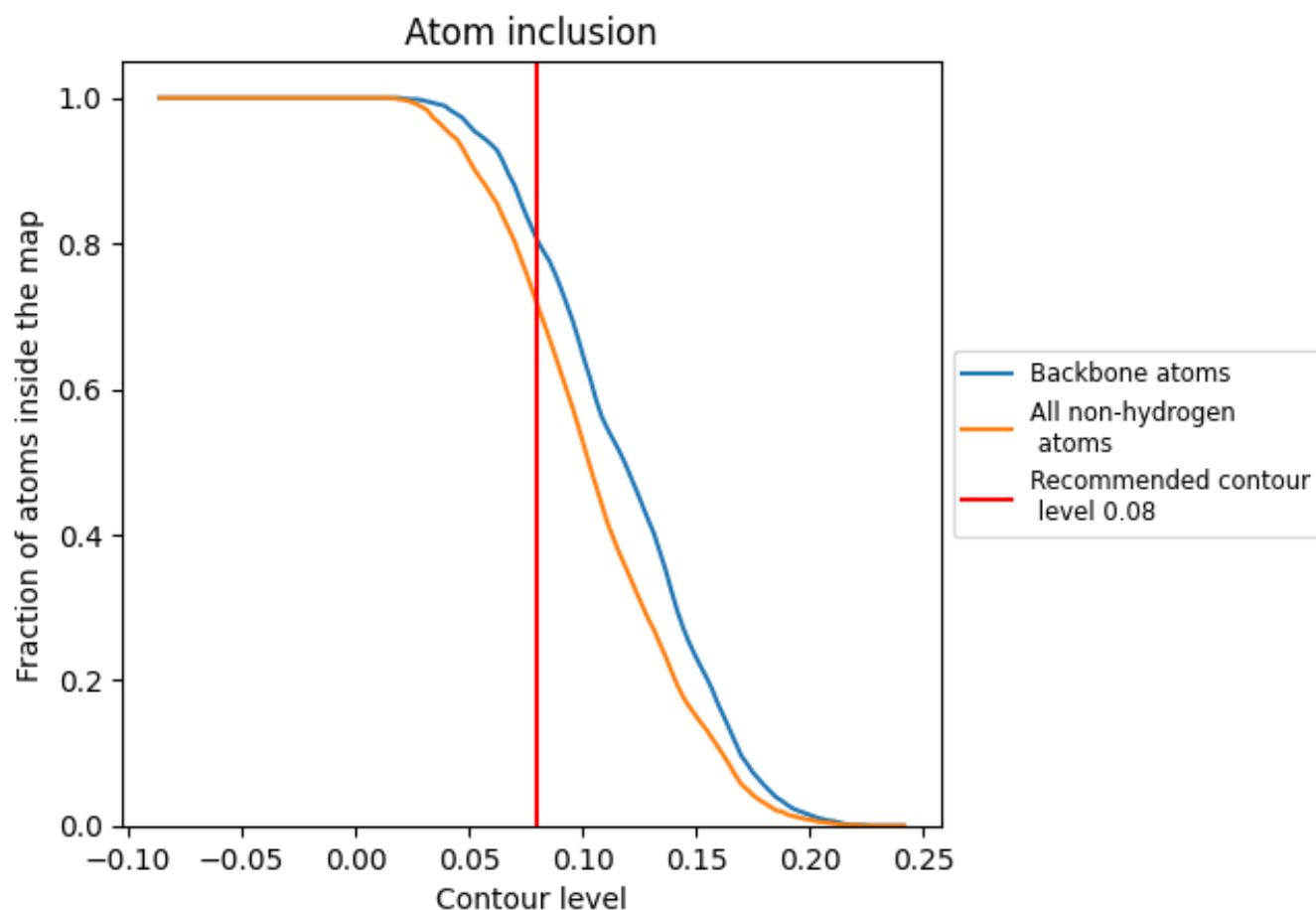
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.08).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7160	 0.4240
0	 0.7060	 0.4330
0A	 0.7150	 0.3950
1	 0.7380	 0.4330
1A	 0.7060	 0.4340
2	 0.7100	 0.4380
2A	 0.7240	 0.4270
3	 0.7200	 0.4280
3A	 0.7060	 0.4370
4	 0.7340	 0.4040
4A	 0.7100	 0.4290
5	 0.7060	 0.4400
5A	 0.7200	 0.3950
6	 0.7100	 0.3780
6A	 0.7010	 0.4370
7	 0.6960	 0.4310
7A	 0.7200	 0.3950
8	 0.7380	 0.4360
8A	 0.7010	 0.4340
9	 0.7100	 0.4380
9A	 0.7340	 0.4290
A	 0.7430	 0.4240
AA	 0.7240	 0.4270
AB	 0.6960	 0.4370
B	 0.7240	 0.4290
BA	 0.7380	 0.4020
BB	 0.7150	 0.4290
C	 0.7200	 0.4260
CA	 0.7200	 0.4460
CB	 0.7240	 0.4000
D	 0.7240	 0.4280
DA	 0.7060	 0.3800
DB	 0.7010	 0.4380
E	 0.7240	 0.4290
EA	 0.6960	 0.4300























































































