



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 08:20 AM BST

PDB ID : 6BV4  
Title : Crystal structure of porcine aminopeptidase-N with Methionine  
Authors : Chen, L.; Lin, Y.-L.; Li, F.  
Deposited on : 2017-12-12  
Resolution : 2.02 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

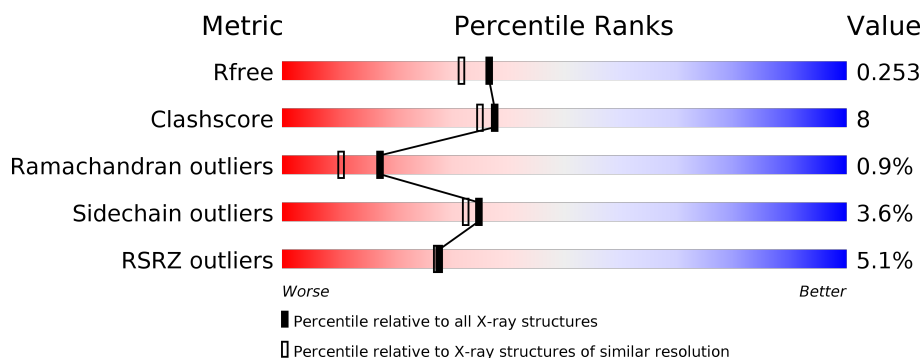
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.02 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.




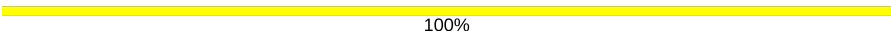


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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  $\leq 5\%$ . 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	902	 5% 86% 12% ..
2	B	3	 33% 67%
2	C	3	 100%
2	F	3	 100%
3	D	2	 50% 50%
3	E	2	 100%

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Mol	Chain	Length	Quality of chain
3	G	2	 50% 50%
3	H	2	 100%
3	I	2	 100%
3	J	2	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	B	3	-	-	-	X
2	NAG	C	2	-	-	-	X
2	NAG	C	3	-	-	-	X
2	NAG	F	3	-	-	-	X
3	NAG	E	2	-	-	-	X
4	NAG	A	1020	-	-	-	X
6	SO4	A	1025	-	-	X	-
6	SO4	A	1026	-	-	X	-
6	SO4	A	1033	-	-	X	-
6	SO4	A	1034	-	-	X	X

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 8472 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.

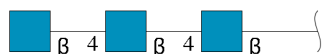
- Molecule 1 is a protein called Aminopeptidase N.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	902	7242	4622	1210	1380	30	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	PHE	LEU	conflict	UNP P15145
A	964	SER	-	expression tag	UNP P15145

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



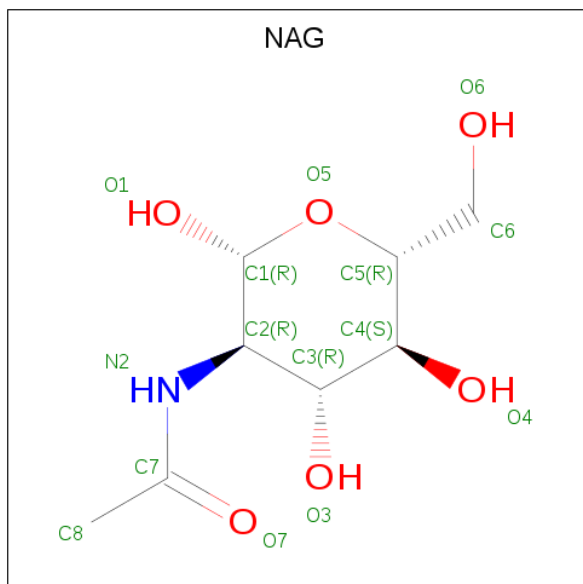
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	3	42	24	3	15	0	0	0
2	C	3	42	24	3	15	0	0	0
2	F	3	42	24	3	15	0	0	0

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



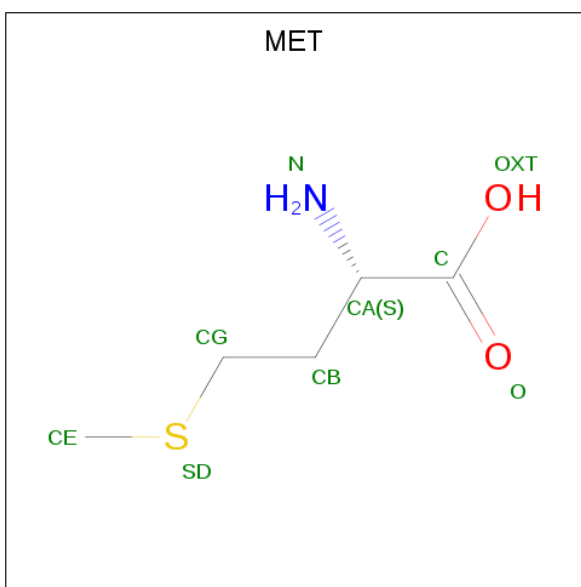
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	J	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

- Molecule 5 is METHIONINE (three-letter code: MET) (formula:  $C_5H_{11}NO_2S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			9	5	1	2	1		

- Molecule 6 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Zn	0	0
			1	1		

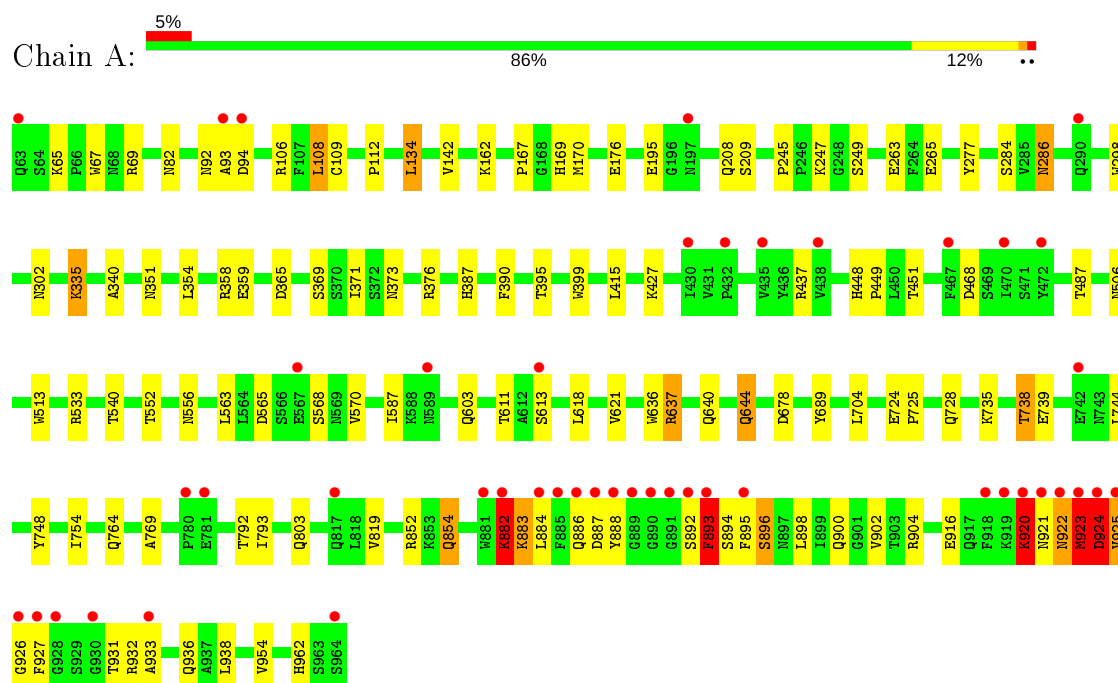
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	838	Total	O	0	0
			838	838		

### 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.

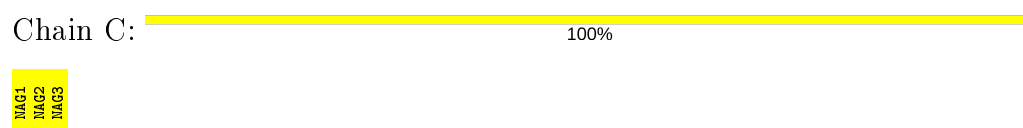
#### • Molecule 1: Aminopeptidase N



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

Chain F:  100%

NAG1  
NAG2  
NAG3

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

Chain D:  50% 50%

NAG1  
NAG2

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

Chain E:  100%

NAG1  
NAG2

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

Chain G:  50% 50%

NAG1  
NAG2

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

Chain H:  100%

NAG1  
NAG2

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

Chain I:  100%

NAG1  
NAG2

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

Chain J:  100%

MAG1  
MAG2

## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	260.66Å 62.87Å 81.62Å 90.00° 100.39° 90.00°	Depositor
Resolution (Å)	50.00 – 2.02 47.63 – 2.02	Depositor EDS
% Data completeness (in resolution range)	98.6 (50.00-2.02) 98.6 (47.63-2.02)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.20 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.205 , 0.246 0.211 , 0.253	Depositor DCC
$R_{free}$ test set	4211 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.4	Xtriage
Anisotropy	0.066	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 37.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8472	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.18% 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: ZN, NAG, SO4

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	0.56	0/7430	0.54	0/10124

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	920	LYS	Peptide
1	A	93	ALA	Peptide

### 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	7242	0	6994	109	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	42	0	37	1	0
2	C	42	0	37	0	0
2	F	42	0	37	0	0
3	D	28	0	25	1	0
3	E	28	0	25	0	0
3	G	28	0	25	0	0
3	H	28	0	25	0	0
3	I	28	0	25	4	0
3	J	28	0	25	2	0
4	A	28	0	26	0	0
5	A	9	0	8	0	0
6	A	60	0	0	11	0
7	A	1	0	0	0	0
8	A	838	0	0	22	1
All	All	8472	0	7289	115	1

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 8.

