



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:58 AM UTC

PDB ID : 3CCC / pdb\_00003ccc  
Title : Crystal Structure of Human DPP4 in complex with a benzimidazole derivative  
Authors : Wallace, M.B.; Skene, R.J.  
Deposited on : 2008-02-25  
Resolution : 2.71 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 : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (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

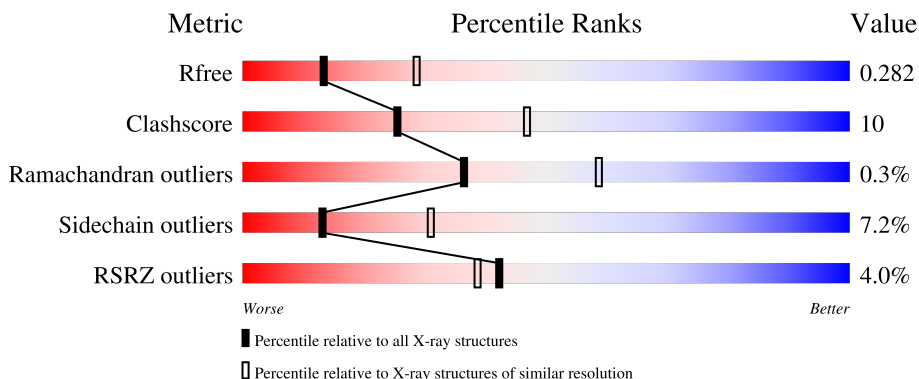
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.71 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.



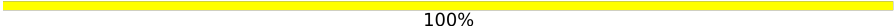

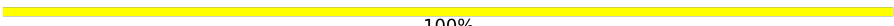
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	4348 (2.74-2.70)
Clashscore	190562	4665 (2.74-2.70)
Ramachandran outliers	187476	4584 (2.74-2.70)
Sidechain outliers	187428	4585 (2.74-2.70)
RSRZ outliers	180081	4348 (2.74-2.70)

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	740	
1	B	740	
1	C	740	
1	D	740	
2	E	2	

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Mol	Chain	Length	Quality of chain
2	F	2	 100%
2	G	2	 50% 50%
2	H	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
3	NAG	C	804	X	-	-	-

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 24357 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	724	5929	3809	974	1120	26	0	0	0
1	B	724	5929	3809	974	1120	26	0	0	0
1	C	724	5929	3809	974	1120	26	0	0	0
1	D	724	5929	3809	974	1120	26	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	ALA	-	expression tag	UNP P27487
A	28	ASP	-	expression tag	UNP P27487
A	29	PRO	-	expression tag	UNP P27487
A	30	GLY	-	expression tag	UNP P27487
A	31	GLY	-	expression tag	UNP P27487
A	32	SER	-	expression tag	UNP P27487
A	33	HIS	-	expression tag	UNP P27487
A	34	HIS	-	expression tag	UNP P27487
A	35	HIS	-	expression tag	UNP P27487
A	36	HIS	-	expression tag	UNP P27487
A	37	HIS	-	expression tag	UNP P27487
A	38	HIS	-	expression tag	UNP P27487
B	27	ALA	-	expression tag	UNP P27487
B	28	ASP	-	expression tag	UNP P27487
B	29	PRO	-	expression tag	UNP P27487
B	30	GLY	-	expression tag	UNP P27487
B	31	GLY	-	expression tag	UNP P27487
B	32	SER	-	expression tag	UNP P27487
B	33	HIS	-	expression tag	UNP P27487
B	34	HIS	-	expression tag	UNP P27487
B	35	HIS	-	expression tag	UNP P27487

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Chain	Residue	Modelled	Actual	Comment	Reference
B	36	HIS	-	expression tag	UNP P27487
B	37	HIS	-	expression tag	UNP P27487
B	38	HIS	-	expression tag	UNP P27487
C	27	ALA	-	expression tag	UNP P27487
C	28	ASP	-	expression tag	UNP P27487
C	29	PRO	-	expression tag	UNP P27487
C	30	GLY	-	expression tag	UNP P27487
C	31	GLY	-	expression tag	UNP P27487
C	32	SER	-	expression tag	UNP P27487
C	33	HIS	-	expression tag	UNP P27487
C	34	HIS	-	expression tag	UNP P27487
C	35	HIS	-	expression tag	UNP P27487
C	36	HIS	-	expression tag	UNP P27487
C	37	HIS	-	expression tag	UNP P27487
C	38	HIS	-	expression tag	UNP P27487
D	27	ALA	-	expression tag	UNP P27487
D	28	ASP	-	expression tag	UNP P27487
D	29	PRO	-	expression tag	UNP P27487
D	30	GLY	-	expression tag	UNP P27487
D	31	GLY	-	expression tag	UNP P27487
D	32	SER	-	expression tag	UNP P27487
D	33	HIS	-	expression tag	UNP P27487
D	34	HIS	-	expression tag	UNP P27487
D	35	HIS	-	expression tag	UNP P27487
D	36	HIS	-	expression tag	UNP P27487
D	37	HIS	-	expression tag	UNP P27487
D	38	HIS	-	expression tag	UNP P27487

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



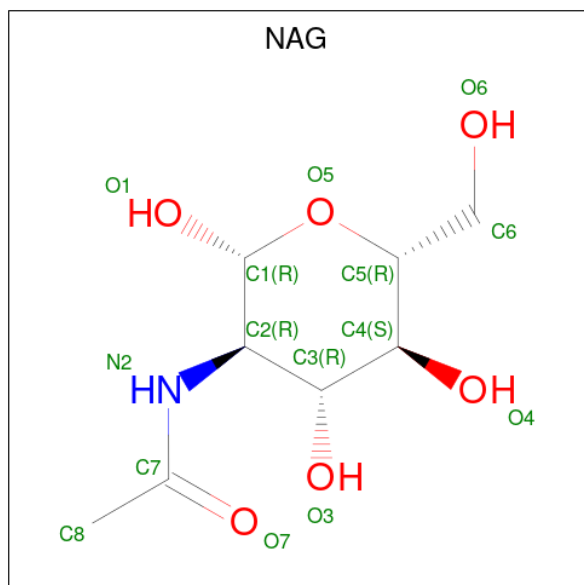
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	G	2	Total	C	N	O	0	0	0
			28	16	2	10			

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

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula:  $C_8H_{15}NO_6$ ).



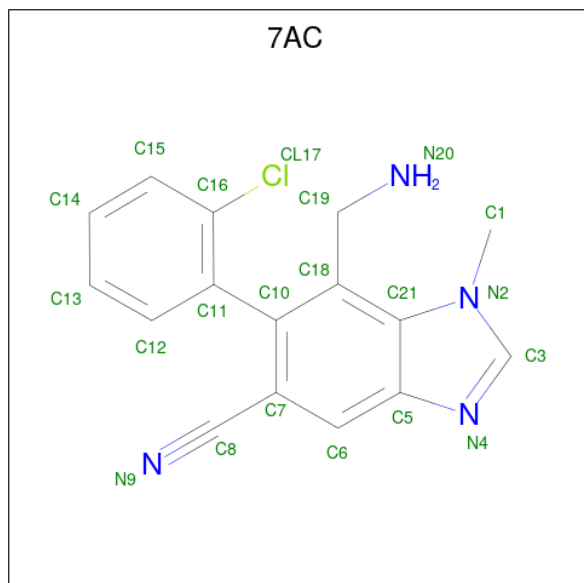
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	14	8	1	5	0	0
3	A	1	14	8	1	5	0	0
3	A	1	14	8	1	5	0	0
3	A	1	14	8	1	5	0	0
3	B	1	14	8	1	5	0	0
3	B	1	14	8	1	5	0	0
3	B	1	14	8	1	5	0	0
3	C	1	14	8	1	5	0	0
3	C	1	14	8	1	5	0	0
3	C	1	14	8	1	5	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is 7-(aminomethyl)-6-(2-chlorophenyl)-1-methyl-1H-benzimidazole-5-carbonitrile (CCD ID: 7AC) (formula: C<sub>16</sub>H<sub>13</sub>ClN<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	Cl	N	0	0
			21	16	1	4		
4	B	1	Total	C	Cl	N	0	0
			21	16	1	4		
4	C	1	Total	C	Cl	N	0	0
			21	16	1	4		
4	D	1	Total	C	Cl	N	0	0
			21	16	1	4		

- Molecule 5 is water.

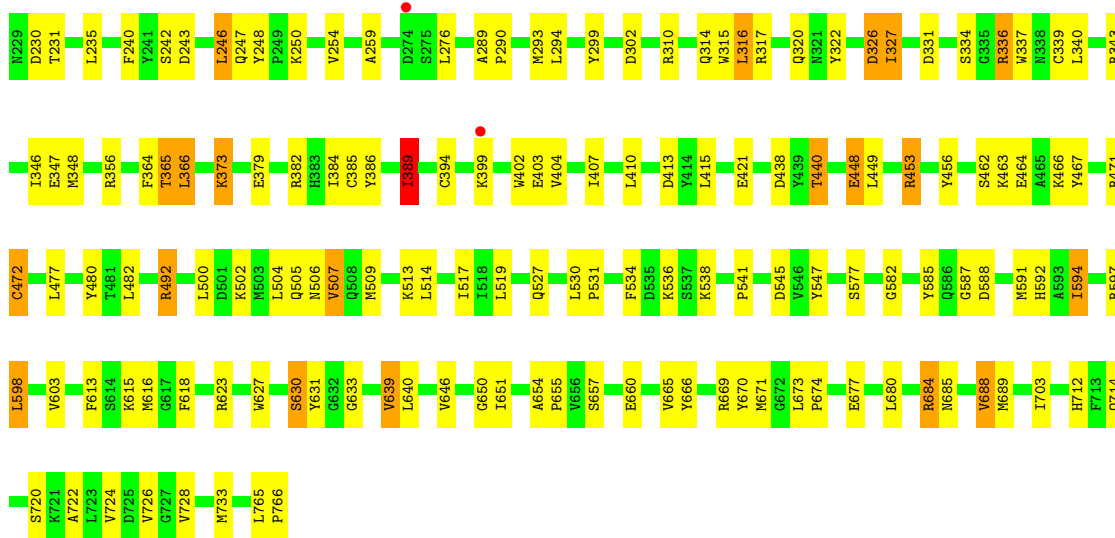
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	85	Total	O	0	0
			85	85		
5	B	106	Total	O	0	0
			106	106		
5	C	56	Total	O	0	0
			56	56		

