Full wwPDB EM Validation Report

Mar 27, 2026 – 04:41 AM UTC

PDB ID	:	9NCJ / pdb_00009ncj
EMDB ID	:	EMD-49258
Title	:	Coiled-coil bundlemer nanotube, R3K (15 proto-filaments)
Authors	:	Das, A.; Conticello, V.
Deposited on	:	2025-02-16
Resolution	:	3.93 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:

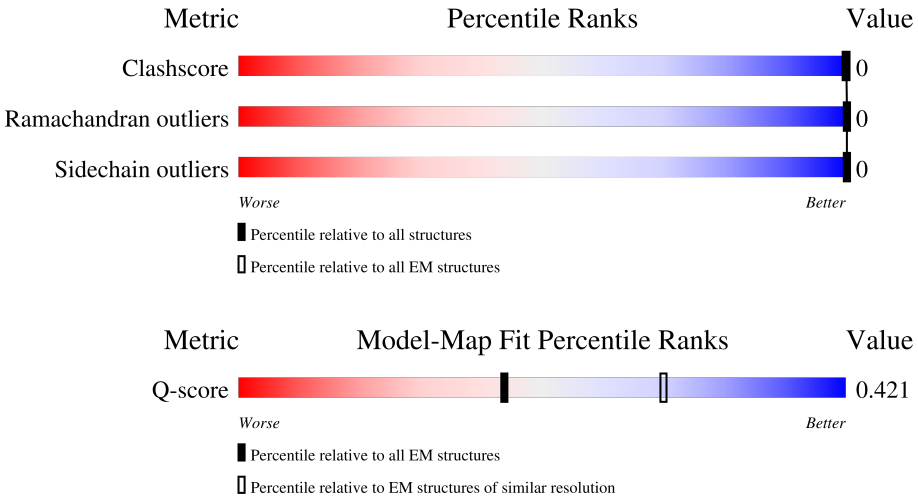
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.93 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	7811 (3.43 - 4.43)

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 <=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	13% 100%
1	0A	30	100%
1	1	30	10% 100%
1	1A	30	13% 100%

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Mol	Chain	Length	Quality of chain
1	2	30	7% 100%
1	2A	30	10% 100%
1	3	30	13% 100%
1	3A	30	7% 100%
1	4	30	7% 100%
1	4A	30	13% 100%
1	5	30	13% 100%
1	5A	30	7% 100%
1	6	30	100%
1	6A	30	13% 100%
1	7	30	13% 100%
1	7A	30	100%
1	8	30	10% 100%
1	8A	30	13% 100%
1	9	30	7% 100%
1	9A	30	13% 100%
1	A	30	7% 100%
1	AA	30	13% 100%
1	AB	30	7% 100%
1	B	30	7% 100%
1	BA	30	7% 100%
1	BB	30	10% 100%
1	C	30	7% 100%
1	CA	30	10% 100%
1	CB	30	7% 100%

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

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Mol	Chain	Length	Quality of chain
1	LA	30	13% 100%
1	LB	30	100%
1	M	30	7% 100%
1	MA	30	10% 100%
1	MB	30	13% 100%
1	N	30	7% 100%
1	NA	30	10% 100%
1	NB	30	13% 100%
1	O	30	7% 100%
1	OA	30	10% 100%
1	OB	30	10% 100%
1	P	30	7% 100%
1	PA	30	7% 100%
1	PB	30	10% 100%
1	Q	30	7% 100%
1	QA	30	10% 100%
1	QB	30	10% 100%
1	R	30	7% 100%
1	RA	30	100%
1	RB	30	10% 100%
1	S	30	13% 100%
1	SA	30	13% 100%
1	SB	30	100%
1	T	30	10% 100%
1	TA	30	10% 100%

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Mol	Chain	Length	Quality of chain
1	TB	30	13% 100%
1	U	30	10% 100%
1	UA	30	10% 100%
1	V	30	7% 100%
1	VA	30	10% 100%
1	W	30	13% 100%
1	WA	30	7% 100%
1	X	30	100%
1	XA	30	10% 100%
1	Y	30	13% 100%
1	YA	30	100%
1	Z	30	10% 100%
1	ZA	30	13% 100%
1	a	30	10% 100%
1	aA	30	13% 100%
1	b	30	13% 100%
1	bA	30	10% 100%
1	c	30	7% 100%
1	cA	30	13% 100%
1	d	30	10% 100%
1	dA	30	10% 100%
1	e	30	7% 100%
1	eA	30	13% 100%
1	f	30	17% 100%
1	fA	30	100%

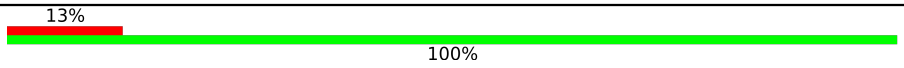
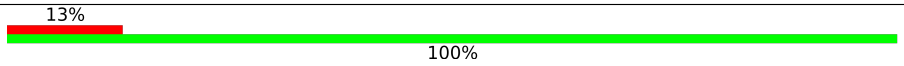
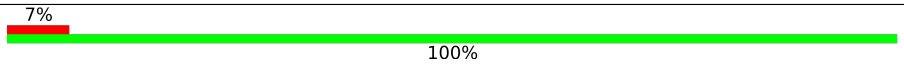
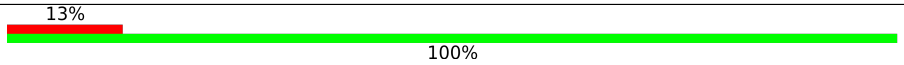
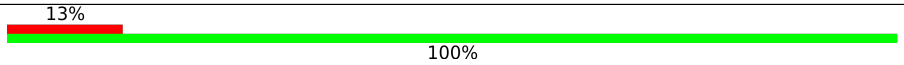
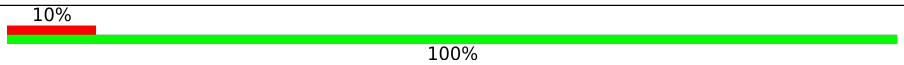
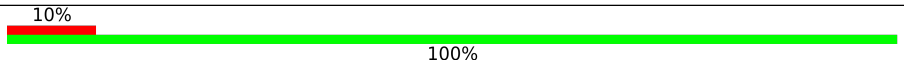
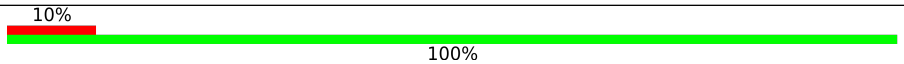
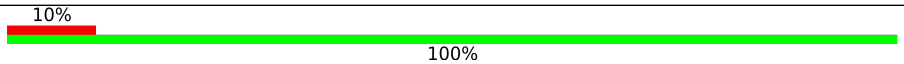
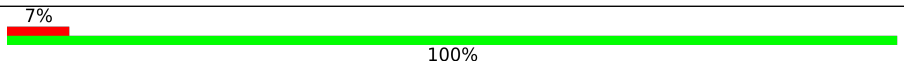
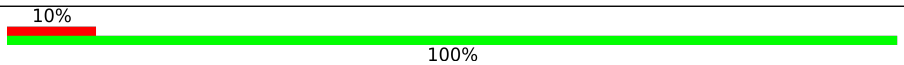
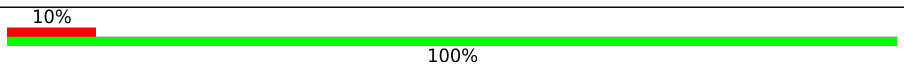
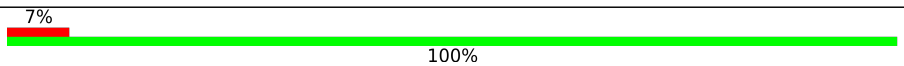
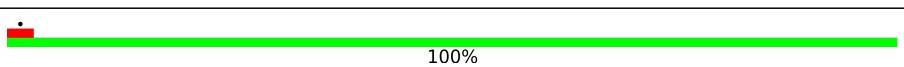
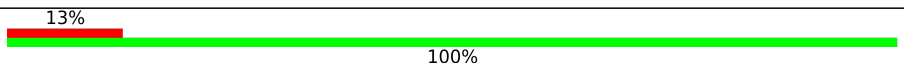
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Mol	Chain	Length	Quality of chain
1	g	30	10% 100%
1	gA	30	13% 100%
1	h	30	10% 100%
1	hA	30	10% 100%
1	i	30	10% 100%
1	iA	30	10% 100%
1	j	30	7% 100%
1	jA	30	10% 100%
1	k	30	10% 100%
1	kA	30	10% 100%
1	l	30	7% 100%
1	lA	30	10% 100%
1	m	30	13% 100%
1	mA	30	100%
1	n	30	13% 100%
1	nA	30	17% 100%
1	o	30	7% 100%
1	oA	30	10% 100%
1	p	30	13% 100%
1	pA	30	10% 100%
1	q	30	7% 100%
1	qA	30	13% 100%
1	r	30	10% 100%
1	rA	30	7% 100%
1	s	30	100%

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Mol	Chain	Length	Quality of chain
1	sA	30	
1	t	30	
1	tA	30	
1	u	30	
1	uA	30	
1	v	30	
1	vA	30	
1	w	30	
1	wA	30	
1	x	30	
1	xA	30	
1	y	30	
1	yA	30	
1	z	30	
1	zA	30	

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 63072 atoms, of which 31680 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 R3K nanotube.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	S	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	T	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	U	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	V	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	W	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	X	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	Y	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	B	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	Z	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	a	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	b	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	c	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	d	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	e	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	f	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	C	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	g	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	h	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	i	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	j	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	k	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	l	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	m	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	D	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	n	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	o	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	p	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	q	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	r	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	s	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	t	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	E	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	u	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	v	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	w	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	x	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	y	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	z	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	0	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	F	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	1	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	2	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	3	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	4	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	5	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	6	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	7	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	G	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	8	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	9	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	AA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	BA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	CA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	DA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	EA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	H	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	FA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	GA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	HA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	IA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	JA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	KA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	LA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	I	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	MA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	NA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	OA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	PA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	QA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	RA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	SA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	J	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	TA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	UA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	VA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	WA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	XA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	YA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	ZA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	K	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	aA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	bA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	cA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	dA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	eA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	fA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	gA	30	Total	C	H	N	O	S	0	1
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1	L	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	hA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	iA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	jA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	kA	30	Total	C	H	N	O	S	0	1
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1	mA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	nA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	M	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	oA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	pA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	qA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	rA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	sA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	tA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	uA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	N	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	vA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	wA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	xA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	yA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	zA	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	0A	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	1A	30	Total	C	H	N	O	S	0	1
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1	O	30	Total	C	H	N	O	S	0	1
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1	6A	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	7A	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	8A	30	Total	C	H	N	O	S	0	1
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1	P	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	9A	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		

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Mol	Chain	Residues	Atoms						AltConf	Trace
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			438	136	220	38	41	3		
1	BB	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	CB	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	DB	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	EB	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	FB	30	Total	C	H	N	O	S	0	1
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1	Q	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	GB	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	HB	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	IB	30	Total	C	H	N	O	S	0	1
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1	JB	30	Total	C	H	N	O	S	0	1
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1	MB	30	Total	C	H	N	O	S	0	1
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1	NB	30	Total	C	H	N	O	S	0	1
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1	OB	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	PB	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	QB	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	RB	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		
1	SB	30	Total	C	H	N	O	S	0	1
			438	136	220	38	41	3		

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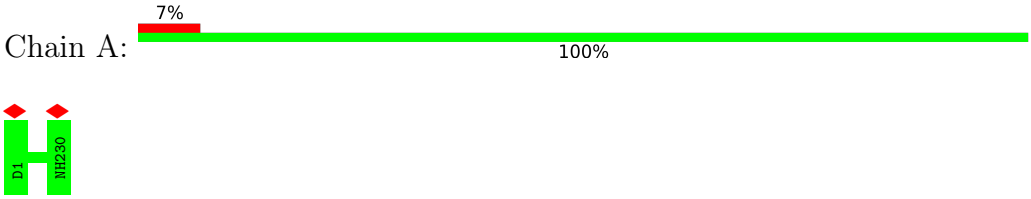
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Mol	Chain	Residues	Atoms						AltConf	Trace
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			438	136	220	38	41	3		

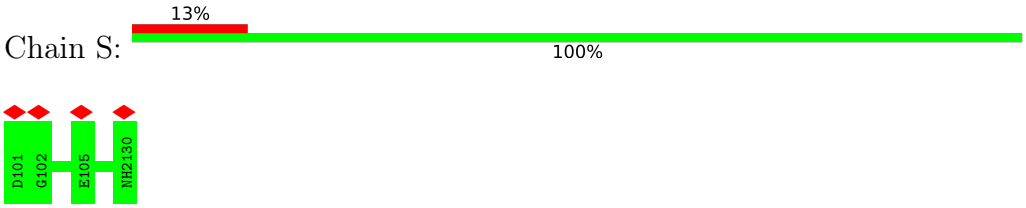
3 Residue-property plots (i)

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.

