



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 03:43 PM UTC

PDB ID : 4QYK / pdb_00004qyk
Title : Crystal structure of a canine parvovirus variant
Authors : Lukk, T.; Organtini, L.J.; Hafenstein, S.U.
Deposited on : 2014-07-24
Resolution : 3.50 Å(reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

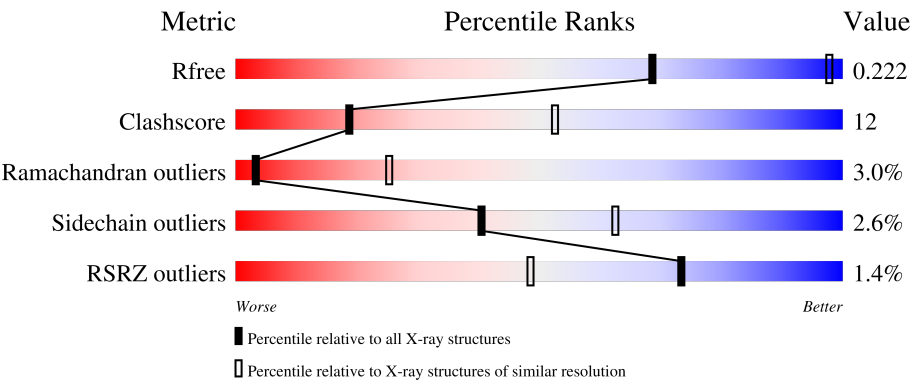
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	584	% 69%22%.. 6%
1	B	584	% 68%23%.. 6%
1	C	584	2% 66%24%.. 6%
1	D	584	% 68%21%.. 6%
1	E	584	% 67%23%.. 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	584	
1	G	584	
1	H	584	
1	I	584	
1	J	584	
1	K	584	
1	L	584	
1	M	584	
1	N	584	
1	O	584	
1	P	584	
1	Q	584	
1	R	584	
1	S	584	
1	T	584	
1	U	584	
1	V	584	
1	W	584	
1	X	584	
1	Y	584	
1	Z	584	
1	a	584	
1	b	584	
1	c	584	
1	d	584	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 130590 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Capsid protein VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	E	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	J	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	N	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	Q	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	B	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	C	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	D	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	F	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	G	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	H	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	I	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	K	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	L	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	M	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	O	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	P	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	R	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	S	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	T	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	U	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	V	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	W	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	X	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	Y	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	Z	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	a	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	b	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	c	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			
1	d	548	Total	C	N	O	S	0	0	0
			4352	2767	740	830	15			

There are 150 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	60	TYR	GLU	conflict	UNP P90456
A	104	GLU	GLN	conflict	UNP P90456
A	426	ASP	ASN	conflict	UNP P90456
A	509	GLN	GLU	conflict	UNP P90456
A	555	VAL	ILE	conflict	UNP P90456
E	60	TYR	GLU	conflict	UNP P90456
E	104	GLU	GLN	conflict	UNP P90456
E	426	ASP	ASN	conflict	UNP P90456
E	509	GLN	GLU	conflict	UNP P90456
E	555	VAL	ILE	conflict	UNP P90456
J	60	TYR	GLU	conflict	UNP P90456

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
J	104	GLU	GLN	conflict	UNP P90456
J	426	ASP	ASN	conflict	UNP P90456
J	509	GLN	GLU	conflict	UNP P90456
J	555	VAL	ILE	conflict	UNP P90456
N	60	TYR	GLU	conflict	UNP P90456
N	104	GLU	GLN	conflict	UNP P90456
N	426	ASP	ASN	conflict	UNP P90456
N	509	GLN	GLU	conflict	UNP P90456
N	555	VAL	ILE	conflict	UNP P90456
Q	60	TYR	GLU	conflict	UNP P90456
Q	104	GLU	GLN	conflict	UNP P90456
Q	426	ASP	ASN	conflict	UNP P90456
Q	509	GLN	GLU	conflict	UNP P90456
Q	555	VAL	ILE	conflict	UNP P90456
B	60	TYR	GLU	conflict	UNP P90456
B	104	GLU	GLN	conflict	UNP P90456
B	426	ASP	ASN	conflict	UNP P90456
B	509	GLN	GLU	conflict	UNP P90456
B	555	VAL	ILE	conflict	UNP P90456
C	60	TYR	GLU	conflict	UNP P90456
C	104	GLU	GLN	conflict	UNP P90456
C	426	ASP	ASN	conflict	UNP P90456
C	509	GLN	GLU	conflict	UNP P90456
C	555	VAL	ILE	conflict	UNP P90456
D	60	TYR	GLU	conflict	UNP P90456
D	104	GLU	GLN	conflict	UNP P90456
D	426	ASP	ASN	conflict	UNP P90456
D	509	GLN	GLU	conflict	UNP P90456
D	555	VAL	ILE	conflict	UNP P90456
F	60	TYR	GLU	conflict	UNP P90456
F	104	GLU	GLN	conflict	UNP P90456
F	426	ASP	ASN	conflict	UNP P90456
F	509	GLN	GLU	conflict	UNP P90456
F	555	VAL	ILE	conflict	UNP P90456
G	60	TYR	GLU	conflict	UNP P90456
G	104	GLU	GLN	conflict	UNP P90456
G	426	ASP	ASN	conflict	UNP P90456
G	509	GLN	GLU	conflict	UNP P90456
G	555	VAL	ILE	conflict	UNP P90456
H	60	TYR	GLU	conflict	UNP P90456
H	104	GLU	GLN	conflict	UNP P90456
H	426	ASP	ASN	conflict	UNP P90456

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
H	509	GLN	GLU	conflict	UNP P90456
H	555	VAL	ILE	conflict	UNP P90456
I	60	TYR	GLU	conflict	UNP P90456
I	104	GLU	GLN	conflict	UNP P90456
I	426	ASP	ASN	conflict	UNP P90456
I	509	GLN	GLU	conflict	UNP P90456
I	555	VAL	ILE	conflict	UNP P90456
K	60	TYR	GLU	conflict	UNP P90456
K	104	GLU	GLN	conflict	UNP P90456
K	426	ASP	ASN	conflict	UNP P90456
K	509	GLN	GLU	conflict	UNP P90456
K	555	VAL	ILE	conflict	UNP P90456
L	60	TYR	GLU	conflict	UNP P90456
L	104	GLU	GLN	conflict	UNP P90456
L	426	ASP	ASN	conflict	UNP P90456
L	509	GLN	GLU	conflict	UNP P90456
L	555	VAL	ILE	conflict	UNP P90456
M	60	TYR	GLU	conflict	UNP P90456
M	104	GLU	GLN	conflict	UNP P90456
M	426	ASP	ASN	conflict	UNP P90456
M	509	GLN	GLU	conflict	UNP P90456
M	555	VAL	ILE	conflict	UNP P90456
O	60	TYR	GLU	conflict	UNP P90456
O	104	GLU	GLN	conflict	UNP P90456
O	426	ASP	ASN	conflict	UNP P90456
O	509	GLN	GLU	conflict	UNP P90456
O	555	VAL	ILE	conflict	UNP P90456
P	60	TYR	GLU	conflict	UNP P90456
P	104	GLU	GLN	conflict	UNP P90456
P	426	ASP	ASN	conflict	UNP P90456
P	509	GLN	GLU	conflict	UNP P90456
P	555	VAL	ILE	conflict	UNP P90456
R	60	TYR	GLU	conflict	UNP P90456
R	104	GLU	GLN	conflict	UNP P90456
R	426	ASP	ASN	conflict	UNP P90456
R	509	GLN	GLU	conflict	UNP P90456
R	555	VAL	ILE	conflict	UNP P90456
S	60	TYR	GLU	conflict	UNP P90456
S	104	GLU	GLN	conflict	UNP P90456
S	426	ASP	ASN	conflict	UNP P90456
S	509	GLN	GLU	conflict	UNP P90456
S	555	VAL	ILE	conflict	UNP P90456

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
T	60	TYR	GLU	conflict	UNP P90456
T	104	GLU	GLN	conflict	UNP P90456
T	426	ASP	ASN	conflict	UNP P90456
T	509	GLN	GLU	conflict	UNP P90456
T	555	VAL	ILE	conflict	UNP P90456
U	60	TYR	GLU	conflict	UNP P90456
U	104	GLU	GLN	conflict	UNP P90456
U	426	ASP	ASN	conflict	UNP P90456
U	509	GLN	GLU	conflict	UNP P90456
U	555	VAL	ILE	conflict	UNP P90456
V	60	TYR	GLU	conflict	UNP P90456
V	104	GLU	GLN	conflict	UNP P90456
V	426	ASP	ASN	conflict	UNP P90456
V	509	GLN	GLU	conflict	UNP P90456
V	555	VAL	ILE	conflict	UNP P90456
W	60	TYR	GLU	conflict	UNP P90456
W	104	GLU	GLN	conflict	UNP P90456
W	426	ASP	ASN	conflict	UNP P90456
W	509	GLN	GLU	conflict	UNP P90456
W	555	VAL	ILE	conflict	UNP P90456
X	60	TYR	GLU	conflict	UNP P90456
X	104	GLU	GLN	conflict	UNP P90456
X	426	ASP	ASN	conflict	UNP P90456
X	509	GLN	GLU	conflict	UNP P90456
X	555	VAL	ILE	conflict	UNP P90456
Y	60	TYR	GLU	conflict	UNP P90456
Y	104	GLU	GLN	conflict	UNP P90456
Y	426	ASP	ASN	conflict	UNP P90456
Y	509	GLN	GLU	conflict	UNP P90456
Y	555	VAL	ILE	conflict	UNP P90456
Z	60	TYR	GLU	conflict	UNP P90456
Z	104	GLU	GLN	conflict	UNP P90456
Z	426	ASP	ASN	conflict	UNP P90456
Z	509	GLN	GLU	conflict	UNP P90456
Z	555	VAL	ILE	conflict	UNP P90456
a	60	TYR	GLU	conflict	UNP P90456
a	104	GLU	GLN	conflict	UNP P90456
a	426	ASP	ASN	conflict	UNP P90456
a	509	GLN	GLU	conflict	UNP P90456
a	555	VAL	ILE	conflict	UNP P90456
b	60	TYR	GLU	conflict	UNP P90456
b	104	GLU	GLN	conflict	UNP P90456

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
b	426	ASP	ASN	conflict	UNP P90456
b	509	GLN	GLU	conflict	UNP P90456
b	555	VAL	ILE	conflict	UNP P90456
c	60	TYR	GLU	conflict	UNP P90456
c	104	GLU	GLN	conflict	UNP P90456
c	426	ASP	ASN	conflict	UNP P90456
c	509	GLN	GLU	conflict	UNP P90456
c	555	VAL	ILE	conflict	UNP P90456
d	60	TYR	GLU	conflict	UNP P90456
d	104	GLU	GLN	conflict	UNP P90456
d	426	ASP	ASN	conflict	UNP P90456
d	509	GLN	GLU	conflict	UNP P90456
d	555	VAL	ILE	conflict	UNP P90456

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0
2	E	2	Total Mg 2 2	0	0
2	J	2	Total Mg 2 2	0	0
2	N	1	Total Mg 1 1	0	0
2	Q	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0
2	G	1	Total Mg 1 1	0	0
2	H	2	Total Mg 2 2	0	0
2	I	1	Total Mg 1 1	0	0
2	K	1	Total Mg 1 1	0	0
2	L	1	Total Mg 1 1	0	0

Continued on next page...

