



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 02:07 AM BST

PDB ID : 6AP9  
Title : Crystal Structure of hGSTP1-1 with S-nitrosation of Cys101  
Authors : Kumari, V.; Ji, X.  
Deposited on : 2017-08-17  
Resolution : 1.55 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](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.

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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 : 2.13.1  
buster-report : 1.1.7 (2018)  
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) : 2.13.1

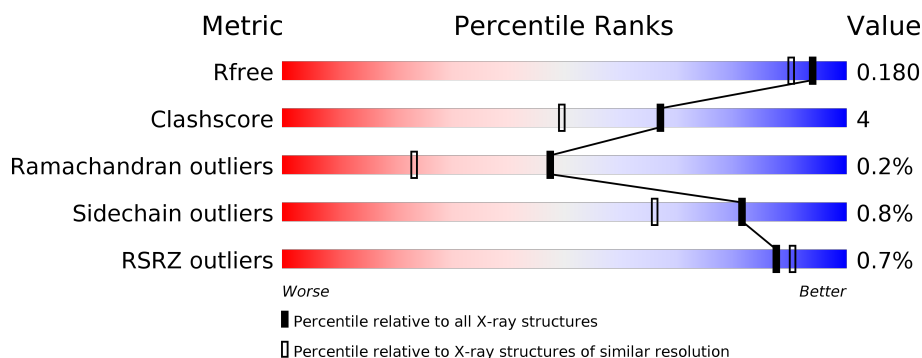
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.55 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	1483 (1.56-1.56)
Clashscore	141614	1529 (1.56-1.56)
Ramachandran outliers	138981	1498 (1.56-1.56)
Sidechain outliers	138945	1495 (1.56-1.56)
RSRZ outliers	127900	1465 (1.56-1.56)

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  $\geq 3$ , 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	211	
1	B	211	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	ACT	A	304[B]	-	-	X	-
5	ACT	B	304[B]	-	-	X	-

## 2 Entry composition [i](#)

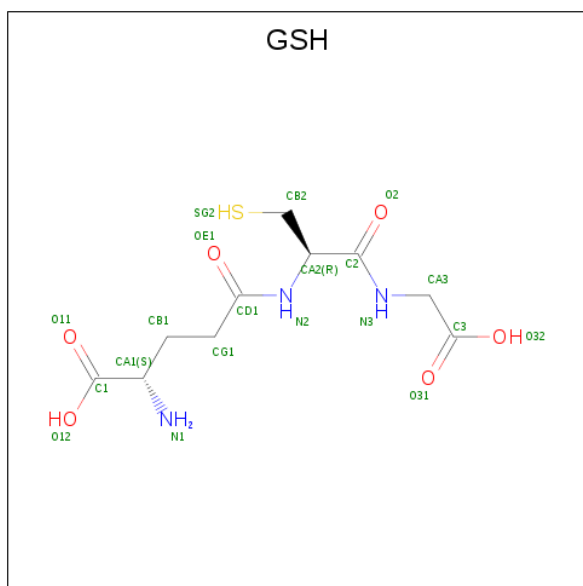
There are 7 unique types of molecules in this entry. The entry contains 4359 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 P.

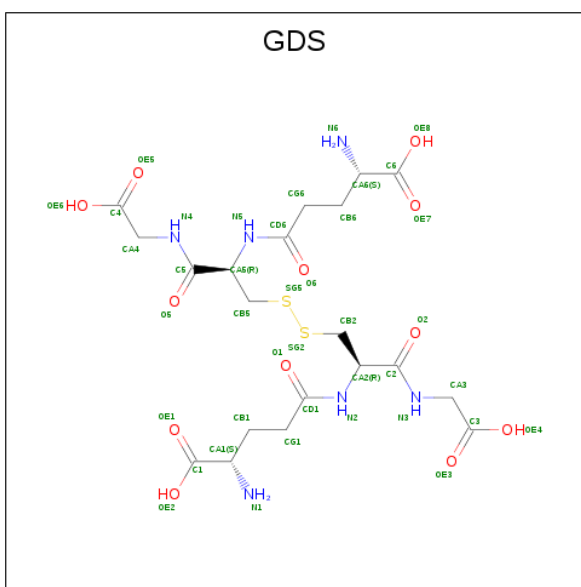
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	210	Total	C	N	O	S	0	14	0
			1720	1109	277	325	9			
1	B	209	Total	C	N	O	S	0	9	0
			1687	1087	276	316	8			

- Molecule 2 is GLUTATHIONE (three-letter code: GSH) (formula:  $C_{10}H_{17}N_3O_6S$ ).



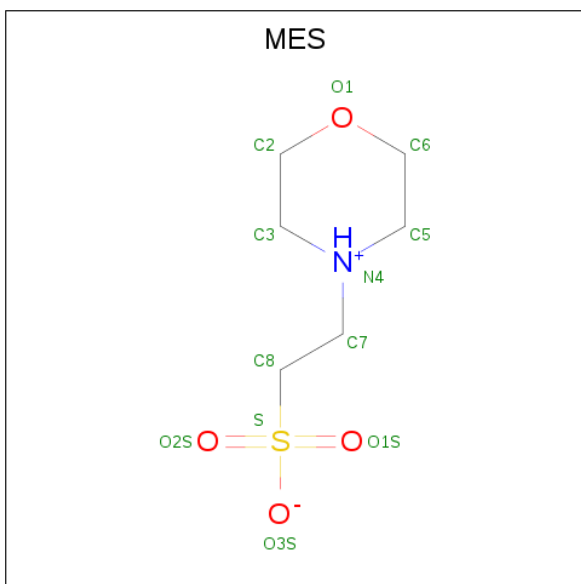
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	1
			20	10	3	6	1		
2	B	1	Total	C	N	O	S	0	1
			20	10	3	6	1		

