



# Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 07:20 AM GMT

PDB ID : 3VDM  
Title : Crystal Structure of VldE, the pseudo-glycosyltransferase which catalyzes non-glycosidic C-N coupling in Validamycin A biosynthesis  
Authors : Cavalier, M.C.; Yim, Y.-S.; Asamizu, S.; Neau, D.; Mahmud, T.; Lee, Y.-H.  
Deposited on : 2012-01-05  
Resolution : 1.98 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>

---

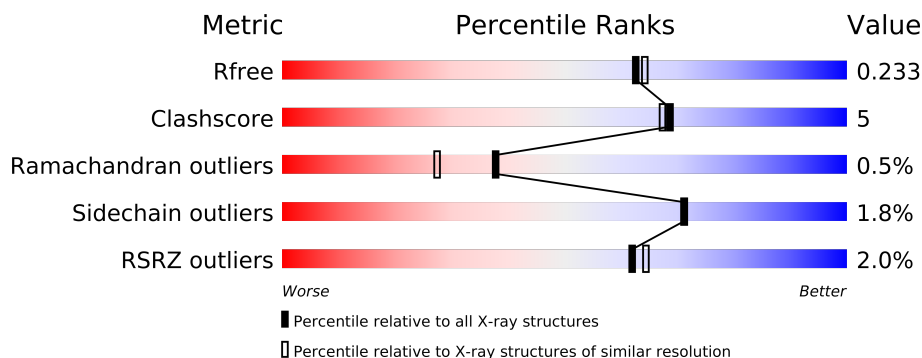
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.98 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	6577 (2.00-1.96)
Clashscore	79885	8091 (2.00-1.96)
Ramachandran outliers	78287	7989 (2.00-1.96)
Sidechain outliers	78261	7987 (2.00-1.96)
RSRZ outliers	66119	6578 (2.00-1.96)

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	497	
1	B	497	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7963 atoms, of which 0 are hydrogen 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 VldE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	479	Total	C	N	O	S	0	0	0
			3739	2336	691	700	12			
1	B	478	Total	C	N	O	S	0	0	0
			3735	2334	690	699	12			

- Molecule 2 is water.

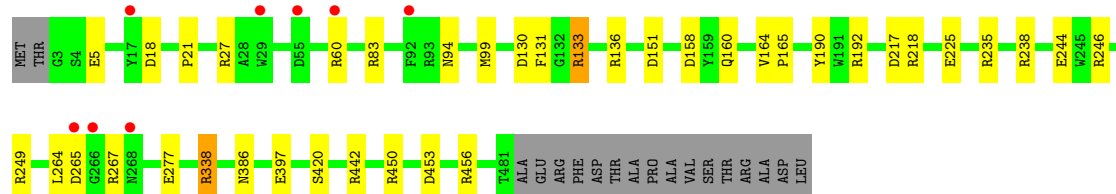
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	245	Total	O	0	0
			245	245		
2	B	244	Total	O	0	0
			244	244		

### 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.

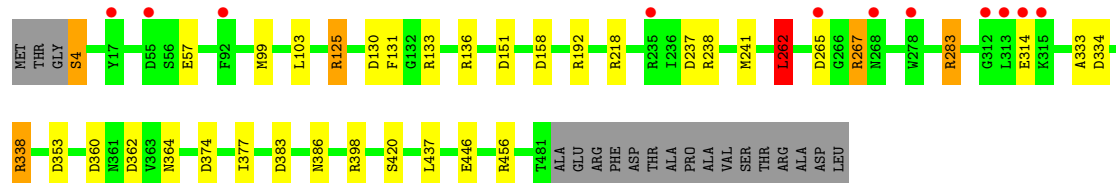
#### • Molecule 1: VldE

Chain A: 



