



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:25 AM UTC

PDB ID : 2VDL / pdb_00002vdl
Title : Re-refinement of Integrin AlphaIIbBeta3 Headpiece
Authors : Springer, T.A.; Zhu, J.; Xiao, T.
Deposited on : 2007-10-10
Resolution : 2.75 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 : 4-5-2 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

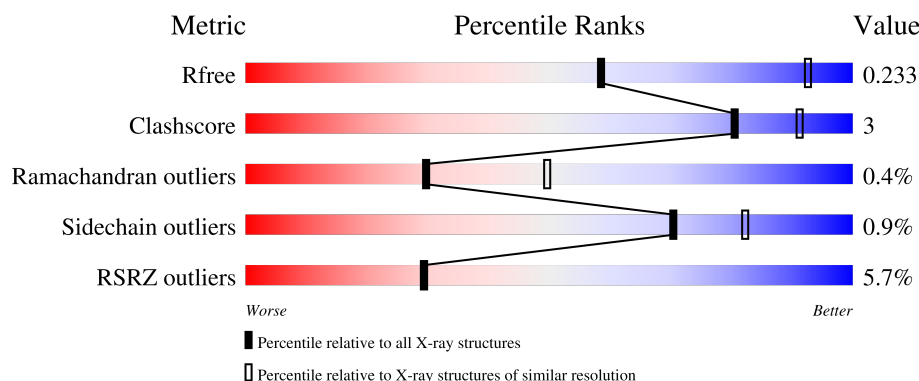
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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	452	% 95% .
2	B	461	12% 90% 8% ..
3	H	221	6% 94% 5% .
4	L	214	% 92% 7%
5	C	5	80% 20%

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Mol	Chain	Length	Quality of chain
6	D	7	 57%43%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	CAC	B	1462	-	X	-	-
5	MAN	C	3	X	-	-	-
6	MAN	D	3	X	-	-	-

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 11800 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 INTEGRIN ALPHA-IIB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	452	Total	C	N	O	S	0	8	0
			3520	2235	612	665	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	282	GLY	ALA	conflict	UNP P08514

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	456	Total	C	N	O	S	0	13	0
			3600	2249	614	704	33			

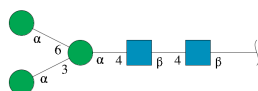
- Molecule 3 is a protein called MONOCLONAL ANTIBODY 10E5 HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	219	Total	C	N	O	S	0	6	0
			1678	1065	270	337	6			

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

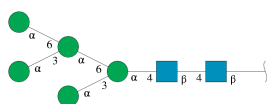
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	214	Total	C	N	O	S	0	7	0
			1663	1035	272	345	11			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



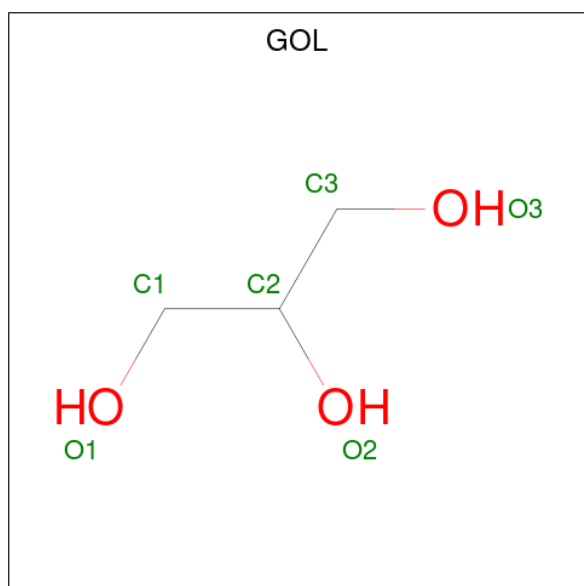
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	C	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 6 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-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	D	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).

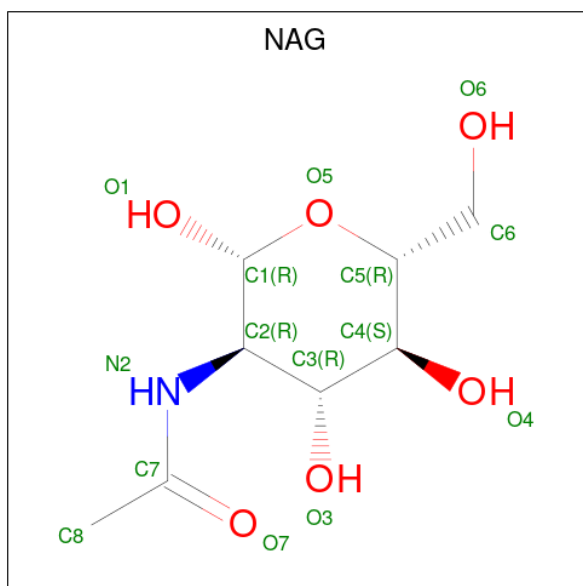


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is CALCIUM ION (CCD ID: CA) (formula: Ca).