- Molecule 3 is OXIDIZED GLUTATHIONE DISULFIDE (three-letter code: GDS) (formula:  $C_{20}H_{32}N_6O_{12}S_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 40	C 20	N 6	O 12	S 2	0	1
3	B	1	Total 40	C 20	N 6	O 12	S 2	0	1

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula:  $\text{C}_6\text{H}_{13}\text{NO}_4\text{S}$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	1
			24	12	2	8	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	1
			24	12	2	8	2		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	1
			4	2	2		
5	B	1	Total	C	O	0	1
			4	2	2		

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	3	Total	Ca	0	0
			3	3		
6	A	2	Total	Ca	0	0
			2	2		

- Molecule 7 is water.

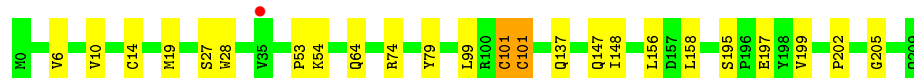
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	368	Total	O	0	18
			380	380		
7	B	380	Total	O	0	15
			391	391		

### 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.

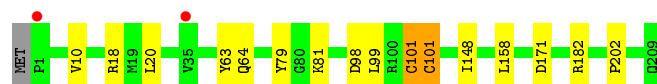
- Molecule 1: Glutathione S-transferase P

Chain A: 



- Molecule 1: Glutathione S-transferase P

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.15Å 90.05Å 68.87Å 90.00° 98.67° 90.00°	Depositor
Resolution (Å)	29.32 – 1.55 29.32 – 1.55	Depositor EDS
% Data completeness (in resolution range)	99.6 (29.32-1.55) 99.7 (29.32-1.55)	Depositor EDS
$R_{merge}$	0.88	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.57 (at 1.55Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, $R_{free}$	0.146 , 0.181 0.146 , 0.180	Depositor DCC
$R_{free}$ test set	1000 reflections (1.47%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	11.5	Xtriage
Anisotropy	0.422	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 49.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	4359	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.56% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GDS, SNC, CA, MES, ACT, GSH

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	0.92	0/1782	0.94	3/2415 (0.1%)
1	B	0.90	0/1738	0.90	4/2355 (0.2%)
All	All	0.91	0/3520	0.92	7/4770 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	74	ARG	NE-CZ-NH2	-12.89	113.86	120.30
1	A	74	ARG	NE-CZ-NH1	10.00	125.30	120.30
1	B	98	ASP	CB-CG-OD2	-6.24	112.68	118.30
1	B	18	ARG	NE-CZ-NH2	-5.91	117.34	120.30
1	A	74	ARG	CG-CD-NE	-5.88	99.45	111.80
1	B	171	ASP	CB-CG-OD2	-5.61	113.26	118.30
1	B	182	ARG	NE-CZ-NH1	5.46	123.03	120.30

There are no chirality outliers.

There are no planarity outliers.

### 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	1720	0	1745	17	0
1	B	1687	0	1707	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	20	0	15	0	0
2	B	20	0	15	0	0
3	A	40	0	28	3	0
3	B	40	0	28	0	0
4	A	24	0	24	3	0
4	B	24	0	24	0	0
5	A	4	0	3	2	0
5	B	4	0	3	2	0
6	A	2	0	0	0	0
6	B	3	0	0	0	0
7	A	380	0	0	7	1
7	B	391	0	0	3	1
All	All	4359	0	3592	28	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 4.

All (28) 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:101[A]:SNC:SG	7:A:653:HOH:O	2.33	0.85
1:B:101[A]:SNC:SG	7:B:678:HOH:O	2.36	0.83
3:A:302[B]:GDS:SG2	7:A:574[B]:HOH:O	2.44	0.76
1:A:197[A]:GLU:OE1	7:A:401[A]:HOH:O	2.09	0.70
1:B:148:ILE:H	5:B:304[B]:ACT:H2	1.58	0.66
1:A:19[B]:MET:SD	7:A:449:HOH:O	2.54	0.64
3:A:302[B]:GDS:HA32	3:A:302[B]:GDS:HN4	1.66	0.61
1:A:99:LEU:HD23	1:A:158[A]:LEU:HD21	1.85	0.58
1:A:137:GLN:HG3	7:A:442[A]:HOH:O	2.03	0.58
1:A:148:ILE:HG22	5:A:304[B]:ACT:H3	1.89	0.55
1:A:28:TRP:CH2	4:A:303[B]:MES:H72	2.44	0.53
1:A:148:ILE:H	5:A:304[B]:ACT:H3	1.77	0.50
1:A:195:SER:O	1:A:199[B]:VAL:HG22	2.12	0.50
1:B:81:LYS:HE2	7:B:715:HOH:O	2.12	0.48
1:A:28:TRP:O	4:A:303[B]:MES:H21	2.14	0.48
1:A:6:VAL:HB	1:A:54:LYS:HB3	1.97	0.46
1:B:63:TYR:O	1:B:64:GLN:HB2	2.15	0.46
1:A:147[B]:GLN:HG3	7:A:554:HOH:O	2.16	0.45
1:B:99:LEU:HD23	1:B:158:LEU:HD21	1.99	0.43
1:A:10[B]:VAL:HG11	1:A:205:GLY:HA2	2.00	0.43
1:B:10[A]:VAL:HG12	1:B:202:PRO:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:304[B]:ACT:H3	7:B:446:HOH:O	2.17	0.42
3:A:302[B]:GDS:HB11	7:A:654:HOH:O	2.20	0.42
1:B:20:LEU:C	1:B:20:LEU:HD23	2.41	0.41
1:A:19[B]:MET:CE	1:A:156:LEU:HD23	2.50	0.41
1:A:10[B]:VAL:HG12	1:A:202:PRO:HG2	2.02	0.41
1:A:28:TRP:CZ3	4:A:303[B]:MES:H72	2.56	0.40
1:A:14:CYS:SG	1:A:53:PRO:HB3	2.62	0.40

