



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 10:13 AM UTC

PDB ID : 3ZE1 / pdb_00003ze1
Title : Integrin alphaIIB beta3 headpiece and RGD peptide complex
Authors : Zhu, J.H.; Zhu, J.Q.; Springer, T.A.
Deposited on : 2012-12-03
Resolution : 3.00 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
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

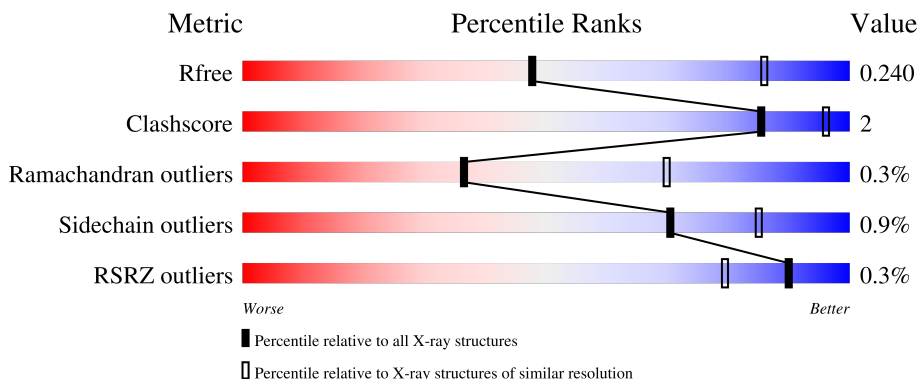
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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.



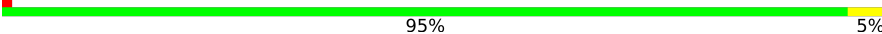
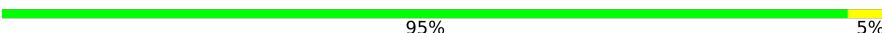
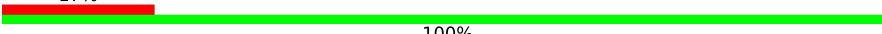
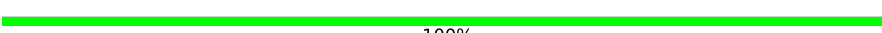
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	457	95% .
1	C	457	93% 6% .
2	B	472	90% 8% .
2	D	472	92% 7% .
3	E	221	91% 6% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	H	221	 90% 7%
4	F	214	 95% 5%
4	L	214	 95% 5%
5	I	6	 83% 17%
5	J	6	 100% 17%
6	G	4	 100%
6	M	4	 75% 25%
7	K	2	 100%
7	N	2	 100%

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 41577 atoms, of which 20215 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 INTEGRIN ALPHA-IIB.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	455	Total	C	H	N	O	S	1	4	0
			6860	2233	3350	604	665	8			
1	C	453	Total	C	H	N	O	S	0	3	0
			6807	2218	3317	601	663	8			

- Molecule 2 is a protein called INTEGRIN BETA-3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	464	Total	C	H	N	O	S	6	1	0
			7083	2233	3498	612	707	33			
2	D	469	Total	C	H	N	O	S	10	2	0
			7146	2253	3526	618	715	34			

- Molecule 3 is a protein called 10E5 FAB HEAVY CHAIN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	E	216	Total	C	H	N	O	S	0	0	0
			3239	1041	1597	266	329	6			
3	H	216	Total	C	H	N	O	S	0	0	0
			3239	1041	1597	266	329	6			

- Molecule 4 is a protein called 10E5 FAB LIGHT CHAIN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	F	214	Total	C	H	N	O	S	0	0	0
			3187	1019	1550	268	341	9			
4	L	214	Total	C	H	N	O	S	0	0	0
			3187	1019	1550	268	341	9			

- Molecule 5 is a protein called RGD PEPTIDE.

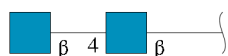
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	6	Total	C	H	N	O	0	0	0
			75	22	34	9	10			
5	J	6	Total	C	H	N	O	0	0	0
			75	22	34	9	10			

- Molecule 6 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	4	Total	C	H	N	O	0	0	0
			93	28	43	2	20			
6	M	4	Total	C	H	N	O	0	0	0
			93	28	43	2	20			

- Molecule 7 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	K	2	Total	C	H	N	O	0	0	0
			53	16	25	2	10			
7	N	2	Total	C	H	N	O	0	0	0
			53	16	25	2	10			

- Molecule 8 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 9 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	4	Total	Ca	0	0
			4	4		
9	C	4	Total	Ca	0	0
			4	4		

- Molecule 10 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	3	Total	Mn	0	0
			3	3		
10	D	3	Total	Mn	0	0
			3	3		

- Molecule 11 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
11	B	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
11	D	1	Total	C	H	N	O	0	0
			27	8	13	1	5		

- Molecule 12 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	C	1	Total	Cl	0	0
			1	1		

- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	161	Total	O	0	0
			161	161		
13	B	61	Total	O	0	0
			61	61		
13	C	50	Total	O	0	0
			50	50		
13	D	16	Total	O	0	0
			16	16		
13	E	2	Total	O	0	0
			2	2		
13	H	5	Total	O	0	0
			5	5		

Continued on next page...

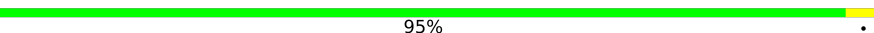
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	I	1	Total 1	O 1	0	0
13	J	1	Total 1	O 1	0	0
13	L	6	Total 6	O 6	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.