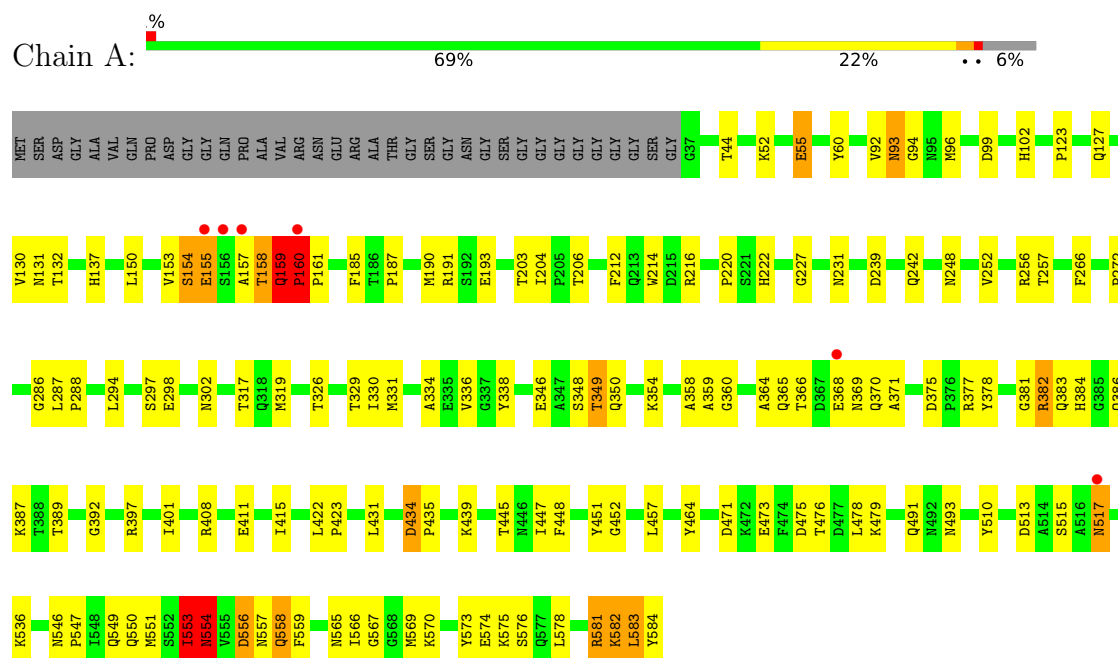
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	M	1	Total 1	Mg 1	0	0
2	O	1	Total 1	Mg 1	0	0
2	P	1	Total 1	Mg 1	0	0
2	R	1	Total 1	Mg 1	0	0
2	S	1	Total 1	Mg 1	0	0
2	T	1	Total 1	Mg 1	0	0
2	W	1	Total 1	Mg 1	0	0
2	X	1	Total 1	Mg 1	0	0
2	Y	2	Total 2	Mg 2	0	0
2	Z	1	Total 1	Mg 1	0	0
2	c	1	Total 1	Mg 1	0	0
2	d	2	Total 2	Mg 2	0	0

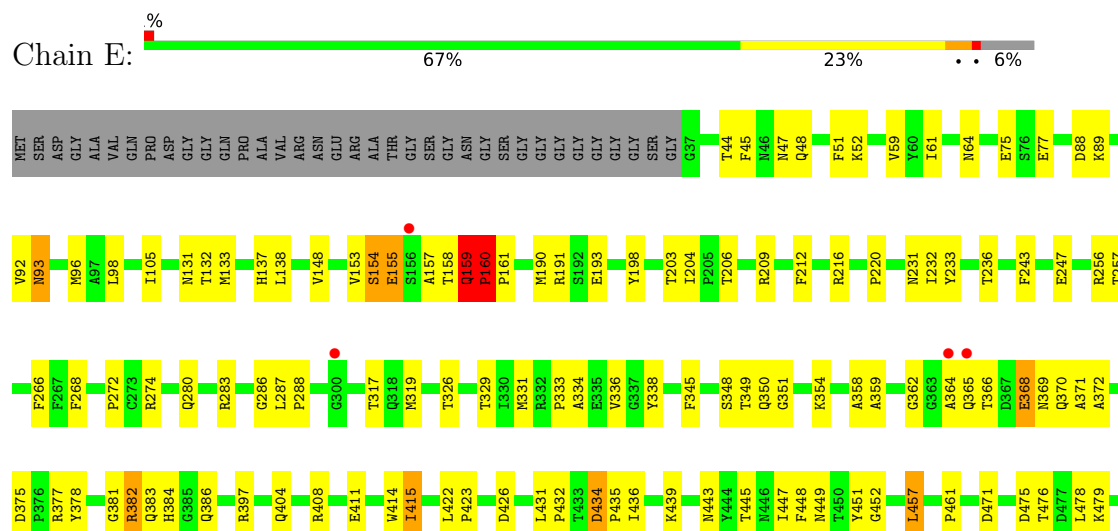
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Capsid protein VP1

