



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 12:24 am BST

PDB ID : 6F05
Title : ARABIDOPSIS THALIANA GSTF9, GSO3 BOUND
Authors : Tossounian, M.A.; Wahni, K.; VanMolle, I.; Vertommen, D.; Rosado, L.;
Messens, J.
Deposited on : 2017-11-17
Resolution : 2.20 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

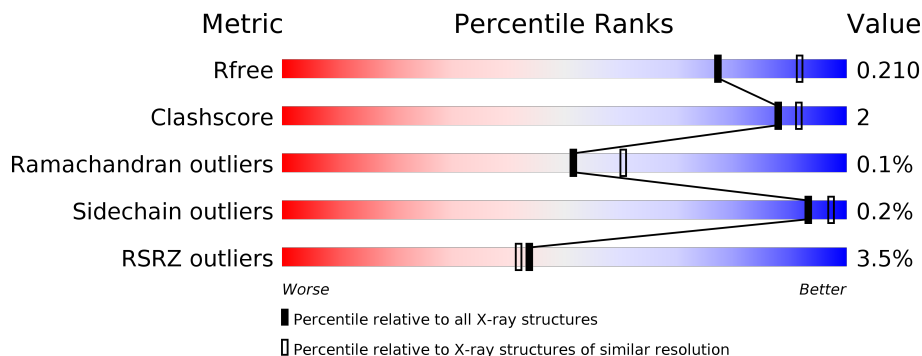
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 ≥ 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	215	 88% 7% 5%
1	B	215	 89% 7% 5%
1	C	215	 90% 6%
1	D	215	 87% 5% 7%
1	E	215	 90% 7%
1	F	215	 89% 5% 6%

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Mol	Chain	Length	Quality of chain
1	G	215	 7% 87% 5% 8%
1	H	215	 % 88% 6% 7%
1	I	215	 90% 6%
1	J	215	 20% 85% 5% 10%

2 Entry composition

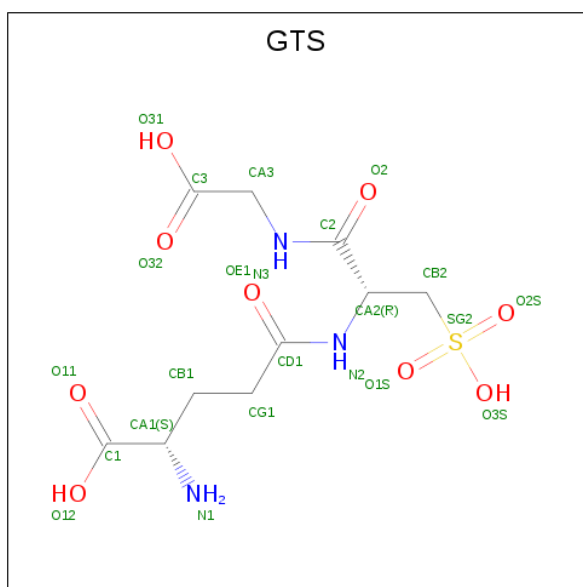
There are 5 unique types of molecules in this entry. The entry contains 16527 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 F9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	204	Total 1578	C 1024	N 260	O 291	S 3	0	0	0
1	B	205	Total 1617	C 1052	N 263	O 298	S 4	0	2	0
1	C	202	Total 1586	C 1030	N 260	O 293	S 3	0	0	0
1	D	199	Total 1524	C 989	N 250	O 282	S 3	0	0	0
1	E	201	Total 1557	C 1011	N 256	O 288	S 2	0	0	0
1	F	203	Total 1575	C 1020	N 259	O 294	S 2	0	1	0
1	G	198	Total 1515	C 983	N 248	O 282	S 2	0	0	0
1	H	201	Total 1547	C 1007	N 254	O 282	S 4	0	0	0
1	I	206	Total 1608	C 1040	N 261	O 303	S 4	0	2	0
1	J	193	Total 1422	C 918	N 235	O 267	S 2	0	0	0

- Molecule 2 is GLUTATHIONE SULFONIC ACID (three-letter code: GTS) (formula: C₁₀H₁₇N₃O₉S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	Total	C	N	O	S	0	0
			23	10	3	9	1		
2	B	1	Total	C	N	O	S	0	0
			23	10	3	9	1		
2	C	1	Total	C	N	O	S	0	0
			23	10	3	9	1		
2	D	1	Total	C	N	O	S	0	0
			23	10	3	9	1		
2	E	1	Total	C	N	O	S	0	0
			23	10	3	9	1		
2	F	1	Total	C	N	O	S	0	0
			23	10	3	9	1		
2	G	1	Total	C	N	O	S	0	0
			23	10	3	9	1		
2	H	1	Total	C	N	O	S	0	0
			23	10	3	9	1		
2	I	1	Total	C	N	O	S	0	0
			23	10	3	9	1		
2	J	1	Total	C	N	O	S	0	0
			23	10	3	9	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	C O	0	0
			6	3 3		
3	A	1	Total	C O	0	0
			6	3 3		
3	B	1	Total	C O	0	0
			6	3 3		
3	B	1	Total	C O	0	0
			6	3 3		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	1	Total	Cl	0	0
			1	1		
4	D	1	Total	Cl	0	0
			1	1		
4	E	1	Total	Cl	0	0
			1	1		
4	H	1	Total	Cl	0	0
			1	1		
4	B	1	Total	Cl	0	0
			1	1		
4	I	1	Total	Cl	0	0
			1	1		
4	C	1	Total	Cl	0	0
			1	1		
4	A	1	Total	Cl	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	F	1	Total	Cl	0	0
			1	1		


- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	123	Total	O	0	0
			123	123		
5	B	127	Total	O	0	0
			127	127		
5	C	119	Total	O	0	0
			119	119		
5	D	47	Total	O	0	0
			47	47		
5	E	92	Total	O	0	0
			92	92		
5	F	52	Total	O	0	0
			52	52		
5	G	21	Total	O	0	0
			21	21		
5	H	44	Total	O	0	0
			44	44		
5	I	102	Total	O	0	0
			102	102		
5	J	8	Total	O	0	0
			8	8		

3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA and DNA 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.

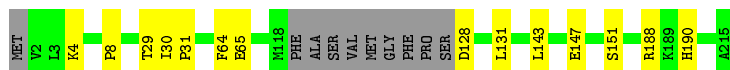
- Molecule 1: Glutathione S-transferase F9

Chain A: 



- Molecule 1: Glutathione S-transferase F9

Chain B: 



- Molecule 1: Glutathione S-transferase F9

Chain C: 




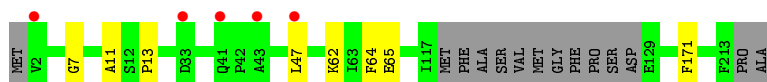
- Molecule 1: Glutathione S-transferase F9

Chain D: 




- Molecule 1: Glutathione S-transferase F9

Chain E: 

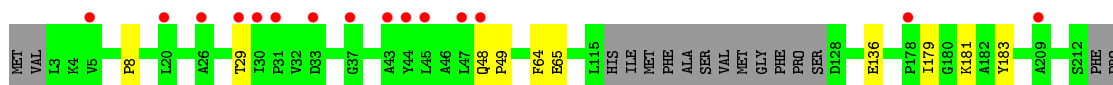
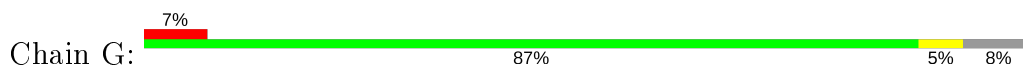


- Molecule 1: Glutathione S-transferase F9

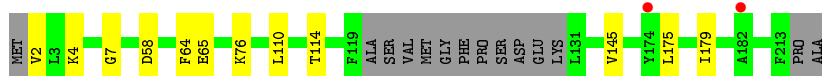
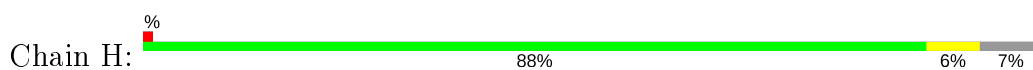
Chain F: 



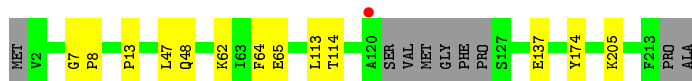
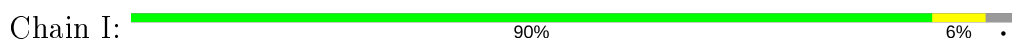
- Molecule 1: Glutathione S-transferase F9



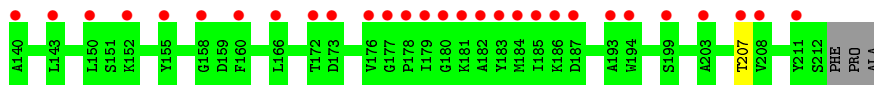
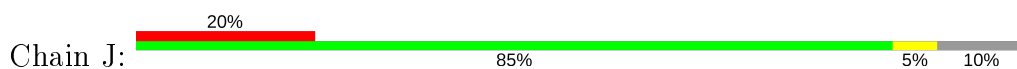
- Molecule 1: Glutathione S-transferase F9



- Molecule 1: Glutathione S-transferase F9



- Molecule 1: Glutathione S-transferase F9



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	61.43Å 93.97Å 107.71Å 93.19° 101.57° 101.97°	Depositor
Resolution (Å)	65.73 – 2.20 65.73 – 2.06	Depositor EDS
% Data completeness (in resolution range)	97.9 (65.73-2.20) 97.7 (65.73-2.06)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 2.07Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.162 , 0.209 0.164 , 0.210	Depositor DCC
R_{free} test set	6862 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	34.1	Xtrriage
Anisotropy	0.305	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 53.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16527	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.69% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, GTS, CL

