



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 03:06 AM UTC

PDB ID : 9CV0 / pdb_00009cv0
EMDB ID : EMD-45955
Title : Bufavirus 1 at pH 7.4
Authors : Gulkis, M.C.; McKenna, R.; Bennett, A.D.
Deposited on : 2024-07-27
Resolution : 2.84 Å (reported)
Based on initial model : 6BWX

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

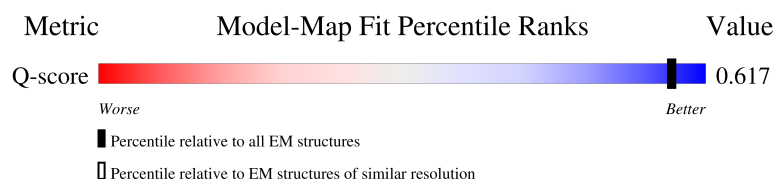
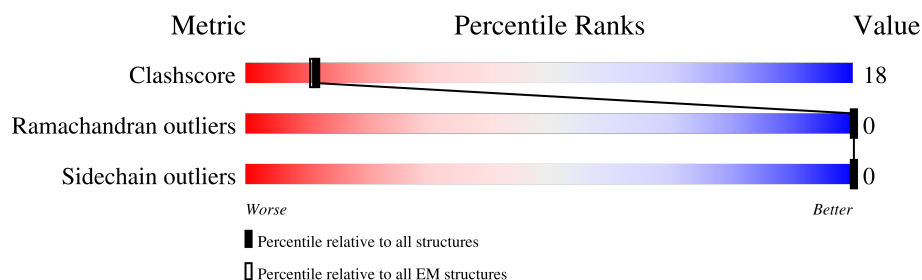
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.84 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.



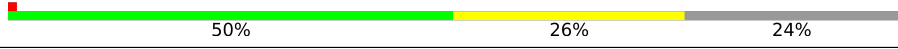
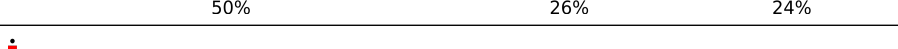
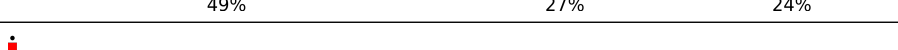
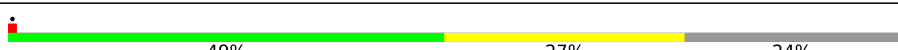
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11884 (2.34 - 3.34)

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	707	
1	2	707	
1	3	707	
1	4	707	

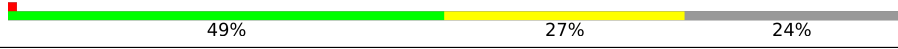
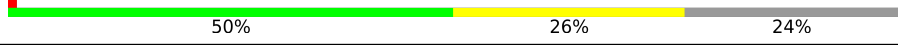
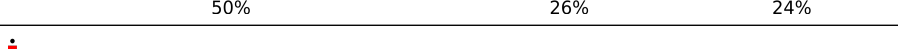
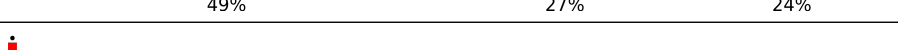
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Mol	Chain	Length	Quality of chain
1	5	707	
1	6	707	
1	7	707	
1	8	707	
1	A	707	
1	B	707	
1	C	707	
1	D	707	
1	E	707	
1	F	707	
1	G	707	
1	H	707	
1	I	707	
1	J	707	
1	K	707	
1	L	707	
1	M	707	
1	N	707	
1	O	707	
1	P	707	
1	Q	707	
1	R	707	
1	S	707	
1	T	707	
1	U	707	

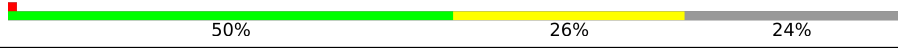
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Mol	Chain	Length	Quality of chain
1	V	707	
1	W	707	
1	X	707	
1	Y	707	
1	Z	707	
1	a	707	
1	b	707	
1	c	707	
1	d	707	
1	e	707	
1	f	707	
1	g	707	
1	h	707	
1	i	707	
1	j	707	
1	k	707	
1	l	707	
1	m	707	
1	n	707	
1	o	707	
1	p	707	
1	q	707	
1	r	707	
1	s	707	
1	t	707	

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Mol	Chain	Length	Quality of chain
1	u	707	
1	v	707	
1	w	707	
1	x	707	
1	y	707	
1	z	707	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 261180 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	B	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	C	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	D	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	E	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	F	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	G	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	H	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	I	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	J	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	K	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	L	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	M	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	N	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	O	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	P	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		
1	Q	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	S	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	T	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	U	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	V	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	W	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	X	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	Y	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	Z	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	a	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	b	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	c	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	d	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	e	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	f	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	g	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	h	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	i	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	j	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	k	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	l	537	Total 4353	C 2754	N 764	O 821	S 14	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	n	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	o	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	p	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	q	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	r	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	s	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	t	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	u	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	v	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	w	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	x	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	y	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	z	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	1	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	2	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	3	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	4	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	5	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	6	537	Total 4353	C 2754	N 764	O 821	S 14	0	0
1	7	537	Total 4353	C 2754	N 764	O 821	S 14	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	537	Total	C	N	O	S	0	0
			4353	2754	764	821	14		

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	35	VAL	ILE	conflict	UNP A0A097PIM0
B	35	VAL	ILE	conflict	UNP A0A097PIM0
C	35	VAL	ILE	conflict	UNP A0A097PIM0
D	35	VAL	ILE	conflict	UNP A0A097PIM0
E	35	VAL	ILE	conflict	UNP A0A097PIM0
F	35	VAL	ILE	conflict	UNP A0A097PIM0
G	35	VAL	ILE	conflict	UNP A0A097PIM0
H	35	VAL	ILE	conflict	UNP A0A097PIM0
I	35	VAL	ILE	conflict	UNP A0A097PIM0
J	35	VAL	ILE	conflict	UNP A0A097PIM0
K	35	VAL	ILE	conflict	UNP A0A097PIM0
L	35	VAL	ILE	conflict	UNP A0A097PIM0
M	35	VAL	ILE	conflict	UNP A0A097PIM0
N	35	VAL	ILE	conflict	UNP A0A097PIM0
O	35	VAL	ILE	conflict	UNP A0A097PIM0
P	35	VAL	ILE	conflict	UNP A0A097PIM0
Q	35	VAL	ILE	conflict	UNP A0A097PIM0
R	35	VAL	ILE	conflict	UNP A0A097PIM0
S	35	VAL	ILE	conflict	UNP A0A097PIM0
T	35	VAL	ILE	conflict	UNP A0A097PIM0
U	35	VAL	ILE	conflict	UNP A0A097PIM0
V	35	VAL	ILE	conflict	UNP A0A097PIM0
W	35	VAL	ILE	conflict	UNP A0A097PIM0
X	35	VAL	ILE	conflict	UNP A0A097PIM0
Y	35	VAL	ILE	conflict	UNP A0A097PIM0
Z	35	VAL	ILE	conflict	UNP A0A097PIM0
a	35	VAL	ILE	conflict	UNP A0A097PIM0
b	35	VAL	ILE	conflict	UNP A0A097PIM0
c	35	VAL	ILE	conflict	UNP A0A097PIM0
d	35	VAL	ILE	conflict	UNP A0A097PIM0
e	35	VAL	ILE	conflict	UNP A0A097PIM0
f	35	VAL	ILE	conflict	UNP A0A097PIM0
g	35	VAL	ILE	conflict	UNP A0A097PIM0
h	35	VAL	ILE	conflict	UNP A0A097PIM0
i	35	VAL	ILE	conflict	UNP A0A097PIM0
j	35	VAL	ILE	conflict	UNP A0A097PIM0

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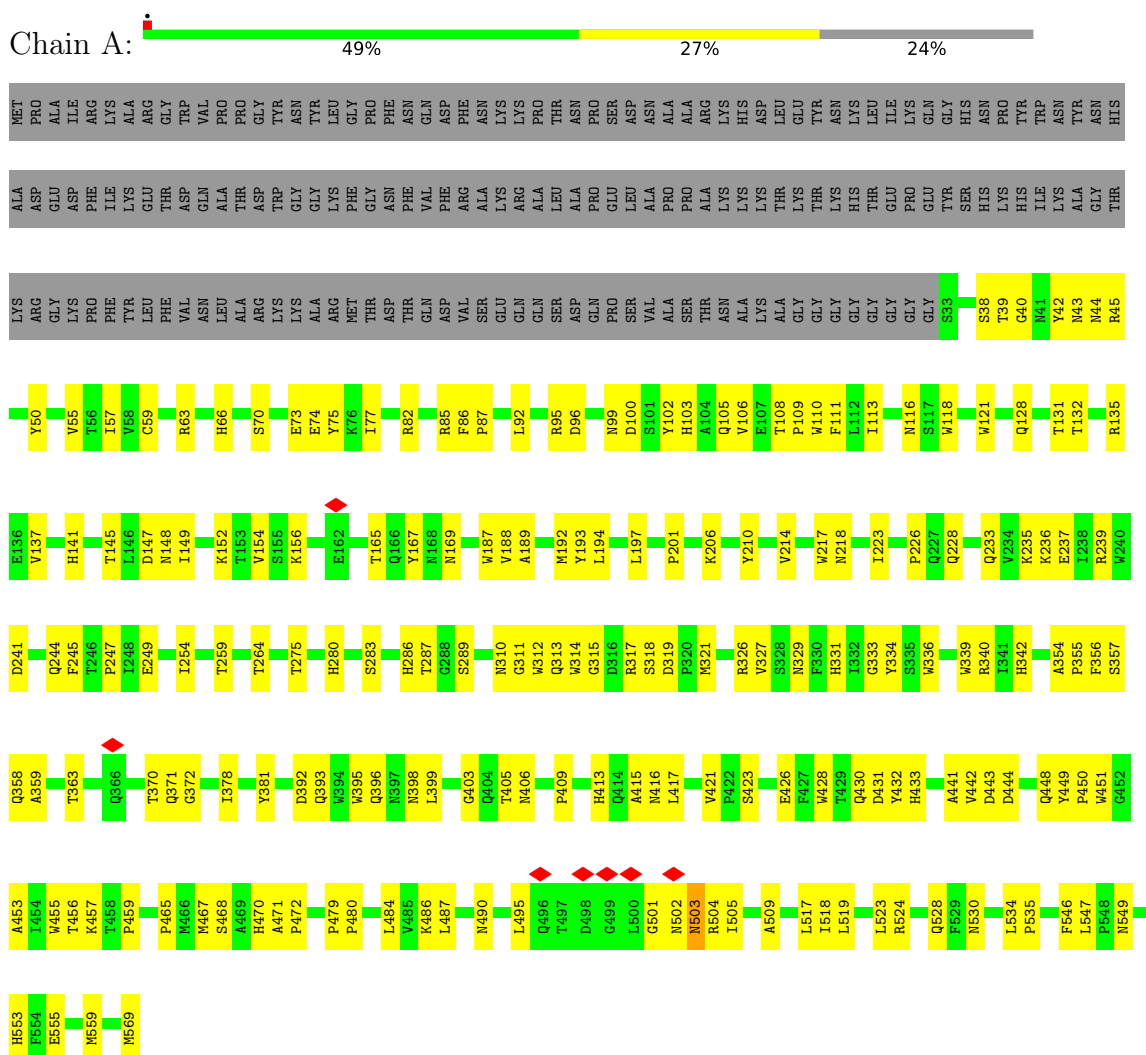
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Chain	Residue	Modelled	Actual	Comment	Reference
k	35	VAL	ILE	conflict	UNP A0A097PIM0
l	35	VAL	ILE	conflict	UNP A0A097PIM0
m	35	VAL	ILE	conflict	UNP A0A097PIM0
n	35	VAL	ILE	conflict	UNP A0A097PIM0
o	35	VAL	ILE	conflict	UNP A0A097PIM0
p	35	VAL	ILE	conflict	UNP A0A097PIM0
q	35	VAL	ILE	conflict	UNP A0A097PIM0
r	35	VAL	ILE	conflict	UNP A0A097PIM0
s	35	VAL	ILE	conflict	UNP A0A097PIM0
t	35	VAL	ILE	conflict	UNP A0A097PIM0
u	35	VAL	ILE	conflict	UNP A0A097PIM0
v	35	VAL	ILE	conflict	UNP A0A097PIM0
w	35	VAL	ILE	conflict	UNP A0A097PIM0
x	35	VAL	ILE	conflict	UNP A0A097PIM0
y	35	VAL	ILE	conflict	UNP A0A097PIM0
z	35	VAL	ILE	conflict	UNP A0A097PIM0
1	35	VAL	ILE	conflict	UNP A0A097PIM0
2	35	VAL	ILE	conflict	UNP A0A097PIM0
3	35	VAL	ILE	conflict	UNP A0A097PIM0
4	35	VAL	ILE	conflict	UNP A0A097PIM0
5	35	VAL	ILE	conflict	UNP A0A097PIM0
6	35	VAL	ILE	conflict	UNP A0A097PIM0
7	35	VAL	ILE	conflict	UNP A0A097PIM0
8	35	VAL	ILE	conflict	UNP A0A097PIM0

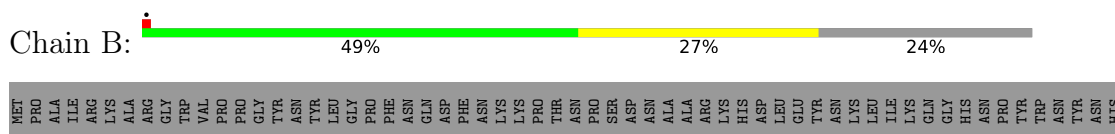
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: VP1



• Molecule 1: VP1



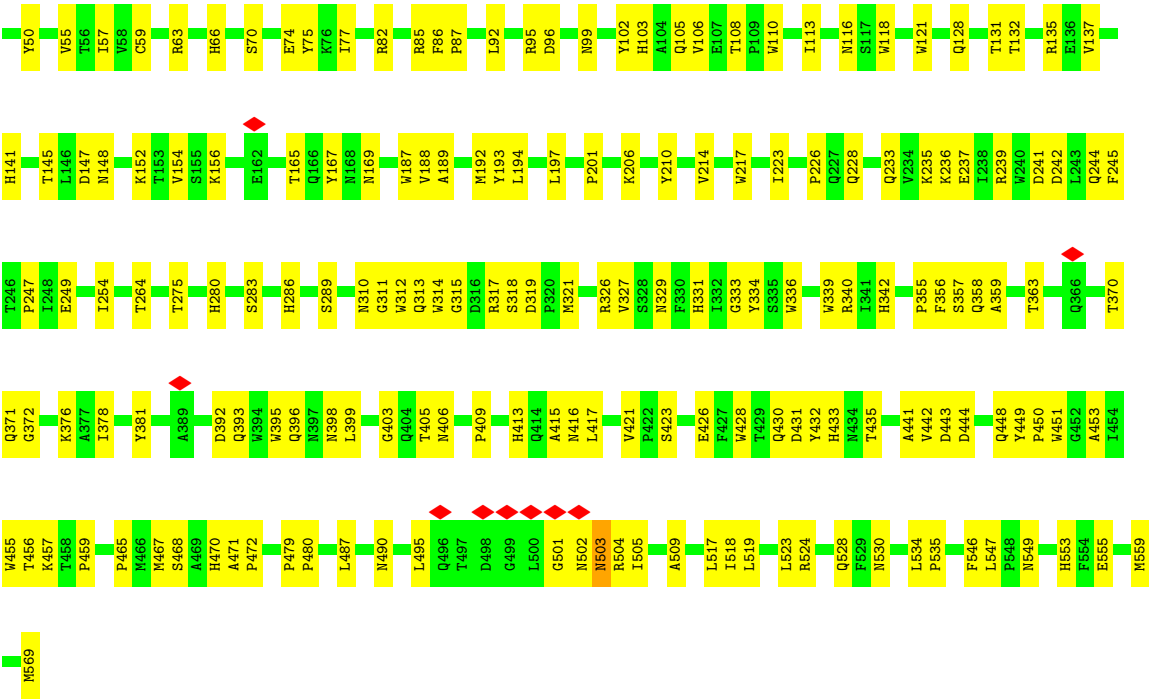
ALA	LYS	R135	R239	F356	G452	H653	LYS
ASP	ARG	E136	W240	S357	A453	H654	ARG
GLU	GLY	V137	D241	Q358	I454	F554	GLY
PRO	LYS	V55	Q244	A359	W455	E555	LYS
PHE	PRO	H141	F245	T363	T456	M559	PHE
ILE	TVR	I57	T246	T366	T458	M659	ILE
LYS	LEU	V58	P247	Q366	P459		LYS
GLU	THR	C59	L146	T370	P465		GLU
THR	VAL	R63	D147	Q371	W466		THR
ASN	ASN	N148	E249	G372	A467		ASN
GLN	LEU	H66	T254	I378	S468		GLN
THR	ALA	S70	R258	Y381	A469		THR
ASP	ARG	E73	T264	P472	H470		ASP
TRP	LYS	S155	T264	Y381	A471		TRP
GLY	ALA	K156	T275	D392	P479		GLY
GLY	ALA	E74	T275	Q393	P480		GLY
PHE	MET	Y75	E162	W394	K486		PHE
GLY	THR	K76	T165	Q395	L487		GLY
ASN	ASP	I77	Q166	W396	K488		ASN
PHE	THR	R82	Y167	Q396	L487		PHE
VAL	GLN	R85	N168	N397	H490		VAL
PHE	ASP	R86	N169	I398			PHE
ARG	VAL	P87	T172	L399			ARG
ALA	SER	L92	W187	Q403	E493		ALA
LYS	GLN	R95	V188	T405	N494		LYS
ARG	ALA	D96	A189	P409	Q496		ARG
LEU	SER	N99	M192	H413	T497		LEU
ALA	GLN	D100	W193	Q414	D498		ALA
PRO	PRO	Y102	L194	A415	Q499		PRO
GLU	ALA	S101	L197	N416	L500		GLU
LEU	VAL	H103	P201	L417	G501		LEU
ALA	SER	A104	Q105	V421	N502		ALA
LYS	THR	E107	K206	S423	N503		LYS
LYS	GLY	V106	M321	E426	I504		LYS
THR	GLY	T108	R326	F427	I505		THR
LYS	GLY	P109	V327	W428	A509		LYS
LYS	GLY	W110	S328	T429	L517		LYS
HIS	GLY	I113	N329	W428	I518		HIS
GLY	GLY	N217	H331	Q430	L519		GLY
GLY	GLY	N218	F330	D431	L523		GLY
PRO	GLY	N116	G333	Y432	R524		PRO
GLU	GLY	S117	Y334	H433			GLU
GLY	GLY	W118	S335	A441	Q528		GLY
TYR	GLY	S33	P226	A441	F529		TYR
SER	SER	W121	Q227	V442	N530		SER
HIS	LYS	S38	Q228	D443	L534		HIS
LYS	T39	G40	W339	D444	P535		LYS
ILE	HIS	Q128	R340	Q448	L546		ILE
LYS	ILE	Y42	T341	Q448	F546		LYS
LYS	LYS	N41	H342	Y449	L547		LYS
GLY	ALA	Y42	R342	P450	P546		GLY
GLY	ALA	N43	A354	W451	F546		GLY
THR	THR	R45	P355	W451	N549		THR

● Molecule 1: VP1

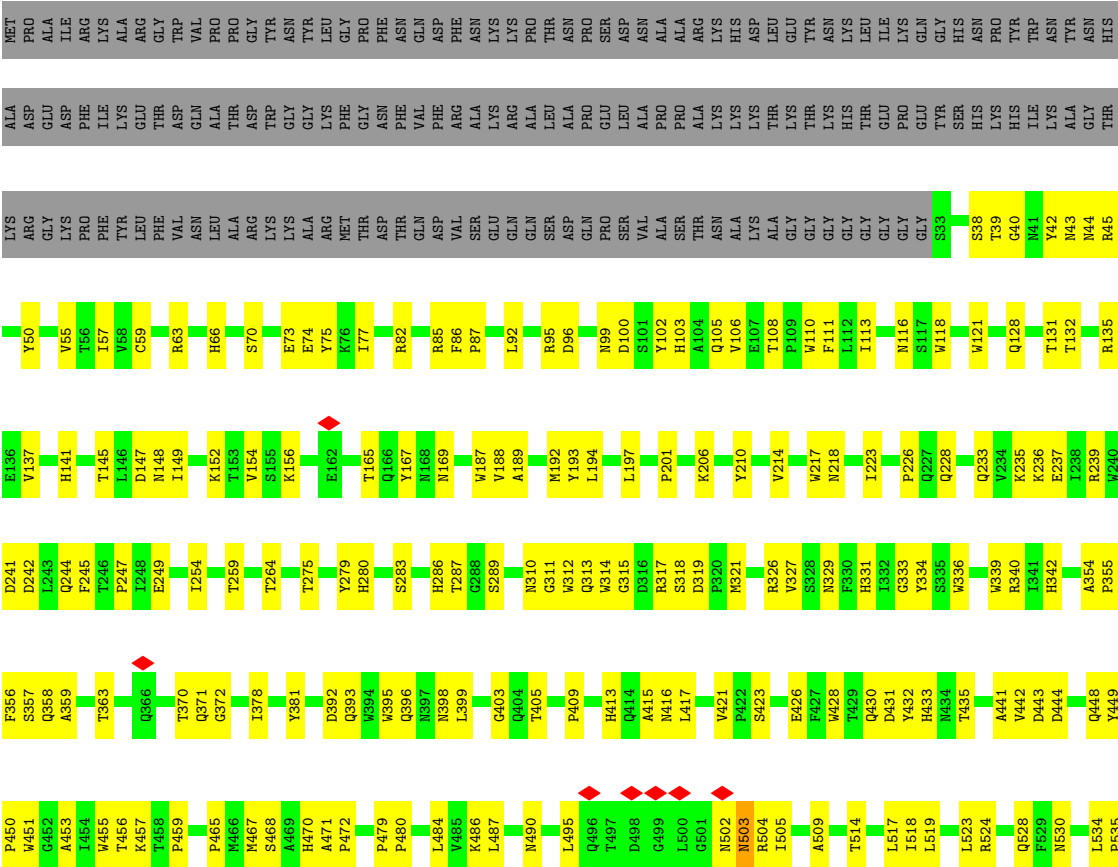


MET	LYS	R45	D241	A359	LYS
PRO	ARG	Y50	Q244	T363	ARG
ALA	GLY	V55	F245	Q366	GLY
ILE	LYS	V56	T246	T370	LYS
LYS	PHE	I57	T248	Q371	PHE
ALA	TYR	V58	E249	G372	ALA
GLY	LEU	C59	T254	I378	GLY
THR	VAL	R63	T259	Y381	THR
ASN	ASN	H66	T264	D392	ASN
VAL	LEU	S70	T275	Q393	VAL
PRO	ALA	E73	Y279	W394	PRO
GLY	THR	E74	H280	Q395	GLY
LYS	ARG	Y75	S283	N397	LYS
LEU	MET	K76	H286	L399	LEU
PRO	THR	I77	T287	G403	PRO
PHE	ASP	R82	N310	Q404	PHE
GLN	VAL	R85	G311	Q404	GLN
ASP	PHE	F86	W312	V188	ASP
PHE	ALA	P87	Q313	A189	PHE
ASN	LYS	L92	W314	M192	ASN
LYS	GLY	R95	G315	Y193	LYS
THR	LEU	D96	R316	L194	THR
PRO	PRO	N99	S318	L197	PRO
ALA	ALA	Y102	D319	P201	ALA
ALA	SER	H103	N321	Q206	ALA
ARG	THR	A104	R326	Y210	ARG
LYS	LYS	Q105	V327	W214	LYS
ASP	ASP	E107	S328	W217	ASP
LYS	LYS	T108	N329	I223	LYS
LEU	LYS	P109	F330	P226	LEU
GLY	GLY	W110	H331	Q227	GLY
GLY	GLY	F111	G332	Q228	GLY
GLY	GLY	I113	Y334	Q233	GLY
GLY	GLY	N116	S335	K235	GLY
GLY	GLY	S117	W336	R236	GLY
GLY	GLY	W118	W339	I238	GLY
S33	S33	W121	R340	R239	S33
H37	H37	Q128	H342	Y240	H37
S38	S38	A125	A354	F355	S38
T39	T39	Q128	P355	I454	T39
G40	G40	T131	S357	I454	G40
N41	N41	T132	Q358	W455	N41
Y42	Y42				Y42
N43	N43				N43
N44	N44				N44





