



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 26, 2022 – 10:18 AM JST

PDB ID : 7DZ4  
Title : Crystal structures of D-allulose 3-epimerase with D-tagatose from *Sinorhizobium fredii*  
Authors : Zhu, Z.L.; Miyakawa, T.; Tanokura, M.; Lu, F.P.; Qin, H.-M.  
Deposited on : 2021-01-23  
Resolution : 1.84 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.

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 : 4.02b-467  
Mogul : ?? (??), CSD ??CSD?? (????)  
Xtriage (Phenix) : 1.13  
EDS : 2.29  
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) : 2.29

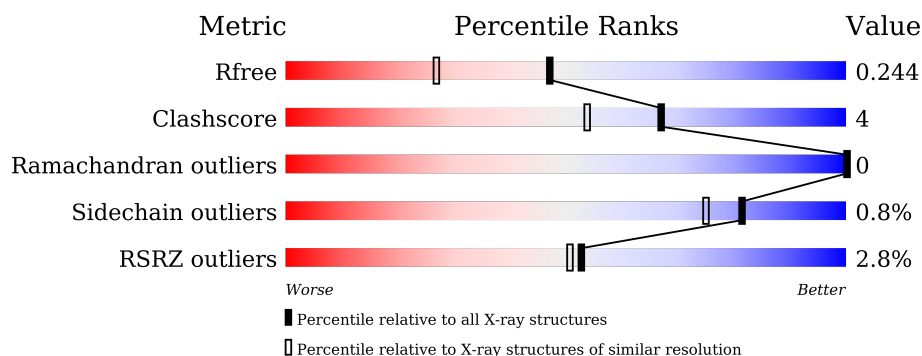
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.84 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	4003 (1.86-1.82)
Clashscore	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)

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  $\geq 3$ , 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	286	 % 91% 8% .
1	B	286	 3% 91% 7% .
1	C	286	 2% 88% 11% .
1	D	286	 5% 90% 10%

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 18238 atoms, of which 8620 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 D-tagatose 3-epimerase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	284	Total	C	H	N	O	S	0	0	0
			4339	1384	2150	382	411	12			
1	B	283	Total	C	H	N	O	S	0	0	0
			4320	1379	2139	381	410	11			
1	C	286	Total	C	H	N	O	S	0	0	0
			4360	1390	2159	385	414	12			
1	D	285	Total	C	H	N	O	S	0	0	0
			4341	1385	2148	384	413	11			

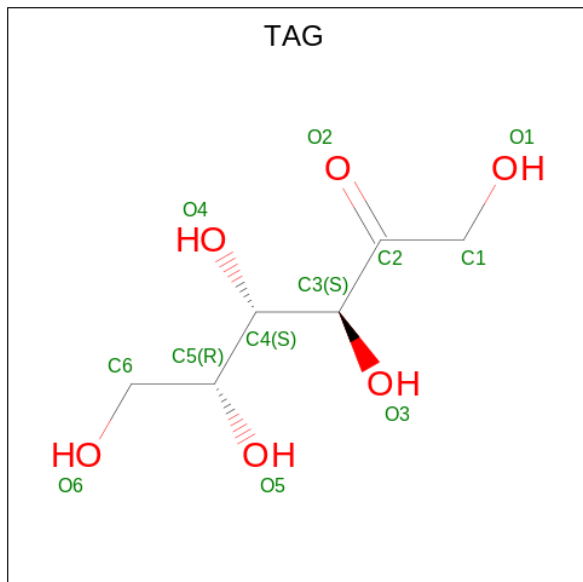
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	285	GLY	-	expression tag	UNP A0A249Q1V1
A	286	ASN	-	expression tag	UNP A0A249Q1V1
B	285	GLY	-	expression tag	UNP A0A249Q1V1
B	286	ASN	-	expression tag	UNP A0A249Q1V1
C	285	GLY	-	expression tag	UNP A0A249Q1V1
C	286	ASN	-	expression tag	UNP A0A249Q1V1
D	284	GLY	-	expression tag	UNP A0A249Q1V1
D	285	ASN	-	expression tag	UNP A0A249Q1V1

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		
2	C	1	Total	Mg	0	0
			1	1		
2	D	1	Total	Mg	0	0
			1	1		

- Molecule 3 is D-tagatose (three-letter code: TAG) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	H	O	0	0
			24	6	12	6		
3	D	1	Total	C	H	O	0	0
			24	6	12	6		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	240	Total	O	0	0
			240	240		
4	B	207	Total	O	0	0
			207	207		
4	C	205	Total	O	0	0
			205	205		
4	D	174	Total	O	0	0
			174	174		

### 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.

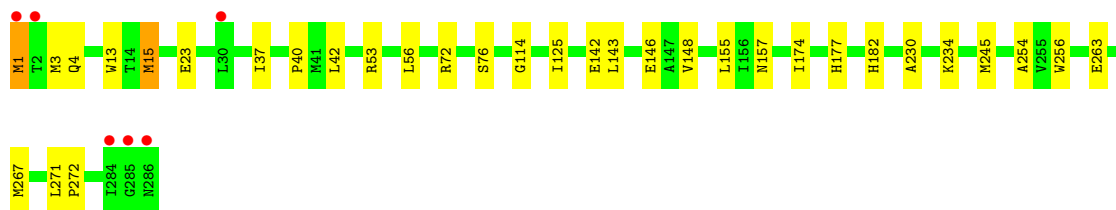
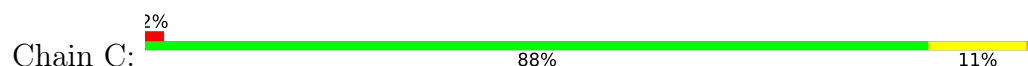
- Molecule 1: D-tagatose 3-epimerase



