



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 03:30 PM UTC

PDB ID : 1JMJ / pdb_00001jnj
Title : Crystal Structure of Native Heparin Cofactor II
Authors : Baglin, T.P.; Carrell, R.W.; Church, F.C.; Huntington, J.A.
Deposited on : 2001-07-18
Resolution : 2.35 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

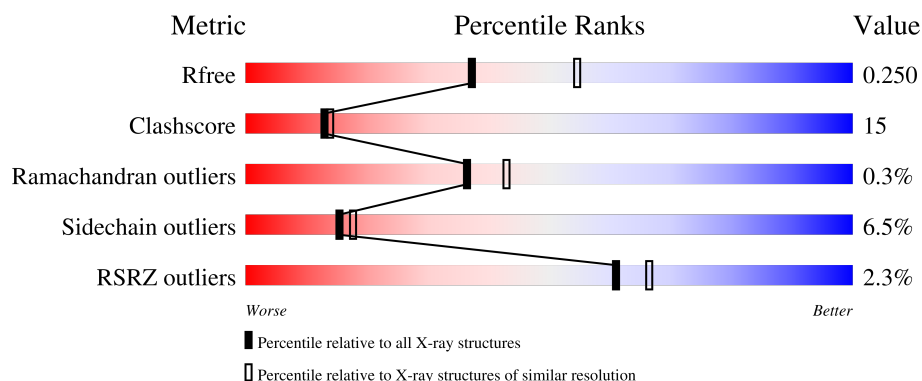
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

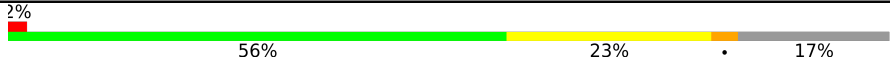
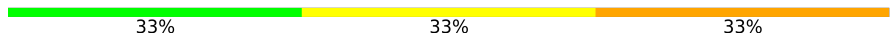
The reported resolution of this entry is 2.35 Å.

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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	480	
1	B	480	
2	C	3	

2 Entry composition [i](#)

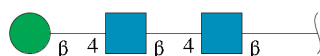
There are 5 unique types of molecules in this entry. The entry contains 6723 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 HEPARIN COFACTOR II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	397	Total	C	N	O	S	20	0	0
			3228	2069	560	579	20			
1	B	387	Total	C	N	O	S	14	0	0
			3144	2017	549	558	20			

- 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.

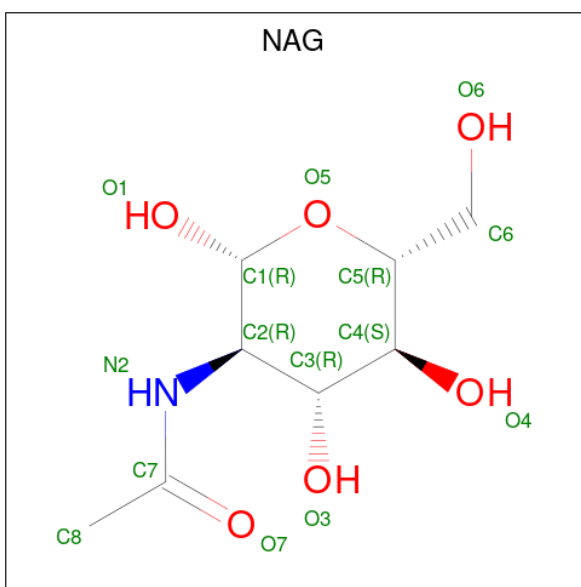


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

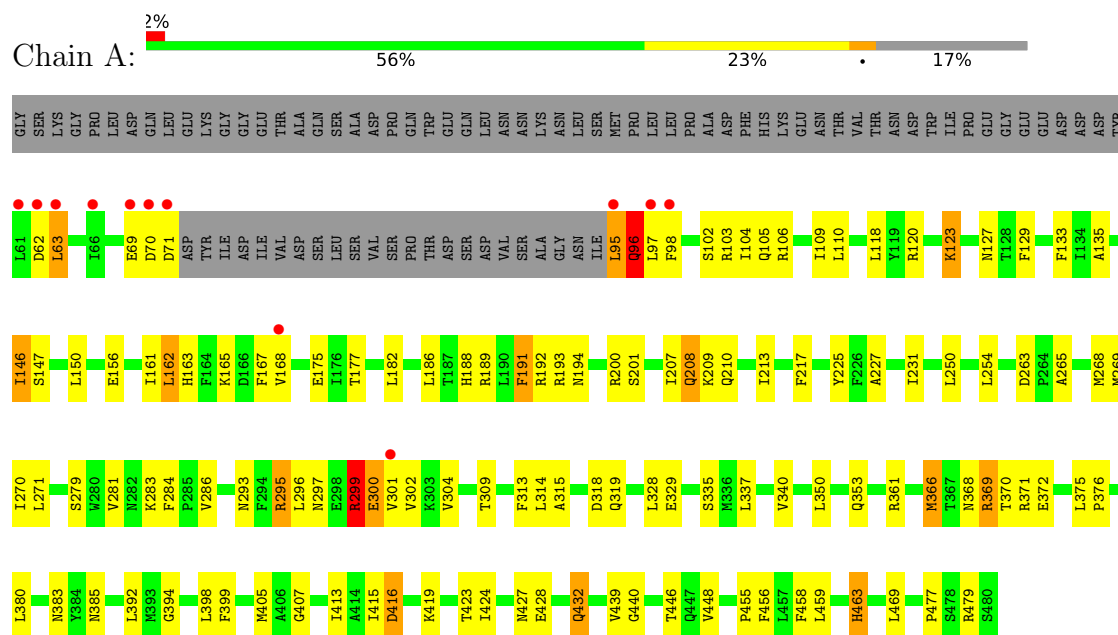
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	157	Total	O	0	0
			157	157		
5	B	140	Total	O	0	0
			140	140		

