



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 06:14 am GMT

PDB ID : 4RS5
Title : Crystal structure of an uncoating intermediate of a EV71 recombinant virus
Authors : Chen, R.; Lyu, K.
Deposited on : 2014-11-07
Resolution : 3.81 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

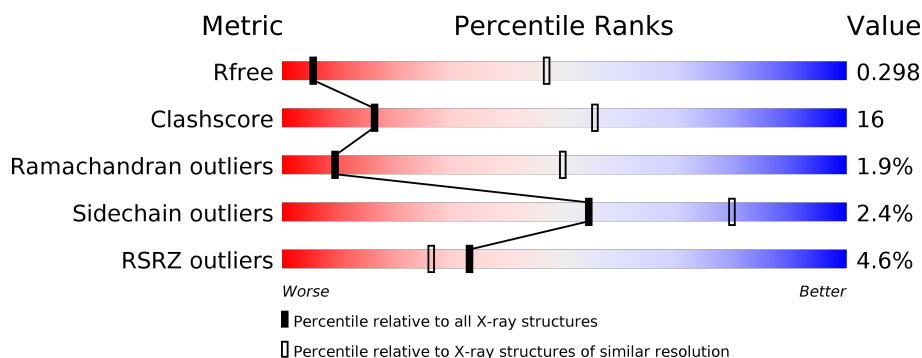
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.81 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}	100719	1019 (4.08-3.52)
Clashscore	112137	1030 (4.04-3.56)
Ramachandran outliers	110173	1011 (4.06-3.54)
Sidechain outliers	110143	1005 (4.06-3.54)
RSRZ outliers	101464	1032 (4.08-3.52)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	B	242	<div> <div>3%</div> <div> <div></div> <div>54%</div> <div>38%</div> <div>8%</div> </div> </div>
1	E	242	<div> <div>2%</div> <div> <div></div> <div>61%</div> <div>31%</div> <div>8%</div> </div> </div>
1	H	242	<div> <div>%</div> <div> <div></div> <div>60%</div> <div>31%</div> <div>8%</div> </div> </div>
1	K	242	<div> <div>%</div> <div> <div></div> <div>65%</div> <div>26%</div> <div>8%</div> </div> </div>
1	N	242	<div> <div>2%</div> <div> <div></div> <div>63%</div> <div>29%</div> <div>8%</div> </div> </div>
2	C	323	<div> <div>5%</div> <div> <div></div> <div>44%</div> <div>27%</div> <div>27%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	F	323	
2	I	323	
2	L	323	
2	O	323	
3	A	313	
3	D	313	
3	G	313	
3	J	313	
3	M	313	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 26425 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 VP3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	223	Total	C	N	O	S	0	0	0
			1699	1093	279	316	11			
1	N	223	Total	C	N	O	S	0	0	0
			1699	1093	279	316	11			
1	B	223	Total	C	N	O	S	0	0	0
			1699	1093	279	316	11			
1	H	223	Total	C	N	O	S	0	0	0
			1699	1093	279	316	11			
1	K	223	Total	C	N	O	S	0	0	0
			1699	1093	279	316	11			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	227	GLN	LYS	engineered mutation	UNP F6KTB0
N	227	GLN	LYS	engineered mutation	UNP F6KTB0
B	227	GLN	LYS	engineered mutation	UNP F6KTB0
H	227	GLN	LYS	engineered mutation	UNP F6KTB0
K	227	GLN	LYS	engineered mutation	UNP F6KTB0

- Molecule 2 is a protein called Capsid protein VP0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	236	Total	C	N	O	S	0	0	0
			1829	1174	303	344	8			
2	O	236	Total	C	N	O	S	0	0	0
			1829	1174	303	344	8			
2	C	236	Total	C	N	O	S	0	0	0
			1829	1174	303	344	8			
2	I	236	Total	C	N	O	S	0	0	0
			1829	1174	303	344	8			
2	L	236	Total	C	N	O	S	0	0	0
			1829	1174	303	344	8			

