Full wwPDB X-ray Structure Validation Report ⓘ

Nov 20, 2023 – 06:03 PM JST

PDB ID	:	7DKW
Title	:	Crystal structure of TxGH116 E441G nucleophile mutant from Thermoanaerobacterium xylanolyticum with autocondensation products from alpha-fluoro glucoside.
Authors	:	Pengthaisong, S.; Ketudat Cairns, J.R.
Deposited on	:	2020-11-25
Resolution	:	1.78 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:

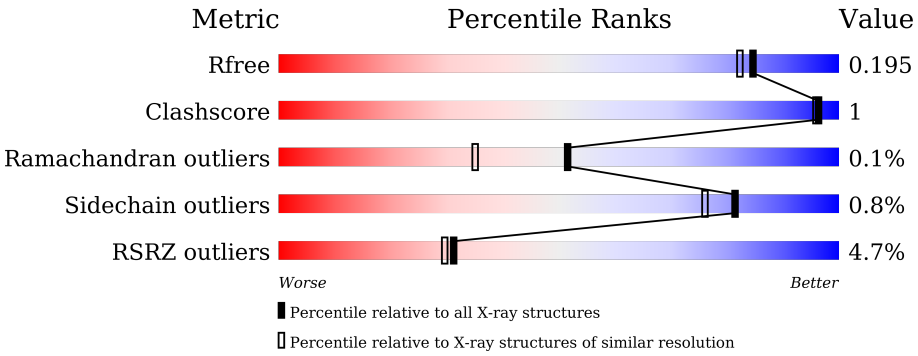
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.78 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	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

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 <=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	799	6% 93%
1	B	799	4% 93%
2	D	4	50% 50%
3	E	3	100%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 13976 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 beta-glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	771	Total	C	N	O	S	0	8	0
			6304	4068	1019	1190	27			
1	B	769	Total	C	N	O	S	0	6	0
			6269	4045	1014	1183	27			

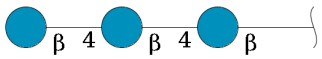
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	ALA	-	expression tag	UNP F6BL85
A	17	MET	-	expression tag	UNP F6BL85
A	18	ALA	-	expression tag	UNP F6BL85
A	441	GLY	GLU	engineered mutation	UNP F6BL85
A	807	LEU	-	expression tag	UNP F6BL85
A	808	GLU	-	expression tag	UNP F6BL85
A	809	HIS	-	expression tag	UNP F6BL85
A	810	HIS	-	expression tag	UNP F6BL85
A	811	HIS	-	expression tag	UNP F6BL85
A	812	HIS	-	expression tag	UNP F6BL85
A	813	HIS	-	expression tag	UNP F6BL85
A	814	HIS	-	expression tag	UNP F6BL85
B	16	ALA	-	expression tag	UNP F6BL85
B	17	MET	-	expression tag	UNP F6BL85
B	18	ALA	-	expression tag	UNP F6BL85
B	441	GLY	GLU	engineered mutation	UNP F6BL85
B	807	LEU	-	expression tag	UNP F6BL85
B	808	GLU	-	expression tag	UNP F6BL85
B	809	HIS	-	expression tag	UNP F6BL85
B	810	HIS	-	expression tag	UNP F6BL85
B	811	HIS	-	expression tag	UNP F6BL85
B	812	HIS	-	expression tag	UNP F6BL85
B	813	HIS	-	expression tag	UNP F6BL85
B	814	HIS	-	expression tag	UNP F6BL85

- Molecule 2 is an oligosaccharide called beta-D-glucopyranose-(1-4)-beta-D-glucopyranose-(1-4)-beta-D-glucopyranose-(1-4)-beta-D-glucopyranose.

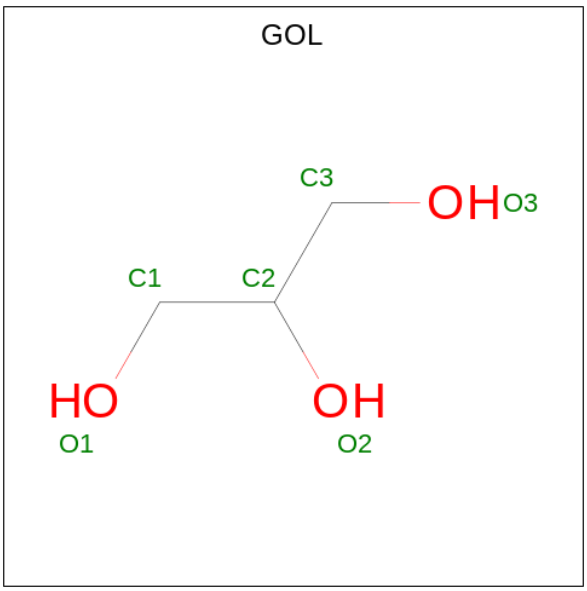
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	D	4	Total C O 45 24 21	0	0	0

- Molecule 3 is an oligosaccharide called beta-D-glucopyranose-(1-4)-beta-D-glucopyranose-(1-4)-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	E	3	Total C O 34 18 16	0	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$) (labeled as "Ligand of Interest" by depositor).



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

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

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Ca 1 1	0	0
5	B	1	Total Ca 1 1	0	0

- Molecule 6 is water.

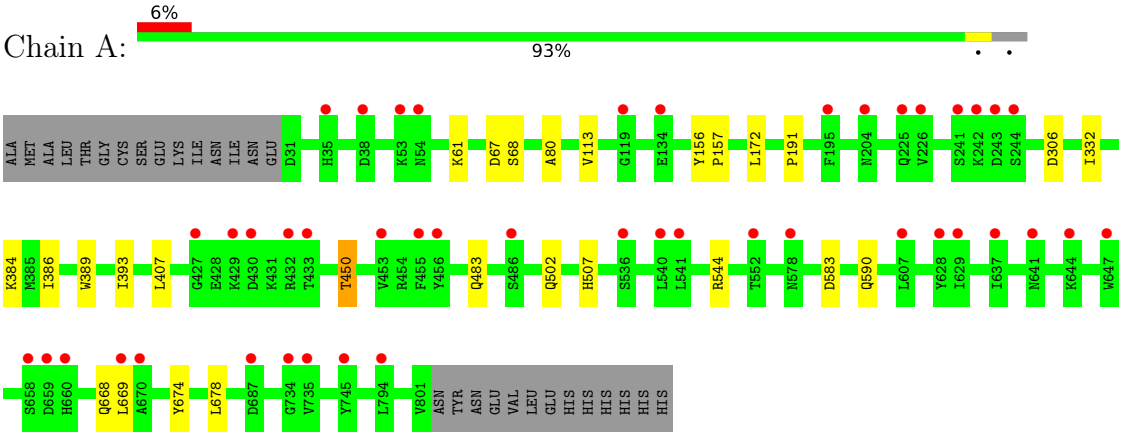
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	593	Total O 593 593	0	0
6	B	687	Total O 687 687	0	0

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.

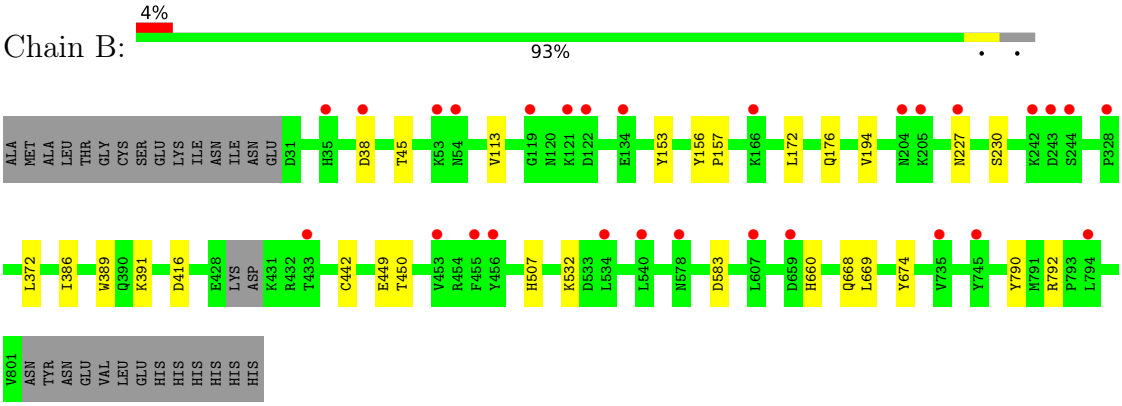
• Molecule 1: beta-glucosidase

Chain A:



• Molecule 1: beta-glucosidase

Chain B:



• Molecule 2: beta-D-glucopyranose-(1-4)-beta-D-glucopyranose-(1-4)-beta-D-glucopyranose-(1-4)-beta-D-glucopyranose

Chain D:

• Molecule 3: beta-D-glucopyranose-(1-4)-beta-D-glucopyranose-(1-4)-beta-D-glucopyranose

Chain E:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	179.21Å 54.60Å 164.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.00 – 1.78 34.64 – 1.78	Depositor EDS
% Data completeness (in resolution range)	97.8 (35.00-1.78) 97.8 (34.64-1.78)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.63 (at 1.78Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.158 , 0.188 0.168 , 0.195	Depositor DCC
R_{free} test set	7479 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å^2)	18.8	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 48.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	13976	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.90% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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, CA, BGC

