



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 11:11 PM BST

PDB ID : 6R2J  
Title : Crystal Structure of Pseudomonas stutzeri endoglucanase Cel5A in complex with cellobiose  
Authors : Dutoit, R.; Delsaute, M.; Berlemont, R.; Van Elder, D.; Galleni, M.; Bauvois, C.  
Deposited on : 2019-03-18  
Resolution : 1.44 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](mailto: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.

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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

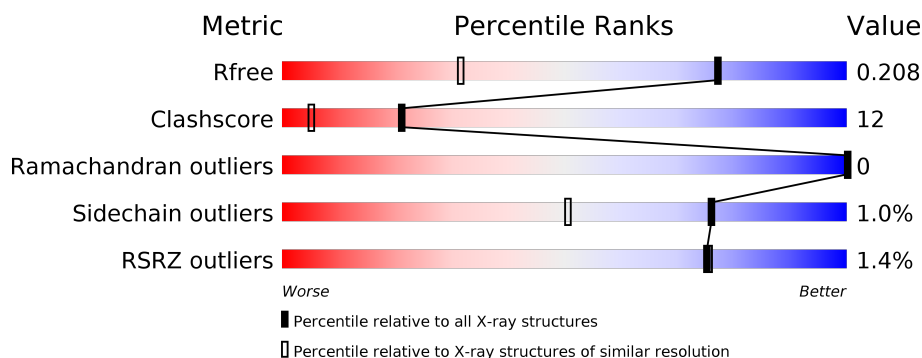
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.44 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	2021 (1.46-1.42)
Clashscore	141614	2086 (1.46-1.42)
Ramachandran outliers	138981	2047 (1.46-1.42)
Sidechain outliers	138945	2047 (1.46-1.42)
RSRZ outliers	127900	1993 (1.46-1.42)

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  $\geq 3$ , 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	330	<div> <div>%</div> <div> <div></div> <div>78%</div> <div>20%</div> <div>..</div> </div> </div>
1	B	330	<div> <div>%</div> <div> <div></div> <div>84%</div> <div>16%</div> </div> </div>
1	C	330	<div> <div>%</div> <div> <div></div> <div>83%</div> <div>15%</div> <div>.</div> </div> </div>
1	D	330	<div> <div>2%</div> <div> <div></div> <div>80%</div> <div>20%</div> </div> </div>
2	E	2	<div> <div></div> <div>100%</div> </div>
2	F	2	<div> <div></div> <div>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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	BGC	E	2	-	-	X	-
2	BGC	F	2	-	-	X	-

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 22940 atoms, of which 10320 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 Endoglucanase(Endo-1,4-beta-glucanase)protein.

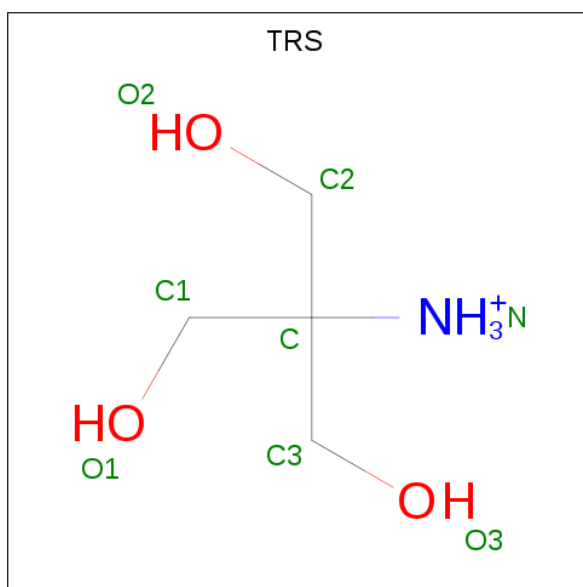
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	326	Total	C	H	N	O	S	0	9	0
			5219	1703	2571	459	477	9			
1	B	330	Total	C	H	N	O	S	0	4	0
			5183	1695	2538	458	483	9			
1	C	325	Total	C	H	N	O	S	0	9	0
			5179	1693	2544	457	476	9			
1	D	329	Total	C	H	N	O	S	0	9	0
			5274	1720	2600	464	481	9			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	2	Total	C	H	O	0	0	0
			44	12	21	11			
2	F	2	Total	C	H	O	0	0	0
			45	12	22	11			