- Molecule 3 is a protein called Capsid protein VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	221	Total	C	N	O	S	0	0	0
			1757	1128	295	323	11			
3	M	221	Total	C	N	O	S	0	0	0
			1757	1128	295	323	11			
3	A	221	Total	C	N	O	S	0	0	0
			1757	1128	295	323	11			
3	G	221	Total	C	N	O	S	0	0	0
			1757	1128	295	323	11			
3	J	221	Total	C	N	O	S	0	0	0
			1757	1128	295	323	11			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	101	SER	-	INSERTION	UNP F6KTB0
D	102	VAL	-	INSERTION	UNP F6KTB0
D	103	LYS	-	INSERTION	UNP F6KTB0
D	104	ARG	-	INSERTION	UNP F6KTB0
D	105	GLY	-	INSERTION	UNP F6KTB0
D	106	THR	-	INSERTION	UNP F6KTB0
D	107	SER	-	INSERTION	UNP F6KTB0
D	108	VAL	-	INSERTION	UNP F6KTB0
D	109	GLY	-	INSERTION	UNP F6KTB0
D	110	MET	-	INSERTION	UNP F6KTB0
D	111	LYS	-	INSERTION	UNP F6KTB0
D	112	PRO	-	INSERTION	UNP F6KTB0
D	113	SER	-	INSERTION	UNP F6KTB0
D	114	PRO	-	INSERTION	UNP F6KTB0
D	115	ARG	-	INSERTION	UNP F6KTB0
D	116	PRO	-	INSERTION	UNP F6KTB0
M	101	SER	-	INSERTION	UNP F6KTB0
M	102	VAL	-	INSERTION	UNP F6KTB0
M	103	LYS	-	INSERTION	UNP F6KTB0
M	104	ARG	-	INSERTION	UNP F6KTB0
M	105	GLY	-	INSERTION	UNP F6KTB0
M	106	THR	-	INSERTION	UNP F6KTB0
M	107	SER	-	INSERTION	UNP F6KTB0
M	108	VAL	-	INSERTION	UNP F6KTB0
M	109	GLY	-	INSERTION	UNP F6KTB0
M	110	MET	-	INSERTION	UNP F6KTB0
M	111	LYS	-	INSERTION	UNP F6KTB0
M	112	PRO	-	INSERTION	UNP F6KTB0

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Chain	Residue	Modelled	Actual	Comment	Reference
M	113	SER	-	INSERTION	UNP F6KTB0
M	114	PRO	-	INSERTION	UNP F6KTB0
M	115	ARG	-	INSERTION	UNP F6KTB0
M	116	PRO	-	INSERTION	UNP F6KTB0
A	101	SER	-	INSERTION	UNP F6KTB0
A	102	VAL	-	INSERTION	UNP F6KTB0
A	103	LYS	-	INSERTION	UNP F6KTB0
A	104	ARG	-	INSERTION	UNP F6KTB0
A	105	GLY	-	INSERTION	UNP F6KTB0
A	106	THR	-	INSERTION	UNP F6KTB0
A	107	SER	-	INSERTION	UNP F6KTB0
A	108	VAL	-	INSERTION	UNP F6KTB0
A	109	GLY	-	INSERTION	UNP F6KTB0
A	110	MET	-	INSERTION	UNP F6KTB0
A	111	LYS	-	INSERTION	UNP F6KTB0
A	112	PRO	-	INSERTION	UNP F6KTB0
A	113	SER	-	INSERTION	UNP F6KTB0
A	114	PRO	-	INSERTION	UNP F6KTB0
A	115	ARG	-	INSERTION	UNP F6KTB0
A	116	PRO	-	INSERTION	UNP F6KTB0
G	101	SER	-	INSERTION	UNP F6KTB0
G	102	VAL	-	INSERTION	UNP F6KTB0
G	103	LYS	-	INSERTION	UNP F6KTB0
G	104	ARG	-	INSERTION	UNP F6KTB0
G	105	GLY	-	INSERTION	UNP F6KTB0
G	106	THR	-	INSERTION	UNP F6KTB0
G	107	SER	-	INSERTION	UNP F6KTB0
G	108	VAL	-	INSERTION	UNP F6KTB0
G	109	GLY	-	INSERTION	UNP F6KTB0
G	110	MET	-	INSERTION	UNP F6KTB0
G	111	LYS	-	INSERTION	UNP F6KTB0
G	112	PRO	-	INSERTION	UNP F6KTB0
G	113	SER	-	INSERTION	UNP F6KTB0
G	114	PRO	-	INSERTION	UNP F6KTB0
G	115	ARG	-	INSERTION	UNP F6KTB0
G	116	PRO	-	INSERTION	UNP F6KTB0
J	101	SER	-	INSERTION	UNP F6KTB0
J	102	VAL	-	INSERTION	UNP F6KTB0
J	103	LYS	-	INSERTION	UNP F6KTB0
J	104	ARG	-	INSERTION	UNP F6KTB0
J	105	GLY	-	INSERTION	UNP F6KTB0
J	106	THR	-	INSERTION	UNP F6KTB0

