



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 7, 2024 – 12:01 pm GMT

PDB ID : 6F2T
Title : Crystal structure of ectonucleotide phosphodiesterase/pyrophosphatase-3 (NPP3)
Authors : Dohler, C.; Zebisch, M.; Strater, N.
Deposited on : 2017-11-27
Resolution : 2.40 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

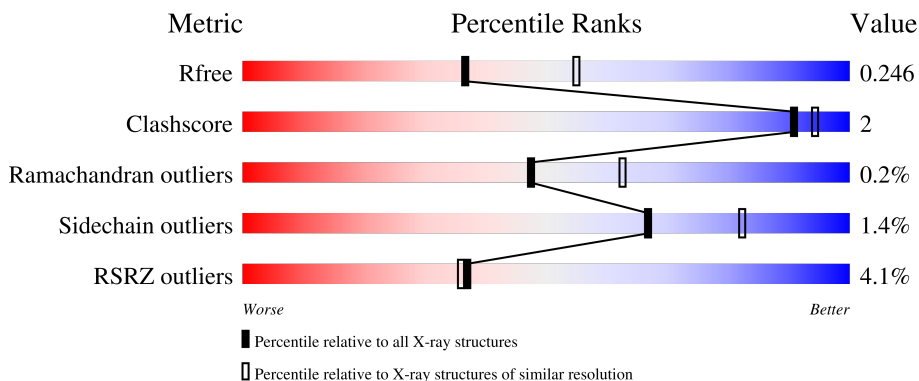
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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.




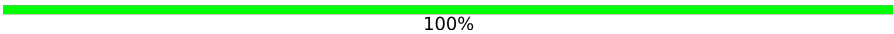
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 $\leq 5\%$. 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	749	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 88%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 6%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">4% 88% 6% 5%</p>
1	B	749	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 90%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 6%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 0%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">4% 90% 6% .</p>
2	C	2	<div style="width: 100%; height: 10px; background-color: yellow;"></div> <p style="text-align: center;">100%</p>
2	D	2	<div style="width: 100%; height: 10px; background-color: green;"></div> <p style="text-align: center;">100%</p>
2	E	2	<div style="display: flex; align-items: center;"> <div style="width: 50%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 50%; height: 10px; background-color: yellow;"></div> </div> <p style="text-align: center;">50% 50%</p>

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Mol	Chain	Length	Quality of chain
3	F	3	 33% 67%
3	G	3	 100%

2 Entry composition i

There are 8 unique types of molecules in this entry. The entry contains 12232 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 Ectonucleotide pyrophosphatase/phosphodiesterase family member 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	710	Total	C	N	O	S	0	0	0
			5715	3666	963	1053	33			
1	B	722	Total	C	N	O	S	0	0	0
			5809	3718	979	1079	33			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	136	ALA	-	expression tag	UNP P97675
A	137	GLU	-	expression tag	UNP P97675
A	138	THR	-	expression tag	UNP P97675
A	139	GLY	-	expression tag	UNP P97675
A	201	VAL	MET	variant	UNP P97675
A	596	ASN	SER	variant	UNP P97675
A	597	ARG	GLY	variant	UNP P97675
A	876	GLY	-	expression tag	UNP P97675
A	877	THR	-	expression tag	UNP P97675
A	878	LYS	-	expression tag	UNP P97675
A	879	HIS	-	expression tag	UNP P97675
A	880	HIS	-	expression tag	UNP P97675
A	881	HIS	-	expression tag	UNP P97675
A	882	HIS	-	expression tag	UNP P97675
A	883	HIS	-	expression tag	UNP P97675
A	884	HIS	-	expression tag	UNP P97675
B	136	ALA	-	expression tag	UNP P97675
B	137	GLU	-	expression tag	UNP P97675
B	138	THR	-	expression tag	UNP P97675
B	139	GLY	-	expression tag	UNP P97675
B	201	VAL	MET	variant	UNP P97675
B	596	ASN	SER	variant	UNP P97675
B	597	ARG	GLY	variant	UNP P97675
B	876	GLY	-	expression tag	UNP P97675

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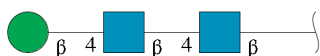
Chain	Residue	Modelled	Actual	Comment	Reference
B	877	THR	-	expression tag	UNP P97675
B	878	LYS	-	expression tag	UNP P97675
B	879	HIS	-	expression tag	UNP P97675
B	880	HIS	-	expression tag	UNP P97675
B	881	HIS	-	expression tag	UNP P97675
B	882	HIS	-	expression tag	UNP P97675
B	883	HIS	-	expression tag	UNP P97675
B	884	HIS	-	expression tag	UNP P97675

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	2	28	16	2	10	0	0	0
2	D	2	28	16	2	10	0	0	0
2	E	2	28	16	2	10	0	0	0

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	F	3	39	22	2	15	0	0	0
3	G	3	39	22	2	15	0	0	0

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O P 5 4 1	0	0
4	B	1	Total O P 5 4 1	0	0

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total Zn 2 2	0	0
5	B	2	Total Zn 2 2	0	0

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Ca 1 1	0	0
6	B	1	Total Ca 1 1	0	0

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
7	A	1	14	8	1	5	0	0
7	A	1	14	8	1	5	0	0
7	B	1	14	8	1	5	0	0
7	B	1	14	8	1	5	0	0

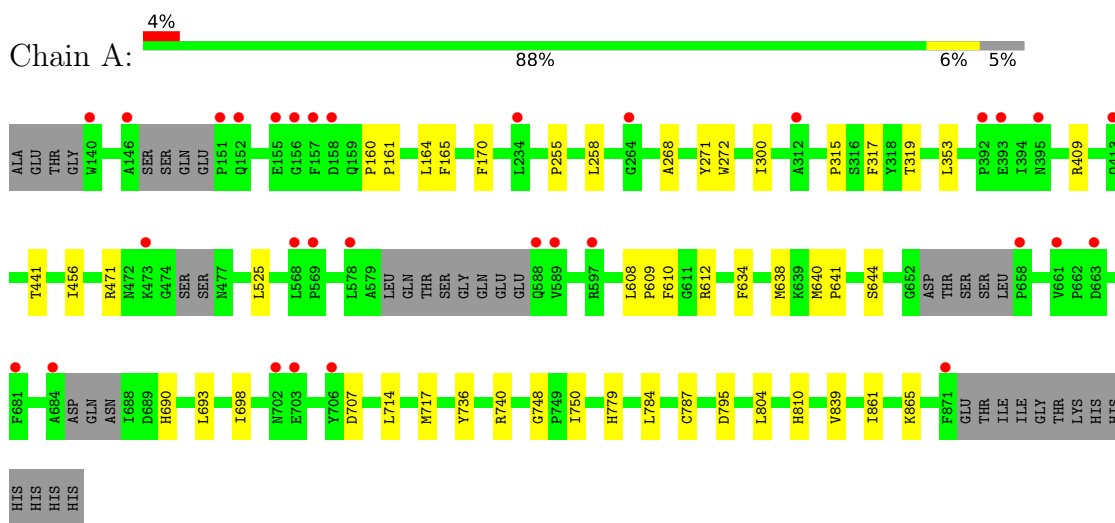
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
8	A	224	224	224	0	0
8	B	250	250	250	0	0

