



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 08:05 AM UTC

PDB ID : 6F2V / pdb_00006f2v
Title : Crystal structure of ectonucleotide phosphodiesterase/pyrophosphatase-3 (NPP3) in complex with AMP
Authors : Dohler, C.; Zebisch, M.; Strater, N.
Deposited on : 2017-11-27
Resolution : 2.50 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

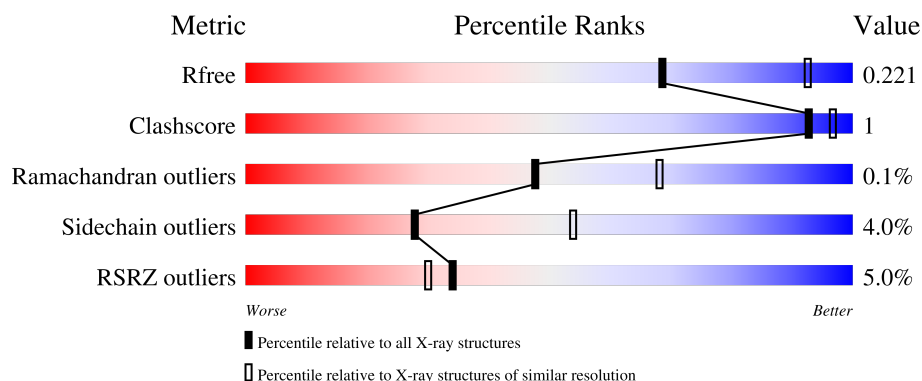
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	6% 88% 8%
1	B	749	4% 88% 8%
2	C	2	100%
2	D	2	50% 50%
2	E	2	50% 50%

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Mol	Chain	Length	Quality of chain
2	G	2	50% 50%
3	F	3	100%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 12350 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
1	A	722	Total	C	N	O	S	0	0	0
			5810	3720	978	1079	33			
1	B	721	Total	C	N	O	S	0	0	0
			5803	3715	977	1078	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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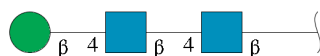
Chain	Residue	Modelled	Actual	Comment	Reference
B	877	THR	-	expression tag	UNP P97675
B	878	LYS	-	expression tag	UNP P97675
B	879	HIS	-	expression tag	UNP P97675
B	880	HIS	-	expression tag	UNP P97675
B	881	HIS	-	expression tag	UNP P97675
B	882	HIS	-	expression tag	UNP P97675
B	883	HIS	-	expression tag	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.



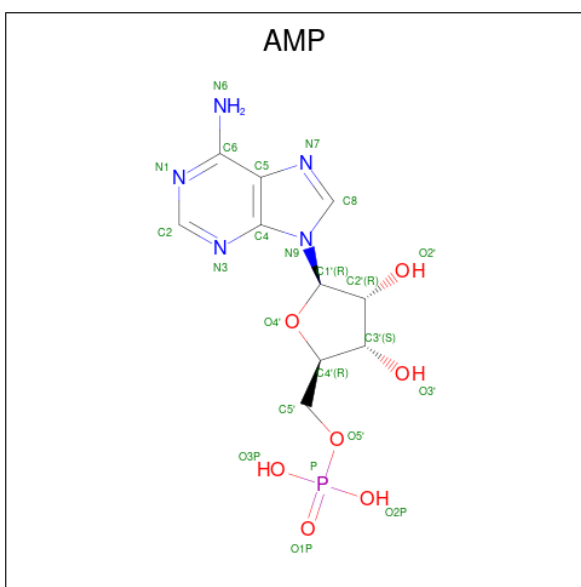
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	G	2	Total	C	N	O	0	0	0
			28	16	2	10			

- 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
3	F	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: C₁₀H₁₄N₅O₇P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
4	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

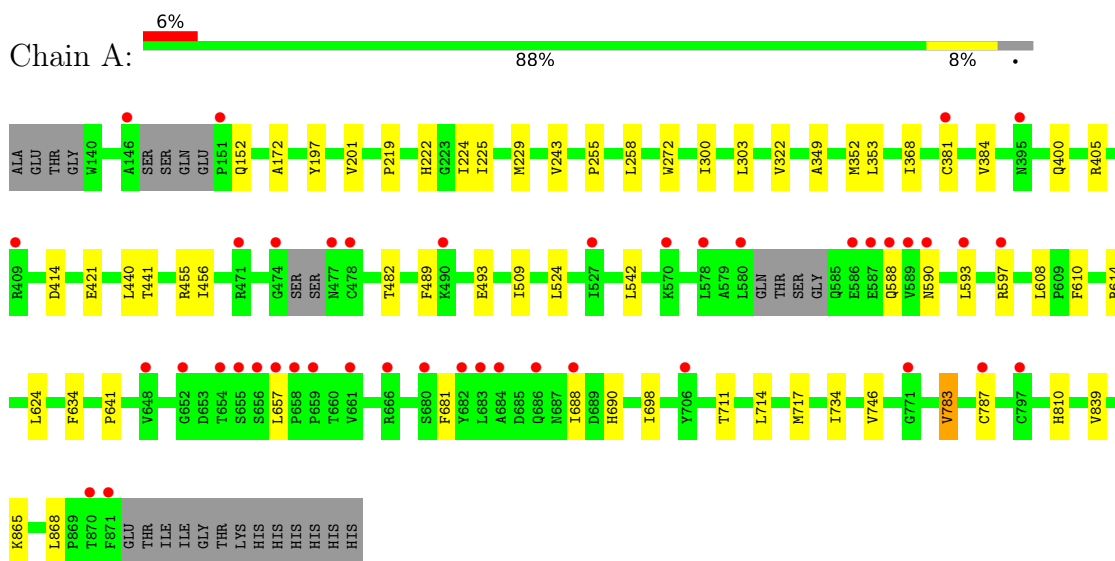
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	230	Total	O	0	0
			230	230		
8	B	234	Total	O	0	0
			234	234		

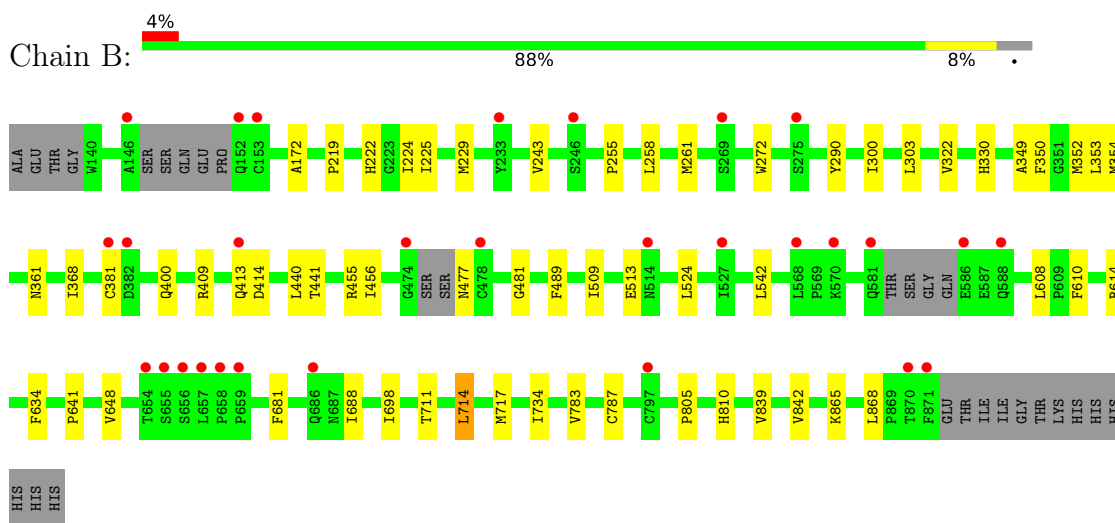
3 Residue-property plots

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: 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

