



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 26, 2022 – 10:18 AM JST

PDB ID : 7DZ3
Title : Crystal structures of D-allulose 3-epimerase with D-fructose from *Sinorhizobium fredii*
Authors : Zhu, Z.L.; Miyakawa, T.; Tanokura, M.; Lu, F.P.; Qin, H.-M.
Deposited on : 2021-01-23
Resolution : 1.88 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 : 4.02b-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

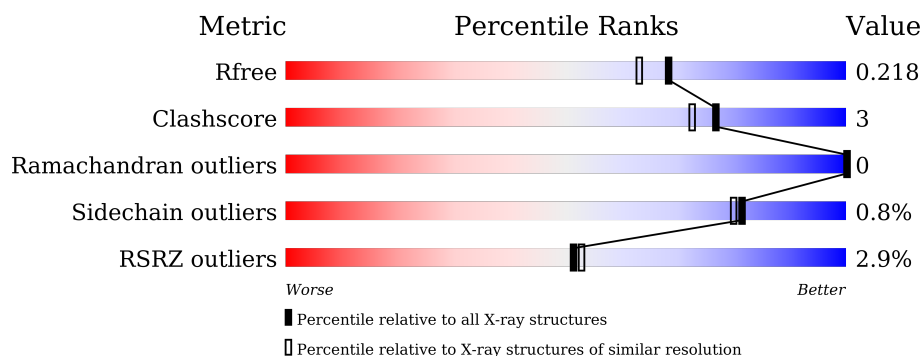
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.88 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	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

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	286	<div> <div>2%</div> <div> <div></div> <div>89%</div> <div>10%</div> <div>.</div> </div> </div>
1	B	286	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>8%</div> <div>.</div> </div> </div>
1	C	286	<div> <div>2%</div> <div> <div></div> <div>94%</div> <div>6%</div> </div> </div>
1	D	286	<div> <div>5%</div> <div> <div></div> <div>91%</div> <div>9%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17745 atoms, of which 8594 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	283	Total	C	H	N	O	S	0	0	0
			4319	1379	2138	381	410	11			
1	B	283	Total	C	H	N	O	S	0	0	0
			4319	1379	2138	381	410	11			
1	C	285	Total	C	H	N	O	S	0	0	0
			4340	1385	2147	384	413	11			
1	D	285	Total	C	H	N	O	S	0	0	0
			4340	1385	2147	384	413	11			

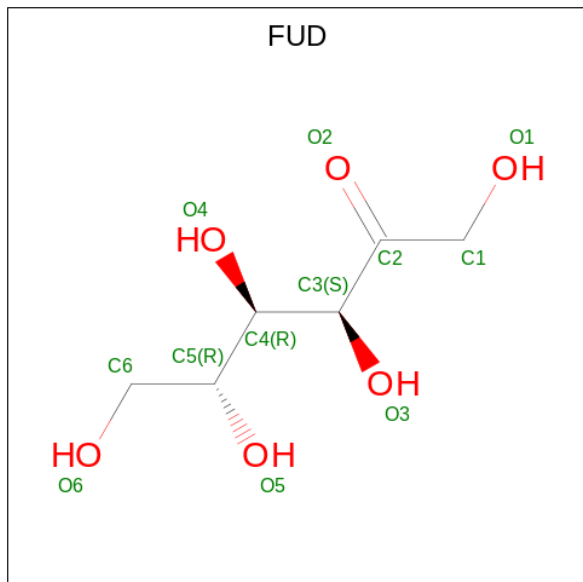
There are 8 discrepancies between the modelled and reference sequences:

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	285	GLY	-	expression tag	UNP A0A249Q1V1
D	286	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-fructose (three-letter code: FUD) (formula: $C_6H_{12}O_6$) (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		

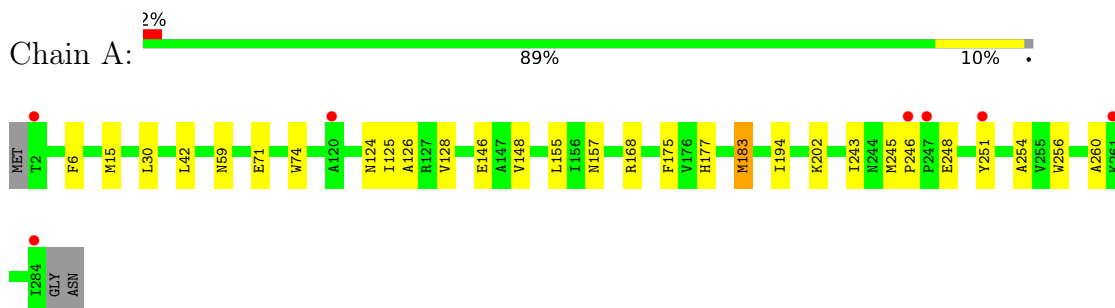
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	102	Total	O	0	0
			102	102		
4	B	83	Total	O	0	0
			83	83		
4	C	131	Total	O	0	0
			131	131		
4	D	59	Total	O	0	0
			59	59		