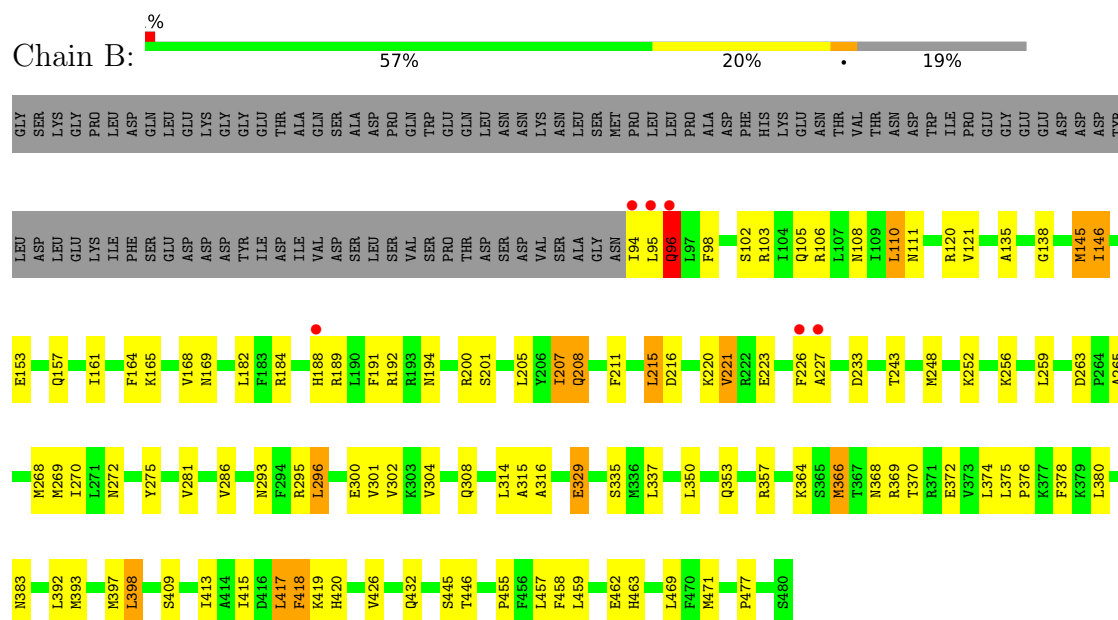
3 Residue-property plots

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: HEPARIN COFACTOR II



• Molecule 1: HEPARIN COFACTOR II



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

Chain C: 33% 33% 33%

MAG1
MAG2
EM13

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.73Å 80.00Å 92.24Å 90.00° 102.04° 90.00°	Depositor
Resolution (Å)	25.00 – 2.35 25.00 – 2.35	Depositor EDS
% Data completeness (in resolution range)	88.0 (25.00-2.35) 88.0 (25.00-2.35)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.57 (at 2.36Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.208 , 0.255 0.209 , 0.250	Depositor DCC
R_{free} test set	995 reflections (2.54%)	wwPDB-VP
Wilson B-factor (Å ²)	31.6	Xtriage
Anisotropy	0.624	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 57.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6723	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.08% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, 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	0.41	0/3291	0.91	12/4431 (0.3%)
1	B	0.41	0/3207	0.90	8/4320 (0.2%)
All	All	0.41	0/6498	0.90	20/8751 (0.2%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	281	VAL	N-CA-C	-8.64	102.00	110.72
1	A	281	VAL	N-CA-C	-8.40	102.24	110.72
1	A	62	ASP	N-CA-C	-7.77	103.78	113.18
1	A	372	GLU	N-CA-C	-6.76	98.23	109.46
1	B	372	GLU	N-CA-C	-6.73	98.25	108.96
1	B	96	GLN	N-CA-C	-6.67	105.11	113.18
1	A	385	ASN	N-CA-C	-6.41	97.96	108.41
1	A	286	VAL	N-CA-C	6.41	120.01	111.17
1	B	463	HIS	N-CA-C	6.38	118.77	111.11
1	A	463	HIS	N-CA-C	6.12	118.49	111.02
1	A	191	PHE	N-CA-C	6.09	119.66	112.72
1	B	462	GLU	N-CA-C	-5.89	99.13	108.73
1	A	299	ARG	N-CA-C	5.88	117.60	109.54
1	B	300	GLU	N-CA-C	5.62	118.73	109.85
1	A	416	ASP	N-CA-C	-5.62	106.56	113.41
1	A	135	ALA	CA-C-N	5.26	124.71	119.24
1	A	135	ALA	C-N-CA	5.26	124.71	119.24
1	B	286	VAL	N-CA-C	5.12	117.45	111.05
1	B	164	PHE	N-CA-C	-5.09	105.92	111.82
1	A	162	LEU	N-CA-C	-5.09	107.02	113.18

