

Full wwPDB X-ray Structure Validation Report (i)

Feb 15, 2021 – 08:02 PM GMT

PDB ID : 4C4Z

Title: Crystal structure of human bifunctional epoxide hydroxylase 2 complexed with

Α8

Authors: Pilger, J.; Mazur, A.; Monecke, P.; Schreuder, H.; Elshorst, B.; Langer, T.;

Schiffer, A.; Krimm, I.; Wegstroth, M.; Lee, D.; Hessler, G.; Wendt, K.-U.;

Becker, S.; Griesinger, C.

Deposited on : 2013-09-09

Resolution : 2.06 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 : 2.17

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)

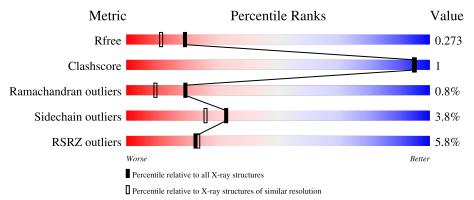
Validation Pipeline (wwPDB-VP) : 2.17

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 2.06 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	2684 (2.08-2.04)
Clashscore	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (2.08-2.04)

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	326	91%	6%	
1	В	326	91%	6%	-



2 Entry composition (i)

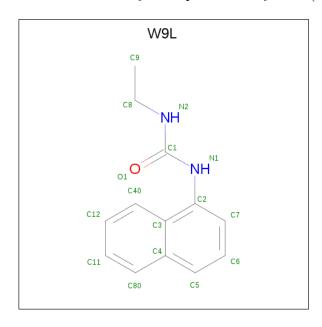
There are 3 unique types of molecules in this entry. The entry contains 5758 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	A	318	Total 2562	C 1645	N 431	O 463	S 23	0	0	0
1	В	318	Total 2562	C 1645	N 431	O 463	S 23	0	0	0

• Molecule 2 is 1-ethyl-3-naphthalen-1-ylurea (three-letter code: W9L) (formula: C₁₃H₁₄N₂O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 16			0	0
2	В	1	Total		N	 0	0

• Molecule 3 is water.



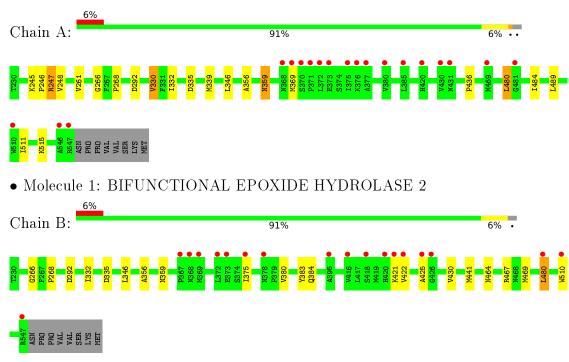
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	334	Total O 334 334	0	0
3	В	268	Total O 268 268	0	0



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 1 21 1	Depositor
Cell constants	46.49Å 79.85Å 87.22Å	Depositor
a, b, c, α , β , γ	90.00° 89.38° 90.00°	Depositor
Resolution (Å)	28.67 - 2.06	Depositor
Resolution (A)	36.30 - 2.06	EDS
% Data completeness	89.9 (28.67-2.06)	Depositor
(in resolution range)	90.0 (36.30-2.06)	EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	6.87 (at 2.06Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
D.D.	0.220 , 0.253	Depositor
R, R_{free}	0.233 , 0.273	DCC
R_{free} test set	2549 reflections (7.17%)	wwPDB-VP
Wilson B-factor (Å ²)	20.4	Xtriage
Anisotropy	0.703	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	$0.32 \; , 32.9$	EDS
L-test for twinning ²	$< L >=0.45, < L^2>=0.28$	Xtriage
Estimated twinning fraction	0.074 for h,-k,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5758	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.72% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities 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: W9L

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
WIOI	Chain	RMSZ	# Z >5	RMSZ	# Z > 5
1	A	0.36	0/2638	0.58	0/3578
1	В	0.36	0/2638	0.56	0/3578
All	All	0.36	0/5276	0.57	0/7156

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	2562	0	2491	7	0
1	В	2562	0	2491	5	0
2	A	16	0	14	0	0
2	В	16	0	14	0	0
3	A	334	0	0	0	0
3	В	268	0	0	0	0
All	All	5758	0	5010	12	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 1.

All (12) close contacts within the same asymmetric unit are listed below, sorted by their clash



magnitude.