#### • Molecule 1: VldE

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	85.24Å 48.56Å 123.05Å 90.00° 91.88° 90.00°	Depositor
Resolution (Å)	49.10 – 1.98 49.10 – 1.98	Depositor EDS
% Data completeness (in resolution range)	98.8 (49.10-1.98) 98.7 (49.10-1.98)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.38 (at 1.98Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, $R_{free}$	0.188 , 0.222 0.201 , 0.233	Depositor DCC
$R_{free}$ test set	3559 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	39.1	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 30.8	EDS
Estimated twinning fraction	0.166 for h,-k,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 70107 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7963	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.12% of the height of the origin peak. No significant pseudotranslation is detected.*

<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	1.09	6/3826 (0.2%)	0.95	9/5216 (0.2%)
1	B	1.03	5/3822 (0.1%)	0.96	7/5211 (0.1%)
All	All	1.06	11/7648 (0.1%)	0.95	16/10427 (0.2%)

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	267	ARG	CZ-NH1	-7.32	1.23	1.33
1	A	420	SER	CB-OG	6.57	1.50	1.42
1	B	192	ARG	CB-CG	-6.44	1.35	1.52
1	A	192	ARG	CZ-NH2	-6.41	1.24	1.33
1	B	192	ARG	CZ-NH2	-5.91	1.25	1.33
1	B	333	ALA	CA-CB	5.82	1.64	1.52
1	A	218	ARG	CG-CD	5.61	1.66	1.51
1	B	314	GLU	CG-CD	5.57	1.60	1.51
1	A	267	ARG	CZ-NH2	5.55	1.40	1.33
1	B	218	ARG	CG-CD	5.34	1.65	1.51
1	A	190	TYR	CB-CG	-5.16	1.44	1.51

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	338	ARG	NE-CZ-NH2	-15.53	112.53	120.30
1	A	192	ARG	NE-CZ-NH1	14.71	127.65	120.30
1	B	192	ARG	NE-CZ-NH1	12.71	126.66	120.30
1	B	192	ARG	NE-CZ-NH2	-12.56	114.02	120.30
1	A	338	ARG	NE-CZ-NH2	-11.65	114.47	120.30
1	A	192	ARG	NE-CZ-NH2	-8.70	115.95	120.30
1	B	262	LEU	CA-CB-CG	7.96	133.62	115.30
1	A	133	ARG	NE-CZ-NH1	6.87	123.74	120.30
1	A	450	ARG	NE-CZ-NH1	6.63	123.61	120.30
1	A	267	ARG	NE-CZ-NH1	5.41	123.00	120.30
1	A	133	ARG	NE-CZ-NH2	-5.37	117.62	120.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	217	ASP	CB-CG-OD1	5.35	123.12	118.30
1	B	338	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	B	237	ASP	CB-CG-OD1	5.23	123.01	118.30
1	A	338	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	B	283	ARG	NE-CZ-NH1	-5.20	117.70	120.30

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	3739	0	0	19	0
1	B	3735	0	0	17	0
2	A	245	0	0	10	0
2	B	244	0	0	8	0
All	All	7963	0	0	36	0

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 5.

All (36) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:4:SER:N	2:B:736:HOH:O	1.85	1.07
1:A:249:ARG:NH1	2:A:601:HOH:O	2.05	0.88
1:A:456:ARG:NH1	2:A:691:HOH:O	2.09	0.86
1:B:125:ARG:NH1	2:B:679:HOH:O	2.10	0.83
1:A:338:ARG:NH2	2:A:600:HOH:O	2.23	0.71
1:B:130:ASP:OD1	1:B:133:ARG:NH1	2.35	0.59
1:A:94:ASN:ND2	1:A:130:ASP:OD2	2.36	0.58
1:B:4:SER:CA	2:B:736:HOH:O	2.45	0.57
1:B:446:GLU:OE1	2:B:713:HOH:O	2.18	0.55
1:B:267:ARG:NH2	1:B:364:ASN:OD1	2.40	0.55
1:B:377:ILE:O	2:B:698:HOH:O	2.18	0.54