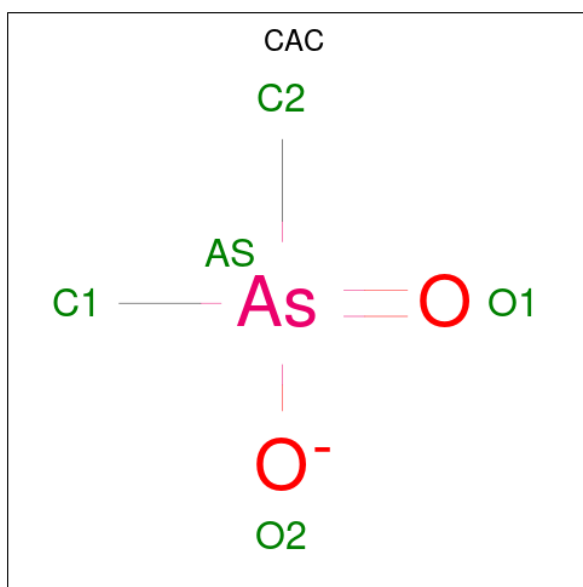
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	4	Total	Ca	0	0
			4	4		
8	B	2	Total	Ca	0	0
			2	2		

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	N	O	0	0
			14	8	1	5		
9	A	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 10 is CACODYLATE ION (CCD ID: CAC) (formula: C₂H₆AsO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	B	1	Total	As	C	O	0	0
			5	1	2	2		

- Molecule 11 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	B	1	Total	Mg	0	0
			1	1		

- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	411	Total	O	0	0
			411	411		
12	B	250	Total	O	0	0
			250	250		
12	H	221	Total	O	0	0
			221	221		
12	L	247	Total	O	0	0
			247	247		

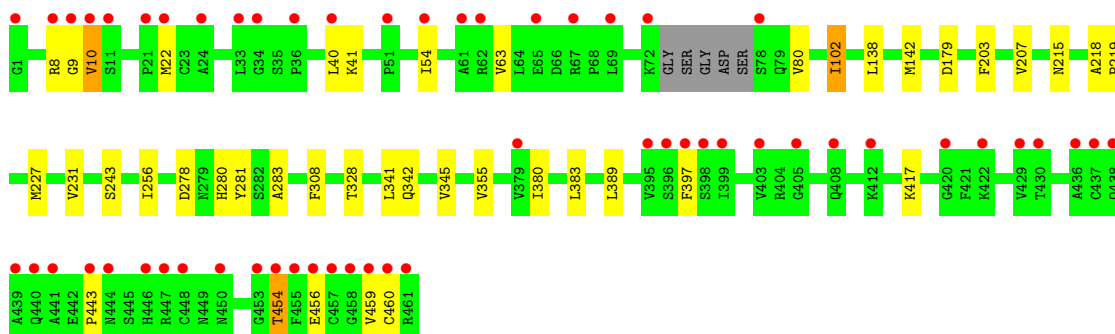
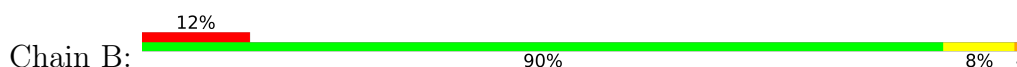
3 Residue-property plots [i](#)

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.

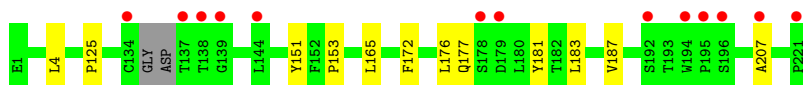
- Molecule 1: INTEGRIN ALPHA-IIB



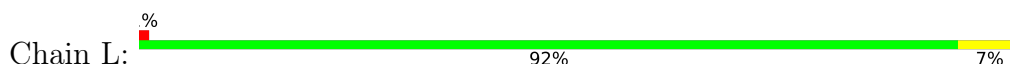
- Molecule 2: INTEGRIN BETA-3



- Molecule 3: MONOCLONAL ANTIBODY 10E5 HEAVY CHAIN



- Molecule 4: MONOCLONAL ANTIBODY 10E5 LIGHT CHAIN



- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyra

nose

Chain C:  80% 20%

MAG1
MAG2
MAN3
MAN4
MAN5

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

Chain D:  57% 43%

MAG1
MAG2
MAN3
MAN4
MAN5
MAN6
MAN7

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	148.93Å 148.93Å 176.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.99 – 2.75 42.99 – 2.75	Depositor EDS
% Data completeness (in resolution range)	95.1 (42.99-2.75) 89.5 (42.99-2.75)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.50 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.3.0037	Depositor
R, R_{free}	0.144 , 0.191 0.194 , 0.233	Depositor DCC
R_{free} test set	2696 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	39.5	Xtriage
Anisotropy	0.005	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 58.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	11800	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% 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: GOL, MAN, CA, NAG, MG, CAC

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	0.44	0/3629	0.65	0/4943
2	B	0.43	0/3688	0.68	0/4995
3	H	0.41	0/1730	0.62	0/2368
4	L	0.42	0/1719	0.61	0/2330
All	All	0.43	0/10766	0.65	0/14636

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	3520	0	3361	12	0
2	B	3600	0	3548	22	0
3	H	1678	0	1634	8	0
4	L	1663	0	1581	14	0
5	C	61	0	52	0	0
6	D	83	0	70	0	0
7	A	6	0	8	0	0
7	B	6	0	8	0	0
8	A	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	B	2	0	0	0	0
9	A	28	0	26	0	0
9	B	14	0	13	0	0
10	B	5	0	0	1	0
11	B	1	0	0	0	0
12	A	411	0	0	2	0
12	B	250	0	0	2	0
12	H	221	0	0	1	0
12	L	247	0	0	3	0
All	All	11800	0	10301	55	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 3.

