



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 27, 2026 – 10:12 PM JST

PDB ID : 22FE / pdb_000022fe
Title : Crystal structure of thioredoxin glutathione reductase from *Schistosoma japonicum* with the U597C mutation in complex with GSH
Authors : Wang, S.Q.; Huang, S.Q.; Lin, T.W.
Deposited on : 2026-01-08
Resolution : 2.12 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

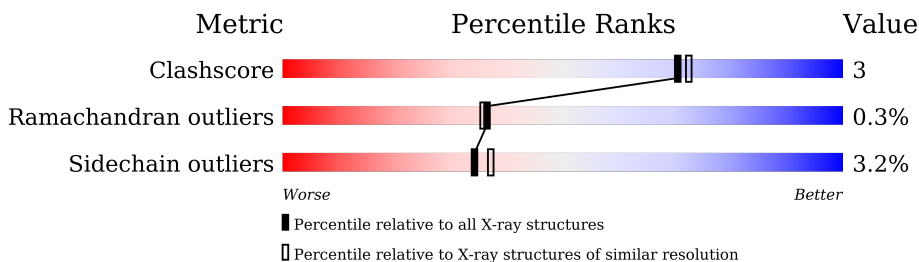
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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))
Clashscore	190562	8817 (2.14-2.10)
Ramachandran outliers	187476	8738 (2.14-2.10)
Sidechain outliers	187428	8739 (2.14-2.10)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	598	
1	B	598	

2 Entry composition [i](#)

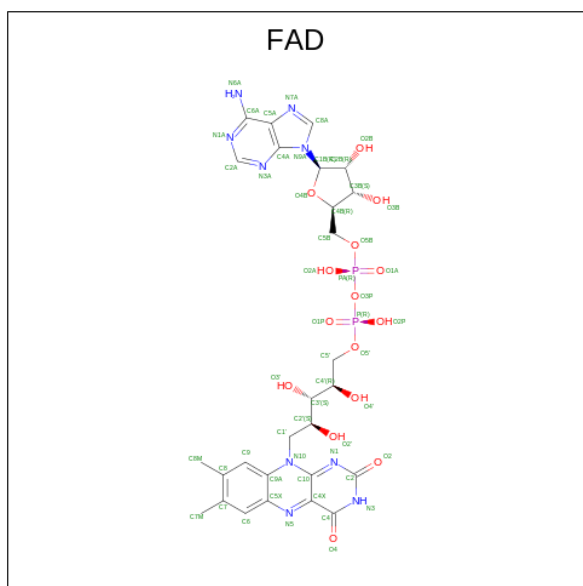
There are 6 unique types of molecules in this entry. The entry contains 9337 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 thioredoxin-disulfide reductase (NADPH).

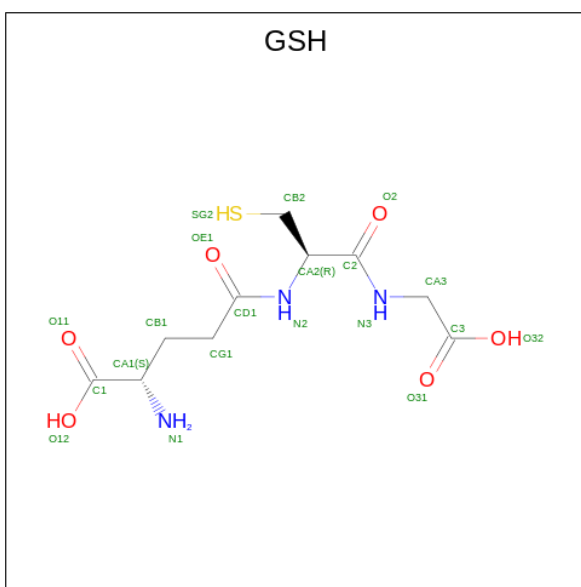
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	591	Total	C	N	O	S	0	2	0
			4536	2868	773	871	24			
1	B	592	Total	C	N	O	S	0	1	0
			4534	2867	770	872	25			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$) (labeled as "Ligand of Interest" by depositor).



