



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 08:11 PM UTC

PDB ID : 5LRR / pdb_00005lrr
Title : The Transcriptional Regulator PrfA from *Listeria Monocytogenes* in complex with glutathione
Authors : Hall, M.; Grundstrom, C.; Begum, A.; Lindberg, M.; Sauer, U.H.; Almqvist, F.; Johansson, J.; Sauer-Eriksson, A.E.
Deposited on : 2016-08-19
Resolution : 2.17 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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

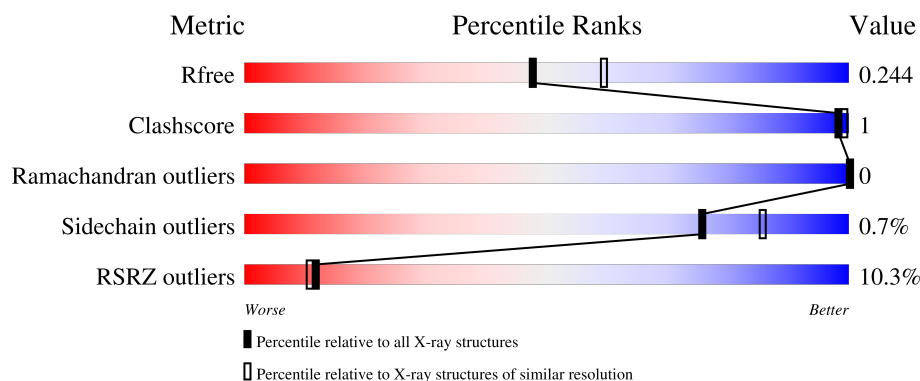
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.17 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}	180053	8975 (2.20-2.16)
Clashscore	190562	9786 (2.20-2.16)
Ramachandran outliers	187476	9664 (2.20-2.16)
Sidechain outliers	187428	9664 (2.20-2.16)
RSRZ outliers	180081	8979 (2.20-2.16)

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	237	5% 97%
1	B	237	3% 97%
1	C	237	4% 99%
1	D	237	22% 98%

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Mol	Chain	Length	Quality of chain
1	E	237	5% 98%
1	F	237	12% 95% • 5%
1	G	237	15% 97% •
1	H	237	15% 91% 5% •

2 Entry composition

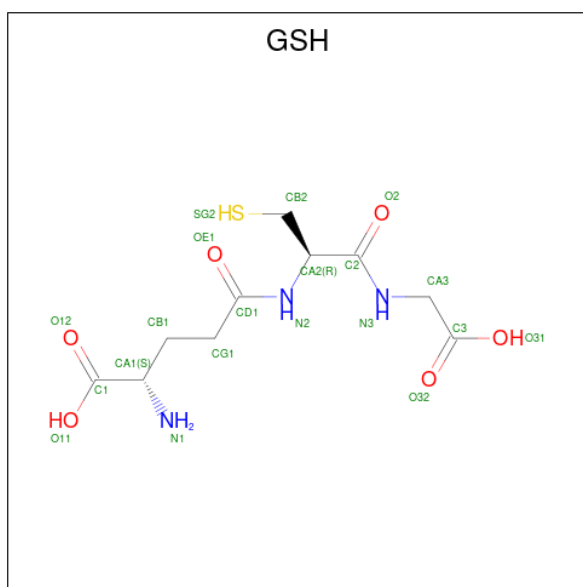
There are 5 unique types of molecules in this entry. The entry contains 31368 atoms, of which 15406 are hydrogens and 0 are deuteriums.

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 Listeriolysin positive regulatory factor A.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
1	A	236	Total	C	H	N	O	S		0	2	0
			3881	1265	1940	308	361	7				
1	B	236	Total	C	H	N	O	S		0	2	0
			3856	1258	1927	302	362	7				
1	C	236	Total	C	H	N	O	S		0	0	0
			3840	1253	1920	301	359	7				
1	D	236	Total	C	H	N	O	S		0	0	0
			3840	1253	1920	301	359	7				
1	E	236	Total	C	H	N	O	S		0	0	0
			3840	1253	1920	301	359	7				
1	F	226	Total	C	H	N	O	S		0	0	0
			3713	1213	1861	289	343	7				
1	G	236	Total	C	H	N	O	S		0	0	0
			3840	1253	1920	301	359	7				
1	H	229	Total	C	H	N	O	S		0	0	0
			3753	1227	1878	292	349	7				

- Molecule 2 is GLUTATHIONE (CCD ID: GSH) (formula: C₁₀H₁₇N₃O₆S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 35	C 10	H 15	N 3	O 6	S 1	0	0
2	B	1	Total 35	C 10	H 15	N 3	O 6	S 1	0	0
2	C	1	Total 35	C 10	H 15	N 3	O 6	S 1	0	0
2	D	1	Total 35	C 10	H 15	N 3	O 6	S 1	0	0
2	E	1	Total 35	C 10	H 15	N 3	O 6	S 1	0	0
2	F	1	Total 35	C 10	H 15	N 3	O 6	S 1	0	0
2	G	1	Total 35	C 10	H 15	N 3	O 6	S 1	0	0
2	H	1	Total 35	C 10	H 15	N 3	O 6	S 1	0	0

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

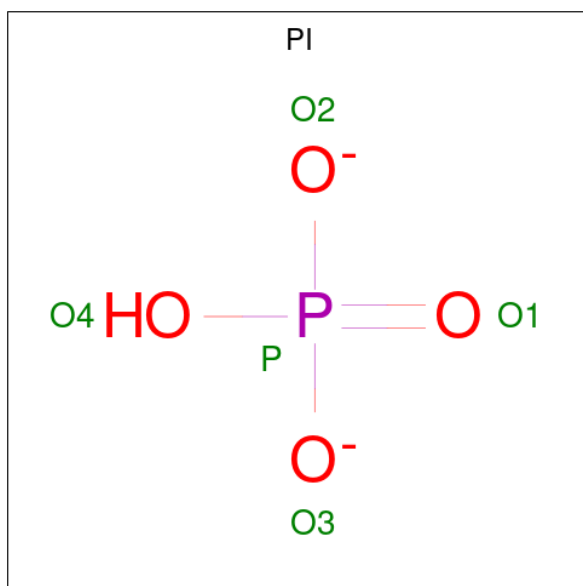
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		
3	D	1	Total	Na	0	0
			1	1		
3	E	1	Total	Na	0	0
			1	1		
3	F	1	Total	Na	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	H	1	Total	Na	0	0
			1	1		

- Molecule 4 is HYDROGENPHOSPHATE ION (CCD ID: PI) (formula: HO_4P).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	99	Total	O	0	0
			99	99		
5	B	86	Total	O	0	0
			86	86		
5	C	70	Total	O	0	1
			71	71		
5	D	40	Total	O	0	0
			40	40		
5	E	78	Total	O	0	0
			78	78		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	F	43	Total 43	O 43	0	0
5	G	58	Total 58	O 58	0	0
5	H	30	Total 30	O 30	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 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: Listeriolysin positive regulatory factor A



