



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 12:16 PM UTC

PDB ID : 7XTJ / pdb_00007xtj
Title : Crystal structure of E88A mutant of GH3 beta-xylosidase from *Aspergillus niger* (AnBX)
Authors : Kaenying, W.; Kongsaree, P.T.; Tagami, T.
Deposited on : 2022-05-17
Resolution : 2.50 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

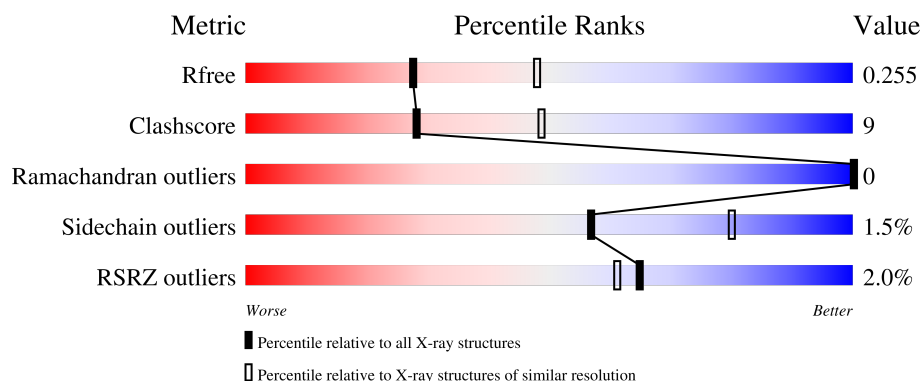
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	788	<div> <div></div> <div>74%</div> <div>20%</div> <div>6%</div> </div>
1	B	788	<div> <div>3%</div> <div>76%</div> <div>18%</div> <div>6%</div> </div>
2	C	6	<div> <div>17%</div> <div>83%</div> </div>
2	E	6	<div> <div>33%</div> <div>67%</div> </div>
3	D	2	<div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
4	F	3	 100%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11809 atoms, of which 16 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.

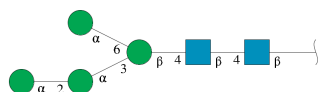
- Molecule 1 is a protein called Xylan 1,4-beta-xylosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	742	Total	C	N	O	S	0	1	0
			5707	3603	968	1124	12			
1	B	743	Total	C	N	O	S	0	0	0
			5704	3599	967	1126	12			

There are 24 discrepancies between the modelled and reference sequences:

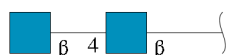
Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	ALA	-	expression tag	UNP A0A023J5W7
A	-9	HIS	-	expression tag	UNP A0A023J5W7
A	-8	HIS	-	expression tag	UNP A0A023J5W7
A	-7	HIS	-	expression tag	UNP A0A023J5W7
A	-6	HIS	-	expression tag	UNP A0A023J5W7
A	-5	HIS	-	expression tag	UNP A0A023J5W7
A	-4	HIS	-	expression tag	UNP A0A023J5W7
A	-3	HIS	-	expression tag	UNP A0A023J5W7
A	-2	HIS	-	expression tag	UNP A0A023J5W7
A	-1	ALA	-	expression tag	UNP A0A023J5W7
A	0	ALA	-	expression tag	UNP A0A023J5W7
A	88	ALA	GLU	engineered mutation	UNP A0A023J5W7
B	-10	ALA	-	expression tag	UNP A0A023J5W7
B	-9	HIS	-	expression tag	UNP A0A023J5W7
B	-8	HIS	-	expression tag	UNP A0A023J5W7
B	-7	HIS	-	expression tag	UNP A0A023J5W7
B	-6	HIS	-	expression tag	UNP A0A023J5W7
B	-5	HIS	-	expression tag	UNP A0A023J5W7
B	-4	HIS	-	expression tag	UNP A0A023J5W7
B	-3	HIS	-	expression tag	UNP A0A023J5W7
B	-2	HIS	-	expression tag	UNP A0A023J5W7
B	-1	ALA	-	expression tag	UNP A0A023J5W7
B	0	ALA	-	expression tag	UNP A0A023J5W7
B	88	ALA	GLU	engineered mutation	UNP A0A023J5W7

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-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.



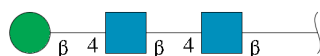
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	6	Total	C	N	O	0	0	0
			72	40	2	30			
2	E	6	Total	C	N	O	0	0	0
			72	40	2	30			

- 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	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 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
4	F	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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	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		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

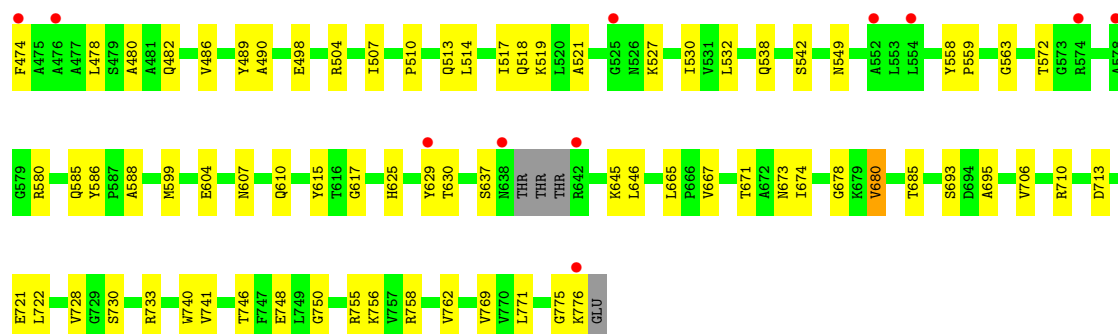
- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			14	3	8	3		
6	B	1	Total	C	H	O	0	0
			14	3	8	3		

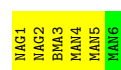
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	23	Total	O	0	0
			23	23		
7	B	10	Total	O	0	0
			10	10		



- Molecule 2: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-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 C: 17% 83%



- Molecule 2: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-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 E: 33% 67%



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

Chain D: 100%



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

Chain F: 100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	120.88Å 120.88Å 266.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.97 – 2.50 49.97 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.97-2.50) 99.8 (49.97-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.24	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.20_4459	Depositor
R, R_{free}	0.214 , 0.256 0.214 , 0.255	Depositor DCC
R_{free} test set	2000 reflections (2.91%)	wwPDB-VP
Wilson B-factor (Å ²)	57.7	Xtriage
Anisotropy	0.488	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 29.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11809	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.25% 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, NAG, BMA

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	0.21	0/5847	0.43	2/7986 (0.0%)
1	B	0.21	0/5843	0.41	2/7982 (0.0%)
All	All	0.21	0/11690	0.42	4/15968 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	289	CYS	CA-C-N	5.43	131.47	121.70
1	A	289	CYS	C-N-CA	5.43	131.47	121.70
1	B	205	TYR	CA-C-N	5.31	131.26	121.70
1	B	205	TYR	C-N-CA	5.31	131.26	121.70

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	5707	0	5438	111	0
1	B	5704	0	5426	91	0
2	C	72	0	61	3	0
2	E	72	0	61	2	0
3	D	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	39	0	34	0	0
5	A	56	0	52	2	0
5	B	70	0	65	3	0
6	A	6	8	8	0	0
6	B	6	8	8	0	0
7	A	23	0	0	1	0
7	B	10	0	0	0	0
All	All	11793	16	11178	205	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 9.