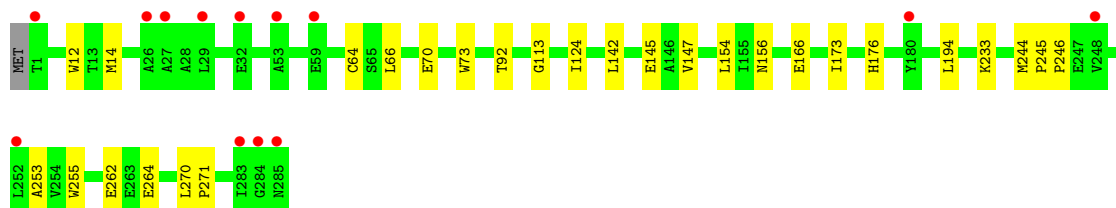
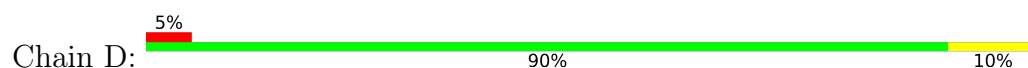
- Molecule 1: D-tagatose 3-epimerase



- Molecule 1: D-tagatose 3-epimerase



- Molecule 1: D-tagatose 3-epimerase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	62.66Å 87.92Å 128.29Å 90.00° 99.31° 90.00°	Depositor
Resolution (Å)	36.11 – 1.84 36.11 – 1.84	Depositor EDS
% Data completeness (in resolution range)	99.8 (36.11-1.84) 99.8 (36.11-1.84)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.96 (at 1.83Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, $R_{free}$	0.203 , 0.245 0.203 , 0.244	Depositor DCC
$R_{free}$ test set	6005 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.4	Xtriage
Anisotropy	0.307	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 49.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	18238	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.30% 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: MG, TAG

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	0.57	0/2238	0.69	0/3035
1	B	0.55	0/2230	0.70	2/3025 (0.1%)
1	C	0.59	1/2250 (0.0%)	0.72	1/3051 (0.0%)
1	D	0.54	0/2242	0.65	0/3041
All	All	0.56	1/8960 (0.0%)	0.69	3/12152 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	267	MET	SD-CE	-5.03	1.49	1.77

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	267	MET	CG-SD-CE	8.46	113.74	100.20
1	B	15	MET	CG-SD-CE	5.48	108.97	100.20
1	B	183	MET	CG-SD-CE	-5.38	91.59	100.20

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	2189	2150	2150	14	0
1	B	2181	2139	2138	13	0
1	C	2201	2159	2159	26	0
1	D	2193	2148	2150	17	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	C	12	12	11	2	0
3	D	12	12	11	1	0
4	A	240	0	0	1	0
4	B	207	0	0	1	0
4	C	205	0	0	4	0
4	D	174	0	0	1	0
All	All	9618	8620	8619	68	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 4.

All (68) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1:MET:HG2	1:C:3:MET:H	1.39	0.85
1:A:279:LYS:HA	1:A:284:ILE:HG22	1.61	0.82
1:A:15:MET:O	1:A:42:LEU:HD12	1.90	0.70
1:D:64:CYS:SG	1:D:92:THR:HG23	2.34	0.67
1:C:40:PRO:HB3	1:C:42:LEU:HD21	1.78	0.65
1:C:234:LYS:HG2	4:C:523:HOH:O	1.98	0.64
1:C:1:MET:N	1:C:142:GLU:OE1	2.32	0.60
1:D:166:GLU:OE2	4:D:401:HOH:O	2.16	0.60
1:C:1:MET:HG2	1:C:3:MET:N	2.16	0.59
1:B:125:ILE:HD11	1:B:155:LEU:HD13	1.84	0.58
1:C:13:TRP:CD1	1:C:263:GLU:HG3	2.38	0.57
1:C:1:MET:CG	1:C:3:MET:HB2	2.34	0.57
1:A:279:LYS:NZ	1:D:264:GLU:OE2	2.40	0.55
3:C:301:TAG:O4	3:C:301:TAG:H11	2.07	0.55
1:C:230:ALA:HB2	1:D:194:LEU:HD21	1.91	0.53
1:C:40:PRO:HB3	1:C:42:LEU:CD2	2.38	0.53
1:A:90:ILE:HG23	1:A:141:ILE:HD11	1.91	0.52
1:C:40:PRO:CB	1:C:42:LEU:CD2	2.88	0.52
1:D:253:ALA:HA	1:D:255:TRP:CZ2	2.45	0.51
1:D:253:ALA:HA	1:D:255:TRP:CH2	2.46	0.50

