wwPDB X-ray Structure Validation Summary Report (i)

Mar 5, 2026 – 04:43 AM UTC

PDB ID	:	4AUE / pdb_00004aue
Title	:	Crystal structure, recombinant expression and mutagenesis studies of the bi-functional catalase-phenol oxidase from Scytalidium thermophilum
Authors	:	Yuzugullu, Y.; Trinh, C.H.; Smith, M.A.; Pearson, A.R.; Phillips, S.E.V.; Sutay Kocabas, D.; Bakir, U.; Ogel, Z.B.; McPherson, M.J.
Deposited on	:	2012-05-17
Resolution	:	2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (i)) were used in the production of this report:

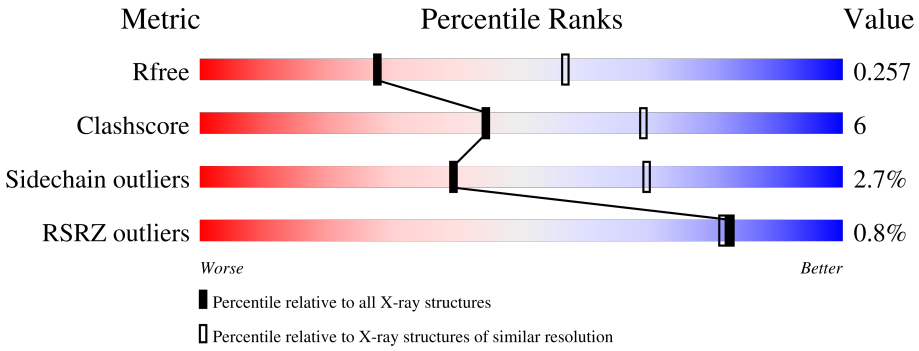
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	717	79% 13% • 7%
1	B	717	79% 14% • 6%
1	C	717	80% 13% • 7%
1	D	717	81% 12% • 7%
2	E	2	100%

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Mol	Chain	Length	Quality of chain
2	F	2	100%
2	G	2	100%
2	H	2	100%
2	I	2	100%
2	J	2	50% 50%
2	K	2	100%
2	L	2	100%
2	M	2	50% 50%
2	N	2	100%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 21804 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 CATALASE-PHENOL OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	669	Total	C	N	O	S	0	8	0
			5274	3328	928	1007	11			
1	B	671	Total	C	N	O	S	0	3	0
			5253	3312	921	1009	11			
1	C	670	Total	C	N	O	S	0	4	0
			5258	3316	925	1006	11			
1	D	669	Total	C	N	O	S	0	2	0
			5232	3300	918	1003	11			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	K	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	L	2	Total	C	N	O	0	0	0
			28	16	2	10			

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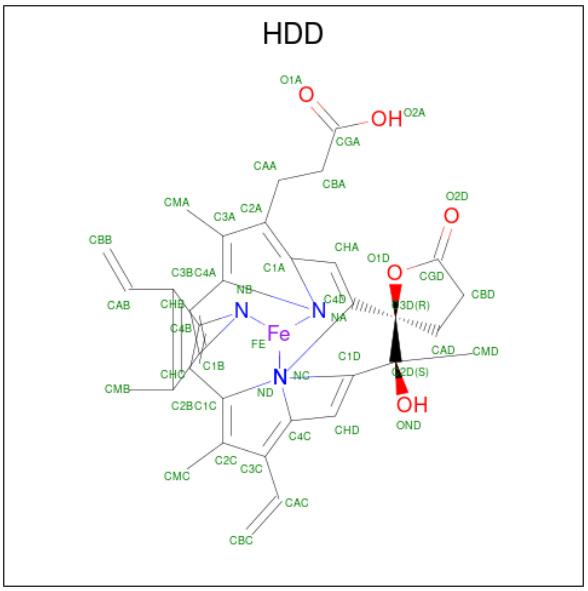
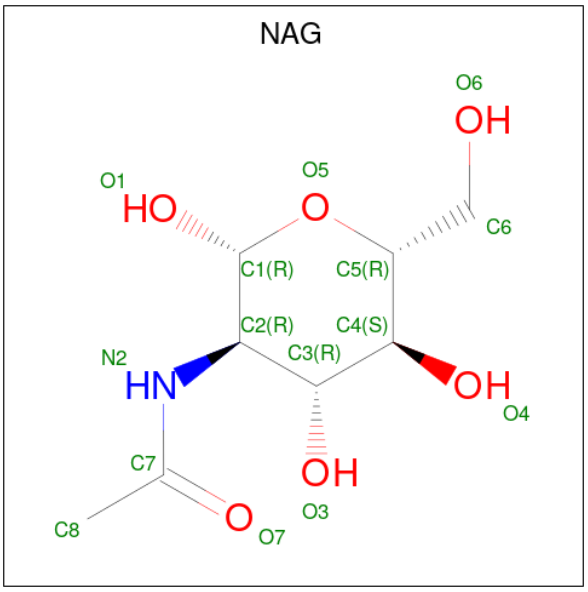
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	M	2	Total C N O 28 16 2 10	0	0	0
2	N	2	Total C N O 28 16 2 10	0	0	0

- Molecule 3 is CIS-HEME D HYDROXYCHLORIN GAMMA-SPIROLACTONE (CCD ID: HDD) (formula: $C_{34}H_{32}FeN_4O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C Fe N O 44 34 1 4 5	0	0
3	B	1	Total C Fe N O 44 34 1 4 5	0	0
3	C	1	Total C Fe N O 44 34 1 4 5	0	0
3	D	1	Total C Fe N O 44 34 1 4 5	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C N O 14 8 1 5	0	0

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 6 is water.

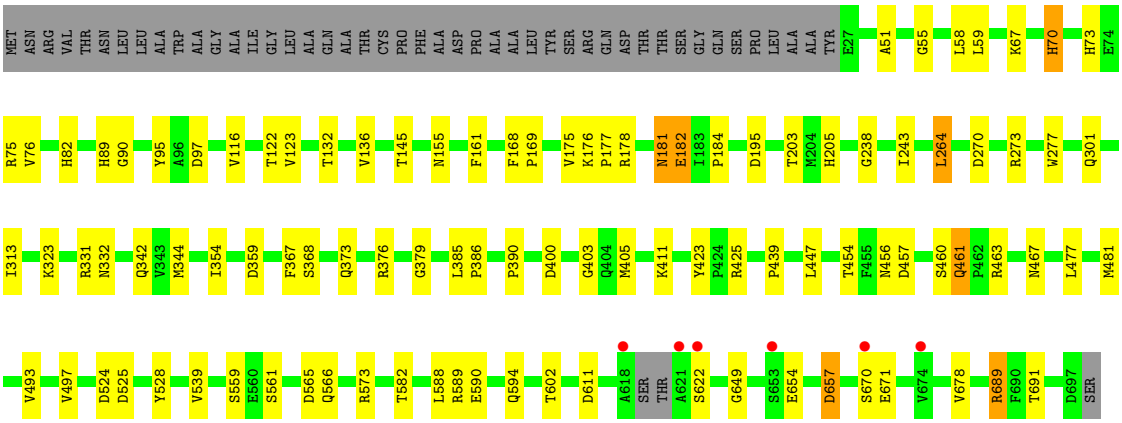
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	128	Total O 128 128	0	0
6	B	75	Total O 75 75	0	0
6	C	51	Total O 51 51	0	0
6	D	62	Total O 62 62	0	0

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.

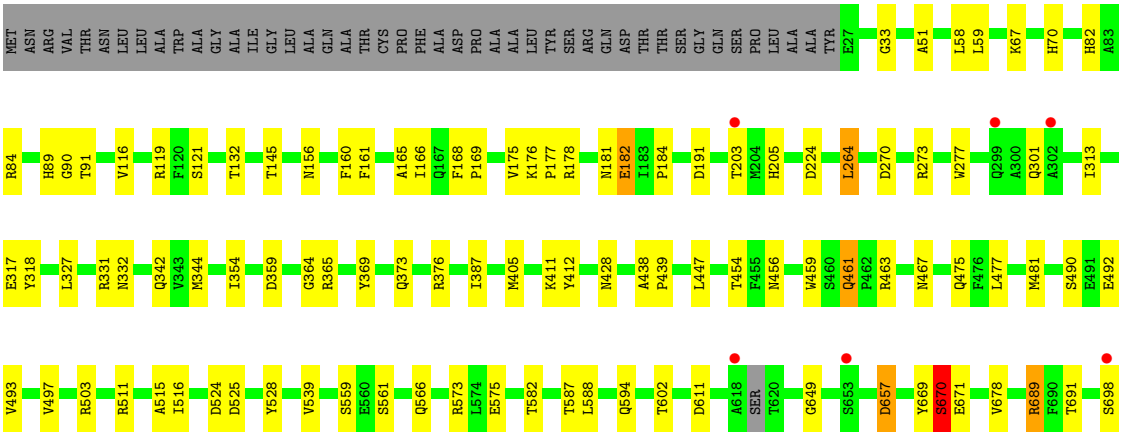
• Molecule 1: CATALASE-PHENOL OXIDASE

Chain A:



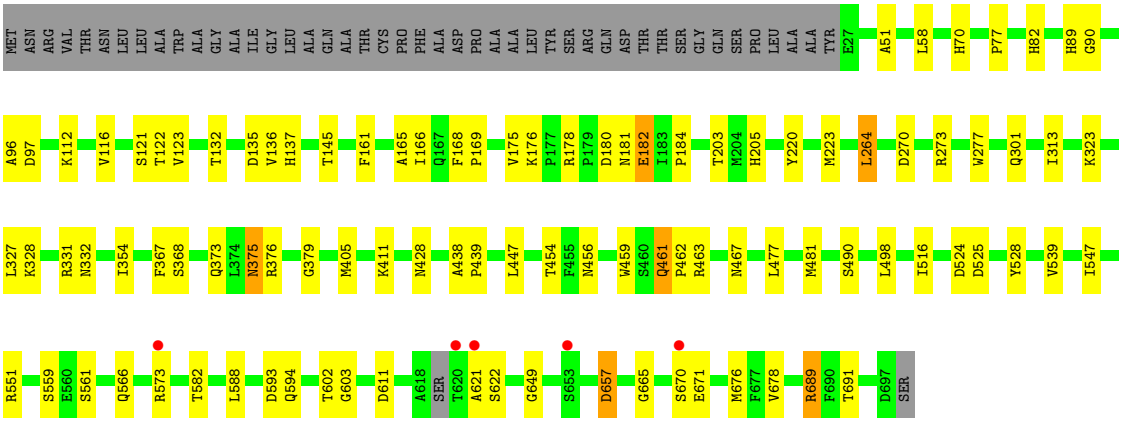
• Molecule 1: CATALASE-PHENOL OXIDASE

Chain B:



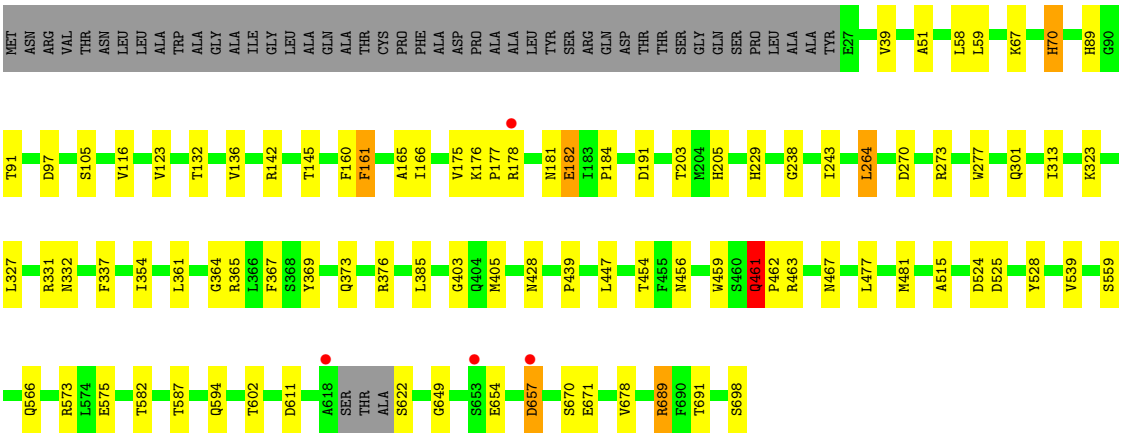
• Molecule 1: CATALASE-PHENOL OXIDASE

Chain C:



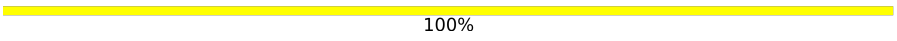
• Molecule 1: CATALASE-PHENOL OXIDASE

Chain D:



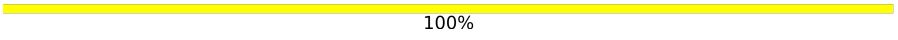
• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:



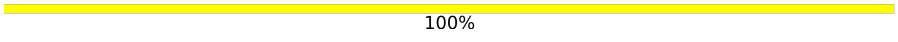
• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:



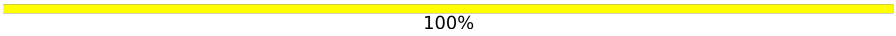
• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:



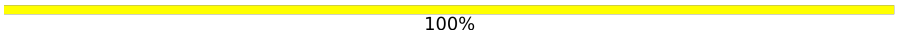
• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:



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

Chain I:

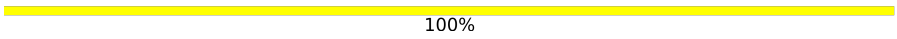


• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:

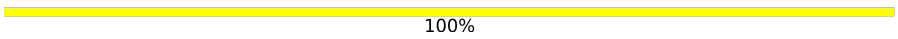
• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:



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

Chain L:

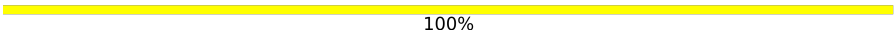


• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:

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

Chain N:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	185.45Å 216.34Å 68.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	141.42 – 2.70 140.80 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.8 (141.42-2.70) 99.8 (140.80-2.70)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.45 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.192 , 0.251 (Not available) , 0.257	Depositor DCC
R_{free} test set	3852 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	49.8	Xtriage
Anisotropy	0.328	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 23.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	21804	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% 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: HDD, NAG, CA

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	0.87	4/5418 (0.1%)	0.93	6/7362 (0.1%)
1	B	0.83	5/5385 (0.1%)	0.92	3/7319 (0.0%)
1	C	0.88	6/5390 (0.1%)	0.95	7/7325 (0.1%)
1	D	0.86	3/5364 (0.1%)	0.93	5/7290 (0.1%)
All	All	0.86	18/21557 (0.1%)	0.93	21/29296 (0.1%)

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	317	GLU	C-N	8.62	1.46	1.33
1	B	575	GLU	C-N	-8.19	1.22	1.33
1	C	112	LYS	C-N	7.98	1.44	1.33
1	A	181	ASN	C-N	7.15	1.42	1.33
1	B	670	SER	C-N	-7.11	1.24	1.33

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	456	ASN	N-CA-C	6.77	121.28	112.89
1	A	456	ASN	N-CA-C	6.25	120.64	112.89
1	C	547	ILE	N-CA-C	-6.21	107.08	113.10
1	A	368	SER	N-CA-C	6.08	118.41	111.11
1	B	33	GLY	N-CA-C	5.86	118.02	112.04

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5274	0	5060	79	0
1	B	5253	0	5019	75	0
1	C	5258	0	5037	71	0
1	D	5232	0	5002	67	0
2	E	28	0	25	0	0
2	F	28	0	25	0	0
2	G	28	0	25	0	0
2	H	28	0	25	0	0
2	I	28	0	25	0	0
2	J	28	0	25	1	0
2	K	28	0	25	0	0
2	L	28	0	25	0	0
2	M	28	0	25	1	0
2	N	28	0	25	0	0
3	A	44	0	31	2	0
3	B	44	0	31	3	0
3	C	44	0	31	1	0
3	D	44	0	31	1	0
4	B	14	0	13	0	0
5	B	1	0	0	0	0
6	A	128	0	0	0	0
6	B	75	0	0	2	0
6	C	51	0	0	2	0
6	D	62	0	0	0	0
All	All	21804	0	20505	253	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 6.