All (115) 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:69:ARG:NH1	6:A:1034:SO4:O2	1.64	1.27
1:A:923:MET:O	1:A:924:ASP:HB2	1.62	0.99
1:A:302:ASN:ND2	6:A:1036:SO4:O4	2.01	0.92
1:A:108:LEU:HD12	1:A:109:CYS:N	1.86	0.89
1:A:265:GLU:HG3	8:A:1764:HOH:O	1.72	0.88
8:A:1608:HOH:O	3:J:2:NAG:H82	1.75	0.86
1:A:552:THR:HB	1:A:611:THR:HG22	1.59	0.85
1:A:637:ARG:NH1	1:A:678:ASP:OD2	2.13	0.81
8:A:1120:HOH:O	3:I:1:NAG:C6	2.27	0.81
1:A:888:TYR:HD1	1:A:895:PHE:HE1	1.28	0.81
1:A:286:ASN:ND2	8:A:1103:HOH:O	1.92	0.76
1:A:82:ASN:HB3	6:A:1026:SO4:O4	1.88	0.72
1:A:888:TYR:CD1	1:A:895:PHE:HE1	2.10	0.70
1:A:176:GLU:OE1	8:A:1104:HOH:O	2.12	0.67
1:A:896:SER:HB2	8:A:1138:HOH:O	1.95	0.66
1:A:399:TRP:CZ3	6:A:1025:SO4:O2	2.50	0.65
1:A:108:LEU:C	1:A:108:LEU:HD12	2.16	0.65
1:A:373:ASN:ND2	8:A:1111:HOH:O	2.29	0.64
1:A:448:HIS:HE1	1:A:468:ASP:OD2	1.81	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:565:ASP:HB3	1:A:568:SER:OG	1.97	0.64
1:A:884:LEU:HD22	1:A:925:VAL:O	1.98	0.64
1:A:371:ILE:HG13	1:A:744:LEU:HD12	1.80	0.63
1:A:556:ASN:HD22	3:I:1:NAG:H83	1.64	0.61
1:A:921:ASN:ND2	8:A:1115:HOH:O	2.32	0.61
1:A:883:LYS:HD3	1:A:883:LYS:C	2.22	0.60
1:A:108:LEU:CD1	1:A:109:CYS:N	2.60	0.59
1:A:637:ARG:HD2	1:A:637:ARG:N	2.17	0.59
1:A:735:LYS:HD2	1:A:739:GLU:CD	2.23	0.59
1:A:754:ILE:HG22	1:A:792:THR:HG21	1.84	0.59
1:A:883:LYS:CD	1:A:883:LYS:C	2.71	0.59
1:A:208:GLN:HE21	1:A:209:SER:HA	1.68	0.58
1:A:728:GLN:NE2	1:A:764:GLN:HE21	2.02	0.58
1:A:884:LEU:HD12	1:A:895:PHE:CE2	2.39	0.57
1:A:621:VAL:HG11	3:J:1:NAG:H82	1.86	0.57
1:A:611:THR:HG21	8:A:1210:HOH:O	2.04	0.57
1:A:883:LYS:HE3	1:A:893:PHE:HE2	1.70	0.57
1:A:954:VAL:HG23	8:A:1313:HOH:O	2.06	0.56
6:A:1033:SO4:O3	3:D:1:NAG:O5	2.22	0.56
3:I:1:NAG:H62	3:I:2:NAG:C1	2.36	0.56
1:A:924:ASP:O	1:A:925:VAL:HG22	2.05	0.56
1:A:896:SER:OG	1:A:933:ALA:HB2	2.06	0.55
1:A:892:SER:O	1:A:893:PHE:HB2	2.05	0.55
1:A:921:ASN:OD1	1:A:921:ASN:O	2.25	0.54
1:A:927:PHE:HB2	1:A:931:THR:HA	1.89	0.54
1:A:565:ASP:HB3	1:A:568:SER:HG	1.72	0.54
1:A:888:TYR:CD1	1:A:895:PHE:CE1	2.95	0.54
1:A:415:LEU:HD22	1:A:427:LYS:HE2	1.91	0.53
1:A:162:LYS:HE2	8:A:1308:HOH:O	2.08	0.53
1:A:644:GLN:HG3	8:A:1597:HOH:O	2.09	0.53
1:A:819:VAL:HG23	8:A:1533:HOH:O	2.08	0.53
1:A:69:ARG:CZ	6:A:1034:SO4:O2	2.49	0.53
1:A:247:LYS:HE2	6:A:1033:SO4:S	2.49	0.52
1:A:395:THR:O	1:A:506:ASN:HA	2.09	0.52
1:A:552:THR:HB	1:A:611:THR:CG2	2.35	0.52
1:A:884:LEU:HD12	1:A:895:PHE:CZ	2.45	0.52
1:A:921:ASN:CG	8:A:1115:HOH:O	2.48	0.52
1:A:883:LYS:HG2	1:A:883:LYS:O	2.10	0.52
1:A:931:THR:O	8:A:1105:HOH:O	2.19	0.52
1:A:900:GLN:NE2	1:A:904:ARG:HD3	2.25	0.51
1:A:563:LEU:HD11	1:A:570:VAL:CG2	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:884:LEU:CD2	1:A:925:VAL:O	2.59	0.51
1:A:371:ILE:CG1	1:A:744:LEU:HD12	2.41	0.50
1:A:365:ASP:O	1:A:369:SER:HB2	2.12	0.50
1:A:735:LYS:O	1:A:738:THR:OG1	2.30	0.50
1:A:358:ARG:NH2	8:A:1116:HOH:O	2.32	0.49
1:A:636:TRP:O	1:A:640:GLN:HG3	2.11	0.49
1:A:108:LEU:CD1	1:A:108:LEU:C	2.81	0.49
1:A:108:LEU:HD13	1:A:169:HIS:O	2.12	0.49
1:A:883:LYS:O	1:A:883:LYS:CG	2.59	0.49
1:A:376:ARG:CZ	6:A:1027:SO4:O4	2.61	0.49
1:A:106:ARG:HG2	1:A:170:MET:HE1	1.94	0.49
1:A:82:ASN:CB	6:A:1026:SO4:O4	2.57	0.49
1:A:728:GLN:HE22	1:A:764:GLN:HE21	1.59	0.48
1:A:134:LEU:HD13	1:A:142:VAL:CG2	2.43	0.48
1:A:263:GLU:OE2	8:A:1106:HOH:O	2.20	0.48
1:A:852:ARG:NH2	1:A:854:GLN:OE1	2.46	0.48
1:A:892:SER:O	1:A:893:PHE:CB	2.61	0.47
1:A:888:TYR:HD1	1:A:895:PHE:CE1	2.19	0.47
1:A:399:TRP:CE3	6:A:1025:SO4:O2	2.68	0.46
1:A:962:HIS:HD2	8:A:1831:HOH:O	1.99	0.46
1:A:286:ASN:ND2	8:A:1145:HOH:O	2.48	0.46
1:A:112:PRO:HD3	1:A:167:PRO:HG3	1.98	0.46
1:A:587:ILE:HG22	1:A:618:LEU:HB3	1.97	0.46
1:A:351:ASN:HB2	1:A:354:LEU:O	2.16	0.46
1:A:195:GLU:HG3	8:A:1631:HOH:O	2.15	0.45
1:A:916:GLU:OE2	1:A:938:LEU:HD22	2.16	0.45
1:A:134:LEU:HD13	1:A:142:VAL:HG22	1.99	0.45
1:A:882:LYS:HG3	1:A:882:LYS:H	1.40	0.45
1:A:448:HIS:CE1	1:A:468:ASP:OD2	2.67	0.44
1:A:247:LYS:HE2	6:A:1033:SO4:O1	2.18	0.44
1:A:245:PRO:HG3	1:A:335:LYS:HG2	2.00	0.44
8:A:1120:HOH:O	3:I:1:NAG:H62	2.04	0.44
1:A:923:MET:H	1:A:923:MET:HG3	1.59	0.44
1:A:448:HIS:HD2	1:A:449:PRO:O	2.01	0.43
1:A:108:LEU:HD12	1:A:109:CYS:O	2.18	0.43
1:A:284:SER:HB3	1:A:298:TRP:CD2	2.53	0.43
1:A:415:LEU:HD22	1:A:427:LYS:CE	2.48	0.43
1:A:451:THR:HG23	1:A:540:THR:HB	2.02	0.42
1:A:769:ALA:HA	1:A:793:ILE:HD12	2.00	0.42
1:A:387:HIS:HA	1:A:390:PHE:O	2.20	0.42
1:A:689:TYR:CD1	1:A:748:TYR:HB3	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2:NAG:H61	2:B:3:NAG:O5	2.19	0.42
1:A:92:ASN:ND2	8:A:1113:HOH:O	2.30	0.42
1:A:208:GLN:HA	1:A:209:SER:HA	1.82	0.41
1:A:924:ASP:C	1:A:926:GLY:H	2.22	0.41
1:A:340:ALA:HB1	1:A:359:GLU:HA	2.02	0.41
1:A:933:ALA:HA	1:A:936:GLN:OE1	2.20	0.41
1:A:724:GLU:N	1:A:725:PRO:CD	2.83	0.41
1:A:924:ASP:O	1:A:926:GLY:N	2.49	0.41
1:A:898:LEU:O	1:A:902:VAL:HG12	2.21	0.41
1:A:900:GLN:HE22	1:A:904:ARG:HD3	1.85	0.41
1:A:65:LYS:HB3	1:A:67:TRP:CE2	2.57	0.40
1:A:922:ASN:O	1:A:924:ASP:N	2.44	0.40
1:A:108:LEU:HD12	1:A:109:CYS:C	2.40	0.40
1:A:704:LEU:HD21	1:A:904:ARG:HG2	2.03	0.40

All (1) 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)
8:A:1247:HOH:O	8:A:1686:HOH:O[4_557]	1.22	0.98

## 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	900/902 (100%)	868 (96%)	24 (3%)	8 (1%)	17 10

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	882	LYS
1	A	893	PHE

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Mol	Chain	Res	Type
1	A	924	ASP
1	A	925	VAL
1	A	894	SER
1	A	923	MET
1	A	920	LYS
1	A	487	THR

### 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	797/797 (100%)	769 (96%)	28 (4%)	36 34

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	ASP
1	A	108	LEU
1	A	134	LEU
1	A	249	SER
1	A	277	TYR
1	A	286	ASN
1	A	335	LYS
1	A	437	ARG
1	A	513	TRP
1	A	533	ARG
1	A	603	GLN
1	A	613	SER
1	A	637	ARG
1	A	644	GLN
1	A	738	THR
1	A	803	GLN
1	A	854	GLN
1	A	882	LYS
1	A	883	LYS
1	A	886	GLN

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Mol	Chain	Res	Type
1	A	887	ASP
1	A	893	PHE
1	A	896	SER
1	A	920	LYS
1	A	922	ASN
1	A	923	MET
1	A	924	ASP
1	A	932	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	208	GLN
1	A	286	ASN
1	A	373	ASN
1	A	448	HIS
1	A	728	GLN
1	A	803	GLN
1	A	886	GLN
1	A	897	ASN
1	A	921	ASN

### 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 ⓘ

21 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	B	1	1,2	14,14,15	0.70	0	17,19,21	1.01	1 (5%)
2	NAG	B	2	2	14,14,15	0.66	0	17,19,21	1.68	5 (29%)
2	NAG	B	3	2	14,14,15	1.01	1 (7%)	17,19,21	1.45	2 (11%)
2	NAG	C	1	1,2	14,14,15	0.49	0	17,19,21	1.03	1 (5%)
2	NAG	C	2	2	14,14,15	0.80	0	17,19,21	1.69	4 (23%)
2	NAG	C	3	2	14,14,15	0.82	0	17,19,21	1.43	2 (11%)
3	NAG	D	1	1,3	14,14,15	0.80	0	17,19,21	1.06	2 (11%)
3	NAG	D	2	3	14,14,15	0.86	0	17,19,21	1.13	2 (11%)
3	NAG	E	1	1,3	14,14,15	0.55	0	17,19,21	0.97	1 (5%)
3	NAG	E	2	3	14,14,15	0.79	0	17,19,21	1.35	2 (11%)
2	NAG	F	1	1,2	14,14,15	0.56	0	17,19,21	1.16	2 (11%)
2	NAG	F	2	2	14,14,15	0.50	0	17,19,21	1.63	4 (23%)
2	NAG	F	3	2	14,14,15	0.55	0	17,19,21	1.17	2 (11%)
3	NAG	G	1	1,3	14,14,15	0.51	0	17,19,21	0.88	0
3	NAG	G	2	3	14,14,15	0.67	0	17,19,21	1.43	3 (17%)
3	NAG	H	1	1,3	14,14,15	0.66	0	17,19,21	1.40	2 (11%)
3	NAG	H	2	3	14,14,15	0.51	0	17,19,21	1.38	3 (17%)
3	NAG	I	1	1,3	14,14,15	0.61	0	17,19,21	1.20	3 (17%)
3	NAG	I	2	3	14,14,15	0.49	0	17,19,21	1.18	1 (5%)
3	NAG	J	1	1,3	14,14,15	0.53	0	17,19,21	0.97	1 (5%)
3	NAG	J	2	3	14,14,15	0.65	0	17,19,21	1.25	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	B	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	4/6/23/26	0/1/1/1
2	NAG	B	3	2	-	2/6/23/26	0/1/1/1
2	NAG	C	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	NAG	C	3	2	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
3	NAG	E	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1
2	NAG	F	3	2	-	2/6/23/26	0/1/1/1
3	NAG	G	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	2/6/23/26	0/1/1/1
3	NAG	H	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	4/6/23/26	0/1/1/1
3	NAG	I	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	I	2	3	-	3/6/23/26	0/1/1/1
3	NAG	J	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3	NAG	C1-C2	2.38	1.55	1.52