Atom-1	Atom-2	$egin{array}{ll} ext{Interatomic} \ ext{distance} \ (ext{\AA}) \end{array}$	Clash overlap (Å)
1:A:266:GLY:HA3	1:A:335:ASP:HB3	1.79	0.64
1:A:246:PRO:O	1:A:247:ARG:HB2	2.00	0.62
1:B:266:GLY:HA3	1:B:335:ASP:HB3	1.82	0.61
1:B:332:ILE:HG12	1:B:356:ALA:HB3	1.87	0.55
1:A:359:ASN:N	1:A:359:ASN:HD22	2.10	0.50
1:A:332:ILE:HG12	1:A:356:ALA:HB3	1.95	0.49
1:A:484:ILE:HB	1:A:511:ILE:HG12	1.93	0.48
1:B:425:ALA:HB1	1:B:430:VAL:HG11	1.99	0.45
1:A:261:VAL:HG22	1:A:330:VAL:HG13	2.01	0.42
1:B:464:ASN:HA	1:B:467:ARG:HD2	2.01	0.42
1:A:245:LYS:HB2	1:A:248:VAL:HB	2.01	0.41
1:B:383:TYR:HB3	1:B:422:VAL:HG21	2.03	0.40

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	316/326 (97%)	305 (96%)	8 (2%)	3 (1%)	17 8
1	В	316/326 (97%)	305 (96%)	9 (3%)	2 (1%)	25 15
All	All	632/652 (97%)	610 (96%)	17 (3%)	5 (1%)	19 9

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	480	LEU
1	A	247	ARG
1	В	480	LEU
1	A	268	PRO
1	В	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	Rotameric	Outliers	Percentiles
1	A	279/287 (97%)	269 (96%)	10 (4%)	35 28
1	В	279/287 (97%)	268 (96%)	11 (4%)	32 25
All	All	558/574 (97%)	537 (96%)	21 (4%)	33 26

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	292	ASP
1	A	330	VAL
1	A	339	MET
1	A	346	LEU
1	A	359	ASN
1	A	369	MET
1	A	436	PRO
1	A	480	LEU
1	A	489	LEU
1	A	515	LYS
1	В	292	ASP
1	В	346	LEU
1	В	359	ASN
1	В	375	ILE
1	В	380	VAL
1	В	384	GLN
1	В	421	LYS
1	В	441	MET
1	В	469	MET
1	В	480	LEU
1	В	510	TRP

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

Mol	Chain	Res	Type
1	Α	359	ASN

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Mol	Chain	Res	Type
1	A	384	GLN
1	A	399	GLN
1	В	399	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)

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).

Mal	Mol Type Chain Res Lin		Link	Во	ond leng	${ m ths}$	В	Bond angles		
MIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	W9L	A	1548	-	17,17,17	1.48	4 (23%)	22,22,22	0.58	0
2	W9L	В	1548	-	17,17,17	1.51	4 (23%)	22,22,22	0.55	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	W9L	A	1548	-	-	0/7/7/7	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	W9L	В	1548	_	=	0/7/7/7	0/2/2/2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(\mathbf{\mathring{A}})$	$\operatorname{Ideal}(ext{\AA})$
2	В	1548	W9L	C1-N2	3.21	1.41	1.35
2	A	1548	W9L	C1-N2	3.12	1.41	1.35
2	A	1548	W9L	C1-N1	2.61	1.42	1.37
2	В	1548	W9L	C1-N1	2.60	1.42	1.37
2	В	1548	W9L	C12-C11	2.17	1.43	1.38
2	A	1548	W9L	C12-C11	2.14	1.43	1.38
2	В	1548	W9L	C6-C7	2.11	1.43	1.38
2	A	1548	W9L	C6-C7	2.06	1.43	1.38

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 $>$	$\#\mathrm{RSRZ}{>}2$		$OWAB(\AA^2)$	Q<0.9
1	A	318/326 (97%)	0.21	19 (5%) 21	22	12, 20, 49, 75	0
1	В	318/326 (97%)	0.34	18 (5%) 23	24	11, 25, 53, 73	0
All	All	636/652 (97%)	0.27	37 (5%) 23	24	11, 22, 52, 75	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	372	LEU	4.9
1	В	510	TRP	4.9
1	A	377	ALA	4.6
1	В	372	LEU	4.4
1	В	480	LEU	3.9
1	В	421	LYS	3.5
1	В	426	GLY	3.5
1	A	481	GLY	3.4
1	A	430	VAL	3.4
1	A	375	ILE	3.4
1	A	376	LYS	3.4
1	В	416	VAL	3.3
1	A	380	VAL	3.2
1	A	370	SER	3.2
1	В	373	GLU	3.1
1	В	420	HIS	3.1
1	A	368	ASN	2.8
1	В	378	ASN	2.8
1	В	375	ILE	2.8
1	В	547	ARG	2.7
1	В	418	SER	2.7
1	В	368	ASN	2.7
1	В	367	PRO	2.6
1	В	369	MET	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	510	TRP	2.5
1	A	369	MET	2.5
1	A	371	PRO	2.5
1	A	469	MET	2.4
1	В	425	ALA	2.3
1	A	385	LEU	2.3
1	A	547	ARG	2.3
1	A	373	GLU	2.2
1	A	431	ASN	2.2
1	В	395	ALA	2.1
1	A	420	HIS	2.1
1	A	546	ALA	2.0
1	В	422	VAL	2.0

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	${f B-factors}({f \AA}^2)$	Q < 0.9
2	W9L	A	1548	16/16	0.79	0.21	33,33,33,34	0
2	W9L	В	1548	16/16	0.83	0.16	38,39,39,39	0

6.5 Other polymers (i)

There are no such residues in this entry.

