



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:47 PM UTC

PDB ID : 6V7N / pdb_00006v7n
Title : Crystal Structure of a human Lysosome Resident Glycoprotein, Lysosomal Acid Lipase, and its Implications in Cholesteryl Ester Storage Disease (CESD)
Authors : Han, S.
Deposited on : 2019-12-09
Resolution : 2.62 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

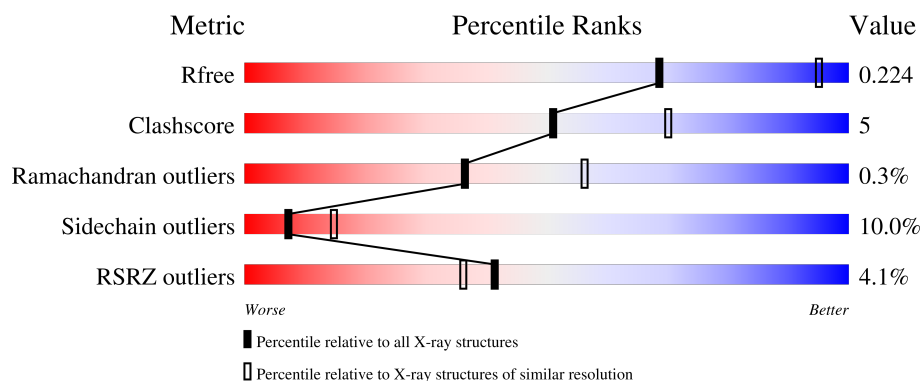
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.62 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	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

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	384	2% 77% 17% • •
1	B	384	6% 75% 18% • •
2	C	2	50% 50%
2	D	2	50% 50%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6241 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 Lysosomal acid lipase/cholesteryl ester hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	369	Total	C	N	O	S	0	0	0
			2982	1933	494	540	15			
1	B	370	Total	C	N	O	S	0	0	0
			2991	1939	496	541	15			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	51	GLN	ASN	engineered mutation	UNP P38571
A	80	GLN	ASN	engineered mutation	UNP P38571
A	300	GLN	ASN	engineered mutation	UNP P38571
A	379	ALA	-	expression tag	UNP P38571
A	380	SER	-	expression tag	UNP P38571
A	381	GLU	-	expression tag	UNP P38571
A	382	ASN	-	expression tag	UNP P38571
A	383	ASN	-	expression tag	UNP P38571
A	384	LEU	-	expression tag	UNP P38571
B	51	GLN	ASN	engineered mutation	UNP P38571
B	80	GLN	ASN	engineered mutation	UNP P38571
B	300	GLN	ASN	engineered mutation	UNP P38571
B	379	ALA	-	expression tag	UNP P38571
B	380	SER	-	expression tag	UNP P38571
B	381	GLU	-	expression tag	UNP P38571
B	382	ASN	-	expression tag	UNP P38571
B	383	ASN	-	expression tag	UNP P38571
B	384	LEU	-	expression tag	UNP P38571

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

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

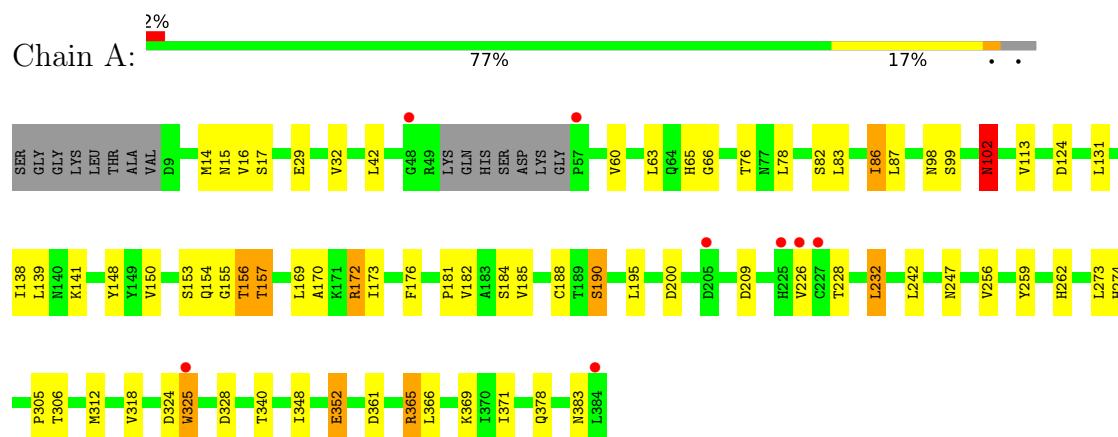
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	77	Total	O	0	0
			77	77		
5	B	78	Total	O	0	0
			78	78		

