



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:40 AM UTC

PDB ID : 6V10 / pdb_00006v10
EMDB ID : EMD-21004
Title : genome-containing AAV8 particles
Authors : Mietzsch, M.; Agbandje-McKenna, M.
Deposited on : 2019-11-19
Resolution : 3.77 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

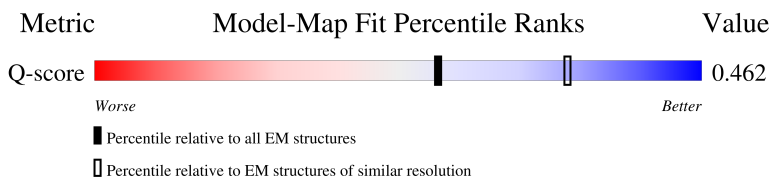
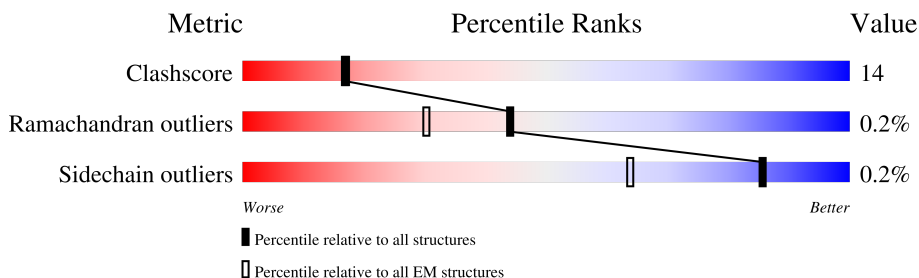
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.77 Å.

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



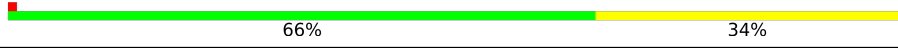
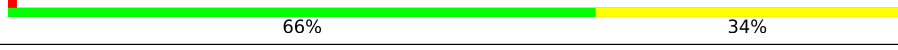
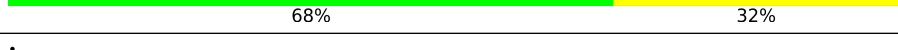
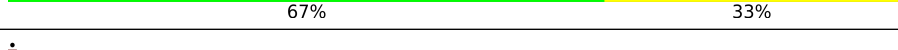
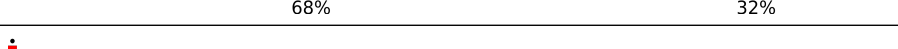
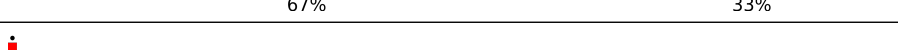
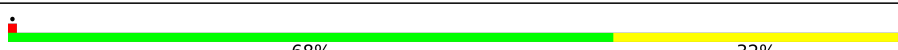
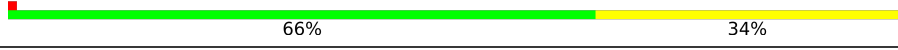
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10146 (3.27 - 4.27)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	521	 66% 34%
1	2	521	 67% 33%
1	3	521	 67% 33%
1	4	521	 67% 33%

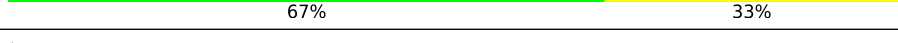
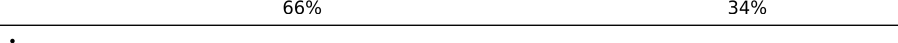
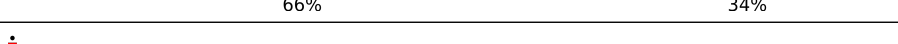
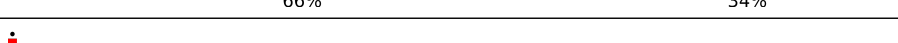
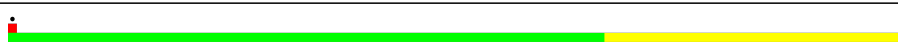
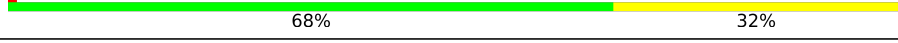
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Mol	Chain	Length	Quality of chain
1	5	521	 67%33%
1	6	521	 67%33%
1	7	521	 66%34%
1	8	521	 66%34%
1	A	521	 67%33%
1	B	521	 67%33%
1	C	521	 68%32%
1	D	521	 67%33%
1	E	521	 68%32%
1	F	521	 67%33%
1	G	521	 67%33%
1	H	521	 67%33%
1	I	521	 66%34%
1	J	521	 67%33%
1	K	521	 67%33%
1	L	521	 68%32%
1	M	521	 66%34%
1	N	521	 68%32%
1	O	521	 68%32%
1	P	521	 67%33%
1	Q	521	 68%32%
1	R	521	 66%34%
1	S	521	 68%32%
1	T	521	 67%33%
1	U	521	 67%33%

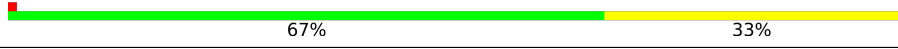
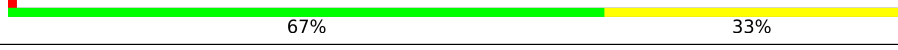
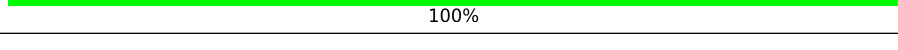
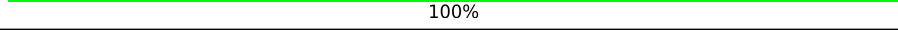
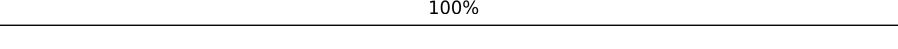
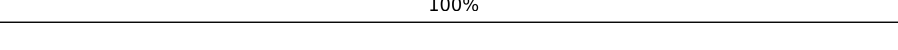
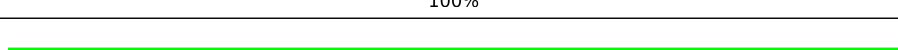
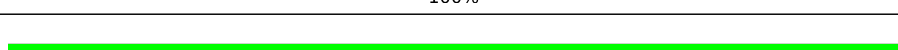
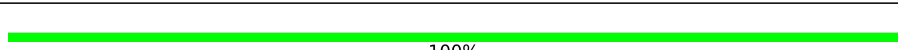
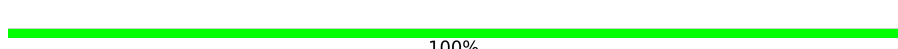
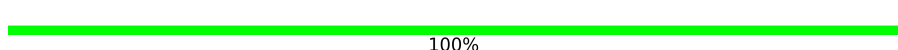
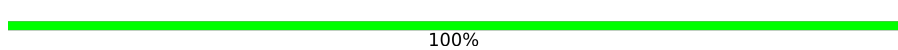
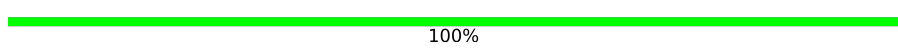
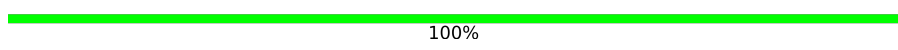
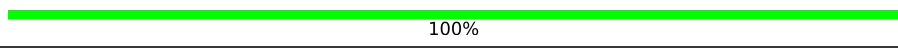
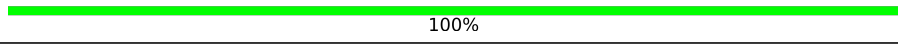
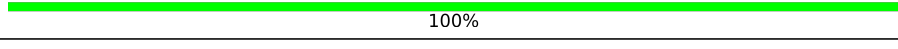
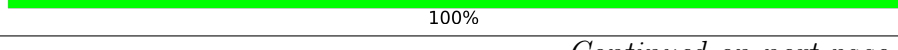
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Mol	Chain	Length	Quality of chain	
1	V	521		
1	W	521		
1	X	521		
1	Y	521		
1	Z	521		
1	a	521		
1	b	521		
1	c	521		
1	d	521		
1	e	521		
1	f	521		
1	g	521		
1	h	521		
1	i	521		
1	j	521		
1	k	521		
1	l	521		
1	m	521		
1	n	521		
1	o	521		
1	p	521		
1	q	521		
1	r	521		
1	s	521		
1	t	521		

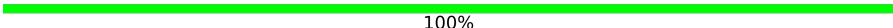
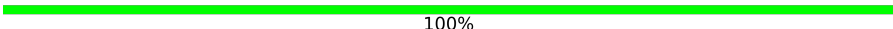
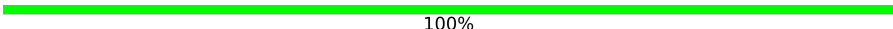
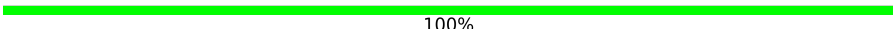
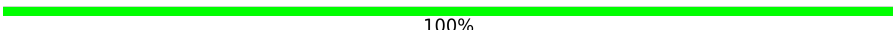
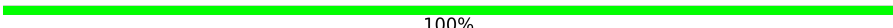
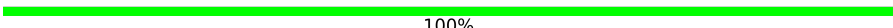
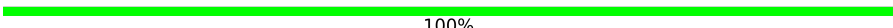
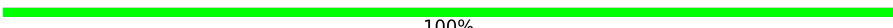
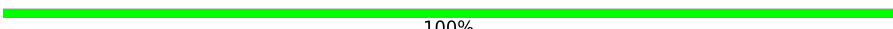
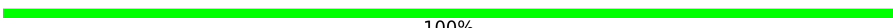
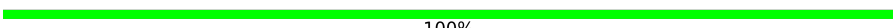
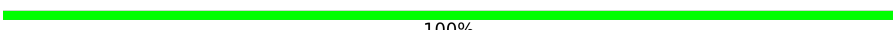
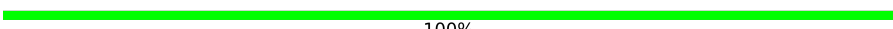
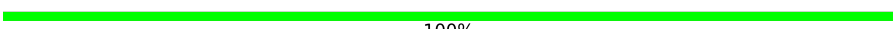
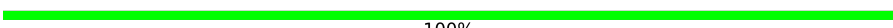
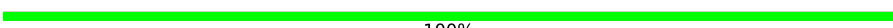
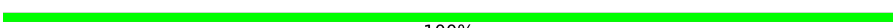
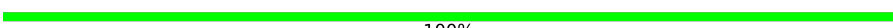
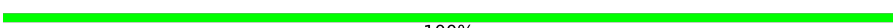
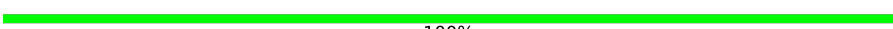
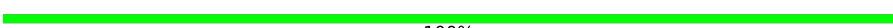
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Mol	Chain	Length	Quality of chain
1	u	521	 67%33%
1	v	521	 67%33%
1	w	521	 67%33%
1	x	521	 67%33%
1	y	521	 67%33%
1	z	521	 68%32%
2	0	2	 100%
2	0A	2	 100%
2	1A	2	 100%
2	2A	2	 100%
2	3A	2	 100%
2	4A	2	 100%
2	5A	2	 100%
2	9	2	 100%
2	AA	2	 100%
2	BA	2	 100%
2	CA	2	 100%
2	DA	2	 100%
2	EA	2	 100%
2	FA	2	 100%
2	GA	2	 100%
2	HA	2	 100%
2	IA	2	 100%
2	JA	2	 100%
2	KA	2	 100%

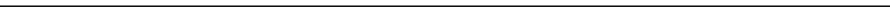
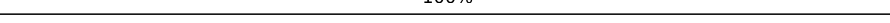
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Mol	Chain	Length	Quality of chain
2	LA	2	 100%
2	MA	2	 100%
2	NA	2	 100%
2	OA	2	 100%
2	PA	2	 100%
2	QA	2	 100%
2	RA	2	 100%
2	SA	2	 100%
2	TA	2	 100%
2	UA	2	 100%
2	VA	2	 100%
2	WA	2	 100%
2	XA	2	 100%
2	YA	2	 100%
2	ZA	2	 100%
2	aA	2	 100%
2	bA	2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

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

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 250920 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	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	B	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	C	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	D	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	E	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	F	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	G	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	H	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	I	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	J	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	K	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	L	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	M	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	N	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	O	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	P	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		
1	Q	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	S	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	T	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	U	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	V	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	W	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	X	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	Y	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	Z	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	a	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	b	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	c	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	d	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	e	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	f	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	g	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	h	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	i	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	j	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	k	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	l	521	Total 4145	C 2614	N 718	O 800	S 13	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	n	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	o	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	p	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	q	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	r	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	s	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	t	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	u	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	v	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	w	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	x	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	y	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	z	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	1	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	2	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	3	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	4	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	5	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	6	521	Total 4145	C 2614	N 718	O 800	S 13	0	0
1	7	521	Total 4145	C 2614	N 718	O 800	S 13	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	521	Total	C	N	O	S	0	0
			4145	2614	718	800	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	0	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	9	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	AA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	BA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	CA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	DA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	EA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	FA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	GA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	HA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	IA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	JA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	KA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	LA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	MA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	NA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	OA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	PA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	QA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	RA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	SA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	TA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	UA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	VA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	WA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	XA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	YA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	ZA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	aA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	bA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	cA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	dA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	eA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	fA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	gA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	hA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	iA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	jA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	kA	2	Total 37	C 19	N 8	O 9	P 1	0	0

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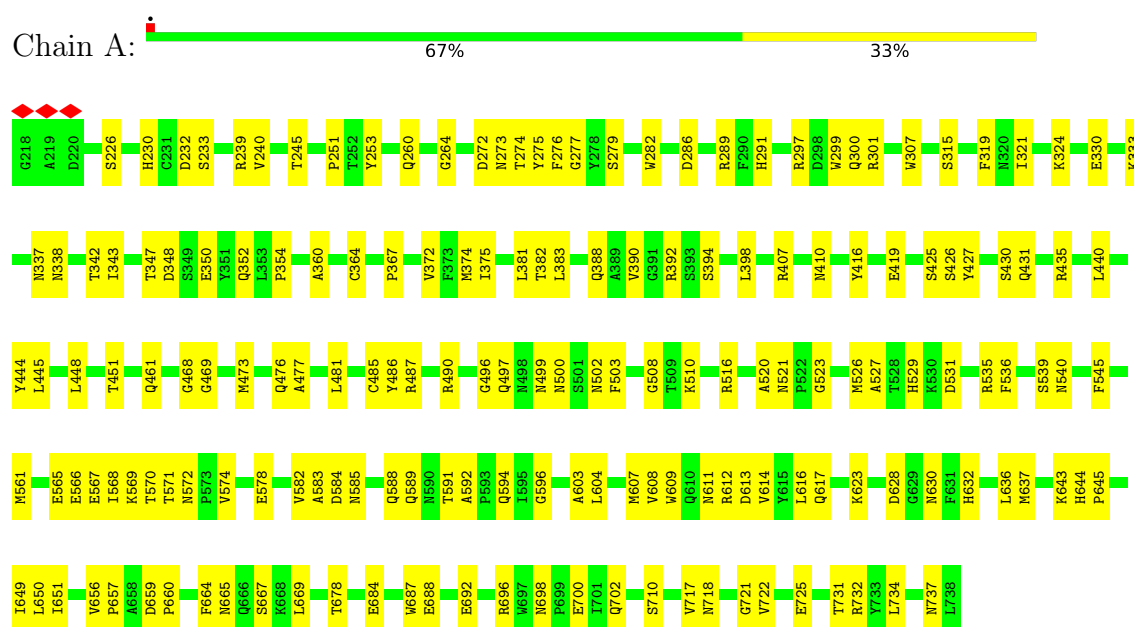
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Mol	Chain	Residues	Atoms					AltConf	Trace
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2	nA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	oA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	pA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	qA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	rA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	sA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	tA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	uA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	vA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	wA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	xA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	yA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	zA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	0A	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	1A	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	2A	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	3A	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	4A	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	5A	2	Total 37	C 19	N 8	O 9	P 1	0	0

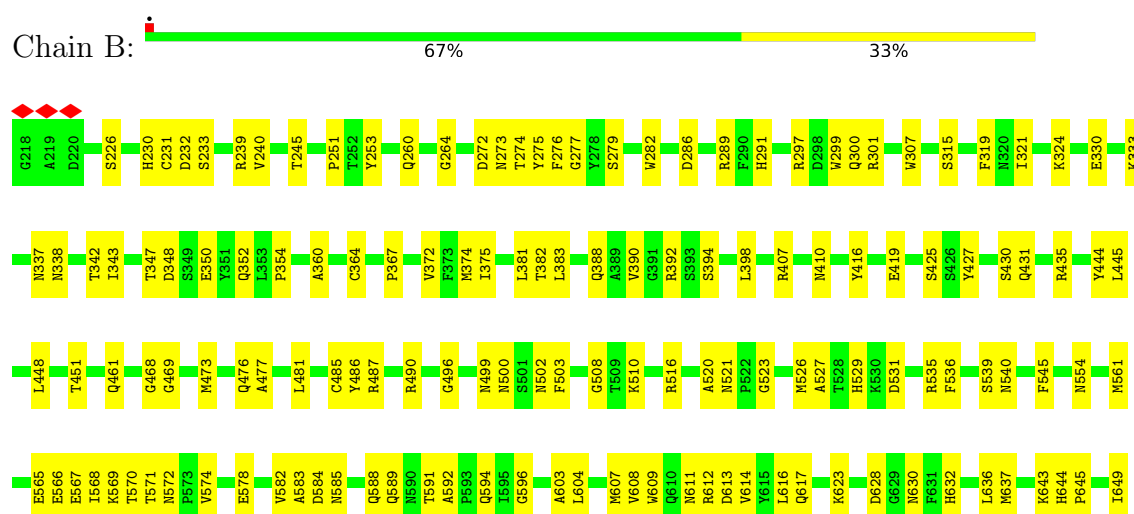
3 Residue-property plots

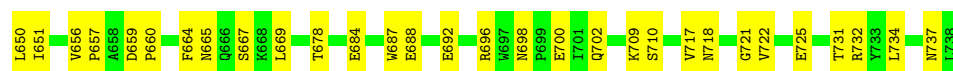
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Capsid protein

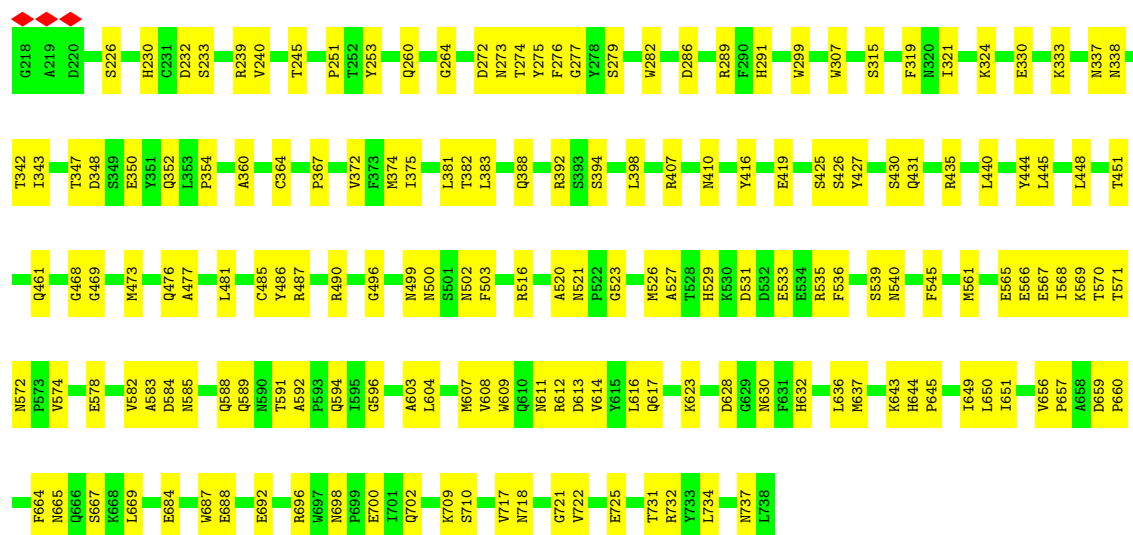


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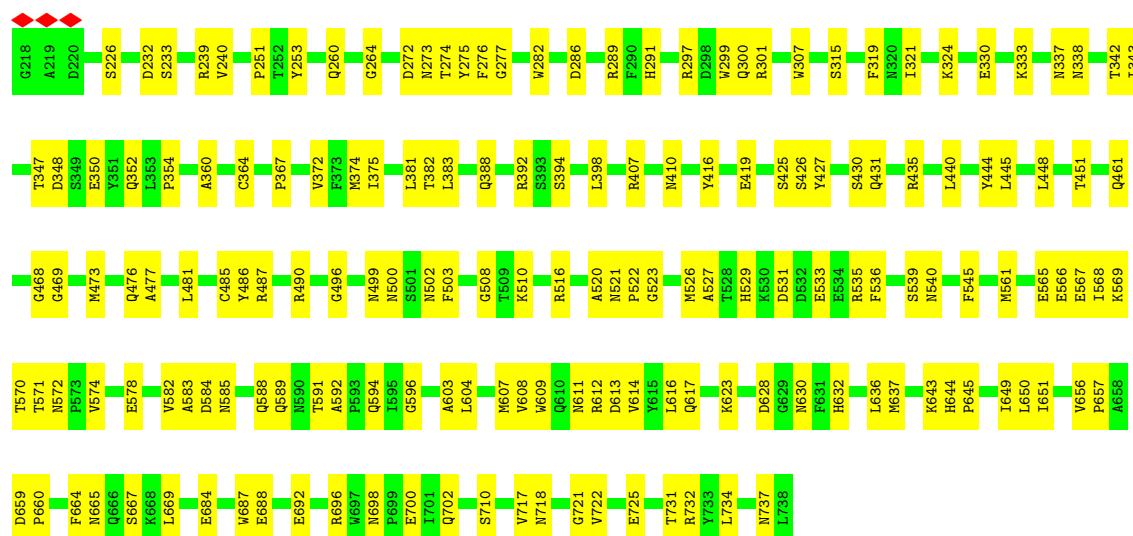