Chain C:  100%

MAG1
MAG2

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

Chain D:  50% 50%

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

Chain G:  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:  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	74.92Å 125.33Å 112.25Å 90.00° 96.91° 90.00°	Depositor
Resolution (Å)	37.81 – 2.50 37.81 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (37.81-2.50) 99.7 (37.81-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.194 , 0.209 0.208 , 0.221	Depositor DCC
R_{free} test set	1423 reflections (1.84%)	wwPDB-VP
Wilson B-factor (Å ²)	41.8	Xtriage
Anisotropy	0.216	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 43.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12350	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% 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: ZN, BMA, NAG, AMP, CA

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	0.69	0/5983	1.21	5/8144 (0.1%)
1	B	0.70	0/5975	1.22	9/8133 (0.1%)
All	All	0.70	0/11958	1.21	14/16277 (0.1%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	513	GLU	CA-C-N	8.22	131.65	120.38
1	B	513	GLU	C-N-CA	8.22	131.65	120.38
1	B	440	LEU	N-CA-C	-6.60	98.51	109.46
1	A	440	LEU	N-CA-C	-6.57	98.56	109.46
1	A	681	PHE	CA-CB-CG	5.87	119.67	113.80
1	B	681	PHE	CA-CB-CG	5.85	119.65	113.80
1	B	489	PHE	CA-CB-CG	5.45	119.25	113.80
1	A	489	PHE	CA-CB-CG	5.44	119.24	113.80
1	B	477	ASN	CA-C-N	5.13	127.67	120.28
1	B	477	ASN	C-N-CA	5.13	127.67	120.28
1	A	172	ALA	CA-C-N	5.12	127.14	120.28
1	A	172	ALA	C-N-CA	5.12	127.14	120.28
1	B	172	ALA	CA-C-N	5.08	127.09	120.28
1	B	172	ALA	C-N-CA	5.08	127.09	120.28

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	5810	0	5596	16	0
1	B	5803	0	5588	18	0
2	C	28	0	25	0	0
2	D	28	0	25	0	0
2	E	28	0	25	0	0
2	G	28	0	25	0	0
3	F	39	0	34	0	0
4	A	23	0	12	0	0
4	B	23	0	12	1	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	28	0	26	0	0
7	B	42	0	39	0	0
8	A	230	0	0	0	0
8	B	234	0	0	0	0
All	All	12350	0	11407	34	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 1.

All (34) 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:A:690:HIS:HB2	1:A:714:LEU:HD22	1.51	0.90
1:B:711:THR:HA	1:B:714:LEU:HD22	1.70	0.72
1:A:255:PRO:HD2	1:A:258:LEU:HD12	1.86	0.57
1:B:255:PRO:HD2	1:B:258:LEU:HD12	1.86	0.57
1:B:783:VAL:HG22	1:B:805:PRO:HB3	1.90	0.53
1:A:300:ILE:HD12	1:A:353:LEU:HB2	1.90	0.53
1:B:300:ILE:HD12	1:B:353:LEU:HB2	1.90	0.53
1:B:634:PHE:HA	1:B:641:PRO:HA	1.92	0.52
1:A:746:VAL:HB	1:A:783:VAL:HG13	1.92	0.51
1:A:634:PHE:HA	1:A:641:PRO:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:711:THR:HA	1:A:714:LEU:HD12	1.92	0.50
1:B:349:ALA:HA	1:B:352:MET:HE3	1.93	0.49
1:B:717:MET:HA	1:B:810:HIS:NE2	2.28	0.49
1:B:224:ILE:HA	1:B:229:MET:HE1	1.95	0.48
1:A:349:ALA:HA	1:A:352:MET:HE3	1.95	0.48
1:A:717:MET:HA	1:A:810:HIS:NE2	2.29	0.48
1:A:224:ILE:HA	1:A:229:MET:HE1	1.95	0.47
1:A:839:VAL:HB	1:A:865:LYS:HA	1.97	0.46
1:B:839:VAL:HB	1:B:865:LYS:HA	1.98	0.46
1:A:590:ASN:HA	1:A:593:LEU:HD13	1.99	0.45
1:B:441:THR:HG21	1:B:456:ILE:HG22	2.00	0.44
1:A:219:PRO:HA	1:A:222:HIS:CE1	2.54	0.43
1:B:509:ILE:HD13	1:B:542:LEU:HD11	2.01	0.42
1:B:711:THR:HA	1:B:714:LEU:CD2	2.45	0.42
1:B:290:TYR:OH	4:B:1001:AMP:H2'	2.19	0.42
1:A:509:ILE:HD13	1:A:542:LEU:HD11	2.01	0.42
1:B:330:HIS:HA	1:B:481:GLY:O	2.20	0.42
1:A:441:THR:HG21	1:A:456:ILE:HG22	2.01	0.42
1:B:219:PRO:HA	1:B:222:HIS:CE1	2.54	0.42
1:B:350:PHE:CE1	1:B:354:MET:HE3	2.56	0.41
1:B:258:LEU:HD23	1:B:261:MET:HE3	2.03	0.41
1:B:219:PRO:HB3	1:B:225:ILE:HA	2.02	0.40
1:A:197:TYR:HB2	1:A:493:GLU:HB3	2.03	0.40
1:A:219:PRO:HB3	1:A:225:ILE:HA	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	714/749 (95%)	684 (96%)	29 (4%)	1 (0%)	48 68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	713/749 (95%)	679 (95%)	33 (5%)	1 (0%)	48 68
All	All	1427/1498 (95%)	1363 (96%)	62 (4%)	2 (0%)	48 68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	272	TRP
1	B	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	646/669 (97%)	618 (96%)	28 (4%)	26 51
1	B	645/669 (96%)	622 (96%)	23 (4%)	31 58
All	All	1291/1338 (96%)	1240 (96%)	51 (4%)	28 54

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	152	GLN
1	A	201	VAL
1	A	243	VAL
1	A	303	LEU
1	A	322	VAL
1	A	368	ILE
1	A	381	CYS
1	A	384	VAL
1	A	400	GLN
1	A	405	ARG
1	A	414	ASP
1	A	421	GLU
1	A	455	ARG
1	A	482	THR

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Mol	Chain	Res	Type
1	A	524	LEU
1	A	588	GLN
1	A	597	ARG
1	A	608	LEU
1	A	610	PHE
1	A	614	ARG
1	A	624	LEU
1	A	657	LEU
1	A	688	ILE
1	A	698	ILE
1	A	734	ILE
1	A	783	VAL
1	A	787	CYS
1	A	868	LEU
1	B	243	VAL
1	B	303	LEU
1	B	322	VAL
1	B	361	ASN
1	B	368	ILE
1	B	381	CYS
1	B	400	GLN
1	B	409	ARG
1	B	413	GLN
1	B	414	ASP
1	B	455	ARG
1	B	524	LEU
1	B	608	LEU
1	B	610	PHE
1	B	614	ARG
1	B	648	VAL
1	B	688	ILE
1	B	698	ILE
1	B	714	LEU
1	B	734	ILE
1	B	787	CYS
1	B	842	VAL
1	B	868	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	159	GLN

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Mol	Chain	Res	Type
1	A	194	HIS
1	A	228	ASN
1	A	687	ASN
1	A	744	ASN
1	A	792	HIS
1	B	152	GLN
1	B	254	GLN
1	B	364	ASN
1	B	519	ASN
1	B	532	ASN
1	B	591	GLN
1	B	594	ASN
1	B	701	ASN
1	B	744	ASN
1	B	792	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 ⓘ

