



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 24, 2026 – 10:46 PM EDT

PDB ID : 1H4P / pdb_00001h4p
Title : Crystal structure of exo-1,3-beta glucanase from *Saccharomyces cerevisiae*
Authors : Ferguson, A.D.
Deposited on : 2001-05-11
Resolution : 1.75 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

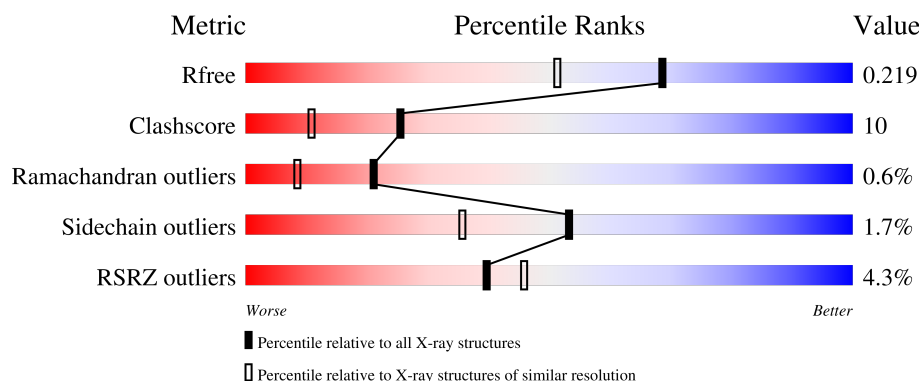
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	408	4% 82% 17% .
1	B	408	5% 83% 15% .
2	C	10	10% 40% 50%
3	D	5	20% 80%
4	E	8	50% 50%

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Mol	Chain	Length	Quality of chain
5	F	2	 100%

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
2	BMA	C	6	-	-	X	-
4	MAN	E	3	X	-	-	-
5	NAG	F	2	X	-	-	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7457 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.

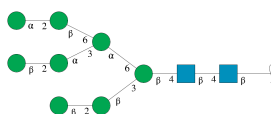
- Molecule 1 is a protein called GLUCAN 1,3-BETA-GLUCOSIDASE I/II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	408	Total	C	N	O	S	0	0	0
			3324	2120	547	645	12			
1	B	408	Total	C	N	O	S	0	0	0
			3324	2120	547	645	12			

There are 10 discrepancies between the modelled and reference sequences:

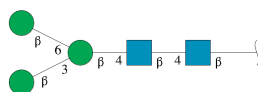
Chain	Residue	Modelled	Actual	Comment	Reference
A	141	ILE	THR	conflict	UNP P23776
A	205	ILE	THR	conflict	UNP P23776
A	223	ILE	THR	conflict	UNP P23776
A	330	ILE	THR	conflict	UNP P23776
A	343	ILE	THR	conflict	UNP P23776
B	141	ILE	THR	conflict	UNP P23776
B	205	ILE	THR	conflict	UNP P23776
B	223	ILE	THR	conflict	UNP P23776
B	330	ILE	THR	conflict	UNP P23776
B	343	ILE	THR	conflict	UNP P23776

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



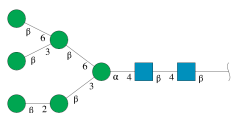
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	10	Total	C	N	O		0	0	0
			116	64	2	50				

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-3)-[beta-D-mannopyranose-(1-6)]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
3	D	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-2)-beta-D-mannopyranose-(1-3)-[beta-D-mannopyranose-(1-3)-[beta-D-mannopyranose-(1-6)]beta-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
4	E	8	Total	C	N	O	0	0	0
			94	52	2	40			

- Molecule 5 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
5	F	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

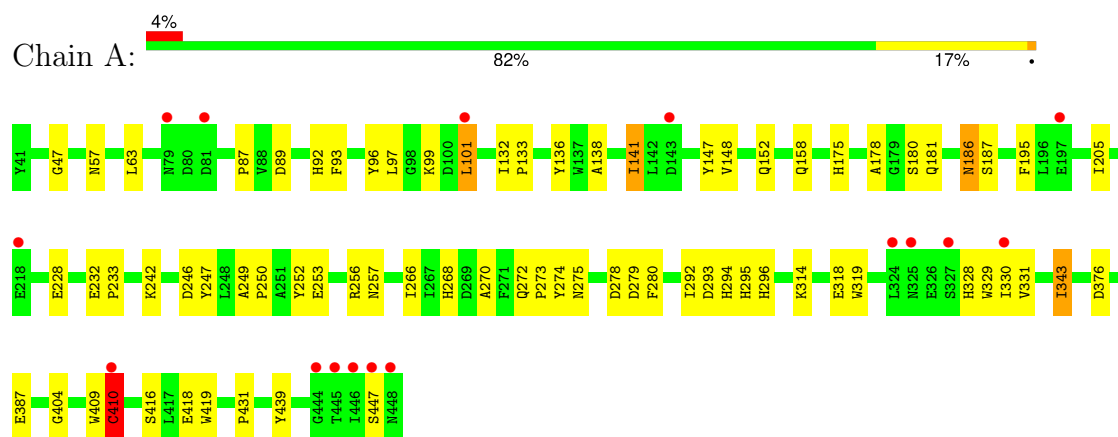
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	228	Total	O	0	0
			228	228		
7	B	228	Total	O	0	0
			228	228		

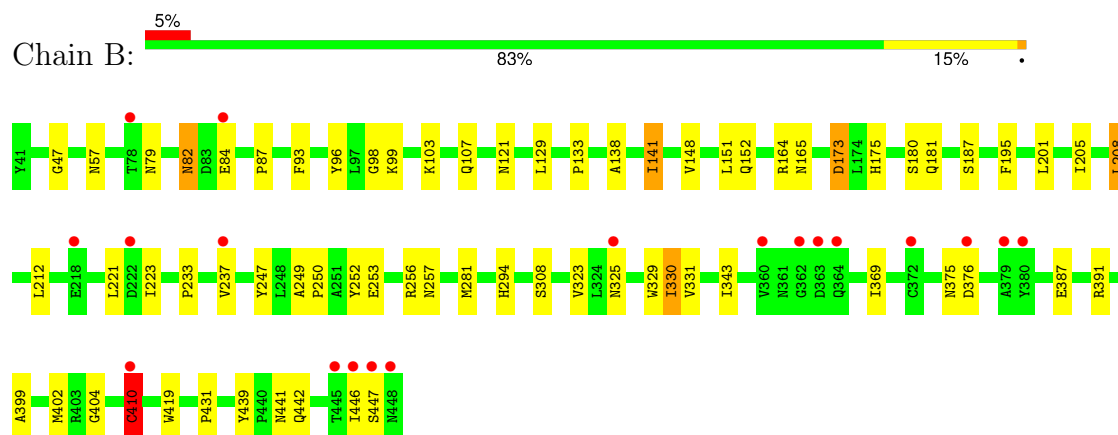
3 Residue-property plots

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: GLUCAN 1,3-BETA-GLUCOSIDASE I/II



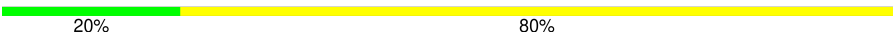
• Molecule 1: GLUCAN 1,3-BETA-GLUCOSIDASE I/II



• Molecule 2: beta-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-beta-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[beta-D-mannopyranose-(1-2)-beta-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



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

Chain D:  20% 80%

MAG1	MAG2	EMA3	EMA4	EMA5
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- Molecule 4: beta-D-mannopyranose-(1-2)-beta-D-mannopyranose-(1-3)-[beta-D-mannopyranose-(1-3)-[beta-D-mannopyranose-(1-6)]beta-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

Chain E:  50% 50%

MAG1	MAG2	MAN3	EMA4	EMA5	EMA6	EMA7	EMA8
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- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  100%