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:130:ASP:OD1	1:A:133:ARG:NH1	2.40	0.54
1:B:374:ASP:OD2	1:B:398:ARG:NE	2.41	0.53
1:A:83:ARG:NE	2:A:723:HOH:O	2.41	0.53
1:A:5:GLU:N	2:A:663:HOH:O	2.44	0.50
1:A:453:ASP:OD1	1:A:456:ARG:NH2	2.44	0.50
1:A:246:ARG:N	2:A:649:HOH:O	2.45	0.50
1:B:136:ARG:NE	2:B:557:HOH:O	2.45	0.49
1:B:456:ARG:NH2	2:B:729:HOH:O	2.46	0.47
1:B:99:MET:CE	1:B:131:PHE:CE1	2.97	0.47
1:A:235:ARG:N	1:A:235:ARG:CD	2.78	0.46
1:A:18:ASP:O	1:A:27:ARG:N	2.49	0.46
1:B:360:ASP:OD1	1:B:362:ASP:N	2.49	0.46
1:A:160:GLN:NE2	2:A:742:HOH:O	2.48	0.46
1:A:277:GLU:CG	2:A:516:HOH:O	2.64	0.45
1:A:397:GLU:N	2:A:563:HOH:O	2.51	0.44
1:B:283:ARG:NH1	1:B:437:LEU:O	2.50	0.44
1:A:136:ARG:NH1	2:A:561:HOH:O	2.50	0.44
1:A:442:ARG:CG	1:A:442:ARG:NH1	2.83	0.42
1:B:262:LEU:O	1:B:265:ASP:N	2.53	0.42
1:B:57:GLU:N	2:B:741:HOH:O	2.53	0.42
1:A:164:VAL:N	1:A:165:PRO:CD	2.83	0.41
1:B:334:ASP:OD2	1:B:338:ARG:CD	2.68	0.41
1:A:99:MET:CE	1:A:131:PHE:CE1	3.04	0.41
1:A:225:GLU:OE2	1:A:238:ARG:NE	2.54	0.40
1:B:238:ARG:O	1:B:241:MET:CE	2.70	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	477/497 (96%)	467 (98%)	8 (2%)	2 (0%)	43	34
1	B	476/497 (96%)	464 (98%)	9 (2%)	3 (1%)	33	23
All	All	953/994 (96%)	931 (98%)	17 (2%)	5 (0%)	38	27

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	386	ASN
1	B	158	ASP
1	A	158	ASP
1	A	386	ASN
1	B	103	LEU

### 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	381/395 (96%)	375 (98%)	6 (2%)	75	75
1	B	381/395 (96%)	373 (98%)	8 (2%)	66	65
All	All	762/790 (96%)	748 (98%)	14 (2%)	71	71

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	PRO
1	A	60	ARG
1	A	151	ASP
1	A	244	GLU
1	A	264	LEU
1	A	265	ASP
1	B	4	SER
1	B	125	ARG
1	B	151	ASP
1	B	262	LEU
1	B	267	ARG
1	B	353	ASP
1	B	383	ASP
1	B	420	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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	479/497 (96%)	0.26	8 (1%) 67 69	24, 40, 65, 96	0
1	B	478/497 (96%)	0.26	11 (2%) 57 60	23, 41, 65, 90	0
All	All	957/994 (96%)	0.26	19 (1%) 62 64	23, 40, 65, 96	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	266	GLY	5.9
1	B	265	ASP	4.4
1	B	314	GLU	4.4
1	A	60	ARG	4.2
1	B	268	ASN	4.1
1	B	312	GLY	4.0
1	A	265	ASP	3.5
1	B	92	PHE	3.3
1	A	29	TRP	3.3
1	A	92	PHE	3.3
1	B	55	ASP	3.1
1	A	55	ASP	3.0
1	A	268	ASN	2.9
1	B	315	LYS	2.5
1	B	313	LEU	2.4
1	B	278	TRP	2.4
1	A	17	TYR	2.3
1	B	17	TYR	2.2
1	B	235	ARG	2.0

### 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.