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C<sub>4</sub>H<sub>12</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	0
			14	4	6	1	3		
3	B	1	Total	C	H	N	O	0	0
			14	4	6	1	3		
3	C	1	Total	C	H	N	O	0	0
			14	4	6	1	3		
3	D	1	Total	C	H	N	O	0	0
			14	4	6	1	3		

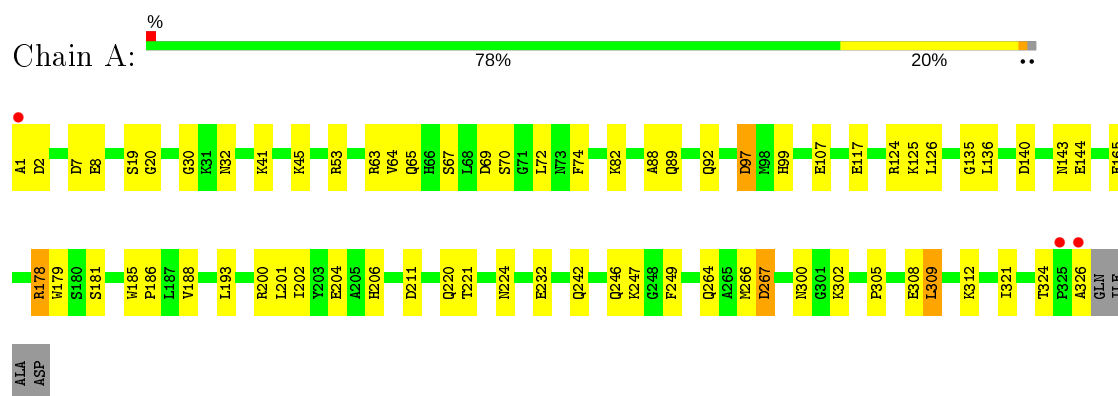
- Molecule 4 is water.

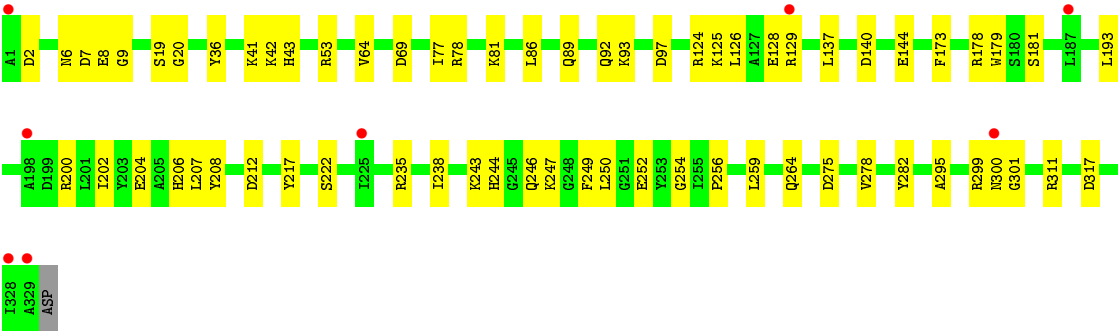
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	458	Total	O	0	0
			458	458		
4	B	517	Total	O	0	0
			517	517		
4	C	468	Total	O	0	0
			468	468		
4	D	497	Total	O	0	0
			497	497		