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)
7:A:445:HOH:O	7:B:462:HOH:O[3_545]	2.03	0.17

## 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	220/211 (104%)	214 (97%)	5 (2%)	1 (0%)	29	9
1	B	214/211 (101%)	208 (97%)	6 (3%)	0	100	100
All	All	434/422 (103%)	422 (97%)	11 (2%)	1 (0%)	47	23

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	64	GLN

### 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	190/177 (107%)	187 (98%)	3 (2%)	62	35
1	B	184/177 (104%)	183 (100%)	1 (0%)	88	78
All	All	374/354 (106%)	370 (99%)	4 (1%)	81	53

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27[A]	SER
1	A	27[B]	SER
1	A	79	TYR
1	B	79	TYR

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

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	SNC	A	101[A]	1	4,7,8	2.44	1 (25%)	1,7,9	3.52	1 (100%)
1	SNC	B	101[A]	1	4,7,8	2.13	1 (25%)	1,7,9	3.57	1 (100%)

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
1	SNC	A	101[A]	1	-	0/0/6/8	-
1	SNC	B	101[A]	1	-	0/0/6/8	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	101[A]	SNC	CA-N	-4.72	1.33	1.48
1	B	101[A]	SNC	CA-N	-3.95	1.36	1.48

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	101[A]	SNC	CA-CB-SG	3.57	120.18	112.76
1	A	101[A]	SNC	CA-CB-SG	3.52	120.06	112.76

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	101[A]	SNC	1	0
1	B	101[A]	SNC	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 5 are monoatomic - leaving 10 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	GSH	B	301[A]	-	12,19,19	0.67	0	15,24,24	1.51	2 (13%)
4	MES	A	303[B]	-	12,12,12	2.89	6 (50%)	14,16,16	7.21	6 (42%)
2	GSH	A	301[A]	-	12,19,19	0.91	1 (8%)	15,24,24	2.02	2 (13%)
4	MES	A	303[A]	-	12,12,12	3.12	5 (41%)	14,16,16	6.78	3 (21%)
4	MES	B	303[A]	-	12,12,12	3.24	6 (50%)	14,16,16	7.76	6 (42%)
4	MES	B	303[B]	-	12,12,12	3.20	6 (50%)	14,16,16	7.50	5 (35%)
5	ACT	B	304[B]	-	1,3,3	2.20	1 (100%)	0,3,3	0.00	-
5	ACT	A	304[B]	-	1,3,3	2.95	1 (100%)	0,3,3	0.00	-
3	GDS	B	302[B]	-	25,39,39	2.19	7 (28%)	32,50,50	1.38	3 (9%)
3	GDS	A	302[B]	-	25,39,39	2.17	7 (28%)	32,50,50	1.69	8 (25%)

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	GSH	B	301[A]	-	-	1/18/24/24	-
4	MES	A	303[B]	-	-	3/6/14/14	0/1/1/1
4	MES	A	303[A]	-	-	3/6/14/14	0/1/1/1
4	MES	B	303[A]	-	-	2/6/14/14	0/1/1/1
4	MES	B	303[B]	-	-	3/6/14/14	0/1/1/1
2	GSH	A	301[A]	-	-	0/18/24/24	-
3	GDS	B	302[B]	-	-	2/39/51/51	-
3	GDS	A	302[B]	-	-	3/39/51/51	-