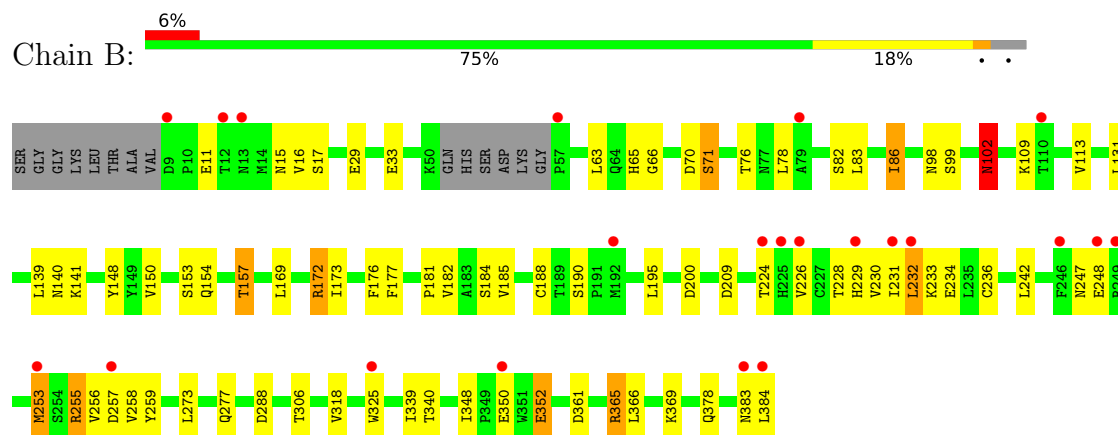
3 Residue-property plots

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: Lysosomal acid lipase/cholesteryl ester hydrolase



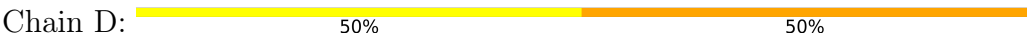
- Molecule 1: Lysosomal acid lipase/cholesteryl ester hydrolase



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	97.14Å 165.49Å 60.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	83.78 – 2.62 83.78 – 2.62	Depositor EDS
% Data completeness (in resolution range)	99.8 (83.78-2.62) 99.8 (83.78-2.62)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 2.62Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.185 , 0.222 0.194 , 0.224	Depositor DCC
R_{free} test set	1518 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	50.4	Xtriage
Anisotropy	0.502	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 66.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6241	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, 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	0.80	2/3074 (0.1%)	1.33	20/4182 (0.5%)
1	B	0.78	1/3083 (0.0%)	1.33	19/4193 (0.5%)
All	All	0.79	3/6157 (0.0%)	1.33	39/8375 (0.5%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	173	ILE	CG1-CD1	-5.39	1.30	1.51
1	B	173	ILE	CG1-CD1	-5.31	1.31	1.51
1	A	228	THR	CA-C	5.26	1.59	1.52

