



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 10, 2020 – 10:51 AM BST

PDB ID : 5GZH
Title : Endo-beta-1,2-glucanase from Chitinophaga pinensis - ligand free form
Authors : Abe, K.; Nakajima, M.; Arakawa, T.; Fushinobu, S.; Taguchi, H.
Deposited on : 2016-09-28
Resolution : 1.80 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

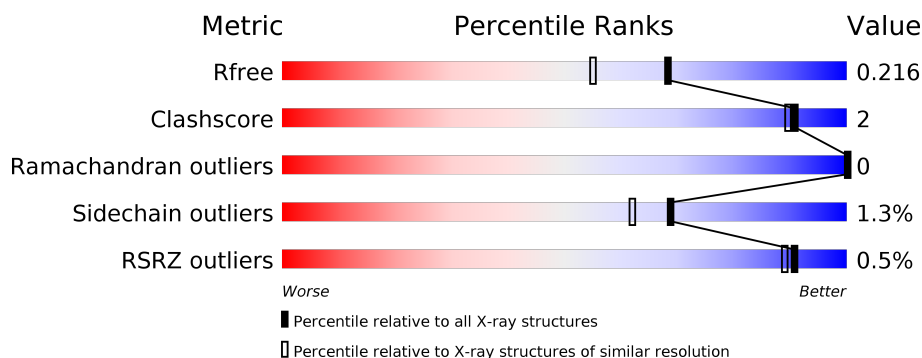
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	449	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 90%, green 90%, grey 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 90% 5% 5% </div> </div>
1	B	449	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 90%, yellow 90%, grey 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 90% • 5% </div> </div>
2	C	2	<div> <div style="width: 100%; height: 10px; background: yellow;"></div> <div style="text-align: center;">100%</div> </div>
2	D	2	<div> <div style="width: 100%; height: 10px; background: yellow;"></div> <div style="text-align: center;">100%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	IOD	A	512	-	-	X	-
3	IOD	B	507	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7659 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 Endo-beta-1,2-glucanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	426	Total	C	N	O	S	0	1	0
			3475	2242	586	630	17			
1	B	426	Total	C	N	O	S	0	1	0
			3475	2242	586	630	17			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	442	LEU	-	expression tag	UNP C7PIC2
A	443	GLU	-	expression tag	UNP C7PIC2
A	444	HIS	-	expression tag	UNP C7PIC2
A	445	HIS	-	expression tag	UNP C7PIC2
A	446	HIS	-	expression tag	UNP C7PIC2
A	447	HIS	-	expression tag	UNP C7PIC2
A	448	HIS	-	expression tag	UNP C7PIC2
A	449	HIS	-	expression tag	UNP C7PIC2
B	442	LEU	-	expression tag	UNP C7PIC2
B	443	GLU	-	expression tag	UNP C7PIC2
B	444	HIS	-	expression tag	UNP C7PIC2
B	445	HIS	-	expression tag	UNP C7PIC2
B	446	HIS	-	expression tag	UNP C7PIC2
B	447	HIS	-	expression tag	UNP C7PIC2
B	448	HIS	-	expression tag	UNP C7PIC2
B	449	HIS	-	expression tag	UNP C7PIC2

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

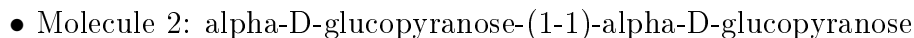
- Molecule 3 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	10	Total	I	0	0
			10	10		
3	A	14	Total	I	0	0
			14	14		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	314	Total	O	0	0
			314	314		
4	B	325	Total	O	0	0
			325	325		

- Molecule 1: Endo-beta-1,2-glucanase



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	90.97Å 90.97Å 124.09Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.74 – 1.80 37.54 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.0 (48.74-1.80) 99.0 (37.54-1.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 1.81Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
R, R_{free}	0.168 , 0.204 0.182 , 0.216	Depositor DCC
R_{free} test set	5317 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	24.0	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 34.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.016 for -h,-k,l 0.458 for h,-h-k,-l 0.017 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7659	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.30% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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, IOD

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	1.06	2/3595 (0.1%)	0.96	8/4881 (0.2%)
1	B	1.06	3/3595 (0.1%)	0.96	8/4881 (0.2%)
All	All	1.06	5/7190 (0.1%)	0.96	16/9762 (0.2%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	291	GLU	CD-OE2	6.03	1.32	1.25
1	A	291	GLU	CD-OE2	5.86	1.32	1.25
1	A	291	GLU	CG-CD	5.59	1.60	1.51
1	B	94	GLU	CG-CD	5.31	1.59	1.51
1	B	40	TYR	CE1-CZ	5.02	1.45	1.38

