



wwPDB X-ray Structure Validation Summary Report

Mar 5, 2026 – 12:19 AM UTC

PDB ID : 2YLA / pdb_00002yla
Title : INHIBITION OF THE PNEUMOCOCCAL VIRULENCE FACTOR STRH AND MOLECULAR INSIGHTS INTO N-GLYCAN RECOGNITION AND HYDROLYSIS
Authors : Pluinage, B.; Higgins, M.A.; Abbott, D.W.; Robb, C.; Dalia, A.B.; Deng, L.; Weiser, J.N.; Parsons, T.B.; Fairbanks, A.J.; Vocadlo, D.J.; Boraston, A.B.
Deposited on : 2011-06-01
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the  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)
Xtrriage (Phenix) : 2.0
EDS : 3.0
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

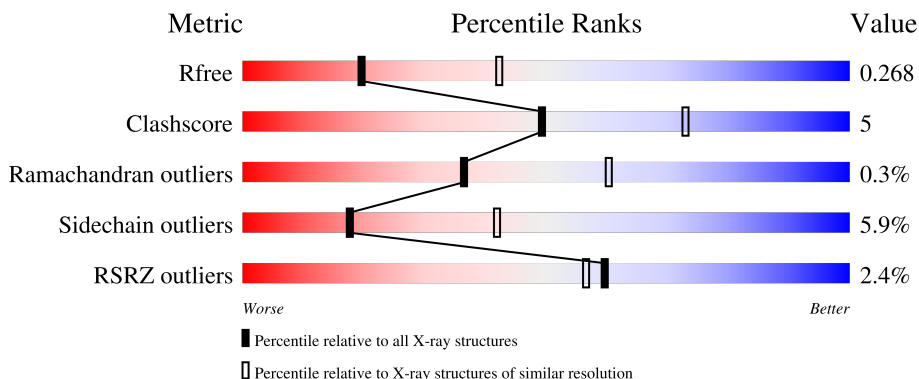
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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



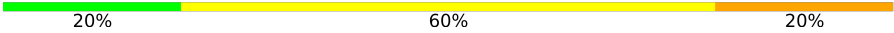

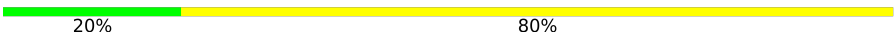

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	442	 2% 79% 13% • 6%
1	B	442	 4% 77% 15% • 6%
1	C	442	 2% 78% 13% • 8%
1	D	442	 % 78% 12% • 8%

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Mol	Chain	Length	Quality of chain
2	E	5	
2	F	5	
2	H	5	
3	G	4	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 14253 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.

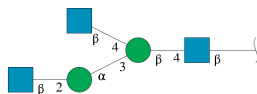
- Molecule 1 is a protein called BETA-N-ACETYLHEXOSAMINIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	416	3321	2128	542	639	12	21	2	0
1	B	417	3317	2126	539	640	12	13	0	0
1	C	408	3267	2097	532	626	12	16	2	0
1	D	408	3261	2092	531	626	12	28	1	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	623	GLY	-	expression tag	UNP P49610
A	624	SER	-	expression tag	UNP P49610
A	625	HIS	-	expression tag	UNP P49610
A	626	MET	-	expression tag	UNP P49610
A	805	GLN	GLU	engineered mutation	UNP P49610
B	623	GLY	-	expression tag	UNP P49610
B	624	SER	-	expression tag	UNP P49610
B	625	HIS	-	expression tag	UNP P49610
B	626	MET	-	expression tag	UNP P49610
B	805	GLN	GLU	engineered mutation	UNP P49610
C	623	GLY	-	expression tag	UNP P49610
C	624	SER	-	expression tag	UNP P49610
C	625	HIS	-	expression tag	UNP P49610
C	626	MET	-	expression tag	UNP P49610
C	805	GLN	GLU	engineered mutation	UNP P49610
D	623	GLY	-	expression tag	UNP P49610
D	624	SER	-	expression tag	UNP P49610
D	625	HIS	-	expression tag	UNP P49610
D	626	MET	-	expression tag	UNP P49610
D	805	GLN	GLU	engineered mutation	UNP P49610

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	E	5	65	36	3	26	0	0	0
2	F	5	65	36	3	26	0	0	0
2	H	5	65	36	3	26	0	0	0

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	G	4	51	28	2	21	0	0	0

- 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	B	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	B	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	B	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	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

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

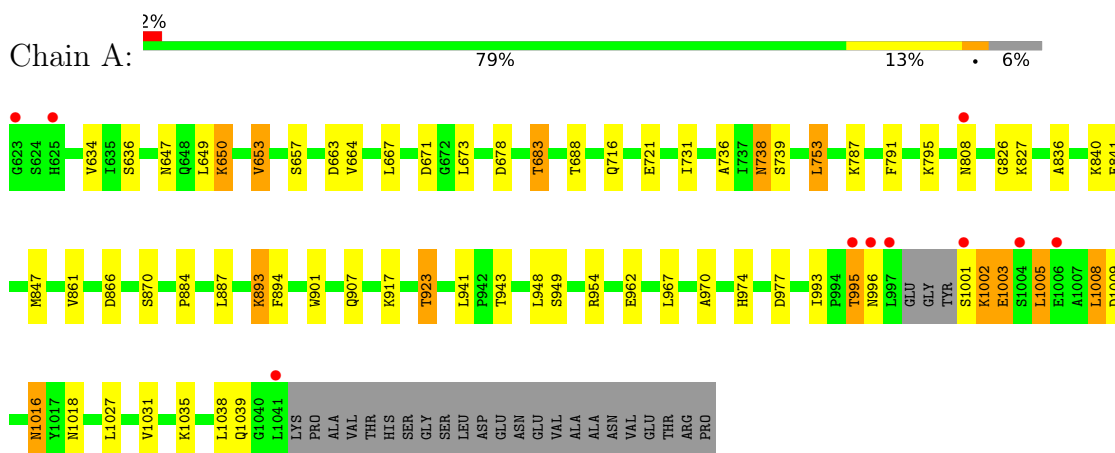
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	172	Total	O	0	2
			174	174		
5	B	197	Total	O	0	3
			200	200		
5	C	235	Total	O	0	2
			237	237		
5	D	168	Total	O	0	2
			170	170		