All (205) 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:221:ASN:HB3	1:B:223:MET:HE3	1.36	1.04
1:B:667:VAL:HG13	1:B:728:VAL:HG22	1.51	0.93
1:A:706:VAL:HG12	1:A:730:SER:HB3	1.59	0.85
1:A:84:GLN:HE21	1:A:86:TRP:H	1.25	0.81
1:A:158:ARG:HH11	1:A:610:GLN:HE22	1.27	0.81
1:A:70:ASN:HD22	1:A:84:GLN:HE22	1.28	0.78
1:B:514:LEU:O	1:B:518:GLN:HG3	1.83	0.77
1:A:436:ASN:HD21	1:A:500:GLU:H	1.34	0.74
1:B:740:TRP:HB2	1:B:771:LEU:HB3	1.68	0.74
1:A:263:CYS:HB3	1:A:317:THR:HG21	1.69	0.73
1:B:158:ARG:HH11	1:B:610:GLN:HE22	1.35	0.73
1:A:422:LEU:HD13	1:A:448:ARG:HA	1.70	0.73
1:B:665:LEU:O	1:B:728:VAL:HG23	1.89	0.73
1:B:452:GLU:HG3	1:B:458:VAL:HG21	1.71	0.71
1:B:667:VAL:CG1	1:B:728:VAL:HG22	2.21	0.70
1:A:610:GLN:O	1:A:611:THR:HB	1.92	0.69
1:A:197:LYS:HD3	1:A:371:TYR:CE1	2.27	0.69
1:B:386:ASN:O	1:B:390:GLN:HG3	1.93	0.68
1:B:155:ASN:ND2	1:B:204:HIS:H	1.90	0.68
1:A:436:ASN:ND2	1:A:500:GLU:H	1.92	0.67
1:A:646:LEU:HD13	1:A:667:VAL:CG2	2.25	0.66
1:B:155:ASN:HD21	1:B:204:HIS:H	1.41	0.66
2:E:1:NAG:H62	2:E:2:NAG:C1	2.26	0.66
1:B:452:GLU:HG3	1:B:458:VAL:CG2	2.26	0.66
1:B:221:ASN:CB	1:B:223:MET:HE3	2.19	0.66
1:A:191:ASP:OD2	1:A:194:SER:HB2	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:671:THR:HA	1:B:722:LEU:O	1.96	0.66
1:A:398:LEU:HD23	1:A:627:LEU:HB2	1.78	0.65
1:A:671:THR:HA	1:A:722:LEU:O	1.97	0.65
1:B:538:GLN:HB3	1:B:585:GLN:HG3	1.79	0.65
1:B:251:MET:HA	1:B:286:SER:O	1.96	0.65
1:B:389:TYR:O	1:B:393:THR:HG23	1.96	0.65
1:B:741:VAL:HG22	1:B:769:VAL:HG22	1.80	0.63
1:A:530:ILE:HD12	1:A:552:ALA:HB3	1.81	0.63
1:A:294:ASN:HA	1:A:297:ASN:O	1.99	0.63
1:A:398:LEU:HA	1:A:554:LEU:HD23	1.79	0.62
1:B:489:TYR:OH	1:B:513:GLN:HB3	2.00	0.62
1:B:402:SER:O	1:B:405:VAL:HG23	1.99	0.62
1:A:611:THR:HG22	1:A:613:LYS:H	1.66	0.61
1:B:420:VAL:CG2	1:B:458:VAL:HG12	2.31	0.61
1:A:47:THR:HG22	1:A:50:ASP:HB2	1.81	0.60
1:B:459:ASN:HB3	1:B:480:ALA:HB1	1.84	0.59
1:B:294:ASN:HA	1:B:297:ASN:O	2.03	0.58
1:A:47:THR:HG23	1:A:50:ASP:H	1.67	0.58
1:B:160:PRO:HG3	1:B:586:TYR:CD2	2.38	0.58
1:A:661:SER:H	1:A:664:GLN:HE21	1.52	0.58
1:A:419:THR:OG1	1:A:484:ALA:HA	2.05	0.57
1:A:667:VAL:HB	1:A:728:VAL:HG12	1.87	0.57
1:A:84:GLN:NE2	1:A:86:TRP:H	1.99	0.57
1:A:488:ILE:HD13	1:A:530:ILE:HB	1.87	0.57
1:B:427:ALA:O	1:B:447:PRO:HD2	2.05	0.57
1:A:706:VAL:CG1	1:A:730:SER:HB3	2.33	0.56
1:A:420:VAL:CG2	1:A:458:VAL:HG22	2.36	0.56
1:B:750:GLY:HA3	1:B:755:ARG:HG2	1.86	0.56
1:B:630:THR:HB	1:B:680:VAL:HG12	1.85	0.56
1:B:158:ARG:NH1	1:B:610:GLN:HE22	2.03	0.56
1:B:221:ASN:HB3	1:B:223:MET:CE	2.23	0.56
1:B:435:GLY:HA2	1:B:558:TYR:CD2	2.41	0.56
1:A:638:ASN:HB3	1:A:642:ARG:NH2	2.21	0.56
5:B:804:NAG:O3	5:B:804:NAG:H82	2.06	0.56
1:B:422:LEU:HD12	1:B:448:ARG:HA	1.89	0.55
1:B:407:PRO:HB2	1:B:572:THR:O	2.07	0.55
1:B:159:HIS:ND1	1:B:161:VAL:HG22	2.21	0.55
1:B:406:LEU:HD23	1:B:408:LEU:HG	1.88	0.55
1:A:741:VAL:HG22	1:A:769:VAL:HG22	1.90	0.54
1:A:754:GLU:HB2	1:A:756:LYS:HE3	1.88	0.54
1:B:208:TYR:HB2	1:B:255:ASN:OD1	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:408:LEU:HD11	1:B:530:ILE:HD11	1.90	0.54
1:A:423:ILE:HA	1:A:461:ALA:O	2.09	0.53
1:A:665:LEU:O	1:A:728:VAL:HG13	2.08	0.53
1:B:471:THR:O	1:B:474:PHE:HB2	2.07	0.53
2:C:1:NAG:H62	2:C:2:NAG:C1	2.38	0.53
1:A:205:TYR:CD1	1:A:206:ALA:HB2	2.44	0.53
1:B:645:LYS:O	1:B:646:LEU:HD23	2.09	0.53
1:A:317:THR:OG1	1:A:325:TYR:OH	2.27	0.52
1:A:398:LEU:HD13	1:A:554:LEU:HD21	1.91	0.52
1:B:28:PHE:HZ	1:B:140:ASN:HD21	1.58	0.52
1:A:697:PRO:O	1:A:733:ARG:NH2	2.43	0.52
1:A:672:ALA:HB2	1:A:757:VAL:HG11	1.90	0.52
1:A:84:GLN:HE21	1:A:86:TRP:N	2.02	0.52
1:A:271:THR:O	1:A:275:ASP:HB2	2.11	0.51
1:B:454:ALA:HB3	1:B:456:TYR:HD1	1.75	0.51
1:B:478:LEU:HD21	1:B:519:LYS:HB3	1.93	0.51
1:A:158:ARG:NH1	1:A:610:GLN:HE22	2.04	0.51
1:A:630:THR:OG1	1:A:678:GLY:HA3	2.10	0.51
1:A:419:THR:HA	1:A:457:ASN:O	2.11	0.51
1:B:423:ILE:HA	1:B:461:ALA:O	2.11	0.51
1:A:131:ILE:HG23	1:A:382:THR:HB	1.92	0.51
1:A:644:ILE:O	1:A:644:ILE:HG22	2.11	0.51
1:A:36:LEU:HD21	1:A:78:LEU:HB3	1.93	0.51
1:A:47:THR:CG2	1:A:50:ASP:H	2.23	0.51
1:A:498:GLU:O	1:A:498:GLU:HG3	2.10	0.51
1:A:429:ALA:HB1	1:A:432:GLN:HB2	1.94	0.50
1:A:251:MET:HA	1:A:286:SER:O	2.10	0.50
1:B:54:SER:O	1:B:58:LEU:HG	2.12	0.50
1:A:232:GLU:HB2	1:A:734:VAL:HG21	1.93	0.50
1:B:423:ILE:O	1:B:489:TYR:HA	2.12	0.50
1:B:706:VAL:HG12	1:B:730:SER:HB3	1.93	0.49
1:A:184:ILE:O	1:A:188:GLN:HG3	2.12	0.49
1:A:663:THR:HA	1:A:728:VAL:CG2	2.43	0.49
1:B:454:ALA:HB3	1:B:456:TYR:CD1	2.48	0.49
1:A:420:VAL:HG22	1:A:458:VAL:HG22	1.94	0.49
1:B:746:THR:HG23	1:B:762:VAL:HG22	1.93	0.49
1:B:75:VAL:HG23	1:B:80:LEU:HD23	1.94	0.48
1:B:161:VAL:HB	1:B:504:ARG:O	2.13	0.48
1:B:510:PRO:HG2	1:B:513:GLN:NE2	2.28	0.48
