



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 23, 2024 – 09:45 AM EDT

PDB ID : 3EIO  
Title : Crystal Structure Analysis of DPPIV Inhibitor  
Authors : Ahn, J.H.; Lee, J.-O.  
Deposited on : 2008-09-17  
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

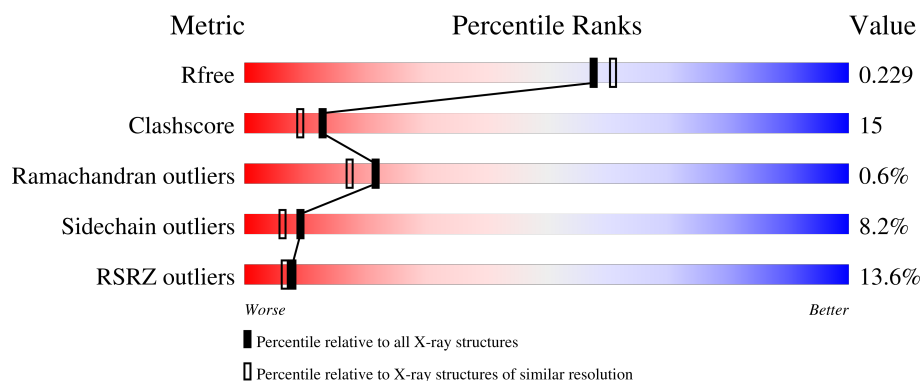
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





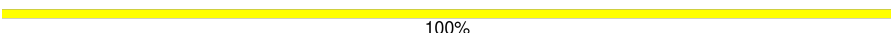
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of 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	728	<div> <div>17%</div> <div>71%</div> <div>26%</div> <div>.</div> </div>
1	B	728	<div> <div>10%</div> <div>74%</div> <div>23%</div> <div>.</div> </div>
2	C	3	<div> <div>67%</div> <div>33%</div> </div>
3	D	2	<div> <div>50%</div> <div>50%</div> </div>
3	E	2	<div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	2	
3	G	2	
3	H	2	

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	C	2	X	-	-	-

## 2 Entry composition [i](#)

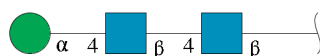
There are 6 unique types of molecules in this entry. The entry contains 12596 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Dipeptidyl peptidase 4 soluble form.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	726	Total	C	N	O	S	0	0	0
			5948	3816	980	1126	26			
1	B	728	Total	C	N	O	S	0	0	0
			5963	3827	982	1128	26			

- Molecule 2 is an oligosaccharide called alpha-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
2	C	3	Total	C	N	O	0	0	0
			39	22	2	15			

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



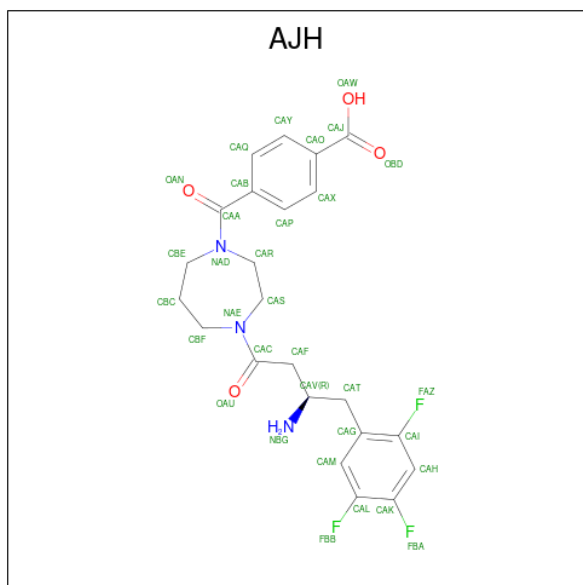
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			

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

- Molecule 4 is 4-({4-[(3R)-3-amino-4-(2,4,5-trifluorophenyl)butanoyl]-1,4-diazepan-1-yl}carbonyl)benzoic acid (three-letter code: AJH) (formula: C<sub>23</sub>H<sub>24</sub>F<sub>3</sub>N<sub>3</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	F	N	O	0	0
			33	23	3	3	4		
4	B	1	Total	C	F	N	O	0	0
			33	23	3	3	4		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



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

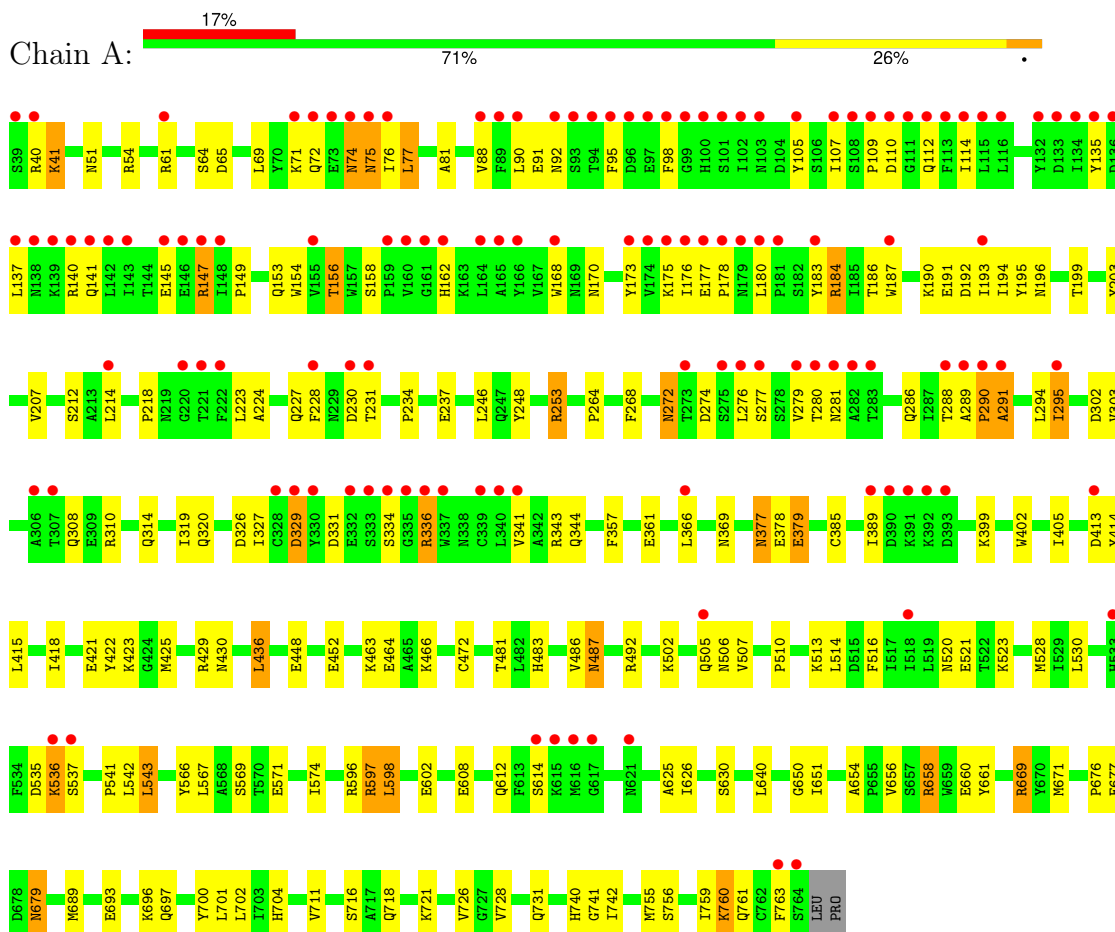
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	147	Total	O	0	0
			147	147		
6	B	153	Total	O	0	0
			153	153		

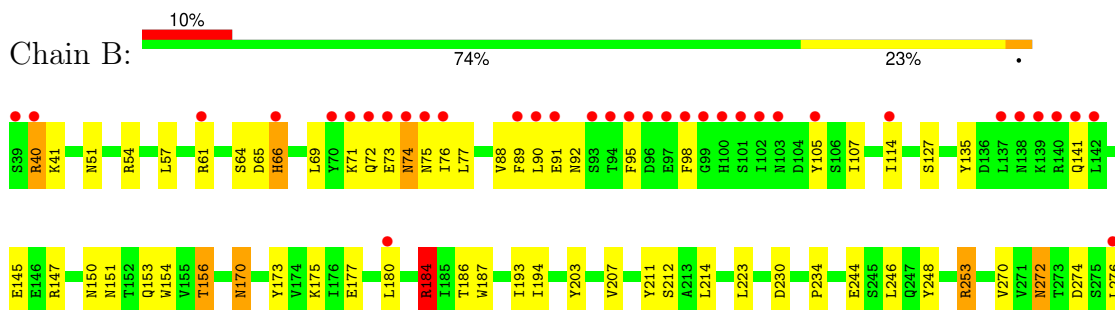
### 3 Residue-property plots

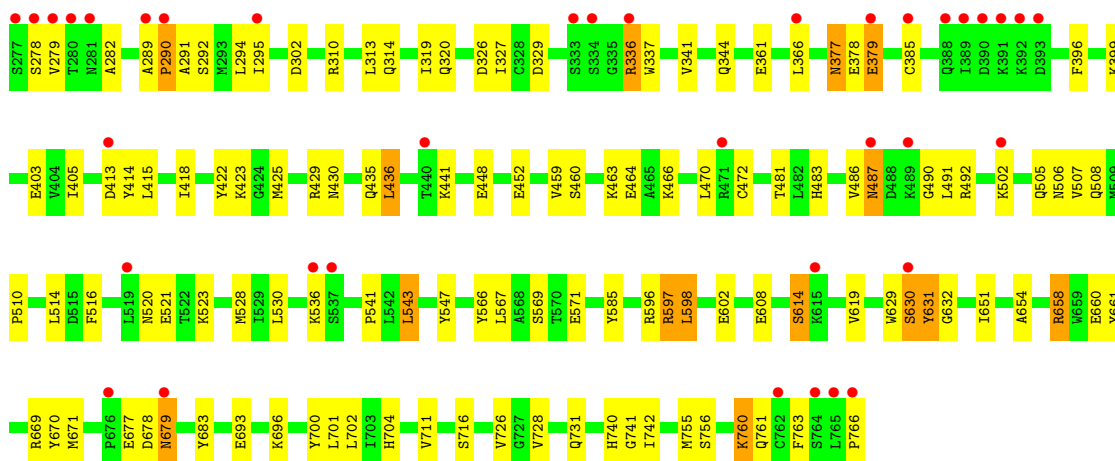
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Dipeptidyl peptidase 4 soluble form



