



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 09:50 AM UTC

PDB ID : 9ME0 / pdb_00009me0
EMDB ID : EMD-48181
Title : Goose Parvovirus Capsid
Authors : Jabbari, K.; Mietzsch, M.; McKenna, R.
Deposited on : 2024-12-05
Resolution : 2.43 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:

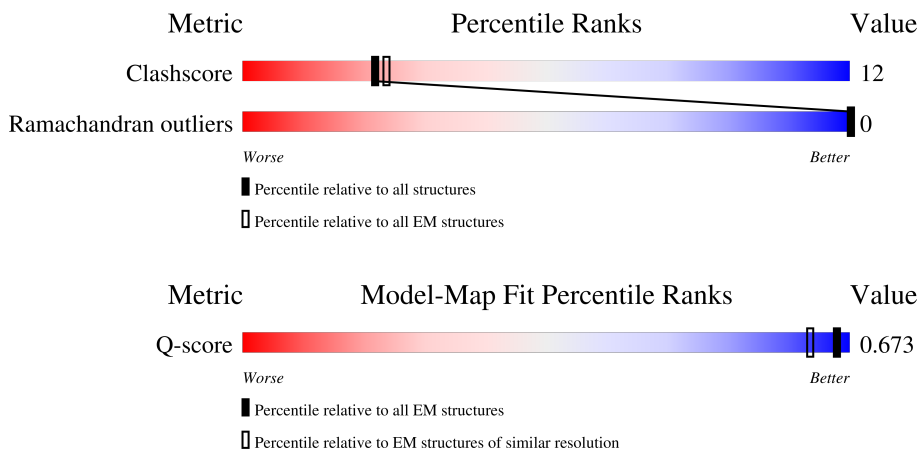
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.43 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	-
Q-score	-	25397	5787 (1.94 - 2.93)

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	732	52% 18% 29%
1	2	732	53% 18% 29%
1	3	732	52% 18% 29%
1	4	732	52% 18% 29%
1	5	732	52% 19% 29%

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Mol	Chain	Length	Quality of chain
1	6	732	
1	7	732	
1	8	732	
1	A	732	
1	B	732	
1	C	732	
1	D	732	
1	E	732	
1	F	732	
1	G	732	
1	H	732	
1	I	732	
1	J	732	
1	K	732	
1	L	732	
1	M	732	
1	N	732	
1	O	732	
1	P	732	
1	Q	732	
1	R	732	
1	S	732	
1	T	732	
1	U	732	
1	V	732	

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Mol	Chain	Length	Quality of chain
1	W	732	
1	X	732	
1	Y	732	
1	Z	732	
1	a	732	
1	b	732	
1	c	732	
1	d	732	
1	e	732	
1	f	732	
1	g	732	
1	h	732	
1	i	732	
1	j	732	
1	k	732	
1	l	732	
1	m	732	
1	n	732	
1	o	732	
1	p	732	
1	q	732	
1	r	732	
1	s	732	
1	t	732	
1	u	732	

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Mol	Chain	Length	Quality of chain
1	v	732	 52% 19% 29%
1	w	732	 52% 18% 29%
1	x	732	 52% 19% 29%
1	y	732	 52% 18% 29%
1	z	732	 53% 18% 29%

2 Entry composition

There is only 1 type of molecule 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 VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	B	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	C	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	D	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	E	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	F	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	G	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	H	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	I	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	J	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	K	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	L	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	M	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	N	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	O	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	P	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	Q	519	Total 4165	C 2640	N 719	O 790	S 16	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	S	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	T	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	U	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	V	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	W	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	X	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	Y	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	Z	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	a	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	b	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	c	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	d	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	e	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	f	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	g	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	h	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	i	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	j	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	k	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	l	519	Total 4165	C 2640	N 719	O 790	S 16	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	n	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	o	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	p	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	q	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	r	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	s	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	t	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	u	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	v	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	w	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	x	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	y	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	z	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	1	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	2	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	3	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	4	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	5	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	6	519	Total 4165	C 2640	N 719	O 790	S 16	0	0
1	7	519	Total 4165	C 2640	N 719	O 790	S 16	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	519	Total	C	N	O	S	0	0
			4165	2640	719	790	16		

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	615	TRP	GLY	conflict	UNP Q67666
B	615	TRP	GLY	conflict	UNP Q67666
C	615	TRP	GLY	conflict	UNP Q67666
D	615	TRP	GLY	conflict	UNP Q67666
E	615	TRP	GLY	conflict	UNP Q67666
F	615	TRP	GLY	conflict	UNP Q67666
G	615	TRP	GLY	conflict	UNP Q67666
H	615	TRP	GLY	conflict	UNP Q67666
I	615	TRP	GLY	conflict	UNP Q67666
J	615	TRP	GLY	conflict	UNP Q67666
K	615	TRP	GLY	conflict	UNP Q67666
L	615	TRP	GLY	conflict	UNP Q67666
M	615	TRP	GLY	conflict	UNP Q67666
N	615	TRP	GLY	conflict	UNP Q67666
O	615	TRP	GLY	conflict	UNP Q67666
P	615	TRP	GLY	conflict	UNP Q67666
Q	615	TRP	GLY	conflict	UNP Q67666
R	615	TRP	GLY	conflict	UNP Q67666
S	615	TRP	GLY	conflict	UNP Q67666
T	615	TRP	GLY	conflict	UNP Q67666
U	615	TRP	GLY	conflict	UNP Q67666
V	615	TRP	GLY	conflict	UNP Q67666
W	615	TRP	GLY	conflict	UNP Q67666
X	615	TRP	GLY	conflict	UNP Q67666
Y	615	TRP	GLY	conflict	UNP Q67666
Z	615	TRP	GLY	conflict	UNP Q67666
a	615	TRP	GLY	conflict	UNP Q67666
b	615	TRP	GLY	conflict	UNP Q67666
c	615	TRP	GLY	conflict	UNP Q67666
d	615	TRP	GLY	conflict	UNP Q67666
e	615	TRP	GLY	conflict	UNP Q67666
f	615	TRP	GLY	conflict	UNP Q67666
g	615	TRP	GLY	conflict	UNP Q67666
h	615	TRP	GLY	conflict	UNP Q67666
i	615	TRP	GLY	conflict	UNP Q67666
j	615	TRP	GLY	conflict	UNP Q67666

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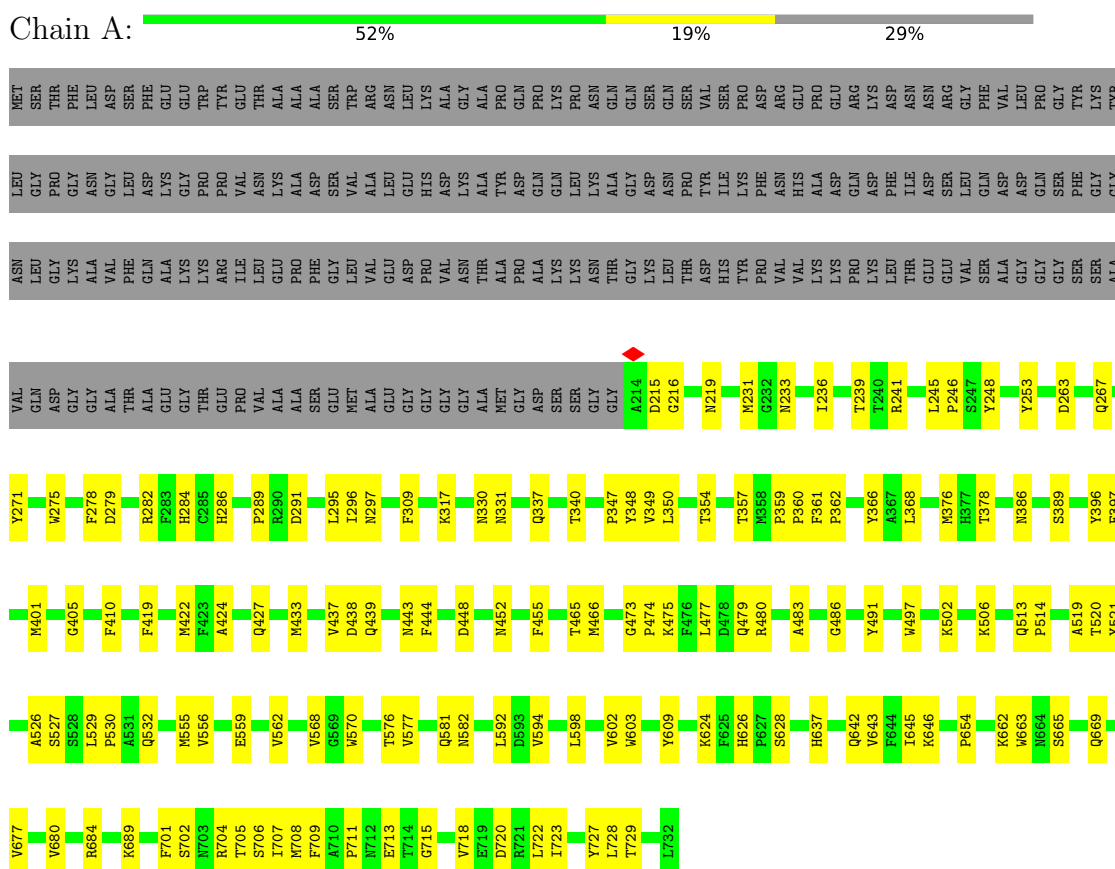
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Chain	Residue	Modelled	Actual	Comment	Reference
k	615	TRP	GLY	conflict	UNP Q67666
l	615	TRP	GLY	conflict	UNP Q67666
m	615	TRP	GLY	conflict	UNP Q67666
n	615	TRP	GLY	conflict	UNP Q67666
o	615	TRP	GLY	conflict	UNP Q67666
p	615	TRP	GLY	conflict	UNP Q67666
q	615	TRP	GLY	conflict	UNP Q67666
r	615	TRP	GLY	conflict	UNP Q67666
s	615	TRP	GLY	conflict	UNP Q67666
t	615	TRP	GLY	conflict	UNP Q67666
u	615	TRP	GLY	conflict	UNP Q67666
v	615	TRP	GLY	conflict	UNP Q67666
w	615	TRP	GLY	conflict	UNP Q67666
x	615	TRP	GLY	conflict	UNP Q67666
y	615	TRP	GLY	conflict	UNP Q67666
z	615	TRP	GLY	conflict	UNP Q67666
1	615	TRP	GLY	conflict	UNP Q67666
2	615	TRP	GLY	conflict	UNP Q67666
3	615	TRP	GLY	conflict	UNP Q67666
4	615	TRP	GLY	conflict	UNP Q67666
5	615	TRP	GLY	conflict	UNP Q67666
6	615	TRP	GLY	conflict	UNP Q67666
7	615	TRP	GLY	conflict	UNP Q67666
8	615	TRP	GLY	conflict	UNP Q67666

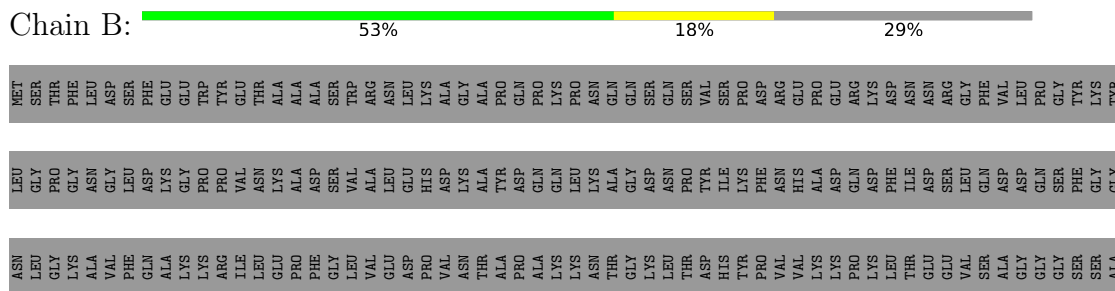
3 Residue-property plots

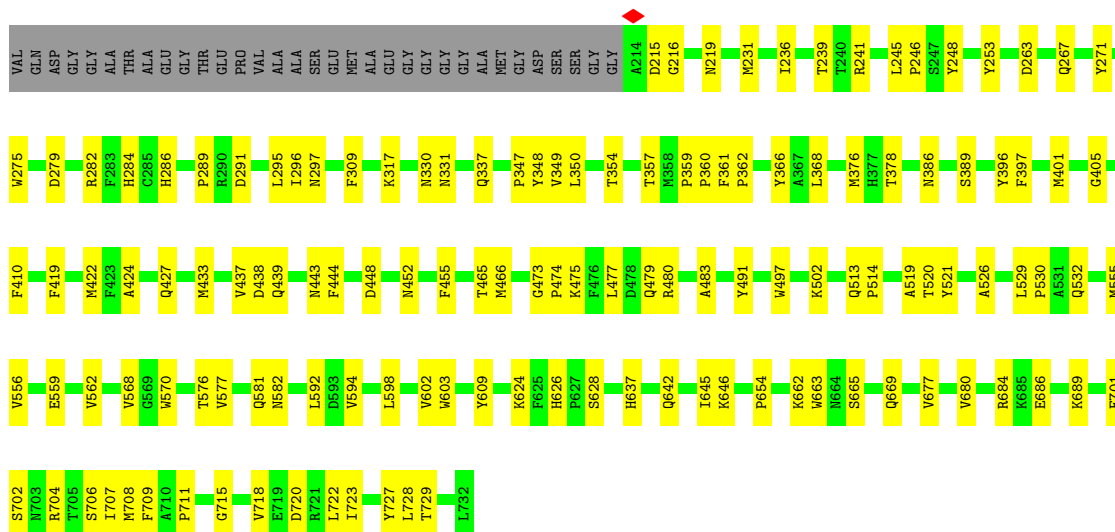
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

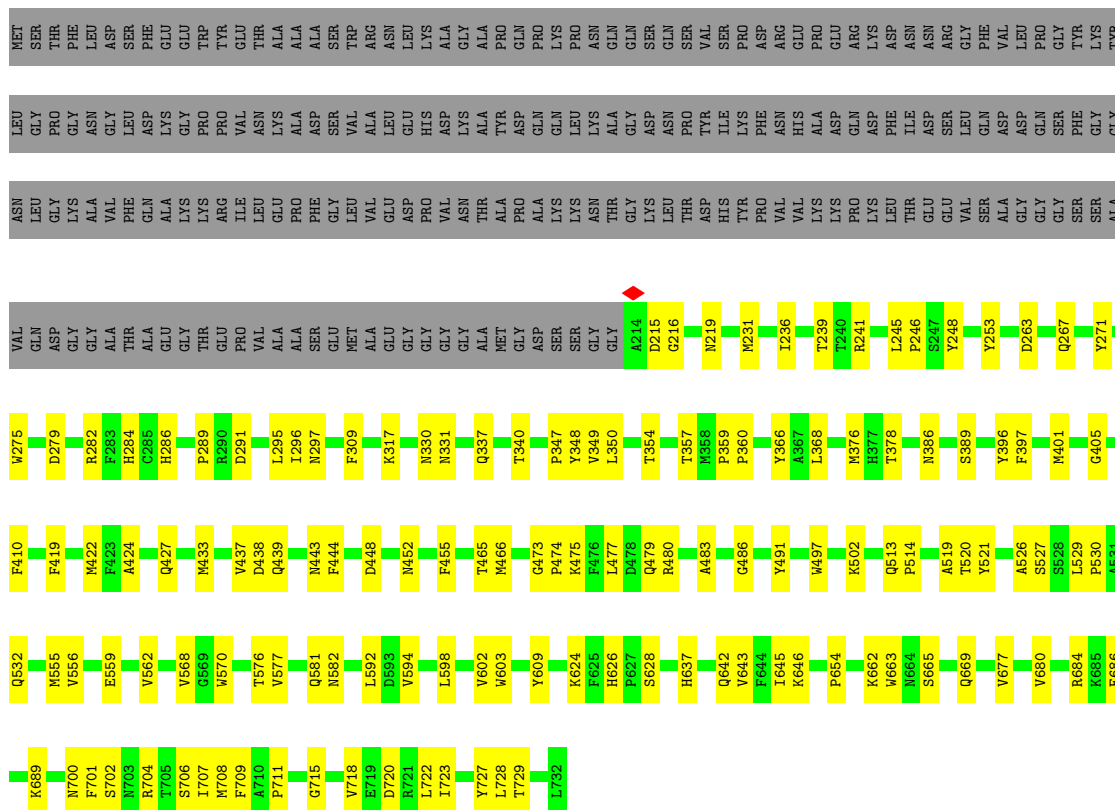


• Molecule 1: VP1

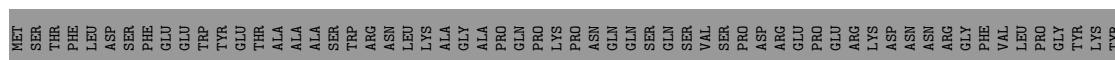




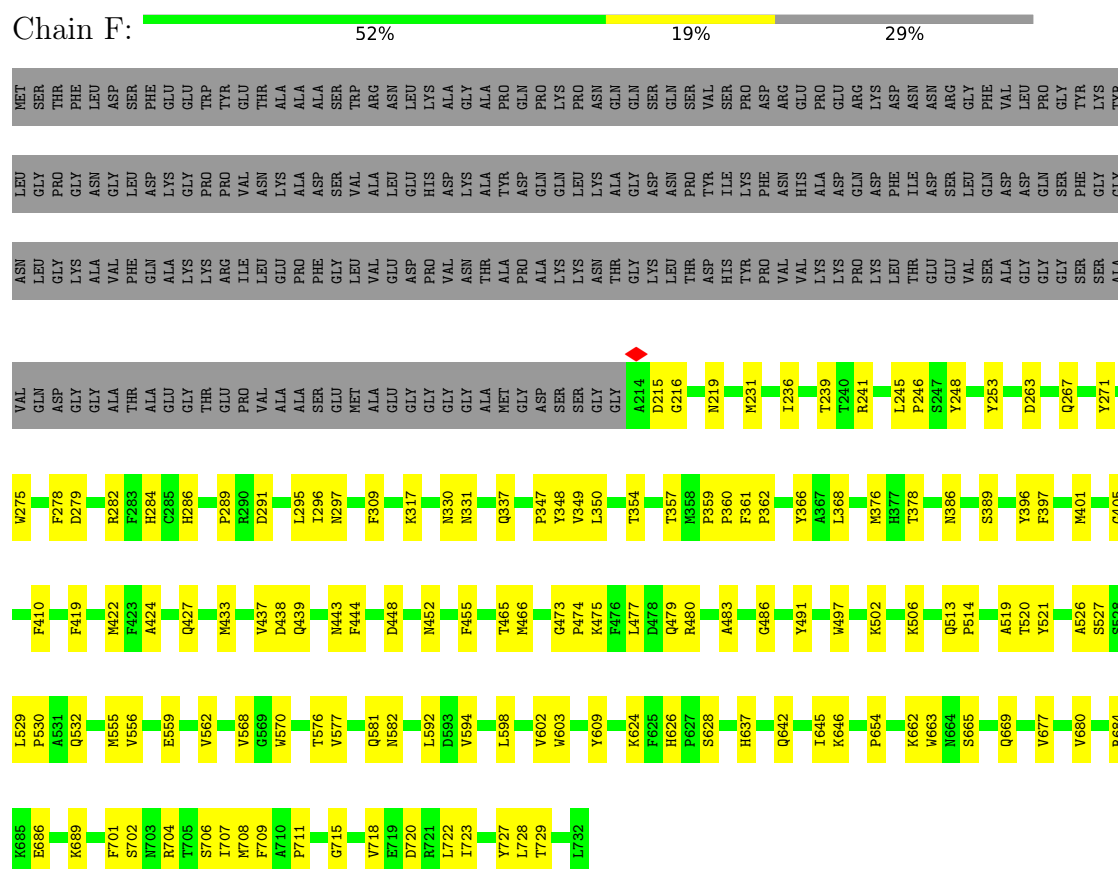
- Molecule 1: VP1



- Molecule 1: VP1

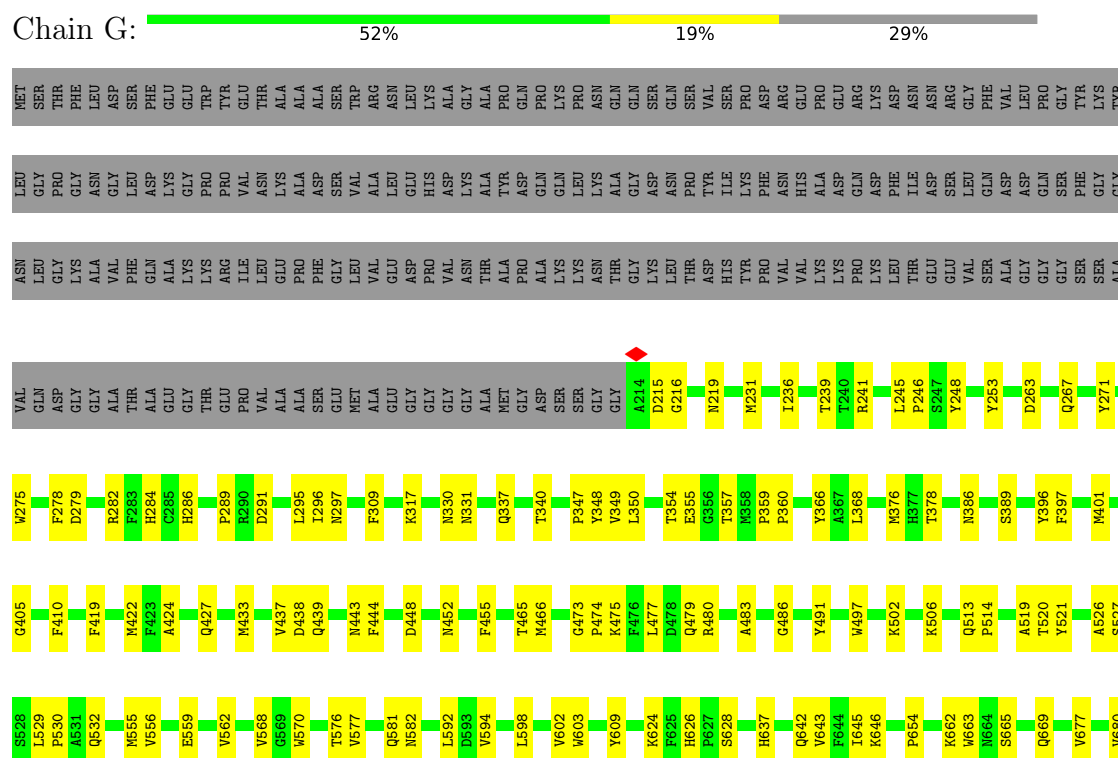


Chain F:

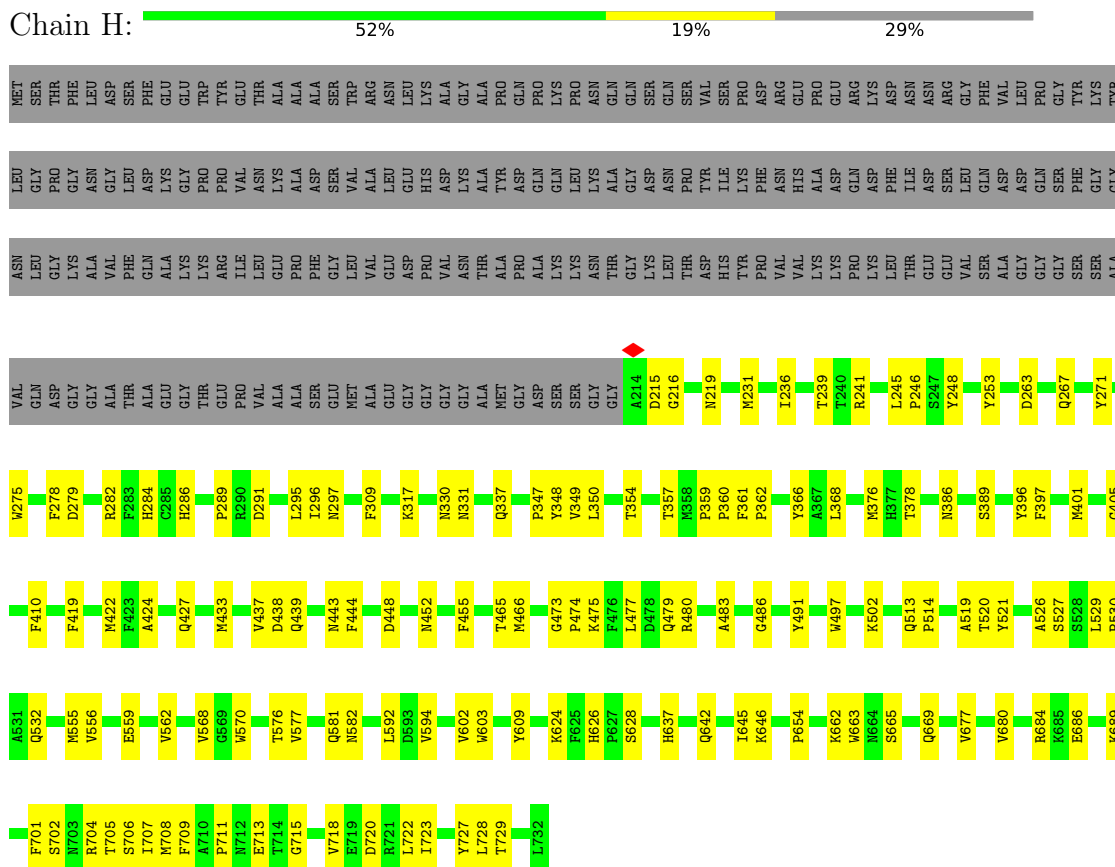


• Molecule 1: VP1

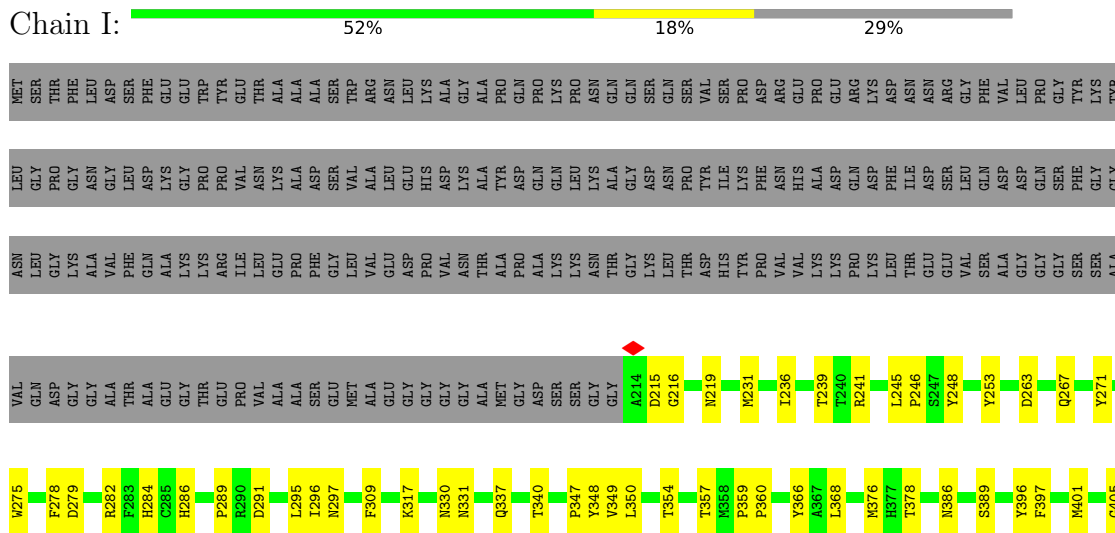
Chain G:

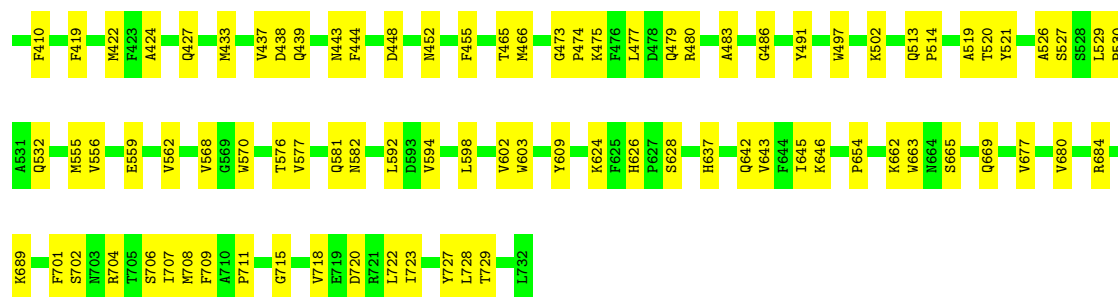


- Molecule 1: VP1



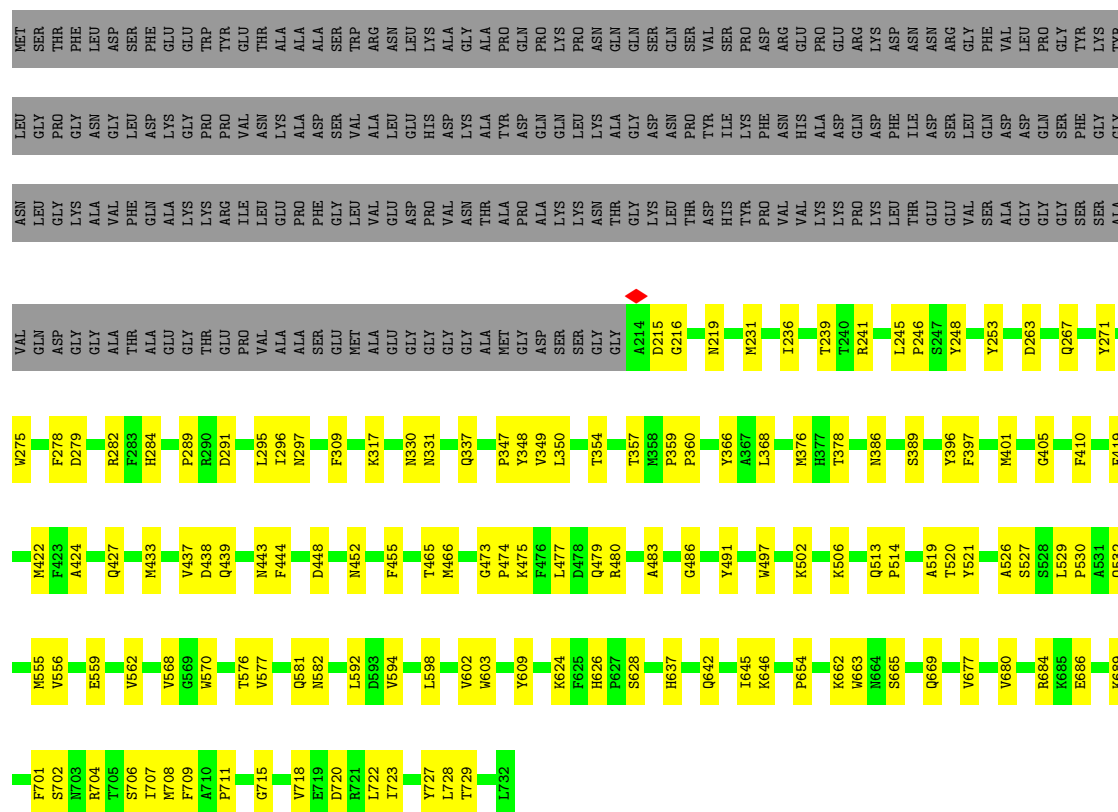
- Molecule 1: VP1





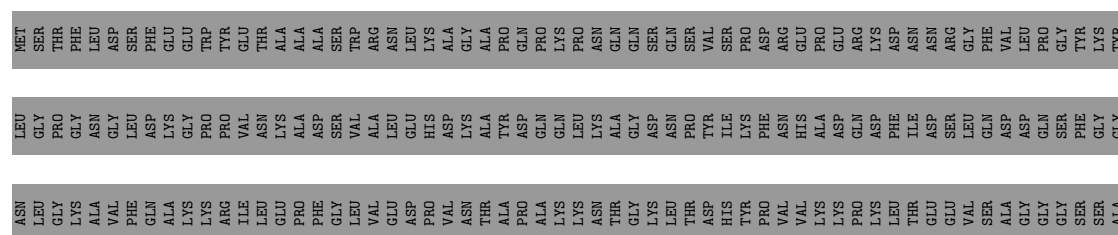
• Molecule 1: VP1

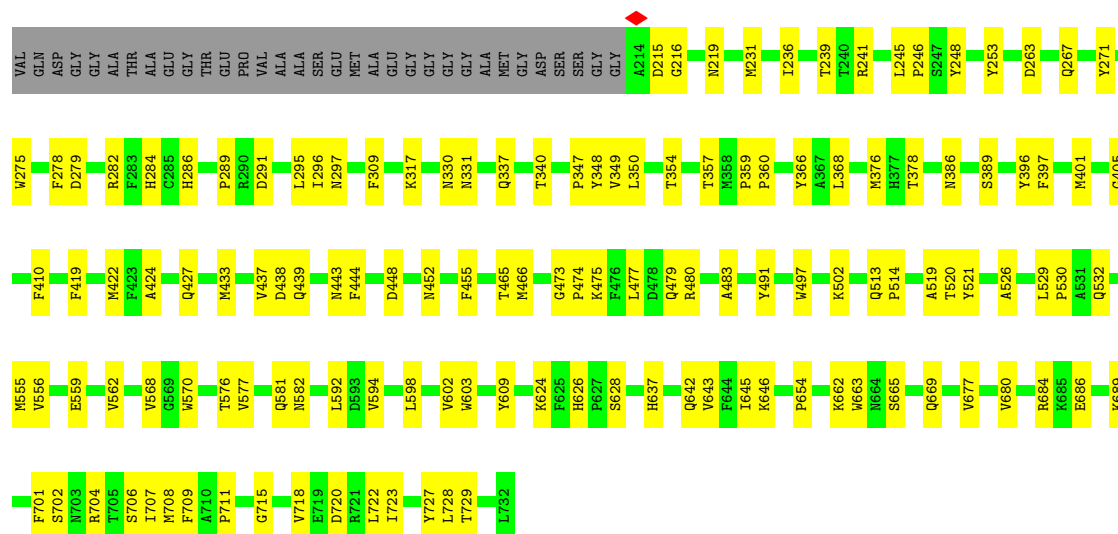
Chain J: 53% 18% 29%



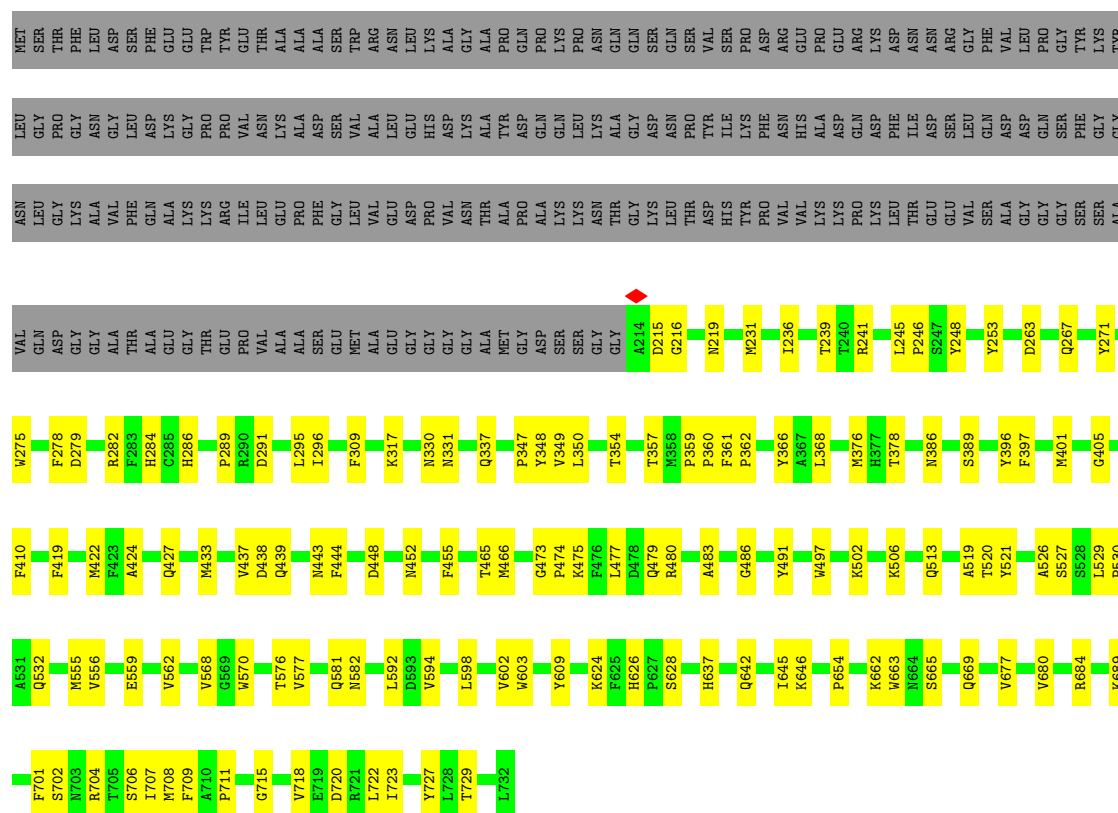
• Molecule 1: VP1

Chain K: 53% 18% 29%

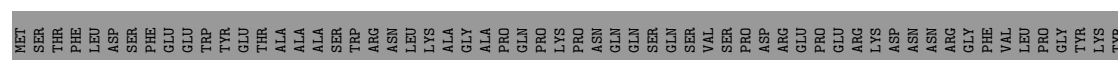


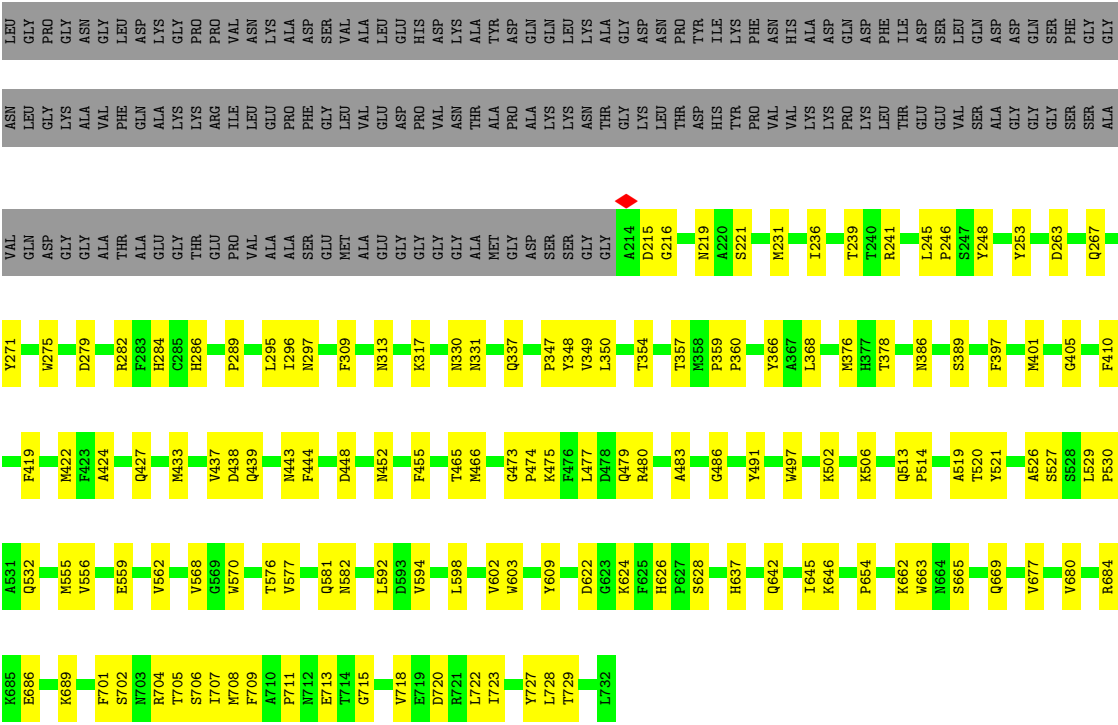


• Molecule 1: VP1

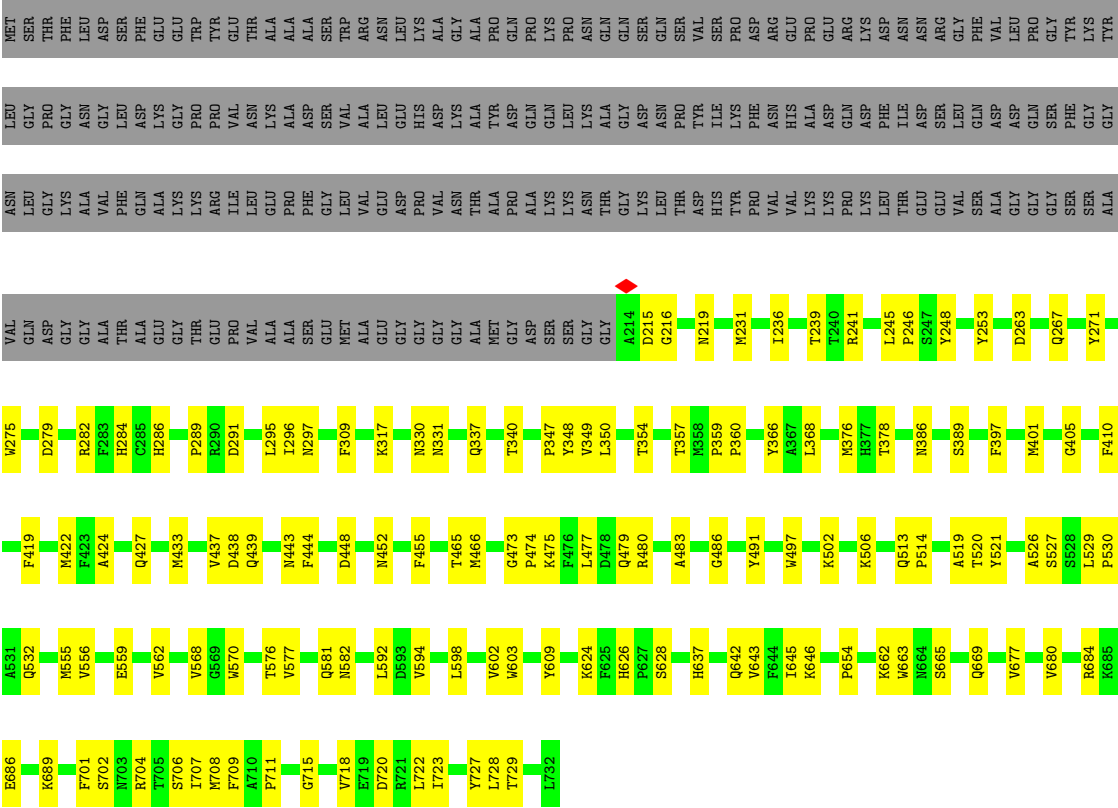


• Molecule 1: VP1





● Molecule 1: VP1



● Molecule 1: VP1

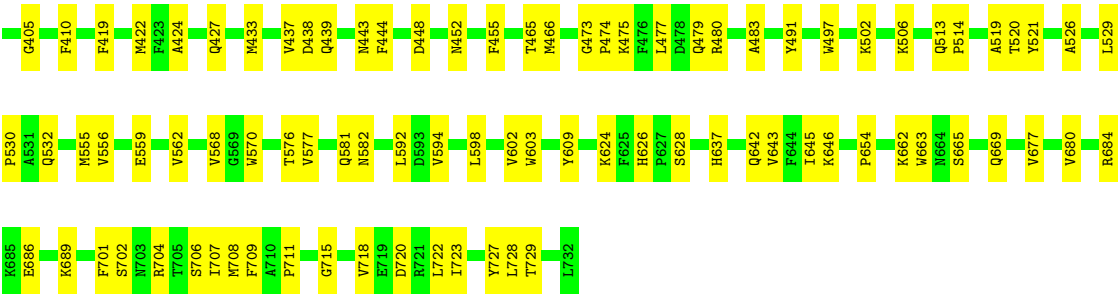
Chain O:  52% 19% 29%

MET	LEU	ASN	VAL	W275	A531	E686
SER	GLY	LEU	GLN	F410	Q552	K689
THR	PRO	GLY	ASP	F419	M555	N700
PHE	ASN	GLY	GLY	M422	V556	F701
LEU	VAL	ALA	ALA	F423	E559	S702
ASP	GLY	VAL	THR	A424	S703	N703
SER	LEU	PHE	ALA	Q427	V562	R704
PHE	ASP	GLN	THR	M433	V568	S705
GLU	GLY	ALA	GLU	V437	G569	T706
TRP	PRO	LYS	THR	D438	I707	M707
TYR	PRO	ARG	PRO	Q439	M433	M708
GLU	VAL	ILE	PRO	M443	W570	F709
THR	ASN	LEU	VAL	F444	T576	A710
ALA	LYS	GLU	ALA	N452	V577	P711
ALA	PRO	ALA	ALA	F455	N581	N712
ALA	ASP	PHE	SER	T465	N582	E713
SER	SER	GLY	GLY	M466	L592	T714
TRP	VAL	LEU	MET	G473	V602	G715
ARG	ALA	VAL	ALA	K475	W603	V718
ASN	ALA	THR	ALA	P474	V594	E719
GLN	TYR	ALA	MET	L477	L598	D720
GLN	GLN	LYS	GLY	Q479	V609	R721
SER	LYS	ASN	GLY	R480	K624	L722
GLN	LEU	THR	GLY	A483	F625	I723
SER	LYS	ASN	GLY	G486	H626	Y727
VAL	TYR	THR	GLY	Y491	P627	L728
SER	ILE	THR	GLY	W497	S628	T729
PRO	PHE	THR	GLY	K502	H637	L732
ARG	ASN	VAL	GLY	Q513	Q642	
GLU	ARG	VAL	GLY	P514	V643	
PRO	GLN	LYS	GLY	A519	F644	
ARG	ASP	LYS	GLY	T520	I645	
LYS	PHE	THR	GLY	Y521	K646	
ASN	ILE	THR	GLY	A526	P654	
ASN	ASP	GLU	GLY	S527	K662	
ARG	ASP	GLU	GLY	S528	W663	
GLY	LEU	VAL	GLY	R684	V664	
VAL	GLN	SER	GLY	K685	S665	
PHE	GLN	ALA	GLY		Q669	
VAL	ASP	ALA	GLY		V677	
LEU	ASP	GLY	GLY		V680	
PRO	GLY	GLY	GLY		R684	
GLY	SER	GLY	GLY		K685	
TYR	PHE	GLY	GLY			
LYS	GLY	GLY	GLY			
TYR	GLY	GLY	GLY			

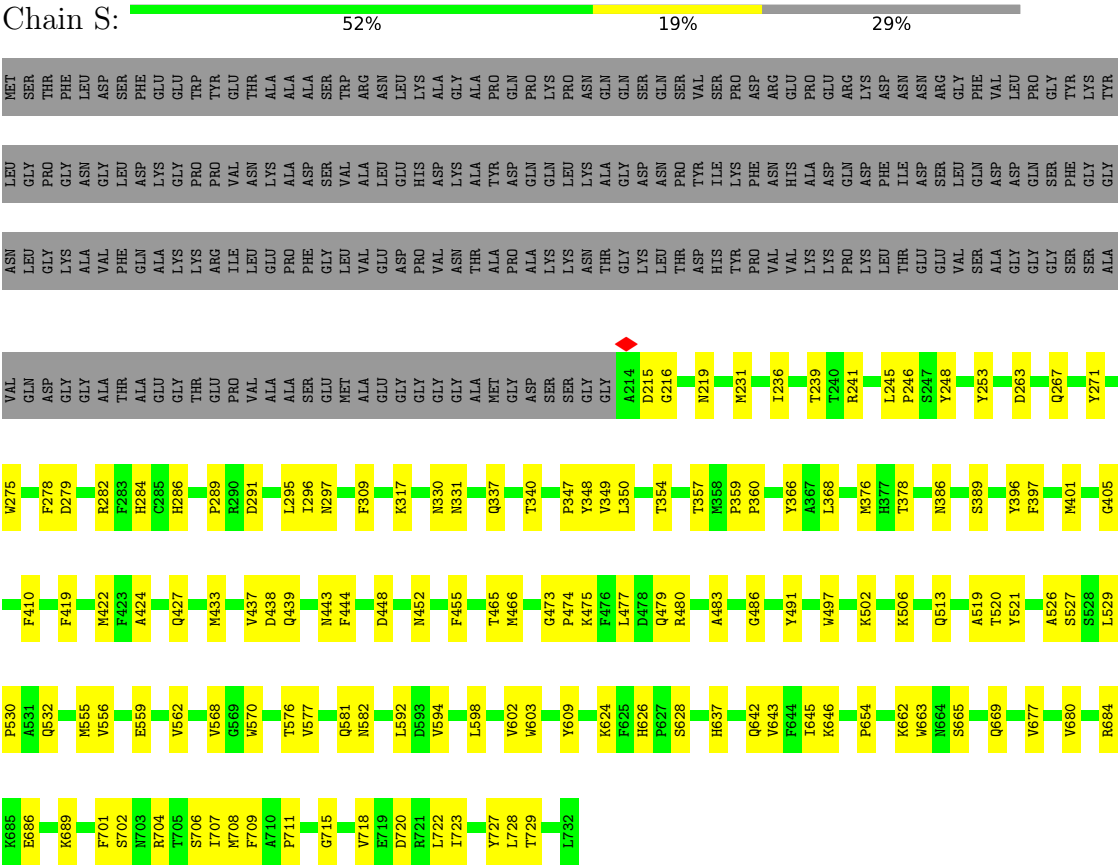
• Molecule 1: VP1

Chain P:  52% 19% 29%

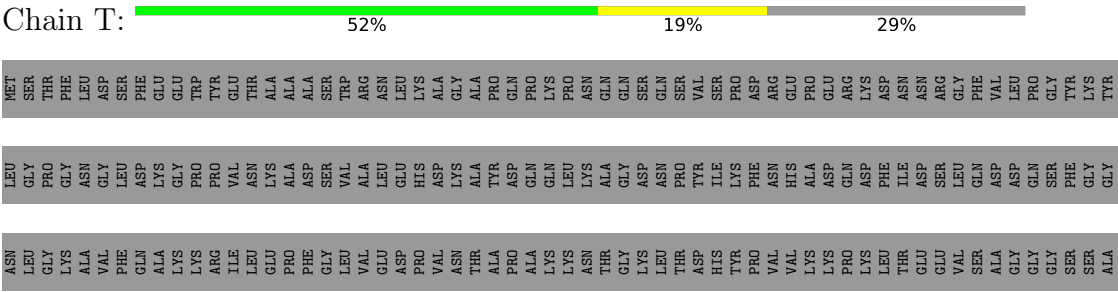
MET	LEU	ASN	VAL	W275	A531	L529
SER	GLY	LEU	GLN	F278	Q532	P530
THR	PRO	GLY	ASP	D279	M555	F532
PHE	ASN	GLY	GLY	R282	V556	A531
LEU	VAL	ALA	ALA	F283	E559	N555
ASP	GLY	PHE	THR	H284	V562	V556
SER	LEU	GLN	ALA	H286	V568	P559
PHE	ASP	GLY	THR	P289	G569	V562
GLU	GLY	ALA	GLU	R290	I570	V568
TRP	PRO	LYS	THR	D291	D438	S569
TYR	PRO	ARG	PRO	L295	Q439	W570
GLU	VAL	ILE	PRO	N297	N443	T576
THR	ASN	LEU	VAL	F309	F444	V577
ALA	LYS	GLU	ALA	K317	D448	Q581
ALA	PRO	ALA	ALA	N330	N452	N582
ALA	ASP	PHE	SER	N331	F455	L592
TRP	VAL	LEU	VAL	Q337	T465	D593
ARG	ALA	VAL	MET	T340	M466	V594
ASN	LEU	VAL	ALA	P347	G473	L598
ASN	LYS	ASN	GLY	Y348	P474	V602
GLN	ALA	THR	GLY	L350	K475	W603
SER	GLY	GLY	GLY	T354	F476	V609
GLN	ASP	ASN	GLY	R480	D478	K624
GLN	LEU	THR	GLY	D215	P627	F625
SER	THR	PRO	GLY	G216	S628	H626
VAL	ASP	TYR	GLY	N219	H637	P627
SER	HIS	ILE	GLY	M231	Q642	S628
PRO	TYR	PHE	GLY	I236	V643	H637
ARG	ASN	ASN	GLY	T239	F644	Q642
GLU	VAL	HIS	GLY	R241	I645	V643
ARG	LYS	VAL	GLY	L245	K646	I645
LYS	LYS	LYS	GLY	P246	P654	K646
LEU	THR	THR	GLY	Y248	A519	P654
ASN	ILE	THR	GLY	Y253	T520	K662
ASN	ASP	GLN	GLY	D263	Y521	W663
ARG	ASP	SER	GLY	Q267	A526	V664
GLY	LEU	GLN	GLY	Y271	S527	S665
VAL	GLN	SER	GLY		R684	K685
ALA	ASP	VAL	GLY			
ALA	ASP	ALA	GLY			
GLY	ASP	GLY	GLY			
PRO	GLY	GLY	GLY			
GLY	SER	GLY	GLY			
TYR	PHE	GLY	GLY			
LYS	GLY	GLY	GLY			
TYR	GLY	GLY	GLY			



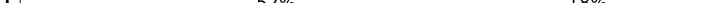
• Molecule 1: VP1



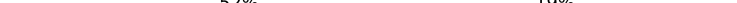
• Molecule 1: VP1

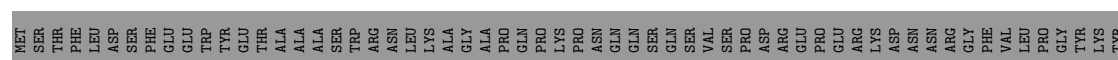


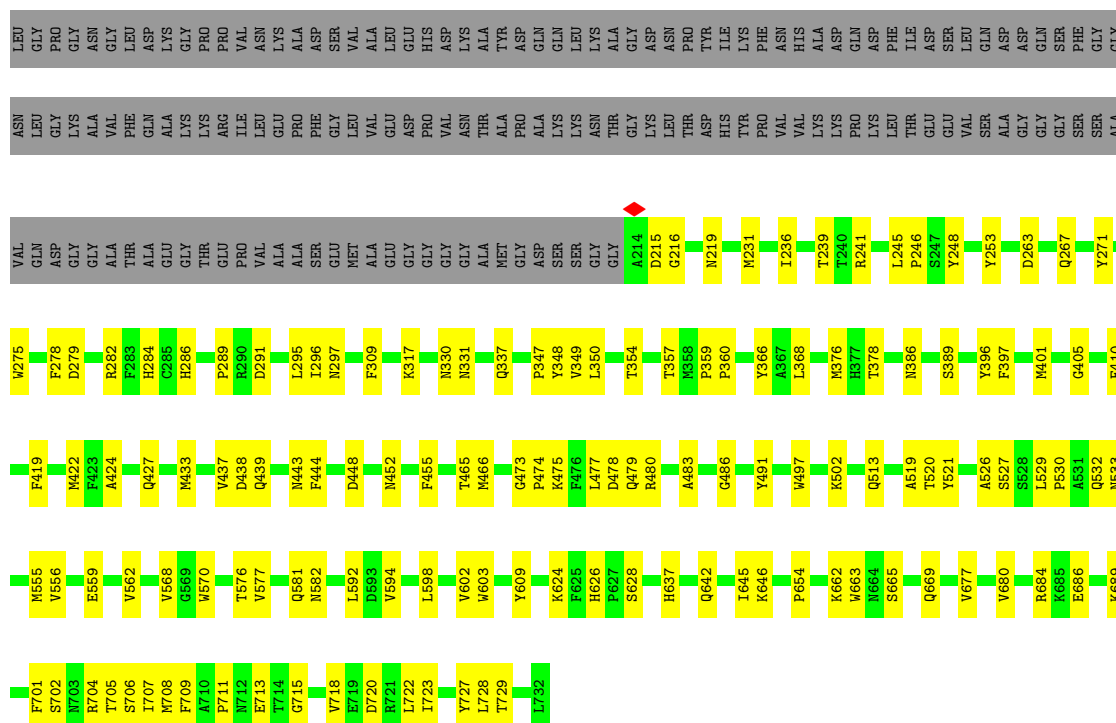
- Molecule 1: VP1

Chain U:  52% 18% 29%

- Molecule 1: VP1

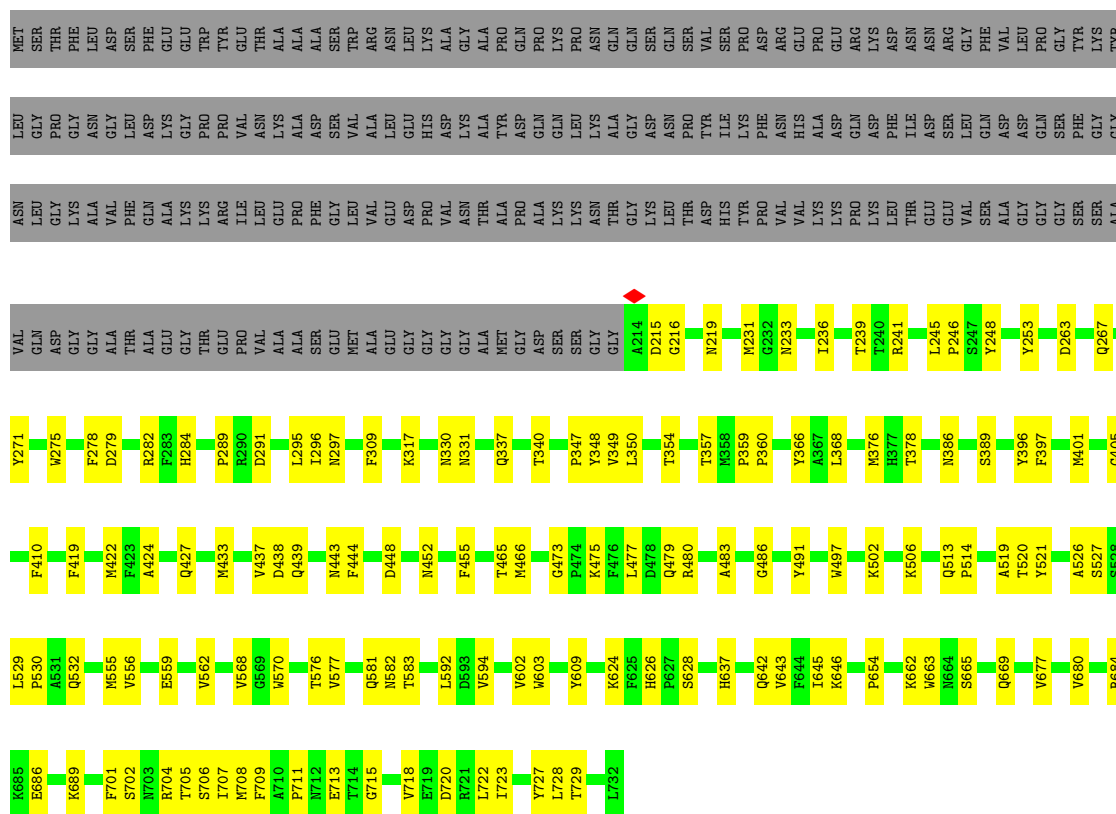
Chain V:  52% 19% 29%





• Molecule 1: VP1

Chain W: 52% 19% 29%



• Molecule 1: VP1

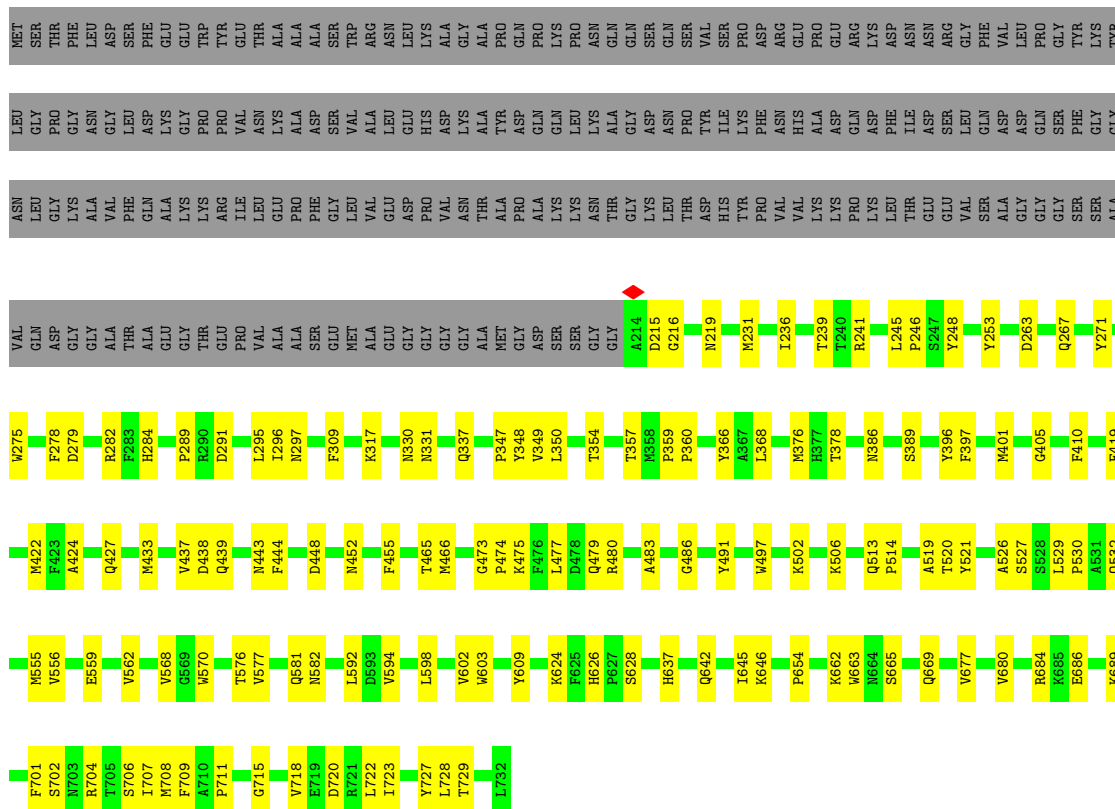
Category	Percentage
Very bad	52%
Bad	19%
Good	29%



