



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 05:39 PM UTC

PDB ID : 6V1G / pdb_00006v1g
EMDB ID : EMD-21011
Title : Genome-containing AAVrh.10
Authors : Mietzsch, M.; Agbandje-McKenna, M.
Deposited on : 2019-11-20
Resolution : 2.98 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:

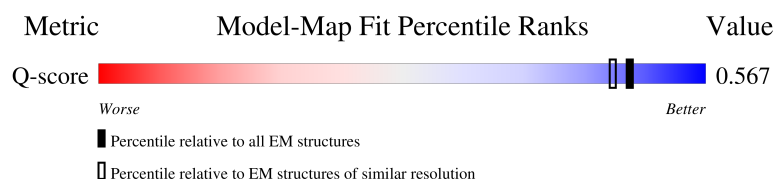
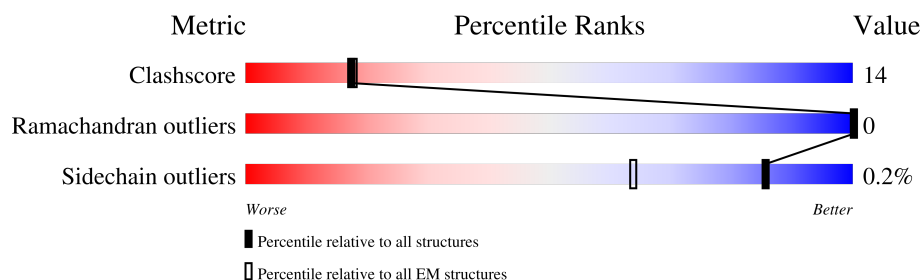
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.98 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.



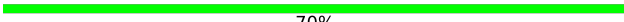
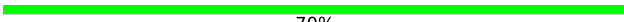
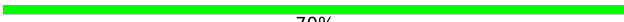
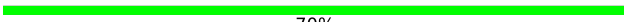
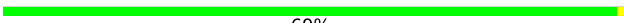
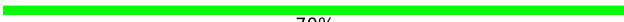
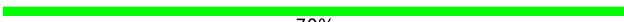
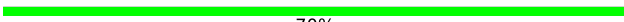
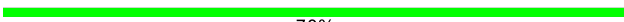
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13236 (2.48 - 3.48)

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	520	 69% 30%
1	2	520	 69% 31%
1	3	520	 70% 30%
1	4	520	 70% 30%

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Mol	Chain	Length	Quality of chain	
1	5	520		30%
1	6	520		30%
1	7	520		29%
1	8	520		30%
1	A	520		30%
1	B	520		30%
1	C	520		29%
1	D	520		30%
1	E	520		29%
1	F	520		30%
1	G	520		31%
1	H	520		30%
1	I	520		31%
1	J	520		30%
1	K	520		30%
1	L	520		30%
1	M	520		30%
1	N	520		30%
1	O	520		30%
1	P	520		29%
1	Q	520		30%
1	R	520		30%
1	S	520		30%
1	T	520		30%
1	U	520		30%

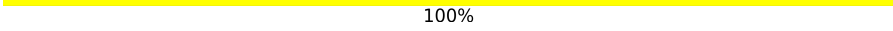
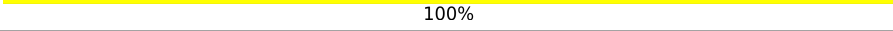
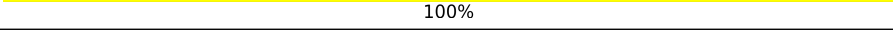
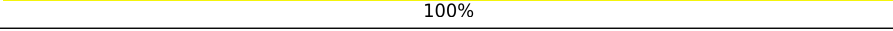
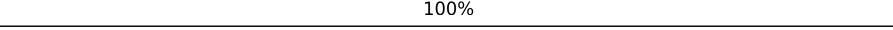
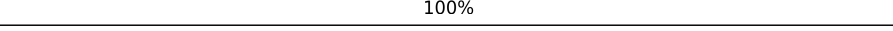
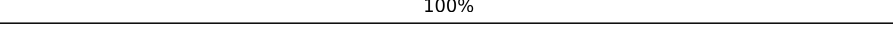
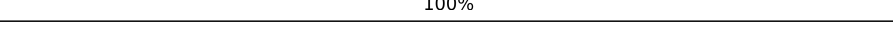
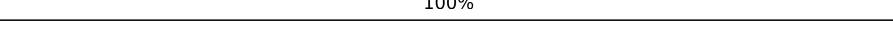
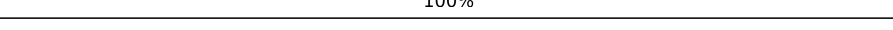
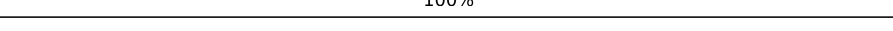
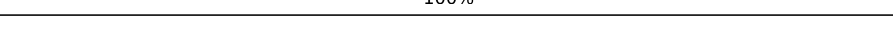
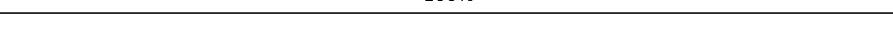
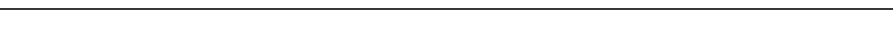
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Mol	Chain	Length	Quality of chain	
1	V	520		30%
1	W	520		30%
1	X	520		30%
1	Y	520		30%
1	Z	520		30%
1	a	520		30%
1	b	520		30%
1	c	520		30%
1	d	520		31%
1	e	520		30%
1	f	520		31%
1	g	520		30%
1	h	520		30%
1	i	520		30%
1	j	520		31%
1	k	520		30%
1	l	520		30%
1	m	520		30%
1	n	520		30%
1	o	520		30%
1	p	520		31%
1	q	520		30%
1	r	520		30%
1	s	520		30%
1	t	520		30%

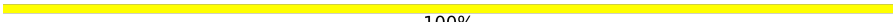
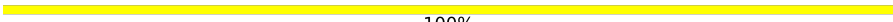
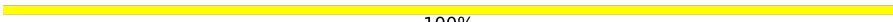
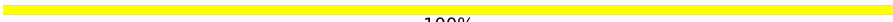
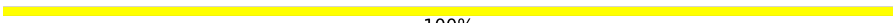
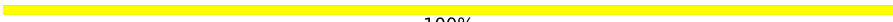
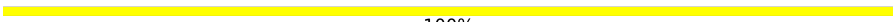
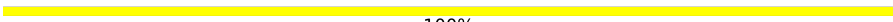
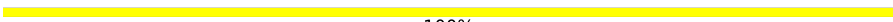
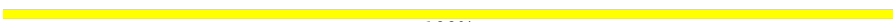
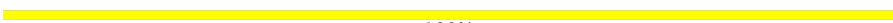
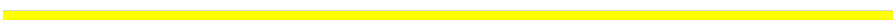
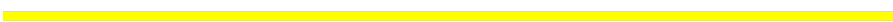
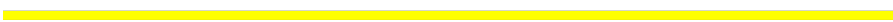
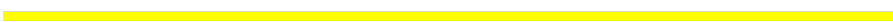
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Mol	Chain	Length	Quality of chain
1	u	520	 70%30%
1	v	520	 70%30%
1	w	520	 70%30%
1	x	520	 70%30%
1	y	520	 69%30%
1	z	520	 70%30%
2	0	2	 100%
2	0A	2	 100%
2	1A	2	 100%
2	2A	2	 100%
2	3A	2	 100%
2	4A	2	 100%
2	5A	2	 100%
2	9	2	 100%
2	AA	2	 100%
2	BA	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%

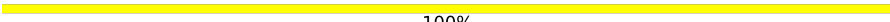
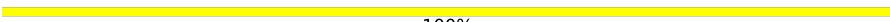
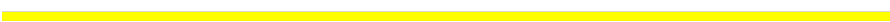
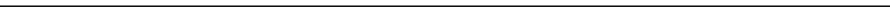
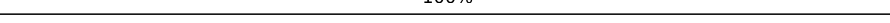
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Mol	Chain	Length	Quality of chain
2	LA	2	 100%
2	MA	2	 100%
2	NA	2	 100%
2	OA	2	 100%
2	PA	2	 100%
2	QA	2	 100%
2	RA	2	 100%
2	SA	2	 100%
2	TA	2	 100%
2	UA	2	 100%
2	VA	2	 100%
2	WA	2	 100%
2	XA	2	 100%
2	YA	2	 100%
2	ZA	2	 100%
2	aA	2	 100%
2	bA	2	 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

There are 2 unique types of molecules in this entry. The entry contains 249900 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	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	B	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	C	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	D	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	E	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	F	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	G	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	H	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	I	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	J	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	K	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	L	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	M	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	N	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	O	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	P	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		
1	Q	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	S	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	T	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	U	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	V	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	W	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	X	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	Y	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	Z	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	a	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	b	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	c	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	d	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	e	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	f	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	g	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	h	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	i	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	j	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	k	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	l	520	Total 4128	C 2608	N 712	O 794	S 14	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	n	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	o	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	p	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	q	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	r	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	s	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	t	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	u	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	v	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	w	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	x	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	y	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	z	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	1	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	2	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	3	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	4	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	5	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	6	520	Total 4128	C 2608	N 712	O 794	S 14	0	0
1	7	520	Total 4128	C 2608	N 712	O 794	S 14	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	520	Total	C	N	O	S	0	0
			4128	2608	712	794	14		

There are 180 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	365	LEU	PRO	conflict	UNP Q6JC62
A	406	LEU	ARG	conflict	UNP Q6JC62
A	720	ASP	GLU	conflict	UNP Q6JC62
B	365	LEU	PRO	conflict	UNP Q6JC62
B	406	LEU	ARG	conflict	UNP Q6JC62
B	720	ASP	GLU	conflict	UNP Q6JC62
C	365	LEU	PRO	conflict	UNP Q6JC62
C	406	LEU	ARG	conflict	UNP Q6JC62
C	720	ASP	GLU	conflict	UNP Q6JC62
D	365	LEU	PRO	conflict	UNP Q6JC62
D	406	LEU	ARG	conflict	UNP Q6JC62
D	720	ASP	GLU	conflict	UNP Q6JC62
E	365	LEU	PRO	conflict	UNP Q6JC62
E	406	LEU	ARG	conflict	UNP Q6JC62
E	720	ASP	GLU	conflict	UNP Q6JC62
F	365	LEU	PRO	conflict	UNP Q6JC62
F	406	LEU	ARG	conflict	UNP Q6JC62
F	720	ASP	GLU	conflict	UNP Q6JC62
G	365	LEU	PRO	conflict	UNP Q6JC62
G	406	LEU	ARG	conflict	UNP Q6JC62
G	720	ASP	GLU	conflict	UNP Q6JC62
H	365	LEU	PRO	conflict	UNP Q6JC62
H	406	LEU	ARG	conflict	UNP Q6JC62
H	720	ASP	GLU	conflict	UNP Q6JC62
I	365	LEU	PRO	conflict	UNP Q6JC62
I	406	LEU	ARG	conflict	UNP Q6JC62
I	720	ASP	GLU	conflict	UNP Q6JC62
J	365	LEU	PRO	conflict	UNP Q6JC62
J	406	LEU	ARG	conflict	UNP Q6JC62
J	720	ASP	GLU	conflict	UNP Q6JC62
K	365	LEU	PRO	conflict	UNP Q6JC62
K	406	LEU	ARG	conflict	UNP Q6JC62
K	720	ASP	GLU	conflict	UNP Q6JC62
L	365	LEU	PRO	conflict	UNP Q6JC62
L	406	LEU	ARG	conflict	UNP Q6JC62
L	720	ASP	GLU	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
M	365	LEU	PRO	conflict	UNP Q6JC62
M	406	LEU	ARG	conflict	UNP Q6JC62
M	720	ASP	GLU	conflict	UNP Q6JC62
N	365	LEU	PRO	conflict	UNP Q6JC62
N	406	LEU	ARG	conflict	UNP Q6JC62
N	720	ASP	GLU	conflict	UNP Q6JC62
O	365	LEU	PRO	conflict	UNP Q6JC62
O	406	LEU	ARG	conflict	UNP Q6JC62
O	720	ASP	GLU	conflict	UNP Q6JC62
P	365	LEU	PRO	conflict	UNP Q6JC62
P	406	LEU	ARG	conflict	UNP Q6JC62
P	720	ASP	GLU	conflict	UNP Q6JC62
Q	365	LEU	PRO	conflict	UNP Q6JC62
Q	406	LEU	ARG	conflict	UNP Q6JC62
Q	720	ASP	GLU	conflict	UNP Q6JC62
R	365	LEU	PRO	conflict	UNP Q6JC62
R	406	LEU	ARG	conflict	UNP Q6JC62
R	720	ASP	GLU	conflict	UNP Q6JC62
S	365	LEU	PRO	conflict	UNP Q6JC62
S	406	LEU	ARG	conflict	UNP Q6JC62
S	720	ASP	GLU	conflict	UNP Q6JC62
T	365	LEU	PRO	conflict	UNP Q6JC62
T	406	LEU	ARG	conflict	UNP Q6JC62
T	720	ASP	GLU	conflict	UNP Q6JC62
U	365	LEU	PRO	conflict	UNP Q6JC62
U	406	LEU	ARG	conflict	UNP Q6JC62
U	720	ASP	GLU	conflict	UNP Q6JC62
V	365	LEU	PRO	conflict	UNP Q6JC62
V	406	LEU	ARG	conflict	UNP Q6JC62
V	720	ASP	GLU	conflict	UNP Q6JC62
W	365	LEU	PRO	conflict	UNP Q6JC62
W	406	LEU	ARG	conflict	UNP Q6JC62
W	720	ASP	GLU	conflict	UNP Q6JC62
X	365	LEU	PRO	conflict	UNP Q6JC62
X	406	LEU	ARG	conflict	UNP Q6JC62
X	720	ASP	GLU	conflict	UNP Q6JC62
Y	365	LEU	PRO	conflict	UNP Q6JC62
Y	406	LEU	ARG	conflict	UNP Q6JC62
Y	720	ASP	GLU	conflict	UNP Q6JC62
Z	365	LEU	PRO	conflict	UNP Q6JC62
Z	406	LEU	ARG	conflict	UNP Q6JC62
Z	720	ASP	GLU	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
a	365	LEU	PRO	conflict	UNP Q6JC62
a	406	LEU	ARG	conflict	UNP Q6JC62
a	720	ASP	GLU	conflict	UNP Q6JC62
b	365	LEU	PRO	conflict	UNP Q6JC62
b	406	LEU	ARG	conflict	UNP Q6JC62
b	720	ASP	GLU	conflict	UNP Q6JC62
c	365	LEU	PRO	conflict	UNP Q6JC62
c	406	LEU	ARG	conflict	UNP Q6JC62
c	720	ASP	GLU	conflict	UNP Q6JC62
d	365	LEU	PRO	conflict	UNP Q6JC62
d	406	LEU	ARG	conflict	UNP Q6JC62
d	720	ASP	GLU	conflict	UNP Q6JC62
e	365	LEU	PRO	conflict	UNP Q6JC62
e	406	LEU	ARG	conflict	UNP Q6JC62
e	720	ASP	GLU	conflict	UNP Q6JC62
f	365	LEU	PRO	conflict	UNP Q6JC62
f	406	LEU	ARG	conflict	UNP Q6JC62
f	720	ASP	GLU	conflict	UNP Q6JC62
g	365	LEU	PRO	conflict	UNP Q6JC62
g	406	LEU	ARG	conflict	UNP Q6JC62
g	720	ASP	GLU	conflict	UNP Q6JC62
h	365	LEU	PRO	conflict	UNP Q6JC62
h	406	LEU	ARG	conflict	UNP Q6JC62
h	720	ASP	GLU	conflict	UNP Q6JC62
i	365	LEU	PRO	conflict	UNP Q6JC62
i	406	LEU	ARG	conflict	UNP Q6JC62
i	720	ASP	GLU	conflict	UNP Q6JC62
j	365	LEU	PRO	conflict	UNP Q6JC62
j	406	LEU	ARG	conflict	UNP Q6JC62
j	720	ASP	GLU	conflict	UNP Q6JC62
k	365	LEU	PRO	conflict	UNP Q6JC62
k	406	LEU	ARG	conflict	UNP Q6JC62
k	720	ASP	GLU	conflict	UNP Q6JC62
l	365	LEU	PRO	conflict	UNP Q6JC62
l	406	LEU	ARG	conflict	UNP Q6JC62
l	720	ASP	GLU	conflict	UNP Q6JC62
m	365	LEU	PRO	conflict	UNP Q6JC62
m	406	LEU	ARG	conflict	UNP Q6JC62
m	720	ASP	GLU	conflict	UNP Q6JC62
n	365	LEU	PRO	conflict	UNP Q6JC62
n	406	LEU	ARG	conflict	UNP Q6JC62
n	720	ASP	GLU	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
o	365	LEU	PRO	conflict	UNP Q6JC62
o	406	LEU	ARG	conflict	UNP Q6JC62
o	720	ASP	GLU	conflict	UNP Q6JC62
p	365	LEU	PRO	conflict	UNP Q6JC62
p	406	LEU	ARG	conflict	UNP Q6JC62
p	720	ASP	GLU	conflict	UNP Q6JC62
q	365	LEU	PRO	conflict	UNP Q6JC62
q	406	LEU	ARG	conflict	UNP Q6JC62
q	720	ASP	GLU	conflict	UNP Q6JC62
r	365	LEU	PRO	conflict	UNP Q6JC62
r	406	LEU	ARG	conflict	UNP Q6JC62
r	720	ASP	GLU	conflict	UNP Q6JC62
s	365	LEU	PRO	conflict	UNP Q6JC62
s	406	LEU	ARG	conflict	UNP Q6JC62
s	720	ASP	GLU	conflict	UNP Q6JC62
t	365	LEU	PRO	conflict	UNP Q6JC62
t	406	LEU	ARG	conflict	UNP Q6JC62
t	720	ASP	GLU	conflict	UNP Q6JC62
u	365	LEU	PRO	conflict	UNP Q6JC62
u	406	LEU	ARG	conflict	UNP Q6JC62
u	720	ASP	GLU	conflict	UNP Q6JC62
v	365	LEU	PRO	conflict	UNP Q6JC62
v	406	LEU	ARG	conflict	UNP Q6JC62
v	720	ASP	GLU	conflict	UNP Q6JC62
w	365	LEU	PRO	conflict	UNP Q6JC62
w	406	LEU	ARG	conflict	UNP Q6JC62
w	720	ASP	GLU	conflict	UNP Q6JC62
x	365	LEU	PRO	conflict	UNP Q6JC62
x	406	LEU	ARG	conflict	UNP Q6JC62
x	720	ASP	GLU	conflict	UNP Q6JC62
y	365	LEU	PRO	conflict	UNP Q6JC62
y	406	LEU	ARG	conflict	UNP Q6JC62
y	720	ASP	GLU	conflict	UNP Q6JC62
z	365	LEU	PRO	conflict	UNP Q6JC62
z	406	LEU	ARG	conflict	UNP Q6JC62
z	720	ASP	GLU	conflict	UNP Q6JC62
1	365	LEU	PRO	conflict	UNP Q6JC62
1	406	LEU	ARG	conflict	UNP Q6JC62
1	720	ASP	GLU	conflict	UNP Q6JC62
2	365	LEU	PRO	conflict	UNP Q6JC62
2	406	LEU	ARG	conflict	UNP Q6JC62
2	720	ASP	GLU	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
3	365	LEU	PRO	conflict	UNP Q6JC62
3	406	LEU	ARG	conflict	UNP Q6JC62
3	720	ASP	GLU	conflict	UNP Q6JC62
4	365	LEU	PRO	conflict	UNP Q6JC62
4	406	LEU	ARG	conflict	UNP Q6JC62
4	720	ASP	GLU	conflict	UNP Q6JC62
5	365	LEU	PRO	conflict	UNP Q6JC62
5	406	LEU	ARG	conflict	UNP Q6JC62
5	720	ASP	GLU	conflict	UNP Q6JC62
6	365	LEU	PRO	conflict	UNP Q6JC62
6	406	LEU	ARG	conflict	UNP Q6JC62
6	720	ASP	GLU	conflict	UNP Q6JC62
7	365	LEU	PRO	conflict	UNP Q6JC62
7	406	LEU	ARG	conflict	UNP Q6JC62
7	720	ASP	GLU	conflict	UNP Q6JC62
8	365	LEU	PRO	conflict	UNP Q6JC62
8	406	LEU	ARG	conflict	UNP Q6JC62
8	720	ASP	GLU	conflict	UNP Q6JC62

- 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		

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Mol	Chain	Residues	Atoms					AltConf	Trace
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
2	LA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	MA	2	Total 37	C 19	N 8	O 9	P 1	0	0
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	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

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Mol	Chain	Residues	Atoms					AltConf	Trace
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
2	lA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	mA	2	Total 37	C 19	N 8	O 9	P 1	0	0
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

