



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 04:39 PM BST

PDB ID : 5DUW
Title : Crystal structure of the human galectin-4 N-terminal carbohydrate recognition domain in complex with lactose-3'-sulfate
Authors : Bum-Erdene, K.; Blanchard, H.
Deposited on : 2015-09-21
Resolution : 1.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

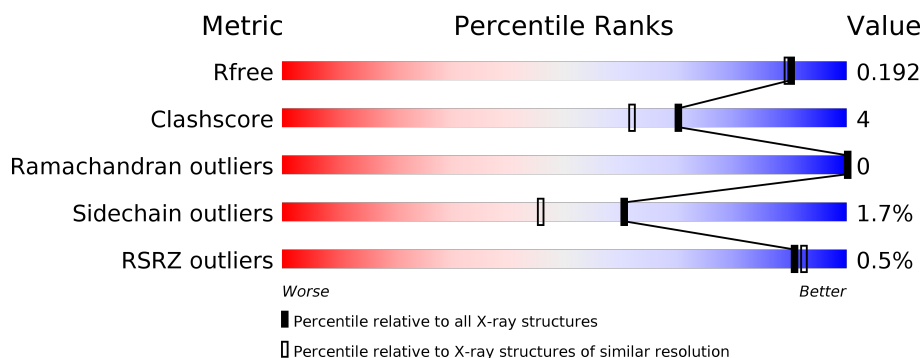
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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.



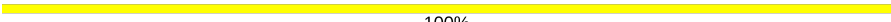
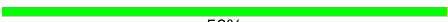
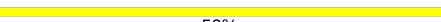
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 on 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	155	<div> <div>84%</div> <div>5%</div> <div>11%</div> </div>
1	B	155	<div> <div>%</div> <div>83%</div> <div>6%</div> <div>10%</div> </div>
1	C	155	<div> <div>%</div> <div>81%</div> <div>7%</div> <div>12%</div> </div>
1	D	155	<div> <div>%</div> <div>80%</div> <div>8%</div> <div>12%</div> </div>
2	E	2	<div> <div>50%</div> <div>50%</div> </div>
2	F	2	<div> <div>50%</div> <div>50%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	G	2	 100%
2	H	2	 50%  50%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5132 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 Galectin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	138	Total	C	N	O	S	0	2	0
			1119	729	191	195	4			
1	B	139	Total	C	N	O	S	0	2	0
			1123	733	190	195	5			
1	C	137	Total	C	N	O	S	0	3	0
			1116	728	189	195	4			
1	D	137	Total	C	N	O	S	0	2	0
			1107	724	186	192	5			

- Molecule 2 is an oligosaccharide called 3-O-sulfo-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	2	Total	C	O	S	0	0	0
			27	12	14	1			
2	F	2	Total	C	O	S	0	0	0
			27	12	14	1			
2	G	2	Total	C	O	S	0	0	0
			27	12	14	1			
2	H	2	Total	C	O	S	0	0	0
			27	12	14	1			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	138	Total	O	0	1
			139	139		

Continued on next page...


Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	141	Total 141	O 141	0	0
3	C	133	Total 133	O 133	0	0
3	D	146	Total 146	O 146	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: Galectin-4

Chain A: 




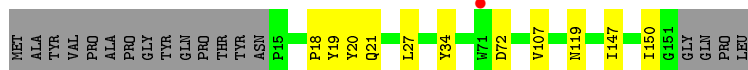
- Molecule 1: Galectin-4

Chain B: 




- Molecule 1: Galectin-4

Chain C: 



- Molecule 1: Galectin-4

Chain D: 



- Molecule 2: 3-O-sulfo-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain E: 



- Molecule 2: 3-O-sulfo-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain F: 

BG01
SGA2

- Molecule 2: 3-O-sulfo-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain G:  100%

BG01
SGA2

- Molecule 2: 3-O-sulfo-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain H:  50%  50%

BG01
SGA2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.18Å 64.05Å 64.65Å 90.00° 91.03° 90.00°	Depositor
Resolution (Å)	64.64 – 1.70 45.59 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.5 (64.64-1.70) 99.5 (45.59-1.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.71 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0131	Depositor
R, R_{free}	0.149 , 0.181 0.162 , 0.192	Depositor DCC
R_{free} test set	2795 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	12.6	Xtriage
Anisotropy	1.074	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 44.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k 0.017 for -h,-l,-k 0.028 for -l,k,h 0.000 for -k,-h,-l 0.000 for k,h,-l 0.000 for k,l,h 0.000 for l,h,k 0.000 for l,-h,-k 0.000 for -k,-l,h 0.030 for h,-k,-l 0.020 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5132	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 30.89 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2124e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SGA, BGC

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.45	0/1157	0.63	0/1566
1	B	0.46	0/1164	0.62	0/1575
1	C	0.44	0/1157	0.64	0/1568
1	D	0.47	0/1148	0.63	0/1554
All	All	0.45	0/4626	0.63	0/6263

There are no bond length outliers.