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	303[A]	MES	C7-N4	-6.60	1.32	1.47
4	B	303[B]	MES	C7-N4	-6.31	1.32	1.47
4	A	303[A]	MES	C7-N4	-6.03	1.33	1.47
4	A	303[B]	MES	C7-N4	-5.94	1.33	1.47
3	A	302[B]	GDS	C5-N4	5.28	1.45	1.33
3	B	302[B]	GDS	C5-N4	5.24	1.45	1.33
3	B	302[B]	GDS	CD6-N5	5.11	1.44	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302[B]	GDS	C2-N3	5.08	1.44	1.33
4	B	303[B]	MES	C8-S	-4.93	1.70	1.77
4	A	303[A]	MES	C3-N4	-4.83	1.33	1.46
4	B	303[A]	MES	C3-N4	-4.79	1.33	1.46
4	B	303[B]	MES	C5-N4	-4.74	1.33	1.46
4	A	303[A]	MES	C5-N4	-4.73	1.33	1.46
4	B	303[A]	MES	C5-N4	-4.69	1.34	1.46
3	B	302[B]	GDS	C2-N3	4.61	1.43	1.33
4	B	303[B]	MES	C3-N4	-4.59	1.34	1.46
4	A	303[B]	MES	C5-N4	-4.55	1.34	1.46
4	A	303[A]	MES	C8-S	-4.45	1.71	1.77
3	A	302[B]	GDS	CD6-N5	4.35	1.43	1.34
4	A	303[B]	MES	C3-N4	-4.25	1.35	1.46
4	B	303[A]	MES	C8-S	-4.24	1.71	1.77
3	A	302[B]	GDS	CD1-N2	3.85	1.42	1.34
3	B	302[B]	GDS	CD1-N2	3.38	1.41	1.34
4	B	303[A]	MES	O1S-S	3.06	1.54	1.45
3	A	302[B]	GDS	CG1-CD1	3.02	1.57	1.51
5	A	304[B]	ACT	CH3-C	2.95	1.52	1.48
4	A	303[B]	MES	C8-S	-2.89	1.73	1.77
2	A	301[A]	GSH	CB2-CA2	2.66	1.56	1.53
4	A	303[B]	MES	O1S-S	2.66	1.52	1.45
3	B	302[B]	GDS	CA1-N1	-2.57	1.41	1.47
4	B	303[A]	MES	O2S-S	2.37	1.52	1.45
4	B	303[B]	MES	O1S-S	2.37	1.52	1.45
3	B	302[B]	GDS	CG1-CD1	2.30	1.55	1.51
4	A	303[B]	MES	O2S-S	2.27	1.51	1.45
3	A	302[B]	GDS	CA6-N6	-2.27	1.42	1.47
4	A	303[A]	MES	O1S-S	2.23	1.51	1.45
5	B	304[B]	ACT	CH3-C	2.20	1.51	1.48
4	B	303[B]	MES	O2S-S	2.17	1.51	1.45
3	A	302[B]	GDS	CA1-N1	-2.16	1.42	1.47
3	B	302[B]	GDS	CA6-N6	-2.15	1.42	1.47

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	303[A]	MES	O1S-S-C8	-20.09	82.73	106.92
4	B	303[B]	MES	O1S-S-C8	-18.74	84.35	106.92
4	A	303[A]	MES	O3S-S-C8	18.47	135.65	105.77
4	A	303[B]	MES	O3S-S-C8	17.94	134.79	105.77
4	B	303[A]	MES	O3S-S-C8	17.44	133.98	105.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	303[B]	MES	O3S-S-C8	17.19	133.57	105.77
4	A	303[A]	MES	O1S-S-C8	-15.57	88.17	106.92
4	A	303[B]	MES	O1S-S-C8	-14.91	88.96	106.92
4	A	303[B]	MES	O3S-S-O1S	-11.37	83.48	111.27
4	B	303[A]	MES	O3S-S-O1S	-9.62	87.77	111.27
4	B	303[B]	MES	O3S-S-O1S	-9.46	88.16	111.27
4	A	303[A]	MES	O3S-S-O1S	-7.37	93.26	111.27
2	A	301[A]	GSH	CA2-CB2-SG2	-6.30	107.11	114.19
4	B	303[B]	MES	O2S-S-C8	5.46	113.50	106.92
4	A	303[B]	MES	O2S-S-C8	5.16	113.13	106.92
3	A	302[B]	GDS	CG1-CD1-N2	4.78	124.13	115.83
4	B	303[A]	MES	O2S-S-C8	4.28	112.06	106.92
4	A	303[B]	MES	C2-C3-N4	4.25	116.54	110.10
3	B	302[B]	GDS	CA4-N4-C5	-4.14	116.38	122.34
4	B	303[B]	MES	C6-C5-N4	3.41	115.28	110.10
4	B	303[A]	MES	C2-C3-N4	3.31	115.13	110.10
3	A	302[B]	GDS	O1-CD1-N2	-3.25	117.46	122.95
2	B	301[A]	GSH	CA3-N3-C2	-3.15	117.80	122.34
2	B	301[A]	GSH	CA2-CB2-SG2	-2.97	110.85	114.19
3	A	302[B]	GDS	CB5-SG5-SG2	2.80	111.08	103.82
4	B	303[A]	MES	C6-C5-N4	2.75	114.27	110.10
3	A	302[B]	GDS	CA4-N4-C5	-2.63	118.56	122.34
3	A	302[B]	GDS	CA2-N2-CD1	-2.53	115.14	121.65
2	A	301[A]	GSH	CG1-CB1-CA1	-2.44	108.15	113.84
4	A	303[B]	MES	C6-C5-N4	2.23	113.49	110.10
3	B	302[B]	GDS	CG1-CD1-N2	2.17	119.60	115.83
3	A	302[B]	GDS	O5-C5-CA5	2.14	124.95	120.45
3	A	302[B]	GDS	CA3-N3-C2	-2.10	119.32	122.34
3	B	302[B]	GDS	O1-CD1-N2	-2.03	119.53	122.95
3	A	302[B]	GDS	CG1-CB1-CA1	-2.02	109.12	113.84

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	303[B]	MES	N4-C7-C8-S
4	A	303[B]	MES	C7-C8-S-O2S
4	A	303[A]	MES	C7-C8-S-O2S
4	A	303[A]	MES	C7-C8-S-O3S
4	B	303[A]	MES	C7-C8-S-O2S
3	B	302[B]	GDS	C1-CA1-CB1-CG1
4	B	303[B]	MES	C7-C8-S-O3S