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	3228	0	3279	102	0
1	B	3144	0	3207	91	0
2	C	39	0	34	4	0
3	A	1	0	0	0	0
4	B	14	0	13	0	0
5	A	157	0	0	2	0
5	B	140	0	0	1	0
All	All	6723	0	6533	193	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 15.

All (193) 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:405:MET:HE1	1:A:413:ILE:HG13	1.40	1.04
1:A:314:LEU:HB3	1:A:366:MET:HG2	1.48	0.96
1:B:96:GLN:NE2	1:B:96:GLN:H	1.64	0.95
1:A:110:LEU:HD12	1:A:167:PHE:HB2	1.59	0.84
2:C:2:NAG:H3	2:C:2:NAG:H82	1.61	0.83
1:A:329:GLU:OE1	1:A:335:SER:HB3	1.80	0.82
1:B:221:VAL:HG13	1:B:227:ALA:HB3	1.60	0.82
1:B:192:ARG:HH11	1:B:192:ARG:HG3	1.43	0.82
1:A:70:ASP:HB3	5:A:631:HOH:O	1.82	0.80
1:B:314:LEU:HB3	1:B:366:MET:HG2	1.65	0.78
1:B:145:MET:HE2	1:B:146:ILE:HA	1.64	0.77
1:B:135:ALA:H	1:B:420:HIS:CE1	2.03	0.77
1:A:405:MET:HE1	1:A:413:ILE:CG1	2.17	0.73
1:A:95:LEU:O	1:A:96:GLN:HB3	1.87	0.73
1:B:398:LEU:HD11	1:B:415:ILE:HD12	1.70	0.73
1:A:370:THR:HG22	1:A:446:THR:HG22	1.69	0.72
1:A:268:MET:HE3	1:A:415:ILE:HD13	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:329:GLU:OE2	1:B:335:SER:HB3	1.90	0.71
1:B:295:ARG:O	1:B:455:PRO:HD3	1.90	0.71
1:B:96:GLN:H	1:B:96:GLN:HE21	1.38	0.70
1:B:350:LEU:HD11	1:B:457:LEU:HD12	1.72	0.70
1:B:215:LEU:HD13	1:B:216:ASP:N	2.08	0.69
1:A:293:ASN:HB3	1:A:301:VAL:HG11	1.74	0.68
1:B:138:GLY:C	1:B:272:ASN:HD21	2.03	0.67
1:B:145:MET:HG2	1:B:221:VAL:HG22	1.75	0.67
1:B:304:VAL:HG11	1:B:477:PRO:HG2	1.77	0.67
1:B:153:GLU:HB3	1:B:397:MET:HE1	1.75	0.66
1:B:145:MET:HE2	1:B:146:ILE:CA	2.26	0.65
1:A:63:LEU:HD22	1:A:63:LEU:H	1.63	0.64
1:A:375:LEU:HD12	1:A:376:PRO:HD2	1.79	0.64
1:A:95:LEU:HD22	1:A:98:PHE:CD1	2.32	0.64
1:B:216:ASP:OD1	1:B:220:LYS:HE2	1.98	0.63
1:B:207:ILE:HD13	1:B:268:MET:HG3	1.80	0.63
1:A:69:GLU:OE2	1:B:445:SER:HB2	1.98	0.63
1:A:95:LEU:O	1:A:96:GLN:CB	2.47	0.63
1:B:375:LEU:HD12	1:B:376:PRO:HD2	1.81	0.63
1:B:146:ILE:HG13	1:B:270:ILE:HD11	1.80	0.62
1:B:98:PHE:CD2	1:B:106:ARG:HD3	2.34	0.62
1:B:252:LYS:HD2	1:B:275:TYR:OH	2.00	0.61
1:B:98:PHE:HZ	1:B:110:LEU:HD21	1.63	0.61
1:B:94:ILE:O	1:B:357:ARG:NH2	2.31	0.61
1:B:350:LEU:CD1	1:B:457:LEU:HD12	2.31	0.60
1:B:94:ILE:HG22	1:B:95:LEU:HG	1.83	0.60
1:B:153:GLU:O	1:B:157:GLN:HG3	2.03	0.59
1:A:96:GLN:HE21	1:A:96:GLN:HA	1.66	0.58
1:A:370:THR:CG2	1:A:446:THR:HG22	2.32	0.58
1:B:135:ALA:H	1:B:420:HIS:HE1	1.46	0.58
1:B:208:GLN:OE1	1:B:208:GLN:HA	2.03	0.58
1:B:192:ARG:HH11	1:B:192:ARG:CG	2.15	0.58
1:B:296:LEU:HD22	1:B:302:VAL:HG13	1.84	0.58
1:B:272:ASN:HD22	1:B:420:HIS:HD2	1.50	0.58
1:B:184:ARG:HG3	1:B:188:HIS:CE1	2.38	0.57
1:A:304:VAL:HG11	1:A:477:PRO:HG2	1.85	0.57
1:A:63:LEU:HD22	1:A:63:LEU:N	2.19	0.56
1:A:102:SER:OG	1:A:104:ILE:HG22	2.05	0.56
1:B:96:GLN:NE2	1:B:96:GLN:N	2.46	0.56
1:A:299:ARG:HB2	1:A:299:ARG:NH1	2.20	0.56
1:B:145:MET:HE2	1:B:146:ILE:N	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:192:ARG:HG3	1:B:192:ARG:NH1	2.19	0.56
1:A:146:ILE:HG13	1:A:270:ILE:HD11	1.87	0.56