- Molecule 1: Dipeptidyl peptidase 4 soluble form





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

Chain C: 67% 33%



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

Chain D: 50% 50%



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

Chain E: 100%



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

Chain F: 50% 50%



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

Chain G: 100%



MAG1  
MAG2

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

Chain H:

100%

MAG1  
MAG2

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	119.37Å 123.39Å 133.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.26 – 2.00 45.26 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.5 (45.26-2.00) 97.5 (45.26-2.00)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.11 (at 2.00Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.239 , 0.272 0.230 , 0.229	Depositor DCC
$R_{free}$ test set	6543 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.0	Xtriage
Anisotropy	0.357	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 32.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.011 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	12596	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.95% 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: AJH, MAN, NAG

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	0/6119	0.84	4/8321 (0.0%)
1	B	0.70	0/6135	0.83	3/8344 (0.0%)
All	All	0.70	0/12254	0.83	7/16665 (0.0%)

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	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	631	TYR	N-CA-CB	5.67	120.81	110.60
1	A	669	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	A	669	ARG	NE-CZ-NH2	-5.49	117.55	120.30
1	A	656	VAL	N-CA-C	-5.30	96.69	111.00
1	B	319	ILE	N-CA-C	-5.09	97.24	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	700	TYR	Sidechain

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Mol	Chain	Res	Type	Group
1	B	700	TYR	Sidechain

## 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	5948	0	5657	190	0
1	B	5963	0	5677	160	0
2	C	39	0	34	2	0
3	D	28	0	25	0	0
3	E	28	0	25	0	0
3	F	28	0	25	0	0
3	G	28	0	25	3	0
3	H	28	0	25	0	0
4	A	33	0	23	5	0
4	B	33	0	23	4	0
5	A	84	0	78	6	0
5	B	56	0	52	4	0
6	A	147	0	0	4	0
6	B	153	0	0	1	0
All	All	12596	0	11669	354	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 15.

The worst 5 of 354 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:760:LYS:HE2	1:B:766:PRO:C	1.60	1.22
4:B:2:AJH:HAP	4:B:2:AJH:HARA	1.17	1.08
1:A:759:ILE:HG23	1:A:763:PHE:CE1	1.90	1.05
1:B:760:LYS:CE	1:B:766:PRO:C	2.24	1.05
1:A:277:SER:CB	1:A:280:THR:HB	1.86	1.04

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	724/728 (100%)	687 (95%)	33 (5%)	4 (1%)	22	17
1	B	726/728 (100%)	692 (95%)	30 (4%)	4 (1%)	22	17
All	All	1450/1456 (100%)	1379 (95%)	63 (4%)	8 (1%)	22	17

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	40	ARG
1	A	291	ALA
1	B	40	ARG
1	B	630	SER
1	A	192	ASP

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	651/653 (100%)	598 (92%)	53 (8%)	9	6
1	B	653/653 (100%)	599 (92%)	54 (8%)	9	6
All	All	1304/1306 (100%)	1197 (92%)	107 (8%)	9	6

5 of 107 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	66	HIS

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Mol	Chain	Res	Type
1	B	253	ARG
1	B	608	GLU
1	B	75	ASN
1	B	156	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	247	GLN
1	B	533	HIS
1	B	272	ASN
1	B	435	GLN
1	B	586	GLN

### 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 ⓘ

13 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	0.83	1 (7%)	17,19,21	0.57	0
2	NAG	C	2	2	14,14,15	2.87	6 (42%)	17,19,21	2.47	7 (41%)
2	MAN	C	3	2	11,11,12	1.53	4 (36%)	15,15,17	1.37	2 (13%)
3	NAG	D	1	3,1	14,14,15	0.97	1 (7%)	17,19,21	1.12	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	D	2	3	14,14,15	0.62	0	17,19,21	0.88	0
3	NAG	E	1	3,1	14,14,15	1.06	1 (7%)	17,19,21	0.74	0
3	NAG	E	2	3	14,14,15	0.85	0	17,19,21	0.92	1 (5%)
3	NAG	F	1	3,1	14,14,15	0.71	0	17,19,21	0.79	0
3	NAG	F	2	3	14,14,15	0.67	0	17,19,21	1.07	1 (5%)
3	NAG	G	1	3,1	14,14,15	0.90	0	17,19,21	1.72	5 (29%)
3	NAG	G	2	3	14,14,15	0.63	0	17,19,21	1.25	2 (11%)
3	NAG	H	1	3,1	14,14,15	0.95	0	17,19,21	1.24	2 (11%)
3	NAG	H	2	3	14,14,15	0.75	0	17,19,21	0.95	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	1/1/5/7	4/6/23/26	0/1/1/1
2	MAN	C	3	2	-	2/2/19/22	0/1/1/1
3	NAG	D	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	D	2	3	-	4/6/23/26	0/1/1/1
3	NAG	E	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	4/6/23/26	0/1/1/1
3	NAG	F	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	4/6/23/26	0/1/1/1
3	NAG	G	1	3,1	-	4/6/23/26	0/1/1/1
3	NAG	G	2	3	-	5/6/23/26	0/1/1/1
3	NAG	H	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	4/6/23/26	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	NAG	O5-C5	5.87	1.54	1.43
2	C	2	NAG	O5-C1	5.08	1.52	1.43
2	C	2	NAG	O4-C4	4.15	1.53	1.43
2	C	2	NAG	C1-C2	3.83	1.57	1.52
2	C	2	NAG	C3-C2	3.17	1.59	1.52

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	NAG	C1-O5-C5	5.83	120.00	112.19
3	G	1	NAG	C6-C5-C4	4.27	123.49	113.02
2	C	2	NAG	O5-C1-C2	-4.21	104.77	111.29
2	C	3	MAN	C1-O5-C5	3.69	117.13	112.19
2	C	2	NAG	C2-N2-C7	-3.59	118.09	122.90

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	2	NAG	C1

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	2	NAG	C8-C7-N2-C2
2	C	2	NAG	O7-C7-N2-C2
3	D	2	NAG	C8-C7-N2-C2
3	D	2	NAG	O7-C7-N2-C2
3	E	2	NAG	C8-C7-N2-C2

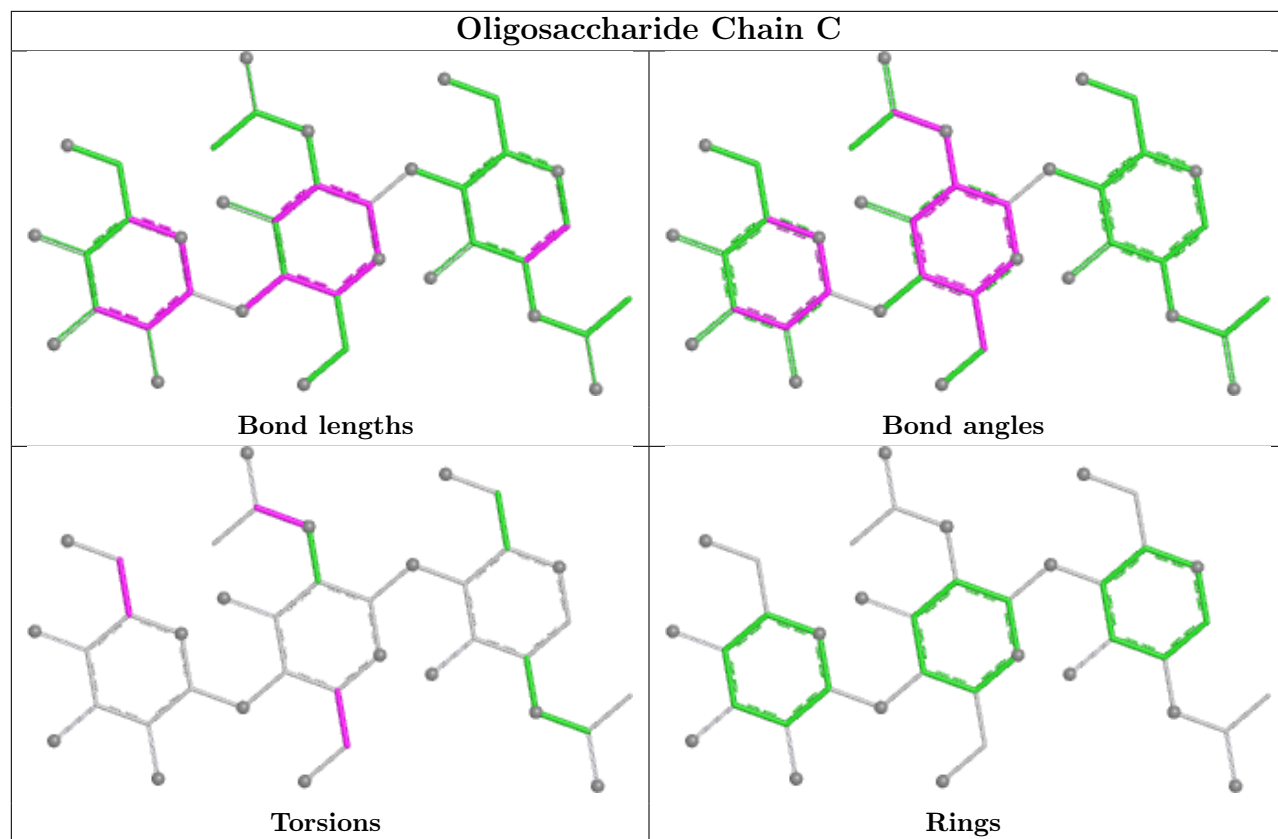
There are no ring outliers.