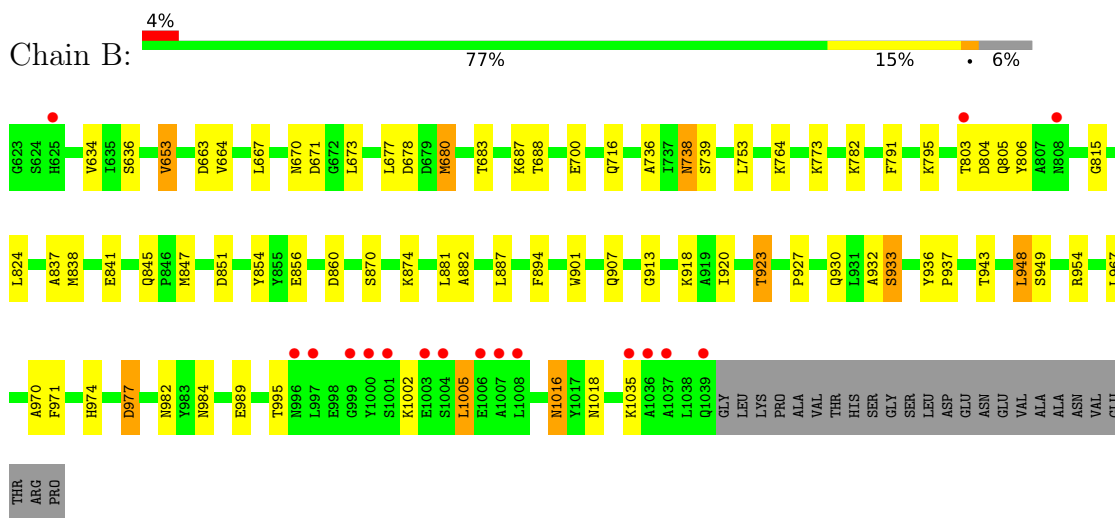
3 Residue-property plots [i](#)

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.

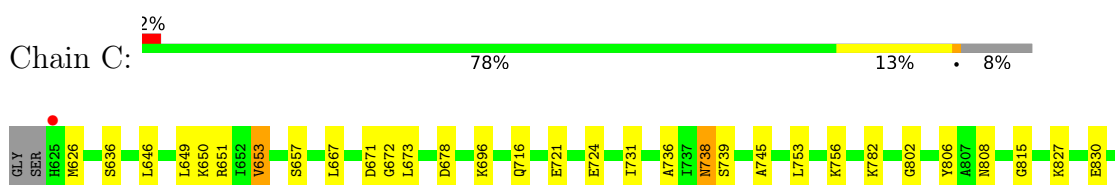
• Molecule 1: BETA-N-ACETYLHEXOSAMINIDASE

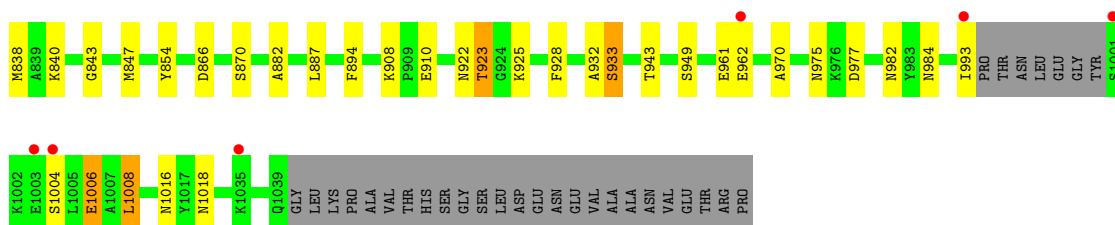


• Molecule 1: BETA-N-ACETYLHEXOSAMINIDASE

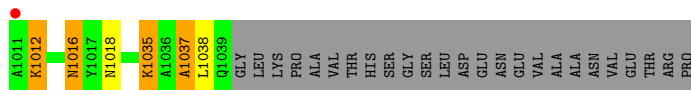
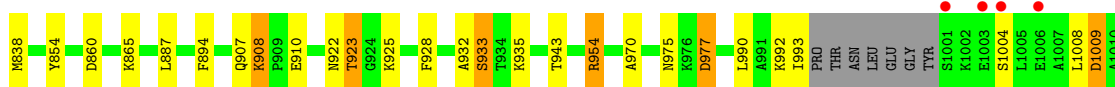
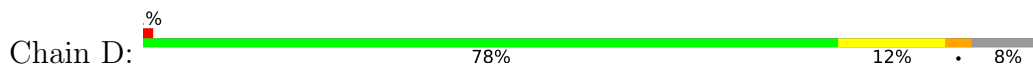


• Molecule 1: BETA-N-ACETYLHEXOSAMINIDASE

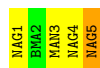




- Molecule 1: BETA-N-ACETYLHEXOSAMINIDASE



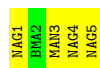
- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



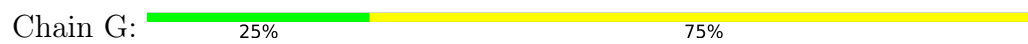
- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-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	67.56Å 115.71Å 132.21Å 90.00° 99.67° 90.00°	Depositor
Resolution (Å)	29.97 – 2.70 29.97 – 2.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.97-2.70) 99.9 (29.97-2.70)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.62 (at 2.68Å)	Xtrriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.223 , 0.273 0.221 , 0.268	Depositor DCC
R_{free} test set	2792 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	16.3	Xtrriage
Anisotropy	0.144	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 27.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14253	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 57.09 % 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 2.4880e-05. 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: BMA, EDO, NAG, MAN

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	0.68	8/3394 (0.2%)	0.86	9/4583 (0.2%)
1	B	0.68	3/3392 (0.1%)	0.81	3/4583 (0.1%)
1	C	0.82	4/3342 (0.1%)	0.92	7/4510 (0.2%)
1	D	1.27	13/3333 (0.4%)	0.86	8/4499 (0.2%)
All	All	0.89	28/13461 (0.2%)	0.86	27/18175 (0.1%)

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	B	0	1

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	1037	ALA	CA-CB	-40.07	0.85	1.53
1	D	756	LYS	CE-NZ	-39.50	0.30	1.49
1	C	724	GLU	CG-CD	30.24	2.27	1.52
1	B	1005	LEU	CA-CB	-25.95	1.10	1.53
1	C	908	LYS	CD-CE	-23.46	0.82	1.52

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	724	GLU	CB-CG-CD	-25.46	69.32	112.60
1	D	908	LYS	CG-CD-CE	17.60	151.78	111.30
1	C	908	LYS	CG-CD-CE	14.41	144.45	111.30
1	A	1035	LYS	CG-CD-CE	12.63	140.35	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	995	THR	N-CA-CB	-11.96	92.13	110.44