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:12:TRP:CD1	1:D:262:GLU:HG3	2.47	0.49
1:B:271:LEU:HB3	1:B:272:PRO:HD3	1.93	0.48
1:C:53:ARG:NH1	4:C:411:HOH:O	2.46	0.48
1:D:14:MET:HG2	1:D:244:MET:O	2.13	0.48
1:D:124:ILE:HD11	1:D:154:LEU:HD13	1.94	0.48
3:D:301:TAG:O4	3:D:301:TAG:H11	2.13	0.48
1:D:145:GLU:HA	1:D:176:HIS:O	2.14	0.48
1:B:148:VAL:O	1:B:157:ASN:HA	2.14	0.48
1:B:60:GLU:OE2	1:B:60:GLU:HA	2.13	0.48
1:B:275:ARG:NE	4:B:404:HOH:O	2.39	0.48
1:C:254:ALA:HA	1:C:256:TRP:CZ2	2.49	0.48
1:C:254:ALA:HA	1:C:256:TRP:CH2	2.49	0.48
1:C:125:ILE:HD11	1:C:155:LEU:HD13	1.96	0.47
1:C:271:LEU:HB3	1:C:272:PRO:HD3	1.96	0.47
1:B:109:ILE:HD12	1:B:152:GLU:HB3	1.97	0.47
1:C:1:MET:HG2	1:C:3:MET:HB2	1.97	0.47
1:C:146:GLU:HA	1:C:177:HIS:O	2.14	0.47
1:C:76:SER:HB3	4:C:459:HOH:O	2.14	0.46
1:A:148:VAL:O	1:A:157:ASN:HA	2.15	0.46
1:B:74:TRP:CE3	1:B:111:GLU:HG2	2.51	0.46
1:D:70:GLU:HA	1:D:73:TRP:CE2	2.52	0.45
1:B:143:LEU:O	1:B:174:ILE:HA	2.18	0.44
1:A:245:MET:HE3	1:A:250:ALA:HA	1.99	0.44
1:D:66:LEU:C	1:D:66:LEU:HD12	2.37	0.44
1:B:11:SER:CB	1:B:15:MET:SD	3.06	0.43
1:C:148:VAL:O	1:C:157:ASN:HA	2.18	0.43
1:A:251:TYR:HB3	1:C:114:GLY:O	2.18	0.43
1:A:146:GLU:HA	1:A:177:HIS:O	2.18	0.43
1:C:182:HIS:HE2	3:C:301:TAG:C1	2.31	0.43
1:D:147:VAL:O	1:D:156:ASN:HA	2.19	0.42
1:B:12:MET:HE3	1:B:243:ILE:CG2	2.49	0.42
1:D:142:LEU:O	1:D:173:ILE:HA	2.18	0.42
1:C:23:GLU:OE2	4:C:401:HOH:O	2.21	0.42
1:A:71:GLU:HA	1:A:74:TRP:CE2	2.54	0.42
1:B:11:SER:HB2	1:B:15:MET:SD	2.59	0.42
1:A:168:ARG:HD3	4:A:406:HOH:O	2.19	0.42
1:B:251:TYR:HB3	1:D:113:GLY:O	2.19	0.42
1:D:270:LEU:HB3	1:D:271:PRO:HD3	2.02	0.41
1:C:1:MET:N	1:C:1:MET:SD	2.88	0.41
1:A:137:LYS:NZ	1:A:172:ASP:OD1	2.51	0.41
1:D:245:PRO:HA	1:D:246:PRO:HD3	1.97	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:134:LYS:HD3	1:B:134:LYS:HA	1.84	0.41
1:A:12:MET:HG2	1:A:243:ILE:CG2	2.51	0.41
1:C:37:ILE:HD11	1:C:56:LEU:HD21	2.02	0.41
1:C:15:MET:HG3	1:C:245:MET:O	2.21	0.41
1:A:44:PRO:N	1:A:45:PRO:CD	2.84	0.40
1:A:276:ASN:O	1:A:279:LYS:HG3	2.22	0.40
1:C:143:LEU:O	1:C:174:ILE:HA	2.22	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	282/286 (99%)	274 (97%)	8 (3%)	0	100	100
1	B	281/286 (98%)	271 (96%)	10 (4%)	0	100	100
1	C	284/286 (99%)	278 (98%)	6 (2%)	0	100	100
1	D	283/286 (99%)	278 (98%)	5 (2%)	0	100	100
All	All	1130/1144 (99%)	1101 (97%)	29 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	223/224 (100%)	222 (100%)	1 (0%)	91	88
1	B	222/224 (99%)	221 (100%)	1 (0%)	88	85
1	C	224/224 (100%)	220 (98%)	4 (2%)	59	44
1	D	223/224 (100%)	222 (100%)	1 (0%)	91	88
All	All	892/896 (100%)	885 (99%)	7 (1%)	81	75

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	LYS
1	B	58	LYS
1	C	1	MET
1	C	4	GLN
1	C	15	MET
1	C	72	ARG
1	D	233	LYS