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	340	THR	N-CA-C	-7.90	98.59	110.28
1	A	324	ASP	CA-C-N	7.43	130.10	120.44
1	A	324	ASP	C-N-CA	7.43	130.10	120.44
1	A	102	ASN	CA-CB-CG	7.34	119.94	112.60
1	A	15	ASN	CA-CB-CG	7.23	119.83	112.60
1	A	176	PHE	CA-CB-CG	7.22	121.02	113.80
1	B	176	PHE	CA-CB-CG	6.94	120.74	113.80
1	B	102	ASN	CA-CB-CG	6.93	119.53	112.60
1	B	15	ASN	CA-CB-CG	6.79	119.39	112.60
1	B	70	ASP	CA-C-N	6.45	130.49	120.82
1	B	70	ASP	C-N-CA	6.45	130.49	120.82
1	A	185	VAL	CA-C-N	6.19	129.42	120.38
1	A	185	VAL	C-N-CA	6.19	129.42	120.38
1	B	185	VAL	CA-C-N	6.18	129.18	120.28
1	B	185	VAL	C-N-CA	6.18	129.18	120.28
1	B	259	TYR	CA-C-N	6.12	128.49	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	259	TYR	C-N-CA	6.12	128.49	120.28
1	B	71	SER	CA-C-N	5.98	129.11	120.38
1	B	71	SER	C-N-CA	5.98	129.11	120.38
1	B	195	LEU	CA-C-N	5.89	126.52	119.98
1	B	195	LEU	C-N-CA	5.89	126.52	119.98
1	A	200	ASP	CA-CB-CG	5.71	118.31	112.60
1	B	140	ASN	CA-CB-CG	5.70	118.30	112.60
1	A	170	ALA	CA-C-N	5.59	128.03	120.38
1	A	170	ALA	C-N-CA	5.59	128.03	120.38
1	B	339	ILE	CA-C-N	5.48	127.62	120.28
1	B	339	ILE	C-N-CA	5.48	127.62	120.28
1	B	148	TYR	N-CA-C	-5.28	101.09	109.76
1	A	259	TYR	CA-C-N	5.20	127.24	120.28
1	A	259	TYR	C-N-CA	5.20	127.24	120.28
1	A	195	LEU	CA-C-N	5.18	125.73	119.98
1	A	195	LEU	C-N-CA	5.18	125.73	119.98
1	A	155	GLY	CA-C-N	5.10	127.38	120.44
1	A	155	GLY	C-N-CA	5.10	127.38	120.44
1	B	247	ASN	CA-CB-CG	5.09	117.69	112.60
1	B	200	ASP	CA-CB-CG	5.08	117.68	112.60
1	A	148	TYR	N-CA-C	-5.05	101.47	109.96
1	A	328	ASP	CA-C-N	5.05	127.11	120.60
1	A	328	ASP	C-N-CA	5.05	127.11	120.60

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	2982	0	2869	32	0
1	B	2991	0	2881	30	0
2	C	28	0	25	1	0
2	D	28	0	25	1	0
3	A	14	0	13	0	0
3	B	28	0	26	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	5	0	0	1	0
4	B	10	0	0	0	0
5	A	77	0	0	1	0
5	B	78	0	0	2	0
All	All	6241	0	5839	62	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 5.