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	803	THR	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	3321	0	3252	42	0
1	B	3317	0	3240	42	0
1	C	3267	0	3207	29	0
1	D	3261	0	3194	28	0
2	E	65	0	57	1	0
2	F	65	0	57	2	0
2	H	65	0	57	0	0
3	G	51	0	45	0	0
4	A	8	0	12	0	0
4	B	40	0	60	2	0
4	C	8	0	12	1	0
4	D	4	0	6	0	0
5	A	174	0	0	0	0
5	B	200	0	0	0	0
5	C	237	0	0	0	0
5	D	170	0	0	0	0
All	All	14253	0	13199	142	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 142 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:982:ASN:HD21	1:B:984:ASN:HD22	1.21	0.87
1:A:907:GLN:NE2	1:A:954:ARG:HH12	1.79	0.80
1:D:907:GLN:NE2	1:D:954:ARG:HH12	1.85	0.75
1:B:678:ASP:H	1:B:716:GLN:HE21	1.34	0.73
1:B:845:GLN:HB2	4:B:1114:EDO:H11	1.70	0.73

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	414/442 (94%)	397 (96%)	16 (4%)	1 (0%)	43 68
1	B	415/442 (94%)	396 (95%)	17 (4%)	2 (0%)	24 48
1	C	406/442 (92%)	389 (96%)	16 (4%)	1 (0%)	43 68
1	D	405/442 (92%)	387 (96%)	17 (4%)	1 (0%)	43 68
All	All	1640/1768 (93%)	1569 (96%)	66 (4%)	5 (0%)	36 60

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	804	ASP
1	D	1037	ALA
1	A	671	ASP
1	B	805	GLN
1	C	671	ASP

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	344/363 (95%)	323 (94%)	21 (6%)	17	40
1	B	343/363 (94%)	325 (95%)	18 (5%)	21	47
1	C	338/363 (93%)	321 (95%)	17 (5%)	22	48
1	D	337/363 (93%)	313 (93%)	24 (7%)	13	33
All	All	1362/1452 (94%)	1282 (94%)	80 (6%)	18	42

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	650	LYS
1	D	954	ARG
1	D	654	ASP
1	D	860	ASP
1	D	1008	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	670	ASN
1	C	974	HIS
1	D	974	HIS
1	C	716	GLN
1	C	907	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

19 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	E	1	2	15,15,15	0.54	0	21,21,21	1.70	5 (23%)
2	BMA	E	2	2	11,11,12	0.87	0	15,15,17	0.80	0
2	MAN	E	3	2	11,11,12	0.52	0	15,15,17	0.89	1 (6%)
2	NAG	E	4	2	14,14,15	0.72	1 (7%)	17,19,21	2.24	3 (17%)
2	NAG	E	5	2	14,14,15	0.61	0	17,19,21	2.25	3 (17%)
2	NAG	F	1	2	15,15,15	0.45	0	21,21,21	0.84	0
2	BMA	F	2	2	11,11,12	0.88	0	15,15,17	0.75	0
2	MAN	F	3	2	11,11,12	0.53	0	15,15,17	1.12	1 (6%)
2	NAG	F	4	2	14,14,15	0.67	1 (7%)	17,19,21	2.20	4 (23%)
2	NAG	F	5	2	14,14,15	0.57	0	17,19,21	2.13	3 (17%)
3	NAG	G	1	3	15,15,15	0.58	0	21,21,21	1.49	4 (19%)
3	BMA	G	2	3	11,11,12	0.79	0	15,15,17	0.83	0
3	MAN	G	3	3	11,11,12	0.49	0	15,15,17	0.92	1 (6%)
3	NAG	G	4	3	14,14,15	0.67	1 (7%)	17,19,21	2.20	3 (17%)
2	NAG	H	1	2	15,15,15	0.57	0	21,21,21	1.49	4 (19%)
2	BMA	H	2	2	11,11,12	0.83	0	15,15,17	0.80	0
2	MAN	H	3	2	11,11,12	0.55	0	15,15,17	0.85	1 (6%)
2	NAG	H	4	2	14,14,15	0.74	1 (7%)	17,19,21	2.15	4 (23%)
2	NAG	H	5	2	14,14,15	0.59	0	17,19,21	1.25	2 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	1	2	-	4/6/26/26	0/1/1/1
2	BMA	E	2	2	-	2/2/19/22	0/1/1/1
2	MAN	E	3	2	-	2/2/19/22	0/1/1/1
2	NAG	E	4	2	-	2/6/23/26	0/1/1/1
2	NAG	E	5	2	-	5/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	F	1	2	-	2/6/26/26	0/1/1/1
2	BMA	F	2	2	-	0/2/19/22	0/1/1/1
2	MAN	F	3	2	-	1/2/19/22	0/1/1/1
2	NAG	F	4	2	-	2/6/23/26	0/1/1/1
2	NAG	F	5	2	-	4/6/23/26	0/1/1/1
3	NAG	G	1	3	-	5/6/26/26	0/1/1/1
3	BMA	G	2	3	-	0/2/19/22	0/1/1/1
3	MAN	G	3	3	-	1/2/19/22	0/1/1/1
3	NAG	G	4	3	-	4/6/23/26	0/1/1/1
2	NAG	H	1	2	-	3/6/26/26	0/1/1/1
2	BMA	H	2	2	-	0/2/19/22	0/1/1/1
2	MAN	H	3	2	-	2/2/19/22	0/1/1/1
2	NAG	H	4	2	-	3/6/23/26	0/1/1/1
2	NAG	H	5	2	-	3/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	4	NAG	C1-C2	2.43	1.55	1.52
2	E	4	NAG	C1-C2	2.35	1.55	1.52
3	G	4	NAG	C1-C2	2.17	1.55	1.52
2	F	4	NAG	C1-C2	2.16	1.55	1.52

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	5	NAG	C2-N2-C7	7.56	133.03	122.90
3	G	4	NAG	C1-O5-C5	7.15	121.76	112.19
2	F	5	NAG	C2-N2-C7	7.14	132.47	122.90
2	F	4	NAG	C1-O5-C5	6.92	121.45	112.19
2	E	4	NAG	C1-O5-C5	6.64	121.08	112.19

There are no chirality outliers.