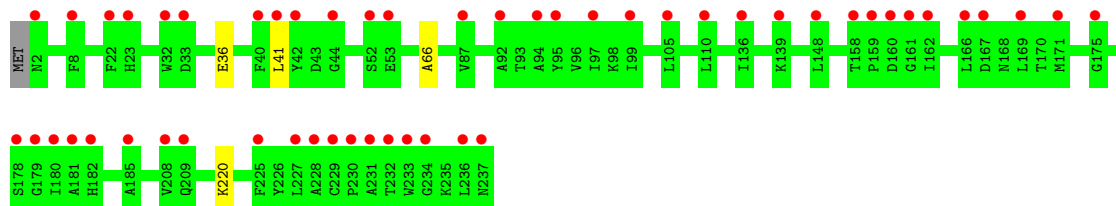
- Molecule 1: Listeriolysin positive regulatory factor A



- Molecule 1: Listeriolysin positive regulatory factor A



- Molecule 1: Listeriolysin positive regulatory factor A



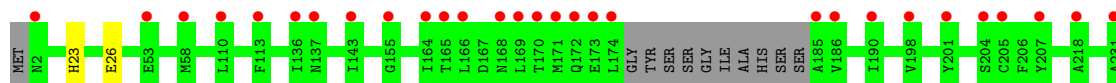
- Molecule 1: Listeriolysin positive regulatory factor A





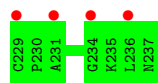
- Molecule 1: Listeriolysin positive regulatory factor A

Chain F: 12% 95% 5%



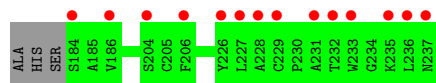
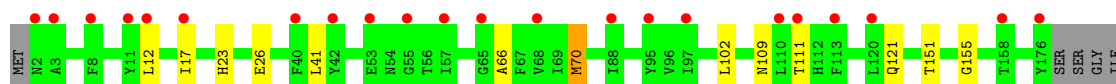
- Molecule 1: Listeriolysin positive regulatory factor A

Chain G: 15% 97% 5%



- Molecule 1: Listeriolysin positive regulatory factor A

Chain H: 15% 91% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	116.27Å 184.23Å 100.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.54 – 2.17 48.54 – 2.17	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.54-2.17) 92.3 (48.54-2.17)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.23 (at 2.18Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.207 , 0.241 0.212 , 0.244	Depositor DCC
R_{free} test set	5706 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	40.0	Xtriage
Anisotropy	0.464	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 35.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	31368	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.69% 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](#)

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

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	0.13	0/1986	0.29	0/2681
1	B	0.14	0/1982	0.28	0/2675
1	C	0.11	0/1964	0.26	0/2652
1	D	0.11	0/1964	0.27	0/2652
1	E	0.12	0/1964	0.29	0/2652
1	F	0.13	0/1893	0.27	0/2556
1	G	0.12	0/1964	0.27	0/2652
1	H	0.12	0/1917	0.26	0/2587
All	All	0.12	0/15634	0.27	0/21107

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	1941	1940	1938	2	0
1	B	1929	1927	1912	3	0
1	C	1920	1920	1920	0	0
1	D	1920	1920	1920	2	0
1	E	1920	1920	1920	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1852	1861	1861	1	0
1	G	1920	1920	1920	3	0
1	H	1875	1878	1878	7	0
2	A	20	15	15	0	0
2	B	20	15	15	0	0
2	C	20	15	15	0	0
2	D	20	15	15	0	0
2	E	20	15	15	0	0
2	F	20	15	15	0	0
2	G	20	15	15	0	0
2	H	20	15	15	0	0
3	A	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	H	1	0	0	0	0
4	A	5	0	0	0	0
4	B	10	0	0	0	0
5	A	99	0	0	0	0
5	B	86	0	0	0	0
5	C	71	0	0	0	0
5	D	40	0	0	0	0
5	E	78	0	0	0	0
5	F	43	0	0	0	0
5	G	58	0	0	0	0
5	H	30	0	0	0	0
All	All	15962	15406	15389	18	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 1.

All (18) 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:G:62:TYR:OH	1:G:173:GLU:OE1	2.27	0.49
1:H:70:MET:HE1	1:H:102:LEU:CD2	2.44	0.48
1:H:41:LEU:O	1:H:66:ALA:HA	2.15	0.46
1:A:24:LYS:O	1:A:25:LYS:HB2	2.17	0.45
1:B:11:TYR:CD1	1:B:112:HIS:CD2	3.06	0.44
1:H:12:LEU:HD22	1:H:17:ILE:HD11	2.01	0.43
1:G:139:LYS:HD2	1:G:180:ILE:HG12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:36:GLU:N	1:D:36:GLU:OE1	2.52	0.42
1:H:109:ASN:OD1	1:H:111:THR:OG1	2.37	0.42
1:A:41:LEU:O	1:A:66:ALA:HA	2.19	0.42
1:H:23:HIS:O	1:H:26:GLU:HG2	2.19	0.42
1:H:151:THR:O	1:H:155:GLY:HA3	2.20	0.42
1:B:11:TYR:CG	1:B:112:HIS:CD2	3.09	0.41
1:D:41:LEU:O	1:D:66:ALA:HA	2.21	0.41
1:G:120:LEU:HD21	1:H:121:GLN:HG3	2.02	0.41
1:B:104:GLU:O	1:B:108:LYS:HD3	2.20	0.41
1:E:41:LEU:O	1:E:66:ALA:HA	2.21	0.40
1:F:23:HIS:N	1:F:26:GLU:OE2	2.41	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	236/237 (100%)	230 (98%)	6 (2%)	0	100	100
1	B	236/237 (100%)	232 (98%)	4 (2%)	0	100	100
1	C	234/237 (99%)	230 (98%)	4 (2%)	0	100	100
1	D	234/237 (99%)	223 (95%)	11 (5%)	0	100	100
1	E	234/237 (99%)	226 (97%)	8 (3%)	0	100	100
1	F	222/237 (94%)	219 (99%)	3 (1%)	0	100	100
1	G	234/237 (99%)	230 (98%)	4 (2%)	0	100	100
1	H	225/237 (95%)	220 (98%)	5 (2%)	0	100	100
All	All	1855/1896 (98%)	1810 (98%)	45 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	213/212 (100%)	210 (99%)	3 (1%)	59	72
1	B	213/212 (100%)	212 (100%)	1 (0%)	81	89
1	C	211/212 (100%)	210 (100%)	1 (0%)	81	89
1	D	211/212 (100%)	210 (100%)	1 (0%)	81	89
1	E	211/212 (100%)	209 (99%)	2 (1%)	70	81
1	F	204/212 (96%)	204 (100%)	0	100	100
1	G	211/212 (100%)	209 (99%)	2 (1%)	70	81
1	H	206/212 (97%)	205 (100%)	1 (0%)	81	89
All	All	1680/1696 (99%)	1669 (99%)	11 (1%)	76	86

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LYS
1	A	36	GLU
1	A	75	ASP
1	B	195	GLN
1	C	36	GLU
1	D	220	LYS
1	E	118	GLN
1	E	120	LEU
1	G	99	ILE
1	G	120	LEU
1	H	70	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	209	GLN
1	B	132	ASN
1	B	137	ASN

