

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

May 29, 2020 – 02:00 am BST

PDB ID : 1BX9

Title : GLUTATHIONE S-TRANSFERASE IN COMPLEX WITH HERBICIDE

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Deposited on : 1998-10-14

Resolution : 2.60 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) : NOT EXECUTED EDS : NOT EXECUTED

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

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

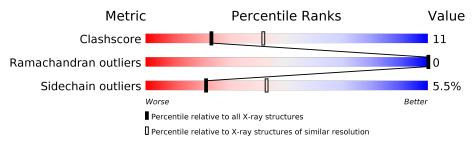
Validation Pipeline (wwPDB-VP) : 2.11

# 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 2.60 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \ resolution} \\ (\#{\rm Entries, \ resolution \ \ range(\AA)}) \end{array}$
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

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 on 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain	
1	A	211	66%	33%
2	В	3	67%	33%



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1797 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 GLUTATHIONE S-TRANSFERASE.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	210	Total 1693	C 1087	N 287	O 317	S 2	0	0	0

• Molecule 2 is a protein called FOE-4053-glutathione conjugate GGL-FOE-GLY.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
9	R	ર	Total	С	F	N	О	S	0	0	0
	ע	9	34	21	1	4	7	1	0	U	0

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	69	Total O 69 69	0	0
3	В	1	Total O 1 1	0	0

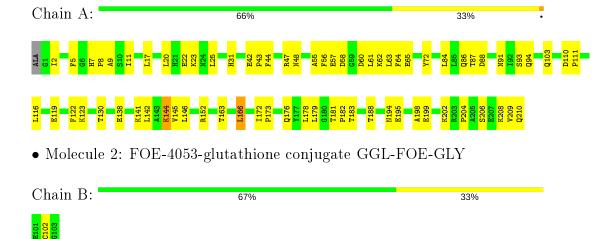


# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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. 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. 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.

Note EDS was not executed.

• Molecule 1: GLUTATHIONE S-TRANSFERASE





# 4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	59.00Å 88.83Å 89.85Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 - 2.60	Depositor
% Data completeness	97.8 (8.00-2.60)	Depositor
(in resolution range)	31.0 (0.00 2.00)	Берозгот
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR 3.8	Depositor
$R, R_{free}$	0.196 , 0.248	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1797	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP



# 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: FOE, GGL

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	0.44	0/1730	0.62	0/2338	
2	В	0.78	0/4	0.73	0/2	
All	All	0.44	0/1734	0.62	0/2340	

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	1693	0	1696	39	0
2	В	34	0	26	1	0
3	A	69	0	0	1	0
3	В	1	0	0	0	0
All	All	1797	0	1722	39	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 11.

