



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 10:58 AM UTC

PDB ID : 5US9 / pdb_00005us9
EMDB ID : EMD-8605
Title : Human bocavirus 4
Authors : Mietzsch, M.; Agbandje-McKenna, M.
Deposited on : 2017-02-13
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

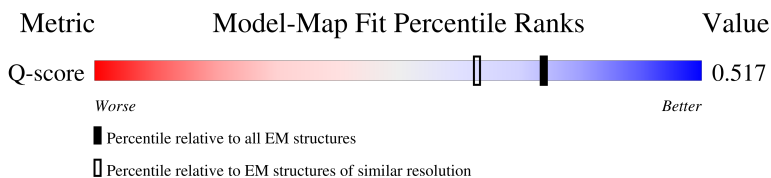
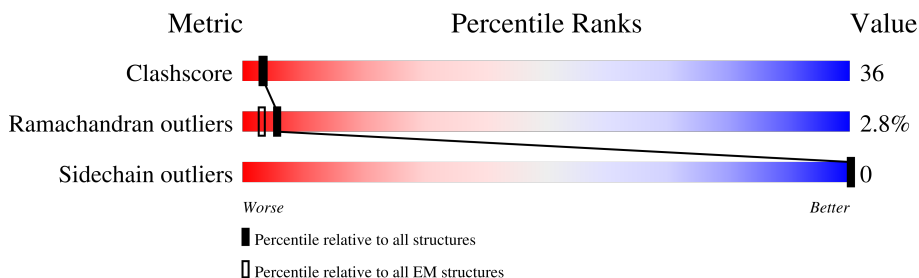
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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.



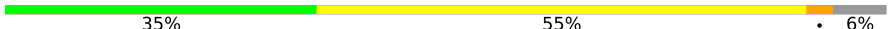
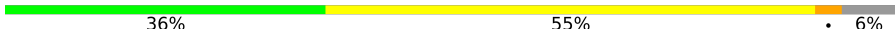
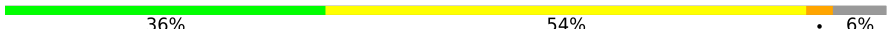
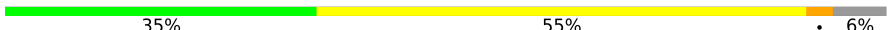
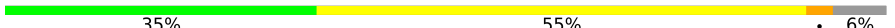
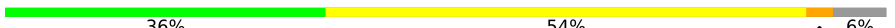
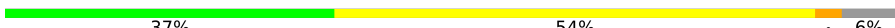
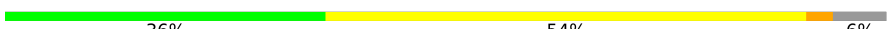
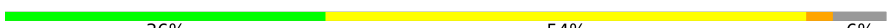
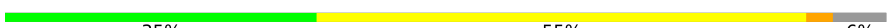
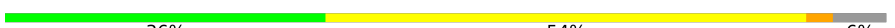
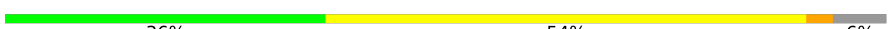
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	541	
1	2	541	
1	3	541	
1	4	541	

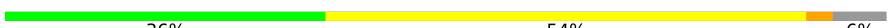
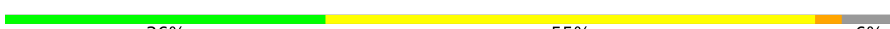
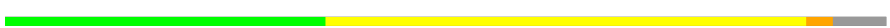
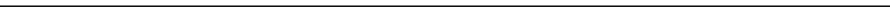
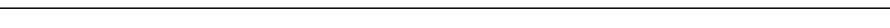
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Mol	Chain	Length	Quality of chain
1	5	541	
1	6	541	
1	7	541	
1	8	541	
1	A	541	
1	B	541	
1	C	541	
1	D	541	
1	E	541	
1	F	541	
1	G	541	
1	H	541	
1	I	541	
1	J	541	
1	K	541	
1	L	541	
1	M	541	
1	N	541	
1	O	541	
1	P	541	
1	Q	541	
1	R	541	
1	S	541	
1	T	541	
1	U	541	

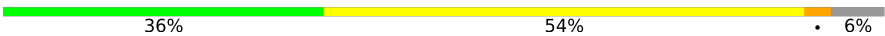
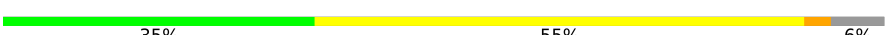
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Mol	Chain	Length	Quality of chain
1	V	541	 35% 55% 6%
1	W	541	 35% 55% 6%
1	X	541	 36% 55% 6%
1	Y	541	 36% 54% 6%
1	Z	541	 36% 55% 6%
1	a	541	 36% 54% 6%
1	b	541	 36% 54% 6%
1	c	541	 36% 54% 6%
1	d	541	 35% 55% 6%
1	e	541	 36% 54% 6%
1	f	541	 35% 55% 6%
1	g	541	 36% 54% 6%
1	h	541	 36% 54% 6%
1	i	541	 36% 55% 6%
1	j	541	 35% 55% 6%
1	k	541	 35% 55% 6%
1	l	541	 36% 54% 6%
1	m	541	 36% 55% 6%
1	n	541	 35% 55% 6%
1	o	541	 36% 54% 6%
1	p	541	 35% 55% 6%
1	q	541	 35% 55% 6%
1	r	541	 35% 55% 6%
1	s	541	 37% 54% 6%
1	t	541	 36% 55% 6%

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Mol	Chain	Length	Quality of chain
1	u	541	
1	v	541	
1	w	541	
1	x	541	
1	y	541	
1	z	541	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 244620 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 VP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	B	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	C	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	D	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	E	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	F	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	G	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	H	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	I	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	J	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	K	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	L	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	M	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	N	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	O	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	P	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		
1	Q	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	S	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	T	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	U	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	V	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	W	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	X	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	Y	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	Z	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	1	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	2	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	3	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	4	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	5	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	6	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	a	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	b	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	c	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	d	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	e	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	f	508	Total 4077	C 2583	N 701	O 771	S 22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	g	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	h	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	i	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	j	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	k	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	l	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	m	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	n	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	o	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	p	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	q	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	r	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	s	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	t	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	u	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	v	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	w	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	x	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	y	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	z	508	Total 4077	C 2583	N 701	O 771	S 22	0	0
1	7	508	Total 4077	C 2583	N 701	O 771	S 22	0	0

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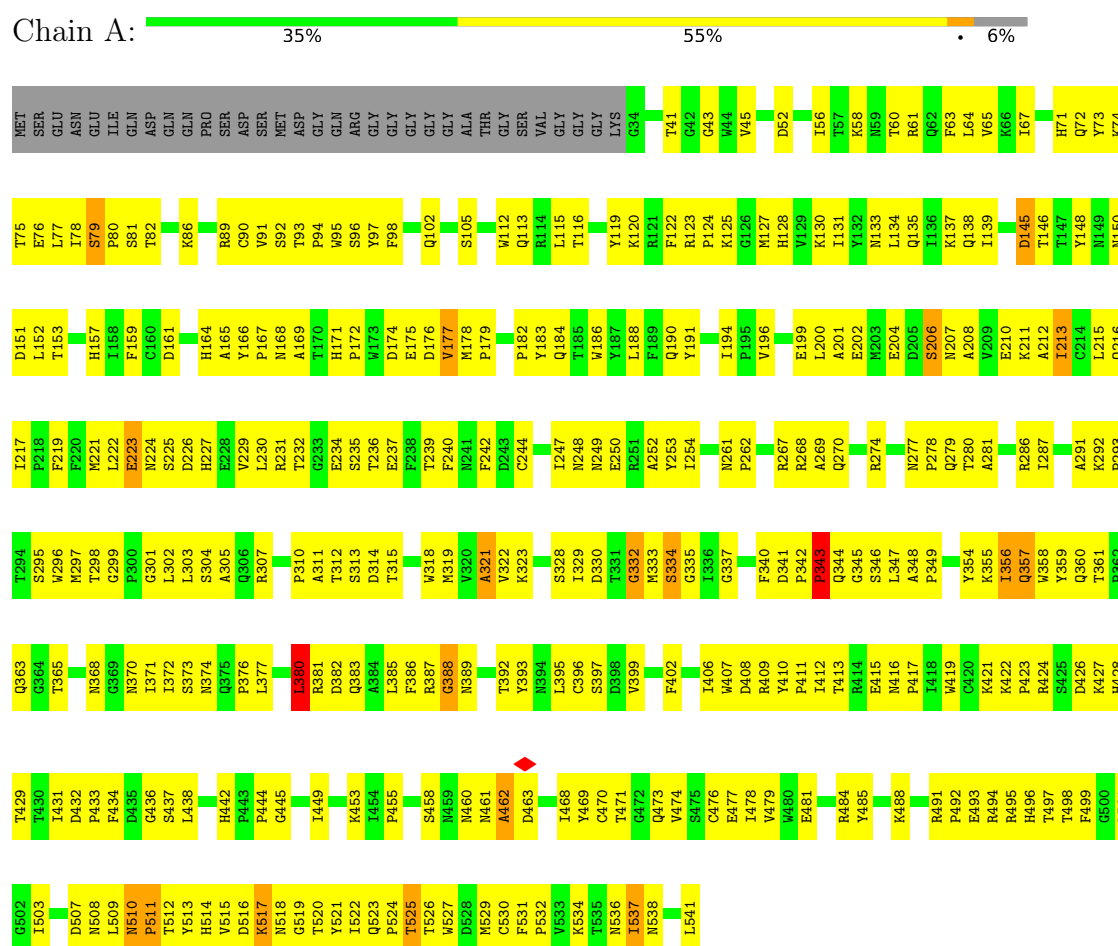
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	508	Total	C	N	O	S	0	0
			4077	2583	701	771	22		

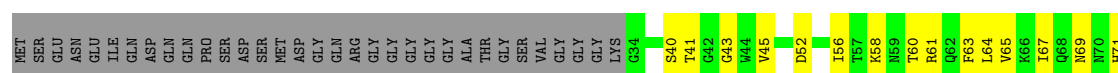
3 Residue-property plots

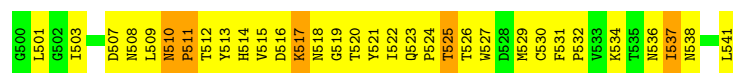
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 VP2



