



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 3OAI
Title : Crystal structure of the extra-cellular domain of human myelin protein zero
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Deposited on : 2010-08-05
Resolution : 2.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

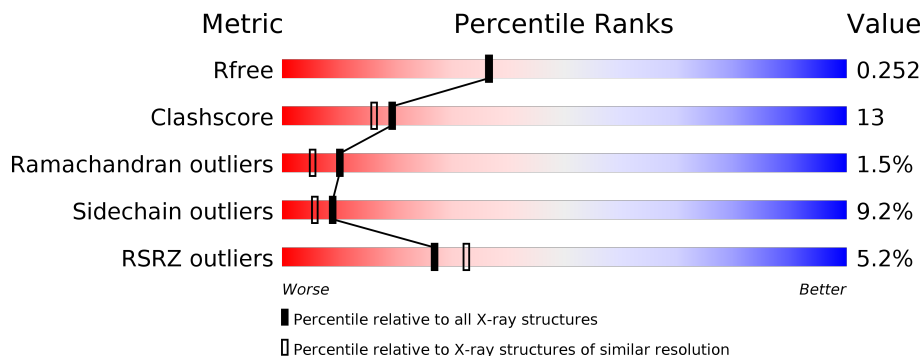
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION





The reported resolution of this entry is 2.10 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}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 on 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	507	
1	B	507	
2	C	2	
2	D	2	

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 8212 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 Maltose-binding periplasmic protein, Myelin protein P0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	488	3831	2463	626	734	8	0	0	0
1	B	488	3831	2463	626	734	8	0	0	0

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	367	ASN	-	linker	UNP D3QK41
A	368	ASN	-	linker	UNP D3QK41
A	369	ASN	-	linker	UNP D3QK41
A	370	ASN	-	linker	UNP D3QK41
A	371	ASN	-	linker	UNP D3QK41
A	372	ASN	-	linker	UNP D3QK41
A	373	ASN	-	linker	UNP D3QK41
A	374	ASN	-	linker	UNP D3QK41
A	375	ASN	-	linker	UNP D3QK41
A	376	ASN	-	linker	UNP D3QK41
A	377	ASN	-	linker	UNP D3QK41
A	378	ASN	-	linker	UNP D3QK41
A	379	ASN	-	linker	UNP D3QK41
A	380	ASN	-	linker	UNP D3QK41
A	381	ASN	-	linker	UNP D3QK41
A	382	ASN	-	linker	UNP D3QK41
A	383	ASN	-	linker	UNP D3QK41
A	384	ASN	-	linker	UNP D3QK41
A	385	ASN	-	linker	UNP D3QK41
A	386	ASN	-	linker	UNP D3QK41
A	1016	GLN	ARG	conflict	UNP P25189
B	367	ASN	-	linker	UNP D3QK41
B	368	ASN	-	linker	UNP D3QK41
B	369	ASN	-	linker	UNP D3QK41
B	370	ASN	-	linker	UNP D3QK41

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Chain	Residue	Modelled	Actual	Comment	Reference
B	371	ASN	-	linker	UNP D3QK41
B	372	ASN	-	linker	UNP D3QK41
B	373	ASN	-	linker	UNP D3QK41
B	374	ASN	-	linker	UNP D3QK41
B	375	ASN	-	linker	UNP D3QK41
B	376	ASN	-	linker	UNP D3QK41
B	377	ASN	-	linker	UNP D3QK41
B	378	ASN	-	linker	UNP D3QK41
B	379	ASN	-	linker	UNP D3QK41
B	380	ASN	-	linker	UNP D3QK41
B	381	ASN	-	linker	UNP D3QK41
B	382	ASN	-	linker	UNP D3QK41
B	383	ASN	-	linker	UNP D3QK41
B	384	ASN	-	linker	UNP D3QK41
B	385	ASN	-	linker	UNP D3QK41
B	386	ASN	-	linker	UNP D3QK41
B	1016	GLN	ARG	conflict	UNP P25189

- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-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 water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	271	Total	O	0	0
			271	271		
3	B	233	Total	O	0	0
			233	233		

