



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 09:29 AM BST

PDB ID : 4TF4  
Title : ENDO/EXOCELLULASE:CELLOPENTAOSE FROM THERMOMONOSPORA  
Authors : Sakon, J.; Wilson, D.B.; Karplus, P.A.  
Deposited on : 1997-05-31  
Resolution : 2.00 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](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

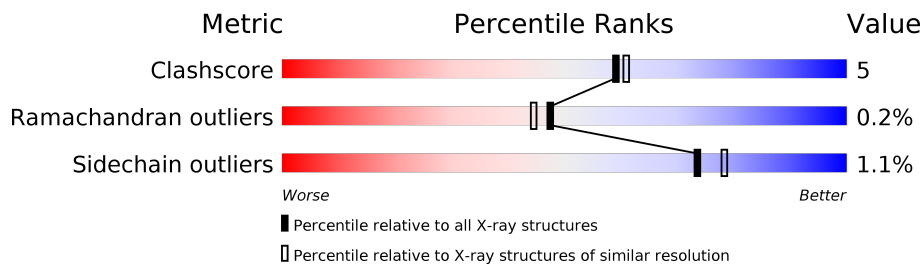
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	605	
1	B	605	
2	C	4	
2	E	4	
3	D	2	
3	F	2	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 11002 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 T. FUSCA ENDO/EXO-CELLULASE E4 CATALYTIC DOMAIN AND CELLULOSE-BINDING DOMAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	605	4757	3027	792	923	15	9	0	0
1	B	605	4757	3027	792	923	15	9	0	0

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
2	C	4	45	24	21	0	0	0
2	E	4	45	24	21	0	0	0

- Molecule 3 is an oligosaccharide called beta-D-glucopyranose-(1-4)-beta-D-glucopyranose.



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

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	2	Total Ca 2 2	0	0
4	A	2	Total Ca 2 2	0	0

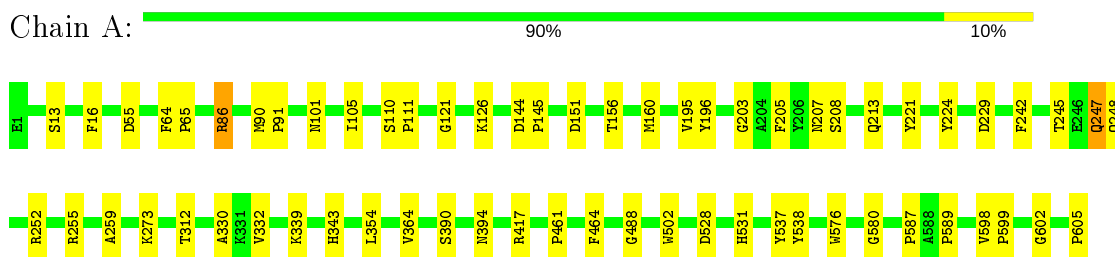
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	687	Total O 687 687	0	0
5	B	661	Total O 661 661	0	0

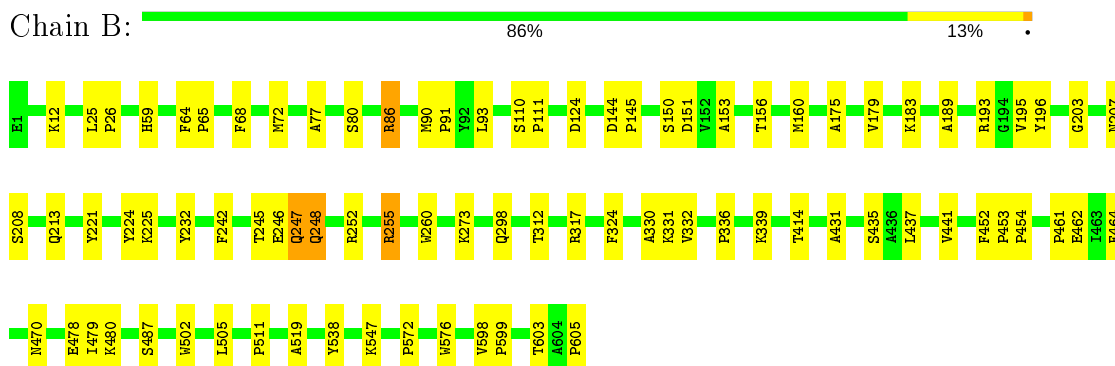
### 3 Residue-property plots [i](#)

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. 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. 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.