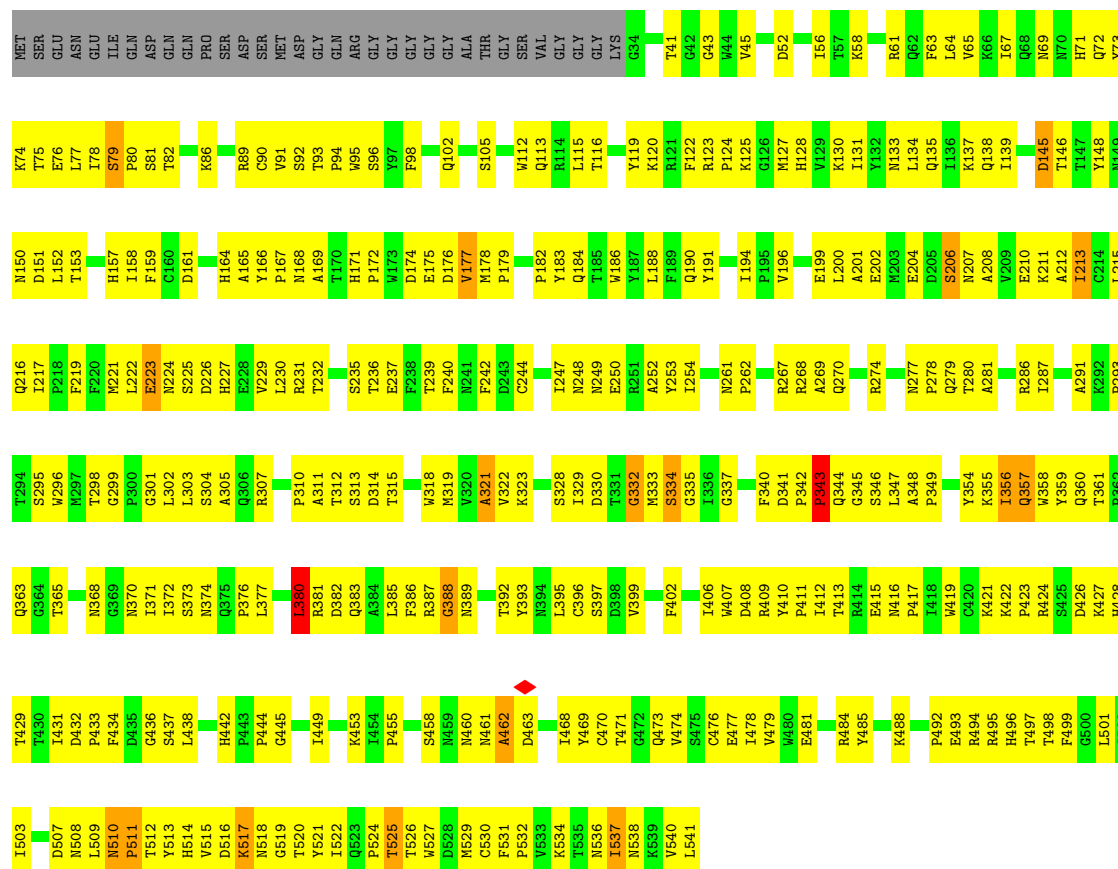
• Molecule 1: Capsid protein VP2





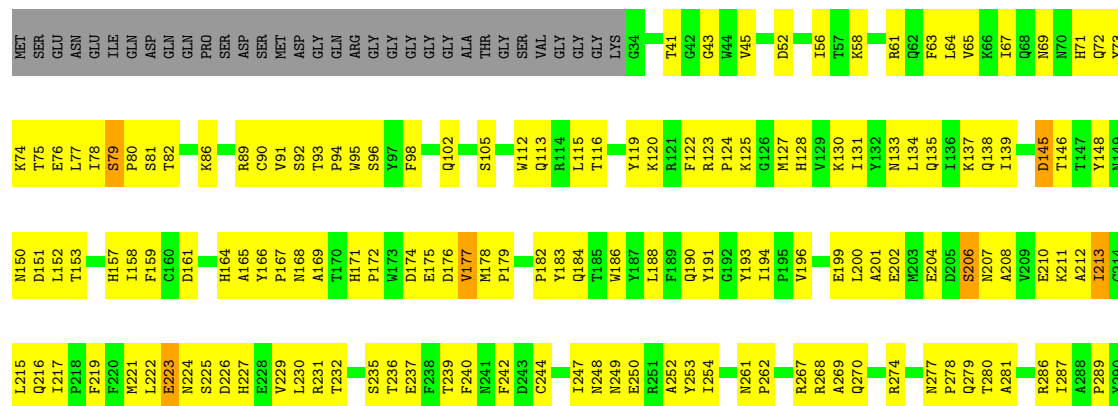
• Molecule 1: Capsid protein VP2

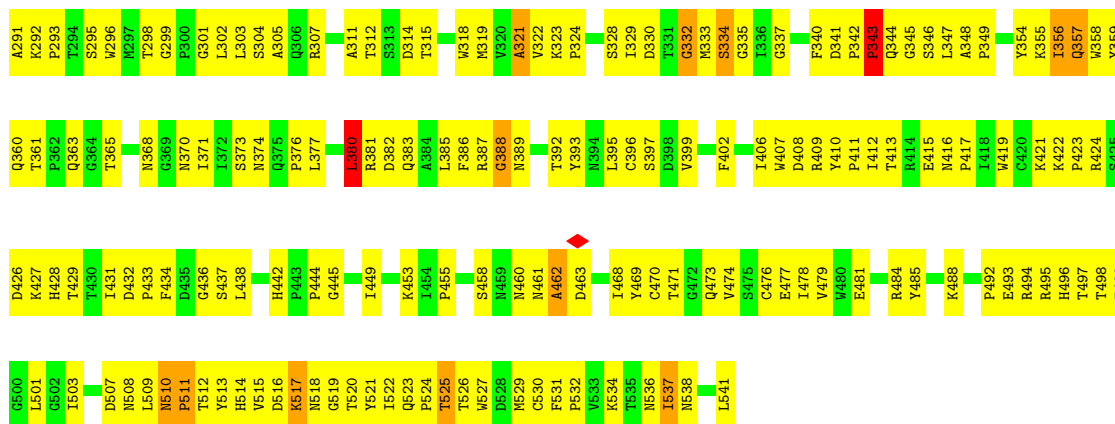
Chain D: 36% 54% 6%



• Molecule 1: Capsid protein VP2

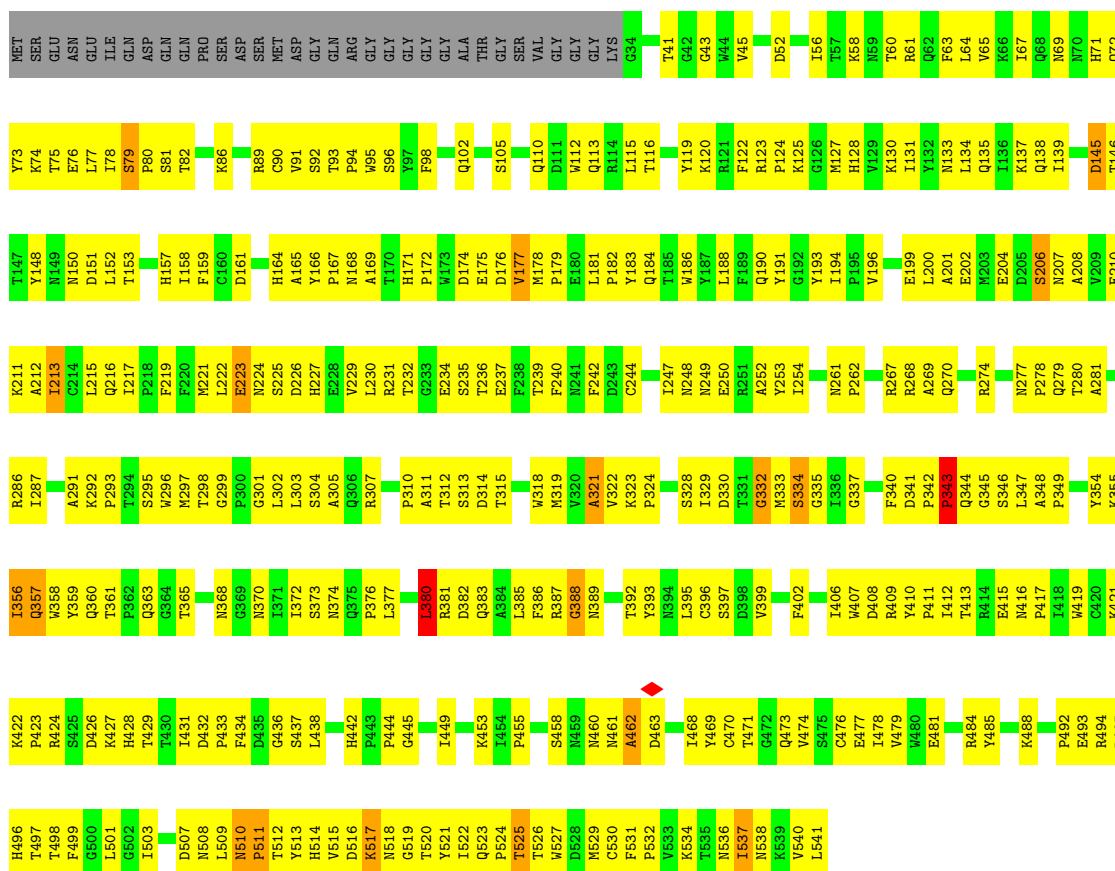
Chain E: 36% 54% 6%





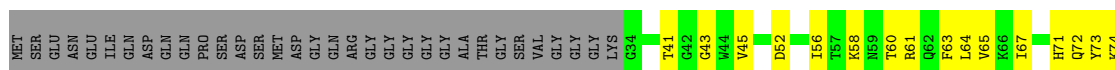
• Molecule 1: Capsid protein VP2

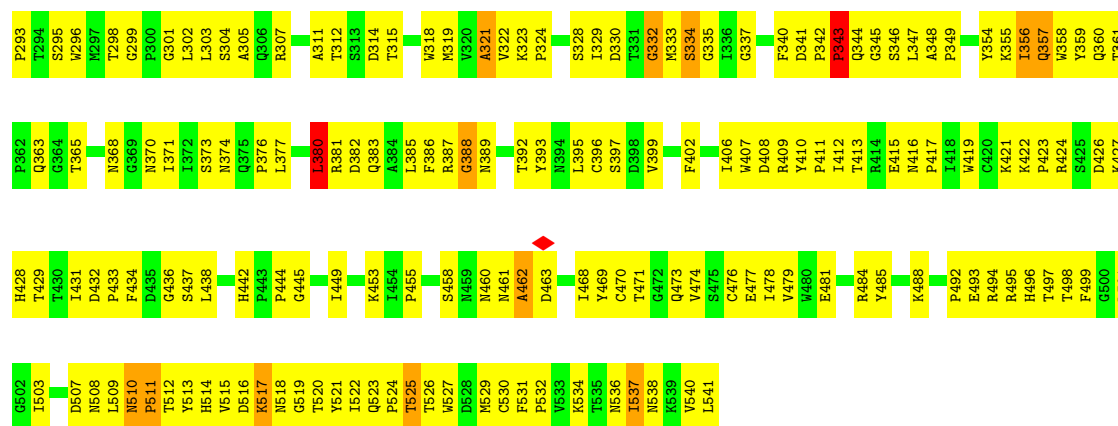
Chain F: 35% 55% 6%



• Molecule 1: Capsid protein VP2

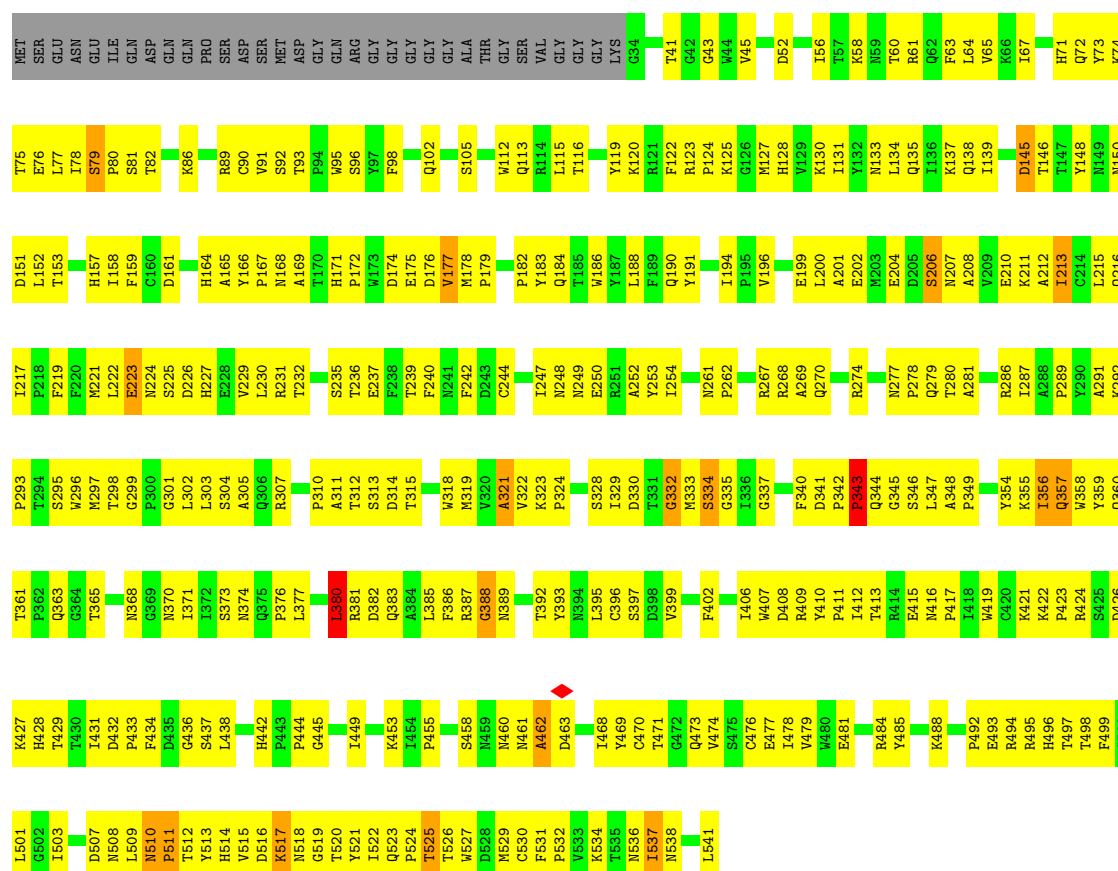
Chain G: 37% 54% 6%





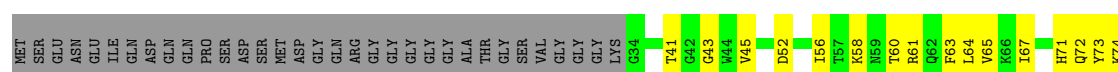
• Molecule 1: Capsid protein VP2

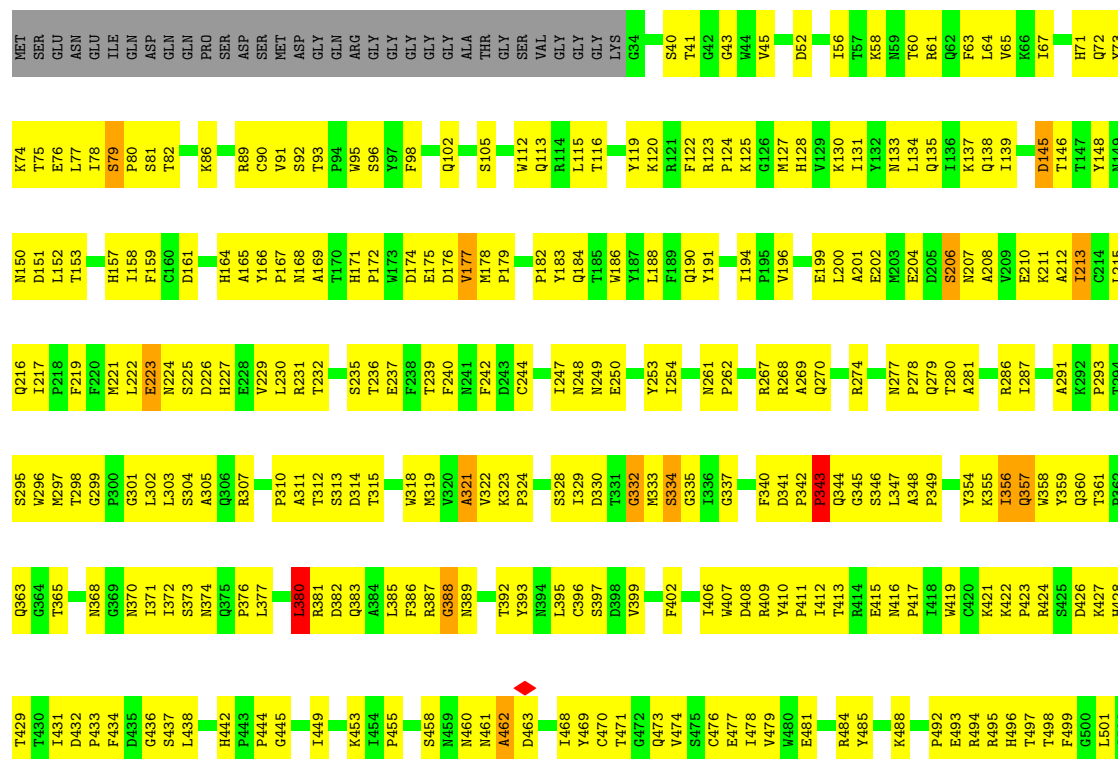
Chain K: 36% 54% 6%



• Molecule 1: Capsid protein VP2

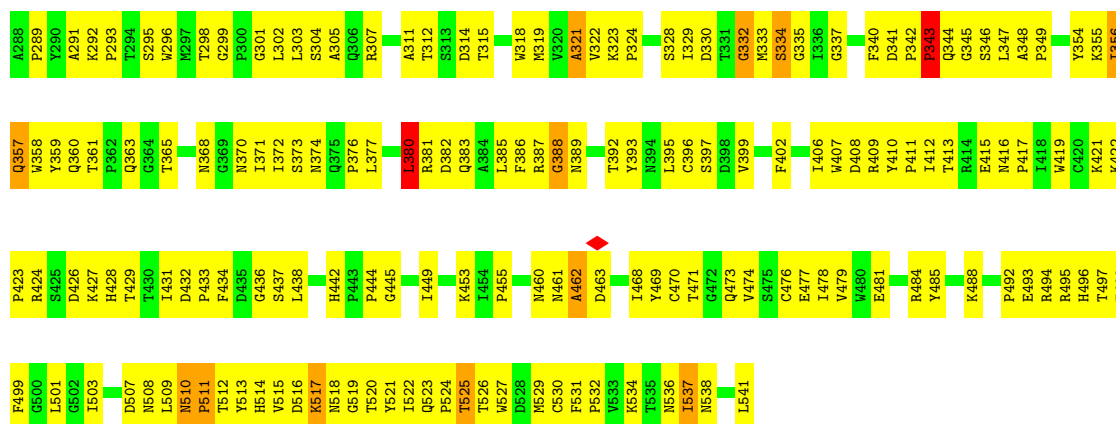
Chain L: 37% 54% 6%





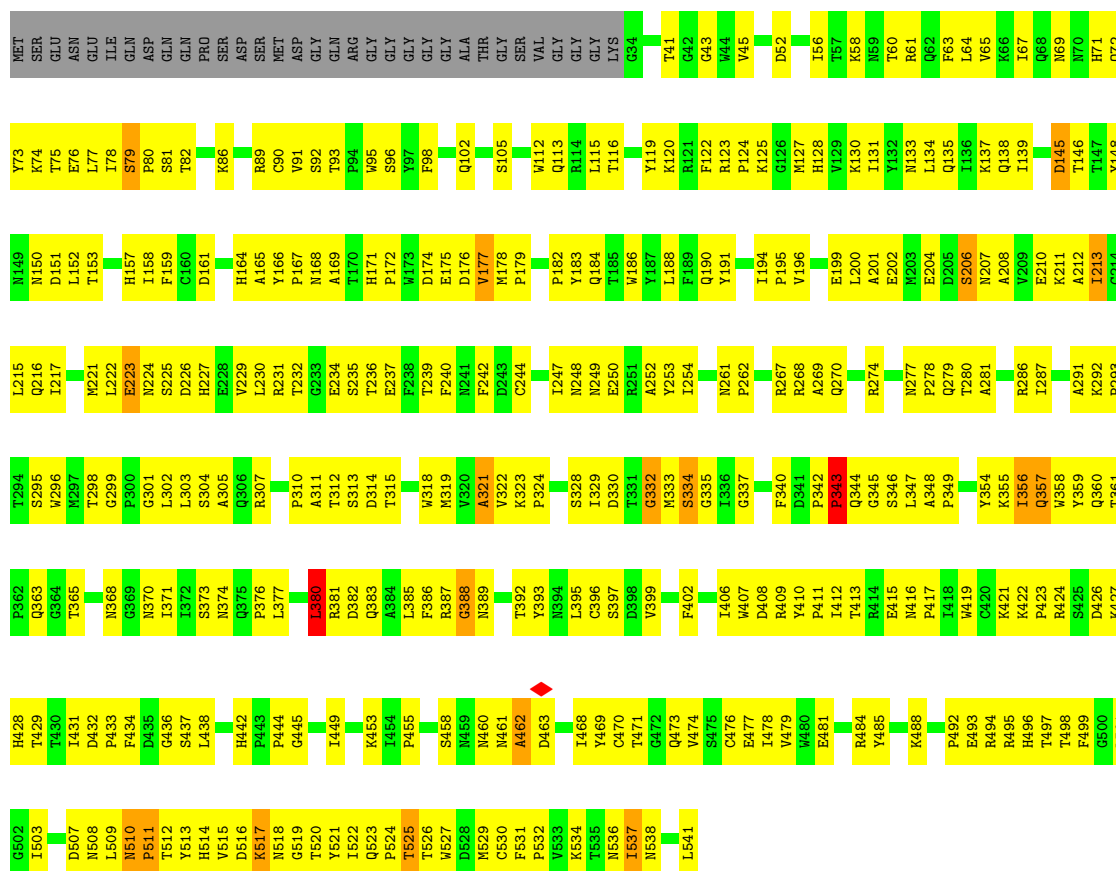
Chain N: 35% 55% • 6%





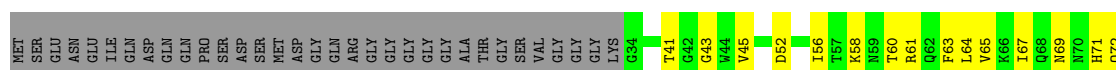
• Molecule 1: Capsid protein VP2

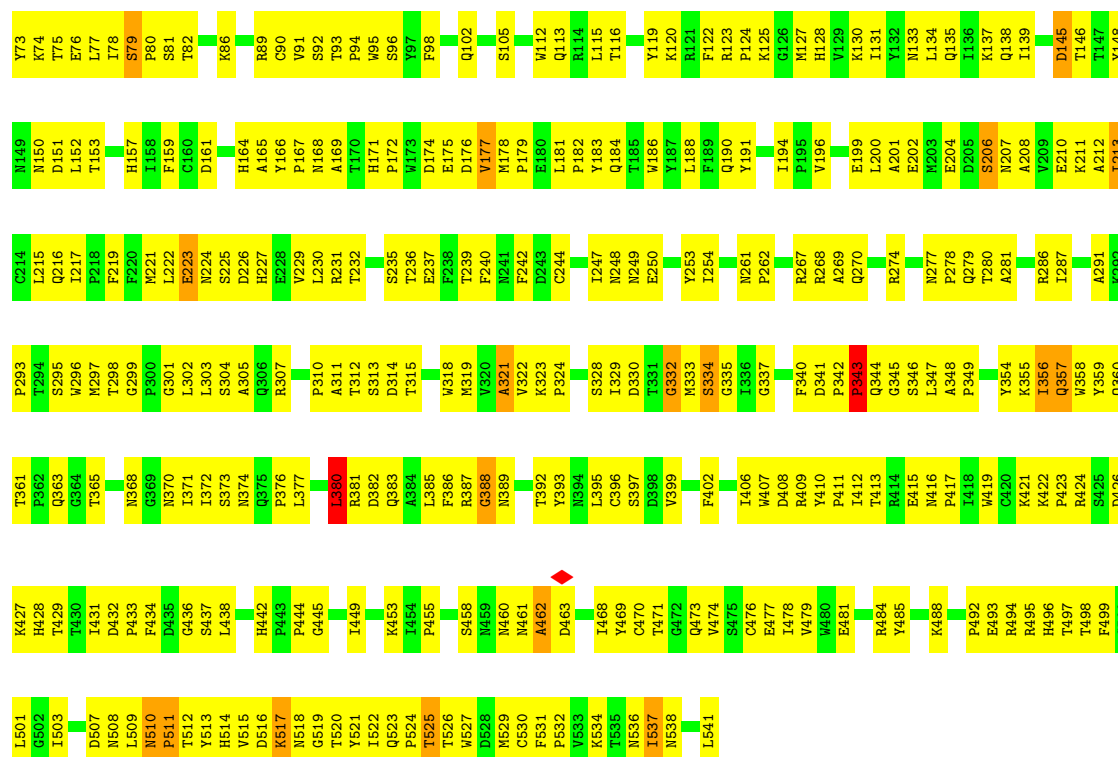
Chain P: 36% 54% 6%



• Molecule 1: Capsid protein VP2