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	66	ASP	CB-CG-OD1	11.41	128.57	118.30
1	A	66	ASP	CB-CG-OD1	10.73	127.96	118.30
1	B	412	ARG	NE-CZ-NH2	-7.38	116.61	120.30
1	B	66	ASP	CB-CG-OD2	-6.67	112.30	118.30
1	A	66	ASP	CB-CG-OD2	-6.62	112.34	118.30

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	3475	0	3263	10	0
1	B	3475	0	3263	7	0
2	C	23	0	21	0	0
2	D	23	0	21	0	0
3	A	14	0	0	7	0
3	B	10	0	0	5	0
4	A	314	0	0	5	1
4	B	325	0	0	1	0
All	All	7659	0	6568	23	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 2.

The worst 5 of 23 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)
3:B:508:IOD:I	4:B:846:HOH:O	2.35	1.11
3:A:515:IOD:I	4:A:789:HOH:O	2.43	1.03
3:A:508:IOD:I	4:A:792:HOH:O	2.56	0.93
3:B:504:IOD:I	3:B:510:IOD:I	3.39	0.80
1:A:443:GLU:HG2	3:A:512:IOD:I	2.53	0.78

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)
4:A:733:HOH:O	4:A:858:HOH:O[2_555]	2.10	0.10

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	425/449 (95%)	409 (96%)	16 (4%)	0	100	100
1	B	425/449 (95%)	410 (96%)	15 (4%)	0	100	100
All	All	850/898 (95%)	819 (96%)	31 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	358/376 (95%)	353 (99%)	5 (1%)	67	59
1	B	358/376 (95%)	354 (99%)	4 (1%)	73	68
All	All	716/752 (95%)	707 (99%)	9 (1%)	69	62

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	442	LEU
1	B	441	LYS
1	B	199	LYS
1	A	204	PHE
1	B	55	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	133	GLN
1	A	247	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	GLC	C	1	2	11,11,12	1.41	2 (18%)	15,15,17	1.52	4 (26%)
2	GLC	C	2	2	12,12,12	0.82	1 (8%)	17,17,17	1.03	1 (5%)
2	GLC	D	1	2	11,11,12	0.81	1 (9%)	15,15,17	1.13	2 (13%)
2	GLC	D	2	2	12,12,12	1.47	2 (16%)	17,17,17	1.03	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
2	GLC	C	1	2	-	0/2/19/22	0/1/1/1
2	GLC	C	2	2	-	0/2/22/22	0/1/1/1
2	GLC	D	1	2	-	0/2/19/22	0/1/1/1
2	GLC	D	2	2	-	0/2/22/22	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	GLC	O3-C3	3.21	1.50	1.43
2	C	1	GLC	O3-C3	3.19	1.50	1.43
2	D	2	GLC	C4-C5	2.75	1.58	1.53
2	C	2	GLC	O1-C1	2.09	1.46	1.39
2	D	1	GLC	C2-C3	2.06	1.55	1.52

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	GLC	C1-O5-C5	2.63	115.76	112.19
2	C	1	GLC	O3-C3-C2	2.56	114.89	109.99
2	C	2	GLC	C3-C4-C5	-2.48	105.82	110.24
2	C	1	GLC	C3-C4-C5	2.43	114.58	110.24
2	C	1	GLC	C1-O5-C5	2.36	115.39	112.19

