



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 12:24 PM UTC

PDB ID : 2AGD / pdb\_00002agd  
Title : Crystal Structure of Human M340H-Beta-1,4-Galactosyltransferase-I(M340H-B4Gal-T1) in Complex with GlcNAc-beta1,4-Man-alpha1,3-Man-beta-OR  
Authors : Ramasamy, V.; Ramakrishnan, B.; Boeggeman, E.; Ratner, D.M.; Seeberger, P.H.; Qasba, P.K.  
Deposited on : 2005-07-26  
Resolution : 1.90 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) 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

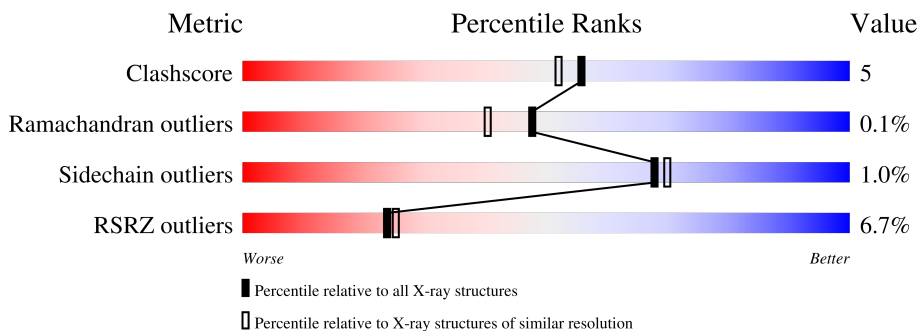
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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))
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	287	 5% 82% 12% • 5%
1	B	287	 4% 82% 13% 5%
1	C	287	 10% 77% 17% • 5%
2	D	3	 67% 33%
2	E	3	 100%
2	F	3	 100%

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 7542 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-1,4-galactosyltransferase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	273	2218	1420	386	401	11	0	0	0
1	B	273	2218	1420	386	401	11	0	0	0
1	C	273	2218	1420	386	401	11	0	0	0

There are 51 discrepancies between the modelled and reference sequences:

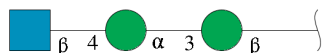
Chain	Residue	Modelled	Actual	Comment	Reference
A	112	ALA	-	SEE REMARK 999	UNP P15291
A	113	SER	-	SEE REMARK 999	UNP P15291
A	114	MET	-	SEE REMARK 999	UNP P15291
A	115	THR	-	SEE REMARK 999	UNP P15291
A	116	GLY	-	SEE REMARK 999	UNP P15291
A	117	GLY	-	SEE REMARK 999	UNP P15291
A	118	GLN	-	SEE REMARK 999	UNP P15291
A	119	GLN	-	SEE REMARK 999	UNP P15291
A	120	MET	-	SEE REMARK 999	UNP P15291
A	121	GLY	-	SEE REMARK 999	UNP P15291
A	122	ARG	-	SEE REMARK 999	UNP P15291
A	123	GLY	-	SEE REMARK 999	UNP P15291
A	124	SER	-	SEE REMARK 999	UNP P15291
A	125	ALA	-	SEE REMARK 999	UNP P15291
A	337	THR	ARG	engineered mutation	UNP P15291
A	338	THR	CYS	engineered mutation	UNP P15291
A	340	HIS	MET	engineered mutation	UNP P15291
B	112	ALA	-	SEE REMARK 999	UNP P15291
B	113	SER	-	SEE REMARK 999	UNP P15291
B	114	MET	-	SEE REMARK 999	UNP P15291
B	115	THR	-	SEE REMARK 999	UNP P15291
B	116	GLY	-	SEE REMARK 999	UNP P15291

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Chain	Residue	Modelled	Actual	Comment	Reference
B	117	GLY	-	SEE REMARK 999	UNP P15291
B	118	GLN	-	SEE REMARK 999	UNP P15291
B	119	GLN	-	SEE REMARK 999	UNP P15291
B	120	MET	-	SEE REMARK 999	UNP P15291
B	121	GLY	-	SEE REMARK 999	UNP P15291
B	122	ARG	-	SEE REMARK 999	UNP P15291
B	123	GLY	-	SEE REMARK 999	UNP P15291
B	124	SER	-	SEE REMARK 999	UNP P15291
B	125	ALA	-	SEE REMARK 999	UNP P15291
B	337	THR	ARG	engineered mutation	UNP P15291
B	338	THR	CYS	engineered mutation	UNP P15291
B	340	HIS	MET	engineered mutation	UNP P15291
C	112	ALA	-	SEE REMARK 999	UNP P15291
C	113	SER	-	SEE REMARK 999	UNP P15291
C	114	MET	-	SEE REMARK 999	UNP P15291
C	115	THR	-	SEE REMARK 999	UNP P15291
C	116	GLY	-	SEE REMARK 999	UNP P15291
C	117	GLY	-	SEE REMARK 999	UNP P15291
C	118	GLN	-	SEE REMARK 999	UNP P15291
C	119	GLN	-	SEE REMARK 999	UNP P15291
C	120	MET	-	SEE REMARK 999	UNP P15291
C	121	GLY	-	SEE REMARK 999	UNP P15291
C	122	ARG	-	SEE REMARK 999	UNP P15291
C	123	GLY	-	SEE REMARK 999	UNP P15291
C	124	SER	-	SEE REMARK 999	UNP P15291
C	125	ALA	-	SEE REMARK 999	UNP P15291
C	337	THR	ARG	engineered mutation	UNP P15291
C	338	THR	CYS	engineered mutation	UNP P15291
C	340	HIS	MET	engineered mutation	UNP P15291

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	D	3	37	20	1	16	0	0	0
2	E	3	37	20	1	16	0	0	0

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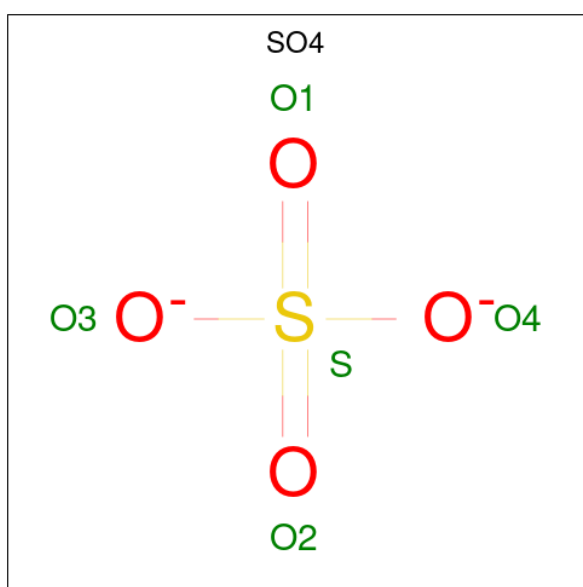
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	F	3	Total	C	N	O	0	0	0
			37	20	1	16			

- Molecule 3 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S).