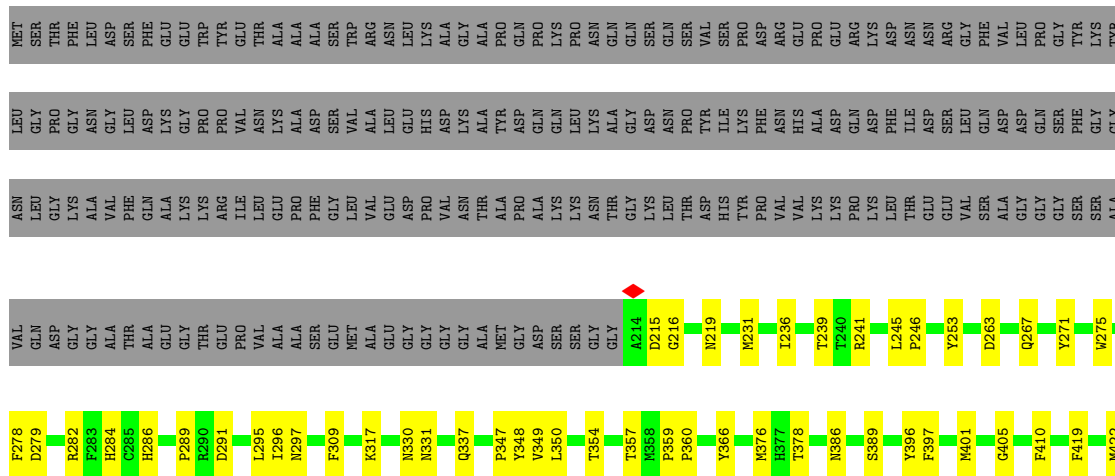
Response	Percentage
Doing a good job	52%
Not doing a good job	18%
Don't know	29%



- Molecule 1: VP1



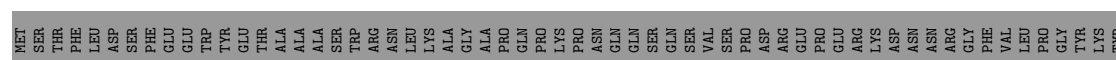
- Molecule 1: VP1



- Molecule 1: VP1



- Molecule 1: VP1



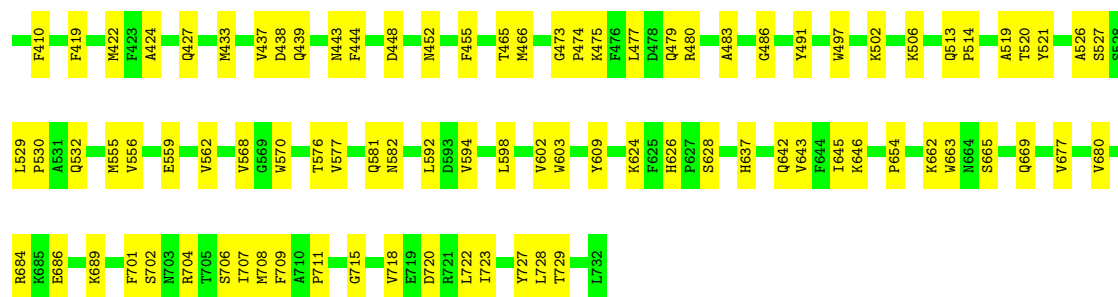


Digital Tool Type	Percentage of Respondents
Video Conferencing Tool	53%
Document Collaboration Tool	18%
Project Management Tool	29%



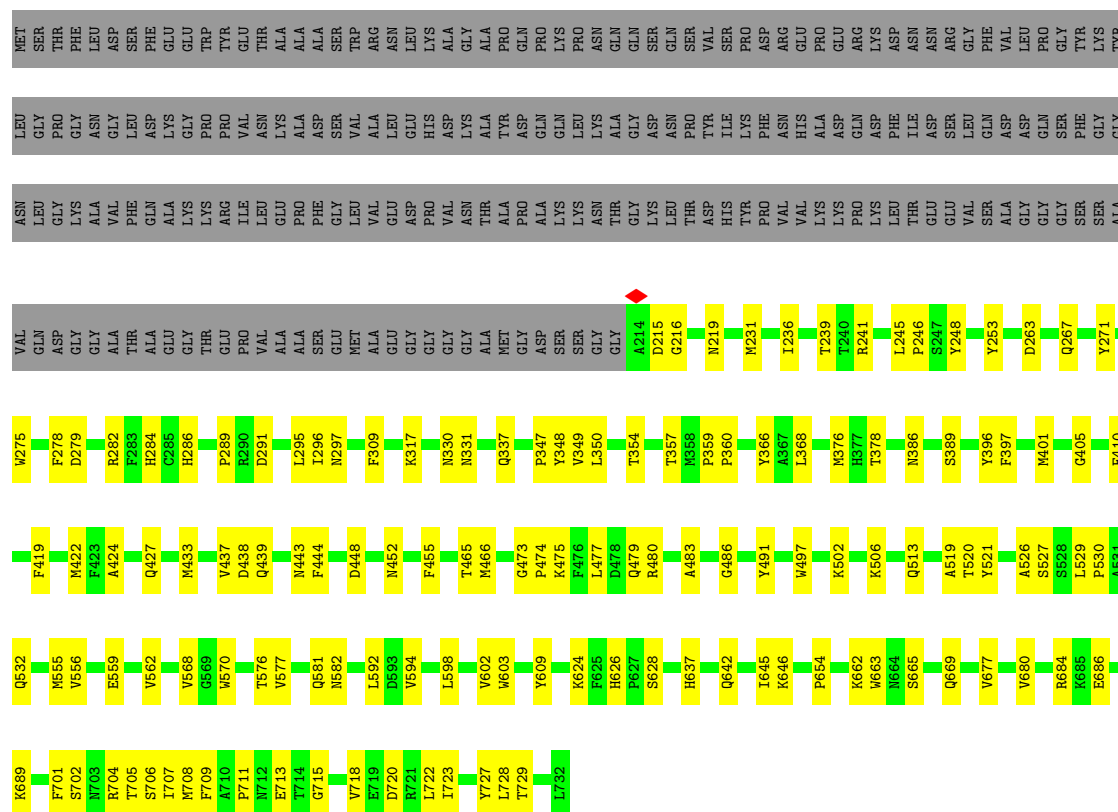
Category	Percentage
Very good	53%
Good	18%
Not good	29%