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	NAG	C4-C3-C2	5.04	118.40	111.02
2	B	2	NAG	C4-C3-C2	4.13	117.07	111.02
2	B	3	NAG	C4-C3-C2	3.96	116.82	111.02
3	E	2	NAG	C1-O5-C5	3.60	117.07	112.19
2	F	2	NAG	C3-C4-C5	3.23	116.01	110.24
2	F	2	NAG	C4-C3-C2	3.21	115.72	111.02
2	C	3	NAG	C4-C3-C2	3.15	115.64	111.02
3	G	2	NAG	C3-C4-C5	-3.13	104.66	110.24
3	H	1	NAG	C1-O5-C5	3.05	116.33	112.19
3	I	2	NAG	C1-O5-C5	3.05	116.32	112.19
2	F	3	NAG	C1-C2-N2	-2.88	105.57	110.49
3	H	1	NAG	C2-N2-C7	-2.87	118.82	122.90
3	J	2	NAG	C1-O5-C5	2.84	116.05	112.19
2	F	3	NAG	C3-C4-C5	2.82	115.27	110.24
2	B	2	NAG	O5-C1-C2	-2.79	106.88	111.29
2	B	2	NAG	C1-O5-C5	-2.71	108.53	112.19
2	F	1	NAG	C2-N2-C7	-2.67	119.10	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3	NAG	C3-C4-C5	2.67	115.01	110.24
2	C	1	NAG	O5-C1-C2	-2.64	107.11	111.29
3	I	1	NAG	O5-C1-C2	-2.63	107.13	111.29
3	D	1	NAG	O5-C5-C6	2.62	111.31	107.20
2	C	3	NAG	C1-C2-N2	-2.61	106.03	110.49
2	C	2	NAG	O5-C1-C2	-2.52	107.30	111.29
3	J	1	NAG	O7-C7-C8	-2.46	117.48	122.06
3	D	2	NAG	O5-C5-C4	-2.42	104.94	110.83
3	H	2	NAG	C2-N2-C7	-2.42	119.46	122.90
3	G	2	NAG	C2-N2-C7	-2.40	119.48	122.90
3	E	2	NAG	C1-C2-N2	2.39	114.57	110.49
2	C	2	NAG	C3-C4-C5	2.38	114.49	110.24
2	F	2	NAG	C1-O5-C5	-2.34	109.03	112.19
2	B	2	NAG	O4-C4-C3	-2.33	104.96	110.35
3	E	1	NAG	O4-C4-C3	-2.32	104.99	110.35
3	G	2	NAG	C6-C5-C4	2.28	118.34	113.00
3	H	2	NAG	C3-C4-C5	2.25	114.25	110.24
3	I	1	NAG	C1-O5-C5	2.18	115.15	112.19
2	C	2	NAG	C1-O5-C5	-2.18	109.25	112.19
3	H	2	NAG	O5-C1-C2	-2.17	107.86	111.29
3	D	1	NAG	C2-N2-C7	-2.08	119.95	122.90
2	F	1	NAG	O5-C1-C2	-2.05	108.05	111.29
2	B	2	NAG	C2-N2-C7	-2.02	120.02	122.90
2	B	1	NAG	C1-O5-C5	2.02	114.93	112.19
2	F	2	NAG	O4-C4-C5	-2.02	104.27	109.30
3	I	1	NAG	C6-C5-C4	-2.02	108.28	113.00
3	D	2	NAG	O5-C1-C2	-2.00	108.13	111.29

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	NAG	O5-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
2	B	3	NAG	O5-C5-C6-O6
2	B	2	NAG	C4-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6
2	C	3	NAG	O5-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6
2	B	3	NAG	C4-C5-C6-O6
3	H	2	NAG	C8-C7-N2-C2
3	H	2	NAG	O7-C7-N2-C2

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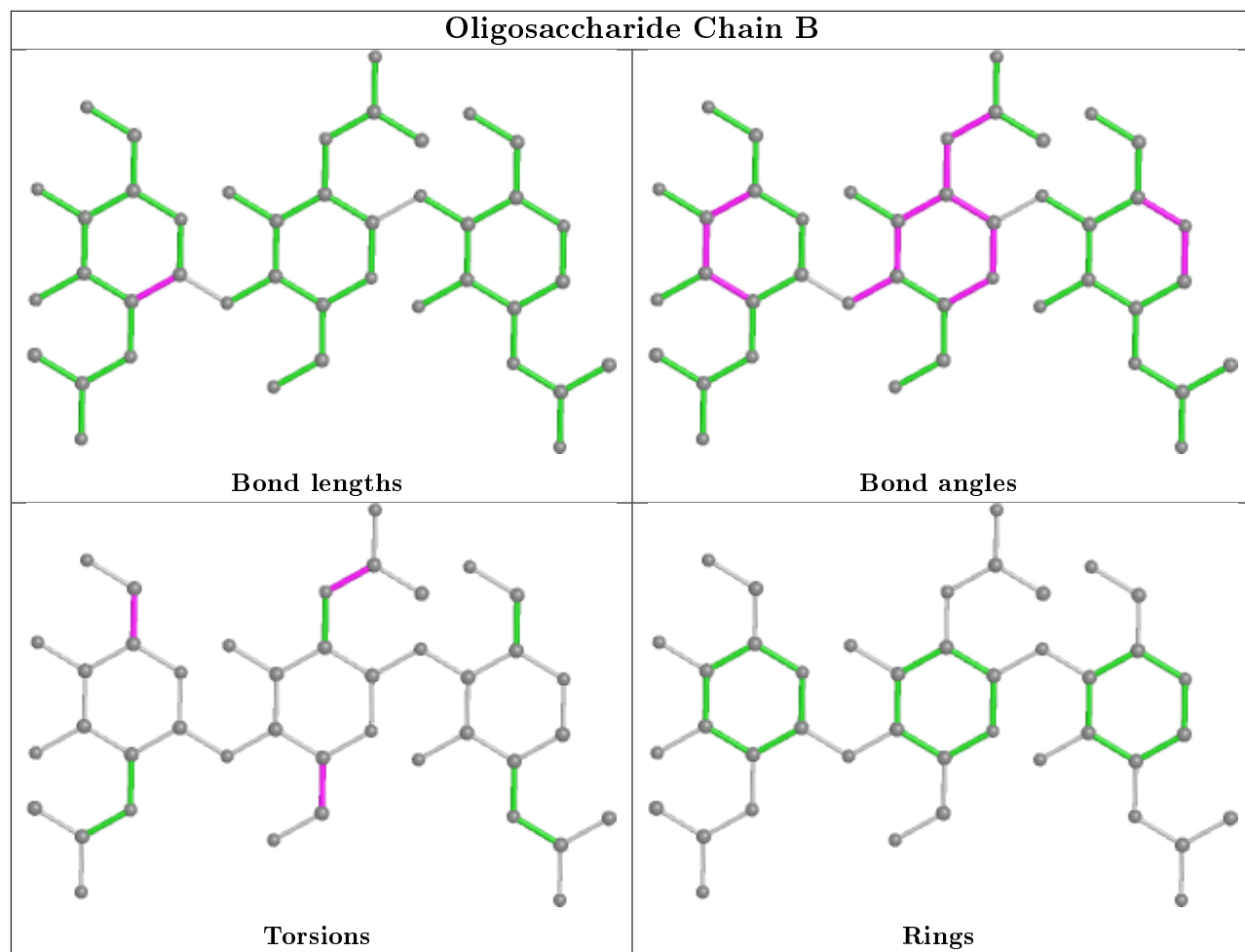
Mol	Chain	Res	Type	Atoms
3	I	2	NAG	C8-C7-N2-C2
3	I	2	NAG	O7-C7-N2-C2
3	I	1	NAG	C8-C7-N2-C2
3	I	1	NAG	O7-C7-N2-C2
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2
3	J	2	NAG	O5-C5-C6-O6
2	F	3	NAG	O5-C5-C6-O6
2	C	3	NAG	C4-C5-C6-O6
3	I	2	NAG	O5-C5-C6-O6
3	J	2	NAG	C4-C5-C6-O6
3	G	2	NAG	O5-C5-C6-O6
3	I	1	NAG	C4-C5-C6-O6
3	I	1	NAG	O5-C5-C6-O6
3	H	2	NAG	C4-C5-C6-O6
2	F	3	NAG	C4-C5-C6-O6
3	H	2	NAG	O5-C5-C6-O6

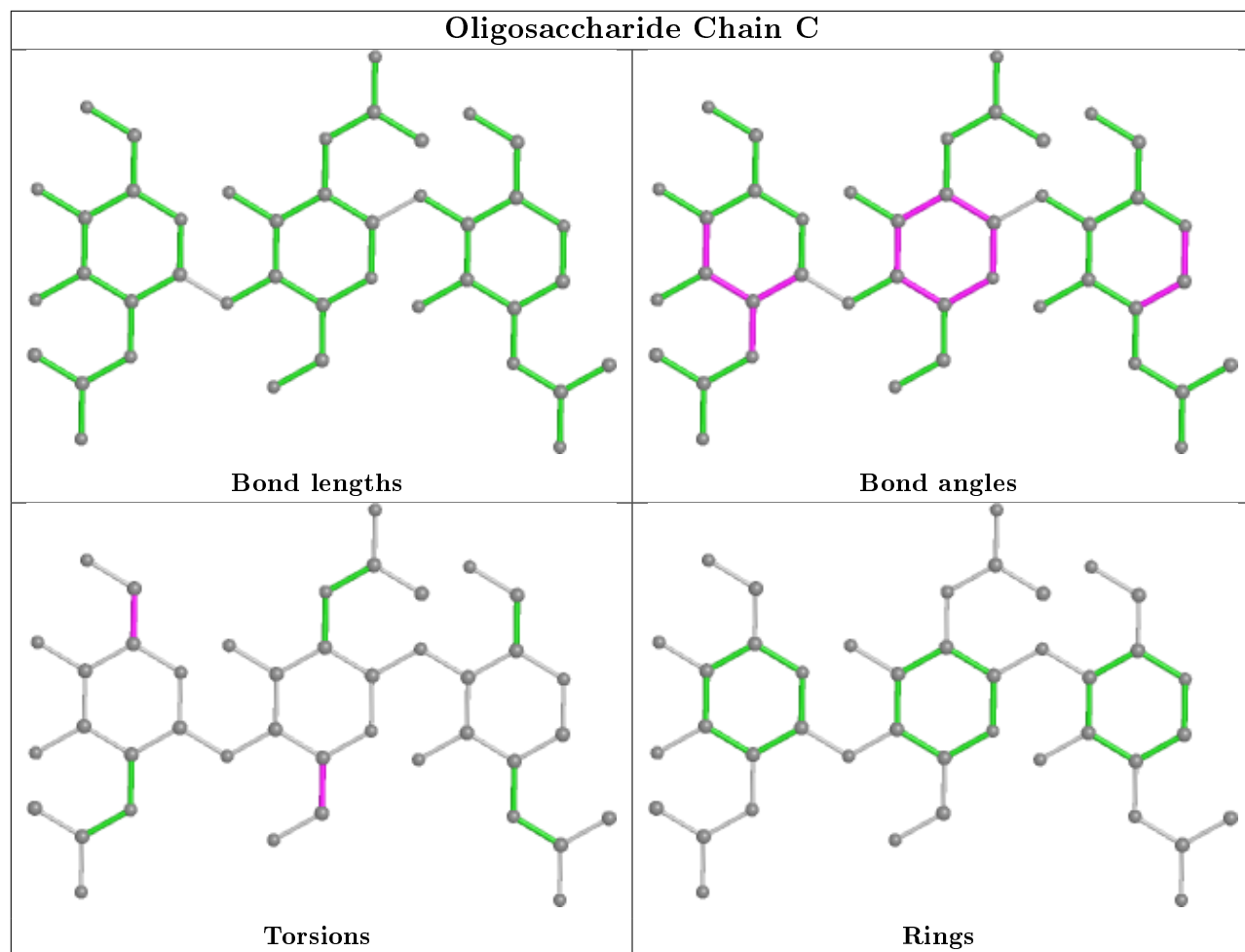
There are no ring outliers.

