



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 04:26 PM UTC

PDB ID : 5KOR / pdb_00005kor
Title : Arabidopsis thaliana fucosyltransferase 1 (FUT1) in complex with GDP and a xylo-oligosaccharide
Authors : Rocha, J.; de Sanctis, D.; Breton, C.
Deposited on : 2016-07-01
Resolution : 2.20 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 ⓘ 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	:	4-5-2 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

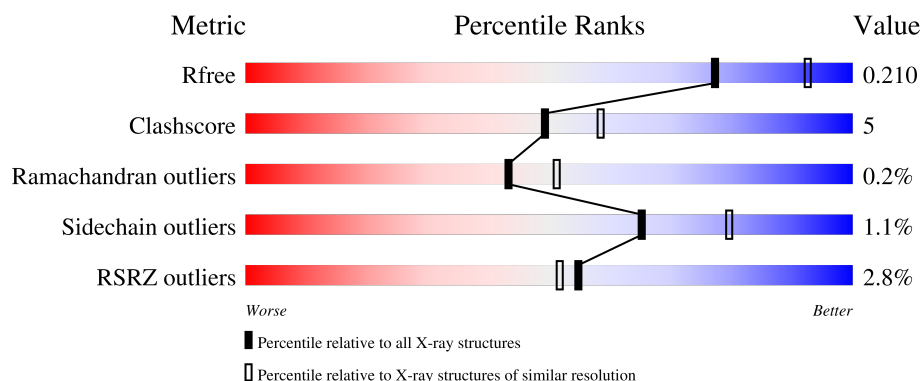
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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

Mol	Chain	Length	Quality of chain
1	A	521	 3% 75% 11% 14%
1	B	521	 2% 77% 8% 14%
1	C	521	 2% 76% 10% 14%
1	D	521	 2% 74% 12% 13%
2	E	9	 11% 89%

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Mol	Chain	Length	Quality of chain
2	F	9	 100%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 15538 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 Galactoside 2-alpha-L-fucosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	450	Total	C	N	O	S	0	2	0
			3638	2345	601	669	23			
1	B	450	Total	C	N	O	S	0	3	0
			3647	2345	608	671	23			
1	C	449	Total	C	N	O	S	0	4	0
			3629	2334	600	671	24			
1	D	452	Total	C	N	O	S	0	2	0
			3659	2352	612	672	23			

There are 124 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	38	HIS	-	expression tag	UNP Q9SWH5
A	39	HIS	-	expression tag	UNP Q9SWH5
A	40	HIS	-	expression tag	UNP Q9SWH5
A	41	HIS	-	expression tag	UNP Q9SWH5
A	42	HIS	-	expression tag	UNP Q9SWH5
A	43	HIS	-	expression tag	UNP Q9SWH5
A	44	GLY	-	expression tag	UNP Q9SWH5
A	45	MET	-	expression tag	UNP Q9SWH5
A	46	ALA	-	expression tag	UNP Q9SWH5
A	47	SER	-	expression tag	UNP Q9SWH5
A	48	MET	-	expression tag	UNP Q9SWH5
A	49	THR	-	expression tag	UNP Q9SWH5
A	50	GLY	-	expression tag	UNP Q9SWH5
A	51	GLY	-	expression tag	UNP Q9SWH5
A	52	GLN	-	expression tag	UNP Q9SWH5
A	53	GLN	-	expression tag	UNP Q9SWH5
A	54	MET	-	expression tag	UNP Q9SWH5
A	55	GLY	-	expression tag	UNP Q9SWH5
A	56	ARG	-	expression tag	UNP Q9SWH5
A	57	ASP	-	expression tag	UNP Q9SWH5
A	58	LEU	-	expression tag	UNP Q9SWH5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	59	TYR	-	expression tag	UNP Q9SWH5
A	60	ASP	-	expression tag	UNP Q9SWH5
A	61	ASP	-	expression tag	UNP Q9SWH5
A	62	ASP	-	expression tag	UNP Q9SWH5
A	63	ASP	-	expression tag	UNP Q9SWH5
A	64	LYS	-	expression tag	UNP Q9SWH5
A	65	SER	-	expression tag	UNP Q9SWH5
A	66	ARG	-	expression tag	UNP Q9SWH5
A	67	LEU	-	expression tag	UNP Q9SWH5
A	68	GLN	-	expression tag	UNP Q9SWH5
B	38	HIS	-	expression tag	UNP Q9SWH5
B	39	HIS	-	expression tag	UNP Q9SWH5
B	40	HIS	-	expression tag	UNP Q9SWH5
B	41	HIS	-	expression tag	UNP Q9SWH5
B	42	HIS	-	expression tag	UNP Q9SWH5
B	43	HIS	-	expression tag	UNP Q9SWH5
B	44	GLY	-	expression tag	UNP Q9SWH5
B	45	MET	-	expression tag	UNP Q9SWH5
B	46	ALA	-	expression tag	UNP Q9SWH5
B	47	SER	-	expression tag	UNP Q9SWH5
B	48	MET	-	expression tag	UNP Q9SWH5
B	49	THR	-	expression tag	UNP Q9SWH5
B	50	GLY	-	expression tag	UNP Q9SWH5
B	51	GLY	-	expression tag	UNP Q9SWH5
B	52	GLN	-	expression tag	UNP Q9SWH5
B	53	GLN	-	expression tag	UNP Q9SWH5
B	54	MET	-	expression tag	UNP Q9SWH5
B	55	GLY	-	expression tag	UNP Q9SWH5
B	56	ARG	-	expression tag	UNP Q9SWH5
B	57	ASP	-	expression tag	UNP Q9SWH5
B	58	LEU	-	expression tag	UNP Q9SWH5
B	59	TYR	-	expression tag	UNP Q9SWH5
B	60	ASP	-	expression tag	UNP Q9SWH5
B	61	ASP	-	expression tag	UNP Q9SWH5
B	62	ASP	-	expression tag	UNP Q9SWH5
B	63	ASP	-	expression tag	UNP Q9SWH5
B	64	LYS	-	expression tag	UNP Q9SWH5
B	65	SER	-	expression tag	UNP Q9SWH5
B	66	ARG	-	expression tag	UNP Q9SWH5
B	67	LEU	-	expression tag	UNP Q9SWH5
B	68	GLN	-	expression tag	UNP Q9SWH5
C	38	HIS	-	expression tag	UNP Q9SWH5

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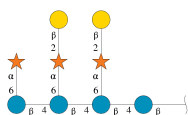
Chain	Residue	Modelled	Actual	Comment	Reference
C	39	HIS	-	expression tag	UNP Q9SWH5
C	40	HIS	-	expression tag	UNP Q9SWH5
C	41	HIS	-	expression tag	UNP Q9SWH5
C	42	HIS	-	expression tag	UNP Q9SWH5
C	43	HIS	-	expression tag	UNP Q9SWH5
C	44	GLY	-	expression tag	UNP Q9SWH5
C	45	MET	-	expression tag	UNP Q9SWH5
C	46	ALA	-	expression tag	UNP Q9SWH5
C	47	SER	-	expression tag	UNP Q9SWH5
C	48	MET	-	expression tag	UNP Q9SWH5
C	49	THR	-	expression tag	UNP Q9SWH5
C	50	GLY	-	expression tag	UNP Q9SWH5
C	51	GLY	-	expression tag	UNP Q9SWH5
C	52	GLN	-	expression tag	UNP Q9SWH5
C	53	GLN	-	expression tag	UNP Q9SWH5
C	54	MET	-	expression tag	UNP Q9SWH5
C	55	GLY	-	expression tag	UNP Q9SWH5
C	56	ARG	-	expression tag	UNP Q9SWH5
C	57	ASP	-	expression tag	UNP Q9SWH5
C	58	LEU	-	expression tag	UNP Q9SWH5
C	59	TYR	-	expression tag	UNP Q9SWH5
C	60	ASP	-	expression tag	UNP Q9SWH5
C	61	ASP	-	expression tag	UNP Q9SWH5
C	62	ASP	-	expression tag	UNP Q9SWH5
C	63	ASP	-	expression tag	UNP Q9SWH5
C	64	LYS	-	expression tag	UNP Q9SWH5
C	65	SER	-	expression tag	UNP Q9SWH5
C	66	ARG	-	expression tag	UNP Q9SWH5
C	67	LEU	-	expression tag	UNP Q9SWH5
C	68	GLN	-	expression tag	UNP Q9SWH5
D	38	HIS	-	expression tag	UNP Q9SWH5
D	39	HIS	-	expression tag	UNP Q9SWH5
D	40	HIS	-	expression tag	UNP Q9SWH5
D	41	HIS	-	expression tag	UNP Q9SWH5
D	42	HIS	-	expression tag	UNP Q9SWH5
D	43	HIS	-	expression tag	UNP Q9SWH5
D	44	GLY	-	expression tag	UNP Q9SWH5
D	45	MET	-	expression tag	UNP Q9SWH5
D	46	ALA	-	expression tag	UNP Q9SWH5
D	47	SER	-	expression tag	UNP Q9SWH5
D	48	MET	-	expression tag	UNP Q9SWH5
D	49	THR	-	expression tag	UNP Q9SWH5