11 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	0.31	0	17,19,21	0.86	1 (5%)
2	NAG	C	2	2	14,14,15	0.31	0	17,19,21	0.84	1 (5%)
2	NAG	D	1	2,1	14,14,15	0.31	0	17,19,21	0.56	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	D	2	2	14,14,15	0.36	0	17,19,21	0.97	2 (11%)
2	NAG	E	1	2,1	14,14,15	0.30	0	17,19,21	0.73	0
2	NAG	E	2	2	14,14,15	0.30	0	17,19,21	0.61	1 (5%)
3	NAG	F	1	3,1	14,14,15	0.31	0	17,19,21	0.86	1 (5%)
3	NAG	F	2	3	14,14,15	0.31	0	17,19,21	0.88	1 (5%)
3	BMA	F	3	3	11,11,12	0.33	0	15,15,17	0.67	1 (6%)
2	NAG	G	1	2,1	14,14,15	0.30	0	17,19,21	0.71	0
2	NAG	G	2	2	14,14,15	0.30	0	17,19,21	0.62	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

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

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	2	NAG	C1-O5-C5	3.24	116.53	112.19
2	C	2	NAG	C1-O5-C5	3.20	116.47	112.19
3	F	1	NAG	O5-C1-C2	-2.84	106.90	111.29
2	C	1	NAG	O5-C1-C2	-2.79	106.97	111.29
2	D	2	NAG	C2-N2-C7	2.47	126.21	122.90
3	F	3	BMA	C1-O5-C5	2.21	115.14	112.19
2	G	2	NAG	C1-O5-C5	2.20	115.13	112.19
2	D	2	NAG	C1-O5-C5	2.14	115.06	112.19
2	E	2	NAG	C1-O5-C5	2.13	115.05	112.19

There are no chirality outliers.

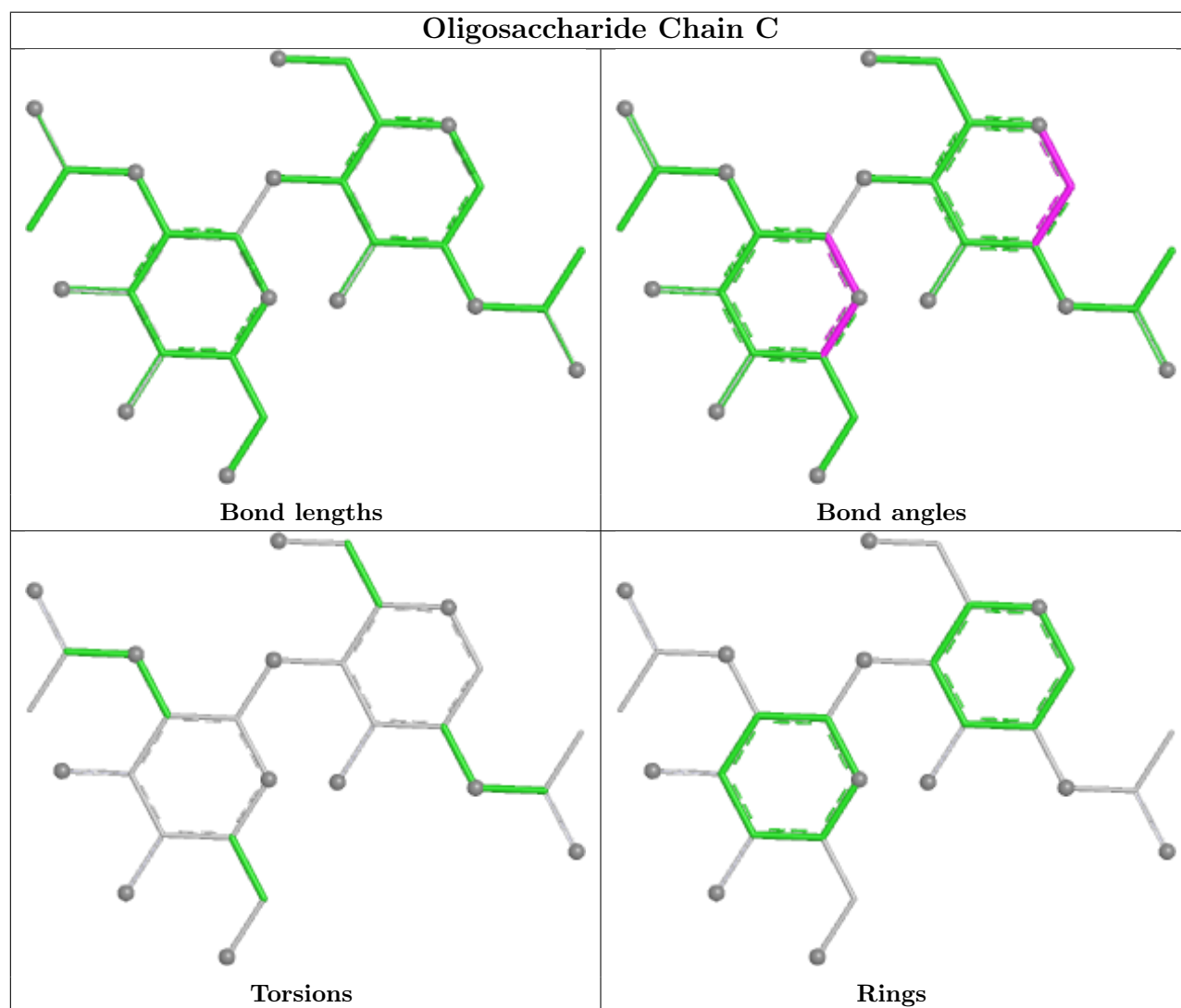
All (3) torsion outliers are listed below:

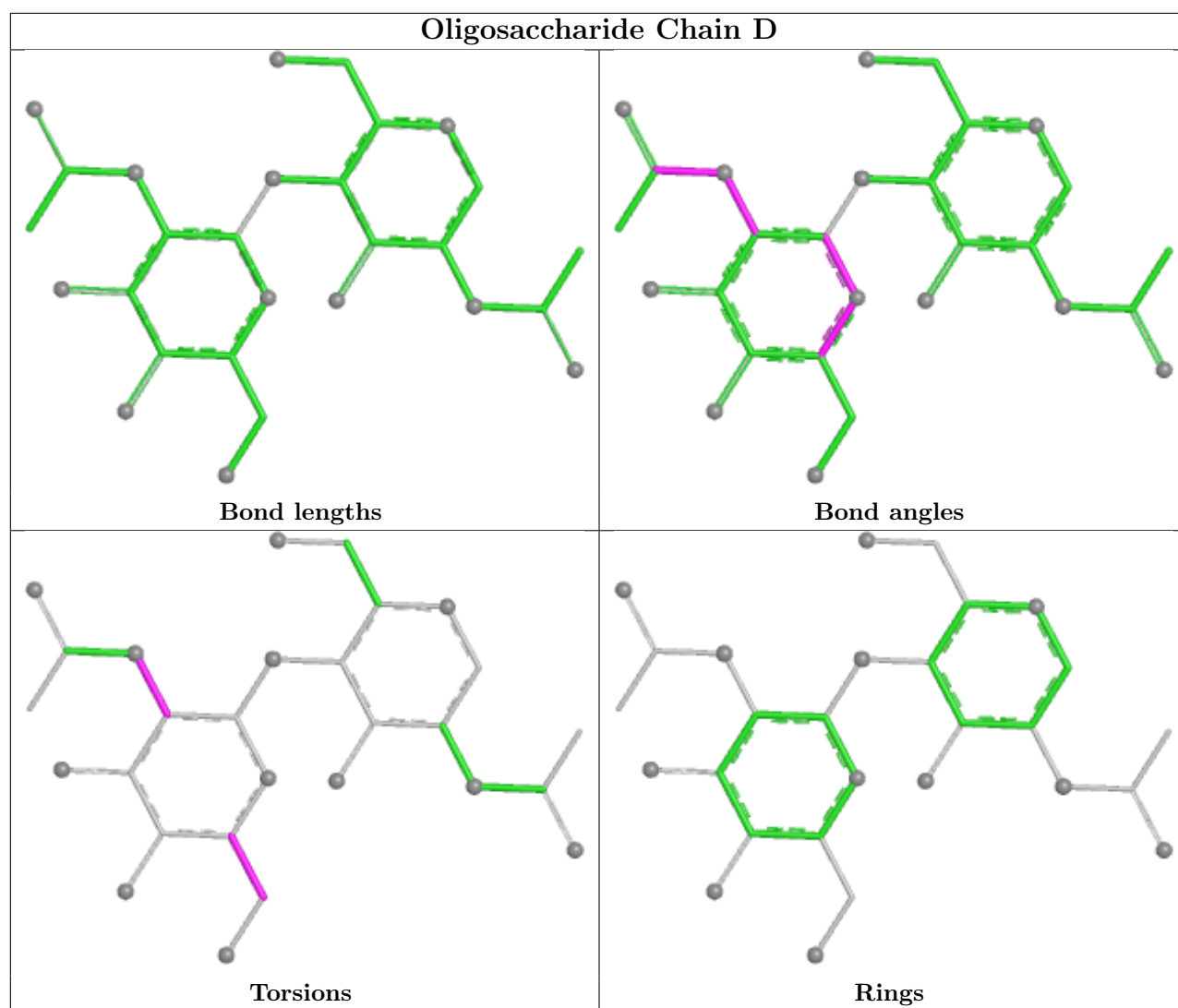
Mol	Chain	Res	Type	Atoms
2	D	2	NAG	C1-C2-N2-C7
2	D	2	NAG	C3-C2-N2-C7
2	D	2	NAG	C4-C5-C6-O6

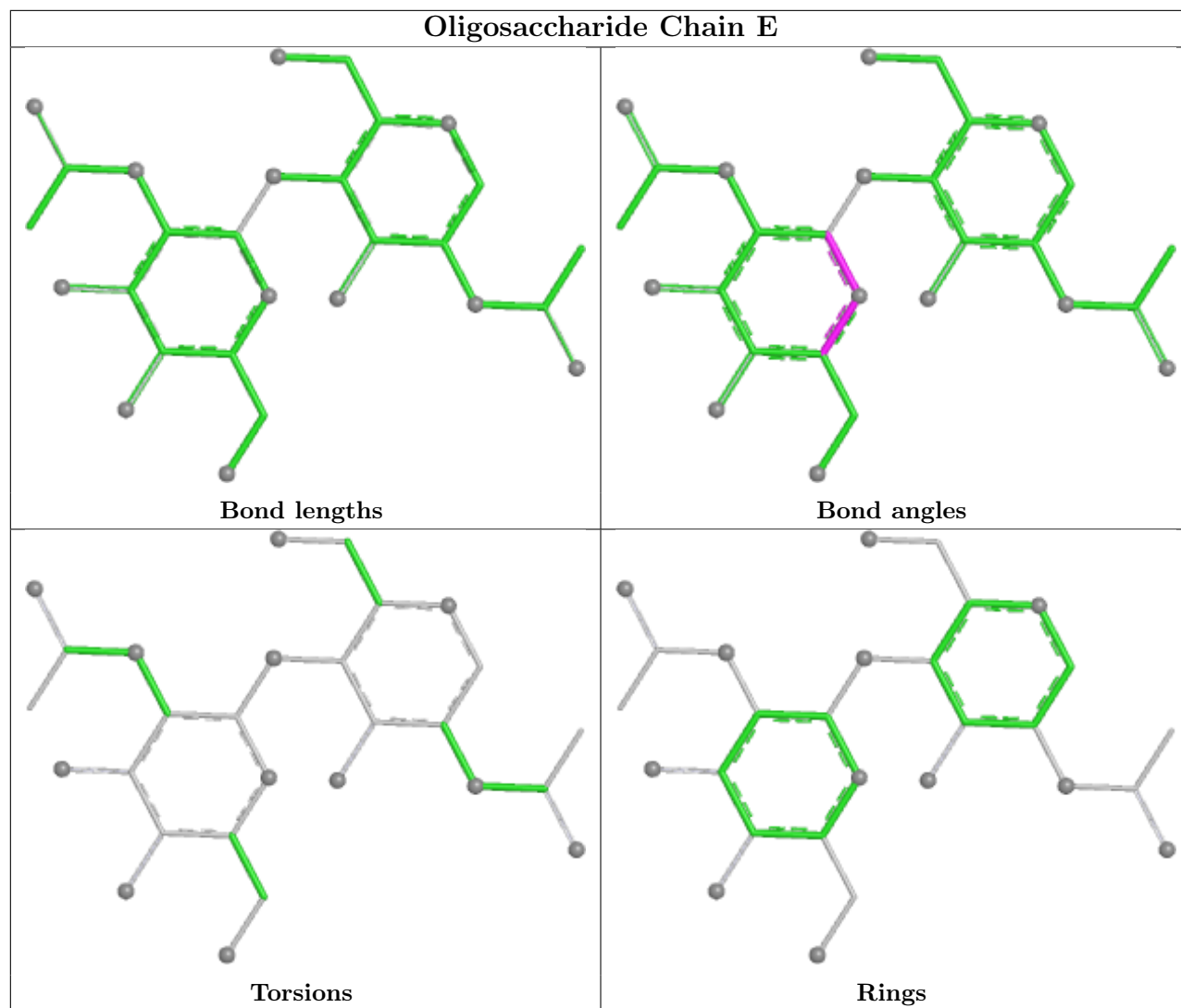
There are no ring outliers.

