



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 06:17 AM UTC

PDB ID : 6B9Q / pdb_00006b9q
EMDB ID : EMD-7071
Title : Single particle cryo-EM structure determination of the LuIII capsid protein
Authors : Pittman, N.C.; Agbandje-McKenna, M.
Deposited on : 2017-10-11
Resolution : 3.17 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:

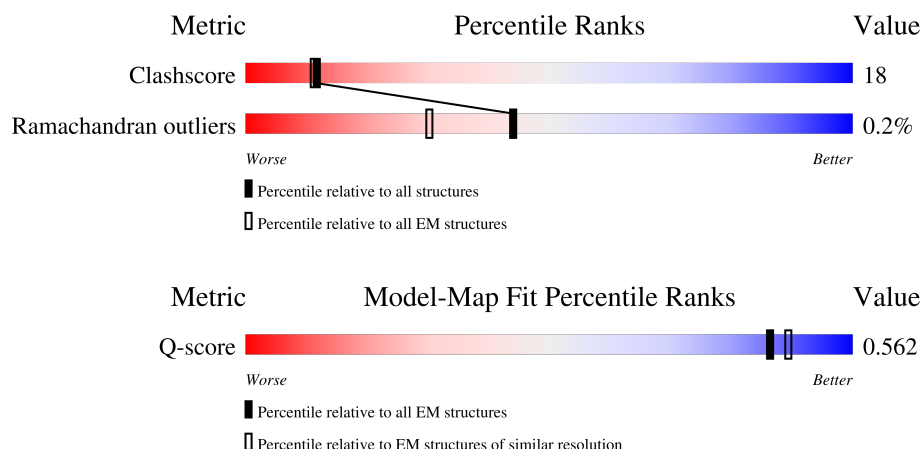
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.17 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	14465 (2.67 - 3.67)

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	587	59% 35% 6%
1	2	587	58% 35% 6%
1	3	587	58% 36% 6%
1	4	587	59% 34% 6%
1	5	587	58% 36% 6%

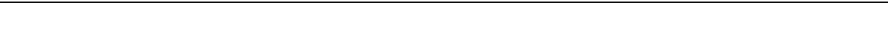
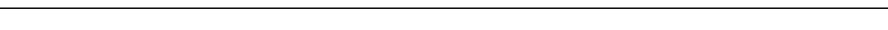
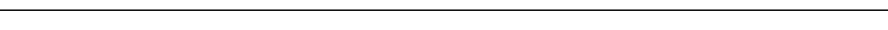
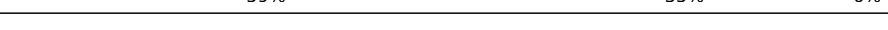
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Mol	Chain	Length	Quality of chain
1	6	587	
1	7	587	
1	8	587	
1	A	587	
1	B	587	
1	C	587	
1	D	587	
1	E	587	
1	F	587	
1	G	587	
1	H	587	
1	I	587	
1	J	587	
1	K	587	
1	L	587	
1	M	587	
1	N	587	
1	O	587	
1	P	587	
1	Q	587	
1	R	587	
1	S	587	
1	T	587	
1	U	587	
1	V	587	

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Mol	Chain	Length	Quality of chain
1	W	587	
1	X	587	
1	Y	587	
1	Z	587	
1	a	587	
1	b	587	
1	c	587	
1	d	587	
1	e	587	
1	f	587	
1	g	587	
1	h	587	
1	i	587	
1	j	587	
1	k	587	
1	l	587	
1	m	587	
1	n	587	
1	o	587	
1	p	587	
1	q	587	
1	r	587	
1	s	587	
1	t	587	
1	u	587	

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Mol	Chain	Length	Quality of chain
1	v	587	 59%35%6%
1	w	587	 59%35%6%
1	x	587	 59%35%6%
1	y	587	 59%35%6%
1	z	587	 58%35%6%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 263940 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	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	B	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	C	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	D	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	E	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	F	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	G	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	H	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	I	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	J	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	K	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	L	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	M	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	N	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	O	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	P	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		
1	Q	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	S	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	T	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	U	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	V	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	W	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	X	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	Y	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	Z	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	1	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	2	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	3	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	4	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	5	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	6	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	a	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	b	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	c	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	d	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	e	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	f	551	Total 4399	C 2766	N 773	O 845	S 15	1	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	g	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	h	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	i	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	j	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	k	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	l	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	m	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	n	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	o	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	p	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	q	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	r	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	s	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	t	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	u	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	v	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	w	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	x	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	y	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	z	551	Total 4399	C 2766	N 773	O 845	S 15	1	0
1	7	551	Total 4399	C 2766	N 773	O 845	S 15	1	0

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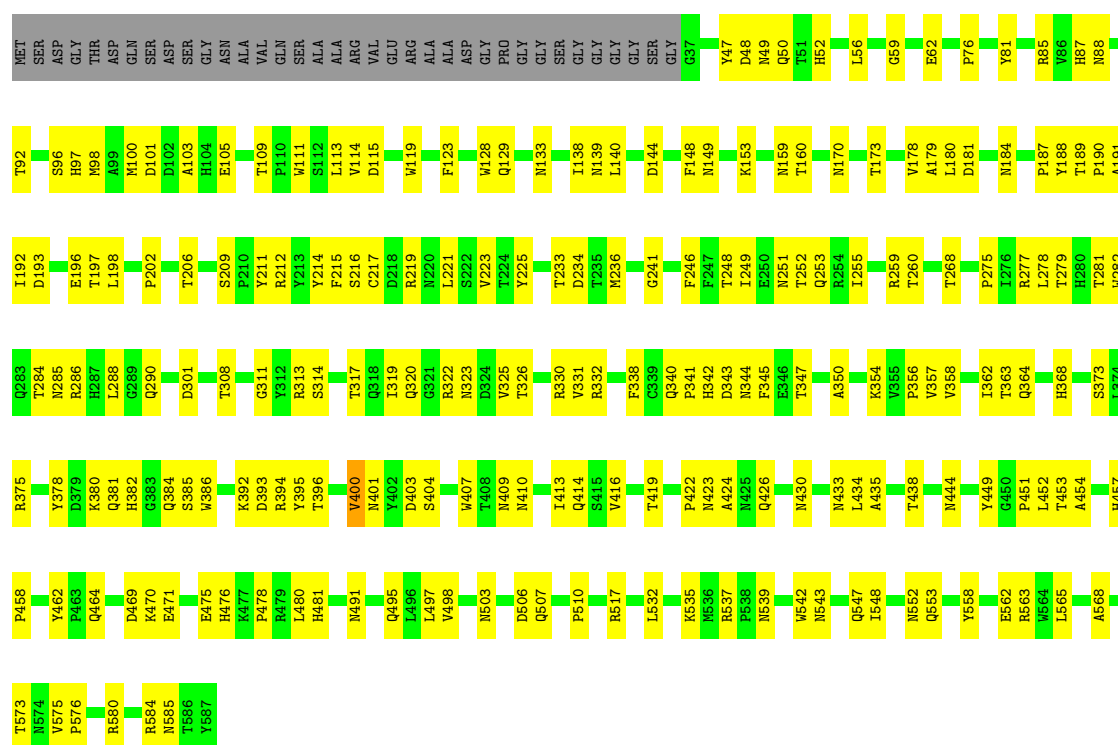
Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	551	Total	C	N	O	S	1	0
			4399	2766	773	845	15		

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.

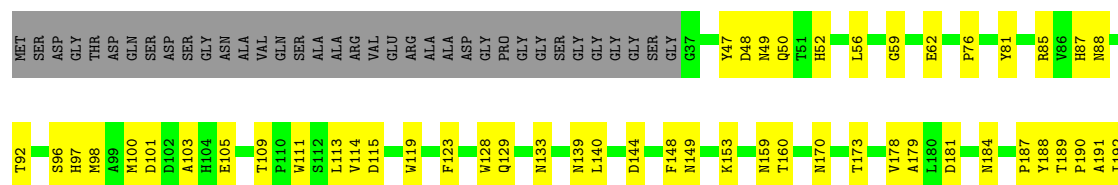
• Molecule 1: Capsid protein VP2

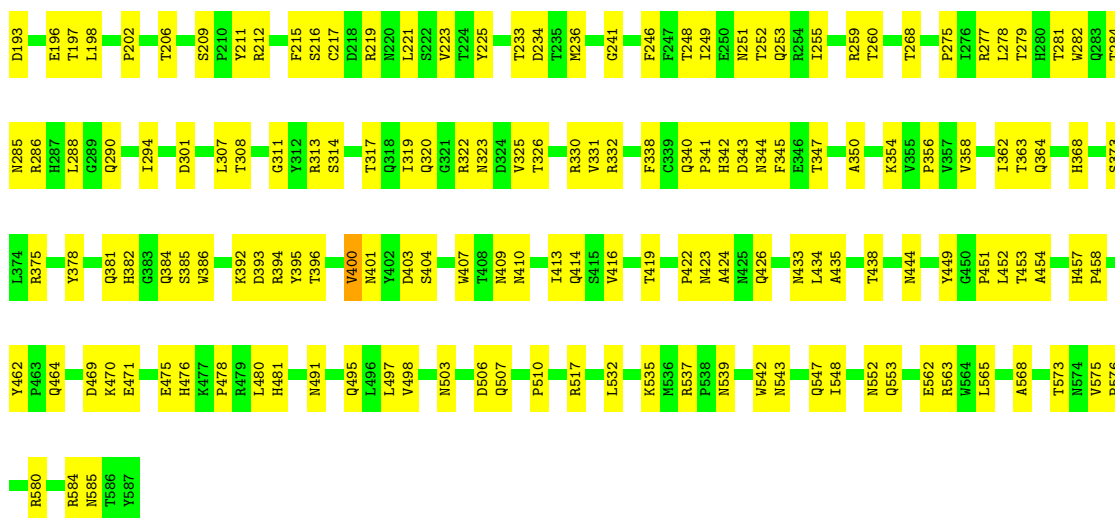
Chain A: 



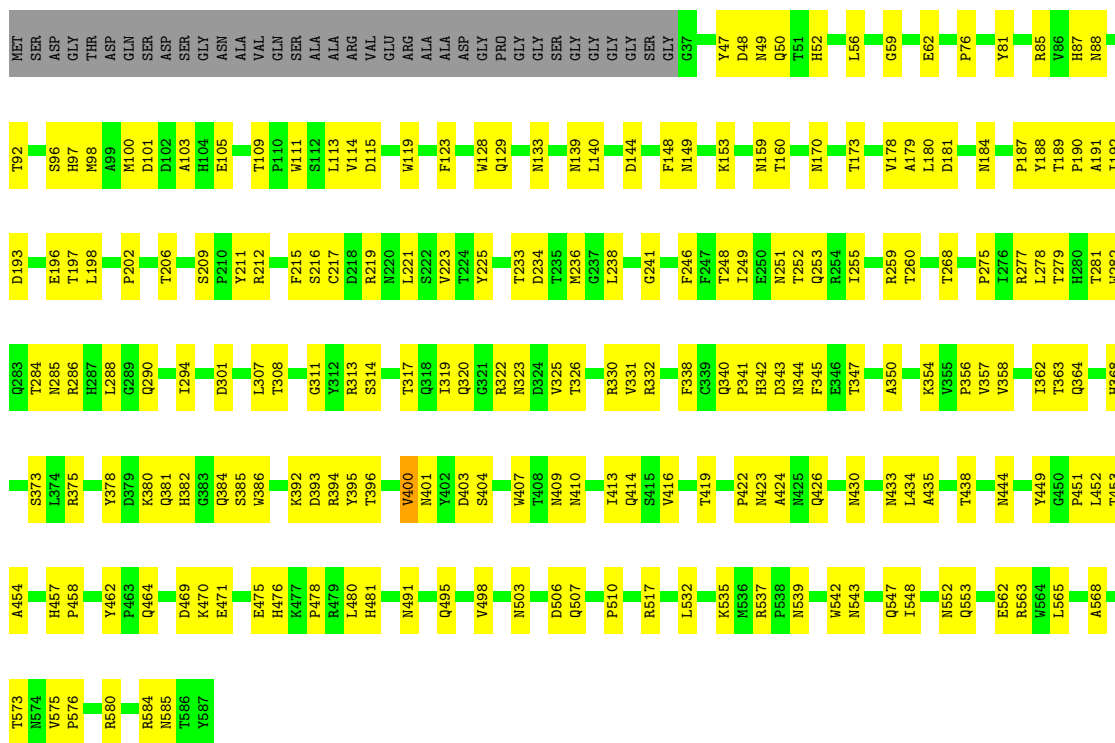
• Molecule 1: Capsid protein VP2

Chain B: 