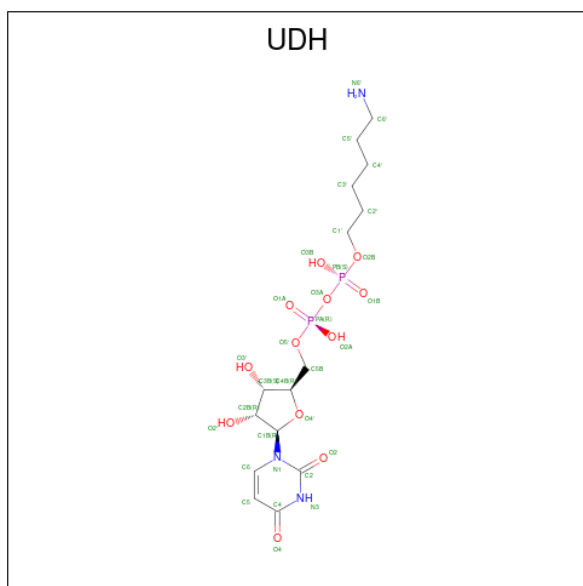
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

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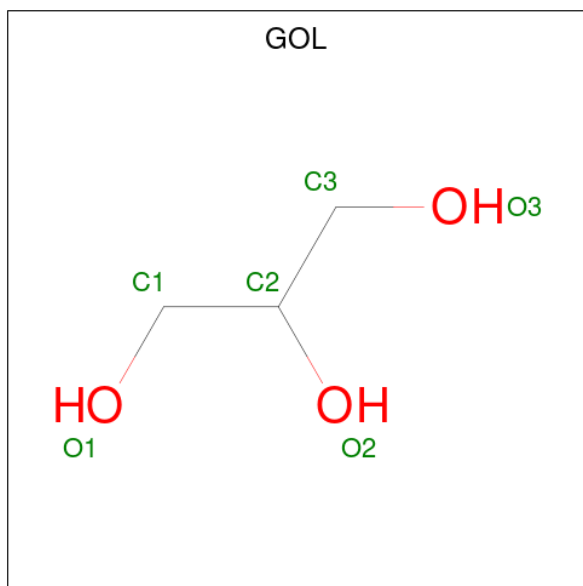
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is 6-AMINOHEXYL-URIDINE-C1,5'-DIPHOSPHATE (CCD ID: UDH) (formula:  $C_{15}H_{27}N_3O_{12}P_2$ ).



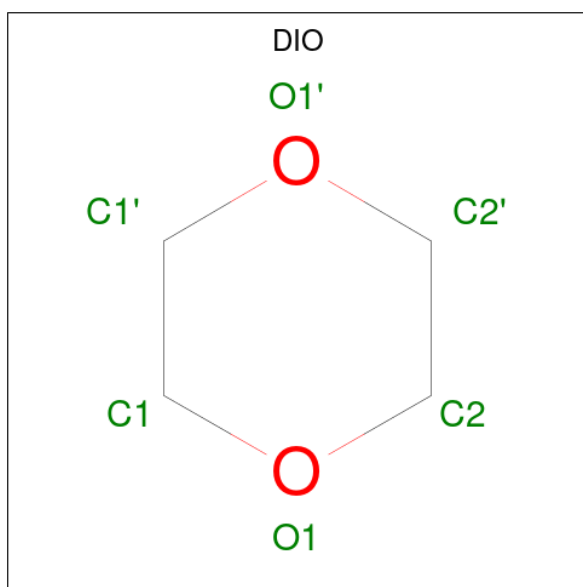
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
5	A	1	32	15	3	12	2	0	0
5	B	1	32	15	3	12	2	0	0
5	C	1	32	15	3	12	2	0	0

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



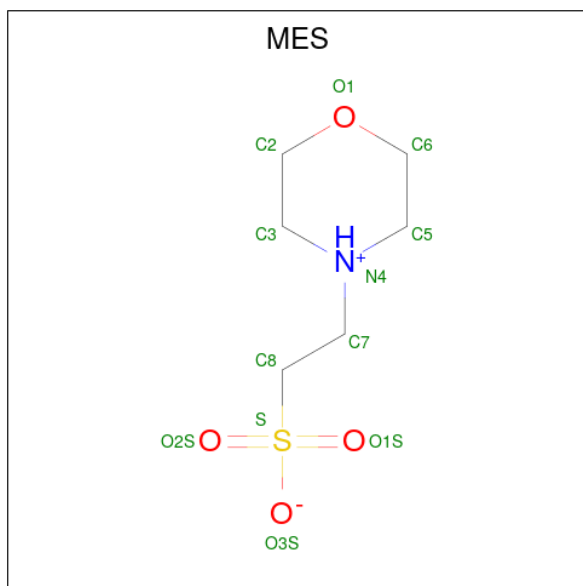
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	A	1	6	3	3	0	0
6	A	1	6	3	3	0	0
6	A	1	6	3	3	0	0
6	B	1	6	3	3	0	0
6	B	1	6	3	3	0	0
6	B	1	6	3	3	0	0
6	B	1	6	3	3	0	0
6	C	1	6	3	3	0	0

- Molecule 7 is 1,4-DIETHYLENE DIOXIDE (CCD ID: DIO) (formula: C<sub>4</sub>H<sub>8</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			6	4	2		

- Molecule 8 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula:  $C_6H_{13}NO_4S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

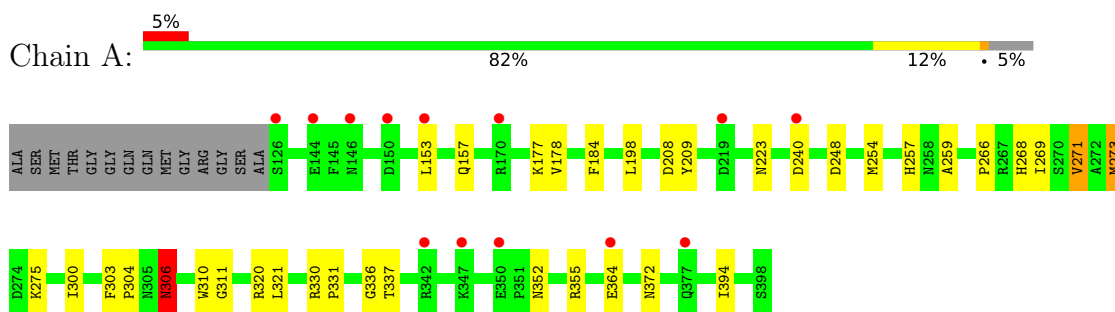
- Molecule 9 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
9	A	182	Total 182	O 182	0	0
9	B	190	Total 190	O 190	0	0
9	C	160	Total 160	O 160	0	0

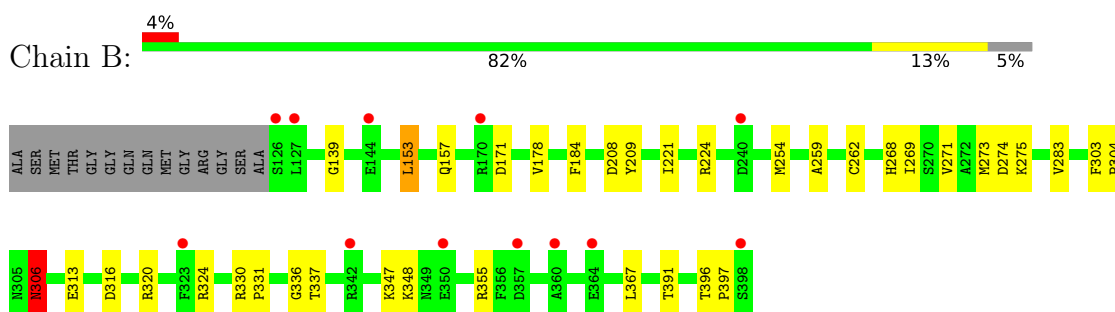
### 3 Residue-property plots [i](#)

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.

