



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 10:42 AM UTC

PDB ID : 7MT0 / pdb_00007mt0
EMDB ID : EMD-23973
Title : Structure of the adeno-associated virus 9 capsid at pH 7.4
Authors : Penzes, J.J.; Chipman, P.; Bhattacharya, N.; Zeher, A.; Huang, R.; McKenna, R.; Agbandje-McKenna, M.
Deposited on : 2021-05-12
Resolution : 2.82 Å(reported)
Based on initial model : 3UX1

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

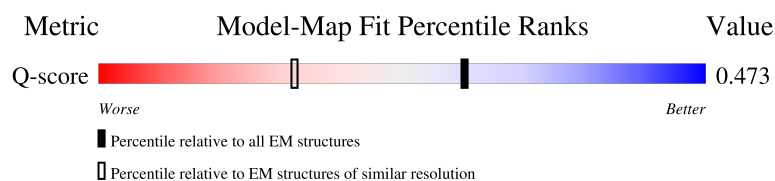
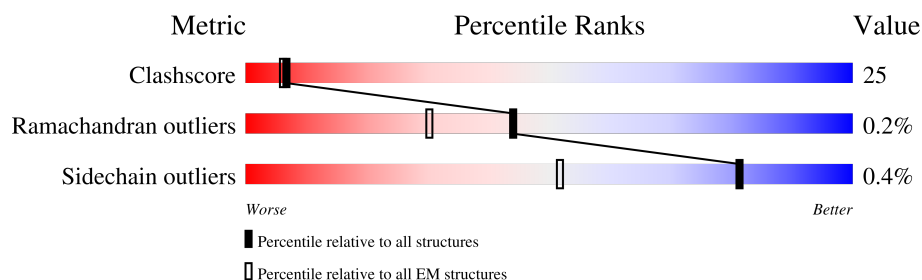
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.82 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	11795 (2.32 - 3.32)

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	518	58% 41% .
1	2	518	58% 41% .
1	3	518	59% 40% .
1	4	518	58% 42% .

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Mol	Chain	Length	Quality of chain	
1	5	518		57% 42%
1	6	518		58% 41%
1	7	518		58% 42%
1	8	518		58% 42%
1	A	518		58% 41%
1	B	518		58% 41%
1	C	518		58% 41%
1	D	518		58% 41%
1	E	518		58% 42%
1	F	518		59% 41%
1	G	518		58% 41%
1	H	518		58% 41%
1	I	518		58% 41%
1	J	518		58% 41%
1	K	518		58% 42%
1	L	518		58% 41%
1	M	518		58% 42%
1	N	518		58% 41%
1	O	518		57% 42%
1	P	518		58% 42%
1	Q	518		58% 41%
1	R	518		59% 40%
1	S	518		59% 41%
1	T	518		59% 41%
1	U	518		58% 41%

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Mol	Chain	Length	Quality of chain	
1	V	518		58% 41%
1	W	518		58% 41%
1	X	518		58% 41%
1	Y	518		59% 41%
1	Z	518		58% 41%
1	a	518		58% 41%
1	b	518		57% 42%
1	c	518		58% 41%
1	d	518		59% 41%
1	e	518		58% 42%
1	f	518		59% 40%
1	g	518		59% 41%
1	h	518		58% 41%
1	i	518		58% 42%
1	j	518		59% 40%
1	k	518		58% 41%
1	l	518		58% 41%
1	m	518		58% 41%
1	n	518		58% 41%
1	o	518		58% 41%
1	p	518		58% 41%
1	q	518		58% 41%
1	r	518		58% 42%
1	s	518		59% 41%
1	t	518		58% 42%

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Mol	Chain	Length	Quality of chain
1	u	518	 58% 42% .
1	v	518	 58% 41% .
1	w	518	 58% 41% .
1	x	518	 59% 40% .
1	y	518	 58% 42% .
1	z	518	 59% 41% .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 247860 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 VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	B	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	C	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	D	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	E	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	F	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	G	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	H	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	I	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	J	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	K	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	L	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	M	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	N	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	O	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	P	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		
1	Q	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	S	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	T	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	U	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	V	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	W	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	X	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	Y	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	Z	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	1	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	2	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	3	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	4	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	5	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	6	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	a	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	b	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	c	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	d	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	e	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	f	518	Total 4131	C 2608	N 718	O 791	S 14	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	g	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	h	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	i	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	j	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	k	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	l	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	m	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	n	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	o	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	p	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	q	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	r	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	s	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	t	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	u	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	v	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	w	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	x	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	y	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	z	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	7	518	Total 4131	C 2608	N 718	O 791	S 14	0	0

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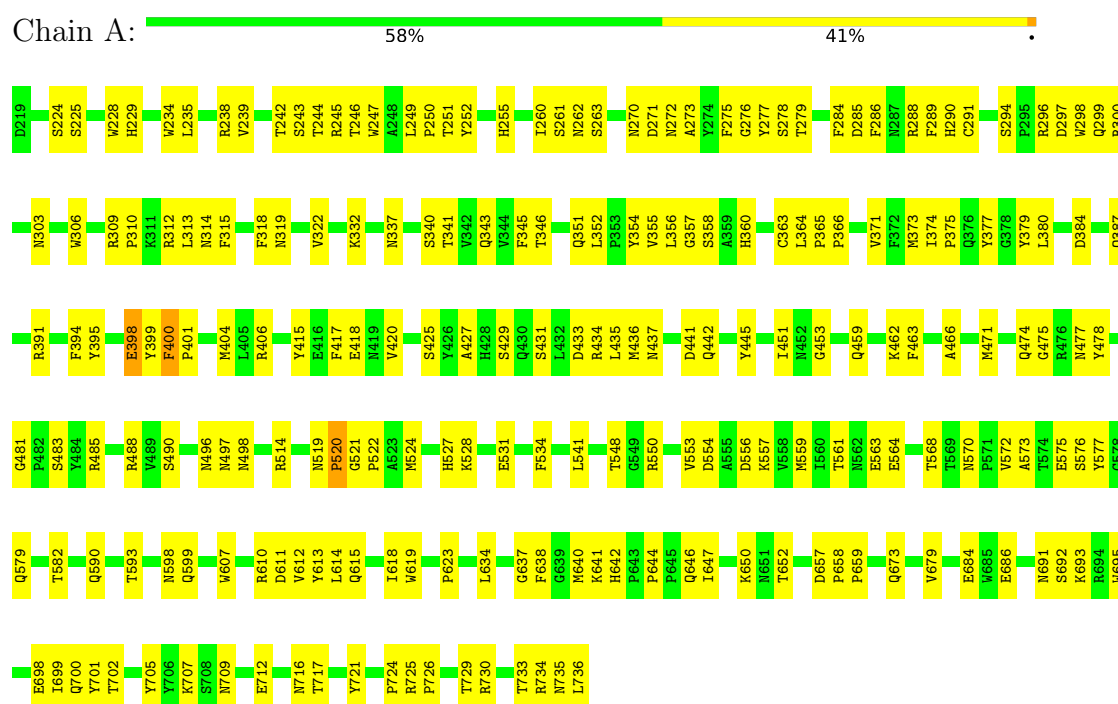
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	518	Total	C	N	O	S	0	0
			4131	2608	718	791	14		

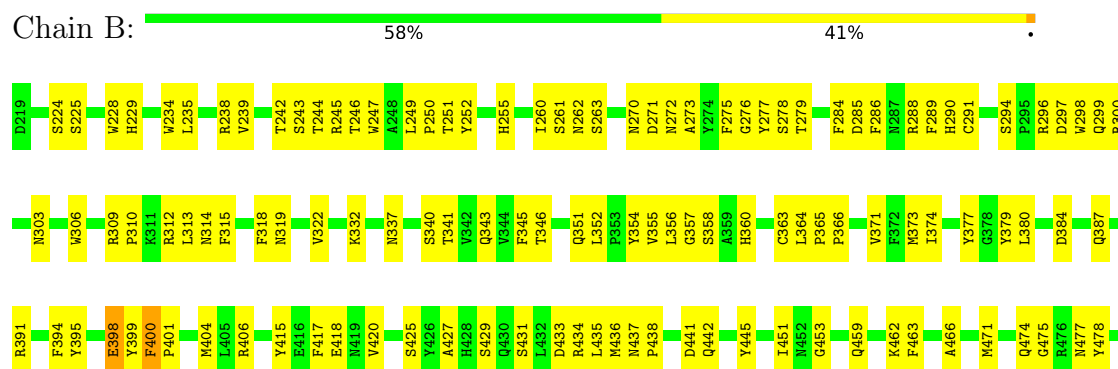
3 Residue-property plots

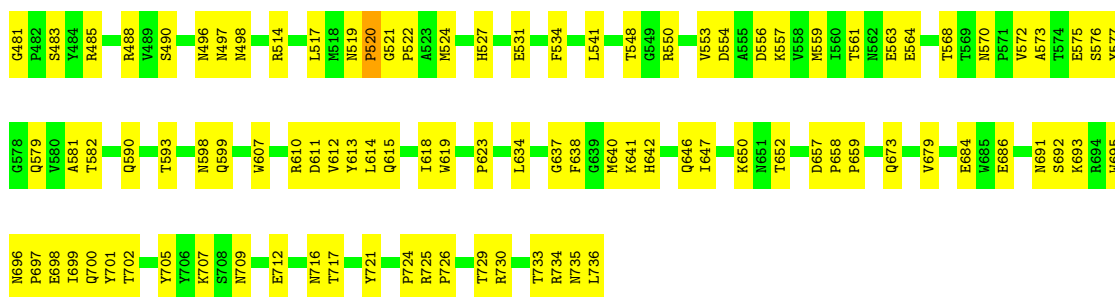
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 VP1