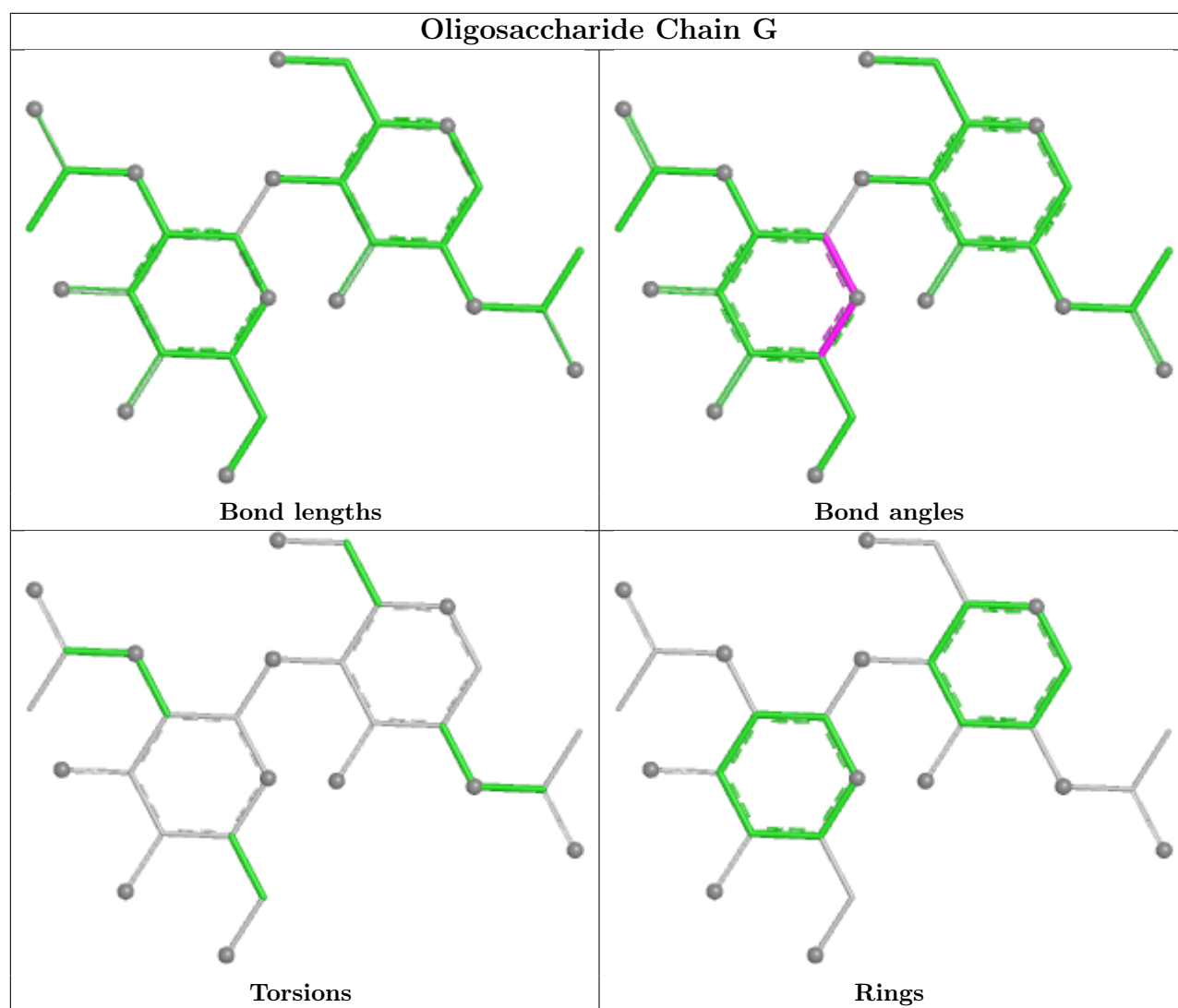
No monomer is involved in short contacts.

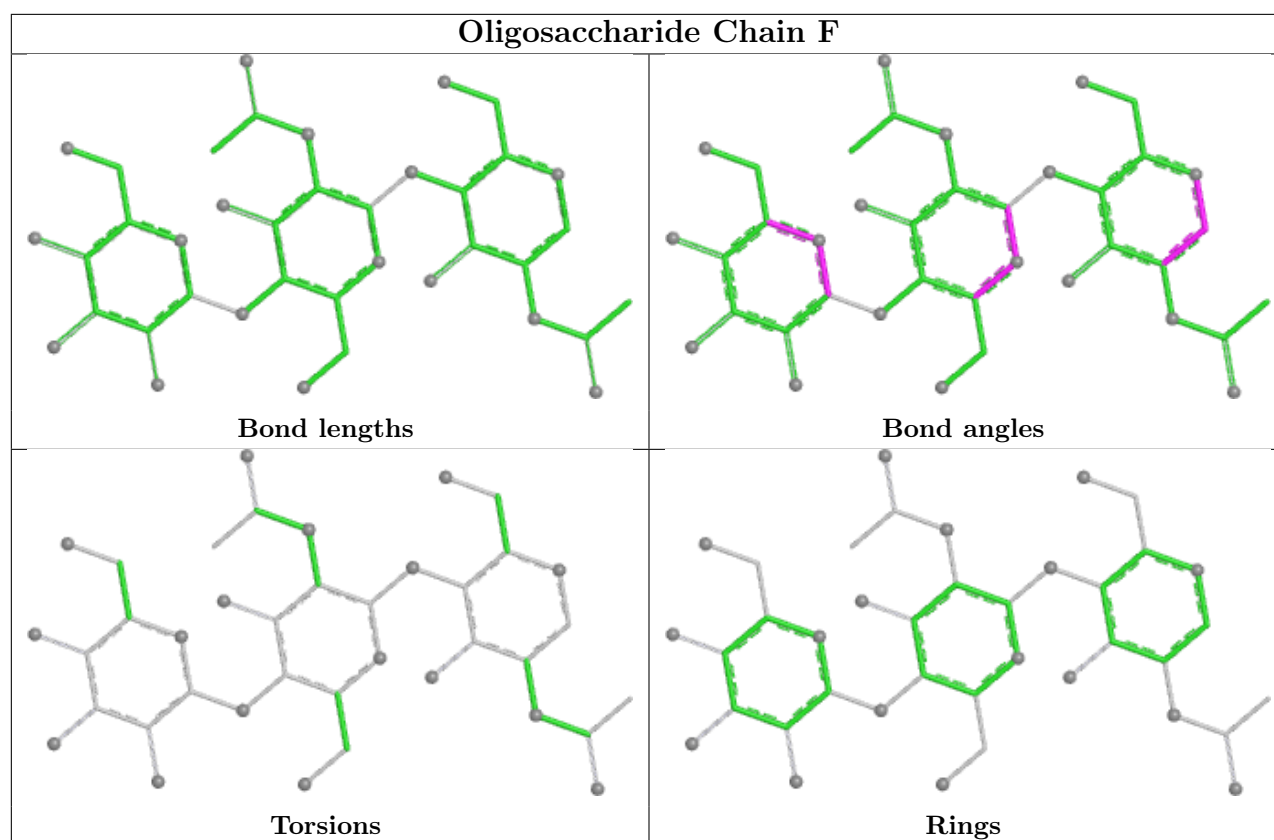
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 6 are monoatomic - leaving 7 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	B	1012	1	14,14,15	0.29	0	17,19,21	0.53	0
4	AMP	A	1001	5	25,25,25	0.38	0	37,38,38	0.41	0
7	NAG	A	1012	1	14,14,15	0.30	0	17,19,21	0.51	0
7	NAG	B	1009	1	14,14,15	0.31	0	17,19,21	0.81	1 (5%)
7	NAG	B	1008	1	14,14,15	0.30	0	17,19,21	0.59	0
7	NAG	A	1007	1	14,14,15	0.29	0	17,19,21	0.82	1 (5%)
4	AMP	B	1001	5	25,25,25	0.36	0	37,38,38	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	B	1012	1	-	0/6/23/26	0/1/1/1
4	AMP	A	1001	5	-	3/10/26/26	0/3/3/3
7	NAG	A	1012	1	-	0/6/23/26	0/1/1/1
7	NAG	B	1009	1	-	1/6/23/26	0/1/1/1
7	NAG	B	1008	1	-	0/6/23/26	0/1/1/1
7	NAG	A	1007	1	-	0/6/23/26	0/1/1/1
4	AMP	B	1001	5	-	2/10/26/26	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	1009	NAG	C1-O5-C5	3.05	116.27	112.19
7	A	1007	NAG	C1-O5-C5	2.50	115.53	112.19

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1001	AMP	C5'-O5'-P-O1P
7	B	1009	NAG	O5-C5-C6-O6
4	A	1001	AMP	C5'-O5'-P-O2P
4	B	1001	AMP	C5'-O5'-P-O3P
4	A	1001	AMP	C5'-O5'-P-O3P
4	B	1001	AMP	C5'-O5'-P-O2P