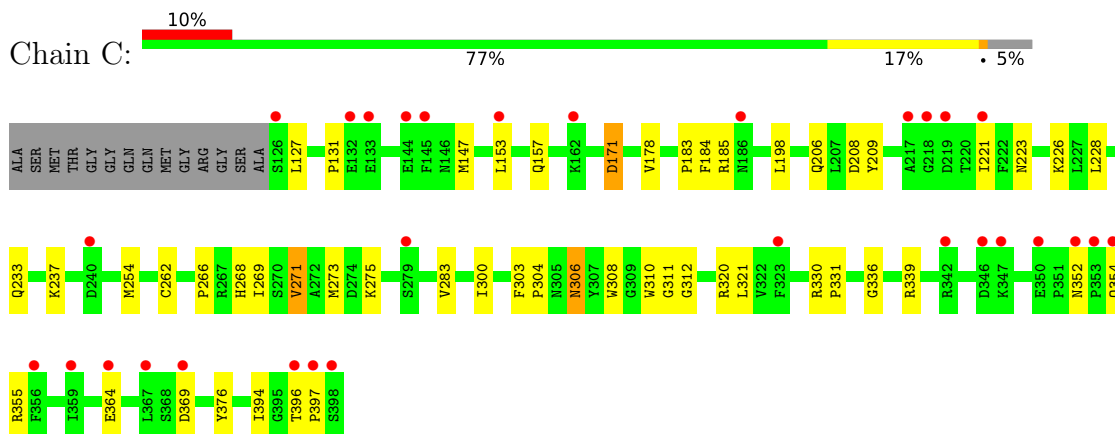
- Molecule 1: Beta-1,4-galactosyltransferase 1




- Molecule 1: Beta-1,4-galactosyltransferase 1



- Molecule 1: Beta-1,4-galactosyltransferase 1




- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose

Chain D:  67% 33%


BM11  
MAN2  
MAG3

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose

Chain E:  100%

BM11  
MAN2  
MAG3

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose

Chain F:  100%

BM11  
MAN2  
MAG3

## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.46Å 194.78Å 143.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 1.90 40.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (40.00-1.90) 99.9 (40.00-1.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.25 (at 1.89Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.202 , 0.228 0.196 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.7	Xtrriage
Anisotropy	0.657	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 40.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	0.000 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.013 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7542	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, SO4, GOL, MN, UDH, MES, MAN, BMA, DIO

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	0.53	1/2280 (0.0%)	1.00	13/3097 (0.4%)
1	B	0.55	0/2280	1.01	18/3097 (0.6%)
1	C	0.48	0/2280	1.00	17/3097 (0.5%)
All	All	0.52	1/6840 (0.0%)	1.00	48/9291 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	273	MET	SD-CE	-5.68	1.65	1.79

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	311	GLY	N-CA-C	9.95	124.52	112.48
1	B	178	VAL	N-CA-C	9.19	121.04	108.17
1	A	178	VAL	N-CA-C	8.00	119.37	108.17
1	C	127	LEU	N-CA-C	7.70	118.45	109.60
1	C	178	VAL	N-CA-C	6.92	117.86	108.17

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	2218	0	2162	19	0
1	B	2218	0	2162	21	0
1	C	2218	0	2162	25	0
2	D	37	0	33	1	0
2	E	37	0	33	0	0
2	F	37	0	33	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	20	0	0	0	0
4	B	35	0	0	0	0
4	C	25	0	0	0	0
5	A	32	0	25	0	0
5	B	32	0	25	0	0
5	C	32	0	25	0	0
6	A	18	0	24	1	0
6	B	24	0	32	3	0
6	C	6	0	8	0	0
7	C	6	0	8	2	0
8	C	12	0	13	3	0
9	A	182	0	0	1	0
9	B	190	0	0	1	0
9	C	160	0	0	0	0
All	All	7542	0	6745	65	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 5.

The worst 5 of 65 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:A:153:LEU:HG	1:A:157:GLN:HE21	1.32	0.93
1:A:273:MET:HE1	1:A:275:LYS:HE2	1.50	0.93
1:C:273:MET:HE1	1:C:275:LYS:HE2	1.61	0.83
1:B:324:ARG:NH1	1:B:367:LEU:HD21	2.01	0.75
1:B:324:ARG:HH11	1:B:367:LEU:HD21	1.52	0.74

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	271/287 (94%)	263 (97%)	8 (3%)	0	100	100
1	B	271/287 (94%)	266 (98%)	5 (2%)	0	100	100
1	C	271/287 (94%)	264 (97%)	6 (2%)	1 (0%)	30	22
All	All	813/861 (94%)	793 (98%)	19 (2%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	185	ARG

### 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	244/252 (97%)	242 (99%)	2 (1%)	73	75
1	B	244/252 (97%)	242 (99%)	2 (1%)	73	75
1	C	244/252 (97%)	241 (99%)	3 (1%)	63	63
All	All	732/756 (97%)	725 (99%)	7 (1%)	68	70

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	306	ASN
1	C	147	MET

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Mol	Chain	Res	Type
1	C	364	GLU
1	C	233	GLN
1	B	153	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	160	ASN
1	B	186	ASN
1	C	257	HIS
1	B	389	GLN
1	C	215	ASN

### 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](#)

9 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	BMA	D	1	2	12,12,12	2.03	4 (33%)	17,17,17	0.57	0
2	MAN	D	2	2	11,11,12	2.48	5 (45%)	15,15,17	1.34	2 (13%)
2	NAG	D	3	2	14,14,15	1.76	3 (21%)	17,19,21	0.88	1 (5%)
2	BMA	E	1	2	12,12,12	1.98	4 (33%)	17,17,17	0.71	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	MAN	E	2	2	11,11,12	2.46	5 (45%)	15,15,17	1.27	2 (13%)
2	NAG	E	3	2	14,14,15	1.70	3 (21%)	17,19,21	0.82	0
2	BMA	F	1	2	12,12,12	1.92	4 (33%)	17,17,17	0.53	0
2	MAN	F	2	2	11,11,12	2.43	5 (45%)	15,15,17	1.32	2 (13%)
2	NAG	F	3	2	14,14,15	1.84	3 (21%)	17,19,21	0.88	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	BMA	D	1	2	-	1/2/22/22	0/1/1/1
2	MAN	D	2	2	-	0/2/19/22	0/1/1/1
2	NAG	D	3	2	-	0/6/23/26	0/1/1/1
2	BMA	E	1	2	-	1/2/22/22	0/1/1/1
2	MAN	E	2	2	-	0/2/19/22	0/1/1/1
2	NAG	E	3	2	-	0/6/23/26	0/1/1/1
2	BMA	F	1	2	-	1/2/22/22	0/1/1/1
2	MAN	F	2	2	-	0/2/19/22	0/1/1/1
2	NAG	F	3	2	-	0/6/23/26	0/1/1/1

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	MAN	O5-C1	4.61	1.51	1.43
2	F	2	MAN	O5-C1	4.52	1.51	1.43
2	E	2	MAN	O5-C5	4.44	1.52	1.43
2	E	2	MAN	O5-C1	4.37	1.51	1.43
2	D	2	MAN	O5-C5	4.24	1.51	1.43

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	2	MAN	C1-O5-C5	3.21	116.49	112.19
2	D	2	MAN	C1-O5-C5	3.09	116.33	112.19
2	E	2	MAN	C1-O5-C5	2.85	116.01	112.19
2	D	2	MAN	O4-C4-C3	2.47	116.19	110.38
2	F	2	MAN	O4-C4-C3	2.35	115.91	110.38

There are no chirality outliers.