All (62) 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:156:THR:HG21	1:A:181:PRO:HA	1.42	1.00
1:B:277:GLN:HE22	1:B:288:ASP:H	1.27	0.82
1:B:154:GLN:HA	1:B:157:THR:HG23	1.72	0.71
1:A:153:SER:O	1:A:156:THR:HB	1.93	0.69
1:A:156:THR:HG21	1:A:181:PRO:CA	2.22	0.65
1:B:65:HIS:HE1	1:B:99:SER:H	1.47	0.62
1:A:190:SER:HB2	1:A:325:TRP:HB3	1.80	0.62
1:B:154:GLN:HA	1:B:157:THR:CG2	2.30	0.61
1:A:65:HIS:HE1	1:A:99:SER:H	1.49	0.58
1:B:348:ILE:HG23	1:B:365:ARG:HH11	1.69	0.56
1:A:102:ASN:HD22	1:A:102:ASN:C	2.14	0.56
1:B:65:HIS:CE1	1:B:99:SER:H	2.24	0.56
1:B:230:VAL:HG12	1:B:233:LYS:H	1.71	0.56
1:A:348:ILE:HG23	1:A:365:ARG:HH11	1.69	0.56
1:A:157:THR:HB	1:A:182:VAL:O	2.06	0.55
1:A:66:GLY:HA3	1:A:153:SER:HB3	1.88	0.55
1:B:66:GLY:HA3	1:B:153:SER:HB3	1.89	0.55
1:A:65:HIS:CE1	1:A:99:SER:H	2.25	0.55
1:B:277:GLN:NE2	1:B:288:ASP:H	2.01	0.55
1:B:188:CYS:HB2	1:B:325:TRP:O	2.06	0.54
1:A:63:LEU:HD23	1:A:150:VAL:HB	1.90	0.54
1:B:71:SER:HB2	1:B:98:ASN:HD21	1.73	0.52
1:A:156:THR:HG21	1:A:182:VAL:H	1.74	0.52
1:B:63:LEU:HD23	1:B:150:VAL:HB	1.91	0.52
1:B:102:ASN:C	1:B:102:ASN:HD22	2.18	0.51
1:B:232:LEU:O	1:B:233:LYS:HG2	2.12	0.50
1:A:156:THR:CG2	1:A:182:VAL:H	2.25	0.49
1:A:154:GLN:HA	1:A:157:THR:HG23	1.95	0.49
1:B:230:VAL:HG21	1:B:236:CYS:SG	2.54	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:181:PRO:HG3	1:B:318:VAL:HG13	1.95	0.47
1:A:181:PRO:HG3	1:A:318:VAL:HG13	1.98	0.46
1:A:305:PRO:HA	4:A:404:SO4:O3	2.15	0.46
1:B:255:ARG:HH21	1:B:258:VAL:HG21	1.81	0.45
1:B:78:LEU:HD11	2:D:1:NAG:HN2	1.81	0.45
1:A:188:CYS:HB2	1:A:325:TRP:O	2.17	0.45
1:B:157:THR:HB	1:B:182:VAL:O	2.15	0.45
1:A:247:ASN:HB2	1:A:352:GLU:HB2	1.98	0.45
1:B:350:GLU:HG2	5:B:524:HOH:O	2.17	0.44
1:B:361:ASP:O	1:B:365:ARG:HG2	2.18	0.44
1:A:78:LEU:HD11	2:C:1:NAG:HN2	1.83	0.44
1:A:154:GLN:HA	1:A:157:THR:CG2	2.48	0.44
1:A:361:ASP:O	1:A:365:ARG:HG2	2.18	0.44
1:A:87:LEU:HD23	1:A:371:ILE:HD13	2.00	0.43
1:B:11:GLU:CD	1:B:255:ARG:HH22	2.26	0.43
1:B:131:LEU:HD23	1:B:131:LEU:HA	1.92	0.43
1:A:124:ASP:OD1	1:A:274:HIS:HE1	2.01	0.43
1:A:139:LEU:CD1	1:A:172:ARG:HG2	2.48	0.43
1:A:82:SER:O	1:A:86:ILE:HG23	2.19	0.42
1:A:60:VAL:HG11	1:A:138:ILE:HG21	2.02	0.42
1:A:352:GLU:HG3	5:A:519:HOH:O	2.19	0.42
1:A:14:MET:O	1:A:262:HIS:HE1	2.03	0.41
1:B:33:GLU:CD	1:B:109:LYS:HD2	2.44	0.41
1:A:65:HIS:HE1	1:A:98:ASN:HA	1.85	0.41
1:B:139:LEU:CD1	1:B:172:ARG:HG2	2.50	0.41
1:B:82:SER:O	1:B:86:ILE:HG23	2.20	0.41
1:B:65:HIS:HE1	1:B:98:ASN:HA	1.86	0.41
1:B:248:GLU:OE1	1:B:253:MET:HE1	2.20	0.41
1:A:131:LEU:HD23	1:A:131:LEU:HA	1.91	0.40
1:A:232:LEU:HD12	1:A:232:LEU:HA	1.90	0.40
1:B:352:GLU:HG3	5:B:514:HOH:O	2.20	0.40
1:A:32:VAL:HG21	1:A:42:LEU:HD22	2.03	0.40
1:B:150:VAL:HG22	1:B:177:PHE:HB2	2.03	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	365/384 (95%)	345 (94%)	19 (5%)	1 (0%)	36	56
1	B	366/384 (95%)	345 (94%)	20 (6%)	1 (0%)	36	56
All	All	731/768 (95%)	690 (94%)	39 (5%)	2 (0%)	36	56

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	226	VAL
1	A	226	VAL

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	324/335 (97%)	295 (91%)	29 (9%)	9	18
1	B	325/335 (97%)	289 (89%)	36 (11%)	6	11
All	All	649/670 (97%)	584 (90%)	65 (10%)	7	15

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	VAL
1	A	17	SER
1	A	29	GLU
1	A	76	THR

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Mol	Chain	Res	Type
1	A	83	LEU
1	A	86	ILE
1	A	102	ASN
1	A	113	VAL
1	A	141	LYS
1	A	156	THR
1	A	157	THR
1	A	169	LEU
1	A	172	ARG
1	A	184	SER
1	A	190	SER
1	A	209	ASP
1	A	232	LEU
1	A	242	LEU
1	A	256	VAL
1	A	273	LEU
1	A	306	THR
1	A	312	MET
1	A	325	TRP
1	A	352	GLU
1	A	365	ARG
1	A	366	LEU
1	A	369	LYS
1	A	378	GLN
1	A	383	ASN
1	B	16	VAL
1	B	17	SER
1	B	29	GLU
1	B	76	THR
1	B	83	LEU
1	B	86	ILE
1	B	102	ASN
1	B	113	VAL
1	B	141	LYS
1	B	157	THR
1	B	169	LEU
1	B	172	ARG
1	B	184	SER
1	B	190	SER
1	B	209	ASP
1	B	224	THR
1	B	228	THR