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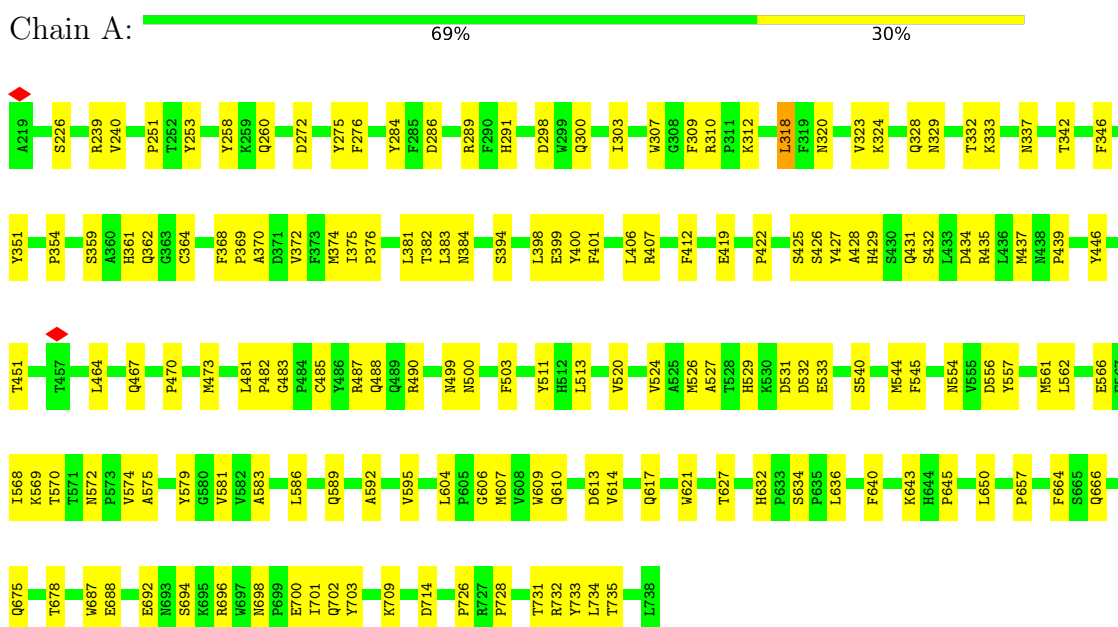
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	yA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	zA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	0A	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	1A	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	2A	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	3A	2	Total 37	C 19	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