Sometimes 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

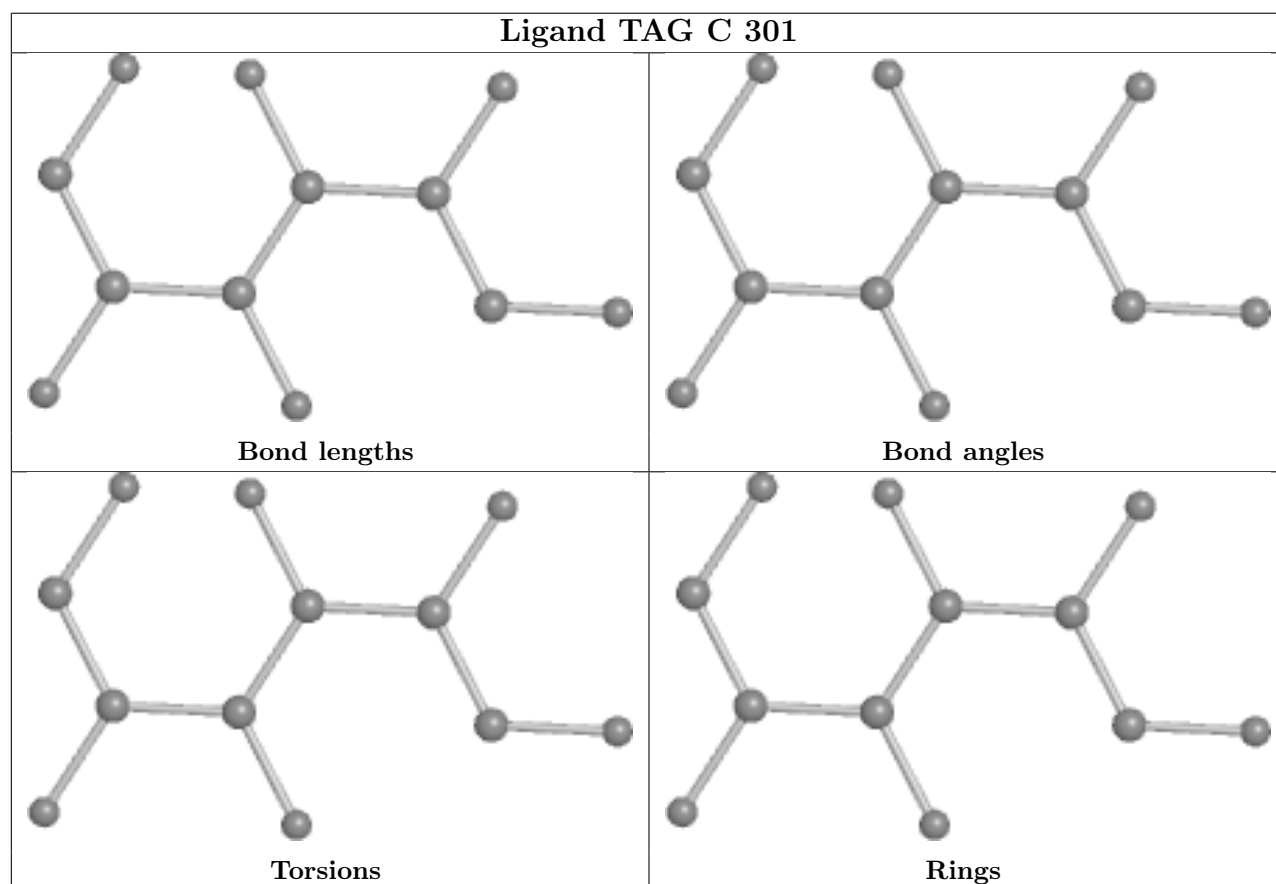
There are no chirality outliers.

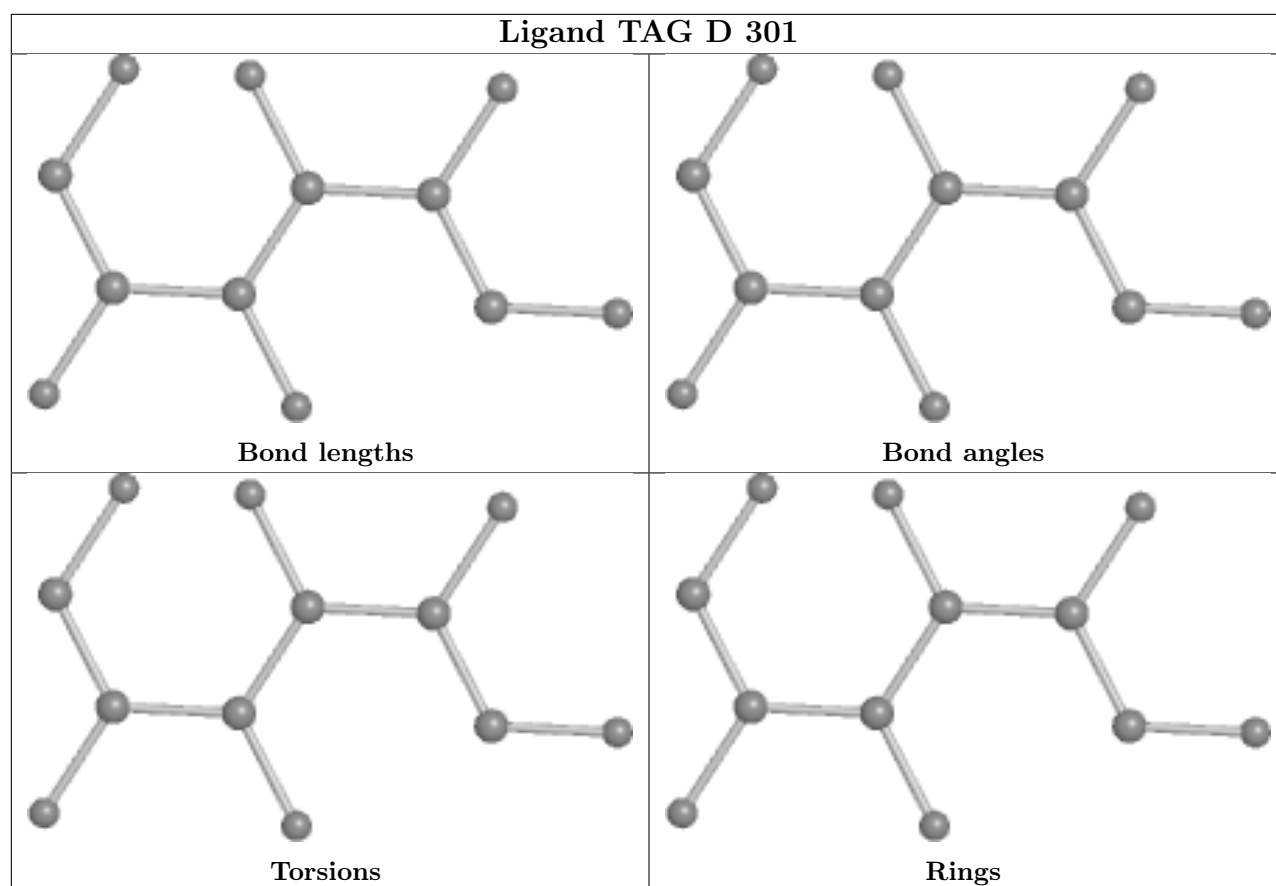
There are no torsion outliers.