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	0.50	0/6487	0.68	0/8789
1	B	0.52	0/6449	0.69	1/8734 (0.0%)
All	All	0.51	0/12936	0.68	1/17523 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	792	ARG	NE-CZ-NH1	5.93	123.27	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6304	0	6035	11	0
1	B	6269	0	6011	12	0
2	D	45	0	39	0	0
3	E	34	0	30	0	0
4	A	18	0	24	1	0
4	B	24	0	32	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	593	0	0	1	0
6	B	687	0	0	0	0
All	All	13976	0	12171	24	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 (24) 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:660[B]:HIS:H	1:B:660[B]:HIS:CD2	2.23	0.56
1:B:450:THR:HG23	1:B:507:HIS:CE1	2.43	0.53
1:A:386:ILE:HA	1:A:389[A]:TRP:CD1	2.46	0.51
1:B:45[A]:THR:HG22	1:B:153:TYR:CD2	2.48	0.49
1:A:393:ILE:HD13	1:A:407:LEU:CD2	2.44	0.48
1:A:668:GLN:HG3	1:A:669:LEU:HG	1.94	0.47
1:B:668:GLN:HG3	1:B:669:LEU:HG	1.97	0.47
1:A:67:ASP:O	1:A:68[A]:SER:CB	2.63	0.47
1:B:227:ASN:HB3	1:B:230:SER:HB2	1.97	0.46
1:A:450:THR:HG23	1:A:507:HIS:CE1	2.49	0.46
1:B:532:LYS:HE2	1:B:583:ASP:O	2.15	0.46
1:B:156:TYR:CD1	1:B:157:PRO:HA	2.50	0.46
1:B:176:GLN:HA	1:B:194:VAL:O	2.16	0.45
1:A:113:VAL:HG21	1:A:172:LEU:HD11	2.00	0.44
1:B:386:ILE:HA	1:B:389:TRP:CD1	2.53	0.43
1:A:483:GLN:HG2	1:A:502:GLN:HB2	2.01	0.42
1:B:442:CYS:HB3	1:B:790:TYR:CD1	2.55	0.42
1:A:156:TYR:CD1	1:A:157:PRO:HA	2.55	0.41
1:B:113:VAL:HG21	1:B:172:LEU:HD11	2.02	0.41
1:B:449:GLU:O	1:B:450:THR:C	2.58	0.41
1:A:544:ARG:HB2	1:A:678:LEU:HD11	2.03	0.40
4:A:1001:GOL:H12	6:A:1323:HOH:O	2.20	0.40
1:A:80:ALA:HB1	1:A:191:PRO:HB3	2.02	0.40
1:A:384[A]:LYS:HZ2	1:A:384[A]:LYS:HG2	1.78	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	777/799 (97%)	751 (97%)	25 (3%)	1 (0%)	51 35
1	B	771/799 (96%)	736 (96%)	35 (4%)	0	100 100
All	All	1548/1598 (97%)	1487 (96%)	60 (4%)	1 (0%)	51 35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	450	THR

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	663/684 (97%)	657 (99%)	6 (1%)	78 72
1	B	660/684 (96%)	655 (99%)	5 (1%)	81 76
All	All	1323/1368 (97%)	1312 (99%)	11 (1%)	81 76

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

Mol	Chain	Res	Type
1	A	61	LYS
1	A	306	ASP
1	A	332	ILE
1	A	583	ASP
1	A	590	GLN

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Mol	Chain	Res	Type
1	A	674	TYR
1	B	38	ASP
1	B	372	LEU
1	B	391	LYS
1	B	416	ASP
1	B	674	TYR

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)

7 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	BGC	D	1	2	12,12,12	0.50	0	17,17,17	1.02	0
2	BGC	D	2	2	11,11,12	0.40	0	15,15,17	1.04	2 (13%)
2	BGC	D	3	2	11,11,12	0.54	0	15,15,17	0.98	1 (6%)
2	BGC	D	4	2	11,11,12	0.38	0	15,15,17	0.57	0
3	BGC	E	1	3	12,12,12	0.42	0	17,17,17	0.51	0
3	BGC	E	2	3	11,11,12	0.48	0	15,15,17	0.68	0
3	BGC	E	3	3	11,11,12	0.48	0	15,15,17	0.62	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	BGC	D	1	2	-	0/2/22/22	0/1/1/1
2	BGC	D	2	2	-	0/2/19/22	0/1/1/1
2	BGC	D	3	2	-	0/2/19/22	0/1/1/1
2	BGC	D	4	2	-	0/2/19/22	0/1/1/1
3	BGC	E	1	3	-	2/2/22/22	0/1/1/1
3	BGC	E	2	3	-	0/2/19/22	0/1/1/1
3	BGC	E	3	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	3	BGC	O5-C5-C6	3.09	112.04	107.20
2	D	2	BGC	O5-C5-C6	2.24	110.72	107.20
2	D	2	BGC	O3-C3-C2	-2.19	105.81	109.99

There are no chirality outliers.

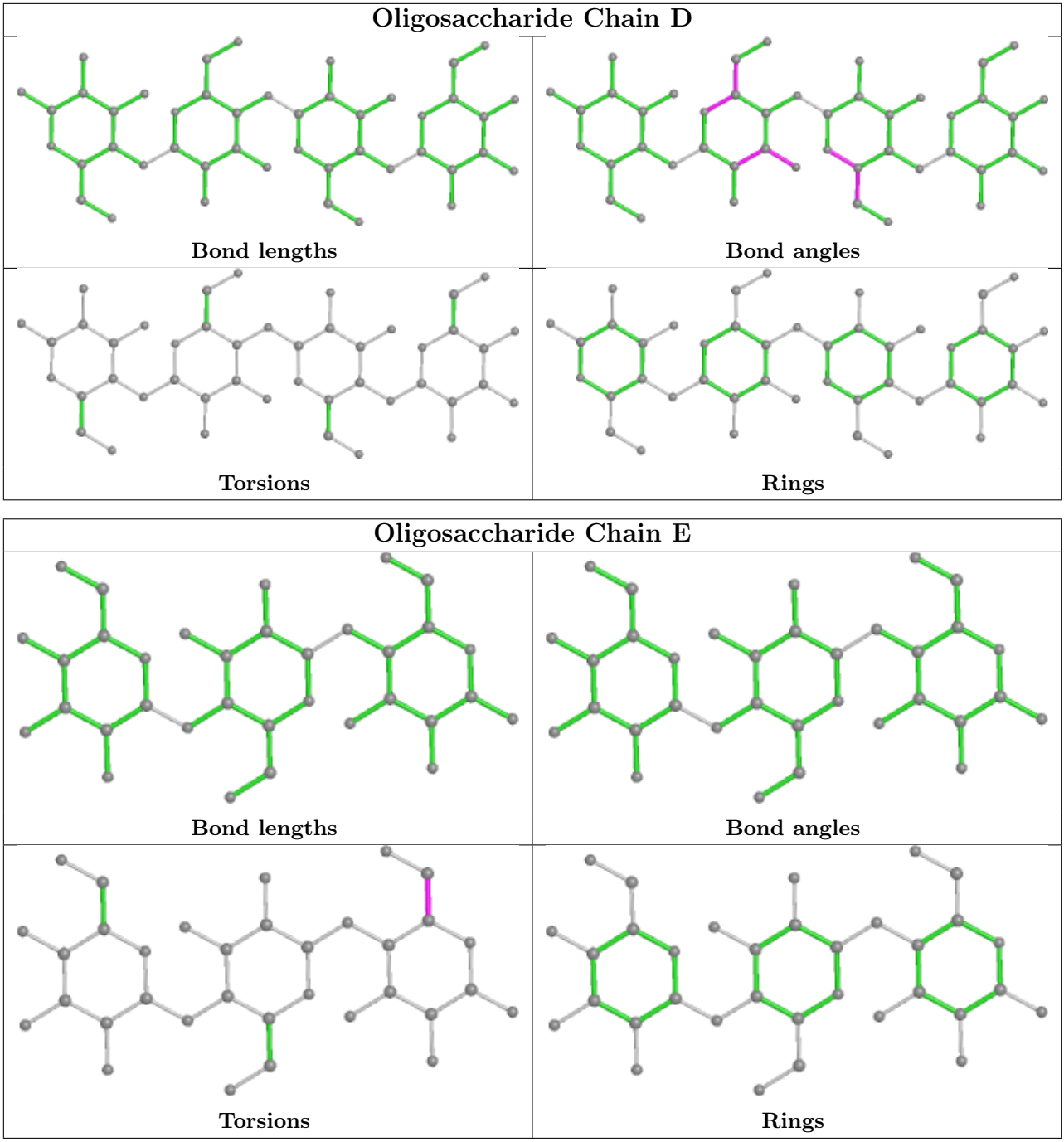
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	1	BGC	O5-C5-C6-O6
3	E	1	BGC	C4-C5-C6-O6

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 oligosaccharide.



5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 2 are monoatomic - leaving 7 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	$\#\|Z\|>2$
4	GOL	B	903	-	5,5,5	0.12	0	5,5,5	0.46	0
4	GOL	B	904	-	5,5,5	0.31	0	5,5,5	0.43	0
4	GOL	B	901	-	5,5,5	0.37	0	5,5,5	0.94	0
4	GOL	A	1001	-	5,5,5	0.29	0	5,5,5	0.83	0
4	GOL	B	902	-	5,5,5	0.49	0	5,5,5	0.60	0
4	GOL	A	1003	-	5,5,5	0.31	0	5,5,5	0.47	0
4	GOL	A	1002	-	5,5,5	0.54	0	5,5,5	0.50	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
4	GOL	B	903	-	-	0/4/4/4	-
4	GOL	B	904	-	-	2/4/4/4	-
4	GOL	B	901	-	-	2/4/4/4	-
4	GOL	A	1001	-	-	2/4/4/4	-
4	GOL	B	902	-	-	0/4/4/4	-
4	GOL	A	1003	-	-	2/4/4/4	-
4	GOL	A	1002	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

