



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:50 PM UTC

PDB ID : 4C53 / pdb_00004c53
Title : Crystal Structure of Guanarito virus GP2 in the post-fusion conformation
Authors : Parsy, M.; Huiskonen, J.T.; Harlos, K.; Bowden, T.A.
Deposited on : 2013-09-10
Resolution : 4.14 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:

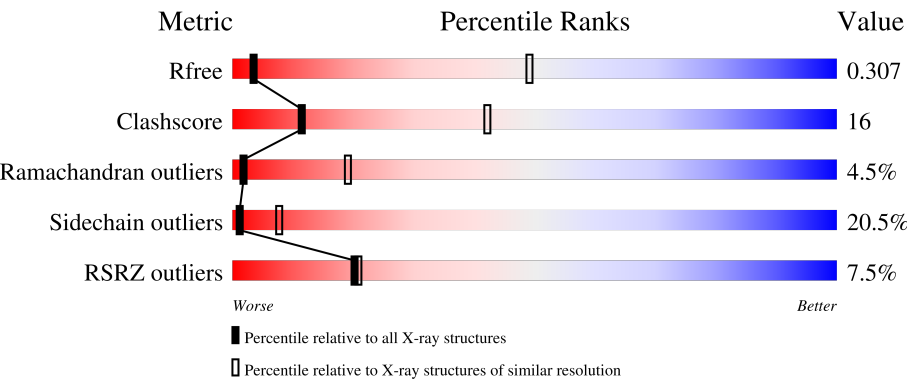
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 4.14 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	1004 (4.46-3.82)
Clashscore	190562	1004 (4.44-3.84)
Ramachandran outliers	187476	1224 (4.48-3.80)
Sidechain outliers	187428	1211 (4.48-3.80)
RSRZ outliers	180081	1001 (4.46-3.82)

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	138	<div><div>7%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>37%27%8%•27%</div></div>
1	B	138	<div><div>6%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>41%29%10%•17%</div></div>
1	C	138	<div><div>4%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>42%25%7%26%</div></div>
2	D	3	<div><div></div><div><div></div><div></div></div><div>33%67%</div></div>
3	E	2	<div><div></div><div><div></div></div><div>100%</div></div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	F	7	 57% 29% 14%
4	G	7	 57% 29% 14%
4	H	7	 71% 29%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3007 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 PRE-GLYCOPROTEIN POLYPROTEIN GP COMPLEX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	101	Total	C	N	O	S	0	0	0
			837	533	143	154	7			
1	B	115	Total	C	N	O	S	0	0	0
			959	607	164	181	7			
1	C	102	Total	C	N	O	S	0	0	0
			853	547	142	157	7			

There are 33 discrepancies between the modelled and reference sequences:

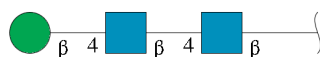
Chain	Residue	Modelled	Actual	Comment	Reference
A	290	THR	-	expression tag	UNP A1A3Z2
A	291	GLY	-	expression tag	UNP A1A3Z2
A	419	GLY	-	expression tag	UNP A1A3Z2
A	420	THR	-	expression tag	UNP A1A3Z2
A	421	LYS	-	expression tag	UNP A1A3Z2
A	422	HIS	-	expression tag	UNP A1A3Z2
A	423	HIS	-	expression tag	UNP A1A3Z2
A	424	HIS	-	expression tag	UNP A1A3Z2
A	425	HIS	-	expression tag	UNP A1A3Z2
A	426	HIS	-	expression tag	UNP A1A3Z2
A	427	HIS	-	expression tag	UNP A1A3Z2
B	290	THR	-	expression tag	UNP A1A3Z2
B	291	GLY	-	expression tag	UNP A1A3Z2
B	419	GLY	-	expression tag	UNP A1A3Z2
B	420	THR	-	expression tag	UNP A1A3Z2
B	421	LYS	-	expression tag	UNP A1A3Z2
B	422	HIS	-	expression tag	UNP A1A3Z2
B	423	HIS	-	expression tag	UNP A1A3Z2
B	424	HIS	-	expression tag	UNP A1A3Z2
B	425	HIS	-	expression tag	UNP A1A3Z2
B	426	HIS	-	expression tag	UNP A1A3Z2
B	427	HIS	-	expression tag	UNP A1A3Z2
C	290	THR	-	expression tag	UNP A1A3Z2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	291	GLY	-	expression tag	UNP A1A3Z2
C	419	GLY	-	expression tag	UNP A1A3Z2
C	420	THR	-	expression tag	UNP A1A3Z2
C	421	LYS	-	expression tag	UNP A1A3Z2
C	422	HIS	-	expression tag	UNP A1A3Z2
C	423	HIS	-	expression tag	UNP A1A3Z2
C	424	HIS	-	expression tag	UNP A1A3Z2
C	425	HIS	-	expression tag	UNP A1A3Z2
C	426	HIS	-	expression tag	UNP A1A3Z2
C	427	HIS	-	expression tag	UNP A1A3Z2

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



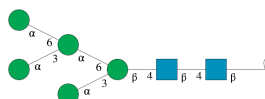
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	3	Total	C	N	O	0	0	0
			39	22	2	15			

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



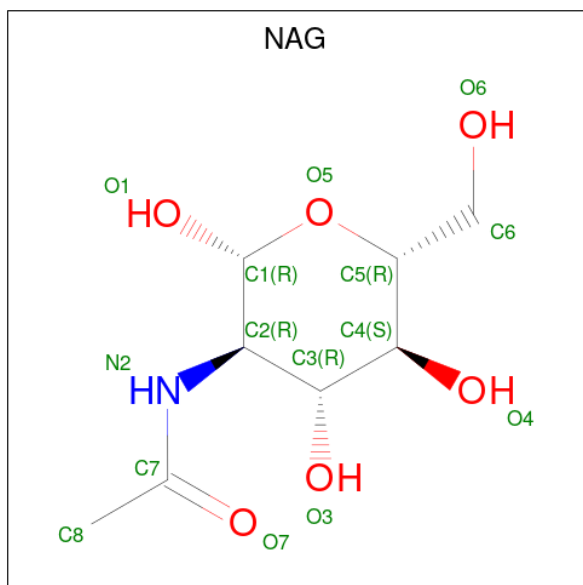
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[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.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	7	Total	C	N	O	0	0	0
			83	46	2	35			
4	G	7	Total	C	N	O	0	0	0
			83	46	2	35			
4	H	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

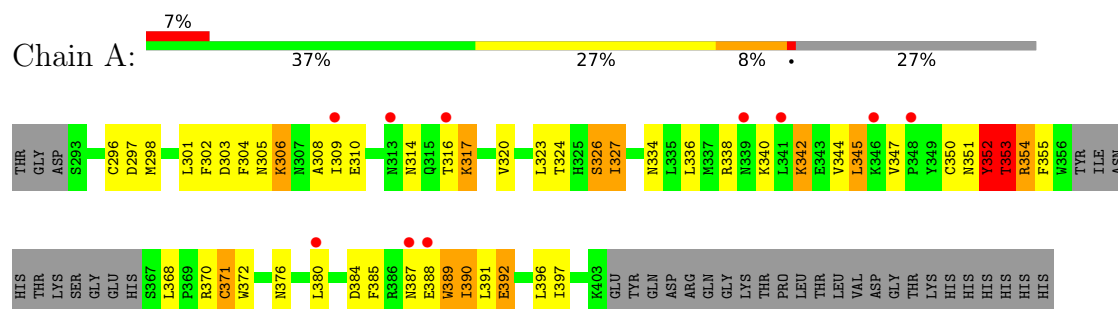


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

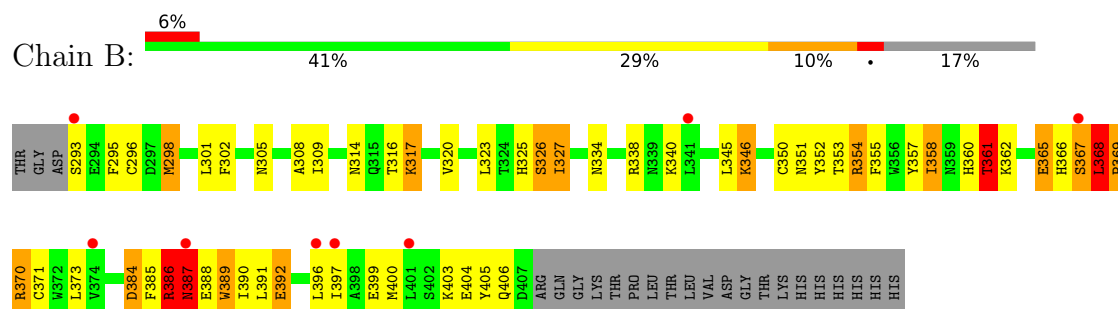
3 Residue-property plots [i](#)

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.