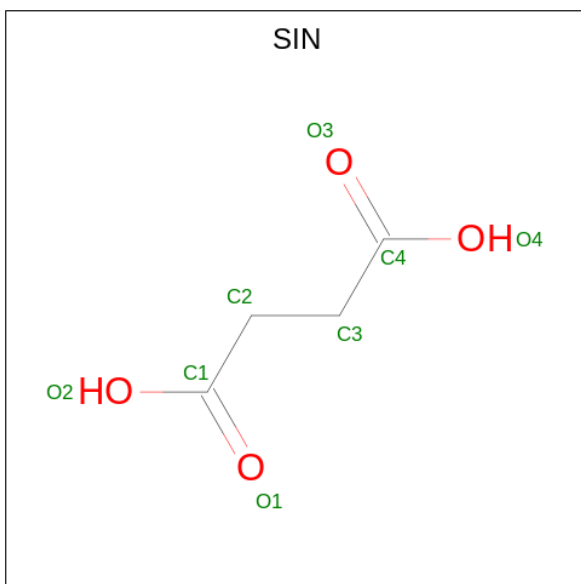
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is Glutathione (CCD ID: GSH) (formula: $C_{10}H_{17}N_3O_6S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			20	10	3	6	1		

- Molecule 4 is SUCCINIC ACID (CCD ID: SIN) (formula: $C_4H_6O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			8	4	4		

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total 1	Na 1	0	0

- Molecule 6 is water.

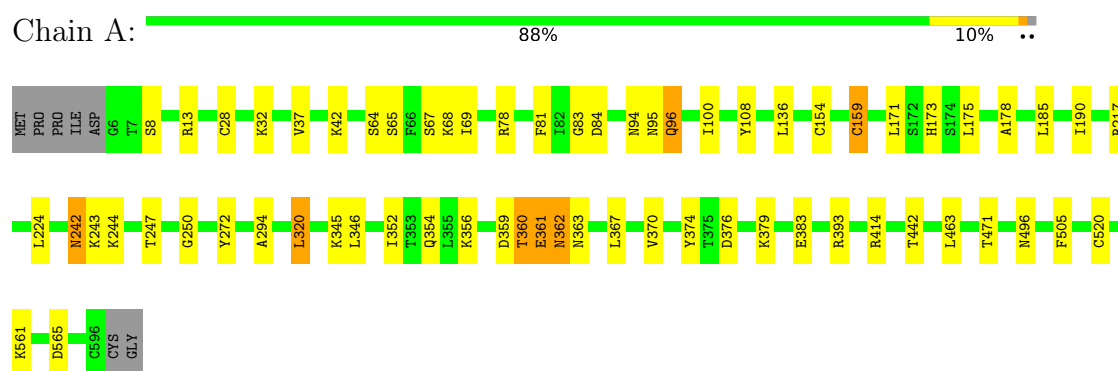
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	87	Total 87	O 87	0	0
6	B	45	Total 45	O 45	0	0

3 Residue-property plots

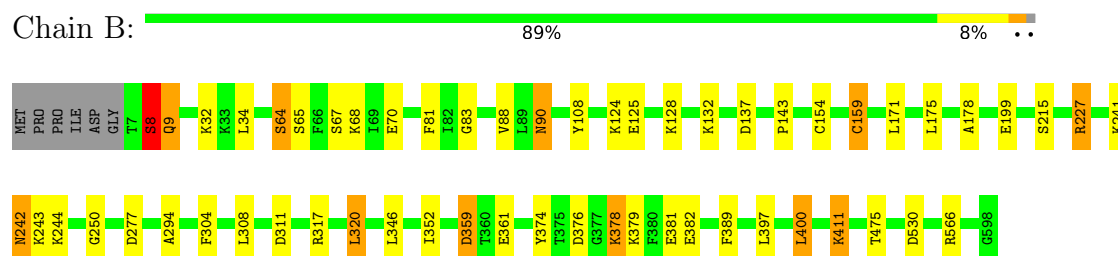
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: thioredoxin-disulfide reductase (NADPH)



- Molecule 1: thioredoxin-disulfide reductase (NADPH)



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	84.56Å 87.58Å 185.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.93 – 2.12	Depositor
% Data completeness (in resolution range)	100.0 (50.93-2.12)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.209 , 0.248	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9337	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FAD, SIN, GSH, NA