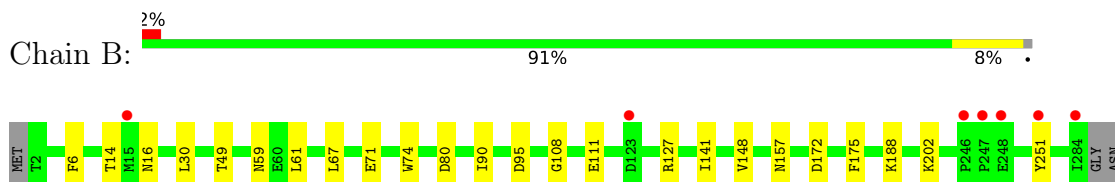
3 Residue-property plots [i](#)

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.

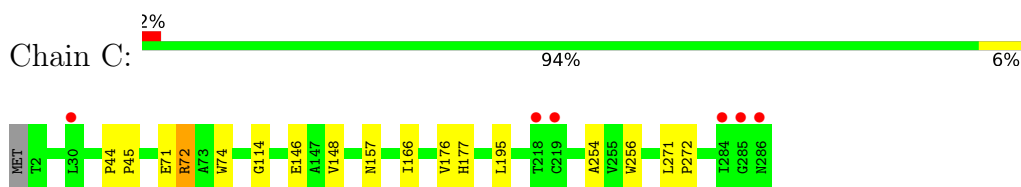
- Molecule 1: D-tagatose 3-epimerase



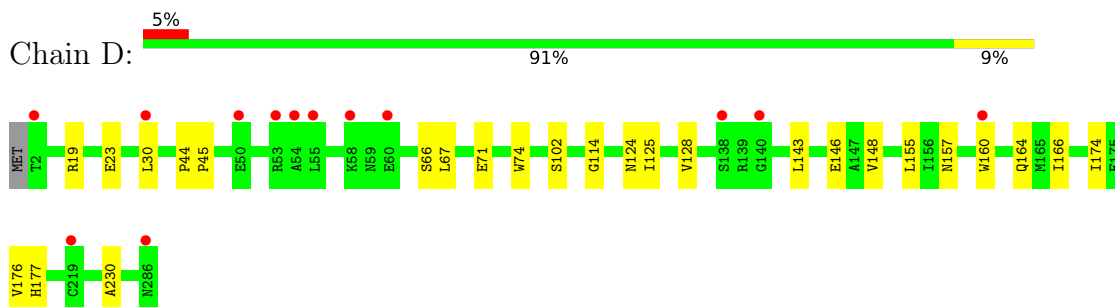
- Molecule 1: D-tagatose 3-epimerase



- Molecule 1: D-tagatose 3-epimerase



- Molecule 1: D-tagatose 3-epimerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.44Å 120.65Å 134.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.92 – 1.88 44.92 – 1.88	Depositor EDS
% Data completeness (in resolution range)	99.1 (44.92-1.88) 99.1 (44.92-1.88)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 1.88Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.182 , 0.218 0.182 , 0.218	Depositor DCC
R_{free} test set	5834 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	26.5	Xtriage
Anisotropy	0.357	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 39.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	17745	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.55 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.5020e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: FUD, MG