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Mol	Chain	Res	Type
1	C	112	HIS
1	D	91	GLN
1	D	112	HIS
1	D	132	ASN
1	E	35	GLN
1	E	100	ASN
1	E	132	ASN
1	E	146	GLN
1	E	168	ASN
1	E	203	ASN
1	F	21	GLN
1	F	137	ASN
1	F	146	GLN
1	G	100	ASN
1	H	4	GLN
1	H	137	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 5 are monoatomic - leaving 11 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	G	301	-	18,19,19	0.74	0	21,24,24	0.68	0
4	PI	B	302	-	4,4,4	0.95	0	6,6,6	0.40	0
2	GSH	A	301	-	18,19,19	0.73	0	21,24,24	0.75	0
2	GSH	D	301	-	18,19,19	0.73	0	21,24,24	0.57	0
2	GSH	H	301	-	18,19,19	0.73	0	21,24,24	0.67	0
4	PI	A	303	-	4,4,4	0.94	0	6,6,6	0.46	0
2	GSH	E	301	-	18,19,19	0.75	0	21,24,24	0.58	0
4	PI	B	303	-	4,4,4	0.93	0	6,6,6	0.50	0
2	GSH	C	301	-	18,19,19	0.72	0	21,24,24	0.66	0
2	GSH	F	301	-	18,19,19	0.72	0	21,24,24	0.71	0
2	GSH	B	301	-	18,19,19	0.71	0	21,24,24	0.85	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	Res	Link	Chirals	Torsions	Rings
2	GSH	G	301	-	-	7/24/24/24	-
2	GSH	A	301	-	-	2/24/24/24	-
2	GSH	D	301	-	-	0/24/24/24	-
2	GSH	H	301	-	-	2/24/24/24	-
2	GSH	E	301	-	-	7/24/24/24	-
2	GSH	C	301	-	-	2/24/24/24	-
2	GSH	F	301	-	-	2/24/24/24	-
2	GSH	B	301	-	-	2/24/24/24	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	301	GSH	O32-C3-CA3-N3
2	E	301	GSH	O31-C3-CA3-N3
2	G	301	GSH	CA1-CB1-CG1-CD1
2	G	301	GSH	N2-CA2-CB2-SG2
2	F	301	GSH	O32-C3-CA3-N3
2	F	301	GSH	O31-C3-CA3-N3