There are no bond angle outliers.

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	1119	0	1087	7	0
1	B	1123	0	1096	7	0
1	C	1116	0	1086	8	0
1	D	1107	0	1082	10	0
2	E	27	0	20	0	0
2	F	27	0	20	1	0
2	G	27	0	20	0	0
2	H	27	0	21	0	0
3	A	139	0	0	5	1

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	141	0	0	3	1
3	C	133	0	0	2	0
3	D	146	0	0	7	0
All	All	5132	0	4432	32	2

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 4.

All (32) 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:D:80:GLN:CD	3:D:302:HOH:O	2.14	0.85
1:D:80:GLN:NE2	3:D:302:HOH:O	2.11	0.83
1:B:34:TYR:OH	1:B:102:GLU:OE2	2.01	0.78
1:B:71:TRP:CZ2	1:B:91:ARG:HG2	2.21	0.75
3:B:301:HOH:O	2:F:2:SGA:O1S	2.08	0.71
1:C:34:TYR:CD1	1:C:150:ILE:HD12	2.27	0.69
1:D:70:GLY:O	3:D:301:HOH:O	2.09	0.69
1:A:69[B]:ASP:OD2	3:A:301:HOH:O	2.11	0.67
1:C:119[A]:ASN:ND2	3:C:302:HOH:O	2.23	0.66
1:C:72:ASP:OD1	3:C:301:HOH:O	2.13	0.66
1:A:110:GLU:OE2	3:A:302:HOH:O	2.14	0.65
1:D:149:PHE:O	3:D:303:HOH:O	2.14	0.65
1:C:34:TYR:CE1	1:C:150:ILE:HD12	2.35	0.61
1:D:80:GLN:CG	3:D:302:HOH:O	2.49	0.61
1:B:89:ARG:HH12	1:C:18:PRO:HG2	1.76	0.51
1:C:19:TYR:CE2	1:C:147:ILE:HD12	2.47	0.49
1:D:73:LYS:HE3	1:D:89:ARG:NH1	2.27	0.49
1:A:83:LYS:HE2	1:A:83:LYS:HA	1.94	0.48
1:C:27:LEU:HD11	1:C:107:VAL:HG21	1.96	0.48
1:B:119:ASN:HB3	3:B:420:HOH:O	2.15	0.46
1:A:30:GLY:CA	3:A:362:HOH:O	2.63	0.45
1:B:72:ASP:OD1	3:B:302:HOH:O	2.21	0.45
1:A:72:ASP:OD1	3:A:304:HOH:O	2.21	0.45
1:B:71:TRP:CH2	1:B:91:ARG:HG2	2.51	0.44
1:D:27:LEU:HD11	1:D:107:VAL:HG21	2.00	0.44
1:B:73:LYS:HD2	1:B:89:ARG:HD3	1.99	0.44
1:D:110:GLU:HG2	3:D:432:HOH:O	2.19	0.42
1:D:57:GLY:O	3:D:304:HOH:O	2.22	0.42
1:A:71:TRP:CH2	1:A:91:ARG:HD3	2.55	0.42
1:D:31[B]:MET:HG3	1:D:150:ILE:O	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:GLY:HA2	3:A:362:HOH:O	2.20	0.41
1:C:19:TYR:OH	1:C:21:GLN:HG2	2.20	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:371:HOH:O	3:B:400:HOH:O[2_854]	1.85	0.35
3:A:374:HOH:O	3:A:417:HOH:O[2_743]	1.97	0.23

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	138/155 (89%)	137 (99%)	1 (1%)	0	100	100
1	B	139/155 (90%)	137 (99%)	2 (1%)	0	100	100
1	C	138/155 (89%)	137 (99%)	1 (1%)	0	100	100
1	D	137/155 (88%)	136 (99%)	1 (1%)	0	100	100
All	All	552/620 (89%)	547 (99%)	5 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	119/131 (91%)	118 (99%)	1 (1%)	81	74
1	B	120/131 (92%)	115 (96%)	5 (4%)	30	12
1	C	120/131 (92%)	119 (99%)	1 (1%)	81	74
1	D	119/131 (91%)	117 (98%)	2 (2%)	60	46
All	All	478/524 (91%)	469 (98%)	9 (2%)	60	41

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	TYR
1	B	20	TYR
1	B	91	ARG
1	B	92	SER
1	B	132[A]	MET
1	B	132[B]	MET
1	C	20	TYR
1	D	20	TYR
1	D	34	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	148	ASN