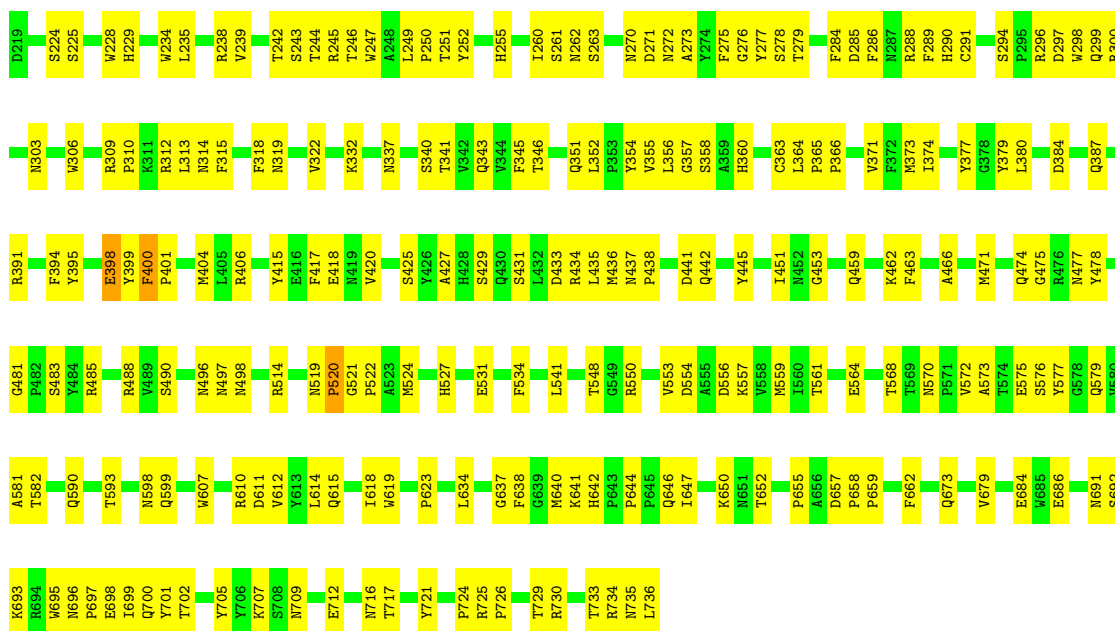
• Molecule 1: Capsid protein VP1





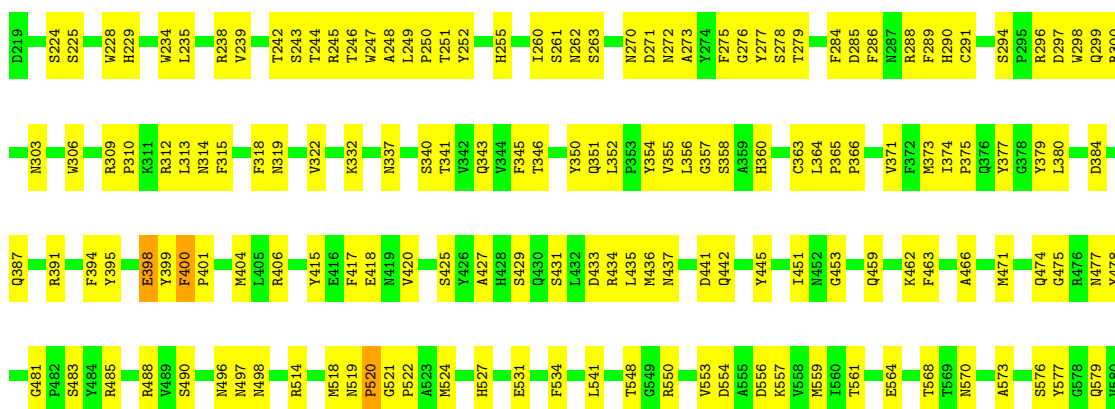
● Molecule 1: Capsid protein VP1

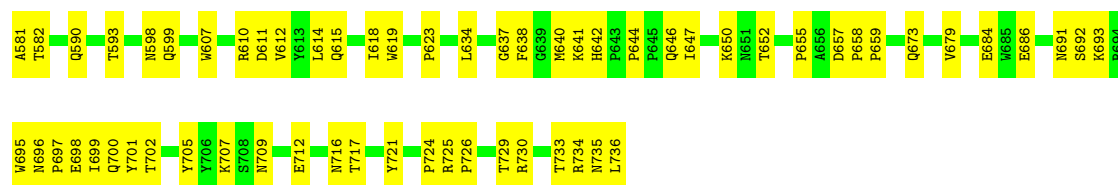
Chain C: 58% 41%



● Molecule 1: Capsid protein VP1

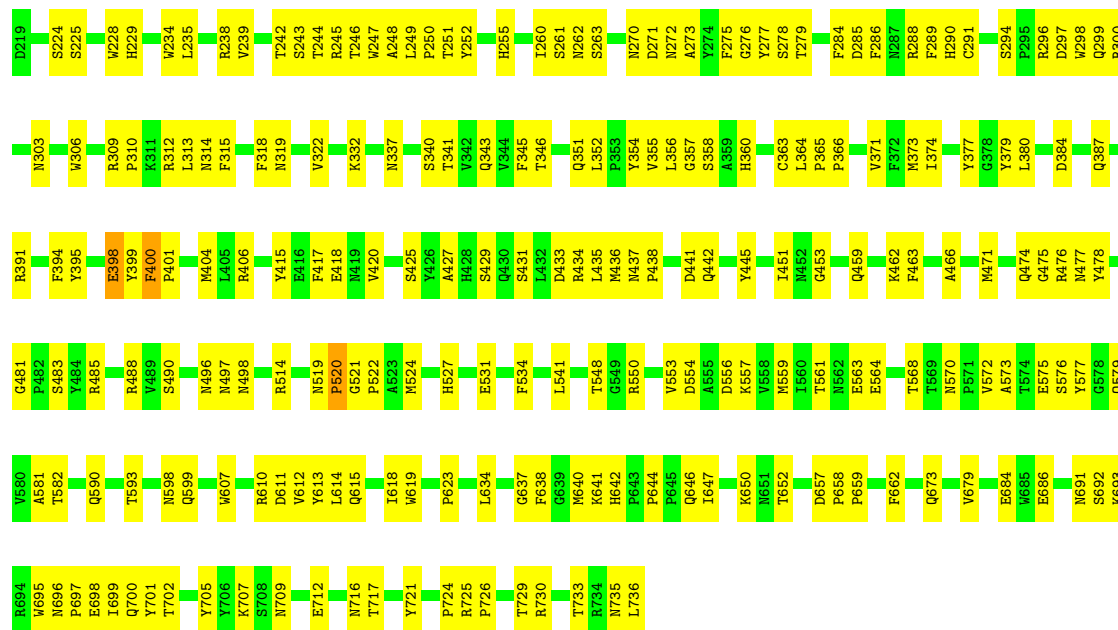
Chain D: 58% 41%





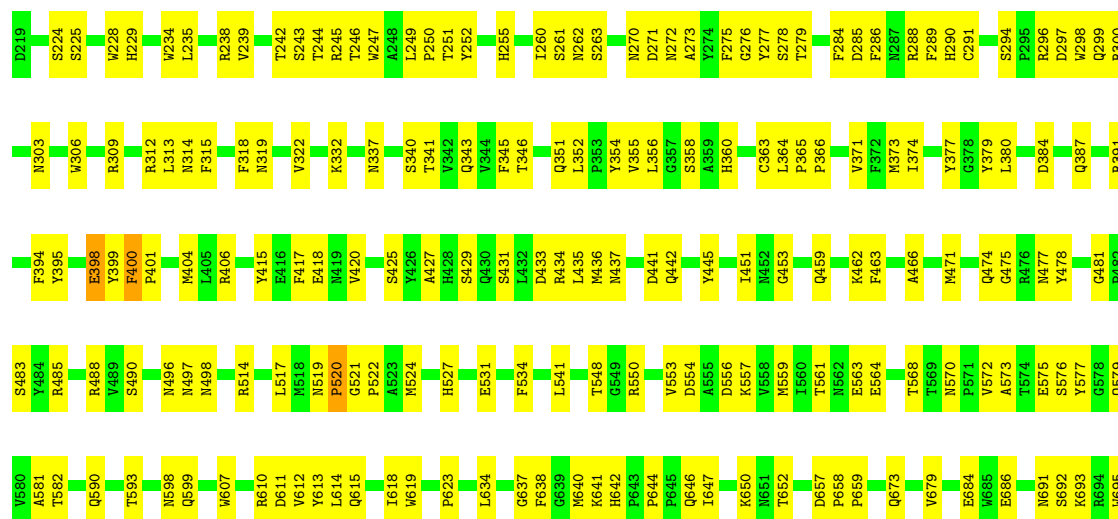
• Molecule 1: Capsid protein VP1

Chain E: 58% 42%



• Molecule 1: Capsid protein VP1

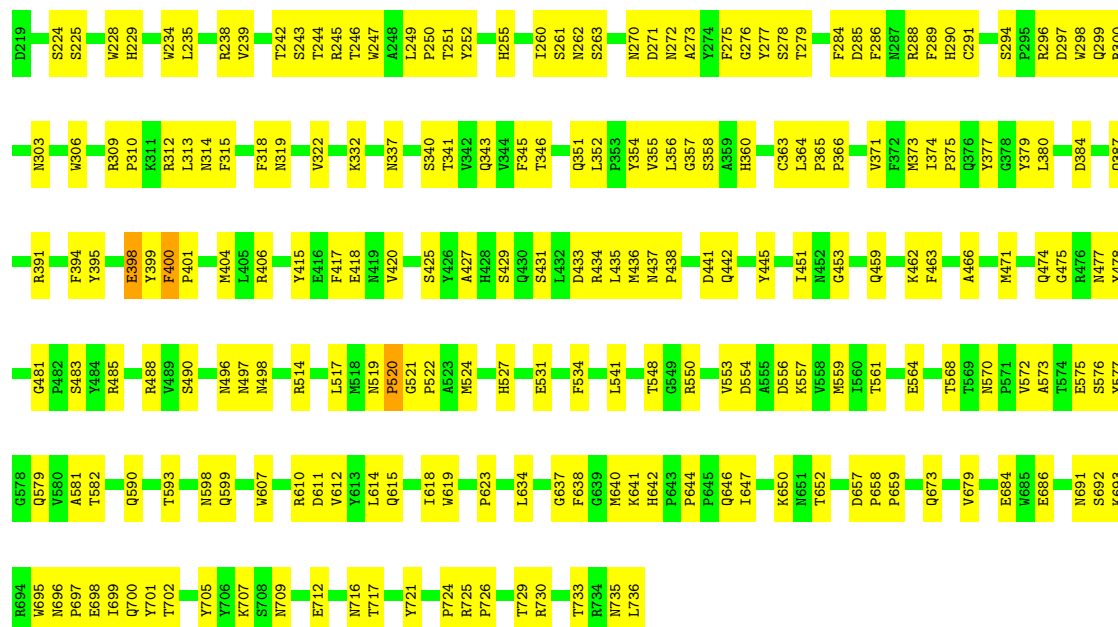
Chain F: 59% 41%





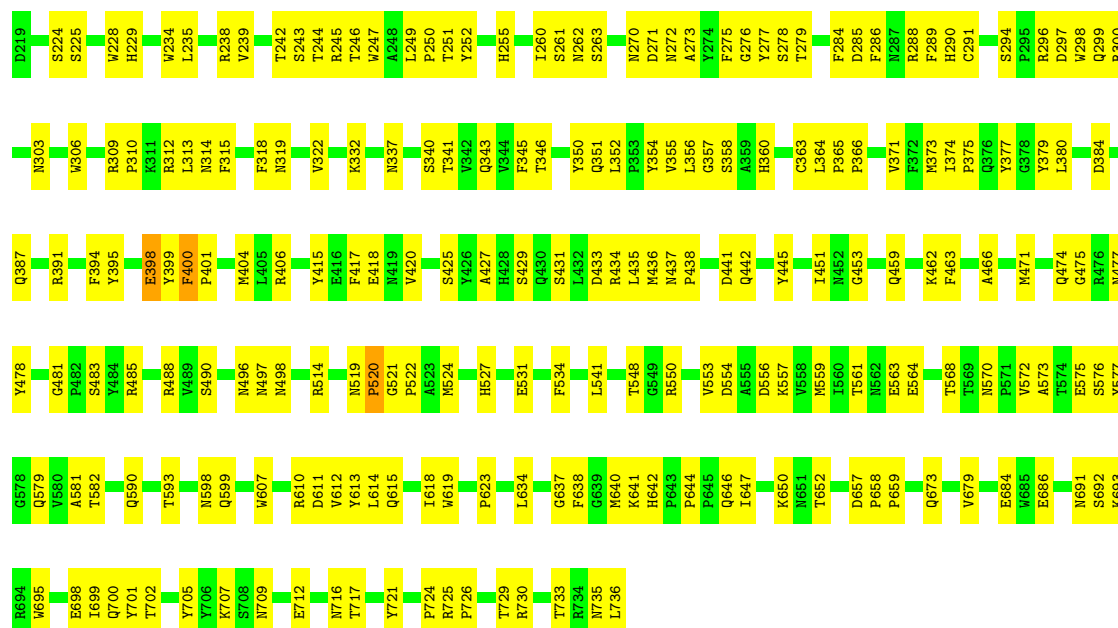
• Molecule 1: Capsid protein VP1

Chain G: 58% 41%



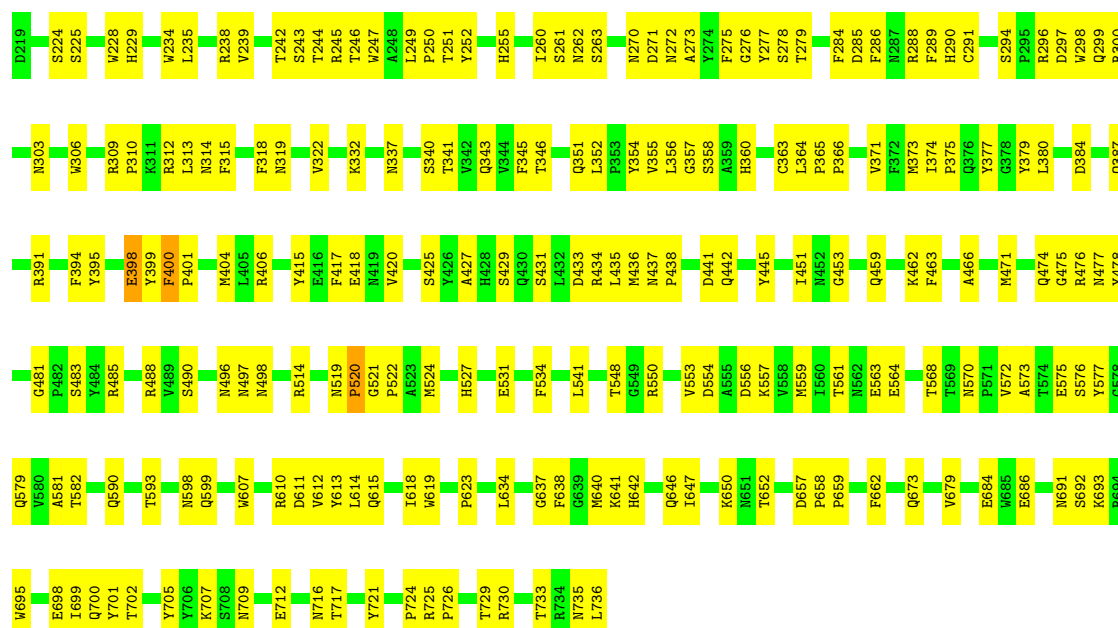
• Molecule 1: Capsid protein VP1

Chain H: 58% 41%



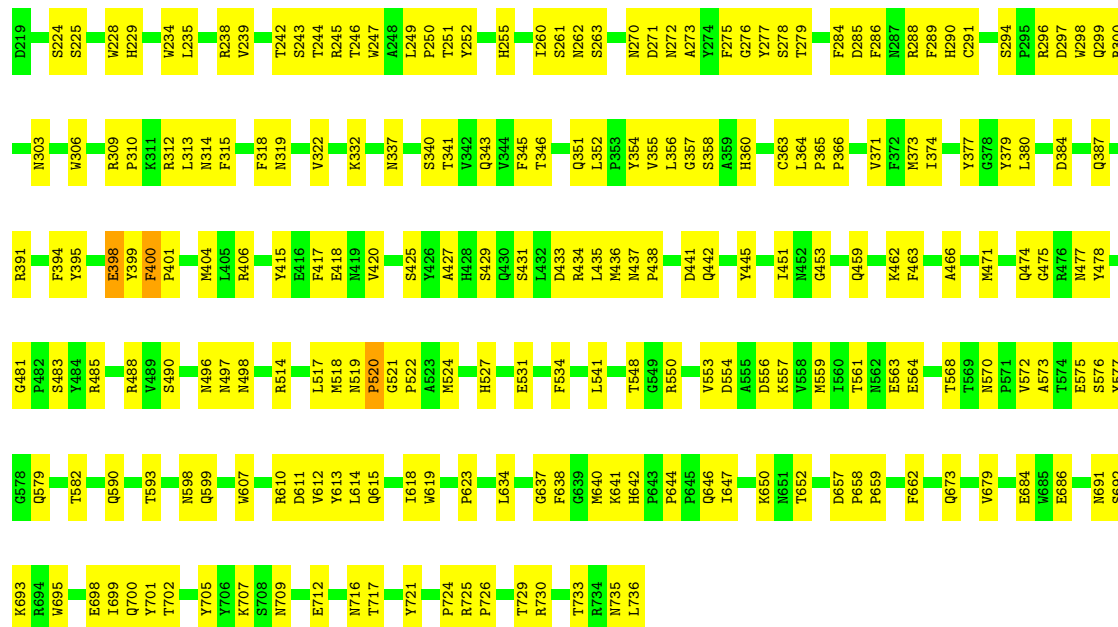
• Molecule 1: Capsid protein VP1

Chain I:  58% 41%



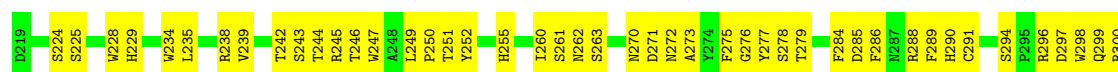
• Molecule 1: Capsid protein VP1

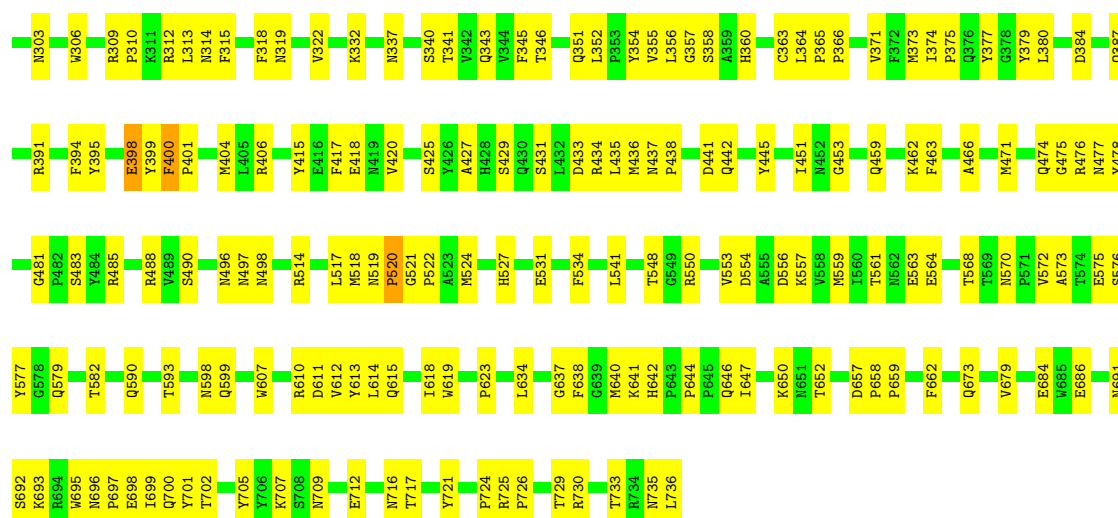
Chain J:  58% 41%



• Molecule 1: Capsid protein VP1

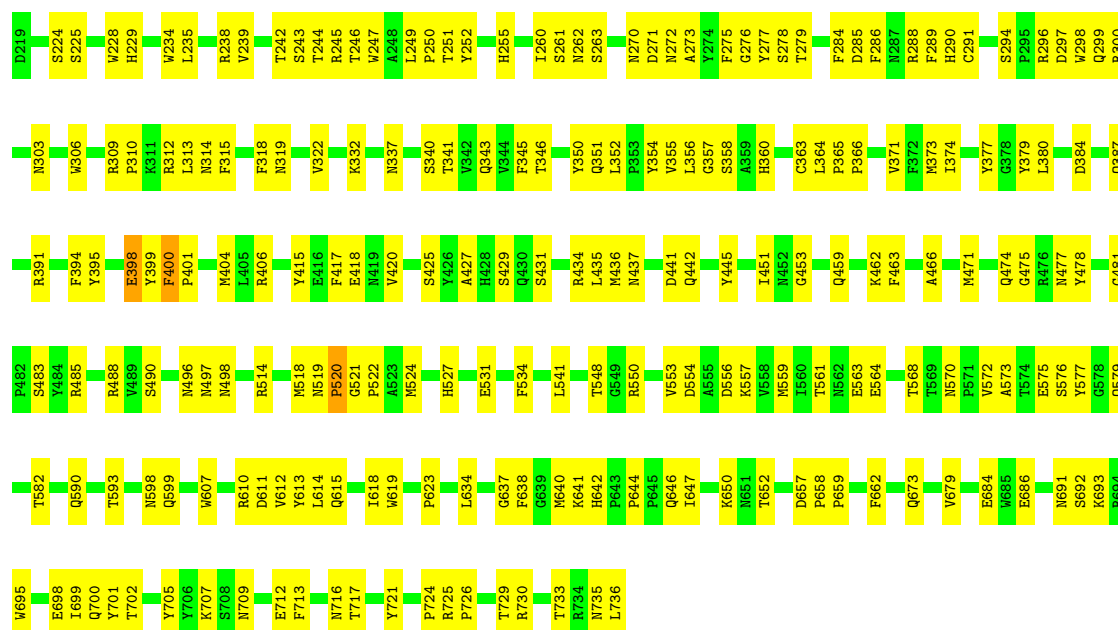
Chain K:  58% 42%





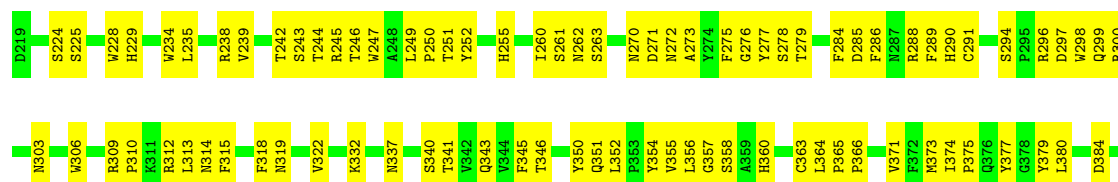
• Molecule 1: Capsid protein VP1

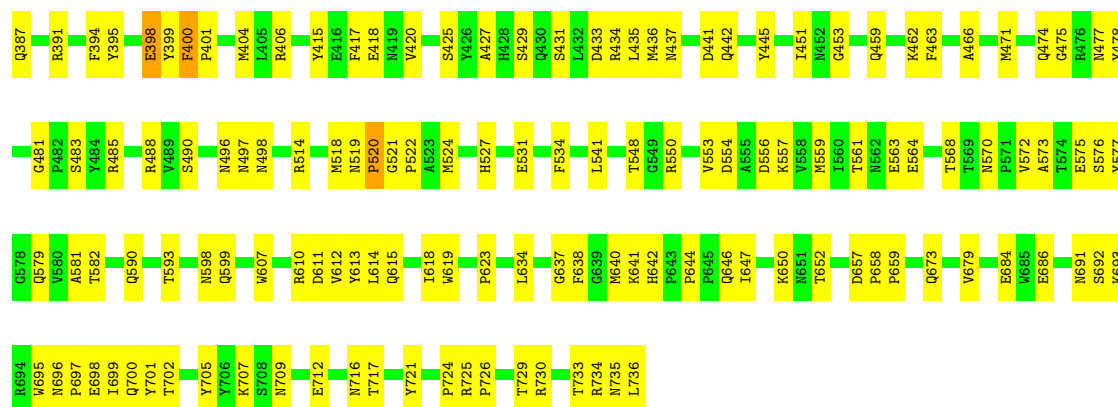
Chain L: 58% 41%



• Molecule 1: Capsid protein VP1

