



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Dec 4, 2019 – 01:43 PM EST

PDB ID : 6V1T
EMDB ID: : EMD-21017
Title : Empty AAVrh.39 particle
Authors : Mietzsch, M.; Agbandje-McKenna, M.
Deposited on : 2019-11-21
Resolution : 3.39 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB 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.

MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

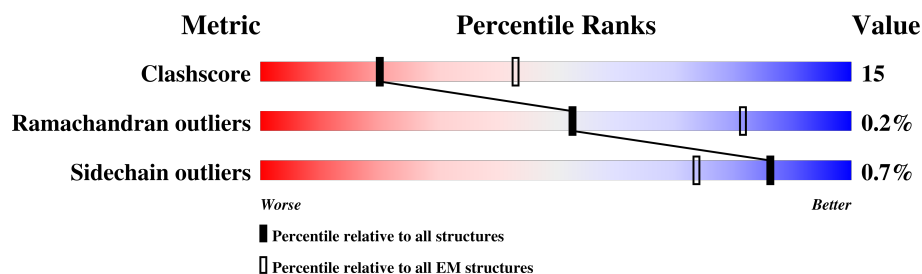
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.39 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)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	1	521	64% 36% .
1	2	521	64% 35% .
1	3	521	64% 35% .
1	4	521	65% 35% .
1	5	521	66% 33% .
1	6	521	65% 35% .
1	7	521	64% 35% .
1	8	521	65% 34% .
1	A	521	63% 36% .

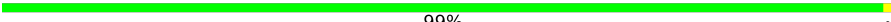














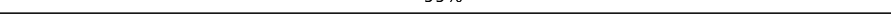
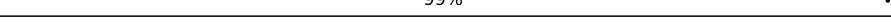
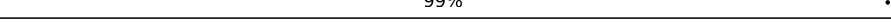
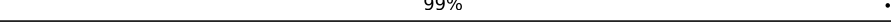
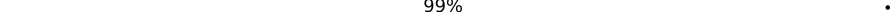
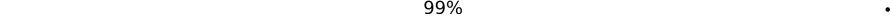
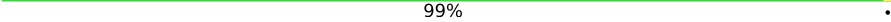
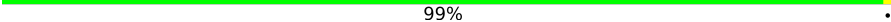

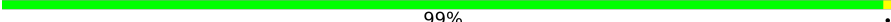
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Mol	Chain	Length	Quality of chain
1	B	521	 65% 34% .
1	C	521	 64% 35% .
1	D	521	 63% 36% .
1	E	521	 64% 36% .
1	F	521	 64% 36% .
1	G	521	 63% 36% .
1	H	521	 63% 36% .
1	I	521	 64% 36% .
1	J	521	 63% 36% .
1	K	521	 63% 37% .
1	L	521	 64% 36% .
1	M	521	 63% 37% .
1	N	521	 64% 36% .
1	O	521	 63% 36% .
1	P	521	 64% 36% .
1	Q	521	 64% 36% .
1	R	521	 63% 36% .
1	S	521	 63% 36% .
1	T	521	 63% 36% .
1	U	521	 63% 36% .
1	V	521	 63% 36% .
1	W	521	 63% 37% .
1	X	521	 64% 36% .
1	Y	521	 62% 37% .
1	Z	521	 63% 37% .

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Mol	Chain	Length	Quality of chain
1	a	521	 99%
1	b	521	 99%
1	c	521	 99%
1	d	521	 99%
1	e	521	 99%
1	f	521	 99%
1	g	521	 99%
1	h	521	 99%
1	i	521	 99%
1	j	521	 99%
1	k	521	 99%
1	l	521	 99%
1	m	521	 99%
1	n	521	 99%
1	o	521	 99%
1	p	521	 99%
1	q	521	 99%
1	r	521	 99%
1	s	521	 99%
1	t	521	 99%
1	u	521	 99%
1	v	521	 99%
1	w	521	 99%
1	x	521	 99%
1	y	521	 99%

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Mol	Chain	Length	Quality of chain
1	z	521	<div><div></div><div>99%</div><div></div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 248280 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	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	B	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	C	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	D	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	E	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	F	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	G	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	H	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	I	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	J	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	K	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	L	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	M	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	N	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	O	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	P	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		
1	Q	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	S	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	T	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	U	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	V	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	W	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	X	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	Y	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	Z	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	a	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	b	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	c	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	d	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	e	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	f	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	g	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	h	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	i	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	j	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	k	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	l	521	Total 4138	C 2612	N 715	O 797	S 14	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	n	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	o	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	p	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	q	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	r	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	s	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	t	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	u	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	v	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	w	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	x	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	y	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	z	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	1	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	2	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	3	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	4	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	5	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	6	521	Total 4138	C 2612	N 715	O 797	S 14	0	0
1	7	521	Total 4138	C 2612	N 715	O 797	S 14	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	521	Total	C	N	O	S	0	0
			4138	2612	715	797	14		

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	315	ASN	SER	conflict	UNP B4Y886
A	417	GLN	THR	conflict	UNP B4Y886
B	315	ASN	SER	conflict	UNP B4Y886
B	417	GLN	THR	conflict	UNP B4Y886
C	315	ASN	SER	conflict	UNP B4Y886
C	417	GLN	THR	conflict	UNP B4Y886
D	315	ASN	SER	conflict	UNP B4Y886
D	417	GLN	THR	conflict	UNP B4Y886
E	315	ASN	SER	conflict	UNP B4Y886
E	417	GLN	THR	conflict	UNP B4Y886
F	315	ASN	SER	conflict	UNP B4Y886
F	417	GLN	THR	conflict	UNP B4Y886
G	315	ASN	SER	conflict	UNP B4Y886
G	417	GLN	THR	conflict	UNP B4Y886
H	315	ASN	SER	conflict	UNP B4Y886
H	417	GLN	THR	conflict	UNP B4Y886
I	315	ASN	SER	conflict	UNP B4Y886
I	417	GLN	THR	conflict	UNP B4Y886
J	315	ASN	SER	conflict	UNP B4Y886
J	417	GLN	THR	conflict	UNP B4Y886
K	315	ASN	SER	conflict	UNP B4Y886
K	417	GLN	THR	conflict	UNP B4Y886
L	315	ASN	SER	conflict	UNP B4Y886
L	417	GLN	THR	conflict	UNP B4Y886
M	315	ASN	SER	conflict	UNP B4Y886
M	417	GLN	THR	conflict	UNP B4Y886
N	315	ASN	SER	conflict	UNP B4Y886
N	417	GLN	THR	conflict	UNP B4Y886
O	315	ASN	SER	conflict	UNP B4Y886
O	417	GLN	THR	conflict	UNP B4Y886
P	315	ASN	SER	conflict	UNP B4Y886
P	417	GLN	THR	conflict	UNP B4Y886
Q	315	ASN	SER	conflict	UNP B4Y886
Q	417	GLN	THR	conflict	UNP B4Y886
R	315	ASN	SER	conflict	UNP B4Y886
R	417	GLN	THR	conflict	UNP B4Y886

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Chain	Residue	Modelled	Actual	Comment	Reference
S	315	ASN	SER	conflict	UNP B4Y886
S	417	GLN	THR	conflict	UNP B4Y886
T	315	ASN	SER	conflict	UNP B4Y886
T	417	GLN	THR	conflict	UNP B4Y886
U	315	ASN	SER	conflict	UNP B4Y886
U	417	GLN	THR	conflict	UNP B4Y886
V	315	ASN	SER	conflict	UNP B4Y886
V	417	GLN	THR	conflict	UNP B4Y886
W	315	ASN	SER	conflict	UNP B4Y886
W	417	GLN	THR	conflict	UNP B4Y886
X	315	ASN	SER	conflict	UNP B4Y886
X	417	GLN	THR	conflict	UNP B4Y886
Y	315	ASN	SER	conflict	UNP B4Y886
Y	417	GLN	THR	conflict	UNP B4Y886
Z	315	ASN	SER	conflict	UNP B4Y886
Z	417	GLN	THR	conflict	UNP B4Y886
a	315	ASN	SER	conflict	UNP B4Y886
a	417	GLN	THR	conflict	UNP B4Y886
b	315	ASN	SER	conflict	UNP B4Y886
b	417	GLN	THR	conflict	UNP B4Y886
c	315	ASN	SER	conflict	UNP B4Y886
c	417	GLN	THR	conflict	UNP B4Y886
d	315	ASN	SER	conflict	UNP B4Y886
d	417	GLN	THR	conflict	UNP B4Y886
e	315	ASN	SER	conflict	UNP B4Y886
e	417	GLN	THR	conflict	UNP B4Y886
f	315	ASN	SER	conflict	UNP B4Y886
f	417	GLN	THR	conflict	UNP B4Y886
g	315	ASN	SER	conflict	UNP B4Y886
g	417	GLN	THR	conflict	UNP B4Y886
h	315	ASN	SER	conflict	UNP B4Y886
h	417	GLN	THR	conflict	UNP B4Y886
i	315	ASN	SER	conflict	UNP B4Y886
i	417	GLN	THR	conflict	UNP B4Y886
j	315	ASN	SER	conflict	UNP B4Y886
j	417	GLN	THR	conflict	UNP B4Y886
k	315	ASN	SER	conflict	UNP B4Y886
k	417	GLN	THR	conflict	UNP B4Y886
l	315	ASN	SER	conflict	UNP B4Y886
l	417	GLN	THR	conflict	UNP B4Y886
m	315	ASN	SER	conflict	UNP B4Y886
m	417	GLN	THR	conflict	UNP B4Y886