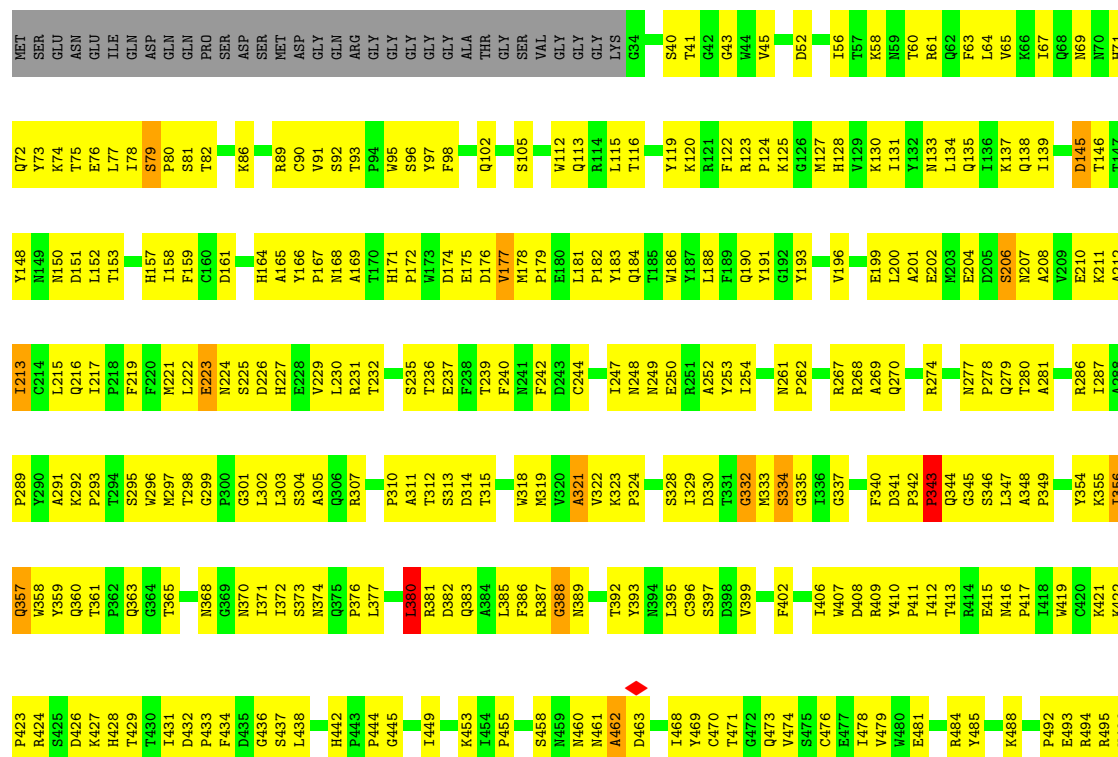
Chain Q: 36% 54% 6%

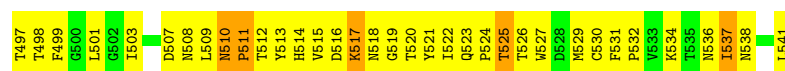




• Molecule 1: Capsid protein VP2

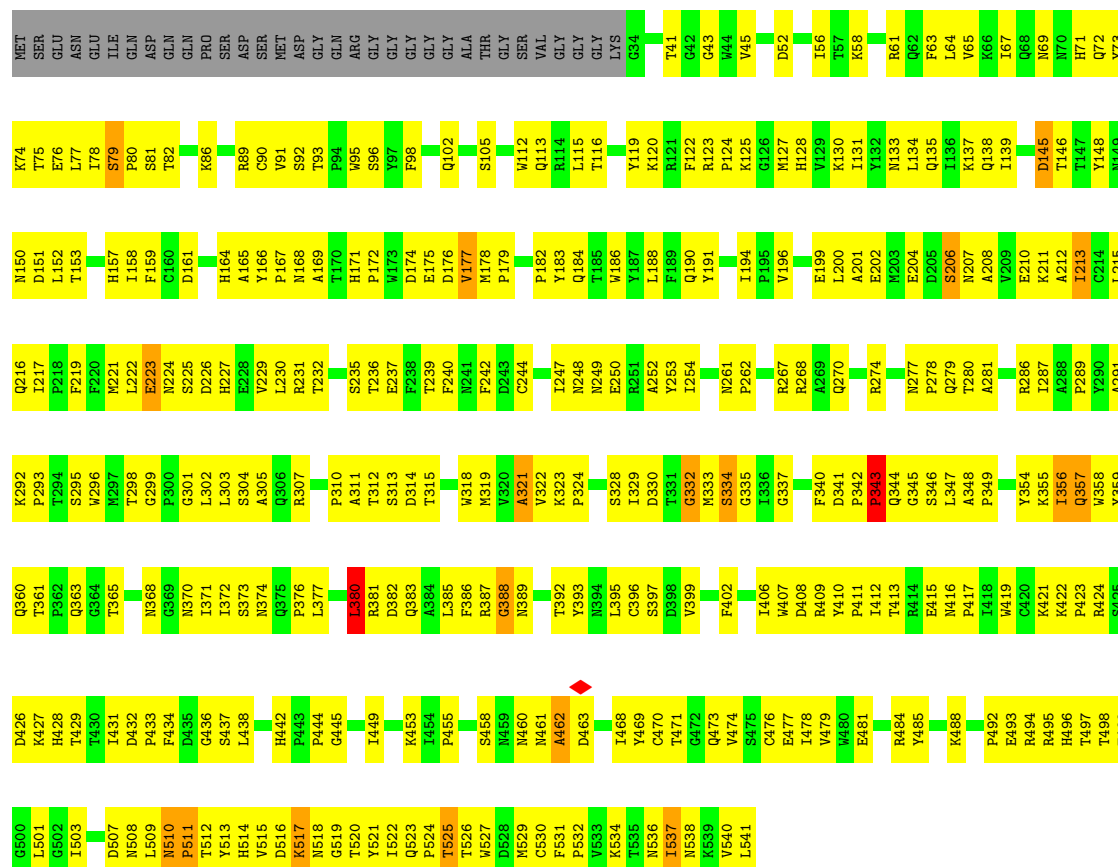
Chain R: 35% 55% 6%





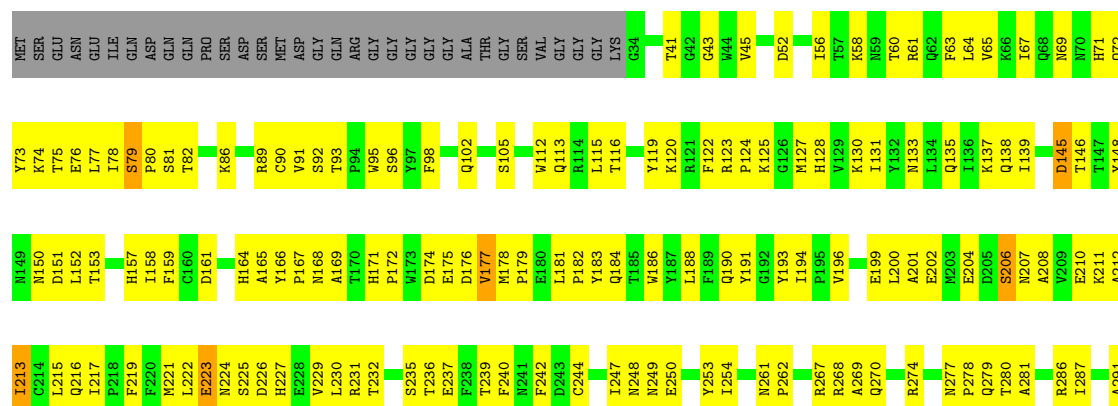
• Molecule 1: Capsid protein VP2

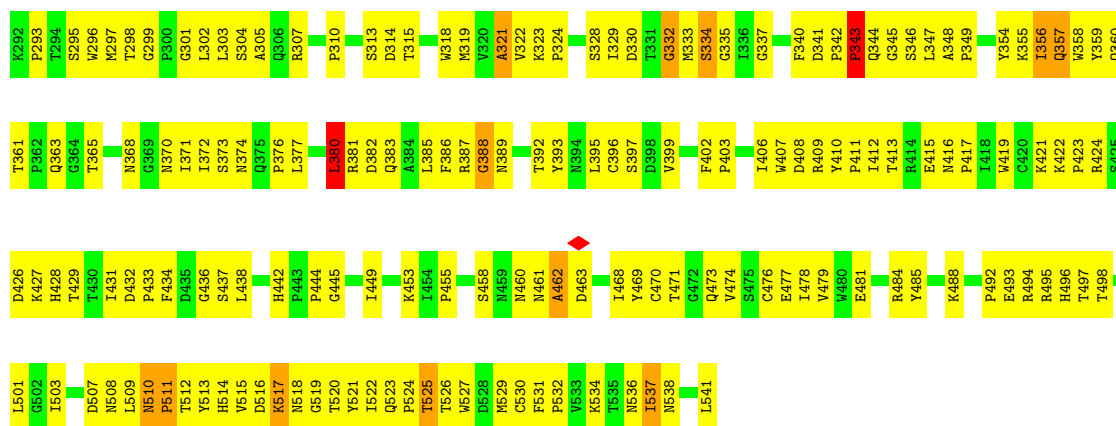
Chain S: 36% 54% 6%



• Molecule 1: Capsid protein VP2

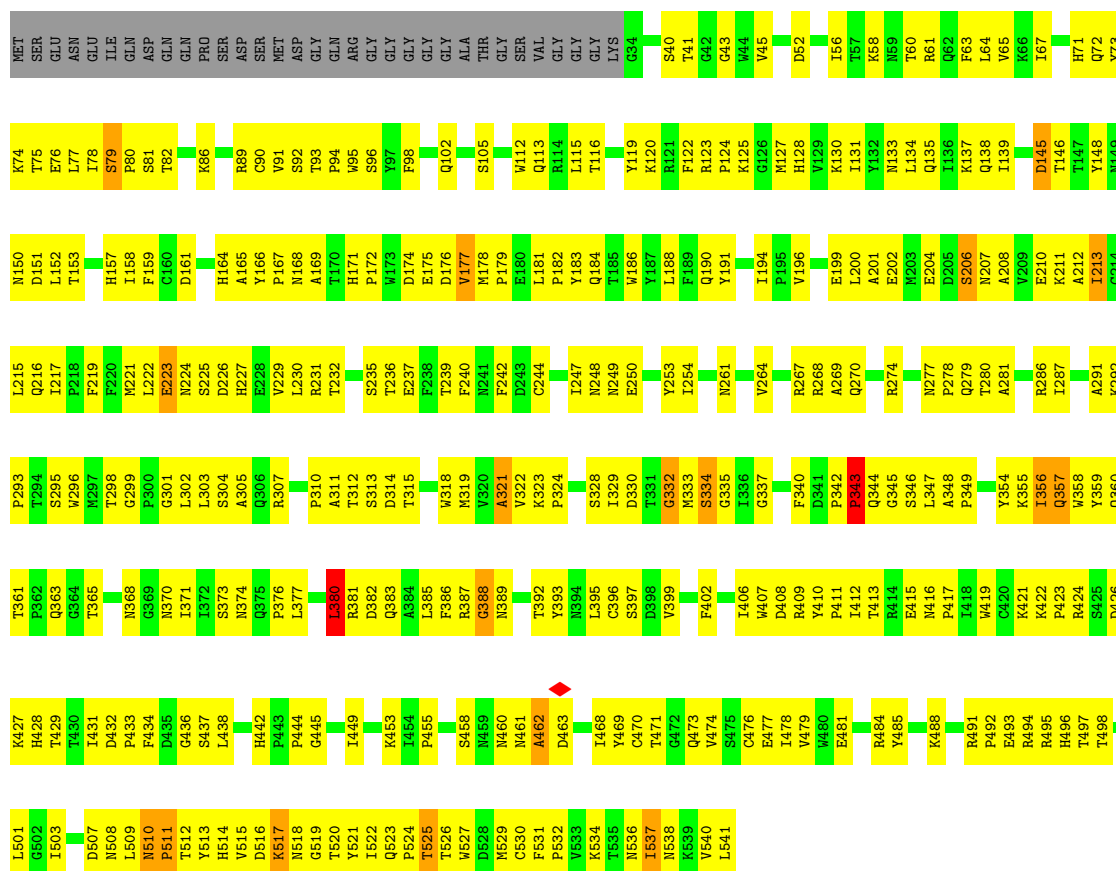
Chain T: 36% 54% 6%





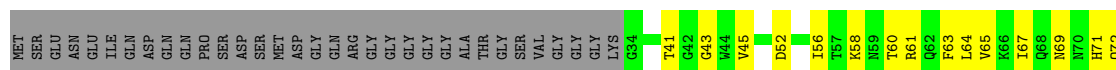
• Molecule 1: Capsid protein VP2

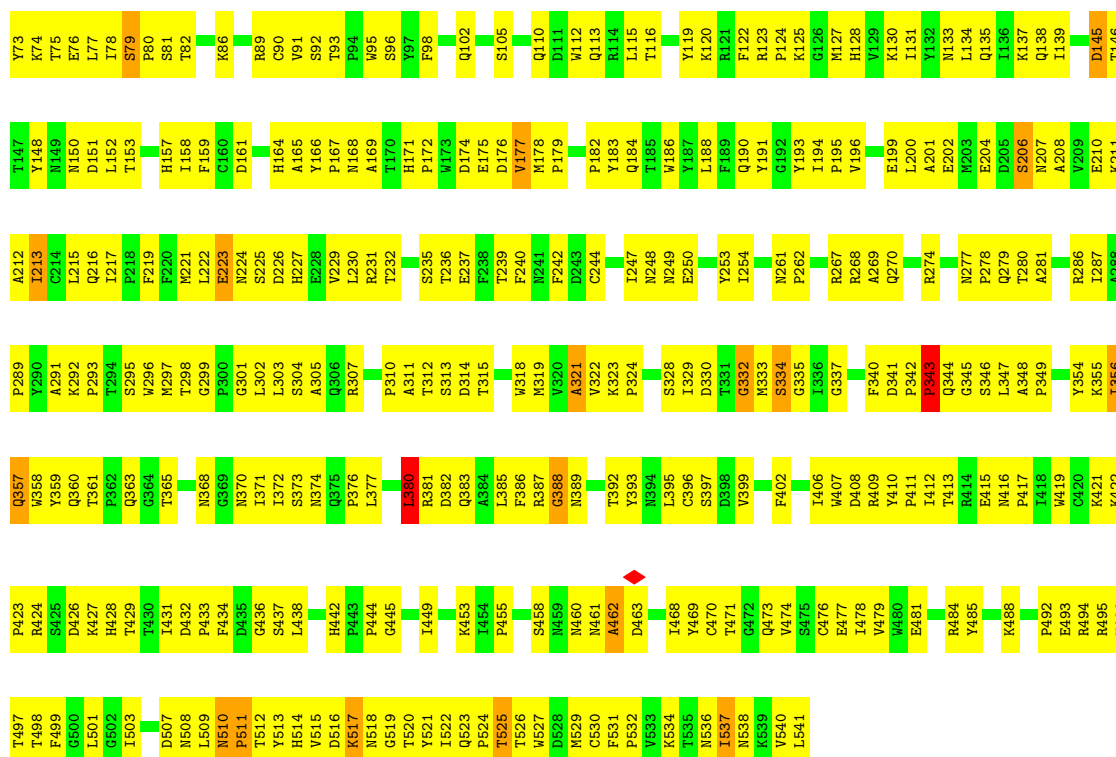
Chain U: 36% 54% 6%



• Molecule 1: Capsid protein VP2

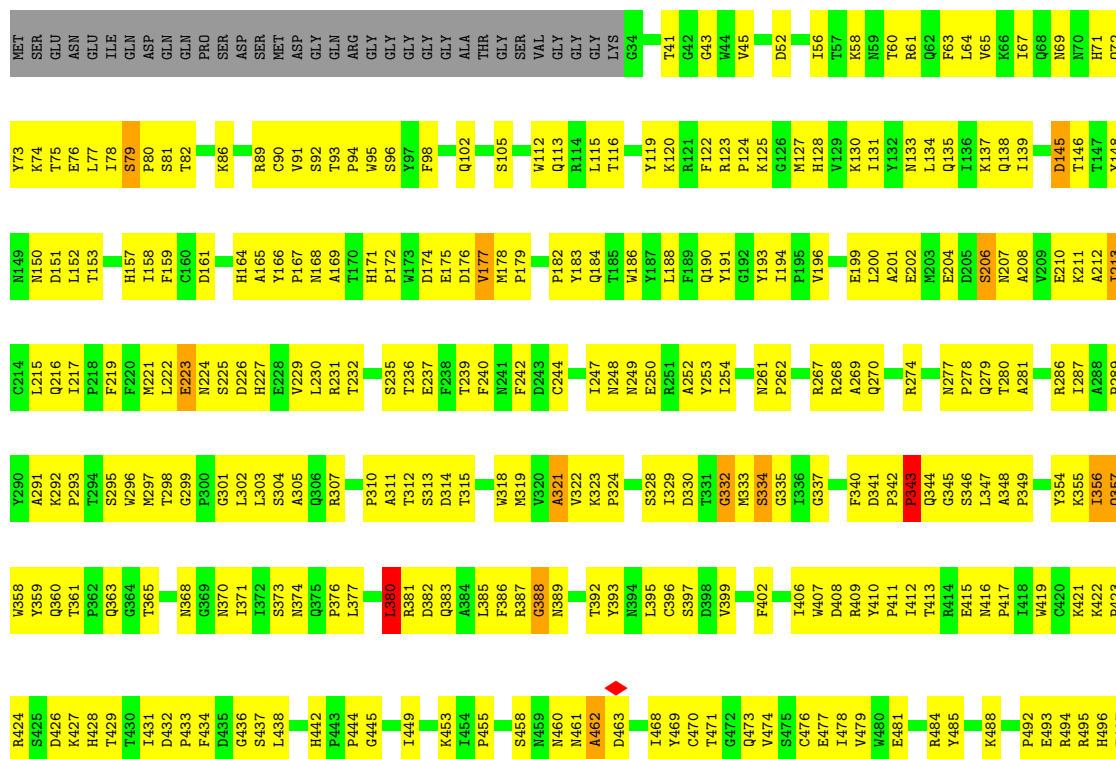
Chain V: 35% 55% 6%

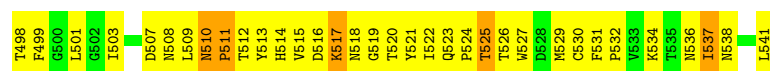




• Molecule 1: Capsid protein VP2

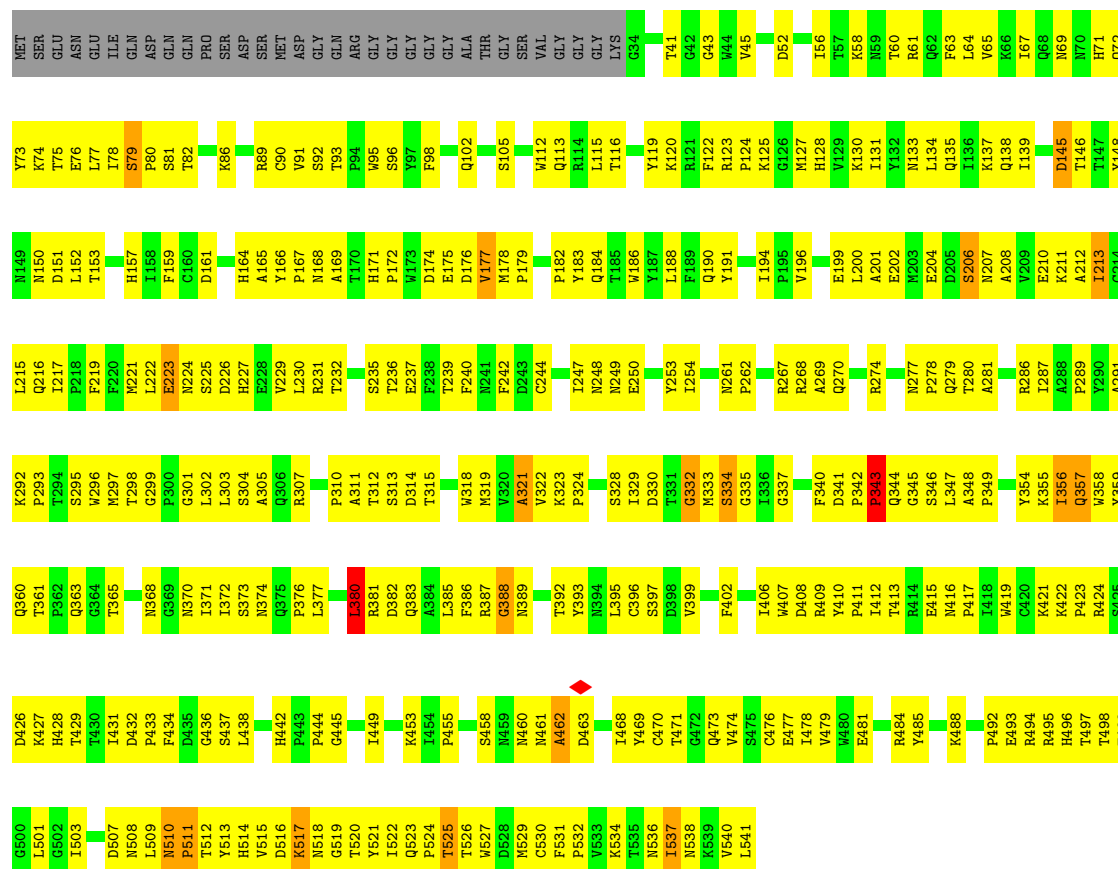
Chain W: 35% 55% 6%





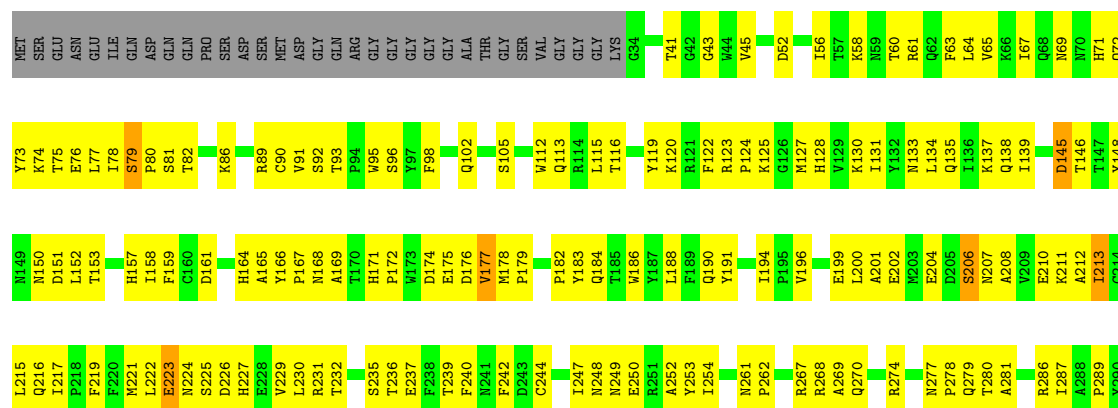
• Molecule 1: Capsid protein VP2

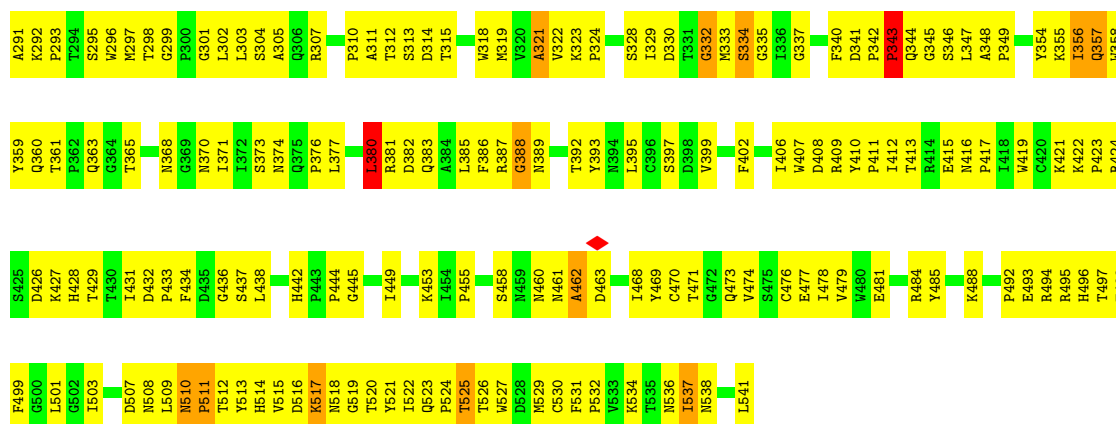
Chain X: 36% 55% 6%



• Molecule 1: Capsid protein VP2

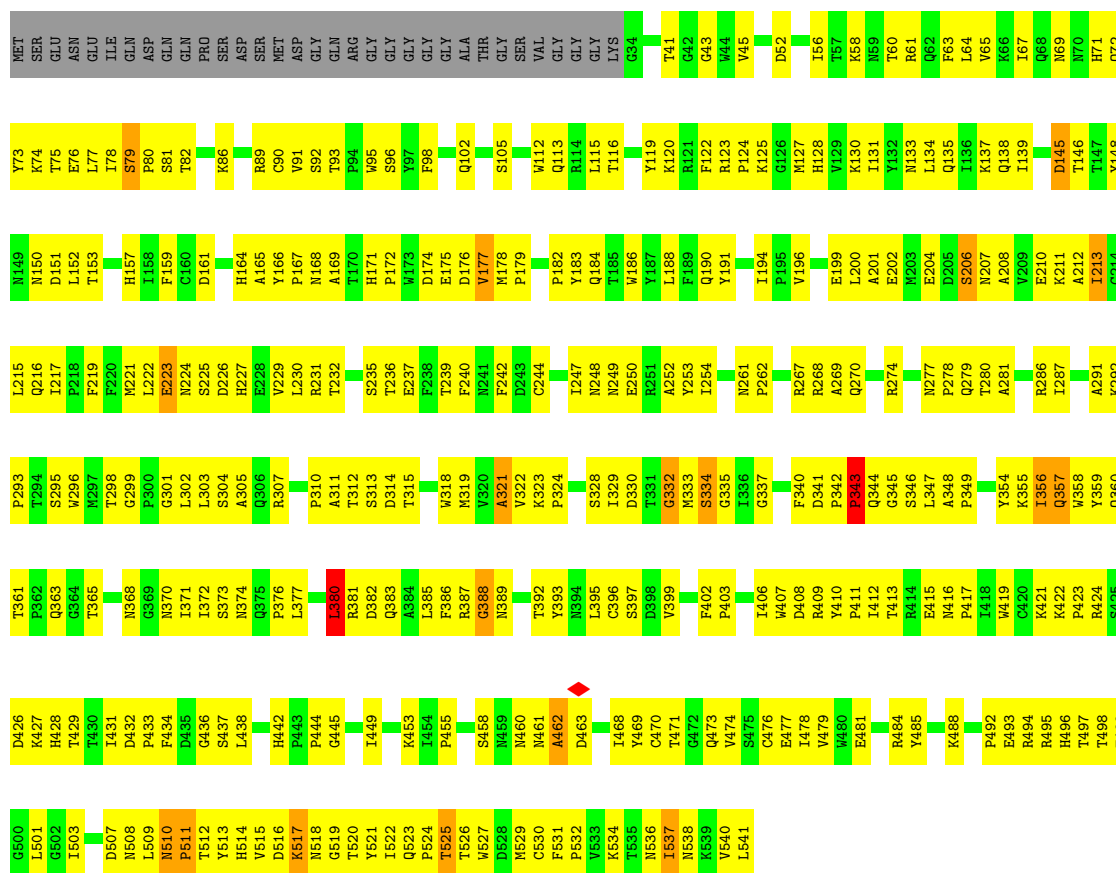
Chain Y: 36% 54% 6%