5 of 45 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	5	NAG	C3-C2-N2-C7
2	F	5	NAG	C3-C2-N2-C7
2	E	3	MAN	O5-C5-C6-O6

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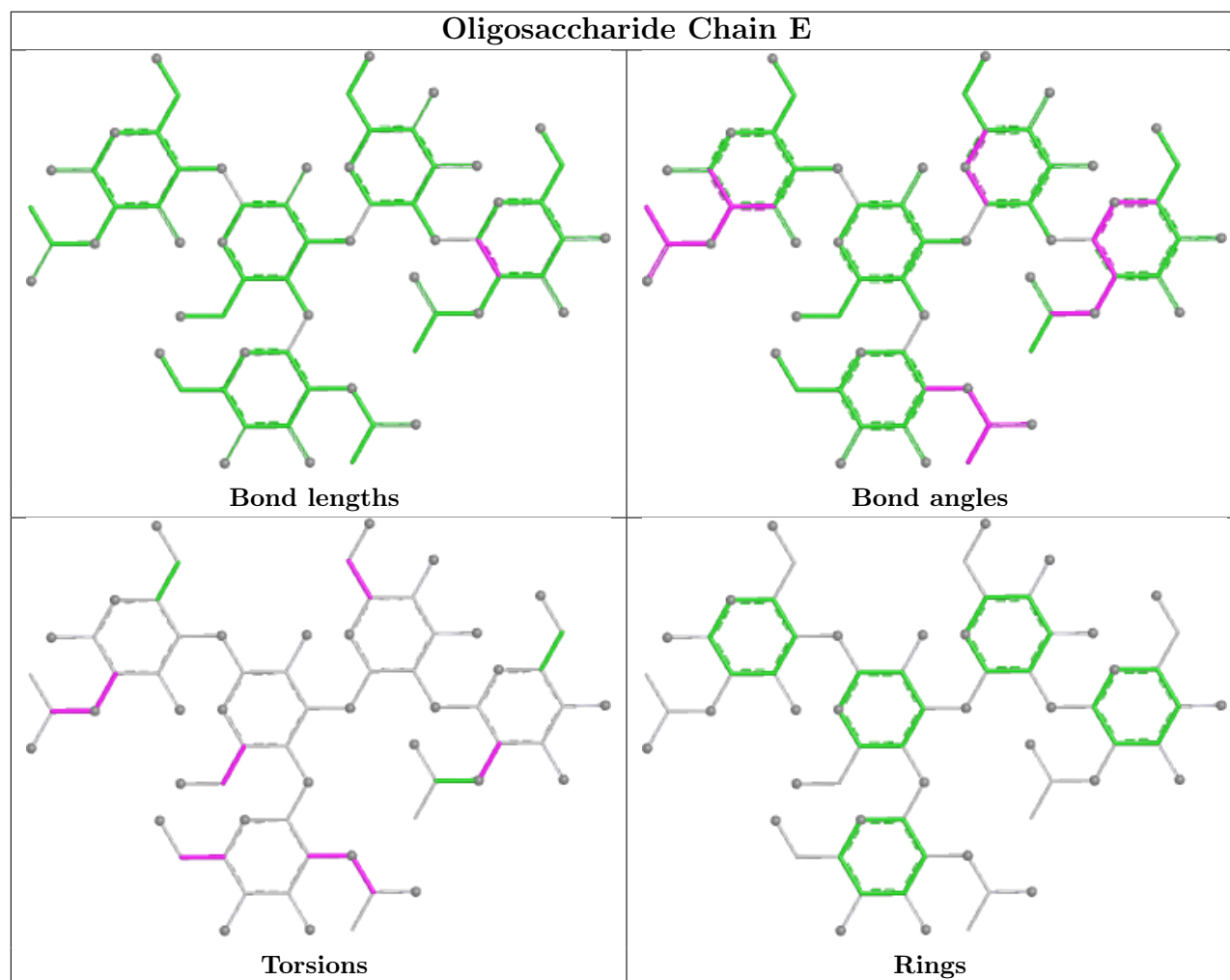
Mol	Chain	Res	Type	Atoms
3	G	4	NAG	O5-C5-C6-O6
2	E	3	MAN	C4-C5-C6-O6

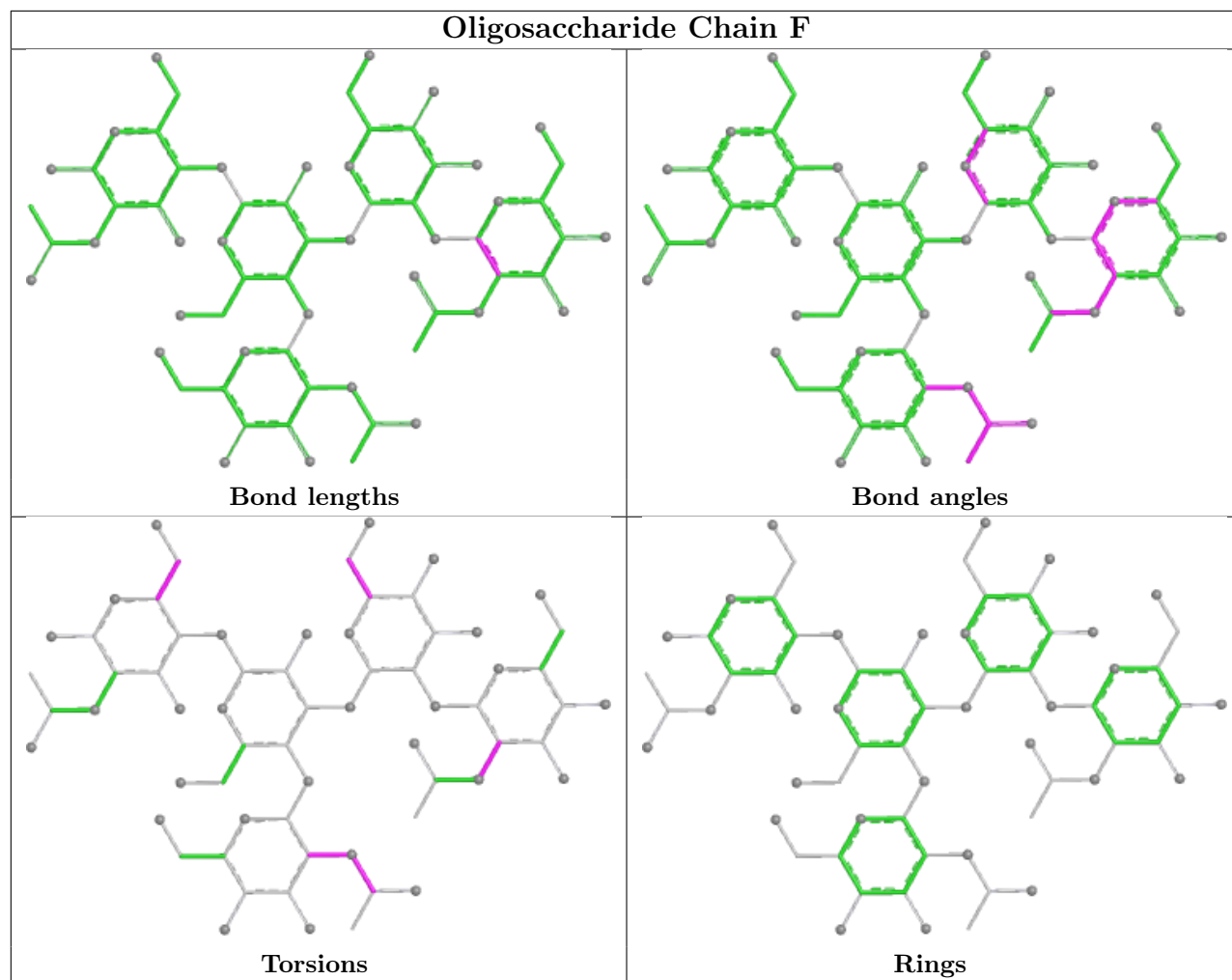
There are no ring outliers.