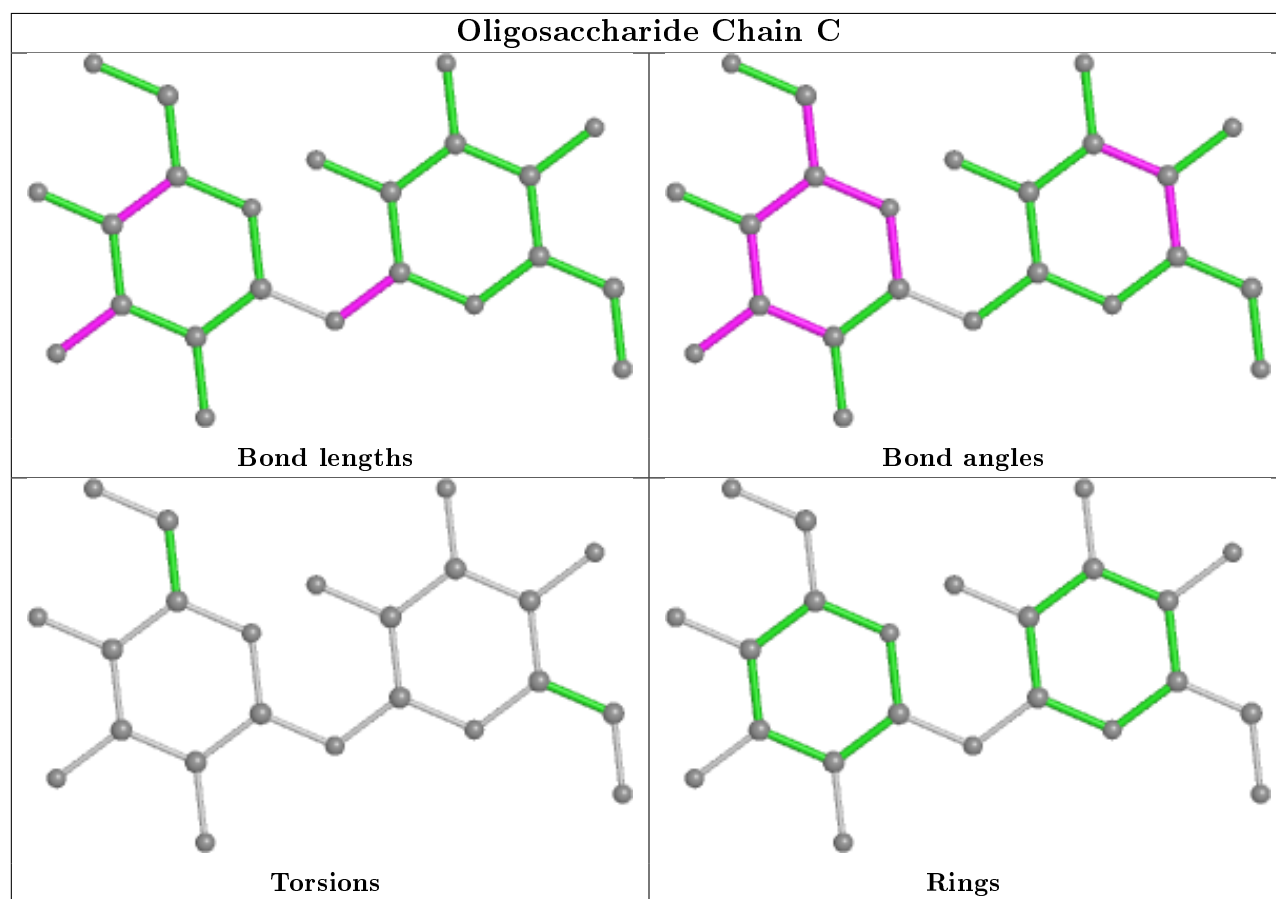
There are no chirality outliers.