7 monomers are involved in 8 short contacts:

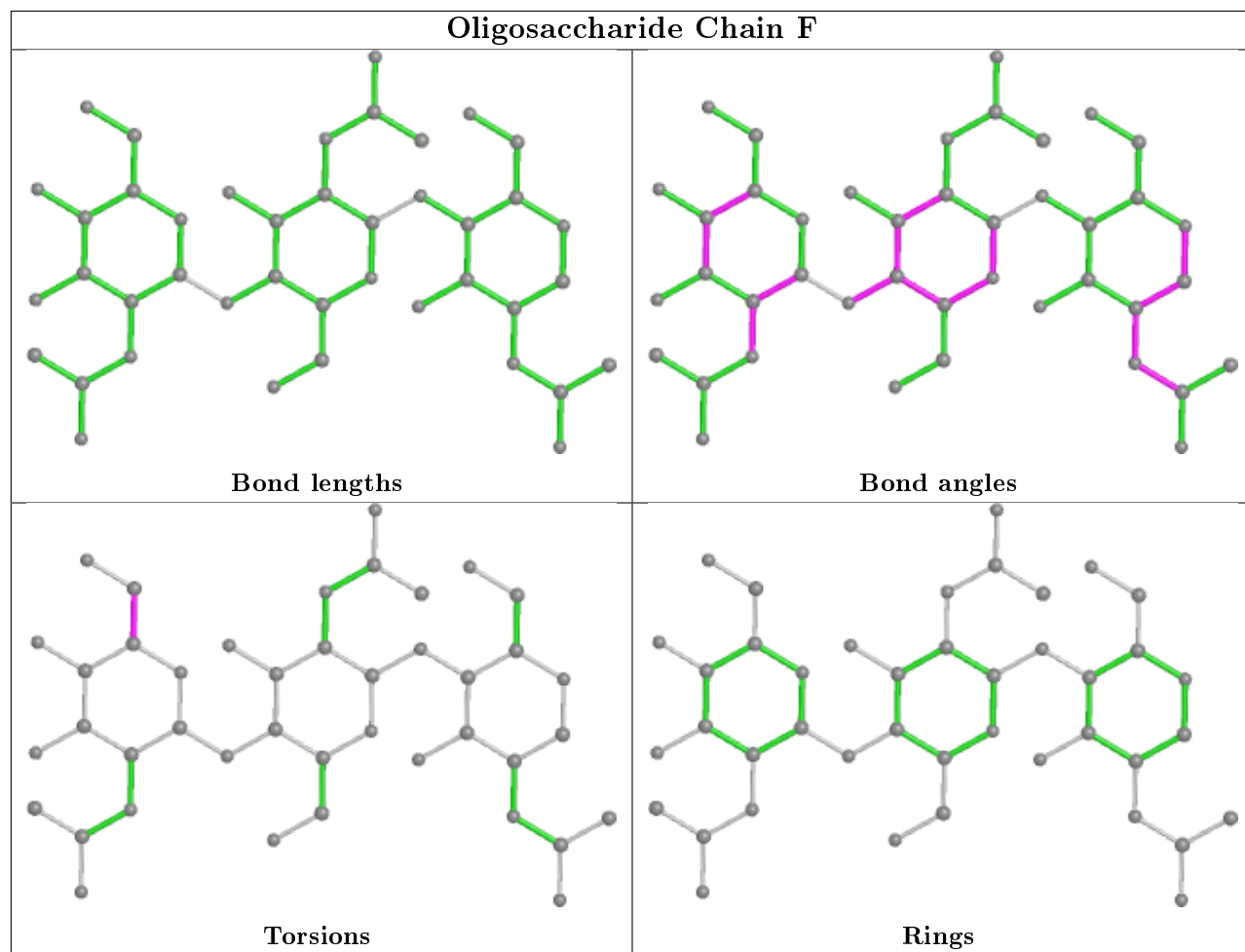
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	J	2	NAG	1	0
3	D	1	NAG	1	0
3	J	1	NAG	1	0
3	I	2	NAG	1	0
3	I	1	NAG	4	0
2	B	3	NAG	1	0
2	B	2	NAG	1	0

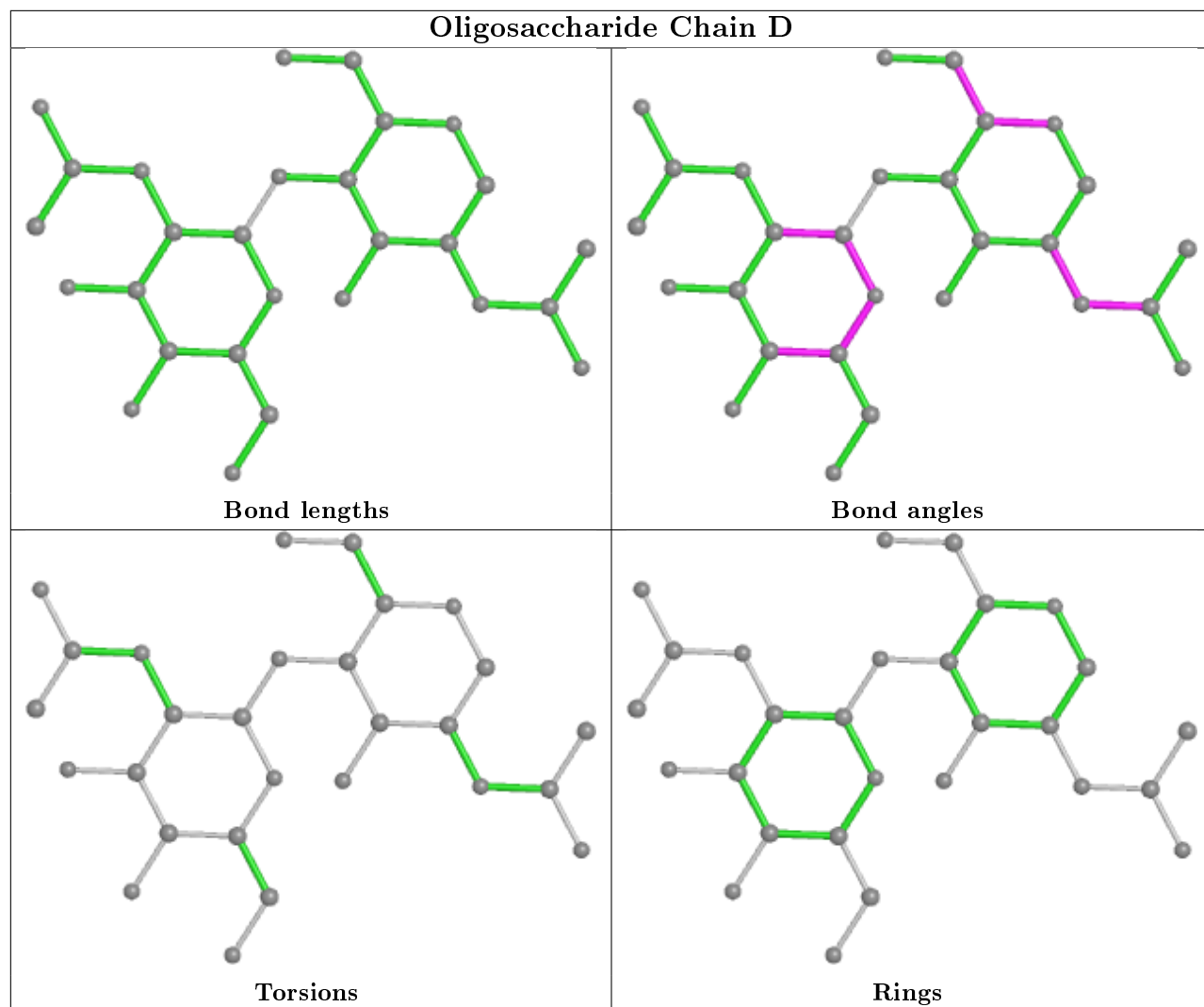
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