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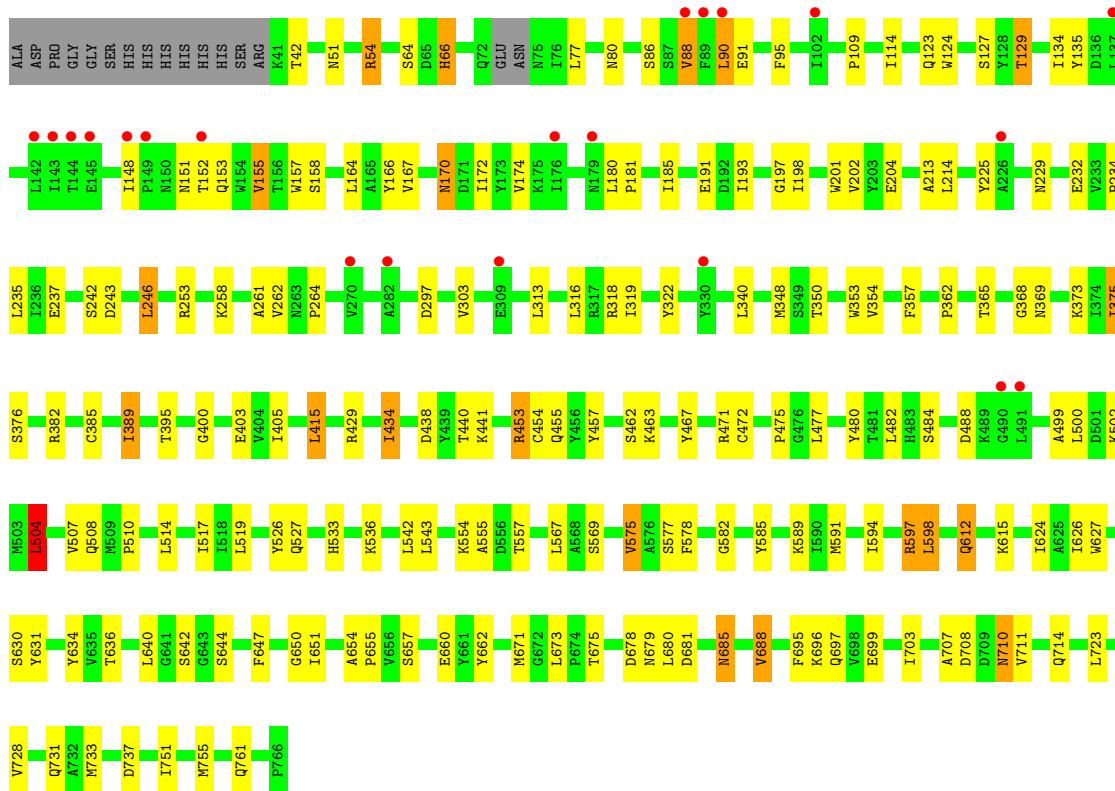
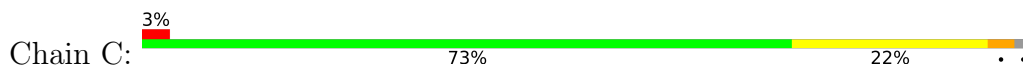
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
5	D	30	Total	O	0	0
			30	30		

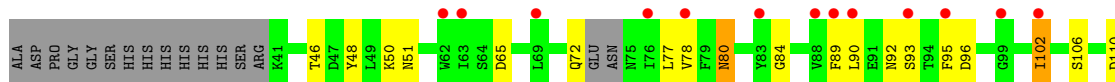


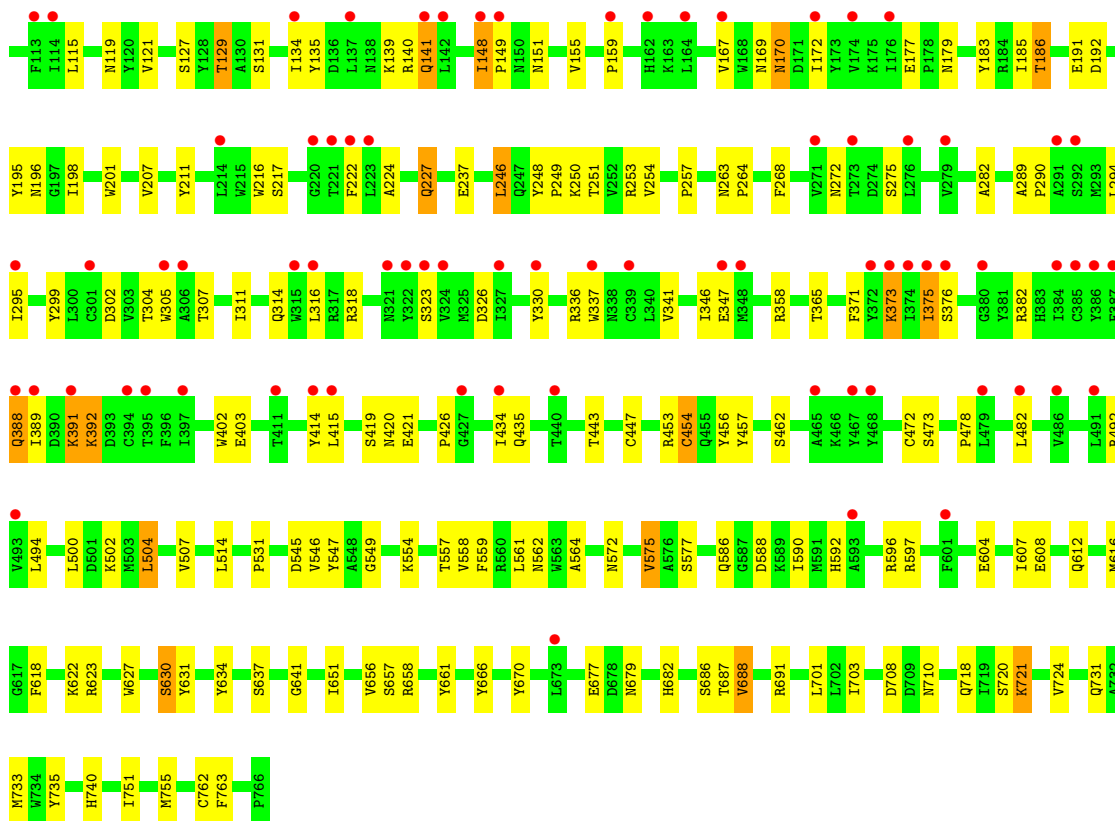


• Molecule 1: Dipeptidyl peptidase 4



• Molecule 1: Dipeptidyl peptidase 4






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

Chain E:  100%



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

Chain F:  100%




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

Chain G:  50%



- Molecule 2: 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 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	121.90Å 121.96Å 144.28Å 90.00° 114.94° 90.00°	Depositor
Resolution (Å)	46.13 – 2.71 46.13 – 2.71	Depositor EDS
% Data completeness (in resolution range)	90.9 (46.13-2.71) 91.0 (46.13-2.71)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.58 (at 2.73Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.200 , 0.267 0.223 , 0.282	Depositor DCC
$R_{free}$ test set	4722 reflections (4.54%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	57.3	Xtrriage
Anisotropy	0.180	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 27.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.023 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	24357	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.11% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, 7AC

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	0.55	0/6100	0.86	4/8296 (0.0%)
1	B	0.58	0/6100	0.87	3/8296 (0.0%)
1	C	0.55	0/6100	0.85	3/8296 (0.0%)
1	D	0.52	0/6100	0.84	3/8296 (0.0%)
All	All	0.55	0/24400	0.85	13/33184 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	140	ARG	N-CA-C	7.39	119.56	110.91
1	A	546	VAL	N-CA-C	6.68	119.14	108.85
1	C	357	PHE	N-CA-C	-6.66	107.03	114.62
1	D	546	VAL	N-CA-C	6.11	116.92	108.12
1	A	96	ASP	N-CA-C	-5.92	106.60	113.88

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5929	0	5649	113	0
1	B	5929	0	5649	124	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	5929	0	5649	104	0
1	D	5929	0	5651	117	0
2	E	28	0	25	0	0
2	F	28	0	25	0	0
2	G	28	0	25	0	0
2	H	28	0	25	0	0
3	A	56	0	52	0	0
3	B	42	0	39	0	0
3	C	42	0	39	0	0
3	D	28	0	26	0	0
4	A	21	0	13	4	0
4	B	21	0	13	3	0
4	C	21	0	13	1	0
4	D	21	0	13	2	0
5	A	85	0	0	1	0
5	B	106	0	0	0	0
5	C	56	0	0	0	0
5	D	30	0	0	0	0
All	All	24357	0	22906	450	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 10.

The worst 5 of 450 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:651:ILE:HD13	1:A:755:MET:HG2	1.40	1.01
1:C:253:ARG:HH21	1:D:253:ARG:HH21	1.05	0.99
1:D:658:ARG:HB2	1:D:687:THR:HG22	1.50	0.93
1:B:640:LEU:HD11	1:B:650:GLY:HA3	1.54	0.90
1:C:235:LEU:HD23	1:C:253:ARG:HB3	1.54	0.86

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	720/740 (97%)	675 (94%)	44 (6%)	1 (0%)	48	72
1	B	720/740 (97%)	667 (93%)	50 (7%)	3 (0%)	30	52
1	C	720/740 (97%)	668 (93%)	50 (7%)	2 (0%)	36	59
1	D	720/740 (97%)	642 (89%)	76 (11%)	2 (0%)	36	59
All	All	2880/2960 (97%)	2652 (92%)	220 (8%)	8 (0%)	36	59

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	678	ASP
1	B	366	LEU
1	A	124	TRP
1	D	282	ALA
1	D	447	CYS

### 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	649/662 (98%)	598 (92%)	51 (8%)	11	27
1	B	649/662 (98%)	601 (93%)	48 (7%)	13	30
1	C	649/662 (98%)	604 (93%)	45 (7%)	14	33
1	D	649/662 (98%)	605 (93%)	44 (7%)	14	33
All	All	2596/2648 (98%)	2408 (93%)	188 (7%)	13	31

5 of 188 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	354	VAL
1	C	761	GLN
1	C	395	THR

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Mol	Chain	Res	Type
1	C	533	HIS
1	D	134	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 77 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	612	GLN
1	D	527	GLN
1	C	731	GLN
1	D	169	ASN
1	D	731	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

8 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	E	1	1,2	14,14,15	0.58	0	17,19,21	0.68	0
2	NAG	E	2	2	14,14,15	0.49	0	17,19,21	0.77	0
2	NAG	F	1	1,2	14,14,15	0.52	0	17,19,21	1.07	1 (5%)
2	NAG	F	2	2	14,14,15	0.55	0	17,19,21	0.99	1 (5%)
2	NAG	G	1	1,2	14,14,15	0.65	0	17,19,21	0.87	0
2	NAG	G	2	2	14,14,15	0.49	0	17,19,21	1.18	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	H	1	1,2	14,14,15	0.48	0	17,19,21	1.07	1 (5%)
2	NAG	H	2	2	14,14,15	0.64	0	17,19,21	1.22	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	E	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	F	2	2	-	3/6/23/26	0/1/1/1
2	NAG	G	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	G	2	2	-	4/6/23/26	0/1/1/1
2	NAG	H	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	H	2	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	2	NAG	C1-O5-C5	3.61	117.03	112.19
2	F	2	NAG	C4-C3-C2	2.67	114.93	111.02
2	F	1	NAG	C2-N2-C7	-2.61	119.40	122.90
2	H	1	NAG	C1-O5-C5	2.28	115.25	112.19
2	H	2	NAG	O4-C4-C5	2.02	114.30	109.32

There are no chirality outliers.