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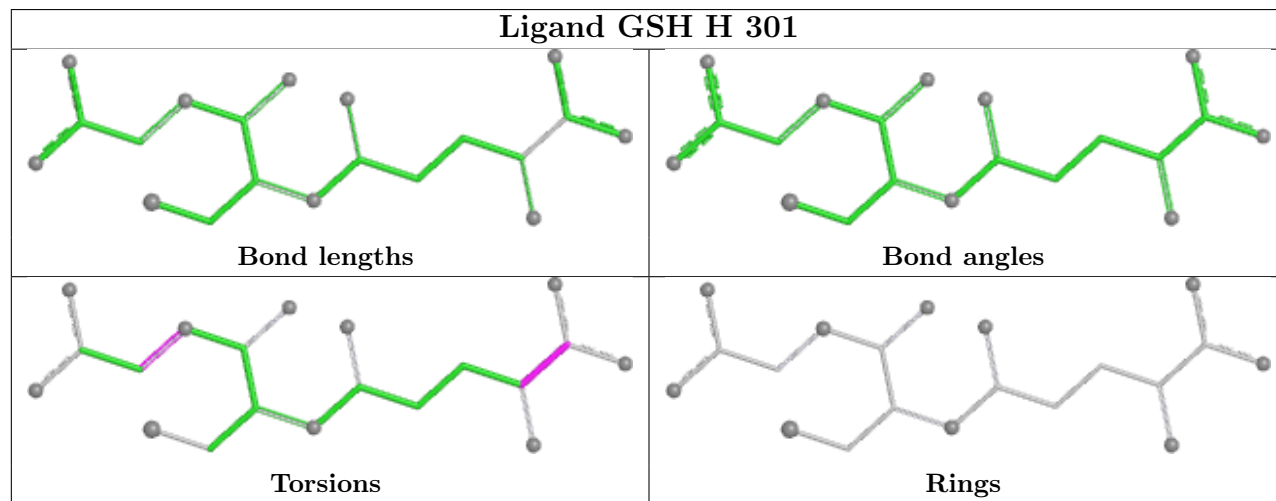
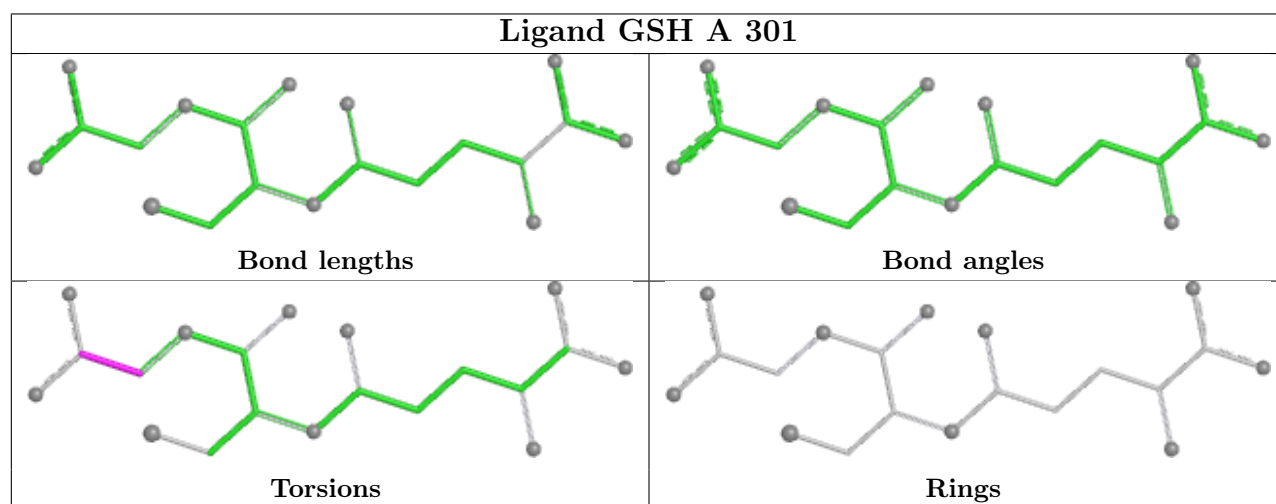
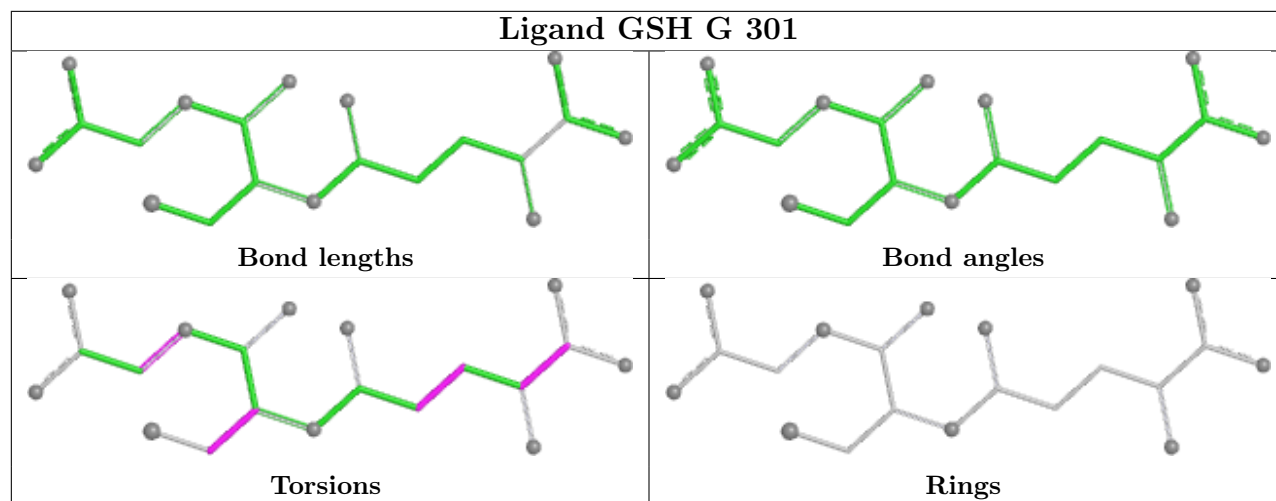
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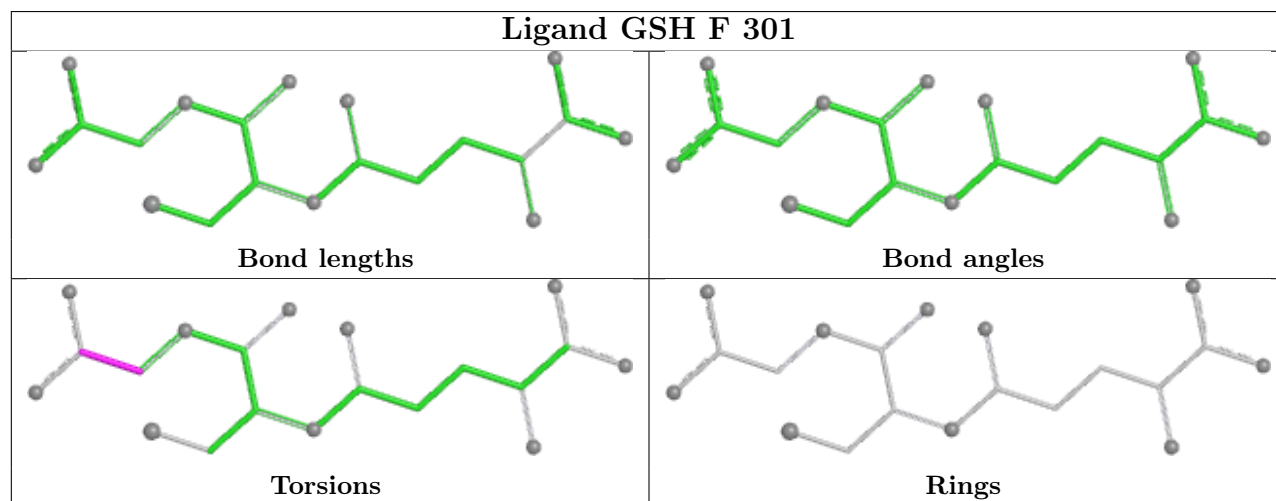
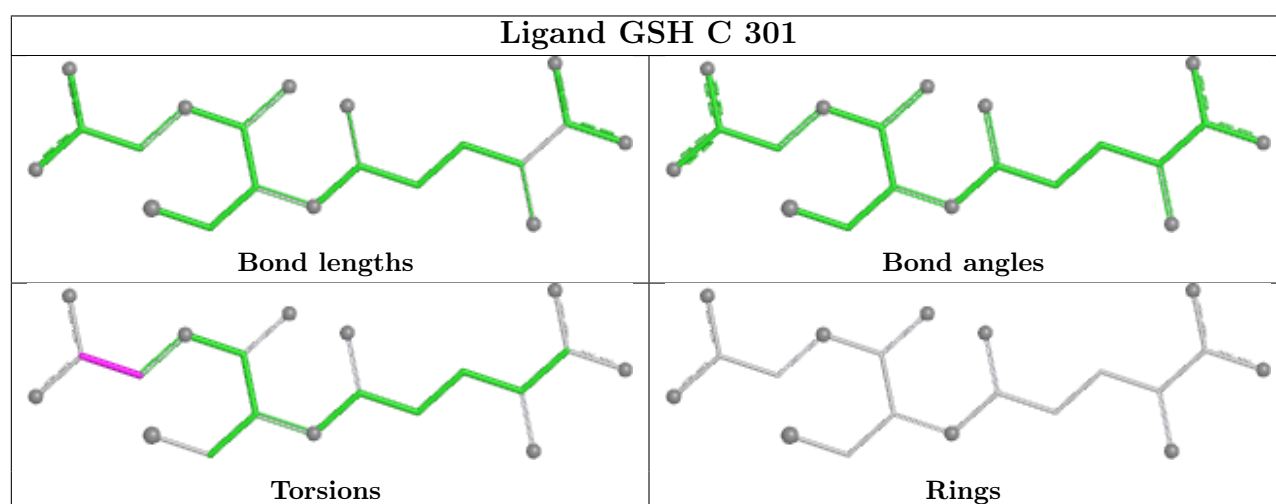
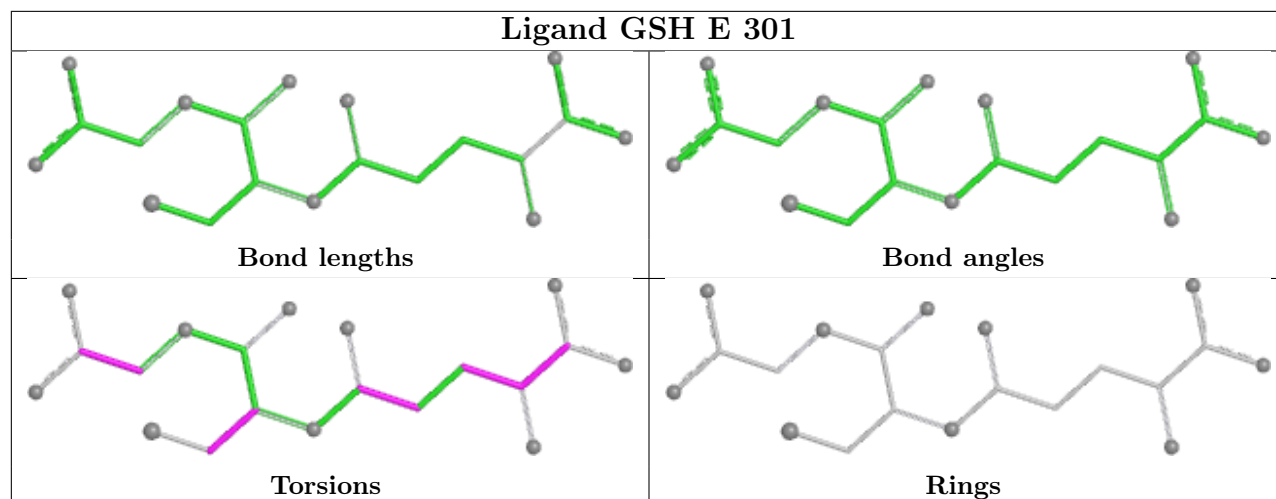
Mol	Chain	Res	Type	Atoms
2	G	301	GSH	C2-CA2-CB2-SG2
2	E	301	GSH	O11-C1-CA1-N1
2	B	301	GSH	O31-C3-CA3-N3
2	G	301	GSH	O11-C1-CA1-CB1
2	E	301	GSH	N1-CA1-CB1-CG1
2	G	301	GSH	O12-C1-CA1-CB1
2	E	301	GSH	N2-CA2-CB2-SG2
2	E	301	GSH	OE1-CD1-CG1-CB1
2	C	301	GSH	O32-C3-CA3-N3
2	H	301	GSH	O12-C1-CA1-N1
2	E	301	GSH	N2-CD1-CG1-CB1
2	A	301	GSH	O32-C3-CA3-N3
2	B	301	GSH	O32-C3-CA3-N3
2	C	301	GSH	O31-C3-CA3-N3
2	G	301	GSH	C3-CA3-N3-C2
2	H	301	GSH	C3-CA3-N3-C2
2	A	301	GSH	O31-C3-CA3-N3
2	G	301	GSH	O11-C1-CA1-N1