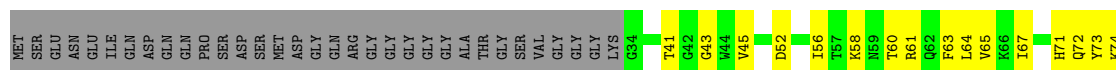
• Molecule 1: Capsid protein VP2

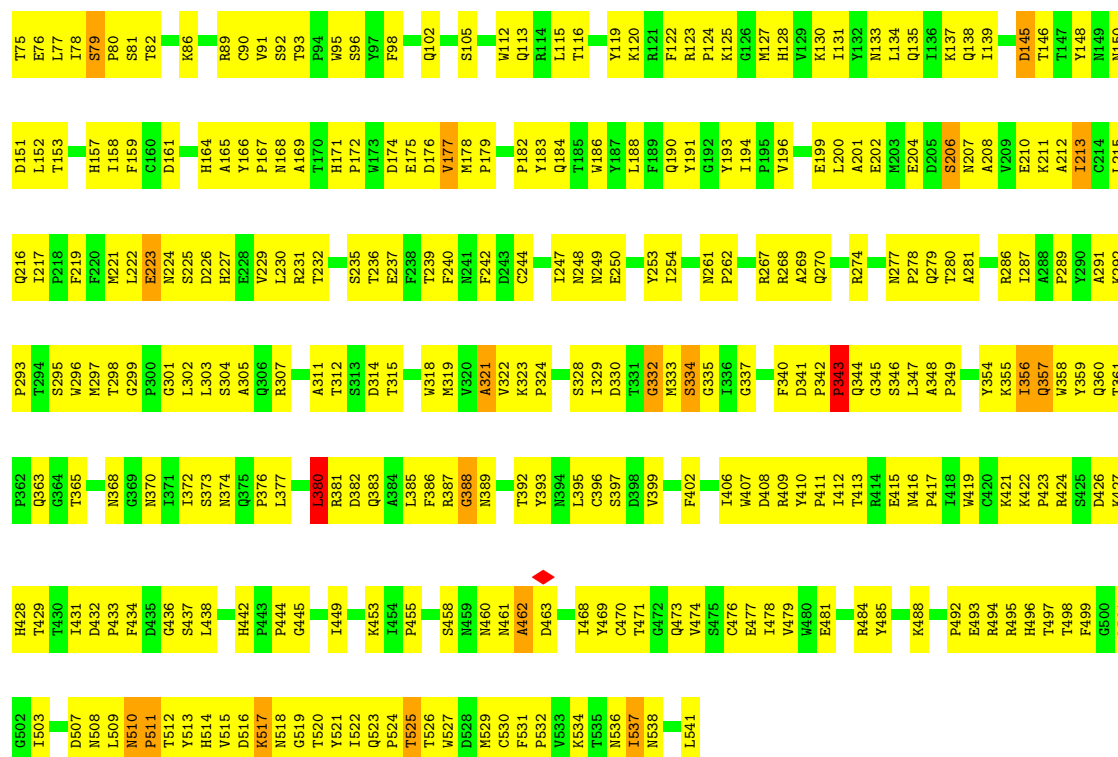
Chain Z: 36% 55% 6%



• Molecule 1: Capsid protein VP2

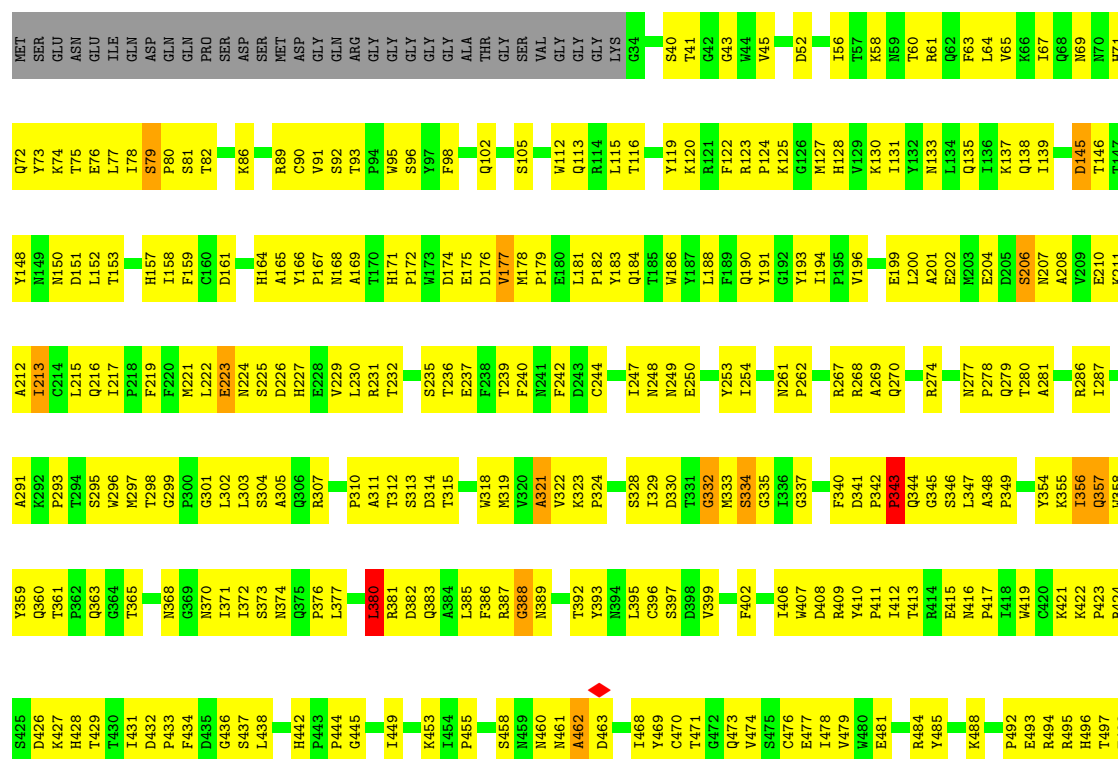
Chain 1: 36% 54% 6%

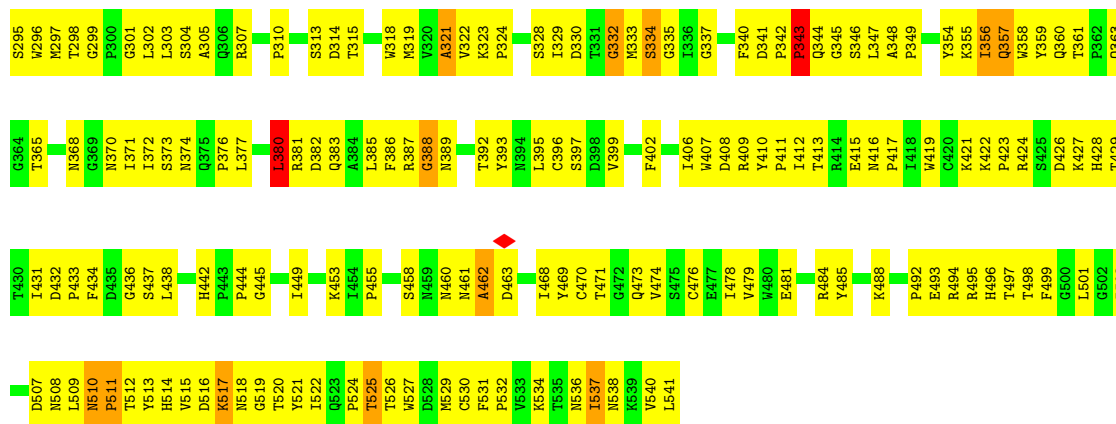




• Molecule 1: Capsid protein VP2

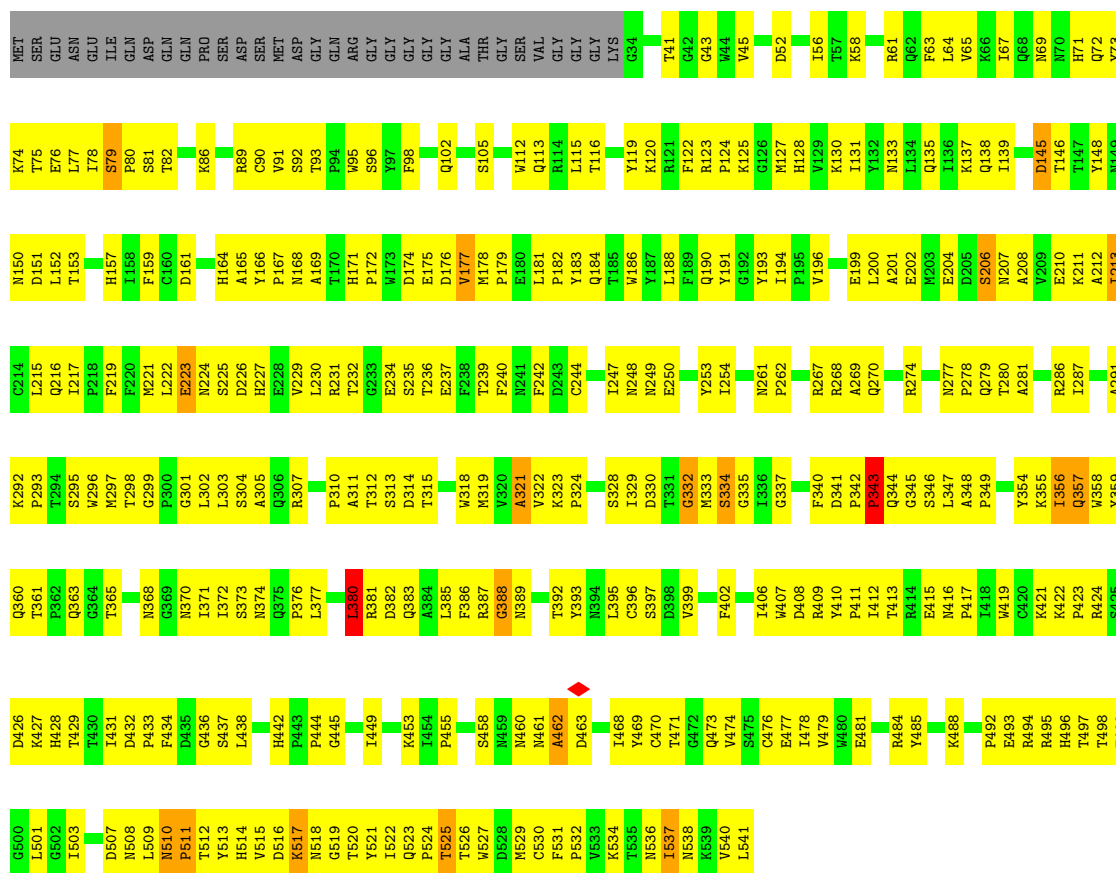
Chain 2: 36% 55% 6%





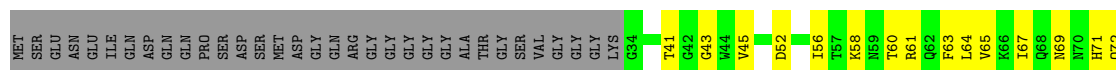
• Molecule 1: Capsid protein VP2

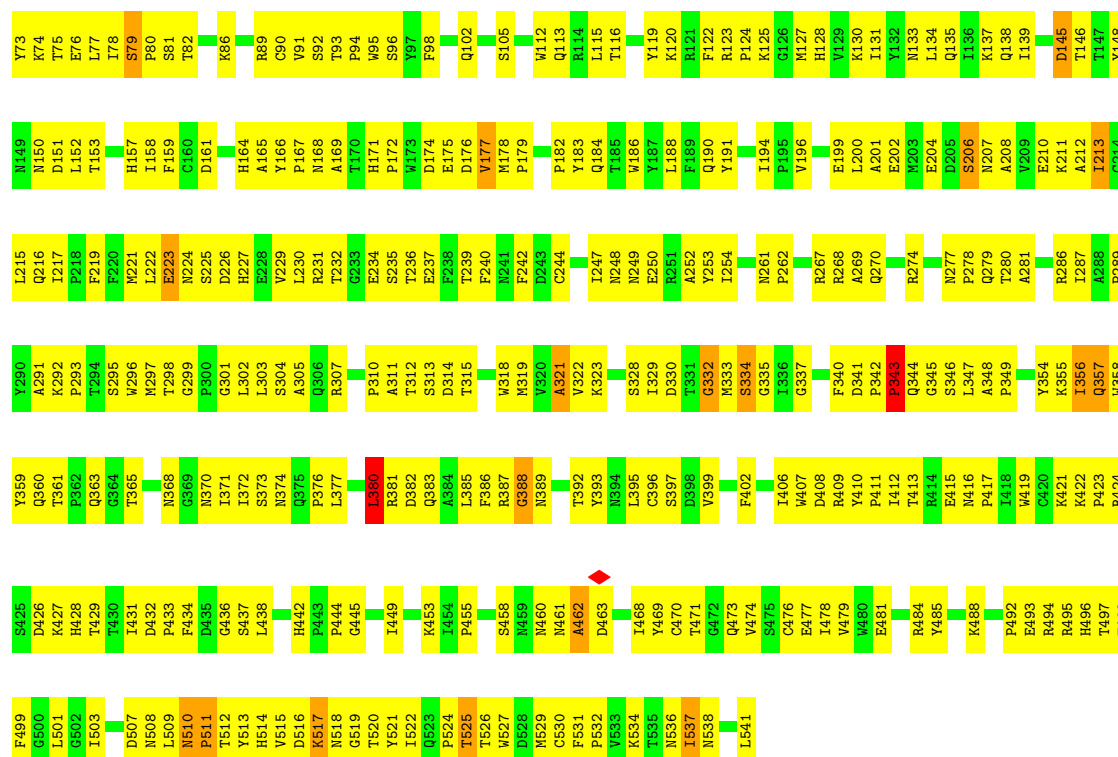
Chain 5: 36% 55% 6%



• Molecule 1: Capsid protein VP2

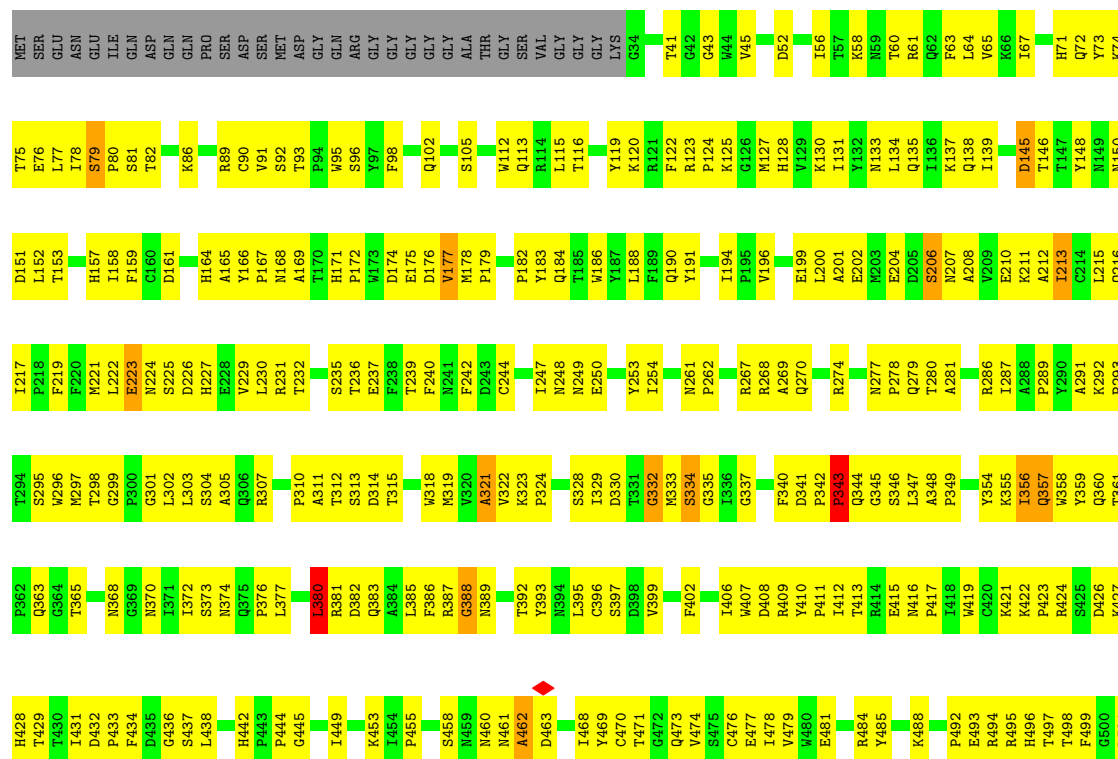
Chain 6: 35% 55% 6%



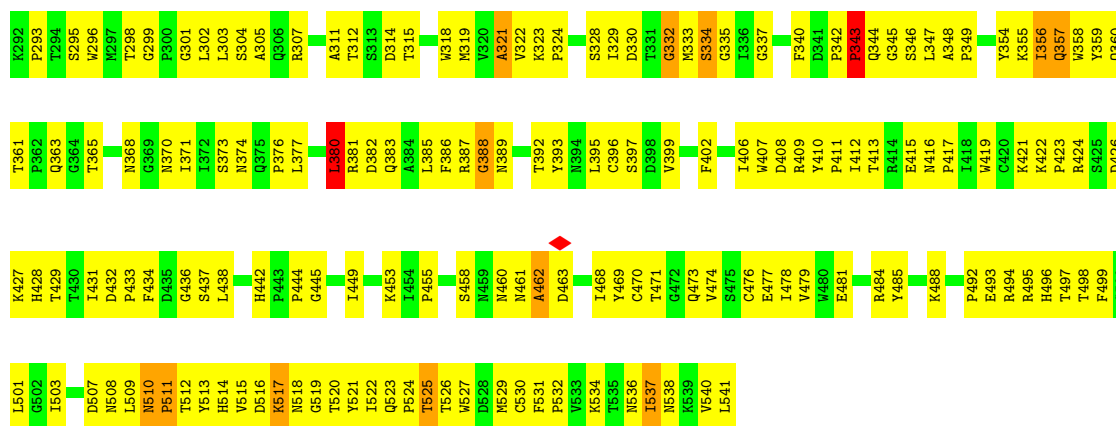


• Molecule 1: Capsid protein VP2

Chain a: 36% 54% 6%

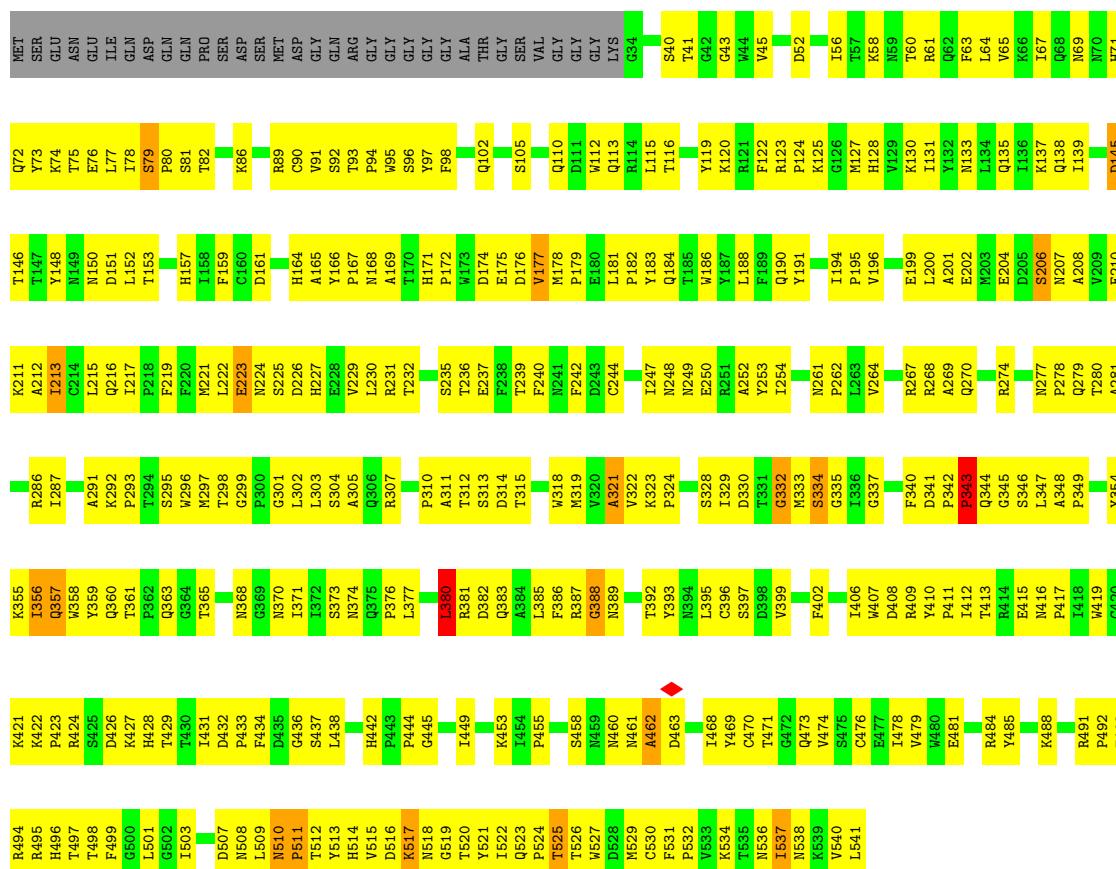






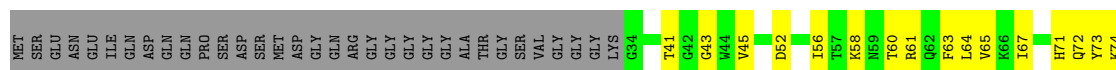
• Molecule 1: Capsid protein VP2

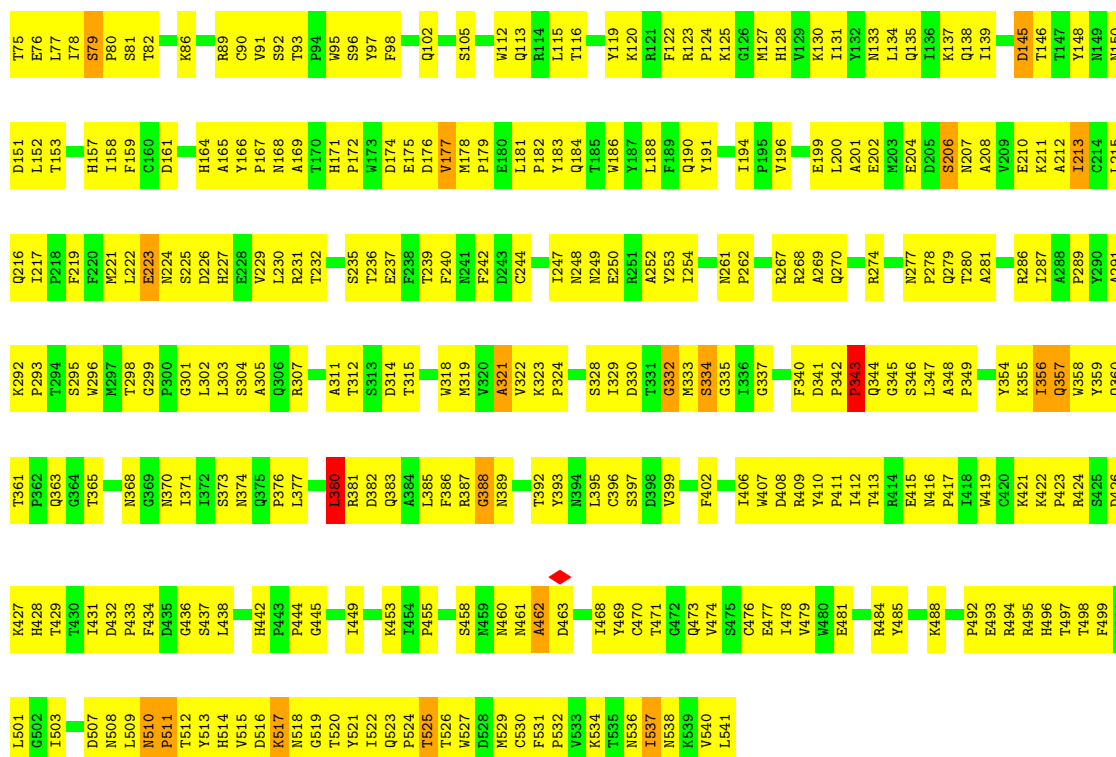
Chain d: 35% 55% 6%



• Molecule 1: Capsid protein VP2

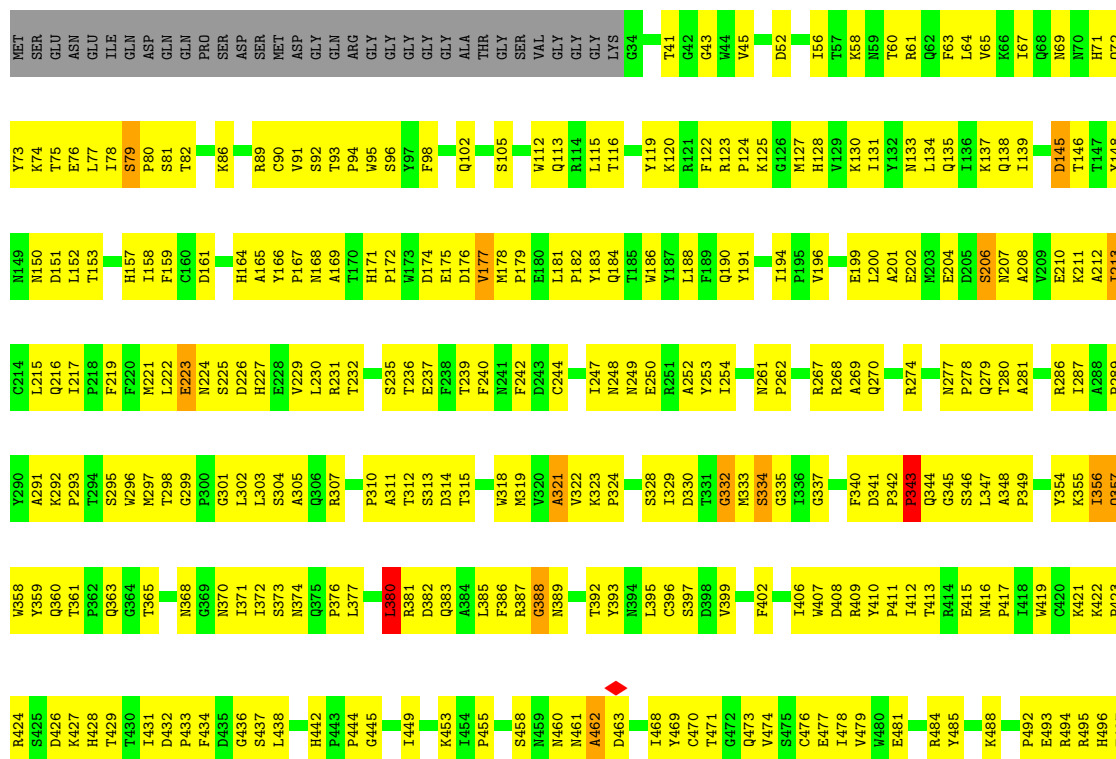
Chain e: 36% 54% 6%

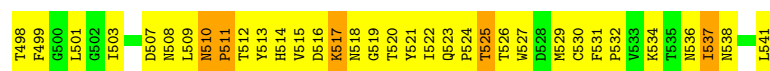




• Molecule 1: Capsid protein VP2