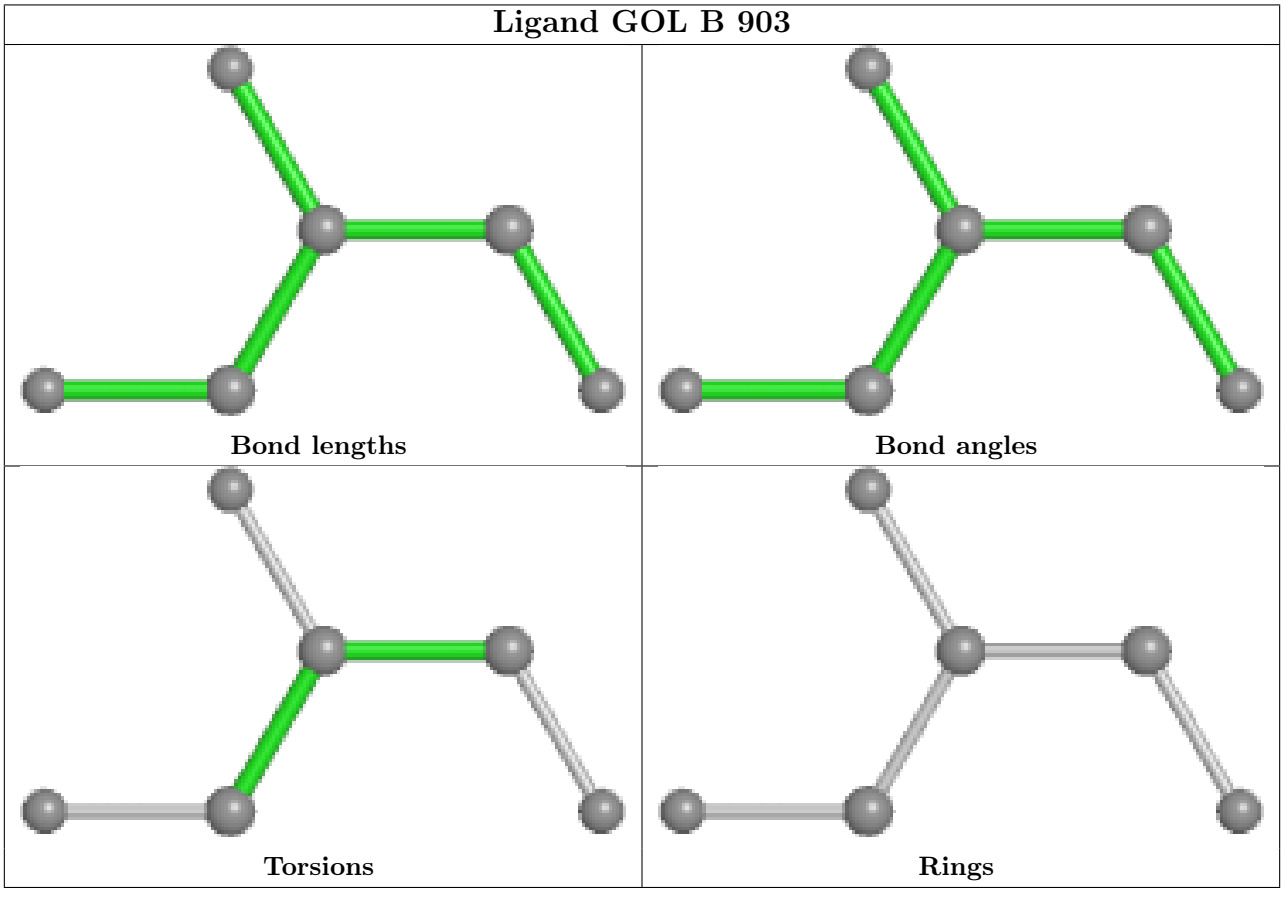
Mol	Chain	Res	Type	Atoms
4	A	1001	GOL	C1-C2-C3-O3
4	A	1001	GOL	O2-C2-C3-O3
4	A	1003	GOL	C1-C2-C3-O3
4	B	901	GOL	O1-C1-C2-C3
4	A	1003	GOL	O2-C2-C3-O3
4	B	904	GOL	O1-C1-C2-C3
4	B	901	GOL	O1-C1-C2-O2
4	B	904	GOL	O1-C1-C2-O2

There are no ring outliers.

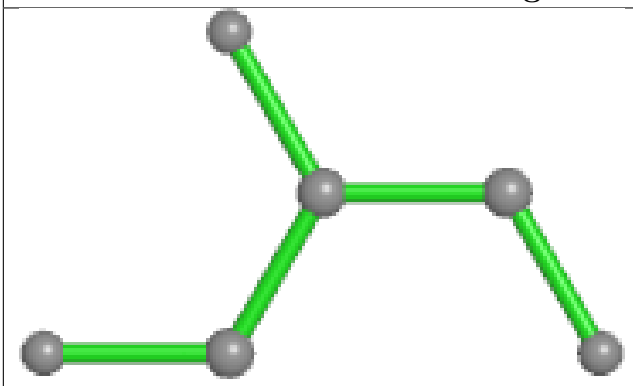
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1001	GOL	1	0

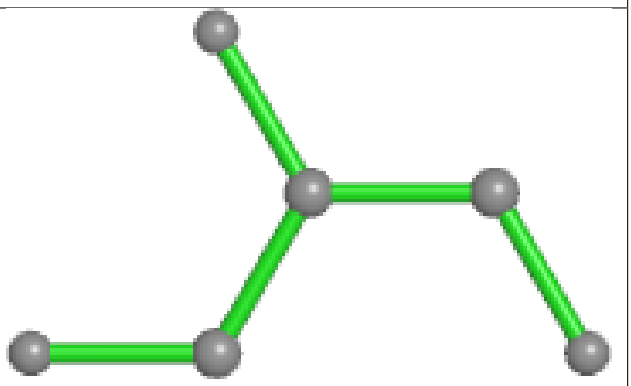
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.



