



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 22, 2024 – 05:02 PM EDT

PDB ID : 4QYK
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	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

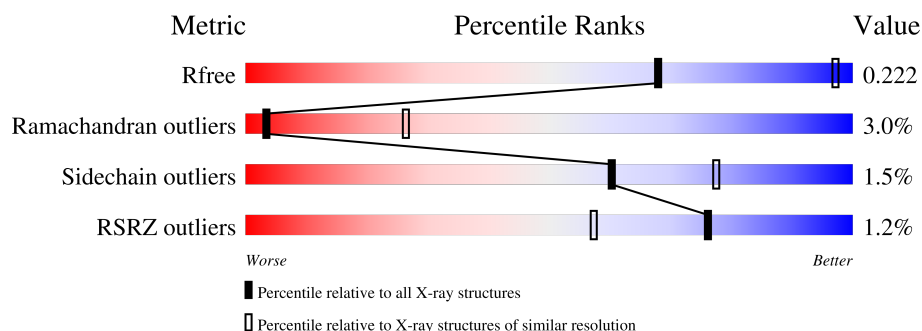
1 Overall quality at a glance ⓘ

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.






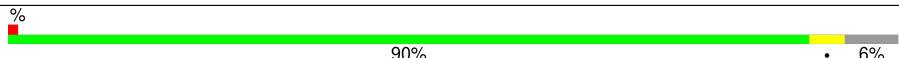
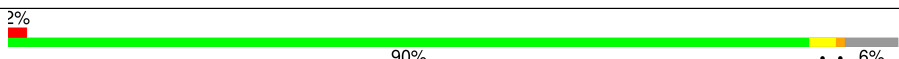
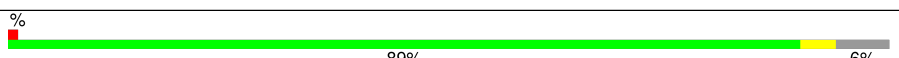
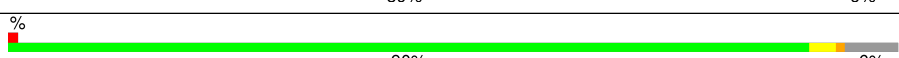
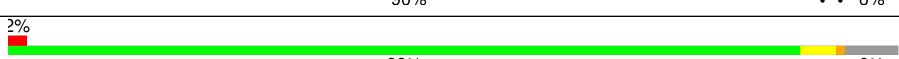
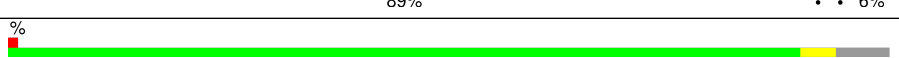
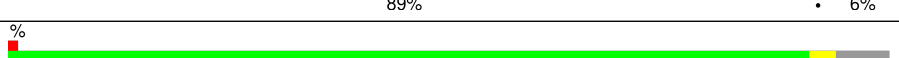

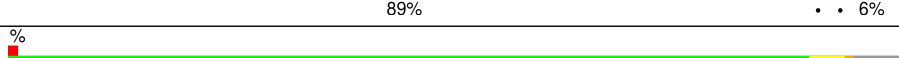
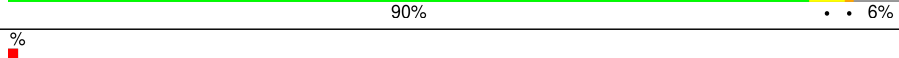
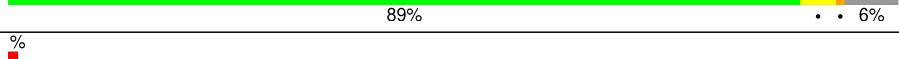
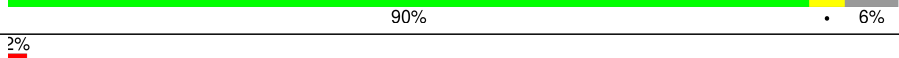
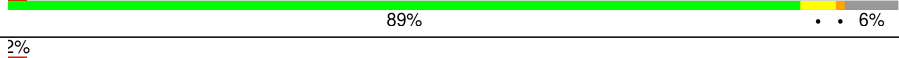
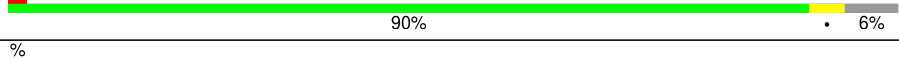
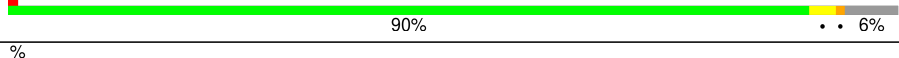

