



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:40 PM UTC

PDB ID : 4UZ6 / pdb_00004uz6
Title : STRUCTURE OF THE WNT DEACYLASE NOTUM - CRYSTAL FORM
V - SOS COMPLEX - 1.9A
Authors : Zebisch, M.; Jones, E.Y.
Deposited on : 2014-09-04
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

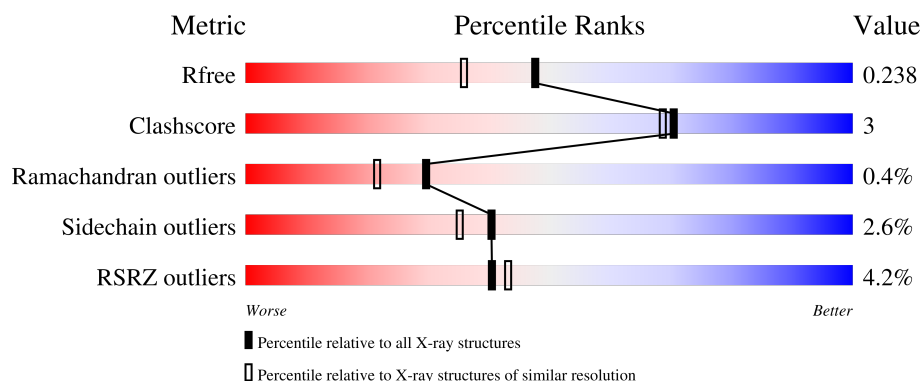
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	383	3% 80% 11% 8%
1	B	383	5% 84% 8% 7%
2	C	2	100%
2	D	2	100%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6042 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 PROTEIN NOTUM HOMOLOG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	351	Total	C	N	O	S	0	2	0
			2829	1786	511	514	18			
1	B	355	Total	C	N	O	S	0	3	0
			2867	1809	519	521	18			

There are 26 discrepancies between the modelled and reference sequences:

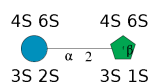
Chain	Residue	Modelled	Actual	Comment	Reference
A	78	GLU	-	expression tag	UNP Q6P988
A	79	THR	-	expression tag	UNP Q6P988
A	80	GLY	-	expression tag	UNP Q6P988
A	452	GLY	-	expression tag	UNP Q6P988
A	453	THR	-	expression tag	UNP Q6P988
A	454	LYS	-	expression tag	UNP Q6P988
A	455	HIS	-	expression tag	UNP Q6P988
A	456	HIS	-	expression tag	UNP Q6P988
A	457	HIS	-	expression tag	UNP Q6P988
A	458	HIS	-	expression tag	UNP Q6P988
A	459	HIS	-	expression tag	UNP Q6P988
A	460	HIS	-	expression tag	UNP Q6P988
A	330	SER	CYS	engineered mutation	UNP Q6P988
B	78	GLU	-	expression tag	UNP Q6P988
B	79	THR	-	expression tag	UNP Q6P988
B	80	GLY	-	expression tag	UNP Q6P988
B	452	GLY	-	expression tag	UNP Q6P988
B	453	THR	-	expression tag	UNP Q6P988
B	454	LYS	-	expression tag	UNP Q6P988
B	455	HIS	-	expression tag	UNP Q6P988
B	456	HIS	-	expression tag	UNP Q6P988
B	457	HIS	-	expression tag	UNP Q6P988
B	458	HIS	-	expression tag	UNP Q6P988
B	459	HIS	-	expression tag	UNP Q6P988
B	460	HIS	-	expression tag	UNP Q6P988

Continued on next page...

Continued from previous page...

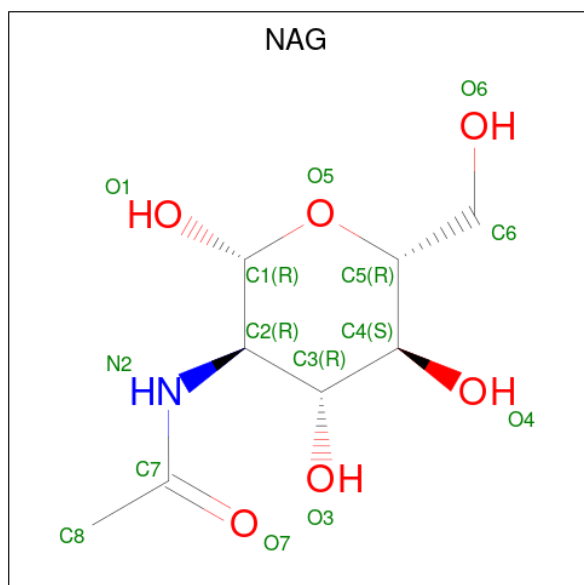
Chain	Residue	Modelled	Actual	Comment	Reference
B	330	SER	CYS	engineered mutation	UNP Q6P988