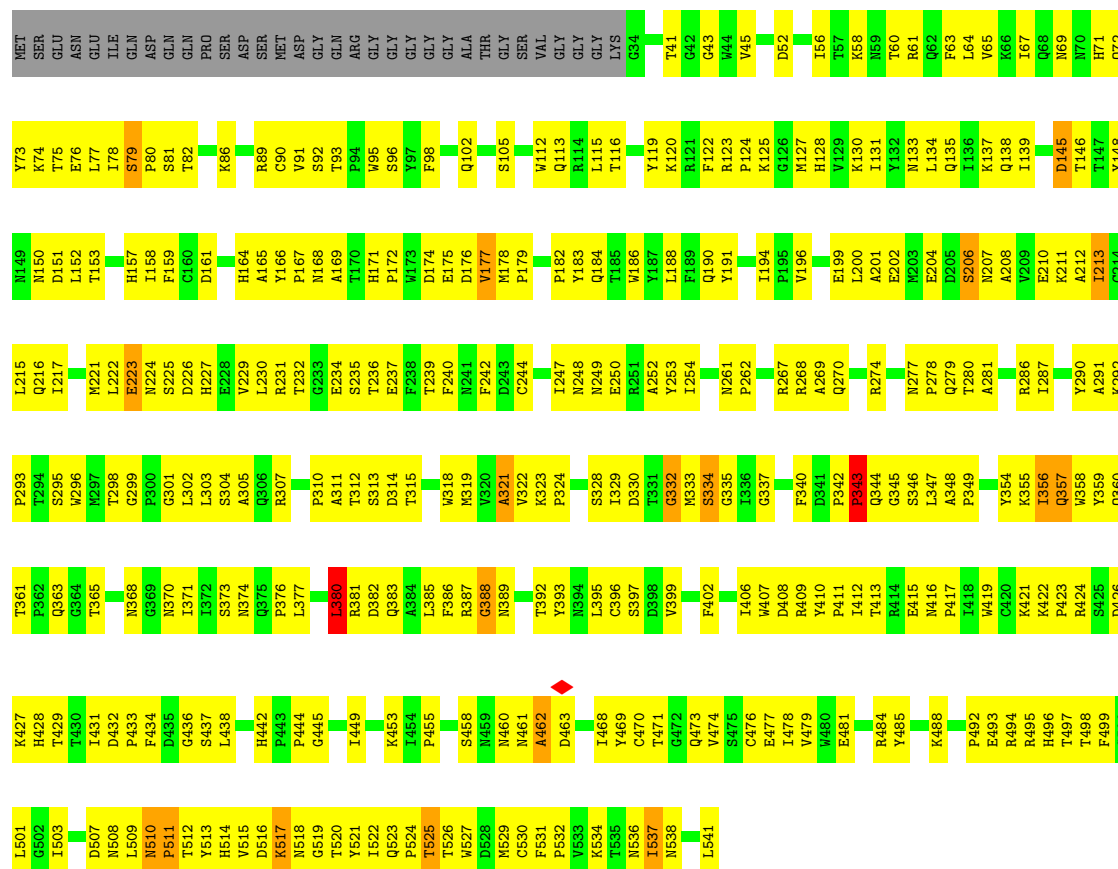
Chain f: 35% 55% 6%





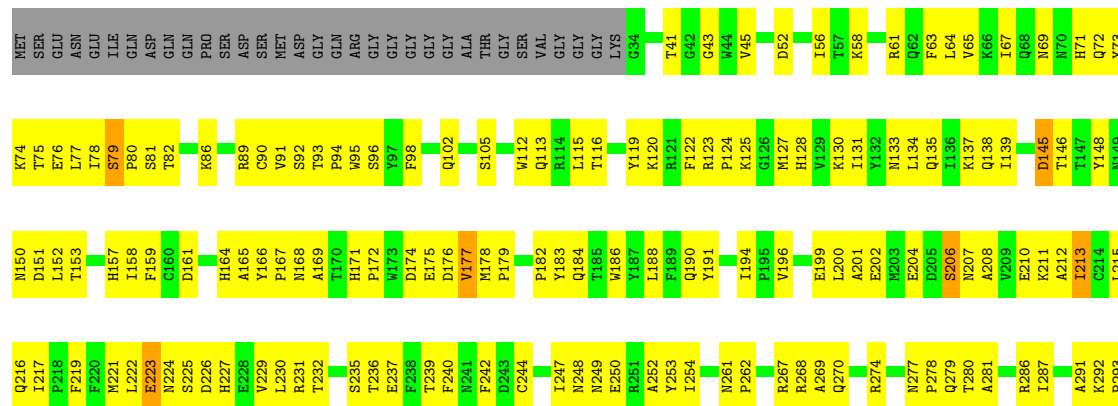
• Molecule 1: Capsid protein VP2

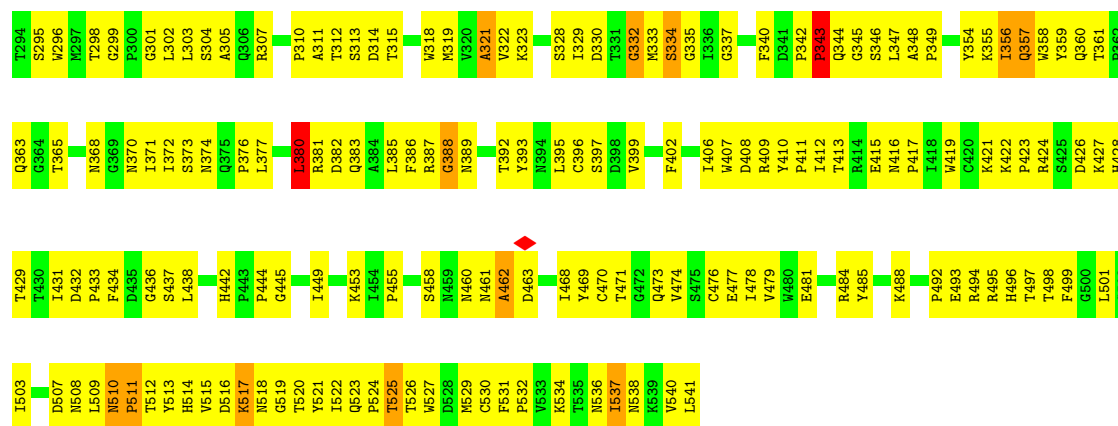
Chain g: 36% 54% 6%



• Molecule 1: Capsid protein VP2

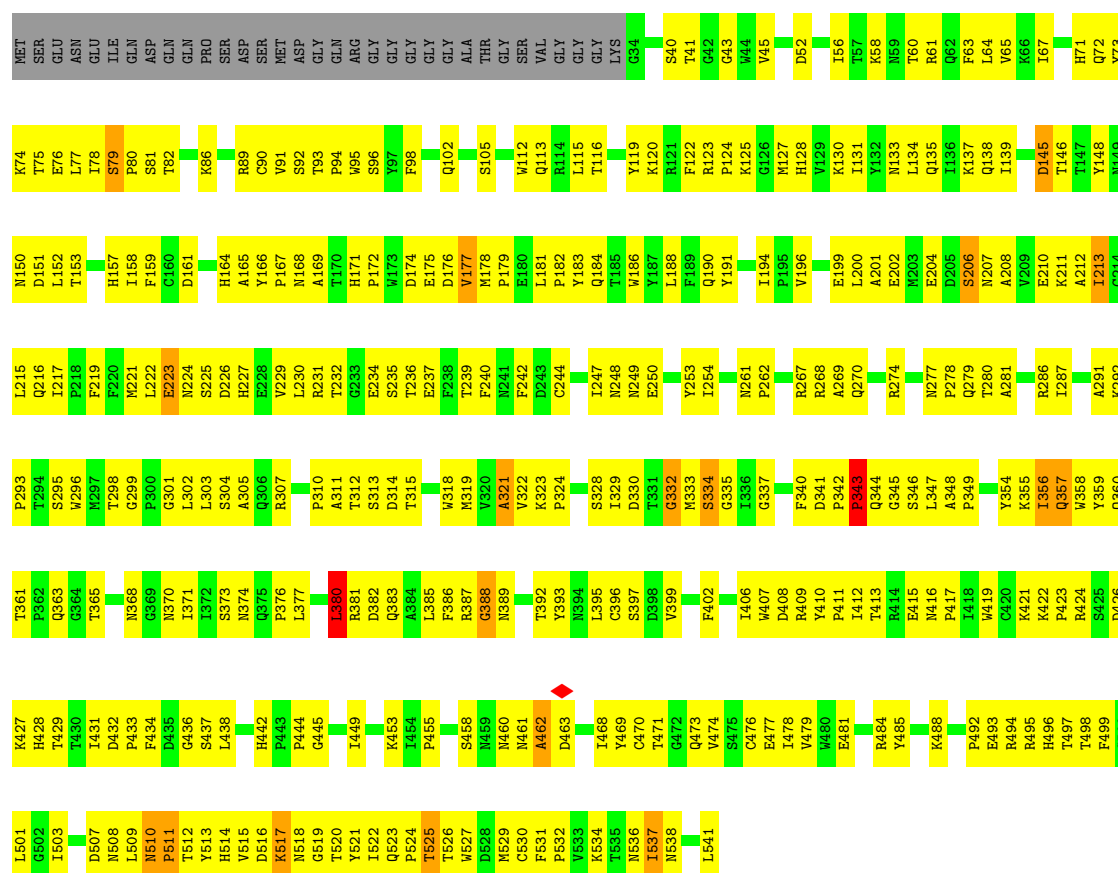
Chain h: 36% 54% 6%





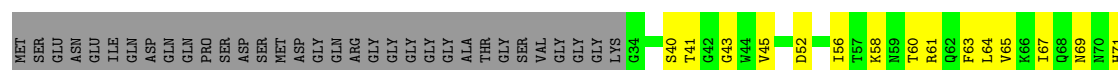
• Molecule 1: Capsid protein VP2

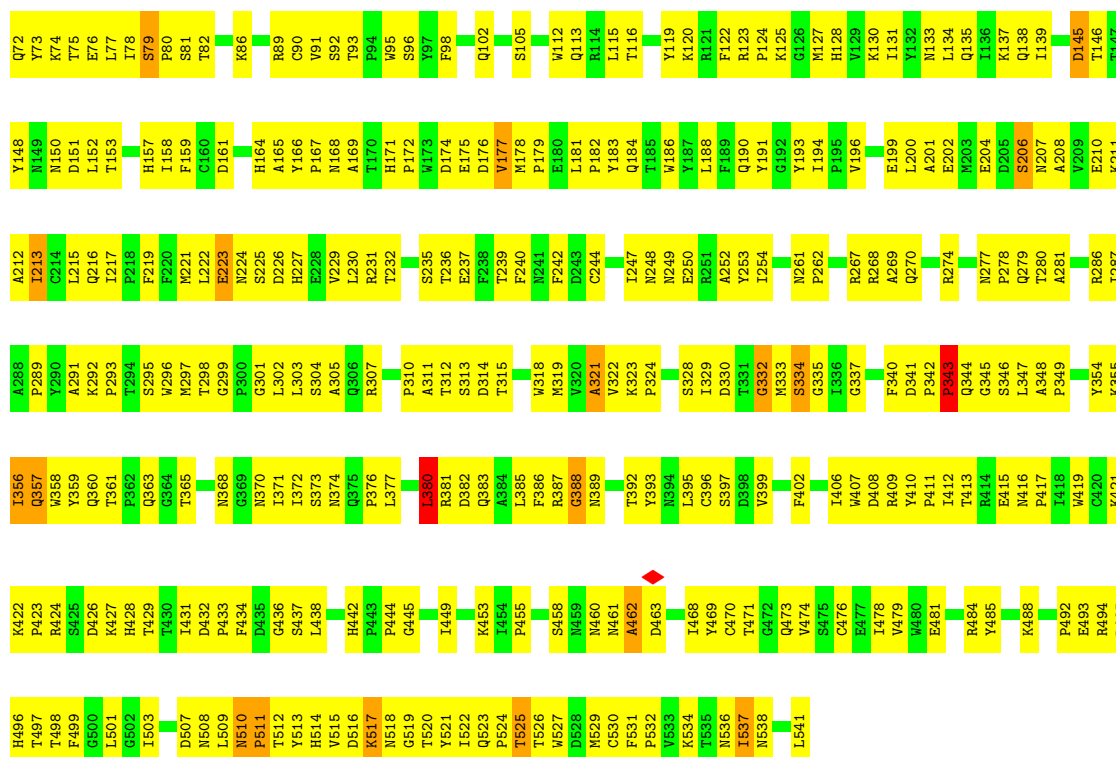
Chain i: 36% 55% 6%



• Molecule 1: Capsid protein VP2

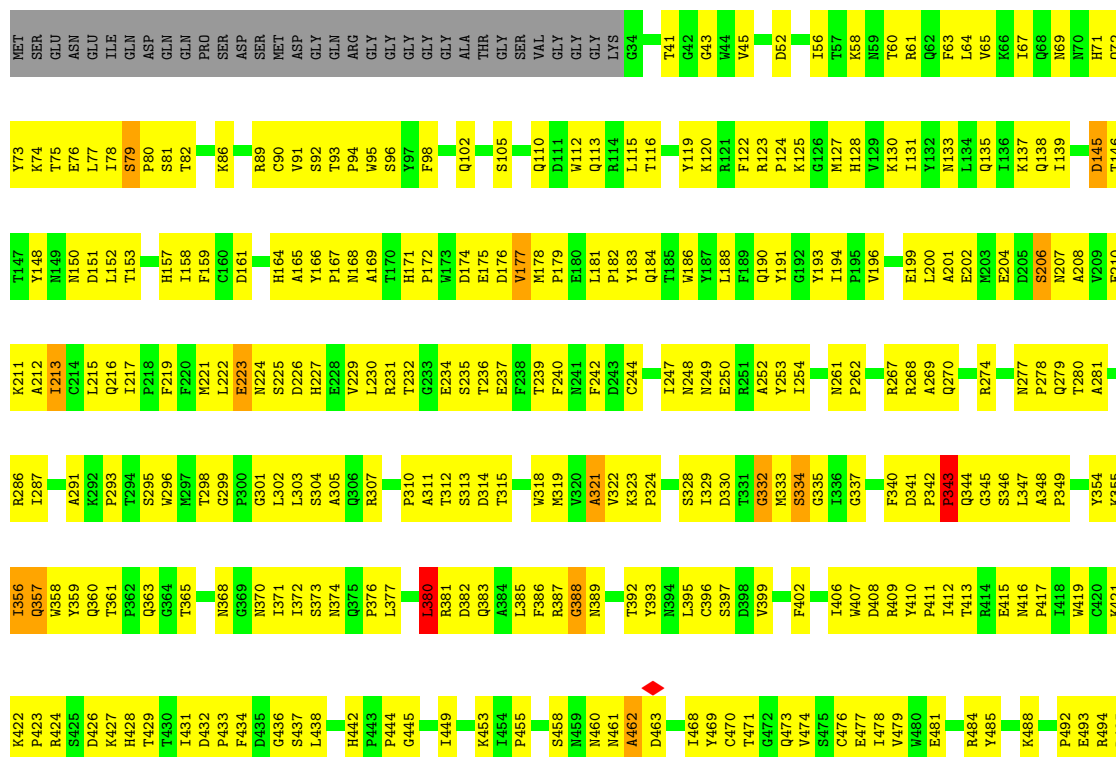
Chain j: 35% 55% 6%

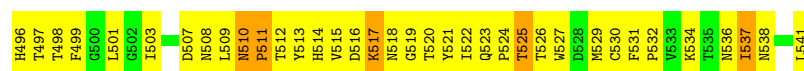




• Molecule 1: Capsid protein VP2

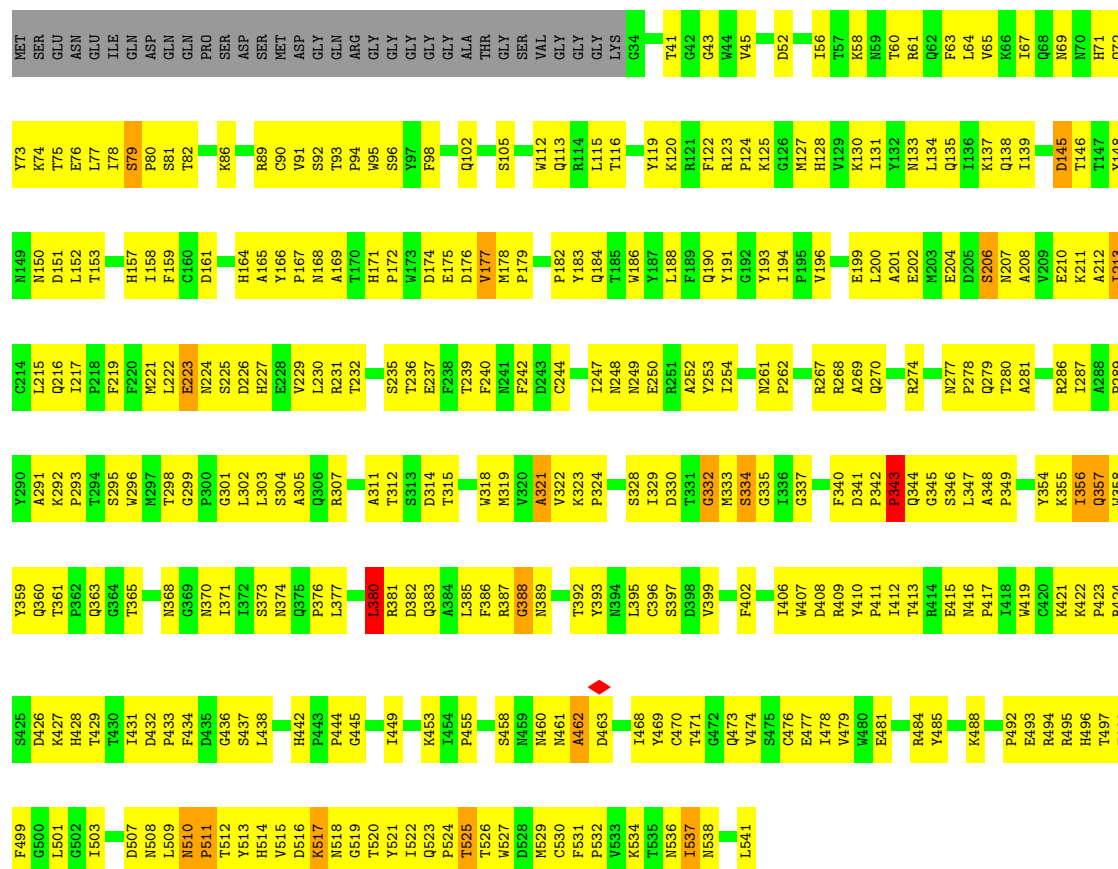
Chain k: 35% 55% 6%





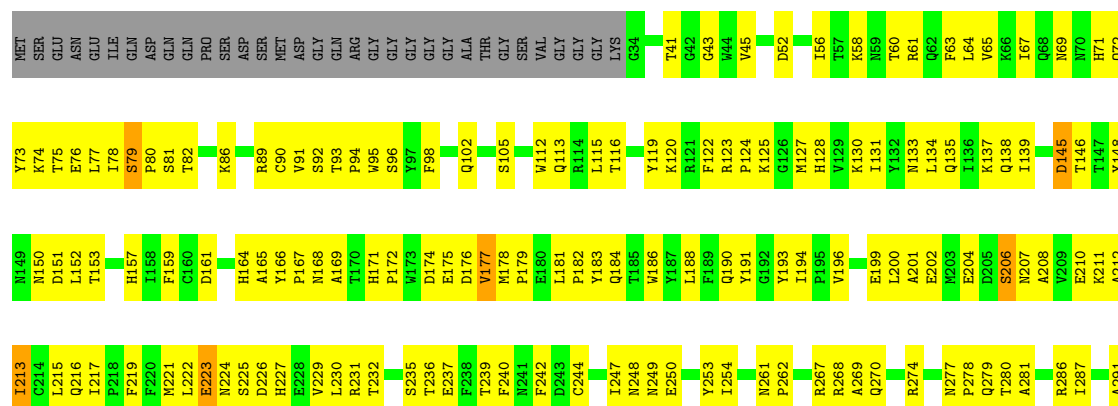
• Molecule 1: Capsid protein VP2

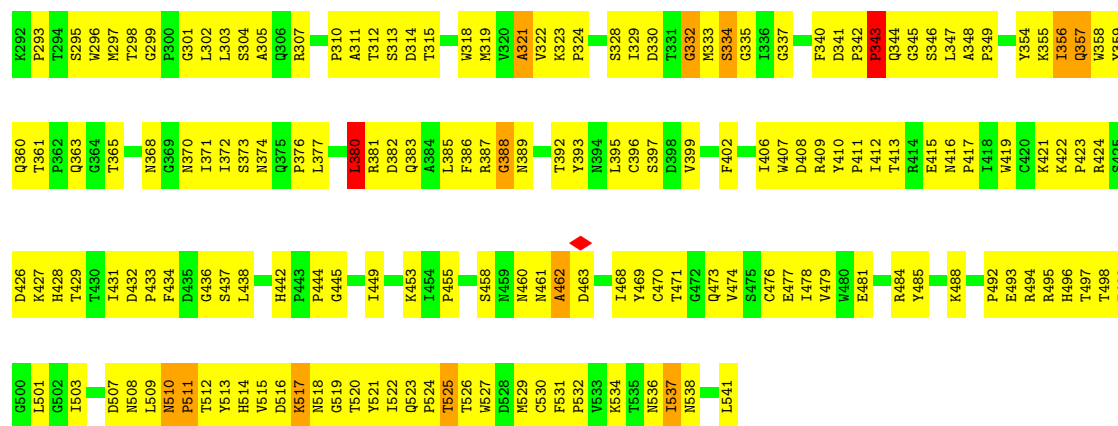
Chain l: 36% 54% 6%



• Molecule 1: Capsid protein VP2

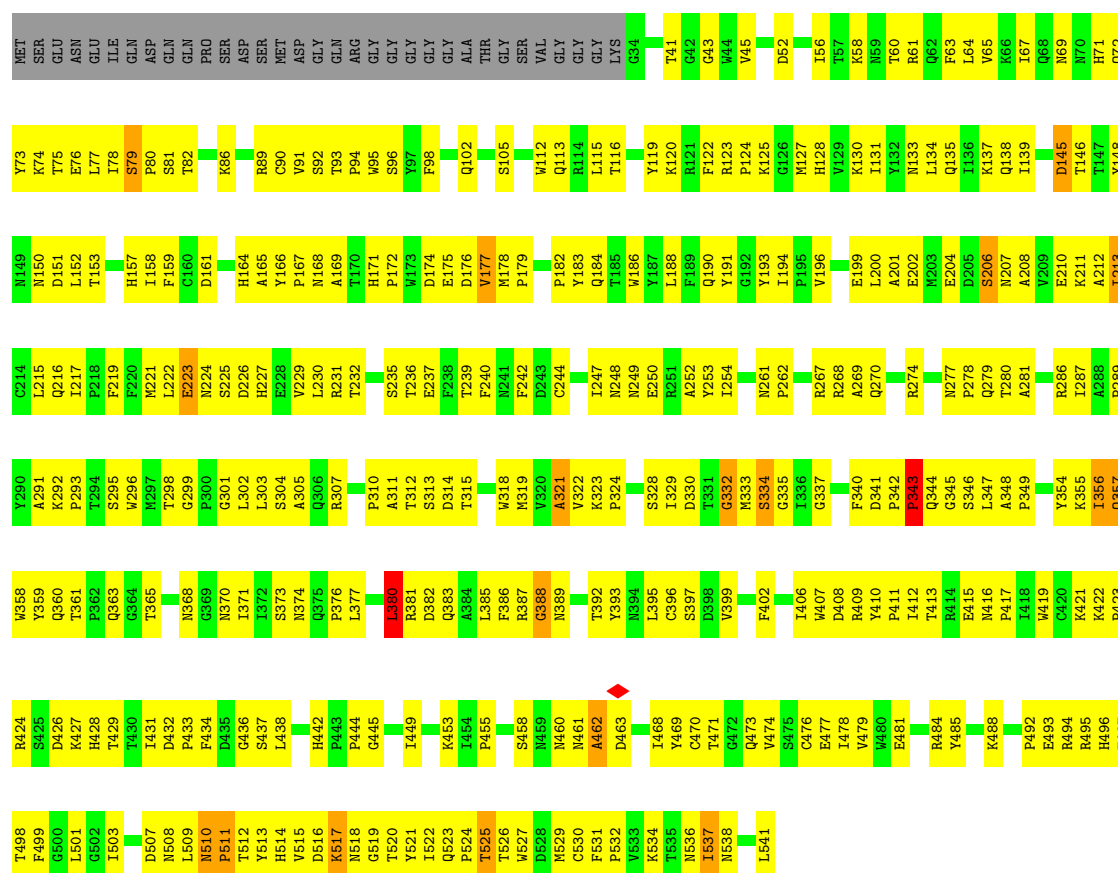
Chain m: 36% 55% 6%





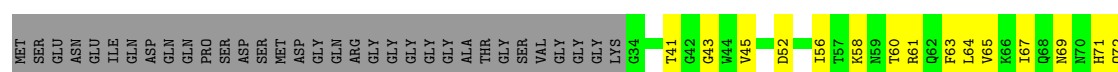
• Molecule 1: Capsid protein VP2

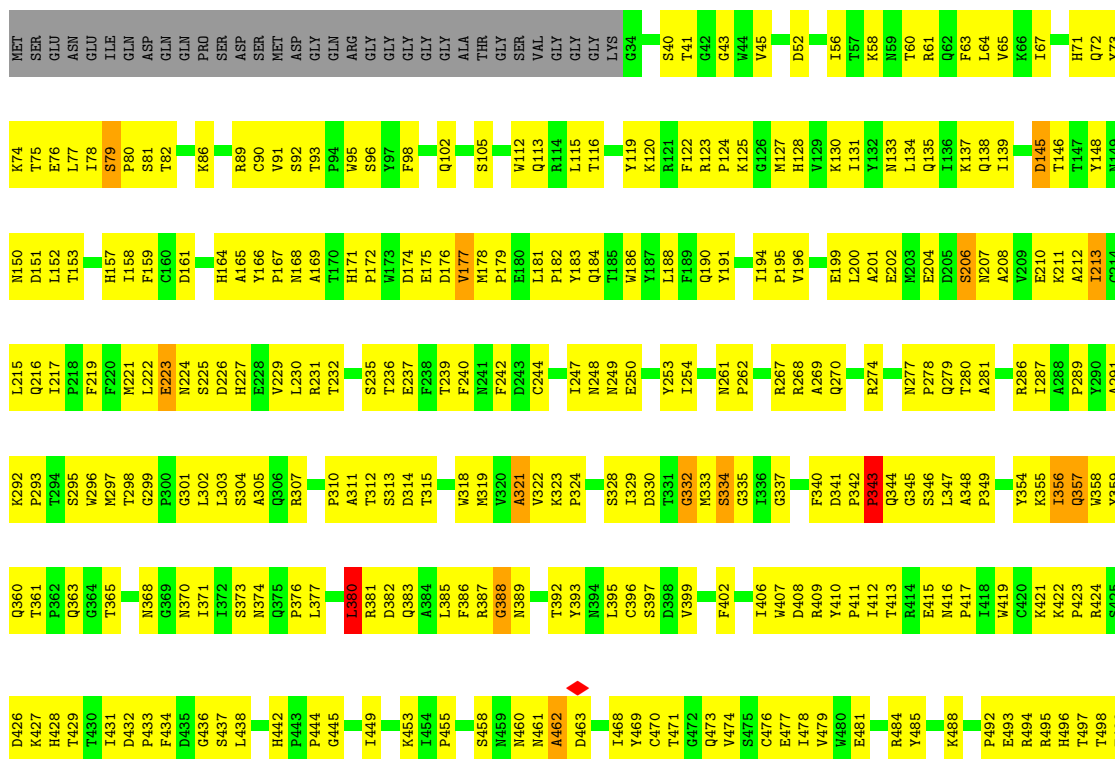