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	0.48	0/1619	0.60	1/2207 (0.0%)
1	B	0.52	0/1667	0.64	0/2269
1	C	0.45	0/1627	0.55	0/2214
1	D	0.37	0/1565	0.52	0/2140
1	E	0.45	0/1598	0.55	0/2180
1	F	0.43	1/1620 (0.1%)	0.57	1/2211 (0.0%)
1	G	0.31	0/1556	0.47	0/2129
1	H	0.35	0/1589	0.50	0/2169
1	I	0.43	0/1656	0.58	1/2259 (0.0%)
1	J	0.29	0/1462	0.48	0/2011
All	All	0.42	1/15959 (0.0%)	0.55	3/21789 (0.0%)

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	F	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	42	PRO	N-CD	5.08	1.54	1.47

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	41	GLN	C-N-CD	5.43	139.81	128.40
1	I	113	LEU	CA-CB-CG	5.27	127.42	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	99	LEU	CA-CB-CG	5.06	126.94	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	107	HIS	Sidechain

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	1578	0	1534	9	0
1	B	1617	0	1589	8	0
1	C	1586	0	1567	5	0
1	D	1524	0	1456	7	0
1	E	1557	0	1512	4	0
1	F	1575	0	1520	9	0
1	G	1515	0	1443	5	0
1	H	1547	0	1492	7	0
1	I	1608	0	1553	8	0
1	J	1422	0	1283	6	0
2	A	23	0	15	0	0
2	B	23	0	15	0	0
2	C	23	0	15	0	0
2	D	23	0	15	0	0
2	E	23	0	15	0	0
2	F	23	0	15	0	0
2	G	23	0	15	0	0
2	H	23	0	15	0	0
2	I	23	0	15	0	0
2	J	23	0	15	0	0
3	A	12	0	16	2	0
3	B	12	0	16	1	0
4	A	1	0	0	1	0
4	B	1	0	0	1	0
4	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1	0	0	1	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	1	0
4	I	1	0	0	1	0
5	A	123	0	0	0	0
5	B	127	0	0	0	0
5	C	119	0	0	0	0
5	D	47	0	0	0	0
5	E	92	0	0	0	0
5	F	52	0	0	0	0
5	G	21	0	0	0	0
5	H	44	0	0	0	0
5	I	102	0	0	0	0
5	J	8	0	0	0	0
All	All	16527	0	15131	63	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (63) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4:LYS:HD3	1:B:30:ILE:HD11	1.73	0.69
1:I:114:THR:HG23	1:I:174:TYR:HE2	1.58	0.68
1:D:136:GLU:OE1	1:D:181:LYS:NZ	2.30	0.60
1:A:4:LYS:HD3	1:A:30:ILE:HD11	1.83	0.59
1:I:114:THR:HG23	1:I:174:TYR:CE2	2.36	0.59
1:F:15:ARG:HH22	1:F:107:HIS:CE1	2.23	0.56
1:D:47:LEU:HA	1:D:62:LYS:HD2	1.89	0.54
1:H:114:THR:HG22	1:H:179:ILE:HG13	1.90	0.53
1:F:107:HIS:CD2	1:F:111:LEU:HB2	2.43	0.53
1:A:186:LYS:HG3	1:F:183:TYR:CZ	2.46	0.51
1:J:21:ILE:HD12	1:J:207:THR:HG23	1.91	0.51
1:A:116:HIS:CB	1:A:132:ILE:HD11	2.43	0.48
1:A:24:GLY:HA3	3:A:302:GOL:H12	1.95	0.48
1:A:64:PHE:O	1:A:65:GLU:HB2	2.14	0.48
1:E:47:LEU:HA	1:E:62:LYS:HD2	1.94	0.48
1:E:64:PHE:O	1:E:65:GLU:HB2	2.14	0.48
1:B:128:ASP:HB3	1:B:131:LEU:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:92:ARG:O	1:C:96:GLU:HG2	2.13	0.48
1:D:36:LYS:HD3	1:I:137:GLU:CD	2.35	0.47
1:F:64:PHE:O	1:F:65:GLU:HB2	2.14	0.47
1:B:64:PHE:O	1:B:65:GLU:HB2	2.15	0.47
1:B:147:GLU:OE1	1:B:188:ARG:HB3	2.16	0.46
1:A:49:PRO:HG3	3:B:303:GOL:H32	1.97	0.46
1:F:112:ASN:O	1:F:116:HIS:HB2	2.16	0.46
1:G:64:PHE:O	1:G:65:GLU:HB2	2.14	0.46
1:A:183:TYR:HA	1:A:186:LYS:HB2	1.98	0.45
1:C:47:LEU:HA	1:C:62:LYS:HD2	1.99	0.45
1:B:151[B]:SER:HG	1:B:190:HIS:CG	2.34	0.45
1:F:100:ASP:OD2	1:J:67:ARG:HB2	2.17	0.45
1:I:47:LEU:HA	1:I:62:LYS:HD2	1.98	0.45
1:C:128:ASP:O	1:C:132:ILE:HG12	2.17	0.45
1:D:102:GLU:HA	1:D:106:TYR:HB3	1.99	0.44
3:A:303:GOL:H11	1:C:81:GLY:HA2	2.00	0.44
1:F:107:HIS:HD2	1:F:111:LEU:HB2	1.83	0.44
1:F:67:ARG:HB2	1:J:100:ASP:OD2	2.18	0.44
1:A:8:PRO:HD2	4:A:304:CL:CL	2.55	0.44
1:D:7:GLY:HA2	4:D:302:CL:CL	2.54	0.44
1:I:7:GLY:O	1:I:13:PRO:HG2	2.18	0.44
1:J:3:LEU:HA	1:J:58:ASP:HA	1.99	0.44
1:H:58:ASP:OD2	1:H:76:LYS:NZ	2.49	0.43
1:I:64:PHE:O	1:I:65:GLU:HB2	2.19	0.43
1:G:136:GLU:OE2	1:G:183:TYR:OH	2.30	0.43
1:C:64:PHE:O	1:C:65:GLU:HB2	2.19	0.43
1:E:7:GLY:O	1:E:13:PRO:HG2	2.19	0.43
1:H:2:VAL:HG13	1:H:4:LYS:HE3	2.00	0.43
1:H:7:GLY:HA2	4:H:302:CL:CL	2.55	0.43
1:J:64:PHE:O	1:J:65:GLU:HB2	2.19	0.42
1:J:92:ARG:O	1:J:96:GLU:HG2	2.20	0.42
1:B:31:PRO:HA	4:B:304:CL:CL	2.57	0.42
1:A:92:ARG:O	1:A:96:GLU:HG2	2.19	0.42
1:D:7:GLY:O	1:D:13:PRO:HG2	2.20	0.42
1:G:179:ILE:HG22	1:G:181:LYS:HG3	2.02	0.42
1:B:143:LEU:HA	1:B:143:LEU:HD23	1.91	0.41
1:H:110:LEU:HD11	1:H:175:LEU:HB2	2.01	0.41
1:F:15:ARG:NH2	1:F:107:HIS:ND1	2.68	0.41
1:I:8:PRO:HD2	4:I:302:CL:CL	2.58	0.41
1:G:49:PRO:HB2	1:H:145:VAL:HG13	2.02	0.41
1:G:8:PRO:HG3	1:G:29:THR:HB	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:99:LEU:HD13	1:D:164:ALA:HA	2.03	0.40
1:B:8:PRO:HG3	1:B:29:THR:HB	2.02	0.40
1:H:64:PHE:O	1:H:65:GLU:HB2	2.20	0.40
1:E:11:ALA:HB3	1:E:171:PHE:CZ	2.56	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	200/215 (93%)	196 (98%)	3 (2%)	1 (0%)	29	31
1	B	203/215 (94%)	200 (98%)	3 (2%)	0	100	100
1	C	198/215 (92%)	196 (99%)	2 (1%)	0	100	100
1	D	195/215 (91%)	193 (99%)	2 (1%)	0	100	100
1	E	197/215 (92%)	195 (99%)	2 (1%)	0	100	100
1	F	200/215 (93%)	198 (99%)	2 (1%)	0	100	100
1	G	194/215 (90%)	192 (99%)	2 (1%)	0	100	100
1	H	197/215 (92%)	195 (99%)	2 (1%)	0	100	100
1	I	204/215 (95%)	202 (99%)	2 (1%)	0	100	100
1	J	189/215 (88%)	187 (99%)	2 (1%)	0	100	100
All	All	1977/2150 (92%)	1954 (99%)	22 (1%)	1 (0%)	51	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	118	MET

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	161/182 (88%)	161 (100%)	0	100	100
1	B	169/182 (93%)	169 (100%)	0	100	100
1	C	166/182 (91%)	166 (100%)	0	100	100
1	D	153/182 (84%)	153 (100%)	0	100	100
1	E	159/182 (87%)	159 (100%)	0	100	100
1	F	162/182 (89%)	161 (99%)	1 (1%)	86	93
1	G	152/182 (84%)	151 (99%)	1 (1%)	84	91
1	H	156/182 (86%)	156 (100%)	0	100	100
1	I	167/182 (92%)	166 (99%)	1 (1%)	86	93
1	J	133/182 (73%)	133 (100%)	0	100	100
All	All	1578/1820 (87%)	1575 (100%)	3 (0%)	93	97

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	116	HIS
1	G	48	GLN
1	I	48	GLN

