



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:08 PM GMT

PDB ID : 4NWW  
Title : Crystal structure of an N-terminally truncated capsid protein mutant of Orsay virus  
Authors : Tao, Y.J.; Guo, Y.R.  
Deposited on : 2013-12-06  
Resolution : 3.75 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

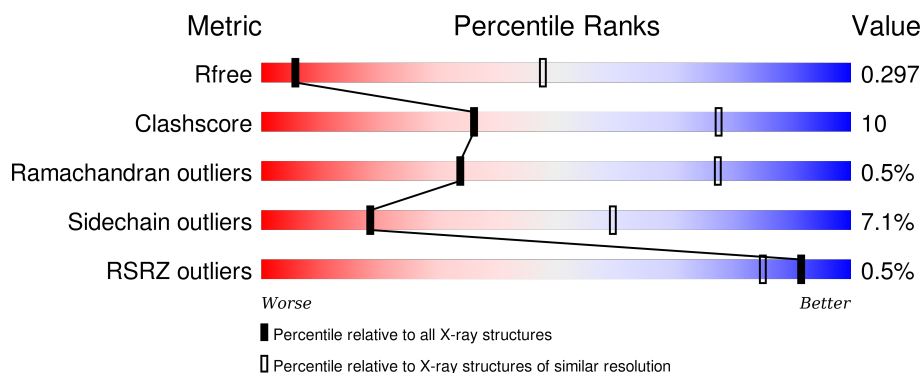
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.75 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))
$R_{free}$	91344	1268 (4.02-3.50)
Clashscore	102246	1407 (4.02-3.50)
Ramachandran outliers	100387	1346 (4.02-3.50)
Sidechain outliers	100360	1342 (4.02-3.50)
RSRZ outliers	91569	1276 (4.02-3.50)

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  $\geq 3$ , 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	A	358	<div> <div></div> <div>72%22%• 5%</div> </div>
1	B	358	<div> <div>%</div> <div>73%21%• •</div> </div>
1	C	358	<div> <div>%</div> <div>74%20%• •</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8019 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	0	0
			2650	1703	443	498	6			
1	B	345	Total	C	N	O	S	0	0	0
			2683	1726	447	504	6			
1	C	345	Total	C	N	O	S	0	0	0
			2683	1726	447	504	6			