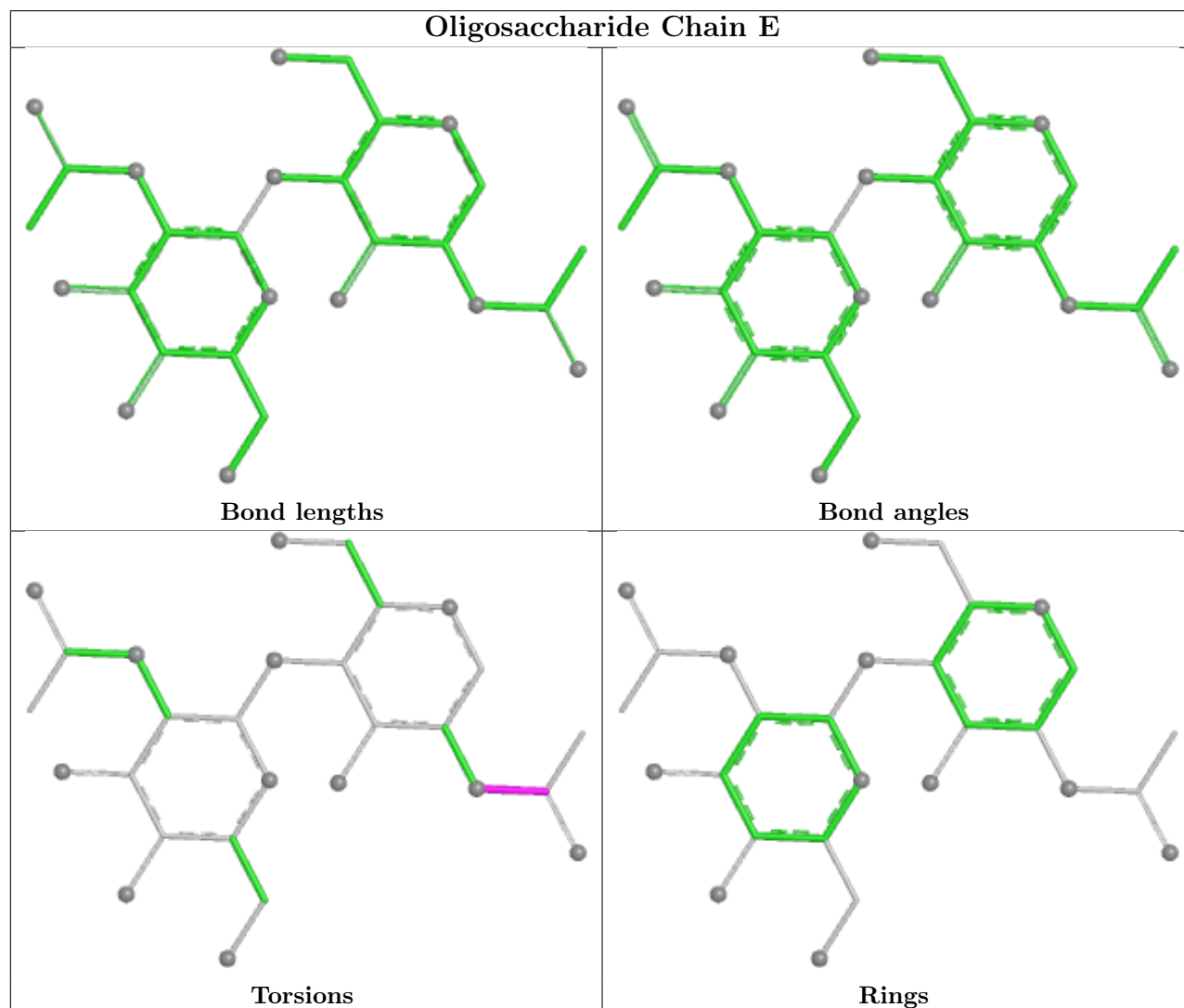
5 of 14 torsion outliers are listed below:

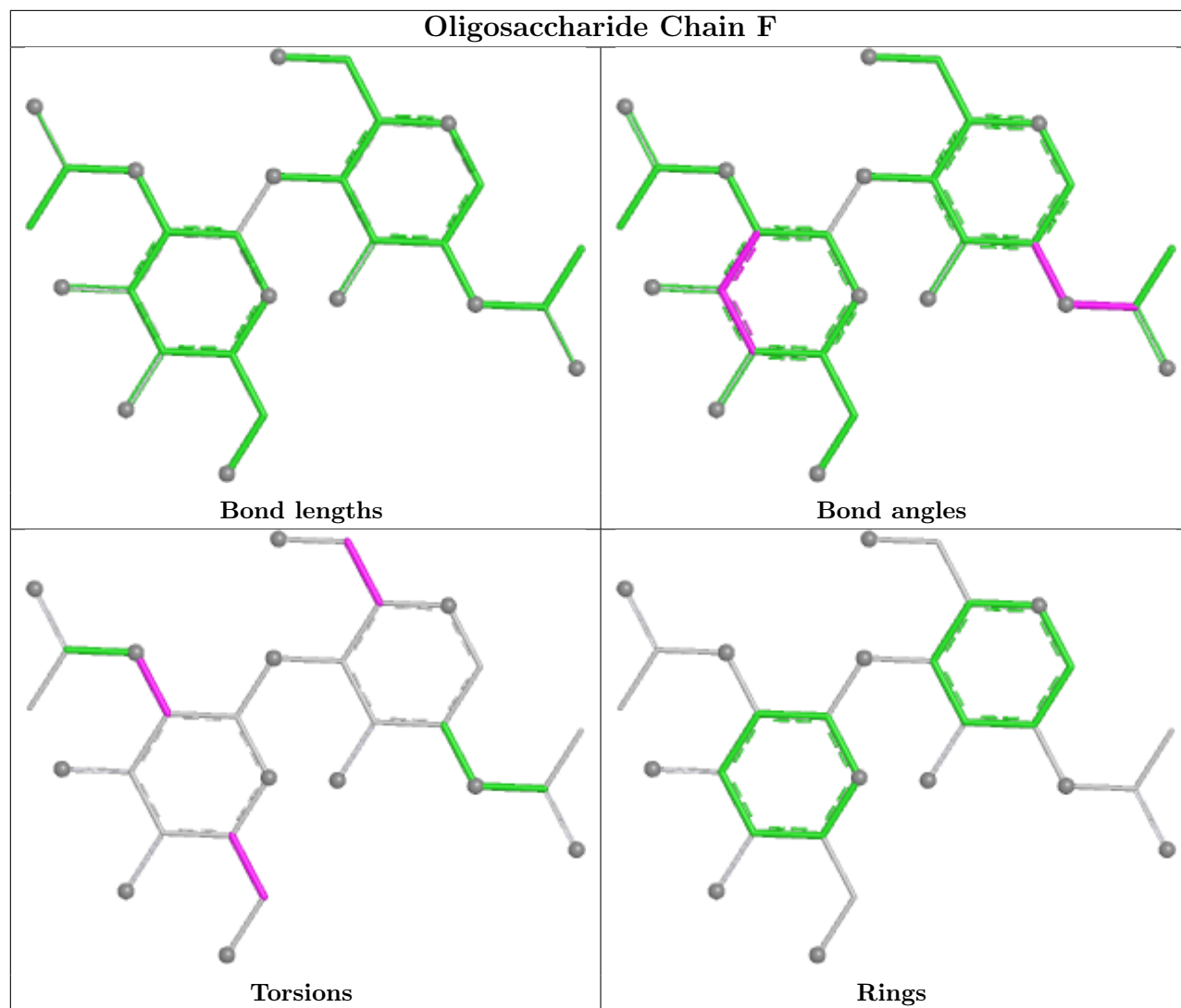
Mol	Chain	Res	Type	Atoms
2	E	1	NAG	C8-C7-N2-C2
2	E	1	NAG	O7-C7-N2-C2
2	G	2	NAG	C8-C7-N2-C2
2	G	2	NAG	O7-C7-N2-C2
2	H	1	NAG	C8-C7-N2-C2