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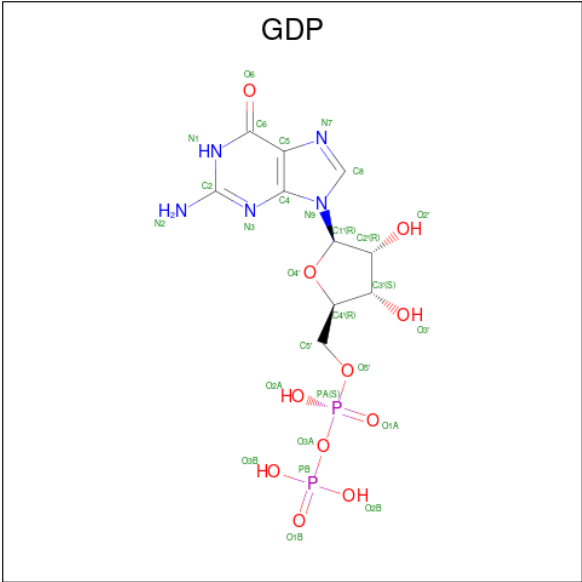
Chain	Residue	Modelled	Actual	Comment	Reference
D	50	GLY	-	expression tag	UNP Q9SWH5
D	51	GLY	-	expression tag	UNP Q9SWH5
D	52	GLN	-	expression tag	UNP Q9SWH5
D	53	GLN	-	expression tag	UNP Q9SWH5
D	54	MET	-	expression tag	UNP Q9SWH5
D	55	GLY	-	expression tag	UNP Q9SWH5
D	56	ARG	-	expression tag	UNP Q9SWH5
D	57	ASP	-	expression tag	UNP Q9SWH5
D	58	LEU	-	expression tag	UNP Q9SWH5
D	59	TYR	-	expression tag	UNP Q9SWH5
D	60	ASP	-	expression tag	UNP Q9SWH5
D	61	ASP	-	expression tag	UNP Q9SWH5
D	62	ASP	-	expression tag	UNP Q9SWH5
D	63	ASP	-	expression tag	UNP Q9SWH5
D	64	LYS	-	expression tag	UNP Q9SWH5
D	65	SER	-	expression tag	UNP Q9SWH5
D	66	ARG	-	expression tag	UNP Q9SWH5
D	67	LEU	-	expression tag	UNP Q9SWH5
D	68	GLN	-	expression tag	UNP Q9SWH5

- Molecule 2 is an oligosaccharide called alpha-D-xylopyranose-(1-6)-beta-D-glucopyranose-(1-4)-[beta-D-galactopyranose-(1-2)-alpha-D-xylopyranose-(1-6)]beta-D-glucopyranose-(1-4)-[beta-D-galactopyranose-(1-2)-alpha-D-xylopyranose-(1-6)]beta-D-glucopyranose-(1-4)-beta-D-glucopyranose.



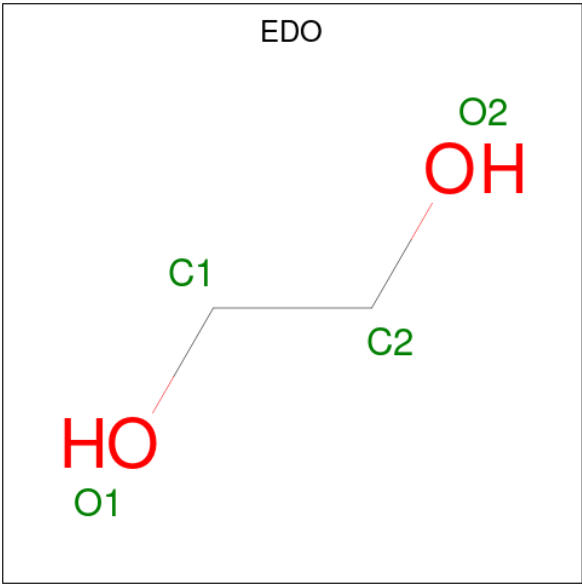
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	9	Total	C	O	0	0	0
			94	51	43			
2	F	9	Total	C	O	0	0	0
			94	51	43			

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
3	B	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
3	C	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
3	D	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Cl 1 1	0	0
5	C	1	Total Cl 1 1	0	0
5	D	1	Total Cl 1 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	129	Total O 129 129	0	0

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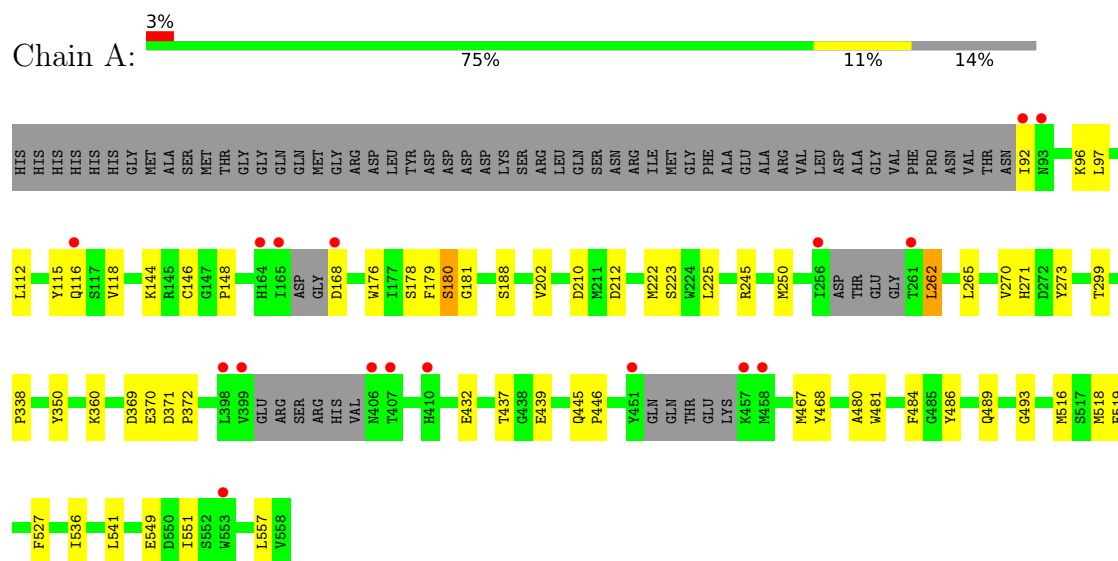
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	152	Total 152	O 152	0	1
6	C	187	Total 187	O 187	0	1
6	D	138	Total 138	O 138	0	0

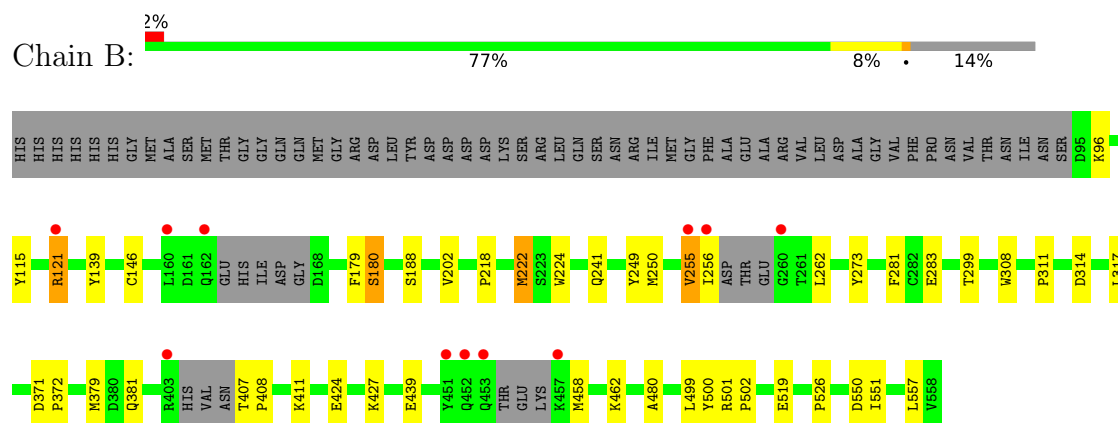
3 Residue-property plots [i](#)

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.

