



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 14, 2023 – 01:48 PM JST

PDB ID : 5ZIC
Title : Crystal structure of human GnT-V luminal domain in complex with acceptor sugar
Authors : Nagae, M.; Yamaguchi, Y.
Deposited on : 2018-03-14
Resolution : 2.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

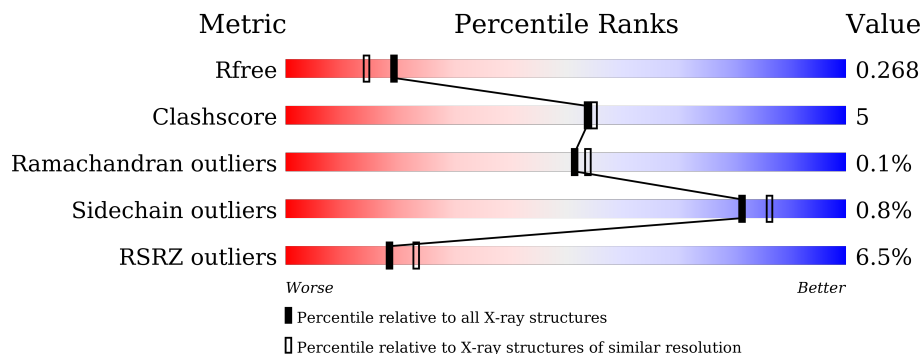
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION




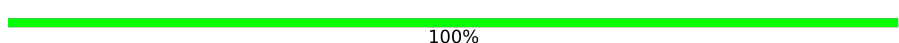
The reported resolution of this entry is 2.10 Å.

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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	523	 5% 82% 11% 7%
1	B	523	 7% 81% 13% 5%
2	C	3	 67% 33%
2	D	3	 100%

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 8253 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 Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyl transferase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	485	3946	2547	677	696	26	0	0	0
1	B	496	4015	2591	687	711	26	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	208	GLY	-	expression tag	UNP Q09328
A	209	LYS	-	expression tag	UNP Q09328
A	210	ASP	-	expression tag	UNP Q09328
A	211	GLY	-	expression tag	UNP Q09328
A	212	SER	-	expression tag	UNP Q09328
A	341	GLY	-	linker	UNP Q09328
A	342	GLY	-	linker	UNP Q09328
A	343	GLY	-	linker	UNP Q09328
A	344	GLY	-	linker	UNP Q09328
B	208	GLY	-	expression tag	UNP Q09328
B	209	LYS	-	expression tag	UNP Q09328
B	210	ASP	-	expression tag	UNP Q09328
B	211	GLY	-	expression tag	UNP Q09328
B	212	SER	-	expression tag	UNP Q09328
B	341	GLY	-	linker	UNP Q09328
B	342	GLY	-	linker	UNP Q09328
B	343	GLY	-	linker	UNP Q09328
B	344	GLY	-	linker	UNP Q09328

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-6-thio-alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	S	0	0	0
			37	20	1	15	1			
2	D	3	Total	C	N	O	S	0	0	0
			37	20	1	15	1			

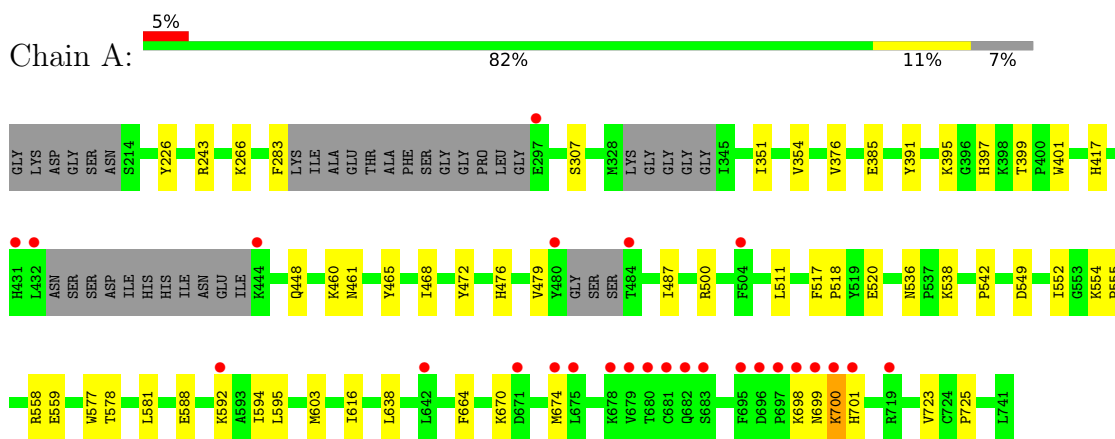
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	126	Total	O	0	0
			126	126		
3	B	92	Total	O	0	0
			92	92		