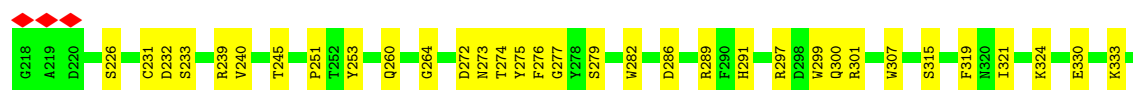
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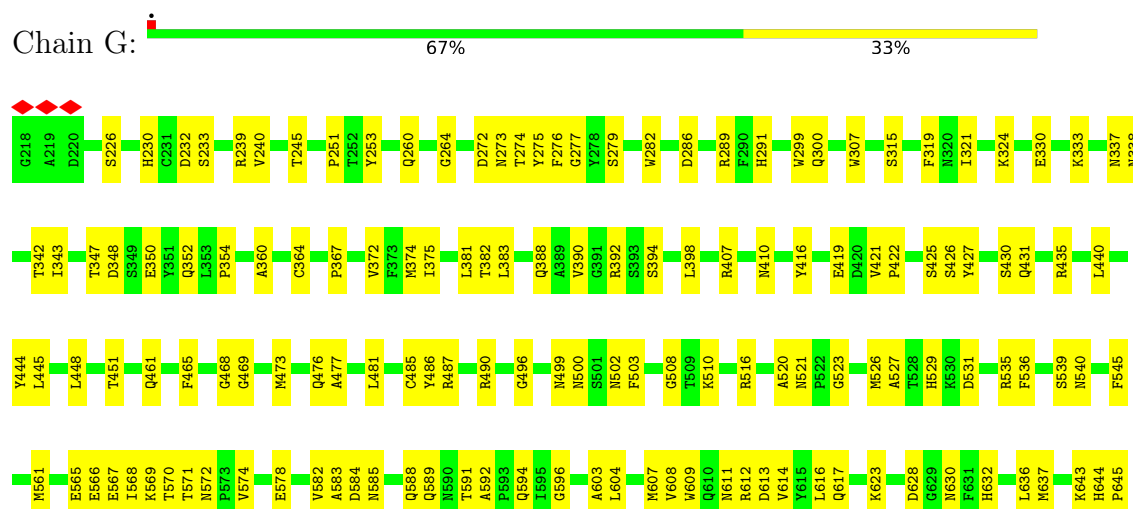


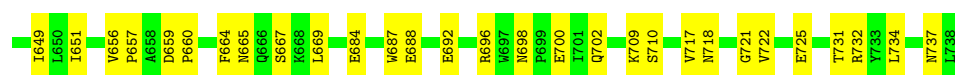
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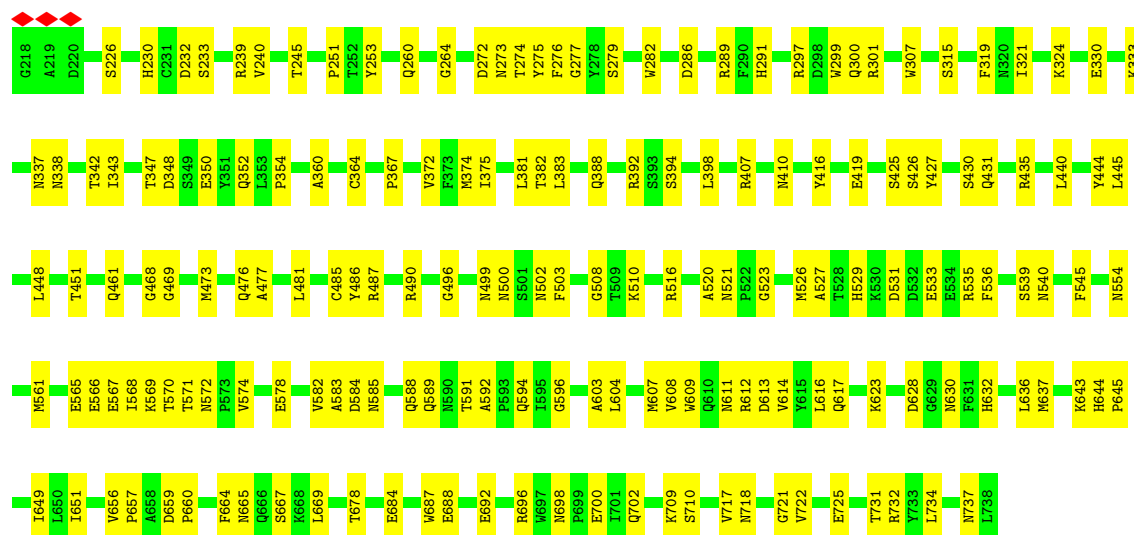
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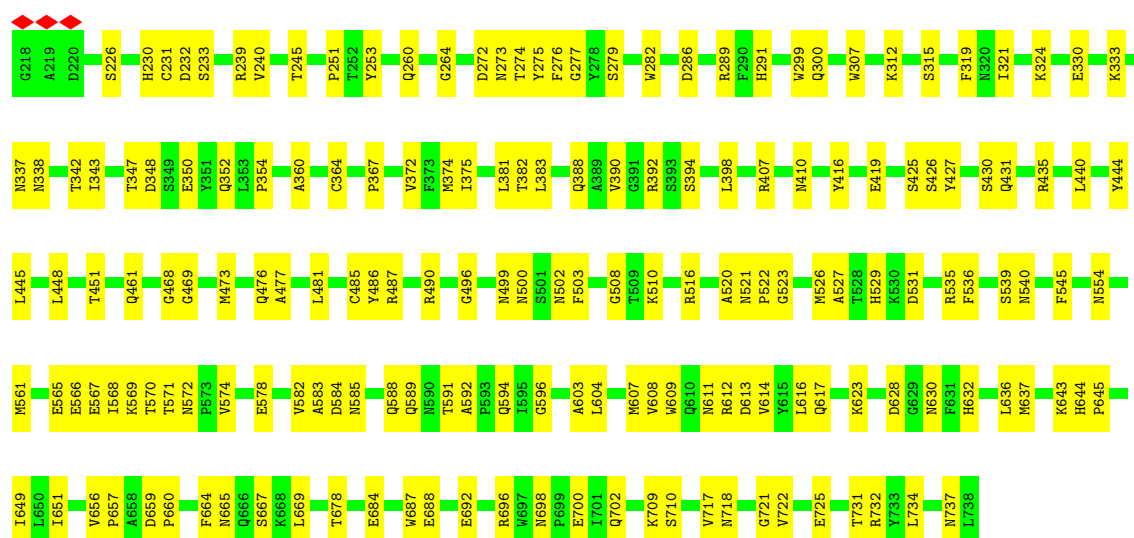




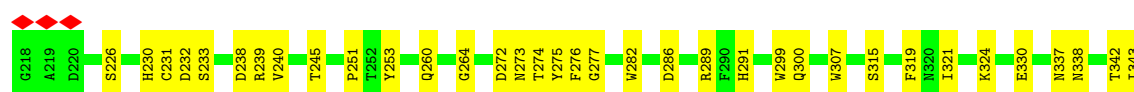
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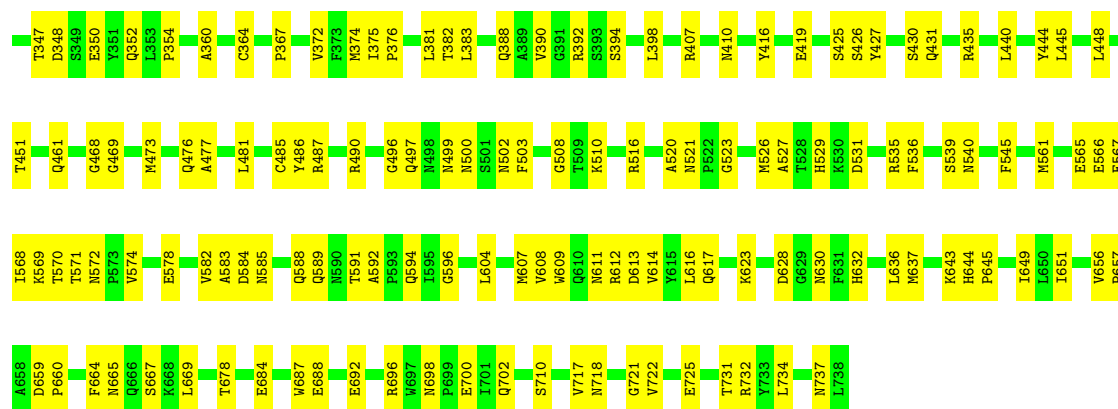


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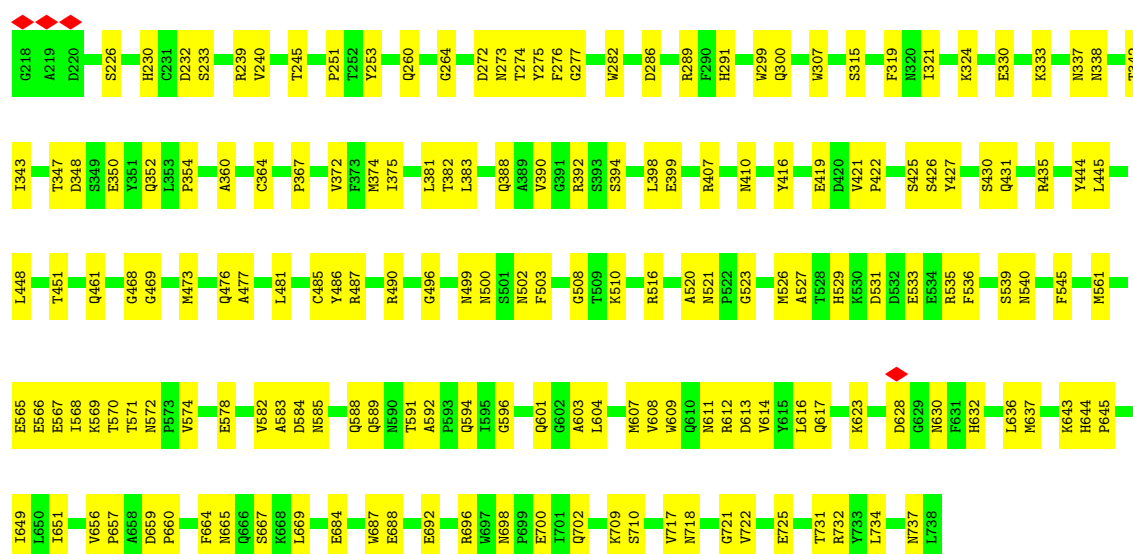


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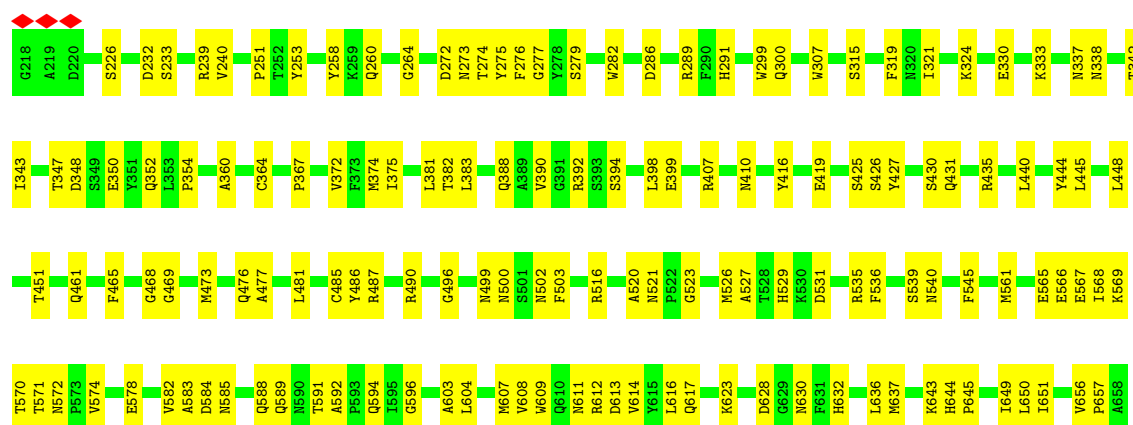




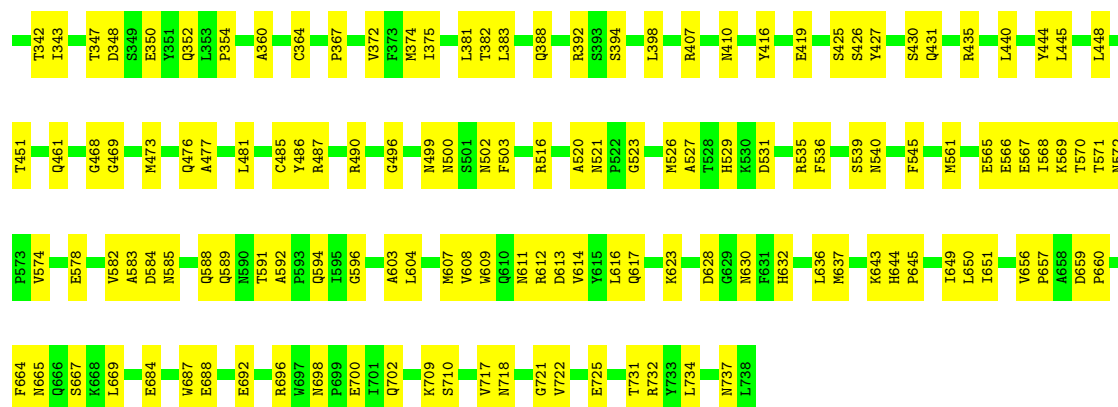
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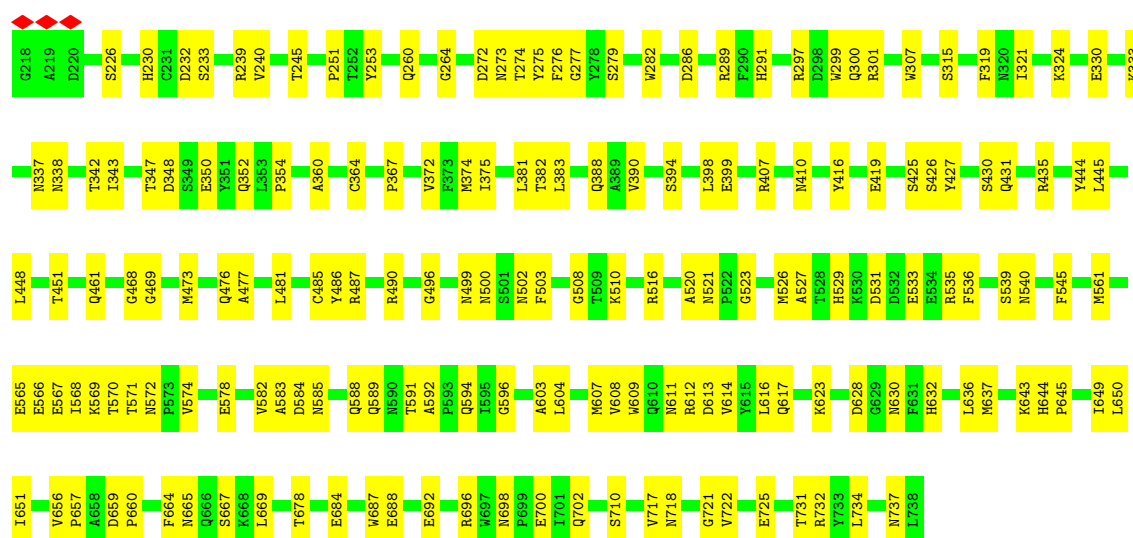
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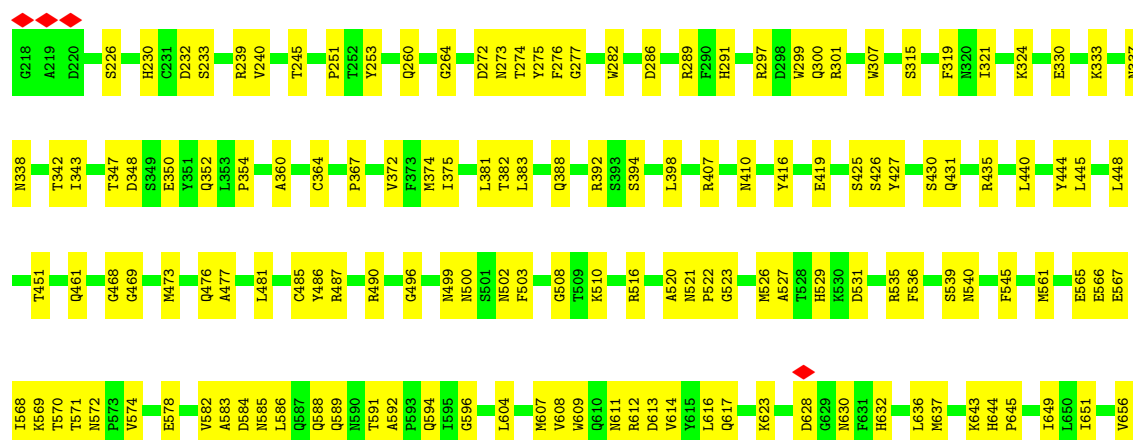


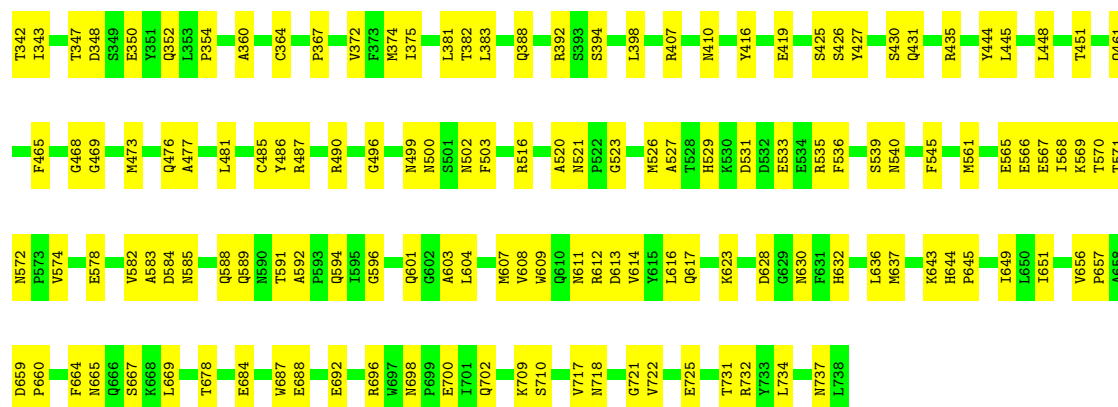


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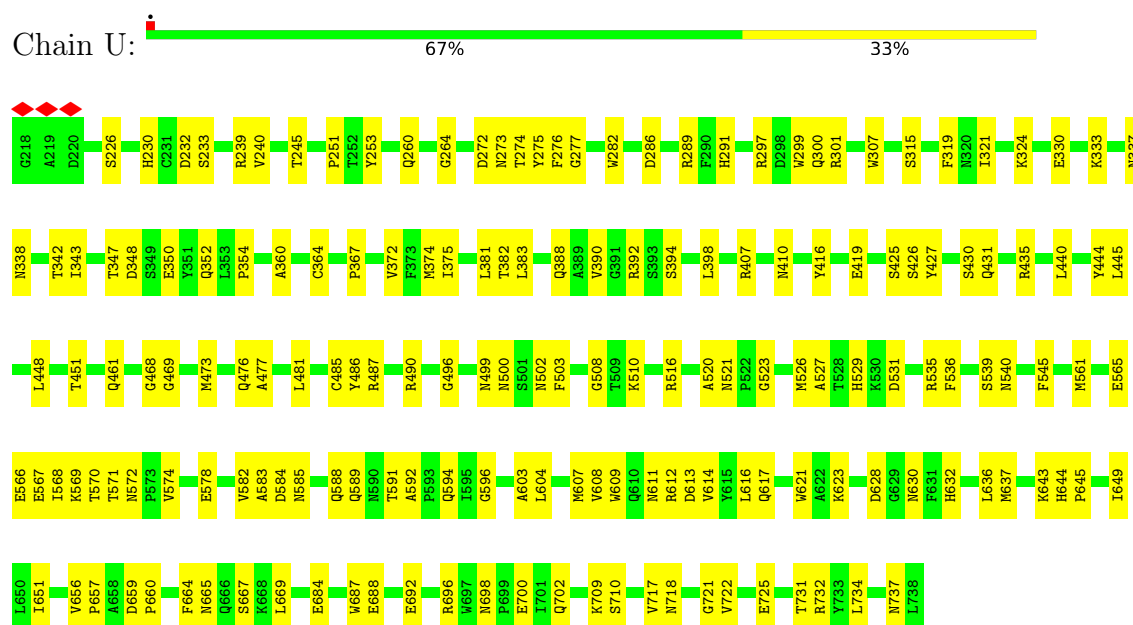