1:A:411:LYS:HD2	1:A:411:LYS:N	2.28	0.48
1:A:389:TYR:O	1:A:393:THR:HG23	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:GLN:OE1	2:C:1:NAG:H83	2.14	0.48
1:A:152:PRO:HB3	1:A:183:TYR:CD1	2.49	0.48
1:A:529:LEU:C	1:A:530:ILE:HD13	2.38	0.48
1:A:178:VAL:HG21	1:A:708:TRP:CZ2	2.49	0.48
1:A:721:GLU:OE1	1:A:723:ARG:NH2	2.46	0.48
1:B:406:LEU:CD2	1:B:408:LEU:HG	2.44	0.47
1:B:673:ASN:C	1:B:674:ILE:HD13	2.39	0.47
1:B:775:GLY:O	1:B:776:LYS:HB3	2.15	0.47
1:A:638:ASN:HB3	1:A:642:ARG:CZ	2.45	0.47
1:B:155:ASN:ND2	1:B:204:HIS:HD2	2.12	0.47
1:A:312:ALA:HB1	1:A:317:THR:OG1	2.15	0.47
1:A:327:TRP:HA	5:A:804:NAG:H62	1.97	0.47
1:A:390:GLN:OE1	2:C:2:NAG:H5	2.15	0.47
1:A:420:VAL:HG12	1:A:486:VAL:HG22	1.95	0.47
1:A:460:PHE:HE2	5:A:802:NAG:H82	1.80	0.47
1:A:507:ILE:HG13	1:A:588:ALA:HA	1.97	0.47
1:B:154:ILE:HG21	1:B:180:ALA:HB2	1.96	0.46
1:B:422:LEU:HD12	1:B:448:ARG:CA	2.45	0.46
1:B:580:ARG:HA	1:B:625:HIS:O	2.14	0.46
1:B:615:TYR:CZ	1:B:617:GLY:HA3	2.50	0.46
1:B:693:SER:OG	5:B:804:NAG:H83	2.15	0.46
1:A:129:ALA:HB1	1:A:187:ILE:HG12	1.97	0.46
1:A:208:TYR:OH	1:A:211:GLU:OE2	2.33	0.46
1:A:340:ARG:O	1:A:344:GLU:HG3	2.15	0.46
1:A:390:GLN:O	1:A:394:GLN:HG3	2.15	0.46
1:A:754:GLU:CB	1:A:756:LYS:HE3	2.46	0.46
1:B:604:GLU:O	1:B:607:ASN:HB3	2.16	0.46
1:A:419:THR:HG22	1:A:457:ASN:HB3	1.98	0.46
1:B:193:ASP:HA	1:B:356:GLN:HE21	1.81	0.46
1:A:646:LEU:HD13	1:A:667:VAL:HG22	1.96	0.45
1:A:310:ALA:HA	1:A:338:LEU:HD23	1.98	0.45
1:B:26:LEU:HG	1:B:26:LEU:O	2.16	0.45
1:B:407:PRO:HB3	1:B:629:TYR:CE2	2.51	0.45
1:B:510:PRO:HG2	1:B:513:GLN:HE21	1.81	0.45
1:A:110:PHE:HB3	1:A:111:PRO:HD2	1.98	0.45
1:A:333:ILE:HD13	1:A:338:LEU:HD12	1.98	0.45
1:B:205:TYR:O	1:B:252:CYS:HA	2.16	0.45
1:A:239:HIS:CD2	1:A:277:PHE:HA	2.52	0.45
1:A:648:ILE:HG23	1:A:742:LEU:HD23	1.98	0.45
1:B:223:MET:HB3	1:B:599:MET:HG3	1.99	0.45
1:A:398:LEU:HD12	1:A:554:LEU:HD23	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:TYR:O	1:A:203:LYS:HE2	2.17	0.44
1:A:117:THR:HG21	1:A:169:PRO:O	2.16	0.44
1:A:205:TYR:O	1:A:252:CYS:HA	2.16	0.44
1:B:630:THR:OG1	1:B:678:GLY:HA3	2.17	0.44
1:A:420:VAL:HG12	1:A:486:VAL:CG2	2.48	0.44
1:B:695:ALA:O	1:B:733:ARG:HD3	2.18	0.44
1:A:137:ARG:NH1	1:A:197:LYS:O	2.44	0.44
1:A:405:VAL:CG1	1:A:528:PRO:HB3	2.47	0.44
1:B:559:PRO:HG2	1:B:563:GLY:HA3	2.00	0.44
1:A:137:ARG:HD3	1:A:197:LYS:O	2.17	0.44
1:A:89:ALA:HA	1:A:92:GLY:O	2.18	0.43
1:A:407:PRO:HB3	1:A:629:TYR:CE2	2.54	0.43
1:B:114:ILE:HG23	1:B:115:LEU:N	2.33	0.43
1:B:91:HIS:NE2	1:B:437:TYR:O	2.51	0.43
1:A:478:LEU:HD23	1:A:520:LEU:HD23	2.00	0.43
1:B:419:THR:HA	1:B:457:ASN:O	2.19	0.43
1:B:710:ARG:HE	2:E:1:NAG:H81	1.84	0.43
1:B:152:PRO:HB3	1:B:183:TYR:CD1	2.54	0.43
1:B:408:LEU:CD1	1:B:486:VAL:HG11	2.48	0.43
1:A:725:PRO:O	1:A:726:ILE:HD13	2.19	0.43
1:A:661:SER:H	1:A:664:GLN:NE2	2.16	0.43
1:B:498:GLU:HG3	1:B:498:GLU:O	2.18	0.43
1:A:263:CYS:CB	1:A:317:THR:HG21	2.45	0.42
1:B:490:ALA:HA	1:B:532:LEU:HB2	1.99	0.42
1:B:26:LEU:N	1:B:26:LEU:HD23	2.35	0.42
1:A:146:GLY:HA3	7:A:909:HOH:O	2.19	0.42
1:A:181:TYR:HA	1:A:245:ALA:HB2	2.01	0.42
1:A:521:ALA:HB1	1:A:549:ASN:HB2	2.01	0.42
1:B:513:GLN:O	1:B:517:ILE:HG13	2.20	0.42
1:B:249:SER:HA	1:B:284:TYR:O	2.19	0.42
1:B:748:GLU:HB3	5:B:804:NAG:HN2	1.84	0.42
1:A:635:SER:OG	1:A:673:ASN:HB2	2.20	0.41
1:B:507:ILE:HG13	1:B:588:ALA:HA	2.02	0.41
1:A:297:ASN:HA	1:A:298:PRO:HA	1.90	0.41
1:A:133:SER:HB2	1:A:197:LYS:HE3	2.02	0.41
1:B:36:LEU:HD21	1:B:78:LEU:HB3	2.02	0.41
1:A:690:ALA:HA	1:A:748:GLU:O	2.21	0.41
1:B:294:ASN:O	1:B:299:HIS:HB2	2.19	0.41
1:B:521:ALA:HB1	1:B:549:ASN:HB3	2.01	0.41
1:B:721:GLU:HG3	1:B:722:LEU:N	2.35	0.41
1:A:128:ILE:O	1:A:132:ILE:HG13	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:ILE:HG21	1:A:180:ALA:HB2	2.02	0.41
1:A:119:ALA:HB1	1:A:394:GLN:HB3	2.02	0.41
1:A:188:GLN:HA	1:A:198:LEU:O	2.21	0.41
1:B:120:LEU:HD12	1:B:685:THR:HB	2.02	0.41
1:A:454:ALA:HB3	1:A:456:TYR:HD1	1.86	0.40
1:B:755:ARG:O	1:B:758:ARG:NH1	2.53	0.40
1:A:36:LEU:HA	1:A:39:HIS:HD2	1.86	0.40
1:A:183:TYR:CE1	1:A:187:ILE:HG13	2.57	0.40
1:A:453:GLU:OE1	1:A:568:ARG:NH1	2.39	0.40
1:A:318:ASP:HB3	1:A:346:GLY:CA	2.52	0.40
1:B:110:PHE:HA	1:B:388:SER:OG	2.22	0.40
1:B:756:LYS:HA	1:B:756:LYS:HD3	1.93	0.40
1:A:161:VAL:HB	1:A:504:ARG:O	2.21	0.40
1:A:230:LEU:HD23	1:A:773:TRP:HZ2	1.86	0.40
1:B:318:ASP:HB3	1:B:346:GLY:CA	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	737/788 (94%)	716 (97%)	21 (3%)	0	100	100
1	B	737/788 (94%)	716 (97%)	21 (3%)	0	100	100
All	All	1474/1576 (94%)	1432 (97%)	42 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	599/638 (94%)	591 (99%)	8 (1%)	61	82
1	B	599/638 (94%)	589 (98%)	10 (2%)	53	78
All	All	1198/1276 (94%)	1180 (98%)	18 (2%)	57	80

