



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 02:10 PM UTC

PDB ID : 4ZNO / pdb_00004zno
Title : Crystal structure of Dln1 complexed with sucrose
Authors : Jia, N.; Jiang, Y.L.; Cheng, W.; Wang, H.W.; Zhou, C.Z.; Chen, Y.
Deposited on : 2015-05-05
Resolution : 1.86 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

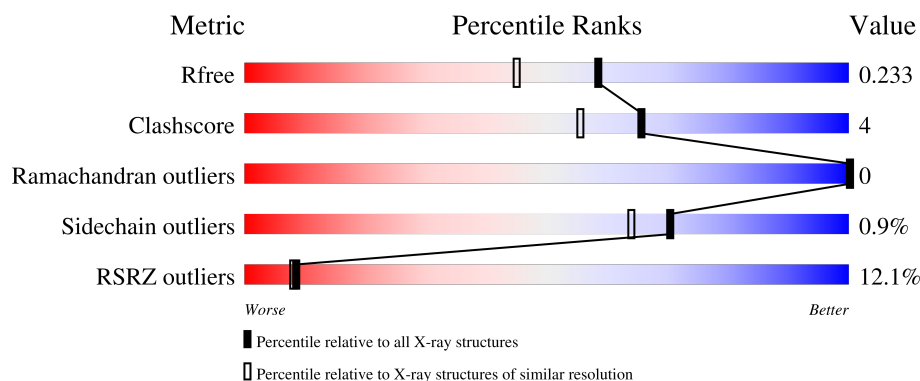
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.86 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	335	11% 89% 6% 5%
1	B	335	12% 85% 10% 5%
2	C	2	100%
2	D	2	100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5625 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 Natterin-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	0	4	0
			2450	1555	400	485	10			
1	B	318	Total	C	N	O	S	0	3	0
			2446	1552	400	484	10			

There are 40 discrepancies between the modelled and reference sequences:

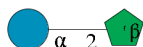
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP Q5CZR5
A	-18	GLY	-	expression tag	UNP Q5CZR5
A	-17	SER	-	expression tag	UNP Q5CZR5
A	-16	SER	-	expression tag	UNP Q5CZR5
A	-15	HIS	-	expression tag	UNP Q5CZR5
A	-14	HIS	-	expression tag	UNP Q5CZR5
A	-13	HIS	-	expression tag	UNP Q5CZR5
A	-12	HIS	-	expression tag	UNP Q5CZR5
A	-11	HIS	-	expression tag	UNP Q5CZR5
A	-10	HIS	-	expression tag	UNP Q5CZR5
A	-9	SER	-	expression tag	UNP Q5CZR5
A	-8	SER	-	expression tag	UNP Q5CZR5
A	-7	GLY	-	expression tag	UNP Q5CZR5
A	-6	LEU	-	expression tag	UNP Q5CZR5
A	-5	VAL	-	expression tag	UNP Q5CZR5
A	-4	PRO	-	expression tag	UNP Q5CZR5
A	-3	ARG	-	expression tag	UNP Q5CZR5
A	-2	GLY	-	expression tag	UNP Q5CZR5
A	-1	SER	-	expression tag	UNP Q5CZR5
A	0	HIS	-	expression tag	UNP Q5CZR5
B	-19	MET	-	expression tag	UNP Q5CZR5
B	-18	GLY	-	expression tag	UNP Q5CZR5
B	-17	SER	-	expression tag	UNP Q5CZR5
B	-16	SER	-	expression tag	UNP Q5CZR5
B	-15	HIS	-	expression tag	UNP Q5CZR5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP Q5CZR5
B	-13	HIS	-	expression tag	UNP Q5CZR5
B	-12	HIS	-	expression tag	UNP Q5CZR5
B	-11	HIS	-	expression tag	UNP Q5CZR5
B	-10	HIS	-	expression tag	UNP Q5CZR5
B	-9	SER	-	expression tag	UNP Q5CZR5
B	-8	SER	-	expression tag	UNP Q5CZR5
B	-7	GLY	-	expression tag	UNP Q5CZR5
B	-6	LEU	-	expression tag	UNP Q5CZR5
B	-5	VAL	-	expression tag	UNP Q5CZR5
B	-4	PRO	-	expression tag	UNP Q5CZR5
B	-3	ARG	-	expression tag	UNP Q5CZR5
B	-2	GLY	-	expression tag	UNP Q5CZR5
B	-1	SER	-	expression tag	UNP Q5CZR5
B	0	HIS	-	expression tag	UNP Q5CZR5