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	0/4624	1.18	12/6261 (0.2%)
1	B	0.66	0/4622	1.13	9/6259 (0.1%)
All	All	0.69	0/9246	1.15	21/12520 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	3
All	All	0	5

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	471	THR	CA-CB-OG1	-7.66	98.11	109.60
1	A	471	THR	OG1-CB-CG2	7.11	123.52	109.30
1	A	95	ASN	CB-CA-C	-6.64	102.11	111.80
1	A	360	THR	CA-CB-OG1	6.23	118.94	109.60
1	B	90	ASN	CB-CA-C	6.20	120.51	110.96
1	A	361	GLU	CB-CA-C	6.04	122.45	110.42
1	A	393	ARG	CD-NE-CZ	5.99	132.79	124.40
1	B	311	ASP	CB-CA-C	5.91	120.55	110.81
1	B	378	LYS	CB-CA-C	5.87	121.80	109.65
1	B	376	ASP	CA-CB-CG	5.84	118.44	112.60
1	A	363	ASN	CA-CB-CG	-5.61	107.00	112.60
1	A	496	ASN	CA-CB-CG	-5.58	107.02	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	199	GLU	CB-CG-CD	5.56	122.05	112.60
1	B	359	ASP	CA-CB-CG	5.52	118.12	112.60
1	B	277	ASP	CA-CB-CG	5.47	118.07	112.60
1	A	360	THR	N-CA-CB	5.42	119.87	110.39
1	B	530	ASP	CA-CB-CG	5.27	117.87	112.60
1	B	132	LYS	CB-CA-C	5.23	118.86	110.29
1	A	376	ASP	CA-CB-CG	5.11	117.71	112.60
1	A	356	LYS	CB-CA-C	-5.08	101.57	109.20
1	A	414	ARG	CG-CD-NE	-5.05	100.90	112.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	217	ARG	Sidechain
1	A	78	ARG	Sidechain
1	B	227	ARG	Sidechain
1	B	317	ARG	Sidechain
1	B	566	ARG	Sidechain

5.2 Too-close contacts

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	4536	0	4521	34	0
1	B	4534	0	4514	33	0
2	A	53	0	31	0	0
2	B	53	0	31	3	0
3	A	20	0	15	3	0
4	A	8	0	4	0	0
5	A	1	0	0	0	0
6	A	87	0	0	0	0
6	B	45	0	0	0	0
All	All	9337	0	9116	61	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 3.

