

# Full wwPDB X-ray Structure Validation Report (i)

#### Sep 13, 2020 – 11:36 AM BST

PDB ID : 3LKV

Title : Crystal structure of conserved domain protein from vibrio cholerae o1 biovar

eltor str. n16961

Authors: Nocek, B.; Duggan, E.; Abdullah, J.; Joachimiak, A.; Midwest Center for

Structural Genomics (MCSG)

Deposited on : 2010-01-27

Resolution : 2.20 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
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : FAILED

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

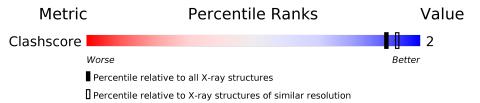
Validation Pipeline (wwPDB-VP) : 2.14.4.dev1

### 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	Similar resolution		
Metric	$(\#  ext{Entries})$	$(\#  ext{Entries},  ext{resolution range}( ext{Å}))$		
Clashscore	141614	5594 (2.20-2.20)		

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 respectively. 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 <=5%

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain				
1	A	302	93%	5% •			



## 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 2310 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.

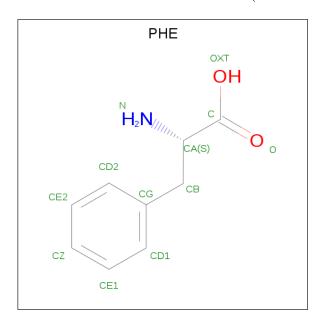
• Molecule 1 is a protein called uncharacterized CONSERVED DOMAIN PROTEIN.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	296	Total	С	N	О	Se	0	0	0
			2173	1379	362	430	2			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	SER	-	expression tag	UNP Q9KT04
A	21	ASN	-	expression tag	UNP Q9KT04
A	22	ALA	-	expression tag	UNP Q9KT04

• Molecule 2 is PHENYLALANINE (three-letter code: PHE) (formula: C<sub>9</sub>H<sub>11</sub>NO<sub>2</sub>).



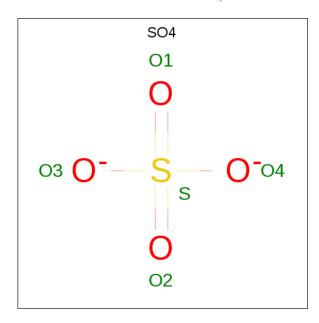
$\mid N$	Iol	Chain	Residues	Atoms				ZeroOcc	AltConf
	2	A	1	Total	С	N	0	0	0



• Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

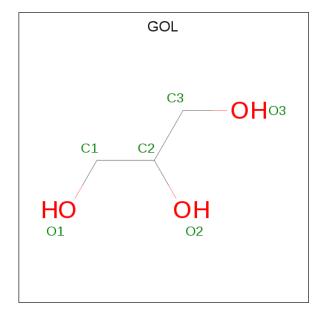
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	3	Total Zn 3 3	0	0

 $\bullet$  Molecule 4 is SULFATE ION (three-letter code: SO4) (formula:  $\mathrm{O_4S}).$ 



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
4	A	1	Total 5	O 4	S 1	0	0

• Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
5	A	1	Total 6	C 3	O 3	0	0

### • Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	111	Total O 111 111	0	0

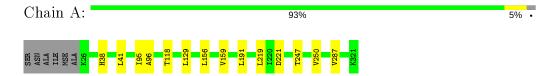


## 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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. 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. 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.

Note EDS failed to run properly.

• Molecule 1: uncharacterized CONSERVED DOMAIN PROTEIN





## 4 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 41 3 2	Depositor
Cell constants	144.26Å 144.26Å 144.26Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 - 2.20	Depositor
% Data completeness	94.4 (40.00-2.20)	Depositor
(in resolution range)	34.4 (40.00-2.20)	Depositor
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$7.56 \; ({\rm at} \; 2.20 {\rm \AA})$	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
$R, R_{free}$	0.178 , $0.203$	Depositor
Wilson B-factor (Å <sup>2</sup> )	34.6	Xtriage
Anisotropy	0.000	Xtriage
L-test for twinning <sup>2</sup>	$ < L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2310	wwPDB-VP
Average B, all atoms $(\mathring{A}^2)$	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.32% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $< L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

## 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: GOL, ZN, SO4

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).

Mal	Chain	Bond	lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z >5	RMSZ	# Z  > 5	
1	A	0.96	0/2199	0.81	0/2990	

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	2173	0	2248	8	0
2	A	12	0	8	1	0
3	A	3	0	0	0	0
4	A	5	0	0	0	0
5	A	6	0	8	0	0
6	A	111	0	0	0	0
All	All	2310	0	2264	8	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 2.

All (8) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${f distance}({ m \AA})$	overlap $( m \AA)$
1:A:247:THR:O	1:A:250:VAL:HG12	1.93	0.68
1:A:118:THR:HG1	2:A:601:PHE:N	2.05	0.53
1:A:156:LEU:O	1:A:159:VAL:HG23	2.09	0.53
1:A:38:HIS:CE1	1:A:41:LEU:HG	2.48	0.48
1:A:129:LEU:HD22	1:A:287:VAL:HG11	1.97	0.47
1:A:219:LEU:CD1	1:A:221:ASP:HB2	2.46	0.45
1:A:95:ILE:O	1:A:96:ALA:HB3	2.17	0.44
1:A:191:LEU:HA	1:A:191:LEU:HD23	1.88	0.40

There are no symmetry-related clashes.

#### 5.3 Torsion angles (i)

#### 5.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

#### 5.3.2 Protein sidechains (i)

There are no protein residues with a non-rotameric sidechain to report in this entry.

#### 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 monosaccharides in this entry.

### 5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and



the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Mol Type Chain Res			Link	Bond lengths			Bond angles		
MIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	PHE	A	601	-	9,12,12	1.12	1 (11%)	10,15,15	0.55	0
5	GOL	A	1001	-	5,5,5	0.55	0	5,5,5	0.69	0
4	SO4	A	501	-	4,4,4	0.22	0	6,6,6	0.28	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PHE	A	601	_	-	0/4/8/8	0/1/1/1
5	GOL	A	1001	_	-	2/4/4/4	-

#### All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
2	A	601	PHE	CA-N	2.29	1.52	1.47

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	$\operatorname{Res}$	Type	Atoms
5	A	1001	GOL	C1-C2-C3-O3
5	A	1001	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	PHE	1	0



## 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)

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

#### 6.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

#### 6.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

### 6.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.