- Molecule 2 is an oligosaccharide called beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	C	2	Total	C	O	0	0	0
			23	12	11			
2	D	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

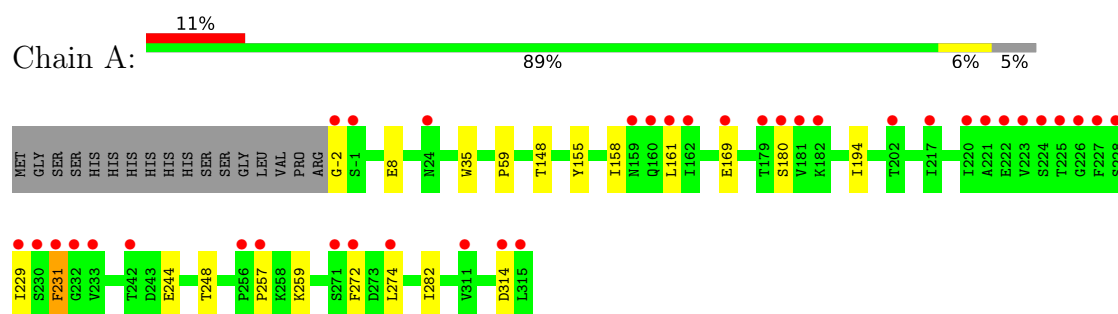
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	333	Total	O	0	0
			333	333		
5	B	333	Total	O	0	0
			333	333		

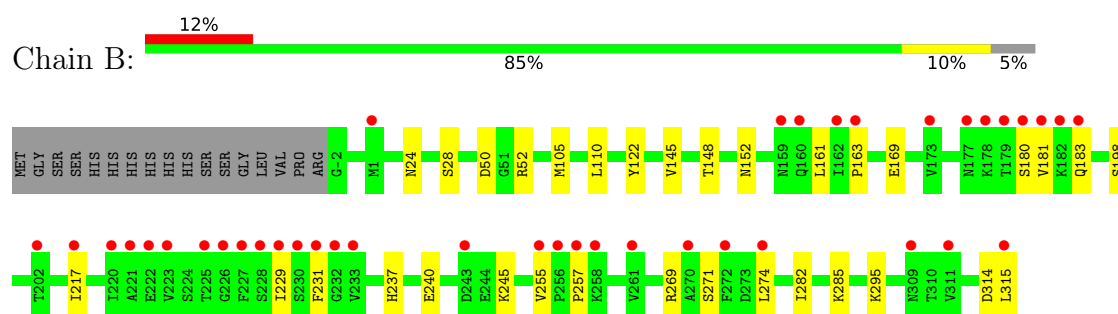
3 Residue-property plots

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.

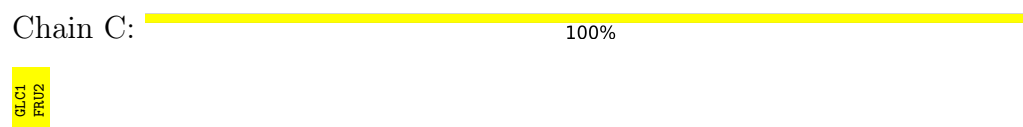
- Molecule 1: Natterin-like protein



- Molecule 1: Natterin-like protein



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose



- Molecule 2: beta-D-fructofuranose-(2-1)-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	57.64Å 95.17Å 148.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.66 – 1.86 35.66 – 1.86	Depositor EDS
% Data completeness (in resolution range)	97.6 (35.66-1.86) 97.6 (35.66-1.86)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 1.87Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.189 , 0.225 0.197 , 0.233	Depositor DCC
R_{free} test set	3431 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	23.5	Xtriage
Anisotropy	0.470	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5625	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.89% 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: FRU, GLC, CL, EPE

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	0.69	0/2515	0.82	0/3406
1	B	0.67	0/2508	0.81	1/3396 (0.0%)
All	All	0.68	0/5023	0.81	1/6802 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	180	SER	N-CA-C	-6.96	101.88	110.65

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	2450	0	2417	17	0
1	B	2446	0	2410	21	0
2	C	23	0	21	0	0
2	D	23	0	21	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	B	15	0	18	0	0
5	A	333	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	333	0	0	6	0
All	All	5625	0	4887	37	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 4.