1:A:209:LYS:HB2	1:A:231:ILE:HD11	1.87	0.56
1:A:299:ARG:O	1:A:300:GLU:HB3	2.05	0.56
1:A:70:ASP:O	1:A:71:ASP:HB2	2.06	0.55
1:B:308:GLN:HG3	1:B:374:LEU:HG	1.88	0.55
1:B:417:LEU:HD11	1:B:419:LYS:HB2	1.87	0.55
1:A:95:LEU:O	1:A:95:LEU:HG	2.05	0.55
1:B:95:LEU:HD22	1:B:98:PHE:CE1	2.41	0.55
1:A:69:GLU:CD	1:B:445:SER:HB2	2.32	0.55
1:A:192:ARG:HH11	1:A:192:ARG:HG3	1.73	0.54
1:A:188:HIS:O	1:A:192:ARG:HG2	2.08	0.54
1:A:168:VAL:HG13	1:A:175:GLU:HA	1.90	0.54
1:B:398:LEU:CD1	1:B:415:ILE:HD12	2.38	0.53
1:B:205:LEU:HD12	1:B:269:MET:O	2.09	0.53
1:B:370:THR:HG22	1:B:446:THR:HG22	1.91	0.53
1:A:147:SER:HA	1:A:150:LEU:HG	1.91	0.53
1:A:337:LEU:O	1:A:458:PHE:HA	2.09	0.53
1:A:398:LEU:HD13	1:A:398:LEU:O	2.09	0.53
1:A:263:ASP:OD1	1:A:265:ALA:HB3	2.09	0.52
1:A:368:ASN:HD22	2:C:1:NAG:H83	1.74	0.52
1:B:102:SER:O	1:B:106:ARG:HG3	2.10	0.52
1:A:110:LEU:CD1	1:A:167:PHE:HB2	2.37	0.51
1:A:335:SER:OG	1:A:463:HIS:HE1	1.92	0.51
1:A:405:MET:CE	1:A:413:ILE:HG13	2.26	0.51
1:B:96:GLN:HE21	1:B:96:GLN:N	2.05	0.51
1:B:184:ARG:O	1:B:188:HIS:ND1	2.44	0.51
1:A:175:GLU:HG3	1:A:177:THR:CG2	2.41	0.50
1:A:295:ARG:O	1:A:455:PRO:HD3	2.11	0.50
1:B:94:ILE:HG22	1:B:95:LEU:N	2.26	0.50
1:A:208:GLN:CA	1:A:208:GLN:HE21	2.24	0.50
1:B:208:GLN:OE1	1:B:233:ASP:HA	2.11	0.50
1:A:209:LYS:CB	1:A:231:ILE:HD11	2.42	0.50
1:B:157:GLN:NE2	1:B:397:MET:HE3	2.26	0.50
1:B:192:ARG:HH12	1:B:194:ASN:CG	2.19	0.49
1:B:184:ARG:HD3	1:B:223:GLU:O	2.11	0.49
1:A:299:ARG:CB	1:A:299:ARG:HH11	2.26	0.49
1:A:104:ILE:HG23	1:A:105:GLN:N	2.26	0.49
1:A:254:LEU:HD21	1:A:423:THR:HB	1.95	0.49
1:B:188:HIS:CE1	1:B:226:PHE:CZ	3.00	0.49
1:B:368:ASN:O	1:B:369:ARG:HD2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:268:MET:HE3	1:B:415:ILE:HG13	1.94	0.49
1:A:313:PHE:HB2	1:A:371:ARG:HD2	1.94	0.49
1:B:215:LEU:HD22	1:B:215:LEU:C	2.38	0.48
1:A:315:ALA:HB3	1:A:371:ARG:CZ	2.43	0.48
1:B:215:LEU:HD22	1:B:215:LEU:O	2.12	0.48
1:B:268:MET:HE3	1:B:415:ILE:CG1	2.44	0.48
1:B:296:LEU:HD22	1:B:302:VAL:CG1	2.43	0.48
1:A:439:VAL:HG22	1:A:440:GLY:N	2.28	0.48
1:A:371:ARG:HG2	1:A:448:VAL:CG2	2.43	0.48
2:C:2:NAG:H82	2:C:2:NAG:C3	2.39	0.48
1:A:314:LEU:HD23	1:A:368:ASN:HA	1.96	0.48
1:A:279:SER:HB2	1:A:283:LYS:NZ	2.29	0.48
2:C:2:NAG:H3	2:C:2:NAG:C8	2.39	0.48
1:A:123:LYS:HD2	5:A:605:HOH:O	2.13	0.48
1:B:188:HIS:O	1:B:192:ARG:HG2	2.14	0.48
1:A:63:LEU:H	1:A:63:LEU:CD2	2.27	0.47
1:A:103:ARG:HG2	1:A:182:LEU:HD11	1.97	0.47
1:A:104:ILE:HD11	1:A:186:LEU:HB2	1.96	0.47
1:A:217:PHE:HB2	1:A:407:GLY:O	2.15	0.47
1:A:318:ASP:OD2	1:A:361:ARG:NH2	2.40	0.46
1:B:383:ASN:HD21	1:B:419:LYS:HE3	1.80	0.46
1:A:127:ASN:HB3	1:A:129:PHE:CE1	2.50	0.46
1:A:192:ARG:NH1	1:A:194:ASN:OD1	2.48	0.46
1:B:315:ALA:C	1:B:366:MET:HG3	2.41	0.46
1:A:405:MET:CE	1:A:413:ILE:O	2.64	0.46
1:A:268:MET:HG2	1:A:415:ILE:HD13	1.98	0.46
1:B:293:ASN:HB3	1:B:301:VAL:HG11	1.97	0.46
1:B:316:ALA:CB	1:B:366:MET:HE3	2.46	0.46
1:A:424:ILE:HA	1:A:432:GLN:HE22	1.80	0.46
1:B:153:GLU:HB3	1:B:397:MET:CE	2.45	0.45