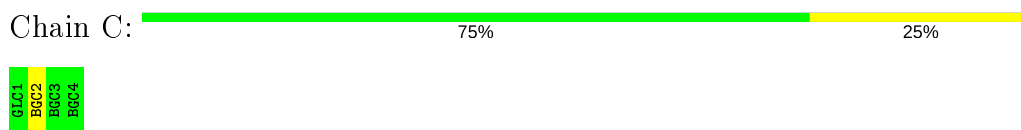
- Molecule 1: T. FUSCA ENDO/EXO-CELLULASE E4 CATALYTIC DOMAIN AND CELLULOSE-BINDING DOMAIN



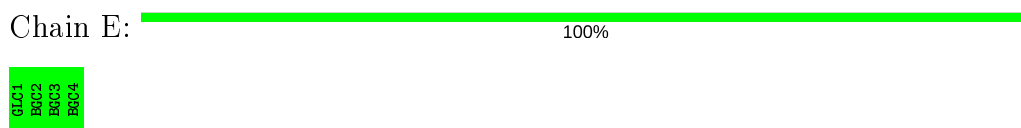
- Molecule 1: T. FUSCA ENDO/EXO-CELLULASE E4 CATALYTIC DOMAIN AND CELLULOSE-BINDING DOMAIN



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



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



- Molecule 3: beta-D-glucopyranose-(1-4)-beta-D-glucopyranose

Chain D:  100%

BG01  
BG02

- Molecule 3: beta-D-glucopyranose-(1-4)-beta-D-glucopyranose

Chain F:  100%

BG01  
BG02

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	145.68Å 145.68Å 157.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.00 8.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	91.0 (8.00-2.00) 28.4 (8.00-2.00)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	0.25	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.89 (at 2.00Å)	Xtrriage
Refinement program	X-PLOR 3.8	Depositor
R, $R_{free}$	0.215 , (Not available) 0.187 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.6	Xtrriage
Anisotropy	0.077	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.25 , 87.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	11002	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.97% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GLC, CA, 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	0.35	0/4912	0.60	3/6716 (0.0%)
1	B	0.36	0/4912	0.58	4/6716 (0.1%)
All	All	0.36	0/9824	0.59	7/13432 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	255	ARG	NE-CZ-NH2	-6.59	117.01	120.30
1	B	255	ARG	NE-CZ-NH1	6.55	123.58	120.30
1	A	255	ARG	NE-CZ-NH2	-6.53	117.04	120.30
1	A	86	ARG	NE-CZ-NH2	-5.76	117.42	120.30
1	B	86	ARG	NE-CZ-NH1	5.74	123.17	120.30
1	B	86	ARG	NE-CZ-NH2	-5.53	117.54	120.30
1	A	255	ARG	NE-CZ-NH1	5.49	123.05	120.30

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	4757	0	4384	36	0
1	B	4757	0	4384	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	45	0	39	0	0
2	E	45	0	39	0	0
3	D	23	0	21	0	0
3	F	23	0	21	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	687	0	0	7	0
5	B	661	0	0	10	0
All	All	11002	0	8888	87	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 5.