There are 312 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	41	GLY	-	EXPRESSION TAG	UNP E9KNV5
A	42	THR	-	EXPRESSION TAG	UNP E9KNV5
A	43	THR	-	EXPRESSION TAG	UNP E9KNV5
A	44	SER	-	EXPRESSION TAG	UNP E9KNV5
A	45	SER	-	EXPRESSION TAG	UNP E9KNV5
A	46	ASN	-	EXPRESSION TAG	UNP E9KNV5
A	47	SER	-	EXPRESSION TAG	UNP E9KNV5
A	48	ILE	-	EXPRESSION TAG	UNP E9KNV5
A	49	LEU	-	EXPRESSION TAG	UNP E9KNV5
A	50	LEU	-	EXPRESSION TAG	UNP E9KNV5
A	51	LYS	-	EXPRESSION TAG	UNP E9KNV5
A	52	GLY	-	EXPRESSION TAG	UNP E9KNV5
A	53	CYS	-	EXPRESSION TAG	UNP E9KNV5
A	54	ASP	-	EXPRESSION TAG	UNP E9KNV5
A	55	ARG	-	EXPRESSION TAG	UNP E9KNV5
A	56	ILE	-	EXPRESSION TAG	UNP E9KNV5
A	57	VAL	-	EXPRESSION TAG	UNP E9KNV5
A	58	THR	-	EXPRESSION TAG	UNP E9KNV5
A	59	VAL	-	EXPRESSION TAG	UNP E9KNV5
A	60	VAL	-	EXPRESSION TAG	UNP E9KNV5
A	61	ASP	-	EXPRESSION TAG	UNP E9KNV5
A	62	ALA	-	EXPRESSION TAG	UNP E9KNV5
A	63	SER	-	EXPRESSION TAG	UNP E9KNV5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	64	THR	-	EXPRESSION TAG	UNP E9KNV5
A	65	TYR	-	EXPRESSION TAG	UNP E9KNV5
A	66	ASP	-	EXPRESSION TAG	UNP E9KNV5
A	67	ALA	-	EXPRESSION TAG	UNP E9KNV5
A	68	GLY	-	EXPRESSION TAG	UNP E9KNV5
A	69	SER	-	EXPRESSION TAG	UNP E9KNV5
A	70	ALA	-	EXPRESSION TAG	UNP E9KNV5
A	71	ILE	-	EXPRESSION TAG	UNP E9KNV5
A	72	VAL	-	EXPRESSION TAG	UNP E9KNV5
A	73	SER	-	EXPRESSION TAG	UNP E9KNV5
A	74	ILE	-	EXPRESSION TAG	UNP E9KNV5
A	75	PRO	-	EXPRESSION TAG	UNP E9KNV5
A	76	ILE	-	EXPRESSION TAG	UNP E9KNV5
A	77	THR	-	EXPRESSION TAG	UNP E9KNV5
A	78	PRO	-	EXPRESSION TAG	UNP E9KNV5
A	79	ASP	-	EXPRESSION TAG	UNP E9KNV5
A	80	ILE	-	EXPRESSION TAG	UNP E9KNV5
A	81	ALA	-	EXPRESSION TAG	UNP E9KNV5
A	82	TYR	-	EXPRESSION TAG	UNP E9KNV5
A	83	ARG	-	EXPRESSION TAG	UNP E9KNV5
A	84	LEU	-	EXPRESSION TAG	UNP E9KNV5
A	85	GLY	-	EXPRESSION TAG	UNP E9KNV5
A	86	SER	-	EXPRESSION TAG	UNP E9KNV5
A	87	THR	-	EXPRESSION TAG	UNP E9KNV5
A	88	ALA	-	EXPRESSION TAG	UNP E9KNV5
A	89	ARG	-	EXPRESSION TAG	UNP E9KNV5
A	90	THR	-	EXPRESSION TAG	UNP E9KNV5
A	91	PHE	-	EXPRESSION TAG	UNP E9KNV5
A	92	GLN	-	EXPRESSION TAG	UNP E9KNV5
A	93	ARG	-	EXPRESSION TAG	UNP E9KNV5
A	94	ILE	-	EXPRESSION TAG	UNP E9KNV5
A	95	LYS	-	EXPRESSION TAG	UNP E9KNV5
A	96	TYR	-	EXPRESSION TAG	UNP E9KNV5
A	97	ARG	-	EXPRESSION TAG	UNP E9KNV5
A	98	SER	-	EXPRESSION TAG	UNP E9KNV5
A	99	LEU	-	EXPRESSION TAG	UNP E9KNV5
A	100	LYS	-	EXPRESSION TAG	UNP E9KNV5
A	101	PHE	-	EXPRESSION TAG	UNP E9KNV5
A	102	ARG	-	EXPRESSION TAG	UNP E9KNV5
A	103	VAL	-	EXPRESSION TAG	UNP E9KNV5
A	104	ASN	-	EXPRESSION TAG	UNP E9KNV5
A	105	ALA	-	EXPRESSION TAG	UNP E9KNV5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	106	GLN	-	EXPRESSION TAG	UNP E9KNV5
A	107	CYS	-	EXPRESSION TAG	UNP E9KNV5
A	108	ALA	-	EXPRESSION TAG	UNP E9KNV5
A	109	THR	-	EXPRESSION TAG	UNP E9KNV5
A	110	THR	-	EXPRESSION TAG	UNP E9KNV5
A	111	THR	-	EXPRESSION TAG	UNP E9KNV5
A	112	ALA	-	EXPRESSION TAG	UNP E9KNV5
A	113	GLY	-	EXPRESSION TAG	UNP E9KNV5
A	114	GLY	-	EXPRESSION TAG	UNP E9KNV5
A	115	TYR	-	EXPRESSION TAG	UNP E9KNV5
A	116	VAL	-	EXPRESSION TAG	UNP E9KNV5
A	117	ALA	-	EXPRESSION TAG	UNP E9KNV5
A	118	GLY	-	EXPRESSION TAG	UNP E9KNV5
A	119	PHE	-	EXPRESSION TAG	UNP E9KNV5
A	120	VAL	-	EXPRESSION TAG	UNP E9KNV5
A	121	LYS	-	EXPRESSION TAG	UNP E9KNV5
A	122	ASP	-	EXPRESSION TAG	UNP E9KNV5
A	123	ALA	-	EXPRESSION TAG	UNP E9KNV5
A	124	ALA	-	EXPRESSION TAG	UNP E9KNV5
A	125	ASP	-	EXPRESSION TAG	UNP E9KNV5
A	126	VAL	-	EXPRESSION TAG	UNP E9KNV5
A	127	LEU	-	EXPRESSION TAG	UNP E9KNV5
A	128	PRO	-	EXPRESSION TAG	UNP E9KNV5
A	129	THR	-	EXPRESSION TAG	UNP E9KNV5
A	130	GLY	-	EXPRESSION TAG	UNP E9KNV5
A	131	THR	-	EXPRESSION TAG	UNP E9KNV5
A	132	ALA	-	EXPRESSION TAG	UNP E9KNV5
A	133	SER	-	EXPRESSION TAG	UNP E9KNV5
A	134	ILE	-	EXPRESSION TAG	UNP E9KNV5
A	135	PRO	-	EXPRESSION TAG	UNP E9KNV5
A	136	TYR	-	EXPRESSION TAG	UNP E9KNV5
A	137	LEU	-	EXPRESSION TAG	UNP E9KNV5
A	392	GLY	-	EXPRESSION TAG	UNP E9KNV5
A	393	HIS	-	EXPRESSION TAG	UNP E9KNV5
A	394	HIS	-	EXPRESSION TAG	UNP E9KNV5
A	395	HIS	-	EXPRESSION TAG	UNP E9KNV5
A	396	HIS	-	EXPRESSION TAG	UNP E9KNV5
A	397	HIS	-	EXPRESSION TAG	UNP E9KNV5
A	398	HIS	-	EXPRESSION TAG	UNP E9KNV5
B	41	GLY	-	EXPRESSION TAG	UNP E9KNV5
B	42	THR	-	EXPRESSION TAG	UNP E9KNV5
B	43	THR	-	EXPRESSION TAG	UNP E9KNV5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	44	SER	-	EXPRESSION TAG	UNP E9KNV5
B	45	SER	-	EXPRESSION TAG	UNP E9KNV5
B	46	ASN	-	EXPRESSION TAG	UNP E9KNV5
B	47	SER	-	EXPRESSION TAG	UNP E9KNV5
B	48	ILE	-	EXPRESSION TAG	UNP E9KNV5
B	49	LEU	-	EXPRESSION TAG	UNP E9KNV5
B	50	LEU	-	EXPRESSION TAG	UNP E9KNV5
B	51	LYS	-	EXPRESSION TAG	UNP E9KNV5
B	52	GLY	-	EXPRESSION TAG	UNP E9KNV5
B	53	CYS	-	EXPRESSION TAG	UNP E9KNV5
B	54	ASP	-	EXPRESSION TAG	UNP E9KNV5
B	55	ARG	-	EXPRESSION TAG	UNP E9KNV5
B	56	ILE	-	EXPRESSION TAG	UNP E9KNV5
B	57	VAL	-	EXPRESSION TAG	UNP E9KNV5
B	58	THR	-	EXPRESSION TAG	UNP E9KNV5
B	59	VAL	-	EXPRESSION TAG	UNP E9KNV5
B	60	VAL	-	EXPRESSION TAG	UNP E9KNV5
B	61	ASP	-	EXPRESSION TAG	UNP E9KNV5
B	62	ALA	-	EXPRESSION TAG	UNP E9KNV5
B	63	SER	-	EXPRESSION TAG	UNP E9KNV5
B	64	THR	-	EXPRESSION TAG	UNP E9KNV5
B	65	TYR	-	EXPRESSION TAG	UNP E9KNV5
B	66	ASP	-	EXPRESSION TAG	UNP E9KNV5
B	67	ALA	-	EXPRESSION TAG	UNP E9KNV5
B	68	GLY	-	EXPRESSION TAG	UNP E9KNV5
B	69	SER	-	EXPRESSION TAG	UNP E9KNV5
B	70	ALA	-	EXPRESSION TAG	UNP E9KNV5
B	71	ILE	-	EXPRESSION TAG	UNP E9KNV5
B	72	VAL	-	EXPRESSION TAG	UNP E9KNV5
B	73	SER	-	EXPRESSION TAG	UNP E9KNV5
B	74	ILE	-	EXPRESSION TAG	UNP E9KNV5
B	75	PRO	-	EXPRESSION TAG	UNP E9KNV5
B	76	ILE	-	EXPRESSION TAG	UNP E9KNV5
B	77	THR	-	EXPRESSION TAG	UNP E9KNV5
B	78	PRO	-	EXPRESSION TAG	UNP E9KNV5
B	79	ASP	-	EXPRESSION TAG	UNP E9KNV5
B	80	ILE	-	EXPRESSION TAG	UNP E9KNV5
B	81	ALA	-	EXPRESSION TAG	UNP E9KNV5
B	82	TYR	-	EXPRESSION TAG	UNP E9KNV5
B	83	ARG	-	EXPRESSION TAG	UNP E9KNV5
B	84	LEU	-	EXPRESSION TAG	UNP E9KNV5
B	85	GLY	-	EXPRESSION TAG	UNP E9KNV5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	86	SER	-	EXPRESSION TAG	UNP E9KNV5
B	87	THR	-	EXPRESSION TAG	UNP E9KNV5
B	88	ALA	-	EXPRESSION TAG	UNP E9KNV5
B	89	ARG	-	EXPRESSION TAG	UNP E9KNV5
B	90	THR	-	EXPRESSION TAG	UNP E9KNV5
B	91	PHE	-	EXPRESSION TAG	UNP E9KNV5