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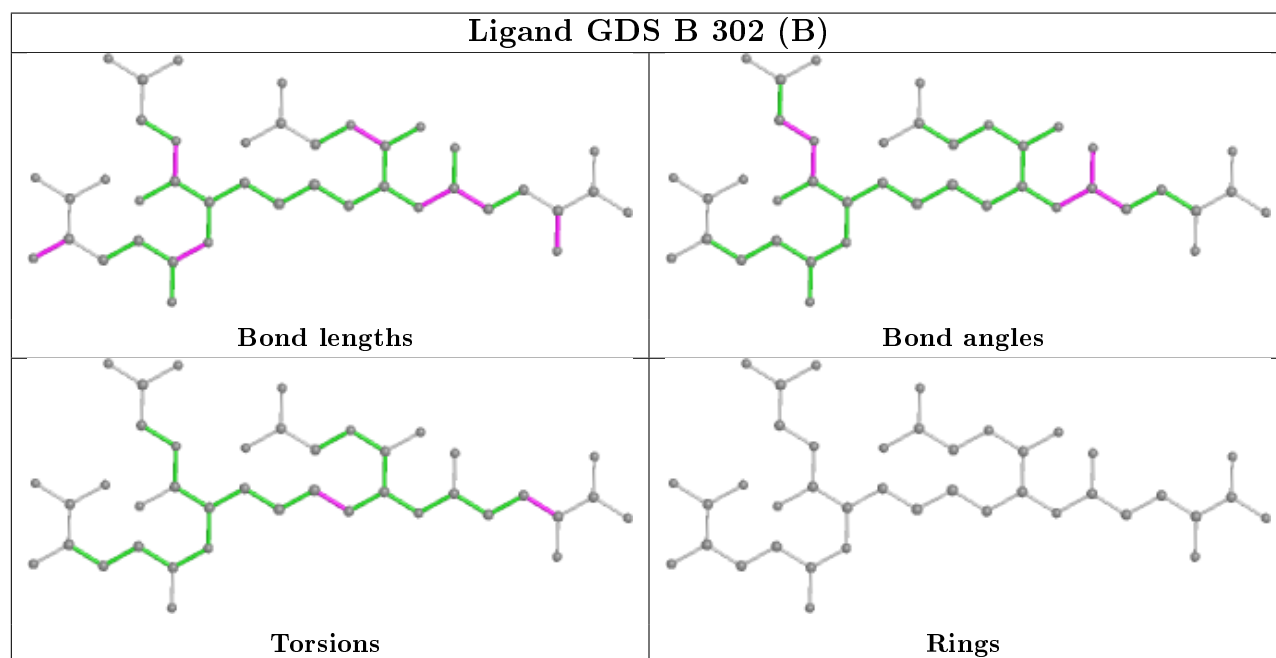
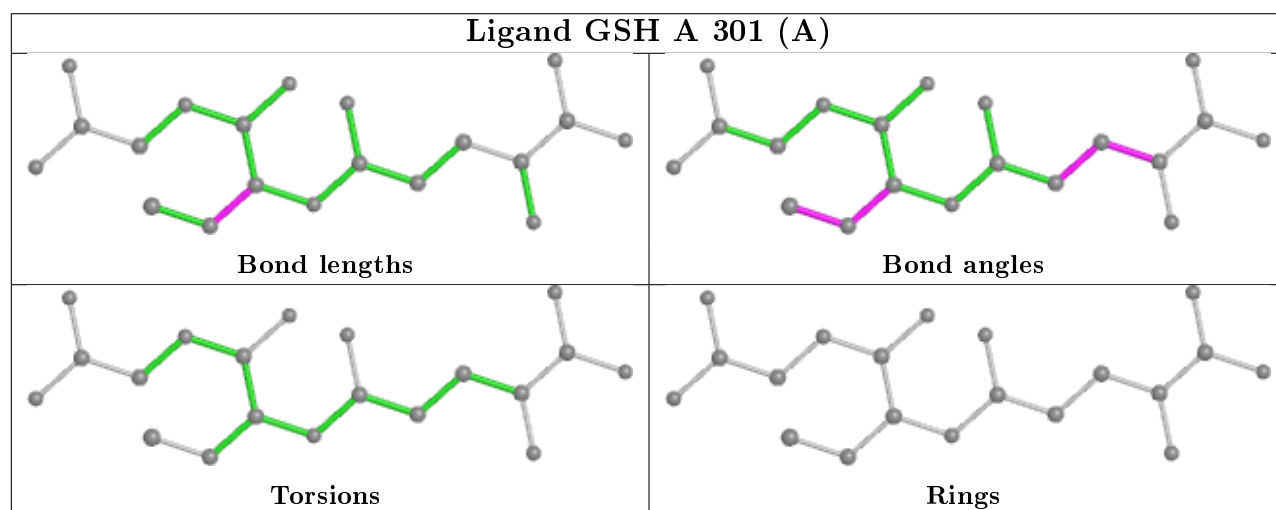
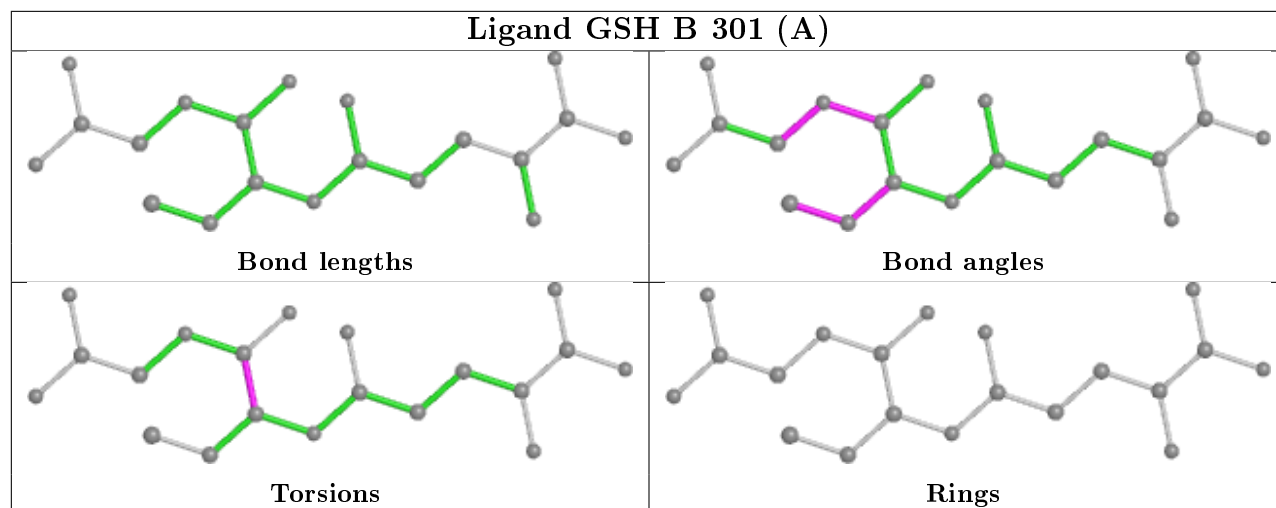
Mol	Chain	Res	Type	Atoms
3	A	302[B]	GDS	O1-CD1-CG1-CB1
3	A	302[B]	GDS	N2-CD1-CG1-CB1
4	B	303[B]	MES	C8-C7-N4-C3
4	B	303[B]	MES	C8-C7-N4-C5
4	A	303[B]	MES	C7-C8-S-O1S
4	A	303[A]	MES	C7-C8-S-O1S
4	B	303[A]	MES	C7-C8-S-O1S
2	B	301[A]	GSH	N3-C2-CA2-N2
3	B	302[B]	GDS	CA2-CB2-SG2-SG5
3	A	302[B]	GDS	CA2-CB2-SG2-SG5