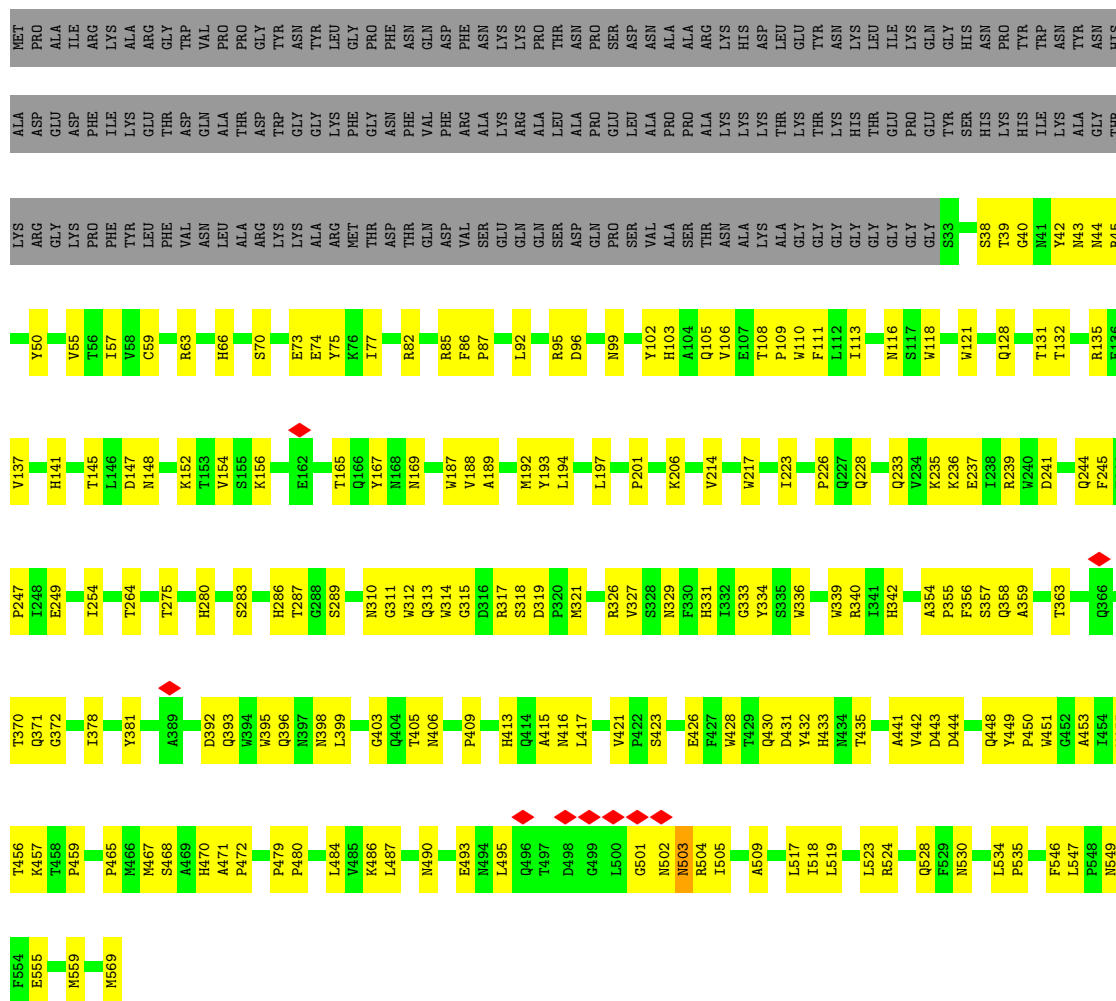
• Molecule 1: VP1





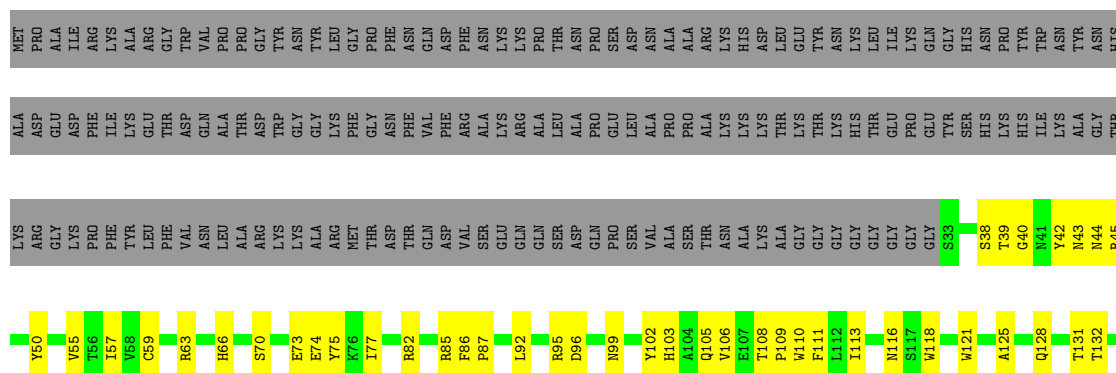
• Molecule 1: VP1

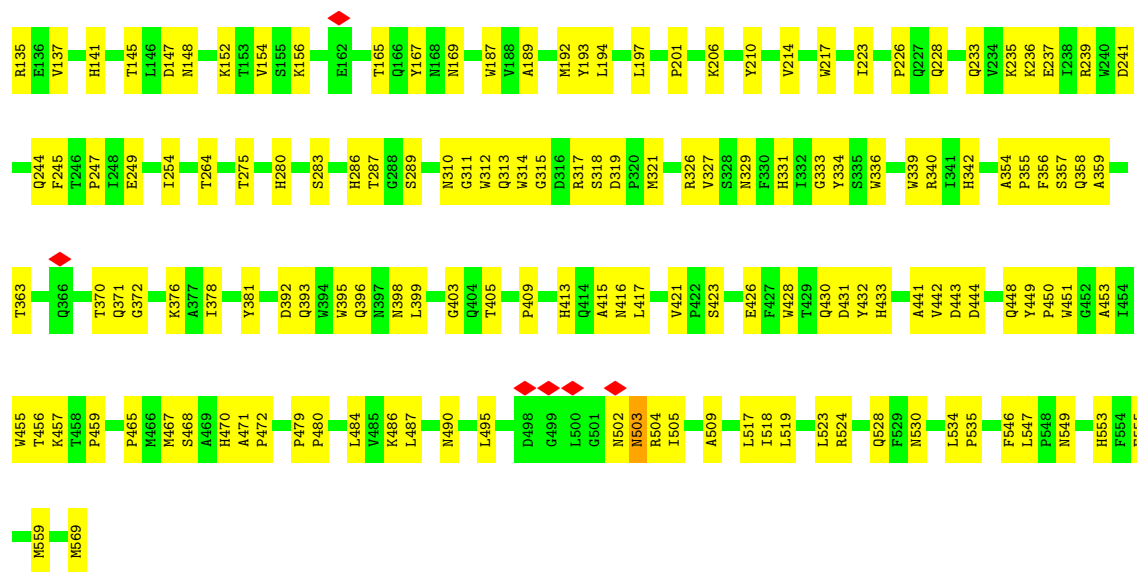
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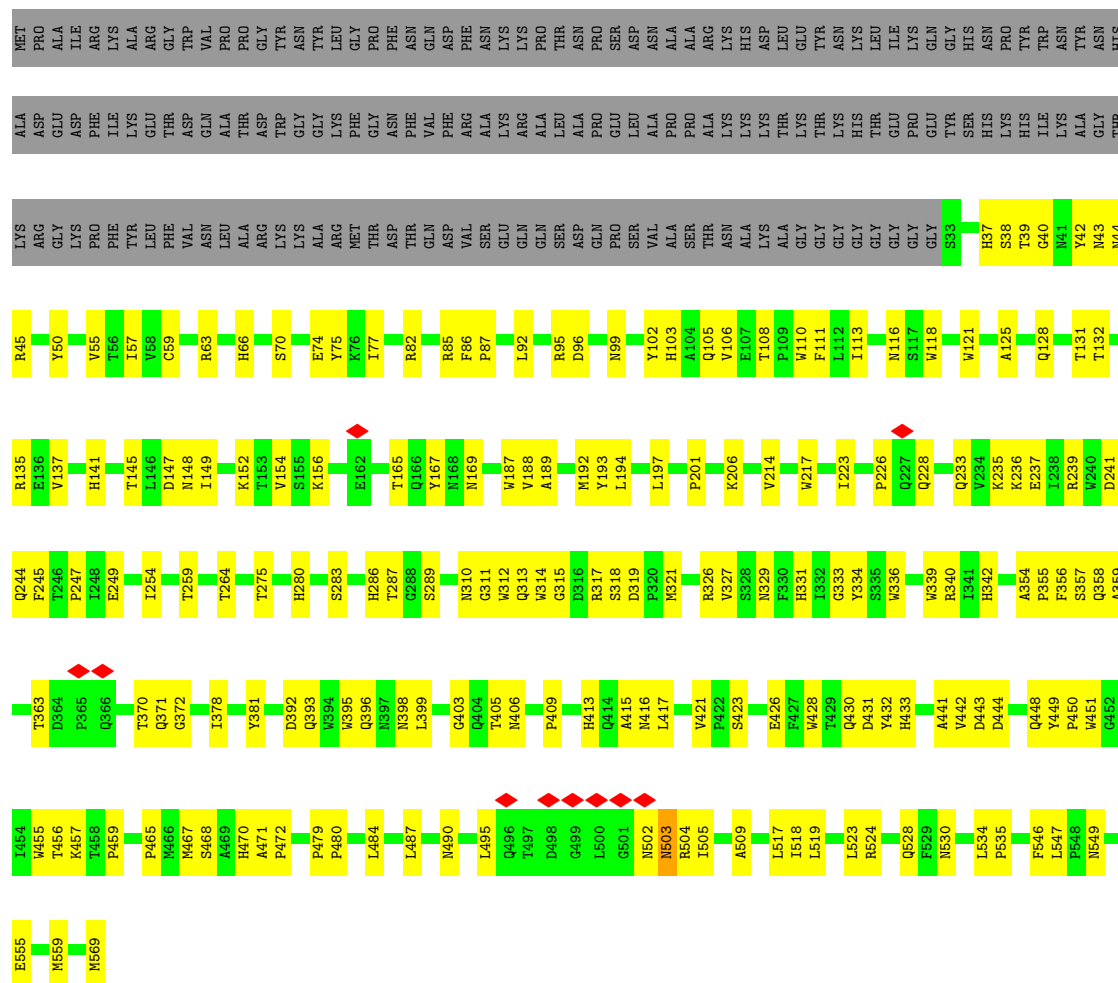
• Molecule 1: VP1

Chain H:



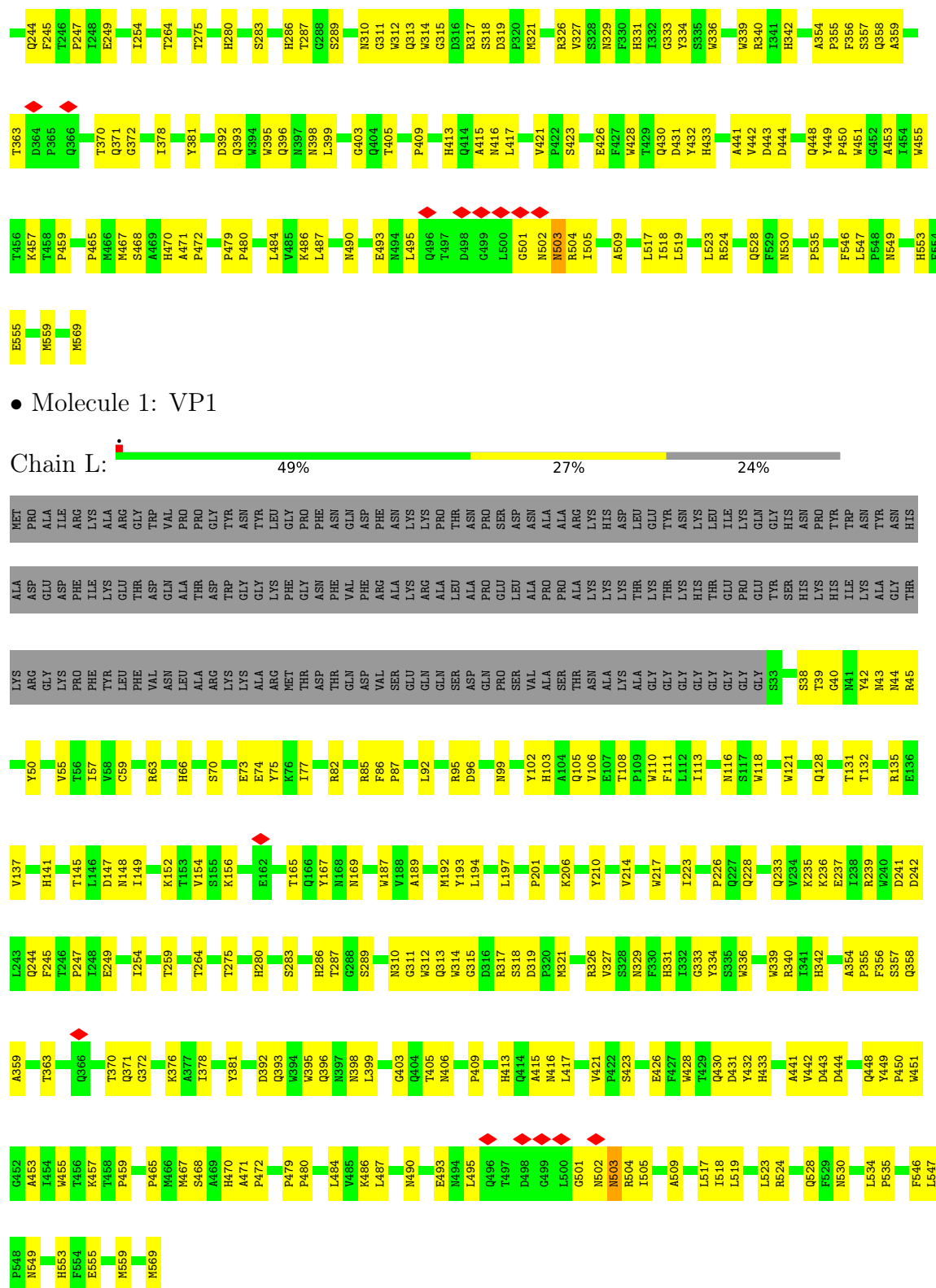


• Molecule 1: VP1



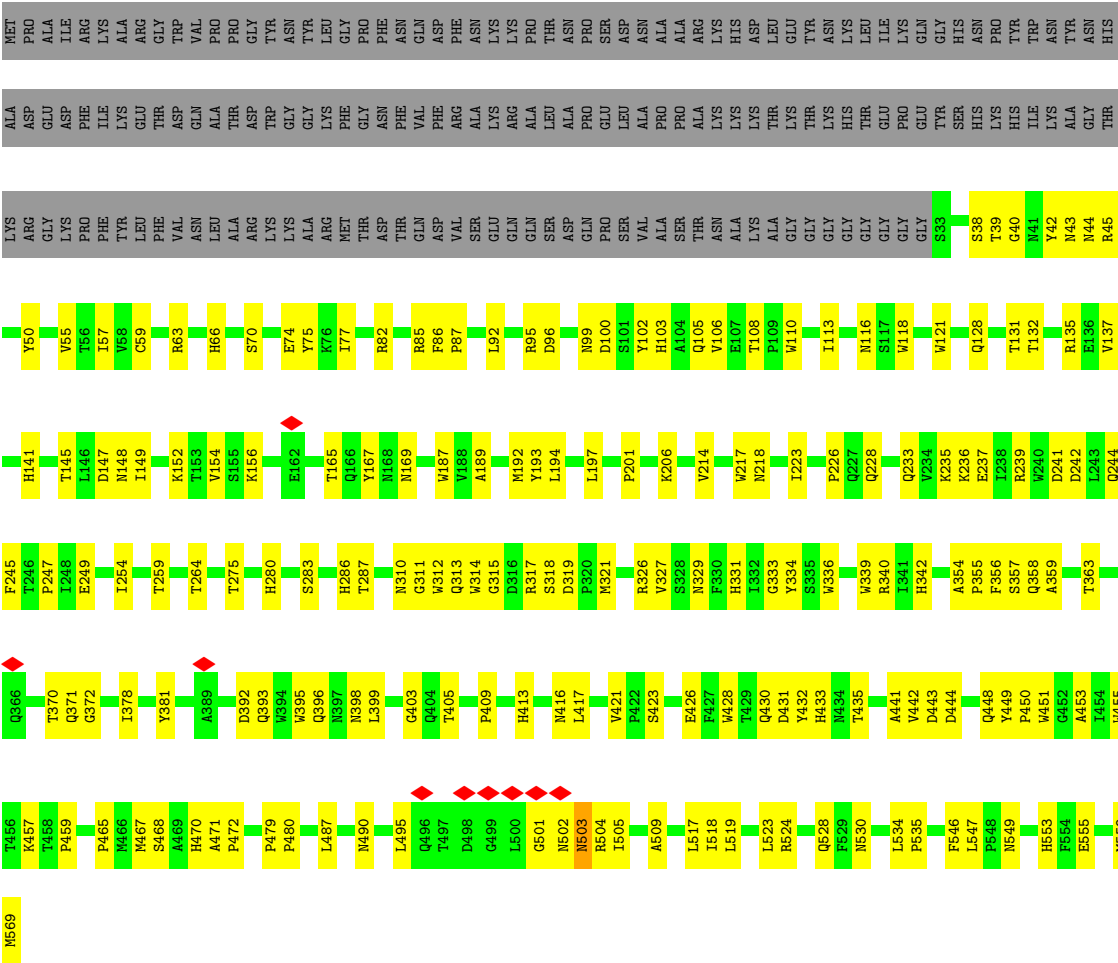
• Molecule 1: VP1



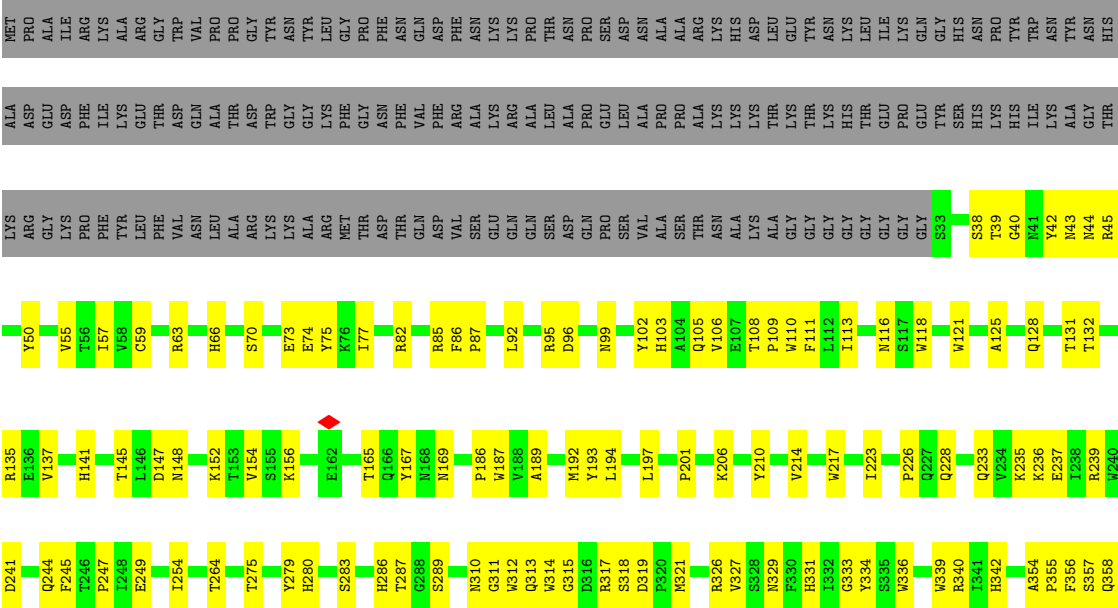


• Molecule 1: VP1

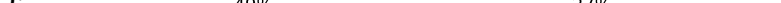


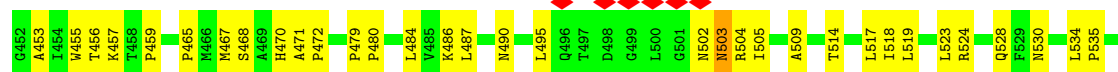
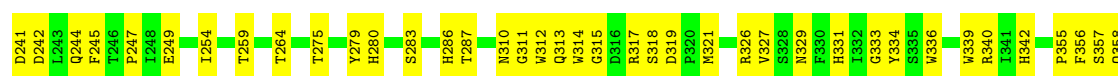
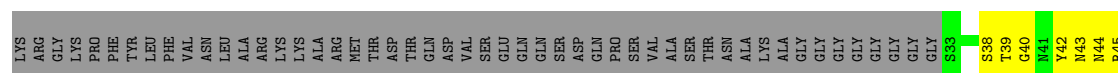
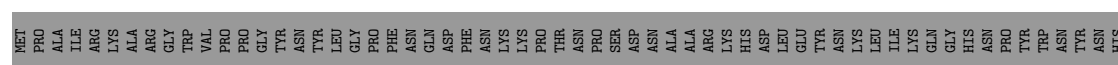


● Molecule 1: VP1



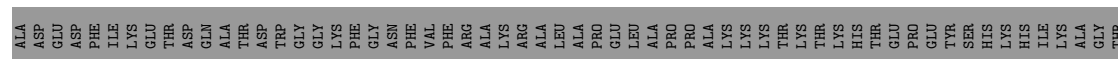
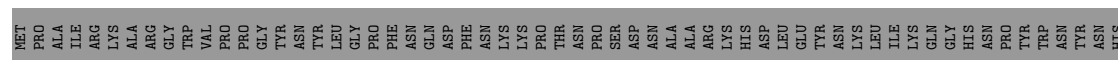
- Molecule 1: VP1

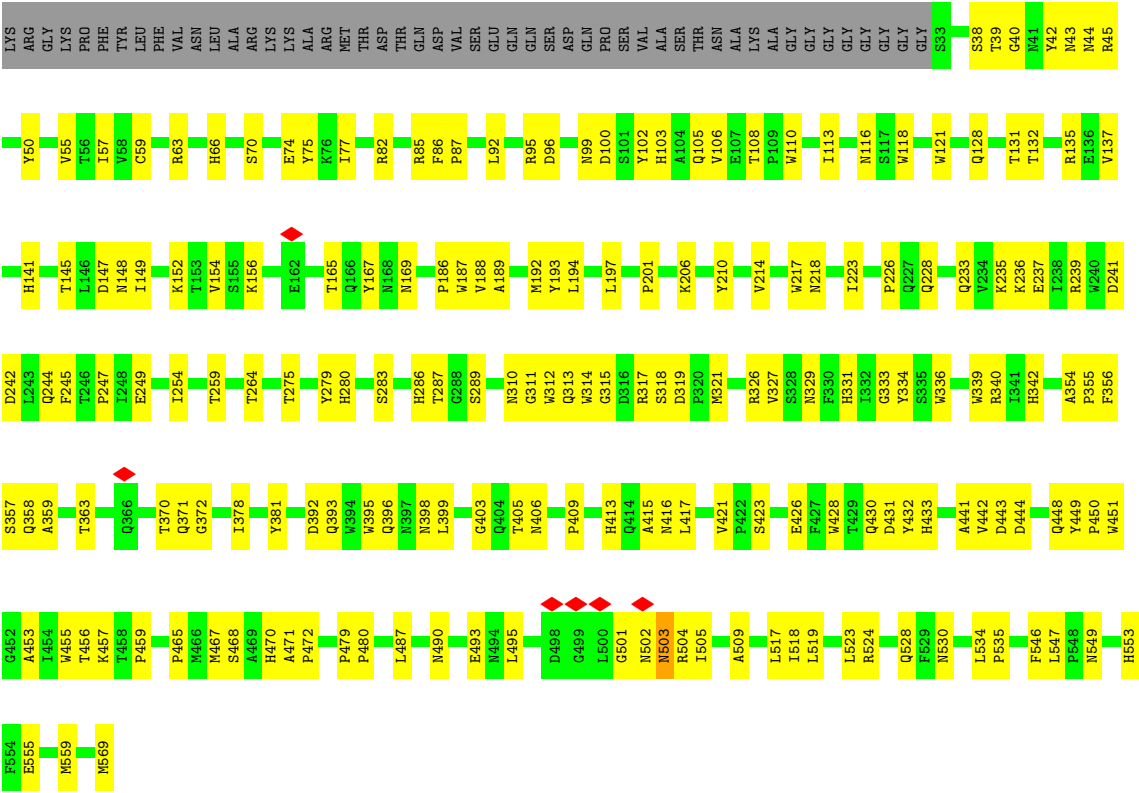
Chain O: 