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 ⓘ

8 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	0.40	0	17,17,17	0.75	0
2	SGA	E	2	2	15,15,16	0.68	0	17,22,24	0.86	1 (5%)
2	BGC	F	1	2	12,12,12	0.52	0	17,17,17	0.63	0
2	SGA	F	2	2	15,15,16	0.58	0	17,22,24	0.63	0
2	BGC	G	1	2	12,12,12	0.48	0	17,17,17	0.91	1 (5%)
2	SGA	G	2	2	15,15,16	0.83	1 (6%)	17,22,24	0.94	1 (5%)
2	BGC	H	1	2	12,12,12	0.60	0	17,17,17	0.73	0
2	SGA	H	2	2	15,15,16	0.73	1 (6%)	17,22,24	0.98	1 (5%)

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	-	0/2/22/22	0/1/1/1
2	SGA	E	2	2	-	0/7/24/27	0/1/1/1
2	BGC	F	1	2	-	0/2/22/22	0/1/1/1
2	SGA	F	2	2	-	2/7/24/27	0/1/1/1
2	BGC	G	1	2	-	0/2/22/22	0/1/1/1
2	SGA	G	2	2	-	0/7/24/27	0/1/1/1
2	BGC	H	1	2	-	0/2/22/22	0/1/1/1
2	SGA	H	2	2	-	0/7/24/27	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	2	SGA	O3-C3	-2.53	1.41	1.46
2	G	2	SGA	O3-C3	-2.48	1.41	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	2	SGA	C1-O5-C5	-2.56	108.72	112.19
2	E	2	SGA	C1-C2-C3	2.53	112.23	109.17
2	G	2	SGA	C1-C2-C3	2.45	112.13	109.17

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	1	BGC	C1-O5-C5	-2.32	109.28	113.66

There are no chirality outliers.

All (2) torsion outliers are listed below:

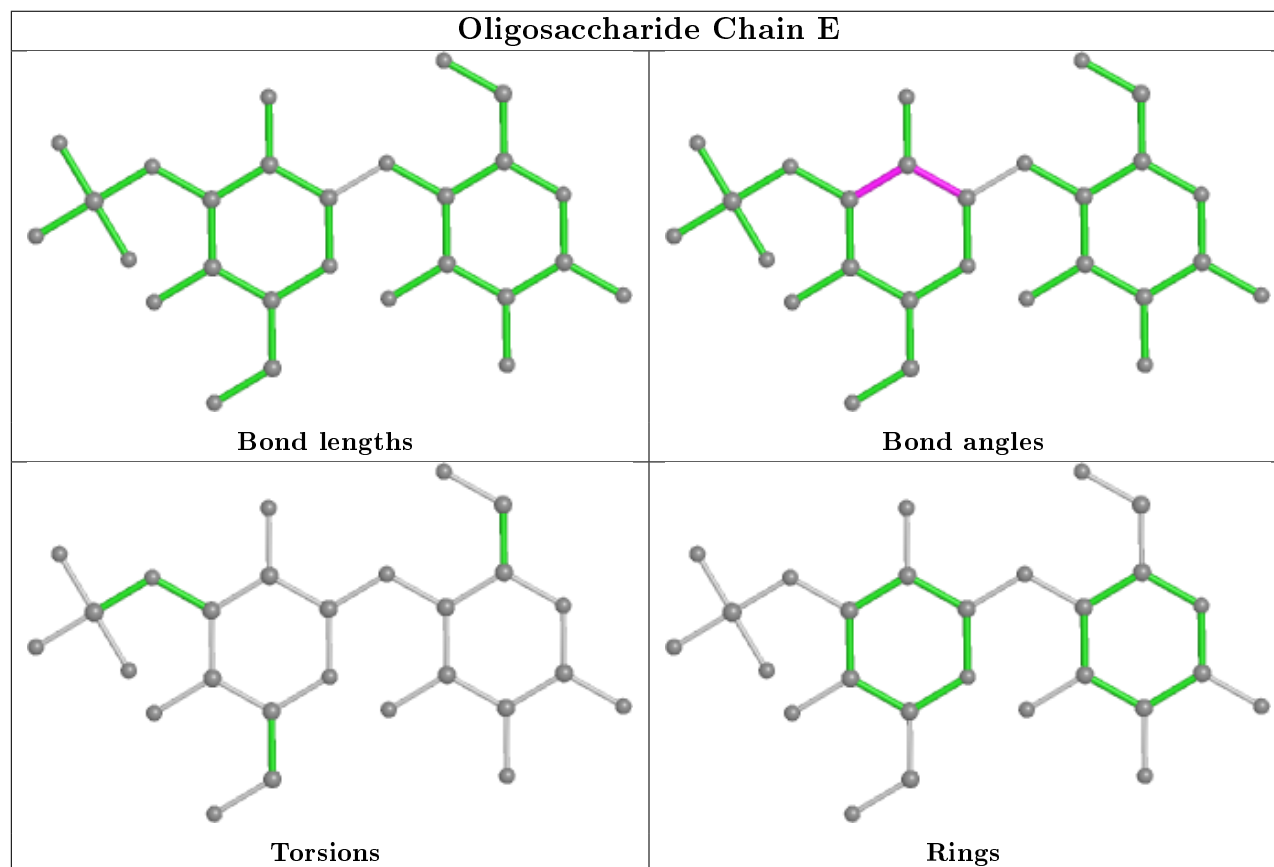
Mol	Chain	Res	Type	Atoms
2	F	2	SGA	C4-C3-O3-S
2	F	2	SGA	C2-C3-O3-S