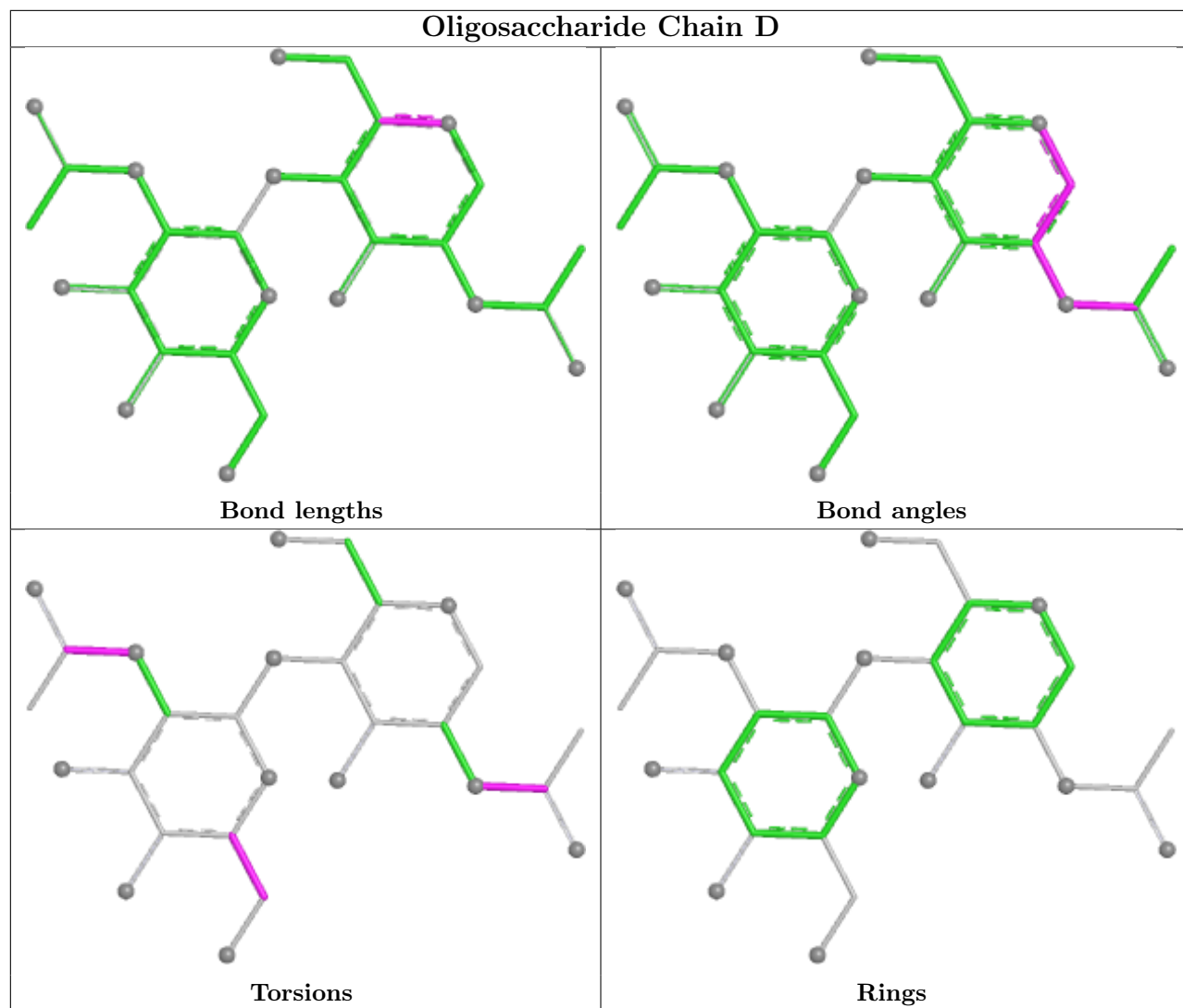
3 monomers are involved in 5 short contacts:

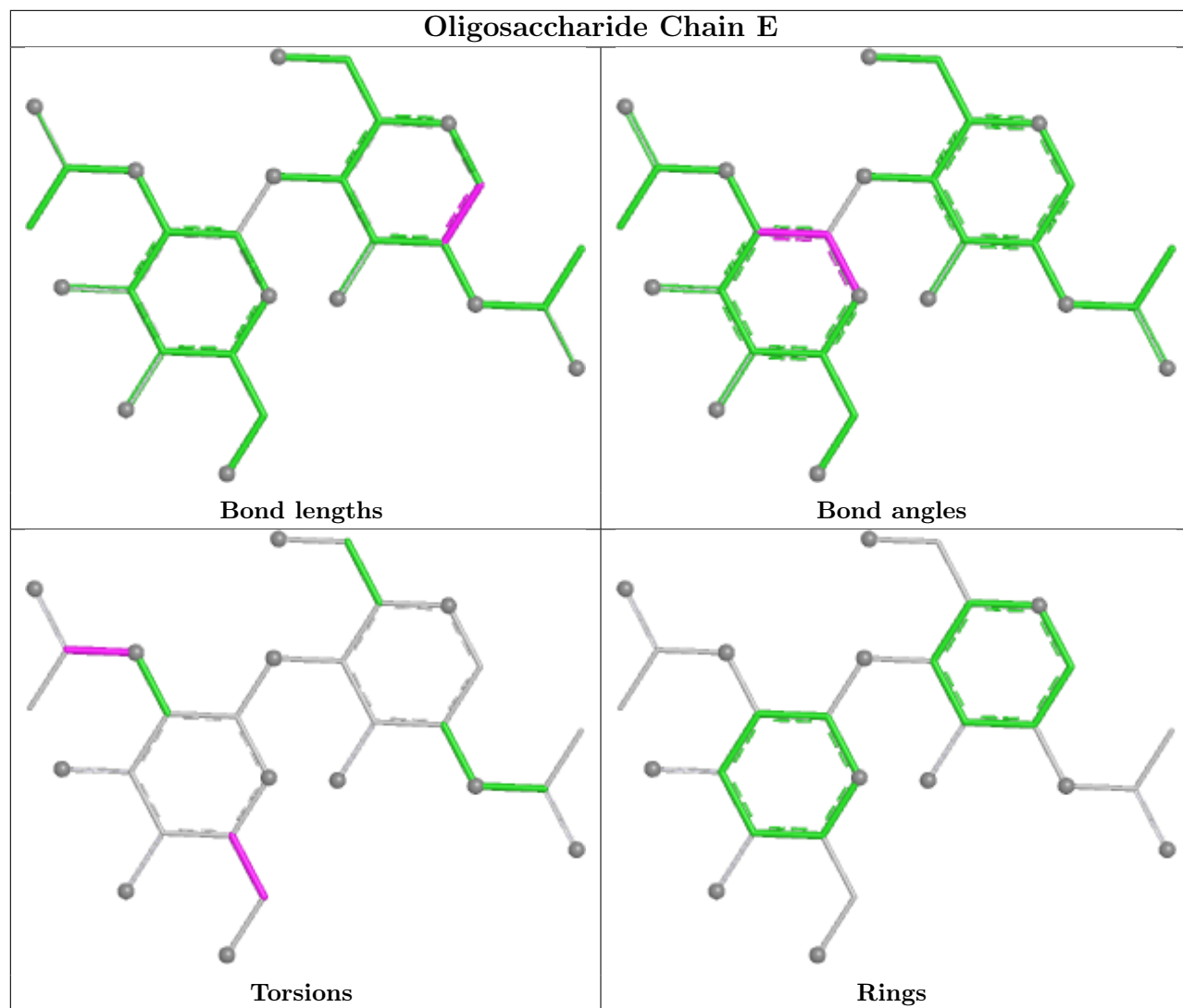
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	NAG	2	0
3	G	1	NAG	3	0
3	G	2	NAG	3	0