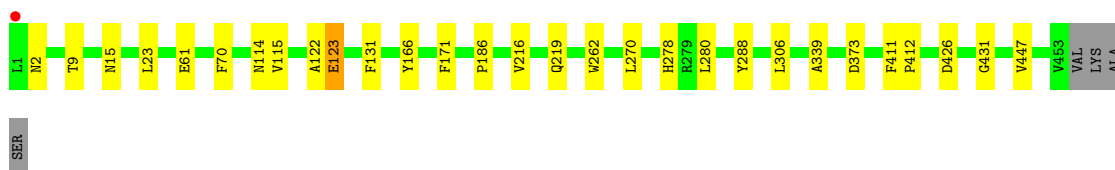
- Molecule 1: INTEGRIN ALPHA-IIB

Chain A:  95% .



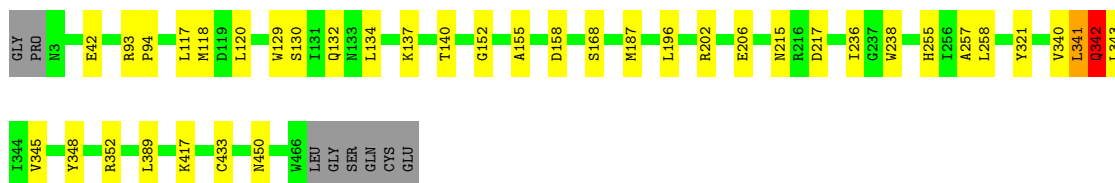
- Molecule 1: INTEGRIN ALPHA-IIB

Chain C:  93% 6% .

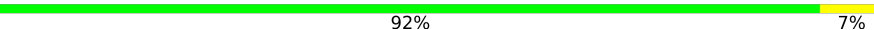


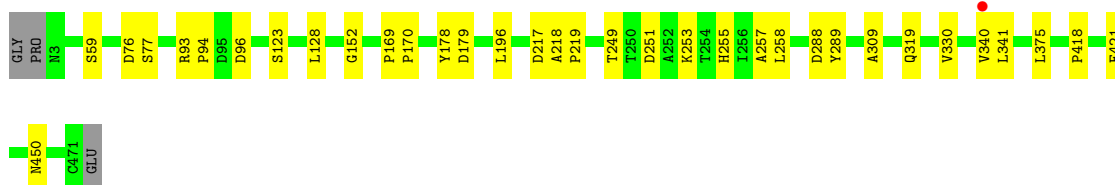
- Molecule 2: INTEGRIN BETA-3

Chain B:  90% 8% .



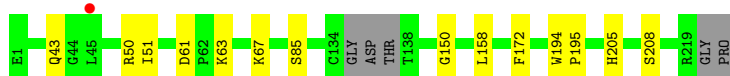
- Molecule 2: INTEGRIN BETA-3

Chain D:  92% 7% .



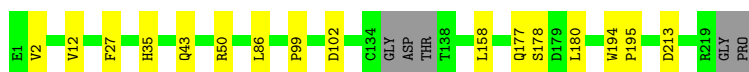
- Molecule 3: 10E5 FAB HEAVY CHAIN

Chain E:  91% 6%

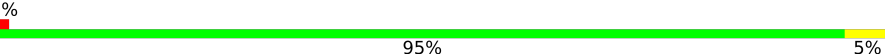


- Molecule 3: 10E5 FAB HEAVY CHAIN

Chain H:  90% 7%

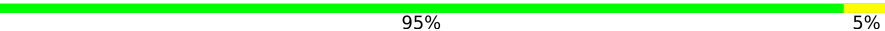


- Molecule 4: 10E5 FAB LIGHT CHAIN

Chain F:  95% 5%



- Molecule 4: 10E5 FAB LIGHT CHAIN

Chain L:  95% 5%

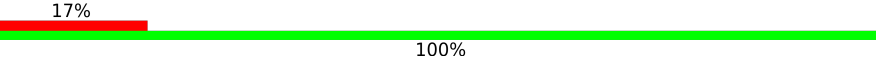


- Molecule 5: RGD PEPTIDE

Chain I:  83% 17%

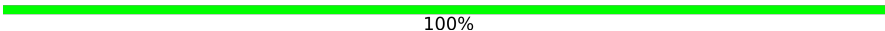


- Molecule 5: RGD PEPTIDE

Chain J:  100%



- Molecule 6: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  100%



- Molecule 6: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:  75% 25%

MAG1
MAG2
BGL3
MAN4

- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  100%

MAG1
MAG2

- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:  100%

MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	258.97Å 144.56Å 104.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.23 – 3.00 48.23 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.1 (48.23-3.00) 98.1 (48.23-3.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.14 (at 3.01Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.175 , 0.233 0.184 , 0.240	Depositor DCC
R_{free} test set	1053 reflections (1.35%)	wwPDB-VP
Wilson B-factor (Å ²)	64.5	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 95.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	41577	wwPDB-VP
Average B, all atoms (Å ²)	115.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.27% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, CL, BMA, MN, MAN, NAG, SO4

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	0.27	0/3619	0.65	2/4932 (0.0%)
1	C	0.26	0/3596	0.62	0/4900
2	B	0.26	0/3654	0.65	1/4954 (0.0%)
2	D	0.25	0/3692	0.61	0/5005
3	E	0.24	0/1684	0.60	0/2305
3	H	0.24	0/1684	0.59	0/2305
4	F	0.23	0/1673	0.57	0/2269
4	L	0.24	0/1673	0.59	0/2269
5	I	0.26	0/41	0.60	0/52
5	J	0.22	0/41	0.59	0/52
All	All	0.25	0/21357	0.62	3/29043 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	342	GLN	N-CA-C	-8.20	103.07	113.23
1	A	144	SER	CA-C-N	5.36	125.03	119.56
1	A	144	SER	C-N-CA	5.36	125.03	119.56

There are no chirality outliers.