1:A:162:LEU:O	1:A:163:HIS:HB2	2.16	0.45
1:A:368:ASN:O	1:A:369:ARG:HD3	2.16	0.45
1:A:207:ILE:HD12	1:A:213:ILE:HG12	1.97	0.45
1:A:297:ASN:ND2	1:A:300:GLU:HG2	2.31	0.45
1:B:248:MET:SD	1:B:256:LYS:HG2	2.56	0.45
1:A:192:ARG:O	1:A:193:ARG:C	2.59	0.45
1:A:192:ARG:HH11	1:A:192:ARG:CG	2.29	0.45
1:B:357:ARG:HH11	1:B:357:ARG:HG2	1.82	0.45
1:B:350:LEU:C	1:B:350:LEU:HD13	2.42	0.45
1:A:95:LEU:HD23	1:A:97:LEU:HB2	1.99	0.45
1:A:105:GLN:O	1:A:109:ILE:HG13	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:PHE:O	1:A:428:GLU:HB3	2.16	0.44
1:A:133:PHE:CZ	1:A:424:ILE:HB	2.52	0.44
1:A:156:GLU:OE1	1:A:165:LYS:NZ	2.40	0.44
1:A:405:MET:HE1	1:A:413:ILE:C	2.43	0.44
1:A:250:LEU:C	1:A:250:LEU:HD23	2.42	0.44
1:A:370:THR:HG22	1:A:446:THR:HA	1.99	0.44
1:B:98:PHE:HZ	1:B:110:LEU:CD2	2.30	0.44
1:A:398:LEU:HD12	1:A:399:PHE:CE2	2.53	0.44
1:A:427:ASN:C	1:A:427:ASN:OD1	2.61	0.44
1:B:418:PHE:CD2	1:B:418:PHE:C	2.96	0.44
1:A:315:ALA:HB3	1:A:371:ARG:NH1	2.34	0.43
1:B:103:ARG:HG2	1:B:182:LEU:HD11	2.00	0.43
1:B:458:PHE:O	1:B:471:MET:HA	2.18	0.43
1:A:95:LEU:CD2	1:A:97:LEU:HB2	2.49	0.43
1:A:161:ILE:HD11	1:A:394:GLY:HA3	2.00	0.43
1:A:268:MET:HE3	1:A:415:ILE:CD1	2.45	0.43
1:B:108:ASN:HA	1:B:111:ASN:HB2	2.00	0.43
1:B:102:SER:OG	1:B:105:GLN:HG3	2.19	0.43
1:A:301:VAL:HG12	1:A:302:VAL:N	2.32	0.43
1:B:378:PHE:CZ	1:B:426:VAL:HG21	2.53	0.43
1:B:200:ARG:NH2	1:B:252:LYS:HE3	2.34	0.42
1:A:225:TYR:C	1:A:227:ALA:N	2.77	0.42
1:A:340:VAL:HG22	1:A:456:PHE:HB3	2.01	0.42
1:A:269:MET:HE2	1:A:271:LEU:HB2	2.01	0.42
1:A:299:ARG:HB2	1:A:299:ARG:HH11	1.82	0.42
1:B:191:PHE:CZ	1:B:201:SER:HB2	2.54	0.42
1:A:104:ILE:CG2	1:A:105:GLN:N	2.82	0.42
1:A:118:LEU:HD13	1:A:118:LEU:C	2.44	0.42
1:B:409:SER:HB3	1:B:413:ILE:HD11	2.02	0.42
1:B:418:PHE:C	1:B:418:PHE:HD2	2.28	0.42
1:A:98:PHE:CD2	1:A:106:ARG:HD3	2.55	0.41
1:A:129:PHE:HD2	1:A:479:ARG:NH1	2.18	0.41
1:A:191:PHE:CZ	1:A:201:SER:HB2	2.55	0.41
1:A:208:GLN:NE2	1:A:208:GLN:HA	2.35	0.41
1:A:210:GLN:N	1:A:210:GLN:CD	2.78	0.41
1:B:316:ALA:HB3	1:B:366:MET:HE3	2.02	0.41
1:A:284:PHE:HA	1:A:309:THR:HB	2.02	0.41
1:B:121:VAL:HG21	1:B:393:MET:HG2	2.03	0.41
1:B:263:ASP:OD1	1:B:265:ALA:HB3	2.20	0.41
1:A:383:ASN:OD1	1:A:419:LYS:HE3	2.21	0.41
1:B:165:LYS:O	1:B:169:ASN:HB2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:337:LEU:O	1:B:458:PHE:HA	2.20	0.41
1:A:175:GLU:HG3	1:A:177:THR:HG23	2.02	0.41
1:B:243:THR:HG21	1:B:259:LEU:CD1	2.51	0.41
1:A:297:ASN:CG	1:A:300:GLU:HG2	2.45	0.41
1:A:319:GLN:HG3	1:B:364:LYS:O	2.21	0.41
1:A:268:MET:HE1	1:A:405:MET:SD	2.61	0.41
1:A:424:ILE:HG23	1:A:424:ILE:O	2.20	0.41
1:B:192:ARG:CG	1:B:192:ARG:NH1	2.74	0.40
1:A:370:THR:CG2	1:A:446:THR:HA	2.51	0.40
1:B:191:PHE:CE1	1:B:201:SER:HB2	2.56	0.40
1:B:211:PHE:CD1	1:B:211:PHE:N	2.89	0.40
1:B:189:ARG:HB2	5:B:576:HOH:O	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	393/480 (82%)	374 (95%)	17 (4%)	2 (0%)	24	27
1	B	385/480 (80%)	375 (97%)	10 (3%)	0	100	100
All	All	778/960 (81%)	749 (96%)	27 (4%)	2 (0%)	36	43