All (3) torsion outliers are listed below:

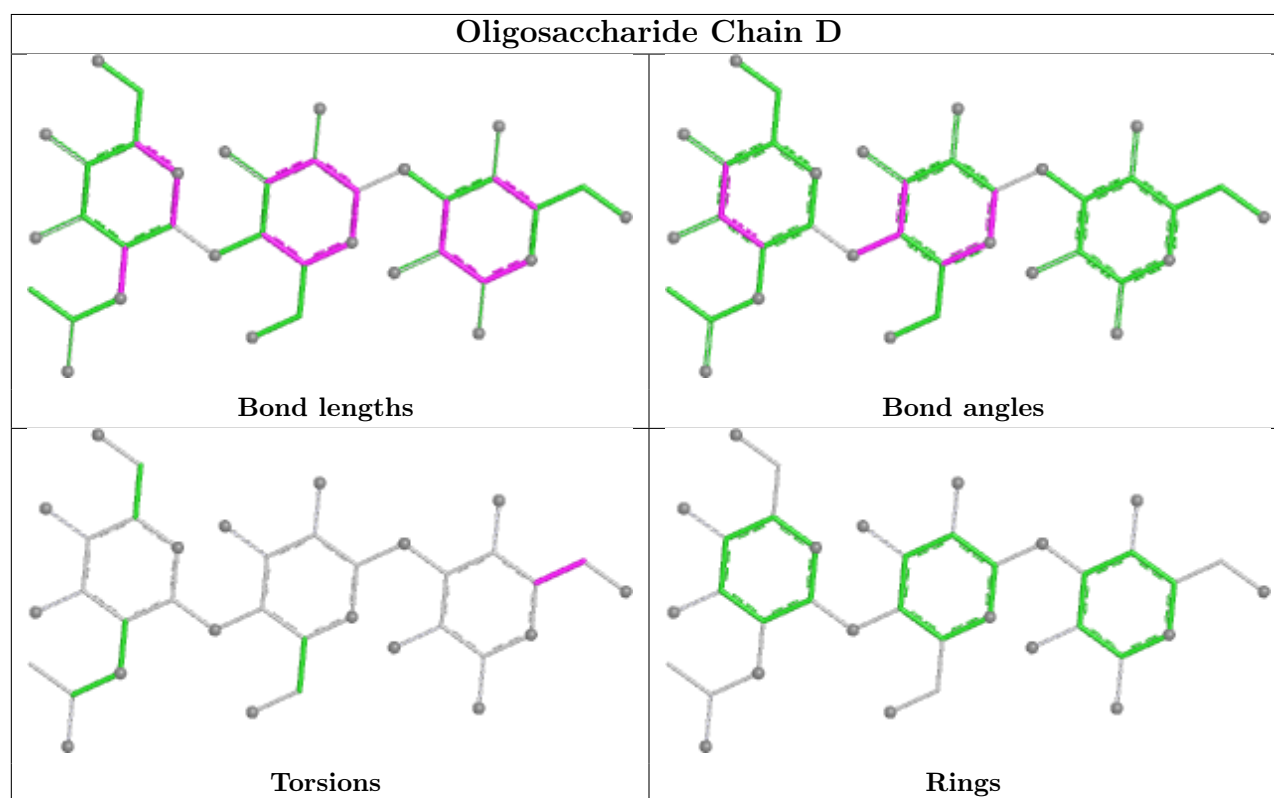
Mol	Chain	Res	Type	Atoms
2	D	1	BMA	O5-C5-C6-O6
2	E	1	BMA	O5-C5-C6-O6
2	F	1	BMA	O5-C5-C6-O6

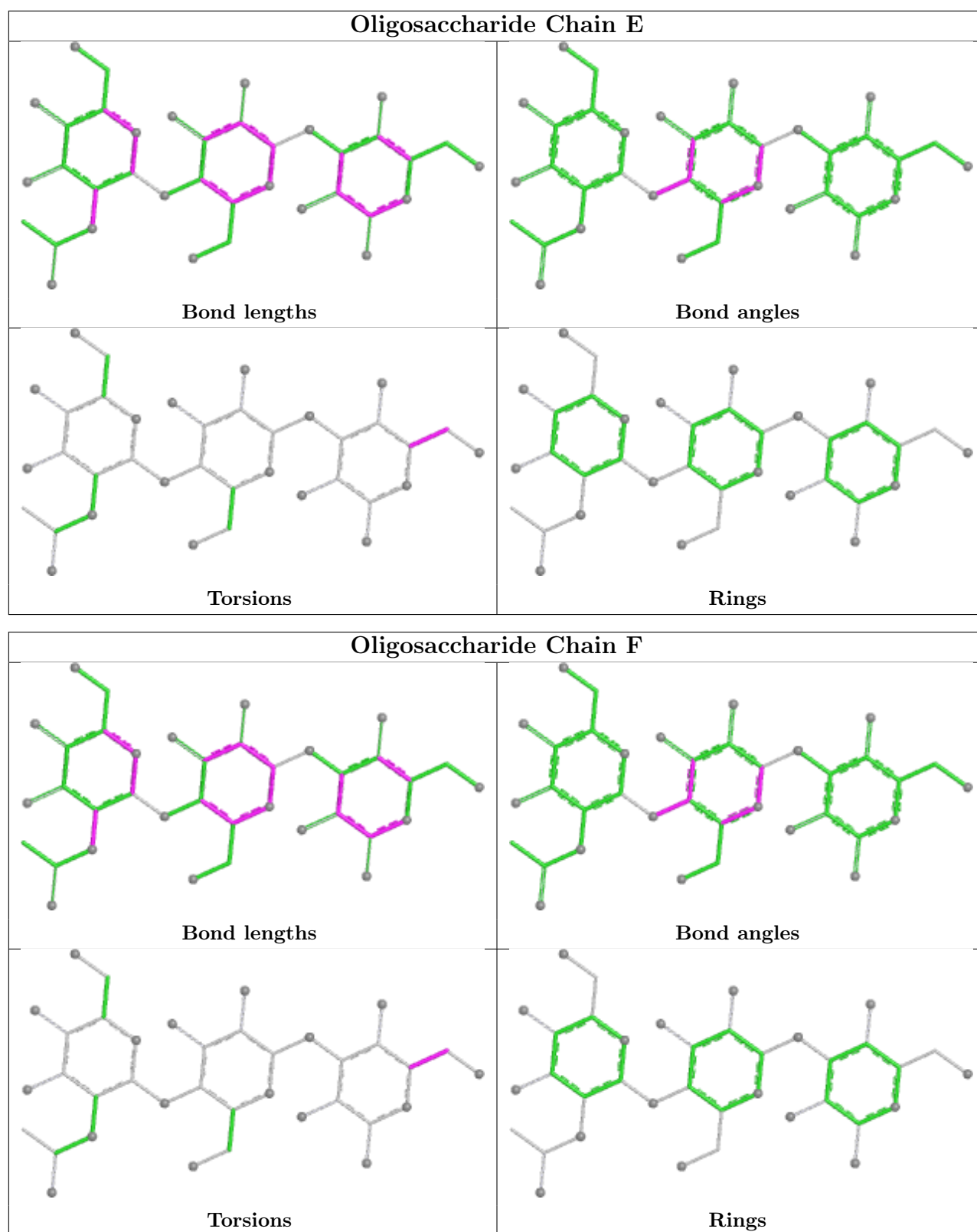
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	3	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.