MAG1	MAG2
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4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	102.60Å 102.60Å 203.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.27 – 1.75 36.27 – 1.75	Depositor EDS
% Data completeness (in resolution range)	94.9 (36.27-1.75) 95.0 (36.27-1.75)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 1.75Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.206 , 0.228 0.200 , 0.219	Depositor DCC
R_{free} test set	5400 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	22.5	Xtriage
Anisotropy	0.186	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 34.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7457	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.74% 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: BMA, GOL, 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	0.36	0/3420	0.90	11/4655 (0.2%)
1	B	0.35	0/3420	0.92	12/4655 (0.3%)
All	All	0.36	0/6840	0.91	23/9310 (0.2%)

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	132	ILE	N-CA-C	7.61	115.74	107.60
1	B	47	GLY	N-CA-C	7.33	119.93	111.36
1	B	369	ILE	N-CA-C	-6.45	106.53	111.62
1	B	329	TRP	N-CA-C	-6.26	102.23	110.43
1	A	329	TRP	N-CA-C	-6.17	102.34	110.43
1	B	98	GLY	N-CA-C	-5.93	105.64	112.29
1	B	148	VAL	N-CA-C	-5.78	100.09	108.87
1	B	93	PHE	N-CA-C	-5.71	104.96	111.07
1	B	187	SER	N-CA-C	-5.69	106.38	113.38
1	A	147	TYR	N-CA-C	5.50	117.39	110.24
1	A	187	SER	N-CA-C	-5.48	106.64	113.38
1	B	308	SER	N-CA-C	-5.47	103.47	110.53
1	A	148	VAL	N-CA-C	-5.37	100.85	108.58
1	A	47	GLY	N-CA-C	5.35	118.82	111.54
1	B	221	LEU	N-CA-C	5.27	118.50	111.75
1	A	431	PRO	N-CA-C	5.27	119.84	111.26
1	A	410	CYS	N-CA-C	5.24	121.96	110.80
1	A	99	LYS	N-CA-C	5.23	117.40	111.02
1	A	93	PHE	N-CA-C	-5.22	105.58	111.28
1	B	233	PRO	N-CA-C	-5.18	103.06	111.19
1	A	233	PRO	N-CA-C	-5.15	103.11	111.19
1	B	99	LYS	N-CA-C	5.13	117.26	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	431	PRO	N-CA-C	5.08	119.17	111.15

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	3324	0	3069	51	0
1	B	3324	0	3069	57	0
2	C	116	0	97	15	0
3	D	61	0	52	3	0
4	E	94	0	79	3	0
5	F	28	0	25	2	0
6	A	24	0	32	3	0
6	B	30	0	40	1	0
7	A	228	0	0	2	0
7	B	228	0	0	6	0
All	All	7457	0	6463	129	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 10.