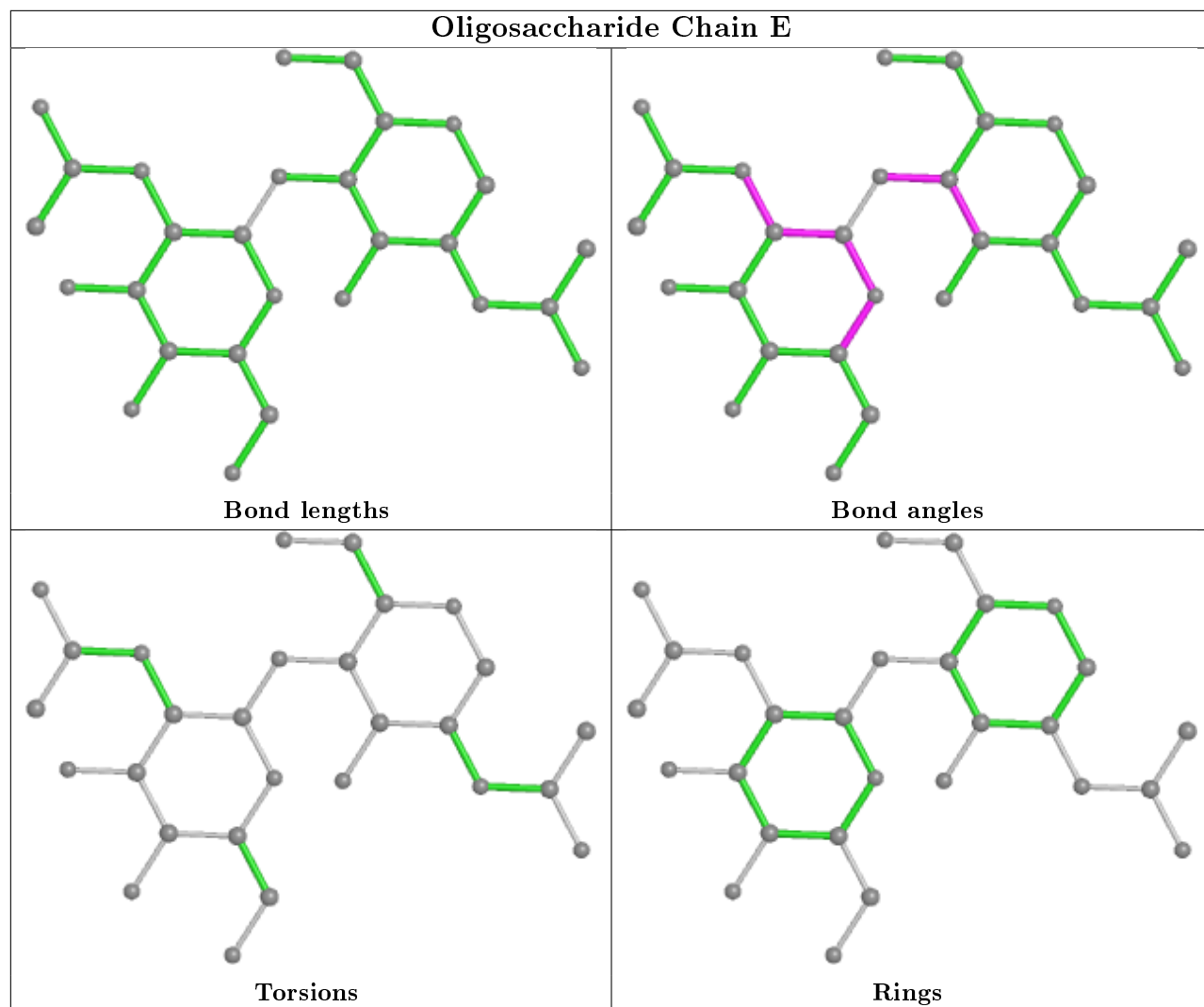


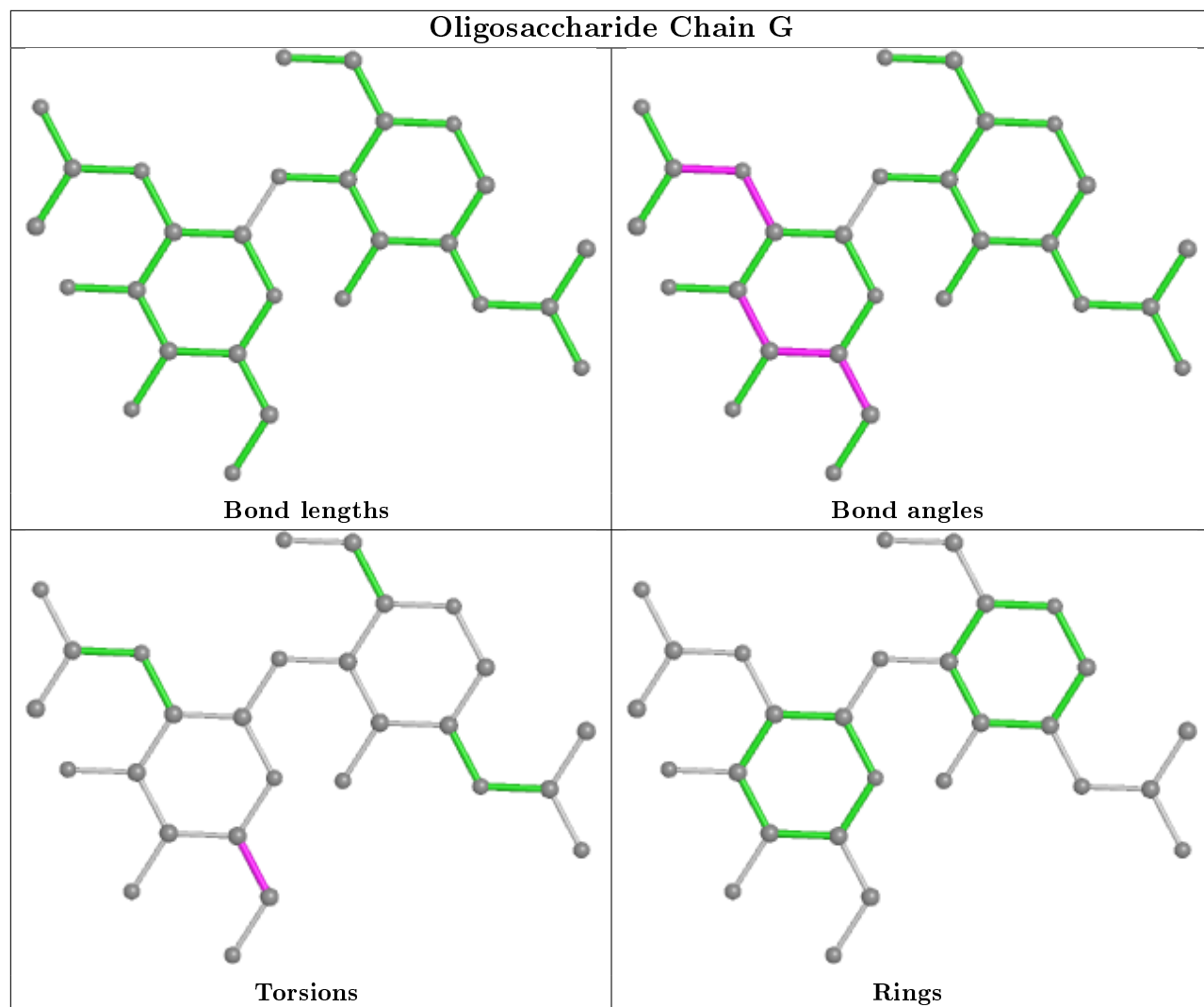


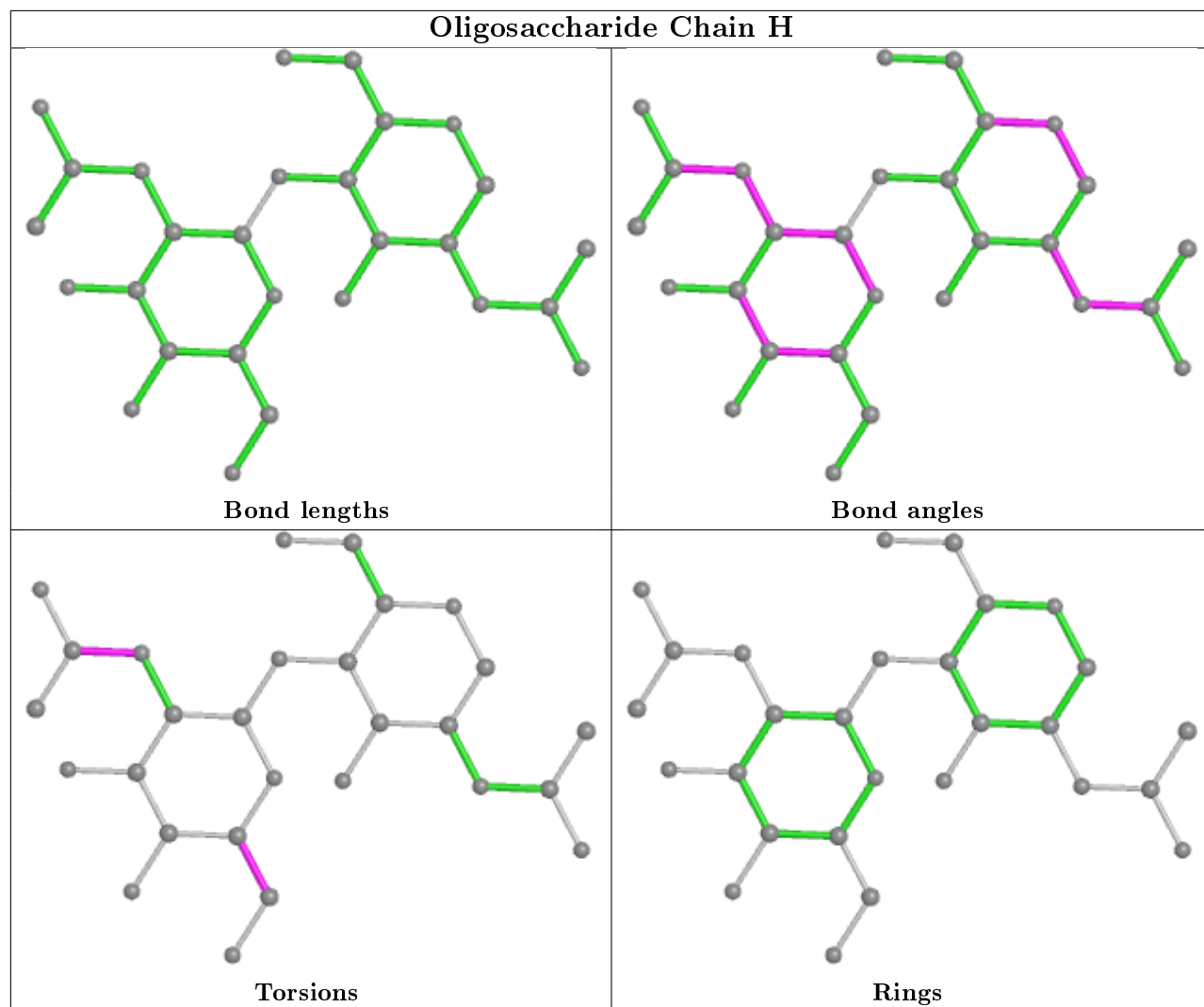


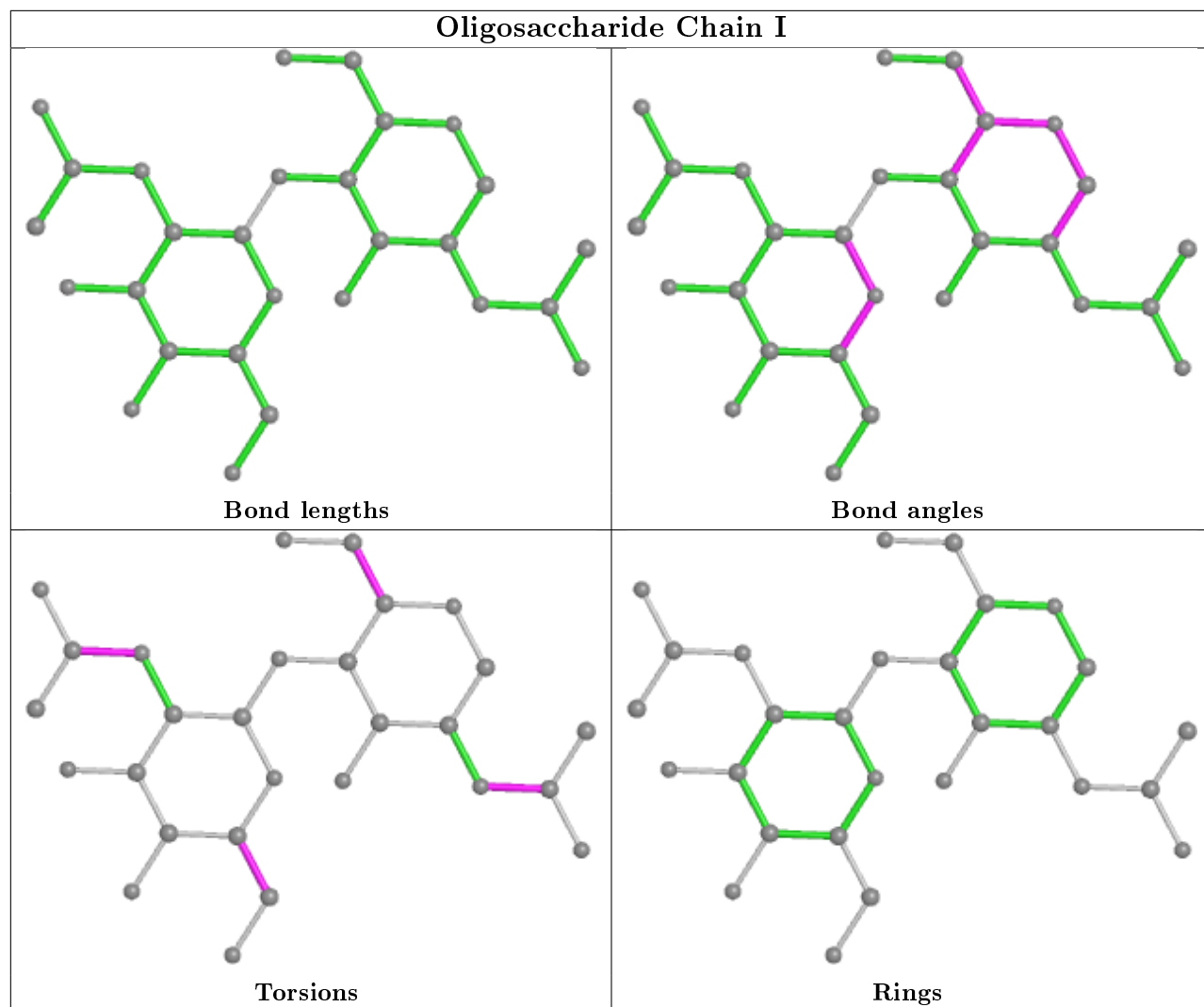


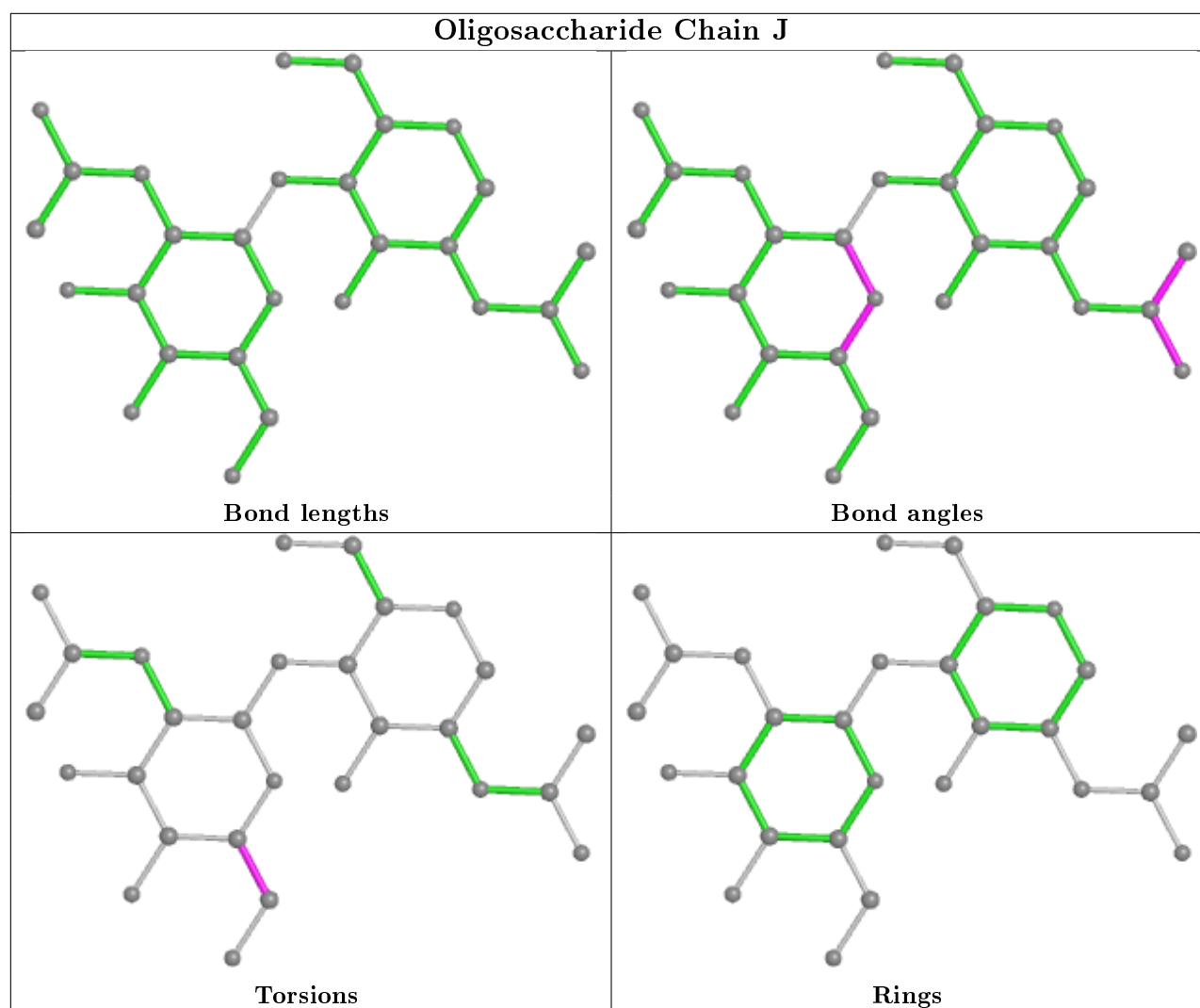












## 5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 1 is monoatomic - leaving 15 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	$\# Z  > 2$
6	SO4	A	1035	-	4,4,4	1.29	0	6,6,6	0.61	0
6	SO4	A	1025	-	4,4,4	1.41	1 (25%)	6,6,6	1.76	2 (33%)
6	SO4	A	1028	-	4,4,4	1.45	1 (25%)	6,6,6	0.68	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	A	1023	1	14,14,15	0.77	0	17,19,21	1.17	3 (17%)
6	SO4	A	1031	-	4,4,4	1.77	1 (25%)	6,6,6	0.53	0
6	SO4	A	1036	-	4,4,4	1.51	1 (25%)	6,6,6	0.42	0
4	NAG	A	1020	1	14,14,15	0.72	0	17,19,21	1.26	2 (11%)
6	SO4	A	1034	-	4,4,4	1.55	0	6,6,6	0.45	0
6	SO4	A	1026	-	4,4,4	1.63	1 (25%)	6,6,6	0.69	0
6	SO4	A	1030	-	4,4,4	1.17	1 (25%)	6,6,6	0.28	0
6	SO4	A	1029	-	4,4,4	1.06	0	6,6,6	0.32	0
6	SO4	A	1033	-	4,4,4	1.70	1 (25%)	6,6,6	0.44	0
6	SO4	A	1027	-	4,4,4	1.60	1 (25%)	6,6,6	0.30	0
6	SO4	A	1032	-	4,4,4	1.52	1 (25%)	6,6,6	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. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	1020	1	-	3/6/23/26	0/1/1/1
4	NAG	A	1023	1	-	2/6/23/26	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1033	SO4	O1-S	2.87	1.61	1.46
6	A	1031	SO4	O2-S	2.72	1.60	1.46
6	A	1036	SO4	O2-S	2.47	1.59	1.46
6	A	1027	SO4	O2-S	2.40	1.59	1.46
6	A	1026	SO4	O1-S	2.39	1.59	1.46
6	A	1032	SO4	O1-S	2.07	1.57	1.46
6	A	1025	SO4	O1-S	2.02	1.56	1.46
6	A	1030	SO4	O2-S	2.01	1.56	1.46
6	A	1028	SO4	O2-S	2.01	1.56	1.46

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1020	NAG	C2-N2-C7	3.28	127.57	122.90
6	A	1025	SO4	O4-S-O2	-2.72	95.12	109.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1023	NAG	C4-C3-C2	2.66	114.92	111.02