## 5.6 Ligand geometry [i](#)

Of 32 ligands modelled in this entry, 3 are monoatomic - leaving 29 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
6	GOL	A	417	-	5,5,5	0.26	0	5,5,5	0.67	0
6	GOL	A	421	-	5,5,5	0.39	0	5,5,5	0.63	0
5	UDH	A	399	3	33,33,33	1.68	5 (15%)	44,47,47	1.46	9 (20%)
6	GOL	A	420	-	5,5,5	0.40	0	5,5,5	0.59	0
6	GOL	B	415	-	5,5,5	0.30	0	5,5,5	0.62	0
6	GOL	C	418	-	5,5,5	0.34	0	5,5,5	0.69	0
4	SO4	A	424	-	4,4,4	1.83	2 (50%)	6,6,6	0.82	0
4	SO4	C	431	-	4,4,4	1.88	2 (50%)	6,6,6	0.84	0
6	GOL	B	414	-	5,5,5	0.56	0	5,5,5	0.92	0
4	SO4	B	434	-	4,4,4	1.84	2 (50%)	6,6,6	0.85	0
6	GOL	B	419	-	5,5,5	0.40	0	5,5,5	0.59	0
4	SO4	C	427	-	4,4,4	1.80	1 (25%)	6,6,6	0.85	0
4	SO4	B	437	-	4,4,4	1.87	2 (50%)	6,6,6	0.83	0
4	SO4	B	429	-	4,4,4	1.79	1 (25%)	6,6,6	0.79	0
4	SO4	A	433	-	4,4,4	1.85	2 (50%)	6,6,6	0.82	0
5	UDH	C	403	3	33,33,33	1.52	4 (12%)	44,47,47	1.44	7 (15%)
4	SO4	B	432	-	4,4,4	1.85	2 (50%)	6,6,6	0.83	0
4	SO4	C	430	-	4,4,4	1.82	2 (50%)	6,6,6	0.83	0
7	DIO	C	438	-	6,6,6	0.95	0	6,6,6	0.73	0
4	SO4	C	435	-	4,4,4	1.87	2 (50%)	6,6,6	0.82	0
4	SO4	B	428	-	4,4,4	1.78	2 (50%)	6,6,6	0.87	0
4	SO4	B	425	-	4,4,4	1.85	2 (50%)	6,6,6	0.83	0
4	SO4	A	423	-	4,4,4	1.79	2 (50%)	6,6,6	0.82	0
4	SO4	A	422	-	4,4,4	1.85	2 (50%)	6,6,6	0.84	0
6	GOL	B	416	-	5,5,5	0.45	0	5,5,5	0.50	0
5	UDH	B	401	3	33,33,33	1.61	5 (15%)	44,47,47	1.40	8 (18%)
4	SO4	B	426	-	4,4,4	1.86	2 (50%)	6,6,6	0.83	0
4	SO4	C	436	-	4,4,4	1.87	2 (50%)	6,6,6	0.81	0
8	MES	C	439	-	12,12,12	1.52	3 (25%)	15,16,16	0.67	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
6	GOL	C	418	-	-	0/4/4/4	-
6	GOL	A	417	-	-	2/4/4/4	-
6	GOL	A	421	-	-	4/4/4/4	-
5	UDH	A	399	3	-	4/25/41/41	0/2/2/2
6	GOL	B	416	-	-	2/4/4/4	-
5	UDH	C	403	3	-	3/25/41/41	0/2/2/2
6	GOL	B	414	-	-	2/4/4/4	-
5	UDH	B	401	3	-	4/25/41/41	0/2/2/2
6	GOL	A	420	-	-	2/4/4/4	-
6	GOL	B	415	-	-	2/4/4/4	-
7	DIO	C	438	-	-	-	0/1/1/1
6	GOL	B	419	-	-	2/4/4/4	-
8	MES	C	439	-	-	2/6/14/14	0/1/1/1

The worst 5 of 47 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	399	UDH	PA-O3A	7.18	1.67	1.59
5	B	401	UDH	PA-O3A	6.37	1.66	1.59
5	C	403	UDH	PA-O3A	6.15	1.66	1.59
4	B	437	SO4	O1-S	3.13	1.63	1.44
4	C	431	SO4	O1-S	3.09	1.63	1.44

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	399	UDH	O3A-PB-O1B	-3.56	100.00	110.70
5	C	403	UDH	O3A-PB-O1B	-3.56	100.00	110.70
5	B	401	UDH	O4'-C4B-C3B	-3.37	98.47	105.15
5	A	399	UDH	O4'-C4B-C3B	-3.33	98.55	105.15
5	B	401	UDH	O3A-PB-O1B	-3.24	100.96	110.70

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

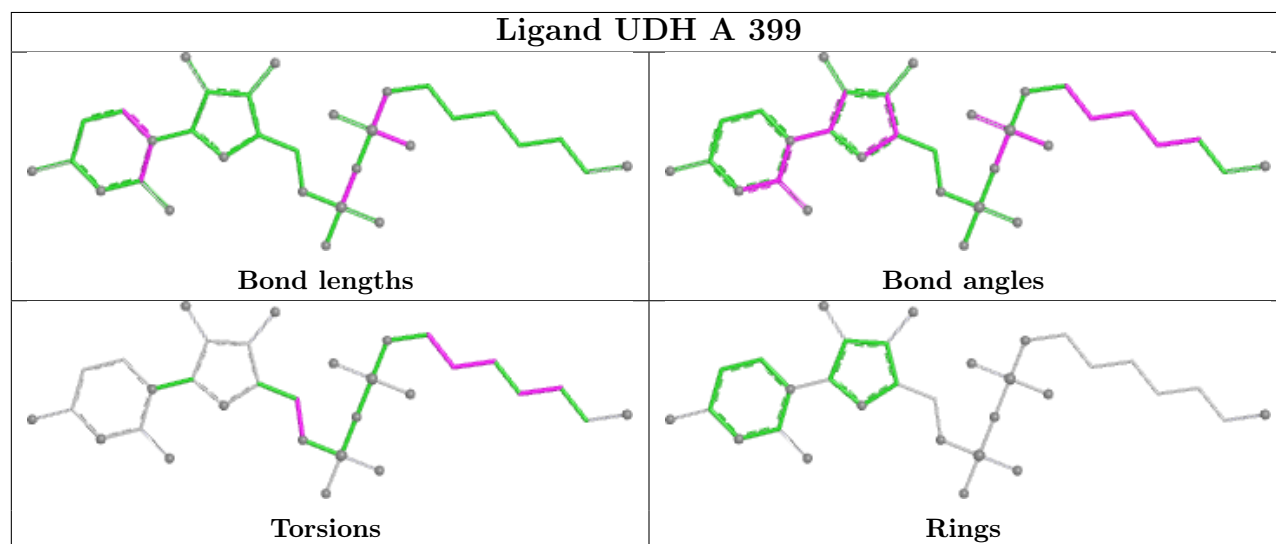
Mol	Chain	Res	Type	Atoms
6	A	421	GOL	C1-C2-C3-O3
6	A	421	GOL	O2-C2-C3-O3
6	B	419	GOL	O2-C2-C3-O3
6	A	417	GOL	O1-C1-C2-C3
6	A	420	GOL	O1-C1-C2-C3