All (129) 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:A:343:ILE:HD12	1:A:419:TRP:HD1	1.22	1.00
1:B:294:HIS:HD2	1:B:330:ILE:HD11	1.25	0.97
1:B:57:ASN:HB2	1:B:410:CYS:H	1.33	0.92
1:A:292:ILE:O	1:A:330:ILE:HD12	1.72	0.90
1:B:294:HIS:HD2	1:B:330:ILE:CD1	1.90	0.85
1:A:410:CYS:HB3	1:A:419:TRP:O	1.79	0.83
1:A:343:ILE:HD12	1:A:419:TRP:CD1	2.11	0.82
1:A:278:ASP:HB2	3:D:2:NAG:H62	1.59	0.81
2:C:4:MAN:H62	2:C:8:MAN:H5	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:ILE:H	1:A:141:ILE:HD13	1.46	0.81
1:B:57:ASN:O	1:B:410:CYS:HA	1.83	0.79
2:C:5:MAN:H3	2:C:6:BMA:H61	1.65	0.78
1:B:399:ALA:HA	1:B:402:MET:HE3	1.64	0.78
1:B:201:LEU:O	1:B:205:ILE:HG12	1.82	0.77
2:C:2:NAG:H3	2:C:6:BMA:H3	1.64	0.77
1:B:141:ILE:H	1:B:141:ILE:HD13	1.51	0.76
1:B:343:ILE:HG12	7:B:2168:HOH:O	1.87	0.75
1:B:343:ILE:HG13	1:B:419:TRP:CD1	2.21	0.75
1:B:294:HIS:CD2	1:B:330:ILE:HD11	2.17	0.75
1:A:232:GLU:HA	1:A:268:HIS:CD2	2.25	0.72
1:A:158:GLN:HG2	2:C:2:NAG:H81	1.70	0.71
1:B:343:ILE:HG13	1:B:419:TRP:HD1	1.55	0.70
1:A:343:ILE:HG13	7:A:2160:HOH:O	1.91	0.70
1:B:173:ASP:OD2	1:B:175:HIS:HD2	1.75	0.70
1:A:292:ILE:O	1:A:330:ILE:CD1	2.40	0.69
1:B:325:ASN:HB2	7:B:2159:HOH:O	1.92	0.67
1:A:232:GLU:OE2	1:A:295:HIS:HD2	1.77	0.66
1:B:387:GLU:HG3	1:B:439:TYR:OH	1.95	0.66
1:A:330:ILE:HD12	1:A:331:VAL:H	1.61	0.65
1:A:343:ILE:CD1	1:A:419:TRP:HD1	2.04	0.64
1:B:223:ILE:HG13	7:B:2100:HOH:O	1.98	0.63
2:C:2:NAG:C3	2:C:6:BMA:H3	2.30	0.62
1:A:87:PRO:HG3	1:A:96:TYR:CD2	2.37	0.60
1:A:387:GLU:HG3	1:A:439:TYR:OH	2.00	0.60
2:C:9:BMA:H4	2:C:10:BMA:C1	2.32	0.60
1:B:294:HIS:CD2	1:B:330:ILE:CD1	2.80	0.60
1:B:103:LYS:O	1:B:107:GLN:HG3	2.01	0.59
1:A:268:HIS:CD2	1:A:270:ALA:H	2.20	0.59
1:B:82:ASN:C	1:B:82:ASN:HD22	2.11	0.59
1:B:253:GLU:HG3	1:B:257:ASN:HD22	1.68	0.58
1:A:97:LEU:HD22	1:A:101:LEU:HD13	1.86	0.57
1:A:141:ILE:HD13	1:A:141:ILE:N	2.18	0.57
1:B:82:ASN:HD22	1:B:84:GLU:H	1.51	0.57
1:B:223:ILE:HD12	1:B:223:ILE:N	2.21	0.55
1:A:314:LYS:O	1:A:318:GLU:HG3	2.06	0.55
4:E:1:NAG:H61	4:E:2:NAG:N2	2.22	0.55
1:B:87:PRO:HG3	1:B:96:TYR:CD2	2.42	0.55
1:B:79:ASN:HD21	1:B:82:ASN:ND2	2.05	0.55
1:B:205:ILE:CD1	1:B:247:TYR:HD1	2.21	0.54
2:C:5:MAN:C3	2:C:6:BMA:H61	2.36	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:205:ILE:HD11	1:B:247:TYR:HD1	1.72	0.53
1:A:181:GLN:HA	1:A:195:PHE:HB2	1.90	0.53
1:A:253:GLU:CD	1:A:257:ASN:HD22	2.16	0.53
1:B:330:ILE:HG12	1:B:331:VAL:N	2.22	0.53
1:B:103:LYS:HE2	1:B:151:LEU:HD11	1.91	0.53
1:B:141:ILE:HD13	1:B:141:ILE:N	2.23	0.53
1:B:391:ARG:HH11	1:B:442:GLN:NE2	2.07	0.52
1:B:330:ILE:CD1	7:B:2165:HOH:O	2.58	0.52
2:C:6:BMA:O6	2:C:10:BMA:H4	2.11	0.51
4:E:3:MAN:H4	4:E:6:BMA:O2	2.10	0.51
2:C:2:NAG:HN2	2:C:6:BMA:H3	1.76	0.51
1:A:343:ILE:HD12	1:A:416:SER:HG	1.76	0.51
1:A:343:ILE:CD1	1:A:416:SER:OG	2.58	0.50
1:B:330:ILE:O	1:B:404:GLY:HA3	2.12	0.50
5:F:1:NAG:O3	5:F:1:NAG:H83	2.12	0.50
1:B:237:VAL:O	1:B:237:VAL:HG12	2.10	0.50
2:C:3:BMA:H2	2:C:9:BMA:H2	1.93	0.50
1:A:92:HIS:HE1	7:A:2032:HOH:O	1.95	0.49
2:C:4:MAN:C6	2:C:8:MAN:H5	2.38	0.49
1:B:391:ARG:HH11	1:B:442:GLN:HE21	1.60	0.49
1:A:330:ILE:HD12	1:A:331:VAL:N	2.26	0.49
1:B:205:ILE:HD13	1:B:247:TYR:CD1	2.48	0.49
1:B:208:LEU:HD22	1:B:212:LEU:HG	1.95	0.49
2:C:3:BMA:O3	2:C:10:BMA:H61	2.13	0.48
1:B:173:ASP:OD2	1:B:175:HIS:CD2	2.62	0.48
1:A:249:ALA:HB3	1:A:250:PRO:HD3	1.96	0.48
1:A:293:ASP:OD2	1:A:295:HIS:HE1	1.97	0.48
1:B:323:VAL:HG11	1:B:330:ILE:CD1	2.44	0.48
1:A:409:TRP:O	1:A:410:CYS:HB2	2.14	0.47
1:A:252:TYR:CE1	1:A:256:ARG:HG3	2.49	0.47
1:A:228:GLU:HA	1:A:266:ILE:HB	1.95	0.47
1:B:330:ILE:HD11	7:B:2165:HOH:O	2.15	0.47
1:A:205:ILE:HD11	1:A:247:TYR:CD1	2.49	0.47
1:B:164:ARG:HB2	1:B:223:ILE:HG12	1.97	0.46
1:B:82:ASN:ND2	1:B:84:GLU:H	2.11	0.46
2:C:4:MAN:H2	2:C:6:BMA:C1	2.46	0.46
3:D:1:NAG:O3	3:D:1:NAG:H83	2.15	0.46
1:B:253:GLU:HG3	1:B:257:ASN:ND2	2.31	0.46
1:B:205:ILE:CD1	1:B:247:TYR:CD1	2.98	0.46
1:A:294:HIS:CD2	1:A:330:ILE:CD1	2.99	0.46
1:A:280:PHE:O	1:A:328:HIS:CE1	2.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:LYS:O	1:A:246:ASP:HB2	2.17	0.45
1:A:409:TRP:O	1:A:410:CYS:CB	2.65	0.45
1:A:138:ALA:HB1	1:A:152:GLN:HB2	1.99	0.45
1:B:79:ASN:HD21	1:B:82:ASN:HD21	1.63	0.45
6:B:1449:GOL:H31	7:B:2166:HOH:O	2.17	0.44
1:A:136:TYR:CE2	1:A:178:ALA:HA	2.52	0.44
1:A:343:ILE:HD11	1:A:418:GLU:HB2	1.98	0.44
1:A:97:LEU:HB3	1:A:101:LEU:HB3	1.99	0.44
1:B:343:ILE:HD13	1:B:375:ASN:HD22	1.83	0.44
1:A:272:GLN:HE21	1:A:273:PRO:HD2	1.83	0.44
1:B:252:TYR:CZ	1:B:256:ARG:HG3	2.52	0.44
1:A:343:ILE:CD1	1:A:376:ASP:OD1	2.65	0.43
2:C:9:BMA:C4	2:C:10:BMA:C1	2.95	0.43
1:A:133:PRO:HB3	1:A:175:HIS:CG	2.53	0.43
1:A:296:HIS:HB3	1:A:319:TRP:CZ3	2.54	0.43
1:B:138:ALA:HB1	1:B:152:GLN:HB2	1.99	0.43
1:A:57:ASN:HB2	1:A:410:CYS:H	1.82	0.43
5:F:1:NAG:H62	5:F:2:NAG:N2	2.34	0.42
1:A:63:LEU:HD13	1:A:175:HIS:HB3	2.02	0.42
1:B:133:PRO:HB3	1:B:175:HIS:CG	2.55	0.42
3:D:3:BMA:O4	3:D:4:BMA:H2	2.20	0.42
1:A:330:ILE:O	1:A:404:GLY:HA3	2.20	0.42
1:B:446:ILE:HG22	1:B:447:SER:N	2.34	0.42
6:A:1452:GOL:C1	1:B:121:ASN:HD21	2.32	0.42
1:B:249:ALA:N	1:B:250:PRO:HD2	2.35	0.42
1:B:343:ILE:CD1	1:B:376:ASP:OD1	2.68	0.41
1:B:252:TYR:HB2	1:B:281:MET:HE1	2.03	0.41
1:B:223:ILE:N	1:B:223:ILE:CD1	2.84	0.41
1:A:279:ASP:OD1	1:A:279:ASP:C	2.64	0.41
1:A:296:HIS:HB3	1:A:319:TRP:CH2	2.55	0.41
1:B:181:GLN:HA	1:B:195:PHE:HB2	2.02	0.41
1:A:89:ASP:OD1	1:A:92:HIS:HD2	2.04	0.41
6:A:1452:GOL:O1	1:B:121:ASN:ND2	2.52	0.41
1:B:165:ASN:CG	4:E:1:NAG:N2	2.78	0.41
1:B:129:LEU:C	1:B:129:LEU:HD23	2.45	0.40
1:A:186:ASN:OD1	6:A:1450:GOL:H12	2.21	0.40
1:A:274:TYR:O	1:A:275:ASN:HB2	2.21	0.40
2:C:5:MAN:O3	2:C:5:MAN:H61	2.22	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	406/408 (100%)	387 (95%)	16 (4%)	3 (1%)	18	7
1	B	406/408 (100%)	387 (95%)	17 (4%)	2 (0%)	24	11
All	All	812/816 (100%)	774 (95%)	33 (4%)	5 (1%)	21	8

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	410	CYS
1	A	410	CYS
1	A	447	SER
1	A	180	SER
1	B	180	SER

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	352/352 (100%)	347 (99%)	5 (1%)	59	44
1	B	352/352 (100%)	345 (98%)	7 (2%)	48	29
All	All	704/704 (100%)	692 (98%)	12 (2%)	53	36

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	LEU

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Mol	Chain	Res	Type
1	A	141	ILE
1	A	186	ASN
1	A	343	ILE
1	A	410	CYS
1	B	82	ASN
1	B	141	ILE
1	B	173	ASP
1	B	208	LEU
1	B	330	ILE
1	B	410	CYS
1	B	441	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	HIS
1	A	107	GLN
1	A	117	GLN
1	A	121	ASN
1	A	125	GLN
1	A	257	ASN
1	A	268	HIS
1	A	272	GLN
1	A	284	ASN
1	A	295	HIS
1	A	361	ASN
1	A	364	GLN
1	A	396	GLN
1	A	422	GLN
1	A	427	ASN
1	B	82	ASN
1	B	107	GLN
1	B	121	ASN
1	B	166	ASN
1	B	175	HIS
1	B	200	ASN
1	B	245	ASN
1	B	257	ASN
1	B	361	ASN
1	B	364	GLN
1	B	396	GLN
1	B	422	GLN

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Mol	Chain	Res	Type
1	B	441	ASN
1	B	442	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 ⓘ

