



## wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 09:30 PM UTC

PDB ID : 9DCB / pdb\_00009dcb  
EMDB ID : EMD-46748  
Title : The Structure of AAV5 at 4 Degrees  
Authors : Bennett, A.B.; McKenna, R.  
Deposited on : 2024-08-25  
Resolution : 2.89 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

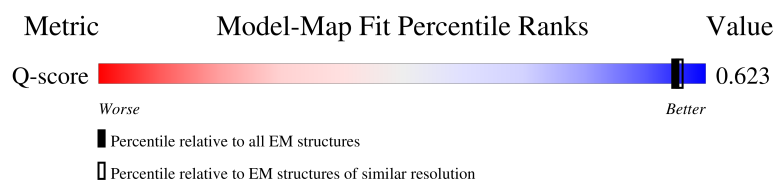
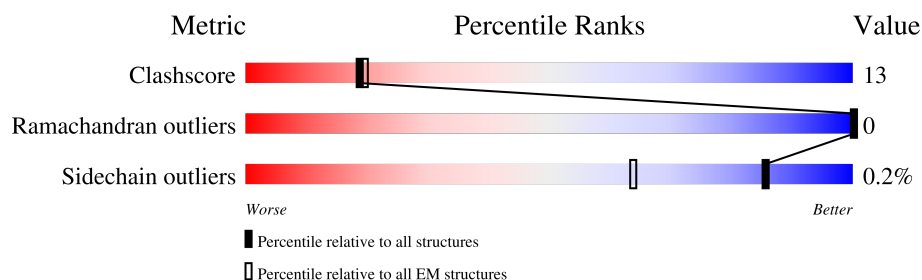
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance

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





The reported resolution of this entry is 2.89 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.









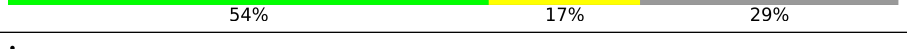
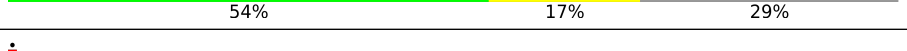
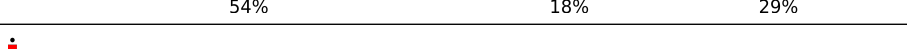
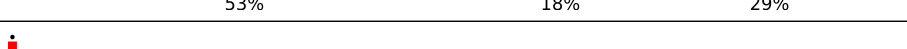
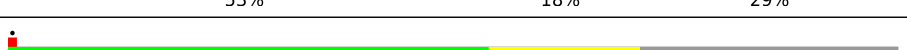

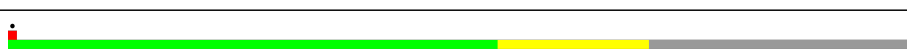

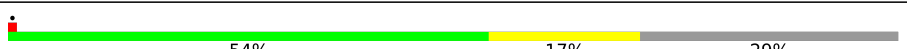





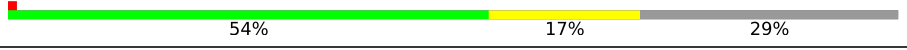
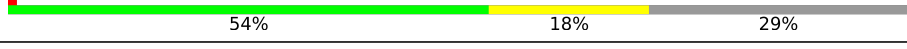



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12148 ( 2.39 - 3.39 )

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . 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	1	724	 53% 18% 29%
1	2	724	 54% 17% 29%
1	3	724	 54% 17% 29%
1	4	724	 53% 18% 29%



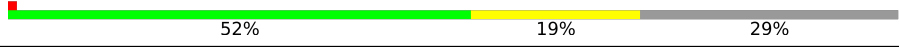




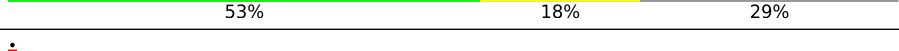
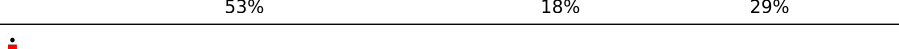
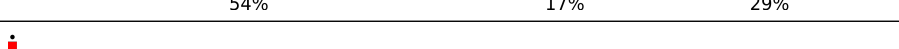
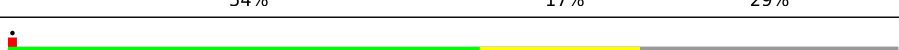

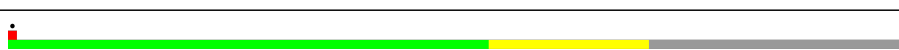

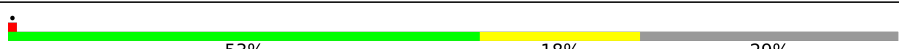





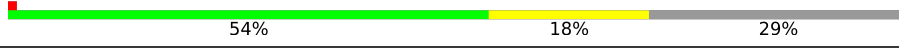
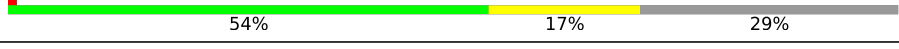



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Mol	Chain	Length	Quality of chain
1	5	724	
1	6	724	
1	7	724	
1	8	724	
1	A	724	
1	B	724	
1	C	724	
1	D	724	
1	E	724	
1	F	724	
1	G	724	
1	H	724	
1	I	724	
1	J	724	
1	K	724	
1	L	724	
1	M	724	
1	N	724	
1	O	724	
1	P	724	
1	Q	724	
1	R	724	
1	S	724	
1	T	724	
1	U	724	







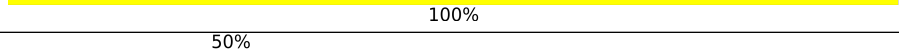
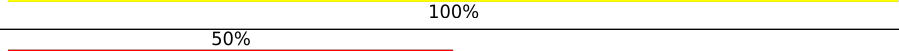
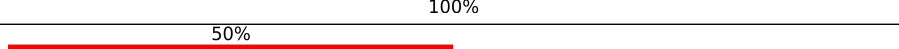
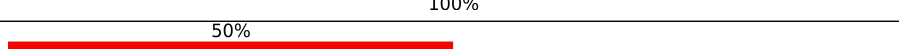
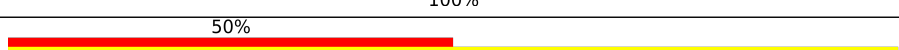
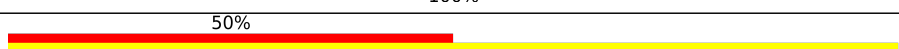

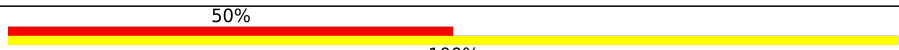
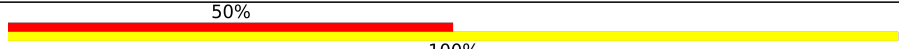


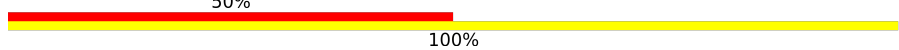
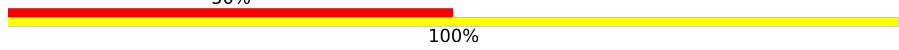

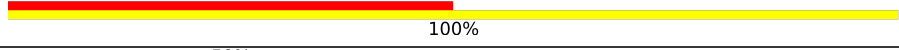
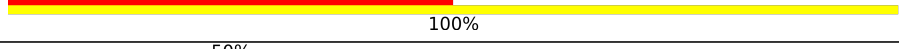
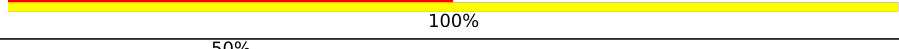
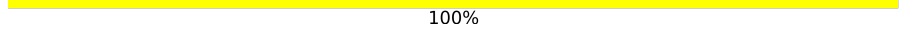

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Mol	Chain	Length	Quality of chain
1	V	724	
1	W	724	
1	X	724	
1	Y	724	
1	Z	724	
1	a	724	
1	b	724	
1	c	724	
1	d	724	
1	e	724	
1	f	724	
1	g	724	
1	h	724	
1	i	724	
1	j	724	
1	k	724	
1	l	724	
1	m	724	
1	n	724	
1	o	724	
1	p	724	
1	q	724	
1	r	724	
1	s	724	
1	t	724	

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Mol	Chain	Length	Quality of chain
1	u	724	
1	v	724	
1	w	724	
1	x	724	
1	y	724	
1	z	724	
2	0	2	
2	0A	2	
2	1A	2	
2	2A	2	
2	3A	2	
2	4A	2	
2	5A	2	
2	9	2	
2	AA	2	
2	BA	2	
2	CA	2	
2	DA	2	
2	EA	2	
2	FA	2	
2	GA	2	
2	HA	2	
2	IA	2	
2	JA	2	
2	KA	2	

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Mol	Chain	Length	Quality of chain	
2	LA	2	50%	100%
2	MA	2	50%	100%
2	NA	2	50%	100%
2	OA	2	50%	100%
2	PA	2	50%	100%
2	QA	2	50%	100%
2	RA	2	50%	100%
2	SA	2	50%	100%
2	TA	2	50%	100%
2	UA	2	50%	100%
2	VA	2	50%	100%
2	WA	2	50%	100%
2	XA	2	50%	100%
2	YA	2	50%	100%
2	ZA	2	50%	100%
2	aA	2	50%	100%
2	bA	2	50%	100%
2	cA	2	50%	100%
2	dA	2	50%	100%
2	eA	2	50%	100%
2	fA	2	50%	100%
2	gA	2	50%	100%
2	hA	2	50%	100%
2	iA	2	50%	100%
2	jA	2	50%	100%

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Mol	Chain	Length	Quality of chain
2	kA	2	<div> <div>50%</div> <div>100%</div> </div>
2	lA	2	<div> <div>50%</div> <div>100%</div> </div>
2	mA	2	<div> <div>50%</div> <div>100%</div> </div>
2	nA	2	<div> <div>50%</div> <div>100%</div> </div>
2	oA	2	<div> <div>50%</div> <div>100%</div> </div>
2	pA	2	<div> <div>50%</div> <div>100%</div> </div>
2	qA	2	<div> <div>50%</div> <div>100%</div> </div>
2	rA	2	<div> <div>50%</div> <div>100%</div> </div>
2	sA	2	<div> <div>50%</div> <div>100%</div> </div>
2	tA	2	<div> <div>50%</div> <div>100%</div> </div>
2	uA	2	<div> <div>50%</div> <div>100%</div> </div>
2	vA	2	<div> <div>50%</div> <div>100%</div> </div>
2	wA	2	<div> <div>50%</div> <div>100%</div> </div>
2	xA	2	<div> <div>50%</div> <div>100%</div> </div>
2	yA	2	<div> <div>50%</div> <div>100%</div> </div>
2	zA	2	<div> <div>50%</div> <div>100%</div> </div>

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 249480 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	B	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	C	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	D	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	E	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	F	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	G	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	H	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	I	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	J	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	K	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	L	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	M	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	N	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	O	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	P	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	Q	517	Total 4116	C 2603	N 706	O 791	S 16	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	S	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	T	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	U	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	V	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	W	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	X	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	Y	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	Z	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	a	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	b	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	c	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	d	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	e	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	f	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	g	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	h	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	i	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	j	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	k	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	l	517	Total 4116	C 2603	N 706	O 791	S 16	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	n	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	o	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	p	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	q	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	r	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	s	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	t	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	u	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	v	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	w	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	x	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	y	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	z	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	1	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	2	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	3	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	4	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	5	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	6	517	Total 4116	C 2603	N 706	O 791	S 16	0	0
1	7	517	Total 4116	C 2603	N 706	O 791	S 16	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	517	Total	C	N	O	S	0	0
			4116	2603	706	791	16		

- Molecule 2 is a DNA chain called DNA (5'-D(P\*AP\*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
2	0	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	JA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	UA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	fA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	qA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	1A	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	3A	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	4A	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	5A	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	9	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	AA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	BA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	CA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	DA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	EA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	FA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	GA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	HA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	IA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	KA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	LA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	MA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	NA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	OA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	PA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	QA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	RA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	SA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	TA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	VA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	WA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	XA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	YA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	ZA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	aA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	bA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	cA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	dA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	eA	2	Total 42	C 20	N 10	O 10	P 2	0	0

*Continued on next page...*

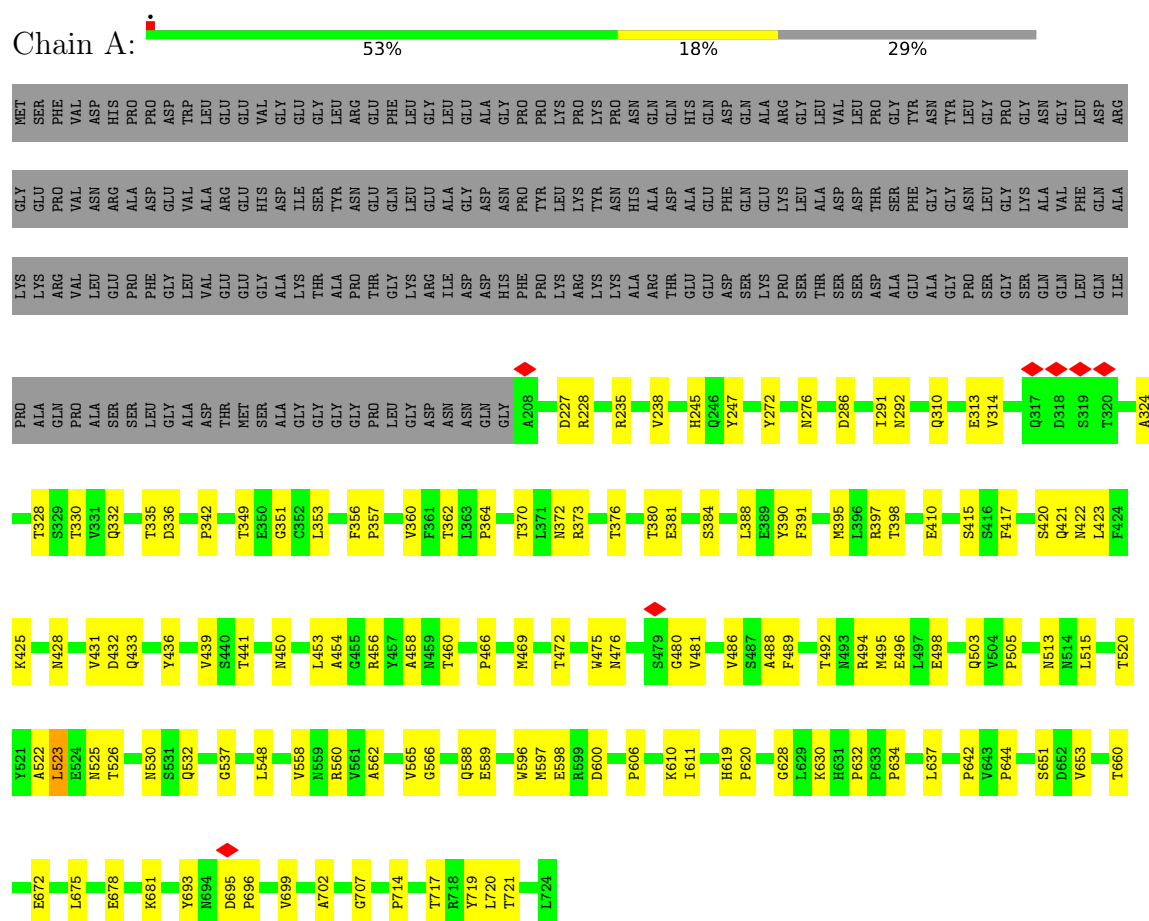
*Continued from previous page...*

Mol	Chain	Residues	Atoms					AltConf	Trace
2	gA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	hA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	iA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	jA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	kA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	lA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	mA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	nA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	oA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	pA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	rA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	sA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	tA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	uA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	vA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	wA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	xA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	yA	2	Total 42	C 20	N 10	O 10	P 2	0	0
2	zA	2	Total 42	C 20	N 10	O 10	P 2	0	0
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2	2A	2	Total 42	C 20	N 10	O 10	P 2	0	0

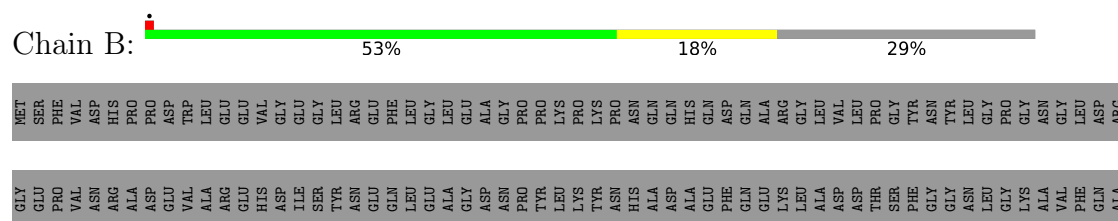
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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: Capsid protein