There are no planarity outliers.

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	3510	3350	3359	10	0
1	C	3490	3317	3328	14	0
2	B	3585	3498	3504	21	0
2	D	3620	3526	3537	19	0
3	E	1642	1597	1600	8	0
3	H	1642	1597	1600	9	0
4	F	1637	1550	1553	5	0
4	L	1637	1550	1553	5	0
5	I	41	34	34	1	0
5	J	41	34	34	0	0
6	G	50	43	43	0	0
6	M	50	43	43	0	0
7	K	28	25	25	0	0
7	N	28	25	25	2	0
8	A	10	0	0	0	0
8	L	5	0	0	0	0
9	A	4	0	0	0	0
9	C	4	0	0	0	0
10	B	3	0	0	0	0
10	D	3	0	0	0	0
11	B	14	13	13	0	0
11	D	14	13	13	2	0
12	C	1	0	0	0	0
13	A	161	0	0	3	1
13	B	61	0	0	1	0
13	C	50	0	0	1	1
13	D	16	0	0	0	0
13	E	2	0	0	0	0
13	H	5	0	0	0	0
13	I	1	0	0	0	0
13	J	1	0	0	0	0
13	L	6	0	0	0	0
All	All	21362	20215	20264	91	1

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 2.

The worst 5 of 91 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)
11:D:3099:NAG:HO6	7:N:2:NAG:HO6	1.39	0.64
1:C:15:ASN:ND2	13:C:4007:HOH:O	2.33	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A:4048:HOH:O	2:B:168:SER:O	2.17	0.58
2:B:202:ARG:NH2	2:B:206:GLU:OE2	2.38	0.57
2:D:76:ASP:OD1	2:D:77:SER:N	2.39	0.56

All (1) 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)
13:A:4055:HOH:O	13:C:4041:HOH:O[1_554]	2.16	0.04

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	457/457 (100%)	438 (96%)	18 (4%)	1 (0%)	43	76
1	C	454/457 (99%)	423 (93%)	30 (7%)	1 (0%)	43	76
2	B	463/472 (98%)	433 (94%)	28 (6%)	2 (0%)	30	65
2	D	469/472 (99%)	433 (92%)	36 (8%)	0	100	100
3	E	212/221 (96%)	194 (92%)	17 (8%)	1 (0%)	24	60
3	H	212/221 (96%)	197 (93%)	14 (7%)	1 (0%)	24	60
4	F	212/214 (99%)	200 (94%)	10 (5%)	2 (1%)	14	48
4	L	212/214 (99%)	200 (94%)	11 (5%)	1 (0%)	24	60
5	I	4/6 (67%)	4 (100%)	0	0	100	100
5	J	4/6 (67%)	4 (100%)	0	0	100	100
All	All	2699/2740 (98%)	2526 (94%)	164 (6%)	9 (0%)	36	70

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	341	LEU
1	A	123	GLU
4	L	138	ASN
2	B	343	LEU
1	C	123	GLU

5.3.2 Protein sidechains ⓘ

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	367/364 (101%)	362 (99%)	5 (1%)	59	80
1	C	364/364 (100%)	358 (98%)	6 (2%)	55	79
2	B	412/417 (99%)	404 (98%)	8 (2%)	50	76
2	D	417/417 (100%)	416 (100%)	1 (0%)	87	92
3	E	187/190 (98%)	187 (100%)	0	100	100
3	H	187/190 (98%)	187 (100%)	0	100	100
4	F	188/188 (100%)	187 (100%)	1 (0%)	81	89
4	L	188/188 (100%)	188 (100%)	0	100	100
5	I	4/4 (100%)	4 (100%)	0	100	100
5	J	4/4 (100%)	4 (100%)	0	100	100
All	All	2318/2326 (100%)	2297 (99%)	21 (1%)	70	85

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	61	GLU
1	C	288	TYR
4	F	104	LEU
1	C	373	ASP
1	C	270	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	219	GLN
4	F	190	ASN
1	C	333	GLN
4	L	27	GLN
2	D	450	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 ⓘ