The worst 5 of 253 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:689:ARG:HG3	1:B:689:ARG:HH11	1.17	1.10
1:C:689:ARG:HG3	1:C:689:ARG:HH11	1.13	1.08
1:A:689:ARG:HG3	1:A:689:ARG:HH11	1.17	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:689:ARG:HG3	1:D:689:ARG:HH11	1.17	1.05
1:A:590:GLU:HA	1:A:590:GLU:OE1	1.62	0.97

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

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	561/590 (95%)	548 (98%)	13 (2%)	44	73
1	B	558/590 (95%)	541 (97%)	17 (3%)	36	66
1	C	559/590 (95%)	544 (97%)	15 (3%)	39	69
1	D	556/590 (94%)	541 (97%)	15 (3%)	39	69
All	All	2234/2360 (95%)	2174 (97%)	60 (3%)	39	69

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	689	ARG
1	D	559	SER
1	C	323	LYS
1	D	461	GLN
1	D	698	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	566	GLN
1	D	467	ASN
1	C	594	GLN
1	D	346	GLN
1	D	594	GLN

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)

20 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	NAG	E	1	2,1	14,14,15	0.79	1 (7%)	17,19,21	2.06	4 (23%)
2	NAG	E	2	2	14,14,15	0.72	0	17,19,21	1.43	3 (17%)
2	NAG	F	1	2,1	14,14,15	0.68	0	17,19,21	1.23	2 (11%)
2	NAG	F	2	2	14,14,15	0.51	0	17,19,21	1.57	4 (23%)
2	NAG	G	1	2,1	14,14,15	0.68	0	17,19,21	1.40	1 (5%)
2	NAG	G	2	2	14,14,15	1.17	1 (7%)	17,19,21	2.22	7 (41%)
2	NAG	H	1	2,1	14,14,15	0.59	0	17,19,21	1.45	2 (11%)
2	NAG	H	2	2	14,14,15	0.67	0	17,19,21	1.39	1 (5%)
2	NAG	I	1	2,1	14,14,15	0.54	0	17,19,21	1.32	1 (5%)
2	NAG	I	2	2	14,14,15	0.51	0	17,19,21	1.76	5 (29%)
2	NAG	J	1	2,1	14,14,15	0.65	0	17,19,21	1.26	2 (11%)
2	NAG	J	2	2	14,14,15	0.54	0	17,19,21	1.93	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	NAG	K	1	2,1	14,14,15	0.90	1 (7%)	17,19,21	1.13	0
2	NAG	K	2	2	14,14,15	0.73	1 (7%)	17,19,21	1.75	4 (23%)
2	NAG	L	1	2,1	14,14,15	0.56	0	17,19,21	1.34	1 (5%)
2	NAG	L	2	2	14,14,15	0.52	0	17,19,21	1.35	3 (17%)
2	NAG	M	1	2,1	14,14,15	0.53	0	17,19,21	2.82	6 (35%)
2	NAG	M	2	2	14,14,15	0.54	0	17,19,21	1.89	4 (23%)
2	NAG	N	1	2,1	14,14,15	0.72	0	17,19,21	1.27	2 (11%)
2	NAG	N	2	2	14,14,15	0.79	1 (7%)	17,19,21	1.78	2 (11%)

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	NAG	E	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	NAG	F	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	2/6/23/26	0/1/1/1
2	NAG	G	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1
2	NAG	H	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	H	2	2	-	0/6/23/26	0/1/1/1
2	NAG	I	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	I	2	2	-	0/6/23/26	0/1/1/1
2	NAG	J	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	J	2	2	-	1/6/23/26	0/1/1/1
2	NAG	K	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	K	2	2	-	2/6/23/26	0/1/1/1
2	NAG	L	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	L	2	2	-	0/6/23/26	0/1/1/1
2	NAG	M	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	M	2	2	-	2/6/23/26	0/1/1/1
2	NAG	N	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	N	2	2	-	0/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	2	NAG	C1-C2	3.56	1.57	1.52
2	K	1	NAG	C1-C2	2.47	1.55	1.52
2	N	2	NAG	C1-C2	2.26	1.55	1.52
2	K	2	NAG	C1-C2	2.25	1.55	1.52
2	E	1	NAG	C1-C2	2.06	1.55	1.52

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	M	1	NAG	C1-O5-C5	7.57	122.33	112.19
2	E	1	NAG	C1-O5-C5	5.69	119.81	112.19
2	J	2	NAG	O5-C1-C2	-4.74	103.95	111.29
2	M	1	NAG	O5-C1-C2	4.73	118.61	111.29
2	I	2	NAG	C1-O5-C5	4.52	118.25	112.19

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	L	1	NAG	C4-C5-C6-O6
2	J	1	NAG	C4-C5-C6-O6
2	H	1	NAG	C4-C5-C6-O6
2	J	1	NAG	O5-C5-C6-O6
2	L	1	NAG	O5-C5-C6-O6

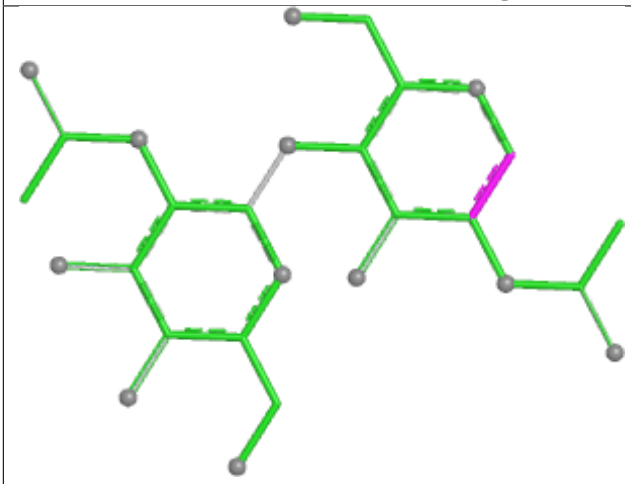
There are no ring outliers.

2 monomers are involved in 2 short contacts:

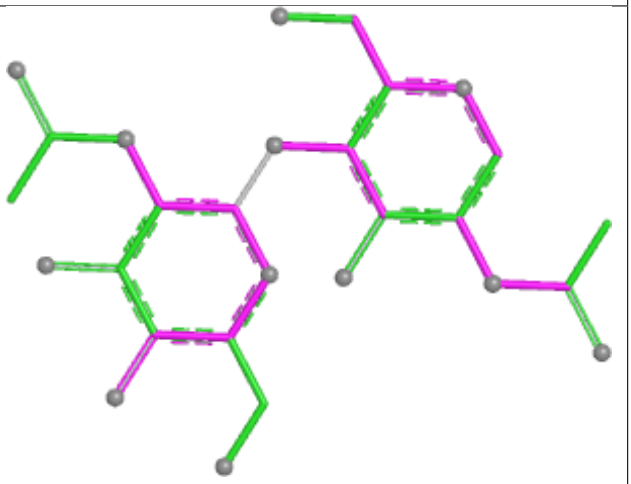
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	J	2	NAG	1	0
2	M	1	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