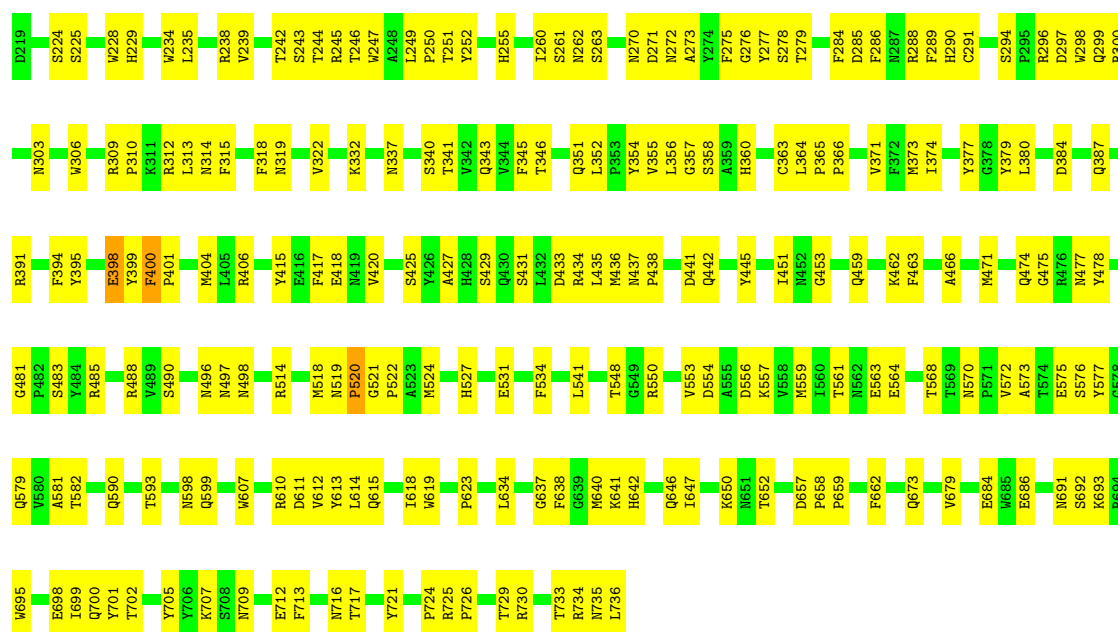
Chain M: 58% 42%





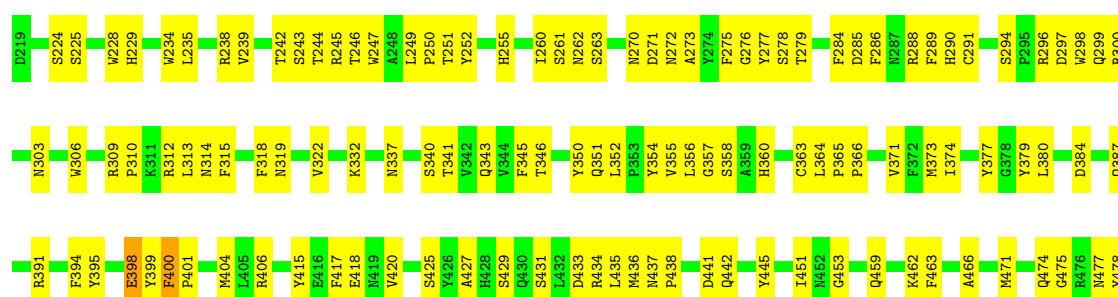
• Molecule 1: Capsid protein VP1

Chain N: 58% 41%



• Molecule 1: Capsid protein VP1

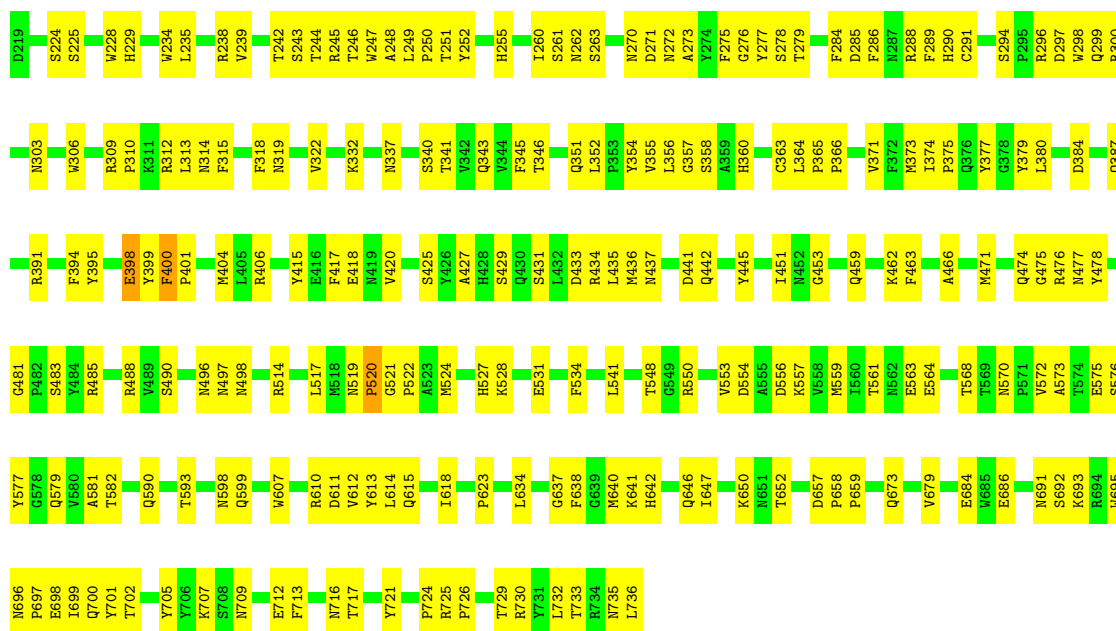
Chain O: 57% 42%





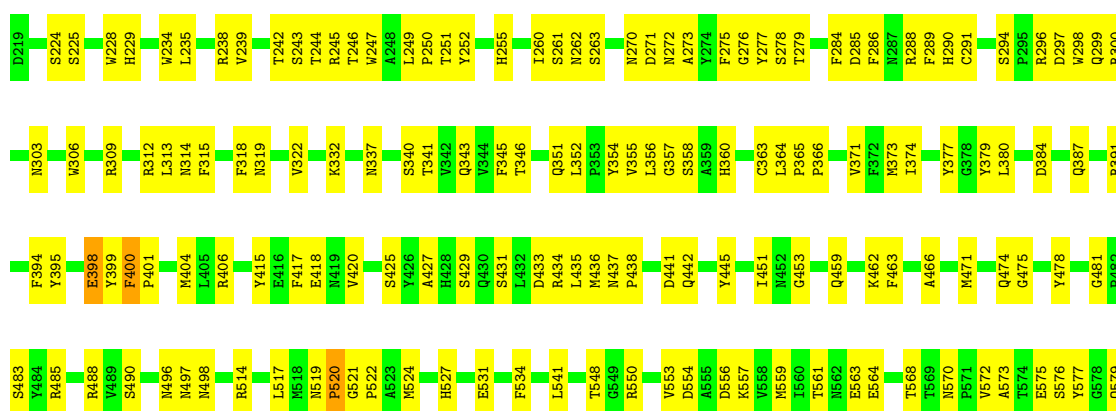
• Molecule 1: Capsid protein VP1

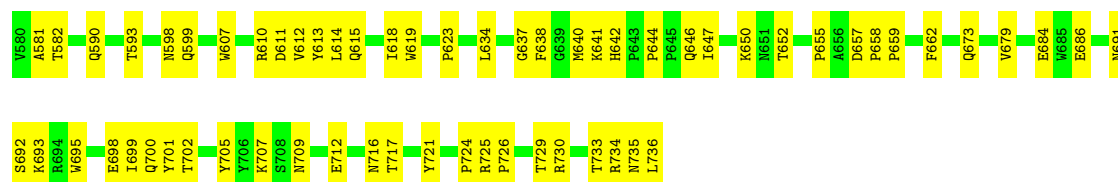
Chain P: 58% 42%



• Molecule 1: Capsid protein VP1

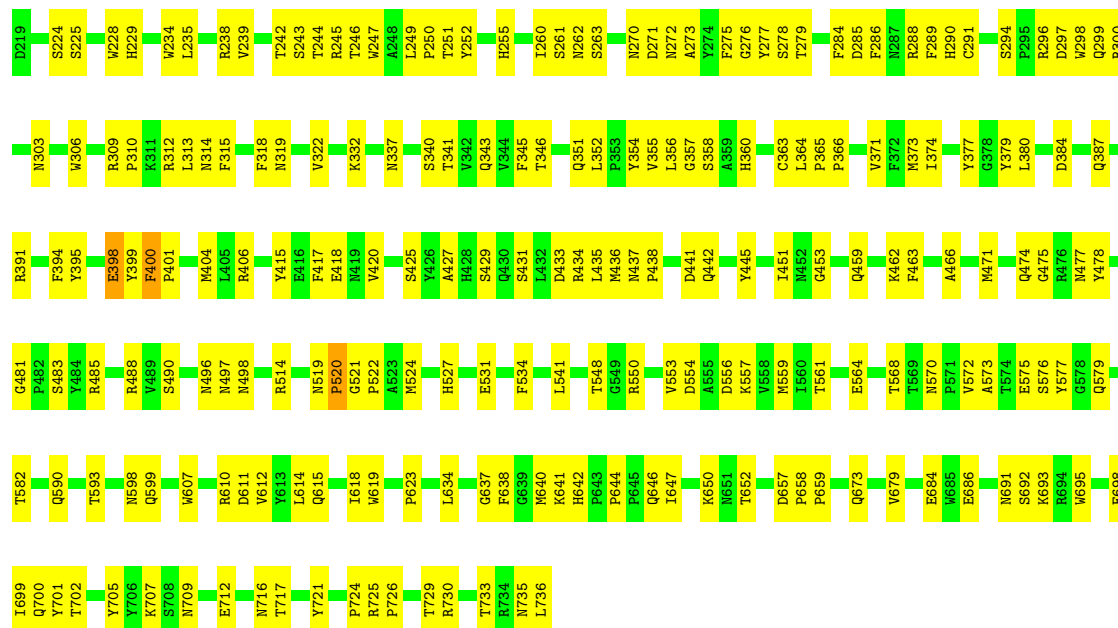
Chain Q: 58% 41%





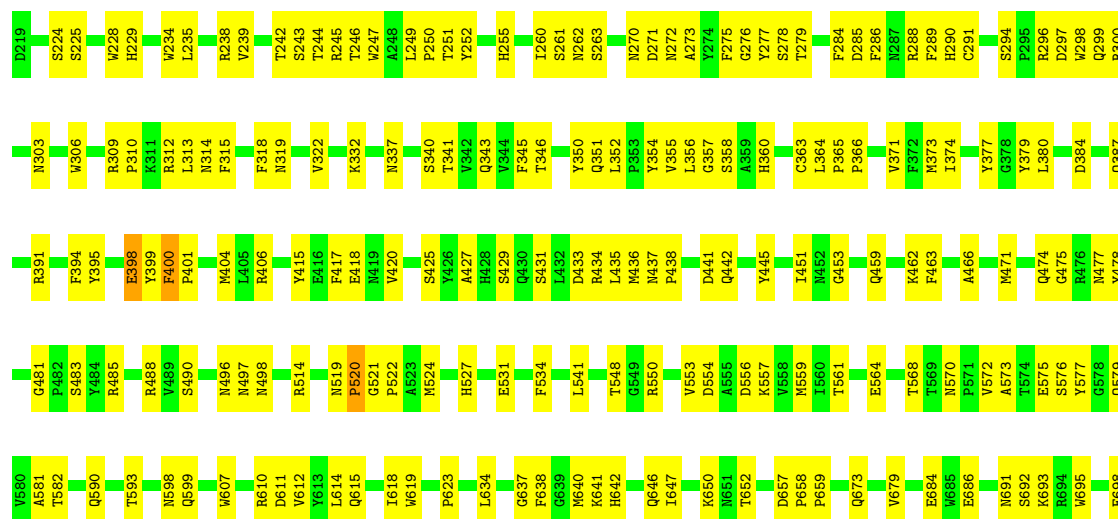
• Molecule 1: Capsid protein VP1

Chain R: 59% 40%



• Molecule 1: Capsid protein VP1

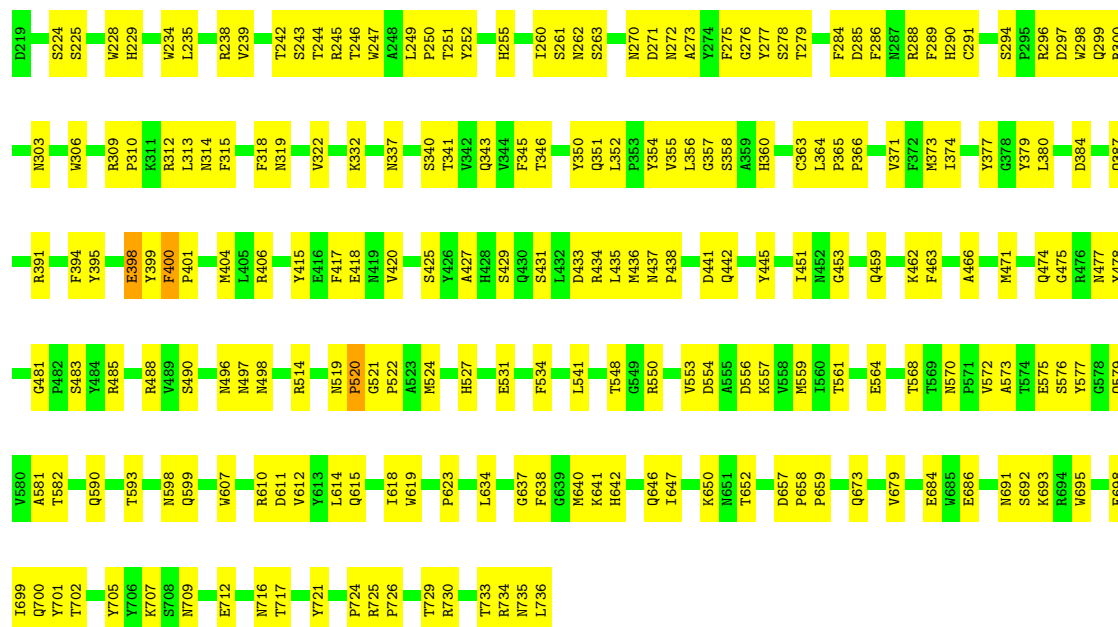
Chain S: 59% 41%





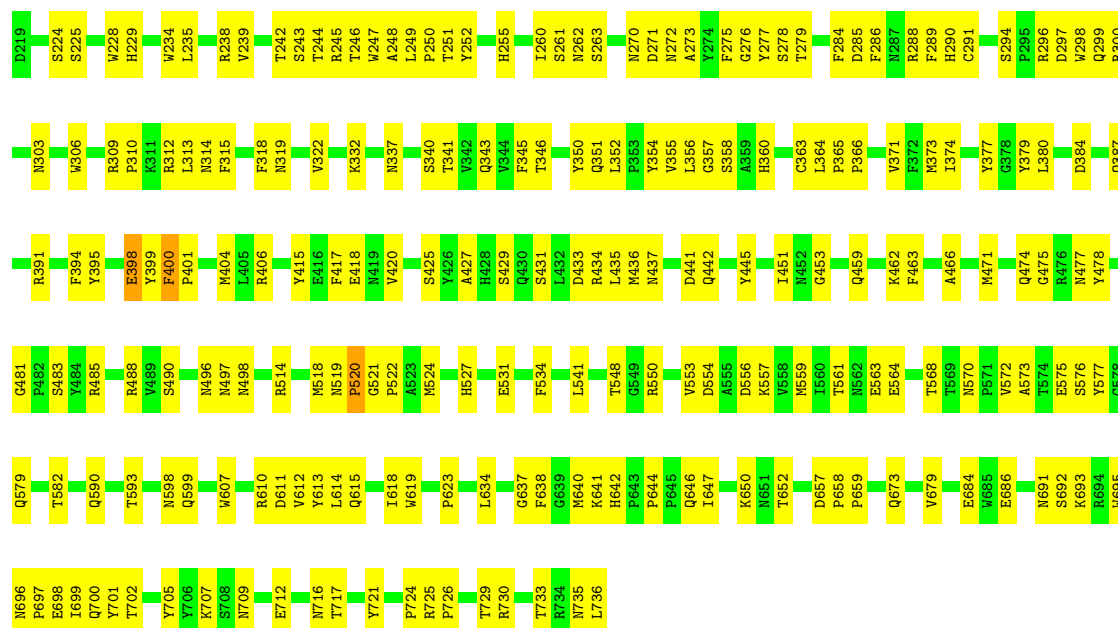
● Molecule 1: Capsid protein VP1

Chain T: 59% 41%



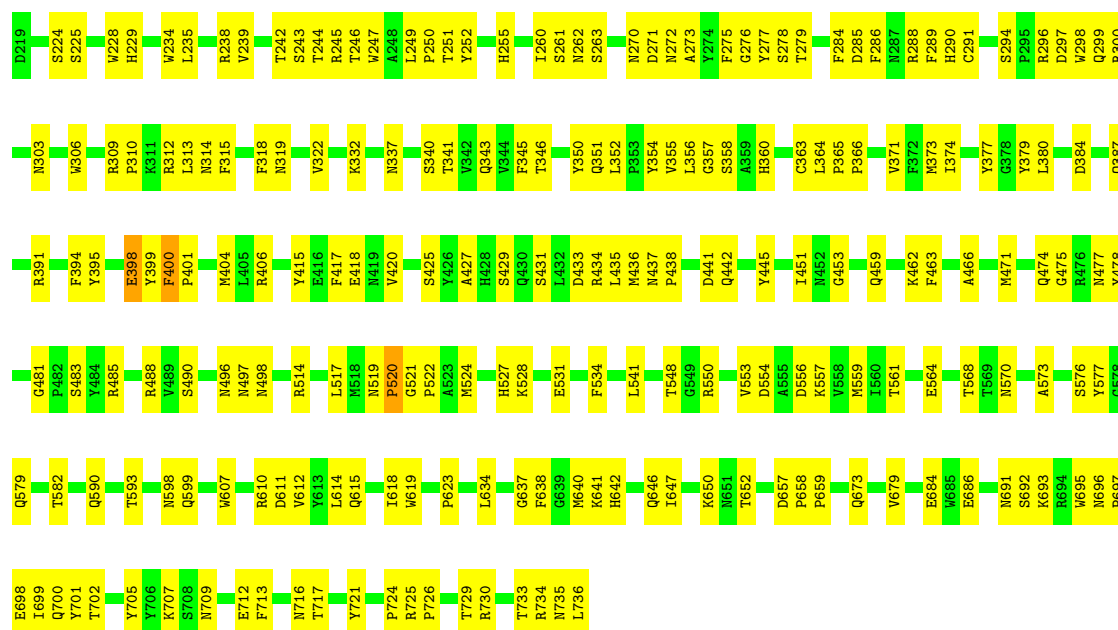
● Molecule 1: Capsid protein VP1

Chain U: 58% 41%



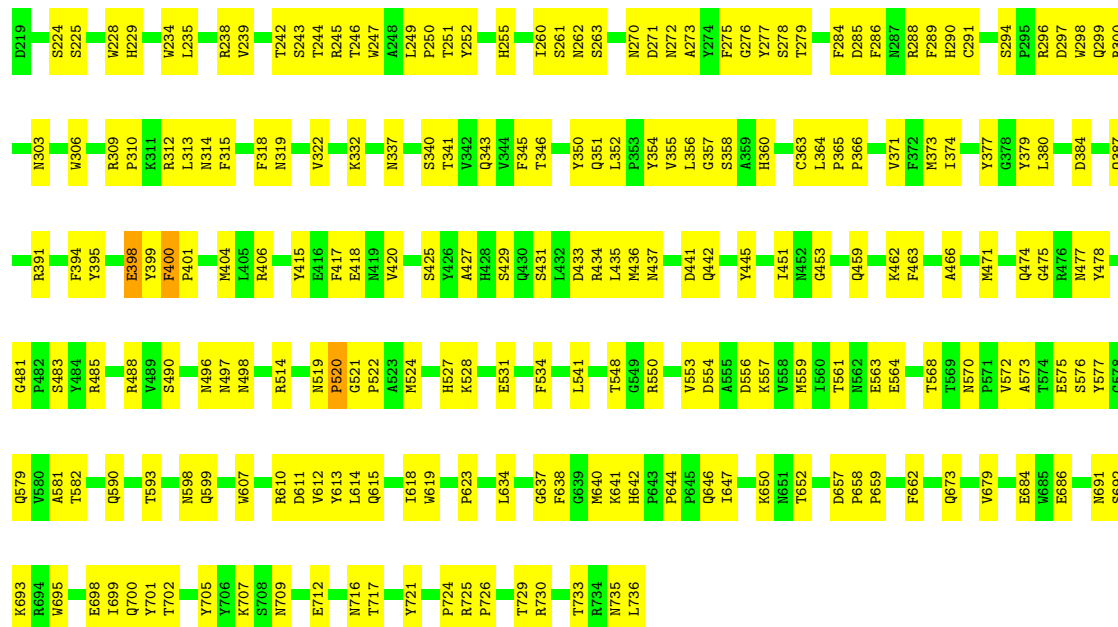
● Molecule 1: Capsid protein VP1

Chain V:  58% 41%



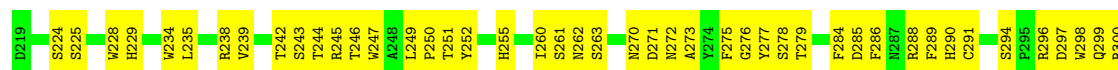
• Molecule 1: Capsid protein VP1

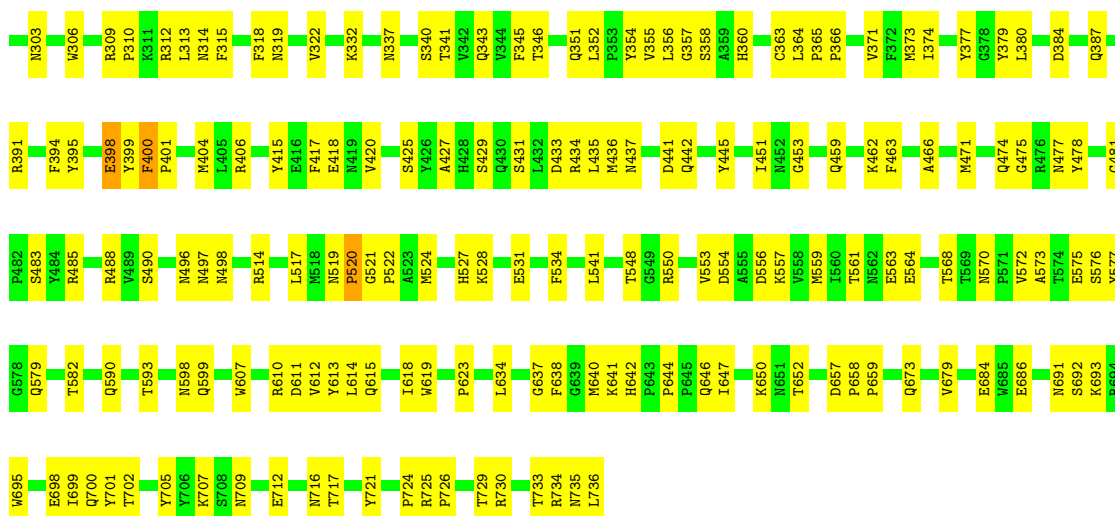
Chain W:  58% 41%



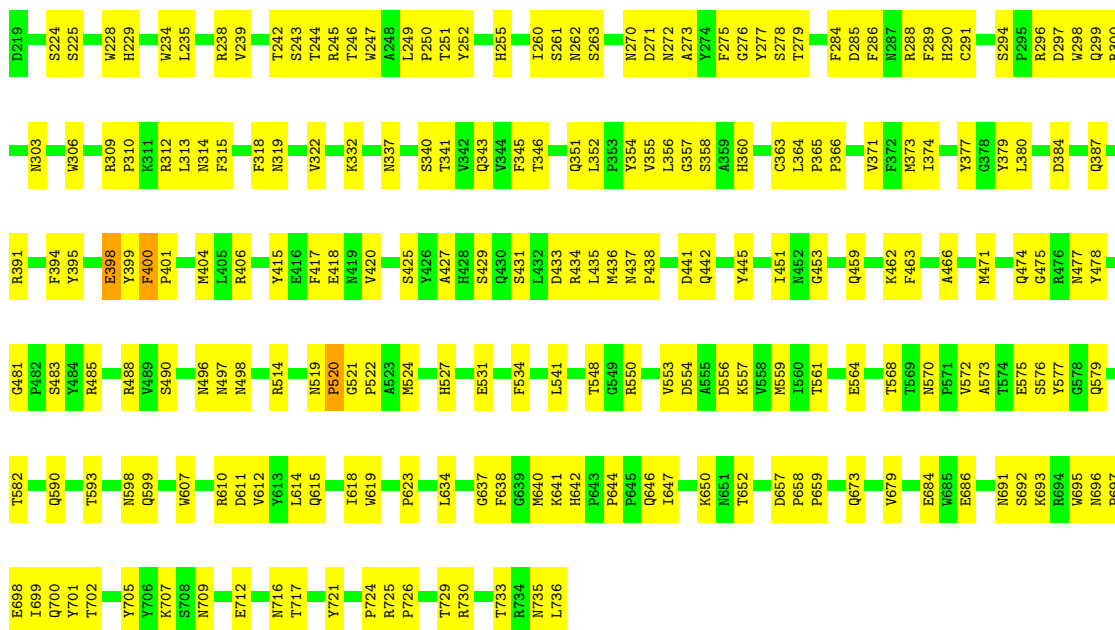
• Molecule 1: Capsid protein VP1

Chain X:  58% 41%