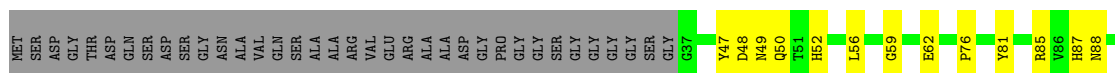


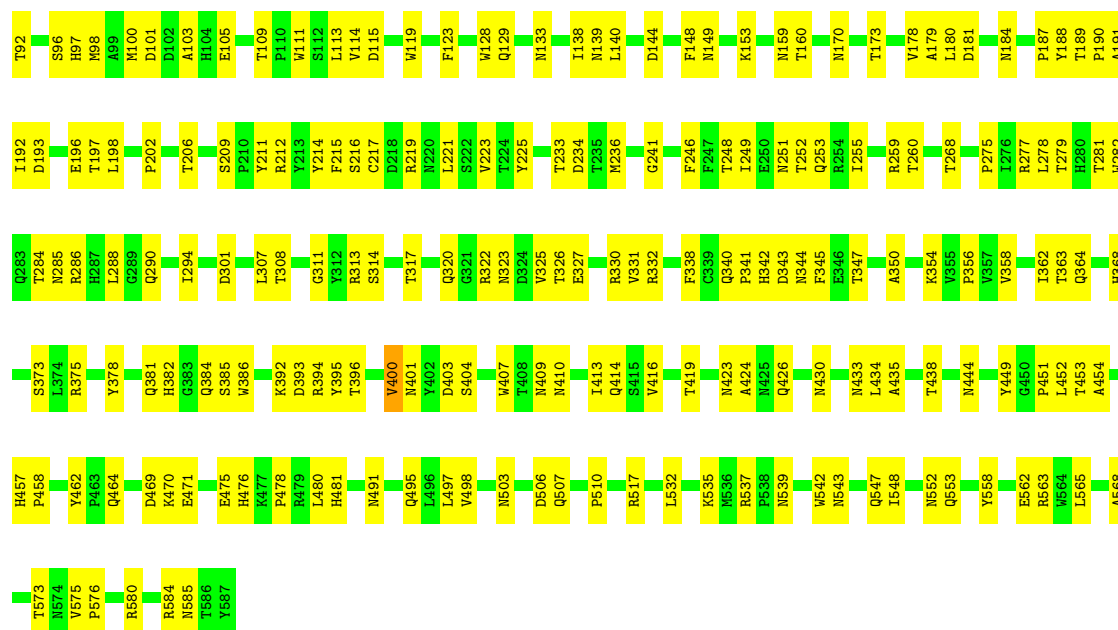


- Molecule 1: Capsid protein VP2



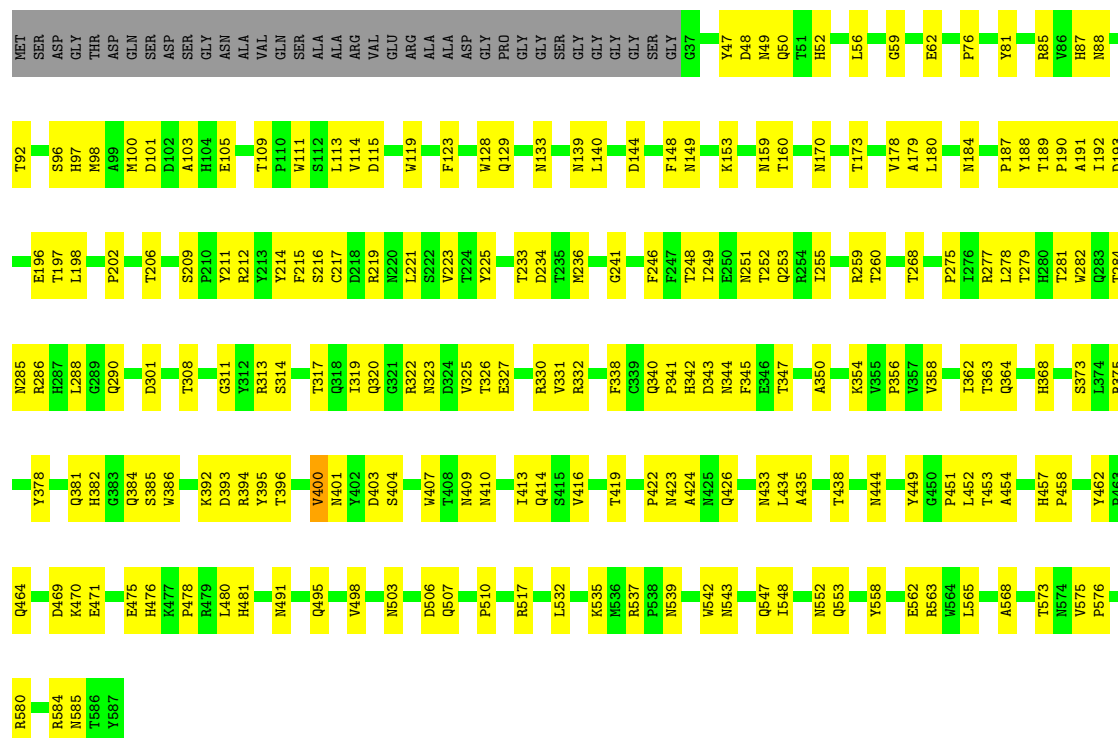
- Molecule 1: Capsid protein VP2





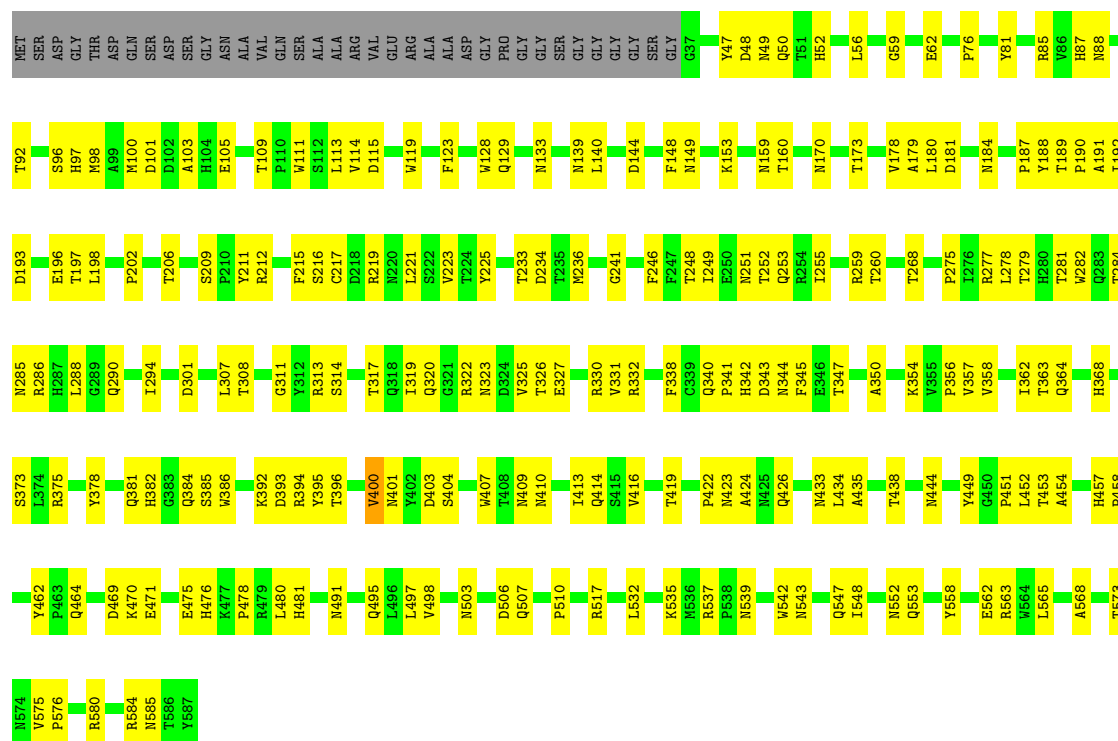
• Molecule 1: Capsid protein VP2

Chain E: 59% 35% 6%



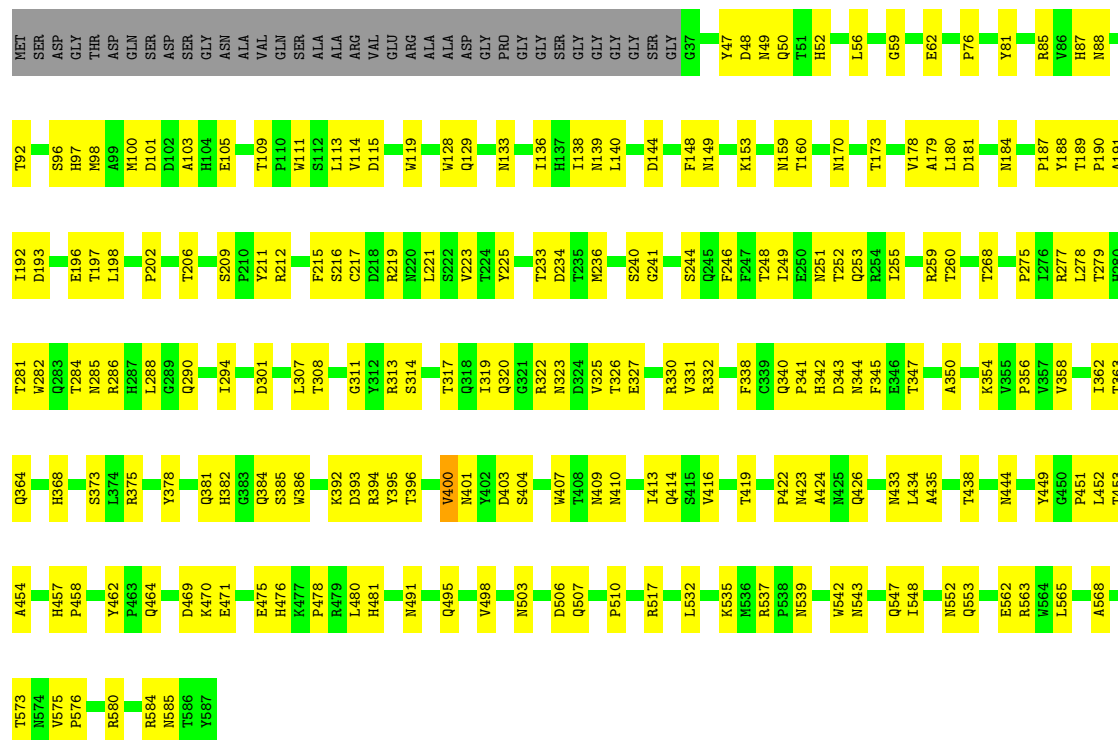
• Molecule 1: Capsid protein VP2

Chain F: 58% 35% 6%



• Molecule 1: Capsid protein VP2

Chain G: 58% 35% 6%



• Molecule 1: Capsid protein VP2

MET	T92	P190	T281	H368	P468	V575
	SR	A191	W282	S373	Y462	P576
	ASP	I192	Q283	S373	Y462	P576
	GLY	D193	T284	L374	P463	R580
	THR	N98	N285	R375	Q464	R580
	ASP	A99	R286			R584
	GLN	E196	H287	Y378	D469	N585
	GLN	T197	L288	Q381	K470	T586
	SR	D100	G289	H382	E471	Y587
	ASP	D102	Q290			
SR	A103	P202	H382	E471		
GLY	H104		G383	E475		
ASN	E105	T206	Q384	H476		
ALA			S385	K477		
VAL	T109	S209	W386	P478		
GLN	P110	P210	T308			
SR	W111	Y211	G311	K392	H481	
ALA	S112	R212	T312	D393	N491	
ALA	L113			R394		
ARG	W114	F215	S314	Y395	Q495	
VAL	D115	S216		T396		
GLU	C217					
ARG	W119	D218	T317	W400	V498	
ALA		R219	Q318	W401		
ALA	F123	W220	I319	Y402	N503	
ASP		L221	Q320	D403		
GLY	W128	S222	G321	S404	D506	
PRO	Q129	V223	R322		Q507	
GLY	T224	N224	W407	W408	P510	
GLY	Y225		D324	M409		
SR		T233	V325	M410	R517	
GLY	T136	D234	E327	Q414	L532	
GLY	H137	T235		S415		
GLY	N138	M236	R330	W416	K535	
GLY	N139		V331		R537	
SR	L140	G241	R332	T419		
GLY	D144					
G37		F246	F338	P422	P538	
Y47	F148	C247	C339	N423	N539	
D48	N149	T248	Q340	M424		
N49		I249	P341	N425	W542	
Q50	K153	E250	H342	Q426	N543	
T51	N251		D343			
H52	N159	T252	N344	N433	Q547	
L56	T160	Q253	E345	L434	I548	
		R254	T347	A435	N552	
	N170	I255			Q553	
G59			A350	T438	Y558	
E62	T173	R259	K354	N444		
P76	V178	T260	P355	Y449	E562	
	L180	Y269	V356		R563	
Y61	D181		V357	G450	W564	
		P275	V358	P451	L565	
R85	N184	T276		L452	A568	
V86	R277	L376	I362	T453		
H87	T278	R277	Q362	A454		
N88	Y188	T279	Q364		T573	
	T189	W290		W457	N574	

T573	A454	S373	T281	I192	T592	MET
N574	H457	L374	W282	D193	SER	GLY
V575	P458	R375	Q283	E196	ASP	ALA
R580	Y462	Y378	N285	T197	THR	GLN
			R286	L198	ASP	GLY
N584	P463	Q381	H287	P202	M100	GLN
V585	Q464	R382	L288	G289	D102	ASP
T586	D469	G383	G289	Q290	A103	SER
Y587	K470	S385	D301	T206	H104	GLY
	E471	W386		S209	E105	ASN
R590	E475	K392	T308	P210	T109	ALA
	H476	D393	G311	Y211	P110	VAL
N594	K477	R394		Y213	R212	GLN
V595	P478	Y395	Y312	Y214	SER	GLY
T596	E479	T396	R313	F215	S112	ALA
	L480	V400	S314	S216	L113	ALA
R598	H481	N401	T317	D218	V114	ARG
	N491	Y402	Q320	R219	D115	VAL
N599	Q495	D403	G321	N220	W119	GLU
V600	W498	S404	R322	L221	F123	ALA
T601	N503	W407	N323	S222	ASP	ALA
	D506	T408	D324	T223	GLY	GLY
Q507	N409	N410	V325	Y225	Q129	GLY
P510	I413	Q414	R330	T233	N133	GLY
R512	S415	V416	V331	D234	T138	SER
	R517	T419	R332	M236	N139	GLY
L522	K535	P422	F338	G241	L140	GLY
N525	M536	N423	C339	F246	D144	GLY
R527	R537	A424	Q341	K153	F148	GLY
P538	R538	Q426	H342	T248	D48	GLY
N539	N539	I427	D343	L249	N49	GLY
W542	W542	L428	N344	E250	Q50	GLY
N543	N430	T429	F345	N251	T160	GLY
Q547	Q547	N433	T347	T252	H52	GLY
I548	I548	L434	A350	Q253	N170	GLY
N552	N552	A435	R354	R254	L56	GLY
Q553	Q553	T438	V355	I255	T173	GLY
R562	E562	N444	V357	G59	V178	GLY
	R563	Y449	R362	E62	A179	GLY
N564	L565	G450	Q364	T260	L180	GLY
T566	A568	P451	V368	D181	P76	GLY
		L452	T268	N184	Y81	GLY
Y567		T452	I362	P276	R85	GLY
		T452	T363	I276	V86	GLY
		T452	Q364	R277	Y188	GLY
		T452	H368	T278	T189	GLY
		T452	H368	T279	P190	GLY
		T452	H368	H590	A192	GLY