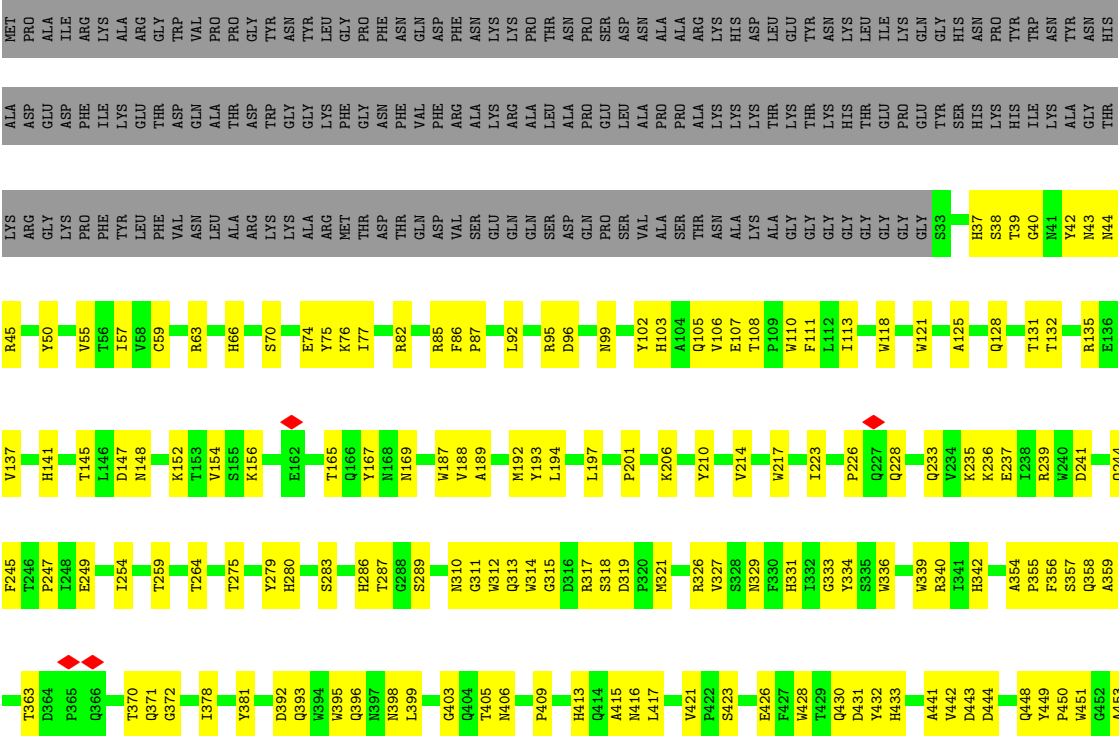
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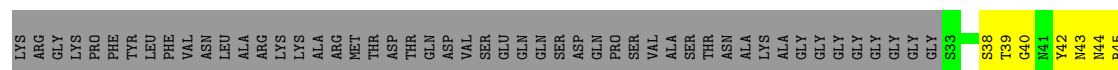
Chain P: 49% 27% 24%





• Molecule 1: VP1

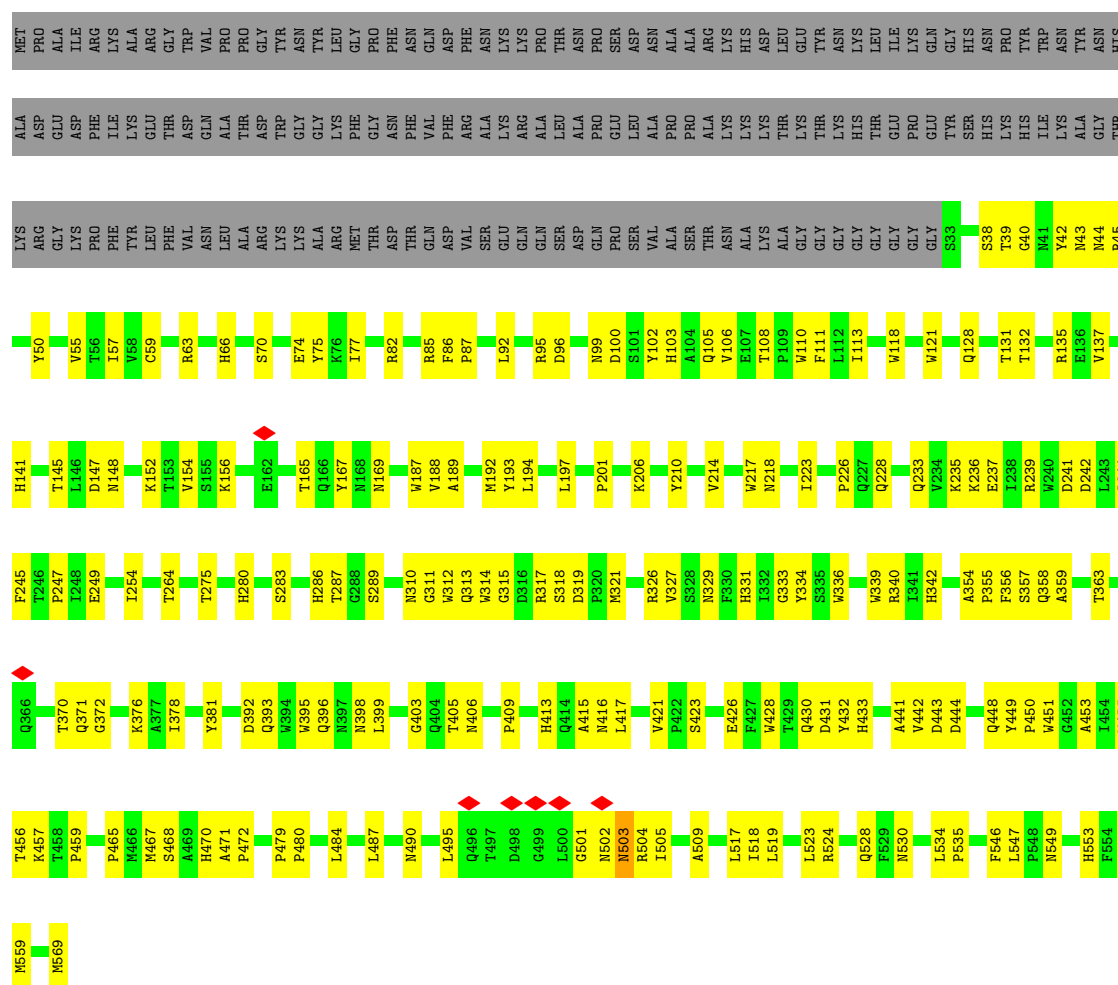




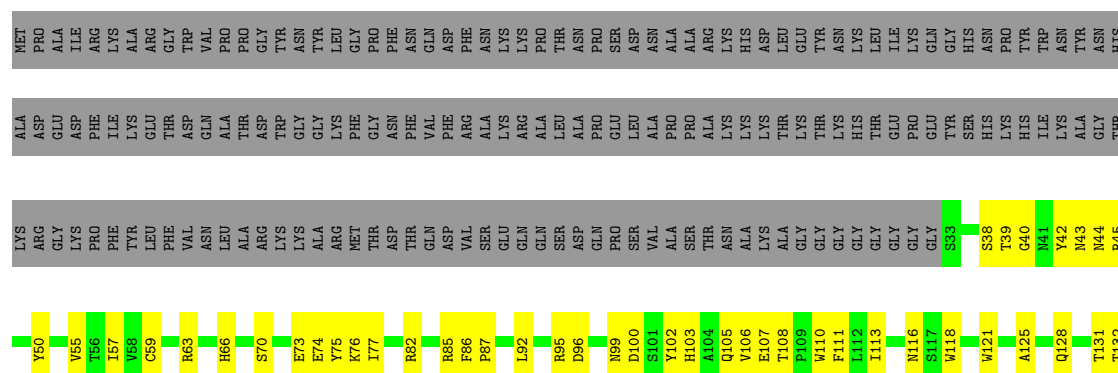


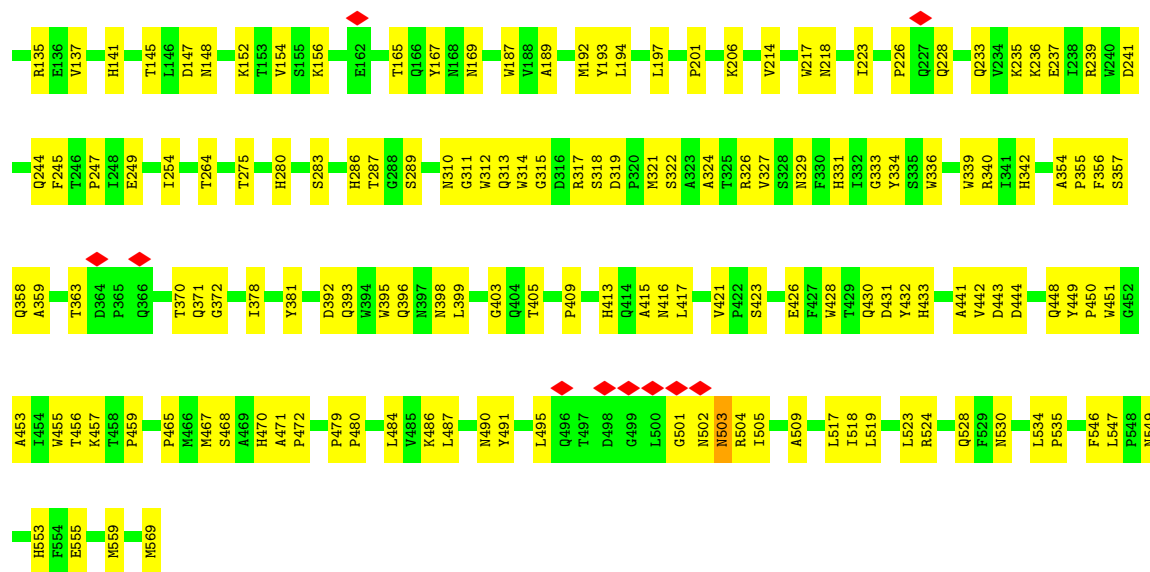


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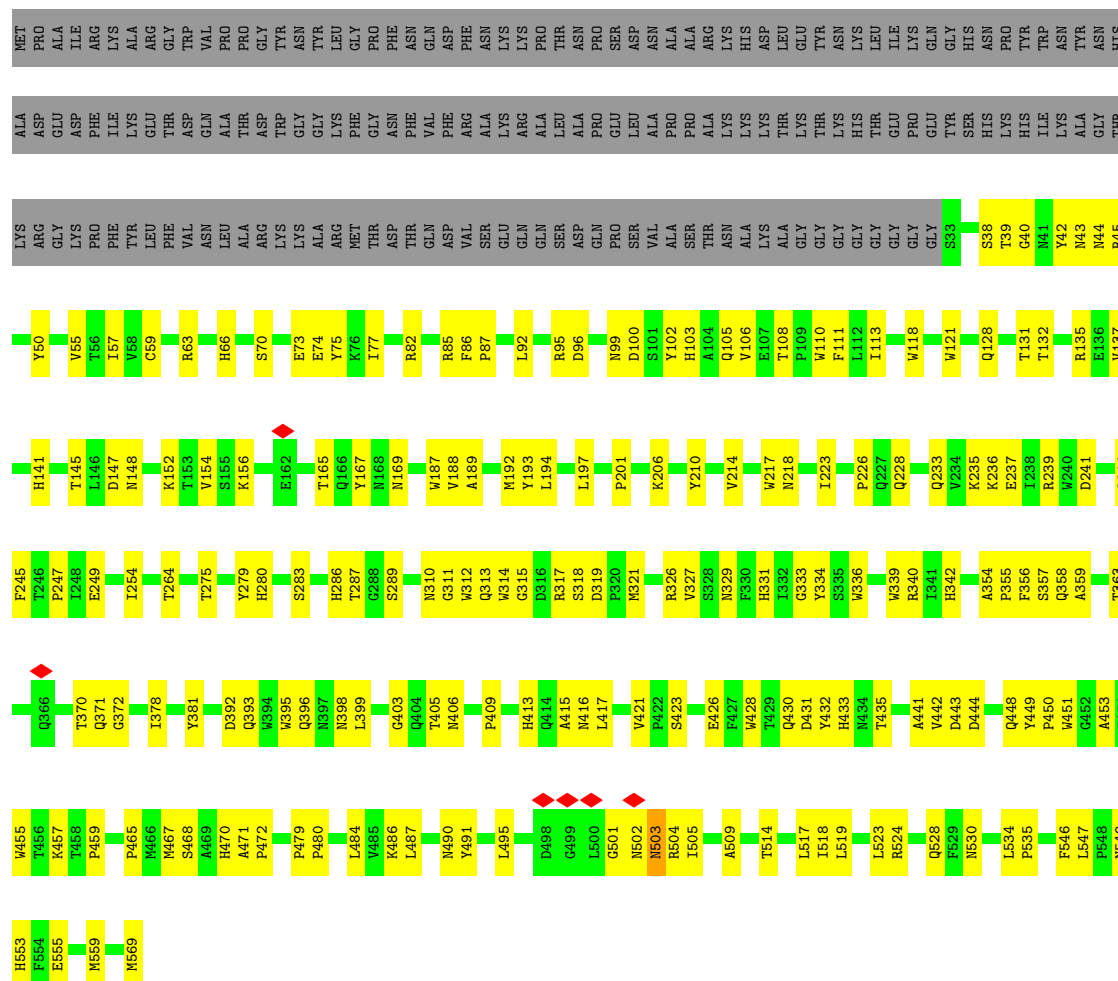


• Molecule 1: VP1



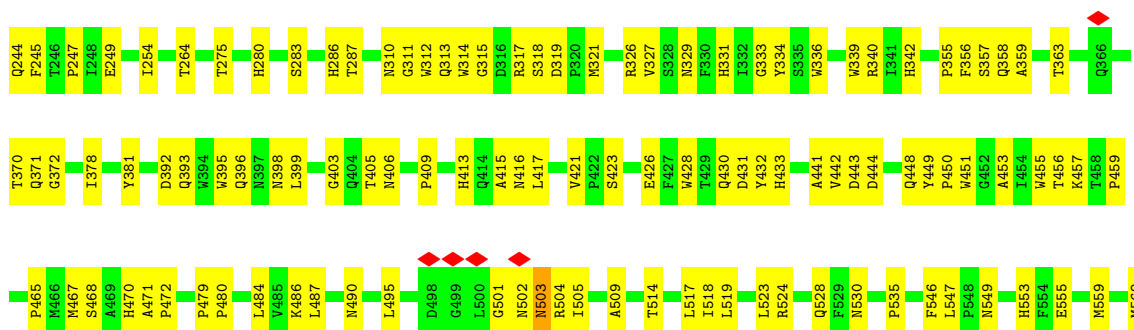


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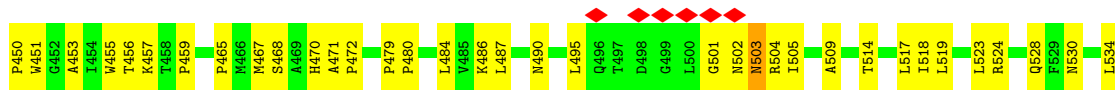
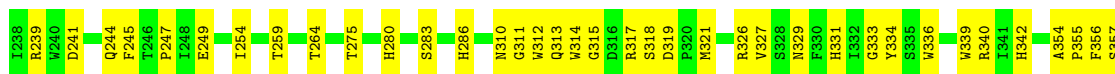
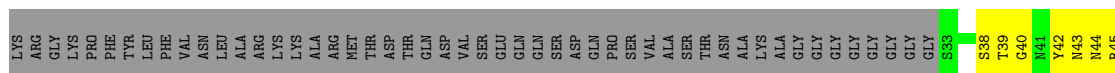
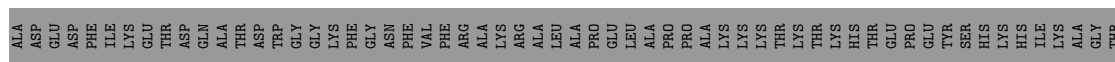
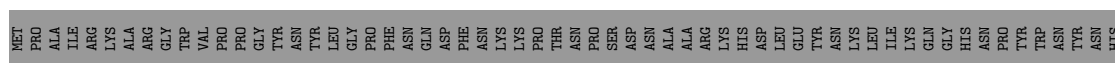


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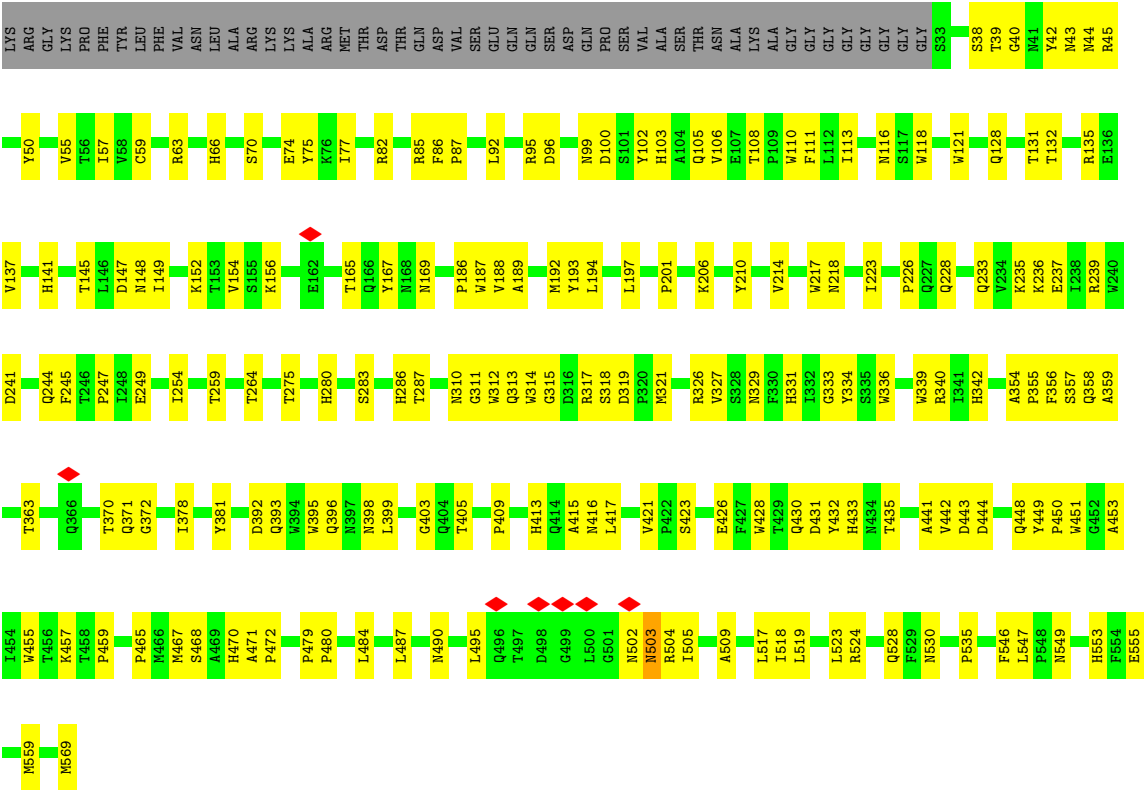


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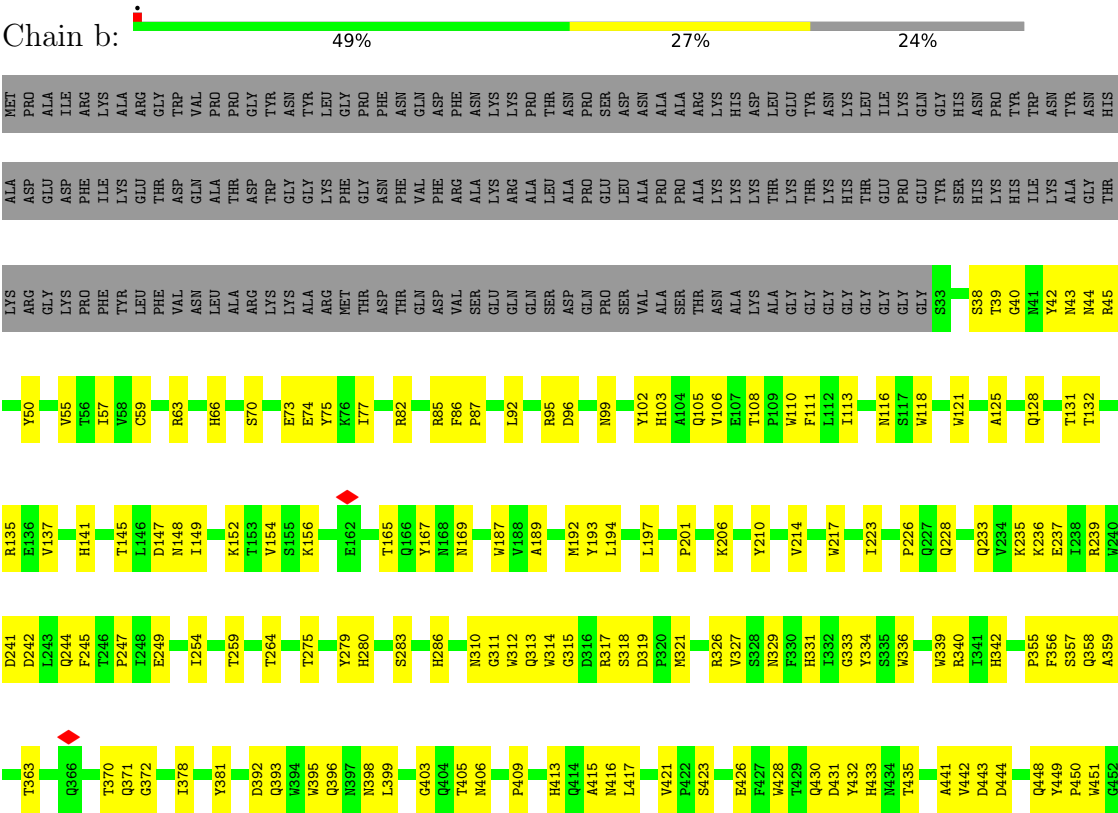


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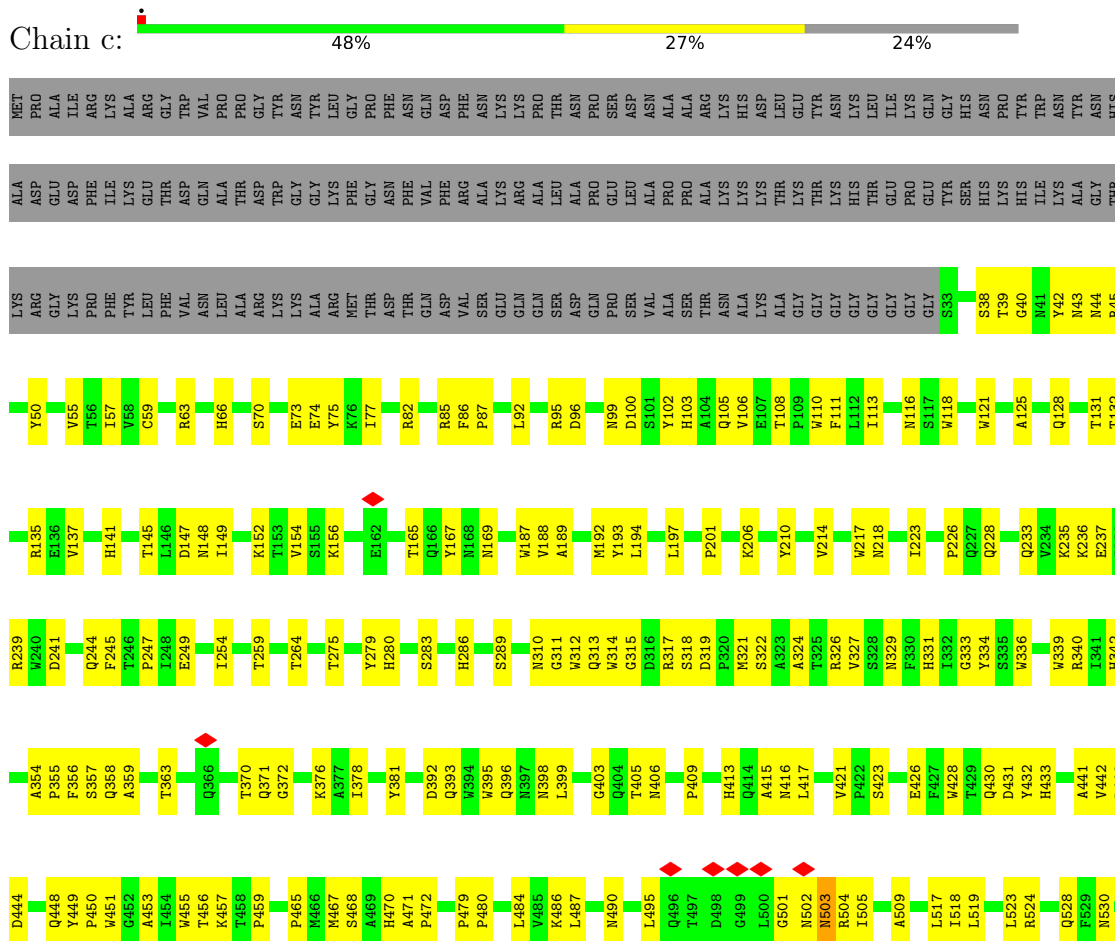