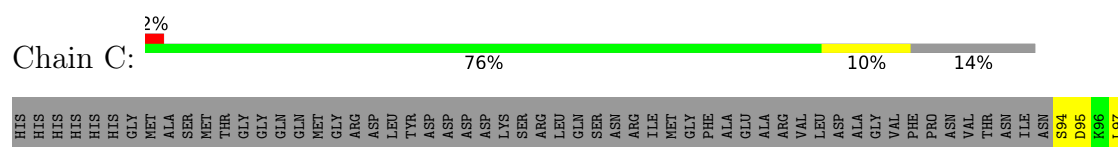
- Molecule 1: Galactoside 2-alpha-L-fucosyltransferase

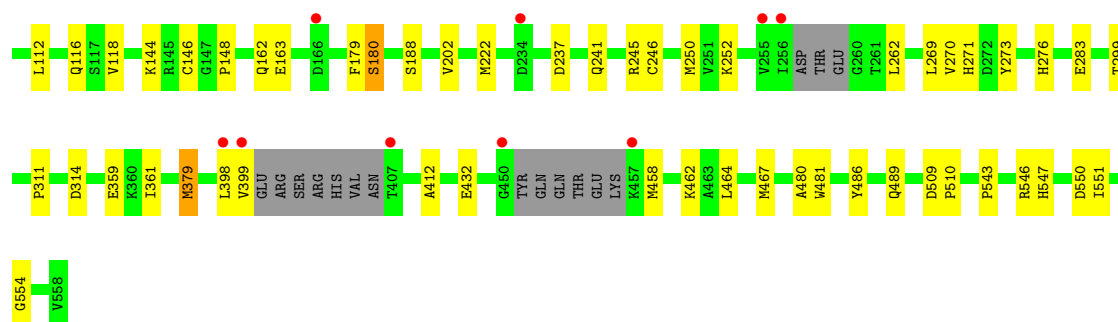


- Molecule 1: Galactoside 2-alpha-L-fucosyltransferase

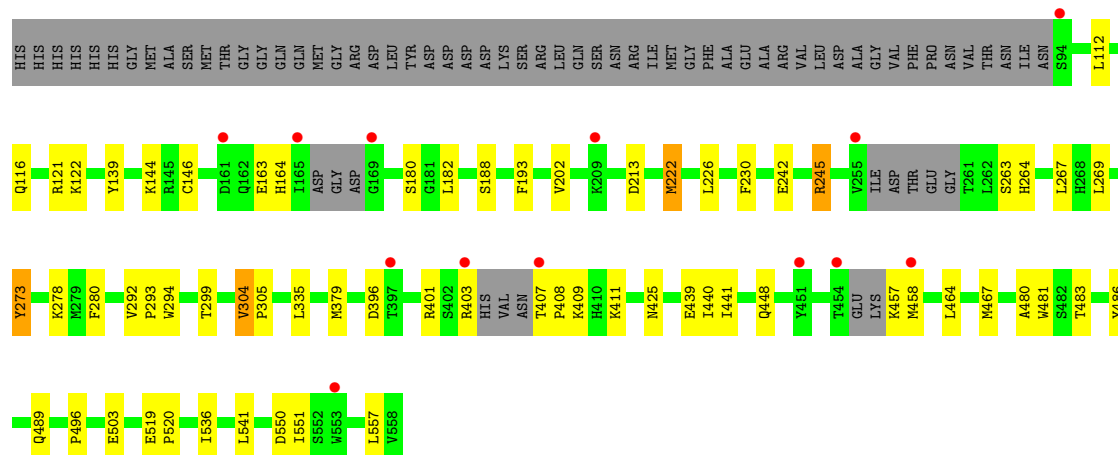
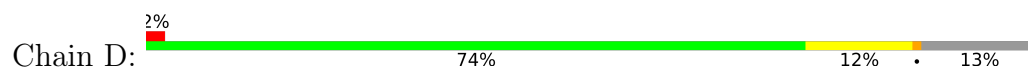


- Molecule 1: Galactoside 2-alpha-L-fucosyltransferase





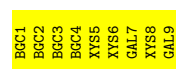
- Molecule 1: Galactoside 2-alpha-L-fucosyltransferase



- Molecule 2: alpha-D-xylopyranose-(1-6)-beta-D-glucopyranose-(1-4)-[beta-D-galactopyranose-(1-2)-alpha-D-xylopyranose-(1-6)]beta-D-glucopyranose-(1-4)-[beta-D-galactopyranose-(1-2)-alpha-D-xylopyranose-(1-6)]beta-D-glucopyranose-(1-4)-beta-D-glucopyranose



- Molecule 2: alpha-D-xylopyranose-(1-6)-beta-D-glucopyranose-(1-4)-[beta-D-galactopyranose-(1-2)-alpha-D-xylopyranose-(1-6)]beta-D-glucopyranose-(1-4)-[beta-D-galactopyranose-(1-2)-alpha-D-xylopyranose-(1-6)]beta-D-glucopyranose-(1-4)-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.97Å 85.81Å 150.72Å 90.00° 96.19° 90.00°	Depositor
Resolution (Å)	39.68 – 2.20 39.68 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.68-2.20) 99.8 (39.68-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.20Å)	Xtriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.179 , 0.215 0.174 , 0.210	Depositor DCC
R_{free} test set	5666 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	29.2	Xtriage
Anisotropy	0.714	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15538	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.28% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BGC, YYS, GAL, EDO, GDP, CL

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	0.48	0/3741	0.61	1/5071 (0.0%)
1	B	0.48	0/3749	0.62	1/5078 (0.0%)
1	C	0.51	0/3731	0.63	0/5056
1	D	0.48	1/3761 (0.0%)	0.60	0/5094
All	All	0.49	1/14982 (0.0%)	0.62	2/20299 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	304	VAL	CA-CB	5.20	1.56	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	255	VAL	CB-CA-C	-6.58	103.49	111.85
1	A	210	ASP	N-CA-C	5.32	122.13	110.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	379[B]	MET	Mainchain

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	3638	0	3532	39	0
1	B	3647	0	3539	35	0
1	C	3629	0	3520	41	0
1	D	3659	0	3558	47	0
2	E	94	0	78	0	0
2	F	94	0	78	0	0
3	A	28	0	12	0	0
3	B	28	0	12	0	0
3	C	28	0	12	0	0
3	D	28	0	12	0	0
4	A	12	0	18	0	0
4	B	8	0	12	1	0
4	C	24	0	36	4	0
4	D	12	0	18	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	A	129	0	0	0	0
6	B	152	0	0	0	0
6	C	187	0	0	0	0
6	D	138	0	0	1	0
All	All	15538	0	14437	159	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 159 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:398:LEU:O	1:C:399:VAL:CG1	1.73	1.34
1:C:398:LEU:O	1:C:399:VAL:HG12	1.01	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:398:LEU:C	1:C:399:VAL:HG12	1.87	1.00
1:C:250:MET:HE1	1:C:262:LEU:HD11	1.49	0.94
1:B:255:VAL:HG12	1:B:255:VAL:O	1.65	0.94

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	442/521 (85%)	427 (97%)	14 (3%)	1 (0%)	43	51
1	B	443/521 (85%)	427 (96%)	15 (3%)	1 (0%)	43	51
1	C	445/521 (85%)	433 (97%)	11 (2%)	1 (0%)	43	51
1	D	444/521 (85%)	428 (96%)	15 (3%)	1 (0%)	43	51
All	All	1774/2084 (85%)	1715 (97%)	55 (3%)	4 (0%)	43	51

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	180	SER
1	A	180	SER
1	C	180	SER
1	D	180	SER

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	403/460 (88%)	400 (99%)	3 (1%)	76	87
1	B	403/460 (88%)	396 (98%)	7 (2%)	53	69
1	C	402/460 (87%)	399 (99%)	3 (1%)	76	87
1	D	405/460 (88%)	400 (99%)	5 (1%)	63	78
All	All	1613/1840 (88%)	1595 (99%)	18 (1%)	65	79

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	245	ARG
1	D	503	GLU
1	D	409	LYS
1	B	424[B]	GLU
1	D	222	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	301	ASN
1	D	276	HIS
1	D	301	ASN
1	B	184	ASN
1	B	323	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