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, 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	284/286 (99%)	-0.15	4 (1%) 75 75	18, 26, 42, 62	0
1	B	283/286 (98%)	0.12	9 (3%) 47 44	19, 30, 45, 67	0
1	C	286/286 (100%)	-0.05	6 (2%) 63 62	17, 26, 43, 69	0
1	D	285/286 (99%)	0.21	13 (4%) 32 29	20, 31, 49, 87	0
All	All	1138/1144 (99%)	0.03	32 (2%) 53 51	17, 28, 45, 87	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	2	THR	7.4
1	D	1	THR	6.2
1	D	29	LEU	5.0
1	B	247	PRO	4.5
1	B	284	ILE	4.1
1	C	1	MET	3.8
1	B	2	THR	3.7
1	C	285	GLY	3.5
1	C	30	LEU	3.4
1	A	1	MET	3.3
1	A	2	THR	3.2
1	B	248	GLU	3.2
1	D	248	VAL	3.1
1	A	284	ILE	2.9
1	D	284	GLY	2.9
1	D	283	ILE	2.7
1	C	284	ILE	2.7
1	B	246	PRO	2.6
1	D	285	ASN	2.4
1	B	249	VAL	2.4
1	D	26	ALA	2.4

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	247	PRO	2.4
1	D	59	GLU	2.4
1	D	27	ALA	2.3
1	D	53	ALA	2.3
1	D	252	LEU	2.3
1	D	180	TYR	2.2
1	B	261	LYS	2.1
1	C	286	ASN	2.0
1	B	251	TYR	2.0
1	B	58	LYS	2.0
1	D	32	GLU	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

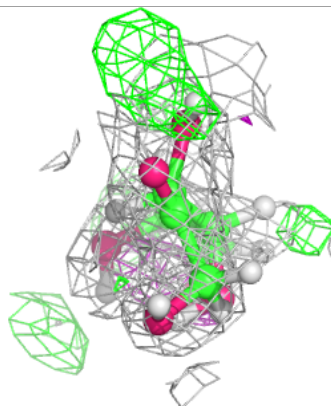
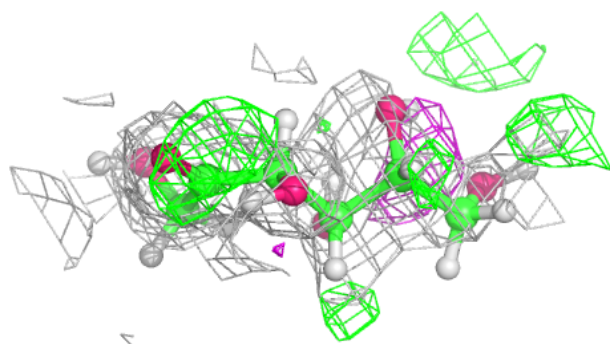
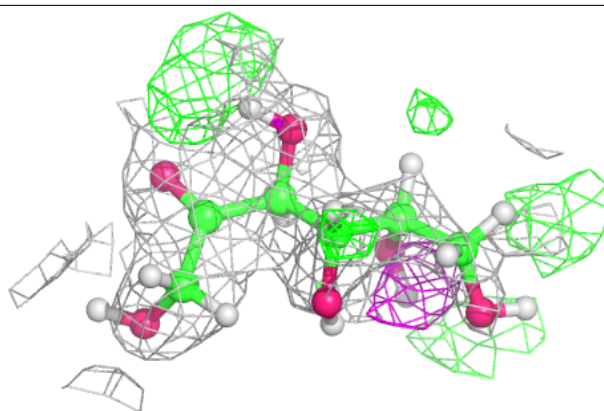
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<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
3	TAG	C	301	12/12	0.84	0.19	26,46,61,63	0
3	TAG	D	301	12/12	0.91	0.16	31,48,68,80	0
2	MG	C	302	1/1	0.99	0.22	12,12,12,12	0
2	MG	D	302	1/1	0.99	0.21	13,13,13,13	0
2	MG	A	301	1/1	0.99	0.15	11,11,11,11	0
2	MG	B	301	1/1	0.99	0.20	14,14,14,14	0