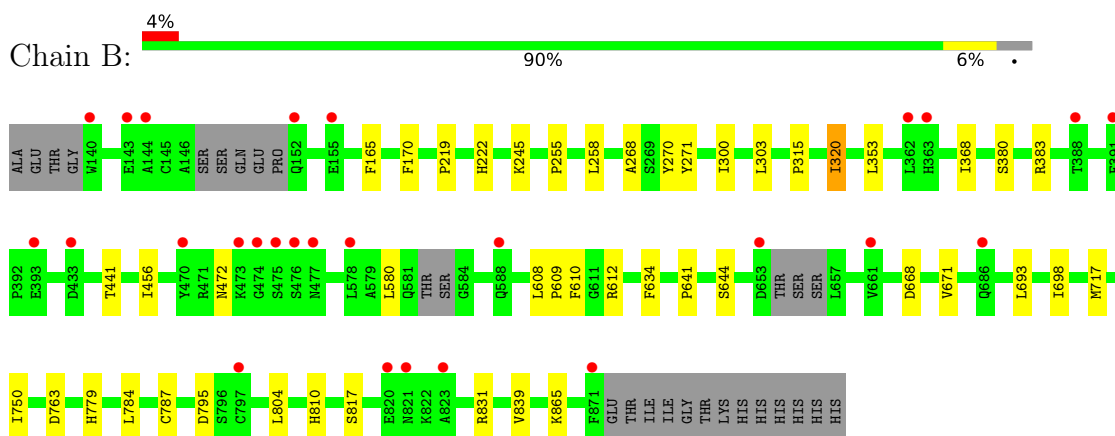
3 Residue-property plots [i](#)

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 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.

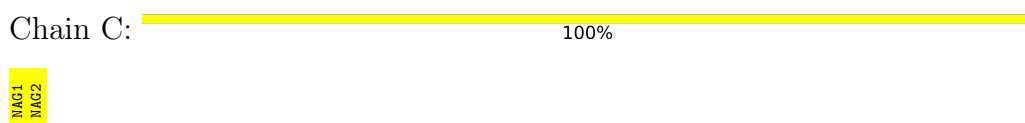
- Molecule 1: Ectonucleotide pyrophosphatase/phosphodiesterase family member 3



- Molecule 1: Ectonucleotide pyrophosphatase/phosphodiesterase family member 3



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



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

Chain D:  100%

MAG1
MAG2

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

Chain E:  50% 50%

MAG1
MAG2

- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  33% 67%

MAG1
MAG2
BMA3

- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  100%

MAG1
MAG2
BMA3

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.84Å 124.06Å 110.67Å 90.00° 97.03° 90.00°	Depositor
Resolution (Å)	47.35 – 2.40 47.35 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.5 (47.35-2.40) 99.5 (47.35-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.67 (at 2.39Å)	Xtrriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.215 , 0.229 0.228 , 0.246	Depositor DCC
R_{free} test set	1539 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	48.2	Xtrriage
Anisotropy	0.513	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 34.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12232	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.52% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, CA, NAG, ZN, PO4

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	0.38	0/5886	0.59	0/8008
1	B	0.38	0/5981	0.59	0/8140
All	All	0.38	0/11867	0.59	0/16148

There are no bond length outliers.

There are no bond angle outliers.

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	5715	0	5514	21	0
1	B	5809	0	5593	17	0
2	C	28	0	25	0	0
2	D	28	0	25	0	0
2	E	28	0	25	0	0
3	F	39	0	34	0	0
3	G	39	0	34	0	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	28	0	26	0	0
7	B	28	0	26	0	0
8	A	224	0	0	0	0
8	B	250	0	0	0	0
All	All	12232	0	11302	38	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 2.

All (38) 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:380:SER:HB3	1:B:383:ARG:HB2	1.82	0.60
1:A:736:TYR:O	1:A:740:ARG:HG2	2.04	0.57
1:B:817:SER:HA	1:B:831:ARG:HH11	1.74	0.53
1:B:300:ILE:HD12	1:B:353:LEU:HB2	1.90	0.53
1:A:255:PRO:HD2	1:A:258:LEU:HD12	1.91	0.52
1:A:300:ILE:HD12	1:A:353:LEU:HB2	1.91	0.52
1:B:255:PRO:HD2	1:B:258:LEU:HD12	1.90	0.52
1:B:219:PRO:HA	1:B:222:HIS:CE1	2.46	0.49
1:B:270:TYR:HB3	1:B:320:ILE:HD12	1.95	0.49
1:A:409:ARG:HH12	1:A:471:ARG:HH21	1.60	0.48
1:B:717:MET:HA	1:B:810:HIS:NE2	2.30	0.47
1:B:839:VAL:HB	1:B:865:LYS:HA	1.98	0.46
1:A:717:MET:HA	1:A:810:HIS:NE2	2.31	0.46
1:A:690:HIS:HB2	1:A:714:LEU:HD22	1.97	0.46
1:A:839:VAL:HB	1:A:865:LYS:HA	1.98	0.46
1:B:644:SER:HB2	1:B:693:LEU:HD23	1.97	0.46
1:A:784:LEU:HD12	1:A:804:LEU:HD23	1.99	0.45
1:A:268:ALA:HB2	1:A:315:PRO:HG2	1.99	0.45
1:A:609:PRO:HB3	1:A:795:ASP:HA	1.99	0.45
1:A:644:SER:HB2	1:A:693:LEU:HD23	1.97	0.45
1:B:784:LEU:HD12	1:B:804:LEU:HD23	1.99	0.45
1:B:268:ALA:HB2	1:B:315:PRO:HG2	1.99	0.44
1:B:609:PRO:HB3	1:B:795:ASP:HA	1.99	0.44
1:B:634:PHE:HA	1:B:641:PRO:HA	1.99	0.44
1:B:668:ASP:HB3	1:B:671:VAL:HG12	2.00	0.44
1:A:634:PHE:HA	1:A:641:PRO:HA	1.99	0.43
1:A:441:THR:HG21	1:A:456:ILE:HG22	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:608:LEU:HD22	1:B:612:ARG:HA	2.03	0.41
1:B:441:THR:HG21	1:B:456:ILE:HG22	2.02	0.41
1:B:750:ILE:HB	1:B:779:HIS:HB2	2.03	0.41
1:A:160:PRO:HA	1:A:161:PRO:HD3	1.99	0.41
1:A:164:LEU:HB3	1:A:319:THR:HG22	2.03	0.41
1:A:608:LEU:HD22	1:A:612:ARG:HA	2.03	0.40
1:A:638:MET:HG3	1:A:640:MET:HG2	2.04	0.40
1:A:750:ILE:HB	1:A:779:HIS:HB2	2.03	0.40
1:A:693:LEU:HD21	1:A:748:GLY:HA2	2.04	0.40
1:A:317:PHE:HB2	1:A:525:LEU:HD21	2.03	0.40
1:A:861:ILE:HG22	1:A:865:LYS:HE3	2.02	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	698/749 (93%)	669 (96%)	27 (4%)	2 (0%)	41	55
1	B	714/749 (95%)	683 (96%)	30 (4%)	1 (0%)	51	68
All	All	1412/1498 (94%)	1352 (96%)	57 (4%)	3 (0%)	47	62