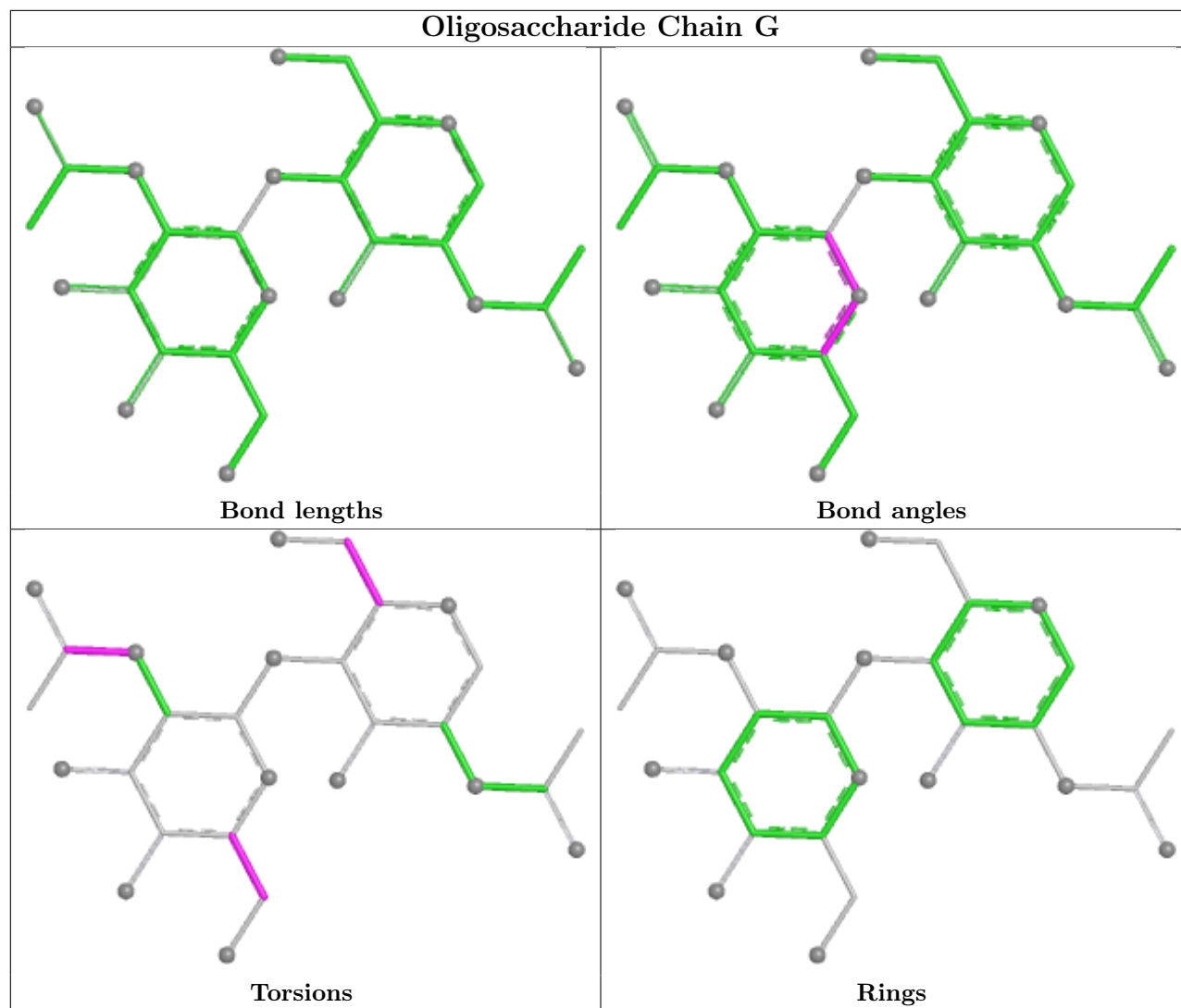
There are no ring outliers.

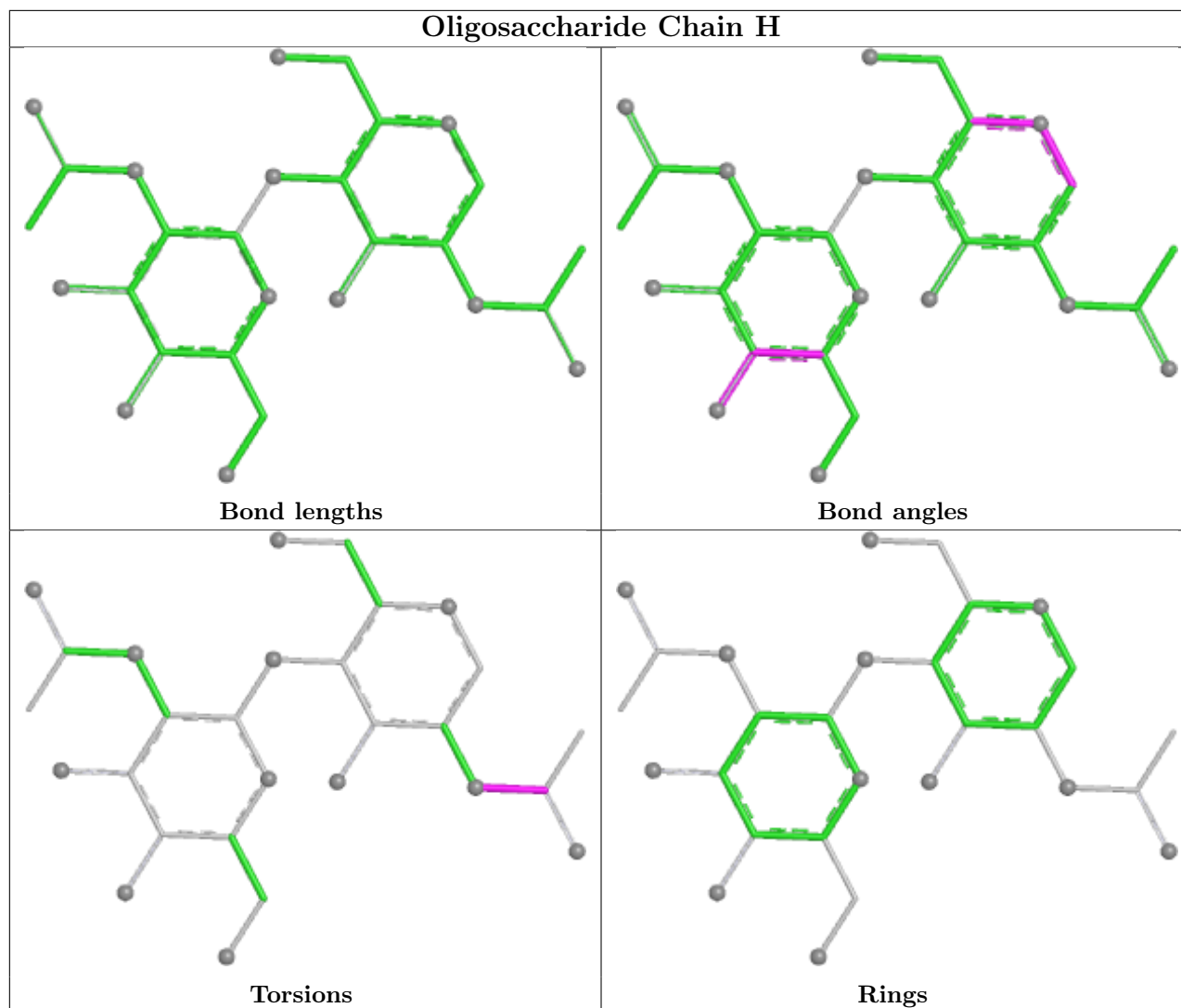
No monomer is involved in short contacts.

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](#)

16 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
3	NAG	C	804	1	14,14,15	0.82	1 (7%)	17,19,21	1.24	2 (11%)
3	NAG	D	804	1	14,14,15	0.74	1 (7%)	17,19,21	1.29	1 (5%)
3	NAG	A	803	1	14,14,15	0.67	0	17,19,21	1.00	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	C	801	1	14,14,15	0.73	0	17,19,21	1.24	1 (5%)
4	7AC	A	800	-	23,23,23	0.73	1 (4%)	26,33,33	1.80	4 (15%)
4	7AC	C	800	-	23,23,23	0.69	1 (4%)	26,33,33	1.50	3 (11%)
3	NAG	B	802	1	14,14,15	0.84	1 (7%)	17,19,21	1.64	2 (11%)
4	7AC	B	800	-	23,23,23	0.78	0	26,33,33	1.65	4 (15%)
3	NAG	D	801	1	14,14,15	0.65	0	17,19,21	1.41	1 (5%)
3	NAG	C	805	1	14,14,15	0.64	0	17,19,21	1.48	1 (5%)
3	NAG	B	805	1	14,14,15	0.63	0	17,19,21	1.42	1 (5%)
3	NAG	A	801	1	14,14,15	0.60	0	17,19,21	1.34	2 (11%)
4	7AC	D	800	-	23,23,23	0.65	1 (4%)	26,33,33	1.85	4 (15%)
3	NAG	A	806	1	14,14,15	0.56	0	17,19,21	1.70	2 (11%)
3	NAG	B	801	1	14,14,15	0.60	0	17,19,21	1.10	1 (5%)
3	NAG	A	802	1	14,14,15	0.53	0	17,19,21	1.55	2 (11%)

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
3	NAG	C	804	1	1/1/5/7	2/6/23/26	0/1/1/1
3	NAG	D	804	1	-	4/6/23/26	0/1/1/1
3	NAG	A	803	1	-	2/6/23/26	0/1/1/1
3	NAG	C	801	1	-	4/6/23/26	0/1/1/1
4	7AC	A	800	-	-	0/7/8/8	0/3/3/3
4	7AC	C	800	-	-	0/7/8/8	0/3/3/3
3	NAG	B	802	1	-	5/6/23/26	0/1/1/1
4	7AC	B	800	-	-	0/7/8/8	0/3/3/3
3	NAG	D	801	1	-	2/6/23/26	0/1/1/1
3	NAG	C	805	1	-	2/6/23/26	0/1/1/1
3	NAG	B	805	1	-	4/6/23/26	0/1/1/1
3	NAG	A	801	1	-	4/6/23/26	0/1/1/1
4	7AC	D	800	-	-	0/7/8/8	0/3/3/3
3	NAG	A	806	1	-	2/6/23/26	0/1/1/1
3	NAG	B	801	1	-	4/6/23/26	0/1/1/1
3	NAG	A	802	1	-	2/6/23/26	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	804	NAG	C1-C2	2.49	1.55	1.52
3	D	804	NAG	C1-C2	2.31	1.55	1.52
3	B	802	NAG	C1-C2	2.22	1.55	1.52
4	A	800	7AC	C11-C10	-2.07	1.47	1.50
4	D	800	7AC	C5-N4	-2.06	1.35	1.39

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	800	7AC	C10-C11-C16	-6.01	115.40	122.31
4	A	800	7AC	C10-C11-C16	-5.70	115.76	122.31
3	A	806	NAG	C1-O5-C5	5.16	119.10	112.19
3	D	801	NAG	C1-O5-C5	5.06	118.97	112.19
4	B	800	7AC	C10-C11-C16	-5.05	116.51	122.31