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	CYS
1	A	448	ARG
1	A	548	THR
1	A	583	THR
1	A	693	SER
1	A	728	VAL
1	A	748	GLU
1	A	760	LYS
1	B	193	ASP
1	B	260	VAL
1	B	353	THR
1	B	422	LEU
1	B	482	GLN
1	B	527	LYS
1	B	542	SER
1	B	637	SER
1	B	680	VAL
1	B	713	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	84	GLN
1	A	140	ASN
1	A	214	HIS
1	A	228	GLN
1	A	239	HIS
1	A	248	HIS
1	A	305	GLN
1	A	436	ASN

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Mol	Chain	Res	Type
1	A	610	GLN
1	A	664	GLN
1	B	112	GLN
1	B	140	ASN
1	B	155	ASN
1	B	204	HIS
1	B	239	HIS
1	B	282	HIS
1	B	294	ASN
1	B	356	GLN
1	B	432	GLN
1	B	459	ASN
1	B	482	GLN
1	B	610	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 ⓘ

17 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	1,2	14,14,15	0.32	0	17,19,21	0.59	0
2	NAG	C	2	2	14,14,15	0.31	0	17,19,21	0.61	0
2	BMA	C	3	2	11,11,12	1.00	1 (9%)	15,15,17	0.96	1 (6%)
2	MAN	C	4	2	11,11,12	0.95	1 (9%)	15,15,17	1.07	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MAN	C	5	2	11,11,12	1.08	1 (9%)	15,15,17	0.77	0
2	MAN	C	6	2	11,11,12	0.99	0	15,15,17	0.90	0
3	NAG	D	1	1,3	14,14,15	0.69	1 (7%)	17,19,21	0.49	0
3	NAG	D	2	3	14,14,15	0.48	0	17,19,21	0.71	1 (5%)
2	NAG	E	1	1,2	14,14,15	0.27	0	17,19,21	0.57	0
2	NAG	E	2	2	14,14,15	0.55	0	17,19,21	0.67	0
2	BMA	E	3	2	11,11,12	0.62	0	15,15,17	0.93	0
2	MAN	E	4	2	11,11,12	0.78	0	15,15,17	1.11	1 (6%)
2	MAN	E	5	2	11,11,12	0.82	0	15,15,17	0.80	0
2	MAN	E	6	2	11,11,12	1.15	1 (9%)	15,15,17	1.00	1 (6%)
4	NAG	F	1	1,4	14,14,15	0.23	0	17,19,21	0.39	0
4	NAG	F	2	4	14,14,15	0.31	0	17,19,21	0.42	0
4	BMA	F	3	4	11,11,12	0.99	0	15,15,17	0.84	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	C	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	BMA	C	3	2	-	1/2/19/22	0/1/1/1
2	MAN	C	4	2	-	0/2/19/22	0/1/1/1
2	MAN	C	5	2	-	0/2/19/22	0/1/1/1
2	MAN	C	6	2	-	0/2/19/22	0/1/1/1
3	NAG	D	1	1,3	-	3/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
2	NAG	E	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
2	BMA	E	3	2	-	1/2/19/22	0/1/1/1
2	MAN	E	4	2	-	0/2/19/22	0/1/1/1
2	MAN	E	5	2	-	0/2/19/22	0/1/1/1
2	MAN	E	6	2	-	0/2/19/22	0/1/1/1
4	NAG	F	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	F	2	4	-	0/6/23/26	0/1/1/1
4	BMA	F	3	4	-	0/2/19/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	5	MAN	C2-C3	2.31	1.56	1.52
3	D	1	NAG	O5-C1	-2.26	1.39	1.43
2	E	6	MAN	O5-C5	2.23	1.47	1.43
2	C	3	BMA	C1-C2	2.08	1.57	1.52
2	C	4	MAN	C1-C2	2.04	1.57	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	4	MAN	C1-O5-C5	2.98	116.18	112.19
2	C	4	MAN	C1-O5-C5	2.76	115.88	112.19
2	E	6	MAN	C1-O5-C5	2.68	115.78	112.19
3	D	2	NAG	C1-O5-C5	2.13	115.04	112.19
2	C	3	BMA	O2-C2-C3	-2.12	105.76	110.15

There are no chirality outliers.

All (15) torsion outliers are listed below:

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

There are no ring outliers.

