

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

#### Aug 17, 2022 – 03:03 PM EDT

PDB ID : 3WKB

Title : Crystal structure of soluble epoxide hydrolase in complex with fragment in-

hibitor

Authors: Amano, Y.; Yamaguchi, T.; Tanabe, E.

Deposited on : 2013-10-18

Resolution : 2.20 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:

MolProbity : 4.02b-467

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

Xtriage (Phenix) : 1.13 EDS : 2.29

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

Refmac : 5.8.0158

CCP4 : 7.0.044 (Gargrove)

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

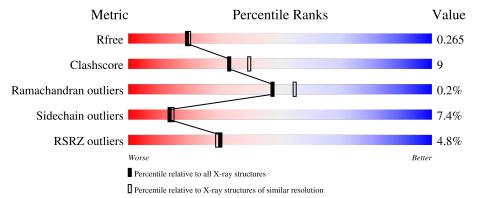
Validation Pipeline (wwPDB-VP) : 2.29

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY\ DIFFRACTION$ 

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	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (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 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		
			5%		
1	A	561	76%	19%	



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4417 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 Bifunctional epoxide hydrolase 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Λ	546	Total	С	N	О	S	0	0	0
1	A	040	4323	2771	728	788	36			U

There are 6 discrepancies between the modelled and reference sequences:

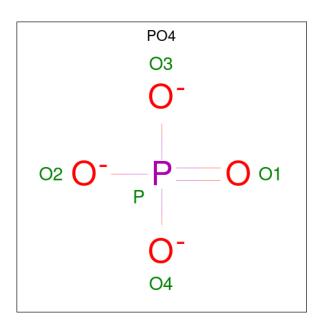
Chain	Residue	Modelled	Actual	Comment	Reference
A	556	HIS	-	expression tag	UNP P34913
A	557	HIS	-	expression tag	UNP P34913
A	558	HIS	-	expression tag	UNP P34913
A	559	HIS	_	expression tag	UNP P34913
A	560	HIS	-	expression tag	UNP P34913
A	561	HIS	-	expression tag	UNP P34913

• Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0

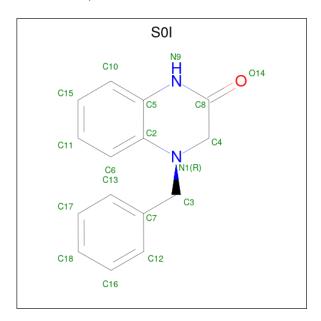
• Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).





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

 $\bullet$  Molecule 4 is 4-benzyl-3,4-dihydroquinoxalin-2(1H)-one (three-letter code: S0I) (formula:  $C_{15}H_{14}N_2O).$ 



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 18	C 15	N 2	O 1	0	0

• Molecule 5 is water.



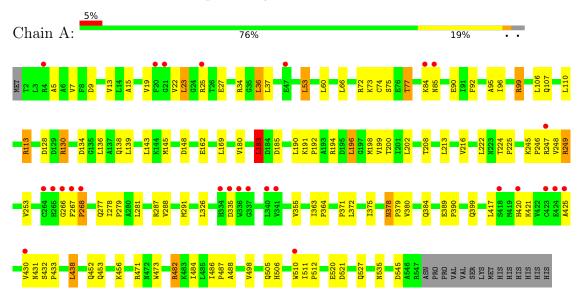
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	70	Total O 70 70	0	0



# 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: Bifunctional epoxide hydrolase 2





# 4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 65 2 2	Depositor	
Cell constants	92.46Å 92.46Å 245.01Å	Donogitor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor	
Resolution (Å)	28.59 - 2.20	Depositor	
resolution (A)	28.59 - 2.20	EDS	
% Data completeness	97.7 (28.59-2.20)	Depositor	
(in resolution range)	97.8 (28.59-2.20)	EDS	
$R_{merge}$	(Not available)	Depositor	
$R_{sym}$	(Not available)	Depositor	
$< I/\sigma(I) > 1$	9.09 (at 2.20Å)	Xtriage	
Refinement program	REFMAC 5.7.0029	Depositor	
P. P.	0.204 , 0.271	Depositor	
$R, R_{free}$	0.202 , $0.265$	DCC	
$R_{free}$ test set	1610 reflections (5.09%)	wwPDB-VP	
Wilson B-factor (Å <sup>2</sup> )	38.7	Xtriage	
Anisotropy	0.026	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.38, 41.3	EDS	
L-test for twinning <sup>2</sup>	$ < L > = 0.51, < L^2> = 0.34$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
$F_o, F_c$ correlation	0.95	EDS	
Total number of atoms	4417	wwPDB-VP	
Average B, all atoms $(Å^2)$	41.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.28% 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: PO4, S0I, MG