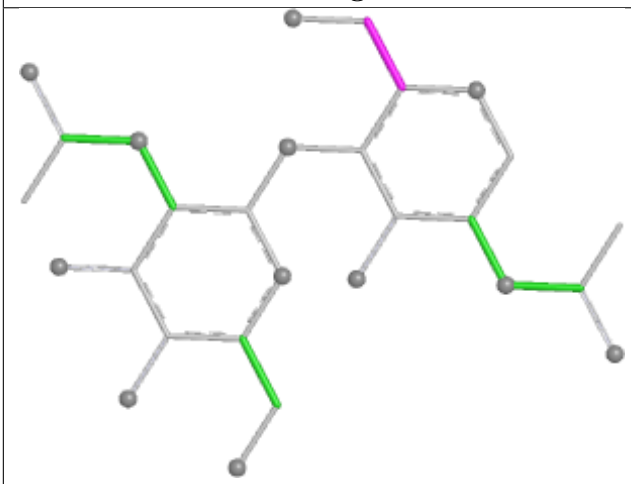
Oligosaccharide Chain E



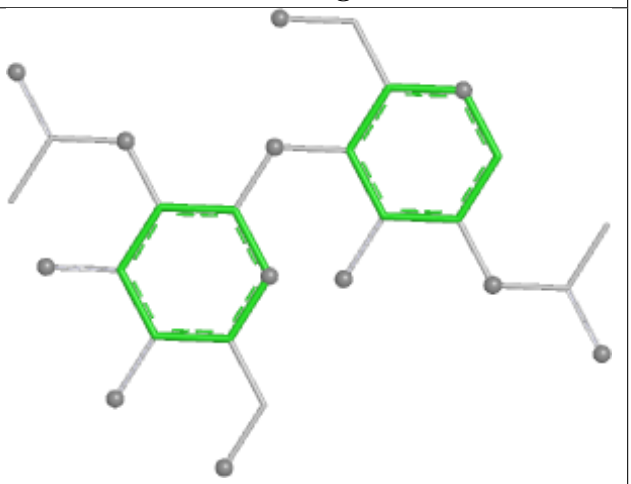
Bond lengths



Bond angles

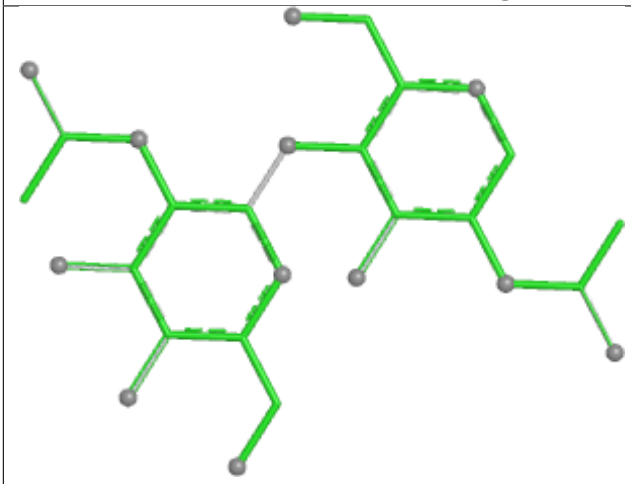


Torsions

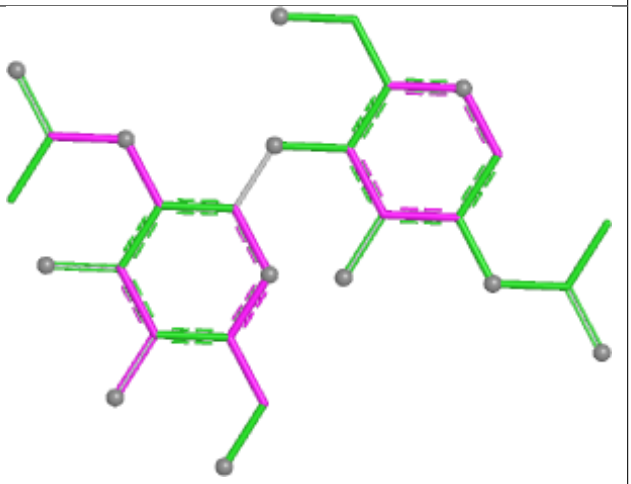


Rings

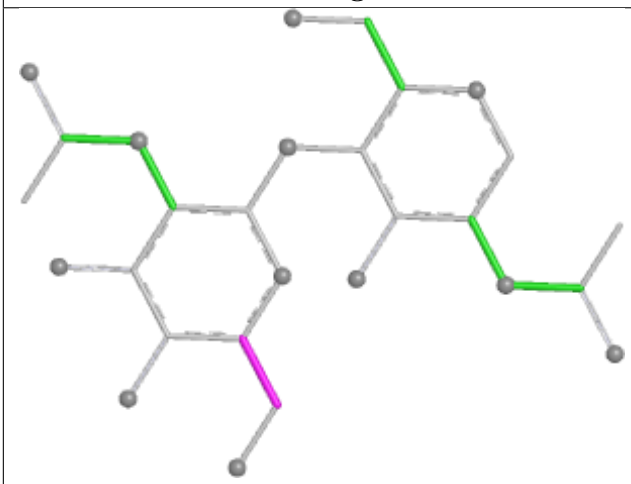
Oligosaccharide Chain F



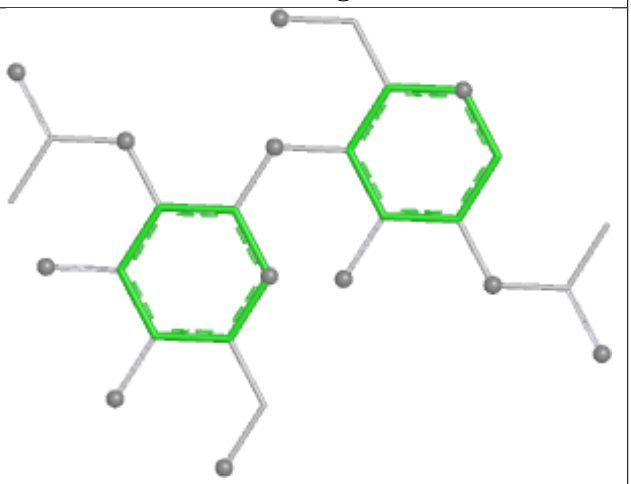
Bond lengths



Bond angles

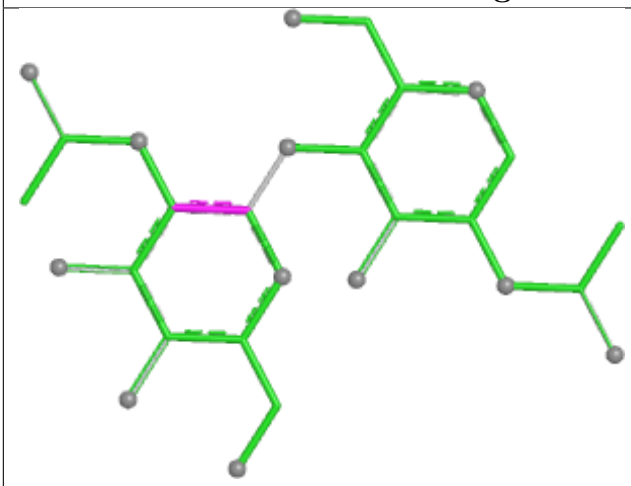


Torsions

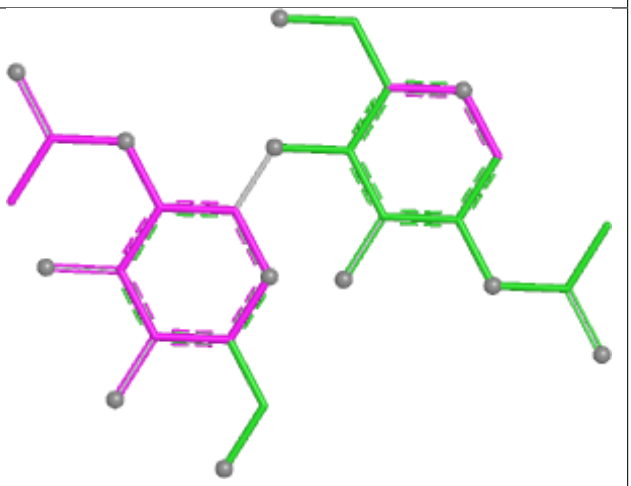


Rings

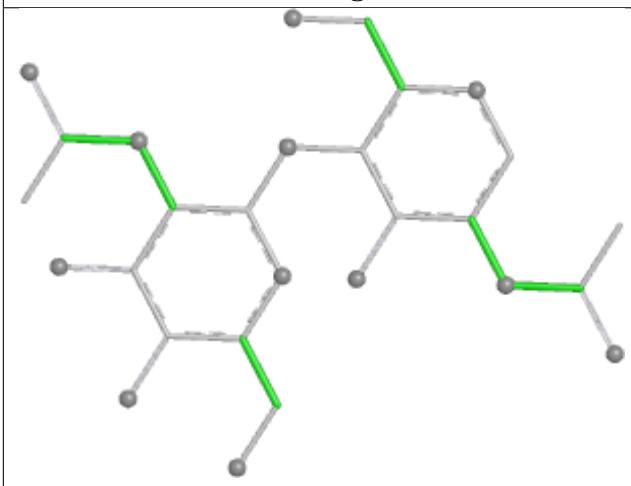
Oligosaccharide Chain G



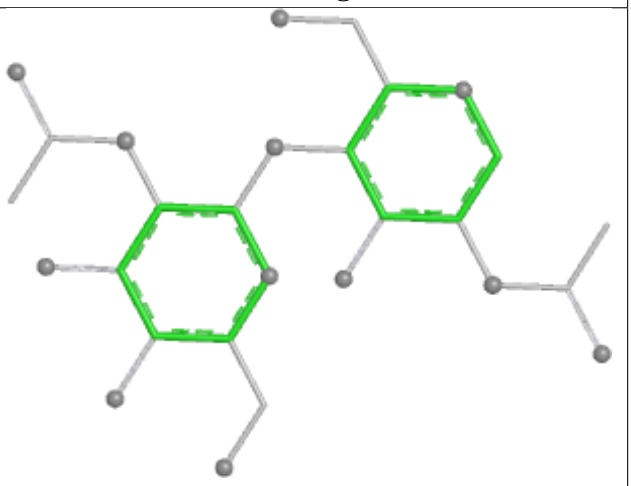
Bond lengths



Bond angles

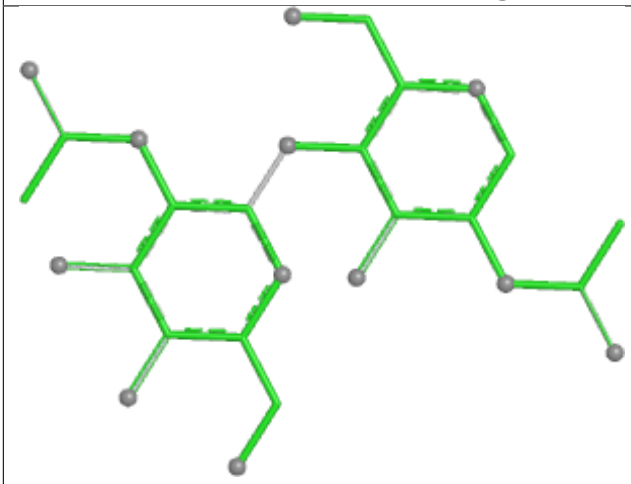


Torsions

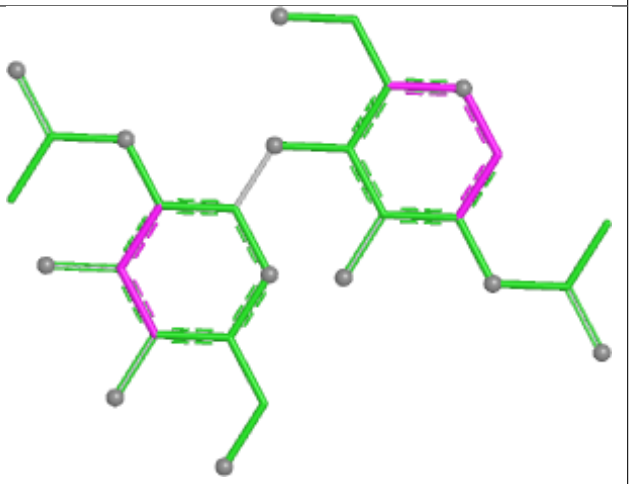


Rings

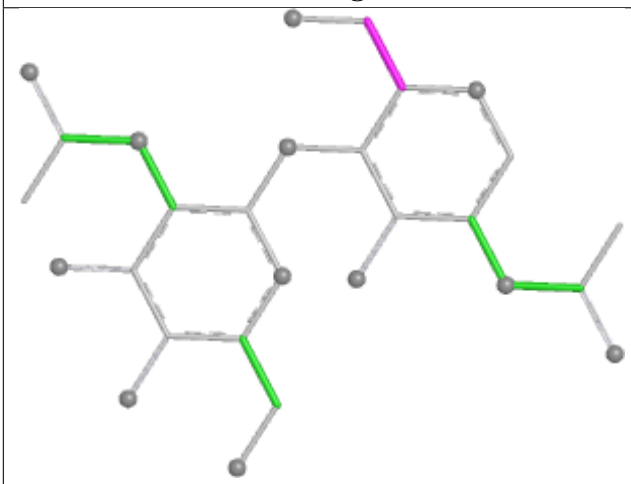
Oligosaccharide Chain H



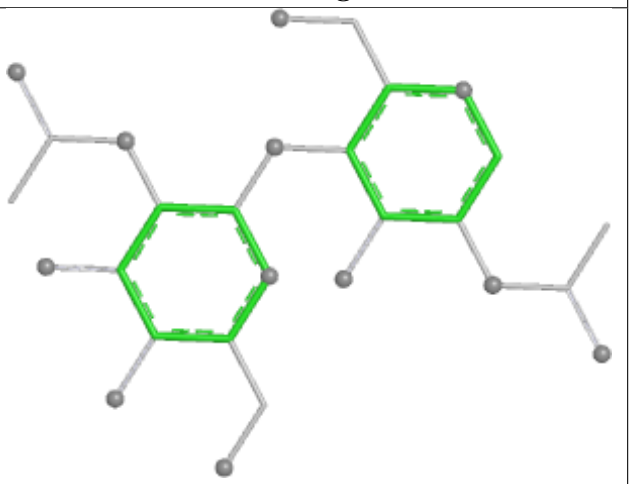
Bond lengths



Bond angles

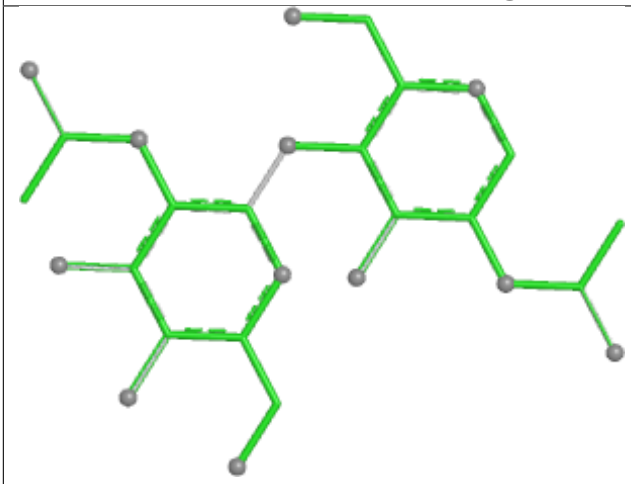


Torsions

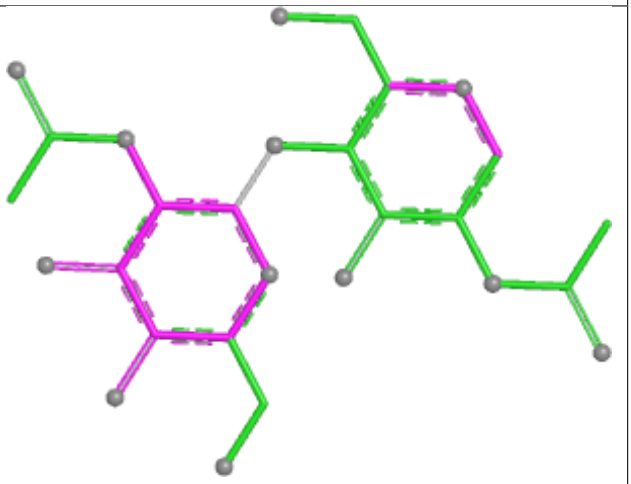


Rings

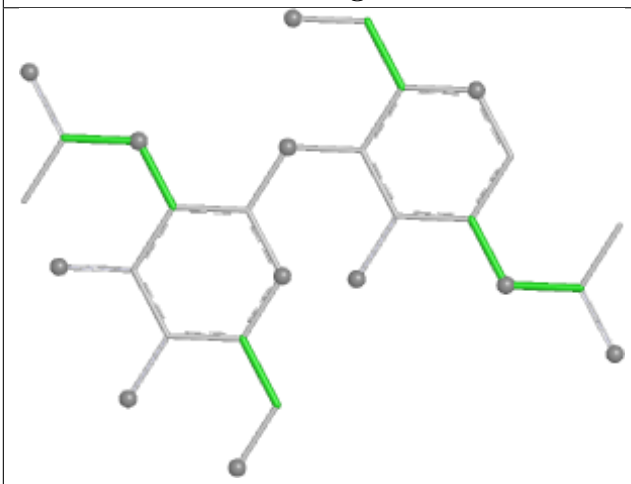
Oligosaccharide Chain I



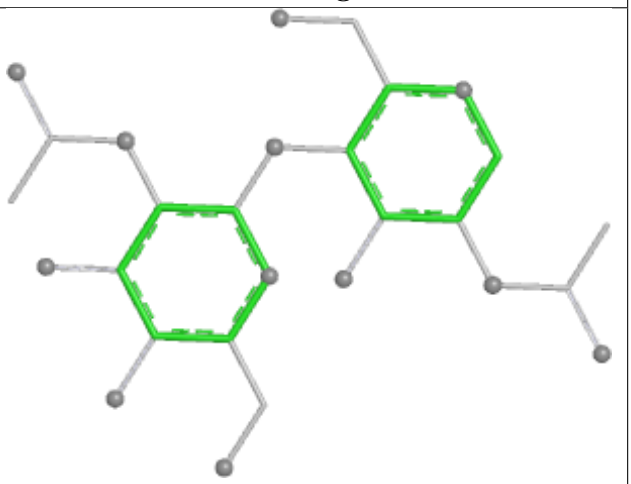
Bond lengths



Bond angles

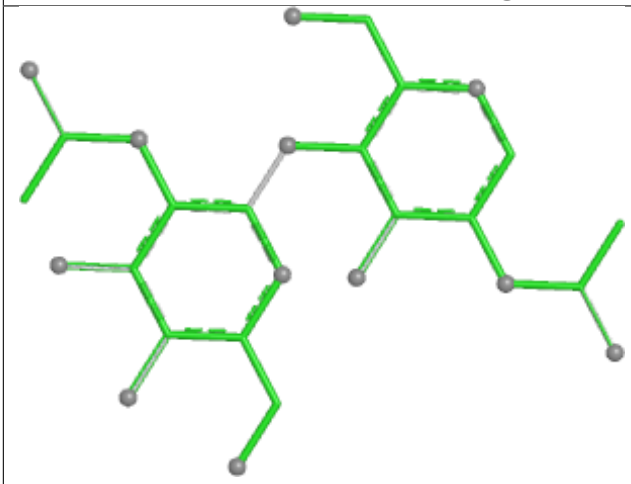


Torsions

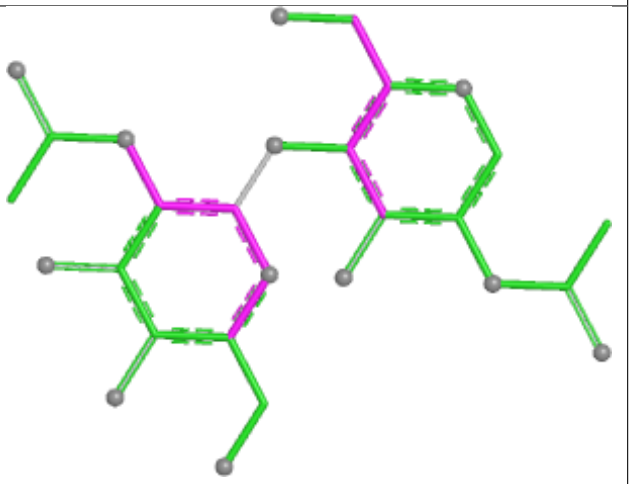


Rings

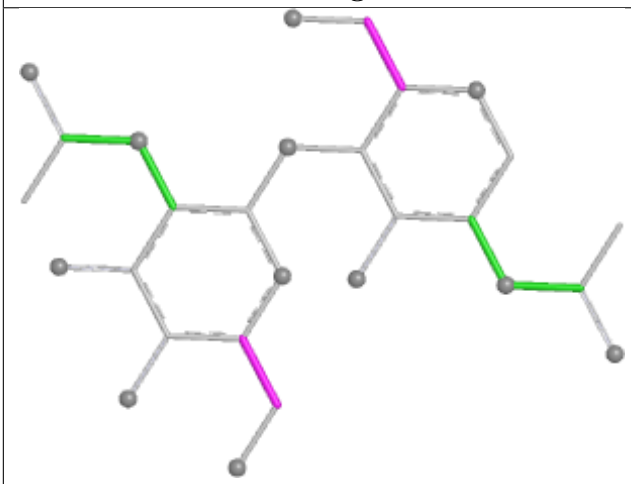
Oligosaccharide Chain J



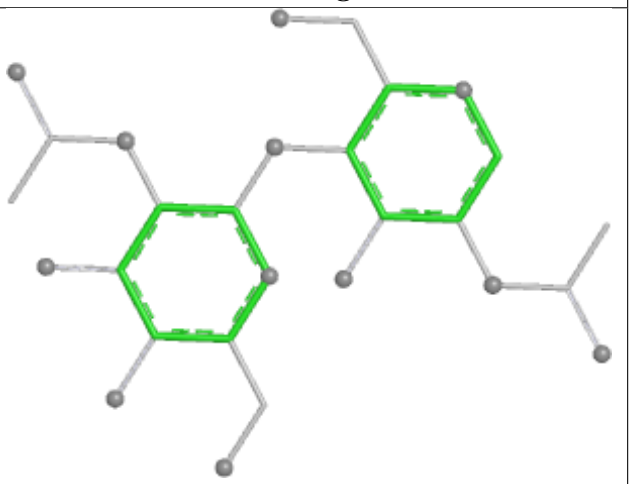