Chain C:  100%

GLC1
GLC2

- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain D:  50%  50%

GLC1
GLC2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.90Å 54.89Å 146.07Å 90.00° 98.54° 90.00°	Depositor
Resolution (Å)	19.96 – 2.10 19.96 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.96-2.10) 99.8 (19.96-2.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 2.09Å)	Xtrriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.183 , 0.252 0.185 , 0.252	Depositor DCC
R_{free} test set	2895 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	26.7	Xtrriage
Anisotropy	0.028	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 58.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8212	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.93% 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: GLC

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	0.61	0/3930	0.69	3/5340 (0.1%)
1	B	0.59	0/3930	0.66	2/5340 (0.0%)
All	All	0.60	0/7860	0.67	5/10680 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
1	B	0	3
All	All	0	8

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	1104	PRO	N-CA-C	6.75	129.64	112.10
1	B	122	LEU	CA-CB-CG	6.34	129.88	115.30
1	A	1032	ASP	N-CA-C	6.32	128.06	111.00
1	B	1103	PRO	C-N-CD	5.52	140.00	128.40
1	A	1103	PRO	C-N-CD	-5.33	108.86	120.60

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1031	ASP	Peptide

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Mol	Chain	Res	Type	Group
1	A	1102	ASN	Peptide
1	A	1103	PRO	Peptide
1	A	1104	PRO	Peptide
1	A	3	GLU	Peptide

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	3831	0	3739	81	0
1	B	3831	0	3739	110	0
2	C	23	0	21	3	0
2	D	23	0	21	0	0
3	A	271	0	0	6	1
3	B	233	0	0	23	0
All	All	8212	0	7520	194	1

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 13.

The worst 5 of 194 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1104:PRO:O	3:B:484:HOH:O	1.52	1.23
1:B:30:ASP:HB2	3:B:478:HOH:O	1.45	1.16
1:B:367:ASN:C	3:B:496:HOH:O	1.84	1.14
1:B:1045:ARG:HH11	1:B:1045:ARG:HG3	0.97	1.07
1:A:12:ASN:ND2	1:A:14:ASP:OD1	1.89	1.04

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1156:HOH:O	3:A:1308:HOH:O 2_556]	2.13	0.07

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	484/507 (96%)	466 (96%)	11 (2%)	7 (1%)	11	6
1	B	484/507 (96%)	456 (94%)	20 (4%)	8 (2%)	9	4
All	All	968/1014 (96%)	922 (95%)	31 (3%)	15 (2%)	10	5

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1031	ASP
1	A	1104	PRO
1	A	1105	ASP
1	B	31	THR
1	B	1061	ASP

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	402/421 (96%)	366 (91%)	36 (9%)	9	6
1	B	402/421 (96%)	364 (90%)	38 (10%)	8	5
All	All	804/842 (96%)	730 (91%)	74 (9%)	9	6

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1106	ILE

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Mol	Chain	Res	Type
1	B	79	ILE
1	B	1103	PRO
1	A	1117	VAL
1	B	33	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1052	HIS
1	A	1093	ASN
1	B	203	HIS
1	A	241	ASN
1	B	218	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

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	12,12,12	0.40	0	17,17,17	1.50	2 (11%)
2	GLC	C	2	2	11,11,12	0.42	0	15,15,17	2.44	4 (26%)
2	GLC	D	1	2	12,12,12	0.63	0	17,17,17	1.00	0
2	GLC	D	2	2	11,11,12	0.55	0	15,15,17	2.02	5 (33%)

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	-	0/2/22/22	0/1/1/1
2	GLC	C	2	2	-	0/2/19/22	0/1/1/1
2	GLC	D	1	2	-	0/2/22/22	0/1/1/1
2	GLC	D	2	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	GLC	C1-O5-C5	6.34	120.78	112.19
2	D	2	GLC	C1-O5-C5	5.56	119.72	112.19
2	C	2	GLC	O5-C1-C2	5.33	118.99	110.77
2	D	2	GLC	O5-C1-C2	3.54	116.24	110.77
2	C	1	GLC	O5-C1-C2	3.26	116.10	110.28

There are no chirality outliers.