12 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	$\# Z > 2$
6	NAG	G	1	2,6	14,14,15	0.53	0	17,19,21	0.68	0
6	NAG	G	2	6	14,14,15	0.56	0	17,19,21	0.69	0
6	BMA	G	3	6	11,11,12	0.61	0	15,15,17	0.73	0
6	MAN	G	4	6	11,11,12	0.61	0	15,15,17	0.58	0
7	NAG	K	1	2,7	14,14,15	0.57	0	17,19,21	0.83	0
7	NAG	K	2	7	14,14,15	0.53	0	17,19,21	0.55	0
6	NAG	M	1	2,6	14,14,15	0.52	0	17,19,21	0.73	0
6	NAG	M	2	6	14,14,15	0.56	0	17,19,21	0.59	0
6	BMA	M	3	6	11,11,12	0.64	0	15,15,17	0.78	1 (6%)
6	MAN	M	4	6	11,11,12	0.65	0	15,15,17	0.57	0
7	NAG	N	1	2,7	14,14,15	0.61	0	17,19,21	1.00	1 (5%)
7	NAG	N	2	7	14,14,15	0.52	0	17,19,21	0.59	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	G	1	2,6	-	2/6/23/26	0/1/1/1
6	NAG	G	2	6	-	0/6/23/26	0/1/1/1
6	BMA	G	3	6	-	0/2/19/22	0/1/1/1
6	MAN	G	4	6	-	0/2/19/22	0/1/1/1
7	NAG	K	1	2,7	-	2/6/23/26	0/1/1/1
7	NAG	K	2	7	-	1/6/23/26	0/1/1/1
6	NAG	M	1	2,6	-	0/6/23/26	0/1/1/1
6	NAG	M	2	6	-	2/6/23/26	0/1/1/1
6	BMA	M	3	6	-	0/2/19/22	0/1/1/1
6	MAN	M	4	6	-	0/2/19/22	0/1/1/1
7	NAG	N	1	2,7	-	0/6/23/26	0/1/1/1
7	NAG	N	2	7	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	N	1	NAG	C4-C3-C2	2.43	114.58	111.02
6	M	3	BMA	C1-C2-C3	2.17	112.80	109.64

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	M	2	NAG	O7-C7-N2-C2
6	M	2	NAG	C8-C7-N2-C2
7	N	2	NAG	O7-C7-N2-C2
7	N	2	NAG	C8-C7-N2-C2
7	K	1	NAG	C8-C7-N2-C2

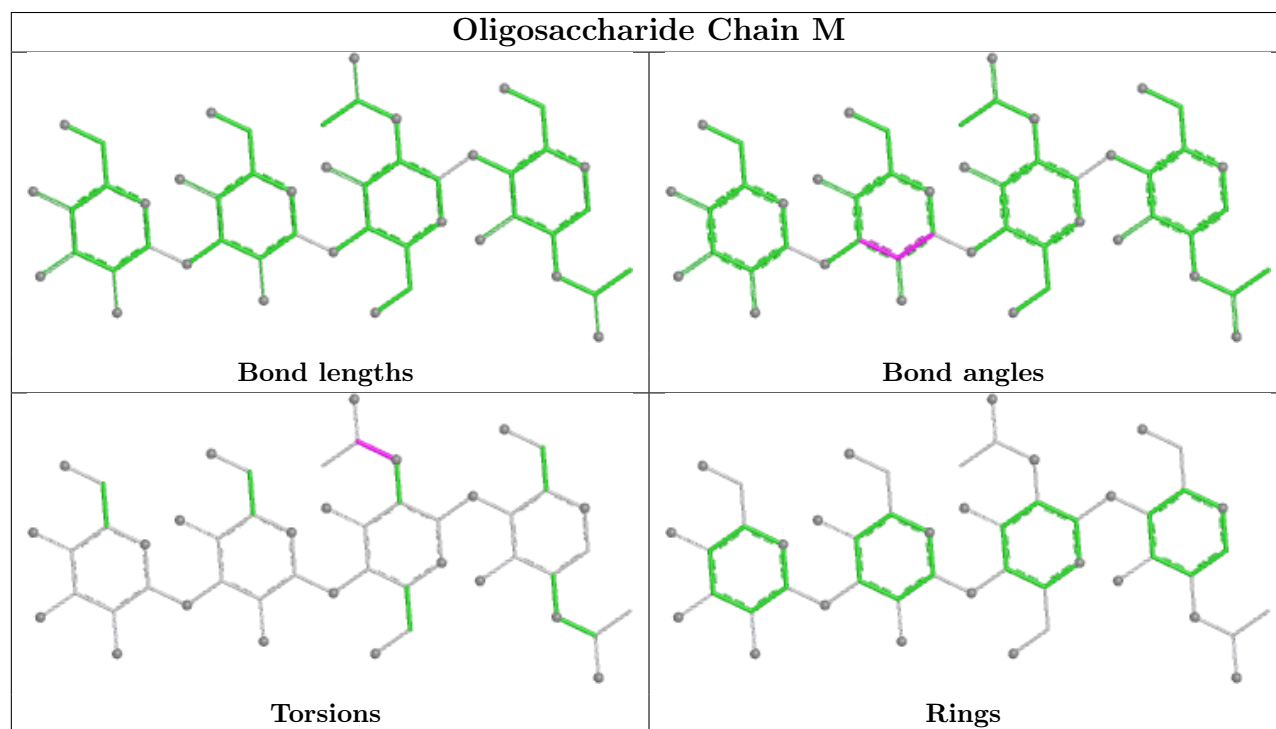
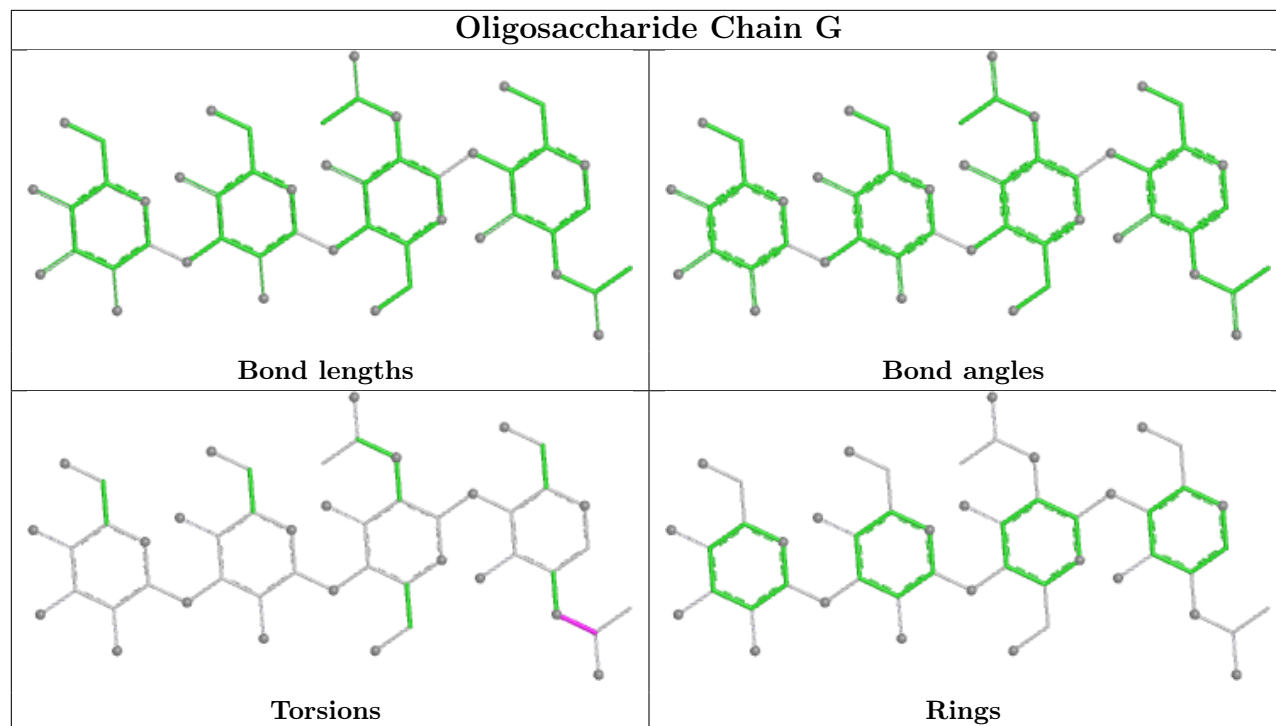
There are no ring outliers.