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 23 ligands modelled in this entry, 9 are monoatomic - leaving 14 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	GTS	H	301	-	15,22,22	2.29	5 (33%)	19,30,30	1.94	4 (21%)
3	GOL	B	302	-	5,5,5	0.32	0	5,5,5	0.29	0
2	GTS	B	301	-	15,22,22	2.10	4 (26%)	19,30,30	2.15	7 (36%)
2	GTS	A	301	-	15,22,22	2.10	5 (33%)	19,30,30	3.00	11 (57%)
2	GTS	F	301	-	15,22,22	2.30	6 (40%)	19,30,30	1.93	4 (21%)
2	GTS	E	301	-	15,22,22	2.25	4 (26%)	19,30,30	1.96	6 (31%)
2	GTS	D	301	-	15,22,22	2.22	4 (26%)	19,30,30	2.15	6 (31%)
2	GTS	C	301	-	15,22,22	2.25	6 (40%)	19,30,30	1.89	7 (36%)
3	GOL	A	302	-	5,5,5	0.46	0	5,5,5	0.29	0
2	GTS	G	301	-	15,22,22	2.29	5 (33%)	19,30,30	2.31	9 (47%)
3	GOL	B	303	-	5,5,5	0.38	0	5,5,5	0.75	0
3	GOL	A	303	-	5,5,5	0.37	0	5,5,5	0.35	0
2	GTS	J	301	-	15,22,22	2.35	5 (33%)	19,30,30	2.30	6 (31%)
2	GTS	I	301	-	15,22,22	2.24	4 (26%)	19,30,30	2.25	9 (47%)

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	GTS	H	301	-	-	1/21/27/27	-
3	GOL	B	302	-	-	2/4/4/4	-
2	GTS	B	301	-	-	4/21/27/27	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GTS	A	301	-	-	4/21/27/27	-
2	GTS	F	301	-	-	1/21/27/27	-
2	GTS	E	301	-	-	3/21/27/27	-
2	GTS	D	301	-	-	1/21/27/27	-
2	GTS	C	301	-	-	3/21/27/27	-
3	GOL	A	302	-	-	4/4/4/4	-
2	GTS	G	301	-	-	4/21/27/27	-
3	GOL	B	303	-	-	0/4/4/4	-
3	GOL	A	303	-	-	2/4/4/4	-
2	GTS	J	301	-	-	3/21/27/27	-
2	GTS	I	301	-	-	3/21/27/27	-

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	301	GTS	C2-N3	5.71	1.46	1.33
2	C	301	GTS	C2-N3	5.65	1.45	1.33
2	F	301	GTS	C2-N3	5.62	1.45	1.33
2	I	301	GTS	C2-N3	5.62	1.45	1.33
2	H	301	GTS	C2-N3	5.54	1.45	1.33
2	D	301	GTS	C2-N3	5.42	1.45	1.33
2	G	301	GTS	C2-N3	5.37	1.45	1.33
2	E	301	GTS	C2-N3	5.22	1.45	1.33
2	B	301	GTS	C2-N3	4.86	1.44	1.33
2	J	301	GTS	CD1-N2	4.53	1.43	1.34
2	E	301	GTS	CD1-N2	4.49	1.43	1.34
2	F	301	GTS	CD1-N2	4.46	1.43	1.34
2	A	301	GTS	C2-N3	4.36	1.43	1.33
2	G	301	GTS	CD1-N2	4.33	1.43	1.34
2	H	301	GTS	CD1-N2	4.18	1.42	1.34
2	B	301	GTS	CD1-N2	4.07	1.42	1.34
2	I	301	GTS	CD1-N2	3.96	1.42	1.34
2	D	301	GTS	CD1-N2	3.90	1.42	1.34
2	A	301	GTS	CD1-N2	3.84	1.42	1.34
2	C	301	GTS	CD1-N2	3.71	1.41	1.34
2	D	301	GTS	CG1-CD1	3.30	1.57	1.51
2	J	301	GTS	CG1-CD1	2.73	1.56	1.51
2	I	301	GTS	CG1-CD1	2.52	1.56	1.51
2	A	301	GTS	O1S-SG2	2.46	1.52	1.45
2	E	301	GTS	O1S-SG2	2.40	1.52	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	301	GTS	CG1-CD1	2.37	1.55	1.51
2	F	301	GTS	CA1-N1	-2.34	1.41	1.47
2	G	301	GTS	O2S-SG2	2.32	1.51	1.45
2	H	301	GTS	CA1-N1	-2.28	1.42	1.47
2	I	301	GTS	CA1-N1	-2.27	1.42	1.47
2	F	301	GTS	O1S-SG2	2.27	1.51	1.45
2	H	301	GTS	O1S-SG2	2.25	1.51	1.45
2	D	301	GTS	O1S-SG2	2.21	1.51	1.45
2	C	301	GTS	CG1-CD1	2.21	1.55	1.51
2	G	301	GTS	CG1-CD1	2.21	1.55	1.51
2	F	301	GTS	CG1-CD1	2.18	1.55	1.51
2	A	301	GTS	O2S-SG2	2.14	1.51	1.45
2	B	301	GTS	CG1-CD1	2.12	1.55	1.51
2	J	301	GTS	O2S-SG2	2.11	1.51	1.45
2	H	301	GTS	CG1-CD1	2.11	1.55	1.51
2	C	301	GTS	O1S-SG2	2.08	1.51	1.45
2	F	301	GTS	O2S-SG2	2.06	1.51	1.45
2	J	301	GTS	O1S-SG2	2.05	1.51	1.45
2	B	301	GTS	CA2-N2	-2.05	1.41	1.45
2	G	301	GTS	O1S-SG2	2.05	1.51	1.45
2	C	301	GTS	CA1-N1	-2.04	1.42	1.47
2	A	301	GTS	CG1-CD1	2.01	1.55	1.51
2	C	301	GTS	O2S-SG2	2.00	1.50	1.45

All (69) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	GTS	C3-CA3-N3	-7.14	96.66	110.43
2	J	301	GTS	O1S-SG2-CB2	5.34	113.29	106.94
2	H	301	GTS	O1S-SG2-CB2	5.02	112.90	106.94
2	A	301	GTS	CA3-N3-C2	4.95	129.47	122.34
2	B	301	GTS	CA3-N3-C2	-4.91	115.28	122.34
2	I	301	GTS	O3S-SG2-CB2	4.76	113.32	105.74
2	B	301	GTS	O2S-SG2-CB2	4.63	112.44	106.94
2	A	301	GTS	CA2-C2-N3	4.59	125.81	116.54
2	F	301	GTS	O3S-SG2-CB2	4.49	112.90	105.74
2	I	301	GTS	O3S-SG2-O2S	-4.36	100.63	111.27
2	G	301	GTS	O3S-SG2-O2S	-4.22	100.95	111.27
2	A	301	GTS	O2-C2-N3	-4.19	113.99	122.99
2	G	301	GTS	O1S-SG2-CB2	4.08	111.79	106.94
2	J	301	GTS	O3S-SG2-O2S	-4.01	101.48	111.27
2	E	301	GTS	O1S-SG2-CB2	4.00	111.69	106.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	301	GTS	O2S-SG2-O1S	-3.91	100.42	113.95
2	D	301	GTS	O2S-SG2-O1S	-3.79	100.83	113.95
2	D	301	GTS	OE1-CD1-N2	-3.61	116.86	122.95
2	J	301	GTS	CG1-CD1-N2	3.59	122.05	115.83
2	D	301	GTS	O3S-SG2-CB2	3.53	111.36	105.74
2	G	301	GTS	CG1-CD1-N2	3.46	121.83	115.83
2	D	301	GTS	O1S-SG2-CB2	3.40	110.97	106.94
2	E	301	GTS	O3S-SG2-O1S	-3.39	103.00	111.27
2	D	301	GTS	O2S-SG2-CB2	3.25	110.80	106.94
2	B	301	GTS	CG1-CB1-CA1	-3.25	106.27	113.84
2	E	301	GTS	CG1-CD1-N2	3.22	121.42	115.83
2	G	301	GTS	O3S-SG2-CB2	3.18	110.81	105.74
2	F	301	GTS	CG1-CD1-N2	3.15	121.30	115.83
2	I	301	GTS	O2S-SG2-CB2	3.15	110.69	106.94
2	J	301	GTS	O3S-SG2-CB2	3.14	110.74	105.74
2	J	301	GTS	O2S-SG2-CB2	3.14	110.67	106.94
2	F	301	GTS	O2S-SG2-O1S	-3.08	103.27	113.95
2	A	301	GTS	O3S-SG2-O1S	-3.08	103.75	111.27
2	G	301	GTS	CA2-C2-N3	3.08	122.75	116.54
2	D	301	GTS	CG1-CD1-N2	3.04	121.11	115.83
2	G	301	GTS	O2S-SG2-CB2	3.00	110.50	106.94
2	C	301	GTS	O1S-SG2-CB2	2.98	110.48	106.94
2	C	301	GTS	O2S-SG2-CB2	2.95	110.44	106.94
2	I	301	GTS	CA3-N3-C2	-2.94	118.11	122.34
2	C	301	GTS	O2S-SG2-O1S	-2.93	103.81	113.95
2	C	301	GTS	O3S-SG2-CB2	2.89	110.34	105.74
2	A	301	GTS	O3S-SG2-CB2	2.81	110.22	105.74
2	F	301	GTS	O2S-SG2-CB2	2.74	110.20	106.94
2	H	301	GTS	CB2-CA2-C2	-2.73	103.89	109.86
2	A	301	GTS	OE1-CD1-N2	-2.71	118.38	122.95
2	J	301	GTS	OE1-CD1-N2	-2.67	118.45	122.95
2	I	301	GTS	CG1-CD1-N2	2.63	120.40	115.83
2	A	301	GTS	C2-CA2-N2	-2.62	104.02	111.16
2	H	301	GTS	O3S-SG2-CB2	2.59	109.88	105.74
2	A	301	GTS	CG1-CD1-N2	2.59	120.32	115.83
2	E	301	GTS	O3S-SG2-CB2	2.58	109.85	105.74
2	A	301	GTS	O2S-SG2-CB2	2.54	109.96	106.94
2	G	301	GTS	O2-C2-N3	-2.54	117.54	122.99
2	C	301	GTS	CB2-CA2-C2	-2.52	104.33	109.86
2	I	301	GTS	OE1-CD1-N2	-2.50	118.73	122.95
2	G	301	GTS	OE1-CD1-N2	-2.48	118.76	122.95
2	C	301	GTS	OE1-CD1-N2	-2.48	118.77	122.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	301	GTS	C3-CA3-N3	-2.42	105.76	110.43
2	B	301	GTS	OE1-CD1-N2	-2.38	118.93	122.95
2	A	301	GTS	O1S-SG2-CB2	2.31	109.68	106.94
2	I	301	GTS	CB2-CA2-C2	-2.30	104.83	109.86
2	C	301	GTS	CA3-N3-C2	-2.30	119.03	122.34
2	E	301	GTS	OE1-CD1-N2	-2.28	119.10	122.95
2	E	301	GTS	O2S-SG2-CB2	2.23	109.59	106.94
2	B	301	GTS	CB2-CA2-C2	-2.19	105.06	109.86
2	I	301	GTS	O1S-SG2-CB2	2.16	109.50	106.94
2	B	301	GTS	CG1-CD1-N2	2.14	119.55	115.83
2	B	301	GTS	CA2-C2-N3	2.13	120.84	116.54
2	I	301	GTS	CG1-CB1-CA1	-2.12	108.90	113.84

