



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:50 AM UTC

PDB ID : 4C4Y / pdb_00004c4y
Title : Crystal structure of human bifunctional epoxide hydroxylase 2 complexed with A4
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 : 2.41 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

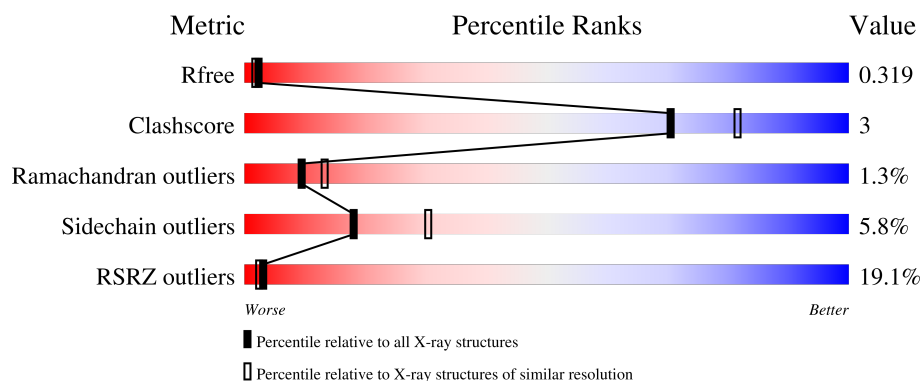
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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}	180053	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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 $\leq 5\%$. 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	18% 84% 11% ••

2 Entry composition [i](#)

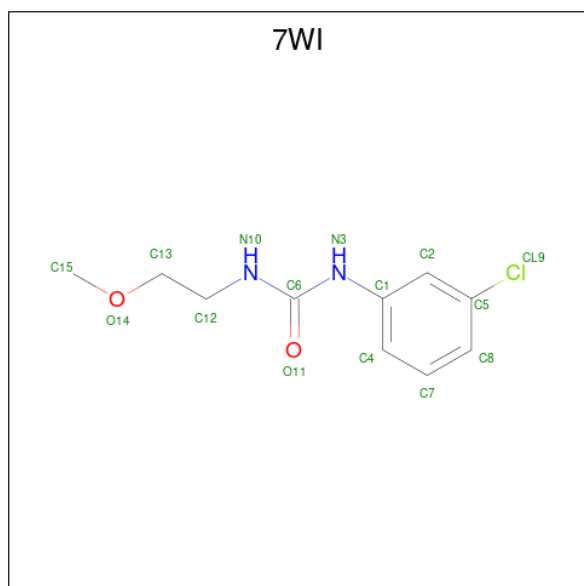
There are 3 unique types of molecules in this entry. The entry contains 2689 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	314	Total	C	N	O	S	0	0	0
			2535	1631	426	456	22			

- Molecule 2 is 1-(3-chlorophenyl)-3-(2-methoxyethyl)urea (CCD ID: 7WI) (formula: $C_{10}H_{13}ClN_2O_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			15	10	1	2	2		

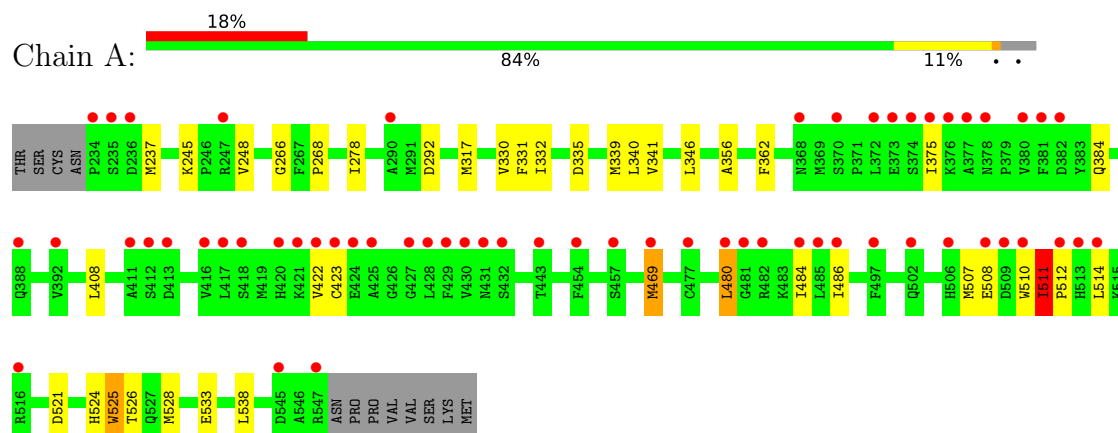
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	139	Total	O	0	0
			139	139		

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

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants a, b, c, α , β , γ	81.64Å 46.34Å 80.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.82 – 2.41 40.82 – 2.41	Depositor EDS
% Data completeness (in resolution range)	96.8 (40.82-2.41) 96.9 (40.82-2.41)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.27 (at 2.42Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.258 , 0.315 0.277 , 0.319	Depositor DCC
R_{free} test set	579 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	29.1	Xtriage
Anisotropy	0.677	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.058 for l,-k,h	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	2689	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.32% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: 7WI

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	0.70	0/2611	1.25	2/3540 (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	525	TRP	CA-C-N	5.15	128.54	120.82
1	A	525	TRP	C-N-CA	5.15	128.54	120.82

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	2535	0	2469	17	0
2	A	15	0	13	4	0
3	A	139	0	0	0	1
All	All	2689	0	2482	17	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 3.