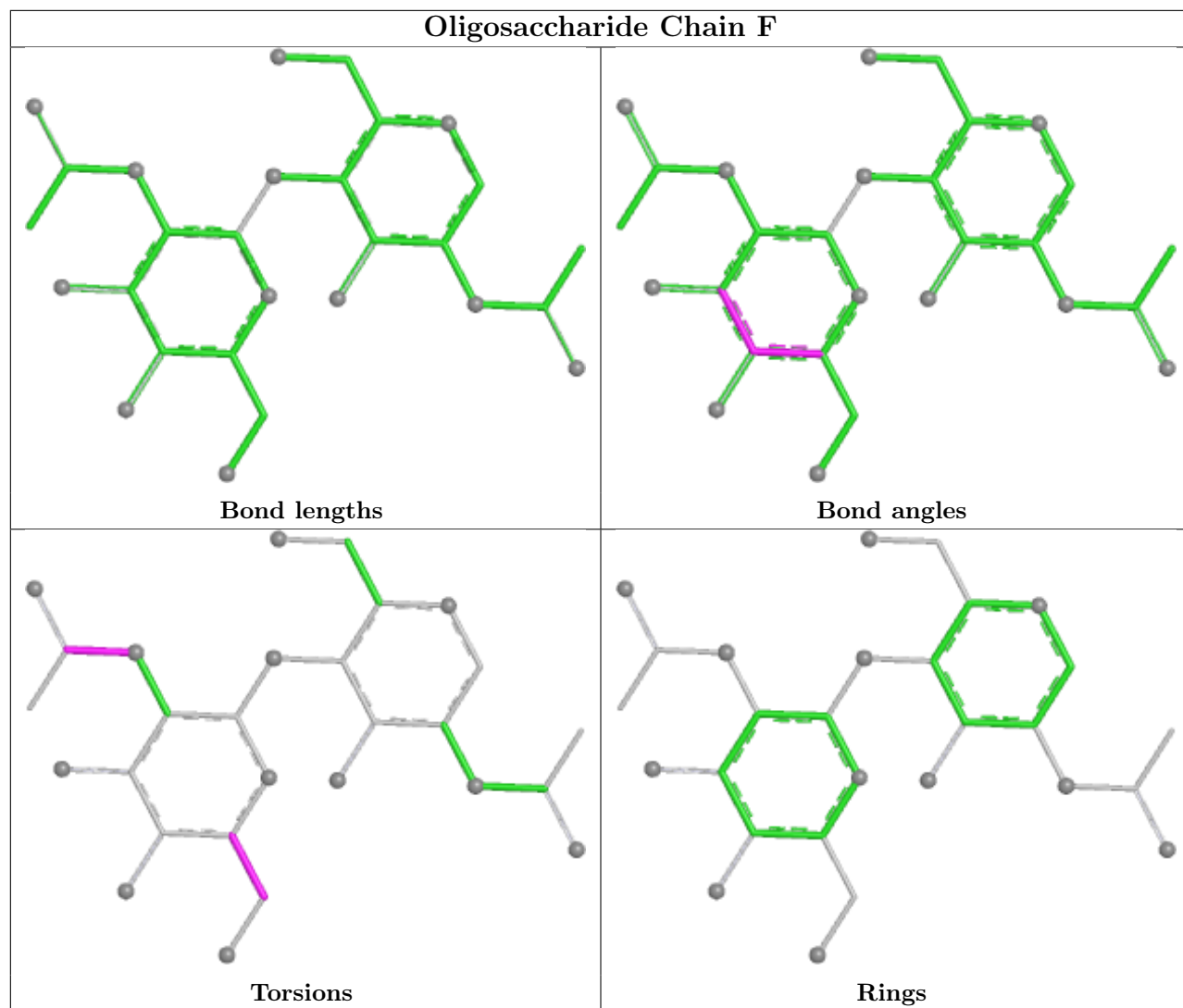
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