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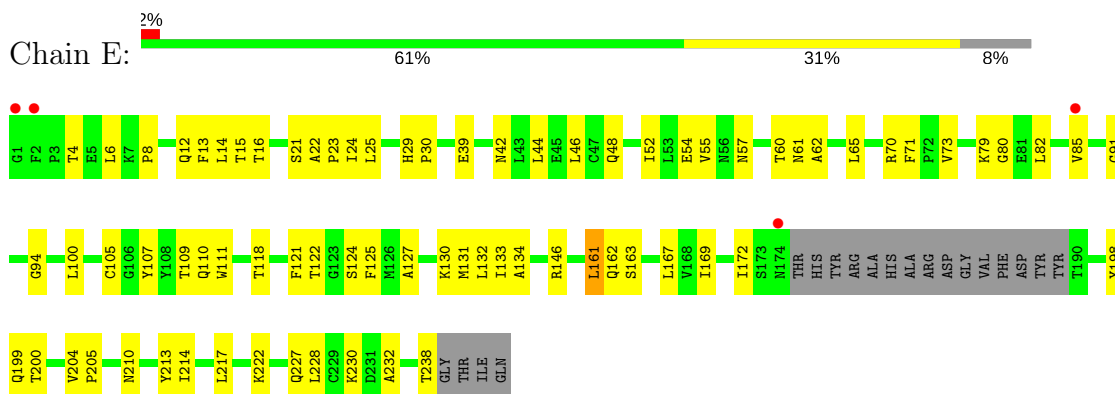
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Chain	Residue	Modelled	Actual	Comment	Reference
J	107	SER	-	INSERTION	UNP F6KTB0
J	108	VAL	-	INSERTION	UNP F6KTB0
J	109	GLY	-	INSERTION	UNP F6KTB0
J	110	MET	-	INSERTION	UNP F6KTB0
J	111	LYS	-	INSERTION	UNP F6KTB0
J	112	PRO	-	INSERTION	UNP F6KTB0
J	113	SER	-	INSERTION	UNP F6KTB0
J	114	PRO	-	INSERTION	UNP F6KTB0
J	115	ARG	-	INSERTION	UNP F6KTB0
J	116	PRO	-	INSERTION	UNP F6KTB0

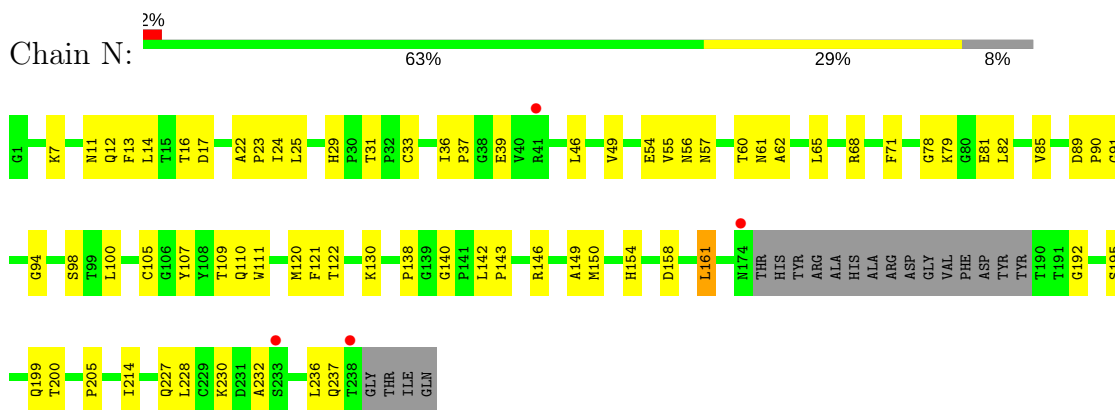
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 ($\text{RSRZ} > 2$). 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.

