



# Full wwPDB X-ray Structure Validation Report

Sep 18, 2014 – 11:10 AM EDT

PDB ID : 3WL7  
Title : The complex structure of pOPH S172C with ligand, ACA  
Authors : Yang, Y.; Ko, T.P.; Li, J.H.; Liu, L.; Huang, C.H.; Chan, H.C.; Ren, F.F.;  
Jia, D.X.; Wang, A.H.-J.; Guo, R.T.; Chen, J.; Du, G.C.  
Deposited on : 2013-11-08  
Resolution : 1.67 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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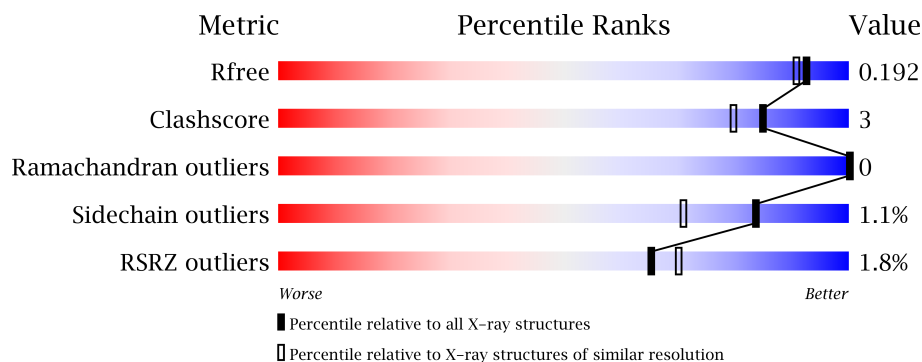
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.16 November 2013  
Xtriage (Phenix) : dev-1439  
EDS : stable23489  
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) : stable23489

# 1 Overall quality at a glance

The reported resolution of this entry is 1.67 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	3587 (1.70-1.66)
Clashscore	79885	4225 (1.70-1.66)
Ramachandran outliers	78287	4144 (1.70-1.66)
Sidechain outliers	78261	4143 (1.70-1.66)
RSRZ outliers	66119	3587 (1.70-1.66)

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	364	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	P2D	A	901	-	X
3	CIT	A	902	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2962 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.

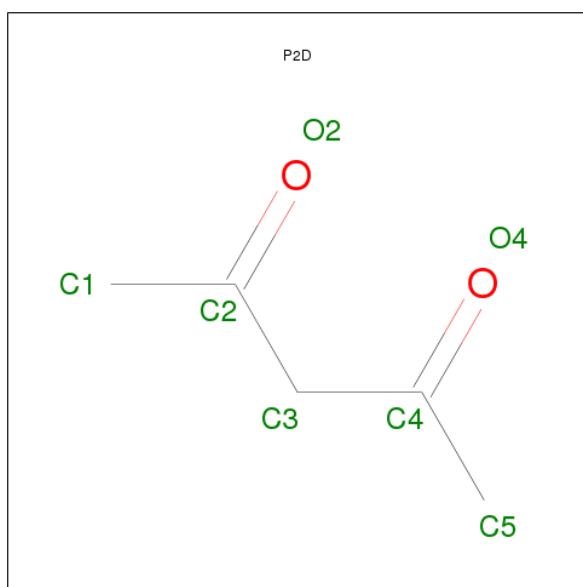
- Molecule 1 is a protein called Oxidized polyvinyl alcohol hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	336	2580	1630	457	478	15	0	0	0

There are 15 discrepancies between the modelled and reference sequences:

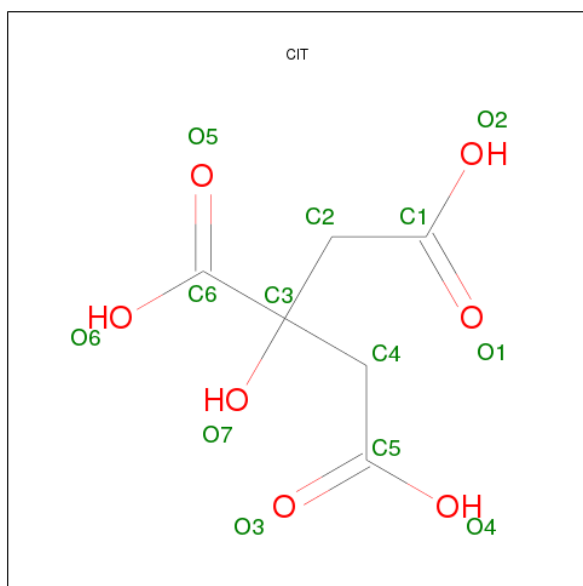
Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	ALA	-	EXPRESSION TAG	UNP Q9LCQ7
A	-3	GLY	-	EXPRESSION TAG	UNP Q9LCQ7
A	-2	ALA	-	EXPRESSION TAG	UNP Q9LCQ7
A	172	OCS	SER	ENGINEERED MUTATION	UNP Q9LCQ7
A	349	ALA	-	EXPRESSION TAG	UNP Q9LCQ7
A	350	SER	-	EXPRESSION TAG	UNP Q9LCQ7
A	351	ALA	-	EXPRESSION TAG	UNP Q9LCQ7
A	352	TRP	-	EXPRESSION TAG	UNP Q9LCQ7
A	353	SER	-	EXPRESSION TAG	UNP Q9LCQ7
A	354	HIS	-	EXPRESSION TAG	UNP Q9LCQ7
A	355	PRO	-	EXPRESSION TAG	UNP Q9LCQ7
A	356	GLN	-	EXPRESSION TAG	UNP Q9LCQ7
A	357	PHE	-	EXPRESSION TAG	UNP Q9LCQ7
A	358	GLU	-	EXPRESSION TAG	UNP Q9LCQ7
A	359	LYS	-	EXPRESSION TAG	UNP Q9LCQ7

- Molecule 2 is PENTANE-2,4-DIONE (three-letter code: P2D) (formula: C<sub>5</sub>H<sub>8</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			7	5	2		

- Molecule 3 is CITRIC ACID (three-letter code: CIT) (formula:  $C_6H_8O_7$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is water.

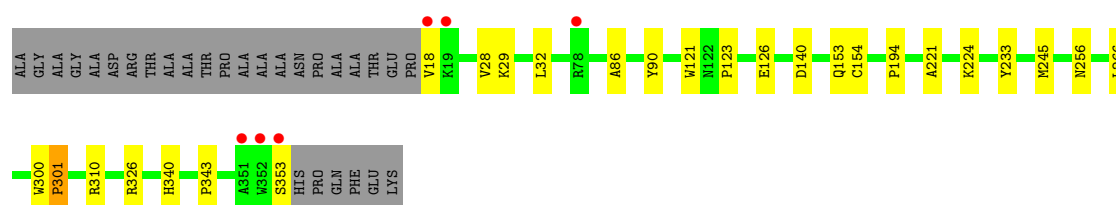
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	362	Total 362	O 362	0	0

### 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 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: Oxidized polyvinyl alcohol hydrolase

Chain A: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	58.60Å 65.53Å 84.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 1.67 24.07 – 1.67	Depositor EDS
% Data completeness (in resolution range)	(Not available) (25.00-1.67) 98.1 (24.07-1.67)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.73 (at 1.68Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.158 , 0.190 0.159 , 0.192	Depositor DCC
$R_{free}$ test set	1868 reflections (4.99%)	DCC
Wilson B-factor (Å <sup>2</sup> )	14.9	Xtriage
Anisotropy	0.481	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 38.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 37449 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2962	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.80% 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

Bond lengths and bond angles in the following residue types are not validated in this section: P2D, OCS, CIT

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	0.90	0/2656	0.94	2/3626 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	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( $^{\circ}$ )
1	A	310	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	A	140	ASP	CB-CG-OD1	5.13	122.92	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	233	TYR	Sidechain

### 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	2580	0	2431	14	0
2	A	7	0	0	0	0
3	A	13	0	5	0	0
4	A	362	0	0	4	0
All	All	2962	0	2436	14	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 3.

