W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 12, 2023 – 04:43 pm GMT

PDB ID	:	2Y24
Title	:	STRUCTURAL BASIS FOR SUBSTRATE RECOGNITION BY ERWINIA CHRYSANTHEMI GH5 GLUCURONOXYLANASE
Authors	:	Urbanikova, L.; Vrsanska, M.; Krogh, K.B.; Hoff, T.; Biely, P.
Deposited on	:	2010-12-13
Resolution	:	1.39 Å(reported)

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

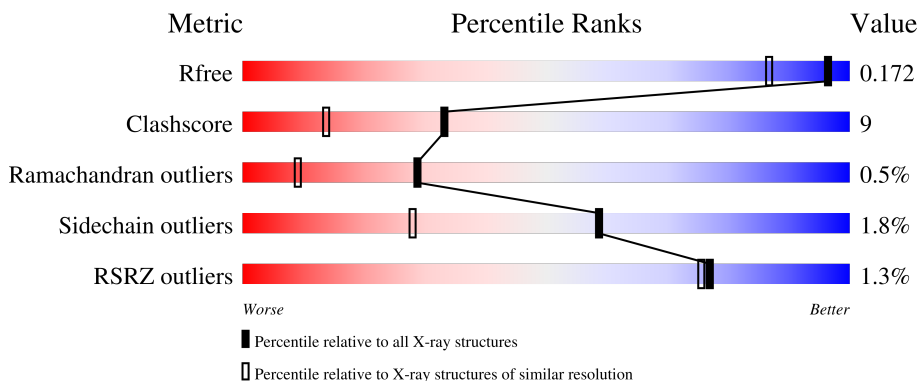|		
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1   Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
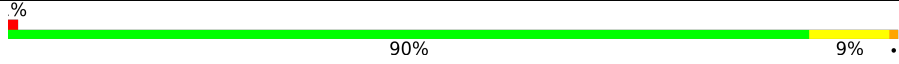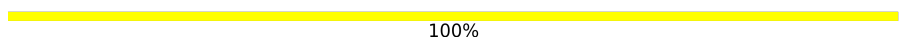*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.39 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	Percentile Ranks	Value
Rfree		0.172
Clashscore		9
Ramachandran outliers		0.5%
Sidechain outliers		1.8%
RSRZ outliers		1.3%

Worse ... *Better*

▮ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	1714 (1.40-1.40)
Clashscore	141614	1812 (1.40-1.40)
Ramachandran outliers	138981	1763 (1.40-1.40)
Sidechain outliers	138945	1762 (1.40-1.40)
RSRZ outliers	127900	1674 (1.40-1.40)

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 <=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	90% ... 9% ·
2	B	4	100%

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 criteria:

| Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PG4	A	1005	-	-	X	-
3	PG4	A	1006	-	-	X	-
4	PGE	A	1007	-	-	X	-

2 Entry composition ⓘ

There are 6 unique types of molecules in this entry. The entry contains 3683 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 XYLANASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	383	Total 3030	C 1910	N 510	O 598	S 12	0	17	0

- Molecule 2 is an oligosaccharide called 4-O-methyl-alpha-D-glucopyranuronic acid-(1-2)-[beta-D-xylopyranose-(1-4)]beta-D-xylopyranose-(1-4)-beta-D-xylopyranose.
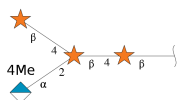
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	B	4	Total 41	C 22	O 19	0	0	0