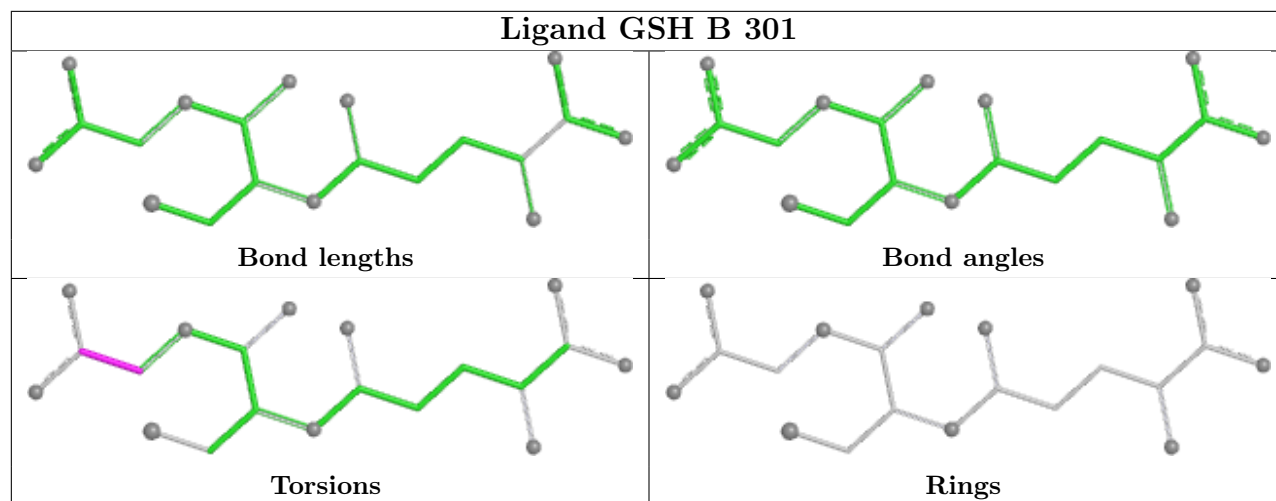
There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

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	236/237 (99%)	0.36	13 (5%)	30 30	26, 51, 79, 99	2 (0%)
1	B	236/237 (99%)	0.31	7 (2%)	52 52	31, 50, 78, 96	1 (0%)
1	C	236/237 (99%)	0.60	10 (4%)	40 40	40, 56, 85, 113	0
1	D	236/237 (99%)	1.25	52 (22%)	2 2	50, 81, 107, 124	0
1	E	236/237 (99%)	0.36	11 (4%)	36 35	35, 50, 75, 103	0
1	F	226/237 (95%)	0.93	29 (12%)	7 6	35, 67, 118, 151	0
1	G	236/237 (99%)	0.91	35 (14%)	5 5	35, 63, 100, 119	0
1	H	229/237 (96%)	1.00	36 (15%)	5 4	40, 66, 102, 115	0
All	All	1871/1896 (98%)	0.71	193 (10%)	12 11	26, 60, 99, 151	3 (0%)

All (193) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	57	ILE	5.4
1	H	55	GLY	5.2
1	F	164	ILE	4.6
1	F	174	LEU	4.5
1	G	32	TRP	4.4
1	H	227	LEU	4.2
1	D	231	ALA	4.1
1	G	80	VAL	4.0
1	H	110	LEU	4.0
1	G	37	TYR	3.9
1	F	113	PHE	3.8
1	D	181	ALA	3.8
1	D	110	LEU	3.8
1	D	161	GLY	3.7
1	B	34	PRO	3.7
1	B	33	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	105	LEU	3.6
1	F	186	VAL	3.5
1	H	232	THR	3.5
1	H	3	ALA	3.5
1	G	2	ASN	3.5
1	H	113	PHE	3.5
1	G	63	TYR	3.5
1	E	88	ILE	3.4
1	D	97	ILE	3.4
1	D	236	LEU	3.4
1	G	82	TYR	3.4
1	E	167	ASP	3.3
1	F	185	ALA	3.3
1	G	74	ILE	3.3
1	G	231	ALA	3.3
1	D	167	ASP	3.2
1	D	230	PRO	3.2
1	C	110	LEU	3.2
1	A	188[A]	ARG	3.2
1	G	83	TYR	3.1
1	H	226	TYR	3.1
1	C	136	ILE	3.1
1	D	158	THR	3.1
1	G	67	PHE	3.1
1	A	136	ILE	3.1
1	H	97	ILE	3.1
1	H	2	ASN	3.1
1	D	171	MET	3.1
1	D	233	TRP	3.0
1	D	159	PRO	3.0
1	A	181	ALA	3.0
1	D	92	ALA	3.0
1	G	31	GLN	3.0
1	E	168	ASN	3.0
1	D	136	ILE	3.0
1	A	182	HIS	3.0
1	G	29	PHE	3.0
1	H	237	ASN	2.9
1	D	234	GLY	2.9
1	G	56	THR	2.9
1	D	175	GLY	2.9
1	G	81	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	H	40	PHE	2.9
1	F	172	GLN	2.8
1	D	99	ILE	2.8
1	H	176	TYR	2.8
1	D	182	HIS	2.8
1	E	181	ALA	2.8
1	D	32	TRP	2.8
1	G	28	ILE	2.8
1	G	55	GLY	2.8
1	H	228	ALA	2.8
1	G	39	ILE	2.8
1	G	99	ILE	2.8
1	F	2	ASN	2.8
1	D	228	ALA	2.8
1	C	25	LYS	2.7
1	D	166	LEU	2.7
1	H	111	THR	2.7
1	H	184	SER	2.7
1	D	160	ASP	2.7
1	D	225	PHE	2.7
1	F	201	TYR	2.7
1	C	168	ASN	2.7
1	C	2	ASN	2.7
1	G	71	SER	2.7
1	D	44	GLY	2.7
1	C	3	ALA	2.6
1	D	53	GLU	2.6
1	G	236	LEU	2.6
1	D	180	ILE	2.6
1	B	35	GLN	2.6
1	A	23[A]	HIS	2.6
1	D	232	THR	2.6
1	D	237	ASN	2.6
1	E	236	LEU	2.6
1	E	204	SER	2.6
1	H	11	TYR	2.6
1	F	173	GLU	2.6
1	D	42	TYR	2.6
1	F	171	MET	2.6
1	G	54	ASN	2.6
1	H	236	LEU	2.6
1	E	179	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	G	97	ILE	2.5
1	B	201	TYR	2.5
1	F	168	ASN	2.5
1	H	229	CYS	2.5
1	F	170	THR	2.5
1	D	94	ALA	2.5
1	F	218	ALA	2.5
1	G	228	ALA	2.5
1	D	41	LEU	2.5
1	F	169	LEU	2.5
1	D	8	PHE	2.5
1	F	58	MET	2.5
1	B	99	ILE	2.5
1	F	207	TYR	2.5
1	G	78	THR	2.5
1	D	23	HIS	2.5
1	A	161	GLY	2.5
1	H	42	TYR	2.4
1	H	231	ALA	2.4
1	D	139	LYS	2.4
1	E	118	GLN	2.4
1	D	33	ASP	2.4
1	G	34	PRO	2.4
1	D	227	LEU	2.4
1	D	40	PHE	2.4
1	G	23	HIS	2.4
1	F	166	LEU	2.4
1	F	198	VAL	2.4
1	H	17	ILE	2.4
1	H	95	TYR	2.3
1	D	2	ASN	2.3
1	C	114	PHE	2.3
1	A	74	ILE	2.3
1	F	190	ILE	2.3
1	G	229	CYS	2.3
1	D	179	GLY	2.3
1	H	235	LYS	2.3
1	G	73	PHE	2.3
1	H	206	PHE	2.3
1	A	2	ASN	2.3
1	A	55	GLY	2.3
1	B	159	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	H	65	GLY	2.3
1	C	58	MET	2.3
1	D	148	LEU	2.3
1	C	17	ILE	2.2
1	H	68	VAL	2.2
1	F	205	CYS	2.2
1	A	180	ILE	2.2
1	D	162	ILE	2.2
1	D	178	SER	2.2
1	F	204	SER	2.2
1	H	204	SER	2.2
1	H	186	VAL	2.2
1	G	53	GLU	2.2
1	G	234	GLY	2.2
1	D	169	LEU	2.2
1	D	52	SER	2.2
1	D	87	VAL	2.1
1	F	231	ALA	2.1
1	H	120	LEU	2.1
1	G	9	LYS	2.1
1	A	20	LYS	2.1
1	E	169	LEU	2.1
1	F	110	LEU	2.1
1	G	85	LEU	2.1
1	H	12	LEU	2.1
1	F	53	GLU	2.1
1	G	62	TYR	2.1
1	G	14	THR	2.1
1	F	136	ILE	2.1
1	H	8	PHE	2.1
1	D	209	GLN	2.1
1	B	37	TYR	2.1
1	C	159	PRO	2.1
1	E	176	TYR	2.1
1	F	143	ILE	2.1
1	G	17	ILE	2.1
1	A	184	SER	2.1
1	D	185	ALA	2.1
1	H	53	GLU	2.0
1	F	137	ASN	2.0
1	A	167	ASP	2.0
1	D	95	TYR	2.0