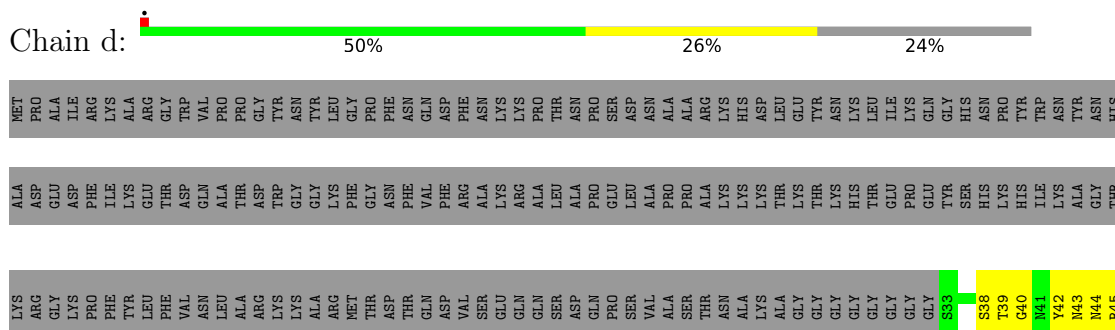
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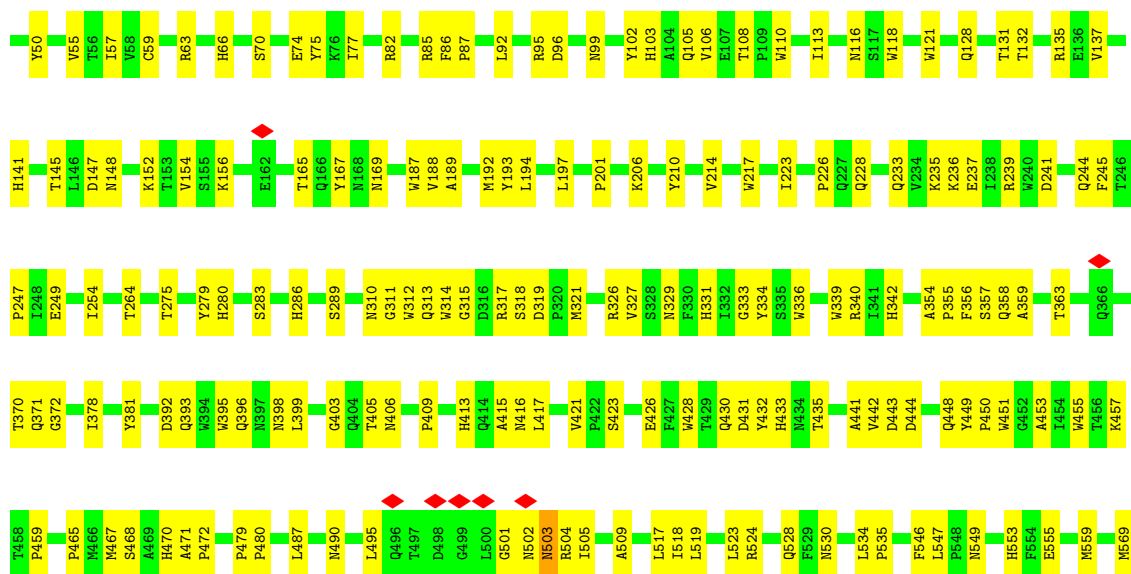


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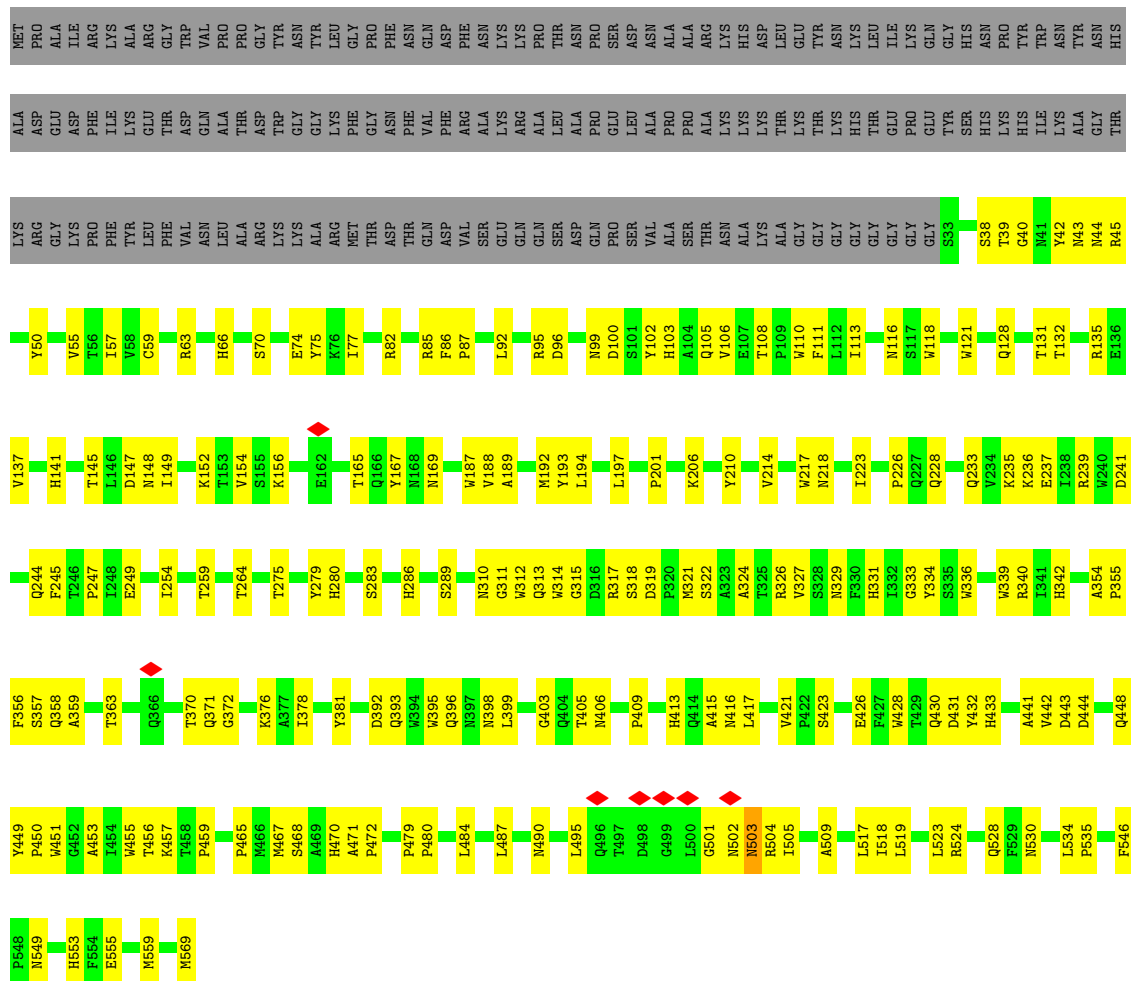


- Molecule 1: VP1





• Molecule 1: VP1



• Molecule 1: VP1

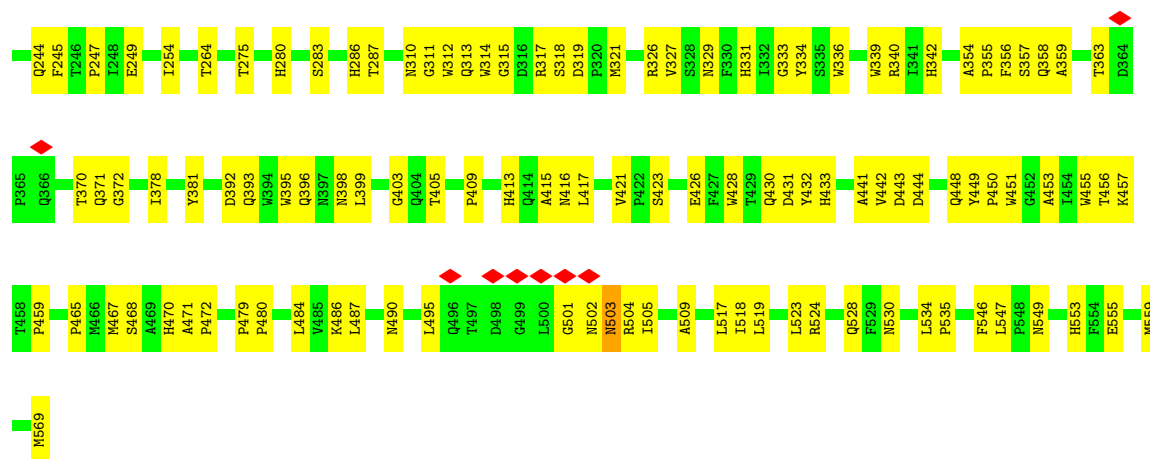


MET	ALA	LYS	Y60	V137	Q244	Q366	T456	M559
PRO	ASP	ARG	Y50	H141	F245	Q366	K457	M559
ALA	GLU	GLY	V55	T246	T246	T370	T458	M569
ILE	ASP	LYS	T56	T145	P247	Q371	P459	
ARG	PHE	PRO	I57	T145	E249	G372	P465	
LYS	ILE	PHE	V58	D147	T254	I378	K466	
ALA	LYS	TYR	C59	N148	T259	Y381	K467	
ARG	GLU	LEU	R63	N149	T264	Y381	K468	
GLY	TRP	VAL	H66	K152	T275	D392	K469	
PRO	ASP	ASN	S70	V154	Y279	Q393	K470	
GLY	THR	ALA	E73	S155	H280	Q393	A471	
TYR	ASP	ARG	E74	K156	Y279	Q396	A472	
ASN	GLY	LYS	Y75	E162	H286	Q396	P479	
LEU	PHE	ALA	K76	T165	T287	N397	P480	
TYR	GLY	LYS	I77	Q166	S283	N398	P480	
PRO	GLY	ARG	R82	Y167	Y286	N399	L484	
ASP	PHE	MET	R85	N168	H287	L399	K485	
ASN	VAL	THR	P87	N169	Q403	T405	K486	
LYS	ARG	GLN	L92	Y187	Q404	P409	L487	
PRO	ALA	VAL	R95	V188	T405	H413	N490	
THR	LYS	SER	D96	A189	H413	H413	L496	
ASN	ALA	GLN	N99	M192	A415	D414	Q496	
PRO	ALA	ASP	Y102	Y193	N416	L417	T497	
ASP	PRO	GLN	H103	L194	S318	V421	D498	
ALA	LEU	PRO	Q105	L197	S319	P422	L500	
ARG	THR	VAL	E107	P201	D321	S423	G501	
HIS	LYS	SER	T108	K206	K326	E426	N503	
LEU	LYS	ASN	P109	Y210	V327	F427	R504	
GLU	LYS	ALA	W110	V214	S328	W428	I505	
TYR	GLY	THR	L112	W217	N329	T429	A509	
ASN	GLY	LYS	I113	I223	H331	Q430	L517	
LEU	GLY	GLY	N116	P226	Q332	Y432	I518	
ILE	GLY	THR	S117	Q227	Y334	H433	L519	
LYS	PRO	GLY	W118	Q228	S335	T435	L523	
GLN	GLY	GLY	W121	Q233	W336	T435	R524	
GLY	TYR	SER	Q128	K235	V339	A441	G528	
HIS	HIS	HIS	T131	K236	R340	W442	F529	
ASN	PRO	LYS	T132	E237	H342	D443	N530	
TRP	TRP	GLY	R135	R238	P355	Q448	L534	
ASN	ILE	GLY	E136	T239	F356	Y449	P535	
TYR	LYS	ALA		R239	Q358	P450	F546	
ASN	GLY	THR		D241	A359	W451	L547	
HIS	THR	GLY			T363	G452	P548	
						A453	N549	
						L454	H553	
						W455	F554	
							E555	

• Molecule 1: VP1



MET	ALA	LYS	Y60	R135
PRO	ASP	ARG	Y50	E136
ALA	GLU	GLY	V55	V137
ILE	ASP	PHE	T56	H141
ARG	PHE	PRO	I57	T145
LYS	ILE	PHE	V58	L146
ALA	LYS	TYR	C59	N148
ARG	GLU	LEU	R63	K152
GLY	TRP	VAL	H66	T153
PRO	ASP	ASN	S70	V154
GLY	THR	ALA	E73	S155
TYR	ASP	ARG	E74	K156
ASN	GLY	LYS	Y75	E162
LEU	PHE	MET	K76	T165
GLY	GLY	THR	I77	Q166
PRO	ASN	ASP	R82	Y167
PHE	PHE	THR	R85	N168
ASN	VAL	GLN	P87	N169
GLN	ARG	VAL	L92	W187
ASP	PHE	SER	R95	V188
ASN	ALA	GLU	D96	A189
PRO	ALA	LYS	N99	M192
GLU	PRO	ASN	Y102	Y193
ASP	LEU	PRO	H103	L194
ALA	ALA	GLN	Q105	L197
ARG	ALA	VAL	E107	P201
LYS	LYS	SER	T108	K206
ASP	LYS	ASN	P109	Y210
LEU	LYS	ALA	W110	V214
GLU	LYS	GLY	F111	W217
TYR	LYS	GLY	L112	I223
ASN	HIS	GLY	I113	P226
LYS	LYS	GLY	N116	Q227
LEU	ILE	GLY	S117	Q228
ILE	GLU	PRO	W118	Q233
GLN	GLU	TYR	W121	V234
GLY	TYR	SER	A125	K235
HIS	HIS	HIS	Q128	K236
ASN	PRO	LYS	T131	E237
TRP	TRP	ILE	T132	I238
ASN	LYS	LYS	R135	R239
TYR	ALA	GLY	E136	W240
ASN	THR	GLY		D241
HIS	THR			



• Molecule 1: VP1

Chain h: 50% 26% 24%

MET PRO ALA ASP ILE LYS ARG LYS ALA ARG GLY THR ASP TRP VAL PRO PRO GLY TYR D392 Q393 W394 W395 W396 W397 N398 L399 G403 Q404 T405 P409 H413 Q414 A415 S318 M416 L417 V421 P422 S423 E426 F427 W428 T429 Q430 D431 Y432 H433 A441 V442 D443 D444 Q448 Y449 P450 W451 G452 A453 T454 W455 T456 E555 M559

ALA ASP GLU LYS ASP PHE ILE LYS GLU THR PHE VAL ALA THR ASP TRP GLY LYS GLY ALA LYS PHE VAL PHE ARG ARG ALA LYS ARG ALA LYS LEU ASP PRO GLU LEU SER ASP ASN ALA PRO ALA ARG LYS HIS T428 T429 T430 T431 T432 T433 T434 T435 T436 T437 T438 T439 T440 T441 T442 T443 T444 T445 T446 T447 T448 T449 T450 T451 T452 T453 T454 T455 T456 T457 T458 T459 T460 T461 T462 T463 T464 T465 T466 T467 T468 T469 T470 T471 T472 T473 T474 T475 T476 T477 T478 T479 T480 T481 T482 T483 T484 T485 T486 T487 T488 T489 T490 T491 T492 T493 T494 T495 T496 T497 T498 T499 T500 T501 T502 T503 T504 T505 T506 T507 T508 T509 T510 T511 T512 T513 T514 T515 T516 T517 T518 T519 T520 T521 T522 T523 T524 T525 T526 T527 T528 T529 T530 T531 T532 T533 T534 T535 T536 T537 T538 T539 T540 T541 T542 T543 T544 T545 T546 T547 T548 T549 T550 T551 T552 T553 T554 T555 T556 T557 T558 T559 T560 T561 T562 T563 T564 T565 T566 T567 T568 T569 T570 T571 T572 T573 T574 T575 T576 T577 T578 T579 T580 T581 T582 T583 T584 T585 T586 T587 T588 T589 T590 T591 T592 T593 T594 T595 T596 T597 T598 T599 T600 T601 T602 T603 T604 T605 T606 T607 T608 T609 T610 T611 T612 T613 T614 T615 T616 T617 T618 T619 T620 T621 T622 T623 T624 T625 T626 T627 T628 T629 T630 T631 T632 T633 T634 T635 T636 T637 T638 T639 T640 T641 T642 T643 T644 T645 T646 T647 T648 T649 T650 T651 T652 T653 T654 T655 T656 T657 T658 T659 T660 T661 T662 T663 T664 T665 T666 T667 T668 T669 T670 T671 T672 T673 T674 T675 T676 T677 T678 T679 T680 T681 T682 T683 T684 T685 T686 T687 T688 T689 T690 T691 T692 T693 T694 T695 T696 T697 T698 T699 T700 T701 T702 T703 T704 T705 T706 T707 T708 T709 T710 T711 T712 T713 T714 T715 T716 T717 T718 T719 T720 T721 T722 T723 T724 T725 T726 T727 T728 T729 T730 T731 T732 T733 T734 T735 T736 T737 T738 T739 T740 T741 T742 T743 T744 T745 T746 T747 T748 T749 T750 T751 T752 T753 T754 T755 T756 T757 T758 T759 T760 T761 T762 T763 T764 T765 T766 T767 T768 T769 T770 T771 T772 T773 T774 T775 T776 T777 T778 T779 T780 T781 T782 T783 T784 T785 T786 T787 T788 T789 T790 T791 T792 T793 T794 T795 T796 T797 T798 T799 T800 T801 T802 T803 T804 T805 T806 T807 T808 T809 T810 T811 T812 T813 T814 T815 T816 T817 T818 T819 T820 T821 T822 T823 T824 T825 T826 T827 T828 T829 T830 T831 T832 T833 T834 T835 T836 T837 T838 T839 T840 T841 T842 T843 T844 T845 T846 T847 T848 T849 T850 T851 T852 T853 T854 T855 T856 T857 T858 T859 T860 T861 T862 T863 T864 T865 T866 T867 T868 T869 T870 T871 T872 T873 T874 T875 T876 T877 T878 T879 T880 T881 T882 T883 T884 T885 T886 T887 T888 T889 T890 T891 T892 T893 T894 T895 T896 T897 T898 T899 T900 T901 T902 T903 T904 T905 T906 T907 T908 T909 T910 T911 T912 T913 T914 T915 T916 T917 T918 T919 T920 T921 T922 T923 T924 T925 T926 T927 T928 T929 T930 T931 T932 T933 T934 T935 T936 T937 T938 T939 T940 T941 T942 T943 T944 T945 T946 T947 T948 T949 T950 T951 T952 T953 T954 T955 T956 T957 T958 T959 T960 T961 T962 T963 T964 T965 T966 T967 T968 T969 T970 T971 T972 T973 T974 T975 T976 T977 T978 T979 T980 T981 T982 T983 T984 T985 T986 T987 T988 T989 T990 T991 T992 T993 T994 T995 T996 T997 T998 T999

LYS ARG GLY LYS ASP PHE ILE LYS GLU THR PHE VAL ALA THR ASP TRP GLY LYS GLY ALA LYS PHE VAL PHE ARG ARG ALA LYS ARG ALA LYS LEU ASP PRO GLU LEU SER ASP ASN ALA PRO ALA ARG LYS HIS T428 T429 T430 T431 T432 T433 T434 T435 T436 T437 T438 T439 T440 T441 T442 T443 T444 T445 T446 T447 T448 T449 T450 T451 T452 T453 T454 T455 T456 T457 T458 T459 T460 T461 T462 T463 T464 T465 T466 T467 T468 T469 T470 T471 T472 T473 T474 T475 T476 T477 T478 T479 T480 T481 T482 T483 T484 T485 T486 T487 T488 T489 T490 T491 T492 T493 T494 T495 T496 T497 T498 T499 T500 T501 T502 T503 T504 T505 T506 T507 T508 T509 T510 T511 T512 T513 T514 T515 T516 T517 T518 T519 T520 T521 T522 T523 T524 T525 T526 T527 T528 T529 T530 T531 T532 T533 T534 T535 T536 T537 T538 T539 T540 T541 T542 T543 T544 T545 T546 T547 T548 T549 T550 T551 T552 T553 T554 T555 T556 T557 T558 T559 T560 T561 T562 T563 T564 T565 T566 T567 T568 T569 T570 T571 T572 T573 T574 T575 T576 T577 T578 T579 T580 T581 T582 T583 T584 T585 T586 T587 T588 T589 T590 T591 T592 T593 T594 T595 T596 T597 T598 T599 T600 T601 T602 T603 T604 T605 T606 T607 T608 T609 T610 T611 T612 T613 T614 T615 T616 T617 T618 T619 T620 T621 T622 T623 T624 T625 T626 T627 T628 T629 T630 T631 T632 T633 T634 T635 T636 T637 T638 T639 T640 T641 T642 T643 T644 T645 T646 T647 T648 T649 T650 T651 T652 T653 T654 T655 T656 T657 T658 T659 T660 T661 T662 T663 T664 T665 T666 T667 T668 T669 T670 T671 T672 T673 T674 T675 T676 T677 T678 T679 T680 T681 T682 T683 T684 T685 T686 T687 T688 T689 T690 T691 T692 T693 T694 T695 T696 T697 T698 T699 T700 T701 T702 T703 T704 T705 T706 T707 T708 T709 T710 T711 T712 T713 T714 T715 T716 T717 T718 T719 T720 T721 T722 T723 T724 T725 T726 T727 T728 T729 T730 T731 T732 T733 T734 T735 T736 T737 T738 T739 T740 T741 T742 T743 T744 T745 T746 T747 T748 T749 T750 T751 T752 T753 T754 T755 T756 T757 T758 T759 T760 T761 T762 T763 T764 T765 T766 T767 T768 T769 T770 T771 T772 T773 T774 T775 T776 T777 T778 T779 T780 T781 T782 T783 T784 T785 T786 T787 T788 T789 T790 T791 T792 T793 T794 T795 T796 T797 T798 T799 T800 T801 T802 T803 T804 T805 T806 T807 T808 T809 T810 T811 T812 T813 T814 T815 T816 T817 T818 T819 T820 T821 T822 T823 T824 T825 T826 T827 T828 T829 T830 T831 T832 T833 T834 T835 T836 T837 T838 T839 T840 T841 T842 T843 T844 T845 T846 T847 T848 T849 T850 T851 T852 T853 T854 T855 T856 T857 T858 T859 T860 T861 T862 T863 T864 T865 T866 T867 T868 T869 T870 T871 T872 T873 T874 T875 T876 T877 T878 T879 T880 T881 T882 T883 T884 T885 T886 T887 T888 T889 T890 T891 T892 T893 T894 T895 T896 T897 T898 T899 T900 T901 T902 T903 T904 T905 T906 T907 T908 T909 T910 T911 T912 T913 T914 T915 T916 T917 T918 T919 T920 T921 T922 T923 T924 T925 T926 T927 T928 T929 T930 T931 T932 T933 T934 T935 T936 T937 T938 T939 T940 T941 T942 T943 T944 T945 T946 T947 T948 T949 T950 T951 T952 T953 T954 T955 T956 T957 T958 T959 T960 T961 T962 T963 T964 T965 T966 T967 T968 T969 T970 T971 T972 T973 T974 T975 T976 T977 T978 T979 T980 T981 T982 T983 T984 T985 T986 T987 T988 T989 T990 T991 T992 T993 T994 T995 T996 T997 T998 T999

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H141 T145 L146 D147 M148 N149 K152 T153 V154 S155 K156 E162 T165 Q166 Y167 M168 N169 W187 V188 A189 M192 Y193 L194 L197 P201 K206 V214 W217 N218 T223 P226 Q227 Q228 Q233 V234 K235 E237 T238 R239 W240 D241 D242 L243 Q244

F245 T246 P247 I248 E249 T254 T259 T264 T275 H280 S283 H286 T287 G288 S289 N310 G311 W312 Q313 W314 G315 D316 R317 S318 S319 M321 R326 V327 S328 N329 H331 G333 Y334 W335 W339 R340 T341 H342 A354 P355 F356 S357 Q358 A359