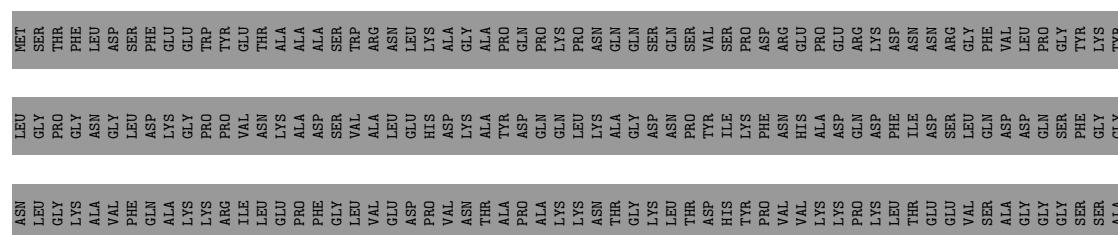
• Molecule 1: VP1

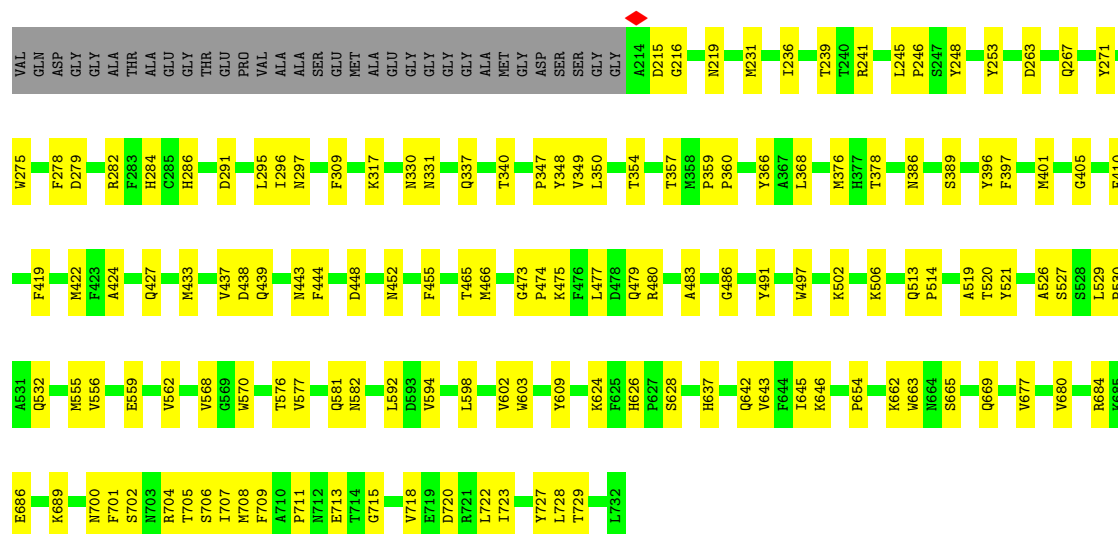
Chain k: 52% 19% 29%



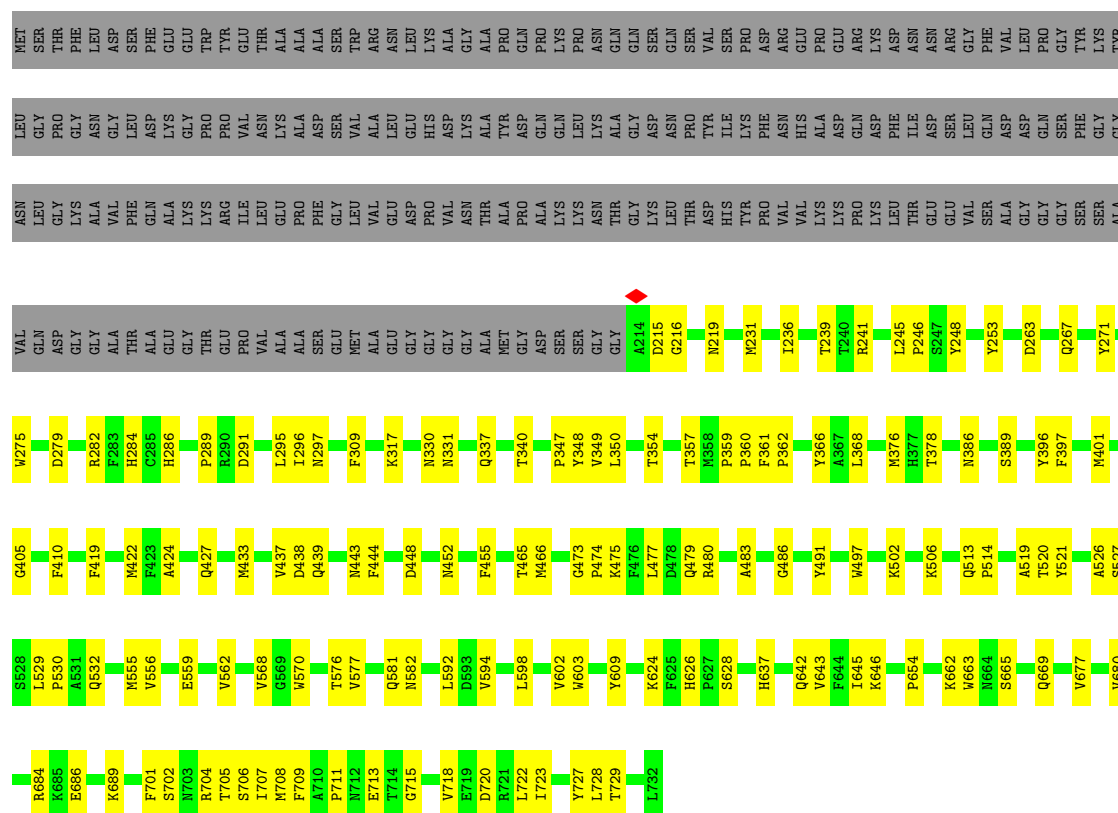
• Molecule 1: VP1

Chain l: 52% 19% 29%

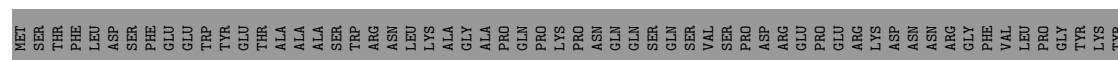


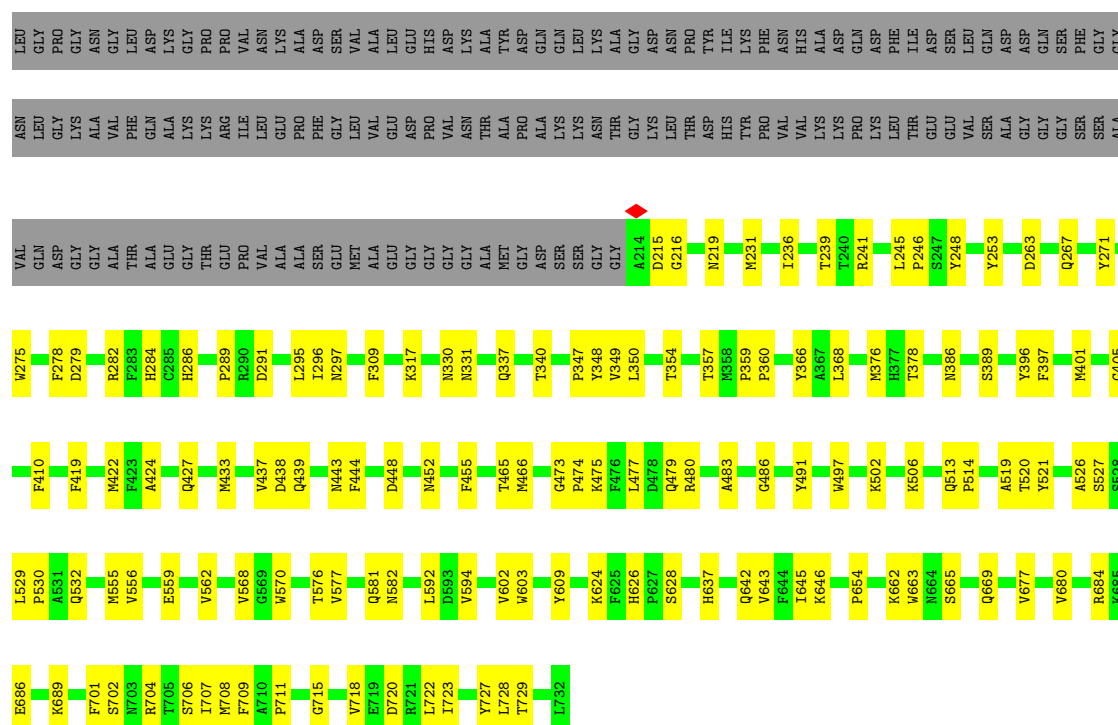


• Molecule 1: VP1

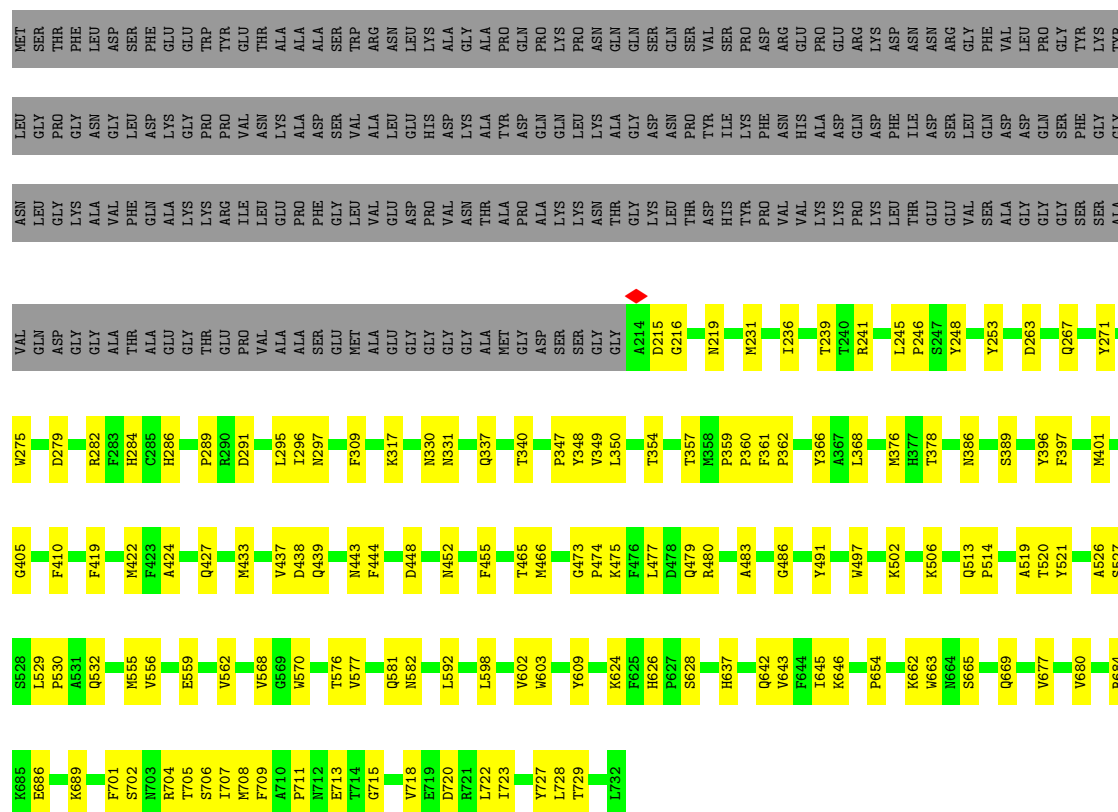


• Molecule 1: VP1



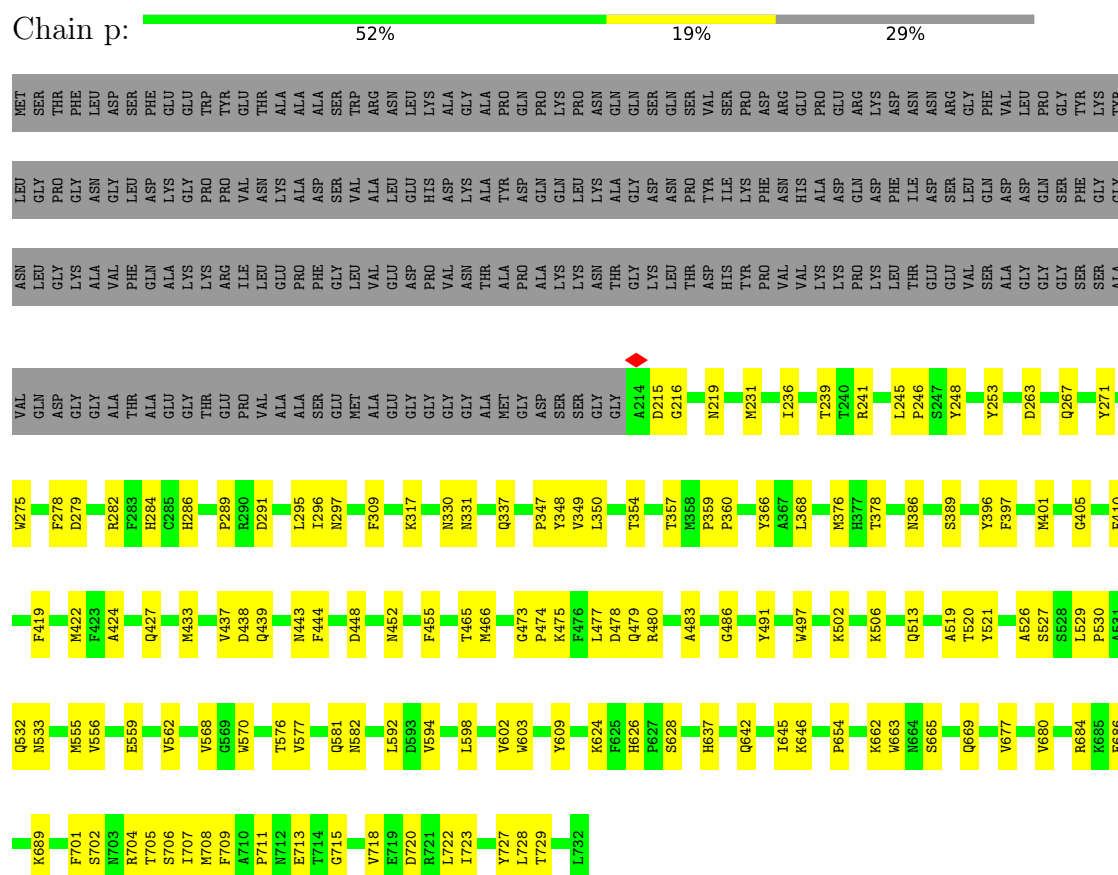


- Molecule 1: VP1



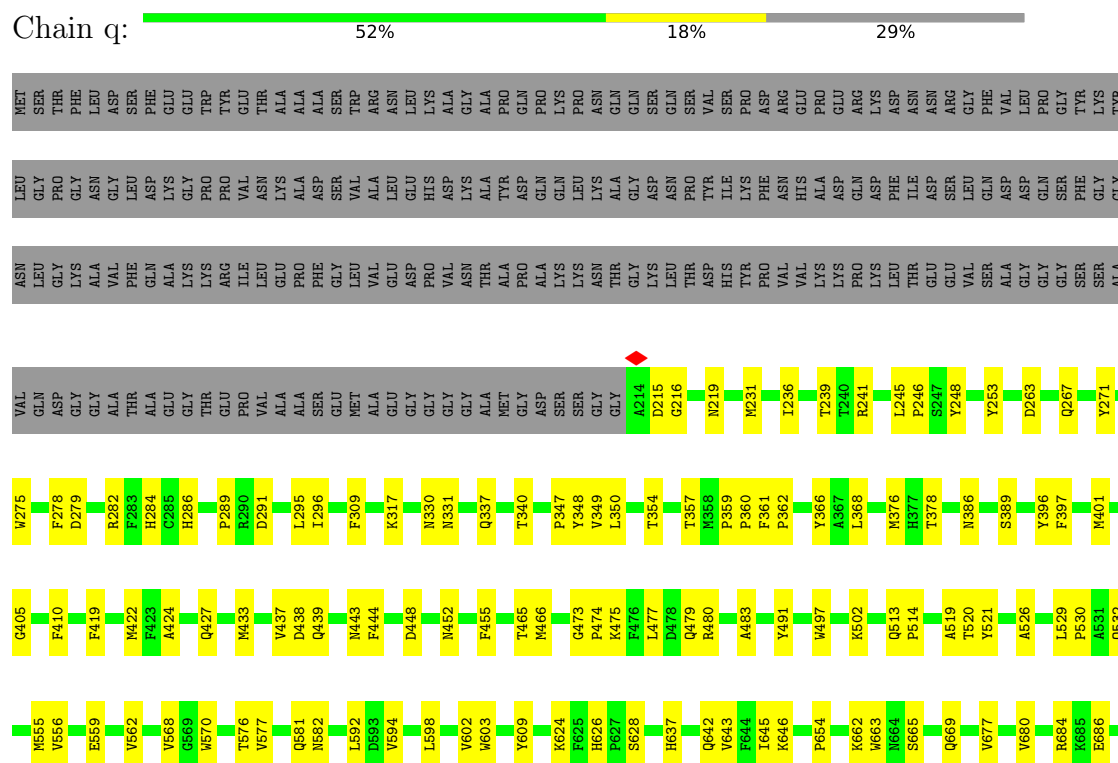
- Molecule 1: VP1

Chain p:



• Molecule 1: VP1

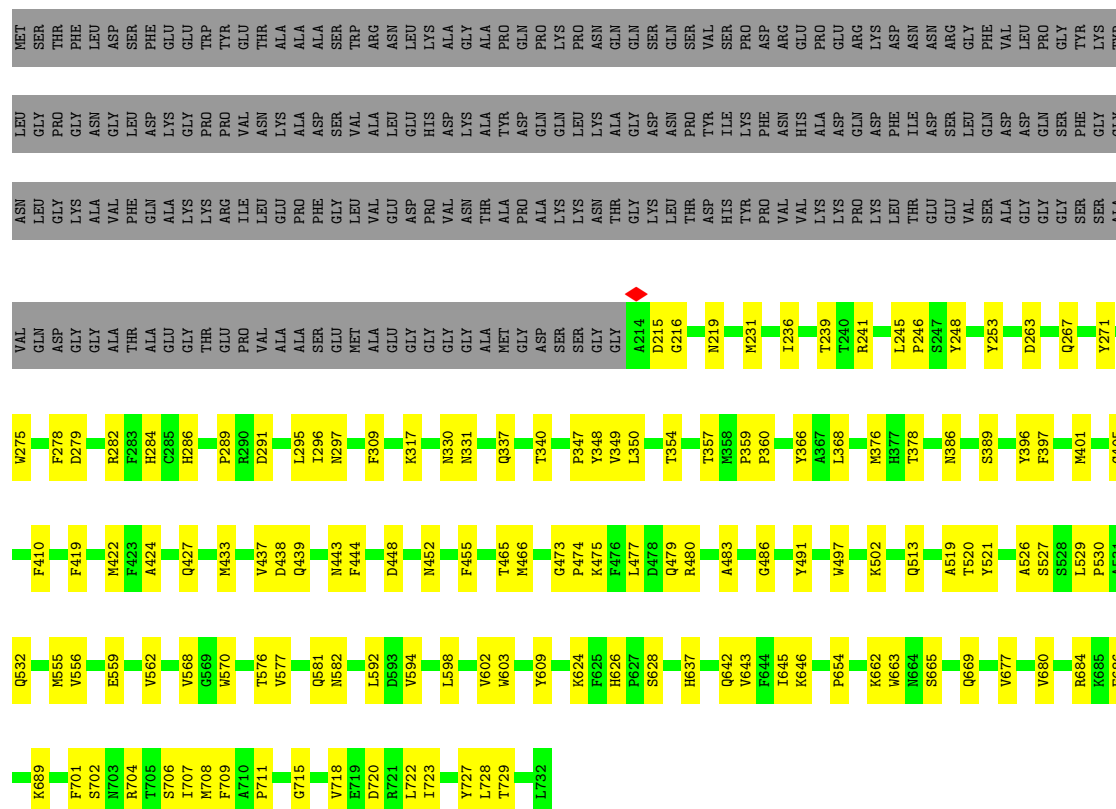
Chain q:





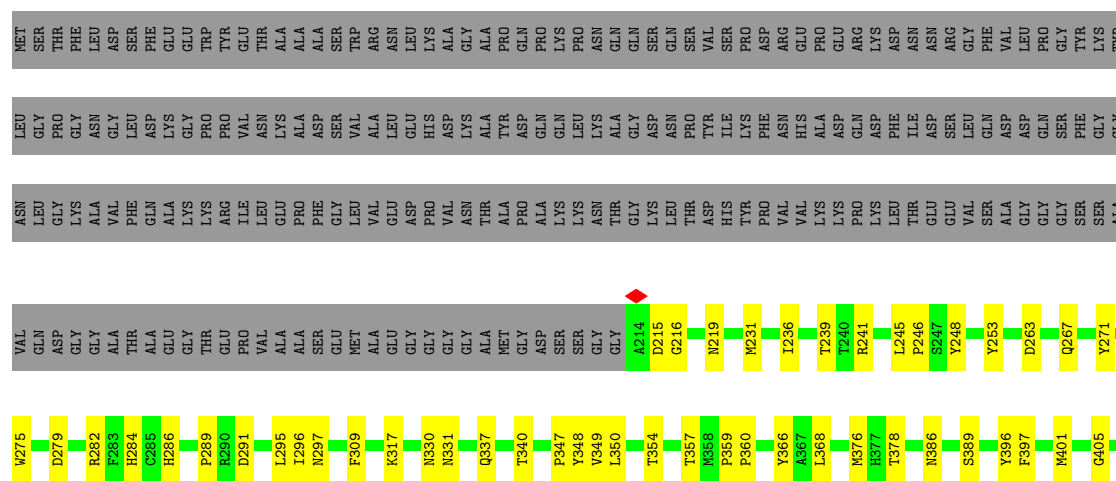
• Molecule 1: VP1

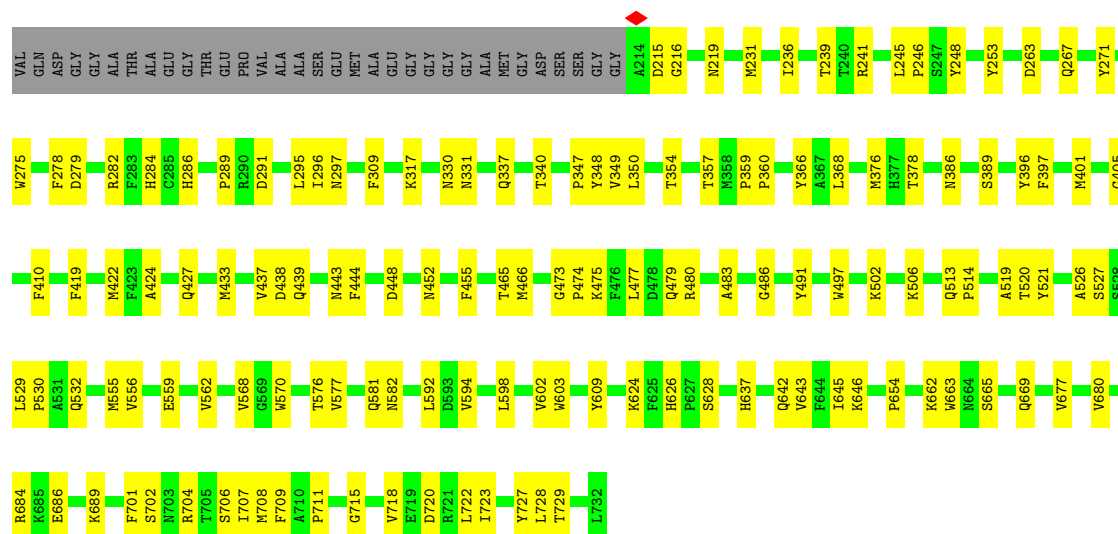
Chain r: 52% 18% 29%



• Molecule 1: VP1

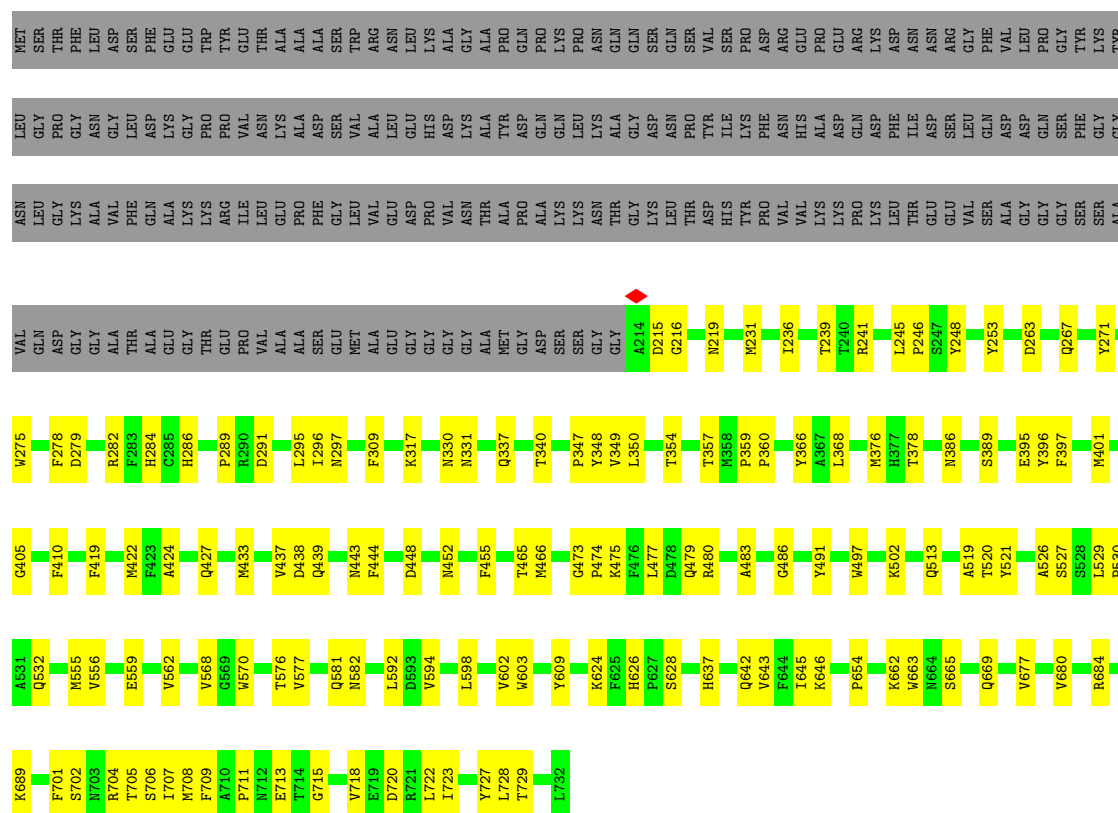
Chain s: 53% 18% 29%





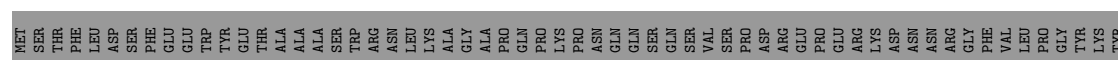
• Molecule 1: VP1

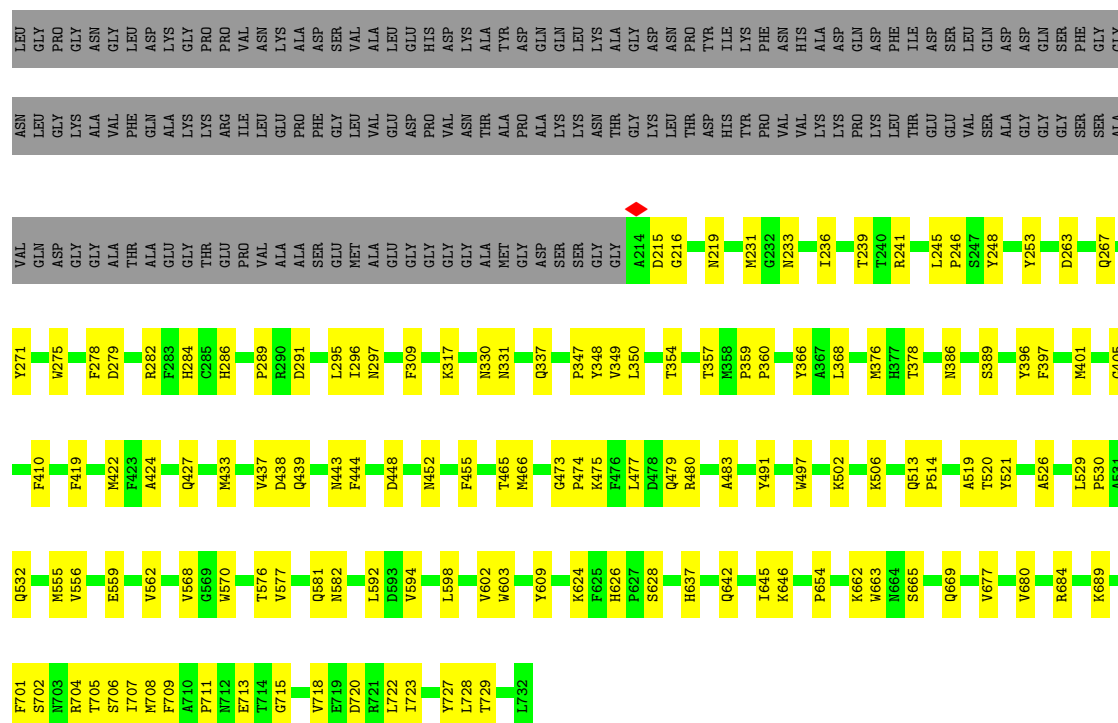
Chain v: 52% 19% 29%



• Molecule 1: VP1

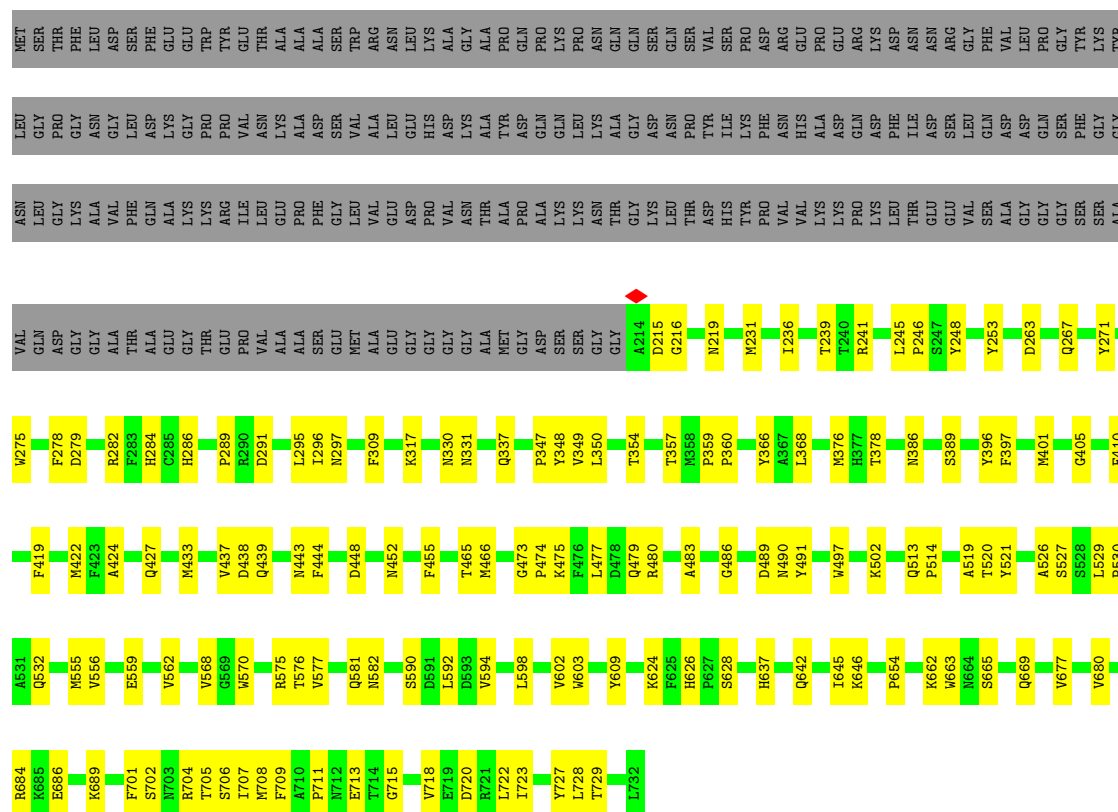
Chain w: 52% 18% 29%





• Molecule 1: VP1

Chain x: 52% 19% 29%



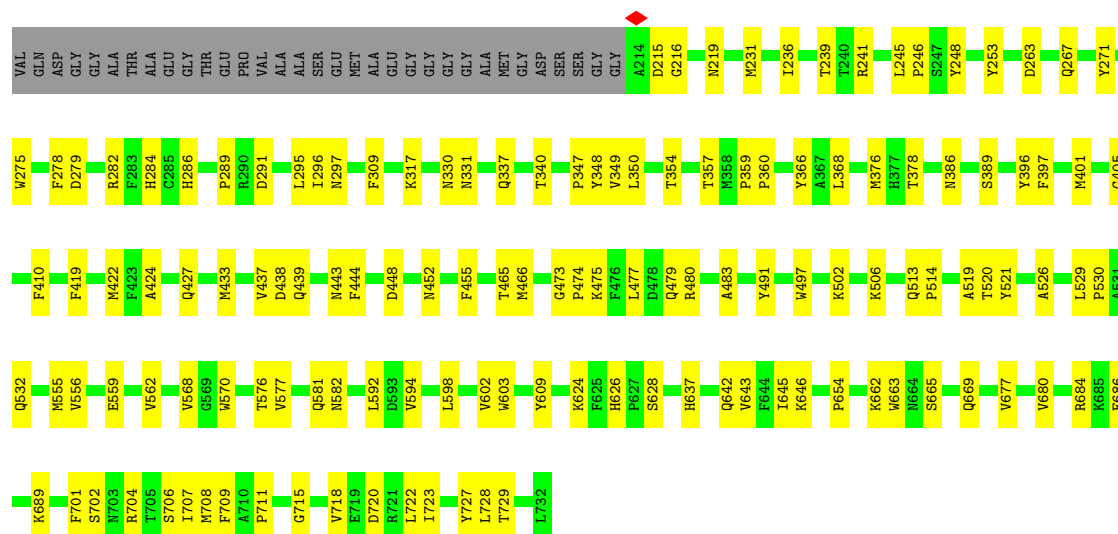
• Molecule 1: VP1

Response	Percentage
Best for the country	52%
Not the best for the country	18%
Don't know	29%