- Molecule 2 is an oligosaccharide called 1,3,4,6-tetra-O-sulfo-beta-D-fructofuranose-(2-1)-2,3,4,6-tetra-O-sulfonato-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	O	S	0	0	0
			55	12	35	8			
2	D	2	Total	C	O	S	0	0	0
			55	12	35	8			

- 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		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Cl 1	0	0
4	B	1	Total 1	Cl 1	0	0

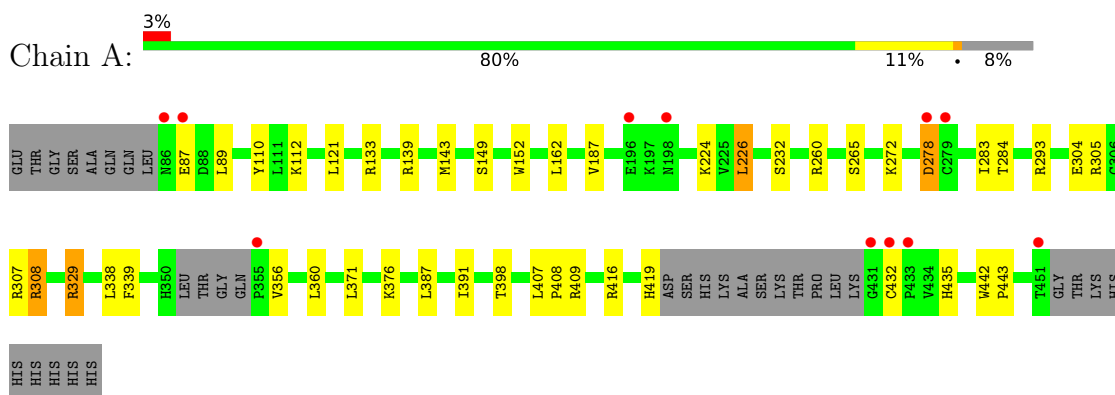
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	121	Total 122	O 122	0	1
5	B	83	Total 84	O 84	0	1

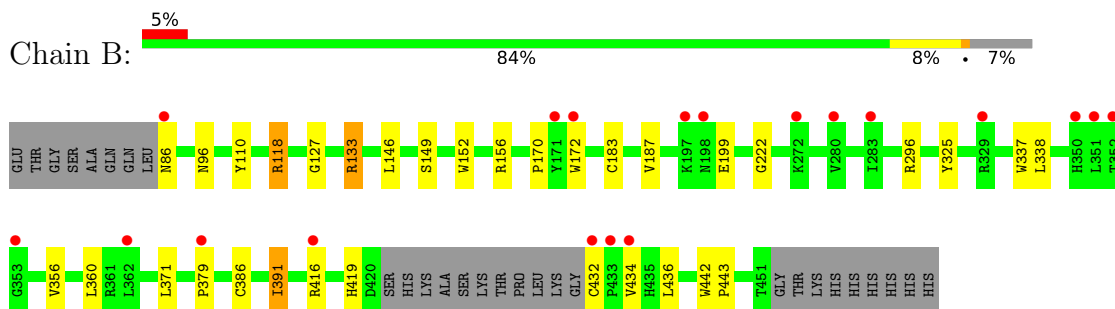
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

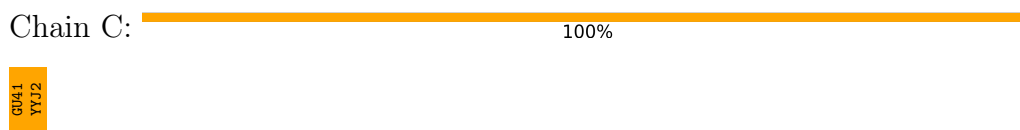
• Molecule 1: PROTEIN NOTUM HOMOLOG



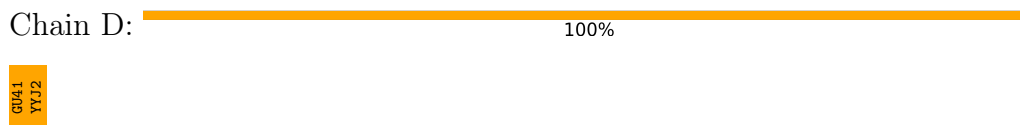
• Molecule 1: PROTEIN NOTUM HOMOLOG



• Molecule 2: 1,3,4,6-tetra-O-sulfo-beta-D-fructofuranose-(2-1)-2,3,4,6-tetra-O-sulfonato-alpha-D-glucopyranose