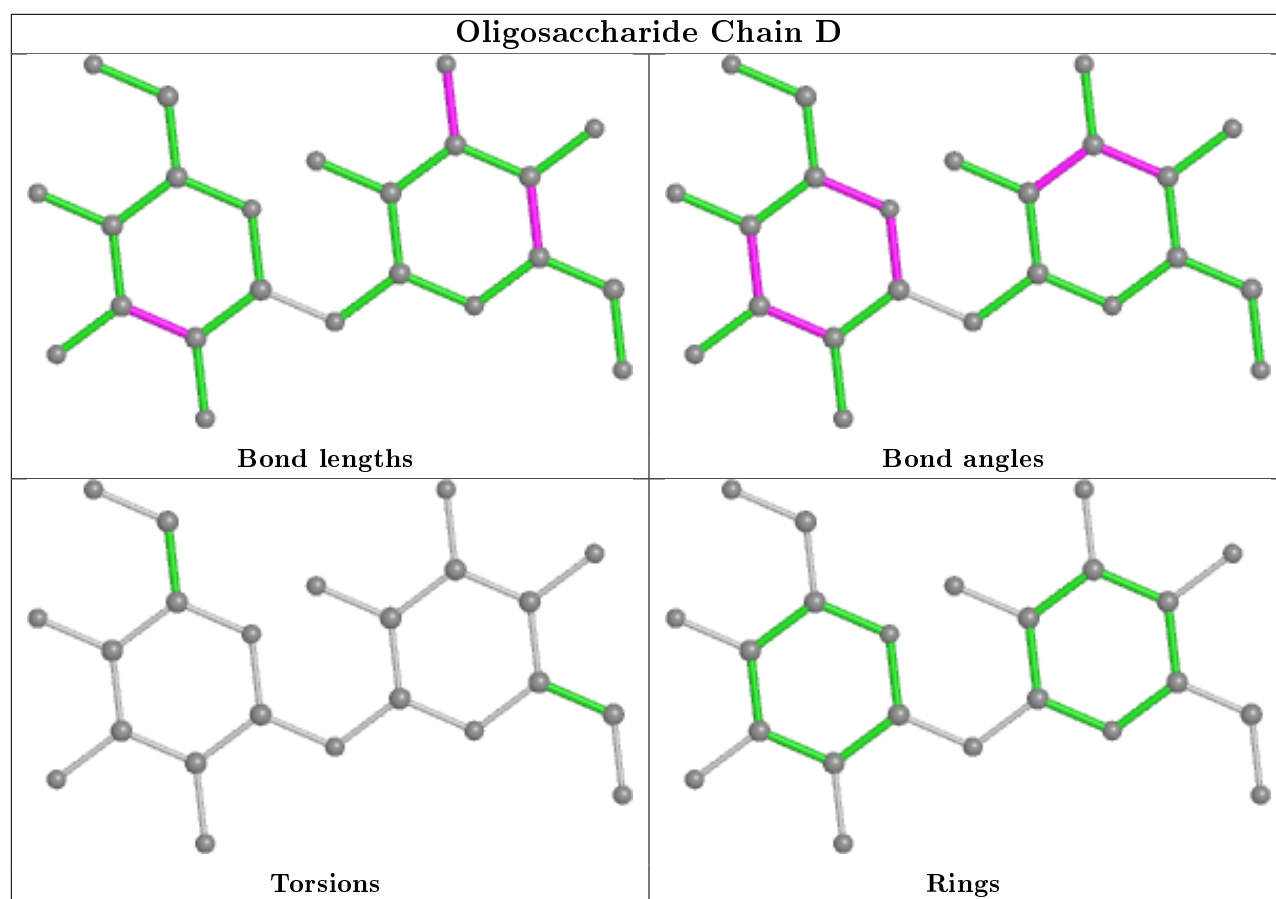
There are no torsion outliers.

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 24 ligands modelled in this entry, 24 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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 [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	426/449 (94%)	-0.53	3 (0%) 87 86	18, 26, 42, 73	0
1	B	426/449 (94%)	-0.52	1 (0%) 95 93	18, 26, 42, 72	0
All	All	852/898 (94%)	-0.53	4 (0%) 91 89	18, 26, 42, 73	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	442	LEU	3.4
1	A	63	PRO	2.8
1	A	61	ASN	2.3
1	B	63	PRO	2.1