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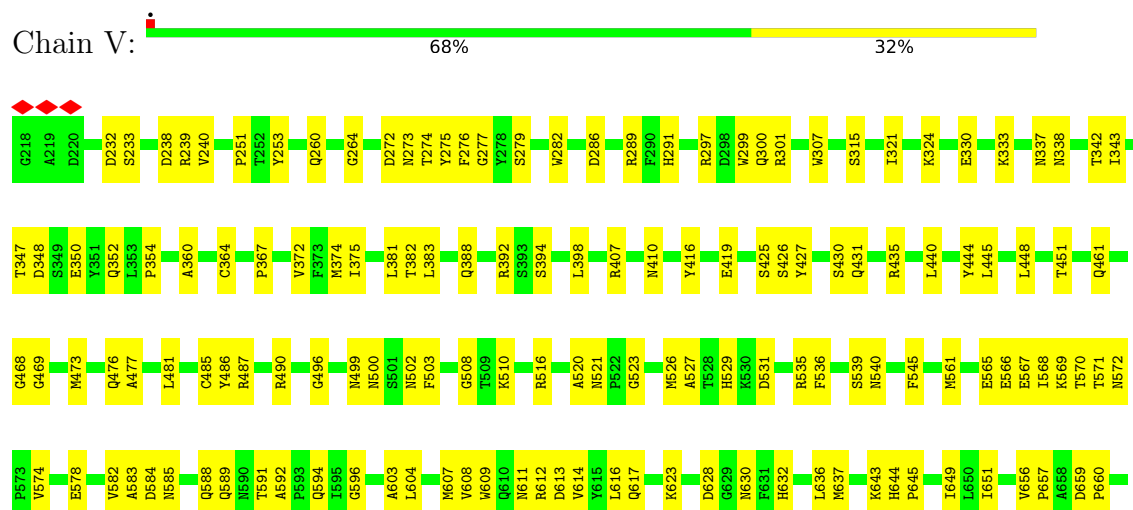




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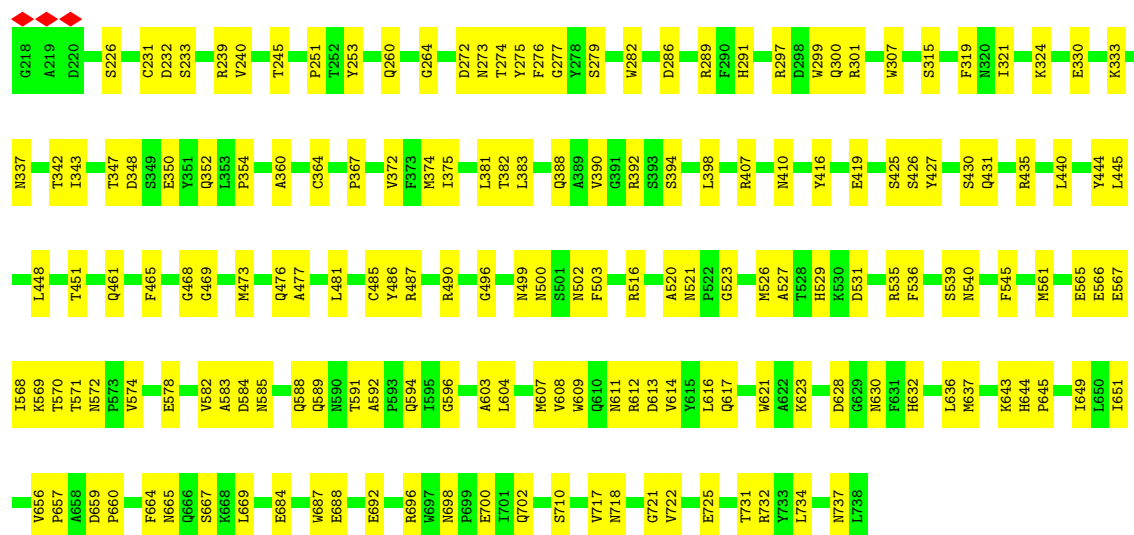


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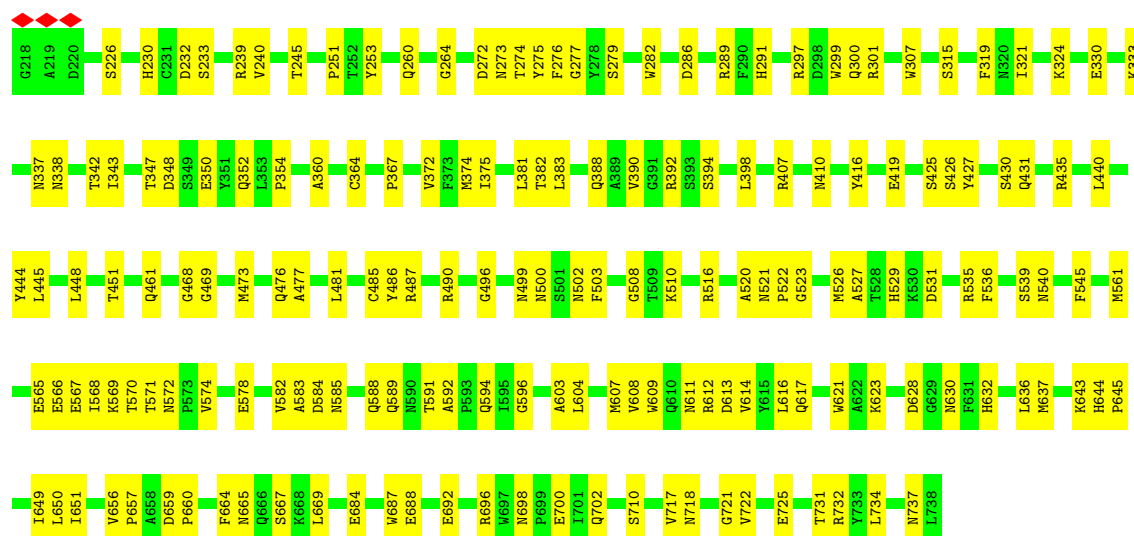




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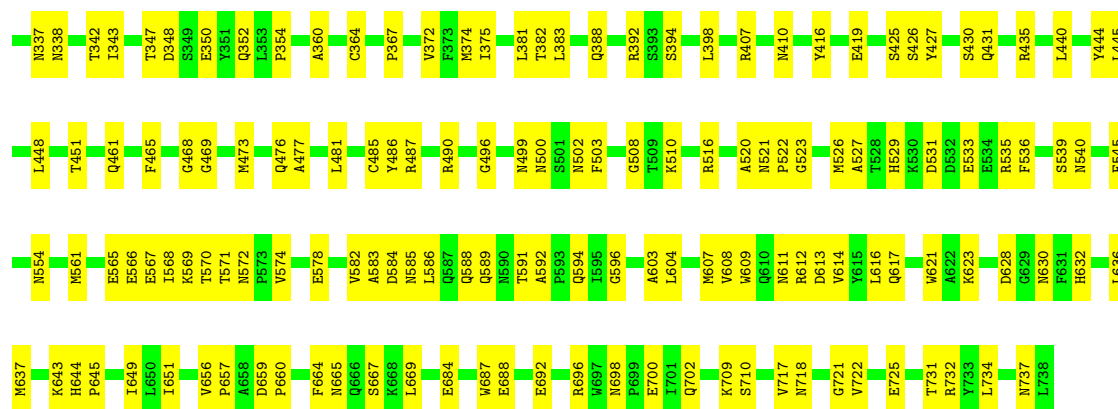


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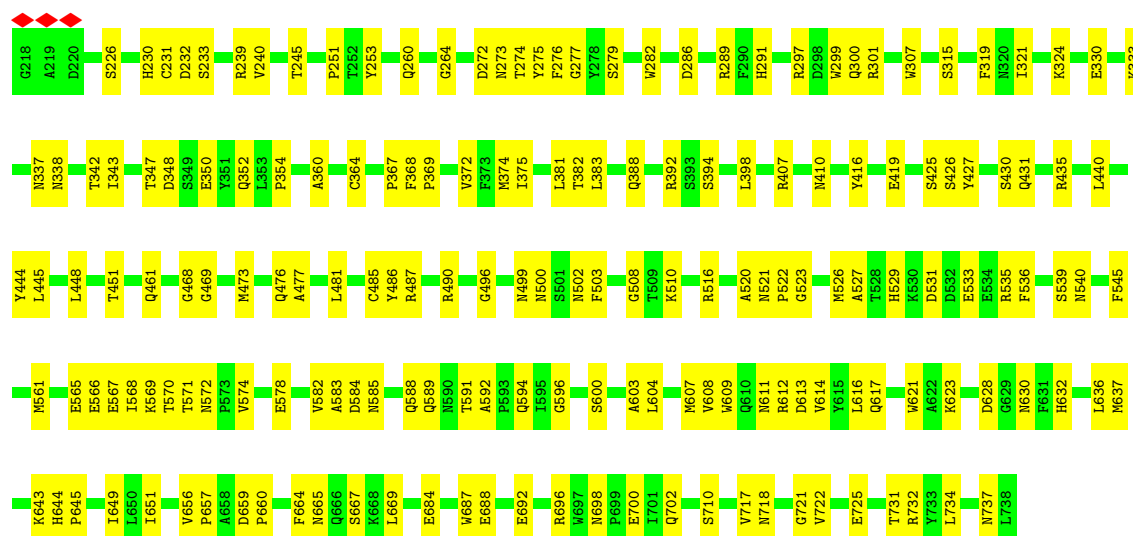


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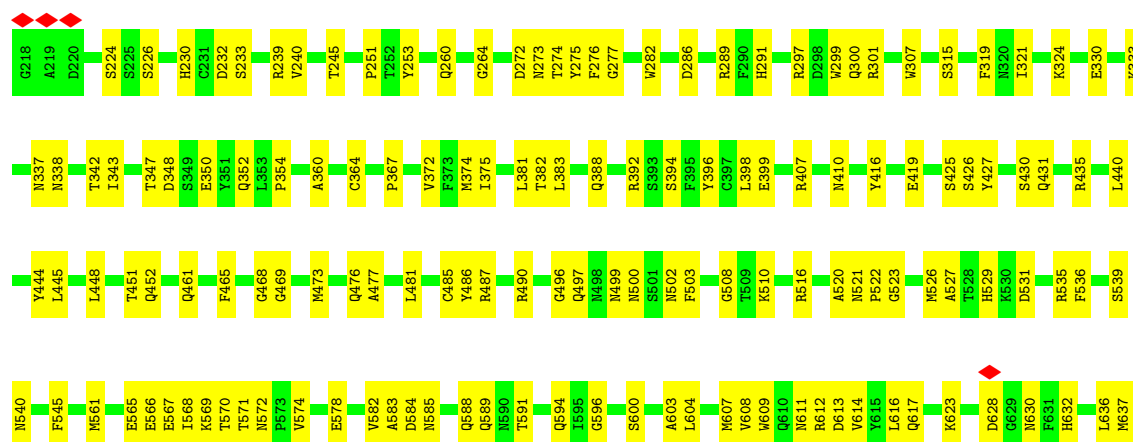




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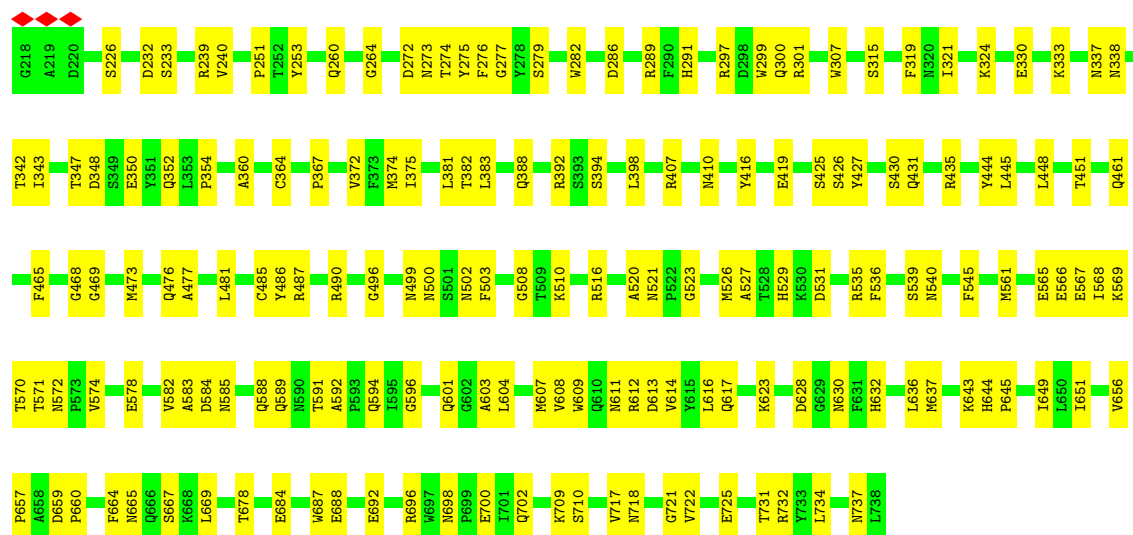


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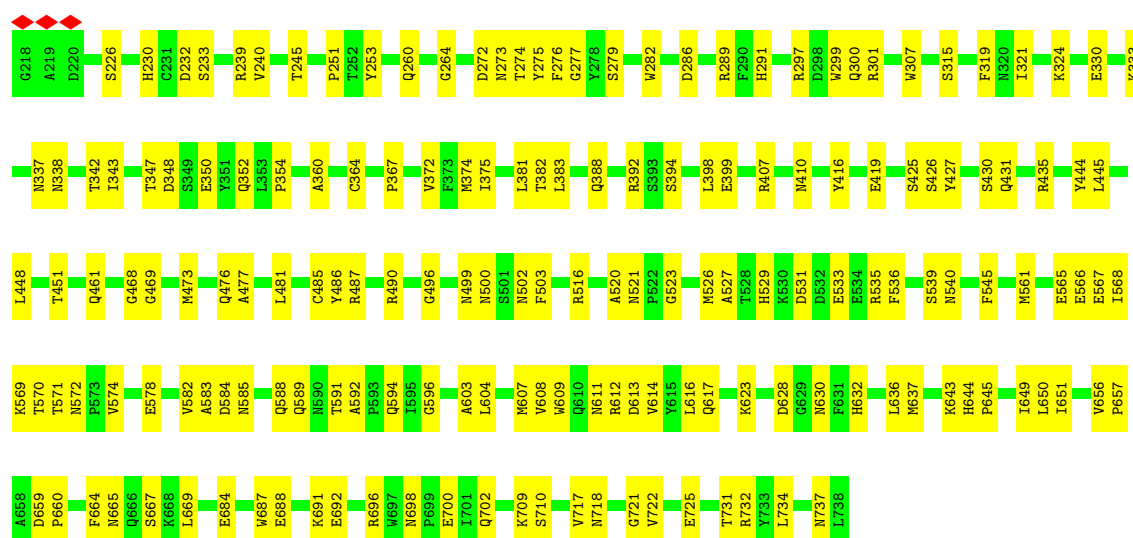




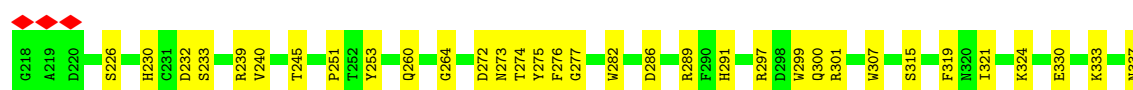
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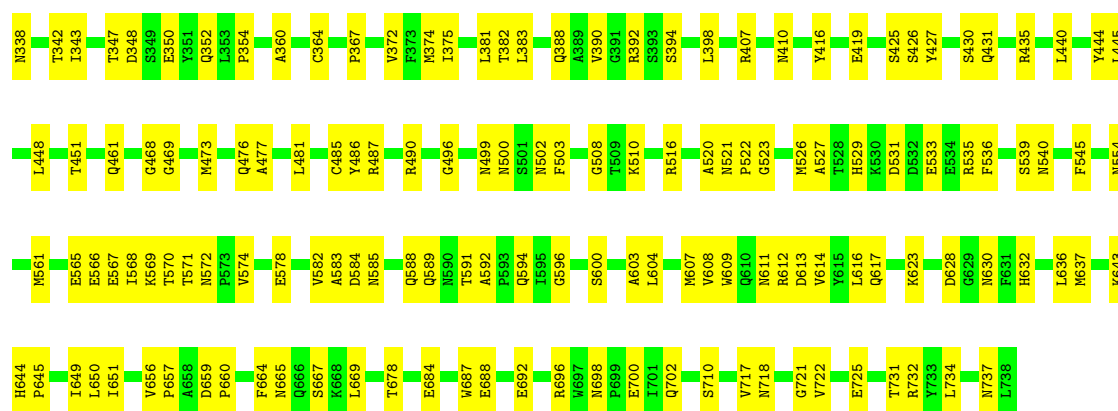


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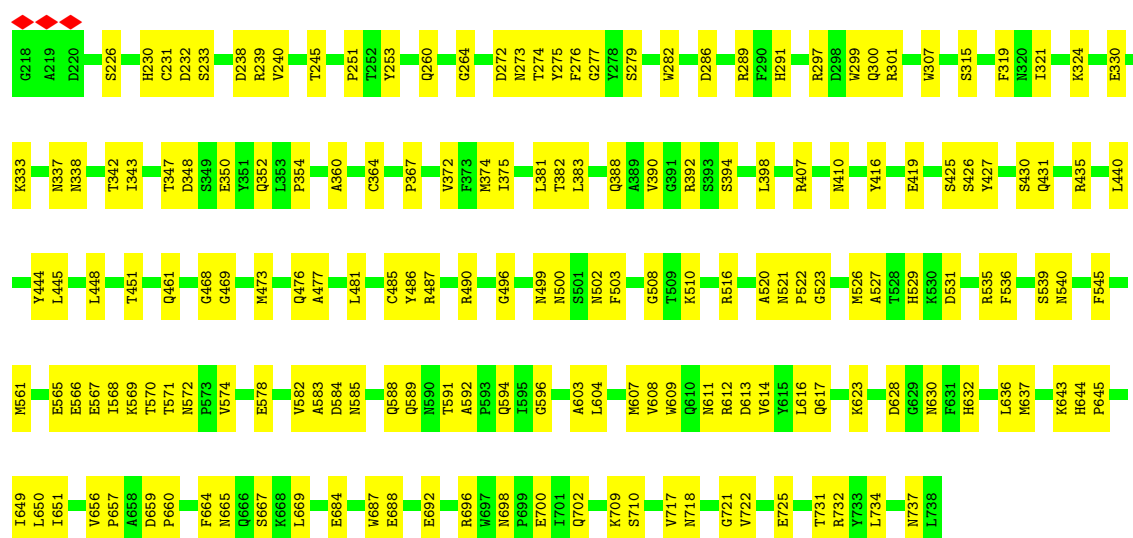


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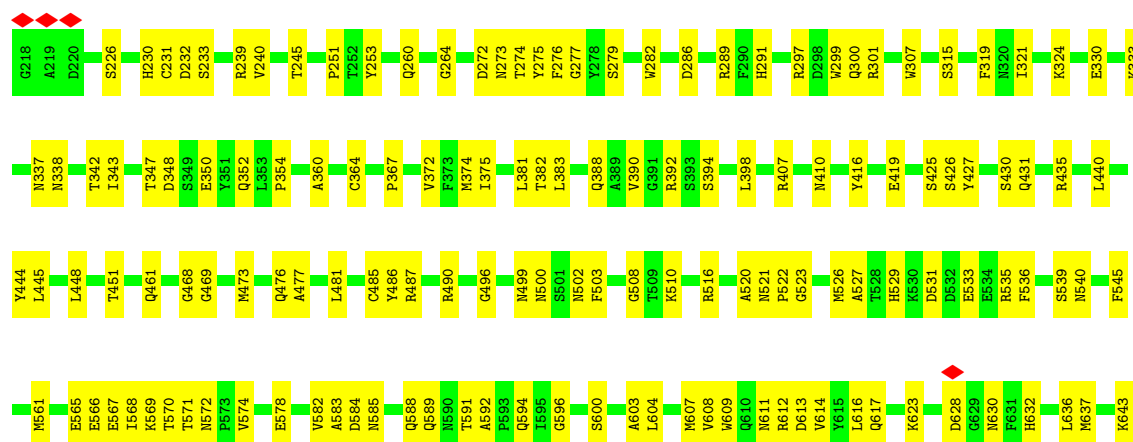