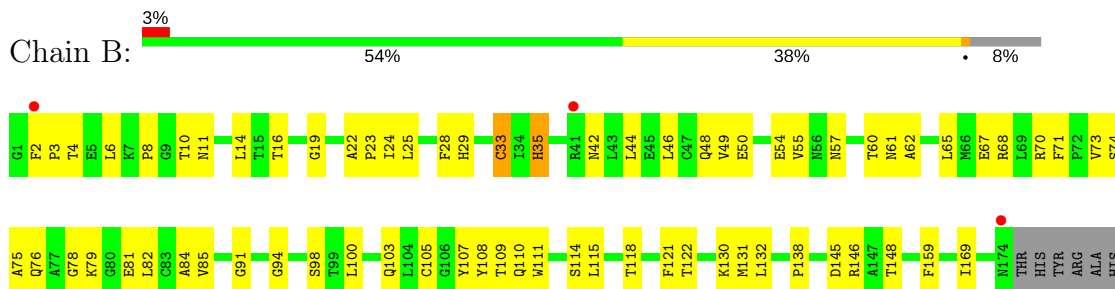
• Molecule 1: Capsid protein VP3

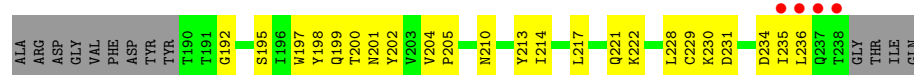


• Molecule 1: Capsid protein VP3

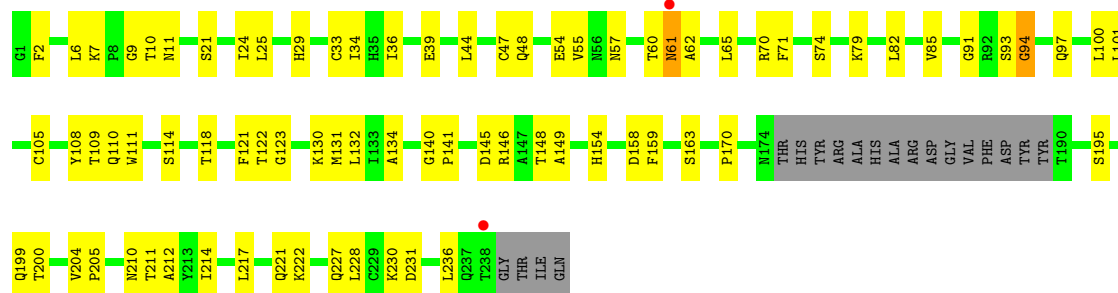


• Molecule 1: Capsid protein VP3