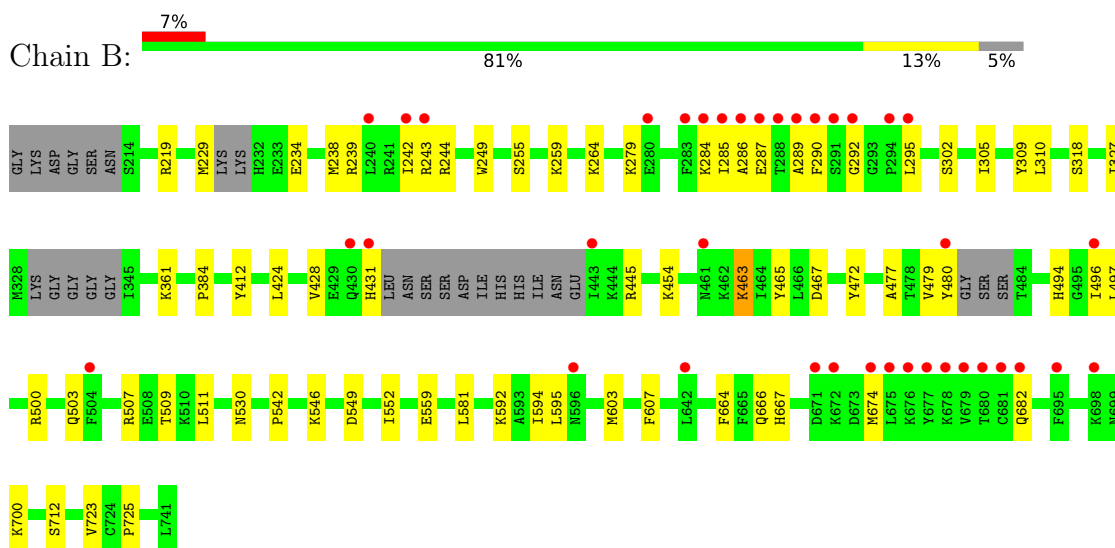
3 Residue-property plots [i](#)

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: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A



- Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-6-thio-alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose



BVAL
Z4Y2
MAG3

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-6-thio-alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose

Chain D:

100%

BVAL
Z4Y2
MAG3

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	70.42Å 89.20Å 92.23Å 90.00° 105.55° 90.00°	Depositor
Resolution (Å)	44.60 – 2.10 44.60 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.3 (44.60-2.10) 98.3 (44.60-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 2.10Å)	Xtrriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.215 , 0.268 0.215 , 0.268	Depositor DCC
R_{free} test set	3197 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	36.5	Xtrriage
Anisotropy	0.018	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8253	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.85% 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: BMA, Z4Y, NAG

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	0.25	0/4047	0.44	0/5463
1	B	0.27	0/4118	0.46	0/5561
All	All	0.26	0/8165	0.45	0/11024

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	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	700	LYS	Peptide
1	B	234	GLU	Peptide

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	3946	0	3935	35	0
1	B	4015	0	3997	50	0
2	C	37	0	24	1	0
2	D	37	0	24	0	0
3	A	126	0	0	0	0
3	B	92	0	0	0	0
All	All	8253	0	7980	85	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.