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	GLN
1	A	300	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	360/433 (83%)	337 (94%)	23 (6%)	16	18
1	B	350/433 (81%)	327 (93%)	23 (7%)	15	17
All	All	710/866 (82%)	664 (94%)	46 (6%)	15	18

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	63	LEU
1	A	95	LEU
1	A	96	GLN
1	A	120	ARG
1	A	123	LYS
1	A	146	ILE
1	A	189	ARG
1	A	200	ARG
1	A	208	GLN
1	A	295	ARG
1	A	296	LEU
1	A	299	ARG
1	A	328	LEU
1	A	350	LEU
1	A	353	GLN
1	A	366	MET
1	A	369	ARG
1	A	380	LEU
1	A	392	LEU
1	A	416	ASP
1	A	432	GLN
1	A	459	LEU
1	A	469	LEU
1	B	96	GLN
1	B	110	LEU
1	B	120	ARG
1	B	145	MET

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Mol	Chain	Res	Type
1	B	146	ILE
1	B	161	ILE
1	B	168	VAL
1	B	207	ILE
1	B	208	GLN
1	B	215	LEU
1	B	221	VAL
1	B	296	LEU
1	B	329	GLU
1	B	353	GLN
1	B	366	MET
1	B	380	LEU
1	B	392	LEU
1	B	398	LEU
1	B	417	LEU
1	B	418	PHE
1	B	432	GLN
1	B	459	LEU
1	B	469	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	GLN
1	A	125	GLN
1	A	208	GLN
1	A	342	HIS
1	A	353	GLN
1	A	363	GLN
1	A	421	GLN
1	A	447	GLN
1	A	463	HIS
1	B	96	GLN
1	B	159	HIS
1	B	169	ASN
1	B	272	ASN
1	B	411	GLN
1	B	420	HIS
1	B	447	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 ⓘ

3 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	0.58	0	17,19,21	0.76	0
2	NAG	C	2	2	14,14,15	0.60	0	17,19,21	1.06	1 (5%)
2	BMA	C	3	2	11,11,12	0.45	0	15,15,17	0.35	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	-	4/6/23/26	0/1/1/1
2	BMA	C	3	2	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	NAG	C3-C4-C5	2.20	114.23	110.23

There are no chirality outliers.