### 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: Endoglucanase(Endo-1,4-beta-glucanase)protein





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

Chain E: 100%



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

Chain F: 100%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.25Å 82.82Å 104.68Å 90.00° 91.97° 90.00°	Depositor
Resolution (Å)	48.19 – 1.44 48.19 – 1.44	Depositor EDS
% Data completeness (in resolution range)	99.2 (48.19-1.44) 89.6 (48.19-1.44)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.46 (at 1.43Å)	Xtriage
Refinement program	PHENIX V.1.14-3260	Depositor
R, $R_{free}$	0.179 , 0.224 0.187 , 0.208	Depositor DCC
$R_{free}$ test set	10832 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	11.2	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 42.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.109 for h,-k,-l	Xtriage
Reported twinning fraction	0.140 for h,-k,-l	Depositor
Outliers	0 of 216633 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	22940	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.70% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TRS, BGC

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	0.60	0/2764	0.75	2/3752 (0.1%)
1	B	0.59	0/2738	0.73	1/3721 (0.0%)
1	C	0.60	0/2743	0.73	1/3727 (0.0%)
1	D	0.57	0/2785	0.71	0/3780
All	All	0.59	0/11030	0.73	4/14980 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	207	LEU	CA-CB-CG	5.86	128.78	115.30
1	A	200	ARG	NE-CZ-NH1	-5.79	117.41	120.30
1	C	210	ASP	CB-CG-OD1	5.33	123.09	118.30
1	A	97	ASP	CB-CG-OD2	-5.19	113.63	118.30

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.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2648	2571	2560	74	1
1	B	2645	2538	2537	52	0
1	C	2635	2544	2537	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2674	2600	2604	77	1
2	E	23	21	19	11	0
2	F	23	22	21	13	0
3	A	8	6	12	0	0
3	B	8	6	12	0	0
3	C	8	6	12	0	0
3	D	8	6	12	1	0
4	A	458	0	0	43	5
4	B	517	0	0	31	8
4	C	468	0	0	29	7
4	D	497	0	0	35	11
All	All	12620	10320	10326	254	17

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 12.

The worst 5 of 254 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)
2:E:1:BGC:O3	2:E:2:BGC:O5	1.82	0.97
1:A:178:ARG:NH1	2:E:2:BGC:O2	1.99	0.94
1:D:247:LYS:HE3	4:D:833:HOH:O	1.67	0.93
1:D:2[B]:ASP:OD1	1:D:93[B]:LYS:NZ	2.00	0.93
1:D:41[B]:LYS:NZ	1:D:89:GLN:OE1	2.03	0.91

The worst 5 of 17 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:B:1007:HOH:O	4:B:1017:HOH:O[2_543]	1.86	0.34
4:A:846:HOH:O	4:C:858:HOH:O[2_554]	1.87	0.33
4:A:534:HOH:O	4:C:666:HOH:O[2_554]	1.99	0.21
4:B:569:HOH:O	4:D:527:HOH:O[2_443]	2.01	0.19
1:A:8:GLU:OE1	1:D:78:ARG:NH2[2_444]	2.07	0.13

## 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	334/330 (101%)	327 (98%)	7 (2%)	0	100	100
1	B	332/330 (101%)	327 (98%)	5 (2%)	0	100	100
1	C	332/330 (101%)	325 (98%)	7 (2%)	0	100	100
1	D	337/330 (102%)	330 (98%)	7 (2%)	0	100	100
All	All	1335/1320 (101%)	1309 (98%)	26 (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	273/267 (102%)	268 (98%)	5 (2%)	59	25
1	B	270/267 (101%)	268 (99%)	2 (1%)	84	64
1	C	271/267 (102%)	268 (99%)	3 (1%)	73	47
1	D	275/267 (103%)	274 (100%)	1 (0%)	91	80
All	All	1089/1068 (102%)	1078 (99%)	11 (1%)	76	50

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	309	LEU
1	B	177	GLU
1	C	178	ARG