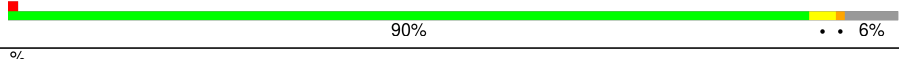
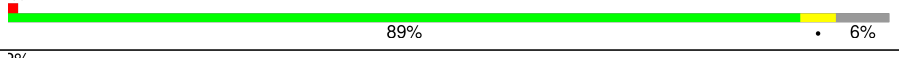
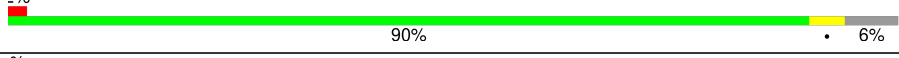
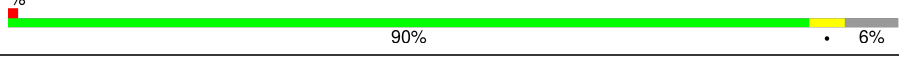

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	1094 (3.56-3.44)
Ramachandran outliers	177936	1032 (3.54-3.46)
Sidechain outliers	177891	1033 (3.54-3.46)
RSRZ outliers	164620	1093 (3.56-3.44)

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	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>6%</div> </div> </div>
1	B	584	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>6%</div> </div> </div>
1	C	584	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>6%</div> </div> </div>
1	D	584	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>6%</div> </div> </div>
1	E	584	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>6%</div> </div> </div>
1	F	584	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>6%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
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

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			

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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

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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

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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

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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

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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 (three-letter code: MG) (formula: Mg).

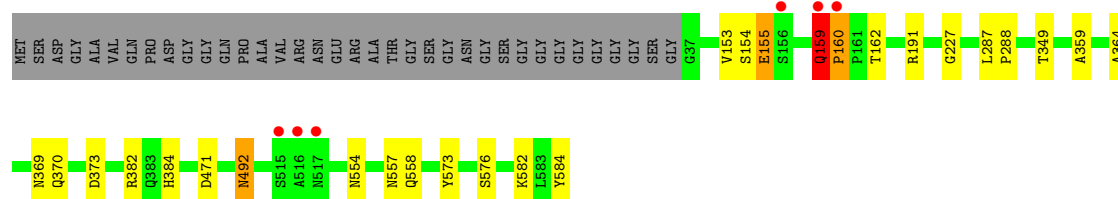
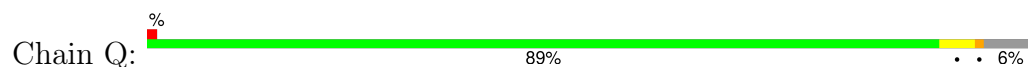
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0
2	E	2	Total Mg 2 2	0	0
2	J	2	Total Mg 2 2	0	0
2	N	1	Total Mg 1 1	0	0
2	Q	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0
2	G	1	Total Mg 1 1	0	0
2	H	2	Total Mg 2 2	0	0
2	I	1	Total Mg 1 1	0	0
2	K	1	Total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

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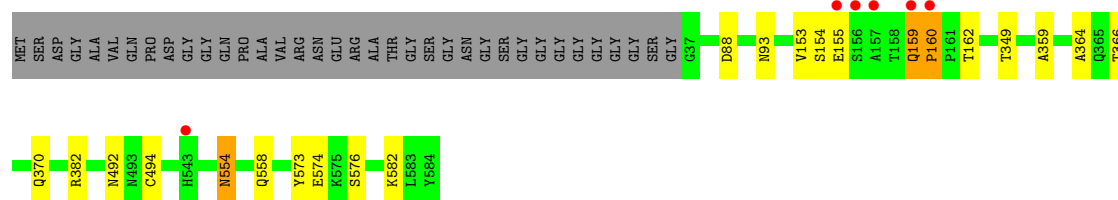
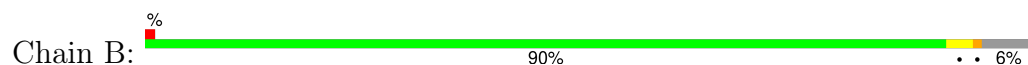
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	M	1	Total 1	Mg 1	0	0
2	O	1	Total 1	Mg 1	0	0
2	P	1	Total 1	Mg 1	0	0
2	R	1	Total 1	Mg 1	0	0
2	S	1	Total 1	Mg 1	0	0
2	T	1	Total 1	Mg 1	0	0
2	W	1	Total 1	Mg 1	0	0
2	X	1	Total 1	Mg 1	0	0
2	Y	2	Total 2	Mg 2	0	0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

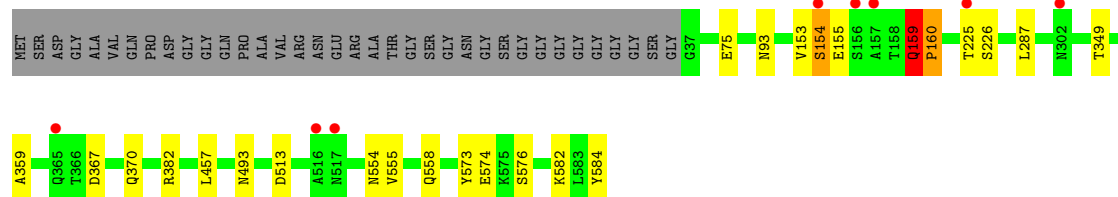
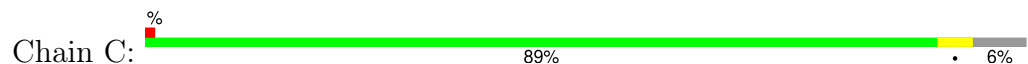
- Molecule 1: Capsid protein VP1