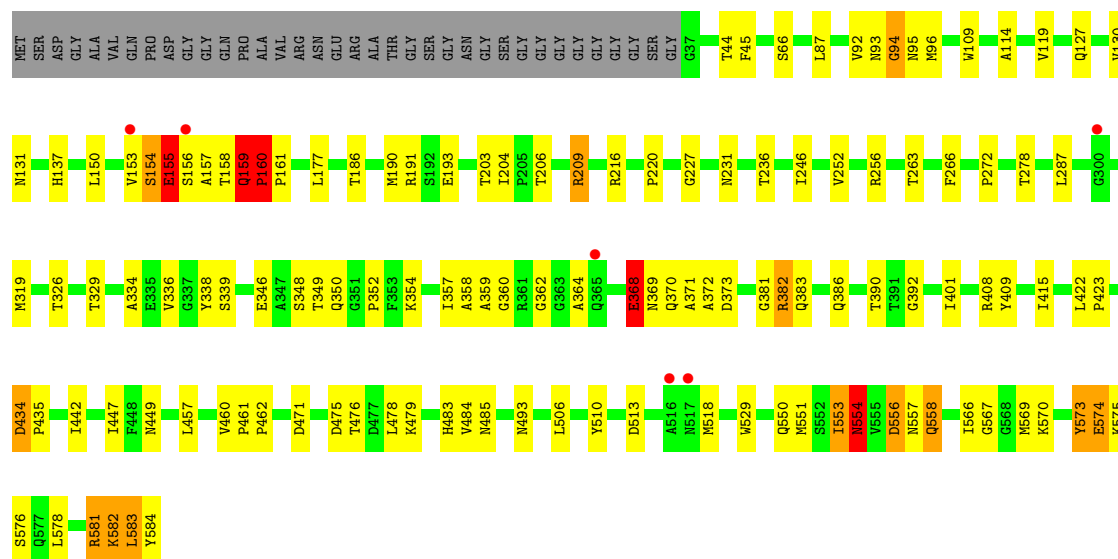


• Molecule 1: Capsid protein VP1

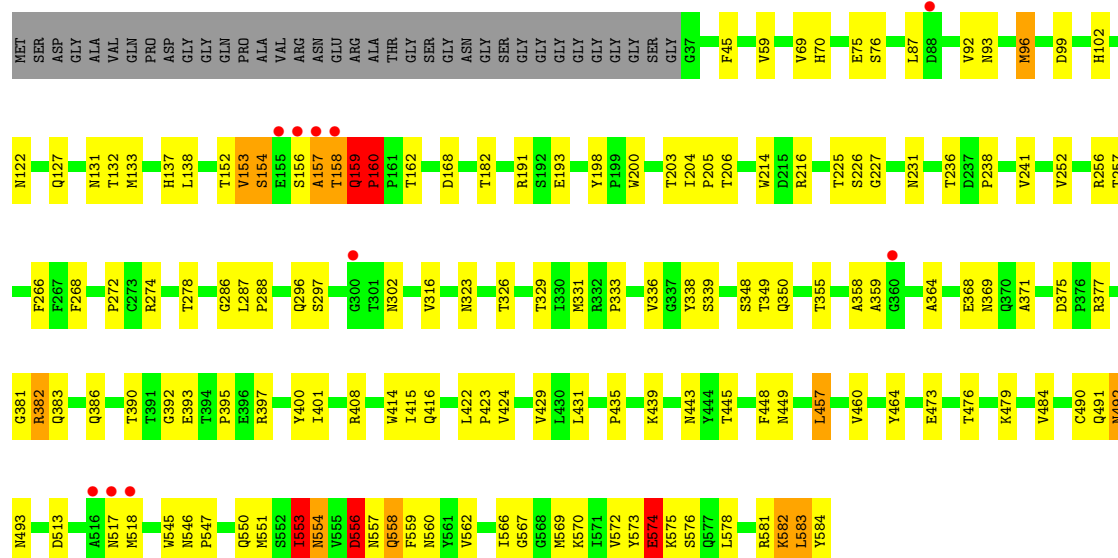




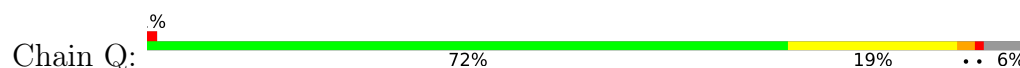
• Molecule 1: Capsid protein VP1

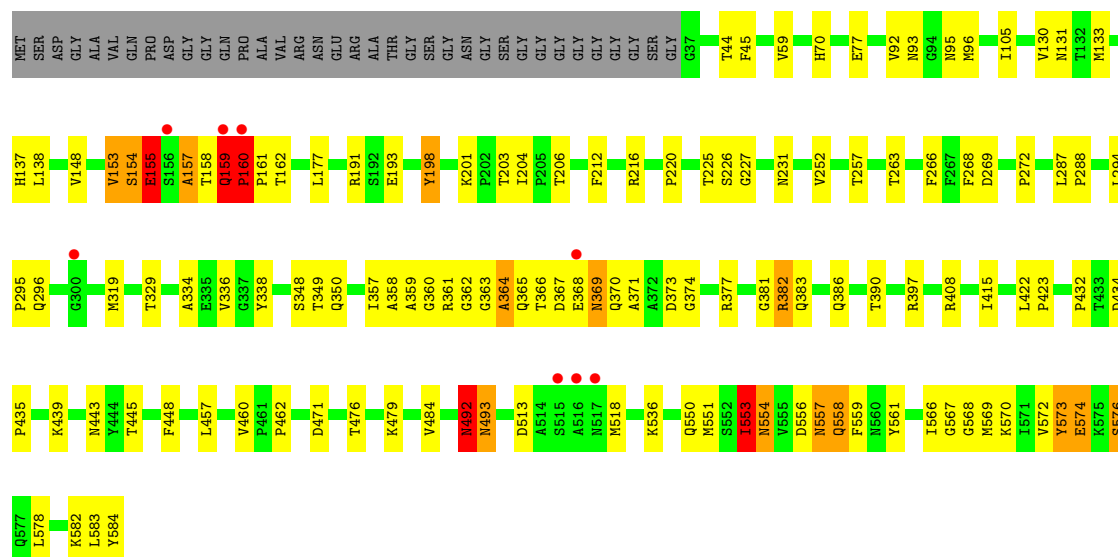


• Molecule 1: Capsid protein VP1

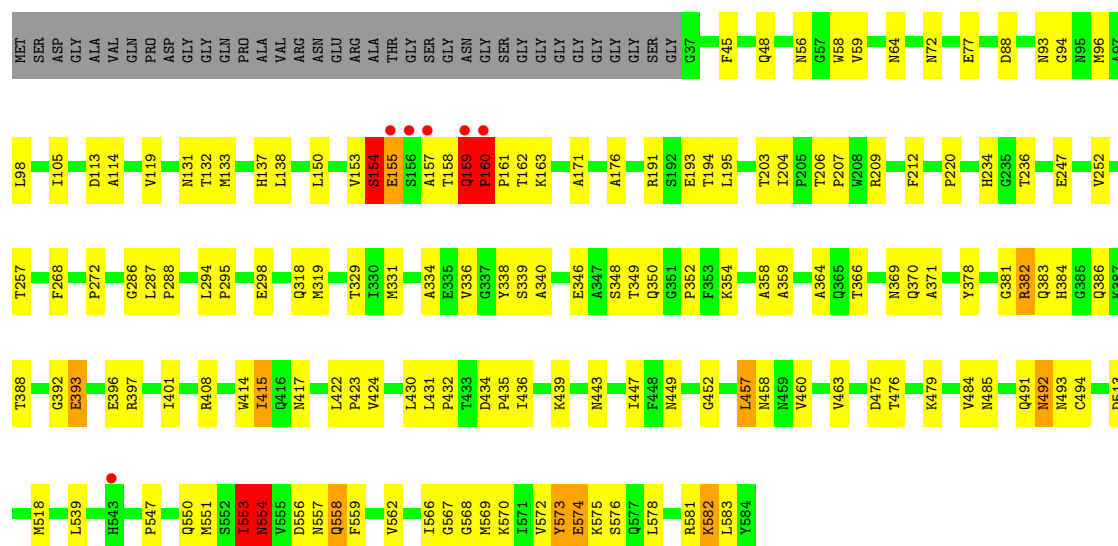


• Molecule 1: Capsid protein VP1

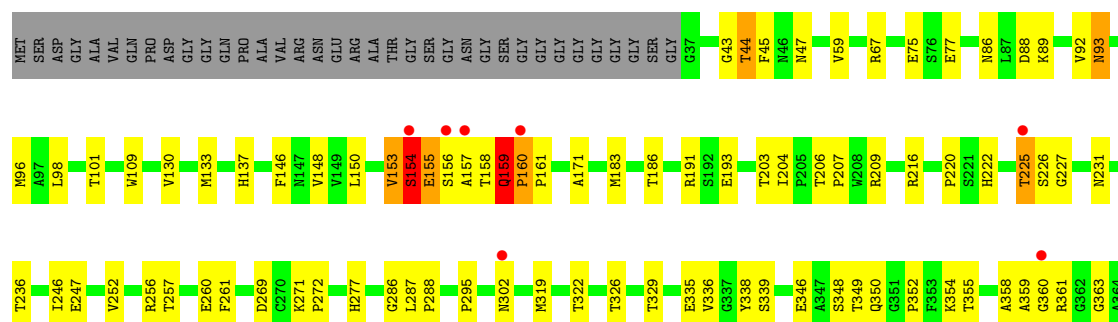


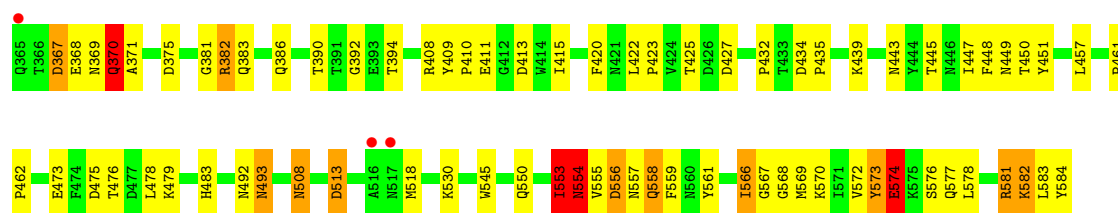


• Molecule 1: Capsid protein VP1

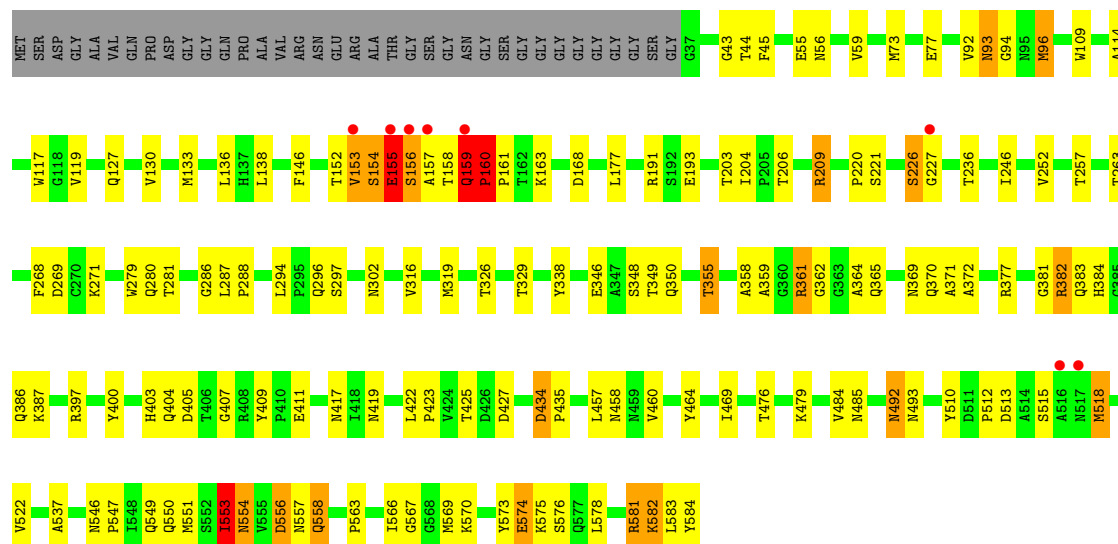


• Molecule 1: Capsid protein VP1

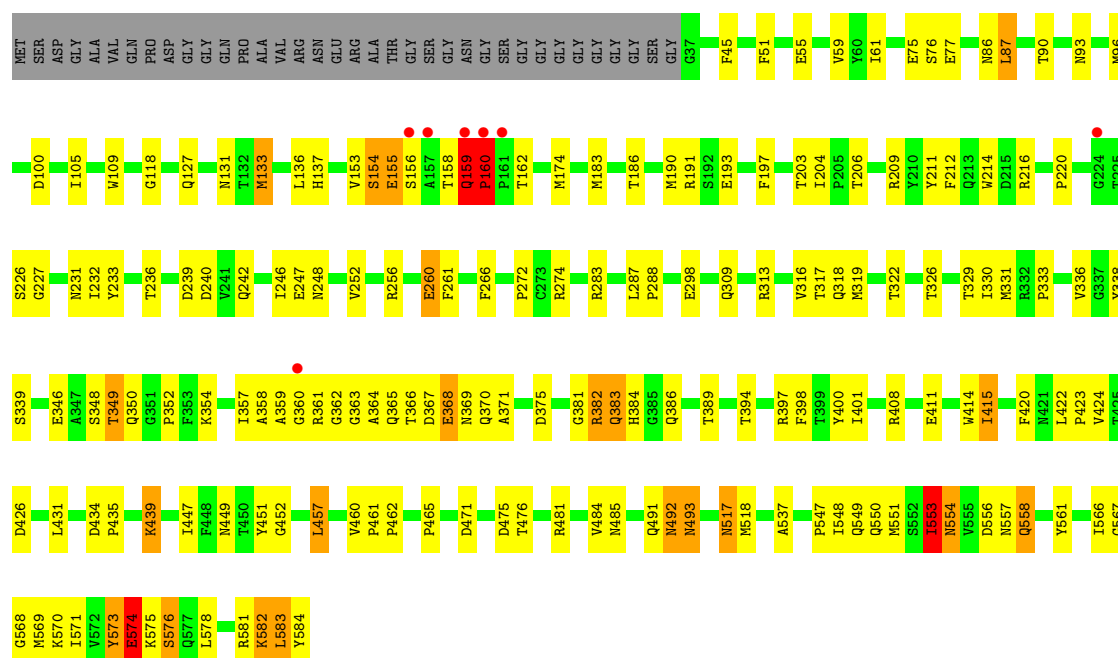


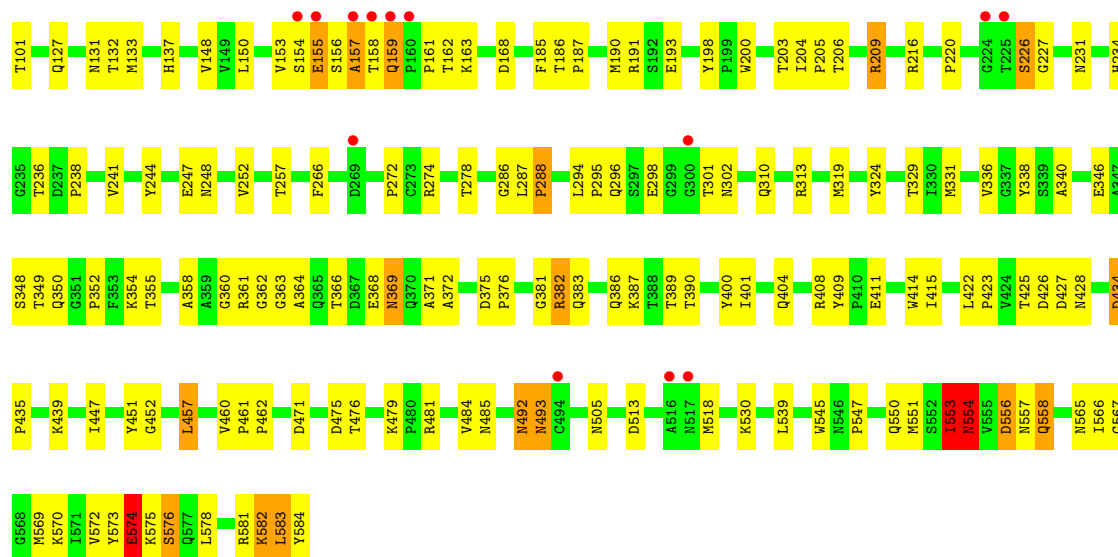


• Molecule 1: Capsid protein VP1

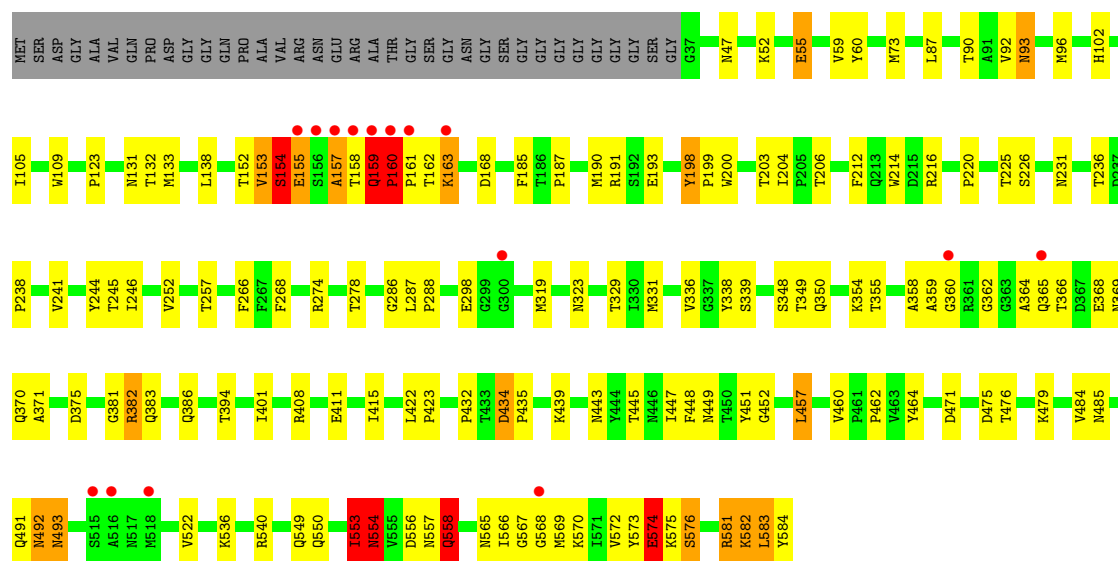


• Molecule 1: Capsid protein VP1

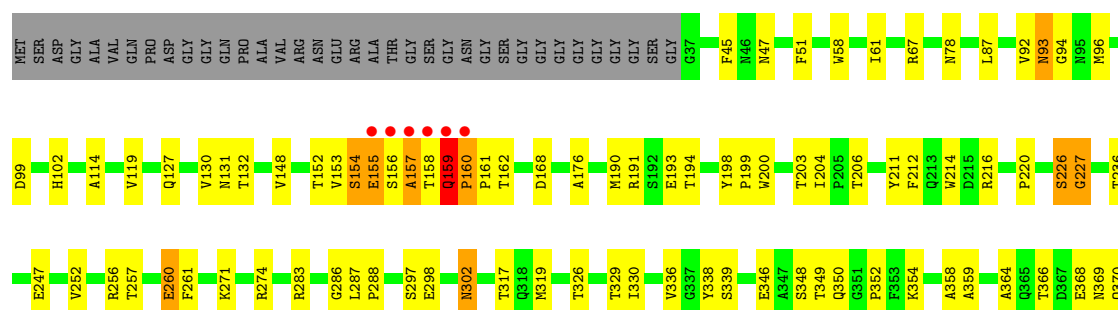




• Molecule 1: Capsid protein VP1

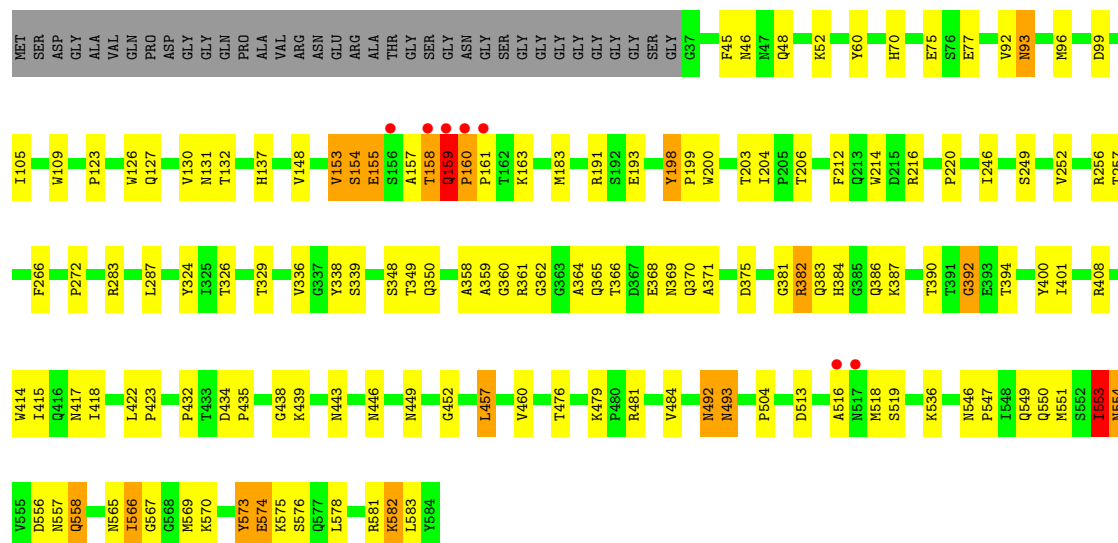


• Molecule 1: Capsid protein VP1

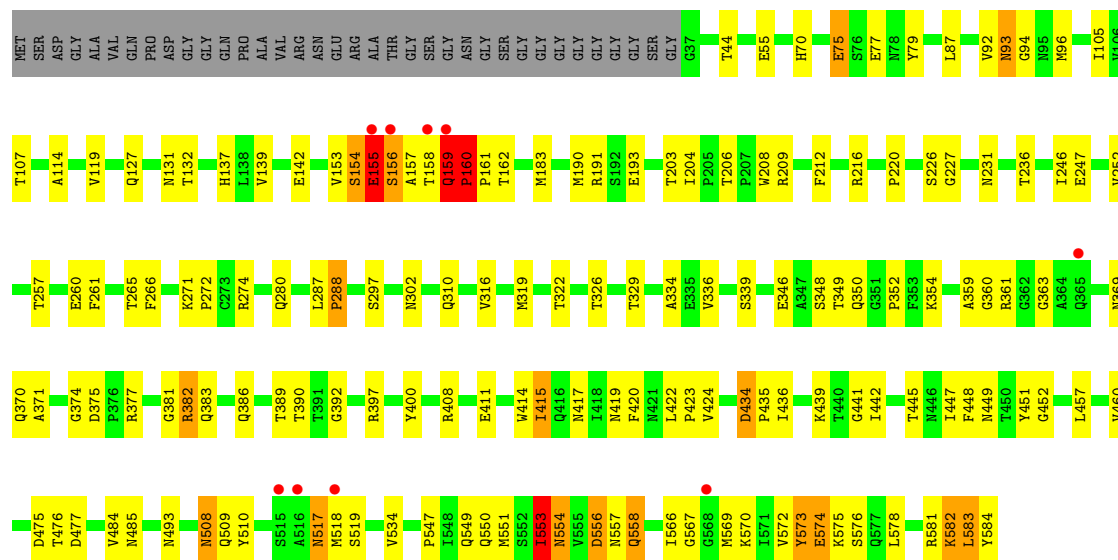




• Molecule 1: Capsid protein VP1

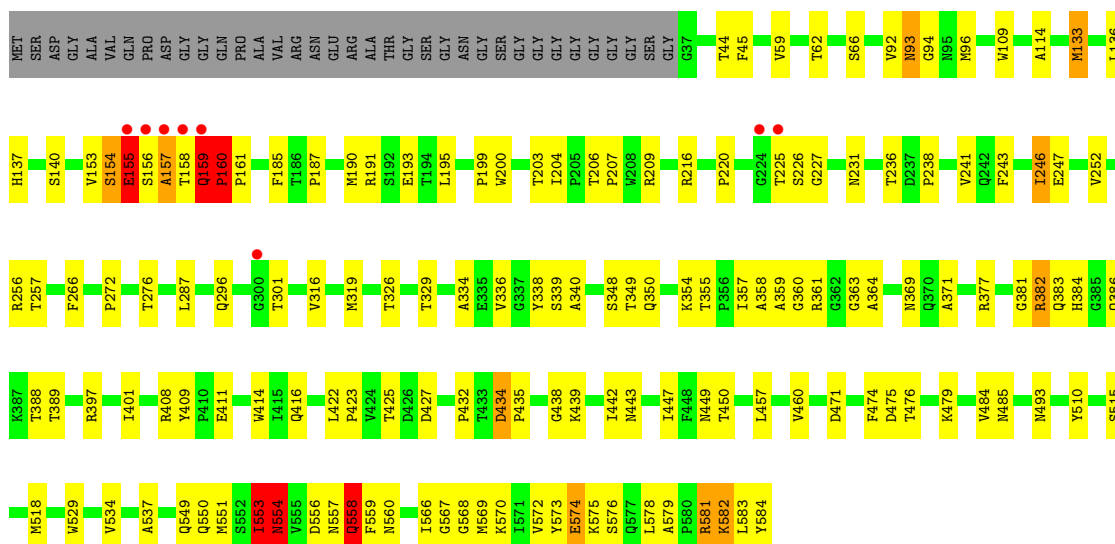


• Molecule 1: Capsid protein VP1

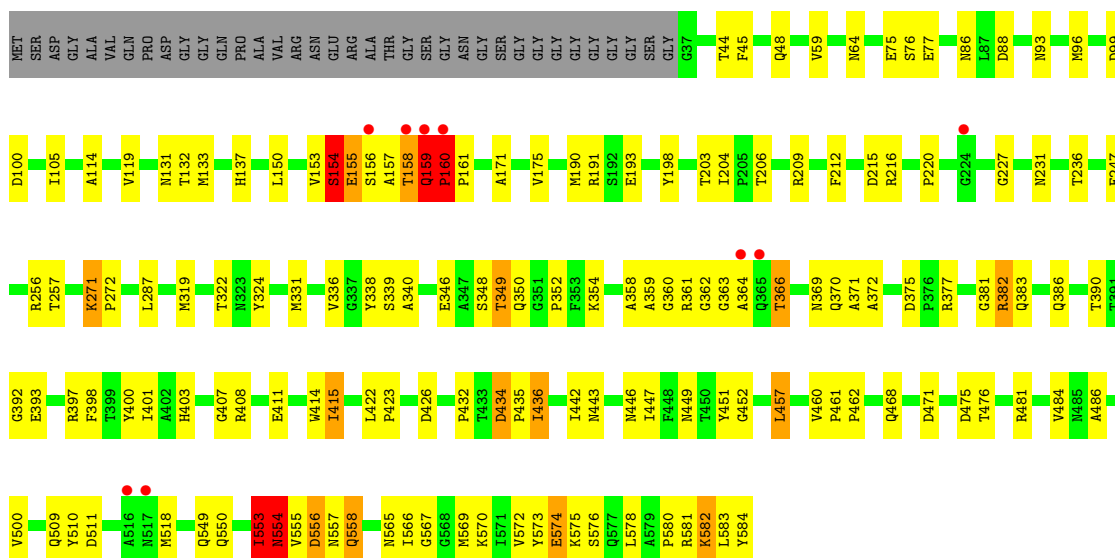


• Molecule 1: Capsid protein VP1

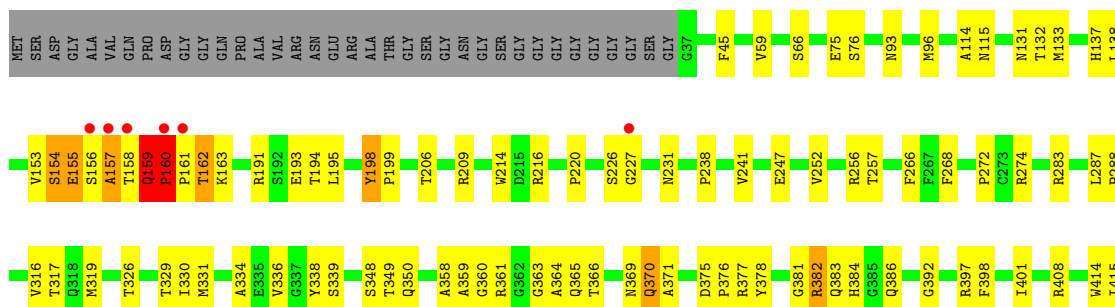


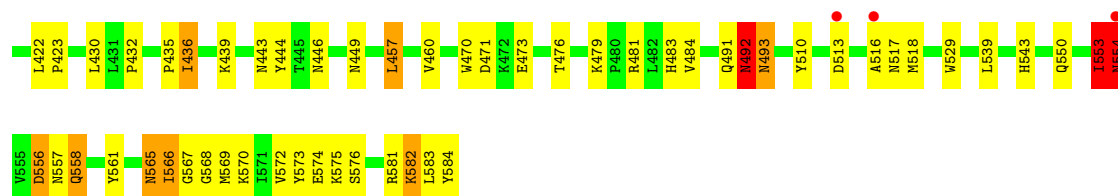


- Molecule 1: Capsid protein VP1

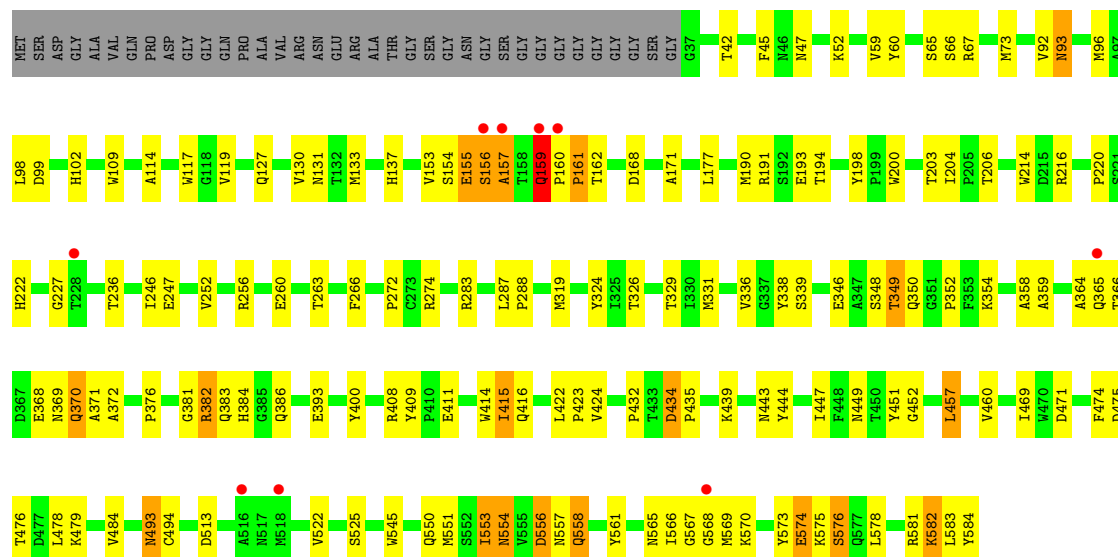