All (61) 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:28:CYS:SG	3:A:602:GSH:SG2	2.67	0.75
1:B:352:ILE:HD11	1:B:389:PHE:HZ	1.54	0.73
1:A:175:LEU:HD23	1:B:175:LEU:HD23	1.71	0.72
1:B:137:ASP:HA	2:B:601:FAD:H8A	1.73	0.70
1:B:359:ASP:OD1	1:B:361:GLU:HB3	1.93	0.69
1:B:242:ASN:HD21	1:B:244:LYS:HG3	1.61	0.66
1:A:242:ASN:HD21	1:A:244:LYS:HG3	1.60	0.65
1:B:242:ASN:ND2	1:B:244:LYS:HG3	2.14	0.62
1:B:352:ILE:HD11	1:B:389:PHE:CZ	2.33	0.60
1:A:175:LEU:CD2	1:B:175:LEU:HD23	2.30	0.60
1:B:241:LYS:HA	1:B:241:LYS:HE2	1.83	0.60
1:B:67:SER:O	1:B:68:LYS:HB2	2.03	0.57
1:B:381:GLU:O	1:B:382[B]:GLU:HG2	2.05	0.57
1:A:67:SER:O	1:A:68:LYS:HB2	2.05	0.55
1:A:242:ASN:ND2	1:A:244:LYS:HG3	2.20	0.54
1:A:294:ALA:HB1	1:A:320:LEU:HD12	1.89	0.53
1:A:362:ASN:OD1	1:A:362:ASN:N	2.41	0.53
1:B:108:TYR:O	1:B:250:GLY:HA2	2.09	0.53
1:A:242:ASN:C	1:A:242:ASN:HD22	2.16	0.52
1:A:42:LYS:N	1:A:42:LYS:HD2	2.24	0.52
1:A:185:LEU:HD12	1:A:190:ILE:CD1	2.38	0.52
1:B:242:ASN:C	1:B:242:ASN:HD22	2.18	0.52
1:A:561:LYS:NZ	1:A:565:ASP:OD1	2.44	0.50
1:B:294:ALA:HB1	1:B:320:LEU:HD12	1.92	0.50
1:B:81:PHE:CZ	1:B:83:GLY:HA2	2.46	0.50
1:B:411:LYS:HD3	1:B:411:LYS:C	2.37	0.49
1:A:154:CYS:SG	1:A:159:CYS:CB	3.00	0.49
1:A:13:ARG:HG2	1:A:13:ARG:HH21	1.79	0.48
1:B:154:CYS:SG	1:B:159:CYS:CB	3.01	0.48
1:B:64:SER:OG	1:B:70:GLU:CG	2.63	0.46
1:B:227:ARG:HG3	2:B:601:FAD:N6A	2.31	0.46
1:B:137:ASP:OD1	2:B:601:FAD:H1B	2.15	0.46
1:A:175:LEU:HD23	1:B:175:LEU:CD2	2.43	0.45
1:B:125:GLU:O	1:B:128:LYS:HB2	2.15	0.45
1:B:346:LEU:O	1:B:374:TYR:HA	2.16	0.45
1:A:84:ASP:HB2	3:A:602:GSH:O11	2.17	0.45
1:A:346:LEU:O	1:A:374:TYR:HA	2.17	0.45
1:A:94:ASN:HB3	1:A:96:GLN:OE1	2.17	0.44
1:A:175:LEU:CD2	1:B:175:LEU:CD2	2.95	0.44
1:A:352:ILE:HD12	1:A:370:VAL:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:CYS:HG	3:A:602:GSH:CB2	2.30	0.44
1:A:81:PHE:CZ	1:A:83:GLY:HA2	2.53	0.43
1:A:359:ASP:OD1	1:A:361:GLU:HG2	2.17	0.43
1:B:397:LEU:HD22	1:B:400:LEU:HD22	1.99	0.43
1:A:64:SER:HB3	1:A:69:ILE:O	2.19	0.43
1:A:367:LEU:HD11	1:A:383:GLU:HG3	2.01	0.43
1:B:64:SER:OG	1:B:70:GLU:HG2	2.18	0.43
1:A:505:PHE:CZ	1:A:520:CYS:HB3	2.55	0.42
1:A:108:TYR:O	1:A:250:GLY:HA2	2.19	0.42
1:A:272:TYR:CE1	1:A:354:GLN:HB2	2.55	0.42
1:B:304:PHE:O	1:B:308:LEU:HG	2.20	0.42
1:A:178:ALA:HA	1:B:171:LEU:HD13	2.02	0.41
1:B:34:LEU:HD11	1:B:88:VAL:HG11	2.01	0.41
1:A:171:LEU:HD13	1:B:178:ALA:HA	2.02	0.41
1:B:9:GLN:CD	1:B:9:GLN:H	2.26	0.41
1:A:242:ASN:ND2	1:A:244:LYS:CG	2.83	0.41
1:B:8:SER:HB3	1:B:9:GLN:H	1.75	0.41
1:A:96:GLN:O	1:A:100:ILE:HG13	2.21	0.40
1:B:124:LYS:HD3	1:B:215:SER:OG	2.21	0.40
1:A:13:ARG:HG2	1:A:13:ARG:NH2	2.37	0.40
1:A:136:LEU:CD2	1:A:224:LEU:HD12	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	591/598 (99%)	572 (97%)	18 (3%)	1 (0%)	43	44
1	B	591/598 (99%)	568 (96%)	21 (4%)	2 (0%)	36	36
All	All	1182/1196 (99%)	1140 (96%)	39 (3%)	3 (0%)	36	36

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	8	SER
1	A	243	LYS
1	B	243	LYS

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	492/496 (99%)	476 (97%)	16 (3%)	33	36
1	B	492/496 (99%)	477 (97%)	15 (3%)	36	40
All	All	984/992 (99%)	953 (97%)	31 (3%)	34	37