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Mol	Chain	Res	Type
1	A	300	ASN
1	C	42	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	191	ASN
1	D	220	GLN
1	C	300	ASN
1	B	169	GLN
1	D	105	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	BGC	E	1	2	12,12,12	1.43	1 (8%)	17,17,17	2.79	7 (41%)
2	BGC	E	2	2	11,11,12	1.95	3 (27%)	15,15,17	5.49	11 (73%)
2	BGC	F	1	2	12,12,12	1.47	1 (8%)	17,17,17	2.13	5 (29%)
2	BGC	F	2	2	11,11,12	1.71	3 (27%)	15,15,17	2.57	10 (66%)

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	BGC	E	1	2	-	1/2/22/22	0/1/1/1
2	BGC	E	2	2	-	0/2/19/22	0/1/1/1
2	BGC	F	1	2	-	2/2/22/22	0/1/1/1
2	BGC	F	2	2	-	0/2/19/22	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	1	BGC	O5-C1	4.48	1.54	1.42
2	E	1	BGC	O5-C1	3.95	1.52	1.42
2	E	2	BGC	O5-C5	3.80	1.51	1.43
2	E	2	BGC	O5-C1	3.32	1.49	1.43
2	F	2	BGC	O5-C5	2.97	1.49	1.43

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	2	BGC	C1-C2-C3	14.21	127.14	109.67
2	E	2	BGC	C1-O5-C5	-9.49	99.33	112.19
2	E	2	BGC	O4-C4-C3	-5.60	97.39	110.35
2	E	1	BGC	C4-C3-C2	-5.19	101.77	110.82
2	E	1	BGC	O4-C4-C3	5.12	122.18	110.35

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	1	BGC	O5-C5-C6-O6
2	F	1	BGC	C4-C5-C6-O6
2	E	1	BGC	O5-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 24 short contacts:

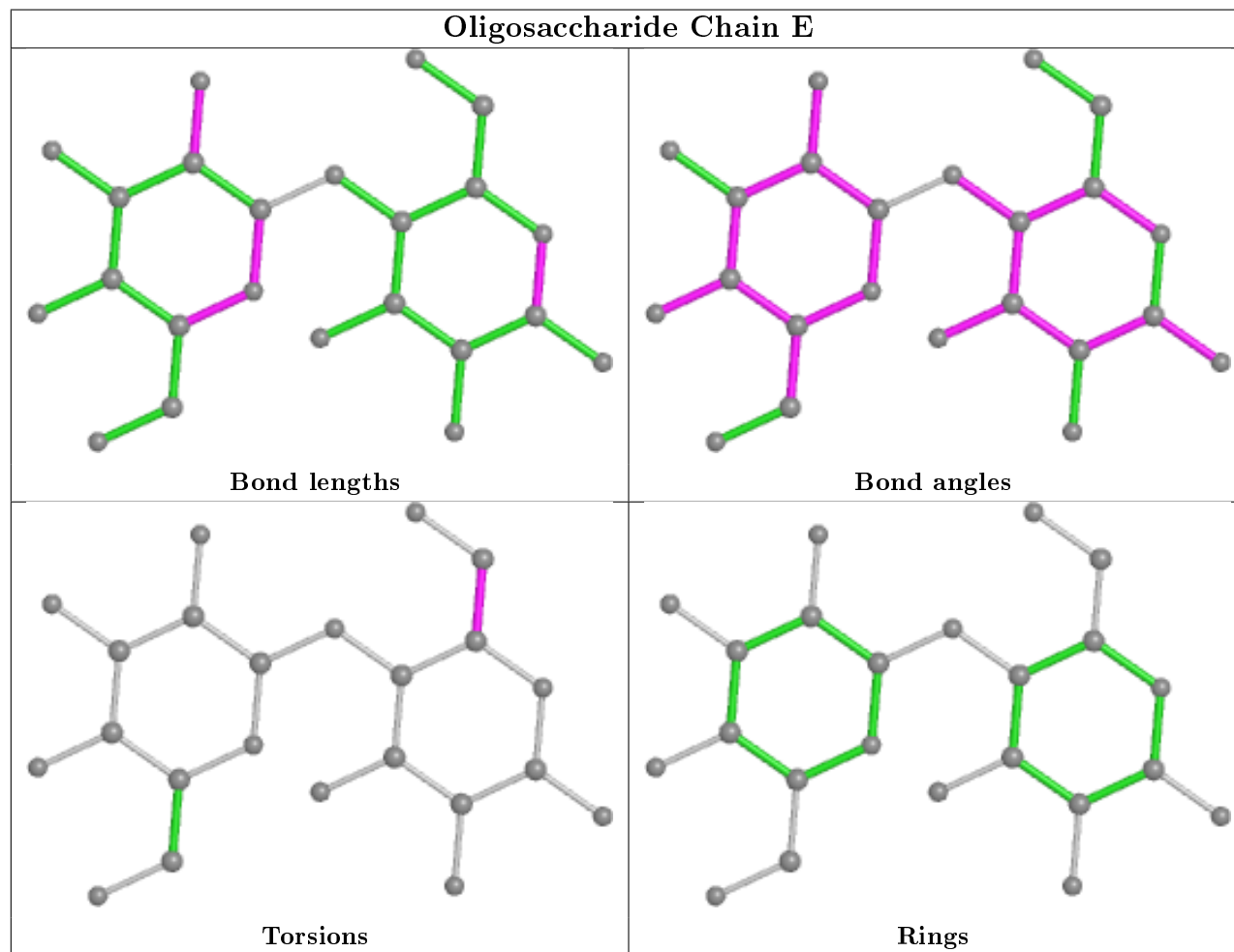
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	1	BGC	3	0
2	F	2	BGC	10	0