• Molecule 2: 1,3,4,6-tetra-O-sulfo-beta-D-fructofuranose-(2-1)-2,3,4,6-tetra-O-sulfonato-alpha-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	66.45Å 69.95Å 195.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	97.90 – 1.90 97.90 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.9 (97.90-1.90) 98.9 (97.90-1.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.195 , 0.235 0.205 , 0.238	Depositor DCC
R_{free} test set	1038 reflections (1.44%)	wwPDB-VP
Wilson B-factor (Å ²)	29.9	Xtriage
Anisotropy	0.180	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 35.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.032 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6042	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.66% 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: YYJ, GU4, CL, 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	1.00	0/2911	1.01	5/3955 (0.1%)
1	B	0.99	1/2953 (0.0%)	0.99	5/4015 (0.1%)
All	All	0.99	1/5864 (0.0%)	1.00	10/7970 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	118	ARG	CA-CB	-5.18	1.46	1.53

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	260	ARG	CA-C-N	-7.54	115.80	121.61
1	A	260	ARG	C-N-CA	-7.54	115.80	121.61
1	B	432	CYS	CA-C-N	-7.03	113.07	120.03
1	B	432	CYS	C-N-CA	-7.03	113.07	120.03
1	A	278	ASP	N-CA-C	-6.40	102.08	110.53
1	B	172	TRP	N-CA-C	5.22	119.20	112.41
1	B	325	TYR	CA-C-N	-5.21	114.25	119.56
1	B	325	TYR	C-N-CA	-5.21	114.25	119.56
1	A	407	LEU	CA-C-N	-5.06	113.72	119.28
1	A	407	LEU	C-N-CA	-5.06	113.72	119.28

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	2829	0	2726	25	0
1	B	2867	0	2770	15	0
2	C	55	0	6	3	0
2	D	55	0	6	3	0
3	A	14	0	13	0	0
3	B	14	0	13	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	122	0	0	1	0
5	B	84	0	0	0	0
All	All	6042	0	5534	39	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 3.

All (39) 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:283:ILE:HD12	1:A:284:THR:HG23	1.59	0.83
1:B:356:VAL:HG13	1:B:360:LEU:HD22	1.60	0.83
1:B:419:HIS:NE2	2:D:1:GU4:O27	2.25	0.69
1:A:283:ILE:CD1	1:A:284:THR:HG23	2.26	0.65
1:A:139:ARG:HA	1:A:143:MET:HE3	1.78	0.65
1:A:416:ARG:NH2	2:C:2:YYJ:O3S3	2.30	0.65
1:A:409:ARG:HH11	1:A:409:ARG:HG2	1.62	0.64
1:A:338:LEU:HA	1:A:371:LEU:HD23	1.78	0.63
1:A:87:GLU:OE2	1:A:112:LYS:NZ	2.35	0.59
1:B:118:ARG:HD2	1:B:222:GLY:O	2.05	0.56
1:A:409:ARG:HG2	1:A:409:ARG:NH1	2.21	0.56
1:A:232:SER:HA	1:A:265:SER:O	2.05	0.56
1:A:304:GLU:OE2	1:A:308:ARG:HD3	2.06	0.55
1:B:416[B]:ARG:NH2	2:D:2:YYJ:O3S3	2.40	0.54
1:A:89:LEU:HB3	1:A:110:TYR:HB3	1.91	0.53
1:A:398:THR:HG22	1:A:408:PRO:HG2	1.91	0.53
1:B:338:LEU:HA	1:B:371:LEU:HD23	1.90	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:VAL:HG23	1:A:360:LEU:HD23	1.91	0.52
1:A:419:HIS:CE1	2:C:1:GU4:O27	2.63	0.51
1:A:416:ARG:NH2	2:C:2:YYJ:O1S1	2.39	0.51
1:B:419:HIS:HD2	2:D:1:GU4:O11	1.94	0.50
1:A:293:ARG:NH2	1:B:170:PRO:O	2.48	0.47
1:B:442:TRP:CD2	1:B:443:PRO:HD2	2.49	0.47
1:A:339:PHE:O	1:A:387:LEU:HA	2.15	0.47
1:B:133:ARG:CZ	1:B:199:GLU:HG3	2.45	0.47
1:A:435:HIS:NE2	5:A:2115:HOH:O	2.36	0.46
1:A:226:LEU:C	1:A:226:LEU:HD23	2.42	0.45
1:A:304:GLU:HG2	1:A:307:ARG:NH1	2.32	0.44
1:B:110:TYR:CD2	1:B:156:ARG:HG2	2.53	0.44
1:B:96:ASN:OD1	1:B:96:ASN:C	2.60	0.43
1:A:121:LEU:HD22	1:A:162:LEU:CD2	2.49	0.43
1:B:337:TRP:CE3	1:B:386:CYS:HB2	2.54	0.43
1:B:379:PRO:O	1:B:434:VAL:HG23	2.20	0.42
1:B:149:SER:HA	1:B:152:TRP:CE2	2.55	0.41
1:A:149:SER:HA	1:A:152:TRP:CE2	2.56	0.41
1:A:442:TRP:CD2	1:A:443:PRO:HD2	2.56	0.40
1:B:146:LEU:O	1:B:183:CYS:HA	2.21	0.40
1:A:121:LEU:HD22	1:A:162:LEU:HD21	2.03	0.40
1:A:305:ARG:CZ	1:A:329:ARG:HD3	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	347/383 (91%)	338 (97%)	8 (2%)	1 (0%)	36	29
1	B	354/383 (92%)	343 (97%)	9 (2%)	2 (1%)	21	13
All	All	701/766 (92%)	681 (97%)	17 (2%)	3 (0%)	30	22