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	271	TYR
1	A	271	TYR
1	A	272	TRP

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	634/669 (95%)	628 (99%)	6 (1%)	78 90
1	B	645/669 (96%)	633 (98%)	12 (2%)	57 75
All	All	1279/1338 (96%)	1261 (99%)	18 (1%)	67 82

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	165	PHE
1	A	170	PHE
1	A	610	PHE
1	A	698	ILE
1	A	707	ASP
1	A	787	CYS
1	B	165	PHE
1	B	170	PHE
1	B	245	LYS
1	B	303	LEU
1	B	320	ILE
1	B	368	ILE
1	B	472	ASN
1	B	580	LEU
1	B	610	PHE
1	B	698	ILE
1	B	763	ASP
1	B	787	CYS

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

Mol	Chain	Res	Type
1	A	194	HIS
1	A	472	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	NAG	C	1	2,1	14,14,15	0.29	0	17,19,21	0.93	1 (5%)
2	NAG	C	2	2	14,14,15	0.29	0	17,19,21	0.77	1 (5%)
2	NAG	D	1	2,1	14,14,15	0.28	0	17,19,21	0.62	0
2	NAG	D	2	2	14,14,15	0.28	0	17,19,21	0.60	0
2	NAG	E	1	2,1	14,14,15	0.28	0	17,19,21	0.59	0
2	NAG	E	2	2	14,14,15	0.30	0	17,19,21	0.60	1 (5%)
3	NAG	F	1	1,3	14,14,15	0.29	0	17,19,21	0.96	1 (5%)
3	NAG	F	2	3	14,14,15	0.29	0	17,19,21	0.73	1 (5%)
3	BMA	F	3	3	11,11,12	0.32	0	15,15,17	0.60	0
3	NAG	G	1	1,3	14,14,15	0.29	0	17,19,21	0.70	0
3	NAG	G	2	3	14,14,15	0.29	0	17,19,21	0.60	0
3	BMA	G	3	3	11,11,12	0.31	0	15,15,17	0.49	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	D	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	1/6/23/26	0/1/1/1
2	NAG	E	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
3	NAG	F	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
3	BMA	F	3	3	-	0/2/19/22	0/1/1/1
3	NAG	G	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	BMA	G	3	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	NAG	O5-C1-C2	-2.96	106.61	111.29
3	F	1	NAG	O5-C1-C2	-2.96	106.62	111.29
3	F	2	NAG	C1-O5-C5	2.67	115.81	112.19
2	C	2	NAG	C1-O5-C5	2.66	115.80	112.19
2	E	2	NAG	C1-O5-C5	2.15	115.11	112.19

There are no chirality outliers.

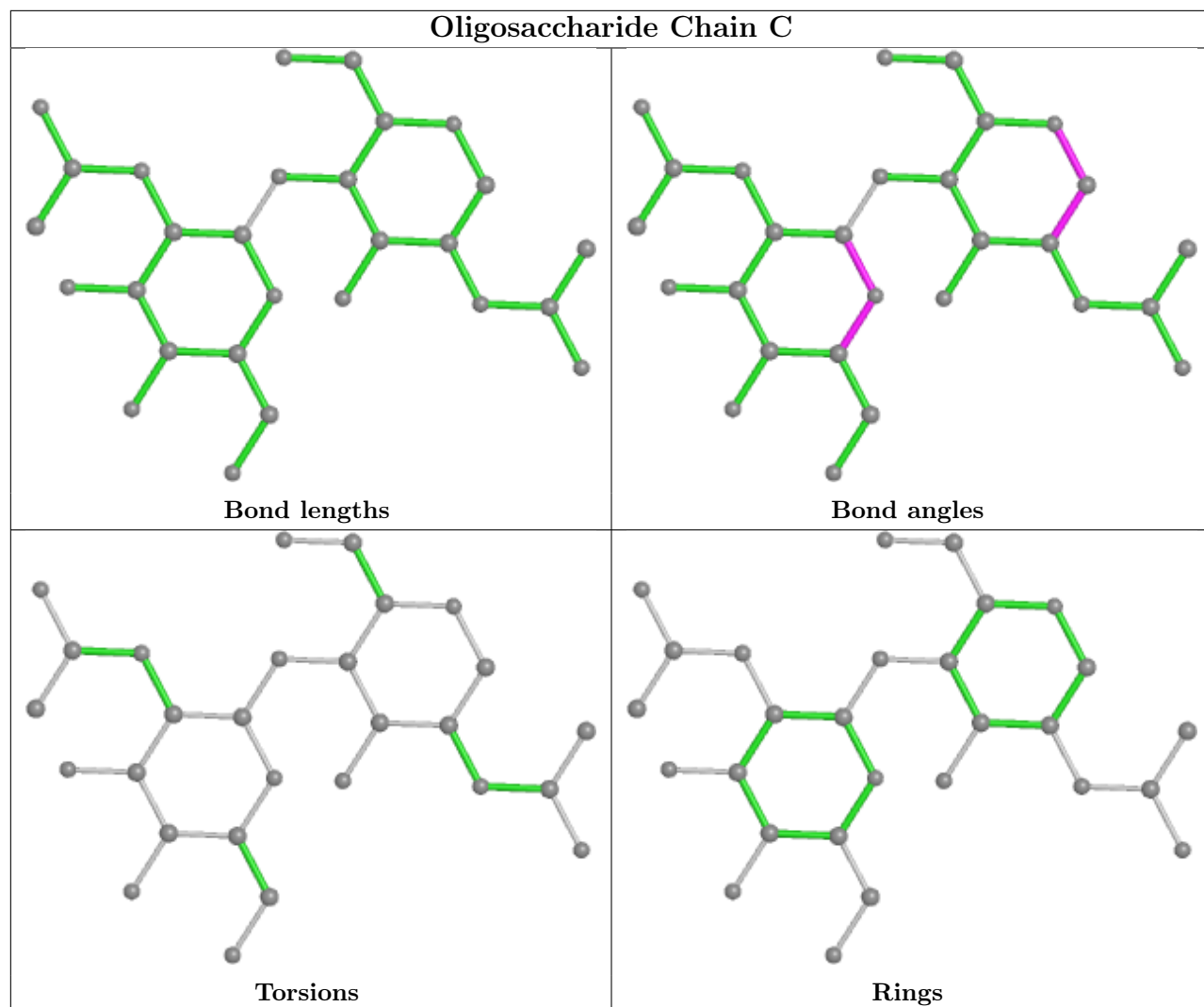
All (1) torsion outliers are listed below:

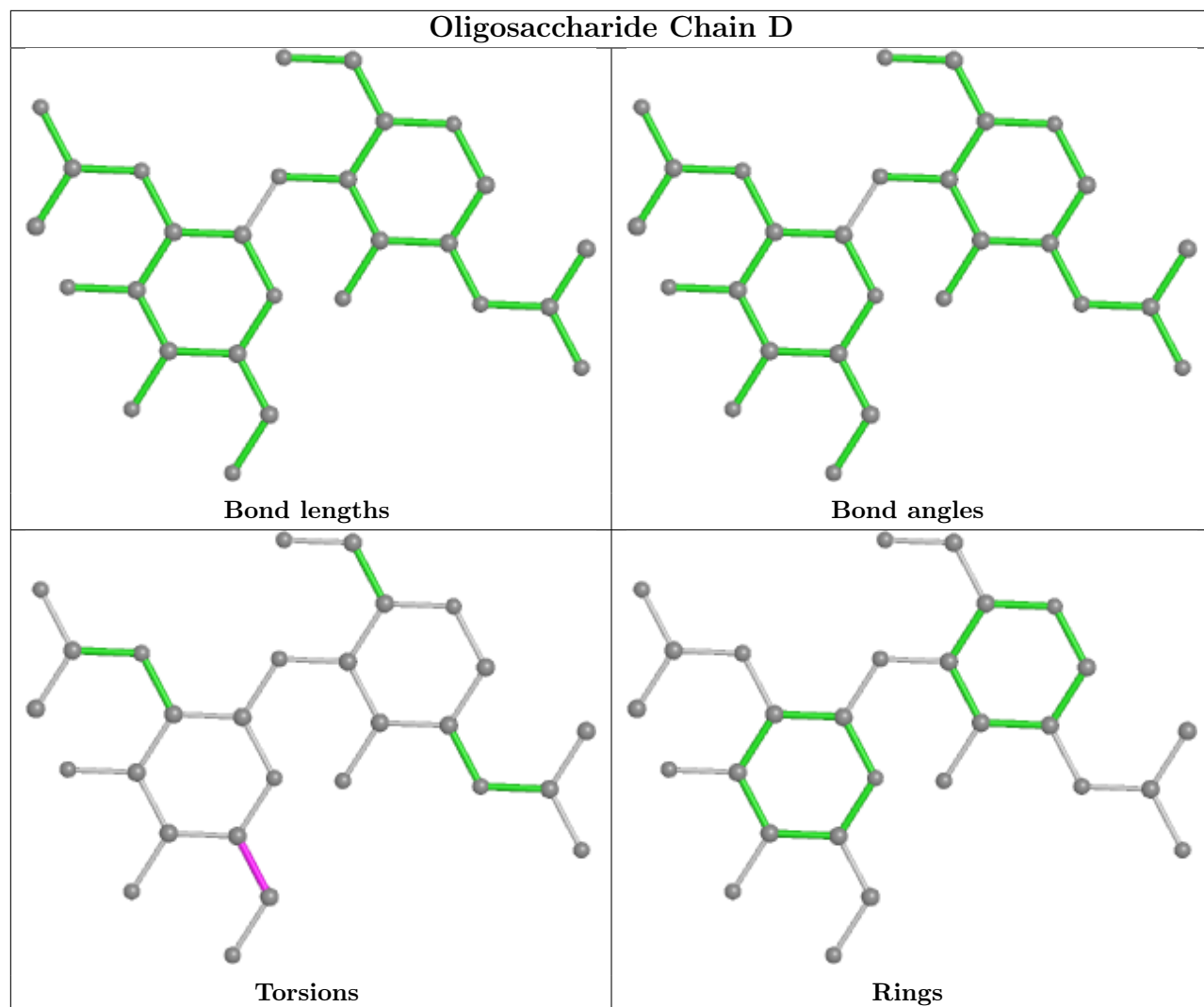
Mol	Chain	Res	Type	Atoms
2	D	2	NAG	O5-C5-C6-O6

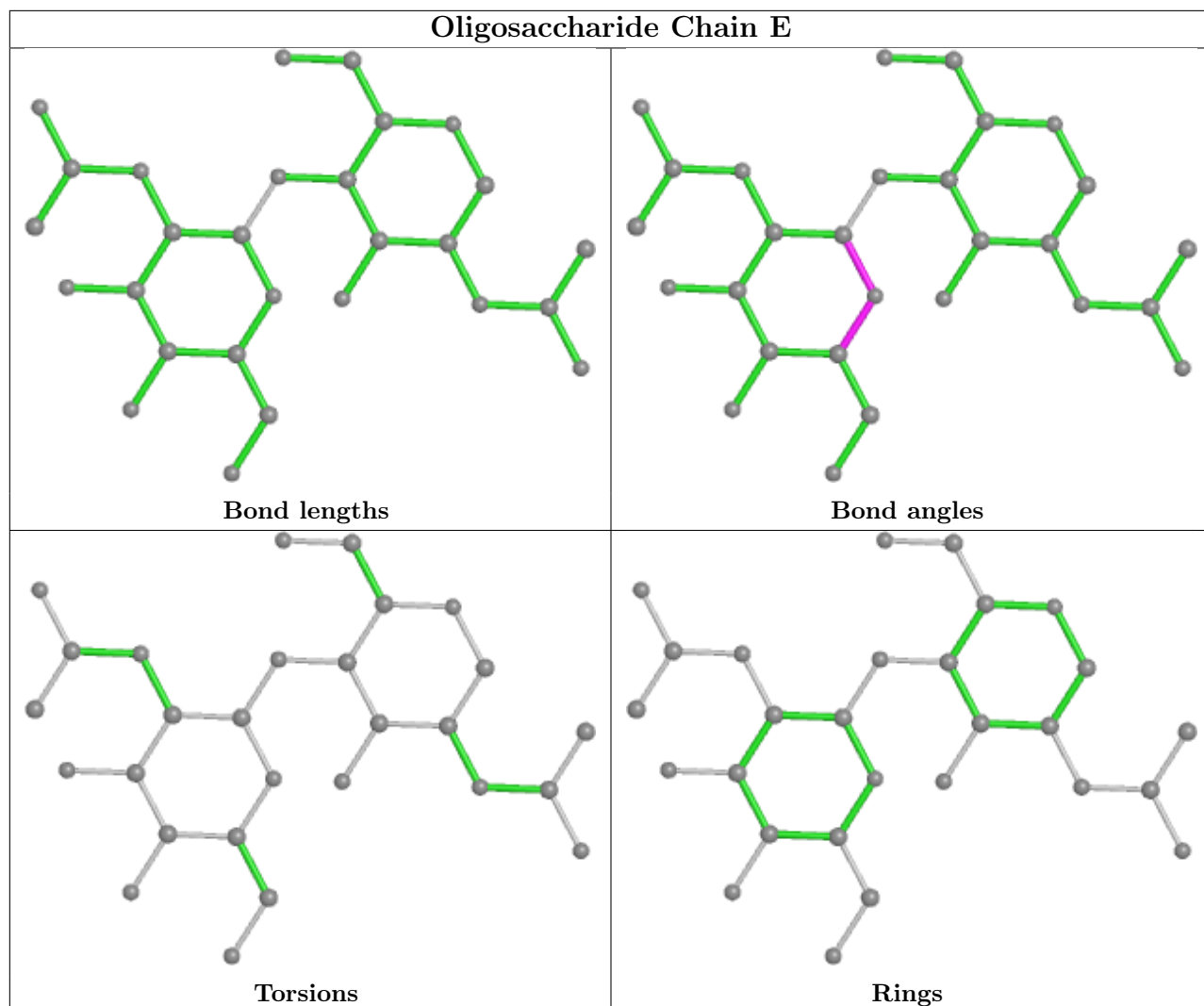
There are no ring outliers.