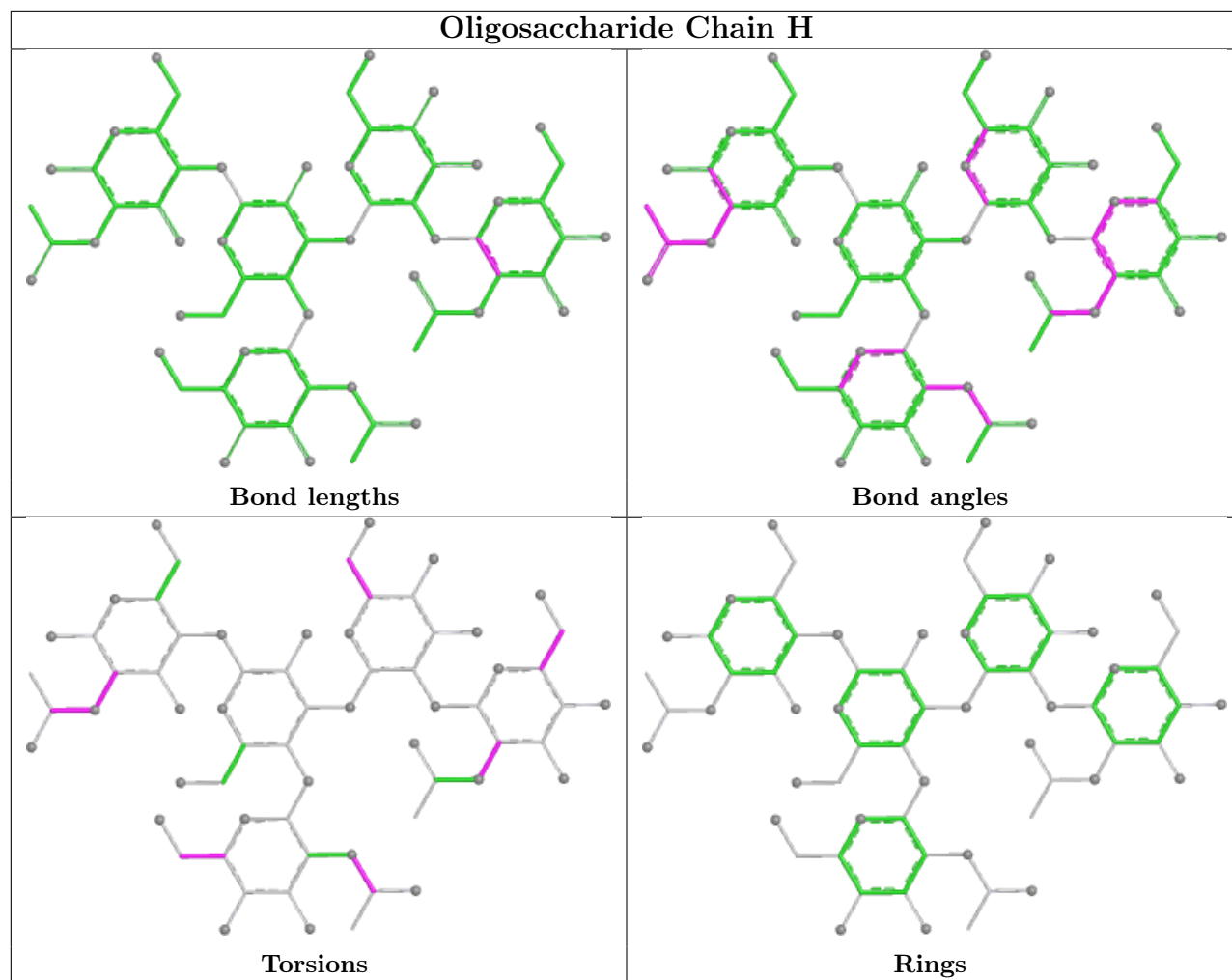
2 monomers are involved in 3 short contacts:

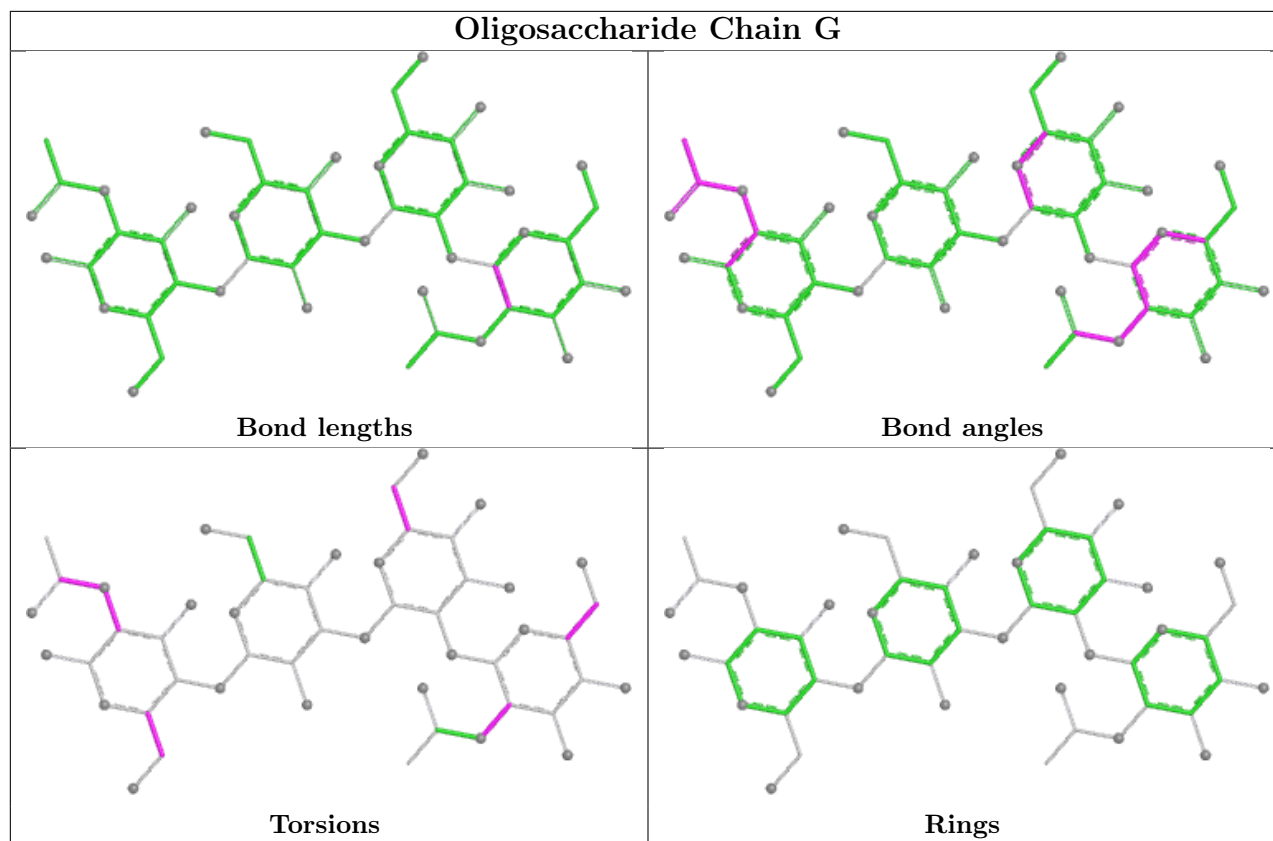
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	5	NAG	2	0
2	E	5	NAG	1	0

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](#)

15 ligands 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	$\# Z > 2$
4	EDO	B	1115	-	3,3,3	0.44	0	2,2,2	0.35	0
4	EDO	A	1107	-	3,3,3	0.45	0	2,2,2	0.35	0
4	EDO	B	1109	-	3,3,3	0.43	0	2,2,2	0.36	0
4	EDO	B	1114	-	3,3,3	0.45	0	2,2,2	0.20	0
4	EDO	C	1106	-	3,3,3	0.42	0	2,2,2	0.36	0
4	EDO	B	1110	-	3,3,3	0.45	0	2,2,2	0.36	0
4	EDO	B	1108	-	3,3,3	0.47	0	2,2,2	0.33	0
4	EDO	A	1106	-	3,3,3	0.44	0	2,2,2	0.36	0
4	EDO	B	1107	-	3,3,3	0.47	0	2,2,2	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	B	1113	-	3,3,3	0.45	0	2,2,2	0.36	0
4	EDO	B	1111	-	3,3,3	0.46	0	2,2,2	0.28	0
4	EDO	B	1106	-	3,3,3	0.43	0	2,2,2	0.35	0
4	EDO	D	1106	-	3,3,3	0.45	0	2,2,2	0.32	0
4	EDO	C	1105	-	3,3,3	0.45	0	2,2,2	0.37	0
4	EDO	B	1112	-	3,3,3	0.43	0	2,2,2	0.34	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	B	1115	-	-	0/1/1/1	-
4	EDO	A	1107	-	-	0/1/1/1	-
4	EDO	B	1109	-	-	0/1/1/1	-
4	EDO	B	1114	-	-	0/1/1/1	-
4	EDO	C	1106	-	-	1/1/1/1	-
4	EDO	B	1110	-	-	0/1/1/1	-
4	EDO	B	1108	-	-	1/1/1/1	-
4	EDO	A	1106	-	-	1/1/1/1	-
4	EDO	B	1107	-	-	1/1/1/1	-
4	EDO	B	1113	-	-	0/1/1/1	-
4	EDO	B	1111	-	-	1/1/1/1	-
4	EDO	B	1106	-	-	1/1/1/1	-
4	EDO	D	1106	-	-	1/1/1/1	-
4	EDO	C	1105	-	-	1/1/1/1	-
4	EDO	B	1112	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1106	EDO	O1-C1-C2-O2
4	B	1106	EDO	O1-C1-C2-O2
4	C	1105	EDO	O1-C1-C2-O2
4	B	1107	EDO	O1-C1-C2-O2
4	B	1111	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1114	EDO	1	0
4	C	1106	EDO	1	0
4	B	1110	EDO	1	0

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	416/442 (94%)	0.07	10 (2%) 59 56	4, 12, 31, 46	16 (3%)
1	B	417/442 (94%)	0.17	17 (4%) 41 37	3, 11, 36, 54	17 (4%)
1	C	408/442 (92%)	0.08	7 (1%) 69 67	4, 11, 31, 52	15 (3%)
1	D	408/442 (92%)	0.09	6 (1%) 72 70	5, 13, 33, 53	22 (5%)
All	All	1649/1768 (93%)	0.10	40 (2%) 59 56	3, 12, 33, 54	70 (4%)

The worst 5 of 40 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1008	LEU	7.5
1	B	1003	GLU	6.3
1	D	1003	GLU	5.5
1	C	1003	GLU	5.1
1	B	1004	SER	4.7

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.