All (37) 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:161:LEU:HD23	1:A:229:ILE:CD1	2.15	0.77
1:B:169:GLU:HG3	5:B:772:HOH:O	2.00	0.60
1:B:183:GLN:HG2	5:B:752:HOH:O	2.02	0.60
1:A:229:ILE:HG23	1:A:272:PHE:CE1	2.37	0.59
1:B:24[B]:ASN:CG	5:B:518:HOH:O	2.45	0.59
1:B:163:PRO:HB3	1:B:229:ILE:HD11	1.88	0.56
1:B:198:SER:HB2	1:B:240:GLU:OE1	2.08	0.54
1:B:152[A]:ASN:ND2	5:B:505:HOH:O	2.42	0.53
1:B:145:VAL:HG11	1:B:148:THR:HG23	1.92	0.52
1:A:161:LEU:HD21	5:A:534:HOH:O	2.11	0.51
1:B:181:VAL:N	1:B:257:PRO:HB3	2.25	0.50
1:B:314:ASP:O	1:B:315:LEU:HB2	2.11	0.50
1:B:269:ARG:HD3	5:B:764:HOH:O	2.13	0.49
1:A:248:THR:OG1	1:B:285:LYS:HE3	2.12	0.49
1:A:148[B]:THR:HG22	1:A:282:ILE:HG12	1.95	0.48
1:A:161:LEU:HB3	1:A:229:ILE:HD12	1.96	0.47
1:B:161:LEU:HD22	1:B:274:LEU:HD23	1.97	0.46
1:A:180:SER:C	1:A:257:PRO:HB3	2.40	0.46
1:A:8:GLU:HG3	5:A:744:HOH:O	2.15	0.46
1:B:50:ASP:OD2	1:B:52:ARG:HD3	2.16	0.45
1:A:259:LYS:HD3	1:A:314:ASP:HA	1.99	0.44
1:B:105:MET:HE2	1:B:110:LEU:HD23	2.00	0.44
1:A:155:TYR:CD1	1:A:274:LEU:HD11	2.53	0.44
1:B:217:ILE:HD12	1:B:237:HIS:NE2	2.32	0.44
1:B:314:ASP:O	1:B:315:LEU:CB	2.66	0.44
1:A:-2:GLY:N	5:A:505:HOH:O	2.50	0.43
1:B:148:THR:HG22	1:B:282:ILE:HG12	2.00	0.43
1:A:229:ILE:HG23	1:A:272:PHE:CZ	2.52	0.43
1:B:50:ASP:CG	1:B:52:ARG:HD3	2.43	0.43
1:A:169:GLU:HG3	5:A:567:HOH:O	2.18	0.42
1:A:194:ILE:HG12	1:A:244:GLU:HG2	2.01	0.42
1:A:35:TRP:CE2	1:A:59:PRO:HB3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:245:LYS:HD3	5:B:719:HOH:O	2.19	0.41
1:A:158:ILE:HD13	1:A:231:PHE:HB2	2.01	0.41
1:B:28:SER:HB3	1:B:122:TYR:CZ	2.55	0.40
1:A:229:ILE:CG2	1:A:272:PHE:CE1	3.04	0.40
1:B:161:LEU:HD23	1:B:229:ILE:HD13	2.02	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	320/335 (96%)	316 (99%)	4 (1%)	0	100	100
1	B	319/335 (95%)	311 (98%)	8 (2%)	0	100	100
All	All	639/670 (95%)	627 (98%)	12 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	275/286 (96%)	274 (100%)	1 (0%)	84	82
1	B	274/286 (96%)	270 (98%)	4 (2%)	57	47
All	All	549/572 (96%)	544 (99%)	5 (1%)	70	64