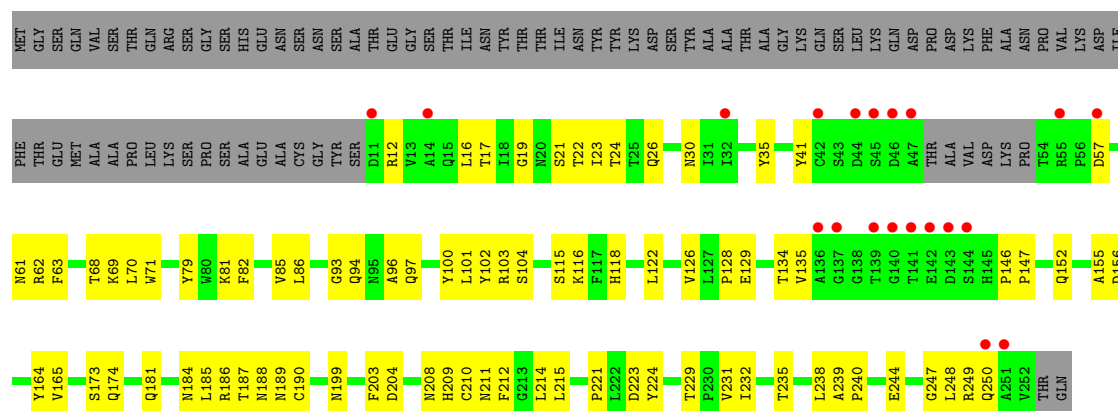
• Molecule 1: Capsid protein VP3



• Molecule 1: Capsid protein VP3

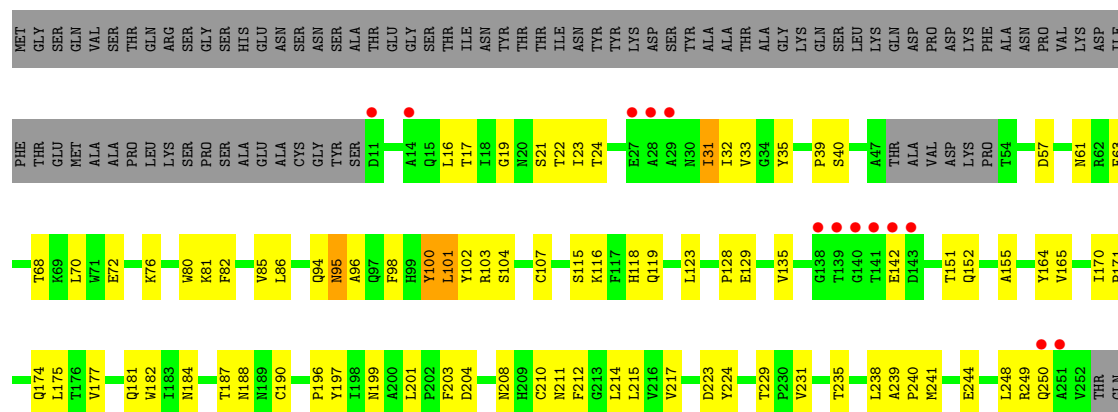


• Molecule 2: Capsid protein VP0

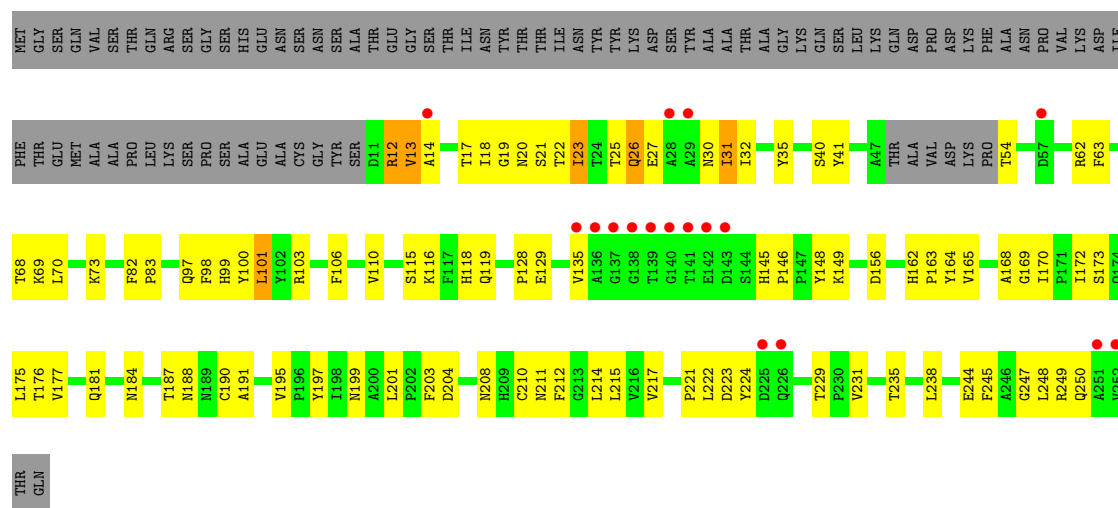
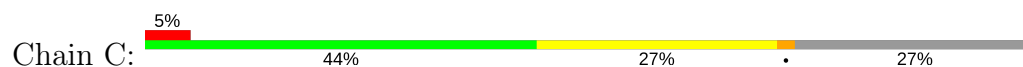