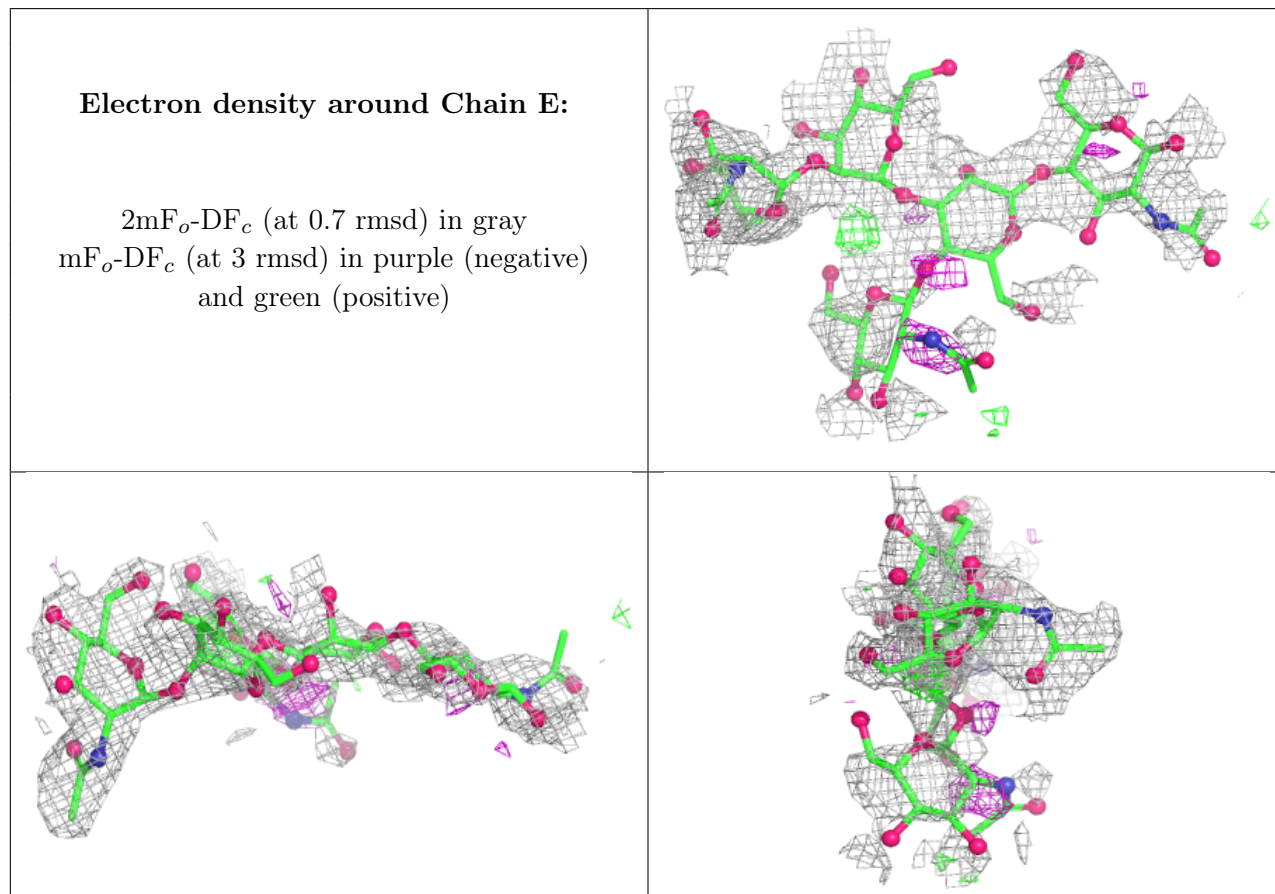
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	BMA	G	2	11/12	0.45	0.26	57,58,59,59	0
2	NAG	F	1	15/15	0.47	0.27	61,62,62,62	0

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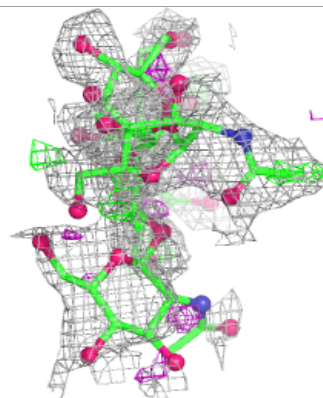
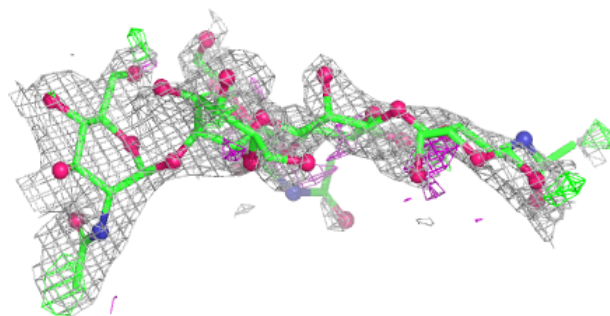
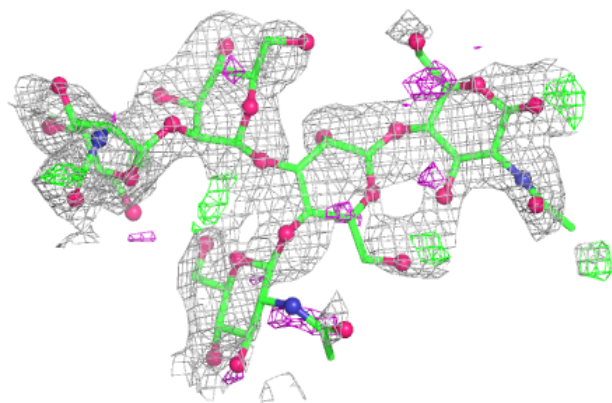
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	BMA	E	2	11/12	0.50	0.25	68,70,70,71	0
2	NAG	E	5	14/15	0.55	0.32	72,72,72,72	0
2	NAG	H	1	15/15	0.56	0.25	64,65,66,66	0
2	BMA	H	2	11/12	0.58	0.20	62,63,64,64	0
2	BMA	F	2	11/12	0.62	0.23	58,61,61,61	0
2	NAG	F	5	14/15	0.65	0.27	62,63,63,63	0
2	MAN	H	3	11/12	0.66	0.20	59,60,61,61	0
2	NAG	E	1	15/15	0.66	0.23	70,71,72,72	0
2	MAN	E	3	11/12	0.67	0.21	65,66,67,67	0
2	NAG	H	5	14/15	0.71	0.24	64,64,64,64	0
3	MAN	G	3	11/12	0.71	0.22	53,55,56,56	0
3	NAG	G	1	15/15	0.73	0.21	60,61,62,62	0
2	MAN	F	3	11/12	0.75	0.21	54,56,57,57	0
2	NAG	F	4	14/15	0.81	0.23	50,52,53,53	0
2	NAG	H	4	14/15	0.85	0.22	56,57,57,58	0
2	NAG	E	4	14/15	0.87	0.20	62,62,63,63	0
3	NAG	G	4	14/15	0.90	0.18	49,50,51,52	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.