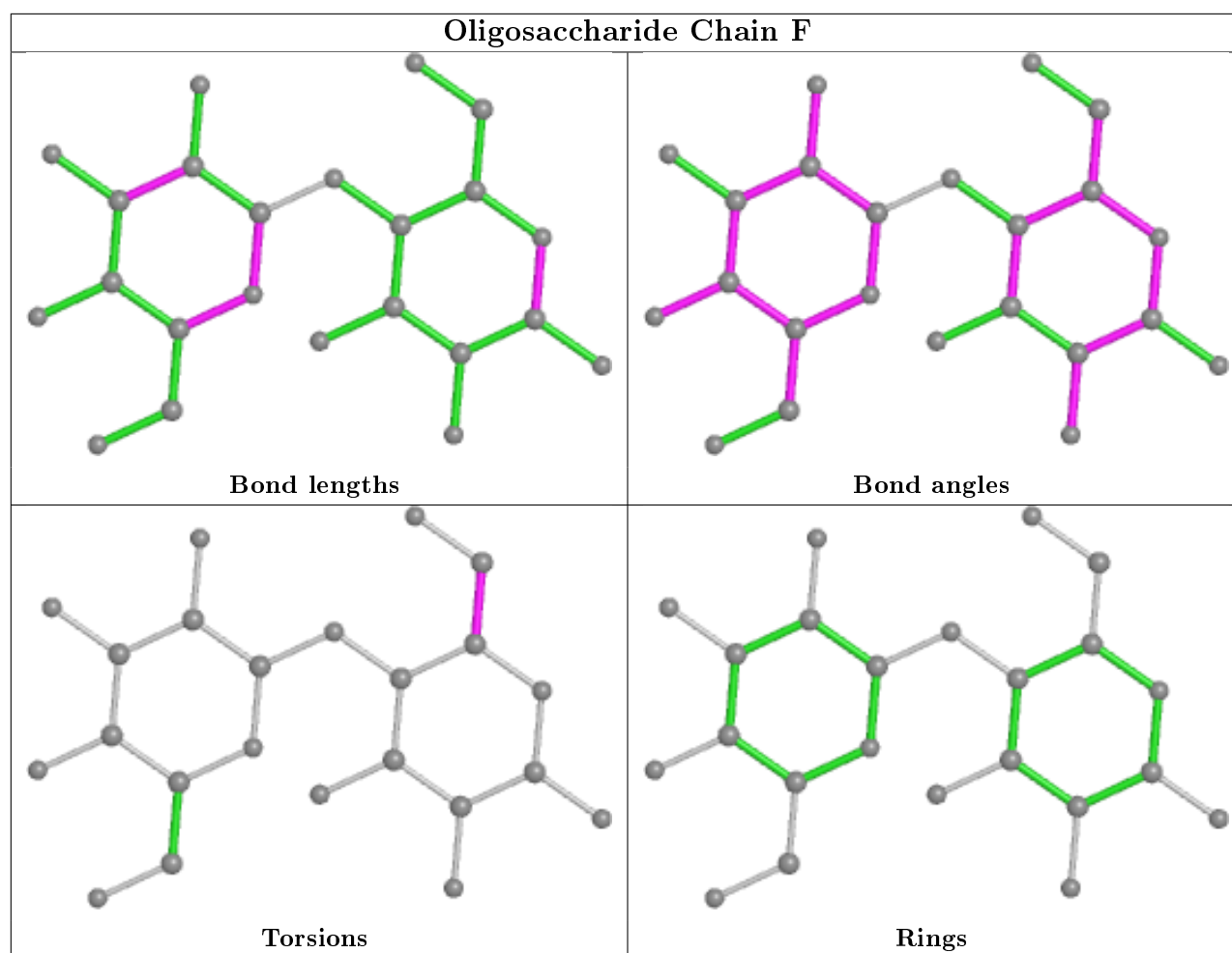
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	BGC	3	0
2	E	2	BGC	10	0