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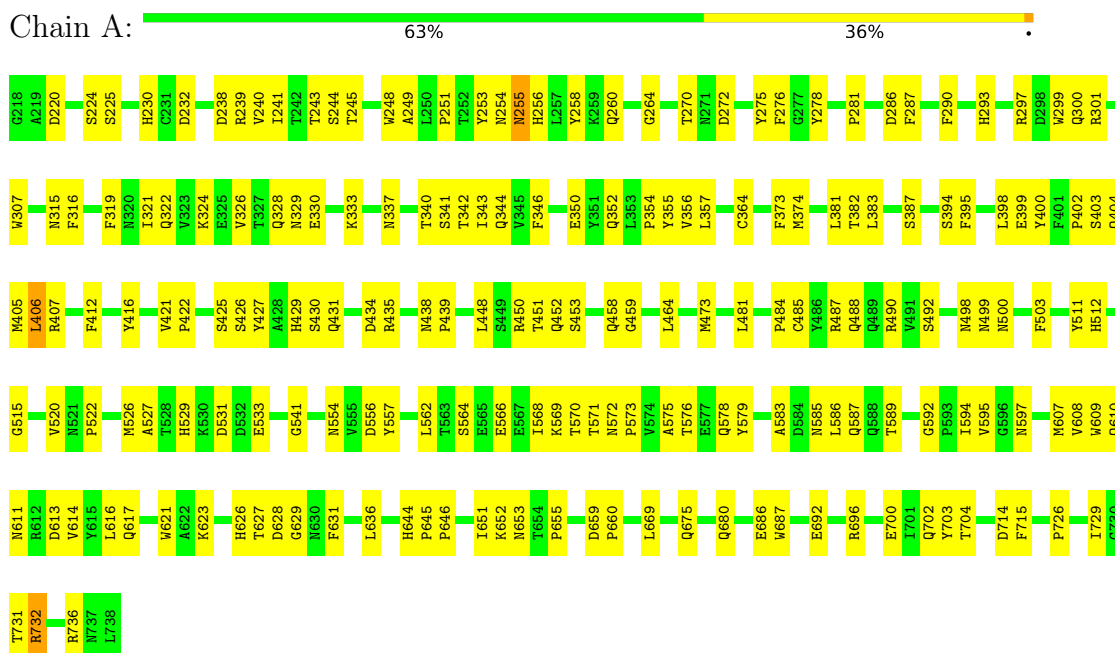
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Chain	Residue	Modelled	Actual	Comment	Reference
n	315	ASN	SER	conflict	UNP B4Y886
n	417	GLN	THR	conflict	UNP B4Y886
o	315	ASN	SER	conflict	UNP B4Y886
o	417	GLN	THR	conflict	UNP B4Y886
p	315	ASN	SER	conflict	UNP B4Y886
p	417	GLN	THR	conflict	UNP B4Y886
q	315	ASN	SER	conflict	UNP B4Y886
q	417	GLN	THR	conflict	UNP B4Y886
r	315	ASN	SER	conflict	UNP B4Y886
r	417	GLN	THR	conflict	UNP B4Y886
s	315	ASN	SER	conflict	UNP B4Y886
s	417	GLN	THR	conflict	UNP B4Y886
t	315	ASN	SER	conflict	UNP B4Y886
t	417	GLN	THR	conflict	UNP B4Y886
u	315	ASN	SER	conflict	UNP B4Y886
u	417	GLN	THR	conflict	UNP B4Y886
v	315	ASN	SER	conflict	UNP B4Y886
v	417	GLN	THR	conflict	UNP B4Y886
w	315	ASN	SER	conflict	UNP B4Y886
w	417	GLN	THR	conflict	UNP B4Y886
x	315	ASN	SER	conflict	UNP B4Y886
x	417	GLN	THR	conflict	UNP B4Y886
y	315	ASN	SER	conflict	UNP B4Y886
y	417	GLN	THR	conflict	UNP B4Y886
z	315	ASN	SER	conflict	UNP B4Y886
z	417	GLN	THR	conflict	UNP B4Y886
1	315	ASN	SER	conflict	UNP B4Y886
1	417	GLN	THR	conflict	UNP B4Y886
2	315	ASN	SER	conflict	UNP B4Y886
2	417	GLN	THR	conflict	UNP B4Y886
3	315	ASN	SER	conflict	UNP B4Y886
3	417	GLN	THR	conflict	UNP B4Y886
4	315	ASN	SER	conflict	UNP B4Y886
4	417	GLN	THR	conflict	UNP B4Y886
5	315	ASN	SER	conflict	UNP B4Y886
5	417	GLN	THR	conflict	UNP B4Y886
6	315	ASN	SER	conflict	UNP B4Y886
6	417	GLN	THR	conflict	UNP B4Y886
7	315	ASN	SER	conflict	UNP B4Y886
7	417	GLN	THR	conflict	UNP B4Y886
8	315	ASN	SER	conflict	UNP B4Y886
8	417	GLN	THR	conflict	UNP B4Y886

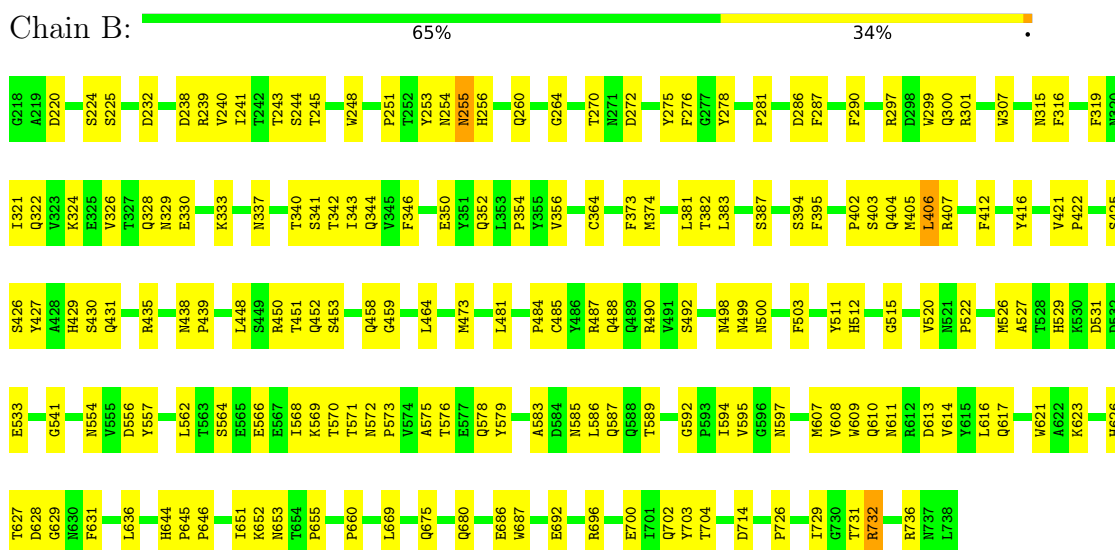
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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. 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. 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.