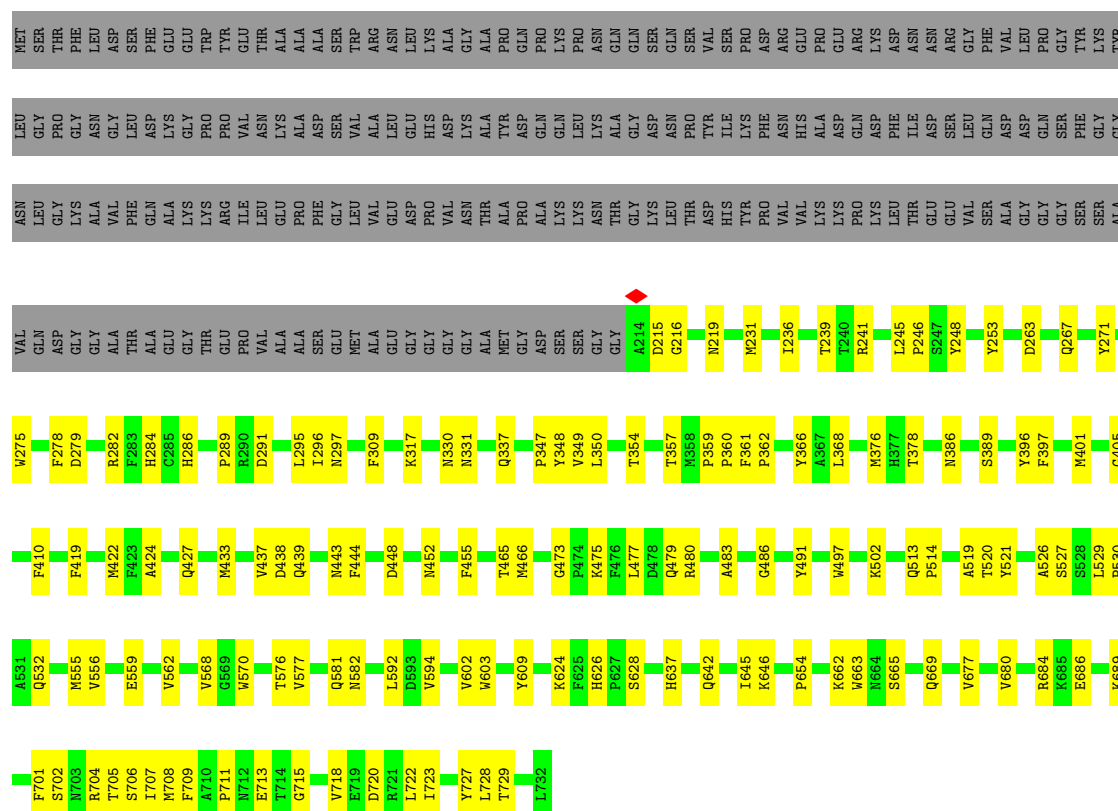
App Type	Percentage
Shopping app	53%
Social media app	18%
Productivity app	29%



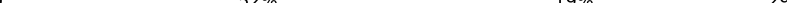


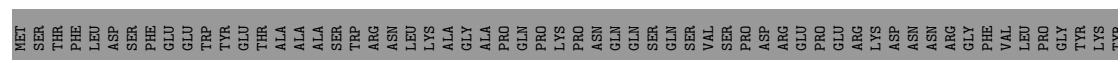
- Molecule 1: VP1

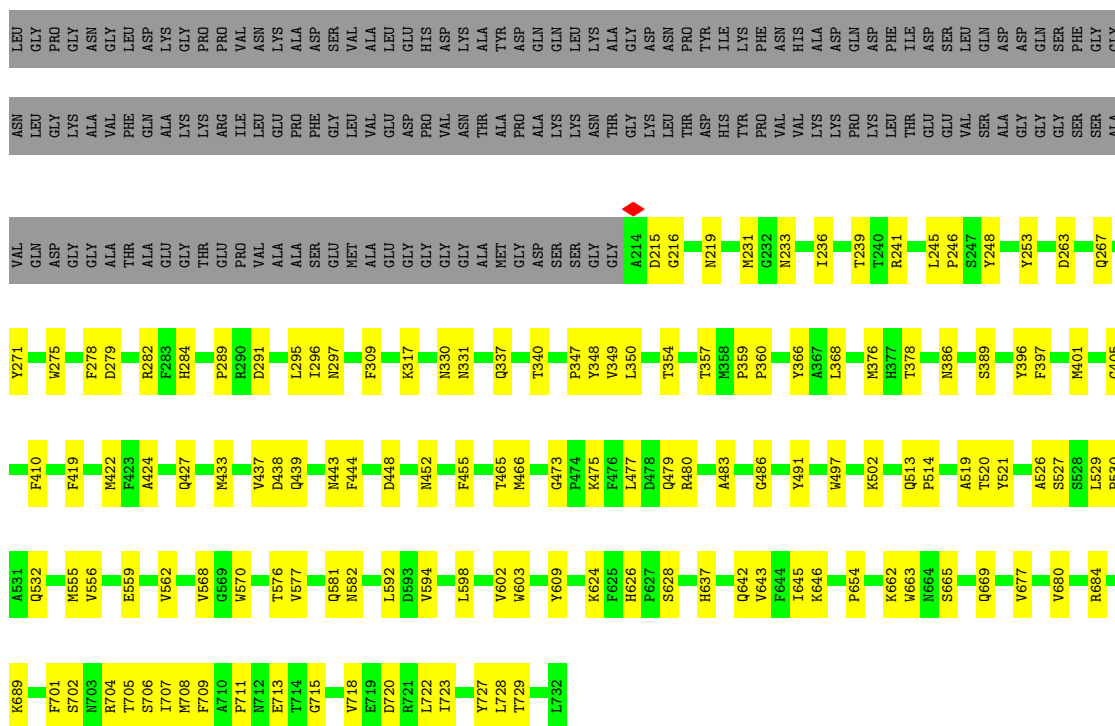
Chain 5: 52% 19% 29%



- Molecule 1: VP1

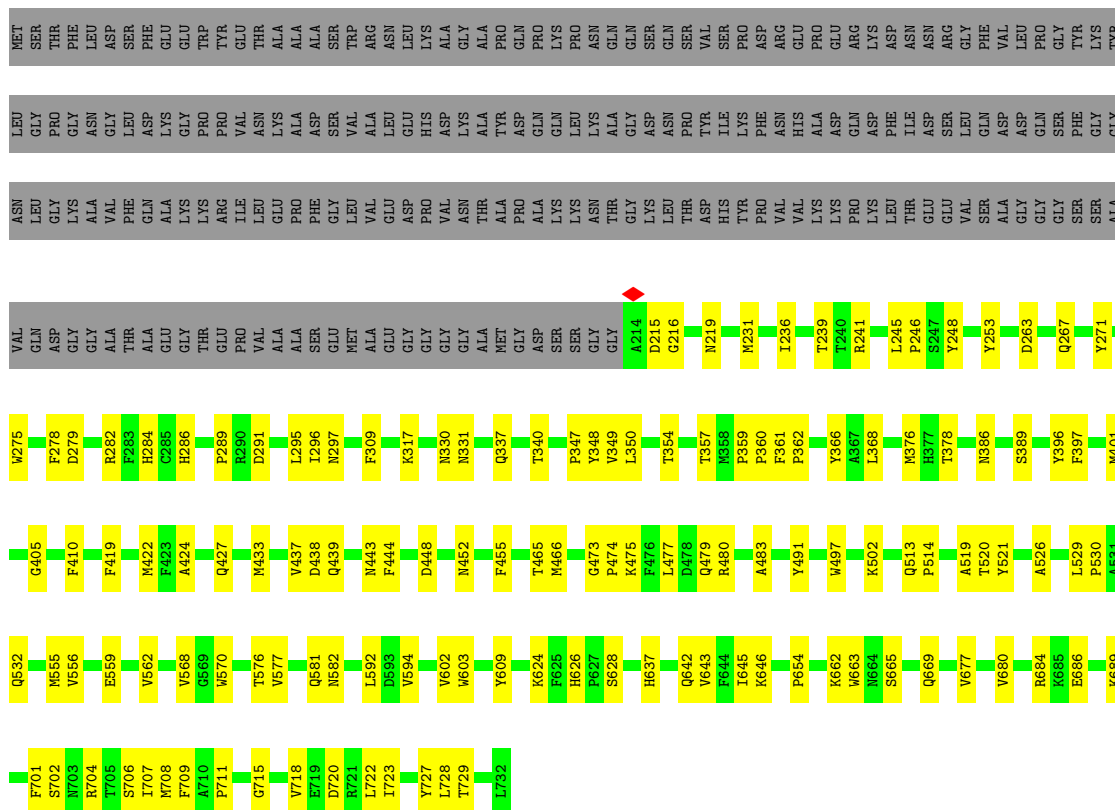
Chain 6:  52% 19% 29%





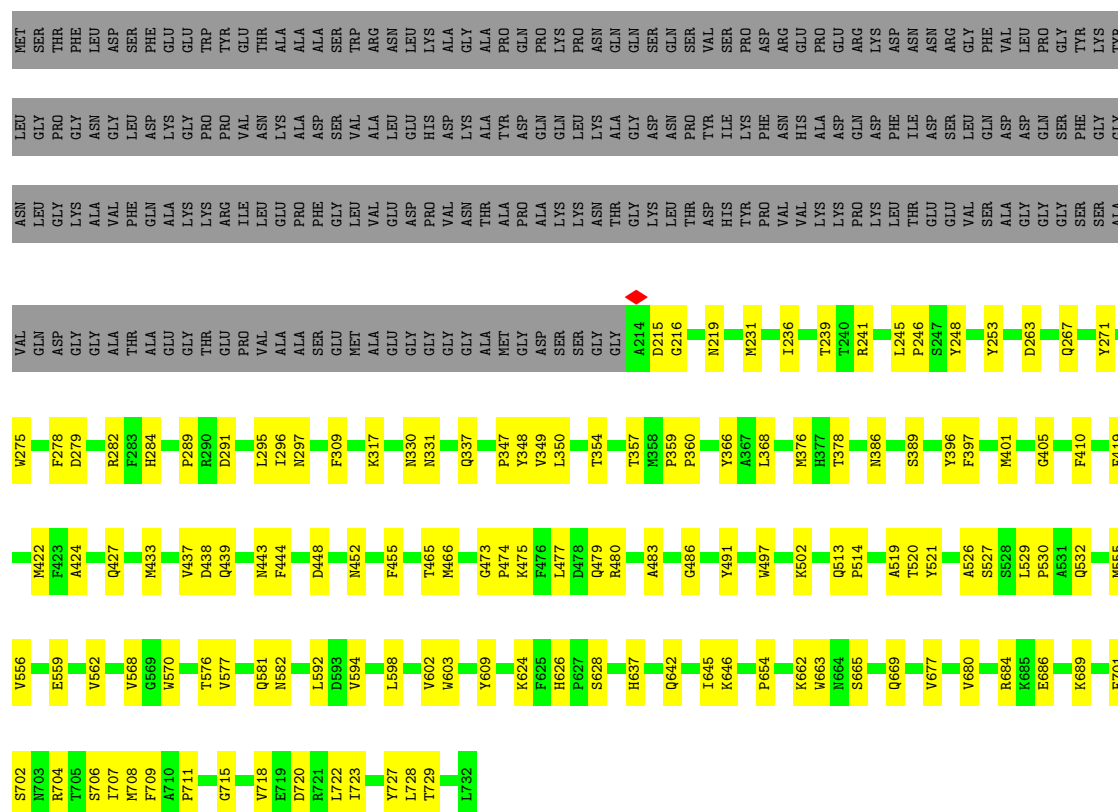
- Molecule 1: VP1

Chain 7: 52% 18% 29%



- Molecule 1: VP1

Response	Percentage
Yes, the U.S. should take action to reduce greenhouse gas emissions	53%
No, the U.S. should focus on other issues	18%
Don't know	29%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15471	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	4700	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	16.594	Depositor
Minimum map value	-8.236	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size (Å)	411.0, 411.0, 411.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.822, 0.822, 0.822	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.45	0/4294	0.58	0/5859
1	2	0.45	0/4294	0.58	1/5859 (0.0%)
1	3	0.45	0/4294	0.58	1/5859 (0.0%)
1	4	0.45	0/4294	0.58	1/5859 (0.0%)
1	5	0.45	0/4294	0.58	0/5859
1	6	0.45	0/4294	0.58	0/5859
1	7	0.45	0/4294	0.58	0/5859
1	8	0.45	0/4294	0.58	0/5859
1	A	0.45	0/4294	0.58	1/5859 (0.0%)
1	B	0.45	0/4294	0.58	0/5859
1	C	0.45	0/4294	0.58	0/5859
1	D	0.45	0/4294	0.58	0/5859
1	E	0.45	0/4294	0.58	0/5859
1	F	0.45	0/4294	0.58	1/5859 (0.0%)
1	G	0.45	0/4294	0.58	1/5859 (0.0%)
1	H	0.45	0/4294	0.58	0/5859
1	I	0.45	0/4294	0.58	0/5859
1	J	0.45	0/4294	0.58	1/5859 (0.0%)
1	K	0.45	0/4294	0.58	0/5859
1	L	0.45	0/4294	0.58	1/5859 (0.0%)
1	M	0.45	0/4294	0.58	1/5859 (0.0%)
1	N	0.45	0/4294	0.58	1/5859 (0.0%)
1	O	0.45	0/4294	0.58	0/5859
1	P	0.45	0/4294	0.58	1/5859 (0.0%)
1	Q	0.45	0/4294	0.58	1/5859 (0.0%)
1	R	0.45	0/4294	0.58	1/5859 (0.0%)
1	S	0.45	0/4294	0.58	1/5859 (0.0%)
1	T	0.45	0/4294	0.58	1/5859 (0.0%)
1	U	0.45	0/4294	0.58	1/5859 (0.0%)
1	V	0.45	0/4294	0.58	0/5859
1	W	0.45	0/4294	0.58	1/5859 (0.0%)
1	X	0.45	0/4294	0.58	1/5859 (0.0%)
1	Y	0.45	0/4294	0.58	1/5859 (0.0%)
1	Z	0.45	0/4294	0.58	1/5859 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.45	0/4294	0.58	1/5859 (0.0%)
1	b	0.45	0/4294	0.58	0/5859
1	c	0.45	0/4294	0.58	1/5859 (0.0%)
1	d	0.45	0/4294	0.58	0/5859
1	e	0.45	0/4294	0.58	1/5859 (0.0%)
1	f	0.45	0/4294	0.58	0/5859
1	g	0.45	0/4294	0.58	0/5859
1	h	0.45	0/4294	0.58	0/5859
1	i	0.45	0/4294	0.58	1/5859 (0.0%)
1	j	0.45	0/4294	0.58	1/5859 (0.0%)
1	k	0.45	0/4294	0.58	1/5859 (0.0%)
1	l	0.45	0/4294	0.58	1/5859 (0.0%)
1	m	0.45	0/4294	0.58	1/5859 (0.0%)
1	n	0.45	0/4294	0.58	1/5859 (0.0%)
1	o	0.45	0/4294	0.58	1/5859 (0.0%)
1	p	0.45	0/4294	0.58	1/5859 (0.0%)
1	q	0.45	0/4294	0.58	0/5859
1	r	0.45	0/4294	0.58	0/5859
1	s	0.45	0/4294	0.58	1/5859 (0.0%)
1	t	0.45	0/4294	0.58	0/5859
1	u	0.45	0/4294	0.58	1/5859 (0.0%)
1	v	0.45	0/4294	0.58	0/5859
1	w	0.45	0/4294	0.58	1/5859 (0.0%)
1	x	0.45	0/4294	0.58	0/5859
1	y	0.45	0/4294	0.58	1/5859 (0.0%)
1	z	0.45	0/4294	0.58	0/5859
All	All	0.45	0/257640	0.58	35/351540 (0.0%)

There are no bond length outliers.

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	U	506	LYS	CB-CA-C	-5.07	110.71	116.54
1	s	506	LYS	CB-CA-C	-5.07	110.71	116.54
1	X	506	LYS	CB-CA-C	-5.06	110.72	116.54
1	w	506	LYS	CB-CA-C	-5.05	110.73	116.54
1	Y	506	LYS	CB-CA-C	-5.05	110.74	116.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	4165	0	3933	108	0
1	2	4165	0	3933	106	0
1	3	4165	0	3933	106	0
1	4	4165	0	3933	106	0
1	5	4165	0	3933	108	0
1	6	4165	0	3933	107	0
1	7	4165	0	3933	108	0
1	8	4165	0	3933	109	0
1	A	4165	0	3933	115	0
1	B	4165	0	3933	106	0
1	C	4165	0	3933	111	0
1	D	4165	0	3933	107	0
1	E	4165	0	3933	112	0
1	F	4165	0	3933	110	0
1	G	4165	0	3933	109	0
1	H	4165	0	3933	109	0
1	I	4165	0	3933	107	0
1	J	4165	0	3933	107	0
1	K	4165	0	3933	108	0
1	L	4165	0	3933	105	0
1	M	4165	0	3933	110	0
1	N	4165	0	3933	108	0
1	O	4165	0	3933	109	0
1	P	4165	0	3933	108	0
1	Q	4165	0	3933	109	0
1	R	4165	0	3933	107	0
1	S	4165	0	3933	109	0
1	T	4165	0	3933	108	0
1	U	4165	0	3933	108	0
1	V	4165	0	3933	109	0
1	W	4165	0	3933	108	0
1	X	4165	0	3933	110	0
1	Y	4165	0	3933	108	0
1	Z	4165	0	3933	108	0
1	a	4165	0	3933	105	0
1	b	4165	0	3933	113	0
1	c	4165	0	3933	111	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	d	4165	0	3933	107	0
1	e	4165	0	3933	111	0
1	f	4165	0	3933	114	0
1	g	4165	0	3933	109	0
1	h	4165	0	3933	110	0
1	i	4165	0	3933	110	0
1	j	4165	0	3933	108	0
1	k	4165	0	3933	107	0
1	l	4165	0	3933	109	0
1	m	4165	0	3933	110	0
1	n	4165	0	3933	107	0
1	o	4165	0	3933	111	0
1	p	4165	0	3933	109	0
1	q	4165	0	3933	106	0
1	r	4165	0	3933	109	0
1	s	4165	0	3933	107	0
1	t	4165	0	3933	109	0
1	u	4165	0	3933	109	0
1	v	4165	0	3933	111	0
1	w	4165	0	3933	109	0
1	x	4165	0	3933	108	0
1	y	4165	0	3933	108	0
1	z	4165	0	3933	105	0
All	All	249900	0	235980	5619	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 12.