There are no ring outliers.

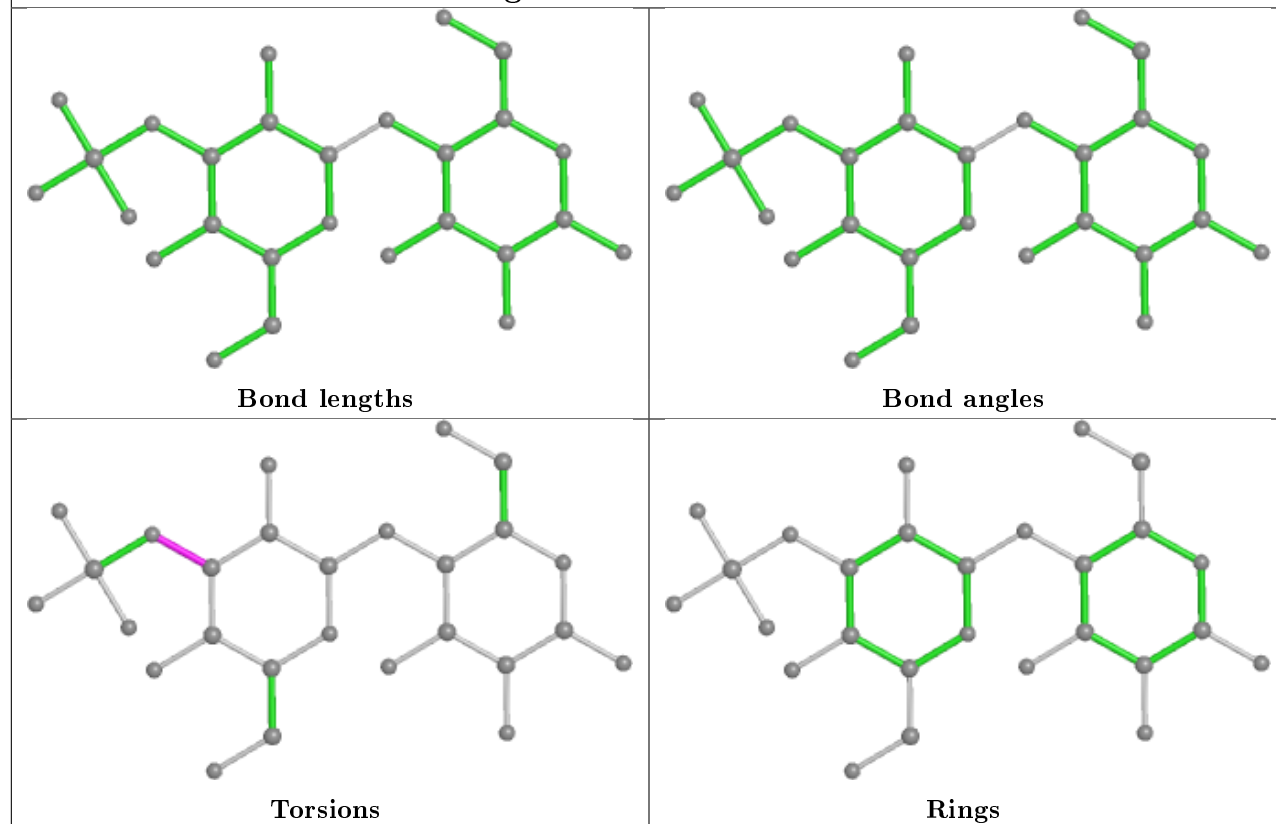
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	2	SGA	1	0