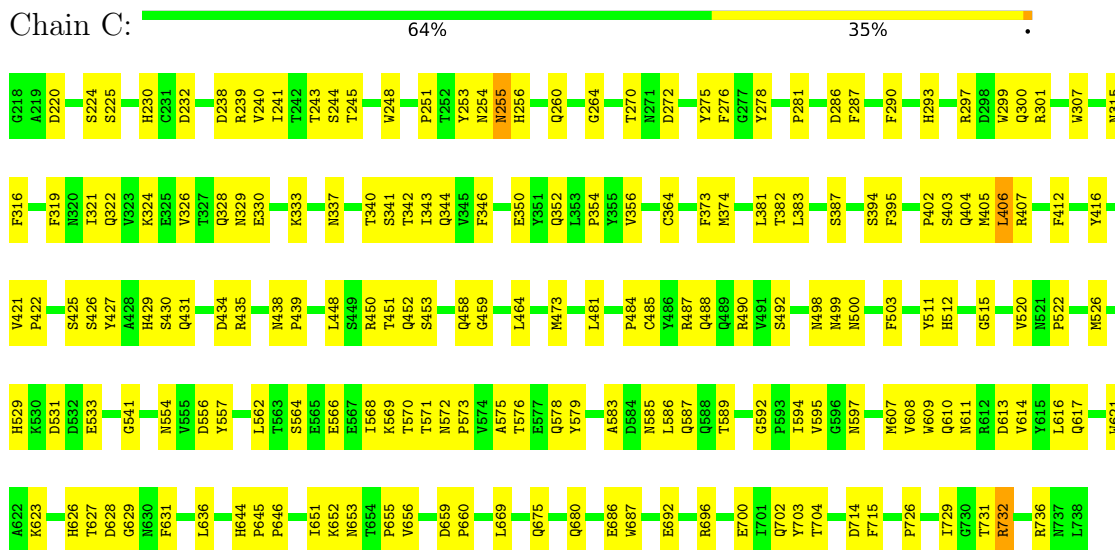
• Molecule 1: Capsid protein VP1



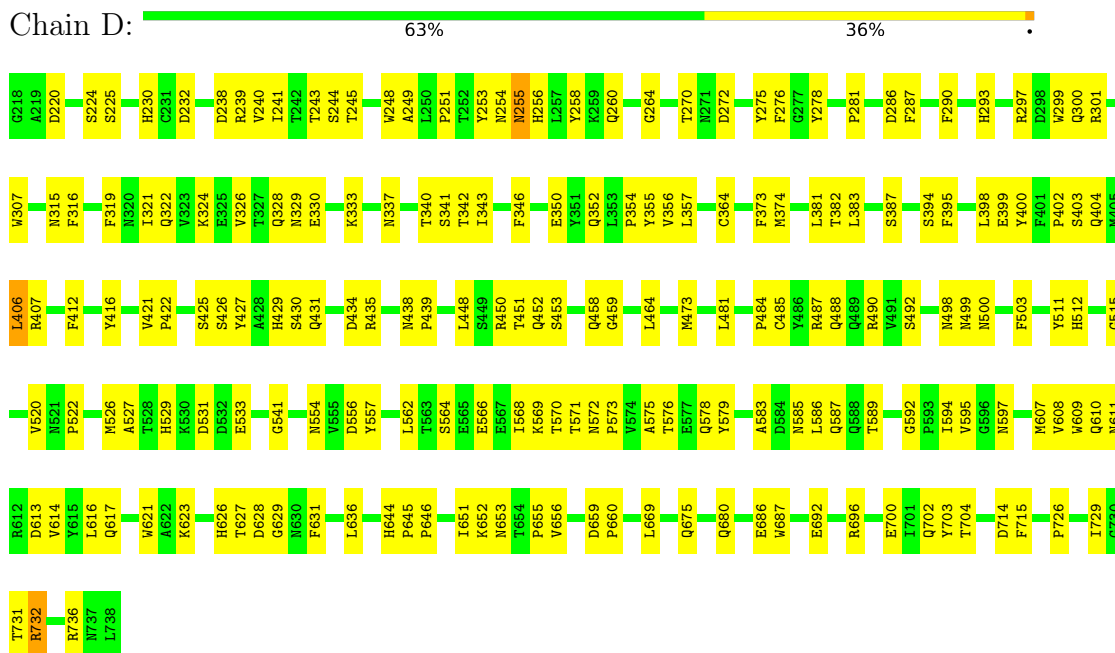
• Molecule 1: Capsid protein VP1



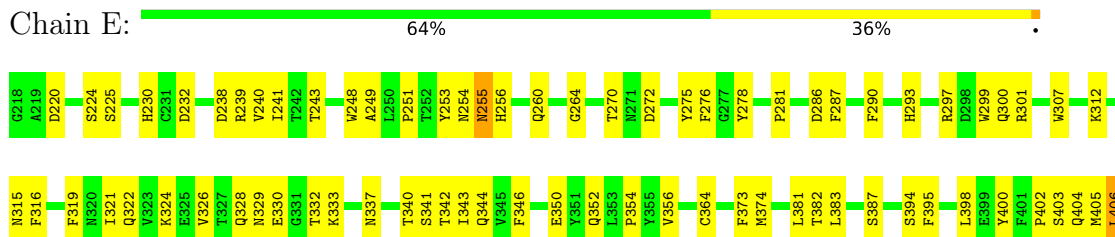
- Molecule 1: Capsid protein VP1

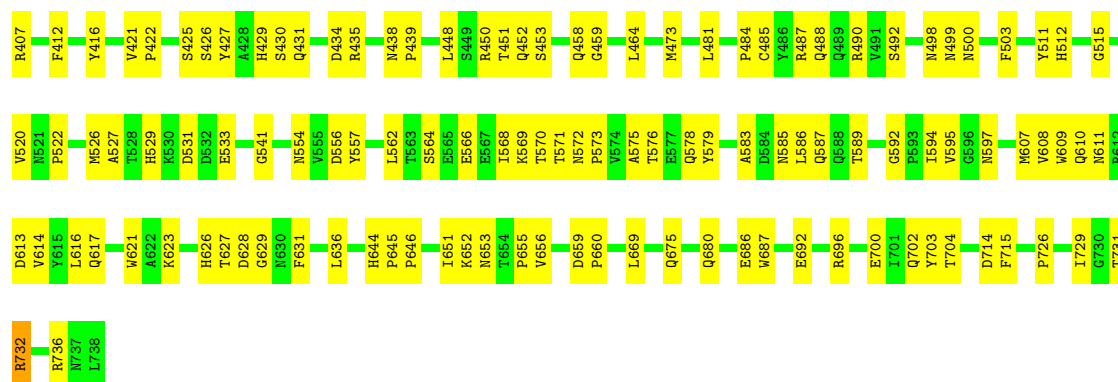


- Molecule 1: Capsid protein VP1



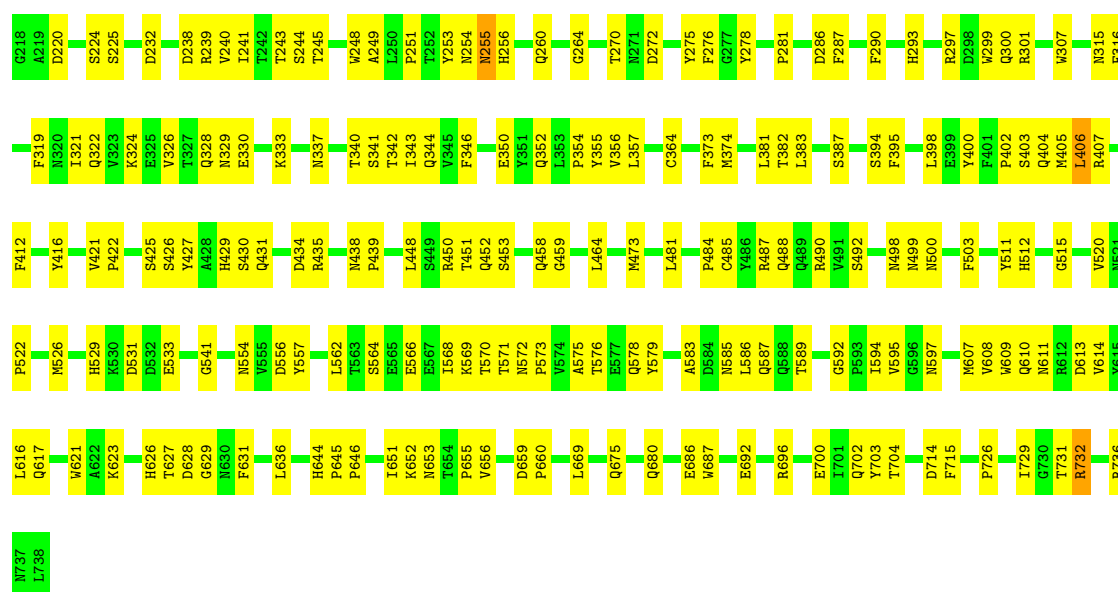
- Molecule 1: Capsid protein VP1





• Molecule 1: Capsid protein VP1

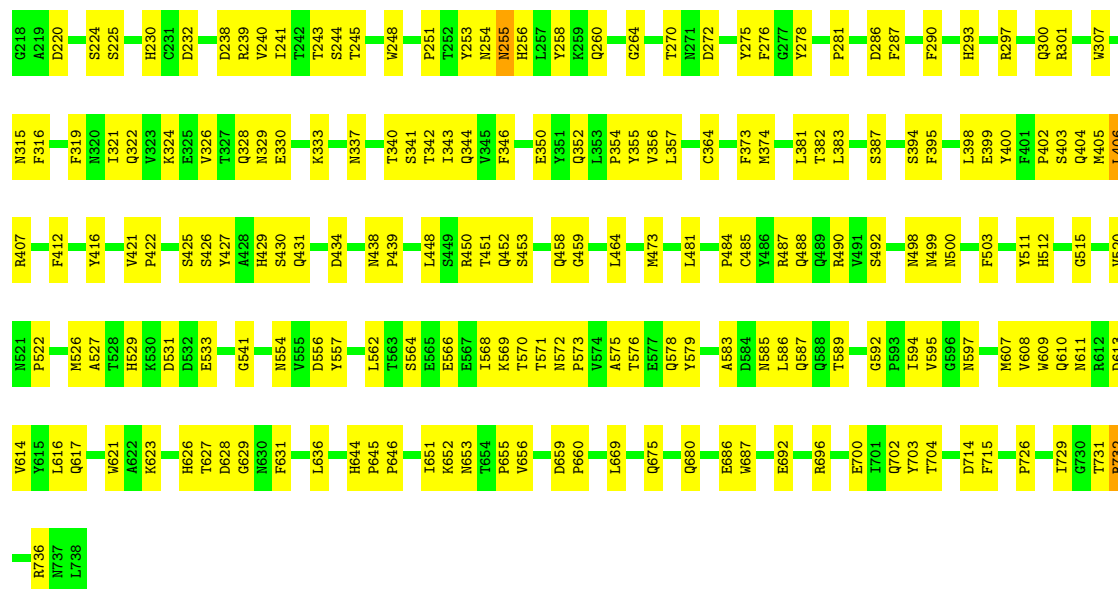
Chain F: 64% 36%





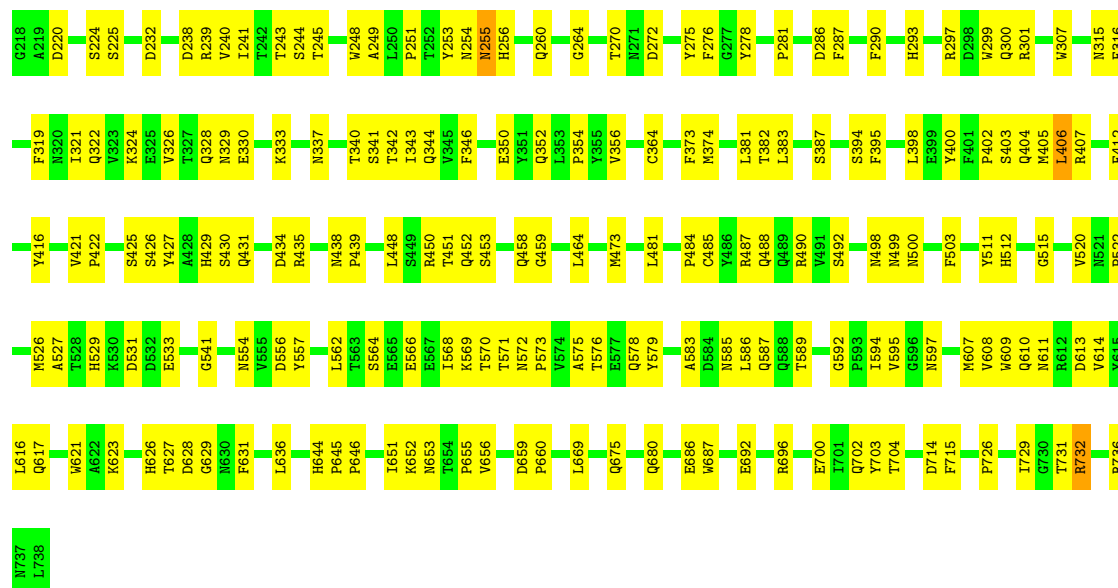
- Molecule 1: Capsid protein VP1

Chain H:  63% 36%