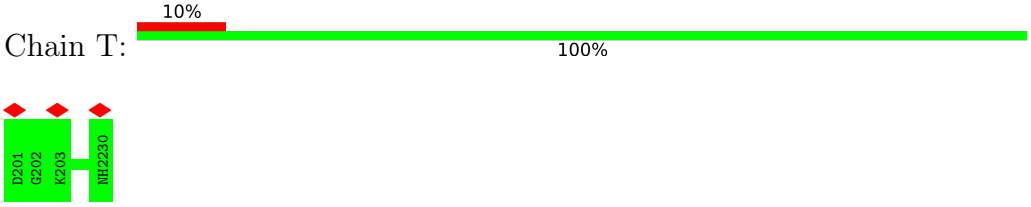
• Molecule 1: R3K nanotube



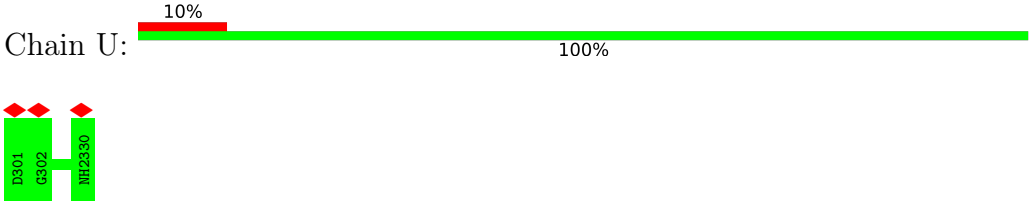
• Molecule 1: R3K nanotube



• Molecule 1: R3K nanotube



• Molecule 1: R3K nanotube



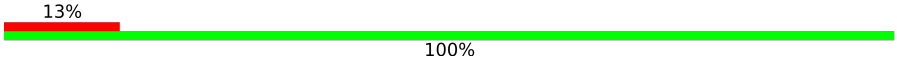
• Molecule 1: R3K nanotube

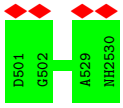




• Molecule 1: R3K nanotube

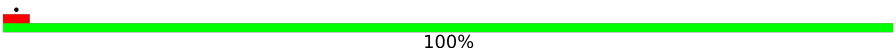
Chain W:





• Molecule 1: R3K nanotube

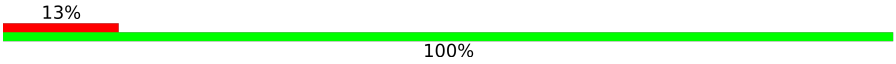
Chain X:

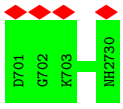




• Molecule 1: R3K nanotube

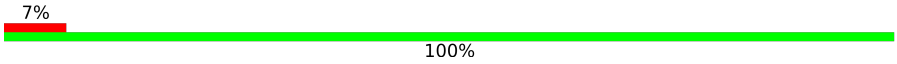
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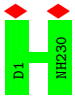




• Molecule 1: R3K nanotube

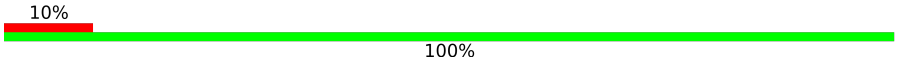
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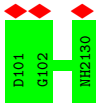




• Molecule 1: R3K nanotube

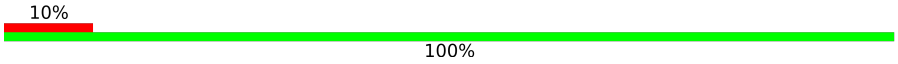
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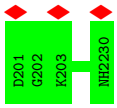




• Molecule 1: R3K nanotube

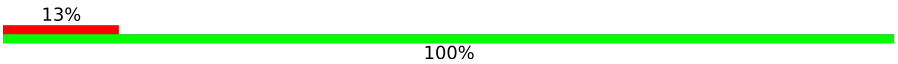
Chain a:

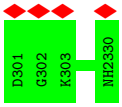




• Molecule 1: R3K nanotube

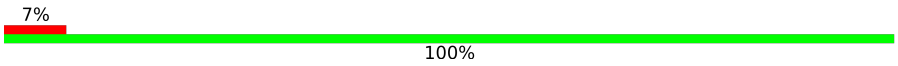
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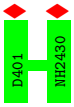




• Molecule 1: R3K nanotube

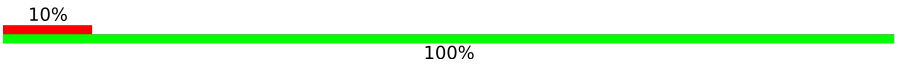
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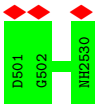




• Molecule 1: R3K nanotube

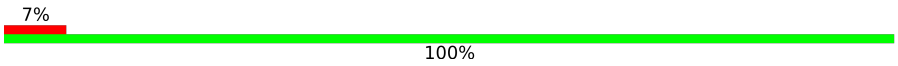
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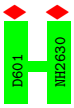




• Molecule 1: R3K nanotube

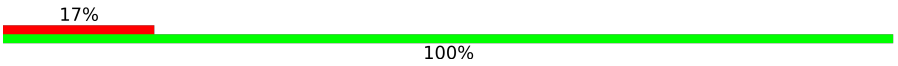
Chain e:

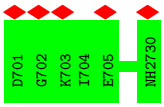




• Molecule 1: R3K nanotube

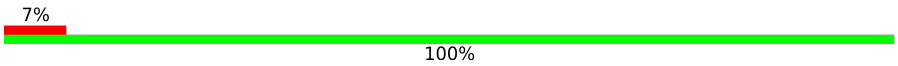
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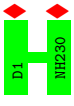




• Molecule 1: R3K nanotube

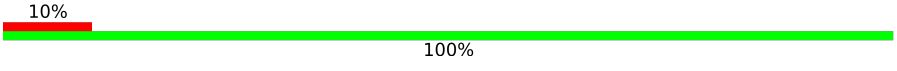
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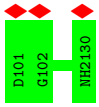




• Molecule 1: R3K nanotube

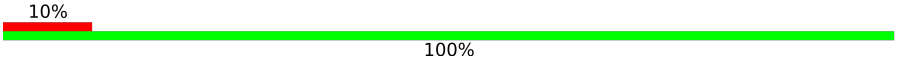
Chain g:

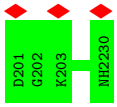




• Molecule 1: R3K nanotube

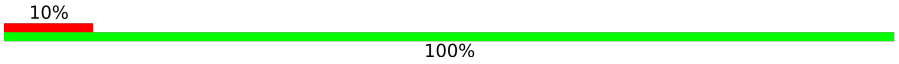
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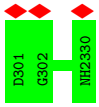




• Molecule 1: R3K nanotube

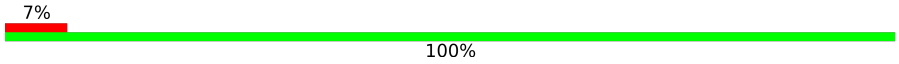
Chain i:





• Molecule 1: R3K nanotube

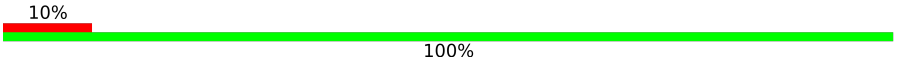
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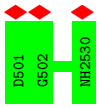




• Molecule 1: R3K nanotube

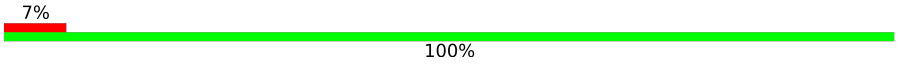
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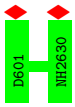




• Molecule 1: R3K nanotube

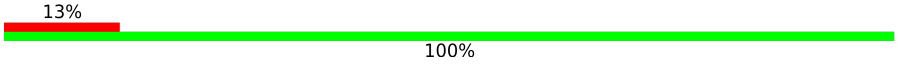
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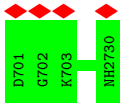




• Molecule 1: R3K nanotube

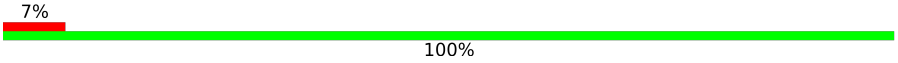
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• Molecule 1: R3K nanotube

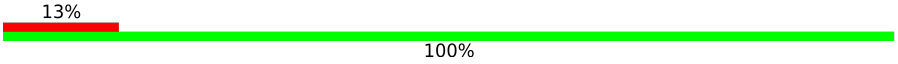
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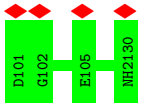




• Molecule 1: R3K nanotube

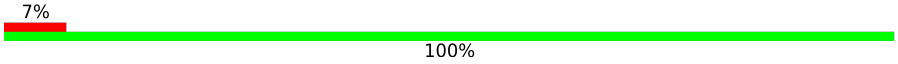
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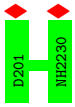




• Molecule 1: R3K nanotube

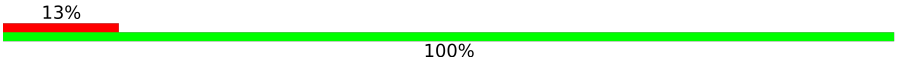
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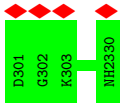




• Molecule 1: R3K nanotube

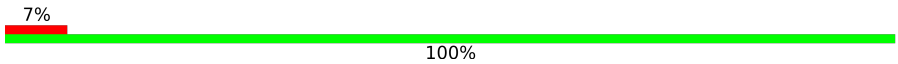
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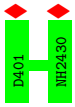




• Molecule 1: R3K nanotube

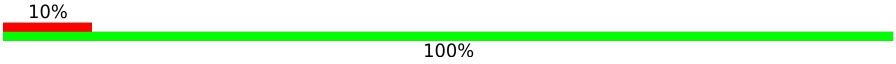
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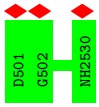




• Molecule 1: R3K nanotube

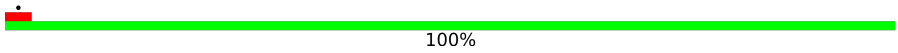
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• Molecule 1: R3K nanotube

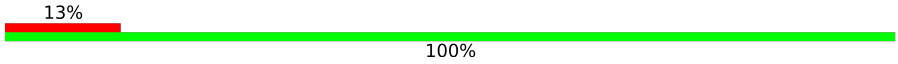
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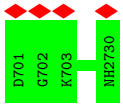




• Molecule 1: R3K nanotube

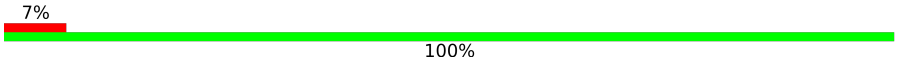
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• Molecule 1: R3K nanotube

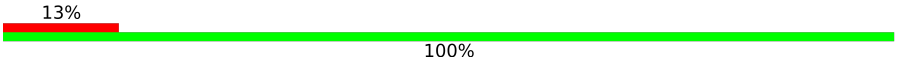
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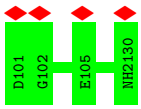




• Molecule 1: R3K nanotube

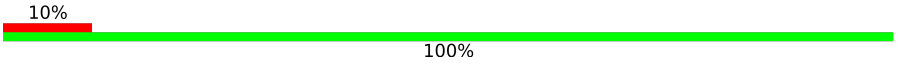
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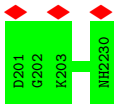




• Molecule 1: R3K nanotube

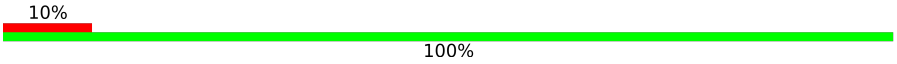
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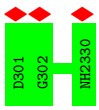




• Molecule 1: R3K nanotube

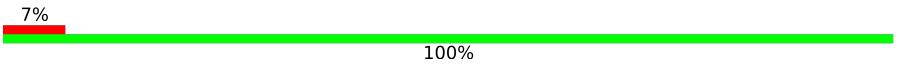
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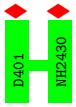




• Molecule 1: R3K nanotube

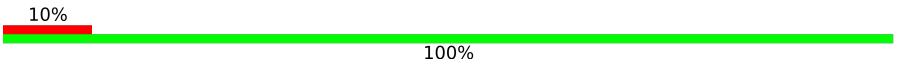
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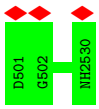




• Molecule 1: R3K nanotube

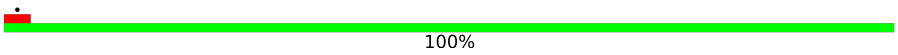
Chain y:





• Molecule 1: R3K nanotube

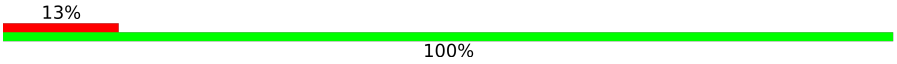
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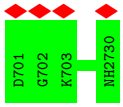




• Molecule 1: R3K nanotube

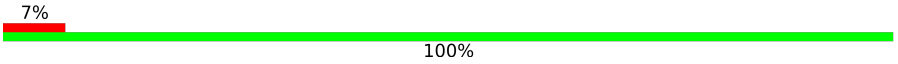
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• Molecule 1: R3K nanotube

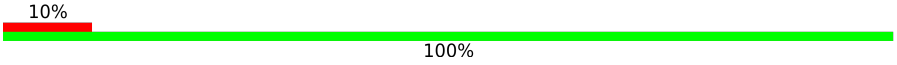
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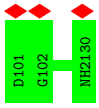




• Molecule 1: R3K nanotube

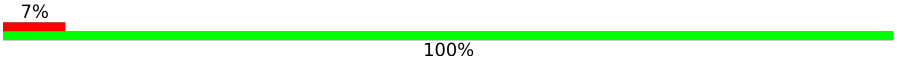
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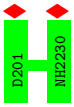




• Molecule 1: R3K nanotube

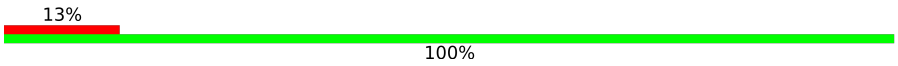
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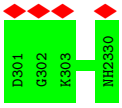




• Molecule 1: R3K nanotube

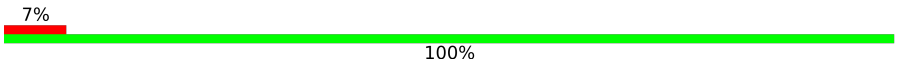
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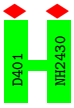




• Molecule 1: R3K nanotube

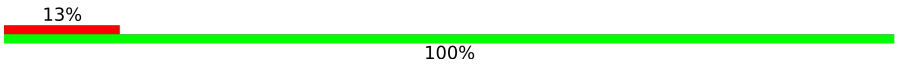
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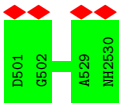