- Molecule 1: Capsid protein VP1

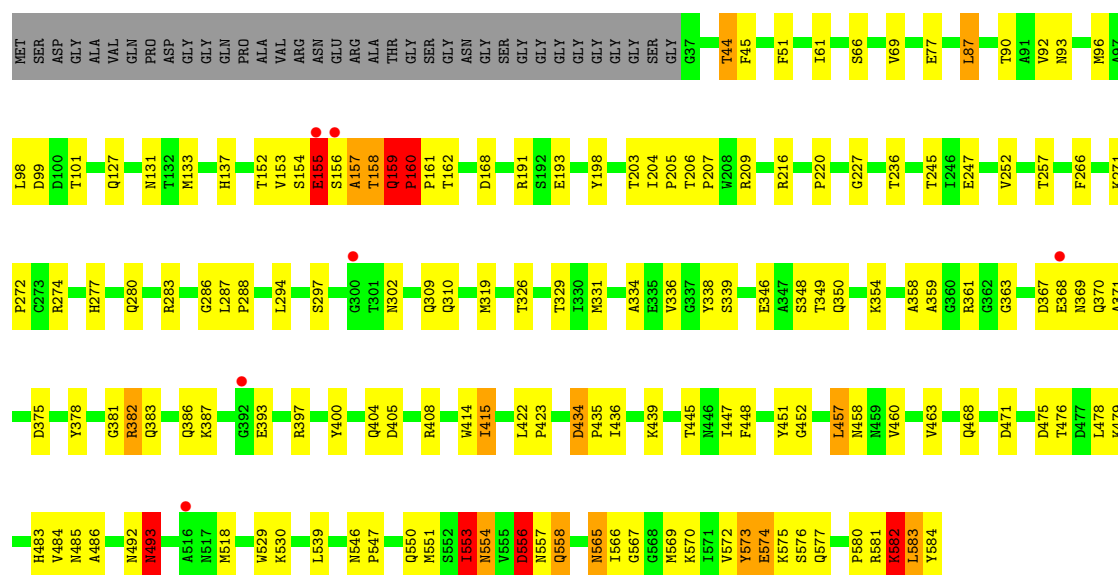




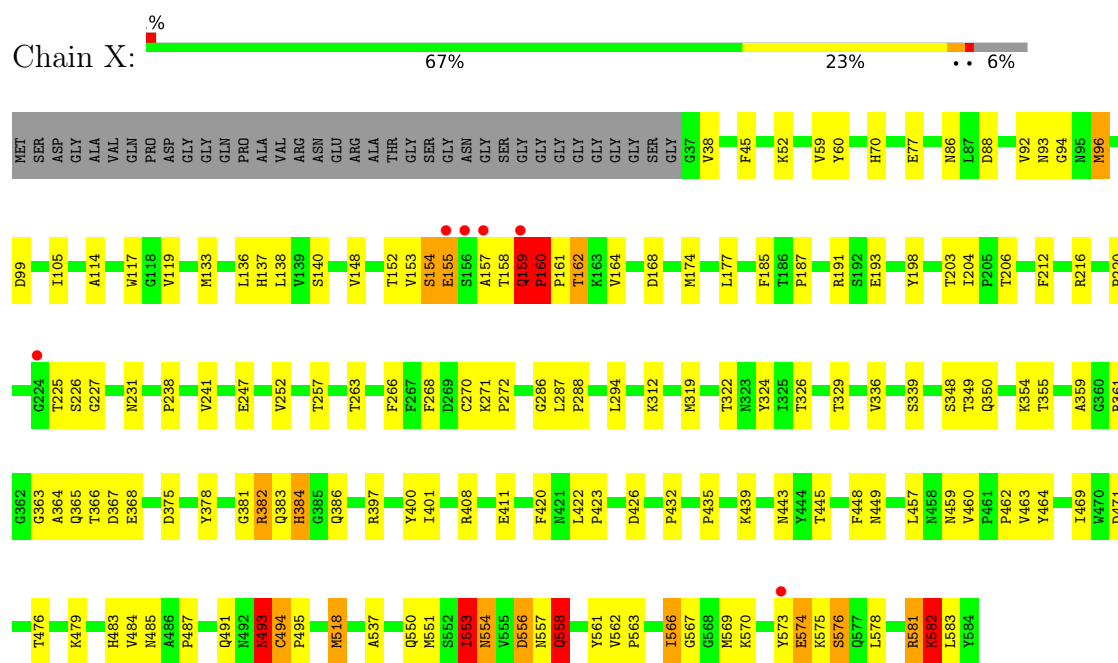
• Molecule 1: Capsid protein VP1



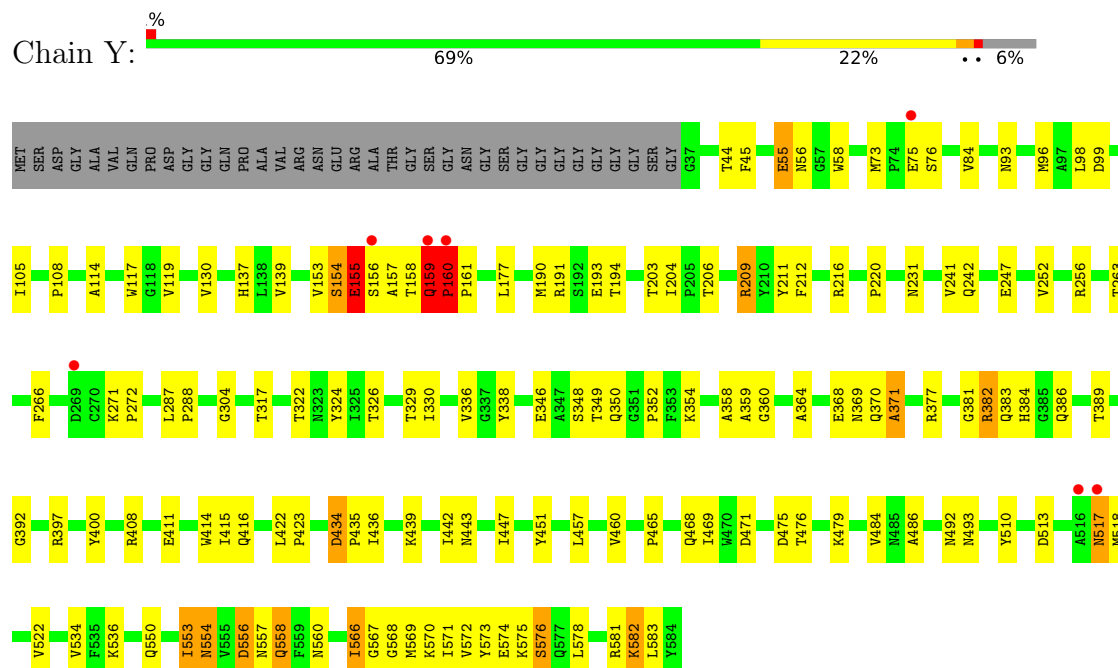
• Molecule 1: Capsid protein VP1



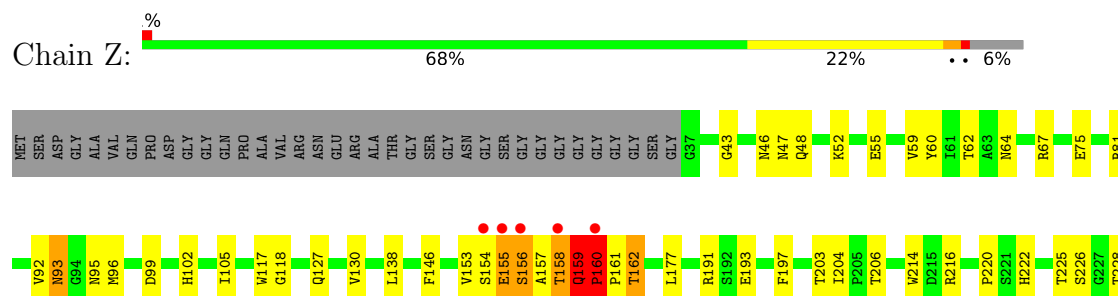
• Molecule 1: Capsid protein VP1

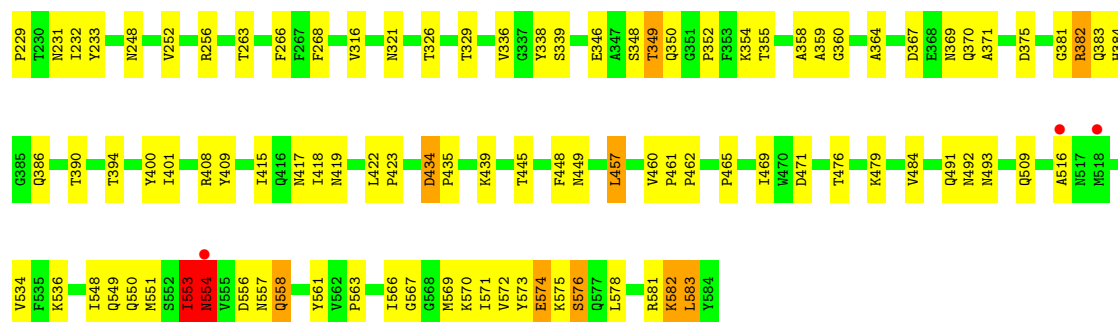


• Molecule 1: Capsid protein VP1

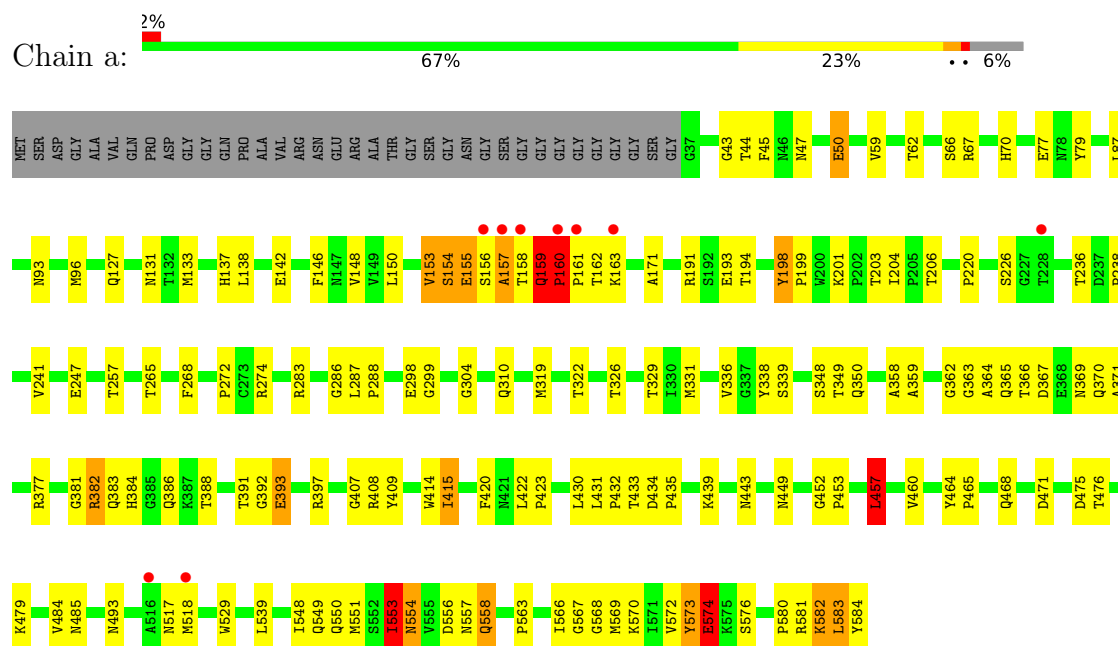


• Molecule 1: Capsid protein VP1

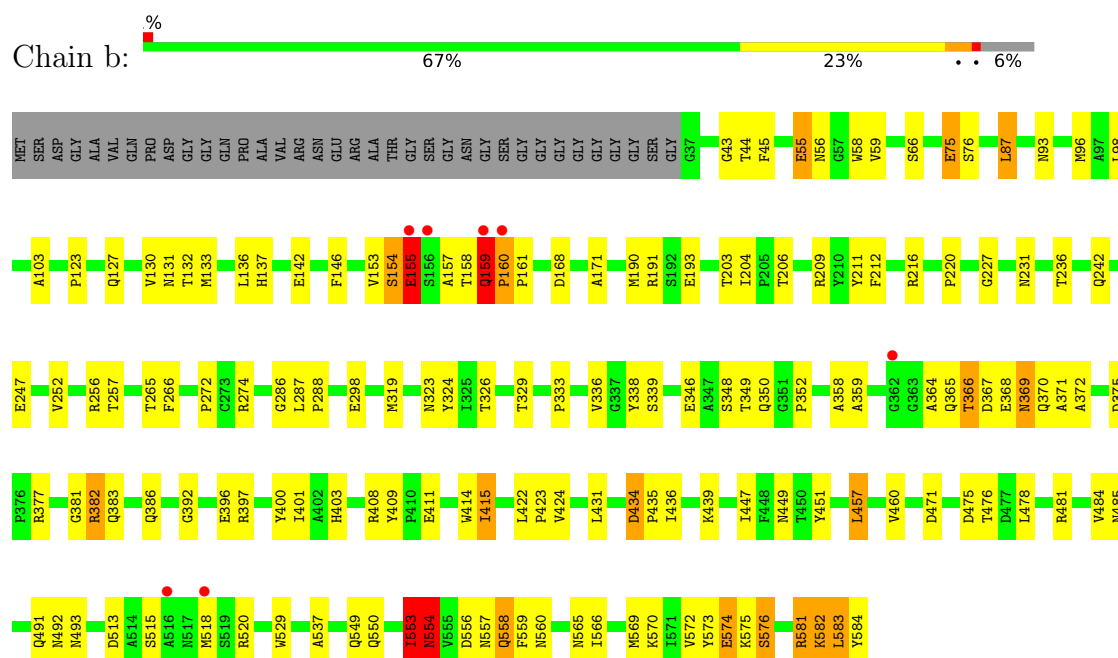




● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	453.10Å 453.10Å 319.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.99 – 3.50 49.99 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.99-3.50) 96.4 (49.99-3.50)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.30 (at 3.48Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.180 , 0.221 0.183 , 0.222	Depositor DCC
R_{free} test set	20538 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	41.7	Xtriage
Anisotropy	0.304	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	130590	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.53% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	A	0.86	1/4483 (0.0%)	1.06	24/6134 (0.4%)
1	B	0.83	2/4483 (0.0%)	1.18	16/6134 (0.3%)
1	C	0.78	0/4483	1.15	24/6134 (0.4%)
1	D	0.77	0/4483	1.12	23/6134 (0.4%)