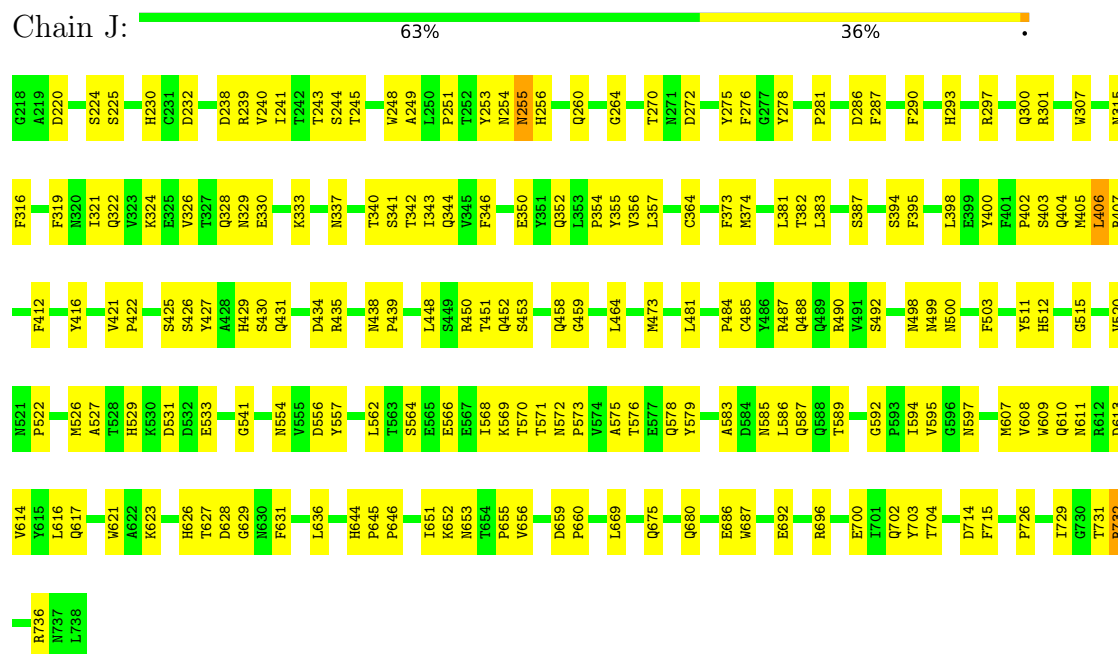


- Molecule 1: Capsid protein VP1

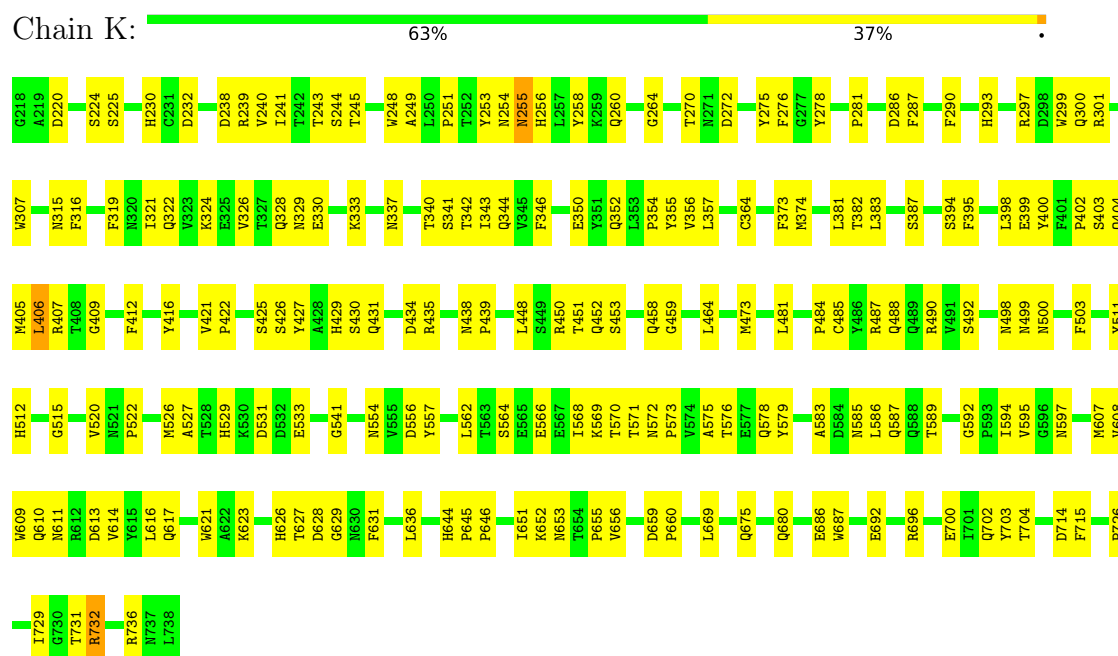
Chain I:  64% 36%



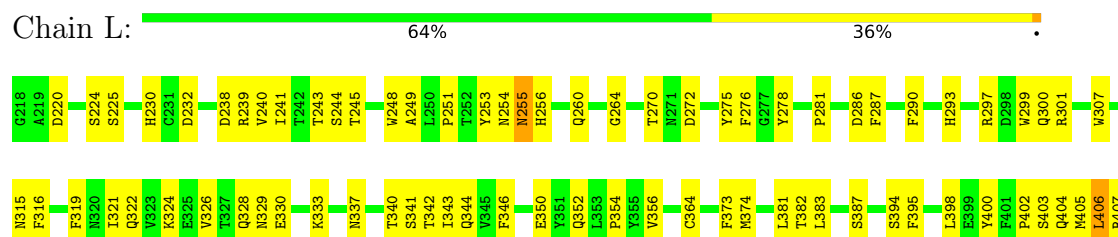
- Molecule 1: Capsid protein VP1

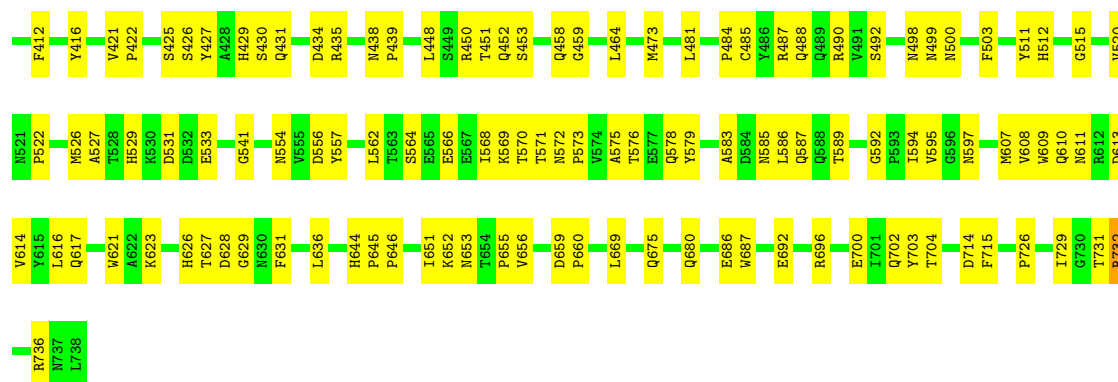


• Molecule 1: Capsid protein VP1



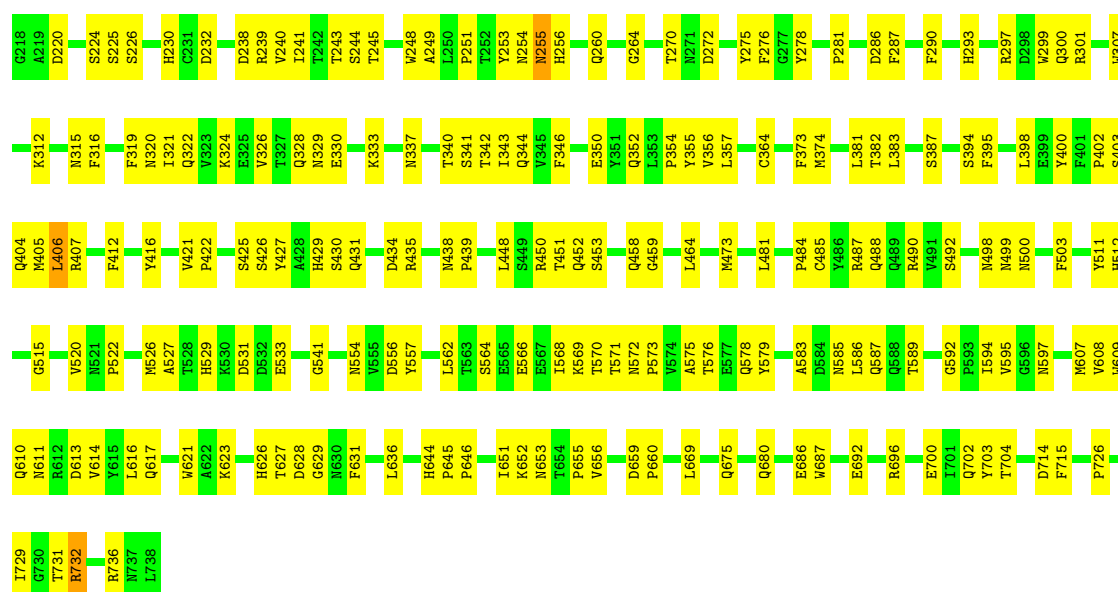
• Molecule 1: Capsid protein VP1





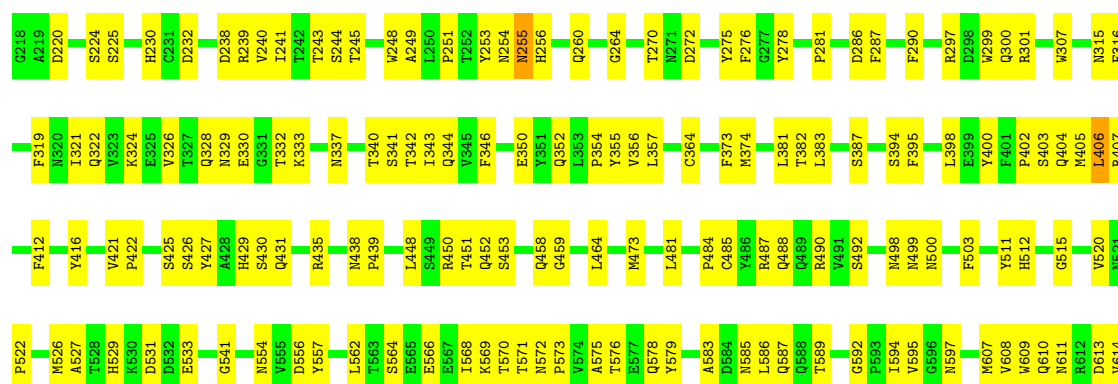
• Molecule 1: Capsid protein VP1

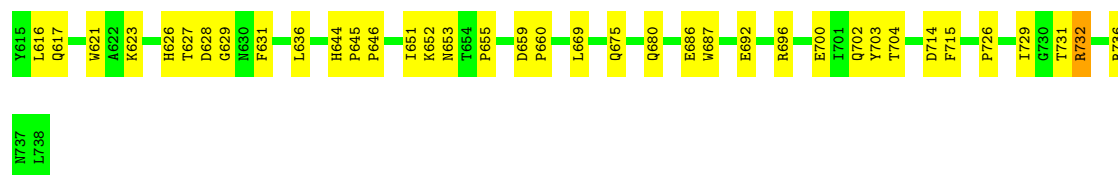
Chain M: 63% 37% .



• Molecule 1: Capsid protein VP1

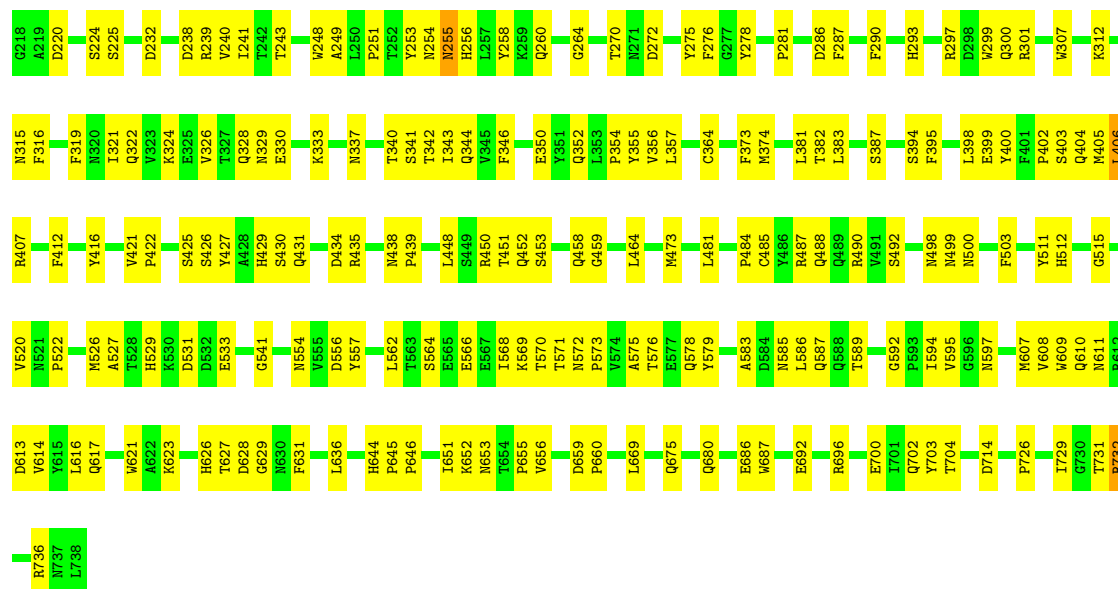
Chain N: 64% 36% .