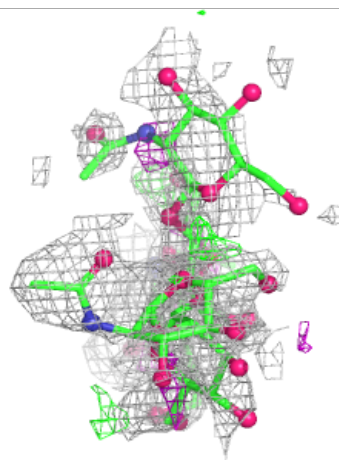
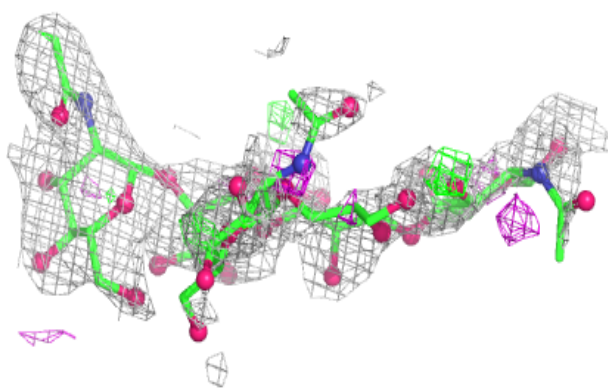
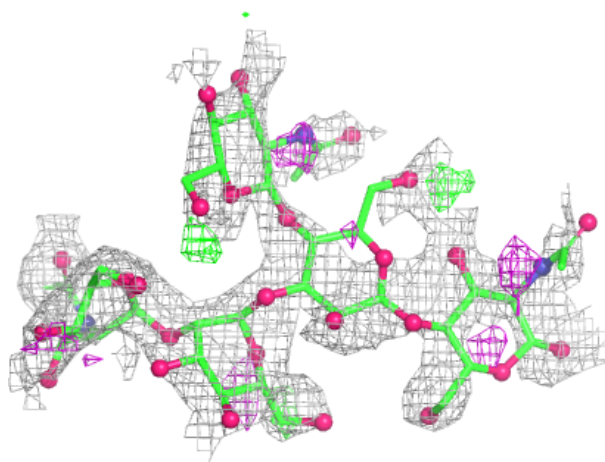
Electron density around Chain F:

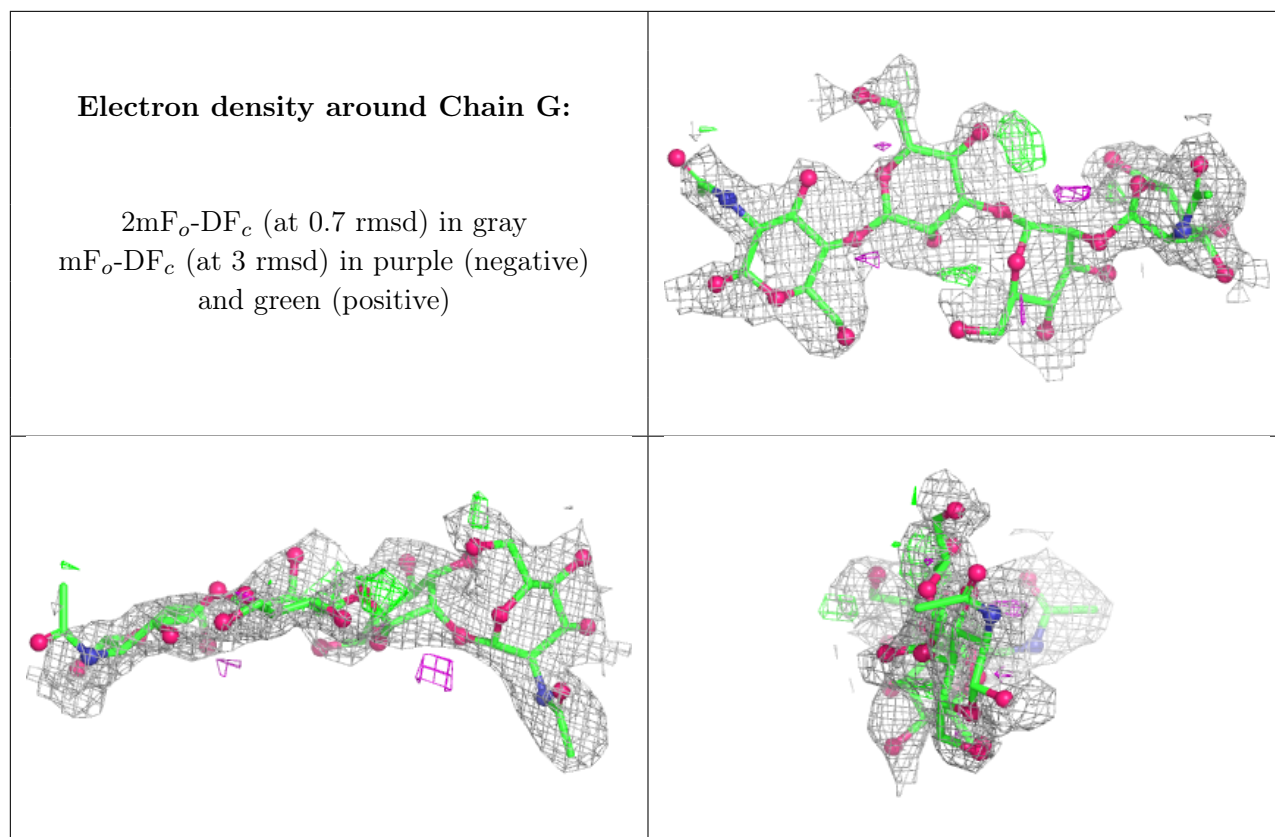
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain H:

$2mF_o-DF_c$ (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, 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
4	EDO	B	1108	4/4	0.64	0.19	39,39,39,39	0
4	EDO	B	1114	4/4	0.73	0.25	29,30,30,31	0
4	EDO	A	1106	4/4	0.74	0.19	37,37,37,37	0
4	EDO	B	1111	4/4	0.76	0.22	36,36,36,37	0
4	EDO	A	1107	4/4	0.77	0.26	63,63,63,63	0
4	EDO	B	1113	4/4	0.78	0.36	85,85,85,85	0
4	EDO	D	1106	4/4	0.79	0.17	38,38,38,38	0
4	EDO	B	1115	4/4	0.81	0.20	41,42,42,42	0
4	EDO	C	1106	4/4	0.82	0.18	42,42,42,43	0
4	EDO	B	1112	4/4	0.83	0.19	49,49,49,49	0
4	EDO	B	1107	4/4	0.83	0.18	27,28,28,28	0
4	EDO	C	1105	4/4	0.86	0.16	20,20,21,21	0
4	EDO	B	1110	4/4	0.88	0.22	36,37,37,37	0
4	EDO	B	1106	4/4	0.92	0.11	43,43,43,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	EDO	B	1109	4/4	0.93	0.10	31,31,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.