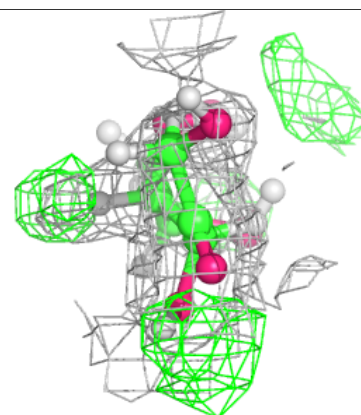
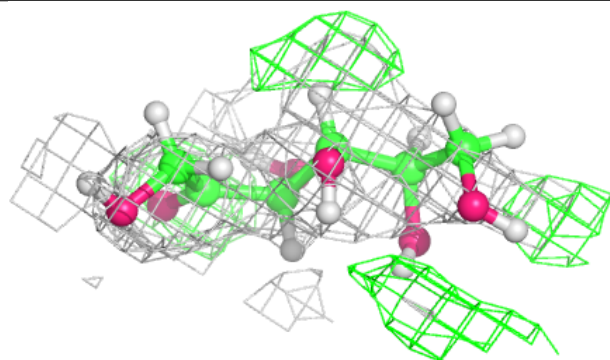
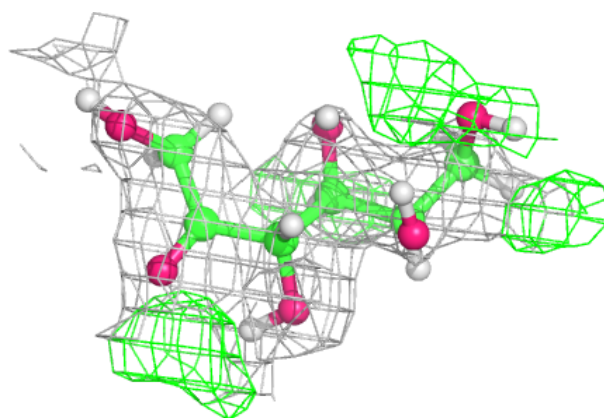
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around TAG 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 TAG D 301:**

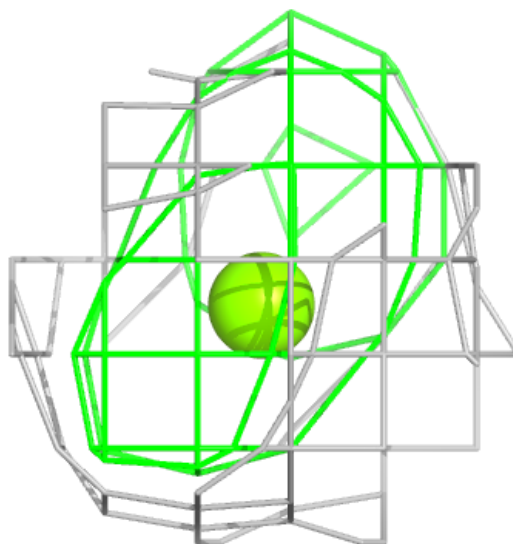
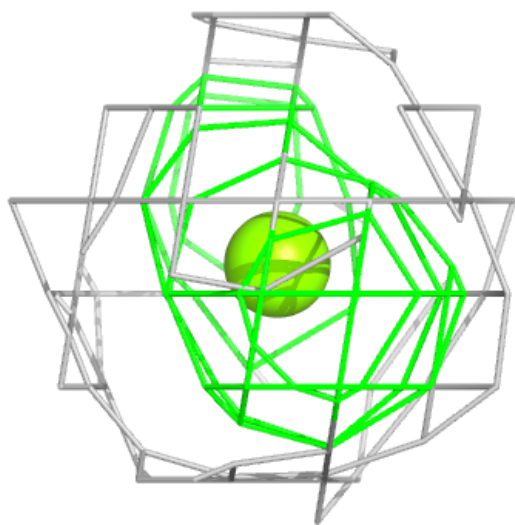
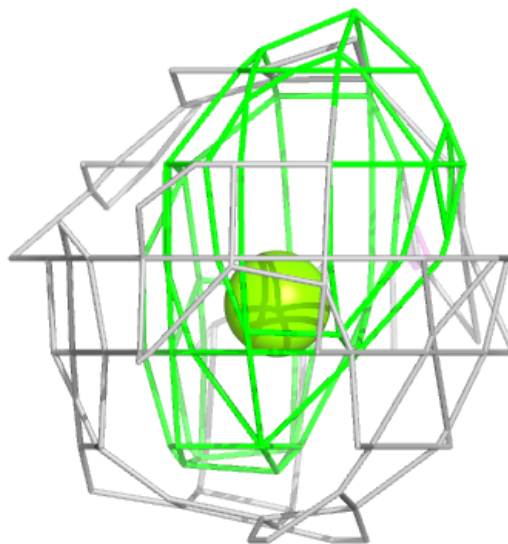
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