Chain J: 59% 35% 6%



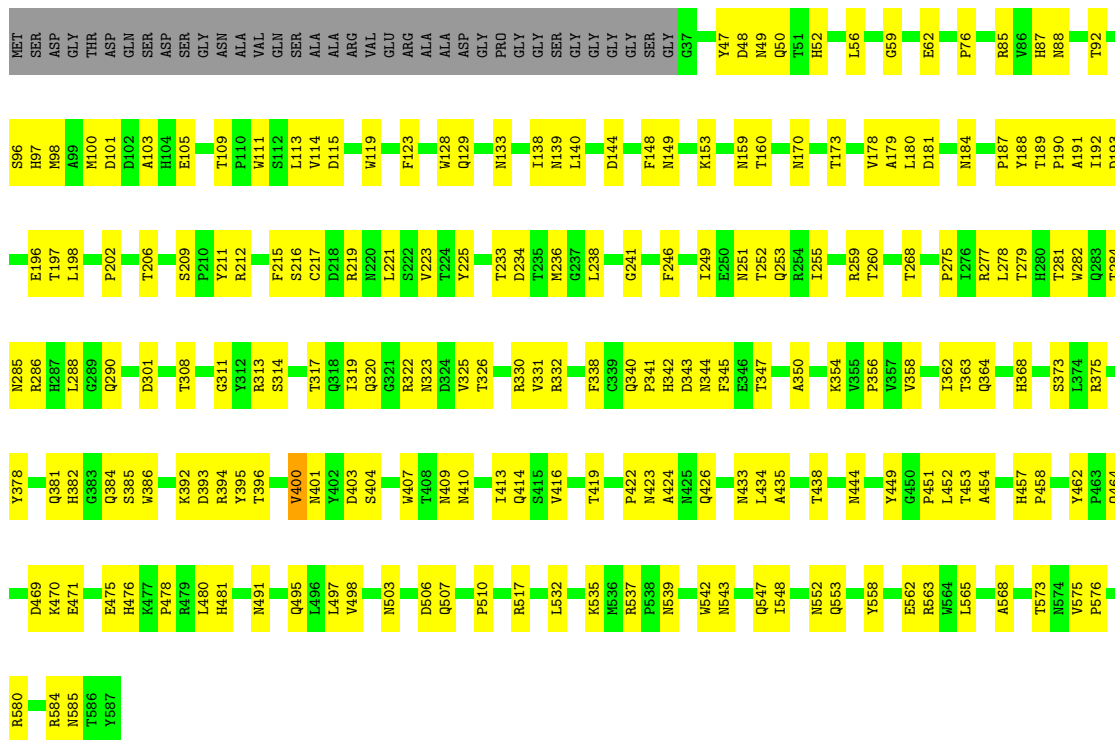
Chain K: 58% 35% 6%





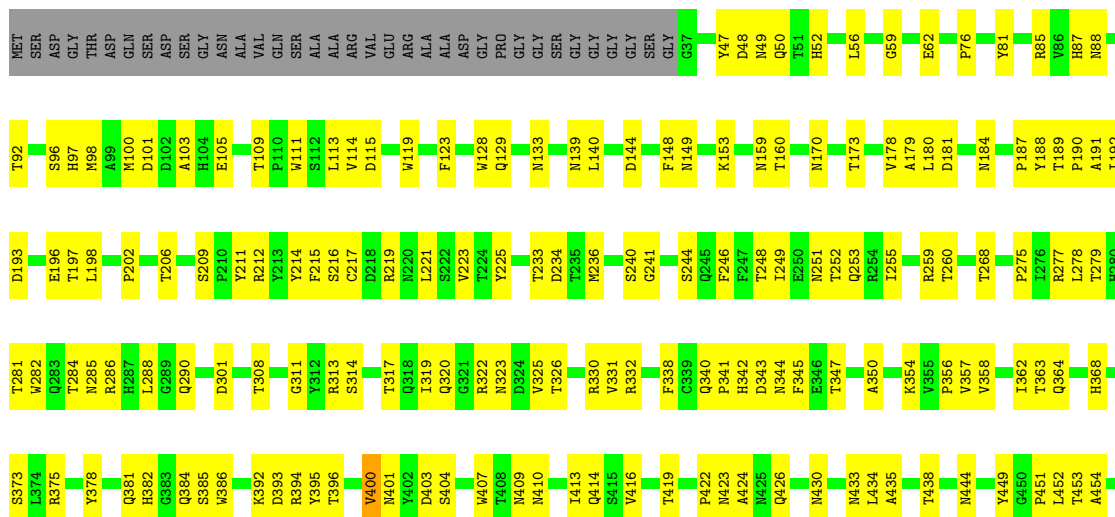
• Molecule 1: Capsid protein VP2

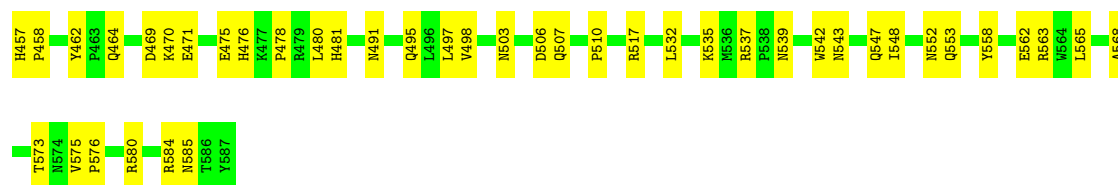
Chain L:  59% 35% 6%



• Molecule 1: Capsid protein VP2

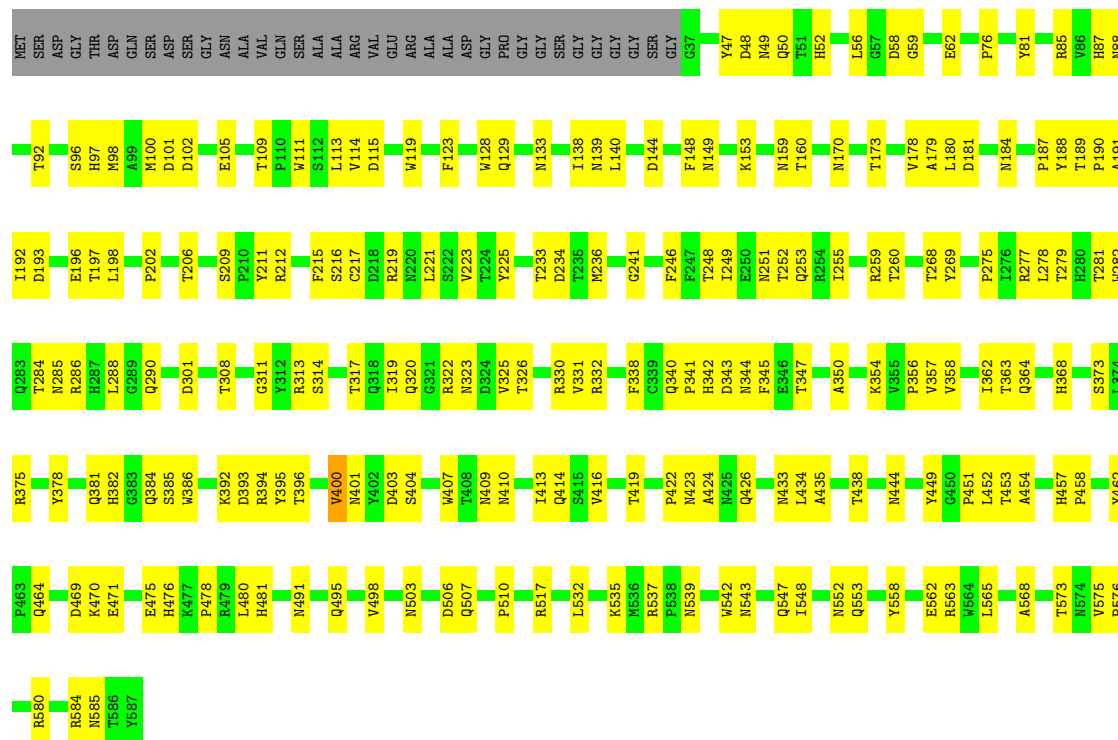
Chain M:  58% 35% 6%





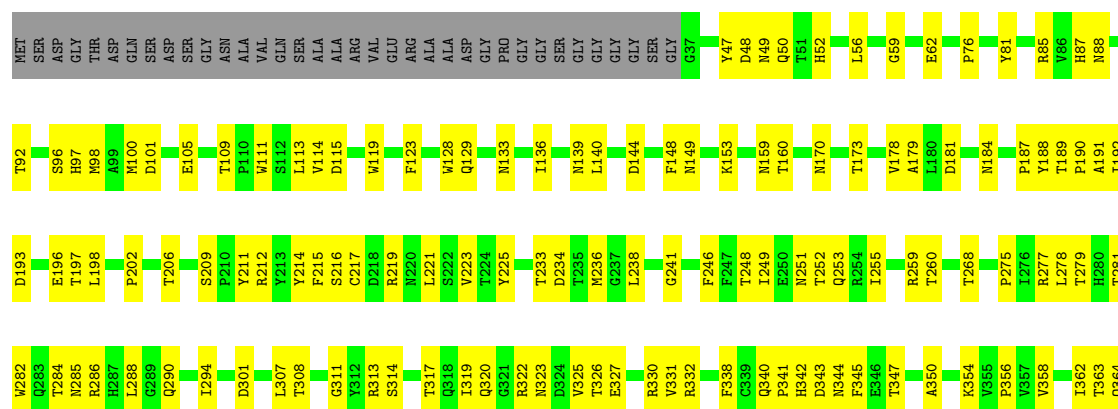
• Molecule 1: Capsid protein VP2

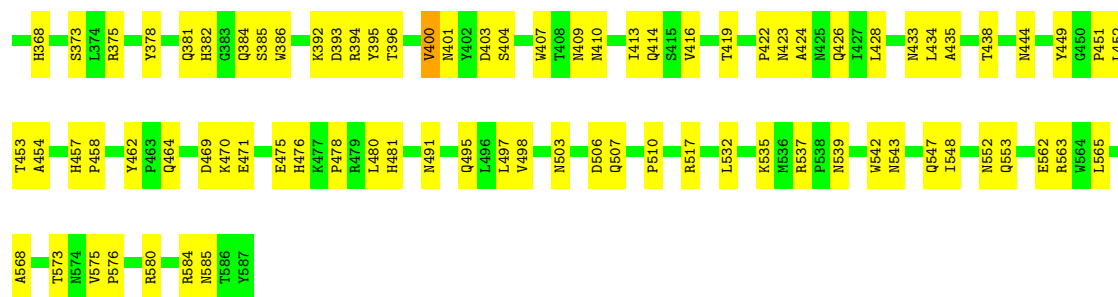
Chain N: 59% 35% 6%



• Molecule 1: Capsid protein VP2

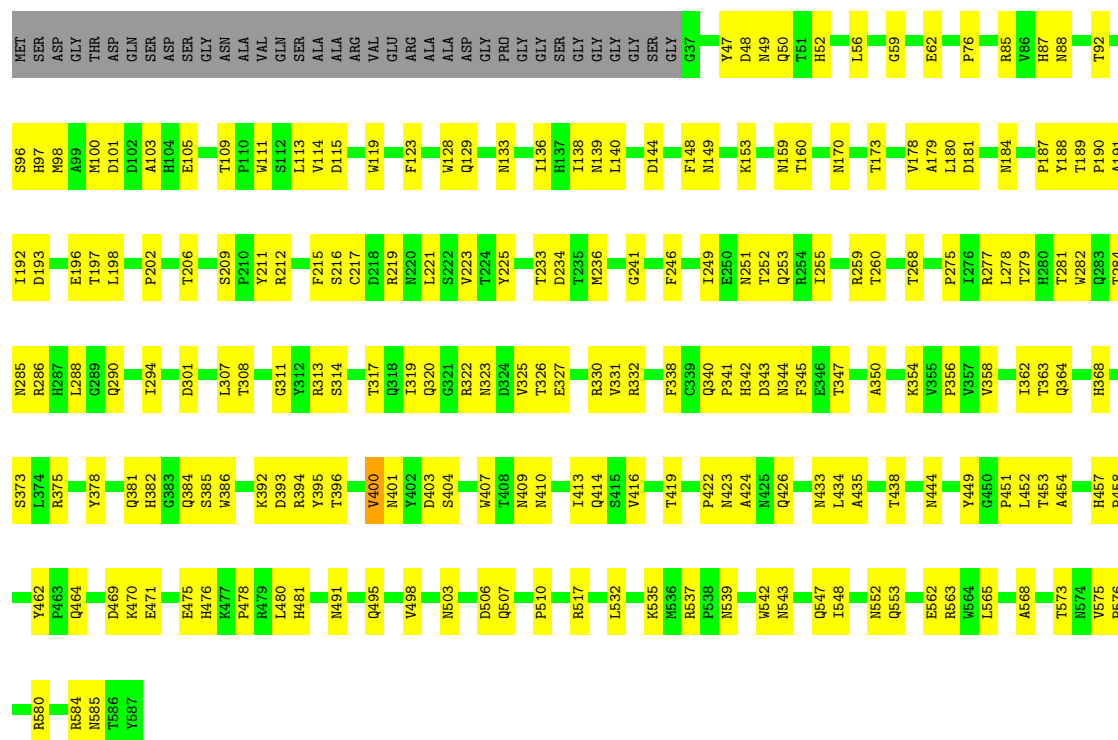
Chain O: 58% 35% 6%





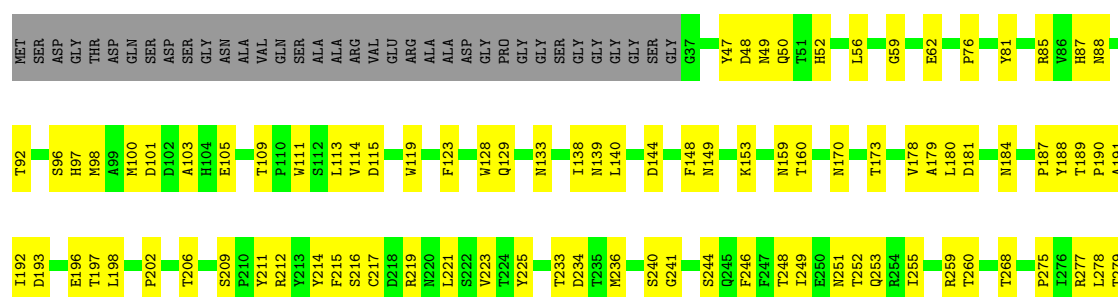
• Molecule 1: Capsid protein VP2

Chain P: 59% 35% 6%



• Molecule 1: Capsid protein VP2

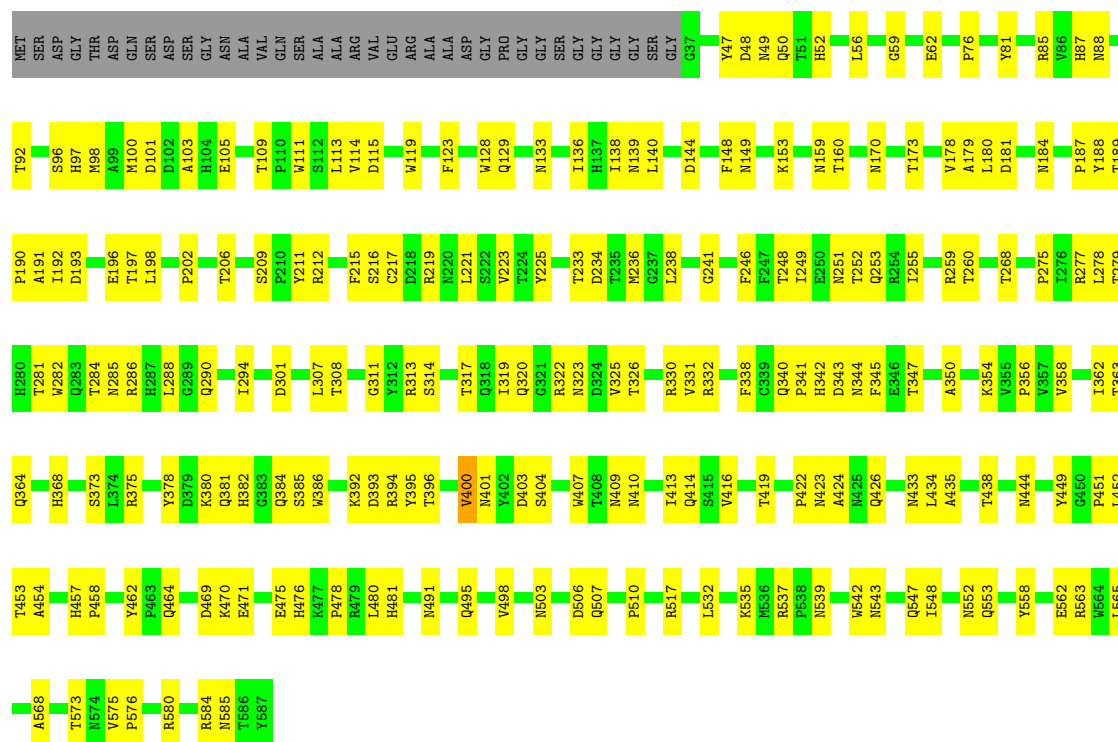
Chain Q: 58% 35% 6%





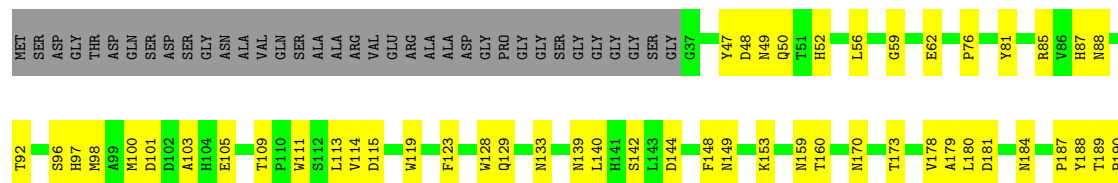
• Molecule 1: Capsid protein VP2

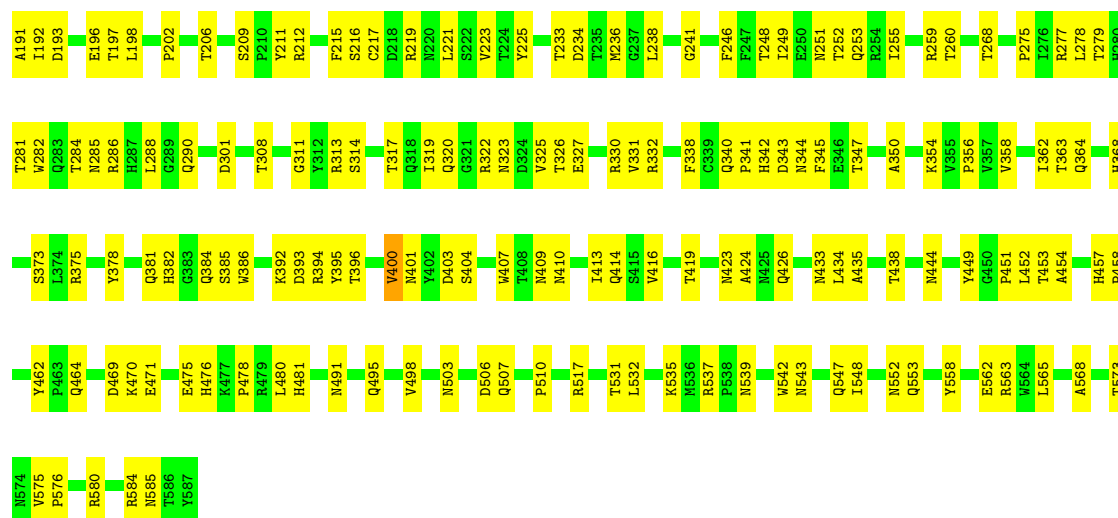
Chain R: 58% 35% 6%



• Molecule 1: Capsid protein VP2

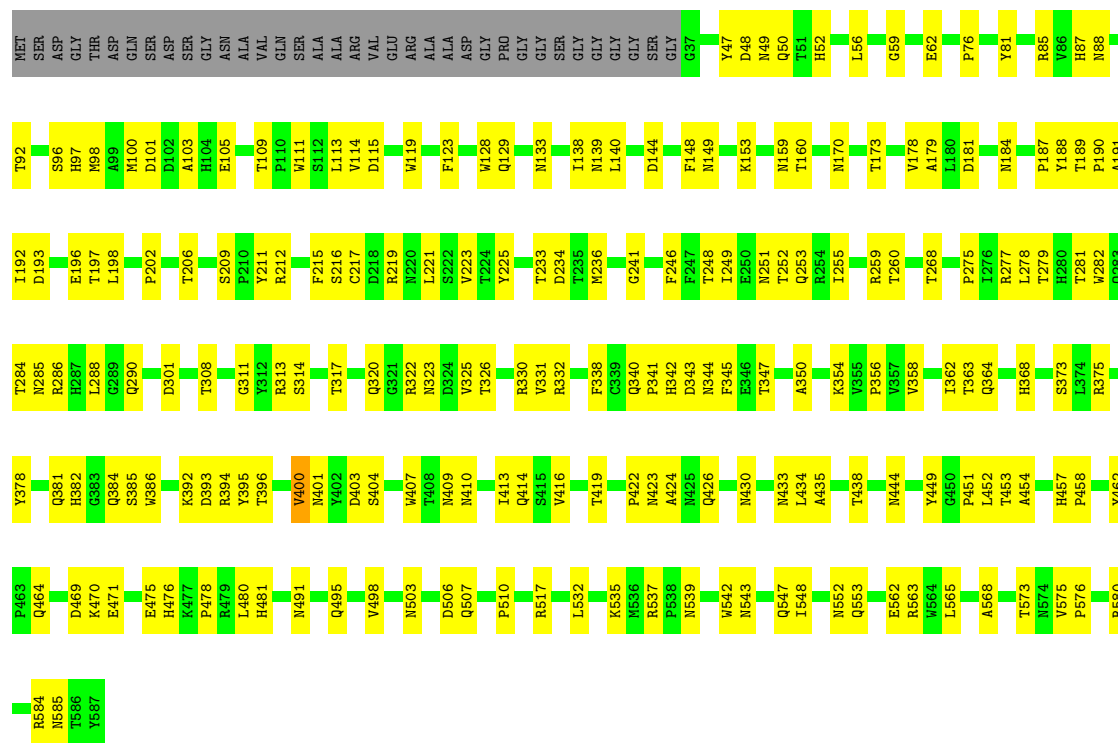
Chain S: 59% 35% 6%

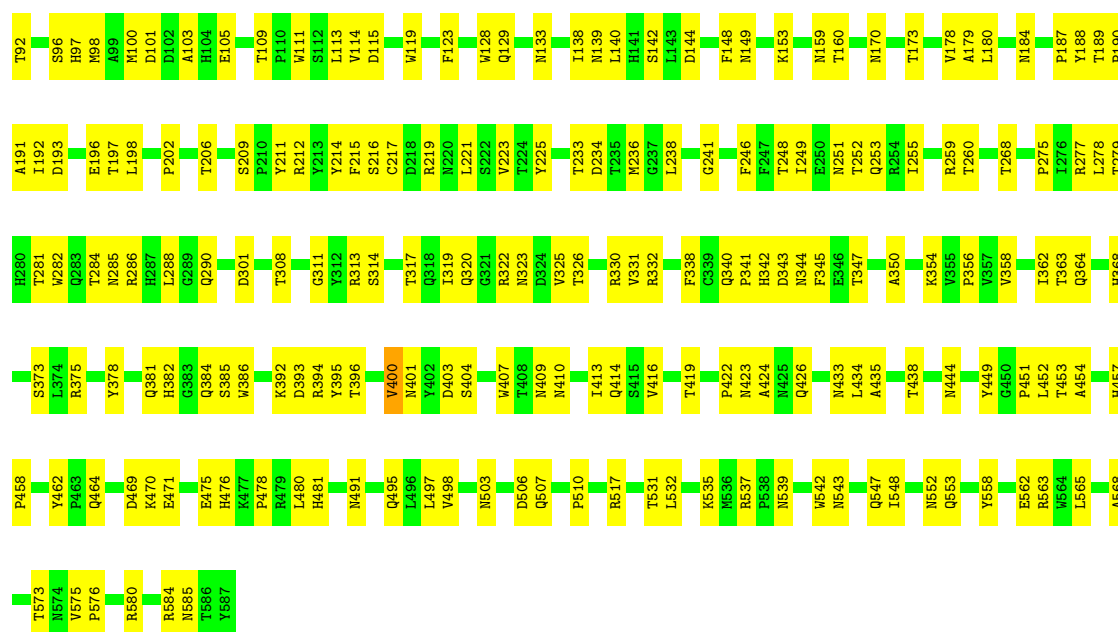




• Molecule 1: Capsid protein VP2

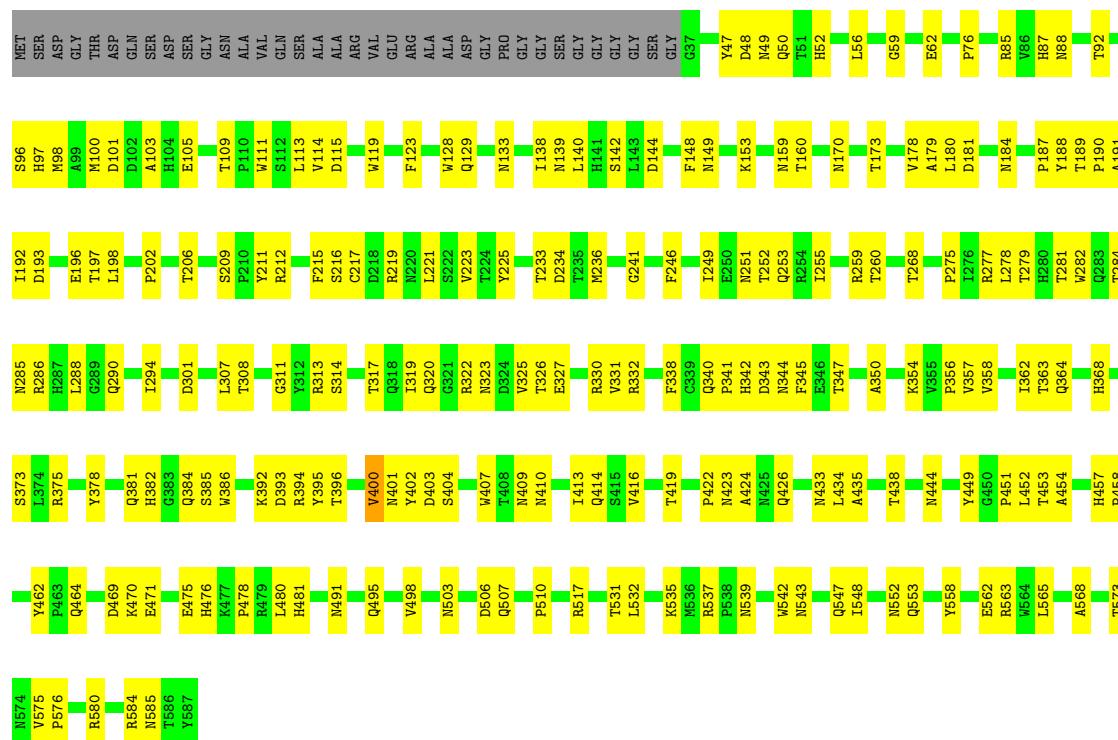
Chain T: 59% 34% 6%





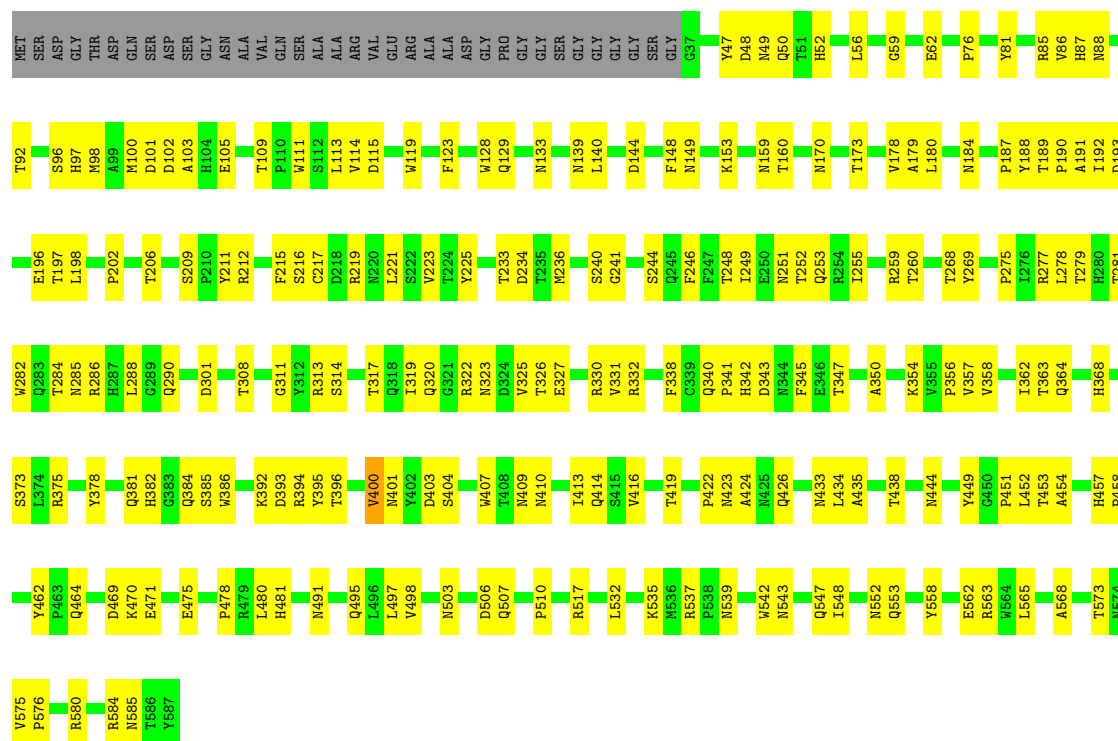
• Molecule 1: Capsid protein VP2

Chain V: 58% 35% 6%



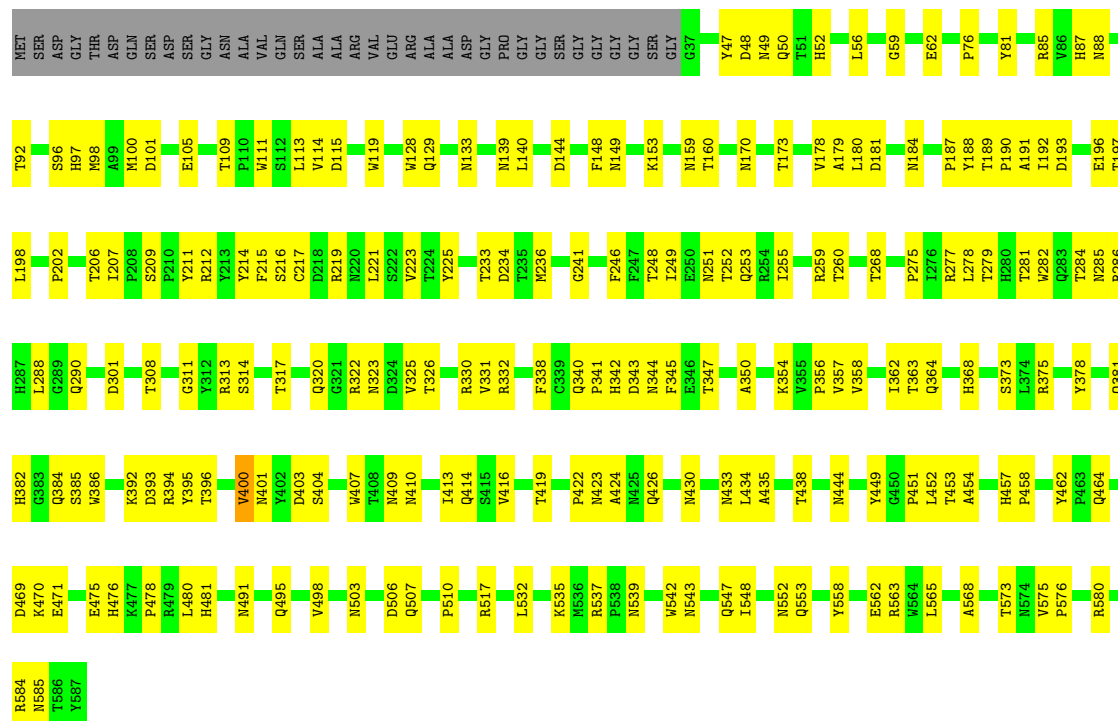
• Molecule 1: Capsid protein VP2

Chain W: 58% 35% 6%



• Molecule 1: Capsid protein VP2

Chain X: 59% 35% 6%



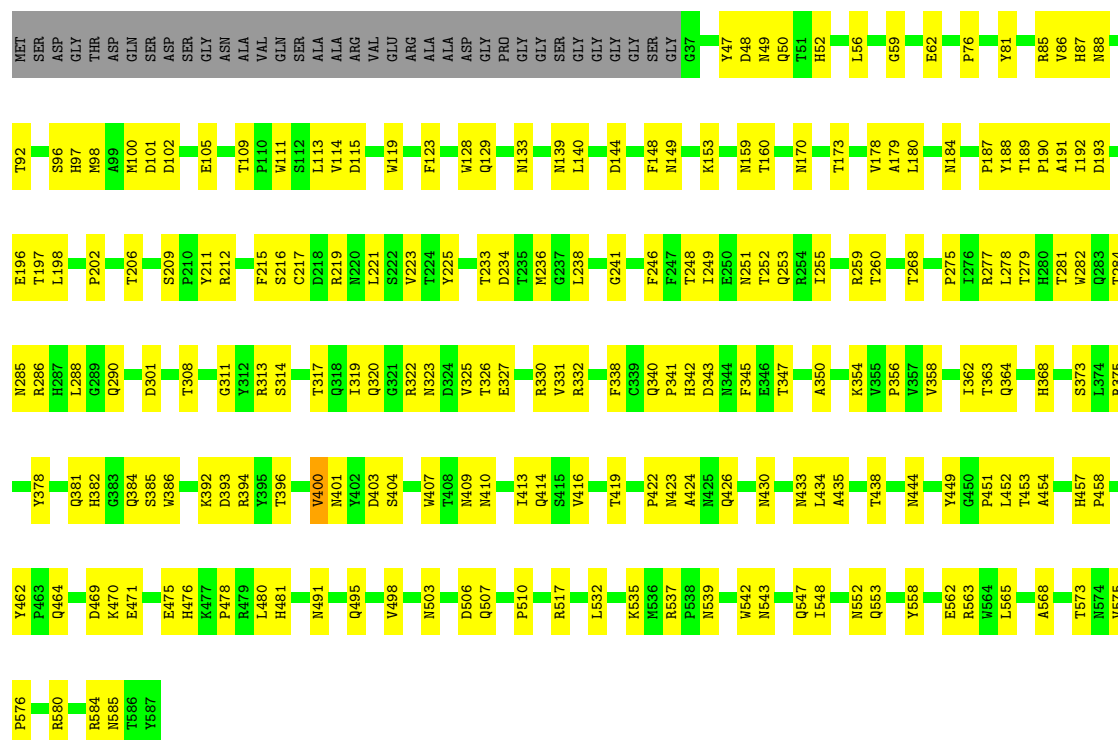
• Molecule 1: Capsid protein VP2