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](#)

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	TRS	A	401	-	7,7,7	0.39	0	9,9,9	0.45	0
3	TRS	C	401	-	7,7,7	0.38	0	9,9,9	0.66	0
3	TRS	B	401	-	7,7,7	0.42	0	9,9,9	0.81	0
3	TRS	D	401	-	7,7,7	0.64	0	9,9,9	1.83	3 (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
3	TRS	A	401	-	-	3/9/9/9	-
3	TRS	C	401	-	-	3/9/9/9	-
3	TRS	B	401	-	-	5/9/9/9	-
3	TRS	D	401	-	-	6/9/9/9	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	401	TRS	C3-C-C2	3.65	122.12	110.81
3	D	401	TRS	C3-C-C1	-2.76	102.25	110.81
3	D	401	TRS	O3-C3-C	2.46	118.81	111.00

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	401	TRS	C2-C-C1-O1
3	A	401	TRS	C3-C-C1-O1
3	B	401	TRS	C2-C-C1-O1
3	B	401	TRS	C3-C-C1-O1
3	B	401	TRS	N-C-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	401	TRS	1	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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	326/330 (98%)	-0.06	3 (0%) 84 84	6, 12, 23, 45	0
1	B	330/330 (100%)	-0.10	3 (0%) 84 84	5, 11, 22, 42	0
1	C	325/330 (98%)	-0.04	4 (1%) 79 79	6, 13, 23, 38	0
1	D	329/330 (99%)	0.01	8 (2%) 59 60	5, 13, 26, 44	0
All	All	1310/1320 (99%)	-0.05	18 (1%) 75 75	5, 12, 24, 45	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	329	ALA	5.9
1	A	325	PRO	5.5
1	C	1	ALA	4.5
1	D	328	ILE	4.5
1	D	329	ALA	4.4

### 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, 95<sup>th</sup> 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.