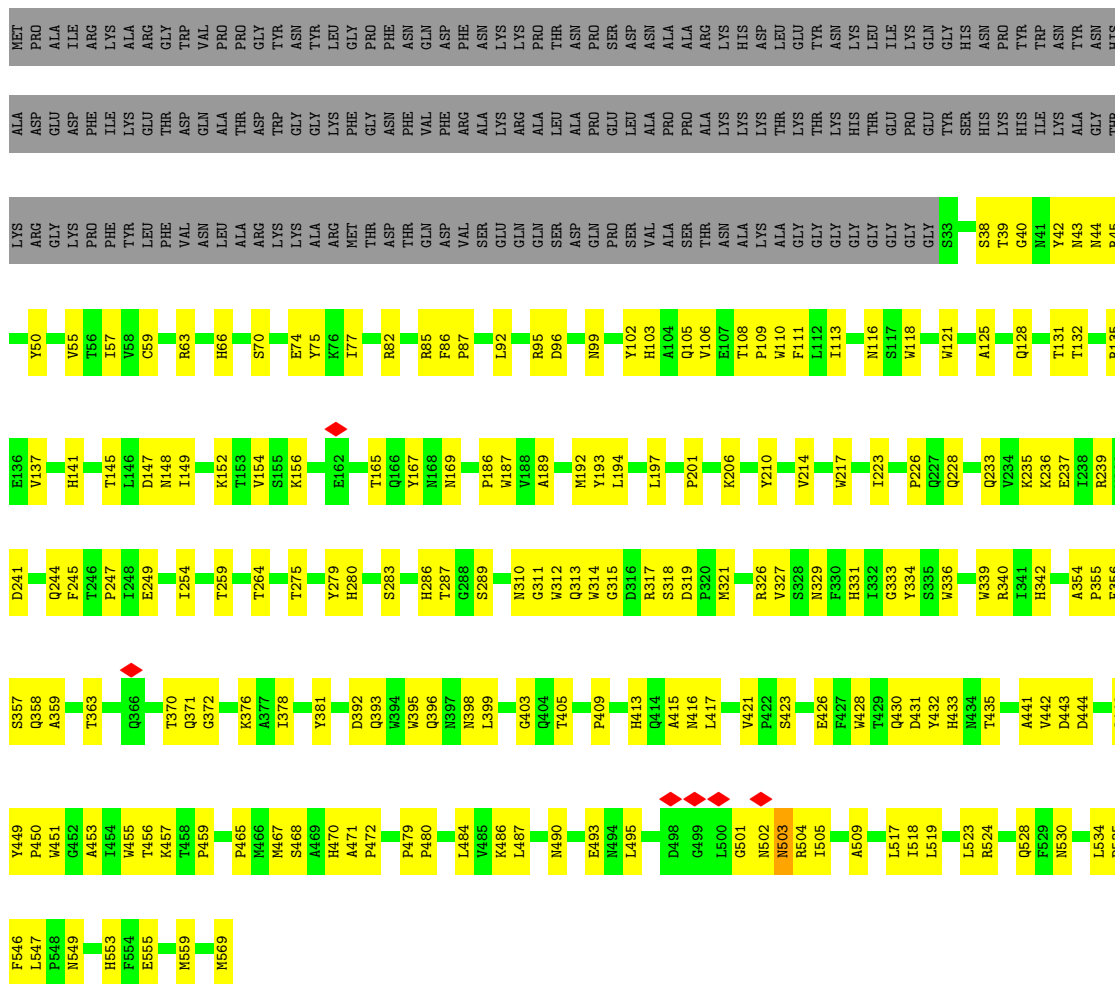
T363 D364 P365 Q366 T370 Q371 G372 T378 Y381 A389 D392 Q393 W394 W395 W396 W397 N398 L399 G403 Q404 T405 P409 H413 Q414 A415 M416 L417 V421 P422 S423 E426 F427 W428 T429 Q430 D431 Y432 H433 T434 T435 A441 V442 D443 D444 Q448 Y449 P450 W451

G452 A453 W454 W455 T456 T457 T458 T459 T460 T461 T462 T463 T464 T465 T466 T467 T468 T469 T470 T471 T472 T473 T474 T475 T476 T477 T478 T479 T480 T481 T482 T483 T484 T485 T486 T487 T488 T489 T490 T491 T492 T493 T494 T495 T496 T497 T498 T499 T500 T501 T502 T503 T504 T505 T506 T507 T508 T509 T510 T511 T512 T513 T514 T515 T516 T517 T518 T519 T520 T521 T522 T523 T524 T525 T526 T527 T528 T529 T530 T531 T532 T533 T534 T535 T536 T537 T538 T539 T540 T541 T542 T543 T544 T545 T546 T547 T548 T549 T550 T551 T552 T553 T554