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Mol	Chain	Res	Type
1	B	229	HIS
1	B	231	ILE
1	B	232	LEU
1	B	234	GLU
1	B	242	LEU
1	B	253	MET
1	B	255	ARG
1	B	256	VAL
1	B	257	ASP
1	B	273	LEU
1	B	306	THR
1	B	340	THR
1	B	352	GLU
1	B	365	ARG
1	B	366	LEU
1	B	369	LYS
1	B	378	GLN
1	B	383	ASN
1	B	384	LEU

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	13	ASN
1	A	47	HIS
1	A	65	HIS
1	A	102	ASN
1	A	144	GLN
1	A	271	ASN
1	A	285	GLN
1	A	298	HIS
1	A	372	ASN
1	A	383	ASN
1	B	13	ASN
1	B	47	HIS
1	B	65	HIS
1	B	73	ASN
1	B	102	ASN
1	B	144	GLN
1	B	271	ASN
1	B	277	GLN
1	B	285	GLN

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Mol	Chain	Res	Type
1	B	341	ASN
1	B	378	GLN
1	B	383	ASN

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 ⓘ

4 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	C	1	2,1	14,14,15	0.31	0	17,19,21	1.64	4 (23%)
2	NAG	C	2	2	14,14,15	0.36	0	17,19,21	1.41	3 (17%)
2	NAG	D	1	2,1	14,14,15	0.29	0	17,19,21	1.65	4 (23%)
2	NAG	D	2	2	14,14,15	0.35	0	17,19,21	1.41	4 (23%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	NAG	D	1	2,1	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	NAG	C1-C2-N2	3.96	116.67	110.43
2	C	1	NAG	C1-C2-N2	3.90	116.57	110.43
2	D	1	NAG	C1-O5-C5	3.54	116.93	112.19
2	C	1	NAG	C1-O5-C5	3.37	116.70	112.19
2	C	2	NAG	C1-O5-C5	3.23	116.52	112.19
2	C	2	NAG	C1-C2-N2	3.21	115.49	110.43
2	D	2	NAG	C1-C2-N2	3.14	115.39	110.43
2	D	2	NAG	C1-O5-C5	3.12	116.37	112.19
2	D	1	NAG	C2-N2-C7	2.56	126.33	122.90
2	D	2	NAG	C2-N2-C7	2.48	126.23	122.90
2	C	1	NAG	C2-N2-C7	2.43	126.16	122.90
2	C	1	NAG	O5-C1-C2	-2.37	107.63	111.29
2	C	2	NAG	C2-N2-C7	2.31	126.00	122.90
2	D	1	NAG	O5-C1-C2	-2.29	107.74	111.29
2	D	2	NAG	O5-C1-C2	-2.19	107.90	111.29

There are no chirality outliers.

All (6) torsion outliers are listed below:

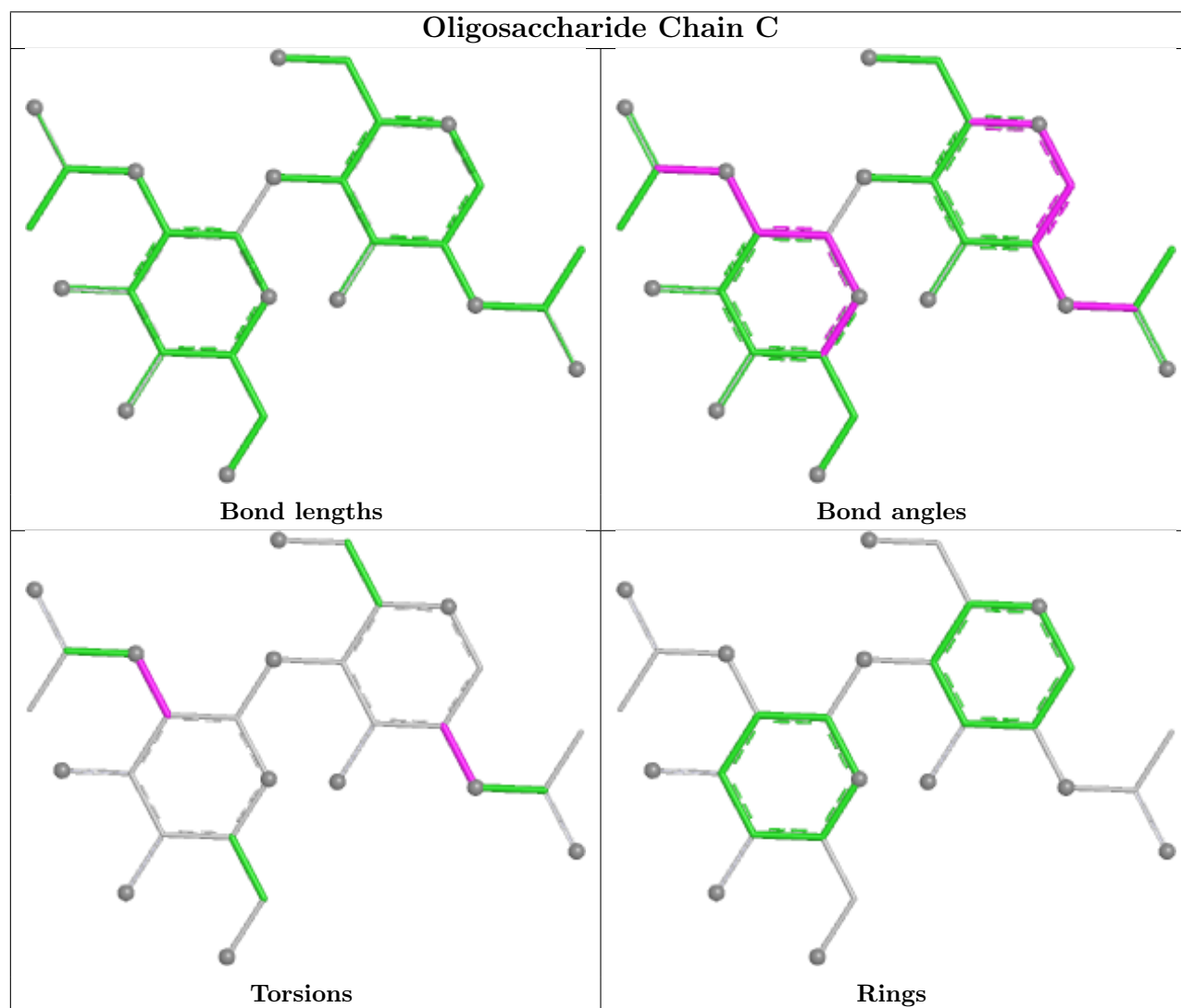
Mol	Chain	Res	Type	Atoms
2	C	1	NAG	C1-C2-N2-C7
2	C	2	NAG	C1-C2-N2-C7
2	D	1	NAG	C1-C2-N2-C7
2	D	2	NAG	C1-C2-N2-C7
2	C	2	NAG	C3-C2-N2-C7
2	D	2	NAG	C3-C2-N2-C7