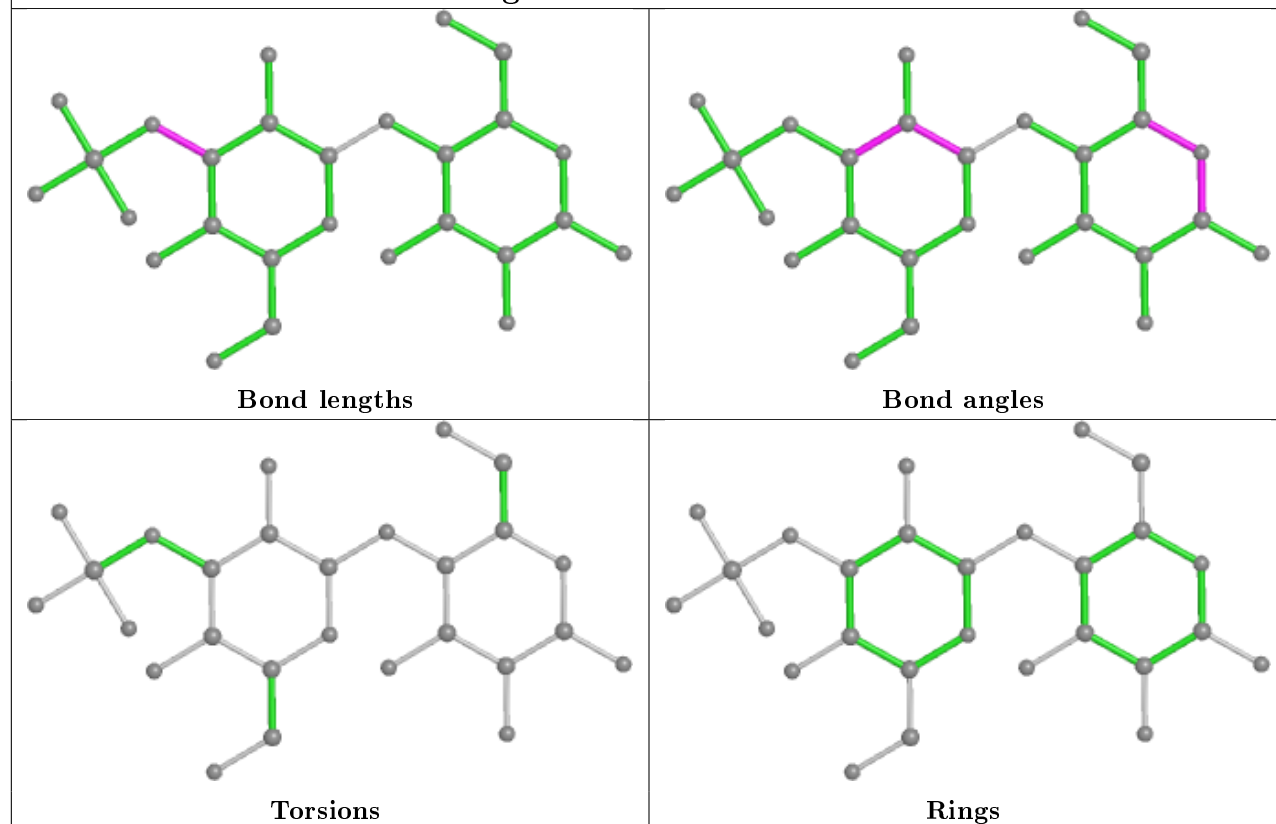
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