Chain n: 35% 55% 6%

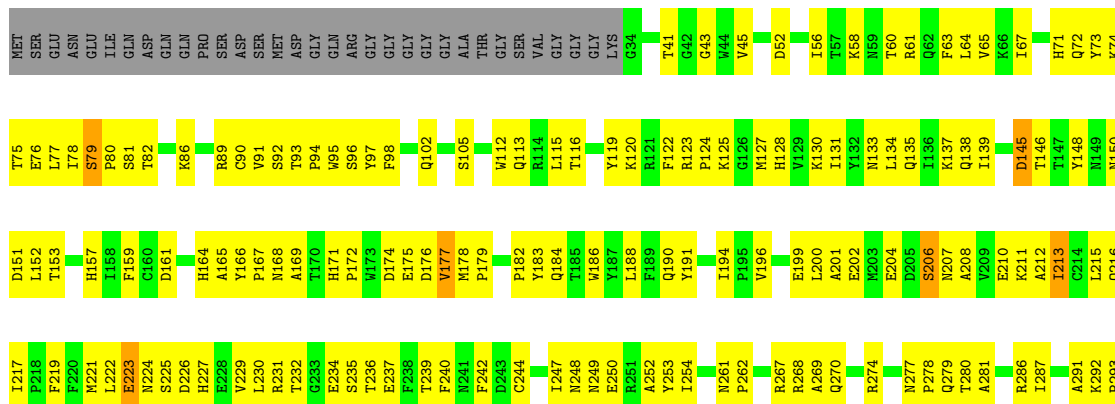


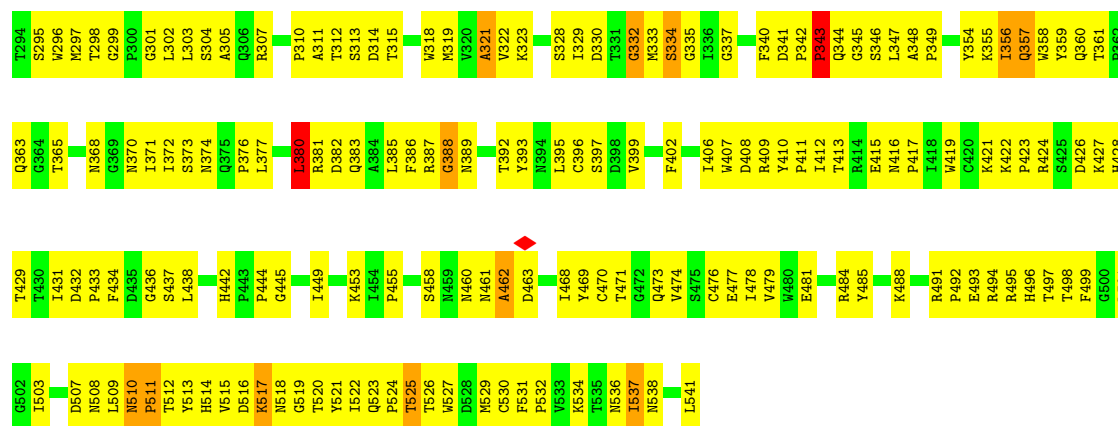
• Molecule 1: Capsid protein VP2

Chain o: 36% 54% 6%



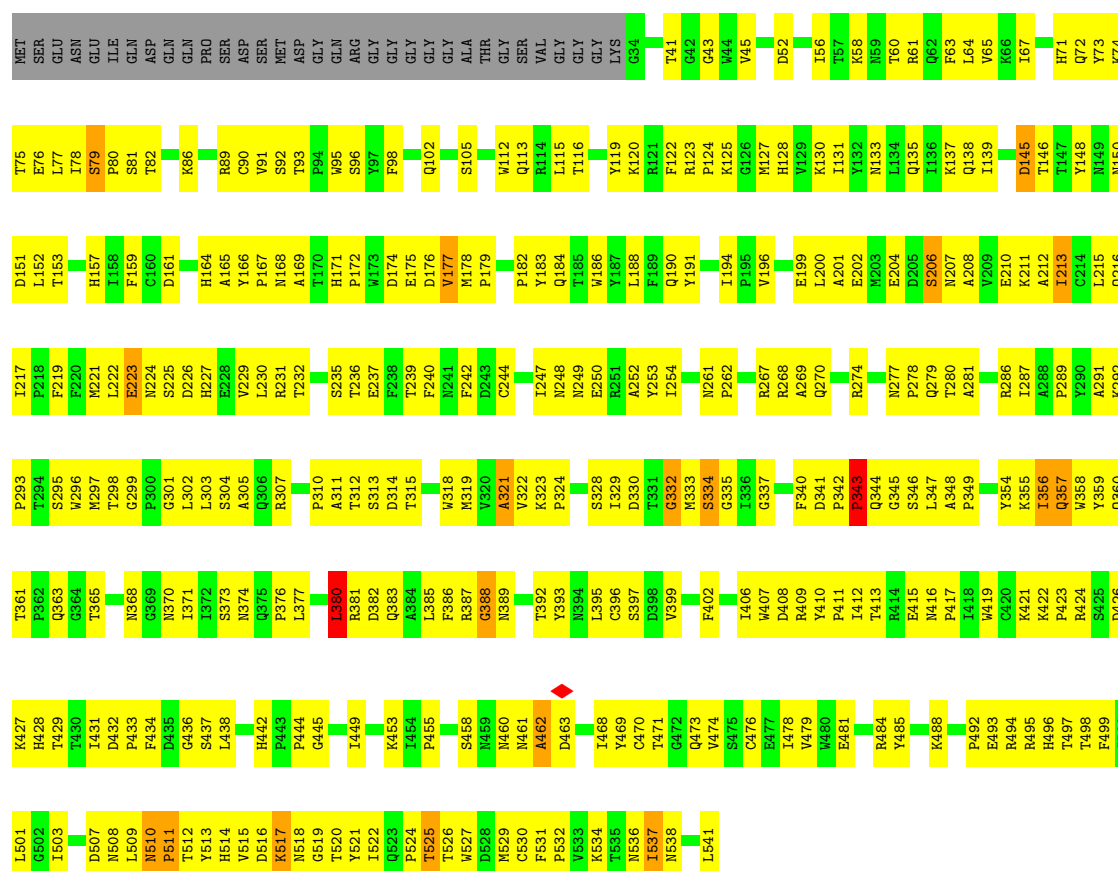






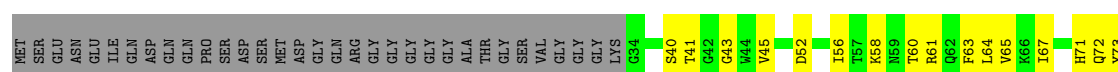
• Molecule 1: Capsid protein VP2

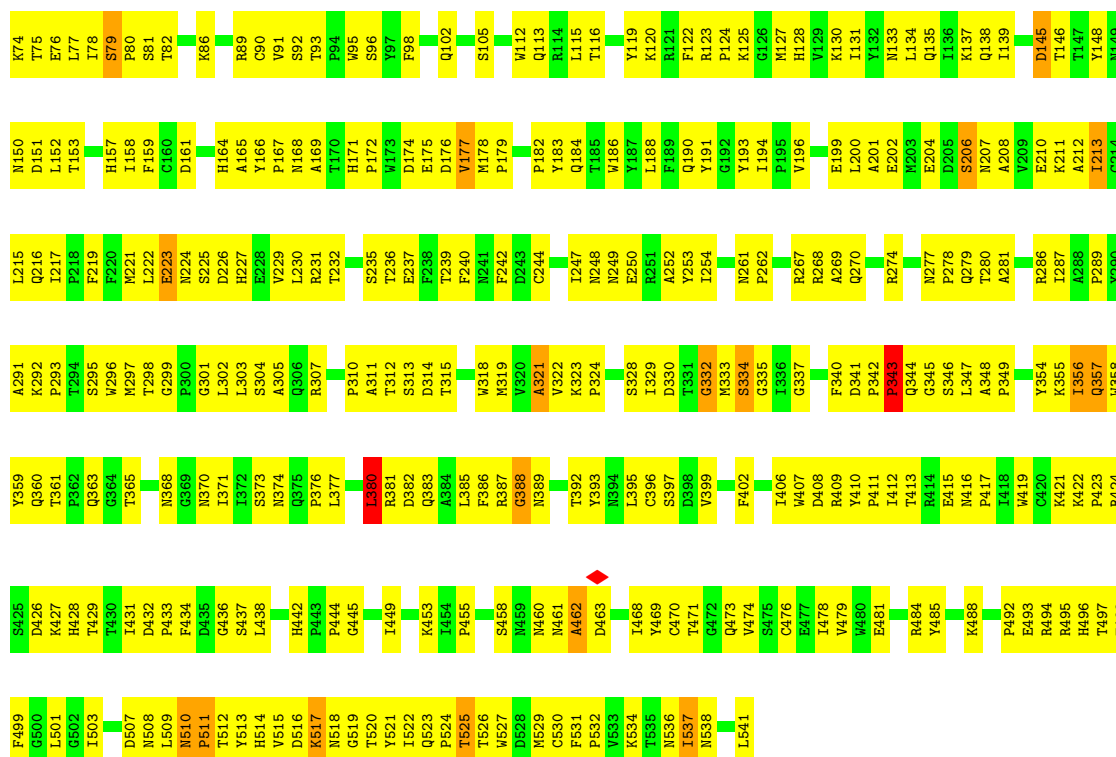
Chain s: 37% 54% 6%



• Molecule 1: Capsid protein VP2

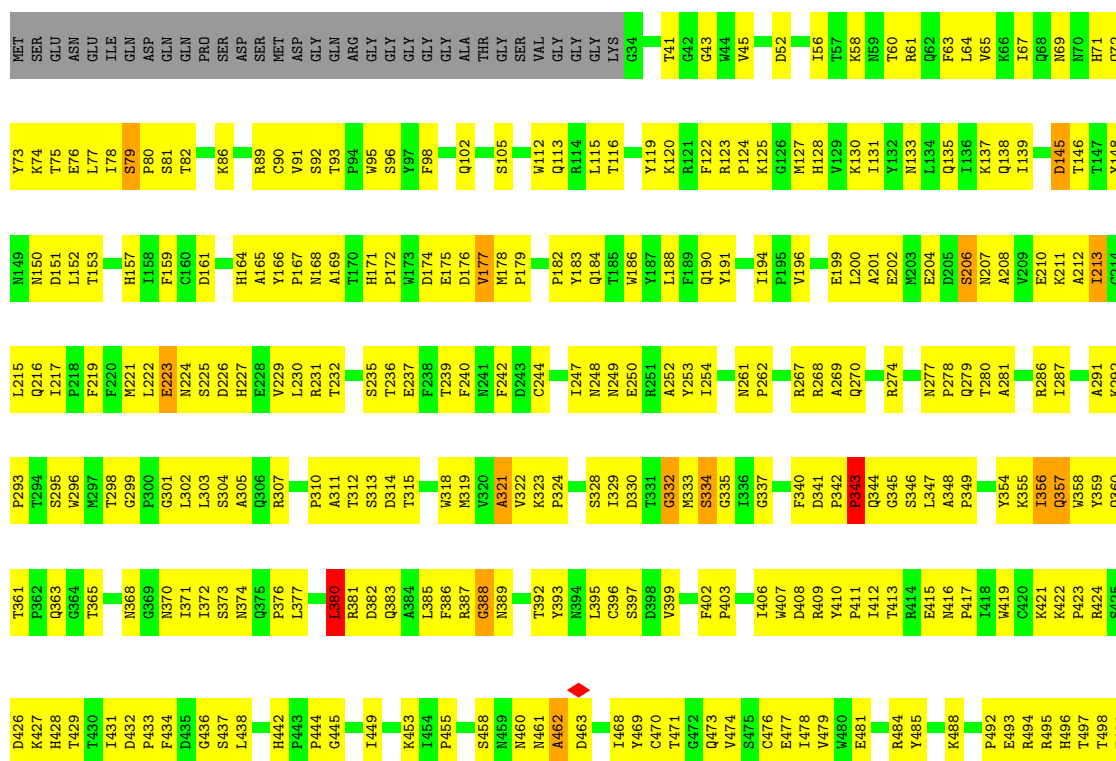
Chain t: 36% 55% 6%

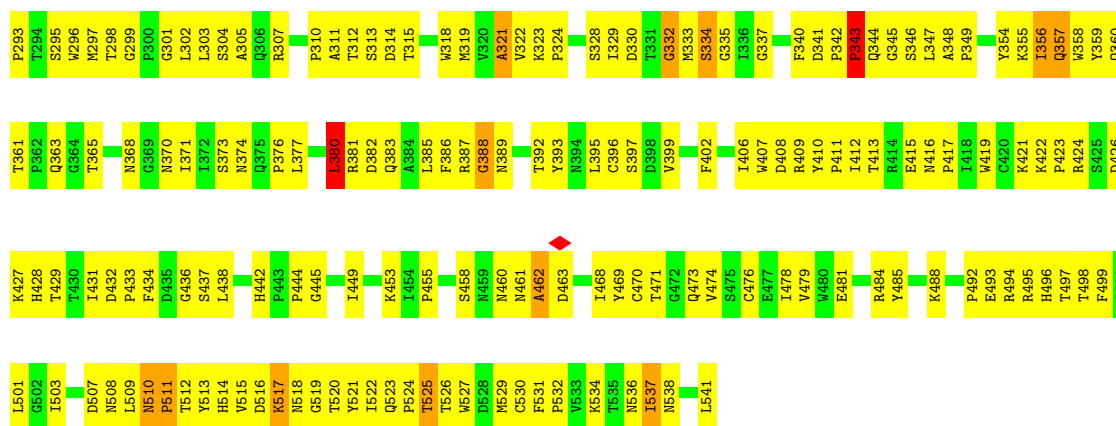




• Molecule 1: Capsid protein VP2

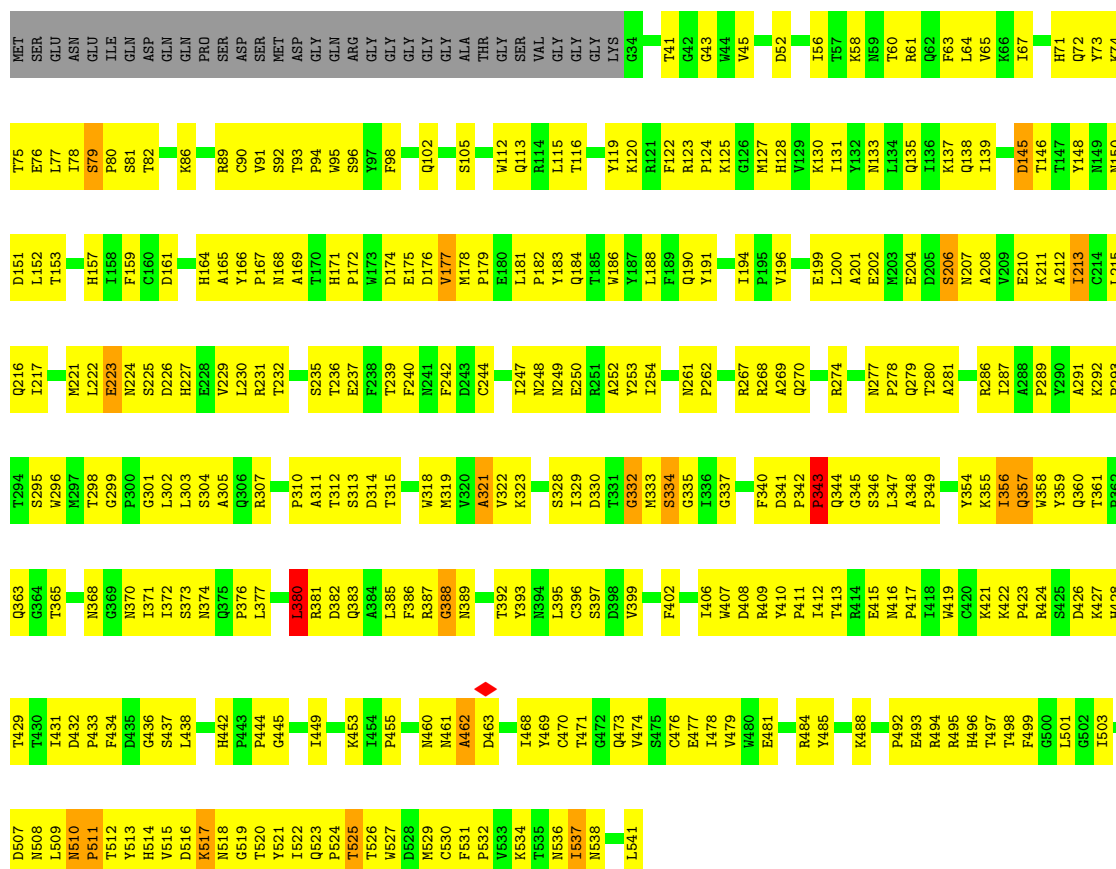
Chain u: 36% 54% 6%





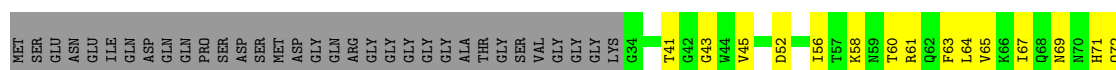
• Molecule 1: Capsid protein VP2

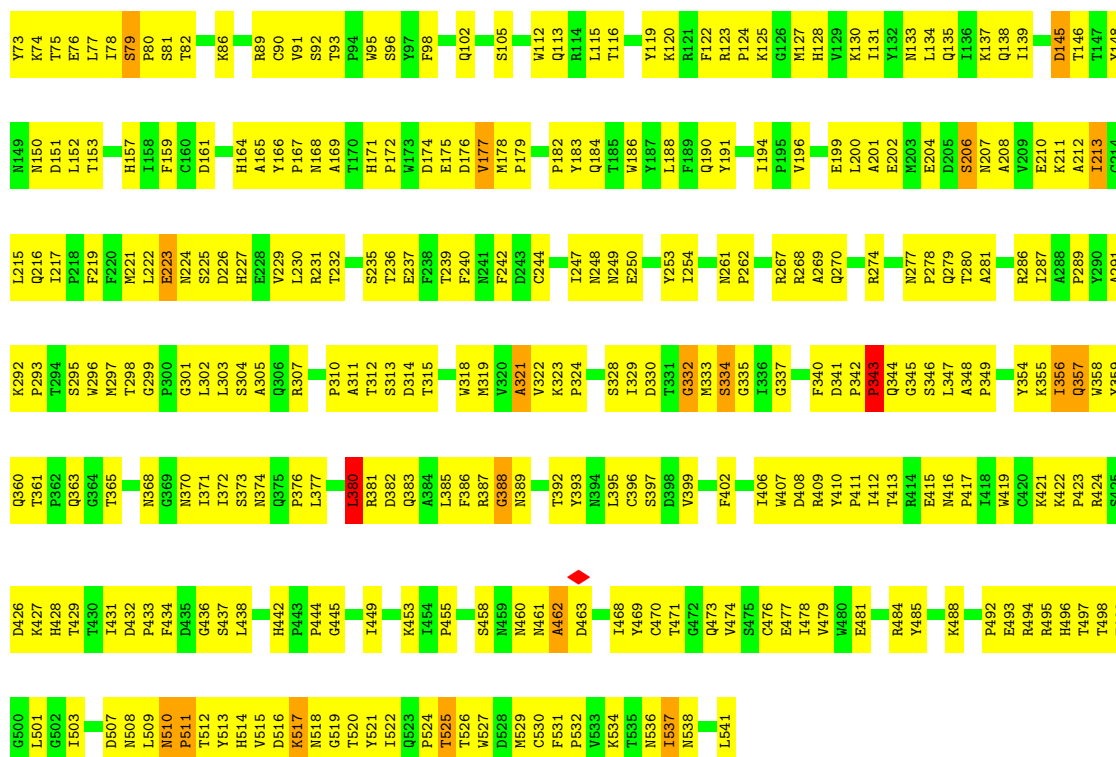
Chain x: 36% 54% 6%



• Molecule 1: Capsid protein VP2

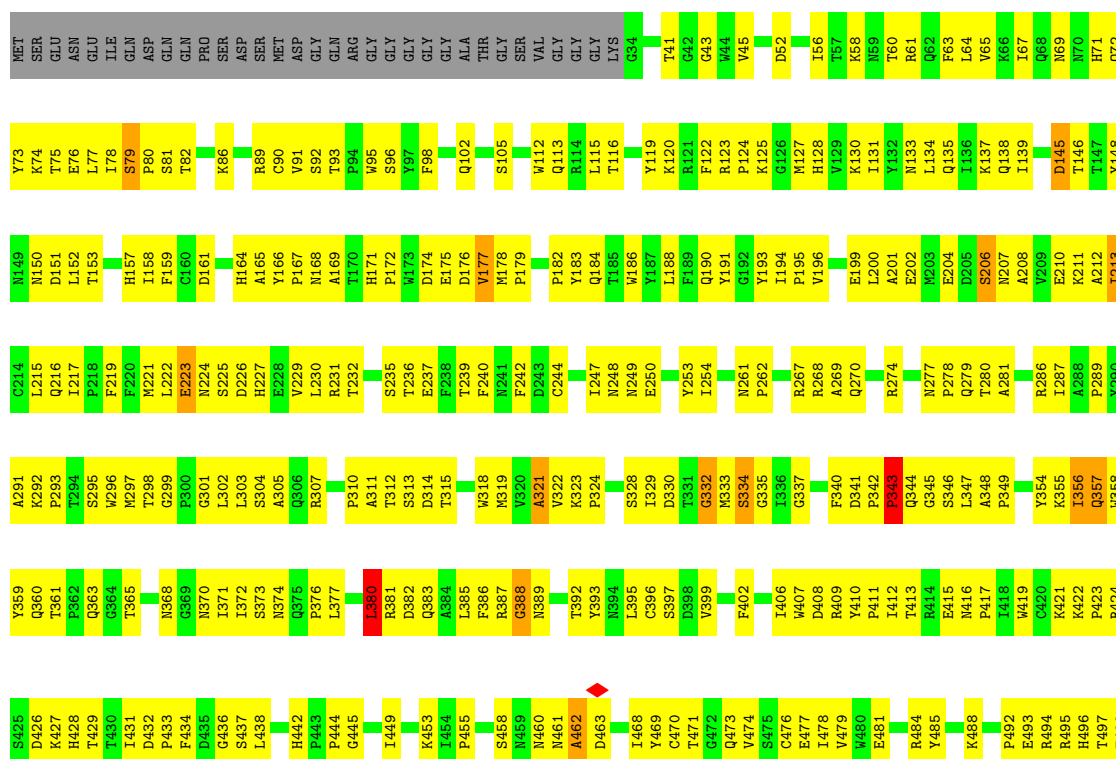
Chain y: 36% 54% 6%

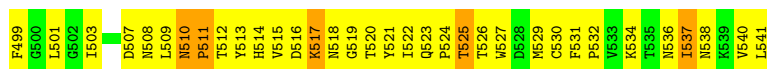




• Molecule 1: Capsid protein VP2

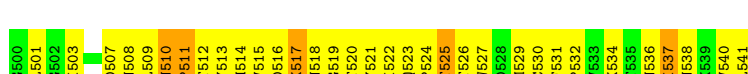
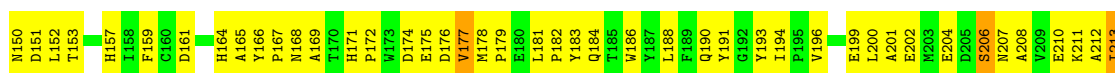
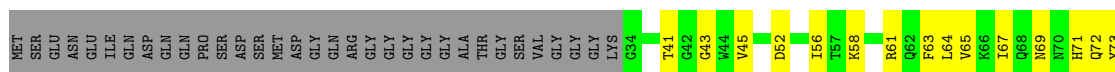
Chain z: 35% 55% 6%





