



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 07:25 AM UTC

PDB ID : 4BTW / pdb_00004btw
Title : Crystal structure of human vascular adhesion protein-1 in complex with pyridazinone inhibitors
Authors : Bligt-Linden, E.; Pihlavisto, M.; Szatmari, I.; Otwinowski, Z.; Smith, D.J.; Lazar, L.; Fulop, F.; Salminen, T.A.
Deposited on : 2013-06-19
Resolution : 2.80 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

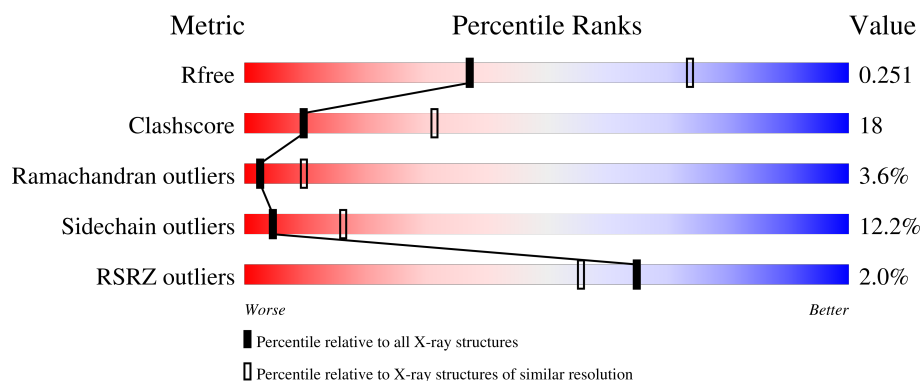
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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.



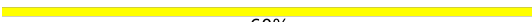
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	737	2% 56% 32% 8% ...
1	B	737	2% 57% 30% 8% ...
2	C	3	67% 33%
3	D	2	100%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	F	2	 100%
4	E	5	 60%  40%

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
7	NAG	A	1770	X	-	-	-
7	NAG	A	1771	X	-	-	-
7	NAG	B	1774	X	-	-	-

2 Entry composition [i](#)

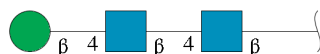
There are 9 unique types of molecules in this entry. The entry contains 11573 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 MEMBRANE PRIMARY AMINE OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	711	Total	C	N	O	S	0	0	0
			5609	3599	970	1020	20			
1	B	705	Total	C	N	O	S	0	0	0
			5562	3571	959	1012	20			

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



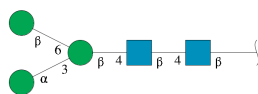
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			39	22	2	15			

- 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	F	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[beta-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	5	Total	C	N	O	0	0	0
			61	34	2	25			

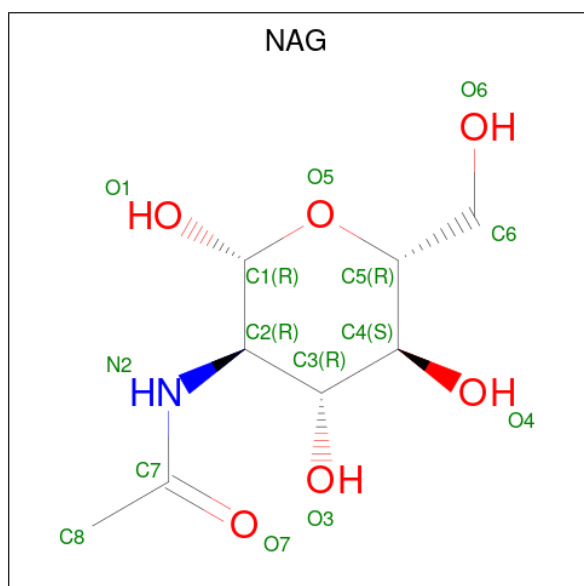
- Molecule 5 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cu	0	0
			1	1		
5	B	1	Total	Cu	0	0
			1	1		

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

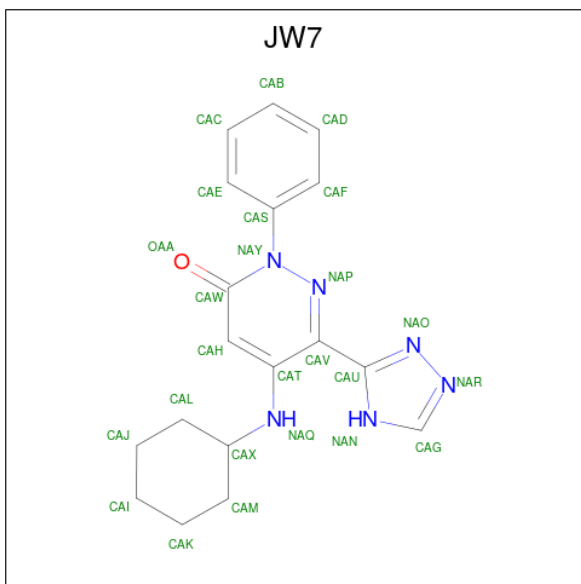
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Ca	0	0
			2	2		
6	B	2	Total	Ca	0	0
			2	2		