• Molecule 2: Capsid protein VP0

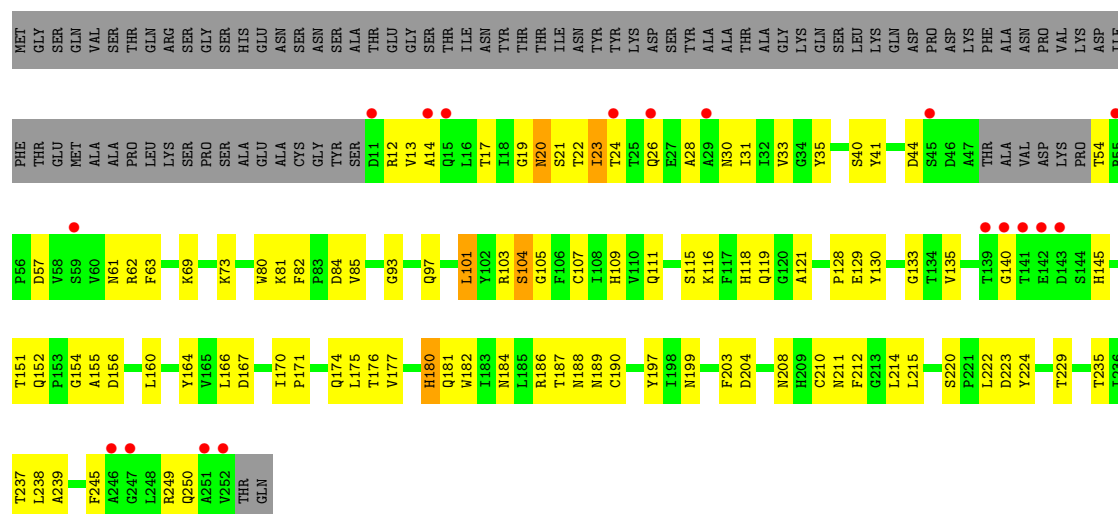
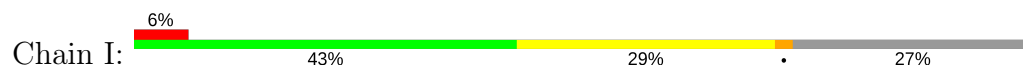




• Molecule 2: Capsid protein VP0



• Molecule 2: Capsid protein VP0



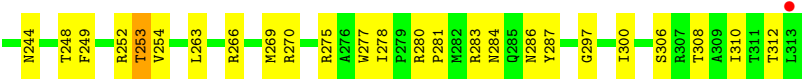
[illegible][illegible]

Chain M:

40% 28% 29%

2%

Amino Acid	Frequency (%)
GLY	2%
ASP	2%
VAL	2%
ALA	2%
ASP	2%
VAL	2%
ILE	2%
GLU	2%
GLY	2%
SER	2%
SER	2%
ILE	2%
GLY	2%
ASP	2%
SER	2%
VAL	2%
SER	2%
ARG	2%
ALA	2%
LEU	2%
THR	2%
HIS	2%
ALA	2%
LEU	2%
PRO	2%
ALA	2%
PRO	2%
THR	2%
THR	2%
GLN	2%
ASN	2%
GLN	2%
THR	2%
GLN	2%
VAL	2%
SER	2%
SER	2%
HIS	2%
ARG	2%
LEU	2%
ASP	2%
THR	2%
THR	2%
GLY	2%
LYS	2%
VAL	2%
PRO	2%
ASN	2%
PRO	2%
ARG	2%
THR	2%
THR	2%
VAL	2%
ASN	2%
ALA	2%
LEU	2%
GLN	2%
ALA	2%
ALA	2%
GLU	2%
ILE	2%
GLY	2%
SER	2%
ASN	2%
ALA	2%
SER	2%
ASP	2%
GLY	2%
GLU	2%
SER	2%
MET	2%
ILE	2%
THR	2%
ARG	2%
CYS	2%
VAL	2%
LEU	2%
ASN	2%
SER	2%
H73	2%
E77	2%
D81	2%
S82	2%
S85	2%
R86	2%
V90	2%
E96	2%
GLY	2%
THR	2%
SER	2%
VAL	2%
LYS	2%
ARG	2%
GLY	2%
THR	2%
SER	2%
VAL	2%
GLY	2%
MET	2%
LYS	2%
PRO	2%
SER	2%
PRO	2%
PRO	2%
ARG	2%
PRO	2%
THR	2%
ASN	2%
P119	2%
W125	2%
D126	2%
I127	2%
D128	2%
I129	2%
T130	2%
G131	2%
Y132	2%
A133	2%
A134	2%
M135	2%
P136	2%
P137	2%
K138	2%
V139	2%
E140	2%
Y144	2%
N145	2%
R146	2%
F147	2%
D148	2%
A149	2%
E150	2%
F151	2%
T152	2%
F153	2%
T157	2%
E161	2%
V162	2%
V163	2%
P164	2%
Q165	2%
L166	2%
L167	2%
F171	2%
V172	2%
P173	2%
R182	2%
E183	2%
W187	2%
Q188	2%
T189	2%
A190	2%
T191	2%
N192	2%
P193	2%
S194	2%
V195	2%
F196	2%
V197	2%
K198	2%
L199	2%
S200	2%
D201	2%
A204	2%
Q205	2%
V206	2%
S207	2%
V208	2%
P209	2%
F210	2%
T211	2%
S212	2%
P213	2%
S217	2%
D222	2%
G223	2%
Y224	2%
G225	2%
T226	2%
F227	2%
G228	2%
E229	2%
H230	2%
K231	2%
G232	2%
E233	2%
K234	2%
D235	2%
C241	2%
N244	2%
M245	2%
M246	2%
F249	2%
R252	2%
T253	2%
V254	2%
K260	2%
L263	2%
Y268	2%
M269	2%
R270	2%
H273	2%
V274	2%
R275	2%
A276	2%
W277	2%
R280	2%
P281	2%
M282	2%
R283	2%
M284	2%
Q285	2%
R286	2%
Y287	2%
L288	2%
F289	2%
K290	2%
A291	2%
N292	2%
G297	2%
L300	2%
R301	2%