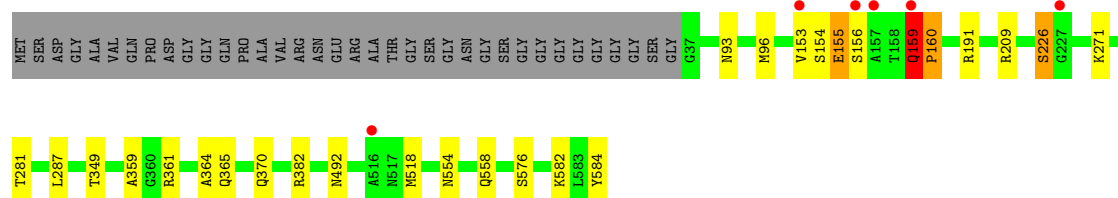
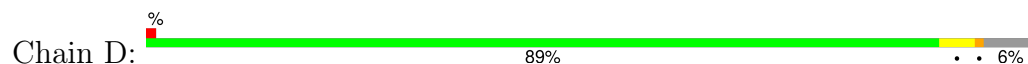
- Molecule 1: Capsid protein VP1



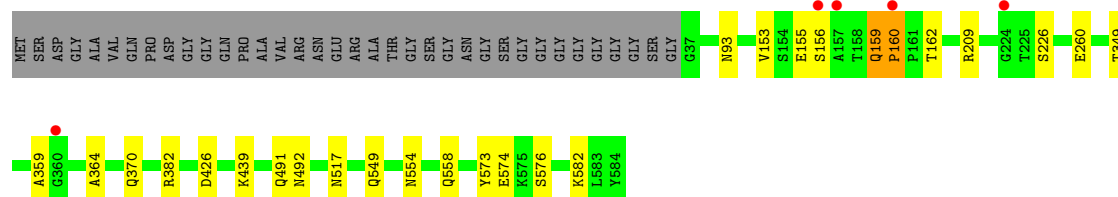
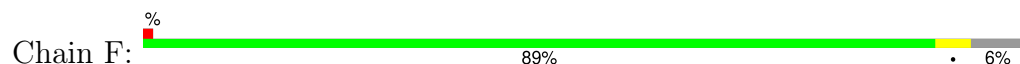
- Molecule 1: Capsid protein VP1



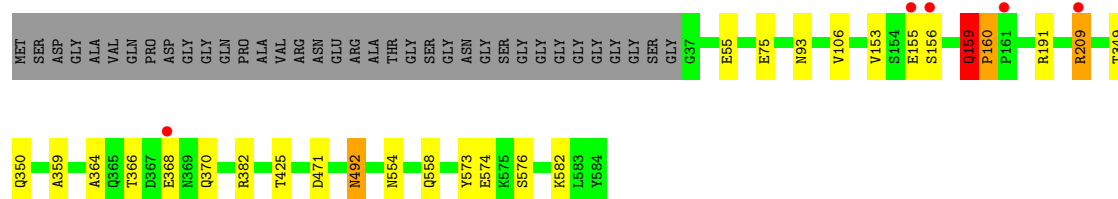
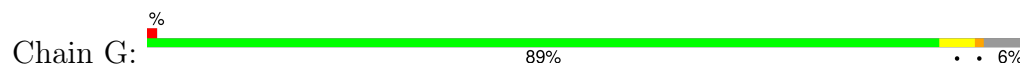
- Molecule 1: Capsid protein VP1



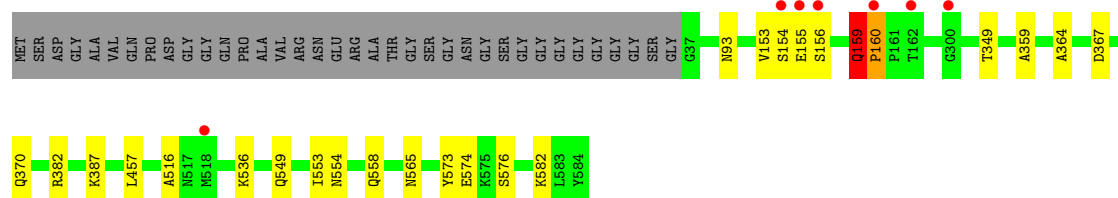
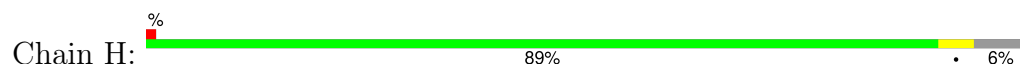
- Molecule 1: Capsid protein VP1