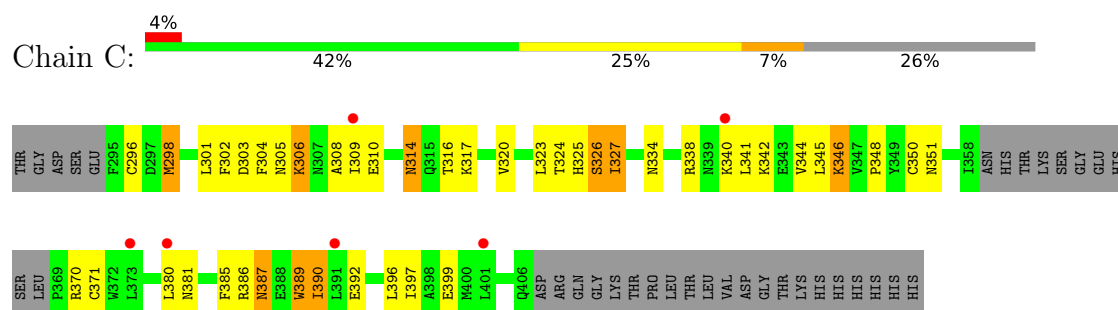
• Molecule 1: PRE-GLYCOPROTEIN POLYPROTEIN GP COMPLEX



• Molecule 1: PRE-GLYCOPROTEIN POLYPROTEIN GP COMPLEX



• Molecule 1: PRE-GLYCOPROTEIN POLYPROTEIN GP COMPLEX



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





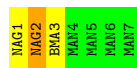
- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  100%



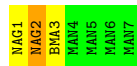
- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  57% 29% 14%



- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[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:  57% 29% 14%



- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[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 H:  71% 29%



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	98.50Å 98.50Å 78.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.44 – 4.14 38.44 – 4.14	Depositor EDS
% Data completeness (in resolution range)	99.6 (38.44-4.14) 99.5 (38.44-4.14)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 4.13Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.255 , 0.276 0.281 , 0.307	Depositor DCC
R_{free} test set	260 reflections (4.46%)	wwPDB-VP
Wilson B-factor (Å ²)	192.1	Xtriage
Anisotropy	0.228	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 219.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.061 for h,-k,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3007	wwPDB-VP
Average B, all atoms (Å ²)	222.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.35% 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, MAN, NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.83	0/853	1.53	13/1150 (1.1%)
1	B	0.87	0/980	1.60	10/1323 (0.8%)
1	C	0.83	1/871 (0.1%)	1.46	5/1175 (0.4%)
All	All	0.84	1/2704 (0.0%)	1.53	28/3648 (0.8%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	390	ILE	CG1-CD1	5.34	1.72	1.51

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	381	ASN	OD1-CG-ND2	-11.51	111.09	122.60
1	C	341	LEU	N-CA-C	-9.65	97.50	111.30
1	B	355	PHE	CA-CB-CG	9.22	123.02	113.80
1	A	314	ASN	CA-CB-CG	9.16	121.76	112.60
1	C	346	LYS	N-CA-C	-8.78	102.00	112.89
1	B	314	ASN	CA-CB-CG	8.44	121.04	112.60
1	B	346	LYS	N-CA-C	-8.39	102.48	112.89
1	C	381	ASN	CB-CG-ND2	7.42	127.53	116.40
1	B	404	GLU	N-CA-C	-7.14	103.73	113.30
1	B	387	ASN	CA-CB-CG	7.06	119.66	112.60
1	C	314	ASN	CA-CB-CG	6.99	119.59	112.60
1	A	351	ASN	CA-C-N	6.79	134.50	121.54
1	A	351	ASN	C-N-CA	6.79	134.50	121.54
1	A	352	TYR	CA-C-N	6.17	133.33	121.54
1	A	352	TYR	C-N-CA	6.17	133.33	121.54
1	A	345	LEU	CA-C-N	6.10	129.06	120.28
1	A	345	LEU	C-N-CA	6.10	129.06	120.28

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	387	ASN	CA-C-N	5.94	128.55	120.54
1	B	387	ASN	C-N-CA	5.94	128.55	120.54
1	B	386	ARG	N-CA-C	5.77	118.85	108.17
1	B	404	GLU	CA-C-N	5.51	132.06	121.54
1	B	404	GLU	C-N-CA	5.51	132.06	121.54
1	A	314	ASN	CB-CG-ND2	-5.24	108.54	116.40
1	A	384	ASP	CA-C-N	-5.24	115.45	122.42
1	A	384	ASP	C-N-CA	-5.24	115.45	122.42
1	A	314	ASN	OD1-CG-ND2	5.15	127.75	122.60
1	A	384	ASP	CA-CB-CG	5.10	117.70	112.60
1	A	376	ASN	CA-CB-CG	5.06	117.66	112.60

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	837	0	823	36	0
1	B	959	0	928	38	0
1	C	853	0	833	34	0
2	D	39	0	34	0	0
3	E	28	0	25	0	0
4	F	83	0	70	2	0
4	G	83	0	70	2	0
4	H	83	0	70	8	0
5	A	28	0	26	0	0
5	B	14	0	13	0	0
All	All	3007	0	2892	93	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 16.