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Mol	Chain	Res	Type	RSRZ
1	H	88	ILE	2.0
1	D	22	PHE	2.0
1	D	208	VAL	2.0
1	H	233	TRP	2.0
1	D	229	CYS	2.0
1	E	23	HIS	2.0
1	F	165	THR	2.0
1	H	158	THR	2.0
1	F	155	GLY	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 oligosaccharides in this entry.

6.4 Ligands [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, 95th 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.

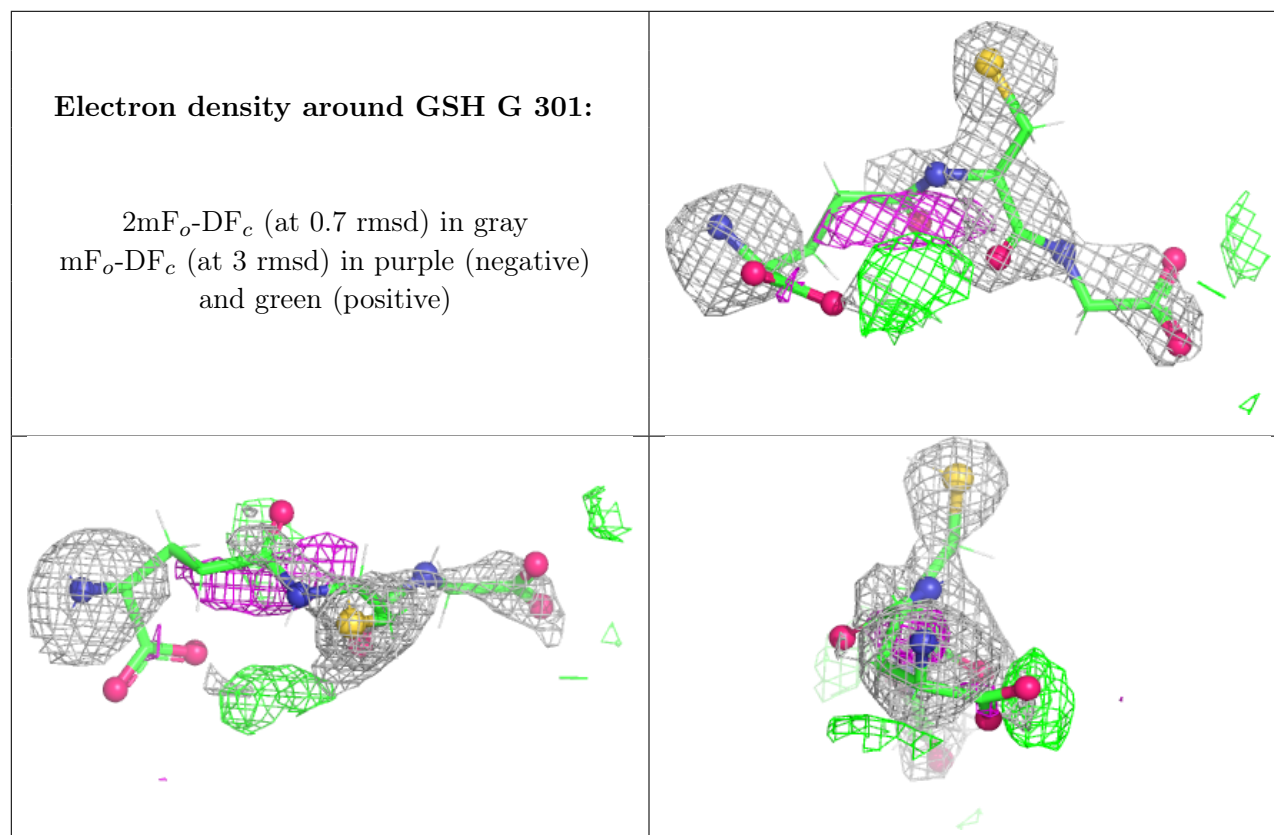
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	PI	A	303	5/5	0.54	0.12	102,102,106,119	0
2	GSH	G	301	20/20	0.64	0.23	70,92,110,112	0
4	PI	B	302	5/5	0.64	0.12	59,69,79,103	0
4	PI	B	303	5/5	0.71	0.14	68,76,90,96	0
2	GSH	E	301	20/20	0.74	0.20	50,74,87,98	0
2	GSH	H	301	20/20	0.81	0.13	55,69,78,87	0
2	GSH	F	301	20/20	0.85	0.12	62,71,85,87	0
3	NA	D	302	1/1	0.92	0.10	56,56,56,56	0
2	GSH	D	301	20/20	0.92	0.10	50,59,71,76	0
2	GSH	C	301	20/20	0.94	0.09	41,52,63,63	0
3	NA	E	302	1/1	0.94	0.06	41,41,41,41	0
3	NA	H	302	1/1	0.94	0.12	43,43,43,43	0
2	GSH	B	301	20/20	0.95	0.08	33,44,53,57	0
3	NA	F	302	1/1	0.95	0.14	37,37,37,37	0