4	A	1023	NAG	O5-C5-C6	2.45	111.05	107.20
6	A	1025	SO4	O4-S-O3	2.17	118.33	109.06
4	A	1020	NAG	C4-C3-C2	-2.16	107.85	111.02
4	A	1023	NAG	O5-C5-C4	-2.06	105.83	110.83

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1020	NAG	C3-C2-N2-C7
4	A	1020	NAG	O5-C5-C6-O6
4	A	1023	NAG	O5-C5-C6-O6
4	A	1020	NAG	C4-C5-C6-O6
4	A	1023	NAG	C4-C5-C6-O6

There are no ring outliers.

6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1025	SO4	2	0
6	A	1036	SO4	1	0
6	A	1034	SO4	2	0
6	A	1026	SO4	2	0
6	A	1033	SO4	3	0
6	A	1027	SO4	1	0

## 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, 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	902/902 (100%)	0.34	46 (5%)	28 27	24, 33, 41, 45	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	889	GLY	10.7
1	A	885	PHE	10.3
1	A	888	TYR	8.4
1	A	925	VAL	7.6
1	A	890	GLY	6.9
1	A	93	ALA	6.8
1	A	893	PHE	6.8
1	A	923	MET	6.0
1	A	926	GLY	5.8
1	A	881	TRP	5.6
1	A	63	GLN	5.4
1	A	882	LYS	5.4
1	A	927	PHE	5.3
1	A	891	GLY	5.3
1	A	886	GLN	5.0
1	A	892	SER	4.9
1	A	922	ASN	4.1
1	A	781	GLU	3.8
1	A	197	ASN	3.6
1	A	918	PHE	3.5
1	A	94	ASP	3.2
1	A	924	ASP	3.2
1	A	290	GLN	3.2
1	A	930	GLY	3.1
1	A	884	LEU	3.0
1	A	928	GLY	2.9
1	A	613	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	430	ILE	2.7
1	A	438	VAL	2.7
1	A	964	SER	2.7
1	A	472	TYR	2.6
1	A	895	PHE	2.6
1	A	920	LYS	2.6
1	A	921	ASN	2.5
1	A	887	ASP	2.4
1	A	919	LYS	2.4
1	A	742	GLU	2.3
1	A	589	ASN	2.3
1	A	567	GLU	2.3
1	A	933	ALA	2.3
1	A	817	GLN	2.2
1	A	470	ILE	2.2
1	A	780	PRO	2.2
1	A	467	PHE	2.1
1	A	435	VAL	2.0
1	A	432	PRO	2.0

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

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

## 6.3 Carbohydrates ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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.

