

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

#### Sep 13, 2023 – 03:02 AM EDT

PDB ID : 4OD7

Title: Complex structure of Proteus mirablis DsbA (C30S) with a non-covalently

bound peptide PWATCDS

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Deposited on : 2014-01-10

Resolution : 1.60 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
A user guide is available at

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

 $Mol Probity \quad : \quad 4.02b\text{--}467$ 

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

Xtriage (Phenix) : 1.13 EDS : 2.35.1

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

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

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

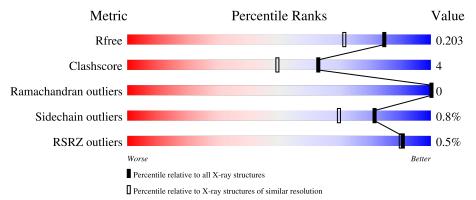
Validation Pipeline (wwPDB-VP) : 2.35.1

# 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 1.60 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{\rm A})}) \end{array}$
$R_{free}$	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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 of 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% 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	190	94%	5	5% •
1	В	190	85%	13%	
1	С	190	83%	16%	•
2	D	9	78%	22%	
2	Е	9	100%		

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Mol	Chain	Length	Quality of chain	
2	F	9	89%	11%



# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9477 atoms, of which 4405 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 Thiol:disulfide interchange protein.

Mol	Chain	Residues		Atoms					ZeroOcc	AltConf	Trace
1 A	187	Total	С	Н	N	О	S	0	0	0	
	101	2839	913	1402	237	281	6				
1	1 B	187	Total	С	Н	N	О	S	0	1	0
1		101	2885	925	1429	240	285	6			
1	1 C	187	Total	С	Н	N	О	S	0	0	0
1			2884	923	1430	240	285	6			

There are 12 discrepancies between the modelled and reference sequences:

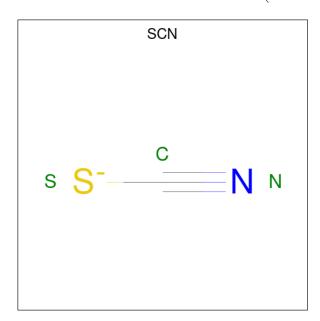
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP B4EZ68
A	0	ASN	-	expression tag	UNP B4EZ68
A	1	ALA	-	expression tag	UNP B4EZ68
A	30	SER	CYS	engineered mutation	UNP B4EZ68
В	-1	SER	-	expression tag	UNP B4EZ68
В	0	ASN	-	expression tag	UNP B4EZ68
В	1	ALA	-	expression tag	UNP B4EZ68
В	30	SER	CYS	engineered mutation	UNP B4EZ68
С	-1	SER	-	expression tag	UNP B4EZ68
С	0	ASN	-	expression tag	UNP B4EZ68
С	1	ALA	-	expression tag	UNP B4EZ68
С	30	SER	CYS	engineered mutation	UNP B4EZ68

• Molecule 2 is a protein called (ACE)PWATCDS(NH2) Peptide.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	D	9	Total 105		H 48			S 1	0	0	1
2	Е	9	Total 105		H 48			S 1	0	0	1
2	F	9	Total 105		H 48		O 12	S 1	0	0	1



• Molecule 3 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	А	1	Total	С	N	S	0	0	
<i>J</i> 11	1	3	1	1	1	U			
3	Δ	1	Total	$\mathbf{C}$	Ν	S	0	0	
3	3 A	1	3	1	1	1	0		
3	C	1	Total	С	N	S	0	0	
3		1	3	1	1	1	0	U	
3	С	1	Total	С	N	S	0	0	
3			3	1	1	1		U	

• Molecule 4 is water.

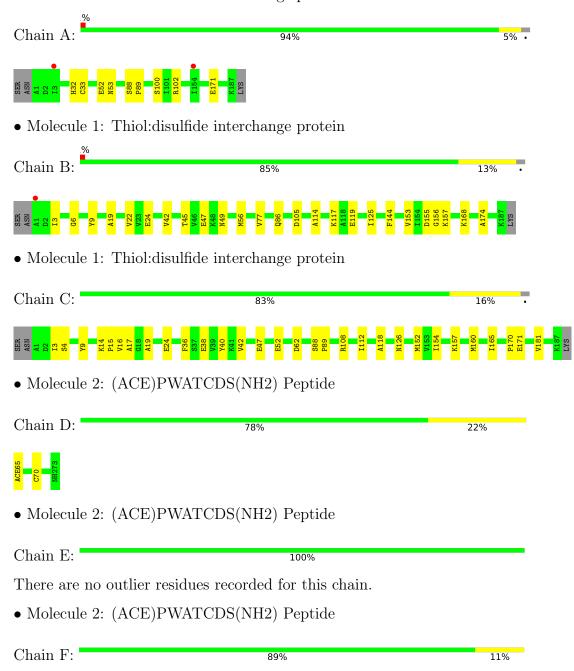
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	161	Total O 161 161	0	0
4	В	171	Total O 171 171	0	0
4	С	173	Total O 173 173	0	0
4	D	11	Total O 11 11	0	0
4	Е	10	Total O 10 10	0	0
4	F	16	Total O 16 16	0	0



# 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 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: Thiol:disulfide interchange protein









# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants	74.06Å 74.06Å 93.27Å	D t
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	37.72 - 1.60	Depositor
Resolution (A)	52.85 - 1.60	EDS
% Data completeness	98.6 (37.72-1.60)	Depositor
(in resolution range)	98.6 (52.85-1.60)	EDS
$R_{merge}$	0.08	Depositor
$R_{sum}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.28 (at 1.60Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
υ .	0.172 , 0.200	Depositor
$R, R_{free}$	0.175 , $0.203$	DCC
$R_{free}$ test set	3765  reflections  (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.7	Xtriage
Anisotropy	0.330	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.36, 38.0	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.45, < L^2> = 0.27$	Xtriage
	0.046 for -h,-k,l	
Estimated twinning fraction	0.488  for h,-h-k,-l	Xtriage
	0.046  for -k,-h,-l	
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	9477	wwPDB-VP
Average B, all atoms $(\mathring{A}^2)$	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.02% 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: SCN, NH2, ACE