18 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	E	1	2	12,12,12	0.67	0	17,17,17	1.22	3 (17%)
2	BGC	E	2	2	11,11,12	0.37	0	15,15,17	1.17	1 (6%)
2	BGC	E	3	2	11,11,12	0.47	0	15,15,17	0.92	0
2	BGC	E	4	2	11,11,12	0.64	0	15,15,17	1.01	1 (6%)
2	XYS	E	5	2	9,9,10	0.90	1 (11%)	10,12,14	1.95	1 (10%)
2	XYS	E	6	2	9,9,10	0.75	0	10,12,14	2.21	1 (10%)
2	GAL	E	7	2	11,11,12	1.44	1 (9%)	15,15,17	0.70	0
2	XYS	E	8	2	9,9,10	1.03	1 (11%)	10,12,14	1.33	2 (20%)
2	GAL	E	9	2	11,11,12	1.30	2 (18%)	15,15,17	0.99	0
2	BGC	F	1	2	12,12,12	0.50	0	17,17,17	0.91	1 (5%)
2	BGC	F	2	2	11,11,12	0.57	0	15,15,17	1.18	1 (6%)
2	BGC	F	3	2	11,11,12	0.52	0	15,15,17	1.24	2 (13%)
2	BGC	F	4	2	11,11,12	0.55	0	15,15,17	1.25	1 (6%)
2	XYS	F	5	2	9,9,10	1.04	1 (11%)	10,12,14	1.83	3 (30%)
2	XYS	F	6	2	9,9,10	0.93	1 (11%)	10,12,14	1.75	2 (20%)
2	GAL	F	7	2	11,11,12	1.55	2 (18%)	15,15,17	1.08	1 (6%)
2	XYS	F	8	2	9,9,10	1.10	1 (11%)	10,12,14	1.93	1 (10%)
2	GAL	F	9	2	11,11,12	1.44	3 (27%)	15,15,17	0.98	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	E	1	2	-	1/2/22/22	0/1/1/1
2	BGC	E	2	2	-	0/2/19/22	0/1/1/1
2	BGC	E	3	2	-	1/2/19/22	0/1/1/1
2	BGC	E	4	2	-	0/2/19/22	0/1/1/1
2	XYS	E	5	2	-	-	0/1/1/1
2	XYS	E	6	2	-	-	0/1/1/1
2	GAL	E	7	2	-	2/2/19/22	0/1/1/1
2	XYS	E	8	2	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GAL	E	9	2	-	1/2/19/22	0/1/1/1
2	BGC	F	1	2	-	2/2/22/22	0/1/1/1
2	BGC	F	2	2	-	0/2/19/22	0/1/1/1
2	BGC	F	3	2	-	2/2/19/22	0/1/1/1
2	BGC	F	4	2	-	0/2/19/22	0/1/1/1
2	XYS	F	5	2	-	-	0/1/1/1
2	XYS	F	6	2	-	-	0/1/1/1
2	GAL	F	7	2	-	2/2/19/22	0/1/1/1
2	XYS	F	8	2	-	-	0/1/1/1
2	GAL	F	9	2	-	1/2/19/22	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	7	GAL	C4-C3	2.70	1.59	1.52
2	F	7	GAL	O5-C5	2.69	1.48	1.43
2	E	9	GAL	C1-C2	2.60	1.58	1.52
2	F	9	GAL	O5-C5	2.50	1.48	1.43
2	F	8	XYS	O5-C1	-2.45	1.38	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	6	XYS	C5-O5-C1	6.25	121.50	111.42
2	E	5	XYS	C5-O5-C1	5.13	119.69	111.42
2	F	8	XYS	C5-O5-C1	5.08	119.61	111.42
2	F	5	XYS	C5-O5-C1	4.51	118.70	111.42
2	F	6	XYS	C5-O5-C1	3.94	117.78	111.42

There are no chirality outliers.

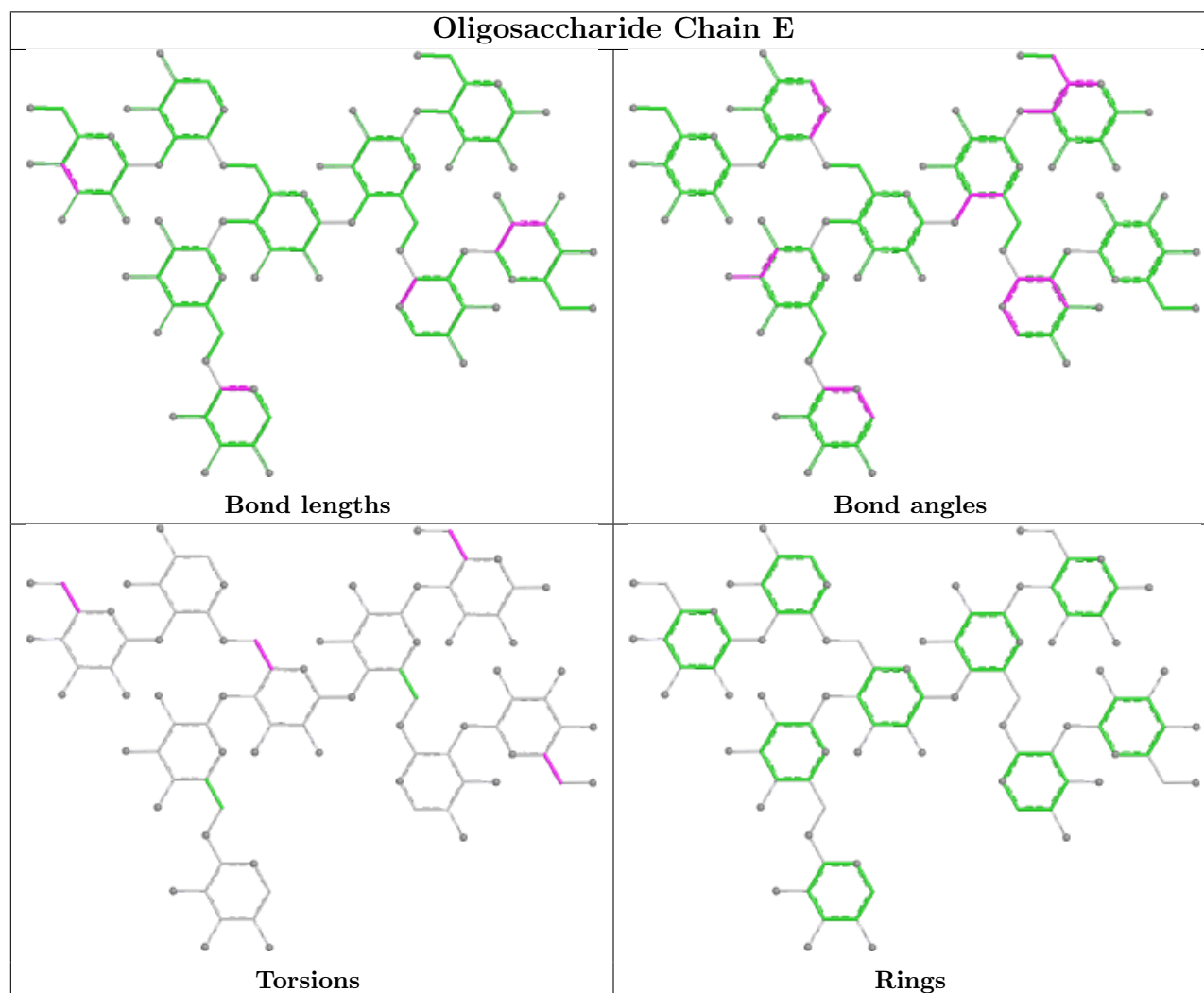
5 of 12 torsion outliers are listed below:

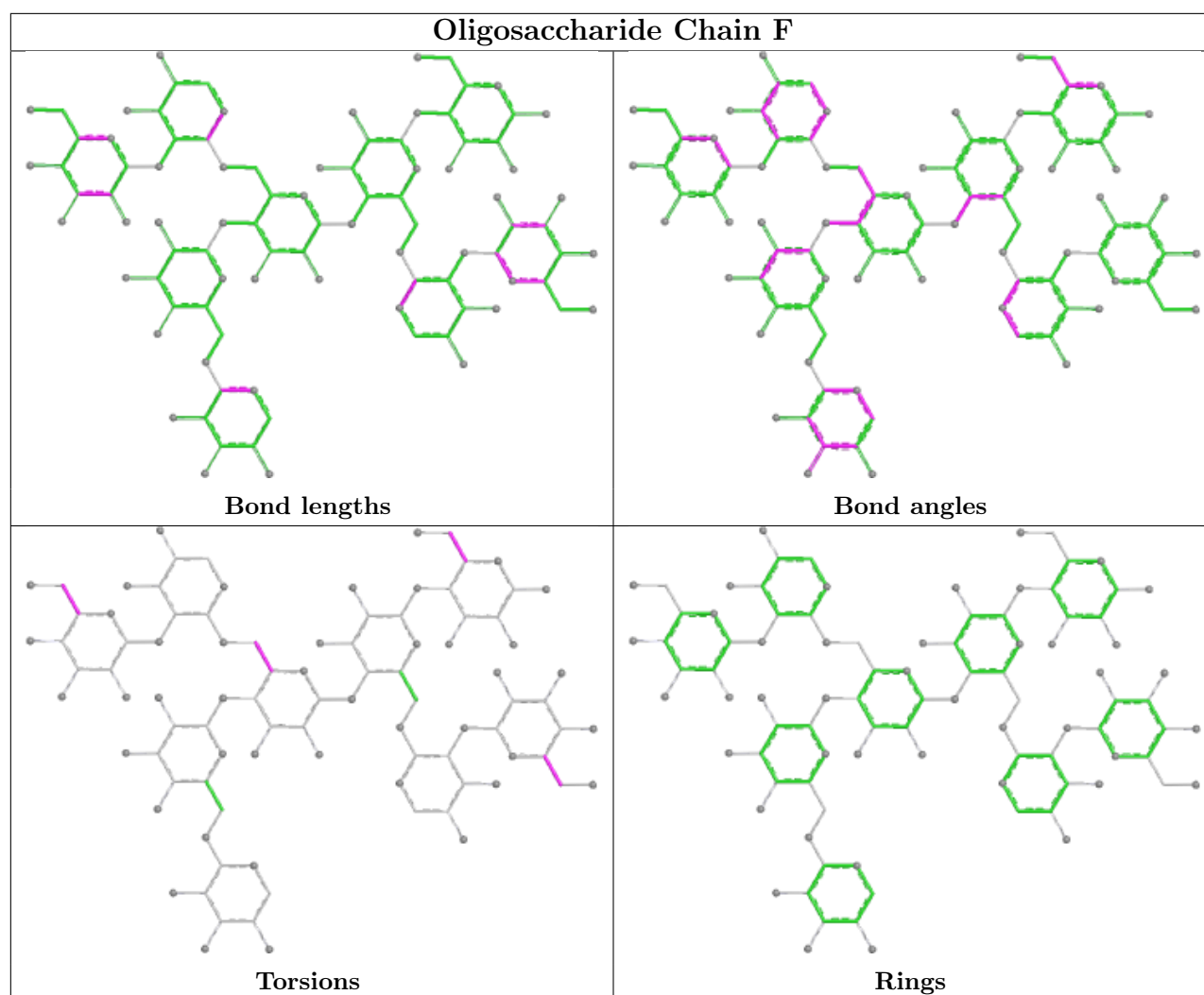
Mol	Chain	Res	Type	Atoms
2	E	7	GAL	O5-C5-C6-O6
2	E	7	GAL	C4-C5-C6-O6
2	F	3	BGC	O5-C5-C6-O6
2	F	9	GAL	O5-C5-C6-O6
2	E	9	GAL	O5-C5-C6-O6

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 21 ligands modelled in this entry, 3 are monoatomic - leaving 18 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	$\# Z > 2$
3	GDP	B	601	-	29,30,30	1.44	5 (17%)	45,47,47	1.71	8 (17%)
4	EDO	C	615	-	3,3,3	0.43	0	2,2,2	0.36	0
4	EDO	C	612	-	3,3,3	0.31	0	2,2,2	0.44	0
4	EDO	C	611	-	3,3,3	0.53	0	2,2,2	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	C	613	-	3,3,3	0.71	0	2,2,2	0.89	0
4	EDO	C	614	-	3,3,3	0.29	0	2,2,2	0.29	0
4	EDO	D	603	-	3,3,3	0.52	0	2,2,2	0.26	0
4	EDO	B	611	-	3,3,3	0.43	0	2,2,2	0.33	0
4	EDO	D	604	-	3,3,3	0.43	0	2,2,2	0.35	0
4	EDO	B	612	-	3,3,3	0.42	0	2,2,2	0.44	0
4	EDO	A	603	-	3,3,3	0.48	0	2,2,2	0.35	0
3	GDP	A	601	-	29,30,30	1.55	5 (17%)	45,47,47	1.67	9 (20%)
3	GDP	D	601	-	29,30,30	1.48	6 (20%)	45,47,47	1.54	8 (17%)
4	EDO	A	604	-	3,3,3	0.37	0	2,2,2	0.84	0
3	GDP	C	601	-	29,30,30	1.41	5 (17%)	45,47,47	1.55	7 (15%)
4	EDO	C	616	-	3,3,3	0.56	0	2,2,2	0.21	0
4	EDO	A	602	-	3,3,3	0.41	0	2,2,2	0.52	0
4	EDO	D	602	-	3,3,3	0.38	0	2,2,2	0.55	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
3	GDP	B	601	-	-	5/16/32/32	0/3/3/3
4	EDO	C	615	-	-	0/1/1/1	-
4	EDO	C	612	-	-	1/1/1/1	-
4	EDO	C	611	-	-	0/1/1/1	-
4	EDO	C	613	-	-	1/1/1/1	-
4	EDO	C	614	-	-	1/1/1/1	-
4	EDO	D	603	-	-	1/1/1/1	-
4	EDO	B	611	-	-	0/1/1/1	-
4	EDO	D	604	-	-	0/1/1/1	-
4	EDO	B	612	-	-	1/1/1/1	-
4	EDO	A	603	-	-	0/1/1/1	-
3	GDP	A	601	-	-	7/16/32/32	0/3/3/3
3	GDP	D	601	-	-	5/16/32/32	0/3/3/3
4	EDO	A	604	-	-	1/1/1/1	-
3	GDP	C	601	-	-	7/16/32/32	0/3/3/3
4	EDO	C	616	-	-	0/1/1/1	-
4	EDO	A	602	-	-	0/1/1/1	-
4	EDO	D	602	-	-	0/1/1/1	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	GDP	PA-O3A	4.43	1.64	1.59
3	B	601	GDP	C6-N1	-3.65	1.32	1.38
3	A	601	GDP	C6-N1	-3.34	1.32	1.38
3	D	601	GDP	C6-N1	-3.24	1.32	1.38
3	C	601	GDP	C5-C4	3.19	1.47	1.38

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	601	GDP	C5-C4-N3	-6.28	118.39	128.39
3	A	601	GDP	C5-C4-N3	-5.70	119.31	128.39
3	D	601	GDP	C5-C4-N3	-5.64	119.41	128.39
3	C	601	GDP	C5-C4-N3	-5.51	119.62	128.39
3	B	601	GDP	N9-C4-N3	4.72	135.39	125.95

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	GDP	PA-O3A-PB-O3B
3	B	601	GDP	PA-O3A-PB-O2B
3	C	601	GDP	PA-O3A-PB-O3B
3	D	601	GDP	PA-O3A-PB-O2B
3	C	601	GDP	C3'-C4'-C5'-O5'