25 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	C	1	2,1	14,14,15	0.60	0	17,19,21	0.74	1 (5%)
2	BMA	C	10	2	11,11,12	0.62	0	15,15,17	0.84	1 (6%)
2	NAG	C	2	2	14,14,15	0.54	0	17,19,21	0.79	0
2	BMA	C	3	2	11,11,12	0.55	0	15,15,17	0.55	0
2	MAN	C	4	2	11,11,12	0.63	0	15,15,17	0.66	1 (6%)
2	MAN	C	5	2	11,11,12	0.60	0	15,15,17	0.65	1 (6%)
2	BMA	C	6	2	11,11,12	0.57	0	15,15,17	0.84	1 (6%)
2	BMA	C	7	2	11,11,12	0.59	0	15,15,17	0.43	0
2	MAN	C	8	2	11,11,12	0.48	0	15,15,17	0.62	1 (6%)
2	BMA	C	9	2	11,11,12	0.76	0	15,15,17	0.63	0
3	NAG	D	1	3,1	14,14,15	0.53	0	17,19,21	0.68	0
3	NAG	D	2	3	14,14,15	0.62	0	17,19,21	0.73	0
3	BMA	D	3	3	11,11,12	0.62	0	15,15,17	0.31	0
3	BMA	D	4	3	11,11,12	0.54	0	15,15,17	0.46	0
3	BMA	D	5	3	11,11,12	0.60	0	15,15,17	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	E	1	4,1	14,14,15	0.61	0	17,19,21	0.69	0
4	NAG	E	2	4	14,14,15	0.52	0	17,19,21	0.66	0
4	MAN	E	3	4	11,11,12	0.54	0	15,15,17	0.28	0
4	BMA	E	4	4	11,11,12	0.57	0	15,15,17	0.49	0
4	BMA	E	5	4	11,11,12	0.49	0	15,15,17	0.46	0
4	BMA	E	6	4	11,11,12	0.69	0	15,15,17	0.67	0
4	BMA	E	7	4	11,11,12	0.53	0	15,15,17	0.46	0
4	BMA	E	8	4	11,11,12	0.55	0	15,15,17	0.44	0
5	NAG	F	1	5,1	14,14,15	0.57	0	17,19,21	0.80	1 (5%)
5	NAG	F	2	5	14,14,15	0.61	0	17,19,21	0.71	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	2,1	-	2/6/23/26	0/1/1/1
2	BMA	C	10	2	-	2/2/19/22	1/1/1/1
2	NAG	C	2	2	-	3/6/23/26	0/1/1/1
2	BMA	C	3	2	-	0/2/19/22	0/1/1/1
2	MAN	C	4	2	-	2/2/19/22	0/1/1/1
2	MAN	C	5	2	-	1/2/19/22	0/1/1/1
2	BMA	C	6	2	-	1/2/19/22	1/1/1/1
2	BMA	C	7	2	-	0/2/19/22	0/1/1/1
2	MAN	C	8	2	-	0/2/19/22	0/1/1/1
2	BMA	C	9	2	-	0/2/19/22	0/1/1/1
3	NAG	D	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	D	2	3	-	5/6/23/26	0/1/1/1
3	BMA	D	3	3	-	2/2/19/22	0/1/1/1
3	BMA	D	4	3	-	0/2/19/22	0/1/1/1
3	BMA	D	5	3	-	0/2/19/22	0/1/1/1
4	NAG	E	1	4,1	-	5/6/23/26	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1
4	MAN	E	3	4	1/1/4/5	0/2/19/22	0/1/1/1
4	BMA	E	4	4	-	2/2/19/22	0/1/1/1
4	BMA	E	5	4	-	0/2/19/22	0/1/1/1
4	BMA	E	6	4	-	0/2/19/22	0/1/1/1
4	BMA	E	7	4	-	2/2/19/22	0/1/1/1
4	BMA	E	8	4	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	F	1	5,1	-	4/6/23/26	0/1/1/1
5	NAG	F	2	5	1/1/5/7	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	10	BMA	C1-O5-C5	2.81	115.96	112.19
2	C	6	BMA	C1-O5-C5	2.77	115.90	112.19
5	F	1	NAG	C2-N2-C7	-2.35	119.75	122.90
2	C	1	NAG	C2-N2-C7	-2.19	119.96	122.90
2	C	5	MAN	C1-O5-C5	2.16	115.09	112.19
5	F	2	NAG	C2-N2-C7	-2.14	120.04	122.90
2	C	4	MAN	C1-O5-C5	2.04	114.92	112.19
2	C	8	MAN	C1-O5-C5	2.04	114.91	112.19

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	E	3	MAN	C1
5	F	2	NAG	C1

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	1	NAG	C8-C7-N2-C2
3	D	1	NAG	O7-C7-N2-C2
3	D	2	NAG	C8-C7-N2-C2
3	D	2	NAG	O7-C7-N2-C2
4	E	1	NAG	C8-C7-N2-C2
4	E	1	NAG	O7-C7-N2-C2
4	E	2	NAG	C8-C7-N2-C2
4	E	2	NAG	O7-C7-N2-C2
5	F	1	NAG	C8-C7-N2-C2
5	F	1	NAG	O7-C7-N2-C2
5	F	2	NAG	C8-C7-N2-C2
5	F	2	NAG	O7-C7-N2-C2
2	C	10	BMA	O5-C5-C6-O6
2	C	10	BMA	C4-C5-C6-O6
3	D	2	NAG	O5-C5-C6-O6
2	C	4	MAN	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
2	C	1	NAG	C8-C7-N2-C2
2	C	2	NAG	C8-C7-N2-C2
2	C	4	MAN	C4-C5-C6-O6
4	E	1	NAG	O5-C5-C6-O6
2	C	1	NAG	O7-C7-N2-C2
2	C	2	NAG	O7-C7-N2-C2
4	E	4	BMA	O5-C5-C6-O6
4	E	7	BMA	C4-C5-C6-O6
4	E	1	NAG	C4-C5-C6-O6
4	E	7	BMA	O5-C5-C6-O6
5	F	1	NAG	O5-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6
3	D	3	BMA	C4-C5-C6-O6
2	C	6	BMA	C4-C5-C6-O6
4	E	4	BMA	C4-C5-C6-O6
3	D	2	NAG	C3-C2-N2-C7
4	E	1	NAG	C3-C2-N2-C7
2	C	5	MAN	O5-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6
3	D	3	BMA	O5-C5-C6-O6
5	F	1	NAG	C4-C5-C6-O6

All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	6	BMA	C1-C2-C3-C4-C5-O5
2	C	10	BMA	C1-C2-C3-C4-C5-O5

18 monomers are involved in 23 short contacts:

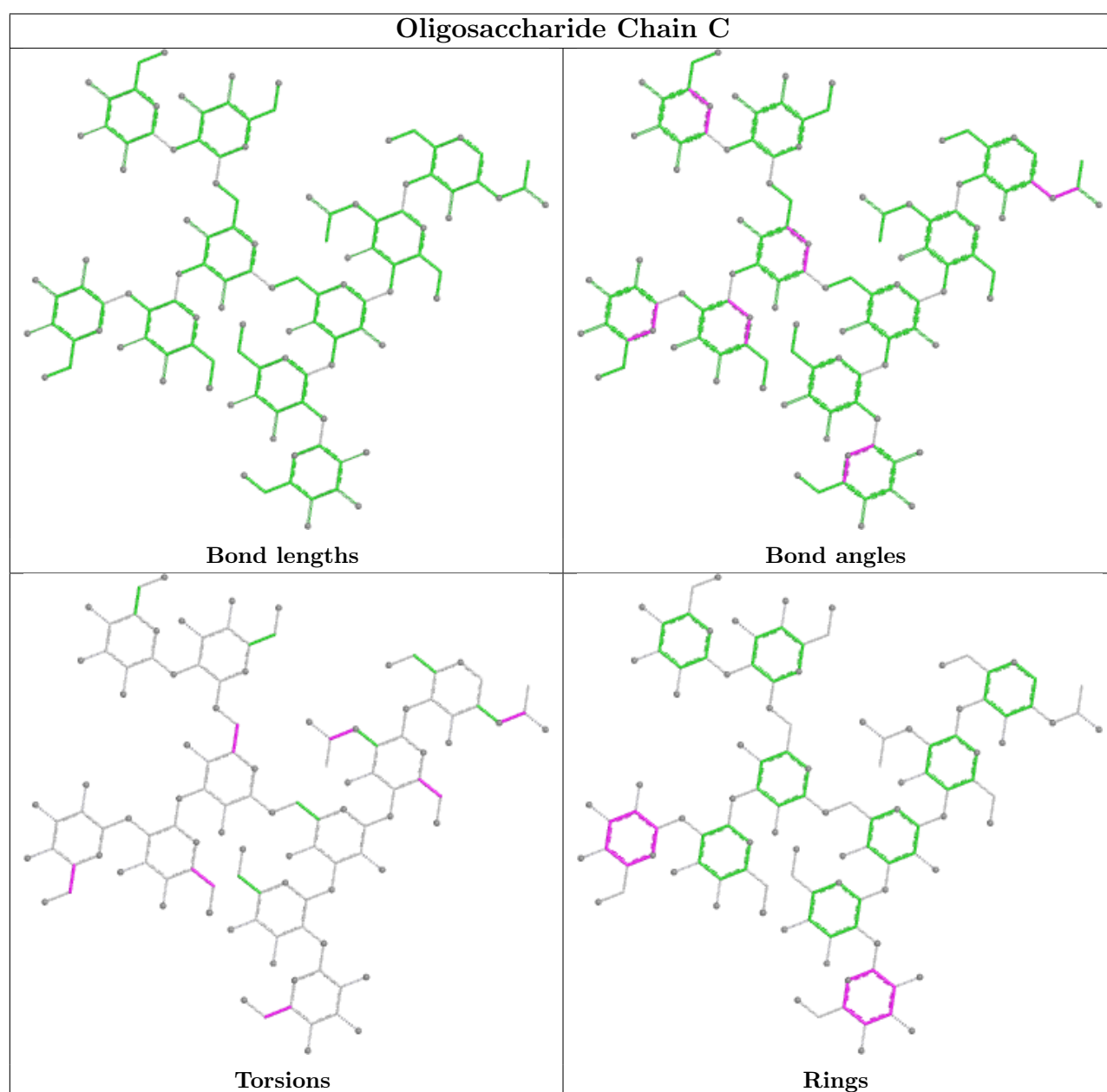
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	9	BMA	3	0
4	E	3	MAN	1	0
3	D	1	NAG	1	0
2	C	2	NAG	4	0
2	C	10	BMA	4	0
2	C	3	BMA	2	0
2	C	4	MAN	3	0
5	F	2	NAG	1	0
4	E	1	NAG	2	0
4	E	2	NAG	1	0
2	C	6	BMA	7	0