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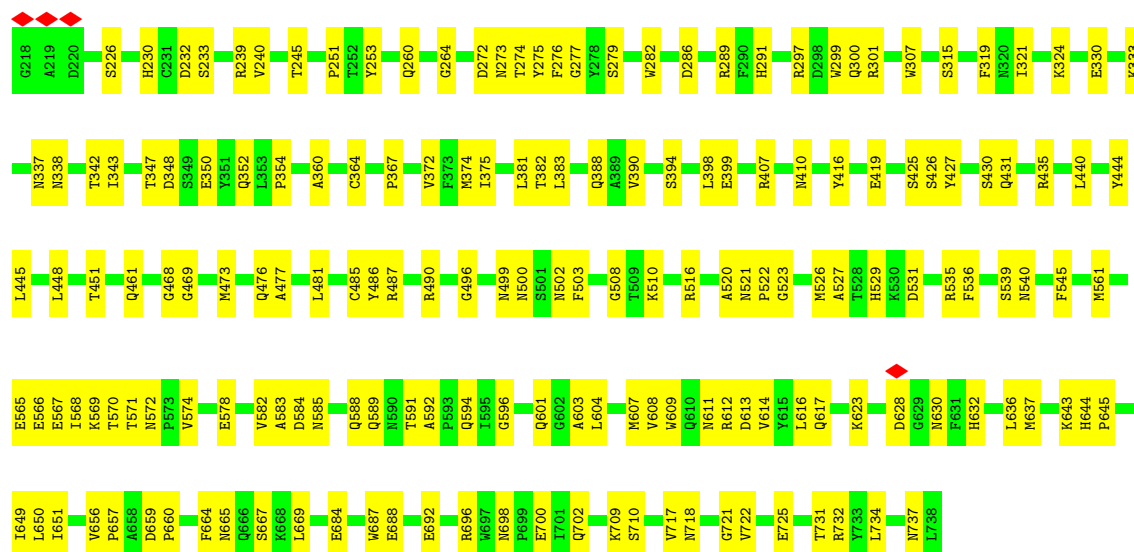


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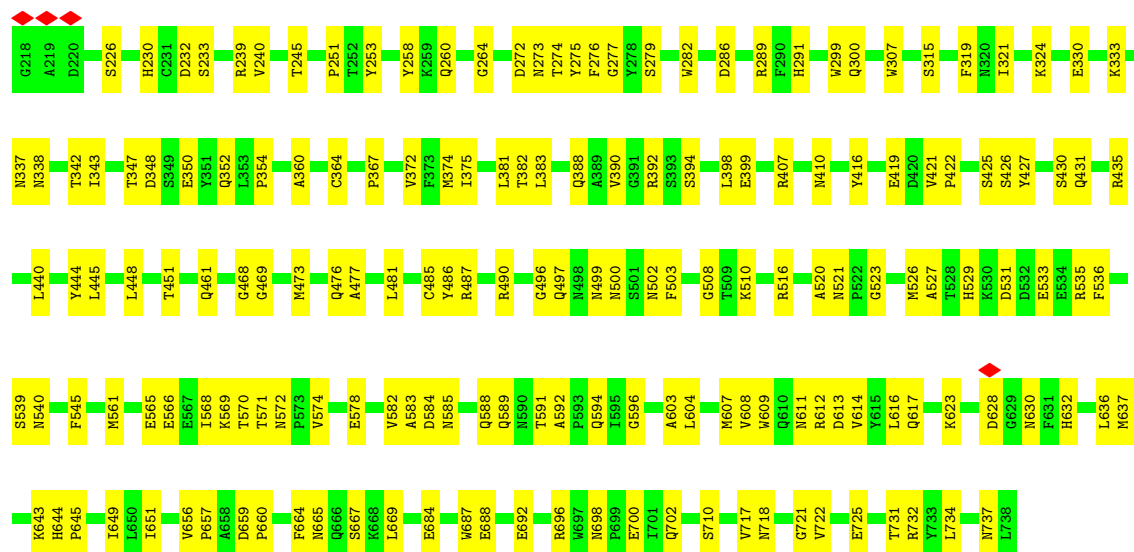




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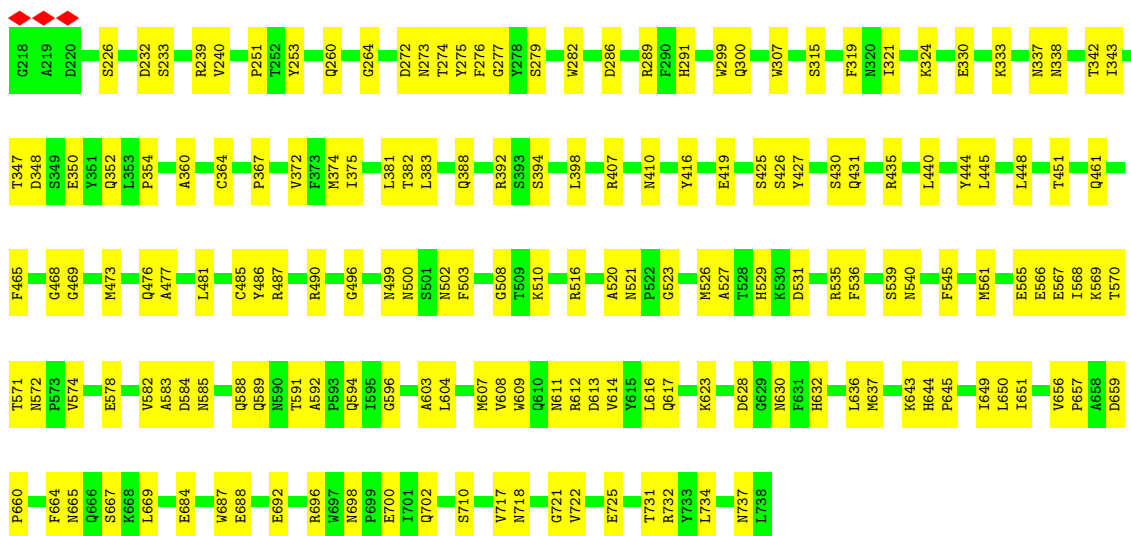


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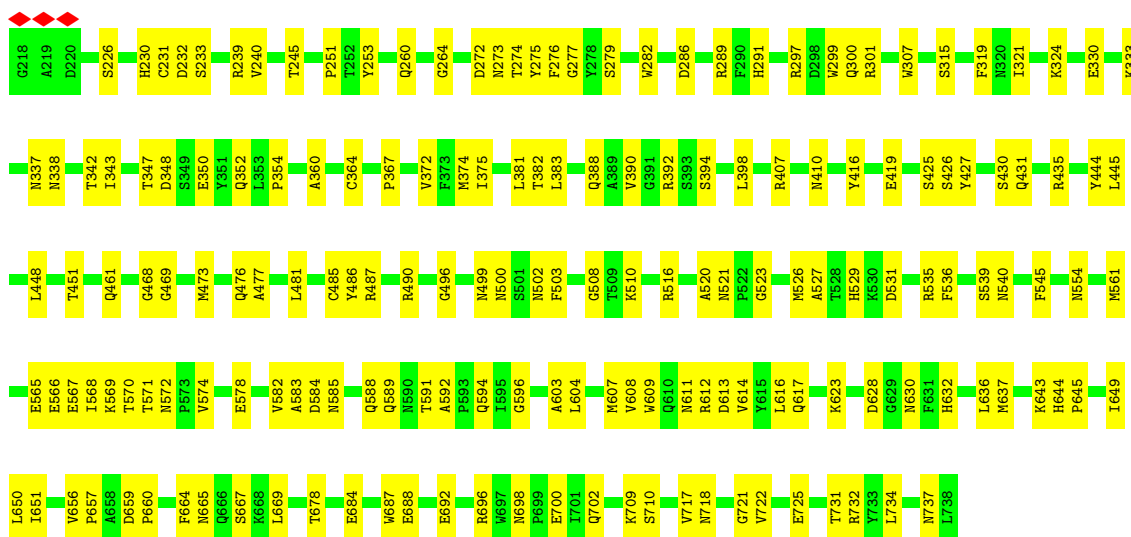


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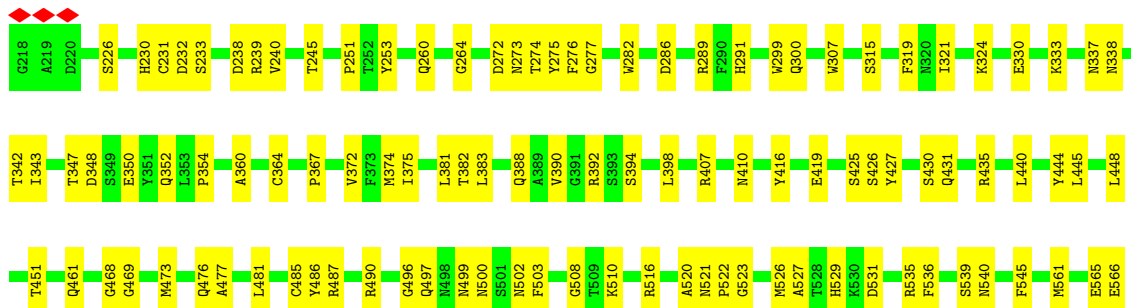


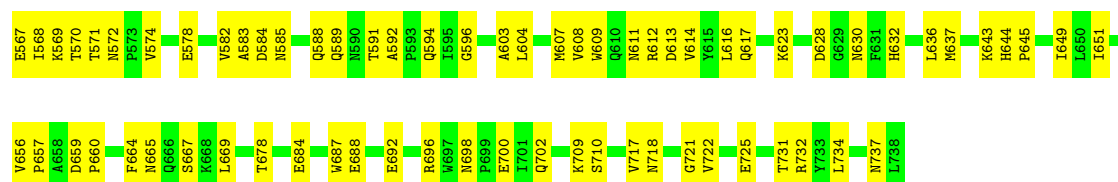


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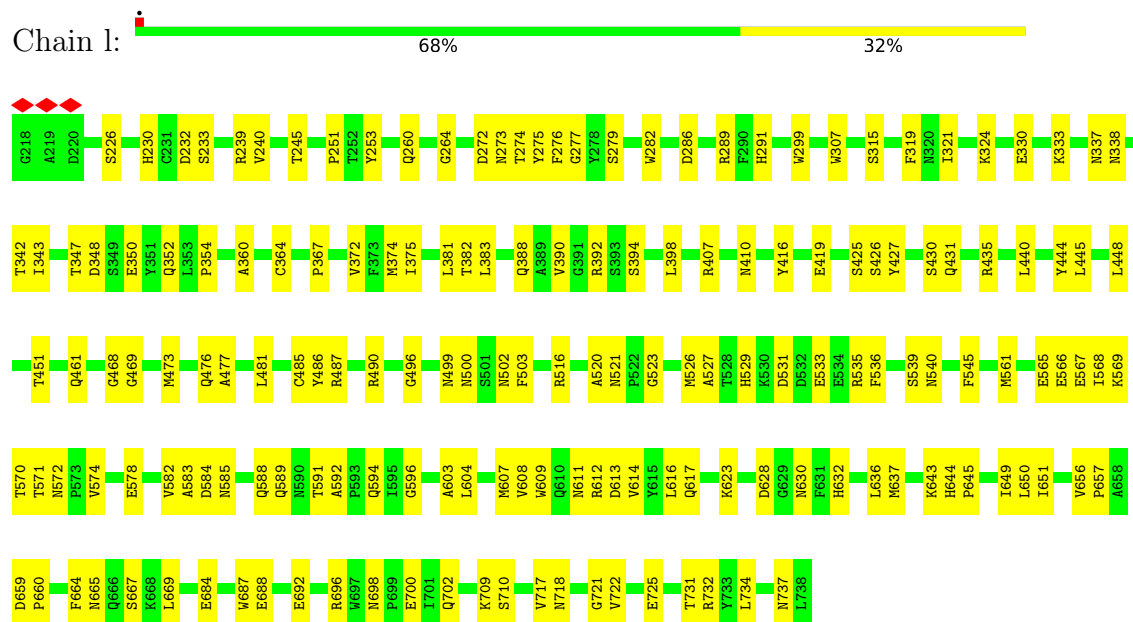


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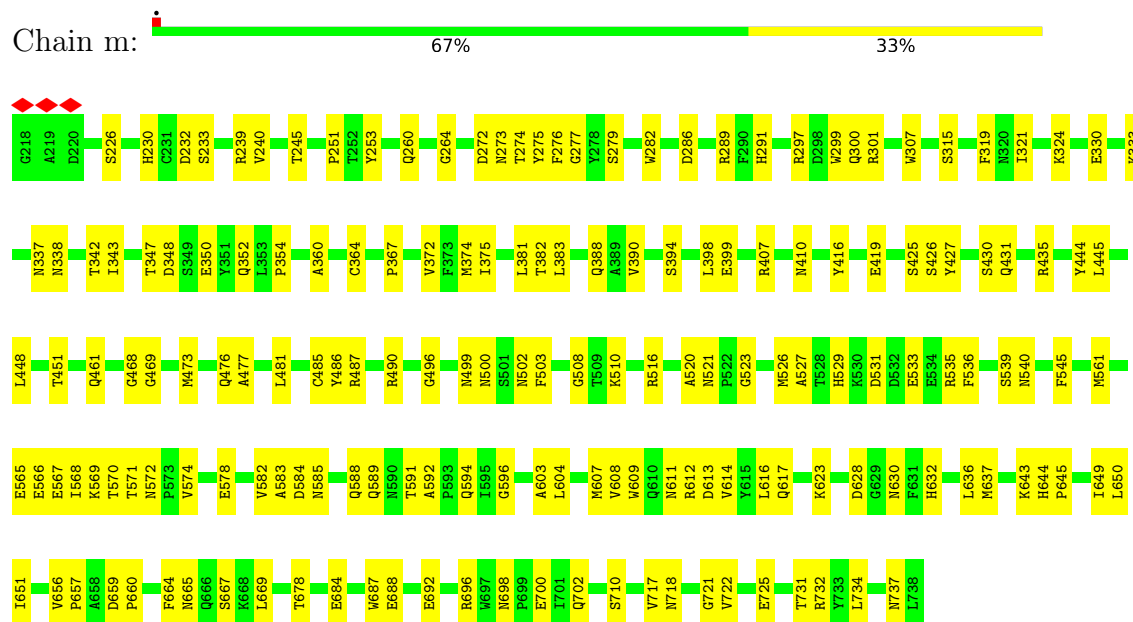




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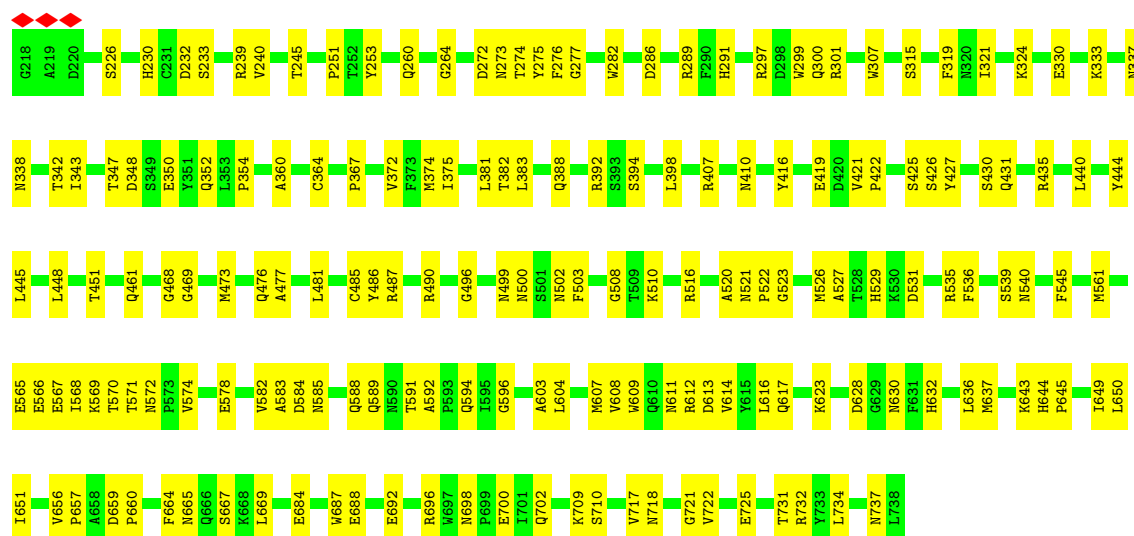


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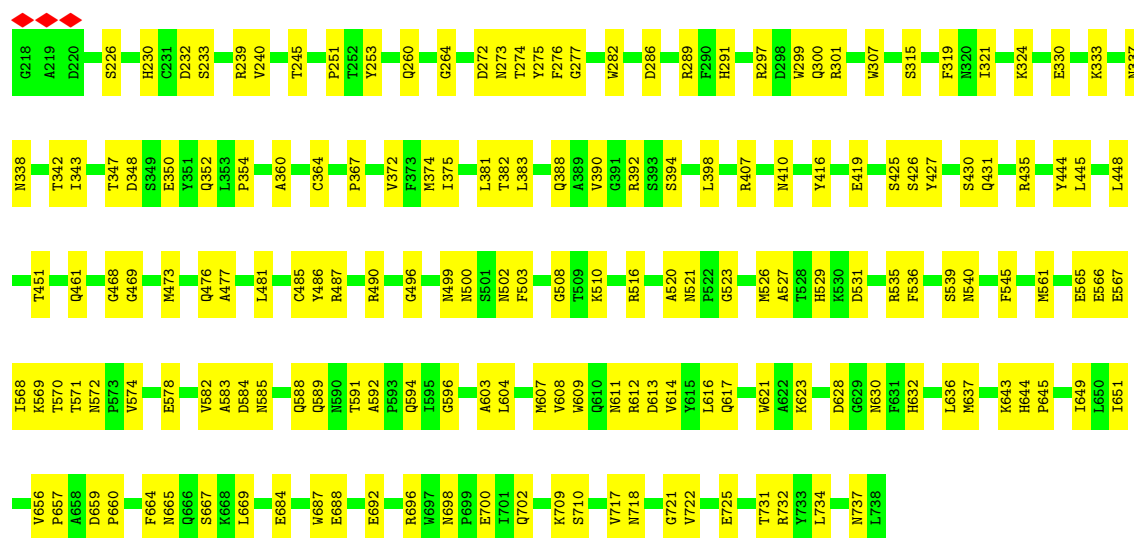


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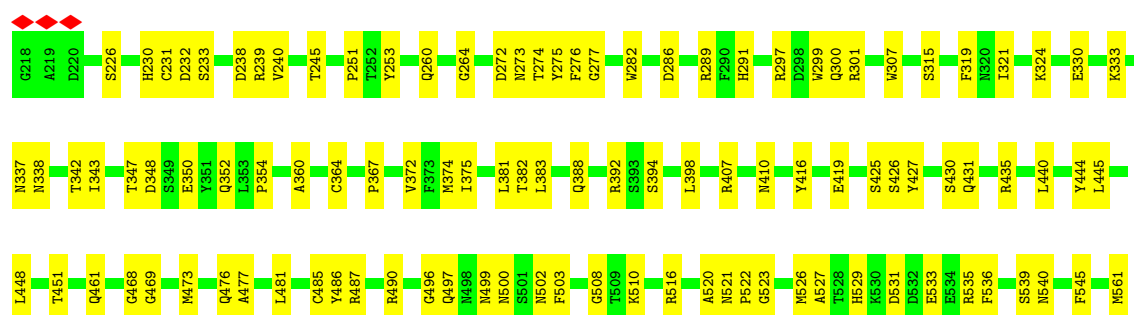