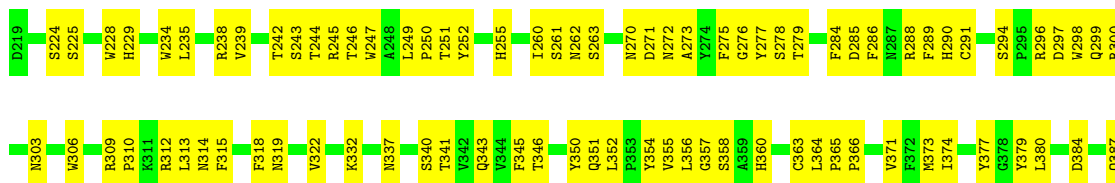


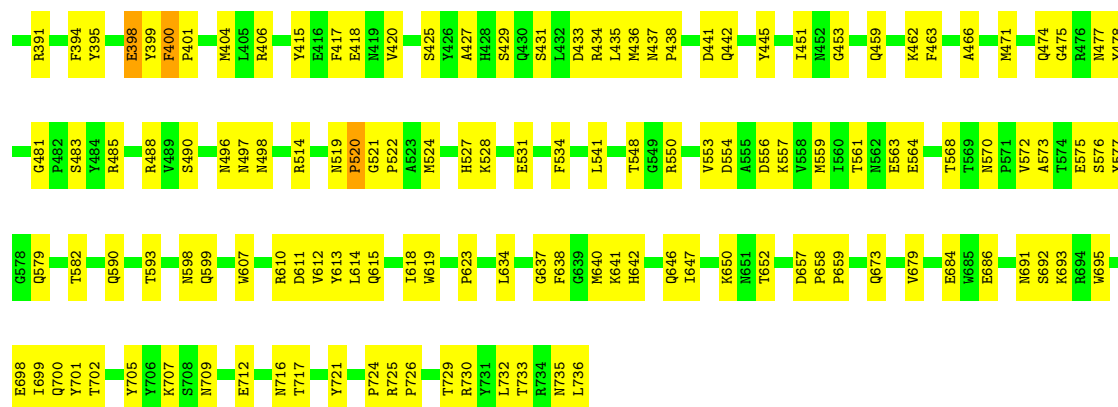


- Molecule 1: Capsid protein VP1



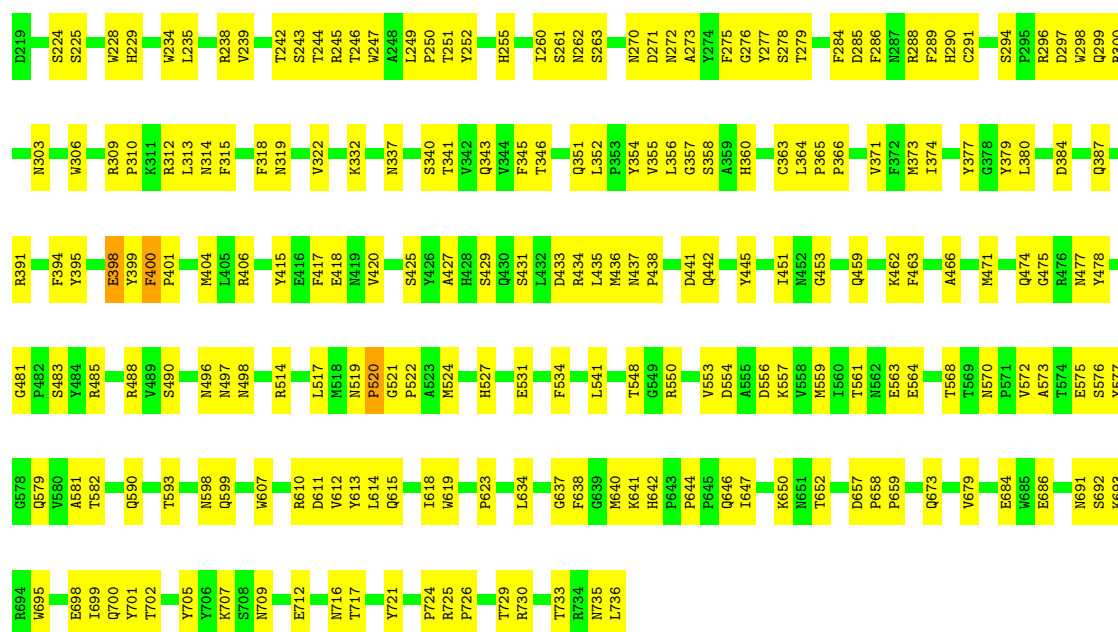
- Molecule 1: Capsid protein VP1





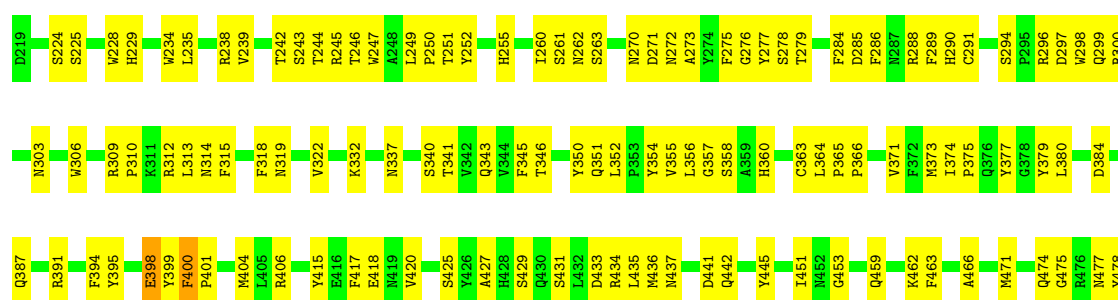
• Molecule 1: Capsid protein VP1

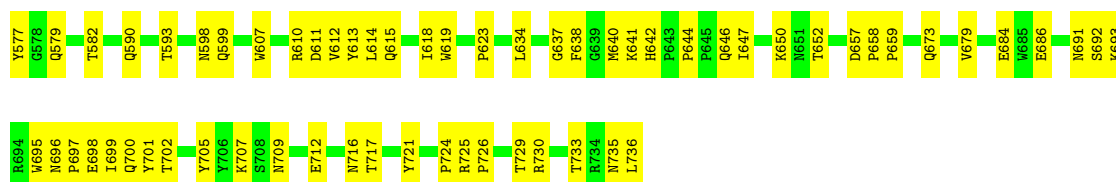
Chain 1: 58% 41%



• Molecule 1: Capsid protein VP1

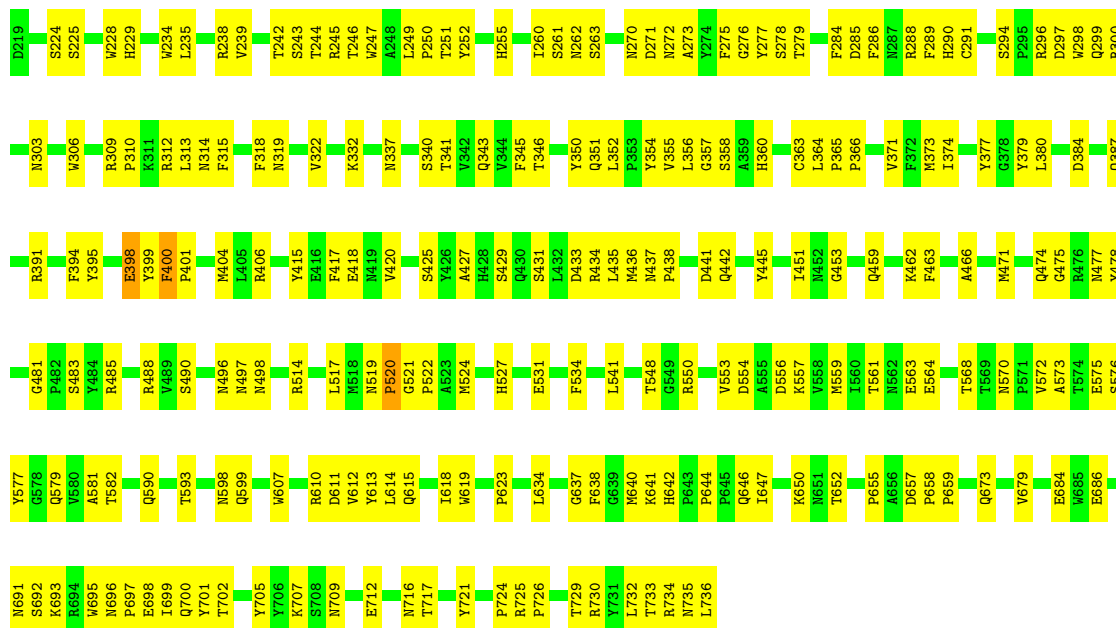
Chain 2: 58% 41%





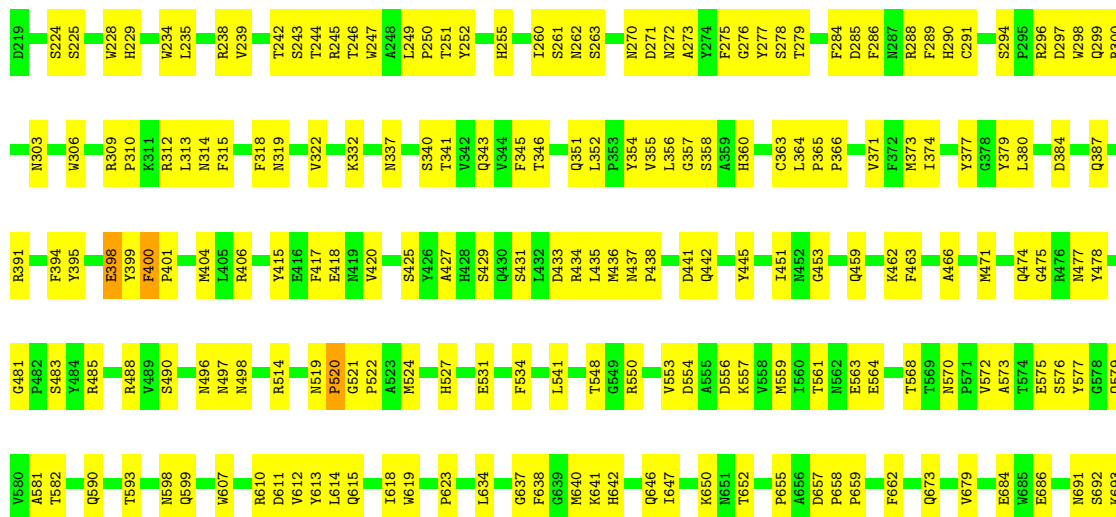
• Molecule 1: Capsid protein VP1

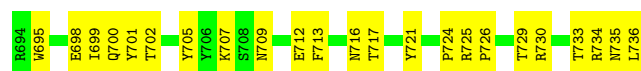
Chain 5: 57% 42%



• Molecule 1: Capsid protein VP1

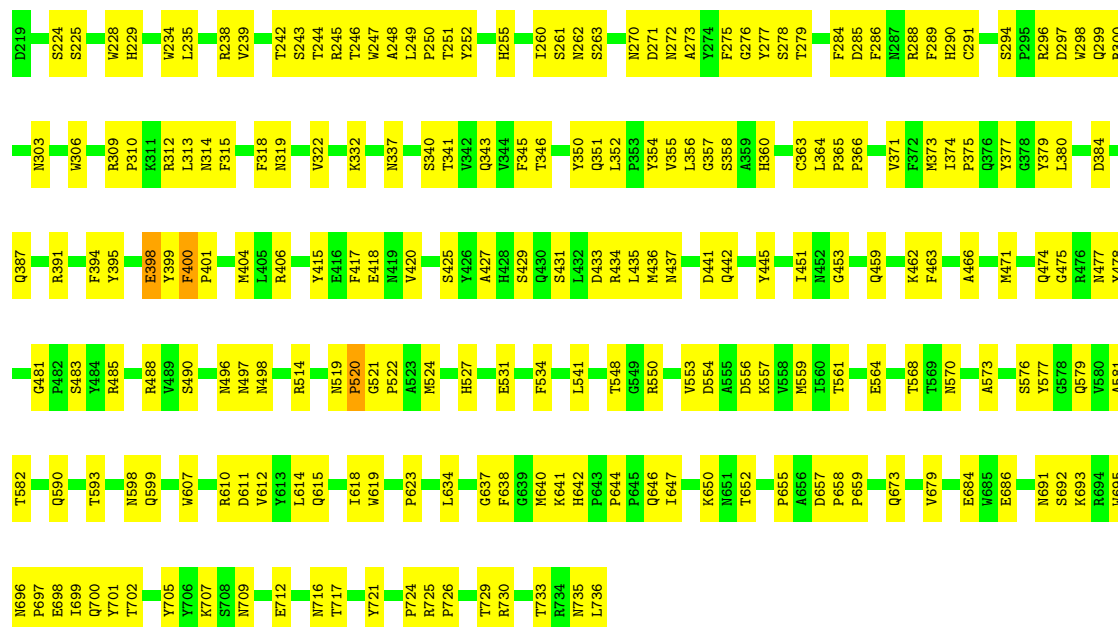
Chain 6: 58% 41%





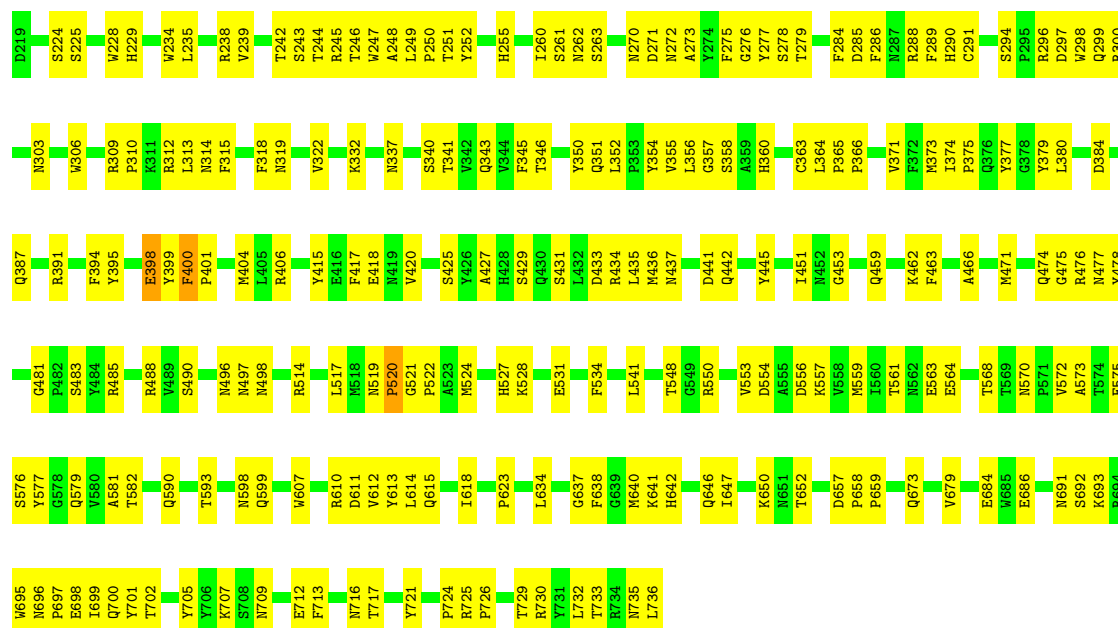
• Molecule 1: Capsid protein VP1

Chain a: 58% 41%



• Molecule 1: Capsid protein VP1

Chain b: 57% 42%



• Molecule 1: Capsid protein VP1

Opinion	Percentage
Doing a good job	58%
Doing a bad job	41%

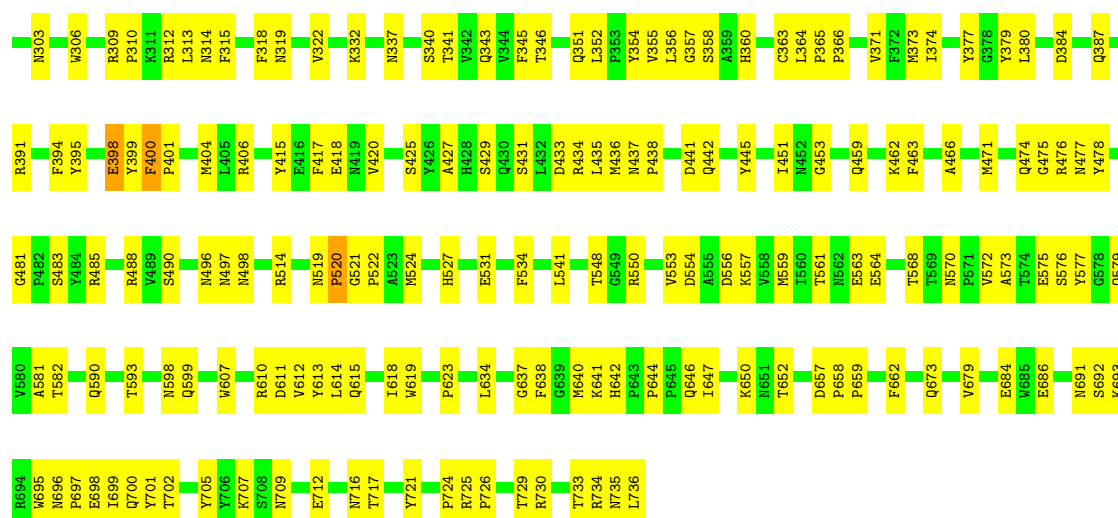


Response	Percentage
U.S. should take more action to protect the environment	59%
U.S. should take less action to protect the environment	41%



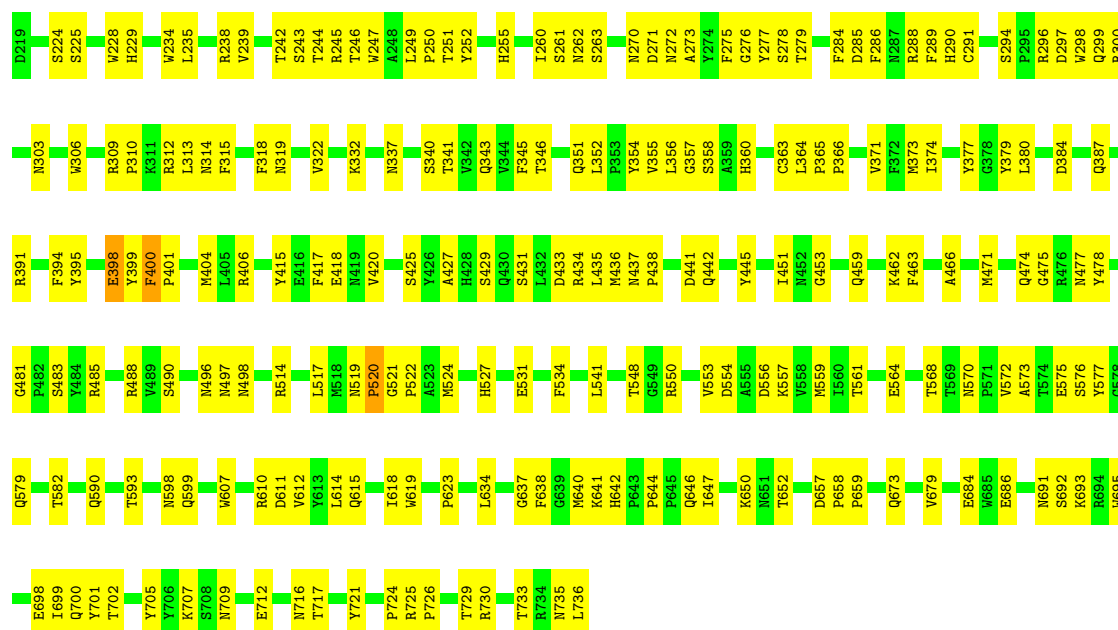
Category	Percentage
Satisfied	58%
Dissatisfied	42%