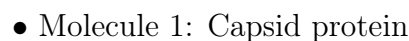
#### • Molecule 1: Capsid protein



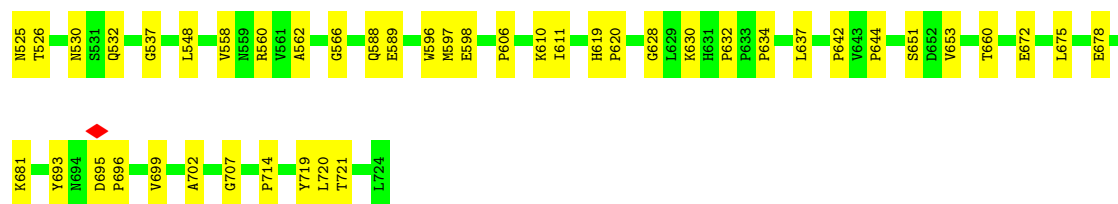
- Molecule 1: Capsid protein



- Molecule 1: Capsid protein

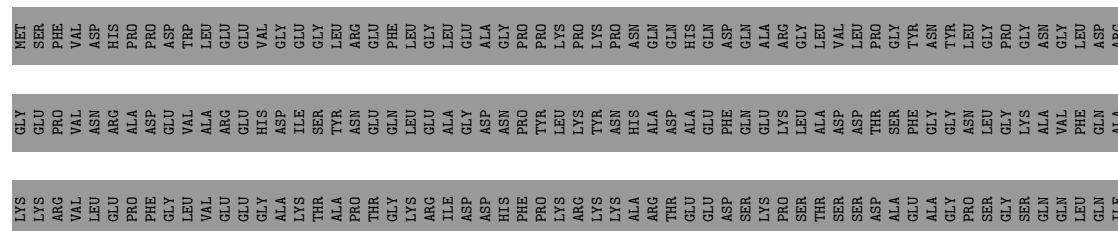






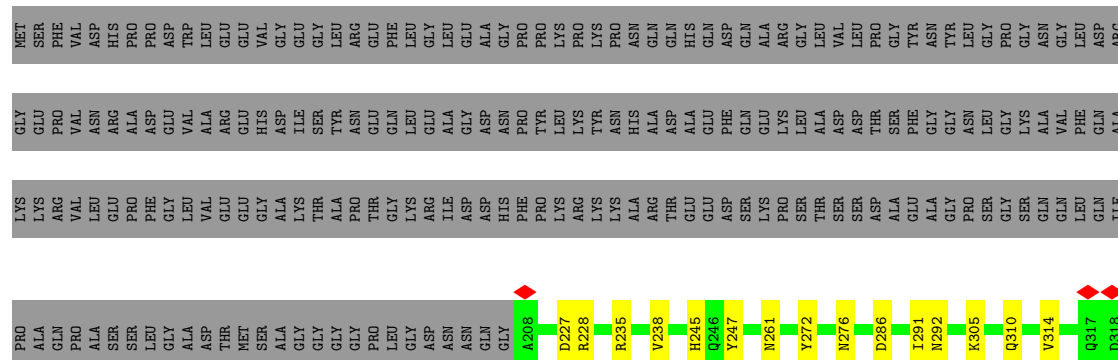
• Molecule 1: Capsid protein

Chain F: 53% 18% 29%

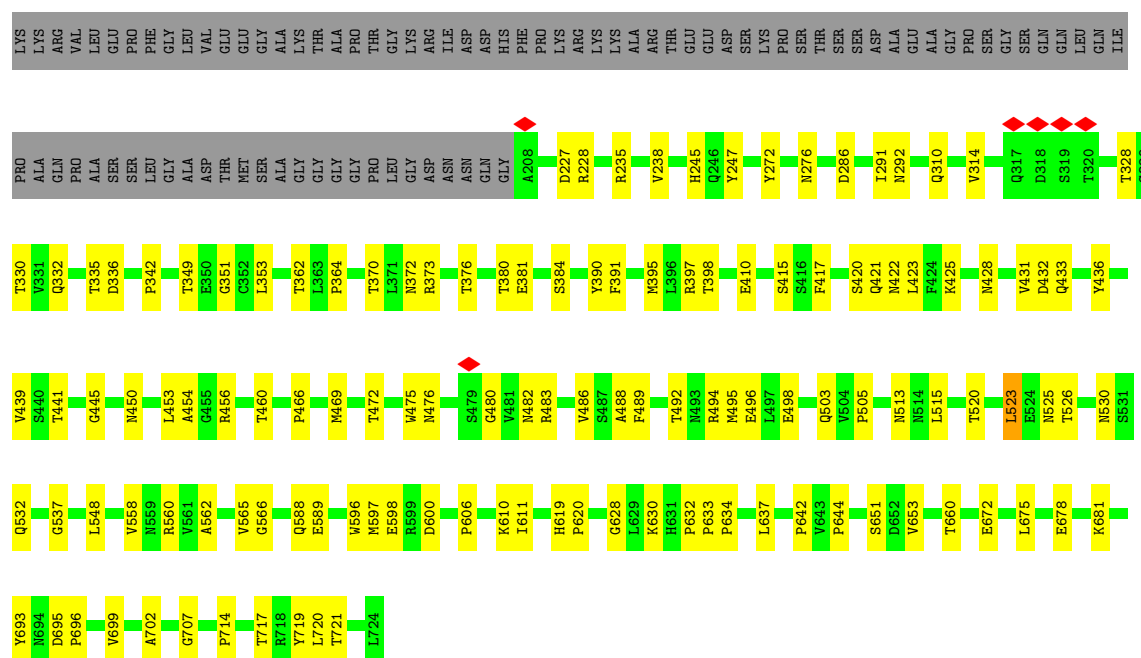


• Molecule 1: Capsid protein

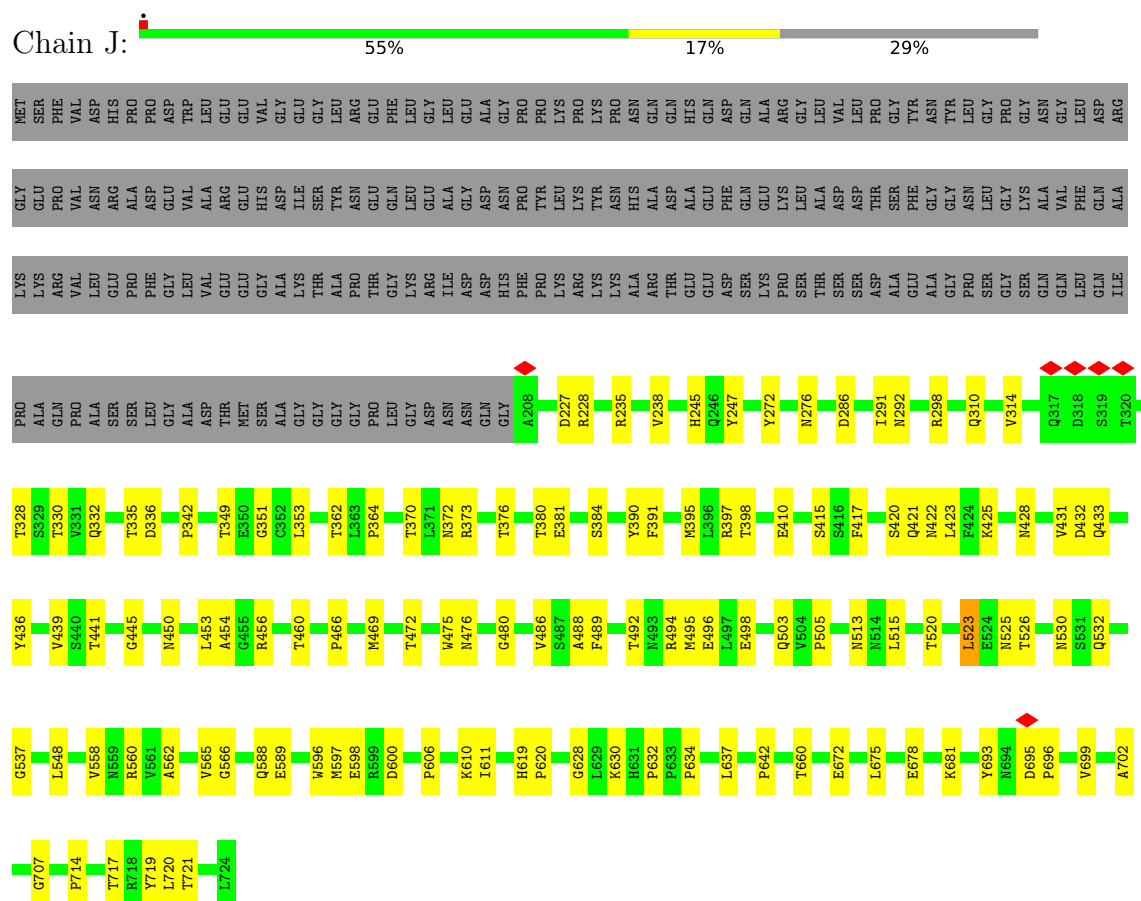
Chain G: 53% 18% 29%





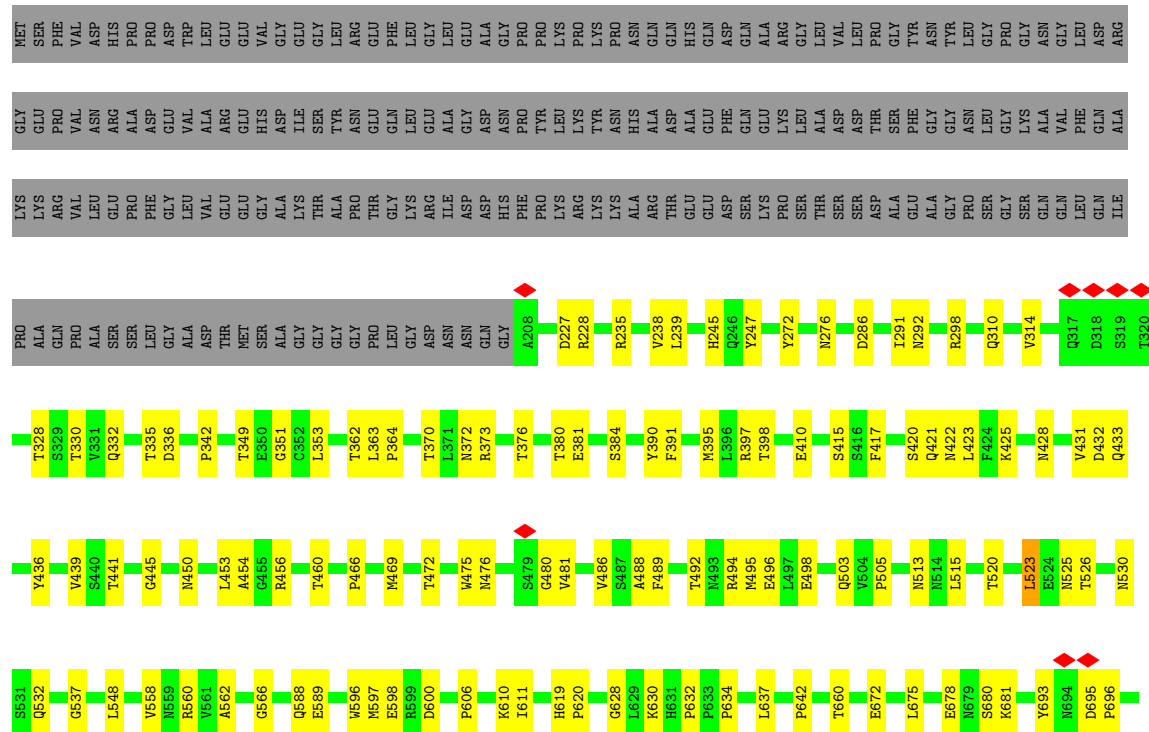


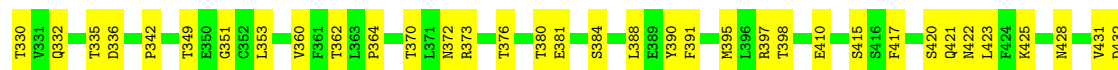
### • Molecule 1: Capsid protein

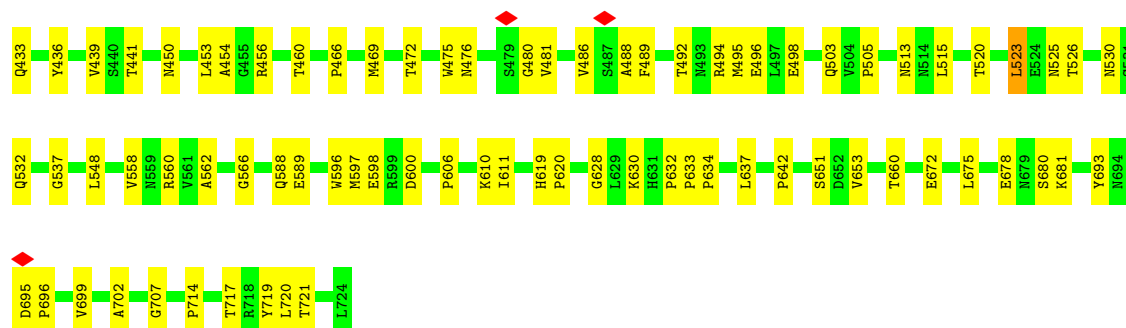


### • Molecule 1: Capsid protein

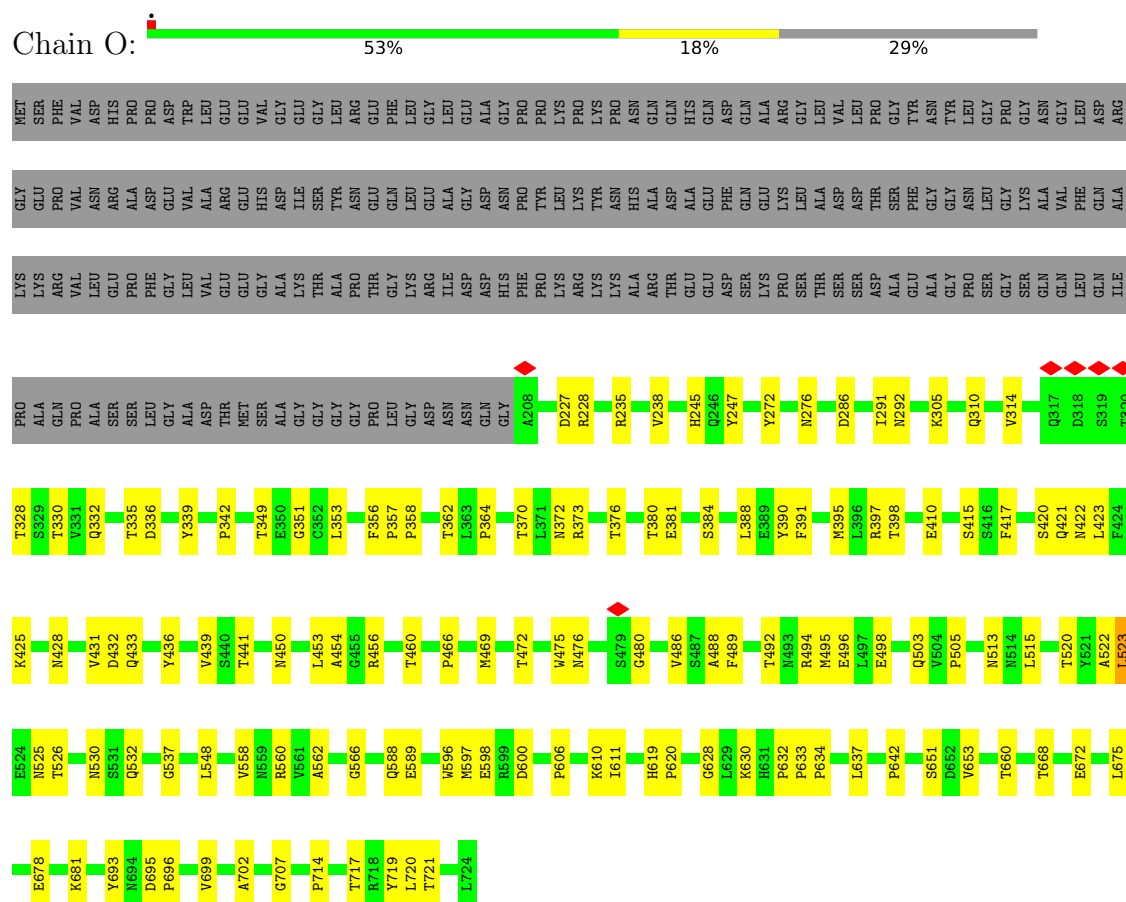




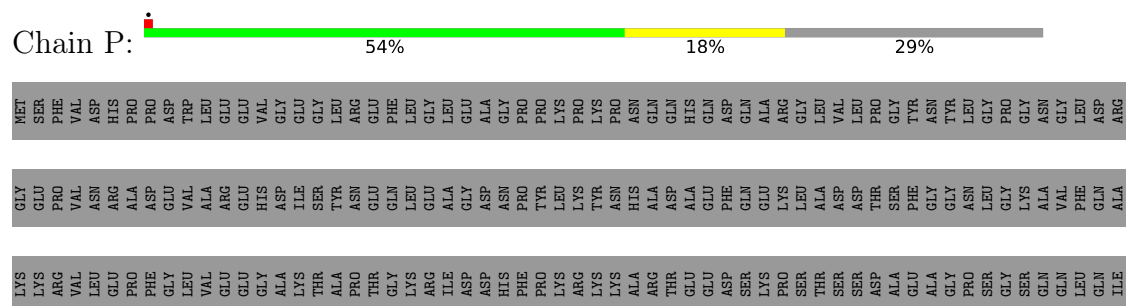


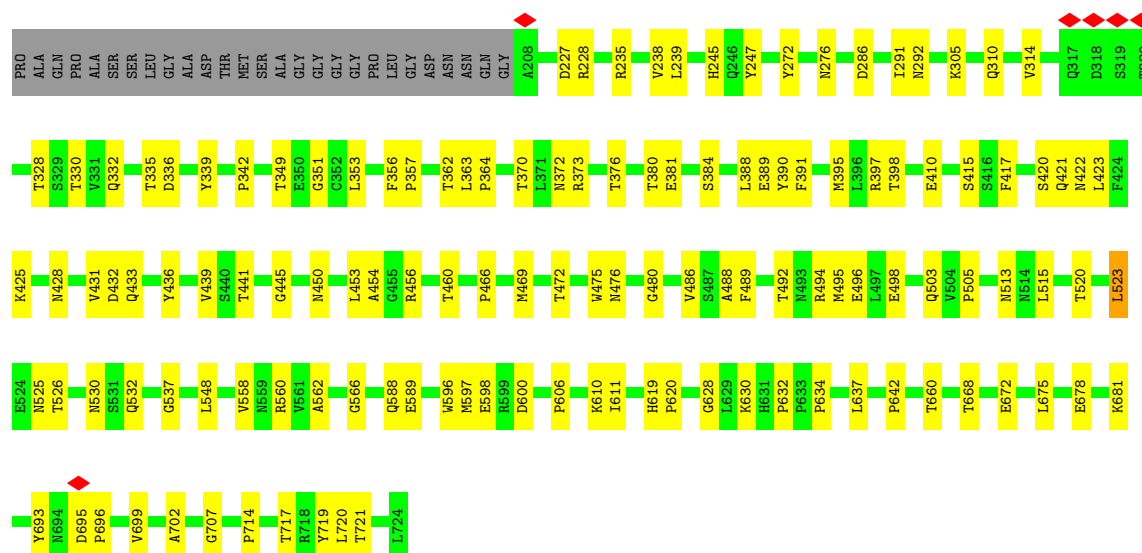


### • Molecule 1: Capsid protein

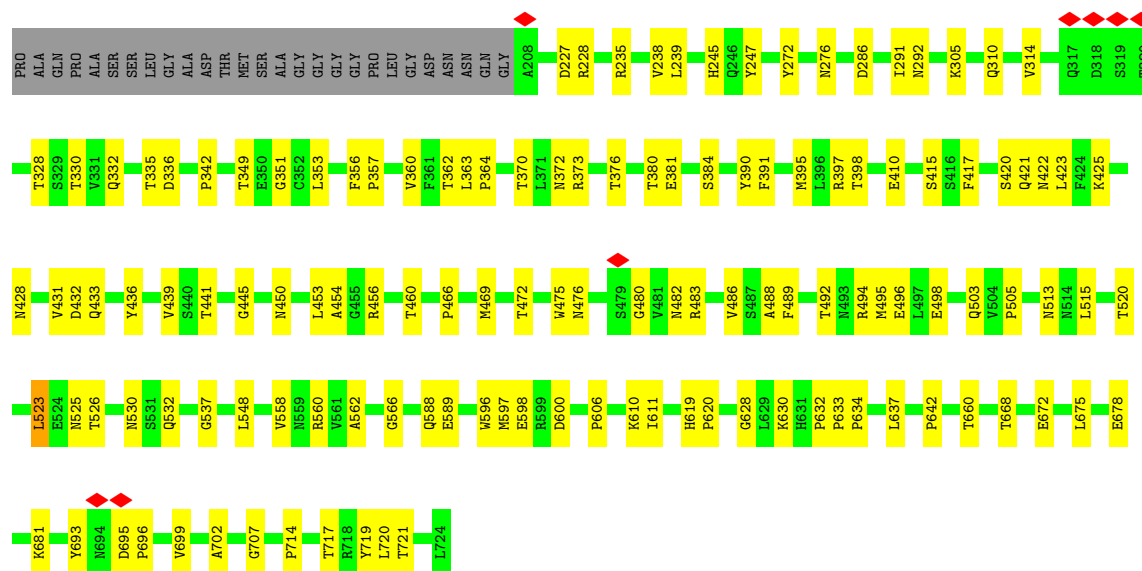
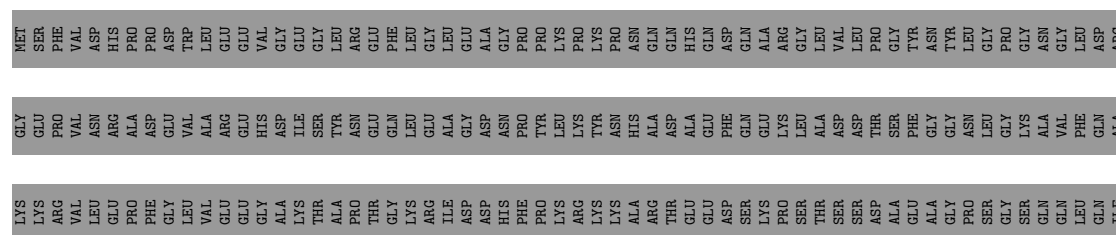