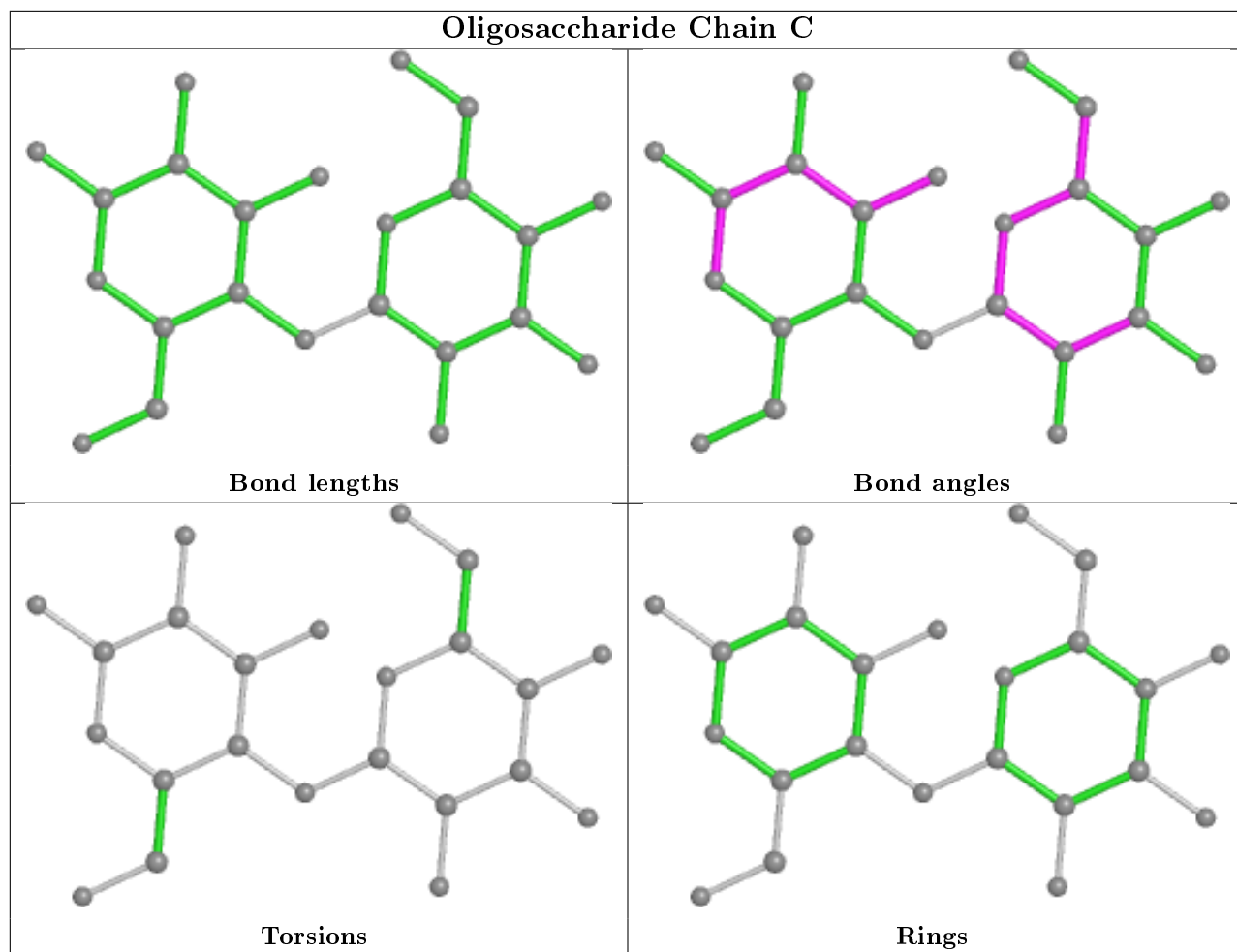
There are no torsion outliers.