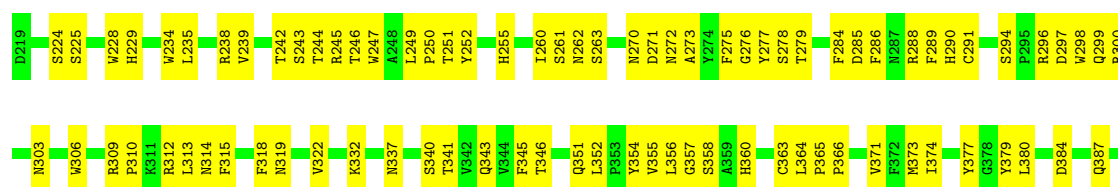
• Molecule 1: Capsid protein VP1

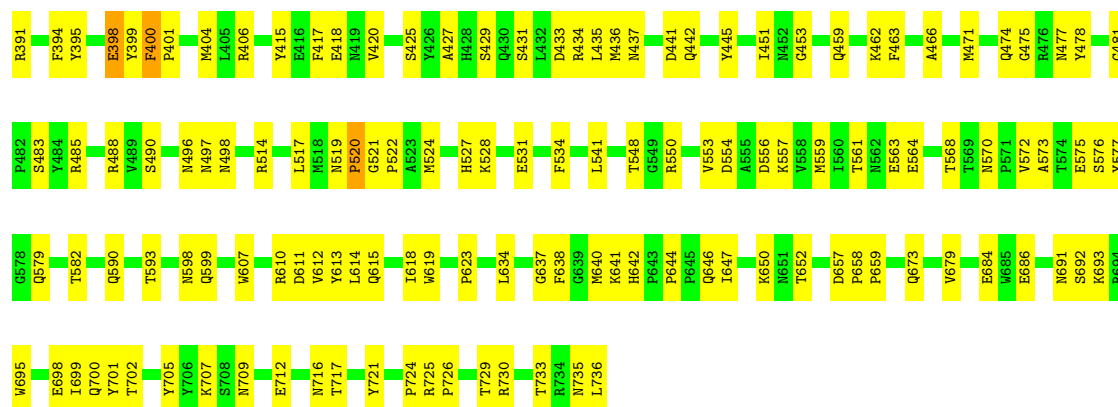
Chain f: 59% 40%



• Molecule 1: Capsid protein VP1

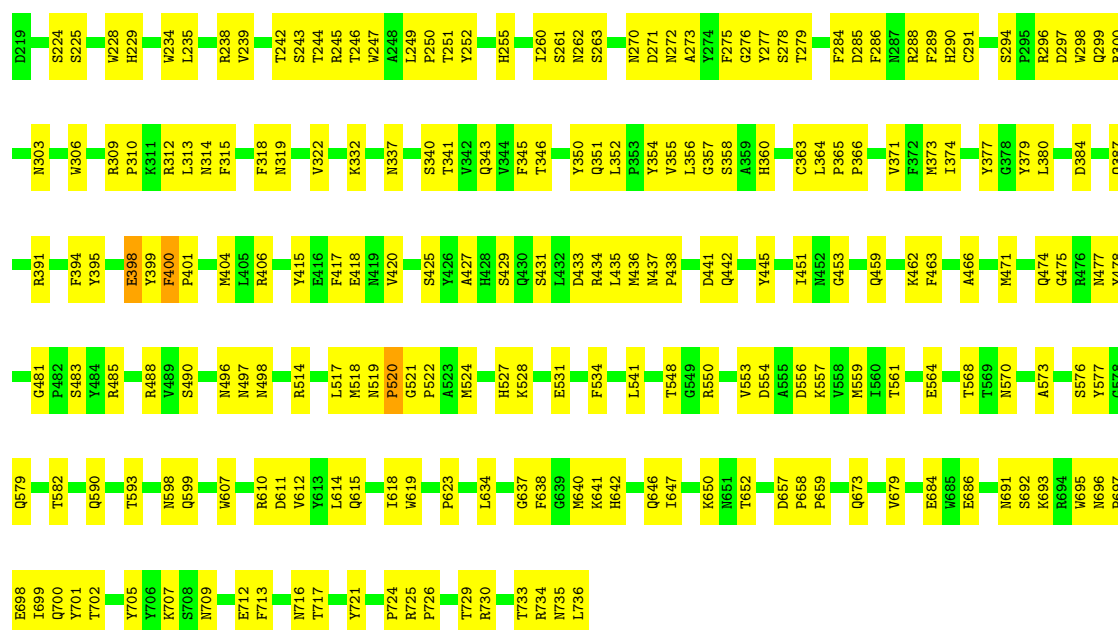
Chain g: 59% 41%





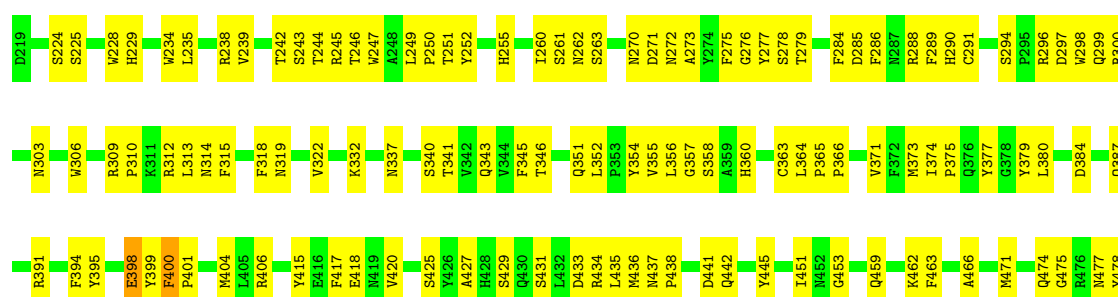
• Molecule 1: Capsid protein VP1

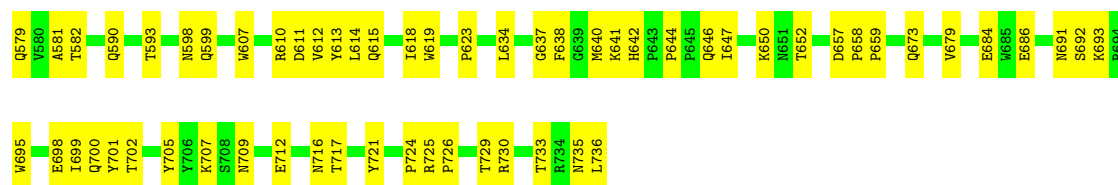
Chain h: 58% 41%



• Molecule 1: Capsid protein VP1

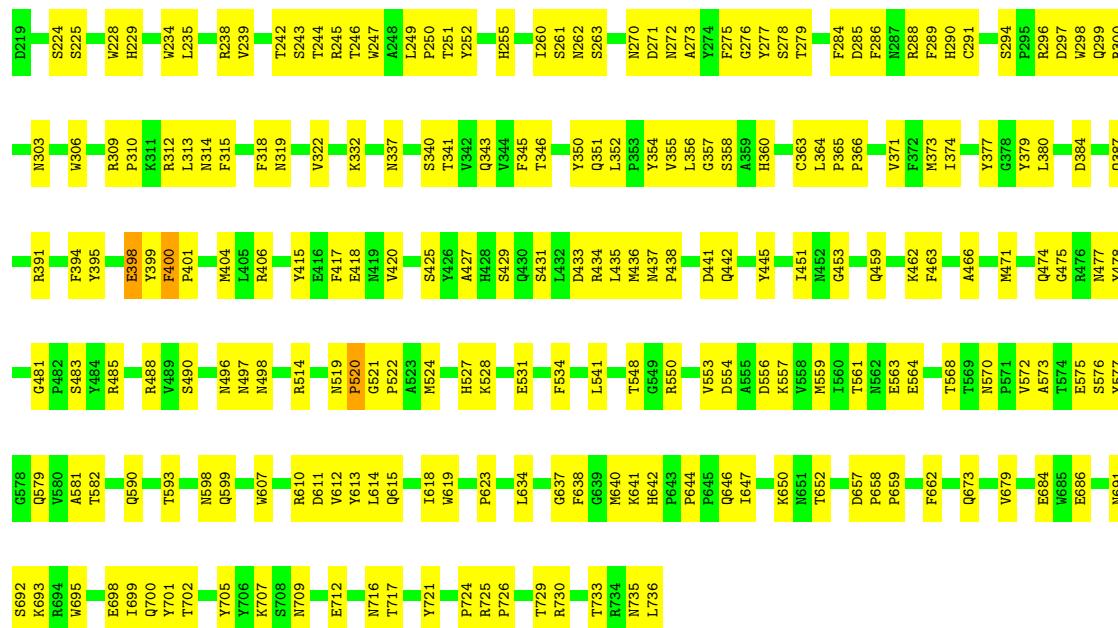
Chain i: 58% 42%





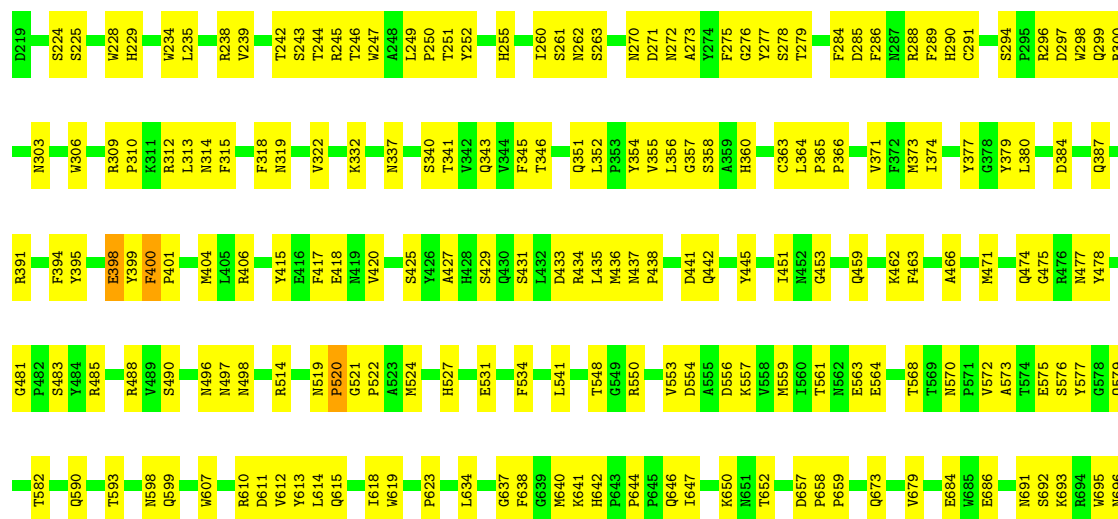
• Molecule 1: Capsid protein VP1

Chain l: 58% 41% .



• Molecule 1: Capsid protein VP1

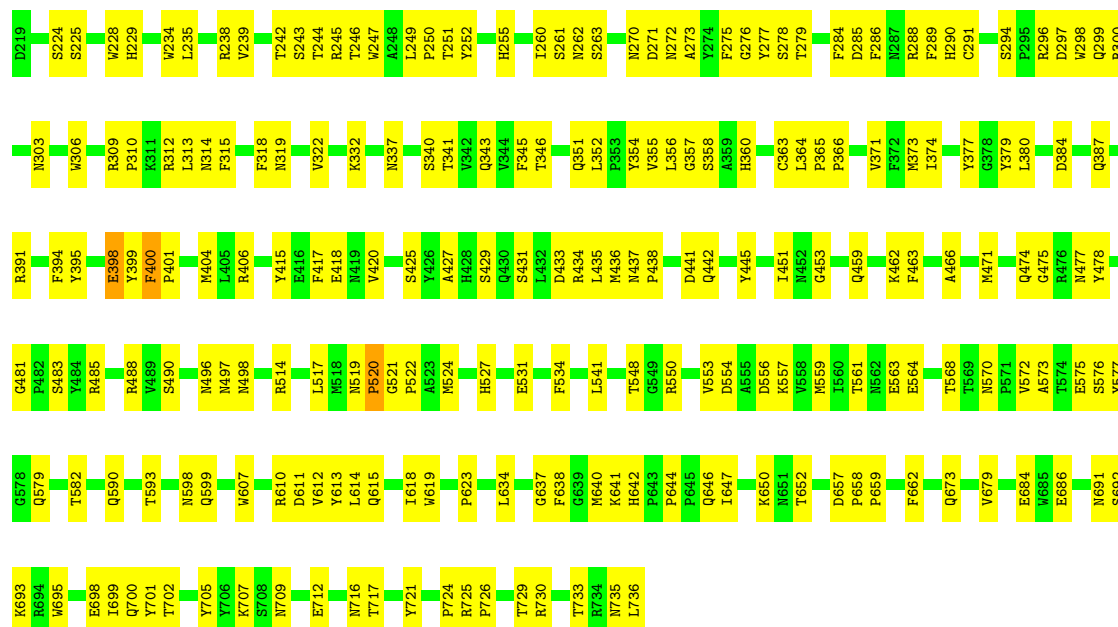
Chain m: 58% 41% .