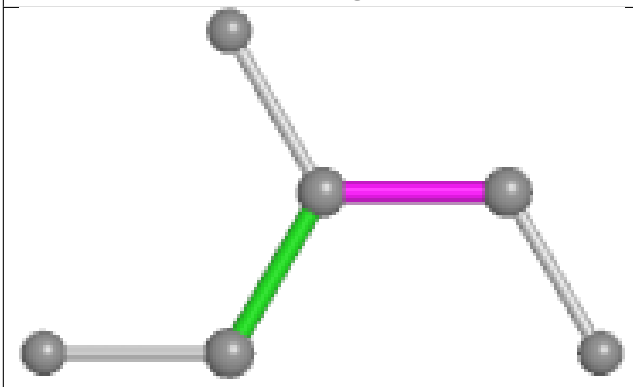
Ligand GOL B 904



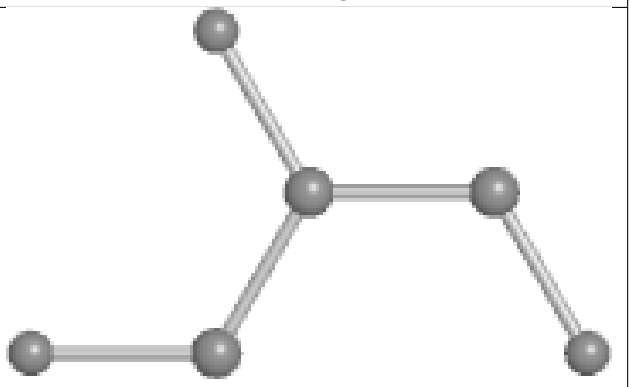
Bond lengths



Bond angles

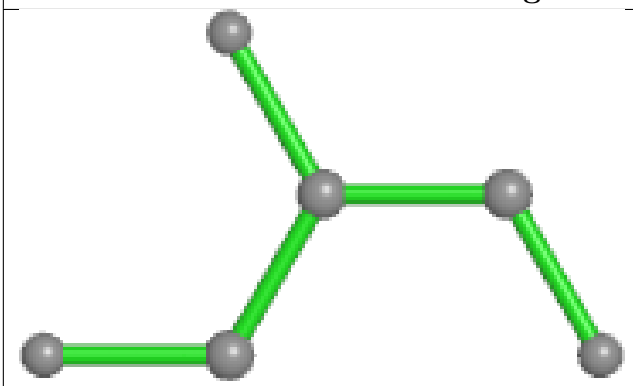


Torsions

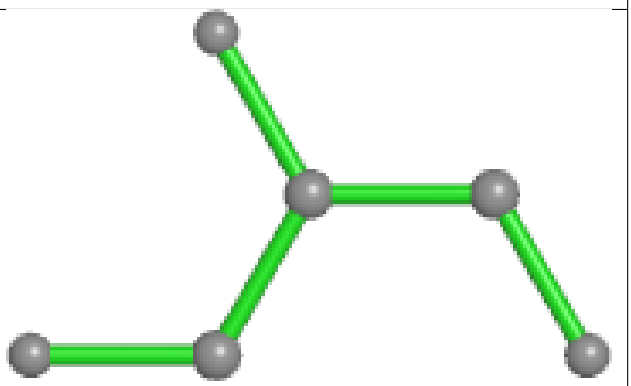


Rings

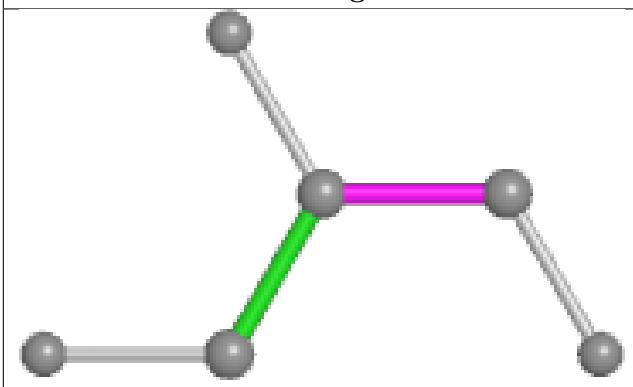
Ligand GOL B 901



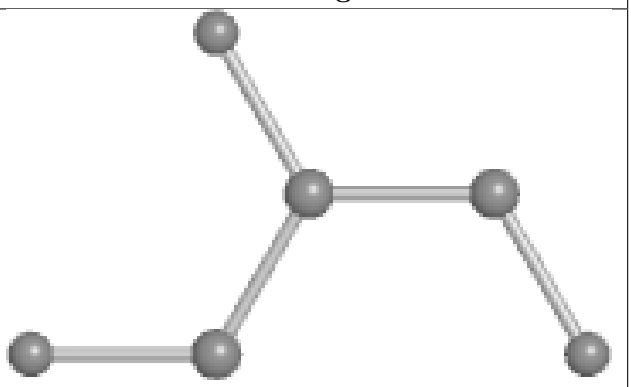
Bond lengths



Bond angles

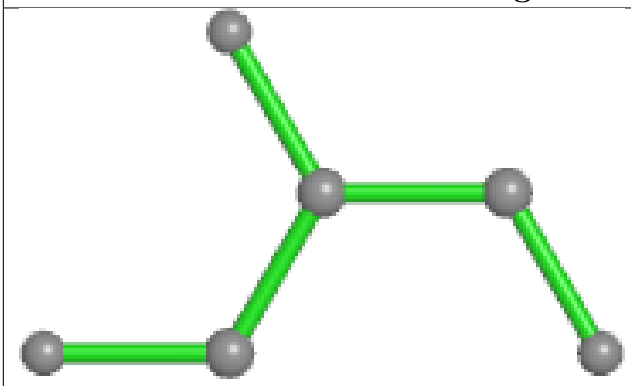


Torsions

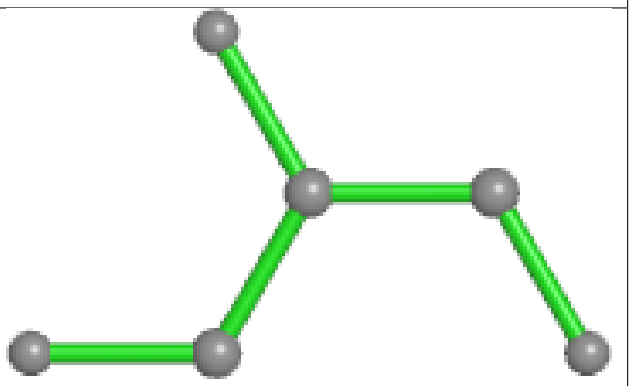


Rings

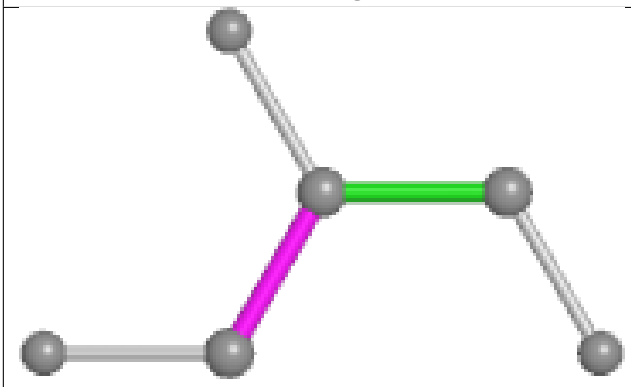
Ligand GOL A 1001



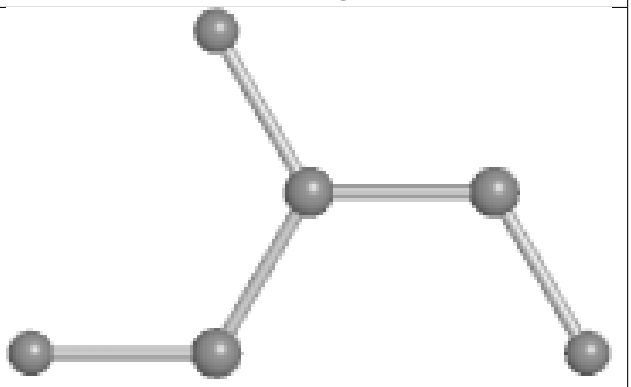
Bond lengths



Bond angles

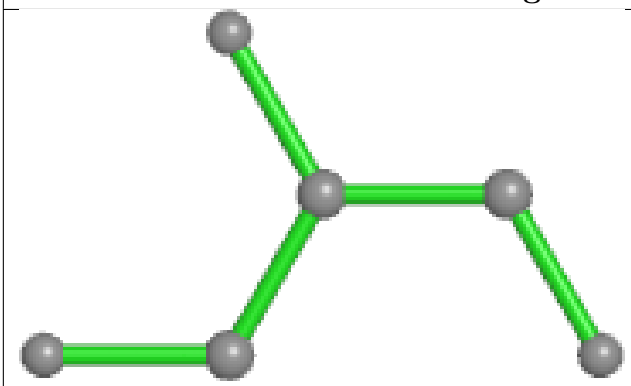


Torsions

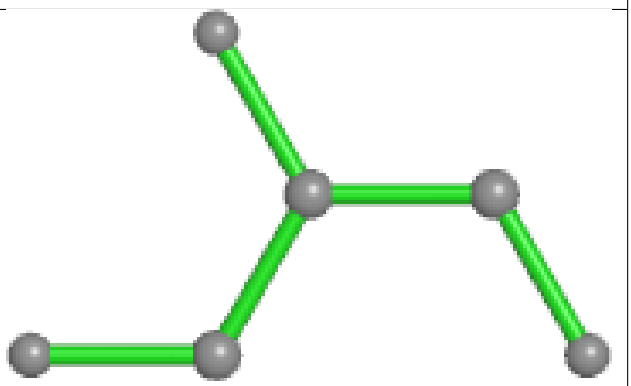


Rings

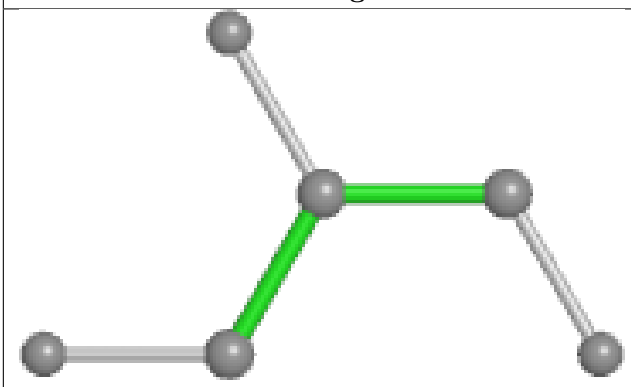
Ligand GOL B 902



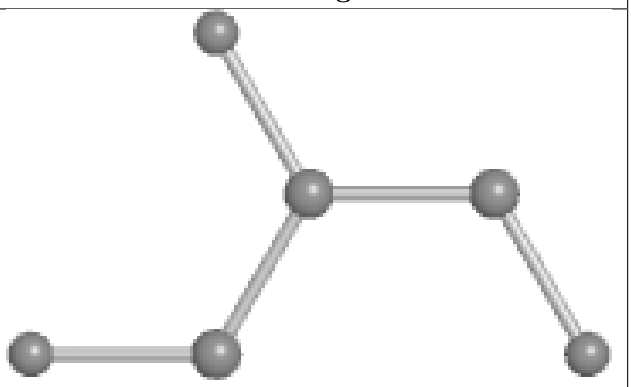
Bond lengths



Bond angles

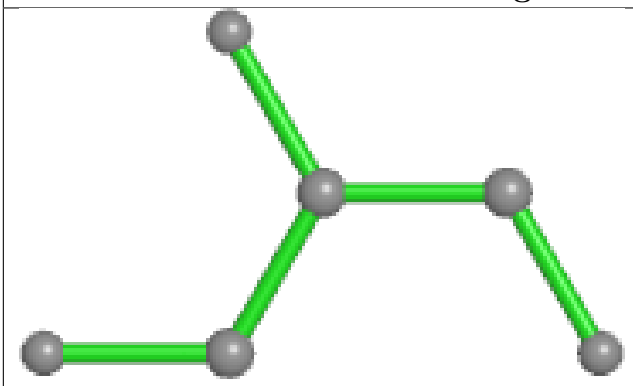


Torsions

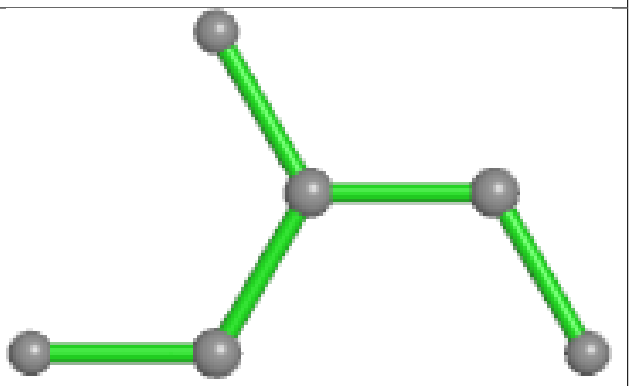


Rings

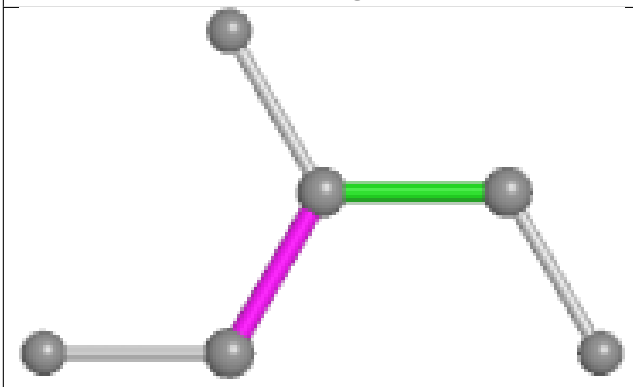
Ligand GOL A 1003



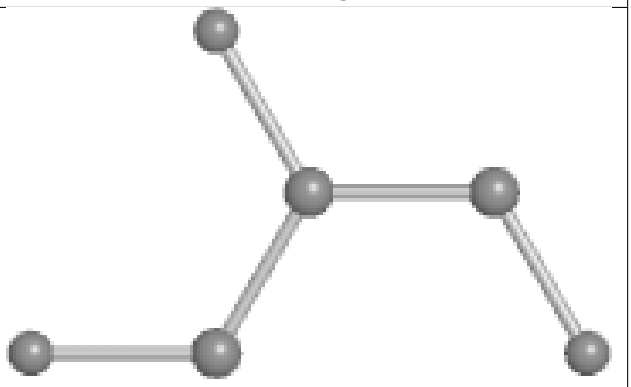
Bond lengths



Bond angles

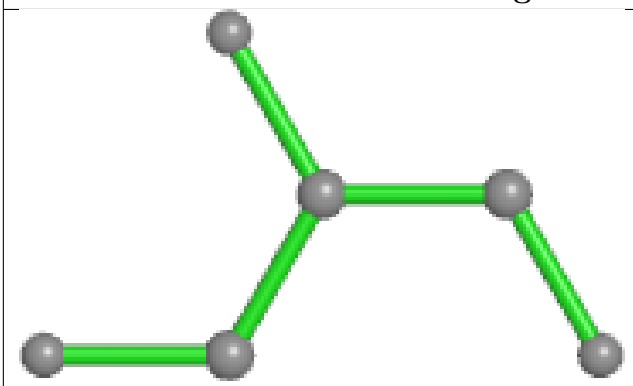


Torsions

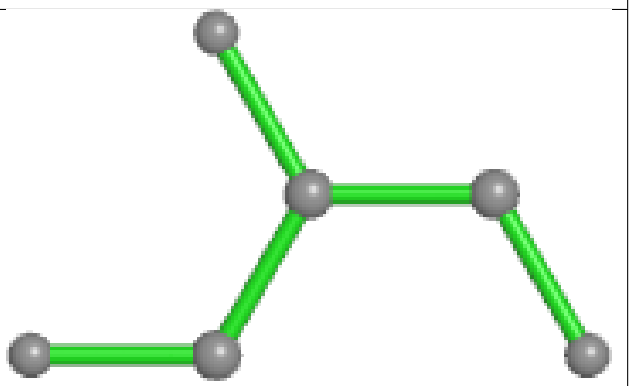


Rings

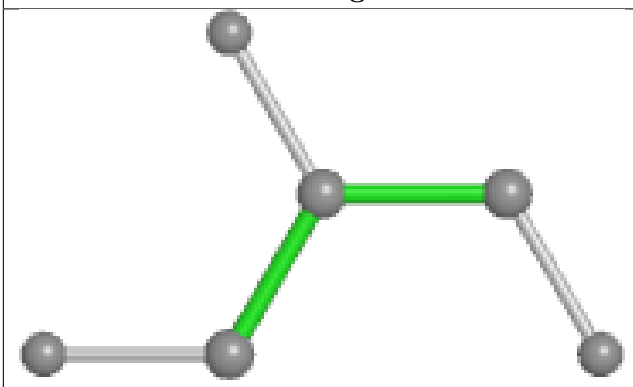
Ligand GOL A 1002



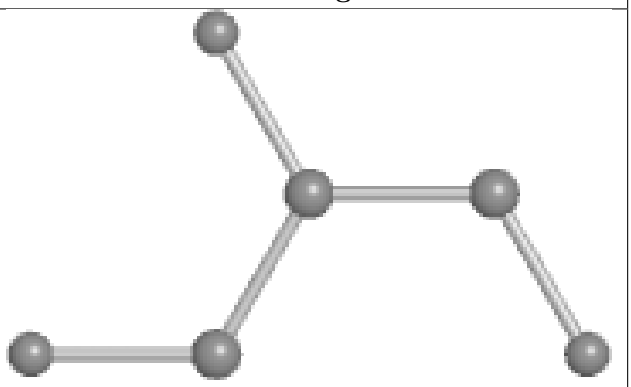
Bond lengths



Bond angles



Torsions



Rings

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^{th} 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	771/799 (96%)	0.22	45 (5%)	23	22	10, 20, 41, 64	0
1	B	769/799 (96%)	0.07	28 (3%)	42	41	10, 18, 36, 58	0
All	All	1540/1598 (96%)	0.14	73 (4%)	31	29	10, 19, 40, 64	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	433	THR	4.5
1	A	225	GLN	4.2
1	B	35	HIS	4.0
1	B	244	SER	3.9
1	B	54	ASN	3.9