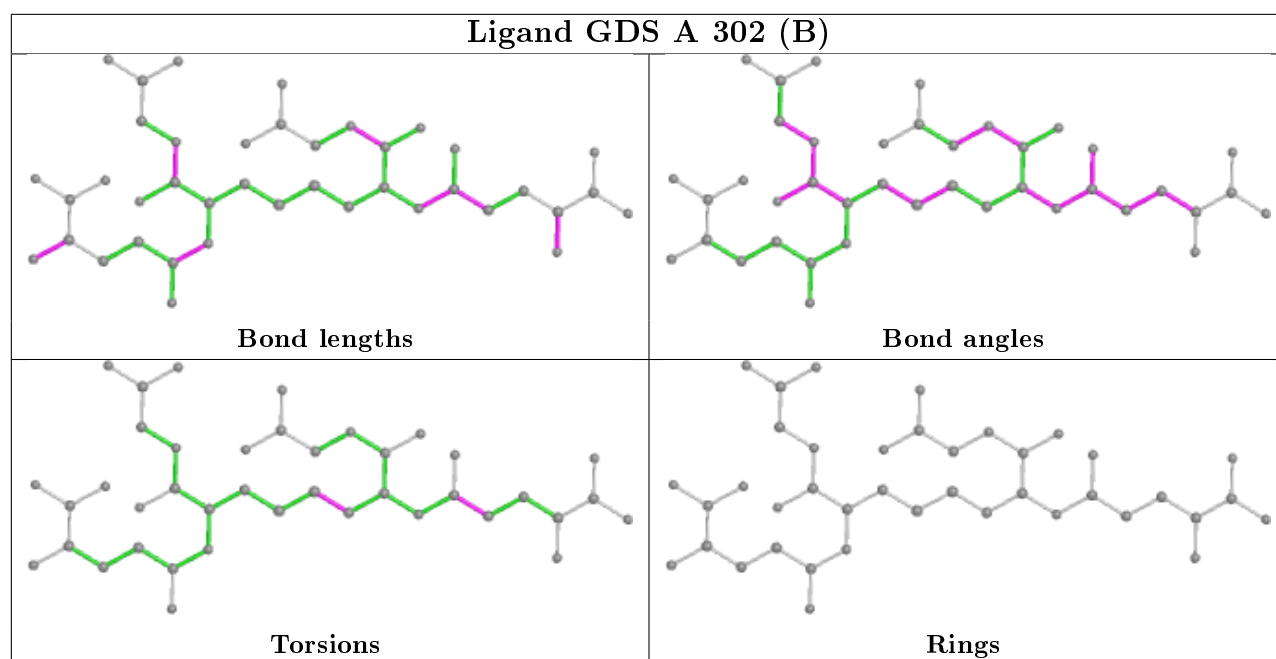
There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	303[B]	MES	3	0
5	B	304[B]	ACT	2	0
5	A	304[B]	ACT	2	0
3	A	302[B]	GDS	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 [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	209/211 (99%)	-0.55	1 (0%) 91 93	6, 12, 28, 37	0
1	B	208/211 (98%)	-0.47	2 (0%) 82 86	6, 13, 33, 52	0
All	All	417/422 (98%)	-0.51	3 (0%) 87 90	6, 12, 31, 52	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	PRO	4.1
1	B	35	VAL	3.3
1	A	35	VAL	2.0