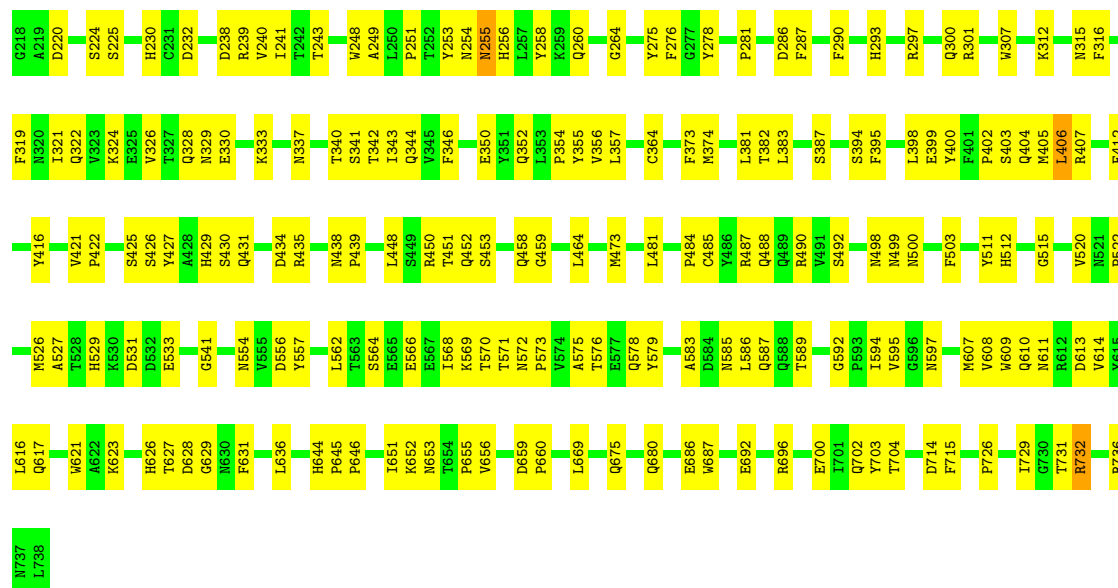
• Molecule 1: Capsid protein VP1

Chain O: 63% 36%



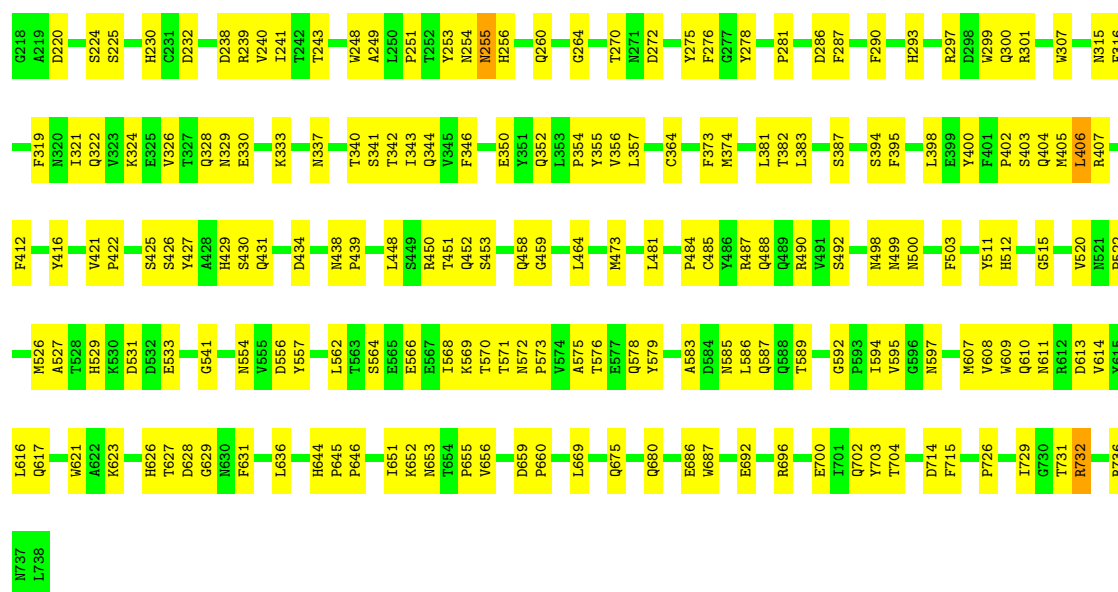
• Molecule 1: Capsid protein VP1

Chain P: 64% 36%



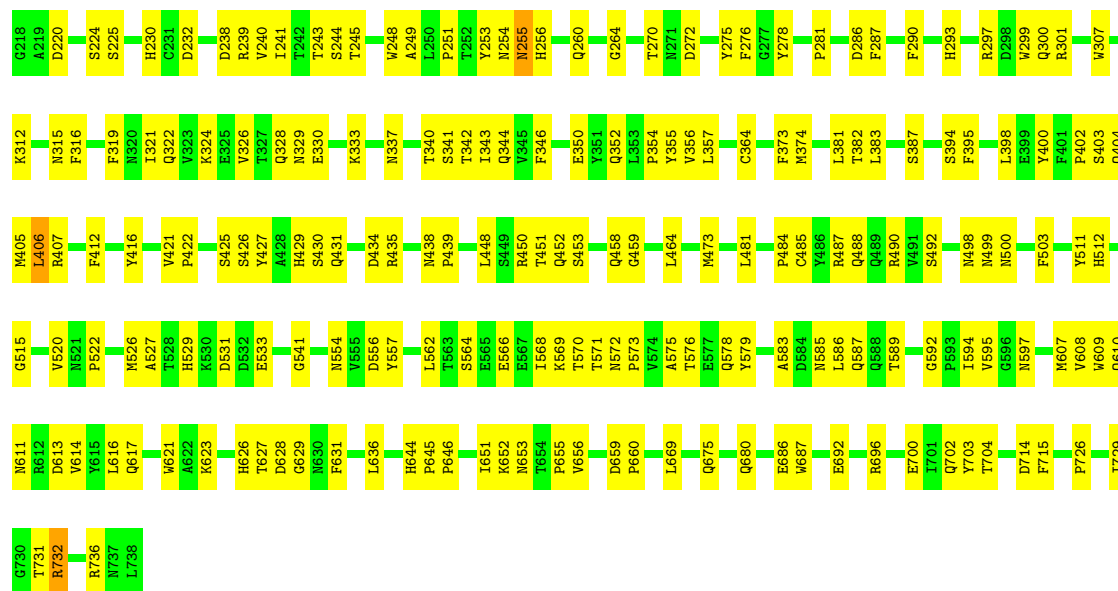
• Molecule 1: Capsid protein VP1

Chain Q:  64% 36%



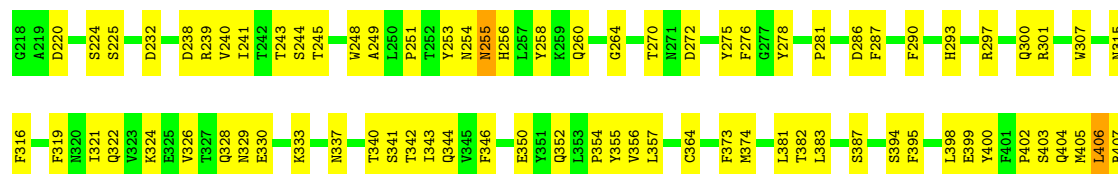
• Molecule 1: Capsid protein VP1

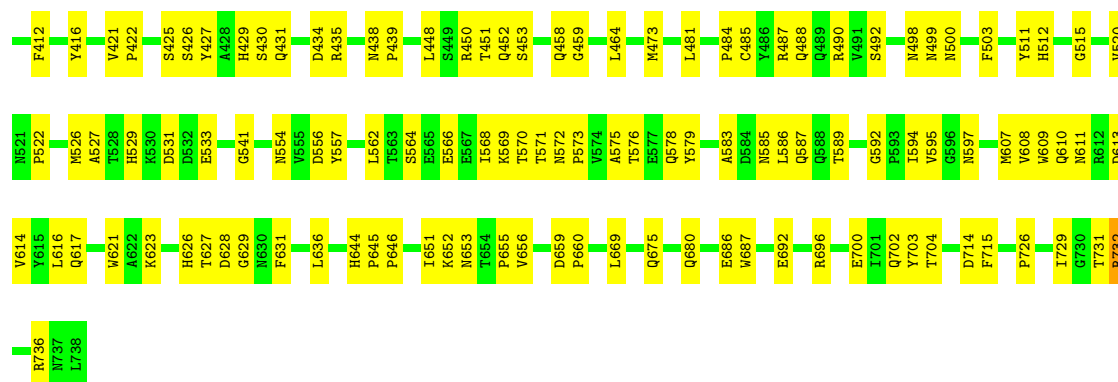
Chain R:  63% 36%



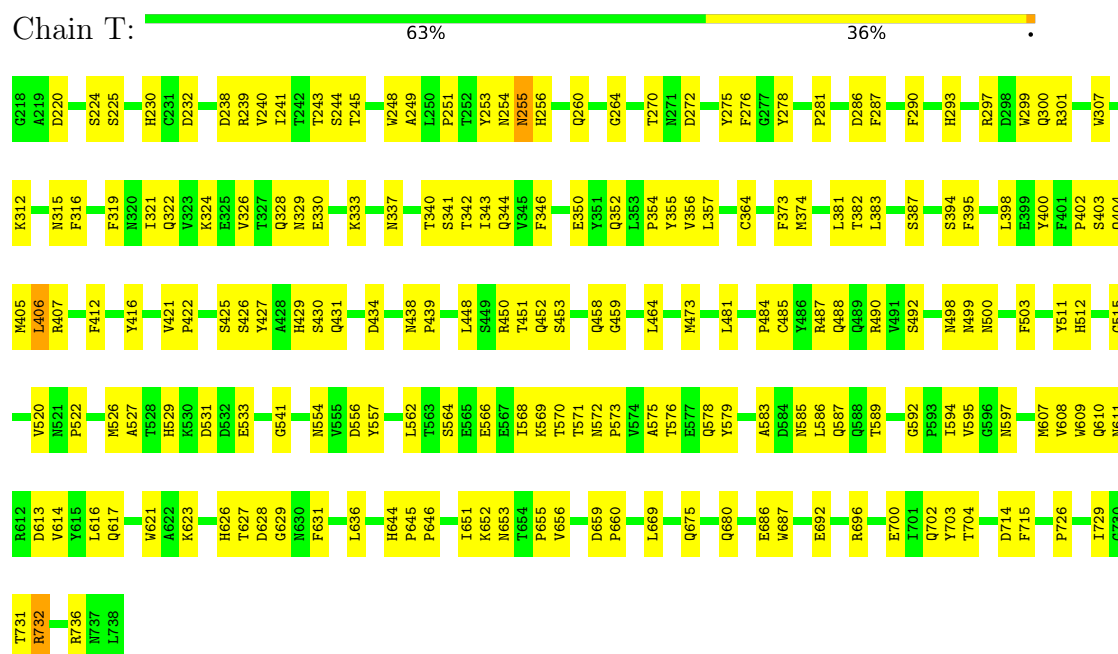
• Molecule 1: Capsid protein VP1

Chain S:  63% 36%

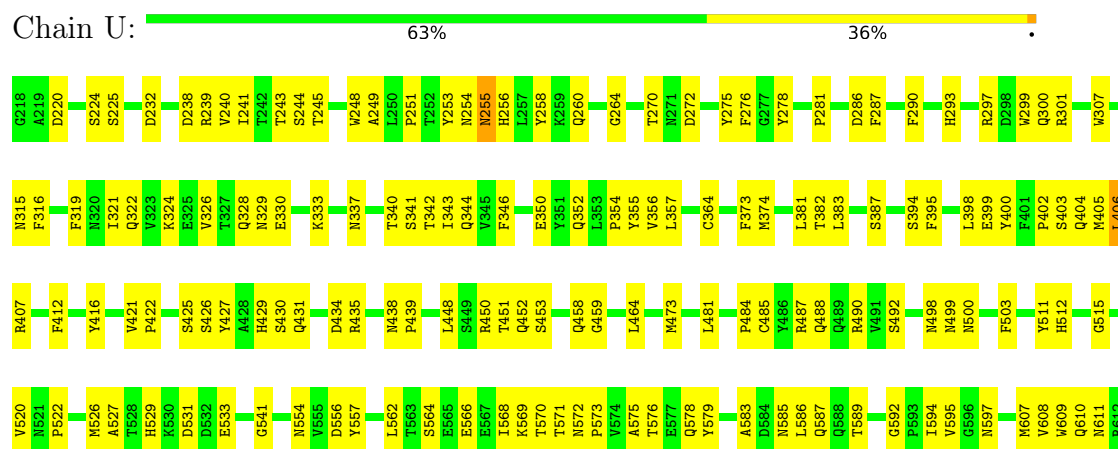


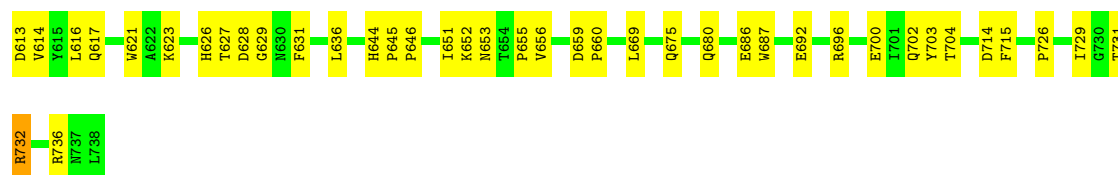


• Molecule 1: Capsid protein VP1



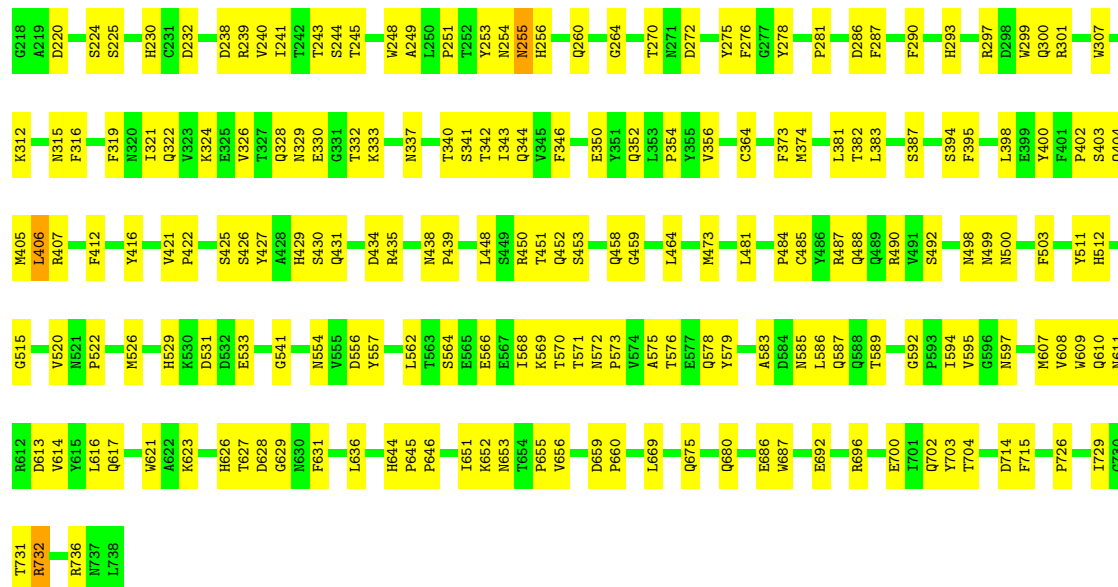
• Molecule 1: Capsid protein VP1





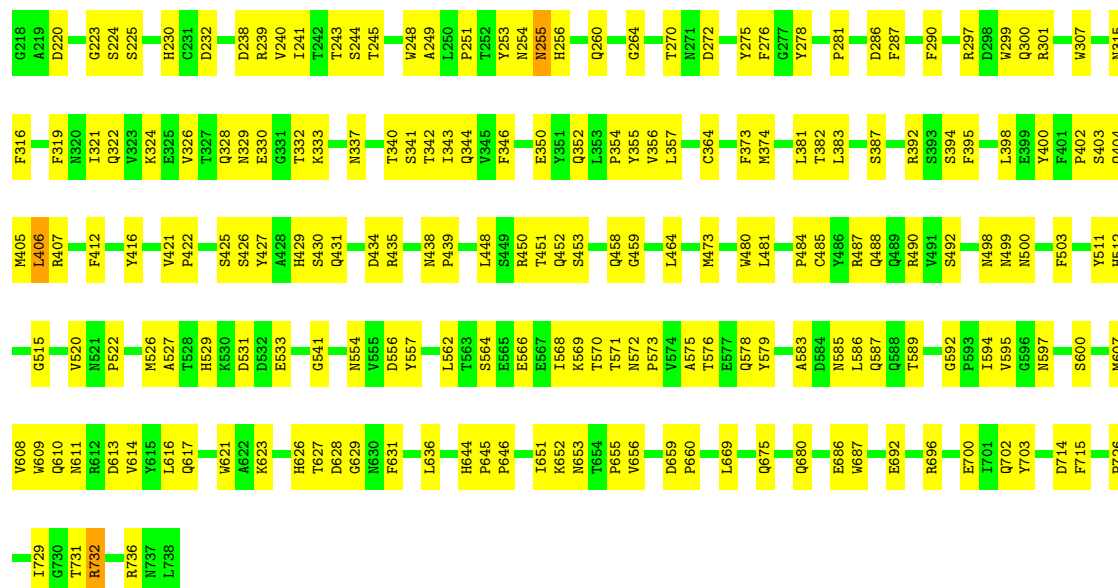
• Molecule 1: Capsid protein VP1

Chain V: 63% 36%



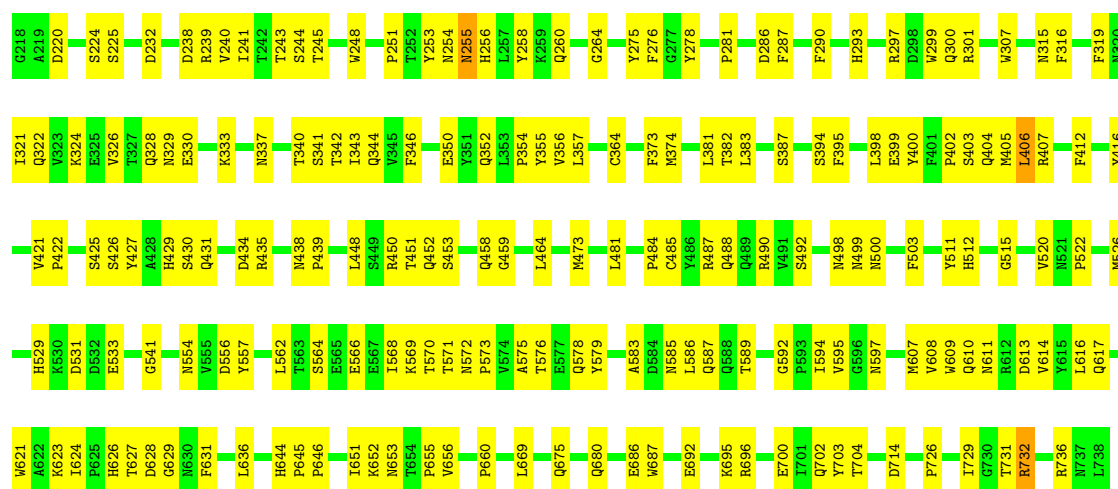