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	0.54	0/2230	0.67	1/3025 (0.0%)
1	B	0.50	0/2230	0.66	0/3025
1	C	0.59	0/2242	0.71	2/3041 (0.1%)
1	D	0.49	0/2242	0.64	0/3041
All	All	0.53	0/8944	0.67	3/12132 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	72	ARG	NE-CZ-NH1	-6.95	116.83	120.30
1	C	72	ARG	NE-CZ-NH2	6.59	123.59	120.30
1	A	183	MET	CG-SD-CE	-5.87	90.80	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	2181	2138	2138	17	0
1	B	2181	2138	2138	12	0
1	C	2193	2147	2147	12	0
1	D	2193	2147	2147	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	0	0
3	D	12	12	12	0	0
4	A	102	0	0	0	0
4	B	83	0	0	0	0
4	C	131	0	0	0	0
4	D	59	0	0	0	0
All	All	9151	8594	8593	52	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (52) 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:166:ILE:HD12	1:C:176:VAL:HG23	1.76	0.66
1:D:19:ARG:O	1:D:23:GLU:HG2	1.99	0.62
1:D:166:ILE:HD12	1:D:176:VAL:HG23	1.80	0.61
1:B:30:LEU:HD11	1:B:59:ASN:OD1	2.04	0.57
1:A:148:VAL:O	1:A:157:ASN:HA	2.08	0.53
1:B:90:ILE:HG23	1:B:141:ILE:HD11	1.90	0.53
1:A:251:TYR:HB3	1:D:114:GLY:O	2.10	0.52
1:B:175:PHE:HB3	1:B:202:LYS:HD2	1.94	0.50
1:C:166:ILE:HD12	1:C:176:VAL:CG2	2.42	0.49
1:D:71:GLU:HA	1:D:74:TRP:CE2	2.48	0.49
1:A:243:ILE:HD13	1:A:260:ALA:HB3	1.95	0.49
1:B:14:THR:CG2	1:B:16:ASN:O	2.61	0.48
1:D:124:ASN:O	1:D:128:VAL:HG23	2.14	0.48
1:D:44:PRO:N	1:D:45:PRO:HD2	2.29	0.48
1:A:30:LEU:HD21	1:A:59:ASN:HB3	1.96	0.48
1:B:148:VAL:O	1:B:157:ASN:HA	2.13	0.48
1:A:175:PHE:HB3	1:A:202:LYS:HD3	1.95	0.48
1:D:146:GLU:HA	1:D:177:HIS:O	2.14	0.48
1:A:248:GLU:H	1:A:248:GLU:CD	2.17	0.47
1:C:254:ALA:HA	1:C:256:TRP:CZ2	2.50	0.47
1:B:49:THR:HG21	1:B:95:ASP:HB2	1.97	0.47
1:A:183:MET:HE1	1:A:194:ILE:HG13	1.96	0.46
1:A:245:MET:HG3	1:A:246:PRO:HD2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:71:GLU:HA	1:B:74:TRP:CE2	2.50	0.46
1:C:271:LEU:HB3	1:C:272:PRO:HD3	1.98	0.46
1:C:148:VAL:O	1:C:157:ASN:HA	2.15	0.45
1:A:254:ALA:HA	1:A:256:TRP:CZ2	2.52	0.45
1:C:71:GLU:HA	1:C:74:TRP:CE2	2.52	0.45
1:B:74:TRP:CE3	1:B:111:GLU:HG2	2.52	0.44
1:C:146:GLU:HA	1:C:177:HIS:O	2.16	0.44
1:A:146:GLU:HA	1:A:177:HIS:O	2.17	0.44
1:D:143:LEU:O	1:D:174:ILE:HA	2.19	0.43
1:A:71:GLU:HA	1:A:74:TRP:NE1	2.34	0.43
1:D:148:VAL:O	1:D:157:ASN:HA	2.18	0.43
1:A:71:GLU:HA	1:A:74:TRP:CD1	2.54	0.43
1:B:80:ASP:OD1	1:B:127:ARG:NH2	2.52	0.42
1:D:160:TRP:O	1:D:164:GLN:HG2	2.19	0.42
1:A:15:MET:HE3	1:A:42:LEU:HD13	2.02	0.42
1:B:74:TRP:NE1	1:B:108:GLY:HA3	2.35	0.42
1:A:126:ALA:HB2	1:A:168:ARG:HD2	2.02	0.42
1:C:166:ILE:CD1	1:C:176:VAL:HG23	2.45	0.41
1:D:66:SER:HA	1:D:102:SER:O	2.20	0.41
1:D:125:ILE:HD11	1:D:155:LEU:HD13	2.02	0.41
1:C:44:PRO:N	1:C:45:PRO:CD	2.84	0.41
1:D:67:LEU:C	1:D:67:LEU:HD12	2.40	0.41
1:A:125:ILE:HD11	1:A:155:LEU:HD13	2.03	0.41
1:A:71:GLU:HA	1:A:74:TRP:CE2	2.56	0.41
1:A:124:ASN:O	1:A:128:VAL:HG23	2.21	0.41
1:B:251:TYR:HB3	1:C:114:GLY:O	2.21	0.41
1:B:67:LEU:C	1:B:67:LEU:HD12	2.41	0.41
1:C:195:LEU:HD21	1:D:230:ALA:HB2	2.03	0.40
1:C:254:ALA:HA	1:C:256:TRP:CH2	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	281/286 (98%)	275 (98%)	6 (2%)	0	100	100
1	B	281/286 (98%)	274 (98%)	7 (2%)	0	100	100
1	C	283/286 (99%)	280 (99%)	3 (1%)	0	100	100
1	D	283/286 (99%)	279 (99%)	4 (1%)	0	100	100
All	All	1128/1144 (99%)	1108 (98%)	20 (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	222/224 (99%)	221 (100%)	1 (0%)	88	88
1	B	222/224 (99%)	218 (98%)	4 (2%)	59	52
1	C	223/224 (100%)	222 (100%)	1 (0%)	91	90
1	D	223/224 (100%)	222 (100%)	1 (0%)	91	90
All	All	890/896 (99%)	883 (99%)	7 (1%)	81	80

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

Mol	Chain	Res	Type
1	A	6	PHE
1	B	6	PHE
1	B	61	LEU
1	B	172	ASP
1	B	188	LYS
1	C	72	ARG
1	D	30	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	GLN

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Mol	Chain	Res	Type
1	B	16	ASN
1	C	164	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

