



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 03:54 am GMT

PDB ID : 1OHF  
Title : THE REFINED STRUCTURE OF NUDAURELIA CAPENSIS OMEGA VIRUS  
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Deposited on : 2003-05-26  
Resolution : 2.80 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](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
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28755
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

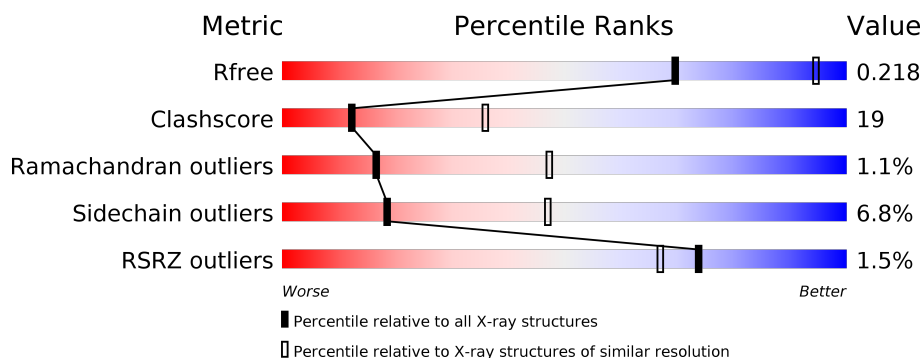
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

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	644	<div> <div>%</div> <div> <div></div> <div>51%</div> <div>29%</div> <div>•</div> <div>16%</div> </div> </div>
1	B	644	<div> <div>2%</div> <div> <div></div> <div>54%</div> <div>27%</div> <div>•</div> <div>15%</div> </div> </div>
1	C	644	<div> <div>%</div> <div> <div></div> <div>64%</div> <div>25%</div> <div>•</div> <div>8%</div> </div> </div>
1	D	644	<div> <div>%</div> <div> <div></div> <div>62%</div> <div>24%</div> <div>•</div> <div>9%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17851 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 NUDAURELIA CAPENSIS OMEGA VIRUS CAPSID PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	539	Total	C	N	O	S	0	0	0
			4134	2632	683	806	13			
1	B	547	Total	C	N	O	S	0	0	0
			4187	2659	694	821	13			
1	C	590	Total	C	N	O	S	0	0	0
			4519	2861	770	874	14			
1	D	587	Total	C	N	O	S	0	0	0
			4491	2846	761	870	14			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	235	VAL	CYS	SEE REMARK 999	UNP Q90063
A	283	VAL	GLU	SEE REMARK 999	UNP Q90063
B	235	VAL	CYS	SEE REMARK 999	UNP Q90063
B	283	VAL	GLU	SEE REMARK 999	UNP Q90063
C	235	VAL	CYS	SEE REMARK 999	UNP Q90063
C	283	VAL	GLU	SEE REMARK 999	UNP Q90063
D	235	VAL	CYS	SEE REMARK 999	UNP Q90063
D	283	VAL	GLU	SEE REMARK 999	UNP Q90063