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	391	ILE
1	A	391	ILE
1	B	127	GLY

5.3.2 Protein sidechains [i](#)

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	308/333 (92%)	298 (97%)	10 (3%)	34	27
1	B	313/333 (94%)	307 (98%)	6 (2%)	50	47
All	All	621/666 (93%)	605 (97%)	16 (3%)	40	35

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	133	ARG
1	A	187	VAL
1	A	224	LYS
1	A	226	LEU
1	A	272	LYS
1	A	278	ASP
1	A	308	ARG
1	A	329	ARG
1	A	376	LYS
1	A	432	CYS
1	B	86	ASN
1	B	133	ARG
1	B	187	VAL
1	B	296	ARG
1	B	391	ILE
1	B	436	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	86	ASN
1	A	135	ASN
1	A	209	GLN
1	A	258	GLN
1	A	350	HIS
1	A	419	HIS
1	B	299	ASN
1	B	373	HIS
1	B	389	HIS
1	B	401	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 ⓘ

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	GU4	C	1	2	27,27,28	1.65	5 (18%)	32,43,45	1.26	3 (9%)
2	YYJ	C	2	2	27,28,28	1.83	5 (18%)	33,46,46	1.35	3 (9%)
2	GU4	D	1	2	27,27,28	1.81	6 (22%)	32,43,45	1.38	5 (15%)
2	YYJ	D	2	2	27,28,28	1.85	6 (22%)	33,46,46	1.64	8 (24%)

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	GU4	C	1	2	-	1/21/38/41	0/1/1/1
2	YYJ	C	2	2	-	3/23/42/42	0/1/1/1
2	GU4	D	1	2	-	3/21/38/41	0/1/1/1
2	YYJ	D	2	2	-	2/23/42/42	0/1/1/1

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	YYJ	O3S4-S4	4.40	1.64	1.45
2	D	1	GU4	O23-S6	4.38	1.64	1.45
2	C	1	GU4	O26-S4	4.36	1.64	1.45
2	C	2	YYJ	O3S6-S6	4.28	1.63	1.45
2	D	2	YYJ	O3S3-S3	4.22	1.63	1.45
2	C	2	YYJ	O3S3-S3	4.19	1.63	1.45
2	C	2	YYJ	O3S1-S1	4.19	1.63	1.45
2	C	1	GU4	O27-S3	4.15	1.63	1.45
2	D	1	GU4	O27-S3	3.95	1.62	1.45
2	D	1	GU4	O26-S4	3.93	1.62	1.45
2	C	1	GU4	O23-S6	3.67	1.61	1.45
2	D	2	YYJ	O3S6-S6	3.64	1.61	1.45
2	D	1	GU4	O2-C2	-3.56	1.42	1.47
2	C	2	YYJ	O3S4-S4	3.54	1.60	1.45
2	D	2	YYJ	O3S1-S1	3.42	1.60	1.45
2	C	2	YYJ	O3-C3	-3.27	1.41	1.47
2	D	2	YYJ	O3-C3	-3.13	1.41	1.47
2	C	1	GU4	O2-C2	-2.50	1.43	1.47
2	D	1	GU4	O5-C1	-2.15	1.40	1.43
2	D	2	YYJ	O3-S3	-2.13	1.50	1.57
2	D	1	GU4	O4-C4	-2.06	1.41	1.46
2	C	1	GU4	O10-S2	2.05	1.63	1.50

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	YYJ	C3-O3-S3	4.58	123.35	117.69
2	D	1	GU4	C1-O5-C5	-3.22	107.88	112.19
2	D	2	YYJ	O1S3-S3-O2S3	2.99	119.02	108.56
2	D	2	YYJ	O6-S6-O3S6	2.97	116.00	106.92
2	D	1	GU4	O6-C6-C5	-2.87	102.46	107.57
2	D	2	YYJ	O1-S1-O3S1	-2.84	98.23	106.92
2	C	1	GU4	O2-C2-C3	2.82	109.77	106.65
2	D	1	GU4	C6-C5-C4	-2.75	106.72	113.35

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	YYJ	O1S1-S1-O1	2.73	112.64	106.37
2	D	2	YYJ	O3S3-S3-O2S3	-2.73	101.72	112.24
2	C	1	GU4	C1-C2-C3	2.70	113.44	109.40
2	D	2	YYJ	O4-C4-C3	2.43	114.20	108.91
2	C	1	GU4	O6-S6-O22	2.42	114.32	106.92
2	C	2	YYJ	O5-C5-C4	2.36	107.37	103.54
2	D	1	GU4	O10-S2-O2	-2.35	100.98	106.37
2	D	2	YYJ	O2-C2-O5	2.32	113.78	109.33
2	D	1	GU4	O6-S6-O22	2.23	113.72	106.92
2	D	2	YYJ	O3-C3-C4	2.18	115.29	109.27
2	D	2	YYJ	O1S1-S1-O3S1	2.00	115.57	108.56

There are no chirality outliers.