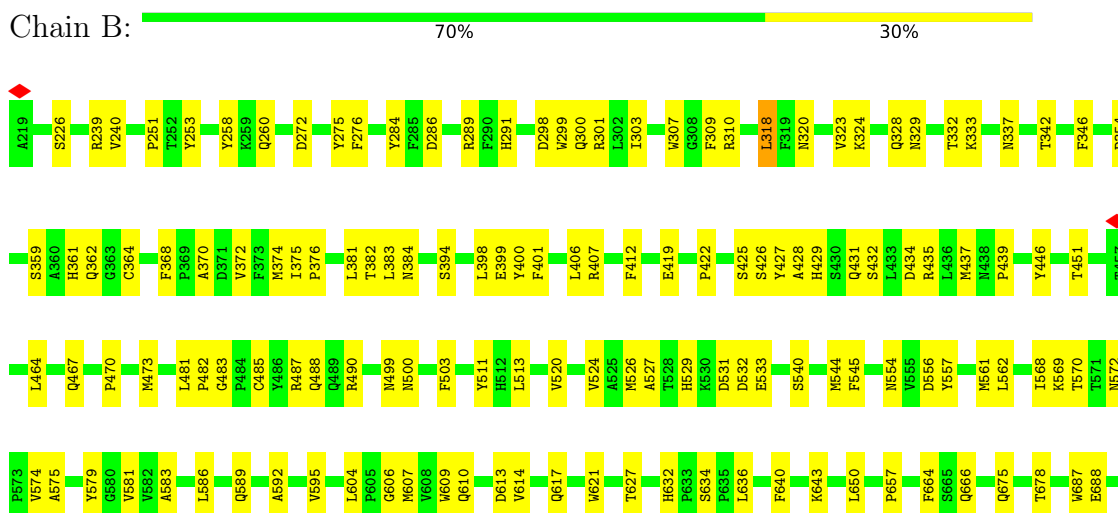
3 Residue-property plots

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 VP1



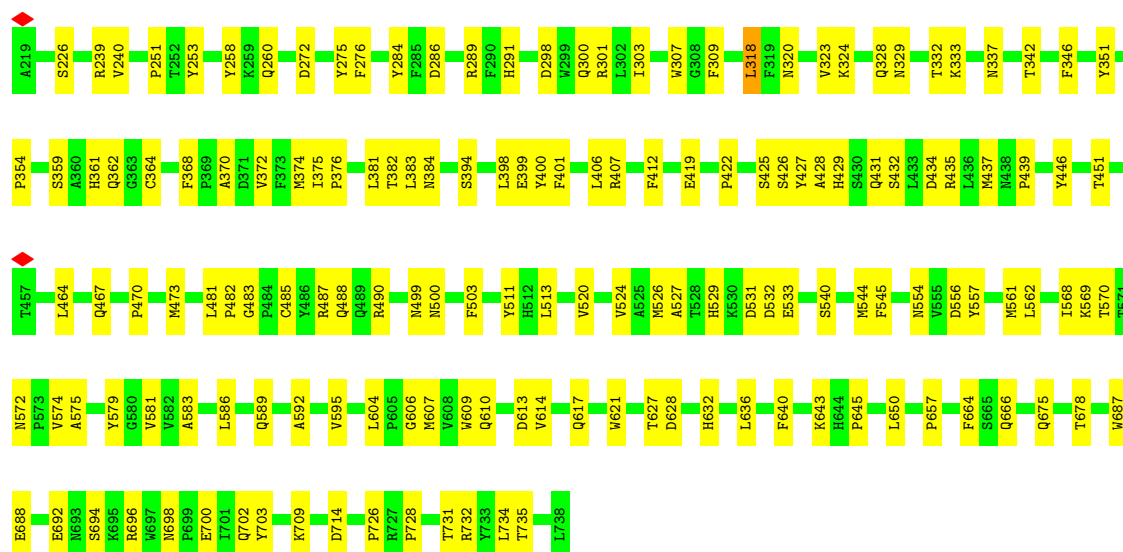
• Molecule 1: Capsid protein VP1





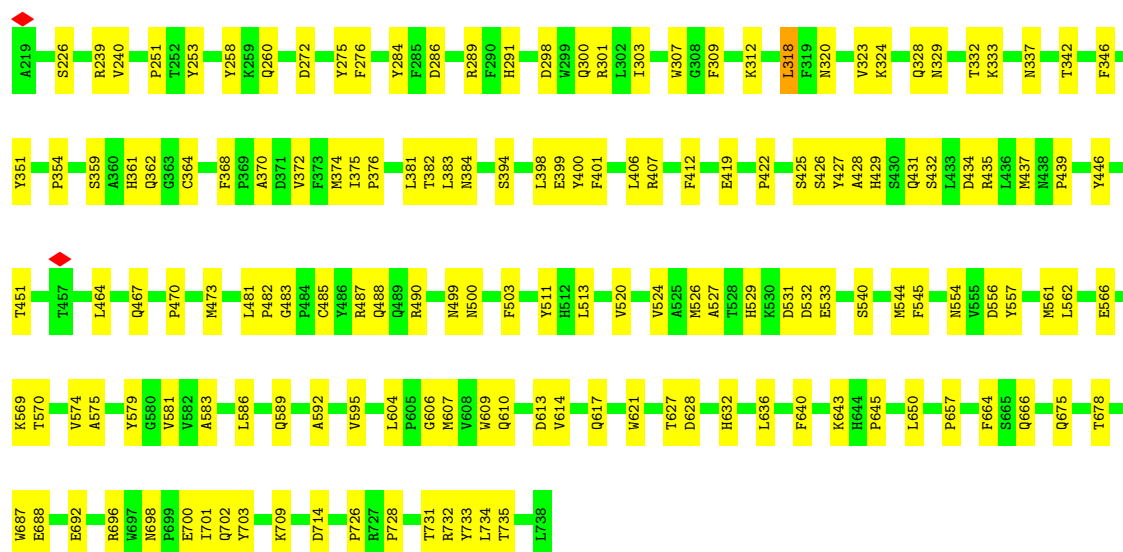
• Molecule 1: Capsid protein VP1

Chain C: 70% 29%



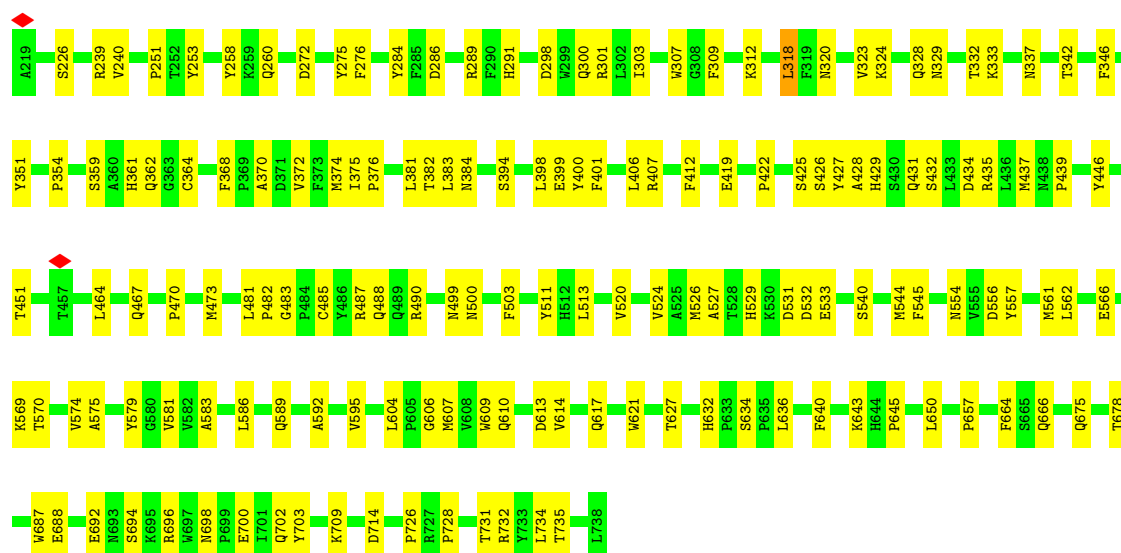
• Molecule 1: Capsid protein VP1

Chain D: 70% 30%



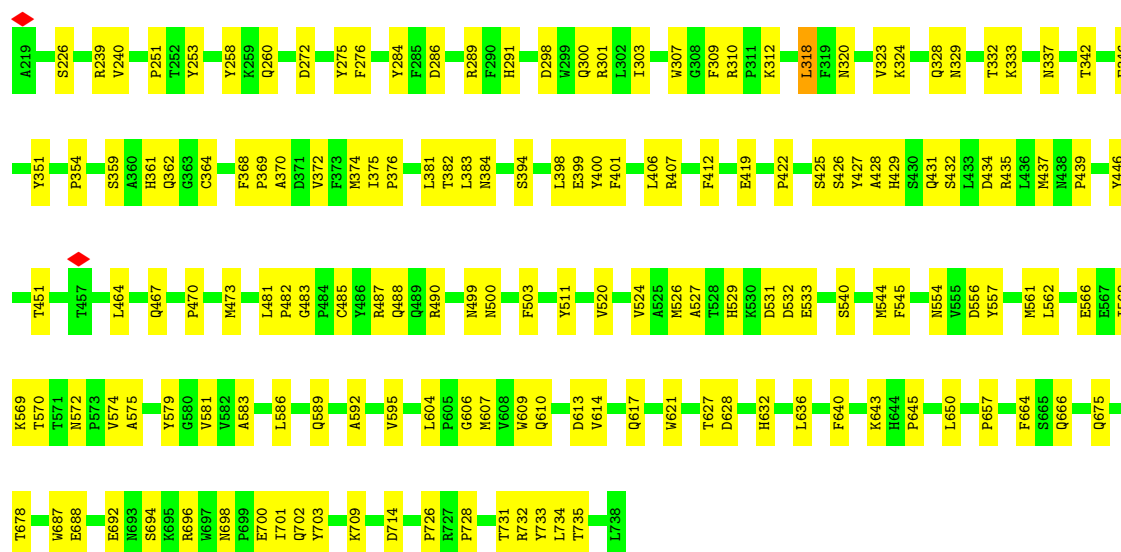
• Molecule 1: Capsid protein VP1

Chain E: 70% 29%



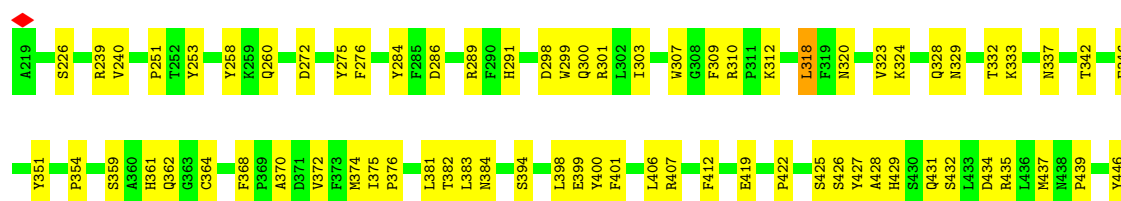
• Molecule 1: Capsid protein VP1

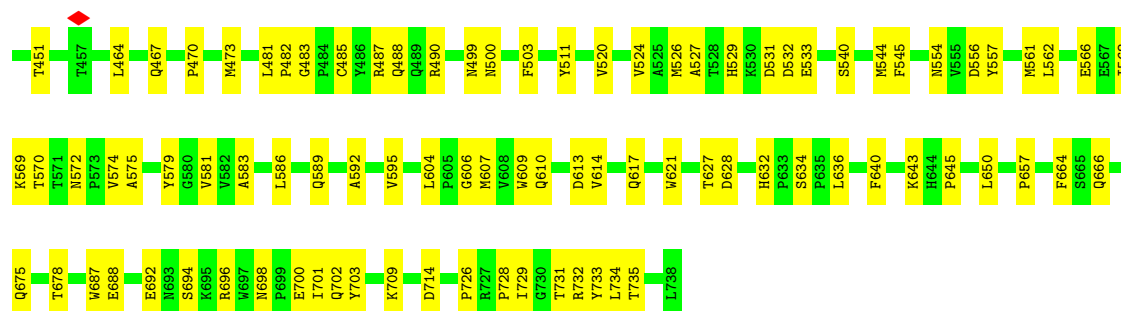
Chain F: 69% 30%



• Molecule 1: Capsid protein VP1

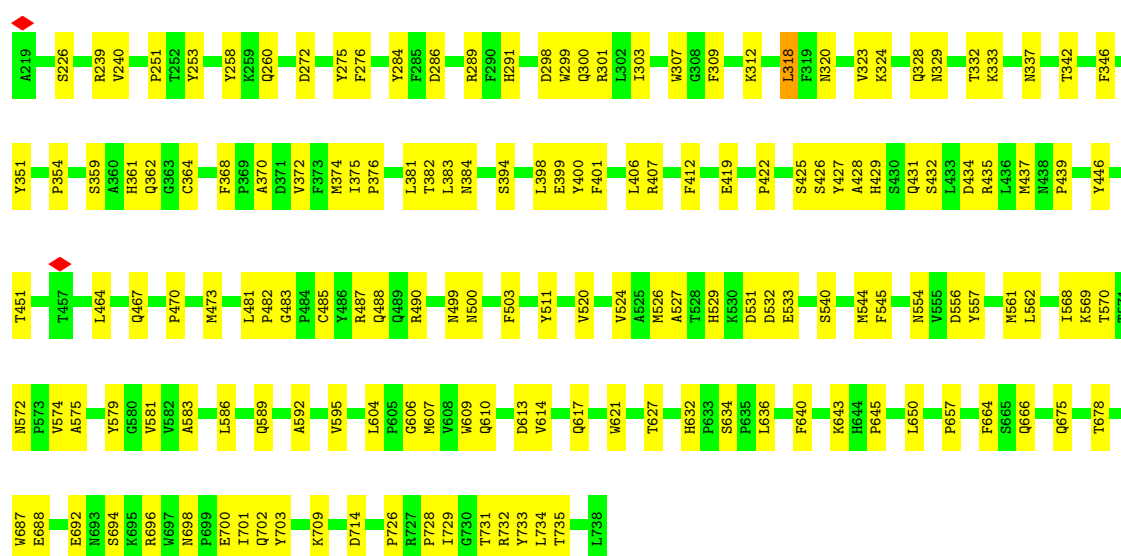
Chain G: 69% 31%





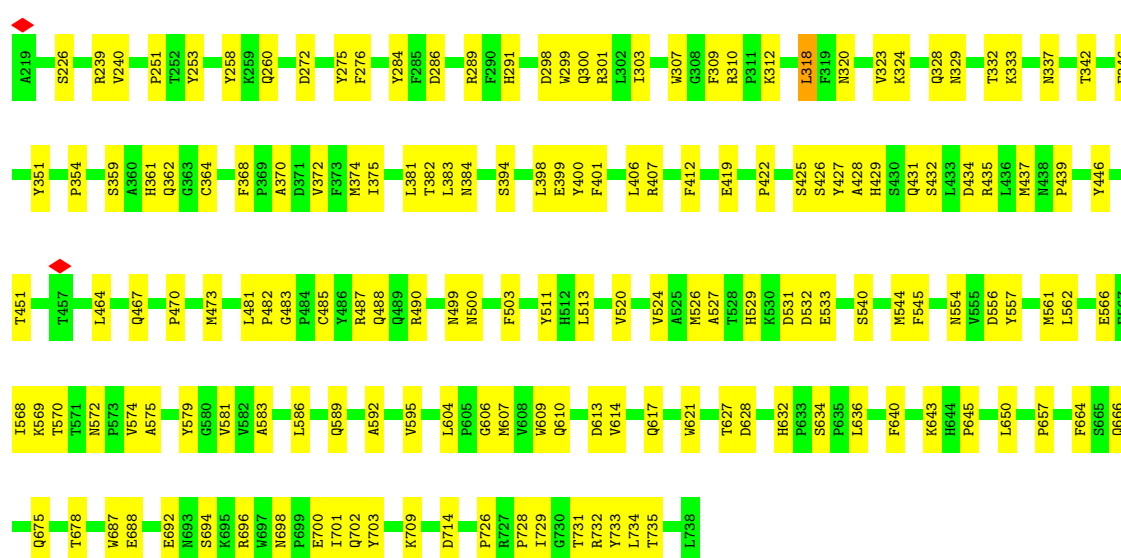
• Molecule 1: Capsid protein VP1

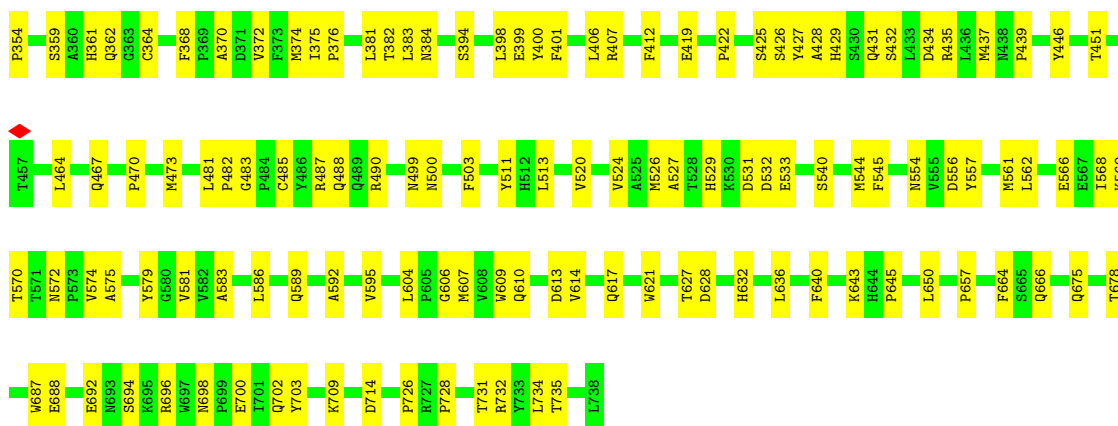
Chain H: 70% 30%



• Molecule 1: Capsid protein VP1

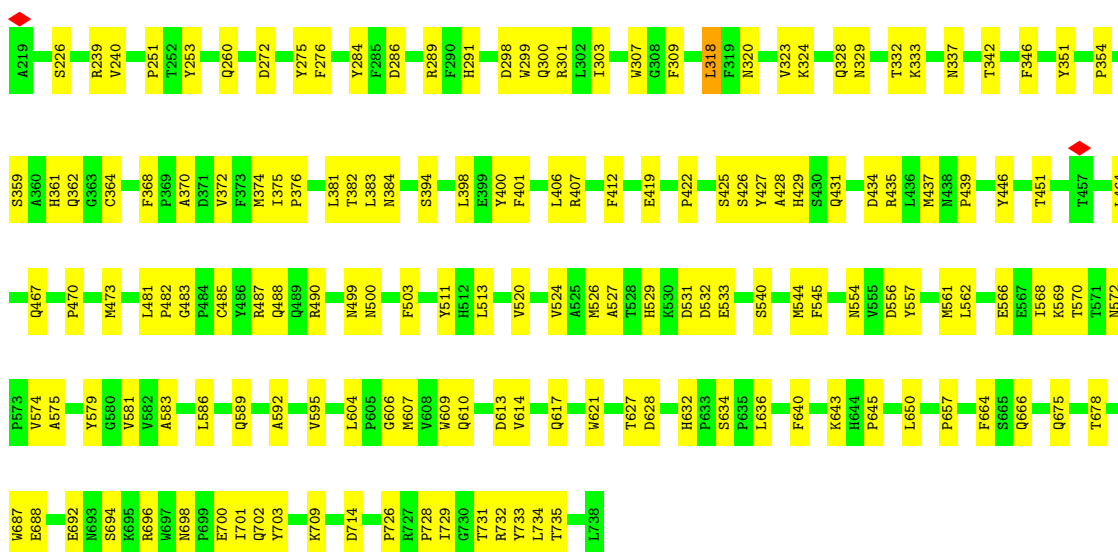
Chain I: 69% 31%





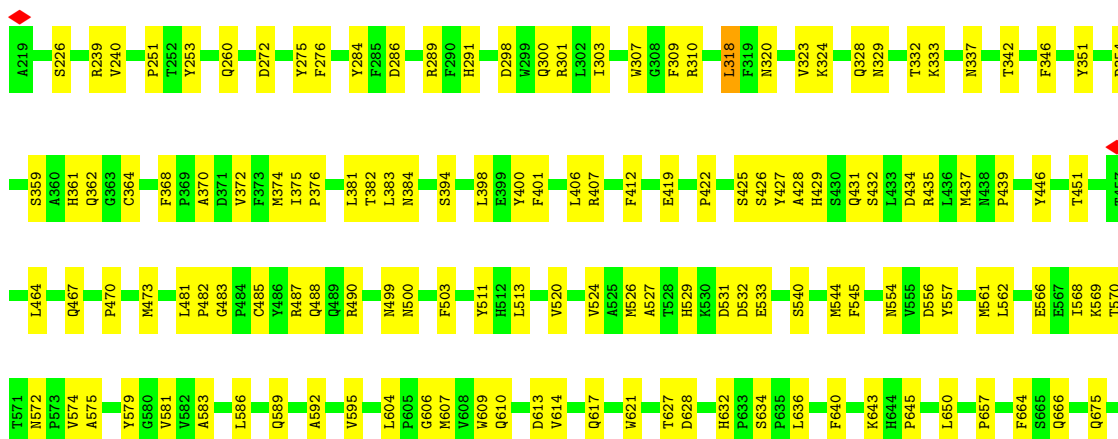
• Molecule 1: Capsid protein VP1

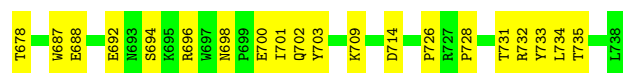
Chain M: 70% 30%



• Molecule 1: Capsid protein VP1

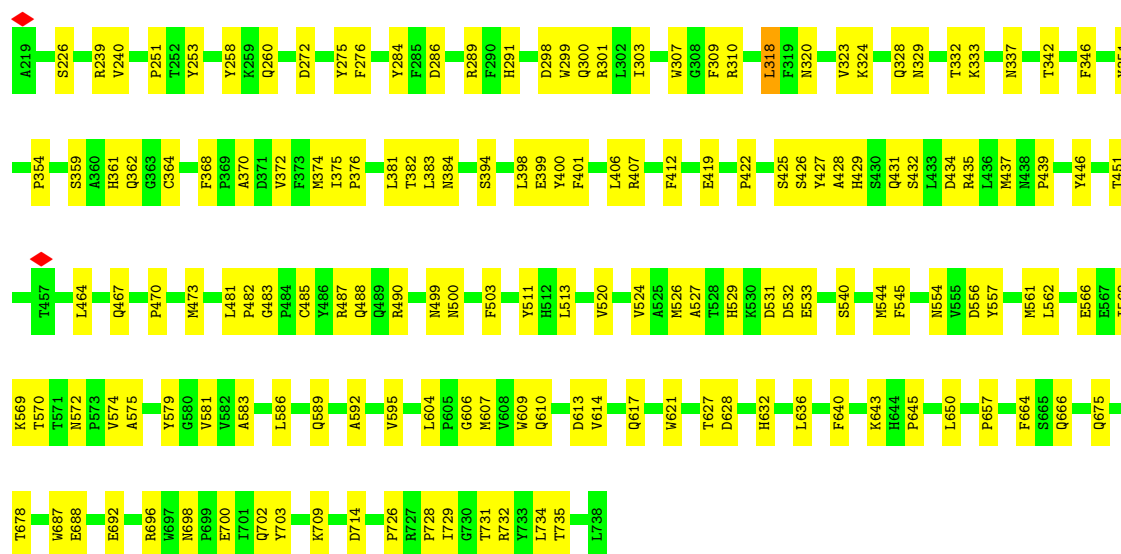
Chain N: 70% 30%





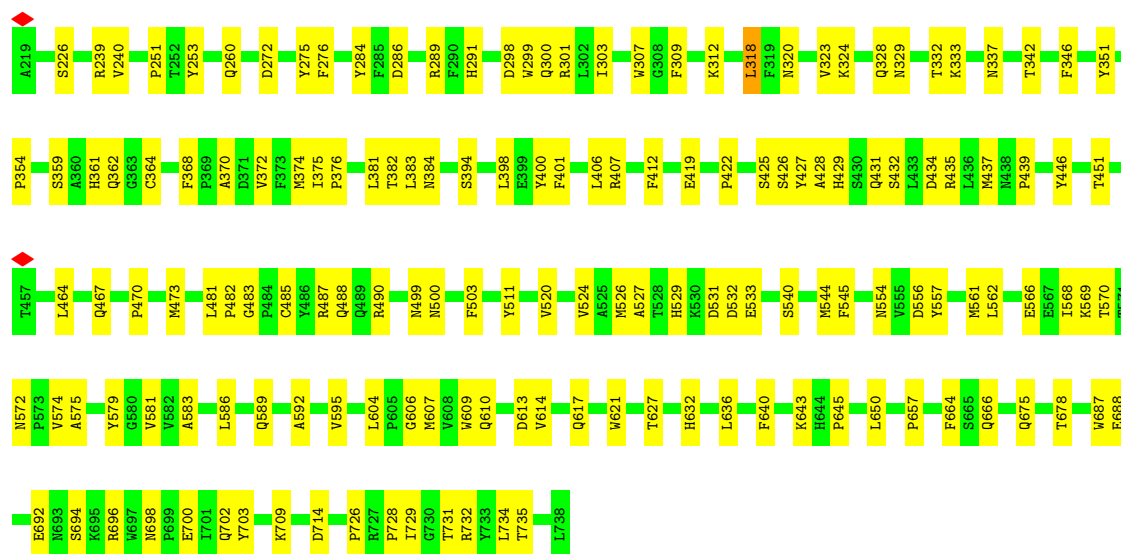
• Molecule 1: Capsid protein VP1

Chain O: 70% 30%



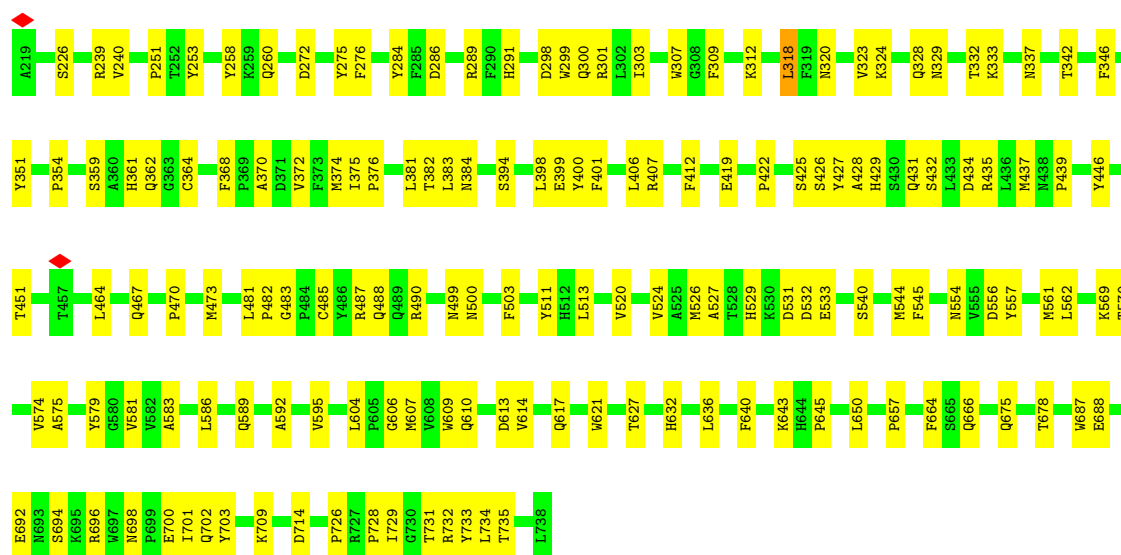
• Molecule 1: Capsid protein VP1

Chain P: 70% 29%



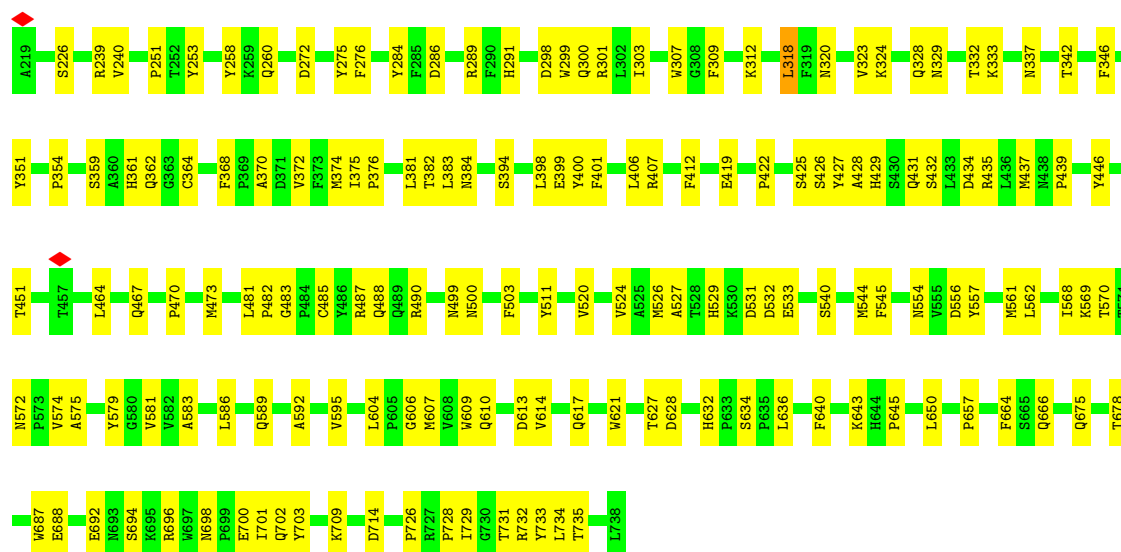
• Molecule 1: Capsid protein VP1

Chain Q: 70% 30%



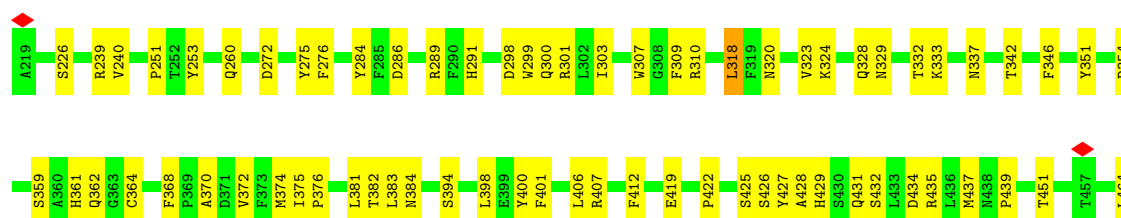
• Molecule 1: Capsid protein VP1

Chain R: 69% 30%

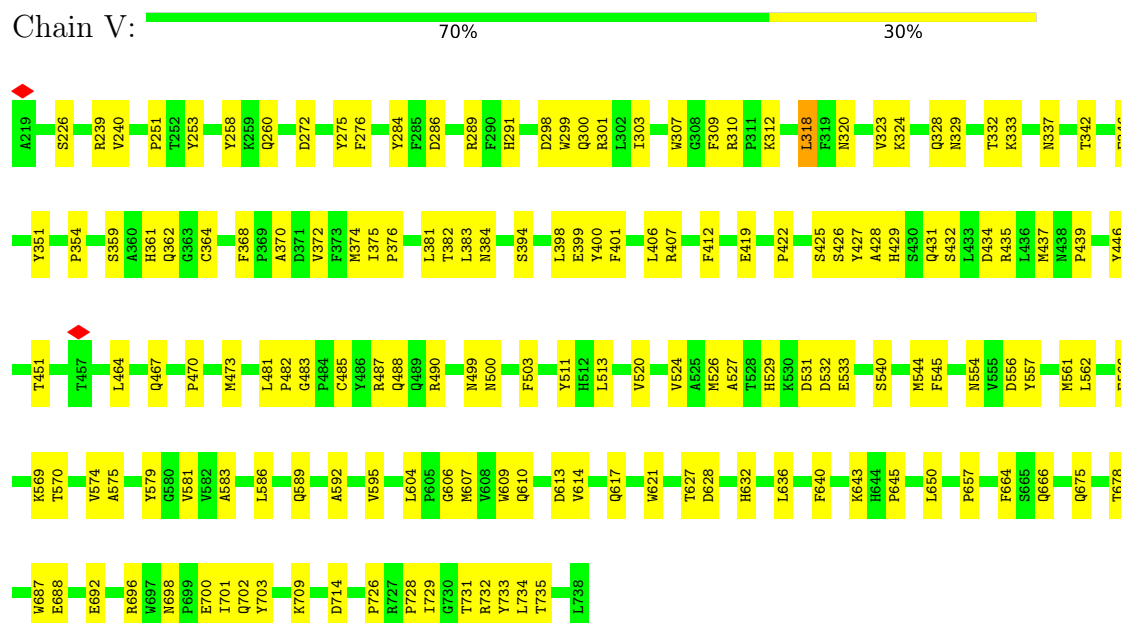