B	92	GLN	-	EXPRESSION TAG	UNP E9KNV5
B	93	ARG	-	EXPRESSION TAG	UNP E9KNV5
B	94	ILE	-	EXPRESSION TAG	UNP E9KNV5
B	95	LYS	-	EXPRESSION TAG	UNP E9KNV5
B	96	TYR	-	EXPRESSION TAG	UNP E9KNV5
B	97	ARG	-	EXPRESSION TAG	UNP E9KNV5
B	98	SER	-	EXPRESSION TAG	UNP E9KNV5
B	99	LEU	-	EXPRESSION TAG	UNP E9KNV5
B	100	LYS	-	EXPRESSION TAG	UNP E9KNV5
B	101	PHE	-	EXPRESSION TAG	UNP E9KNV5
B	102	ARG	-	EXPRESSION TAG	UNP E9KNV5
B	103	VAL	-	EXPRESSION TAG	UNP E9KNV5
B	104	ASN	-	EXPRESSION TAG	UNP E9KNV5
B	105	ALA	-	EXPRESSION TAG	UNP E9KNV5
B	106	GLN	-	EXPRESSION TAG	UNP E9KNV5
B	107	CYS	-	EXPRESSION TAG	UNP E9KNV5
B	108	ALA	-	EXPRESSION TAG	UNP E9KNV5
B	109	THR	-	EXPRESSION TAG	UNP E9KNV5
B	110	THR	-	EXPRESSION TAG	UNP E9KNV5
B	111	THR	-	EXPRESSION TAG	UNP E9KNV5
B	112	ALA	-	EXPRESSION TAG	UNP E9KNV5
B	113	GLY	-	EXPRESSION TAG	UNP E9KNV5
B	114	GLY	-	EXPRESSION TAG	UNP E9KNV5
B	115	TYR	-	EXPRESSION TAG	UNP E9KNV5
B	116	VAL	-	EXPRESSION TAG	UNP E9KNV5
B	117	ALA	-	EXPRESSION TAG	UNP E9KNV5
B	118	GLY	-	EXPRESSION TAG	UNP E9KNV5
B	119	PHE	-	EXPRESSION TAG	UNP E9KNV5
B	120	VAL	-	EXPRESSION TAG	UNP E9KNV5
B	121	LYS	-	EXPRESSION TAG	UNP E9KNV5
B	122	ASP	-	EXPRESSION TAG	UNP E9KNV5
B	123	ALA	-	EXPRESSION TAG	UNP E9KNV5
B	124	ALA	-	EXPRESSION TAG	UNP E9KNV5
B	125	ASP	-	EXPRESSION TAG	UNP E9KNV5
B	126	VAL	-	EXPRESSION TAG	UNP E9KNV5
B	127	LEU	-	EXPRESSION TAG	UNP E9KNV5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	128	PRO	-	EXPRESSION TAG	UNP E9KNV5
B	129	THR	-	EXPRESSION TAG	UNP E9KNV5
B	130	GLY	-	EXPRESSION TAG	UNP E9KNV5
B	131	THR	-	EXPRESSION TAG	UNP E9KNV5
B	132	ALA	-	EXPRESSION TAG	UNP E9KNV5
B	133	SER	-	EXPRESSION TAG	UNP E9KNV5
B	134	ILE	-	EXPRESSION TAG	UNP E9KNV5
B	135	PRO	-	EXPRESSION TAG	UNP E9KNV5
B	136	TYR	-	EXPRESSION TAG	UNP E9KNV5
B	137	LEU	-	EXPRESSION TAG	UNP E9KNV5
B	392	GLY	-	EXPRESSION TAG	UNP E9KNV5
B	393	HIS	-	EXPRESSION TAG	UNP E9KNV5
B	394	HIS	-	EXPRESSION TAG	UNP E9KNV5
B	395	HIS	-	EXPRESSION TAG	UNP E9KNV5
B	396	HIS	-	EXPRESSION TAG	UNP E9KNV5
B	397	HIS	-	EXPRESSION TAG	UNP E9KNV5
B	398	HIS	-	EXPRESSION TAG	UNP E9KNV5
C	41	GLY	-	EXPRESSION TAG	UNP E9KNV5
C	42	THR	-	EXPRESSION TAG	UNP E9KNV5
C	43	THR	-	EXPRESSION TAG	UNP E9KNV5
C	44	SER	-	EXPRESSION TAG	UNP E9KNV5
C	45	SER	-	EXPRESSION TAG	UNP E9KNV5
C	46	ASN	-	EXPRESSION TAG	UNP E9KNV5
C	47	SER	-	EXPRESSION TAG	UNP E9KNV5
C	48	ILE	-	EXPRESSION TAG	UNP E9KNV5
C	49	LEU	-	EXPRESSION TAG	UNP E9KNV5
C	50	LEU	-	EXPRESSION TAG	UNP E9KNV5
C	51	LYS	-	EXPRESSION TAG	UNP E9KNV5
C	52	GLY	-	EXPRESSION TAG	UNP E9KNV5
C	53	CYS	-	EXPRESSION TAG	UNP E9KNV5
C	54	ASP	-	EXPRESSION TAG	UNP E9KNV5
C	55	ARG	-	EXPRESSION TAG	UNP E9KNV5
C	56	ILE	-	EXPRESSION TAG	UNP E9KNV5
C	57	VAL	-	EXPRESSION TAG	UNP E9KNV5
C	58	THR	-	EXPRESSION TAG	UNP E9KNV5
C	59	VAL	-	EXPRESSION TAG	UNP E9KNV5
C	60	VAL	-	EXPRESSION TAG	UNP E9KNV5
C	61	ASP	-	EXPRESSION TAG	UNP E9KNV5
C	62	ALA	-	EXPRESSION TAG	UNP E9KNV5
C	63	SER	-	EXPRESSION TAG	UNP E9KNV5
C	64	THR	-	EXPRESSION TAG	UNP E9KNV5
C	65	TYR	-	EXPRESSION TAG	UNP E9KNV5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	66	ASP	-	EXPRESSION TAG	UNP E9KNV5
C	67	ALA	-	EXPRESSION TAG	UNP E9KNV5
C	68	GLY	-	EXPRESSION TAG	UNP E9KNV5
C	69	SER	-	EXPRESSION TAG	UNP E9KNV5
C	70	ALA	-	EXPRESSION TAG	UNP E9KNV5
C	71	ILE	-	EXPRESSION TAG	UNP E9KNV5
C	72	VAL	-	EXPRESSION TAG	UNP E9KNV5
C	73	SER	-	EXPRESSION TAG	UNP E9KNV5
C	74	ILE	-	EXPRESSION TAG	UNP E9KNV5
C	75	PRO	-	EXPRESSION TAG	UNP E9KNV5
C	76	ILE	-	EXPRESSION TAG	UNP E9KNV5
C	77	THR	-	EXPRESSION TAG	UNP E9KNV5
C	78	PRO	-	EXPRESSION TAG	UNP E9KNV5
C	79	ASP	-	EXPRESSION TAG	UNP E9KNV5
C	80	ILE	-	EXPRESSION TAG	UNP E9KNV5
C	81	ALA	-	EXPRESSION TAG	UNP E9KNV5
C	82	TYR	-	EXPRESSION TAG	UNP E9KNV5
C	83	ARG	-	EXPRESSION TAG	UNP E9KNV5
C	84	LEU	-	EXPRESSION TAG	UNP E9KNV5
C	85	GLY	-	EXPRESSION TAG	UNP E9KNV5
C	86	SER	-	EXPRESSION TAG	UNP E9KNV5
C	87	THR	-	EXPRESSION TAG	UNP E9KNV5
C	88	ALA	-	EXPRESSION TAG	UNP E9KNV5
C	89	ARG	-	EXPRESSION TAG	UNP E9KNV5
C	90	THR	-	EXPRESSION TAG	UNP E9KNV5
C	91	PHE	-	EXPRESSION TAG	UNP E9KNV5
C	92	GLN	-	EXPRESSION TAG	UNP E9KNV5
C	93	ARG	-	EXPRESSION TAG	UNP E9KNV5
C	94	ILE	-	EXPRESSION TAG	UNP E9KNV5
C	95	LYS	-	EXPRESSION TAG	UNP E9KNV5
C	96	TYR	-	EXPRESSION TAG	UNP E9KNV5
C	97	ARG	-	EXPRESSION TAG	UNP E9KNV5
C	98	SER	-	EXPRESSION TAG	UNP E9KNV5
C	99	LEU	-	EXPRESSION TAG	UNP E9KNV5
C	100	LYS	-	EXPRESSION TAG	UNP E9KNV5
C	101	PHE	-	EXPRESSION TAG	UNP E9KNV5
C	102	ARG	-	EXPRESSION TAG	UNP E9KNV5
C	103	VAL	-	EXPRESSION TAG	UNP E9KNV5
C	104	ASN	-	EXPRESSION TAG	UNP E9KNV5
C	105	ALA	-	EXPRESSION TAG	UNP E9KNV5
C	106	GLN	-	EXPRESSION TAG	UNP E9KNV5
C	107	CYS	-	EXPRESSION TAG	UNP E9KNV5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	108	ALA	-	EXPRESSION TAG	UNP E9KNV5
C	109	THR	-	EXPRESSION TAG	UNP E9KNV5
C	110	THR	-	EXPRESSION TAG	UNP E9KNV5
C	111	THR	-	EXPRESSION TAG	UNP E9KNV5
C	112	ALA	-	EXPRESSION TAG	UNP E9KNV5
C	113	GLY	-	EXPRESSION TAG	UNP E9KNV5
C	114	GLY	-	EXPRESSION TAG	UNP E9KNV5
C	115	TYR	-	EXPRESSION TAG	UNP E9KNV5
C	116	VAL	-	EXPRESSION TAG	UNP E9KNV5
C	117	ALA	-	EXPRESSION TAG	UNP E9KNV5
C	118	GLY	-	EXPRESSION TAG	UNP E9KNV5
C	119	PHE	-	EXPRESSION TAG	UNP E9KNV5
C	120	VAL	-	EXPRESSION TAG	UNP E9KNV5
C	121	LYS	-	EXPRESSION TAG	UNP E9KNV5
C	122	ASP	-	EXPRESSION TAG	UNP E9KNV5
C	123	ALA	-	EXPRESSION TAG	UNP E9KNV5
C	124	ALA	-	EXPRESSION TAG	UNP E9KNV5
C	125	ASP	-	EXPRESSION TAG	UNP E9KNV5
C	126	VAL	-	EXPRESSION TAG	UNP E9KNV5
C	127	LEU	-	EXPRESSION TAG	UNP E9KNV5
C	128	PRO	-	EXPRESSION TAG	UNP E9KNV5
C	129	THR	-	EXPRESSION TAG	UNP E9KNV5
C	130	GLY	-	EXPRESSION TAG	UNP E9KNV5
C	131	THR	-	EXPRESSION TAG	UNP E9KNV5
C	132	ALA	-	EXPRESSION TAG	UNP E9KNV5
C	133	SER	-	EXPRESSION TAG	UNP E9KNV5
C	134	ILE	-	EXPRESSION TAG	UNP E9KNV5
C	135	PRO	-	EXPRESSION TAG	UNP E9KNV5
C	136	TYR	-	EXPRESSION TAG	UNP E9KNV5
C	137	LEU	-	EXPRESSION TAG	UNP E9KNV5
C	392	GLY	-	EXPRESSION TAG	UNP E9KNV5
C	393	HIS	-	EXPRESSION TAG	UNP E9KNV5
C	394	HIS	-	EXPRESSION TAG	UNP E9KNV5
C	395	HIS	-	EXPRESSION TAG	UNP E9KNV5
C	396	HIS	-	EXPRESSION TAG	UNP E9KNV5
C	397	HIS	-	EXPRESSION TAG	UNP E9KNV5
C	398	HIS	-	EXPRESSION TAG	UNP E9KNV5