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	SER
1	A	32	LYS
1	A	37	VAL
1	A	65	SER
1	A	96	GLN
1	A	159	CYS
1	A	173	HIS
1	A	242	ASN
1	A	247	THR
1	A	320	LEU
1	A	345	LYS
1	A	360	THR
1	A	362	ASN
1	A	379	LYS
1	A	442	THR
1	A	463	LEU
1	B	8	SER
1	B	9	GLN
1	B	32	LYS
1	B	64	SER

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Mol	Chain	Res	Type
1	B	65	SER
1	B	90	ASN
1	B	143	PRO
1	B	159	CYS
1	B	242	ASN
1	B	320	LEU
1	B	378	LYS
1	B	379	LYS
1	B	400	LEU
1	B	411	LYS
1	B	475	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	93	ASN
1	A	156	ASN
1	A	204	HIS
1	A	209	ASN
1	A	225	ASN
1	A	237	GLN
1	A	242	ASN
1	A	354	GLN
1	A	447	HIS
1	B	9	GLN
1	B	92	HIS
1	B	93	ASN
1	B	156	ASN
1	B	180	HIS
1	B	204	HIS
1	B	209	ASN
1	B	225	ASN
1	B	242	ASN
1	B	354	GLN
1	B	447	HIS
1	B	496	ASN

5.3.3 RNA ⓘ

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](#)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 for Mogul analysis.

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	FAD	B	601	-	56,58,58	0.61	0	81,89,89	1.04	4 (4%)
3	GSH	A	602	-	18,19,19	0.72	0	23,24,24	1.17	2 (8%)
2	FAD	A	601	-	56,58,58	0.63	0	81,89,89	0.68	0
4	SIN	A	603	-	7,7,7	1.44	1 (14%)	8,8,8	2.15	3 (37%)

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	FAD	B	601	-	-	9/34/50/50	0/6/6/6
3	GSH	A	602	-	-	2/24/24/24	-
2	FAD	A	601	-	-	3/34/50/50	0/6/6/6
4	SIN	A	603	-	-	3/5/5/5	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	SIN	O3-C4	2.25	1.29	1.22

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	603	SIN	C2-C3-C4	4.39	123.05	113.60
2	B	601	FAD	C2B-C1B-N9A	3.54	122.26	113.30
3	A	602	GSH	O32-C3-CA3	3.33	124.29	112.74
3	A	602	GSH	O31-C3-CA3	-3.04	110.42	122.68
2	B	601	FAD	O4B-C1B-C2B	-2.76	100.62	106.64
4	A	603	SIN	C3-C2-C1	2.46	118.90	113.60
2	B	601	FAD	O2B-C2B-C1B	2.44	118.17	110.02
4	A	603	SIN	O2-C1-C2	2.36	121.60	114.03
2	B	601	FAD	C4A-N9A-C1B	2.10	131.59	126.59

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	FAD	C5B-O5B-PA-O1A
2	B	601	FAD	C5B-O5B-PA-O2A
2	B	601	FAD	C5B-O5B-PA-O3P
4	A	603	SIN	C1-C2-C3-C4
2	B	601	FAD	PA-O3P-P-O1P
2	A	601	FAD	PA-O3P-P-O5'
2	B	601	FAD	PA-O3P-P-O5'
2	B	601	FAD	C2B-C1B-N9A-C4A
2	B	601	FAD	C2B-C1B-N9A-C8A
2	A	601	FAD	P-O3P-PA-O1A
2	B	601	FAD	O4B-C4B-C5B-O5B
3	A	602	GSH	O32-C3-CA3-N3
3	A	602	GSH	CA1-CB1-CG1-CD1
2	A	601	FAD	O4B-C4B-C5B-O5B
2	B	601	FAD	O4B-C1B-N9A-C8A
4	A	603	SIN	O2-C1-C2-C3
4	A	603	SIN	O1-C1-C2-C3