• Molecule 1: Capsid protein VP1

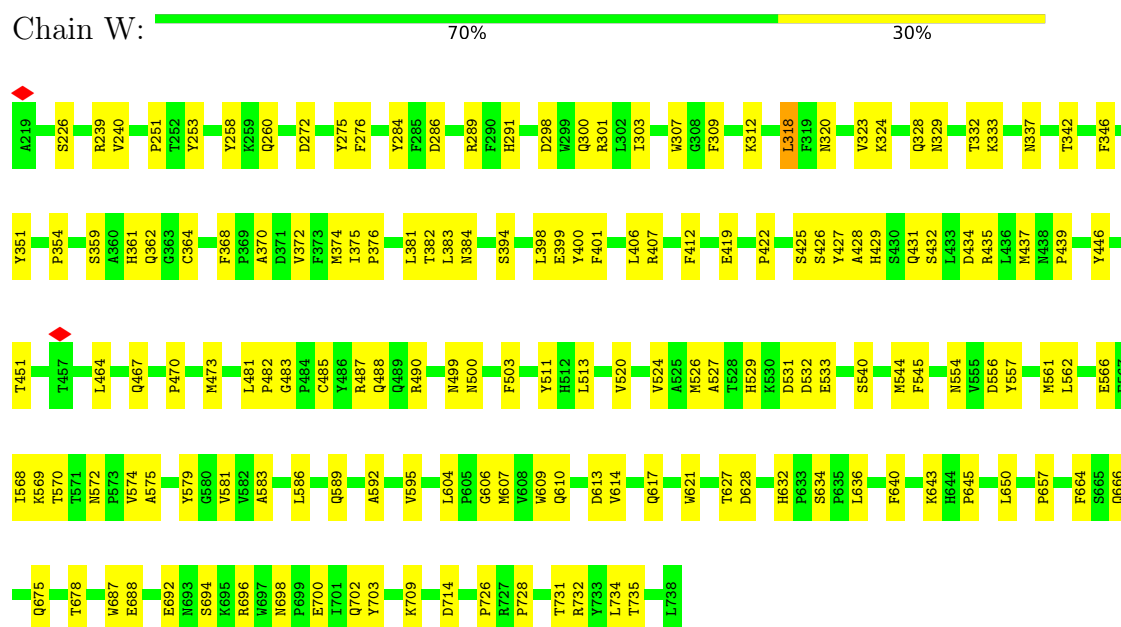
Chain S: 70% 30%



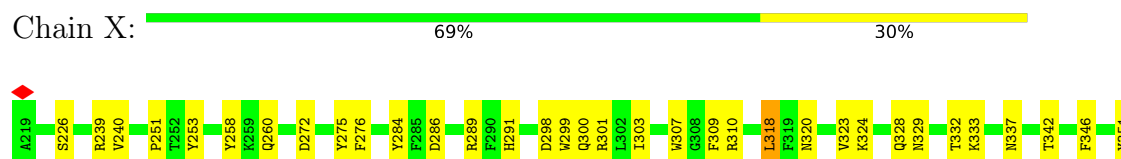
- Molecule 1: Capsid protein VP1



- Molecule 1: Capsid protein VP1



- Molecule 1: Capsid protein VP1

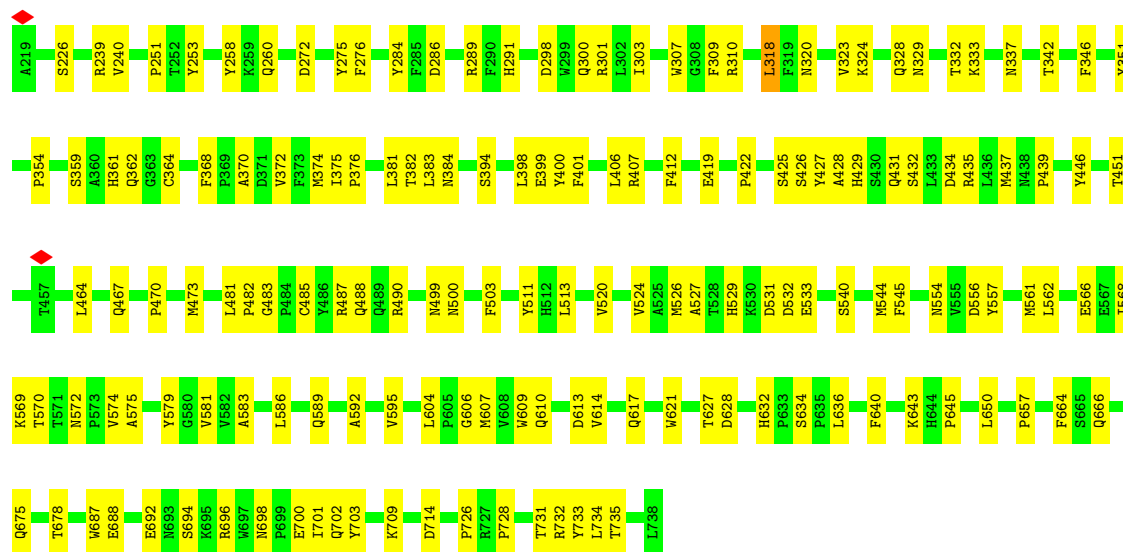






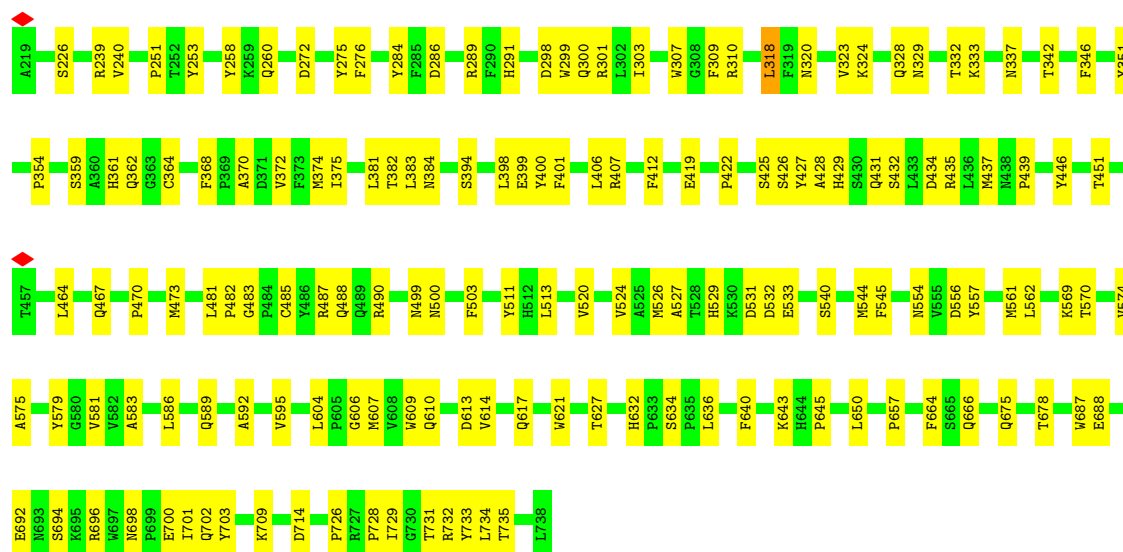
• Molecule 1: Capsid protein VP1

Chain a: 69% 30%



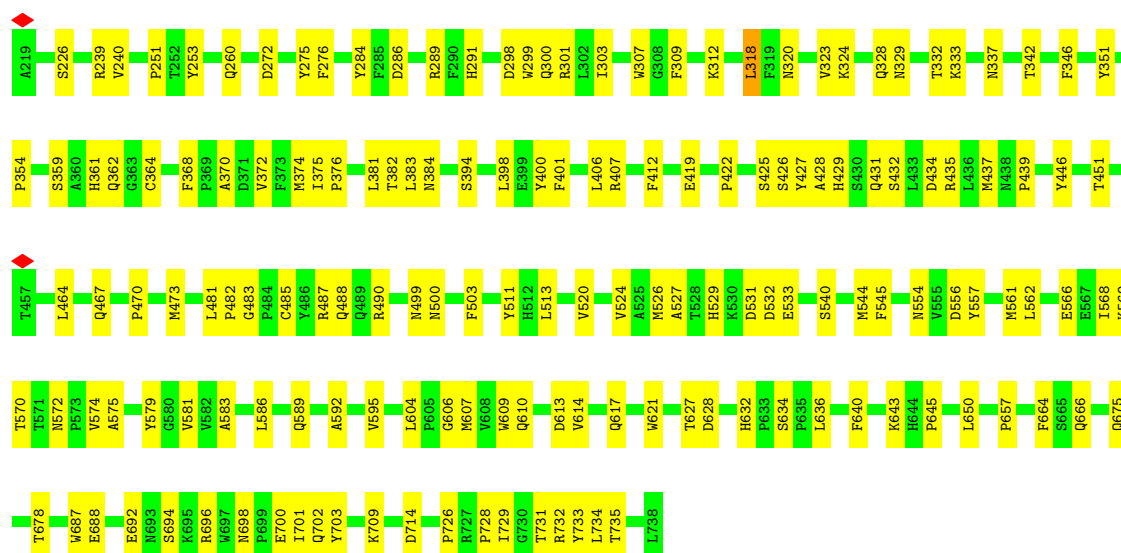
• Molecule 1: Capsid protein VP1

Chain b: 70% 30%

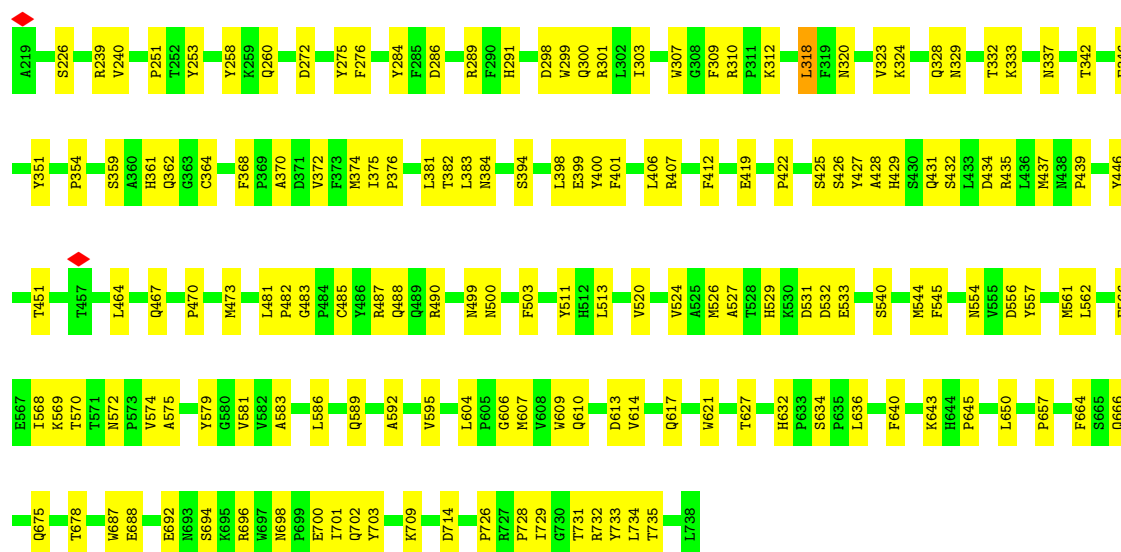


• Molecule 1: Capsid protein VP1

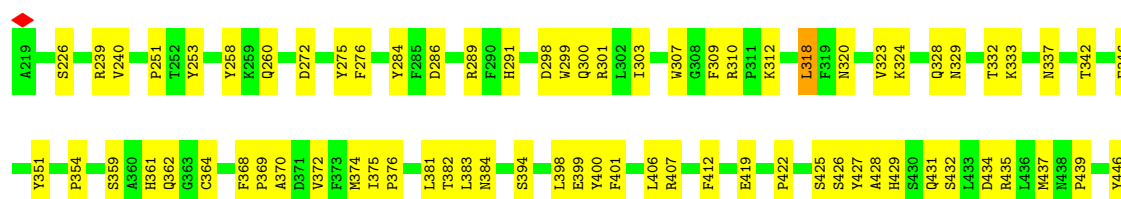
Chain c: 69% 30%

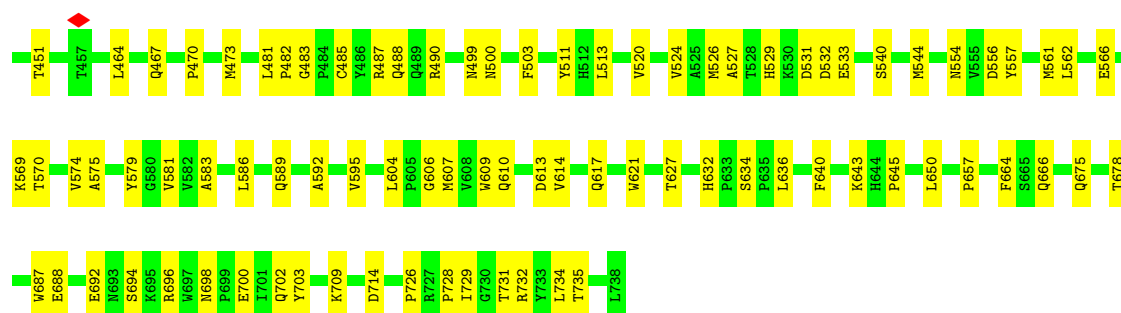


• Molecule 1: Capsid protein VP1



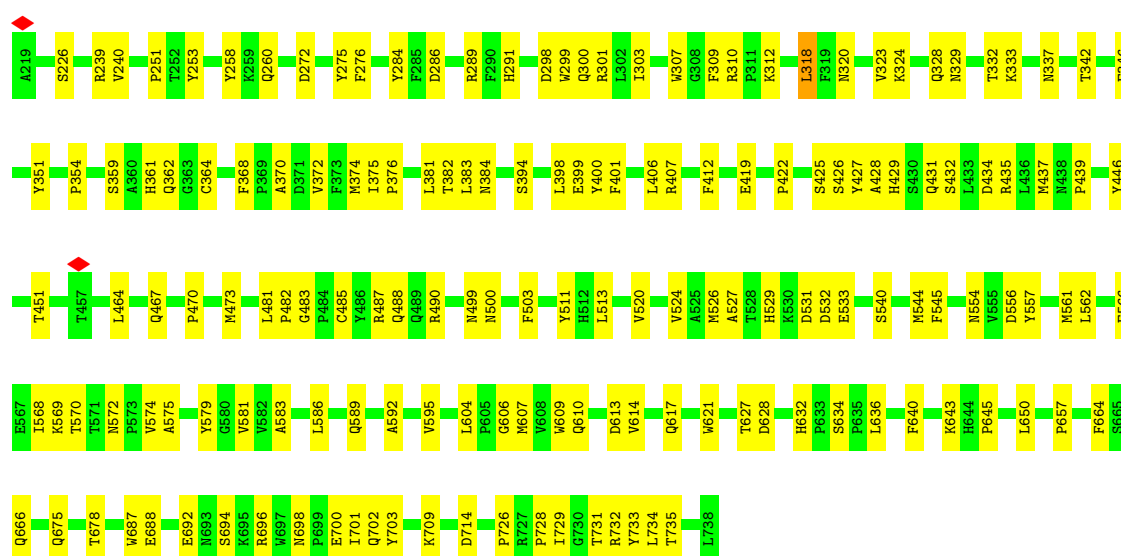
• Molecule 1: Capsid protein VP1





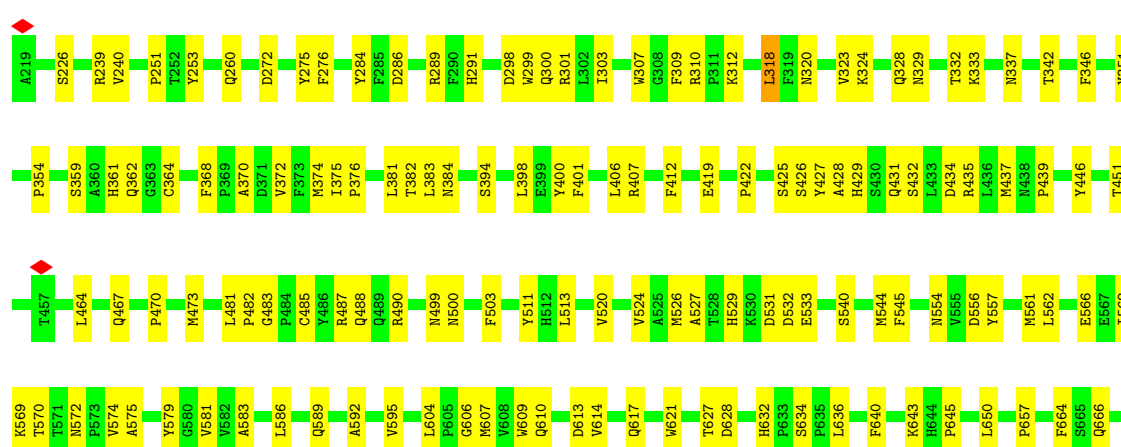
• Molecule 1: Capsid protein VP1

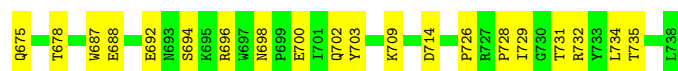
Chain f: 69% 31%



• Molecule 1: Capsid protein VP1

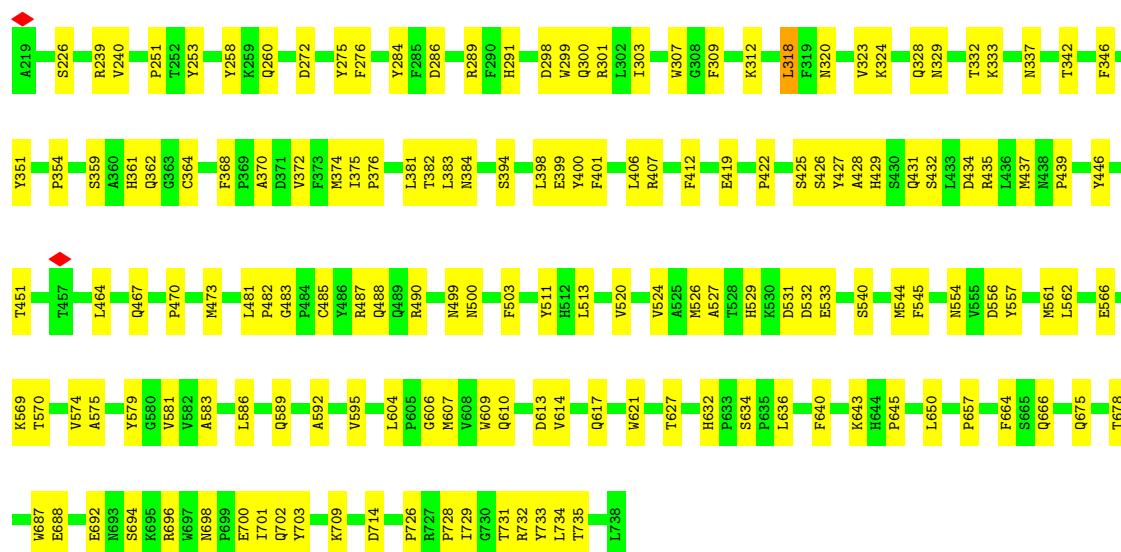
Chain g: 70% 30%





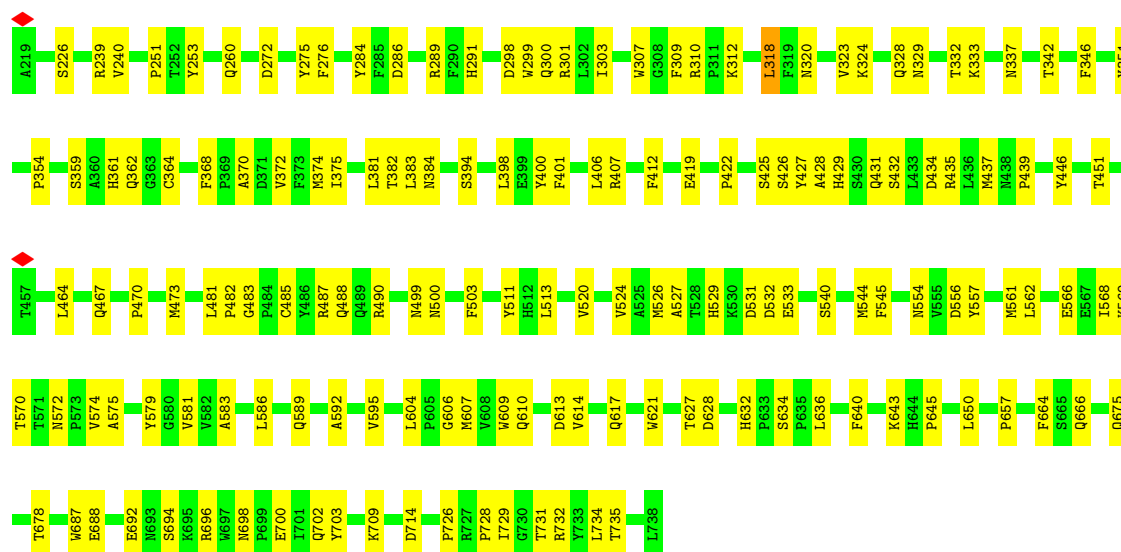
• Molecule 1: Capsid protein VP1

Chain h: 70% 30%



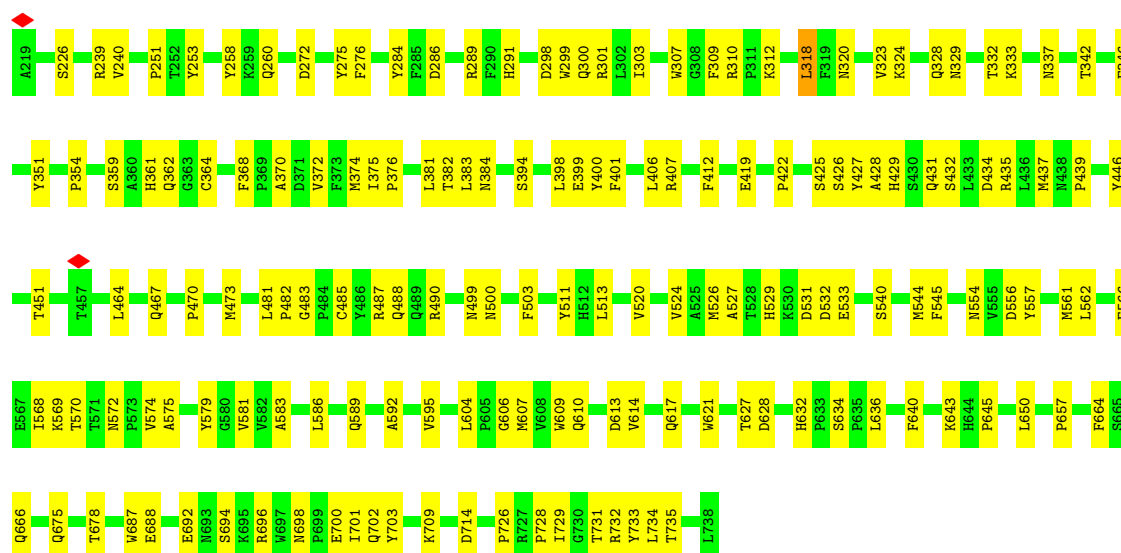
• Molecule 1: Capsid protein VP1

Chain i: 70% 30%



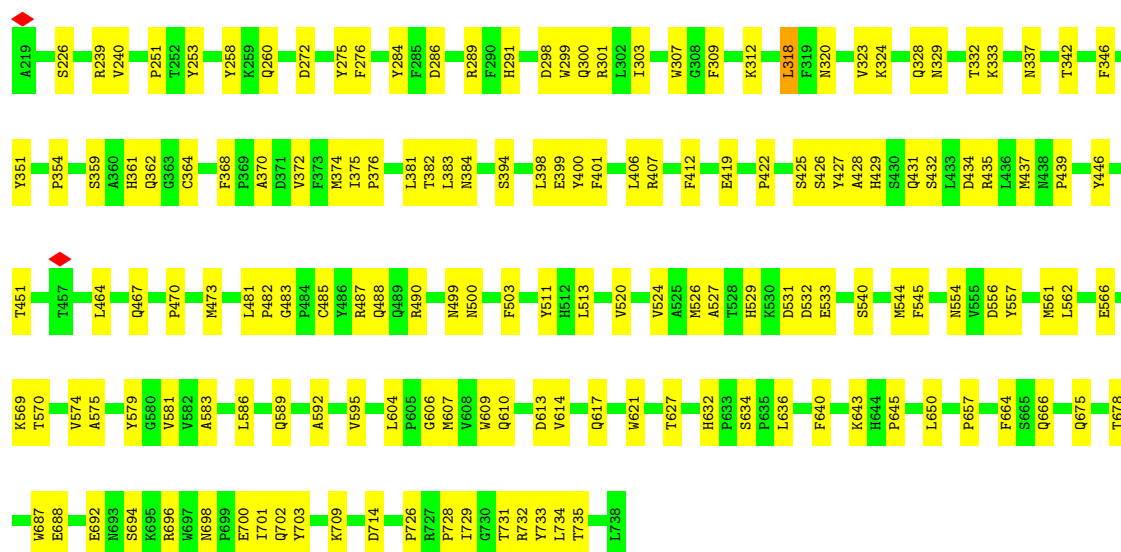
• Molecule 1: Capsid protein VP1

Chain j: 69% 31%



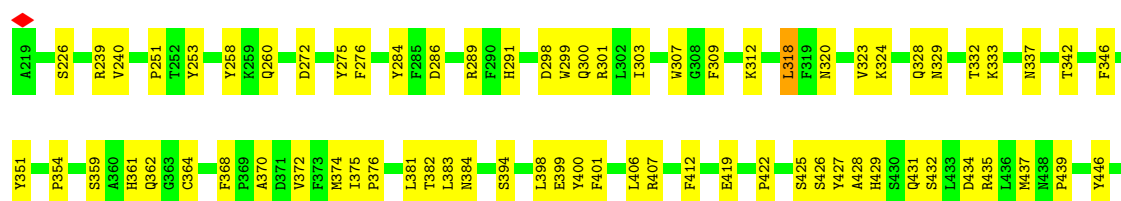
• Molecule 1: Capsid protein VP1

Chain k: 70% 30%



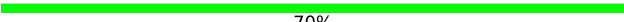
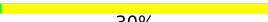
• Molecule 1: Capsid protein VP1

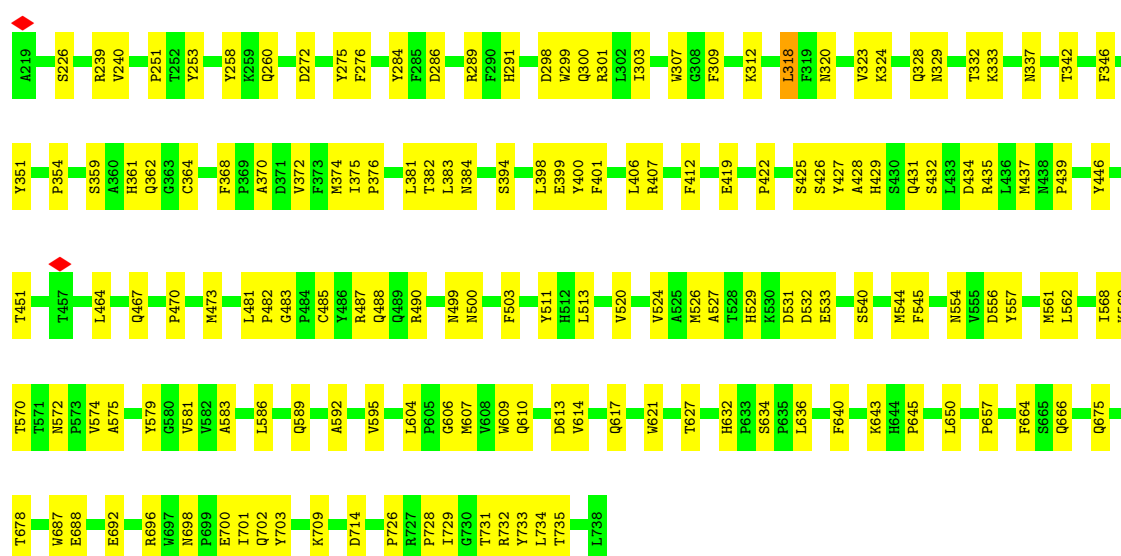
Chain l: 70% 30%



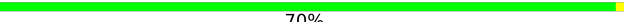
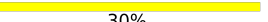