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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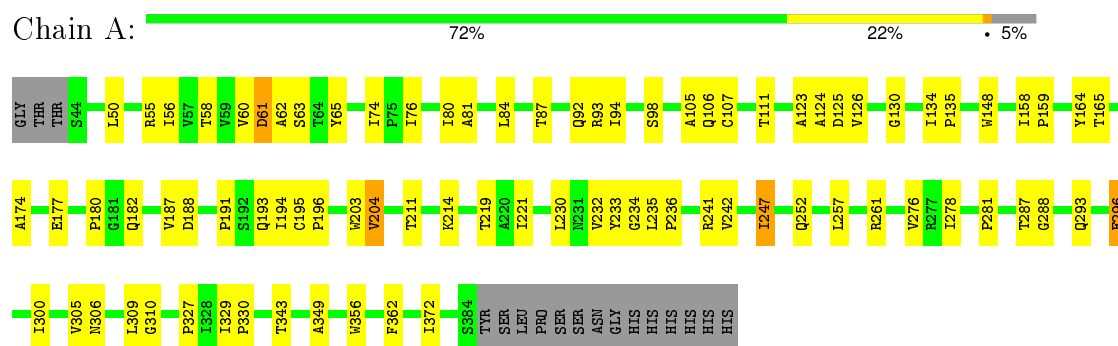
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
-----	-------	----------	-------	---------	---------