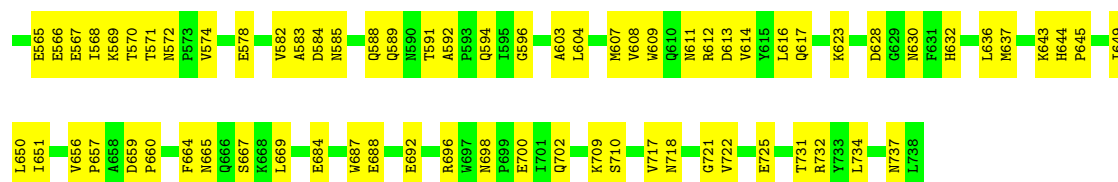


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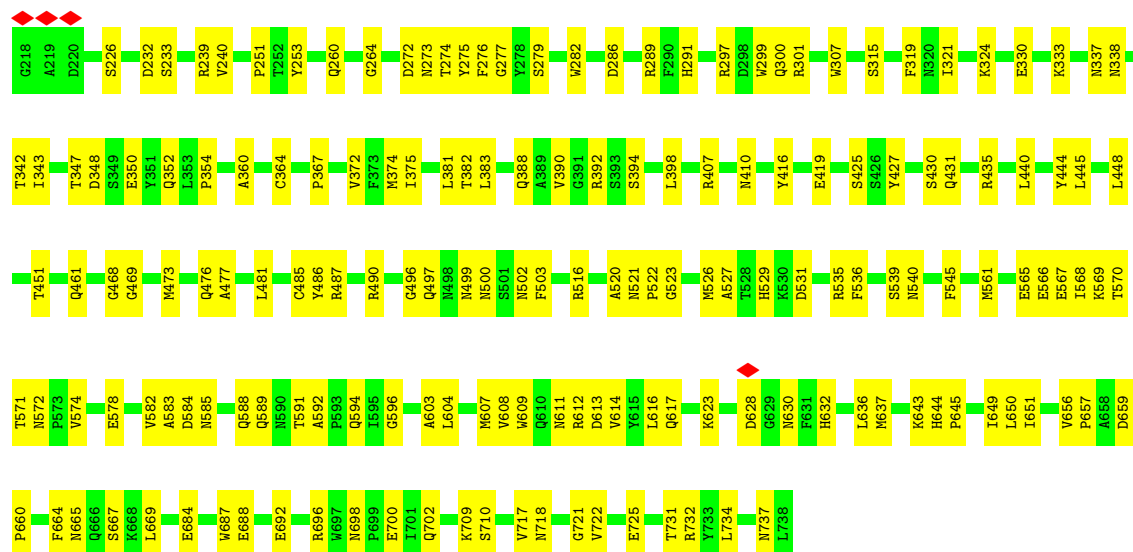


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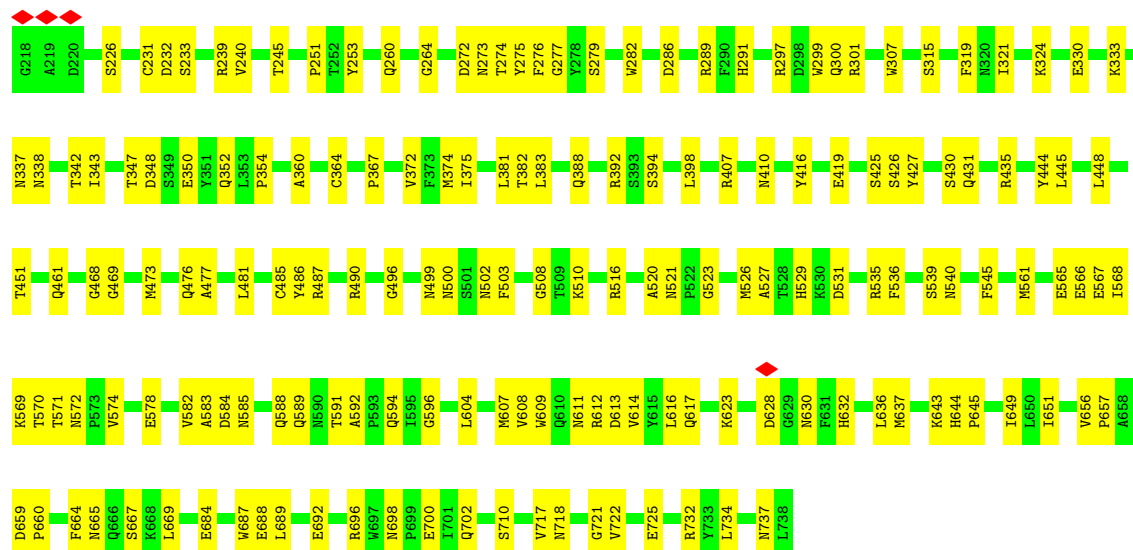




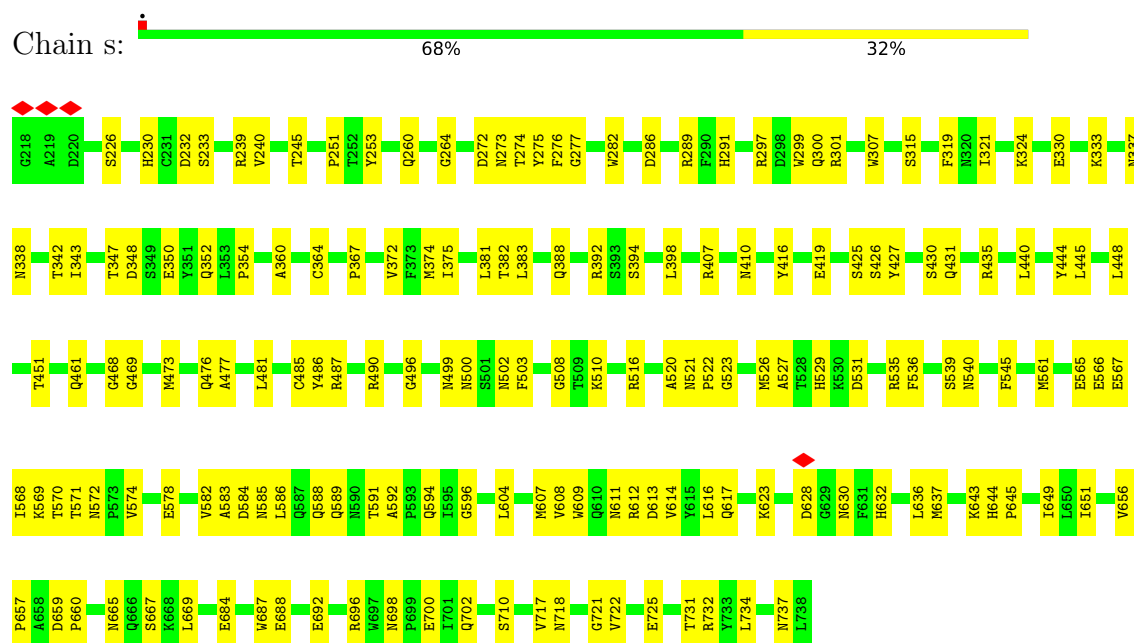
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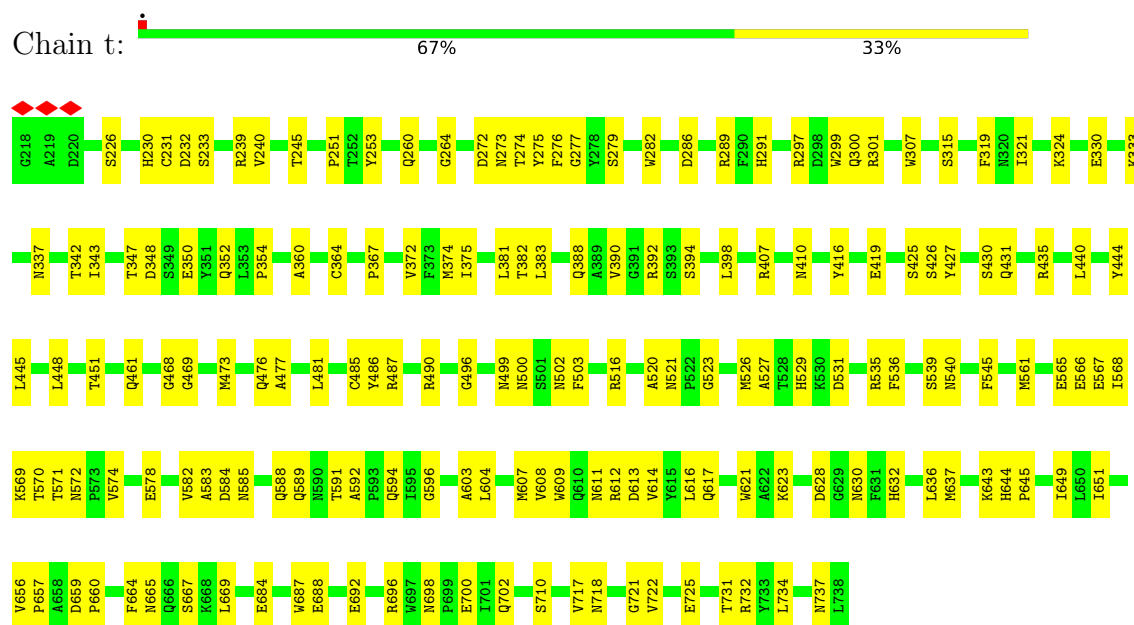
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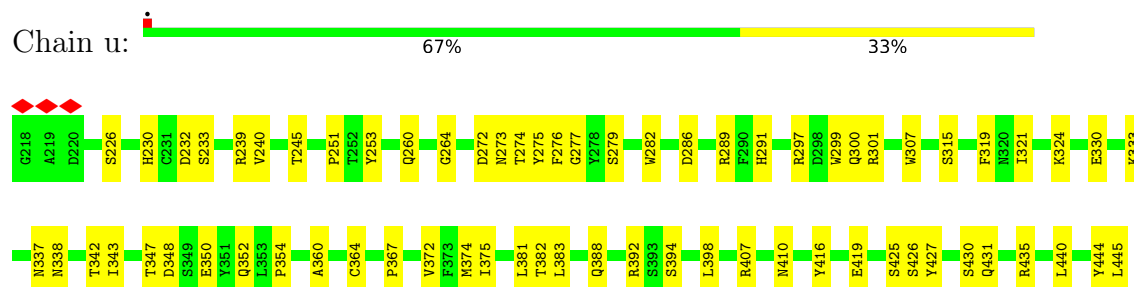
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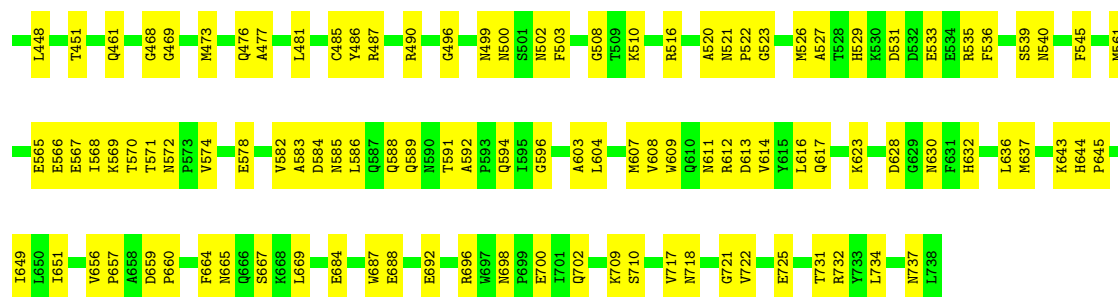


- Molecule 1: Capsid protein

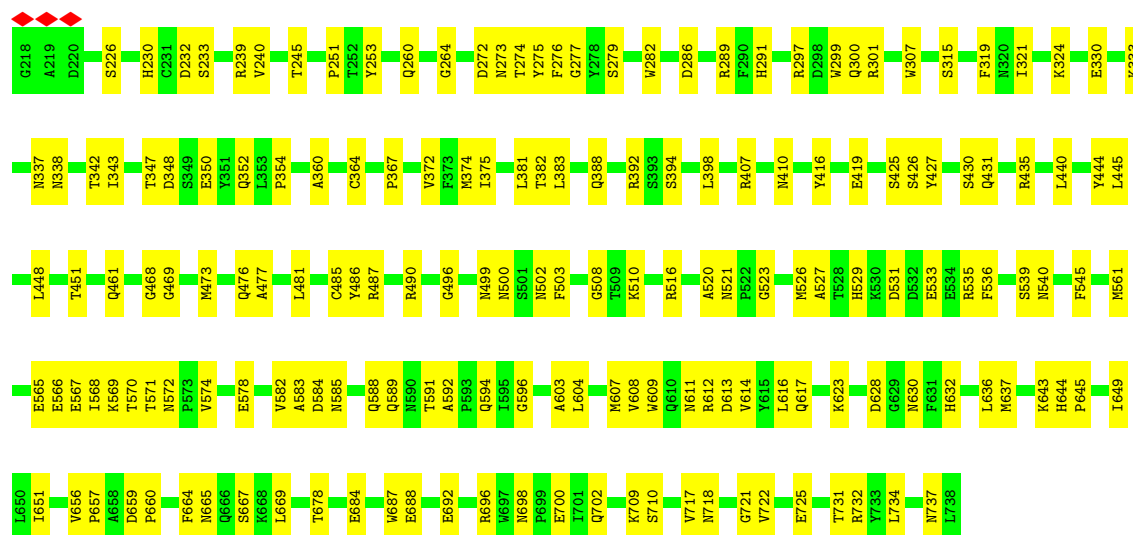


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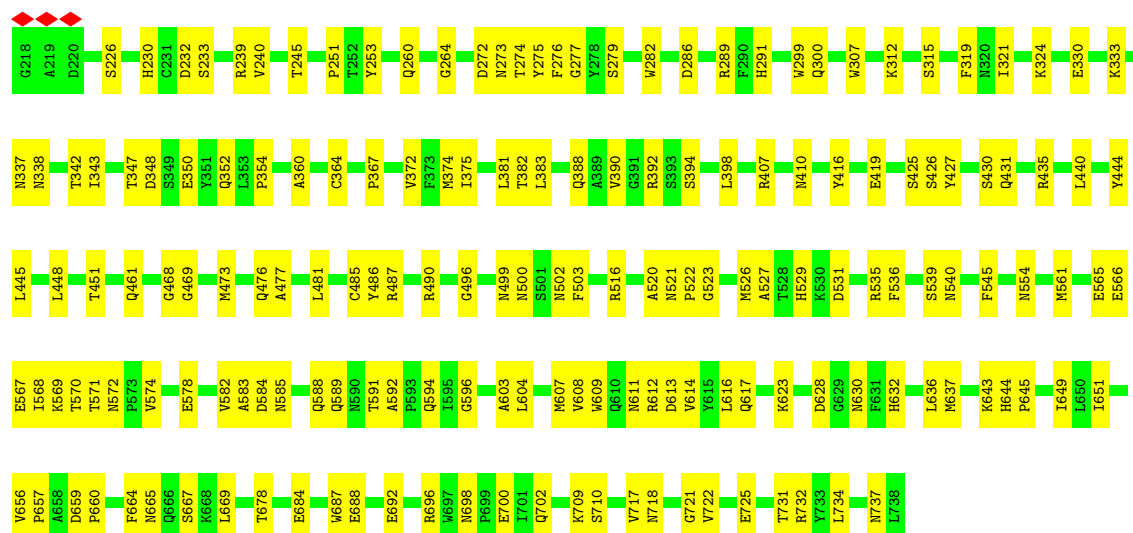




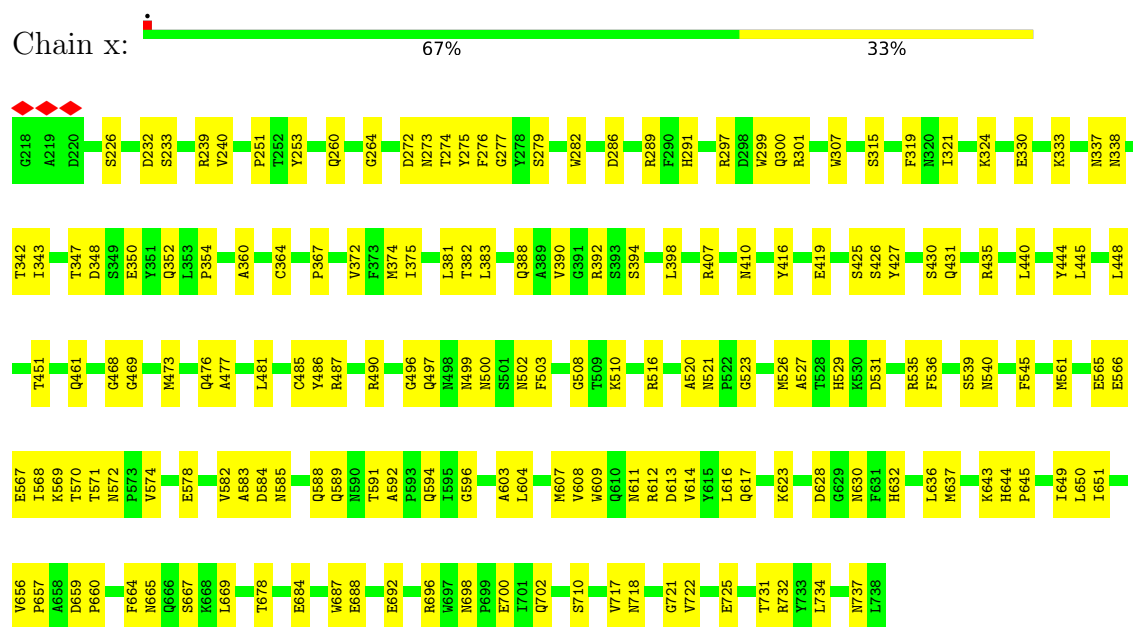
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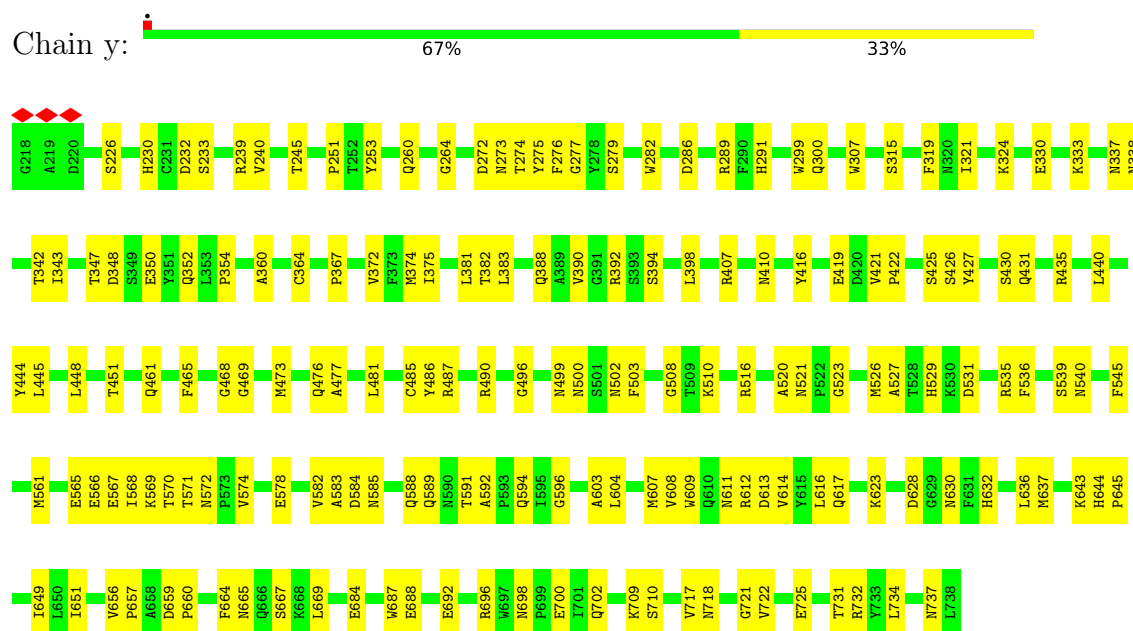
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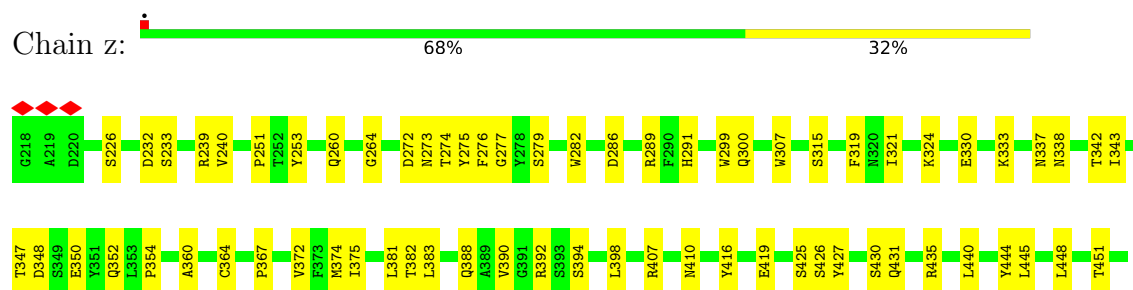
• Molecule 1: Capsid protein