All (55) 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)
10:B:1462:CAC:C1	12:B:4099:HOH:O	2.23	0.86
3:H:177[A]:GLN:HB3	4:L:160:LEU:HD11	1.76	0.66
1:A:270:LEU:HD23	1:A:276:ARG:HA	1.80	0.62
2:B:138:LEU:HD23	2:B:341[A]:LEU:HD23	1.84	0.59
1:A:235:TRP:HZ2	1:A:270:LEU:HD11	1.72	0.55
2:B:456:GLU:O	2:B:459:VAL:HG12	2.06	0.55
4:L:4:MET:HE3	4:L:23:CYS:SG	2.47	0.54
3:H:177[A]:GLN:NE2	12:H:4196:HOH:O	2.38	0.53
2:B:278:ASP:CG	2:B:280[B]:HIS:HD1	2.17	0.53
2:B:355:VAL:HG23	2:B:389:LEU:HD22	1.91	0.52
1:A:235:TRP:CZ2	1:A:270:LEU:HD11	2.45	0.52
1:A:390:LEU:HD12	1:A:390:LEU:N	2.25	0.51
1:A:421:LEU:CD2	1:A:437:VAL:HG22	2.40	0.51
2:B:142[A]:MET:HE1	2:B:345:VAL:HG23	1.93	0.51
2:B:281:TYR:CE1	2:B:283:ALA:HB3	2.46	0.50
1:A:1:LEU:HB2	1:A:393:LEU:HD11	1.94	0.50
2:B:41:LYS:HG3	2:B:54:ILE:HG21	1.93	0.49
4:L:136:LEU:HD12	4:L:136:LEU:N	2.29	0.48
1:A:278[A]:HIS:CD2	1:A:339:ALA:HB1	2.48	0.48
1:A:451:GLN:NE2	12:A:4408:HOH:O	2.47	0.48
3:H:172:PHE:CD1	4:L:164:THR:HG23	2.49	0.47
4:L:122:SER:O	4:L:126:THR:HG23	2.16	0.46
2:B:102:ILE:HG22	2:B:397:PHE:HB2	1.97	0.46
2:B:63:VAL:HG23	2:B:63:VAL:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:165:LEU:CD2	3:H:187:VAL:HG21	2.46	0.46
3:H:4:LEU:HD12	3:H:4:LEU:N	2.31	0.46
2:B:308:PHE:CE2	2:B:328:THR:HG21	2.50	0.45
4:L:117:ILE:HG13	4:L:134[B]:CYS:SG	2.57	0.45
4:L:161:ASN:HB3	4:L:175:MET:HE3	1.98	0.45
3:H:176:LEU:HD13	3:H:181:TYR:CE1	2.51	0.45
2:B:203:PHE:O	2:B:207:VAL:HG23	2.17	0.45
2:B:22:MET:HE2	2:B:40:LEU:HD22	1.99	0.44
2:B:8:ARG:O	2:B:10:VAL:N	2.51	0.44
3:H:125:PRO:HB3	3:H:151:TYR:HB3	2.00	0.44
4:L:181:LEU:HD23	4:L:181:LEU:N	2.33	0.44
2:B:218:ALA:HB3	2:B:219:PRO:HD3	2.00	0.43
4:L:45:MET:HE3	12:L:4067:HOH:O	2.18	0.43
1:A:436:ILE:HG22	1:A:447:VAL:HG22	1.99	0.43
2:B:459:VAL:HG22	2:B:460:CYS:O	2.19	0.43
2:B:278:ASP:OD2	2:B:280[B]:HIS:ND1	2.51	0.43
4:L:105:GLU:HG3	4:L:173:TYR:OH	2.19	0.43
1:A:122:ALA:O	1:A:123:GLU:HB2	2.18	0.42
1:A:194:LEU:HD12	1:A:194:LEU:C	2.44	0.42
2:B:142[A]:MET:HE2	2:B:341[A]:LEU:HD22	2.01	0.42
2:B:227:MET:O	2:B:231:VAL:HG22	2.19	0.42
2:B:380:ILE:HG21	2:B:383:LEU:HD22	2.01	0.42
2:B:417:LYS:NZ	12:B:4224:HOH:O	2.53	0.42
1:A:53:VAL:HG21	1:A:106:ALA:CB	2.49	0.42
4:L:117:ILE:HA	4:L:134[B]:CYS:SG	2.60	0.42
2:B:443:PRO:HA	2:B:454:THR:HG22	2.02	0.42
4:L:106:ILE:HD12	12:L:4203:HOH:O	2.21	0.41
12:A:4301:HOH:O	2:B:256:ILE:HD12	2.21	0.41
4:L:188[B]:ARG:NH2	12:L:4224:HOH:O	2.54	0.40
3:H:153:PRO:HD2	3:H:207:ALA:CB	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	457/452 (101%)	445 (97%)	11 (2%)	1 (0%)	43	64
2	B	463/461 (100%)	442 (96%)	17 (4%)	4 (1%)	14	28
3	H	218/221 (99%)	213 (98%)	5 (2%)	0	100	100
4	L	218/214 (102%)	211 (97%)	7 (3%)	0	100	100
All	All	1356/1348 (101%)	1311 (97%)	40 (3%)	5 (0%)	30	50