- Molecule 3 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).
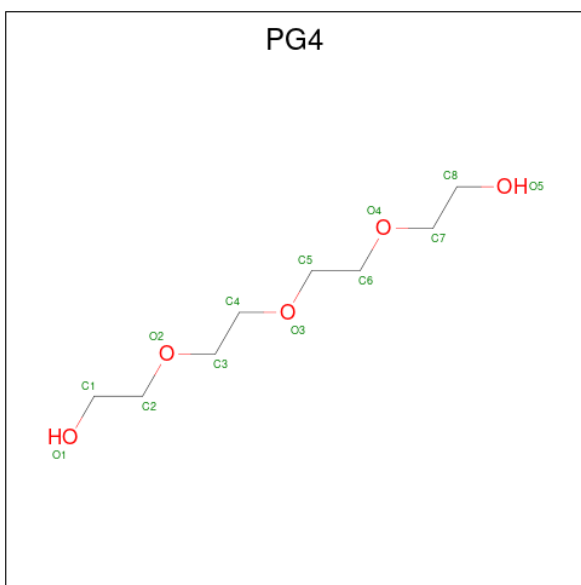
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 13	C 8	O 5	0	0
3	A	1	Total 13	C 8	O 5	0	0

- Molecule 4 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).
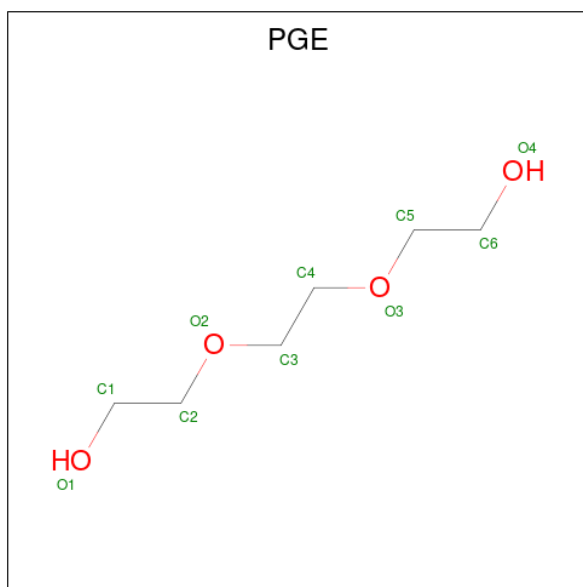
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 10	C 6	O 4	0	0

- Molecule 5 is IMIDAZOLE (three-letter code: IMD) (formula: $C_3H_5N_2$).
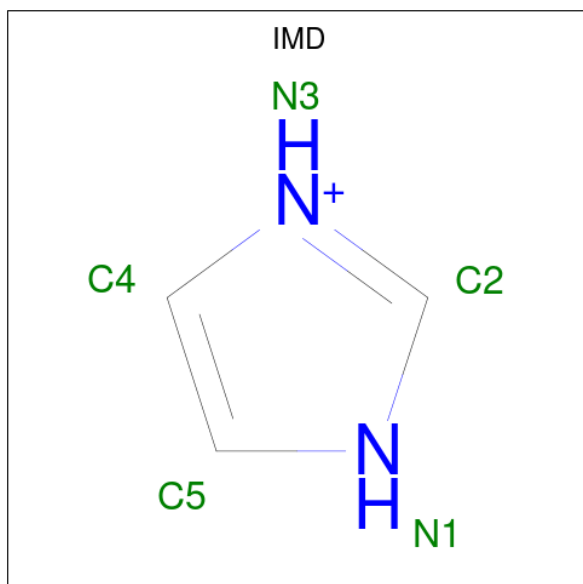
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 5	C 3	N 2	0	0

• Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	571	Total 571	O 571	0	0

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: XYLANASE

Chain A:
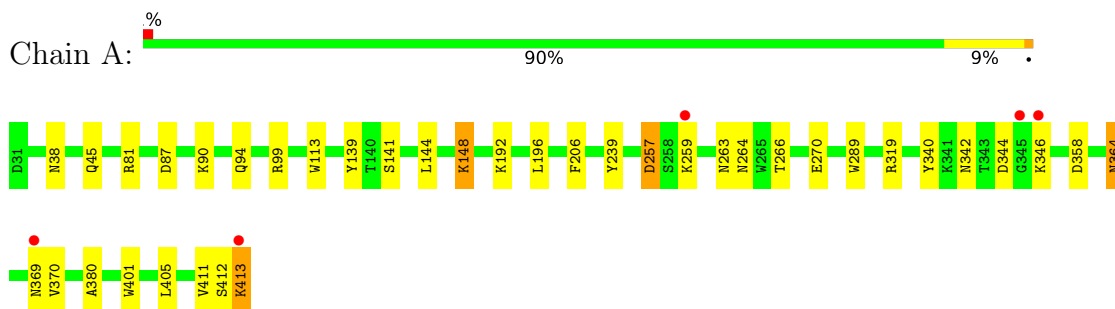
• Molecule 2: 4-O-methyl-alpha-D-glucopyranuronic acid-(1-2)-[beta-D-xylopyranose-(1-4)]beta-D-xylopyranose-(1-4)-beta-D-xylopyranose