Bond lengths



Bond angles

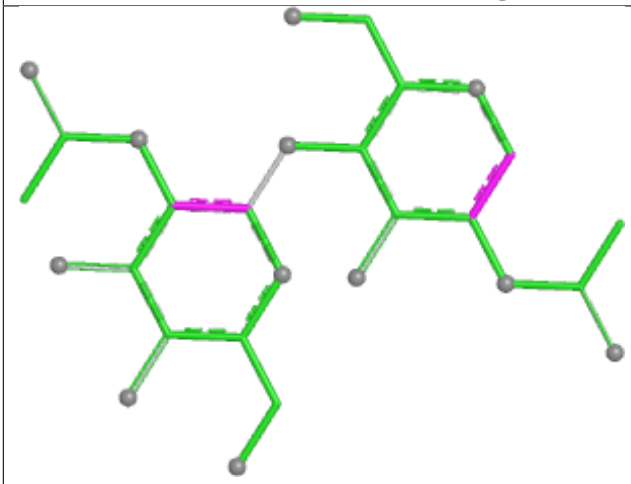


Torsions

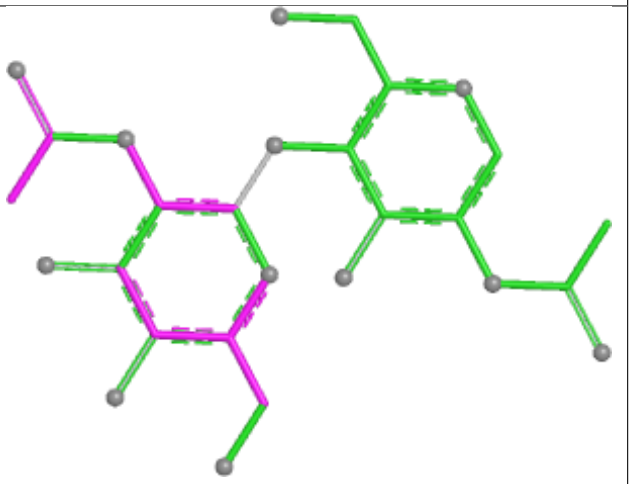


Rings

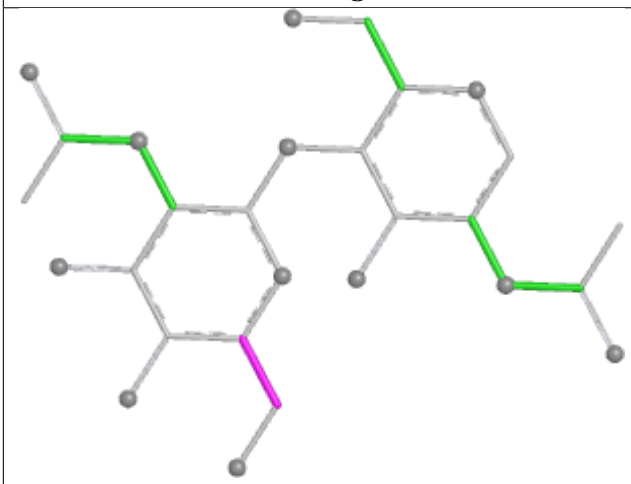
Oligosaccharide Chain K



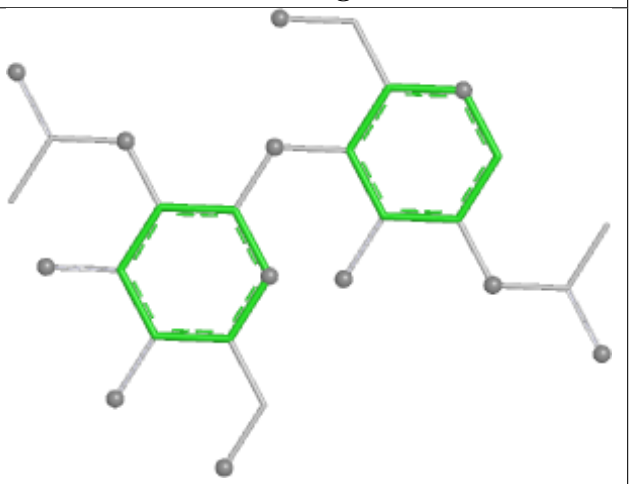
Bond lengths



Bond angles

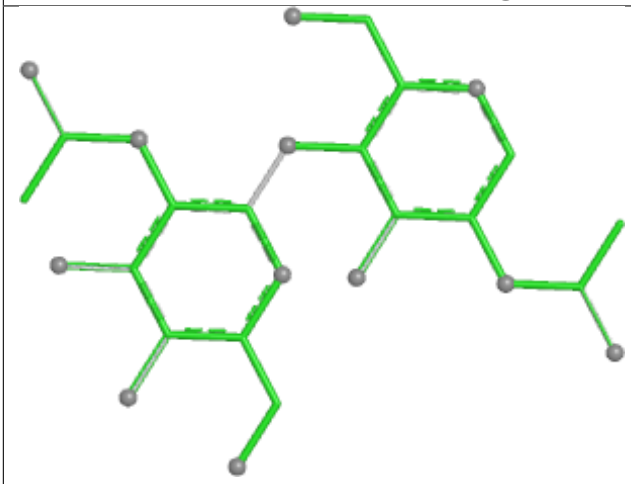


Torsions

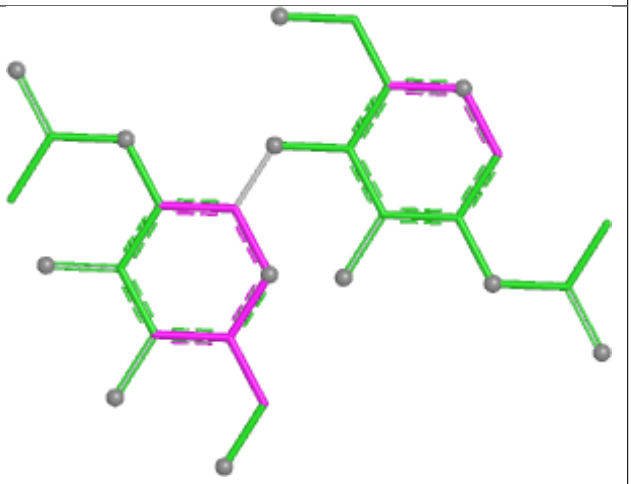


Rings

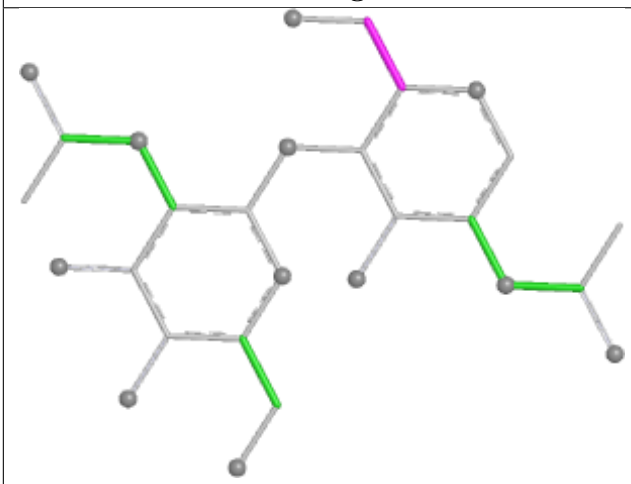
Oligosaccharide Chain L



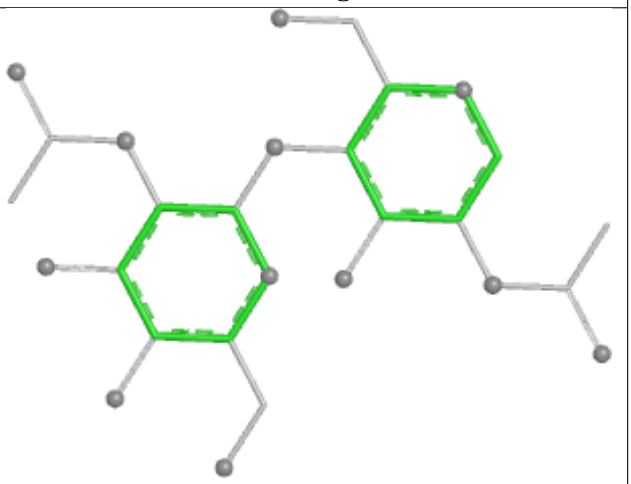
Bond lengths



Bond angles

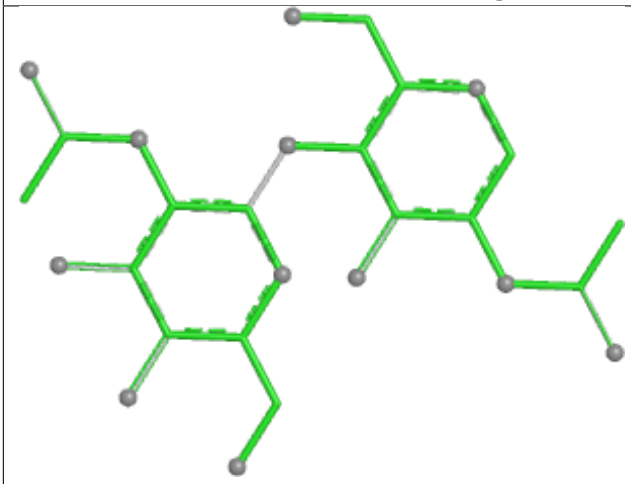


Torsions

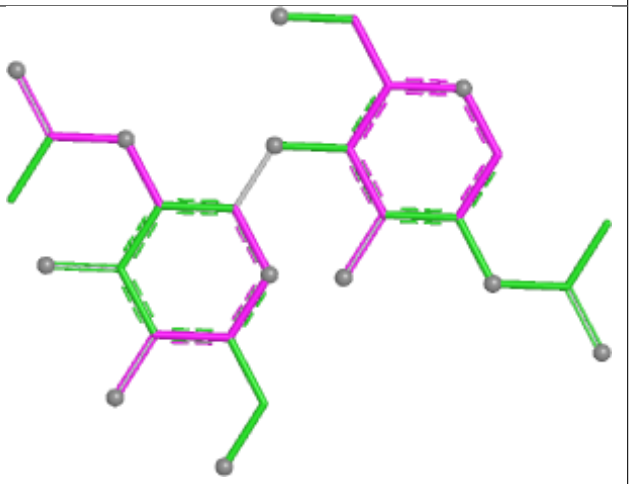


Rings

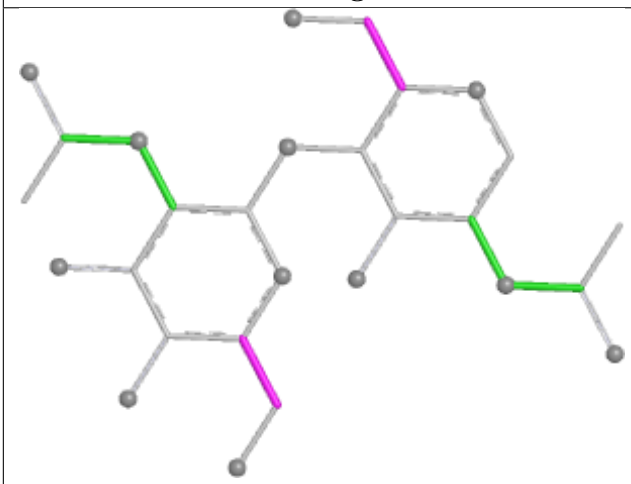
Oligosaccharide Chain M



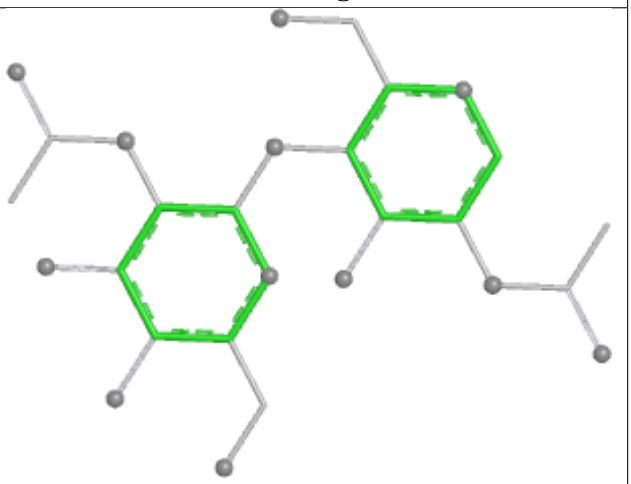
Bond lengths



Bond angles

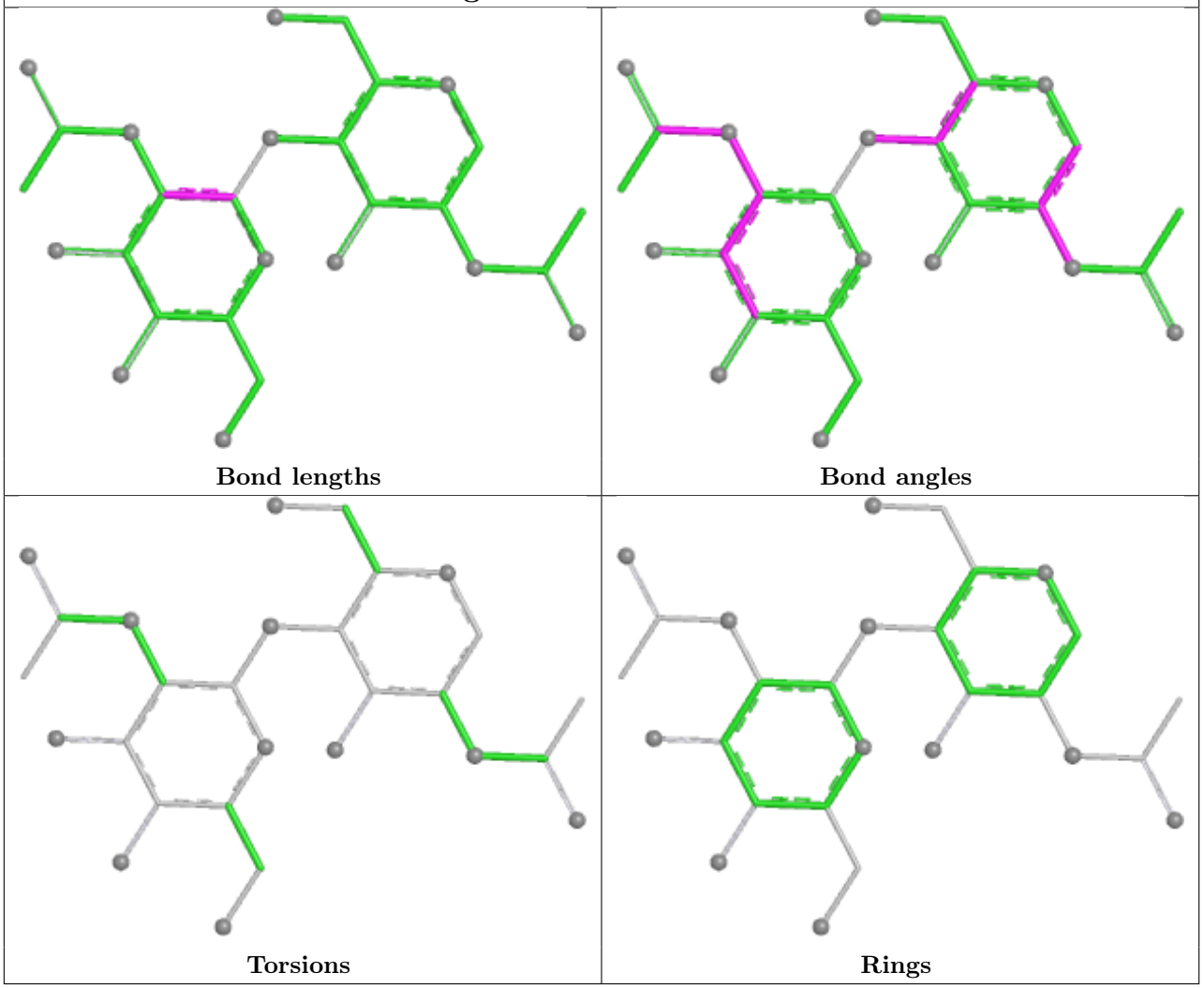


Torsions



Rings

Oligosaccharide Chain N



5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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	NAG	B	905	1	14,14,15	0.64	0	17,19,21	1.67	2 (11%)
3	HDD	A	900	1	46,52,52	2.07	16 (34%)	62,89,89	2.39	22 (35%)
3	HDD	C	900	1	46,52,52	2.30	17 (36%)	62,89,89	2.47	21 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	HDD	D	900	1	46,52,52	2.27	18 (39%)	62,89,89	2.36	24 (38%)
3	HDD	B	900	1	46,52,52	2.30	18 (39%)	62,89,89	2.36	24 (38%)