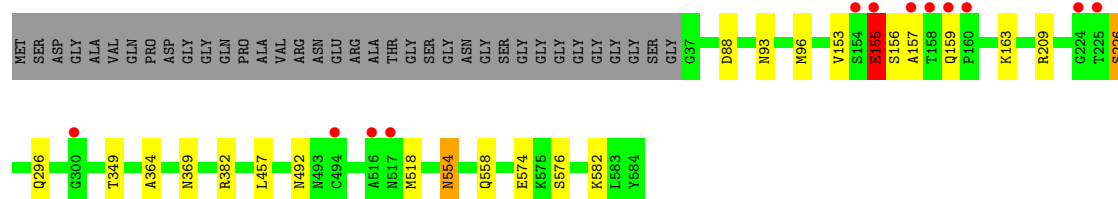
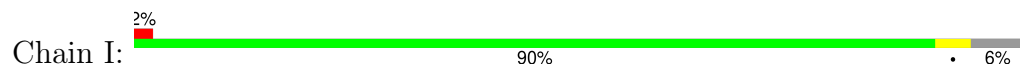
- Molecule 1: Capsid protein VP1



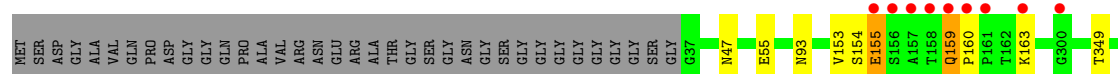
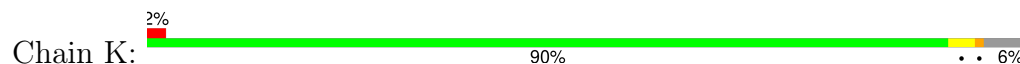
- Molecule 1: Capsid protein VP1

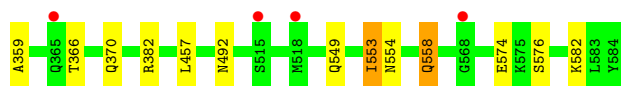


- Molecule 1: Capsid protein VP1

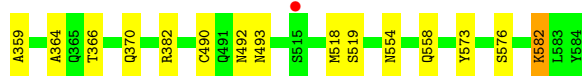
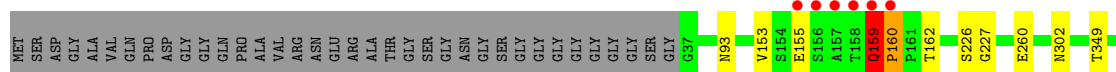
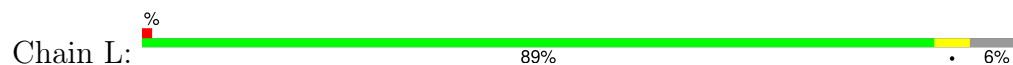


- Molecule 1: Capsid protein VP1

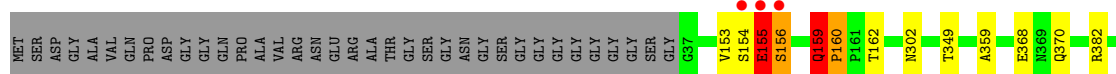
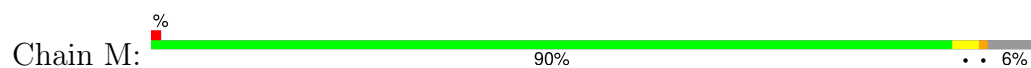




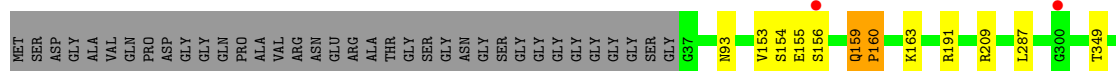
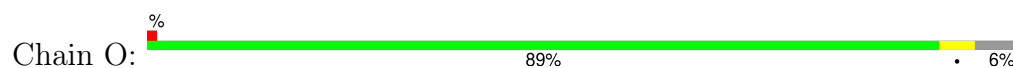
- Molecule 1: Capsid protein VP1



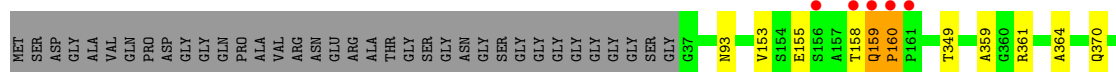
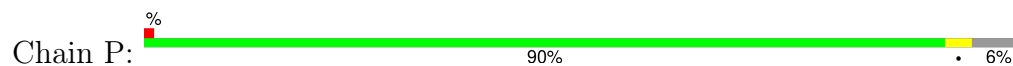
- Molecule 1: Capsid protein VP1