All (10) torsion outliers are listed below:

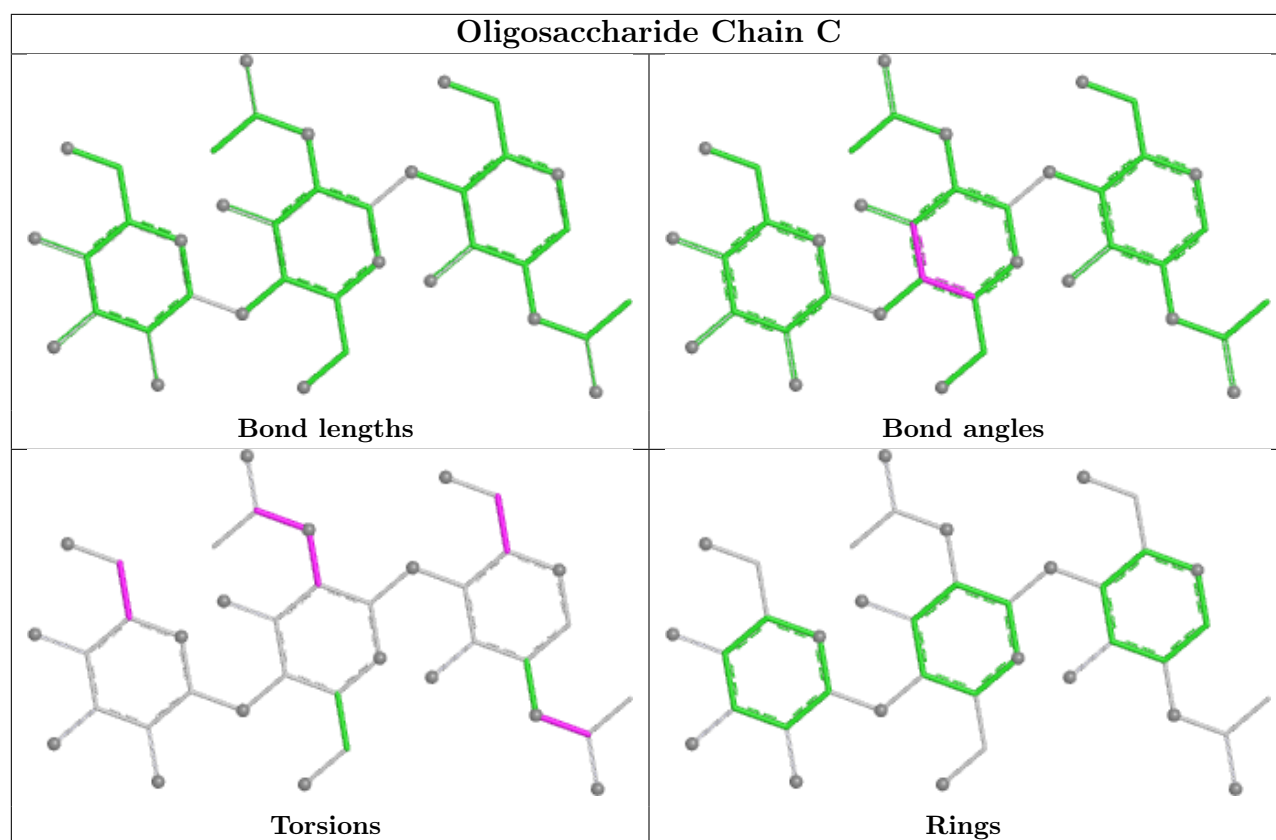
Mol	Chain	Res	Type	Atoms
2	C	2	NAG	C8-C7-N2-C2
2	C	2	NAG	O7-C7-N2-C2
2	C	3	BMA	O5-C5-C6-O6
2	C	3	BMA	C4-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
2	C	1	NAG	C8-C7-N2-C2
2	C	1	NAG	O7-C7-N2-C2
2	C	1	NAG	O5-C5-C6-O6
2	C	2	NAG	C1-C2-N2-C7
2	C	2	NAG	C3-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	NAG	3	0
2	C	1	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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	B	481	1	14,14,15	0.57	0	17,19,21	0.64	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
4	NAG	B	481	1	-	5/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	481	NAG	C8-C7-N2-C2
4	B	481	NAG	O7-C7-N2-C2
4	B	481	NAG	C3-C2-N2-C7
4	B	481	NAG	O5-C5-C6-O6
4	B	481	NAG	C1-C2-N2-C7