### • Molecule 1: Capsid protein





• Molecule 1: Capsid protein



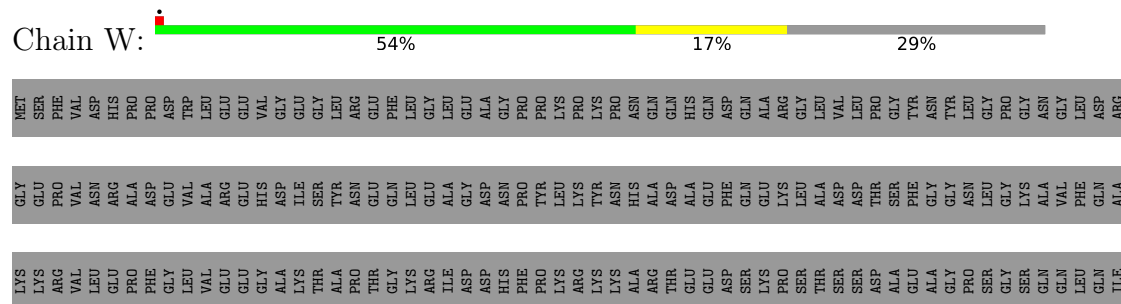
• Molecule 1: Capsid protein

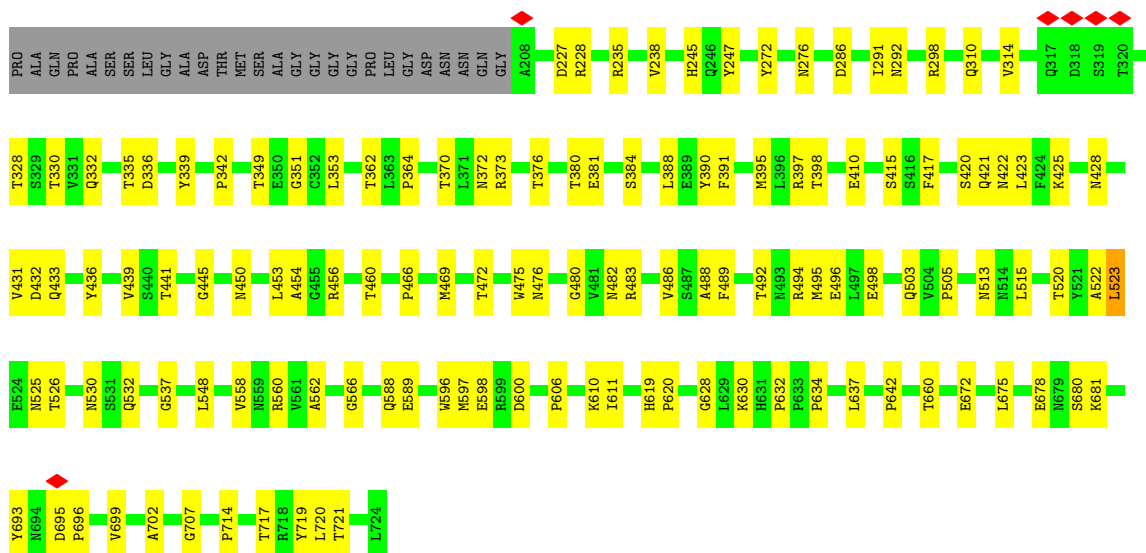




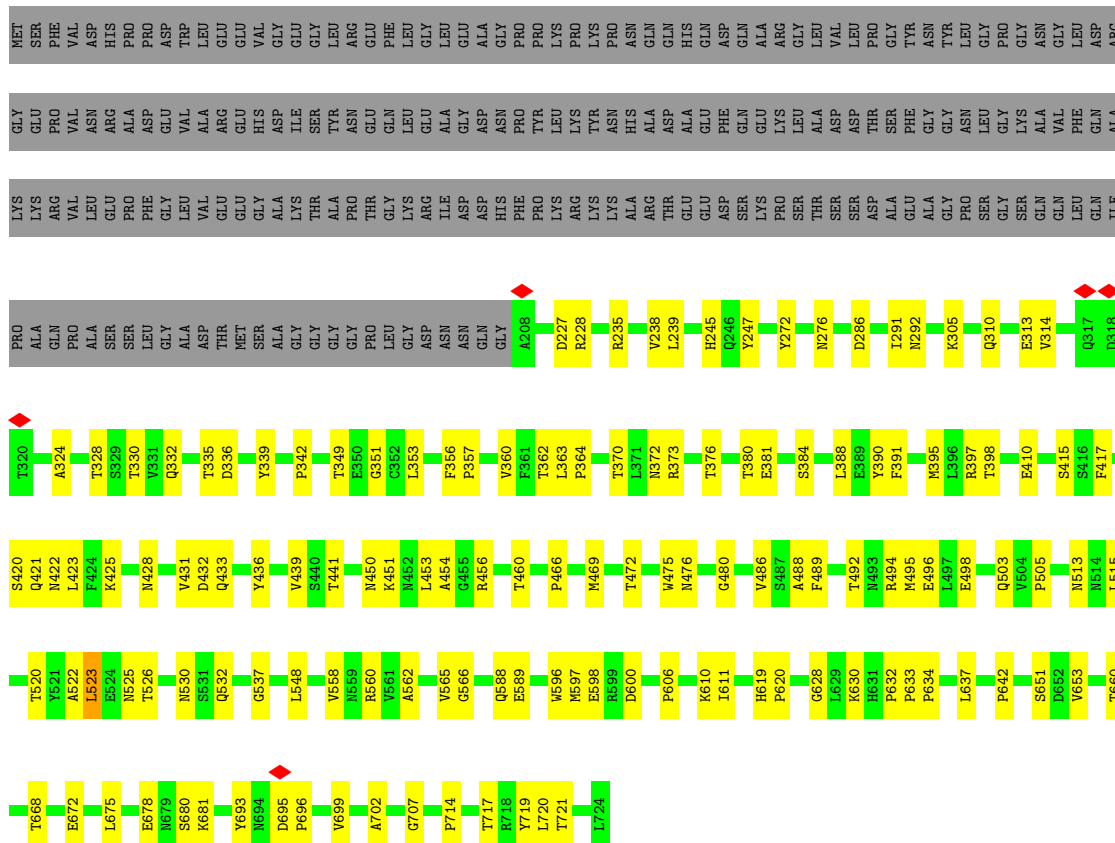






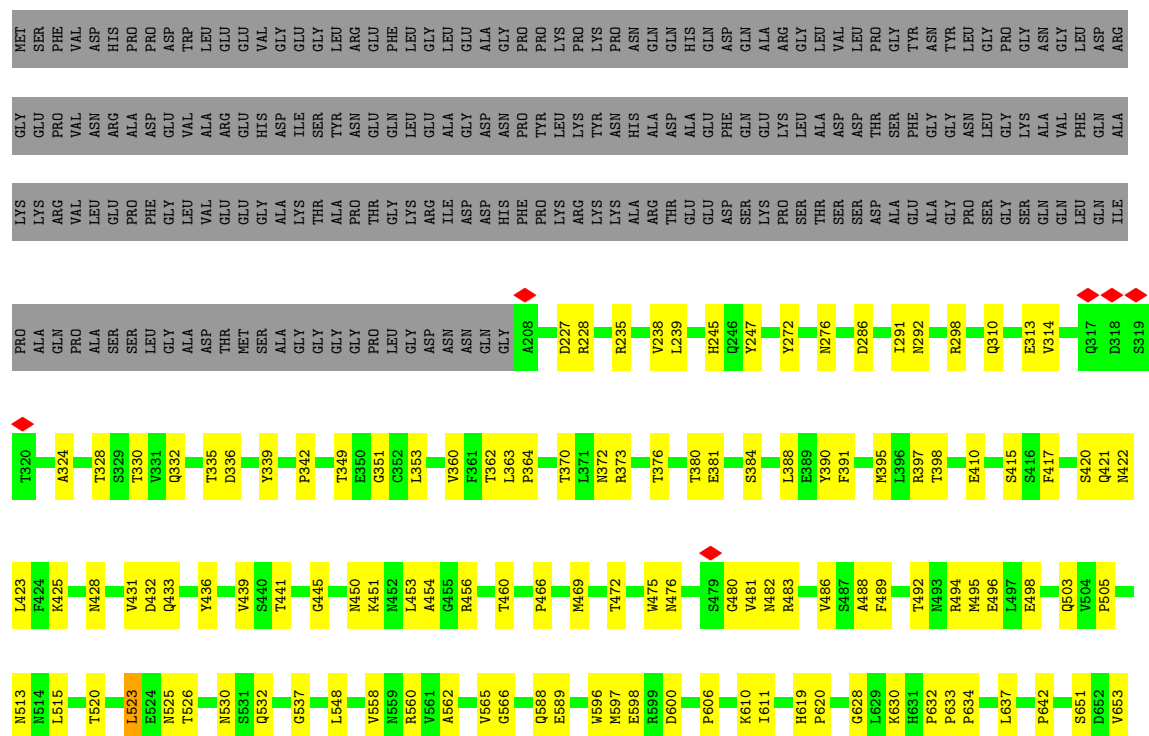


- Molecule 1: Capsid protein

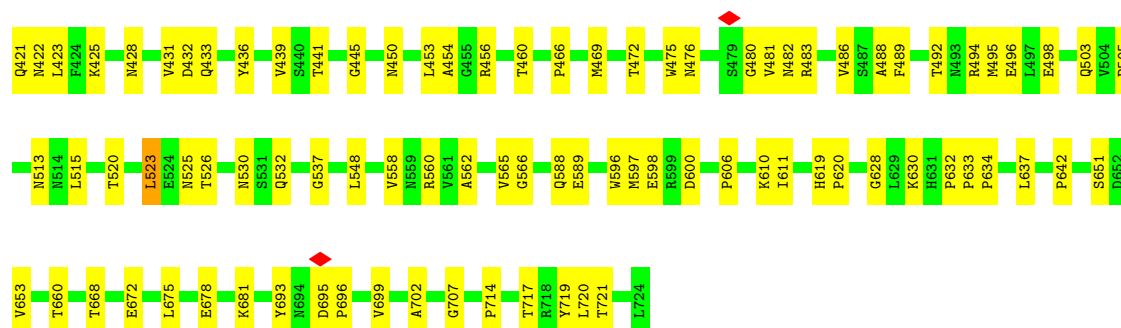


- Molecule 1: Capsid protein

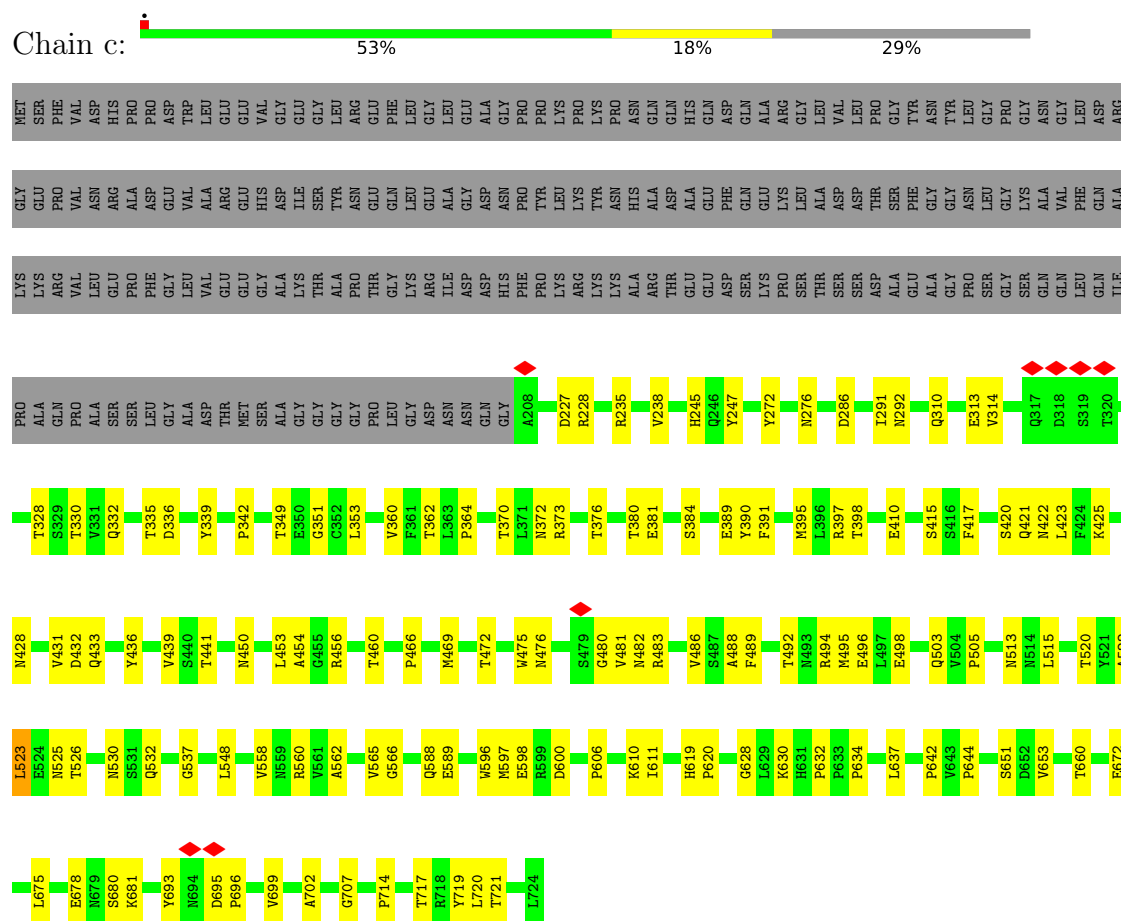




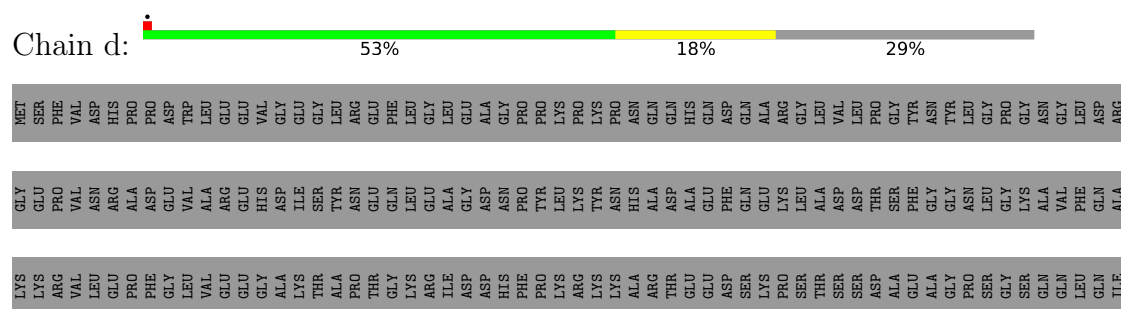


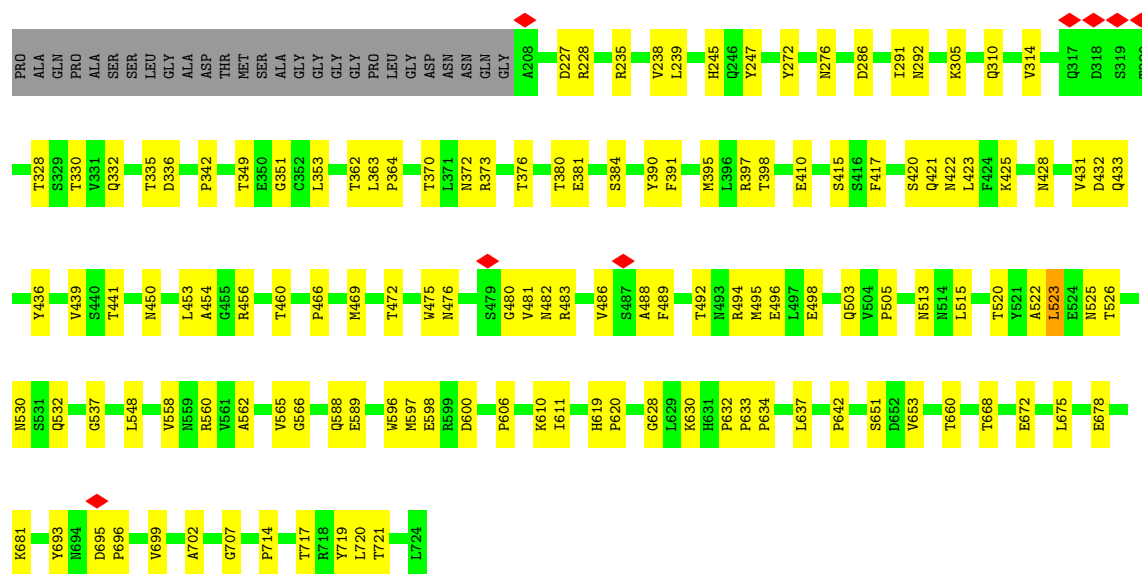


- Molecule 1: Capsid protein

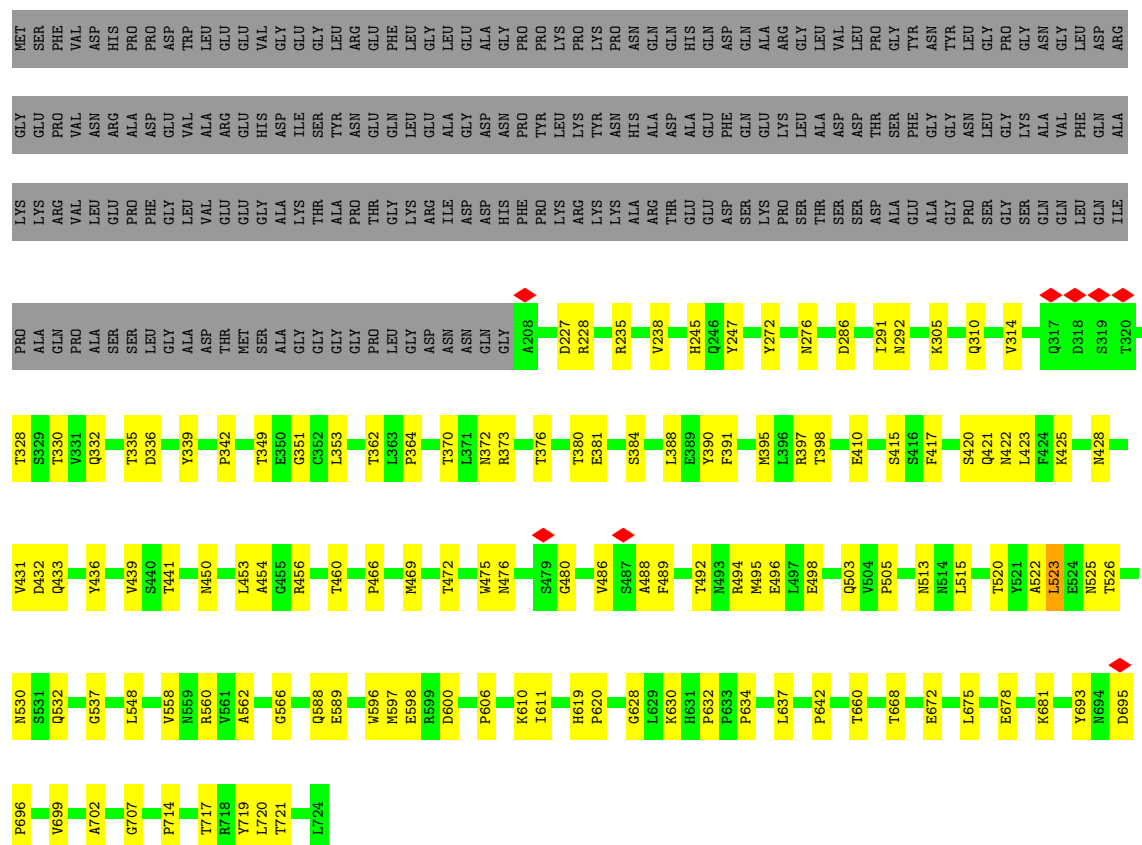


- Molecule 1: Capsid protein





- Molecule 1: Capsid protein