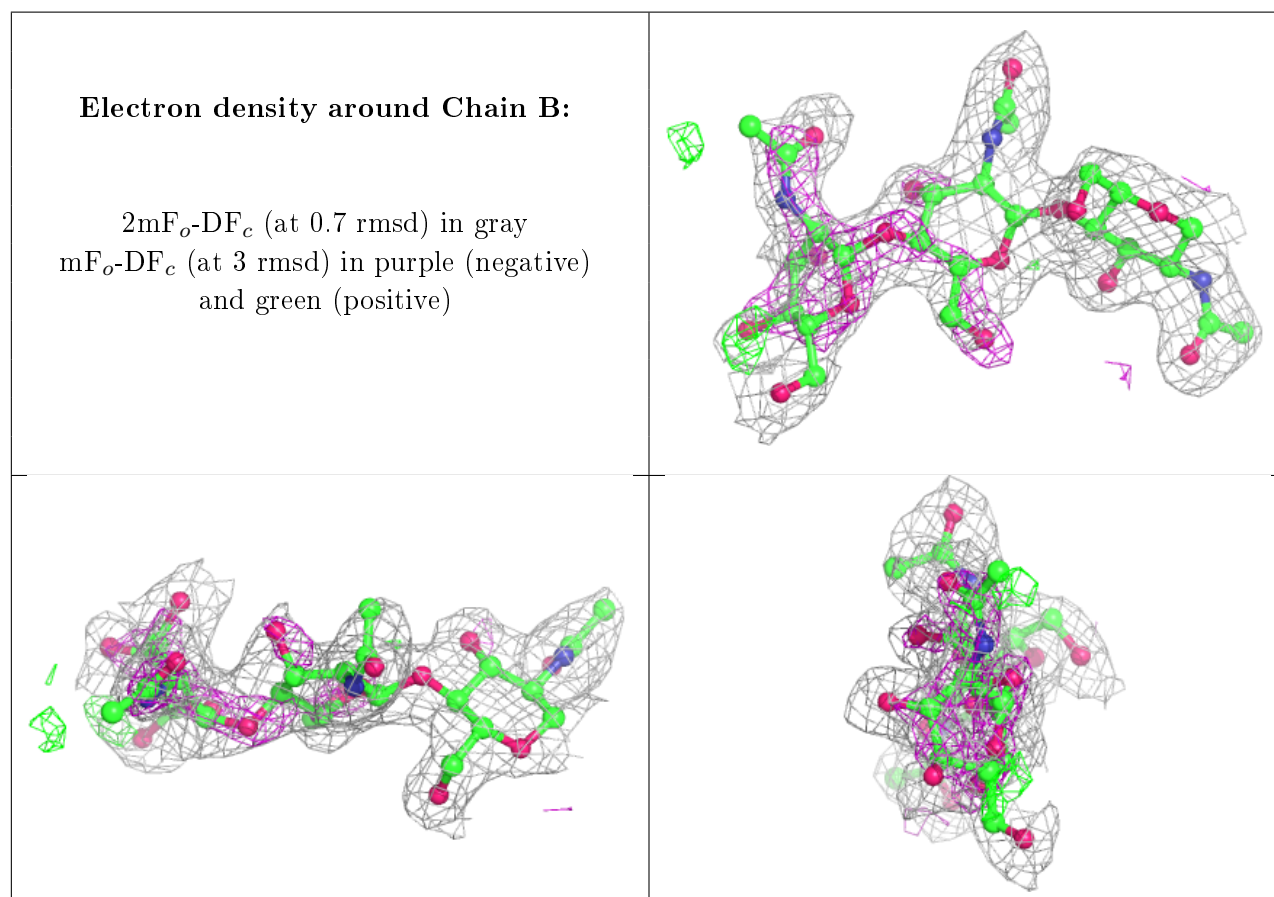
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	C	3	14/15	0.44	0.57	34,36,41,41	0
2	NAG	F	3	14/15	0.49	0.50	33,35,41,42	0
3	NAG	E	2	14/15	0.69	0.44	33,35,40,40	0
2	NAG	F	2	14/15	0.70	0.26	33,35,37,38	0
2	NAG	B	3	14/15	0.73	0.42	34,35,39,40	0
2	NAG	C	2	14/15	0.74	0.41	34,35,39,40	0
3	NAG	G	2	14/15	0.77	0.35	33,35,42,42	0
3	NAG	G	1	14/15	0.80	0.23	32,35,37,38	0
3	NAG	J	2	14/15	0.81	0.26	33,35,37,38	0

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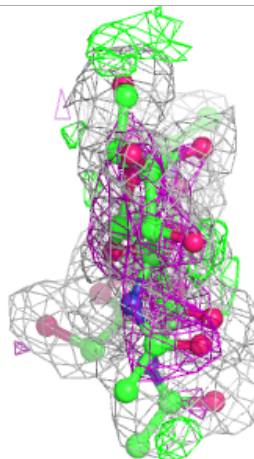
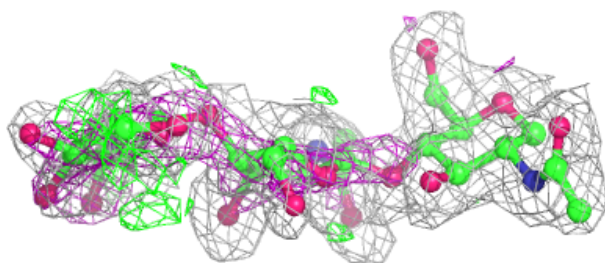
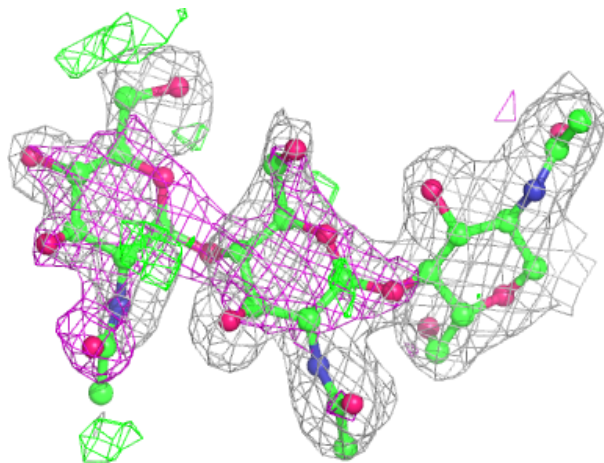
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAG	I	2	14/15	0.83	0.41	33,35,40,40	0
3	NAG	I	1	14/15	0.84	0.24	32,34,38,38	0
3	NAG	E	1	14/15	0.85	0.22	32,35,39,39	0
2	NAG	B	2	14/15	0.85	0.27	33,34,38,39	0
2	NAG	F	1	14/15	0.86	0.22	31,34,36,36	0
3	NAG	H	2	14/15	0.87	0.18	32,33,38,41	0
3	NAG	D	2	14/15	0.91	0.18	31,34,38,42	0
3	NAG	D	1	14/15	0.92	0.10	27,31,33,36	0
3	NAG	H	1	14/15	0.92	0.12	27,31,33,33	0
2	NAG	C	1	14/15	0.92	0.15	31,32,35,37	0
3	NAG	J	1	14/15	0.93	0.09	31,34,37,37	0
2	NAG	B	1	14/15	0.95	0.11	29,32,33,35	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.



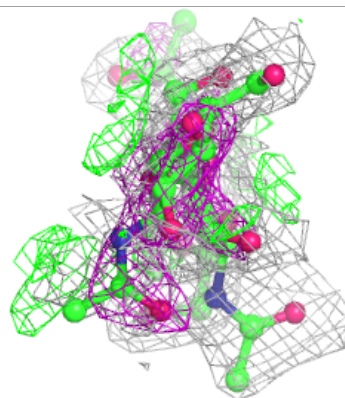
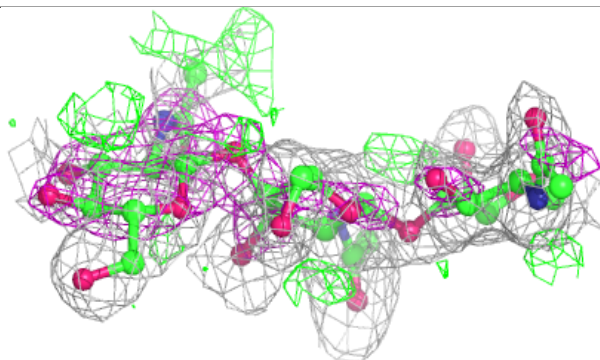
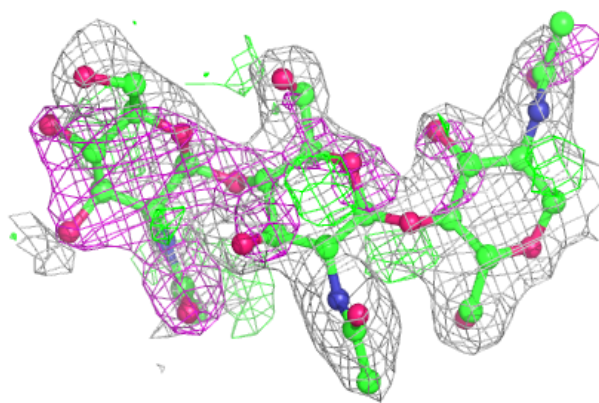
**Electron density around Chain C:**

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



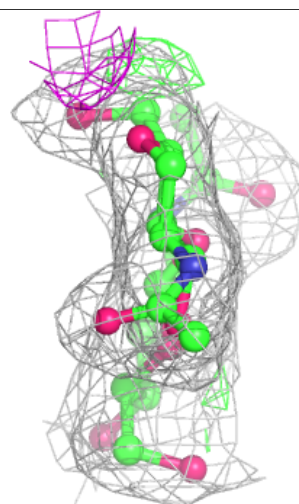
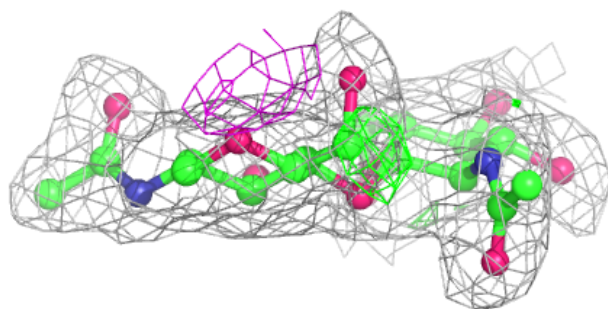
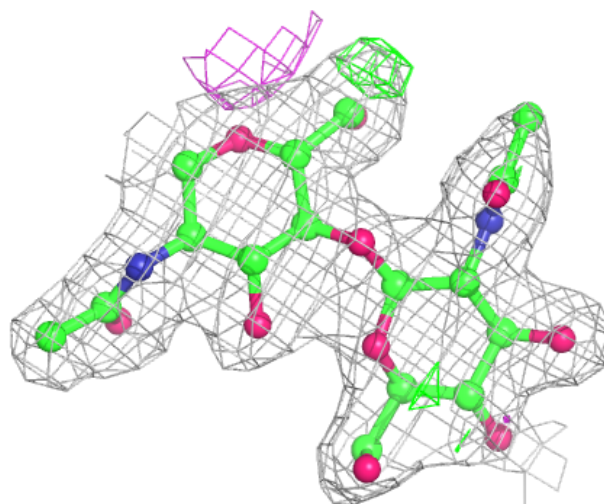
**Electron density around Chain F:**

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



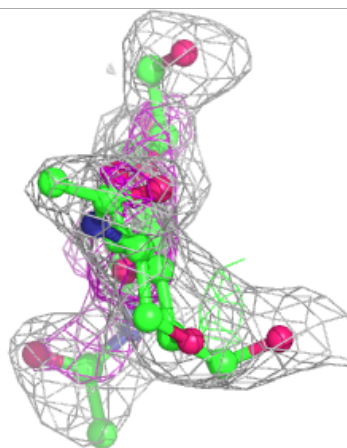
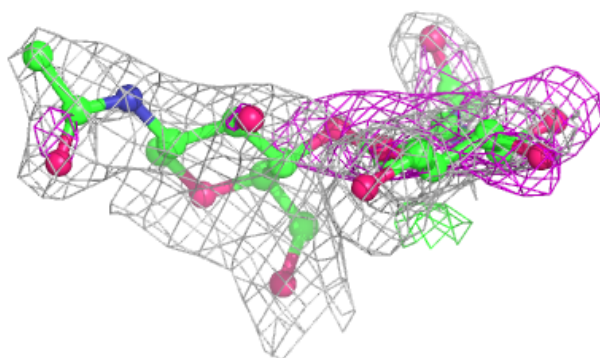
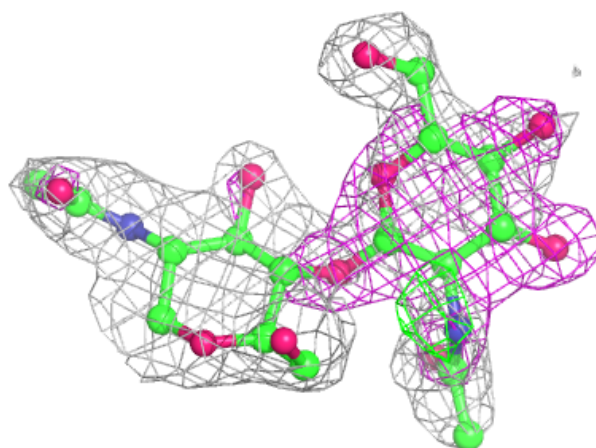
**Electron density around Chain D:**