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	NAG	B	905	1	-	1/6/23/26	0/1/1/1
3	HDD	A	900	1	-	4/9/89/89	0/1/9/9
3	HDD	C	900	1	-	4/9/89/89	0/1/9/9
3	HDD	D	900	1	-	6/9/89/89	0/1/9/9
3	HDD	B	900	1	-	4/9/89/89	0/1/9/9

The worst 5 of 69 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	900	HDD	O1D-CGD	6.54	1.45	1.35
3	D	900	HDD	O1D-CGD	6.25	1.45	1.35
3	C	900	HDD	O1D-CGD	6.11	1.45	1.35
3	C	900	HDD	C3B-C2B	4.81	1.46	1.37
3	D	900	HDD	CHB-C1B	4.72	1.47	1.38

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	900	HDD	C3B-C2B-C1B	-7.92	99.55	107.05
3	A	900	HDD	C3B-C2B-C1B	-7.11	100.32	107.05
3	D	900	HDD	C3B-C2B-C1B	-6.91	100.51	107.05
3	B	900	HDD	C3B-C2B-C1B	-6.73	100.68	107.05
3	C	900	HDD	C3C-C2C-C1C	-5.97	100.13	107.17

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	900	HDD	C2B-C3B-CAB-CBB
3	A	900	HDD	C4B-C3B-CAB-CBB
3	B	900	HDD	C2B-C3B-CAB-CBB

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Mol	Chain	Res	Type	Atoms
3	D	900	HDD	C2B-C3B-CAB-CBB
3	D	900	HDD	C4B-C3B-CAB-CBB

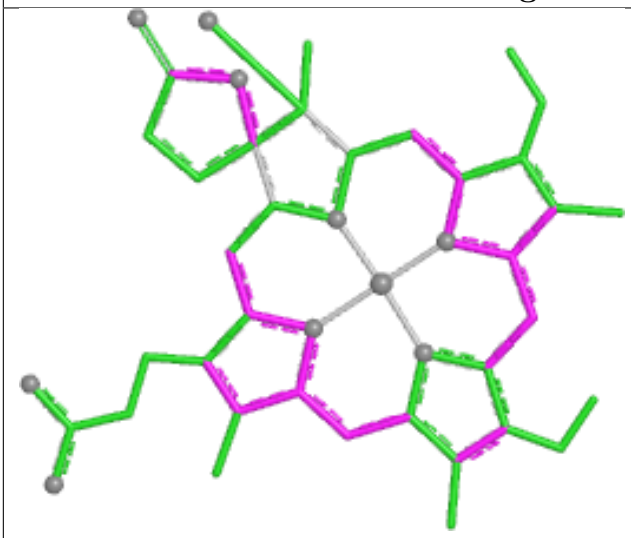
There are no ring outliers.

4 monomers are involved in 7 short contacts:

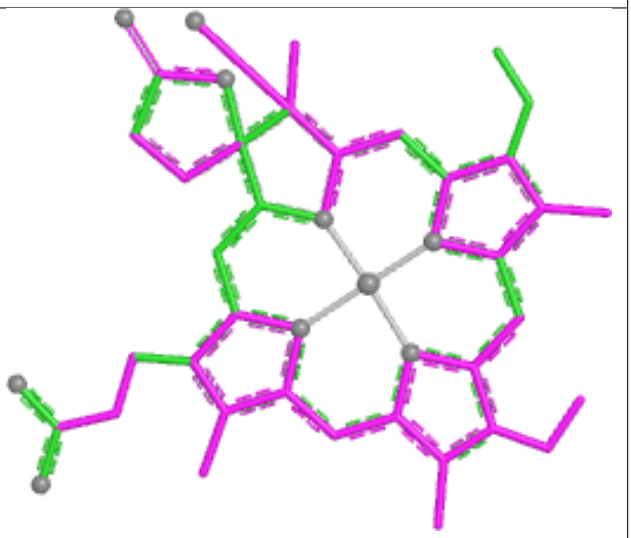
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	900	HDD	2	0
3	C	900	HDD	1	0
3	D	900	HDD	1	0
3	B	900	HDD	3	0

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.