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	123	GLU
2	B	9	GLY
2	B	80	VAL
2	B	454	THR
2	B	10	VAL

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	367/360 (102%)	364 (99%)	3 (1%)	73	84
2	B	417/409 (102%)	412 (99%)	5 (1%)	63	78
3	H	192/190 (101%)	191 (100%)	1 (0%)	81	89
4	L	194/188 (103%)	193 (100%)	1 (0%)	81	89
All	All	1170/1147 (102%)	1160 (99%)	10 (1%)	70	82

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	LEU
1	A	166	TYR
1	A	288	TYR

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Mol	Chain	Res	Type
2	B	102	ILE
2	B	179	ASP
2	B	215	ASN
2	B	243	SER
2	B	342	GLN
3	H	183	LEU
4	L	105	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	64	GLN
1	A	158	ASN
1	A	372	ASN
2	B	199	GLN
2	B	301	GLN
2	B	428	GLN
2	B	438	GLN
2	B	440	GLN
3	H	3	GLN
3	H	177[A]	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

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	$\# Z > 2$
5	NAG	C	1	2,5	14,14,15	0.58	0	17,19,21	0.76	0
5	NAG	C	2	5	14,14,15	0.71	0	17,19,21	0.91	0
5	MAN	C	3	5	11,11,12	0.62	0	15,15,17	0.54	0
5	MAN	C	4	5	11,11,12	0.51	0	15,15,17	0.66	0
5	MAN	C	5	5	11,11,12	0.56	0	15,15,17	1.38	2 (13%)
6	NAG	D	1	6,2	14,14,15	0.69	0	17,19,21	1.04	1 (5%)
6	NAG	D	2	6	14,14,15	0.49	0	17,19,21	0.96	0
6	MAN	D	3	6	11,11,12	0.55	0	15,15,17	0.78	0
6	MAN	D	4	6	11,11,12	0.69	0	15,15,17	1.04	1 (6%)
6	MAN	D	5	6	11,11,12	0.55	0	15,15,17	0.89	0
6	MAN	D	6	6	11,11,12	0.57	0	15,15,17	0.67	0
6	MAN	D	7	6	11,11,12	0.60	0	15,15,17	1.07	1 (6%)

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
5	NAG	C	1	2,5	-	0/6/23/26	0/1/1/1
5	NAG	C	2	5	-	1/6/23/26	0/1/1/1
5	MAN	C	3	5	1/1/4/5	0/2/19/22	0/1/1/1
5	MAN	C	4	5	-	0/2/19/22	0/1/1/1
5	MAN	C	5	5	-	0/2/19/22	0/1/1/1
6	NAG	D	1	6,2	-	0/6/23/26	0/1/1/1
6	NAG	D	2	6	-	0/6/23/26	0/1/1/1
6	MAN	D	3	6	1/1/4/5	2/2/19/22	0/1/1/1
6	MAN	D	4	6	-	0/2/19/22	0/1/1/1
6	MAN	D	5	6	-	0/2/19/22	0/1/1/1
6	MAN	D	6	6	-	2/2/19/22	0/1/1/1
6	MAN	D	7	6	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	5	MAN	C1-O5-C5	3.75	117.21	112.19
6	D	4	MAN	C1-O5-C5	3.04	116.26	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	5	MAN	C1-C2-C3	2.84	113.78	109.64
6	D	7	MAN	C3-C4-C5	2.67	115.06	110.23
6	D	1	NAG	O5-C1-C2	-2.38	107.61	111.29