• Molecule 1: Capsid protein VP1

Chain m:  70%  30%

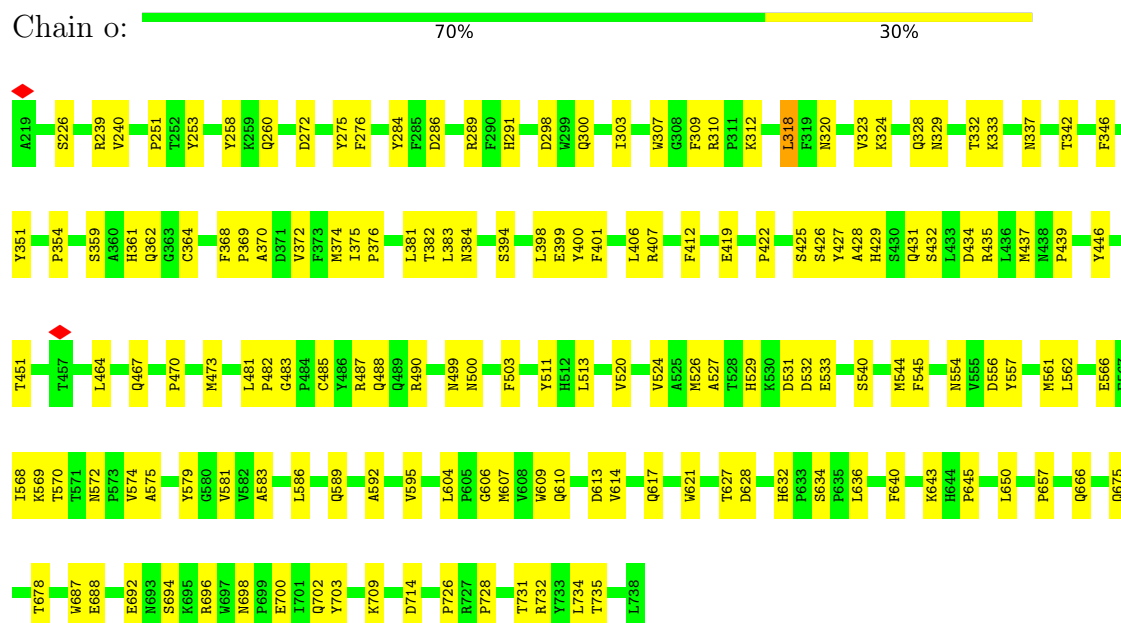


• Molecule 1: Capsid protein VP1

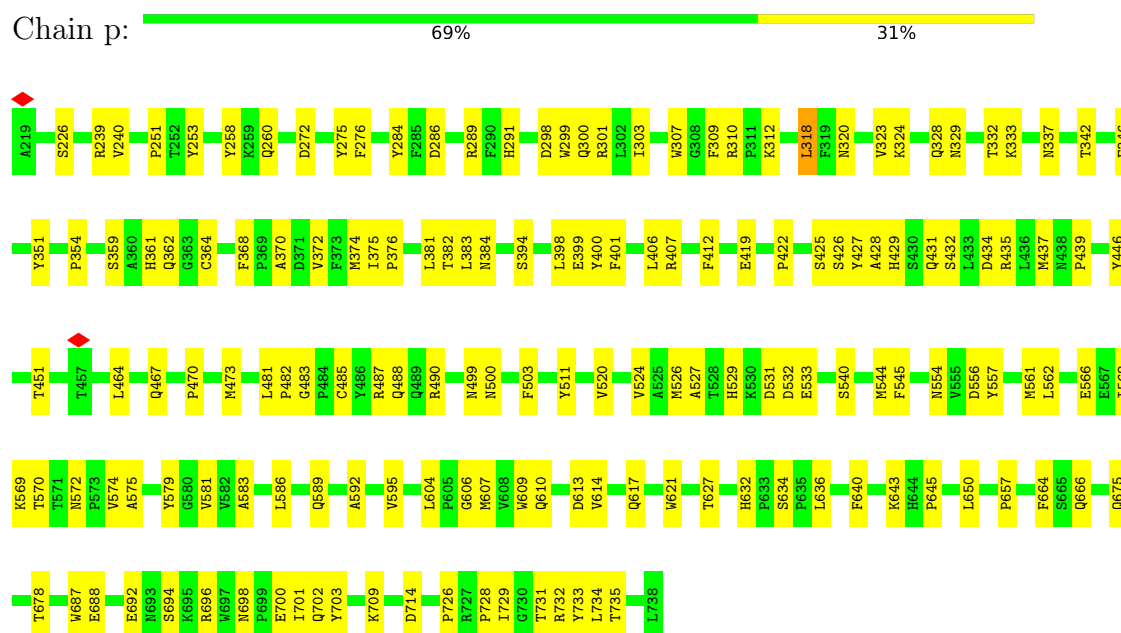
Chain n:  70%  30%



- Molecule 1: Capsid protein VP1

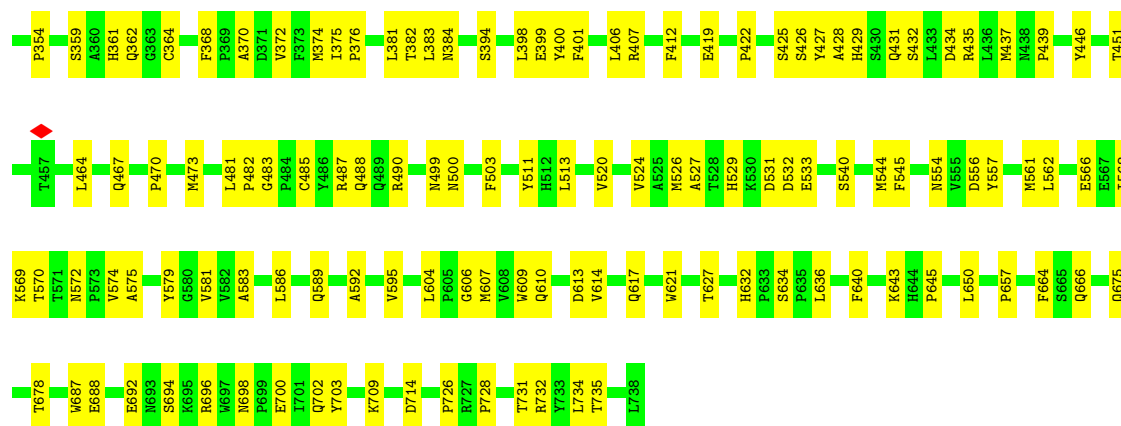


- Molecule 1: Capsid protein VP1



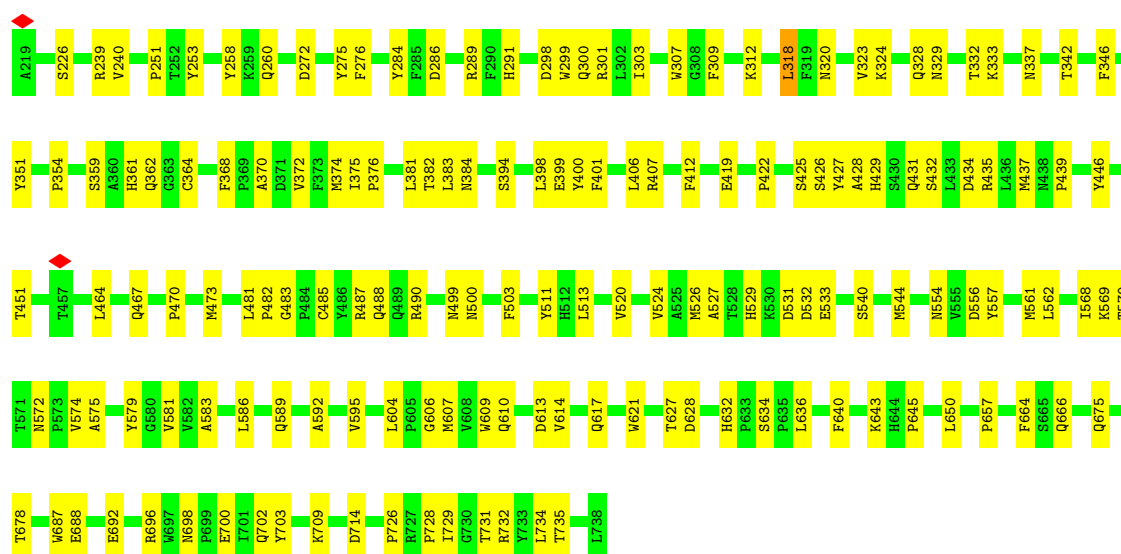
- Molecule 1: Capsid protein VP1





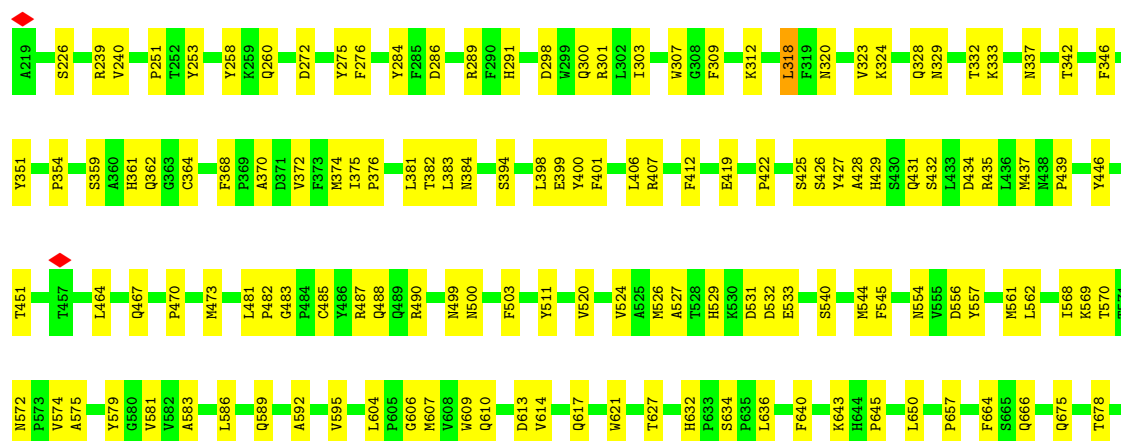
• Molecule 1: Capsid protein VP1

Chain r: 70% 30%



• Molecule 1: Capsid protein VP1

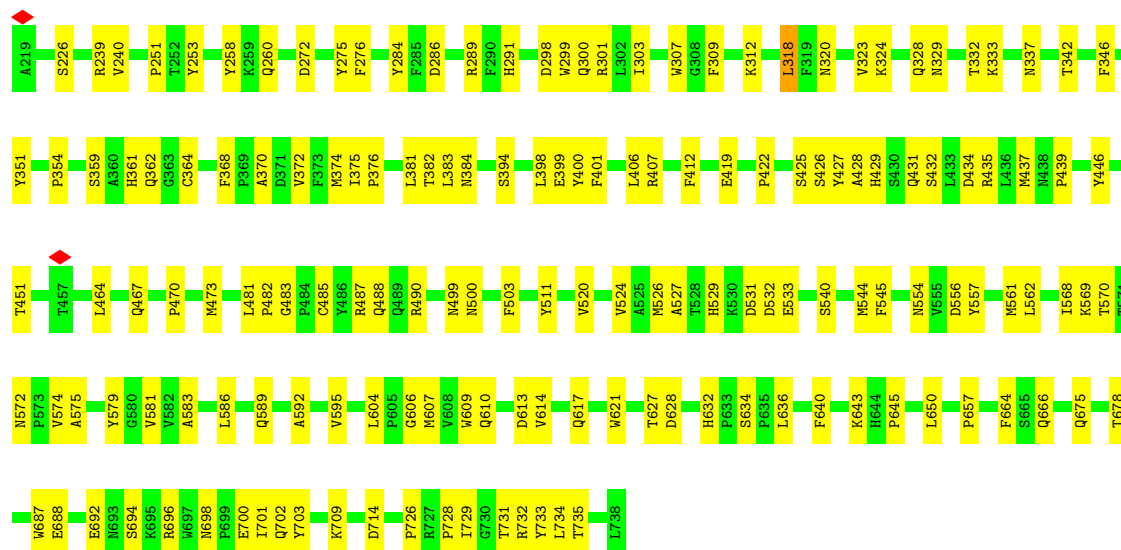
Chain s: 70% 30%





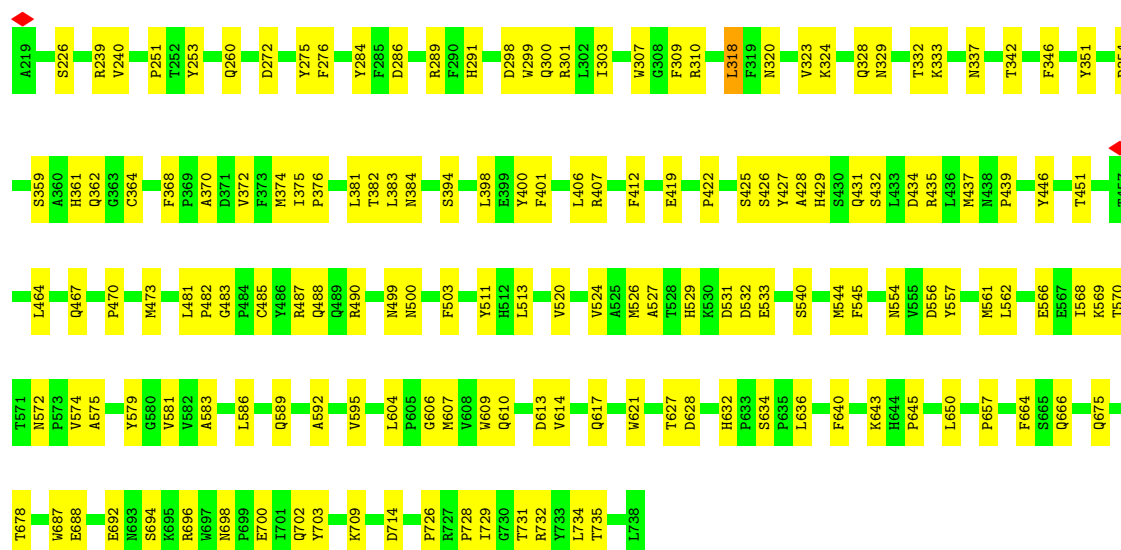
• Molecule 1: Capsid protein VP1

Chain t: 69% 30%



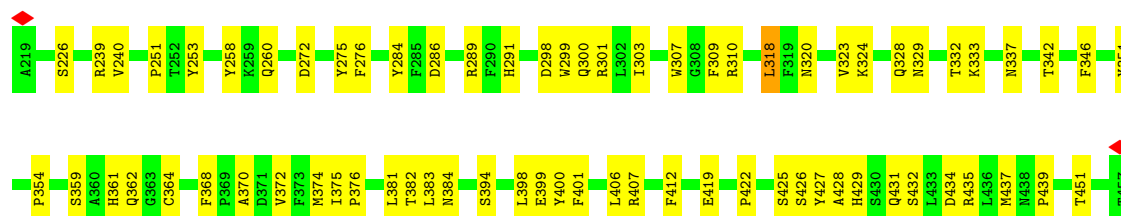
• Molecule 1: Capsid protein VP1

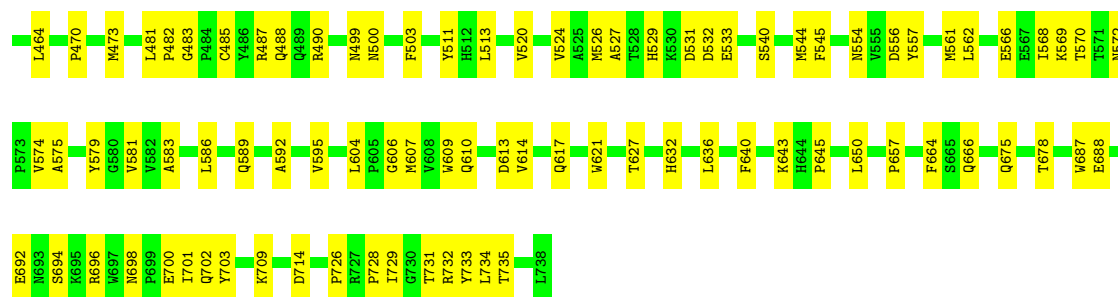
Chain u: 70% 30%



• Molecule 1: Capsid protein VP1

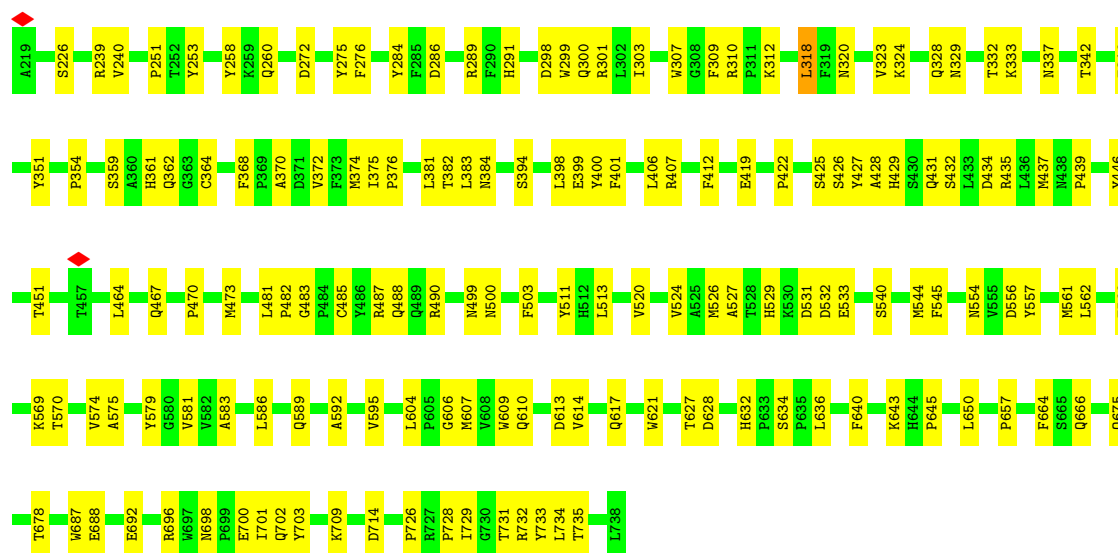
Chain v: 70% 30%





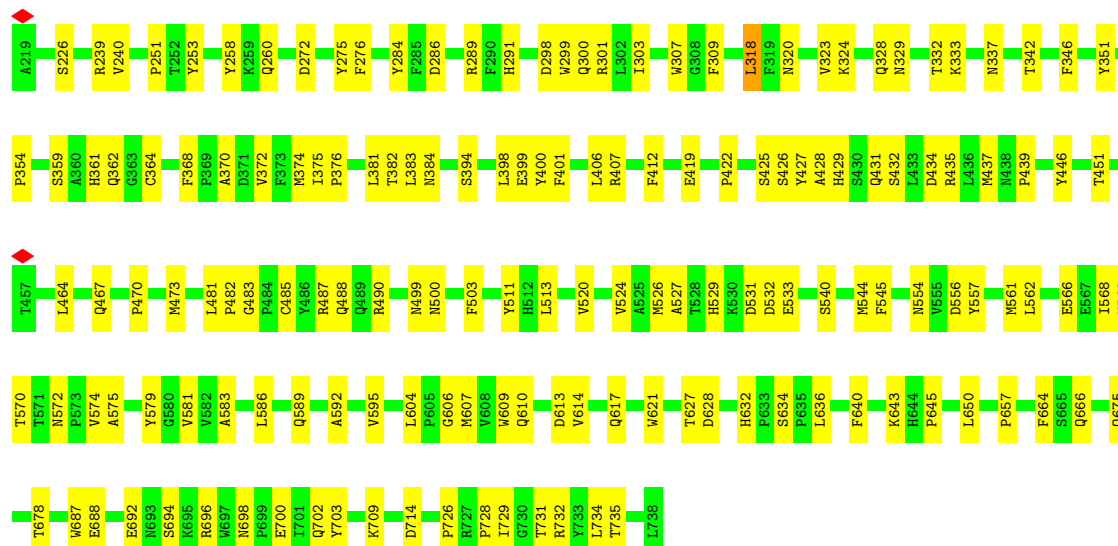
• Molecule 1: Capsid protein VP1

Chain y: 69% 30%

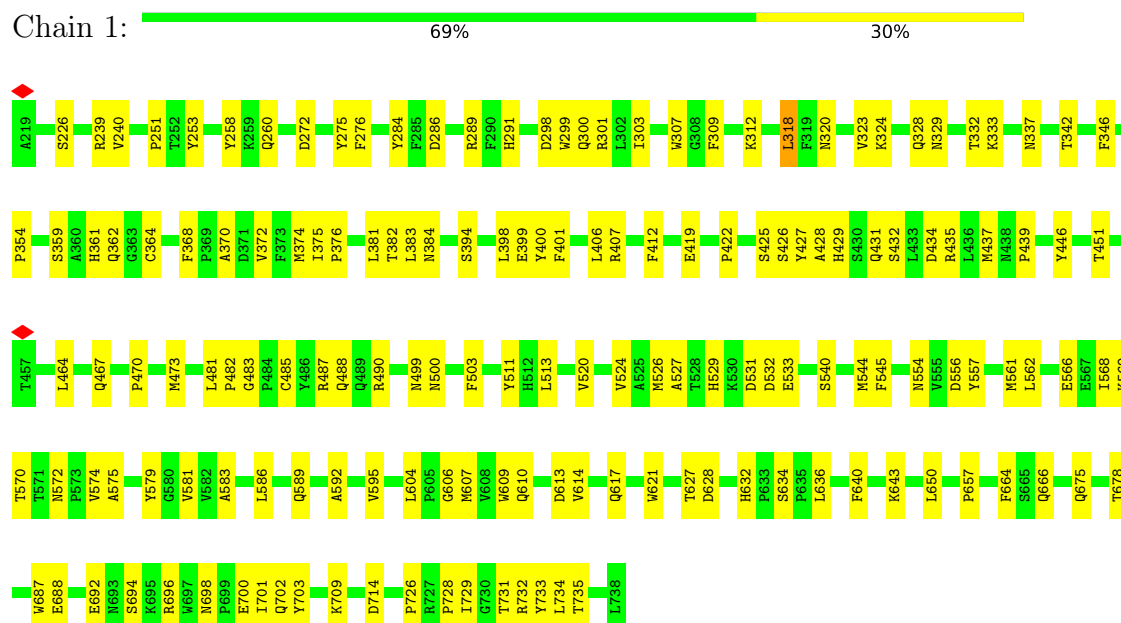


• Molecule 1: Capsid protein VP1

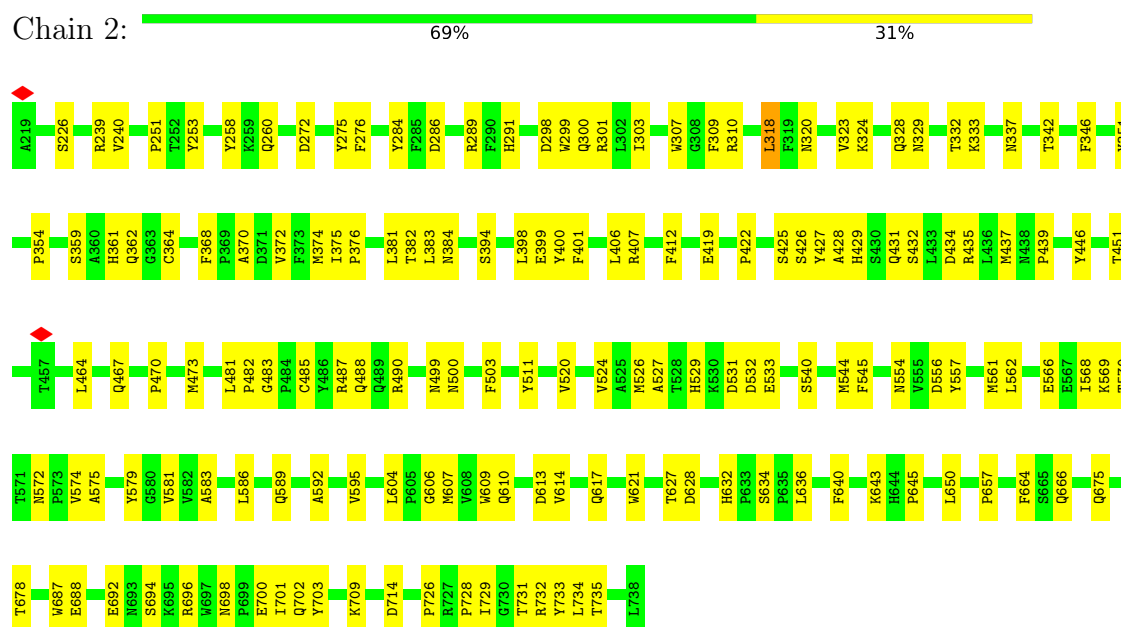
Chain z: 70% 30%



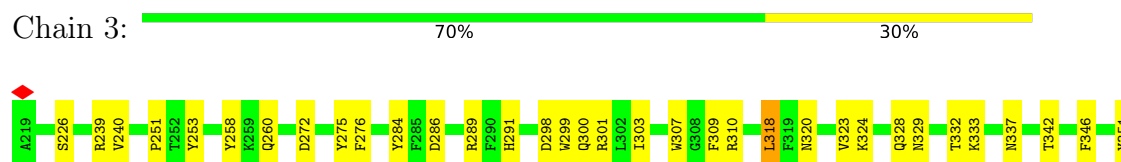
- Molecule 1: Capsid protein VP1

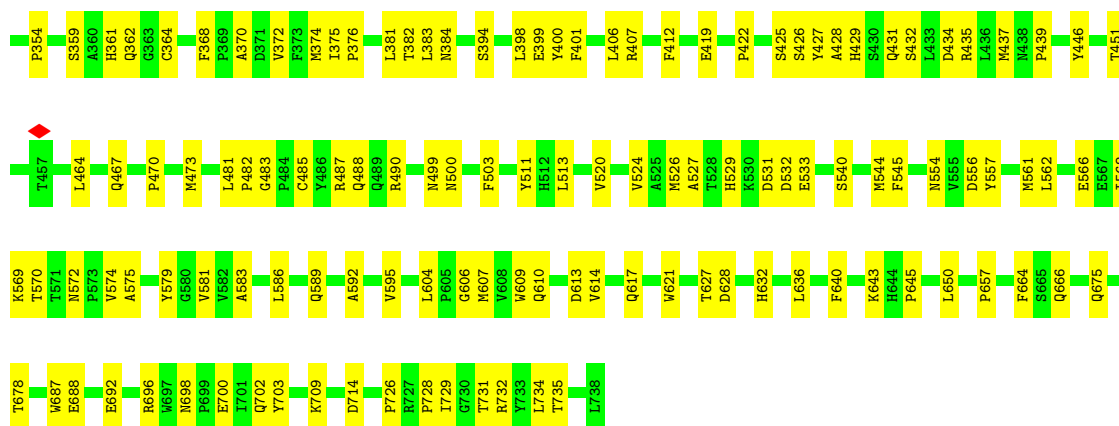


- Molecule 1: Capsid protein VP1

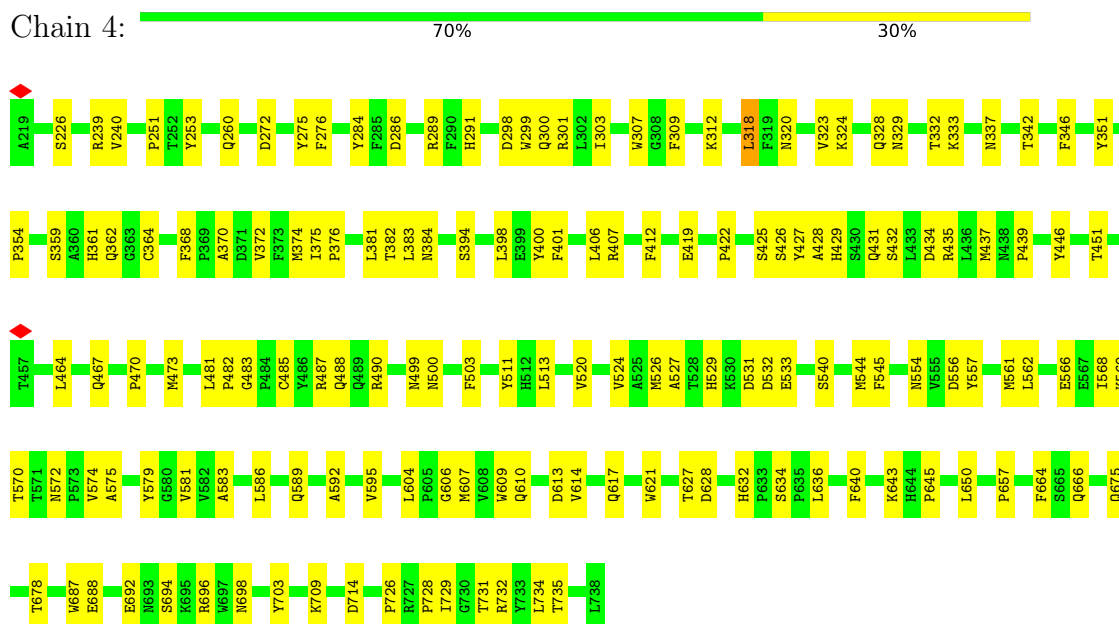


- Molecule 1: Capsid protein VP1

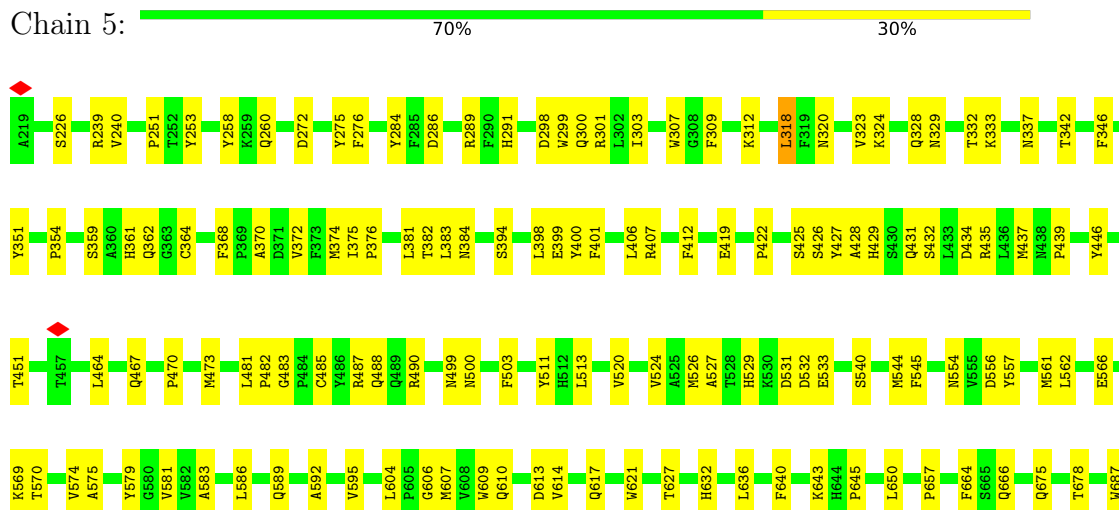




• Molecule 1: Capsid protein VP1



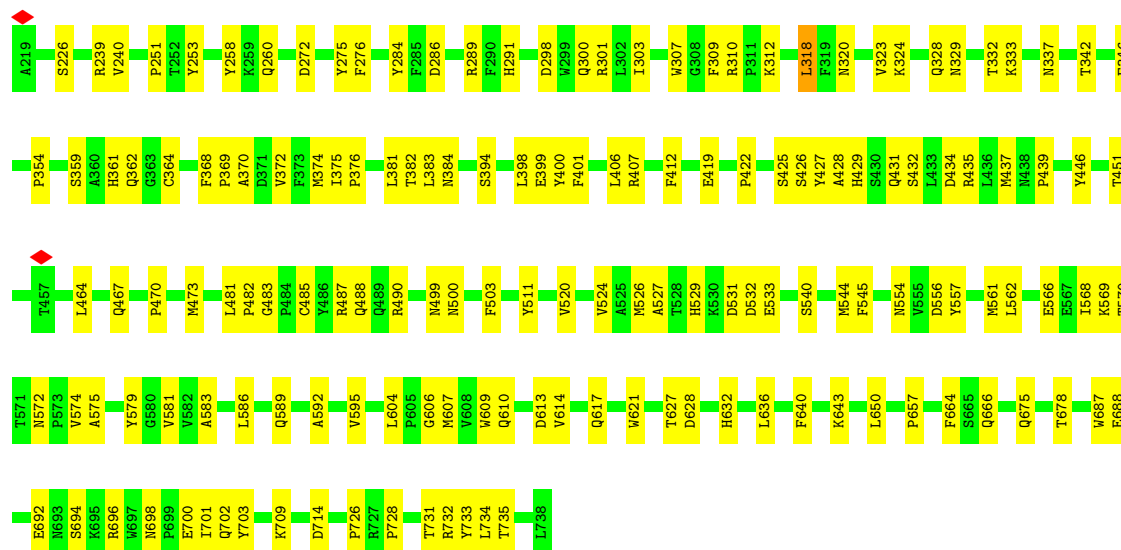
• Molecule 1: Capsid protein VP1





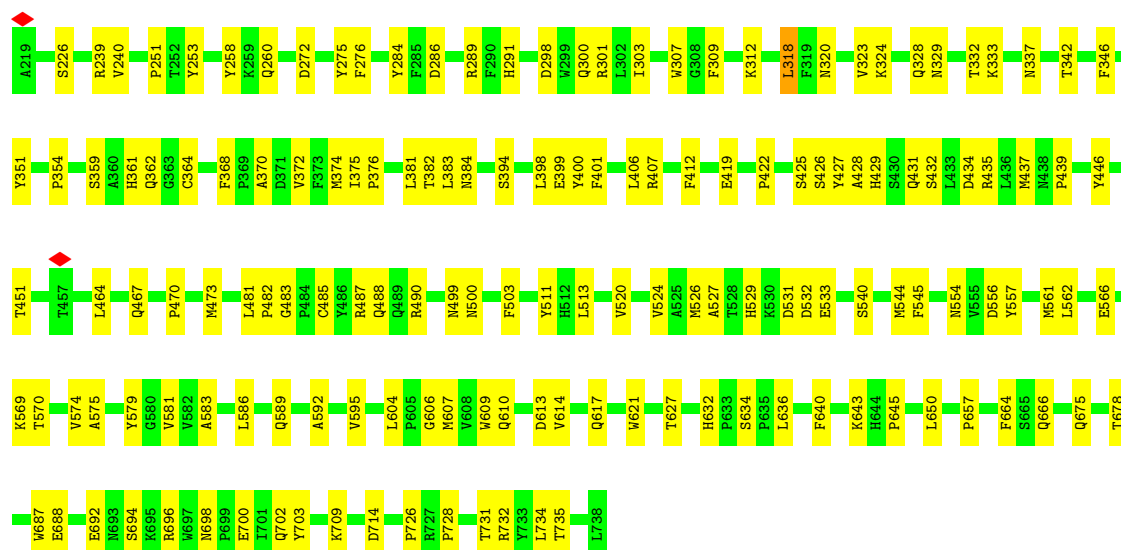
• Molecule 1: Capsid protein VP1

Chain 6: 70% 30%



• Molecule 1: Capsid protein VP1

Chain 7: 70% 29%



• Molecule 1: Capsid protein VP1

Chain 8: 70% 30%



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

Chain 0: 100%

C901
A902

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

Chain 9: 100%

C903
A904

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

Chain AA: 100%

C905
A906

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

Chain BA: 100%

C907
A908

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

Chain CA: 100%

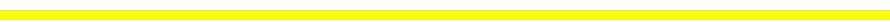
C909
A910

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

Chain DA:  100%

C911
A912

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

Chain EA:  100%

C913
A914

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

Chain FA:  100%

C915
A916

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

Chain GA:  100%

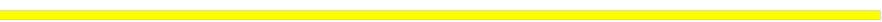
C917
A918

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

Chain HA:  100%

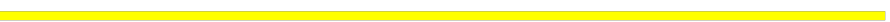
C919
A920

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

Chain IA:  100%

C921
A922

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

Chain JA:  100%

C923
A924

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

Chain KA:  100%

C925
A926

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

Chain LA:  100%C927
A928

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

Chain MA:  100%C929
A930

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

Chain NA:  100%C931
A932

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

Chain OA:  100%C933
A934

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

Chain PA:  100%C935
A936

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

Chain QA:  100%C937
A938

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

Chain RA:  100%C939
A940

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

Chain SA:  100%

C941
A942

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

Chain TA:  100%

C943
A944

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

Chain UA:  100%

C945
A946

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

Chain VA:  100%

C947
A948

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

Chain WA:  100%

C949
A950

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

Chain XA:  100%

C951
A952

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

Chain YA:  100%

C953
A954

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

Chain ZA:  100%

C955
A956

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

Chain aA:  100%C957
A958

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

Chain bA:  100%C959
A960

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

Chain cA:  100%C961
A962

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

Chain dA:  100%C963
A964

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

Chain eA:  100%C965
A966

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

Chain fA:  100%C967
A968

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

Chain gA:  100%C969
A970

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

Chain hA:  100%

C971