All (93) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:323:LEU:O	1:B:327:ILE:HG22	1.75	0.86
1:C:323:LEU:O	1:C:327:ILE:HG22	1.79	0.82
1:C:350:CYS:HG	1:C:371:CYS:HG	0.82	0.81
1:A:323:LEU:O	1:A:327:ILE:HG22	1.79	0.80
1:A:303:ASP:HA	1:A:306:LYS:HG2	1.69	0.74
1:A:308:ALA:HB2	1:B:389:TRP:HB3	1.70	0.73
1:B:301:LEU:HD23	1:C:396:LEU:HD23	1.70	0.72
1:A:327:ILE:HD11	1:C:326:SER:HB3	1.70	0.72
1:B:350:CYS:HG	1:B:371:CYS:HG	0.74	0.72
1:C:387:ASN:HA	1:C:390:ILE:HD13	1.72	0.72
1:B:326:SER:HB3	1:C:327:ILE:HD11	1.73	0.71
1:A:301:LEU:HD23	1:B:396:LEU:HD23	1.74	0.70
1:A:326:SER:HB3	1:B:327:ILE:HD11	1.72	0.70
1:A:389:TRP:HB3	1:C:308:ALA:HB2	1.75	0.69
1:B:358:ILE:HG21	1:B:373:LEU:HD13	1.75	0.68
1:A:310:GLU:HG2	1:A:390:ILE:HG13	1.76	0.66
4:H:4:MAN:O4	4:H:6:MAN:H5	1.98	0.63
1:A:396:LEU:HD23	1:C:301:LEU:HD23	1.80	0.63
1:B:351:ASN:O	1:B:353:THR:N	2.31	0.62
1:A:302:PHE:CD2	1:C:301:LEU:HB3	2.35	0.61
4:H:3:BMA:H2	4:H:7:MAN:H5	1.82	0.61
1:A:327:ILE:CD1	1:C:326:SER:HB3	2.31	0.61
1:B:301:LEU:HB3	1:C:302:PHE:CD2	2.37	0.60
1:B:302:PHE:HE1	1:B:397:ILE:HD11	1.66	0.60
4:G:2:NAG:H62	4:G:3:BMA:C1	2.32	0.60
1:B:308:ALA:HB2	1:C:389:TRP:HB3	1.85	0.59
1:A:302:PHE:HE1	1:A:397:ILE:HD11	1.68	0.58
1:C:338:ARG:HG2	1:C:345:LEU:HD21	1.85	0.58
4:F:2:NAG:H62	4:F:3:BMA:C1	2.33	0.57
1:B:316:THR:O	1:B:320:VAL:HG23	2.05	0.57
1:B:358:ILE:HG21	1:B:373:LEU:CD1	2.34	0.57
1:C:302:PHE:HE1	1:C:397:ILE:HD11	1.69	0.57
1:A:350:CYS:HG	1:A:371:CYS:CB	2.18	0.56
1:B:293:SER:C	1:B:295:PHE:H	2.13	0.56
1:B:298:MET:SD	1:C:298:MET:HB3	2.46	0.55
1:C:324:THR:HG23	1:C:380:LEU:HB2	1.88	0.55
1:A:347:VAL:HG11	1:A:372:TRP:CZ3	2.42	0.55
1:C:316:THR:O	1:C:320:VAL:HG23	2.05	0.54
1:B:305:ASN:O	1:B:309:ILE:HG13	2.08	0.54
1:B:338:ARG:HG2	1:B:345:LEU:HD21	1.89	0.54
1:A:301:LEU:HD11	1:B:400:MET:HG3	1.90	0.53
1:A:316:THR:O	1:A:320:VAL:HG23	2.08	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:314:ASN:OD1	4:H:1:NAG:H83	2.08	0.53
1:B:370:ARG:HG3	1:B:371:CYS:SG	2.49	0.53
1:A:305:ASN:O	1:A:309:ILE:HG13	2.09	0.52
1:C:306:LYS:O	1:C:310:GLU:HG3	2.09	0.52
1:C:303:ASP:HA	1:C:306:LYS:HG2	1.91	0.52
1:A:323:LEU:HD11	1:B:320:VAL:HG13	1.92	0.52
1:A:388:GLU:O	1:A:391:LEU:HG	2.10	0.51
1:A:303:ASP:O	1:A:306:LYS:HG3	2.11	0.51
1:B:317:LYS:HE3	1:B:385:PHE:H	1.76	0.51
1:B:386:ARG:C	1:B:388:GLU:H	2.18	0.51
1:C:305:ASN:O	1:C:309:ILE:HG13	2.11	0.50
1:B:357:TYR:O	1:B:361:THR:HG22	2.11	0.50
1:A:301:LEU:HB3	1:B:302:PHE:CD2	2.47	0.49
1:A:387:ASN:HB3	1:A:390:ILE:HD12	1.93	0.49
1:A:324:THR:HG23	1:A:380:LEU:HB2	1.94	0.49
1:B:354:ARG:HH21	1:B:370:ARG:CZ	2.26	0.49
1:A:338:ARG:HD3	1:A:372:TRP:CE2	2.48	0.48
1:A:297:ASP:HB3	1:B:400:MET:SD	2.53	0.48
1:A:320:VAL:HG13	1:C:323:LEU:HD11	1.96	0.48
1:B:350:CYS:HB3	1:B:354:ARG:HB3	1.96	0.47
1:B:301:LEU:CD2	1:C:396:LEU:HD23	2.41	0.47
1:C:350:CYS:HG	1:C:371:CYS:CB	2.25	0.47
4:H:4:MAN:O4	4:H:5:MAN:H3	2.15	0.46
1:A:396:LEU:HD23	1:C:301:LEU:CD2	2.45	0.46
1:A:326:SER:HB3	1:B:327:ILE:CD1	2.43	0.46
4:H:4:MAN:H3	4:H:5:MAN:H2	1.65	0.46
1:B:326:SER:HB3	1:C:327:ILE:CD1	2.43	0.45
1:C:317:LYS:HG3	1:C:385:PHE:HD1	1.80	0.45
1:C:317:LYS:HE3	1:C:385:PHE:H	1.82	0.45
1:C:310:GLU:HG2	1:C:390:ILE:CG2	2.46	0.45
1:A:392:GLU:HB3	1:C:304:PHE:CE2	2.51	0.45
4:H:3:BMA:H4	4:H:5:MAN:H2	1.98	0.45
1:A:304:PHE:CE2	1:B:392:GLU:HB3	2.51	0.45
1:A:353:THR:HG22	1:A:354:ARG:HD2	1.98	0.45
1:C:303:ASP:O	1:C:306:LYS:HG3	2.17	0.45
1:C:348:PRO:HG2	1:C:370:ARG:HH21	1.81	0.44
1:B:367:SER:O	1:B:368:LEU:C	2.61	0.44
4:H:4:MAN:O4	4:H:6:MAN:H3	2.18	0.44
1:B:317:LYS:HE3	1:B:384:ASP:HA	2.00	0.43
4:G:2:NAG:C6	4:G:3:BMA:C1	2.96	0.43
4:F:2:NAG:C6	4:F:3:BMA:C1	2.97	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:306:LYS:HD2	1:A:397:ILE:HD11	2.01	0.42
1:A:342:LYS:O	1:A:342:LYS:HG3	2.19	0.41
1:A:336:LEU:HD13	1:B:369:PRO:HB3	2.02	0.41
1:A:317:LYS:HE3	1:A:385:PHE:H	1.85	0.41
4:H:1:NAG:O3	4:H:2:NAG:C1	2.68	0.41
1:B:350:CYS:HG	1:B:371:CYS:CB	2.27	0.41
1:C:310:GLU:HG2	1:C:390:ILE:HG23	2.03	0.41
1:B:302:PHE:CD1	1:B:302:PHE:C	2.99	0.40
1:B:323:LEU:HD11	1:C:320:VAL:HG13	2.03	0.40
1:A:302:PHE:CD1	1:A:302:PHE:C	3.00	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	97/138 (70%)	91 (94%)	3 (3%)	3 (3%)	3	25
1	B	113/138 (82%)	98 (87%)	5 (4%)	10 (9%)	0	10
1	C	98/138 (71%)	92 (94%)	5 (5%)	1 (1%)	12	46
All	All	308/414 (74%)	281 (91%)	13 (4%)	14 (4%)	2	19

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	353	THR
1	A	371	CYS
1	B	352	TYR
1	B	365	GLU
1	B	367	SER
1	B	369	PRO
1	B	405	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	406	GLN
1	A	352	TYR
1	B	361	THR
1	B	362	LYS
1	B	387	ASN
1	C	351	ASN
1	B	368	LEU

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	96/130 (74%)	76 (79%)	20 (21%)	1	7
1	B	110/130 (85%)	84 (76%)	26 (24%)	1	5
1	C	97/130 (75%)	81 (84%)	16 (16%)	2	12
All	All	303/390 (78%)	241 (80%)	62 (20%)	1	8

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	296	CYS
1	A	298	MET
1	A	306	LYS
1	A	317	LYS
1	A	326	SER
1	A	327	ILE
1	A	334	ASN
1	A	340	LYS
1	A	342	LYS
1	A	344	VAL
1	A	345	LEU
1	A	352	TYR
1	A	353	THR
1	A	354	ARG
1	A	355	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	368	LEU
1	A	370	ARG
1	A	389	TRP
1	A	390	ILE
1	A	392	GLU
1	B	296	CYS
1	B	298	MET
1	B	317	LYS
1	B	325	HIS
1	B	326	SER
1	B	327	ILE
1	B	334	ASN
1	B	340	LYS
1	B	346	LYS
1	B	354	ARG
1	B	358	ILE
1	B	360	HIS
1	B	361	THR
1	B	365	GLU
1	B	366	HIS
1	B	368	LEU
1	B	370	ARG
1	B	384	ASP
1	B	386	ARG
1	B	387	ASN
1	B	389	TRP
1	B	390	ILE
1	B	391	LEU
1	B	392	GLU
1	B	399	GLU
1	B	403	LYS
1	C	296	CYS
1	C	298	MET
1	C	306	LYS
1	C	325	HIS
1	C	326	SER
1	C	327	ILE
1	C	334	ASN
1	C	340	LYS
1	C	342	LYS
1	C	344	VAL
1	C	346	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	386	ARG
1	C	387	ASN
1	C	389	TRP
1	C	392	GLU
1	C	399	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	307	ASN
1	B	307	ASN
1	B	376	ASN
1	C	307	ASN
1	C	376	ASN
1	C	406	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 ⓘ

