



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 27, 2021 – 11:01 pm GMT

PDB ID : 6SSR
Title : Crystal structure of Human Microsomal Glutathione S-Transferase 2 at 3.8 Angstroms resolution
Authors : Thulasingham, M.; Nji, E.; Rinaldo-Matthis, A.; Haeggstrom, J.Z.
Deposited on : 2019-09-09
Resolution : 3.80 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.18
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) : 2.18

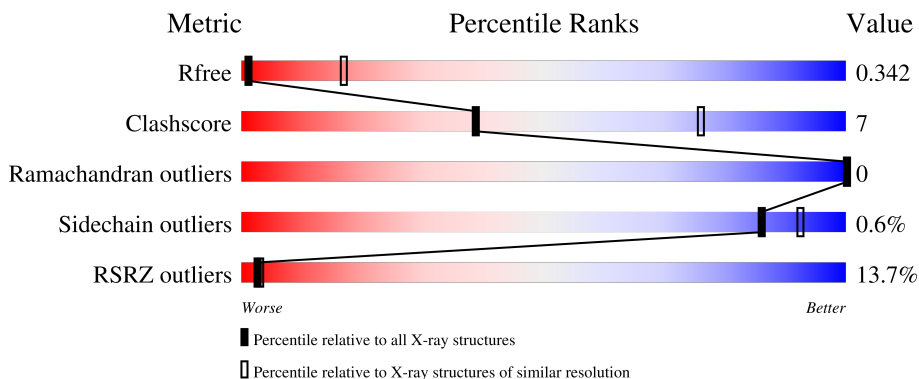
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 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	1212 (4.00-3.60)
Clashscore	141614	1288 (4.00-3.60)
Ramachandran outliers	138981	1243 (4.00-3.60)
Sidechain outliers	138945	1237 (4.00-3.60)
RSRZ outliers	127900	1121 (4.00-3.60)

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 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	153	 12% 80% 8% 12%
1	B	153	 19% 77% 12% 11%
1	C	153	 5% 73% 12% 15%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3148 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 Microsomal glutathione S-transferase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	135	1054	701	172	177	4	0	0	0
1	B	136	1065	707	174	180	4	0	0	0
1	C	130	1029	683	168	174	4	0	0	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	initiating methionine	UNP Q99735
A	-4	HIS	-	expression tag	UNP Q99735
A	-3	HIS	-	expression tag	UNP Q99735
A	-2	HIS	-	expression tag	UNP Q99735
A	-1	HIS	-	expression tag	UNP Q99735
A	0	HIS	-	expression tag	UNP Q99735
A	1	HIS	-	expression tag	UNP Q99735
B	-5	MET	-	initiating methionine	UNP Q99735
B	-4	HIS	-	expression tag	UNP Q99735
B	-3	HIS	-	expression tag	UNP Q99735
B	-2	HIS	-	expression tag	UNP Q99735
B	-1	HIS	-	expression tag	UNP Q99735
B	0	HIS	-	expression tag	UNP Q99735
B	1	HIS	-	expression tag	UNP Q99735
C	-5	MET	-	initiating methionine	UNP Q99735
C	-4	HIS	-	expression tag	UNP Q99735
C	-3	HIS	-	expression tag	UNP Q99735
C	-2	HIS	-	expression tag	UNP Q99735
C	-1	HIS	-	expression tag	UNP Q99735
C	0	HIS	-	expression tag	UNP Q99735
C	1	HIS	-	expression tag	UNP Q99735

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	109.94Å 151.15Å 70.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.45 – 3.80 44.45 – 3.80	Depositor EDS
% Data completeness (in resolution range)	99.3 (44.45-3.80) 99.4 (44.45-3.80)	Depositor EDS
R_{merge}	0.42	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 3.77Å)	Xtrriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.305 , 0.337 0.312 , 0.342	Depositor DCC
R_{free} test set	301 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	131.2	Xtrriage
Anisotropy	0.584	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 75.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.21$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	3148	wwPDB-VP
Average B, all atoms (Å ²)	142.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.38% 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

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	0.51	0/1082	0.63	0/1472
1	B	0.50	0/1093	0.64	0/1486
1	C	0.48	0/1057	0.65	0/1435
All	All	0.49	0/3232	0.64	0/4393

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	1054	0	1054	13	0
1	B	1065	0	1067	26	0
1	C	1029	0	1034	22	0
All	All	3148	0	3155	47	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 7.