Chain B:
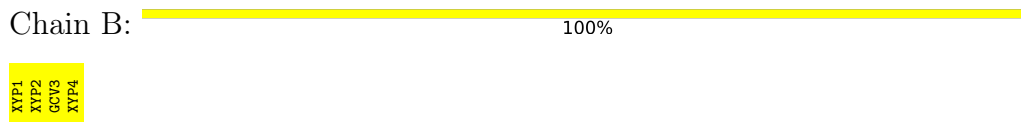
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	59.58Å 59.58Å 168.30Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.37 – 1.39 19.37 – 1.39	Depositor EDS
% Data completeness (in resolution range)	98.9 (19.37-1.39) 96.8 (19.37-1.39)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.53 (at 1.39Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.120 , 0.169 0.129 , 0.172	Depositor DCC
R_{free} test set	3468 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å²)	10.4	Xtriage
Anisotropy	0.906	Xtriage
Bulk solvent k_{sol}(e/Å³), B_{sol}(Å²)	0.35 , 43.1	EDS
L-test for twinning[2]	$< \lvert L \rvert > = 0.47, < L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.034 for -h,-k,l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	3683	wwPDB-VP
Average B, all atoms (Å²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.93% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< \lvert L \rvert >$, $< L^2 >$ 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: PGE, XYP, PG4, GCV, IMD

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	1.13	5/3167 (0.2%)	0.98	7/4301 (0.2%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	270	GLU	CB-CG	7.03	1.65	1.52
1	A	270	GLU	CG-CD	6.31	1.61	1.51
1	A	148	LYS	CD-CE	5.82	1.65	1.51
1	A	270	GLU	CD-OE2	5.71	1.31	1.25
1	A	340	TYR	CE1-CZ	5.11	1.45	1.38

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	81	ARG	NE-CZ-NH1	12.15	126.38	120.30
1	A	81	ARG	NE-CZ-NH2	-7.76	116.42	120.30
1	A	99	ARG	NE-CZ-NH2	-7.47	116.56	120.30
1	A	99	ARG	NE-CZ-NH1	6.28	123.44	120.30
1	A	319	ARG	NE-CZ-NH2	-6.26	117.17	120.30

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.

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3030	0	2962	41	0
2	B	41	0	9	0	0
3	A	26	0	36	22	0
4	A	10	0	14	10	0
5	A	5	0	5	0	0
6	A	571	0	0	18	2
All	All	3683	0	3026	53	2

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 9.

The worst 5 of 53 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:A:1005:PG4:C8	6:A:1361:HOH:O	2.12	0.97
1:A:38[B]:ASN:OD1	6:A:1101:HOH:O	1.84	0.95
1:A:148:LYS:HG3	6:A:1161:HOH:O	1.66	0.95
1:A:346[A]:LYS:HD2	1:A:411[A]:VAL:CG1	1.96	0.94
3:A:1005:PG4:H42	6:A:1533:HOH:O	1.65	0.94

All (2) 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)
6:A:1604:HOH:O	6:A:1604:HOH:O[4_645]	1.97	0.23
6:A:1647:HOH:O	6:A:1647:HOH:O[6_554]	2.00	0.20

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	399/383 (104%)	389 (98%)	8 (2%)	2 (0%)	29	9

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	257	ASP
1	A	289	TRP

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	342/325 (105%)	336 (98%)	6 (2%)	59	28