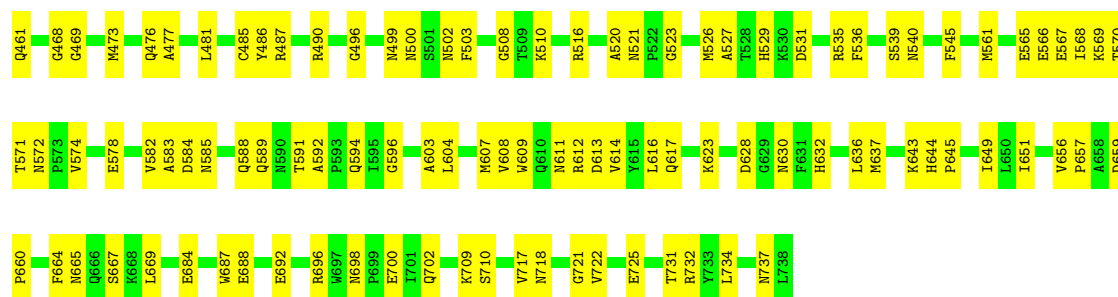


● Molecule 1: Capsid protein

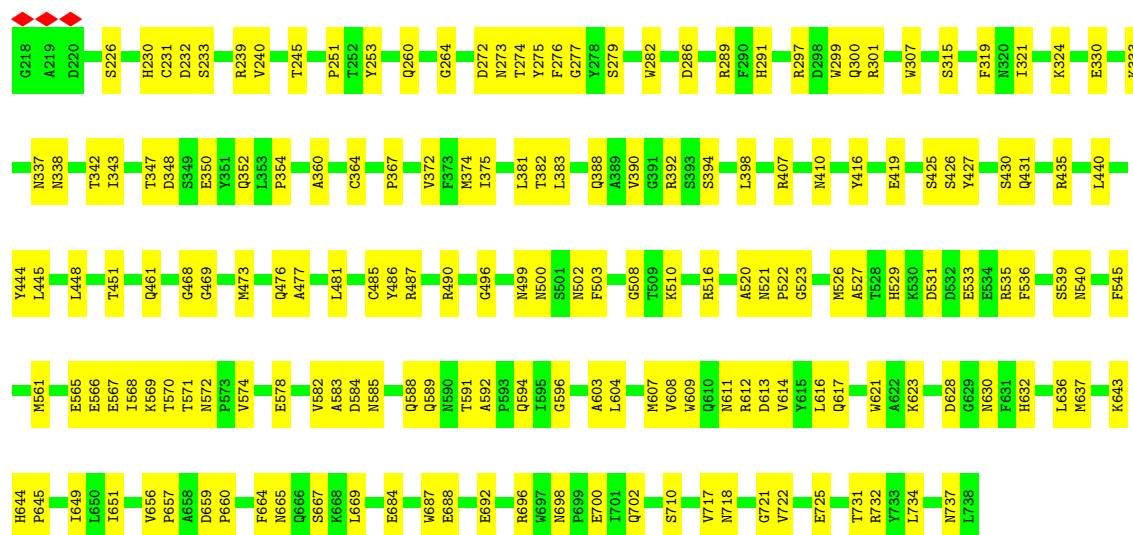


● Molecule 1: Capsid protein

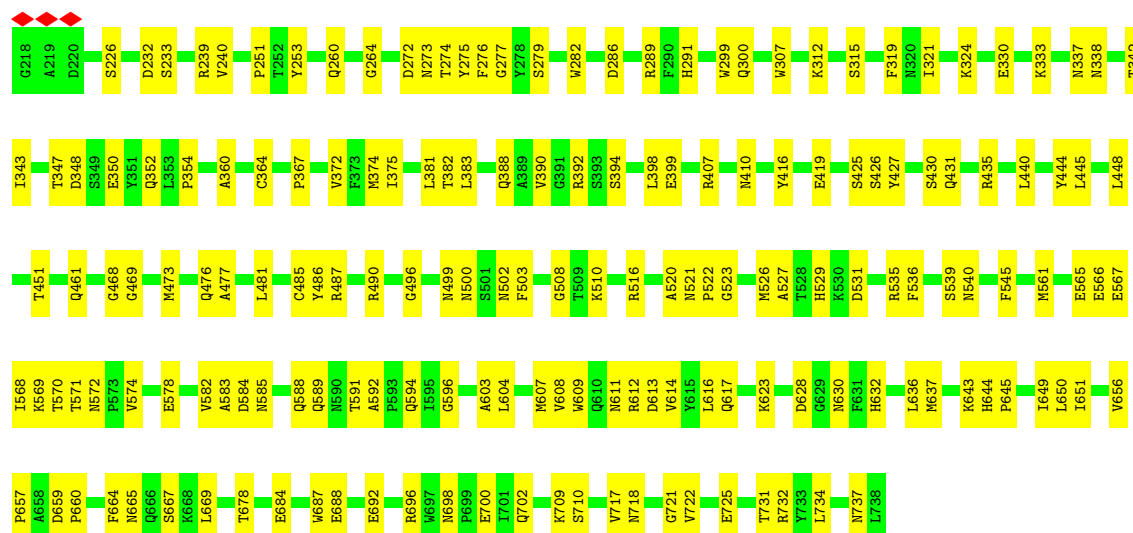




• Molecule 1: Capsid protein

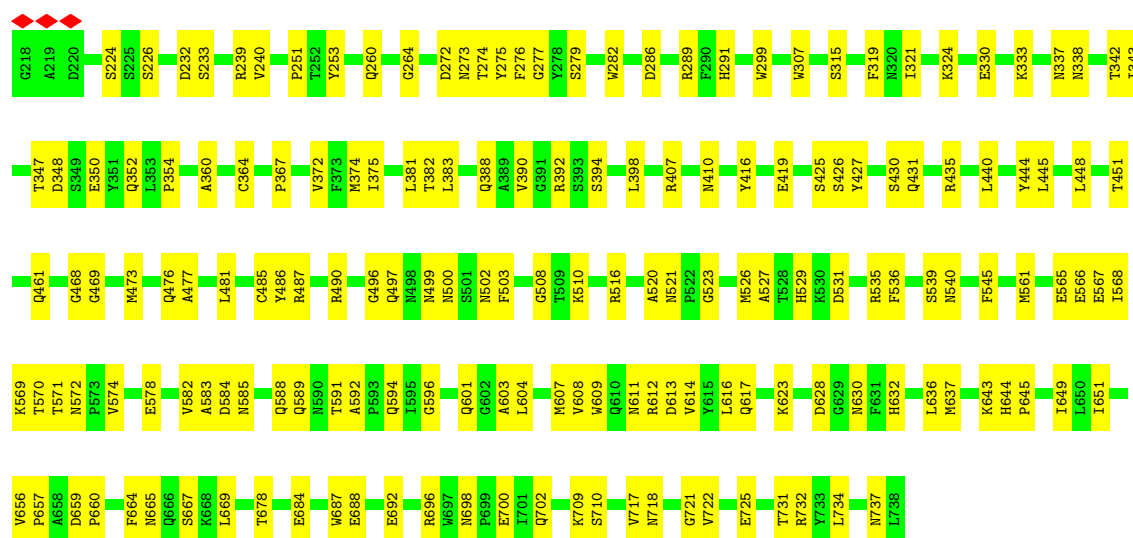


• Molecule 1: Capsid protein



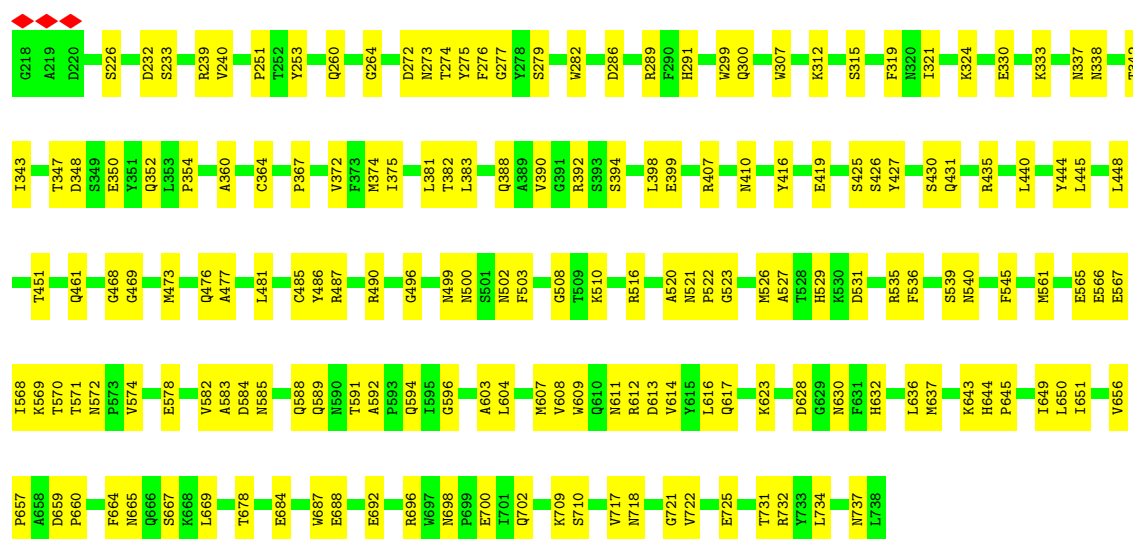
• Molecule 1: Capsid protein

Chain 3:  67% 33%



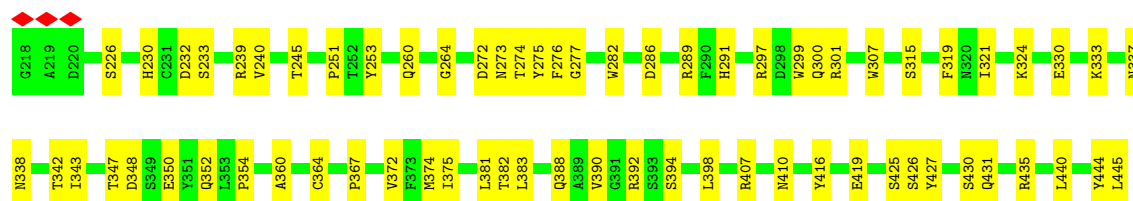
• Molecule 1: Capsid protein

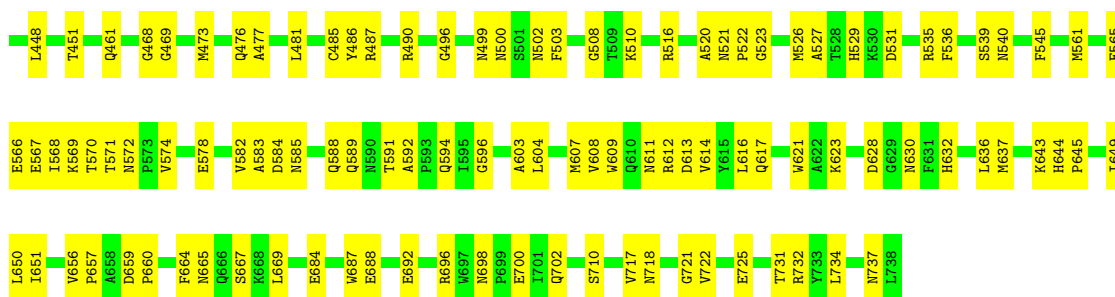
Chain 4:  67% 33%



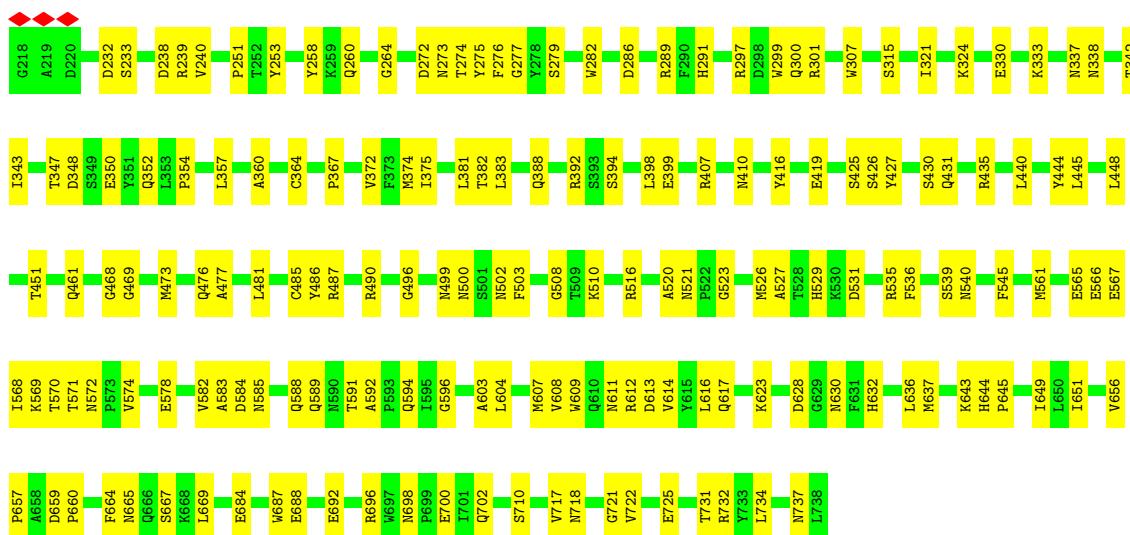
• Molecule 1: Capsid protein

Chain 5:  67% 33%

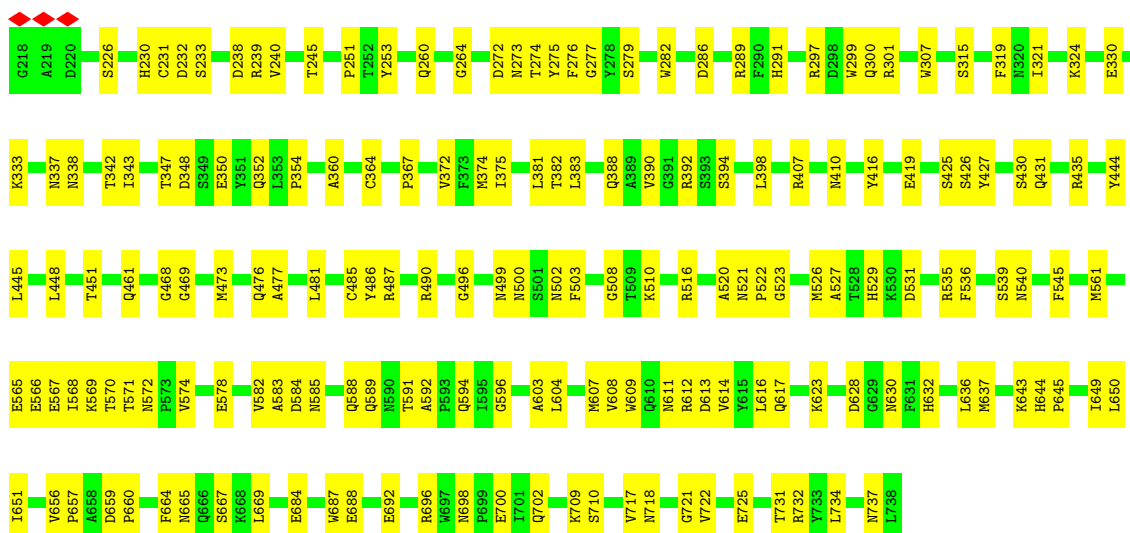




• Molecule 1: Capsid protein



• Molecule 1: Capsid protein



• Molecule 1: Capsid protein

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain EA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain FA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain GA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain HA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain IA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain JA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain KA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain LA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain MA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain NA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain OA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain PA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain QA:  100%

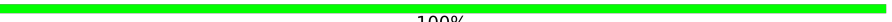
There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain RA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain SA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain TA:  100%

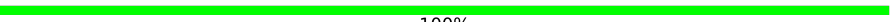
There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain UA:  100%

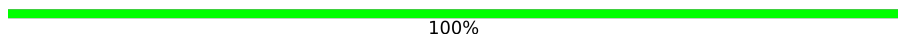
There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain VA:  100%

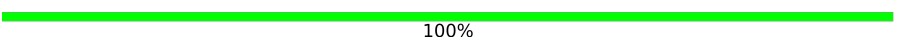
There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain WA:  100%

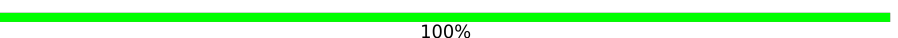
There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain XA:  100%

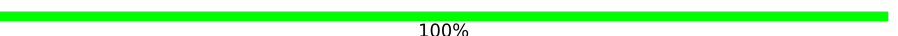
There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain YA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain ZA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain aA:  100%

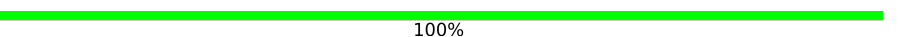
There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain bA:  100%

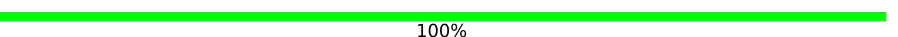
There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain cA:  100%

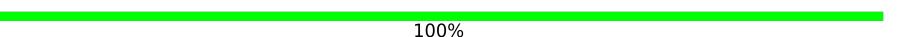
There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain dA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain eA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain fA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain gA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain hA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain iA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain jA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain kA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain lA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain mA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain nA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain oA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain pA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain qA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain rA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain sA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain tA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain uA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain vA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain wA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain xA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain yA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain zA:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain 0A:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain 1A:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain 2A:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain 3A:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain 4A:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain 5A:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	1072	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	67	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	DIRECT ELECTRON DE-20 (5k x 3k)	Depositor
Maximum map value	13.200	Depositor
Minimum map value	-8.260	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1	Depositor
Map size (Å)	387.03, 387.03, 387.03	wwPDB
Map dimensions	399, 399, 399	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.96999997, 0.96999997, 0.96999997	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	0.43	0/4268	0.47	1/5823 (0.0%)
1	2	0.43	0/4268	0.47	1/5823 (0.0%)
1	3	0.43	0/4268	0.47	1/5823 (0.0%)
1	4	0.43	0/4268	0.47	1/5823 (0.0%)
1	5	0.43	0/4268	0.47	1/5823 (0.0%)
1	6	0.43	0/4268	0.47	1/5823 (0.0%)
1	7	0.43	0/4268	0.47	1/5823 (0.0%)
1	8	0.43	0/4268	0.47	1/5823 (0.0%)
1	A	0.43	0/4268	0.47	1/5823 (0.0%)
1	B	0.43	0/4268	0.47	1/5823 (0.0%)
1	C	0.43	0/4268	0.47	1/5823 (0.0%)
1	D	0.43	0/4268	0.47	1/5823 (0.0%)
1	E	0.43	0/4268	0.47	1/5823 (0.0%)
1	F	0.43	0/4268	0.47	1/5823 (0.0%)
1	G	0.43	0/4268	0.47	1/5823 (0.0%)
1	H	0.43	0/4268	0.47	1/5823 (0.0%)
1	I	0.43	0/4268	0.47	1/5823 (0.0%)
1	J	0.43	0/4268	0.47	1/5823 (0.0%)
1	K	0.43	0/4268	0.47	1/5823 (0.0%)
1	L	0.43	0/4268	0.47	1/5823 (0.0%)
1	M	0.43	0/4268	0.47	1/5823 (0.0%)
1	N	0.43	0/4268	0.47	1/5823 (0.0%)
1	O	0.43	0/4268	0.47	1/5823 (0.0%)
1	P	0.43	0/4268	0.47	1/5823 (0.0%)
1	Q	0.43	0/4268	0.47	1/5823 (0.0%)
1	R	0.43	0/4268	0.47	1/5823 (0.0%)
1	S	0.43	0/4268	0.47	1/5823 (0.0%)
1	T	0.43	0/4268	0.47	1/5823 (0.0%)
1	U	0.43	0/4268	0.47	1/5823 (0.0%)
1	V	0.43	0/4268	0.47	1/5823 (0.0%)
1	W	0.43	0/4268	0.47	1/5823 (0.0%)
1	X	0.43	0/4268	0.47	1/5823 (0.0%)
1	Y	0.43	0/4268	0.47	1/5823 (0.0%)
1	Z	0.43	0/4268	0.47	1/5823 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.43	0/4268	0.47	1/5823 (0.0%)
1	b	0.43	0/4268	0.47	1/5823 (0.0%)
1	c	0.43	0/4268	0.47	1/5823 (0.0%)
1	d	0.43	0/4268	0.47	1/5823 (0.0%)
1	e	0.43	0/4268	0.47	1/5823 (0.0%)
1	f	0.43	0/4268	0.47	1/5823 (0.0%)
1	g	0.43	0/4268	0.47	1/5823 (0.0%)
1	h	0.43	0/4268	0.47	1/5823 (0.0%)
1	i	0.43	0/4268	0.47	1/5823 (0.0%)
1	j	0.43	0/4268	0.47	1/5823 (0.0%)
1	k	0.43	0/4268	0.47	1/5823 (0.0%)
1	l	0.43	0/4268	0.47	1/5823 (0.0%)
1	m	0.43	0/4268	0.47	1/5823 (0.0%)
1	n	0.43	0/4268	0.47	1/5823 (0.0%)
1	o	0.43	0/4268	0.47	1/5823 (0.0%)
1	p	0.43	0/4268	0.47	1/5823 (0.0%)
1	q	0.43	0/4268	0.47	1/5823 (0.0%)
1	r	0.43	0/4268	0.47	1/5823 (0.0%)
1	s	0.43	0/4268	0.47	1/5823 (0.0%)
1	t	0.43	0/4268	0.47	1/5823 (0.0%)
1	u	0.43	0/4268	0.47	1/5823 (0.0%)
1	v	0.43	0/4268	0.47	1/5823 (0.0%)
1	w	0.43	0/4268	0.47	1/5823 (0.0%)
1	x	0.43	0/4268	0.47	1/5823 (0.0%)
1	y	0.43	0/4268	0.47	1/5823 (0.0%)
1	z	0.43	0/4268	0.47	1/5823 (0.0%)
2	0	0.25	0/41	0.32	0/61
2	0A	0.25	0/41	0.32	0/61
2	1A	0.25	0/41	0.32	0/61
2	2A	0.25	0/41	0.32	0/61
2	3A	0.25	0/41	0.32	0/61
2	4A	0.25	0/41	0.32	0/61
2	5A	0.25	0/41	0.32	0/61
2	9	0.25	0/41	0.32	0/61
2	AA	0.25	0/41	0.32	0/61
2	BA	0.25	0/41	0.32	0/61
2	CA	0.25	0/41	0.32	0/61
2	DA	0.25	0/41	0.32	0/61
2	EA	0.25	0/41	0.32	0/61
2	FA	0.25	0/41	0.32	0/61
2	GA	0.25	0/41	0.32	0/61
2	HA	0.25	0/41	0.32	0/61
2	IA	0.25	0/41	0.32	0/61