All (85) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:480:TYR:CZ	1:B:496:ILE:HD11	2.12	0.83
1:B:454:LYS:HD2	1:B:480:TYR:OH	1.87	0.73
1:A:699:ASN:O	1:A:701:HIS:N	2.23	0.71
1:B:682:GLN:HG2	1:B:700:LYS:HB2	1.74	0.69
1:B:454:LYS:HD2	1:B:480:TYR:CZ	2.29	0.67
1:B:454:LYS:HB3	1:B:480:TYR:CE2	2.29	0.66
1:B:285:ILE:O	1:B:289:ALA:N	2.20	0.65
1:B:431:HIS:CE1	1:B:503:GLN:HG3	2.33	0.64
1:B:284:LYS:HB3	1:B:287:GLU:HG2	1.81	0.62
1:B:480:TYR:CE1	1:B:496:ILE:HD11	2.34	0.62
1:A:307:SER:HB3	1:A:616:ILE:HG21	1.81	0.61
1:B:445:ARG:NH2	1:B:530:ASN:O	2.24	0.59
1:B:244:ARG:HD2	1:B:431:HIS:CD2	2.38	0.58
1:A:511:LEU:HD13	1:A:594:ILE:HD13	1.86	0.58
1:B:229:MET:HB2	1:B:239:ARG:HH21	1.68	0.58
1:B:431:HIS:CD2	1:B:500:ARG:HG3	2.38	0.58
1:A:399:THR:HG22	1:A:401:TRP:H	1.68	0.57
1:B:229:MET:O	1:B:239:ARG:NH2	2.39	0.56
1:A:542:PRO:HB2	1:A:559:GLU:HB3	1.89	0.55
1:B:290:PHE:O	1:B:480:TYR:HD1	1.90	0.55
1:B:249:TRP:HB3	1:B:310:LEU:HD11	1.90	0.53
1:A:520:GLU:OE2	1:A:558:ARG:NH1	2.39	0.53
1:B:445:ARG:NH1	1:B:509:THR:O	2.41	0.53
1:B:549:ASP:HA	1:B:552:ILE:HG13	1.91	0.52
1:B:428:VAL:HG23	1:B:607:PHE:HB3	1.92	0.52
1:A:664:PHE:HB2	1:A:725:PRO:HB2	1.92	0.51
1:B:664:PHE:HB2	1:B:725:PRO:HB2	1.91	0.51
1:A:674:MET:HE1	1:A:723:VAL:HG11	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:468:ILE:HG23	1:A:588:GLU:HG3	1.94	0.49
1:B:229:MET:CB	1:B:239:ARG:HH21	2.26	0.48
1:A:670:LYS:O	1:A:674:MET:HG2	2.15	0.47
1:B:666:GLN:HG3	1:B:667:HIS:CD2	2.49	0.47
1:B:238:MET:O	1:B:242:ILE:HD12	2.14	0.47
1:A:391:TYR:CZ	1:A:395:LYS:HE3	2.50	0.47
1:A:479:VAL:HG21	1:A:487:ILE:HD11	1.96	0.47
1:B:511:LEU:HD13	1:B:594:ILE:HD13	1.97	0.47
1:B:238:MET:HG2	1:B:302:SER:HB2	1.96	0.46
1:B:494:HIS:CB	1:B:497:LEU:HD11	2.45	0.46
1:B:674:MET:HE2	1:B:723:VAL:HG21	1.97	0.46
1:A:592:LYS:HZ2	1:A:595:LEU:HB3	1.81	0.46
1:A:417:HIS:HB2	1:A:558:ARG:HD2	1.98	0.46
1:B:286:ALA:O	1:B:290:PHE:HB2	2.14	0.46
1:B:454:LYS:HB3	1:B:480:TYR:CD2	2.51	0.46
1:B:465:TYR:CD1	1:B:581:LEU:HG	2.52	0.45
1:A:465:TYR:CE1	1:A:581:LEU:HD22	2.52	0.45
1:A:266:LYS:HE3	1:A:266:LYS:HB2	1.68	0.45
1:B:496:ILE:HG23	1:B:496:ILE:HD12	1.55	0.45
1:B:465:TYR:CG	1:B:581:LEU:HG	2.52	0.45
1:B:477:ALA:HB1	1:B:479:VAL:HG23	1.99	0.44
1:B:255:SER:OG	1:B:259:LYS:NZ	2.50	0.44
1:A:592:LYS:NZ	1:A:595:LEU:HD13	2.32	0.43
1:A:592:LYS:HA	1:A:592:LYS:HD2	1.72	0.43
1:B:503:GLN:O	1:B:507:ARG:N	2.44	0.43
1:B:292:GLY:O	1:B:454:LYS:HE3	2.19	0.43
1:A:351:ILE:O	1:A:376:VAL:HA	2.19	0.43
1:A:592:LYS:HZ3	1:A:595:LEU:HD13	1.84	0.43
1:B:238:MET:HE1	1:B:305:ILE:HD12	2.00	0.43
1:B:318:SER:HB2	1:B:327:ILE:HD12	2.01	0.42
1:A:517:PHE:CG	1:A:518:PRO:HA	2.54	0.42
1:A:603:MET:HE2	1:A:603:MET:HB2	1.91	0.42
1:B:496:ILE:HA	1:B:496:ILE:HD13	1.69	0.42
1:A:538:LYS:HB2	1:A:578:THR:HG22	2.01	0.42
1:B:384:PRO:HG2	1:B:712:SER:HA	2.00	0.42
1:B:542:PRO:HB2	1:B:559:GLU:HB3	2.01	0.42
1:B:412:TYR:HB3	1:B:424:LEU:HB2	2.01	0.42
1:B:472:TYR:OH	1:B:592:LYS:HE2	2.20	0.42
1:B:494:HIS:HB3	1:B:497:LEU:HD11	2.02	0.42
1:A:226:TYR:OH	1:A:243:ARG:HG2	2.20	0.41
1:A:460:LYS:HG2	1:A:461:ASN:OD1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:385:GLU:CD	1:A:397:HIS:HE2	2.22	0.41
1:B:264:LYS:HD2	1:B:264:LYS:HA	1.86	0.41
1:A:283:PHE:CE2	1:A:354:VAL:HG21	2.55	0.41
1:A:536:ASN:O	1:A:578:THR:HA	2.20	0.41
1:A:549:ASP:HA	1:A:552:ILE:HG13	2.02	0.41
1:A:638:LEU:HD13	1:A:664:PHE:HB3	2.03	0.41
1:B:279:LYS:H	1:B:279:LYS:CD	2.34	0.41
1:B:472:TYR:HB3	1:B:595:LEU:HD11	2.03	0.41
1:A:472:TYR:HB3	1:A:595:LEU:HD12	2.03	0.41
1:A:399:THR:HG21	1:A:555:PRO:HB3	2.02	0.41
1:A:448:GLN:HB2	1:A:476:HIS:CD2	2.56	0.40
1:A:554:LYS:HD2	2:C:3:NAG:O6	2.21	0.40
1:B:219:ARG:HD2	1:B:309:TYR:CZ	2.56	0.40
1:B:463:LYS:HE3	1:B:467:ASP:OD1	2.21	0.40
1:A:577:TRP:CD1	1:A:594:ILE:HD11	2.57	0.40
1:B:546:LYS:HA	1:B:546:LYS:HD2	1.90	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	475/523 (91%)	460 (97%)	14 (3%)	1 (0%)	47	49
1	B	486/523 (93%)	473 (97%)	13 (3%)	0	100	100
All	All	961/1046 (92%)	933 (97%)	27 (3%)	1 (0%)	51	54