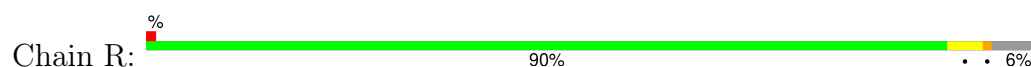
- Molecule 1: Capsid protein VP1

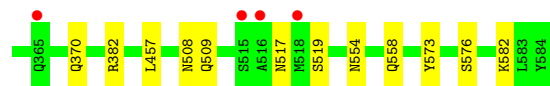
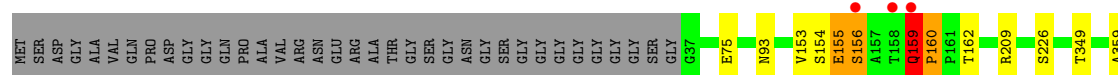


- Molecule 1: Capsid protein VP1

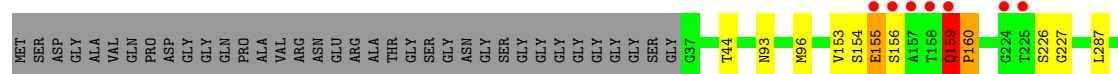
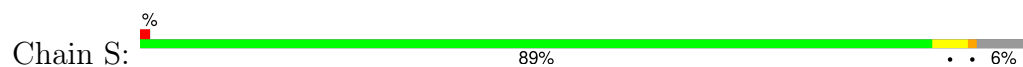


- Molecule 1: Capsid protein VP1

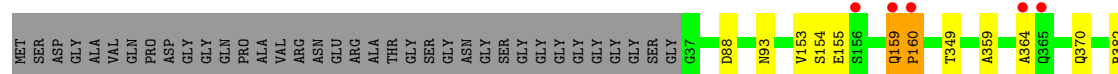
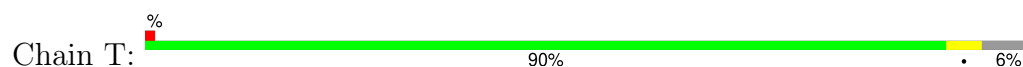




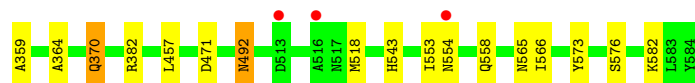
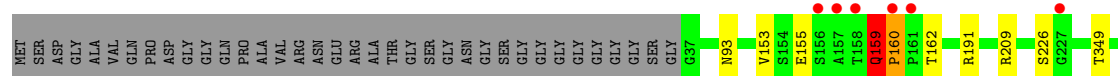
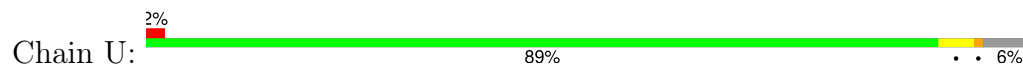
• Molecule 1: Capsid protein VP1



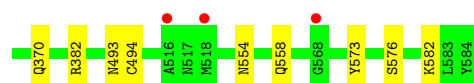
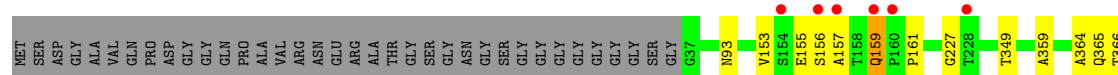
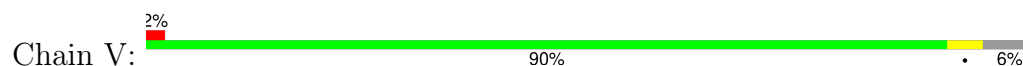
• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1

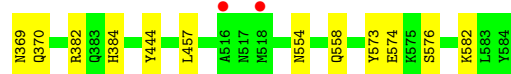
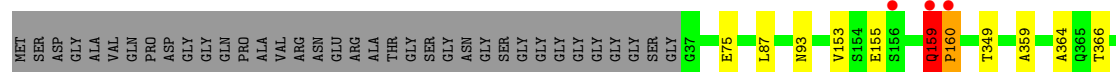
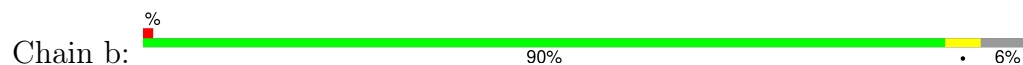


• Molecule 1: Capsid protein VP1

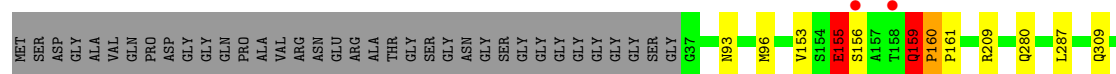
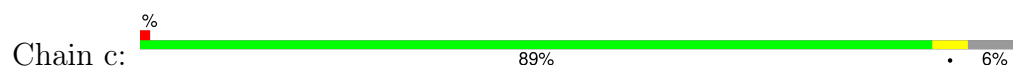