All (87) 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:247:GLN:NE2	1:B:255:ARG:HH22	1.95	0.64
1:A:273:LYS:HG3	1:A:332:VAL:HG11	1.82	0.62
1:B:576:TRP:CG	1:B:605:PRO:HG3	2.36	0.61
1:A:259:ALA:HB3	5:A:6198:HOH:O	2.01	0.60
1:B:195:VAL:HG13	1:B:208:SER:HB3	1.83	0.60
1:A:195:VAL:HG13	1:A:208:SER:HB3	1.84	0.60
1:B:245:THR:HA	1:B:252:ARG:HA	1.84	0.59
1:B:175:ALA:O	1:B:179:VAL:HG23	2.03	0.58
1:B:576:TRP:CD1	1:B:605:PRO:HG3	2.38	0.58
1:B:461:PRO:HB2	1:B:464:PHE:CD1	2.39	0.57
1:A:101:ASN:O	1:A:105:ILE:HG13	2.06	0.55
1:A:203:GLY:O	1:A:207:ASN:HB2	2.06	0.55
1:A:576:TRP:CD1	1:A:605:PRO:HG3	2.41	0.55
1:A:502:TRP:CD1	1:A:538:TYR:HB3	2.42	0.55
1:B:203:GLY:O	1:B:207:ASN:HB2	2.08	0.54
1:B:153:ALA:HB3	1:B:189:ALA:HB2	1.90	0.54
1:B:462:GLU:HB3	1:B:487:SER:HA	1.90	0.54
1:A:247:GLN:HG3	1:A:248:GLN:H	1.72	0.53
1:A:90:MET:N	1:A:91:PRO:HD2	2.24	0.53
1:B:273:LYS:HG3	1:B:332:VAL:HG11	1.90	0.53
1:A:55:ASP:HB2	5:A:6029:HOH:O	2.10	0.52
1:B:336:PRO:HG3	5:B:6263:HOH:O	2.10	0.51
1:B:247:GLN:HG3	1:B:248:GLN:H	1.76	0.51
1:B:90:MET:N	1:B:91:PRO:HD2	2.26	0.51
1:A:394:ASN:OD1	1:A:417:ARG:HD3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:PRO:HB2	5:B:6029:HOH:O	2.12	0.49
1:A:245:THR:HA	1:A:252:ARG:HA	1.94	0.49
1:B:225:LYS:HE2	1:B:225:LYS:HA	1.95	0.48
1:B:519:ALA:HB3	5:B:6041:HOH:O	2.12	0.48
1:B:183:LYS:HD2	1:B:232:TYR:OH	2.14	0.48
1:B:505:LEU:HD21	1:B:511:PRO:HD3	1.96	0.48
1:A:343:HIS:HD2	5:A:6050:HOH:O	1.95	0.48
1:B:255:ARG:NH1	1:B:298:GLN:HE22	2.13	0.47
1:B:156:THR:O	1:B:160:MET:HG3	2.14	0.47
1:B:195:VAL:CG1	1:B:208:SER:HB3	2.43	0.47
1:A:576:TRP:CG	1:A:605:PRO:HG3	2.50	0.47
1:A:531:HIS:HB2	1:A:537:TYR:CE2	2.50	0.47
1:B:603:THR:HG23	5:B:6267:HOH:O	2.15	0.47
1:B:221:TYR:O	1:B:224:TYR:HB3	2.14	0.47
1:A:195:VAL:CG1	1:A:208:SER:HB3	2.45	0.47
1:B:246:GLU:OE1	1:B:255:ARG:HG3	2.15	0.47
1:A:144:ASP:HB2	1:A:145:PRO:CD	2.46	0.46
1:B:195:VAL:HG13	1:B:208:SER:CB	2.45	0.46
1:B:331:LYS:HD2	5:B:6439:HOH:O	2.15	0.46
1:B:437:LEU:O	1:B:441:VAL:HG23	2.16	0.46
1:A:589:PRO:O	1:A:602:GLY:HA2	2.16	0.46
1:B:330:ALA:O	1:B:339:LYS:HE2	2.17	0.45
1:B:144:ASP:HB2	1:B:145:PRO:CD	2.46	0.45
1:A:330:ALA:O	1:A:339:LYS:HE2	2.17	0.45
1:B:502:TRP:CD1	1:B:538:TYR:HB3	2.53	0.44
1:A:221:TYR:O	1:A:224:TYR:HB3	2.18	0.44
1:A:156:THR:O	1:A:160:MET:HG3	2.18	0.44
1:A:229:ASP:HA	5:A:6200:HOH:O	2.17	0.43
1:B:80:SER:HB2	5:B:6431:HOH:O	2.17	0.43
1:A:461:PRO:HB2	1:A:464:PHE:CD1	2.52	0.43
1:B:414:THR:HB	5:B:6468:HOH:O	2.17	0.43
1:B:110:SER:HB2	1:B:111:PRO:HD2	2.00	0.43
1:A:126:LYS:HG3	5:A:6292:HOH:O	2.18	0.43
1:A:598:VAL:HA	1:A:599:PRO:HD3	1.92	0.43
1:A:121:GLY:HA3	1:A:205:PHE:CZ	2.54	0.43
1:B:213:GLN:HG2	1:B:242:PHE:O	2.19	0.42
1:B:453:PRO:HA	1:B:454:PRO:HD3	1.93	0.42
1:A:354:LEU:HD23	1:A:364:VAL:HG21	2.01	0.42
1:B:12:LYS:HG2	1:B:452:PHE:CE2	2.55	0.42
1:B:77:ALA:HB2	1:B:93:LEU:HD21	2.02	0.42
1:A:144:ASP:HB2	1:A:145:PRO:HD2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:479:ILE:HG22	1:B:480:LYS:N	2.35	0.42
1:B:25:LEU:HA	1:B:26:PRO:HD3	1.80	0.41
1:A:64:PHE:HB3	1:A:65:PRO:HD3	2.02	0.41
1:B:324:PHE:CE1	1:B:435:SER:HB3	2.56	0.41
1:B:64:PHE:HB3	1:B:65:PRO:CD	2.50	0.41
1:B:150:SER:OG	1:B:193:ARG:HA	2.21	0.41
1:A:13:SER:O	1:A:16:PHE:HB3	2.21	0.41
1:A:390:SER:HB3	5:A:6513:HOH:O	2.19	0.41
1:A:580:GLY:HA3	5:A:6163:HOH:O	2.19	0.41
1:B:598:VAL:HA	1:B:599:PRO:HD3	1.94	0.41
1:B:414:THR:HA	5:B:6667:HOH:O	2.19	0.41
1:B:470:ASN:HB3	1:B:478:GLU:HG2	2.02	0.41
1:A:110:SER:HB2	1:A:111:PRO:HD2	2.02	0.41
1:B:68:PHE:CG	1:B:260:TRP:HA	2.56	0.41
1:B:72:MET:HB2	1:B:431:ALA:HB1	2.03	0.41
1:A:64:PHE:HB3	1:A:65:PRO:CD	2.51	0.41
1:B:59:HIS:HB2	1:B:124:ASP:OD1	2.21	0.40
1:A:213:GLN:HG2	1:A:242:PHE:O	2.21	0.40
1:A:587:PRO:O	1:A:589:PRO:HD3	2.20	0.40
1:B:572:PRO:HG3	5:B:6085:HOH:O	2.21	0.40
1:B:547:LYS:HE2	5:B:6396:HOH:O	2.21	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	603/605 (100%)	578 (96%)	23 (4%)	2 (0%)	41 37
1	B	603/605 (100%)	578 (96%)	24 (4%)	1 (0%)	47 44
All	All	1206/1210 (100%)	1156 (96%)	47 (4%)	3 (0%)	47 44

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	247	GLN
1	B	247	GLN
1	A	488	GLY