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



**Electron density around Chain E:**

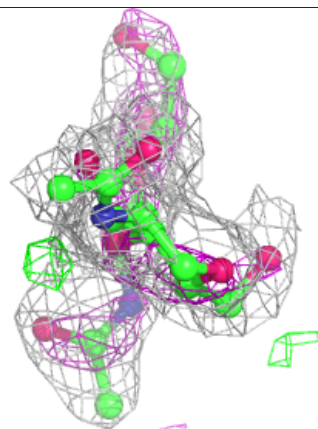
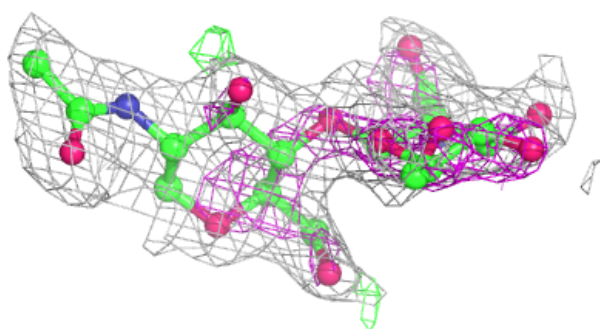
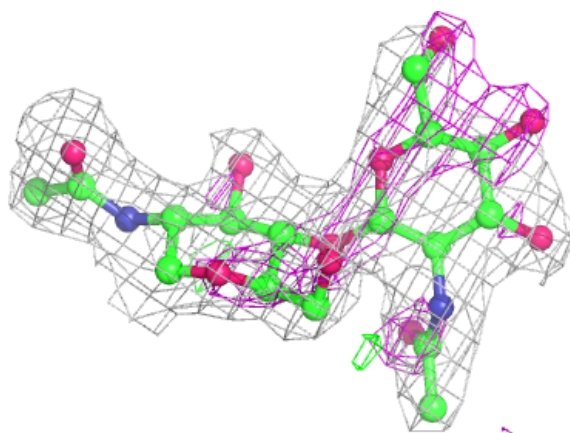
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





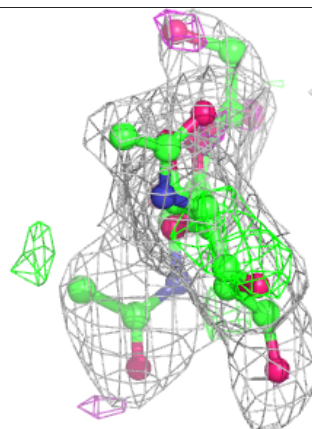
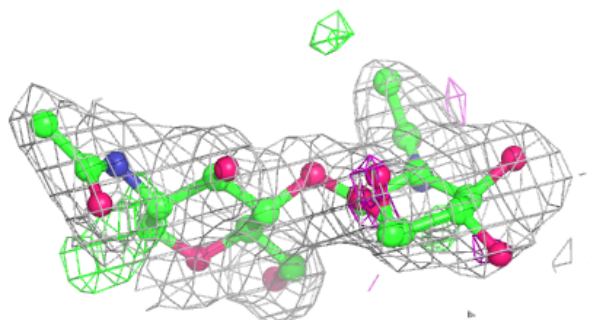
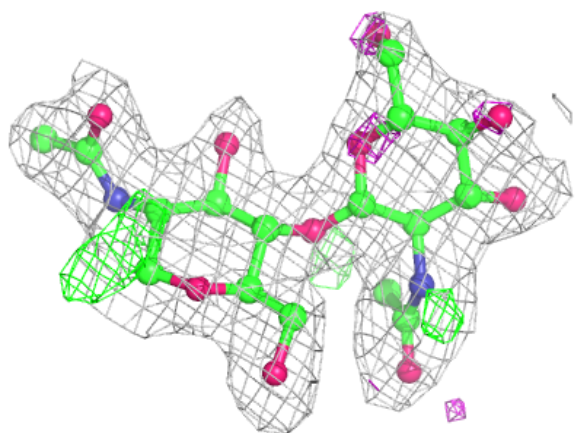
**Electron density around Chain G:**

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



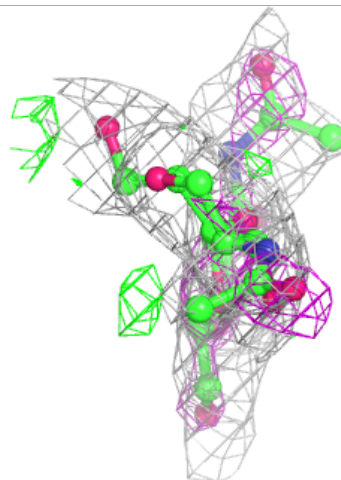
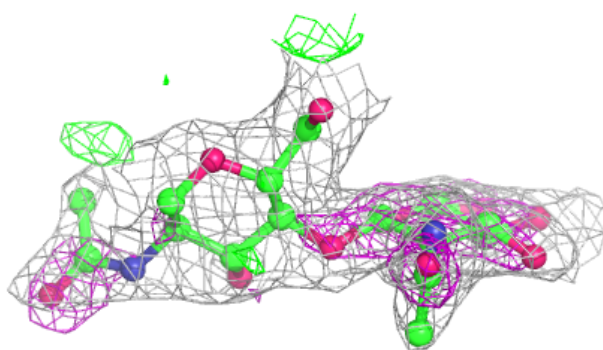
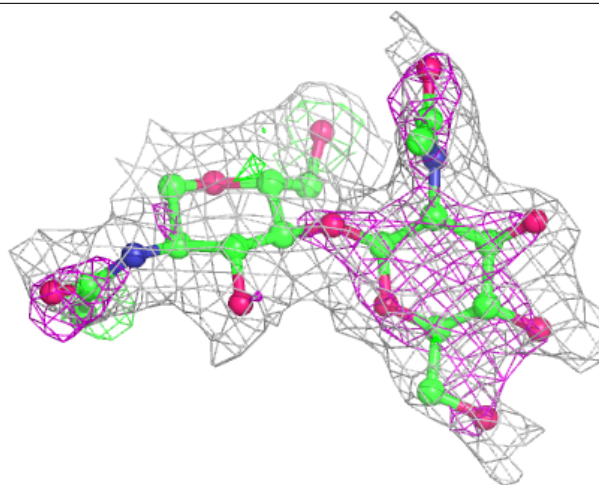
**Electron density around Chain H:**

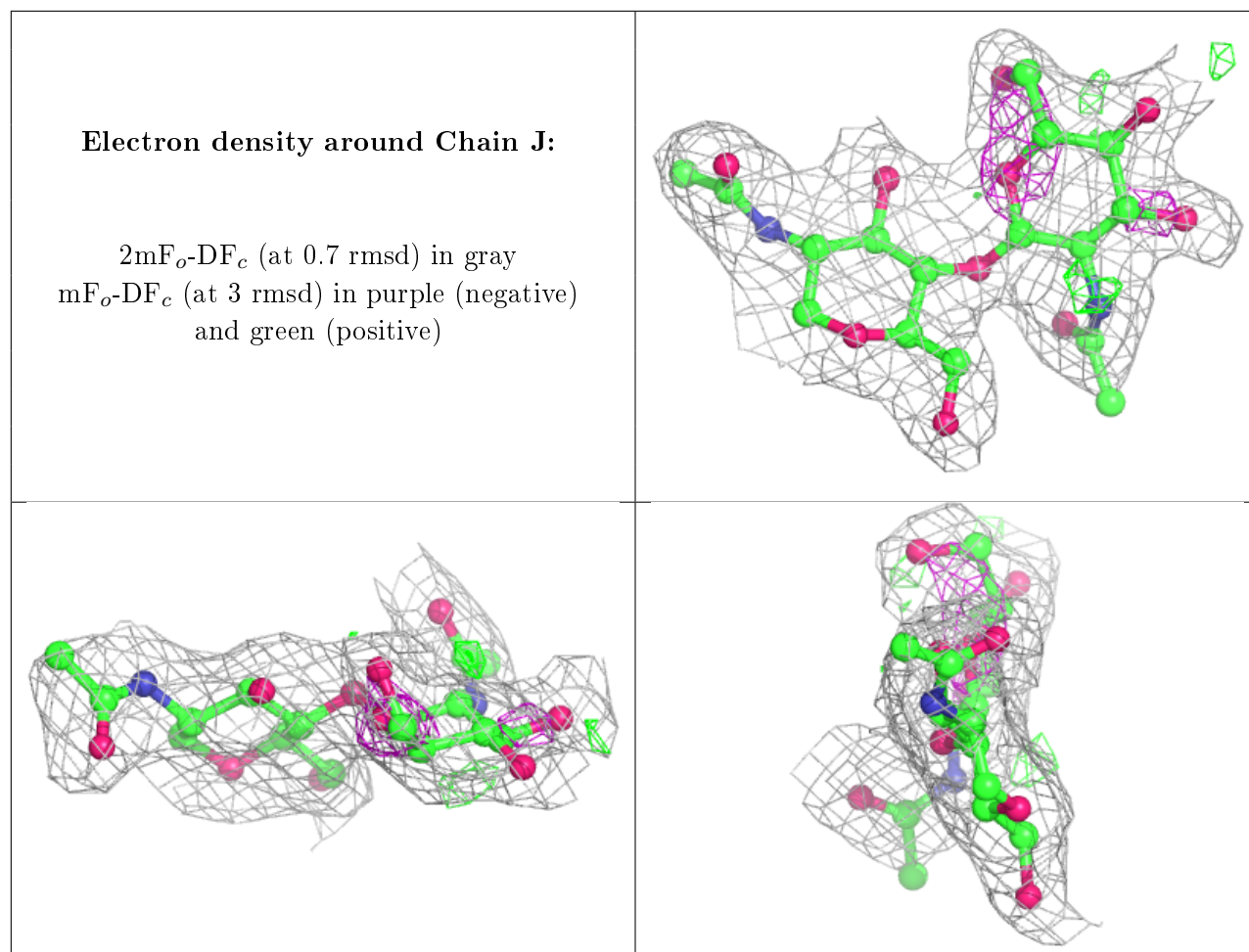
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around Chain I:**

$2mF_o-DF_c$  (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, 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
5	MET	A	1024	9/9	0.69	0.32	30,33,40,40	0
6	SO4	A	1034	5/5	0.76	0.53	37,37,39,40	0
4	NAG	A	1020	14/15	0.77	0.53	33,35,40,42	0
6	SO4	A	1035	5/5	0.80	0.36	37,37,39,40	0
4	NAG	A	1023	14/15	0.81	0.41	32,35,41,42	0
6	SO4	A	1027	5/5	0.81	0.39	39,39,41,41	0
6	SO4	A	1028	5/5	0.83	0.38	35,37,40,40	0
6	SO4	A	1033	5/5	0.84	0.57	35,36,41,42	0
6	SO4	A	1032	5/5	0.84	0.42	35,37,38,39	0
6	SO4	A	1031	5/5	0.87	0.53	36,37,39,40	0
6	SO4	A	1025	5/5	0.90	0.25	32,33,39,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
6	SO4	A	1036	5/5	0.93	0.39	36,38,39,40	0
6	SO4	A	1026	5/5	0.94	0.60	31,38,39,40	0
6	SO4	A	1029	5/5	0.96	0.27	36,38,38,39	0
6	SO4	A	1030	5/5	0.96	0.25	36,37,37,39	0
7	ZN	A	1037	1/1	1.00	0.18	25,25,25,25	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.