• Molecule 1: R3K nanotube

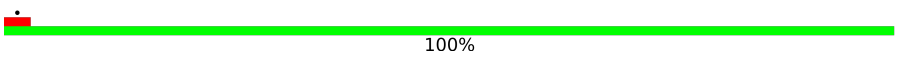
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• Molecule 1: R3K nanotube

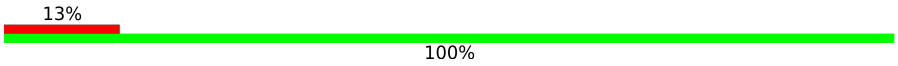
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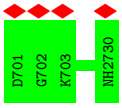




• Molecule 1: R3K nanotube

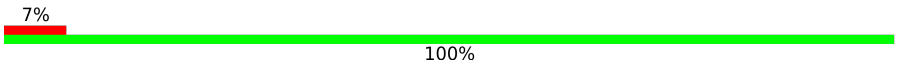
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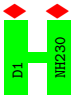




• Molecule 1: R3K nanotube

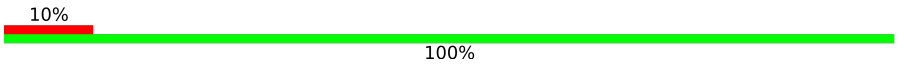
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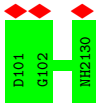




• Molecule 1: R3K nanotube

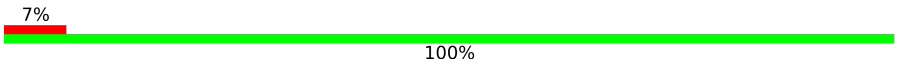
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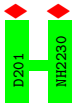




• Molecule 1: R3K nanotube

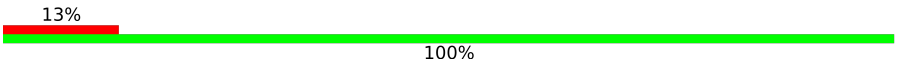
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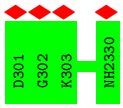




• Molecule 1: R3K nanotube

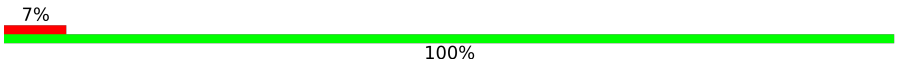
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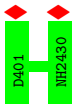




• Molecule 1: R3K nanotube

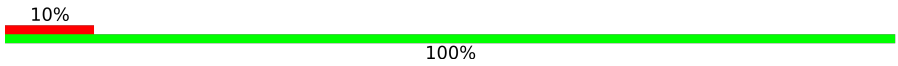
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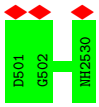




• Molecule 1: R3K nanotube

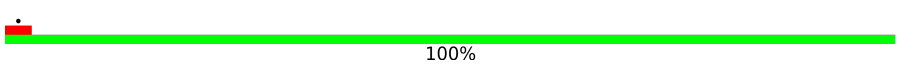
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• Molecule 1: R3K nanotube

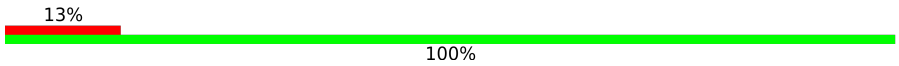
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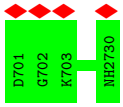




• Molecule 1: R3K nanotube

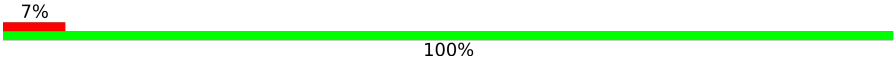
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• Molecule 1: R3K nanotube

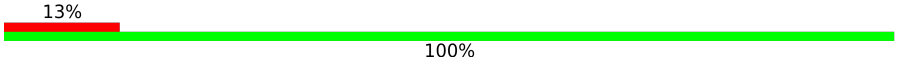
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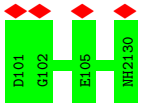




• Molecule 1: R3K nanotube

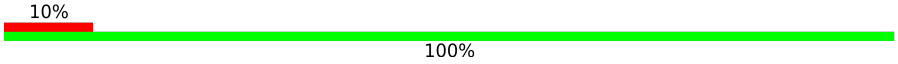
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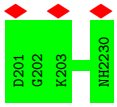




• Molecule 1: R3K nanotube

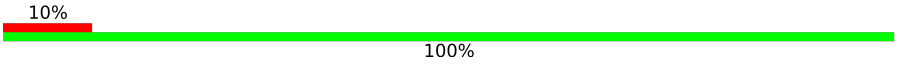
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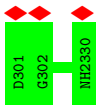




• Molecule 1: R3K nanotube

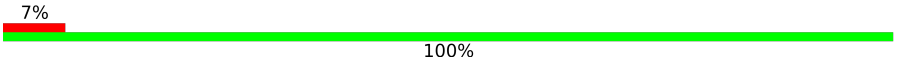
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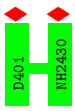




• Molecule 1: R3K nanotube

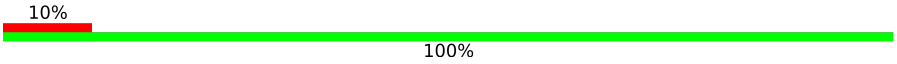
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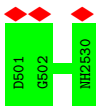




• Molecule 1: R3K nanotube

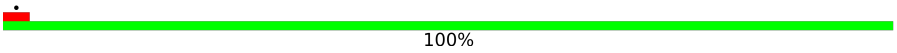
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• Molecule 1: R3K nanotube

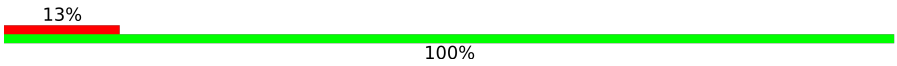
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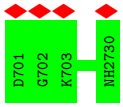




• Molecule 1: R3K nanotube

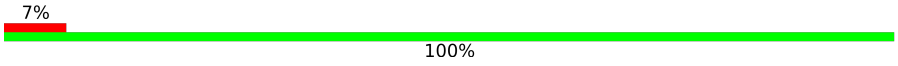
Chain LA:





• Molecule 1: R3K nanotube

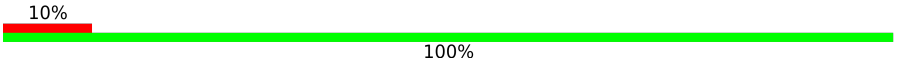
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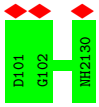




• Molecule 1: R3K nanotube

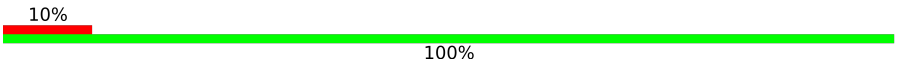
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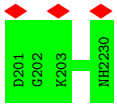




• Molecule 1: R3K nanotube

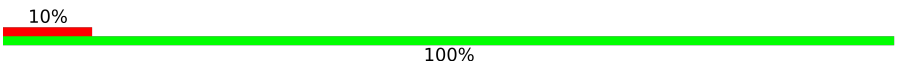
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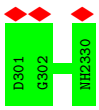




• Molecule 1: R3K nanotube

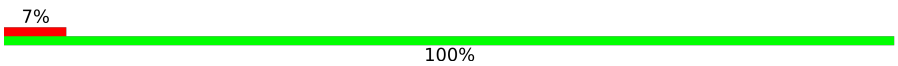
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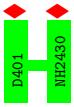




• Molecule 1: R3K nanotube

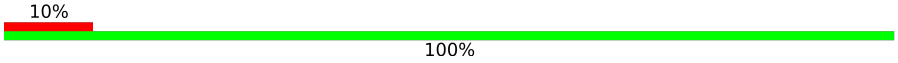
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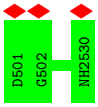




• Molecule 1: R3K nanotube

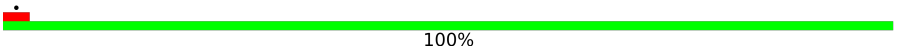
Chain QA:





• Molecule 1: R3K nanotube

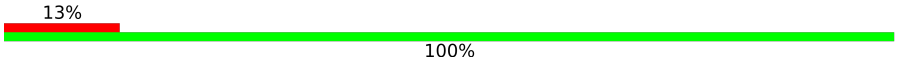
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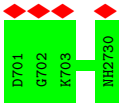




• Molecule 1: R3K nanotube

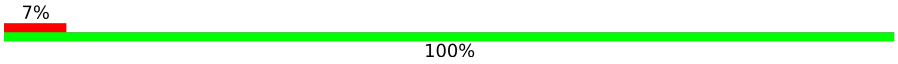
Chain SA:





• Molecule 1: R3K nanotube

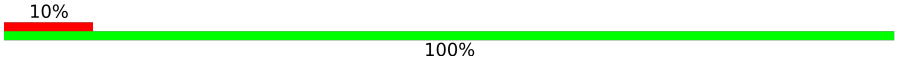
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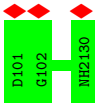




• Molecule 1: R3K nanotube

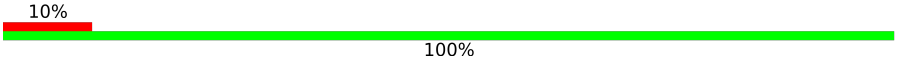
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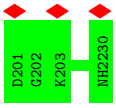




• Molecule 1: R3K nanotube

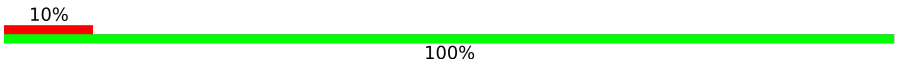
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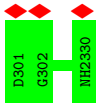




• Molecule 1: R3K nanotube

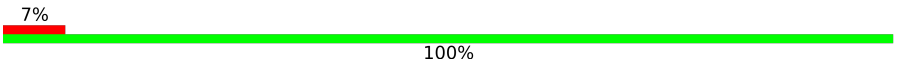
Chain VA:





• Molecule 1: R3K nanotube

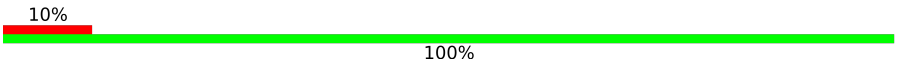
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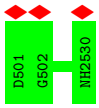




• Molecule 1: R3K nanotube

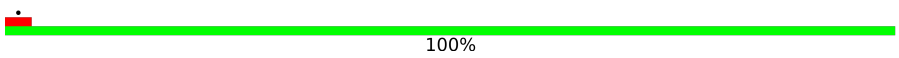
Chain XA:





• Molecule 1: R3K nanotube

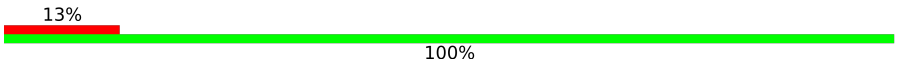
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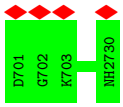




• Molecule 1: R3K nanotube

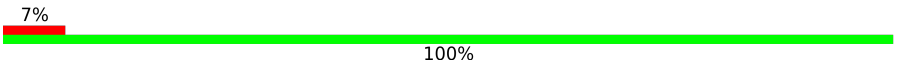
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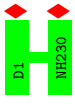




• Molecule 1: R3K nanotube

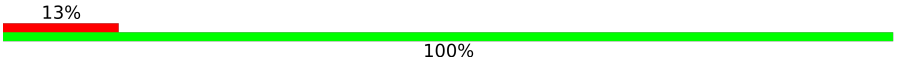
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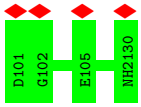




• Molecule 1: R3K nanotube

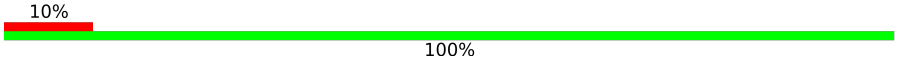
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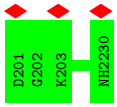




• Molecule 1: R3K nanotube

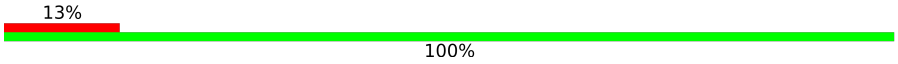
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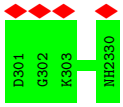




• Molecule 1: R3K nanotube

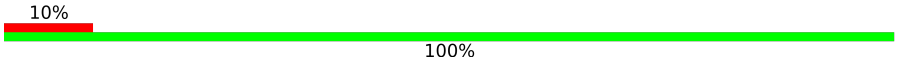
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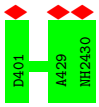




• Molecule 1: R3K nanotube

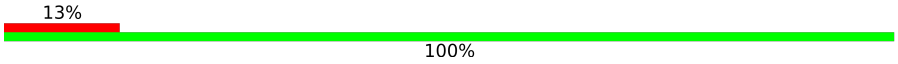
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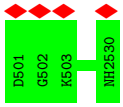




• Molecule 1: R3K nanotube

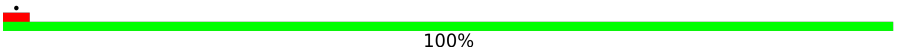
Chain eA:





• Molecule 1: R3K nanotube

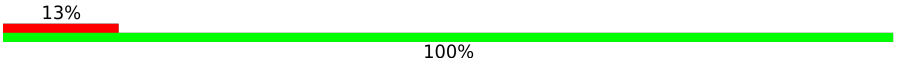
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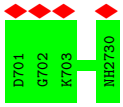




• Molecule 1: R3K nanotube

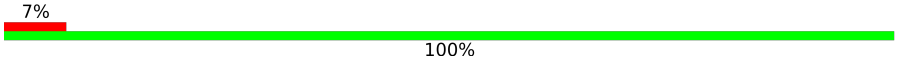
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• Molecule 1: R3K nanotube