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	364	ASN
1	A	369	ASN
1	A	413	LYS
1	A	206	PHE
1	A	113	TRP

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	244	ASN
1	A	334	ASN
1	A	364	ASN
1	A	391	GLN

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 ⓘ

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	XYP	B	1	2	10,10,10	2.19	4 (40%)	14,14,14	1.69	5 (35%)
2	XYP	B	2	2	9,9,10	1.12	0	10,12,14	1.07	1 (10%)
2	GCV	B	3	2	13,13,14	0.90	0	14,18,20	1.38	2 (14%)
2	XYP	B	4	2	9,9,10	0.90	0	10,12,14	1.58	4 (40%)

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	XYP	B	1	2	-	-	0/1/1/1
2	XYP	B	2	2	-	-	0/1/1/1
2	GCV	B	3	2	-	1/6/23/26	0/1/1/1
2	XYP	B	4	2	-	-	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	XYP	O5-C1	-4.70	1.36	1.43
2	B	1	XYP	C1-C2	2.89	1.59	1.52
2	B	1	XYP	C4-C3	-2.61	1.48	1.52
2	B	1	XYP	C5-C4	2.49	1.57	1.52

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	4	XYP	C5-C4-C3	-2.92	106.08	109.67
2	B	3	GCV	O5-C1-C2	-2.87	106.34	110.77
2	B	1	XYP	C5-C4-C3	-2.80	106.23	109.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	3	GCV	C1-C2-C3	2.54	112.78	109.67
2	B	1	XYP	O5-C1-C2	2.51	113.15	109.43

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	3	GCV	O5-C5-C6-O6A

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.