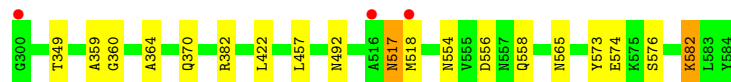
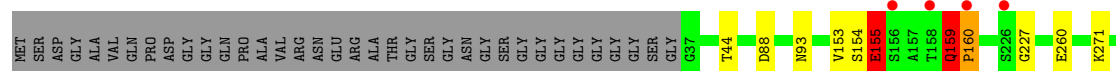
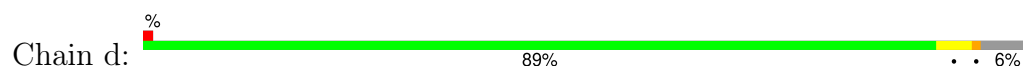
• Molecule 1: Capsid protein VP1



• 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	0.66	0/4483	0.70	2/6134 (0.0%)
1	B	0.63	0/4483	0.73	5/6134 (0.1%)
1	C	0.59	0/4483	0.73	4/6134 (0.1%)
1	D	0.58	0/4483	0.73	5/6134 (0.1%)
1	E	0.62	0/4483	0.73	4/6134 (0.1%)
1	F	0.63	1/4483 (0.0%)	0.84	9/6134 (0.1%)
1	G	0.59	0/4483	0.74	6/6134 (0.1%)
1	H	0.57	0/4483	0.72	3/6134 (0.0%)
1	I	0.64	0/4483	0.71	1/6134 (0.0%)
1	J	0.61	0/4483	0.71	5/6134 (0.1%)
1	K	0.67	0/4483	0.74	2/6134 (0.0%)
1	L	0.61	0/4483	0.73	3/6134 (0.0%)
1	M	0.66	0/4483	0.74	5/6134 (0.1%)
1	N	0.66	0/4483	0.72	6/6134 (0.1%)
1	O	0.58	0/4483	0.71	3/6134 (0.0%)
1	P	0.61	0/4483	0.73	4/6134 (0.1%)
1	Q	0.61	0/4483	0.72	5/6134 (0.1%)
1	R	0.63	0/4483	0.73	3/6134 (0.0%)
1	S	0.63	1/4483 (0.0%)	0.76	9/6134 (0.1%)
1	T	0.65	0/4483	0.72	4/6134 (0.1%)
1	U	0.60	0/4483	0.73	4/6134 (0.1%)
1	V	0.60	0/4483	0.70	1/6134 (0.0%)
1	W	0.55	0/4483	0.72	3/6134 (0.0%)
1	X	0.61	1/4483 (0.0%)	0.76	7/6134 (0.1%)
1	Y	0.56	0/4483	0.73	5/6134 (0.1%)
1	Z	0.60	2/4483 (0.0%)	0.74	4/6134 (0.1%)
1	a	0.55	0/4483	0.75	2/6134 (0.0%)
1	b	0.57	0/4483	0.73	3/6134 (0.0%)
1	c	0.58	0/4483	0.73	4/6134 (0.1%)
1	d	0.60	0/4483	0.76	7/6134 (0.1%)
All	All	0.61	5/134490 (0.0%)	0.73	128/184020 (0.1%)

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

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Z	222	HIS	CG-CD2	-8.08	1.22	1.35
1	F	426	ASP	CB-CG	-7.62	1.35	1.51
1	S	438	GLY	C-O	-5.81	1.14	1.23
1	X	426	ASP	CB-CG	-5.05	1.41	1.51
1	Z	273	CYS	CB-SG	-5.00	1.73	1.81

The worst 5 of 128 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	426	ASP	CB-CG-OD2	-27.25	93.78	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	a	159	GLN	C-N-CD	-18.61	79.65	120.60
1	X	159	GLN	C-N-CD	-16.06	85.27	120.60
1	F	426	ASP	CB-CG-OD1	15.33	132.10	118.30
1	C	159	GLN	C-N-CD	-13.92	89.97	120.60