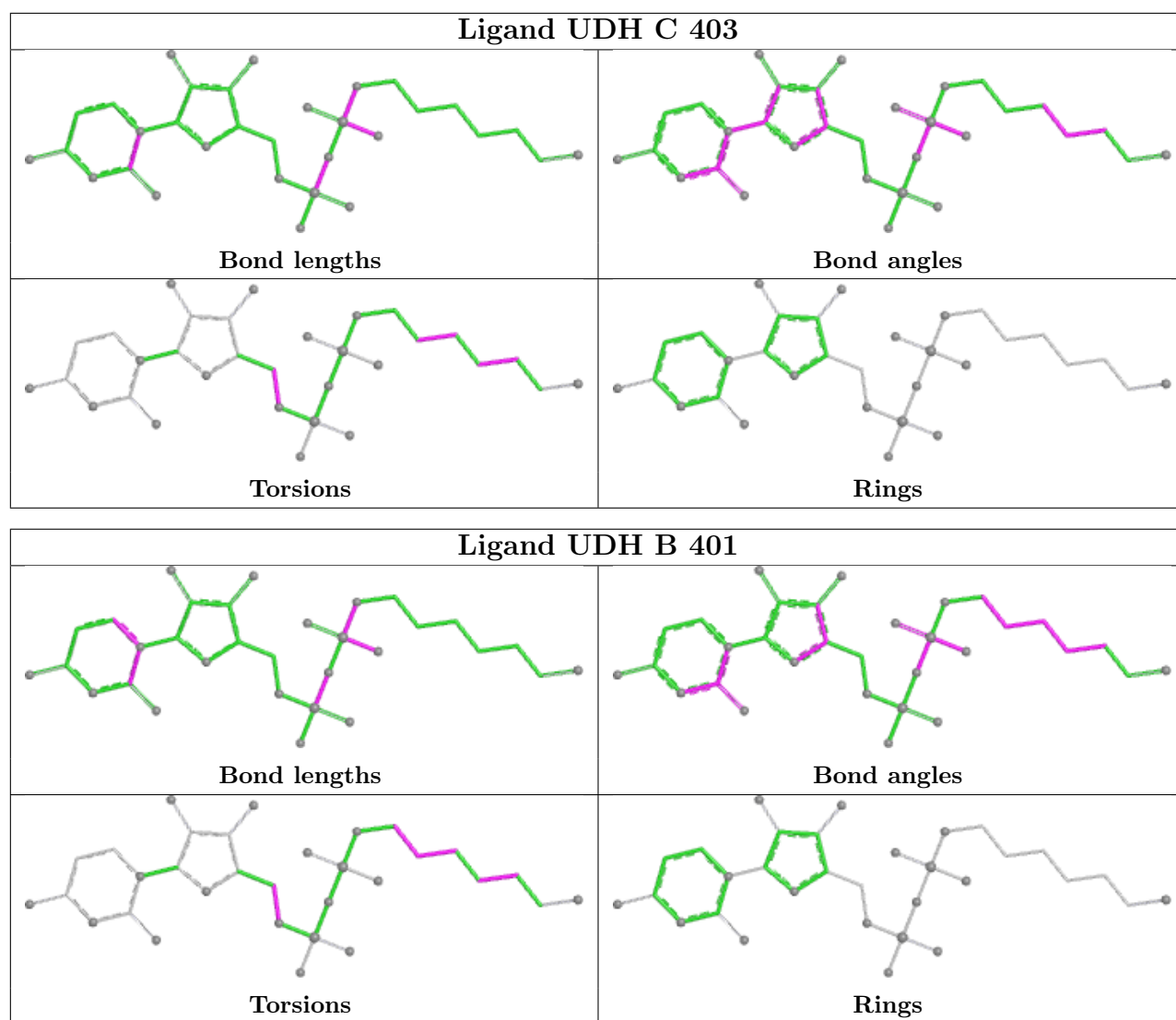
There are no ring outliers.

5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	417	GOL	1	0
6	B	414	GOL	2	0
6	B	419	GOL	1	0
7	C	438	DIO	2	0
8	C	439	MES	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 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	273/287 (95%)	0.32	13 (4%) 35 38	17, 25, 42, 50	0
1	B	273/287 (95%)	0.03	12 (4%) 39 41	15, 22, 36, 51	0
1	C	273/287 (95%)	0.73	30 (10%) 10 11	20, 29, 47, 58	0
All	All	819/861 (95%)	0.36	55 (6%) 24 25	15, 25, 43, 58	0

The worst 5 of 55 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	126	SER	5.1
1	C	398	SER	4.3
1	C	126	SER	4.1
1	A	126	SER	3.8
1	C	240	ASP	3.6

### 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<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

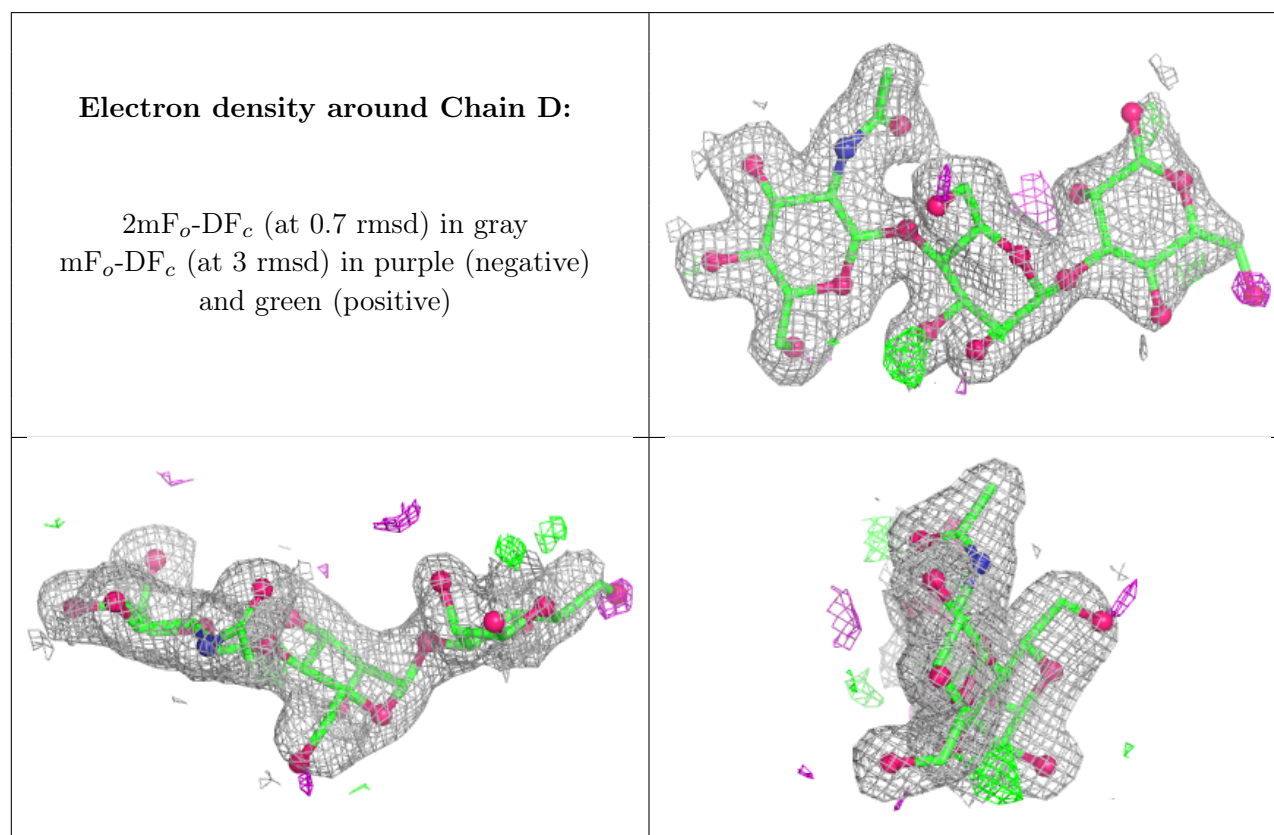
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	BMA	F	1	12/12	0.62	0.21	60,67,69,71	0
2	BMA	D	1	12/12	0.67	0.19	54,62,64,67	0
2	BMA	E	1	12/12	0.71	0.18	46,53,55,57	0