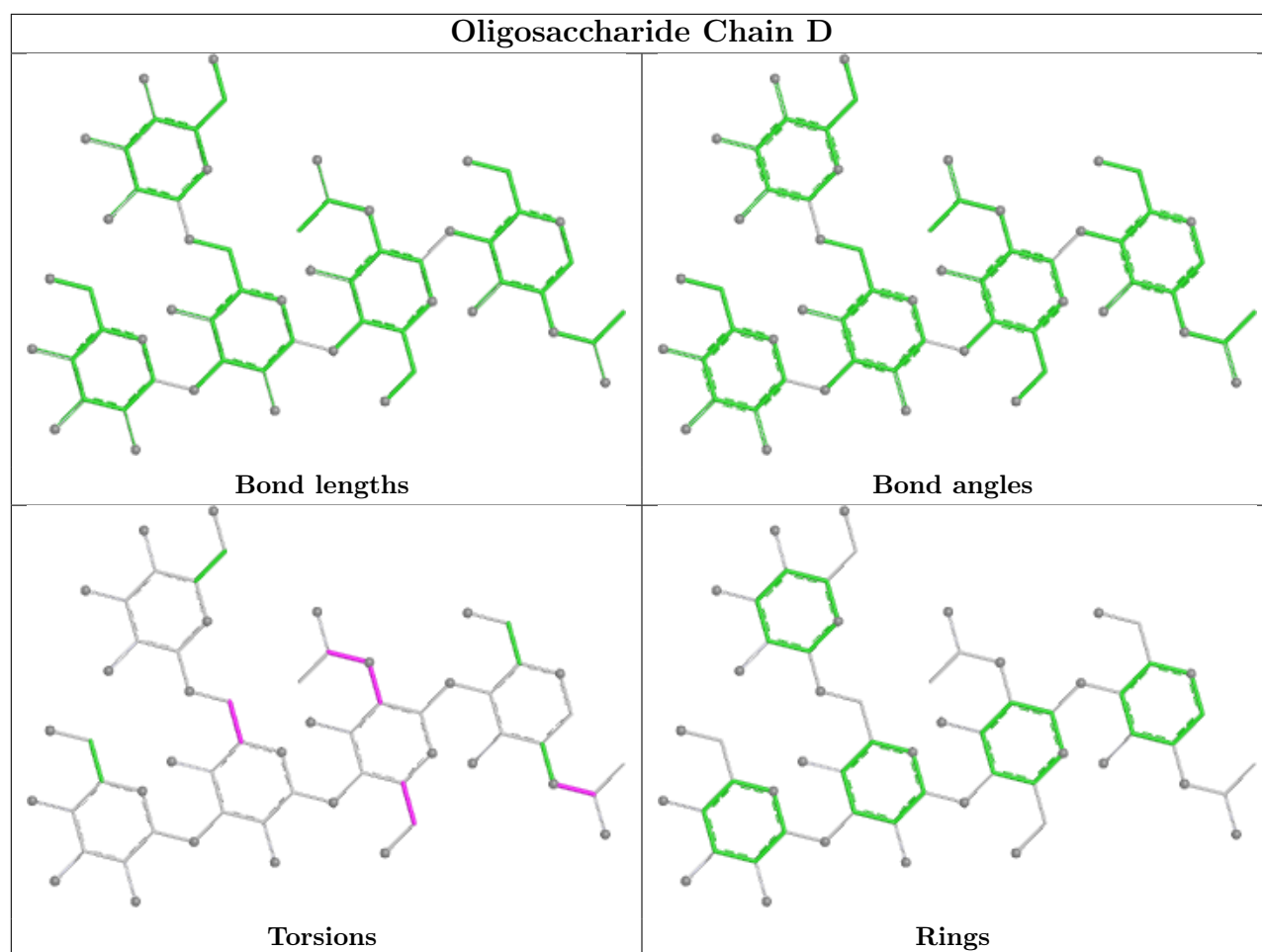
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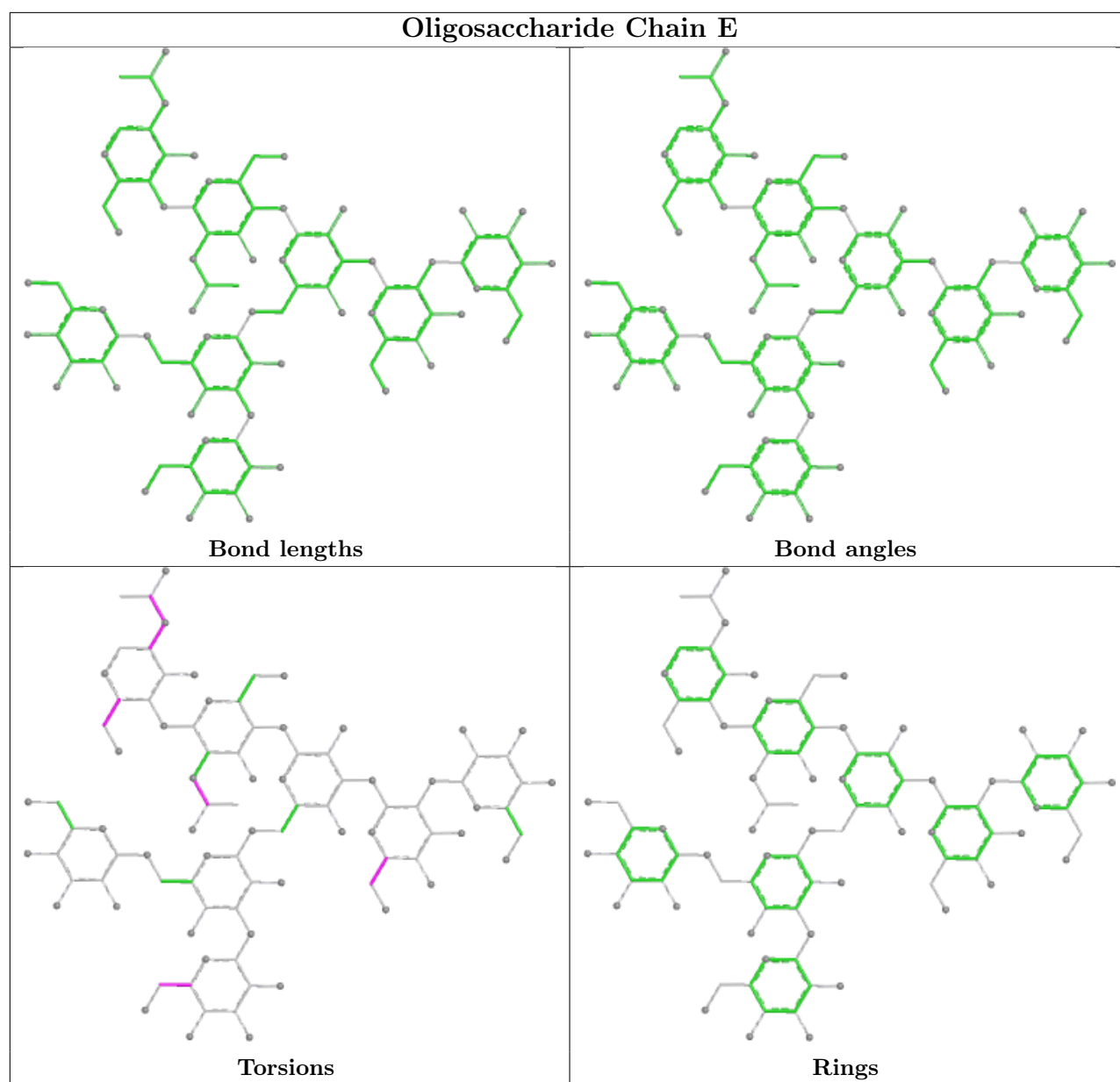
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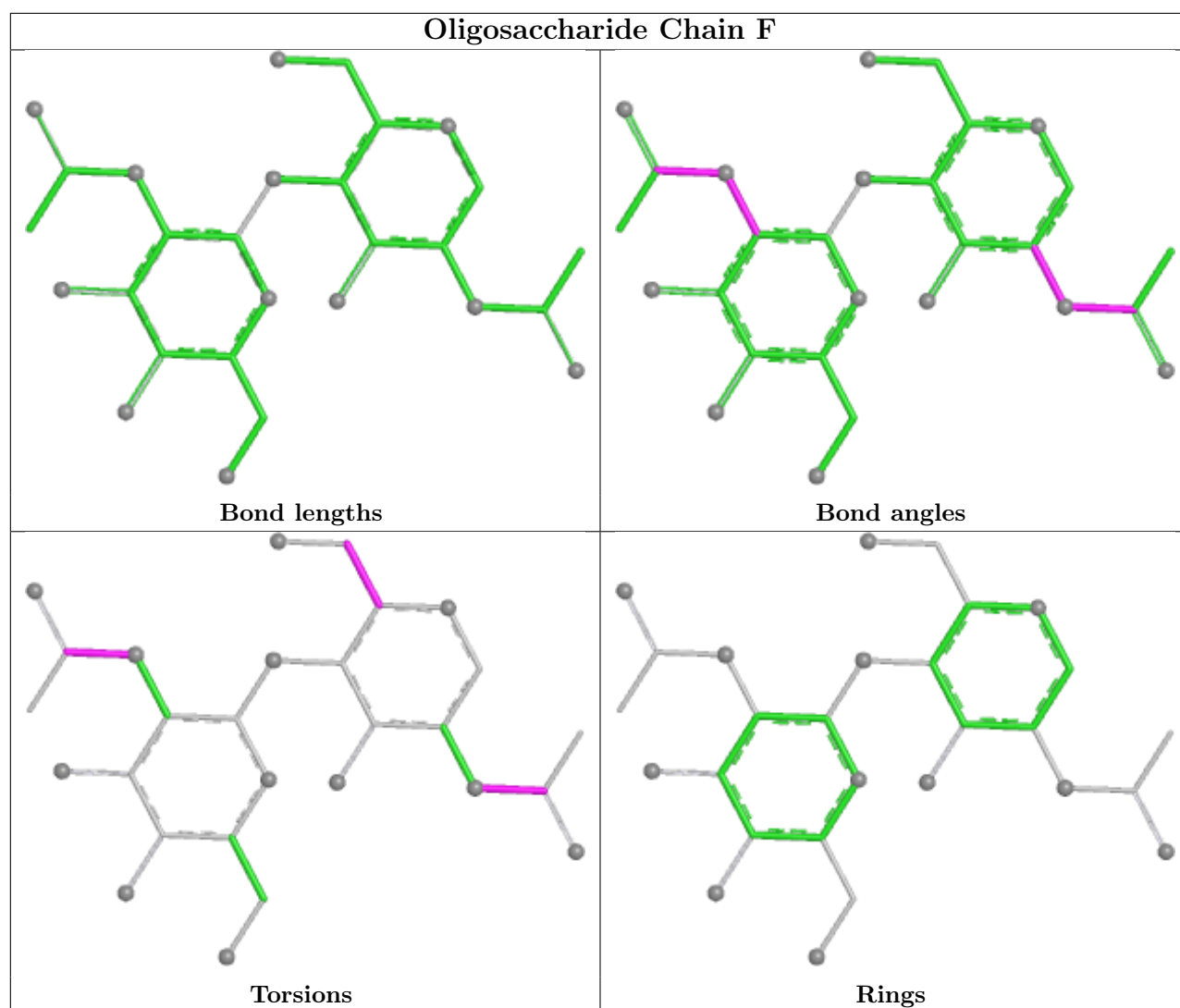
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	6	BMA	1	0
2	C	8	MAN	2	0
5	F	1	NAG	2	0
3	D	2	NAG	1	0
3	D	3	BMA	1	0
3	D	4	BMA	1	0
2	C	5	MAN	3	0

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](#)

9 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	$\# Z > 2$
6	GOL	A	1449	-	5,5,5	0.90	0	5,5,5	0.40	0
6	GOL	A	1450	-	5,5,5	0.83	0	5,5,5	0.44	0
6	GOL	B	1449	-	5,5,5	0.95	0	5,5,5	0.34	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	GOL	B	1451	-	5,5,5	0.87	0	5,5,5	0.39	0
6	GOL	B	1453	-	5,5,5	0.84	0	5,5,5	0.42	0
6	GOL	A	1451	-	5,5,5	0.87	0	5,5,5	0.40	0
6	GOL	A	1452	-	5,5,5	0.85	0	5,5,5	0.48	0
6	GOL	B	1450	-	5,5,5	0.81	0	5,5,5	0.46	0
6	GOL	B	1452	-	5,5,5	0.86	0	5,5,5	0.48	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	GOL	A	1449	-	-	0/4/4/4	-
6	GOL	A	1450	-	-	0/4/4/4	-
6	GOL	B	1449	-	-	0/4/4/4	-
6	GOL	B	1451	-	-	0/4/4/4	-
6	GOL	B	1453	-	-	0/4/4/4	-
6	GOL	A	1451	-	-	0/4/4/4	-
6	GOL	A	1452	-	-	0/4/4/4	-
6	GOL	B	1450	-	-	0/4/4/4	-
6	GOL	B	1452	-	-	0/4/4/4	-

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.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1450	GOL	1	0
6	B	1449	GOL	1	0
6	A	1452	GOL	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	408/408 (100%)	0.25	16 (3%) 43 49	15, 24, 37, 80	0
1	B	408/408 (100%)	0.35	19 (4%) 36 42	15, 24, 37, 78	0
All	All	816/816 (100%)	0.30	35 (4%) 40 46	15, 24, 37, 80	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	447	SER	6.1
1	B	446	ILE	5.8
1	A	446	ILE	5.5
1	B	448	ASN	4.4
1	B	363	ASP	4.2
1	A	325	ASN	3.8
1	B	362	GLY	3.7
1	A	448	ASN	3.7
1	B	325	ASN	3.7
1	B	410	CYS	3.6
1	B	380	TYR	3.6
1	A	447	SER	3.5
1	A	79	ASN	3.4
1	A	445	THR	3.3
1	B	360	VAL	3.2
1	A	444	GLY	2.8
1	A	81	ASP	2.7
1	B	445	THR	2.7
1	B	222	ASP	2.7
1	B	376	ASP	2.7
1	A	327	SER	2.6
1	B	379	ALA	2.6
1	A	101	LEU	2.4
1	A	218	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	237	VAL	2.3
1	A	330	ILE	2.3
1	B	78	THR	2.2
1	B	364	GLN	2.2
1	A	197	GLU	2.2
1	A	410	CYS	2.2
1	A	324	LEU	2.2
1	B	218	GLU	2.1
1	B	372	CYS	2.1
1	B	84	GLU	2.1
1	A	143	ASP	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.