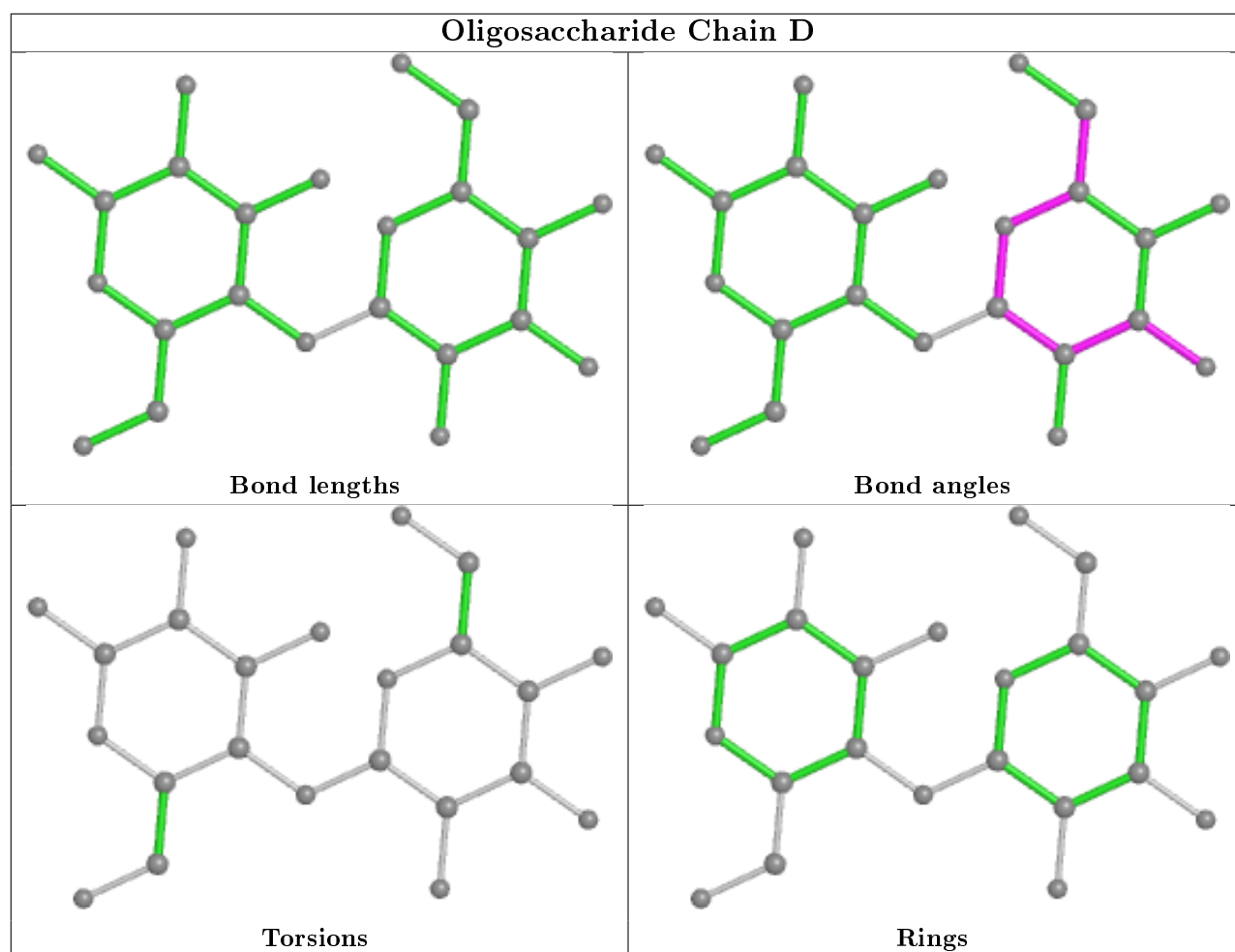
There are no ring outliers.

2 monomers are involved in 3 short contacts:

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

There are no ligands in this entry.