There are no chirality outliers.

All (35) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	302	GOL	O1-C1-C2-C3
2	C	301	GTS	CA2-CB2-SG2-O1S
3	A	303	GOL	O1-C1-C2-O2
2	E	301	GTS	CA2-CB2-SG2-O1S
2	E	301	GTS	CA2-CB2-SG2-O2S
2	E	301	GTS	CA2-CB2-SG2-O3S
2	G	301	GTS	N1-CA1-CB1-CG1
2	G	301	GTS	C1-CA1-CB1-CG1
2	I	301	GTS	CA2-CB2-SG2-O3S
2	B	301	GTS	CA2-CB2-SG2-O3S
3	A	302	GOL	O1-C1-C2-C3
3	A	302	GOL	C1-C2-C3-O3
2	J	301	GTS	CA2-CB2-SG2-O1S
2	J	301	GTS	CA2-CB2-SG2-O2S
2	J	301	GTS	CA2-CB2-SG2-O3S
2	G	301	GTS	O2-C2-N3-CA3
2	A	301	GTS	O2-C2-N3-CA3
2	G	301	GTS	CA2-C2-N3-CA3
2	A	301	GTS	CA2-C2-N3-CA3
3	A	303	GOL	O1-C1-C2-C3
3	B	302	GOL	O1-C1-C2-O2
2	C	301	GTS	CA2-CB2-SG2-O2S
2	B	301	GTS	CA2-CB2-SG2-O1S
2	B	301	GTS	CA2-CB2-SG2-O2S
3	A	302	GOL	O1-C1-C2-O2

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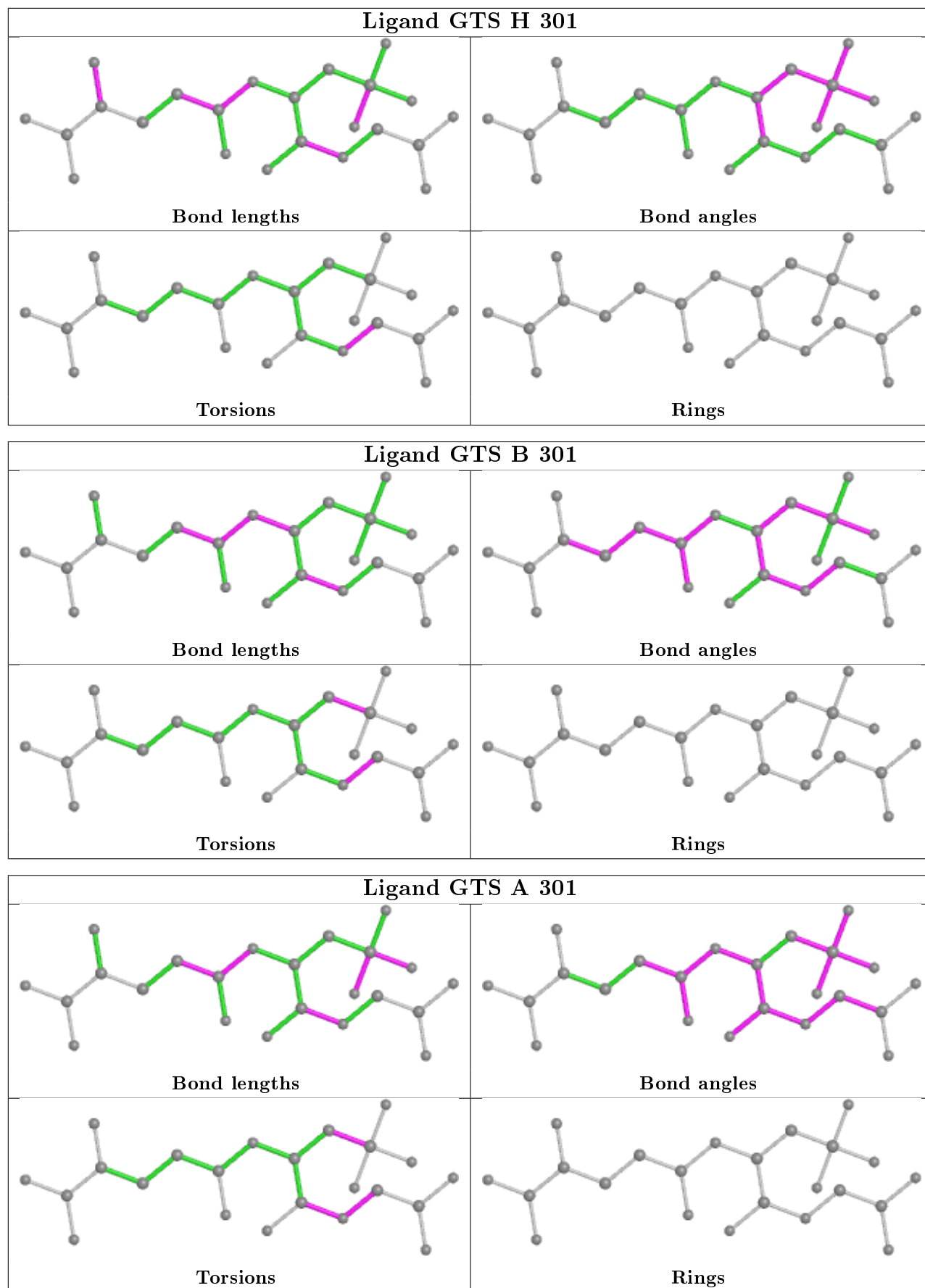
Mol	Chain	Res	Type	Atoms
3	A	302	GOL	O2-C2-C3-O3
2	C	301	GTS	CA2-CB2-SG2-O3S
2	D	301	GTS	CA2-CB2-SG2-O1S
2	A	301	GTS	C3-CA3-N3-C2
2	F	301	GTS	C3-CA3-N3-C2
2	I	301	GTS	C3-CA3-N3-C2
2	I	301	GTS	CA2-CB2-SG2-O1S
2	A	301	GTS	CA2-CB2-SG2-O1S
2	H	301	GTS	C3-CA3-N3-C2
2	B	301	GTS	C3-CA3-N3-C2

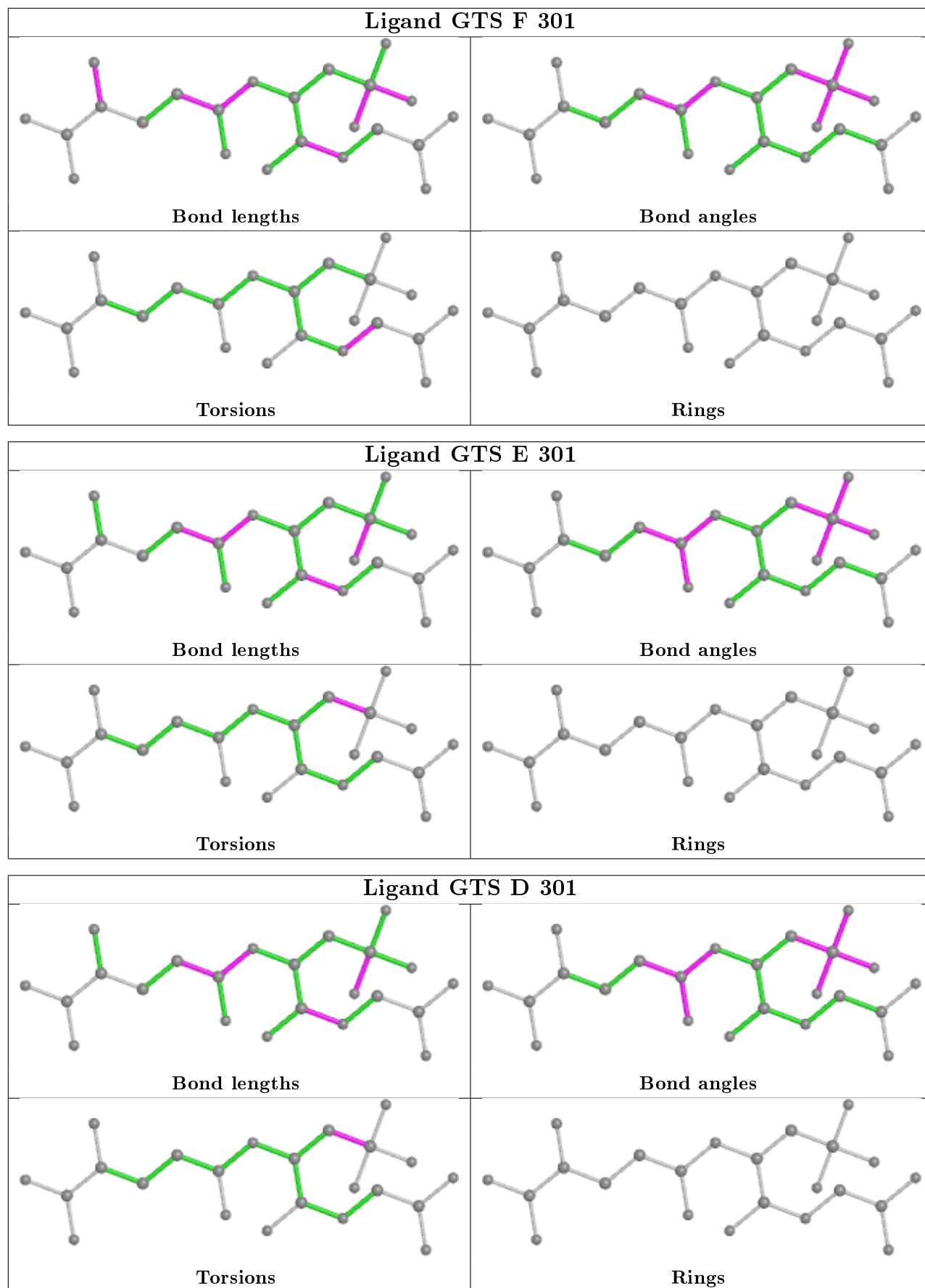
There are no ring outliers.