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

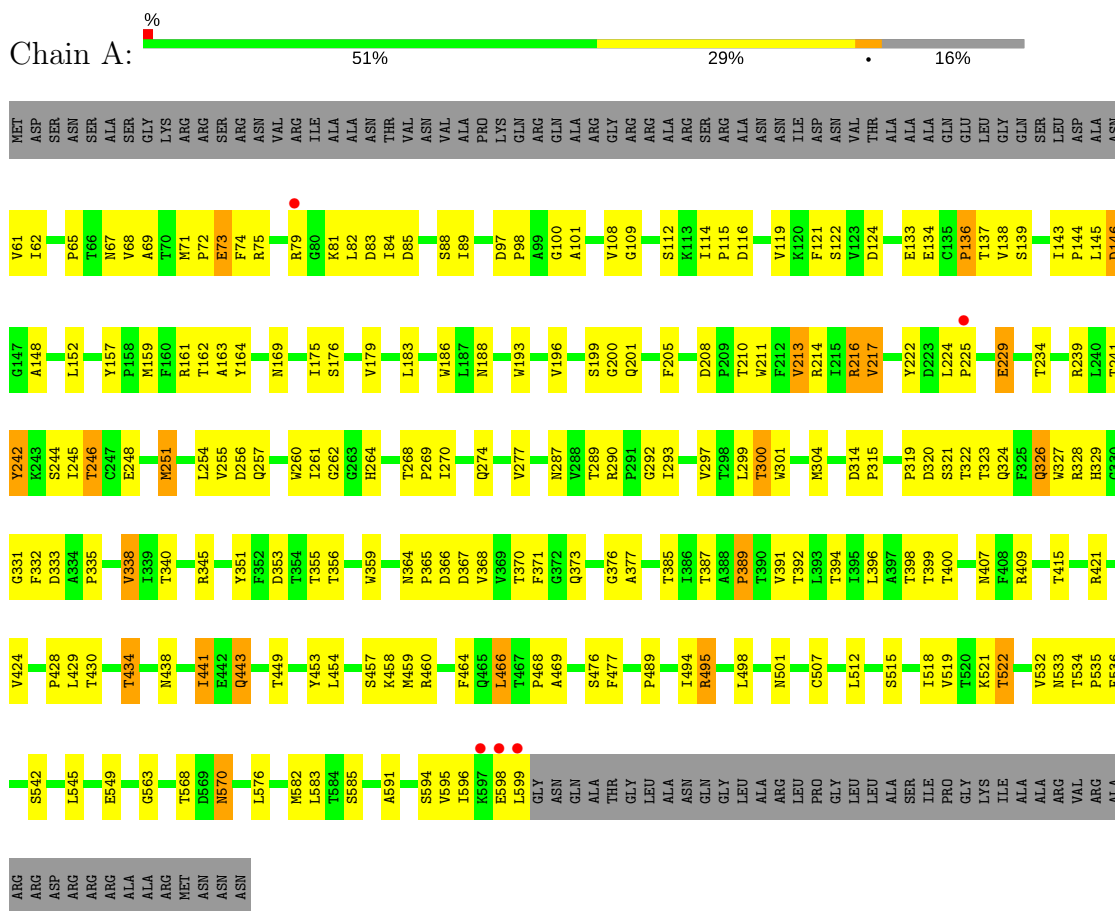
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	97	Total 97	O 97	0	0
3	B	127	Total 127	O 127	0	0
3	C	148	Total 148	O 148	0	0
3	D	144	Total 144	O 144	0	0

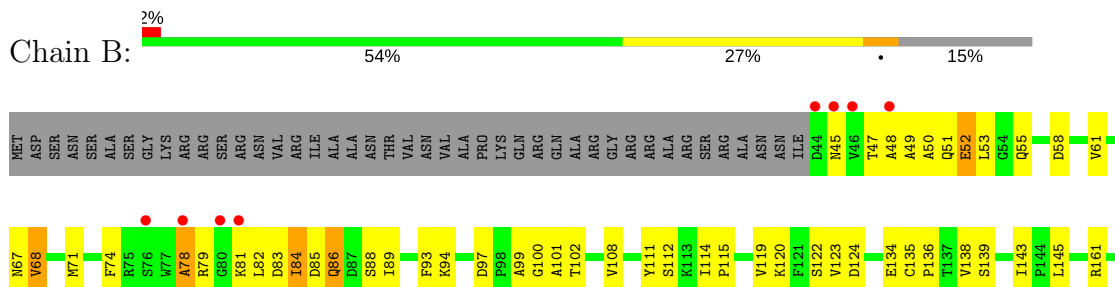
### 3 Residue-property plots

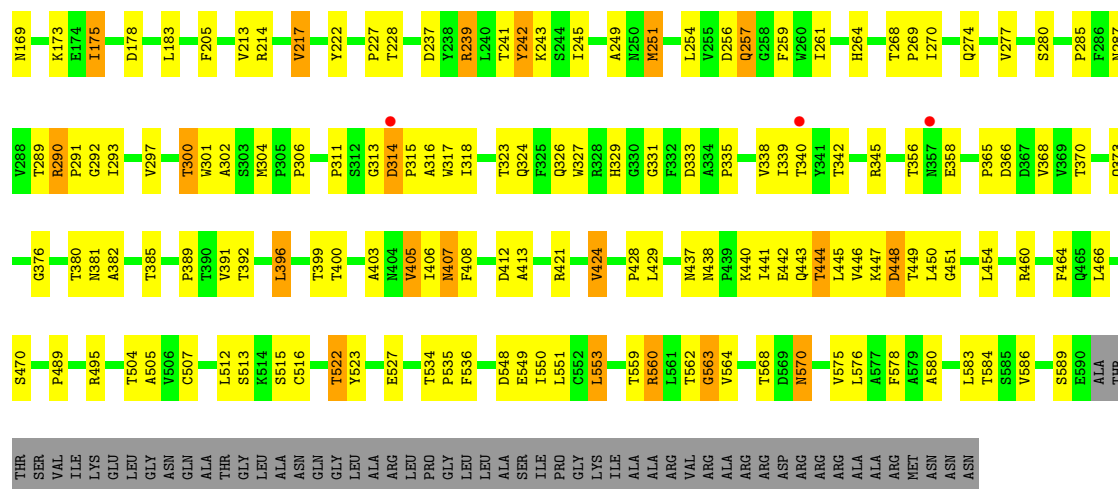
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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 ( $RSRZ > 2$ ). 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: NUDAURELIA CAPENSIS OMEGA VIRUS CAPSID PROTEIN