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	488/507 (96%)	0.08	22 (4%) 33 38	14, 26, 43, 66	2 (0%)
1	B	488/507 (96%)	0.25	29 (5%) 22 27	15, 28, 49, 68	2 (0%)
All	All	976/1014 (96%)	0.17	51 (5%) 27 32	14, 27, 48, 68	4 (0%)

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1063	VAL	9.5
1	A	1063	VAL	6.9
1	B	1121	VAL	6.2
1	B	1044	GLY	6.1
1	B	31	THR	5.8

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

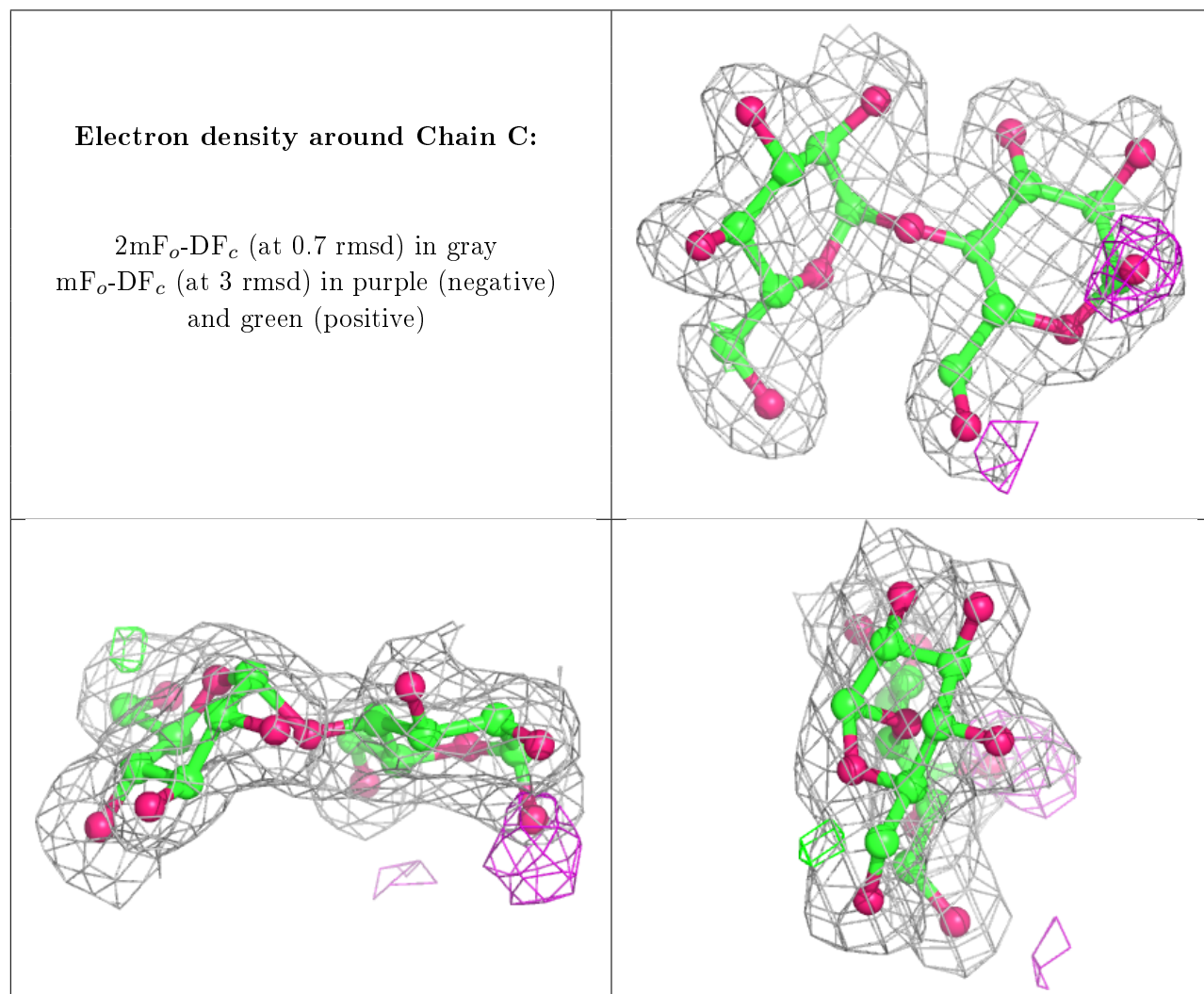
There are no non-standard protein/DNA/RNA residues in this entry.