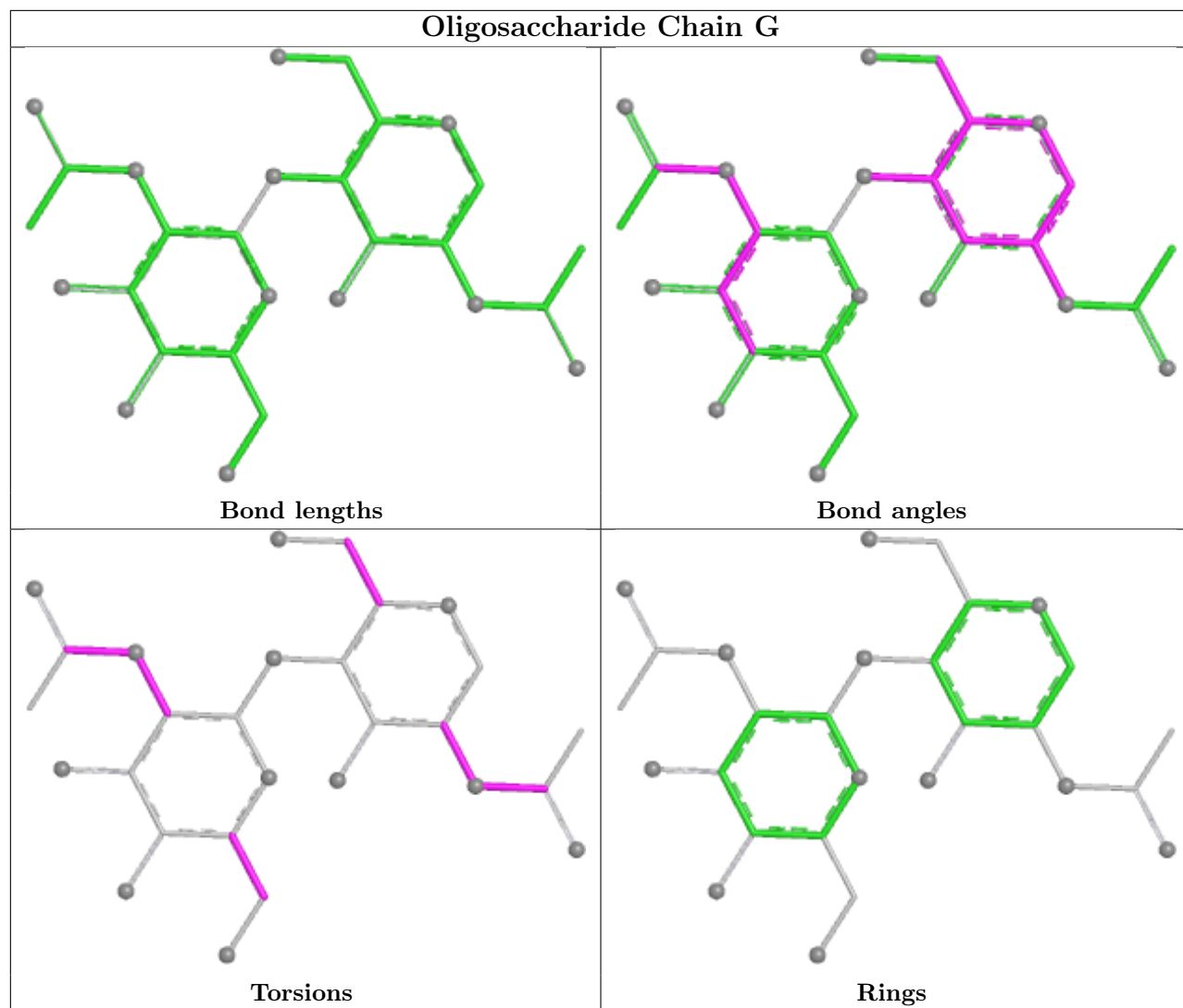


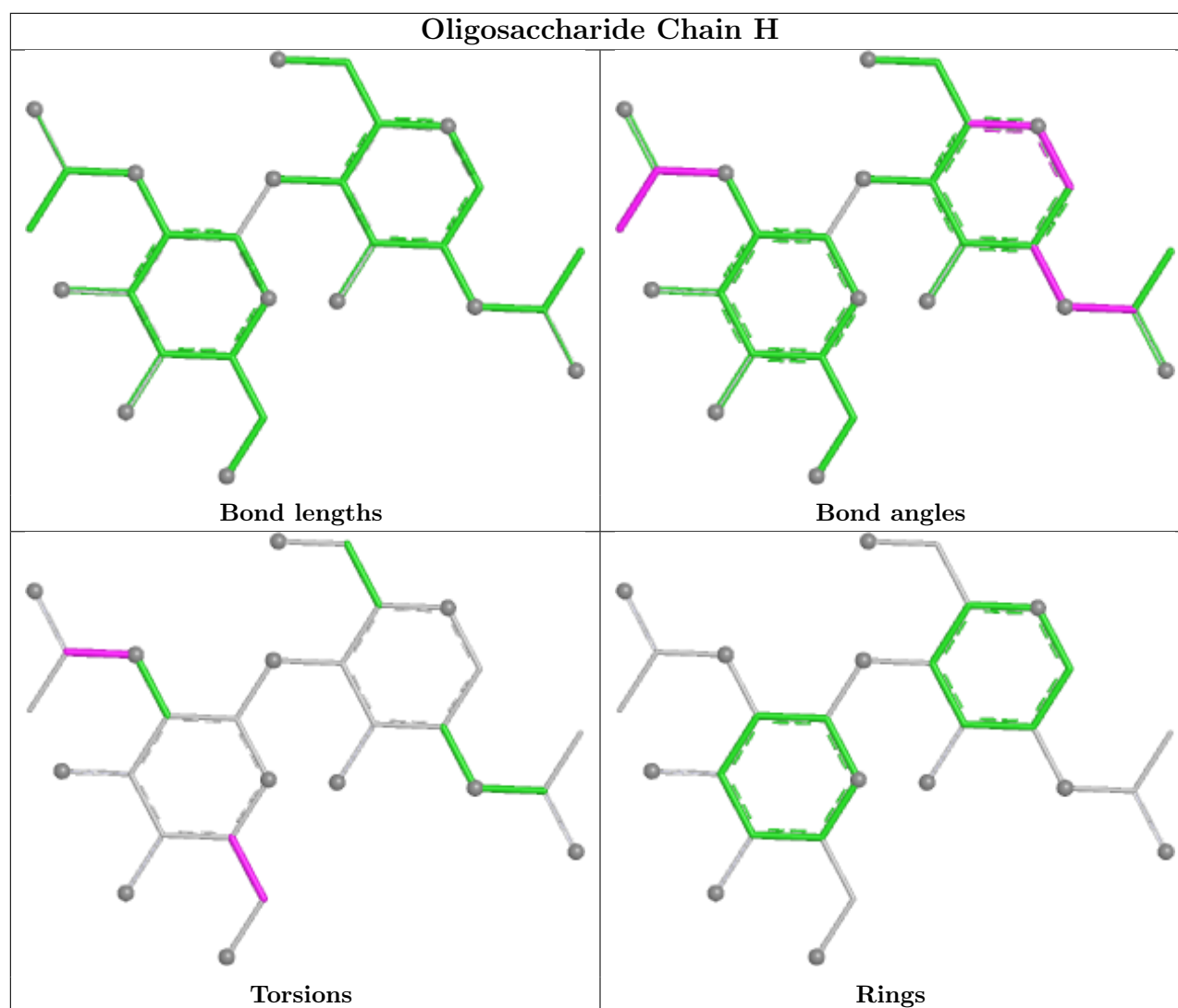












## 5.6 Ligand geometry [i](#)

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
5	NAG	A	871	1	14,14,15	0.63	0	17,19,21	1.31	3 (17%)
5	NAG	A	801	1	14,14,15	1.52	1 (7%)	17,19,21	1.21	4 (23%)
4	AJH	A	1	-	35,35,35	1.76	2 (5%)	43,49,49	1.41	7 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	NAG	A	831	1	14,14,15	0.83	1 (7%)	17,19,21	0.57	0
5	NAG	A	851	1	14,14,15	1.11	2 (14%)	17,19,21	0.70	0
5	NAG	B	911	1	14,14,15	0.70	0	17,19,21	0.64	0
5	NAG	B	921	1	14,14,15	0.74	0	17,19,21	0.62	0
5	NAG	B	971	1	14,14,15	0.63	0	17,19,21	0.86	1 (5%)
4	AJH	B	2	-	35,35,35	1.76	1 (2%)	43,49,49	1.38	5 (11%)
5	NAG	B	941	1	14,14,15	0.91	0	17,19,21	1.72	5 (29%)
5	NAG	A	821	1	14,14,15	1.20	1 (7%)	17,19,21	1.14	2 (11%)
5	NAG	A	811	1	14,14,15	0.99	1 (7%)	17,19,21	0.83	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
5	NAG	A	871	1	-	0/6/23/26	0/1/1/1
5	NAG	A	801	1	-	3/6/23/26	0/1/1/1
4	AJH	A	1	-	-	7/22/35/35	0/2/3/3
5	NAG	A	831	1	-	0/6/23/26	0/1/1/1
5	NAG	A	851	1	-	5/6/23/26	0/1/1/1
5	NAG	B	911	1	-	4/6/23/26	0/1/1/1
5	NAG	B	921	1	-	3/6/23/26	0/1/1/1
5	NAG	B	971	1	-	1/6/23/26	0/1/1/1
4	AJH	B	2	-	-	6/22/35/35	0/2/3/3
5	NAG	B	941	1	-	3/6/23/26	0/1/1/1
5	NAG	A	821	1	-	0/6/23/26	0/1/1/1
5	NAG	A	811	1	-	3/6/23/26	0/1/1/1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1	AJH	CAB-CAA	-9.37	1.34	1.50
4	B	2	AJH	CAB-CAA	-9.36	1.34	1.50
5	A	801	NAG	C1-C2	5.03	1.59	1.52
5	A	851	NAG	C1-C2	3.05	1.56	1.52
5	A	811	NAG	O5-C5	2.71	1.48	1.43

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	2	AJH	CAB-CAA-NAD	4.69	124.52	118.66
5	B	941	NAG	C6-C5-C4	4.25	123.46	113.02
4	A	1	AJH	CAB-CAA-NAD	4.19	123.89	118.66
5	B	941	NAG	C1-O5-C5	-3.12	108.00	112.19
4	A	1	AJH	CAS-CAR-NAD	-3.11	107.61	113.22

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	921	NAG	C1-C2-N2-C7
5	A	811	NAG	C4-C5-C6-O6
4	A	1	AJH	OAW-CAJ-CAO-CAX
4	A	1	AJH	OAW-CAJ-CAO-CAY
4	A	1	AJH	OBD-CAJ-CAO-CAX

There are no ring outliers.

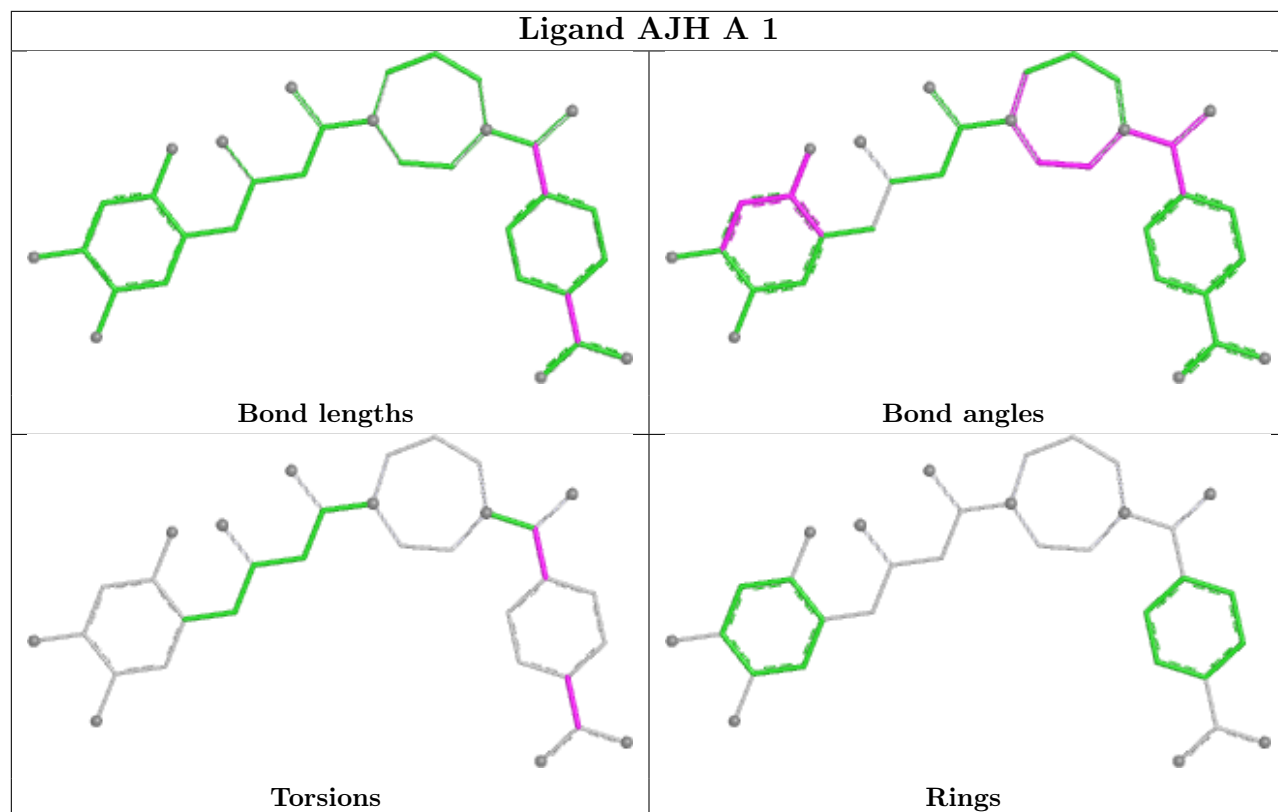
5 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1	AJH	5	0
5	B	911	NAG	4	0
4	B	2	AJH	4	0
5	A	821	NAG	2	0
5	A	811	NAG	4	0