4 monomers are involved in 5 short contacts:

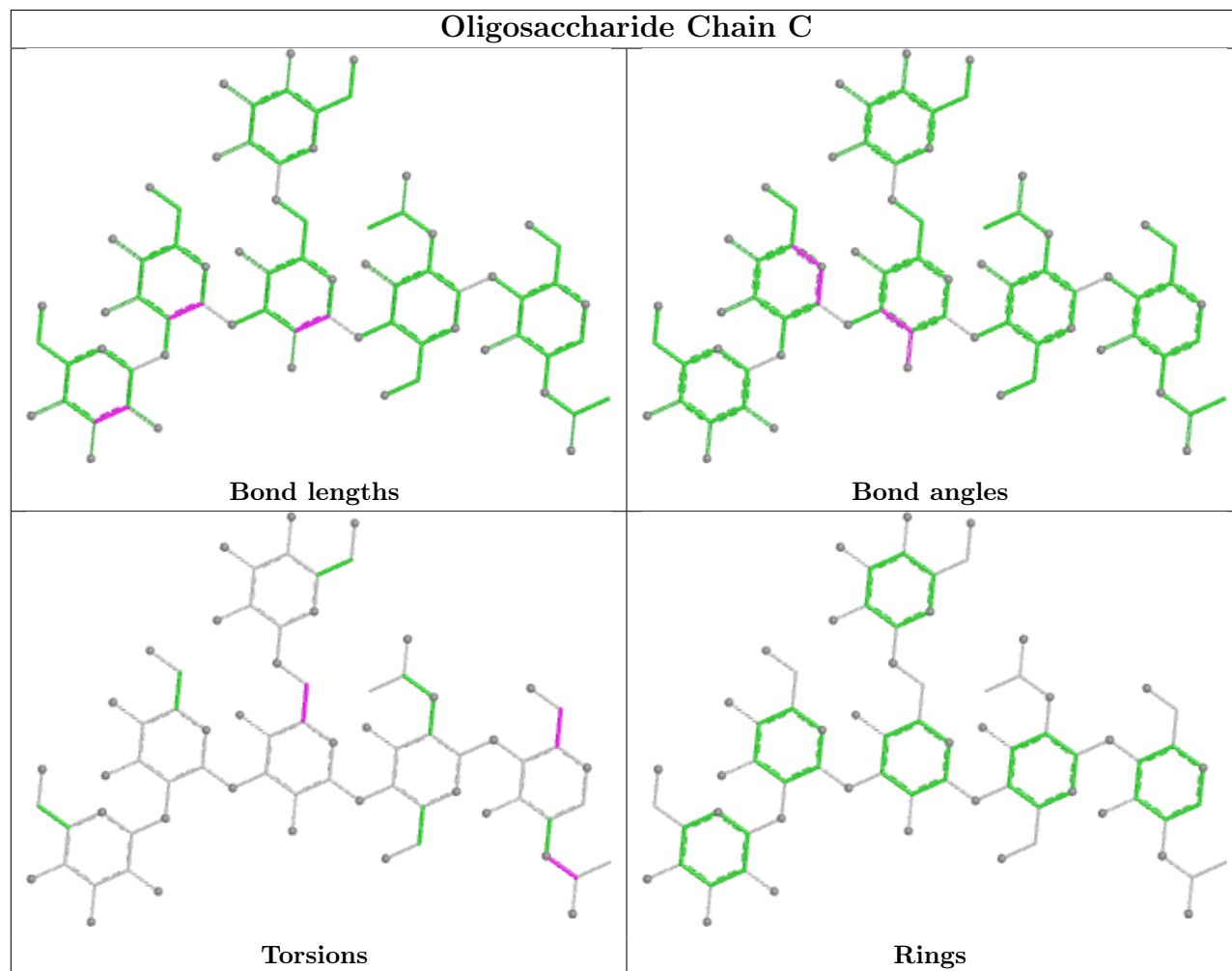
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	NAG	2	0
2	E	1	NAG	2	0
2	C	1	NAG	2	0