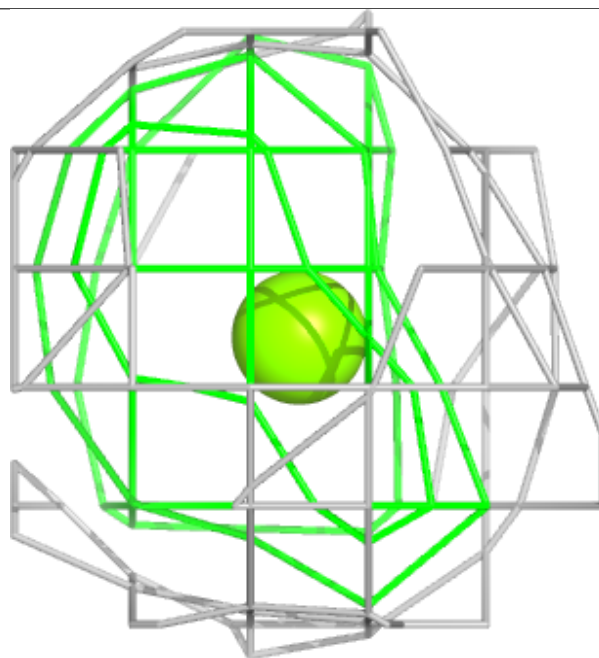
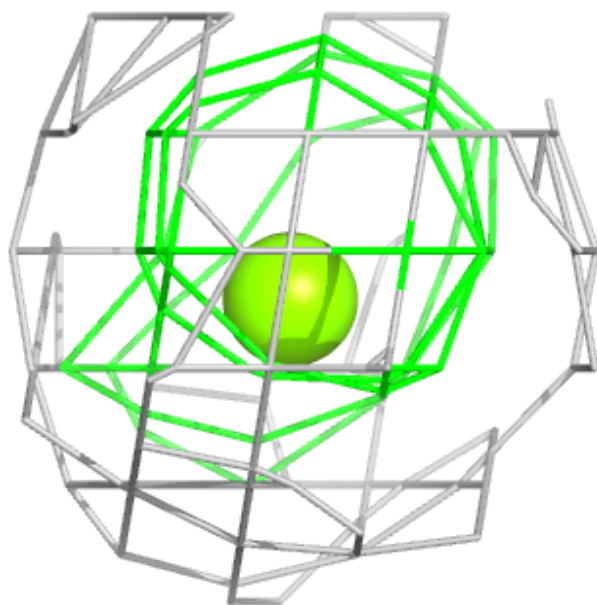
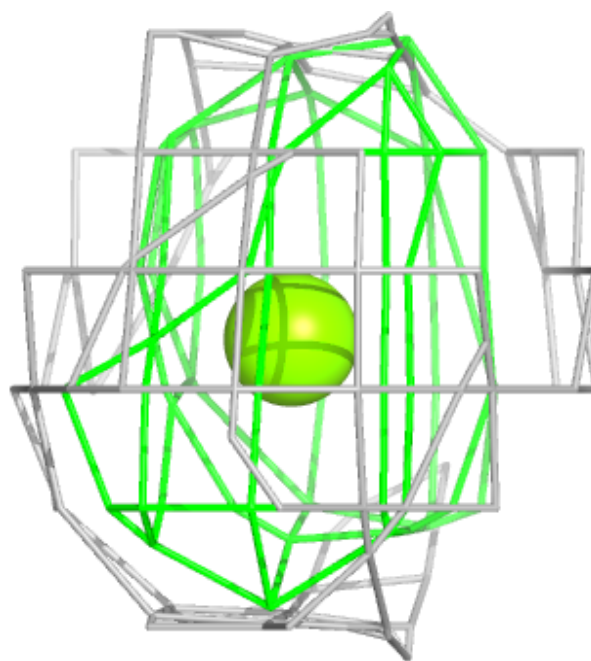
**Electron density around MG C 302:**