### 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	485/485 (100%)	480 (99%)	5 (1%)	76	81
1	B	485/485 (100%)	479 (99%)	6 (1%)	71	76
All	All	970/970 (100%)	959 (99%)	11 (1%)	73	78

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	ARG
1	A	151	ASP
1	A	196	TYR
1	A	312	THR
1	A	528	ASP
1	B	86	ARG
1	B	151	ASP
1	B	196	TYR
1	B	248	GLN
1	B	312	THR
1	B	317	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	180	GLN
1	A	247	GLN
1	A	248	GLN

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Mol	Chain	Res	Type
1	A	278	GLN
1	A	285	ASN
1	A	343	HIS
1	A	370	ASN
1	A	561	GLN
1	A	583	ASN
1	B	180	GLN
1	B	213	GLN
1	B	247	GLN
1	B	248	GLN
1	B	278	GLN
1	B	285	ASN
1	B	486	GLN
1	B	553	GLN
1	B	561	GLN
1	B	583	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](#)

12 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	0.38	0
2	BGC	C	2	2	11,11,12	0.47	0	15,15,17	0.81	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	BGC	C	3	2	11,11,12	0.52	0	15,15,17	0.35	0
2	BGC	C	4	2	11,11,12	0.28	0	15,15,17	0.35	0
3	BGC	D	1	3	12,12,12	0.18	0	17,17,17	0.34	0
3	BGC	D	2	3	11,11,12	0.46	0	15,15,17	0.44	0
2	GLC	E	1	2	12,12,12	0.44	0	17,17,17	0.44	0
2	BGC	E	2	2	11,11,12	0.51	0	15,15,17	0.73	0
2	BGC	E	3	2	11,11,12	0.48	0	15,15,17	0.32	0
2	BGC	E	4	2	11,11,12	0.35	0	15,15,17	0.49	0
3	BGC	F	1	3	12,12,12	0.36	0	17,17,17	0.49	0
3	BGC	F	2	3	11,11,12	0.40	0	15,15,17	0.36	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
2	GLC	C	1	2	-	0/2/22/22	0/1/1/1
2	BGC	C	2	2	-	0/2/19/22	0/1/1/1
2	BGC	C	3	2	-	0/2/19/22	0/1/1/1
2	BGC	C	4	2	-	0/2/19/22	0/1/1/1
3	BGC	D	1	3	-	0/2/22/22	0/1/1/1
3	BGC	D	2	3	-	0/2/19/22	0/1/1/1
2	GLC	E	1	2	-	0/2/22/22	0/1/1/1
2	BGC	E	2	2	-	0/2/19/22	0/1/1/1
2	BGC	E	3	2	-	0/2/19/22	0/1/1/1
2	BGC	E	4	2	-	0/2/19/22	0/1/1/1
3	BGC	F	1	3	-	0/2/22/22	0/1/1/1
3	BGC	F	2	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	BGC	C1-C2-C3	2.23	112.41	109.67

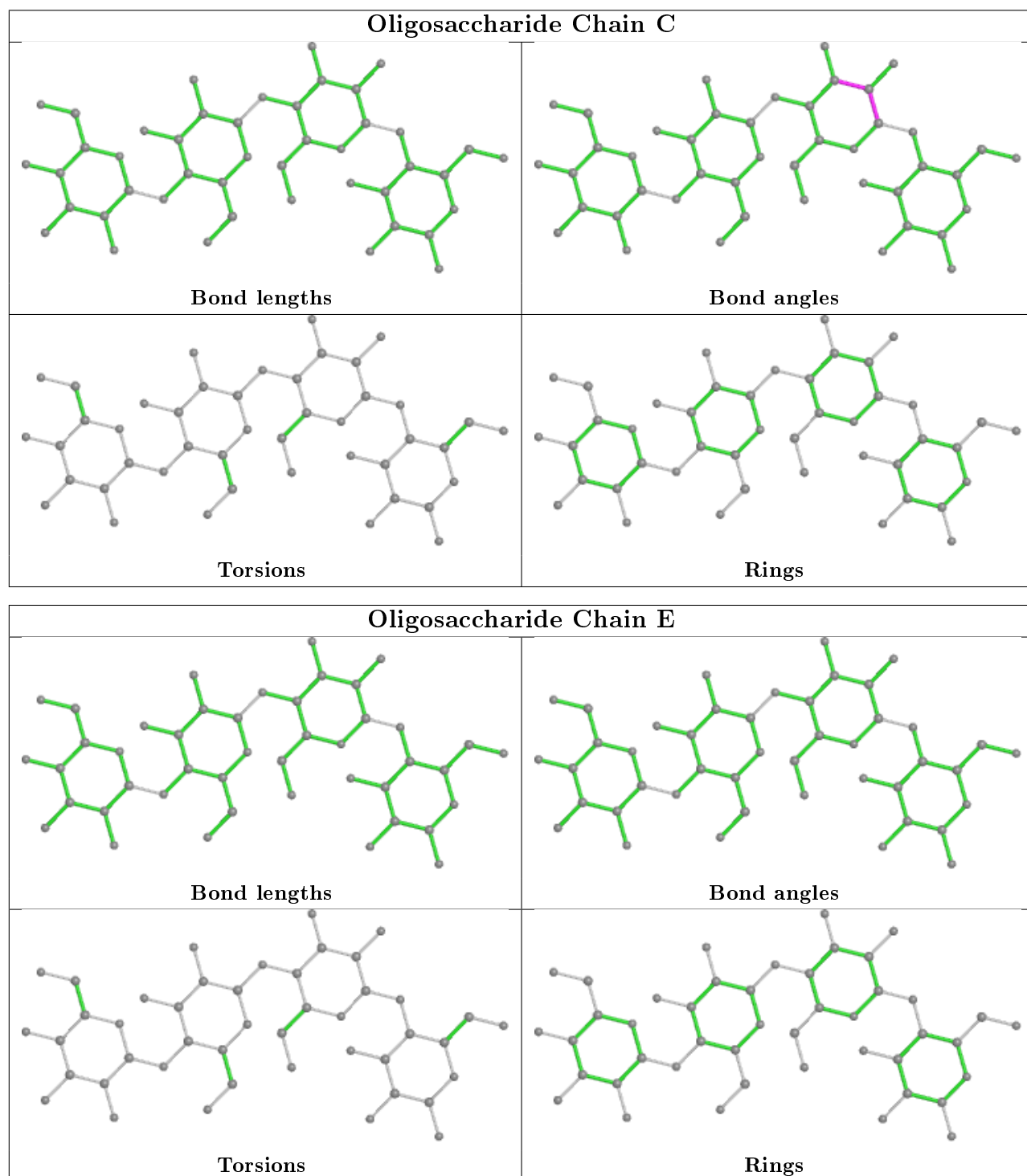
There are no chirality outliers.