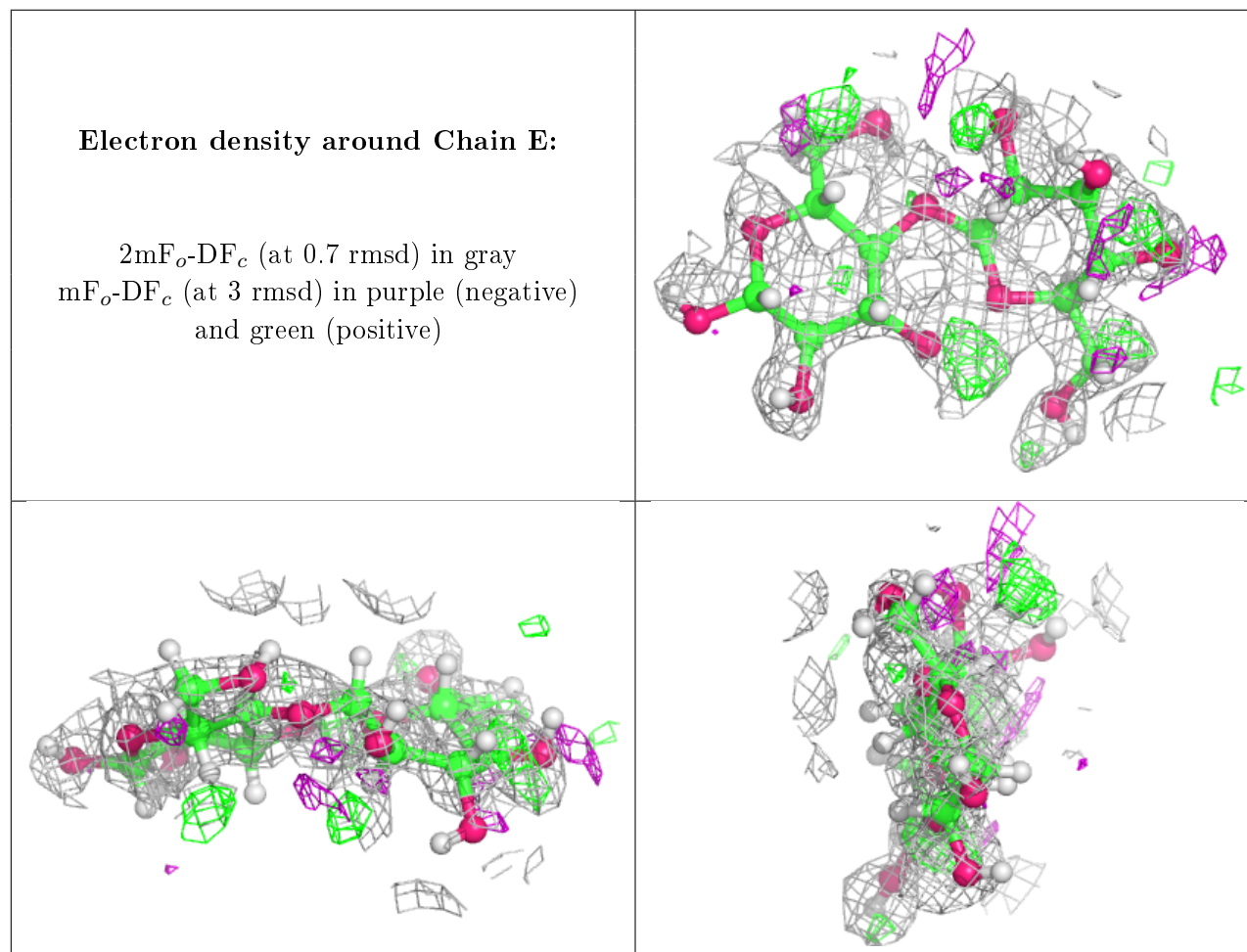
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	BGC	E	1	12/12	0.70	0.25	13,28,46,76	22
2	BGC	E	2	11/12	0.72	0.26	7,18,39,62	22