All (9) torsion outliers are listed below:

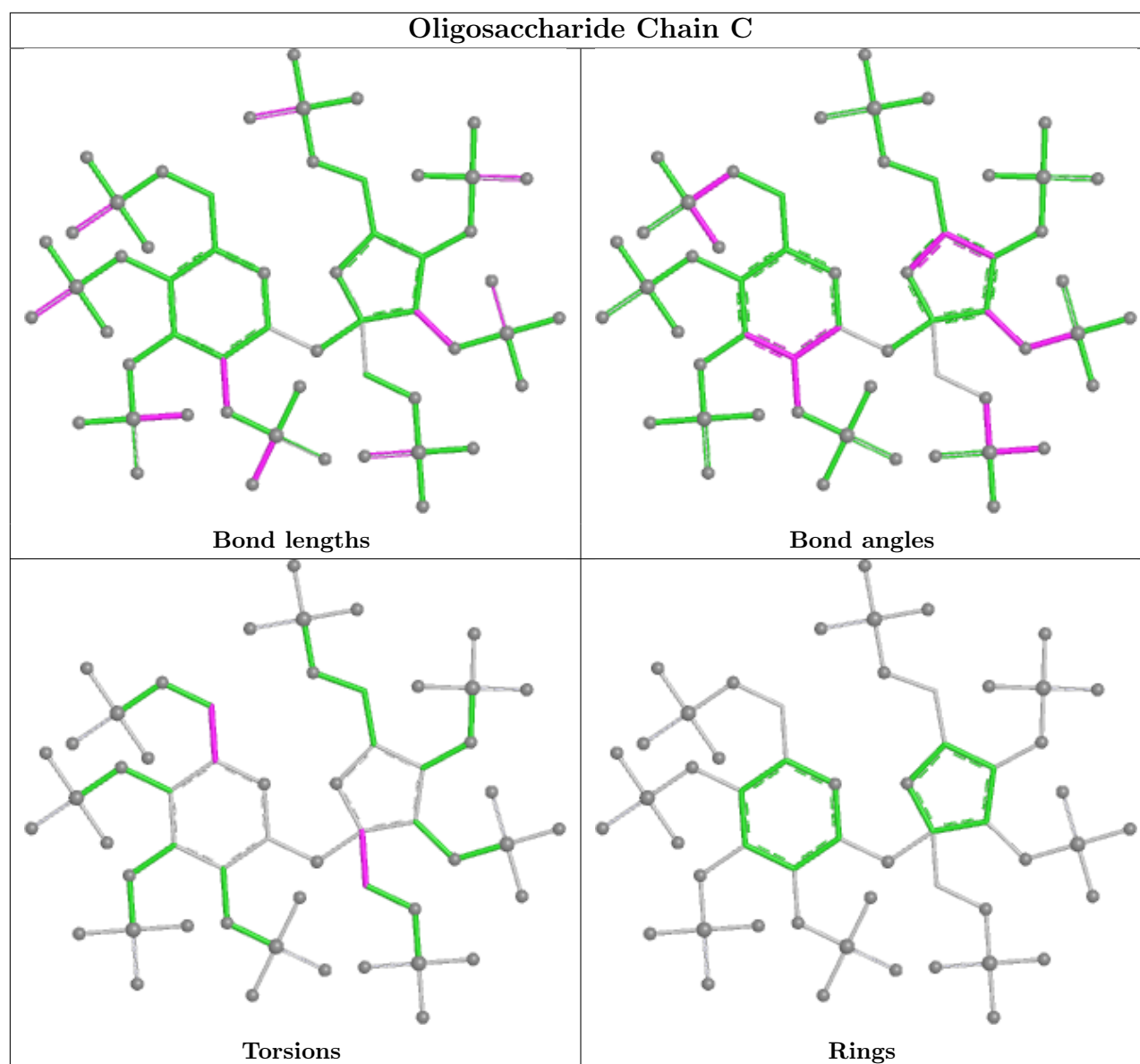
Mol	Chain	Res	Type	Atoms
2	C	2	YYJ	O1-C1-C2-C3
2	C	2	YYJ	O1-C1-C2-O2
2	C	2	YYJ	O1-C1-C2-O5
2	D	1	GU4	C4-O4-S4-O26
2	D	1	GU4	C4-O4-S4-O24
2	D	2	YYJ	C4-C5-C6-O6
2	D	2	YYJ	O5-C5-C6-O6
2	D	1	GU4	C4-O4-S4-O25
2	C	1	GU4	C4-C5-C6-O6