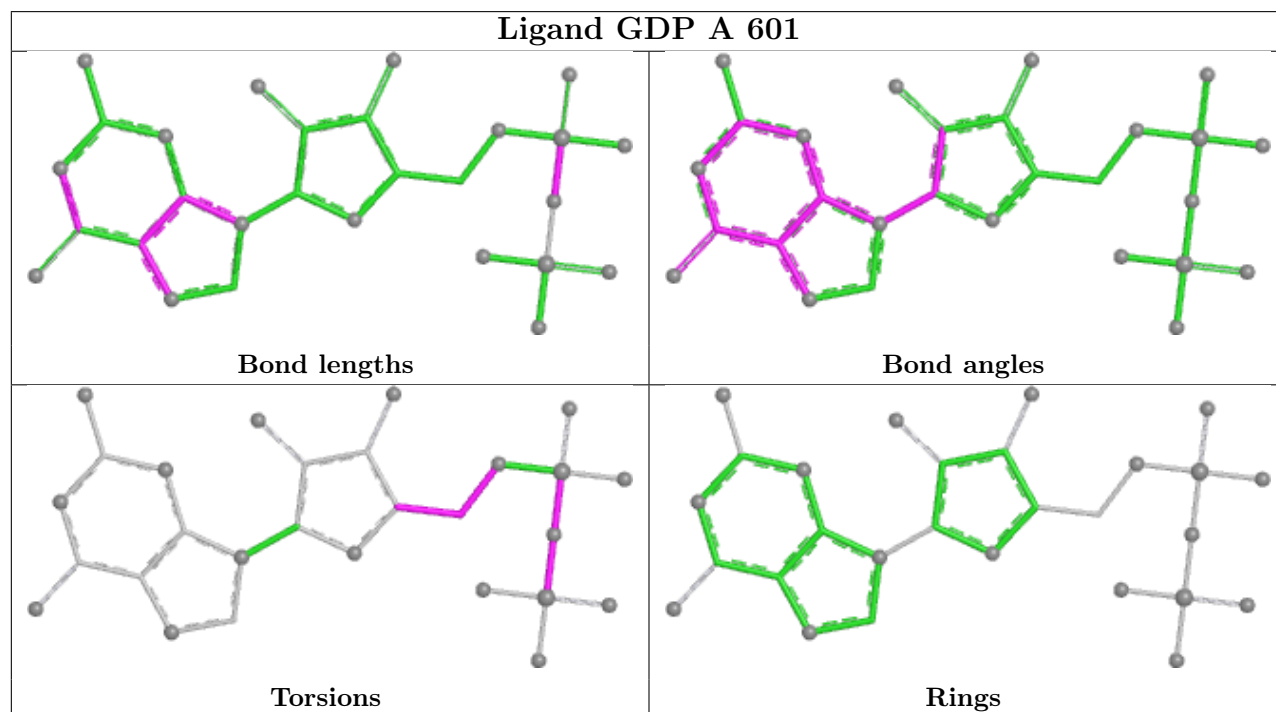
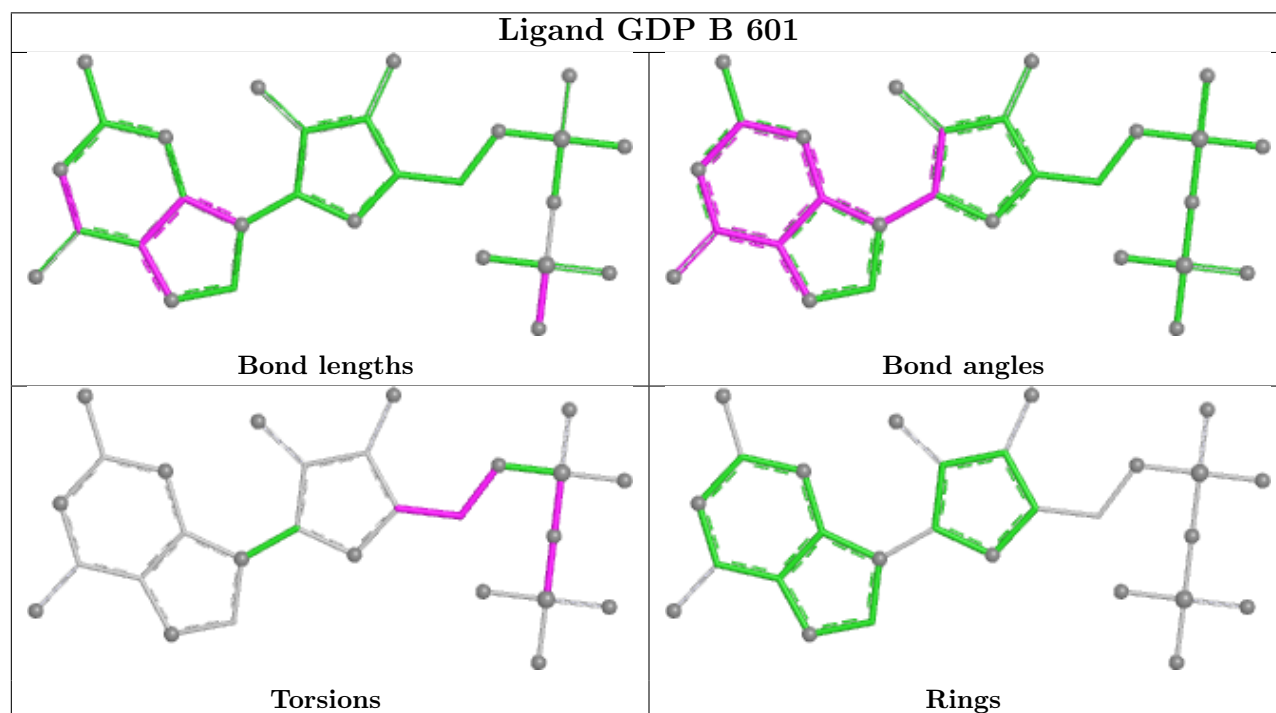
There are no ring outliers.

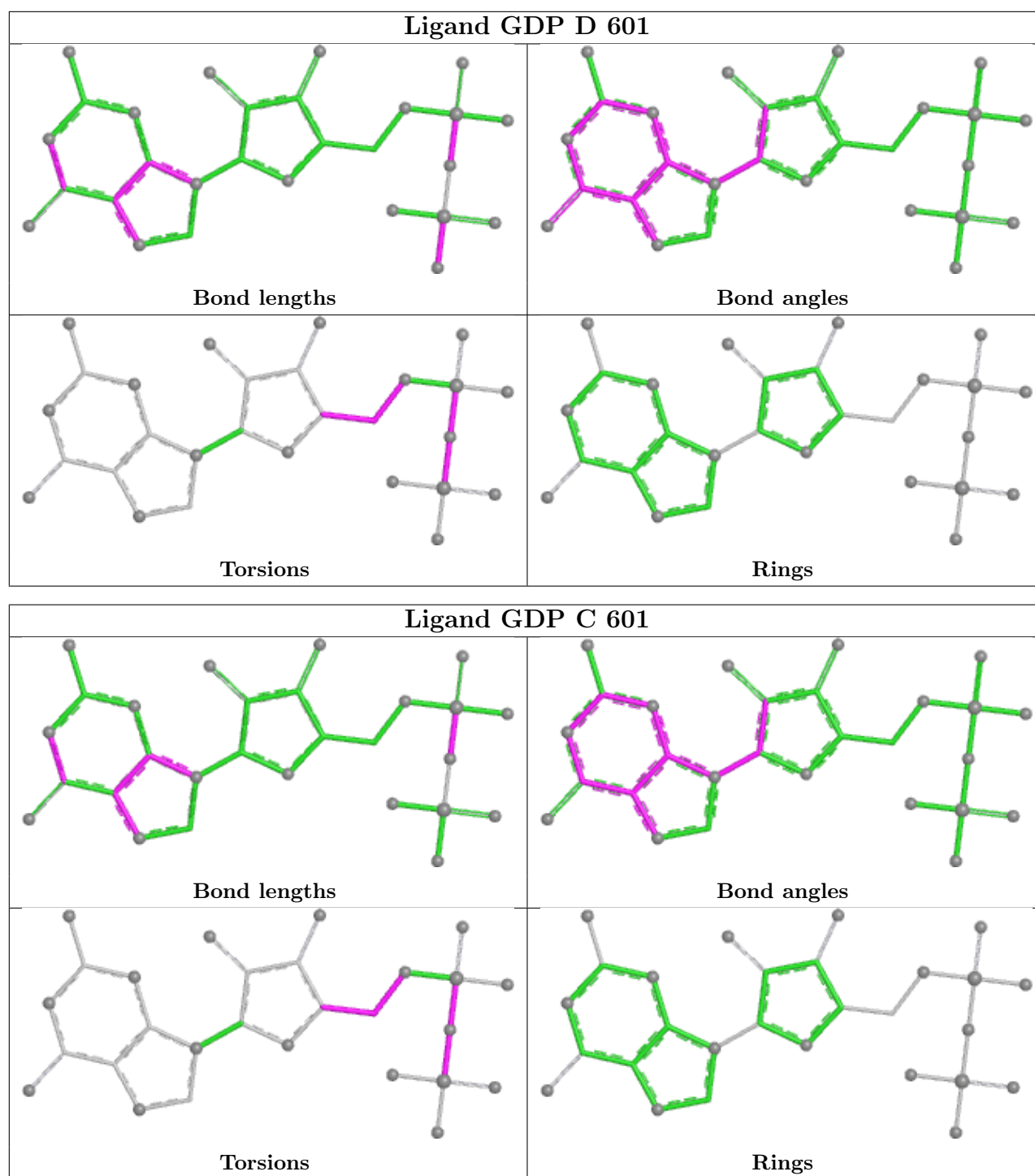
3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	613	EDO	3	0
4	C	614	EDO	1	0
4	B	612	EDO	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 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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	450/521 (86%)	-0.15	17 (3%) 44 41	13, 35, 73, 120	2 (0%)
1	B	450/521 (86%)	-0.24	11 (2%) 59 56	18, 35, 71, 111	3 (0%)
1	C	449/521 (86%)	-0.41	9 (2%) 65 62	15, 30, 58, 99	4 (0%)
1	D	452/521 (86%)	-0.19	13 (2%) 53 50	18, 36, 74, 119	2 (0%)
All	All	1801/2084 (86%)	-0.25	50 (2%) 55 52	13, 34, 71, 120	11 (0%)