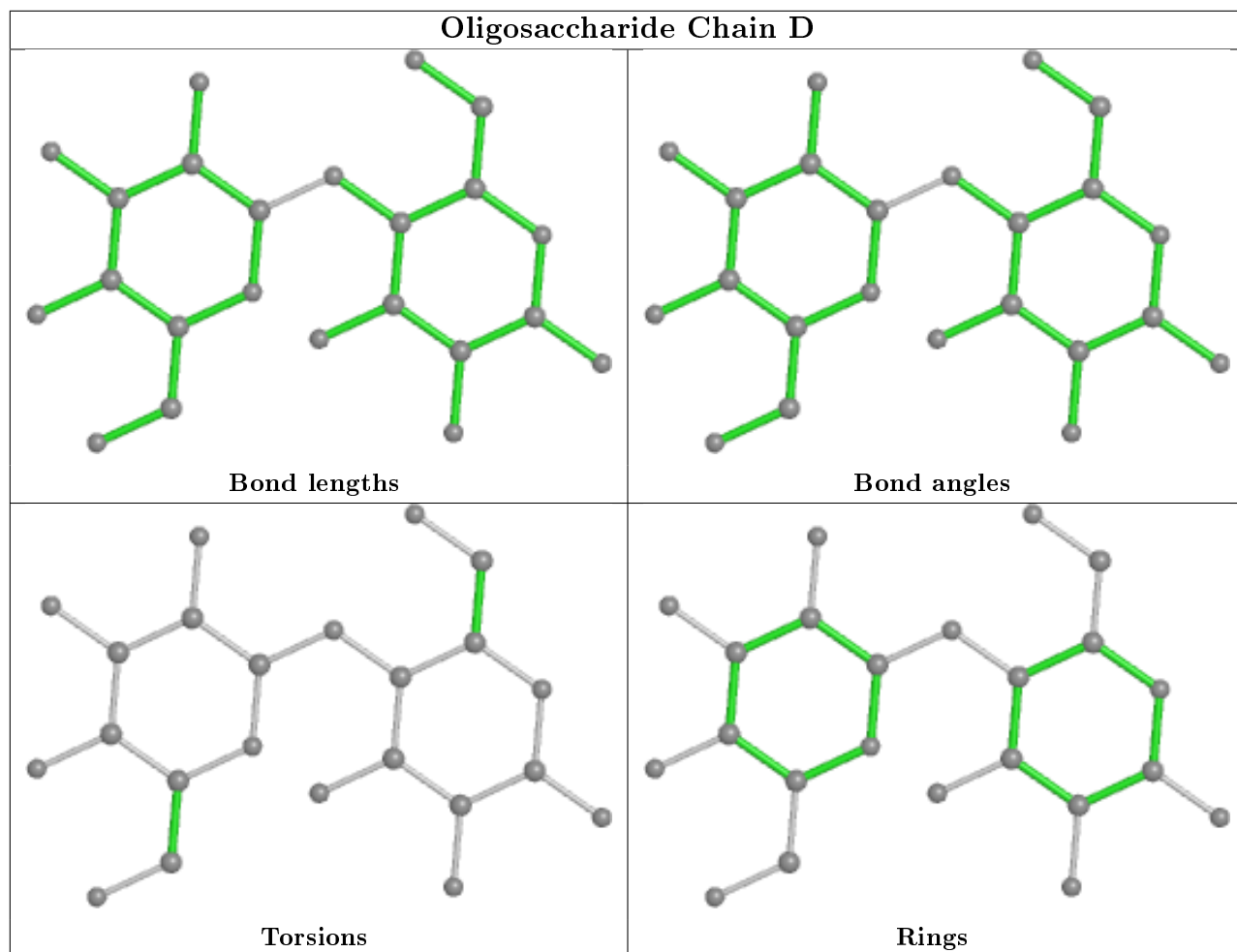
There are no torsion outliers.