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



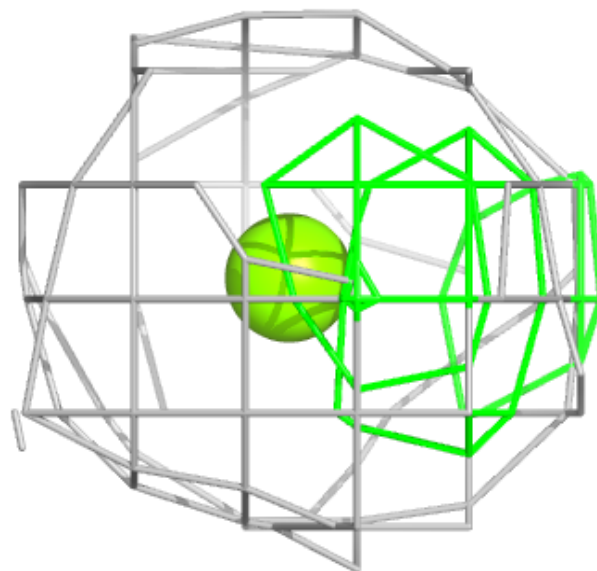
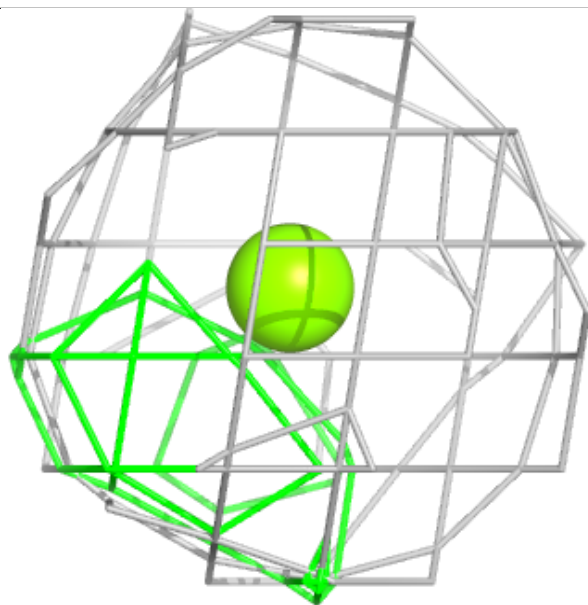
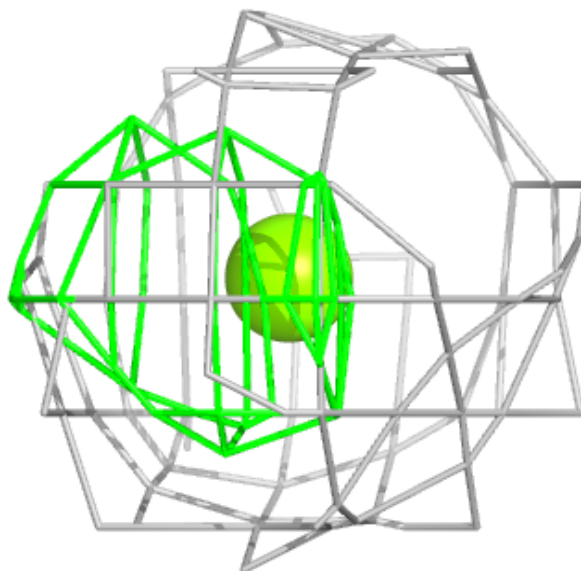
**Electron density around MG D 302:**

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



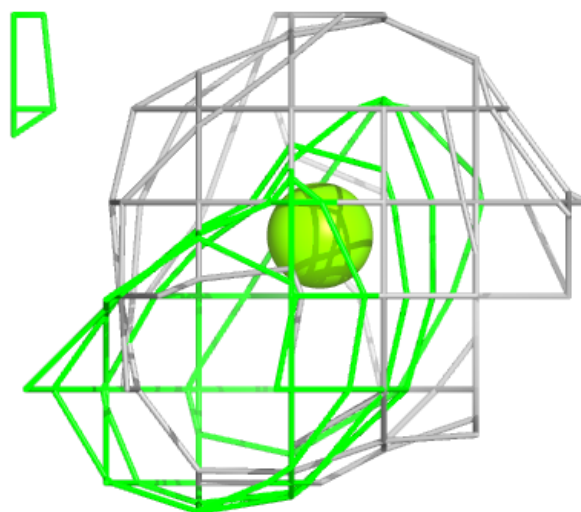
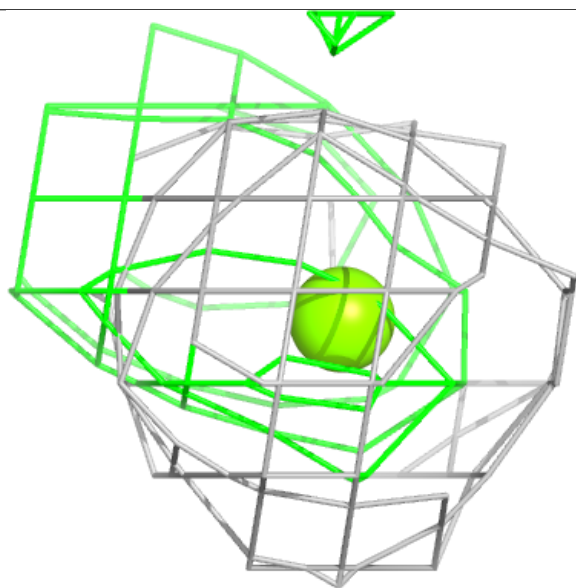
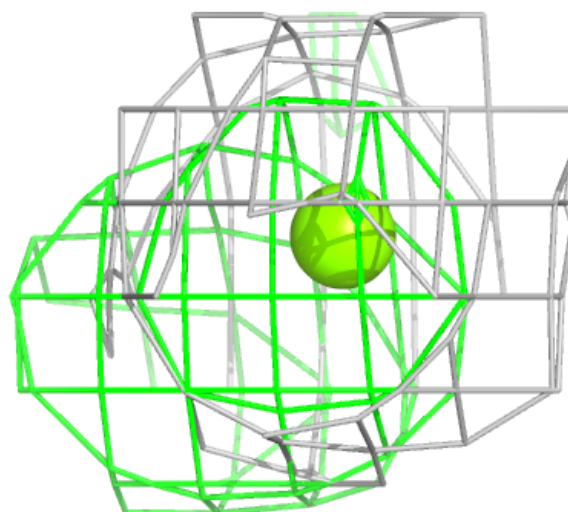
**Electron density around MG A 301:**

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



**Electron density around MG 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 [i](#)

There are no such residues in this entry.