The worst 5 of 5619 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:H:284:HIS:HD2	1:H:360:PRO:HB3	1.45	0.82
1:b:284:HIS:HD2	1:b:360:PRO:HB3	1.45	0.82
1:f:284:HIS:HD2	1:f:360:PRO:HB3	1.45	0.82
1:p:284:HIS:HD2	1:p:360:PRO:HB3	1.45	0.82
1:V:284:HIS:HD2	1:V:360:PRO:HB3	1.45	0.82

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	2	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	3	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	4	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	5	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	6	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	7	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	8	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	A	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	B	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	C	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	D	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	E	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	F	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	G	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	H	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	I	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	J	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	K	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	L	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	M	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	N	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	O	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	P	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	Q	517/732 (71%)	504 (98%)	13 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	S	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	T	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	U	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	V	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	W	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	X	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	Y	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	Z	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	a	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	b	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	c	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	d	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	e	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	f	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	g	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	h	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	i	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	j	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	k	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	l	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	m	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	n	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	o	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	p	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	q	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	r	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	s	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	t	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	u	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	v	517/732 (71%)	504 (98%)	13 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	w	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	x	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	y	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
1	z	517/732 (71%)	504 (98%)	13 (2%)	0	100	100
All	All	31020/43920 (71%)	30240 (98%)	780 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

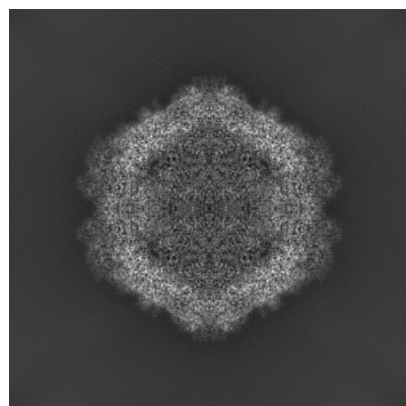
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48181. These allow visual inspection of the internal detail of the map and identification of artifacts.

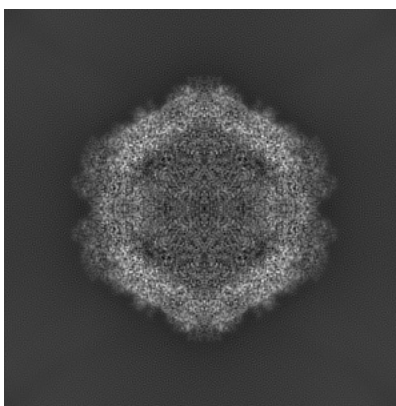
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

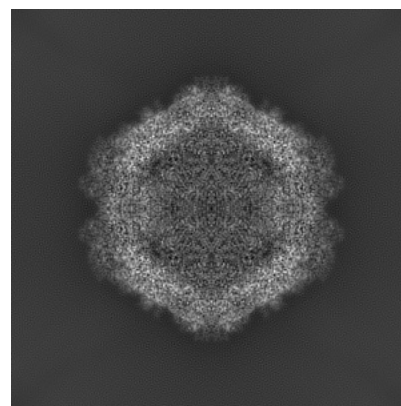
6.1.1 Primary map



X

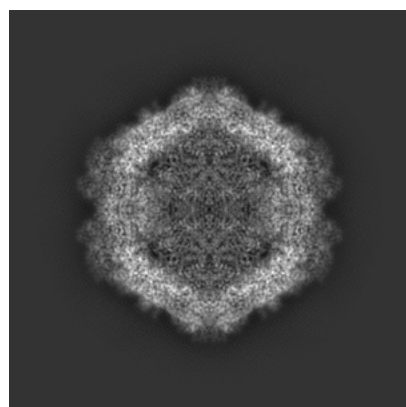


Y

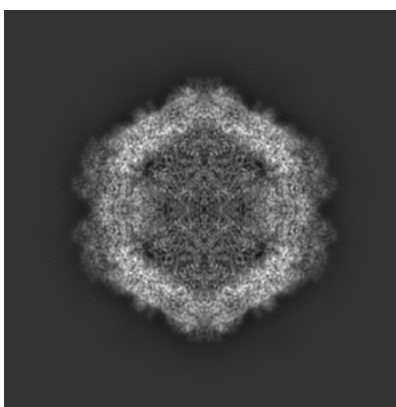


Z

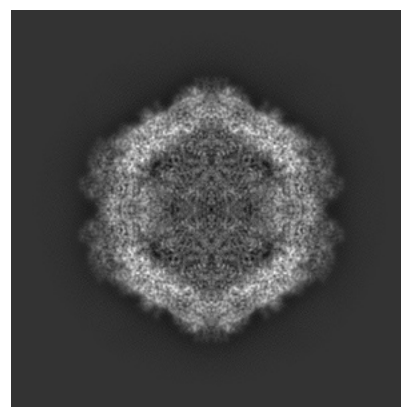
6.1.2 Raw map



X



Y

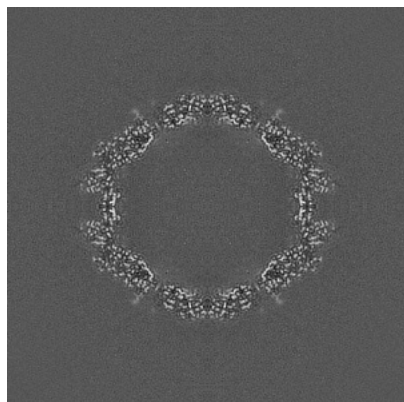


Z

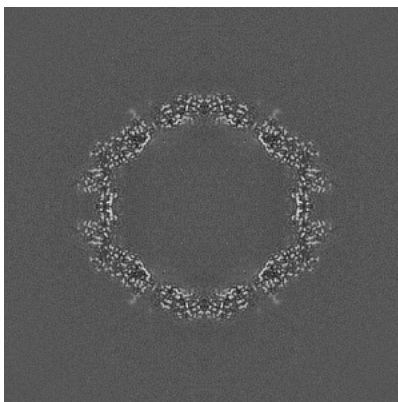
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

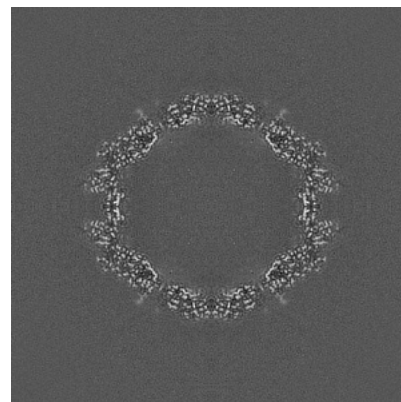
6.2.1 Primary map



X Index: 250

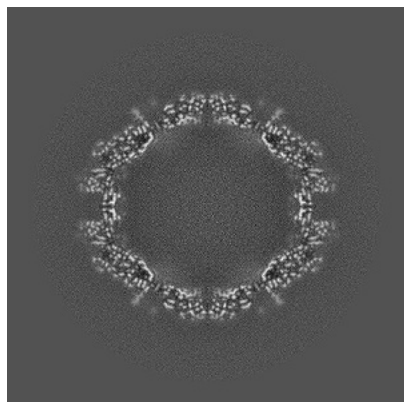


Y Index: 250

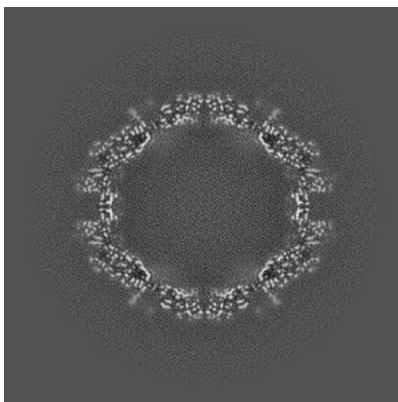


Z Index: 250

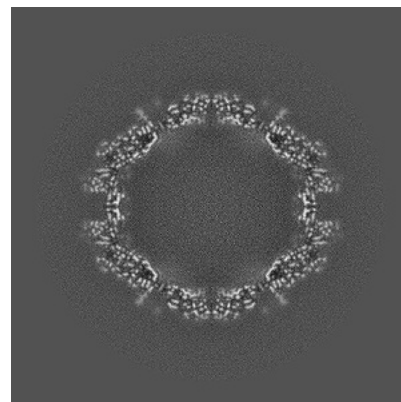
6.2.2 Raw map



X Index: 250



Y Index: 250

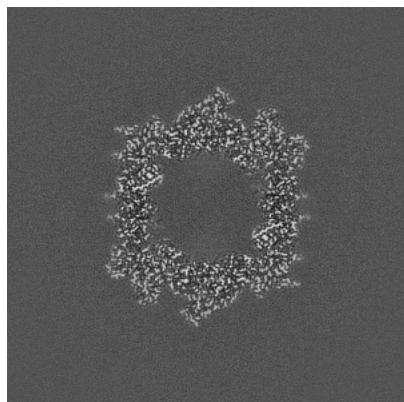


Z Index: 250

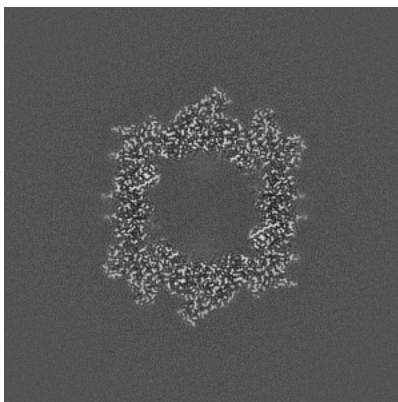
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

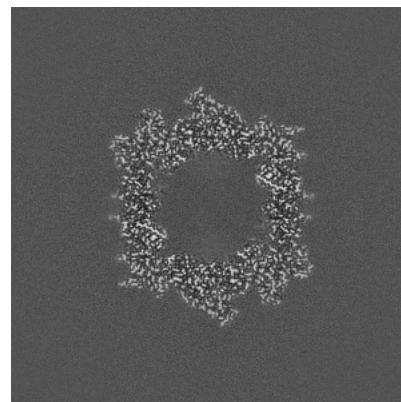
6.3.1 Primary map



X Index: 329

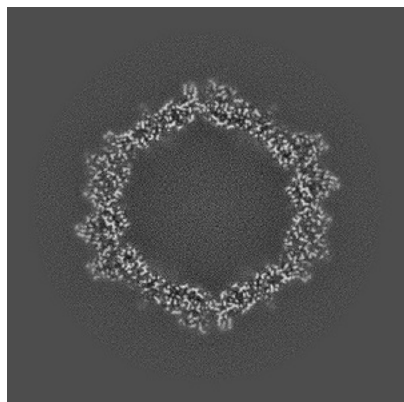


Y Index: 329

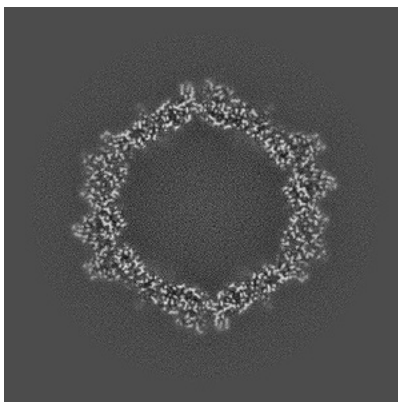


Z Index: 171

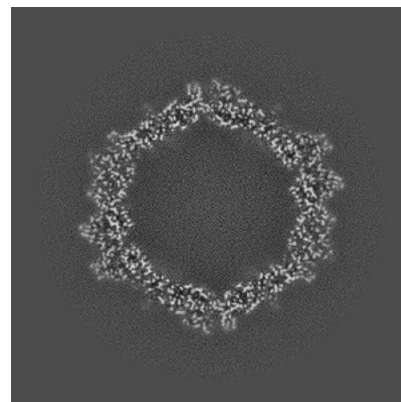
6.3.2 Raw map



X Index: 232



Y Index: 232

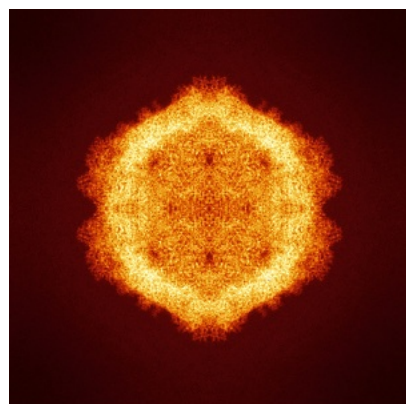


Z Index: 232

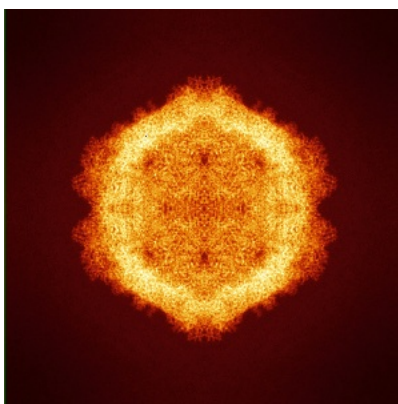
The images above show the largest variance slices of the map in three orthogonal directions.

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

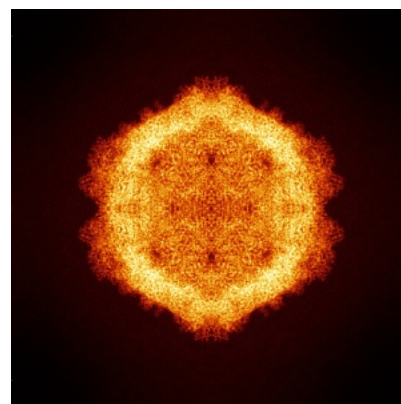
6.4.1 Primary map



X

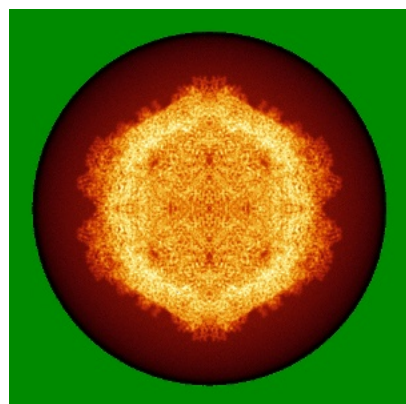


Y

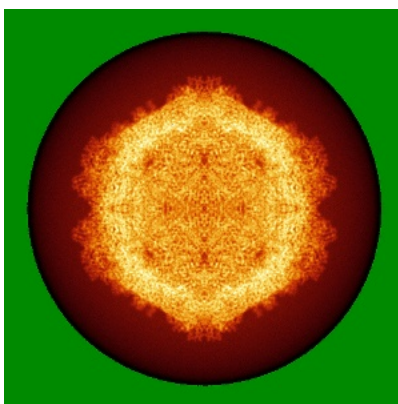


Z

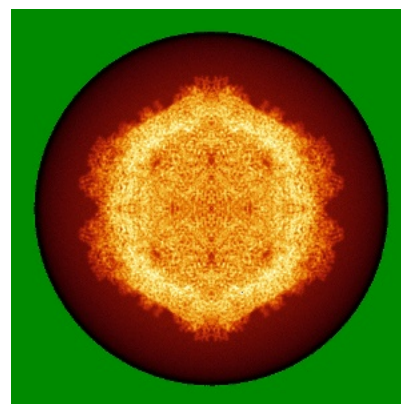
6.4.2 Raw map



X



Y

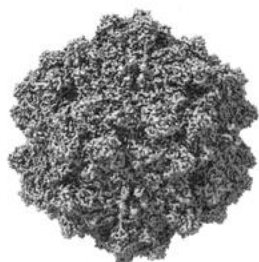


Z

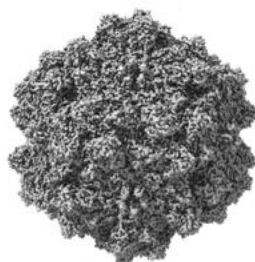
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

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

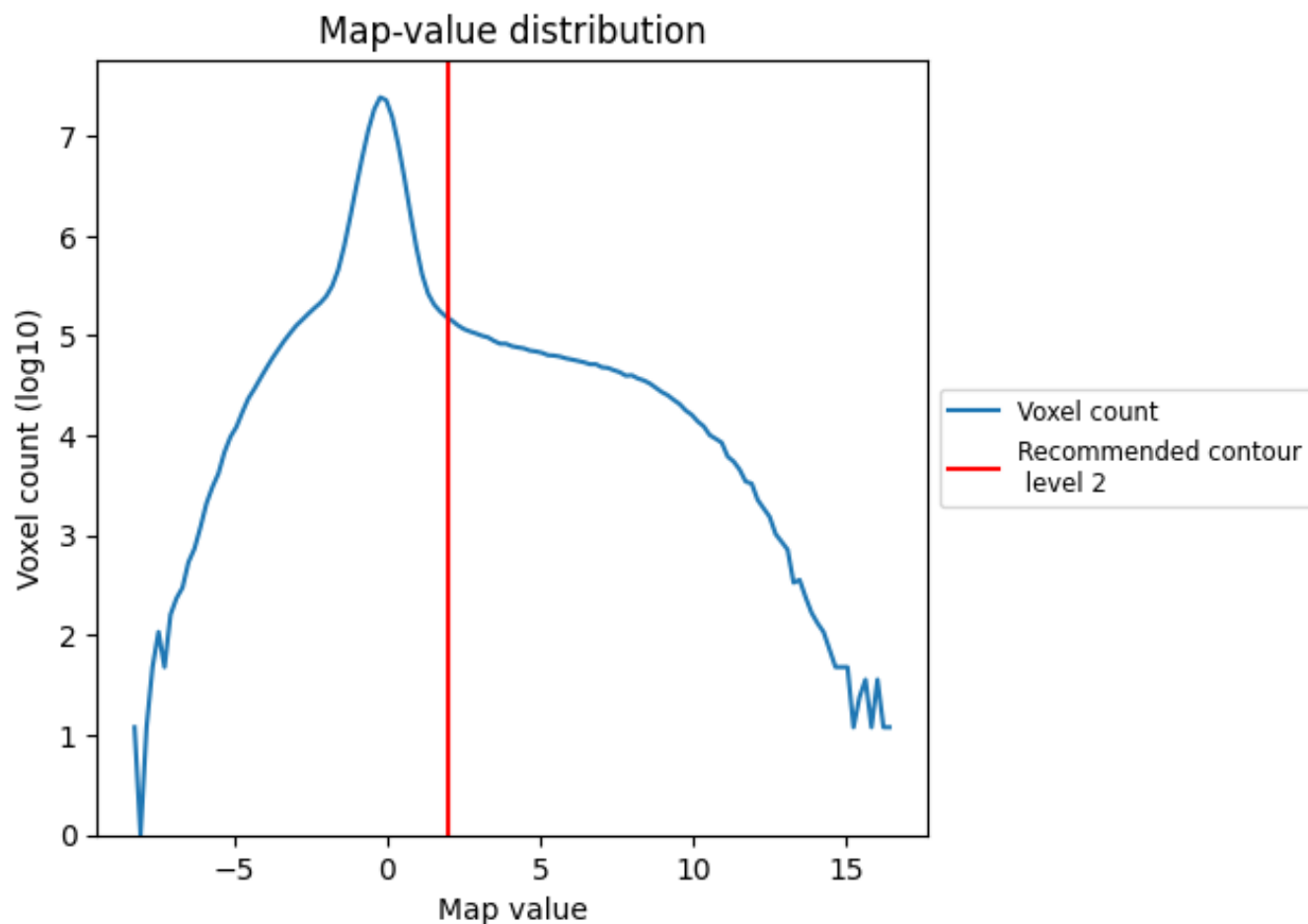
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