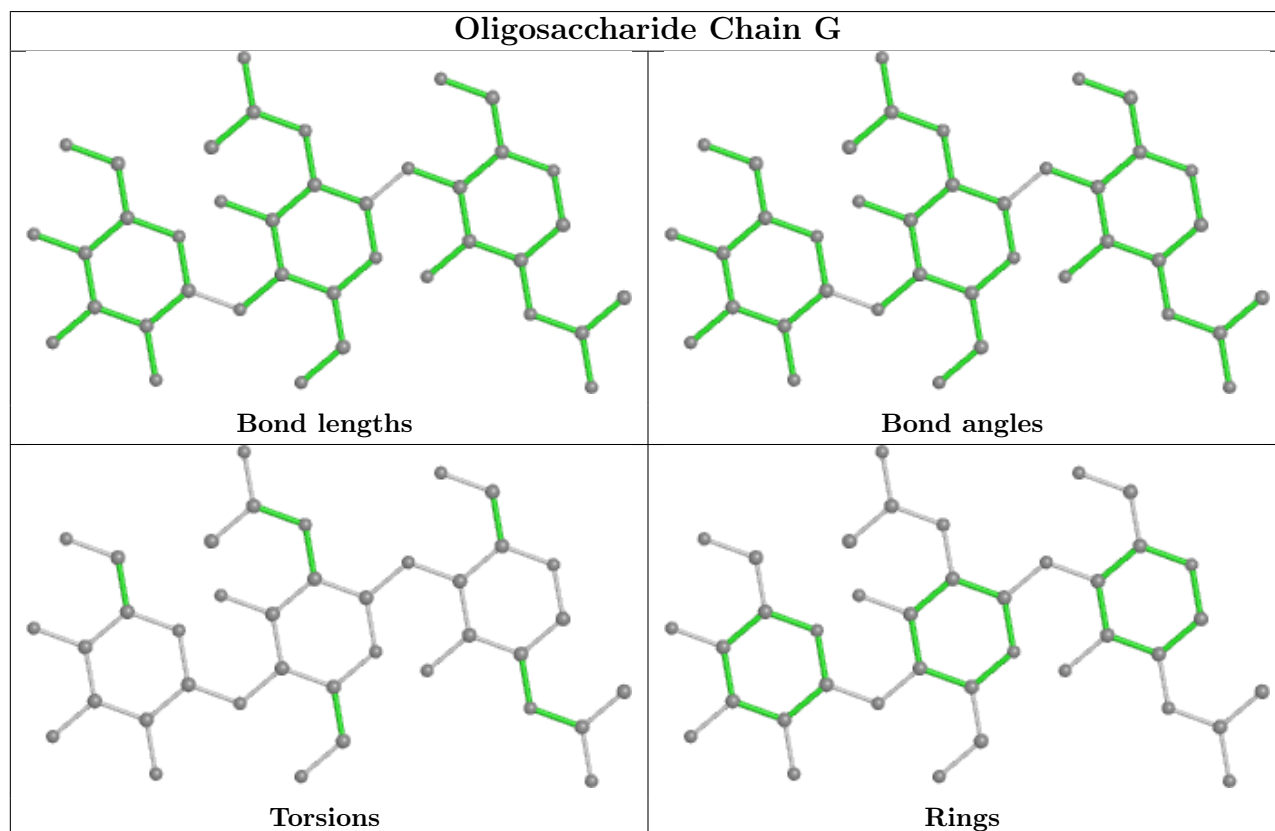
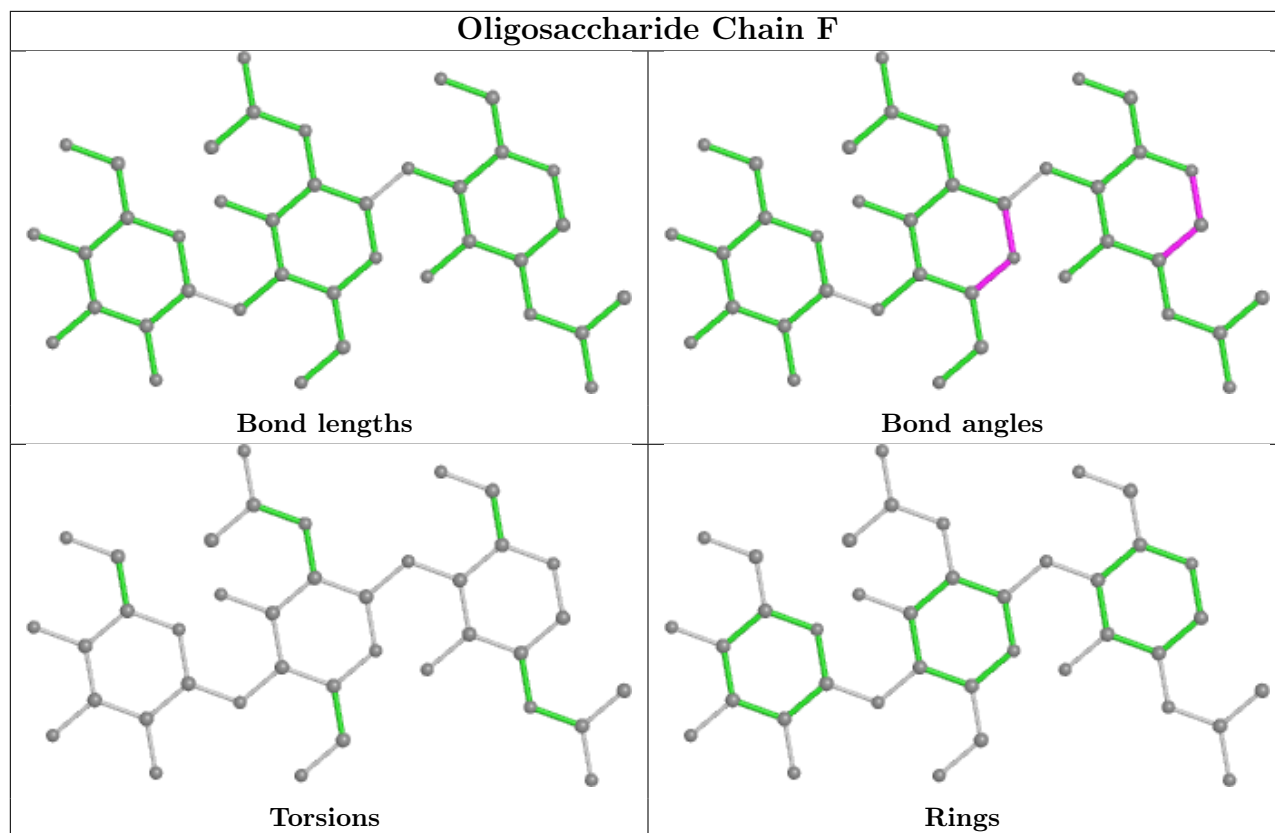
No monomer is involved in short contacts.