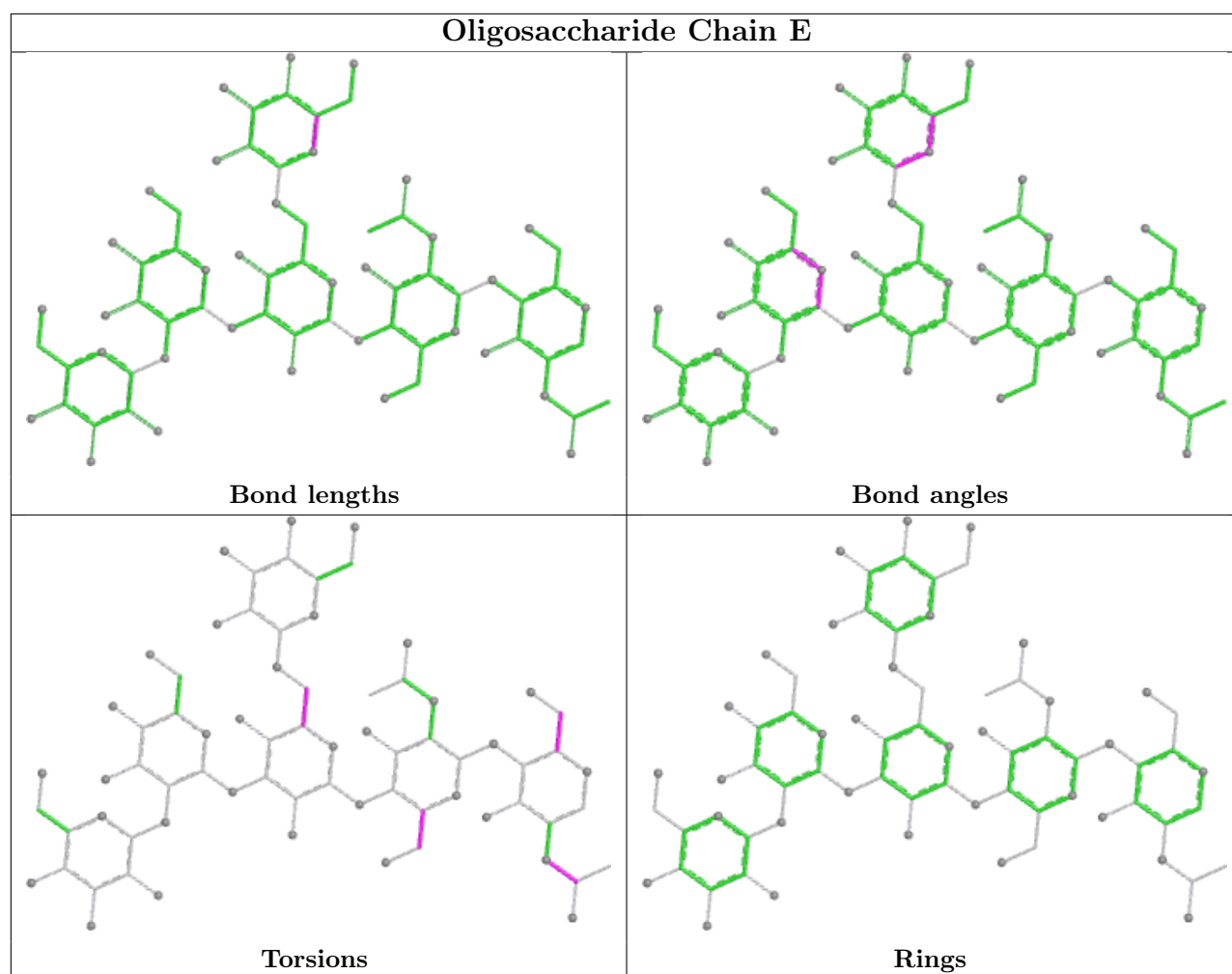
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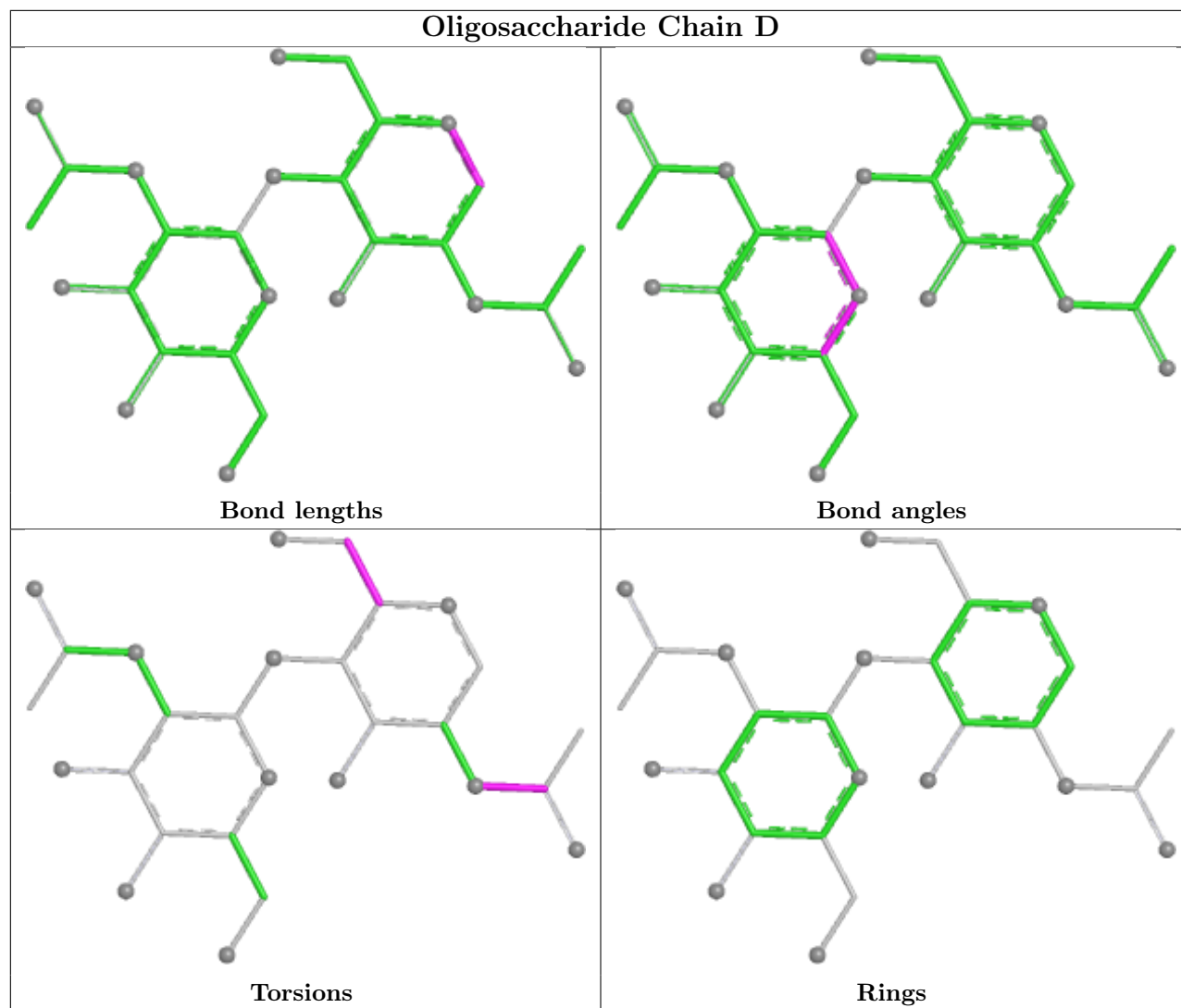
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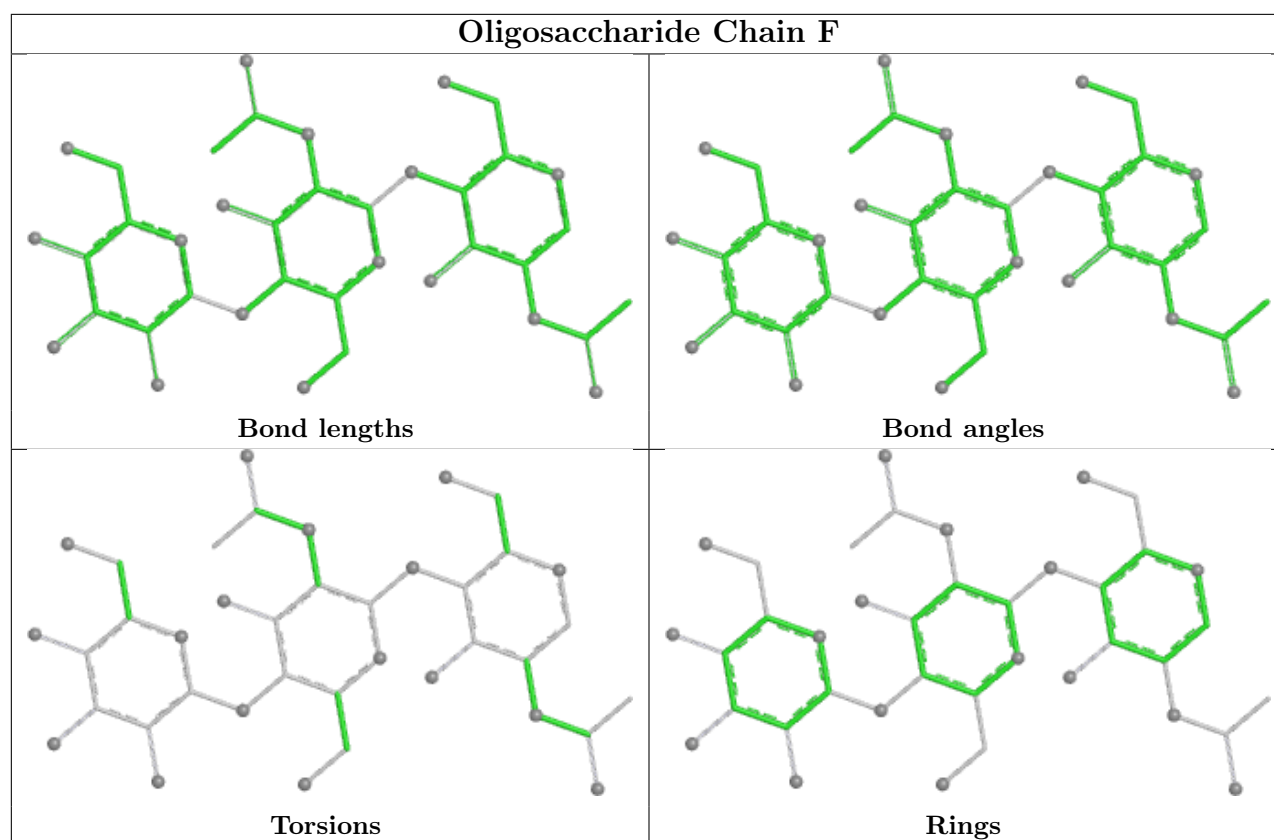
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	2	NAG	1	0