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

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, 95<sup>th</sup> 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(Å <sup>2</sup> )	Q<0.9
1	SNC	A	101[A]	8/9	0.97	0.06	8,14,17,25	8
1	SNC	B	101[A]	8/9	0.98	0.06	8,11,17,29	8

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands

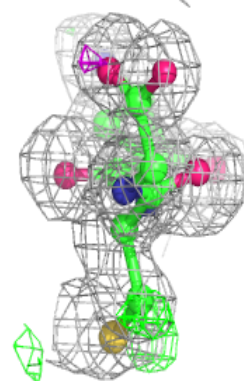
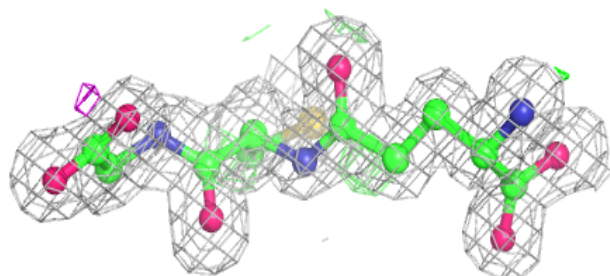
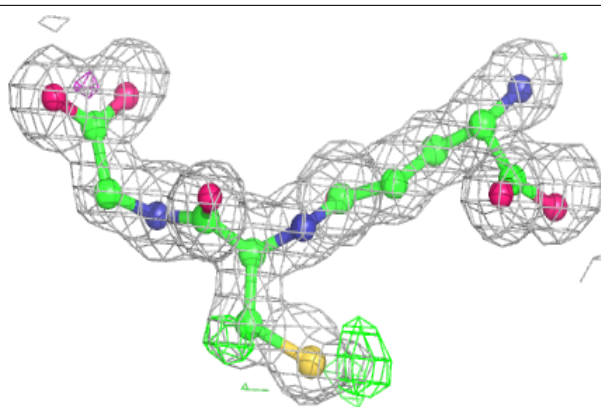
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	ACT	A	304[B]	4/4	0.91	0.14	12,16,18,24	4
5	ACT	B	304[B]	4/4	0.93	0.10	11,13,14,17	4
2	GSH	A	301[A]	20/20	0.95	0.08	7,12,16,19	20
3	GDS	B	302[B]	40/40	0.95	0.11	8,22,56,60	40
4	MES	B	303[A]	12/12	0.96	0.09	10,17,20,28	12
6	CA	B	306	1/1	0.96	0.06	17,17,17,17	1
4	MES	B	303[B]	12/12	0.96	0.09	8,16,23,32	12
4	MES	A	303[B]	12/12	0.96	0.11	6,14,22,27	12
4	MES	A	303[A]	12/12	0.96	0.11	2,14,17,18	12
2	GSH	B	301[A]	20/20	0.96	0.07	6,15,22,26	20
3	GDS	A	302[B]	40/40	0.96	0.11	6,17,55,63	40
6	CA	A	305	1/1	0.97	0.09	15,15,15,15	1
6	CA	A	306	1/1	0.98	0.05	14,14,14,14	1
6	CA	B	307	1/1	0.99	0.09	16,16,16,16	1
6	CA	B	305	1/1	1.00	0.02	11,11,11,11	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

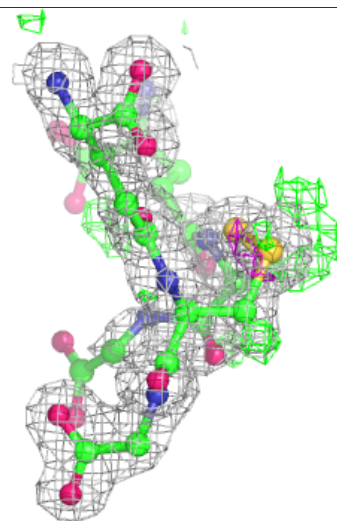
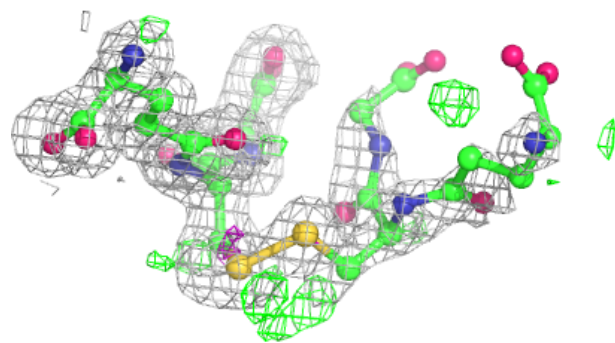
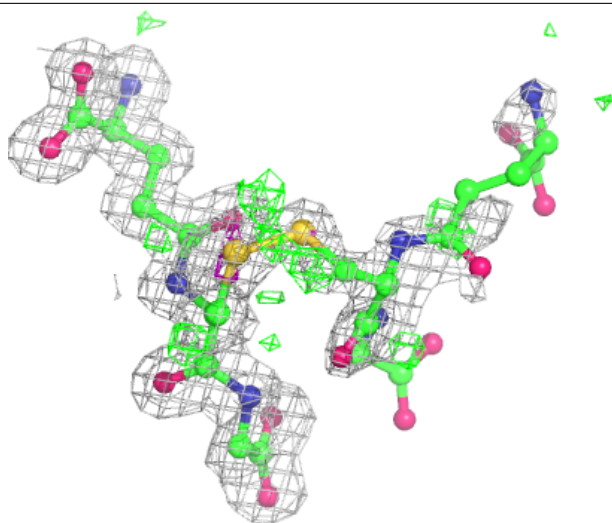
**Electron density around GSH A 301 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