A568	H457	S373	T281	T192	T92	MET
T573	P458	L374	W282	D193		SER
N574		R375	Q283		S96	ASP
W575	Y462	N285	T284	E196	H97	GLY
P576	P463	R286	N287	T197	M98	THR
	Q464		R287	L198	A99	ASP
R580		Q381	L288	P202	M100	GLN
	D469	H382	L289	D101	D102	SER
R584	K470	G383	Q290	T206	A103	ASP
N585	E471	Q384	Q290		H104	GLY
T586		S385	D301	S209	E105	ASN
Y587	E475	W386		P210		ALA
	K476		L307	Y211	T109	VAL
	H477	K392	T308	R212	P110	GLN
	P478	D393		Y213	W111	SER
	P479	R394	G311	Y214	S112	ALA
	L480	Y395	T312	F215	L113	ALA
	H481	T396	R313	S216	V114	ARG
			S314	C217	D115	VAL
	N491	V400		D218		GLU
	M401	M401	T317	R219	W119	ARG
	Q495	Y402	Q318	N220		ALA
	V498	D403	I319	L221	F123	ALA
		S404	Q320	S222		ASP
	N503		G321	T223	W128	GLY
	D506	W407	R322	T224	Q129	PRO
Q607		T408	N323	Y225		GLY
	P510	M409	D324		M133	GLY
	R517	M410	V325	T233		SER
		I413	T326	D234	T138	GLY
		Q414	R330	T235	M139	GLY
		S415	M331	M236	L140	GLY
		V416	R332	G237		GLY
	L532			L238	D144	SER
	K535	T419	F338	G241	F148	GLY
M536		P422	C339		N149	G37
R537	P537	N423	Q340	F246		Y47
N539		A424	H342	T248	D48	D48
	Q426	H425	D343	T249	N49	N49
W542		Q426	R344	E250	Q50	Q50
N543		M430	F345	N251	T160	T51
	Q547	M433	E346	T252	H52	H52
L548	S549	L434	T347	Q253	M170	L56
		A435		R254	T173	
N552		T438	K354	T255		G59
Q553			V355	R269	V178	
		M444	P356	T260	A179	E62
	Y558		H557	D181		P76
		Y449	V358	T268		
E562	G450		I362	P276	M184	Y61
R563	P451			T276	P187	R85
W564	L452		Q364	R277	Y188	V86
L565	T453			T278	T189	H87
	M564		H369	T279	P190	N88
				H529	A191	

[illegible]