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









5.6 Ligand geometry [i](#)

11 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	B	804	1	14,14,15	0.69	0	17,19,21	0.47	0
5	NAG	A	803	1	14,14,15	0.67	1 (7%)	17,19,21	0.61	0
6	GOL	A	805	-	5,5,5	0.80	0	5,5,5	0.70	0
5	NAG	A	804	1	14,14,15	0.36	0	17,19,21	0.50	0
5	NAG	B	801	1	14,14,15	0.24	0	17,19,21	0.35	0
5	NAG	B	805	1	14,14,15	0.48	0	17,19,21	0.42	0
6	GOL	B	806	-	5,5,5	1.11	0	5,5,5	1.49	1 (20%)
5	NAG	A	801	1	14,14,15	0.19	0	17,19,21	0.51	0
5	NAG	A	802	1	14,14,15	0.33	0	17,19,21	0.56	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	B	802	1	14,14,15	0.24	0	17,19,21	0.51	0
5	NAG	B	803	1	14,14,15	0.46	0	17,19,21	0.49	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
5	NAG	B	804	1	-	3/6/23/26	0/1/1/1
5	NAG	A	803	1	-	2/6/23/26	0/1/1/1
6	GOL	A	805	-	-	1/4/4/4	-
5	NAG	A	804	1	-	0/6/23/26	0/1/1/1
5	NAG	B	801	1	-	0/6/23/26	0/1/1/1
5	NAG	B	805	1	-	0/6/23/26	0/1/1/1
6	GOL	B	806	-	-	0/4/4/4	-
5	NAG	A	801	1	-	2/6/23/26	0/1/1/1
5	NAG	A	802	1	-	0/6/23/26	0/1/1/1
5	NAG	B	802	1	-	2/6/23/26	0/1/1/1
5	NAG	B	803	1	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	803	NAG	C1-C2	2.14	1.55	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	806	GOL	C3-C2-C1	-3.00	100.78	111.80

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	801	NAG	C8-C7-N2-C2
5	A	801	NAG	O7-C7-N2-C2
5	A	803	NAG	C8-C7-N2-C2
5	A	803	NAG	O7-C7-N2-C2
5	B	802	NAG	C8-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
5	B	802	NAG	O7-C7-N2-C2
5	B	803	NAG	C8-C7-N2-C2
5	B	803	NAG	O7-C7-N2-C2
5	B	804	NAG	C8-C7-N2-C2
5	B	804	NAG	O7-C7-N2-C2
5	B	804	NAG	O5-C5-C6-O6
6	A	805	GOL	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	804	NAG	3	0
5	A	804	NAG	1	0
5	A	802	NAG	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	742/788 (94%)	0.13	6 (0%) 82 80	26, 56, 74, 103	1 (0%)
1	B	743/788 (94%)	0.32	23 (3%) 51 47	46, 60, 80, 99	0
All	All	1485/1576 (94%)	0.22	29 (1%) 65 61	26, 58, 78, 103	1 (0%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	25	PRO	6.0
1	A	370	PRO	4.8
1	B	26	LEU	4.7
1	B	578	ALA	4.5
1	B	94	ASP	3.8
1	A	639	THR	3.1
1	A	776	LYS	3.0
1	B	642	ARG	2.8
1	B	395	GLY	2.7
1	B	629	TYR	2.7
1	B	552	ALA	2.7
1	B	638	ASN	2.6
1	B	474	PHE	2.5
1	B	525	GLY	2.5
1	A	26	LEU	2.4
1	B	411	LYS	2.4
1	B	776	LYS	2.4
1	B	362	SER	2.3
1	B	338	LEU	2.3
1	B	476	ALA	2.3
1	B	554	LEU	2.2
1	B	412	ALA	2.2
1	B	574	ARG	2.2
1	B	417	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	27	SER	2.1
1	B	416	SER	2.1
1	B	437	TYR	2.1
1	A	642	ARG	2.1
1	B	32	GLN	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](#)

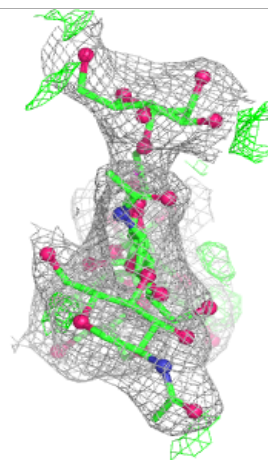
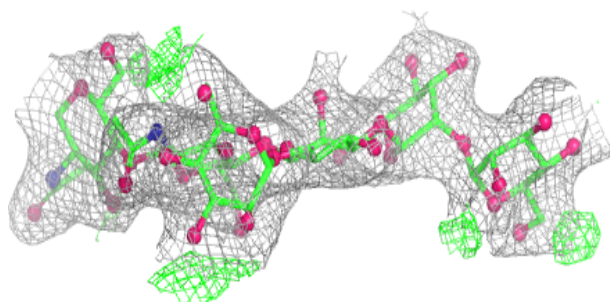
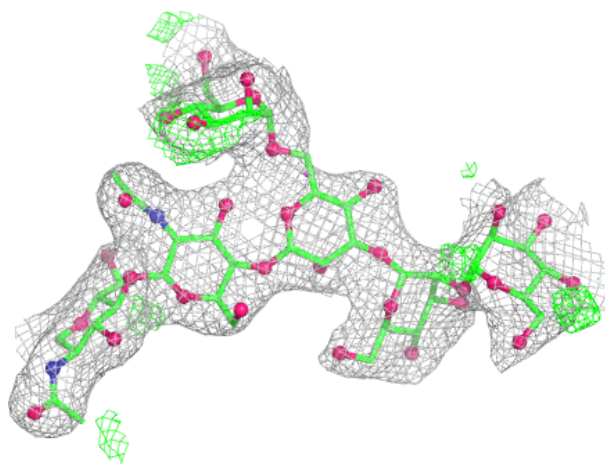
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	MAN	E	5	11/12	0.48	0.16	91,97,101,101	0
2	MAN	C	5	11/12	0.58	0.15	80,85,90,92	0
2	MAN	E	6	11/12	0.62	0.16	74,77,82,82	0
4	BMA	F	3	11/12	0.70	0.14	76,80,84,86	0
2	MAN	C	6	11/12	0.80	0.12	70,72,74,76	0
3	NAG	D	2	14/15	0.85	0.12	57,62,66,67	0
2	MAN	C	4	11/12	0.89	0.10	68,73,76,79	0
2	NAG	E	2	14/15	0.90	0.10	63,66,71,72	0
3	NAG	D	1	14/15	0.90	0.10	56,62,65,72	0
4	NAG	F	2	14/15	0.91	0.09	59,68,73,79	0
2	NAG	E	1	14/15	0.91	0.10	58,62,65,66	0
2	BMA	C	3	11/12	0.92	0.10	65,71,75,77	0
2	BMA	E	3	11/12	0.92	0.08	72,75,78,79	0
2	MAN	E	4	11/12	0.92	0.08	70,79,81,90	0
2	NAG	C	1	14/15	0.93	0.09	52,58,64,66	0
2	NAG	C	2	14/15	0.94	0.08	60,65,68,74	0
4	NAG	F	1	14/15	0.94	0.08	60,64,67,67	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.