• Molecule 1: Capsid protein VP1

Chain W: 63% 37%



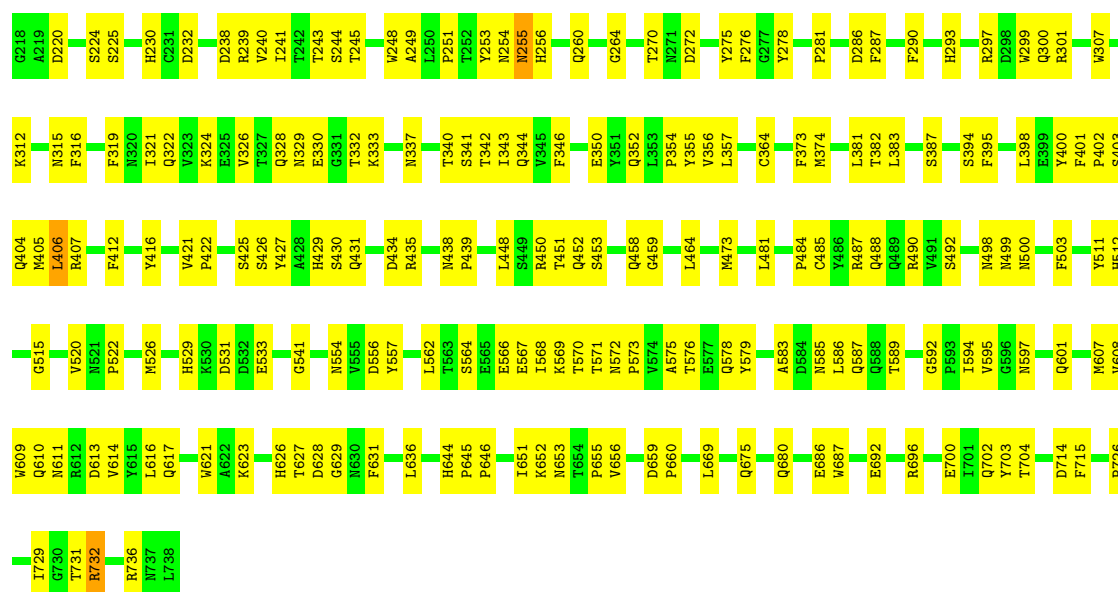
• Molecule 1: Capsid protein VP1

Chain X:  64% 36%



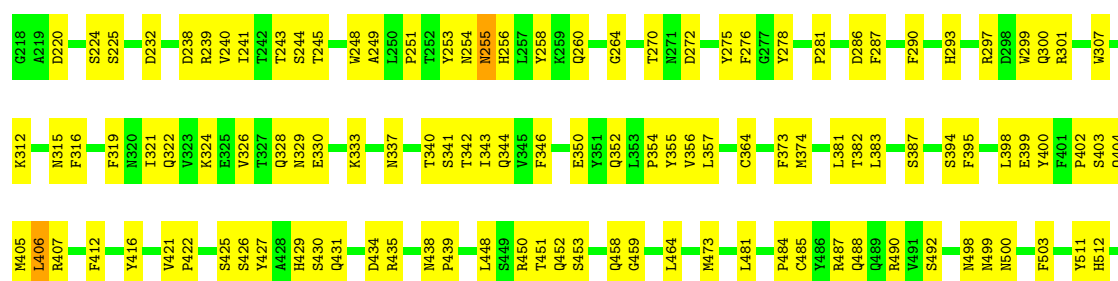
• Molecule 1: Capsid protein VP1

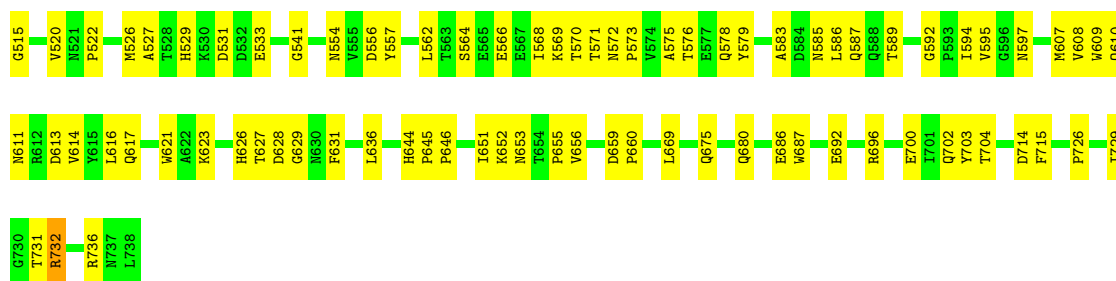
Chain Y:  62% 37%



• Molecule 1: Capsid protein VP1

Chain Z:  63% 37%





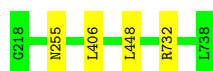
- Molecule 1: Capsid protein VP1

Chain a: 99%



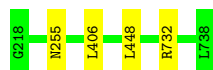
- Molecule 1: Capsid protein VP1

Chain b: 99%



- Molecule 1: Capsid protein VP1

Chain c: 99%



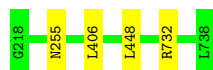
- Molecule 1: Capsid protein VP1

Chain d: 99%



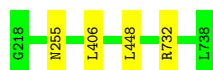
- Molecule 1: Capsid protein VP1

Chain e: 99%



- Molecule 1: Capsid protein VP1

Chain f: 99%



- Molecule 1: Capsid protein VP1

Chain g:  99% .