4 Data and refinement statistics

Property	Value	Source
Space group	P 4 ₂ 3 2	Depositor
Cell constants a, b, c, α , β , γ	350.15Å 350.15Å 350.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.79 – 3.81 46.79 – 3.81	Depositor EDS
% Data completeness (in resolution range)	(Not available) (46.79-3.81) 77.3 (46.79-3.81)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 3.77Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.271 , 0.299 0.269 , 0.298	Depositor DCC
R_{free} test set	1998 reflections (3.00%)	DCC
Wilson B-factor (Å ²)	103.6	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 38.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	26425	wwPDB-VP
Average B, all atoms (Å ²)	108.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.64% 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 [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	B	0.29	0/1744	0.51	0/2387
1	E	0.28	0/1744	0.50	0/2387
1	H	0.30	0/1744	0.54	1/2387 (0.0%)
1	K	0.28	0/1744	0.50	0/2387
1	N	0.28	0/1744	0.50	0/2387
2	C	0.29	0/1882	0.51	0/2580
2	F	0.28	0/1882	0.48	0/2580
2	I	0.30	0/1882	0.52	0/2580
2	L	0.30	0/1882	0.51	0/2580
2	O	0.28	0/1882	0.52	0/2580
3	A	0.29	0/1811	0.50	0/2464
3	D	0.30	0/1811	0.49	0/2464
3	G	0.29	0/1811	0.50	0/2464
3	J	0.29	0/1811	0.51	0/2464
3	M	0.29	0/1811	0.51	0/2464
All	All	0.29	0/27185	0.51	1/37155 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	61	ASN	N-CA-C	-5.29	96.72	111.00

There are no chirality outliers.

There are no planarity outliers.

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	B	1699	0	1691	73	0
1	E	1699	0	1691	65	0
1	H	1699	0	1691	73	0
1	K	1699	0	1691	51	0
1	N	1699	0	1691	63	0
2	C	1829	0	1765	67	0
2	F	1829	0	1765	62	0
2	I	1829	0	1765	80	0
2	L	1829	0	1765	53	0
2	O	1829	0	1765	65	0
3	A	1757	0	1707	82	0
3	D	1757	0	1707	73	0
3	G	1757	0	1707	77	0
3	J	1757	0	1707	64	0
3	M	1757	0	1707	95	0
All	All	26425	0	25815	838	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 16.

The worst 5 of 838 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)
2:C:12:ARG:O	2:C:26:GLN:NE2	2.10	0.84
3:J:191:THR:HG21	1:N:230:LYS:HA	1.61	0.82
3:A:136:ARG:HD3	1:B:236:LEU:HD12	1.60	0.82
3:A:253:THR:H	3:A:254:VAL:HA	1.44	0.81
1:E:121:PHE:O	2:F:184:ASN:ND2	2.13	0.81