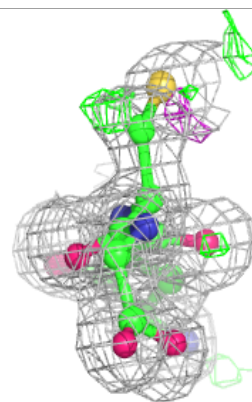
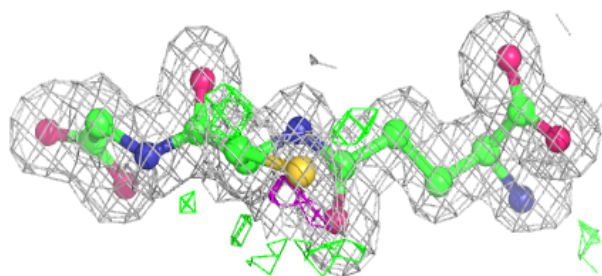
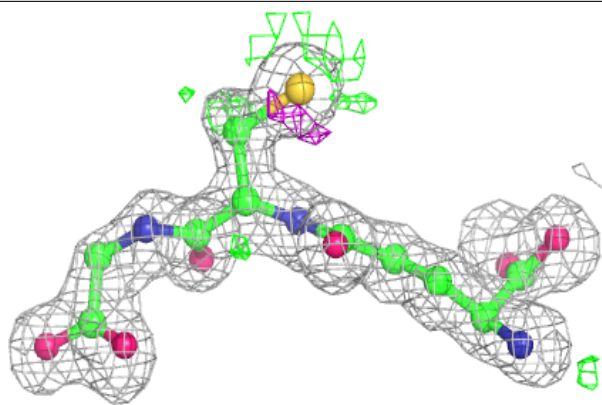
**Electron density around GDS B 302 (B):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around GSH B 301 (A):**

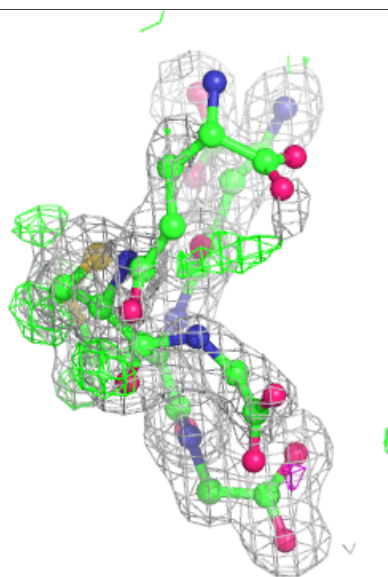
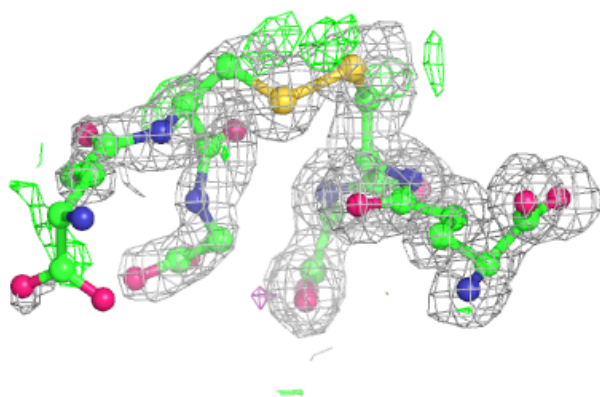
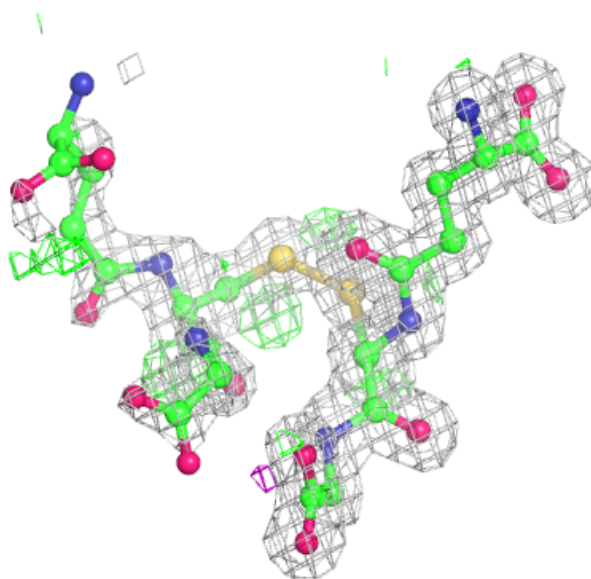
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around GDS A 302 (B):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.