All (17) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:511:ILE:HB	1:A:512:PRO:HA	1.74	0.69
1:A:511:ILE:HB	1:A:512:PRO:CA	2.25	0.66
1:A:339:MET:HE2	2:A:1548:7WI:H151	1.83	0.61
1:A:266:GLY:HA3	1:A:335:ASP:HB3	1.88	0.54
1:A:525:TRP:CH2	2:A:1548:7WI:H7	2.42	0.54
1:A:524:HIS:NE2	2:A:1548:7WI:H4	2.23	0.53
1:A:408:LEU:HD22	2:A:1548:7WI:H8	1.92	0.52
1:A:375:ILE:HD11	1:A:469:MET:HG2	1.93	0.50
1:A:245:LYS:HB2	1:A:248:VAL:HB	1.94	0.49
1:A:332:ILE:HG12	1:A:356:ALA:HB3	1.94	0.49
1:A:317:MET:HG3	1:A:340:LEU:HD21	1.98	0.46
1:A:237:MET:HE1	1:A:278:ILE:HG21	1.98	0.45
1:A:511:ILE:HB	1:A:512:PRO:C	2.42	0.44
1:A:332:ILE:HD13	1:A:538:LEU:HD22	2.02	0.42
1:A:362:PHE:HB3	1:A:507:MET:HE3	2.02	0.42
1:A:484:ILE:O	1:A:512:PRO:HB3	2.20	0.41
1:A:331:PHE:HB3	1:A:341:VAL:HG12	2.03	0.41

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	Interatomic distance (Å)	Clash overlap (Å)
3:A:2026:HOH:O	3:A:2121:HOH:O[3_597]	2.09	0.11

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	312/326 (96%)	295 (95%)	13 (4%)	4 (1%)	9 13

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	511	ILE
1	A	514	LEU
1	A	480	LEU
1	A	268	PRO

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	275/287 (96%)	259 (94%)	16 (6%)	18	30

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	292	ASP
1	A	330	VAL
1	A	346	LEU
1	A	384	GLN
1	A	422	VAL
1	A	423	CYS
1	A	469	MET
1	A	480	LEU
1	A	486	ILE
1	A	508	GLU
1	A	510	TRP
1	A	511	ILE
1	A	521	ASP
1	A	526	THR
1	A	528	MET
1	A	533	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	378	ASN
1	A	453	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand 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	$\# Z > 2$
2	7WI	A	1548	-	15,15,15	0.13	0	18,18,18	0.46	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	7WI	A	1548	-	-	1/9/9/9	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1548	7WI	N10-C12-C13-O14

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1548	7WI	4	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 ⓘ

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, 95th 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 ²)	Q<0.9
1	A	314/326 (96%)	1.26	60 (19%) 3 2	16, 34, 64, 82	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	416	VAL	4.4
1	A	423	CYS	4.2
1	A	425	ALA	4.1
1	A	234	PRO	4.0
1	A	380	VAL	3.9
1	A	484	ILE	3.8
1	A	424	GLU	3.8
1	A	430	VAL	3.6
1	A	377	ALA	3.5
1	A	547	ARG	3.5
1	A	509	ASP	3.3
1	A	485	LEU	3.3
1	A	381	PHE	3.2
1	A	372	LEU	3.2
1	A	375	ILE	3.2
1	A	417	LEU	3.1
1	A	506	HIS	3.0
1	A	480	LEU	2.9
1	A	378	ASN	2.9
1	A	428	LEU	2.9
1	A	412	SER	2.8
1	A	429	PHE	2.8
1	A	421	LYS	2.8
1	A	420	HIS	2.8
1	A	388	GLN	2.8
1	A	235	SER	2.7
1	A	370	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	481	GLY	2.6
1	A	431	ASN	2.6
1	A	508	GLU	2.6
1	A	512	PRO	2.6
1	A	376	LYS	2.5
1	A	247	ARG	2.5
1	A	545	ASP	2.5
1	A	368	ASN	2.4
1	A	411	ALA	2.4
1	A	432	SER	2.4
1	A	374	SER	2.4
1	A	497	PHE	2.4
1	A	513	HIS	2.3
1	A	514	LEU	2.3
1	A	457	SER	2.3
1	A	236	ASP	2.3
1	A	516	ARG	2.2
1	A	382	ASP	2.2
1	A	482	ARG	2.2
1	A	510	TRP	2.2
1	A	427	GLY	2.2
1	A	477	CYS	2.2
1	A	454	PHE	2.2
1	A	422	VAL	2.1
1	A	469	MET	2.1
1	A	486	ILE	2.1
1	A	418	SER	2.1
1	A	443	THR	2.1
1	A	373	GLU	2.1
1	A	290	ALA	2.1
1	A	392	VAL	2.0
1	A	502	GLN	2.0
1	A	413	ASP	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 oligosaccharides 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. The B-factors column lists the minimum, median, 95th 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	B-factors($\text{\AA}^2$)	Q<0.9
2	7WI	A	1548	15/15	0.81	0.18	46,49,51,51	0

6.5 Other polymers

There are no such residues in this entry.