Full wwPDB EM Validation Report ⓘ

Apr 5, 2025 – 03:23 PM EDT

PDB ID	:	9DCC / pdb_00009dcc
EMDB ID	:	EMD-46749
Title	:	The Structure of AAV5 at 55 Degrees Celsius
Authors	:	Bennett, A.B.; McKenna, R.
Deposited on	:	2024-08-25
Resolution	:	3.12 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:

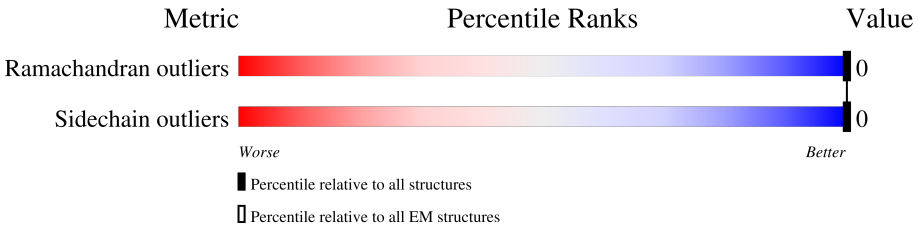
EMDB validation analysis	:	0.0.1.dev117
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

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 3.12 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=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	1	724	71% 28%
1	2	724	71% 28%
1	3	724	71% 28%
1	4	724	71% 28%
1	5	724	71% 28%
1	6	724	71% 28%
1	7	724	71% 28%
1	8	724	71% 28%
1	A	724	71% 28%

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Mol	Chain	Length	Quality of chain
1	B	724	71% 28%
1	C	724	71% 28%
1	D	724	71% 28%
1	E	724	71% 28%
1	F	724	71% 28%
1	G	724	71% 28%
1	H	724	71% 28%
1	I	724	71% 28%
1	J	724	71% 28%
1	K	724	71% 28%
1	L	724	71% 28%
1	M	724	71% 28%
1	N	724	71% 28%
1	O	724	71% 28%
1	P	724	71% 28%
1	Q	724	71% 28%
1	R	724	71% 28%
1	S	724	71% 28%
1	T	724	71% 28%
1	U	724	71% 28%
1	V	724	71% 28%
1	W	724	71% 28%
1	X	724	71% 28%
1	Y	724	71% 28%
1	Z	724	71% 28%

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Mol	Chain	Length	Quality of chain
1	a	724	71% 28%
1	b	724	71% 28%
1	c	724	71% 28%
1	d	724	71% 28%
1	e	724	71% 28%
1	f	724	71% 28%
1	g	724	71% 28%
1	h	724	71% 28%
1	i	724	71% 28%
1	j	724	71% 28%
1	k	724	71% 28%
1	l	724	71% 28%
1	m	724	71% 28%
1	n	724	71% 28%
1	o	724	71% 28%
1	p	724	71% 28%
1	q	724	71% 28%
1	r	724	71% 28%
1	s	724	71% 28%
1	t	724	71% 28%
1	u	724	71% 28%
1	v	724	71% 28%
1	w	724	71% 28%
1	x	724	71% 28%
1	y	724	71% 28%

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Mol	Chain	Length	Quality of chain
1	z	724	71% 28%
2	0	2	50% 100%
2	0A	2	50% 100%
2	1A	2	50% 100%
2	2A	2	50% 100%
2	3A	2	50% 100%
2	4A	2	50% 100%
2	5A	2	50% 100%
2	9	2	100%
2	AA	2	50% 100%
2	BA	2	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	100%
2	IA	2	100%
2	JA	2	100%
2	KA	2	50% 100%
2	LA	2	100%
2	MA	2	50% 100%
2	NA	2	50% 100%
2	OA	2	50% 100%
2	PA	2	50% 100%

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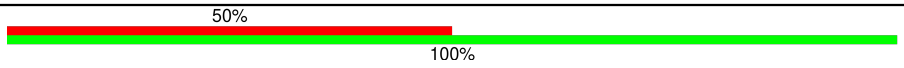
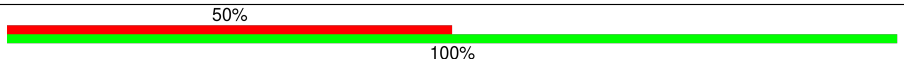
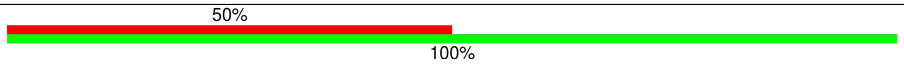
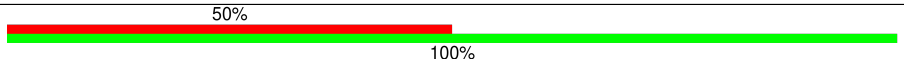
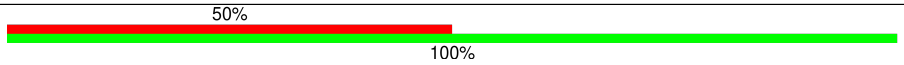
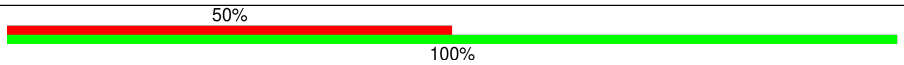
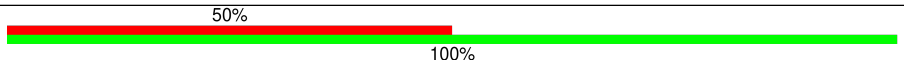
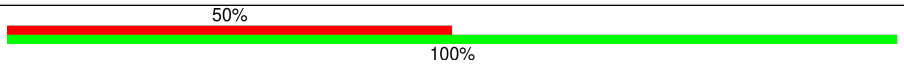
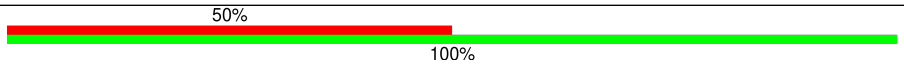
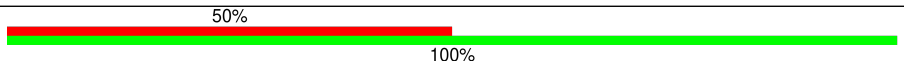
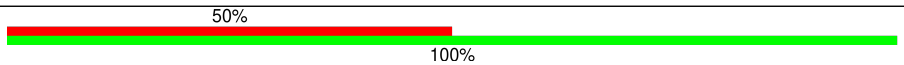
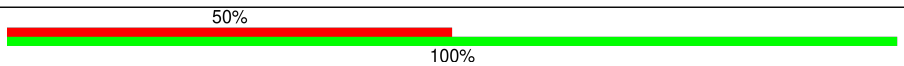
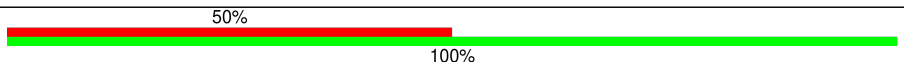
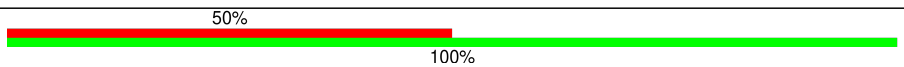
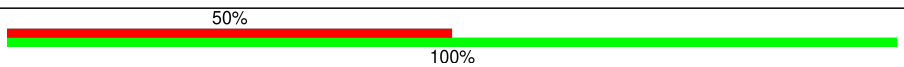
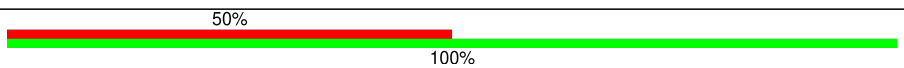
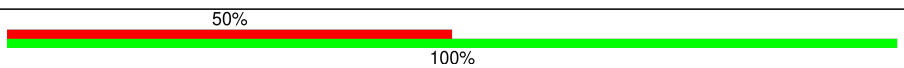
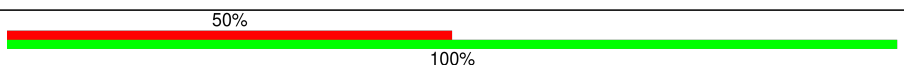
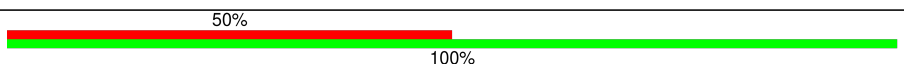
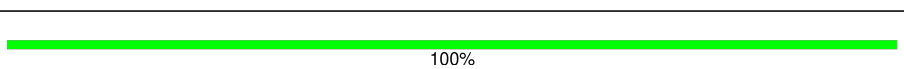
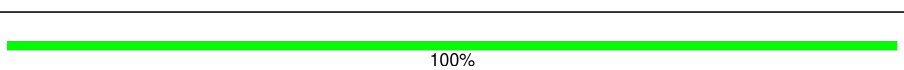
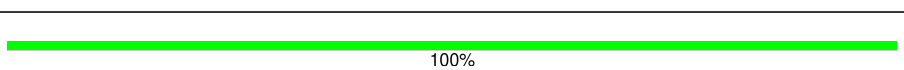
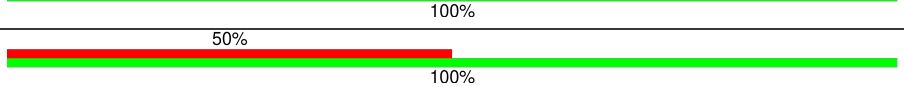
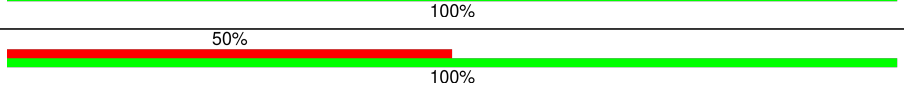
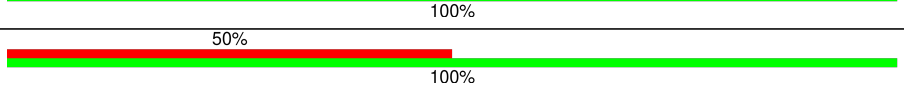
Mol	Chain	Length	Quality of chain
2	QA	2	
2	RA	2	
2	SA	2	
2	TA	2	
2	UA	2	
2	VA	2	
2	WA	2	
2	XA	2	
2	YA	2	
2	ZA	2	
2	aA	2	
2	bA	2	
2	cA	2	
2	dA	2	
2	eA	2	
2	fA	2	
2	gA	2	
2	hA	2	
2	iA	2	
2	jA	2	
2	kA	2	
2	lA	2	
2	mA	2	
2	nA	2	
2	oA	2	

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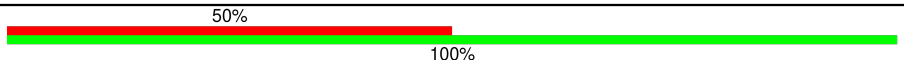
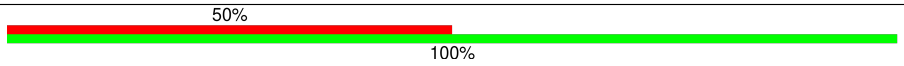
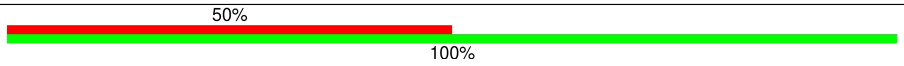
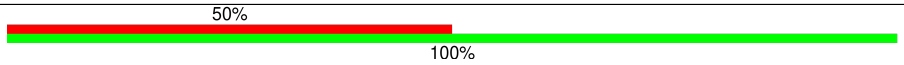
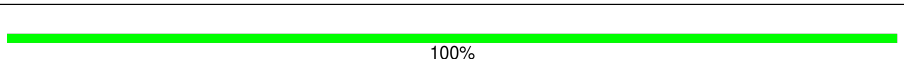
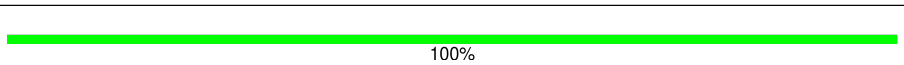
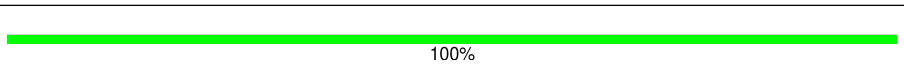
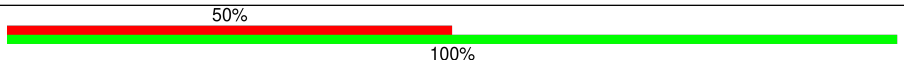
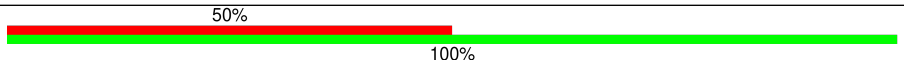
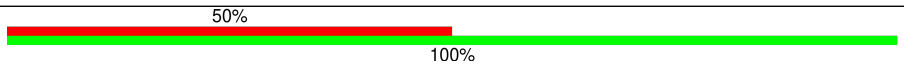
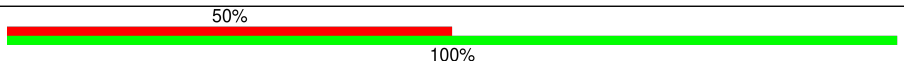
Mol	Chain	Length	Quality of chain
2	pA	2	
2	qA	2	
2	rA	2	
2	sA	2	
2	tA	2	
2	uA	2	
2	vA	2	
2	wA	2	
2	xA	2	
2	yA	2	
2	zA	2	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 249720 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	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	B	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	C	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	D	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	E	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	F	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	G	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	H	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	I	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	J	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	K	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	L	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	M	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	N	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	O	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	P	518	Total 4120	C 2605	N 707	O 792	S 16	0	0
1	Q	518	Total 4120	C 2605	N 707	O 792	S 16	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	S	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	T	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	U	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	V	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	W	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	X	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	Y	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	Z	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	a	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	b	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	c	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	d	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	e	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	f	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	g	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	h	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	i	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	j	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	k	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	l	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	n	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	o	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	p	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	q	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	r	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	s	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	t	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	u	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	v	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	w	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	x	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	y	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	z	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	1	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	2	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	3	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	4	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	5	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	6	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		
1	7	518	Total	C	N	O	S	0	0
			4120	2605	707	792	16		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	518	Total	C	N	O	S	0	0
			4120	2605	707	792	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	C	N	O	P	0	0
			42	20	10	10	2		
2	KA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	LA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	MA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	NA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	OA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	PA	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	RA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	SA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	TA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	VA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	WA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	XA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	YA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	ZA	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		

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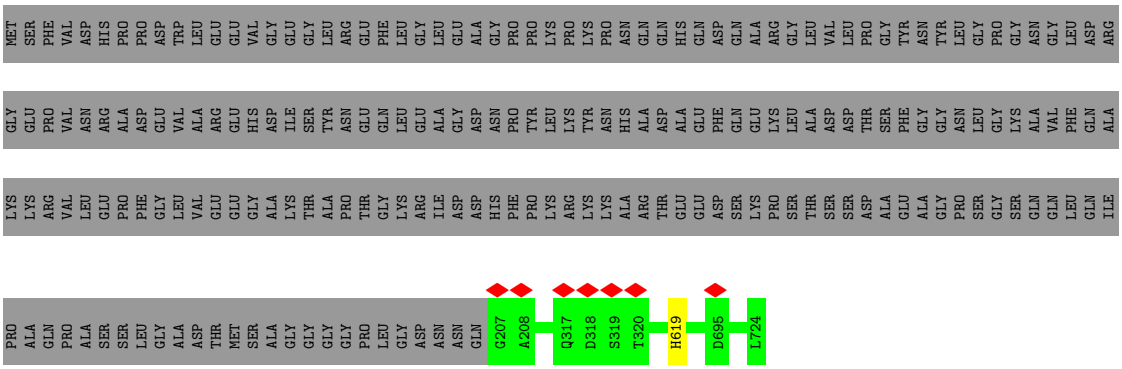
Mol	Chain	Residues	Atoms					AltConf	Trace
2	gA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	hA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	iA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	jA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	kA	2	Total	C	N	O	P	0	0
			42	20	10	10	2		
2	lA	2	Total	C	N	O	P	0	0
			42	20	10	10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

3 Residue-property plots (i)

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

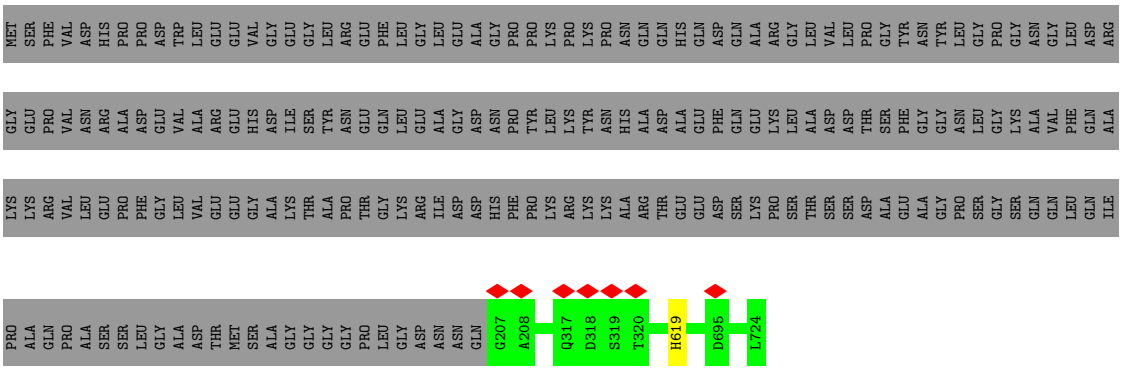
• Molecule 1: Capsid protein

Chain A:



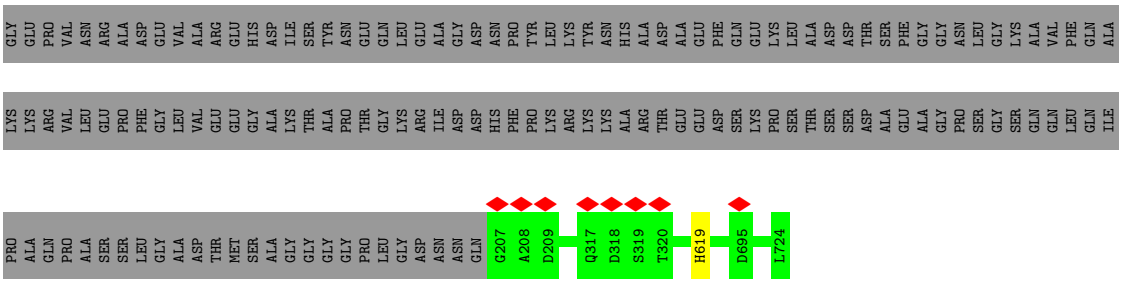
• Molecule 1: Capsid protein

Chain B:



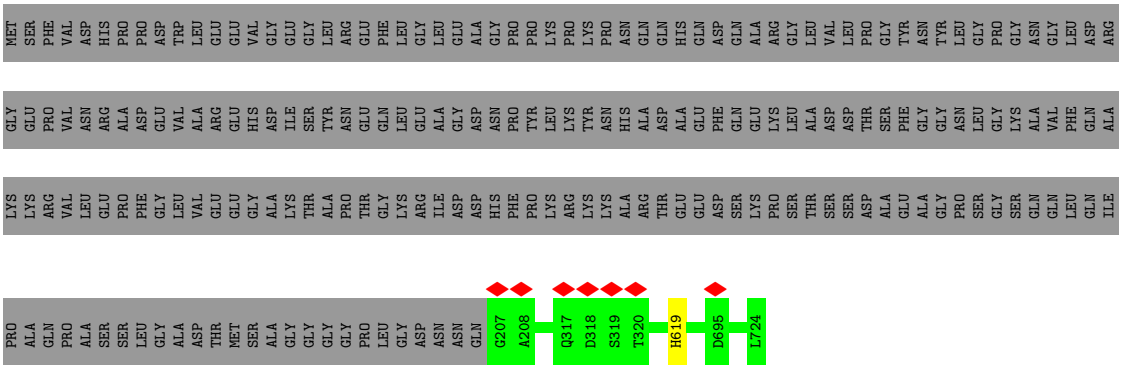
• Molecule 1: Capsid protein

Chain C:



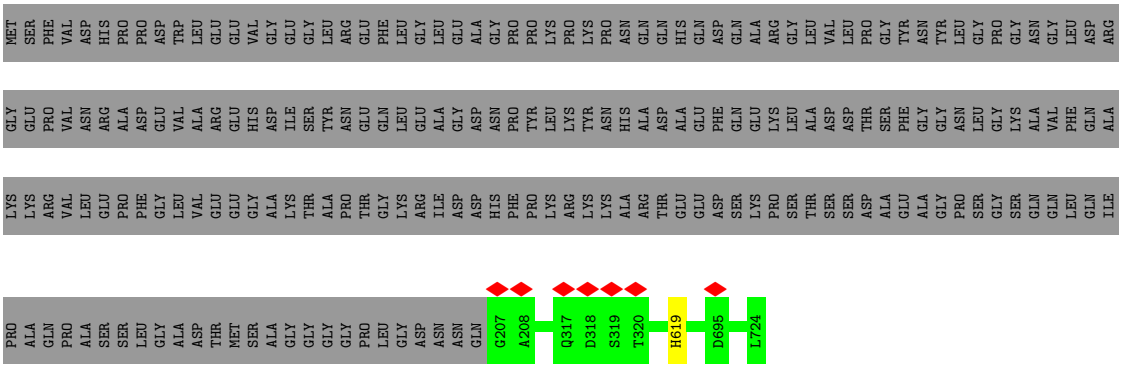
• Molecule 1: Capsid protein

Chain D:



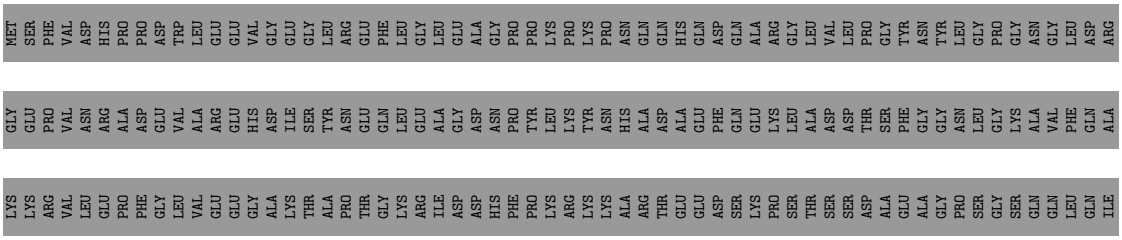
• Molecule 1: Capsid protein

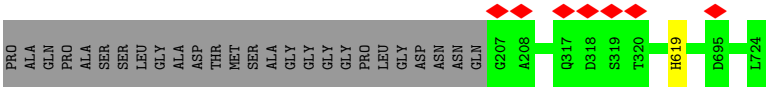
Chain E:



• Molecule 1: Capsid protein

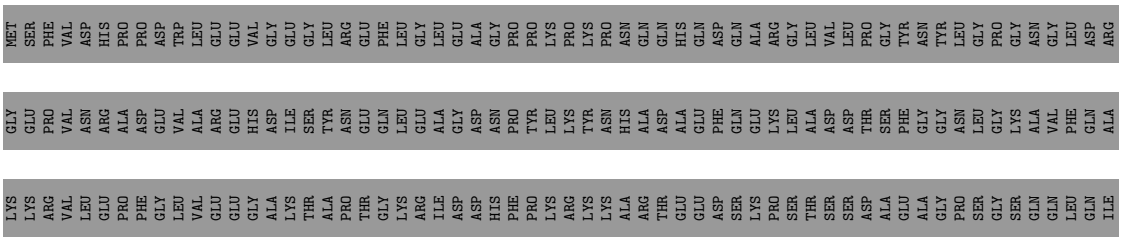
Chain F:

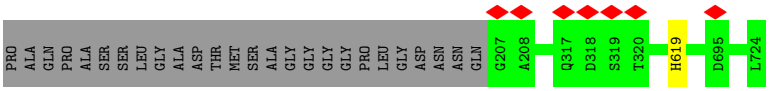




• Molecule 1: Capsid protein

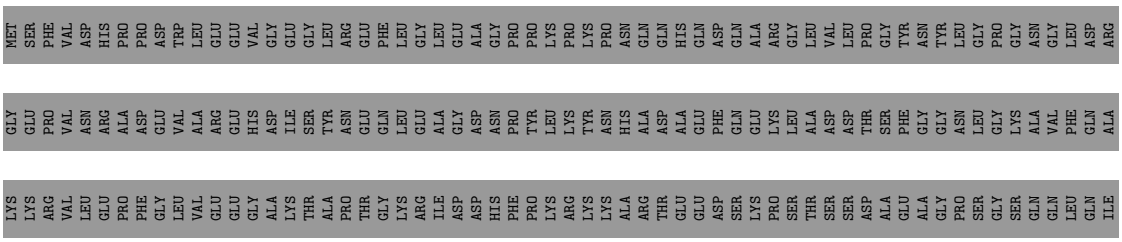
Chain G:

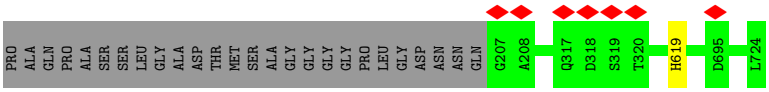




• Molecule 1: Capsid protein

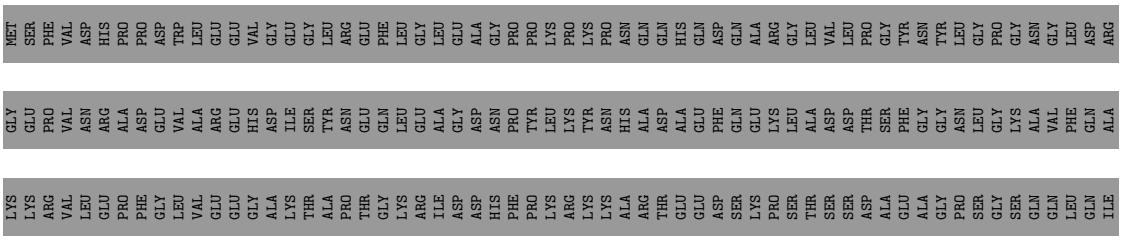
Chain H:

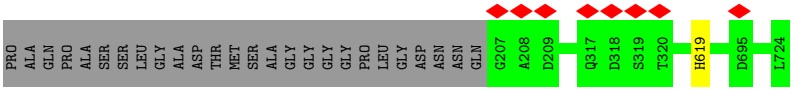




• Molecule 1: Capsid protein

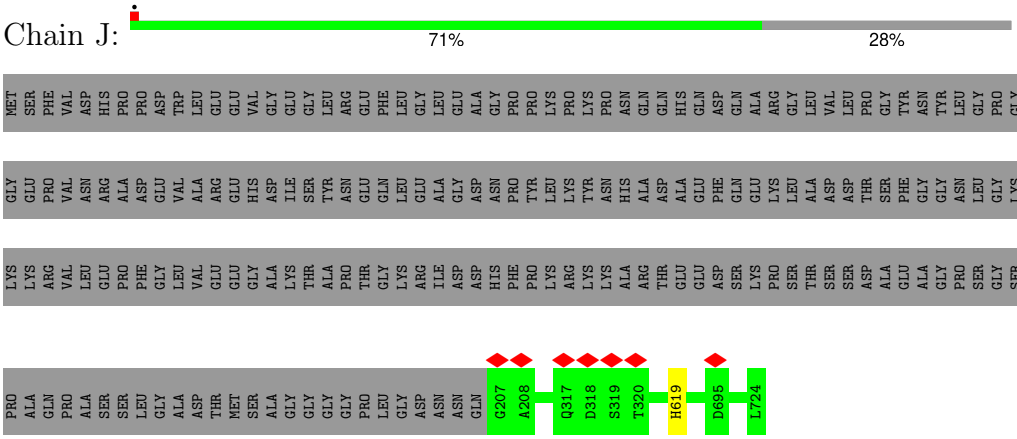
Chain I:





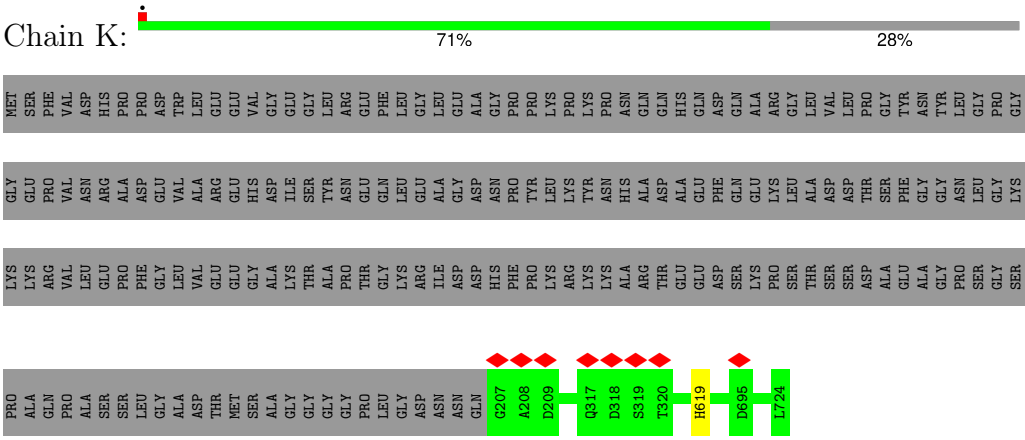
• Molecule 1: Capsid protein

Chain J:



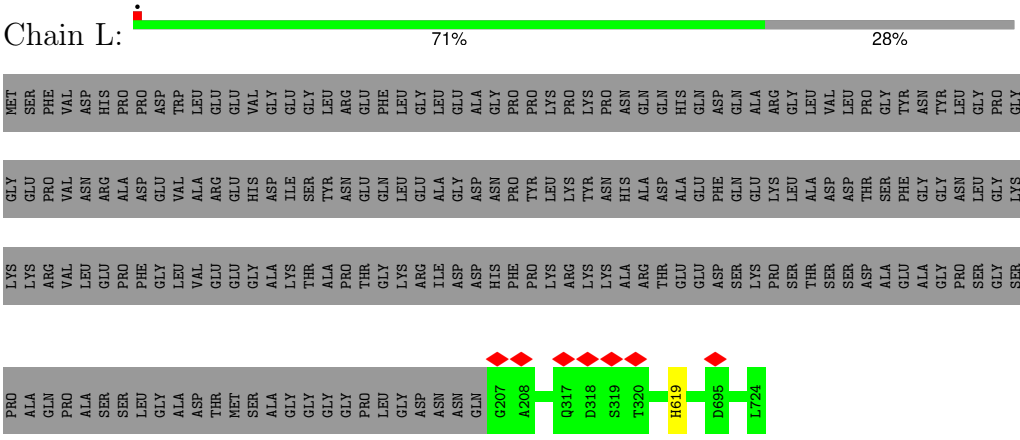
- Molecule 1: Capsid protein

Chain K:



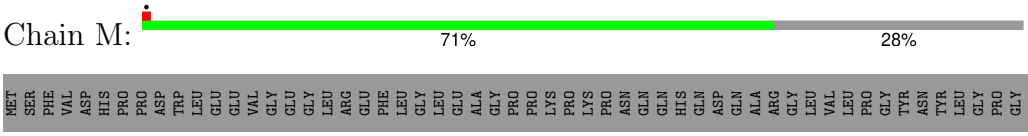
- Molecule 1: Capsid protein

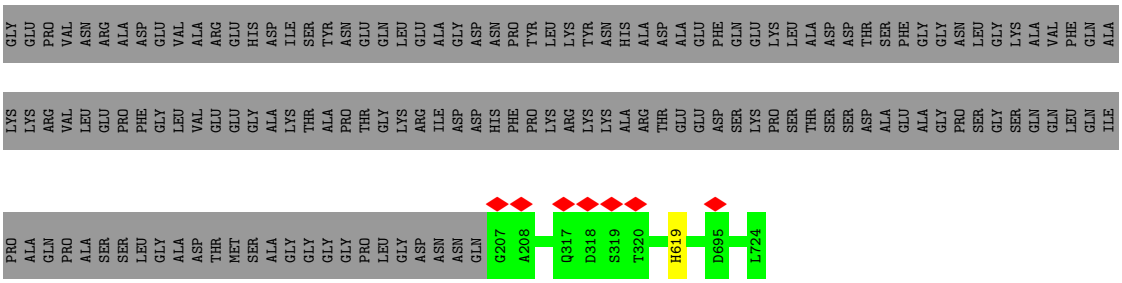
Chain L:



- Molecule 1: Capsid protein

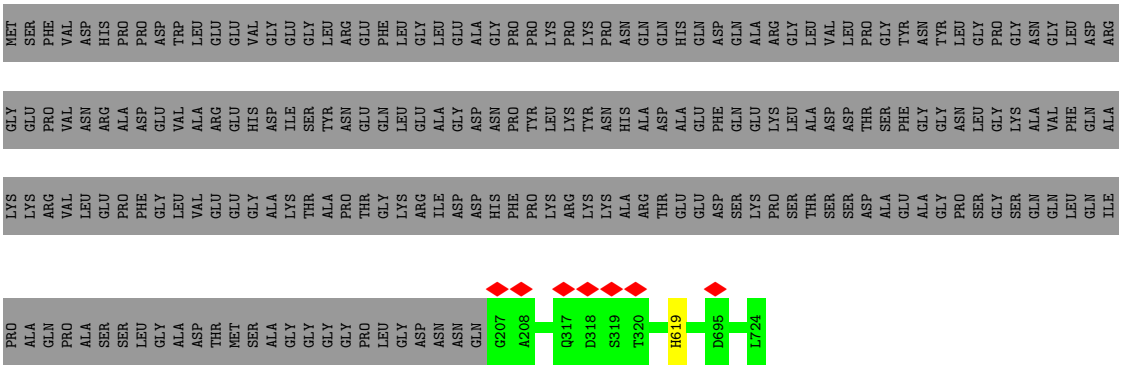
Chain M:





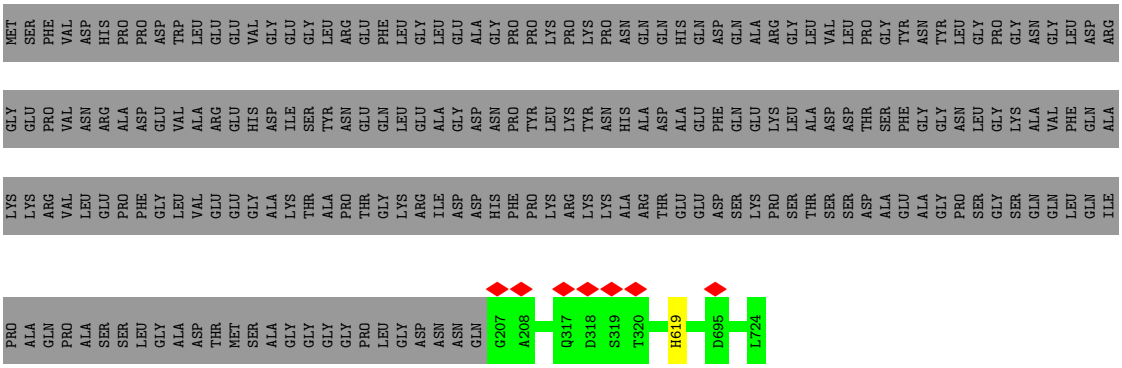
• Molecule 1: Capsid protein

Chain N:



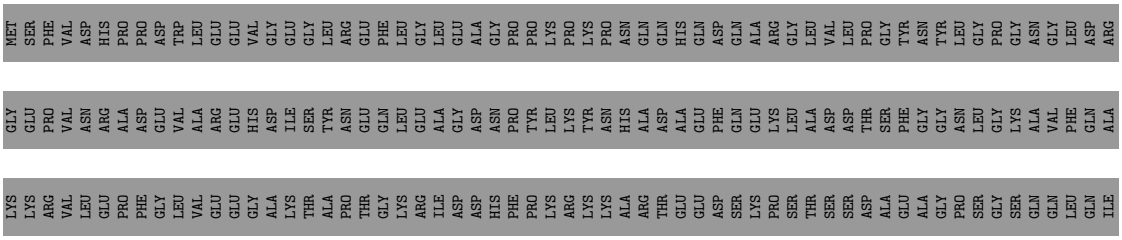
• Molecule 1: Capsid protein

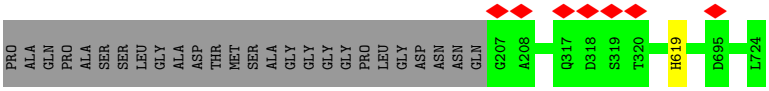
Chain O:



• Molecule 1: Capsid protein

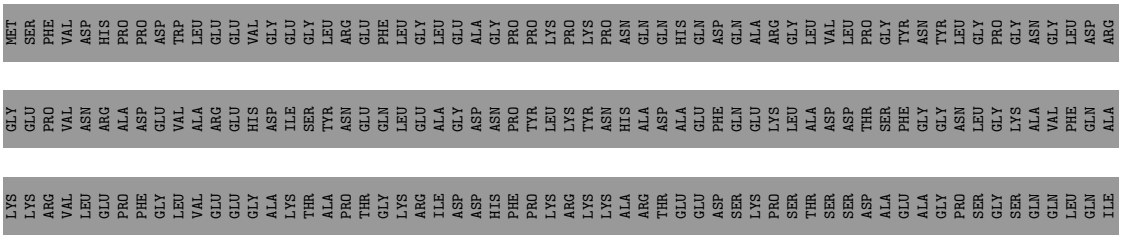
Chain P:

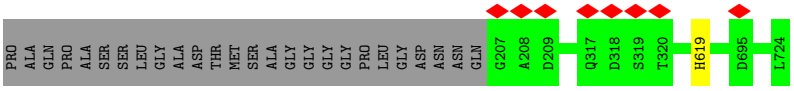




• Molecule 1: Capsid protein

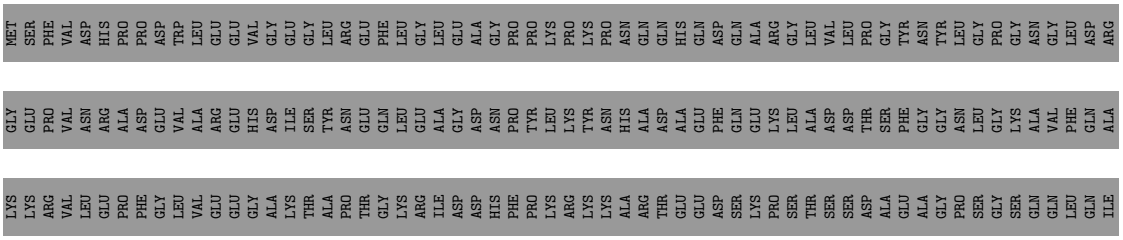
Chain Q:

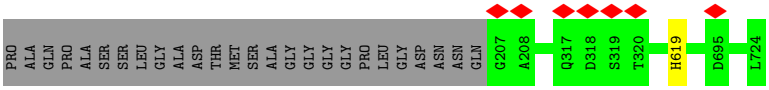




• Molecule 1: Capsid protein

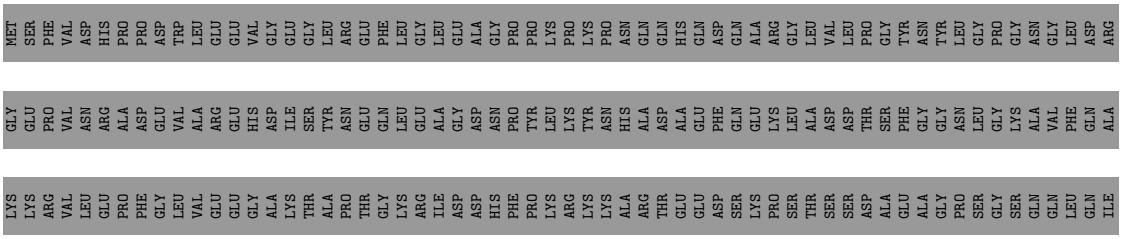
Chain R:

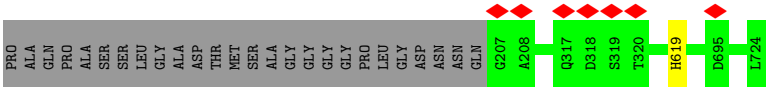




• Molecule 1: Capsid protein

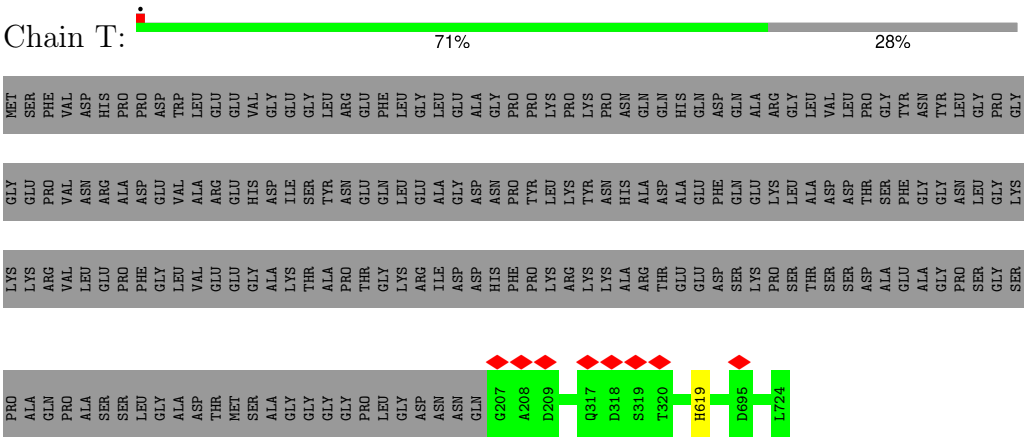
Chain S:





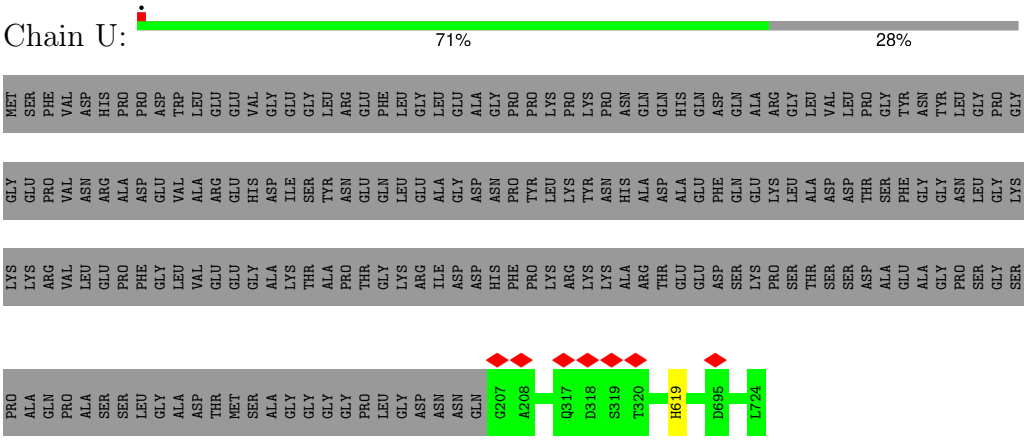
• Molecule 1: Capsid protein

Chain T:



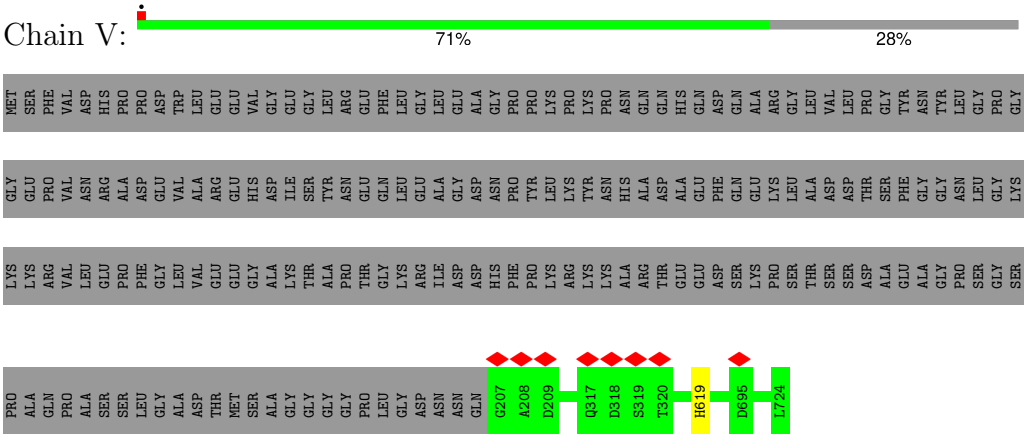
• Molecule 1: Capsid protein

Chain U:



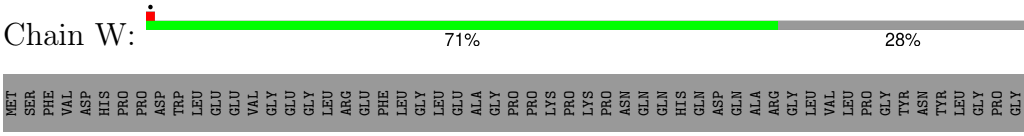
• Molecule 1: Capsid protein

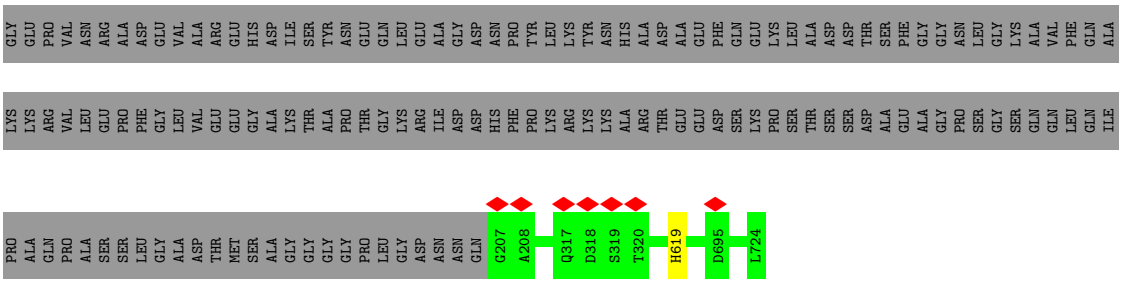
Chain V:



• Molecule 1: Capsid protein

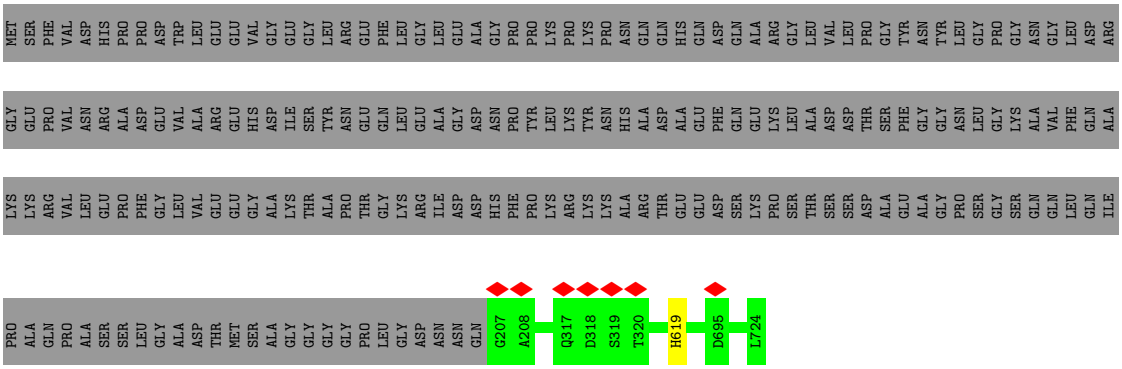
Chain W:





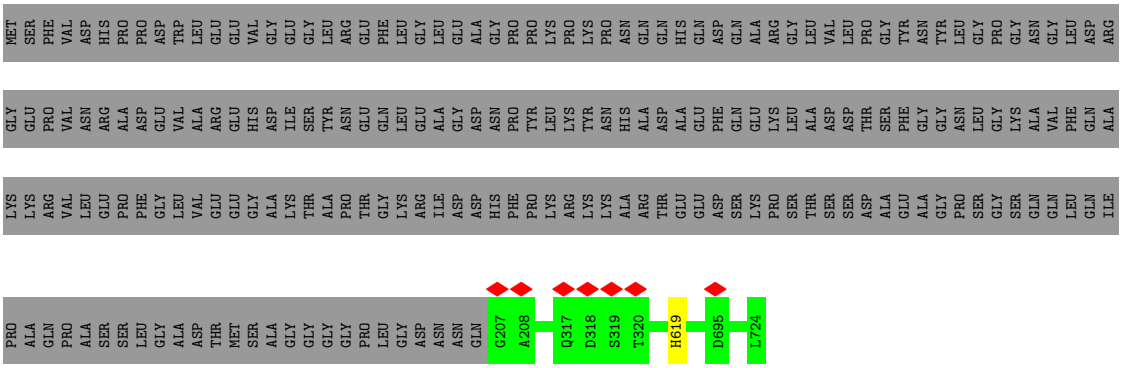
• Molecule 1: Capsid protein

Chain X:



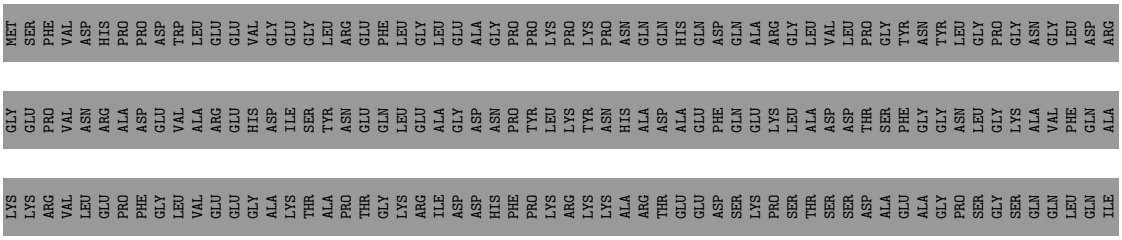
• Molecule 1: Capsid protein

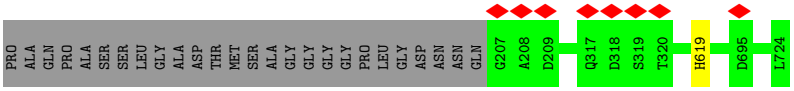
Chain Y:



• Molecule 1: Capsid protein

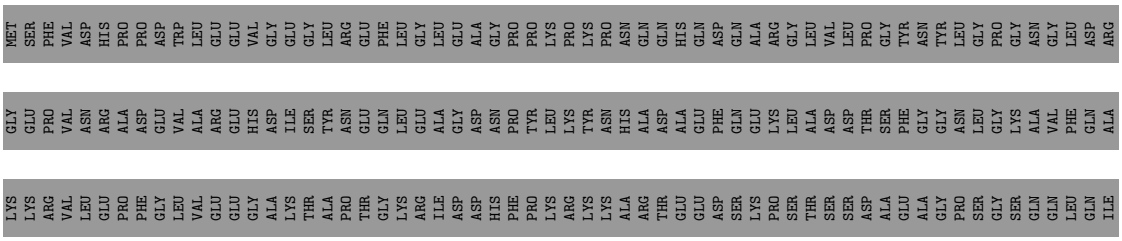
Chain Z:

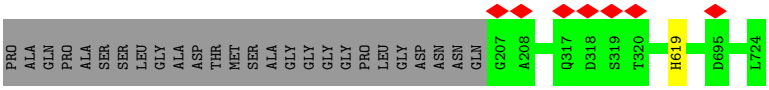




• Molecule 1: Capsid protein

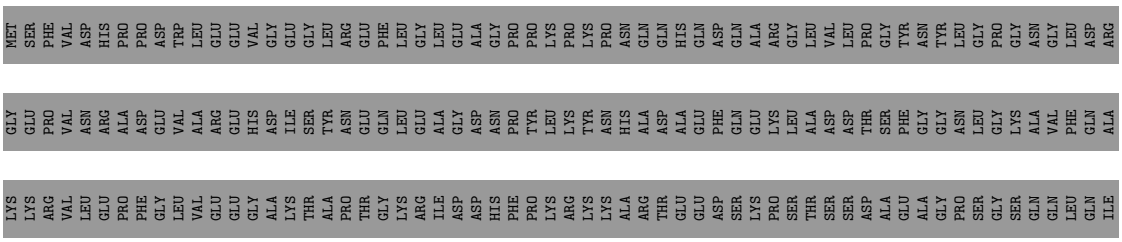
Chain a:

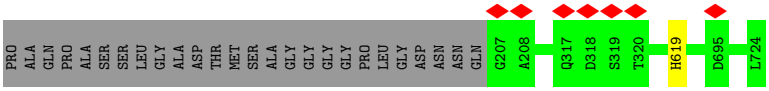




• Molecule 1: Capsid protein

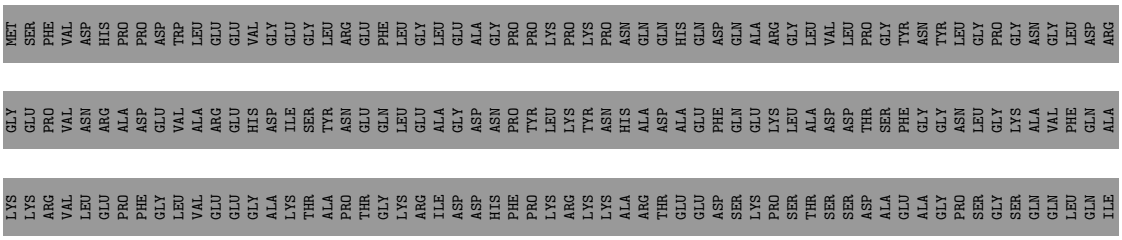
Chain b:

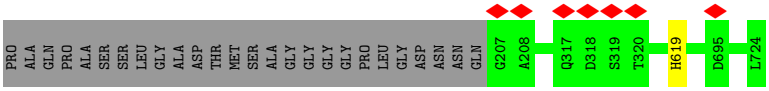




• Molecule 1: Capsid protein

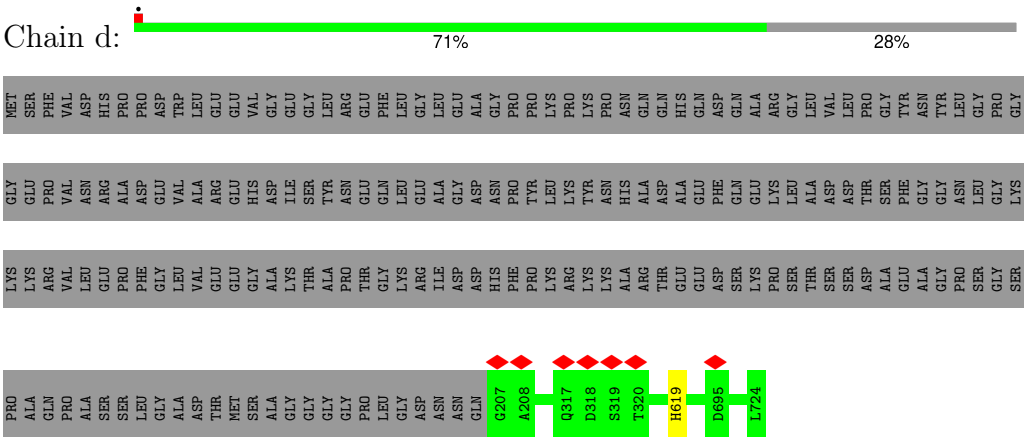
Chain c:





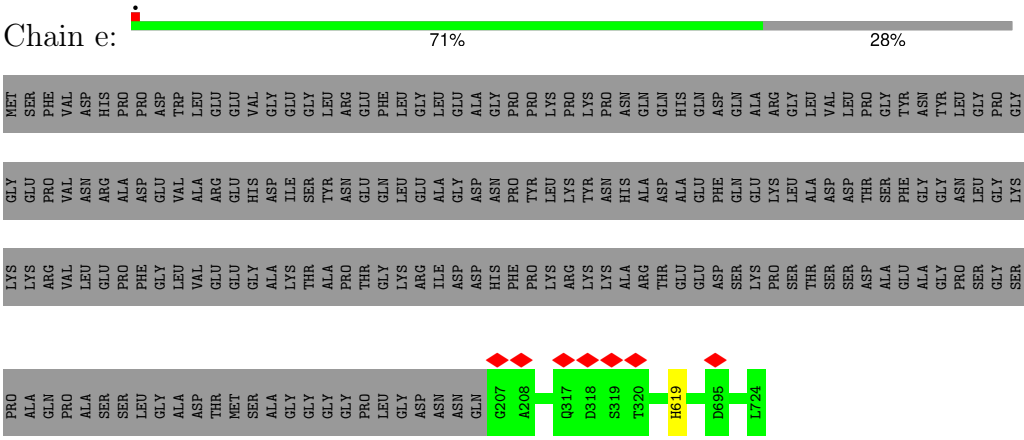
• Molecule 1: Capsid protein

Chain d:



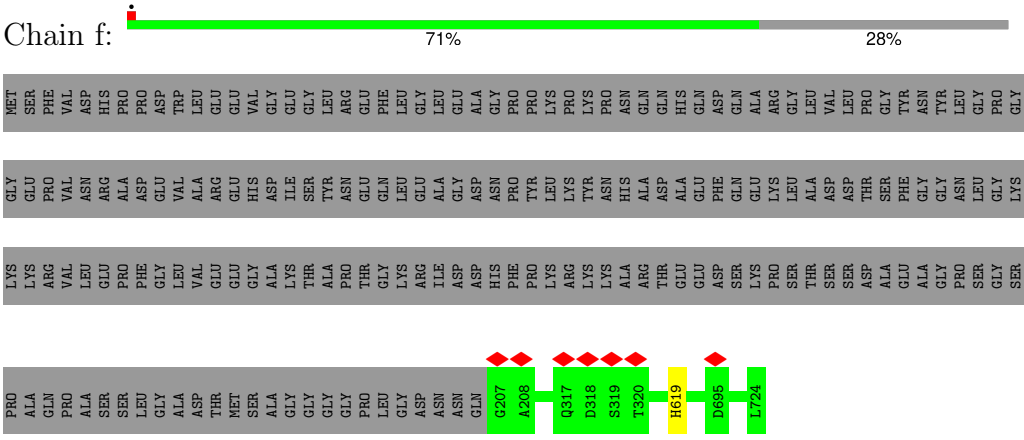
• Molecule 1: Capsid protein

Chain e:



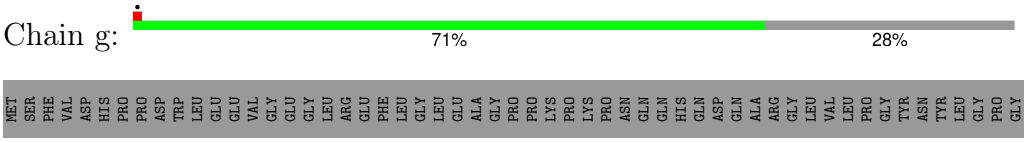
• Molecule 1: Capsid protein

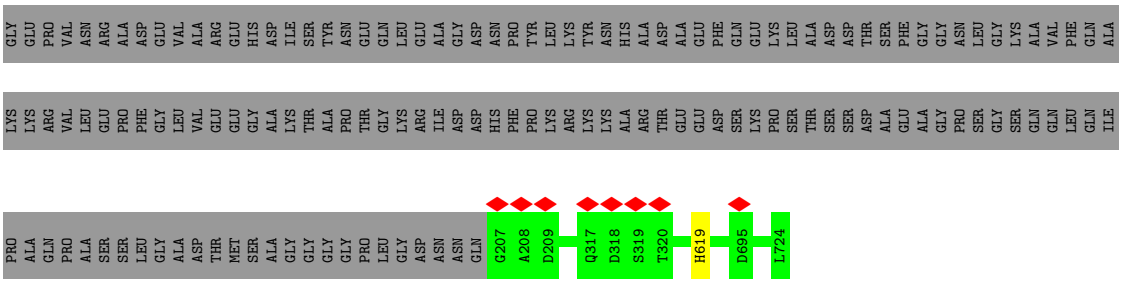
Chain f:



• Molecule 1: Capsid protein

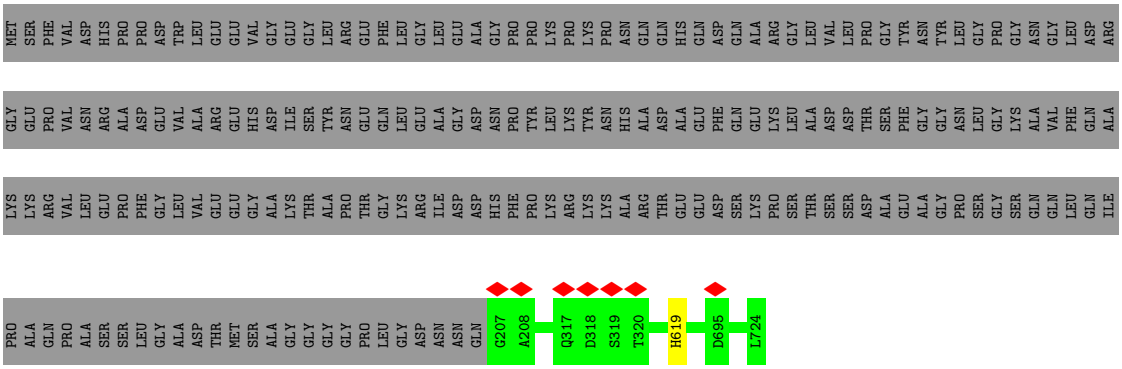
Chain g:





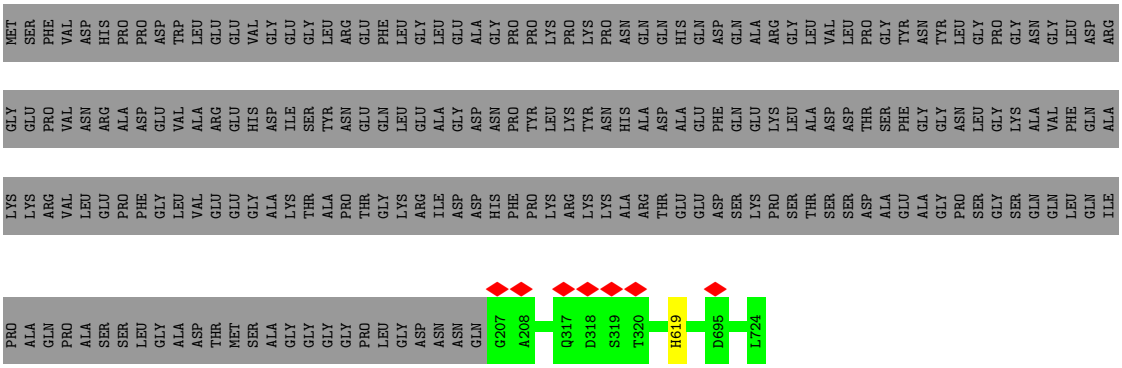
• Molecule 1: Capsid protein

Chain h:



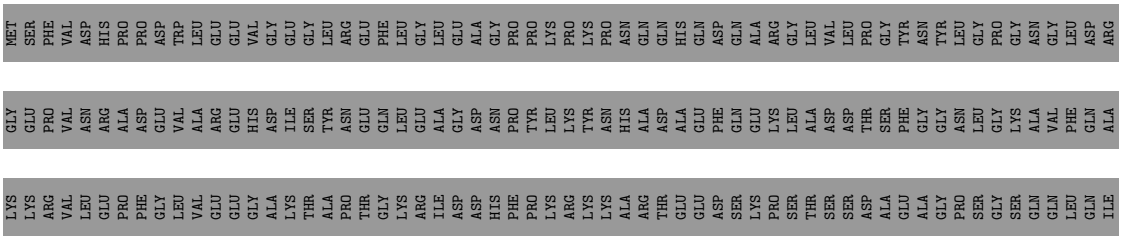
• Molecule 1: Capsid protein

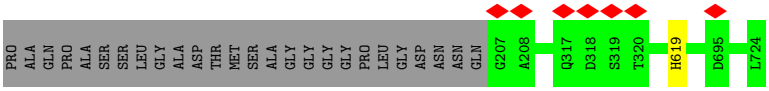
Chain i:



• Molecule 1: Capsid protein

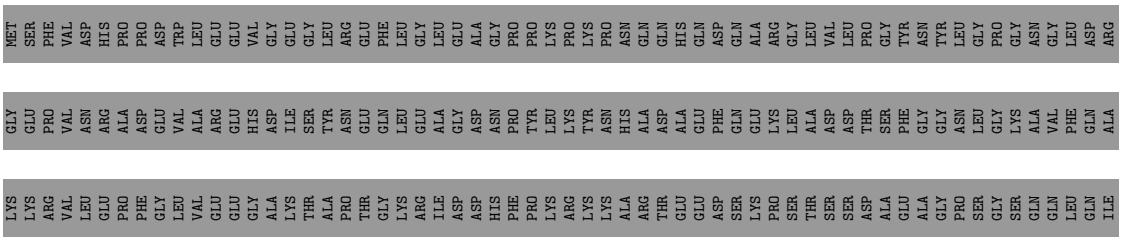
Chain j:

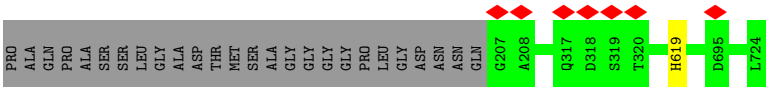




• Molecule 1: Capsid protein

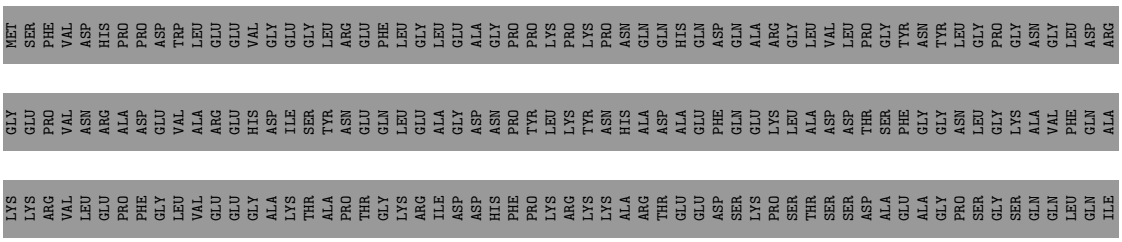
Chain k:

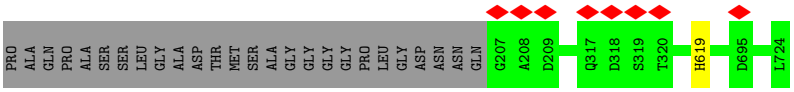




• Molecule 1: Capsid protein

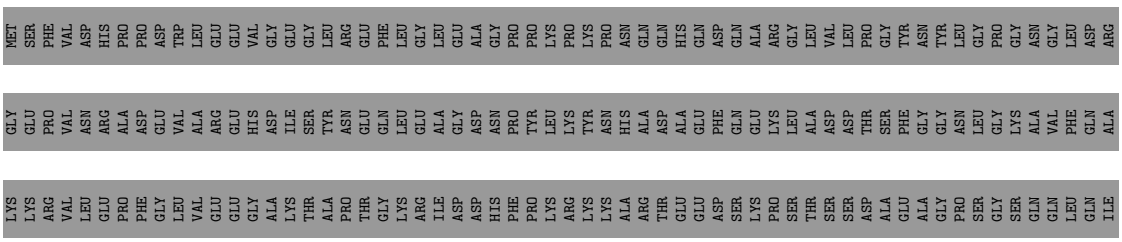
Chain l:

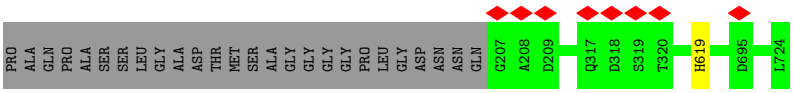




• Molecule 1: Capsid protein

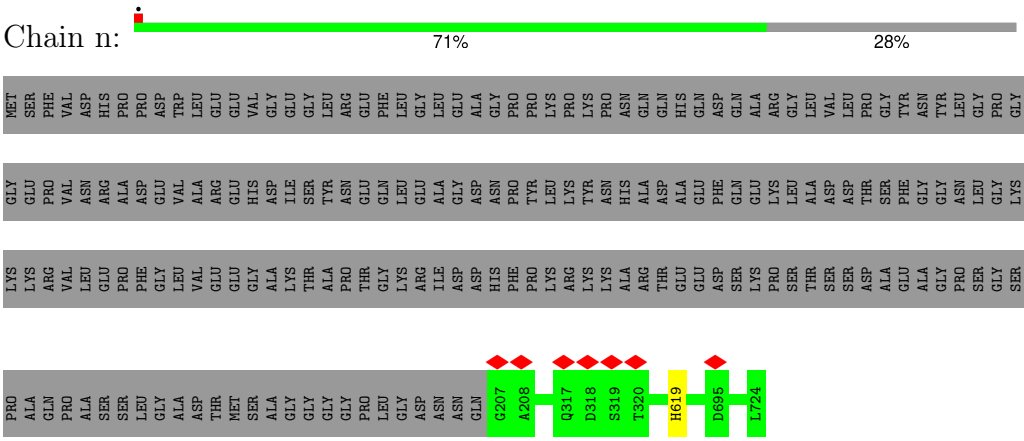
Chain m:





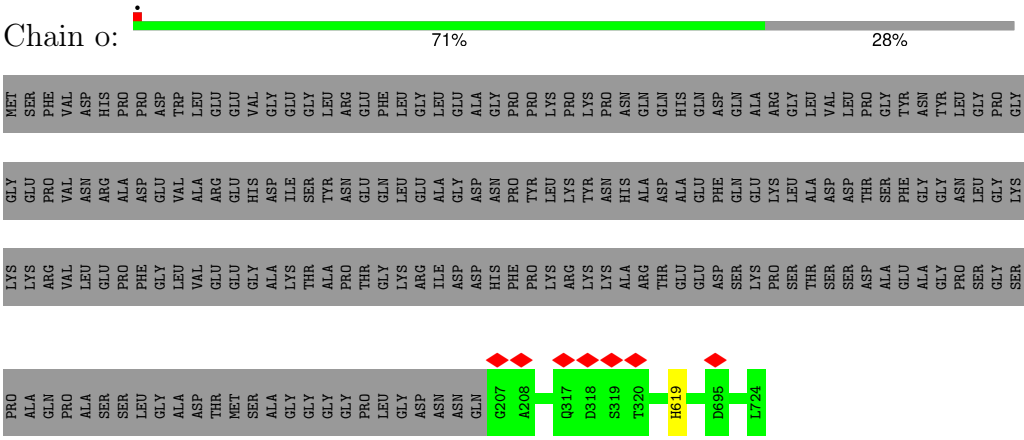
• Molecule 1: Capsid protein

Chain n:



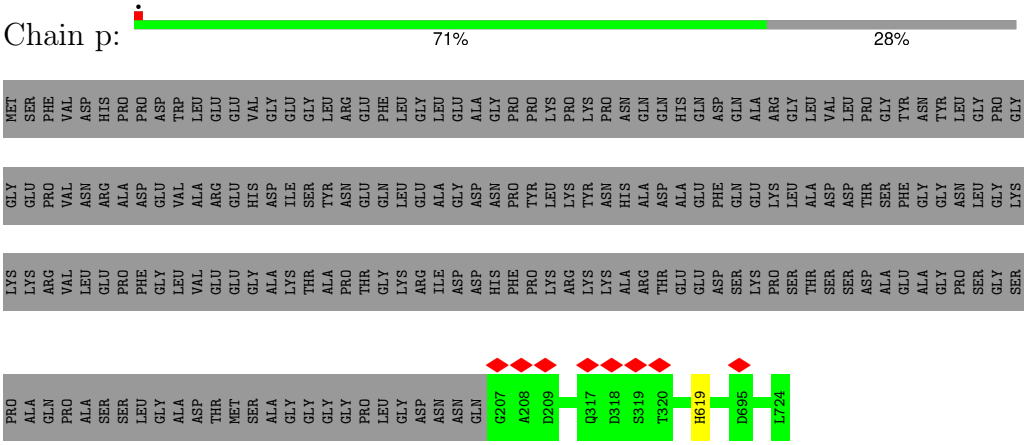
• Molecule 1: Capsid protein

Chain o:



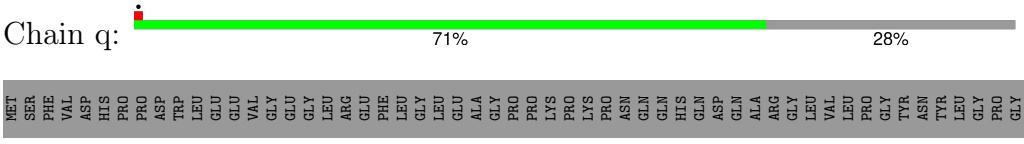
• Molecule 1: Capsid protein

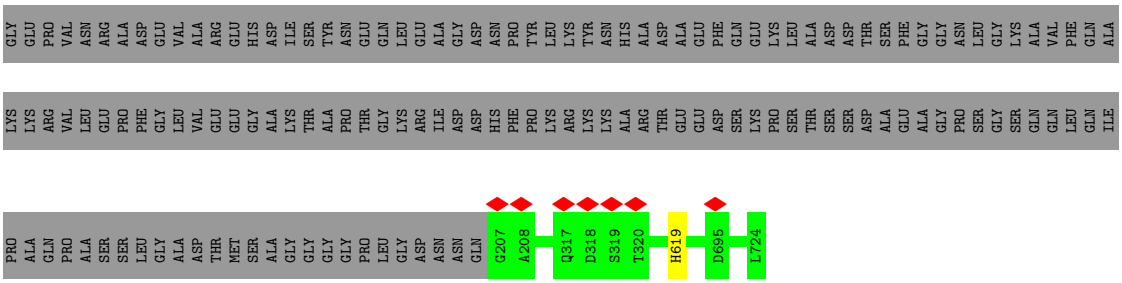
Chain p:



• Molecule 1: Capsid protein

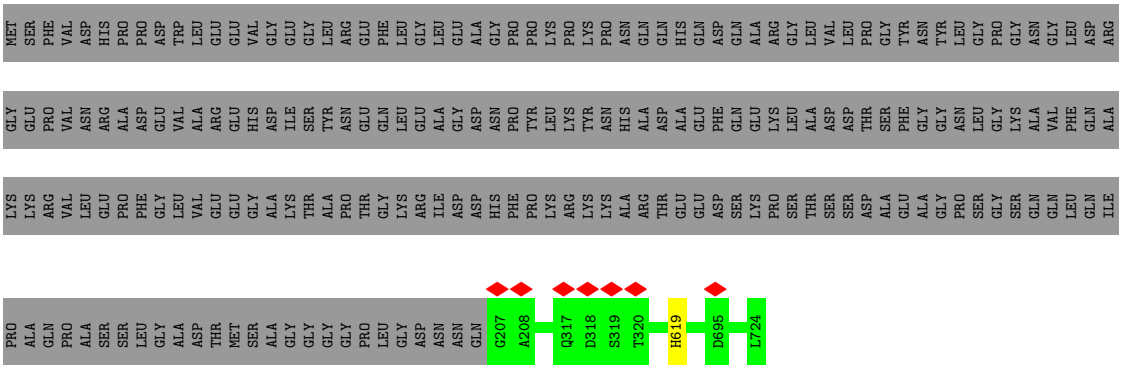
Chain q:





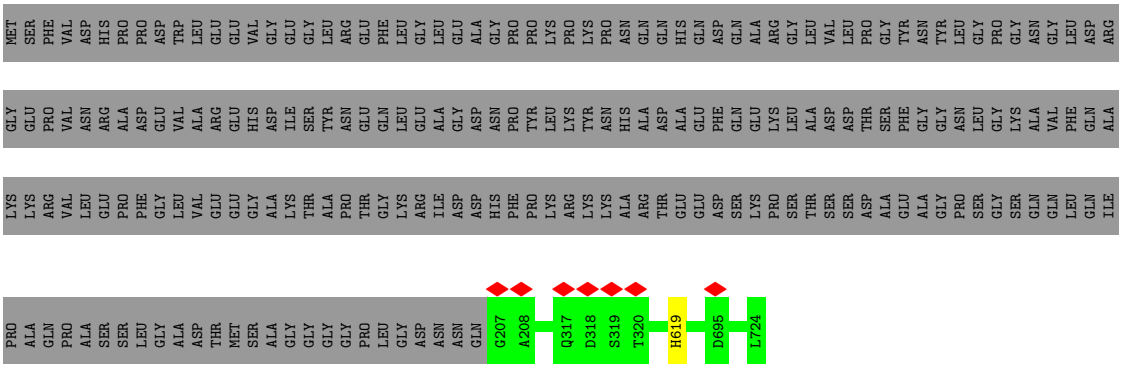
• Molecule 1: Capsid protein

Chain r:



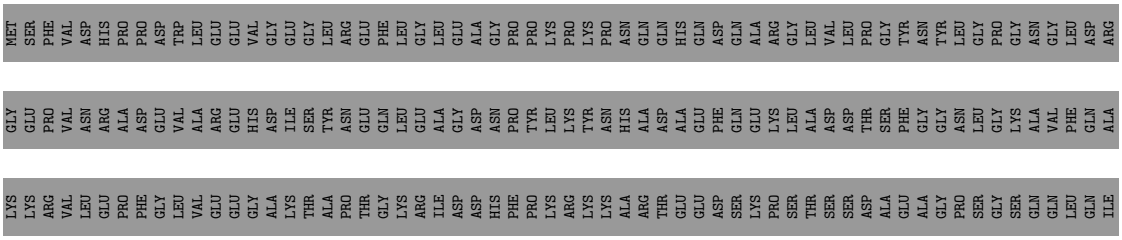
• Molecule 1: Capsid protein

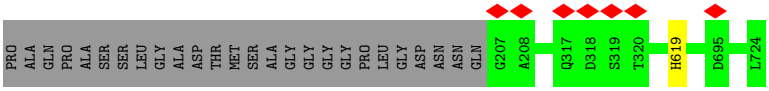
Chain s:



• Molecule 1: Capsid protein

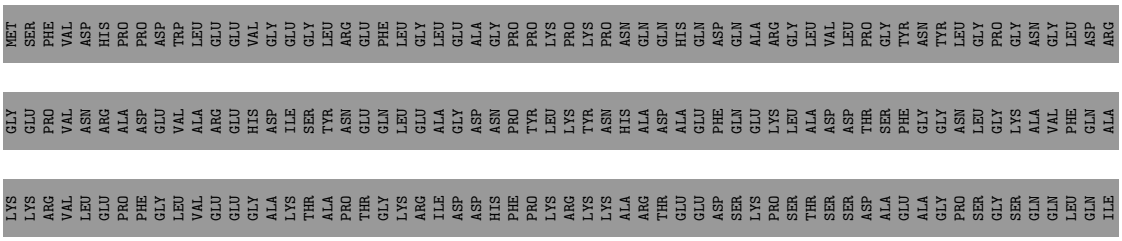
Chain t:

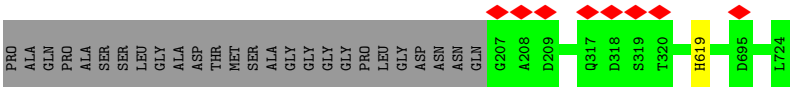




• Molecule 1: Capsid protein

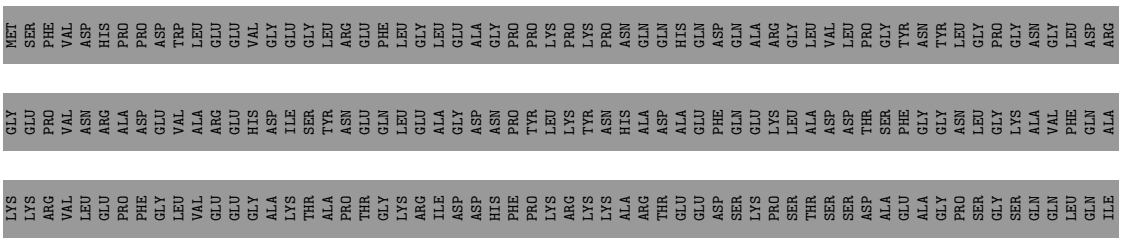
Chain u:

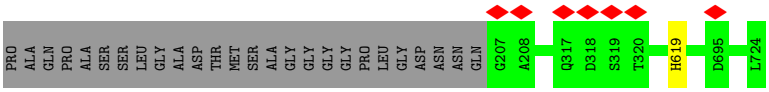




• Molecule 1: Capsid protein

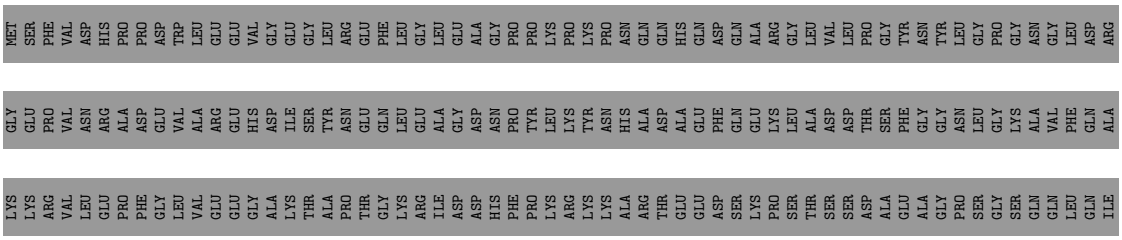
Chain v:

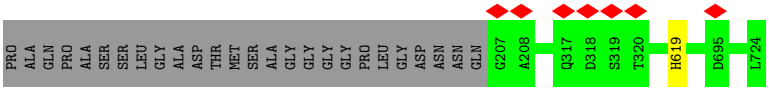




• Molecule 1: Capsid protein

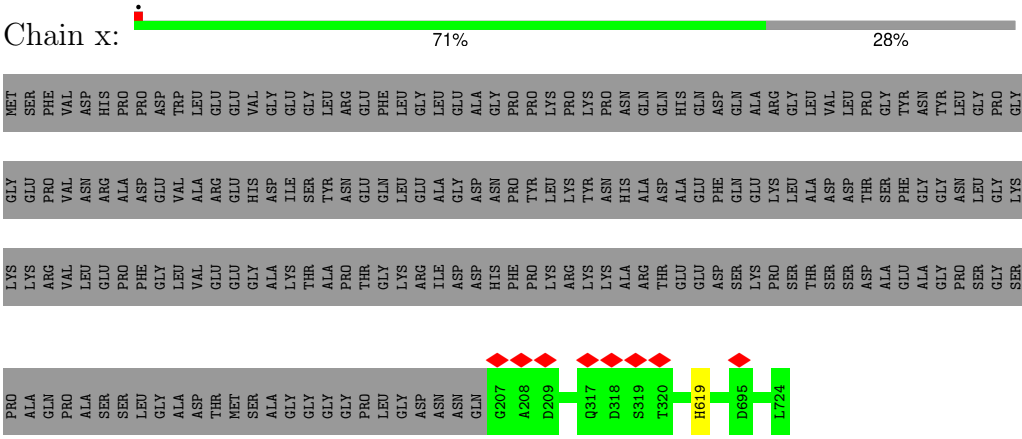
Chain w:





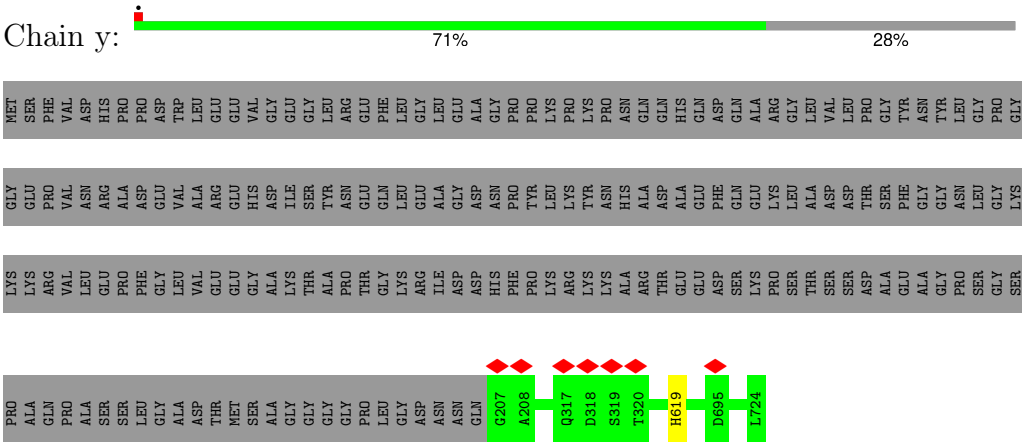
• Molecule 1: Capsid protein

Chain x:



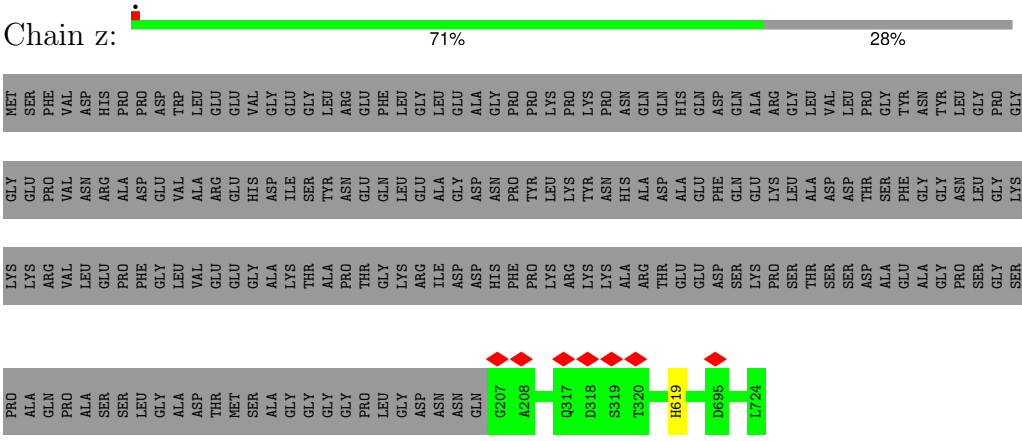
• Molecule 1: Capsid protein

Chain y:



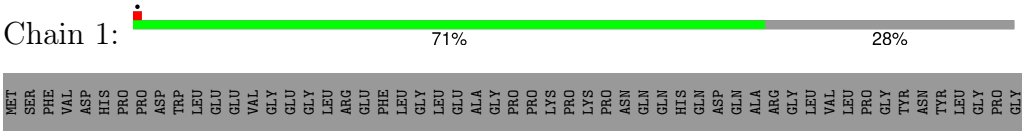
• Molecule 1: Capsid protein

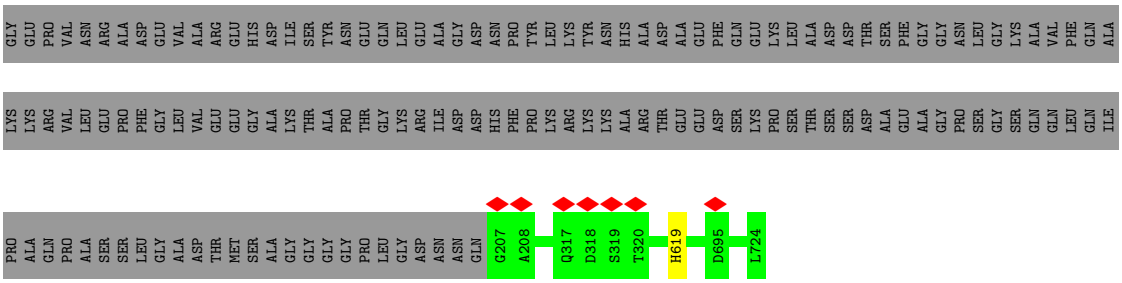
Chain z:



• Molecule 1: Capsid protein

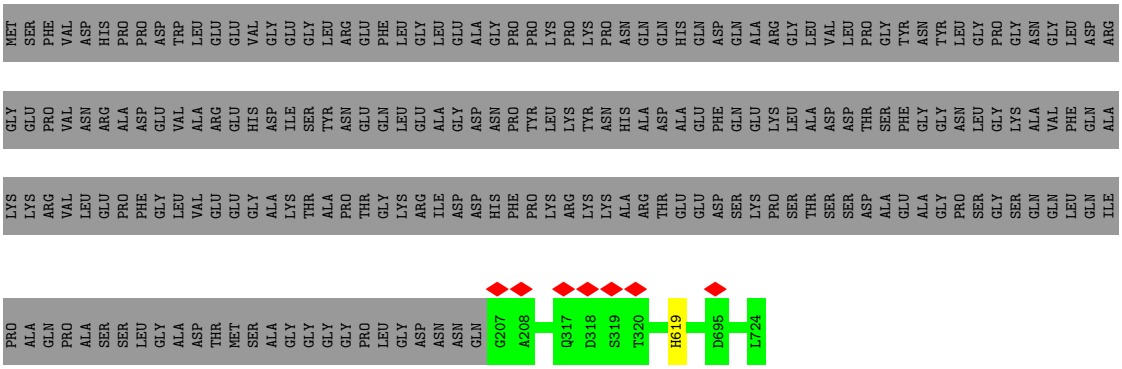
Chain 1:





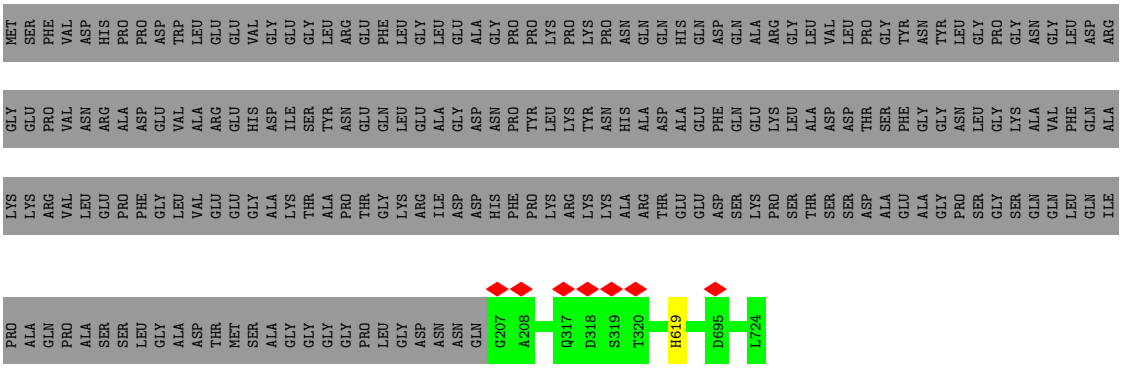
• Molecule 1: Capsid protein

Chain 2:



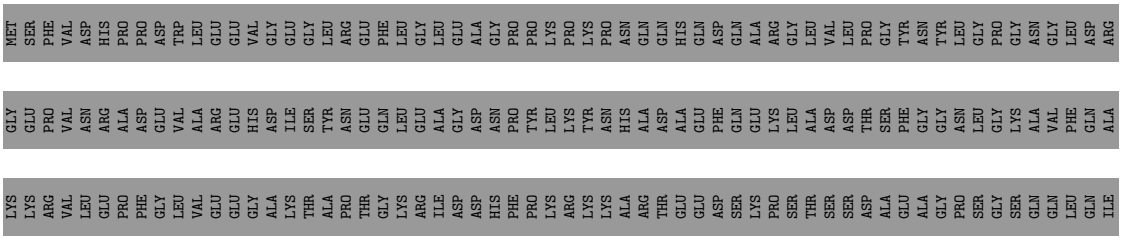
• Molecule 1: Capsid protein

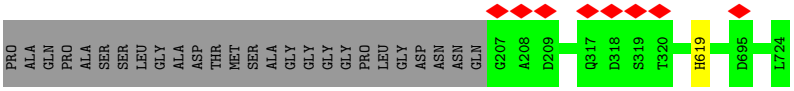
Chain 3:



• Molecule 1: Capsid protein

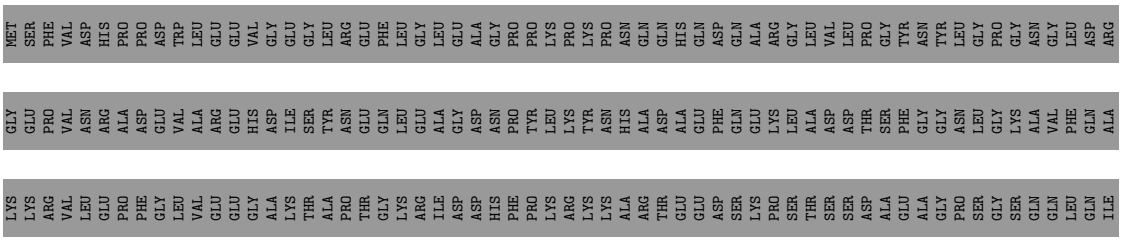
Chain 4:





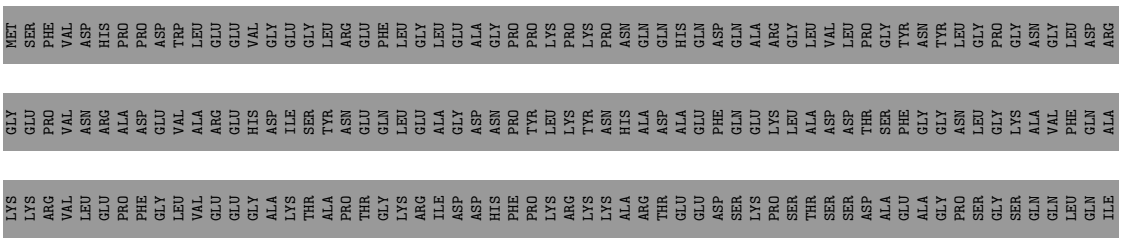
• Molecule 1: Capsid protein

Chain 5:



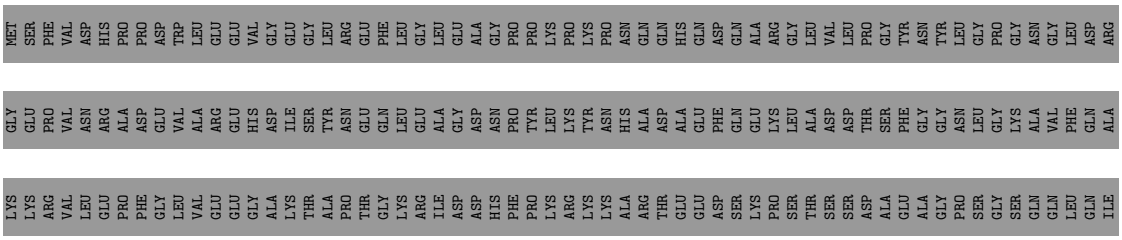
• Molecule 1: Capsid protein

Chain 6:



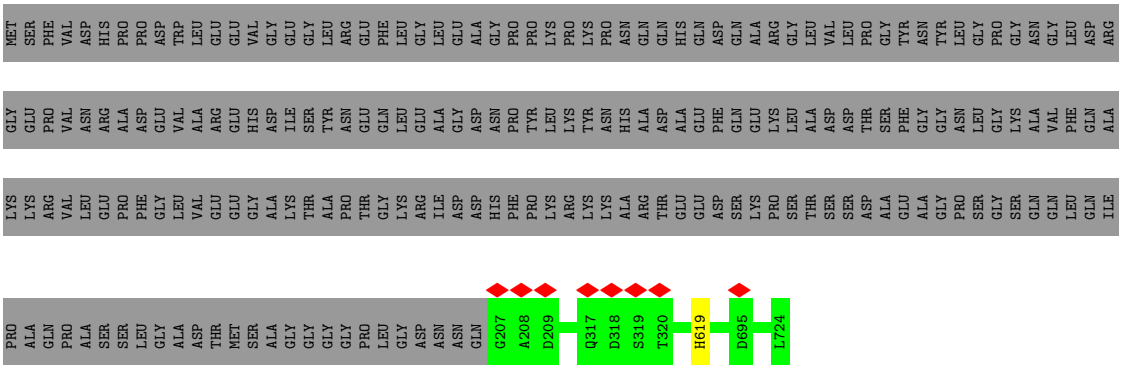
• Molecule 1: Capsid protein

Chain 7:



• Molecule 1: Capsid protein

Chain 8:



• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain 0:

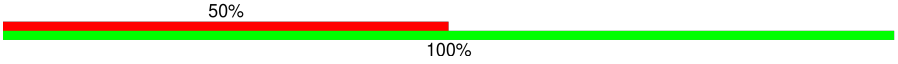
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain JA:

There are no outlier residues recorded for this chain.

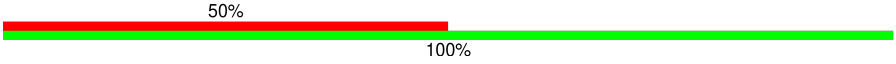
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain UA:



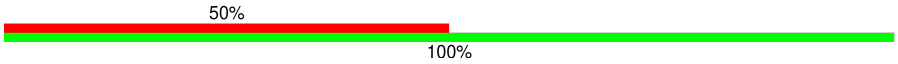
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain fA:

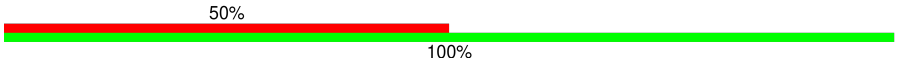


• Molecule 2: DNA (5'-D(P*AP*A)-3')

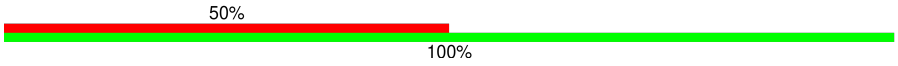
Chain qA:



• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain 1A: 

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain 3A: 

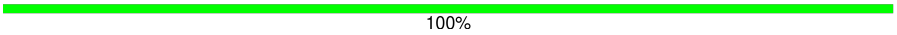
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain 4A:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain 5A:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

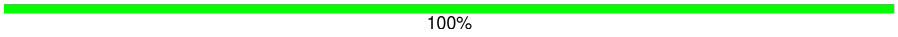
Chain 9: 

There are no outlier residues recorded for this chain.

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain AA:

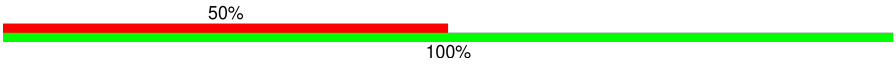
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain BA: 

There are no outlier residues recorded for this chain.

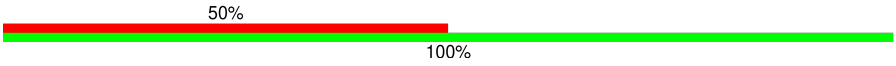
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain CA:



• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain DA:



• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain EA:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

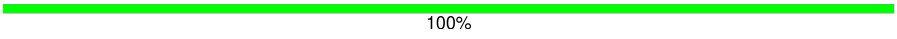
Chain FA:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain GA:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

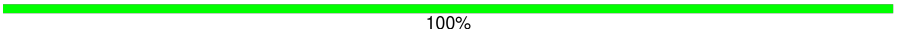
Chain HA:



There are no outlier residues recorded for this chain.

• Molecule 2: DNA (5'-D(P*AP*A)-3')

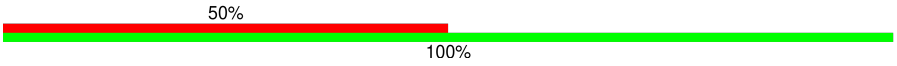
Chain IA:



There are no outlier residues recorded for this chain.

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain KA:



• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain LA:

There are no outlier residues recorded for this chain.

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain MA:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain NA:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain OA:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

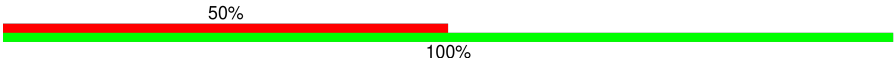
Chain PA:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain QA:

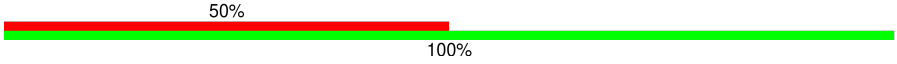
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain RA:



• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain SA:



• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain TA:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain VA:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain WA:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

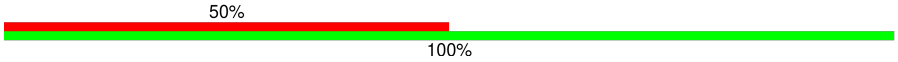
Chain XA:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain YA:

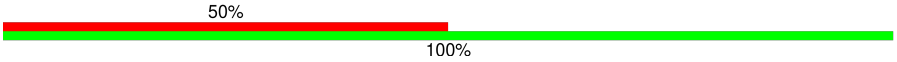
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain ZA:



• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain aA:



• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain bA:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain cA:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

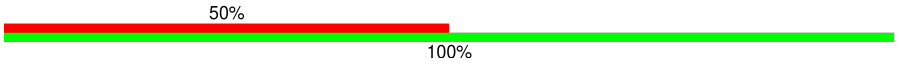
Chain dA:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain eA:

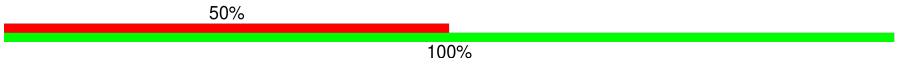
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain gA:



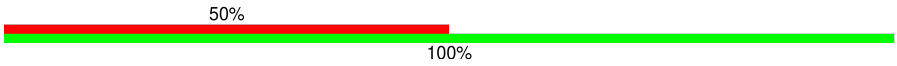
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain hA:



• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain iA:



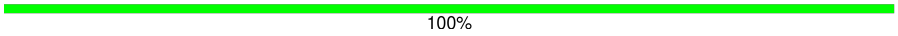
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain jA:

There are no outlier residues recorded for this chain.

• Molecule 2: DNA (5'-D(P*AP*A)-3')

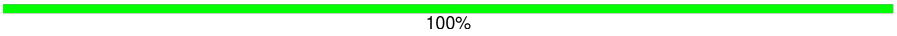
Chain kA:



There are no outlier residues recorded for this chain.

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain lA:



There are no outlier residues recorded for this chain.

• Molecule 2: DNA (5'-D(P*AP*A)-3')

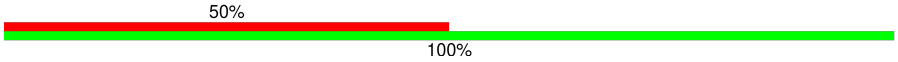
Chain mA:

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain nA:

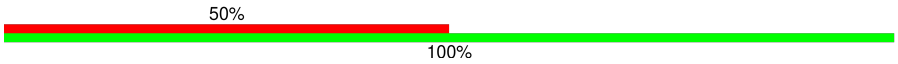
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain oA:



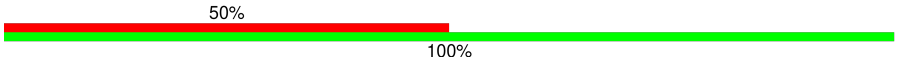
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain pA:



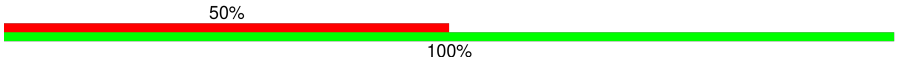
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain rA:



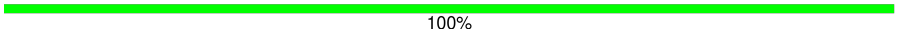
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain sA:



• Molecule 2: DNA (5'-D(P*AP*A)-3')

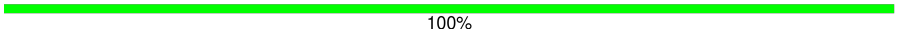
Chain tA:



There are no outlier residues recorded for this chain.

• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain uA:



There are no outlier residues recorded for this chain.

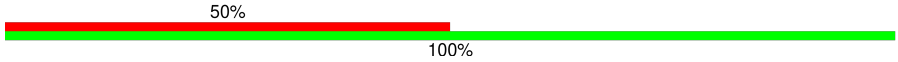
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain vA:

There are no outlier residues recorded for this chain.

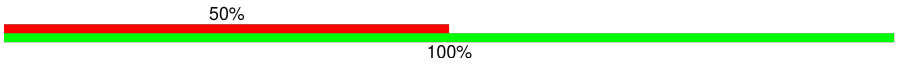
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain wA:



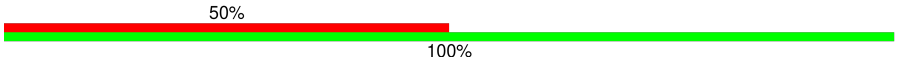
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain xA:



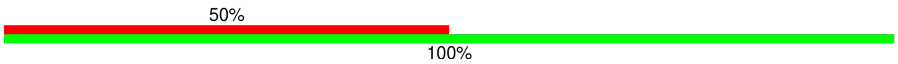
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain yA:



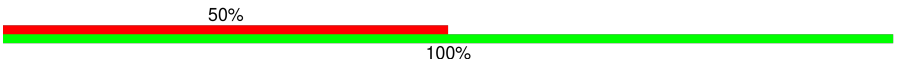
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain zA:



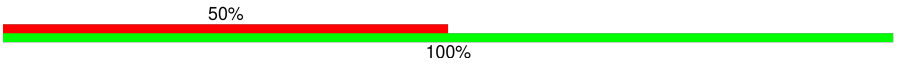
• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain 0A:



• Molecule 2: DNA (5'-D(P*AP*A)-3')

Chain 2A:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	42158	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 ($e^-/Å^2$)	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	22.036	Depositor
Minimum map value	-17.362	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	0.48	1/4248 (0.0%)	0.59	0/5805
1	2	0.48	1/4248 (0.0%)	0.59	0/5805
1	3	0.48	1/4248 (0.0%)	0.59	0/5805
1	4	0.48	1/4248 (0.0%)	0.59	0/5805
1	5	0.48	1/4248 (0.0%)	0.59	0/5805
1	6	0.48	1/4248 (0.0%)	0.59	0/5805
1	7	0.48	1/4248 (0.0%)	0.59	0/5805
1	8	0.48	1/4248 (0.0%)	0.59	0/5805
1	A	0.48	1/4248 (0.0%)	0.59	0/5805
1	B	0.48	1/4248 (0.0%)	0.59	0/5805
1	C	0.48	1/4248 (0.0%)	0.59	0/5805
1	D	0.48	1/4248 (0.0%)	0.59	0/5805
1	E	0.48	1/4248 (0.0%)	0.59	0/5805
1	F	0.48	1/4248 (0.0%)	0.59	0/5805
1	G	0.48	1/4248 (0.0%)	0.59	0/5805
1	H	0.48	1/4248 (0.0%)	0.59	0/5805
1	I	0.48	1/4248 (0.0%)	0.59	0/5805
1	J	0.48	1/4248 (0.0%)	0.59	0/5805
1	K	0.48	1/4248 (0.0%)	0.59	0/5805
1	L	0.48	1/4248 (0.0%)	0.59	0/5805
1	M	0.48	1/4248 (0.0%)	0.59	0/5805
1	N	0.48	1/4248 (0.0%)	0.59	0/5805
1	O	0.48	1/4248 (0.0%)	0.59	0/5805
1	P	0.48	1/4248 (0.0%)	0.59	0/5805
1	Q	0.48	1/4248 (0.0%)	0.59	0/5805
1	R	0.48	1/4248 (0.0%)	0.59	0/5805
1	S	0.48	1/4248 (0.0%)	0.59	0/5805
1	T	0.48	1/4248 (0.0%)	0.59	0/5805
1	U	0.48	1/4248 (0.0%)	0.59	0/5805
1	V	0.48	1/4248 (0.0%)	0.59	0/5805
1	W	0.48	1/4248 (0.0%)	0.59	0/5805
1	X	0.48	1/4248 (0.0%)	0.59	0/5805
1	Y	0.48	1/4248 (0.0%)	0.59	0/5805
1	Z	0.48	1/4248 (0.0%)	0.59	0/5805