- Molecule 1: Capsid protein VP1

Chain h:  99% .



- Molecule 1: Capsid protein VP1

Chain i:  99% .



- Molecule 1: Capsid protein VP1

Chain j:  99% .



- Molecule 1: Capsid protein VP1

Chain k:  99% .



- Molecule 1: Capsid protein VP1

Chain l:  99% .

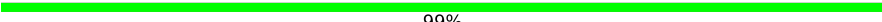


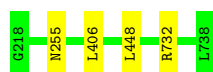
- Molecule 1: Capsid protein VP1

Chain m:  99% .



- Molecule 1: Capsid protein VP1

Chain n:  99%



- Molecule 1: Capsid protein VP1

Chain o:  99%



- Molecule 1: Capsid protein VP1

Chain p:  99%



- Molecule 1: Capsid protein VP1

Chain q:  99%



- Molecule 1: Capsid protein VP1

Chain r:  99%



- Molecule 1: Capsid protein VP1

Chain s:  99%



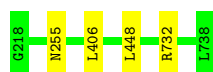
- Molecule 1: Capsid protein VP1

Chain t:  99%



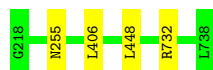
- Molecule 1: Capsid protein VP1

Chain u:  99%



- Molecule 1: Capsid protein VP1

Chain v: 99%



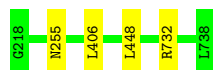
- Molecule 1: Capsid protein VP1

Chain w: 99%



- Molecule 1: Capsid protein VP1

Chain x: 99%



- Molecule 1: Capsid protein VP1

Chain y: 99%



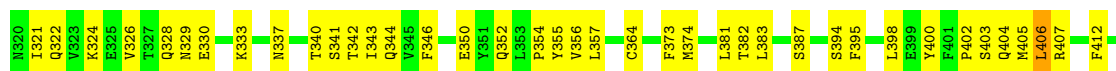
- Molecule 1: Capsid protein VP1

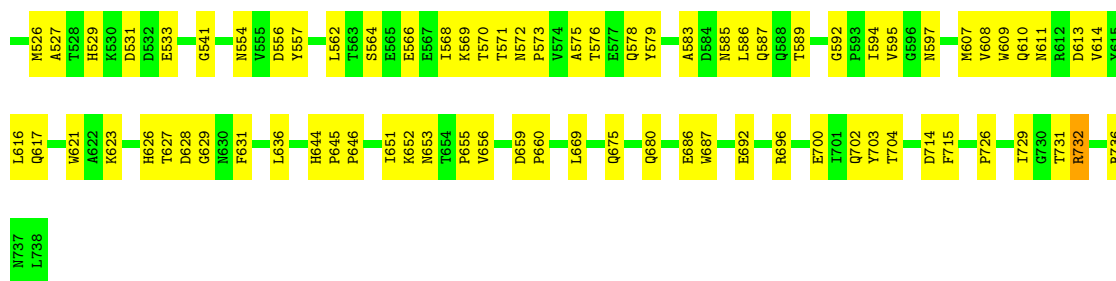
Chain z: 99%

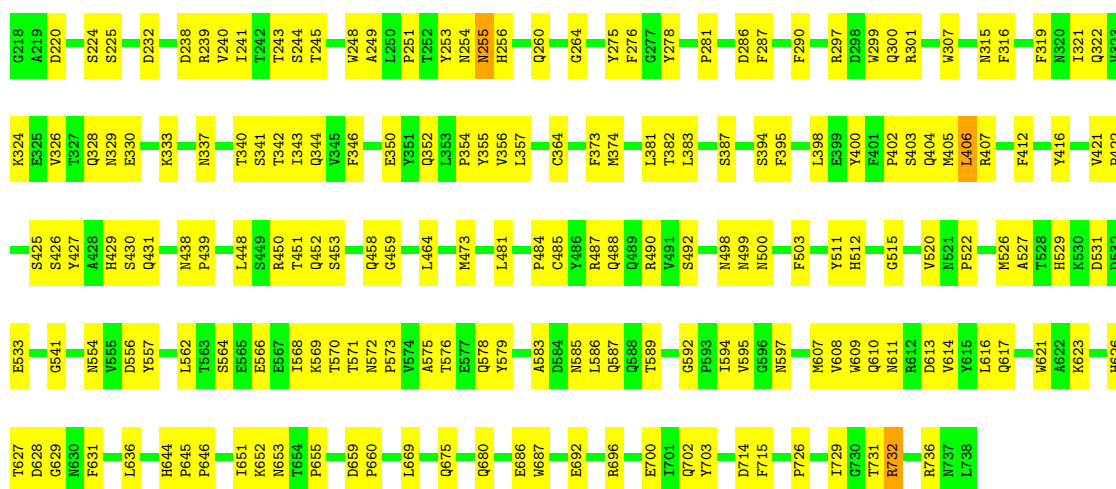


- Molecule 1: Capsid protein VP1

Chain 1: 64%

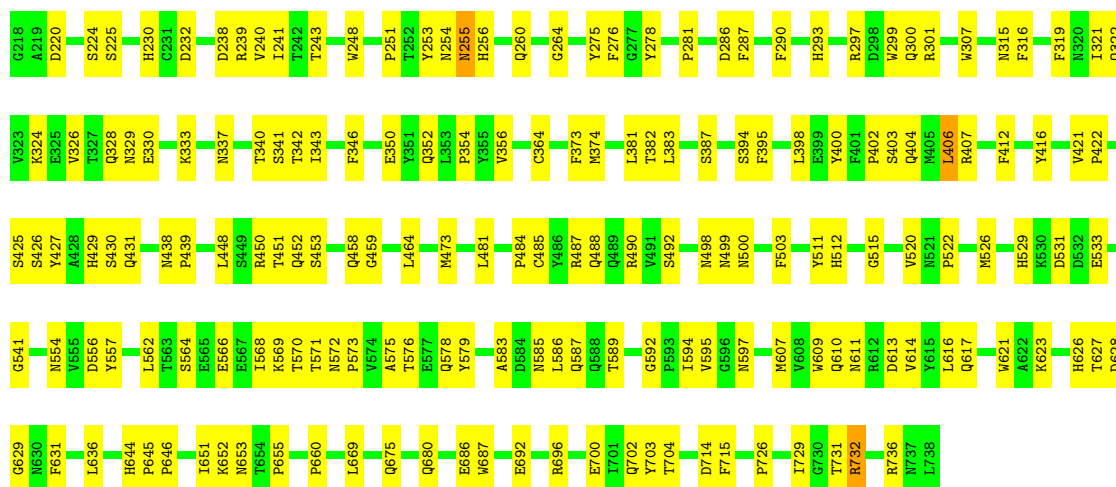






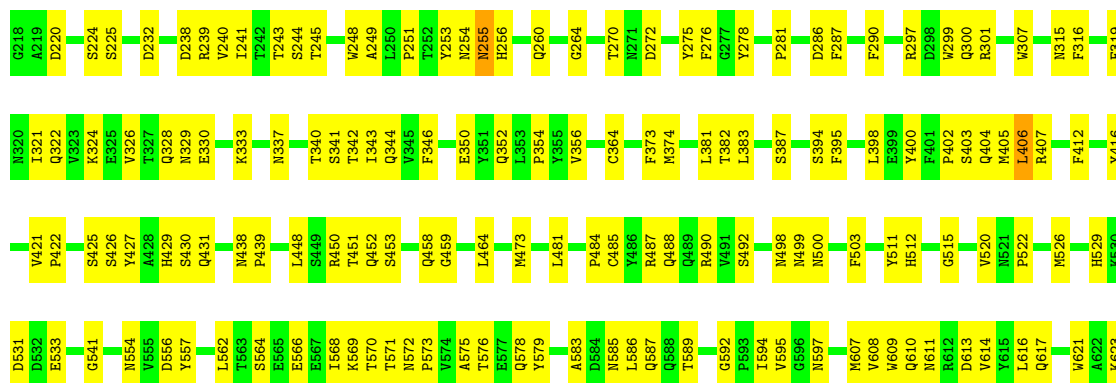
• Molecule 1: Capsid protein VP1

Chain 5: 66% 33% .



• Molecule 1: Capsid protein VP1

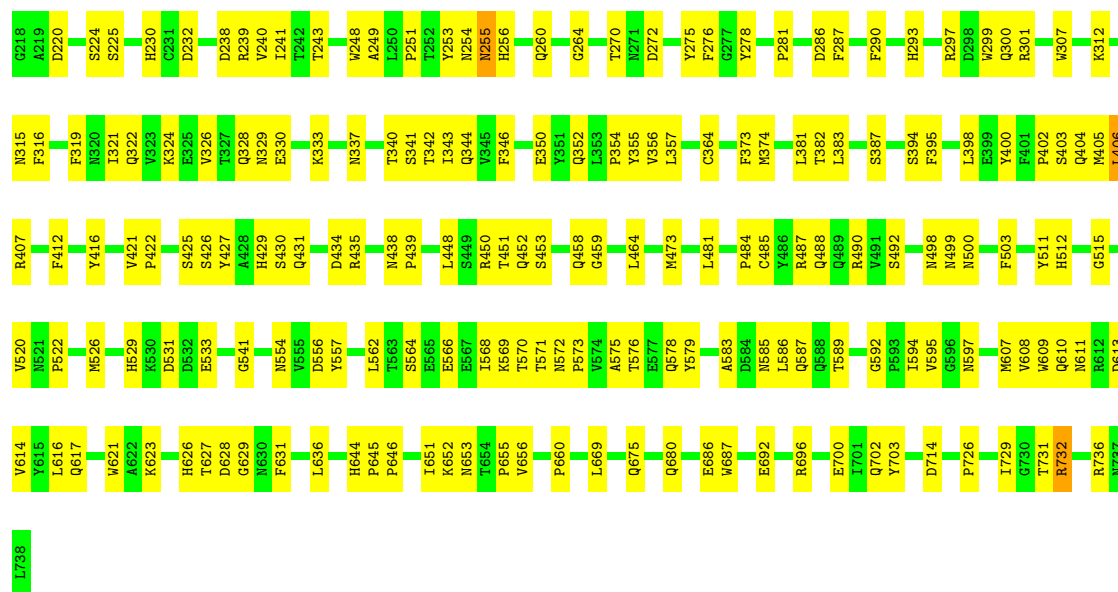
Chain 6: 65% 35% .