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	C	804	NAG	C1

5 of 37 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	801	NAG	C8-C7-N2-C2
3	A	801	NAG	O7-C7-N2-C2
3	A	803	NAG	C8-C7-N2-C2
3	A	803	NAG	O7-C7-N2-C2
3	B	801	NAG	C8-C7-N2-C2

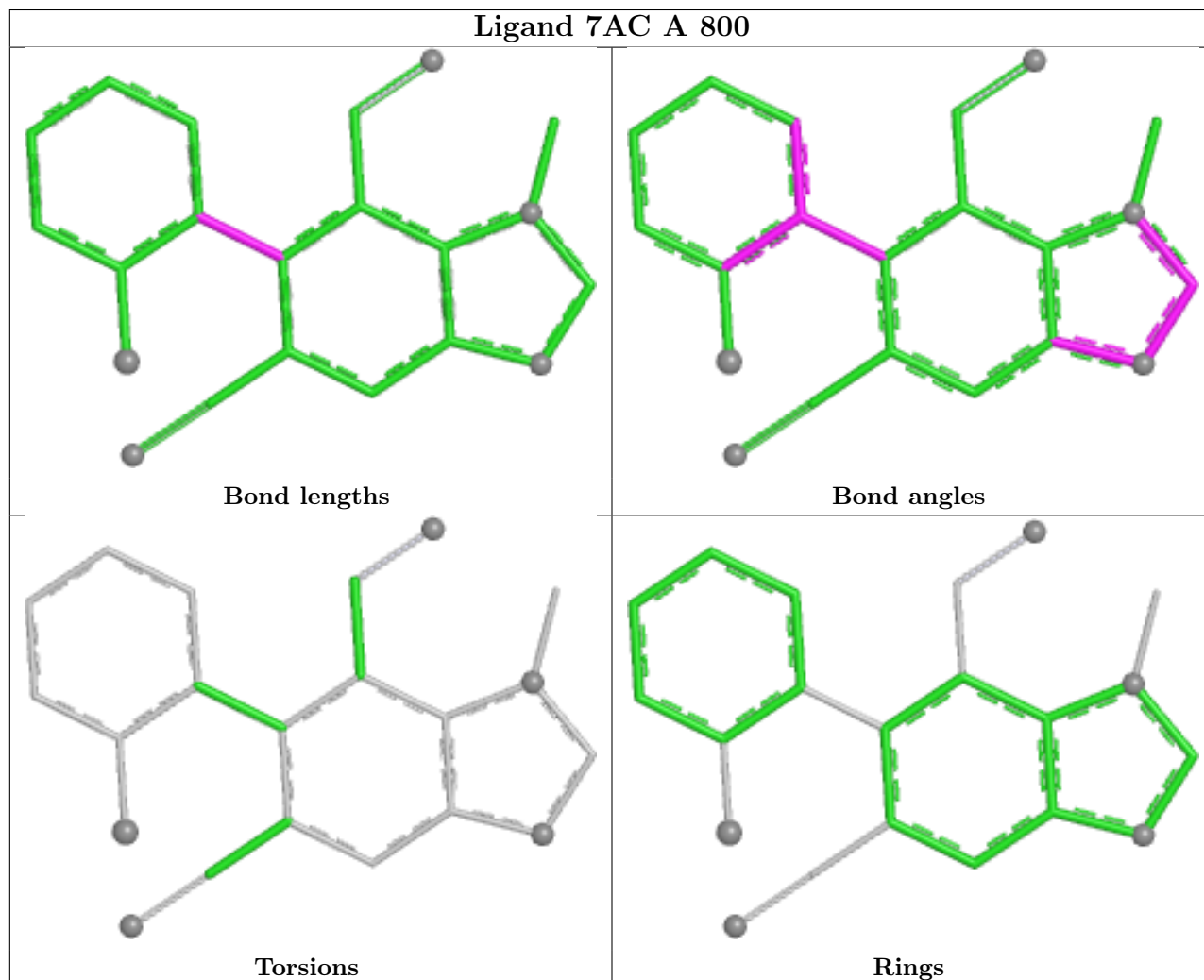
There are no ring outliers.

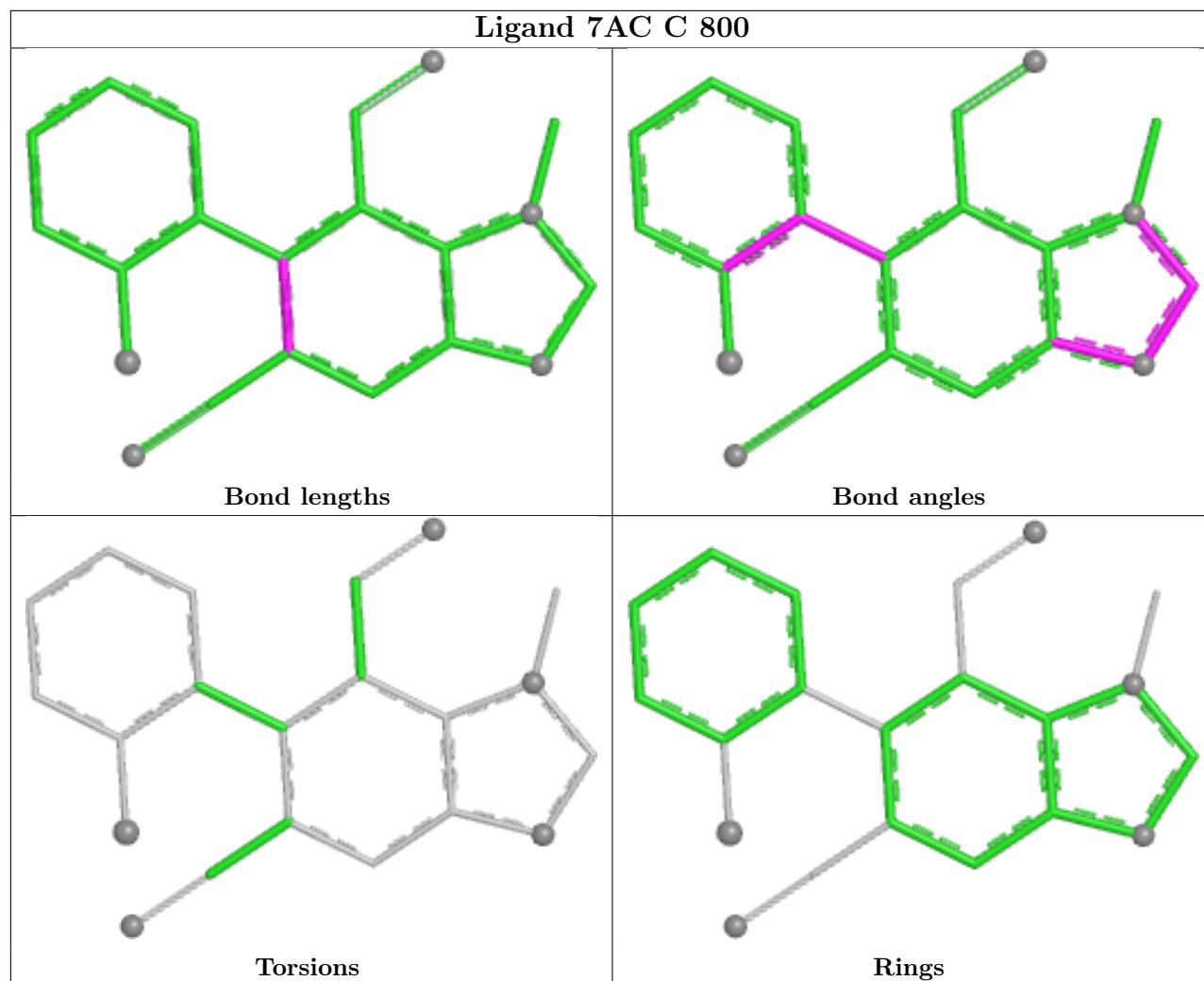
4 monomers are involved in 10 short contacts:

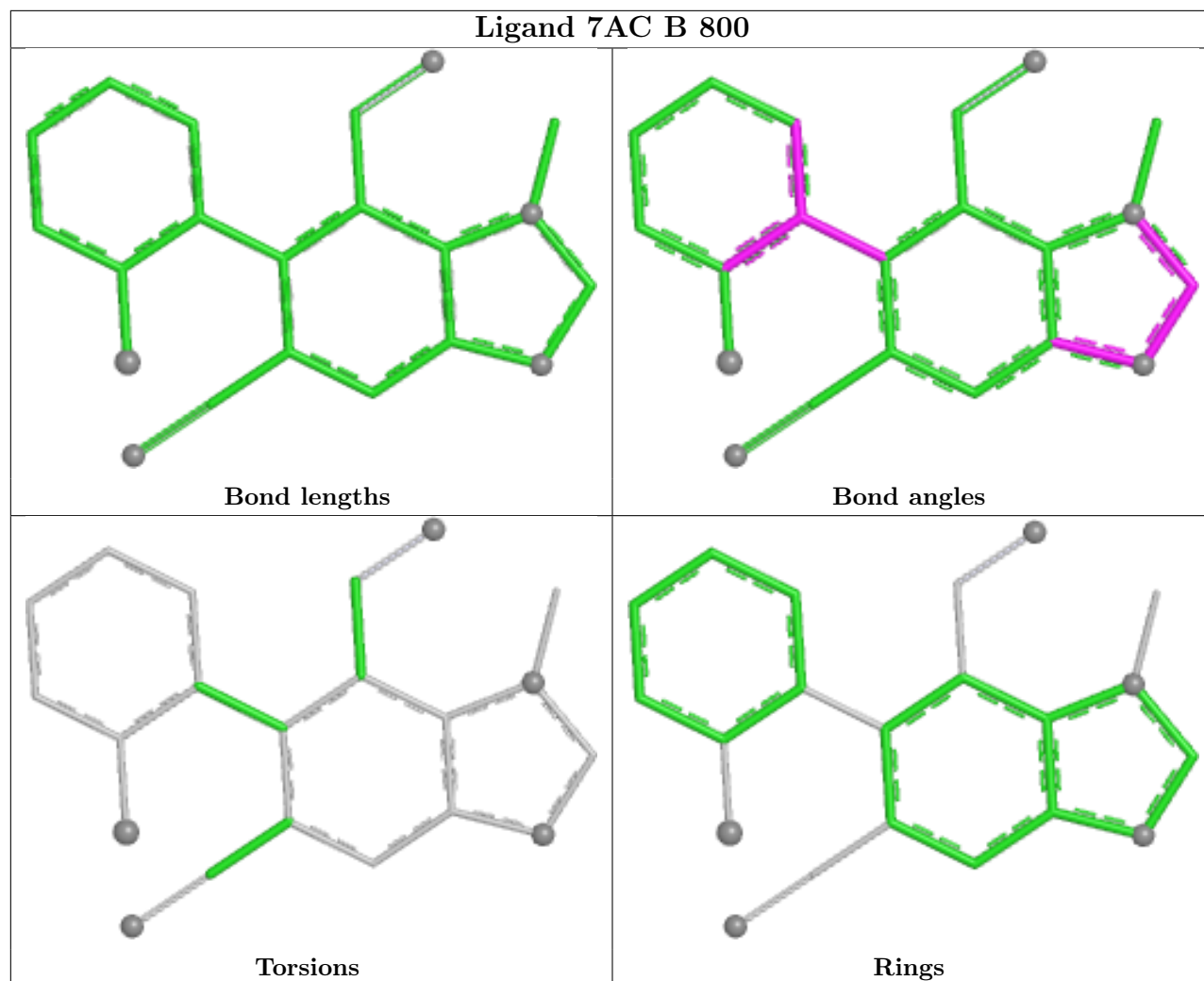
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	800	7AC	4	0
4	C	800	7AC	1	0
4	B	800	7AC	3	0
4	D	800	7AC	2	0