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 [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	397/480 (82%)	-0.02	12 (3%) 52 59	19, 34, 68, 95	7 (1%)
1	B	387/480 (80%)	-0.05	6 (1%) 70 76	17, 34, 60, 85	4 (1%)
All	All	784/960 (81%)	-0.04	18 (2%) 61 66	17, 34, 61, 95	11 (1%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	94	ILE	4.5
1	A	61	LEU	4.2
1	A	95	LEU	3.9
1	B	226	PHE	3.2
1	B	95	LEU	3.1
1	A	71	ASP	3.1
1	A	66	ILE	3.1
1	A	70	ASP	3.0
1	A	63	LEU	2.8
1	A	62	ASP	2.6
1	A	98	PHE	2.6
1	B	96	GLN	2.5
1	B	188	HIS	2.5
1	A	97	LEU	2.4
1	A	168	VAL	2.3
1	A	301	VAL	2.1
1	B	227	ALA	2.0
1	A	69	GLU	2.0

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

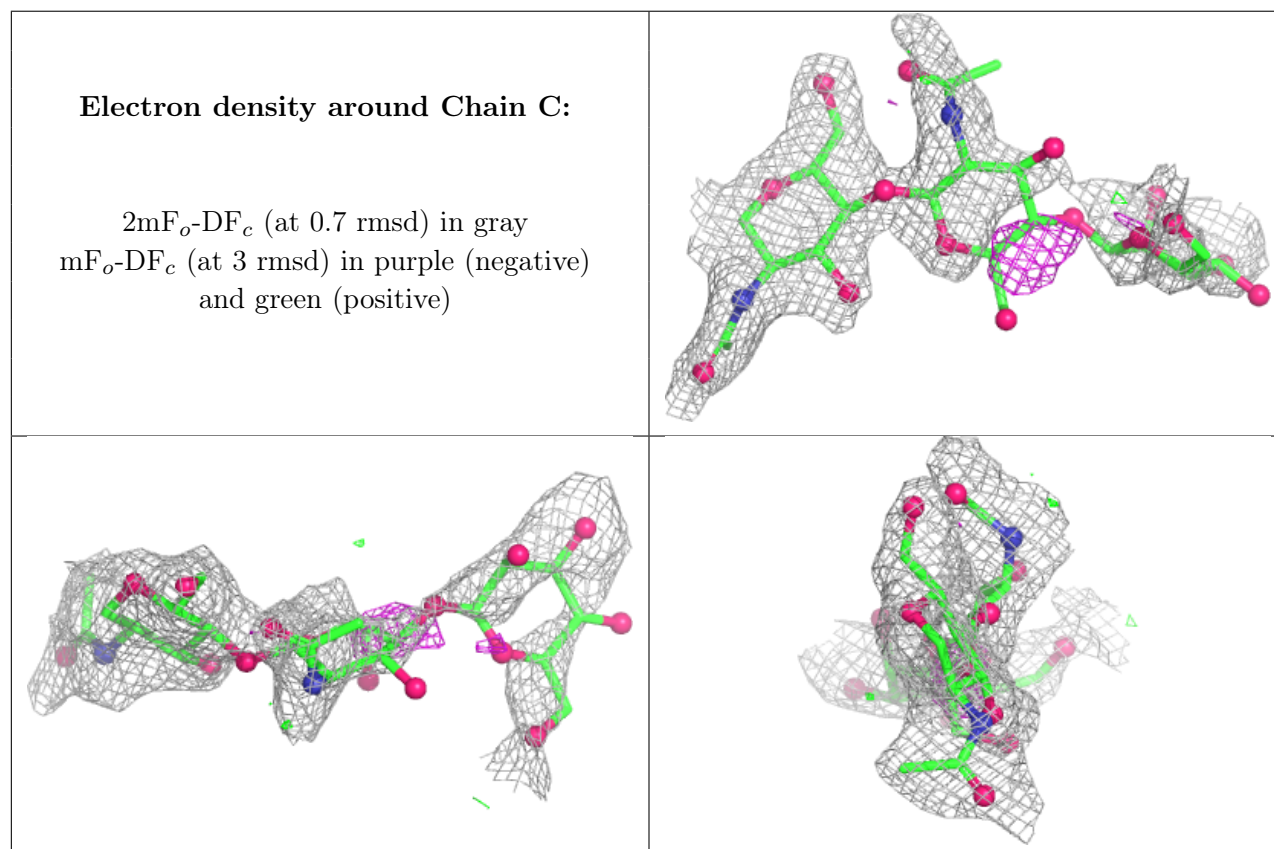
There are no non-standard protein/DNA/RNA residues in this entry.

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($\text{\AA}^2$)	Q<0.9
2	NAG	C	2	14/15	0.46	0.21	86,90,93,95	0
2	BMA	C	3	11/12	0.50	0.16	96,97,97,97	0
2	NAG	C	1	14/15	0.79	0.13	61,65,71,80	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.



6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	B	481	14/15	0.75	0.15	51,56,58,59	0
3	CA	A	501	1/1	0.95	0.08	44,44,44,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.