



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 24, 2024 – 11:52 AM EDT

PDB ID : 6N8U  
Title : DRAFT model of Schistosoma japonicum Glutathione S-transferase expression tag  
Authors : Tempel, W.; Dong, C.  
Deposited on : 2018-11-30  
Resolution : 1.96 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](mailto: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>.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.37.1  
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) : 2.37.1

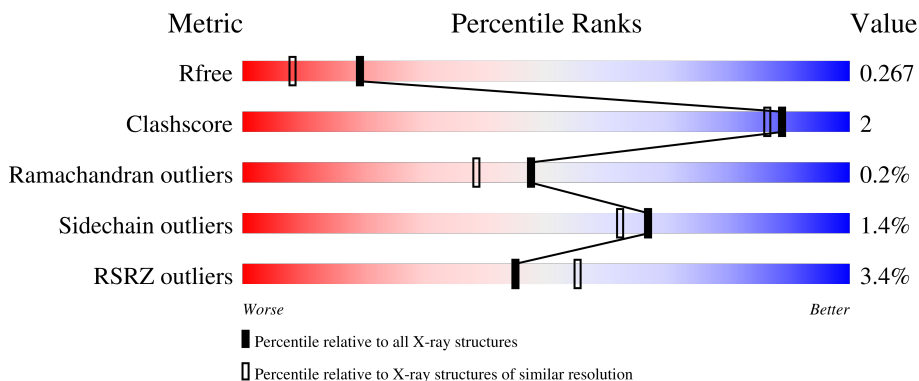
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.96 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))
$R_{free}$	130704	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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  $\geq 3$ , 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	240	
1	B	240	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3495 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 class-mu 26 kDa isozyme.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	217	1755	1147	278	318	4	8	0	1	0
1	B	216	1740	1136	281	311	4	8	0	2	0

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	219	SER	-	expression tag	UNP P08515
A	220	ASP	-	expression tag	UNP P08515
A	221	GLY	-	expression tag	UNP P08515
A	222	SER	-	expression tag	UNP P08515
A	223	SER	-	expression tag	UNP P08515
A	224	MSE	-	expression tag	UNP P08515
A	225	GLY	-	expression tag	UNP P08515
A	226	SER	-	expression tag	UNP P08515
A	227	SER	-	expression tag	UNP P08515
A	228	HIS	-	expression tag	UNP P08515
A	229	HIS	-	expression tag	UNP P08515
A	230	HIS	-	expression tag	UNP P08515
A	231	HIS	-	expression tag	UNP P08515
A	232	HIS	-	expression tag	UNP P08515
A	233	HIS	-	expression tag	UNP P08515
A	234	SER	-	expression tag	UNP P08515
A	235	SER	-	expression tag	UNP P08515
A	236	GLY	-	expression tag	UNP P08515
A	237	LEU	-	expression tag	UNP P08515
A	238	VAL	-	expression tag	UNP P08515
A	239	PRO	-	expression tag	UNP P08515
A	240	ARG	-	expression tag	UNP P08515
B	219	SER	-	expression tag	UNP P08515
B	220	ASP	-	expression tag	UNP P08515
B	221	GLY	-	expression tag	UNP P08515

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Chain	Residue	Modelled	Actual	Comment	Reference
B	222	SER	-	expression tag	UNP P08515
B	223	SER	-	expression tag	UNP P08515
B	224	MSE	-	expression tag	UNP P08515
B	225	GLY	-	expression tag	UNP P08515
B	226	SER	-	expression tag	UNP P08515
B	227	SER	-	expression tag	UNP P08515
B	228	HIS	-	expression tag	UNP P08515
B	229	HIS	-	expression tag	UNP P08515
B	230	HIS	-	expression tag	UNP P08515
B	231	HIS	-	expression tag	UNP P08515
B	232	HIS	-	expression tag	UNP P08515
B	233	HIS	-	expression tag	UNP P08515
B	234	SER	-	expression tag	UNP P08515
B	235	SER	-	expression tag	UNP P08515
B	236	GLY	-	expression tag	UNP P08515
B	237	LEU	-	expression tag	UNP P08515
B	238	VAL	-	expression tag	UNP P08515
B	239	PRO	-	expression tag	UNP P08515
B	240	ARG	-	expression tag	UNP P08515

### 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.

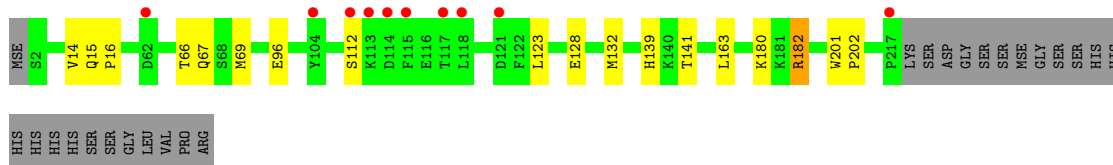
- Molecule 1: Glutathione S-transferase class-mu 26 kDa isozyme

Chain A:  2% 86% 10%



- Molecule 1: Glutathione S-transferase class-mu 26 kDa isozyme

Chain B:  4% 82% 7% 10%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	93.92Å 102.77Å 48.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.96 – 1.96 46.96 – 1.96	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.96-1.96) 99.9 (46.96-1.96)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.51 (at 1.97Å)	Xtrriage
Refinement program	REFMAC 5.8.0238	Depositor
R, $R_{free}$	0.212 , 0.256 0.227 , 0.267	Depositor DCC
$R_{free}$ test set	1711 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.9	Xtrriage
Anisotropy	0.268	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 32.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3495	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.34% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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](#)

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	0.71	0/1796	0.81	0/2419
1	B	0.70	0/1786	0.83	1/2406 (0.0%)
All	All	0.70	0/3582	0.82	1/4825 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	182	ARG	NE-CZ-NH1	5.88	123.24	120.30

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	1755	0	1707	4	0
1	B	1740	0	1681	10	0
All	All	3495	0	3388	13	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 2.

The worst 5 of 13 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:B:69:MSE:HE2	1:B:96:GLU:CD	2.23	0.59
1:A:201:TRP:CG	1:A:202:PRO:HA	2.42	0.54
1:B:141:THR:HG23	1:B:182:ARG:HD3	1.94	0.49
1:A:150:HIS:CG	1:A:151:PRO:HD3	2.49	0.48
1:B:128:GLU:OE2	1:B:132:MSE:HE2	2.14	0.47

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	215/240 (90%)	208 (97%)	6 (3%)	1 (0%)	29	17
1	B	215/240 (90%)	211 (98%)	4 (2%)	0	100	100
All	All	430/480 (90%)	419 (97%)	10 (2%)	1 (0%)	47	38

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	61	GLY

### 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	184/203 (91%)	181 (98%)	3 (2%)	62	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	179/203 (88%)	177 (99%)	2 (1%)	73	71
All	All	363/406 (89%)	358 (99%)	5 (1%)	67	62

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	VAL
1	A	138	CYS
1	A	214	ASP
1	B	14	VAL
1	B	112	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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](#)

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](#)

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<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	209/240 (87%)	0.13	4 (1%) 66 74	23, 33, 54, 71	1 (0%)
1	B	208/240 (86%)	0.38	10 (4%) 30 40	25, 36, 60, 79	1 (0%)
All	All	417/480 (86%)	0.25	14 (3%) 45 55	23, 35, 58, 79	2 (0%)

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	62	ASP	3.9
1	B	115	PHE	3.3
1	B	112	SER	3.0
1	B	217	PRO	3.0
1	A	215	HIS	2.9

### 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](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.