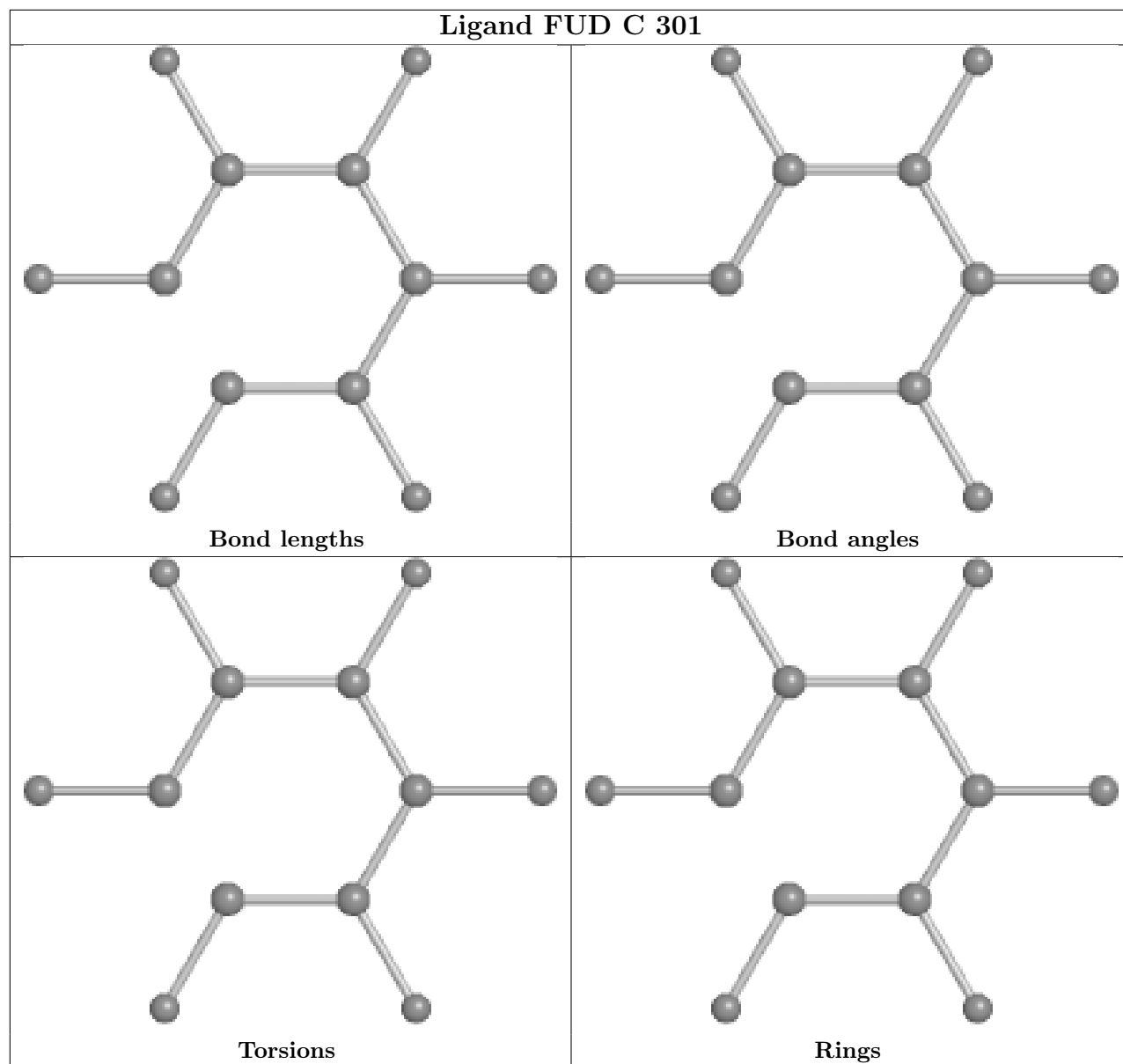
There are no chirality outliers.