26 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	D	1	2,1	14,14,15	0.69	0	17,19,21	1.10	1 (5%)
2	NAG	D	2	2	14,14,15	0.88	0	17,19,21	1.01	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	BMA	D	3	2	11,11,12	0.72	0	15,15,17	0.74	0
3	NAG	E	1	3,1	14,14,15	0.81	0	17,19,21	1.26	3 (17%)
3	NAG	E	2	3	14,14,15	0.68	0	17,19,21	1.01	2 (11%)
4	NAG	F	1	4,1	14,14,15	0.69	0	17,19,21	1.29	2 (11%)
4	NAG	F	2	4	14,14,15	0.76	0	17,19,21	1.07	1 (5%)
4	BMA	F	3	4	11,11,12	0.55	0	15,15,17	0.72	0
4	MAN	F	4	4	11,11,12	0.71	0	15,15,17	0.70	0
4	MAN	F	5	4	11,11,12	0.59	0	15,15,17	0.74	0
4	MAN	F	6	4	11,11,12	0.65	0	15,15,17	0.68	0
4	MAN	F	7	4	11,11,12	0.51	0	15,15,17	0.73	0
4	NAG	G	1	4,1	14,14,15	0.77	0	17,19,21	1.34	2 (11%)
4	NAG	G	2	4	14,14,15	0.79	0	17,19,21	1.10	1 (5%)
4	BMA	G	3	4	11,11,12	0.55	0	15,15,17	0.79	0
4	MAN	G	4	4	11,11,12	0.65	0	15,15,17	0.82	0
4	MAN	G	5	4	11,11,12	0.60	0	15,15,17	0.73	0
4	MAN	G	6	4	11,11,12	0.67	0	15,15,17	0.70	0
4	MAN	G	7	4	11,11,12	0.50	0	15,15,17	0.72	0
4	NAG	H	1	4,1	14,14,15	0.77	0	17,19,21	1.34	2 (11%)
4	NAG	H	2	4	14,14,15	0.63	0	17,19,21	1.09	3 (17%)
4	BMA	H	3	4	11,11,12	0.77	0	15,15,17	0.63	0
4	MAN	H	4	4	11,11,12	0.72	0	15,15,17	0.83	0
4	MAN	H	5	4	11,11,12	0.72	0	15,15,17	0.57	0
4	MAN	H	6	4	11,11,12	0.73	0	15,15,17	0.64	0
4	MAN	H	7	4	11,11,12	0.55	0	15,15,17	0.65	0

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

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

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MAN	F	4	4	-	2/2/19/22	0/1/1/1
4	MAN	F	5	4	-	0/2/19/22	0/1/1/1
4	MAN	F	6	4	-	0/2/19/22	0/1/1/1
4	MAN	F	7	4	-	0/2/19/22	0/1/1/1
4	NAG	G	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	G	2	4	-	0/6/23/26	0/1/1/1
4	BMA	G	3	4	-	2/2/19/22	0/1/1/1
4	MAN	G	4	4	-	2/2/19/22	0/1/1/1
4	MAN	G	5	4	-	0/2/19/22	0/1/1/1
4	MAN	G	6	4	-	0/2/19/22	0/1/1/1
4	MAN	G	7	4	-	0/2/19/22	0/1/1/1
4	NAG	H	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	H	2	4	-	2/6/23/26	0/1/1/1
4	BMA	H	3	4	-	2/2/19/22	0/1/1/1
4	MAN	H	4	4	-	2/2/19/22	0/1/1/1
4	MAN	H	5	4	-	2/2/19/22	0/1/1/1
4	MAN	H	6	4	-	0/2/19/22	0/1/1/1
4	MAN	H	7	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	1	NAG	C8-C7-N2	3.36	121.69	116.12
3	E	1	NAG	C8-C7-N2	3.11	121.27	116.12
4	G	1	NAG	C8-C7-N2	2.95	121.01	116.12
4	F	1	NAG	C8-C7-N2	2.81	120.78	116.12
2	D	1	NAG	C8-C7-N2	2.80	120.77	116.12
4	H	1	NAG	C4-C3-C2	-2.73	107.02	111.02
4	F	1	NAG	C4-C3-C2	-2.55	107.29	111.02
3	E	1	NAG	C1-O5-C5	-2.46	108.89	112.19
4	H	2	NAG	C4-C3-C2	-2.36	107.56	111.02
2	D	2	NAG	C8-C7-N2	2.33	119.99	116.12
4	G	1	NAG	C4-C3-C2	-2.30	107.64	111.02
4	G	2	NAG	C8-C7-N2	2.26	119.86	116.12
4	F	2	NAG	C8-C7-N2	2.25	119.85	116.12
4	H	2	NAG	C8-C7-N2	2.16	119.70	116.12
3	E	2	NAG	C8-C7-N2	2.16	119.69	116.12
3	E	2	NAG	C4-C3-C2	-2.13	107.89	111.02
4	H	2	NAG	C1-O5-C5	-2.11	109.36	112.19

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	NAG	C4-C3-C2	-2.09	107.95	111.02
3	E	1	NAG	C4-C3-C2	-2.05	108.02	111.02

There are no chirality outliers.

All (43) torsion outliers are listed below:

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

Continued on next page...

Continued from previous page...

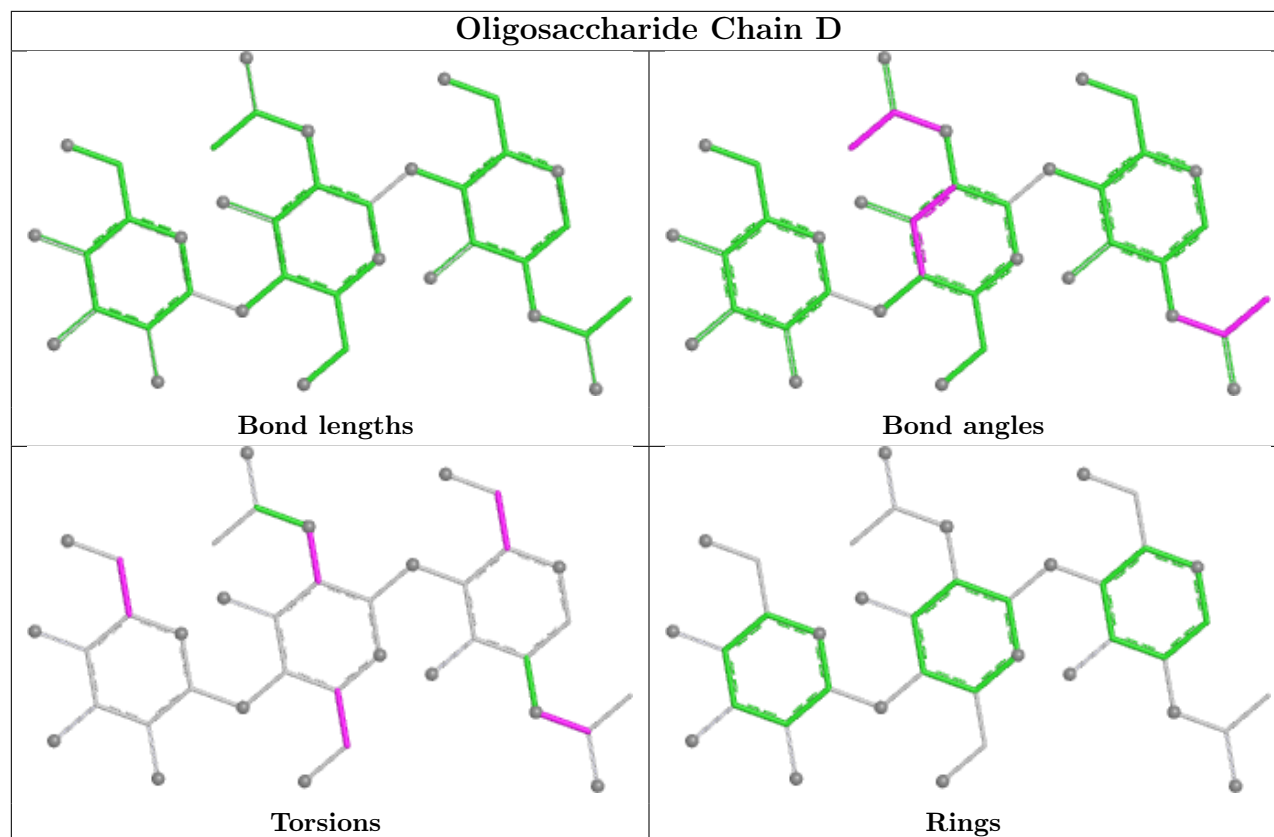
Mol	Chain	Res	Type	Atoms
3	E	1	NAG	O7-C7-N2-C2
4	F	1	NAG	C8-C7-N2-C2
4	F	1	NAG	O7-C7-N2-C2
4	G	1	NAG	C8-C7-N2-C2
4	G	1	NAG	O7-C7-N2-C2
4	H	1	NAG	C8-C7-N2-C2
4	H	1	NAG	O7-C7-N2-C2
2	D	2	NAG	C1-C2-N2-C7