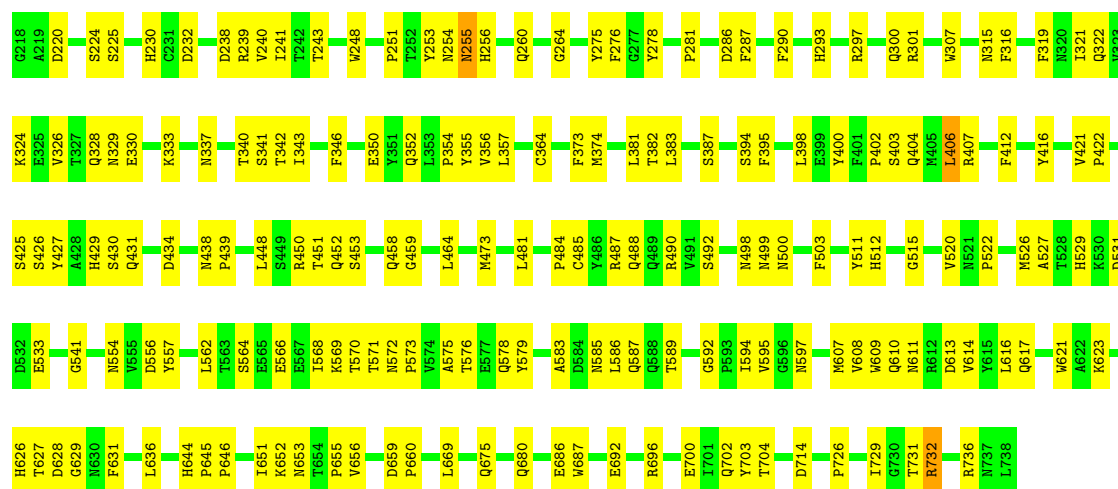
• Molecule 1: Capsid protein VP1

Chain 7: 64% 35%



• Molecule 1: Capsid protein VP1

Chain 8: 65% 34%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	52912	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	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	DIRECT ELECTRON DE-20 (5k x 3k)	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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	1	0.52	0/4261	0.55	0/5810
1	2	0.52	0/4261	0.55	0/5810
1	3	0.52	0/4261	0.55	0/5810
1	4	0.52	0/4261	0.55	0/5810
1	5	0.52	0/4261	0.55	0/5810
1	6	0.52	0/4261	0.55	0/5810
1	7	0.52	0/4261	0.55	0/5810
1	8	0.52	0/4261	0.55	0/5810
1	A	0.52	0/4261	0.55	0/5810
1	B	0.52	0/4261	0.55	0/5810
1	C	0.52	0/4261	0.55	0/5810
1	D	0.52	0/4261	0.55	0/5810
1	E	0.52	0/4261	0.55	0/5810
1	F	0.52	0/4261	0.55	0/5810
1	G	0.52	0/4261	0.55	0/5810
1	H	0.52	0/4261	0.55	0/5810
1	I	0.52	0/4261	0.55	0/5810
1	J	0.52	0/4261	0.55	0/5810
1	K	0.52	0/4261	0.55	0/5810
1	L	0.52	0/4261	0.55	0/5810
1	M	0.52	0/4261	0.55	0/5810
1	N	0.52	0/4261	0.55	0/5810
1	O	0.52	0/4261	0.55	0/5810
1	P	0.52	0/4261	0.55	0/5810
1	Q	0.52	0/4261	0.55	0/5810
1	R	0.52	0/4261	0.55	0/5810
1	S	0.52	0/4261	0.55	0/5810
1	T	0.52	0/4261	0.55	0/5810
1	U	0.52	0/4261	0.55	0/5810
1	V	0.52	0/4261	0.55	0/5810
1	W	0.52	0/4261	0.55	0/5810
1	X	0.52	0/4261	0.55	0/5810
1	Y	0.52	0/4261	0.55	0/5810
1	Z	0.52	0/4261	0.55	0/5810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	a	0.52	0/4261	0.55	0/5810
1	b	0.52	0/4261	0.55	0/5810
1	c	0.52	0/4261	0.55	0/5810
1	d	0.52	0/4261	0.55	0/5810
1	e	0.52	0/4261	0.55	0/5810
1	f	0.52	0/4261	0.55	0/5810
1	g	0.52	0/4261	0.55	0/5810
1	h	0.52	0/4261	0.55	0/5810
1	i	0.52	0/4261	0.55	0/5810
1	j	0.52	0/4261	0.55	0/5810
1	k	0.52	0/4261	0.55	0/5810
1	l	0.52	0/4261	0.55	0/5810
1	m	0.52	0/4261	0.55	0/5810
1	n	0.52	0/4261	0.55	0/5810
1	o	0.52	0/4261	0.55	0/5810
1	p	0.52	0/4261	0.55	0/5810
1	q	0.52	0/4261	0.55	0/5810
1	r	0.52	0/4261	0.55	0/5810
1	s	0.52	0/4261	0.55	0/5810
1	t	0.52	0/4261	0.55	0/5810
1	u	0.52	0/4261	0.55	0/5810
1	v	0.52	0/4261	0.55	0/5810
1	w	0.52	0/4261	0.55	0/5810
1	x	0.52	0/4261	0.55	0/5810
1	y	0.52	0/4261	0.55	0/5810
1	z	0.52	0/4261	0.55	0/5810
All	All	0.52	0/255660	0.55	0/348600

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	4138	0	3900	217	0
1	2	4138	0	3900	215	0
1	3	4138	0	3900	217	0
1	4	4138	0	3900	214	0
1	5	4138	0	3900	211	0
1	6	4138	0	3900	212	0
1	7	4138	0	3900	217	0
1	8	4138	0	3900	213	0
1	A	4138	0	3900	299	0
1	B	4138	0	3900	282	0
1	C	4138	0	3900	292	0
1	D	4138	0	3900	296	0
1	E	4138	0	3900	298	0
1	F	4138	0	3900	294	0
1	G	4138	0	3900	298	0
1	H	4138	0	3900	283	0
1	I	4138	0	3900	280	0
1	J	4138	0	3900	291	0
1	K	4138	0	3900	300	0
1	L	4138	0	3900	296	0
1	M	4138	0	3900	293	0
1	N	4138	0	3900	292	0
1	O	4138	0	3900	296	0
1	P	4138	0	3900	283	0
1	Q	4138	0	3900	283	0
1	R	4138	0	3900	272	0
1	S	4138	0	3900	274	0
1	T	4138	0	3900	292	0
1	U	4138	0	3900	299	0
1	V	4138	0	3900	298	0
1	W	4138	0	3900	308	0
1	X	4138	0	3900	297	0
1	Y	4138	0	3900	302	0
1	Z	4138	0	3900	298	0
1	a	4138	0	3900	0	0
1	b	4138	0	3900	0	0
1	c	4138	0	3900	0	0
1	d	4138	0	3900	0	0
1	e	4138	0	3900	0	0
1	f	4138	0	3900	0	0
1	g	4138	0	3900	0	0
1	h	4138	0	3900	0	0
1	i	4138	0	3900	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	j	4138	0	3900	0	0
1	k	4138	0	3900	0	0
1	l	4138	0	3900	0	0
1	m	4138	0	3900	0	0
1	n	4138	0	3900	0	0
1	o	4138	0	3900	0	0
1	p	4138	0	3900	0	0
1	q	4138	0	3900	0	0
1	r	4138	0	3900	0	0
1	s	4138	0	3900	0	0
1	t	4138	0	3900	0	0
1	u	4138	0	3900	0	0
1	v	4138	0	3900	0	0
1	w	4138	0	3900	0	0
1	x	4138	0	3900	0	0
1	y	4138	0	3900	0	0
1	z	4138	0	3900	0	0
All	All	248280	0	234000	7130	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 15.

The worst 5 of 7130 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:G:613:ASP:HB3	1:G:732:ARG:HD2	1.28	1.16
1:P:613:ASP:HB3	1:P:732:ARG:HD2	1.28	1.16
1:H:613:ASP:HB3	1:H:732:ARG:HD2	1.28	1.16
1:K:613:ASP:HB3	1:K:732:ARG:HD2	1.28	1.16
1:C:613:ASP:HB3	1:C:732:ARG:HD2	1.28	1.15

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	2	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	3	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	4	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	5	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	6	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	7	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	8	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	A	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	B	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	C	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	D	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	E	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	F	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	G	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	H	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	I	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	J	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	K	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	L	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	M	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	N	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	O	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	P	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	Q	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	R	519/521 (100%)	501 (96%)	17 (3%)	1 (0%)	49	82
1	S	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	T	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	U	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	V	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	W	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	X	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	Y	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	Z	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	a	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	b	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	c	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	d	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	e	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	f	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	g	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	h	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	i	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	j	519/521 (100%)	501 (96%)	17 (3%)	1 (0%)	49	82
1	k	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	l	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	m	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	n	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	o	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	p	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	q	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	r	519/521 (100%)	501 (96%)	17 (3%)	1 (0%)	49	82
1	s	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	t	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	u	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	v	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	w	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	x	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	y	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
1	z	519/521 (100%)	500 (96%)	18 (4%)	1 (0%)	49	82
All	All	31140/31260 (100%)	30003 (96%)	1077 (4%)	60 (0%)	53	82

5 of 60 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	255	ASN
1	B	255	ASN
1	C	255	ASN
1	D	255	ASN
1	E	255	ASN

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	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	2	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	3	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	4	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	5	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	6	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	7	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	8	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	A	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	B	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	C	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	D	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	E	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	F	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	G	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	H	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	I	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	J	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	K	454/454 (100%)	451 (99%)	3 (1%)	85	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	M	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	N	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	O	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	P	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	Q	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	R	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	S	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	T	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	U	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	V	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	W	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	X	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	Y	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	Z	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	a	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	b	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	c	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	d	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	e	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	f	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	g	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	h	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	i	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	j	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	k	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	l	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	m	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	n	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	o	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	p	454/454 (100%)	451 (99%)	3 (1%)	85	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	q	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	r	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	s	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	t	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	u	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	v	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	w	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	x	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	y	454/454 (100%)	451 (99%)	3 (1%)	85	93
1	z	454/454 (100%)	451 (99%)	3 (1%)	85	93
All	All	27240/27240 (100%)	27060 (99%)	180 (1%)	86	93

5 of 180 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	406	LEU
1	h	448	LEU
1	4	448	LEU
1	b	732	ARG
1	e	448	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 780 such sidechains are listed below:

Mol	Chain	Res	Type
1	b	328	GLN
1	h	601	GLN
1	4	587	GLN
1	b	737	ASN
1	e	597	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates 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.