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	700	LYS

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	435/462 (94%)	433 (100%)	2 (0%)	88	92
1	B	441/462 (96%)	436 (99%)	5 (1%)	73	79
All	All	876/924 (95%)	869 (99%)	7 (1%)	81	86

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	500	ARG
1	A	698	LYS
1	B	243	ARG
1	B	295	LEU
1	B	361	LYS
1	B	463	LYS
1	B	603	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	232	HIS
1	A	596	ASN
1	A	699	ASN
1	B	431	HIS

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

6 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	C	1	2	12,12,12	0.48	0	17,17,17	0.70	0
2	Z4Y	C	2	2	11,11,12	0.22	0	15,15,17	0.76	0
2	NAG	C	3	2	14,14,15	0.22	0	17,19,21	0.42	0
2	BMA	D	1	2	12,12,12	0.47	0	17,17,17	0.78	0
2	Z4Y	D	2	2	11,11,12	0.24	0	15,15,17	0.75	0
2	NAG	D	3	2	14,14,15	0.33	0	17,19,21	0.33	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	C	1	2	-	0/2/22/22	0/1/1/1
2	Z4Y	C	2	2	-	0/2/19/22	0/1/1/1
2	NAG	C	3	2	-	0/6/23/26	0/1/1/1
2	BMA	D	1	2	-	0/2/22/22	0/1/1/1
2	Z4Y	D	2	2	-	0/2/19/22	0/1/1/1
2	NAG	D	3	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