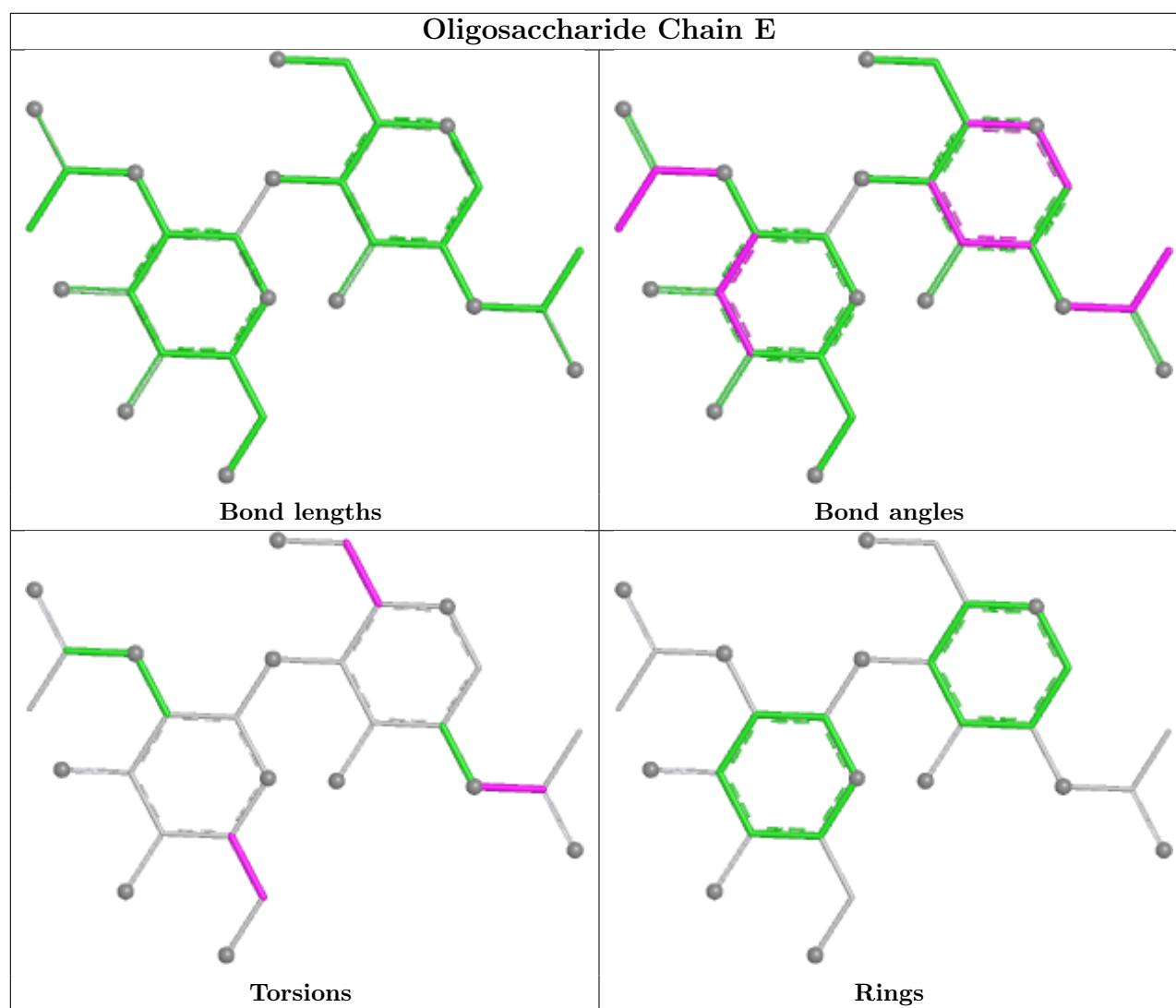
There are no ring outliers.

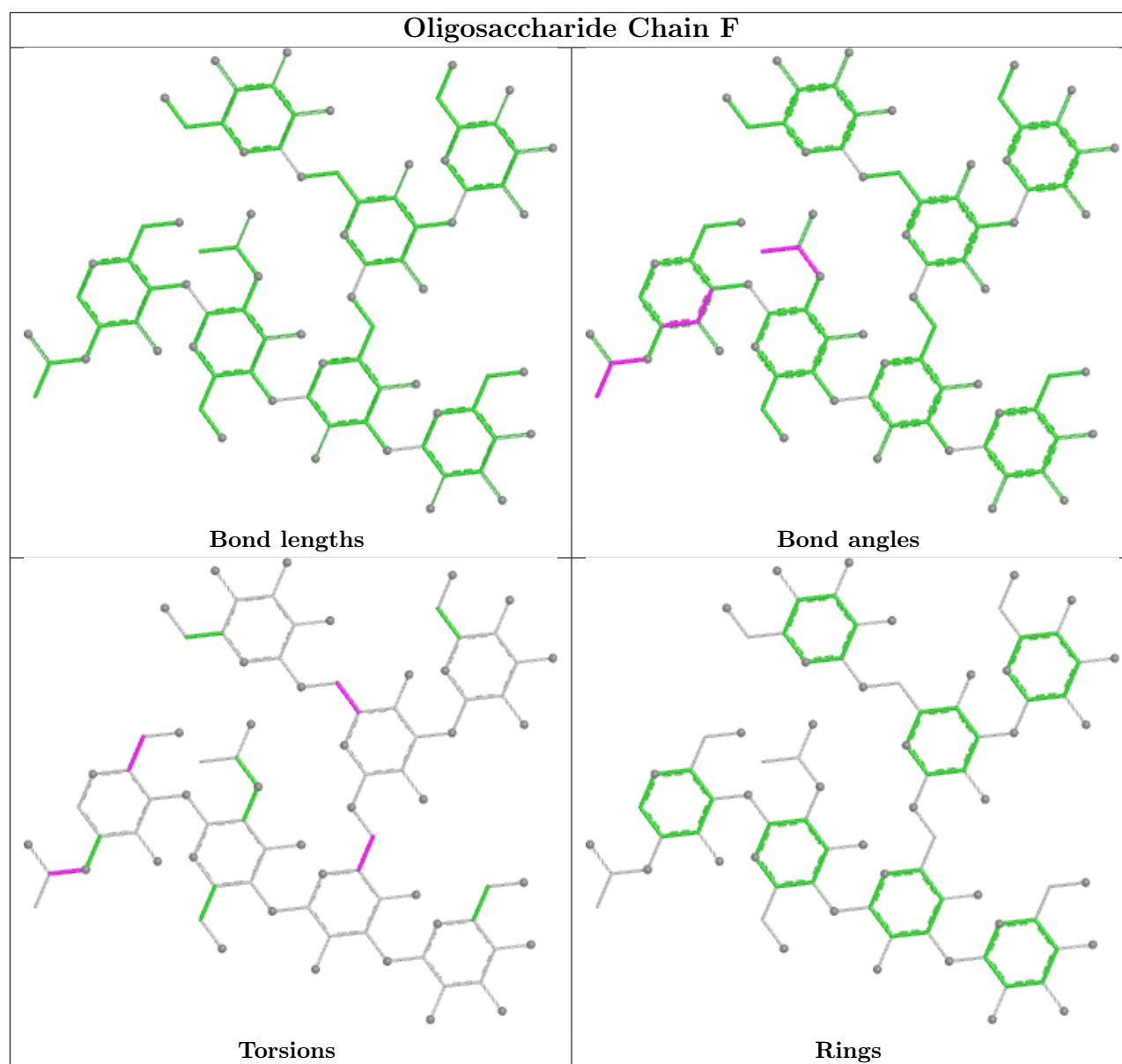
11 monomers are involved in 12 short contacts:

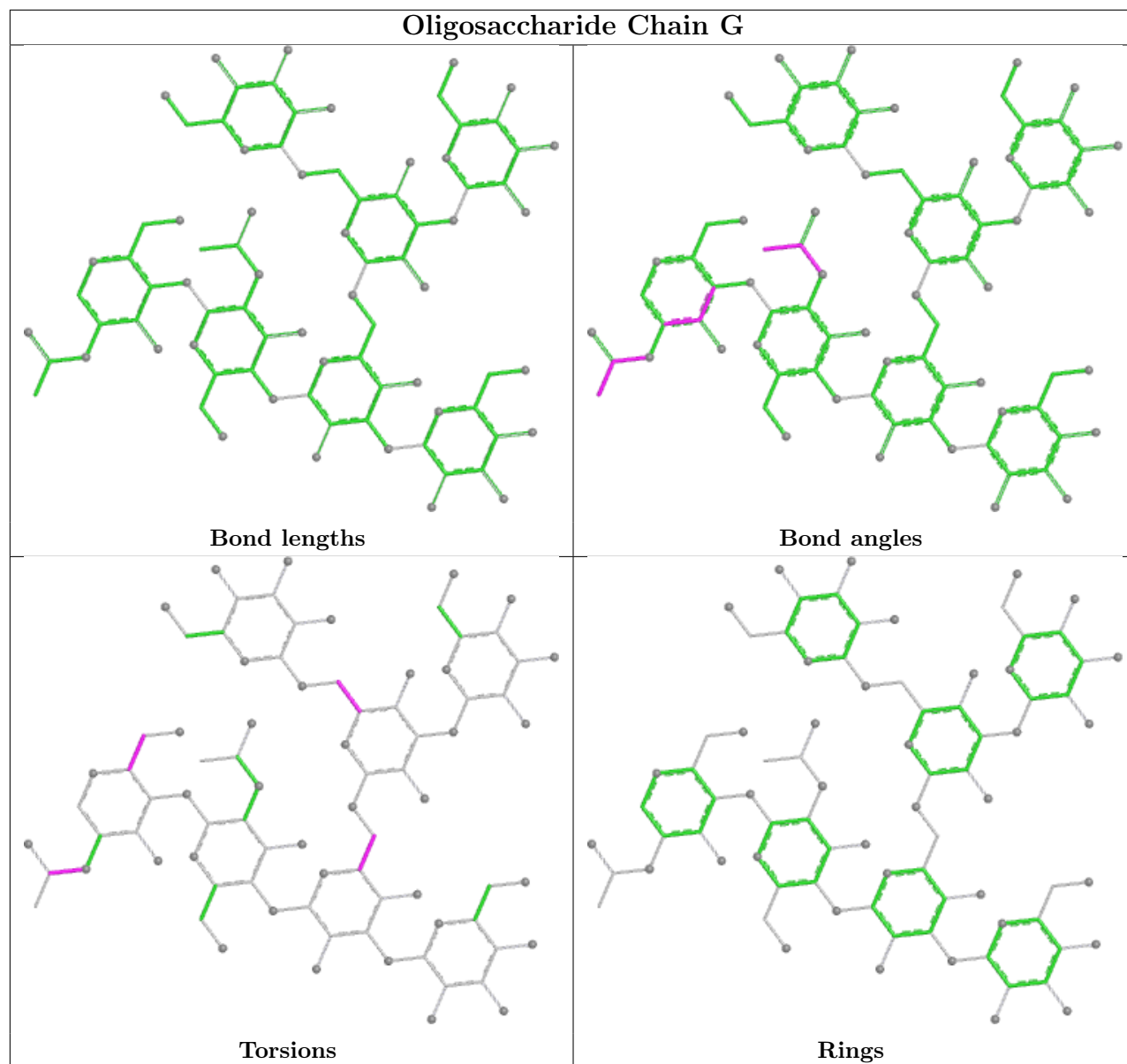
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	6	MAN	2	0
4	H	5	MAN	3	0
4	G	3	BMA	2	0
4	H	1	NAG	2	0
4	H	4	MAN	4	0
4	F	2	NAG	2	0
4	H	2	NAG	1	0
4	H	3	BMA	2	0
4	F	3	BMA	2	0
4	H	7	MAN	1	0
4	G	2	NAG	2	0

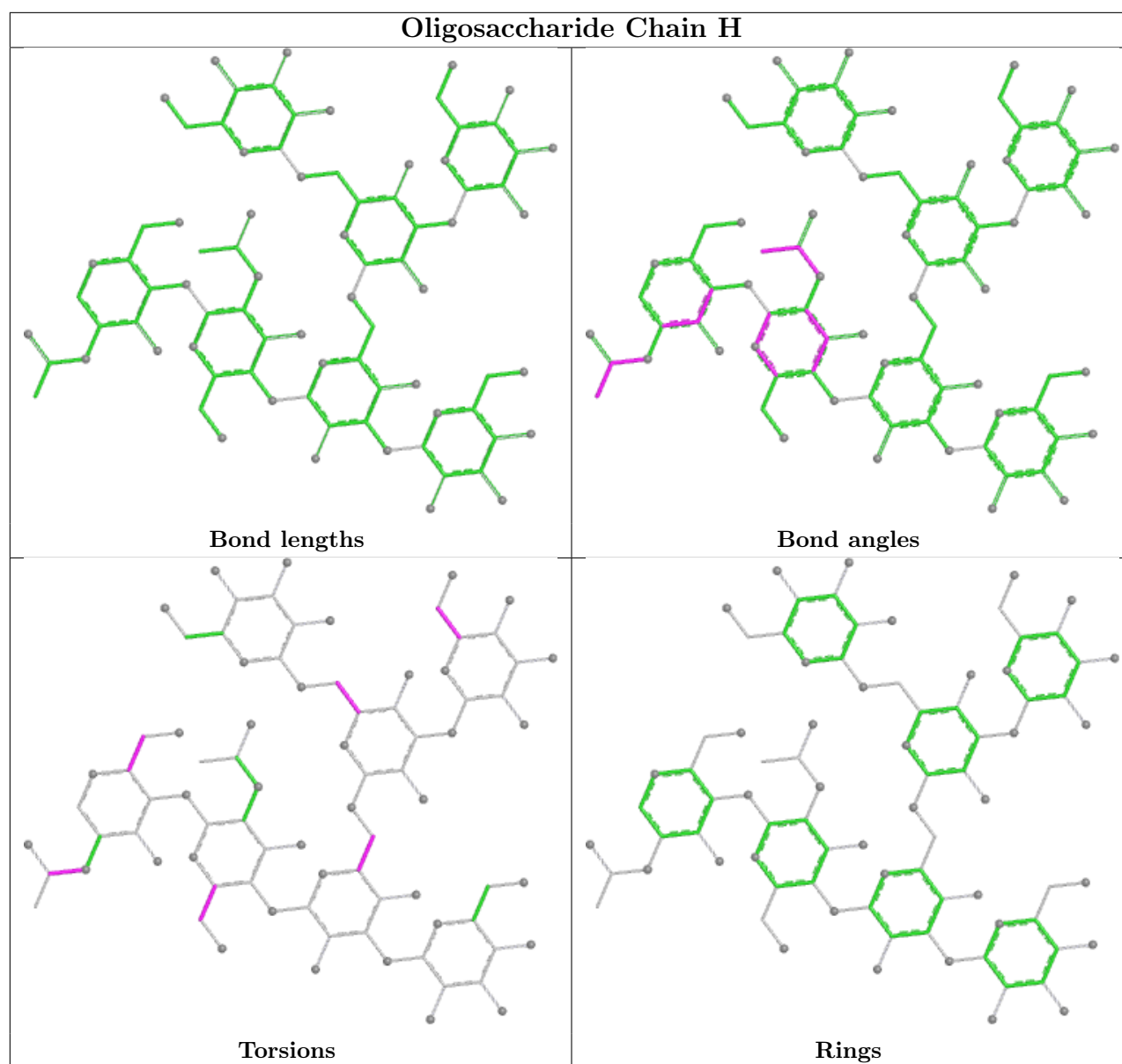
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

3 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
5	NAG	A	1408	1	14,14,15	0.69	0	17,19,21	1.32	3 (17%)
5	NAG	B	1417	1	14,14,15	0.79	0	17,19,21	1.19	2 (11%)
5	NAG	A	1407	1	14,14,15	0.81	0	17,19,21	1.18	2 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	1408	1	-	4/6/23/26	0/1/1/1
5	NAG	B	1417	1	-	4/6/23/26	0/1/1/1
5	NAG	A	1407	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1417	NAG	C8-C7-N2	2.98	121.07	116.12
5	A	1408	NAG	C8-C7-N2	2.90	120.93	116.12
5	A	1407	NAG	C8-C7-N2	2.86	120.85	116.12
5	A	1408	NAG	C4-C3-C2	-2.41	107.49	111.02
5	B	1417	NAG	C4-C3-C2	-2.37	107.55	111.02
5	A	1407	NAG	C4-C3-C2	-2.34	107.58	111.02
5	A	1408	NAG	C2-N2-C7	-2.24	119.90	122.90