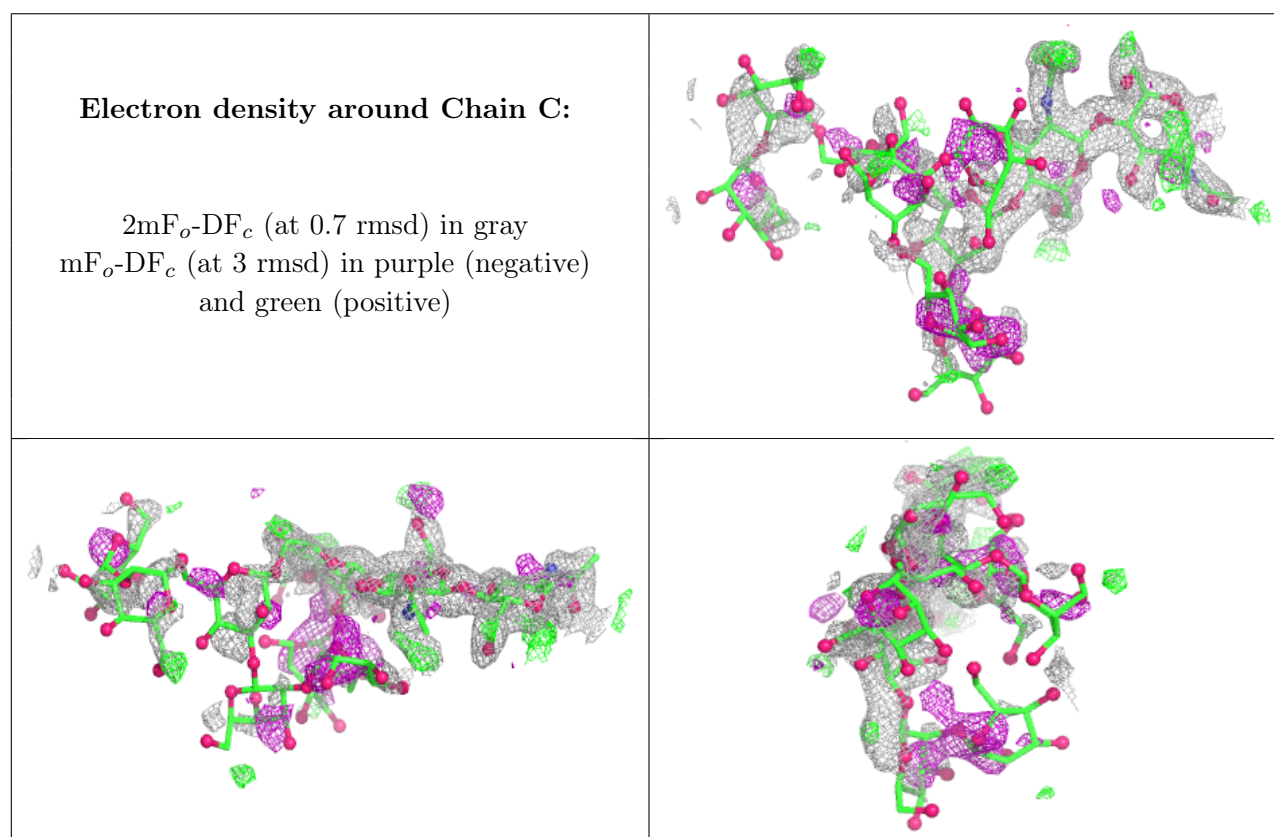
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	BMA	C	7	11/12	-0.01	0.23	93,94,94,95	0
2	MAN	C	5	11/12	0.01	0.27	94,94,95,95	0
2	MAN	C	8	11/12	0.02	0.26	95,96,96,96	0
2	BMA	C	10	11/12	0.03	0.26	91,92,93,93	0
4	BMA	E	7	11/12	0.05	0.24	90,90,90,91	0
4	BMA	E	5	11/12	0.11	0.27	88,89,89,90	0
2	BMA	C	9	11/12	0.14	0.26	85,87,88,90	0
3	BMA	D	5	11/12	0.15	0.27	98,99,99,99	0
3	BMA	D	4	11/12	0.17	0.27	95,96,96,96	0
4	BMA	E	6	11/12	0.23	0.23	86,88,89,90	0
2	BMA	C	6	11/12	0.28	0.22	95,95,96,96	0
2	MAN	C	4	11/12	0.29	0.21	88,91,92,93	0
4	BMA	E	8	11/12	0.29	0.22	91,91,91,91	0
5	NAG	F	2	14/15	0.30	0.22	73,75,76,76	0
3	NAG	D	2	14/15	0.31	0.28	84,86,88,91	0
4	BMA	E	4	11/12	0.35	0.20	84,85,86,87	0
3	BMA	D	3	11/12	0.39	0.24	93,95,96,98	0

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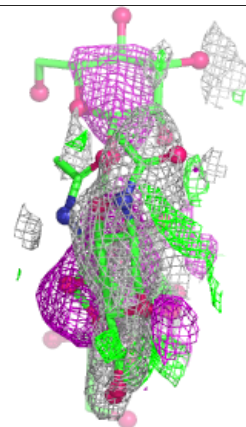
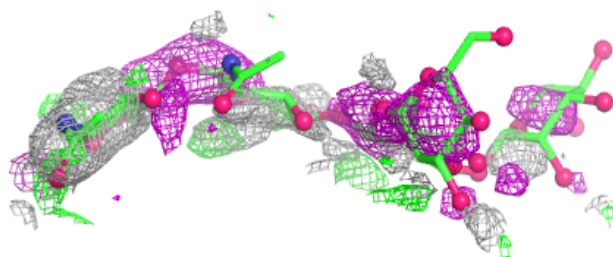
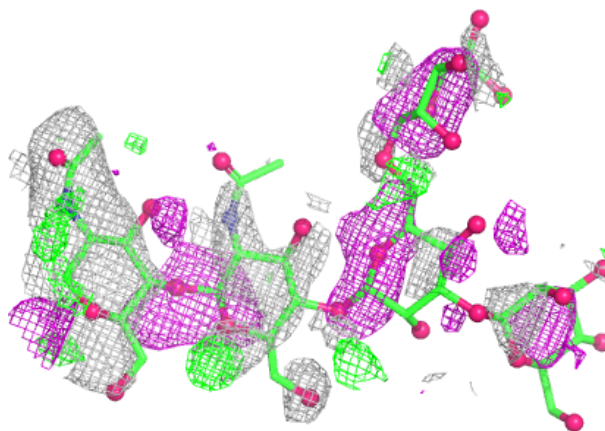
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	D	1	14/15	0.42	0.26	69,72,75,80	0
2	BMA	C	3	11/12	0.54	0.22	74,79,82,86	0
5	NAG	F	1	14/15	0.56	0.22	61,65,67,70	0
2	NAG	C	2	14/15	0.61	0.18	57,60,64,69	0
4	NAG	E	2	14/15	0.62	0.20	62,65,67,72	0
2	NAG	C	1	14/15	0.72	0.17	42,46,48,51	0
4	MAN	E	3	11/12	0.76	0.19	76,79,82,84	0
4	NAG	E	1	14/15	0.76	0.16	49,52,54,58	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.