1	E	0.82	1/4483 (0.0%)	1.11	24/6134 (0.4%)
1	F	0.83	1/4483 (0.0%)	1.17	26/6134 (0.4%)
1	G	0.78	1/4483 (0.0%)	1.15	28/6134 (0.5%)
1	H	0.76	1/4483 (0.0%)	1.10	24/6134 (0.4%)
1	I	0.84	0/4483	1.05	22/6134 (0.4%)
1	J	0.81	2/4483 (0.0%)	1.11	25/6134 (0.4%)
1	K	0.87	0/4483	1.14	28/6134 (0.5%)
1	L	0.81	0/4483	1.10	21/6134 (0.3%)
1	M	0.87	1/4483 (0.0%)	1.12	32/6134 (0.5%)
1	N	0.86	0/4483	1.11	22/6134 (0.4%)
1	O	0.76	0/4483	1.08	21/6134 (0.3%)
1	P	0.79	0/4483	1.10	25/6134 (0.4%)
1	Q	0.80	1/4483 (0.0%)	1.12	20/6134 (0.3%)
1	R	0.85	2/4483 (0.0%)	1.10	21/6134 (0.3%)
1	S	0.84	3/4483 (0.1%)	1.12	21/6134 (0.3%)
1	T	0.87	0/4483	1.10	26/6134 (0.4%)
1	U	0.78	1/4483 (0.0%)	1.14	24/6134 (0.4%)
1	V	0.78	0/4483	1.02	12/6134 (0.2%)
1	W	0.74	1/4483 (0.0%)	1.12	24/6134 (0.4%)
1	X	0.81	0/4483	1.23	25/6134 (0.4%)
1	Y	0.75	0/4483	1.11	20/6134 (0.3%)
1	Z	0.82	4/4483 (0.1%)	1.13	25/6134 (0.4%)
1	a	0.72	1/4483 (0.0%)	1.20	16/6134 (0.3%)
1	b	0.74	0/4483	1.10	21/6134 (0.3%)
1	c	0.77	0/4483	1.12	16/6134 (0.3%)
1	d	0.79	2/4483 (0.0%)	1.12	30/6134 (0.5%)
All	All	0.80	25/134490 (0.0%)	1.12	686/184020 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	2
1	D	0	2
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
1	L	0	2
1	M	0	3
1	N	0	1
1	Q	0	1
1	R	0	2
1	S	0	2
1	U	0	1
1	W	0	1
1	X	0	1
1	Y	0	2
1	Z	0	1
1	a	0	1
1	b	0	1