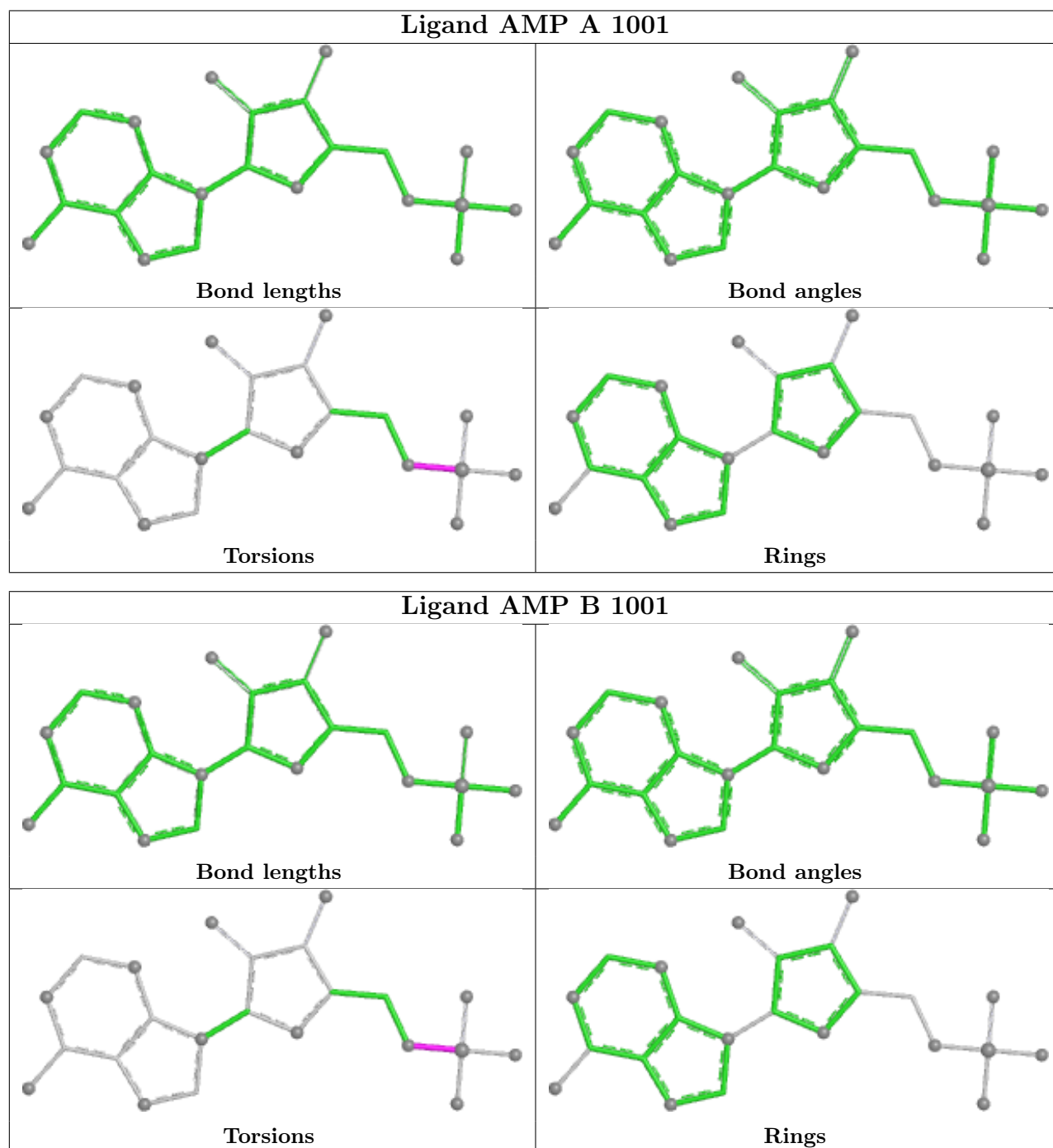
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1001	AMP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	722/749 (96%)	0.39	43 (5%)	27 24	27, 50, 95, 153	1 (0%)
1	B	721/749 (96%)	0.31	29 (4%)	42 38	28, 50, 89, 123	1 (0%)
All	All	1443/1498 (96%)	0.35	72 (4%)	34 30	27, 50, 93, 153	2 (0%)

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	657	LEU	5.7
1	B	657	LEU	4.7
1	A	146	ALA	4.4
1	B	581	GLN	4.2
1	A	589	VAL	3.9
1	B	152	GLN	3.7
1	B	146	ALA	3.7
1	A	381	CYS	3.6
1	B	797	CYS	3.6
1	A	587	GLU	3.6
1	A	474	GLY	3.4
1	B	586	GLU	3.4
1	B	655	SER	3.3
1	B	654	THR	3.2
1	B	568	LEU	3.2
1	B	381	CYS	3.2
1	B	658	PRO	3.1
1	A	661	VAL	3.1
1	A	871	PHE	3.1
1	A	648	VAL	3.1
1	A	580	LEU	3.1
1	A	151	PRO	3.0
1	A	684	ALA	3.0
1	A	654	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	656	SER	3.0
1	A	797	CYS	3.0
1	A	588	GLN	3.0
1	A	578	LEU	2.9
1	B	870	THR	2.8
1	A	471	ARG	2.8
1	A	683	LEU	2.8
1	A	658	PRO	2.8
1	B	474	GLY	2.7
1	B	871	PHE	2.7
1	A	590	ASN	2.7
1	A	570	LYS	2.6
1	A	395	ASN	2.6
1	A	787	CYS	2.6
1	B	413	GLN	2.6
1	A	680	SER	2.6
1	A	706	TYR	2.6
1	B	656	SER	2.5
1	A	409	ARG	2.5
1	A	682	TYR	2.5
1	A	593	LEU	2.5
1	B	527	ILE	2.5
1	A	688	ILE	2.4
1	A	478	CYS	2.4
1	B	514	ASN	2.4
1	B	275	SER	2.4
1	A	666	ARG	2.4
1	A	870	THR	2.4
1	B	269	SER	2.3
1	B	570	LYS	2.3
1	B	246	SER	2.3
1	B	686	GLN	2.3
1	A	771	GLY	2.3
1	A	586	GLU	2.3
1	B	153	CYS	2.2
1	A	652	GLY	2.2
1	A	659	PRO	2.2
1	A	477	ASN	2.2
1	B	659	PRO	2.2
1	B	478	CYS	2.1
1	A	490	LYS	2.1
1	A	597	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	655	SER	2.1
1	A	527	ILE	2.1
1	B	233	TYR	2.1
1	A	686	GLN	2.0
1	B	588	GLN	2.0
1	B	382	ASP	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 [i](#)