1	A	119	GLY	3.9
1	B	119	GLY	3.8
1	A	226	VAL	3.8
1	B	121	LYS	3.7
1	A	453	VAL	3.6
1	B	242	LYS	3.6
1	A	427	GLY	3.5
1	B	455	PHE	3.3
1	A	433	THR	3.3
1	B	243	ASP	3.3
1	A	745	TYR	3.2
1	B	735	VAL	3.2
1	A	456	TYR	3.2
1	A	54	ASN	3.2
1	B	134	GLU	3.1
1	A	204	ASN	3.1
1	A	243	ASP	2.9
1	A	735	VAL	2.9
1	B	794	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	607	LEU	2.9
1	A	628	TYR	2.9
1	A	647	TRP	2.8
1	B	204	ASN	2.8
1	B	53	LYS	2.8
1	A	644	LYS	2.8
1	A	134	GLU	2.8
1	A	660[A]	HIS	2.7
1	A	578	ASN	2.7
1	A	35	HIS	2.7
1	A	637	ILE	2.7
1	A	53	LYS	2.7
1	B	534	LEU	2.7
1	A	38	ASP	2.7
1	B	659	ASP	2.7
1	B	456	TYR	2.6
1	B	745	TYR	2.6
1	A	659	ASP	2.6
1	A	429	LYS	2.5
1	A	552	THR	2.5
1	A	687	ASP	2.5
1	B	38	ASP	2.5
1	B	453	VAL	2.5
1	A	794	LEU	2.5
1	B	205	LYS	2.5
1	B	607	LEU	2.4
1	B	166	LYS	2.4
1	A	455	PHE	2.4
1	A	670	ALA	2.4
1	B	578	ASN	2.4
1	A	430	ASP	2.3
1	A	641	ASN	2.3
1	A	244	SER	2.3
1	A	241	SER	2.3
1	A	242	LYS	2.2
1	A	540	LEU	2.2
1	A	432	ARG	2.2
1	A	541	LEU	2.2
1	A	669	LEU	2.2
1	B	328	PRO	2.1
1	A	658	SER	2.1
1	A	486	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	536	SER	2.1
1	A	734	GLY	2.0
1	A	629	ILE	2.0
1	B	227	ASN	2.0
1	A	195	PHE	2.0
1	B	540	LEU	2.0
1	B	122	ASP	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)

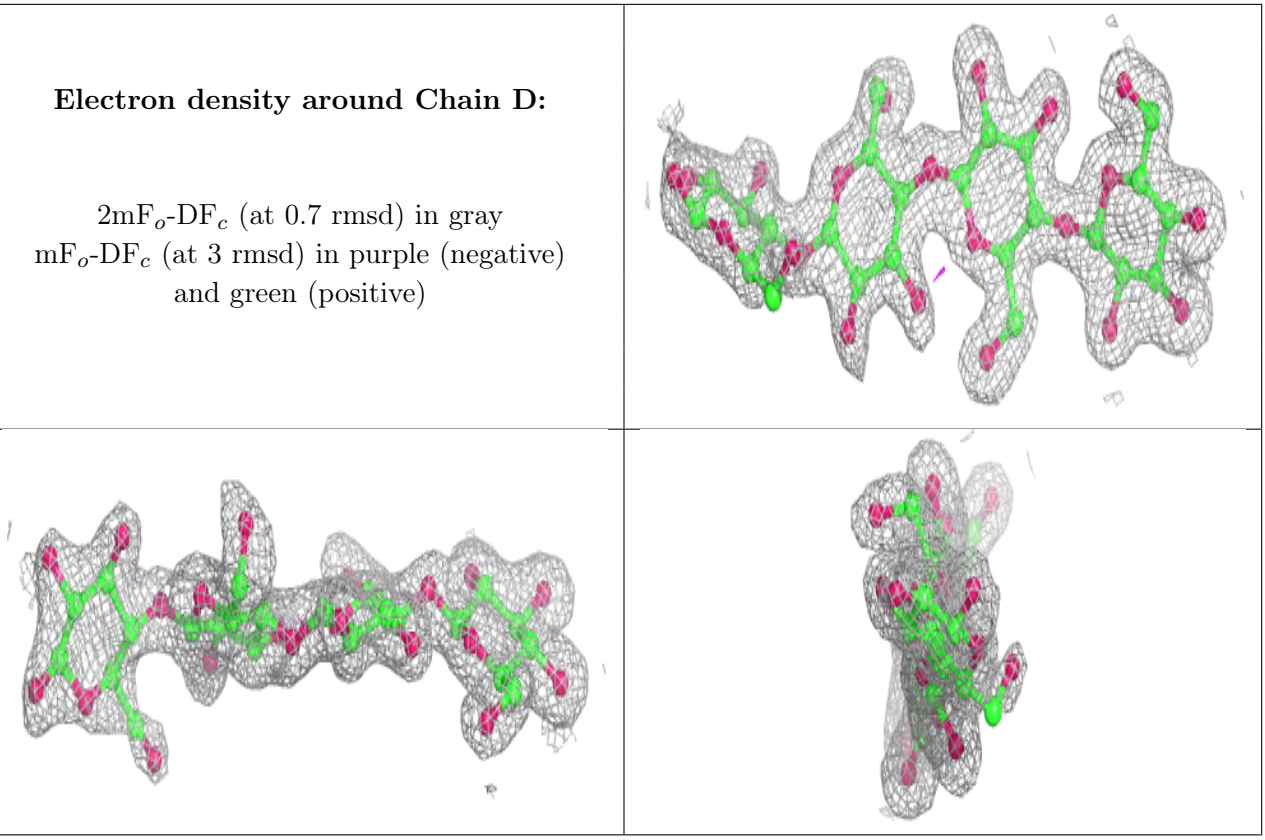
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	BGC	E	1	12/12	0.76	0.23	42,57,60,64	0
2	BGC	D	1	12/12	0.86	0.21	41,44,48,49	0
2	BGC	D	2	11/12	0.90	0.15	33,38,40,42	0
3	BGC	E	2	11/12	0.92	0.10	24,28,35,35	0
2	BGC	D	3	11/12	0.93	0.14	29,30,30,30	0
2	BGC	D	4	11/12	0.94	0.08	23,25,26,27	0
3	BGC	E	3	11/12	0.97	0.06	19,20,21,22	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

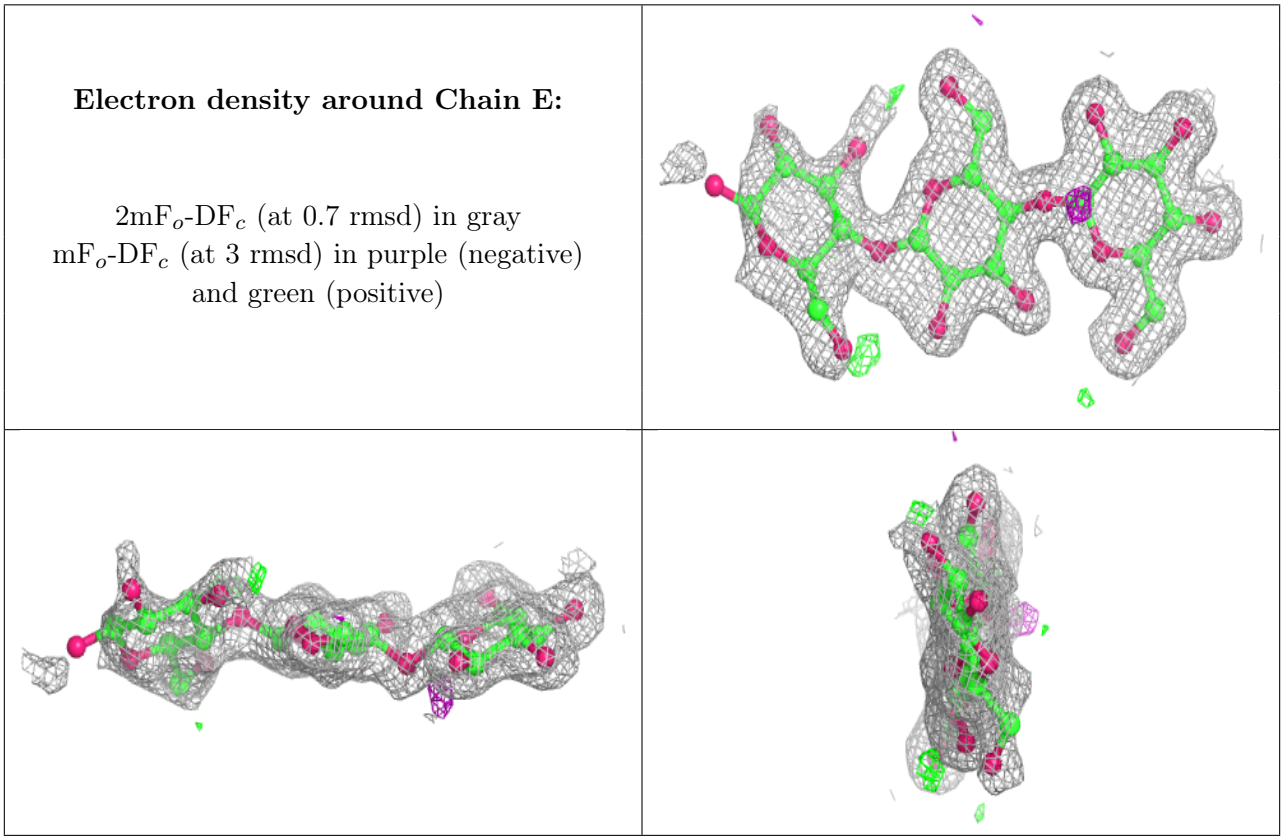
Electron density around Chain D:

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



Electron density around Chain E:

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



6.4 Ligands (i)

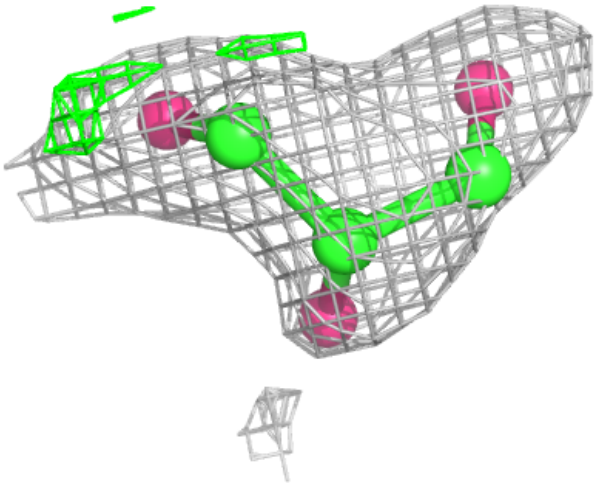
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

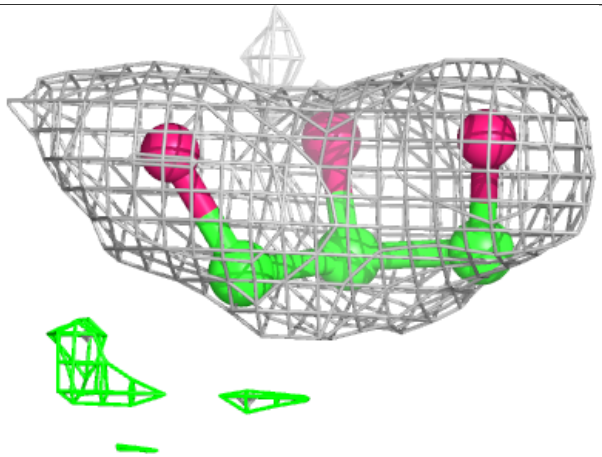
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	GOL	B	904	6/6	0.80	0.19	38,45,48,51	0
4	GOL	B	903	6/6	0.82	0.20	41,42,46,48	0
4	GOL	A	1003	6/6	0.83	0.25	43,46,50,56	0
4	GOL	A	1001	6/6	0.92	0.17	29,30,31,31	0
4	GOL	A	1002	6/6	0.93	0.13	22,25,26,28	0
4	GOL	B	902	6/6	0.94	0.13	21,23,24,24	0
4	GOL	B	901	6/6	0.95	0.17	23,25,26,26	0
5	CA	A	1004	1/1	0.95	0.08	36,36,36,36	0
5	CA	B	905	1/1	0.97	0.04	27,27,27,27	0

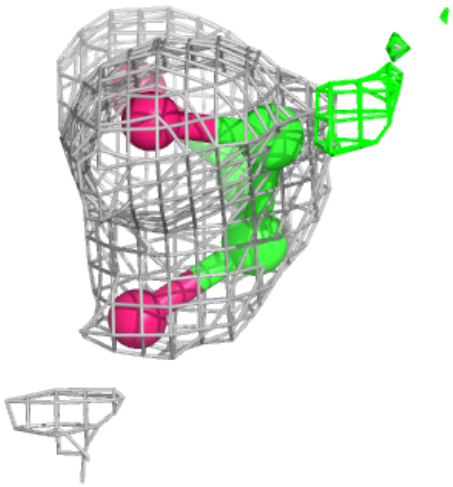
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around GOL B 904:

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

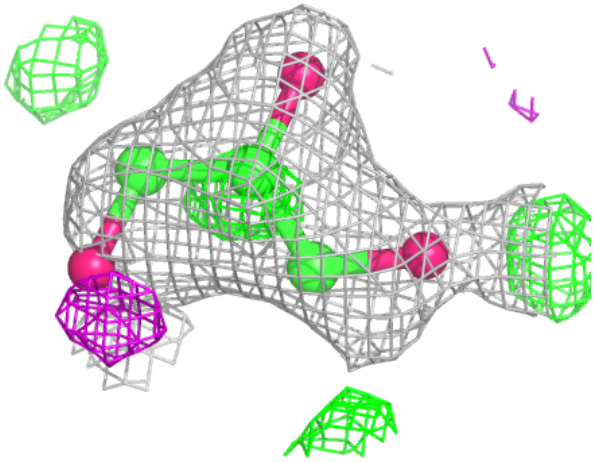


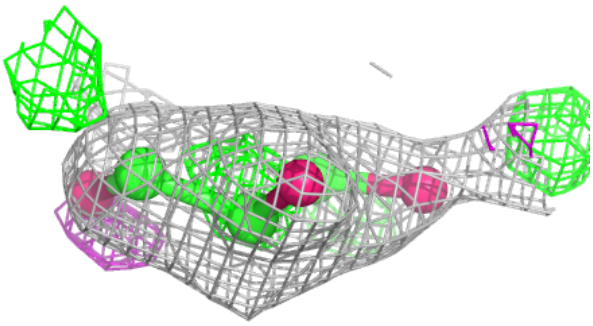


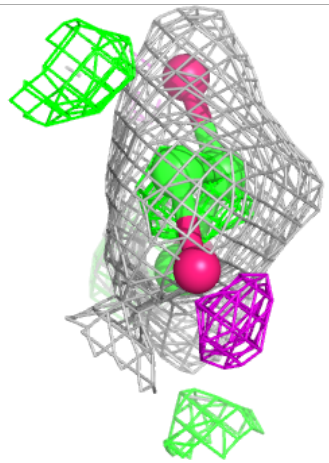


Electron density around GOL B 903:

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

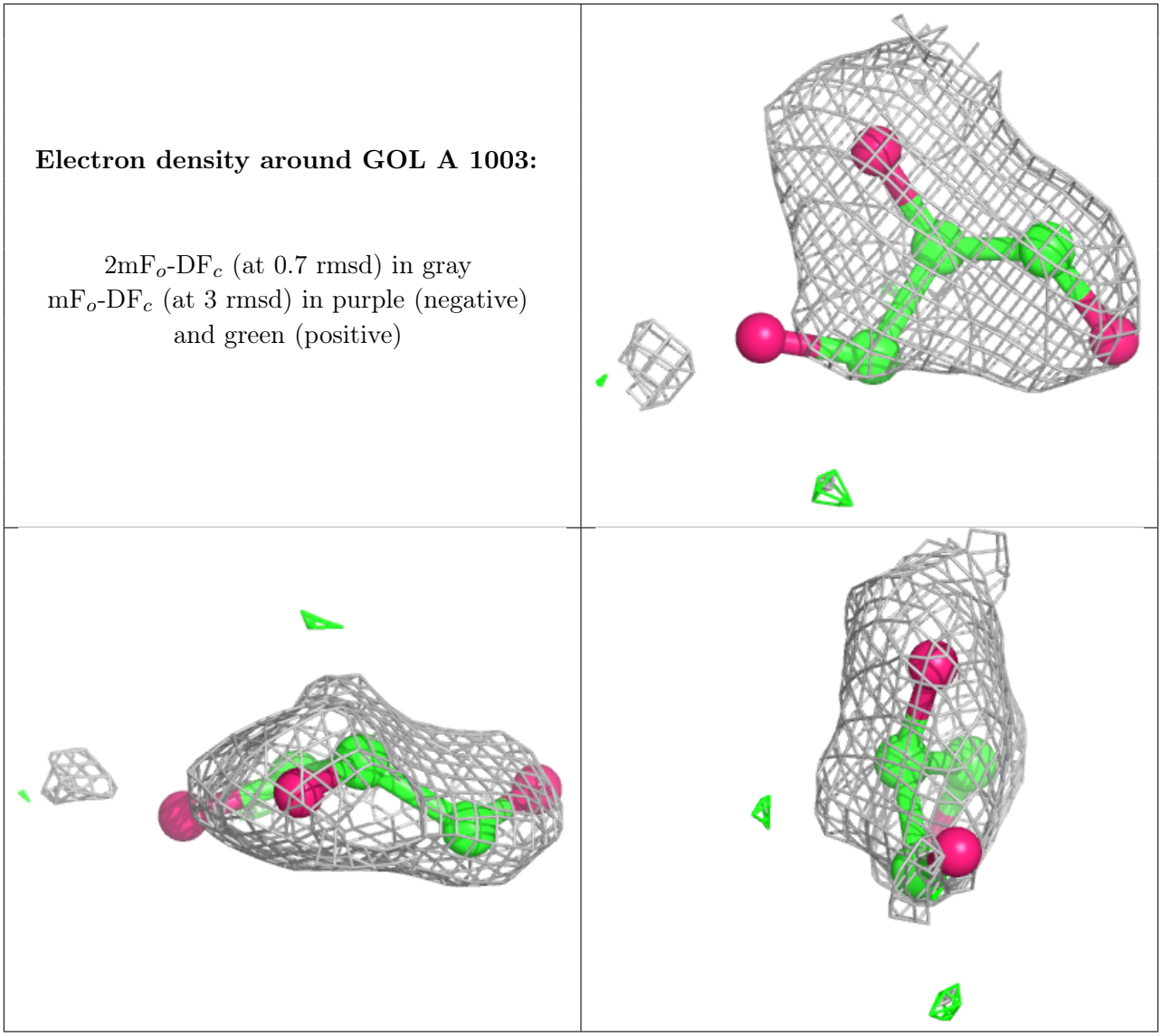






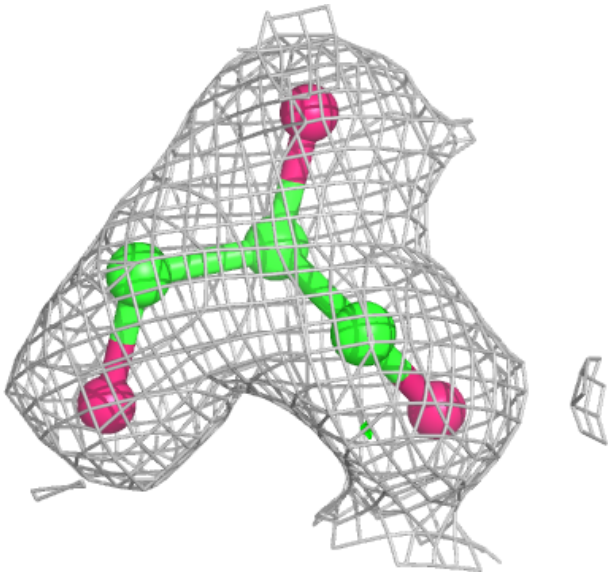
Electron density around GOL A 1003:

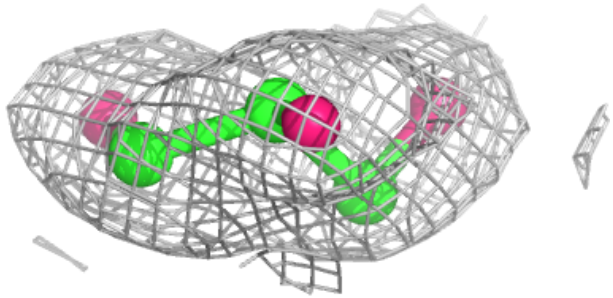
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

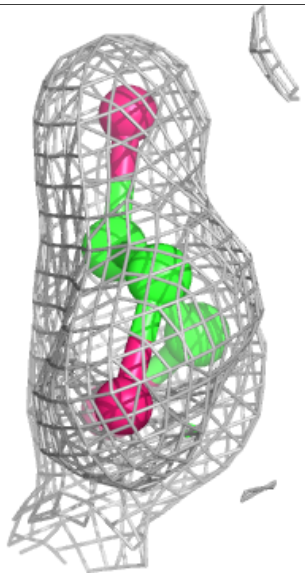


Electron density around GOL A 1001:

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

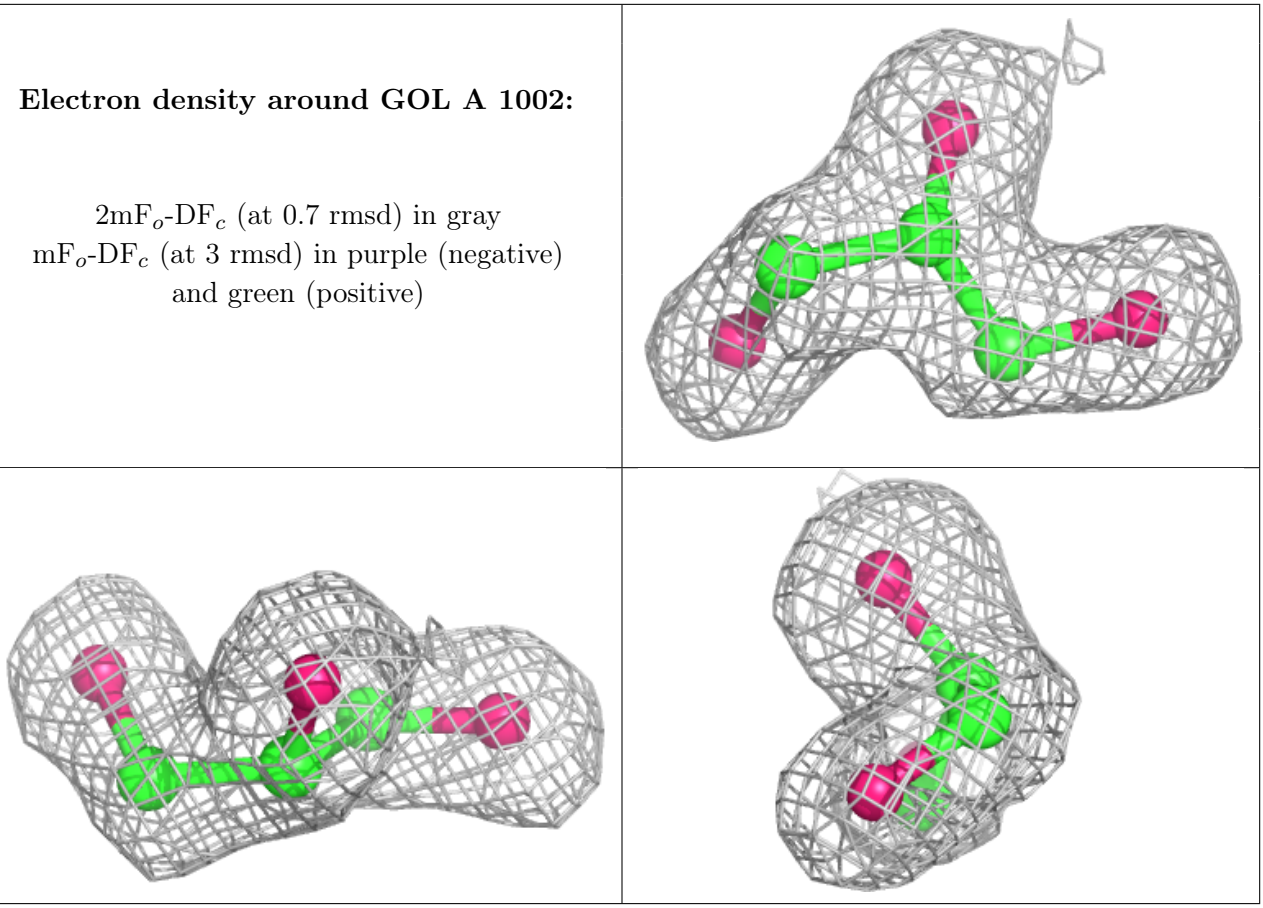






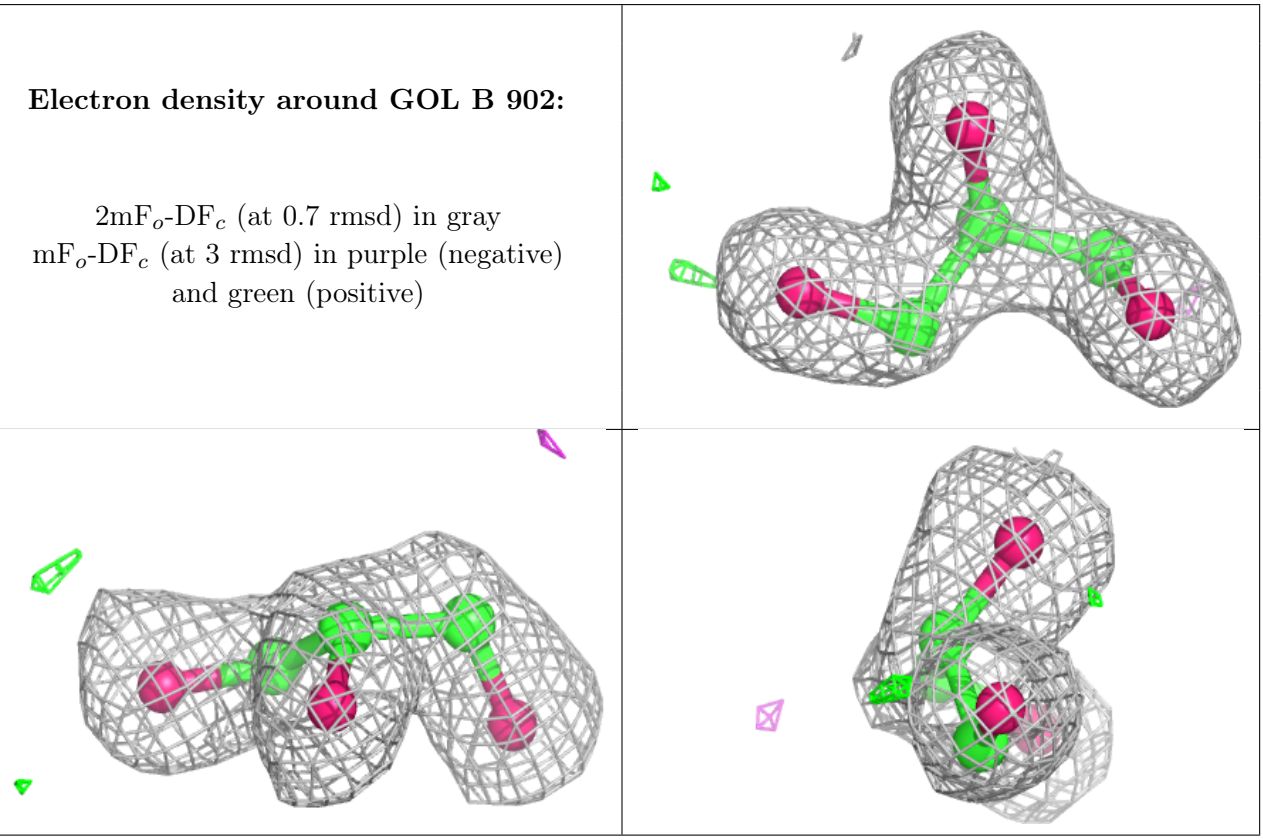
Electron density around GOL A 1002:

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



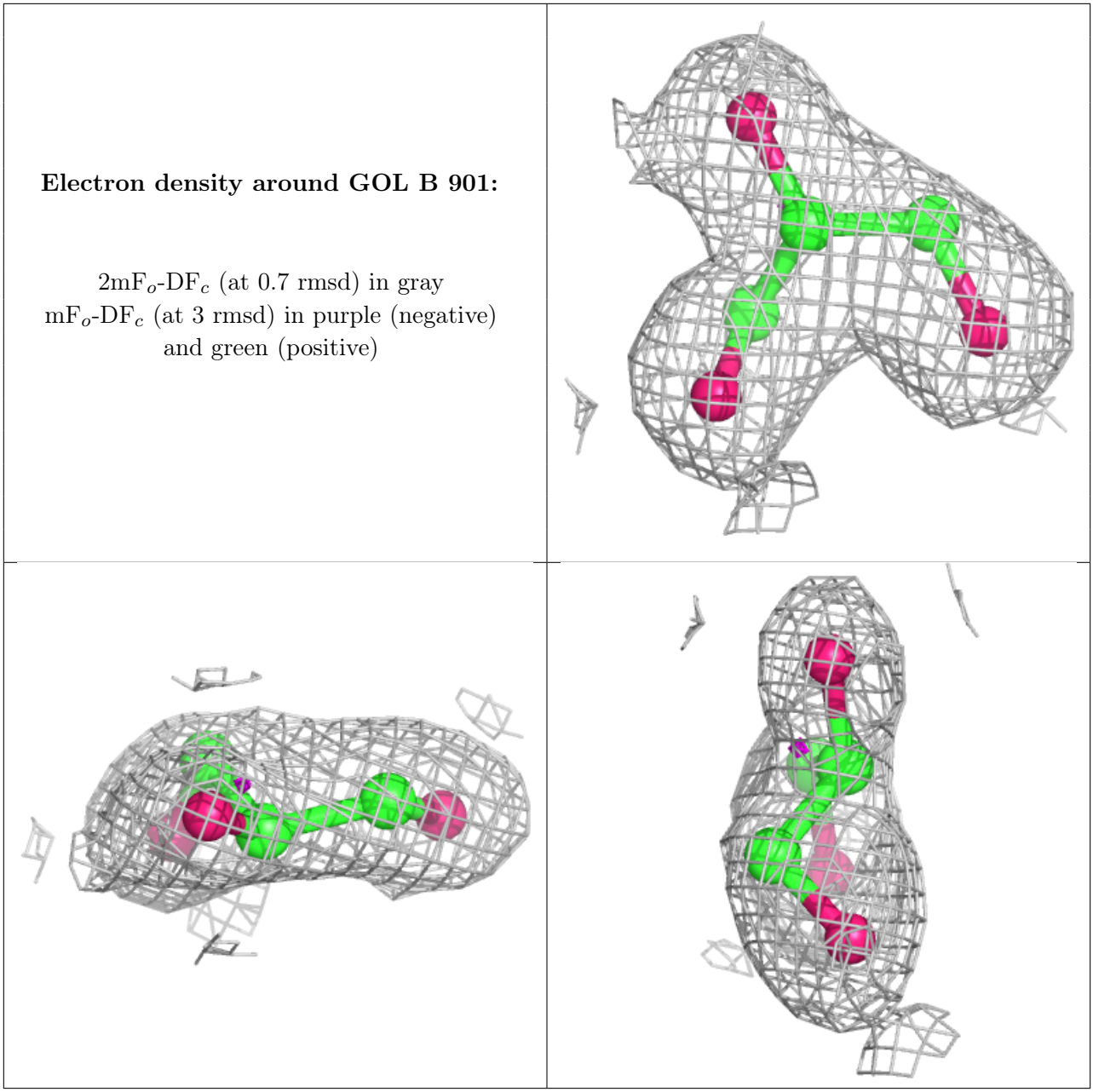
Electron density around GOL B 902:

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



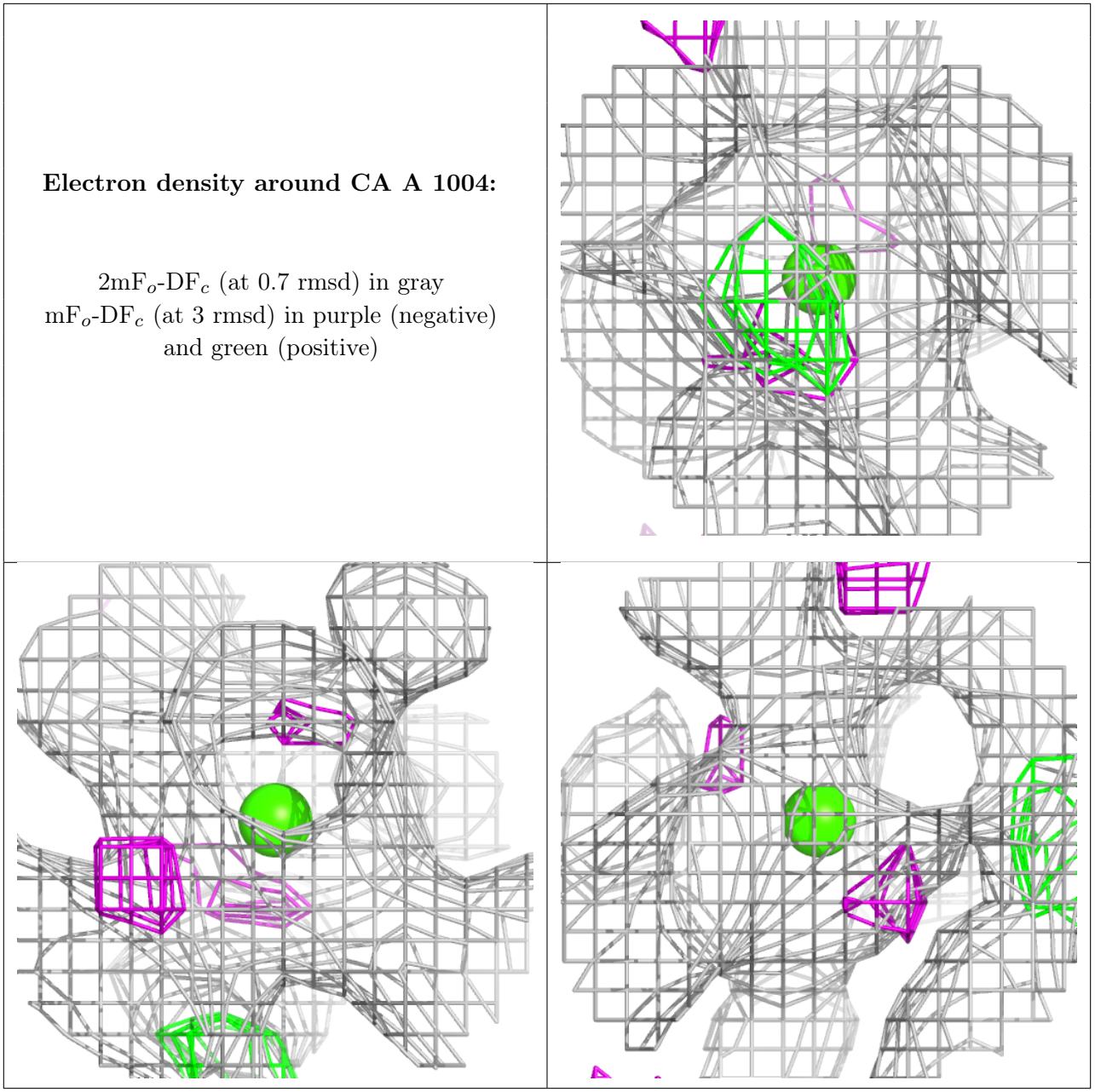
Electron density around GOL B 901:

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



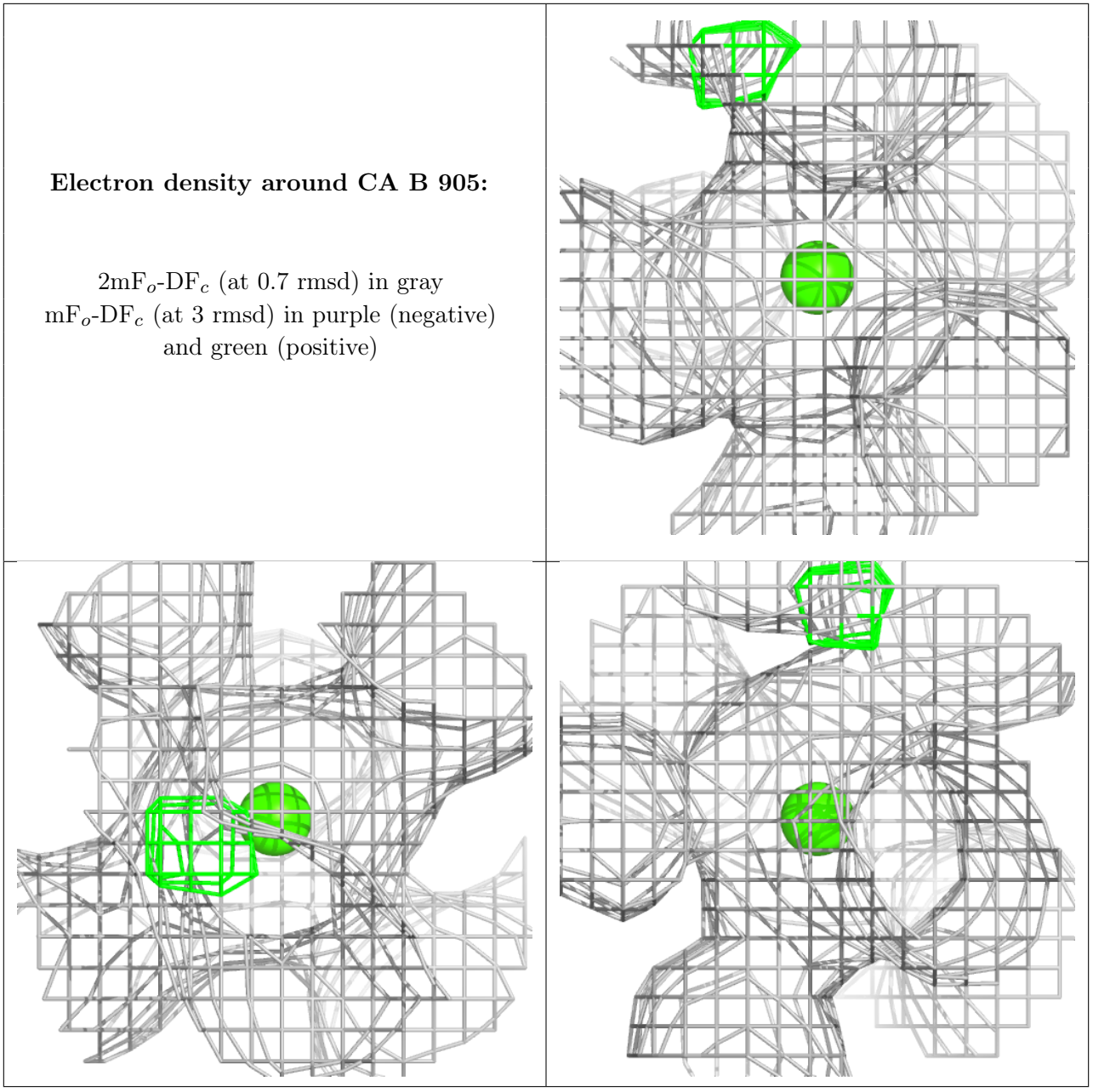
Electron density around CA A 1004:

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



Electron density around CA B 905:

$2mF_o$-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.