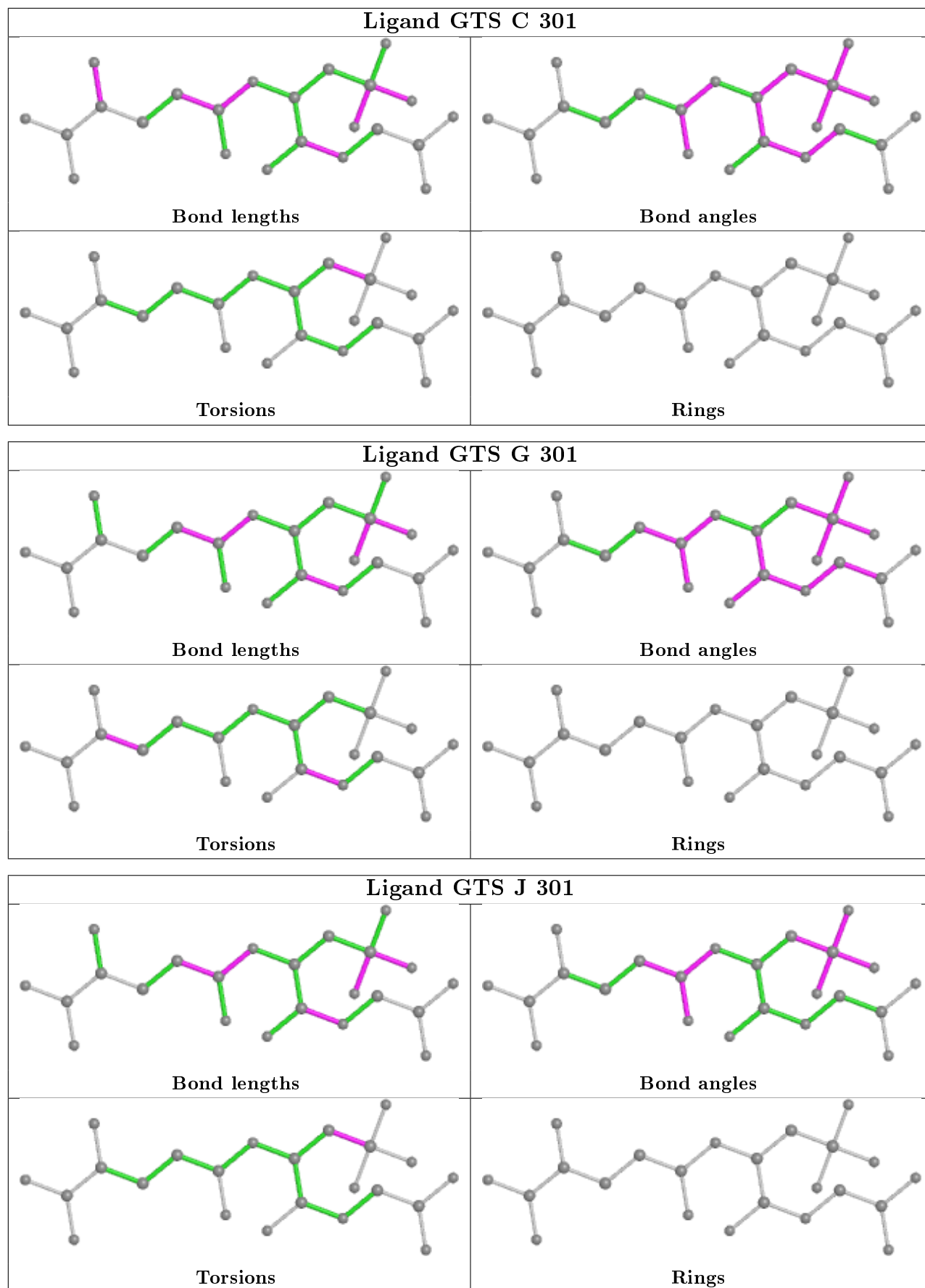
3 monomers are involved in 3 short contacts:

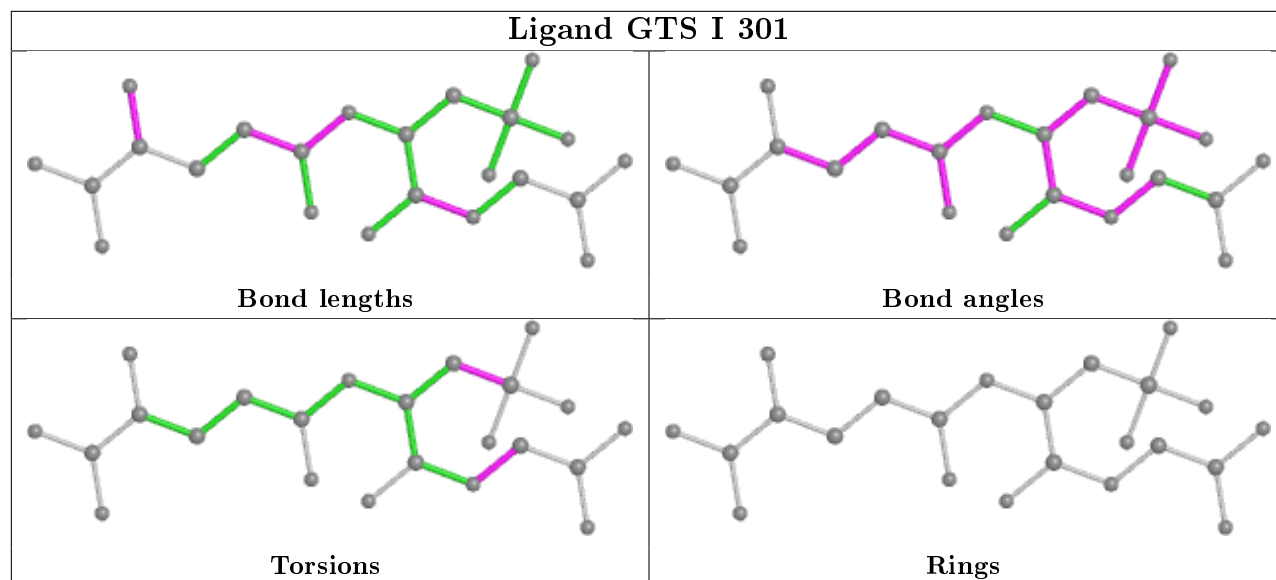
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	302	GOL	1	0
3	B	303	GOL	1	0
3	A	303	GOL	1	0

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

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	204/215 (94%)	-0.17	1 (0%) 91 90	22, 32, 54, 91	0
1	B	205/215 (95%)	-0.15	0 100 100	21, 31, 62, 97	1 (0%)
1	C	202/215 (93%)	-0.27	0 100 100	23, 35, 62, 89	0
1	D	199/215 (92%)	-0.09	1 (0%) 91 90	29, 55, 70, 78	0
1	E	201/215 (93%)	-0.10	5 (2%) 57 55	23, 37, 74, 99	0
1	F	203/215 (94%)	-0.20	3 (1%) 73 72	36, 49, 72, 102	0
1	G	198/215 (92%)	0.27	15 (7%) 13 12	38, 57, 76, 87	1 (0%)
1	H	201/215 (93%)	-0.15	2 (0%) 82 81	34, 52, 71, 86	0
1	I	206/215 (95%)	-0.29	1 (0%) 91 90	24, 39, 58, 86	0
1	J	193/215 (89%)	1.07	42 (21%) 0 0	52, 77, 97, 102	0
All	All	2012/2150 (93%)	-0.01	70 (3%) 44 42	21, 46, 81, 102	2 (0%)

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	37	GLY	7.6
1	J	158	GLY	6.2
1	J	194	TRP	6.0
1	J	3	LEU	5.8
1	G	43	ALA	4.7
1	J	176	VAL	4.6
1	G	47	LEU	4.5
1	J	208	VAL	4.3
1	G	44	TYR	4.1
1	J	180	GLY	4.0
1	J	203	ALA	4.0
1	D	86	GLY	3.7
1	J	179	ILE	3.7