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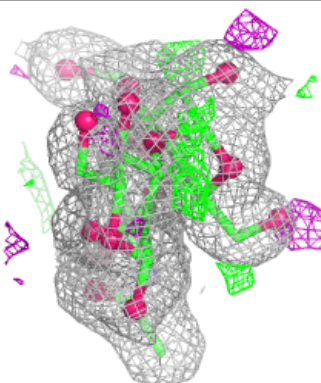
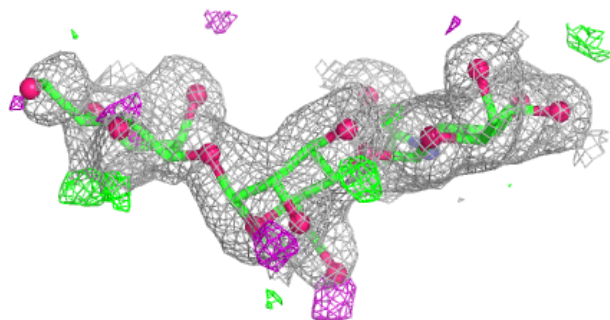
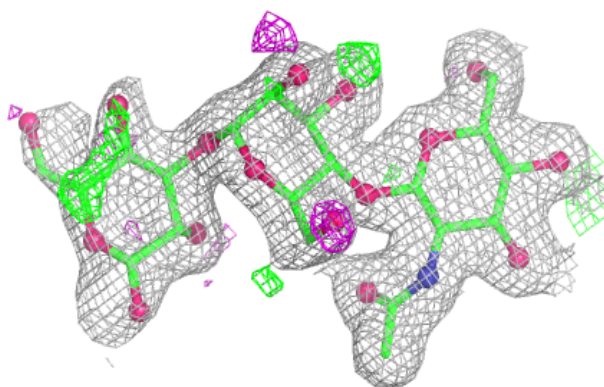
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MAN	D	2	11/12	0.86	0.13	36,45,49,51	0
2	MAN	F	2	11/12	0.87	0.13	46,53,56,56	0
2	MAN	E	2	11/12	0.88	0.12	30,37,40,43	0
2	NAG	F	3	14/15	0.90	0.12	35,39,40,42	0
2	NAG	E	3	14/15	0.96	0.07	19,23,24,25	0
2	NAG	D	3	14/15	0.96	0.07	22,28,29,30	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.

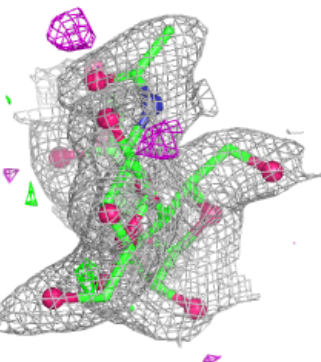
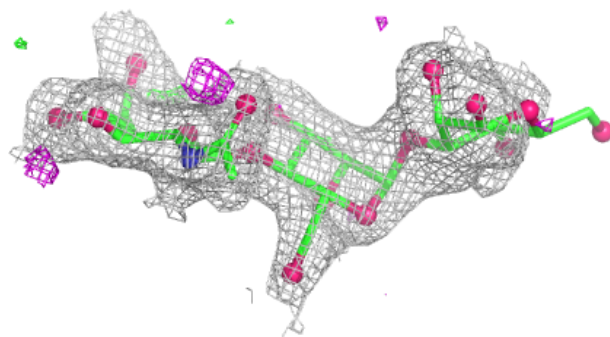
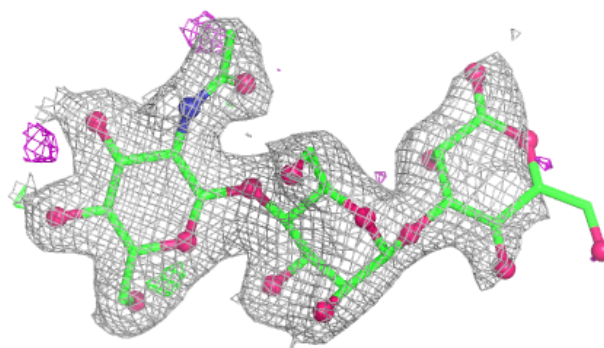


**Electron density around Chain E:**

$2mF_o-DF_c$  (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)