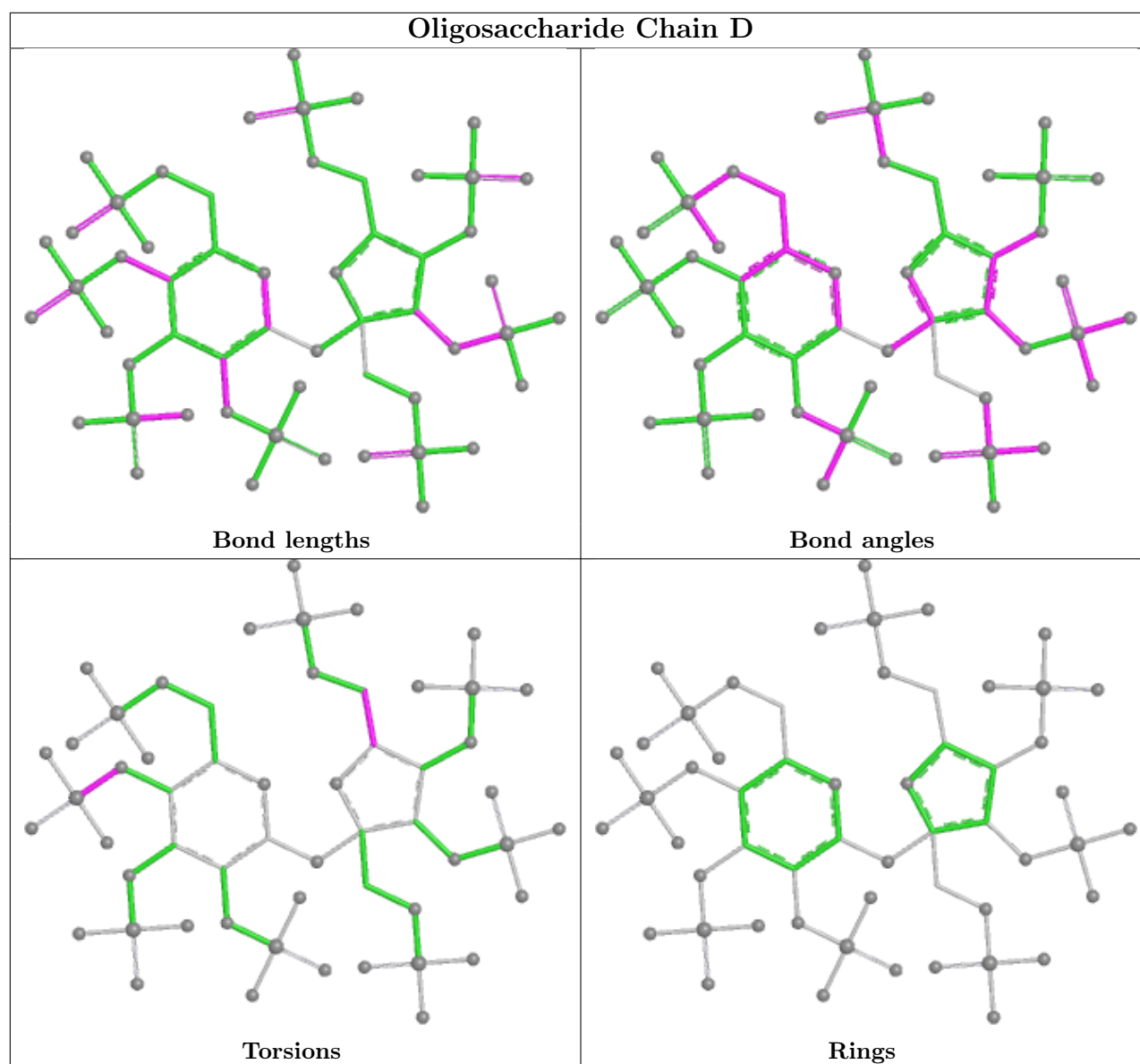
There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	2	YYJ	1	0
2	D	1	GU4	2	0
2	C	2	YYJ	2	0
2	C	1	GU4	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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
3	NAG	B	1452	1	14,14,15	0.64	0	17,19,21	1.47	5 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	A	1452	1	14,14,15	0.87	1 (7%)	17,19,21	1.48	3 (17%)

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	1452	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1452	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1452	NAG	O5-C1	-2.09	1.40	1.43