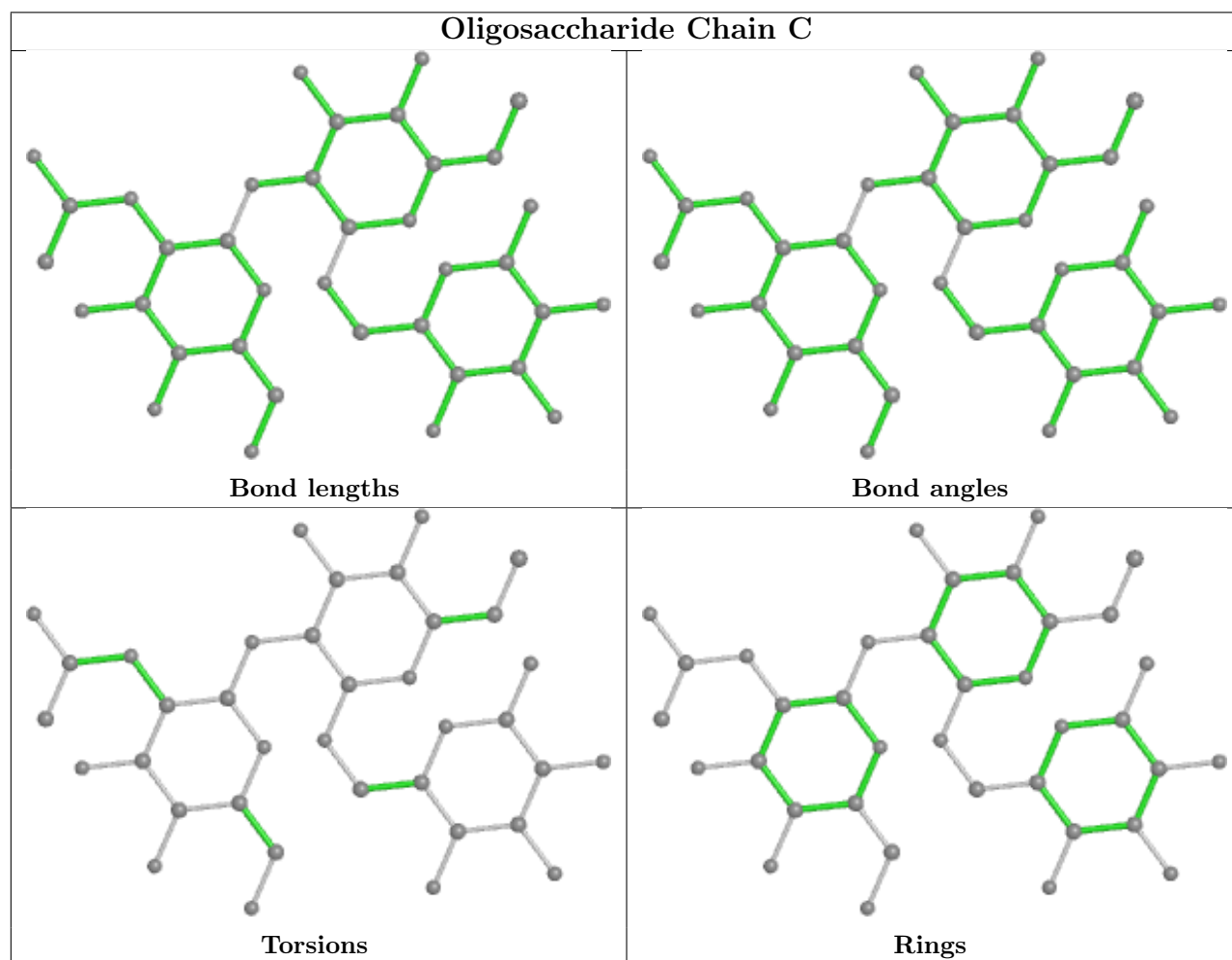
There are no torsion outliers.