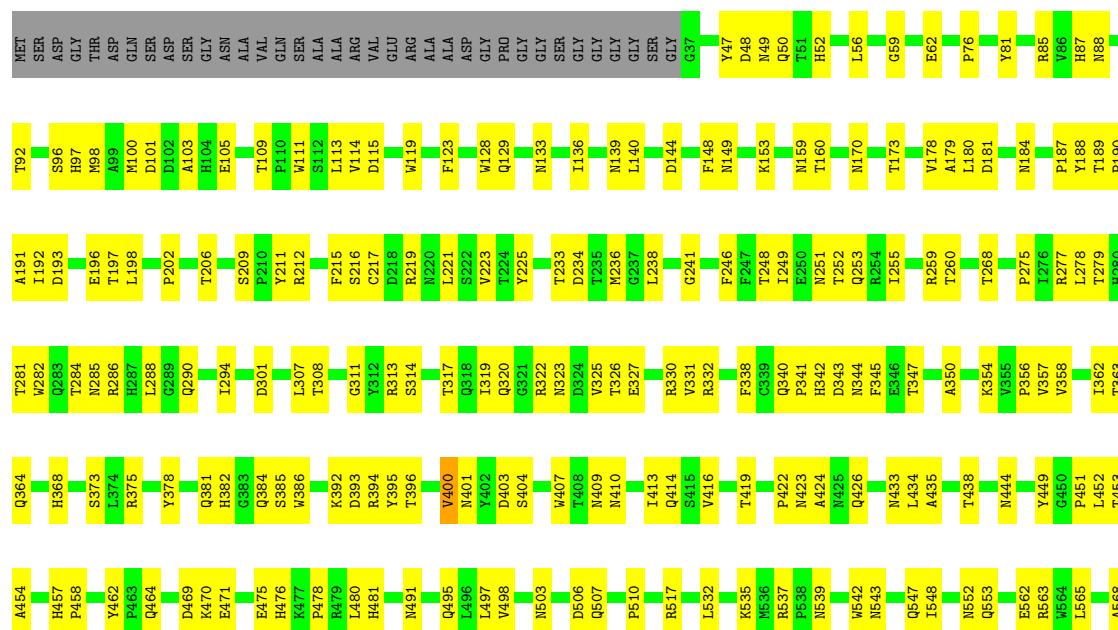
- Molecule 1: Capsid protein VP2

Chain 1:  59% 35% 6%



- Molecule 1: Capsid protein VP2

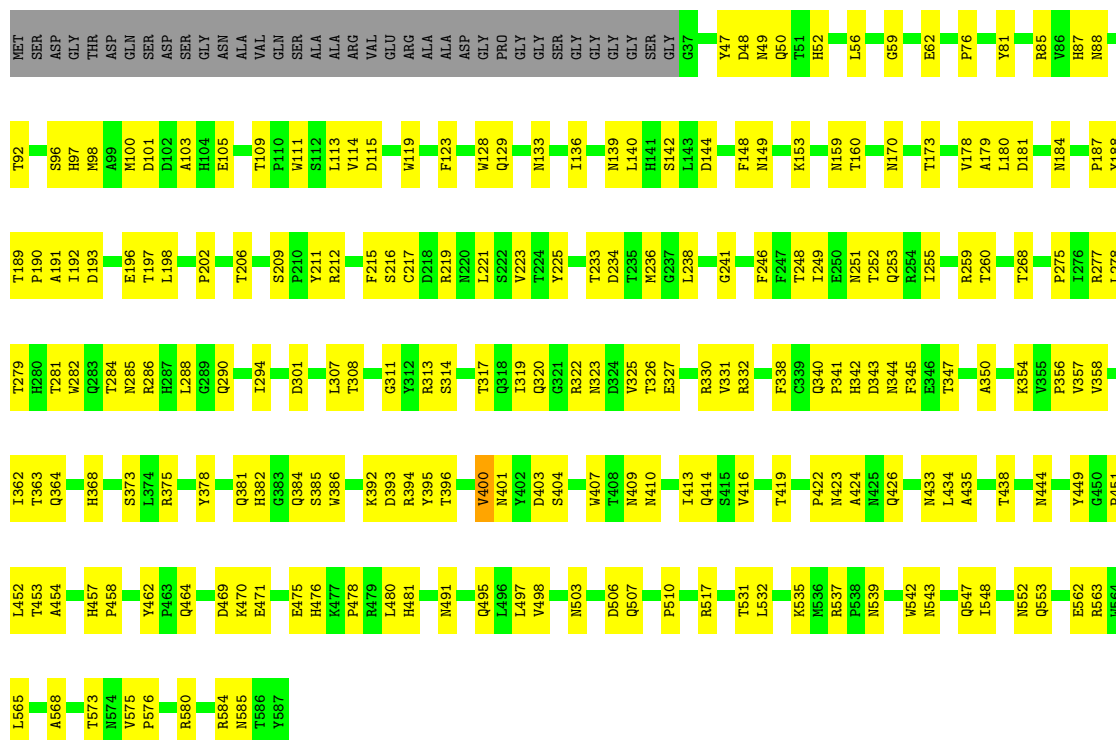
Chain 2:  58% 35% 6%





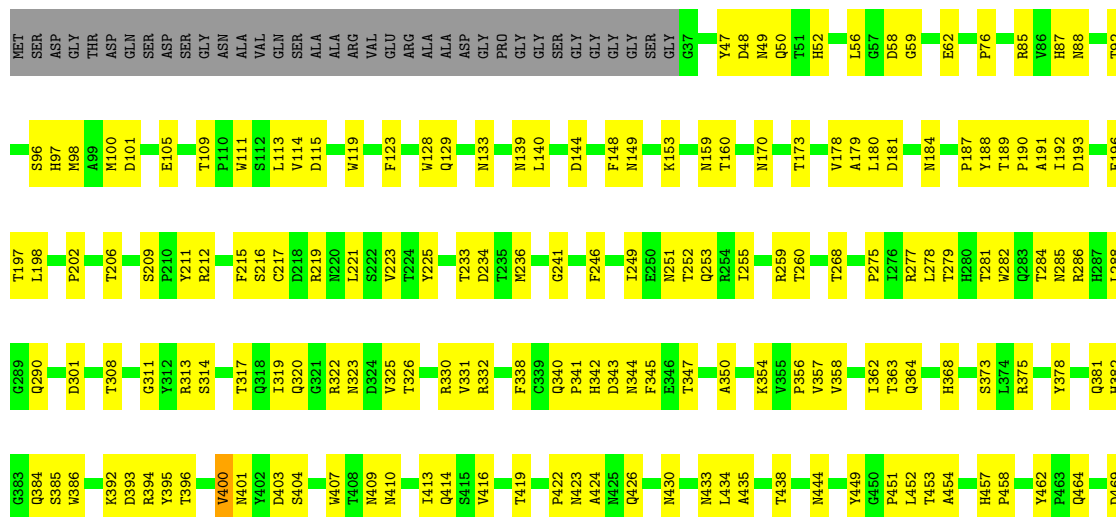
• Molecule 1: Capsid protein VP2

Chain 3: 58% 36% 6%



• Molecule 1: Capsid protein VP2

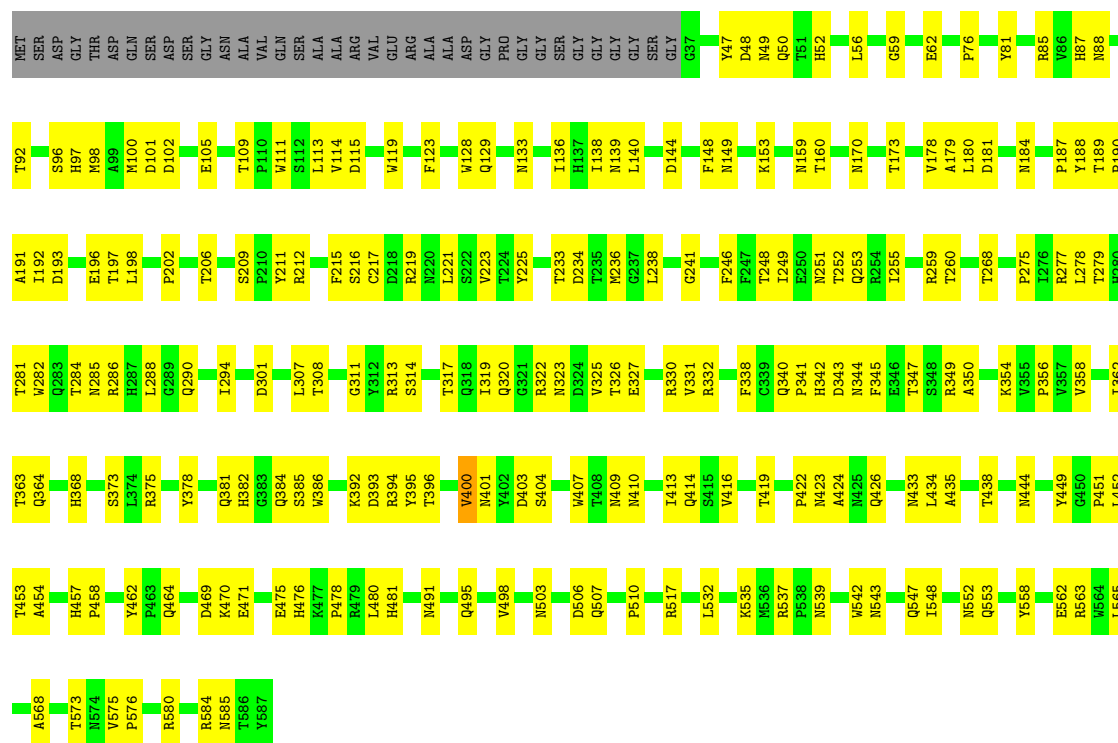
Chain 4: 59% 34% 6%





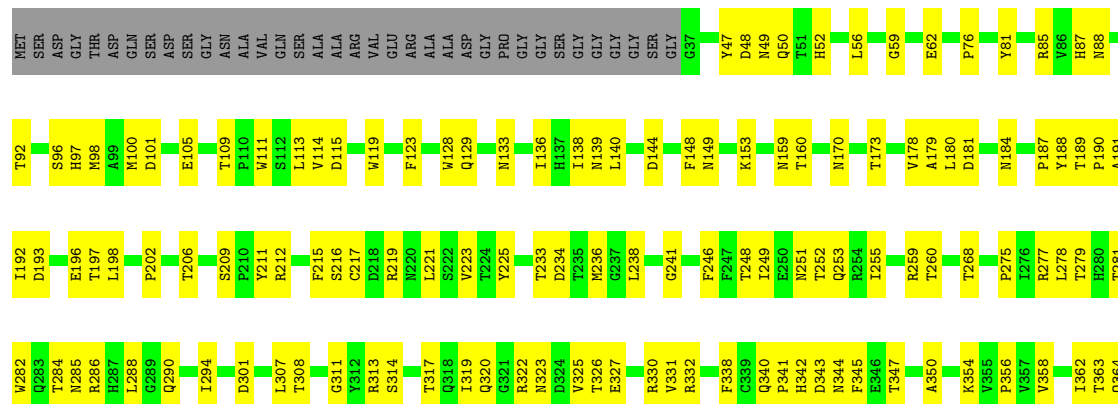
• Molecule 1: Capsid protein VP2

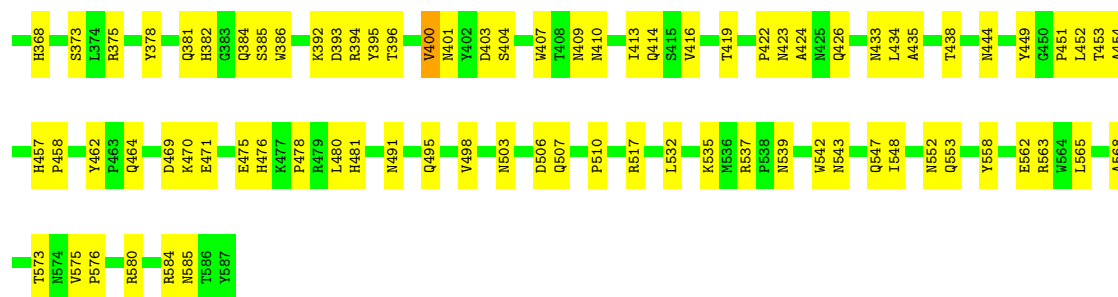
Chain 5: 58% 36% 6%



• Molecule 1: Capsid protein VP2

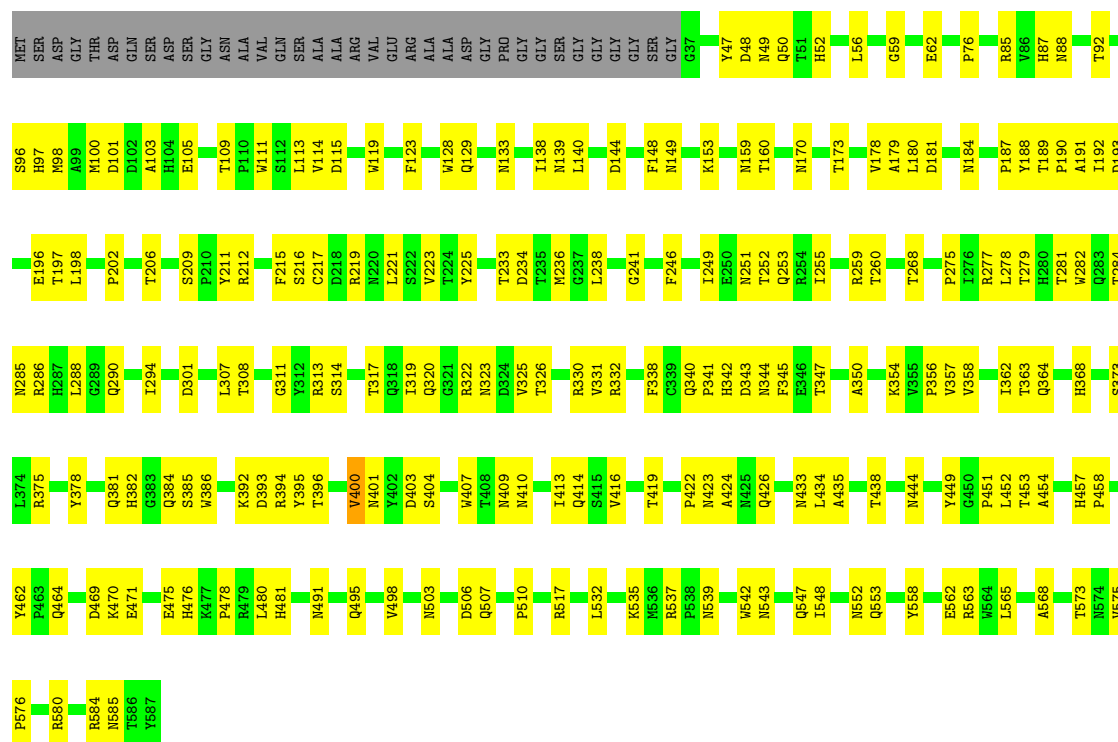
Chain 6: 58% 35% 6%





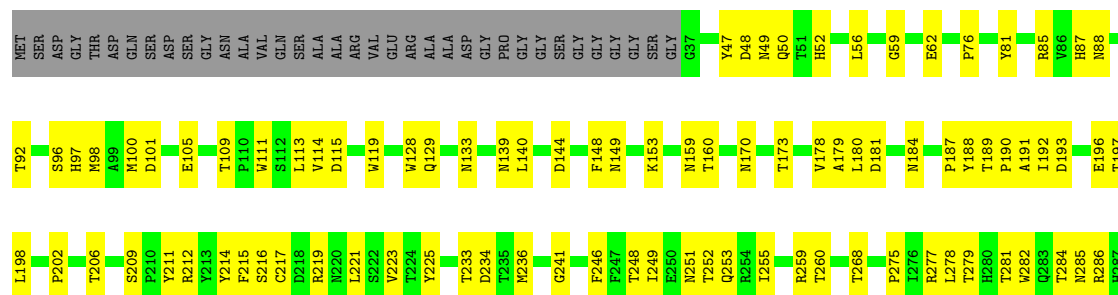
• Molecule 1: Capsid protein VP2

Chain a: 59% 35% 6%



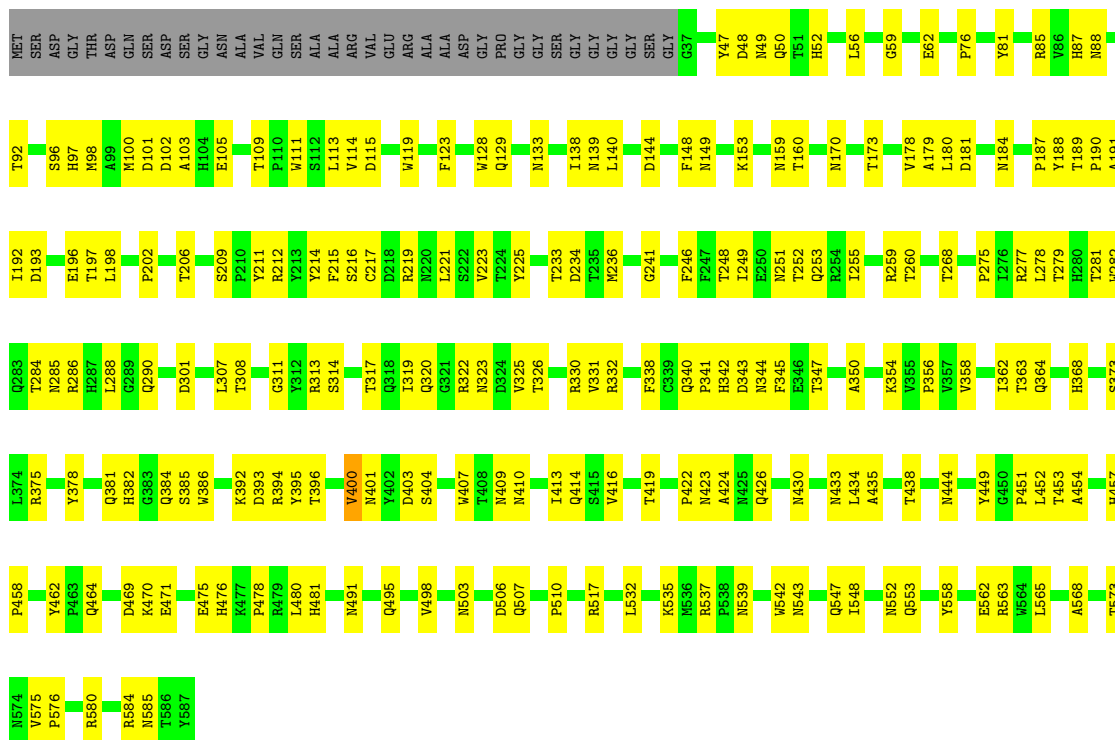
• Molecule 1: Capsid protein VP2

Chain b: 59% 34% 6%

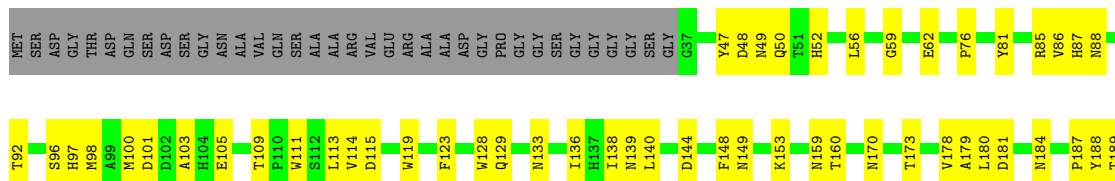


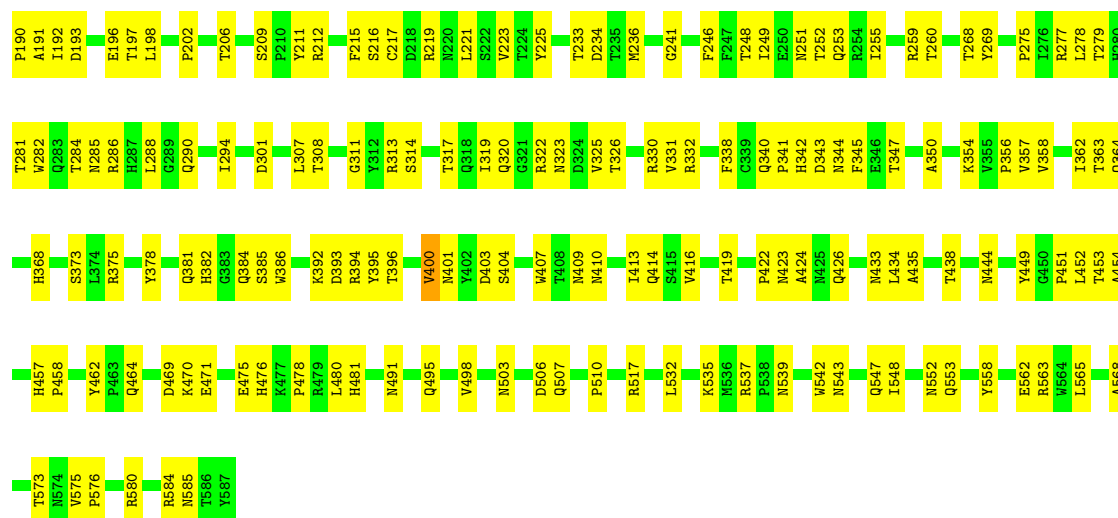


- Molecule 1: Capsid protein VP2



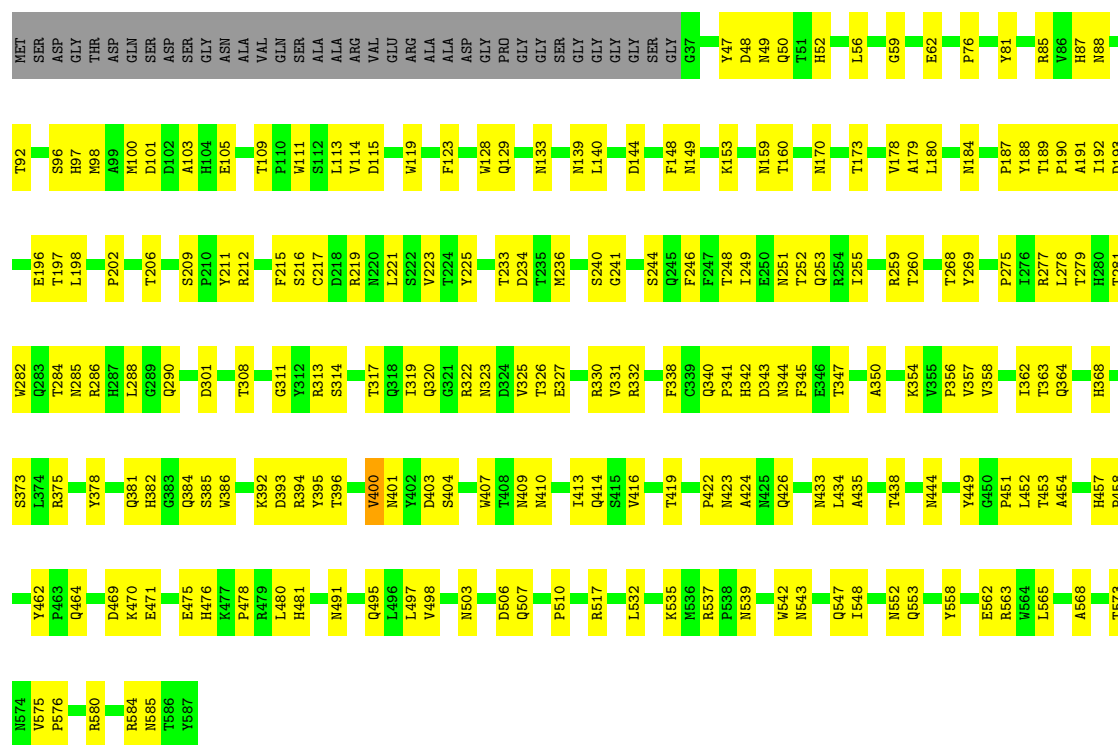
- Molecule 1: Capsid protein VP2





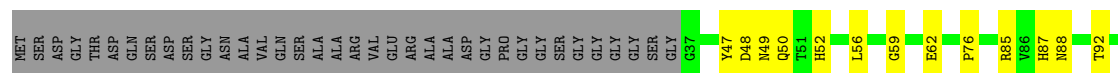
• Molecule 1: Capsid protein VP2

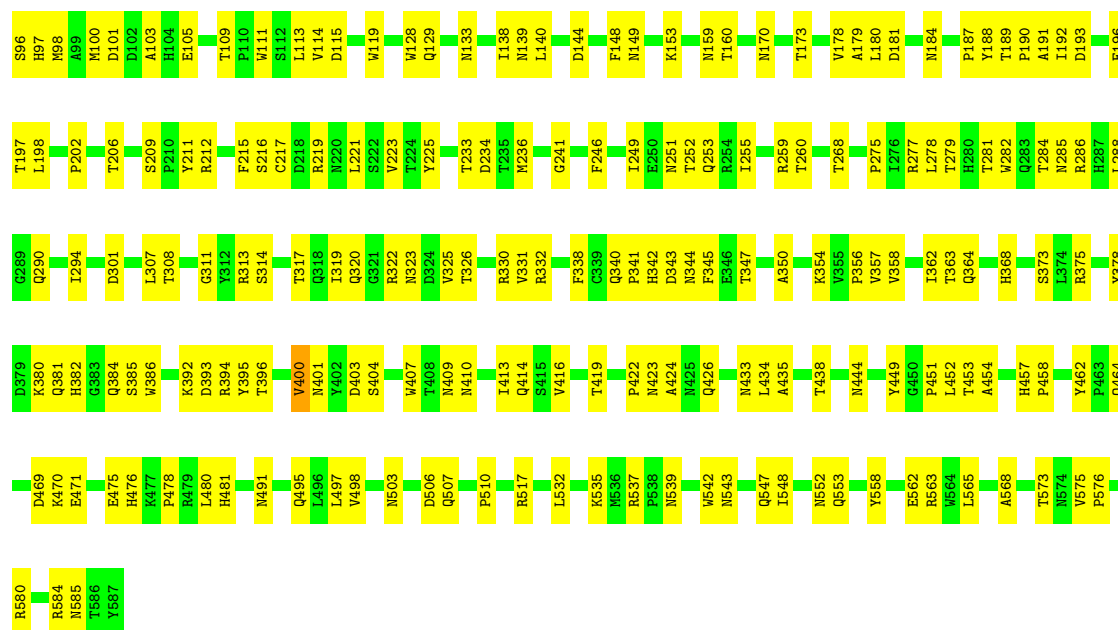
Chain e: 58% 35% 6%



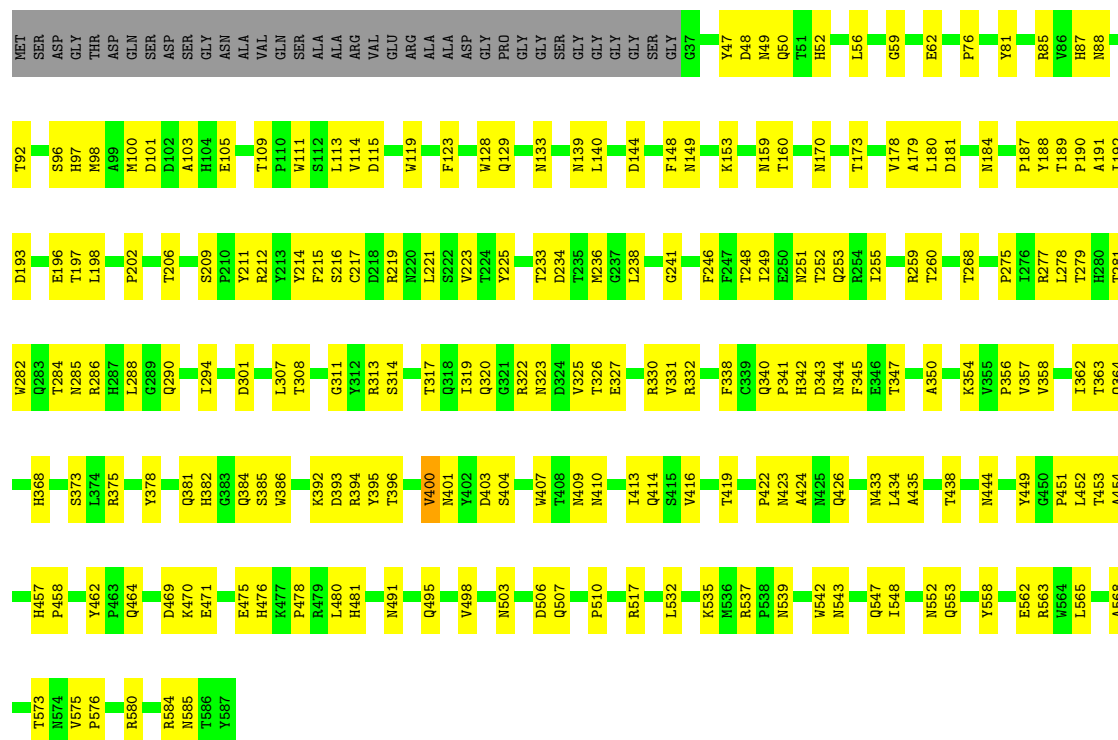
• Molecule 1: Capsid protein VP2

Chain f: 59% 35% 6%



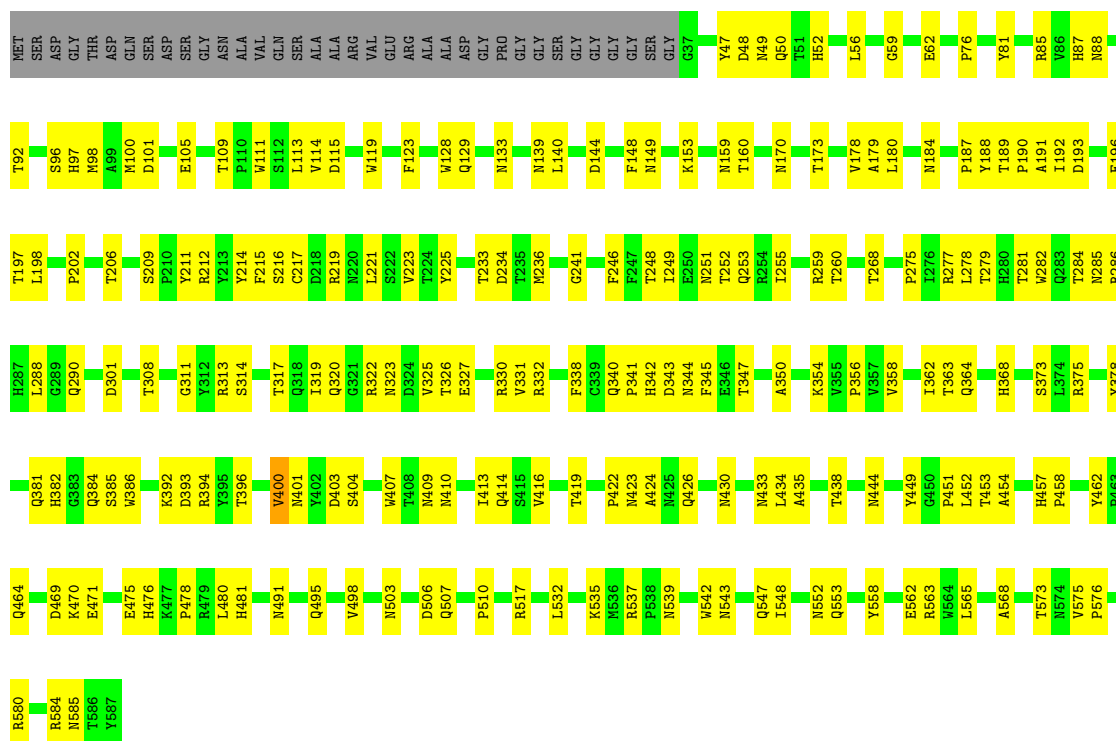


- Molecule 1: Capsid protein VP2



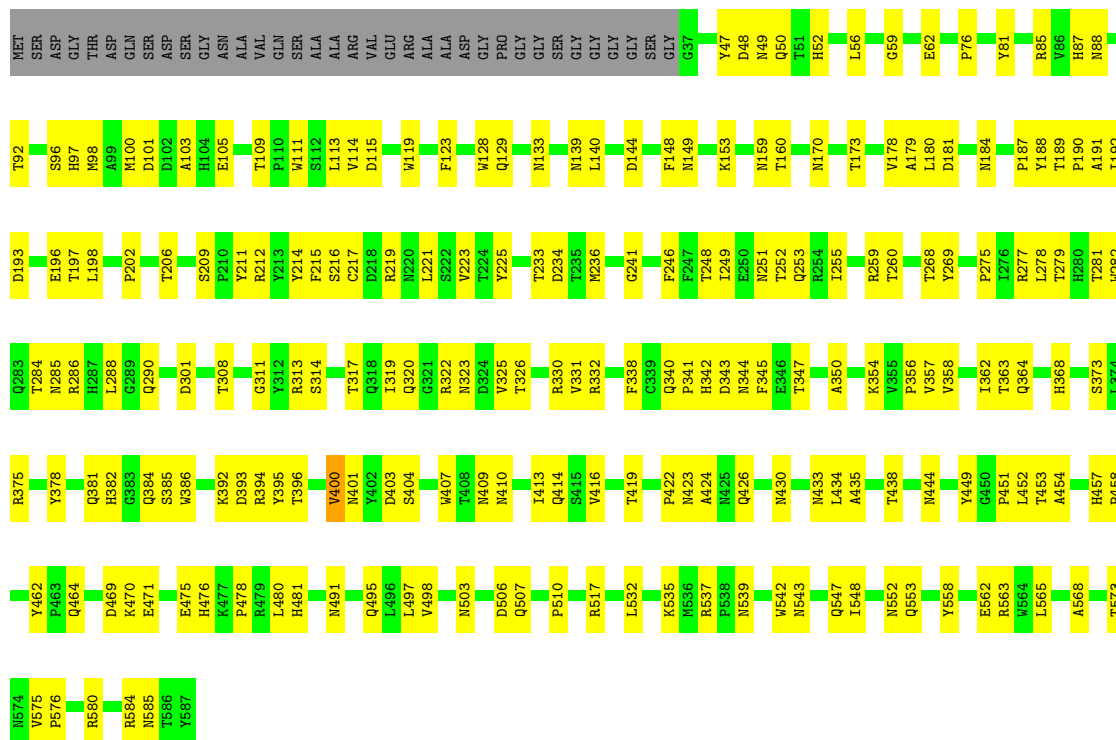
- Molecule 1: Capsid protein VP2





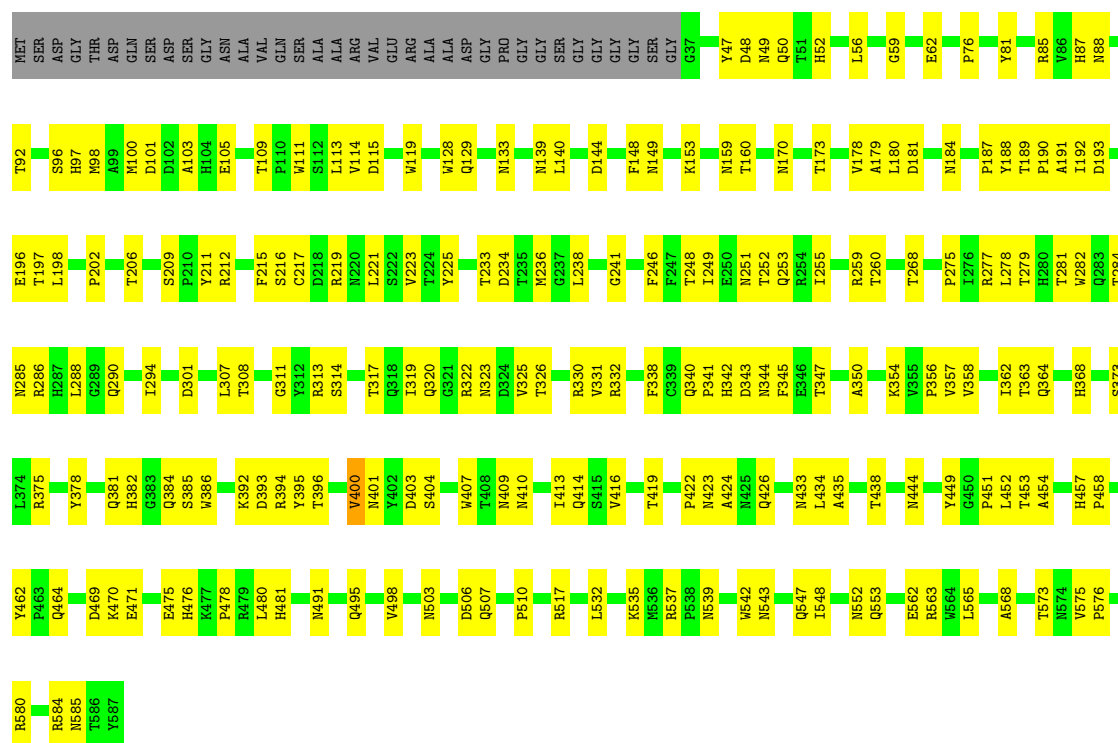
• Molecule 1: Capsid protein VP2

Chain i:



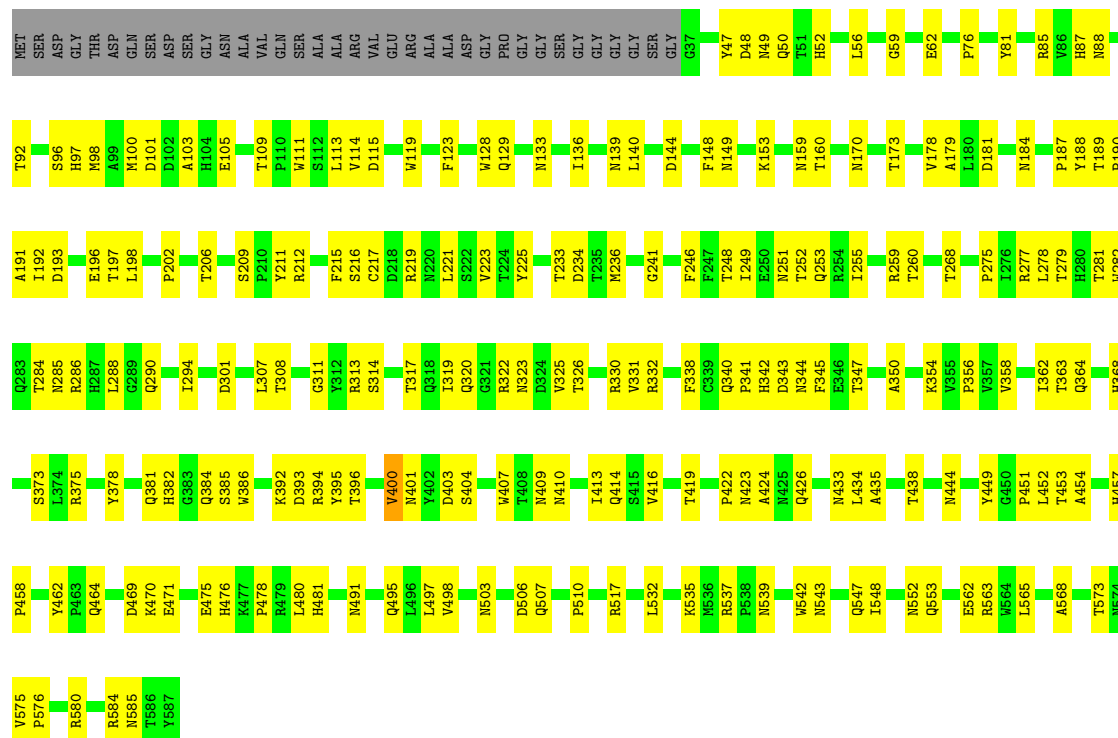
• Molecule 1: Capsid protein VP2

Response	Percentage
U.S. is responsible	59%
U.S. is not responsible	35%
Don't know	6%



- Molecule 1: Capsid protein VP2

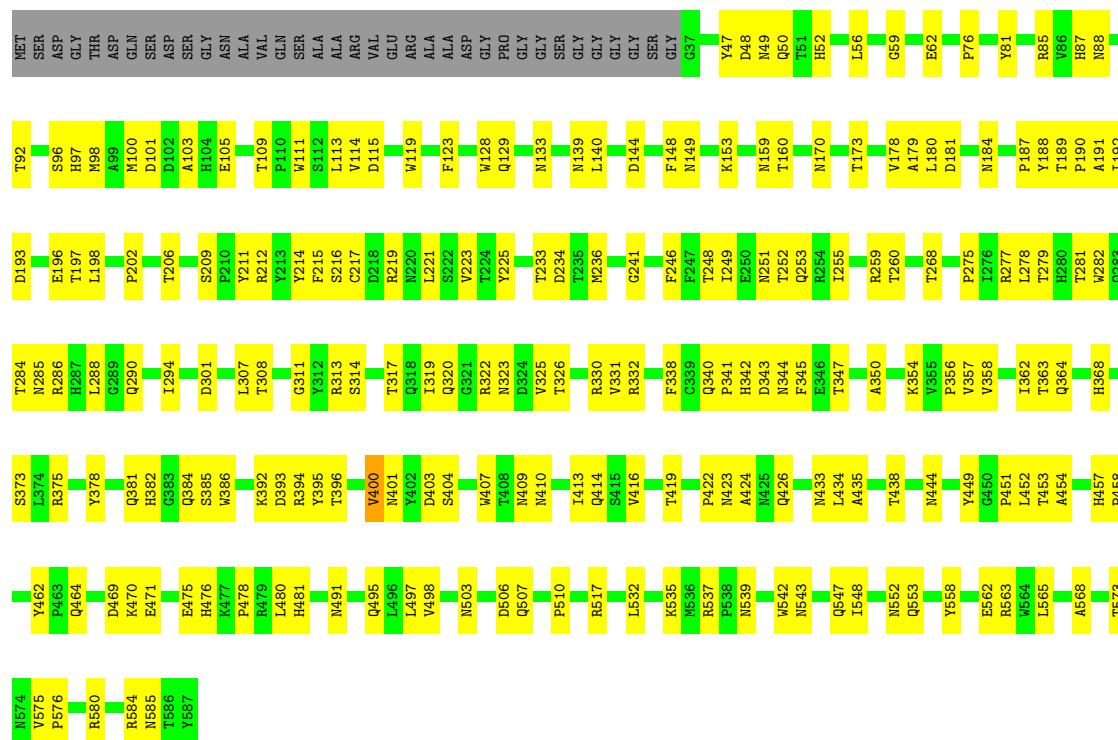
Response	Percentage
Yes, the U.S. should take action to protect the environment	59%
No, the U.S. should not take action to protect the environment	35%
Don't know	6%