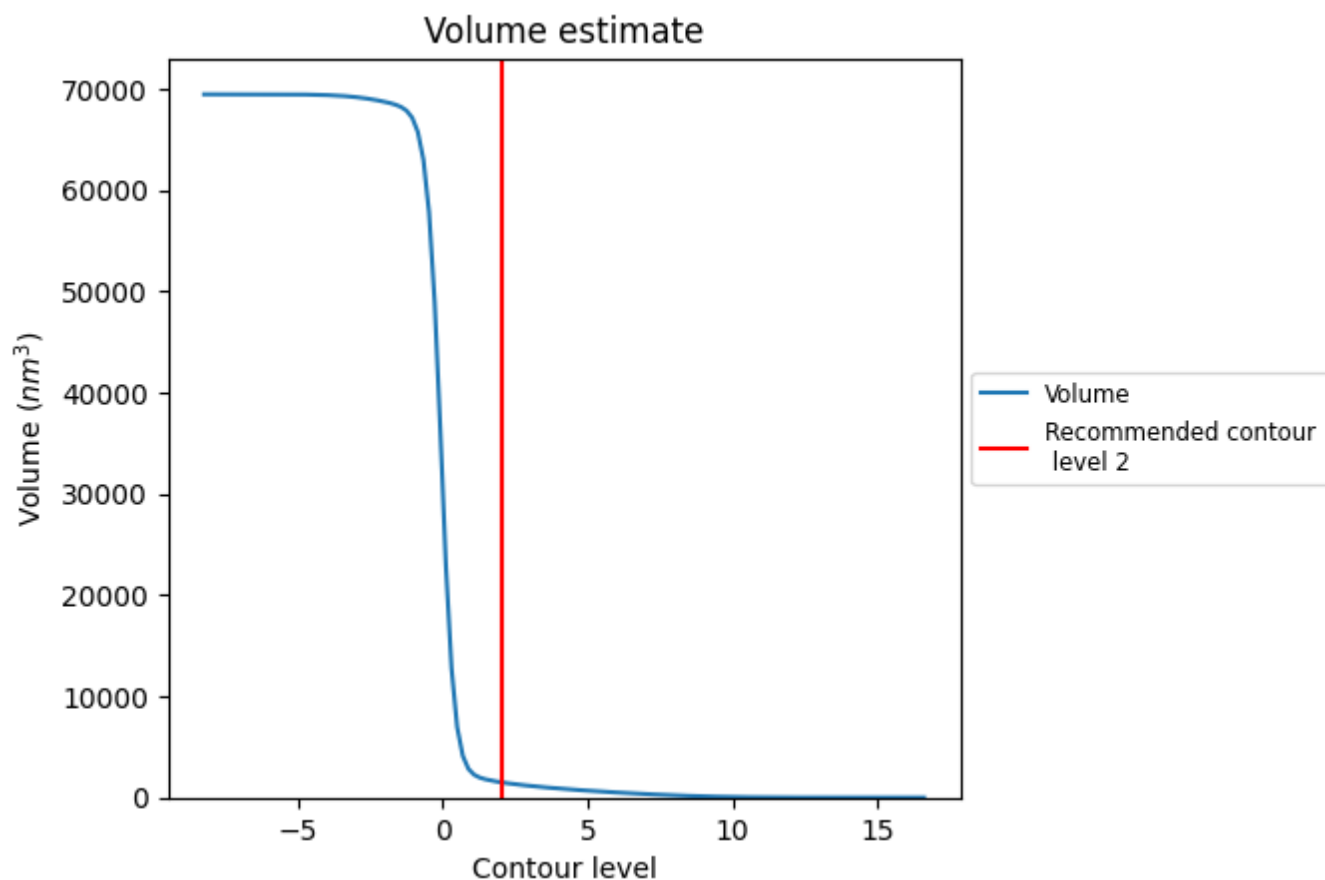
This section contains the results of statistical analysis of the map.

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.

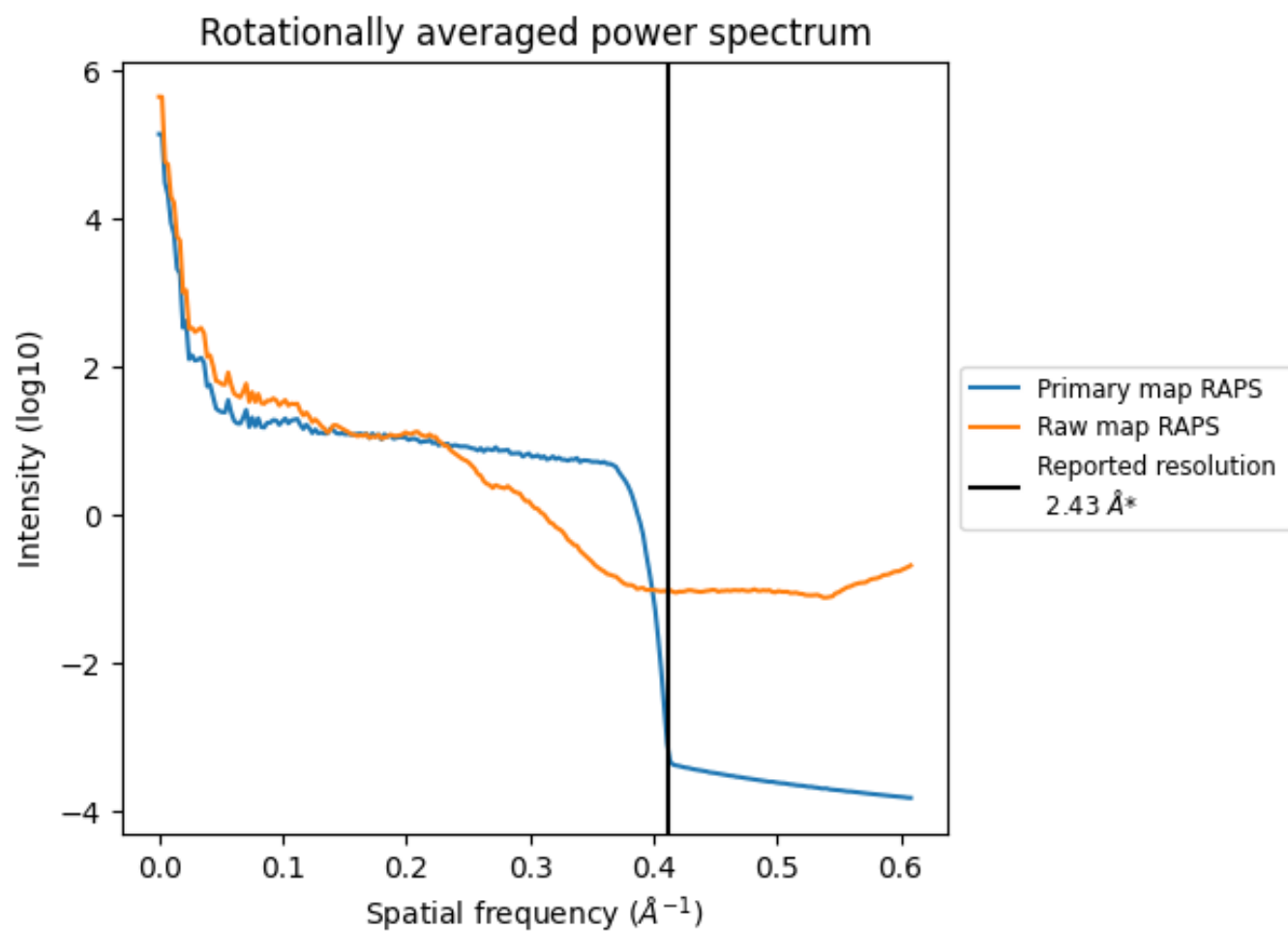
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1512 nm³; this corresponds to an approximate mass of 1366 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 ⓘ

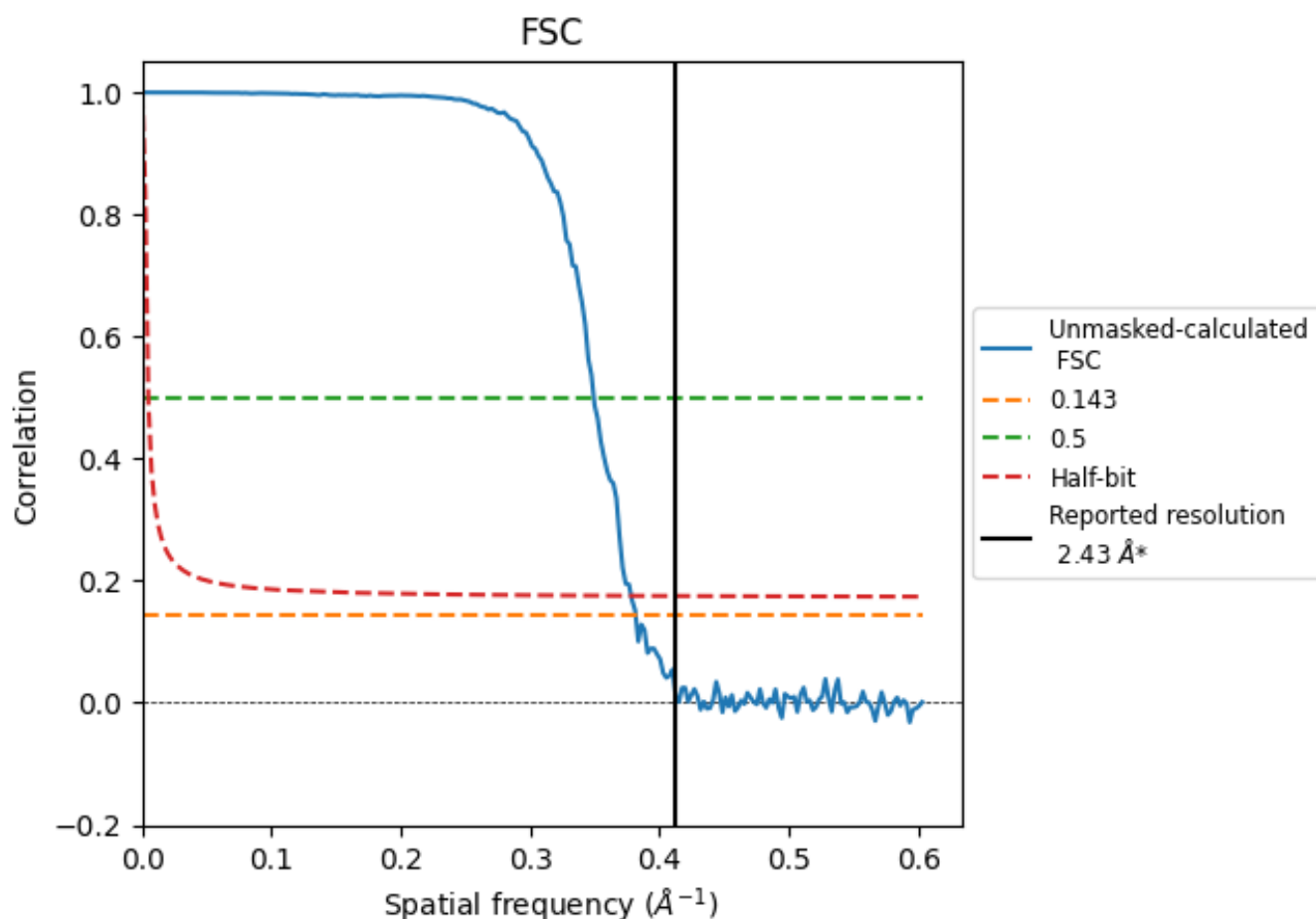


*Reported resolution corresponds to spatial frequency of $0.412 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.412 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.43	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.62	2.86	2.64

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

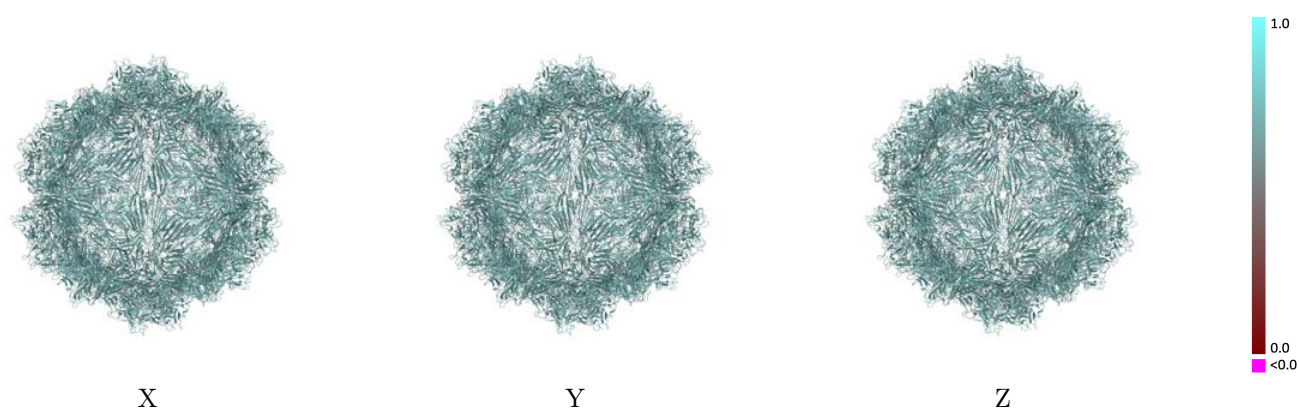
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-48181 and PDB model 9ME0. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

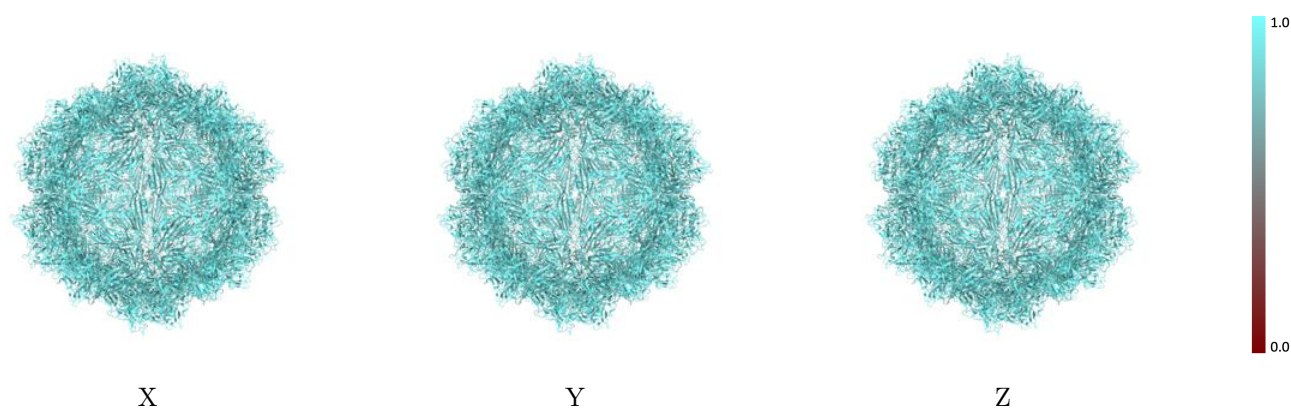
This section was not generated.

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



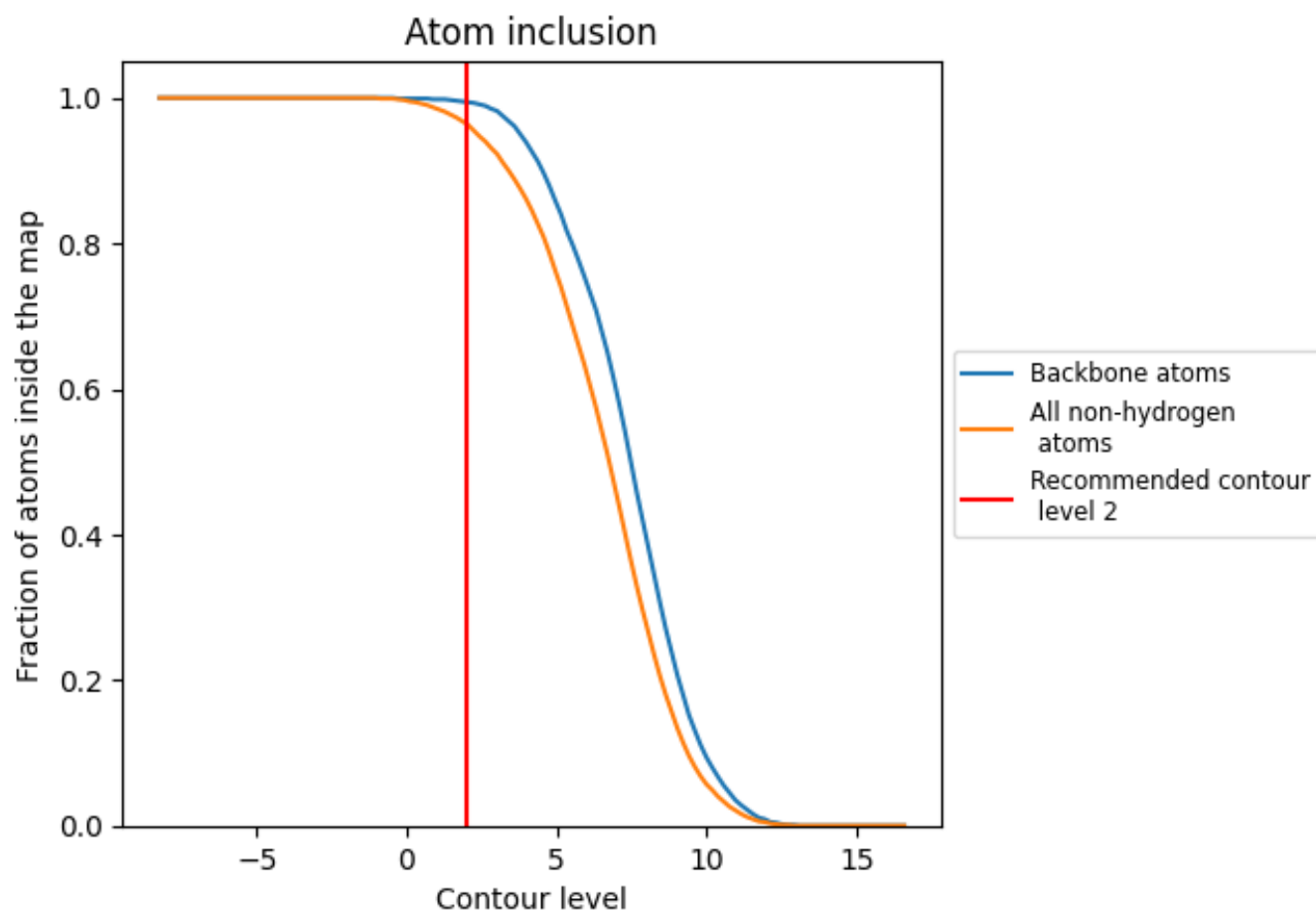
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9640	 0.6730
1	 0.9630	 0.6730
2	 0.9630	 0.6730
3	 0.9640	 0.6730
4	 0.9650	 0.6730
5	 0.9650	 0.6740
6	 0.9650	 0.6740
7	 0.9650	 0.6730
8	 0.9640	 0.6730
A	 0.9640	 0.6740
B	 0.9630	 0.6730
C	 0.9650	 0.6730
D	 0.9650	 0.6730
E	 0.9640	 0.6730
F	 0.9640	 0.6730
G	 0.9640	 0.6730
H	 0.9650	 0.6740
I	 0.9650	 0.6730
J	 0.9630	 0.6730
K	 0.9650	 0.6730
L	 0.9630	 0.6730
M	 0.9640	 0.6730
N	 0.9650	 0.6730
O	 0.9640	 0.6730
P	 0.9650	 0.6730
Q	 0.9650	 0.6730
R	 0.9630	 0.6730
S	 0.9630	 0.6730
T	 0.9650	 0.6730
U	 0.9630	 0.6730
V	 0.9650	 0.6730
W	 0.9650	 0.6740
X	 0.9640	 0.6730
Y	 0.9650	 0.6730
Z	 0.9640	 0.6740



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Chain	Atom inclusion	Q-score
a	 0.9640	 0.6730
b	 0.9640	 0.6740
c	 0.9640	 0.6740
d	 0.9640	 0.6730
e	 0.9640	 0.6730
f	 0.9640	 0.6740
g	 0.9650	 0.6730
h	 0.9640	 0.6730
i	 0.9650	 0.6740
j	 0.9650	 0.6730
k	 0.9650	 0.6730
l	 0.9640	 0.6730
m	 0.9650	 0.6730
n	 0.9640	 0.6740
o	 0.9640	 0.6730
p	 0.9650	 0.6730
q	 0.9630	 0.6730
r	 0.9630	 0.6730
s	 0.9630	 0.6730
t	 0.9640	 0.6730
u	 0.9650	 0.6720
v	 0.9640	 0.6730
w	 0.9640	 0.6730
x	 0.9650	 0.6730
y	 0.9640	 0.6730
z	 0.9630	 0.6720