Oligosaccharide Chain B

Bond lengths

Bond angles

Torsions

Rings
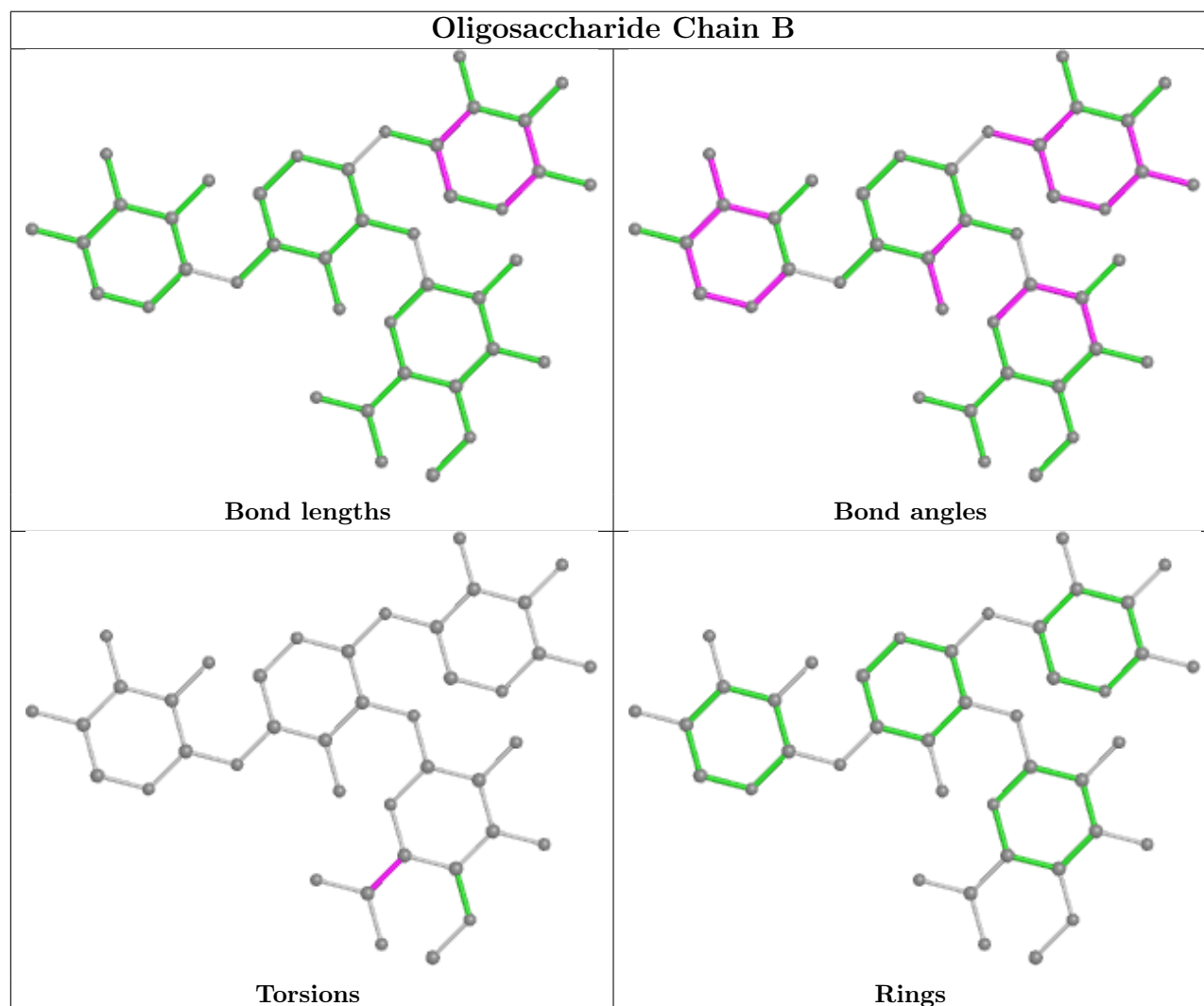
5.6 Ligand geometry ⓘ

4 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	PG4	A	1006	-	12,12,12	0.87	0	11,11,11	1.20	1 (9%)
5	IMD	A	1008	-	3,5,5	0.38	0	4,5,5	0.27	0
4	PGE	A	1007	-	9,9,9	0.92	0	8,8,8	1.34	2 (25%)
3	PG4	A	1005	-	12,12,12	0.72	0	11,11,11	0.98	0

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	PG4	A	1006	-	-	4/10/10/10	-
5	IMD	A	1008	-	-	-	0/1/1/1
4	PGE	A	1007	-	-	4/7/7/7	-
3	PG4	A	1005	-	-	5/10/10/10	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1006	PG4	O3-C5-C6	3.16	124.64	110.39
4	A	1007	PGE	C5-O3-C4	2.56	124.38	113.29
4	A	1007	PGE	O4-C6-C5	2.12	124.11	111.81

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1006	PG4	O3-C5-C6-O4

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Mol	Chain	Res	Type	Atoms
3	A	1005	PG4	O4-C7-C8-O5
3	A	1006	PG4	O1-C1-C2-O2
4	A	1007	PGE	O2-C3-C4-O3
4	A	1007	PGE	O3-C5-C6-O4

There are no ring outliers.

3 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1006	PG4	8	0
4	A	1007	PGE	10	0
3	A	1005	PG4	14	0

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	383/383 (100%)	-0.09	5 (1%)	77	75	6, 11, 20, 31	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	413	LYS	3.3
1	A	369	ASN	2.9
1	A	345[A]	GLY	2.9
1	A	259[A]	LYS	2.3
1	A	346[A]	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