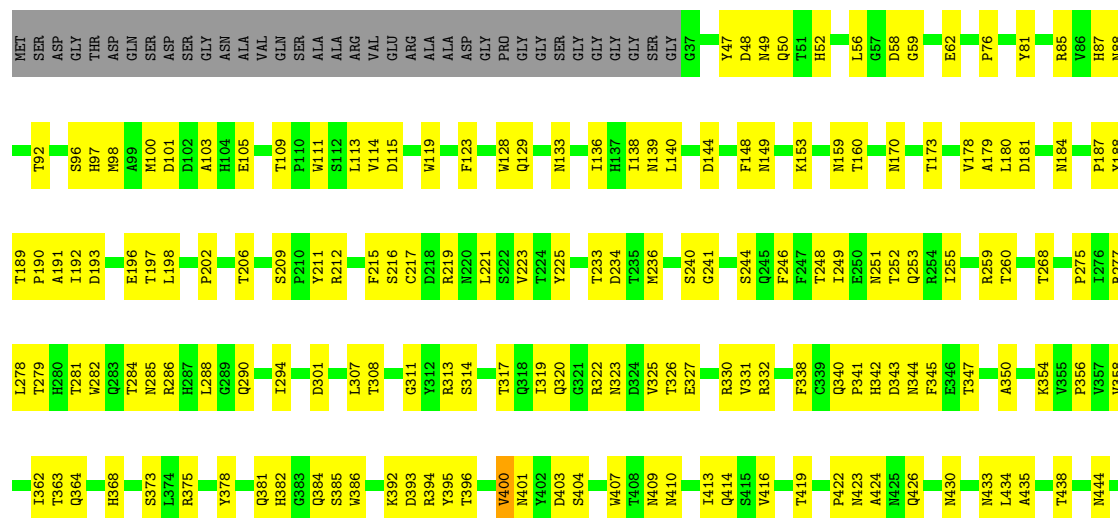
• Molecule 1: Capsid protein VP2

Chain p:  58% 35% 6%



• Molecule 1: Capsid protein VP2

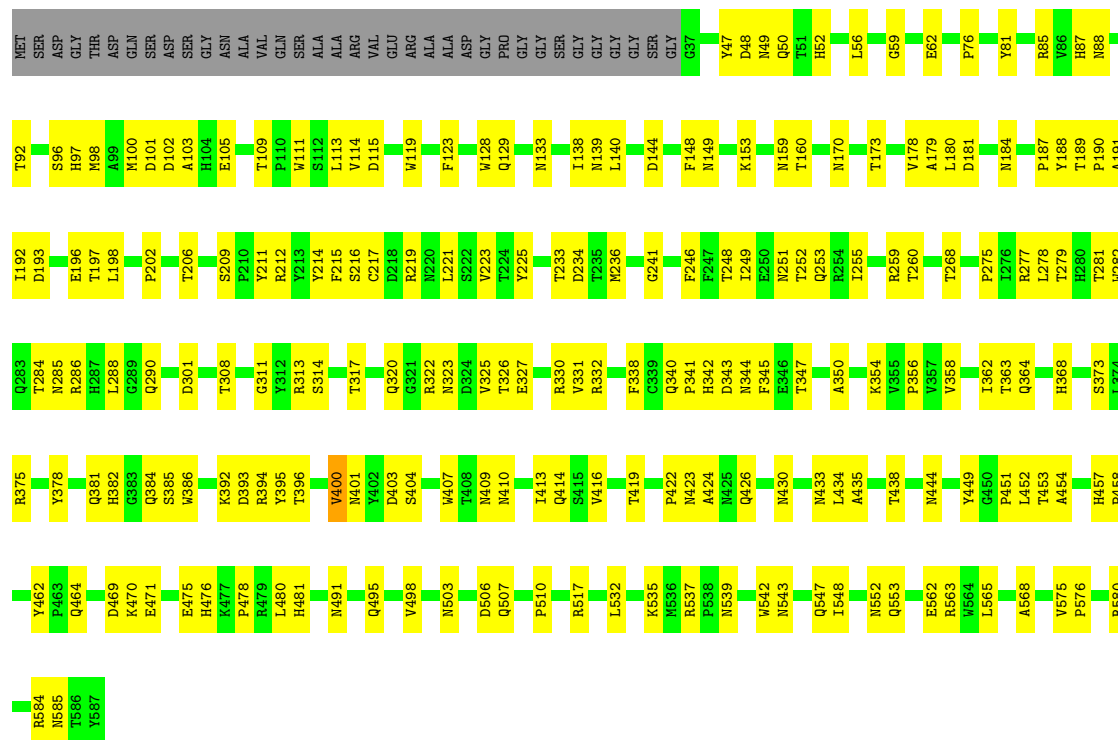
Chain q:  58% 36% 6%





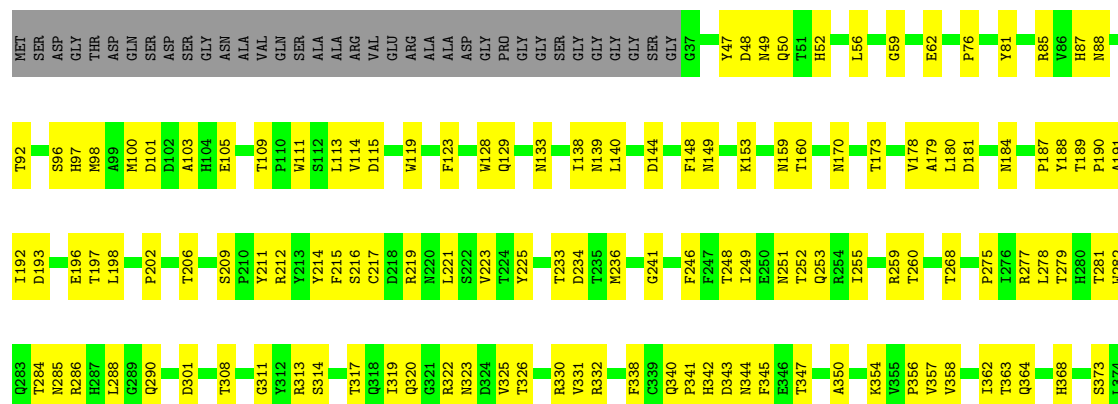
• Molecule 1: Capsid protein VP2

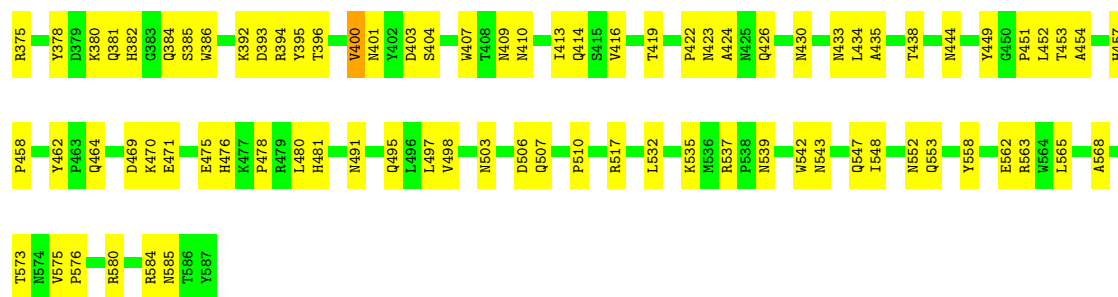
Chain r: 59% 35% 6%



• Molecule 1: Capsid protein VP2

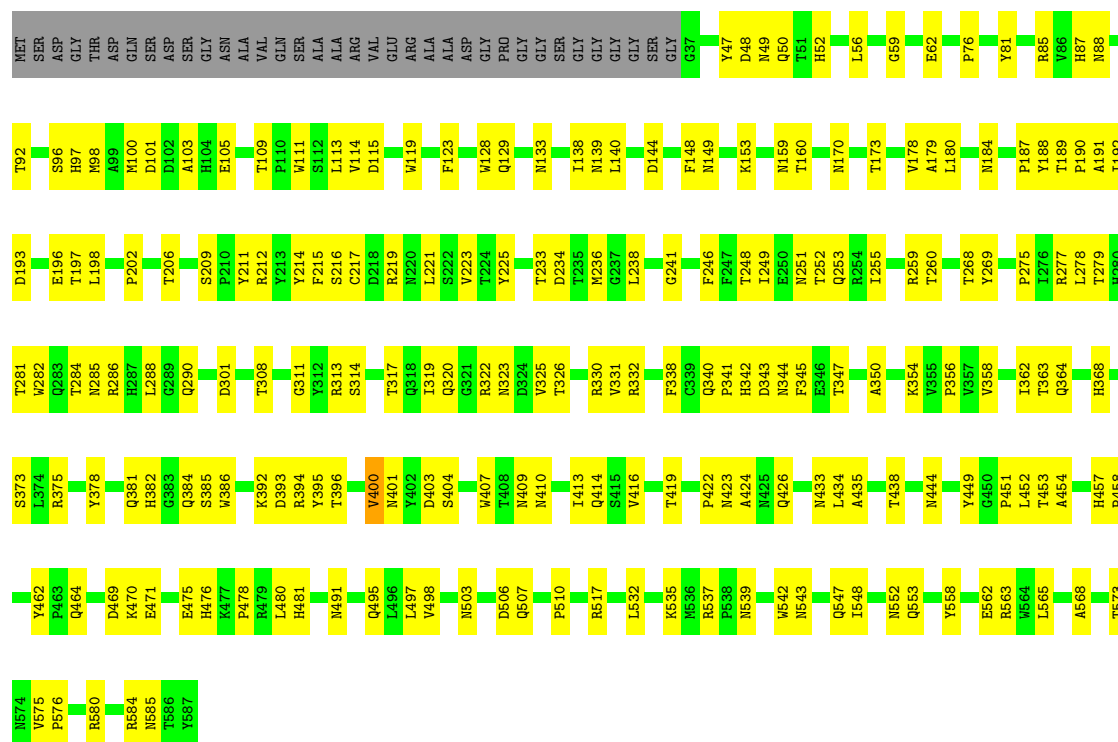
Chain s: 58% 35% 6%





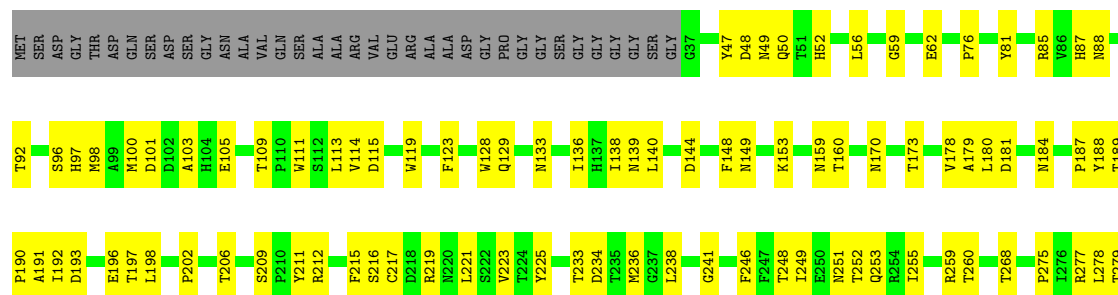
• Molecule 1: Capsid protein VP2

Chain t: 59% 35% 6%



• Molecule 1: Capsid protein VP2

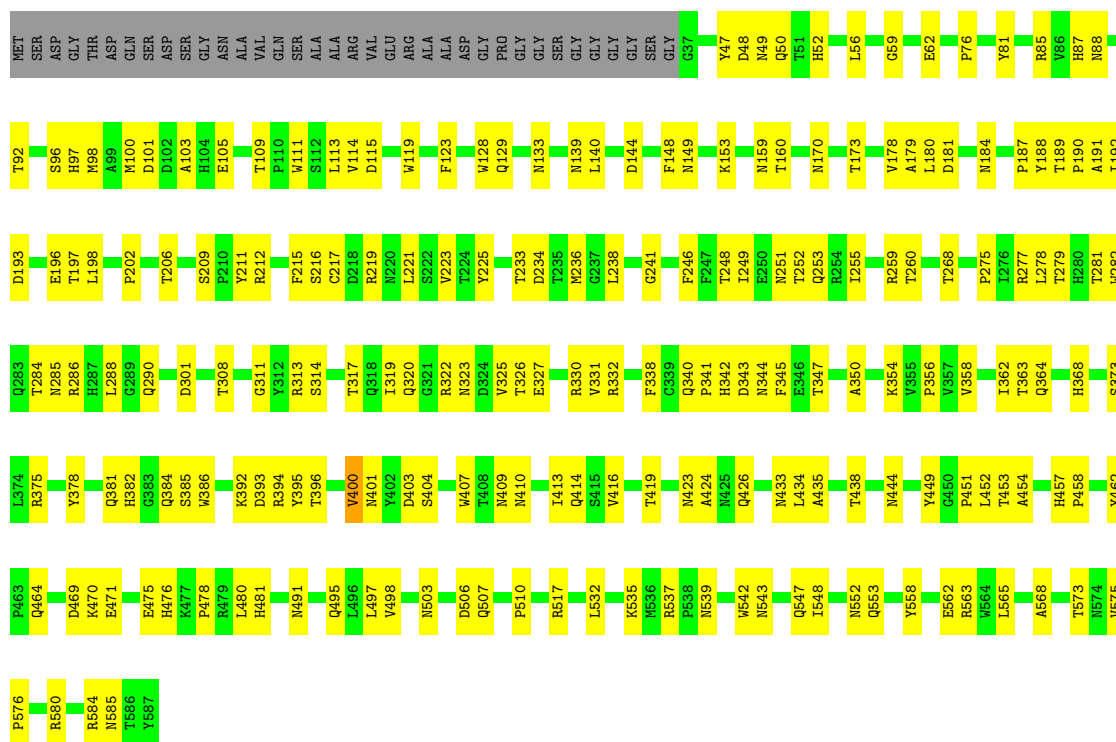
Chain u: 58% 35% 6%





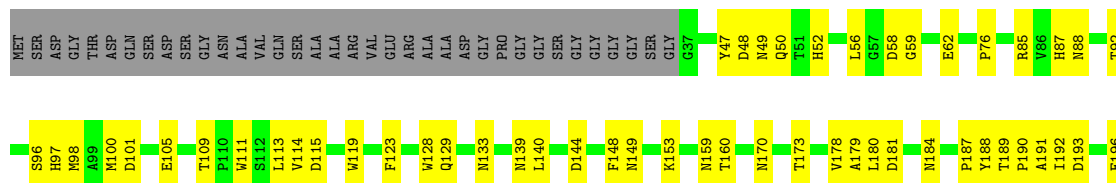
• Molecule 1: Capsid protein VP2

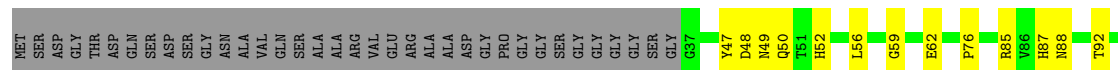
Chain v: 59% 35% 6%

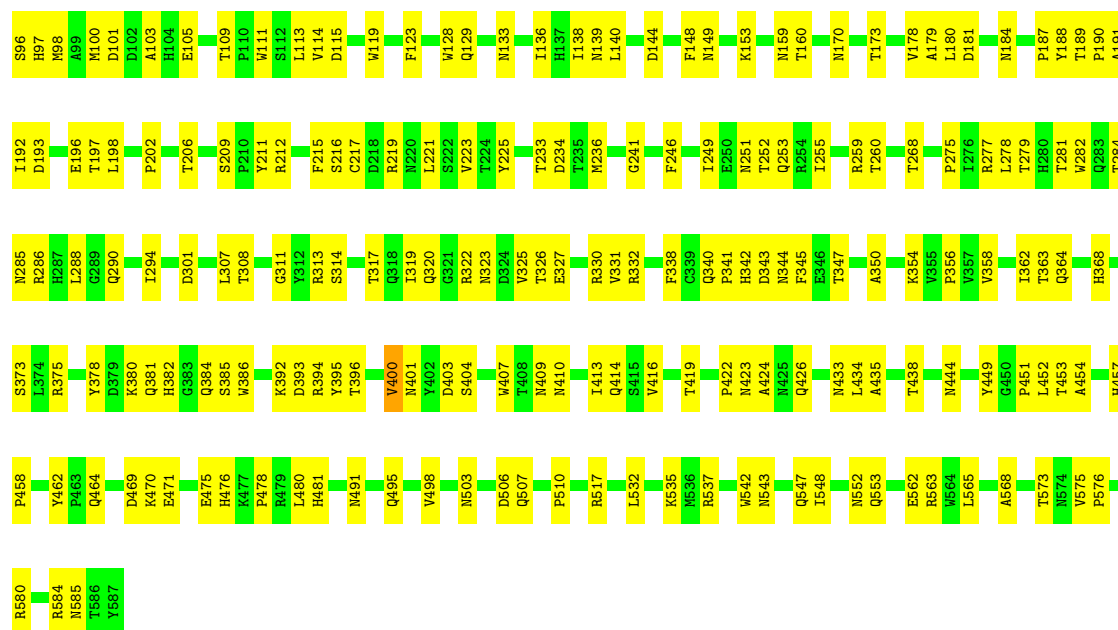


• Molecule 1: Capsid protein VP2

Chain w: 59% 35% 6%

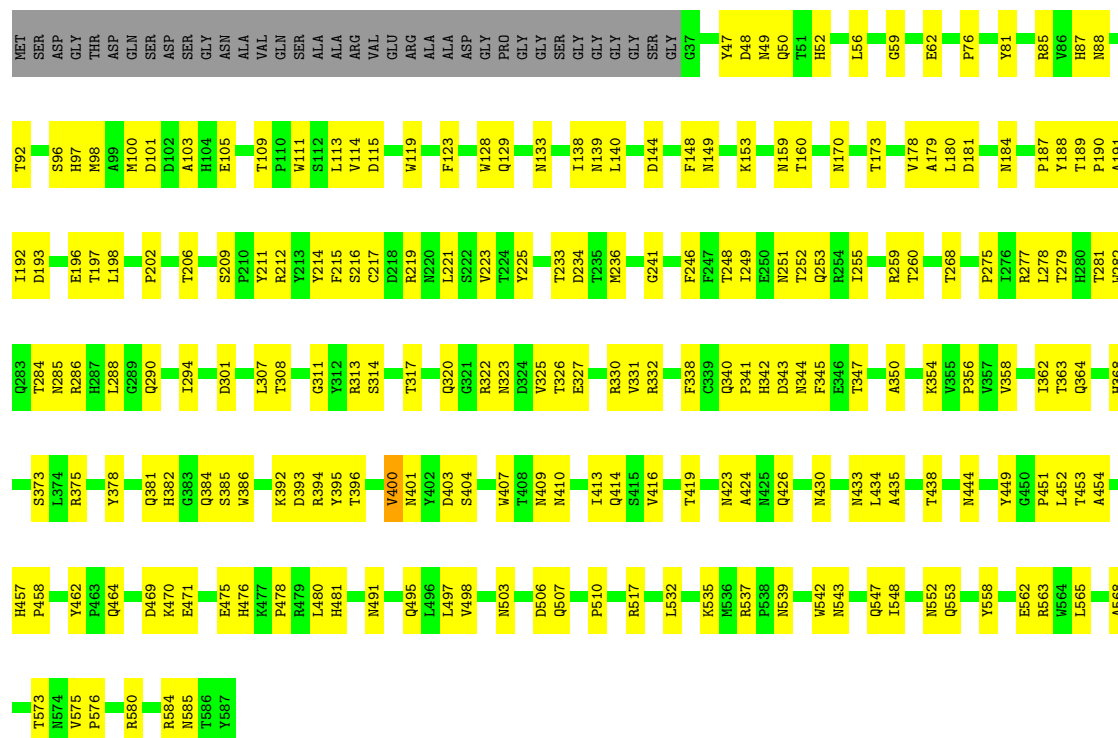






• Molecule 1: Capsid protein VP2

Chain z: 58% 35% 6%



• Molecule 1: Capsid protein VP2

Chain 7: 59% 35% 6%

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18134	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 ($e^-/\text{\AA}^2$)	1.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	14.712	Depositor
Minimum map value	-7.755	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1	Depositor
Map size (Å)	381.976, 381.976, 381.976	wwPDB
Map dimensions	359, 359, 359	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.064, 1.064, 1.064	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	0.41	0/4528	0.49	0/6193
1	2	0.41	0/4528	0.49	0/6193
1	3	0.41	0/4528	0.49	0/6193
1	4	0.41	0/4528	0.49	0/6193
1	5	0.41	0/4528	0.49	0/6193
1	6	0.41	0/4528	0.49	0/6193
1	7	0.41	0/4528	0.49	0/6193
1	8	0.41	0/4528	0.49	0/6193
1	A	0.41	0/4528	0.49	0/6193
1	B	0.41	0/4528	0.49	0/6193
1	C	0.41	0/4528	0.49	0/6193
1	D	0.41	0/4528	0.49	0/6193
1	E	0.41	0/4528	0.49	0/6193
1	F	0.41	0/4528	0.49	0/6193
1	G	0.41	0/4528	0.49	0/6193
1	H	0.41	0/4528	0.49	0/6193
1	I	0.41	0/4528	0.49	0/6193
1	J	0.41	0/4528	0.49	0/6193
1	K	0.41	0/4528	0.49	0/6193
1	L	0.41	0/4528	0.49	0/6193
1	M	0.41	0/4528	0.49	0/6193
1	N	0.41	0/4528	0.49	0/6193
1	O	0.41	0/4528	0.49	0/6193
1	P	0.41	0/4528	0.49	0/6193
1	Q	0.41	0/4528	0.49	0/6193
1	R	0.41	0/4528	0.49	0/6193
1	S	0.41	0/4528	0.49	0/6193
1	T	0.41	0/4528	0.49	0/6193
1	U	0.41	0/4528	0.49	0/6193
1	V	0.41	0/4528	0.49	0/6193
1	W	0.41	0/4528	0.49	0/6193
1	X	0.41	0/4528	0.49	0/6193
1	Y	0.41	0/4528	0.49	0/6193
1	Z	0.41	0/4528	0.49	0/6193

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.41	0/4528	0.49	0/6193
1	b	0.41	0/4528	0.49	0/6193
1	c	0.41	0/4528	0.49	0/6193
1	d	0.41	0/4528	0.49	0/6193
1	e	0.41	0/4528	0.49	0/6193
1	f	0.41	0/4528	0.49	0/6193
1	g	0.41	0/4528	0.49	0/6193
1	h	0.41	0/4528	0.49	0/6193
1	i	0.41	0/4528	0.49	0/6193
1	j	0.41	0/4528	0.49	0/6193
1	k	0.41	0/4528	0.49	0/6193
1	l	0.41	0/4528	0.49	0/6193
1	m	0.41	0/4528	0.49	0/6193
1	n	0.41	0/4528	0.49	0/6193
1	o	0.41	0/4528	0.49	0/6193
1	p	0.41	0/4528	0.49	0/6193
1	q	0.41	0/4528	0.49	0/6193
1	r	0.41	0/4528	0.49	0/6193
1	s	0.41	0/4528	0.49	0/6193
1	t	0.41	0/4528	0.49	0/6193
1	u	0.41	0/4528	0.49	0/6193
1	v	0.41	0/4528	0.49	0/6193
1	w	0.41	0/4528	0.49	0/6193
1	x	0.41	0/4528	0.49	0/6193
1	y	0.41	0/4528	0.49	0/6193
1	z	0.41	0/4528	0.49	0/6193
All	All	0.41	0/271680	0.49	0/371580

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	4399	0	4169	181	0
1	2	4399	0	4169	190	0
1	3	4399	0	4169	192	0
1	4	4399	0	4169	185	0
1	5	4399	0	4169	192	0
1	6	4399	0	4169	190	0
1	7	4399	0	4169	186	0
1	8	4399	0	4169	185	0
1	A	4399	0	4169	189	0
1	B	4399	0	4169	184	0
1	C	4399	0	4169	189	0
1	D	4399	0	4169	189	0
1	E	4399	0	4169	183	0
1	F	4399	0	4169	186	0
1	G	4399	0	4169	185	0
1	H	4399	0	4169	190	0
1	I	4399	0	4169	188	0
1	J	4399	0	4169	186	0
1	K	4399	0	4169	188	0
1	L	4399	0	4169	189	0
1	M	4399	0	4169	189	0
1	N	4399	0	4169	188	0
1	O	4399	0	4169	184	0
1	P	4399	0	4169	184	0
1	Q	4399	0	4169	188	0
1	R	4399	0	4169	187	0
1	S	4399	0	4169	185	0
1	T	4399	0	4169	184	0
1	U	4399	0	4169	188	0
1	V	4399	0	4169	189	0
1	W	4399	0	4169	187	0
1	X	4399	0	4169	187	0
1	Y	4399	0	4169	193	0
1	Z	4399	0	4169	187	0
1	a	4399	0	4169	187	0
1	b	4399	0	4169	185	0
1	c	4399	0	4169	190	0
1	d	4399	0	4169	191	0
1	e	4399	0	4169	190	0
1	f	4399	0	4169	186	0
1	g	4399	0	4169	189	0
1	h	4399	0	4169	182	0
1	i	4399	0	4169	188	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	j	4399	0	4169	186	0
1	k	4399	0	4169	185	0
1	l	4399	0	4169	185	0
1	m	4399	0	4169	188	0
1	n	4399	0	4169	183	0
1	o	4399	0	4169	187	0
1	p	4399	0	4169	186	0
1	q	4399	0	4169	191	0
1	r	4399	0	4169	185	0
1	s	4399	0	4169	191	0
1	t	4399	0	4169	188	0
1	u	4399	0	4169	188	0
1	v	4399	0	4169	187	0
1	w	4399	0	4169	185	0
1	x	4399	0	4169	186	0
1	y	4399	0	4169	184	0
1	z	4399	0	4169	189	0
All	All	263940	0	250140	9055	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 18.

The worst 5 of 9055 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:S:340:GLN:HE22	1:S:358:VAL:HG22	1.34	0.93
1:v:340:GLN:HE22	1:v:358:VAL:HG22	1.34	0.93
1:t:340:GLN:HE22	1:t:358:VAL:HG22	1.34	0.93
1:G:340:GLN:HE22	1:G:358:VAL:HG22	1.34	0.93
1:U:340:GLN:HE22	1:U:358:VAL:HG22	1.34	0.93

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	2	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	3	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	4	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	5	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	6	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	7	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	8	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	A	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	B	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	C	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	D	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	E	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	F	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	G	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	H	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	I	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	J	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	K	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	L	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	M	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	N	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	O	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	P	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	Q	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	R	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	S	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	T	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	U	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	V	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	W	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	X	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	Y	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	Z	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	a	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	b	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	c	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	d	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	e	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	f	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	g	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	h	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	i	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	j	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	k	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	l	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	m	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	n	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	o	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	p	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	q	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	r	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	s	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	t	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	u	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	v	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	w	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	x	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	y	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
1	z	550/587 (94%)	538 (98%)	11 (2%)	1 (0%)	43	72
All	All	33000/35220 (94%)	32280 (98%)	660 (2%)	60 (0%)	44	72

5 of 60 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	400	VAL
1	B	400	VAL
1	C	400	VAL
1	D	400	VAL
1	E	400	VAL

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.

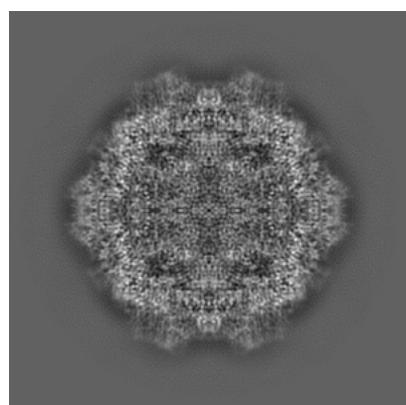
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7071. These allow visual inspection of the internal detail of the map and identification of artifacts.

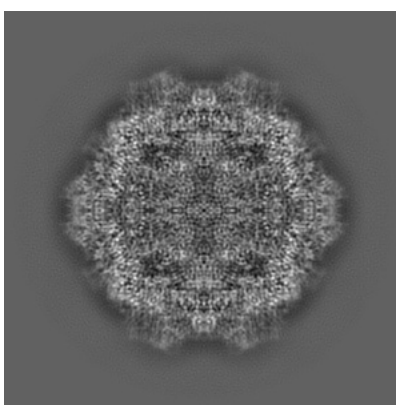
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

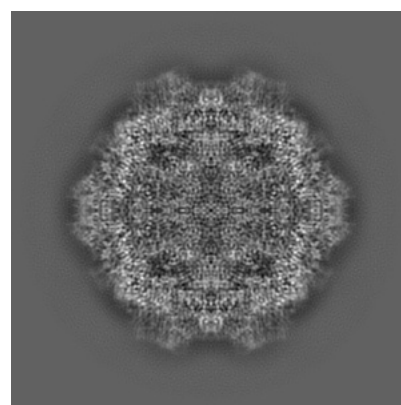
6.1.1 Primary map



X



Y

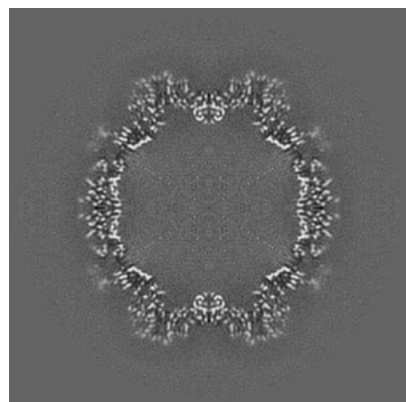


Z

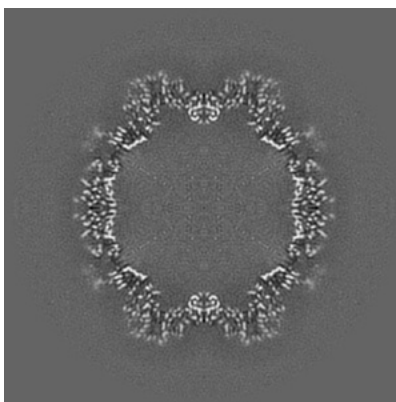
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

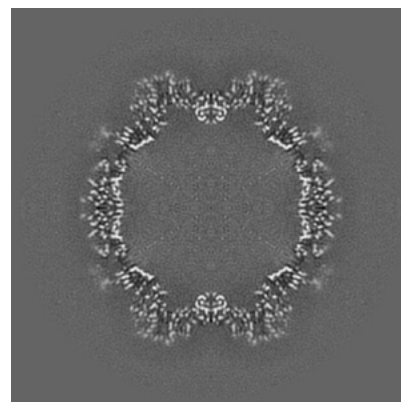
6.2.1 Primary map



X Index: 179



Y Index: 179

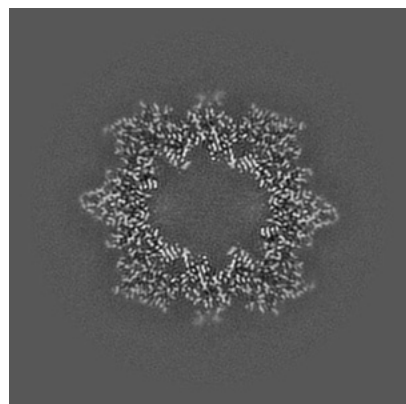


Z Index: 179

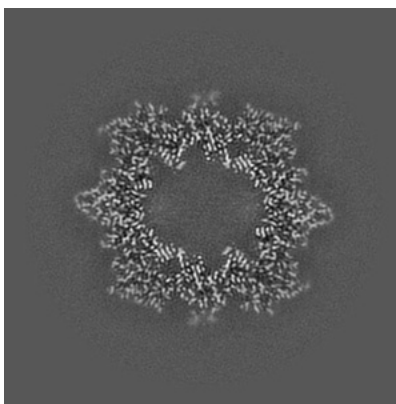
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

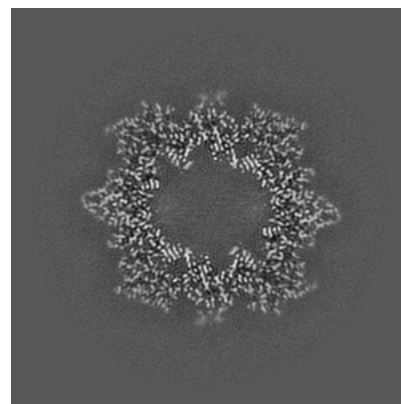
6.3.1 Primary map



X Index: 115



Y Index: 115

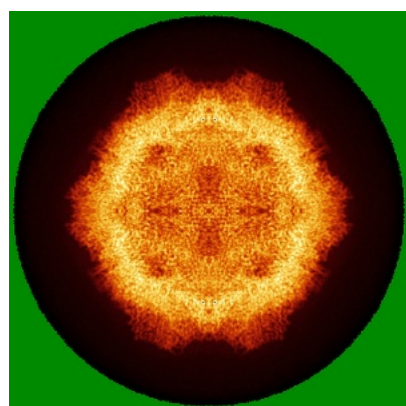


Z Index: 115

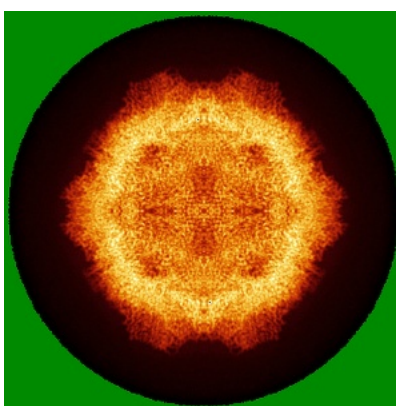
The images above show the largest variance slices of the map in three orthogonal directions.