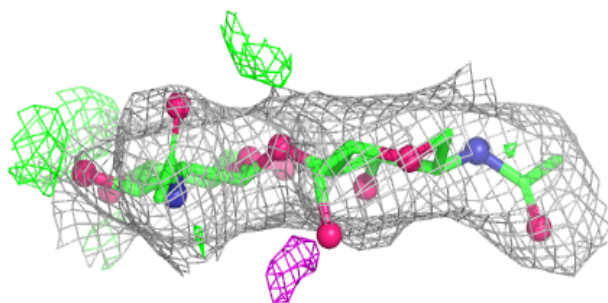
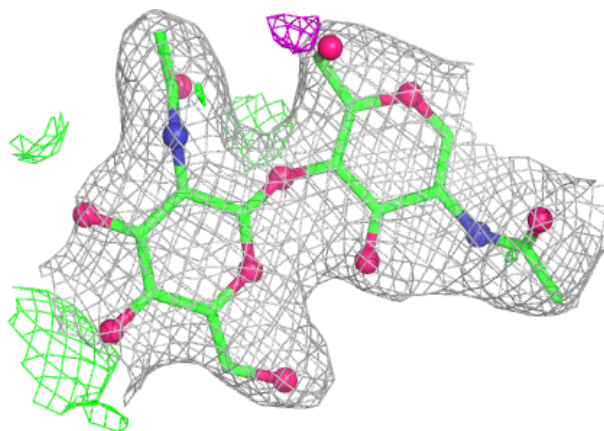
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	BMA	F	3	11/12	0.64	0.15	84,85,85,85	0
2	NAG	D	2	14/15	0.75	0.14	63,65,66,66	0
2	NAG	C	2	14/15	0.83	0.14	64,65,67,68	0
2	NAG	E	2	14/15	0.84	0.14	56,59,61,62	0
2	NAG	G	2	14/15	0.85	0.12	61,63,65,65	0
2	NAG	D	1	14/15	0.85	0.12	53,57,62,62	0
3	NAG	F	2	14/15	0.86	0.15	78,80,83,83	0
2	NAG	C	1	14/15	0.88	0.11	58,60,63,64	0
3	NAG	F	1	14/15	0.90	0.12	68,71,73,76	0
2	NAG	G	1	14/15	0.95	0.09	47,53,55,58	0
2	NAG	E	1	14/15	0.97	0.07	40,45,48,52	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.

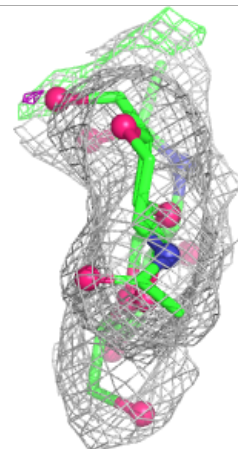
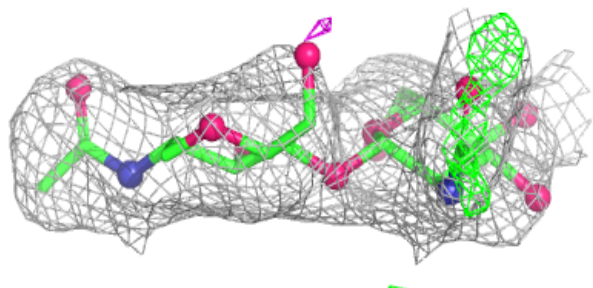
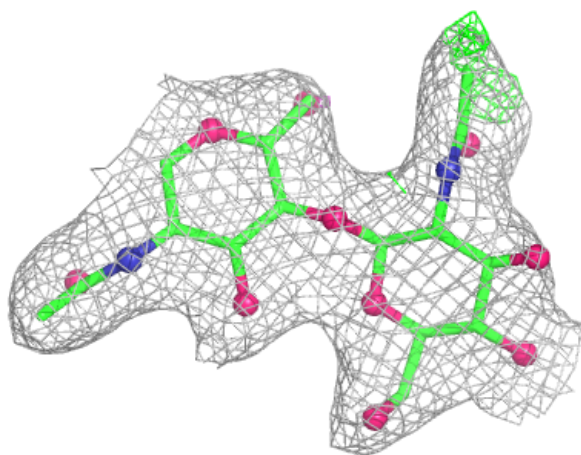
Electron density around Chain C:

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



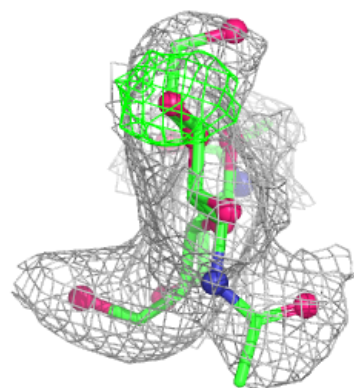
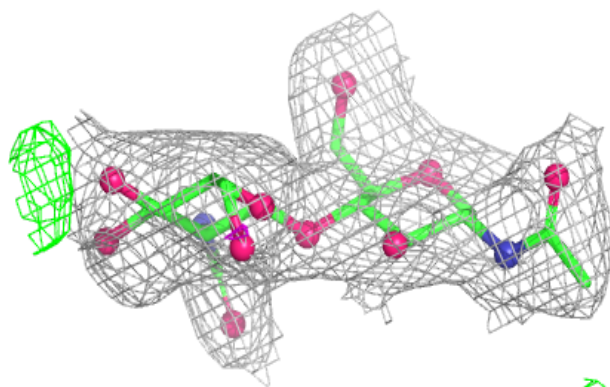
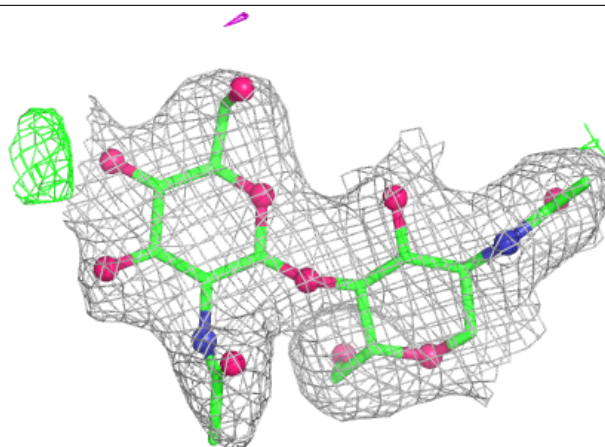
Electron density around Chain D:

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

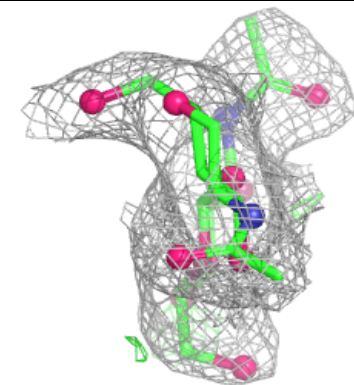
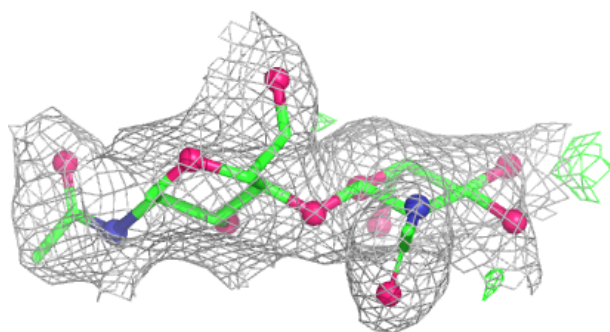
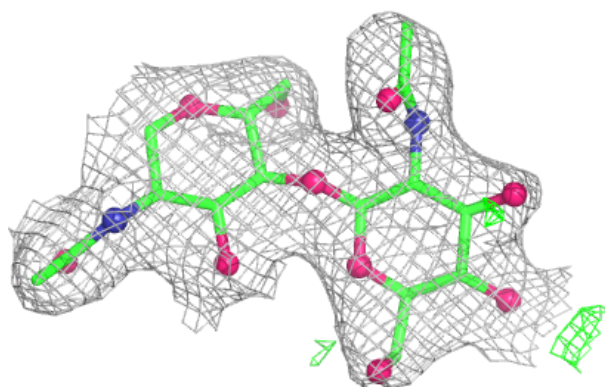