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 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 for Mogul analysis.

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
7	NAG	A	1007	1	14,14,15	0.30	0	17,19,21	0.75	1 (5%)
7	NAG	B	1008	1	14,14,15	0.29	0	17,19,21	0.44	0
4	PO4	B	1001	5	4,4,4	1.99	1 (25%)	6,6,6	0.40	0
4	PO4	A	1001	5	4,4,4	1.92	0	6,6,6	0.38	0
7	NAG	A	1012	1	14,14,15	0.29	0	17,19,21	0.48	0
7	NAG	B	1012	1	14,14,15	0.30	0	17,19,21	0.43	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
7	NAG	A	1012	1	-	0/6/23/26	0/1/1/1
7	NAG	A	1007	1	-	0/6/23/26	0/1/1/1
7	NAG	B	1008	1	-	0/6/23/26	0/1/1/1
7	NAG	B	1012	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1001	PO4	P-O1	2.08	1.55	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	1007	NAG	C1-O5-C5	2.80	115.98	112.19

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

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	710/749 (94%)	0.22	31 (4%) 34 33	37, 56, 91, 125	1 (0%)
1	B	722/749 (96%)	0.22	27 (3%) 41 41	38, 54, 79, 119	1 (0%)
All	All	1432/1498 (95%)	0.22	58 (4%) 37 36	37, 55, 85, 125	2 (0%)

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	578	LEU	7.2
1	A	151	PRO	5.3
1	B	144	ALA	4.8
1	A	146	ALA	4.8
1	A	156	GLY	4.5
1	B	578	LEU	4.3
1	A	706	TYR	4.1
1	A	568	LEU	3.9
1	B	823	ALA	3.9
1	B	475	SER	3.8
1	B	155	GLU	3.4
1	B	821	ASN	3.3
1	A	155	GLU	3.3
1	A	597	ARG	3.2
1	B	363	HIS	3.1
1	A	588	GLN	2.9
1	B	474	GLY	2.9
1	A	663	ASP	2.9
1	A	684	ALA	2.8
1	A	569	PRO	2.8
1	A	681	PHE	2.8
1	B	393	GLU	2.8
1	B	143	GLU	2.7
1	A	264	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	653	ASP	2.6
1	A	589	VAL	2.6
1	A	312	ALA	2.6
1	A	661	VAL	2.6
1	A	392	PRO	2.6
1	A	158	ASP	2.6
1	A	393	GLU	2.6
1	B	820	GLU	2.6
1	B	871	PHE	2.5
1	B	476	SER	2.5
1	A	140	TRP	2.5
1	A	157	PHE	2.5
1	A	395	ASN	2.4
1	B	391	PHE	2.4
1	A	703	GLU	2.4
1	A	413	GLN	2.4
1	B	152	GLN	2.4
1	B	473	LYS	2.3
1	A	234	LEU	2.3
1	B	661	VAL	2.3
1	B	470	TYR	2.3
1	A	702	ASN	2.2
1	A	473	LYS	2.2
1	B	388	THR	2.2
1	B	686	GLN	2.2
1	B	140	TRP	2.2
1	A	152	GLN	2.1
1	B	433	ASP	2.1
1	A	658	PRO	2.1
1	B	588	GLN	2.1
1	B	797	CYS	2.1
1	B	477	ASN	2.0
1	B	362	LEU	2.0
1	A	871	PHE	2.0