## 6.4 Ligands [i](#)

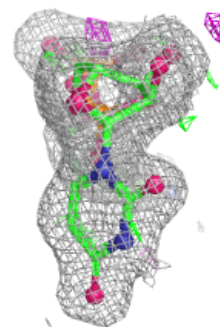
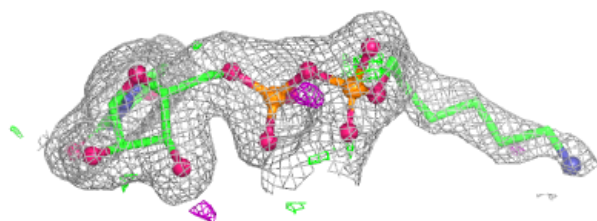
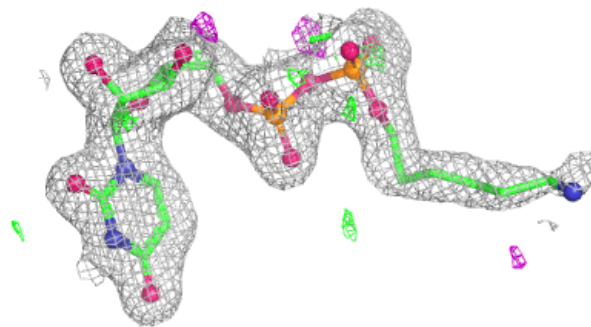
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
8	MES	C	439	12/12	0.62	0.27	57,60,69,70	0
7	DIO	C	438	6/6	0.67	0.33	67,67,67,68	0
4	SO4	C	435	5/5	0.67	0.19	86,86,87,87	0
4	SO4	A	424	5/5	0.71	0.18	79,79,80,80	0
4	SO4	B	425	5/5	0.73	0.18	72,73,73,74	0
4	SO4	C	436	5/5	0.73	0.15	92,92,93,93	0
6	GOL	A	421	6/6	0.74	0.26	58,61,61,61	0
6	GOL	B	415	6/6	0.76	0.22	36,41,43,48	0
4	SO4	C	431	5/5	0.77	0.13	93,93,93,94	0
4	SO4	B	437	5/5	0.79	0.14	80,81,81,81	0
4	SO4	B	426	5/5	0.81	0.15	88,88,88,89	0
6	GOL	B	419	6/6	0.82	0.22	49,51,52,54	0
6	GOL	A	420	6/6	0.83	0.16	39,48,49,50	0
4	SO4	A	433	5/5	0.83	0.12	88,88,88,88	0
4	SO4	B	429	5/5	0.84	0.17	55,58,58,59	0
4	SO4	B	434	5/5	0.84	0.16	67,68,69,70	0
4	SO4	A	423	5/5	0.85	0.14	54,57,57,57	0
6	GOL	B	414	6/6	0.87	0.15	24,32,33,39	0
4	SO4	A	422	5/5	0.88	0.14	73,73,74,74	0
6	GOL	C	418	6/6	0.88	0.15	35,37,38,41	0
4	SO4	C	430	5/5	0.89	0.15	76,76,76,76	0
4	SO4	B	428	5/5	0.89	0.15	69,69,70,71	0
6	GOL	A	417	6/6	0.90	0.13	27,33,36,38	0
4	SO4	B	432	5/5	0.90	0.10	77,77,78,78	0
4	SO4	C	427	5/5	0.90	0.18	44,46,47,47	0
5	UDH	C	403	32/32	0.96	0.09	26,30,51,55	0
5	UDH	A	399	32/32	0.97	0.08	22,26,47,51	0
6	GOL	B	416	6/6	0.97	0.06	20,21,22,25	0
5	UDH	B	401	32/32	0.98	0.08	15,19,49,52	0
3	MN	C	404	1/1	0.98	0.04	30,30,30,30	0
3	MN	B	402	1/1	0.99	0.02	20,20,20,20	0
3	MN	A	400	1/1	1.00	0.02	27,27,27,27	0

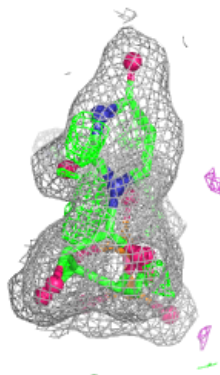
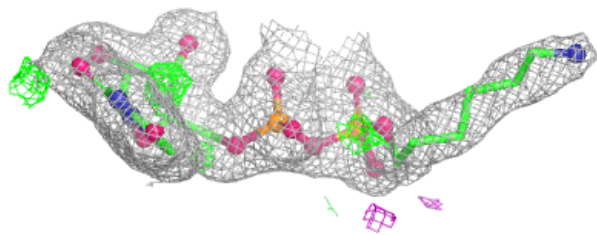
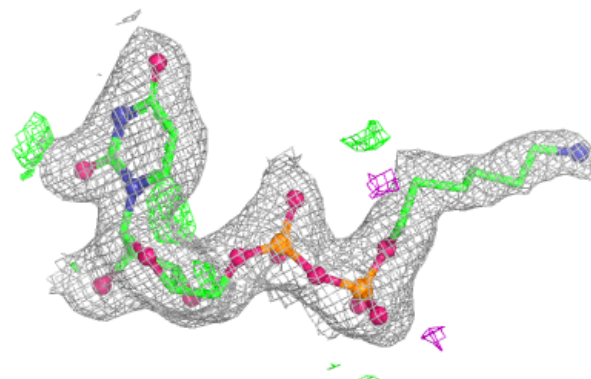
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

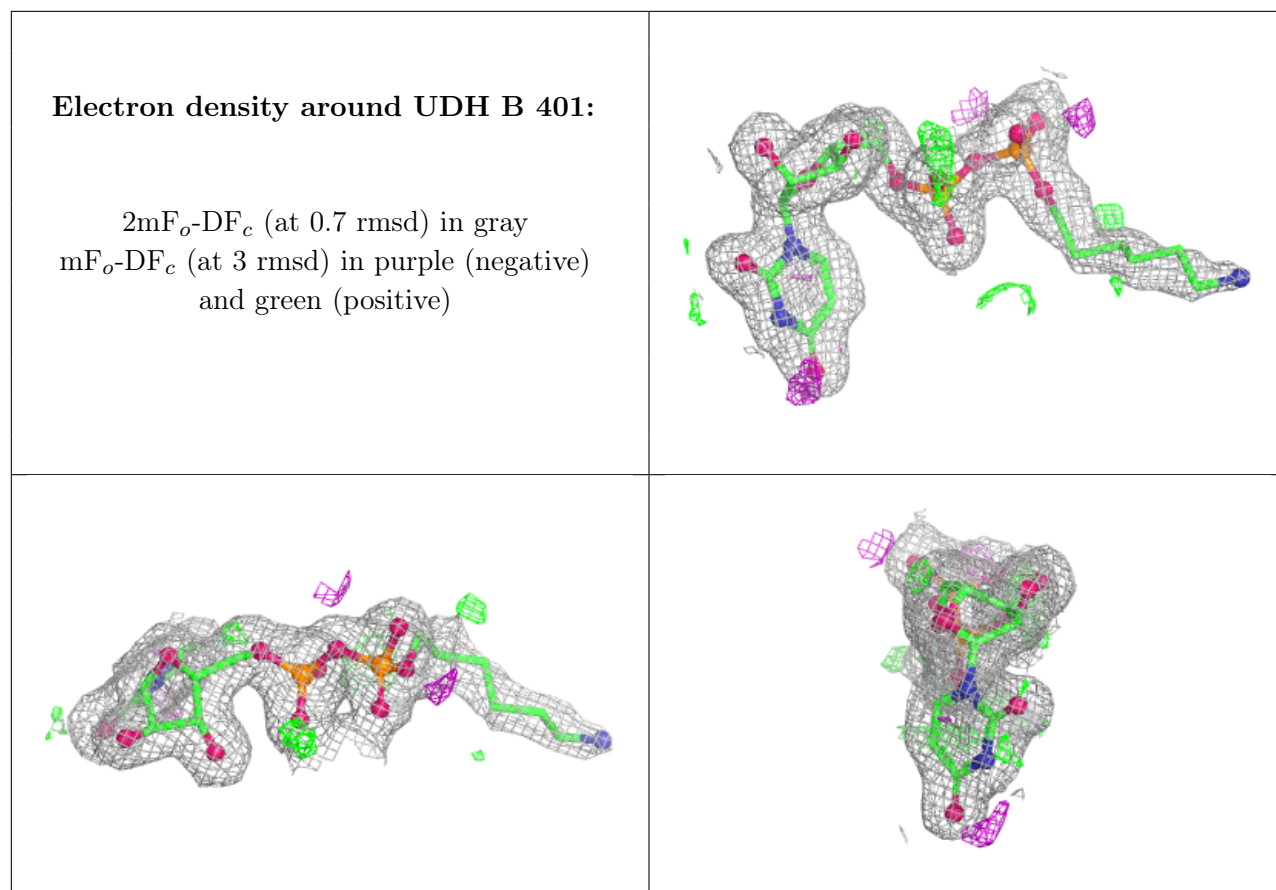
**Electron density around UDH C 403:**

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

**Electron density around UDH A 399:**

$2mF_o-DF_c$  (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.