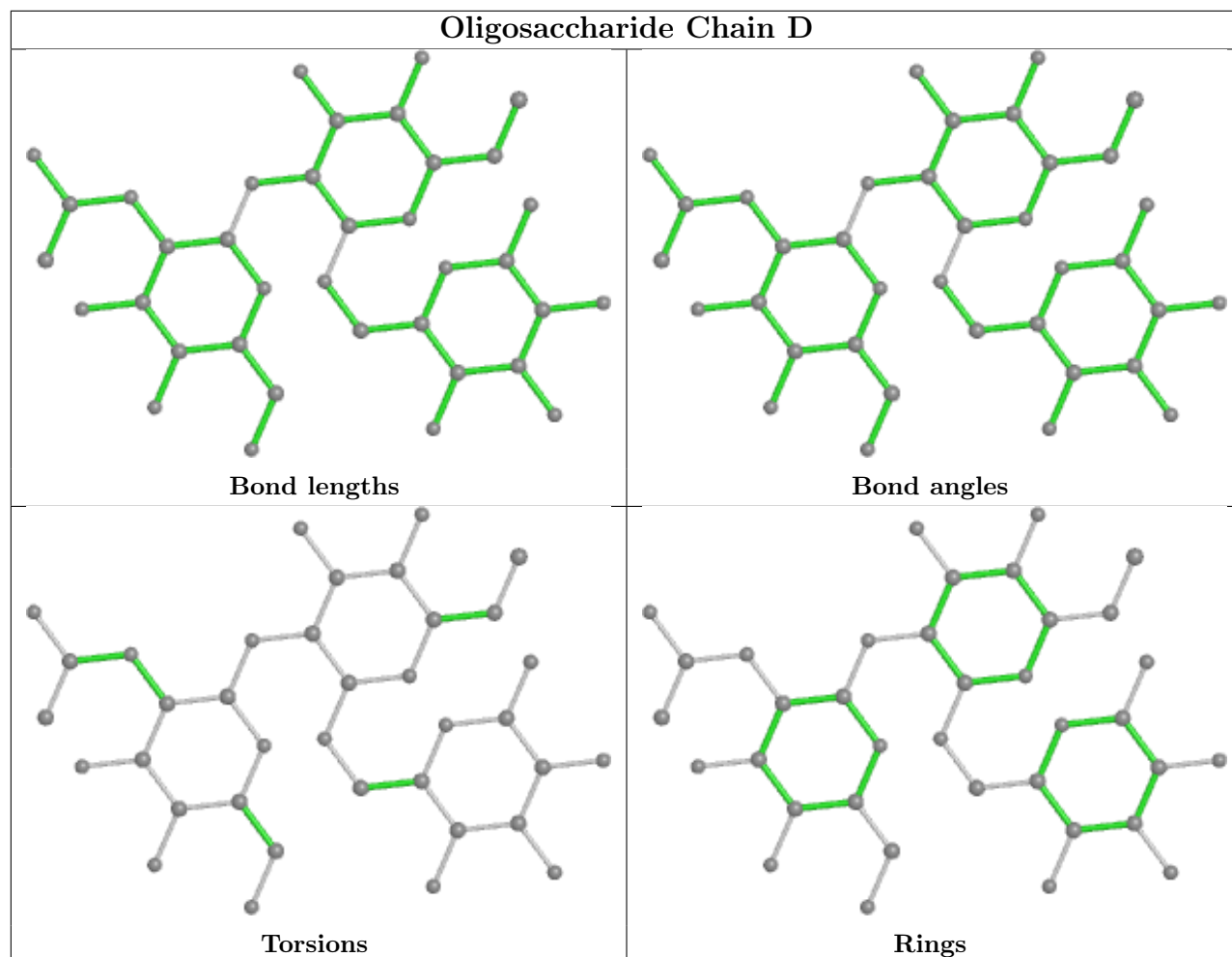
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	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](#)

