



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 01:05 AM GMT

PDB ID : 3W3C  
Title : Crystal structure of VirB core domain complexed with the cis-acting site upstream icsb promoter  
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Deposited on : 2012-12-19  
Resolution : 2.43 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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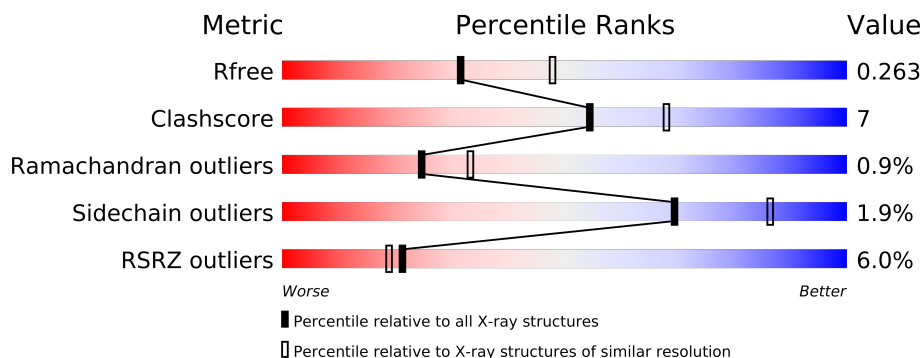
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.43 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))
$R_{free}$	66092	2989 (2.48-2.40)
Clashscore	79885	3698 (2.48-2.40)
Ramachandran outliers	78287	3639 (2.48-2.40)
Sidechain outliers	78261	3640 (2.48-2.40)
RSRZ outliers	66119	2993 (2.48-2.40)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	143	
2	B	26	
3	C	26	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3033 atoms, of which 972 are hydrogens and 0 are deuterium.

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 Virulence regulon transcriptional activator VirB.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	116	1903	601	972	153	176	1	12	0	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	108	MET	-	EXPRESSION TAG	UNP P0A247
A	109	GLY	-	EXPRESSION TAG	UNP P0A247
A	110	SER	-	EXPRESSION TAG	UNP P0A247
A	111	SER	-	EXPRESSION TAG	UNP P0A247
A	112	HIS	-	EXPRESSION TAG	UNP P0A247
A	113	HIS	-	EXPRESSION TAG	UNP P0A247
A	114	HIS	-	EXPRESSION TAG	UNP P0A247
A	115	HIS	-	EXPRESSION TAG	UNP P0A247
A	116	HIS	-	EXPRESSION TAG	UNP P0A247
A	117	HIS	-	EXPRESSION TAG	UNP P0A247
A	118	SER	-	EXPRESSION TAG	UNP P0A247
A	119	SER	-	EXPRESSION TAG	UNP P0A247
A	120	GLY	-	EXPRESSION TAG	UNP P0A247
A	121	LEU	-	EXPRESSION TAG	UNP P0A247
A	122	VAL	-	EXPRESSION TAG	UNP P0A247
A	123	PRO	-	EXPRESSION TAG	UNP P0A247
A	124	ARG	-	EXPRESSION TAG	UNP P0A247
A	125	GLY	-	EXPRESSION TAG	UNP P0A247
A	126	SER	-	EXPRESSION TAG	UNP P0A247
A	127	HIS	-	EXPRESSION TAG	UNP P0A247
A	128	MET	-	EXPRESSION TAG	UNP P0A247

- Molecule 2 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	26	Total	C	N	O	P	0	0	0
			538	258	99	156	25			

- Molecule 3 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	26	Total	C	N	O	P	0	0	0
			522	252	93	152	25			

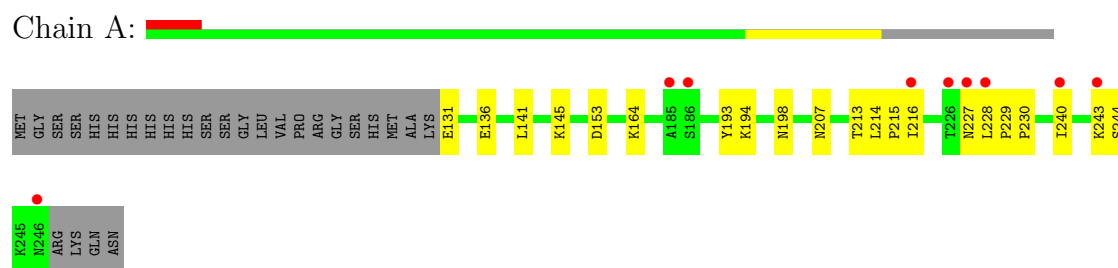
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	37	Total	O	0	0
			37	37		
4	B	19	Total	O	0	0
			19	19		
4	C	14	Total	O	0	0
			14	14		