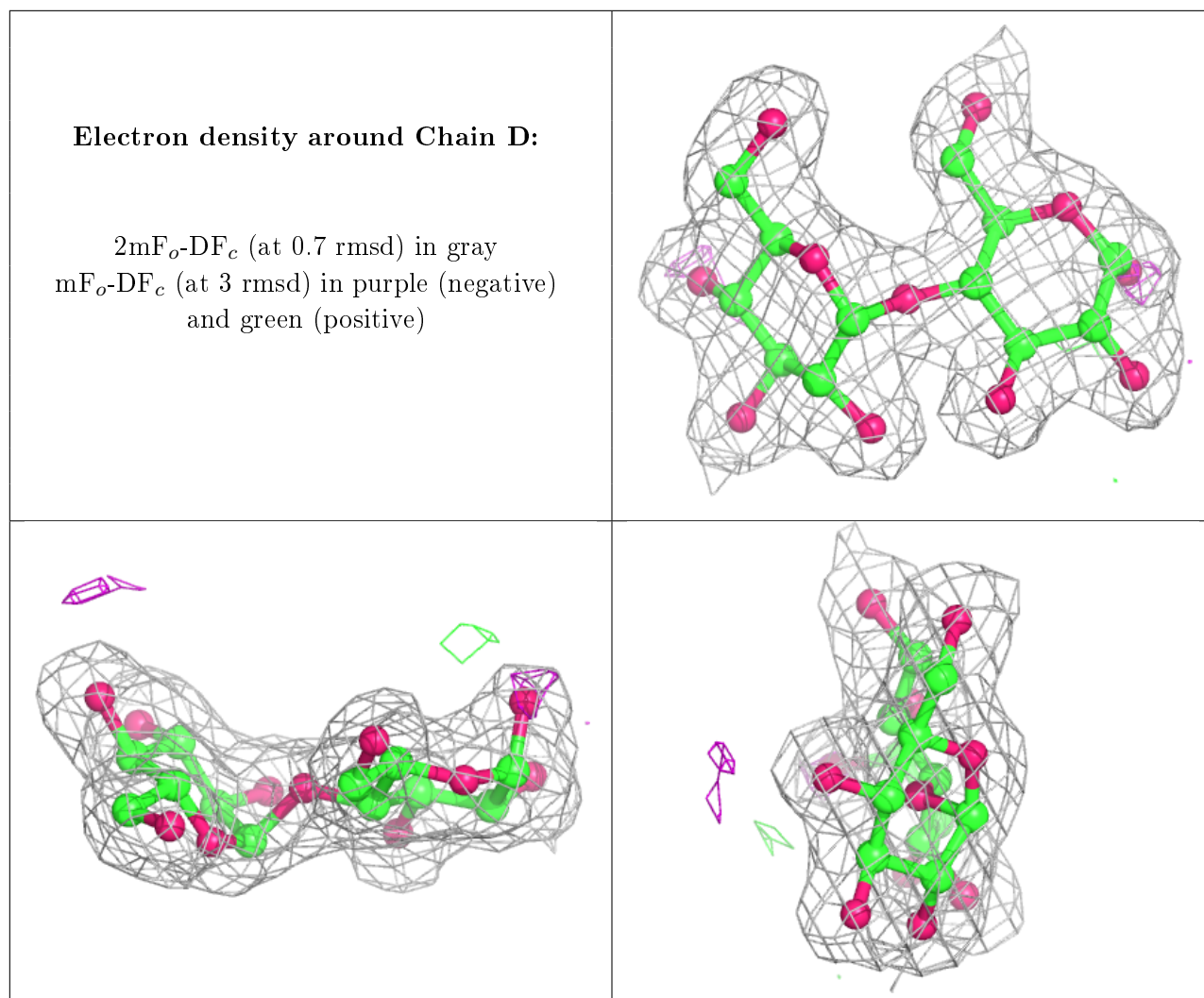
6.3 Carbohydrates [i](#)

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	GLC	C	1	12/12	0.93	0.10	14,19,22,23	0
2	GLC	D	1	12/12	0.96	0.08	16,18,21,22	0
2	GLC	C	2	11/12	0.97	0.10	13,16,20,20	0
2	GLC	D	2	11/12	0.98	0.12	14,14,17,19	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.