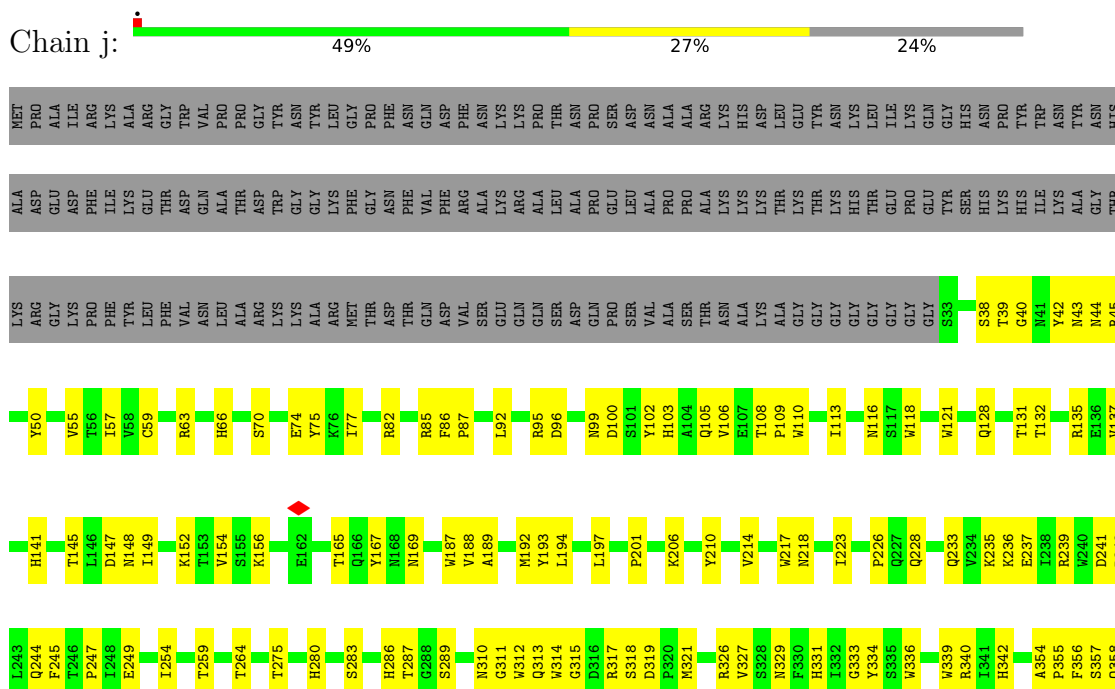
E555 M559 M569

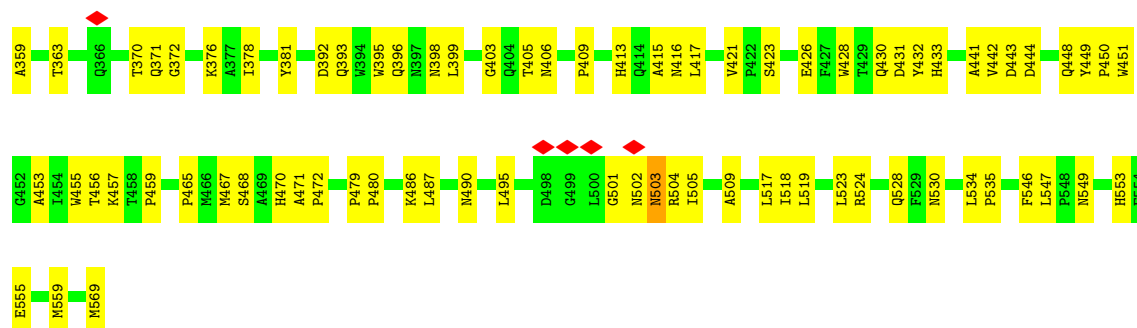
• Molecule 1: VP1

Chain i: 49% 27% 24%

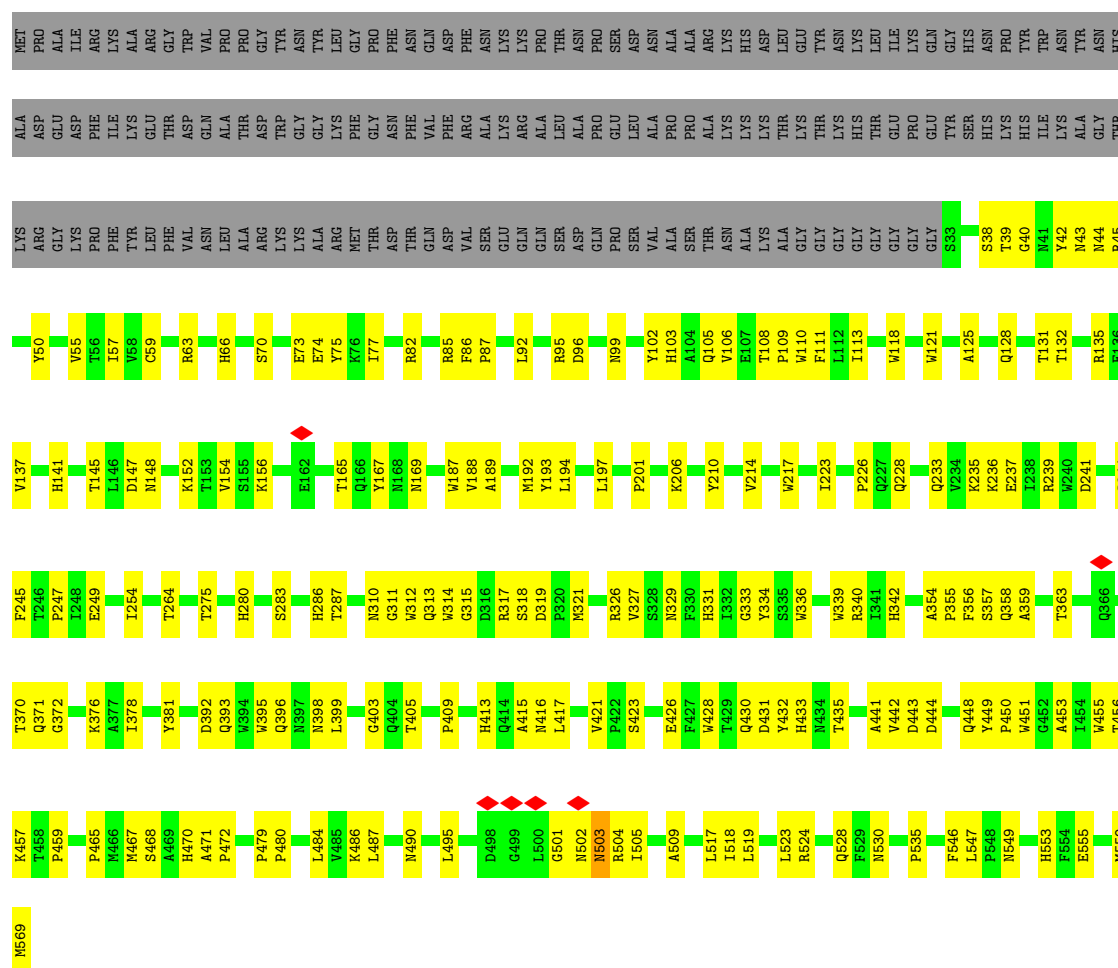


- Molecule 1: VP1

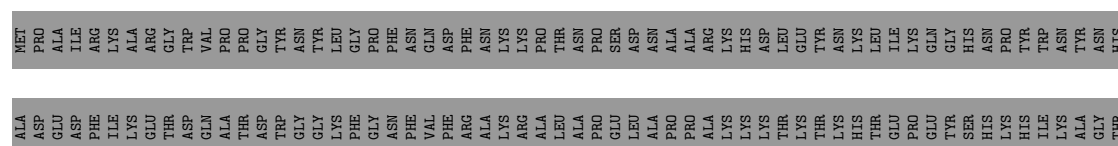


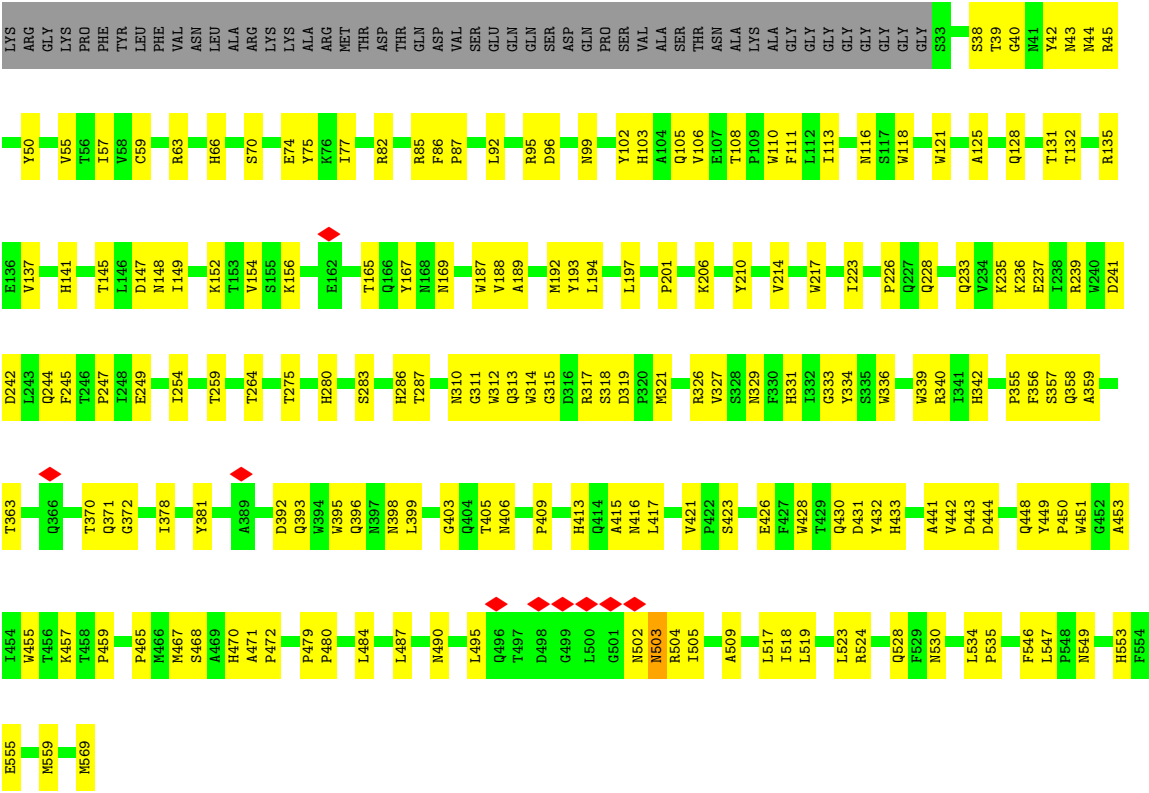


• Molecule 1: VP1

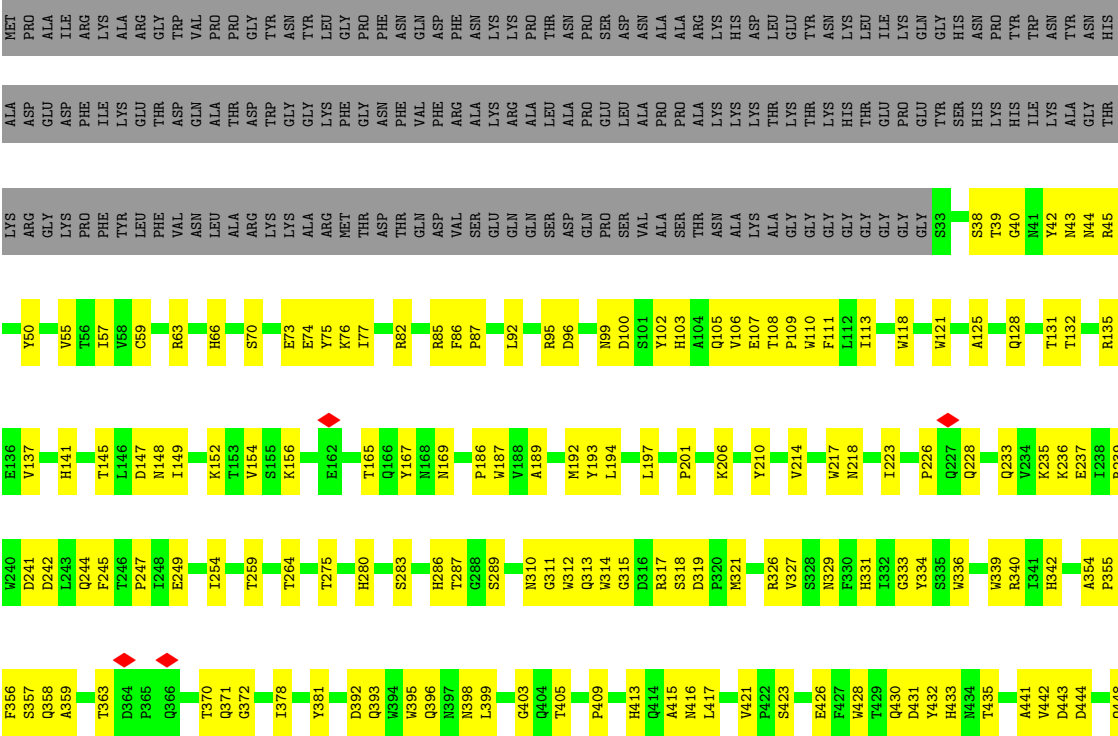


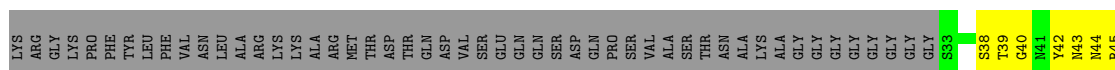
• Molecule 1: VP1

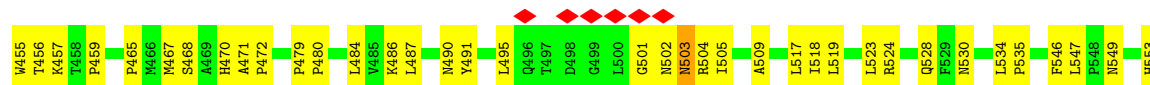


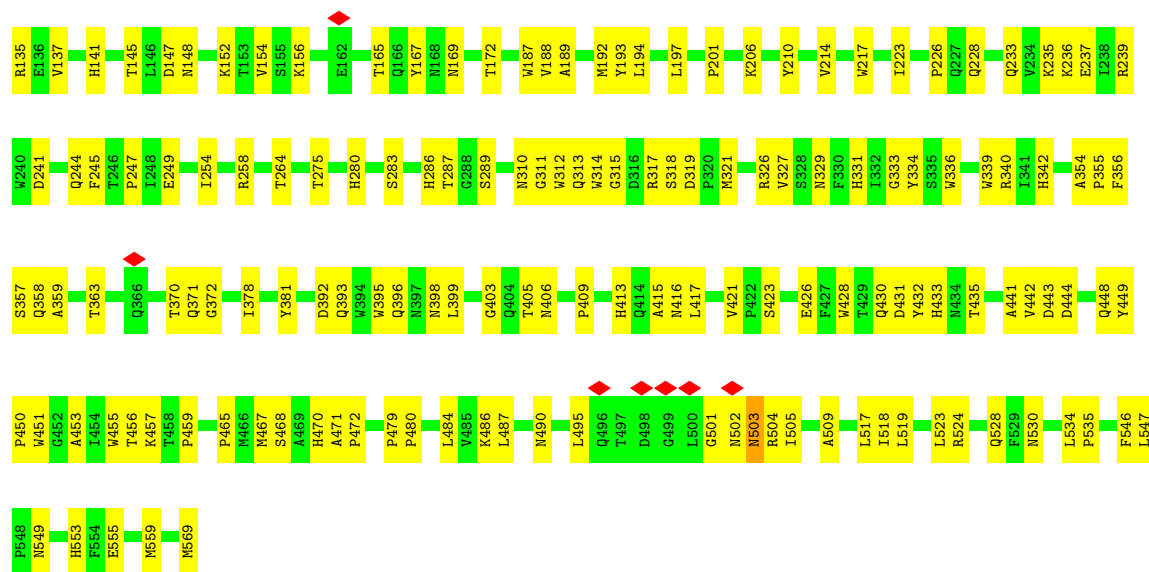


• Molecule 1: VP1

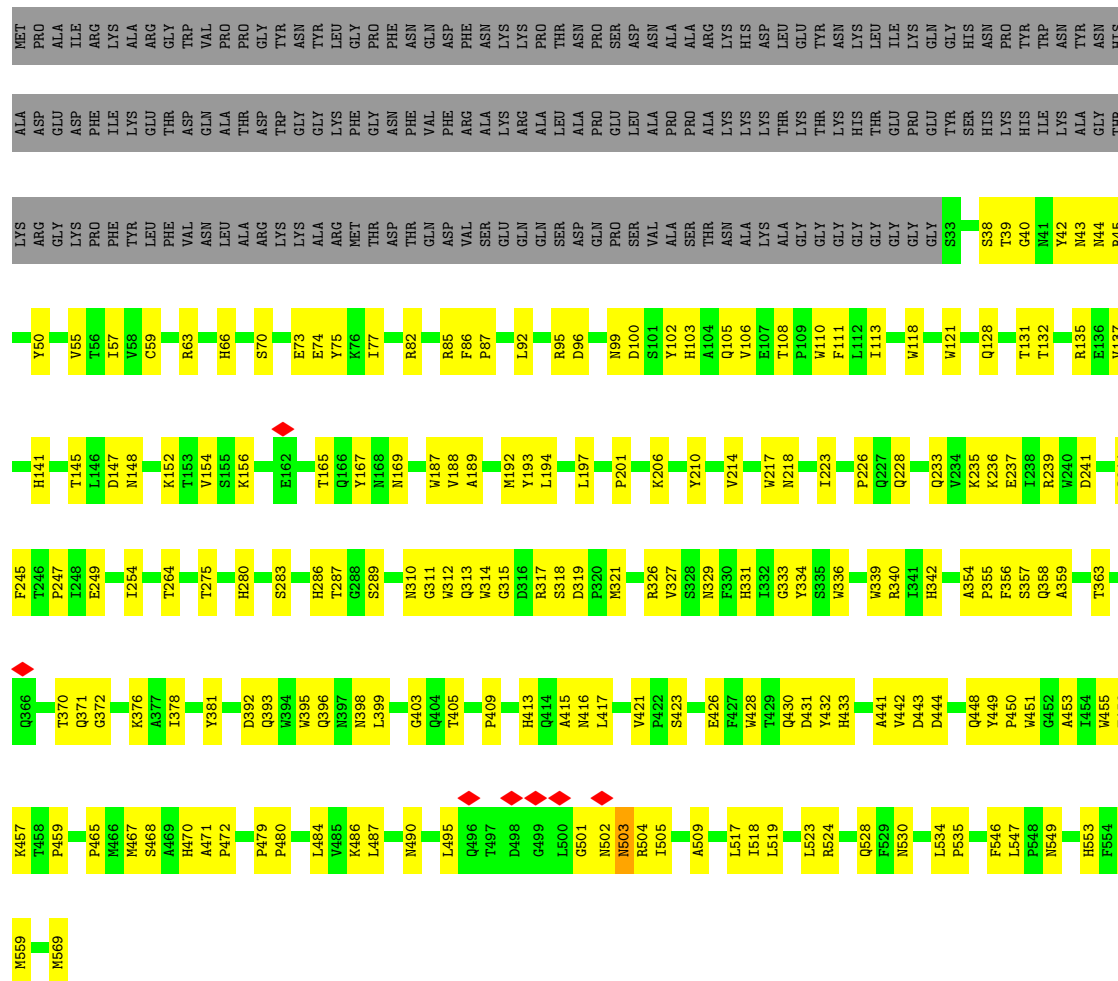






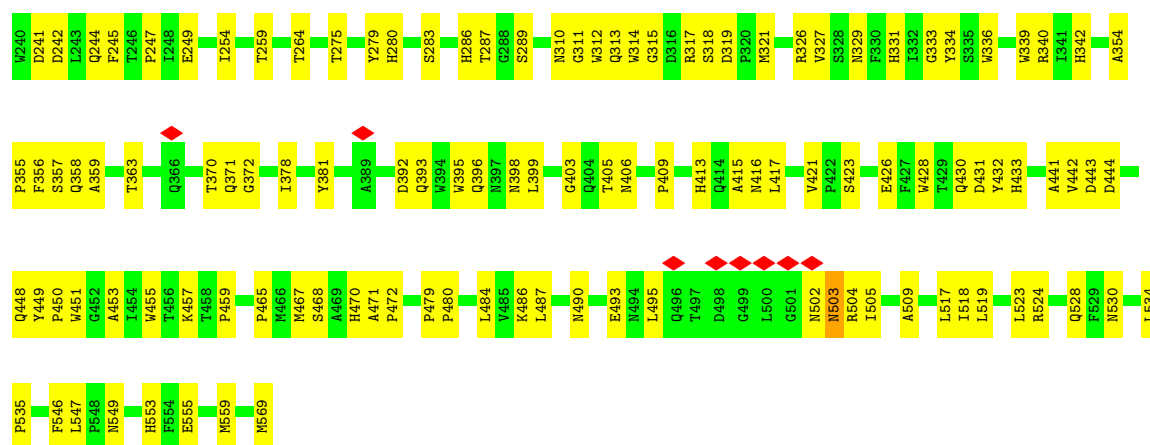


• Molecule 1: VP1

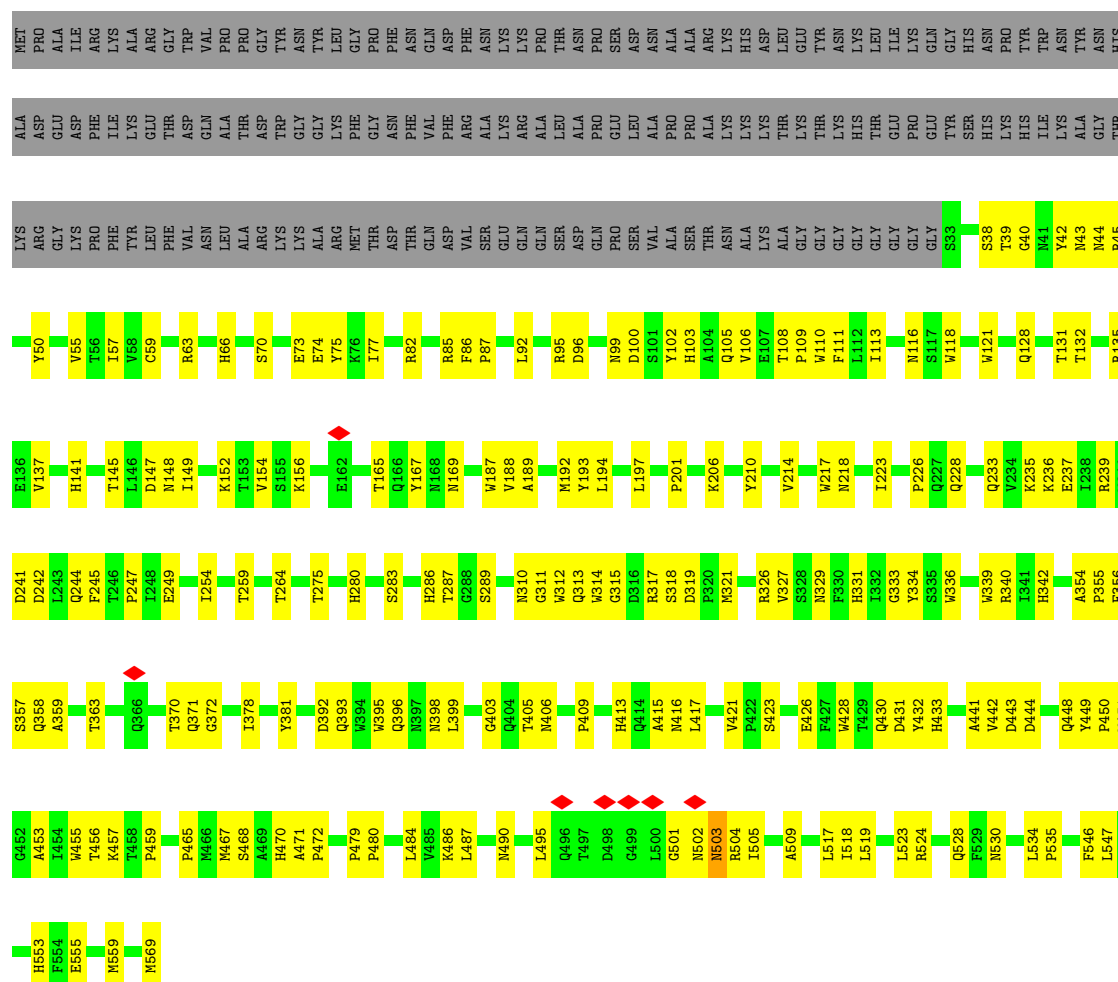


• Molecule 1: VP1



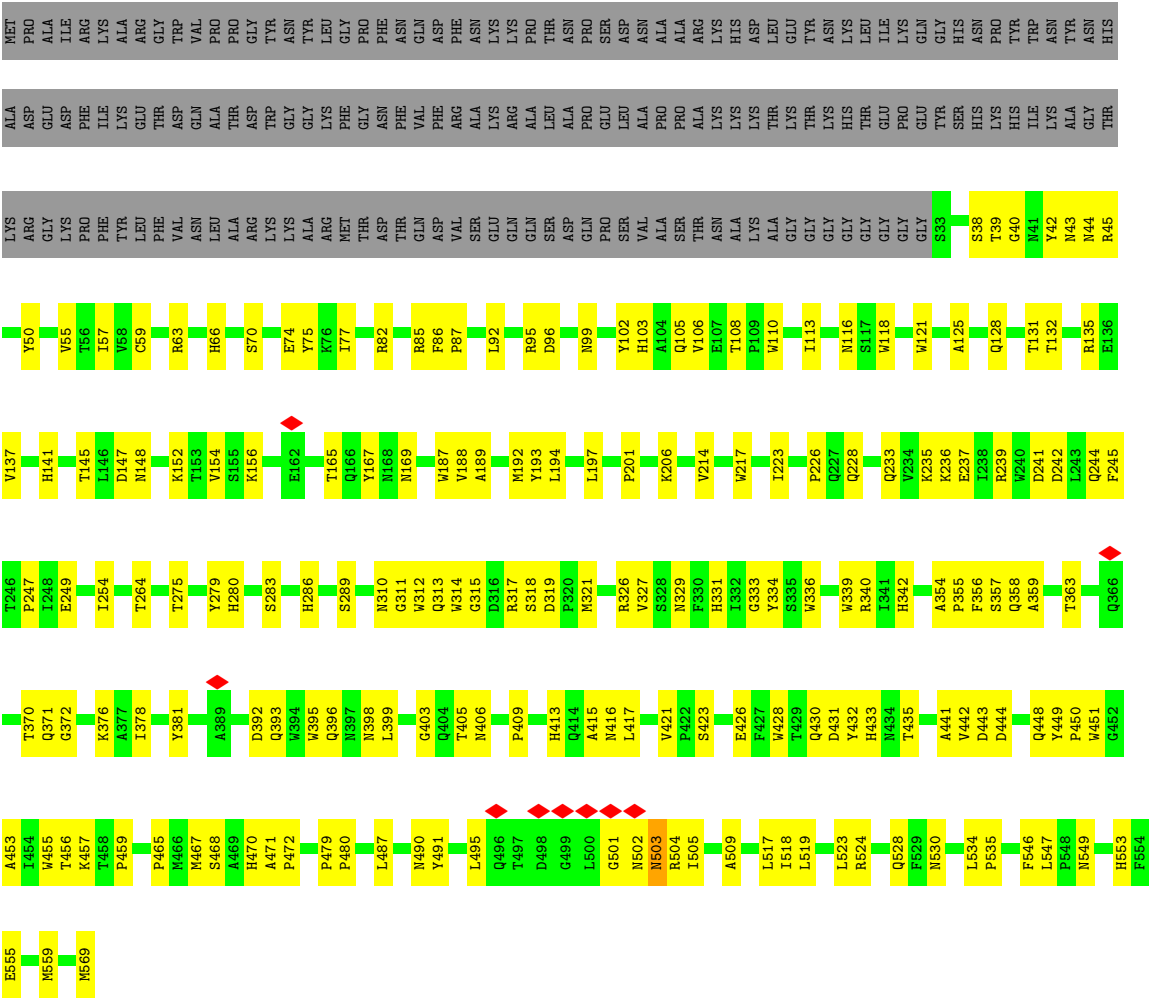


• Molecule 1: VP1

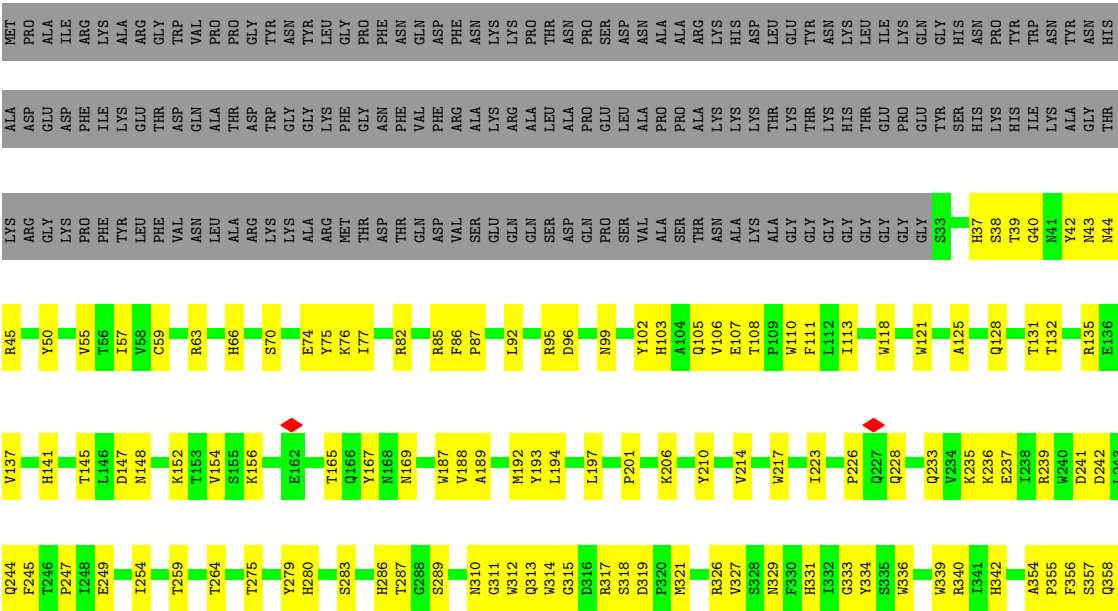


• Molecule 1: VP1

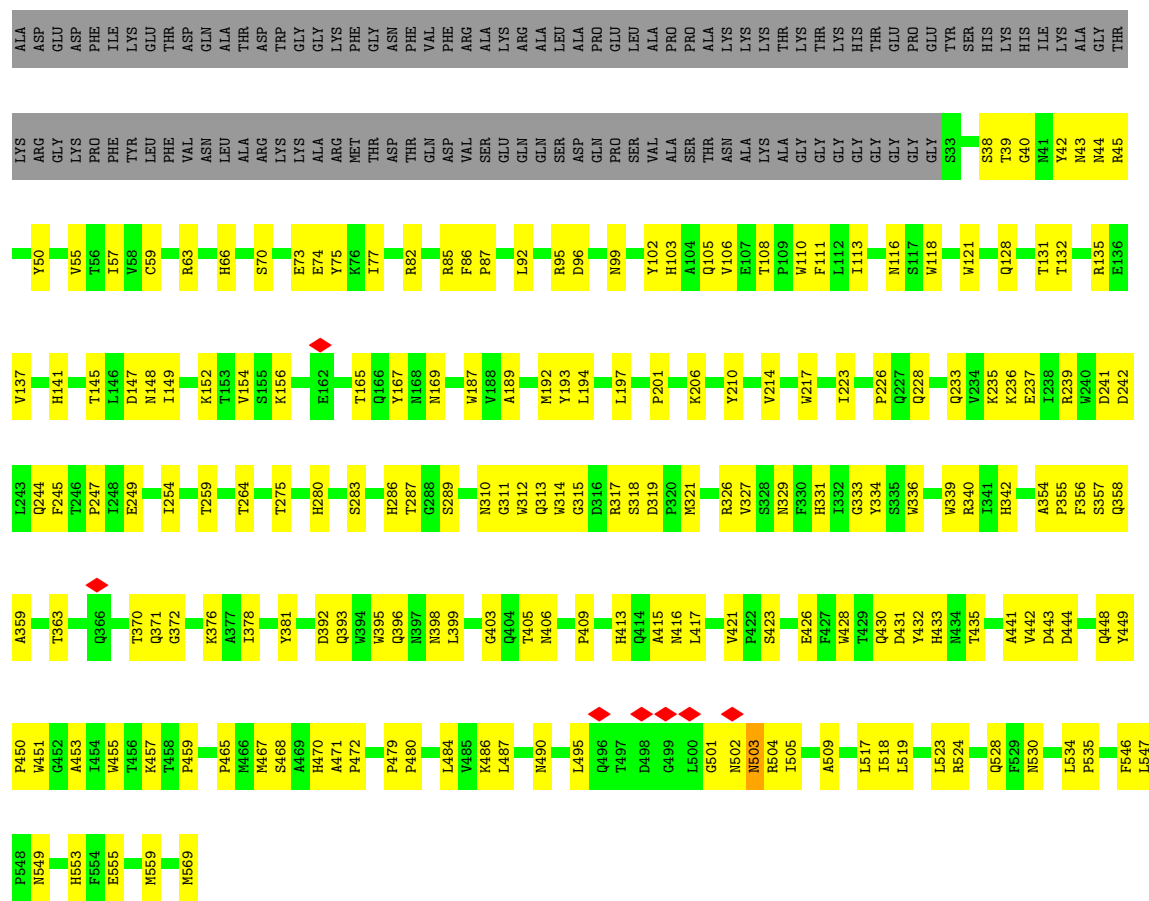




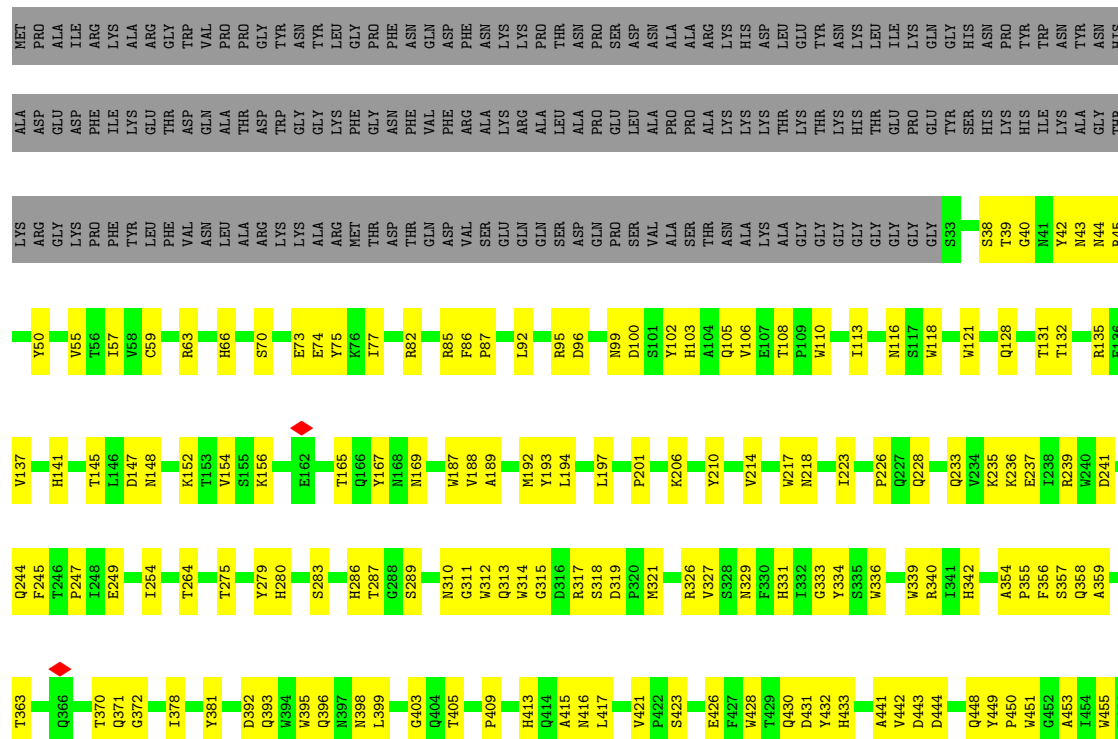
• Molecule 1: VP1

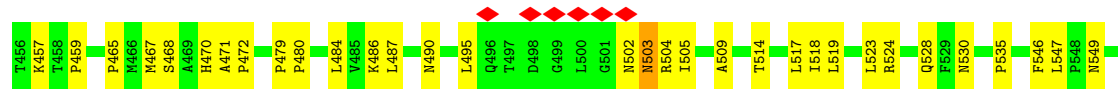




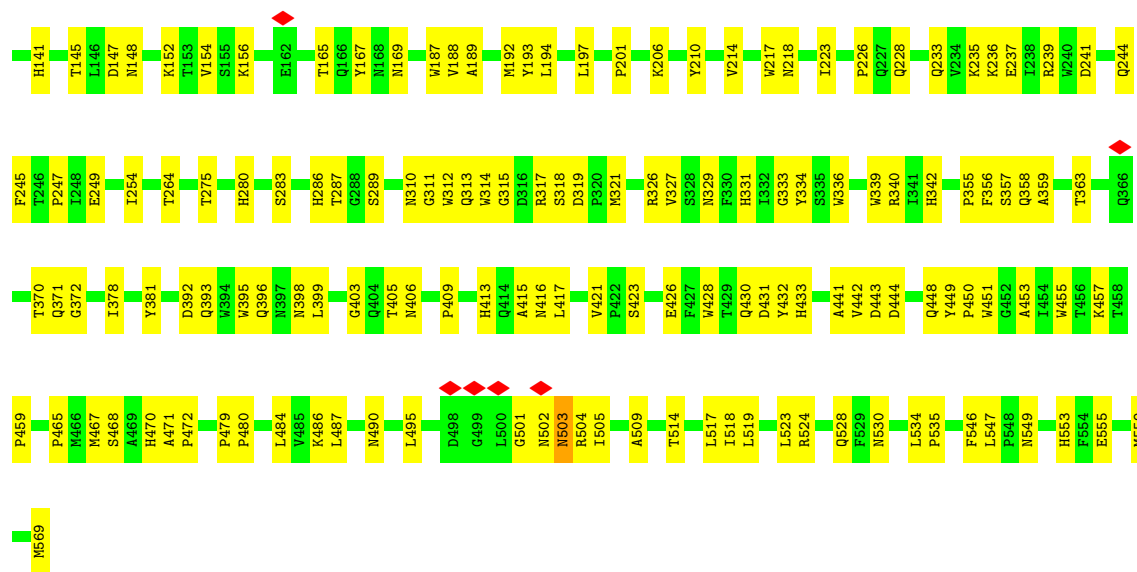


● Molecule 1: VP1

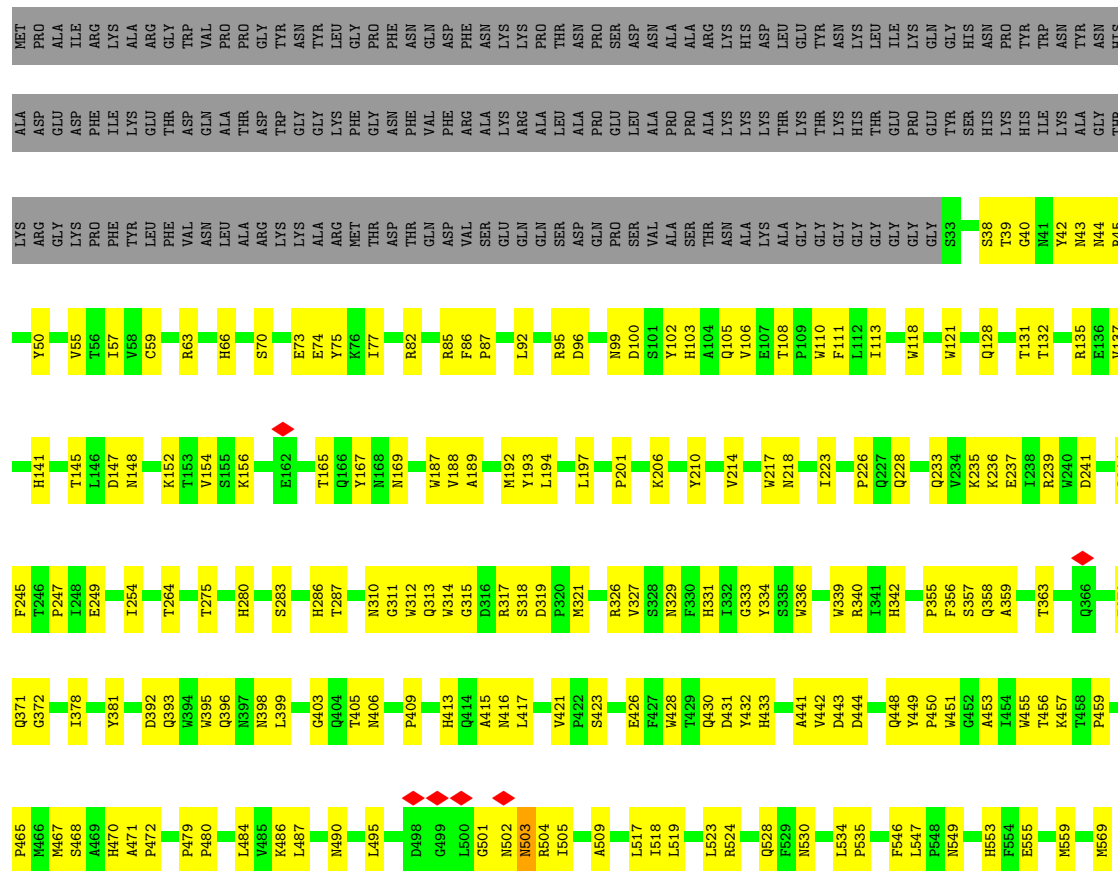








• Molecule 1: VP1



• Molecule 1: VP1



P548	P450	Q368	I238	Y50	LYS	ALA
N549	W451	A359	R239	R135	ARG	ASP
	G452		W240	E136	GLY	GLU
H553	A453	T363	D241	V137	LVS	ASP
F554	W454			T556	PRQ	PHE
E555	W455	Q366	Q244	H441	PHE	ILE
	T456		F245		LVS	LYS
M559	K457	T370	T246	T145	TYR	ALA
	T458	Q371	P247	L146	PHE	GLU
M569	P459	G372	I248	D147	LEU	THR
			E249	N148	VAL	TRP
				I149	ASN	VAL
	P465	I378	I254	H66	LEU	GLN
	M466			S70	ALA	ALA
	M467	Y381	T259	K152	ALA	THR
	S468			T153	ARG	PRO
	A469			LVS	ASP	PRO
	H470	A389	T264	E73	LYS	GLY
	A471			ET74	ALA	TYR
	P472	D392	T275	Y75	LVS	GLY
		Q393		K76	PHE	LEU
		K394	H280	E162	MET	GLY
	P479	W395		I77	THR	PRO
	P480	Q396	S283	R82	ASP	PHE
	L484	N397		T165	ASN	ASN
	W485	N398	H286	Q166	PHE	GLN
	K486	L399		Y167	VAL	VAL
	L487			N168	ARG	PHE
				N169	ALA	ASP
	M490	G403	N310	L92	LVS	ASN
		Q404	G311	P186	GLU	GLN
		T405	W312	W187	GLN	ALA
			Q313	V188	LEU	THR
	L496	P409	W314	A189	ALA	ASN
	Q496		G315	D96	GLN	PRO
T497	T497	H413	D316	N99	PRO	PRO
		Q414	R317	M192	GLU	GLU
G499	A415	A415	S318	D100	LEU	ASP
		N416	D319	S101	VAL	ASN
L500	L500	L417	P320	Y102	ALA	ALA
			L197	H103	PRO	ALA
G501			K321	A104	PRO	ALA
	N502	W421	R326	P201	ASN	LYS
M503	P422	P422	V327	Q105	LYS	LYS
R504	S423	S423	S328	V106	LYS	LYS
I505			N329	E107	LYS	ASP
	A509	E426	F427	T108	THR	LEU
		W428	H331	P109	LYS	GLU
L517		T429	R332	Y210	GLY	TYR
I518		Q430	G333	V214	GLY	LYS
L519		D431	Y334	I112	GLY	LYS
		Y432	S335	W217	GLY	LEU
		H433	W336	N218	GLY	LEU
L523				N116	GLY	ILE
R524		M434		S117	GLY	LYS
		T435	W339	W118	GLY	GLN
			R340		TYR	GLY
Q528			H342		GLY	HIS
F529			T341		THR	ASN
N530		A441	R340	W121	SER	ASN
		V442	Q228	A125	HIS	LYS
N534		D443	Q228		LYS	PRO
L534		D444	Q233	Q128	ILE	TYR
P535		Q448	A354		LYS	TRP
			P355	W234	ASN	ASN
			F356	K235	ALA	TYR
			S257	K236	GLY	HIS
					THR	ASN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	55466	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	75	Depositor
Minimum defocus (nm)	100	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	22.842	Depositor
Minimum map value	-14.265	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size (Å)	493.49997, 493.49997, 493.49997	wwPDB
Map dimensions	470, 470, 470	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.52	0/4500	0.72	7/6156 (0.1%)
1	2	0.52	0/4500	0.72	8/6156 (0.1%)
1	3	0.52	0/4500	0.72	8/6156 (0.1%)
1	4	0.52	0/4500	0.72	7/6156 (0.1%)
1	5	0.52	0/4500	0.72	8/6156 (0.1%)
1	6	0.52	0/4500	0.72	7/6156 (0.1%)
1	7	0.52	0/4500	0.72	7/6156 (0.1%)
1	8	0.52	0/4500	0.72	7/6156 (0.1%)
1	A	0.52	0/4500	0.72	7/6156 (0.1%)
1	B	0.52	0/4500	0.72	8/6156 (0.1%)
1	C	0.52	0/4500	0.72	7/6156 (0.1%)
1	D	0.52	0/4500	0.72	7/6156 (0.1%)
1	E	0.52	0/4500	0.72	7/6156 (0.1%)
1	F	0.52	0/4500	0.72	7/6156 (0.1%)
1	G	0.52	0/4500	0.72	8/6156 (0.1%)
1	H	0.52	0/4500	0.72	7/6156 (0.1%)
1	I	0.52	0/4500	0.72	7/6156 (0.1%)
1	J	0.52	0/4500	0.72	7/6156 (0.1%)
1	K	0.52	0/4500	0.72	8/6156 (0.1%)
1	L	0.52	0/4500	0.72	8/6156 (0.1%)
1	M	0.52	0/4500	0.72	7/6156 (0.1%)
1	N	0.52	0/4500	0.72	7/6156 (0.1%)
1	O	0.52	0/4500	0.72	7/6156 (0.1%)
1	P	0.52	0/4500	0.72	8/6156 (0.1%)
1	Q	0.52	0/4500	0.72	7/6156 (0.1%)
1	R	0.52	0/4500	0.72	7/6156 (0.1%)
1	S	0.52	0/4500	0.72	8/6156 (0.1%)
1	T	0.52	0/4500	0.72	8/6156 (0.1%)
1	U	0.52	0/4500	0.72	7/6156 (0.1%)
1	V	0.52	0/4500	0.72	7/6156 (0.1%)
1	W	0.52	0/4500	0.72	7/6156 (0.1%)
1	X	0.52	0/4500	0.72	7/6156 (0.1%)
1	Y	0.52	0/4500	0.72	7/6156 (0.1%)
1	Z	0.52	0/4500	0.72	7/6156 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.52	0/4500	0.72	7/6156 (0.1%)
1	b	0.52	0/4500	0.72	7/6156 (0.1%)
1	c	0.52	0/4500	0.72	7/6156 (0.1%)
1	d	0.52	0/4500	0.72	7/6156 (0.1%)
1	e	0.52	0/4500	0.72	7/6156 (0.1%)
1	f	0.52	0/4500	0.72	7/6156 (0.1%)
1	g	0.52	0/4500	0.72	7/6156 (0.1%)
1	h	0.52	0/4500	0.72	7/6156 (0.1%)
1	i	0.52	0/4500	0.72	8/6156 (0.1%)
1	j	0.52	0/4500	0.72	7/6156 (0.1%)
1	k	0.52	0/4500	0.72	7/6156 (0.1%)
1	l	0.52	0/4500	0.72	7/6156 (0.1%)
1	m	0.52	0/4500	0.72	8/6156 (0.1%)
1	n	0.52	0/4500	0.72	7/6156 (0.1%)
1	o	0.52	0/4500	0.72	7/6156 (0.1%)
1	p	0.52	0/4500	0.72	7/6156 (0.1%)
1	q	0.52	0/4500	0.72	8/6156 (0.1%)
1	r	0.52	0/4500	0.72	7/6156 (0.1%)
1	s	0.52	0/4500	0.72	7/6156 (0.1%)
1	t	0.52	0/4500	0.72	8/6156 (0.1%)
1	u	0.52	0/4500	0.72	8/6156 (0.1%)
1	v	0.52	0/4500	0.72	7/6156 (0.1%)
1	w	0.52	0/4500	0.72	7/6156 (0.1%)
1	x	0.52	0/4500	0.72	7/6156 (0.1%)
1	y	0.52	0/4500	0.72	7/6156 (0.1%)
1	z	0.52	0/4500	0.72	7/6156 (0.1%)
All	All	0.52	0/270000	0.72	435/369360 (0.1%)

There are no bond length outliers.

The worst 5 of 435 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	503	ASN	N-CA-CB	-10.88	93.38	110.46
1	5	503	ASN	N-CA-CB	-10.88	93.38	110.46
1	m	503	ASN	N-CA-CB	-10.87	93.39	110.46
1	J	503	ASN	N-CA-CB	-10.87	93.40	110.46
1	U	503	ASN	N-CA-CB	-10.87	93.40	110.46

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	4353	0	4079	179	0
1	2	4353	0	4079	177	0
1	3	4353	0	4079	172	0
1	4	4353	0	4079	172	0
1	5	4353	0	4079	181	0
1	6	4353	0	4079	178	0
1	7	4353	0	4079	178	0
1	8	4353	0	4079	178	0
1	A	4353	0	4079	179	0
1	B	4353	0	4079	181	0
1	C	4353	0	4079	180	0
1	D	4353	0	4079	181	0
1	E	4353	0	4079	176	0
1	F	4353	0	4079	183	0
1	G	4353	0	4079	179	0
1	H	4353	0	4079	178	0
1	I	4353	0	4079	181	0
1	J	4353	0	4079	177	0
1	K	4353	0	4079	173	0
1	L	4353	0	4079	176	0
1	M	4353	0	4079	176	0
1	N	4353	0	4079	183	0
1	O	4353	0	4079	181	0
1	P	4353	0	4079	180	0
1	Q	4353	0	4079	184	0
1	R	4353	0	4079	183	0
1	S	4353	0	4079	185	0
1	T	4353	0	4079	181	0
1	U	4353	0	4079	182	0
1	V	4353	0	4079	181	0
1	W	4353	0	4079	182	0
1	X	4353	0	4079	183	0
1	Y	4353	0	4079	180	0
1	Z	4353	0	4079	179	0
1	a	4353	0	4079	174	0
1	b	4353	0	4079	179	0
1	c	4353	0	4079	180	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	d	4353	0	4079	173	0
1	e	4353	0	4079	178	0
1	f	4353	0	4079	176	0
1	g	4353	0	4079	179	0
1	h	4353	0	4079	177	0
1	i	4353	0	4079	183	0
1	j	4353	0	4079	182	0
1	k	4353	0	4079	178	0
1	l	4353	0	4079	178	0
1	m	4353	0	4079	184	0
1	n	4353	0	4079	177	0
1	o	4353	0	4079	183	0
1	p	4353	0	4079	179	0
1	q	4353	0	4079	182	0
1	r	4353	0	4079	184	0
1	s	4353	0	4079	181	0
1	t	4353	0	4079	180	0
1	u	4353	0	4079	182	0
1	v	4353	0	4079	181	0
1	w	4353	0	4079	180	0
1	x	4353	0	4079	186	0
1	y	4353	0	4079	182	0
1	z	4353	0	4079	177	0
All	All	261180	0	244740	8940	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 8940 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:495:LEU:HD12	1:H:503:ASN:HD21	1.26	1.01
1:K:495:LEU:HD12	1:K:503:ASN:HD21	1.26	1.01
1:P:495:LEU:HD12	1:P:503:ASN:HD21	1.26	1.01
1:U:495:LEU:HD12	1:U:503:ASN:HD21	1.26	1.01
1:m:495:LEU:HD12	1:m:503:ASN:HD21	1.26	1.01