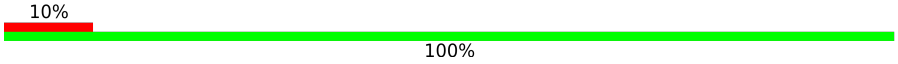
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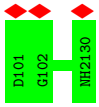




• Molecule 1: R3K nanotube

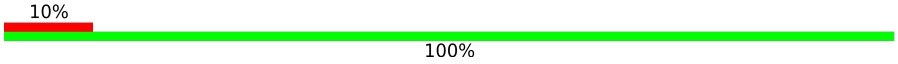
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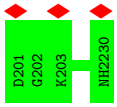




• Molecule 1: R3K nanotube

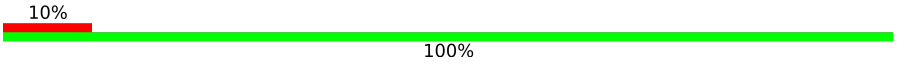
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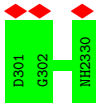




• Molecule 1: R3K nanotube

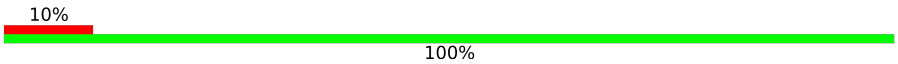
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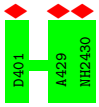




• Molecule 1: R3K nanotube

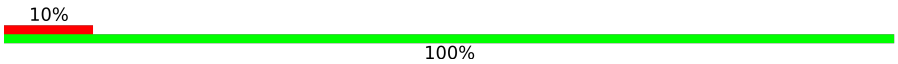
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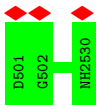




• Molecule 1: R3K nanotube

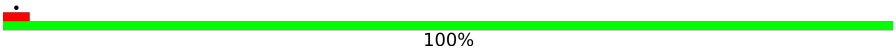
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• Molecule 1: R3K nanotube

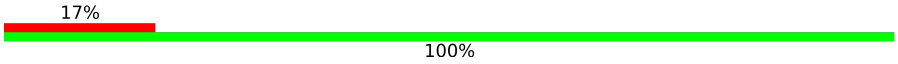
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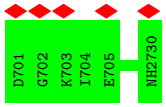




• Molecule 1: R3K nanotube

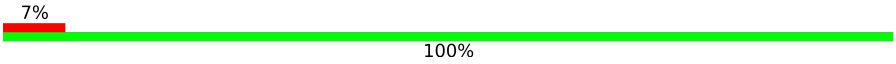
Chain nA:





• Molecule 1: R3K nanotube

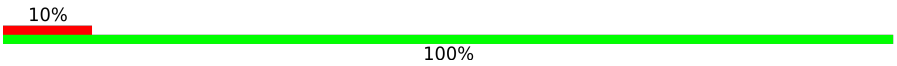
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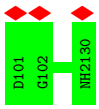




• Molecule 1: R3K nanotube

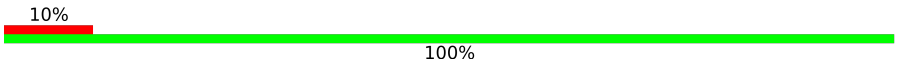
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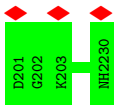




• Molecule 1: R3K nanotube

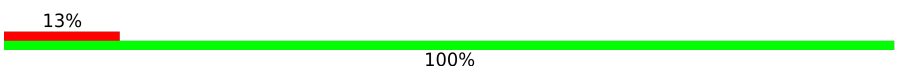
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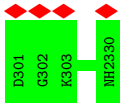




• Molecule 1: R3K nanotube

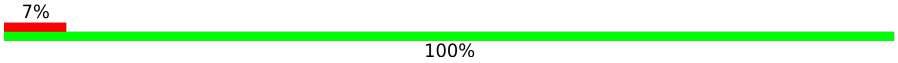
Chain qA:





• Molecule 1: R3K nanotube

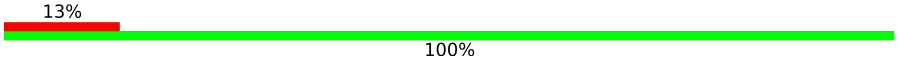
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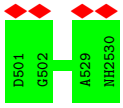




• Molecule 1: R3K nanotube

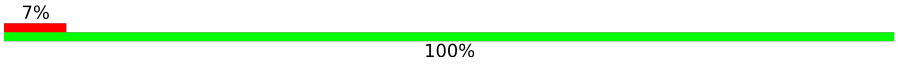
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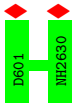




• Molecule 1: R3K nanotube

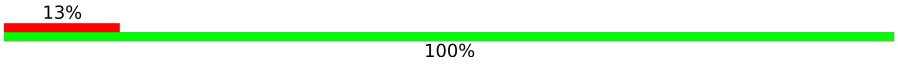
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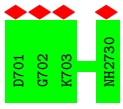




• Molecule 1: R3K nanotube

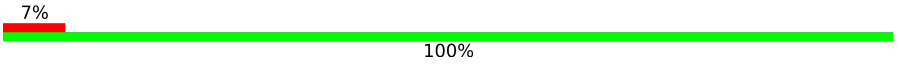
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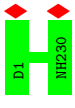




• Molecule 1: R3K nanotube

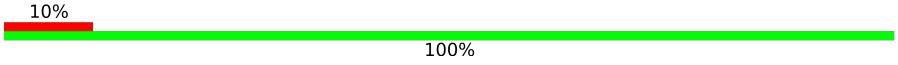
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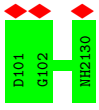




• Molecule 1: R3K nanotube

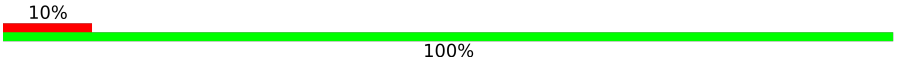
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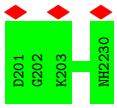




• Molecule 1: R3K nanotube

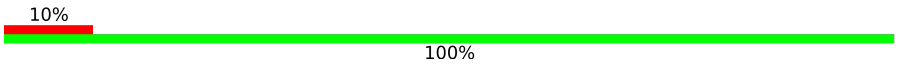
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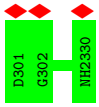




• Molecule 1: R3K nanotube

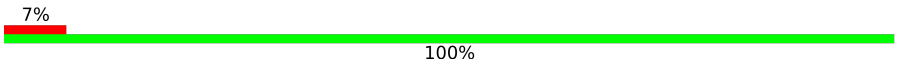
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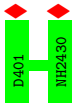




• Molecule 1: R3K nanotube

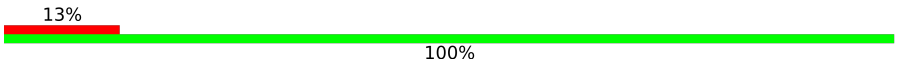
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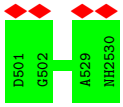




• Molecule 1: R3K nanotube

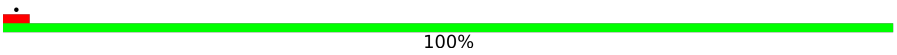
Chain zA:





• Molecule 1: R3K nanotube

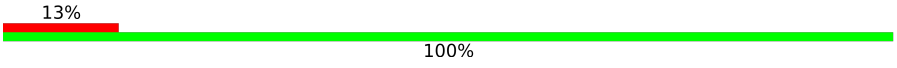
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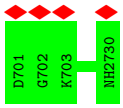




• Molecule 1: R3K nanotube

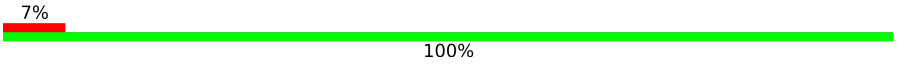
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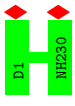




• Molecule 1: R3K nanotube

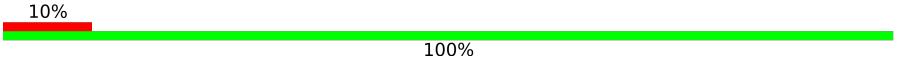
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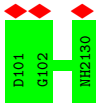




• Molecule 1: R3K nanotube

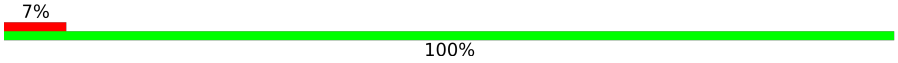
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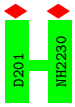




• Molecule 1: R3K nanotube

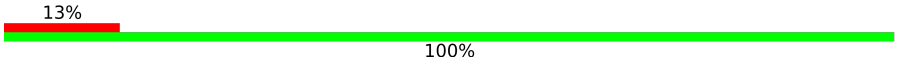
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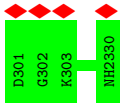




• Molecule 1: R3K nanotube

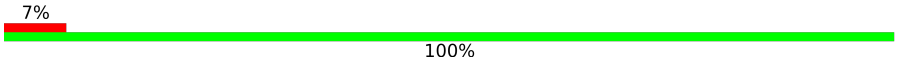
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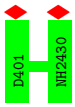




• Molecule 1: R3K nanotube

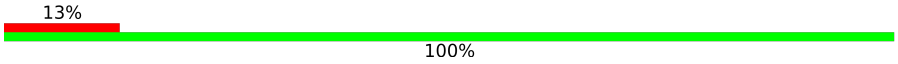
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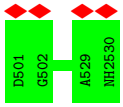




• Molecule 1: R3K nanotube

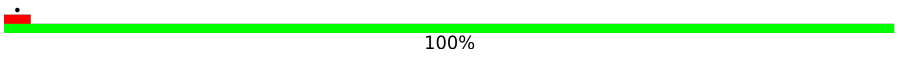
Chain 6A:





• Molecule 1: R3K nanotube

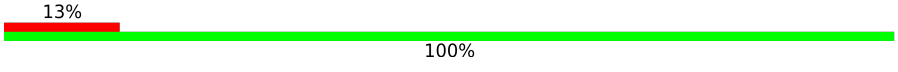
Chain 7A:

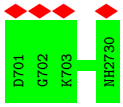




• Molecule 1: R3K nanotube

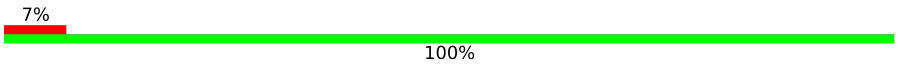
Chain 8A:





• Molecule 1: R3K nanotube

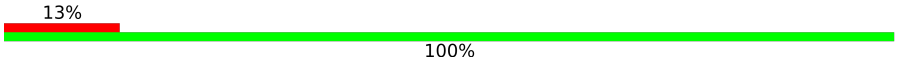
Chain P:

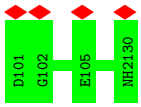




• Molecule 1: R3K nanotube

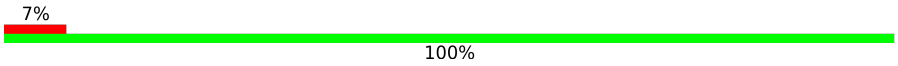
Chain 9A:

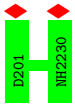




• Molecule 1: R3K nanotube

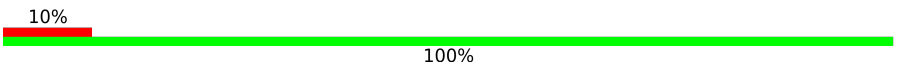
Chain AB:

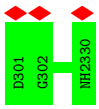




• Molecule 1: R3K nanotube

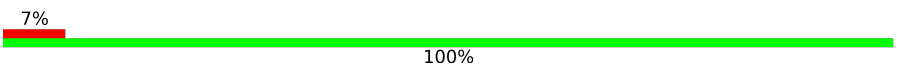
Chain BB:





• Molecule 1: R3K nanotube

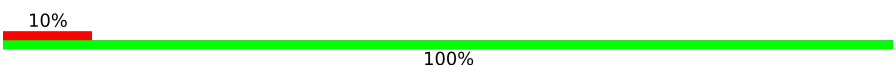
Chain CB:

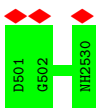




• Molecule 1: R3K nanotube

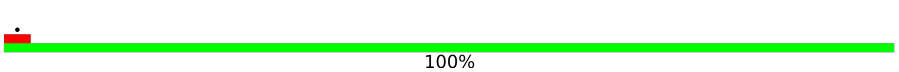
Chain DB:





• Molecule 1: R3K nanotube

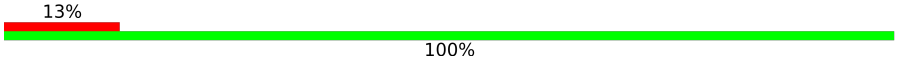
Chain EB:

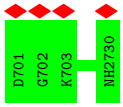




• Molecule 1: R3K nanotube

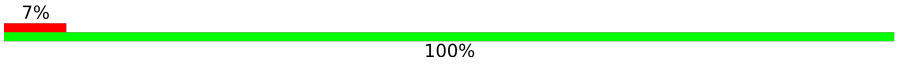
Chain FB:





• Molecule 1: R3K nanotube

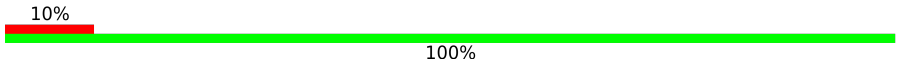
Chain Q:

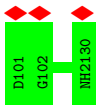




• Molecule 1: R3K nanotube

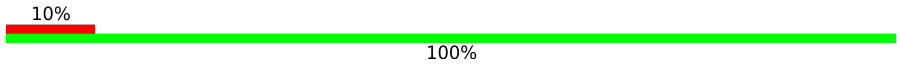
Chain GB:

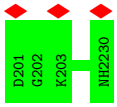




• Molecule 1: R3K nanotube

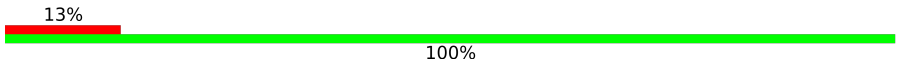
Chain HB:

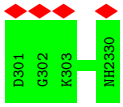




• Molecule 1: R3K nanotube

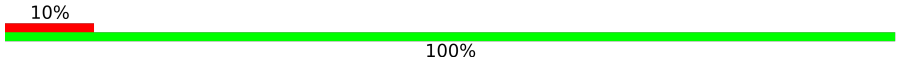
Chain IB:

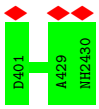




• Molecule 1: R3K nanotube

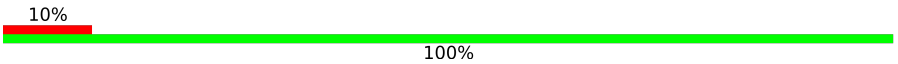
Chain JB:

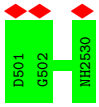




• Molecule 1: R3K nanotube

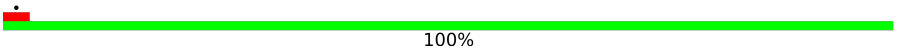
Chain KB:





• Molecule 1: R3K nanotube

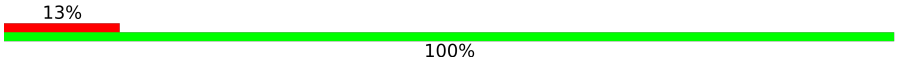
Chain LB:

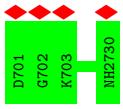




• Molecule 1: R3K nanotube

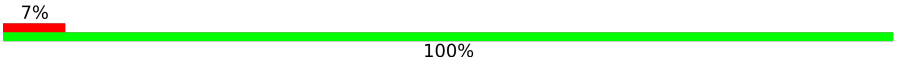
Chain MB:

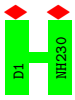




• Molecule 1: R3K nanotube

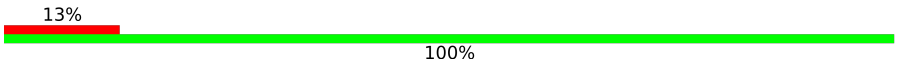
Chain R:

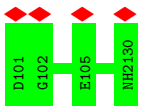




• Molecule 1: R3K nanotube

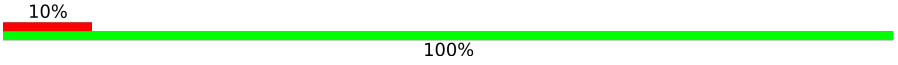
Chain NB:

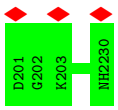




• Molecule 1: R3K nanotube

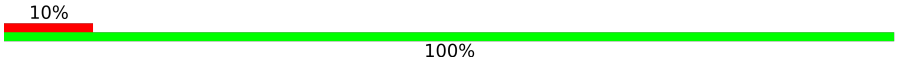
Chain OB:

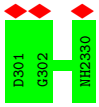




• Molecule 1: R3K nanotube

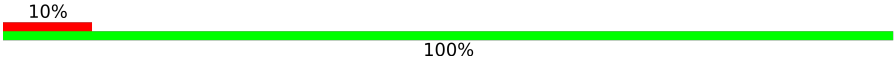
Chain PB:

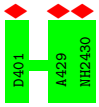




• Molecule 1: R3K nanotube

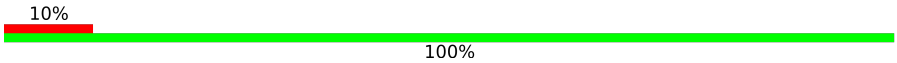
Chain QB:

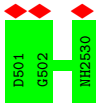




• Molecule 1: R3K nanotube

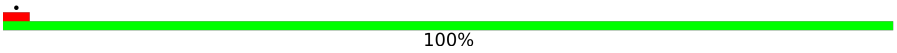
Chain RB:





• Molecule 1: R3K nanotube

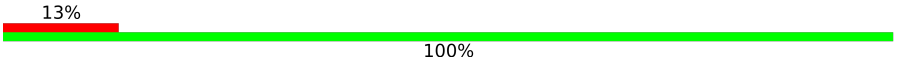
Chain SB:

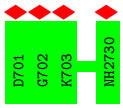




• Molecule 1: R3K nanotube

Chain TB:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=24.347°, rise=4.441 Å, axial sym=C1	Depositor
Number of segments used	66965	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 ($e^-/Å^2$)	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	1.282	Depositor
Minimum map value	-0.604	Depositor
Average map value	0.057	Depositor
Map value standard deviation	0.154	Depositor
Recommended contour level	0.374	Depositor
Map size (Å)	201.04681, 201.04681, 644.35925	wwPDB
Map dimensions	239, 239, 766	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84120005, 0.84120005, 0.84120005	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	0.78	0/219	0.97	0/290
1	0A	0.78	0/219	1.00	0/290
1	1	0.78	0/219	0.96	0/290
1	1A	0.78	0/219	0.97	0/290
1	2	0.79	0/219	0.99	0/290
1	2A	0.77	0/219	0.96	0/290
1	3	0.80	0/219	0.99	0/290
1	3A	0.79	0/219	1.00	0/290
1	4	0.81	0/219	1.03	0/290
1	4A	0.80	0/219	1.00	0/290
1	5	0.79	0/219	0.98	0/290
1	5A	0.81	0/219	1.03	0/290
1	6	0.80	0/219	1.11	0/290
1	6A	0.79	0/219	0.97	0/290
1	7	0.78	0/219	0.97	0/290
1	7A	0.78	0/219	1.00	0/290
1	8	0.78	0/219	0.96	0/290
1	8A	0.78	0/219	0.97	0/290
1	9	0.80	0/219	1.00	0/290
1	9A	0.79	0/219	1.05	0/290
1	A	0.79	0/219	0.97	0/290
1	AA	0.80	0/219	0.98	0/290
1	AB	0.78	0/219	1.00	0/290
1	B	0.80	0/219	0.99	0/290
1	BA	0.80	0/219	0.99	0/290
1	BB	0.79	0/219	0.99	0/290
1	C	0.79	0/219	0.97	0/290
1	CA	0.79	0/219	0.98	0/290
1	CB	0.81	0/219	1.02	0/290
1	D	0.79	0/219	0.97	0/290
1	DA	0.78	0/219	1.00	0/290
1	DB	0.77	0/219	1.04	0/290

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	E	0.80	0/219	0.99	0/290
1	EA	0.78	0/219	0.99	0/290
1	EB	0.77	0/219	1.00	0/290
1	F	0.78	0/219	0.97	0/290
1	FA	0.78	0/219	0.97	0/290
1	FB	0.79	0/219	0.99	0/290
1	G	0.79	0/219	0.97	0/290
1	GA	0.80	0/219	1.00	0/290
1	GB	0.78	0/219	0.96	0/290
1	H	0.80	0/219	0.96	0/290
1	HA	0.79	0/219	0.99	0/290
1	HB	0.78	0/219	0.99	0/290
1	I	0.79	0/219	0.96	0/290
1	IA	0.82	0/219	1.08	0/290
1	IB	0.81	0/219	1.00	0/290
1	J	0.79	0/219	0.97	0/290
1	JA	0.79	0/219	0.98	0/290
1	JB	0.82	0/219	1.07	0/290
1	K	0.79	0/219	0.96	0/290
1	KA	0.78	0/219	1.00	0/290
1	KB	0.78	0/219	1.05	0/290
1	L	0.81	0/219	1.00	0/290
1	LA	0.80	0/219	0.97	0/290
1	LB	0.78	0/219	0.99	0/290
1	M	0.78	0/219	0.97	0/290
1	MA	0.78	0/219	0.98	0/290
1	MB	0.79	0/219	1.00	0/290
1	N	0.80	0/219	1.01	0/290
1	NA	0.80	0/219	0.99	0/290
1	NB	0.79	0/219	0.97	0/290
1	O	0.78	0/219	0.97	0/290
1	OA	0.80	0/219	0.99	0/290
1	OB	0.81	0/219	0.98	0/290
1	P	0.79	0/219	0.99	0/290
1	PA	0.80	0/219	1.00	0/290
1	PB	0.79	0/219	1.00	0/290
1	Q	0.81	0/219	1.01	0/290
1	QA	0.79	0/219	0.98	0/290
1	QB	0.83	0/219	1.06	0/290
1	R	0.80	0/219	1.01	0/290
1	RA	0.77	0/219	1.01	0/290
1	RB	0.77	0/219	1.04	0/290
1	S	0.78	0/219	1.03	0/290

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	SA	0.79	0/219	0.95	0/290
1	SB	0.78	0/219	0.97	0/290
1	T	0.79	0/219	1.02	0/290
1	TA	0.79	0/219	0.99	0/290
1	TB	0.78	0/219	0.99	0/290
1	U	0.79	0/219	0.98	0/290
1	UA	0.79	0/219	0.98	0/290
1	V	0.80	0/219	1.02	0/290
1	VA	0.80	0/219	0.99	0/290
1	W	0.80	0/219	1.00	0/290
1	WA	0.81	0/219	1.13	0/290
1	X	0.79	0/219	1.02	0/290
1	XA	0.79	0/219	0.97	0/290
1	Y	0.79	0/219	0.96	0/290
1	YA	0.80	0/219	1.02	0/290
1	Z	0.79	0/219	0.95	0/290
1	ZA	0.78	0/219	0.96	0/290
1	a	0.81	0/219	0.96	0/290
1	aA	0.78	0/219	0.98	0/290
1	b	0.80	0/219	0.96	0/290
1	bA	0.80	0/219	0.99	0/290
1	c	0.81	0/219	1.01	0/290
1	cA	0.79	0/219	0.99	0/290
1	d	0.81	0/219	0.98	0/290
1	dA	0.80	0/219	0.99	0/290
1	e	0.78	0/219	1.02	0/290
1	eA	0.80	0/219	0.98	0/290
1	f	0.80	0/219	0.93	0/290
1	fA	0.80	0/219	1.01	0/290
1	g	0.78	0/219	0.97	0/290
1	gA	0.79	0/219	0.96	0/290
1	h	0.79	0/219	1.04	0/290
1	hA	0.78	0/219	0.99	0/290
1	i	0.79	0/219	1.01	0/290
1	iA	0.79	0/219	0.99	0/290
1	j	0.81	0/219	1.02	0/290
1	jA	0.80	0/219	0.99	0/290
1	k	0.80	0/219	0.98	0/290
1	kA	0.81	0/219	0.99	0/290
1	l	0.77	0/219	1.03	0/290
1	lA	0.78	0/219	0.99	0/290
1	m	0.79	0/219	0.96	0/290
1	mA	0.78	0/219	1.00	0/290

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	n	0.78	0/219	0.99	0/290
1	nA	0.78	0/219	0.97	0/290
1	o	0.78	0/219	0.99	0/290
1	oA	0.78	0/219	0.97	0/290
1	p	0.80	0/219	0.99	0/290
1	pA	0.79	0/219	0.99	0/290
1	q	0.80	0/219	0.99	0/290
1	qA	0.80	0/219	0.99	0/290
1	r	0.79	0/219	0.96	0/290
1	rA	0.80	0/219	1.02	0/290
1	s	0.77	0/219	1.01	0/290
1	sA	0.79	0/219	0.97	0/290
1	t	0.79	0/219	0.98	0/290
1	tA	0.78	0/219	1.00	0/290
1	u	0.79	0/219	1.01	0/290
1	uA	0.79	0/219	0.96	0/290
1	v	0.80	0/219	0.99	0/290
1	vA	0.78	0/219	0.98	0/290
1	w	0.80	0/219	0.99	0/290
1	wA	0.79	0/219	0.99	0/290
1	x	0.81	0/219	1.00	0/290
1	xA	0.80	0/219	0.99	0/290
1	y	0.79	0/219	0.96	0/290
1	yA	0.80	0/219	0.99	0/290
1	z	0.79	0/219	1.01	0/290
1	zA	0.79	0/219	0.96	0/290
All	All	0.79	0/31536	0.99	0/41760