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	231	PHE
1	B	231	PHE
1	B	255	VAL
1	B	271	SER
1	B	295	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	A	64	GLN
1	A	159	ASN
1	B	0	HIS

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	GLC	C	1	2	11,11,12	0.48	0	15,15,17	1.25	1 (6%)
2	FRU	C	2	2	11,12,12	1.20	1 (9%)	10,18,18	1.51	3 (30%)
2	GLC	D	1	2	11,11,12	0.46	0	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	FRU	D	2	2	11,12,12	0.93	1 (9%)	10,18,18	1.26	2 (20%)

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	GLC	C	1	2	-	0/2/19/22	0/1/1/1
2	FRU	C	2	2	-	3/5/24/24	0/1/1/1
2	GLC	D	1	2	-	0/2/19/22	0/1/1/1
2	FRU	D	2	2	-	0/5/24/24	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	FRU	O2-C2	3.28	1.46	1.40
2	D	2	FRU	O2-C2	2.62	1.45	1.40

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	GLC	C1-O5-C5	4.21	117.82	112.19
2	C	2	FRU	O5-C5-C6	2.90	116.80	108.89
2	C	2	FRU	C6-C5-C4	-2.42	109.37	115.10
2	D	2	FRU	O1-C1-C2	-2.18	106.85	111.67
2	C	2	FRU	O2-C2-O5	2.18	113.51	109.33
2	D	2	FRU	O5-C5-C6	2.17	114.81	108.89
2	D	1	GLC	C1-O5-C5	2.17	115.09	112.19

There are no chirality outliers.

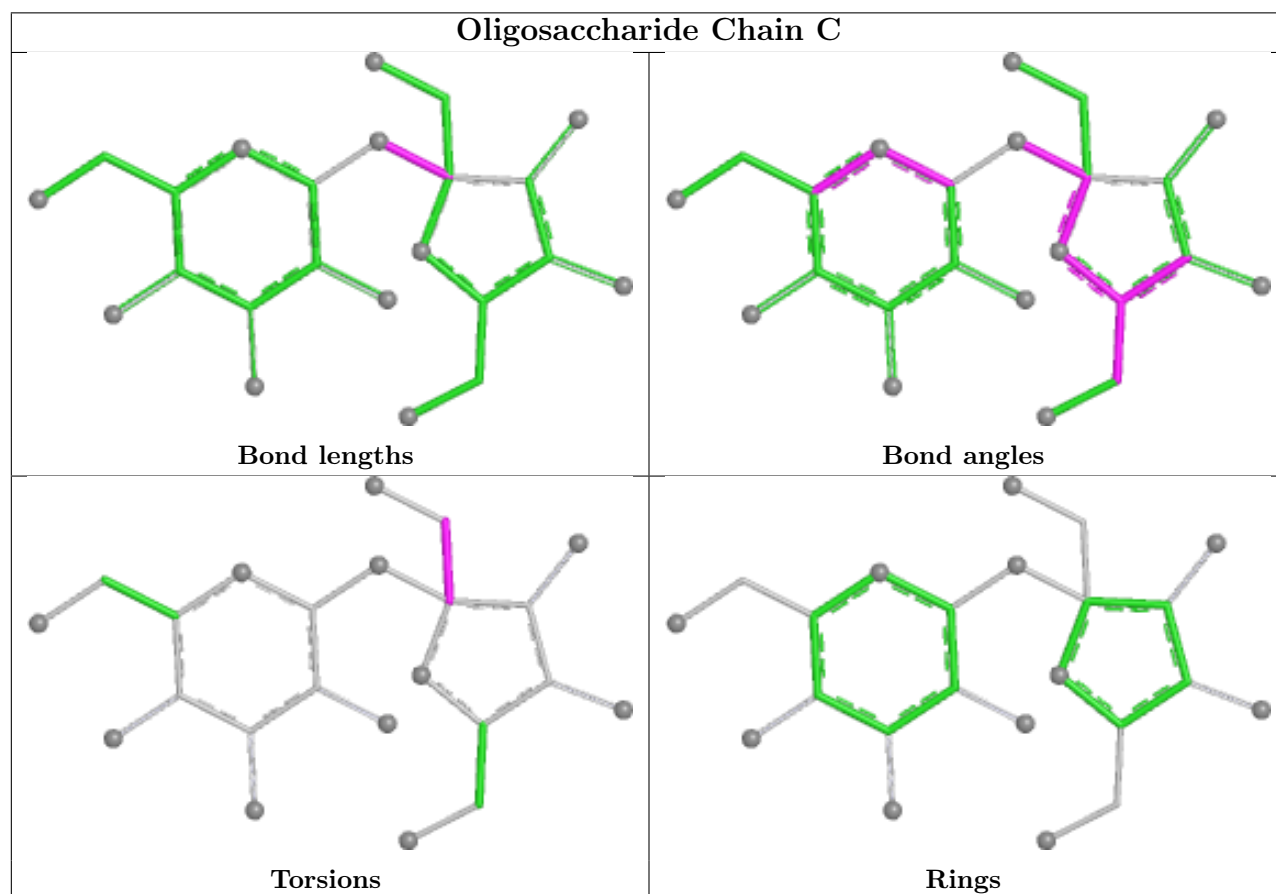
All (3) torsion outliers are listed below:

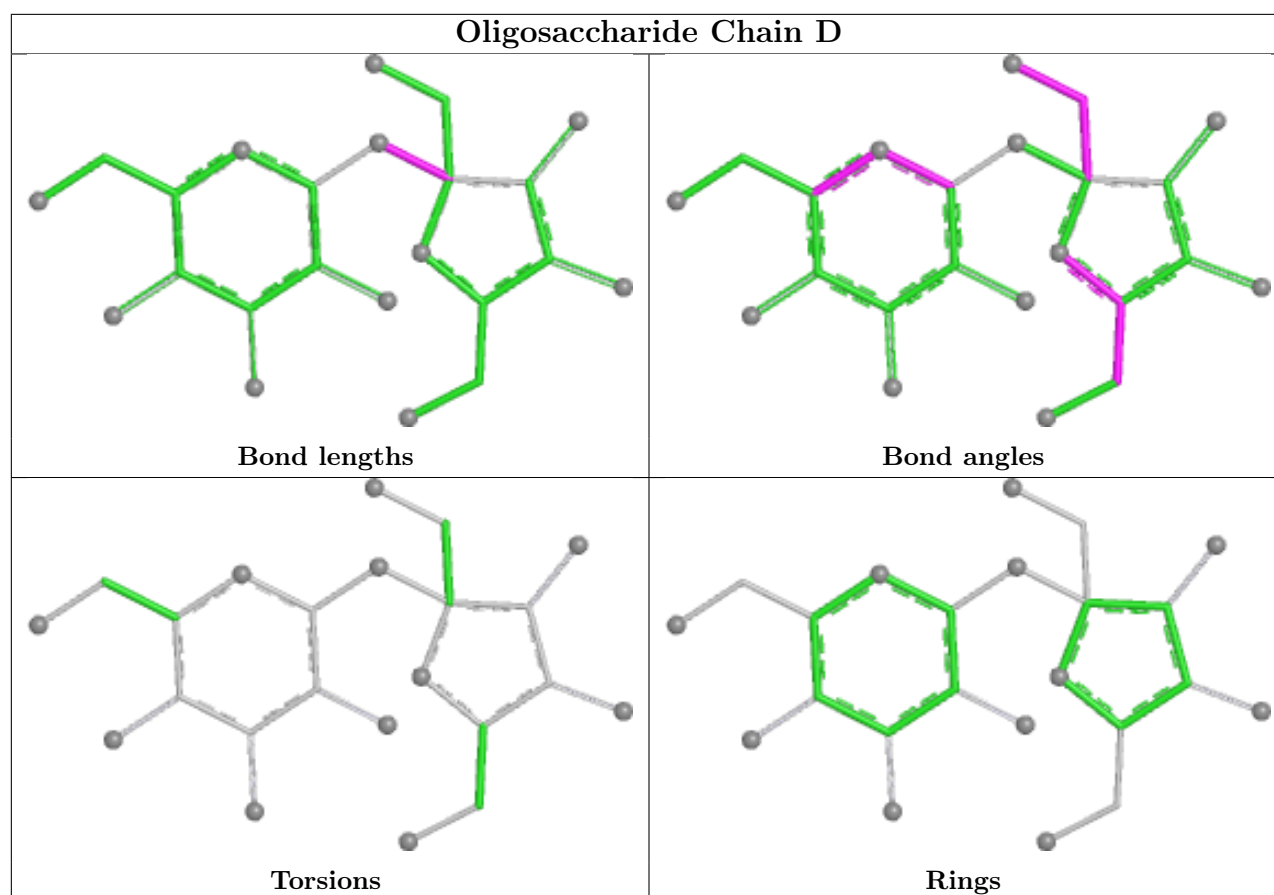
Mol	Chain	Res	Type	Atoms
2	C	2	FRU	O1-C1-C2-C3
2	C	2	FRU	O1-C1-C2-O2
2	C	2	FRU	O1-C1-C2-O5