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](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	28
1	B	546/584 (94%)	496 (91%)	32 (6%)	18 (3%)	3	25
1	C	546/584 (94%)	493 (90%)	39 (7%)	14 (3%)	4	28
1	D	546/584 (94%)	497 (91%)	32 (6%)	17 (3%)	3	26
1	E	546/584 (94%)	497 (91%)	33 (6%)	16 (3%)	3	27
1	F	546/584 (94%)	496 (91%)	33 (6%)	17 (3%)	3	26
1	G	546/584 (94%)	497 (91%)	32 (6%)	17 (3%)	3	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	546/584 (94%)	491 (90%)	38 (7%)	17 (3%)	3	26
1	I	546/584 (94%)	499 (91%)	34 (6%)	13 (2%)	5	30
1	J	546/584 (94%)	498 (91%)	33 (6%)	15 (3%)	4	28
1	K	546/584 (94%)	499 (91%)	31 (6%)	16 (3%)	3	27
1	L	546/584 (94%)	494 (90%)	35 (6%)	17 (3%)	3	26
1	M	546/584 (94%)	491 (90%)	40 (7%)	15 (3%)	4	28
1	N	546/584 (94%)	497 (91%)	34 (6%)	15 (3%)	4	28
1	O	546/584 (94%)	492 (90%)	35 (6%)	19 (4%)	3	24
1	P	546/584 (94%)	497 (91%)	32 (6%)	17 (3%)	3	26
1	Q	546/584 (94%)	496 (91%)	34 (6%)	16 (3%)	3	27
1	R	546/584 (94%)	490 (90%)	39 (7%)	17 (3%)	3	26
1	S	546/584 (94%)	500 (92%)	32 (6%)	14 (3%)	4	28
1	T	546/584 (94%)	501 (92%)	30 (6%)	15 (3%)	4	28
1	U	546/584 (94%)	496 (91%)	32 (6%)	18 (3%)	3	25
1	V	546/584 (94%)	492 (90%)	37 (7%)	17 (3%)	3	26
1	W	546/584 (94%)	491 (90%)	40 (7%)	15 (3%)	4	28
1	X	546/584 (94%)	495 (91%)	34 (6%)	17 (3%)	3	26
1	Y	546/584 (94%)	498 (91%)	30 (6%)	18 (3%)	3	25
1	Z	546/584 (94%)	497 (91%)	31 (6%)	18 (3%)	3	25
1	a	546/584 (94%)	497 (91%)	33 (6%)	16 (3%)	3	27
1	b	546/584 (94%)	489 (90%)	41 (8%)	16 (3%)	3	27
1	c	546/584 (94%)	499 (91%)	31 (6%)	16 (3%)	3	27
1	d	546/584 (94%)	498 (91%)	32 (6%)	16 (3%)	3	27
All	All	16380/17520 (94%)	14873 (91%)	1020 (6%)	487 (3%)	3	26

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%)	468 (98%)	8 (2%)	56	75
1	B	476/495 (96%)	472 (99%)	4 (1%)	79	88
1	C	476/495 (96%)	467 (98%)	9 (2%)	52	73
1	D	476/495 (96%)	470 (99%)	6 (1%)	65	81
1	E	476/495 (96%)	471 (99%)	5 (1%)	70	83
1	F	476/495 (96%)	470 (99%)	6 (1%)	65	81
1	G	476/495 (96%)	468 (98%)	8 (2%)	56	75
1	H	476/495 (96%)	468 (98%)	8 (2%)	56	75
1	I	476/495 (96%)	463 (97%)	13 (3%)	40	65
1	J	476/495 (96%)	471 (99%)	5 (1%)	70	83
1	K	476/495 (96%)	467 (98%)	9 (2%)	52	73
1	L	476/495 (96%)	467 (98%)	9 (2%)	52	73
1	M	476/495 (96%)	470 (99%)	6 (1%)	65	81
1	N	476/495 (96%)	470 (99%)	6 (1%)	65	81
1	O	476/495 (96%)	473 (99%)	3 (1%)	84	91
1	P	476/495 (96%)	472 (99%)	4 (1%)	79	88
1	Q	476/495 (96%)	470 (99%)	6 (1%)	65	81
1	R	476/495 (96%)	468 (98%)	8 (2%)	56	75
1	S	476/495 (96%)	465 (98%)	11 (2%)	45	69
1	T	476/495 (96%)	468 (98%)	8 (2%)	56	75
1	U	476/495 (96%)	468 (98%)	8 (2%)	56	75
1	V	476/495 (96%)	471 (99%)	5 (1%)	70	83
1	W	476/495 (96%)	468 (98%)	8 (2%)	56	75
1	X	476/495 (96%)	468 (98%)	8 (2%)	56	75
1	Y	476/495 (96%)	474 (100%)	2 (0%)	89	95
1	Z	476/495 (96%)	471 (99%)	5 (1%)	70	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	a	476/495 (96%)	471 (99%)	5 (1%)	70	83
1	b	476/495 (96%)	468 (98%)	8 (2%)	56	75
1	c	476/495 (96%)	463 (97%)	13 (3%)	40	65
1	d	476/495 (96%)	465 (98%)	11 (2%)	45	69
All	All	14280/14850 (96%)	14065 (98%)	215 (2%)	60	77

5 of 215 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	R	75	GLU
1	U	370	GLN
1	c	416	GLN
1	R	508	ASN
1	S	549	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 102 such sidechains are listed below:

Mol	Chain	Res	Type
1	P	558	GLN
1	U	446	ASN
1	c	554	ASN
1	R	137	HIS
1	T	302	ASN

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

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

There are no such residues in this entry.