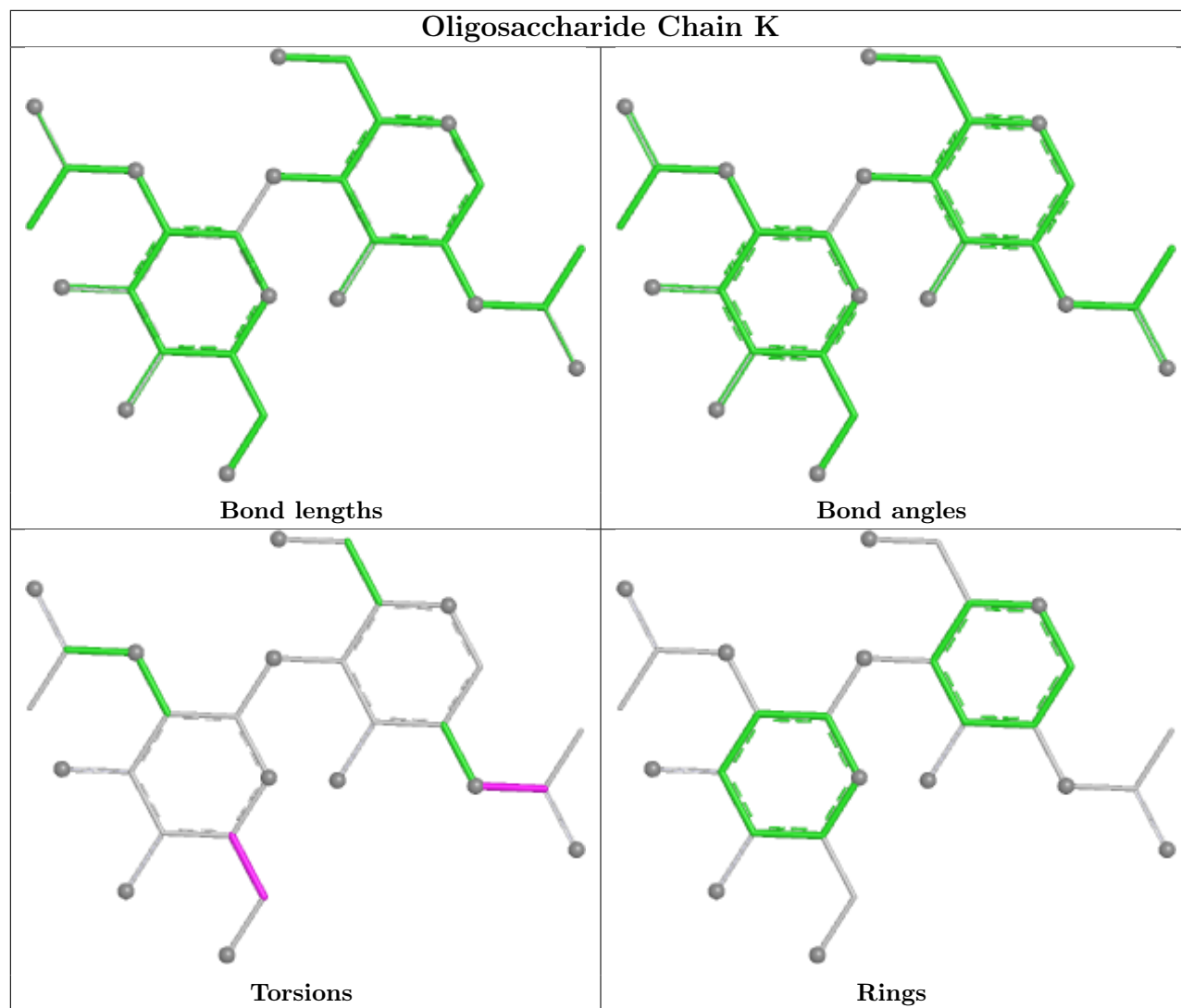
1 monomer is involved in 2 short contacts:

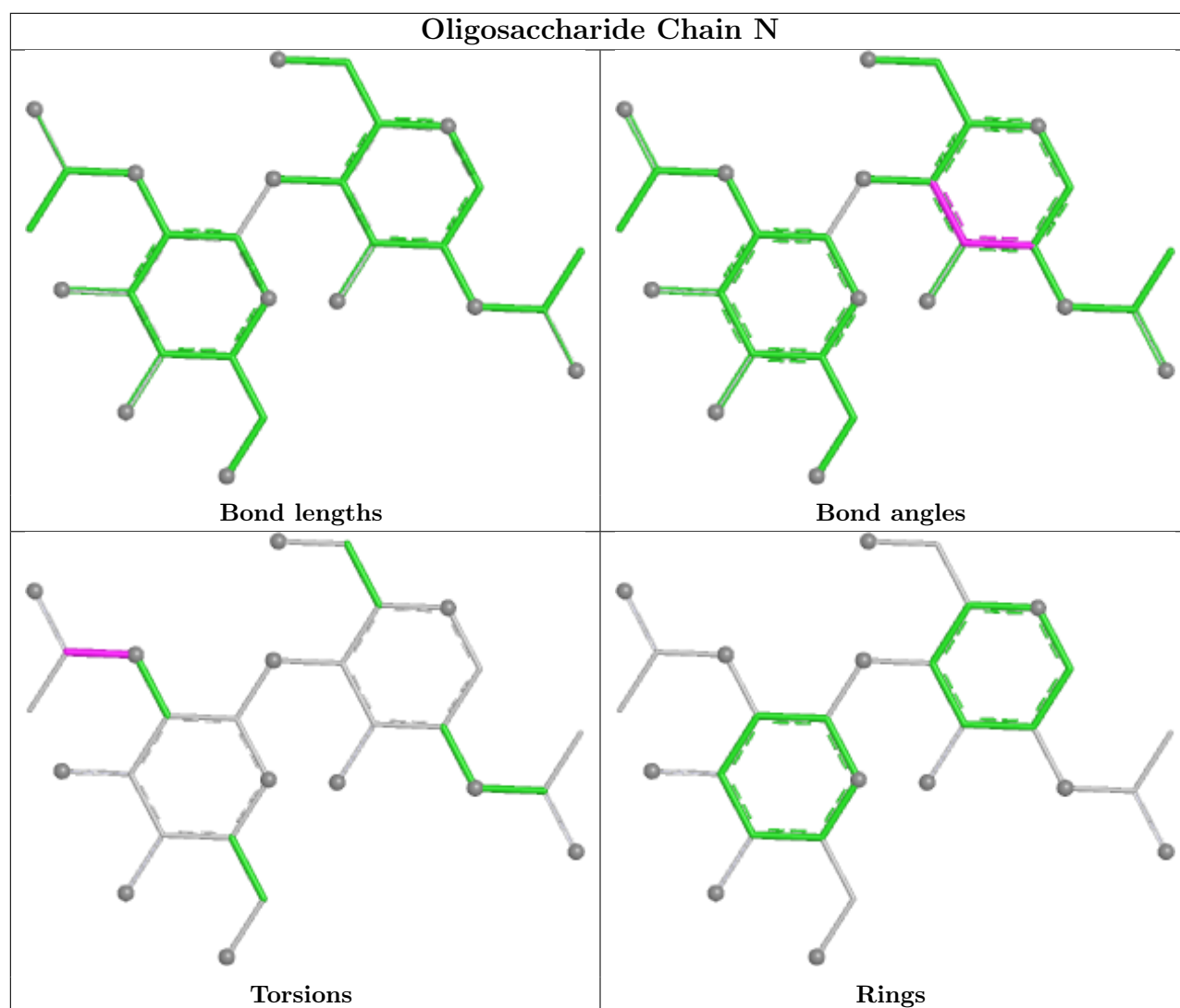
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	N	2	NAG	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for oligosaccharide.