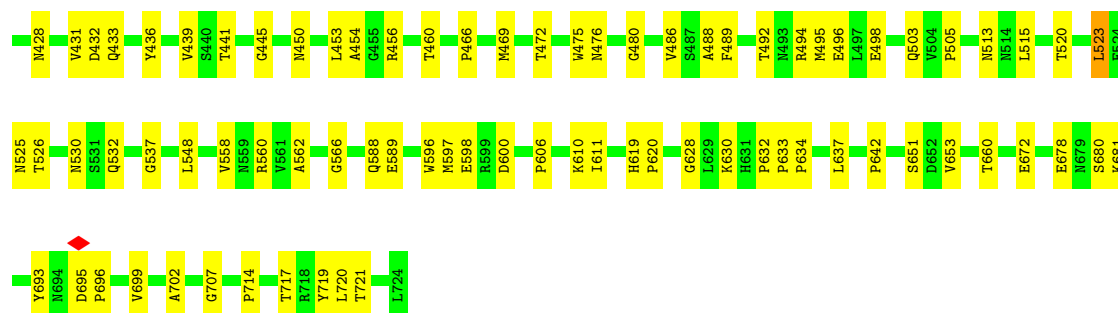
- Molecule 1: Capsid protein



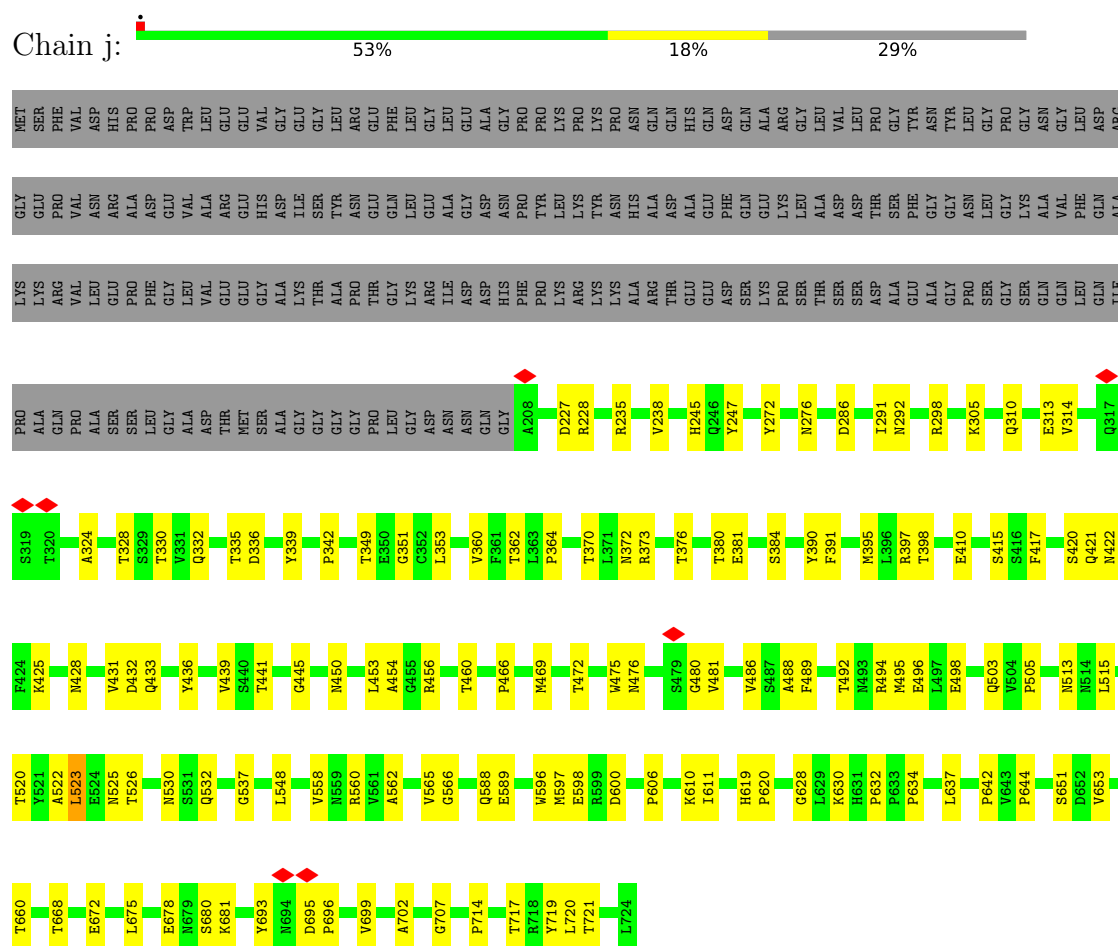




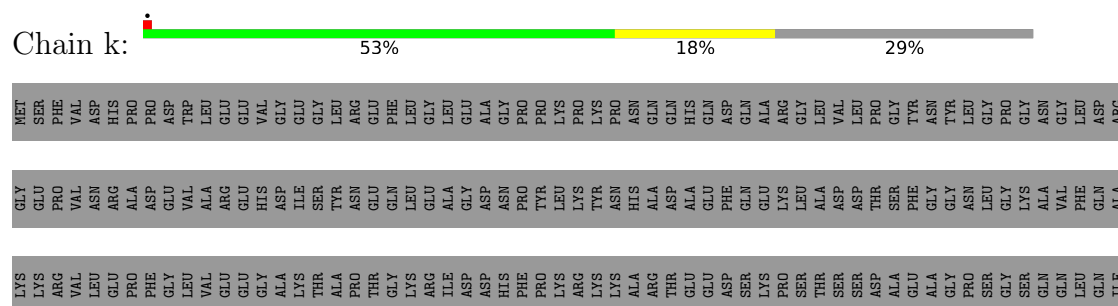


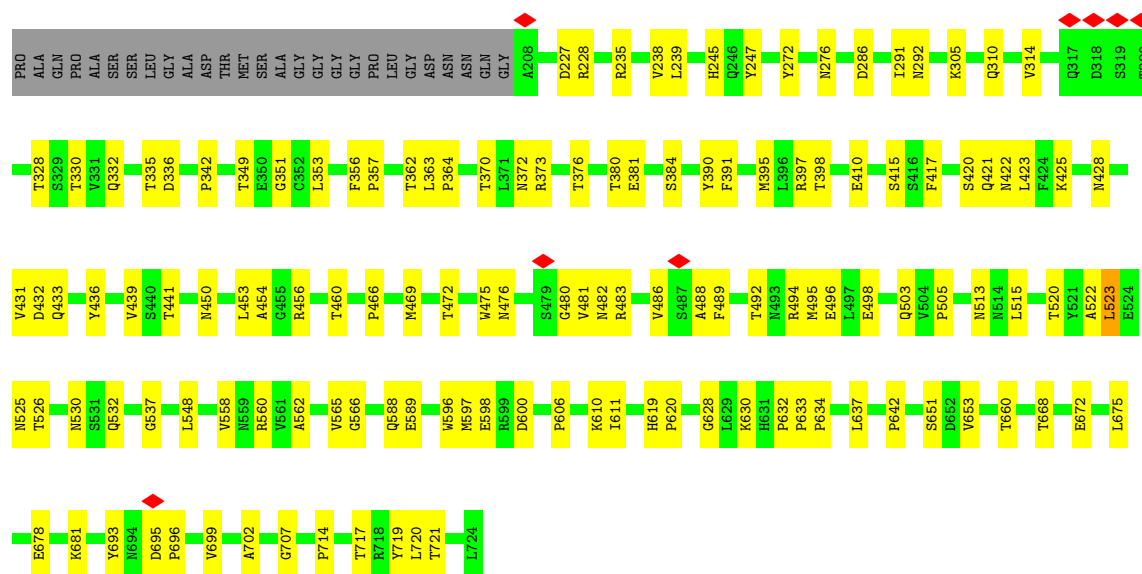


### • Molecule 1: Capsid protein

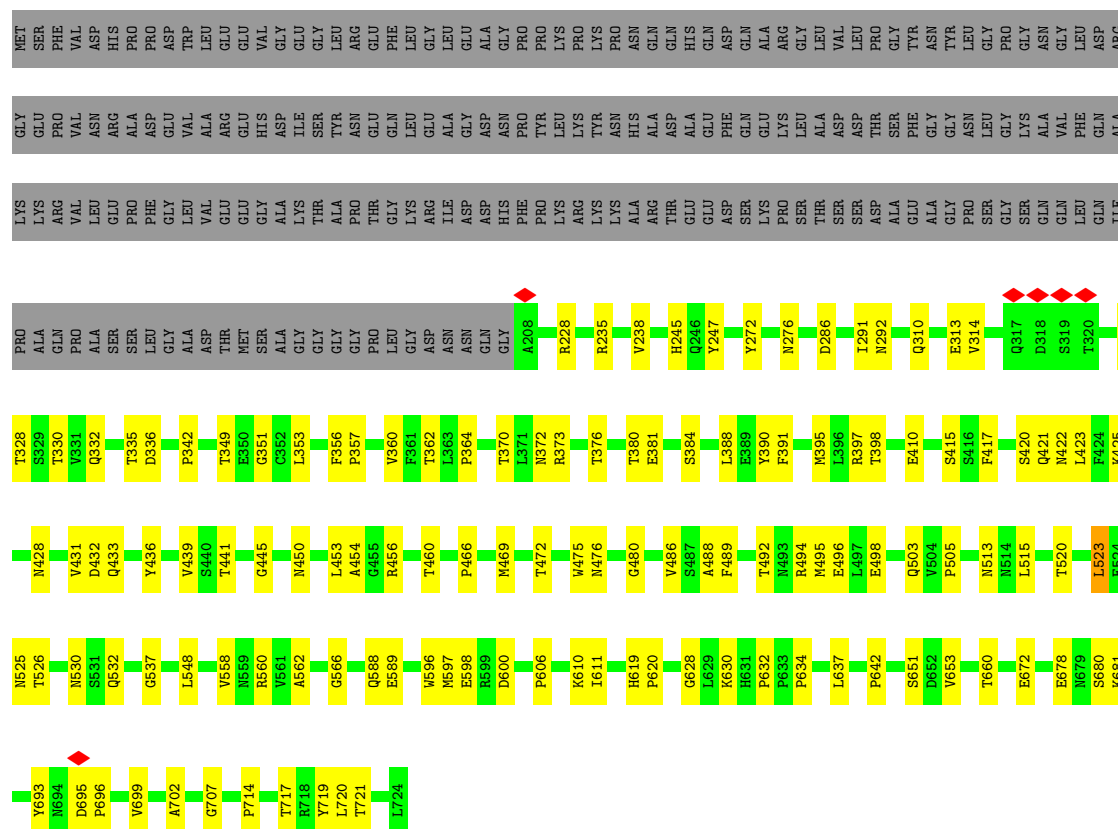


### • Molecule 1: Capsid protein



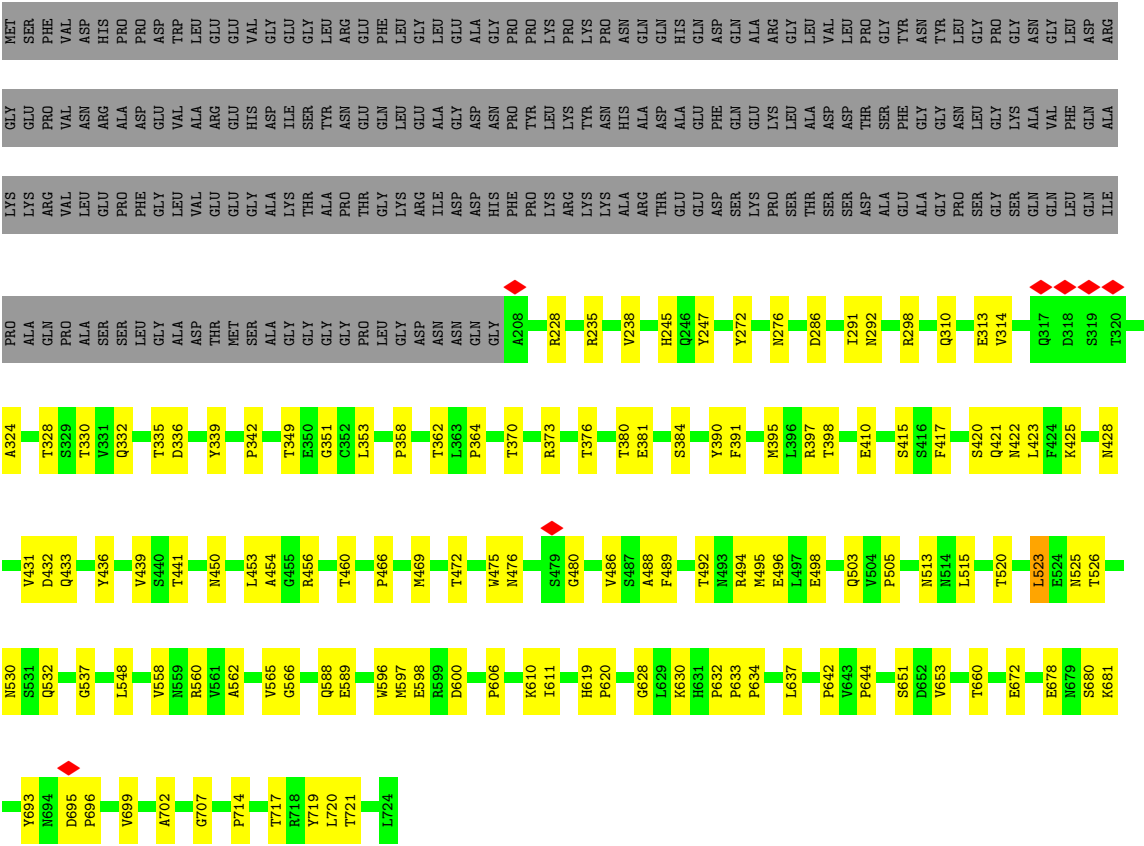


• Molecule 1: Capsid protein

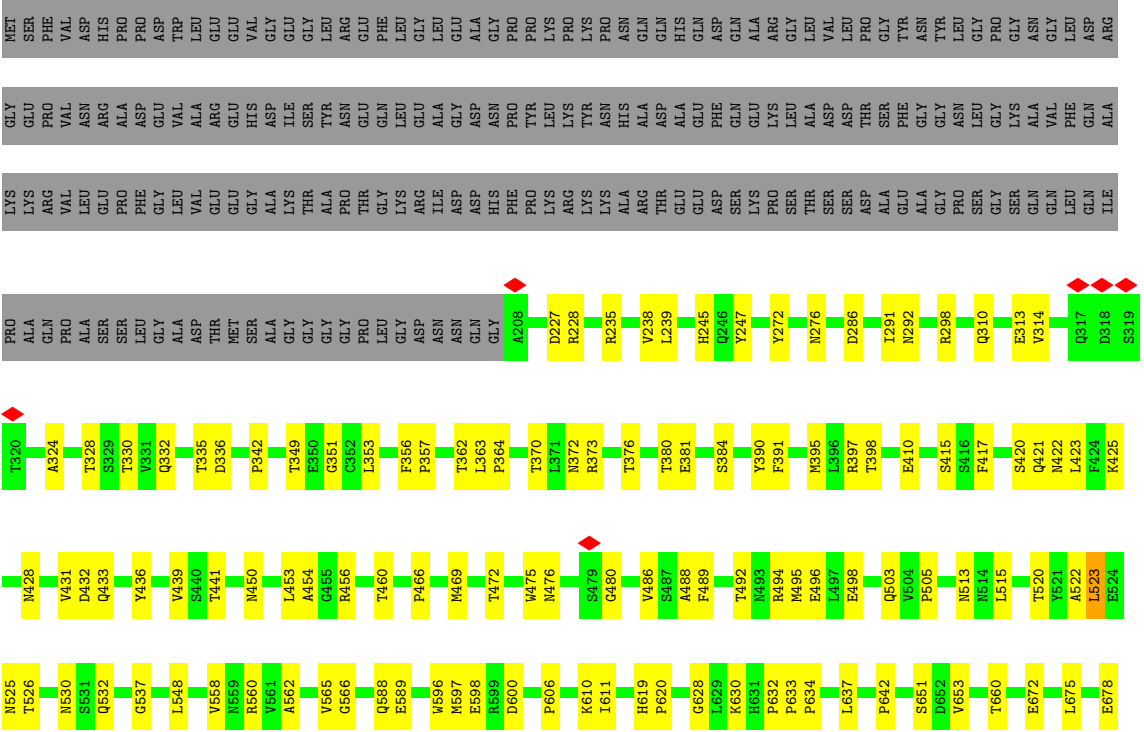


• Molecule 1: Capsid protein

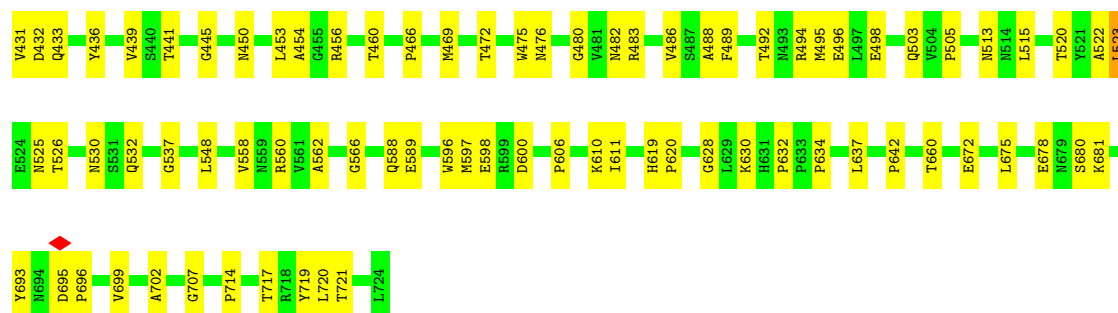




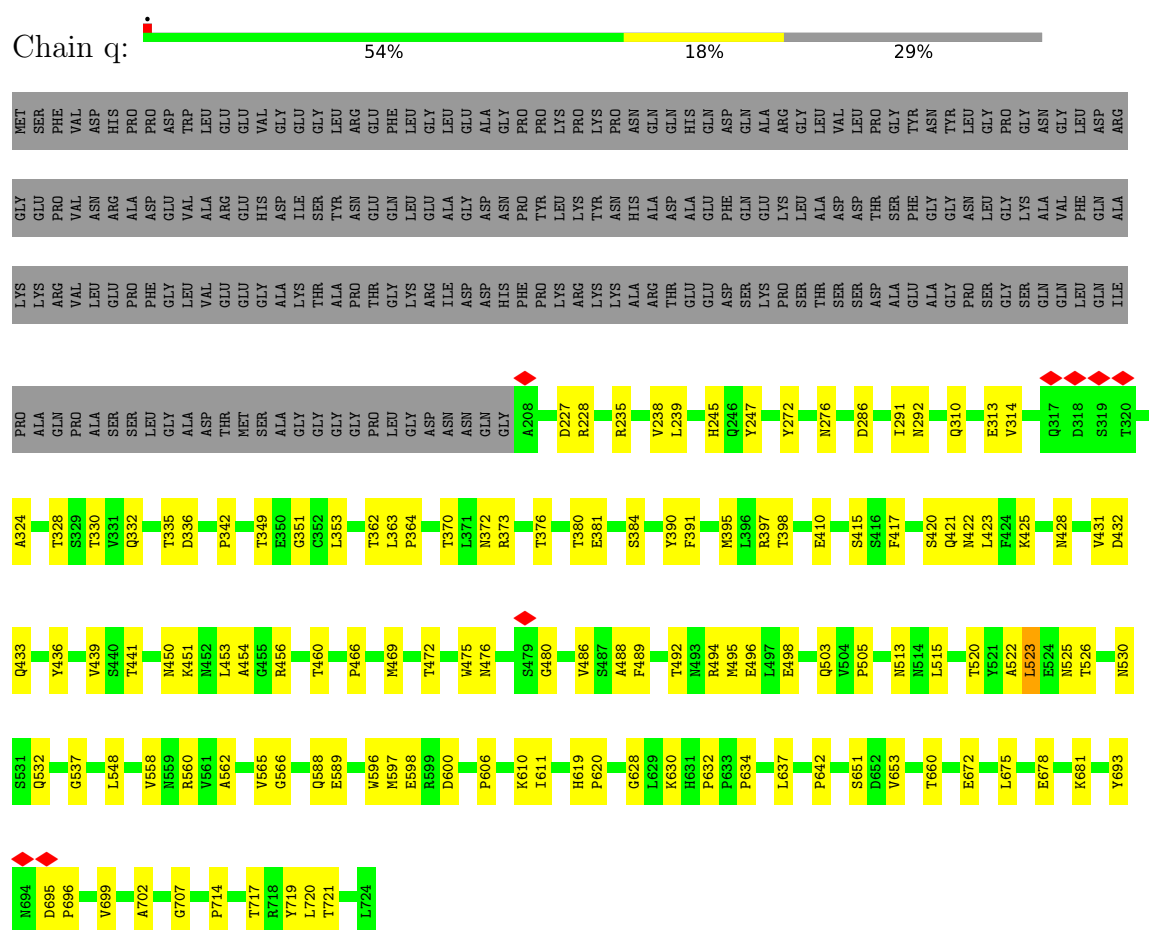
● Molecule 1: Capsid protein



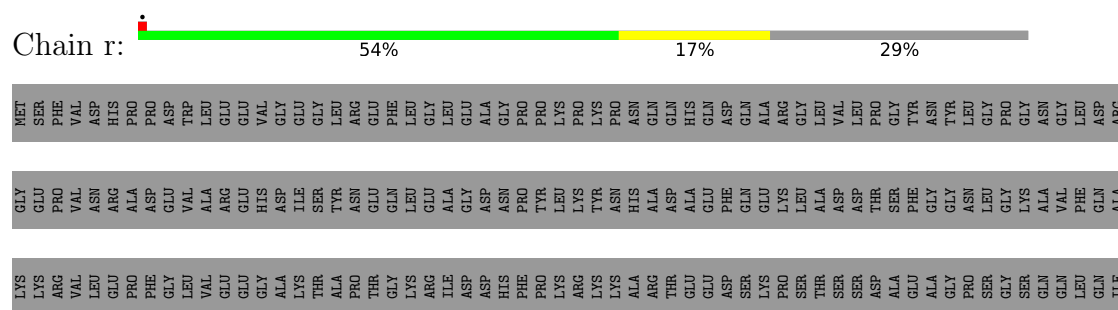