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	C	3	MAN	C1
6	D	3	MAN	C1

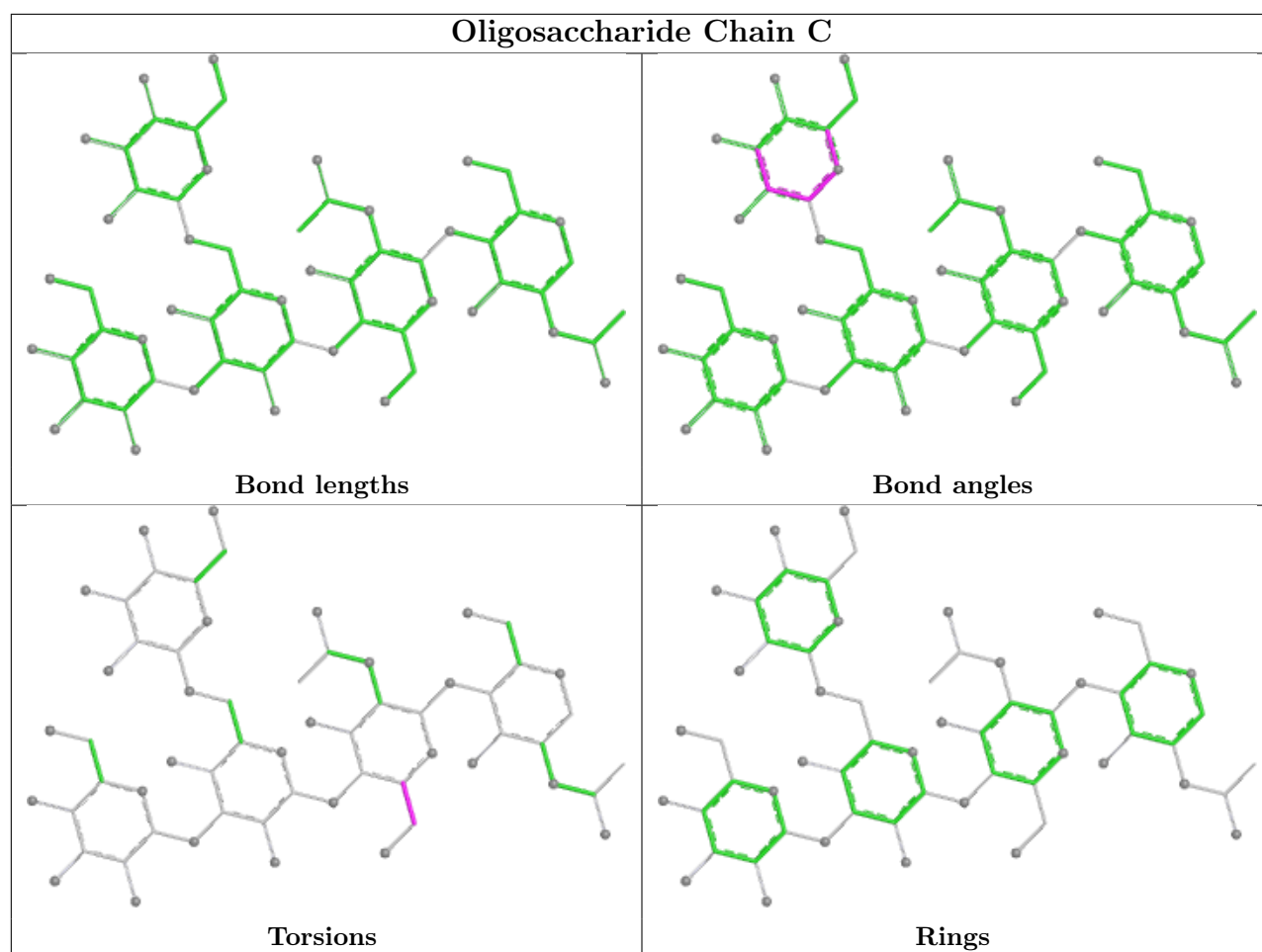
All (5) torsion outliers are listed below:

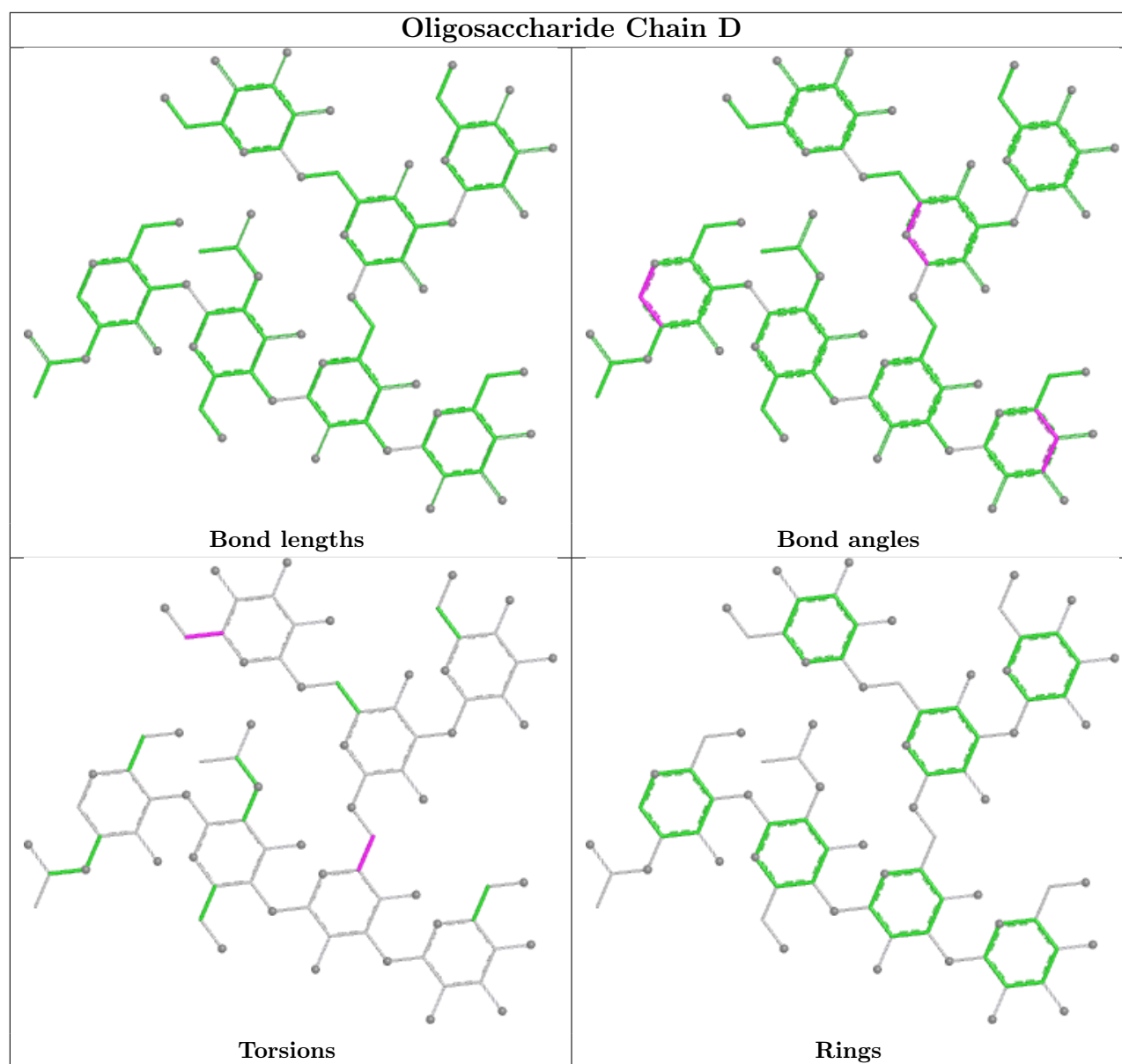
Mol	Chain	Res	Type	Atoms
6	D	3	MAN	O5-C5-C6-O6
6	D	6	MAN	C4-C5-C6-O6
6	D	6	MAN	O5-C5-C6-O6
6	D	3	MAN	C4-C5-C6-O6
5	C	2	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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