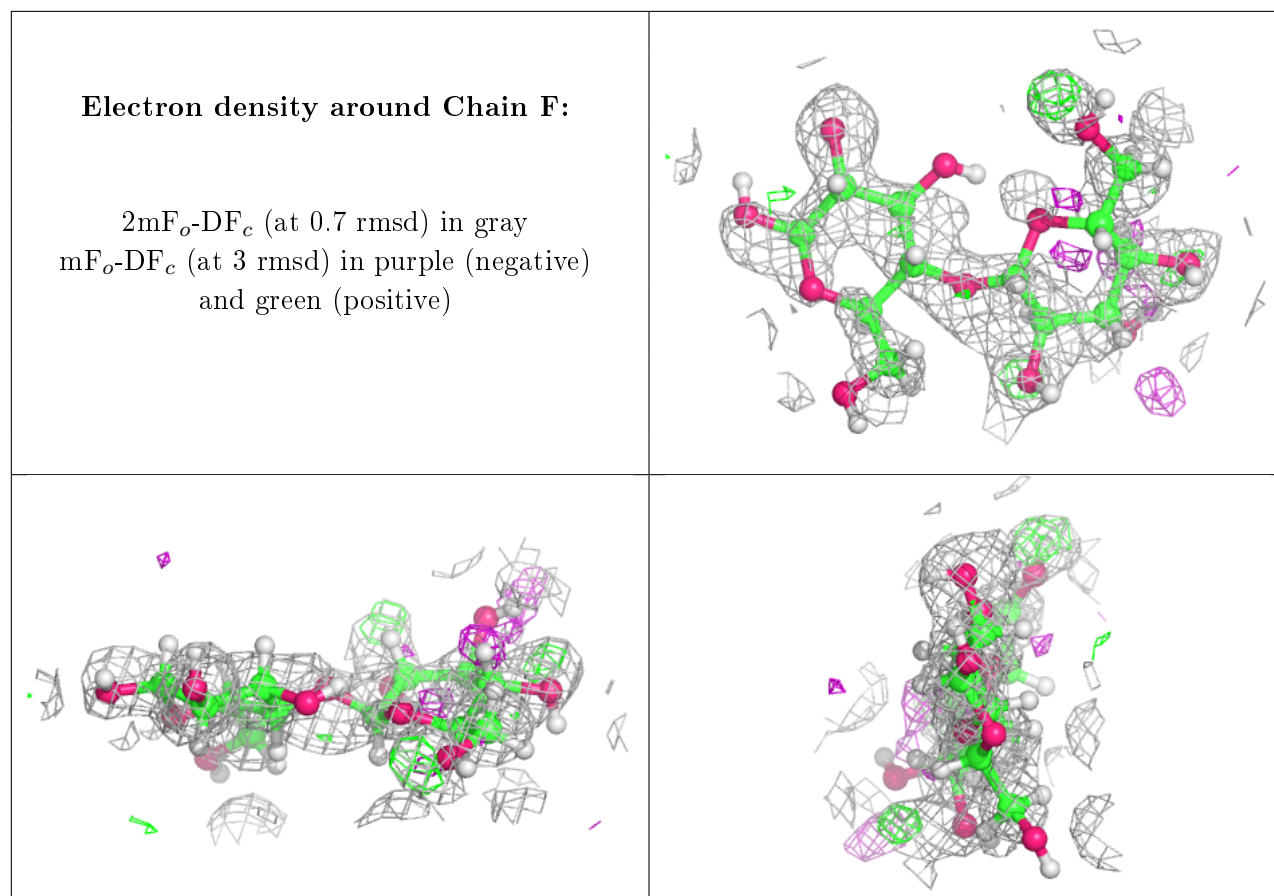
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	BGC	F	1	12/12	0.80	0.22	16,31,75,90	0
2	BGC	F	2	11/12	0.81	0.27	3,28,66,87	0

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](#)

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, 95<sup>th</sup> 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
3	TRS	A	401	8/8	0.89	0.17	9,34,59,71	0
3	TRS	C	401	8/8	0.90	0.11	15,21,29,29	0
3	TRS	B	401	8/8	0.90	0.13	9,20,33,33	0
3	TRS	D	401	8/8	0.93	0.15	9,15,41,94	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.