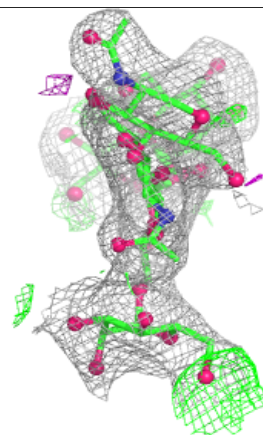
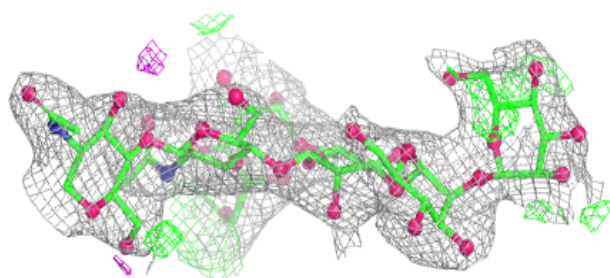
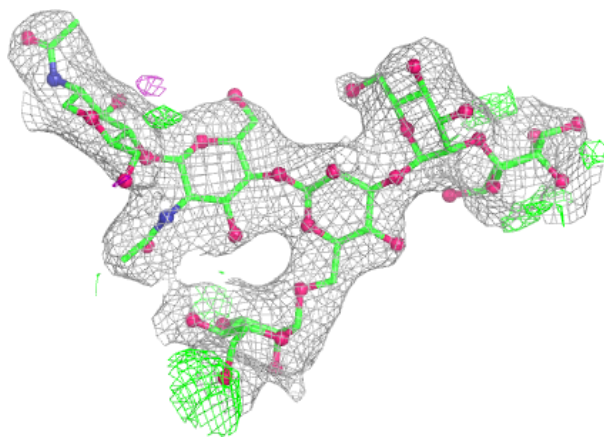
Electron density around Chain C:

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

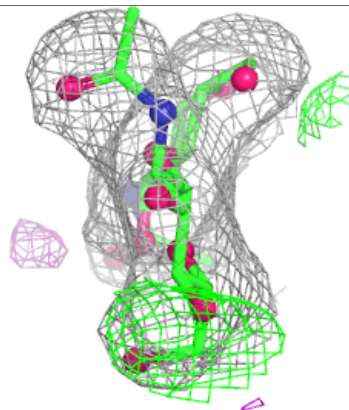
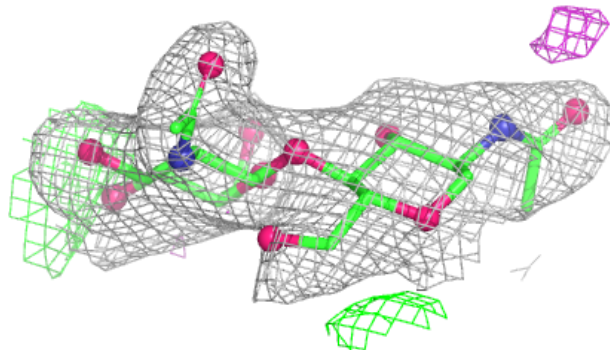
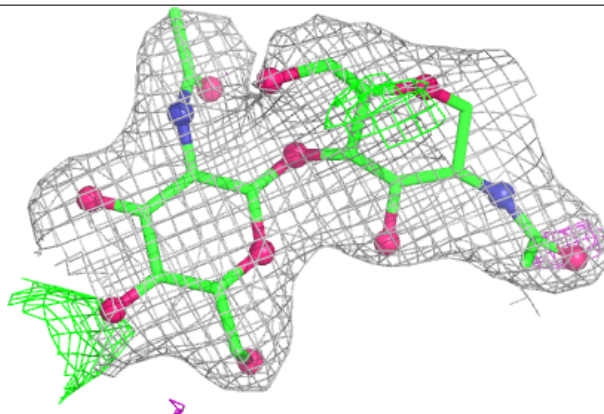


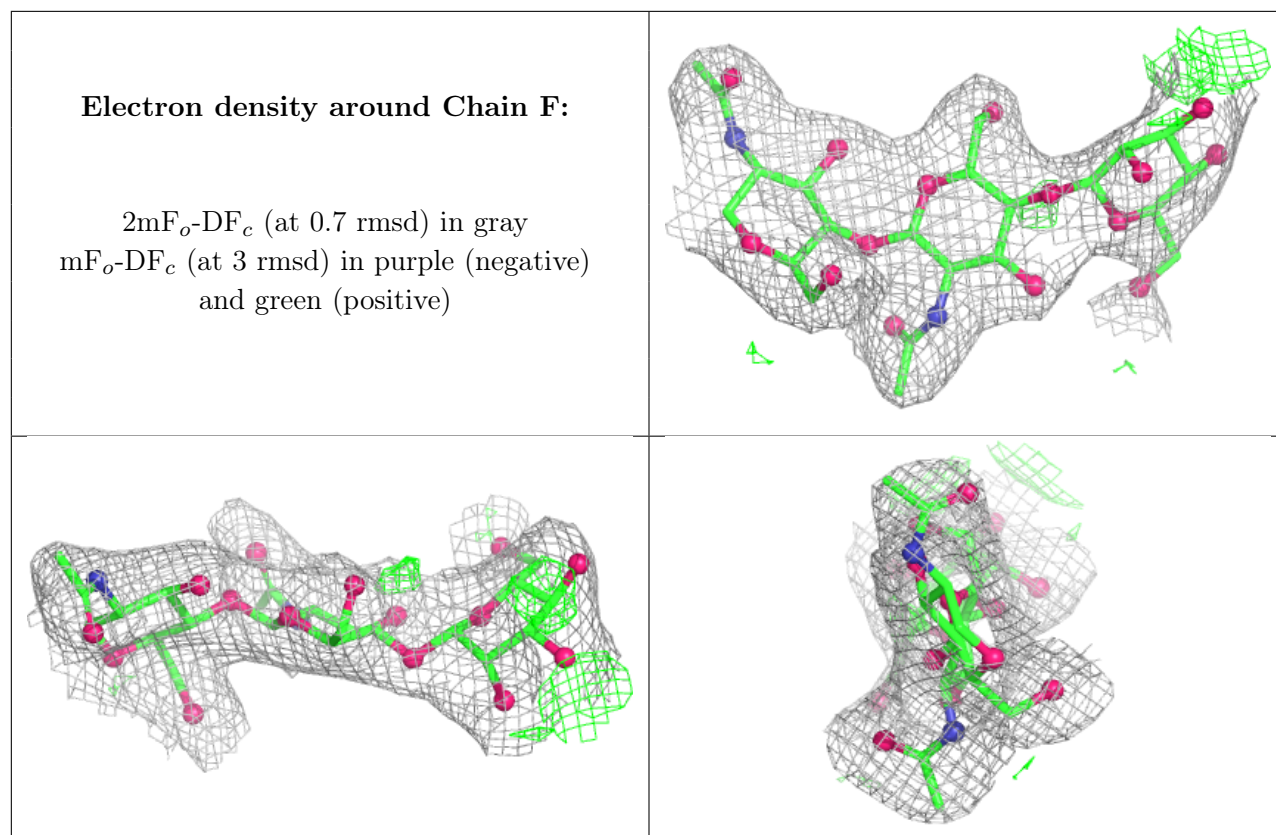
Electron density around Chain E:

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

**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)





6.4 Ligands ⓘ

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	B	804	14/15	0.43	0.18	79,89,94,103	0
5	NAG	A	804	14/15	0.56	0.19	75,85,91,92	0
5	NAG	A	803	14/15	0.64	0.16	75,84,89,89	0
6	GOL	A	805	6/6	0.66	0.22	47,60,69,73	0
5	NAG	B	802	14/15	0.67	0.15	77,82,83,84	0
5	NAG	B	803	14/15	0.72	0.14	71,88,92,93	0
5	NAG	B	805	14/15	0.73	0.15	66,77,83,87	0
6	GOL	B	806	6/6	0.73	0.25	73,88,99,99	0
5	NAG	B	801	14/15	0.77	0.14	80,86,90,92	0
5	NAG	A	801	14/15	0.84	0.12	74,82,85,88	0
5	NAG	A	802	14/15	0.85	0.12	64,71,75,76	0

6.5 Other polymers [i](#)

There are no such residues in this entry.