5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 7 are monoatomic - leaving 6 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
9	NAG	B	3099	2	14,14,15	0.58	0	17,19,21	0.97	0
9	NAG	A	3249	1	14,14,15	0.52	0	17,19,21	1.16	2 (11%)
7	GOL	A	1453	-	5,5,5	0.43	0	5,5,5	0.17	0
7	GOL	B	1463	8	5,5,5	0.37	0	5,5,5	0.25	0
10	CAC	B	1462	11	2,4,4	2.80	2 (100%)	4,6,6	2.09	2 (50%)
9	NAG	A	3015	1	14,14,15	0.48	0	17,19,21	1.00	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
9	NAG	B	3099	2	-	2/6/23/26	0/1/1/1
9	NAG	A	3249	1	-	2/6/23/26	0/1/1/1
7	GOL	A	1453	-	-	2/4/4/4	-
7	GOL	B	1463	8	-	0/4/4/4	-
9	NAG	A	3015	1	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	1462	CAC	AS-C2	2.85	1.97	1.90
10	B	1462	CAC	AS-C1	2.76	1.96	1.90

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	B	1462	CAC	O2-AS-C1	2.72	112.43	105.84
10	B	1462	CAC	O2-AS-C2	2.57	112.06	105.84
9	A	3249	NAG	C1-O5-C5	2.25	115.20	112.19
9	A	3249	NAG	C1-C2-N2	2.12	113.77	110.43

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	1453	GOL	O1-C1-C2-O2
7	A	1453	GOL	O1-C1-C2-C3
9	A	3249	NAG	O5-C5-C6-O6
9	A	3249	NAG	C4-C5-C6-O6
9	B	3099	NAG	O5-C5-C6-O6
9	B	3099	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	B	1462	CAC	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

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	452/452 (100%)	0.17	5 (1%) 78 77	18, 41, 58, 79	9 (1%)
2	B	456/461 (98%)	0.79	56 (12%) 8 6	17, 50, 92, 105	13 (2%)
3	H	219/221 (99%)	0.28	13 (5%) 28 28	22, 39, 62, 102	6 (2%)
4	L	214/214 (100%)	0.10	3 (1%) 73 73	17, 35, 51, 74	8 (3%)
All	All	1341/1348 (99%)	0.39	77 (5%) 29 29	17, 41, 83, 105	36 (2%)

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	452	PRO	8.6
1	A	1	LEU	5.2
4	L	214	CYS	5.0
2	B	1	GLY	4.6
2	B	439	ALA	4.4
2	B	440	GLN	4.3
2	B	405	GLY	4.0
2	B	458	GLY	3.8
2	B	34	GLY	3.8
2	B	72	LYS	3.8
2	B	459	VAL	3.8
1	A	337[A]	PRO	3.7
3	H	221	PRO	3.6
2	B	33	LEU	3.6
2	B	437	CYS	3.6
2	B	453	GLY	3.5
2	B	441	ALA	3.5
2	B	454	THR	3.4
3	H	137	THR	3.4
2	B	438	GLN	3.4
2	B	461	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
2	B	10	VAL	3.2
2	B	11	SER	3.2
2	B	395	VAL	3.1
2	B	69	LEU	3.0
3	H	207	ALA	3.0
2	B	78	SER	3.0
2	B	398	SER	3.0
2	B	457	CYS	2.9
2	B	24	ALA	2.9
3	H	195	PRO	2.9
3	H	138	THR	2.8
2	B	456	GLU	2.8
4	L	100	GLY	2.8
2	B	21	PRO	2.8
2	B	51	PRO	2.8
2	B	379	VAL	2.8
3	H	194	TRP	2.7
2	B	9	GLY	2.7
2	B	54	ILE	2.7
2	B	61	ALA	2.7
3	H	139	GLY	2.7
2	B	22	MET	2.6
2	B	36	PRO	2.6
2	B	8	ARG	2.5
2	B	448	CYS	2.5
2	B	460	CYS	2.5
3	H	192	SER	2.5
2	B	40	LEU	2.5
2	B	447	ARG	2.5
2	B	429	VAL	2.5
2	B	443	PRO	2.4
2	B	422	LYS	2.4
2	B	436	ALA	2.4
2	B	399	ILE	2.3
3	H	179[A]	ASP	2.3
2	B	403	VAL	2.3
2	B	420	GLY	2.2
3	H	196	SER	2.2
2	B	412[A]	LYS	2.2
2	B	396	SER	2.2
2	B	446	HIS	2.1
2	B	397	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	65	GLU	2.1
3	H	134	CYS	2.1
2	B	444	ASN	2.1
3	H	178	SER	2.1
1	A	402[A]	ARG	2.1
2	B	67	ARG	2.0
2	B	408	GLN	2.0
3	H	144	LEU	2.0
1	A	338	HIS	2.0
2	B	450	ASN	2.0
4	L	212	ASN	2.0
2	B	62	ARG	2.0
2	B	455	PHE	2.0
2	B	430	THR	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.