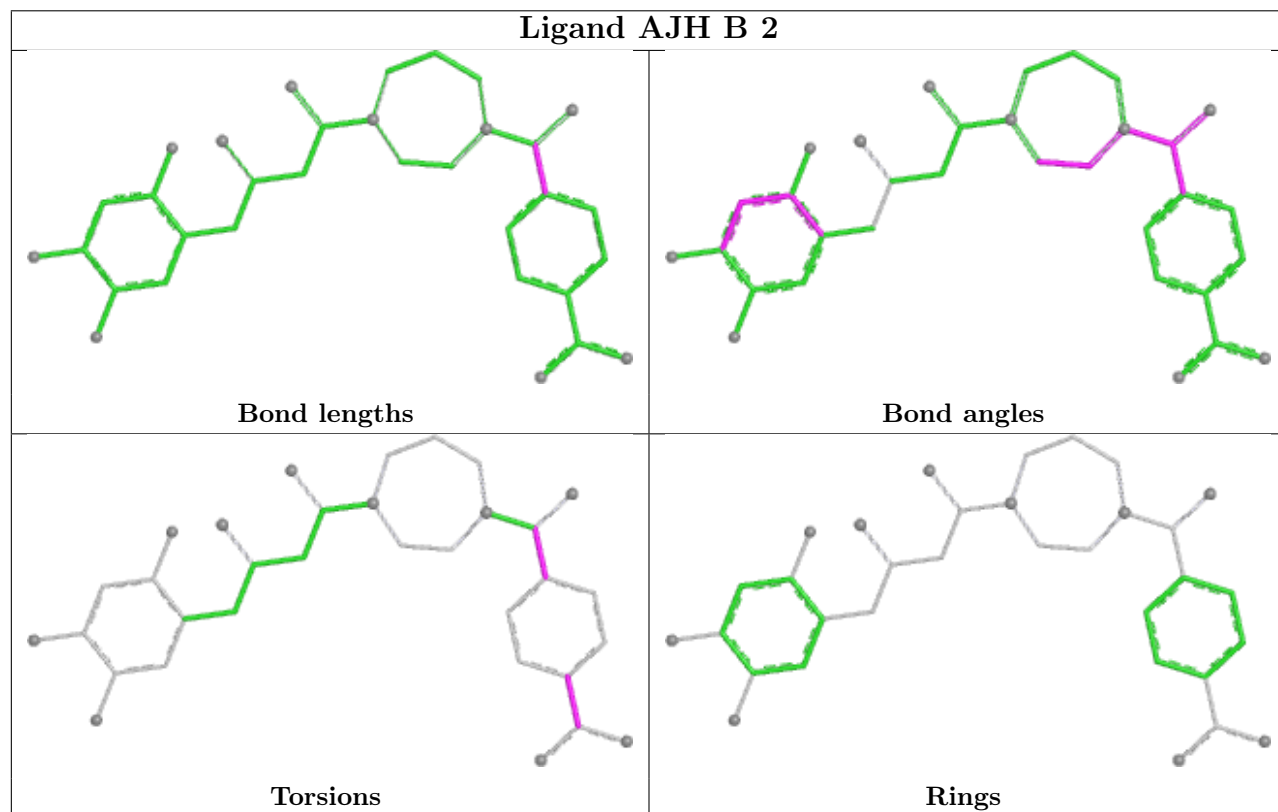
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



## Ligand AJH A 1



## Ligand AJH B 2



## 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 [i](#)

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	726/728 (99%)	0.60	126 (17%) 5 4	13, 28, 67, 96	0
1	B	728/728 (100%)	0.34	72 (9%) 14 13	13, 27, 57, 94	0
All	All	1454/1456 (99%)	0.47	198 (13%) 8 7	13, 28, 64, 96	0

The worst 5 of 198 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	765	LEU	10.0
1	B	766	PRO	8.7
1	A	289	ALA	8.3
1	A	763	PHE	6.9
1	B	487	ASN	6.7

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

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

### 6.3 Carbohydrates [i](#)

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

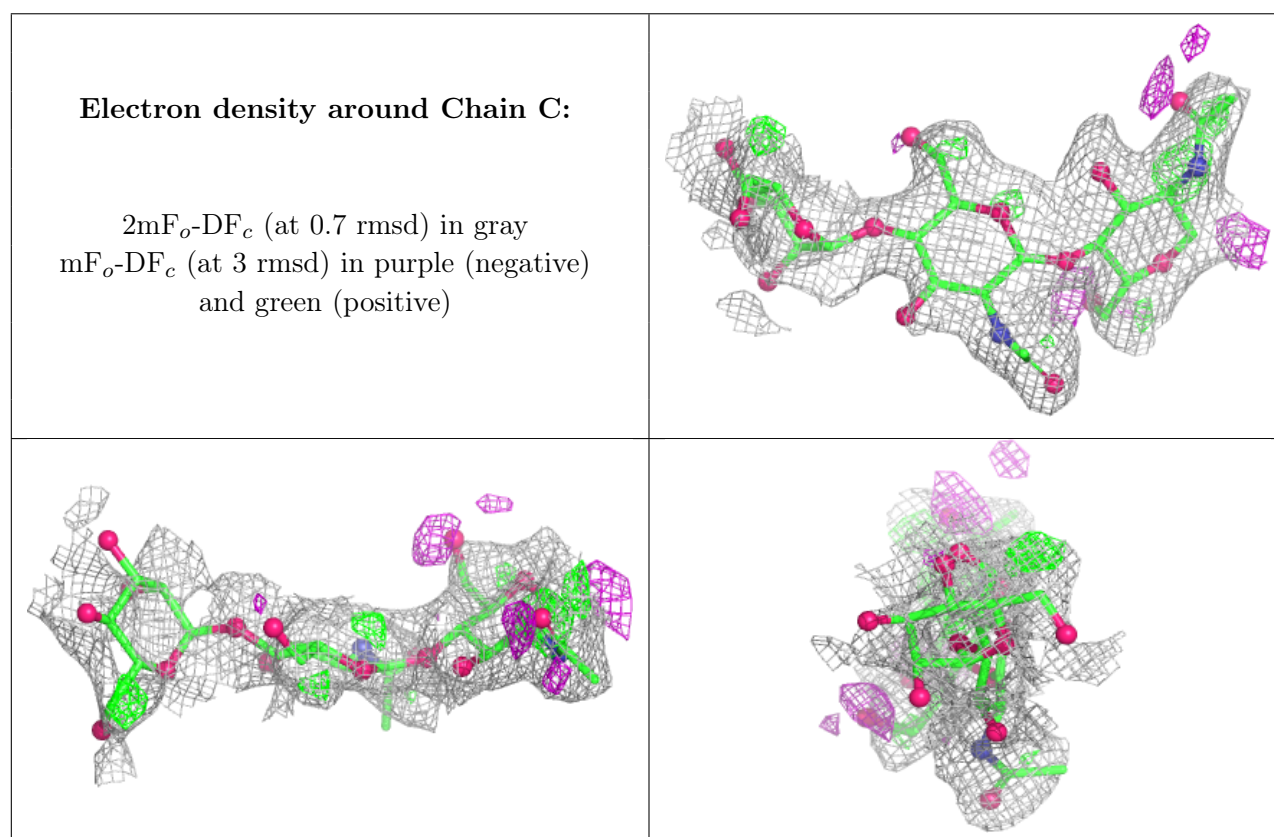
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	MAN	C	3	11/12	0.36	0.20	78,80,82,85	0
3	NAG	D	2	14/15	0.50	0.21	75,79,81,84	0
3	NAG	H	2	14/15	0.52	0.17	68,74,76,77	0
3	NAG	E	2	14/15	0.59	0.18	80,84,86,88	0
3	NAG	G	2	14/15	0.63	0.32	67,72,76,79	0

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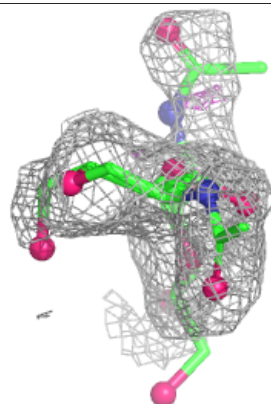
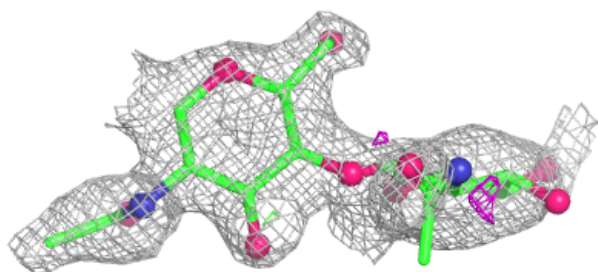
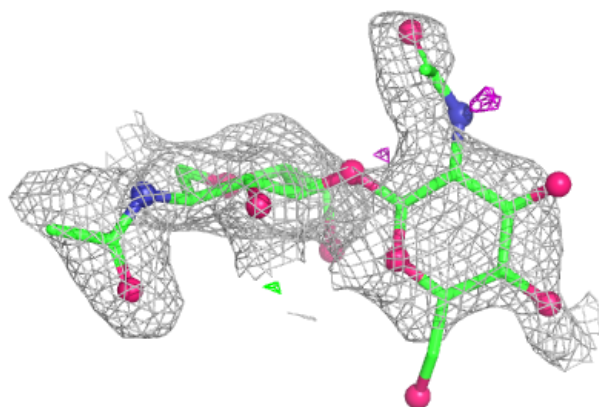
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	C	2	14/15	0.63	0.21	65,72,74,76	0
3	NAG	F	2	14/15	0.64	0.18	66,70,71,73	0
3	NAG	E	1	14/15	0.68	0.17	56,61,73,75	0
3	NAG	G	1	14/15	0.68	0.23	48,50,57,60	0
2	NAG	C	1	14/15	0.69	0.25	56,63,66,68	0
3	NAG	H	1	14/15	0.71	0.17	47,51,58,61	0
3	NAG	D	1	14/15	0.75	0.15	52,56,63,71	0
3	NAG	F	1	14/15	0.82	0.12	42,51,57,60	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.