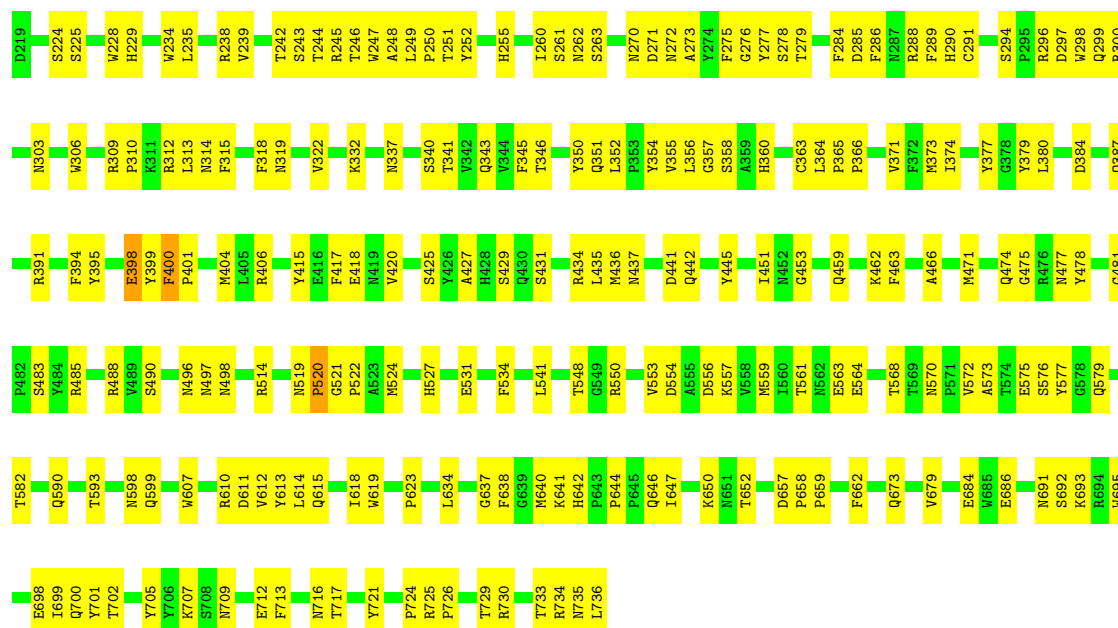
● Molecule 1: Capsid protein VP1

Chain n: 58% 41%



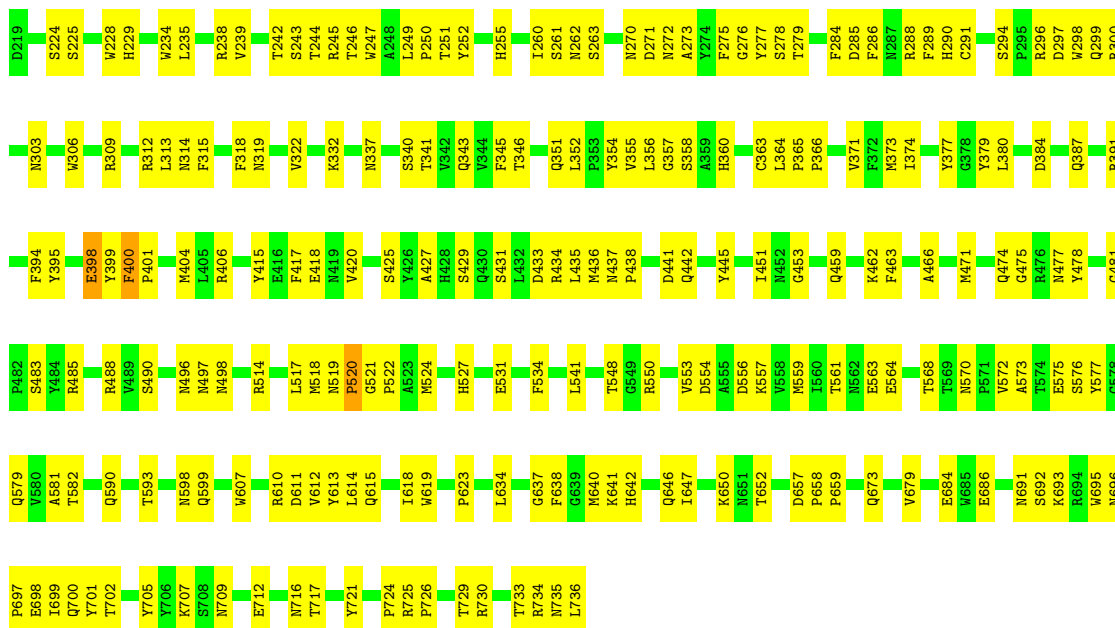
● Molecule 1: Capsid protein VP1

Chain o: 58% 41%



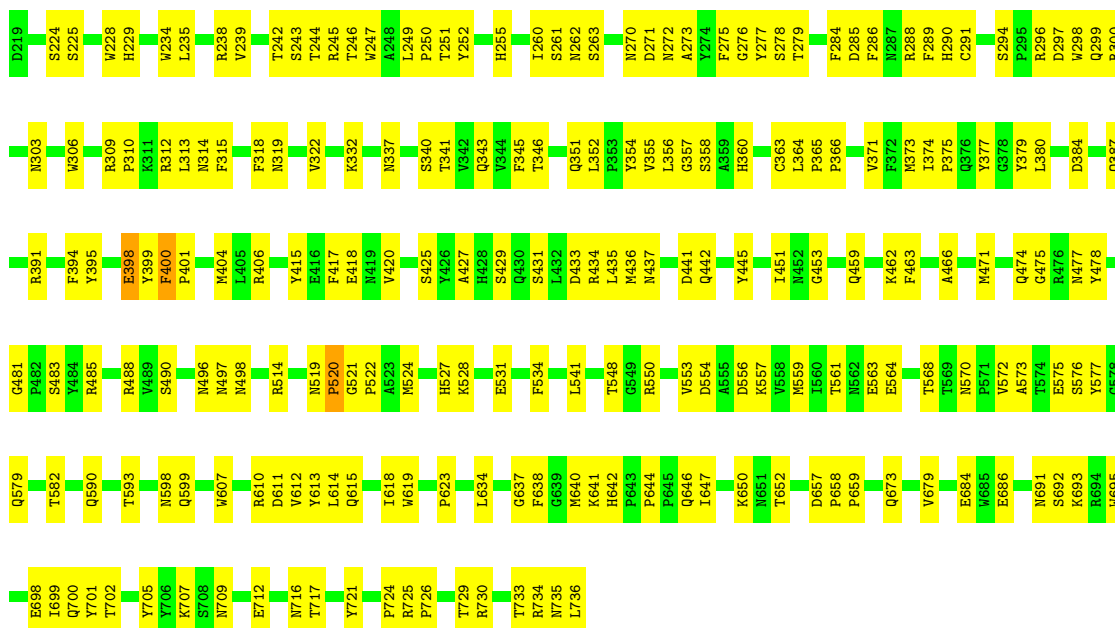
● Molecule 1: Capsid protein VP1

Chain p:  58% 41%



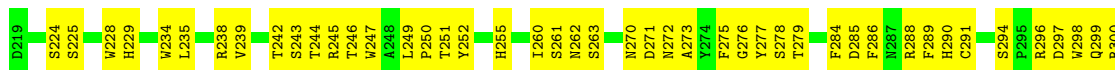
• Molecule 1: Capsid protein VP1

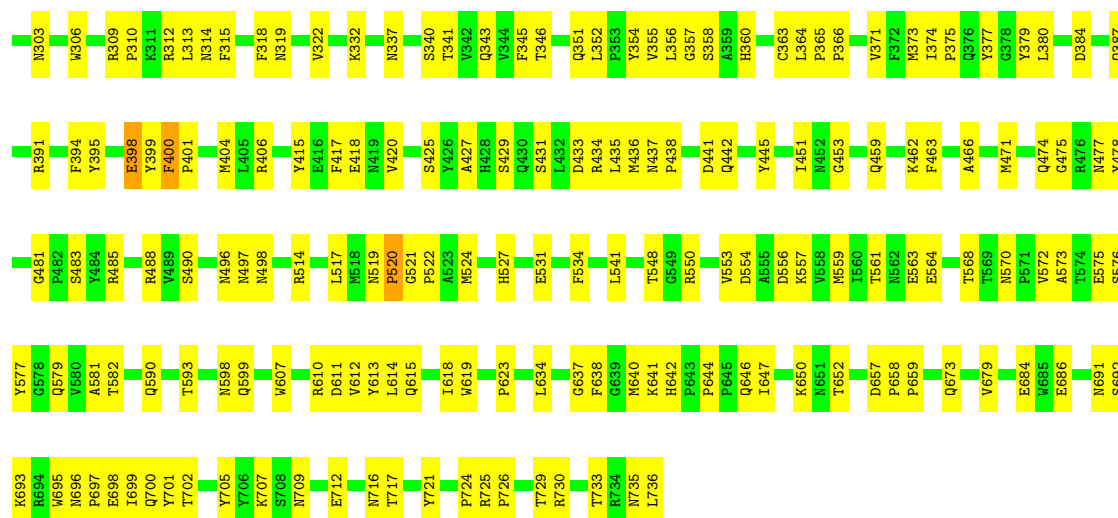
Chain q:  58% 41%



• Molecule 1: Capsid protein VP1

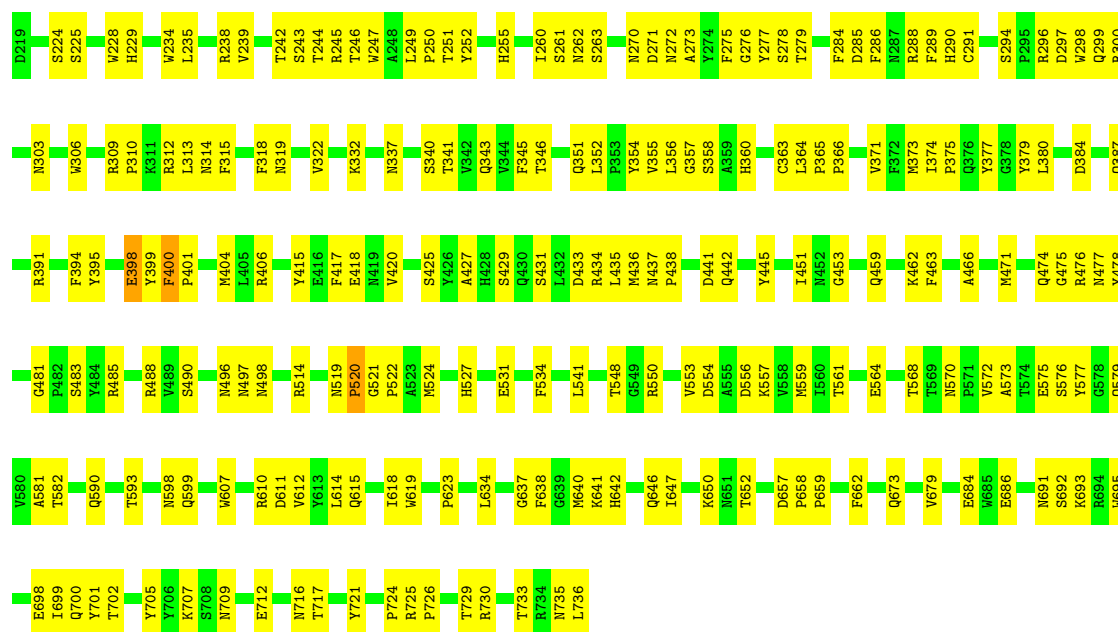
Chain r:  58% 42%





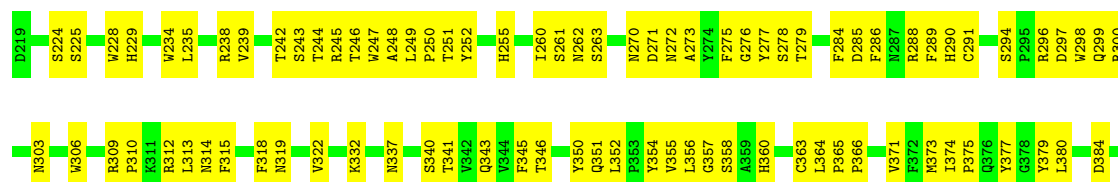
● Molecule 1: Capsid protein VP1

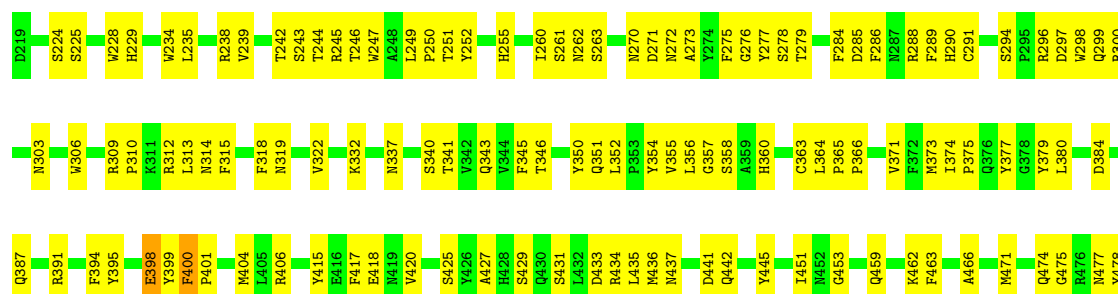
Chain s: 59% 41%



● Molecule 1: Capsid protein VP1

Chain t: 58% 42%

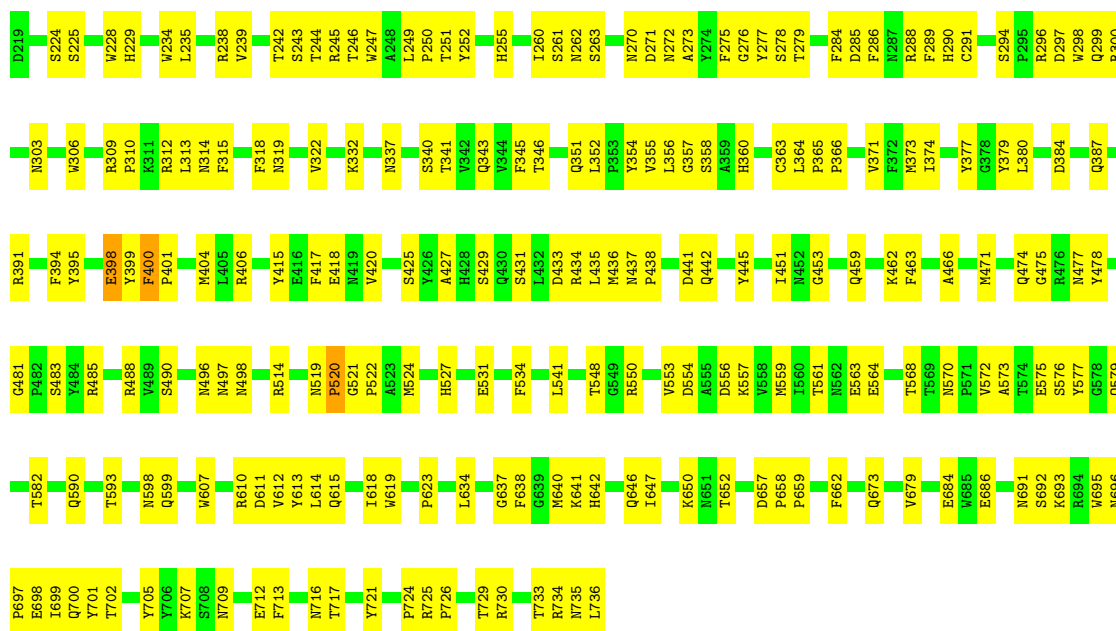






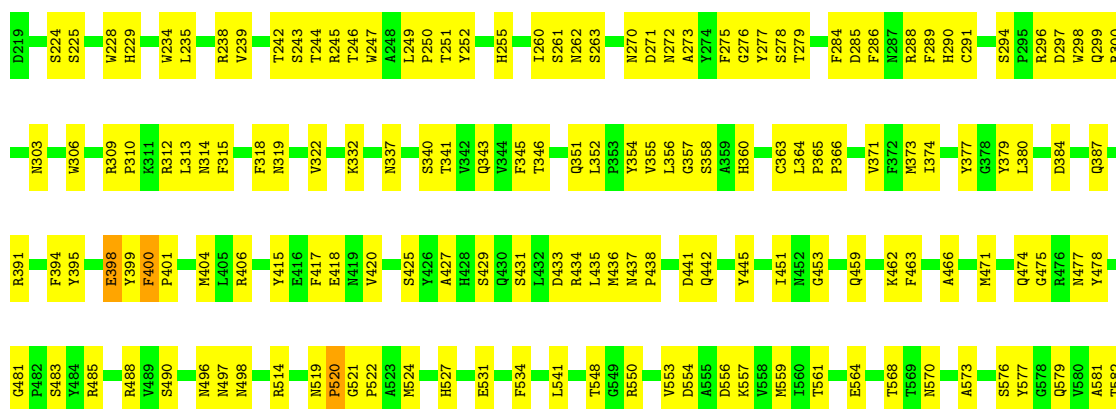
• Molecule 1: Capsid protein VP1

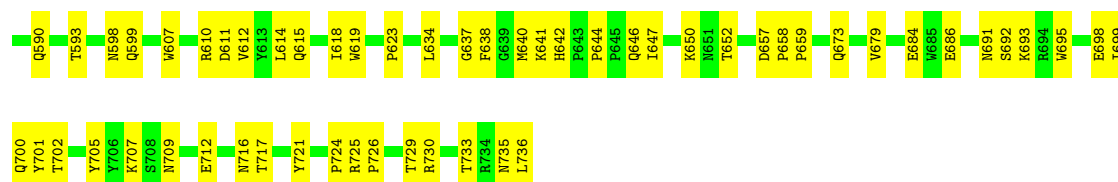
Chain w: 58% 41%



• Molecule 1: Capsid protein VP1

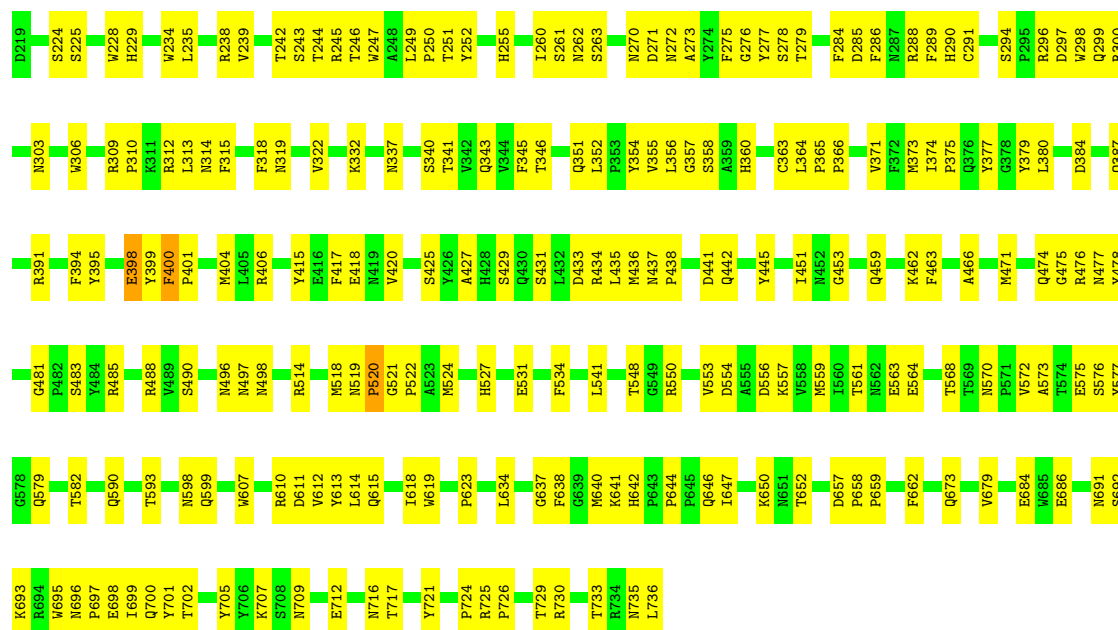
Chain x: 59% 40%





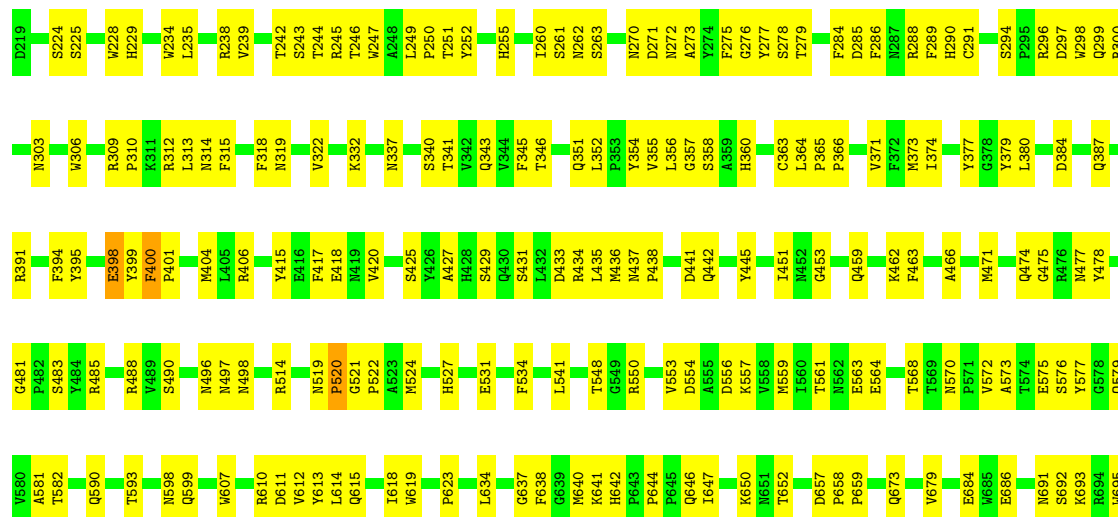
- Molecule 1: Capsid protein VP1

Chain y: 58% 42%



- Molecule 1: Capsid protein VP1

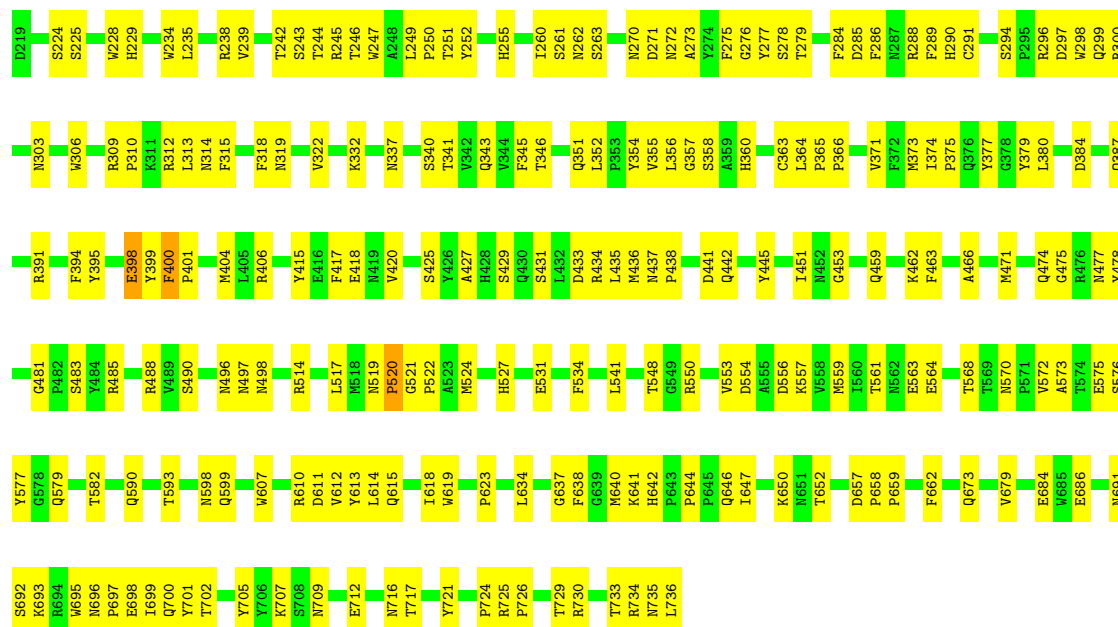
Chain z: 59% 41%





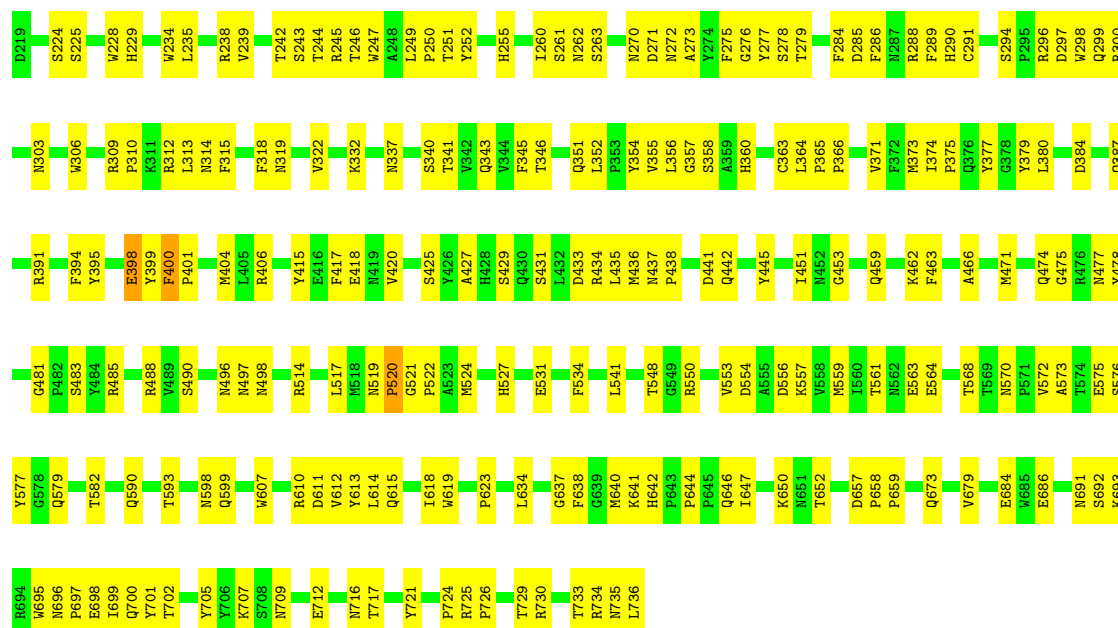
• Molecule 1: Capsid protein VP1

Chain 7: 58% 42%



• Molecule 1: Capsid protein VP1

Chain 8: 58% 42%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	150469	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	17.699	Depositor
Minimum map value	-9.359	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1	Depositor
Map size ($\text{\AA}$)	390.574, 390.574, 390.574	wwPDB
Map dimensions	401, 401, 401	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.97400004, 0.97400004, 0.97400004	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.46	0/4256	0.56	1/5800 (0.0%)
1	2	0.46	0/4256	0.56	1/5800 (0.0%)
1	3	0.46	0/4256	0.56	1/5800 (0.0%)
1	4	0.46	0/4256	0.56	2/5800 (0.0%)
1	5	0.46	0/4256	0.56	1/5800 (0.0%)
1	6	0.46	0/4256	0.56	1/5800 (0.0%)
1	7	0.46	0/4256	0.56	1/5800 (0.0%)
1	8	0.46	0/4256	0.56	1/5800 (0.0%)
1	A	0.46	0/4256	0.56	1/5800 (0.0%)
1	B	0.46	0/4256	0.56	1/5800 (0.0%)
1	C	0.46	0/4256	0.56	1/5800 (0.0%)
1	D	0.46	0/4256	0.56	2/5800 (0.0%)
1	E	0.46	0/4256	0.56	1/5800 (0.0%)
1	F	0.46	0/4256	0.56	1/5800 (0.0%)
1	G	0.46	0/4256	0.56	1/5800 (0.0%)
1	H	0.46	0/4256	0.56	1/5800 (0.0%)
1	I	0.46	0/4256	0.56	1/5800 (0.0%)
1	J	0.46	0/4256	0.56	2/5800 (0.0%)
1	K	0.46	0/4256	0.56	2/5800 (0.0%)
1	L	0.46	0/4256	0.56	2/5800 (0.0%)
1	M	0.46	0/4256	0.56	2/5800 (0.0%)
1	N	0.46	0/4256	0.56	2/5800 (0.0%)
1	O	0.46	0/4256	0.56	2/5800 (0.0%)
1	P	0.46	0/4256	0.56	1/5800 (0.0%)
1	Q	0.46	0/4256	0.56	1/5800 (0.0%)
1	R	0.46	0/4256	0.56	1/5800 (0.0%)
1	S	0.46	0/4256	0.56	1/5800 (0.0%)
1	T	0.46	0/4256	0.56	1/5800 (0.0%)
1	U	0.46	0/4256	0.56	2/5800 (0.0%)
1	V	0.46	0/4256	0.56	1/5800 (0.0%)
1	W	0.46	0/4256	0.56	1/5800 (0.0%)
1	X	0.46	0/4256	0.56	1/5800 (0.0%)
1	Y	0.46	0/4256	0.56	1/5800 (0.0%)
1	Z	0.46	0/4256	0.56	1/5800 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.46	0/4256	0.56	1/5800 (0.0%)
1	b	0.46	0/4256	0.56	1/5800 (0.0%)
1	c	0.46	0/4256	0.56	2/5800 (0.0%)
1	d	0.46	0/4256	0.56	1/5800 (0.0%)
1	e	0.46	0/4256	0.56	1/5800 (0.0%)
1	f	0.46	0/4256	0.56	1/5800 (0.0%)
1	g	0.46	0/4256	0.56	1/5800 (0.0%)
1	h	0.46	0/4256	0.56	2/5800 (0.0%)
1	i	0.46	0/4256	0.56	1/5800 (0.0%)
1	j	0.46	0/4256	0.56	1/5800 (0.0%)
1	k	0.46	0/4256	0.56	1/5800 (0.0%)
1	l	0.46	0/4256	0.56	1/5800 (0.0%)
1	m	0.46	0/4256	0.56	1/5800 (0.0%)
1	n	0.46	0/4256	0.56	1/5800 (0.0%)
1	o	0.46	0/4256	0.56	1/5800 (0.0%)
1	p	0.46	0/4256	0.56	2/5800 (0.0%)
1	q	0.46	0/4256	0.56	1/5800 (0.0%)
1	r	0.46	0/4256	0.56	1/5800 (0.0%)
1	s	0.46	0/4256	0.56	1/5800 (0.0%)
1	t	0.46	0/4256	0.56	1/5800 (0.0%)
1	u	0.46	0/4256	0.56	1/5800 (0.0%)
1	v	0.46	0/4256	0.56	1/5800 (0.0%)
1	w	0.46	0/4256	0.56	1/5800 (0.0%)
1	x	0.46	0/4256	0.56	1/5800 (0.0%)
1	y	0.46	0/4256	0.56	2/5800 (0.0%)
1	z	0.46	0/4256	0.56	1/5800 (0.0%)
All	All	0.46	0/255360	0.56	73/348000 (0.0%)

There are no bond length outliers.

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	398	GLU	N-CA-C	5.67	119.45	112.54
1	U	398	GLU	N-CA-C	5.67	119.45	112.54
1	4	398	GLU	N-CA-C	5.67	119.45	112.54
1	m	398	GLU	N-CA-C	5.66	119.45	112.54
1	q	398	GLU	N-CA-C	5.66	119.45	112.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	4131	0	3884	247	0
1	2	4131	0	3884	248	0
1	3	4131	0	3884	241	0
1	4	4131	0	3884	247	0
1	5	4131	0	3884	251	0
1	6	4131	0	3884	245	0
1	7	4131	0	3884	249	0
1	8	4131	0	3884	247	0
1	A	4131	0	3884	245	0
1	B	4131	0	3884	243	0
1	C	4131	0	3884	249	0
1	D	4131	0	3884	247	0
1	E	4131	0	3884	248	0
1	F	4131	0	3884	243	0
1	G	4131	0	3884	243	0
1	H	4131	0	3884	245	0
1	I	4131	0	3884	246	0
1	J	4131	0	3884	243	0
1	K	4131	0	3884	251	0
1	L	4131	0	3884	243	0
1	M	4131	0	3884	245	0
1	N	4131	0	3884	245	0
1	O	4131	0	3884	250	0
1	P	4131	0	3884	249	0
1	Q	4131	0	3884	246	0
1	R	4131	0	3884	241	0
1	S	4131	0	3884	244	0
1	T	4131	0	3884	243	0
1	U	4131	0	3884	245	0
1	V	4131	0	3884	244	0
1	W	4131	0	3884	246	0
1	X	4131	0	3884	246	0
1	Y	4131	0	3884	240	0
1	Z	4131	0	3884	247	0
1	a	4131	0	3884	246	0
1	b	4131	0	3884	251	0
1	c	4131	0	3884	248	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	d	4131	0	3884	239	0
1	e	4131	0	3884	248	0
1	f	4131	0	3884	238	0
1	g	4131	0	3884	245	0
1	h	4131	0	3884	245	0
1	i	4131	0	3884	245	0
1	j	4131	0	3884	244	0
1	k	4131	0	3884	244	0
1	l	4131	0	3884	248	0
1	m	4131	0	3884	242	0
1	n	4131	0	3884	243	0
1	o	4131	0	3884	246	0
1	p	4131	0	3884	245	0
1	q	4131	0	3884	245	0
1	r	4131	0	3884	243	0
1	s	4131	0	3884	245	0
1	t	4131	0	3884	246	0
1	u	4131	0	3884	250	0
1	v	4131	0	3884	250	0
1	w	4131	0	3884	245	0
1	x	4131	0	3884	241	0
1	y	4131	0	3884	250	0
1	z	4131	0	3884	245	0
All	All	247860	0	233040	11887	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 25.

The worst 5 of 11887 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:N:559:MET:SD	1:N:726:PRO:HD3	1.26	1.75
1:I:559:MET:SD	1:I:726:PRO:HD3	1.26	1.75
1:b:559:MET:SD	1:b:726:PRO:HD3	1.26	1.75
1:P:559:MET:SD	1:P:726:PRO:HD3	1.26	1.75
1:6:559:MET:SD	1:6:726:PRO:HD3	1.26	1.75

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	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	2	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	3	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	4	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	5	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	6	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	7	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	8	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	A	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	B	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	C	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	D	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	E	516/518 (100%)	504 (98%)	11 (2%)	1 (0%)	43	71