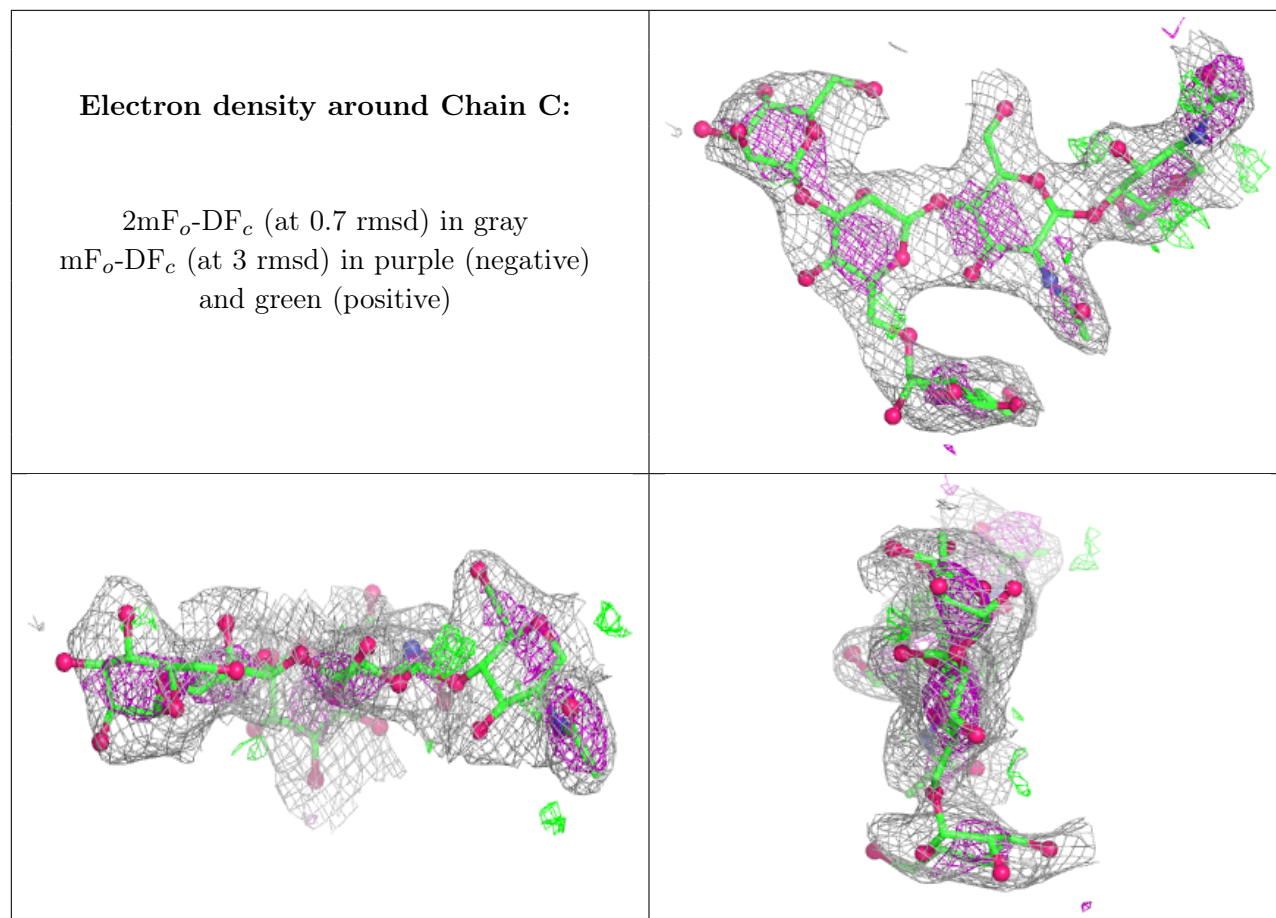
6.3 Carbohydrates [i](#)