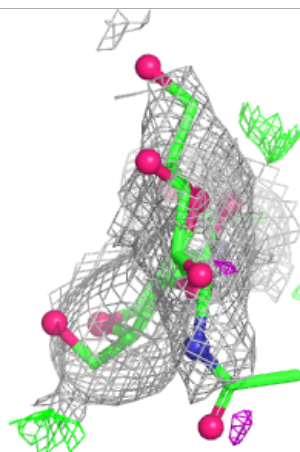
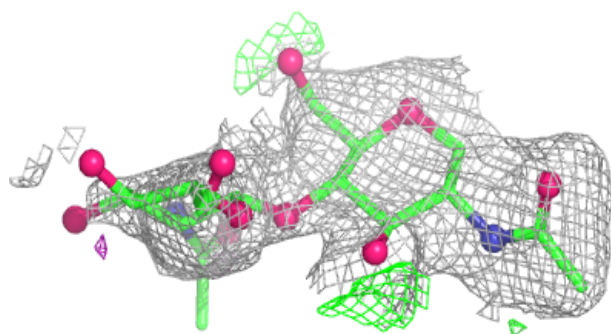
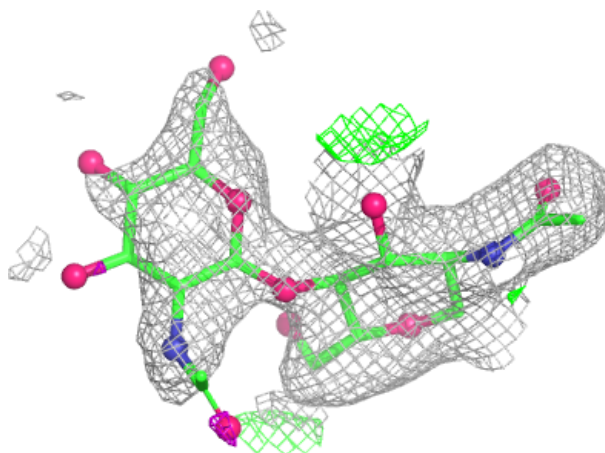
**Electron density around Chain D:**

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



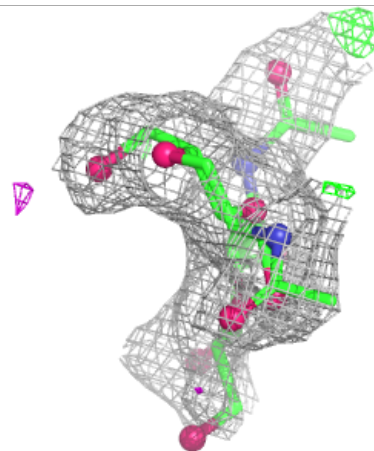
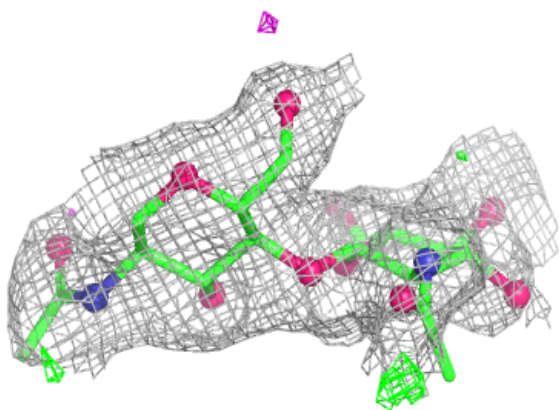
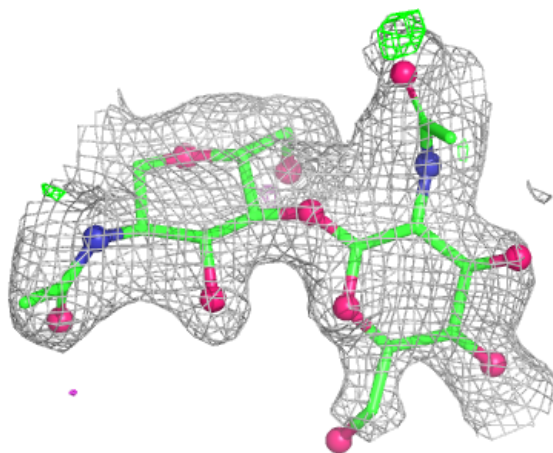
**Electron density around Chain E:**

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



**Electron density around Chain F:**

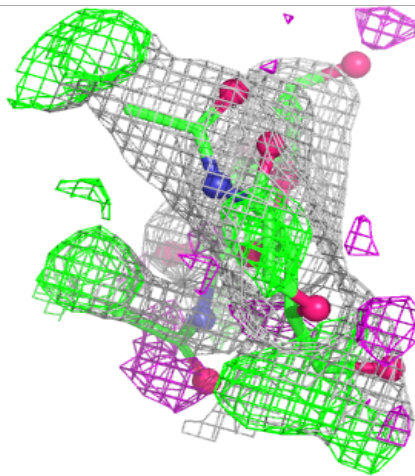
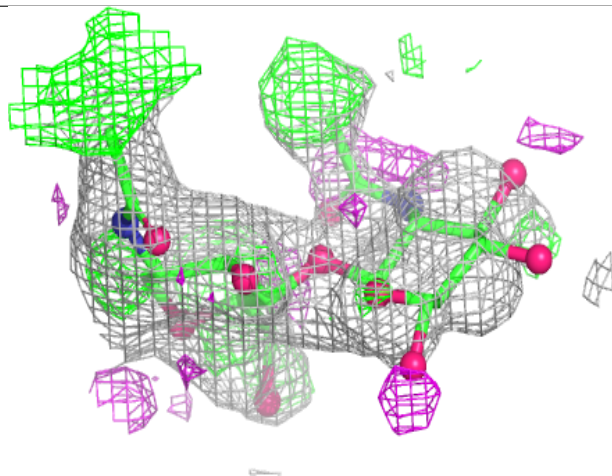
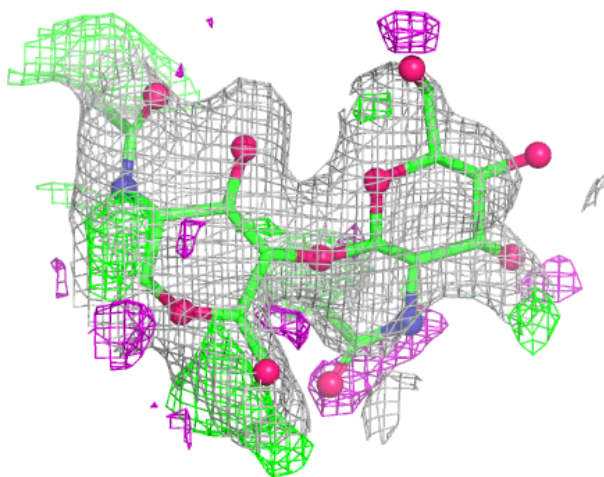
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