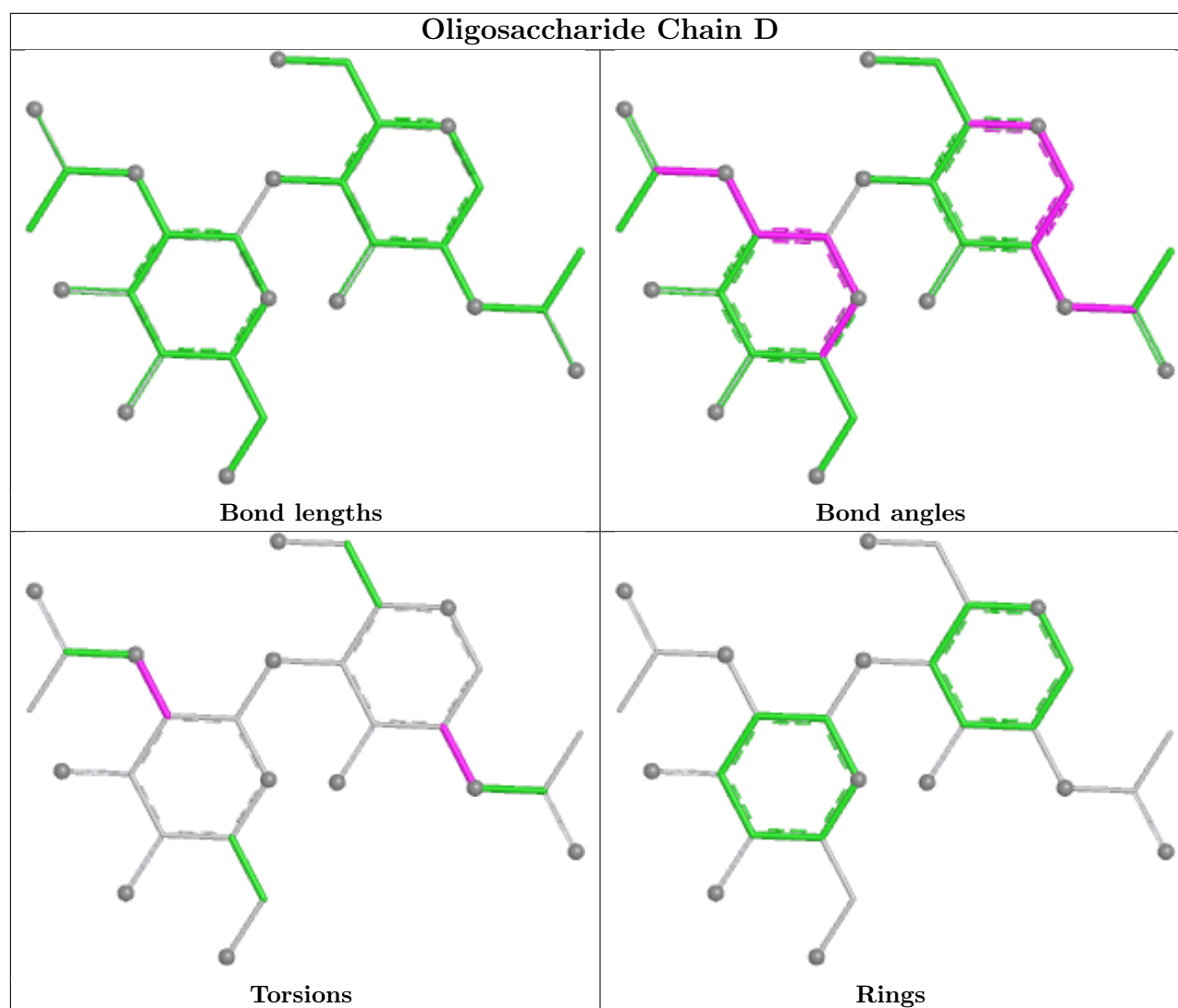
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1	NAG	1	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](#)

6 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	$\# Z > 2$
3	NAG	A	401	1	14,14,15	0.31	0	17,19,21	0.48	0
4	SO4	A	404	-	4,4,4	0.29	0	6,6,6	0.33	0
4	SO4	B	406	-	4,4,4	0.32	0	6,6,6	0.09	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	B	401	1	14,14,15	0.31	0	17,19,21	0.45	0
4	SO4	B	405	-	4,4,4	0.17	0	6,6,6	0.14	0
3	NAG	B	402	1	14,14,15	0.44	0	17,19,21	0.83	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	B	402	1	-	0/6/23/26	0/1/1/1
3	NAG	A	401	1	-	0/6/23/26	0/1/1/1
3	NAG	B	401	1	-	0/6/23/26	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(°)
3	B	402	NAG	O5-C1-C2	2.05	114.47	111.29

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	404	SO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	369/384 (96%)	0.10	8 (2%) 62 57	34, 54, 82, 102	0
1	B	370/384 (96%)	0.22	22 (5%) 28 23	32, 55, 94, 134	0
All	All	739/768 (96%)	0.16	30 (4%) 41 36	32, 55, 89, 134	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	384	LEU	5.5
1	B	325	TRP	4.0
1	A	384	LEU	3.5
1	B	13	ASN	3.2
1	A	227	CYS	3.1
1	A	226	VAL	3.1
1	A	225	HIS	2.9
1	A	48	GLY	2.8
1	B	79	ALA	2.7
1	B	249	ARG	2.6
1	B	225	HIS	2.6
1	B	12	THR	2.5
1	A	205	ASP	2.5
1	B	246	PHE	2.5
1	B	224	THR	2.5
1	B	248	GLU	2.4
1	B	57	PRO	2.4
1	B	253	MET	2.3
1	B	232	LEU	2.3
1	B	192	MET	2.3
1	A	57	PRO	2.3
1	B	110	THR	2.3
1	B	350	GLU	2.2
1	B	257	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	325	TRP	2.2
1	B	226	VAL	2.2
1	B	231	ILE	2.1
1	B	229	HIS	2.1
1	B	383	ASN	2.0
1	B	9	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