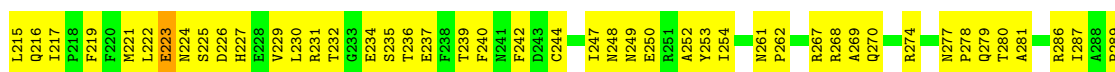
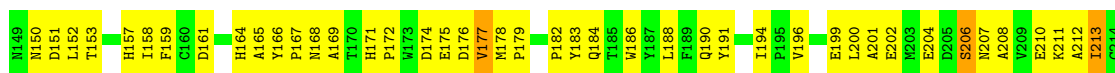
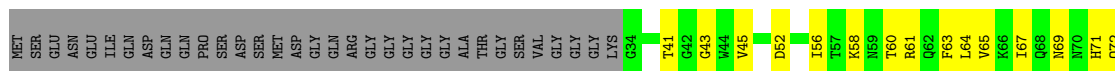
• Molecule 1: Capsid protein VP2

Chain 7: 36% 55% 6%



• Molecule 1: Capsid protein VP2

Chain 8: 36% 54% 6%



L501	G502	L503	D507	N508	L509	N510	P511	T512	Y513	H514	V515	D516	K517	N518	G519	T520	Y521	I522	Q523	P524	T525	T526	W527	D528	M529	C530	F531	P532	V533	K534	T535	N536	I537	N538	L541																			
S425	D426	K427	H428	T429	T430	I431	D432	P433	F434	D435	G436	S437	L438	H442	P443	P444	G445	I449	K453	I454	P455	N460	N461	A462	D463	I468	Y469	C470	T471	G472	Q473	V474	C476	E477	I478	V479	W480	E481	R484	Y485	K488	P492	E493	R494	R495	H496	T497	T498	F499	G500				
Y359	Q360	T361	P362	Q363	G364	T365	N368	G369	N370	I371	I372	S373	N374	Q375	P376	L377	L380	R381	D382	Q383	A384	L385	F386	R387	G388	N389	T392	Y393	N394	L395	C396	S397	D398	V399	F402	I406	W407	D408	R409	Y410	P411	I412	T413	R414	E415	N416	P417	I418	W419	C420	K421	K422	P423	R424
A291	K292	T293	T294	S295	W296	K297	T298	G299	P300	G301	L302	L303	S304	A305	Q306	R307	P310	A311	T312	S313	D314	T315	W318	M319	V320	A321	V322	K323	S328	I329	D330	T331	G332	M333	S334	G335	I336	G337	F340	D341	P342	P343	Q344	G345	S346	L347	A348	P349	Y354	K355	I356	Q357	W358	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	13394	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-20 (5k x 3k)	Depositor
Maximum map value	16.946	Depositor
Minimum map value	-8.800	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1	Depositor
Map size (Å)	379.05, 379.05, 379.05	wwPDB
Map dimensions	399, 399, 399	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	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	0.46	0/4202	0.83	16/5733 (0.3%)
1	2	0.46	0/4202	0.83	16/5733 (0.3%)
1	3	0.46	0/4202	0.83	16/5733 (0.3%)
1	4	0.46	0/4202	0.83	16/5733 (0.3%)
1	5	0.46	0/4202	0.83	16/5733 (0.3%)
1	6	0.46	0/4202	0.83	16/5733 (0.3%)
1	7	0.46	0/4202	0.83	16/5733 (0.3%)
1	8	0.46	0/4202	0.83	16/5733 (0.3%)
1	A	0.46	0/4202	0.83	16/5733 (0.3%)
1	B	0.46	0/4202	0.83	16/5733 (0.3%)
1	C	0.46	0/4202	0.83	16/5733 (0.3%)
1	D	0.46	0/4202	0.83	16/5733 (0.3%)
1	E	0.46	0/4202	0.83	16/5733 (0.3%)
1	F	0.46	0/4202	0.83	16/5733 (0.3%)
1	G	0.46	0/4202	0.83	16/5733 (0.3%)
1	H	0.46	0/4202	0.83	16/5733 (0.3%)
1	I	0.46	0/4202	0.83	16/5733 (0.3%)
1	J	0.46	0/4202	0.83	16/5733 (0.3%)
1	K	0.46	0/4202	0.83	16/5733 (0.3%)
1	L	0.46	0/4202	0.83	16/5733 (0.3%)
1	M	0.46	0/4202	0.83	16/5733 (0.3%)
1	N	0.46	0/4202	0.83	16/5733 (0.3%)
1	O	0.46	0/4202	0.83	16/5733 (0.3%)
1	P	0.46	0/4202	0.83	16/5733 (0.3%)
1	Q	0.46	0/4202	0.83	16/5733 (0.3%)
1	R	0.46	0/4202	0.83	16/5733 (0.3%)
1	S	0.46	0/4202	0.83	16/5733 (0.3%)
1	T	0.46	0/4202	0.83	16/5733 (0.3%)
1	U	0.46	0/4202	0.83	16/5733 (0.3%)
1	V	0.46	0/4202	0.83	16/5733 (0.3%)
1	W	0.46	0/4202	0.83	16/5733 (0.3%)
1	X	0.46	0/4202	0.83	16/5733 (0.3%)
1	Y	0.46	0/4202	0.83	16/5733 (0.3%)
1	Z	0.46	0/4202	0.83	16/5733 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.46	0/4202	0.83	16/5733 (0.3%)
1	b	0.46	0/4202	0.83	16/5733 (0.3%)
1	c	0.46	0/4202	0.83	16/5733 (0.3%)
1	d	0.46	0/4202	0.83	16/5733 (0.3%)
1	e	0.46	0/4202	0.83	16/5733 (0.3%)
1	f	0.46	0/4202	0.83	16/5733 (0.3%)
1	g	0.46	0/4202	0.83	16/5733 (0.3%)
1	h	0.46	0/4202	0.83	16/5733 (0.3%)
1	i	0.46	0/4202	0.83	16/5733 (0.3%)
1	j	0.46	0/4202	0.83	16/5733 (0.3%)
1	k	0.46	0/4202	0.83	16/5733 (0.3%)
1	l	0.46	0/4202	0.83	16/5733 (0.3%)
1	m	0.46	0/4202	0.83	16/5733 (0.3%)
1	n	0.46	0/4202	0.83	16/5733 (0.3%)
1	o	0.46	0/4202	0.83	16/5733 (0.3%)
1	p	0.46	0/4202	0.83	16/5733 (0.3%)
1	q	0.46	0/4202	0.83	16/5733 (0.3%)
1	r	0.46	0/4202	0.83	16/5733 (0.3%)
1	s	0.46	0/4202	0.83	16/5733 (0.3%)
1	t	0.46	0/4202	0.83	16/5733 (0.3%)
1	u	0.46	0/4202	0.83	16/5733 (0.3%)
1	v	0.46	0/4202	0.83	16/5733 (0.3%)
1	w	0.46	0/4202	0.83	16/5733 (0.3%)
1	x	0.46	0/4202	0.83	16/5733 (0.3%)
1	y	0.46	0/4202	0.83	16/5733 (0.3%)
1	z	0.46	0/4202	0.83	16/5733 (0.3%)
All	All	0.46	0/252120	0.83	960/343980 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	0	7
1	2	0	7
1	3	0	7
1	4	0	7
1	5	0	7
1	6	0	7
1	7	0	7
1	8	0	7

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7
1	B	0	7
1	C	0	7
1	D	0	7
1	E	0	7
1	F	0	7
1	G	0	7
1	H	0	7
1	I	0	7
1	J	0	7
1	K	0	7
1	L	0	7
1	M	0	7
1	N	0	7
1	O	0	7
1	P	0	7
1	Q	0	7
1	R	0	7
1	S	0	7
1	T	0	7
1	U	0	7
1	V	0	7
1	W	0	7
1	X	0	7
1	Y	0	7
1	Z	0	7
1	a	0	7
1	b	0	7
1	c	0	7
1	d	0	7
1	e	0	7
1	f	0	7
1	g	0	7
1	h	0	7
1	i	0	7
1	j	0	7
1	k	0	7
1	l	0	7
1	m	0	7
1	n	0	7
1	o	0	7
1	p	0	7

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	q	0	7
1	r	0	7
1	s	0	7
1	t	0	7
1	u	0	7
1	v	0	7
1	w	0	7
1	x	0	7
1	y	0	7
1	z	0	7
All	All	0	420

There are no bond length outliers.

The worst 5 of 960 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	k	517	LYS	N-CA-C	10.88	126.77	113.38
1	G	517	LYS	N-CA-C	10.88	126.76	113.38
1	L	517	LYS	N-CA-C	10.88	126.76	113.38
1	S	517	LYS	N-CA-C	10.88	126.76	113.38
1	c	517	LYS	N-CA-C	10.88	126.76	113.38

There are no chirality outliers.

5 of 420 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	223	GLU	Peptide
1	A	342	PRO	Peptide
1	A	343	PRO	Peptide
1	A	380	LEU	Peptide
1	A	79	SER	Peptide

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.

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	4077	0	3878	342	0
1	2	4077	0	3878	350	0
1	3	4077	0	3878	349	0
1	4	4077	0	3878	341	0
1	5	4077	0	3878	345	0
1	6	4077	0	3878	345	0
1	7	4077	0	3878	345	0
1	8	4077	0	3878	341	0
1	A	4077	0	3878	347	0
1	B	4077	0	3878	350	0
1	C	4077	0	3878	343	0
1	D	4077	0	3878	343	0
1	E	4077	0	3878	346	0
1	F	4077	0	3878	354	0
1	G	4077	0	3878	339	0
1	H	4077	0	3878	347	0
1	I	4077	0	3878	352	0
1	J	4077	0	3878	348	0
1	K	4077	0	3878	339	0
1	L	4077	0	3878	344	0
1	M	4077	0	3878	340	0
1	N	4077	0	3878	347	0
1	O	4077	0	3878	347	0
1	P	4077	0	3878	346	0
1	Q	4077	0	3878	346	0
1	R	4077	0	3878	355	0
1	S	4077	0	3878	344	0
1	T	4077	0	3878	344	0
1	U	4077	0	3878	343	0
1	V	4077	0	3878	349	0
1	W	4077	0	3878	345	0
1	X	4077	0	3878	340	0
1	Y	4077	0	3878	349	0
1	Z	4077	0	3878	345	0
1	a	4077	0	3878	340	0
1	b	4077	0	3878	340	0
1	c	4077	0	3878	348	0
1	d	4077	0	3878	354	0
1	e	4077	0	3878	346	0
1	f	4077	0	3878	347	0
1	g	4077	0	3878	345	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	h	4077	0	3878	346	0
1	i	4077	0	3878	345	0
1	j	4077	0	3878	349	0
1	k	4077	0	3878	350	0
1	l	4077	0	3878	346	0
1	m	4077	0	3878	346	0
1	n	4077	0	3878	343	0
1	o	4077	0	3878	345	0
1	p	4077	0	3878	348	0
1	q	4077	0	3878	354	0
1	r	4077	0	3878	347	0
1	s	4077	0	3878	339	0
1	t	4077	0	3878	339	0
1	u	4077	0	3878	344	0
1	v	4077	0	3878	341	0
1	w	4077	0	3878	337	0
1	x	4077	0	3878	341	0
1	y	4077	0	3878	339	0
1	z	4077	0	3878	349	0
All	All	244620	0	232680	17283	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 36.

The worst 5 of 17283 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:C:177:VAL:O	1:C:186:TRP:NE1	1.99	0.96
1:A:177:VAL:O	1:A:186:TRP:NE1	1.99	0.96
1:5:177:VAL:O	1:5:186:TRP:NE1	1.99	0.96
1:f:177:VAL:O	1:f:186:TRP:NE1	1.99	0.96
1:7:177:VAL:O	1:7:186:TRP:NE1	1.99	0.96

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	506/541 (94%)	407 (80%)	85 (17%)	14 (3%)	4	21
1	2	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	3	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	4	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	5	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	6	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	7	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	8	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	A	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	B	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	C	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	D	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	E	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	F	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	G	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	H	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	I	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	J	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	K	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	L	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	M	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	N	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	O	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	P	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	Q	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	S	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	T	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	U	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	V	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	W	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	X	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	Y	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	Z	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	a	506/541 (94%)	407 (80%)	85 (17%)	14 (3%)	4	21
1	b	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	c	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	d	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	e	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	f	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	g	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	h	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	i	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	j	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	k	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	l	506/541 (94%)	407 (80%)	85 (17%)	14 (3%)	4	21
1	m	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	n	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	o	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	p	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	q	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	r	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	s	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	t	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	u	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	v	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	w	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	x	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	y	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
1	z	506/541 (94%)	408 (81%)	84 (17%)	14 (3%)	4	21
All	All	30360/32460 (94%)	24477 (81%)	5043 (17%)	840 (3%)	6	21

5 of 840 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	213	ILE
1	A	356	ILE
1	B	213	ILE
1	B	356	ILE
1	C	213	ILE

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	449/471 (95%)	449 (100%)	0	100	100
1	2	449/471 (95%)	449 (100%)	0	100	100
1	3	449/471 (95%)	449 (100%)	0	100	100
1	4	449/471 (95%)	449 (100%)	0	100	100
1	5	449/471 (95%)	449 (100%)	0	100	100
1	6	449/471 (95%)	449 (100%)	0	100	100
1	7	449/471 (95%)	449 (100%)	0	100	100
1	8	449/471 (95%)	449 (100%)	0	100	100
1	A	449/471 (95%)	449 (100%)	0	100	100
1	B	449/471 (95%)	449 (100%)	0	100	100
1	C	449/471 (95%)	449 (100%)	0	100	100
1	D	449/471 (95%)	449 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	449/471 (95%)	449 (100%)	0	100	100
1	F	449/471 (95%)	449 (100%)	0	100	100
1	G	449/471 (95%)	449 (100%)	0	100	100
1	H	449/471 (95%)	449 (100%)	0	100	100
1	I	449/471 (95%)	449 (100%)	0	100	100
1	J	449/471 (95%)	449 (100%)	0	100	100
1	K	449/471 (95%)	449 (100%)	0	100	100
1	L	449/471 (95%)	449 (100%)	0	100	100
1	M	449/471 (95%)	449 (100%)	0	100	100
1	N	449/471 (95%)	449 (100%)	0	100	100
1	O	449/471 (95%)	449 (100%)	0	100	100
1	P	449/471 (95%)	449 (100%)	0	100	100
1	Q	449/471 (95%)	449 (100%)	0	100	100
1	R	449/471 (95%)	449 (100%)	0	100	100
1	S	449/471 (95%)	449 (100%)	0	100	100
1	T	449/471 (95%)	449 (100%)	0	100	100
1	U	449/471 (95%)	449 (100%)	0	100	100
1	V	449/471 (95%)	449 (100%)	0	100	100
1	W	449/471 (95%)	449 (100%)	0	100	100
1	X	449/471 (95%)	449 (100%)	0	100	100
1	Y	449/471 (95%)	449 (100%)	0	100	100
1	Z	449/471 (95%)	449 (100%)	0	100	100
1	a	449/471 (95%)	449 (100%)	0	100	100
1	b	449/471 (95%)	449 (100%)	0	100	100
1	c	449/471 (95%)	449 (100%)	0	100	100
1	d	449/471 (95%)	449 (100%)	0	100	100
1	e	449/471 (95%)	449 (100%)	0	100	100
1	f	449/471 (95%)	449 (100%)	0	100	100
1	g	449/471 (95%)	449 (100%)	0	100	100
1	h	449/471 (95%)	449 (100%)	0	100	100
1	i	449/471 (95%)	449 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	j	449/471 (95%)	449 (100%)	0	100	100
1	k	449/471 (95%)	449 (100%)	0	100	100
1	l	449/471 (95%)	449 (100%)	0	100	100
1	m	449/471 (95%)	449 (100%)	0	100	100
1	n	449/471 (95%)	449 (100%)	0	100	100
1	o	449/471 (95%)	449 (100%)	0	100	100
1	p	449/471 (95%)	449 (100%)	0	100	100
1	q	449/471 (95%)	449 (100%)	0	100	100
1	r	449/471 (95%)	449 (100%)	0	100	100
1	s	449/471 (95%)	449 (100%)	0	100	100
1	t	449/471 (95%)	449 (100%)	0	100	100
1	u	449/471 (95%)	449 (100%)	0	100	100
1	v	449/471 (95%)	449 (100%)	0	100	100
1	w	449/471 (95%)	449 (100%)	0	100	100
1	x	449/471 (95%)	449 (100%)	0	100	100
1	y	449/471 (95%)	449 (100%)	0	100	100
1	z	449/471 (95%)	449 (100%)	0	100	100
All	All	26940/28260 (95%)	26940 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1160 such sidechains are listed below:

Mol	Chain	Res	Type
1	p	538	ASN
1	8	102	GLN
1	r	164	HIS
1	p	536	ASN
1	v	248	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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.

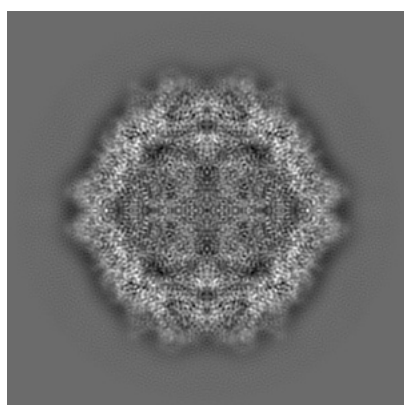
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8605. These allow visual inspection of the internal detail of the map and identification of artifacts.

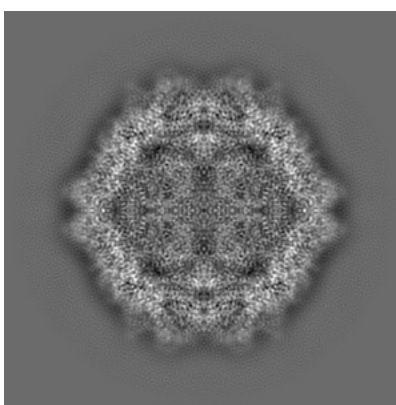
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

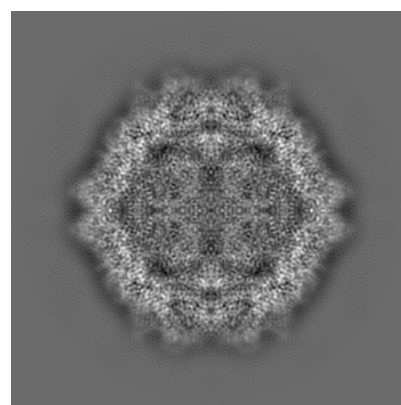
6.1.1 Primary map



X



Y

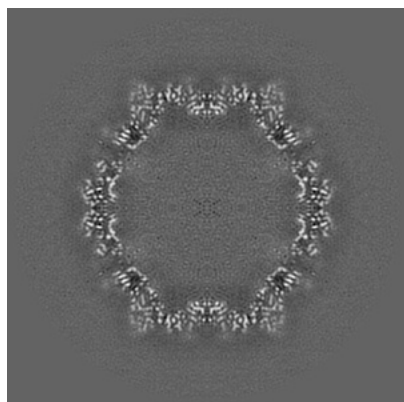


Z

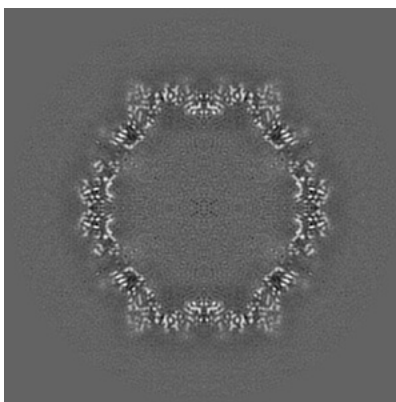
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

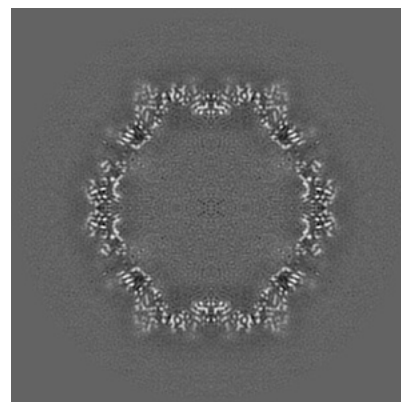
6.2.1 Primary map



X Index: 199



Y Index: 199

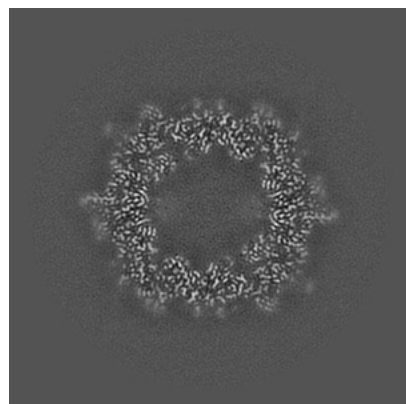


Z Index: 199

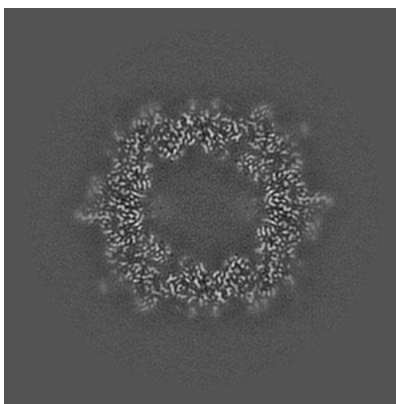
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

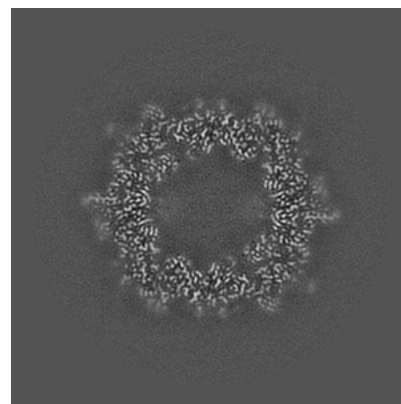
6.3.1 Primary map



X Index: 269



Y Index: 129

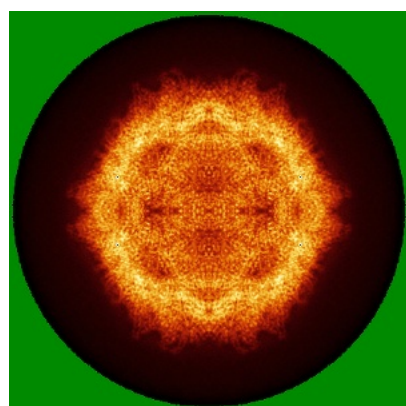


Z Index: 269

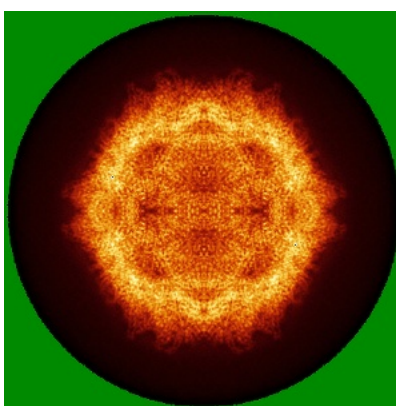
The images above show the largest variance slices of the map in three orthogonal directions.