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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	485/523 (92%)	0.32	26 (5%) 25 31	22, 38, 65, 83	0
1	B	496/523 (94%)	0.44	38 (7%) 13 17	25, 42, 72, 90	0
All	All	981/1046 (93%)	0.38	64 (6%) 18 23	22, 40, 70, 90	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	675	LEU	6.7
1	B	480	TYR	6.4
1	B	290	PHE	6.3
1	B	681	CYS	5.8
1	A	680	THR	5.5
1	B	680	THR	5.2
1	A	480	TYR	4.8
1	B	431	HIS	4.8
1	B	284	LYS	4.7
1	A	681	CYS	4.6
1	A	675	LEU	4.3
1	A	679	VAL	4.1
1	A	697	PRO	4.1
1	B	682	GLN	4.1
1	B	679	VAL	4.0
1	A	682	GLN	3.9
1	A	695	PHE	3.9
1	B	443	ILE	3.9
1	A	297	GLU	3.7
1	A	678	LYS	3.6
1	A	700	LYS	3.6
1	B	285	ILE	3.5
1	B	280	GLU	3.4
1	B	678	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	672	LYS	3.3
1	B	504	PHE	3.3
1	A	696	ASP	3.2
1	B	291	SER	3.0
1	B	292	GLY	3.0
1	B	642	LEU	3.0
1	A	698	LYS	3.0
1	B	430	GLN	3.0
1	B	243	ARG	3.0
1	B	287	GLU	2.8
1	B	677	TYR	2.8
1	A	701	HIS	2.8
1	A	671	ASP	2.8
1	A	683	SER	2.8
1	A	444	LYS	2.8
1	B	695	PHE	2.8
1	B	671	ASP	2.7
1	A	432	LEU	2.7
1	A	699	ASN	2.7
1	B	240	LEU	2.7
1	B	295	LEU	2.6
1	B	242	ILE	2.5
1	B	283	PHE	2.5
1	B	288	THR	2.5
1	A	719	ARG	2.4
1	B	294	PRO	2.4
1	A	642	LEU	2.4
1	B	286	ALA	2.3
1	B	496	ILE	2.3
1	A	674	MET	2.3
1	B	289	ALA	2.3
1	B	596	ASN	2.3
1	B	698	LYS	2.2
1	A	484	THR	2.1
1	A	504	PHE	2.1
1	B	676	LYS	2.1
1	B	674	MET	2.1
1	A	431	HIS	2.0
1	A	592	LYS	2.0
1	B	461	ASN	2.0

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

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

6.3 Carbohydrates [i](#)

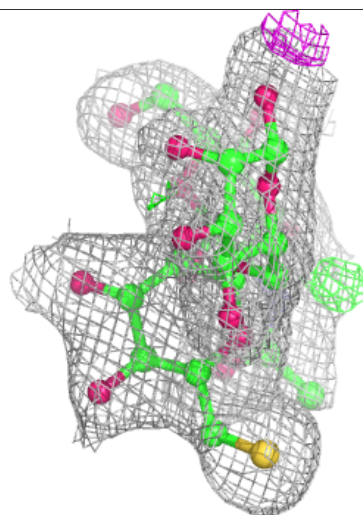
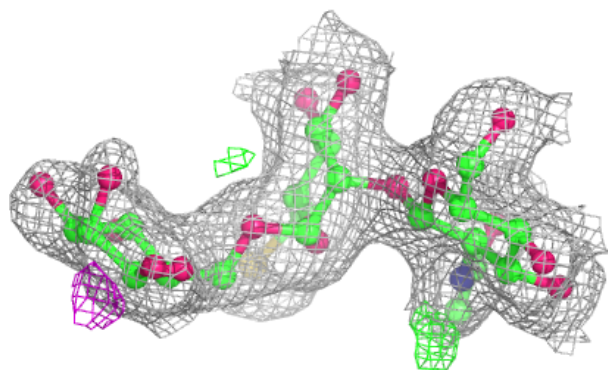
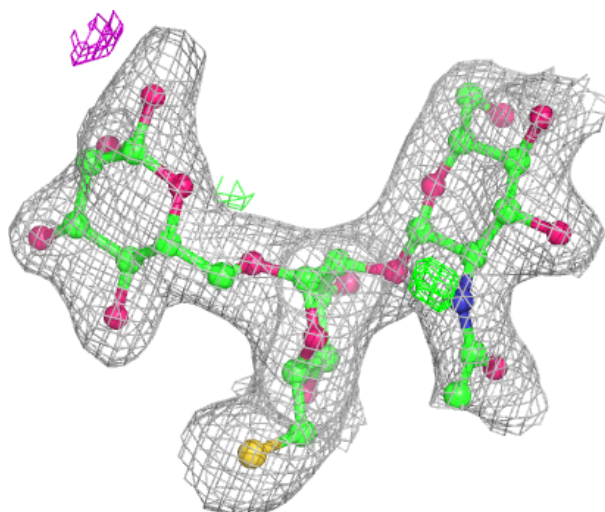
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