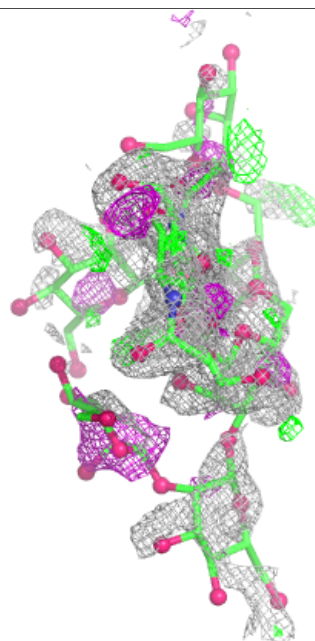
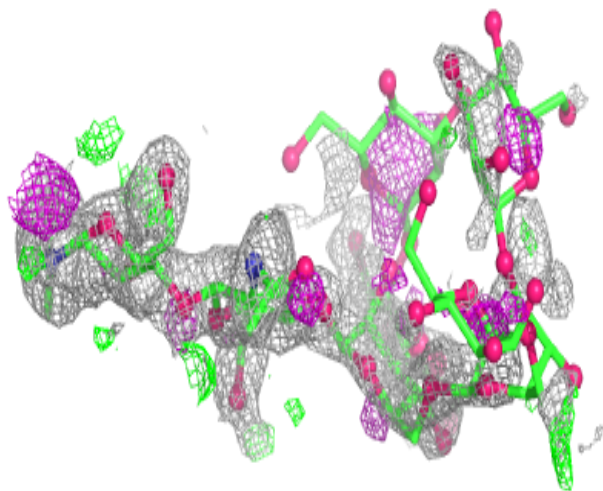
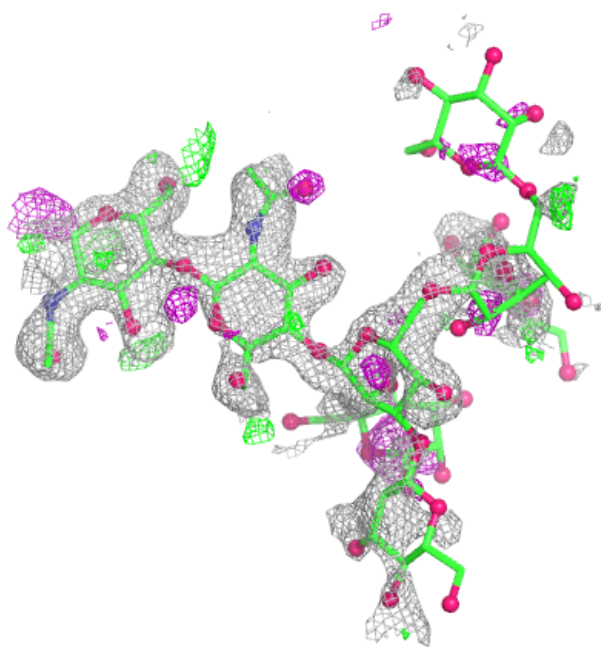
Electron density around Chain D:

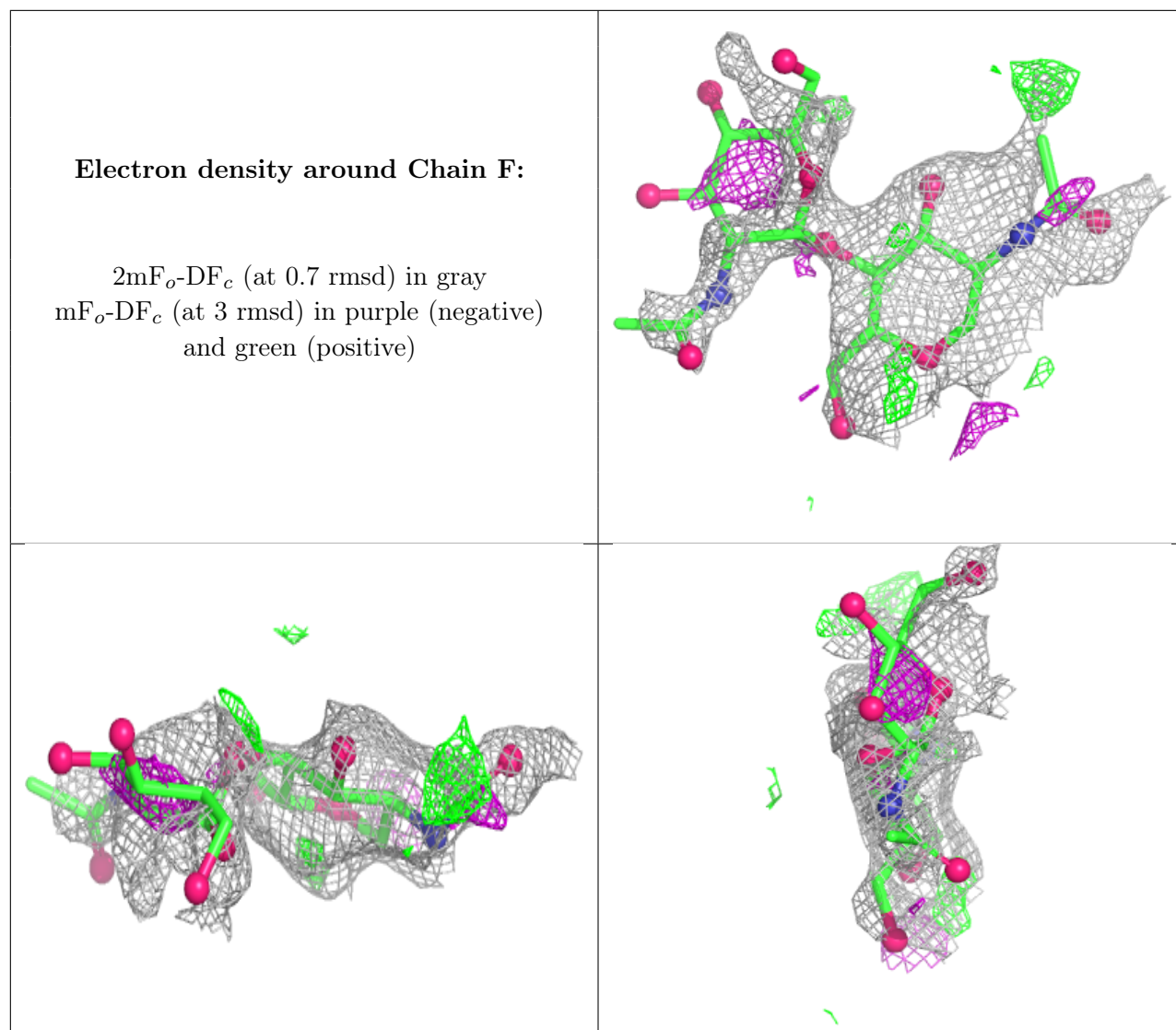
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain E:

$2mF_o-DF_c$ (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(Å ²)	Q<0.9
6	GOL	B	1453	6/6	0.69	0.29	61,62,63,64	0
6	GOL	A	1451	6/6	0.70	0.25	57,58,58,58	0
6	GOL	B	1451	6/6	0.73	0.28	56,57,57,57	0
6	GOL	B	1452	6/6	0.73	0.25	49,54,55,56	0
6	GOL	A	1450	6/6	0.73	0.24	40,41,43,43	0
6	GOL	A	1452	6/6	0.76	0.24	50,52,55,56	0
6	GOL	B	1449	6/6	0.77	0.16	36,40,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	GOL	B	1450	6/6	0.89	0.12	24,29,31,35	0
6	GOL	A	1449	6/6	0.94	0.09	28,30,30,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.