### • Molecule 1: Capsid protein



### • Molecule 1: Capsid protein

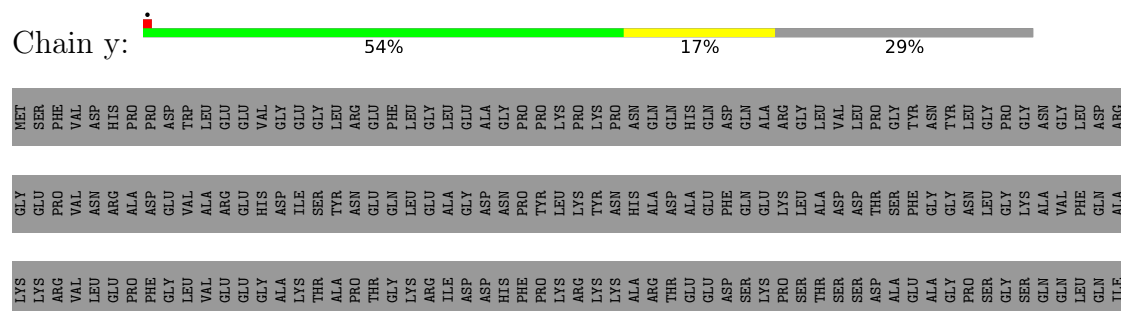








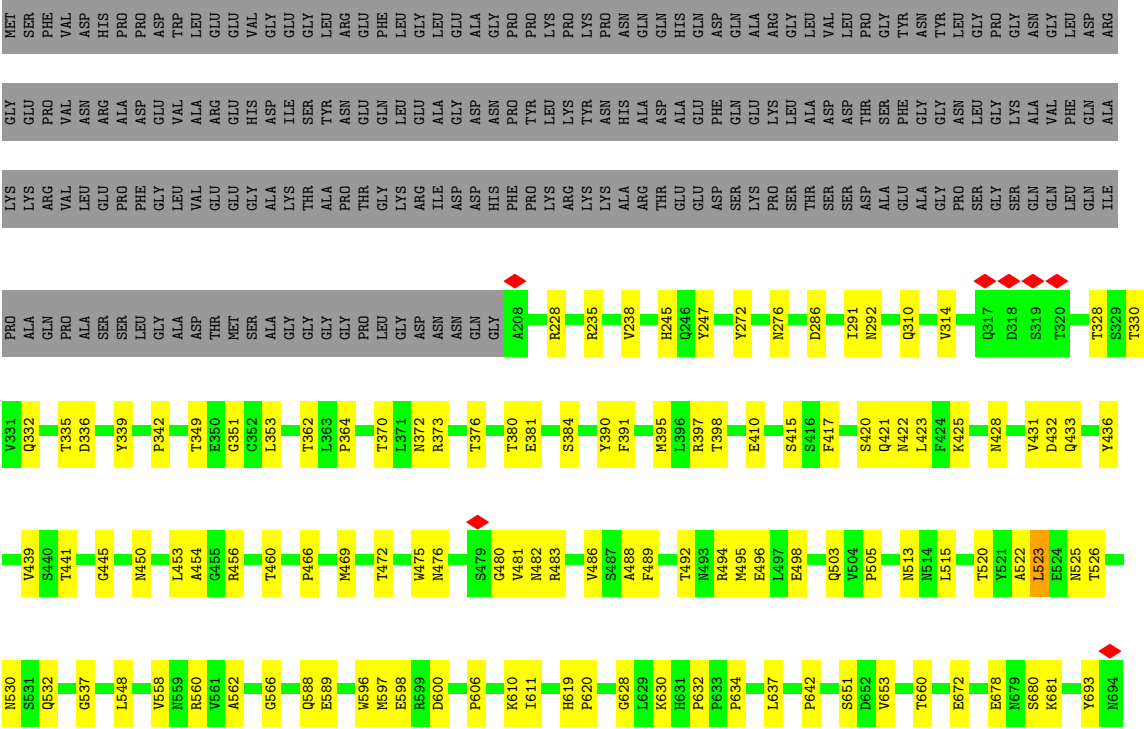




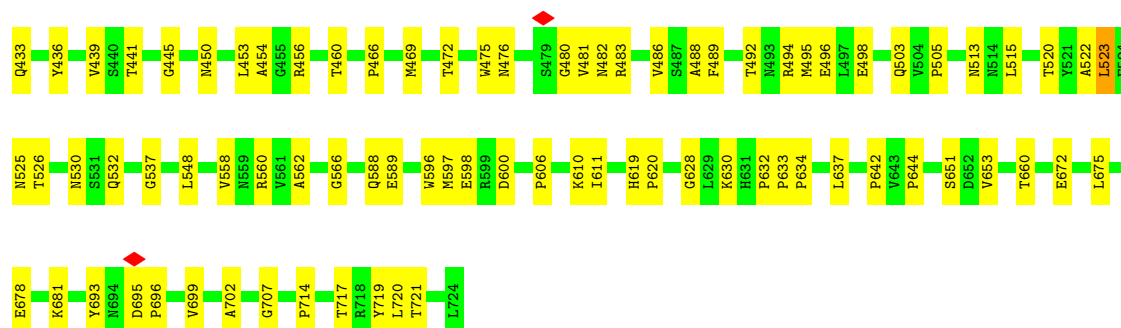




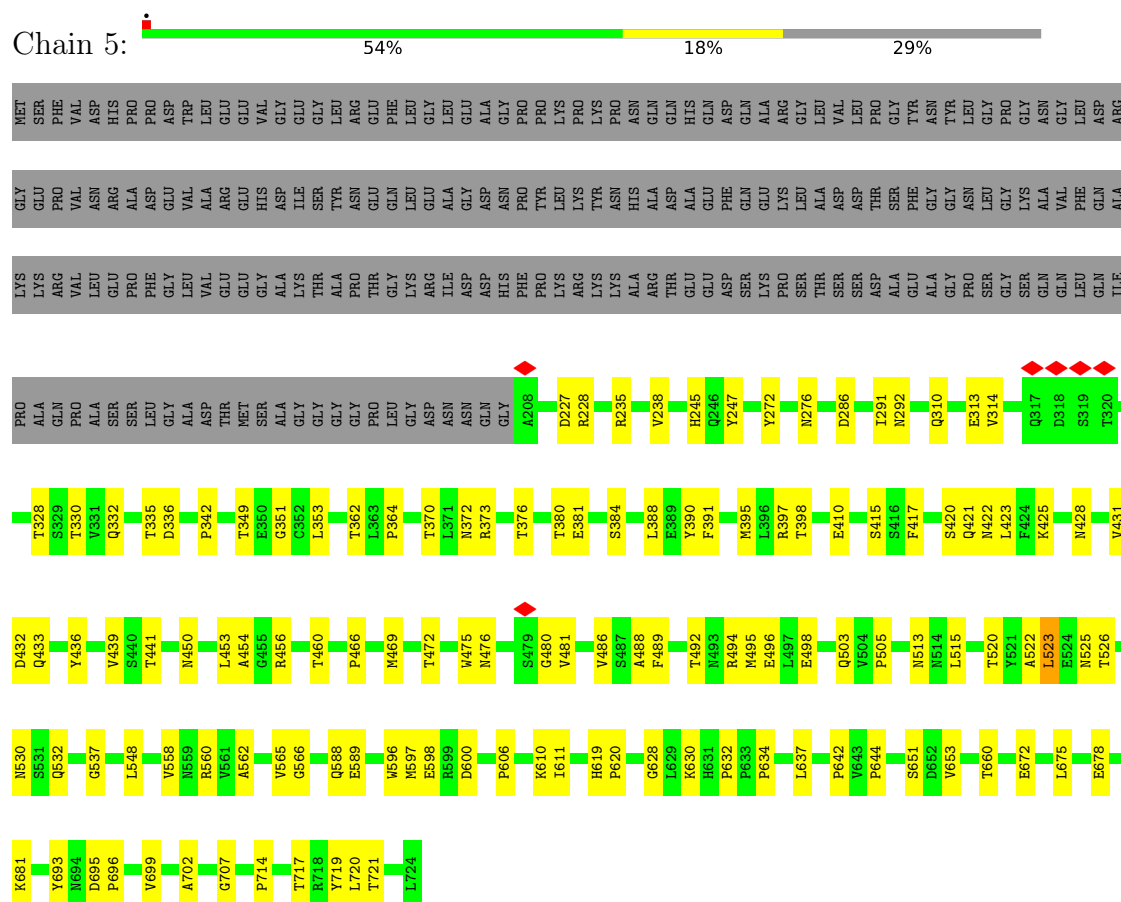
● Molecule 1: Capsid protein



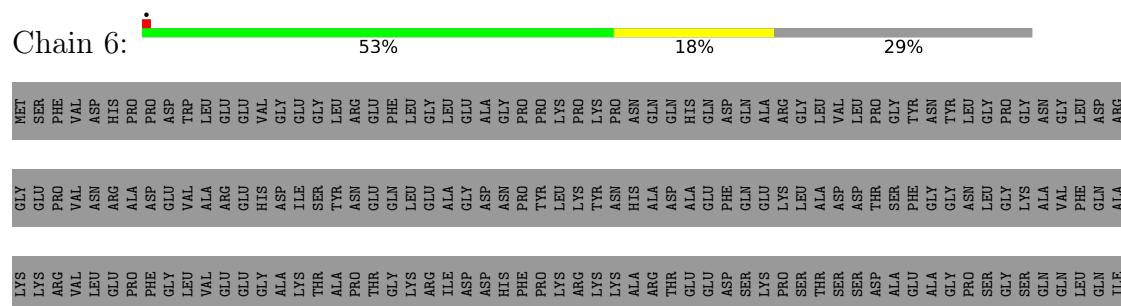


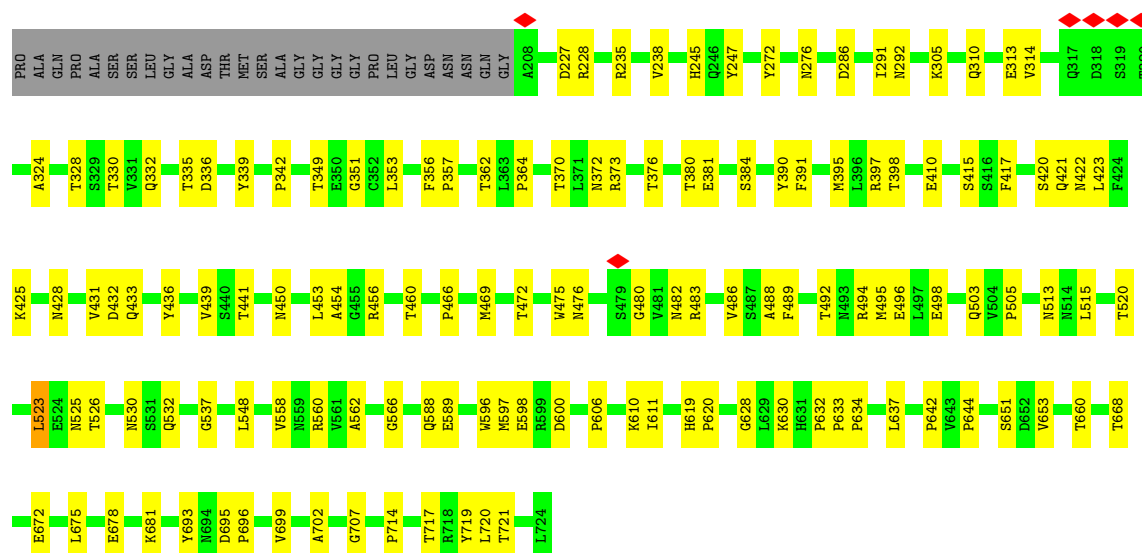


• Molecule 1: Capsid protein

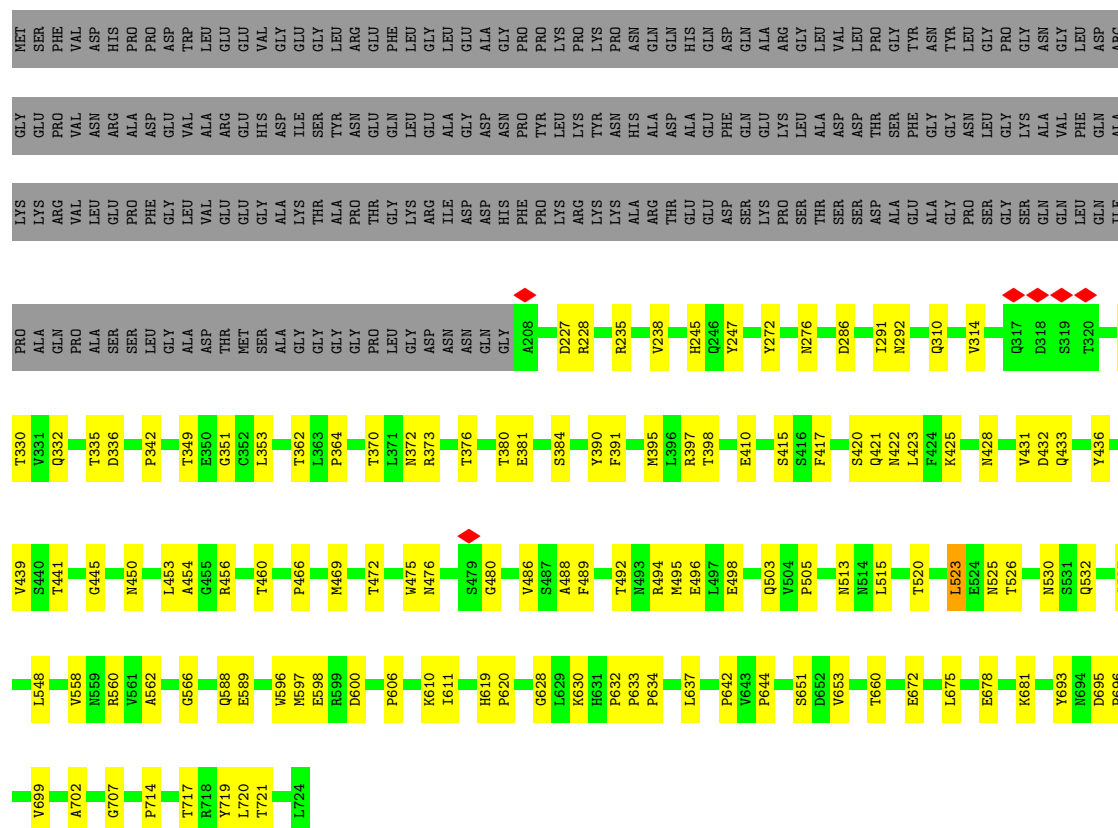


• Molecule 1: Capsid protein

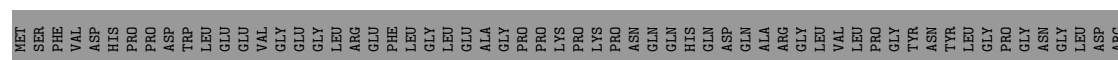


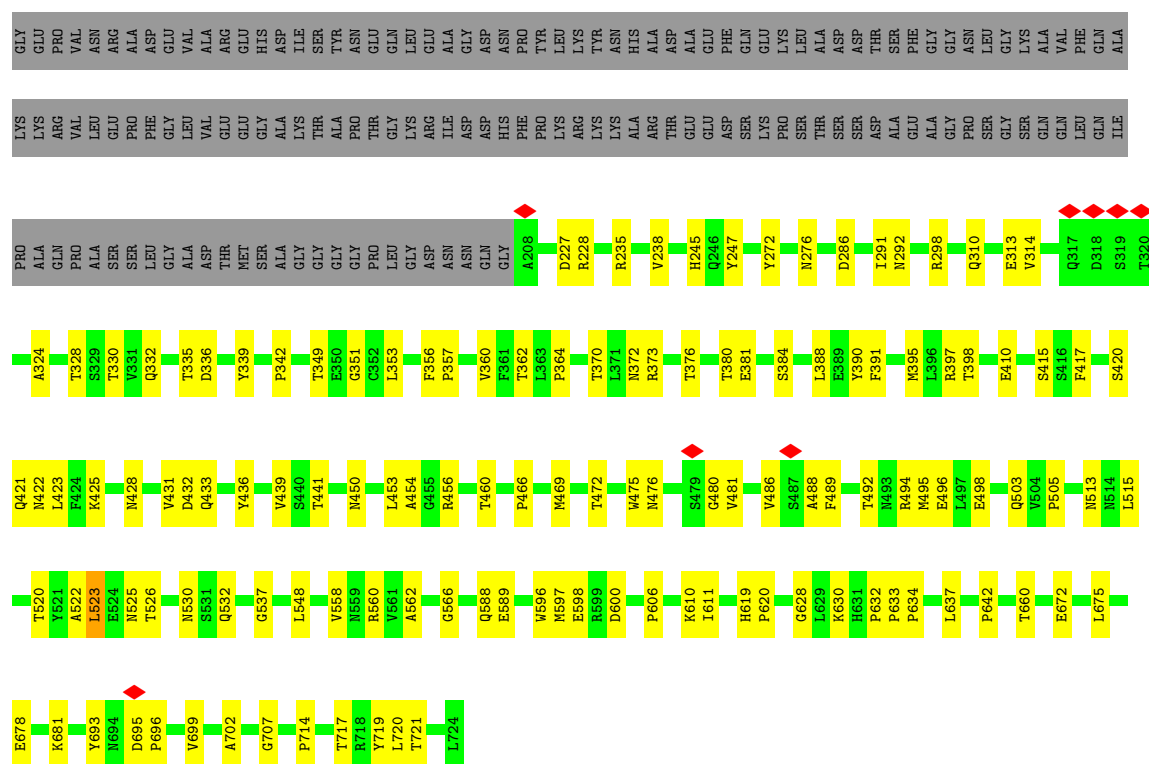


• Molecule 1: Capsid protein



• Molecule 1: Capsid protein





- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')







- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')





- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



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- Molecule 2: DNA (5'-D(P\*AP\*A)-3')





- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



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- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



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- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



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- Molecule 2: DNA (5'-D(P\*AP\*A)-3')







- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



- Molecule 2: DNA (5'-D(P\*AP\*A)-3')



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	45	Depositor
Minimum defocus (nm)	1289	Depositor
Maximum defocus (nm)	3967	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	22.666	Depositor
Minimum map value	-18.405	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size (Å)	467.5, 467.5, 467.5	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.935, 0.935, 0.935	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	1	0.41	0/4244	0.59	0/5800
1	2	0.41	0/4244	0.59	0/5800
1	3	0.41	0/4244	0.59	0/5800
1	4	0.41	0/4244	0.59	0/5800
1	5	0.41	0/4244	0.59	0/5800
1	6	0.41	0/4244	0.59	0/5800
1	7	0.41	0/4244	0.59	0/5800
1	8	0.41	0/4244	0.59	0/5800
1	A	0.41	0/4244	0.59	0/5800
1	B	0.41	0/4244	0.59	0/5800
1	C	0.41	0/4244	0.59	0/5800
1	D	0.41	0/4244	0.59	0/5800
1	E	0.41	0/4244	0.59	0/5800
1	F	0.41	0/4244	0.59	0/5800
1	G	0.41	0/4244	0.59	0/5800
1	H	0.41	0/4244	0.59	0/5800
1	I	0.41	0/4244	0.59	0/5800
1	J	0.41	0/4244	0.59	0/5800
1	K	0.41	0/4244	0.59	0/5800
1	L	0.41	0/4244	0.59	0/5800
1	M	0.41	0/4244	0.59	0/5800
1	N	0.41	0/4244	0.59	0/5800
1	O	0.41	0/4244	0.59	0/5800
1	P	0.41	0/4244	0.59	0/5800
1	Q	0.41	0/4244	0.59	0/5800
1	R	0.41	0/4244	0.59	0/5800
1	S	0.41	0/4244	0.59	0/5800
1	T	0.41	0/4244	0.59	0/5800
1	U	0.41	0/4244	0.59	0/5800
1	V	0.41	0/4244	0.59	0/5800
1	W	0.41	0/4244	0.59	0/5800
1	X	0.41	0/4244	0.59	0/5800
1	Y	0.41	0/4244	0.59	0/5800
1	Z	0.41	0/4244	0.59	0/5800

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	a	0.41	0/4244	0.59	0/5800
1	b	0.41	0/4244	0.59	0/5800
1	c	0.41	0/4244	0.59	0/5800
1	d	0.41	0/4244	0.59	0/5800
1	e	0.41	0/4244	0.59	0/5800
1	f	0.41	0/4244	0.59	0/5800
1	g	0.41	0/4244	0.59	0/5800
1	h	0.41	0/4244	0.59	0/5800
1	i	0.41	0/4244	0.59	0/5800
1	j	0.41	0/4244	0.59	0/5800
1	k	0.41	0/4244	0.59	0/5800
1	l	0.41	0/4244	0.59	0/5800
1	m	0.41	0/4244	0.59	0/5800
1	n	0.41	0/4244	0.59	0/5800
1	o	0.41	0/4244	0.59	0/5800
1	p	0.41	0/4244	0.59	0/5800
1	q	0.41	0/4244	0.59	0/5800
1	r	0.41	0/4244	0.59	0/5800
1	s	0.41	0/4244	0.59	0/5800
1	t	0.41	0/4244	0.59	0/5800
1	u	0.41	0/4244	0.59	0/5800
1	v	0.41	0/4244	0.59	0/5800
1	w	0.41	0/4244	0.59	0/5800
1	x	0.41	0/4244	0.59	0/5800
1	y	0.41	0/4244	0.59	0/5800
1	z	0.41	0/4244	0.59	0/5800
2	0	0.26	0/47	0.42	0/70
2	0A	0.25	0/47	0.42	0/70
2	1A	0.26	0/47	0.42	0/70
2	2A	0.26	0/47	0.42	0/70
2	3A	0.26	0/47	0.42	0/70
2	4A	0.26	0/47	0.42	0/70
2	5A	0.26	0/47	0.42	0/70
2	9	0.27	0/47	0.42	0/70
2	AA	0.27	0/47	0.42	0/70
2	BA	0.25	0/47	0.42	0/70
2	CA	0.27	0/47	0.42	0/70
2	DA	0.26	0/47	0.42	0/70
2	EA	0.26	0/47	0.42	0/70
2	FA	0.25	0/47	0.42	0/70
2	GA	0.25	0/47	0.42	0/70
2	HA	0.26	0/47	0.42	0/70
2	IA	0.26	0/47	0.42	0/70

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
2	JA	0.26	0/47	0.42	0/70
2	KA	0.26	0/47	0.42	0/70
2	LA	0.26	0/47	0.42	0/70
2	MA	0.26	0/47	0.42	0/70
2	NA	0.26	0/47	0.42	0/70
2	OA	0.26	0/47	0.42	0/70
2	PA	0.26	0/47	0.42	0/70
2	QA	0.26	0/47	0.42	0/70
2	RA	0.25	0/47	0.42	0/70
2	SA	0.26	0/47	0.42	0/70
2	TA	0.26	0/47	0.42	0/70
2	UA	0.26	0/47	0.42	0/70
2	VA	0.26	0/47	0.42	0/70
2	WA	0.26	0/47	0.42	0/70
2	XA	0.25	0/47	0.42	0/70
2	YA	0.26	0/47	0.42	0/70
2	ZA	0.25	0/47	0.42	0/70
2	aA	0.25	0/47	0.42	0/70
2	bA	0.26	0/47	0.42	0/70
2	cA	0.26	0/47	0.42	0/70
2	dA	0.26	0/47	0.42	0/70
2	eA	0.26	0/47	0.42	0/70
2	fA	0.25	0/47	0.42	0/70
2	gA	0.26	0/47	0.42	0/70
2	hA	0.26	0/47	0.42	0/70
2	iA	0.25	0/47	0.42	0/70
2	jA	0.26	0/47	0.42	0/70
2	kA	0.26	0/47	0.42	0/70
2	lA	0.26	0/47	0.42	0/70
2	mA	0.26	0/47	0.42	0/70
2	nA	0.26	0/47	0.42	0/70
2	oA	0.25	0/47	0.42	0/70
2	pA	0.26	0/47	0.42	0/70
2	qA	0.25	0/47	0.42	0/70
2	rA	0.26	0/47	0.42	0/70
2	sA	0.26	0/47	0.42	0/70
2	tA	0.26	0/47	0.42	0/70
2	uA	0.26	0/47	0.42	0/70
2	vA	0.25	0/47	0.42	0/70
2	wA	0.26	0/47	0.42	0/70
2	xA	0.26	0/47	0.42	0/70
2	yA	0.26	0/47	0.42	0/70
2	zA	0.26	0/47	0.42	0/70

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
All	All	0.41	0/257460	0.59	0/352200

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	1	4116	0	3863	125	0
1	2	4116	0	3863	122	0
1	3	4116	0	3863	121	0
1	4	4116	0	3863	128	0
1	5	4116	0	3863	123	0
1	6	4116	0	3863	125	0
1	7	4116	0	3863	119	0
1	8	4116	0	3863	124	0
1	A	4116	0	3863	127	0
1	B	4116	0	3863	125	0
1	C	4116	0	3863	119	0
1	D	4116	0	3863	122	0
1	E	4116	0	3863	122	0
1	F	4116	0	3863	127	0
1	G	4116	0	3863	126	0
1	H	4116	0	3863	122	0
1	I	4116	0	3863	121	0
1	J	4116	0	3863	119	0
1	K	4116	0	3863	120	0
1	L	4116	0	3863	123	0
1	M	4116	0	3863	125	0
1	N	4116	0	3863	123	0
1	O	4116	0	3863	126	0
1	P	4116	0	3863	123	0
1	Q	4116	0	3863	121	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	4116	0	3863	122	0
1	S	4116	0	3863	125	0
1	T	4116	0	3863	128	0
1	U	4116	0	3863	124	0
1	V	4116	0	3863	122	0
1	W	4116	0	3863	125	0
1	X	4116	0	3863	130	0
1	Y	4116	0	3863	128	0
1	Z	4116	0	3863	129	0
1	a	4116	0	3863	122	0
1	b	4116	0	3863	129	0
1	c	4116	0	3863	129	0
1	d	4116	0	3863	124	0
1	e	4116	0	3863	122	0
1	f	4116	0	3863	122	0
1	g	4116	0	3863	126	0
1	h	4116	0	3863	125	0
1	i	4116	0	3863	124	0
1	j	4116	0	3863	128	0
1	k	4116	0	3863	125	0
1	l	4116	0	3863	123	0
1	m	4116	0	3863	123	0
1	n	4116	0	3863	126	0
1	o	4116	0	3863	122	0
1	p	4116	0	3863	124	0
1	q	4116	0	3863	123	0
1	r	4116	0	3863	123	0
1	s	4116	0	3863	132	0
1	t	4116	0	3863	125	0
1	u	4116	0	3863	121	0
1	v	4116	0	3863	122	0
1	w	4116	0	3863	126	0
1	x	4116	0	3863	126	0
1	y	4116	0	3863	124	0
1	z	4116	0	3863	122	0
2	0	42	0	23	28	0
2	0A	42	0	23	28	0
2	1A	42	0	23	30	0
2	2A	42	0	23	28	0
2	3A	42	0	23	29	0
2	4A	42	0	23	27	0
2	5A	42	0	23	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	9	42	0	23	29	0
2	AA	42	0	23	29	0
2	BA	42	0	23	30	0
2	CA	42	0	23	28	0
2	DA	42	0	23	28	0
2	EA	42	0	23	28	0
2	FA	42	0	23	28	0
2	GA	42	0	23	26	0
2	HA	42	0	23	28	0
2	IA	42	0	23	28	0
2	JA	42	0	23	28	0
2	KA	42	0	23	30	0
2	LA	42	0	23	29	0
2	MA	42	0	23	27	0
2	NA	42	0	23	29	0
2	OA	42	0	23	28	0
2	PA	42	0	23	28	0
2	QA	42	0	23	28	0
2	RA	42	0	23	30	0
2	SA	42	0	23	28	0
2	TA	42	0	23	28	0
2	UA	42	0	23	26	0
2	VA	42	0	23	27	0
2	WA	42	0	23	28	0
2	XA	42	0	23	29	0
2	YA	42	0	23	28	0
2	ZA	42	0	23	29	0
2	aA	42	0	23	29	0
2	bA	42	0	23	30	0
2	cA	42	0	23	27	0
2	dA	42	0	23	28	0
2	eA	42	0	23	29	0
2	fA	42	0	23	27	0
2	gA	42	0	23	29	0
2	hA	42	0	23	27	0
2	iA	42	0	23	29	0
2	jA	42	0	23	27	0
2	kA	42	0	23	28	0
2	lA	42	0	23	28	0
2	mA	42	0	23	30	0
2	nA	42	0	23	28	0
2	oA	42	0	23	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	pA	42	0	23	28	0
2	qA	42	0	23	27	0
2	rA	42	0	23	28	0
2	sA	42	0	23	28	0
2	tA	42	0	23	28	0
2	uA	42	0	23	28	0
2	vA	42	0	23	27	0
2	wA	42	0	23	26	0
2	xA	42	0	23	28	0
2	yA	42	0	23	28	0
2	zA	42	0	23	28	0
All	All	249480	0	233160	6225	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 13.

The worst 5 of 6225 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:620:PRO:HD2	2:ZA:997:DA:C2'	1.00	1.48
1:n:620:PRO:HD2	2:gA:997:DA:C2'	1.00	1.48
1:z:620:PRO:HD2	2:tA:997:DA:C2'	1.00	1.48
1:N:620:PRO:HD2	2:DA:997:DA:C2'	1.00	1.48
1:f:620:PRO:HD2	2:XA:997:DA:C2'	1.00	1.48

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	1	515/724 (71%)	499 (97%)	16 (3%)	0	<b>100</b> <b>100</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	3	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	4	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	5	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	6	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	7	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	8	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	A	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	B	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	C	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	D	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	E	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	F	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	G	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	H	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	I	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	J	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	K	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	L	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	M	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	N	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	O	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	P	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	Q	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	R	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	S	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	T	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	U	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	V	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	W	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	X	515/724 (71%)	499 (97%)	16 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Y	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	Z	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	a	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	b	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	c	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	d	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	e	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	f	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	g	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	h	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	i	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	j	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	k	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	l	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	m	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	n	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	o	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	p	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	q	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	r	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	s	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	t	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	u	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	v	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	w	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	x	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	y	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
1	z	515/724 (71%)	499 (97%)	16 (3%)	0	100	100
All	All	30900/43440 (71%)	29940 (97%)	960 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	2	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	3	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	4	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	5	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	6	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	7	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	8	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	A	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	B	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	C	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	D	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	E	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	F	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	G	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	H	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	I	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	J	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	K	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	L	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	M	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	N	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	O	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	P	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	Q	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	R	451/613 (74%)	450 (100%)	1 (0%)	87	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	S	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	T	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	U	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	V	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	W	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	X	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	Y	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	Z	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	a	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	b	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	c	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	d	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	e	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	f	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	g	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	h	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	i	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	j	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	k	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	l	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	m	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	n	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	o	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	p	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	q	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	r	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	s	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	t	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	u	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	v	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	w	451/613 (74%)	450 (100%)	1 (0%)	87	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	x	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	y	451/613 (74%)	450 (100%)	1 (0%)	87	96
1	z	451/613 (74%)	450 (100%)	1 (0%)	87	96
All	All	27060/36780 (74%)	27000 (100%)	60 (0%)	85	96

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	c	523	LEU
1	4	523	LEU
1	j	523	LEU
1	3	523	LEU
1	8	523	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 718 such sidechains are listed below:

Mol	Chain	Res	Type
1	m	507	GLN
1	v	525	ASN
1	n	525	ASN
1	m	476	ASN
1	r	261	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

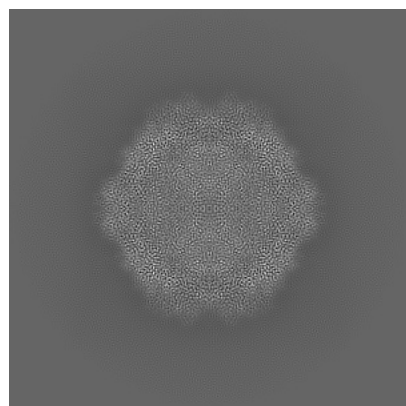
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-46748. These allow visual inspection of the internal detail of the map and identification of artifacts.

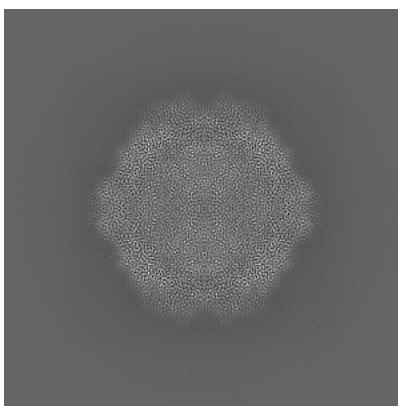
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