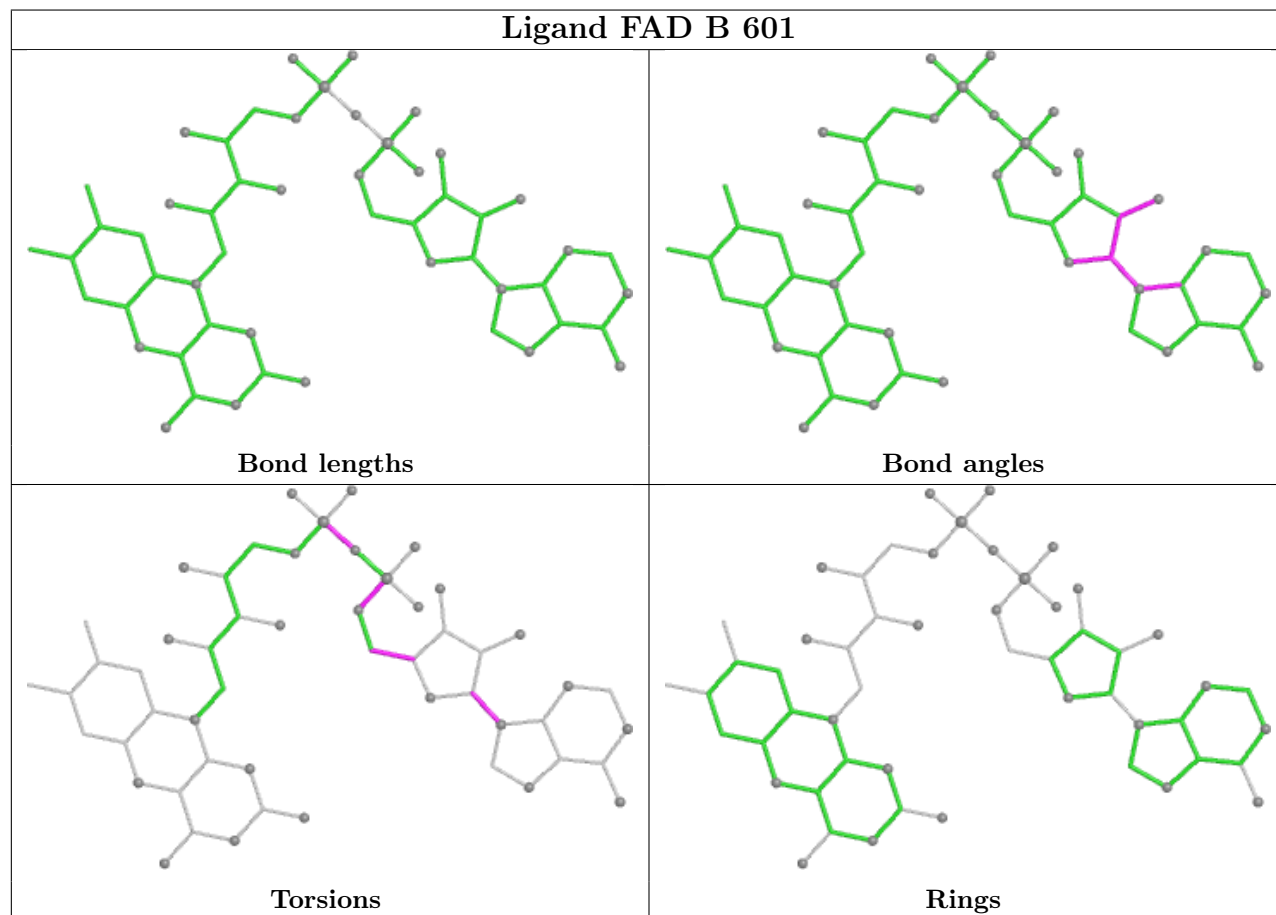
There are no ring outliers.