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	a	0.48	1/4248 (0.0%)	0.59	0/5805
1	b	0.48	1/4248 (0.0%)	0.59	0/5805
1	c	0.48	1/4248 (0.0%)	0.59	0/5805
1	d	0.48	1/4248 (0.0%)	0.59	0/5805
1	e	0.48	1/4248 (0.0%)	0.59	0/5805
1	f	0.48	1/4248 (0.0%)	0.59	0/5805
1	g	0.48	1/4248 (0.0%)	0.59	0/5805
1	h	0.48	1/4248 (0.0%)	0.59	0/5805
1	i	0.48	1/4248 (0.0%)	0.59	0/5805
1	j	0.48	1/4248 (0.0%)	0.59	0/5805
1	k	0.48	1/4248 (0.0%)	0.59	0/5805
1	l	0.48	1/4248 (0.0%)	0.59	0/5805
1	m	0.48	1/4248 (0.0%)	0.59	0/5805
1	n	0.48	1/4248 (0.0%)	0.59	0/5805
1	o	0.48	1/4248 (0.0%)	0.59	0/5805
1	p	0.48	1/4248 (0.0%)	0.59	0/5805
1	q	0.48	1/4248 (0.0%)	0.59	0/5805
1	r	0.48	1/4248 (0.0%)	0.59	0/5805
1	s	0.48	1/4248 (0.0%)	0.59	0/5805
1	t	0.48	1/4248 (0.0%)	0.59	0/5805
1	u	0.48	1/4248 (0.0%)	0.59	0/5805
1	v	0.48	1/4248 (0.0%)	0.59	0/5805
1	w	0.48	1/4248 (0.0%)	0.59	0/5805
1	x	0.48	1/4248 (0.0%)	0.59	0/5805
1	y	0.48	1/4248 (0.0%)	0.59	0/5805
1	z	0.48	1/4248 (0.0%)	0.59	0/5805
2	0	0.60	0/47	0.85	0/70
2	0A	0.60	0/47	0.85	0/70
2	1A	0.61	0/47	0.85	0/70
2	2A	0.59	0/47	0.84	0/70
2	3A	0.60	0/47	0.85	0/70
2	4A	0.60	0/47	0.85	0/70
2	5A	0.60	0/47	0.85	0/70
2	9	0.60	0/47	0.84	0/70
2	AA	0.60	0/47	0.85	0/70
2	BA	0.61	0/47	0.85	0/70
2	CA	0.60	0/47	0.85	0/70
2	DA	0.61	0/47	0.85	0/70
2	EA	0.61	0/47	0.85	0/70
2	FA	0.60	0/47	0.85	0/70
2	GA	0.61	0/47	0.85	0/70
2	HA	0.60	0/47	0.85	0/70
2	IA	0.60	0/47	0.85	0/70

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
2	JA	0.60	0/47	0.84	0/70
2	KA	0.60	0/47	0.85	0/70
2	LA	0.61	0/47	0.85	0/70
2	MA	0.60	0/47	0.85	0/70
2	NA	0.60	0/47	0.85	0/70
2	OA	0.60	0/47	0.85	0/70
2	PA	0.59	0/47	0.85	0/70
2	QA	0.60	0/47	0.85	0/70
2	RA	0.60	0/47	0.85	0/70
2	SA	0.60	0/47	0.85	0/70
2	TA	0.60	0/47	0.85	0/70
2	UA	0.61	0/47	0.85	0/70
2	VA	0.60	0/47	0.85	0/70
2	WA	0.60	0/47	0.85	0/70
2	XA	0.60	0/47	0.85	0/70
2	YA	0.60	0/47	0.85	0/70
2	ZA	0.60	0/47	0.85	0/70
2	aA	0.60	0/47	0.85	0/70
2	bA	0.59	0/47	0.85	0/70
2	cA	0.60	0/47	0.85	0/70
2	dA	0.60	0/47	0.84	0/70
2	eA	0.61	0/47	0.85	0/70
2	fA	0.61	0/47	0.84	0/70
2	gA	0.60	0/47	0.85	0/70
2	hA	0.60	0/47	0.85	0/70
2	iA	0.61	0/47	0.85	0/70
2	jA	0.59	0/47	0.85	0/70
2	kA	0.59	0/47	0.85	0/70
2	lA	0.60	0/47	0.85	0/70
2	mA	0.60	0/47	0.85	0/70
2	nA	0.60	0/47	0.85	0/70
2	oA	0.60	0/47	0.85	0/70
2	pA	0.60	0/47	0.85	0/70
2	qA	0.61	0/47	0.86	0/70
2	rA	0.61	0/47	0.85	0/70
2	sA	0.60	0/47	0.85	0/70
2	tA	0.60	0/47	0.85	0/70
2	uA	0.59	0/47	0.85	0/70
2	vA	0.61	0/47	0.85	0/70
2	wA	0.60	0/47	0.85	0/70
2	xA	0.61	0/47	0.84	0/70
2	yA	0.60	0/47	0.85	0/70
2	zA	0.61	0/47	0.85	0/70

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
All	All	0.48	60/257700 (0.0%)	0.59	0/352500

All (60) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	a	619	HIS	C-N	-5.21	1.24	1.34
1	6	619	HIS	C-N	-5.18	1.24	1.34
1	o	619	HIS	C-N	-5.18	1.24	1.34
1	e	619	HIS	C-N	-5.17	1.24	1.34
1	C	619	HIS	C-N	-5.17	1.24	1.34
1	4	619	HIS	C-N	-5.17	1.24	1.34
1	d	619	HIS	C-N	-5.17	1.24	1.34
1	n	619	HIS	C-N	-5.17	1.24	1.34
1	B	619	HIS	C-N	-5.16	1.24	1.34
1	J	619	HIS	C-N	-5.16	1.24	1.34
1	L	619	HIS	C-N	-5.16	1.24	1.34
1	R	619	HIS	C-N	-5.16	1.24	1.34
1	q	619	HIS	C-N	-5.16	1.24	1.34
1	z	619	HIS	C-N	-5.16	1.24	1.34
1	K	619	HIS	C-N	-5.16	1.24	1.34
1	T	619	HIS	C-N	-5.16	1.24	1.34
1	V	619	HIS	C-N	-5.16	1.24	1.34
1	m	619	HIS	C-N	-5.16	1.24	1.34
1	p	619	HIS	C-N	-5.16	1.24	1.34
1	3	619	HIS	C-N	-5.16	1.24	1.34
1	D	619	HIS	C-N	-5.15	1.24	1.34
1	P	619	HIS	C-N	-5.14	1.24	1.34
1	W	619	HIS	C-N	-5.14	1.24	1.34
1	Y	619	HIS	C-N	-5.14	1.24	1.34
1	i	619	HIS	C-N	-5.14	1.24	1.34
1	k	619	HIS	C-N	-5.14	1.24	1.34
1	7	619	HIS	C-N	-5.14	1.24	1.34
1	E	619	HIS	C-N	-5.13	1.24	1.34
1	G	619	HIS	C-N	-5.13	1.24	1.34
1	M	619	HIS	C-N	-5.13	1.24	1.34
1	O	619	HIS	C-N	-5.13	1.24	1.34
1	X	619	HIS	C-N	-5.13	1.24	1.34
1	Z	619	HIS	C-N	-5.13	1.24	1.34
1	h	619	HIS	C-N	-5.13	1.24	1.34
1	l	619	HIS	C-N	-5.13	1.24	1.34
1	w	619	HIS	C-N	-5.13	1.24	1.34
1	8	619	HIS	C-N	-5.13	1.24	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	619	HIS	C-N	-5.13	1.24	1.34
1	F	619	HIS	C-N	-5.13	1.24	1.34
1	b	619	HIS	C-N	-5.13	1.24	1.34
1	c	619	HIS	C-N	-5.13	1.24	1.34
1	f	619	HIS	C-N	-5.13	1.24	1.34
1	v	619	HIS	C-N	-5.13	1.24	1.34
1	y	619	HIS	C-N	-5.13	1.24	1.34
1	I	619	HIS	C-N	-5.12	1.24	1.34
1	Q	619	HIS	C-N	-5.12	1.24	1.34
1	u	619	HIS	C-N	-5.12	1.24	1.34
1	x	619	HIS	C-N	-5.12	1.24	1.34
1	g	619	HIS	C-N	-5.11	1.24	1.34
1	N	619	HIS	C-N	-5.11	1.24	1.34
1	S	619	HIS	C-N	-5.11	1.24	1.34
1	U	619	HIS	C-N	-5.11	1.24	1.34
1	r	619	HIS	C-N	-5.11	1.24	1.34
1	s	619	HIS	C-N	-5.11	1.24	1.34
1	1	619	HIS	C-N	-5.11	1.24	1.34
1	2	619	HIS	C-N	-5.11	1.24	1.34
1	5	619	HIS	C-N	-5.11	1.24	1.34
1	t	619	HIS	C-N	-5.11	1.24	1.34
1	H	619	HIS	C-N	-5.11	1.24	1.34
1	j	619	HIS	C-N	-5.11	1.24	1.34

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	2	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	3	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	4	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	5	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	6	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	7	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	8	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	A	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	B	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	C	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	D	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	E	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	F	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	G	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	H	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	I	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	J	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	K	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	L	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	M	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	N	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	O	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	P	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	Q	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	R	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	S	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	T	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	U	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	V	516/724 (71%)	503 (98%)	13 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	W	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	X	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	Y	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	Z	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	a	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	b	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	c	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	d	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	e	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	f	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	g	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	h	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	i	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	j	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	k	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	l	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	m	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	n	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	o	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	p	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	q	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	r	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	s	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	t	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	u	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	v	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	w	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	x	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	y	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
1	z	516/724 (71%)	503 (98%)	13 (2%)	0	100	100
All	All	30960/43440 (71%)	30180 (98%)	780 (2%)	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	1	451/613 (74%)	451 (100%)	0	100	100
1	2	451/613 (74%)	451 (100%)	0	100	100
1	3	451/613 (74%)	451 (100%)	0	100	100
1	4	451/613 (74%)	451 (100%)	0	100	100
1	5	451/613 (74%)	451 (100%)	0	100	100
1	6	451/613 (74%)	451 (100%)	0	100	100
1	7	451/613 (74%)	451 (100%)	0	100	100
1	8	451/613 (74%)	451 (100%)	0	100	100
1	A	451/613 (74%)	451 (100%)	0	100	100
1	B	451/613 (74%)	451 (100%)	0	100	100
1	C	451/613 (74%)	451 (100%)	0	100	100
1	D	451/613 (74%)	451 (100%)	0	100	100
1	E	451/613 (74%)	451 (100%)	0	100	100
1	F	451/613 (74%)	451 (100%)	0	100	100
1	G	451/613 (74%)	451 (100%)	0	100	100
1	H	451/613 (74%)	451 (100%)	0	100	100
1	I	451/613 (74%)	451 (100%)	0	100	100
1	J	451/613 (74%)	451 (100%)	0	100	100
1	K	451/613 (74%)	451 (100%)	0	100	100
1	L	451/613 (74%)	451 (100%)	0	100	100
1	M	451/613 (74%)	451 (100%)	0	100	100
1	N	451/613 (74%)	451 (100%)	0	100	100
1	O	451/613 (74%)	451 (100%)	0	100	100
1	P	451/613 (74%)	451 (100%)	0	100	100

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	v	451/613 (74%)	451 (100%)	0	100	100
1	w	451/613 (74%)	451 (100%)	0	100	100
1	x	451/613 (74%)	451 (100%)	0	100	100
1	y	451/613 (74%)	451 (100%)	0	100	100
1	z	451/613 (74%)	451 (100%)	0	100	100
All	All	27060/36780 (74%)	27060 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (483) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	245	HIS
1	A	261	ASN
1	A	308	ASN
1	A	476	ASN
1	A	525	ASN
1	A	574	GLN
1	A	631	HIS
1	A	661	GLN
1	B	245	HIS
1	B	261	ASN
1	B	308	ASN
1	B	476	ASN
1	B	525	ASN
1	B	574	GLN
1	B	631	HIS
1	B	661	GLN
1	C	245	HIS
1	C	261	ASN
1	C	308	ASN
1	C	476	ASN
1	C	525	ASN
1	C	574	GLN
1	C	631	HIS
1	C	661	GLN
1	D	245	HIS
1	D	261	ASN
1	D	308	ASN
1	D	476	ASN

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Mol	Chain	Res	Type
1	D	525	ASN
1	D	574	GLN
1	D	631	HIS
1	D	661	GLN
1	E	245	HIS
1	E	261	ASN
1	E	308	ASN
1	E	476	ASN
1	E	525	ASN
1	E	574	GLN
1	E	631	HIS
1	E	661	GLN
1	F	245	HIS
1	F	261	ASN
1	F	308	ASN
1	F	476	ASN
1	F	525	ASN
1	F	574	GLN
1	F	631	HIS
1	F	661	GLN
1	G	245	HIS
1	G	261	ASN
1	G	308	ASN
1	G	476	ASN
1	G	525	ASN
1	G	574	GLN
1	G	631	HIS
1	G	661	GLN
1	H	245	HIS
1	H	261	ASN
1	H	308	ASN
1	H	476	ASN
1	H	525	ASN
1	H	574	GLN
1	H	631	HIS
1	H	661	GLN
1	I	245	HIS
1	I	261	ASN
1	I	308	ASN
1	I	476	ASN
1	I	525	ASN
1	I	574	GLN

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Mol	Chain	Res	Type
1	I	631	HIS
1	I	661	GLN
1	J	245	HIS
1	J	261	ASN
1	J	308	ASN
1	J	476	ASN
1	J	525	ASN
1	J	574	GLN
1	J	631	HIS
1	J	661	GLN
1	K	245	HIS
1	K	261	ASN
1	K	308	ASN
1	K	476	ASN
1	K	525	ASN
1	K	574	GLN
1	K	631	HIS
1	K	661	GLN
1	L	245	HIS
1	L	261	ASN
1	L	308	ASN
1	L	476	ASN
1	L	525	ASN
1	L	574	GLN
1	L	631	HIS
1	L	661	GLN
1	M	245	HIS
1	M	261	ASN
1	M	308	ASN
1	M	476	ASN
1	M	525	ASN
1	M	574	GLN
1	M	631	HIS
1	M	661	GLN
1	N	245	HIS
1	N	261	ASN
1	N	308	ASN
1	N	476	ASN
1	N	525	ASN
1	N	574	GLN
1	N	631	HIS
1	N	661	GLN

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Mol	Chain	Res	Type
1	O	245	HIS
1	O	261	ASN
1	O	308	ASN
1	O	476	ASN
1	O	525	ASN
1	O	574	GLN
1	O	631	HIS
1	O	661	GLN
1	P	245	HIS
1	P	261	ASN
1	P	308	ASN
1	P	476	ASN
1	P	525	ASN
1	P	574	GLN
1	P	631	HIS
1	P	661	GLN
1	Q	245	HIS
1	Q	261	ASN
1	Q	308	ASN
1	Q	476	ASN
1	Q	525	ASN
1	Q	574	GLN
1	Q	631	HIS
1	Q	661	GLN
1	R	245	HIS
1	R	261	ASN
1	R	308	ASN
1	R	476	ASN
1	R	525	ASN
1	R	574	GLN
1	R	631	HIS
1	R	661	GLN
1	S	245	HIS
1	S	261	ASN
1	S	308	ASN
1	S	476	ASN
1	S	525	ASN
1	S	574	GLN
1	S	631	HIS
1	S	661	GLN
1	T	245	HIS
1	T	261	ASN

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Mol	Chain	Res	Type
1	T	308	ASN
1	T	476	ASN
1	T	525	ASN
1	T	574	GLN
1	T	631	HIS
1	T	661	GLN
1	U	245	HIS
1	U	261	ASN
1	U	308	ASN
1	U	476	ASN
1	U	525	ASN
1	U	574	GLN
1	U	631	HIS
1	U	661	GLN
1	V	245	HIS
1	V	261	ASN
1	V	308	ASN
1	V	476	ASN
1	V	525	ASN
1	V	574	GLN
1	V	631	HIS
1	V	661	GLN
1	W	245	HIS
1	W	261	ASN
1	W	308	ASN
1	W	476	ASN
1	W	525	ASN
1	W	574	GLN
1	W	631	HIS
1	W	661	GLN
1	X	245	HIS
1	X	261	ASN
1	X	308	ASN
1	X	476	ASN
1	X	525	ASN
1	X	574	GLN
1	X	631	HIS
1	X	661	GLN
1	Y	245	HIS
1	Y	261	ASN
1	Y	308	ASN
1	Y	476	ASN

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Mol	Chain	Res	Type
1	Y	525	ASN
1	Y	574	GLN
1	Y	631	HIS
1	Y	661	GLN
1	Z	245	HIS
1	Z	261	ASN
1	Z	308	ASN
1	Z	476	ASN
1	Z	509	ASN
1	Z	525	ASN
1	Z	574	GLN
1	Z	631	HIS
1	Z	661	GLN
1	a	245	HIS
1	a	261	ASN
1	a	308	ASN
1	a	476	ASN
1	a	525	ASN
1	a	574	GLN
1	a	631	HIS
1	a	661	GLN
1	b	245	HIS
1	b	261	ASN
1	b	308	ASN
1	b	476	ASN
1	b	525	ASN
1	b	574	GLN
1	b	631	HIS
1	b	661	GLN
1	c	245	HIS
1	c	261	ASN
1	c	308	ASN
1	c	476	ASN
1	c	525	ASN
1	c	574	GLN
1	c	631	HIS
1	c	661	GLN
1	d	245	HIS
1	d	261	ASN
1	d	308	ASN
1	d	476	ASN
1	d	525	ASN

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Mol	Chain	Res	Type
1	d	574	GLN
1	d	631	HIS
1	d	661	GLN
1	e	245	HIS
1	e	261	ASN
1	e	308	ASN
1	e	476	ASN
1	e	525	ASN
1	e	574	GLN
1	e	631	HIS
1	e	661	GLN
1	f	245	HIS
1	f	261	ASN
1	f	308	ASN
1	f	476	ASN
1	f	525	ASN
1	f	574	GLN
1	f	631	HIS
1	f	661	GLN
1	g	245	HIS
1	g	261	ASN
1	g	308	ASN
1	g	476	ASN
1	g	525	ASN
1	g	574	GLN
1	g	631	HIS
1	g	661	GLN
1	h	245	HIS
1	h	261	ASN
1	h	308	ASN
1	h	476	ASN
1	h	509	ASN
1	h	525	ASN
1	h	574	GLN
1	h	631	HIS
1	h	661	GLN
1	i	245	HIS
1	i	261	ASN
1	i	308	ASN
1	i	476	ASN
1	i	525	ASN
1	i	574	GLN

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Mol	Chain	Res	Type
1	i	631	HIS
1	i	661	GLN
1	j	245	HIS
1	j	261	ASN
1	j	308	ASN
1	j	476	ASN
1	j	525	ASN
1	j	574	GLN
1	j	631	HIS
1	j	661	GLN
1	k	245	HIS
1	k	261	ASN
1	k	308	ASN
1	k	476	ASN
1	k	525	ASN
1	k	574	GLN
1	k	631	HIS
1	k	661	GLN
1	l	245	HIS
1	l	261	ASN
1	l	308	ASN
1	l	476	ASN
1	l	525	ASN
1	l	574	GLN
1	l	631	HIS
1	l	661	GLN
1	m	245	HIS
1	m	261	ASN
1	m	308	ASN
1	m	476	ASN
1	m	525	ASN
1	m	574	GLN
1	m	631	HIS
1	m	661	GLN
1	n	245	HIS
1	n	261	ASN
1	n	308	ASN
1	n	476	ASN
1	n	525	ASN
1	n	574	GLN
1	n	631	HIS
1	n	661	GLN

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Mol	Chain	Res	Type
1	o	245	HIS
1	o	261	ASN
1	o	308	ASN
1	o	476	ASN
1	o	525	ASN
1	o	574	GLN
1	o	631	HIS
1	o	661	GLN
1	p	245	HIS
1	p	261	ASN
1	p	308	ASN
1	p	476	ASN
1	p	525	ASN
1	p	574	GLN
1	p	631	HIS
1	p	661	GLN
1	q	245	HIS
1	q	261	ASN
1	q	308	ASN
1	q	476	ASN
1	q	525	ASN
1	q	574	GLN
1	q	631	HIS
1	q	661	GLN
1	r	245	HIS
1	r	261	ASN
1	r	308	ASN
1	r	476	ASN
1	r	525	ASN
1	r	574	GLN
1	r	631	HIS
1	r	661	GLN
1	s	245	HIS
1	s	261	ASN
1	s	308	ASN
1	s	476	ASN
1	s	525	ASN
1	s	574	GLN
1	s	631	HIS
1	s	661	GLN
1	t	245	HIS
1	t	261	ASN

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Mol	Chain	Res	Type
1	t	308	ASN
1	t	476	ASN
1	t	525	ASN
1	t	574	GLN
1	t	631	HIS
1	t	661	GLN
1	u	245	HIS
1	u	261	ASN
1	u	308	ASN
1	u	476	ASN
1	u	525	ASN
1	u	574	GLN
1	u	631	HIS
1	u	661	GLN
1	v	245	HIS
1	v	261	ASN
1	v	308	ASN
1	v	476	ASN
1	v	525	ASN
1	v	574	GLN
1	v	631	HIS
1	v	661	GLN
1	w	245	HIS
1	w	261	ASN
1	w	308	ASN
1	w	476	ASN
1	w	525	ASN
1	w	574	GLN
1	w	631	HIS
1	w	661	GLN
1	x	245	HIS
1	x	261	ASN
1	x	308	ASN
1	x	476	ASN
1	x	525	ASN
1	x	574	GLN
1	x	631	HIS
1	x	661	GLN
1	y	245	HIS
1	y	261	ASN
1	y	308	ASN
1	y	476	ASN

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Mol	Chain	Res	Type
1	y	525	ASN
1	y	574	GLN
1	y	631	HIS
1	y	661	GLN
1	z	245	HIS
1	z	261	ASN
1	z	308	ASN
1	z	476	ASN
1	z	525	ASN
1	z	574	GLN
1	z	631	HIS
1	z	661	GLN
1	1	245	HIS
1	1	261	ASN
1	1	308	ASN
1	1	476	ASN
1	1	525	ASN
1	1	574	GLN
1	1	631	HIS
1	1	661	GLN
1	2	245	HIS
1	2	261	ASN
1	2	308	ASN
1	2	476	ASN
1	2	525	ASN
1	2	574	GLN
1	2	631	HIS
1	2	661	GLN
1	3	245	HIS
1	3	261	ASN
1	3	308	ASN
1	3	476	ASN
1	3	525	ASN
1	3	574	GLN
1	3	631	HIS
1	3	661	GLN
1	4	245	HIS
1	4	261	ASN
1	4	308	ASN
1	4	476	ASN
1	4	525	ASN
1	4	574	GLN

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Mol	Chain	Res	Type
1	4	631	HIS
1	4	661	GLN
1	5	245	HIS
1	5	261	ASN
1	5	308	ASN
1	5	476	ASN
1	5	525	ASN
1	5	574	GLN
1	5	631	HIS
1	5	661	GLN
1	6	245	HIS
1	6	261	ASN
1	6	308	ASN
1	6	476	ASN
1	6	525	ASN
1	6	574	GLN
1	6	631	HIS
1	6	661	GLN
1	7	245	HIS
1	7	261	ASN
1	7	308	ASN
1	7	476	ASN
1	7	525	ASN
1	7	574	GLN
1	7	631	HIS
1	7	661	GLN
1	8	245	HIS
1	8	261	ASN
1	8	308	ASN
1	8	476	ASN
1	8	509	ASN
1	8	525	ASN
1	8	574	GLN
1	8	631	HIS
1	8	661	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

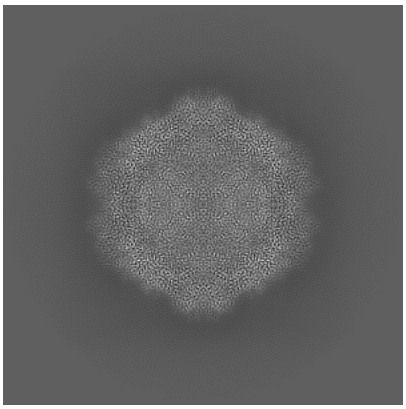
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-46749. These allow visual inspection of the internal detail of the map and identification of artifacts.