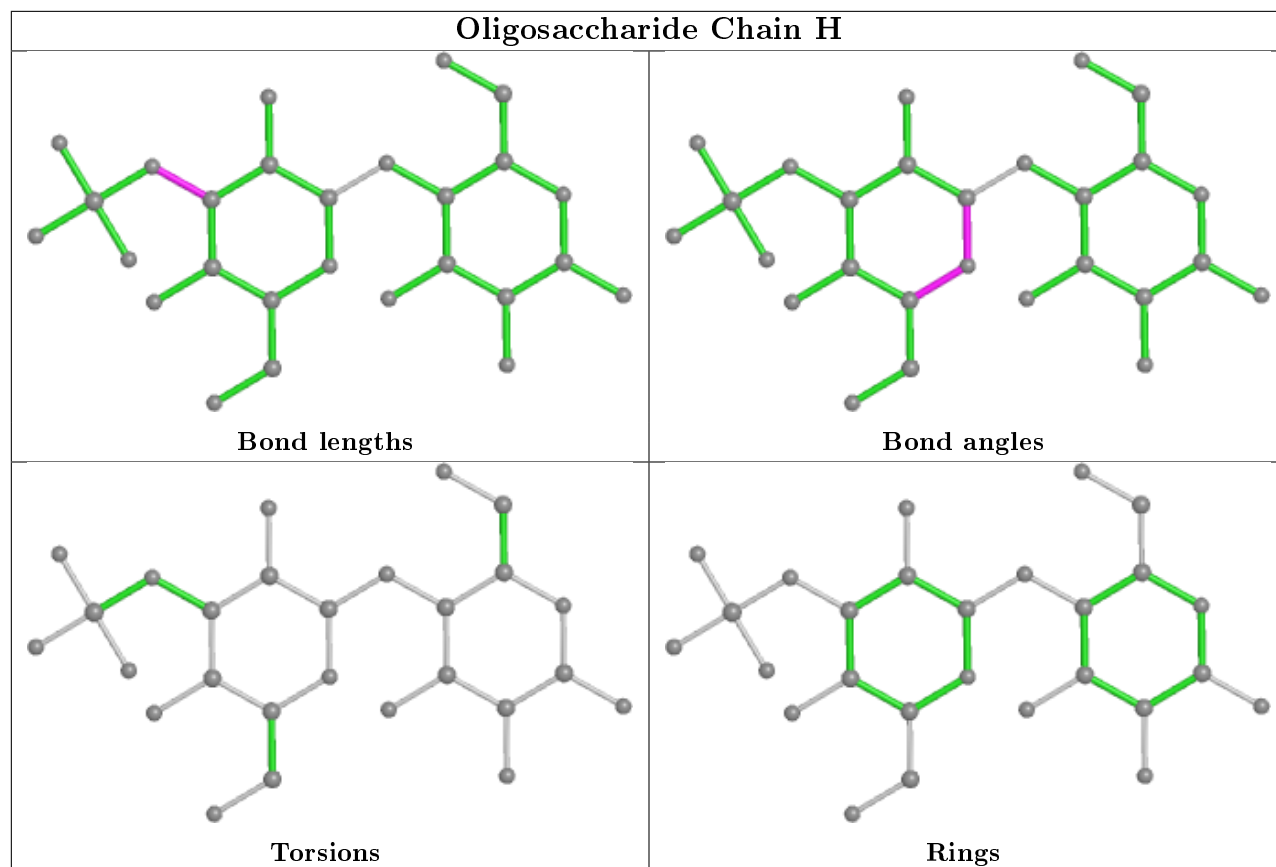


Oligosaccharide Chain F



Oligosaccharide Chain G





5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	138/155 (89%)	-0.33	0 100 100	8, 14, 29, 37	0
1	B	139/155 (89%)	-0.26	1 (0%) 87 90	8, 14, 33, 56	0
1	C	137/155 (88%)	-0.32	1 (0%) 87 90	8, 14, 29, 47	0
1	D	137/155 (88%)	-0.28	1 (0%) 87 90	9, 14, 29, 42	0
All	All	551/620 (88%)	-0.30	3 (0%) 91 92	8, 14, 30, 56	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	71	TRP	2.8
1	B	153	GLN	2.3
1	D	71	TRP	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

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.

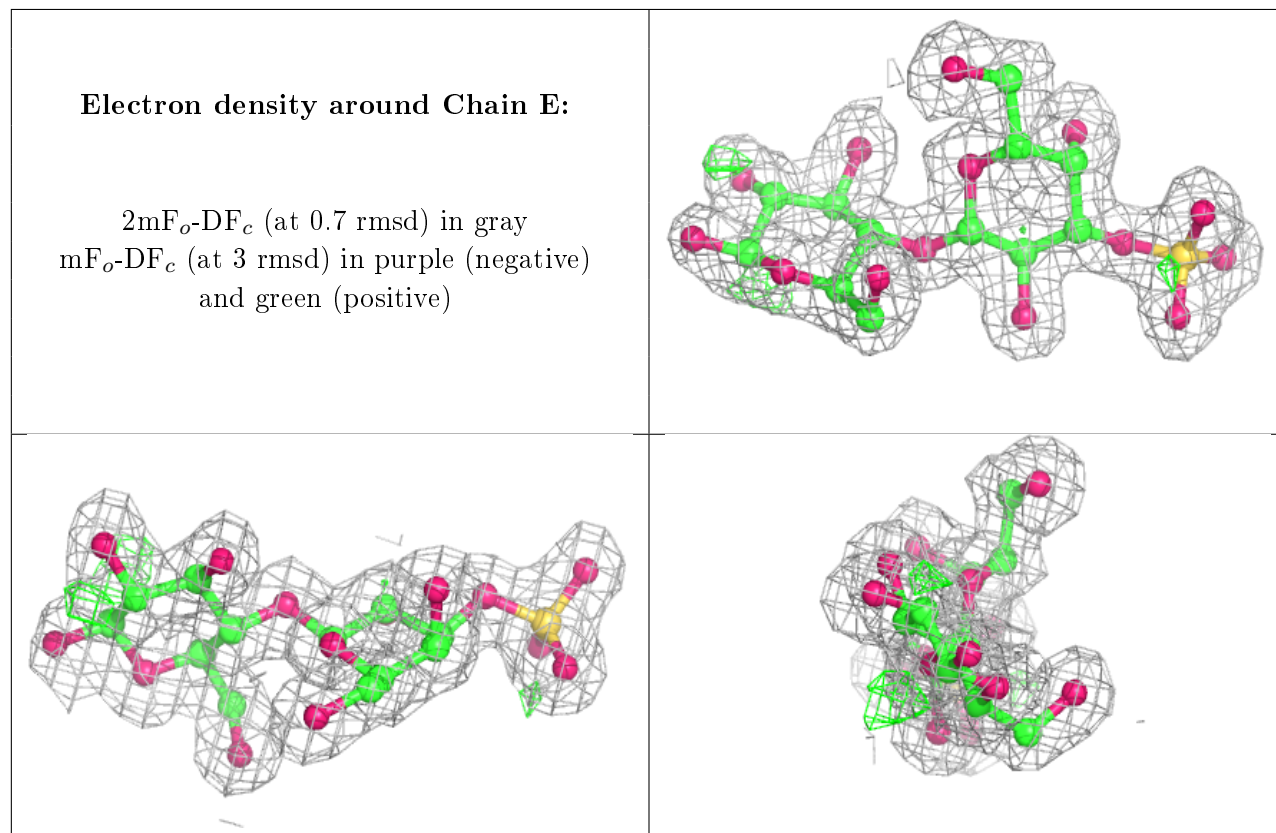
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	BGC	H	1	12/12	0.94	0.10	12,16,23,26	0
2	BGC	E	1	12/12	0.95	0.09	11,13,24,32	0
2	BGC	F	1	12/12	0.95	0.10	14,18,22,26	0
2	BGC	G	1	12/12	0.95	0.09	9,14,18,24	0