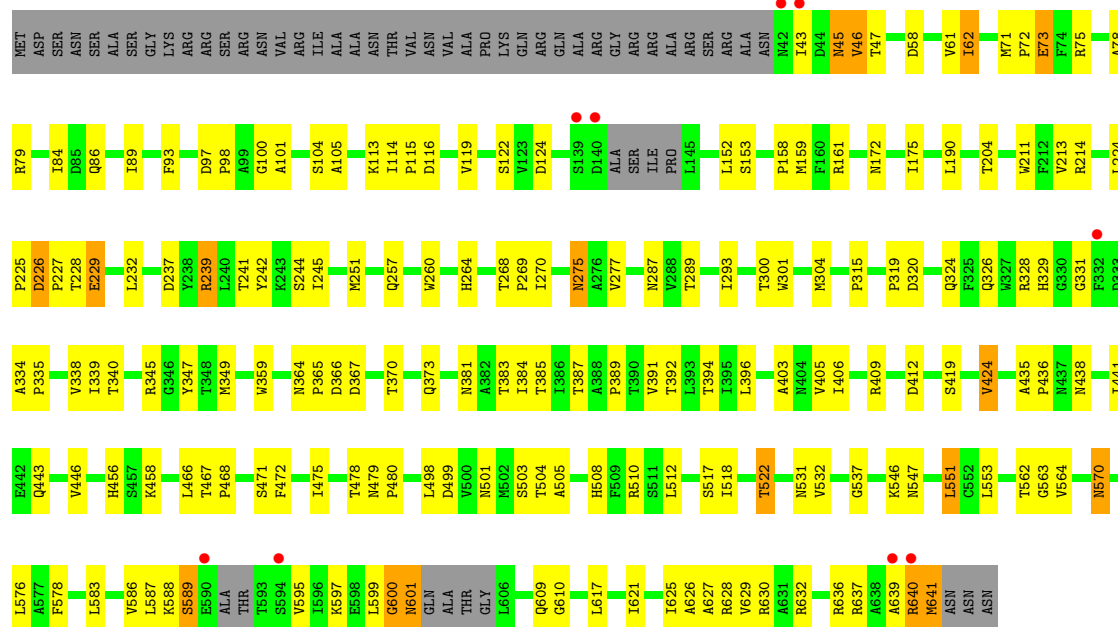


#### • Molecule 1: NUDAURELIA CAPENSIS OMEGA VIRUS CAPSID PROTEIN

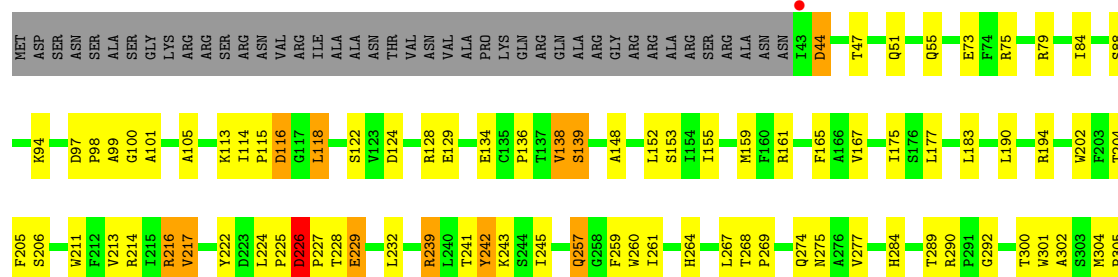




• Molecule 1: NUDAURELIA CAPENSIS OMEGA VIRUS CAPSID PROTEIN



• Molecule 1: NUDAURELIA CAPENSIS OMEGA VIRUS CAPSID PROTEIN





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	413.55Å 410.22Å 419.67Å 59.13° 58.90° 64.04°	Depositor
Resolution (Å)	20.00 – 2.80 20.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	50.9 (20.00-2.80) 46.9 (20.00-2.80)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.07 (at 2.79Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.219 , 0.221 0.215 , 0.218	Depositor DCC
$R_{free}$ test set	24978 reflections (1.02%)	DCC
Wilson B-factor (Å <sup>2</sup> )	36.1	Xtriage
Anisotropy	0.126	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 53.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.045 for h-l,h,h-k 0.045 for k,k-l,-h+k 0.046 for -k,-h,-l 0.046 for -h+l,-k+l,l 0.046 for k-l,h-l,-l 0.046 for -h,-h+l,-h+k 0.046 for -k+l,-k,h-k	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	17851	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.43	0/4244	0.67	0/5816
1	B	0.44	0/4297	0.67	0/5889
1	C	0.42	0/4627	0.65	0/6324
1	D	0.43	0/4602	0.68	0/6296
All	All	0.43	0/17770	0.67	0/24325

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 [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4134	0	3987	189	0
1	B	4187	0	4021	175	0
1	C	4519	0	4389	169	0
1	D	4491	0	4363	154	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	97	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	127	0	0	5	0
3	C	148	0	0	2	0
3	D	144	0	0	4	0
All	All	17851	0	16760	643	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 19.

The worst 5 of 643 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:A:428:PRO:HB2	1:A:434:THR:HG22	1.34	1.08
1:A:175:ILE:HD11	1:A:429:LEU:HB3	1.37	1.06
1:B:342:THR:HG22	1:B:368:VAL:HG22	1.35	1.04