A972

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

Chain iA:  100%

C973
A974

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

Chain jA:  100%

C975
A976

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

Chain kA:  100%

C977
A978

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

Chain lA:  100%

C979
A980

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

Chain mA:  100%

C981
A982

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

Chain nA:  100%

C983
A984

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

Chain oA:  100%

C985
A986

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

Chain pA:  100%C987
A988

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

Chain qA:  100%C989
A990

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

Chain rA:  100%C991
A992

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

Chain sA:  100%C993
A994

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

Chain tA:  100%C995
A996

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

Chain uA:  100%C997
A998

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

Chain vA:  100%C999
A1000

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

Chain wA:  100%

C1001
A1002

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

Chain xA:  100%

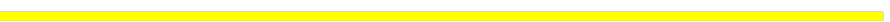
C1003
A1004

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

Chain yA:  100%

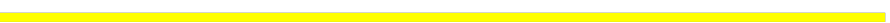
C1005
A1006

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

Chain zA:  100%

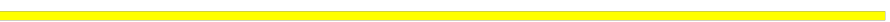
C1007
A1008

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

Chain 0A:  100%

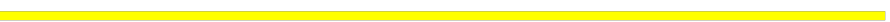
C1009
A1010

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

Chain 1A:  100%

C1011
A1012

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

Chain 2A:  100%

C1013
A1014

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

Chain 3A:  100%

C1015
A1016

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

Chain 4A:  100%

C1017
A1018

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

Chain 5A:  100%

C1019
A1020

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	82463	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	DIRECT ELECTRON DE-64 (8k x 8k)	Depositor
Maximum map value	19.450	Depositor
Minimum map value	-9.472	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1	Depositor
Map size (Å)	390.975, 390.975, 390.975	wwPDB
Map dimensions	401, 401, 401	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.975, 0.975, 0.975	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	0.47	0/4251	0.48	0/5797
1	2	0.47	0/4251	0.48	0/5797
1	3	0.47	0/4251	0.48	0/5797
1	4	0.47	0/4251	0.48	0/5797
1	5	0.47	0/4251	0.48	0/5797
1	6	0.47	0/4251	0.48	0/5797
1	7	0.47	0/4251	0.48	0/5797
1	8	0.47	0/4251	0.48	0/5797
1	A	0.47	0/4251	0.48	0/5797
1	B	0.47	0/4251	0.48	0/5797
1	C	0.47	0/4251	0.48	0/5797
1	D	0.47	0/4251	0.48	0/5797
1	E	0.47	0/4251	0.48	0/5797
1	F	0.47	0/4251	0.48	0/5797
1	G	0.47	0/4251	0.48	0/5797
1	H	0.47	0/4251	0.48	0/5797
1	I	0.47	0/4251	0.49	0/5797
1	J	0.47	0/4251	0.48	0/5797
1	K	0.47	0/4251	0.48	0/5797
1	L	0.47	0/4251	0.48	0/5797
1	M	0.47	0/4251	0.48	0/5797
1	N	0.47	0/4251	0.48	0/5797
1	O	0.47	0/4251	0.48	0/5797
1	P	0.47	0/4251	0.48	0/5797
1	Q	0.47	0/4251	0.48	0/5797
1	R	0.47	0/4251	0.48	0/5797
1	S	0.47	0/4251	0.48	0/5797
1	T	0.47	0/4251	0.48	0/5797
1	U	0.47	0/4251	0.48	0/5797
1	V	0.47	0/4251	0.48	0/5797
1	W	0.47	0/4251	0.48	0/5797
1	X	0.47	0/4251	0.48	0/5797
1	Y	0.47	0/4251	0.48	0/5797
1	Z	0.47	0/4251	0.48	0/5797

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.47	0/4251	0.48	0/5797
1	b	0.47	0/4251	0.48	0/5797
1	c	0.47	0/4251	0.48	0/5797
1	d	0.47	0/4251	0.48	0/5797
1	e	0.47	0/4251	0.48	0/5797
1	f	0.47	0/4251	0.48	0/5797
1	g	0.47	0/4251	0.48	0/5797
1	h	0.47	0/4251	0.48	0/5797
1	i	0.47	0/4251	0.48	0/5797
1	j	0.47	0/4251	0.48	0/5797
1	k	0.47	0/4251	0.48	0/5797
1	l	0.47	0/4251	0.48	0/5797
1	m	0.47	0/4251	0.48	0/5797
1	n	0.47	0/4251	0.48	0/5797
1	o	0.47	0/4251	0.48	0/5797
1	p	0.47	0/4251	0.48	0/5797
1	q	0.47	0/4251	0.48	0/5797
1	r	0.47	0/4251	0.48	0/5797
1	s	0.47	0/4251	0.48	0/5797
1	t	0.47	0/4251	0.48	0/5797
1	u	0.47	0/4251	0.48	0/5797
1	v	0.47	0/4251	0.48	0/5797
1	w	0.47	0/4251	0.48	0/5797
1	x	0.47	0/4251	0.48	0/5797
1	y	0.47	0/4251	0.48	0/5797
1	z	0.47	0/4251	0.48	0/5797
2	0	0.32	0/41	0.38	0/61
2	0A	0.32	0/41	0.38	0/61
2	1A	0.32	0/41	0.38	0/61
2	2A	0.32	0/41	0.38	0/61
2	3A	0.32	0/41	0.38	0/61
2	4A	0.32	0/41	0.38	0/61
2	5A	0.32	0/41	0.38	0/61
2	9	0.31	0/41	0.38	0/61
2	AA	0.31	0/41	0.38	0/61
2	BA	0.32	0/41	0.38	0/61
2	CA	0.32	0/41	0.38	0/61
2	DA	0.32	0/41	0.38	0/61
2	EA	0.32	0/41	0.38	0/61
2	FA	0.32	0/41	0.38	0/61
2	GA	0.32	0/41	0.38	0/61
2	HA	0.32	0/41	0.38	0/61
2	IA	0.32	0/41	0.38	0/61