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

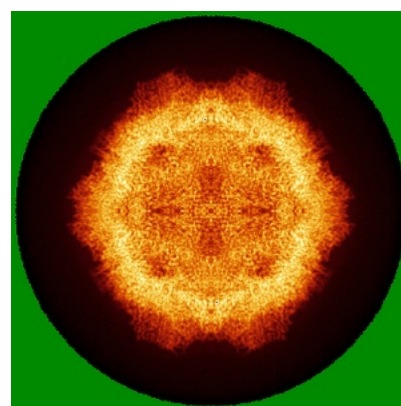
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

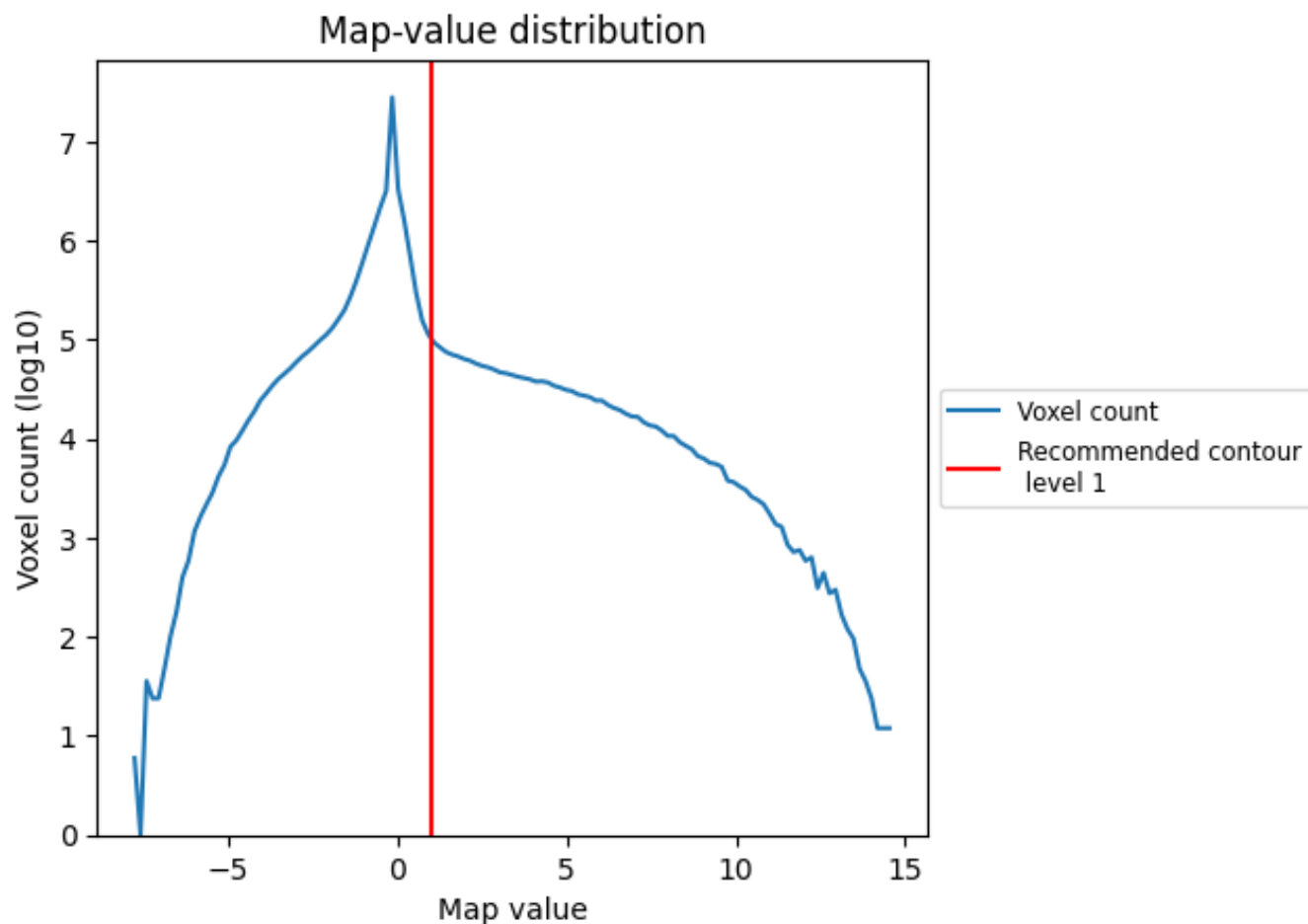
6.6 Mask visualisation

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

7 Map analysis [i](#)

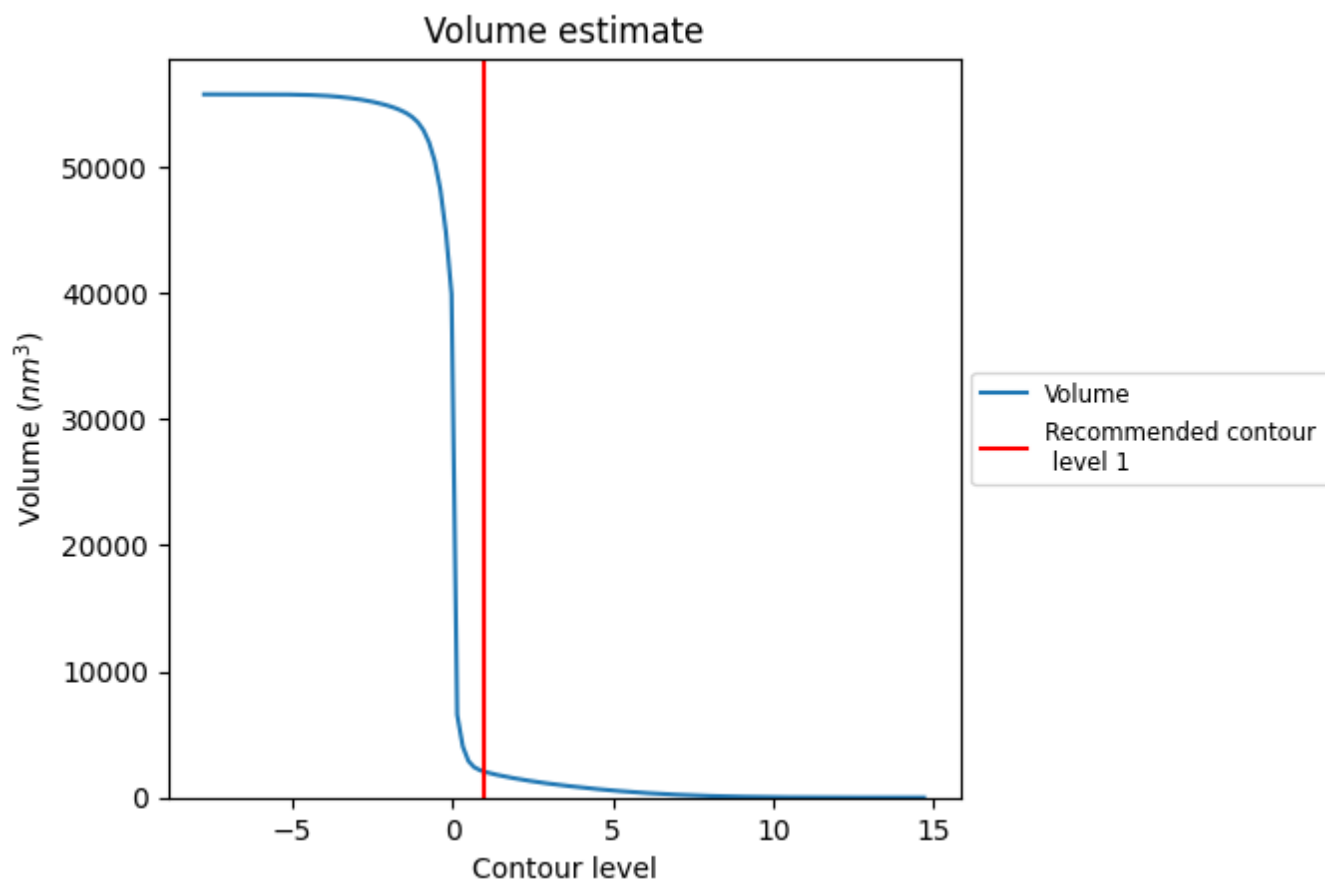
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

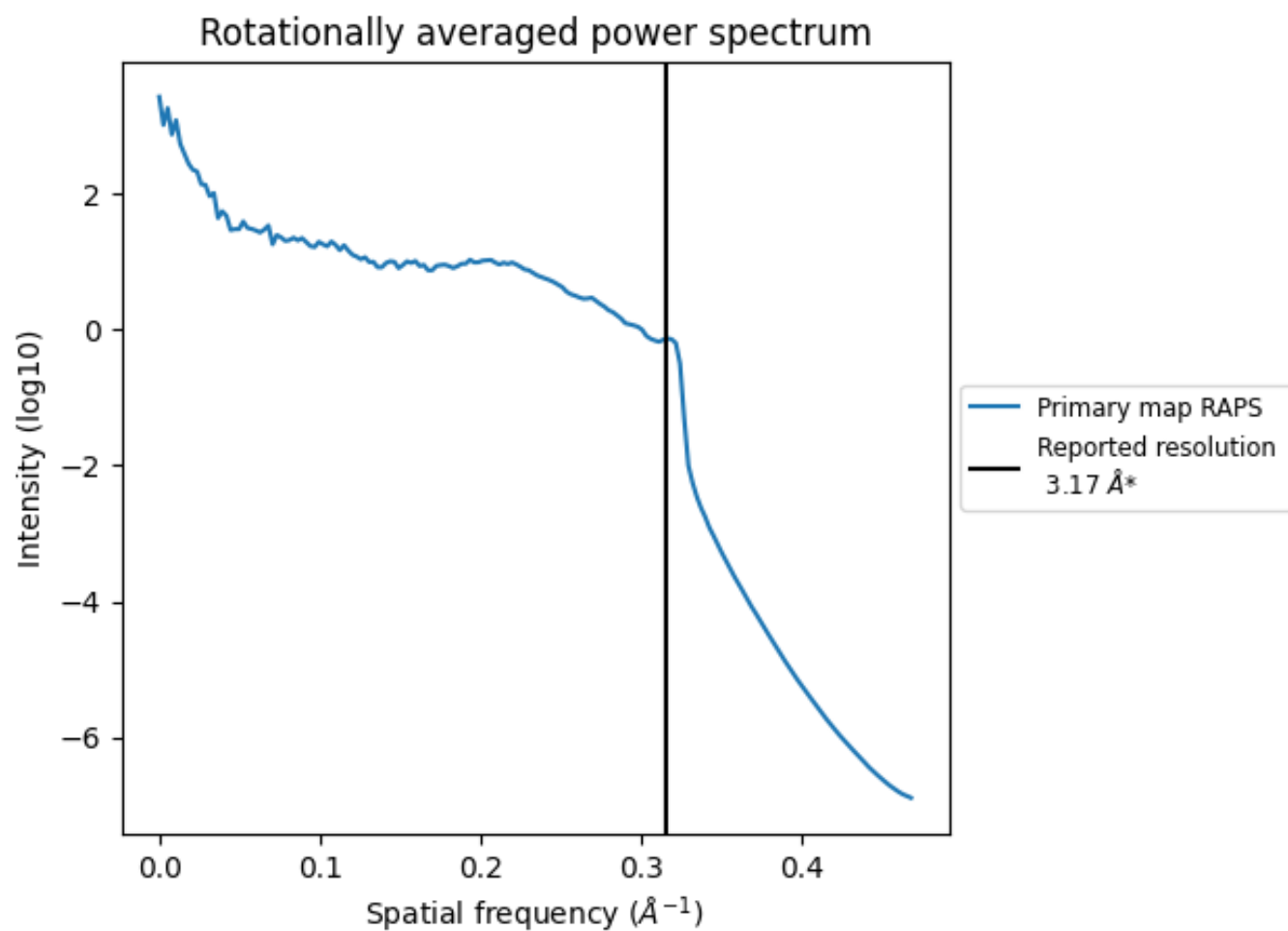
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2048 nm³; this corresponds to an approximate mass of 1850 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 0.315 Å⁻¹

8 Fourier-Shell correlation

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

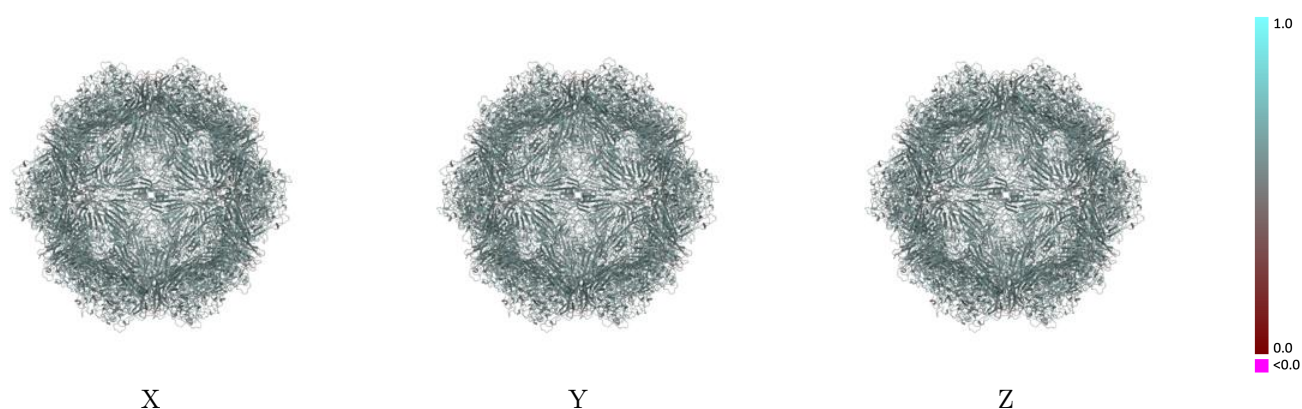
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7071 and PDB model 6B9Q. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)

This section was not generated.

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

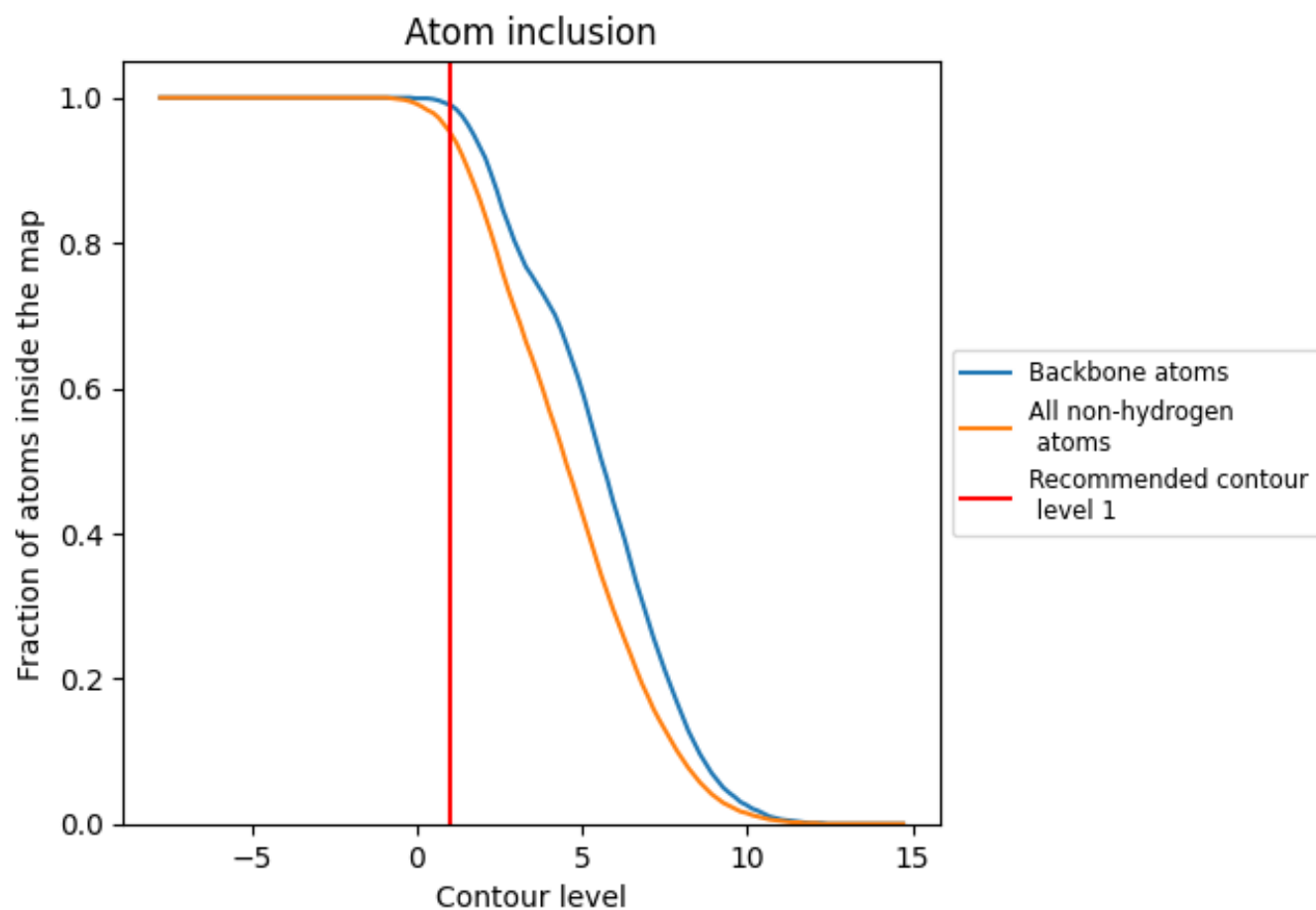


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 95% 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	 0.9530	 0.5620
1	 0.9540	 0.5640
2	 0.9540	 0.5640
3	 0.9540	 0.5640
4	 0.9540	 0.5630
5	 0.9540	 0.5630
6	 0.9540	 0.5630
7	 0.9520	 0.5630
8	 0.9520	 0.5620
A	 0.9540	 0.5630
B	 0.9540	 0.5620
C	 0.9510	 0.5620
D	 0.9530	 0.5620
E	 0.9520	 0.5620
F	 0.9540	 0.5610
G	 0.9520	 0.5620
H	 0.9520	 0.5620
I	 0.9510	 0.5610
J	 0.9540	 0.5620
K	 0.9520	 0.5620
L	 0.9550	 0.5620
M	 0.9520	 0.5640
N	 0.9520	 0.5630
O	 0.9520	 0.5630
P	 0.9520	 0.5620
Q	 0.9510	 0.5610
R	 0.9540	 0.5610
S	 0.9540	 0.5630
T	 0.9510	 0.5620
U	 0.9540	 0.5620
V	 0.9520	 0.5600
W	 0.9520	 0.5610
X	 0.9520	 0.5620
Y	 0.9500	 0.5630
Z	 0.9520	 0.5630



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Chain	Atom inclusion	Q-score
a	 0.9510	 0.5620
b	 0.9520	 0.5630
c	 0.9520	 0.5630
d	 0.9520	 0.5620
e	 0.9530	 0.5630
f	 0.9520	 0.5630
g	 0.9520	 0.5620
h	 0.9540	 0.5640
i	 0.9520	 0.5630
j	 0.9520	 0.5600
k	 0.9540	 0.5610
l	 0.9540	 0.5620
m	 0.9540	 0.5630
n	 0.9520	 0.5620
o	 0.9510	 0.5610
p	 0.9540	 0.5620
q	 0.9520	 0.5630
r	 0.9510	 0.5600
s	 0.9540	 0.5610
t	 0.9540	 0.5620
u	 0.9550	 0.5620
v	 0.9540	 0.5620
w	 0.9540	 0.5620
x	 0.9520	 0.5620
y	 0.9520	 0.5610
z	 0.9530	 0.5620