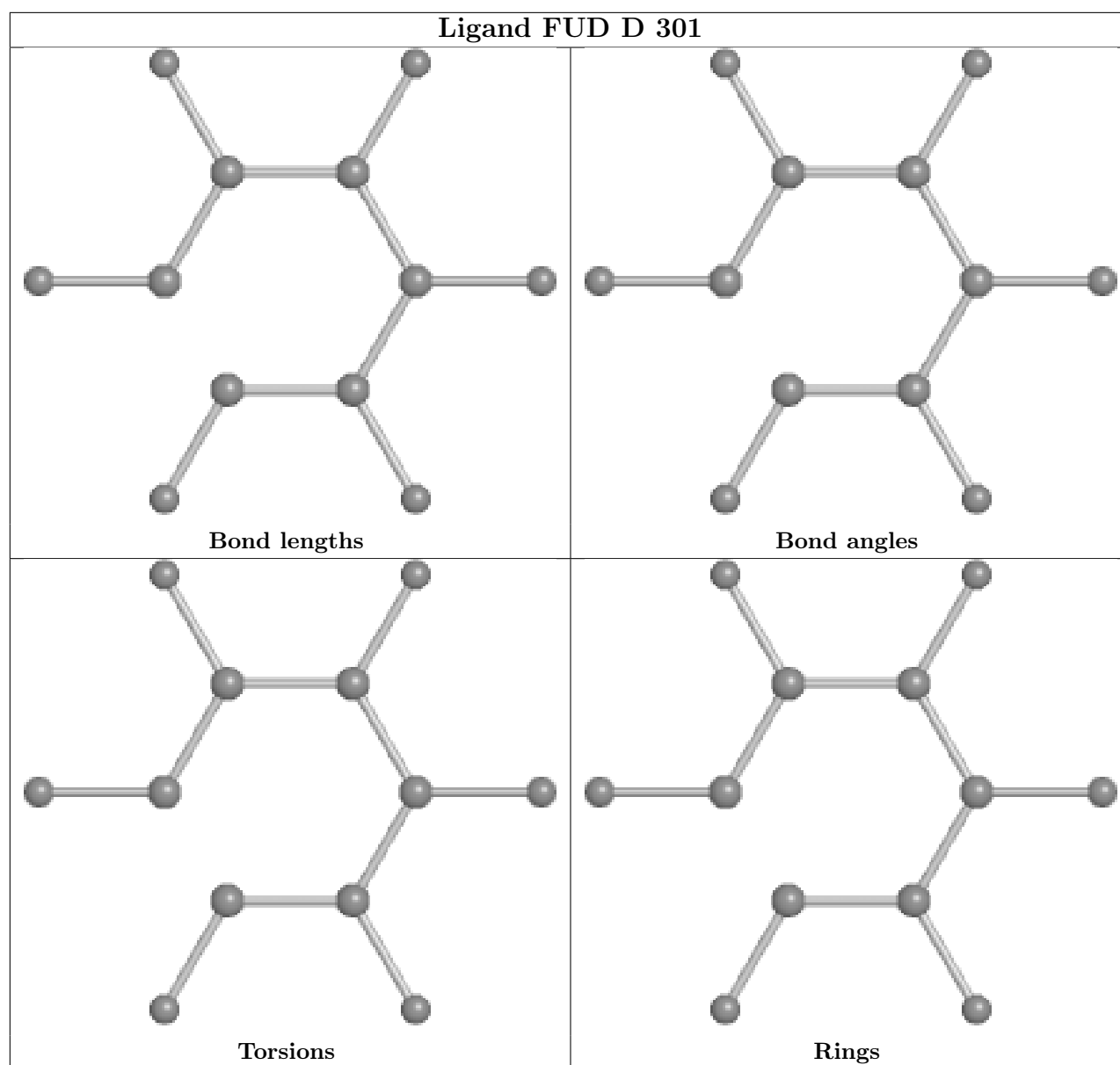
There are no torsion outliers.

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, 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	283/286 (98%)	0.09	7 (2%) 57 59	19, 27, 48, 72	0
1	B	283/286 (98%)	0.16	7 (2%) 57 59	19, 31, 50, 67	0
1	C	285/286 (99%)	0.00	6 (2%) 63 65	17, 24, 39, 62	0
1	D	285/286 (99%)	0.30	13 (4%) 32 34	19, 33, 57, 72	0
All	All	1136/1144 (99%)	0.14	33 (2%) 51 53	17, 28, 51, 72	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	30	LEU	5.1
1	B	284	ILE	4.7
1	B	247	PRO	4.5
1	A	247	PRO	4.4
1	A	284	ILE	4.3
1	D	286	ASN	4.1
1	C	285	GLY	3.9
1	A	251	TYR	3.3
1	C	286	ASN	3.3
1	B	248	GLU	3.2
1	D	54	ALA	2.9
1	C	284	ILE	2.8
1	A	2	THR	2.8
1	A	246	PRO	2.8
1	A	261	LYS	2.7
1	B	251	TYR	2.6
1	D	2	THR	2.6
1	D	160	TRP	2.5
1	B	123	ASP	2.5
1	D	60	GLU	2.5
1	D	58	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	50	GLU	2.3
1	D	219	CYS	2.3
1	D	138	SER	2.3
1	C	30	LEU	2.3
1	C	219	CYS	2.3
1	B	246	PRO	2.2
1	D	140	GLY	2.2
1	B	15	MET	2.2
1	A	120	ALA	2.2
1	D	53	ARG	2.1
1	C	218	THR	2.1
1	D	55	LEU	2.1

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](#)