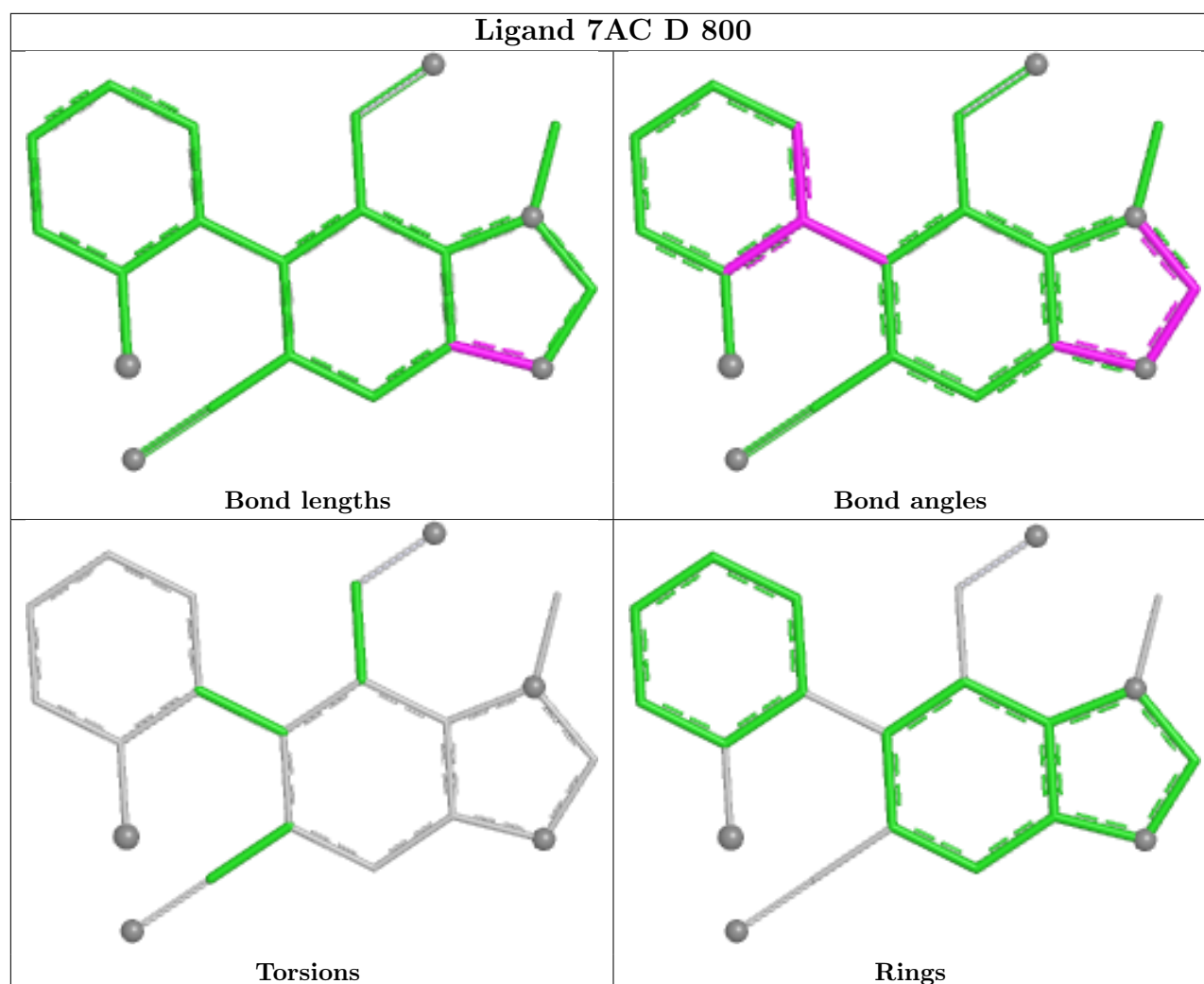
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

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 [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	724/740 (97%)	0.11	4 (0%) 85 85	32, 52, 73, 108	0
1	B	724/740 (97%)	0.00	4 (0%) 85 85	28, 49, 75, 102	0
1	C	724/740 (97%)	0.32	21 (2%) 53 50	30, 57, 84, 99	0
1	D	724/740 (97%)	0.86	88 (12%) 8 8	40, 69, 95, 124	0
All	All	2896/2960 (97%)	0.32	117 (4%) 42 39	28, 55, 86, 124	0

The worst 5 of 117 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	220	GLY	4.1
1	C	143	ILE	4.0
1	D	63	ILE	3.9
1	D	384	ILE	3.9
1	D	102	ILE	3.7

### 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.

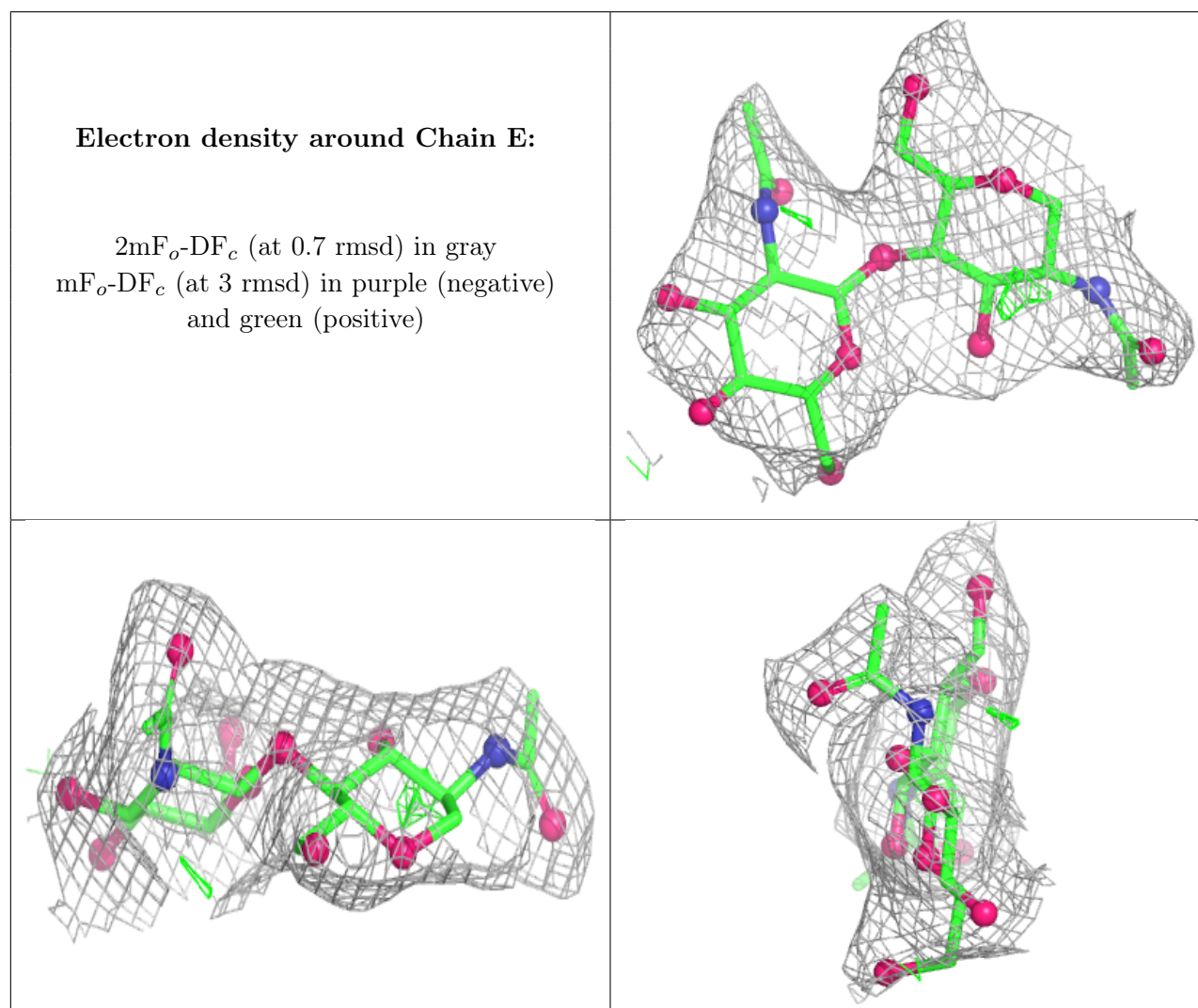
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	NAG	G	2	14/15	0.74	0.12	86,89,90,90	0
2	NAG	H	2	14/15	0.76	0.11	82,83,84,84	0