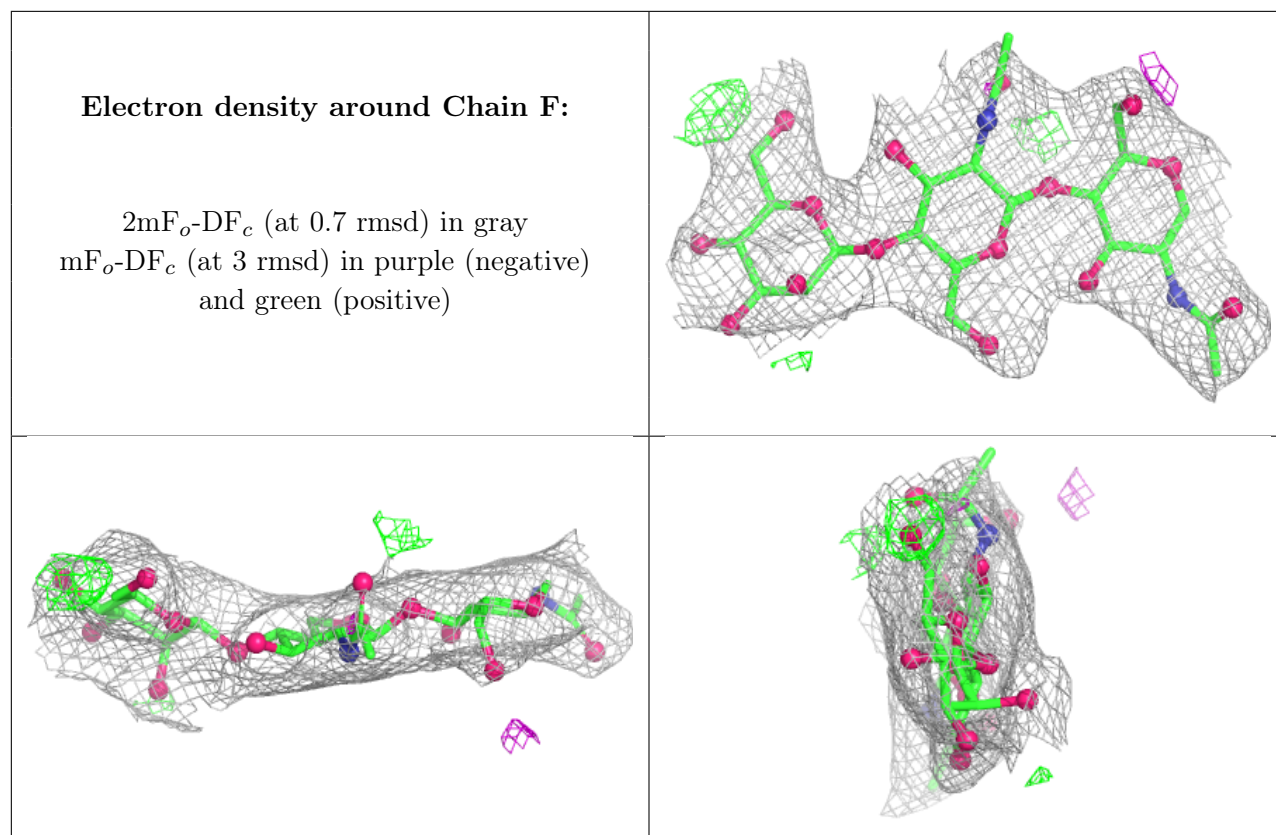
Electron density around Chain E:

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

**Electron density around Chain G:**

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





6.4 Ligands ⓘ

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.

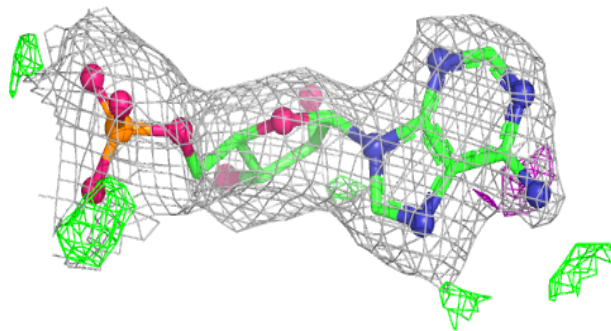
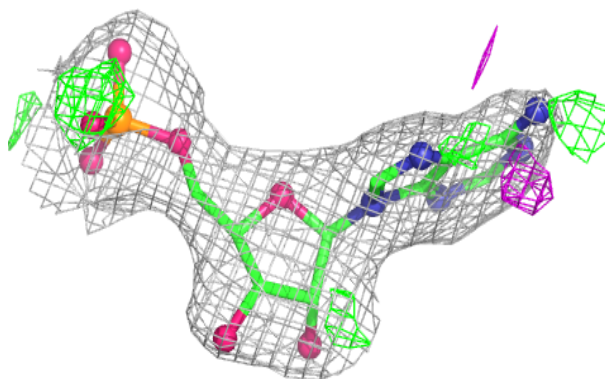
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	NAG	B	1009	14/15	0.67	0.16	87,89,89,90	0
7	NAG	A	1012	14/15	0.73	0.13	85,85,86,86	0
7	NAG	B	1012	14/15	0.78	0.15	79,81,82,82	0
7	NAG	B	1008	14/15	0.85	0.14	77,79,81,81	0
7	NAG	A	1007	14/15	0.90	0.09	50,54,57,58	0
4	AMP	B	1001	23/23	0.91	0.11	51,56,59,60	0
4	AMP	A	1001	23/23	0.94	0.09	39,45,51,52	0
6	CA	A	1004	1/1	0.97	0.10	57,57,57,57	0
6	CA	B	1004	1/1	0.99	0.09	46,46,46,46	0
5	ZN	B	1003	1/1	0.99	0.02	44,44,44,44	0
5	ZN	B	1002	1/1	0.99	0.03	43,43,43,43	0
5	ZN	A	1003	1/1	1.00	0.02	34,34,34,34	0
5	ZN	A	1002	1/1	1.00	0.01	32,32,32,32	0

The following is a graphical depiction of the model fit to experimental electron density of all

instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

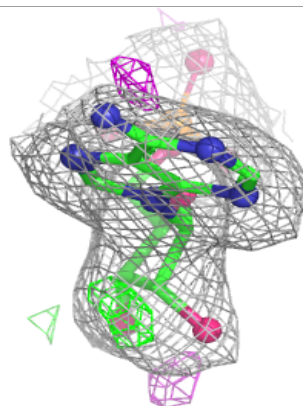
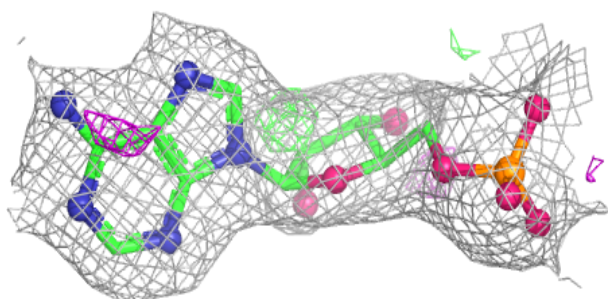
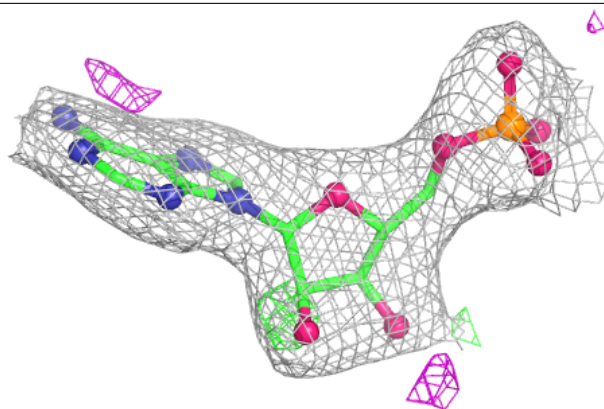
Electron density around AMP B 1001:

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



Electron density around AMP A 1001:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.