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
2	JA	0.32	0/41	0.38	0/61
2	KA	0.32	0/41	0.38	0/61
2	LA	0.32	0/41	0.38	0/61
2	MA	0.32	0/41	0.38	0/61
2	NA	0.32	0/41	0.38	0/61
2	OA	0.32	0/41	0.38	0/61
2	PA	0.32	0/41	0.38	0/61
2	QA	0.32	0/41	0.38	0/61
2	RA	0.32	0/41	0.38	0/61
2	SA	0.32	0/41	0.38	0/61
2	TA	0.32	0/41	0.38	0/61
2	UA	0.32	0/41	0.38	0/61
2	VA	0.32	0/41	0.38	0/61
2	WA	0.32	0/41	0.38	0/61
2	XA	0.32	0/41	0.38	0/61
2	YA	0.32	0/41	0.38	0/61
2	ZA	0.32	0/41	0.38	0/61
2	aA	0.32	0/41	0.38	0/61
2	bA	0.32	0/41	0.38	0/61
2	cA	0.32	0/41	0.38	0/61
2	dA	0.32	0/41	0.38	0/61
2	eA	0.32	0/41	0.38	0/61
2	fA	0.32	0/41	0.38	0/61
2	gA	0.32	0/41	0.38	0/61
2	hA	0.32	0/41	0.38	0/61
2	iA	0.31	0/41	0.38	0/61
2	jA	0.32	0/41	0.38	0/61
2	kA	0.32	0/41	0.38	0/61
2	lA	0.32	0/41	0.38	0/61
2	mA	0.32	0/41	0.38	0/61
2	nA	0.32	0/41	0.38	0/61
2	oA	0.32	0/41	0.38	0/61
2	pA	0.32	0/41	0.38	0/61
2	qA	0.32	0/41	0.38	0/61
2	rA	0.32	0/41	0.38	0/61
2	sA	0.32	0/41	0.38	0/61
2	tA	0.32	0/41	0.38	0/61
2	uA	0.32	0/41	0.38	0/61
2	vA	0.32	0/41	0.38	0/61
2	wA	0.32	0/41	0.38	0/61
2	xA	0.32	0/41	0.38	0/61
2	yA	0.32	0/41	0.38	0/61
2	zA	0.32	0/41	0.38	0/61

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.47	0/257520	0.48	0/351480

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	4128	0	3893	138	0
1	2	4128	0	3893	139	0
1	3	4128	0	3893	135	0
1	4	4128	0	3893	135	0
1	5	4128	0	3893	135	0
1	6	4128	0	3893	136	0
1	7	4128	0	3893	133	0
1	8	4128	0	3893	135	0
1	A	4128	0	3893	139	0
1	B	4128	0	3893	132	0
1	C	4128	0	3893	133	0
1	D	4128	0	3893	134	0
1	E	4128	0	3893	133	0
1	F	4128	0	3893	137	0
1	G	4128	0	3893	137	0
1	H	4128	0	3893	138	0
1	I	4128	0	3893	136	0
1	J	4128	0	3893	135	0
1	K	4128	0	3893	134	0
1	L	4128	0	3893	134	0
1	M	4128	0	3893	134	0
1	N	4128	0	3893	135	0
1	O	4128	0	3893	137	0
1	P	4128	0	3893	134	0
1	Q	4128	0	3893	135	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	4128	0	3893	135	0
1	S	4128	0	3893	135	0
1	T	4128	0	3893	136	0
1	U	4128	0	3893	132	0
1	V	4128	0	3893	136	0
1	W	4128	0	3893	137	0
1	X	4128	0	3893	136	0
1	Y	4128	0	3893	134	0
1	Z	4128	0	3893	133	0
1	a	4128	0	3893	135	0
1	b	4128	0	3893	133	0
1	c	4128	0	3893	135	0
1	d	4128	0	3893	140	0
1	e	4128	0	3893	135	0
1	f	4128	0	3893	141	0
1	g	4128	0	3893	136	0
1	h	4128	0	3893	139	0
1	i	4128	0	3893	135	0
1	j	4128	0	3893	141	0
1	k	4128	0	3893	138	0
1	l	4128	0	3893	136	0
1	m	4128	0	3893	134	0
1	n	4128	0	3893	136	0
1	o	4128	0	3893	136	0
1	p	4128	0	3893	136	0
1	q	4128	0	3893	136	0
1	r	4128	0	3893	134	0
1	s	4128	0	3893	135	0
1	t	4128	0	3893	136	0
1	u	4128	0	3893	136	0
1	v	4128	0	3893	133	0
1	w	4128	0	3893	134	0
1	x	4128	0	3893	134	0
1	y	4128	0	3893	137	0
1	z	4128	0	3893	136	0
2	0	37	0	24	5	0
2	0A	37	0	24	4	0
2	1A	37	0	24	5	0
2	2A	37	0	24	4	0
2	3A	37	0	24	4	0
2	4A	37	0	24	4	0
2	5A	37	0	24	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	9	37	0	24	5	0
2	AA	37	0	24	4	0
2	BA	37	0	24	4	0
2	CA	37	0	24	4	0
2	DA	37	0	24	4	0
2	EA	37	0	24	4	0
2	FA	37	0	24	5	0
2	GA	37	0	24	5	0
2	HA	37	0	24	5	0
2	IA	37	0	24	4	0
2	JA	37	0	24	4	0
2	KA	37	0	24	4	0
2	LA	37	0	24	4	0
2	MA	37	0	24	4	0
2	NA	37	0	24	4	0
2	OA	37	0	24	4	0
2	PA	37	0	24	5	0
2	QA	37	0	24	5	0
2	RA	37	0	24	5	0
2	SA	37	0	24	4	0
2	TA	37	0	24	4	0
2	UA	37	0	24	4	0
2	VA	37	0	24	4	0
2	WA	37	0	24	5	0
2	XA	37	0	24	5	0
2	YA	37	0	24	4	0
2	ZA	37	0	24	5	0
2	aA	37	0	24	5	0
2	bA	37	0	24	5	0
2	cA	37	0	24	5	0
2	dA	37	0	24	5	0
2	eA	37	0	24	5	0
2	fA	37	0	24	5	0
2	gA	37	0	24	5	0
2	hA	37	0	24	5	0
2	iA	37	0	24	5	0
2	jA	37	0	24	4	0
2	kA	37	0	24	5	0
2	lA	37	0	24	5	0
2	mA	37	0	24	5	0
2	nA	37	0	24	4	0
2	oA	37	0	24	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	pA	37	0	24	5	0
2	qA	37	0	24	4	0
2	rA	37	0	24	5	0
2	sA	37	0	24	5	0
2	tA	37	0	24	4	0
2	uA	37	0	24	5	0
2	vA	37	0	24	4	0
2	wA	37	0	24	5	0
2	xA	37	0	24	4	0
2	yA	37	0	24	5	0
2	zA	37	0	24	5	0
All	All	249900	0	235020	6598	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 6598 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:A:473:MET:HE1	1:G:275:TYR:HB3	1.64	0.79
1:T:473:MET:HE1	1:d:275:TYR:HB3	1.65	0.79
1:1:473:MET:HE1	1:2:275:TYR:HB3	1.65	0.79
1:o:473:MET:HE1	1:p:275:TYR:HB3	1.65	0.78
1:H:473:MET:HE1	1:W:275:TYR:HB3	1.66	0.77

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	518/520 (100%)	507 (98%)	11 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	3	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	4	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	5	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	6	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	7	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	8	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	A	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	B	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	C	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	D	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	E	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	F	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	G	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	H	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	I	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	J	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	K	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	L	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	M	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	N	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	O	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	P	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	Q	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	R	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	S	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	T	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	U	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	V	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	W	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	X	518/520 (100%)	507 (98%)	11 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Y	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	Z	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	a	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	b	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	c	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	d	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	e	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	f	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	g	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	h	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	i	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	j	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	k	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	l	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	m	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	n	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	o	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	p	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	q	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	r	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	s	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	t	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	u	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	v	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	w	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	x	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	y	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
1	z	518/520 (100%)	507 (98%)	11 (2%)	0	100	100
All	All	31080/31200 (100%)	30420 (98%)	660 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	2	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	3	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	4	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	5	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	6	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	7	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	8	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	A	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	B	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	C	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	D	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	E	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	F	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	G	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	H	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	I	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	J	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	K	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	L	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	M	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	N	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	O	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	P	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	Q	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	R	452/452 (100%)	451 (100%)	1 (0%)	87	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	S	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	T	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	U	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	V	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	W	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	X	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	Y	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	Z	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	a	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	b	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	c	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	d	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	e	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	f	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	g	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	h	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	i	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	j	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	k	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	l	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	m	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	n	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	o	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	p	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	q	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	r	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	s	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	t	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	u	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	v	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	w	452/452 (100%)	451 (100%)	1 (0%)	87	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	x	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	y	452/452 (100%)	451 (100%)	1 (0%)	87	92
1	z	452/452 (100%)	451 (100%)	1 (0%)	87	92
All	All	27120/27120 (100%)	27060 (100%)	60 (0%)	85	92

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

Mol	Chain	Res	Type
1	c	318	LEU
1	4	318	LEU
1	j	318	LEU
1	3	318	LEU
1	8	318	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 515 such sidechains are listed below:

Mol	Chain	Res	Type
1	3	230	HIS
1	4	610	GLN
1	2	737	ASN
1	W	328	GLN
1	V	653	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

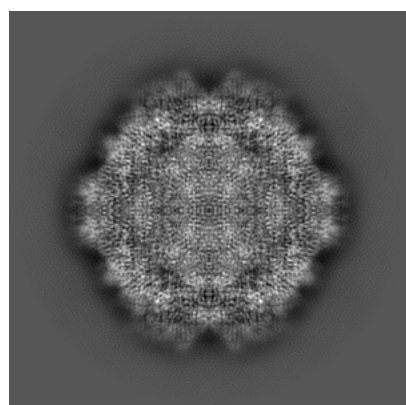
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21011. These allow visual inspection of the internal detail of the map and identification of artifacts.

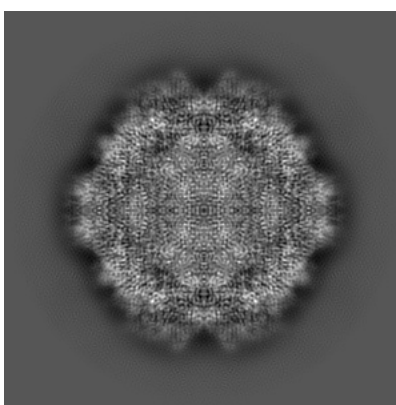
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

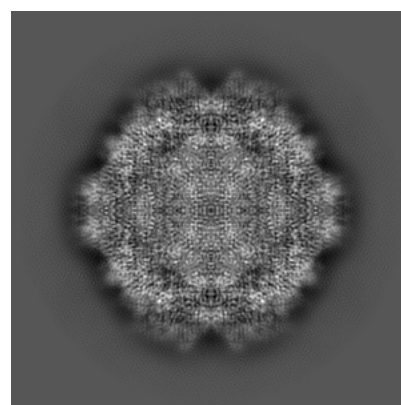
6.1.1 Primary map



X



Y

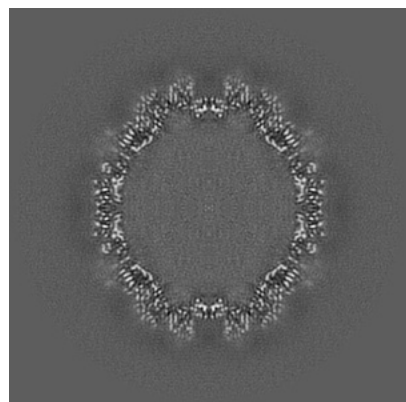


Z

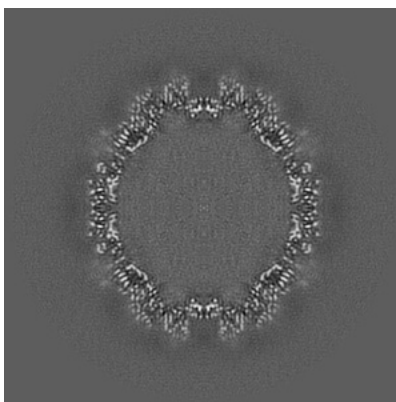
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

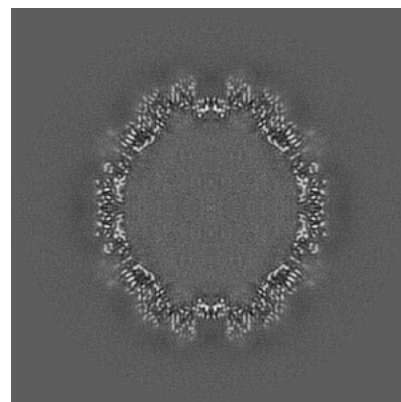
6.2.1 Primary map



X Index: 200



Y Index: 200

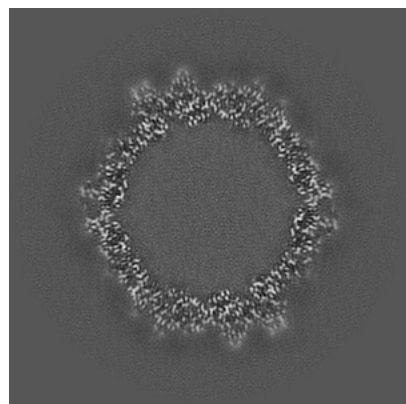


Z Index: 200

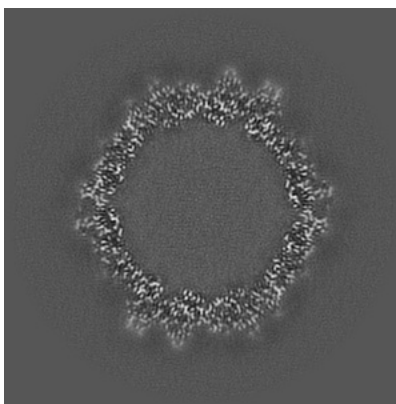
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

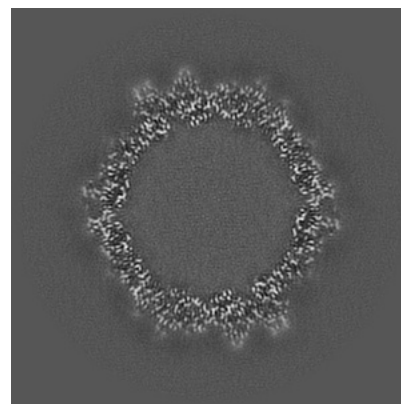
6.3.1 Primary map



X Index: 215



Y Index: 185

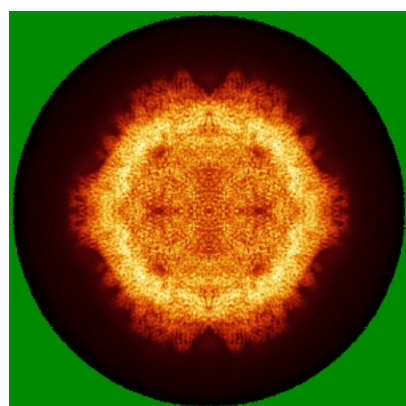


Z Index: 215

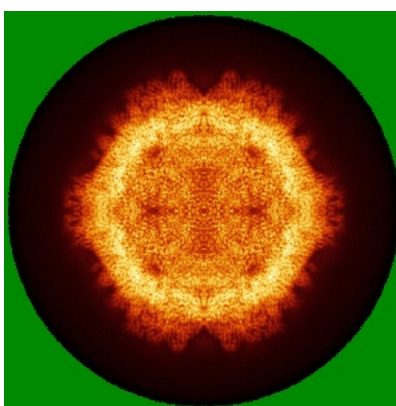
The images above show the largest variance slices of the map in three orthogonal directions.

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

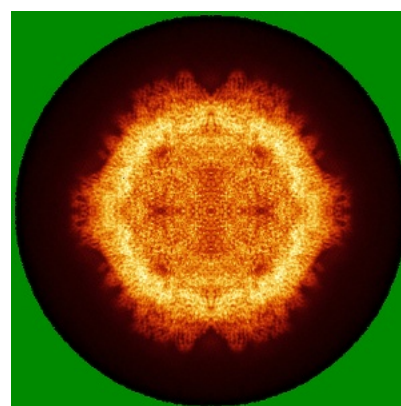
6.4.1 Primary map



X



Y

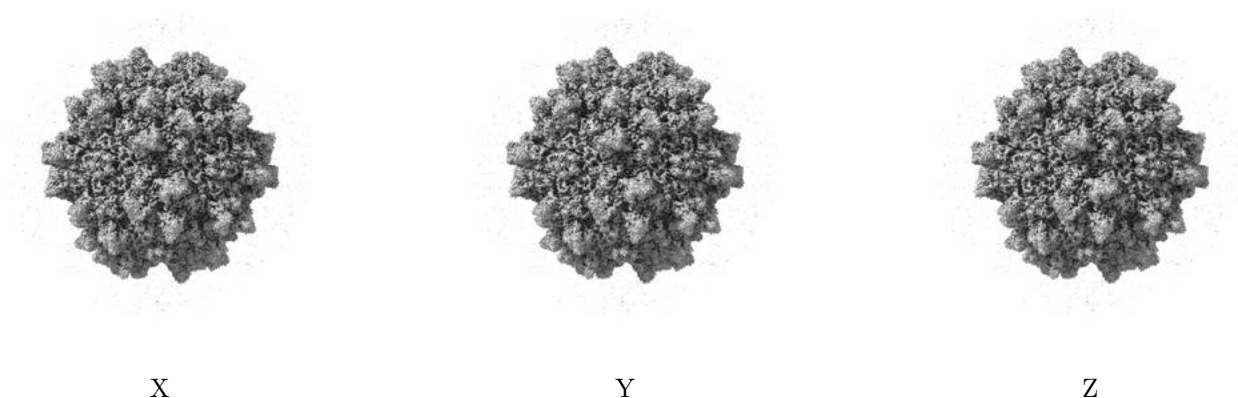


Z

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 [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

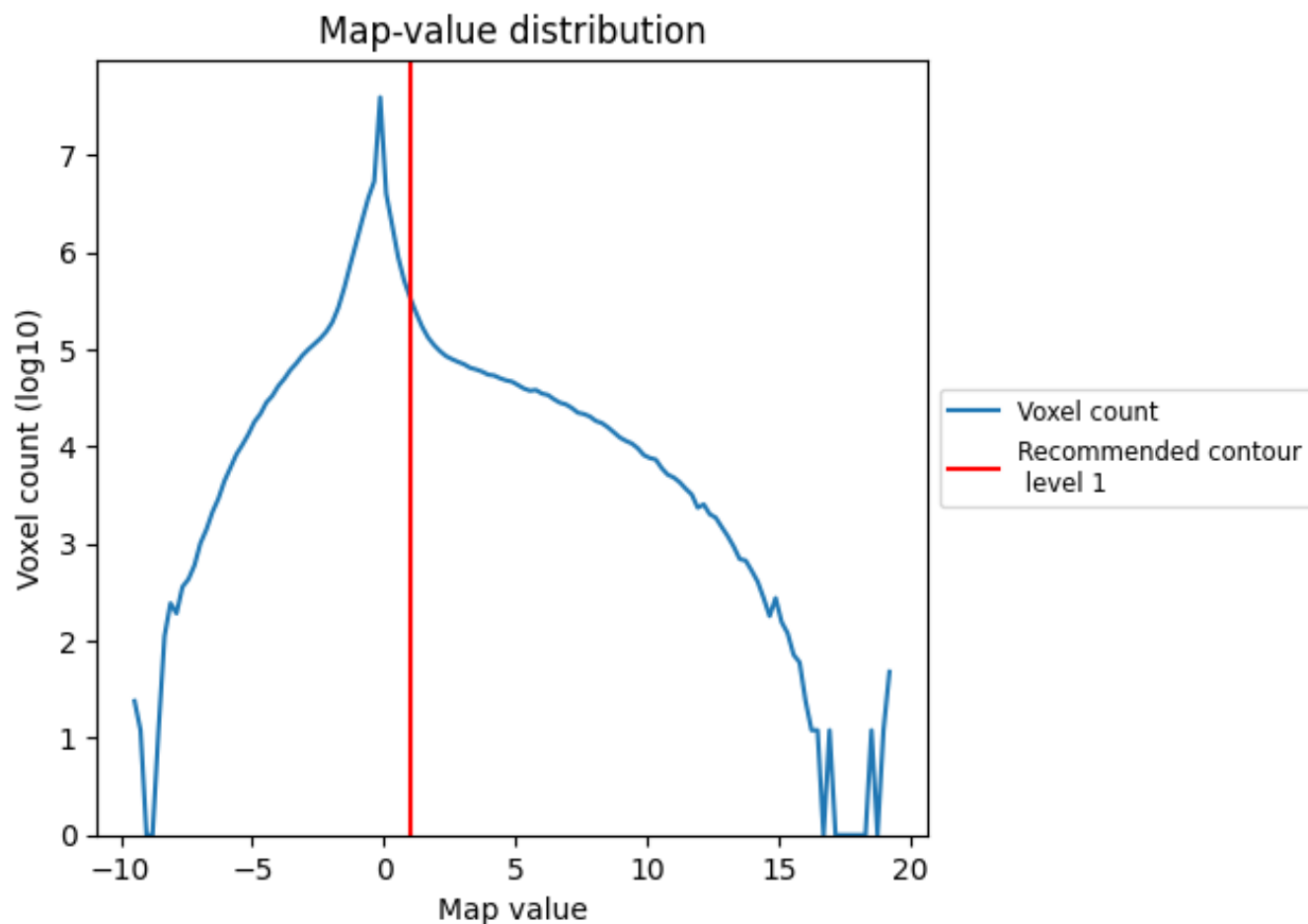
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