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Ca 1 1	0	0
2	A	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0

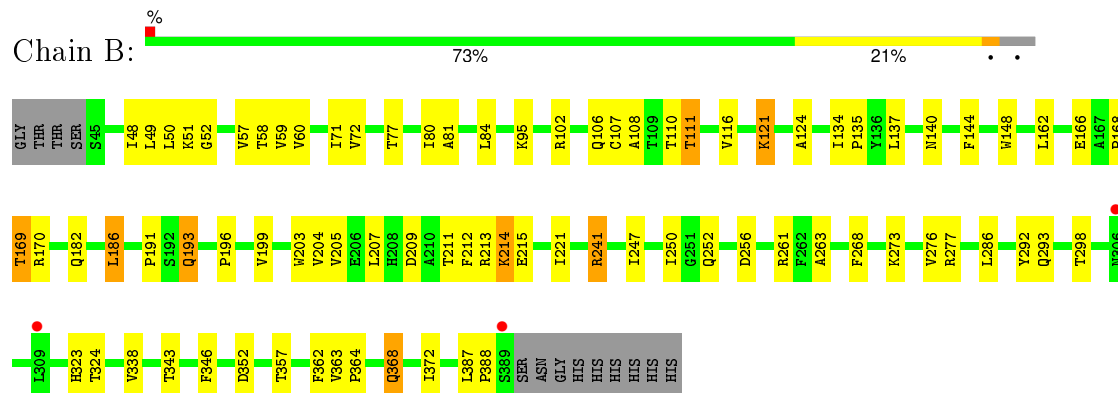
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