1	F	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	G	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	H	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	I	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	J	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	K	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	L	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	M	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	N	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	O	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	P	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	Q	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	S	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	T	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	U	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	V	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	W	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	X	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	Y	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	Z	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	a	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	b	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	c	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	d	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	e	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	f	516/518 (100%)	504 (98%)	11 (2%)	1 (0%)	43	71
1	g	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	h	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	i	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	j	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	k	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	l	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	m	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	n	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	o	516/518 (100%)	504 (98%)	11 (2%)	1 (0%)	43	71
1	p	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	q	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	r	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	s	516/518 (100%)	504 (98%)	11 (2%)	1 (0%)	43	71
1	t	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	u	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	v	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	w	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	x	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	y	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
1	z	516/518 (100%)	503 (98%)	12 (2%)	1 (0%)	43	71
All	All	30960/31080 (100%)	30184 (98%)	716 (2%)	60 (0%)	44	71

5 of 60 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	520	PRO
1	B	520	PRO
1	C	520	PRO
1	D	520	PRO
1	E	520	PRO

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%)	451 (100%)	2 (0%)	84	94
1	2	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	3	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	4	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	5	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	6	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	7	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	8	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	A	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	B	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	C	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	D	453/453 (100%)	451 (100%)	2 (0%)	84	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	F	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	G	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	H	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	I	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	J	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	K	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	L	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	M	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	N	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	O	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	P	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	Q	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	R	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	S	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	T	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	U	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	V	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	W	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	X	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	Y	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	Z	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	a	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	b	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	c	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	d	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	e	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	f	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	g	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	h	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	i	453/453 (100%)	451 (100%)	2 (0%)	84	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	j	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	k	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	l	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	m	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	n	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	o	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	p	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	q	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	r	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	s	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	t	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	u	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	v	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	w	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	x	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	y	453/453 (100%)	451 (100%)	2 (0%)	84	94
1	z	453/453 (100%)	451 (100%)	2 (0%)	84	94
All	All	27180/27180 (100%)	27060 (100%)	120 (0%)	81	94

5 of 120 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	3	400	PHE
1	x	239	VAL
1	d	400	PHE
1	w	400	PHE
1	8	239	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1031 such sidechains are listed below:

Mol	Chain	Res	Type
1	v	691	ASN
1	x	459	GLN
1	v	673	GLN
1	W	527	HIS

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Mol	Chain	Res	Type
1	W	255	HIS

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.

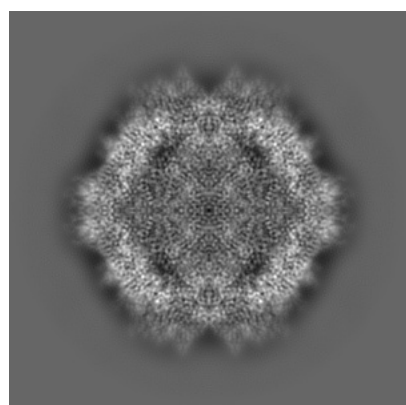
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23973. These allow visual inspection of the internal detail of the map and identification of artifacts.

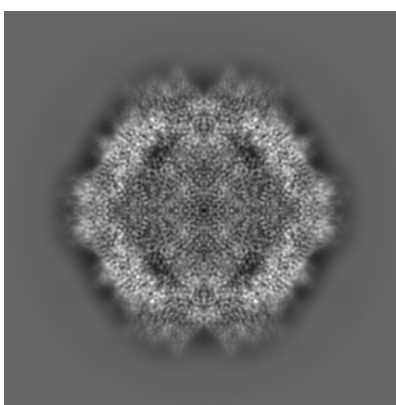
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

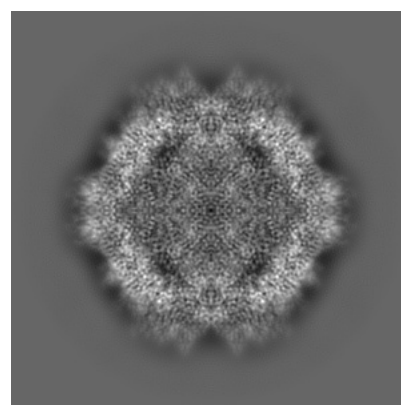
6.1.1 Primary map



X



Y

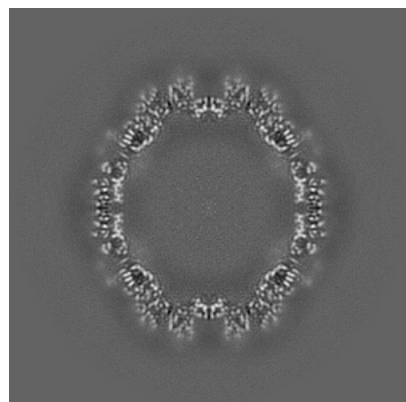


Z

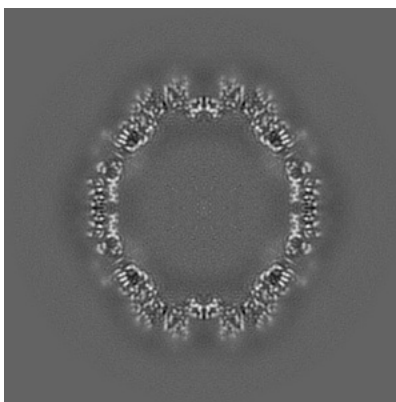
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

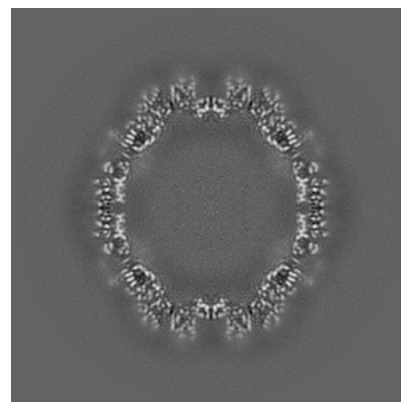
6.2.1 Primary map



X Index: 200



Y Index: 200

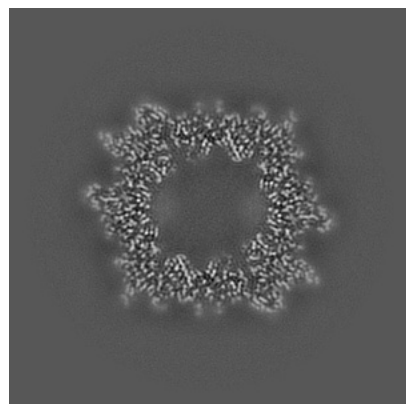


Z Index: 200

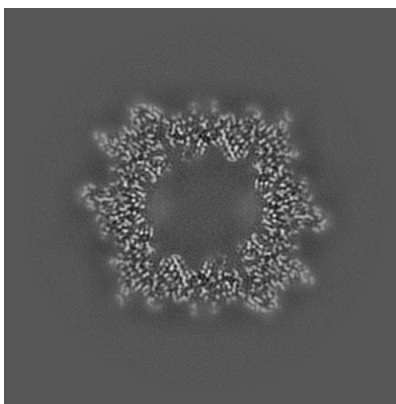
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

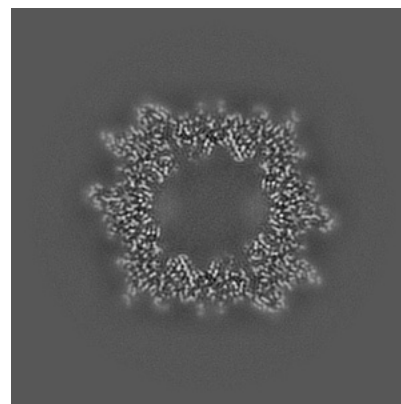
6.3.1 Primary map



X Index: 267



Y Index: 267

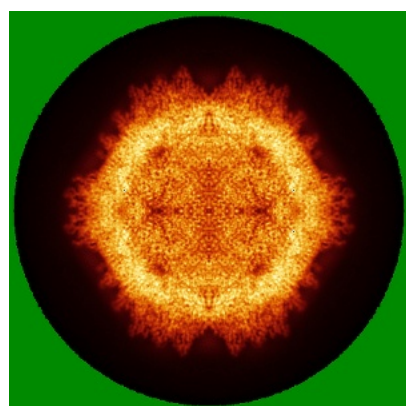


Z Index: 267

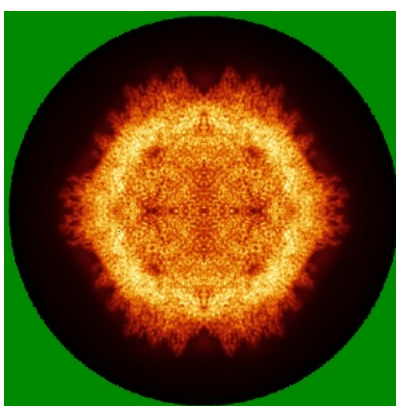
The images above show the largest variance slices of the map in three orthogonal directions.

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

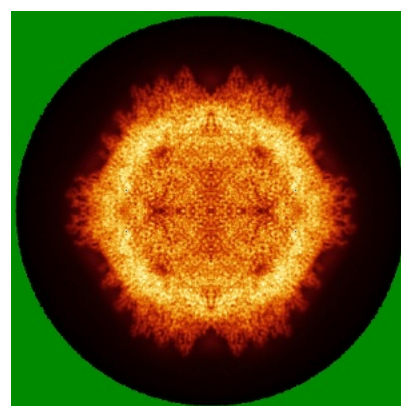
6.4.1 Primary map



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.