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	220	215	0	0
1	0A	218	220	215	0	0
1	1	218	220	215	0	0
1	1A	218	220	215	0	0
1	2	218	220	215	0	0
1	2A	218	220	215	0	0
1	3	218	220	215	0	0
1	3A	218	220	215	0	0
1	4	218	220	215	0	0
1	4A	218	220	215	0	0
1	5	218	220	215	0	0
1	5A	218	220	215	0	0
1	6	218	220	215	0	0
1	6A	218	220	215	0	0
1	7	218	220	215	0	0
1	7A	218	220	215	0	0
1	8	218	220	215	0	0
1	8A	218	220	215	0	0
1	9	218	220	215	0	0
1	9A	218	220	215	0	0
1	A	218	220	218	0	0
1	AA	218	220	215	0	0
1	AB	218	220	215	0	0
1	B	218	220	218	0	0
1	BA	218	220	215	0	0
1	BB	218	220	215	0	0
1	C	218	220	218	0	0
1	CA	218	220	215	0	0
1	CB	218	220	215	0	0
1	D	218	220	218	0	0
1	DA	218	220	215	0	0
1	DB	218	220	215	0	0
1	E	218	220	218	0	0
1	EA	218	220	215	0	0
1	EB	218	220	215	0	0
1	F	218	220	218	0	0
1	FA	218	220	215	0	0
1	FB	218	220	215	0	0
1	G	218	220	218	0	0
1	GA	218	220	215	0	0
1	GB	218	220	215	0	0
1	H	218	220	218	0	0
1	HA	218	220	215	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	HB	218	220	215	0	0
1	I	218	220	218	0	0
1	IA	218	220	215	0	0
1	IB	218	220	215	0	0
1	J	218	220	218	0	0
1	JA	218	220	215	0	0
1	JB	218	220	215	0	0
1	K	218	220	218	0	0
1	KA	218	220	215	0	0
1	KB	218	220	215	0	0
1	L	218	220	218	0	0
1	LA	218	220	215	0	0
1	LB	218	220	215	0	0
1	M	218	220	218	0	0
1	MA	218	220	215	0	0
1	MB	218	220	215	0	0
1	N	218	220	218	0	0
1	NA	218	220	215	0	0
1	NB	218	220	215	0	0
1	O	218	220	218	0	0
1	OA	218	220	215	0	0
1	OB	218	220	215	0	0
1	P	218	220	218	0	0
1	PA	218	220	215	0	0
1	PB	218	220	215	0	0
1	Q	218	220	218	0	0
1	QA	218	220	215	0	0
1	QB	218	220	215	0	0
1	R	218	220	218	0	0
1	RA	218	220	215	0	0
1	RB	218	220	215	0	0
1	S	218	220	215	0	0
1	SA	218	220	215	0	0
1	SB	218	220	215	0	0
1	T	218	220	215	0	0
1	TA	218	220	215	0	0
1	TB	218	220	215	0	0
1	U	218	220	215	0	0
1	UA	218	220	215	0	0
1	V	218	220	215	0	0
1	VA	218	220	215	0	0
1	W	218	220	215	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	WA	218	220	215	0	0
1	X	218	220	215	0	0
1	XA	218	220	215	0	0
1	Y	218	220	215	0	0
1	YA	218	220	215	0	0
1	Z	218	220	215	0	0
1	ZA	218	220	215	0	0
1	a	218	220	215	0	0
1	aA	218	220	215	0	0
1	b	218	220	215	0	0
1	bA	218	220	215	0	0
1	c	218	220	215	0	0
1	cA	218	220	215	0	0
1	d	218	220	215	0	0
1	dA	218	220	215	0	0
1	e	218	220	215	0	0
1	eA	218	220	215	0	0
1	f	218	220	215	0	0
1	fA	218	220	215	0	0
1	g	218	220	215	0	0
1	gA	218	220	215	0	0
1	h	218	220	215	0	0
1	hA	218	220	215	0	0
1	i	218	220	215	0	0
1	iA	218	220	215	0	0
1	j	218	220	215	0	0
1	jA	218	220	215	0	0
1	k	218	220	215	0	0
1	kA	218	220	215	0	0
1	l	218	220	215	0	0
1	lA	218	220	215	0	0
1	m	218	220	215	0	0
1	mA	218	220	215	0	0
1	n	218	220	215	0	0
1	nA	218	220	215	0	0
1	o	218	220	215	0	0
1	oA	218	220	215	0	0
1	p	218	220	215	0	0
1	pA	218	220	215	0	0
1	q	218	220	215	0	0
1	qA	218	220	215	0	0
1	r	218	220	215	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	rA	218	220	215	0	0
1	s	218	220	215	0	0
1	sA	218	220	215	0	0
1	t	218	220	215	0	0
1	tA	218	220	215	0	0
1	u	218	220	215	0	0
1	uA	218	220	215	0	0
1	v	218	220	215	0	0
1	vA	218	220	215	0	0
1	w	218	220	215	0	0
1	wA	218	220	215	0	0
1	x	218	220	215	0	0
1	xA	218	220	215	0	0
1	y	218	220	215	0	0
1	yA	218	220	215	0	0
1	z	218	220	215	0	0
1	zA	218	220	215	0	0
All	All	31392	31680	31014	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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	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
1	a	28/30 (93%)	28 (100%)	0	0	100	100
1	aA	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	c	28/30 (93%)	28 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	cA	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	e	28/30 (93%)	28 (100%)	0	0	100	100
1	eA	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	g	28/30 (93%)	28 (100%)	0	0	100	100
1	gA	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	i	28/30 (93%)	28 (100%)	0	0	100	100
1	iA	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	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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	4032/4320 (93%)	4032 (100%)	0	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	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
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
1	a	19/19 (100%)	19 (100%)	0	100	100
1	aA	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	c	19/19 (100%)	19 (100%)	0	100	100
1	cA	19/19 (100%)	19 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	d	19/19 (100%)	19 (100%)	0	100	100
1	dA	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	f	19/19 (100%)	19 (100%)	0	100	100
1	fA	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	h	19/19 (100%)	19 (100%)	0	100	100
1	hA	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	j	19/19 (100%)	19 (100%)	0	100	100
1	jA	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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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	2736/2736 (100%)	2736 (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. There are no such sidechains identified.

5.3.3 RNA (i)

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.

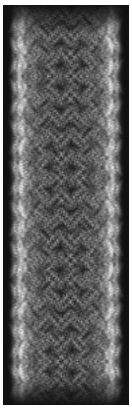
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-49258. These allow visual inspection of the internal detail of the map and identification of artifacts.

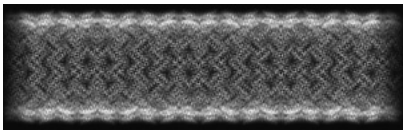
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

6.1.1 Primary map



X

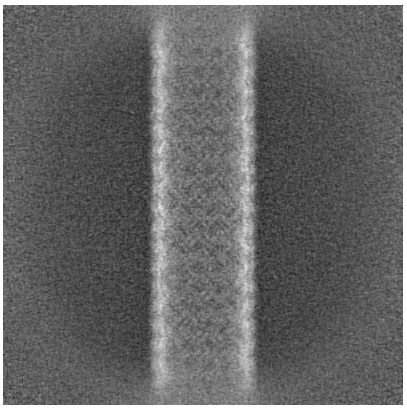


Y

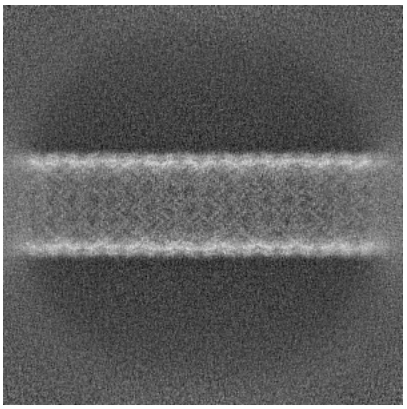


Z

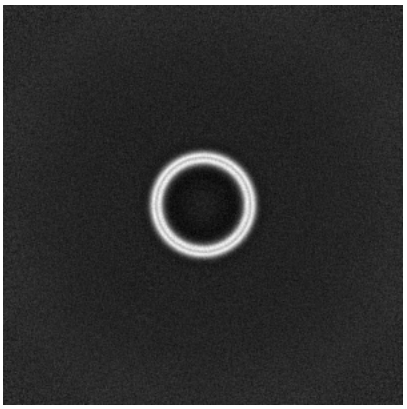
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices (i)

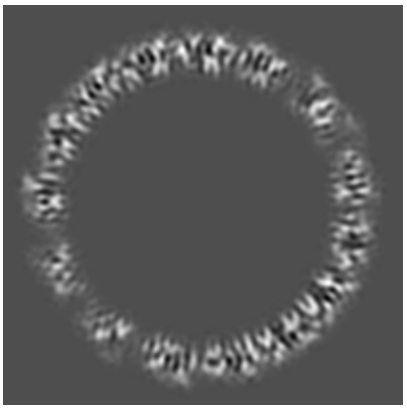
6.2.1 Primary map



X Index: 119

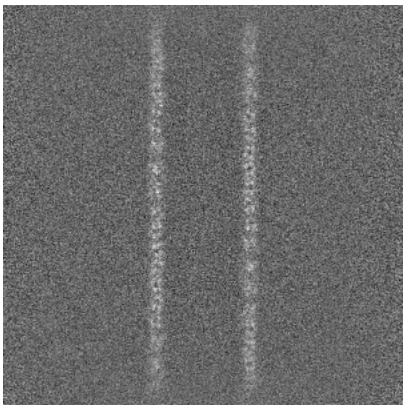


Y Index: 119

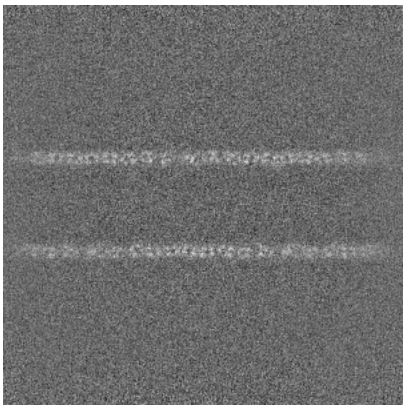


Z Index: 383

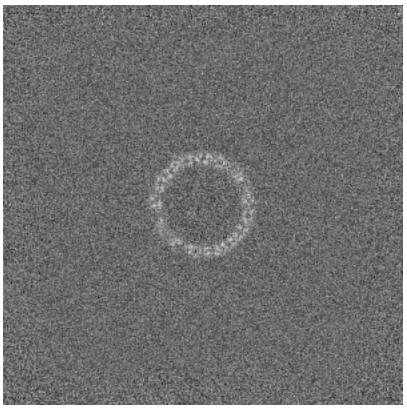
6.2.2 Raw map



X Index: 400



Y Index: 400

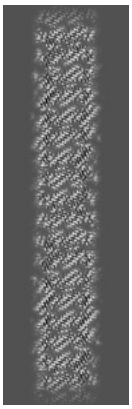


Z Index: 400

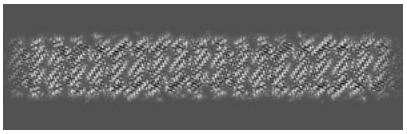
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

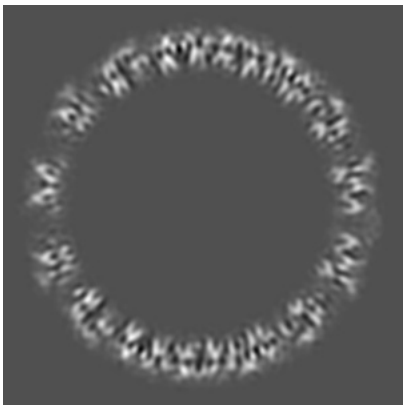
6.3.1 Primary map



X Index: 206

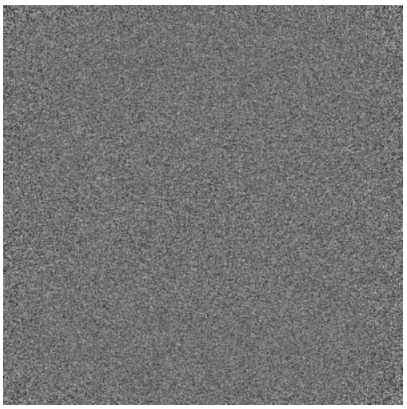


Y Index: 32

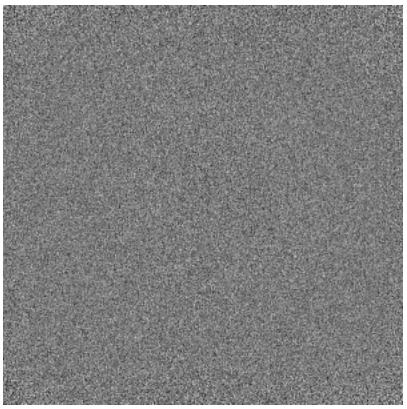


Z Index: 608

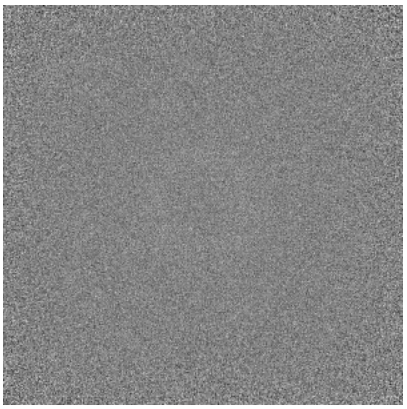
6.3.2 Raw map



X Index: 0



Y Index: 0

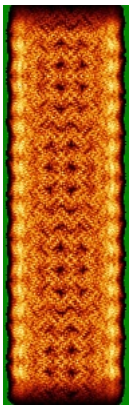


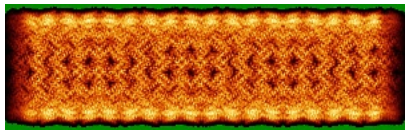
Z Index: 0

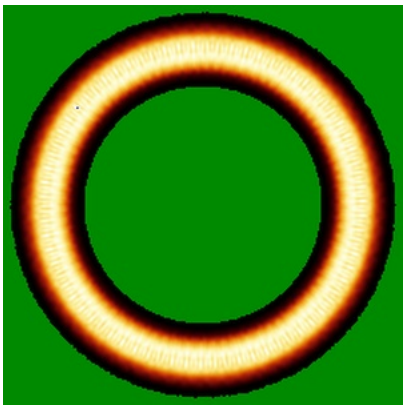
The images above show the largest variance slices of the map in three orthogonal directions.