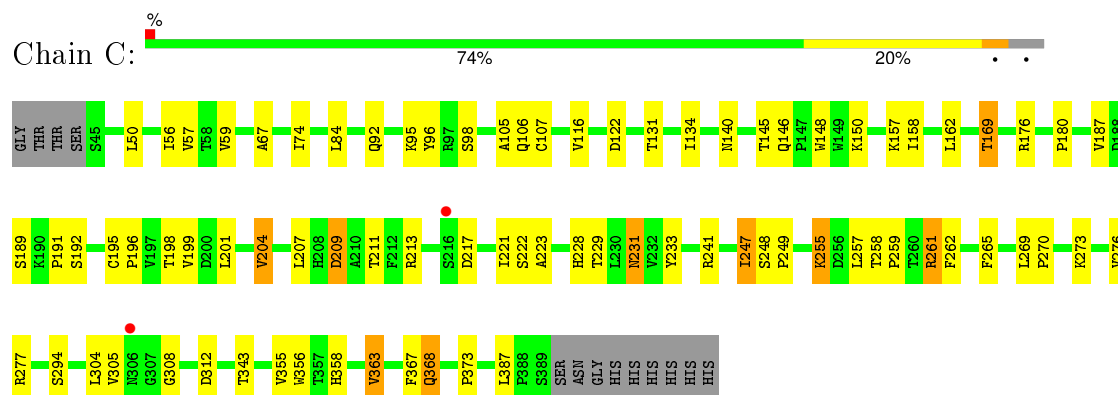
#### • Molecule 1: Capsid protein



#### • Molecule 1: Capsid protein



#### • Molecule 1: Capsid protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	404.92Å 375.15Å 412.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.75 29.90 – 3.74	Depositor EDS
% Data completeness (in resolution range)	64.2 (30.00-3.75) 63.9 (29.90-3.74)	Depositor EDS
$R_{merge}$	0.25	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.50 (at 3.75Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.299 , 0.301 0.296 , 0.297	Depositor DCC
$R_{free}$ test set	10137 reflections (5.24%)	DCC
Wilson B-factor (Å <sup>2</sup> )	60.0	Xtriage
Anisotropy	0.518	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 57.8	EDS
Estimated twinning fraction	0.015 for -l,-k,-h	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	5 of 203989 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.78	EDS
Total number of atoms	8019	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: CA

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	0.32	0/2725	0.56	0/3738
1	B	0.31	0/2760	0.55	0/3787
1	C	0.32	0/2760	0.56	0/3787
All	All	0.32	0/8245	0.56	0/11312

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2650	0	2602	52	0
1	B	2683	0	2634	49	0
1	C	2683	0	2636	64	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
All	All	8019	0	7872	151	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 10.