There are no ring outliers.

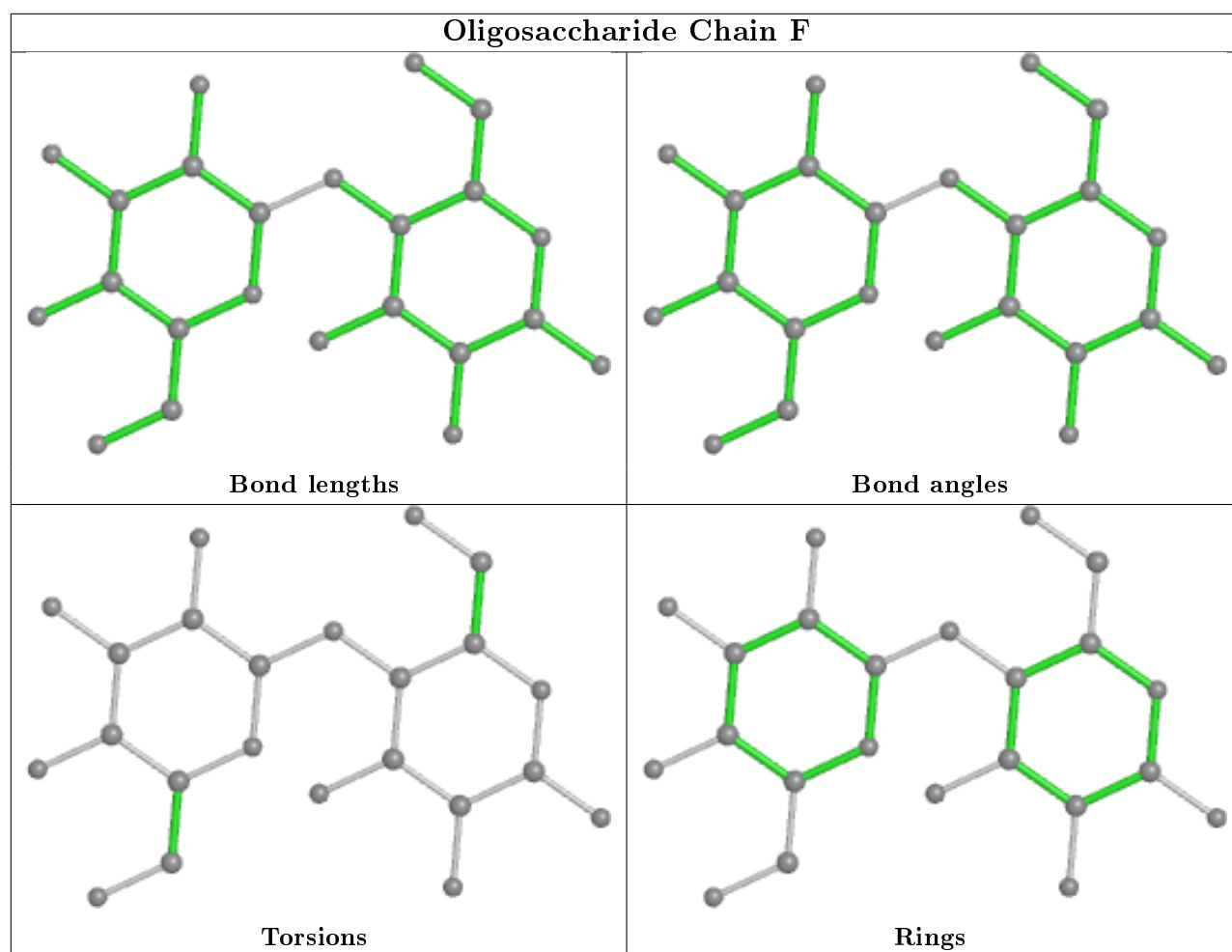
No monomer is involved in short contacts.

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 4 ligands modelled in this entry, 4 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