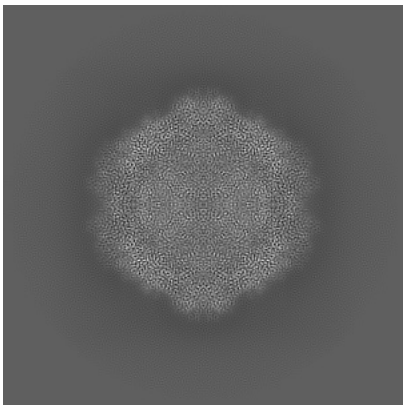
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

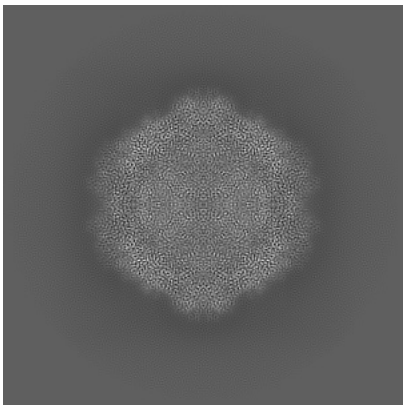
6.1.1 Primary map



X

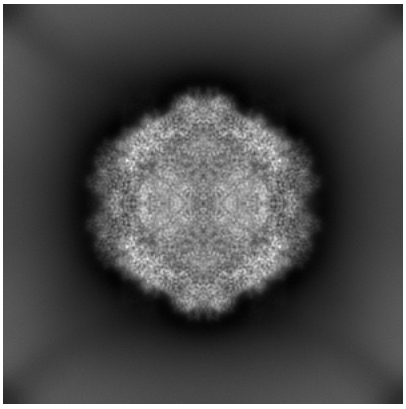


Y

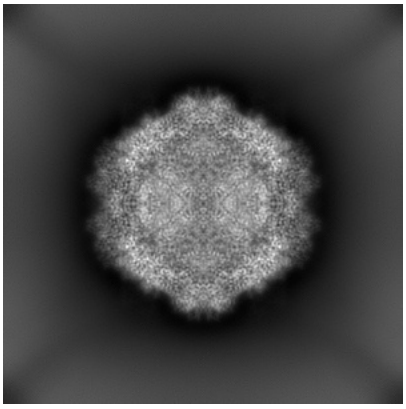


Z

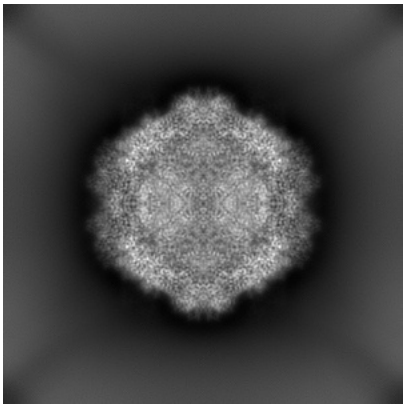
6.1.2 Raw map



X



Y

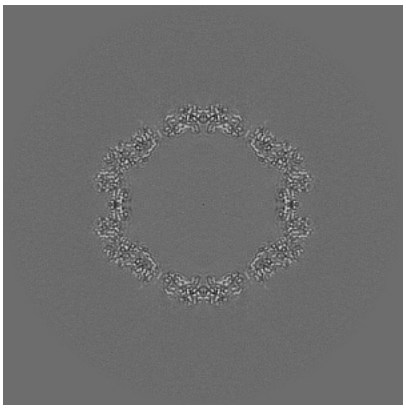


Z

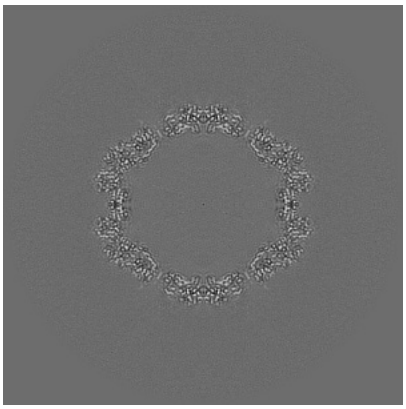
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

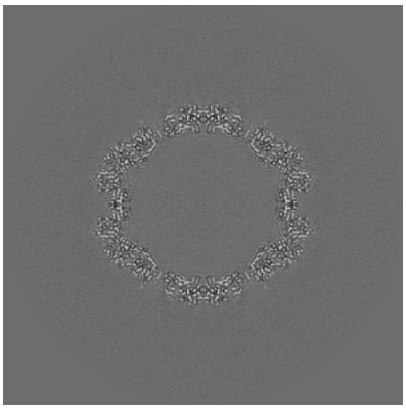
6.2.1 Primary map



X Index: 250

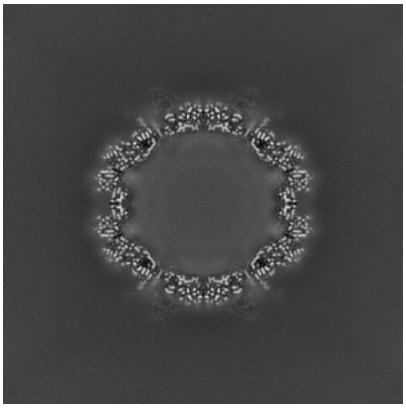


Y Index: 250

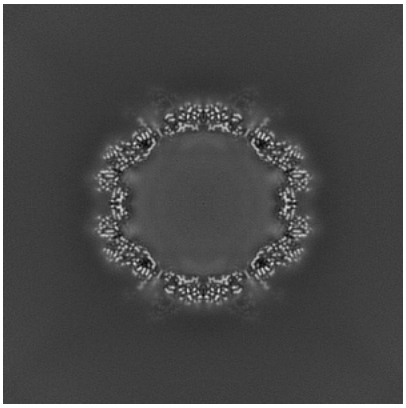


Z Index: 250

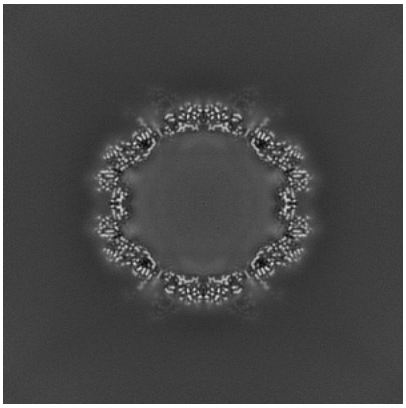
6.2.2 Raw map



X Index: 250



Y Index: 250

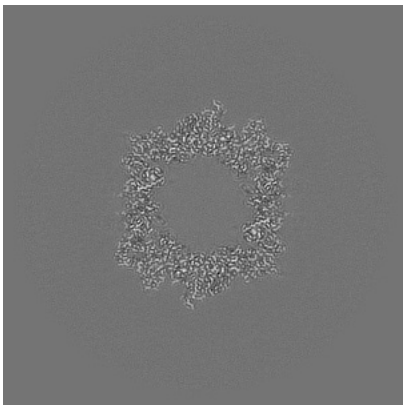


Z Index: 250

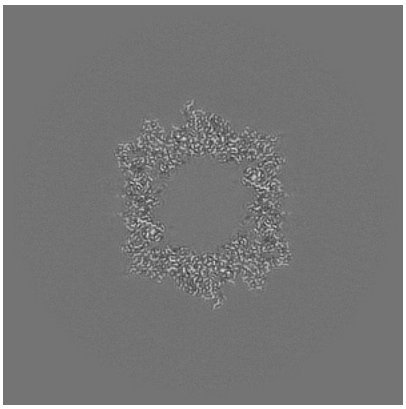
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

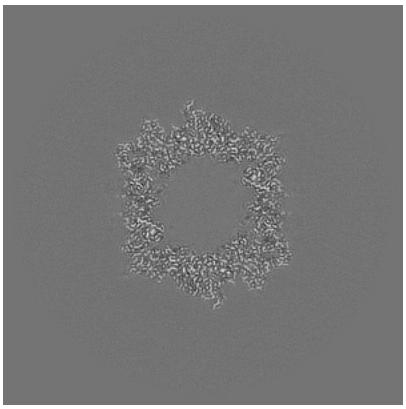
6.3.1 Primary map



X Index: 320

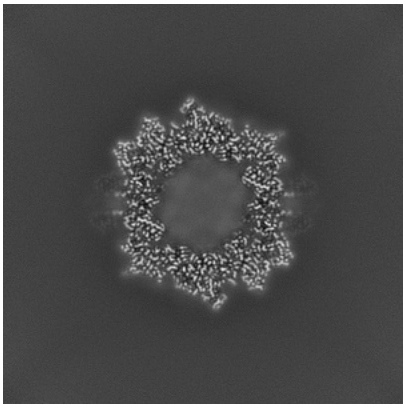


Y Index: 180

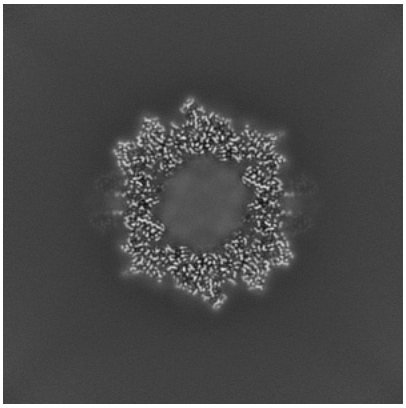


Z Index: 180

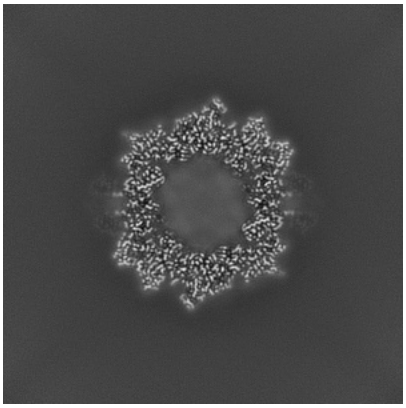
6.3.2 Raw map



X Index: 180



Y Index: 180

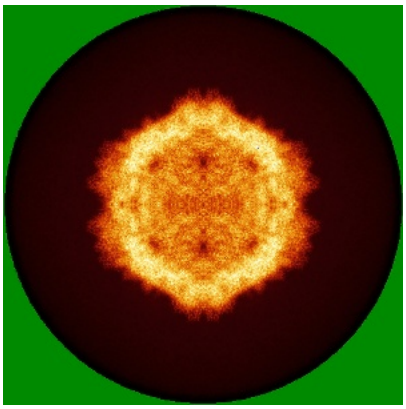


Z Index: 320

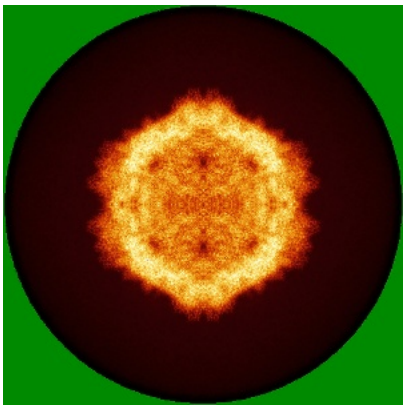
The images above show the largest variance slices of the map in three orthogonal directions.

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

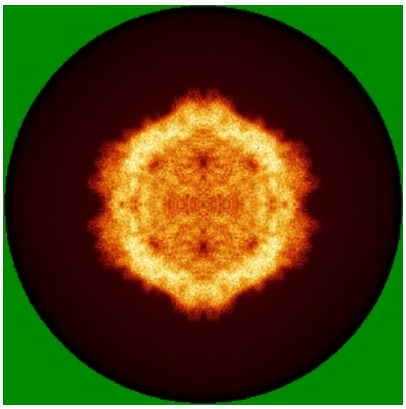
6.4.1 Primary map



X

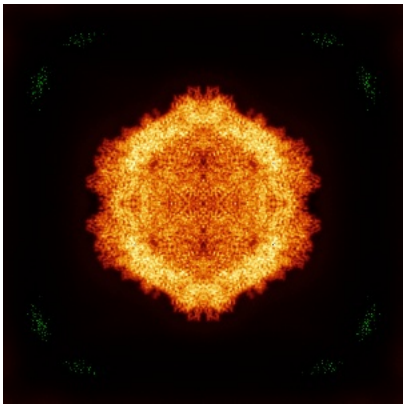


Y

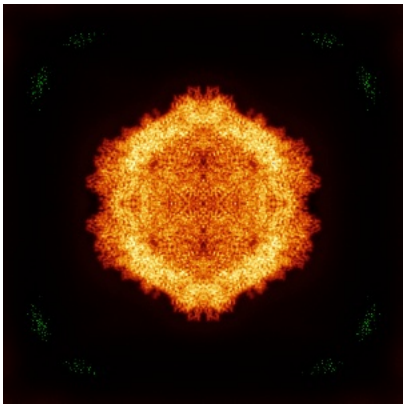


Z

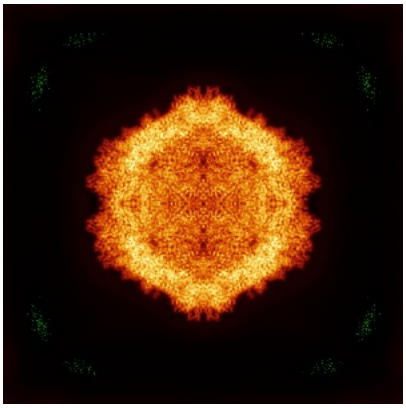
6.4.2 Raw map



X



Y



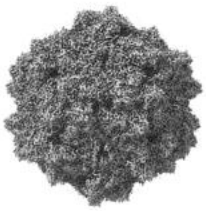
Z

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.

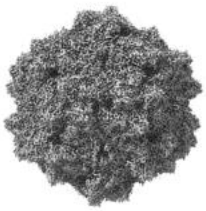
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X



Y

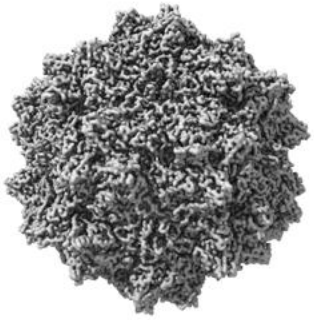


Z

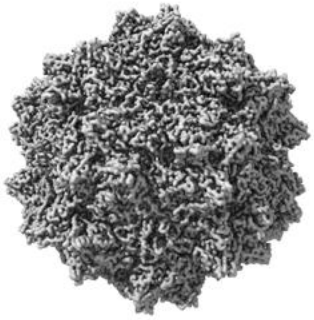
The images above show the 3D surface view of the map at the recommended contour level 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

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.

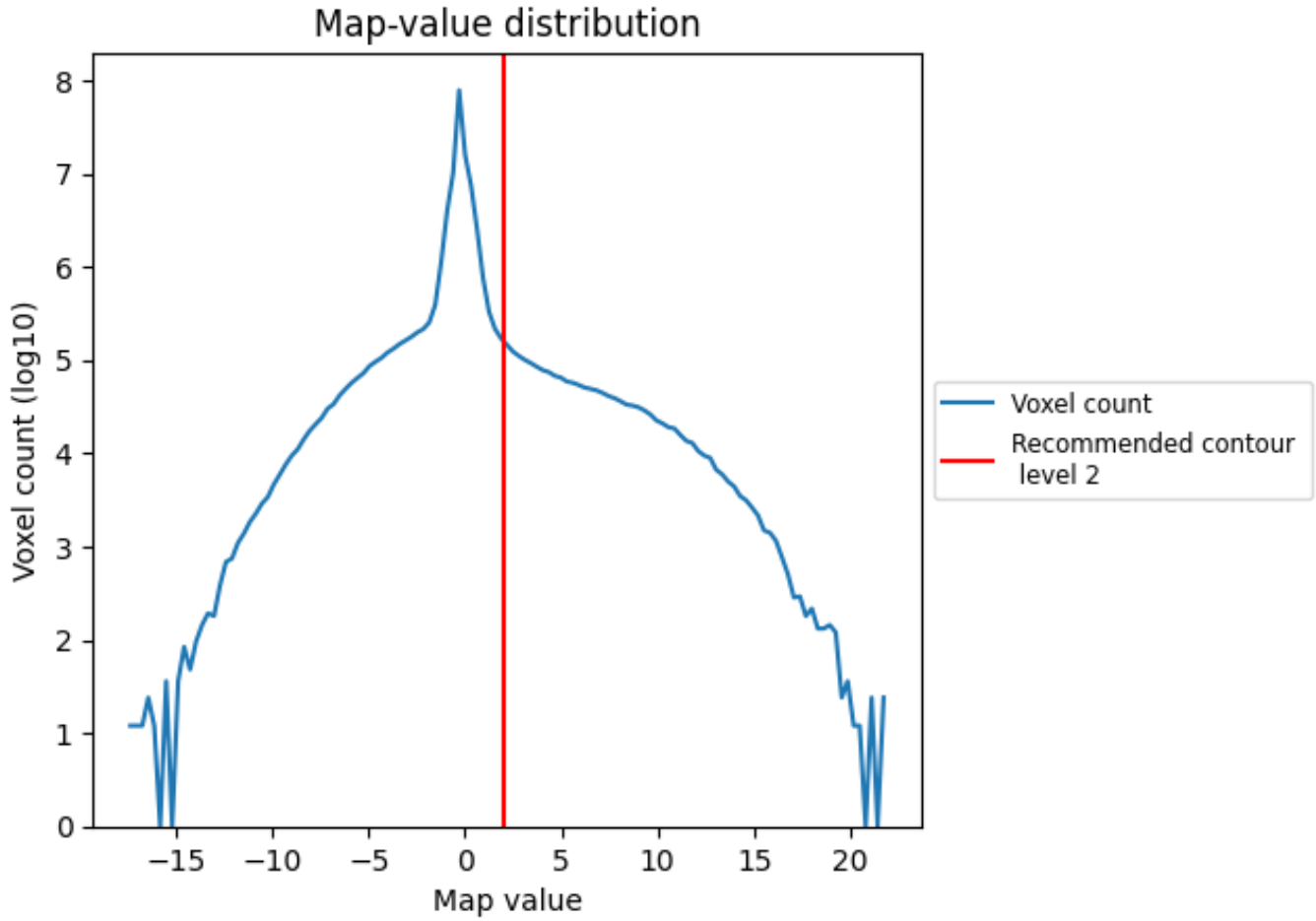
6.6 Mask visualisation (i)

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

7 Map analysis

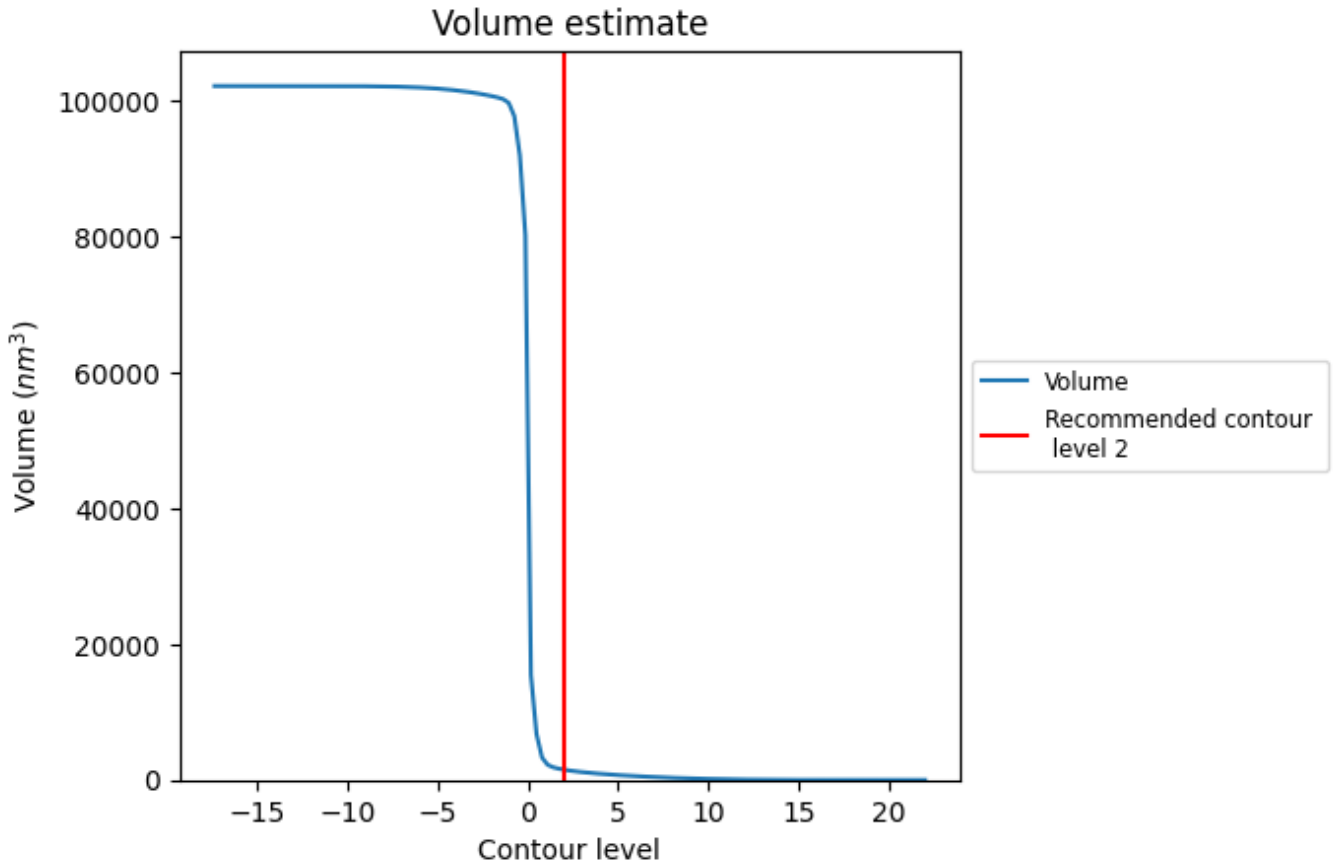
This section contains the results of statistical analysis of the map.