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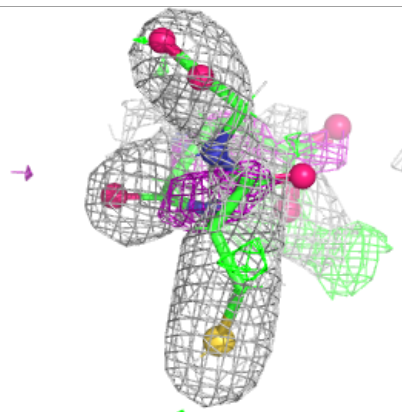
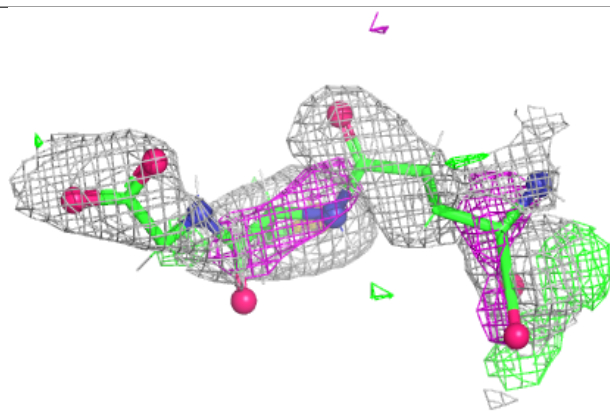
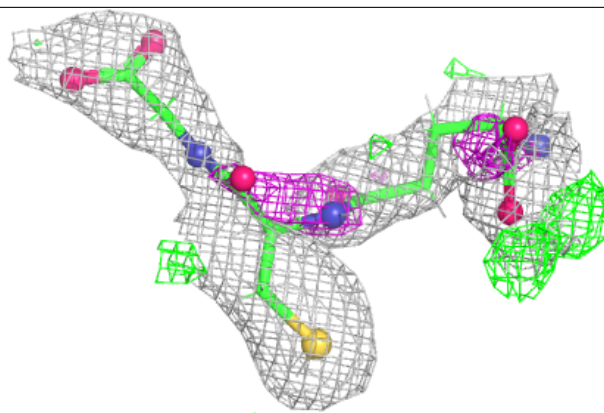
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GSH	A	301	20/20	0.95	0.07	31,41,48,49	0
3	NA	A	302	1/1	0.96	0.12	41,41,41,41	0

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.



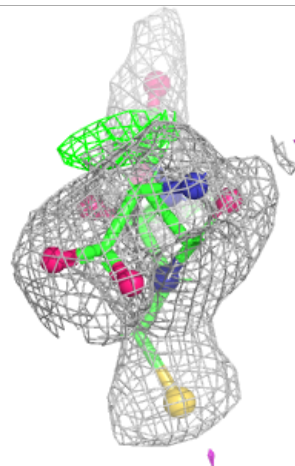
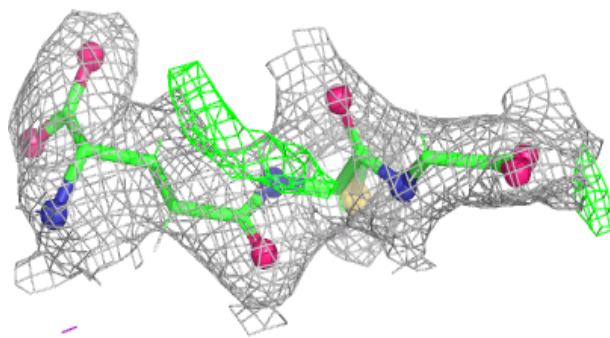
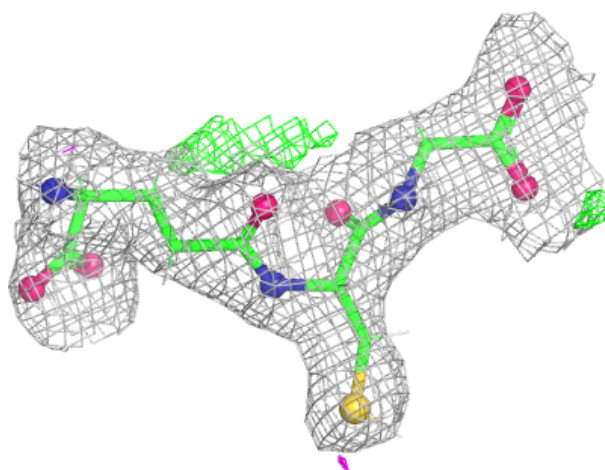
Electron density around GSH E 301:

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



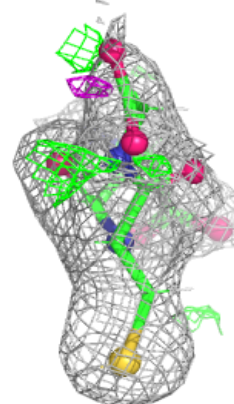
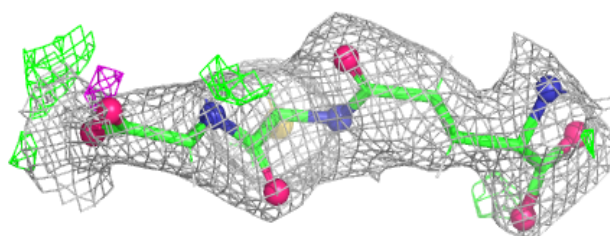
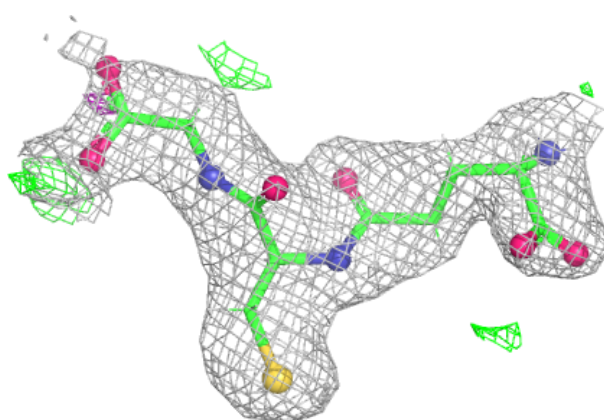
Electron density around GSH H 301:

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

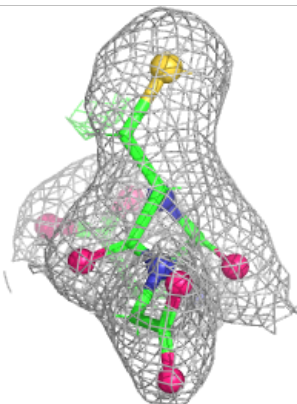
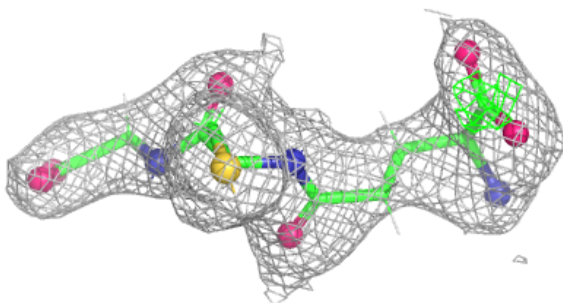
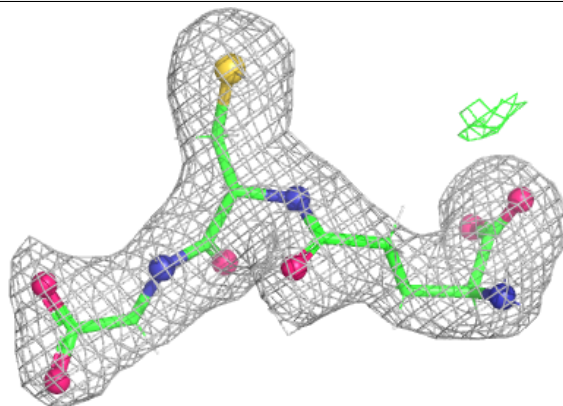


Electron density around GSH F 301:

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

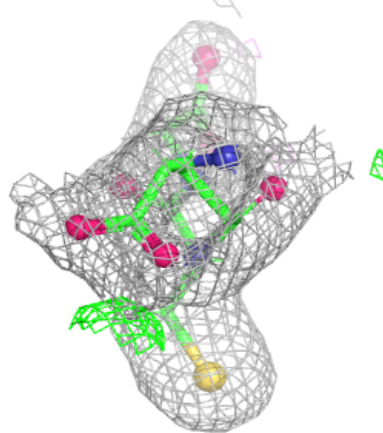
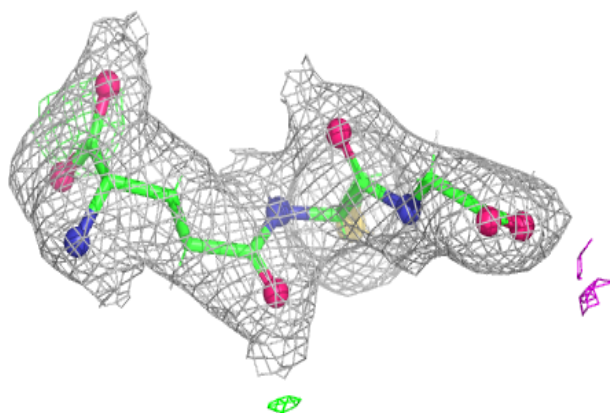
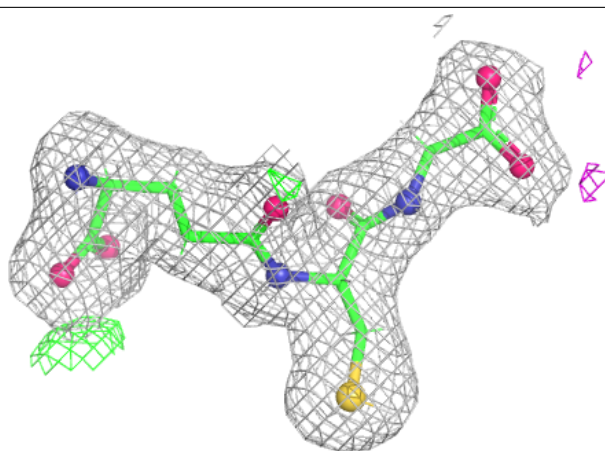
**Electron density around GSH C 301:**

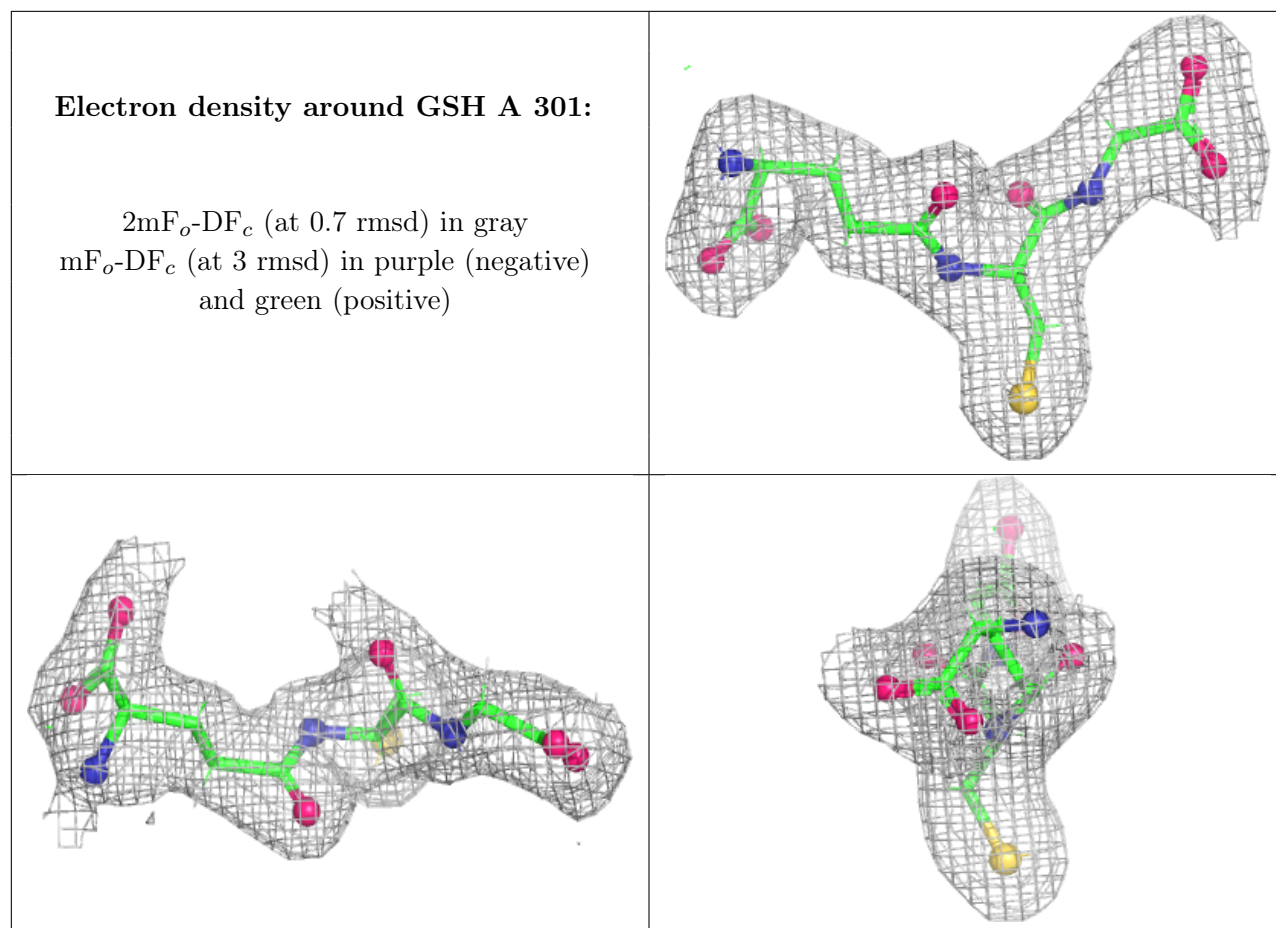
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around GSH B 301:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.