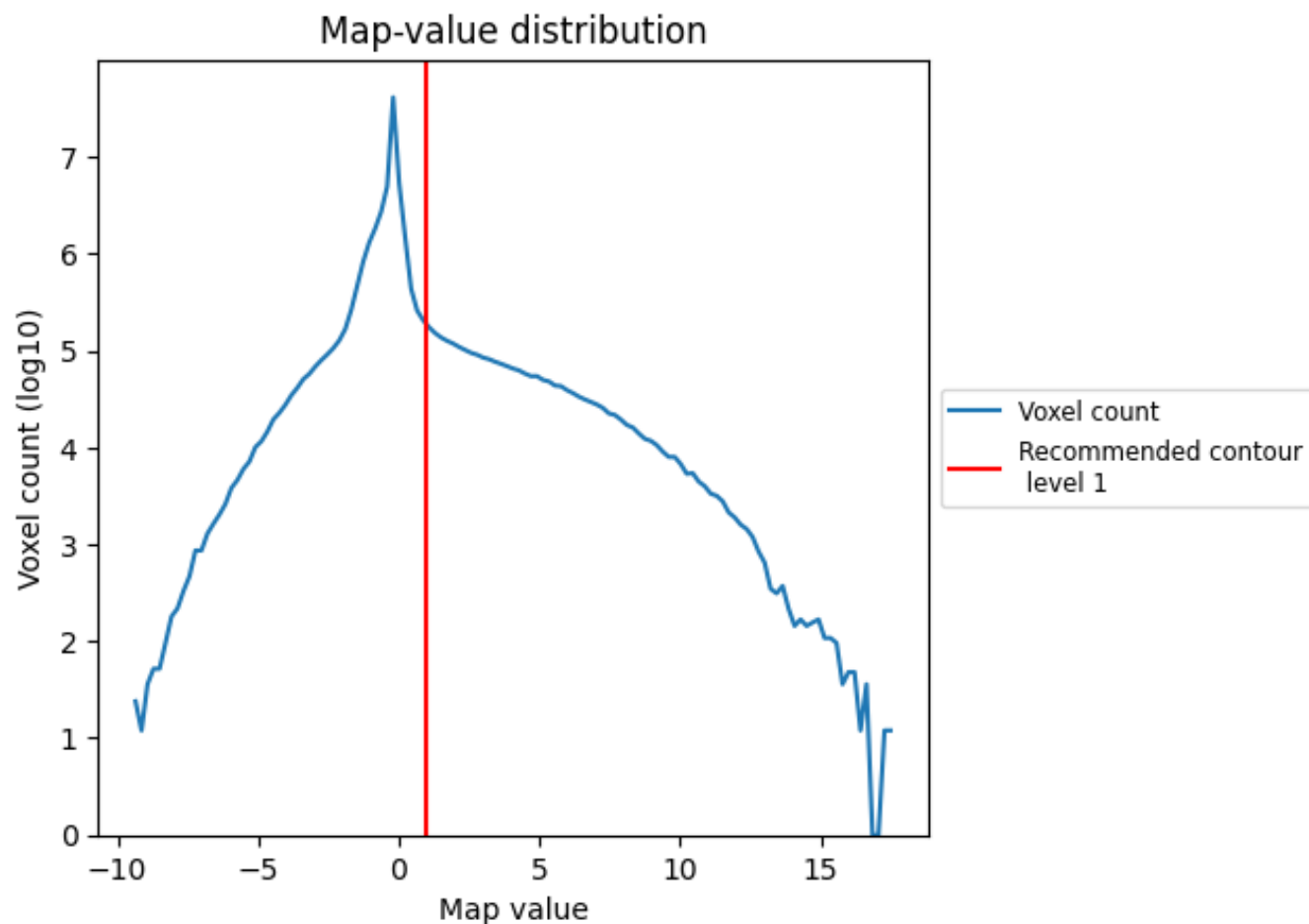
6.6 Mask visualisation

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

7 Map analysis [i](#)

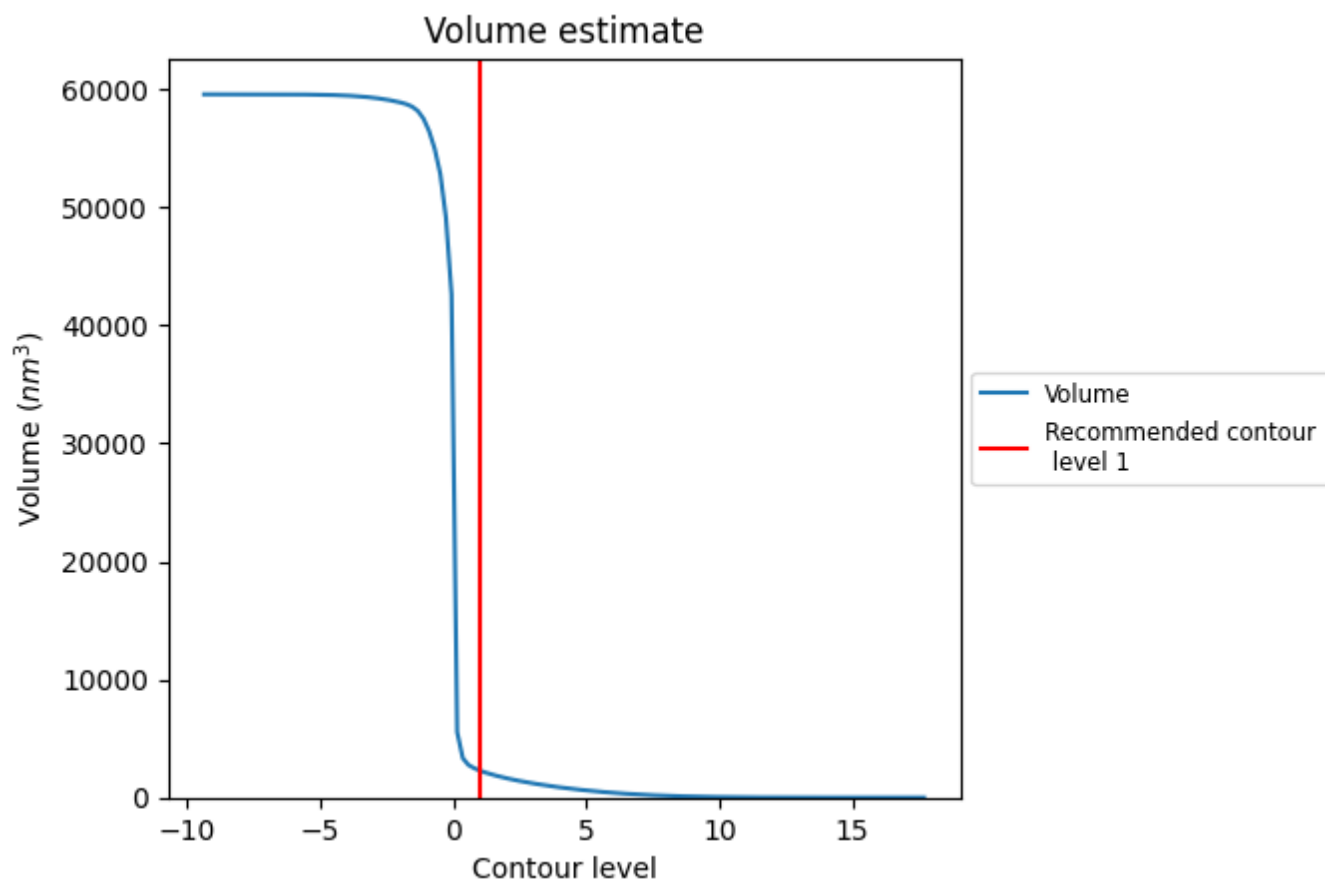
This section contains the results of statistical analysis of the map.

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.

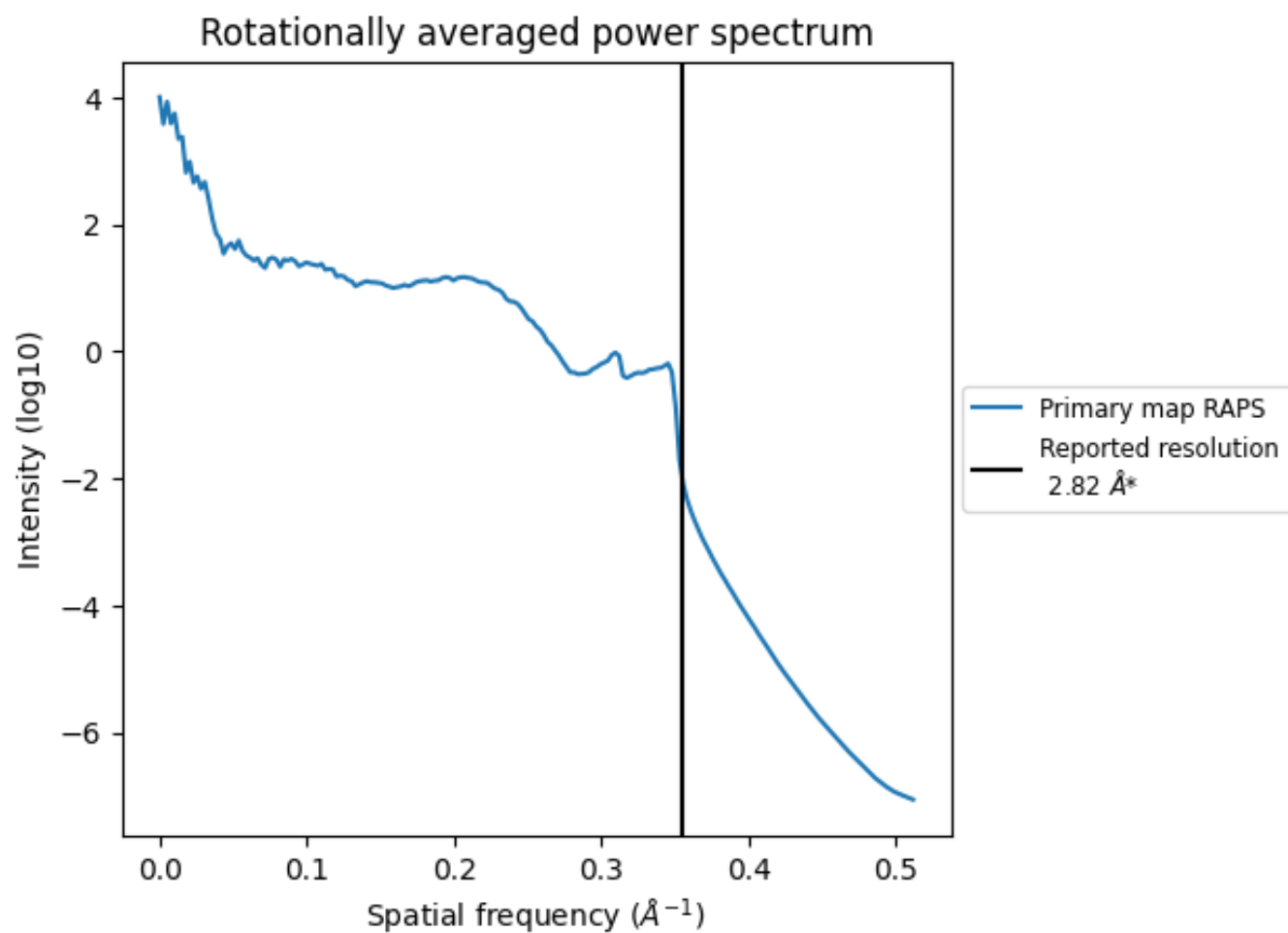
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2292 nm³; this corresponds to an approximate mass of 2070 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 0.355 Å⁻¹

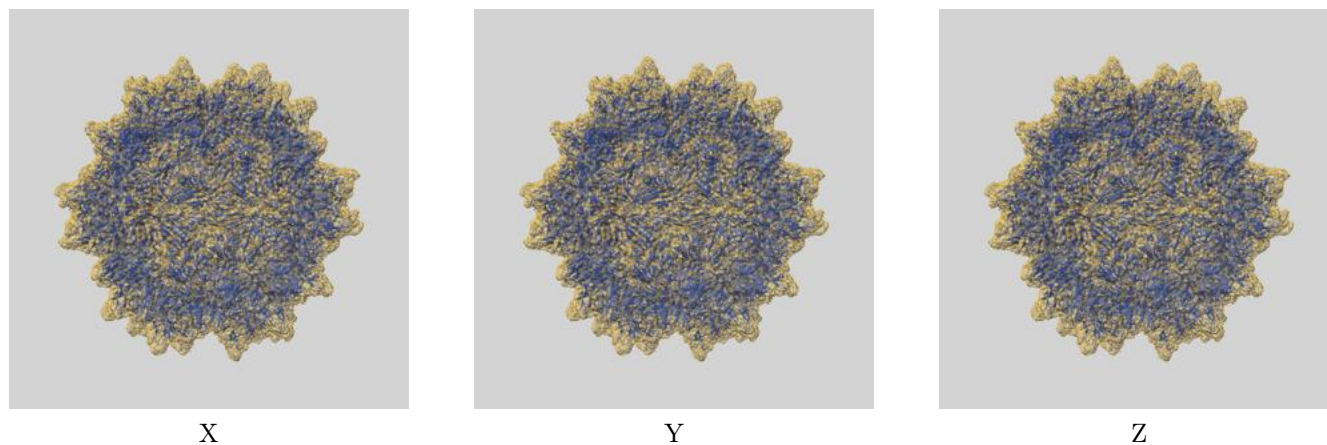
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

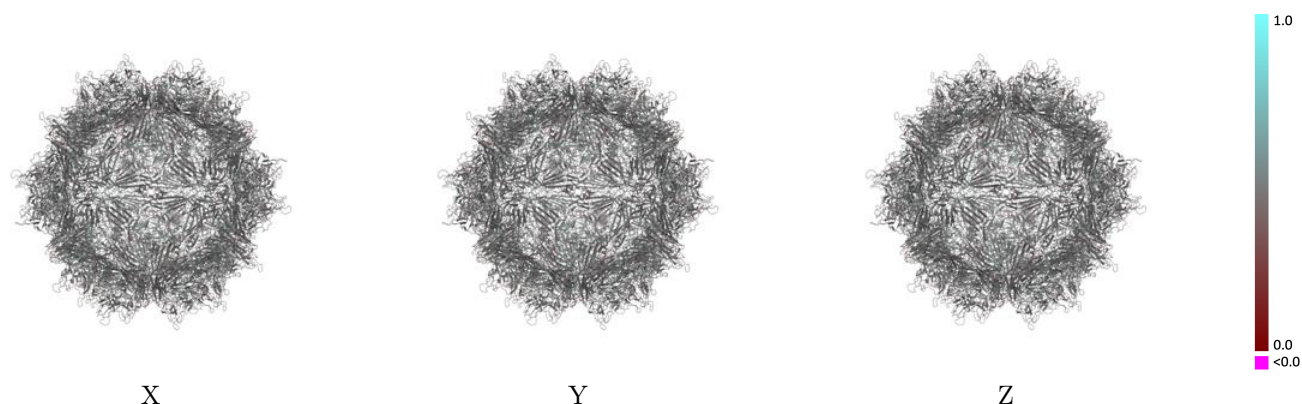
This section contains information regarding the fit between EMDB map EMD-23973 and PDB model 7MT0. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



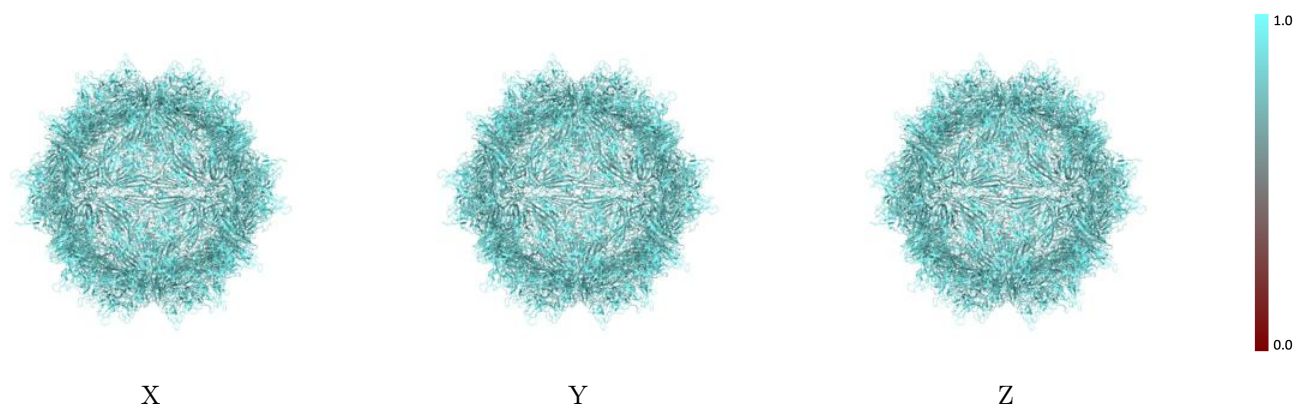
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



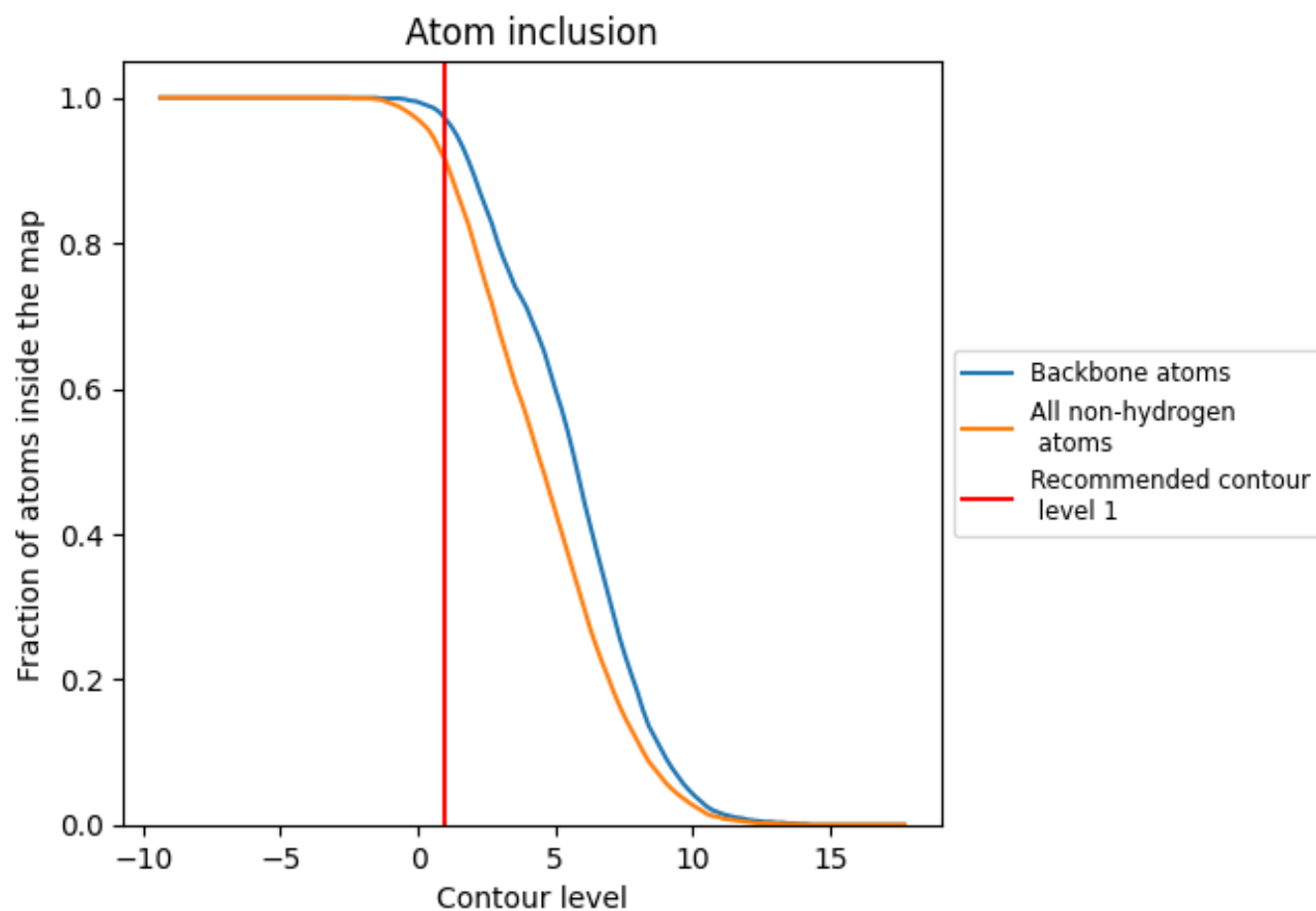
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 91% 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	 0.9140	 0.4730
1	 0.9140	 0.4730
2	 0.9140	 0.4730
3	 0.9160	 0.4740
4	 0.9140	 0.4740
5	 0.9140	 0.4730
6	 0.9140	 0.4750
7	 0.9110	 0.4730
8	 0.9110	 0.4720
A	 0.9130	 0.4710
B	 0.9140	 0.4720
C	 0.9140	 0.4740
D	 0.9110	 0.4730
E	 0.9160	 0.4730
F	 0.9160	 0.4740
G	 0.9110	 0.4730
H	 0.9110	 0.4720
I	 0.9140	 0.4720
J	 0.9140	 0.4710
K	 0.9140	 0.4730
L	 0.9140	 0.4720
M	 0.9110	 0.4730
N	 0.9140	 0.4730
O	 0.9140	 0.4720
P	 0.9140	 0.4740
Q	 0.9160	 0.4740
R	 0.9140	 0.4740
S	 0.9110	 0.4740
T	 0.9110	 0.4730
U	 0.9140	 0.4740
V	 0.9140	 0.4740
W	 0.9140	 0.4730
X	 0.9140	 0.4730
Y	 0.9140	 0.4720
Z	 0.9160	 0.4710



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Chain	Atom inclusion	Q-score
a	 0.9110	 0.4730
b	 0.9140	 0.4720
c	 0.9160	 0.4730
d	 0.9170	 0.4730
e	 0.9150	 0.4740
f	 0.9140	 0.4730
g	 0.9140	 0.4720
h	 0.9140	 0.4720
i	 0.9160	 0.4730
j	 0.9160	 0.4720
k	 0.9110	 0.4720
l	 0.9140	 0.4710
m	 0.9140	 0.4720
n	 0.9140	 0.4720
o	 0.9140	 0.4730
p	 0.9140	 0.4730
q	 0.9130	 0.4730
r	 0.9110	 0.4710
s	 0.9140	 0.4720
t	 0.9110	 0.4720
u	 0.9140	 0.4730
v	 0.9130	 0.4730
w	 0.9160	 0.4730
x	 0.9160	 0.4730
y	 0.9140	 0.4730
z	 0.9140	 0.4740