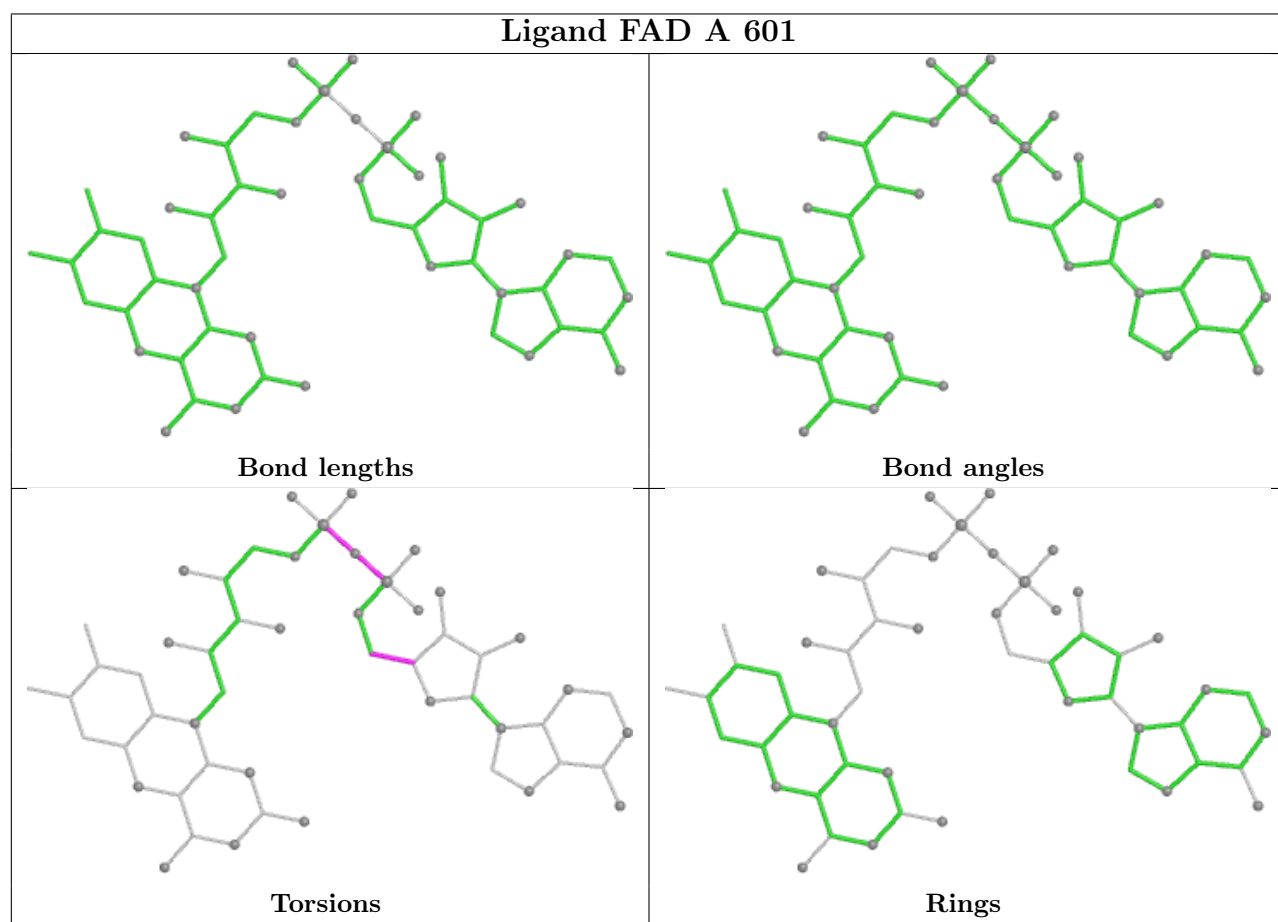
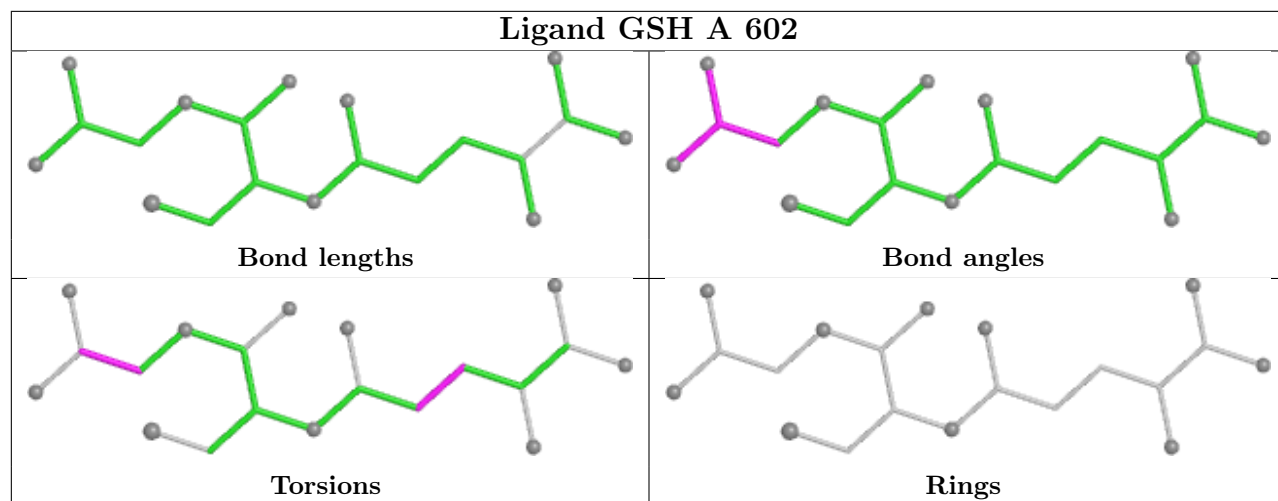
2 monomers are involved in 6 short contacts:

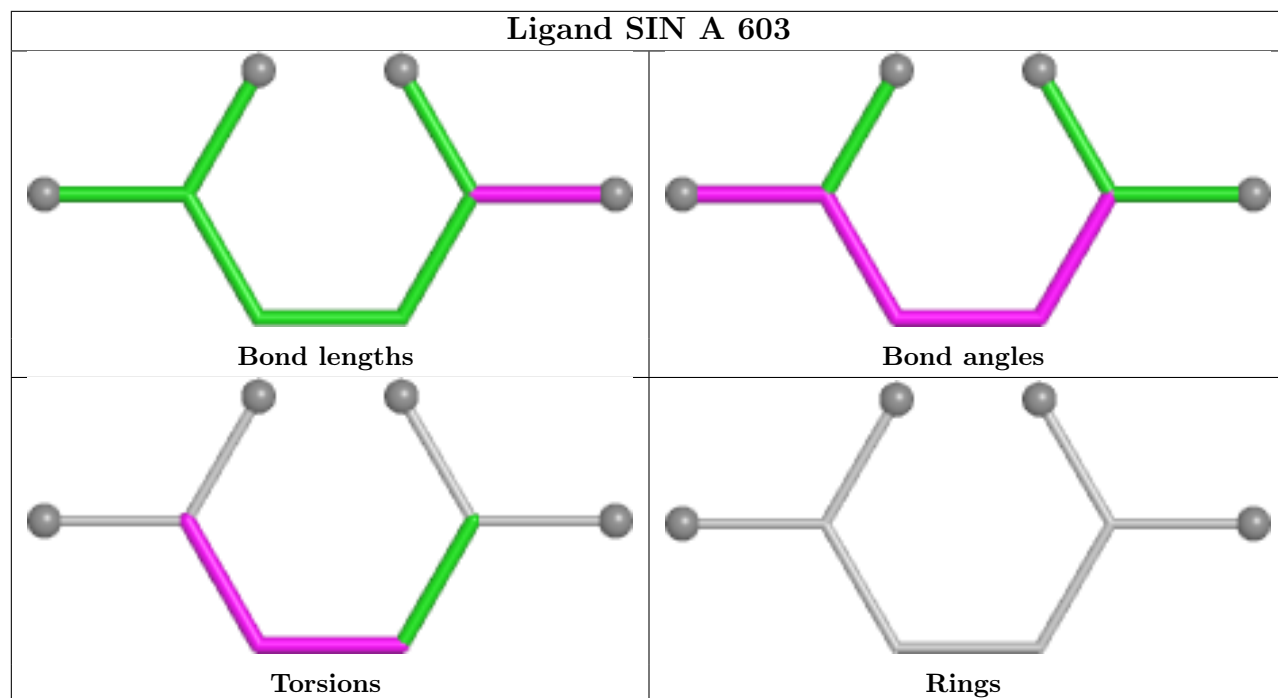
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	FAD	3	0
3	A	602	GSH	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.