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Mol	Chain	Res	Type	RSRZ
1	J	43	ALA	3.7
1	J	182	ALA	3.6
1	G	33	ASP	3.5
1	J	178	PRO	3.5
1	J	211	TYR	3.4
1	J	33	ASP	3.3
1	J	181	LYS	3.3
1	E	33	ASP	3.2
1	G	178	PRO	3.1
1	J	10	PHE	3.1
1	G	31	PRO	3.0
1	J	166	LEU	2.9
1	E	47	LEU	2.9
1	J	207	THR	2.9
1	J	173	ASP	2.8
1	J	183	TYR	2.8
1	J	143	LEU	2.7
1	F	117	ILE	2.7
1	F	41	GLN	2.7
1	J	185	ILE	2.6
1	G	45	LEU	2.6
1	H	174	TYR	2.6
1	J	152	LYS	2.5
1	E	41	GLN	2.5
1	J	150	LEU	2.5
1	J	26	ALA	2.4
1	G	26	ALA	2.4
1	G	209	ALA	2.4
1	J	199	SER	2.4
1	J	172	THR	2.4
1	G	48	GLN	2.4
1	J	177	GLY	2.4
1	E	43	ALA	2.4
1	J	187	ASP	2.3
1	G	30	ILE	2.3
1	J	136	GLU	2.3
1	E	2	VAL	2.3
1	J	12	SER	2.3
1	G	5	VAL	2.2
1	J	160	PHE	2.2
1	G	29	THR	2.2
1	G	37	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	J	2	VAL	2.2
1	A	213	PHE	2.2
1	H	182	ALA	2.1
1	J	186	LYS	2.1
1	J	110	LEU	2.1
1	J	184	MET	2.1
1	J	140	ALA	2.1
1	J	155	TYR	2.1
1	J	114	THR	2.1
1	F	116	HIS	2.1
1	J	73	VAL	2.1
1	G	20	LEU	2.1
1	J	17	LEU	2.0
1	I	120	ALA	2.0
1	J	193	ALA	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 carbohydrates 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
3	GOL	B	303	6/6	0.41	0.31	56,60,61,61	0
3	GOL	B	302	6/6	0.65	0.22	68,74,78,83	0
4	CL	G	302	1/1	0.74	0.28	130,130,130,130	0
3	GOL	A	303	6/6	0.78	0.18	50,66,68,75	0
3	GOL	A	302	6/6	0.91	0.14	55,63,65,68	0
2	GTS	J	301	23/23	0.91	0.16	42,71,76,80	0
2	GTS	G	301	23/23	0.93	0.15	50,65,101,104	0
2	GTS	C	301	23/23	0.94	0.15	30,37,59,65	0

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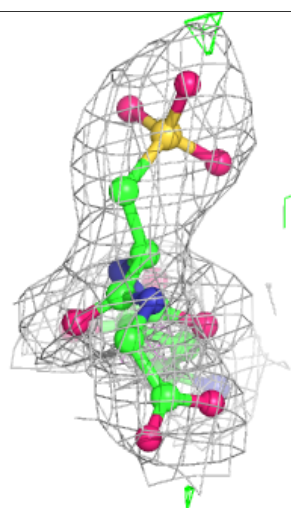
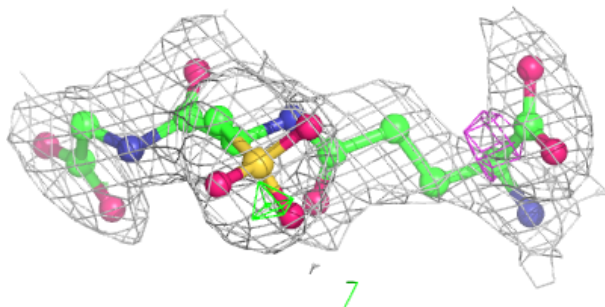
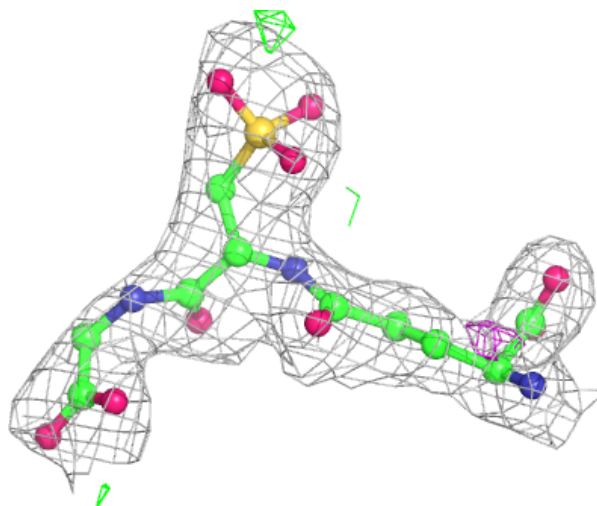
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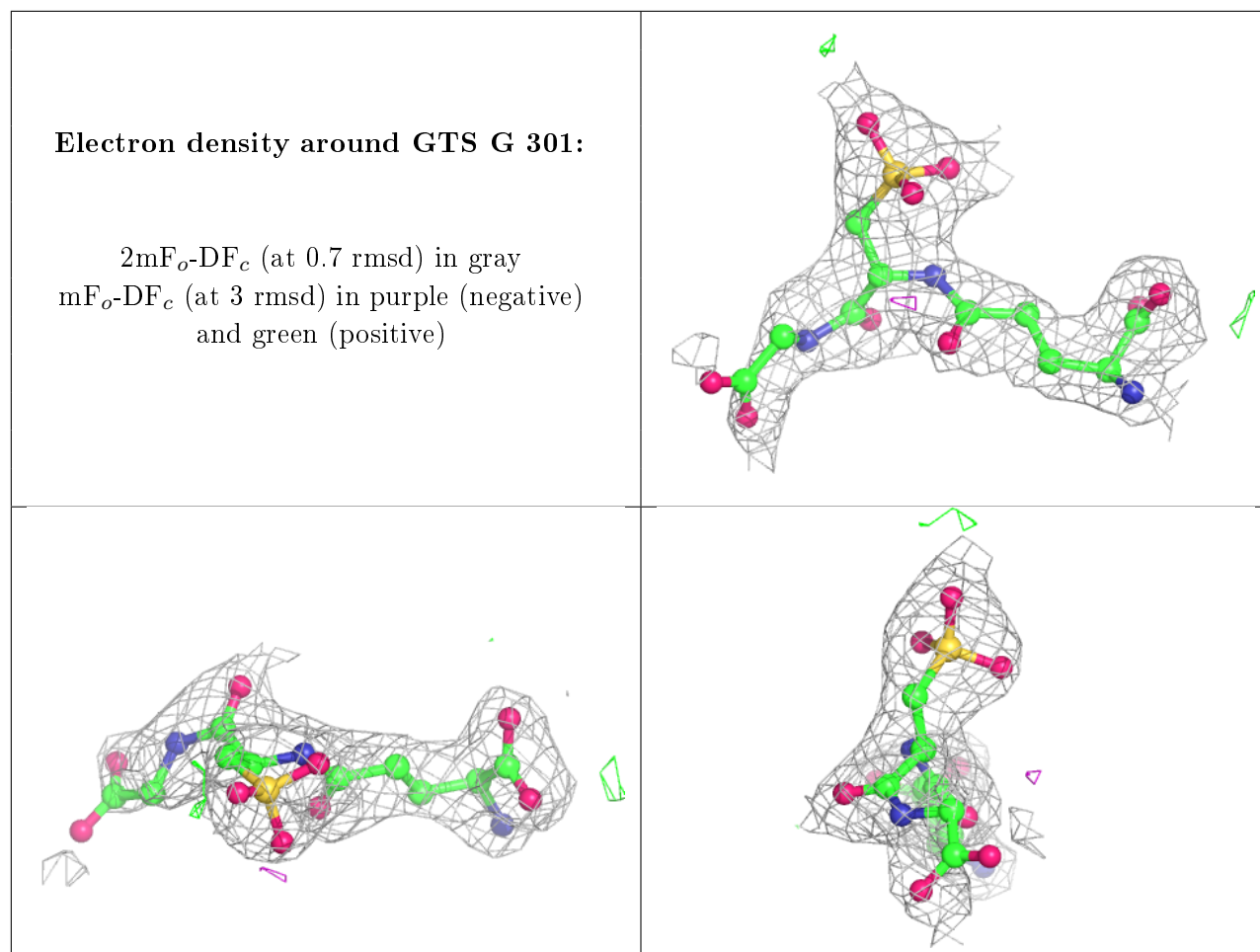
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	GTS	F	301	23/23	0.94	0.15	45,53,62,67	0
2	GTS	A	301	23/23	0.95	0.14	28,34,47,58	0
4	CL	D	302	1/1	0.95	0.14	48,48,48,48	0
2	GTS	E	301	23/23	0.95	0.14	30,47,80,85	0
2	GTS	H	301	23/23	0.96	0.12	40,43,53,55	0
4	CL	C	302	1/1	0.97	0.12	44,44,44,44	0
2	GTS	B	301	23/23	0.97	0.13	23,28,43,48	0
4	CL	F	302	1/1	0.97	0.15	50,50,50,50	0
4	CL	H	302	1/1	0.97	0.12	48,48,48,48	0
2	GTS	D	301	23/23	0.97	0.14	25,36,47,51	0
2	GTS	I	301	23/23	0.98	0.11	22,30,49,54	0
4	CL	A	304	1/1	0.99	0.20	35,35,35,35	0
4	CL	I	302	1/1	0.99	0.12	36,36,36,36	0
4	CL	B	304	1/1	0.99	0.15	34,34,34,34	0
4	CL	E	302	1/1	0.99	0.12	52,52,52,52	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 GTS J 301:

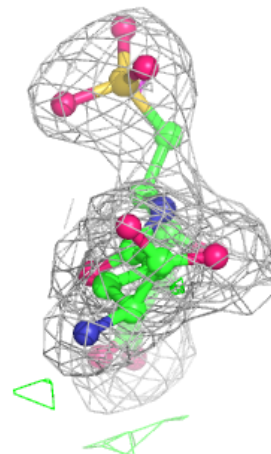
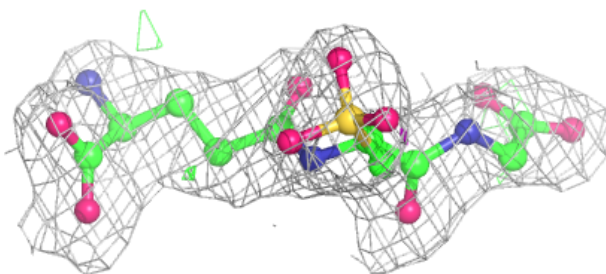
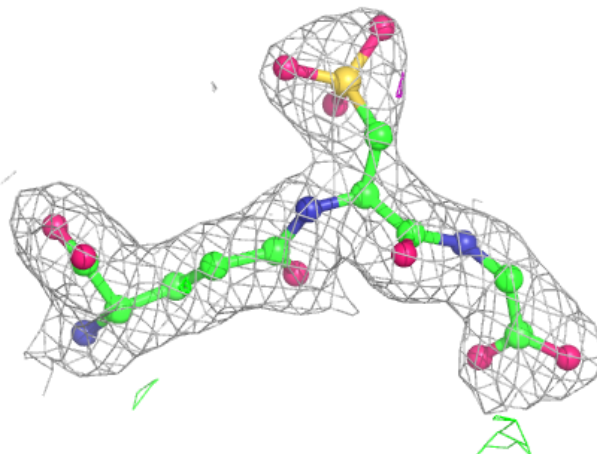
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





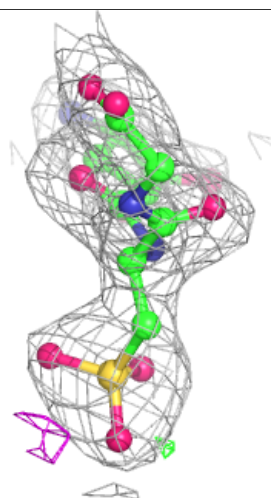
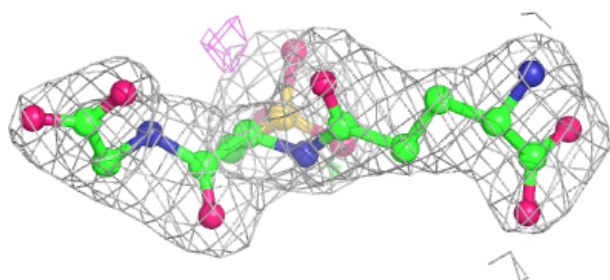
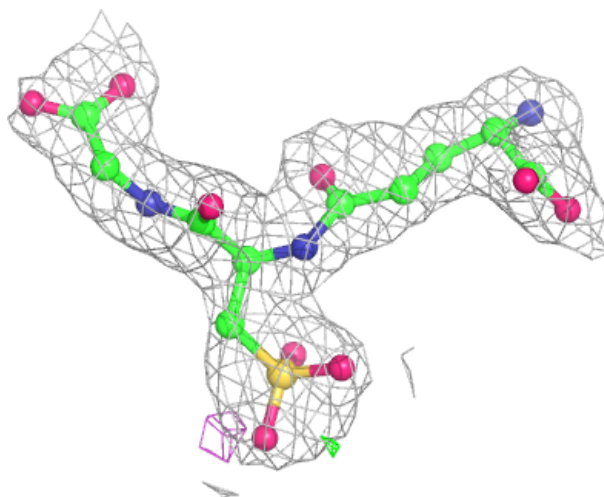
Electron density around GTS C 301:

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



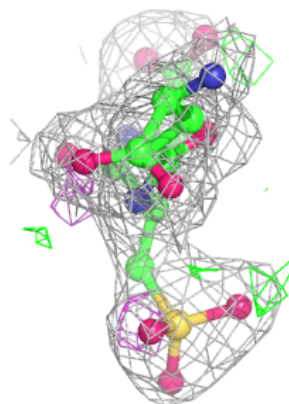
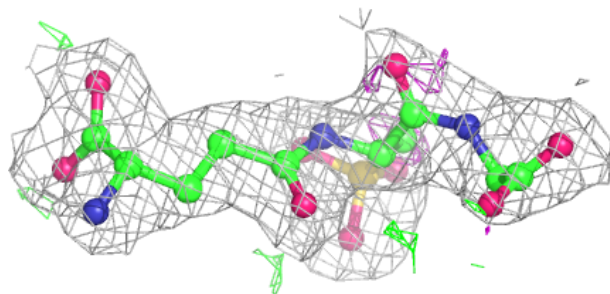
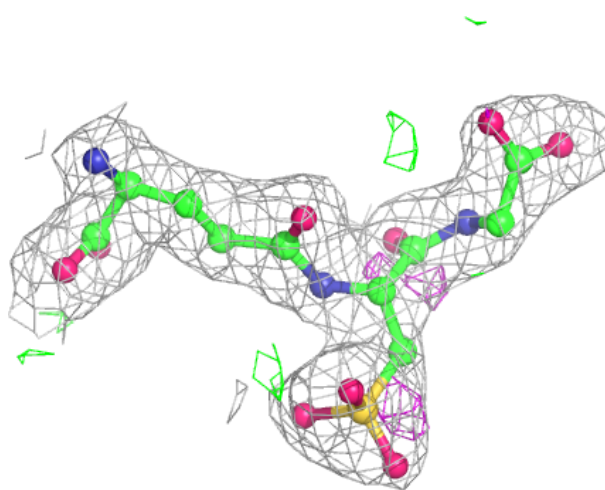
Electron density around GTS F 301:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



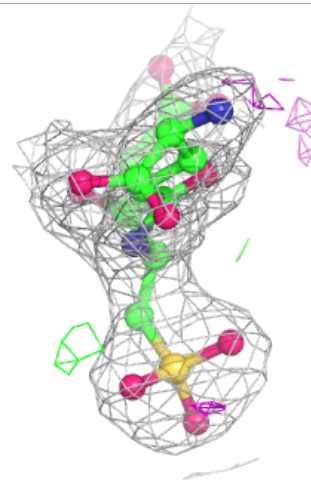
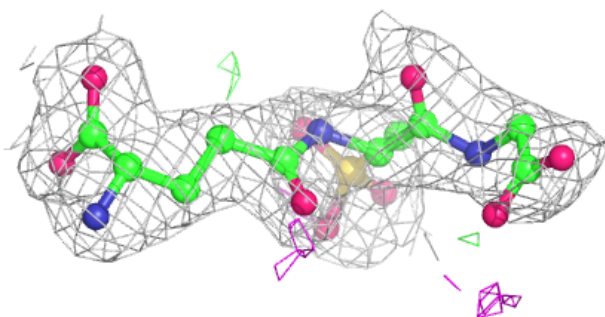
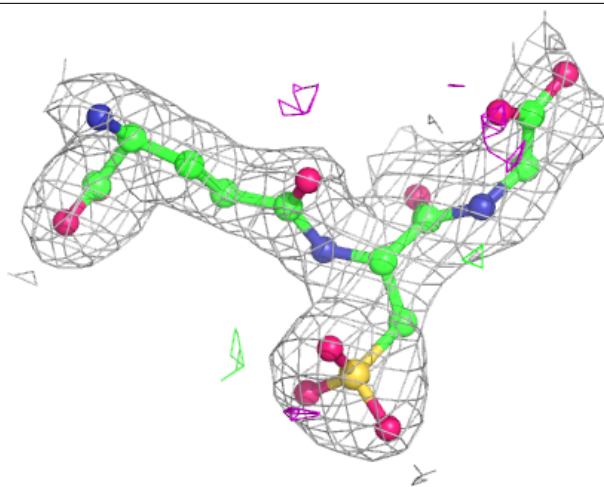
Electron density around GTS A 301:

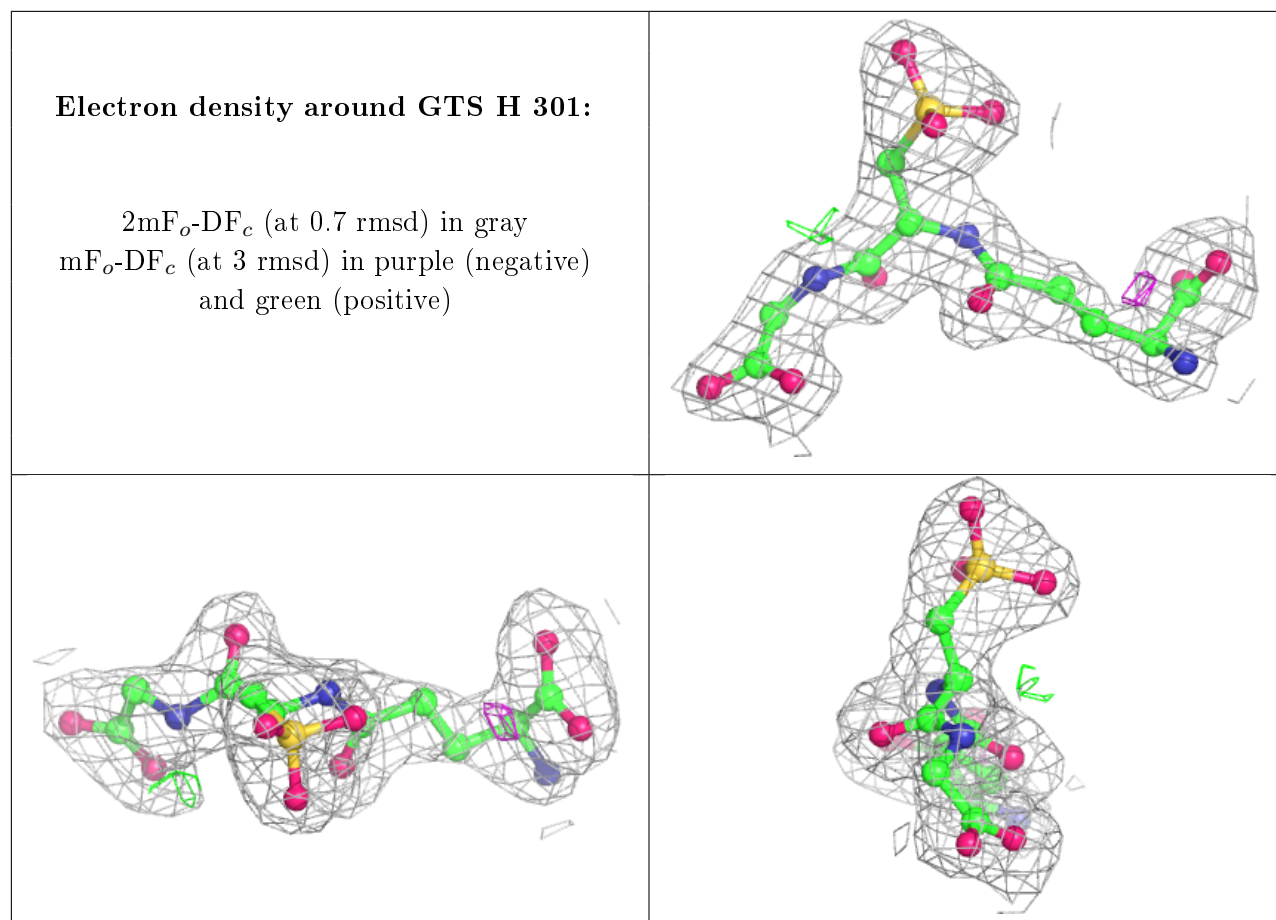
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around GTS E 301:

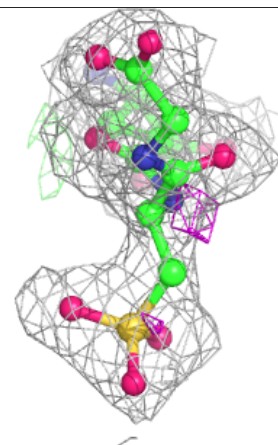
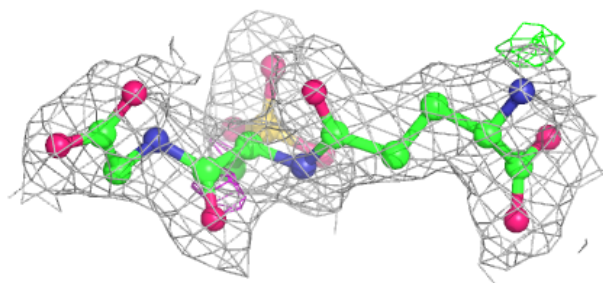
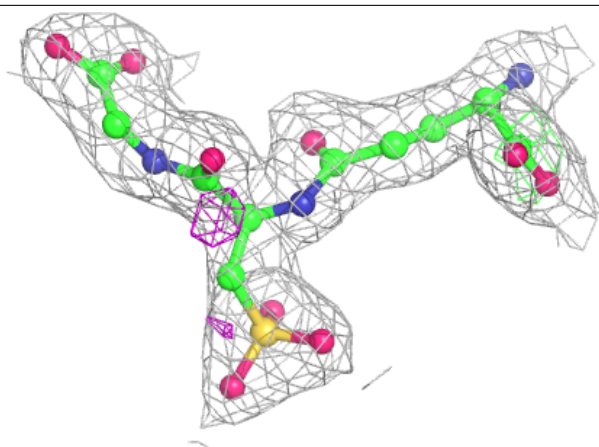
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





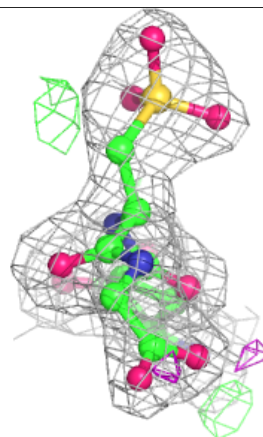
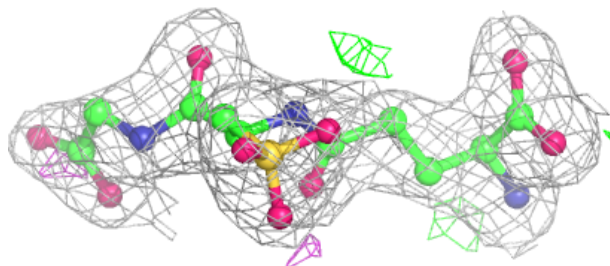
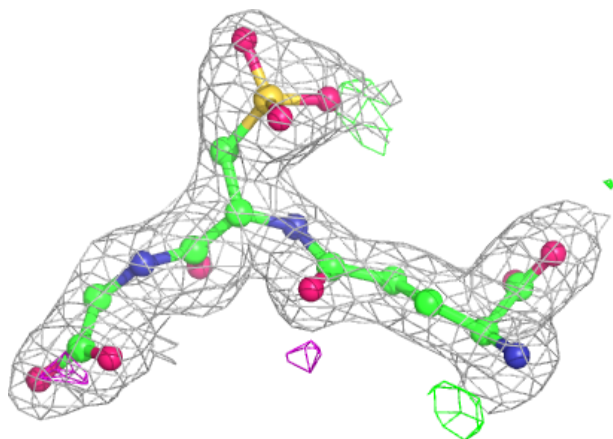
Electron density around GTS B 301:

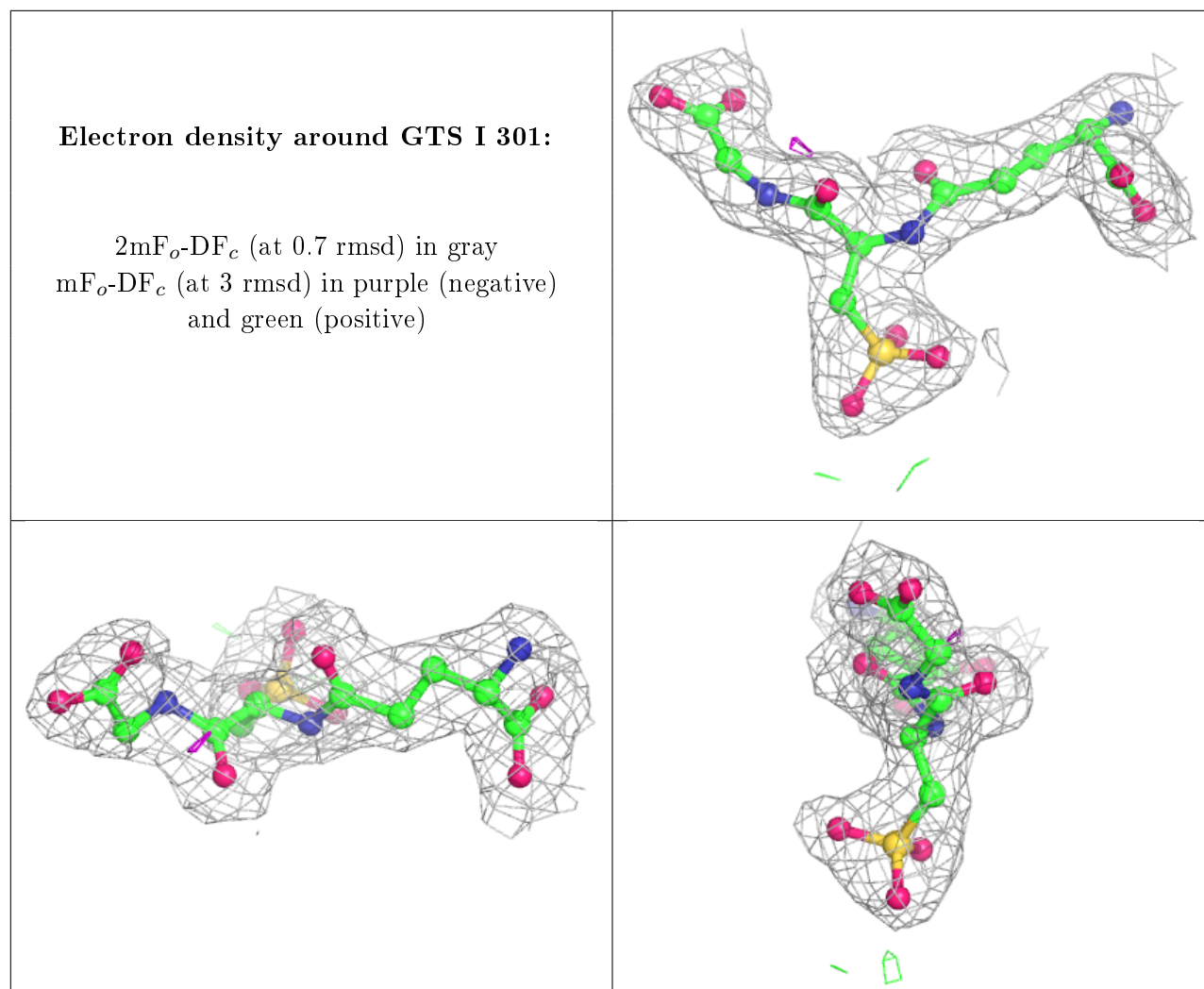
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around GTS D 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 [\(i\)](#)

There are no such residues in this entry.