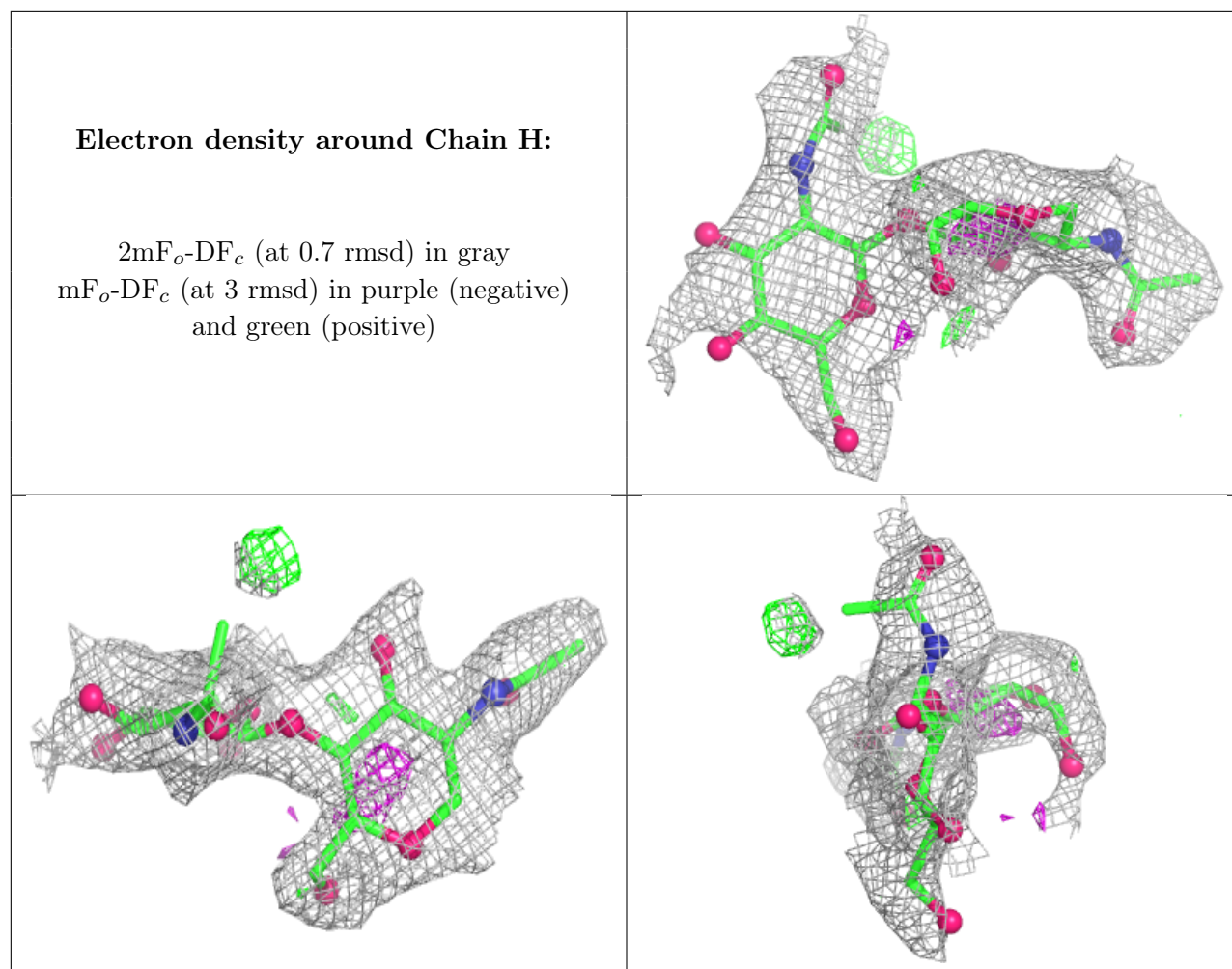


**Electron density around Chain G:**

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







## 6.4 Ligands [i](#)

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

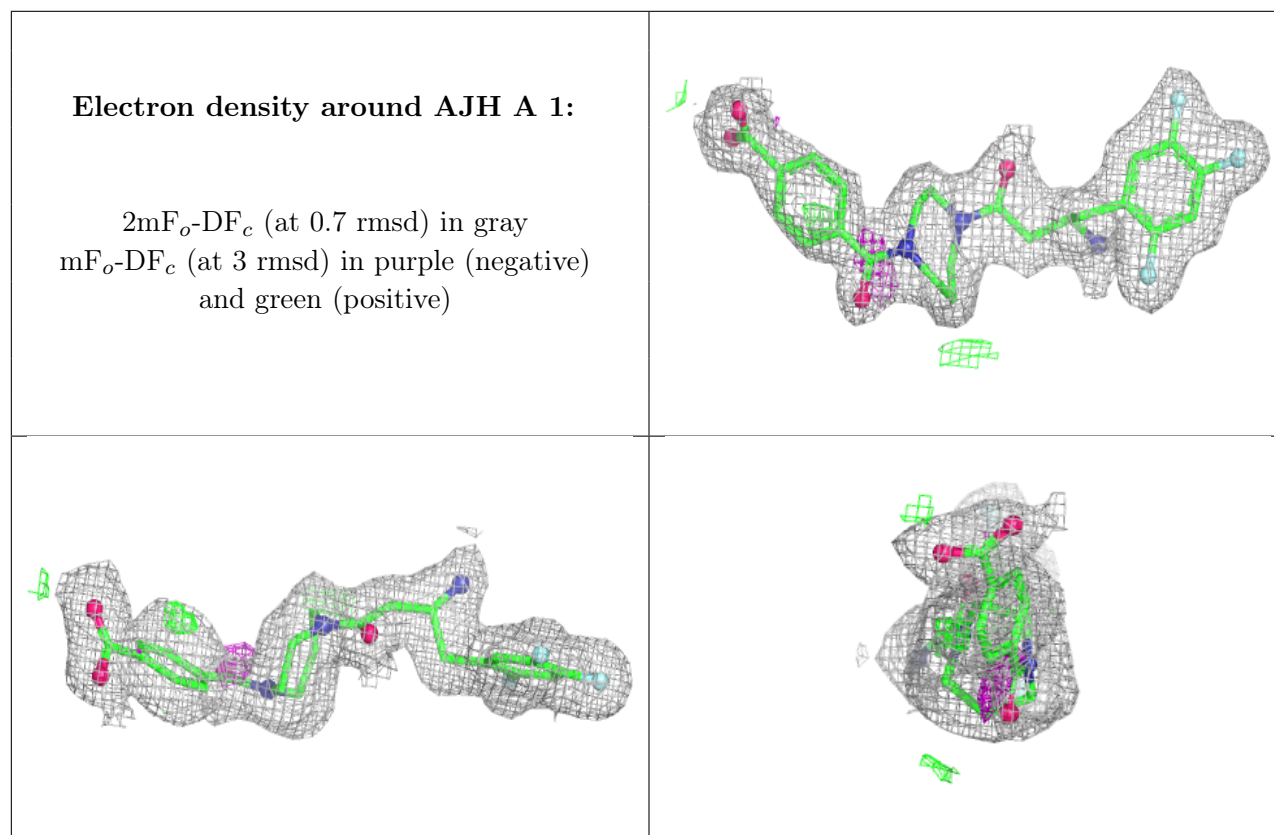
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	NAG	A	811	14/15	0.33	0.22	81,85,87,87	0
5	NAG	A	821	14/15	0.44	0.19	15,20,30,31	0
5	NAG	A	801	14/15	0.48	0.23	55,62,64,67	0
5	NAG	B	911	14/15	0.51	0.19	74,78,79,80	0
5	NAG	B	921	14/15	0.58	0.18	61,67,70,73	0
5	NAG	B	971	14/15	0.59	0.18	63,70,73,77	0
5	NAG	A	851	14/15	0.62	0.20	64,66,69,70	0
5	NAG	B	941	14/15	0.66	0.21	48,50,57,60	0
5	NAG	A	871	14/15	0.66	0.19	69,71,73,74	0
5	NAG	A	831	14/15	0.74	0.15	56,63,66,68	0

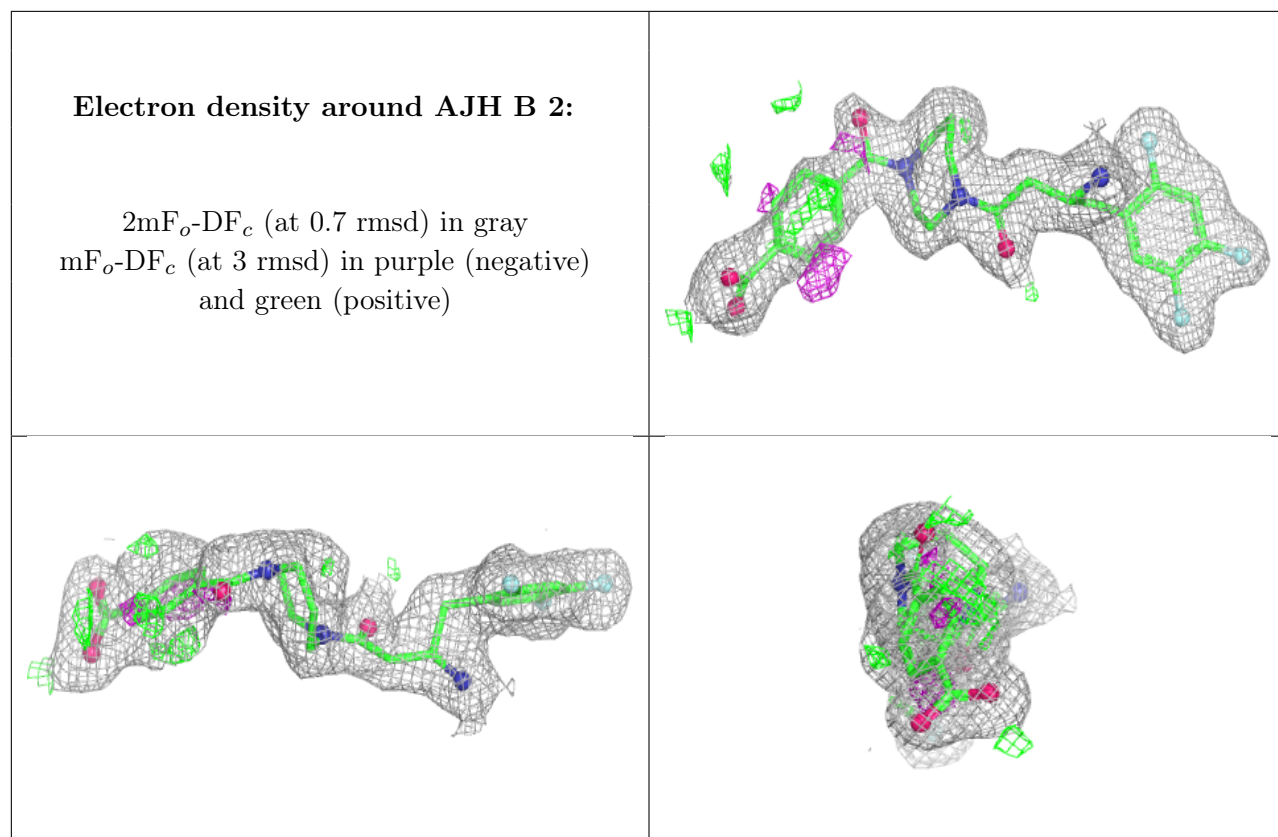
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	AJH	A	1	33/33	0.92	0.11	17,26,49,50	0
4	AJH	B	2	33/33	0.92	0.11	14,23,44,48	0

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.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.