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
2	JA	0.25	0/41	0.32	0/61
2	KA	0.25	0/41	0.32	0/61
2	LA	0.25	0/41	0.32	0/61
2	MA	0.25	0/41	0.32	0/61
2	NA	0.25	0/41	0.32	0/61
2	OA	0.25	0/41	0.32	0/61
2	PA	0.25	0/41	0.32	0/61
2	QA	0.25	0/41	0.32	0/61
2	RA	0.25	0/41	0.32	0/61
2	SA	0.25	0/41	0.32	0/61
2	TA	0.25	0/41	0.32	0/61
2	UA	0.25	0/41	0.32	0/61
2	VA	0.25	0/41	0.32	0/61
2	WA	0.25	0/41	0.32	0/61
2	XA	0.25	0/41	0.32	0/61
2	YA	0.25	0/41	0.32	0/61
2	ZA	0.25	0/41	0.32	0/61
2	aA	0.25	0/41	0.32	0/61
2	bA	0.25	0/41	0.32	0/61
2	cA	0.25	0/41	0.32	0/61
2	dA	0.26	0/41	0.32	0/61
2	eA	0.25	0/41	0.32	0/61
2	fA	0.25	0/41	0.32	0/61
2	gA	0.25	0/41	0.32	0/61
2	hA	0.25	0/41	0.32	0/61
2	iA	0.25	0/41	0.32	0/61
2	jA	0.25	0/41	0.32	0/61
2	kA	0.25	0/41	0.32	0/61
2	lA	0.25	0/41	0.32	0/61
2	mA	0.25	0/41	0.32	0/61
2	nA	0.25	0/41	0.32	0/61
2	oA	0.25	0/41	0.32	0/61
2	pA	0.25	0/41	0.32	0/61
2	qA	0.25	0/41	0.32	0/61
2	rA	0.25	0/41	0.32	0/61
2	sA	0.25	0/41	0.32	0/61
2	tA	0.24	0/41	0.32	0/61
2	uA	0.25	0/41	0.32	0/61
2	vA	0.25	0/41	0.32	0/61
2	wA	0.25	0/41	0.32	0/61
2	xA	0.25	0/41	0.32	0/61
2	yA	0.25	0/41	0.32	0/61
2	zA	0.25	0/41	0.32	0/61

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.43	0/258540	0.47	60/353040 (0.0%)

There are no bond length outliers.

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	330	GLU	CB-CA-C	-6.00	109.64	116.54
1	5	330	GLU	CB-CA-C	-6.00	109.64	116.54
1	S	330	GLU	CB-CA-C	-6.00	109.65	116.54
1	X	330	GLU	CB-CA-C	-6.00	109.65	116.54
1	c	330	GLU	CB-CA-C	-6.00	109.65	116.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	4145	0	3901	146	0
1	2	4145	0	3901	148	0
1	3	4145	0	3901	144	0
1	4	4145	0	3901	148	0
1	5	4145	0	3901	145	0
1	6	4145	0	3901	146	0
1	7	4145	0	3901	146	0
1	8	4145	0	3901	149	0
1	A	4145	0	3901	146	0
1	B	4145	0	3901	147	0
1	C	4145	0	3901	142	0
1	D	4145	0	3901	143	0
1	E	4145	0	3901	140	0
1	F	4145	0	3901	147	0
1	G	4145	0	3901	145	0
1	H	4145	0	3901	145	0
1	I	4145	0	3901	150	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	4145	0	3901	145	0
1	K	4145	0	3901	148	0
1	L	4145	0	3901	141	0
1	M	4145	0	3901	147	0
1	N	4145	0	3901	142	0
1	O	4145	0	3901	142	0
1	P	4145	0	3901	144	0
1	Q	4145	0	3901	141	0
1	R	4145	0	3901	149	0
1	S	4145	0	3901	141	0
1	T	4145	0	3901	143	0
1	U	4145	0	3901	145	0
1	V	4145	0	3901	143	0
1	W	4145	0	3901	143	0
1	X	4145	0	3901	146	0
1	Y	4145	0	3901	149	0
1	Z	4145	0	3901	148	0
1	a	4145	0	3901	150	0
1	b	4145	0	3901	143	0
1	c	4145	0	3901	144	0
1	d	4145	0	3901	148	0
1	e	4145	0	3901	147	0
1	f	4145	0	3901	147	0
1	g	4145	0	3901	147	0
1	h	4145	0	3901	144	0
1	i	4145	0	3901	139	0
1	j	4145	0	3901	147	0
1	k	4145	0	3901	149	0
1	l	4145	0	3901	143	0
1	m	4145	0	3901	145	0
1	n	4145	0	3901	145	0
1	o	4145	0	3901	144	0
1	p	4145	0	3901	149	0
1	q	4145	0	3901	146	0
1	r	4145	0	3901	140	0
1	s	4145	0	3901	141	0
1	t	4145	0	3901	144	0
1	u	4145	0	3901	147	0
1	v	4145	0	3901	145	0
1	w	4145	0	3901	148	0
1	x	4145	0	3901	145	0
1	y	4145	0	3901	145	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	z	4145	0	3901	140	0
2	0	37	0	24	0	0
2	0A	37	0	24	0	0
2	1A	37	0	24	0	0
2	2A	37	0	24	0	0
2	3A	37	0	24	0	0
2	4A	37	0	24	0	0
2	5A	37	0	24	0	0
2	9	37	0	24	0	0
2	AA	37	0	24	0	0
2	BA	37	0	24	0	0
2	CA	37	0	24	0	0
2	DA	37	0	24	0	0
2	EA	37	0	24	0	0
2	FA	37	0	24	0	0
2	GA	37	0	24	0	0
2	HA	37	0	24	0	0
2	IA	37	0	24	0	0
2	JA	37	0	24	0	0
2	KA	37	0	24	0	0
2	LA	37	0	24	0	0
2	MA	37	0	24	0	0
2	NA	37	0	24	0	0
2	OA	37	0	24	0	0
2	PA	37	0	24	0	0
2	QA	37	0	24	0	0
2	RA	37	0	24	0	0
2	SA	37	0	24	0	0
2	TA	37	0	24	0	0
2	UA	37	0	24	0	0
2	VA	37	0	24	0	0
2	WA	37	0	24	0	0
2	XA	37	0	24	0	0
2	YA	37	0	24	0	0
2	ZA	37	0	24	0	0
2	aA	37	0	24	0	0
2	bA	37	0	24	0	0
2	cA	37	0	24	0	0
2	dA	37	0	24	0	0
2	eA	37	0	24	0	0
2	fA	37	0	24	0	0
2	gA	37	0	24	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	hA	37	0	24	0	0
2	iA	37	0	24	0	0
2	jA	37	0	24	0	0
2	kA	37	0	24	0	0
2	lA	37	0	24	0	0
2	mA	37	0	24	0	0
2	nA	37	0	24	0	0
2	oA	37	0	24	0	0
2	pA	37	0	24	0	0
2	qA	37	0	24	0	0
2	rA	37	0	24	0	0
2	sA	37	0	24	0	0
2	tA	37	0	24	0	0
2	uA	37	0	24	0	0
2	vA	37	0	24	0	0
2	wA	37	0	24	0	0
2	xA	37	0	24	0	0
2	yA	37	0	24	0	0
2	zA	37	0	24	0	0
All	All	250920	0	235500	6770	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

The worst 5 of 6770 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:486:TYR:H	1:5:526:MET:HE1	1.48	0.79
1:3:486:TYR:H	1:3:526:MET:HE1	1.48	0.78
1:D:486:TYR:H	1:D:526:MET:HE1	1.49	0.78
1:X:486:TYR:H	1:X:526:MET:HE1	1.49	0.78
1:n:486:TYR:H	1:n:526:MET:HE1	1.49	0.78

There are no symmetry-related clashes.

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	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	2	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	3	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	4	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	5	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	6	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	7	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	8	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	A	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	B	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	C	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	D	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	E	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	F	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	G	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	H	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	I	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	J	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	K	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	L	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	M	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	N	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	O	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	P	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	Q	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	S	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	T	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	U	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	V	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	W	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	X	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	Y	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	Z	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	a	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	b	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	c	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	d	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	e	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	f	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	g	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	h	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	i	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	j	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	k	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	l	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	m	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	n	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	o	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	p	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	q	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	r	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	s	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	t	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	u	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	v	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	w	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	x	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	y	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
1	z	519/521 (100%)	504 (97%)	14 (3%)	1 (0%)	43	72
All	All	31140/31260 (100%)	30240 (97%)	840 (3%)	60 (0%)	44	72

5 of 60 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	539	SER
1	B	539	SER
1	C	539	SER
1	D	539	SER
1	E	539	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	2	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	3	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	4	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	5	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	6	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	7	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	8	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	A	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	B	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	C	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	D	453/453 (100%)	452 (100%)	1 (0%)	87	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	F	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	G	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	H	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	I	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	J	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	K	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	L	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	M	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	N	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	O	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	P	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	Q	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	R	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	S	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	T	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	U	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	V	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	W	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	X	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	Y	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	Z	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	a	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	b	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	c	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	d	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	e	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	f	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	g	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	h	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	i	453/453 (100%)	452 (100%)	1 (0%)	87	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	j	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	k	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	l	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	m	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	n	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	o	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	p	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	q	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	r	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	s	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	t	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	u	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	v	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	w	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	x	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	y	453/453 (100%)	452 (100%)	1 (0%)	87	87
1	z	453/453 (100%)	452 (100%)	1 (0%)	87	87
All	All	27180/27180 (100%)	27120 (100%)	60 (0%)	85	87

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

Mol	Chain	Res	Type
1	c	448	LEU
1	4	448	LEU
1	j	448	LEU
1	3	448	LEU
1	8	448	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 787 such sidechains are listed below:

Mol	Chain	Res	Type
1	j	362	GLN
1	r	653	ASN
1	k	352	GLN
1	j	352	GLN

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Mol	Chain	Res	Type
1	n	548	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

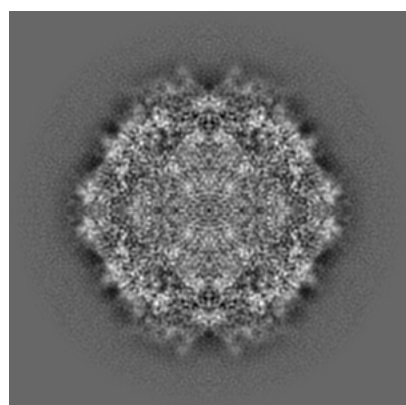
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21004. These allow visual inspection of the internal detail of the map and identification of artifacts.

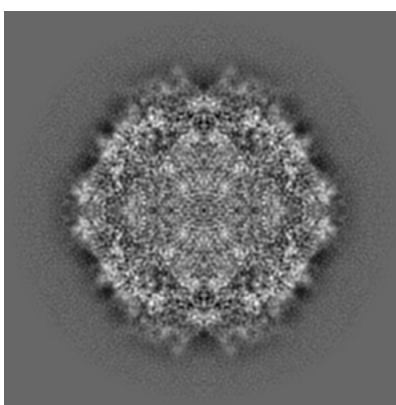
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

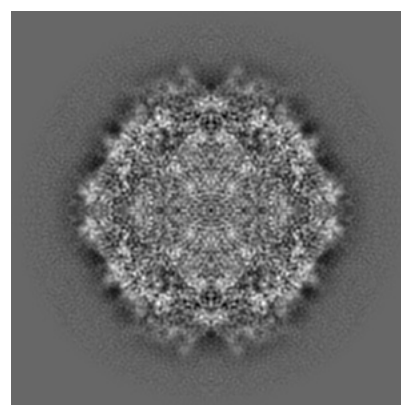
6.1.1 Primary map



X



Y

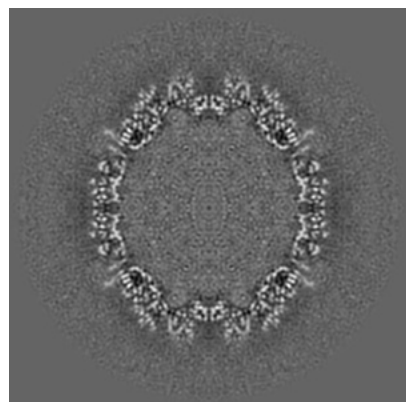


Z

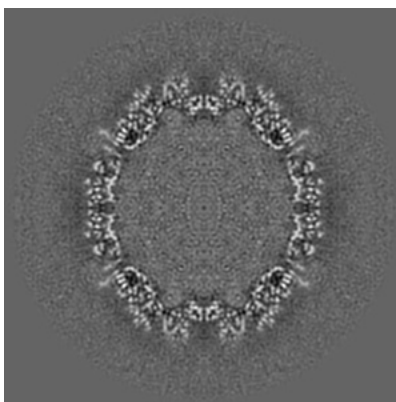
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

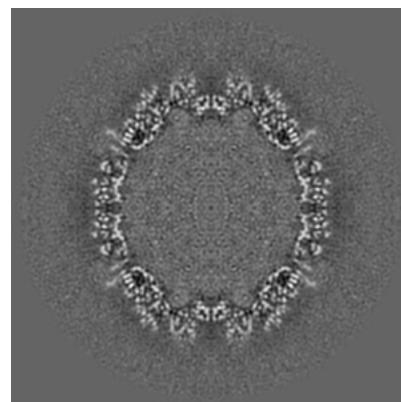
6.2.1 Primary map



X Index: 199



Y Index: 199

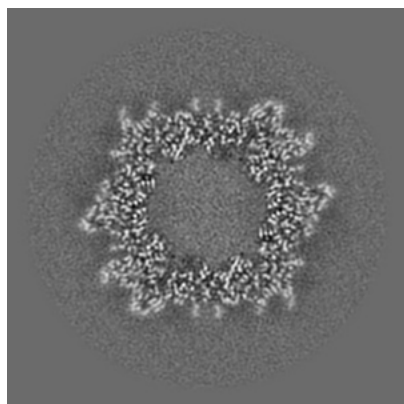


Z Index: 199

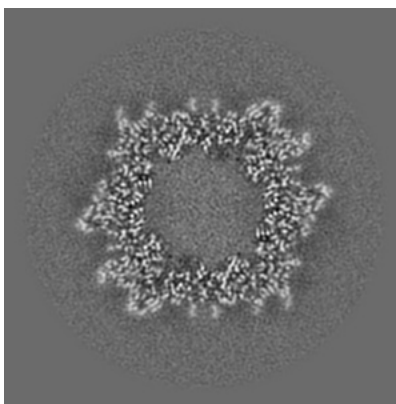
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

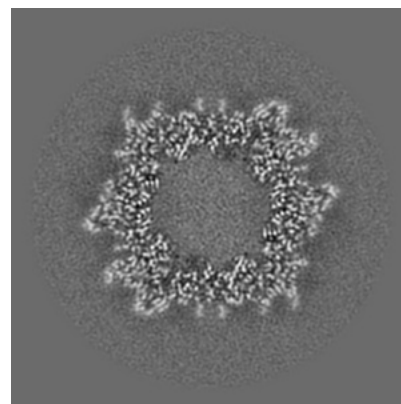
6.3.1 Primary map



X Index: 131



Y Index: 131

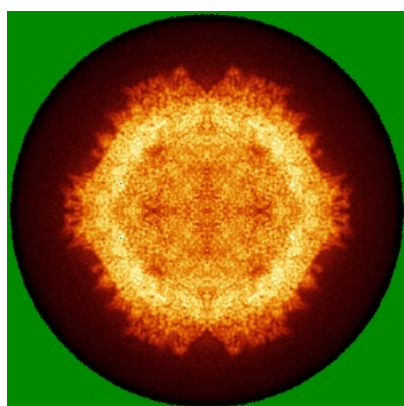


Z Index: 131

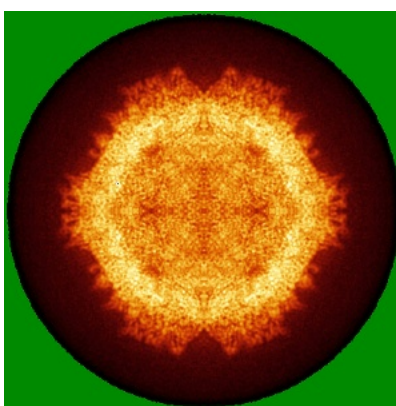
The images above show the largest variance slices of the map in three orthogonal directions.

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

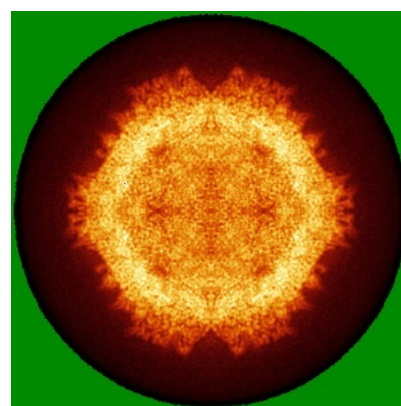
6.4.1 Primary map



X



Y



Z

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

This section was not generated.