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

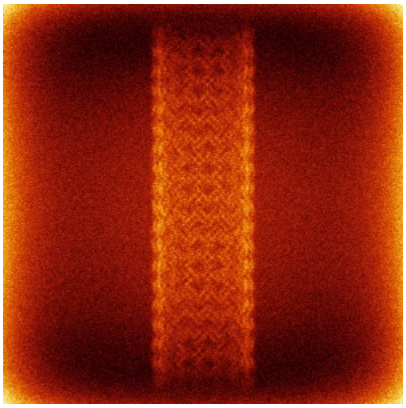
6.4.1 Primary map

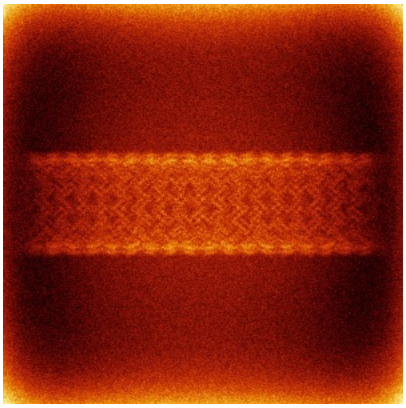

X

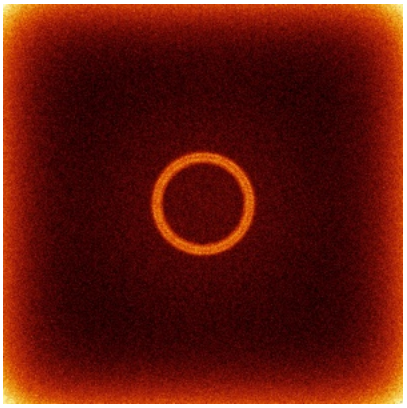

Y


Z

6.4.2 Raw map


X

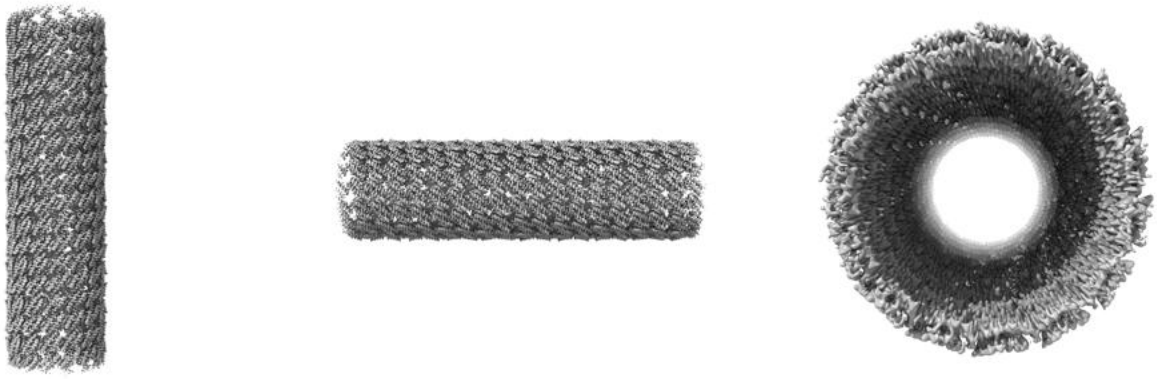

Y


Z

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)

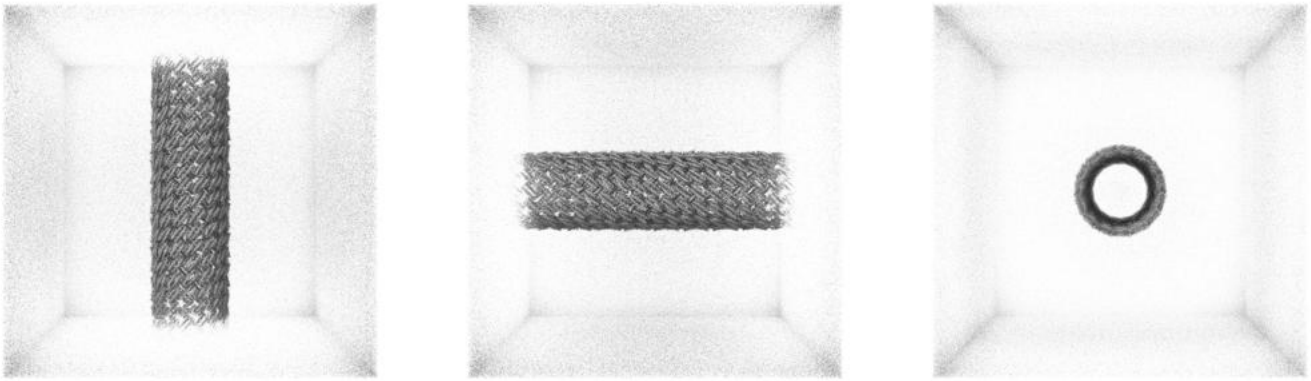
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.374. 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



X Y Z

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.

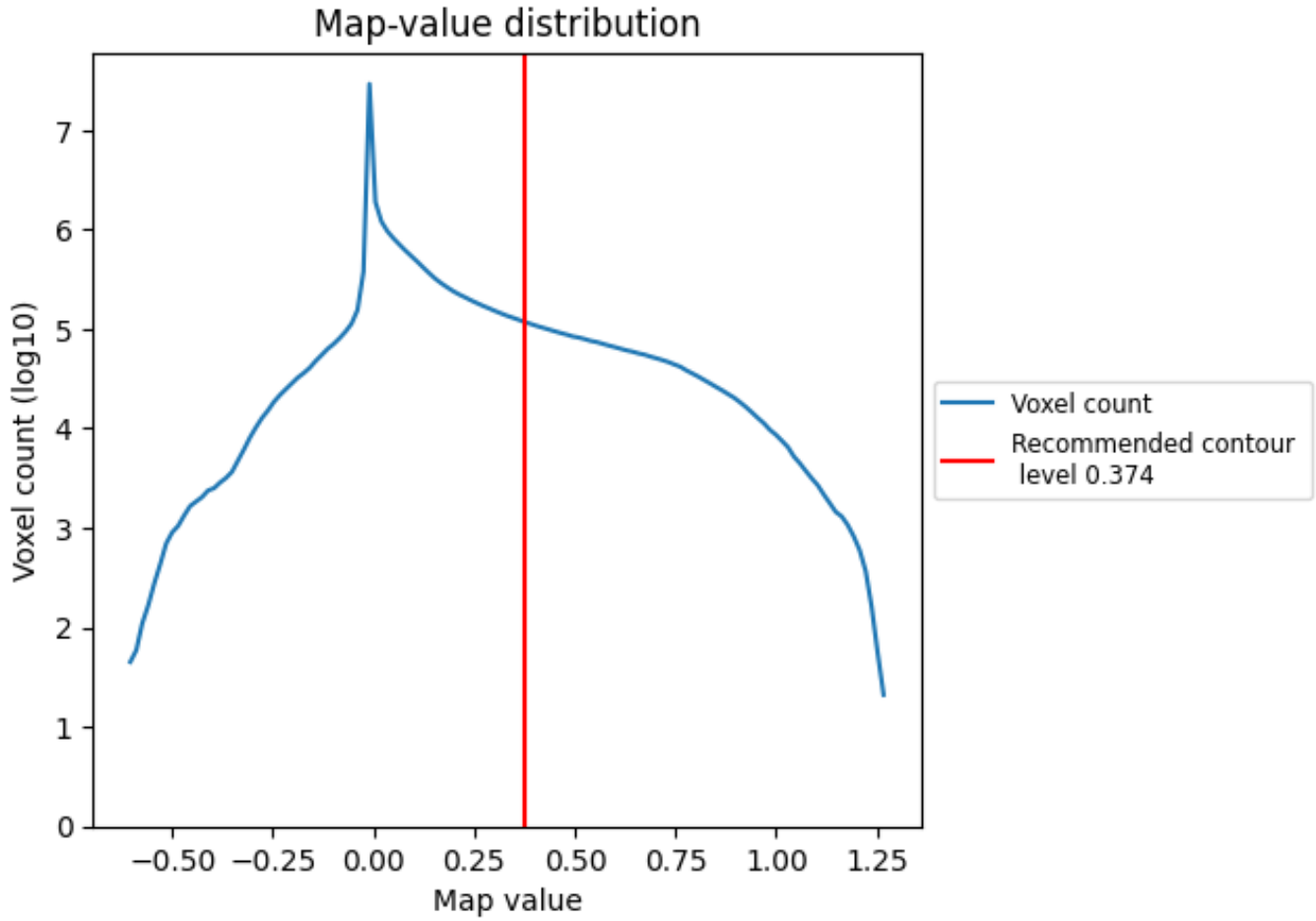
6.6 Mask visualisation (i)

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

7 Map analysis

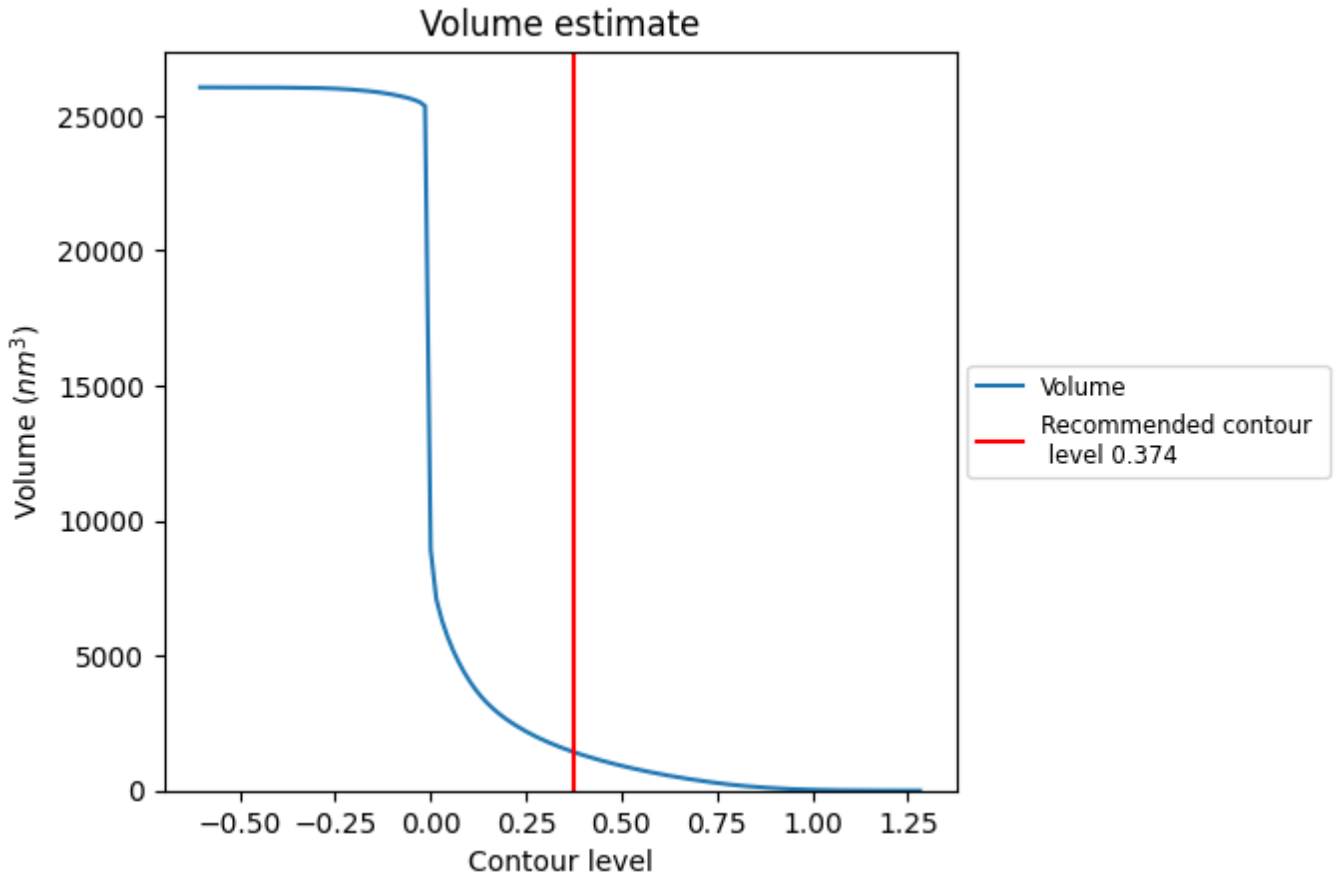
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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



The volume at the recommended contour level is 1432 nm^3; this corresponds to an approximate mass of 1293 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.

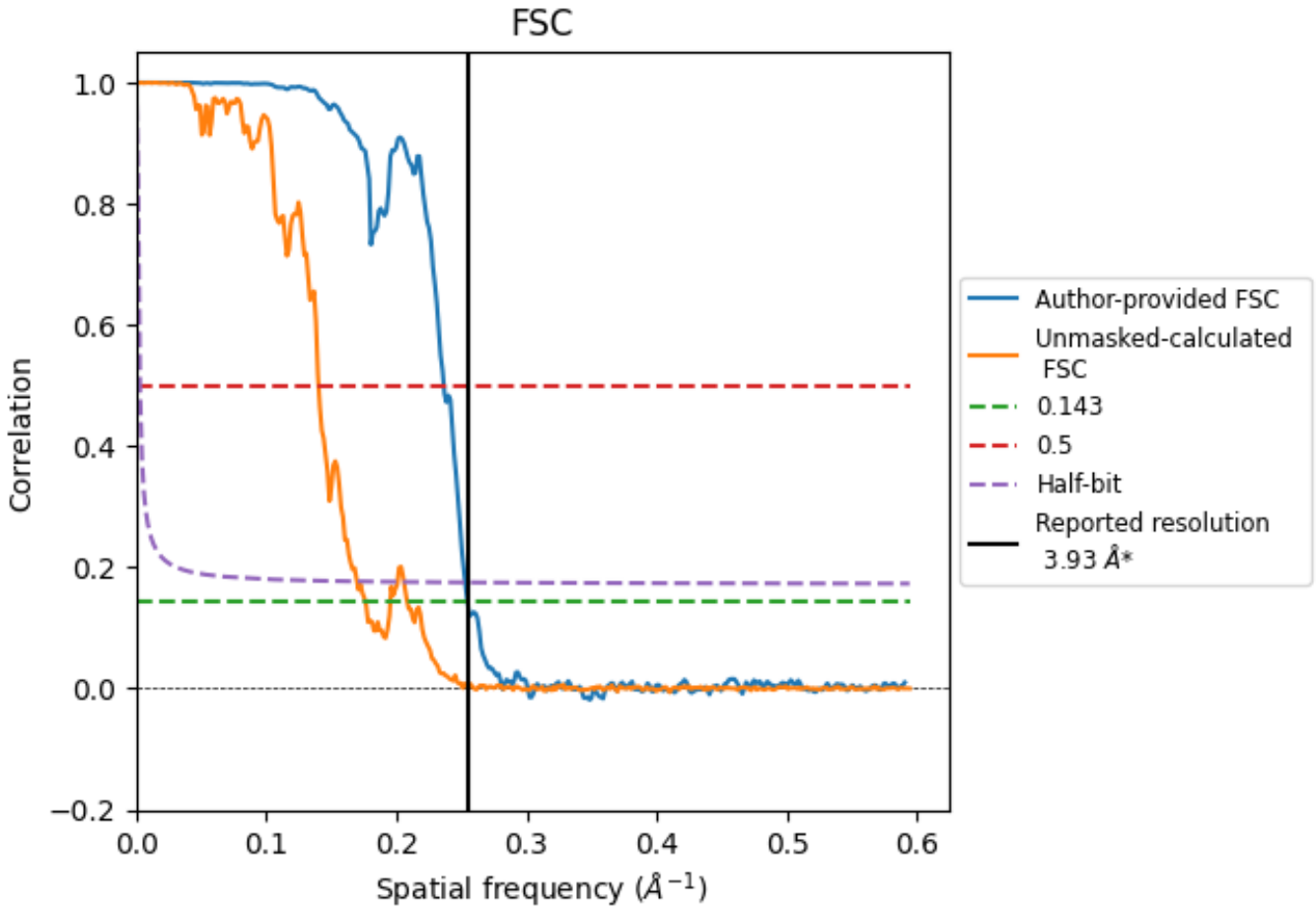
7.3 Rotationally averaged power spectrum

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

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.254 Å^{-1}

8.2 Resolution estimates (i)

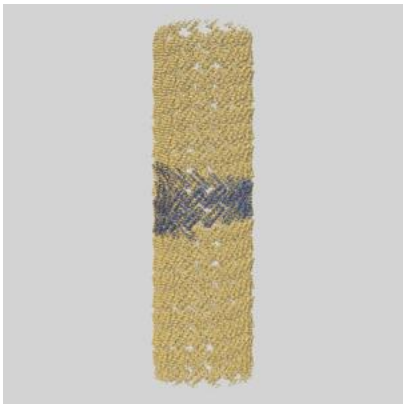
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.93	-	-
Author-provided FSC curve	3.93	4.23	3.96
Unmasked-calculated*	5.68	7.13	5.89

*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 5.68 differs from the reported value 3.93 by more than 10 %

9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-49258 and PDB model 9NCJ. Per-residue inclusion information can be found in section 3 on page 17.