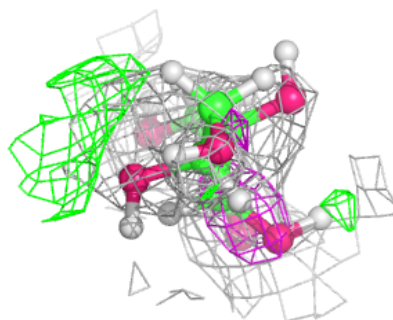
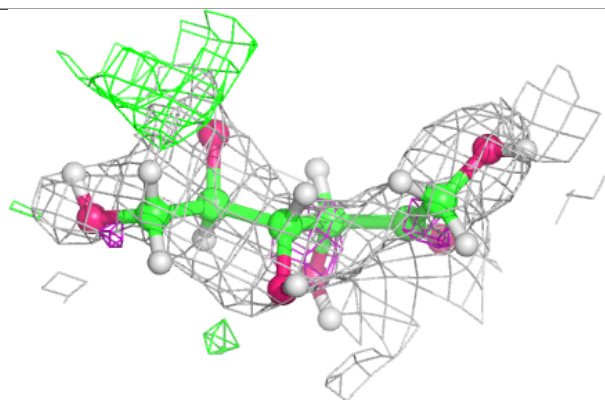
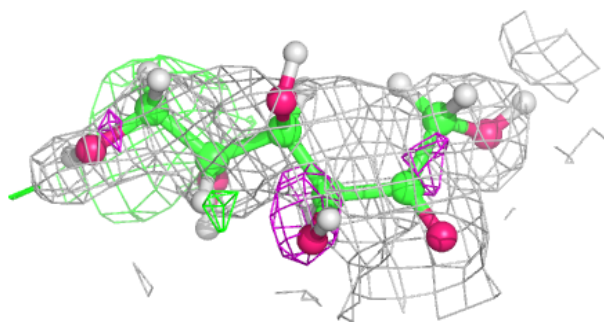
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	FUD	D	301	12/12	0.85	0.20	31,55,68,74	0
3	FUD	C	301	12/12	0.87	0.17	24,47,57,62	0
2	MG	A	301	1/1	0.96	0.07	31,31,31,31	0
2	MG	B	301	1/1	0.96	0.14	38,38,38,38	0
2	MG	D	302	1/1	0.98	0.12	30,30,30,30	0
2	MG	C	302	1/1	0.99	0.10	23,23,23,23	0

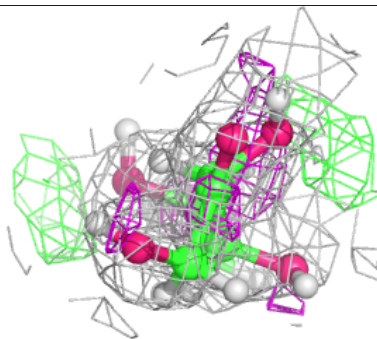
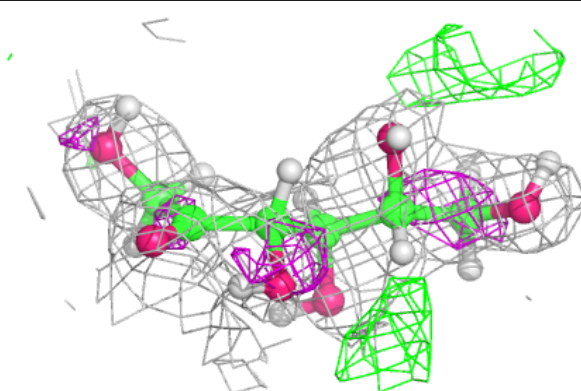
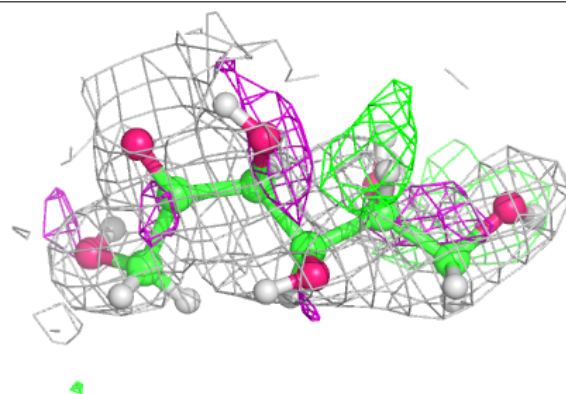
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FUD 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)

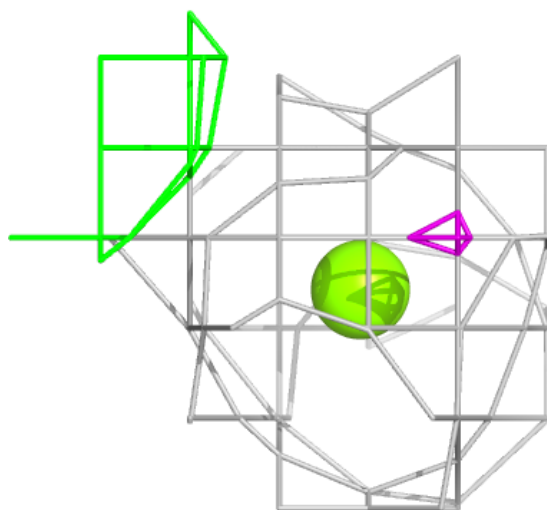
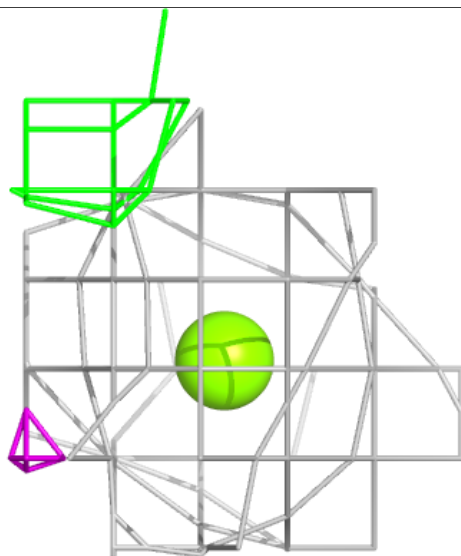
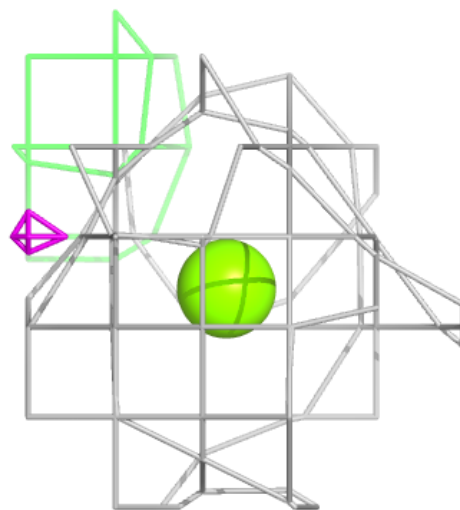
**Electron density around FUD C 301:**