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1452	NAG	O5-C1-C2	-3.29	106.20	111.29
3	A	1452	NAG	C1-C2-N2	2.83	114.90	110.43
3	B	1452	NAG	C3-C4-C5	-2.66	105.42	110.23
3	B	1452	NAG	O5-C5-C4	-2.44	104.90	110.83
3	B	1452	NAG	C8-C7-N2	2.36	120.03	116.12
3	B	1452	NAG	O5-C5-C6	2.13	111.80	107.66
3	A	1452	NAG	O7-C7-N2	2.06	125.63	121.98
3	B	1452	NAG	O7-C7-C8	-2.06	118.39	122.05

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	351/383 (91%)	0.31	11 (3%) 51 55	16, 33, 56, 106	2 (0%)
1	B	355/383 (92%)	0.50	19 (5%) 31 33	15, 36, 65, 101	3 (0%)
All	All	706/766 (92%)	0.41	30 (4%) 40 43	15, 35, 59, 106	5 (0%)

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	433	PRO	4.8
1	B	434	VAL	4.2
1	A	431	GLY	4.0
1	B	432	CYS	3.9
1	B	198	ASN	3.2
1	B	353	GLY	3.0
1	B	352	THR	3.0
1	B	351	LEU	2.9
1	B	362	LEU	2.8
1	A	279	CYS	2.7
1	B	416[A]	ARG	2.7
1	B	329	ARG	2.7
1	A	87	GLU	2.7
1	B	171	TYR	2.6
1	B	86	ASN	2.6
1	B	350	HIS	2.6
1	A	86	ASN	2.6
1	A	433	PRO	2.5
1	B	272	LYS	2.5
1	A	196	GLU	2.5
1	B	197	LYS	2.4
1	A	278	ASP	2.4
1	A	432	CYS	2.3
1	A	355	PRO	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	283	ILE	2.2
1	B	379	PRO	2.2
1	B	172	TRP	2.1
1	A	198	ASN	2.1
1	B	280	VAL	2.1
1	A	451	THR	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](#)

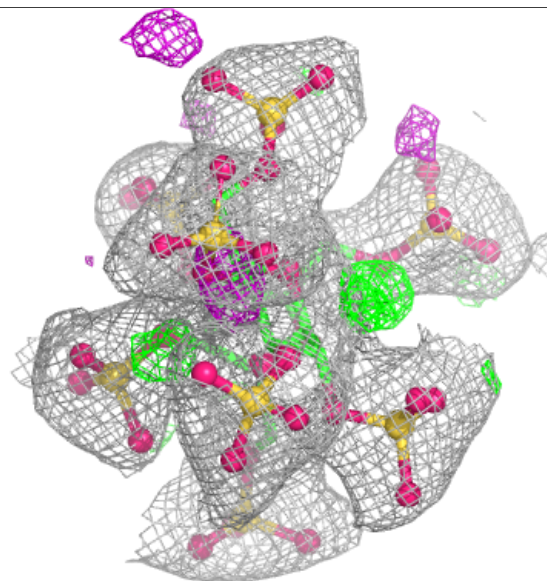
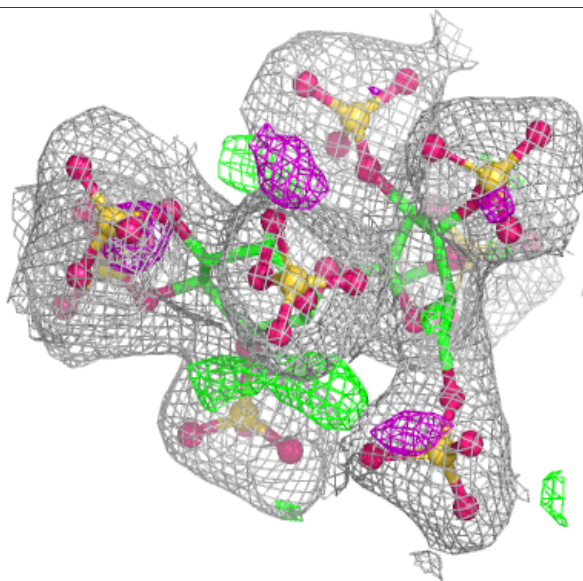
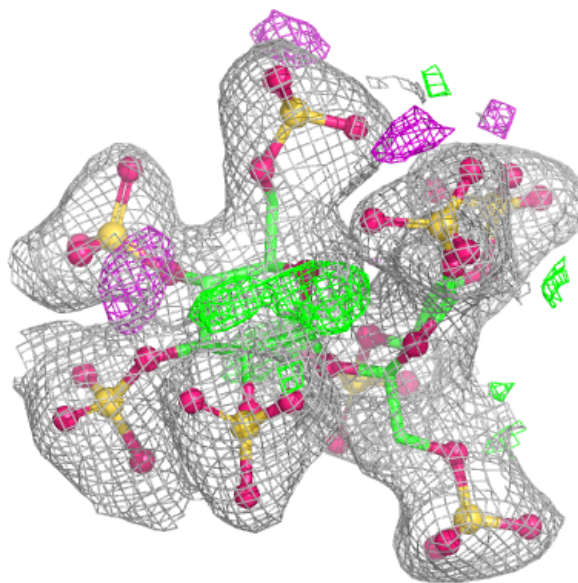
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