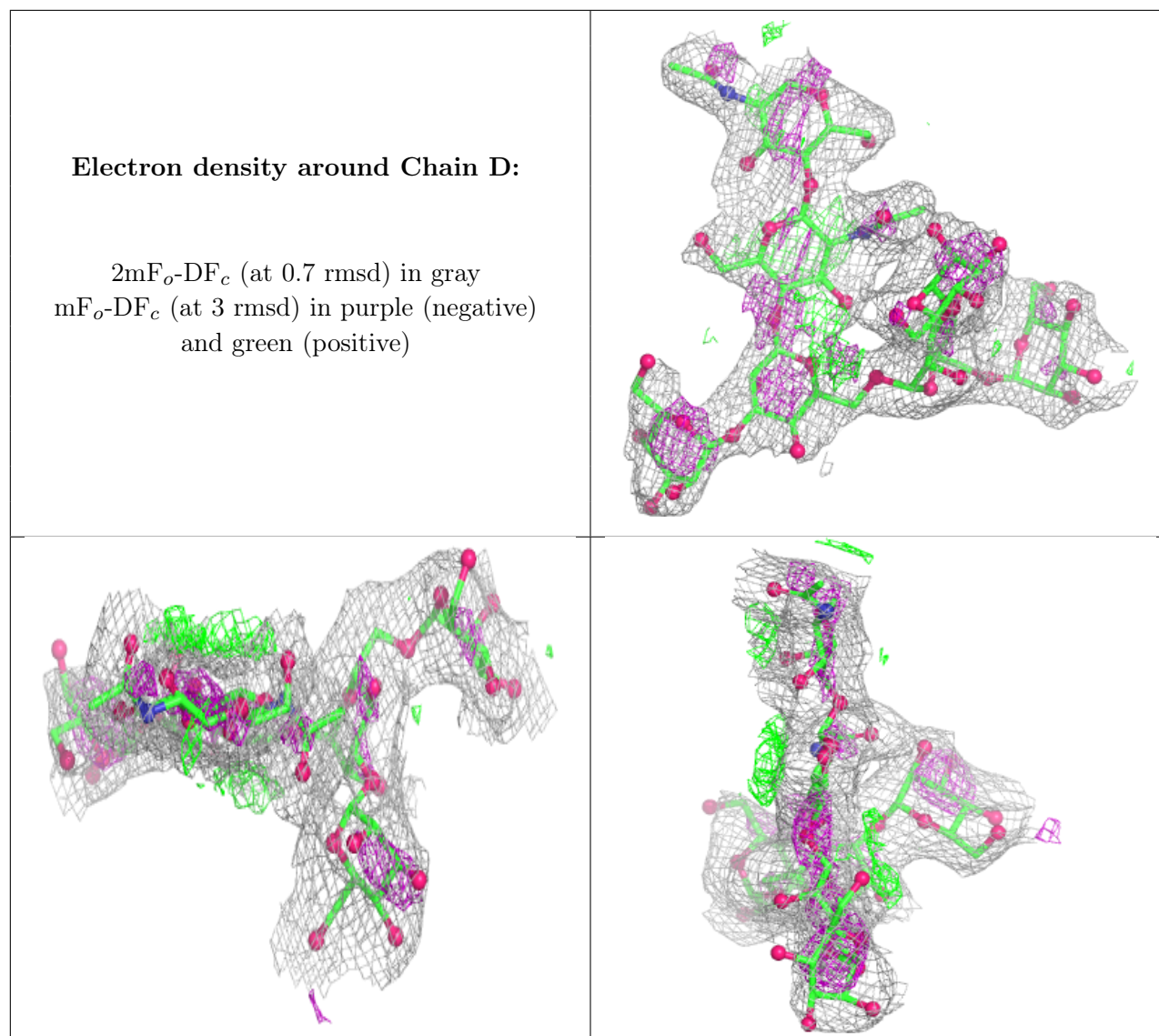
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	C	1	14/15	-	-	41,48,54,60	0
5	NAG	C	2	14/15	-	-	66,69,76,84	0
5	MAN	C	3	11/12	-	-	90,96,101,105	0
5	MAN	C	4	11/12	-	-	91,94,96,96	0
5	MAN	C	5	11/12	-	-	104,106,106,106	0
6	NAG	D	1	14/15	-	-	62,67,71,72	0
6	NAG	D	2	14/15	-	-	56,74,80,84	0
6	MAN	D	3	11/12	-	-	75,86,88,91	0
6	MAN	D	4	11/12	-	-	63,70,74,78	0
6	MAN	D	5	11/12	-	-	53,57,61,62	0
6	MAN	D	6	11/12	-	-	82,85,87,89	0
6	MAN	D	7	11/12	-	-	90,94,95,95	0

The following is a graphical depiction of the model fit to experimental electron density for oligosac-

charide. Each fit is shown from different orientation to approximate a three-dimensional view.





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(Å ²)	Q<0.9
9	NAG	A	3249	14/15	0.23	0.26	85,87,88,89	14
9	NAG	B	3099	14/15	0.60	0.21	94,100,104,104	0
9	NAG	A	3015	14/15	0.66	0.22	73,74,75,76	14
7	GOL	A	1453	6/6	0.89	0.17	58,62,65,66	0
7	GOL	B	1463	6/6	0.92	0.15	57,58,60,61	0
8	CA	A	2006	1/1	0.97	0.13	57,57,57,57	0
10	CAC	B	1462	5/5	0.97	0.18	51,52,53,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	CA	A	2005	1/1	0.98	0.21	41,41,41,41	0
8	CA	A	2004	1/1	0.98	0.13	57,57,57,57	0
8	CA	A	2007	1/1	0.99	0.12	53,53,53,53	0
8	CA	B	2003	1/1	0.99	0.21	25,25,25,25	0
11	MG	B	2001	1/1	0.99	0.15	23,23,23,23	0
8	CA	B	2002	1/1	1.00	0.15	32,32,32,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.