5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 15 are monoatomic - leaving 5 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	$\# Z > 2$
8	SO4	A	1456	-	4,4,4	0.23	0	6,6,6	0.09	0
11	NAG	D	3099	2	14,14,15	0.51	0	17,19,21	0.54	0
8	SO4	A	1457	-	4,4,4	0.24	0	6,6,6	0.07	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	SO4	L	1215	-	4,4,4	0.23	0	6,6,6	0.07	0
11	NAG	B	3099	2	14,14,15	0.52	0	17,19,21	0.62	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
11	NAG	D	3099	2	-	0/6/23/26	0/1/1/1
11	NAG	B	3099	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 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	D	3099	NAG	2	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	455/457 (99%)	-0.70	1 (0%) 91 83	24, 55, 98, 164	5 (1%)
1	C	453/457 (99%)	-0.40	1 (0%) 91 83	46, 91, 141, 215	3 (0%)
2	B	464/472 (98%)	-0.35	0 100 100	30, 98, 201, 238	3 (0%)
2	D	469/472 (99%)	0.07	1 (0%) 91 83	61, 136, 209, 248	3 (0%)
3	E	216/221 (97%)	0.10	1 (0%) 87 72	94, 166, 224, 258	0
3	H	216/221 (97%)	-0.24	0 100 100	63, 129, 200, 240	0
4	F	214/214 (100%)	-0.04	2 (0%) 81 61	96, 168, 246, 308	0
4	L	214/214 (100%)	-0.30	0 100 100	68, 117, 158, 258	0
5	I	6/6 (100%)	-0.10	0 100 100	50, 63, 108, 127	0
5	J	6/6 (100%)	0.77	1 (16%) 4 3	99, 125, 152, 180	2 (33%)
All	All	2713/2740 (99%)	-0.27	7 (0%) 90 79	24, 112, 208, 308	16 (0%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	F	181	LEU	2.7
1	C	1	LEU	2.5
3	E	45	LEU	2.2
4	F	193	THR	2.2
2	D	340	VAL	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

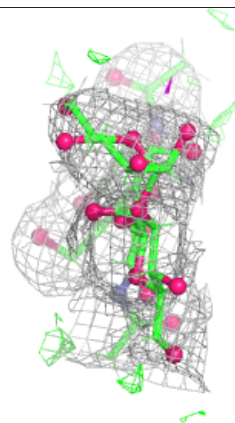
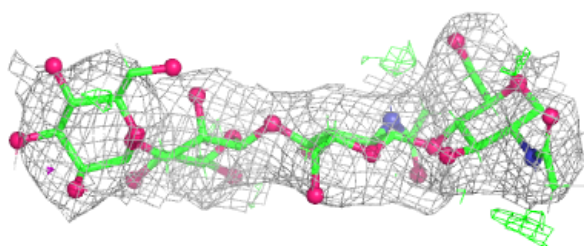
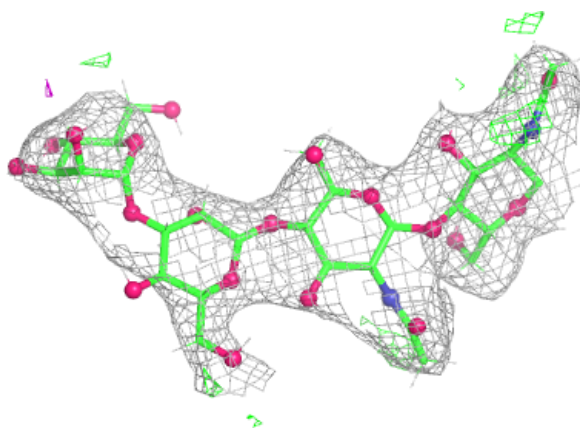
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	NAG	G	1	14/15	-	-	19,59,87,104	0
6	NAG	G	2	14/15	-	-	88,112,146,150	0
6	BMA	G	3	11/12	-	-	143,167,200,201	0
6	MAN	G	4	11/12	-	-	143,163,188,191	0
7	NAG	N	2	14/15	0.15	0.13	163,190,227,228	0
6	BMA	M	3	11/12	0.42	0.11	176,197,235,237	0
6	MAN	M	4	11/12	0.47	0.12	205,211,252,253	0
7	NAG	N	1	14/15	0.77	0.10	137,170,200,210	0
6	NAG	M	2	14/15	0.81	0.10	108,146,181,185	0
7	NAG	K	2	14/15	0.89	0.10	138,171,206,212	0
7	NAG	K	1	14/15	0.97	0.06	116,142,165,172	0
6	NAG	M	1	14/15	0.97	0.08	74,107,135,142	0

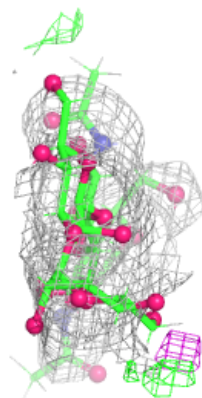
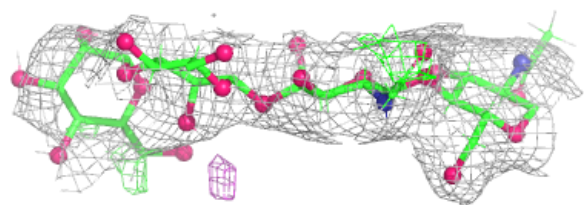
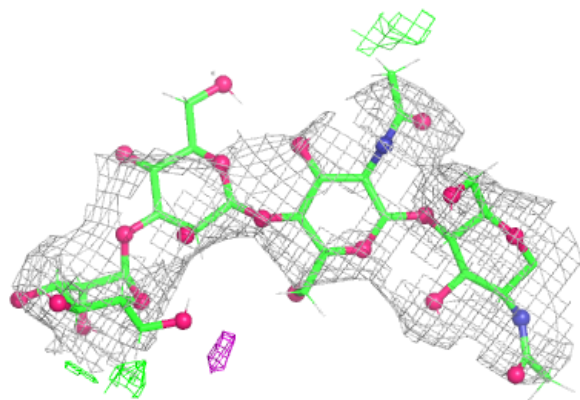
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain G:

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

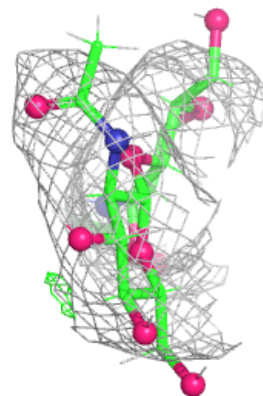
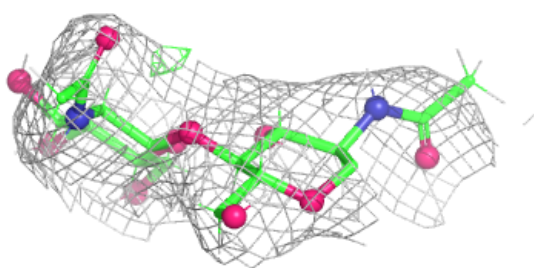
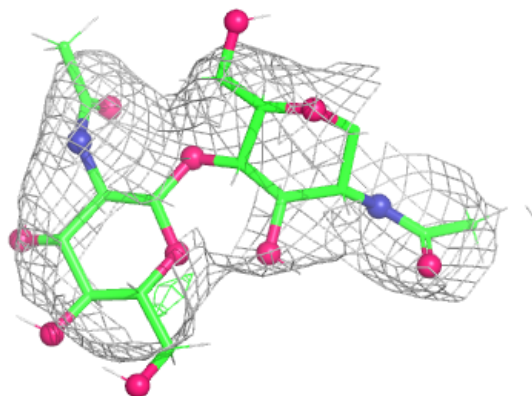
**Electron density around Chain M:**

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

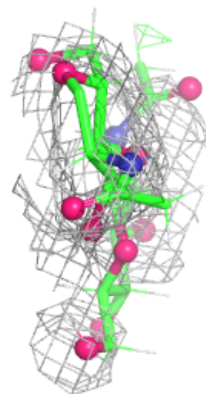
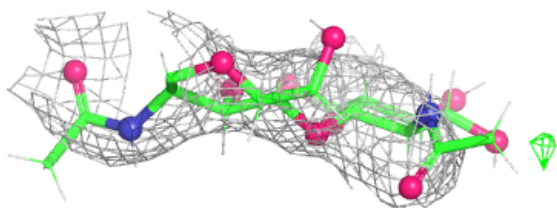
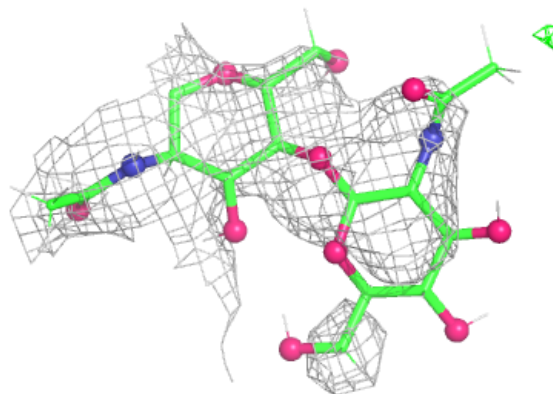


Electron density around Chain K:

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

**Electron density around Chain N:**

$2mF_o-DF_c$ (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($\text{\AA}^2$)	Q<0.9
11	NAG	D	3099	14/15	0.39	0.13	144,168,198,202	0
11	NAG	B	3099	14/15	0.76	0.10	123,153,182,187	0
8	SO4	L	1215	5/5	0.81	0.11	152,153,156,164	0
8	SO4	A	1456	5/5	0.88	0.12	83,99,114,131	0
8	SO4	A	1457	5/5	0.93	0.20	109,126,139,157	0
10	MN	D	2002	1/1	0.95	0.09	174,174,174,174	0
10	MN	D	2003	1/1	0.98	0.04	120,120,120,120	0
10	MN	D	2001	1/1	0.99	0.05	119,119,119,119	0
9	CA	C	2004	1/1	0.99	0.04	113,113,113,113	0
9	CA	C	2005	1/1	0.99	0.03	107,107,107,107	0
9	CA	C	2006	1/1	0.99	0.03	78,78,78,78	0
9	CA	C	2007	1/1	0.99	0.03	71,71,71,71	0
12	CL	C	2001	1/1	0.99	0.09	81,81,81,81	0
10	MN	B	2003	1/1	1.00	0.02	61,61,61,61	0
9	CA	A	2004	1/1	1.00	0.01	47,47,47,47	0
9	CA	A	2005	1/1	1.00	0.03	41,41,41,41	0
9	CA	A	2006	1/1	1.00	0.02	40,40,40,40	0
9	CA	A	2007	1/1	1.00	0.02	49,49,49,49	0
10	MN	B	2001	1/1	1.00	0.05	48,48,48,48	0
10	MN	B	2002	1/1	1.00	0.02	63,63,63,63	0

6.5 Other polymers [i](#)

There are no such residues in this entry.