Continued on next page...

Continued from previous page...

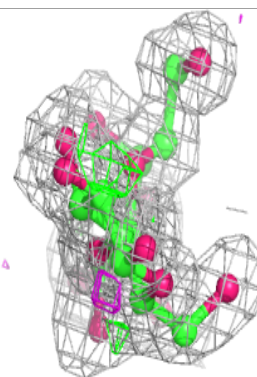
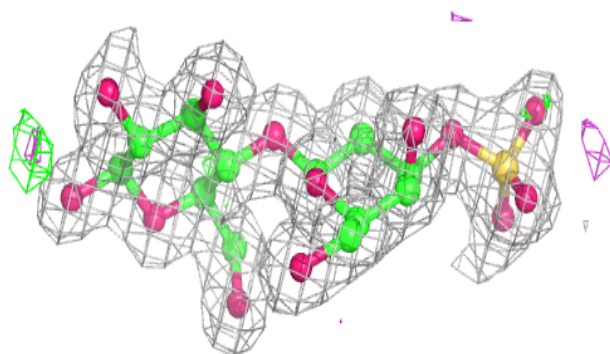
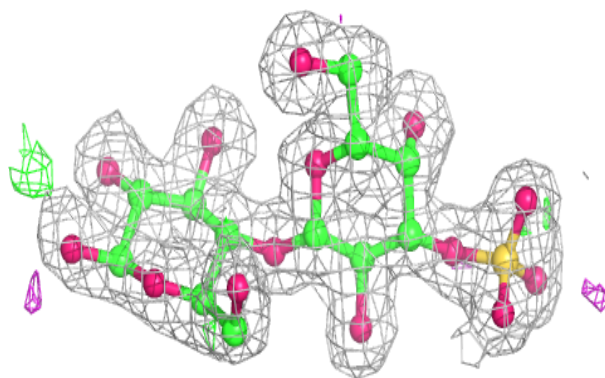
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SGA	F	2	15/16	0.97	0.07	10,14,24,27	0
2	SGA	H	2	15/16	0.98	0.07	10,13,22,24	0
2	SGA	E	2	15/16	0.98	0.07	9,10,16,17	0
2	SGA	G	2	15/16	0.98	0.06	9,10,16,16	0

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.