There are no ring outliers.

No monomer is involved in short contacts.

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 3 ligands modelled in this entry, 2 are 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	EPE	B	403	-	15,15,15	1.95	1 (6%)	19,20,20	2.86	9 (47%)

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	EPE	B	403	-	-	3/9/19/19	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	403	EPE	C10-S	-7.25	1.67	1.77

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	403	EPE	O1S-S-C10	5.21	114.60	106.73
4	B	403	EPE	O2S-S-C10	4.94	114.19	106.73
4	B	403	EPE	C7-N4-C3	4.61	123.53	111.24
4	B	403	EPE	C6-N1-C2	4.14	117.75	108.84
4	B	403	EPE	C9-N1-C6	4.13	122.25	111.24
4	B	403	EPE	C5-N4-C3	4.13	117.73	108.84
4	B	403	EPE	C9-N1-C2	3.25	119.90	111.24
4	B	403	EPE	C7-N4-C5	2.78	118.66	111.24
4	B	403	EPE	O2S-S-O1S	-2.04	107.19	113.82

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	403	EPE	C8-C7-N4-C3
4	B	403	EPE	C10-C9-N1-C6
4	B	403	EPE	N4-C7-C8-O8

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	318/335 (94%)	0.47	37 (11%) 9 9	16, 28, 73, 123	4 (1%)
1	B	318/335 (94%)	0.45	40 (12%) 8 7	16, 27, 72, 101	3 (0%)
All	All	636/670 (94%)	0.46	77 (12%) 8 8	16, 28, 73, 123	7 (1%)

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	223	VAL	6.2
1	A	223	VAL	6.2
1	A	221	ALA	5.7
1	B	183	GLN	5.4
1	A	181	VAL	5.4
1	B	232	GLY	5.4
1	B	315	LEU	5.1
1	B	231	PHE	4.6
1	B	179	THR	4.5
1	A	315	LEU	4.5
1	A	231	PHE	4.5
1	B	229	ILE	4.4
1	A	227	PHE	4.3
1	B	177	ASN	4.3
1	A	220	ILE	4.1
1	B	217	ILE	4.0
1	B	180	SER	3.9
1	B	181	VAL	3.9
1	A	-2	GLY	3.8
1	B	233	VAL	3.7
1	A	232	GLY	3.7
1	A	228	SER	3.6
1	A	179	THR	3.6
1	A	226	GLY	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	228	SER	3.5
1	B	221	ALA	3.5
1	A	224	SER	3.5
1	A	274	LEU	3.5
1	B	163	PRO	3.4
1	A	233	VAL	3.3
1	A	272	PHE	3.2
1	B	226	GLY	3.2
1	A	217	ILE	3.1
1	B	222	GLU	3.0
1	B	311	VAL	3.0
1	B	220	ILE	2.9
1	B	1	MET	2.9
1	B	162	ILE	2.9
1	B	256	PRO	2.8
1	A	229	ILE	2.8
1	B	225	THR	2.8
1	B	257	PRO	2.8
1	A	180	SER	2.8
1	A	242	THR	2.8
1	B	230	SER	2.7
1	B	227	PHE	2.7
1	B	255	VAL	2.7
1	A	225	THR	2.6
1	B	178	LYS	2.6
1	B	173	VAL	2.6
1	B	274	LEU	2.5
1	A	182	LYS	2.5
1	A	160	GLN	2.4
1	A	257	PRO	2.4
1	A	24	ASN	2.4
1	A	230	SER	2.4
1	A	311	VAL	2.4
1	B	272	PHE	2.3
1	A	162	ILE	2.3
1	A	159	ASN	2.3
1	B	159	ASN	2.3
1	A	271	SER	2.3
1	A	256	PRO	2.2
1	A	-1	SER	2.2
1	A	169	GLU	2.2
1	B	160	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	182	LYS	2.2
1	B	258	LYS	2.2
1	B	309	ASN	2.2
1	A	222	GLU	2.1
1	B	243	ASP	2.1
1	A	161	LEU	2.1
1	B	261	VAL	2.1
1	B	270	ALA	2.0
1	A	314	ASP	2.0
1	A	202	THR	2.0
1	B	202	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](#)