All (39) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap(A)
1:A:181:THR:HG22	1:A:183:THR:H	1.36	0.87
1:A:22:GLU:HG2	1:A:84:LEU:HD21	1.62	0.82
1:A:84:LEU:HB3	1:A:166:LEU:HD13	1.65	0.78
1:A:195:GLU:O	1:A:199:GLU:HG2	1.86	0.76
1:A:65:GLU:HG3	3:A:279:HOH:O	1.94	0.65
1:A:5:PHE:HB2	1:A:55:ALA:HB3	1.80	0.64
1:A:172:ILE:HB	1:A:173:PRO:HD3	1.82	0.62
1:A:7:HIS:HD2	1:A:9:ALA:H	1.50	0.59
1:A:44:PHE:HA	1:A:47:ARG:HG3	1.85	0.58
1:A:88:ASP:H	1:A:94:GLN:HE22	1.56	0.54
1:A:176:GLN:HB3	1:A:210:GLN:HE21	1.75	0.52
1:A:198:ALA:HB1	1:A:202:LYS:HE2	1.92	0.51
1:A:181:THR:HG23	1:A:182:PRO:HD2	1.92	0.50
1:A:11:ILE:HG23	1:A:173:PRO:HB2	1.94	0.50
1:A:110:ASP:HB3	1:A:111:PRO:HD3	1.94	0.50
1:A:87:THR:HG23	1:A:88:ASP:N	2.26	0.50
1:A:206:SER:O	1:A:209:VAL:HG22	2.12	0.48
1:A:2:ILE:HA	1:A:57:GLU:O	2.15	0.47
1:A:204:PRO:O	1:A:208:LYS:HG3	2.13	0.47
1:A:61:LEU:HG	1:A:63:LEU:HD11	1.95	0.47
1:A:8:PRO:HD2	1:A:31:HIS:CD2	2.50	0.47
1:A:116:LEU:HD13	1:A:138:GLU:HB2	1.98	0.45
1:A:142:LEU:O	1:A:146:LEU:HG	2.17	0.45
1:A:42:GLU:HG3	1:A:43:PRO:HA	1.98	0.44
1:A:64:PHE:O	1:A:65:GLU:CB	2.67	0.43
1:A:141:LYS:O	1:A:145:VAL:HG23	2.18	0.43
1:A:188:THR:HA	1:A:194:ASN:HD22	1.82	0.42
1:A:86:GLN:OE1	1:A:86:GLN:HA	2.19	0.42
1:A:62:LYS:C	1:A:63:LEU:HD12	2.39	0.42
1:A:61:LEU:HD23	1:A:72:TYR:CE1	2.54	0.42
1:A:141:LYS:O	1:A:144:LYS:HB3	2.20	0.41
1:A:119:GLU:HA	1:A:123:LYS:HD2	2.02	0.41
1:A:119:GLU:O	1:A:130:THR:HG22	2.20	0.41
1:A:91:ASN:OD1	1:A:93:SER:HB3	2.21	0.41
1:A:178:LEU:O	1:A:181:THR:HB	2.20	0.41
1:A:23:LYS:HB3	1:A:25:LEU:CD1	2.50	0.41
1:A:188:THR:HA	1:A:194:ASN:ND2	2.36	0.41
1:A:56:PHE:CE1	1:A:58:ASP:HB2	2.56	0.40
1:A:122:PHE:CE2	2:B:102:FOE:H53	2.56	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	208/211 (99%)	199 (96%)	9 (4%)	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	Analysed Rotameric		Percentiles
1	A	181/181 (100%)	171 (94%)	10 (6%)	21 43

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LEU
1	A	20	LEU
1	A	48	ASN
1	A	60	ASP
1	A	103	GLN
1	A	144	LYS
1	A	152	ARG
1	A	163	THR
1	A	166	LEU
1	A	179	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:



Mol	Chain	Res	Type
1	A	7	HIS
1	A	21	HIS
1	A	24	ASN
1	A	48	ASN
1	A	80	GLN
1	A	83	ASN
1	A	94	GLN
1	A	107	HIS
1	A	108	GLN
1	A	120	GLN
1	A	170	HIS
1	A	176	GLN
1	A	194	ASN
1	A	210	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)

2 non-standard protein/DNA/RNA residues 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	Т	Type Chain I		T in le	Bond lengths			Bond angles		
MIGI	Type	Chain	Res	Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	FOE	В	102	2	19,20,21	1.86	4 (21%)	21,26,28	1.68	4 (19%)
2	GGL	В	101	2	4,8,9	0.78	0	2,9,11	0.60	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	$\mathbf{Res}$	Link	Chirals	Torsions	Rings
2	FOE	В	102	2	-	5/18/20/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GGL	В	101	2	-	0/3/8/9	-

#### All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	${ m Observed}({ m \AA})$	$\operatorname{Ideal}( ext{\AA})$
2	В	102	FOE	C10-N4	-4.98	1.34	1.43
2	В	102	FOE	C1-C2	3.17	1.57	1.51
2	В	102	FOE	C8-C13	2.46	1.41	1.37
2	В	102	FOE	C6-N4	2.02	1.51	1.48

#### All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
2	В	102	FOE	C2-C1-SG	4.57	127.05	113.59
2	В	102	FOE	O3-C2-C1	-3.46	113.26	120.93
2	В	102	FOE	O3-C2-N4	-2.49	118.48	121.58
2	В	102	FOE	C7-C6-C5	-2.47	105.57	112.40

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	102	FOE	C-CA-CB-SG
2	В	102	FOE	SG-C1-C2-O3
2	В	102	FOE	SG-C1-C2-N4
2	В	102	FOE	C5-C6-N4-C2
2	В	102	FOE	N-CA-CB-SG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	${f Res}$	Type	Clashes	Symm-Clashes
2	В	102	FOE	1	0

## 5.5 Carbohydrates (i)

There are no carbohydrates in this entry.



## 5.6 Ligand geometry (i)

There are no ligands in this entry.

## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

$\mathbf{Mol}$	Chain	Number of breaks
2	В	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	В	101:GGL	С	102:FOE	N	5.27



# 6 Fit of model and data (i)

#### 6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

## 6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