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	Bo	nd lengths	Bond angles		
IVIOI		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.78	$1/1466 \ (0.1\%)$	0.75	0/1989	
1	В	0.79	0/1488	0.78	0/2017	
1	С	0.77	0/1483	0.77	1/2010 (0.0%)	
2	D	1.57	$2/56 \ (3.6\%)$	0.75	0/78	
2	Е	0.87	0/56	0.78	0/78	
2	F	1.10	1/56 (1.8%)	0.60	0/78	
All	All	0.80	4/4605 (0.1%)	0.76	$1/6250 \ (0.0\%)$	

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	Observed(A)	$\operatorname{Ideal}( ext{\AA})$
2	D	65	ACE	C-N	9.30	1.51	1.34
2	F	65	ACE	C-N	6.38	1.46	1.34
1	A	33	CYS	CB-SG	-5.21	1.73	1.81
2	D	70	CYS	CB-SG	-5.07	1.73	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
1	С	62	ASP	CB-CG-OD1	5.70	123.43	118.30

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



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1437	1402	1402	6	0
1	В	1456	1429	1432	17	1
1	С	1454	1430	1430	17	0
2	D	57	48	46	0	0
2	Е	57	48	46	0	0
2	F	57	48	46	0	0
3	A	6	0	0	1	0
3	С	6	0	0	0	0
4	A	161	0	0	0	0
4	В	171	0	0	0	0
4	С	173	0	0	3	1
4	D	11	0	0	0	0
4	Е	10	0	0	0	0
4	F	16	0	0	0	0
All	All	5072	4405	4402	38	1

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 4.

The worst 5 of 38 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	Clash overlap (Å)
1:B:155:ASP:HB3	1:B:157:LYS:HE2	1.64	0.80
1:A:171:GLU:OE1	1:A:171:GLU:N	2.26	0.67
1:C:17:ALA:N	4:C:431:HOH:O	2.31	0.61
1:C:108:ARG:NH2	1:C:118:ALA:HB1	2.18	0.58
1:C:15:PRO:HB3	1:C:157:LYS:HG2	1.87	0.56

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	$egin{aligned}  ext{Interatomic} \  ext{distance} \ ( ext{Å}) \end{aligned}$	Clash overlap (Å)
1:B:105:ASP:OD2	4:C:404:HOH:O[1_665]	2.19	0.01



### 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	Perce	entiles
1	A	185/190~(97%)	183 (99%)	2 (1%)	0	100	100
1	В	186/190 (98%)	184 (99%)	2 (1%)	0	100	100
1	С	185/190~(97%)	183 (99%)	2 (1%)	0	100	100
2	D	7/9~(78%)	7 (100%)	0	0	100	100
2	E	7/9 (78%)	7 (100%)	0	0	100	100
2	F	7/9 (78%)	7 (100%)	0	0	100	100
All	All	577/597 (97%)	571 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.

#### 5.3.2 Protein sidechains (i)

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	155/162~(96%)	155 (100%)	0	100	100	
1	В	159/162 (98%)	158 (99%)	1 (1%)	86	77	
1	С	159/162 (98%)	156 (98%)	3 (2%)	57	34	
2	D	6/6 (100%)	6 (100%)	0	100	100	
2	E	6/6 (100%)	6 (100%)	0	100	100	
2	F	6/6 (100%)	6 (100%)	0	100	100	
All	All	491/504 (97%)	487 (99%)	4 (1%)	81	70	



All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	168	LYS
1	С	4	SER
1	С	14	LYS
1	С	52	GLU

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

#### 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)

4 ligands are modelled in this entry.

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 Type (		Chain	Res	Res Link	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	SCN	С	201	-	1,2,2	0.23	0	0,1,1	-	-
3	SCN	A	202	-	1,2,2	0.99	0	0,1,1	-	-
3	SCN	С	202	-	1,2,2	0.79	0	0,1,1	-	-
3	SCN	A	201	-	1,2,2	1.19	0	0,1,1	-	-

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	202	SCN	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)

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,  $95^{th}$  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>	$\#\mathrm{RSRZ}{>}2$	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	A	187/190 (98%)	-0.20	2 (1%) 80 80	12, 22, 49, 76	0
1	В	187/190 (98%)	-0.35	1 (0%) 91 90	15, 22, 38, 60	0
1	С	187/190 (98%)	-0.24	0 100 100	12, 22, 46, 62	0
2	D	7/9 (77%)	-0.39	0 100 100	15, 17, 21, 24	0
2	E	7/9 (77%)	-0.51	0 100 100	16, 19, 21, 24	0
2	F	7/9 (77%)	-0.52	0 100 100	17, 18, 20, 21	0
All	All	582/597 (97%)	-0.27	3 (0%) 91 90	12, 22, 45, 76	0

#### All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	A	3	ILE	4.1	
1	В	1	ALA	3.1	
1	A	154	ILE	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 monosaccharides 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. The B-factors column lists the minimum,



median,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
3	SCN	A	202	3/3	0.97	0.09	21,21,22,23	0
3	SCN	С	202	3/3	0.97	0.08	24,24,25,26	0
3	SCN	A	201	3/3	0.98	0.07	12,12,18,25	0
3	SCN	С	201	3/3	0.99	0.09	16,16,17,20	0

# 6.5 Other polymers (i)

There are no such residues in this entry.