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	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	2	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	3	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	4	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	5	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	6	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	7	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	8	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	A	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	B	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	C	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	D	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	E	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	F	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	G	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	H	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	I	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	J	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	K	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	L	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	M	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	N	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	O	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	P	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	Q	535/707 (76%)	506 (95%)	29 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	S	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	T	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	U	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	V	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	W	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	X	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	Y	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	Z	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	a	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	b	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	c	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	d	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	e	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	f	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	g	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	h	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	i	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	j	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	k	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	l	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	m	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	n	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	o	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	p	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	q	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	r	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	s	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	t	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	u	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	v	535/707 (76%)	506 (95%)	29 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	w	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	x	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	y	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
1	z	535/707 (76%)	506 (95%)	29 (5%)	0	100	100
All	All	32100/42420 (76%)	30360 (95%)	1740 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	473/609 (78%)	473 (100%)	0	100	100
1	2	473/609 (78%)	473 (100%)	0	100	100
1	3	473/609 (78%)	473 (100%)	0	100	100
1	4	473/609 (78%)	473 (100%)	0	100	100
1	5	473/609 (78%)	473 (100%)	0	100	100
1	6	473/609 (78%)	473 (100%)	0	100	100
1	7	473/609 (78%)	473 (100%)	0	100	100
1	8	473/609 (78%)	473 (100%)	0	100	100
1	A	473/609 (78%)	473 (100%)	0	100	100
1	B	473/609 (78%)	473 (100%)	0	100	100
1	C	473/609 (78%)	473 (100%)	0	100	100
1	D	473/609 (78%)	473 (100%)	0	100	100
1	E	473/609 (78%)	473 (100%)	0	100	100
1	F	473/609 (78%)	473 (100%)	0	100	100
1	G	473/609 (78%)	473 (100%)	0	100	100
1	H	473/609 (78%)	473 (100%)	0	100	100
1	I	473/609 (78%)	473 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	473/609 (78%)	473 (100%)	0	100	100
1	K	473/609 (78%)	473 (100%)	0	100	100
1	L	473/609 (78%)	473 (100%)	0	100	100
1	M	473/609 (78%)	473 (100%)	0	100	100
1	N	473/609 (78%)	473 (100%)	0	100	100
1	O	473/609 (78%)	473 (100%)	0	100	100
1	P	473/609 (78%)	473 (100%)	0	100	100
1	Q	473/609 (78%)	473 (100%)	0	100	100
1	R	473/609 (78%)	473 (100%)	0	100	100
1	S	473/609 (78%)	473 (100%)	0	100	100
1	T	473/609 (78%)	473 (100%)	0	100	100
1	U	473/609 (78%)	473 (100%)	0	100	100
1	V	473/609 (78%)	473 (100%)	0	100	100
1	W	473/609 (78%)	473 (100%)	0	100	100
1	X	473/609 (78%)	473 (100%)	0	100	100
1	Y	473/609 (78%)	473 (100%)	0	100	100
1	Z	473/609 (78%)	473 (100%)	0	100	100
1	a	473/609 (78%)	473 (100%)	0	100	100
1	b	473/609 (78%)	473 (100%)	0	100	100
1	c	473/609 (78%)	473 (100%)	0	100	100
1	d	473/609 (78%)	473 (100%)	0	100	100
1	e	473/609 (78%)	473 (100%)	0	100	100
1	f	473/609 (78%)	473 (100%)	0	100	100
1	g	473/609 (78%)	473 (100%)	0	100	100
1	h	473/609 (78%)	473 (100%)	0	100	100
1	i	473/609 (78%)	473 (100%)	0	100	100
1	j	473/609 (78%)	473 (100%)	0	100	100
1	k	473/609 (78%)	473 (100%)	0	100	100
1	l	473/609 (78%)	473 (100%)	0	100	100
1	m	473/609 (78%)	473 (100%)	0	100	100
1	n	473/609 (78%)	473 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	o	473/609 (78%)	473 (100%)	0	100	100
1	p	473/609 (78%)	473 (100%)	0	100	100
1	q	473/609 (78%)	473 (100%)	0	100	100
1	r	473/609 (78%)	473 (100%)	0	100	100
1	s	473/609 (78%)	473 (100%)	0	100	100
1	t	473/609 (78%)	473 (100%)	0	100	100
1	u	473/609 (78%)	473 (100%)	0	100	100
1	v	473/609 (78%)	473 (100%)	0	100	100
1	w	473/609 (78%)	473 (100%)	0	100	100
1	x	473/609 (78%)	473 (100%)	0	100	100
1	y	473/609 (78%)	473 (100%)	0	100	100
1	z	473/609 (78%)	473 (100%)	0	100	100
All	All	28380/36540 (78%)	28380 (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 1370 such sidechains are listed below:

Mol	Chain	Res	Type
1	o	305	ASN
1	y	105	GLN
1	p	430	GLN
1	o	297	ASN
1	t	342	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

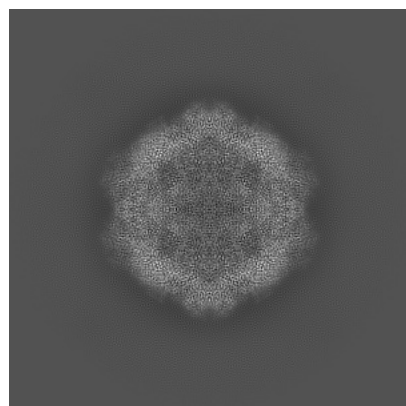
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45955. These allow visual inspection of the internal detail of the map and identification of artifacts.

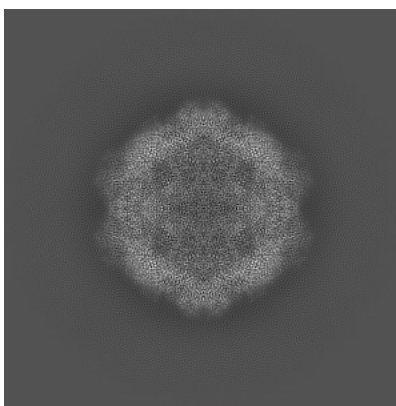
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

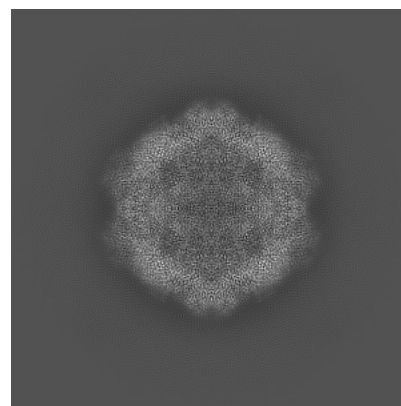
6.1.1 Primary map



X

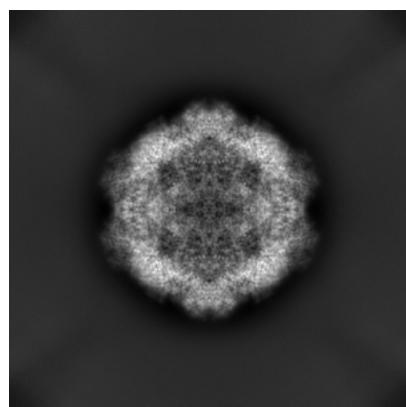


Y

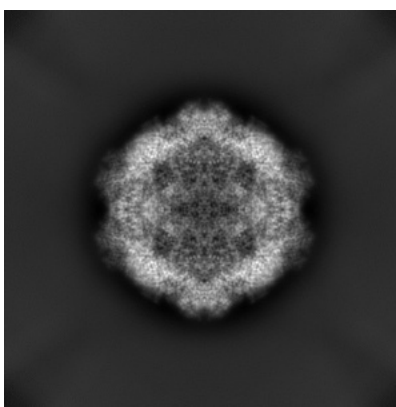


Z

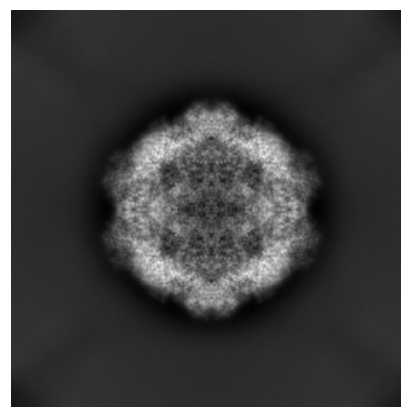
6.1.2 Raw map



X



Y

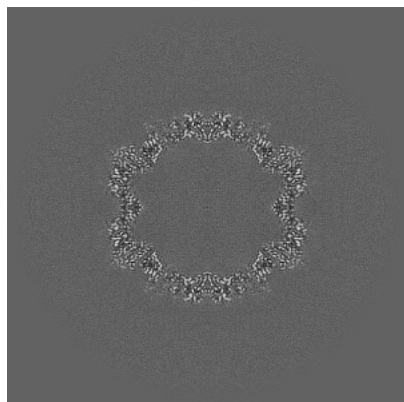


Z

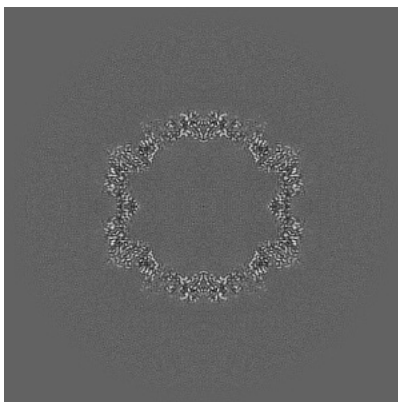
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

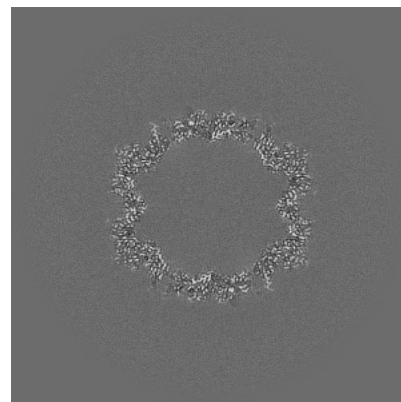
6.2.1 Primary map



X Index: 235

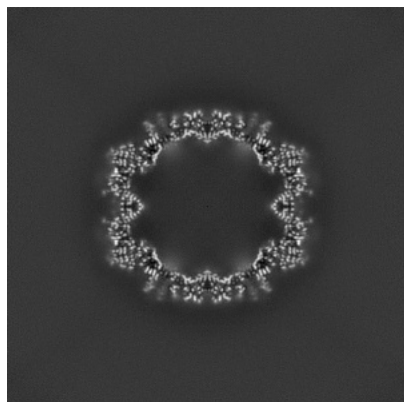


Y Index: 235

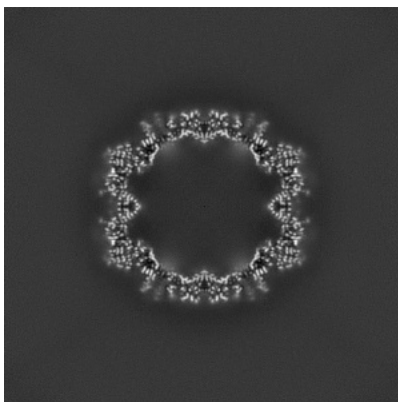


Z Index: 235

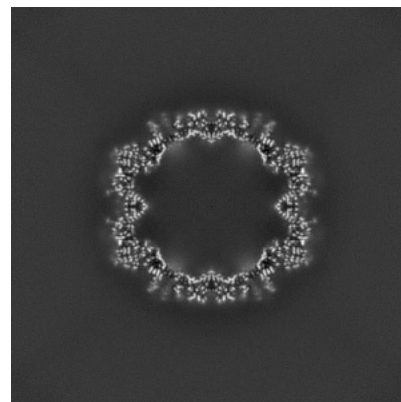
6.2.2 Raw map



X Index: 235



Y Index: 235

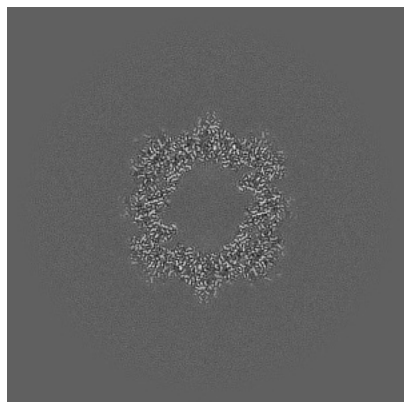


Z Index: 235

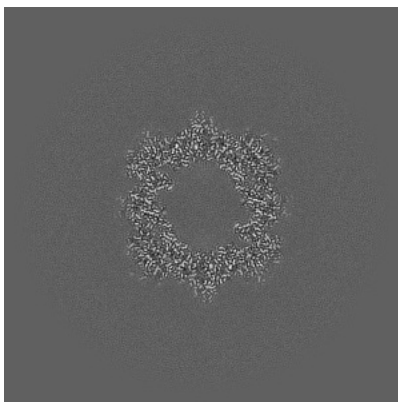
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

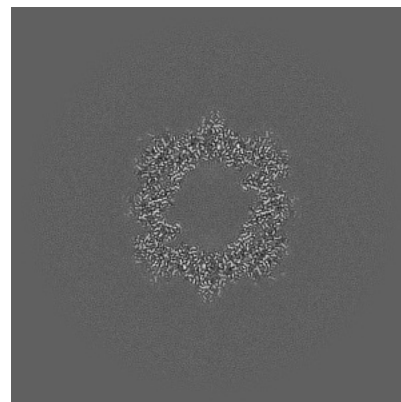
6.3.1 Primary map



X Index: 170

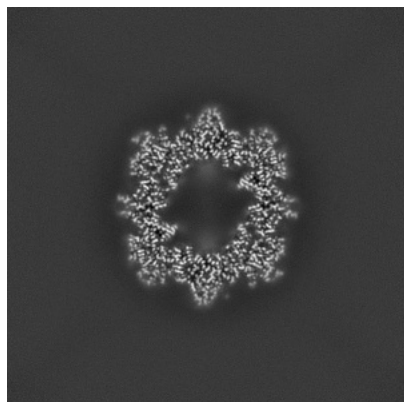


Y Index: 300

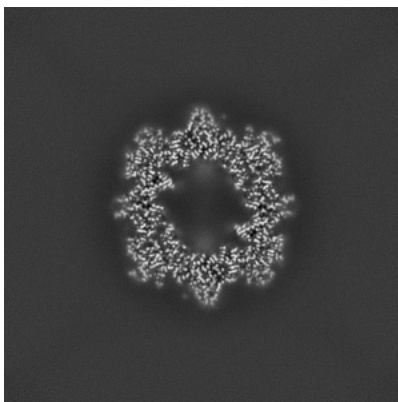


Z Index: 169

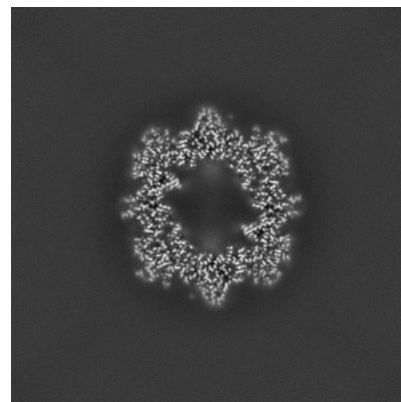
6.3.2 Raw map



X Index: 298



Y Index: 172

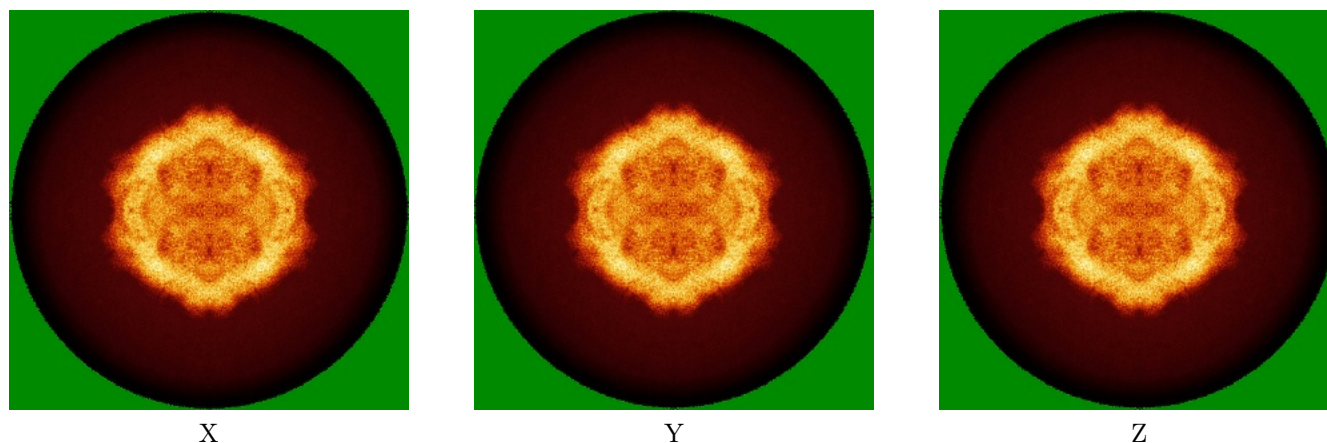


Z Index: 172

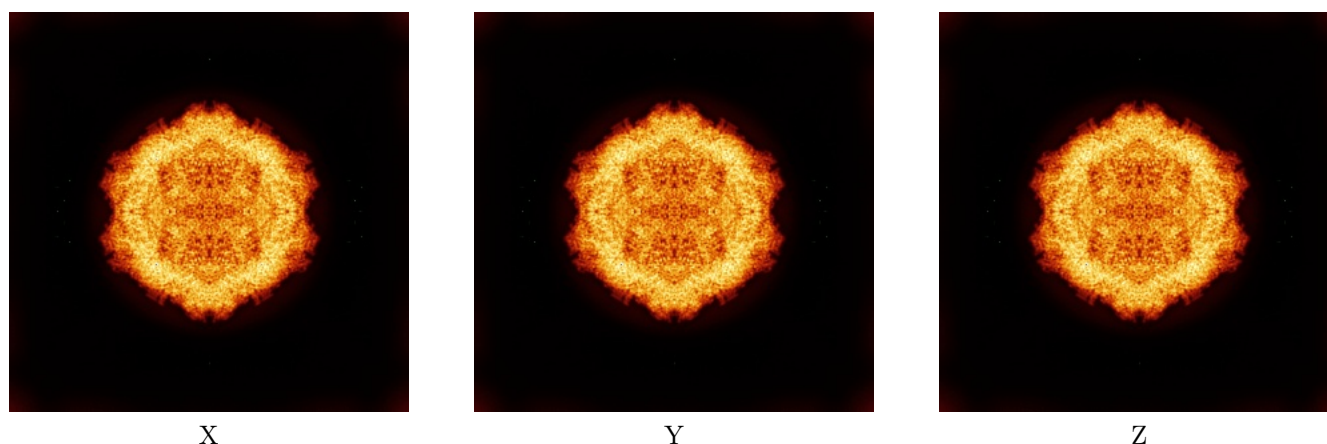
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