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



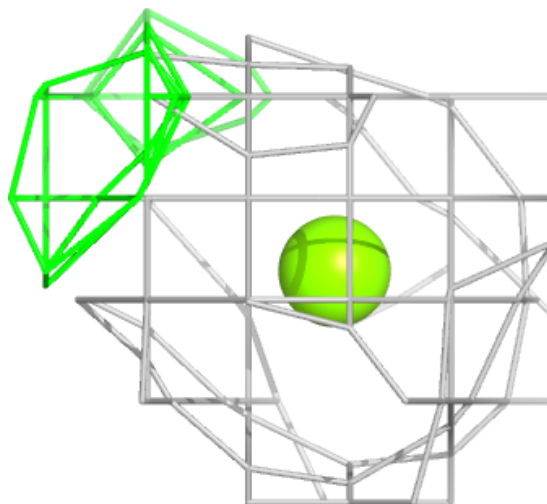
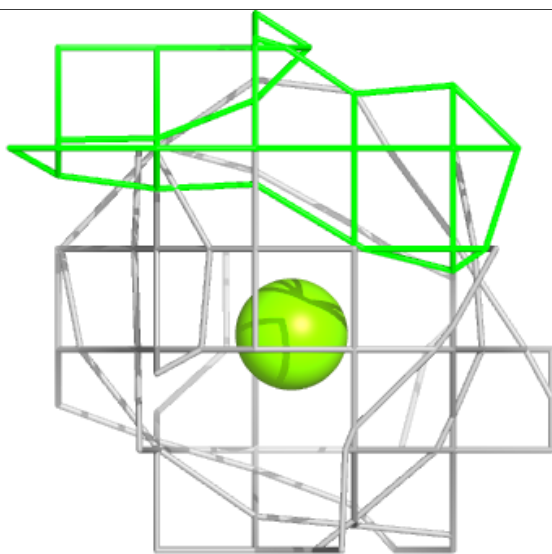
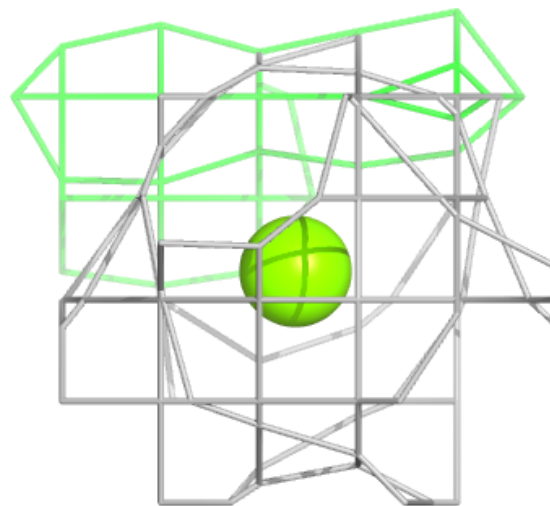
Electron density around MG A 301:

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



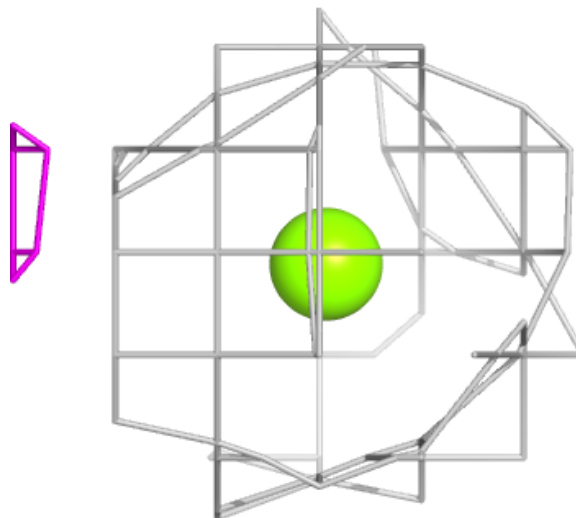
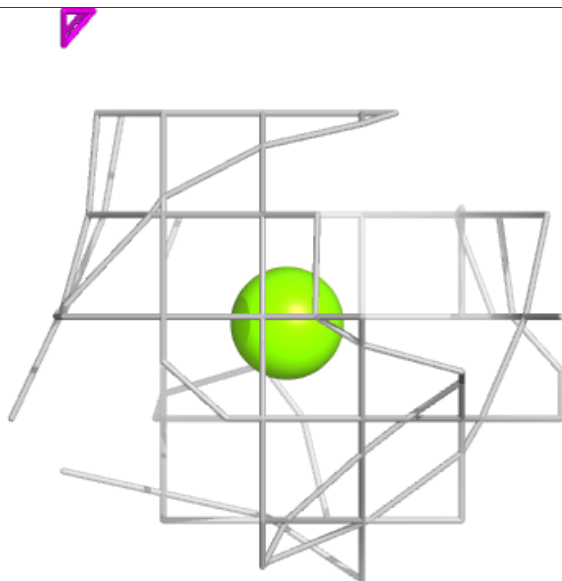
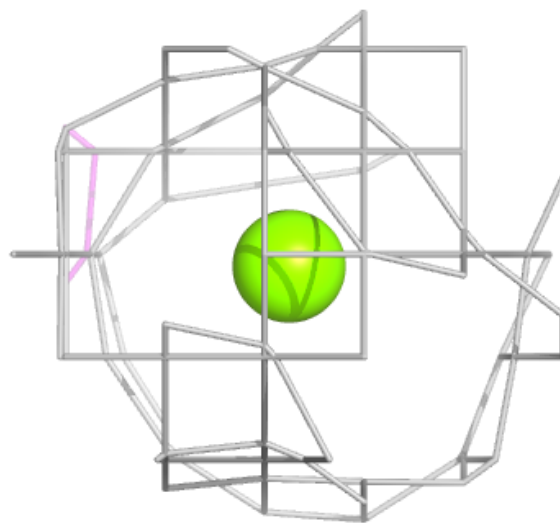
Electron density around MG B 301:

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



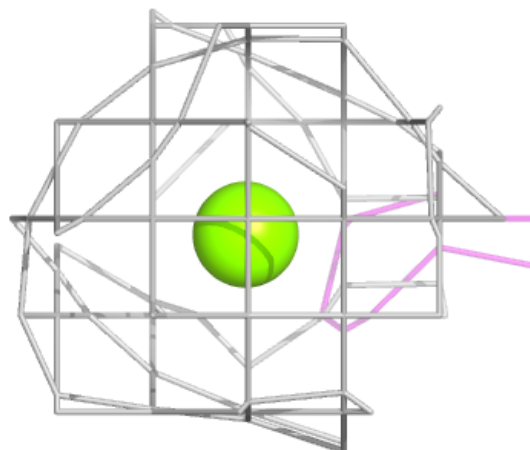
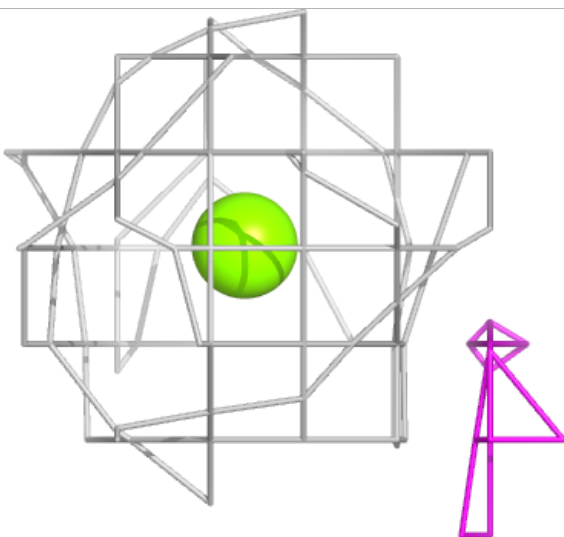
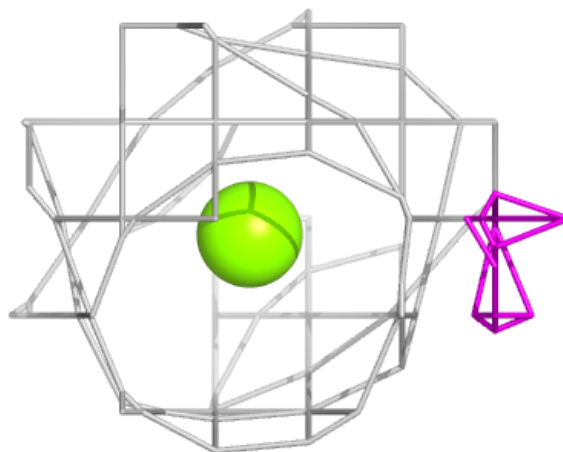
Electron density around MG D 302:

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



Electron density around MG 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.