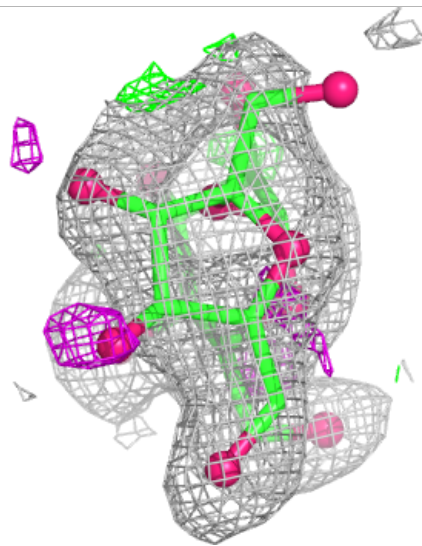
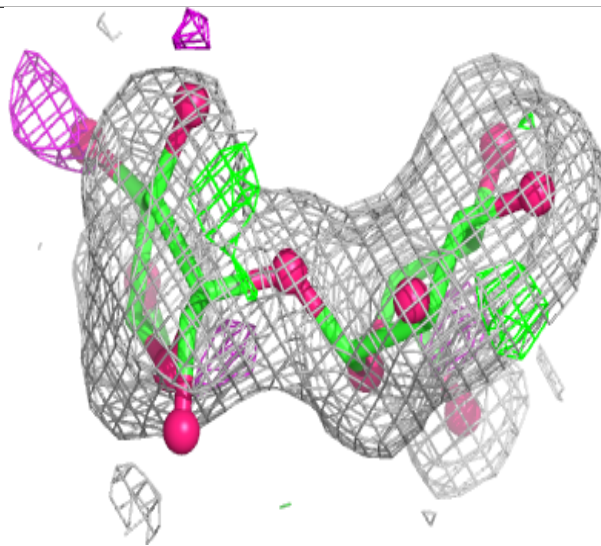
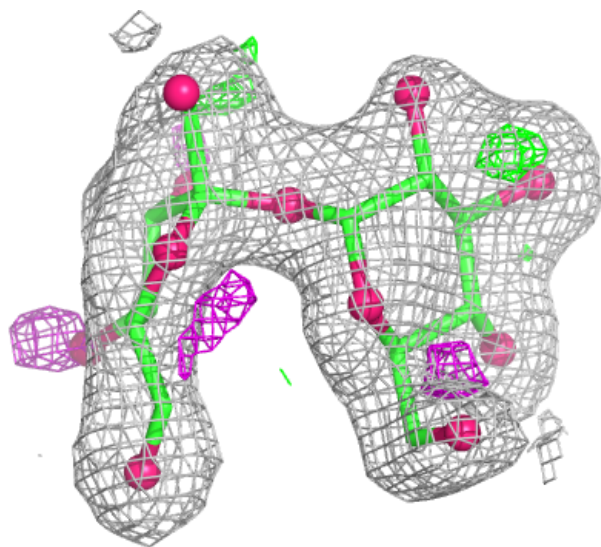
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