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.

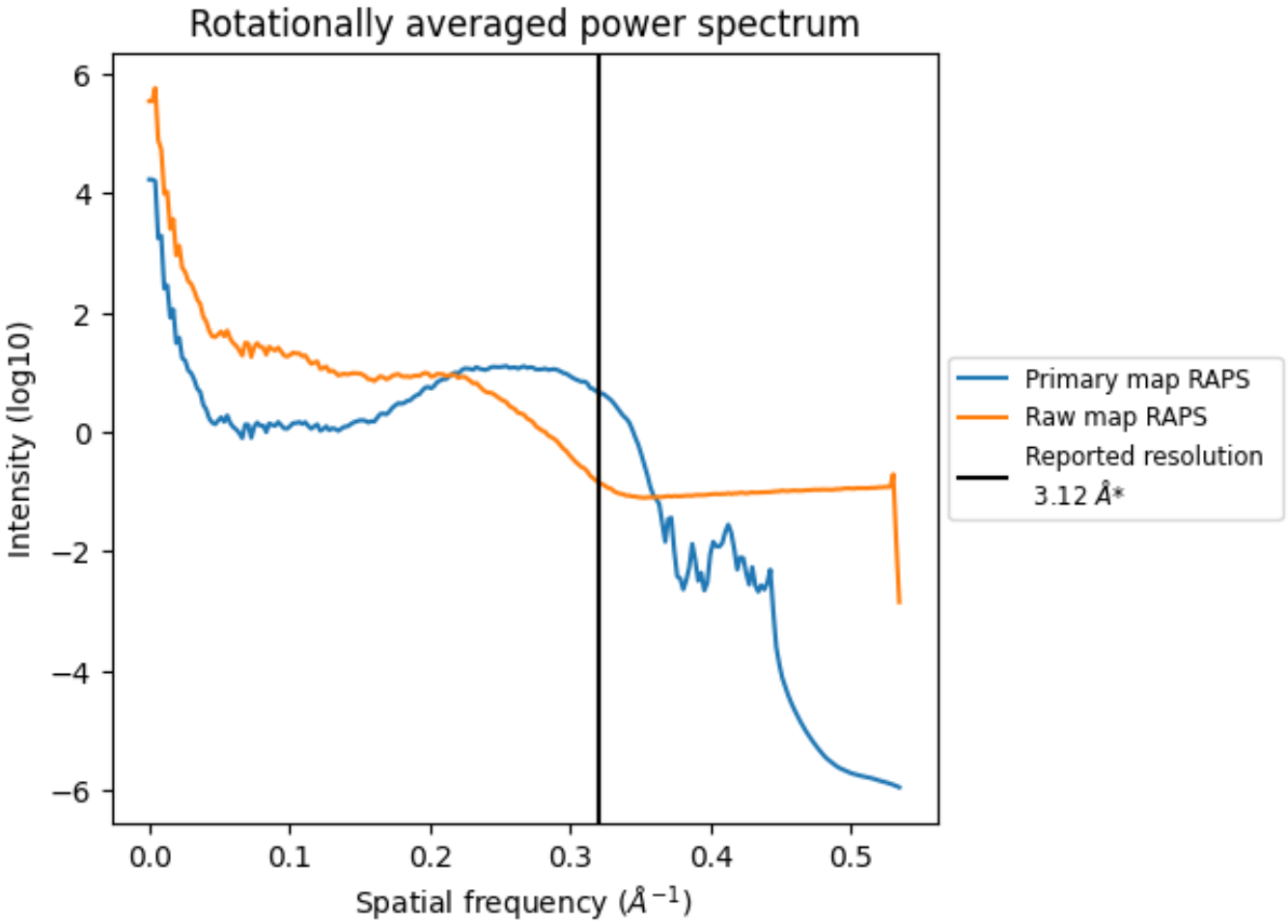
7.2 Volume estimate



The volume at the recommended contour level is 1520 nm^3; this corresponds to an approximate mass of 1373 kDa.

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

7.3 Rotationally averaged power spectrum (i)

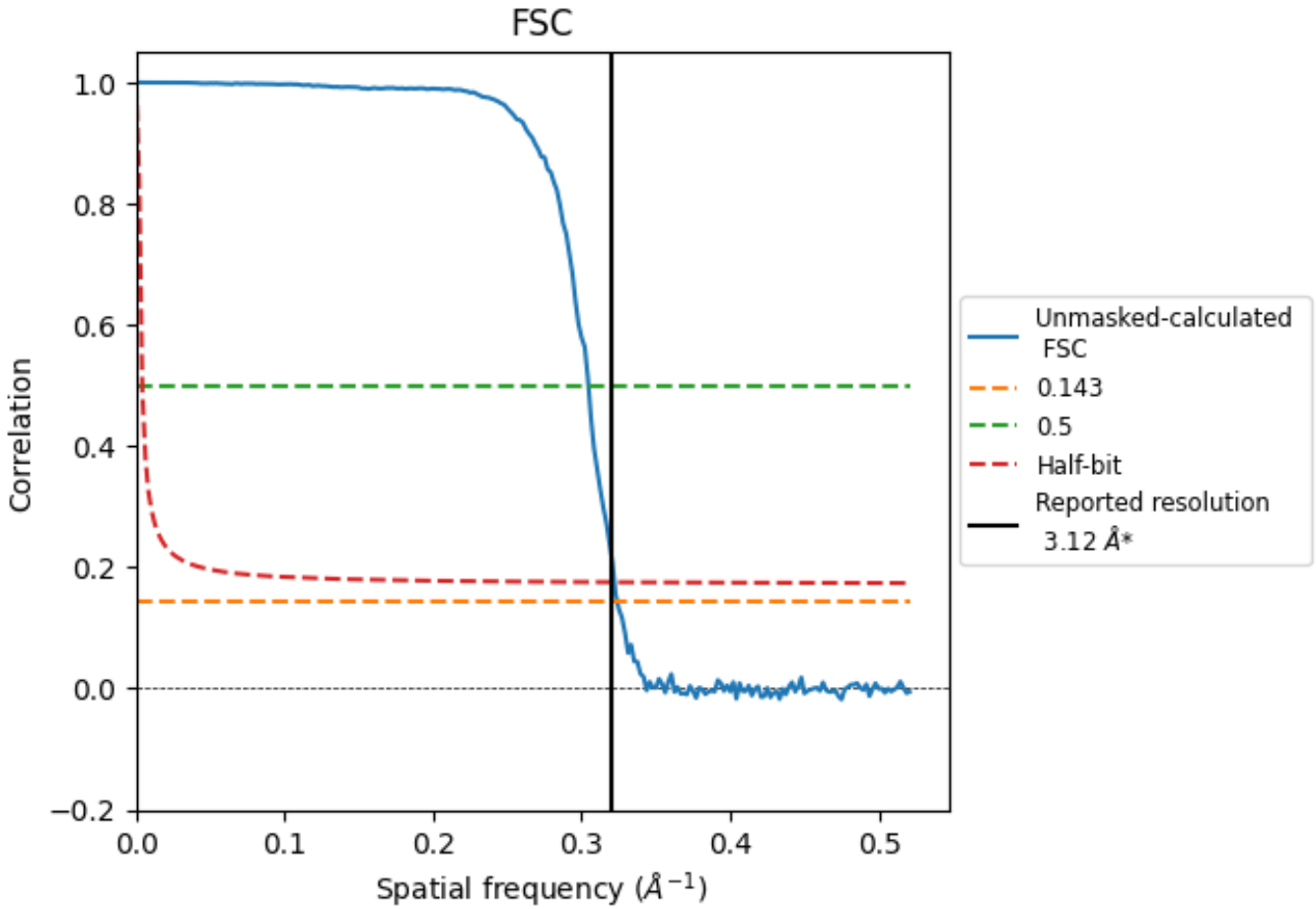


*Reported resolution corresponds to spatial frequency of 0.321 Å^{-1}

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 0.321 Å^{-1}

8.2 Resolution estimates (i)

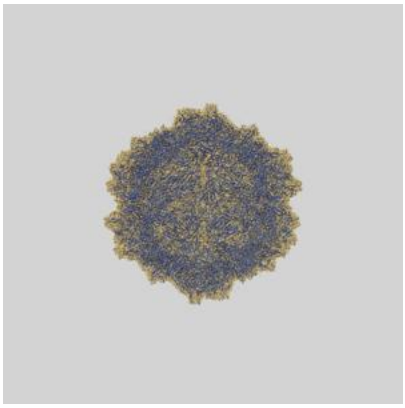
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.12	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.09	3.28	3.10

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

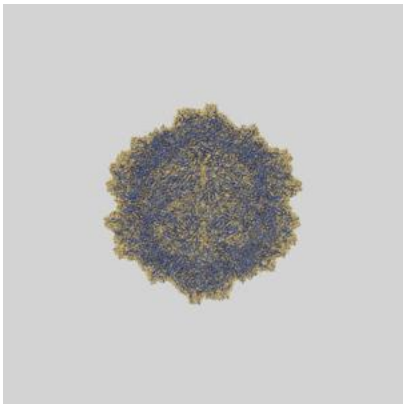
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-46749 and PDB model 9DCC. Per-residue inclusion information can be found in section 3 on page 14.

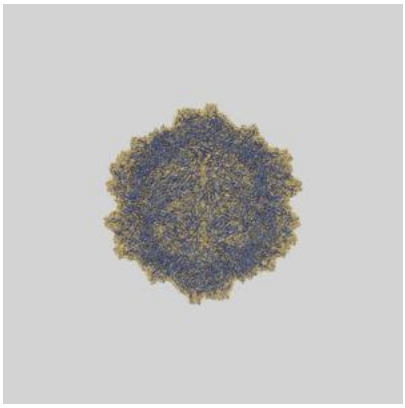
9.1 Map-model overlay



X



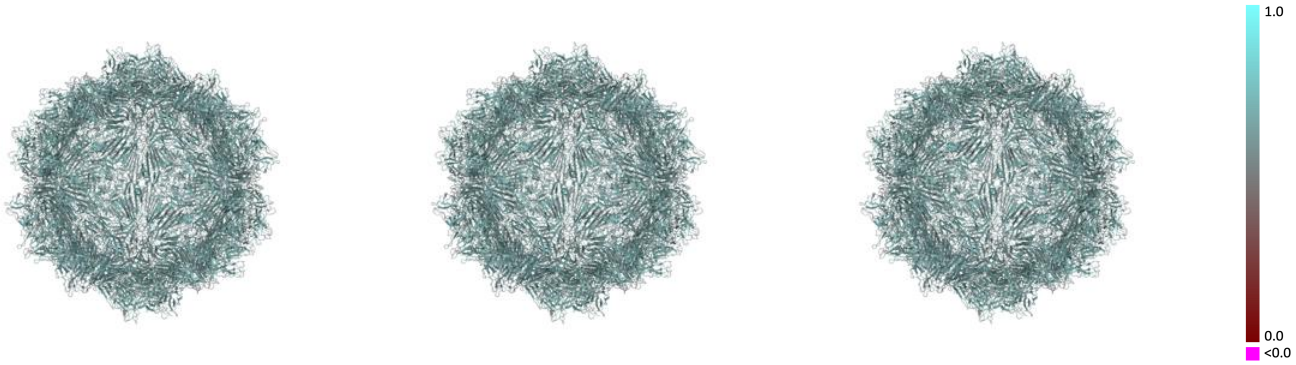
Y



Z

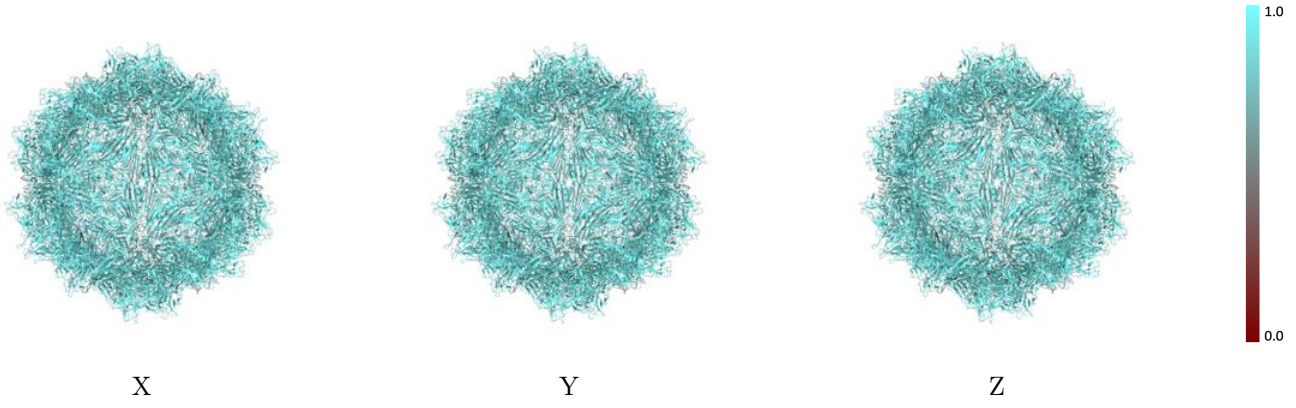
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



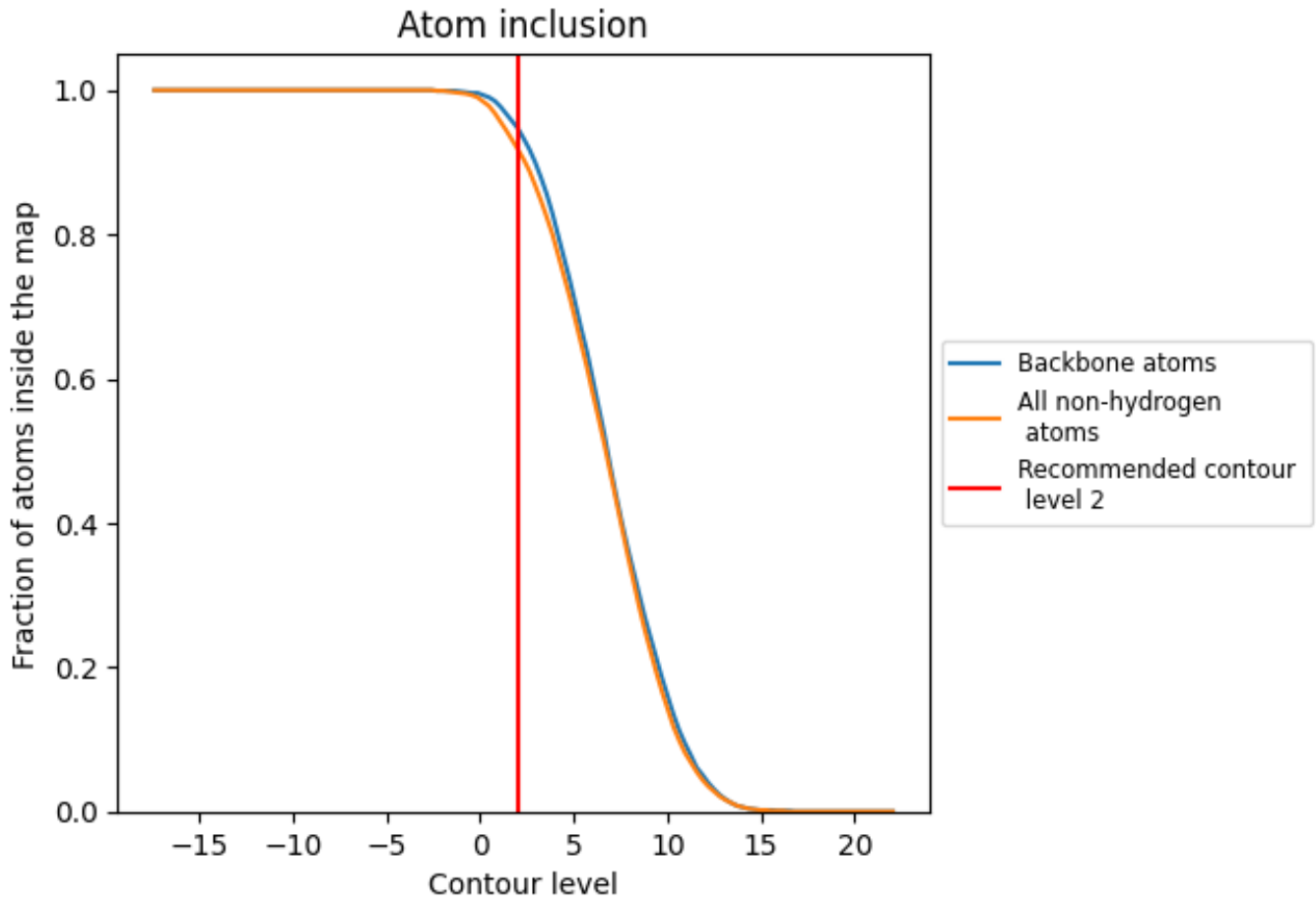
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	0.9190	0.6240
0	0.5480	0.5410
0A	0.5480	0.5400
1	0.9230	0.6250
1A	0.5480	0.5460
2	0.9230	0.6250
2A	0.5710	0.5480
3	0.9230	0.6250
3A	0.5710	0.5540
4	0.9220	0.6250
4A	0.5480	0.5490
5	0.9230	0.6250
5A	0.5480	0.5420
6	0.9230	0.6250
7	0.9230	0.6250
8	0.9240	0.6260
9	0.5950	0.5400
A	0.9240	0.6260
AA	0.5480	0.5340
B	0.9230	0.6250
BA	0.5950	0.5370
C	0.9220	0.6240
CA	0.5710	0.5560
D	0.9230	0.6250
DA	0.5480	0.5380
E	0.9240	0.6260
EA	0.5710	0.5510
F	0.9240	0.6250
FA	0.5480	0.5420
G	0.9230	0.6250
GA	0.5480	0.5430
H	0.9230	0.6250
HA	0.5950	0.5370
I	0.9220	0.6250
IA	0.5950	0.5400

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Chain	Atom inclusion	Q-score
J	0.9230	0.6250
JA	0.5950	0.5400
K	0.9220	0.6240
KA	0.5480	0.5400
L	0.9230	0.6250
LA	0.5950	0.5360
M	0.9240	0.6250
MA	0.5480	0.5390
N	0.9230	0.6250
NA	0.5480	0.5470
O	0.9240	0.6250
OA	0.5710	0.5550
P	0.9230	0.6250
PA	0.5480	0.5380
Q	0.9220	0.6250
QA	0.5710	0.5610
R	0.9230	0.6250
RA	0.5480	0.5440
S	0.9230	0.6250
SA	0.5480	0.5380
T	0.9220	0.6250
TA	0.5480	0.5370
U	0.9230	0.6260
UA	0.5480	0.5390
V	0.9220	0.6250
VA	0.5480	0.5390
W	0.9230	0.6260
WA	0.5480	0.5450
X	0.9240	0.6250
XA	0.5480	0.5420
Y	0.9230	0.6250
YA	0.5480	0.5430
Z	0.9240	0.6260
ZA	0.5710	0.5580
a	0.9240	0.6250
aA	0.5480	0.5310
b	0.9240	0.6250
bA	0.5480	0.5460
c	0.9240	0.6260
cA	0.5480	0.5440
d	0.9240	0.6250
dA	0.5710	0.5590

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Chain	Atom inclusion	Q-score
e	0.9240	0.6260
eA	0.5480	0.5380
f	0.9240	0.6250
fA	0.5480	0.5420
g	0.9220	0.6250
gA	0.5480	0.5460
h	0.9240	0.6260
hA	0.5710	0.5520
i	0.9230	0.6240
iA	0.5480	0.5370
j	0.9230	0.6250
jA	0.5950	0.5350
k	0.9230	0.6260
kA	0.5950	0.5440
l	0.9240	0.6250
lA	0.5950	0.5400
m	0.9220	0.6250
mA	0.5710	0.5530
n	0.9240	0.6250
nA	0.5480	0.5450
o	0.9240	0.6250
oA	0.5480	0.5470
p	0.9220	0.6250
pA	0.5710	0.5540
q	0.9230	0.6250
qA	0.5710	0.5550
r	0.9230	0.6250
rA	0.5480	0.5460
s	0.9230	0.6250
sA	0.5480	0.5390
t	0.9240	0.6250
tA	0.5950	0.5340
u	0.9220	0.6240
uA	0.5950	0.5430
v	0.9240	0.6250
vA	0.5950	0.5340
w	0.9240	0.6250
wA	0.5480	0.5400
x	0.9220	0.6240
xA	0.5480	0.5340
y	0.9240	0.6250
yA	0.5480	0.5380

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Chain	Atom inclusion	Q-score
z	0.9230	0.6250
zA	0.5480	0.5340