The worst 5 of 50 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	256	ILE	6.1
1	A	92	ILE	4.9
1	A	399	VAL	4.7
1	D	165	ILE	4.5
1	A	165	ILE	4.4

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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GAL	F	7	11/12	0.27	0.18	101,107,108,109	0
2	GAL	E	7	11/12	0.28	0.16	103,105,106,106	0

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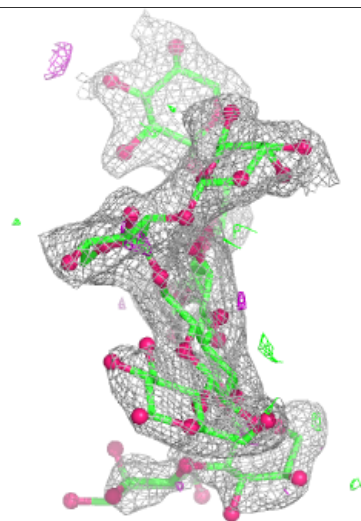
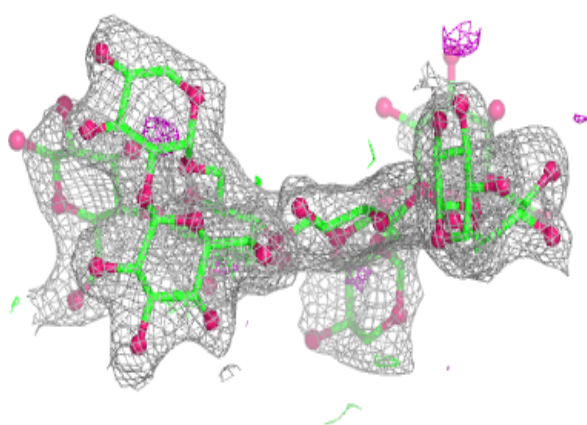
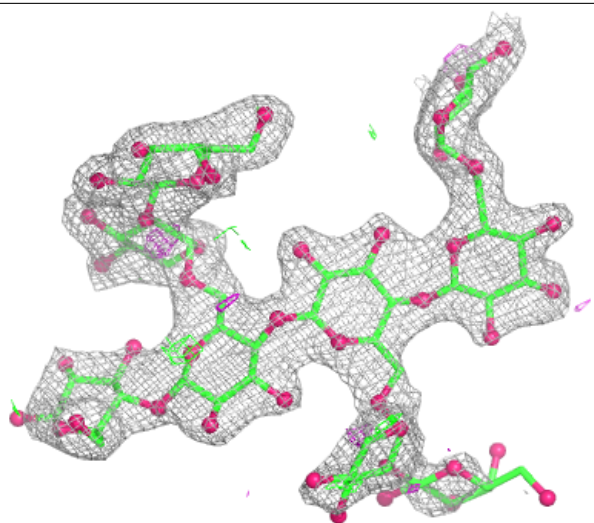
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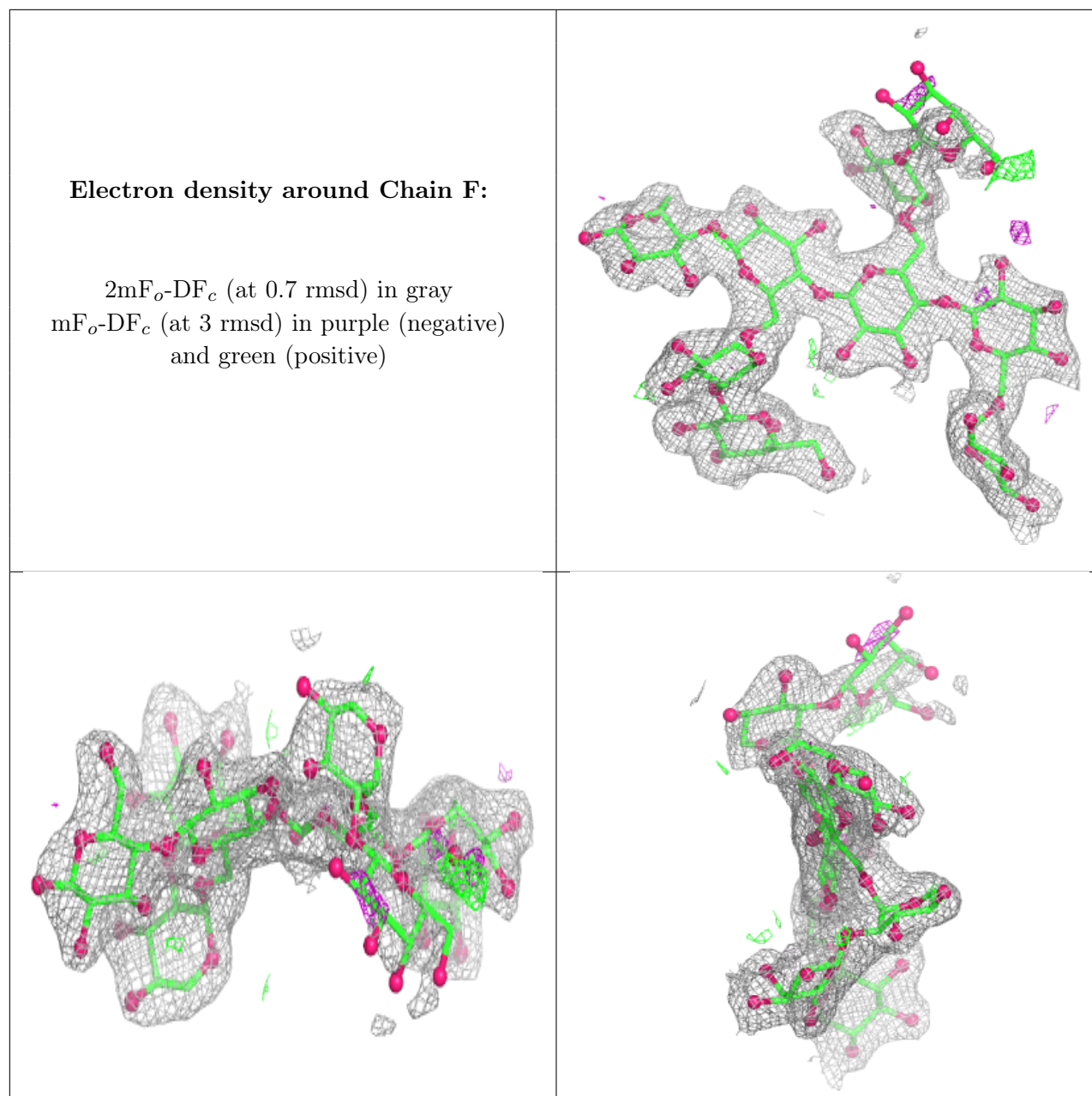
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	XYS	E	6	9/10	0.60	0.16	91,94,96,100	0
2	XYS	F	6	9/10	0.77	0.13	81,83,86,93	0
2	BGC	E	4	11/12	0.82	0.12	64,72,75,77	0
2	BGC	E	1	12/12	0.86	0.10	64,69,70,72	0
2	BGC	F	1	12/12	0.89	0.09	53,59,63,66	0
2	BGC	E	3	11/12	0.90	0.09	62,65,80,86	0
2	XYS	E	5	9/10	0.90	0.10	59,61,62,62	0
2	XYS	E	8	9/10	0.90	0.10	51,54,56,56	0
2	XYS	F	8	9/10	0.91	0.09	39,46,49,53	0
2	BGC	E	2	11/12	0.92	0.08	56,58,61,61	0
2	BGC	F	3	11/12	0.92	0.08	41,50,65,73	0
2	XYS	F	5	9/10	0.92	0.08	42,43,44,44	0
2	BGC	F	2	11/12	0.93	0.07	42,45,48,48	0
2	BGC	F	4	11/12	0.93	0.08	45,49,55,57	0
2	GAL	E	9	11/12	0.95	0.07	40,42,47,48	0
2	GAL	F	9	11/12	0.96	0.06	29,34,36,36	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)





6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	EDO	C	616	4/4	0.75	0.17	63,64,64,65	0
4	EDO	C	613	4/4	0.77	0.21	38,43,44,49	0
4	EDO	A	603	4/4	0.80	0.20	59,61,63,64	0