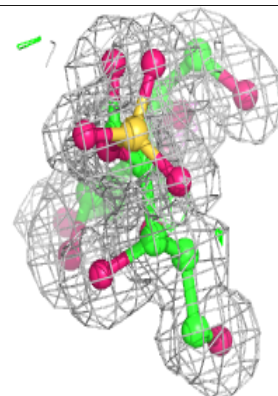
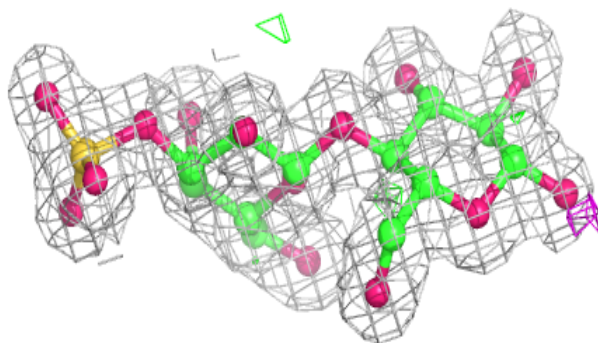
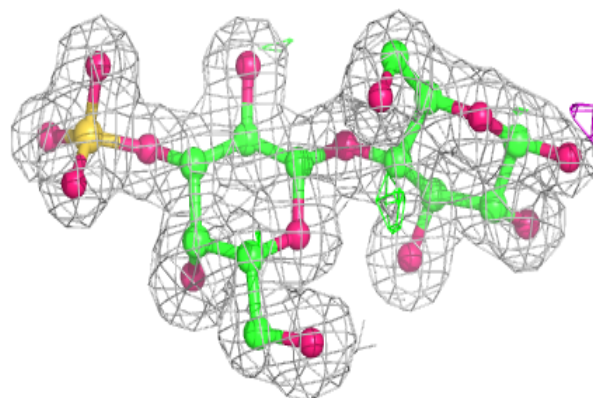


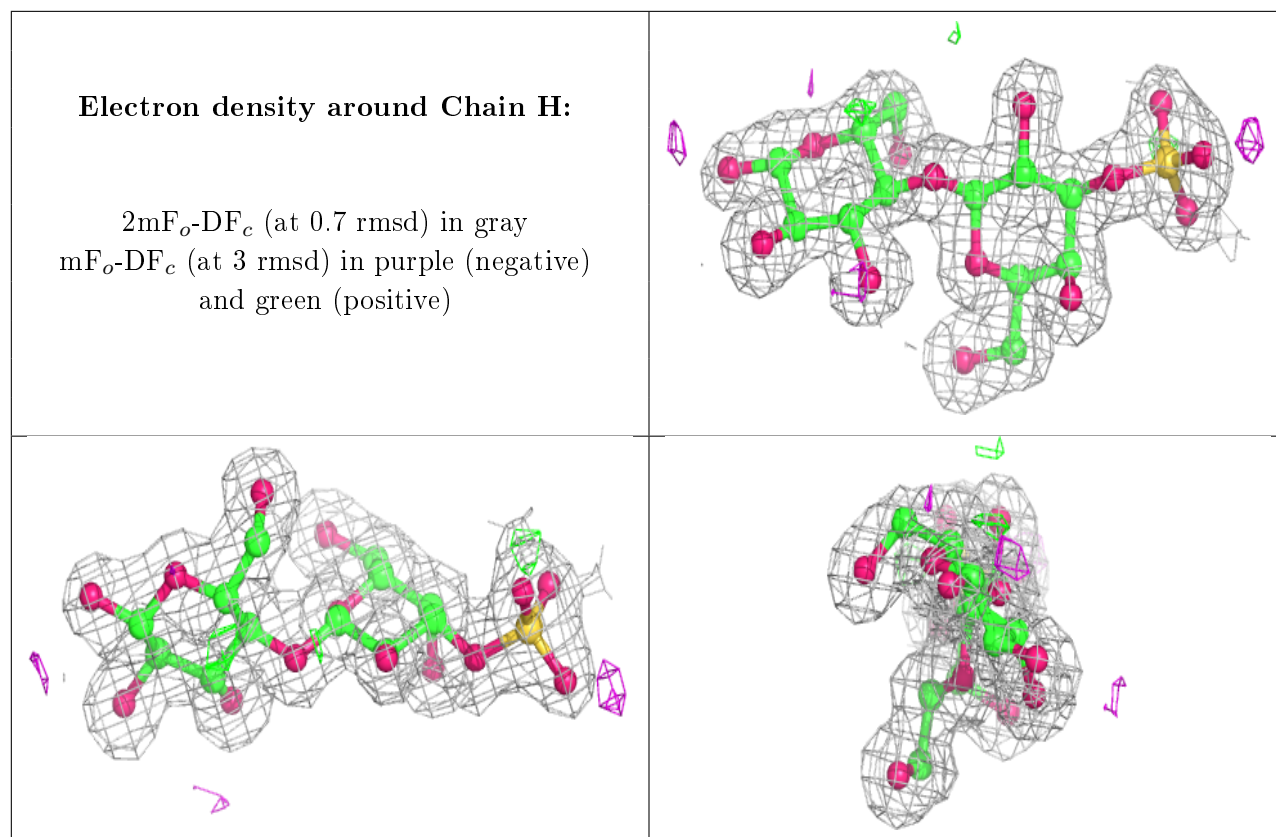
Electron density around Chain F:

$2mF_o - DF_c$ (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)





6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.