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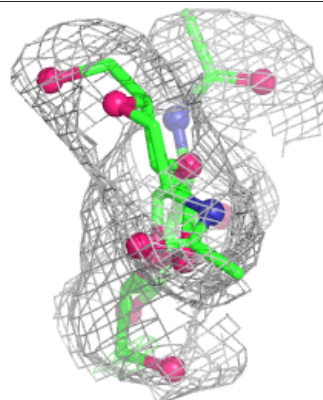
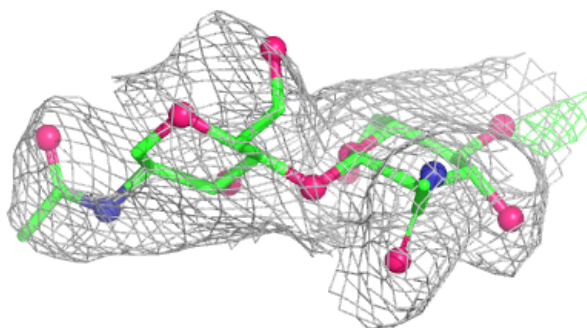
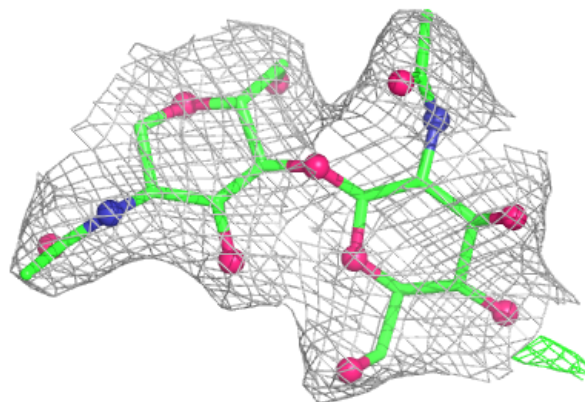
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	E	2	14/15	0.77	0.11	82,83,85,86	0
2	NAG	H	1	14/15	0.85	0.10	76,77,78,80	0
2	NAG	F	2	14/15	0.86	0.09	74,75,77,77	0
2	NAG	E	1	14/15	0.88	0.11	67,71,75,79	0
2	NAG	G	1	14/15	0.89	0.10	71,74,78,82	0
2	NAG	F	1	14/15	0.92	0.10	63,66,69,71	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.

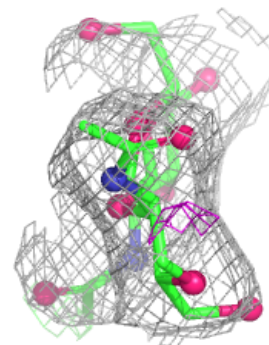
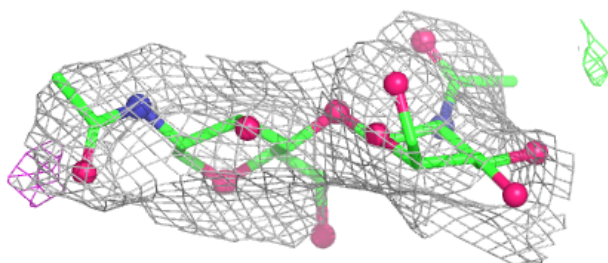
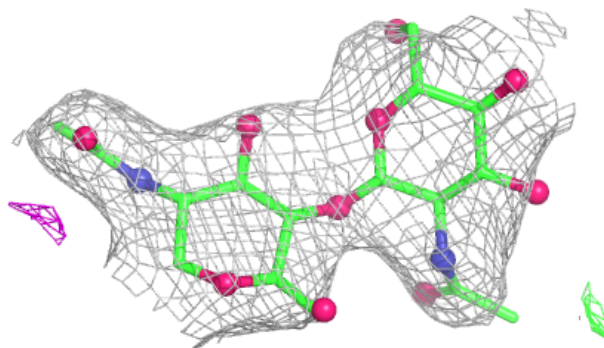


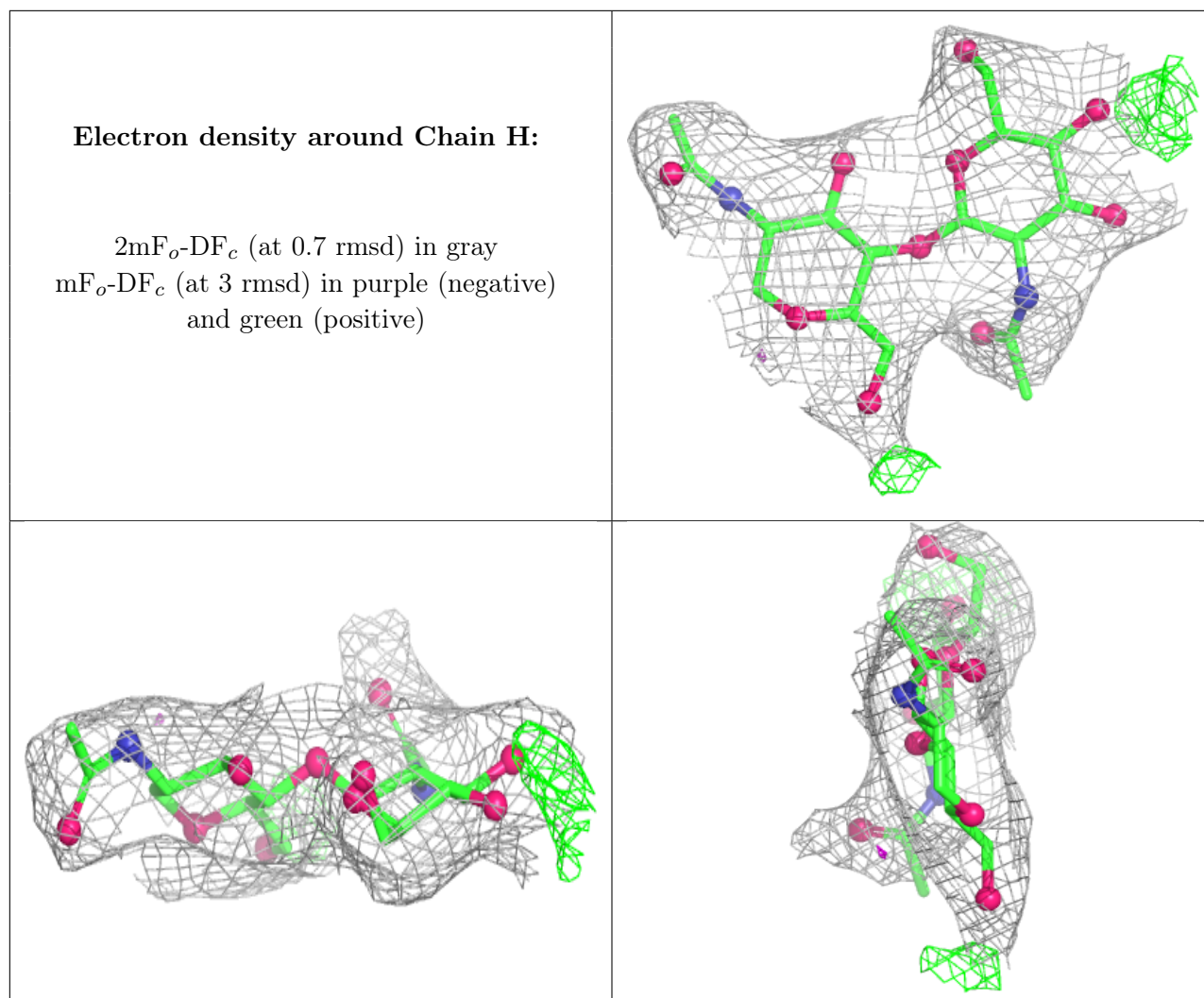
**Electron density around Chain F:**

$2mF_o-DF_c$  (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.

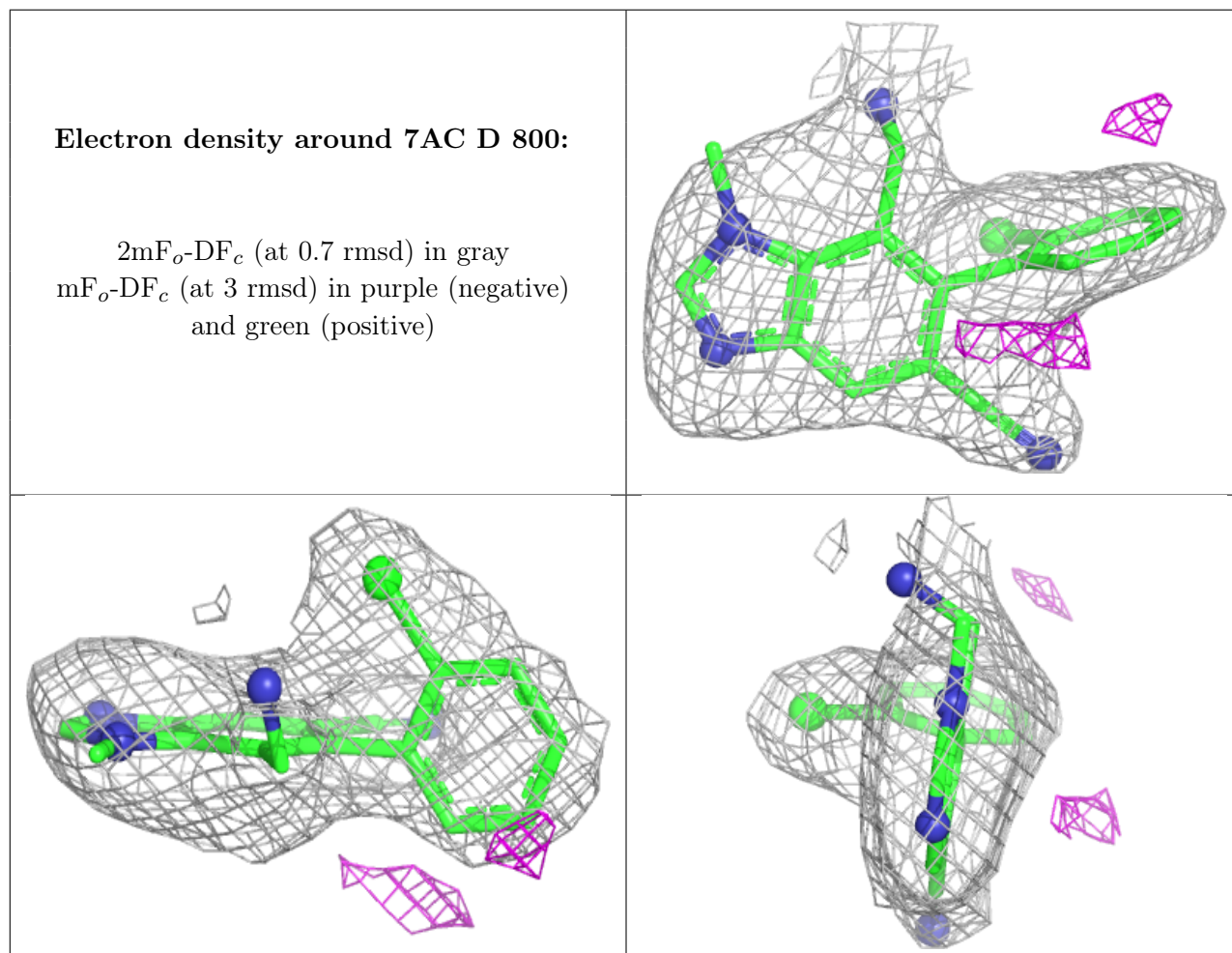
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	NAG	A	801	14/15	0.56	0.17	78,80,81,82	0
3	NAG	B	802	14/15	0.62	0.14	80,83,85,85	0
3	NAG	B	801	14/15	0.65	0.14	76,77,78,78	0
3	NAG	C	804	14/15	0.68	0.13	93,95,96,96	0
3	NAG	C	805	14/15	0.70	0.15	73,76,77,77	0
3	NAG	D	801	14/15	0.70	0.14	71,72,72,72	0
3	NAG	D	804	14/15	0.70	0.13	91,92,93,93	0
3	NAG	A	802	14/15	0.75	0.14	62,67,69,69	0
3	NAG	A	803	14/15	0.75	0.12	73,76,78,79	0