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

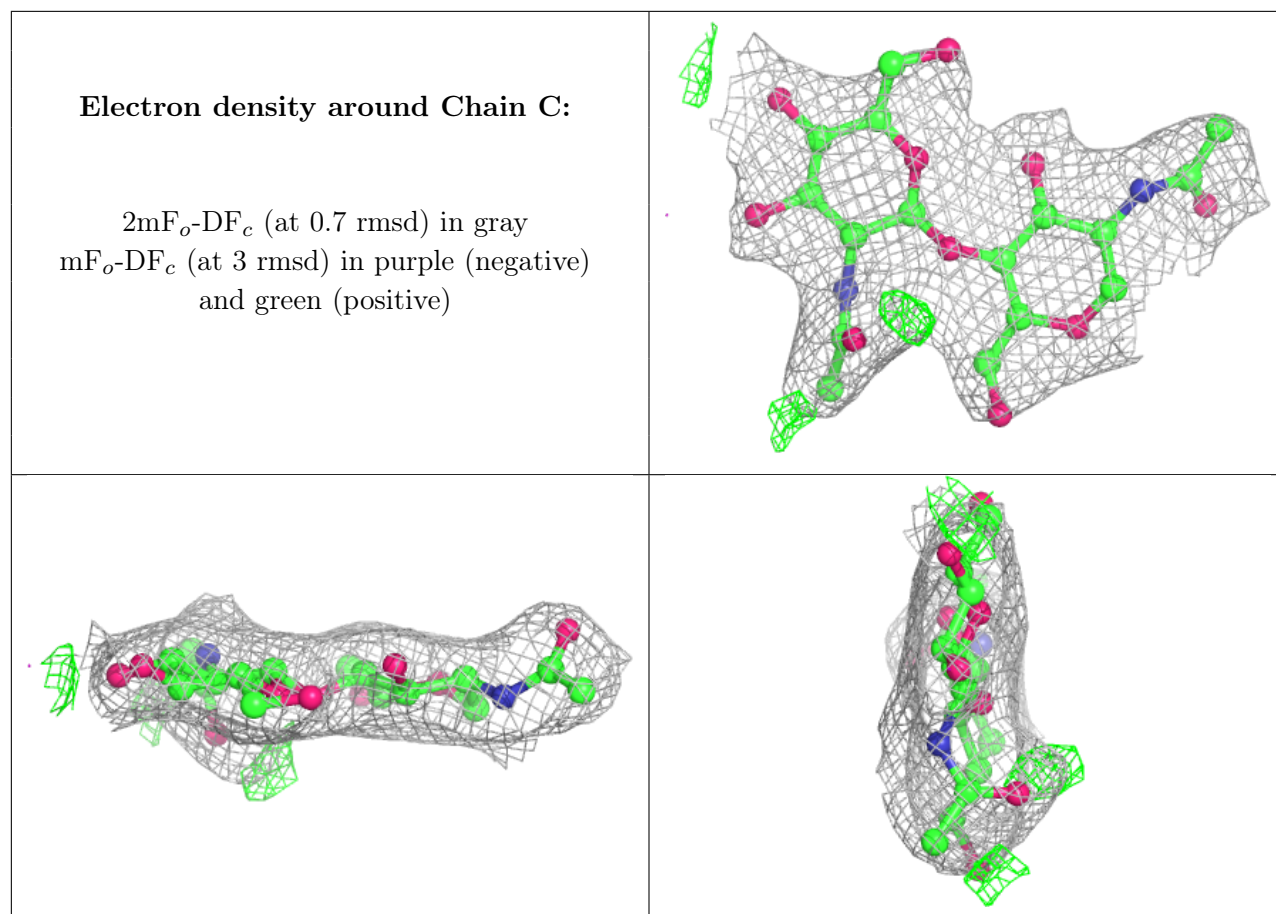
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

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.

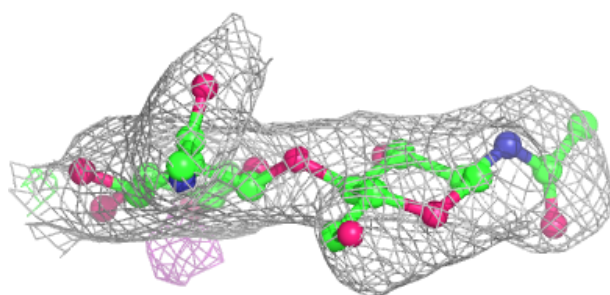
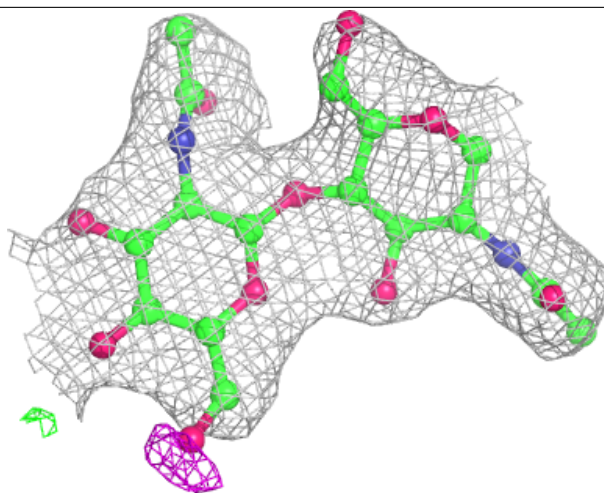
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	BMA	F	3	11/12	0.73	0.28	87,88,89,89	0
3	BMA	G	3	11/12	0.75	0.22	72,74,76,76	0
2	NAG	C	2	14/15	0.87	0.22	65,68,69,69	0
2	NAG	D	2	14/15	0.87	0.20	74,75,76,76	0
3	NAG	G	2	14/15	0.91	0.15	59,63,66,69	0
2	NAG	E	2	14/15	0.91	0.16	56,59,61,62	0
2	NAG	D	1	14/15	0.92	0.15	69,71,73,73	0
2	NAG	E	1	14/15	0.93	0.16	47,50,52,55	0
3	NAG	F	2	14/15	0.94	0.18	80,83,83,85	0
3	NAG	F	1	14/15	0.94	0.16	69,74,75,78	0
2	NAG	C	1	14/15	0.95	0.14	66,67,68,69	0
3	NAG	G	1	14/15	0.96	0.17	47,51,54,57	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.



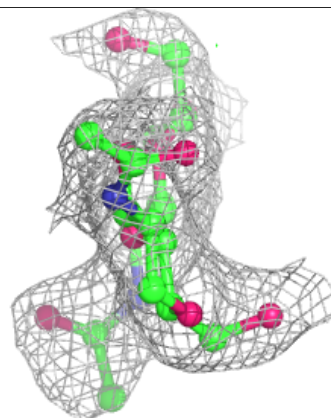
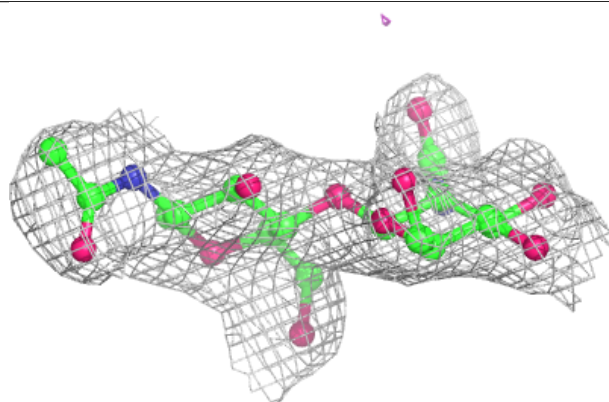
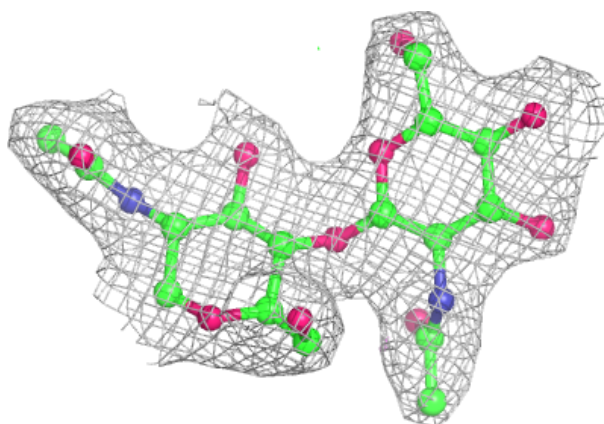
Electron density around Chain D:

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

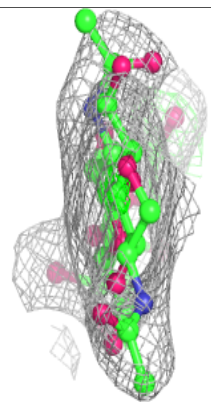
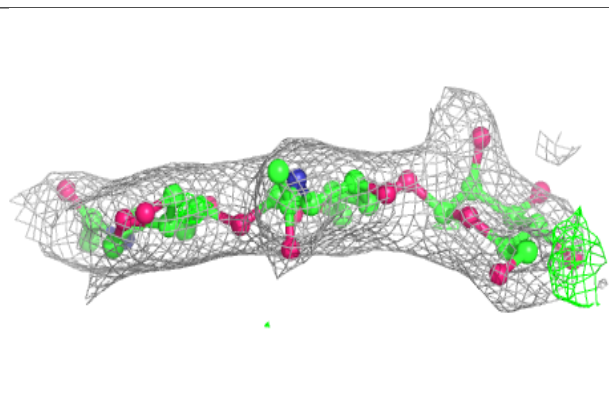
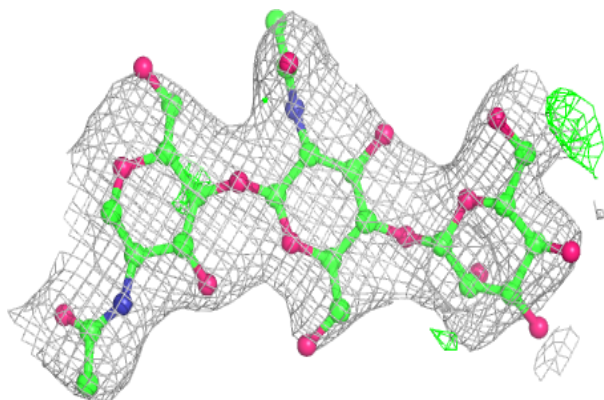


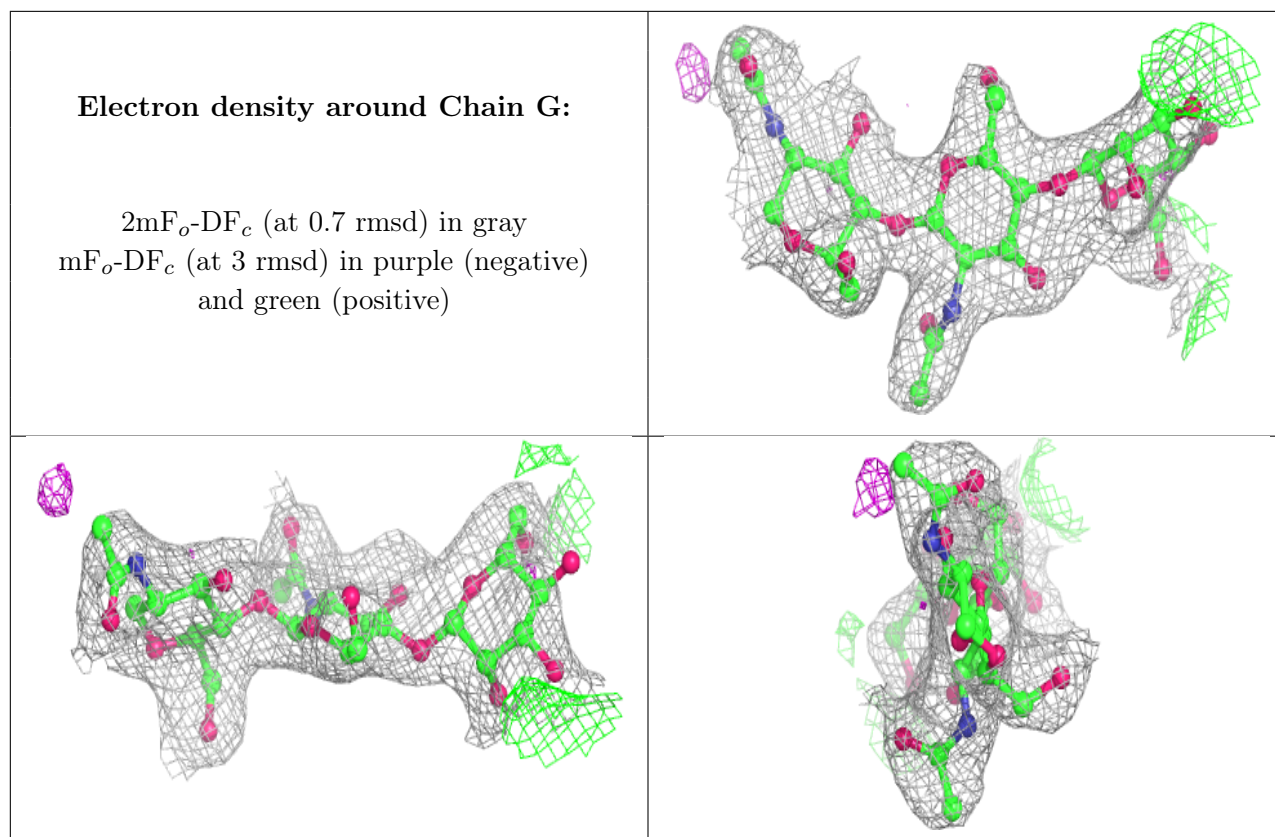
Electron density around Chain E:

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

**Electron density around Chain F:**

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





6.4 Ligands [i](#)

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(\AA^2)	Q<0.9
7	NAG	A	1012	14/15	0.82	0.21	93,93,95,95	0
7	NAG	B	1012	14/15	0.82	0.37	89,89,90,90	0
7	NAG	B	1008	14/15	0.83	0.20	70,73,75,76	0
7	NAG	A	1007	14/15	0.94	0.17	60,63,64,64	0
6	CA	A	1004	1/1	0.96	0.10	48,48,48,48	0
4	PO4	B	1001	5/5	0.97	0.12	63,63,64,65	0
4	PO4	A	1001	5/5	0.98	0.16	67,67,67,68	0
6	CA	B	1004	1/1	0.99	0.15	41,41,41,41	0
5	ZN	A	1003	1/1	0.99	0.13	44,44,44,44	0
5	ZN	B	1002	1/1	0.99	0.12	48,48,48,48	0
5	ZN	B	1003	1/1	0.99	0.12	50,50,50,50	0
5	ZN	A	1002	1/1	0.99	0.11	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.