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

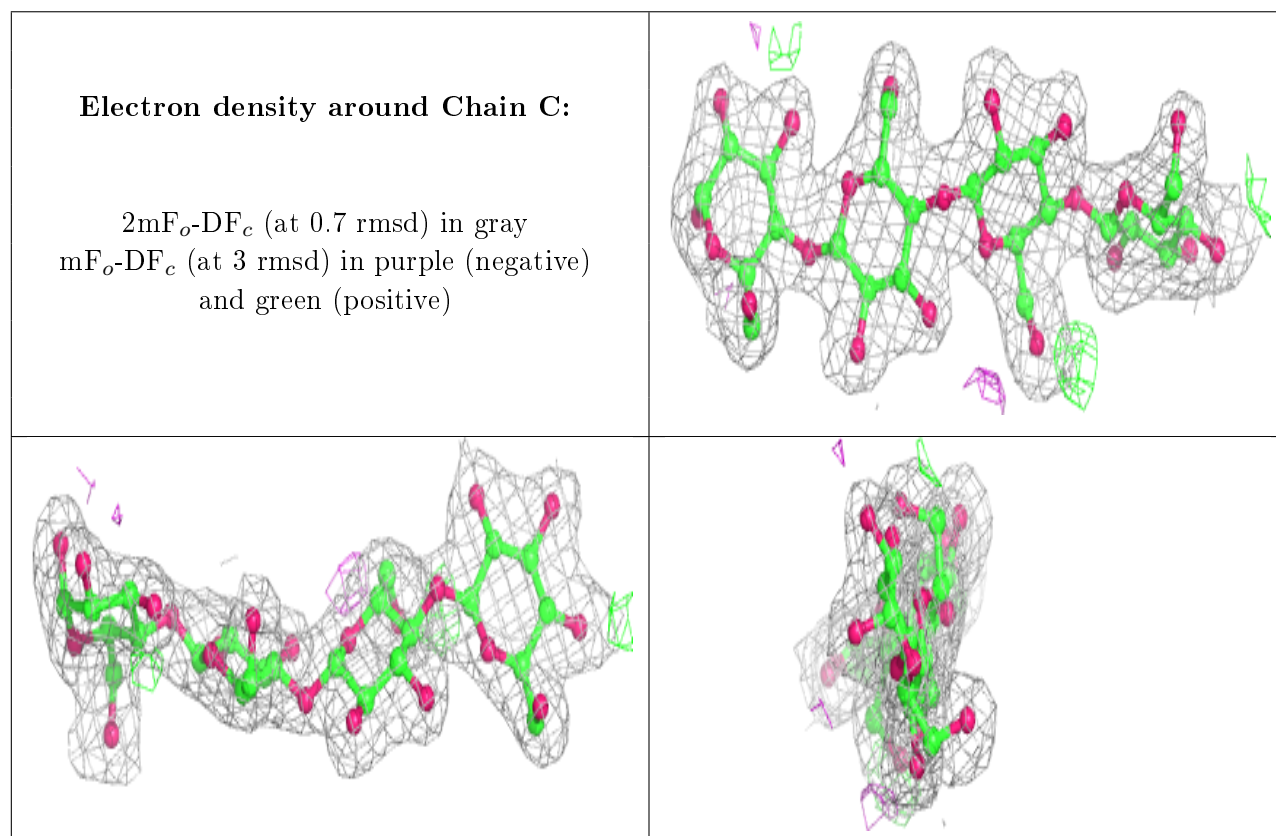
### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

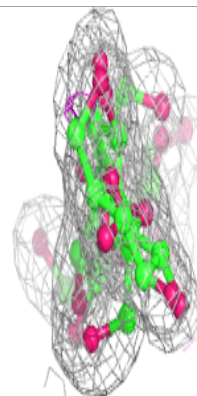
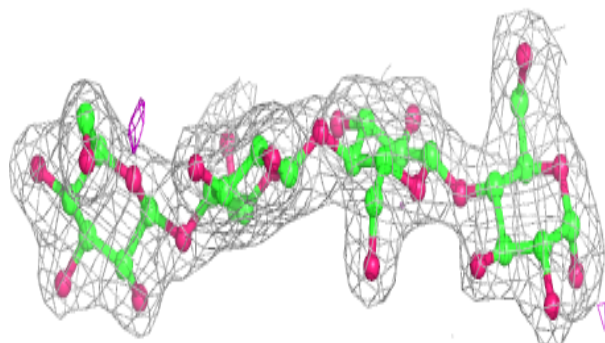
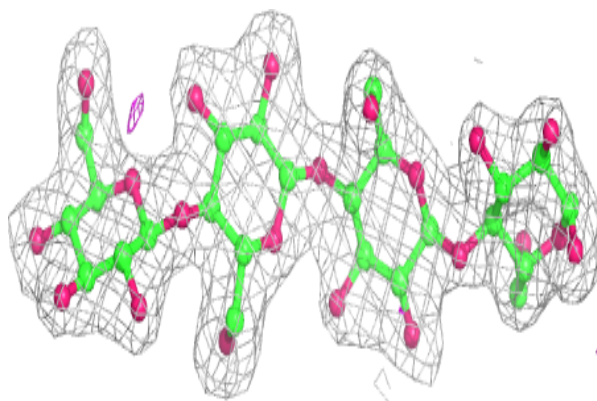
Unable to reproduce the depositors R factor - this section is therefore empty.

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.