All (47) 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:C:127:ALA:O	1:C:131:LEU:CD1	1.81	1.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:127:ALA:O	1:C:131:LEU:HD13	1.09	1.25
1:B:48:ARG:O	1:B:97:TYR:HE2	1.23	1.19
1:B:48:ARG:O	1:B:97:TYR:CE2	1.96	1.17
1:B:52:ALA:HB2	1:B:97:TYR:CD2	2.02	0.94
1:C:127:ALA:C	1:C:131:LEU:HD13	1.90	0.92
1:B:97:TYR:OH	1:C:38:PRO:HB3	1.75	0.87
1:C:128:ASN:HA	1:C:131:LEU:HD22	1.64	0.80
1:B:69:MET:HE1	1:C:9:ALA:HA	1.65	0.76
1:A:66:THR:HG22	1:A:118:LEU:HB3	1.69	0.74
1:B:53:GLN:O	1:B:57:VAL:HG12	1.89	0.72
1:B:52:ALA:HB2	1:B:97:TYR:HD2	1.54	0.71
1:B:48:ARG:O	1:B:97:TYR:CD2	2.47	0.65
1:B:66:THR:HG22	1:B:118:LEU:HB3	1.79	0.65
1:C:127:ALA:C	1:C:131:LEU:CD1	2.57	0.61
1:A:97:TYR:CD2	1:A:101:ALA:HA	2.37	0.60
1:A:65:ILE:HD11	1:B:64:ILE:HG13	1.83	0.59
1:A:57:VAL:HG11	1:C:58:GLU:HG2	1.85	0.58
1:B:51:ARG:HB3	1:B:97:TYR:OH	2.03	0.58
1:C:133:GLU:N	1:C:133:GLU:OE1	2.36	0.57
1:C:19:GLN:HE22	1:C:56:CYS:HB3	1.70	0.56
1:B:69:MET:HE1	1:C:68:TRP:HZ2	1.71	0.56
1:A:64:ILE:HG13	1:C:65:ILE:HD11	1.87	0.55
1:B:48:ARG:C	1:B:97:TYR:CE2	2.77	0.55
1:B:69:MET:CE	1:C:9:ALA:HA	2.34	0.55
1:C:125:GLY:O	1:C:129:SER:HB2	2.07	0.54
1:B:101:ALA:O	1:B:104:ARG:NH2	2.36	0.53
1:B:69:MET:CE	1:C:68:TRP:HZ2	2.23	0.51
1:C:51:ARG:NH1	1:C:55:ASN:OD1	2.45	0.49
1:A:97:TYR:CE2	1:A:101:ALA:HA	2.48	0.49
1:A:57:VAL:HG21	1:C:58:GLU:HB3	1.96	0.48
1:B:97:TYR:HD1	1:B:104:ARG:HD3	1.79	0.48
1:C:131:LEU:CD1	1:C:131:LEU:N	2.79	0.45
1:C:54:GLN:O	1:C:58:GLU:HG3	2.17	0.44
1:B:69:MET:HE1	1:C:68:TRP:CZ2	2.52	0.43
1:A:85:VAL:HG12	1:A:114:ILE:HD11	2.01	0.43
1:B:131:LEU:O	1:B:137:LEU:N	2.36	0.43
1:A:65:ILE:HD11	1:B:64:ILE:CG1	2.49	0.42
1:C:130:PHE:O	1:C:130:PHE:CG	2.72	0.42
1:A:112:LEU:HD23	1:A:112:LEU:HA	1.89	0.42
1:B:48:ARG:C	1:B:97:TYR:HE2	2.10	0.41
1:B:48:ARG:CA	1:B:97:TYR:CE2	3.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:54:GLN:O	1:B:58:GLU:HG3	2.20	0.41
1:B:102:LYS:HA	1:B:102:LYS:HD3	1.87	0.41
1:A:58:GLU:CB	1:B:57:VAL:HG21	2.51	0.41
1:A:9:ALA:HB1	1:C:126:ILE:HD11	2.03	0.40
1:A:62:ILE:HD11	1:B:19:GLN:HB3	2.02	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	133/153 (87%)	131 (98%)	2 (2%)	0	100	100
1	B	134/153 (88%)	130 (97%)	4 (3%)	0	100	100
1	C	128/153 (84%)	125 (98%)	3 (2%)	0	100	100
All	All	395/459 (86%)	386 (98%)	9 (2%)	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	Rotameric	Outliers	Percentiles	
1	A	105/126 (83%)	104 (99%)	1 (1%)	76	86
1	B	106/126 (84%)	106 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	104/126 (82%)	103 (99%)	1 (1%)	76	86
All	All	315/378 (83%)	313 (99%)	2 (1%)	86	92

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	TYR
1	C	97	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	55	ASN
1	C	19	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](#)

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

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	135/153 (88%)	0.69	18 (13%) 3 3	92, 127, 161, 181	0
1	B	136/153 (88%)	0.98	29 (21%) 0 1	83, 139, 181, 216	0
1	C	130/153 (84%)	0.45	8 (6%) 20 16	104, 153, 197, 214	0
All	All	401/459 (87%)	0.71	55 (13%) 3 3	83, 138, 186, 216	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	38	PRO	7.5
1	A	42	GLY	5.5
1	A	36	THR	5.3
1	A	136	ASP	5.1
1	B	32	LYS	5.1
1	B	103	LYS	4.8
1	B	33	TYR	4.8
1	A	99	GLU	4.7
1	B	34	LYS	4.6
1	B	36	THR	4.5
1	B	105	ILE	4.4
1	A	133	GLU	4.1
1	B	107	GLY	4.0
1	C	129	SER	4.0
1	A	35	VAL	4.0
1	C	101	ALA	4.0
1	A	37	PRO	3.8
1	A	39	ALA	3.6
1	B	137	LEU	3.5
1	B	102	LYS	3.5
1	C	125	GLY	3.5
1	B	104	ARG	3.4
1	B	138	ASN	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	103	LYS	3.2
1	B	106	THR	3.2
1	B	76	GLN	3.2
1	C	21	TYR	3.1
1	B	25	GLN	3.0
1	A	41	THR	3.0
1	B	27	GLY	3.0
1	B	96	GLY	3.0
1	B	100	ALA	3.0
1	B	109	ARG	2.9
1	A	75	ASN	2.9
1	A	79	ALA	2.9
1	B	80	THR	2.8
1	C	102	LYS	2.7
1	A	134	TYR	2.7
1	B	97	TYR	2.7
1	C	6	ILE	2.7
1	A	81	CYS	2.6
1	C	131	LEU	2.6
1	B	28	LYS	2.4
1	C	111	SER	2.3
1	B	120	LEU	2.3
1	A	137	LEU	2.3
1	B	35	VAL	2.2
1	B	52	ALA	2.2
1	B	43	SER	2.2
1	B	4	ASN	2.2
1	A	91	HIS	2.1
1	B	31	LEU	2.1
1	B	134	TYR	2.1
1	A	135	LEU	2.1
1	B	20	SER	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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.