1	c	0	2
1	d	0	3
All	All	0	34

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Z	222	HIS	CG-CD2	-12.58	1.22	1.35
1	Z	222	HIS	CD2-NE2	12.06	1.51	1.37
1	R	334	ALA	CA-CB	-8.04	1.47	1.54
1	Z	222	HIS	CG-ND1	7.96	1.47	1.38
1	W	334	ALA	CA-CB	-7.91	1.47	1.54

The worst 5 of 686 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	159	GLN	CA-C-N	33.81	155.21	120.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	159	GLN	C-N-CA	33.81	155.21	120.38
1	a	159	GLN	CA-C-N	32.53	153.89	120.38
1	a	159	GLN	C-N-CA	32.53	153.89	120.38
1	B	159	GLN	CA-C-N	29.76	151.03	120.38

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	159	GLN	Peptide
1	C	159	GLN	Peptide
1	E	368	GLU	Peptide
1	N	226	SER	Peptide
1	Q	159	GLN	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4352	0	4143	123	0
1	B	4352	0	4143	129	0
1	C	4352	0	4143	119	2
1	D	4352	0	4143	101	4
1	E	4352	0	4143	136	0
1	F	4352	0	4143	146	0
1	G	4352	0	4143	129	3
1	H	4352	0	4143	134	0
1	I	4352	0	4143	141	0
1	J	4352	0	4143	86	2
1	K	4352	0	4143	127	0
1	L	4352	0	4143	142	0
1	M	4352	0	4143	132	0
1	N	4352	0	4143	109	2
1	O	4352	0	4143	100	5
1	P	4352	0	4143	111	0
1	Q	4352	0	4143	82	5
1	R	4352	0	4143	129	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	S	4352	0	4143	95	2
1	T	4352	0	4143	119	0
1	U	4352	0	4143	109	3
1	V	4352	0	4143	138	0
1	W	4352	0	4143	134	0