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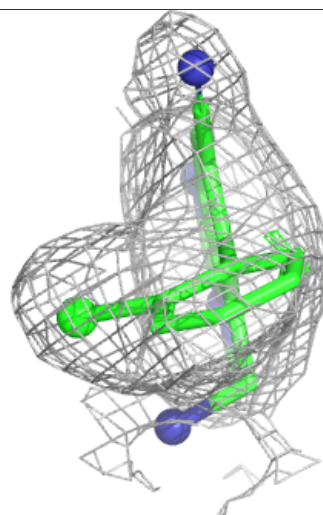
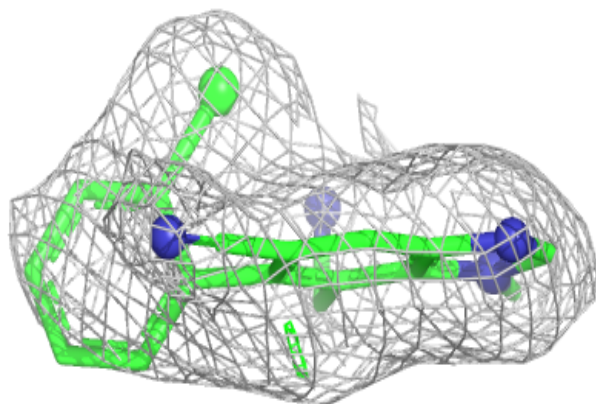
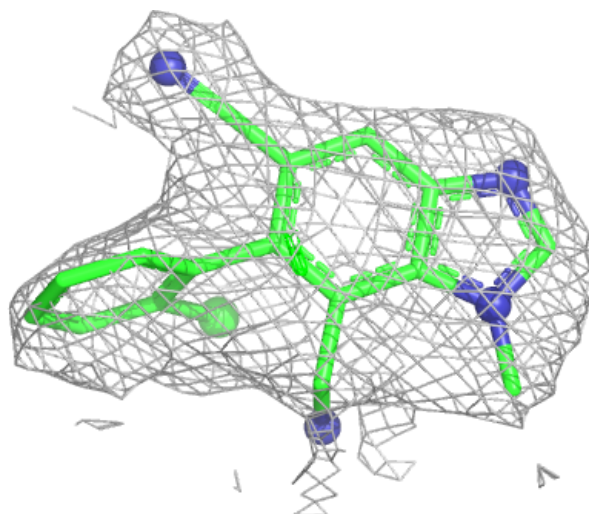
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAG	A	806	14/15	0.77	0.11	65,68,70,70	0
3	NAG	B	805	14/15	0.81	0.12	75,78,79,79	0
3	NAG	C	801	14/15	0.84	0.09	73,75,75,76	0
4	7AC	D	800	21/21	0.91	0.13	67,68,68,68	0
4	7AC	A	800	21/21	0.93	0.12	57,58,59,60	0
4	7AC	C	800	21/21	0.94	0.11	55,59,59,59	0
4	7AC	B	800	21/21	0.94	0.11	55,58,59,59	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.



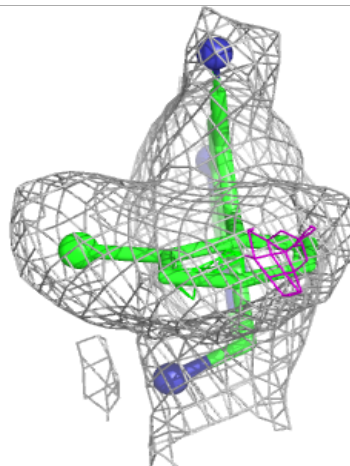
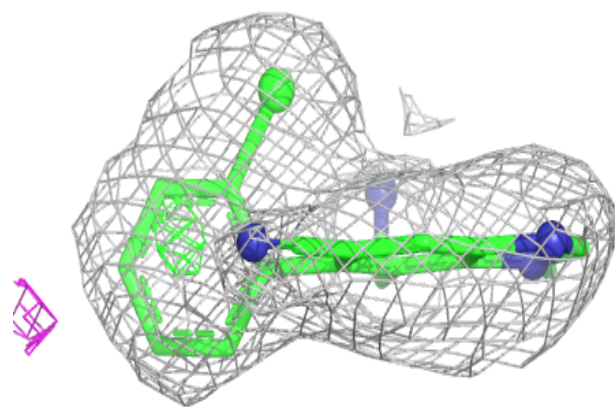
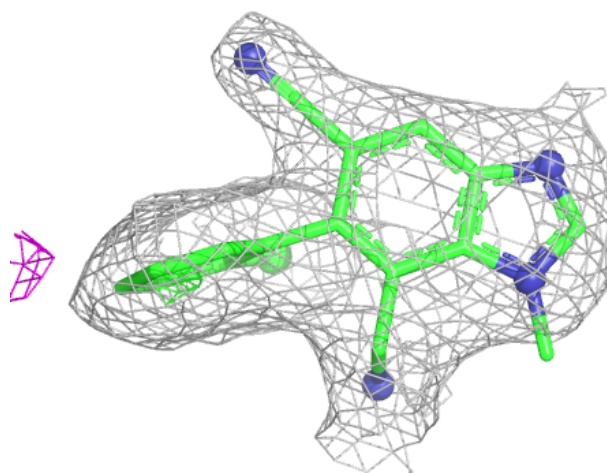
**Electron density around 7AC A 800:**

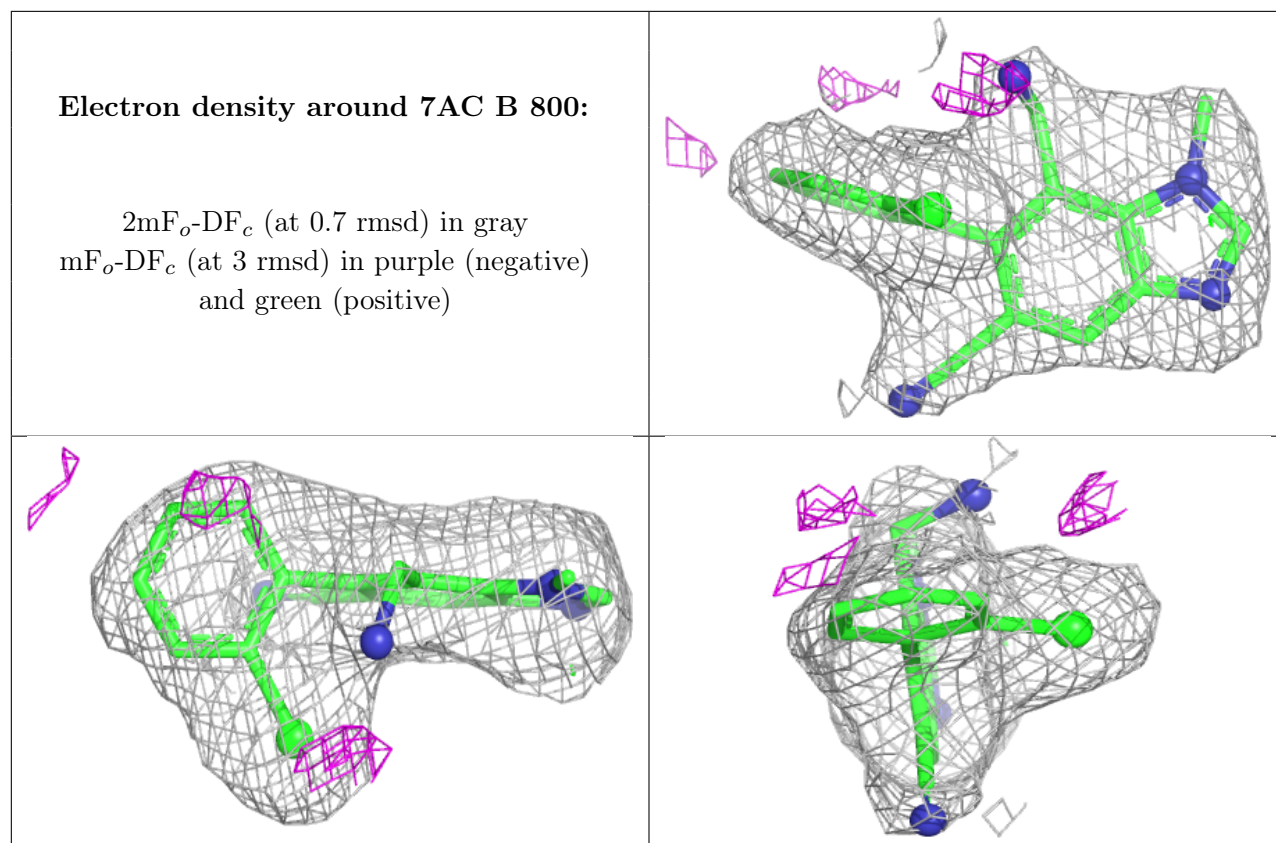
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around 7AC C 800:**

$2mF_o-DF_c$  (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.