All (151) 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:C:228:HIS:HB3	1:C:249:PRO:HA	1.52	0.91
1:C:228:HIS:CB	1:C:249:PRO:HA	2.05	0.86
1:C:169:THR:HG21	1:C:213:ARG:HH21	1.45	0.80
1:C:107:CYS:SG	1:C:148:TRP:HB3	2.23	0.78
1:A:234:GLY:HA2	1:A:242:VAL:HG22	1.75	0.68
1:B:81:ALA:HB3	1:B:84:LEU:HB3	1.77	0.67
1:C:259:PRO:HB2	1:C:270:PRO:HG2	1.78	0.66
1:C:305:VAL:HG21	1:C:312:ASP:HB2	1.79	0.64
1:C:247:ILE:HD11	1:C:257:LEU:HG	1.79	0.64
1:C:92:GLN:HE21	1:C:211:THR:HB	1.63	0.64
1:B:121:LYS:HG2	1:C:209:ASP:HB3	1.80	0.63
1:A:164:TYR:CE2	1:C:176:ARG:HG2	2.35	0.61
1:A:105:ALA:HB1	1:A:107:CYS:SG	2.40	0.61
1:A:56:ILE:HG13	1:A:80:ILE:HG21	1.81	0.61
1:C:107:CYS:HG	1:C:195:CYS:HG	1.39	0.60
1:C:191:PRO:HB3	1:C:195:CYS:SG	2.41	0.60
1:C:107:CYS:CB	1:C:195:CYS:HG	2.13	0.60
1:A:123:ALA:O	1:B:170:ARG:NH1	2.34	0.60
1:C:277:ARG:HB3	1:C:363:VAL:HG13	1.85	0.59
1:A:247:ILE:HD11	1:A:257:LEU:HA	1.84	0.59
1:C:258:THR:OG1	1:C:261:ARG:NH1	2.35	0.58
1:C:107:CYS:HB3	1:C:195:CYS:HG	1.69	0.58
1:B:134:ILE:HD13	1:B:186:LEU:HD23	1.85	0.58
1:A:92:GLN:OE1	1:C:122:ASP:HB2	2.05	0.57
1:C:262:PHE:CD2	1:C:270:PRO:HG3	2.39	0.57
1:C:223:ALA:HB3	1:C:358:HIS:HA	1.87	0.57
1:B:211:THR:HG22	1:B:212:PHE:N	2.20	0.57
1:C:169:THR:CG2	1:C:213:ARG:HH21	2.18	0.56
1:A:63:SER:HA	1:A:191:PRO:HG2	1.88	0.56
1:C:92:GLN:NE2	1:C:211:THR:HB	2.21	0.55
1:A:62:ALA:HB1	1:A:65:TYR:CD2	2.41	0.54
1:C:228:HIS:HB2	1:C:249:PRO:HA	1.87	0.54
1:C:247:ILE:HD13	1:C:261:ARG:HG2	1.90	0.54
1:A:92:GLN:HE21	1:A:211:THR:CB	2.22	0.53
1:B:121:LYS:HB2	1:C:92:GLN:HG3	1.90	0.53
1:A:74:ILE:HD12	1:A:80:ILE:HD13	1.91	0.52
1:B:121:LYS:CG	1:C:209:ASP:HB3	2.39	0.52
1:C:116:VAL:HG21	1:C:134:ILE:HG23	1.91	0.52
1:A:124:ALA:HB1	1:B:168:PRO:HA	1.91	0.52
1:B:352:ASP:OD2	1:C:294:SER:HB3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:134:ILE:HB	1:B:135:PRO:CD	2.41	0.51
1:A:327:PRO:HB2	1:A:329:ILE:HD13	1.91	0.51
1:C:59:VAL:HA	1:C:198:THR:HG22	1.92	0.51
1:C:67:ALA:HA	1:C:187:VAL:HG23	1.92	0.51
1:B:124:ALA:O	1:C:169:THR:HG23	2.11	0.51
1:B:108:ALA:O	1:B:111:THR:HG23	2.10	0.51
1:C:262:PHE:CG	1:C:270:PRO:HG3	2.45	0.51
1:B:277:ARG:HB3	1:B:363:VAL:HG13	1.91	0.51
1:A:92:GLN:HE21	1:A:211:THR:HB	1.75	0.50
1:B:49:LEU:HD12	1:B:205:VAL:O	2.12	0.50
1:C:258:THR:N	1:C:259:PRO:HA	2.27	0.50
1:C:105:ALA:HB1	1:C:148:TRP:O	2.12	0.50
1:C:57:VAL:HG12	1:C:199:VAL:HB	1.93	0.49
1:B:323:HIS:O	1:B:368:GLN:NE2	2.44	0.49
1:A:126:VAL:HG12	1:B:169:THR:HB	1.94	0.49
1:C:74:ILE:O	1:C:74:ILE:HG23	2.12	0.49
1:C:106:GLN:HB2	1:C:196:PRO:HG2	1.94	0.49
1:B:286:LEU:HB3	1:B:346:PHE:CD1	2.48	0.48
1:B:57:VAL:HG11	1:B:72:VAL:HG22	1.96	0.48
1:C:56:ILE:CG1	1:C:201:LEU:HB2	2.43	0.48
1:C:223:ALA:HB2	1:C:265:PHE:CZ	2.49	0.48
1:C:191:PRO:CB	1:C:195:CYS:SG	3.01	0.48
1:B:137:LEU:HD12	1:B:140:ASN:HD21	1.78	0.47
1:B:77:THR:O	1:B:80:ILE:HG22	2.15	0.47
1:C:107:CYS:SG	1:C:195:CYS:CB	3.03	0.47
1:A:211:THR:OG1	1:C:140:ASN:ND2	2.48	0.47
1:A:158:ILE:N	1:A:159:PRO:CD	2.77	0.47
1:B:121:LYS:CB	1:C:92:GLN:HG3	2.45	0.46
1:C:158:ILE:HD12	1:C:180:PRO:HB2	1.96	0.46
1:A:50:LEU:HD11	1:A:87:THR:HG21	1.98	0.46
1:C:367:PHE:O	1:C:368:GLN:HB2	2.15	0.46
1:A:148:TRP:CD1	1:A:191:PRO:HB3	2.50	0.46
1:B:241:ARG:NH1	1:B:256:ASP:HB3	2.30	0.46
1:C:217:ASP:O	1:C:373:PRO:HA	2.16	0.46
1:C:247:ILE:HD12	1:C:255:LYS:O	2.16	0.46
1:B:137:LEU:HD22	1:B:186:LEU:HD22	1.98	0.46
1:B:57:VAL:HA	1:B:388:PRO:HD3	1.98	0.46
1:C:95:LYS:HB2	1:C:162:LEU:HD23	1.97	0.45
1:C:231:ASN:HB3	1:C:355:VAL:HA	1.98	0.45
1:A:278:ILE:HD13	1:A:300:ILE:HG13	1.98	0.45
1:A:281:PRO:HB3	1:A:296:GLU:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:ALA:HB3	1:A:148:TRP:O	2.17	0.45
1:A:56:ILE:HG23	1:A:74:ILE:HD11	1.97	0.45
1:A:158:ILE:CD1	1:A:180:PRO:HB2	2.47	0.45
1:A:158:ILE:HD13	1:A:180:PRO:HB2	1.98	0.45
1:A:111:THR:HG22	1:A:193:GLN:HB2	1.98	0.45
1:A:247:ILE:HD11	1:A:257:LEU:HD23	1.99	0.45
1:C:223:ALA:HB2	1:C:265:PHE:CE2	2.52	0.45
1:B:107:CYS:SG	1:B:111:THR:HG21	2.56	0.45
1:B:57:VAL:HG22	1:B:199:VAL:HB	1.97	0.45
1:C:304:LEU:HB3	1:C:308:GLY:HA2	1.98	0.45
1:B:60:VAL:O	1:B:196:PRO:HA	2.16	0.45
1:A:93:ARG:HG2	1:A:93:ARG:HH11	1.81	0.45
1:C:229:THR:HB	1:C:356:TRP:O	2.16	0.45
1:B:166:GLU:OE1	1:B:213:ARG:HG3	2.16	0.45
1:C:98:SER:HB3	1:C:204:VAL:CG1	2.46	0.45
1:A:81:ALA:HB3	1:A:84:LEU:HB3	1.98	0.44
1:C:57:VAL:CG1	1:C:199:VAL:HB	2.47	0.44
1:B:84:LEU:HB2	1:B:203:TRP:CE2	2.52	0.44
1:C:187:VAL:O	1:C:187:VAL:HG23	2.17	0.44
1:A:233:TYR:HB2	1:B:338:VAL:HG12	2.00	0.44
1:A:134:ILE:HD11	1:A:188:ASP:HA	1.99	0.44
1:B:111:THR:HB	1:B:193:GLN:HG2	1.99	0.44
1:C:59:VAL:HG22	1:C:198:THR:CG2	2.48	0.44
1:A:278:ILE:HA	1:A:278:ILE:HD12	1.94	0.43
1:A:232:VAL:HG23	1:A:356:TRP:HZ3	1.84	0.43
1:A:276:VAL:CG2	1:A:362:PHE:HB3	2.49	0.43
1:A:61:ASP:HB2	1:A:195:CYS:H	1.82	0.43
1:B:137:LEU:CD2	1:B:186:LEU:HD22	2.48	0.43
1:C:96:TYR:HB2	1:C:158:ILE:HG21	1.99	0.43
1:A:235:LEU:HB3	1:A:236:PRO:HD3	2.01	0.43
1:A:309:LEU:HD12	1:A:310:GLY:N	2.34	0.43
1:A:98:SER:HB3	1:A:204:VAL:HG13	2.00	0.43
1:B:276:VAL:CG1	1:B:362:PHE:HB3	2.49	0.43
1:A:60:VAL:O	1:A:61:ASP:C	2.57	0.43
1:A:50:LEU:HB3	1:A:203:TRP:HZ3	1.83	0.43
1:B:214:LYS:O	1:B:215:GLU:C	2.56	0.42
1:B:263:ALA:HA	1:B:268:PHE:O	2.19	0.42
1:B:247:ILE:HD12	1:B:261:ARG:HB3	2.02	0.42
1:B:277:ARG:CB	1:B:363:VAL:HG13	2.50	0.42
1:C:231:ASN:HD21	1:C:248:SER:HB2	1.83	0.42
1:C:257:LEU:N	1:C:257:LEU:HD12	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:ASP:HB3	1:B:213:ARG:HH21	1.84	0.42
1:A:94:ILE:HB	1:A:165:THR:HG22	2.01	0.42
1:A:194:ILE:HG22	1:A:196:PRO:HD3	2.02	0.42
1:B:52:GLY:HA3	1:B:203:TRP:CZ2	2.55	0.42
1:A:134:ILE:N	1:A:135:PRO:HD2	2.35	0.42
1:A:287:THR:OG1	1:A:288:GLY:N	2.52	0.42
1:C:231:ASN:ND2	1:C:233:TYR:OH	2.53	0.41
1:B:71:ILE:HG13	1:B:72:VAL:HG23	2.02	0.41
1:B:148:TRP:CE2	1:B:191:PRO:HG3	2.56	0.41
1:C:221:ILE:HG22	1:C:222:SER:N	2.36	0.41
1:B:58:THR:HG23	1:B:387:LEU:HB2	2.02	0.41
1:A:330:PRO:HG3	1:A:349:ALA:HB2	2.03	0.41
1:B:116:VAL:HG21	1:B:134:ILE:HG23	2.03	0.41
1:B:51:LYS:HG2	1:B:204:VAL:HG22	2.02	0.41
1:A:247:ILE:HD13	1:A:261:ARG:CD	2.51	0.41
1:B:211:THR:CG2	1:B:212:PHE:N	2.84	0.41
1:A:305:VAL:HG12	1:A:310:GLY:HA3	2.03	0.41
1:C:269:LEU:HA	1:C:270:PRO:HD3	1.96	0.41
1:A:76:ILE:HA	1:A:80:ILE:HD11	2.03	0.41
1:B:363:VAL:HA	1:B:364:PRO:HD3	1.97	0.41
1:B:48:ILE:HD11	1:B:207:LEU:HD12	2.03	0.41
1:B:134:ILE:HB	1:B:135:PRO:HD3	2.03	0.41
1:A:305:VAL:HG13	1:A:306:ASN:N	2.36	0.40
1:C:213:ARG:HG3	1:C:213:ARG:HH11	1.86	0.40
1:C:146:GLN:HG3	1:C:150:LYS:HB3	2.03	0.40
1:C:122:ASP:OD1	1:C:176:ARG:NH1	2.54	0.40
1:A:92:GLN:HE21	1:A:211:THR:CG2	2.35	0.40
1:A:174:ALA:HB3	1:A:177:GLU:CD	2.42	0.40
1:B:95:LYS:HB2	1:B:162:LEU:HD23	2.04	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	339/358 (95%)	316 (93%)	21 (6%)	2 (1%)	30	75
1	B	343/358 (96%)	327 (95%)	14 (4%)	2 (1%)	30	75
1	C	343/358 (96%)	329 (96%)	13 (4%)	1 (0%)	46	83
All	All	1025/1074 (95%)	972 (95%)	48 (5%)	5 (0%)	34	77