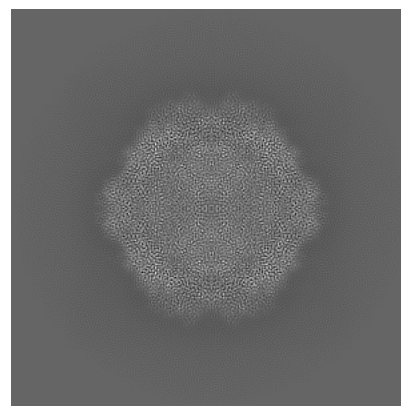
#### 6.1.1 Primary map



X

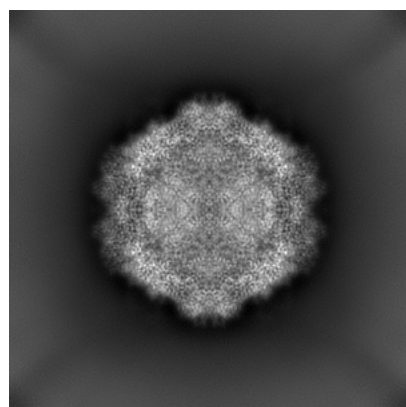


Y

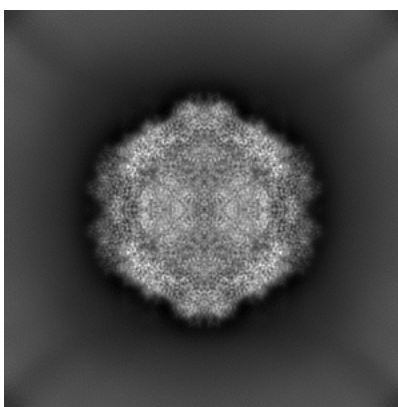


Z

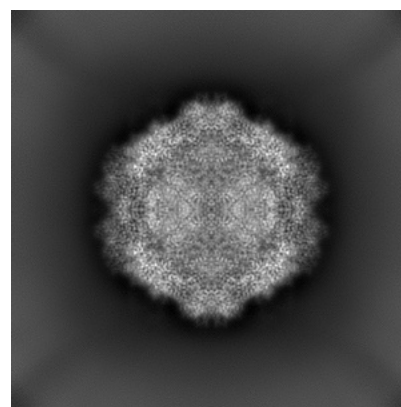
#### 6.1.2 Raw map



X



Y



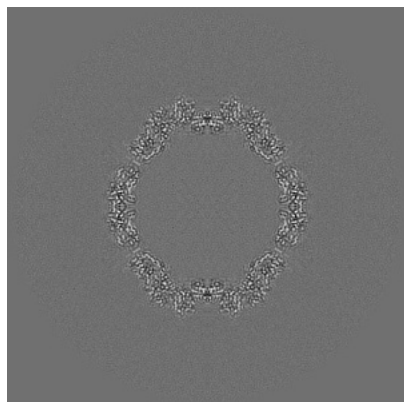
Z

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

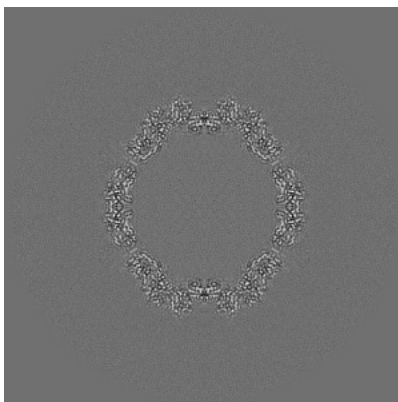


## 6.2 Central slices [i](#)

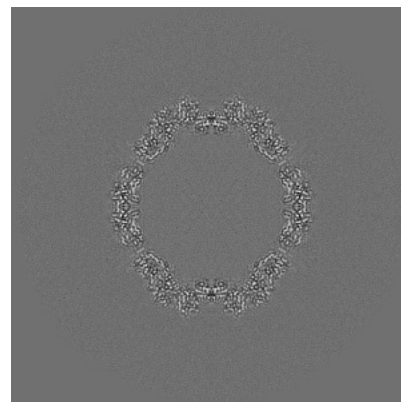
### 6.2.1 Primary map



X Index: 250

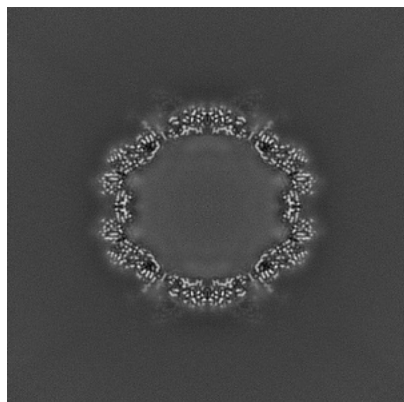


Y Index: 250

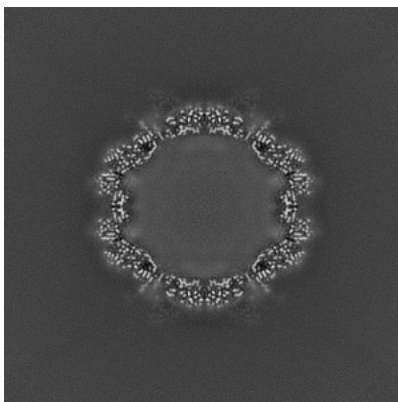


Z Index: 250

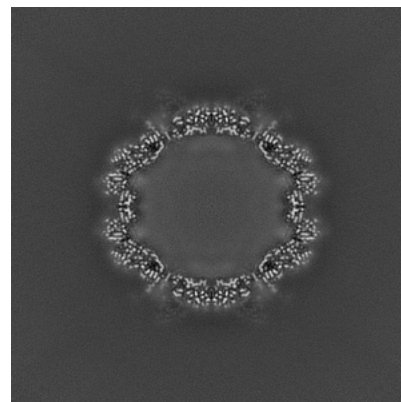
### 6.2.2 Raw map



X Index: 250



Y Index: 250

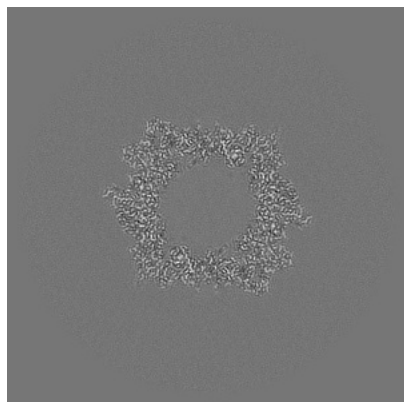


Z Index: 250

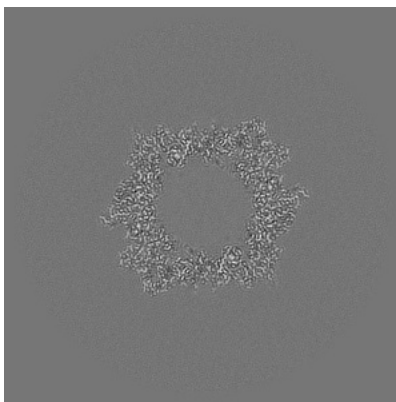
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

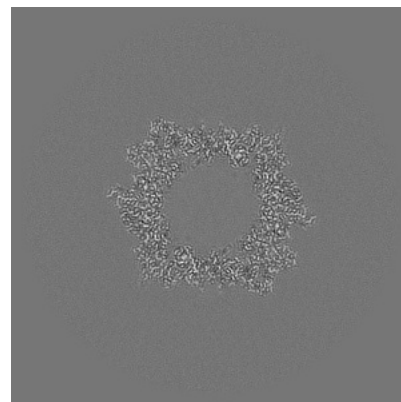
### 6.3.1 Primary map



X Index: 320

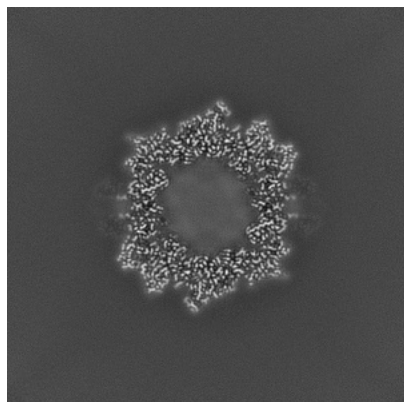


Y Index: 180

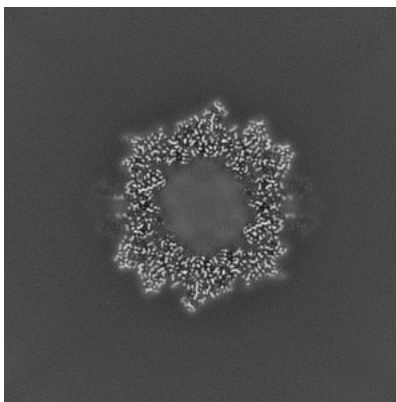


Z Index: 320

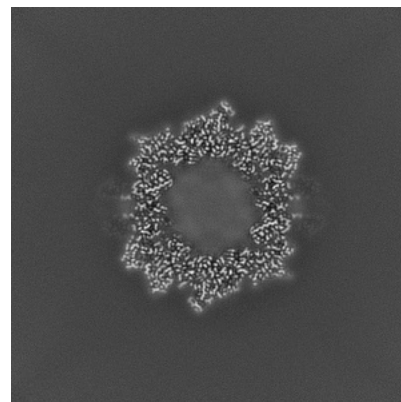
### 6.3.2 Raw map



X Index: 320



Y Index: 320

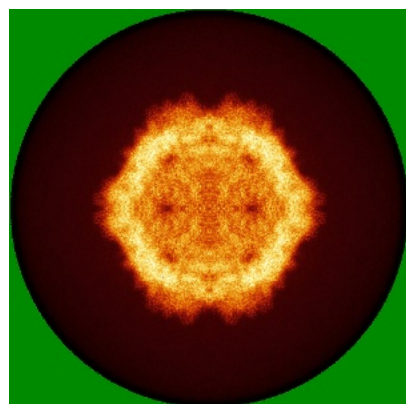


Z Index: 320

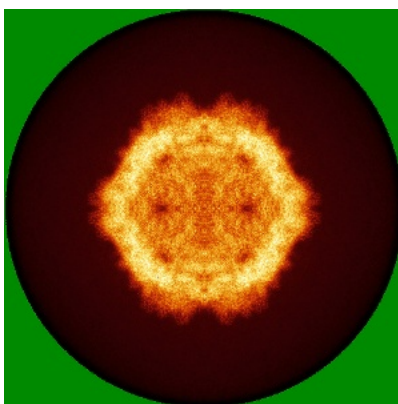
The images above show the largest variance slices of the map in three orthogonal directions.

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

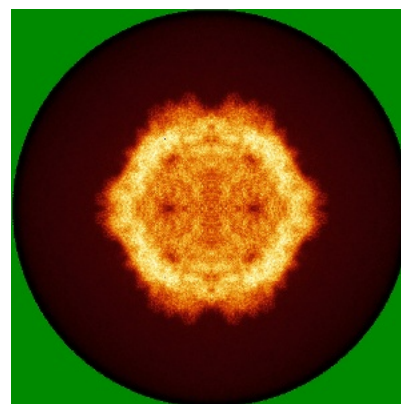
### 6.4.1 Primary map



X

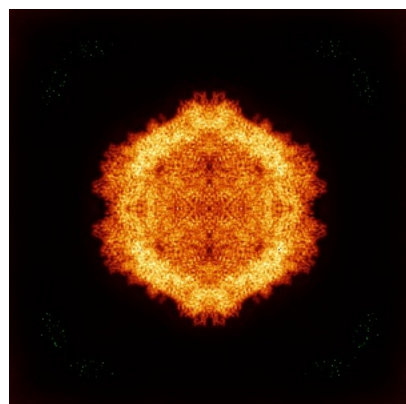


Y

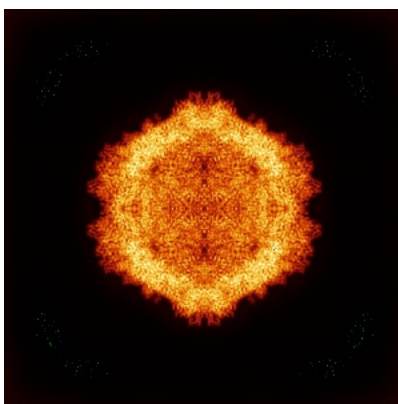


Z

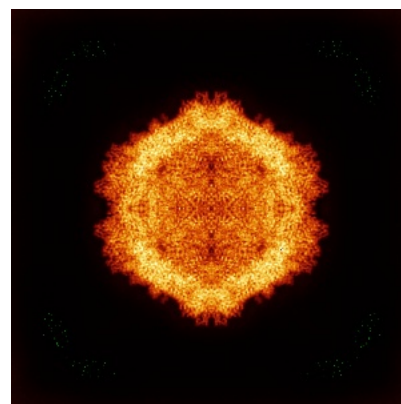
### 6.4.2 Raw map



X



Y

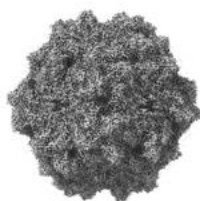


Z

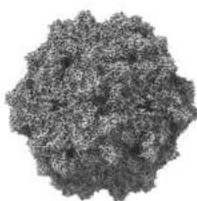
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

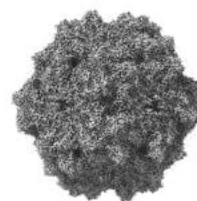
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

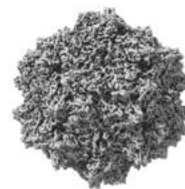
### 6.5.2 Raw map



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.

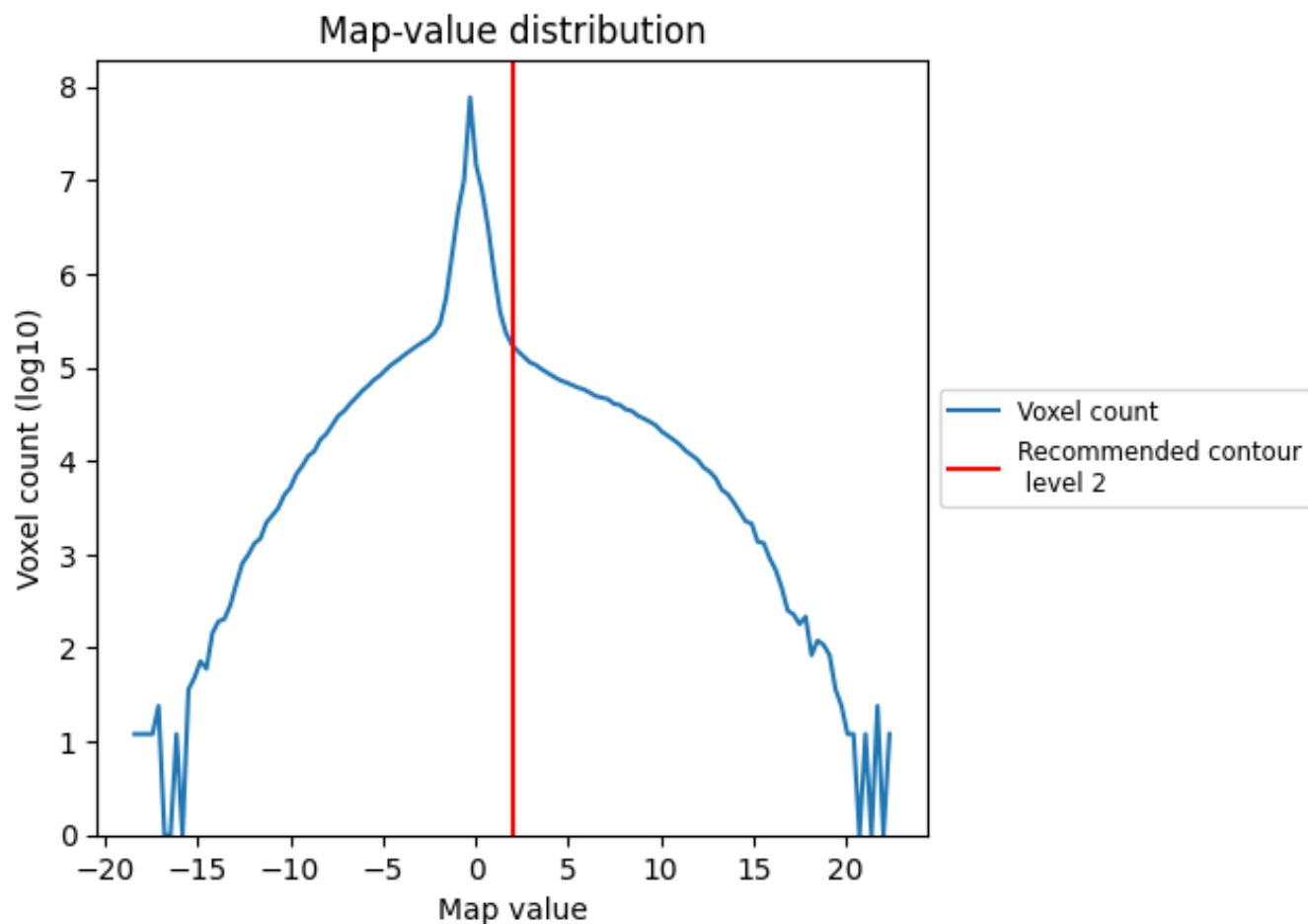
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

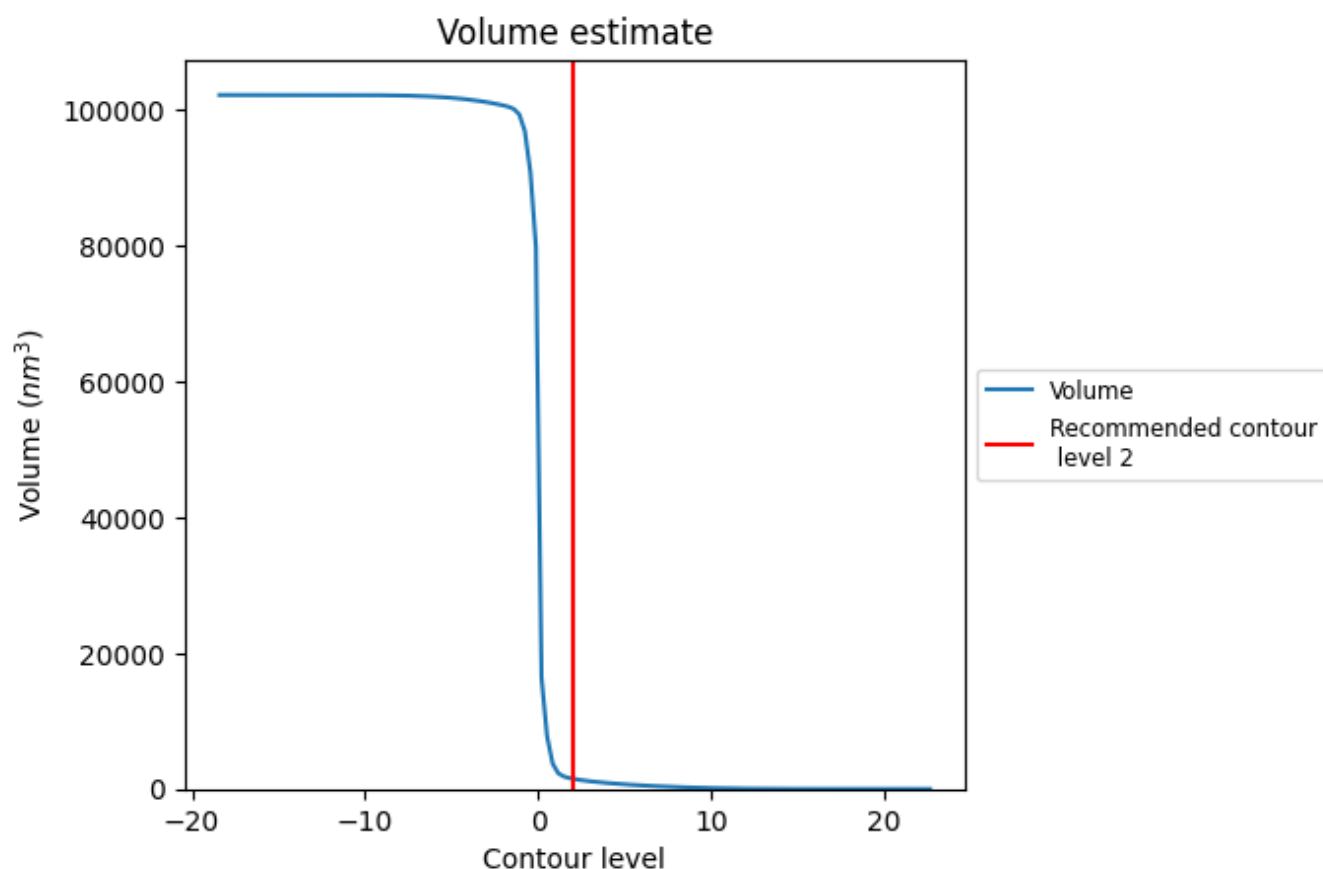
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