All (14) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:340:HIS:HD2	4:A:1342:HOH:O	1.80	0.63
1:A:326:ARG:NH2	4:A:1277:HOH:O	2.37	0.57
1:A:29:LYS:HE3	1:A:32:LEU:O	2.06	0.55
1:A:153:GLN:NE2	4:A:1040:HOH:O	2.39	0.54
1:A:221:ALA:HB1	1:A:224:LYS:HG2	1.90	0.53
1:A:121:TRP:CD1	1:A:123:PRO:HD2	2.44	0.52
1:A:18:VAL:N	4:A:1217:HOH:O	2.44	0.51
1:A:340:HIS:HE1	1:A:343:PRO:O	1.95	0.50
1:A:256:ASN:HD22	1:A:266:LEU:HA	1.79	0.48
1:A:86:ALA:HA	1:A:90:TYR:O	2.14	0.47
1:A:300:TRP:CD1	1:A:301:PRO:HD2	2.50	0.47
1:A:28:VAL:CG2	1:A:154:CYS:SG	3.04	0.46
1:A:194:PRO:HD2	1:A:245:MET:O	2.16	0.46
1:A:221:ALA:CB	1:A:224:LYS:HG2	2.48	0.44

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	333/364 (92%)	325 (98%)	8 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	269/285 (94%)	266 (99%)	3 (1%)	84	71

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	126	GLU
1	A	301	PRO
1	A	353	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	153	GLN
1	A	256	ASN
1	A	302	GLN
1	A	340	HIS

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
1	OCS	A	172	1	8,8,9	6.04	3 (37%)	9,11,13	3.19	4 (44%)

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
1	OCS	A	172	1	-	0/5/7/9	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	172	OCS	O-C	16.43	1.22	1.11
1	A	172	OCS	CB-SG	3.35	1.82	1.77
1	A	172	OCS	CA-C	2.41	1.54	1.49

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	172	OCS	C-CA-N	-7.19	106.65	113.83
1	A	172	OCS	OD3-SG-CB	-3.99	103.31	106.83
1	A	172	OCS	OD2-SG-CB	3.21	109.70	105.89
1	A	172	OCS	CA-CB-SG	3.14	119.68	113.37

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

2 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	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
2	P2D	A	901	-	6,6,6	0.97	0	7,7,7	0.78	0
3	CIT	A	902	-	12,12,12	2.48	5 (41%)	17,17,17	2.16	5 (29%)

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	P2D	A	901	-	-	0/4/4/4	0/0/0/0
3	CIT	A	902	-	-	0/16/16/16	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	902	CIT	O5-C6	4.58	1.37	1.22
3	A	902	CIT	O1-C1	3.75	1.35	1.22
3	A	902	CIT	C2-C3	3.67	1.58	1.53
3	A	902	CIT	C4-C3	2.82	1.57	1.53
3	A	902	CIT	C3-C6	2.34	1.55	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	902	CIT	O6-C6-C3	5.51	120.90	112.89
3	A	902	CIT	O5-C6-C3	-4.12	116.53	122.20
3	A	902	CIT	O7-C3-C4	2.84	114.97	109.25
3	A	902	CIT	C2-C3-C6	-2.74	103.78	110.12
3	A	902	CIT	O7-C3-C6	2.09	111.96	108.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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	336/364 (92%)	-0.28	6 (1%) 65 70	9, 14, 26, 47	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	353	SER	3.7
1	A	19	LYS	3.1
1	A	351	ALA	2.8
1	A	352	TRP	2.6
1	A	78	ARG	2.1
1	A	18	VAL	2.0

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

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	OCS	A	172	9/10	0.07	-1.15	10,13,16,21	0

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	P2D	A	901	7/7	0.16	6.73	32,34,36,37	0
3	CIT	A	902	13/13	0.16	2.10	19,23,33,35	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.