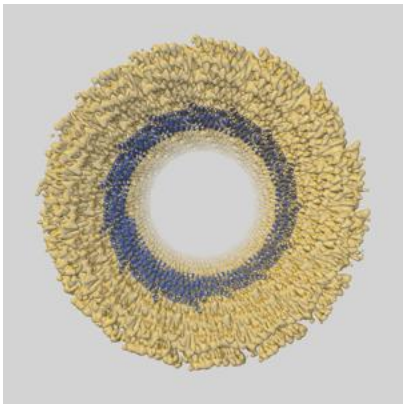
9.1 Map-model overlay



X



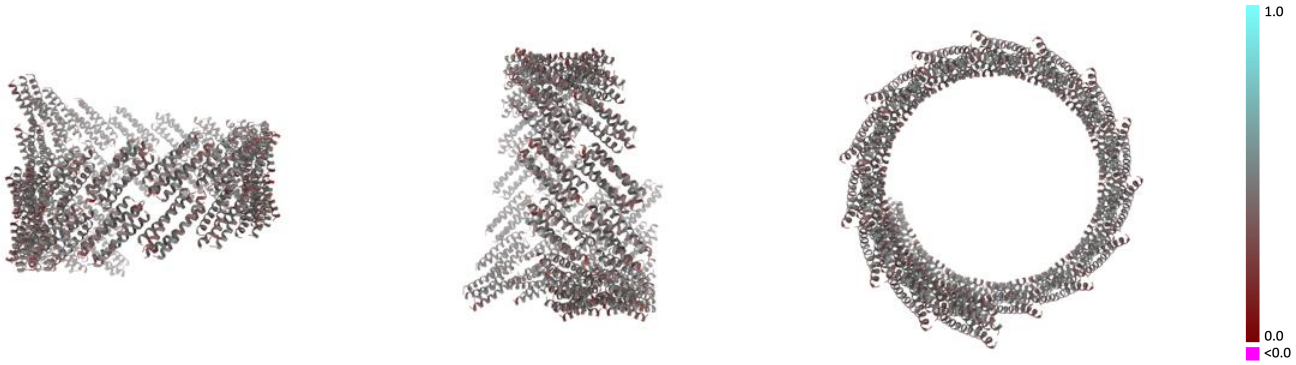
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.374 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

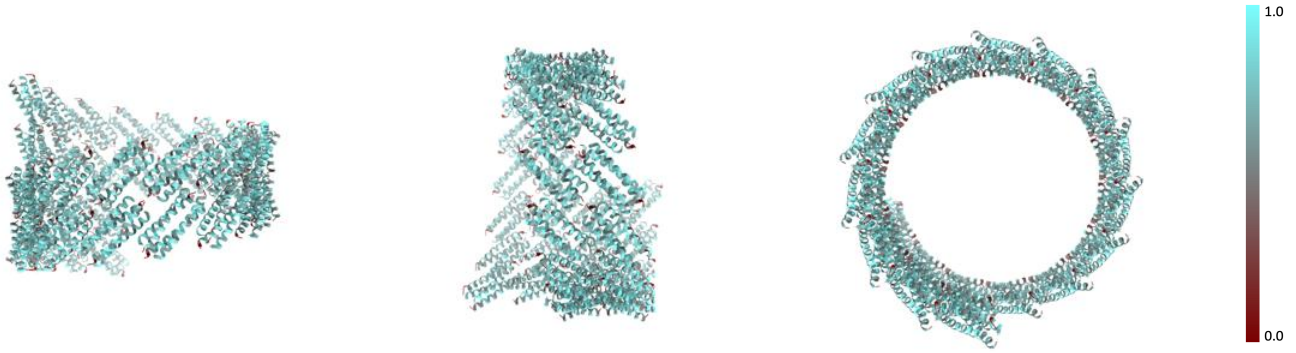
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according 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.

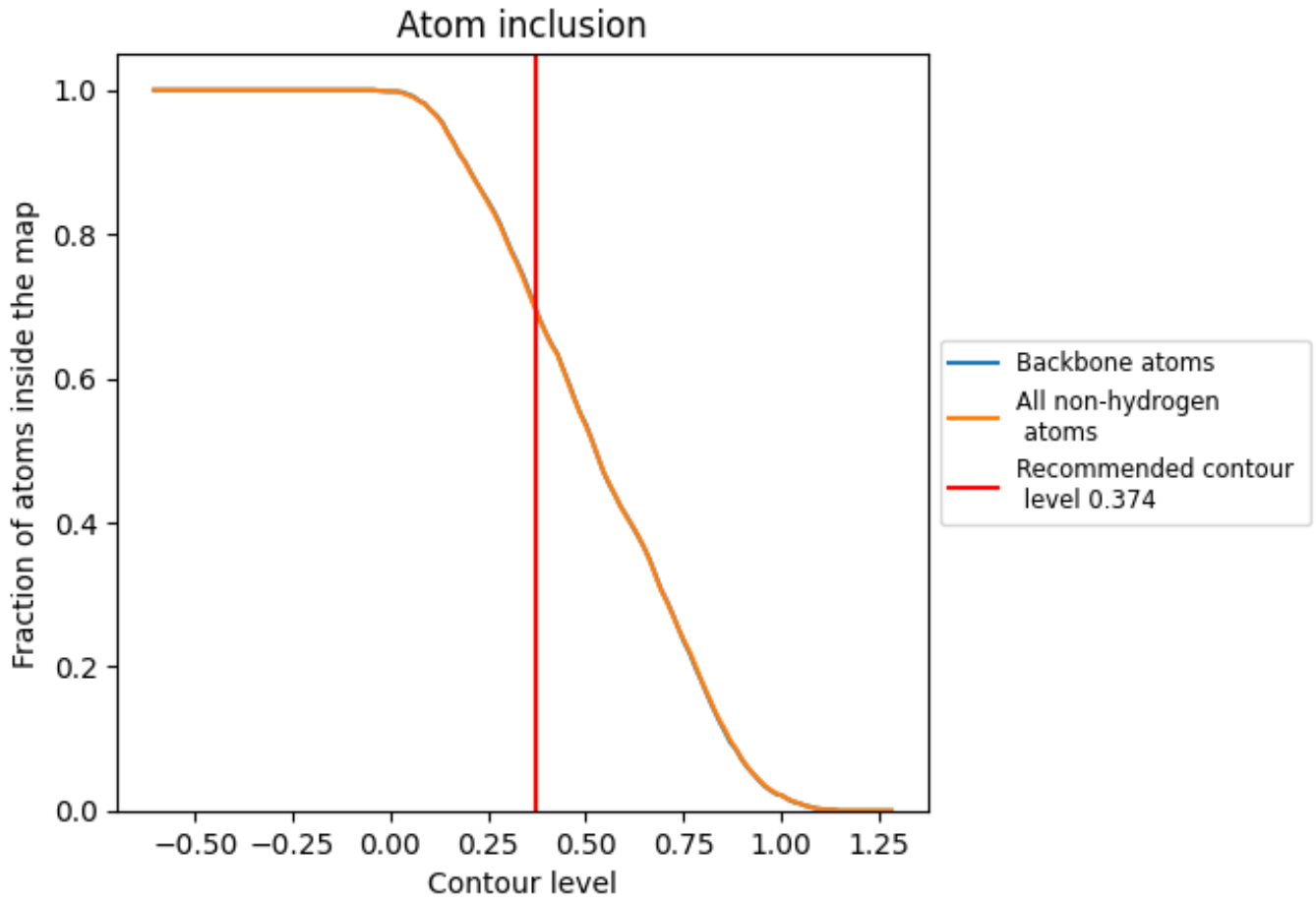
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.374).

9.4 Atom inclusion (i)



At the recommended contour level, 69% of all backbone atoms, 69% 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 (0.374) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6920	0.4210
0	0.6920	0.4270
0A	0.7200	0.4050
1	0.6920	0.4240
1A	0.6920	0.4250
2	0.7150	0.4170
2A	0.6870	0.4280
3	0.6870	0.4430
3A	0.7100	0.4120
4	0.7240	0.4140
4A	0.6820	0.4410
5	0.6920	0.4250
5A	0.7290	0.4130
6	0.7150	0.4100
6A	0.6780	0.4190
7	0.7010	0.4230
7A	0.7200	0.4030
8	0.6780	0.4230
8A	0.6920	0.4250
9	0.7150	0.4130
9A	0.6960	0.4190
A	0.6960	0.4150
AA	0.6870	0.4430
AB	0.7100	0.4180
B	0.7150	0.4160
BA	0.7150	0.4210
BB	0.6920	0.4430
C	0.7100	0.4110
CA	0.6870	0.4210
CB	0.7240	0.4180
D	0.7060	0.4150
DA	0.7240	0.4060
DB	0.6820	0.4190
E	0.6960	0.4110
EA	0.7060	0.4300



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Chain	Atom inclusion	Q-score
EB	0.7150	0.4140
F	0.7060	0.4140
FA	0.6920	0.4230
FB	0.6870	0.4300
G	0.7060	0.4150
GA	0.7100	0.4160
GB	0.6960	0.4250
H	0.7010	0.4110
HA	0.6870	0.4440
HB	0.7100	0.4190
I	0.7060	0.4180
IA	0.7150	0.4250
IB	0.6870	0.4420
J	0.6960	0.4180
JA	0.6780	0.4180
JB	0.7100	0.4100
K	0.7060	0.4150
KA	0.7150	0.4030
KB	0.6820	0.4190
L	0.7010	0.4150
LA	0.7010	0.4260
LB	0.7290	0.4110
M	0.7150	0.4250
MA	0.6870	0.4230
MB	0.6920	0.4210
N	0.7060	0.4220
NA	0.7150	0.4120
NB	0.6870	0.4230
O	0.7060	0.4160
OA	0.6920	0.4460
OB	0.7200	0.4170
P	0.7060	0.4130
PA	0.7240	0.4220
PB	0.6870	0.4380
Q	0.7060	0.4050
QA	0.6960	0.4180
QB	0.7150	0.4170
R	0.7200	0.4180
RA	0.7200	0.3990
RB	0.6780	0.4290
S	0.6870	0.4220
SA	0.6960	0.4230

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Chain	Atom inclusion	Q-score
SB	0.7240	0.4120
T	0.7060	0.4160
TA	0.6920	0.4240
TB	0.7100	0.4240
U	0.6870	0.4400
UA	0.7100	0.4080
V	0.7290	0.4170
VA	0.6920	0.4450
W	0.6730	0.4190
WA	0.7240	0.4160
X	0.7200	0.4080
XA	0.6870	0.4160
Y	0.6960	0.4300
YA	0.7240	0.3980
Z	0.7010	0.4280
ZA	0.6960	0.4260
a	0.7150	0.4230
aA	0.6780	0.4220
b	0.6870	0.4380
bA	0.7150	0.4130
c	0.7240	0.4110
cA	0.6820	0.4440
d	0.6870	0.4230
dA	0.7060	0.4240
e	0.7240	0.4160
eA	0.6730	0.4160
f	0.6920	0.4260
fA	0.7240	0.3940
g	0.6960	0.4250
gA	0.7010	0.4270
h	0.7150	0.4170
hA	0.6820	0.4210
i	0.6870	0.4360
iA	0.7100	0.4090
j	0.7200	0.4130
jA	0.6780	0.4420
k	0.6920	0.4230
kA	0.7150	0.4210
l	0.7060	0.4080
lA	0.6780	0.4170
m	0.7010	0.4270
mA	0.7200	0.4000

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Chain	Atom inclusion	Q-score
n	0.6920	0.4260
nA	0.6820	0.4290
o	0.7150	0.4160
oA	0.6870	0.4270
p	0.6820	0.4360
pA	0.7150	0.4140
q	0.7290	0.4190
qA	0.6920	0.4420
r	0.6730	0.4270
rA	0.7150	0.4200
s	0.7100	0.4090
sA	0.6780	0.4180
t	0.6920	0.4220
tA	0.7200	0.4010
u	0.6920	0.4280
uA	0.6920	0.4240
v	0.7060	0.4220
vA	0.6820	0.4280
w	0.6960	0.4410
wA	0.7100	0.4080
x	0.7290	0.4190
xA	0.6870	0.4430
y	0.6820	0.4210
yA	0.7150	0.4200
z	0.7200	0.4110
zA	0.6730	0.4180