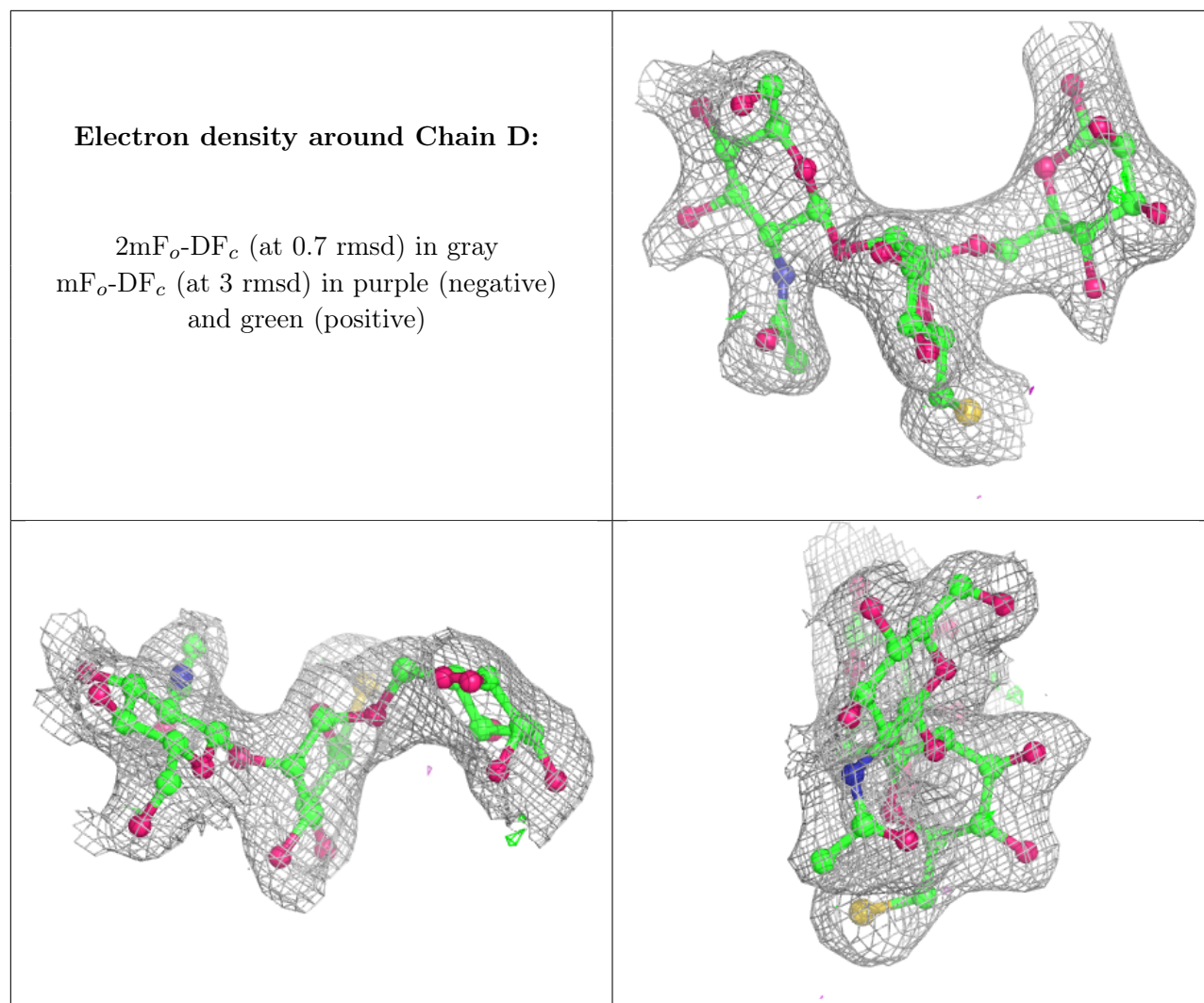
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	BMA	D	1	12/12	0.84	0.12	50,59,62,65	0
2	BMA	C	1	12/12	0.86	0.12	36,45,56,57	0
2	NAG	D	3	14/15	0.92	0.15	31,35,45,50	0
2	Z4Y	C	2	11/12	0.95	0.10	30,34,43,50	0
2	Z4Y	D	2	11/12	0.95	0.12	38,44,49,62	0
2	NAG	C	3	14/15	0.95	0.13	24,29,40,40	0

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 C:

$2mF_o-DF_c$ (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.