1	X	4352	0	4145	98	4
1	Y	4352	0	4143	119	2
1	Z	4352	0	4143	88	2
1	a	4352	0	4143	130	3
1	b	4352	0	4143	139	0
1	c	4352	0	4143	116	1
1	d	4352	0	4143	133	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	2	0	0	0	0
2	G	1	0	0	0	0
2	H	2	0	0	0	0
2	I	1	0	0	0	0
2	J	2	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
2	M	1	0	0	0	0
2	N	1	0	0	0	0
2	O	1	0	0	0	0
2	P	1	0	0	0	0
2	Q	1	0	0	0	0
2	R	1	0	0	0	0
2	S	1	0	0	0	0
2	T	1	0	0	0	0
2	W	1	0	0	0	0
2	X	1	0	0	0	0
2	Y	2	0	0	0	0
2	Z	1	0	0	0	0
2	c	1	0	0	0	0
2	d	2	0	0	0	0
All	All	130590	0	124292	3031	20

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 3031 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:L:553:ILE:HA	1:L:554:ASN:HB2	1.35	1.08
1:b:553:ILE:HA	1:b:554:ASN:HB2	1.37	1.07
1:V:154:SER:HA	1:V:155:GLU:HB2	1.36	1.06
1:R:154:SER:HA	1:R:155:GLU:HG3	1.33	1.06
1:Z:553:ILE:HA	1:Z:554:ASN:HB2	1.37	1.05

The worst 5 of 20 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:209:ARG:NH1	1:Y:288:PRO:O[8_555]	2.04	0.16
1:N:182:THR:O	1:X:582:LYS:NZ[8_555]	2.06	0.14
1:S:584:TYR:OH	1:X:471:ASP:OD1[8_555]	2.07	0.13
1:C:287:LEU:O	1:Z:191:ARG:NH1[8_555]	2.10	0.10
1:O:191:ARG:NH1	1:Y:287:LEU:O[8_555]	2.10	0.10

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 X-ray entries followed by that with respect to entries of similar resolution.