5.8 Polymer linkage issues

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%)	-0.41	4 (0%) 84 69	3, 17, 60, 119	0
1	B	548/584 (93%)	-0.39	6 (1%) 77 59	4, 19, 64, 124	0
1	C	548/584 (93%)	-0.28	8 (1%) 71 53	3, 20, 64, 121	0
1	D	548/584 (93%)	-0.31	6 (1%) 77 59	5, 20, 63, 131	0
1	E	548/584 (93%)	-0.35	6 (1%) 77 59	4, 18, 62, 120	0
1	F	548/584 (93%)	-0.36	5 (0%) 81 64	3, 18, 61, 118	0
1	G	548/584 (93%)	-0.31	5 (0%) 81 64	4, 20, 62, 126	0
1	H	548/584 (93%)	-0.33	7 (1%) 74 56	4, 19, 62, 118	0
1	I	548/584 (93%)	-0.32	12 (2%) 62 43	5, 19, 62, 127	0
1	J	548/584 (93%)	-0.39	5 (0%) 81 64	3, 19, 61, 122	0
1	K	548/584 (93%)	-0.36	13 (2%) 59 41	3, 17, 61, 122	0
1	L	548/584 (93%)	-0.28	7 (1%) 74 56	4, 19, 60, 125	0
1	M	548/584 (93%)	-0.39	4 (0%) 84 69	3, 18, 62, 121	0
1	N	548/584 (93%)	-0.36	9 (1%) 70 51	5, 19, 62, 126	0
1	O	548/584 (93%)	-0.30	4 (0%) 84 69	3, 20, 64, 123	0
1	P	548/584 (93%)	-0.35	7 (1%) 74 56	3, 18, 61, 119	0
1	Q	548/584 (93%)	-0.38	6 (1%) 77 59	4, 19, 61, 130	0
1	R	548/584 (93%)	-0.36	7 (1%) 74 56	4, 18, 62, 121	0
1	S	548/584 (93%)	-0.31	8 (1%) 71 53	5, 19, 61, 131	0
1	T	548/584 (93%)	-0.35	7 (1%) 74 56	4, 18, 64, 120	0
1	U	548/584 (93%)	-0.34	9 (1%) 70 51	3, 18, 65, 118	0
1	V	548/584 (93%)	-0.29	9 (1%) 70 51	4, 19, 62, 126	0
1	W	548/584 (93%)	-0.29	5 (0%) 81 64	4, 21, 66, 121	0
1	X	548/584 (93%)	-0.33	5 (0%) 81 64	4, 19, 60, 131	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	Y	548/584 (93%)	-0.29	7 (1%) 74 56	4, 19, 64, 123	0
1	Z	548/584 (93%)	-0.23	7 (1%) 74 56	3, 20, 64, 116	0
1	a	548/584 (93%)	-0.20	9 (1%) 70 51	4, 21, 67, 123	0
1	b	548/584 (93%)	-0.33	5 (0%) 81 64	3, 20, 66, 124	0
1	c	548/584 (93%)	-0.22	3 (0%) 87 75	4, 22, 61, 130	0
1	d	548/584 (93%)	-0.27	7 (1%) 74 56	4, 19, 64, 125	0
All	All	16440/17520 (93%)	-0.32	202 (1%) 76 57	3, 19, 64, 131	0

The worst 5 of 202 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	a	156	SER	5.2
1	M	156	SER	4.8
1	G	368	GLU	4.6
1	K	156	SER	4.6
1	N	158	THR	4.5

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 monosaccharides 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	0.78	0.36	52,52,52,52	0
2	MG	K	800	1/1	0.82	0.37	39,39,39,39	0
2	MG	D	800	1/1	0.86	0.16	43,43,43,43	0
2	MG	M	800	1/1	0.87	0.29	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MG	d	602	1/1	0.87	0.31	56,56,56,56	0
2	MG	T	800	1/1	0.88	0.29	43,43,43,43	0
2	MG	N	800	1/1	0.89	0.26	39,39,39,39	0
2	MG	G	800	1/1	0.90	0.24	44,44,44,44	0
2	MG	Q	800	1/1	0.90	0.25	41,41,41,41	0
2	MG	H	602	1/1	0.91	0.22	54,54,54,54	0
2	MG	O	800	1/1	0.91	0.18	41,41,41,41	0
2	MG	R	800	1/1	0.91	0.21	37,37,37,37	0
2	MG	W	800	1/1	0.92	0.18	47,47,47,47	0
2	MG	L	800	1/1	0.93	0.19	41,41,41,41	0
2	MG	C	800	1/1	0.94	0.21	41,41,41,41	0
2	MG	Y	601	1/1	0.94	0.17	47,47,47,47	0
2	MG	H	601	1/1	0.94	0.16	36,36,36,36	0
2	MG	c	800	1/1	0.94	0.17	53,53,53,53	0
2	MG	E	601	1/1	0.94	0.17	40,40,40,40	0
2	MG	I	800	1/1	0.95	0.21	43,43,43,43	0
2	MG	J	602	1/1	0.95	0.23	38,38,38,38	0
2	MG	d	601	1/1	0.95	0.14	37,37,37,37	0
2	MG	E	602	1/1	0.95	0.15	38,38,38,38	0
2	MG	X	800	1/1	0.96	0.15	43,43,43,43	0
2	MG	P	800	1/1	0.96	0.19	39,39,39,39	0
2	MG	A	800	1/1	0.96	0.14	32,32,32,32	0
2	MG	S	800	1/1	0.96	0.17	39,39,39,39	0
2	MG	B	800	1/1	0.96	0.17	41,41,41,41	0
2	MG	J	601	1/1	0.96	0.16	40,40,40,40	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.