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1407	NAG	C4-C5-C6-O6
5	A	1408	NAG	C4-C5-C6-O6
5	B	1417	NAG	C4-C5-C6-O6
5	A	1407	NAG	O5-C5-C6-O6
5	A	1408	NAG	O5-C5-C6-O6
5	B	1417	NAG	O5-C5-C6-O6
5	A	1407	NAG	C8-C7-N2-C2
5	A	1407	NAG	O7-C7-N2-C2
5	A	1408	NAG	C8-C7-N2-C2
5	A	1408	NAG	O7-C7-N2-C2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
5	B	1417	NAG	C8-C7-N2-C2
5	B	1417	NAG	O7-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

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	101/138 (73%)	0.62	10 (9%) 13 15	131, 220, 273, 279	0
1	B	115/138 (83%)	0.65	8 (6%) 22 22	124, 215, 260, 270	0
1	C	102/138 (73%)	0.46	6 (5%) 28 26	132, 213, 276, 293	0
All	All	318/414 (76%)	0.58	24 (7%) 20 21	124, 216, 273, 293	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	401	LEU	5.1
1	A	309	ILE	4.7
1	B	374	VAL	4.5
1	C	309	ILE	3.8
1	C	401	LEU	3.7
1	A	313	ASN	3.6
1	B	396	LEU	3.3
1	C	373	LEU	3.2
1	B	387	ASN	3.0
1	B	397	ILE	3.0
1	A	387	ASN	2.9
1	A	339	ASN	2.8
1	A	346	LYS	2.7
1	B	293	SER	2.5
1	A	348	PRO	2.5
1	B	341	LEU	2.5
1	A	316	THR	2.5
1	A	341	LEU	2.3
1	C	391	LEU	2.3
1	A	380	LEU	2.2
1	B	367	SER	2.2
1	A	388	GLU	2.2
1	C	340	LYS	2.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	380	LEU	2.0

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

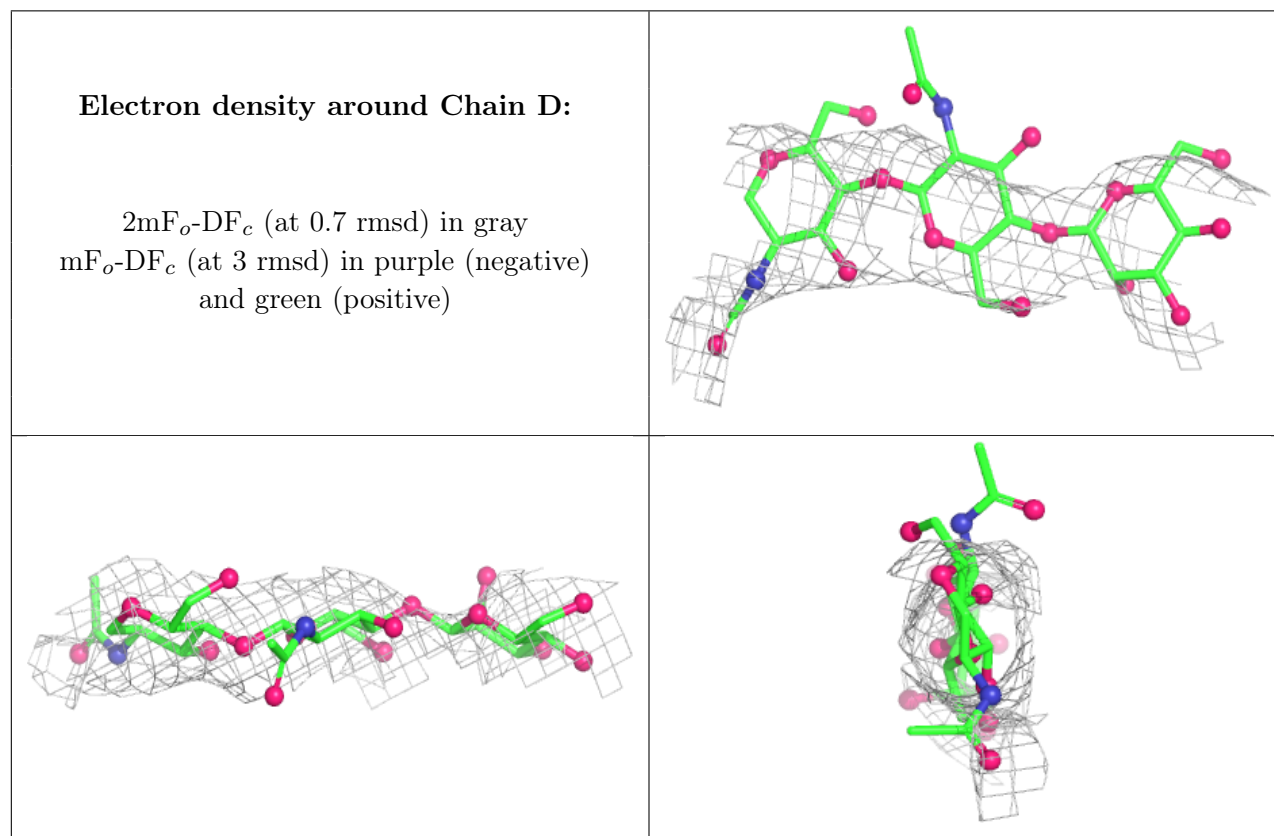
There are no non-standard protein/DNA/RNA residues in this entry.

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.

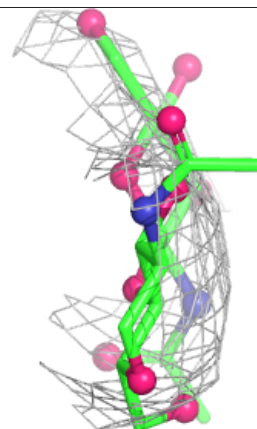
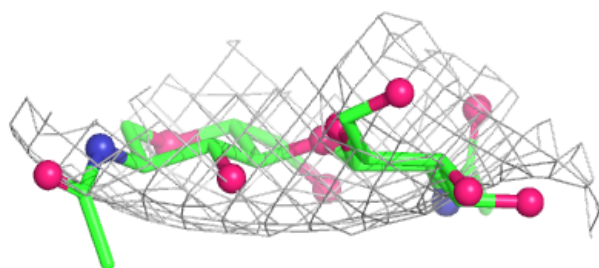
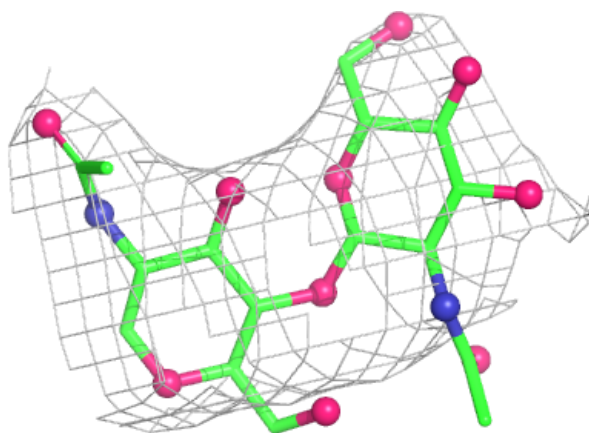
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	BMA	F	3	11/12	-0.34	0.14	297,297,297,297	0
4	MAN	G	4	11/12	-0.10	0.13	300,300,300,300	0
4	BMA	G	3	11/12	-0.09	0.12	298,298,298,298	0
4	MAN	G	5	11/12	0.09	0.13	300,300,300,300	0
4	NAG	F	2	14/15	0.14	0.23	288,288,288,288	0
4	MAN	F	4	11/12	0.15	0.12	300,300,300,300	0
4	MAN	H	4	11/12	0.22	0.12	300,300,300,300	0
2	BMA	D	3	11/12	0.27	0.13	293,293,293,293	0
4	MAN	F	5	11/12	0.33	0.20	300,300,300,300	0
4	MAN	F	7	11/12	0.34	0.17	300,300,300,300	0
4	MAN	F	6	11/12	0.39	0.11	300,300,300,300	0
4	MAN	H	6	11/12	0.40	0.13	300,300,300,300	0
4	BMA	H	3	11/12	0.43	0.11	299,299,299,299	0
4	MAN	H	5	11/12	0.46	0.10	300,300,300,300	0
4	MAN	G	7	11/12	0.46	0.13	297,297,297,297	0
4	MAN	H	7	11/12	0.61	0.18	296,296,296,296	0
4	MAN	G	6	11/12	0.66	0.14	300,300,300,300	0
2	NAG	D	1	14/15	0.67	0.12	283,289,293,293	0
4	NAG	G	2	14/15	0.69	0.14	294,294,294,294	0
4	NAG	G	1	14/15	0.70	0.20	275,282,284,284	0
4	NAG	H	1	14/15	0.72	0.16	275,278,284,287	0
3	NAG	E	2	14/15	0.75	0.13	278,278,278,278	0
4	NAG	F	1	14/15	0.76	0.16	269,274,274,274	0
2	NAG	D	2	14/15	0.79	0.09	292,292,292,292	0
4	NAG	H	2	14/15	0.83	0.16	293,293,293,293	0
3	NAG	E	1	14/15	0.91	0.12	259,262,268,274	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.