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	A	546/584 (94%)	500 (92%)	31 (6%)	15 (3%)	4	27
1	B	546/584 (94%)	496 (91%)	32 (6%)	18 (3%)	3	23
1	C	546/584 (94%)	493 (90%)	39 (7%)	14 (3%)	4	27
1	D	546/584 (94%)	497 (91%)	32 (6%)	17 (3%)	3	25
1	E	546/584 (94%)	497 (91%)	33 (6%)	16 (3%)	3	26
1	F	546/584 (94%)	496 (91%)	33 (6%)	17 (3%)	3	25
1	G	546/584 (94%)	497 (91%)	32 (6%)	17 (3%)	3	25
1	H	546/584 (94%)	491 (90%)	38 (7%)	17 (3%)	3	25
1	I	546/584 (94%)	499 (91%)	34 (6%)	13 (2%)	4	29
1	J	546/584 (94%)	498 (91%)	33 (6%)	15 (3%)	4	27

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	K	546/584 (94%)	499 (91%)	31 (6%)	16 (3%)	3	26
1	L	546/584 (94%)	494 (90%)	35 (6%)	17 (3%)	3	25
1	M	546/584 (94%)	491 (90%)	40 (7%)	15 (3%)	4	27
1	N	546/584 (94%)	497 (91%)	34 (6%)	15 (3%)	4	27
1	O	546/584 (94%)	492 (90%)	35 (6%)	19 (4%)	3	23
1	P	546/584 (94%)	497 (91%)	32 (6%)	17 (3%)	3	25
1	Q	546/584 (94%)	496 (91%)	34 (6%)	16 (3%)	3	26
1	R	546/584 (94%)	490 (90%)	39 (7%)	17 (3%)	3	25
1	S	546/584 (94%)	500 (92%)	32 (6%)	14 (3%)	4	27
1	T	546/584 (94%)	501 (92%)	30 (6%)	15 (3%)	4	27
1	U	546/584 (94%)	496 (91%)	32 (6%)	18 (3%)	3	23
1	V	546/584 (94%)	492 (90%)	37 (7%)	17 (3%)	3	25
1	W	546/584 (94%)	491 (90%)	40 (7%)	15 (3%)	4	27
1	X	546/584 (94%)	495 (91%)	34 (6%)	17 (3%)	3	25
1	Y	546/584 (94%)	498 (91%)	30 (6%)	18 (3%)	3	23
1	Z	546/584 (94%)	497 (91%)	31 (6%)	18 (3%)	3	23
1	a	546/584 (94%)	497 (91%)	33 (6%)	16 (3%)	3	26
1	b	546/584 (94%)	489 (90%)	41 (8%)	16 (3%)	3	26
1	c	546/584 (94%)	499 (91%)	31 (6%)	16 (3%)	3	26
1	d	546/584 (94%)	498 (91%)	32 (6%)	16 (3%)	3	26
All	All	16380/17520 (94%)	14873 (91%)	1020 (6%)	487 (3%)	3	25

5 of 487 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	153	VAL
1	A	155	GLU
1	A	159	GLN
1	A	160	PRO
1	A	349	THR

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 X-ray entries followed by that with respect to entries of similar

resolution.

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	A	476/495 (96%)	463 (97%)	13 (3%)	39	62
1	B	476/495 (96%)	467 (98%)	9 (2%)	50	68
1	C	476/495 (96%)	458 (96%)	18 (4%)	29	55
1	D	476/495 (96%)	462 (97%)	14 (3%)	37	60
1	E	476/495 (96%)	467 (98%)	9 (2%)	50	68
1	F	476/495 (96%)	463 (97%)	13 (3%)	39	62
1	G	476/495 (96%)	462 (97%)	14 (3%)	37	60
1	H	476/495 (96%)	460 (97%)	16 (3%)	32	57
1	I	476/495 (96%)	460 (97%)	16 (3%)	32	57
1	J	476/495 (96%)	466 (98%)	10 (2%)	47	66
1	K	476/495 (96%)	464 (98%)	12 (2%)	42	63
1	L	476/495 (96%)	460 (97%)	16 (3%)	32	57
1	M	476/495 (96%)	464 (98%)	12 (2%)	42	63
1	N	476/495 (96%)	466 (98%)	10 (2%)	47	66
1	O	476/495 (96%)	465 (98%)	11 (2%)	44	64
1	P	476/495 (96%)	469 (98%)	7 (2%)	57	71
1	Q	476/495 (96%)	465 (98%)	11 (2%)	44	64
1	R	476/495 (96%)	461 (97%)	15 (3%)	34	59
1	S	476/495 (96%)	464 (98%)	12 (2%)	42	63
1	T	476/495 (96%)	462 (97%)	14 (3%)	37	60
1	U	476/495 (96%)	463 (97%)	13 (3%)	39	62
1	V	476/495 (96%)	470 (99%)	6 (1%)	61	72
1	W	476/495 (96%)	462 (97%)	14 (3%)	37	60
1	X	476/495 (96%)	464 (98%)	12 (2%)	42	63
1	Y	476/495 (96%)	470 (99%)	6 (1%)	61	72
1	Z	476/495 (96%)	465 (98%)	11 (2%)	44	64
1	a	476/495 (96%)	465 (98%)	11 (2%)	44	64
1	b	476/495 (96%)	465 (98%)	11 (2%)	44	64
1	c	476/495 (96%)	462 (97%)	14 (3%)	37	60

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	d	476/495 (96%)	460 (97%)	16 (3%)	32	57
All	All	14280/14850 (96%)	13914 (97%)	366 (3%)	40	62

5 of 366 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	S	549	GLN
1	X	312	LYS
1	T	44	THR
1	U	553	ILE
1	Y	457	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 204 such sidechains are listed below:

Mol	Chain	Res	Type
1	R	280	GLN
1	U	558	GLN
1	d	302	ASN
1	R	458	ASN
1	T	253	HIS

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](#)

Of 30 ligands modelled in this entry, 30 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	548/584 (93%)	-0.25	6 (1%) 78 54	3, 17, 60, 119	0
1	B	548/584 (93%)	-0.22	6 (1%) 78 54	4, 19, 64, 124	0
1	C	548/584 (93%)	-0.12	10 (1%) 67 42	3, 20, 64, 121	0
1	D	548/584 (93%)	-0.15	8 (1%) 72 47	5, 20, 63, 131	0
1	E	548/584 (93%)	-0.19	7 (1%) 75 50	4, 18, 62, 120	0
1	F	548/584 (93%)	-0.20	7 (1%) 75 50	3, 18, 61, 118	0
1	G	548/584 (93%)	-0.15	5 (0%) 81 58	4, 20, 62, 126	0
1	H	548/584 (93%)	-0.17	7 (1%) 75 50	4, 19, 62, 118	0
1	I	548/584 (93%)	-0.16	13 (2%) 59 35	5, 19, 62, 127	0
1	J	548/584 (93%)	-0.23	6 (1%) 78 54	3, 19, 61, 122	0
1	K	548/584 (93%)	-0.20	15 (2%) 56 33	3, 17, 61, 122	0
1	L	548/584 (93%)	-0.12	7 (1%) 75 50	4, 19, 60, 125	0
1	M	548/584 (93%)	-0.23	6 (1%) 78 54	3, 18, 62, 121	0
1	N	548/584 (93%)	-0.19	10 (1%) 67 42	5, 19, 62, 126	0
1	O	548/584 (93%)	-0.14	6 (1%) 78 54	3, 20, 64, 123	0
1	P	548/584 (93%)	-0.18	7 (1%) 75 50	3, 18, 61, 119	0
1	Q	548/584 (93%)	-0.21	8 (1%) 72 47	4, 19, 61, 130	0
1	R	548/584 (93%)	-0.20	9 (1%) 70 45	4, 18, 62, 121	0
1	S	548/584 (93%)	-0.14	8 (1%) 72 47	5, 19, 61, 131	0
1	T	548/584 (93%)	-0.19	9 (1%) 70 45	4, 18, 64, 120	0
1	U	548/584 (93%)	-0.18	9 (1%) 70 45	3, 18, 65, 118	0
1	V	548/584 (93%)	-0.12	9 (1%) 70 45	4, 19, 62, 126	0
1	W	548/584 (93%)	-0.13	6 (1%) 78 54	4, 21, 66, 121	0
1	X	548/584 (93%)	-0.17	6 (1%) 78 54	4, 19, 60, 131	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	Y	548/584 (93%)	-0.13	7 (1%) 75 50	4, 19, 64, 123	0
1	Z	548/584 (93%)	-0.07	8 (1%) 72 47	3, 20, 64, 116	0
1	a	548/584 (93%)	-0.04	9 (1%) 70 45	4, 21, 67, 123	0
1	b	548/584 (93%)	-0.17	7 (1%) 75 50	3, 20, 66, 124	0
1	c	548/584 (93%)	-0.06	4 (0%) 84 63	4, 22, 61, 130	0
1	d	548/584 (93%)	-0.11	8 (1%) 72 47	4, 19, 64, 125	0
All	All	16440/17520 (93%)	-0.16	233 (1%) 73 48	3, 19, 64, 131	0

The worst 5 of 233 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	368	GLU	4.8
1	a	156	SER	4.7
1	N	158	THR	4.4
1	Q	516	ALA	4.4
1	M	156	SER	4.4

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MG	Y	602	1/1	0.76	0.36	52,52,52,52	0
2	MG	K	800	1/1	0.82	0.35	39,39,39,39	0
2	MG	D	800	1/1	0.86	0.17	43,43,43,43	0
2	MG	T	800	1/1	0.87	0.29	43,43,43,43	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MG	M	800	1/1	0.87	0.29	41,41,41,41	0
2	MG	N	800	1/1	0.88	0.26	39,39,39,39	0
2	MG	O	800	1/1	0.89	0.18	41,41,41,41	0
2	MG	d	602	1/1	0.89	0.32	56,56,56,56	0
2	MG	G	800	1/1	0.90	0.24	44,44,44,44	0
2	MG	H	602	1/1	0.91	0.23	54,54,54,54	0
2	MG	Q	800	1/1	0.91	0.25	41,41,41,41	0
2	MG	R	800	1/1	0.91	0.21	37,37,37,37	0
2	MG	c	800	1/1	0.92	0.18	53,53,53,53	0
2	MG	C	800	1/1	0.93	0.20	41,41,41,41	0
2	MG	L	800	1/1	0.93	0.18	41,41,41,41	0
2	MG	W	800	1/1	0.93	0.19	47,47,47,47	0
2	MG	E	601	1/1	0.94	0.18	40,40,40,40	0
2	MG	H	601	1/1	0.95	0.16	36,36,36,36	0
2	MG	Y	601	1/1	0.95	0.15	47,47,47,47	0
2	MG	P	800	1/1	0.95	0.19	39,39,39,39	0
2	MG	J	602	1/1	0.95	0.22	38,38,38,38	0
2	MG	d	601	1/1	0.95	0.14	37,37,37,37	0
2	MG	I	800	1/1	0.95	0.20	43,43,43,43	0
2	MG	E	602	1/1	0.96	0.14	38,38,38,38	0
2	MG	B	800	1/1	0.96	0.17	41,41,41,41	0
2	MG	X	800	1/1	0.96	0.15	43,43,43,43	0
2	MG	S	800	1/1	0.96	0.16	39,39,39,39	0
2	MG	J	601	1/1	0.97	0.16	40,40,40,40	0
2	MG	A	800	1/1	0.97	0.11	32,32,32,32	0
2	MG	Z	800	1/1	0.99	0.14	47,47,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.