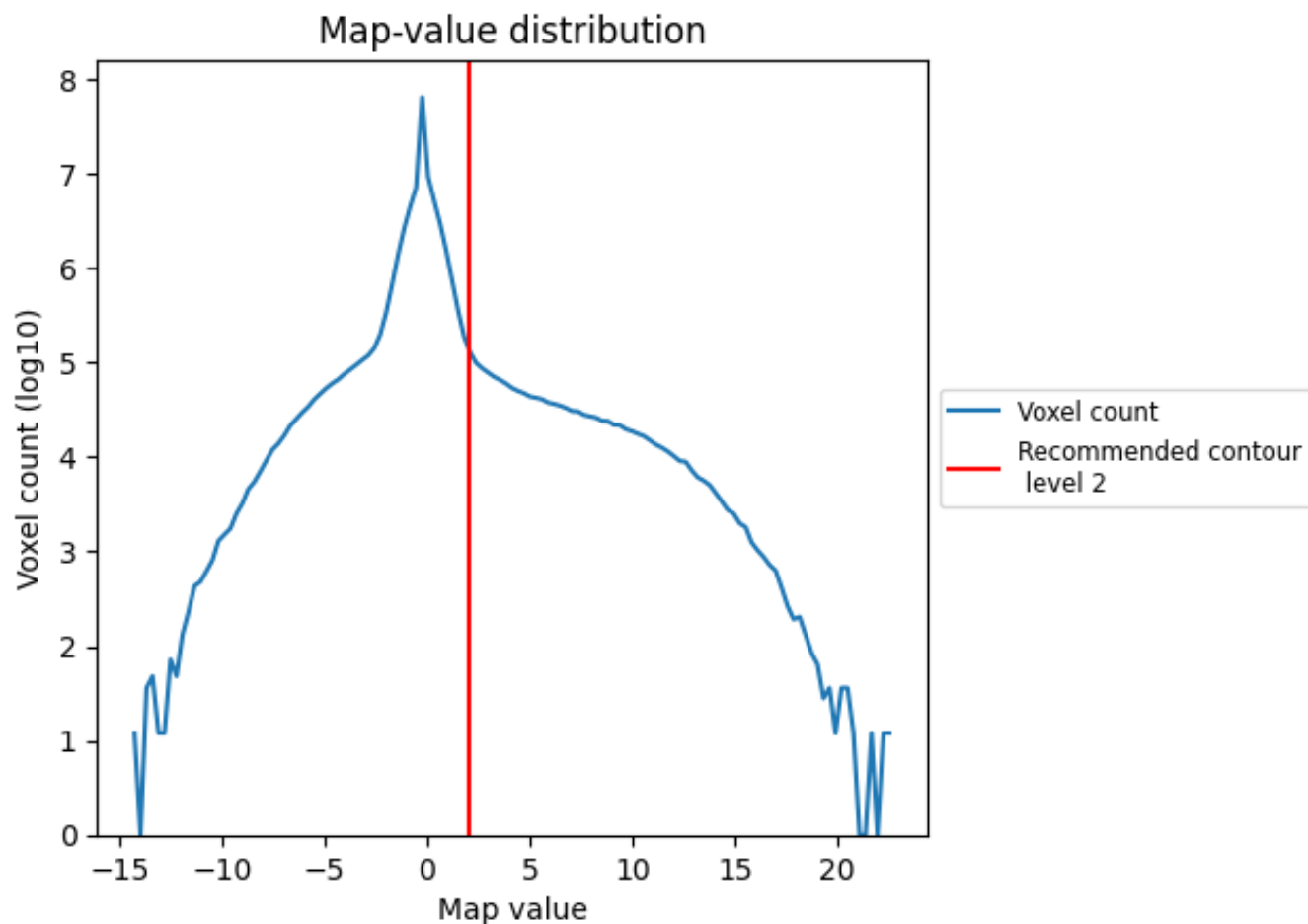
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

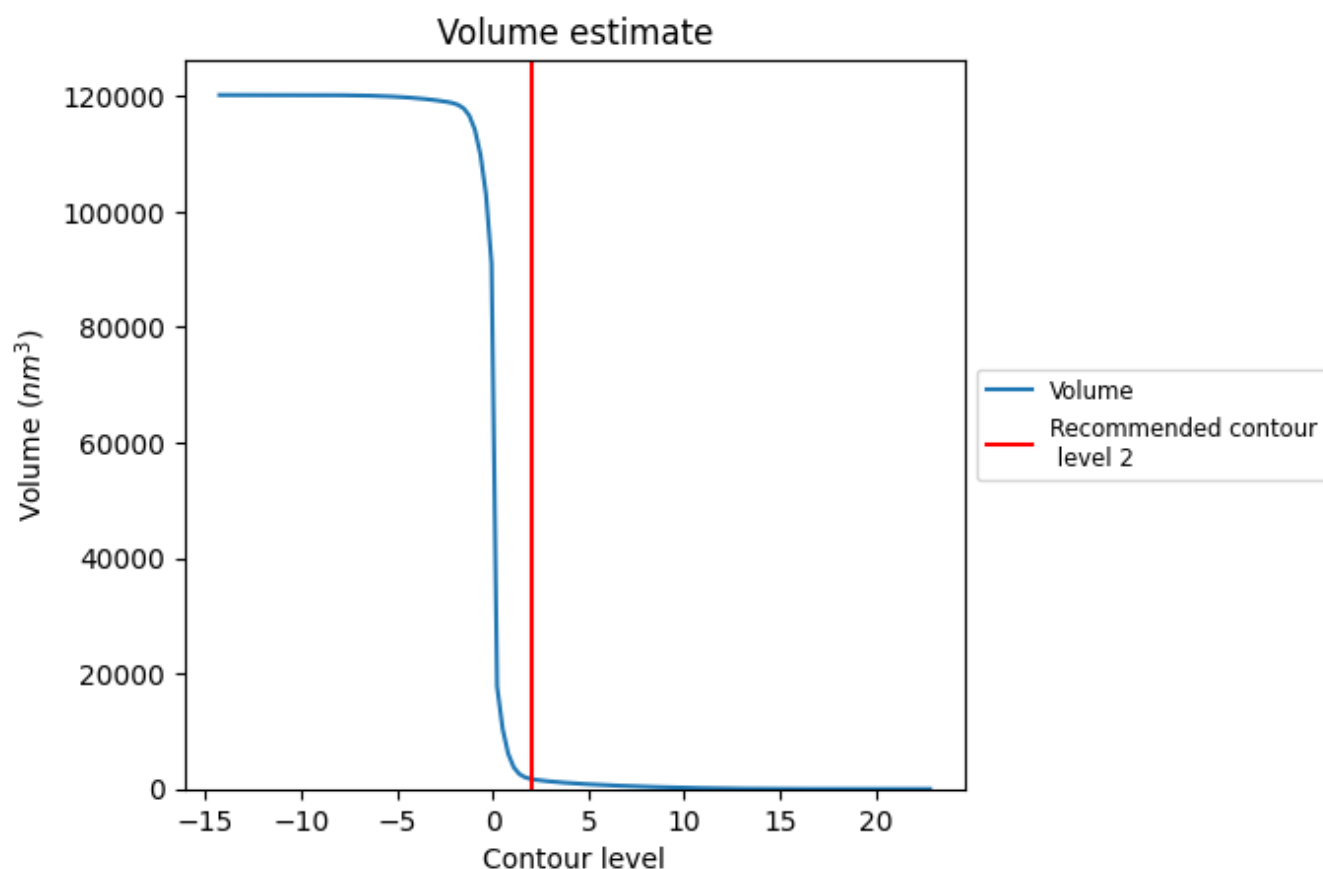
This section contains the results of statistical analysis of the map.

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.

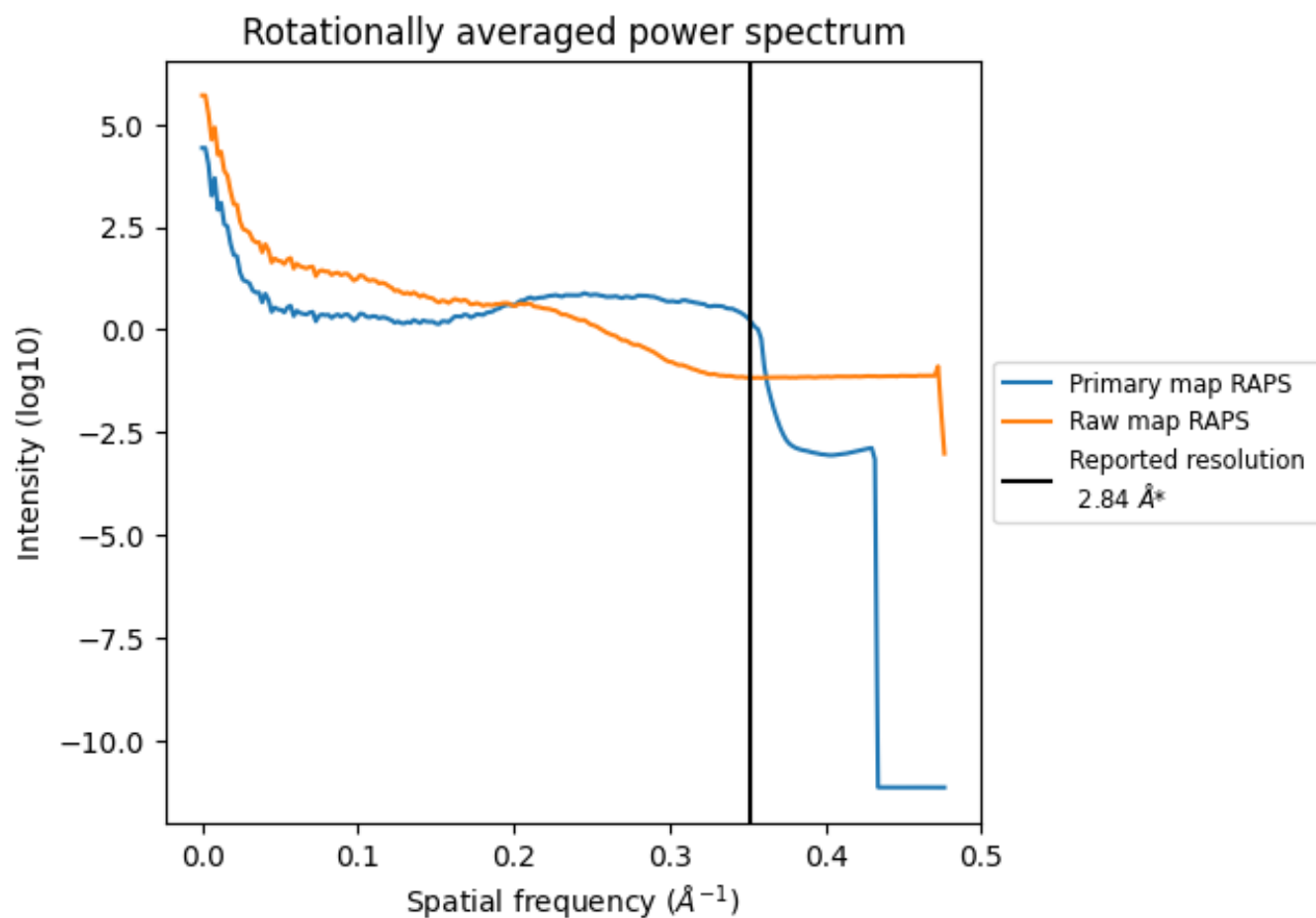
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1736 nm³; this corresponds to an approximate mass of 1569 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 ⓘ

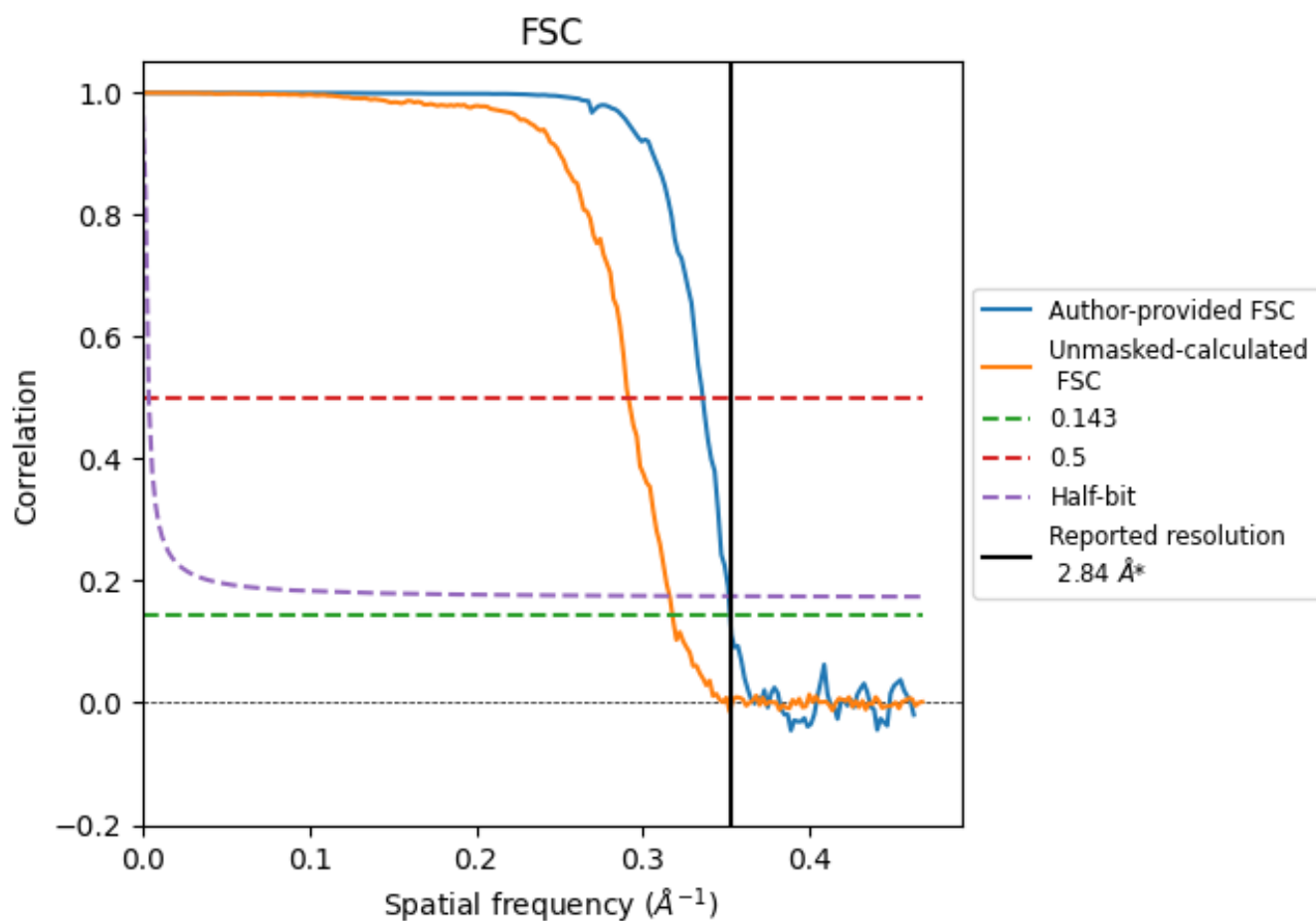


*Reported resolution corresponds to spatial frequency of 0.352 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.352 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.84	-	-
Author-provided FSC curve	2.84	2.98	2.85
Unmasked-calculated*	3.15	3.43	3.17

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.15 differs from the reported value 2.84 by more than 10 %

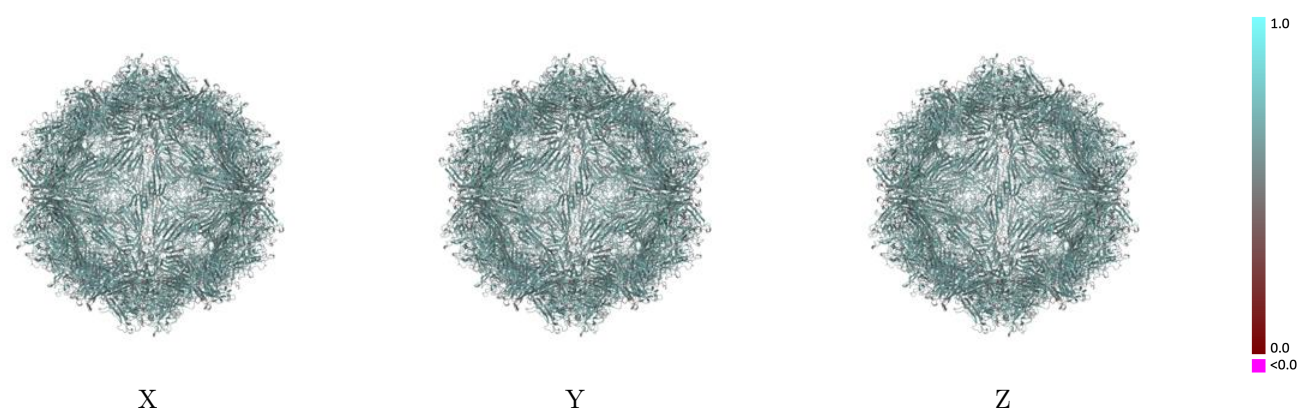
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-45955 and PDB model 9CV0. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

This section was not generated.

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

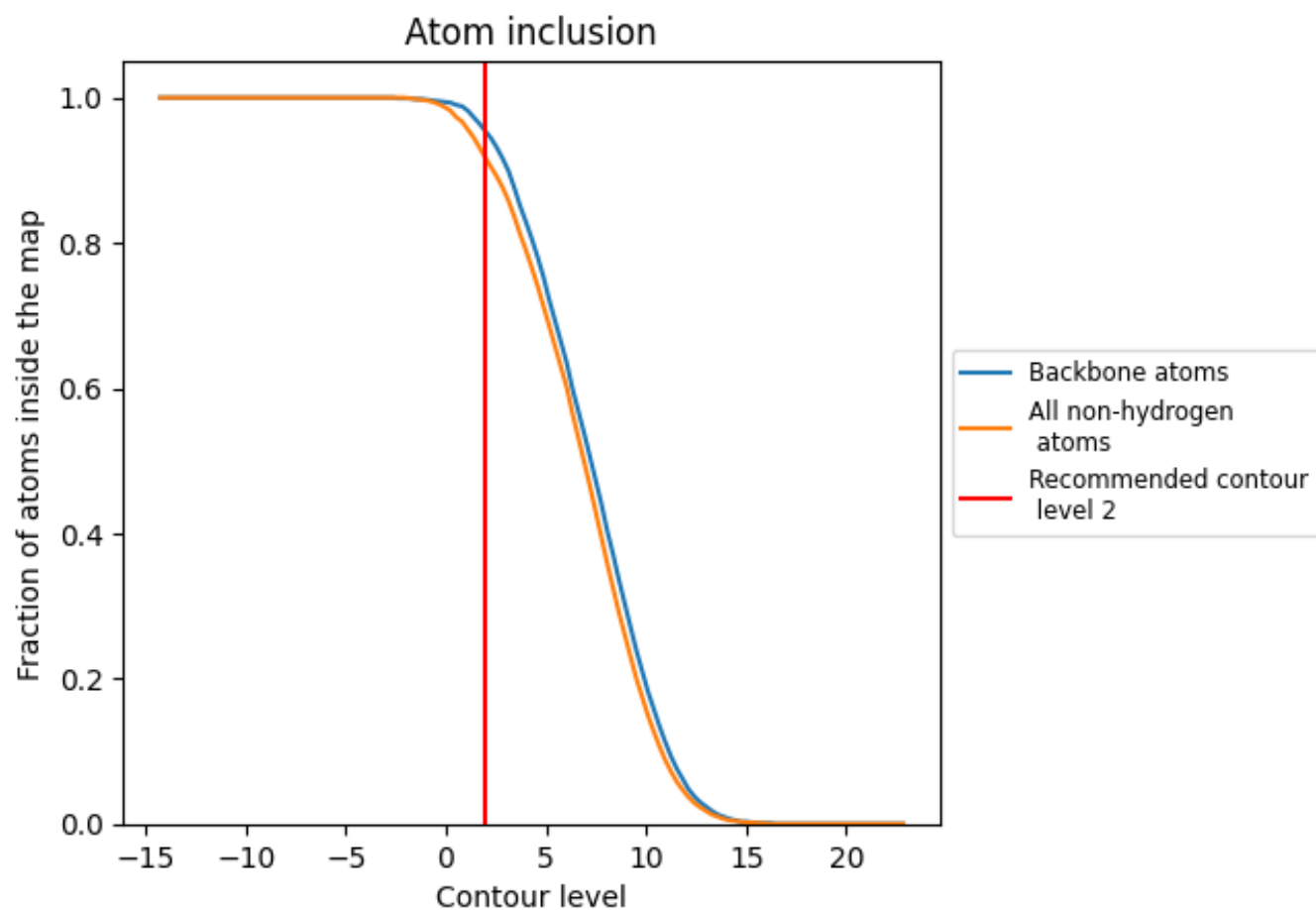


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 95% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

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

Chain	Atom inclusion	Q-score
All	 0.9160	 0.6170
1	 0.9160	 0.6180
2	 0.9160	 0.6170
3	 0.9160	 0.6180
4	 0.9130	 0.6150
5	 0.9170	 0.6160
6	 0.9170	 0.6160
7	 0.9170	 0.6150
8	 0.9160	 0.6170
A	 0.9160	 0.6170
B	 0.9160	 0.6170
C	 0.9150	 0.6150
D	 0.9170	 0.6170
E	 0.9160	 0.6180
F	 0.9160	 0.6170
G	 0.9160	 0.6160
H	 0.9170	 0.6160
I	 0.9130	 0.6150
J	 0.9160	 0.6160
K	 0.9130	 0.6160
L	 0.9160	 0.6170
M	 0.9160	 0.6170
N	 0.9170	 0.6170
O	 0.9160	 0.6170
P	 0.9170	 0.6170
Q	 0.9130	 0.6150
R	 0.9160	 0.6170
S	 0.9160	 0.6180
T	 0.9130	 0.6150
U	 0.9160	 0.6180
V	 0.9130	 0.6150
W	 0.9170	 0.6160
X	 0.9160	 0.6170
Y	 0.9170	 0.6170
Z	 0.9160	 0.6170



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Chain	Atom inclusion	Q-score
a	 0.9160	 0.6170
b	 0.9160	 0.6180
c	 0.9160	 0.6170
d	 0.9160	 0.6180
e	 0.9160	 0.6170
f	 0.9160	 0.6170
g	 0.9130	 0.6160
h	 0.9160	 0.6170
i	 0.9170	 0.6160
j	 0.9170	 0.6150
k	 0.9170	 0.6170
l	 0.9160	 0.6170
m	 0.9130	 0.6160
n	 0.9160	 0.6180
o	 0.9160	 0.6170
p	 0.9130	 0.6150
q	 0.9160	 0.6160
r	 0.9160	 0.6180
s	 0.9160	 0.6170
t	 0.9160	 0.6160
u	 0.9130	 0.6150
v	 0.9160	 0.6170
w	 0.9160	 0.6170
x	 0.9130	 0.6140
y	 0.9160	 0.6170
z	 0.9160	 0.6180