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Chain	Atom inclusion	Q-score
EB	 0.7150	 0.3920
F	 0.7150	 0.4290
FA	 0.7380	 0.4390
FB	 0.6960	 0.4330
G	 0.7240	 0.4250
GA	 0.7200	 0.4380
GB	 0.7290	 0.4300
H	 0.7240	 0.4270
HA	 0.7060	 0.4280
HB	 0.7100	 0.4330
I	 0.7200	 0.4300
IA	 0.7340	 0.3950
IB	 0.7150	 0.4340
J	 0.7240	 0.4350
JA	 0.7100	 0.4390
JB	 0.7200	 0.4030
K	 0.7290	 0.4350
KA	 0.7010	 0.3840
KB	 0.6920	 0.4410
L	 0.7200	 0.4310
LA	 0.6960	 0.4300
LB	 0.7100	 0.3870
M	 0.7100	 0.4360
MA	 0.7430	 0.4320
MB	 0.7060	 0.4310
N	 0.7150	 0.4360
NA	 0.7100	 0.4420
NB	 0.7290	 0.4330
O	 0.7290	 0.4290
OA	 0.7240	 0.4240
OB	 0.7060	 0.4380
P	 0.7200	 0.4290
PA	 0.7240	 0.4000
PB	 0.7240	 0.4370
Q	 0.7290	 0.4280
QA	 0.7060	 0.4450
QB	 0.7150	 0.4040
R	 0.7240	 0.4270
RA	 0.7240	 0.3840
RB	 0.6960	 0.4410
S	 0.7290	 0.4280
SA	 0.7010	 0.4340





















































































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Chain	Atom inclusion	Q-score
SB	 0.7100	 0.3870
T	 0.7340	 0.4330
TA	 0.7380	 0.4300
TB	 0.7010	 0.4320
U	 0.7100	 0.4330
UA	 0.7100	 0.4390
UB	 0.7290	 0.4340
V	 0.7200	 0.3970
VA	 0.7150	 0.4260
VB	 0.7060	 0.4370
W	 0.7150	 0.4370
WA	 0.7290	 0.3940
WB	 0.7200	 0.4450
X	 0.7100	 0.3840
XA	 0.7100	 0.4390
XB	 0.7150	 0.4020
Y	 0.7240	 0.4300
YA	 0.7150	 0.3900
YB	 0.7150	 0.4420
Z	 0.7380	 0.4280
ZA	 0.7010	 0.4230
ZB	 0.7150	 0.3860
a	 0.7240	 0.4430
aA	 0.7340	 0.4250
aB	 0.7100	 0.4320
b	 0.7200	 0.4310
bA	 0.7150	 0.4410
bB	 0.7340	 0.4360
c	 0.7150	 0.4060
cA	 0.7200	 0.4210
cB	 0.7060	 0.4370
d	 0.7010	 0.4370
dA	 0.7240	 0.3940
dB	 0.7240	 0.4460
e	 0.7100	 0.3850
eA	 0.7060	 0.4410
eB	 0.7240	 0.4000
f	 0.7010	 0.4340
fA	 0.7150	 0.3910
fB	 0.7060	 0.4400
g	 0.7290	 0.4370
gA	 0.7060	 0.4310

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Chain	Atom inclusion	Q-score
gB	 0.7200	 0.3930
h	 0.7100	 0.4400
hA	 0.7240	 0.4250
hB	 0.6960	 0.4370
i	 0.7240	 0.4300
iA	 0.7100	 0.4390
iB	 0.7290	 0.4340
j	 0.7100	 0.4020
jA	 0.7200	 0.4260
jB	 0.7060	 0.4360
k	 0.7200	 0.4410
kA	 0.7340	 0.3970
l	 0.7060	 0.3840
lA	 0.7060	 0.4390
m	 0.7010	 0.4310
mA	 0.7100	 0.3900
n	 0.7290	 0.4370
nA	 0.6960	 0.4300
o	 0.7010	 0.4410
oA	 0.7380	 0.4270
p	 0.7150	 0.4320
pA	 0.7150	 0.4410
q	 0.7240	 0.4010
qA	 0.7150	 0.4300
r	 0.7010	 0.4400
rA	 0.7240	 0.3980
s	 0.7150	 0.3820
sA	 0.7010	 0.4400
t	 0.6960	 0.4330
tA	 0.7100	 0.3950
u	 0.7200	 0.4390
uA	 0.7100	 0.4290
v	 0.7150	 0.4410
vA	 0.7240	 0.4300
w	 0.7200	 0.4330
wA	 0.7100	 0.4360
x	 0.7290	 0.4040
xA	 0.7200	 0.4290
y	 0.7150	 0.4370
yA	 0.7240	 0.3970
z	 0.7100	 0.3820
zA	 0.6960	 0.4340