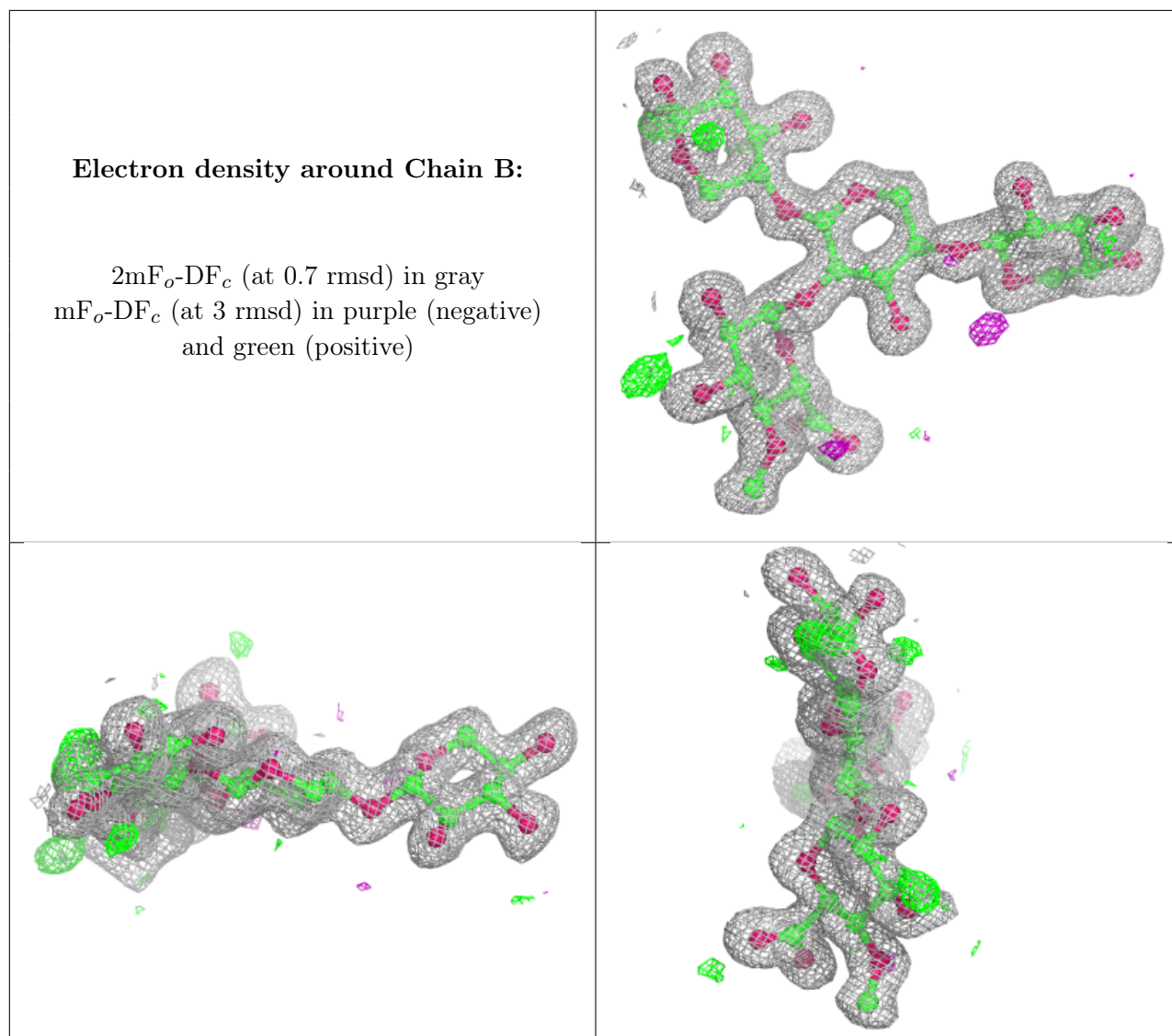There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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	XYP	B	1	10/10	0.97	0.07	9,12,19,20	0
2	GCV	B	3	13/14	0.97	0.07	10,14,18,21	0
2	XYP	B	4	9/10	0.97	0.10	15,17,21,24	0
2	XYP	B	2	9/10	0.98	0.06	11,12,14,14	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 B:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (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	PG4	A	1006	13/13	0.81	0.42	33,37,42,45	0
3	PG4	A	1005	13/13	0.83	0.33	28,32,36,38	0
4	PGE	A	1007	10/10	0.88	0.24	18,27,31,32	0
5	IMD	A	1008	5/5	0.98	0.06	9,11,11,13	0

6.5 Other polymers ⓘ

There are no such residues in this entry.