### 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 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: Virulence regulon transcriptional activator VirB



- Molecule 2: DNA (26-MER)



- Molecule 3: DNA (26-MER)



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.14Å 163.40Å 39.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.85 – 2.43 40.85 – 2.43	Depositor EDS
% Data completeness (in resolution range)	96.3 (40.85-2.43) 96.5 (40.85-2.43)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.34 (at 2.42Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.264 , 0.280 0.249 , 0.263	Depositor DCC
$R_{free}$ test set	694 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	47.9	Xtriage
Anisotropy	0.501	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 32.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	4 of 13927 reflections (0.029%)	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	3033	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.74 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 8.1469e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

## 5 Model quality

### 5.1 Standard geometry

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	0.22	0/946	0.35	0/1271
2	B	0.42	0/604	1.06	1/933 (0.1%)
3	C	0.43	0/584	1.05	1/897 (0.1%)
All	All	0.35	0/2134	0.84	2/3101 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	B	4	DG	O4'-C4'-C3'	-5.80	102.18	104.50
3	C	2	DA	C3'-C2'-C1'	-5.50	95.89	102.50

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	931	972	0	13	1
2	B	538	0	0	4	0
3	C	522	0	0	5	0
4	A	37	0	0	6	1
4	B	19	0	0	1	0
4	C	14	0	0	1	0
All	All	2061	972	0	20	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

All (20) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:244:SER:OG	4:A:304:HOH:O	2.04	0.76
3:C:15:DA:N3	4:C:111:HOH:O	2.21	0.73
1:A:131:GLU:N	1:A:136:GLU:OE2	2.22	0.73
2:B:20:DA:N6	4:B:114:HOH:O	2.21	0.72
1:A:193:TYR:OH	4:A:325:HOH:O	2.13	0.64
1:A:198:ASN:ND2	4:A:321:HOH:O	2.29	0.62
1:A:228:LEU:N	1:A:229:PRO:CD	2.63	0.61
1:A:214:LEU:N	1:A:215:PRO:CD	2.69	0.56
3:C:8:DT:C2'	3:C:9:DT:O5'	2.59	0.51
1:A:164:LYS:NZ	3:C:16:DT:OP2	2.45	0.50
2:B:3:DT:C2'	2:B:4:DG:C5'	2.89	0.50
1:A:213:THR:O	1:A:216:ILE:HG22	2.12	0.49
1:A:240:ILE:HA	1:A:243:LYS:HG2	1.95	0.48
1:A:194:LYS:NZ	4:A:327:HOH:O	2.31	0.47
1:A:227:ASN:N	1:A:227:ASN:OD1	2.49	0.46
1:A:194:LYS:NZ	4:A:316:HOH:O	2.47	0.45
2:B:3:DT:C1'	2:B:4:DG:C5'	2.95	0.44
1:A:145:LYS:HE3	4:A:317:HOH:O	2.19	0.42
2:B:16:DG:N2	3:C:15:DA:C2	2.88	0.41
3:C:7:DG:C5	3:C:8:DT:C4	3.09	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:153:ASP:OD2	4:A:320:HOH:O[4_447]	1.96	0.24

## 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	114/143 (80%)	110 (96%)	3 (3%)	1 (1%)	25 33



All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	230	PRO

### 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	105/128 (82%)	103 (98%)	2 (2%)	69 86

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	141	LEU
1	A	207	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	142	ASN
1	A	170	GLN
1	A	191	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 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, 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	116/143 (81%)	0.52	9 (7%) 13 11	21, 43, 98, 118	1 (0%)
2	B	26/26 (100%)	0.39	1 (3%) 38 36	24, 62, 114, 117	0
3	C	26/26 (100%)	0.37	0 100 100	29, 70, 117, 122	0
All	All	168/195 (86%)	0.47	10 (5%) 21 19	21, 45, 110, 122	1 (0%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	226	THR	4.9
1	A	185	ALA	3.4
1	A	246	ASN	3.0
1	A	228	LEU	2.9
1	A	243	LYS	2.9
1	A	186	SER	2.7
1	A	240	ILE	2.6
1	A	227	ASN	2.5
2	B	26	DG	2.2
1	A	216	ILE	2.1

### 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 carbohydrates in this entry.

## 6.4 Ligands

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.