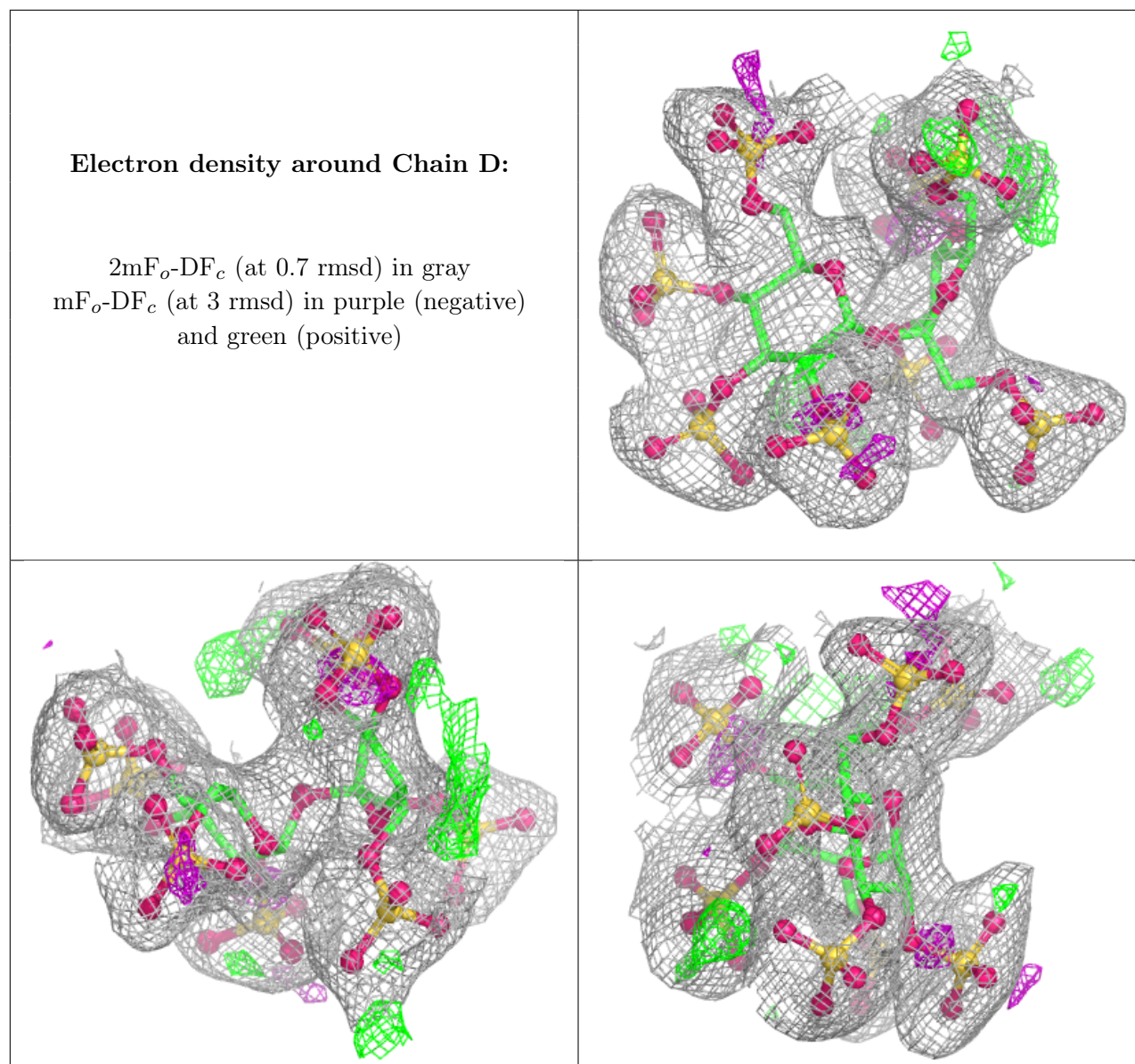
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GU4	C	1	27/28	0.87	0.10	46,58,67,72	0
2	GU4	D	1	27/28	0.89	0.10	46,58,68,83	0
2	YYJ	D	2	28/28	0.89	0.11	39,57,73,76	0
2	YYJ	C	2	28/28	0.93	0.10	36,50,69,72	0

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)





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(Å ²)	Q<0.9
3	NAG	B	1452	14/15	0.84	0.11	49,61,66,67	0
4	CL	B	1454	1/1	0.86	0.20	75,75,75,75	0
3	NAG	A	1452	14/15	0.88	0.10	40,46,52,52	0
4	CL	A	1454	1/1	0.90	0.22	60,60,60,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.