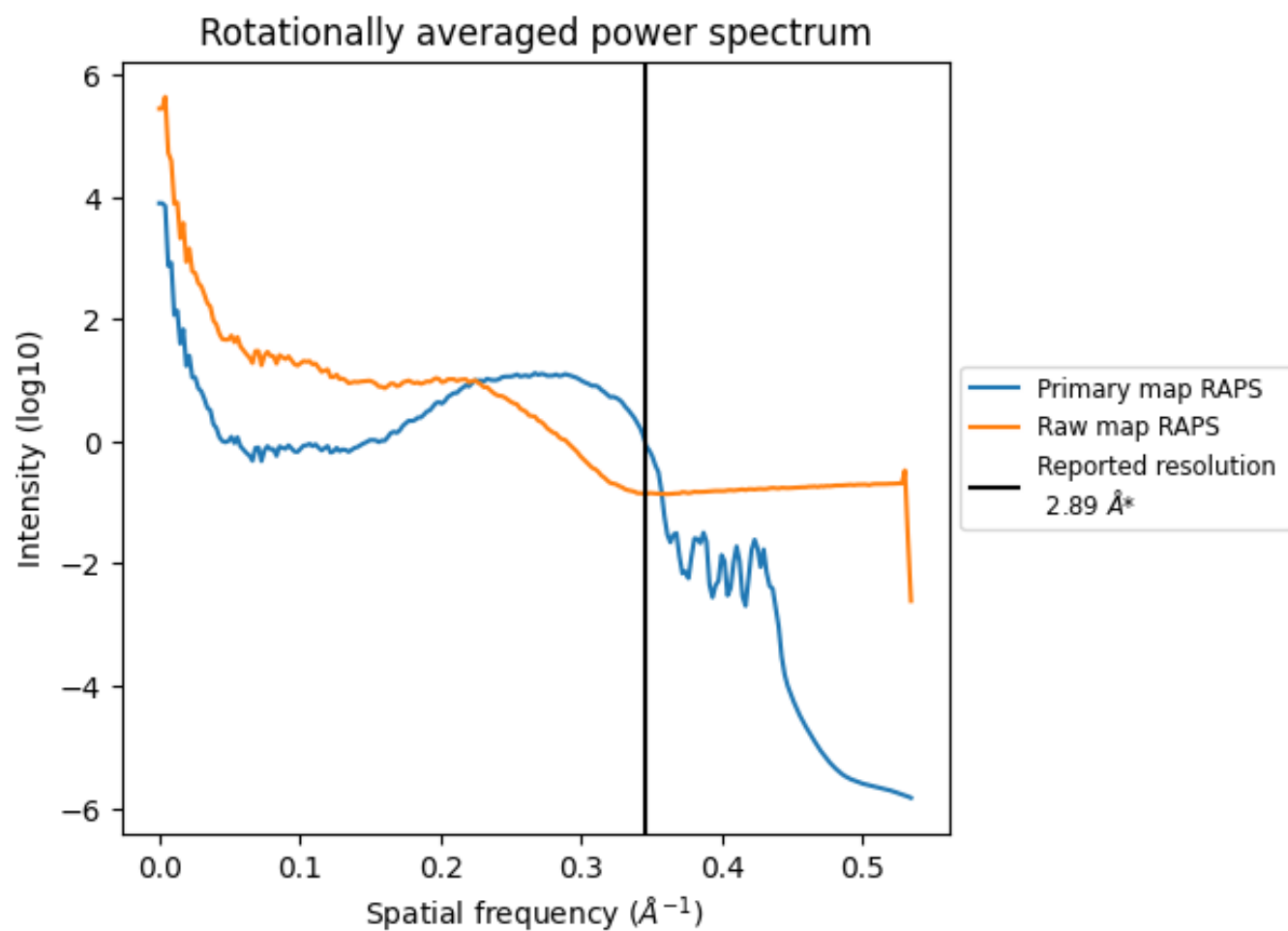
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1513  $\text{nm}^3$ ; this corresponds to an approximate mass of 1367 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 ⓘ

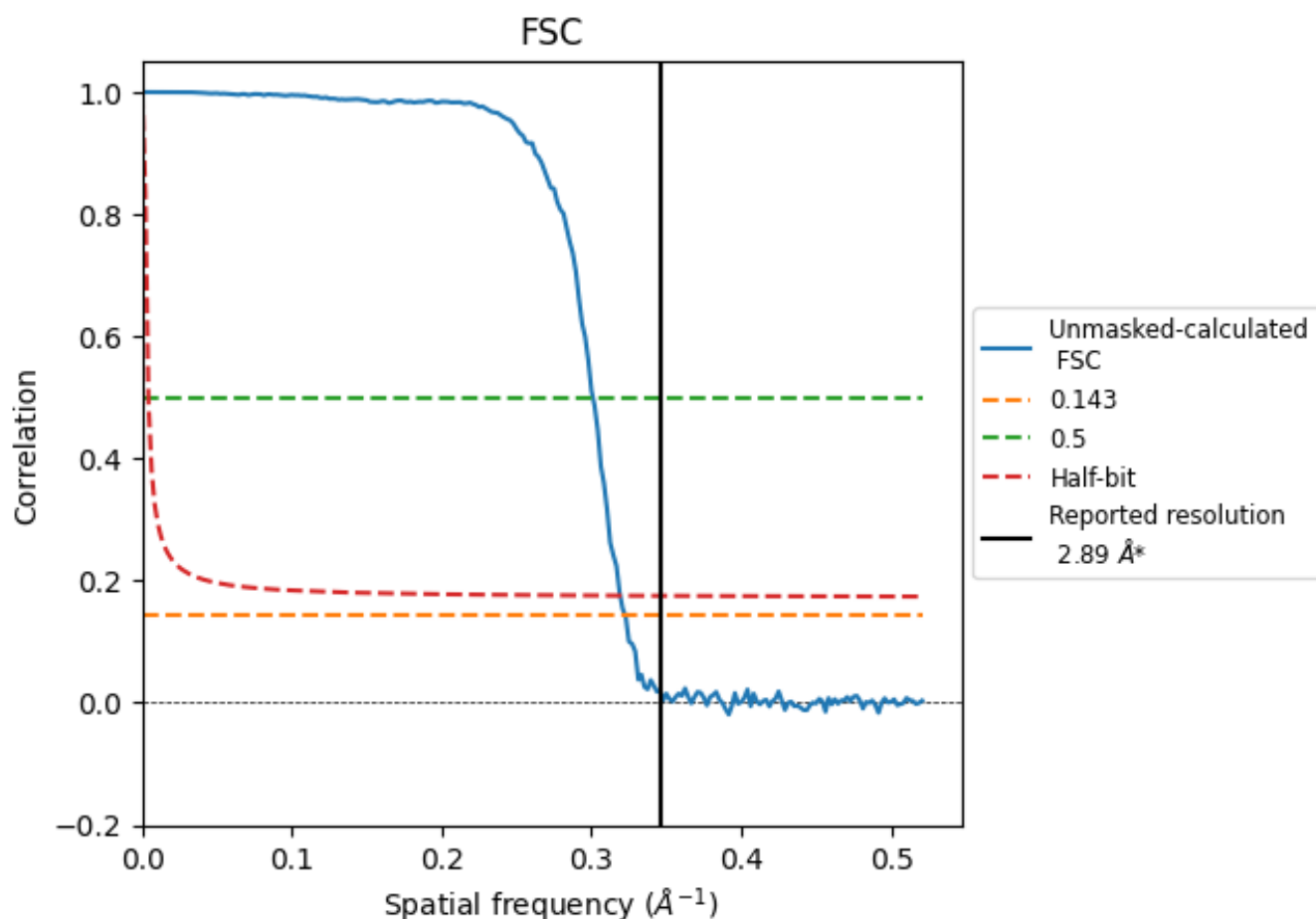


\*Reported resolution corresponds to spatial frequency of 0.346 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.346  $\text{\AA}^{-1}$



## 8.2 Resolution estimates [i](#)

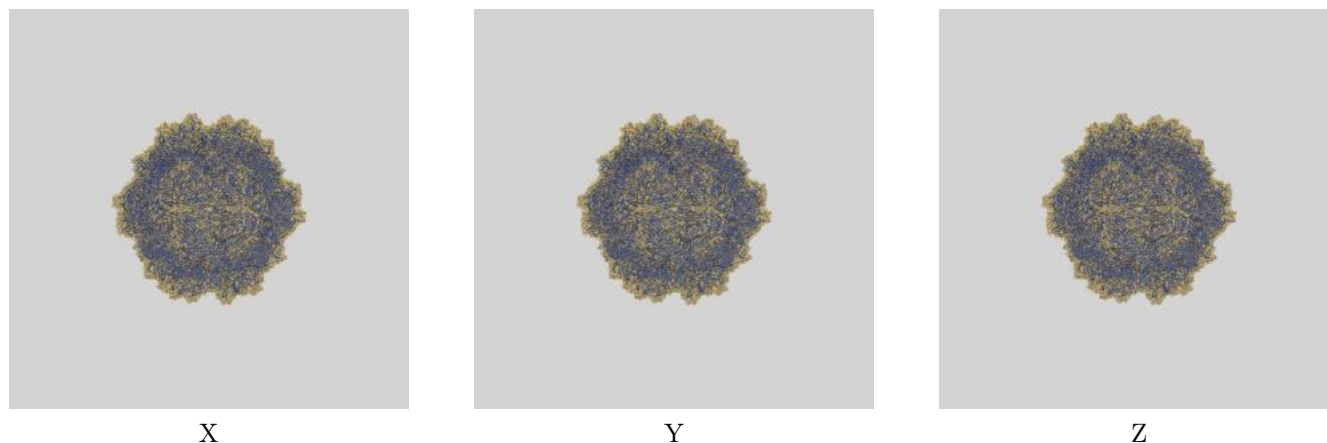
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.89	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.10	3.32	3.13

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

## 9 Map-model fit [i](#)

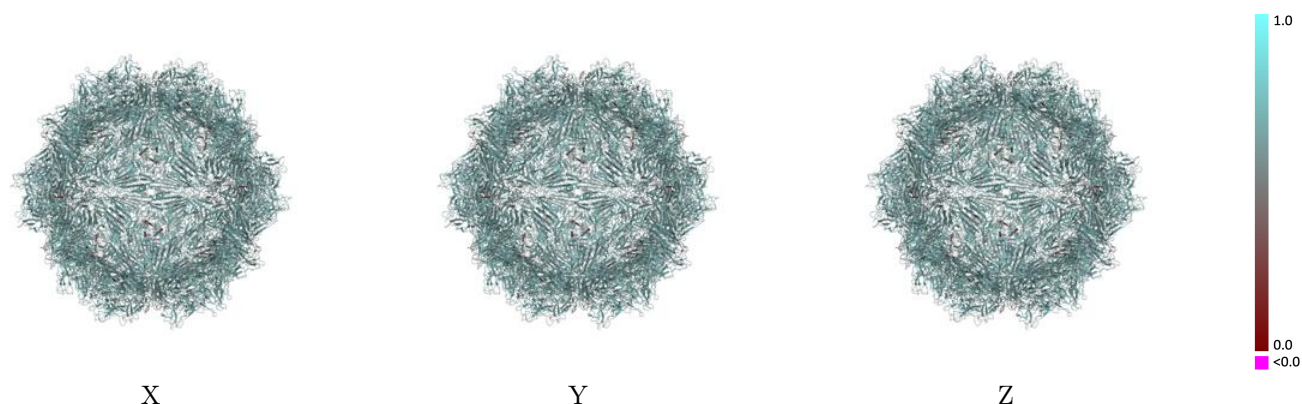
This section contains information regarding the fit between EMDB map EMD-46748 and PDB model 9DCB. Per-residue inclusion information can be found in section [3](#) on page [14](#).

### 9.1 Map-model overlay [i](#)



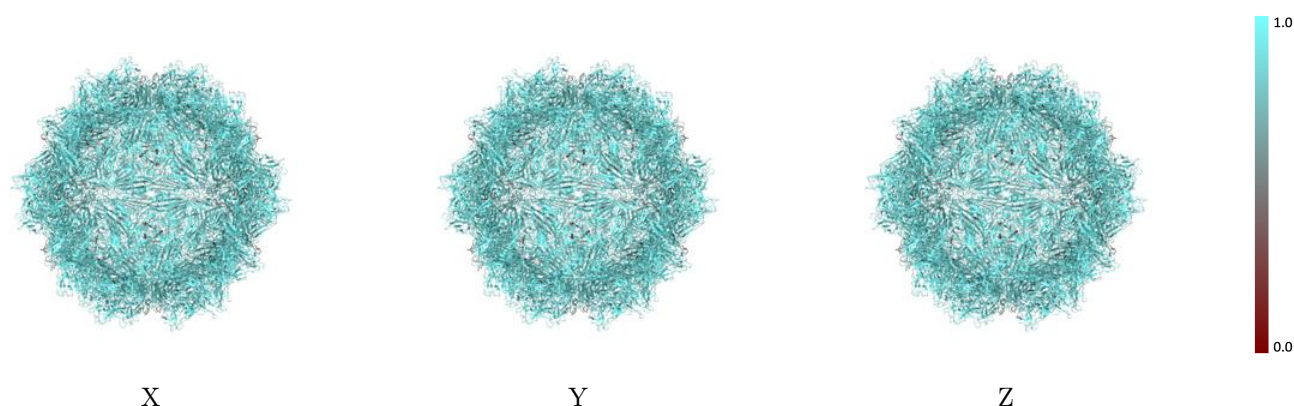
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



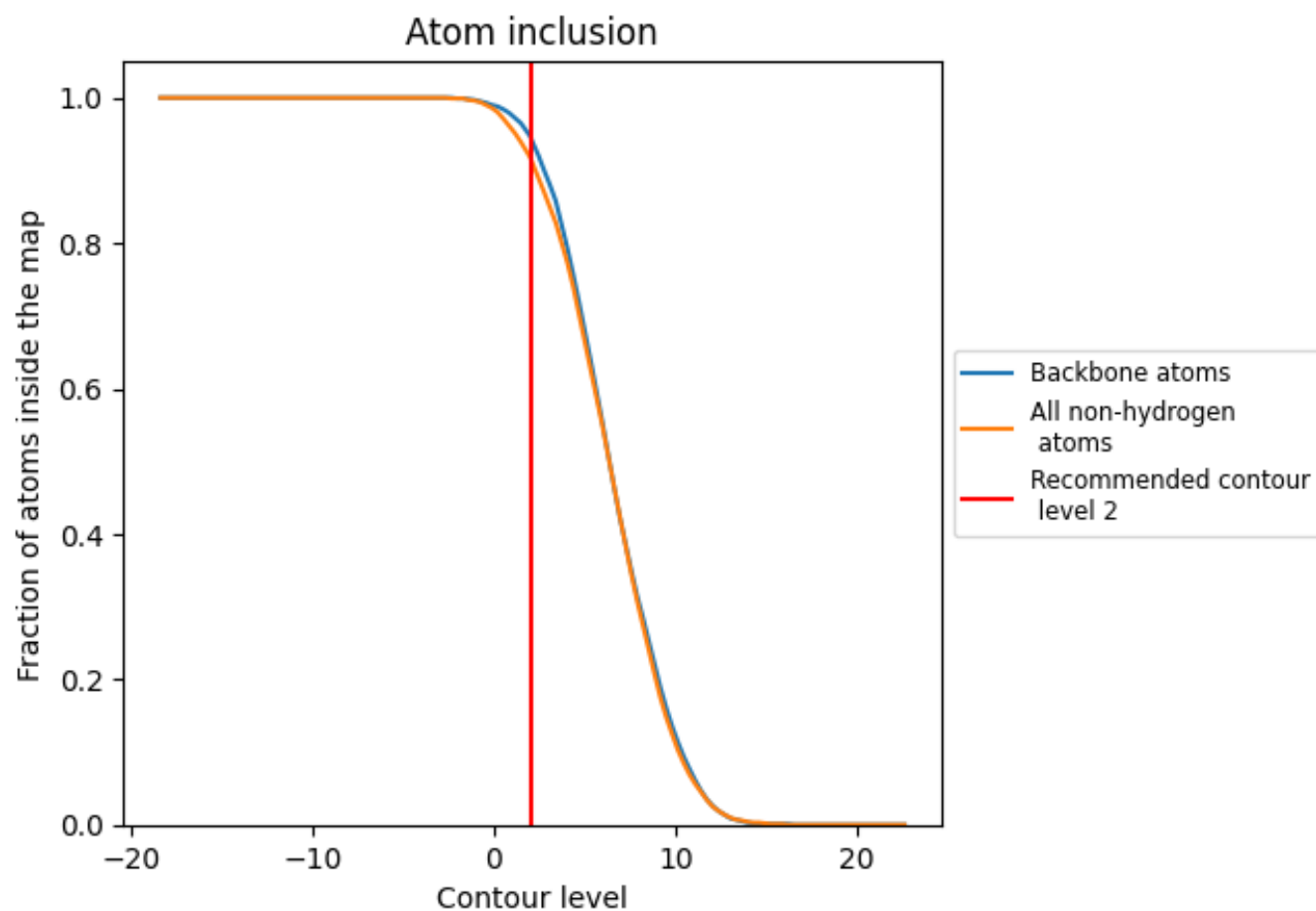
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 92% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9180	 0.6230
0	 0.3330	 0.1870
0A	 0.3330	 0.1970
1	 0.9240	 0.6270
1A	 0.3330	 0.1980
2	 0.9250	 0.6280
2A	 0.3330	 0.1860
3	 0.9230	 0.6270
3A	 0.3330	 0.1900
4	 0.9230	 0.6270
4A	 0.3330	 0.1840
5	 0.9230	 0.6280
5A	 0.3330	 0.1800
6	 0.9230	 0.6270
7	 0.9230	 0.6280
8	 0.9230	 0.6270
9	 0.3090	 0.1940
A	 0.9230	 0.6270
AA	 0.3090	 0.1810
B	 0.9230	 0.6270
BA	 0.3090	 0.1790
C	 0.9230	 0.6280
CA	 0.3330	 0.1730
D	 0.9250	 0.6270
DA	 0.3330	 0.1880
E	 0.9240	 0.6270
EA	 0.3330	 0.1720
F	 0.9230	 0.6270
FA	 0.3090	 0.1930
G	 0.9230	 0.6270
GA	 0.3090	 0.1820
H	 0.9230	 0.6280
HA	 0.3330	 0.1790
I	 0.9230	 0.6270
IA	 0.3330	 0.1770























































































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Chain	Atom inclusion	Q-score
J	 0.9240	 0.6270
JA	 0.3330	 0.1900
K	 0.9240	 0.6280
KA	 0.3090	 0.1750
L	 0.9250	 0.6270
LA	 0.3330	 0.1830
M	 0.9230	 0.6270
MA	 0.3090	 0.1880
N	 0.9230	 0.6270
NA	 0.3090	 0.1900
O	 0.9230	 0.6280
OA	 0.3090	 0.1910
P	 0.9240	 0.6270
PA	 0.3090	 0.1930
Q	 0.9250	 0.6270
QA	 0.3330	 0.1820
R	 0.9230	 0.6270
RA	 0.3090	 0.1800
S	 0.9230	 0.6270
SA	 0.3330	 0.1940
T	 0.9250	 0.6270
TA	 0.3090	 0.1750
U	 0.9230	 0.6280
UA	 0.3330	 0.1850
V	 0.9240	 0.6280
VA	 0.3330	 0.1920
W	 0.9240	 0.6270
WA	 0.3330	 0.1970
X	 0.9240	 0.6280
XA	 0.3330	 0.1900
Y	 0.9240	 0.6270
YA	 0.3330	 0.1730
Z	 0.9230	 0.6270
ZA	 0.3330	 0.1850
a	 0.9250	 0.6270
aA	 0.3090	 0.1970
b	 0.9230	 0.6270
bA	 0.3090	 0.1830
c	 0.9240	 0.6280
cA	 0.3330	 0.1930
d	 0.9230	 0.6270
dA	 0.3090	 0.1830





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Chain	Atom inclusion	Q-score
e	 0.9230	 0.6270
eA	 0.3330	 0.1910
f	 0.9230	 0.6280
fA	 0.3090	 0.1830
g	 0.9230	 0.6270
gA	 0.3330	 0.1880
h	 0.9230	 0.6270
hA	 0.3330	 0.1950
i	 0.9240	 0.6280
iA	 0.3090	 0.1890
j	 0.9250	 0.6270
jA	 0.3090	 0.1820
k	 0.9230	 0.6270
kA	 0.3330	 0.2000
l	 0.9240	 0.6280
lA	 0.3090	 0.1900
m	 0.9230	 0.6280
mA	 0.3330	 0.1950
n	 0.9230	 0.6270
nA	 0.3090	 0.1880
o	 0.9230	 0.6280
oA	 0.3090	 0.1810
p	 0.9240	 0.6270
pA	 0.3330	 0.1870
q	 0.9240	 0.6280
qA	 0.3090	 0.1820
r	 0.9230	 0.6270
rA	 0.3330	 0.1910
s	 0.9230	 0.6280
sA	 0.3330	 0.1790
t	 0.9230	 0.6270
tA	 0.3330	 0.1950
u	 0.9240	 0.6270
uA	 0.3090	 0.2040
v	 0.9250	 0.6260
vA	 0.3090	 0.1830
w	 0.9230	 0.6270
wA	 0.3330	 0.1840
x	 0.9240	 0.6270
xA	 0.3330	 0.1820
y	 0.9230	 0.6270
yA	 0.3330	 0.1790

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Chain	Atom inclusion	Q-score
z	 0.9230	 0.6270
zA	 0.3330	 0.1810