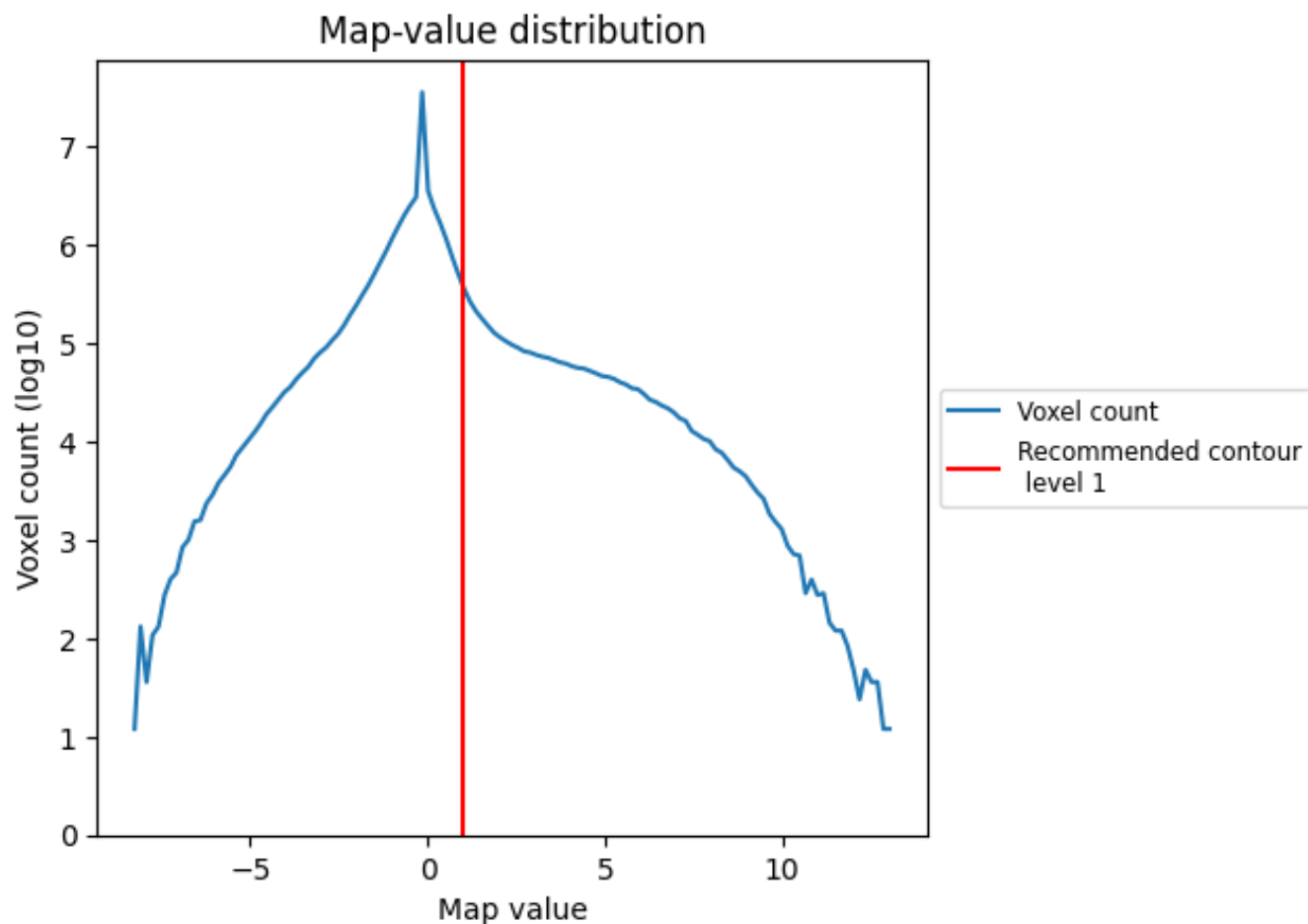
6.6 Mask visualisation

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

7 Map analysis [i](#)

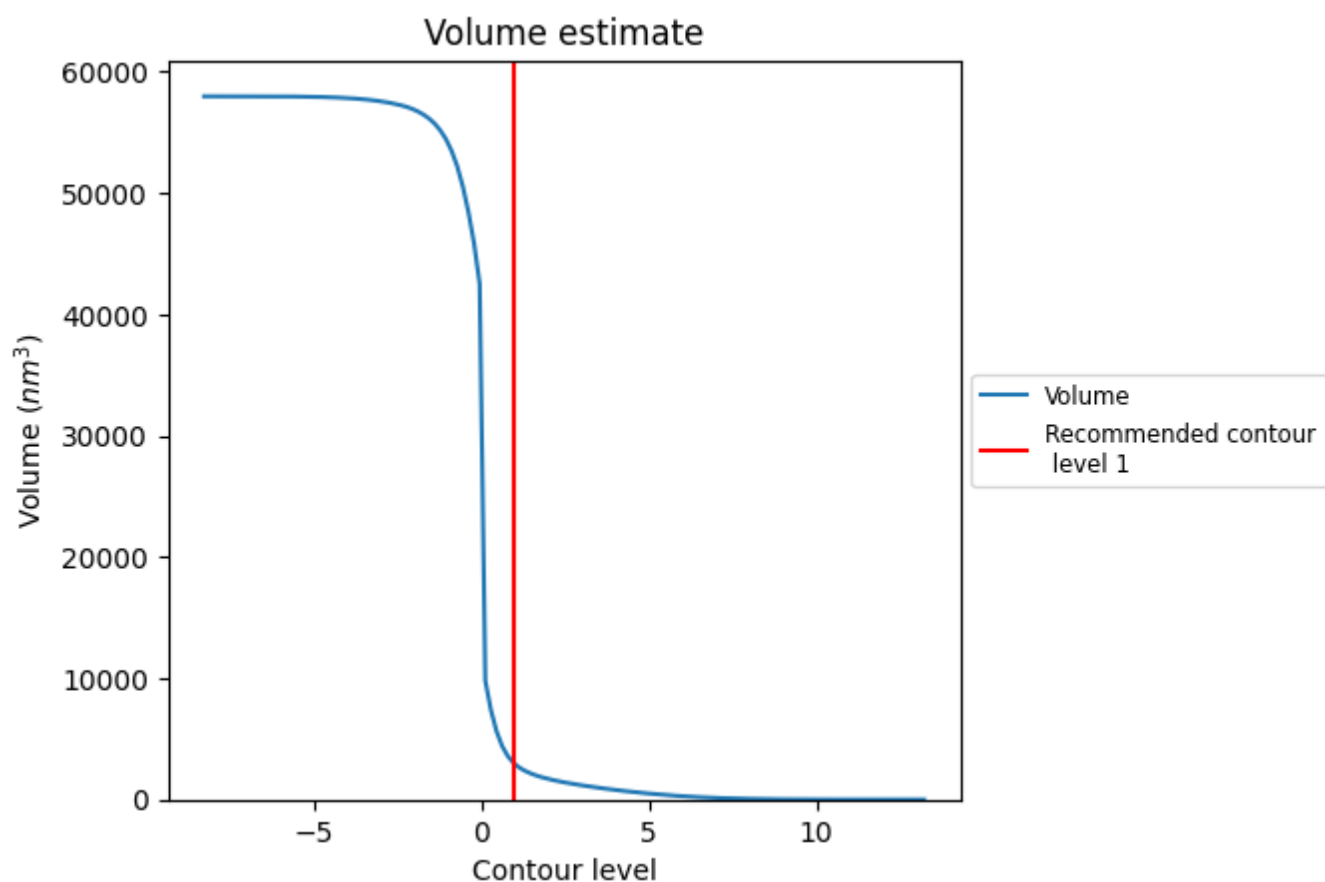
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

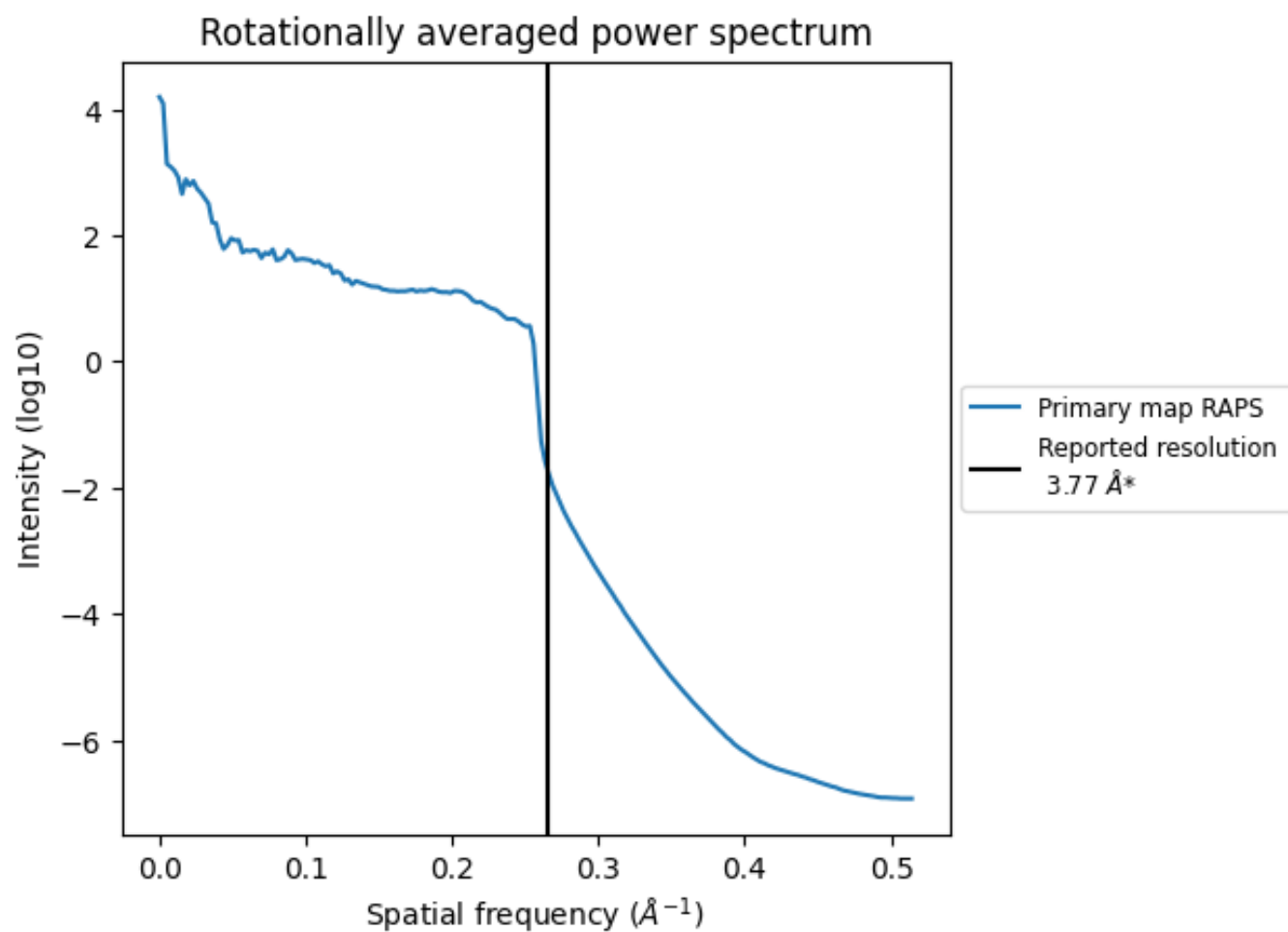
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2942 nm³; this corresponds to an approximate mass of 2657 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.265 Å⁻¹

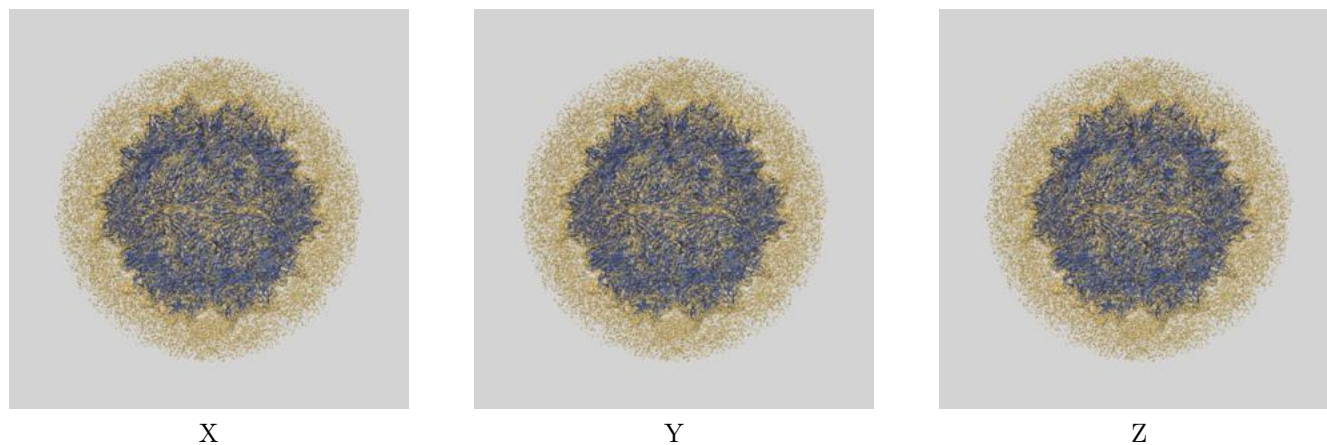
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

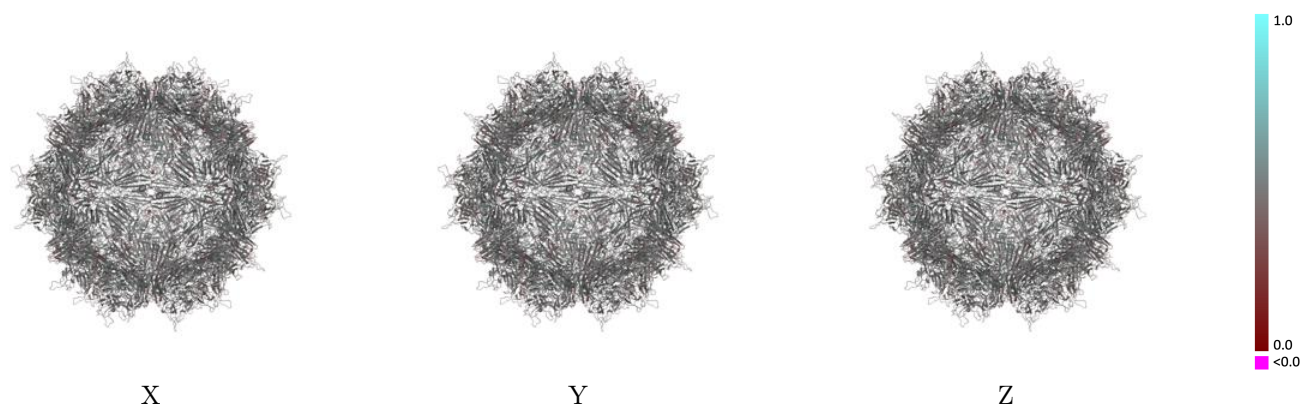
This section contains information regarding the fit between EMDB map EMD-21004 and PDB model 6V10. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 1.0 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](#)

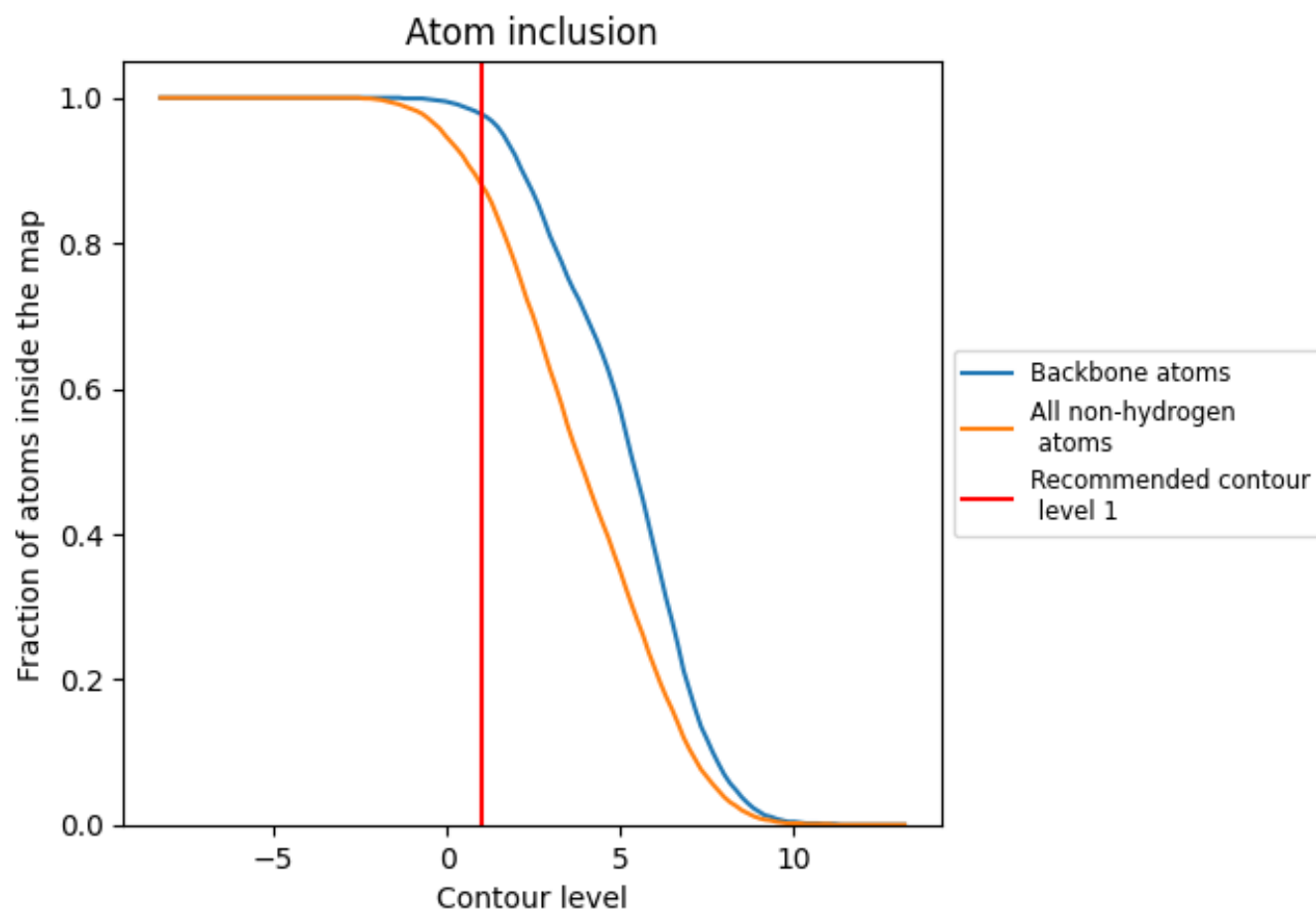


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 88% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8800	 0.4620
0	 0.8380	 0.4360
0A	 0.8380	 0.4330
1	 0.8800	 0.4630
1A	 0.8650	 0.4180
2	 0.8790	 0.4620
2A	 0.8650	 0.4310
3	 0.8810	 0.4630
3A	 0.8650	 0.4270
4	 0.8790	 0.4620
4A	 0.8380	 0.4300
5	 0.8800	 0.4630
5A	 0.8920	 0.4360
6	 0.8790	 0.4610
7	 0.8810	 0.4630
8	 0.8820	 0.4630
9	 0.8650	 0.4270
A	 0.8810	 0.4620
AA	 0.8920	 0.4220
B	 0.8800	 0.4630
BA	 0.8650	 0.4270
C	 0.8800	 0.4630
CA	 0.8920	 0.4320
D	 0.8800	 0.4620
DA	 0.8920	 0.4340
E	 0.8820	 0.4640
EA	 0.8650	 0.4310
F	 0.8820	 0.4630
FA	 0.8920	 0.4230
G	 0.8800	 0.4630
GA	 0.8650	 0.4180
H	 0.8800	 0.4620
HA	 0.8380	 0.4330
I	 0.8800	 0.4620
IA	 0.8920	 0.4350



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Chain	Atom inclusion	Q-score
J	 0.8810	 0.4620
JA	 0.8650	 0.4510
K	 0.8820	 0.4630
KA	 0.8920	 0.4390
L	 0.8800	 0.4620
LA	 0.8650	 0.4170
M	 0.8800	 0.4620
MA	 0.8650	 0.4140
N	 0.8790	 0.4640
NA	 0.8380	 0.4310
O	 0.8790	 0.4630
OA	 0.8920	 0.4390
P	 0.8810	 0.4620
PA	 0.8380	 0.4300
Q	 0.8830	 0.4640
QA	 0.8650	 0.4290
R	 0.8810	 0.4620
RA	 0.8920	 0.4230
S	 0.8800	 0.4630
SA	 0.8650	 0.4280
T	 0.8800	 0.4630
TA	 0.8650	 0.4210
U	 0.8790	 0.4630
UA	 0.8920	 0.4350
V	 0.8790	 0.4630
VA	 0.8650	 0.4350
W	 0.8800	 0.4620
WA	 0.8920	 0.4350
X	 0.8800	 0.4630
XA	 0.8650	 0.4320
Y	 0.8800	 0.4620
YA	 0.8920	 0.4360
Z	 0.8800	 0.4630
ZA	 0.8920	 0.4100
a	 0.8820	 0.4620
aA	 0.8650	 0.4270
b	 0.8800	 0.4620
bA	 0.8920	 0.4370
c	 0.8800	 0.4640
cA	 0.8380	 0.4370
d	 0.8800	 0.4620
dA	 0.8920	 0.4390

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Chain	Atom inclusion	Q-score
e	 0.8810	 0.4630
eA	 0.8920	 0.4380
f	 0.8830	 0.4620
fA	 0.8920	 0.4360
g	 0.8820	 0.4630
gA	 0.8650	 0.4370
h	 0.8820	 0.4630
hA	 0.8650	 0.4110
i	 0.8800	 0.4610
iA	 0.8380	 0.4450
j	 0.8800	 0.4610
jA	 0.8920	 0.4200
k	 0.8810	 0.4620
kA	 0.8380	 0.4310
l	 0.8800	 0.4630
lA	 0.8650	 0.4320
m	 0.8810	 0.4620
mA	 0.8650	 0.4200
n	 0.8800	 0.4630
nA	 0.8380	 0.4310
o	 0.8790	 0.4620
oA	 0.8920	 0.4390
p	 0.8810	 0.4620
pA	 0.8920	 0.4380
q	 0.8820	 0.4630
qA	 0.8920	 0.4390
r	 0.8820	 0.4630
rA	 0.8920	 0.4290
s	 0.8830	 0.4630
sA	 0.8920	 0.4280
t	 0.8800	 0.4620
tA	 0.8920	 0.4240
u	 0.8800	 0.4630
uA	 0.8650	 0.4230
v	 0.8800	 0.4620
vA	 0.8380	 0.4330
w	 0.8800	 0.4630
wA	 0.8650	 0.4370
x	 0.8810	 0.4620
xA	 0.8380	 0.4330
y	 0.8800	 0.4620
yA	 0.8650	 0.4380

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Chain	Atom inclusion	Q-score
z	 0.8810	 0.4620
zA	 0.8650	 0.4200