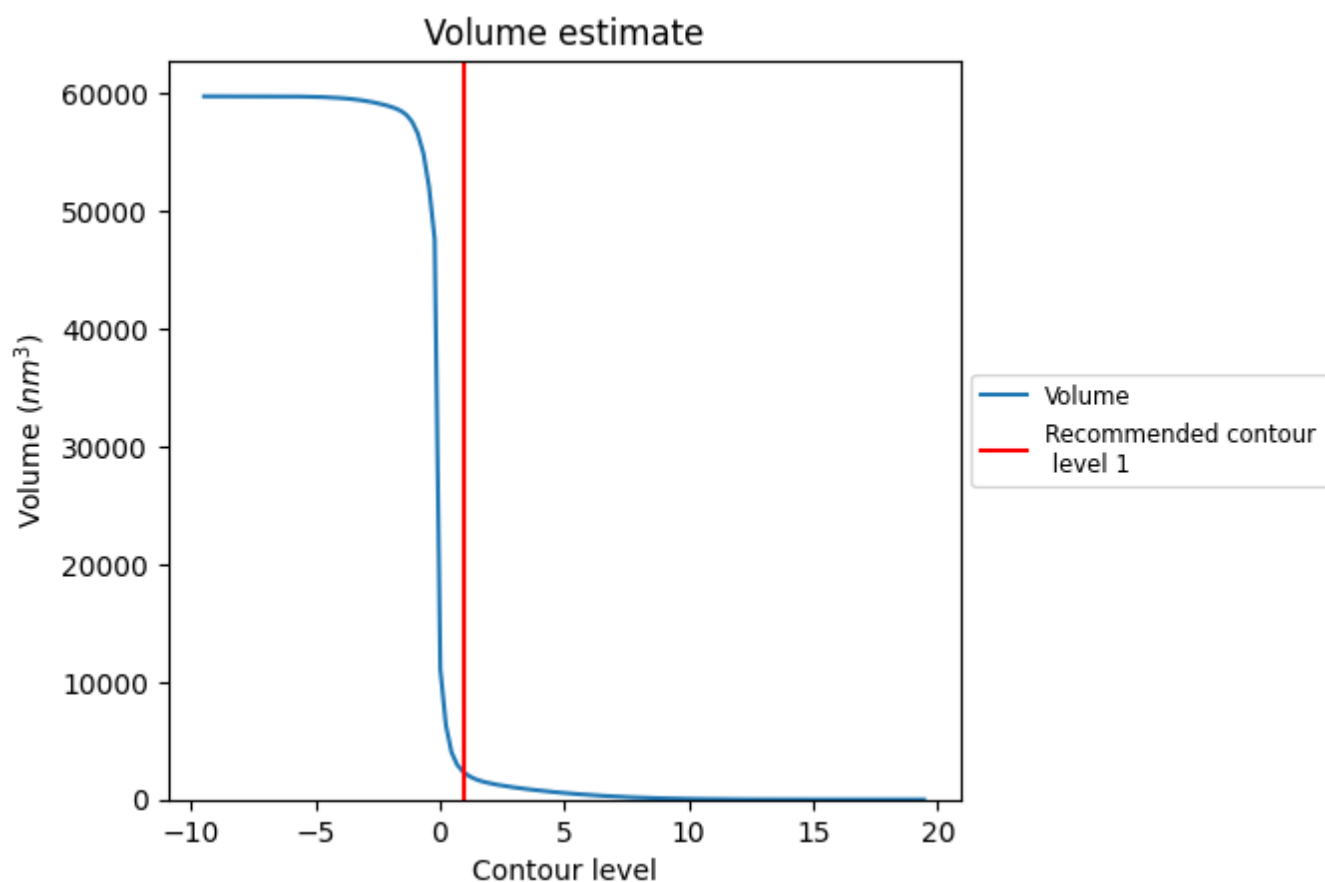
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

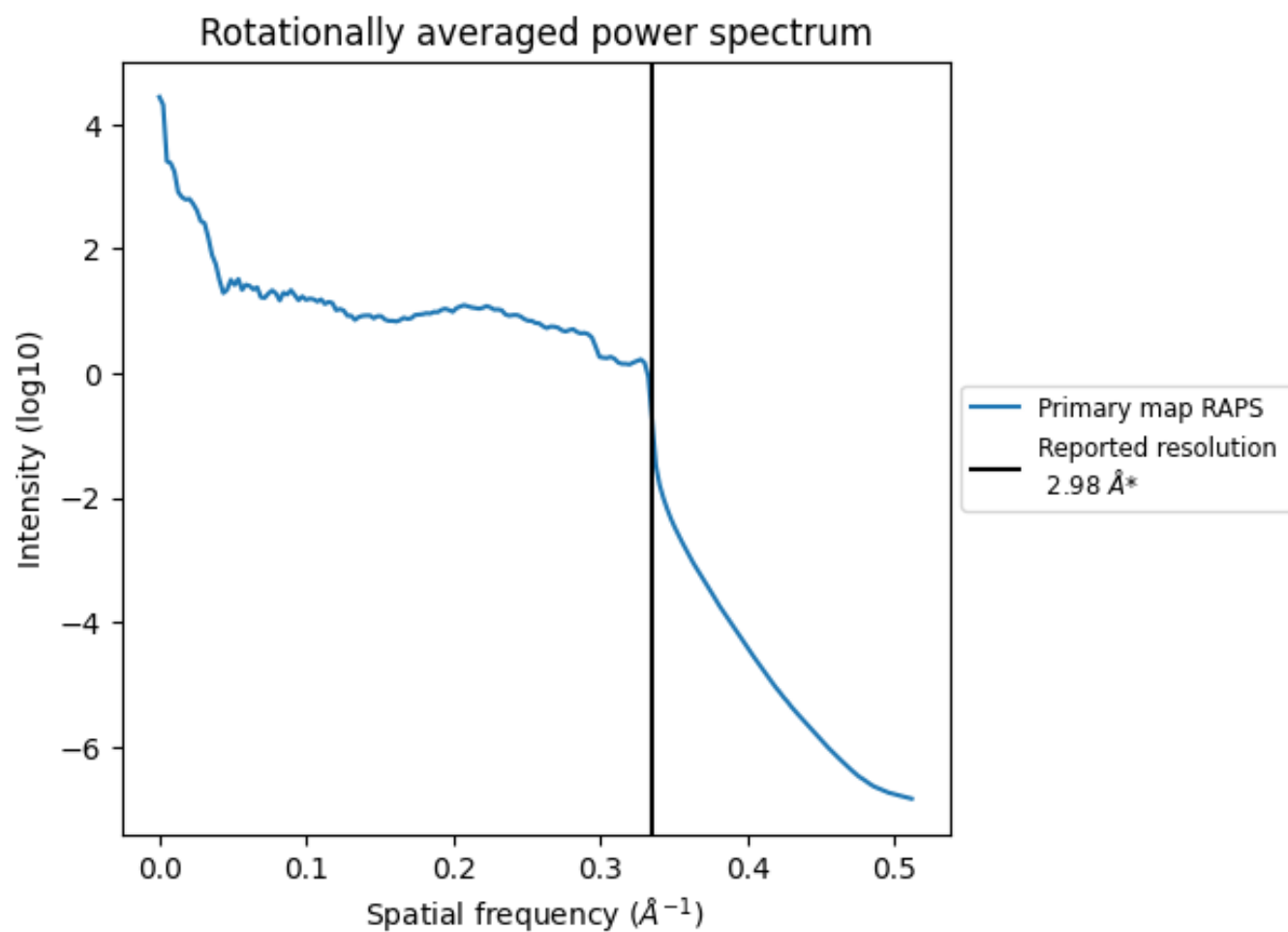
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2269 nm³; this corresponds to an approximate mass of 2050 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 0.336 Å⁻¹

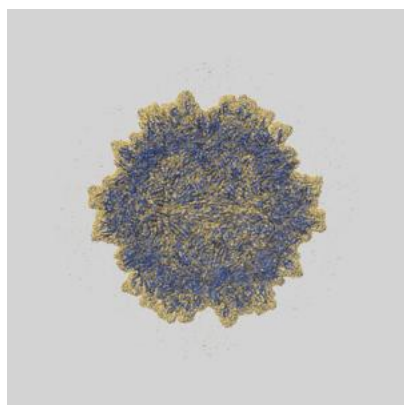
8 Fourier-Shell correlation

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

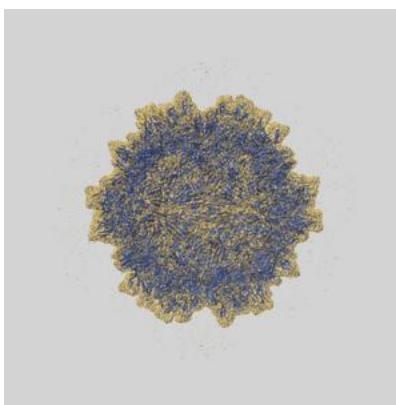
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21011 and PDB model 6V1G. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

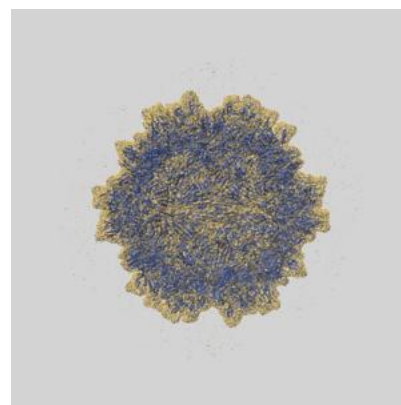
9.1 Map-model overlay [i](#)



X



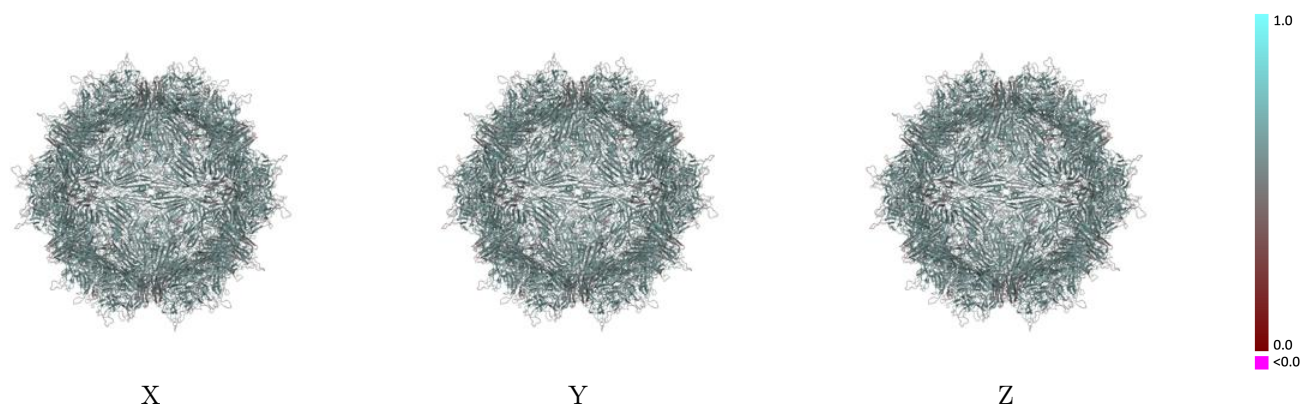
Y



Z

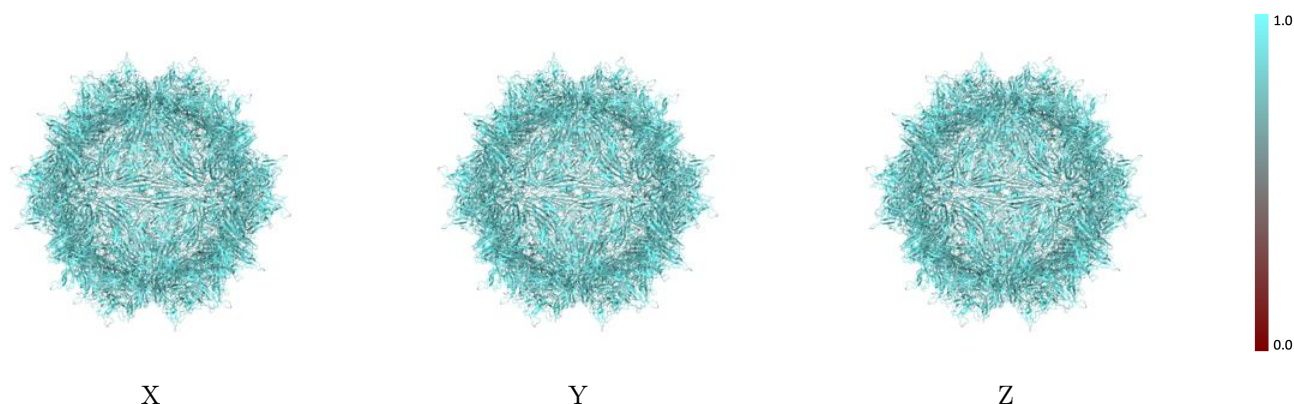
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



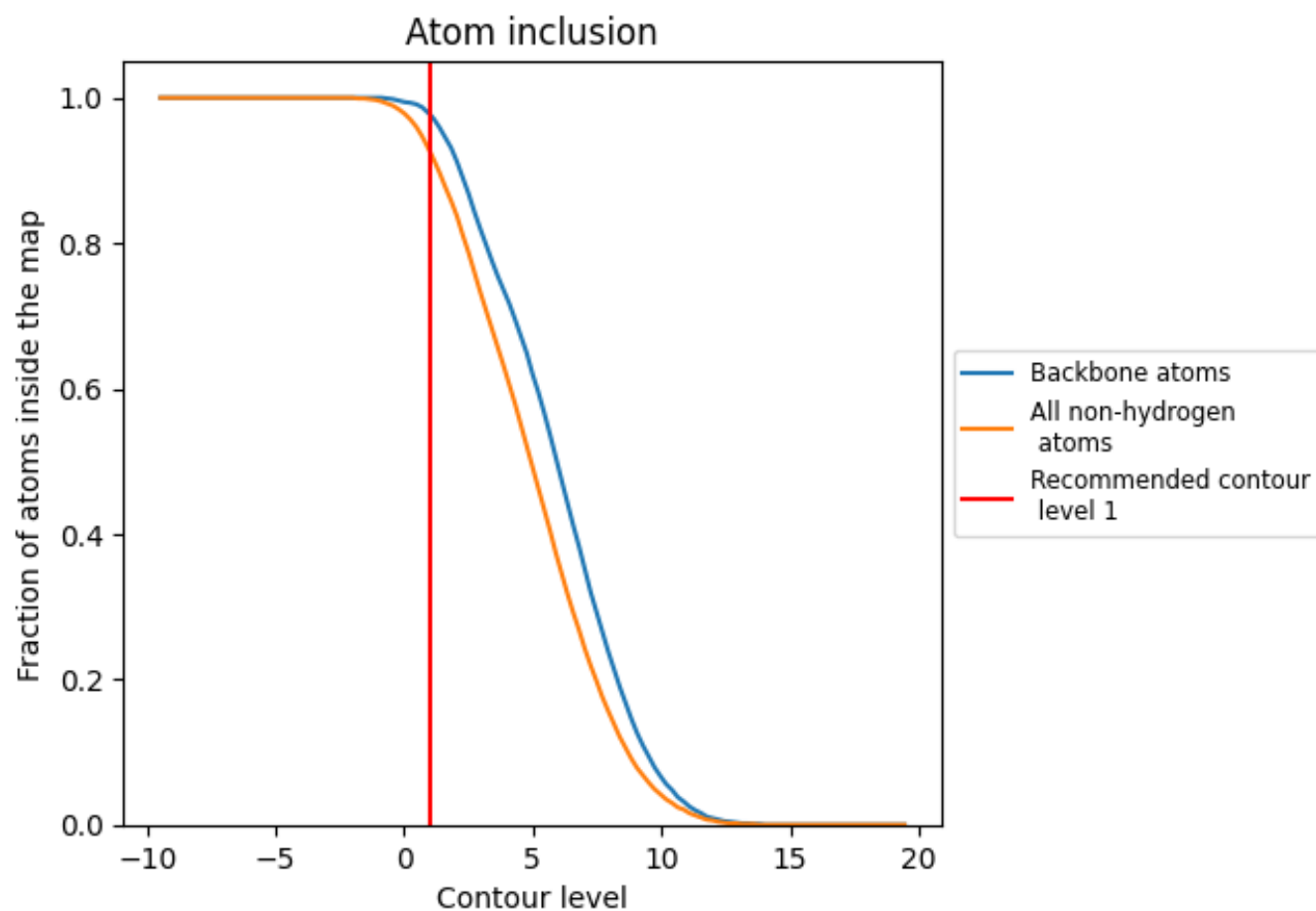
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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, 98% of all backbone atoms, 93% 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	 0.9260	 0.5670
0	 0.6760	 0.4800
0A	 0.6490	 0.4710
1	 0.9300	 0.5680
1A	 0.7030	 0.4900
2	 0.9290	 0.5680
2A	 0.6220	 0.4870
3	 0.9290	 0.5670
3A	 0.7030	 0.4960
4	 0.9270	 0.5670
4A	 0.6490	 0.4850
5	 0.9260	 0.5680
5A	 0.6760	 0.4890
6	 0.9270	 0.5690
7	 0.9280	 0.5670
8	 0.9280	 0.5670
9	 0.7030	 0.4900
A	 0.9290	 0.5670
AA	 0.6220	 0.4880
B	 0.9270	 0.5680
BA	 0.6760	 0.4880
C	 0.9260	 0.5680
CA	 0.6490	 0.4780
D	 0.9290	 0.5680
DA	 0.7030	 0.4890
E	 0.9280	 0.5680
EA	 0.6760	 0.4920
F	 0.9270	 0.5690
FA	 0.7030	 0.4990
G	 0.9300	 0.5670
GA	 0.6760	 0.4880
H	 0.9270	 0.5670
HA	 0.6490	 0.4780
I	 0.9300	 0.5660
IA	 0.6760	 0.4780



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Chain	Atom inclusion	Q-score
J	 0.9290	 0.5680
JA	 0.6220	 0.4910
K	 0.9290	 0.5670
KA	 0.6490	 0.4830
L	 0.9260	 0.5670
LA	 0.6760	 0.4840
M	 0.9290	 0.5690
MA	 0.6490	 0.4810
N	 0.9280	 0.5680
NA	 0.6760	 0.4890
O	 0.9290	 0.5660
OA	 0.6220	 0.4850
P	 0.9280	 0.5680
PA	 0.6220	 0.4940
Q	 0.9260	 0.5680
QA	 0.7030	 0.4920
R	 0.9260	 0.5680
RA	 0.6760	 0.4750
S	 0.9270	 0.5690
SA	 0.6490	 0.4780
T	 0.9300	 0.5670
TA	 0.6760	 0.4820
U	 0.9290	 0.5670
UA	 0.6490	 0.4710
V	 0.9280	 0.5690
VA	 0.6760	 0.4810
W	 0.9290	 0.5660
WA	 0.6220	 0.4870
X	 0.9280	 0.5690
XA	 0.6220	 0.4920
Y	 0.9260	 0.5670
YA	 0.6760	 0.4800
Z	 0.9260	 0.5660
ZA	 0.7030	 0.4910
a	 0.9280	 0.5670
aA	 0.6760	 0.4800
b	 0.9270	 0.5690
bA	 0.6760	 0.4920
c	 0.9300	 0.5680
cA	 0.6760	 0.4860
d	 0.9290	 0.5670
dA	 0.6490	 0.4780

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Chain	Atom inclusion	Q-score
e	 0.9280	 0.5690
eA	 0.7030	 0.4920
f	 0.9290	 0.5680
fA	 0.6220	 0.4930
g	 0.9270	 0.5690
gA	 0.7030	 0.4860
h	 0.9260	 0.5690
hA	 0.6490	 0.4820
i	 0.9270	 0.5680
iA	 0.6220	 0.4900
j	 0.9290	 0.5660
jA	 0.6760	 0.4870
k	 0.9260	 0.5680
kA	 0.6220	 0.4860
l	 0.9300	 0.5660
lA	 0.7030	 0.4950
m	 0.9260	 0.5670
mA	 0.6760	 0.4850
n	 0.9270	 0.5660
nA	 0.6760	 0.4850
o	 0.9300	 0.5680
oA	 0.6490	 0.4740
p	 0.9290	 0.5670
pA	 0.6220	 0.4940
q	 0.9290	 0.5660
qA	 0.7030	 0.4950
r	 0.9260	 0.5660
rA	 0.6220	 0.4880
s	 0.9270	 0.5670
sA	 0.7030	 0.4870
t	 0.9260	 0.5690
tA	 0.6490	 0.4780
u	 0.9270	 0.5690
uA	 0.6760	 0.4850
v	 0.9280	 0.5670
vA	 0.6760	 0.4940
w	 0.9290	 0.5670
wA	 0.6760	 0.4870
x	 0.9280	 0.5670
xA	 0.6760	 0.4900
y	 0.9290	 0.5680
yA	 0.6760	 0.4850

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Chain	Atom inclusion	Q-score
z	 0.9290	 0.5670
zA	 0.6760	 0.4750