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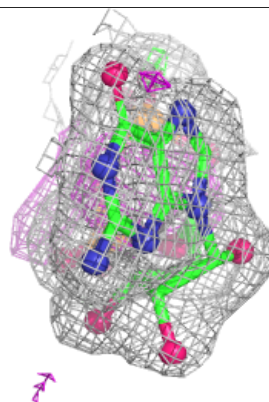
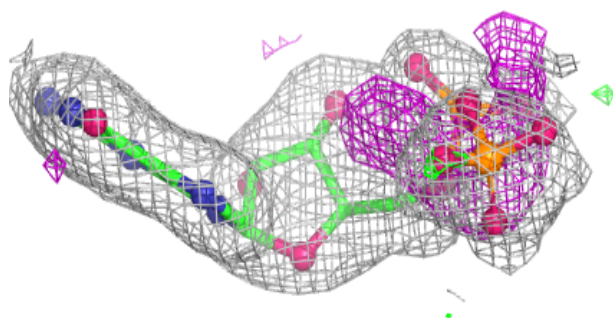
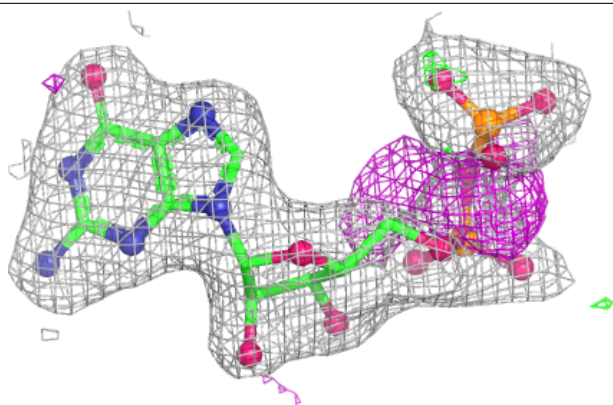
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	EDO	C	614	4/4	0.82	0.20	58,58,59,59	0
4	EDO	C	612	4/4	0.82	0.18	65,66,67,68	0
4	EDO	C	615	4/4	0.88	0.18	63,64,65,66	0
5	CL	B	613	1/1	0.88	0.13	57,57,57,57	0
4	EDO	D	604	4/4	0.90	0.16	60,61,63,64	0
3	GDP	A	601	28/28	0.90	0.11	38,51,67,67	0
4	EDO	A	604	4/4	0.92	0.13	49,54,58,62	0
3	GDP	C	601	28/28	0.93	0.08	24,36,49,51	0
4	EDO	B	612	4/4	0.94	0.10	56,56,58,60	0
4	EDO	D	603	4/4	0.94	0.11	57,57,58,61	0
5	CL	C	617	1/1	0.94	0.12	51,51,51,51	0
5	CL	D	605	1/1	0.94	0.14	58,58,58,58	0
3	GDP	D	601	28/28	0.95	0.07	27,34,40,43	0
3	GDP	B	601	28/28	0.95	0.08	21,34,41,45	0
4	EDO	D	602	4/4	0.96	0.08	42,43,43,44	0
4	EDO	A	602	4/4	0.96	0.07	36,37,37,38	0
4	EDO	B	611	4/4	0.97	0.07	37,37,38,40	0
4	EDO	C	611	4/4	0.98	0.05	31,32,33,34	0

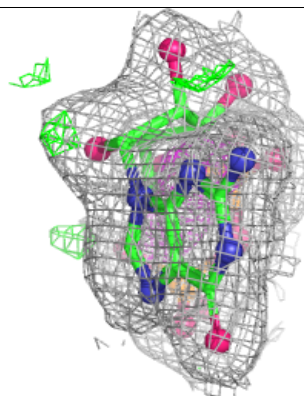
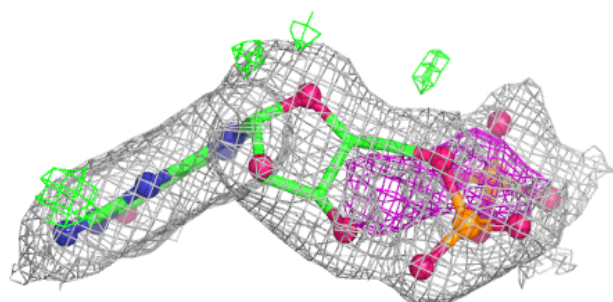
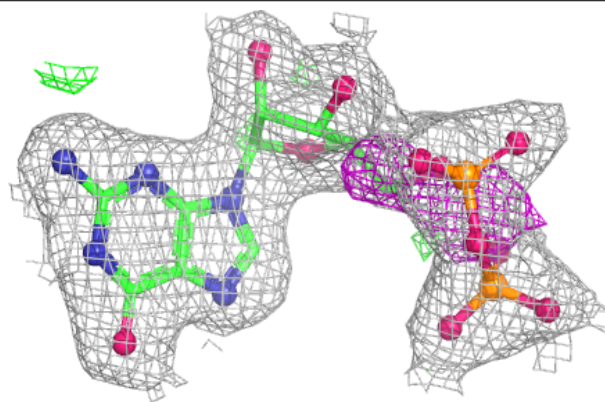
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around GDP A 601:

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

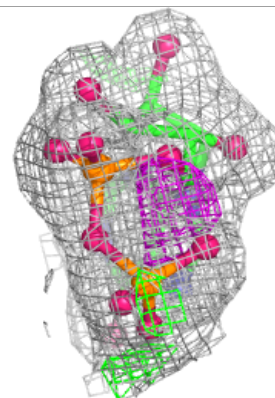
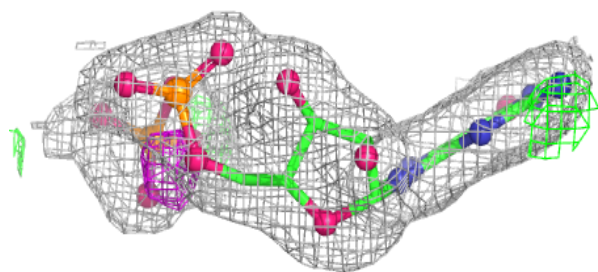
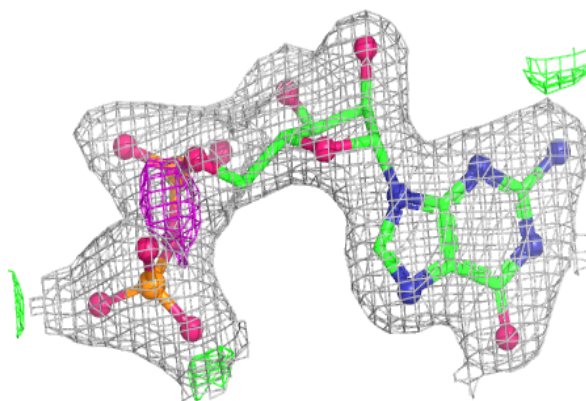
**Electron density around GDP C 601:**

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

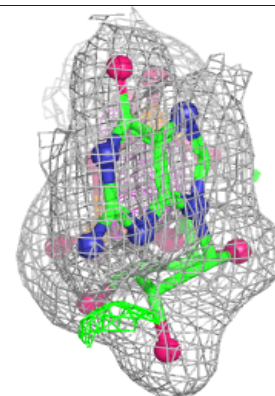
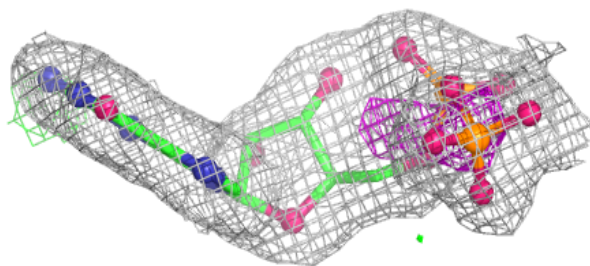
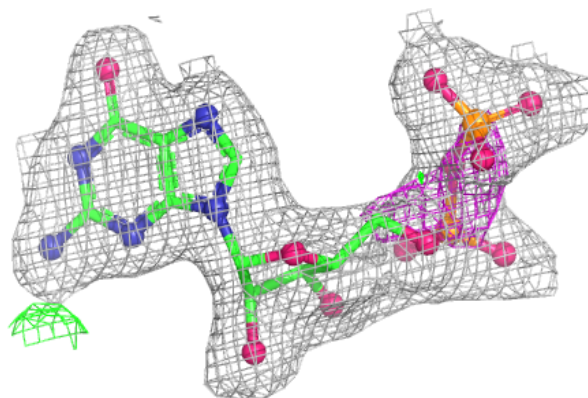


Electron density around GDP D 601:

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

**Electron density around GDP B 601:**

$2mF_o-DF_c$ (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.