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	B	219/242 (90%)	193 (88%)	23 (10%)	3 (1%)	13	54
1	E	219/242 (90%)	192 (88%)	25 (11%)	2 (1%)	20	62
1	H	219/242 (90%)	191 (87%)	26 (12%)	2 (1%)	20	62
1	K	219/242 (90%)	193 (88%)	24 (11%)	2 (1%)	20	62
1	N	219/242 (90%)	194 (89%)	22 (10%)	3 (1%)	13	54
2	C	232/323 (72%)	195 (84%)	30 (13%)	7 (3%)	5	41
2	F	232/323 (72%)	200 (86%)	29 (12%)	3 (1%)	14	56
2	I	232/323 (72%)	201 (87%)	26 (11%)	5 (2%)	8	46
2	L	232/323 (72%)	203 (88%)	24 (10%)	5 (2%)	8	46
2	O	232/323 (72%)	201 (87%)	26 (11%)	5 (2%)	8	46
3	A	217/313 (69%)	192 (88%)	20 (9%)	5 (2%)	7	46
3	D	217/313 (69%)	193 (89%)	20 (9%)	4 (2%)	10	50
3	G	217/313 (69%)	192 (88%)	20 (9%)	5 (2%)	7	46
3	J	217/313 (69%)	189 (87%)	22 (10%)	6 (3%)	6	42
3	M	217/313 (69%)	188 (87%)	24 (11%)	5 (2%)	7	46
All	All	3340/4390 (76%)	2917 (87%)	361 (11%)	62 (2%)	9	50

5 of 62 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	205	PRO
2	F	211	ASN
3	D	130	THR
3	M	130	THR
3	J	234	LYS

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	B	187/202 (93%)	183 (98%)	4 (2%)	59	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	187/202 (93%)	185 (99%)	2 (1%)	78	89
1	H	187/202 (93%)	183 (98%)	4 (2%)	59	82
1	K	187/202 (93%)	184 (98%)	3 (2%)	68	86
1	N	187/202 (93%)	185 (99%)	2 (1%)	78	89
2	C	200/272 (74%)	195 (98%)	5 (2%)	53	79
2	F	200/272 (74%)	198 (99%)	2 (1%)	80	90
2	I	200/272 (74%)	193 (96%)	7 (4%)	41	73
2	L	200/272 (74%)	197 (98%)	3 (2%)	70	87
2	O	200/272 (74%)	193 (96%)	7 (4%)	41	73
3	A	190/265 (72%)	183 (96%)	7 (4%)	39	71
3	D	190/265 (72%)	186 (98%)	4 (2%)	59	82
3	G	190/265 (72%)	181 (95%)	9 (5%)	30	66
3	J	190/265 (72%)	185 (97%)	5 (3%)	51	78
3	M	190/265 (72%)	186 (98%)	4 (2%)	59	82
All	All	2885/3695 (78%)	2817 (98%)	68 (2%)	54	80

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	J	249	PHE
1	B	79	LYS
2	I	101	LEU
3	J	253	THR
1	N	161	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
3	J	205	GLN
1	N	237	GLN
2	I	181	GLN
3	A	244	ASN
2	L	97	GLN

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 carbohydrates 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 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	B	223/242 (92%)	-0.14	7 (3%)	49 39	80, 97, 139, 197	0
1	E	223/242 (92%)	-0.17	4 (1%)	69 60	80, 95, 135, 176	0
1	H	223/242 (92%)	-0.18	2 (0%)	84 77	80, 96, 135, 179	0
1	K	223/242 (92%)	-0.13	2 (0%)	84 77	80, 97, 140, 188	0
1	N	223/242 (92%)	-0.24	4 (1%)	69 60	80, 97, 134, 201	0
2	C	236/323 (73%)	0.16	17 (7%)	16 12	78, 105, 203, 251	0
2	F	236/323 (73%)	0.27	20 (8%)	11 10	78, 103, 198, 239	0
2	I	236/323 (73%)	0.21	18 (7%)	15 11	78, 105, 205, 239	0
2	L	236/323 (73%)	0.22	19 (8%)	13 10	78, 107, 203, 235	0
2	O	236/323 (73%)	0.17	13 (5%)	26 19	78, 105, 205, 234	0
3	A	221/313 (70%)	-0.05	9 (4%)	38 30	75, 95, 166, 239	0
3	D	221/313 (70%)	0.02	11 (4%)	30 23	75, 93, 164, 211	0
3	G	221/313 (70%)	-0.12	10 (4%)	34 27	75, 95, 167, 237	0
3	J	221/313 (70%)	0.03	12 (5%)	26 21	75, 95, 170, 255	0
3	M	221/313 (70%)	-0.03	7 (3%)	48 38	75, 95, 159, 219	0
All	All	3400/4390 (77%)	0.01	155 (4%)	33 26	75, 97, 184, 255	0

The worst 5 of 155 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	J	233	GLU	9.6
2	F	141	THR	8.2
2	F	143	ASP	7.3
3	J	235	ASP	6.9
2	C	139	THR	6.2

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.