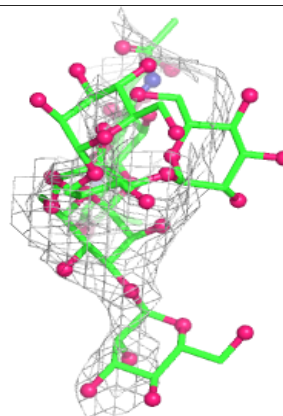
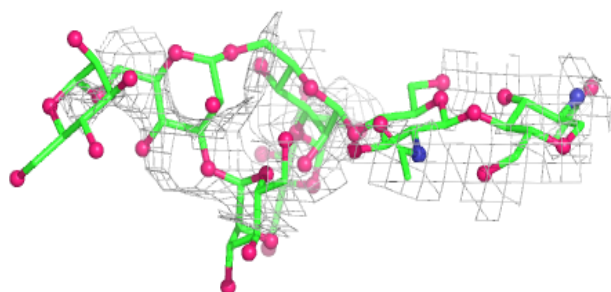
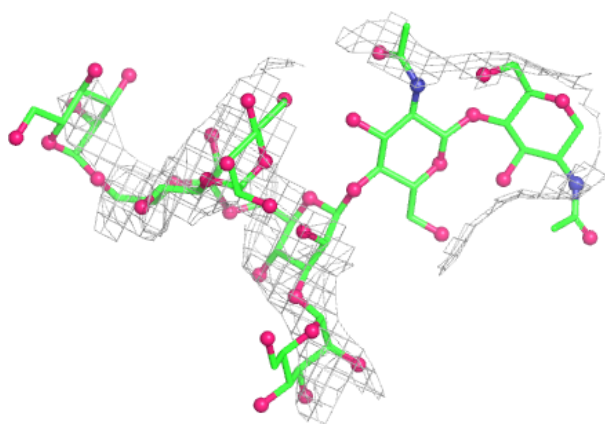
Electron density around Chain E:

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

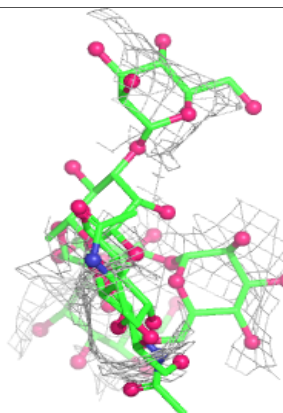
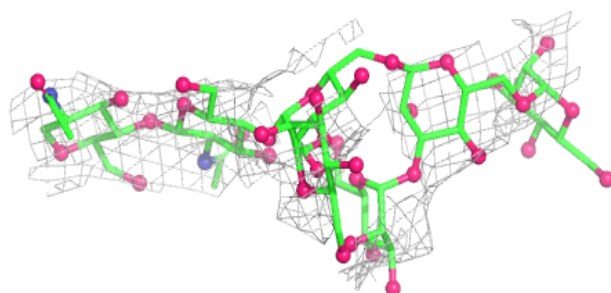
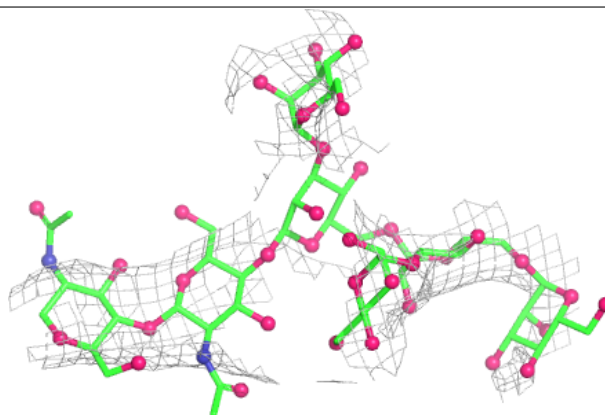


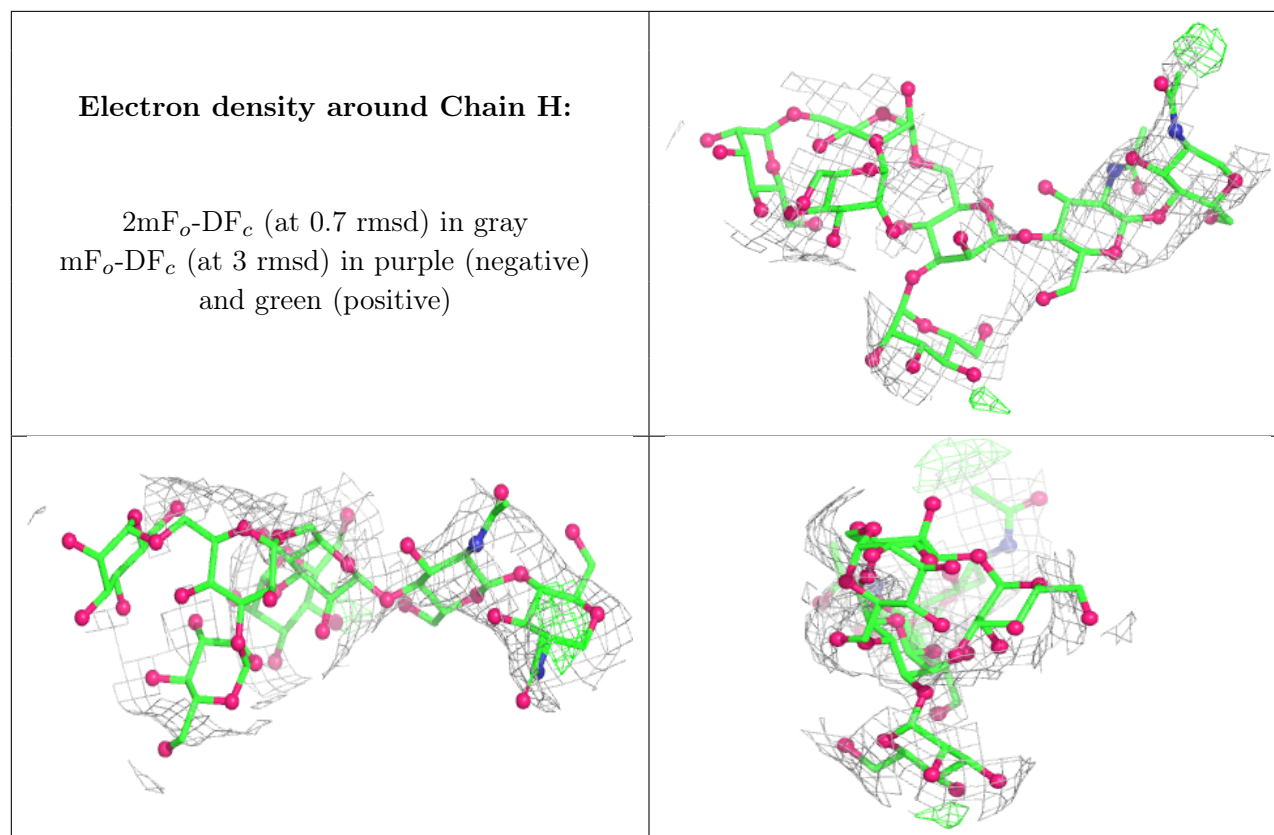
Electron density around Chain F:

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

**Electron density around Chain G:**

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





6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	NAG	A	1407	14/15	0.46	0.18	262,263,265,265	0
5	NAG	A	1408	14/15	0.73	0.13	279,279,279,279	0
5	NAG	B	1417	14/15	0.73	0.12	260,267,269,270	0

6.5 Other polymers [i](#)

There are no such residues in this entry.