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	Во	ond angles
MIOI	ol $\mid$ Chain $\mid$ RN		# Z  > 5	RMSZ	# Z  > 5
1	A	0.87	1/4428 (0.0%)	1.04	$15/6000 \ (0.2\%)$

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 maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

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

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(\text{\AA})$
1	A	162	GLU	CD-OE2	5.35	1.31	1.25

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\mathrm{Ideal}(^{o})$
1	A	287	ARG	NE-CZ-NH2	16.82	128.71	120.30
1	A	287	ARG	NE-CZ-NH1	-14.26	113.17	120.30
1	A	482	ARG	NE-CZ-NH1	-10.37	115.11	120.30
1	A	482	ARG	NE-CZ-NH2	9.19	124.89	120.30
1	A	471	ARG	NE-CZ-NH2	8.16	124.38	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	291	MET	Peptide



## 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	4323	0	4329	73	0
2	A	1	0	0	0	0
3	A	5	0	0	0	0
4	A	18	0	14	3	0
5	A	70	0	0	3	0
All	All	4417	0	4343	75	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 9.

The worst 5 of 75 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned}  ext{Clash} \  ext{overlap } ( ext{Å}) \end{aligned}$	
4:A:603:S0I:H10	4:A:603:S0I:H7	1.51	0.91	
1:A:364:PRO:HG3	1:A:510:TRP:CE2	2.10	0.86	
1:A:180:VAL:CG1	1:A:198:MET:HE2	2.08	0.82	
1:A:73:LYS:O	1:A:77:THR:HG22	1.80	0.82	
1:A:190:LEU:HD22	1:A:200:THR:HB	1.63	0.81	

There are no symmetry-related clashes.

## 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	Percentiles	
1	A	544/561 (97%)	527 (97%)	16 (3%)	1 (0%)	47 55	



All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	268	PRO

#### 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	Analysed Rotameric		Percentiles	
1	A	472/487 (97%)	437 (93%)	35 (7%)	13 14	

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	438	LEU
1	A	452	GLN
1	A	520	GLU
1	A	113	ARG
1	A	110	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	420	HIS
1	A	452	GLN
1	A	535	ASN
1	A	506	HIS
1	A	384	GLN

#### 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 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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 Type	Chain	Chain	Dag	Link	Bo	Bond lengths			Bond angles		
MIOI	туре	Chain	Res	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
4	S0I	A	603	-	20,20,20	1.08	2 (10%)	23,27,27	2.55	7 (30%)	
3	PO4	A	602	2	4,4,4	1.16	1 (25%)	6,6,6	1.23	1 (16%)	

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
4	S0I	A	603	-	-	0/4/16/16	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	$\operatorname{Ideal}(\text{\AA})$
4	A	603	S0I	C8-N9	3.35	1.38	1.35
4	A	603	S0I	C4-C8	2.21	1.54	1.51
3	A	602	PO4	P-O4	-2.13	1.48	1.54

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
4	A	603	S0I	O14-C8-N9	-6.81	115.42	121.43
4	A	603	S0I	C10-C5-C2	4.28	124.22	118.83
4	A	603	S0I	C6-C2-N1	4.09	124.33	118.87
4	A	603	S0I	C6-C2-C5	-4.00	114.66	119.63
4	A	603	S0I	C4-C8-N9	3.75	120.80	116.13



There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	603	S0I	3	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.

Mo	l Chain	in Analysed	<RSRZ $>$	$\# \mathrm{RSRZ}{>}2$		$OWAB(A^2)$	Q<0.9	
1	A	546/561 (97%)	-0.06	26 (4%)	30	29	22, 39, 68, 101	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	247	ARG	4.6
1	A	21	GLY	3.6
1	A	264	CYS	3.4
1	A	25	ARG	3.1
1	A	266	GLY	3.1

## 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
4	S0I	A	603	18/18	0.79	0.17	40,54,57,61	0
2	MG	A	601	1/1	0.97	0.11	38,38,38,38	0
3	PO4	A	602	5/5	0.99	0.14	38,40,42,44	0



# 6.5 Other polymers (i)

There are no such residues in this entry.