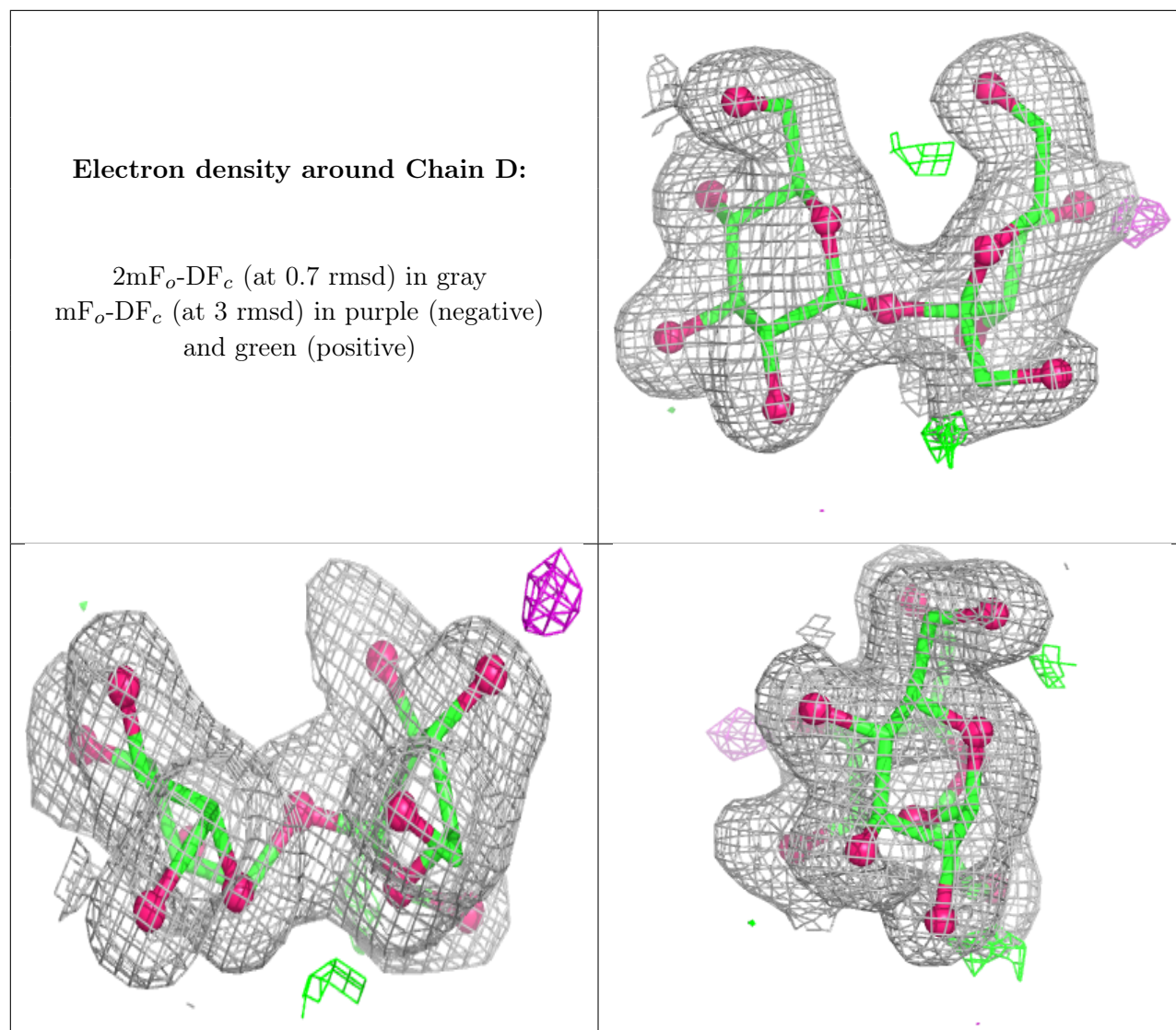
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FRU	C	2	12/12	0.77	0.16	41,49,60,61	0
2	FRU	D	2	12/12	0.88	0.10	33,39,41,43	0
2	GLC	C	1	11/12	0.92	0.09	26,28,38,43	0
2	GLC	D	1	11/12	0.94	0.07	23,25,32,36	0

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 [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	EPE	B	403	15/15	0.93	0.10	37,41,46,47	0
3	CL	A	402	1/1	0.95	0.08	32,32,32,32	0
3	CL	B	402	1/1	0.98	0.09	31,31,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.