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

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

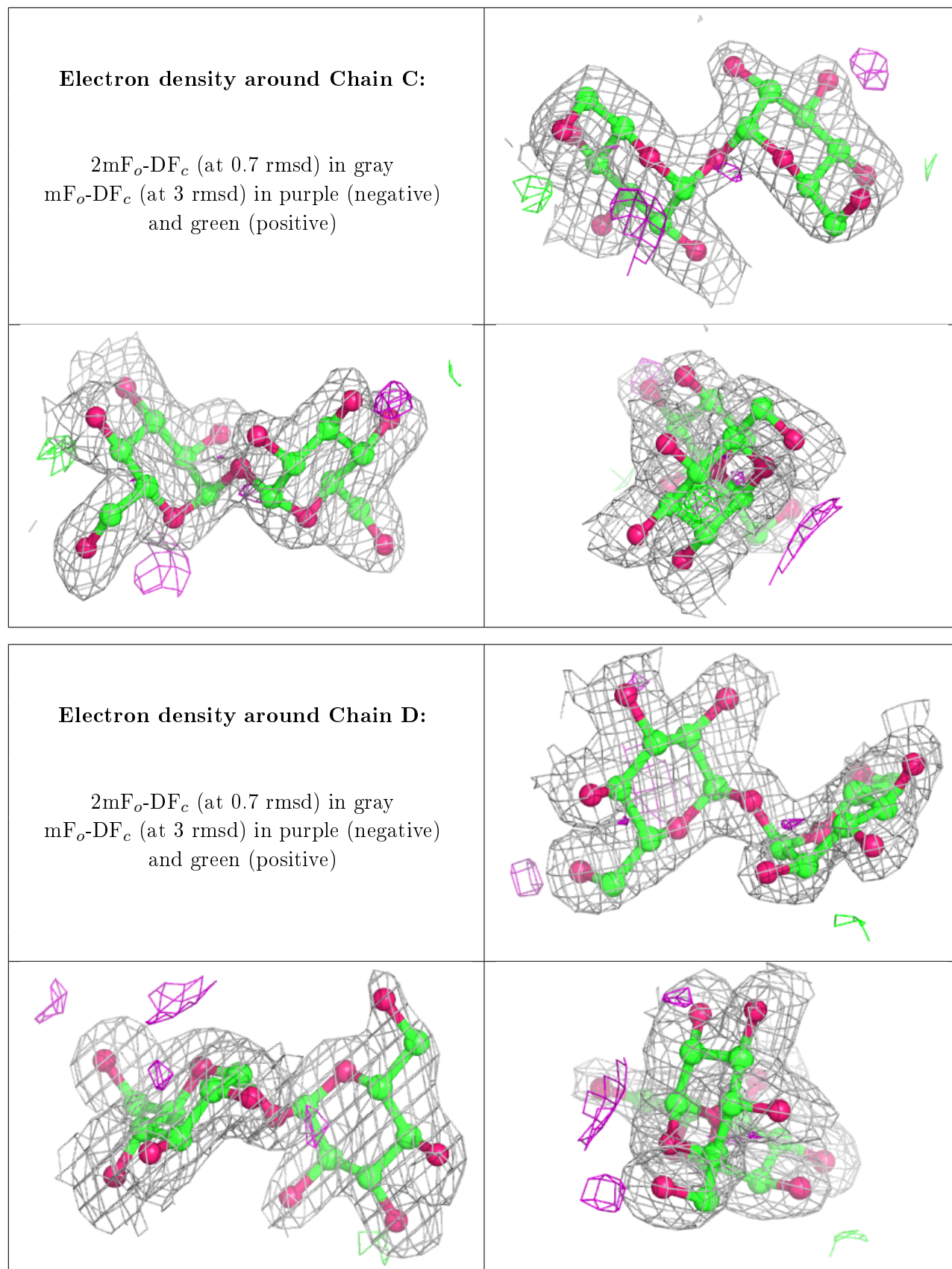
6.3 Carbohydrates [i](#)

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	D	1	11/12	0.83	0.21	37,41,49,55	0
2	GLC	C	1	11/12	0.83	0.11	30,37,40,42	0
2	GLC	C	2	12/12	0.88	0.14	38,42,49,53	0
2	GLC	D	2	12/12	0.89	0.10	34,38,41,43	0

The following is a graphical depiction of the model fit to experimental electron density for oligosac-

charide. Each fit is shown from different orientation to approximate a three-dimensional view.



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	IOD	A	506	1/1	0.83	0.19	96,96,96,96	0
3	IOD	A	504	1/1	0.86	0.09	50,50,50,50	0
3	IOD	B	511	1/1	0.91	0.26	63,63,63,63	0
3	IOD	A	512	1/1	0.92	0.13	79,79,79,79	0
3	IOD	B	509	1/1	0.93	0.10	81,81,81,81	0
3	IOD	A	513	1/1	0.93	0.18	82,82,82,82	0
3	IOD	A	511	1/1	0.94	0.11	73,73,73,73	0
3	IOD	A	510	1/1	0.95	0.16	73,73,73,73	0
3	IOD	A	515	1/1	0.96	0.33	63,63,63,63	0
3	IOD	B	506	1/1	0.96	0.13	74,74,74,74	0
3	IOD	B	507	1/1	0.96	0.12	77,77,77,77	0
3	IOD	B	508	1/1	0.96	0.14	76,76,76,76	0
3	IOD	A	514	1/1	0.96	0.08	89,89,89,89	0
3	IOD	B	505	1/1	0.97	0.10	71,71,71,71	0
3	IOD	A	507	1/1	0.97	0.12	68,68,68,68	0
3	IOD	A	505	1/1	0.97	0.13	66,66,66,66	0
3	IOD	A	509	1/1	0.97	0.09	75,75,75,75	0
3	IOD	A	508	1/1	0.98	0.13	68,68,68,68	0
3	IOD	B	510	1/1	0.98	0.25	58,58,58,58	0
3	IOD	B	504	1/1	0.99	0.09	64,64,64,64	0
3	IOD	B	502	1/1	0.99	0.02	40,40,40,40	0
3	IOD	A	502	1/1	0.99	0.03	40,40,40,40	0
3	IOD	B	503	1/1	1.00	0.03	29,29,29,29	0
3	IOD	A	503	1/1	1.00	0.02	29,29,29,29	0

6.5 Other polymers ⓘ

There are no such residues in this entry.