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	130	GLY
1	B	209	ASP
1	C	209	ASP
1	A	61	ASP
1	B	250	ILE

### 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	293/308 (95%)	276 (94%)	17 (6%)	25	66
1	B	297/308 (96%)	272 (92%)	25 (8%)	14	53
1	C	297/308 (96%)	276 (93%)	21 (7%)	18	59
All	All	887/924 (96%)	824 (93%)	63 (7%)	18	59

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	ARG
1	A	58	THR
1	A	106	GLN
1	A	182	GLN
1	A	187	VAL
1	A	204	VAL
1	A	214	LYS
1	A	219	THR

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Mol	Chain	Res	Type
1	A	221	ILE
1	A	230	LEU
1	A	241	ARG
1	A	247	ILE
1	A	252	GLN
1	A	293	GLN
1	A	296	GLU
1	A	343	THR
1	A	372	ILE
1	B	50	LEU
1	B	59	VAL
1	B	102	ARG
1	B	106	GLN
1	B	110	THR
1	B	111	THR
1	B	121	LYS
1	B	144	PHE
1	B	169	THR
1	B	182	GLN
1	B	186	LEU
1	B	193	GLN
1	B	214	LYS
1	B	221	ILE
1	B	241	ARG
1	B	252	GLN
1	B	273	LYS
1	B	292	TYR
1	B	293	GLN
1	B	298	THR
1	B	324	THR
1	B	343	THR
1	B	357	THR
1	B	368	GLN
1	B	372	ILE
1	C	50	LEU
1	C	84	LEU
1	C	131	THR
1	C	145	THR
1	C	157	LYS
1	C	169	THR
1	C	189	SER
1	C	192	SER

*Continued on next page...*

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Mol	Chain	Res	Type
1	C	204	VAL
1	C	207	LEU
1	C	231	ASN
1	C	241	ARG
1	C	247	ILE
1	C	255	LYS
1	C	261	ARG
1	C	273	LYS
1	C	276	VAL
1	C	343	THR
1	C	363	VAL
1	C	368	GLN
1	C	387	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	GLN
1	A	106	GLN
1	A	184	HIS
1	A	252	GLN
1	A	319	ASN
1	A	354	HIS
1	B	228	HIS
1	B	319	ASN
1	B	368	GLN
1	C	92	GLN
1	C	140	ASN
1	C	182	GLN
1	C	231	ASN
1	C	326	GLN

### 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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	341/358 (95%)	-0.37	0 100 100	25, 60, 107, 156	0
1	B	345/358 (96%)	-0.32	3 (0%) 85 74	30, 66, 113, 159	0
1	C	345/358 (96%)	-0.24	2 (0%) 90 82	30, 68, 122, 175	0
All	All	1031/1074 (95%)	-0.31	5 (0%) 91 85	25, 64, 117, 175	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	306	ASN	3.5
1	B	389	SER	3.0
1	B	309	LEU	2.8
1	B	306	ASN	2.8
1	C	216	SER	2.2

### 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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	CA	C	401	1/1	0.91	0.18	-0.70	55,55,55,55	0
2	CA	B	401	1/1	0.97	0.13	-1.56	40,40,40,40	0
2	CA	A	401	1/1	0.98	0.06	-7.70	49,49,49,49	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.