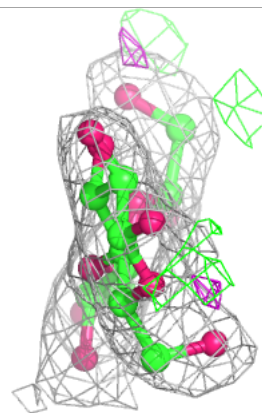
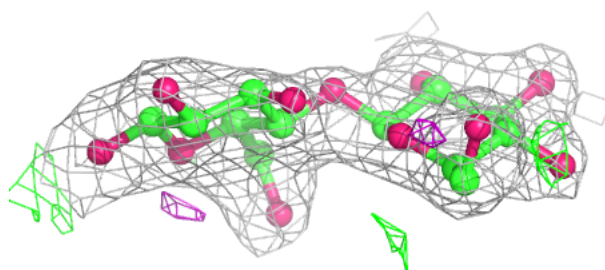
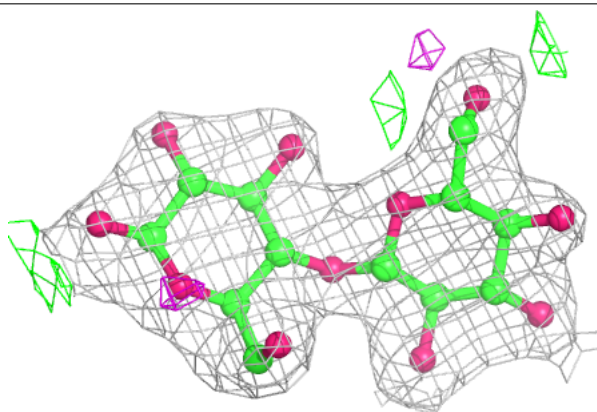


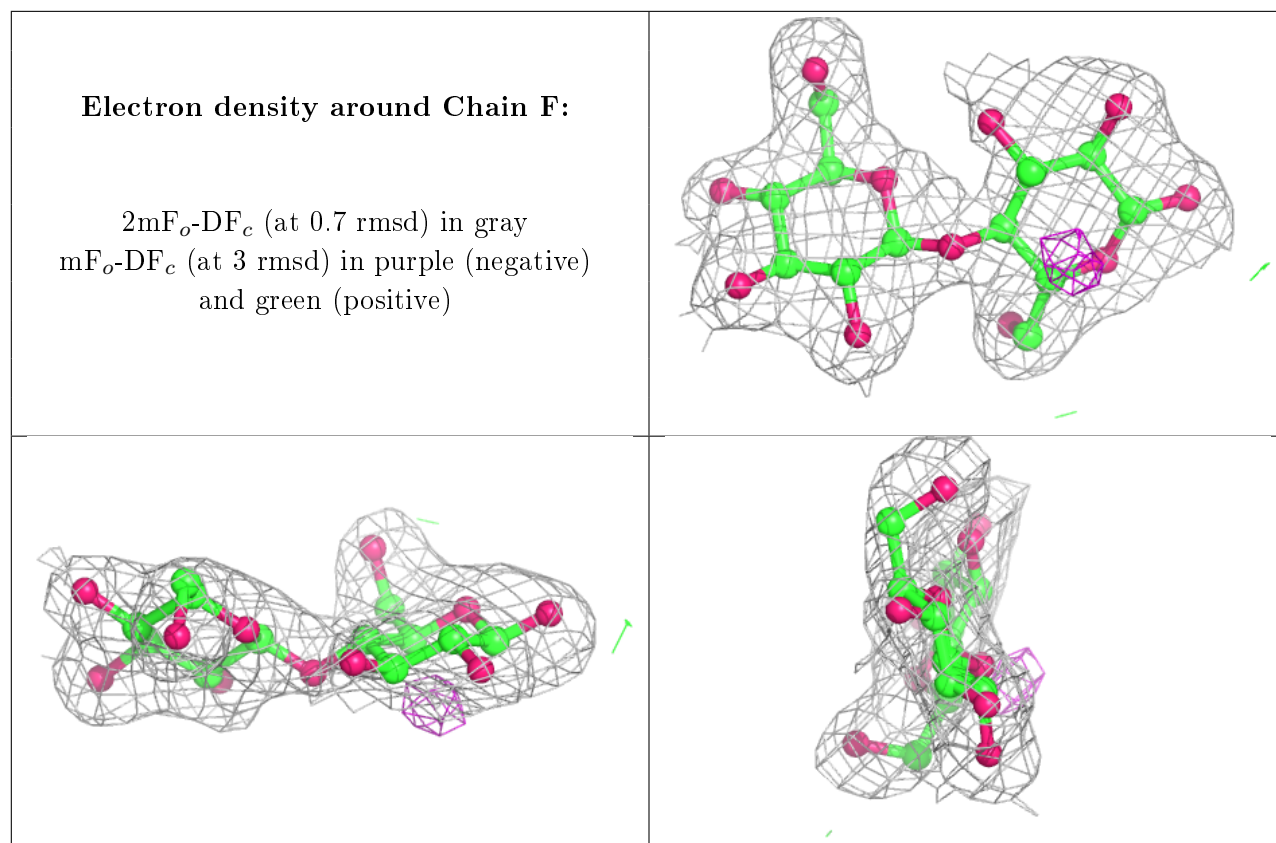
**Electron density around Chain E:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around Chain D:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.4 Ligands [i](#)

Unable to reproduce the depositor's R factor - this section is therefore empty.

## 6.5 Other polymers [i](#)

Unable to reproduce the depositor's R factor - this section is therefore empty.