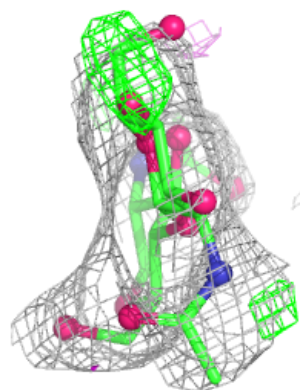
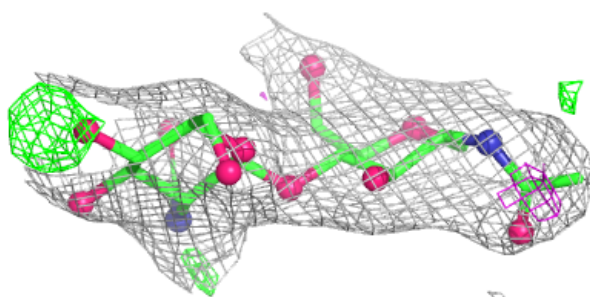
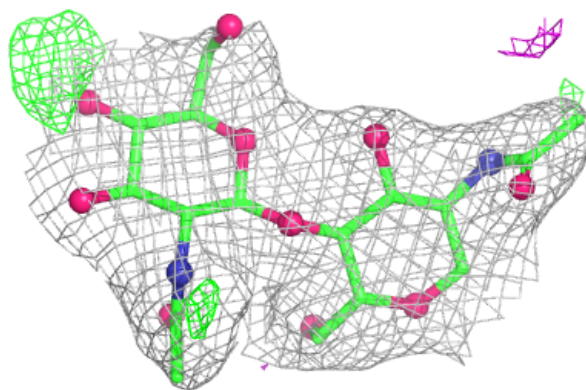
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	C	2	14/15	0.80	0.16	86,91,97,99	0
2	NAG	D	2	14/15	0.80	0.16	103,108,111,117	0
2	NAG	D	1	14/15	0.89	0.12	85,88,93,98	0
2	NAG	C	1	14/15	0.93	0.11	61,67,72,81	0

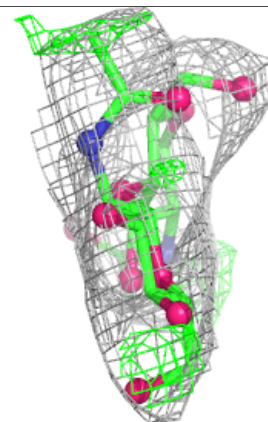
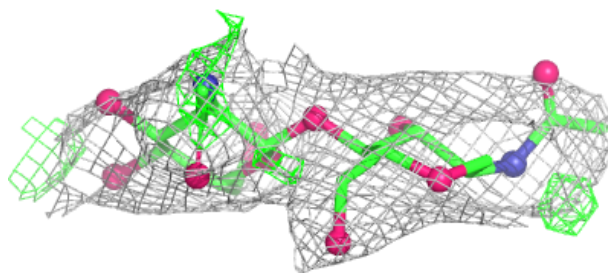
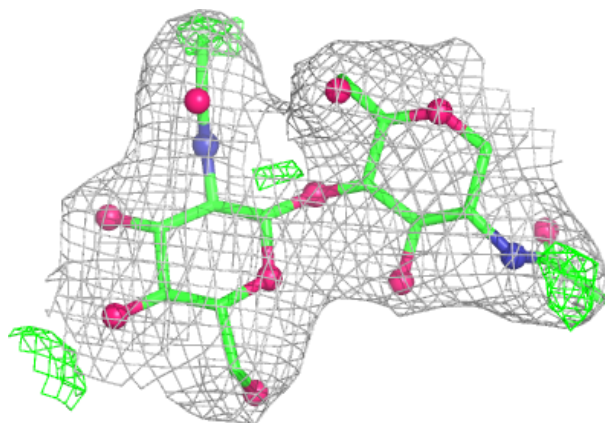
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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 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 [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
3	NAG	B	402	14/15	0.25	0.19	104,108,110,111	0
3	NAG	B	401	14/15	0.83	0.10	68,81,95,98	0
3	NAG	A	401	14/15	0.86	0.11	72,85,95,98	0
4	SO4	B	405	5/5	0.87	0.10	106,107,107,108	0
4	SO4	B	406	5/5	0.88	0.07	96,97,98,98	0
4	SO4	A	404	5/5	0.97	0.06	58,60,61,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.