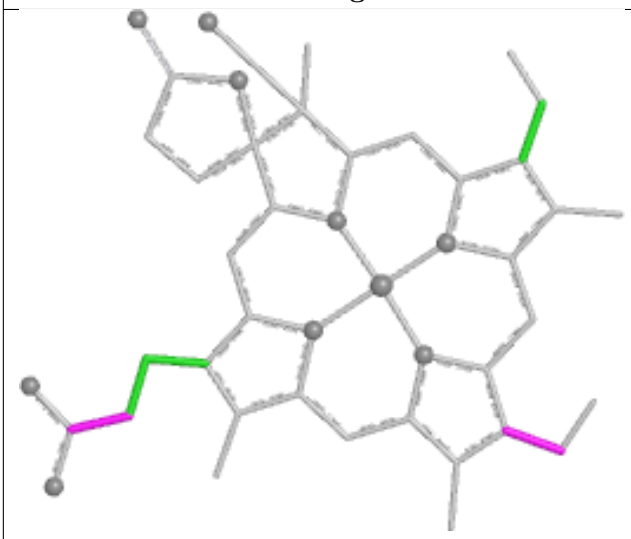
Ligand HDD A 900



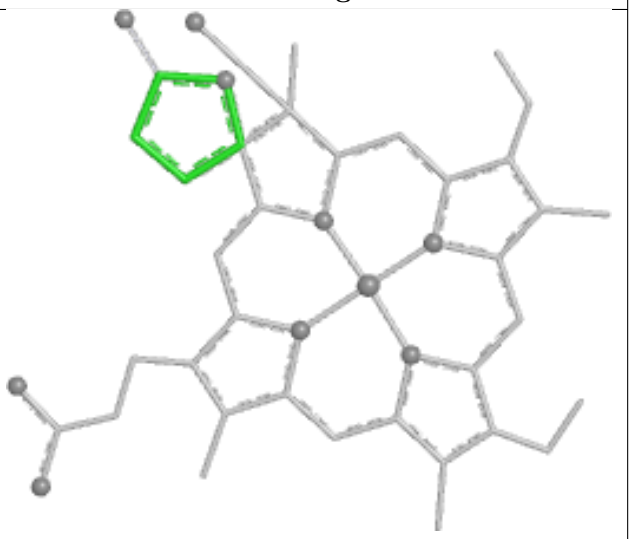
Bond lengths



Bond angles

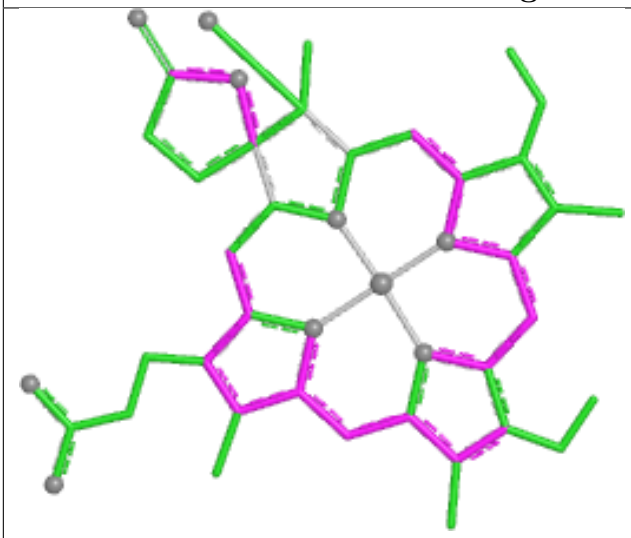


Torsions

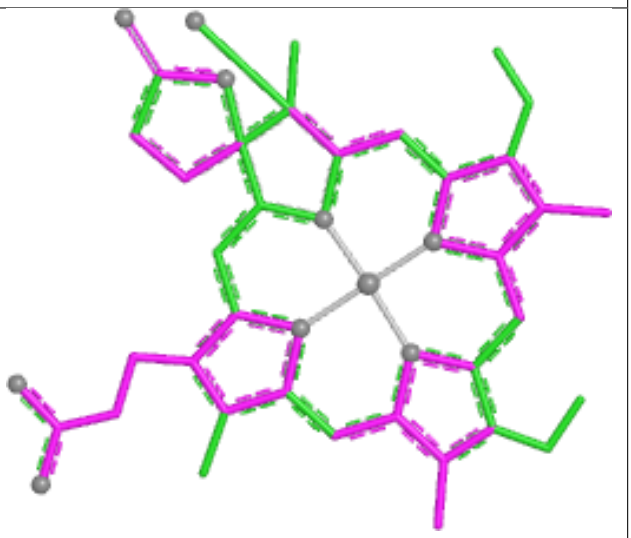


Rings

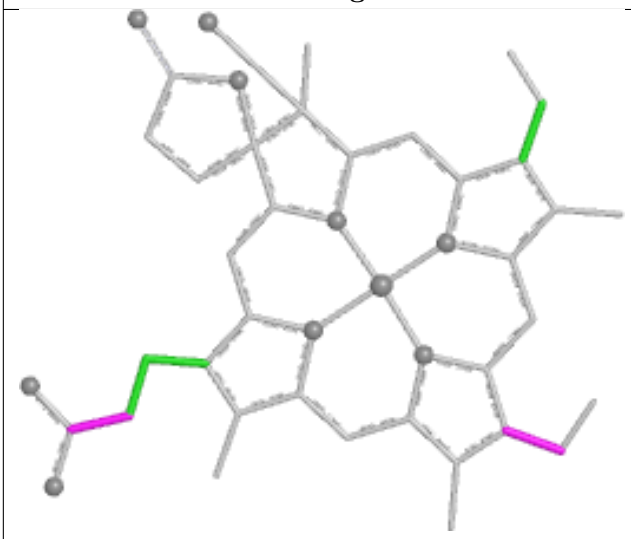
Ligand HDD C 900



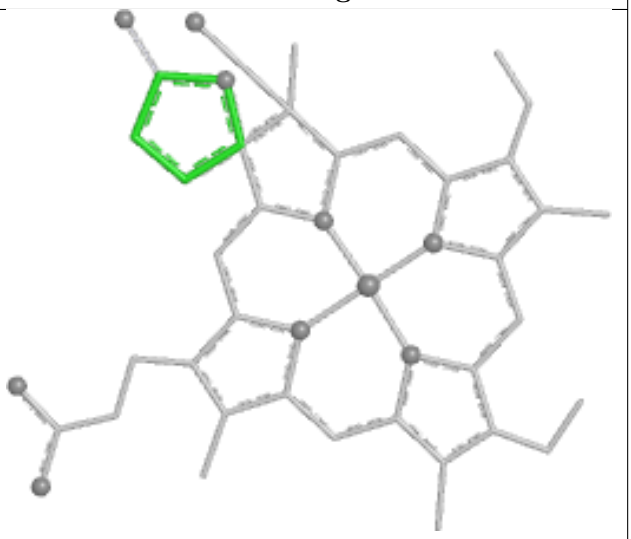
Bond lengths



Bond angles

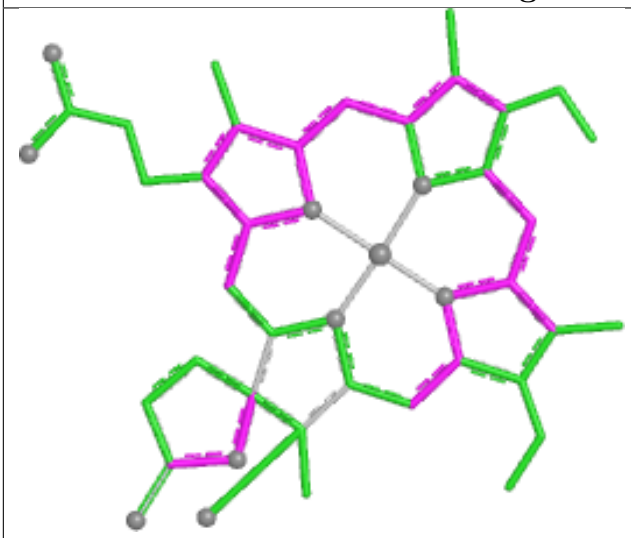


Torsions

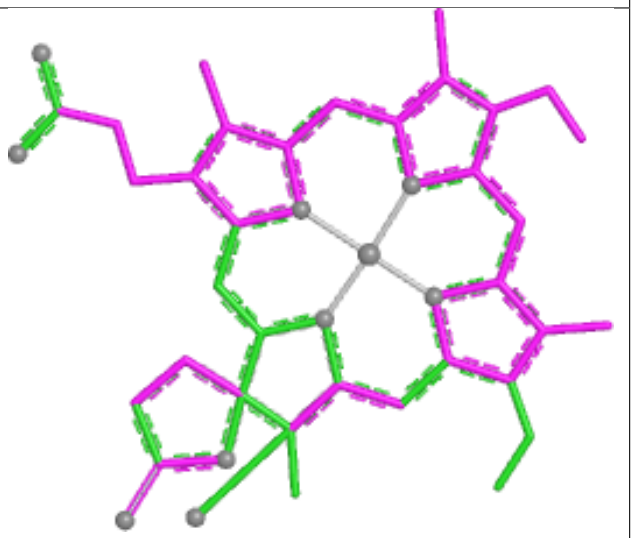


Rings

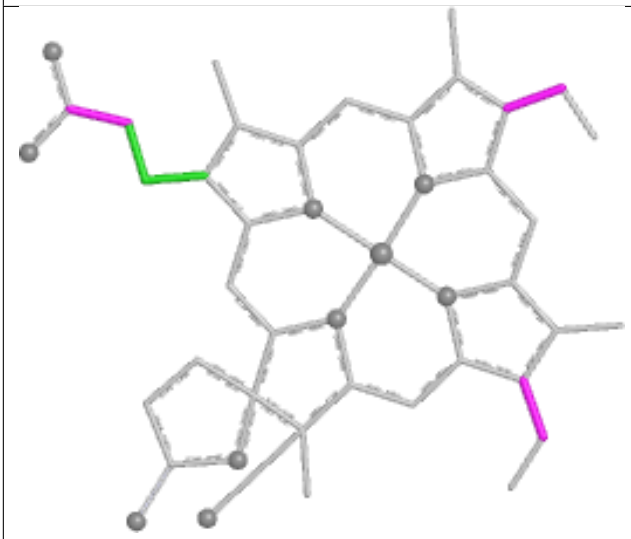
Ligand HDD D 900



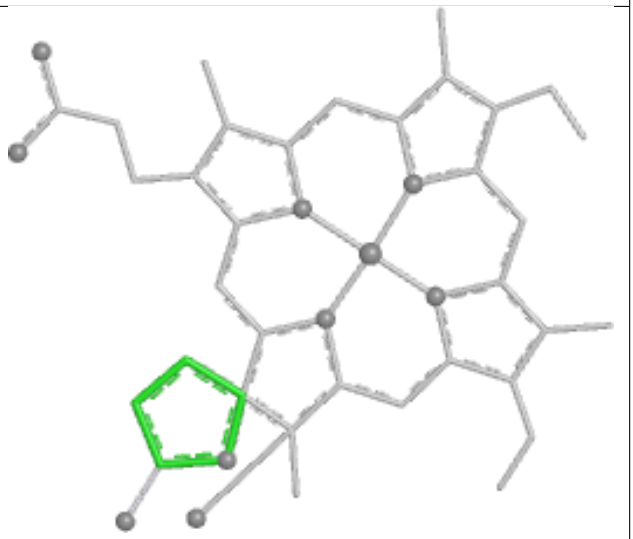
Bond lengths



Bond angles

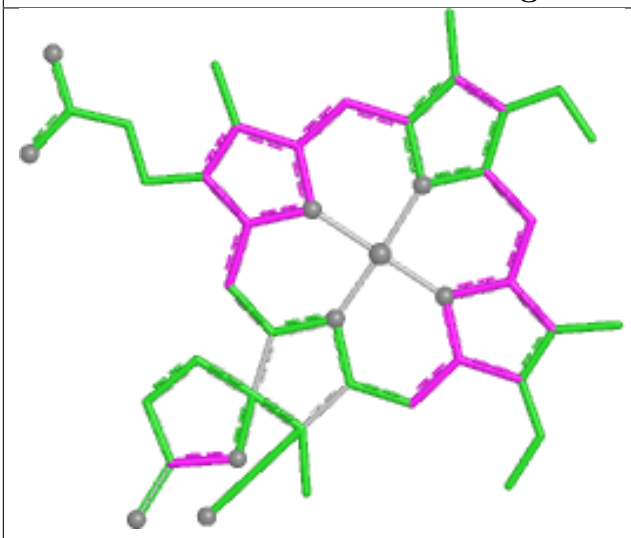


Torsions

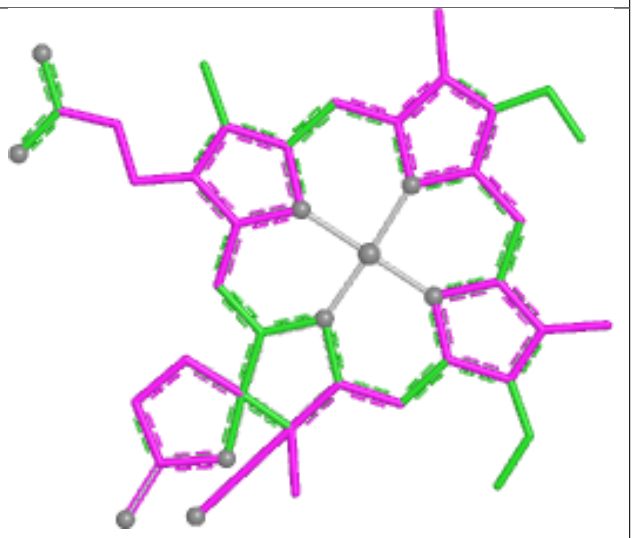


Rings

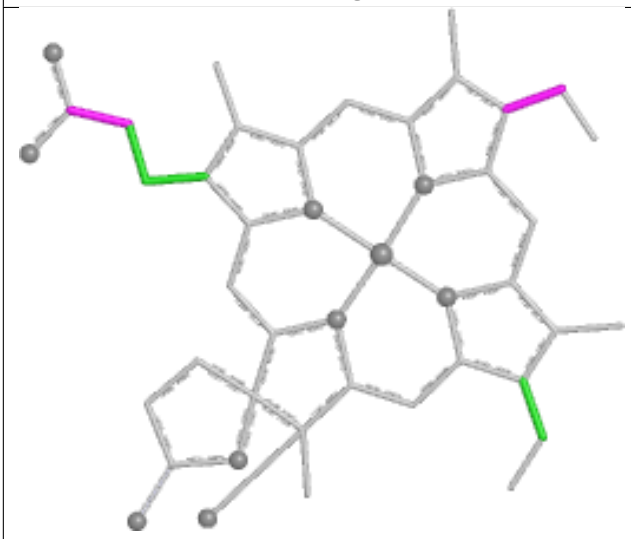
Ligand HDD B 900



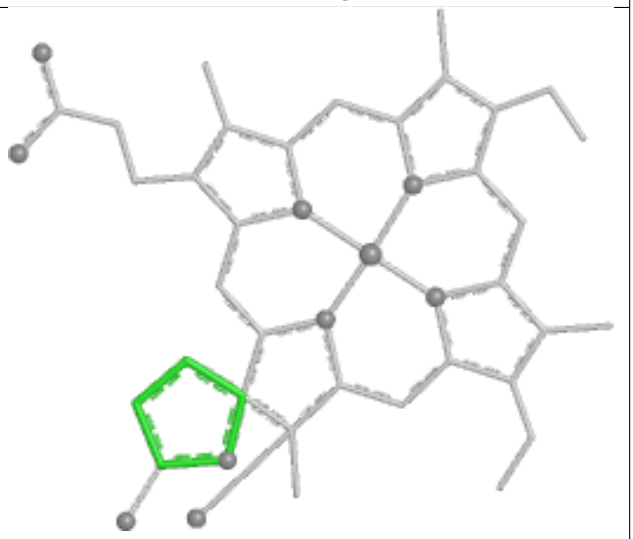
Bond lengths



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	669/717 (93%)	-0.45	6 (0%)	81	80	15, 42, 74, 122	8 (1%)
1	B	671/717 (93%)	-0.16	6 (0%)	81	80	22, 54, 88, 127	3 (0%)
1	C	670/717 (93%)	-0.27	5 (0%)	84	83	18, 46, 82, 119	4 (0%)
1	D	669/717 (93%)	-0.42	4 (0%)	85	85	20, 44, 78, 118	2 (0%)
All	All	2679/2868 (93%)	-0.32	21 (0%)	82	81	15, 46, 83, 127	17 (0%)

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	670	SER	6.1
1	C	653[A]	SER	4.8
1	D	178	ARG	4.2
1	A	621	ALA	3.8
1	D	618	ALA	3.7

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

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
2	NAG	F	2	14/15	0.57	0.14	68,87,100,108	0
2	NAG	J	2	14/15	0.59	0.14	59,92,103,103	0

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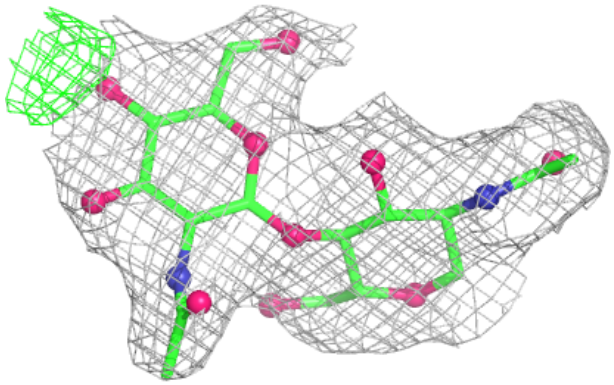
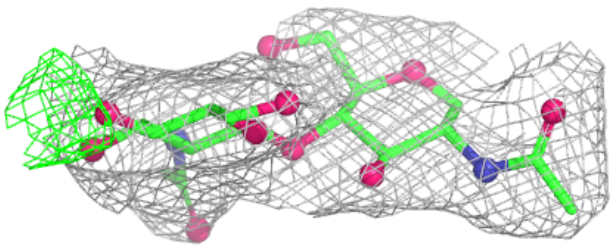
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	N	2	14/15	0.65	0.13	75,90,94,96	0
2	NAG	G	2	14/15	0.69	0.12	70,89,95,96	0
2	NAG	H	2	14/15	0.71	0.12	77,101,106,106	0
2	NAG	K	2	14/15	0.84	0.08	65,69,78,80	0
2	NAG	L	2	14/15	0.84	0.10	68,72,80,84	0
2	NAG	E	2	14/15	0.84	0.09	56,70,75,77	0
2	NAG	H	1	14/15	0.85	0.09	65,82,85,88	0
2	NAG	F	1	14/15	0.85	0.12	54,63,72,81	0
2	NAG	I	1	14/15	0.86	0.08	65,71,81,84	0
2	NAG	I	2	14/15	0.86	0.09	63,75,81,83	0
2	NAG	G	1	14/15	0.86	0.10	67,76,83,84	0
2	NAG	M	1	14/15	0.87	0.10	51,62,66,67	0
2	NAG	K	1	14/15	0.88	0.09	54,62,70,71	0
2	NAG	N	1	14/15	0.89	0.09	62,72,81,88	0
2	NAG	L	1	14/15	0.90	0.08	45,53,63,64	0
2	NAG	J	1	14/15	0.91	0.09	62,65,71,83	0
2	NAG	M	2	14/15	0.91	0.09	53,57,63,69	0
2	NAG	E	1	14/15	0.95	0.07	44,50,56,67	0

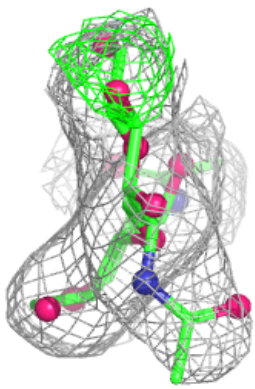
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain E:

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

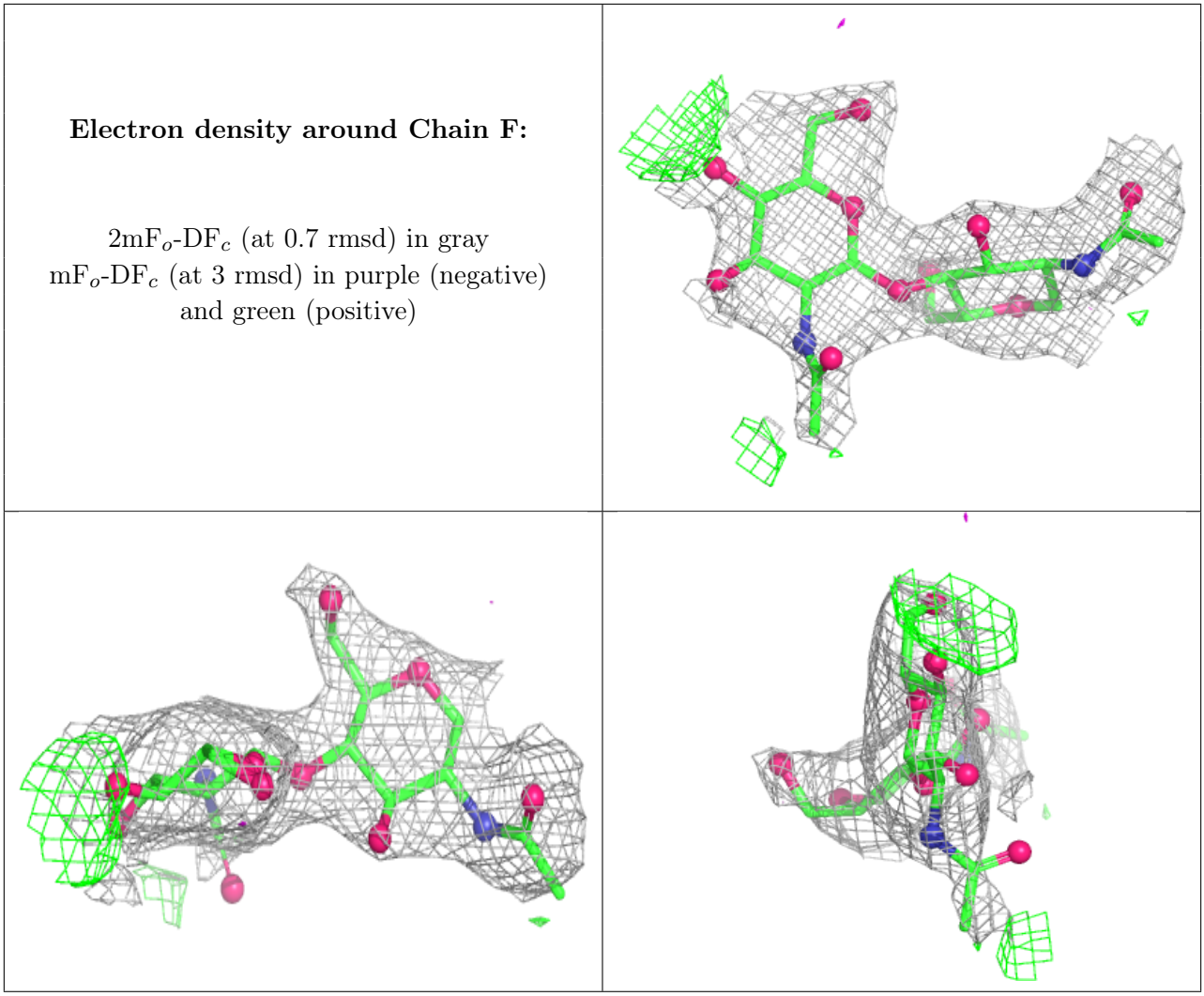






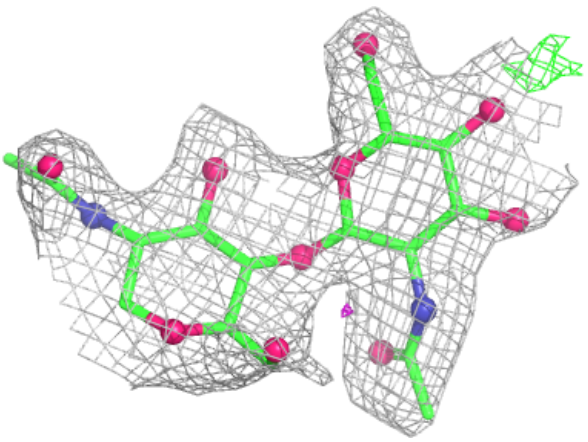
Electron density around Chain F:

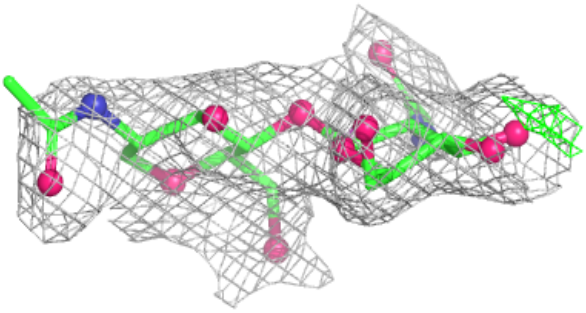
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

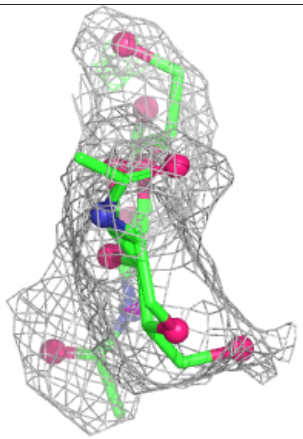


Electron density around Chain G:

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

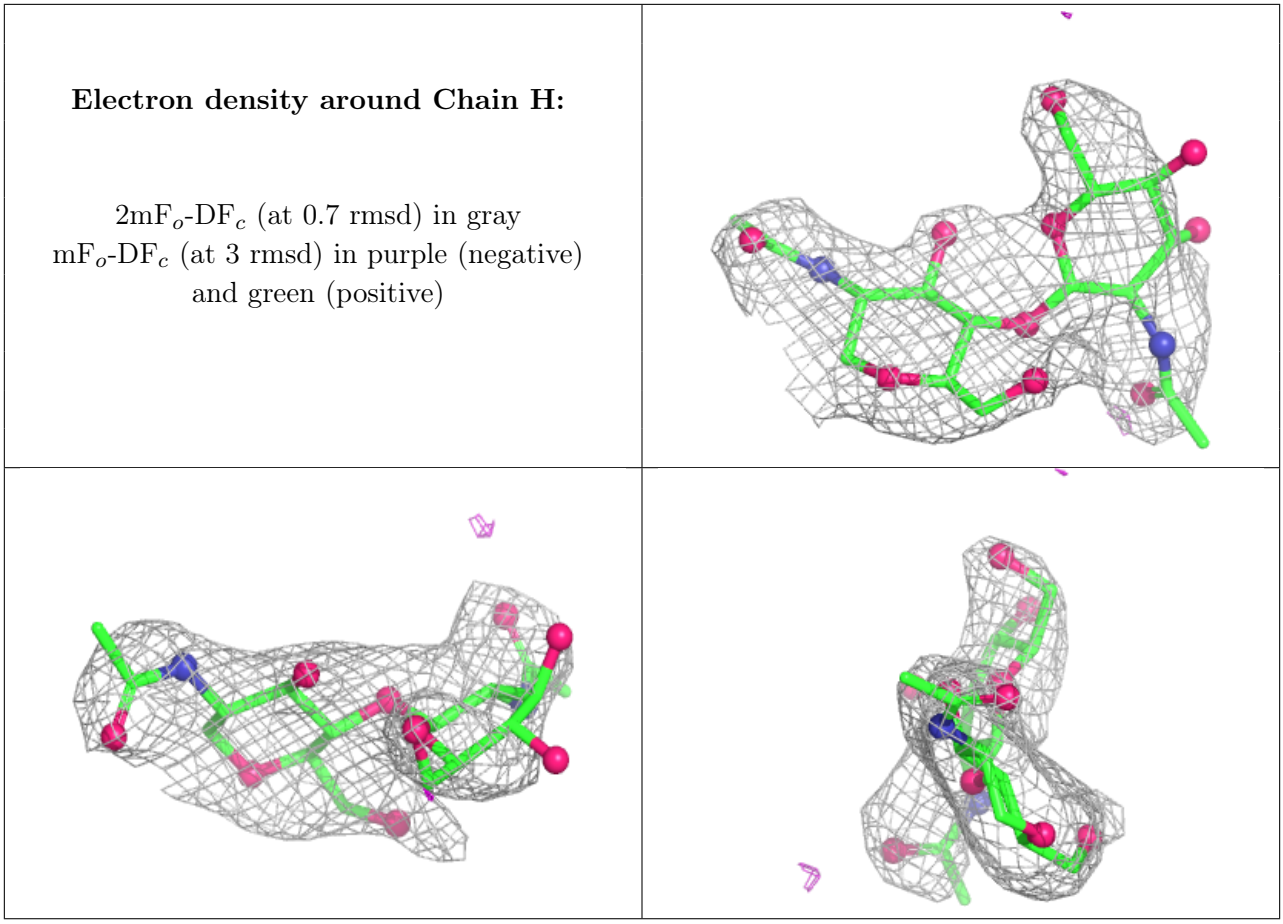






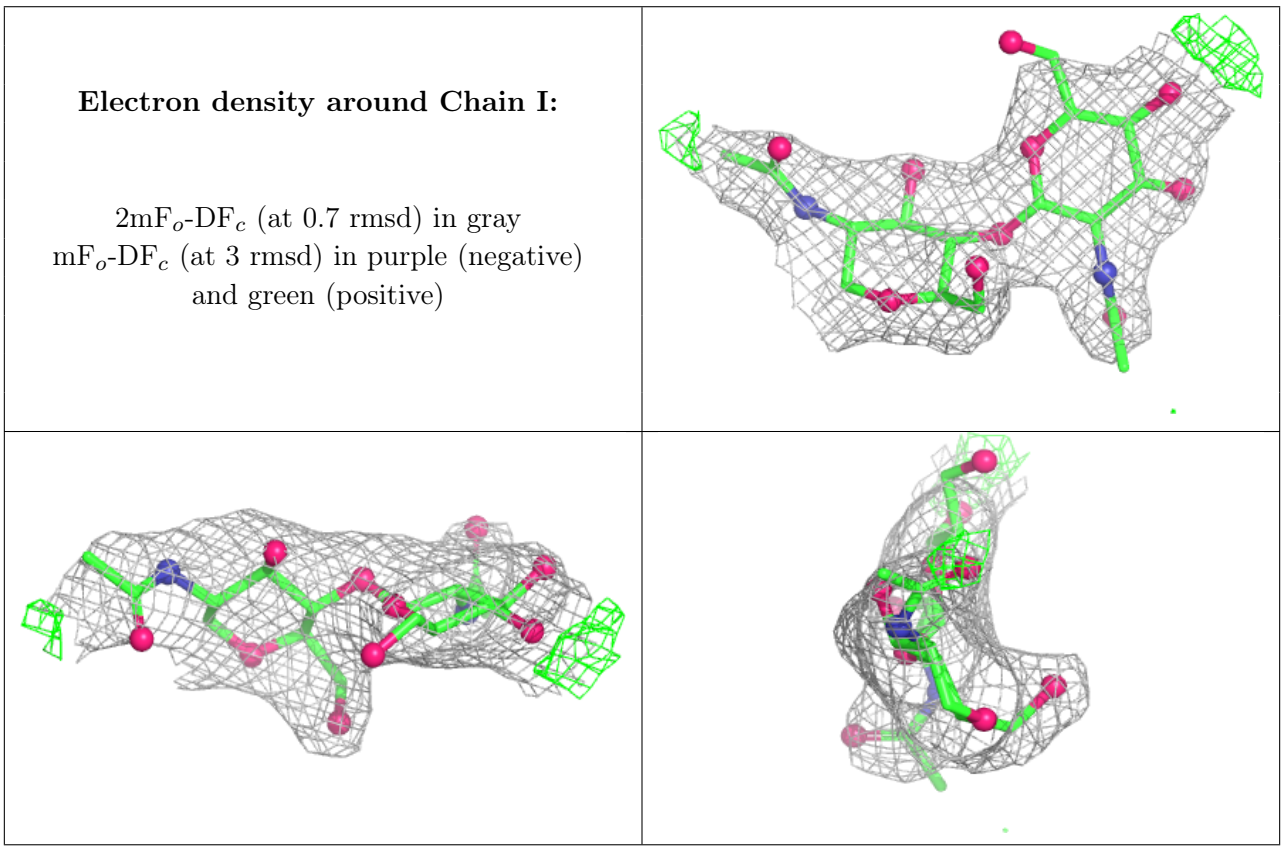
Electron density around Chain H:

$2mF_o$-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 I:

$2mF_o$-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 J:

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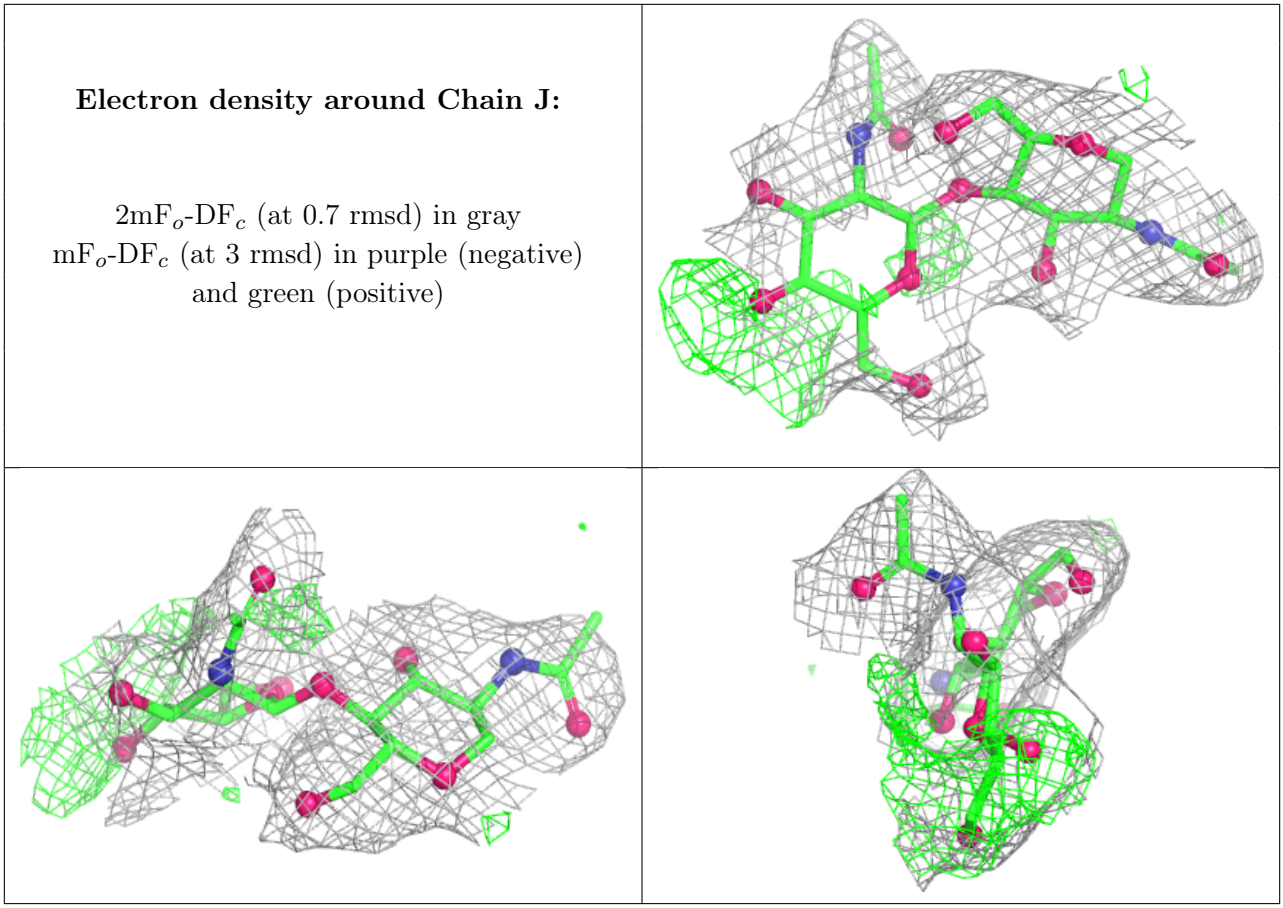
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around Chain K:

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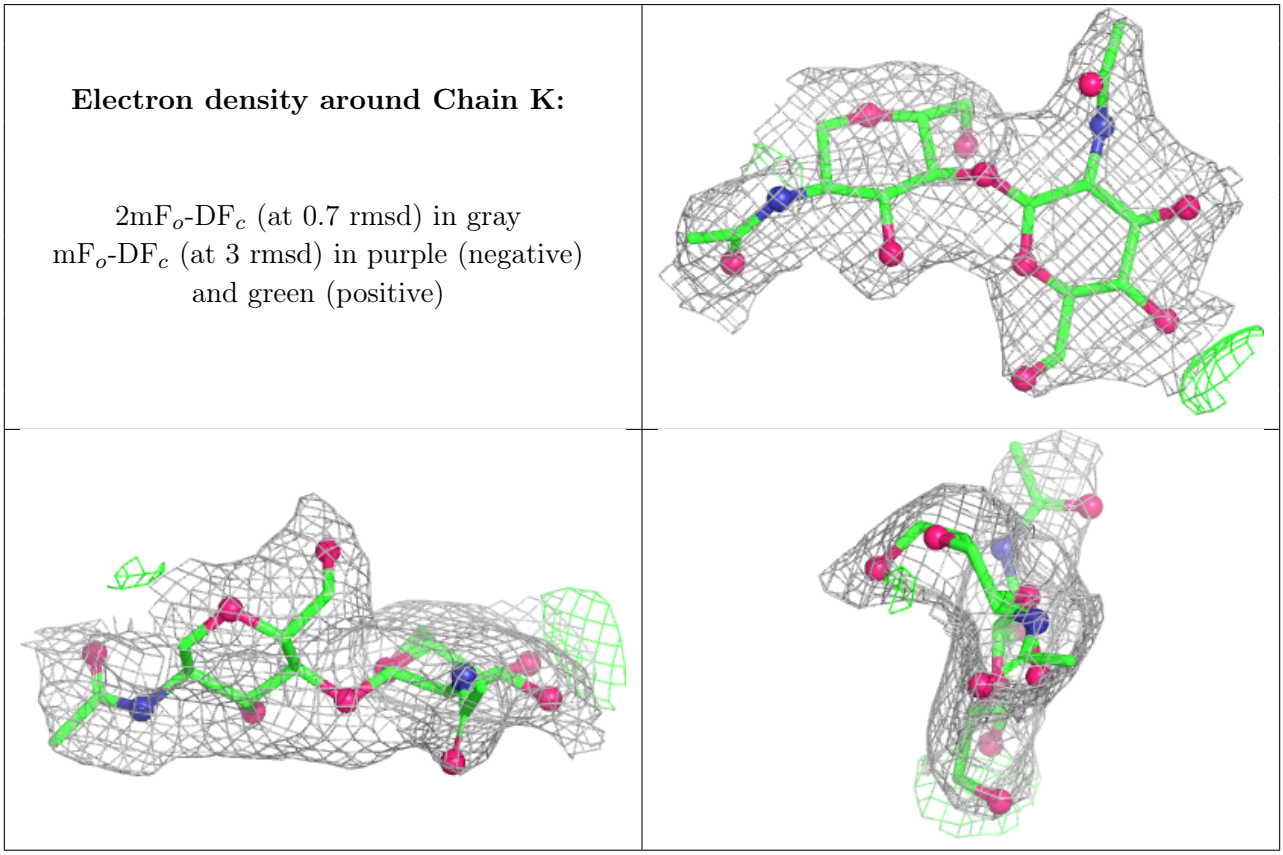
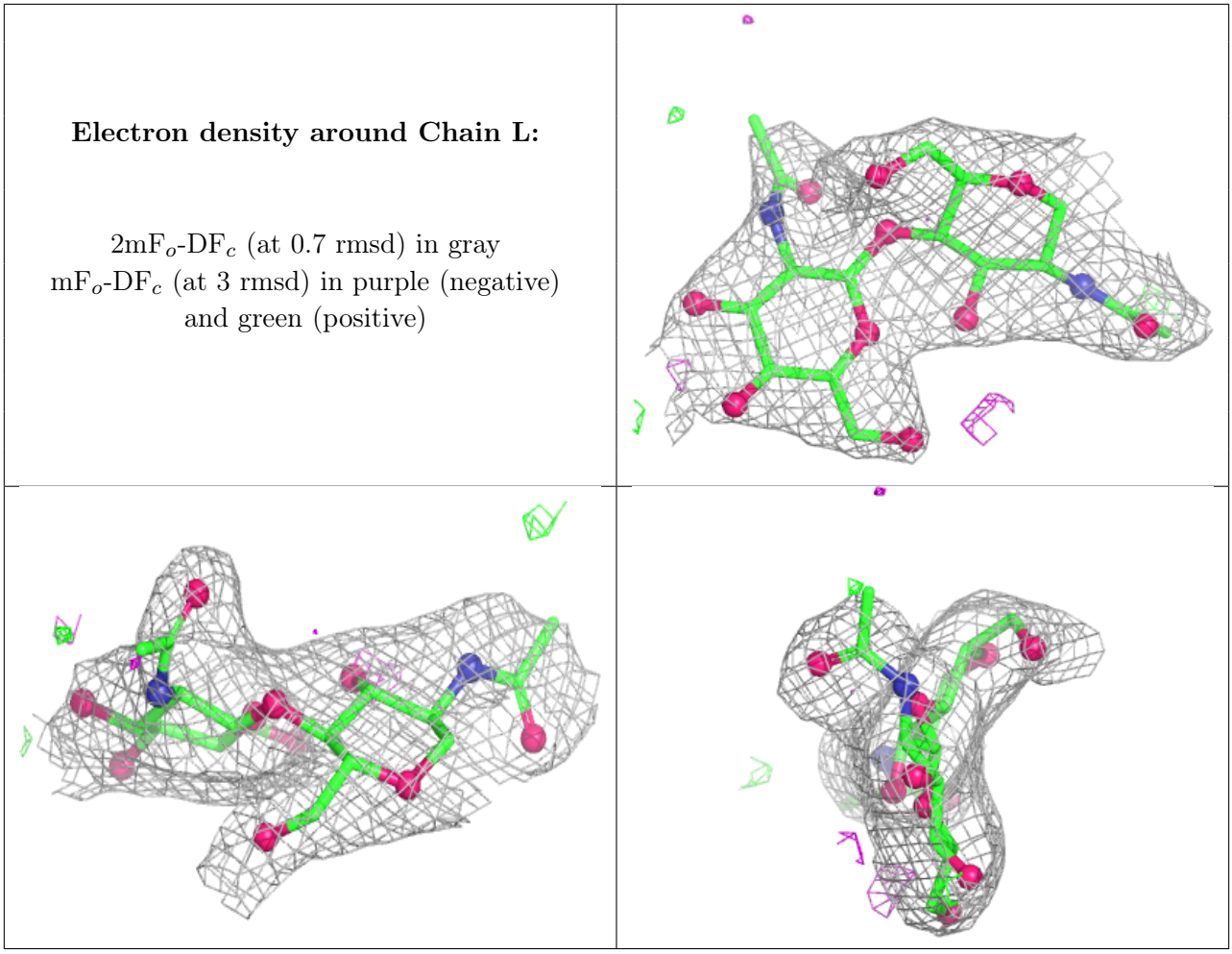
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around Chain L:

$2mF_o$-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 M:

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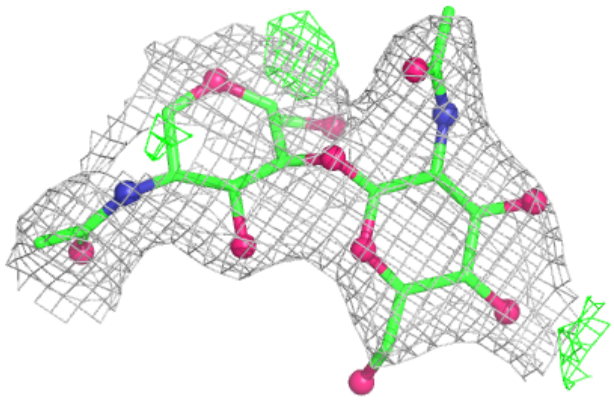
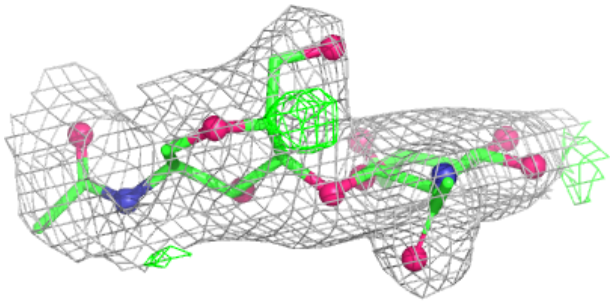
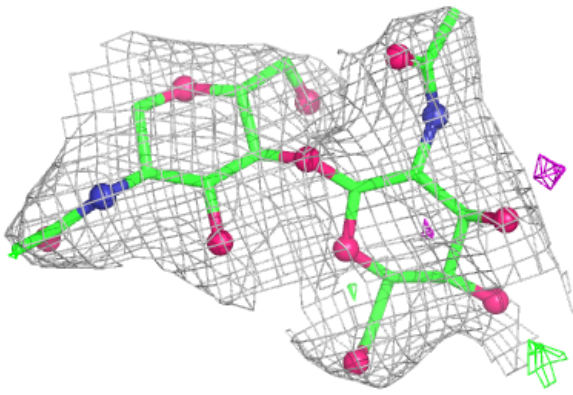
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

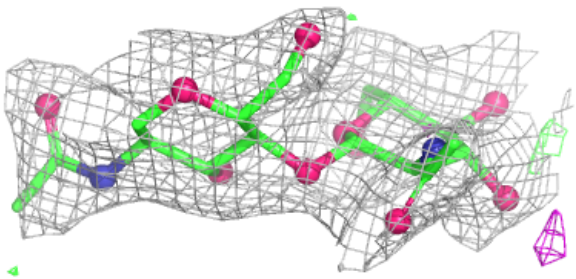


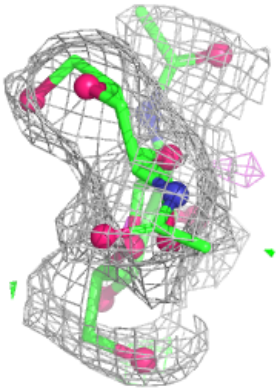


Electron density around Chain N:

$2mF_o$-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)

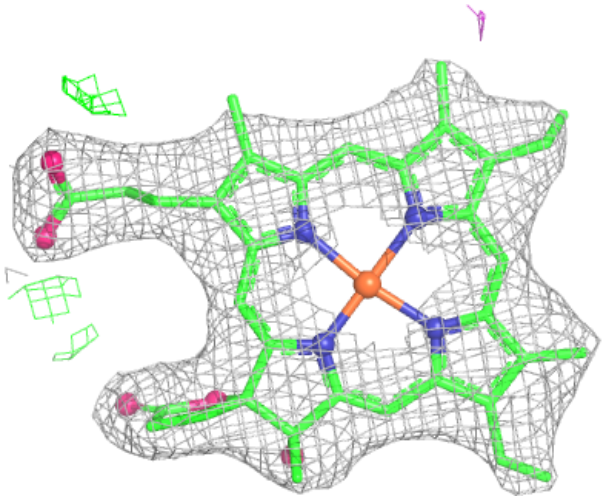
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

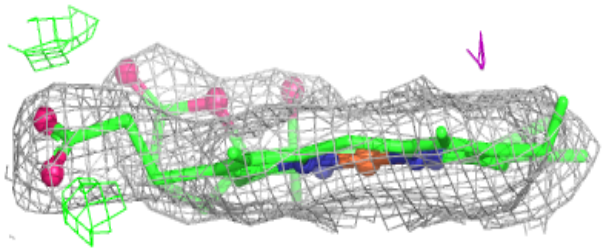
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	NAG	B	905	14/15	0.78	0.12	86,94,99,100	0
3	HDD	C	900	44/44	0.97	0.08	30,40,50,55	0
3	HDD	B	900	44/44	0.97	0.08	36,46,55,58	0
3	HDD	D	900	44/44	0.98	0.06	29,38,44,45	0
3	HDD	A	900	44/44	0.98	0.07	25,38,44,49	0
5	CA	B	910	1/1	0.99	0.07	37,37,37,37	1

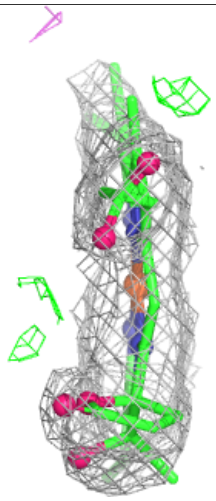
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around HDD C 900:

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

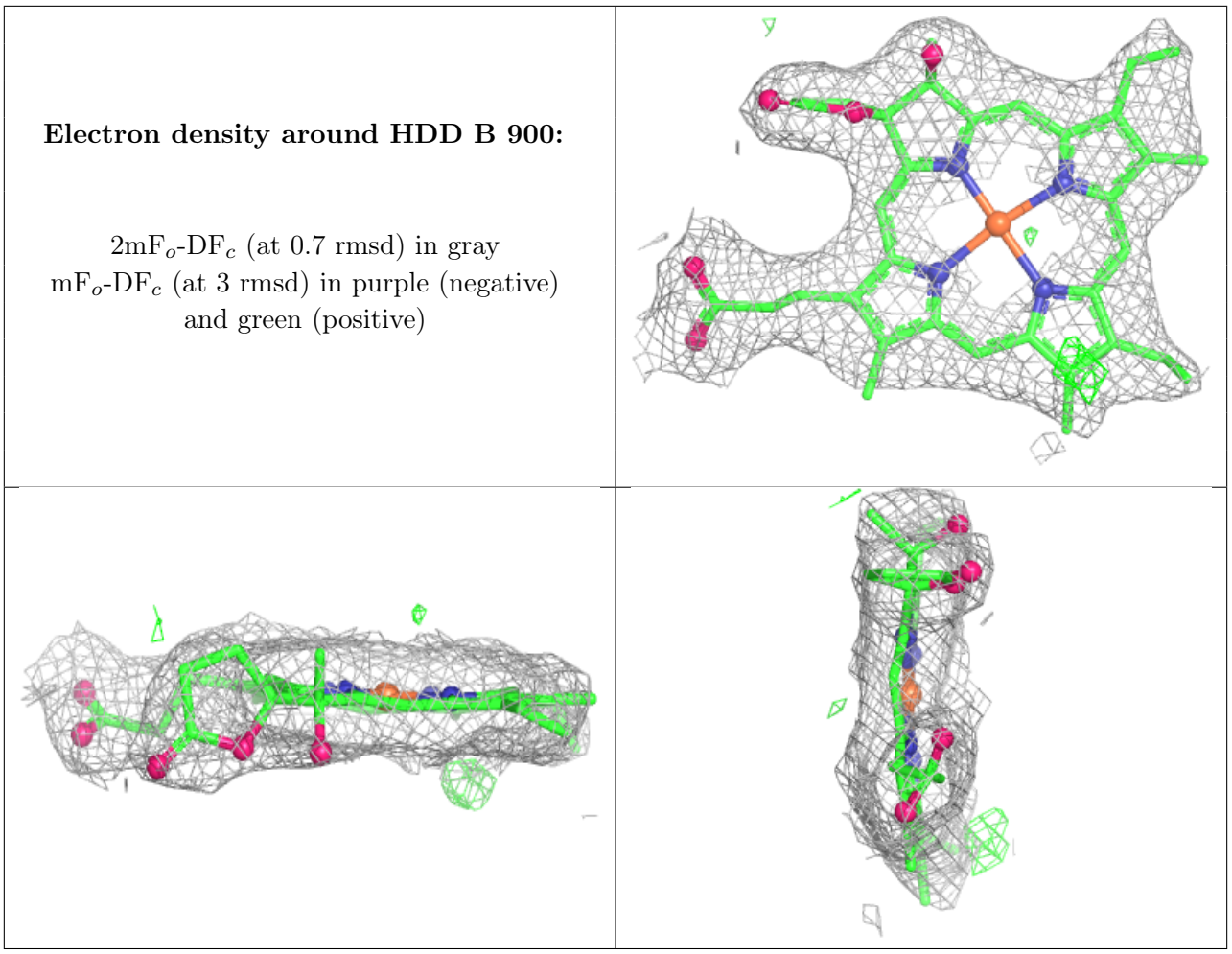






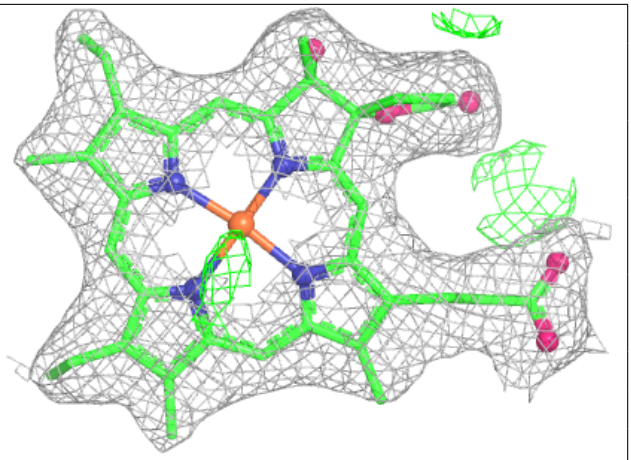
Electron density around HDD B 900:

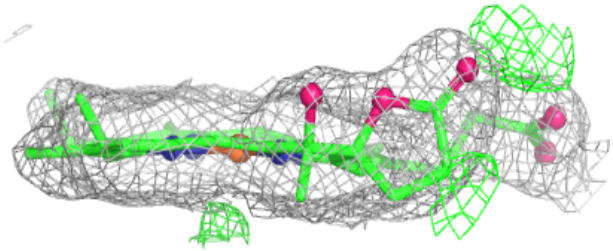
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

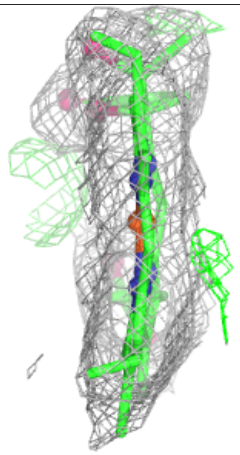


Electron density around HDD D 900:

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

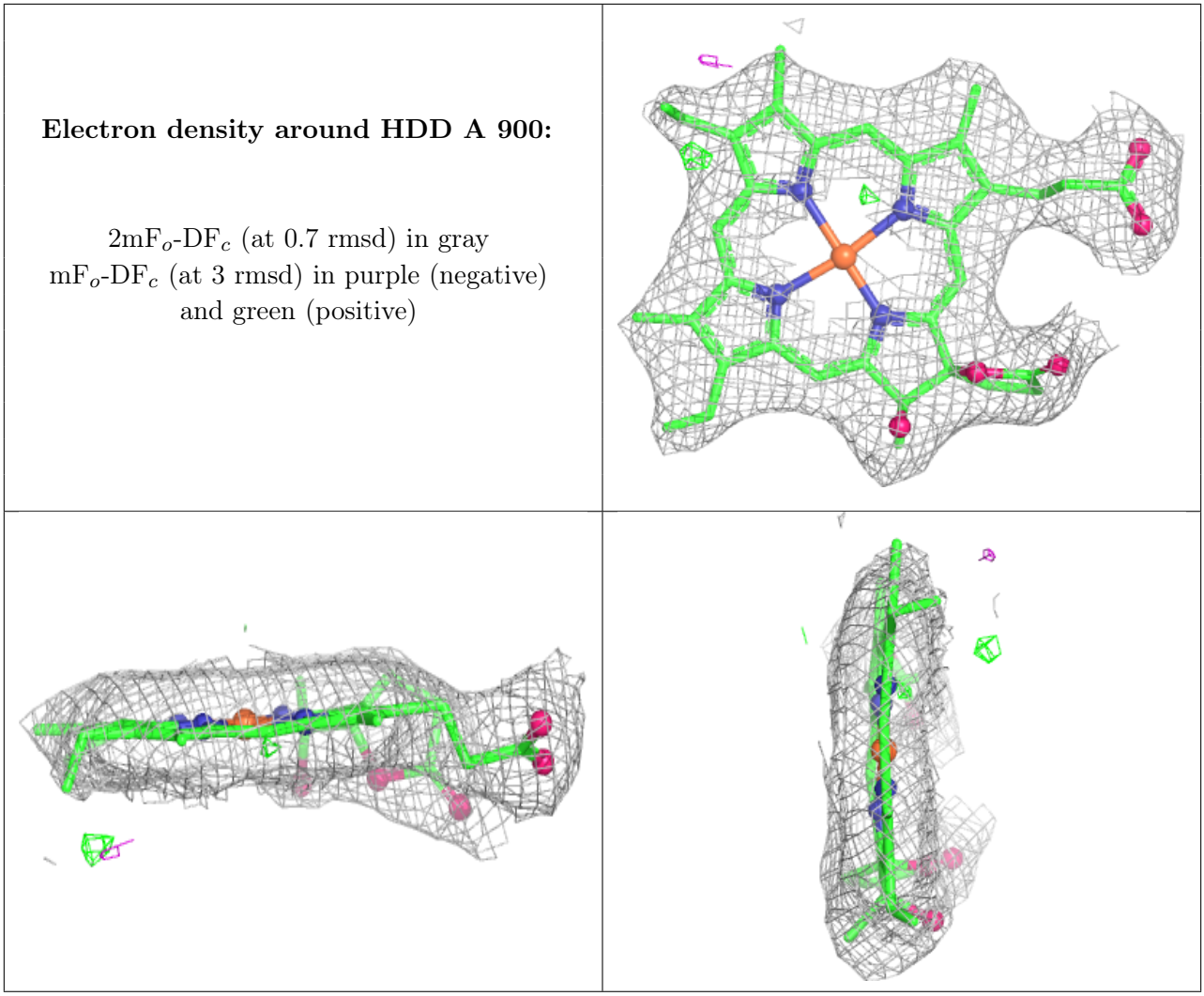






Electron density around HDD A 900:

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



6.5 Other polymers

There are no such residues in this entry.