1:B:269:PRO:HB3	1:B:424:VAL:HG13	1.39	0.99
1:A:329:HIS:CE1	1:A:373:GLN:HE22	1.79	0.98

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	A	535/644 (83%)	495 (92%)	37 (7%)	3 (1%)	28	62
1	B	543/644 (84%)	500 (92%)	36 (7%)	7 (1%)	14	41
1	C	580/644 (90%)	552 (95%)	22 (4%)	6 (1%)	18	50
1	D	581/644 (90%)	540 (93%)	33 (6%)	8 (1%)	13	39
All	All	2239/2576 (87%)	2087 (93%)	128 (6%)	24 (1%)	17	47

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	589	SER
1	D	139	SER
1	D	615	PRO
1	D	640	ARG
1	A	200	GLY

### 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	450/527 (85%)	415 (92%)	35 (8%)	15	39
1	B	454/527 (86%)	421 (93%)	33 (7%)	16	42
1	C	486/527 (92%)	459 (94%)	27 (6%)	25	57
1	D	484/527 (92%)	451 (93%)	33 (7%)	18	47
All	All	1874/2108 (89%)	1746 (93%)	128 (7%)	18	47

5 of 128 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	424	VAL
1	C	86	GLN
1	D	495	ARG
1	B	504	THR
1	B	568	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 52 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	479	ASN
1	C	329	HIS
1	D	533	ASN
1	C	86	GLN
1	C	275	ASN

### 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](#)

Of 4 ligands modelled in this entry, 4 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	539/644 (83%)	-0.76	5 (0%) 84 79	19, 35, 71, 129	0
1	B	547/644 (84%)	-0.73	11 (2%) 65 56	20, 34, 77, 143	0
1	C	590/644 (91%)	-0.80	9 (1%) 74 67	20, 33, 69, 122	0
1	D	587/644 (91%)	-0.80	8 (1%) 75 69	19, 32, 70, 162	0
All	All	2263/2576 (87%)	-0.77	33 (1%) 74 67	19, 34, 74, 162	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	44	ASP	4.8
1	C	42	ASN	4.3
1	C	139	SER	4.2
1	A	599	LEU	4.0
1	D	591	ALA	3.5

### 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	MG	A	1645	1/1	0.94	0.06	-	43,43,43,43	0
2	MG	C	1645	1/1	0.96	0.21	-	40,40,40,40	0
2	MG	B	1645	1/1	0.86	0.09	-	24,24,24,24	0
2	MG	D	1645	1/1	0.98	0.05	-	25,25,25,25	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.