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

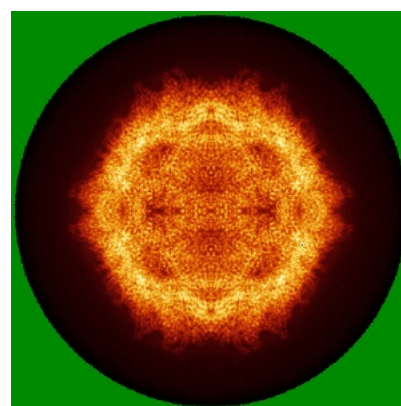
6.4.1 Primary map



X



Y

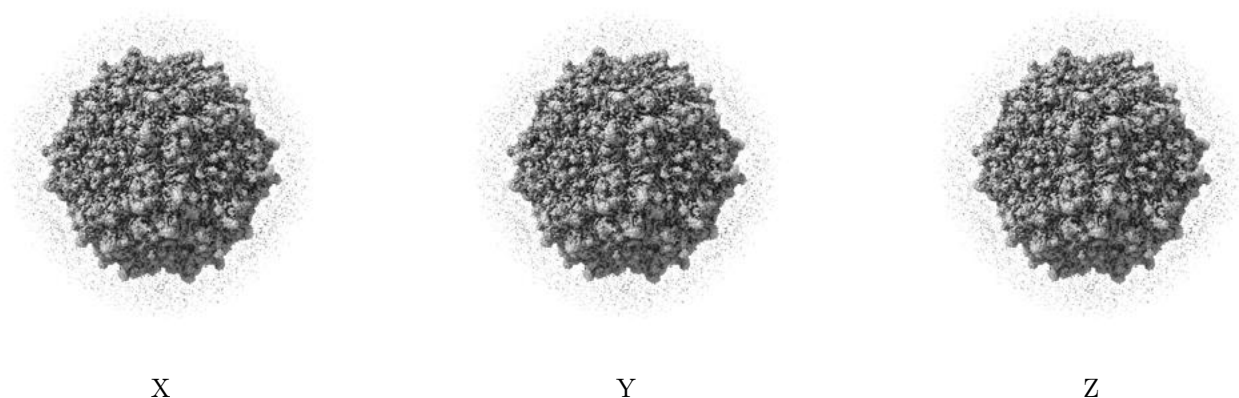


Z

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.

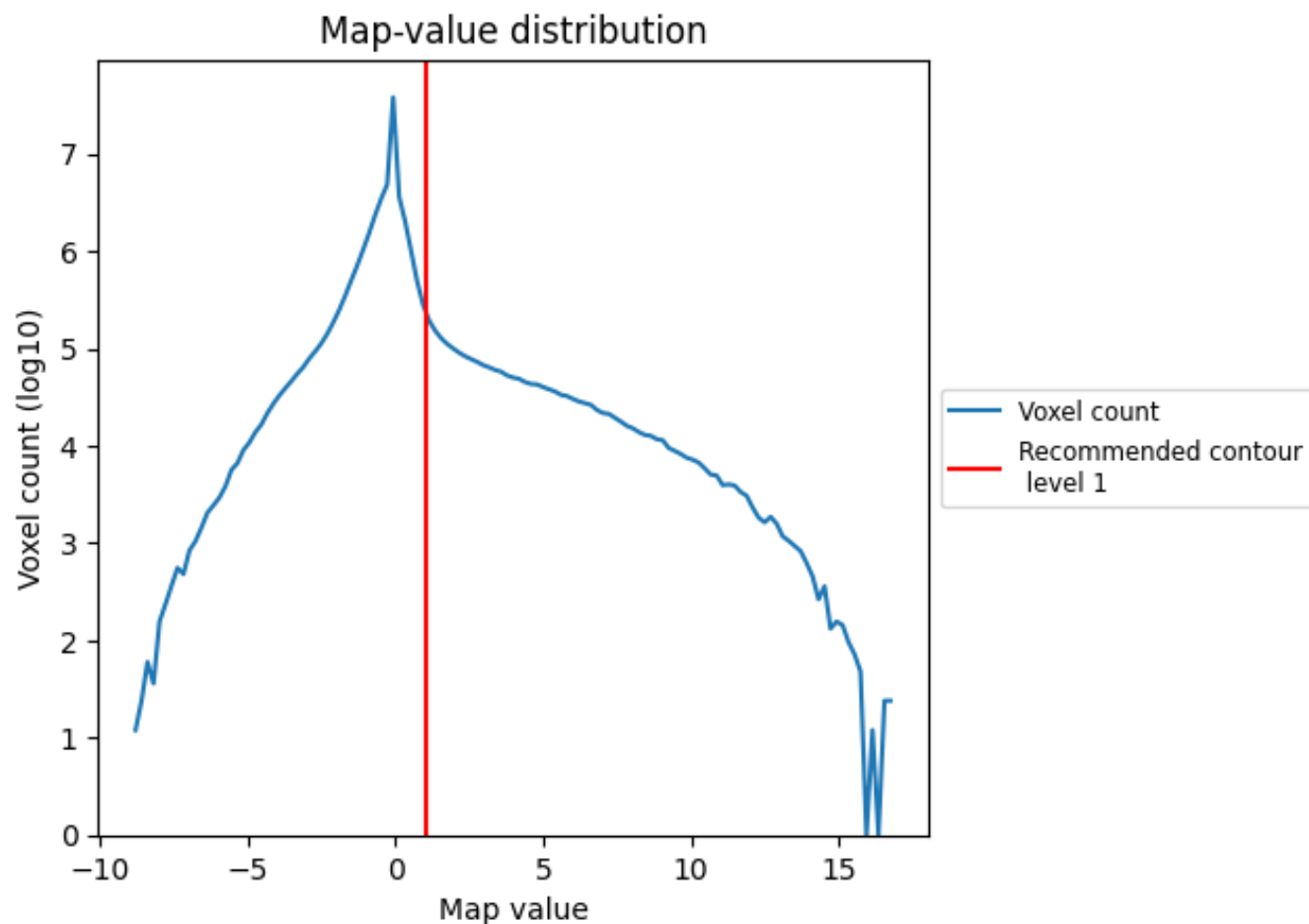
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

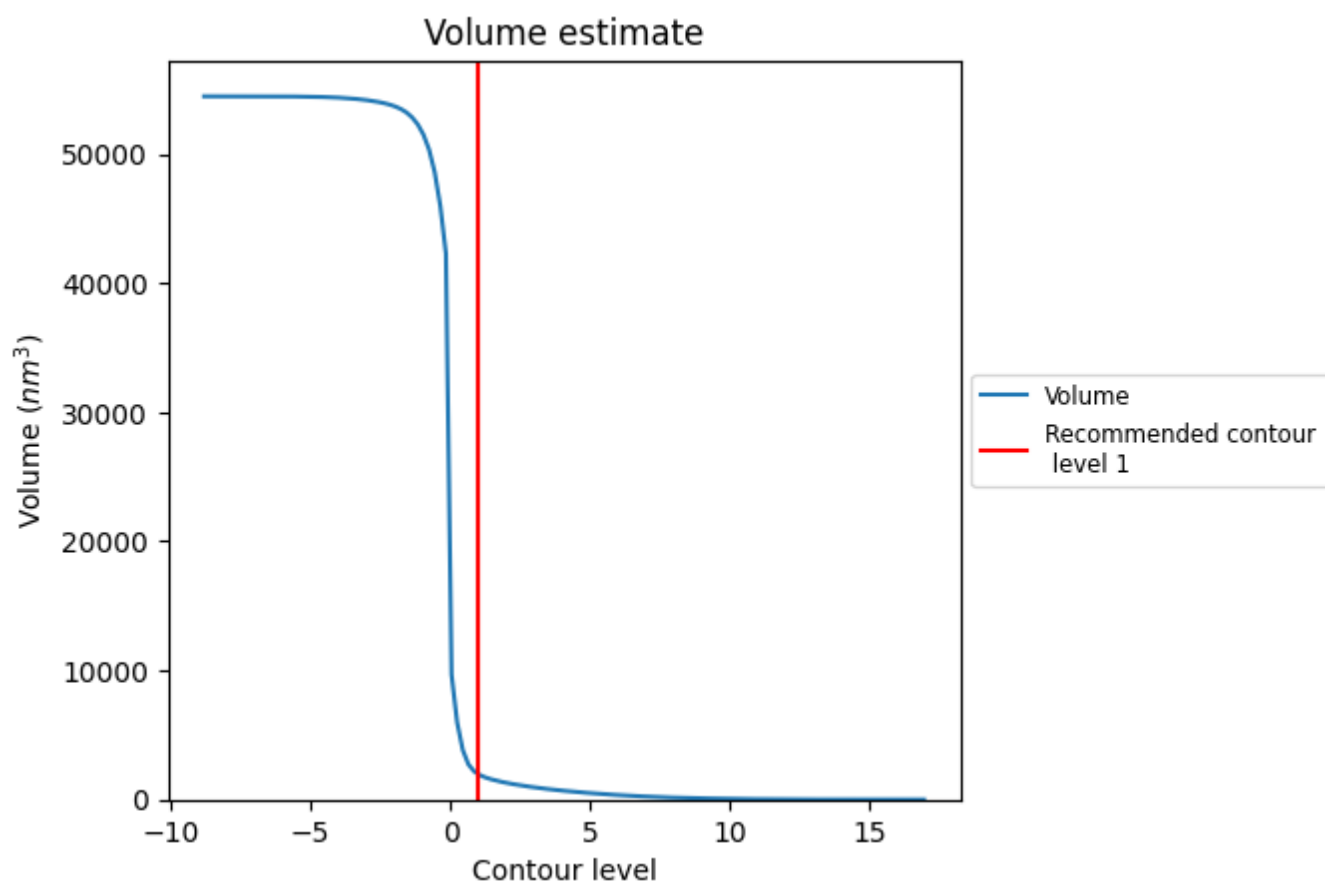
This section contains the results of statistical analysis of the map.

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.

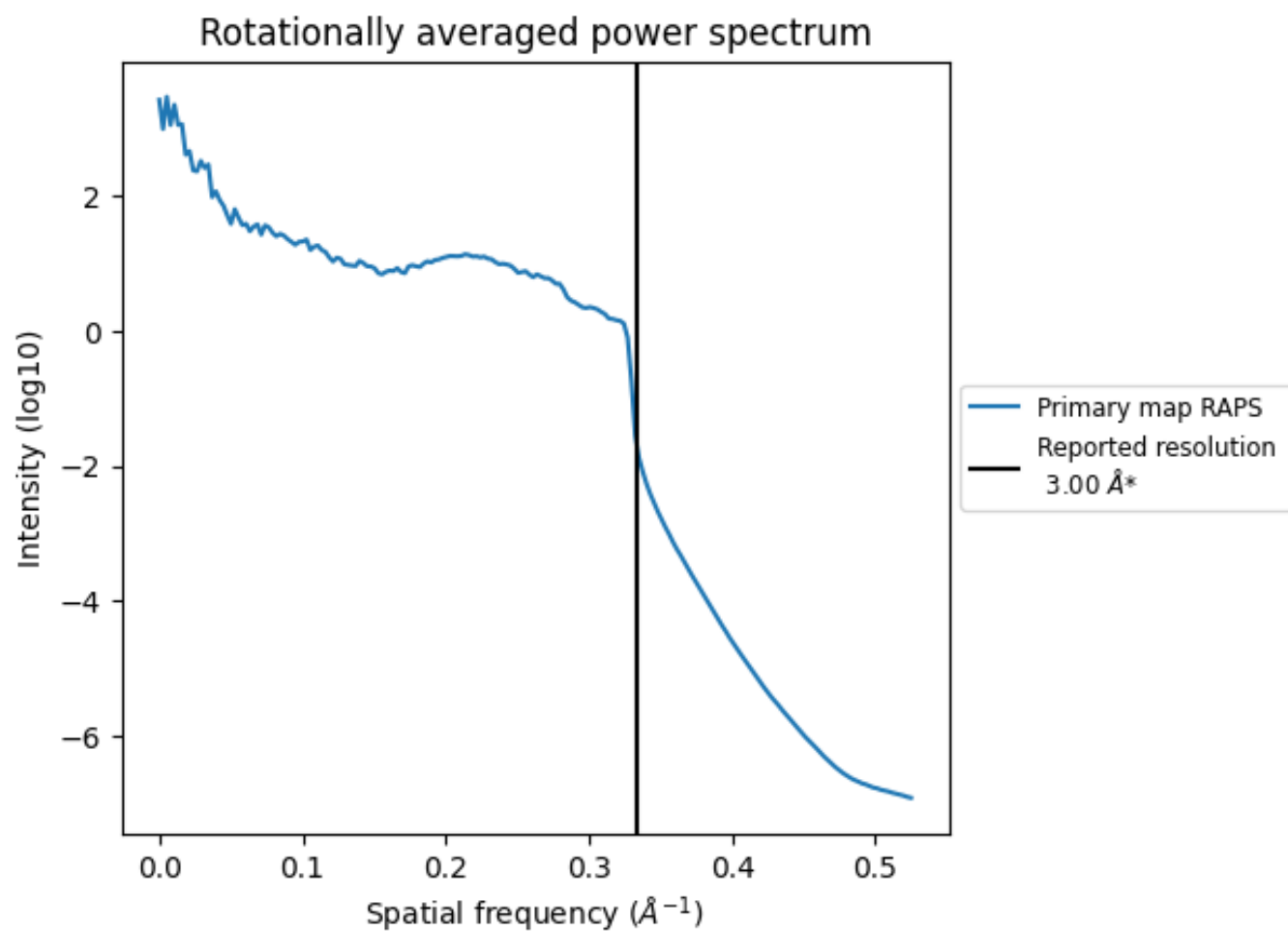
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1984 nm³; this corresponds to an approximate mass of 1793 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 0.333 Å⁻¹

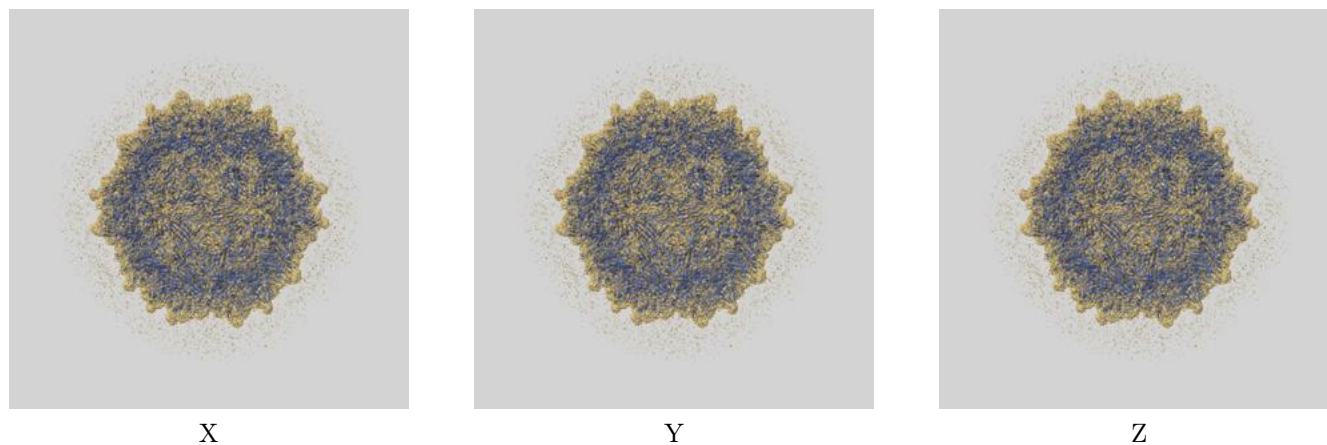
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

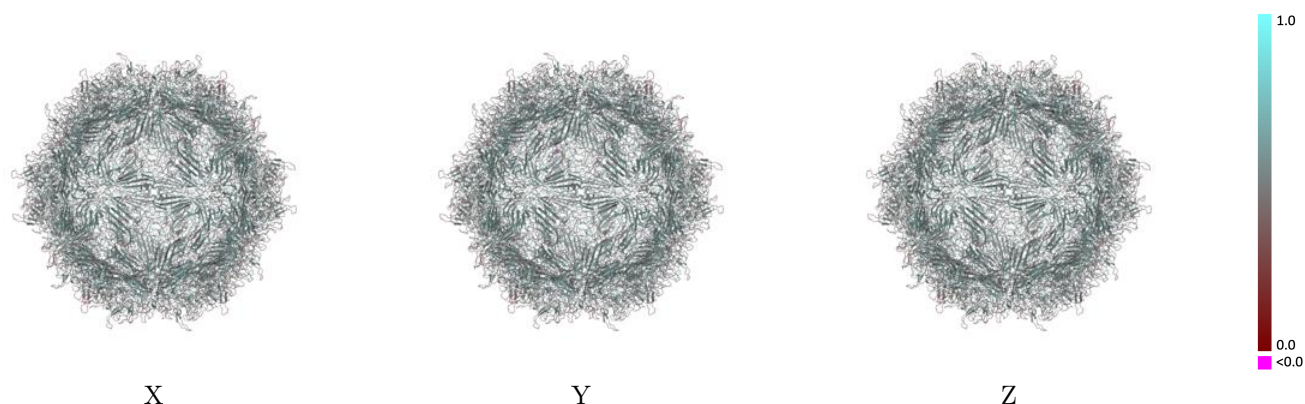
This section contains information regarding the fit between EMDB map EMD-8605 and PDB model 5US9. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



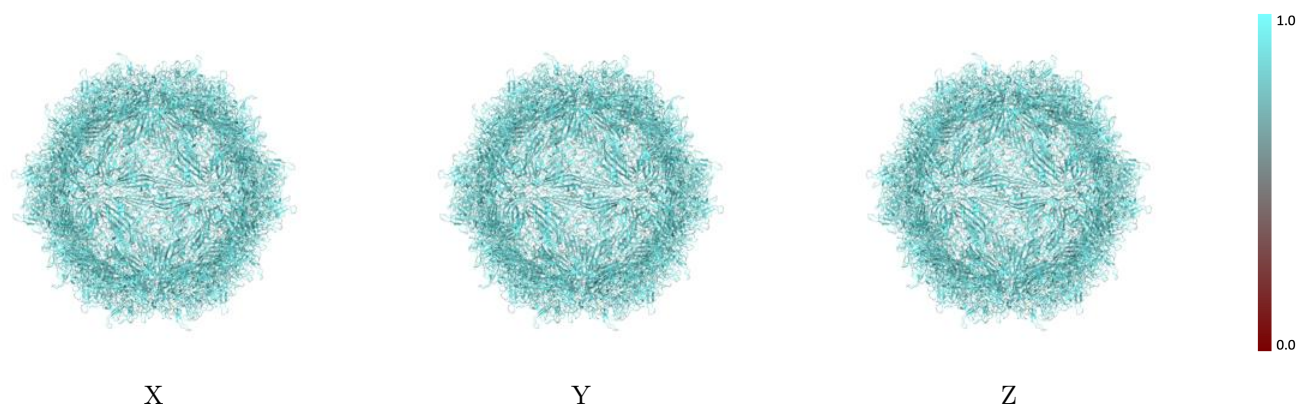
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



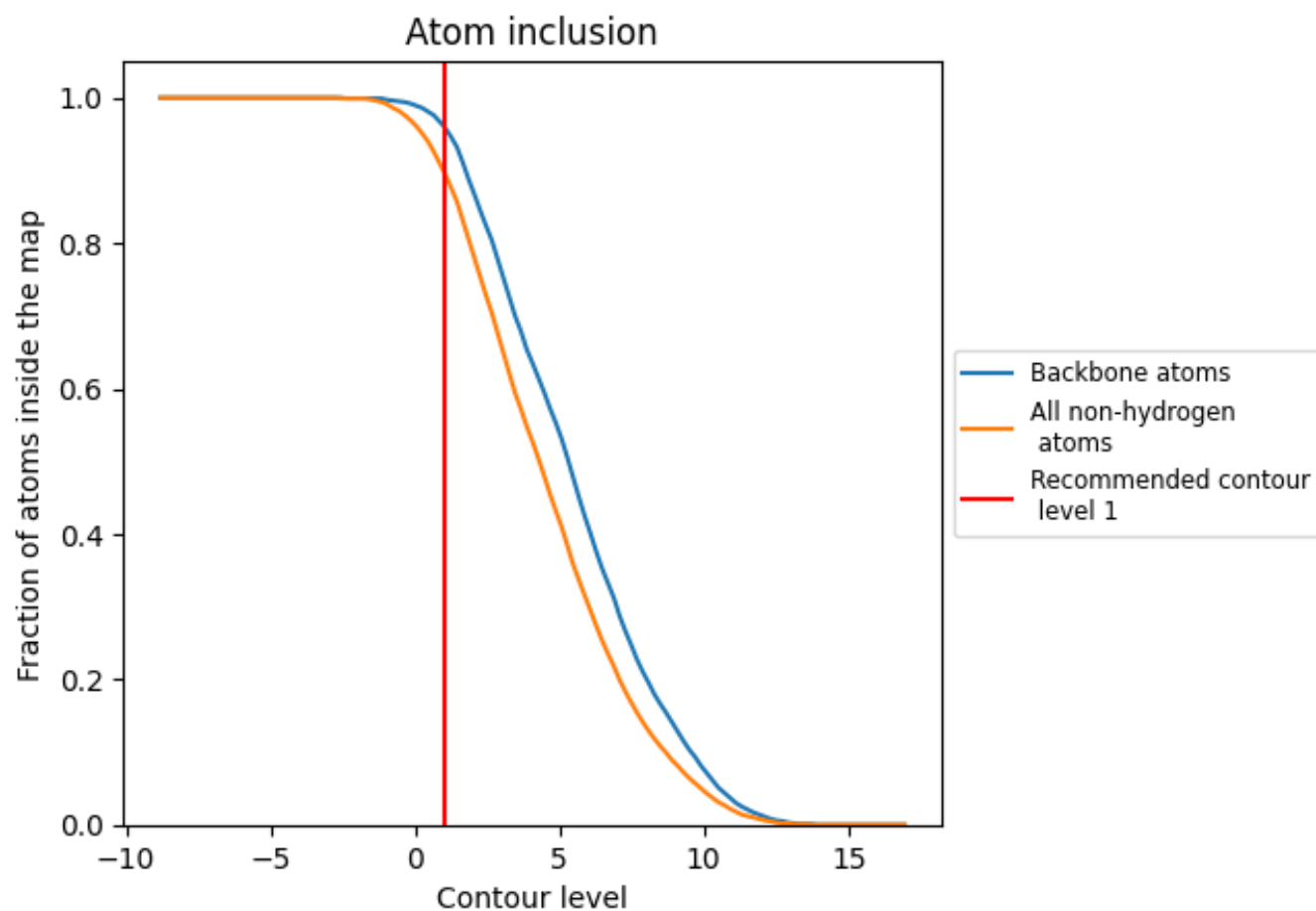
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 96% of all backbone atoms, 90% 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	 0.8990	 0.5170
1	 0.9000	 0.5160
2	 0.8980	 0.5170
3	 0.8990	 0.5170
4	 0.8980	 0.5180
5	 0.8970	 0.5170
6	 0.9000	 0.5180
7	 0.8970	 0.5190
8	 0.9000	 0.5170
A	 0.8970	 0.5180
B	 0.8990	 0.5170
C	 0.8980	 0.5180
D	 0.8990	 0.5170
E	 0.9000	 0.5180
F	 0.9000	 0.5180
G	 0.8990	 0.5170
H	 0.8980	 0.5160
I	 0.8990	 0.5160
J	 0.8970	 0.5170
K	 0.9000	 0.5170
L	 0.8990	 0.5170
M	 0.8980	 0.5170
N	 0.8990	 0.5170
O	 0.8990	 0.5180
P	 0.8970	 0.5190
Q	 0.9000	 0.5180
R	 0.8970	 0.5170
S	 0.9000	 0.5170
T	 0.8980	 0.5180
U	 0.9000	 0.5180
V	 0.8990	 0.5170
W	 0.8980	 0.5180
X	 0.8990	 0.5170
Y	 0.8980	 0.5170
Z	 0.8990	 0.5160



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Chain	Atom inclusion	Q-score
a	 0.9000	 0.5170
b	 0.9000	 0.5180
c	 0.8990	 0.5160
d	 0.8990	 0.5160
e	 0.8970	 0.5160
f	 0.8980	 0.5160
g	 0.8970	 0.5190
h	 0.8990	 0.5160
i	 0.8990	 0.5180
j	 0.8970	 0.5170
k	 0.9000	 0.5170
l	 0.9000	 0.5160
m	 0.9000	 0.5180
n	 0.8980	 0.5170
o	 0.8980	 0.5170
p	 0.8980	 0.5170
q	 0.8990	 0.5160
r	 0.8970	 0.5170
s	 0.8990	 0.5160
t	 0.8970	 0.5180
u	 0.8990	 0.5160
v	 0.8990	 0.5180
w	 0.8970	 0.5180
x	 0.8990	 0.5160
y	 0.8990	 0.5180
z	 0.8990	 0.5160