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



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

- Molecule 8 is 5-(cyclohexylamino)-2-phenyl-6-(1H-1,2,4-triazol-5-yl)-3(2H)-pyridazinone (CCD ID: JW7) (formula: C₁₈H₂₀N₆O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total 25	C 18	N 6	O 1	0	0
8	B	1	Total 25	C 18	N 6	O 1	0	0

- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	64	Total O 64 64	0	0

Continued on next page...

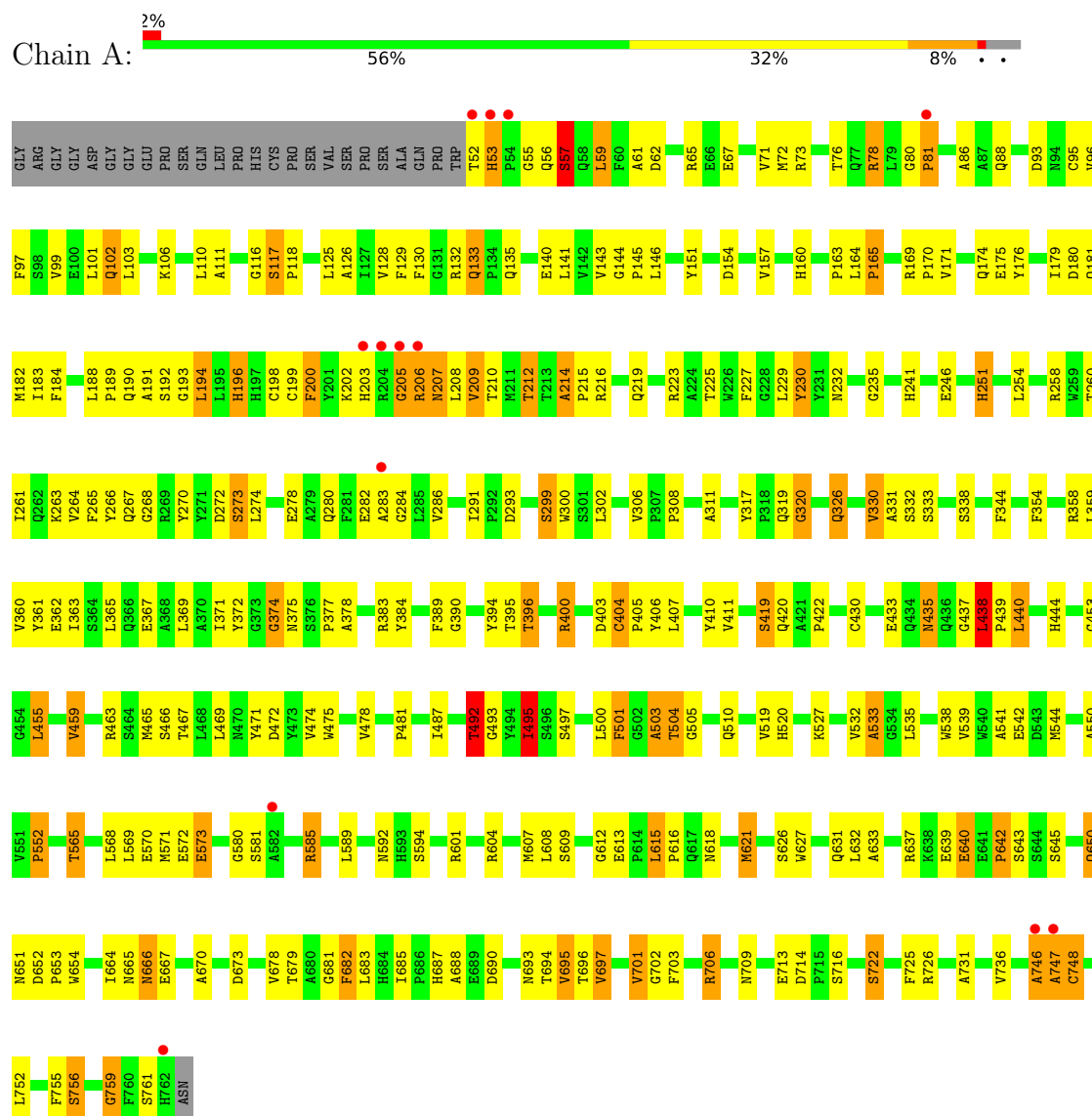
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	42	Total	O	0	0
			42	42		

3 Residue-property plots

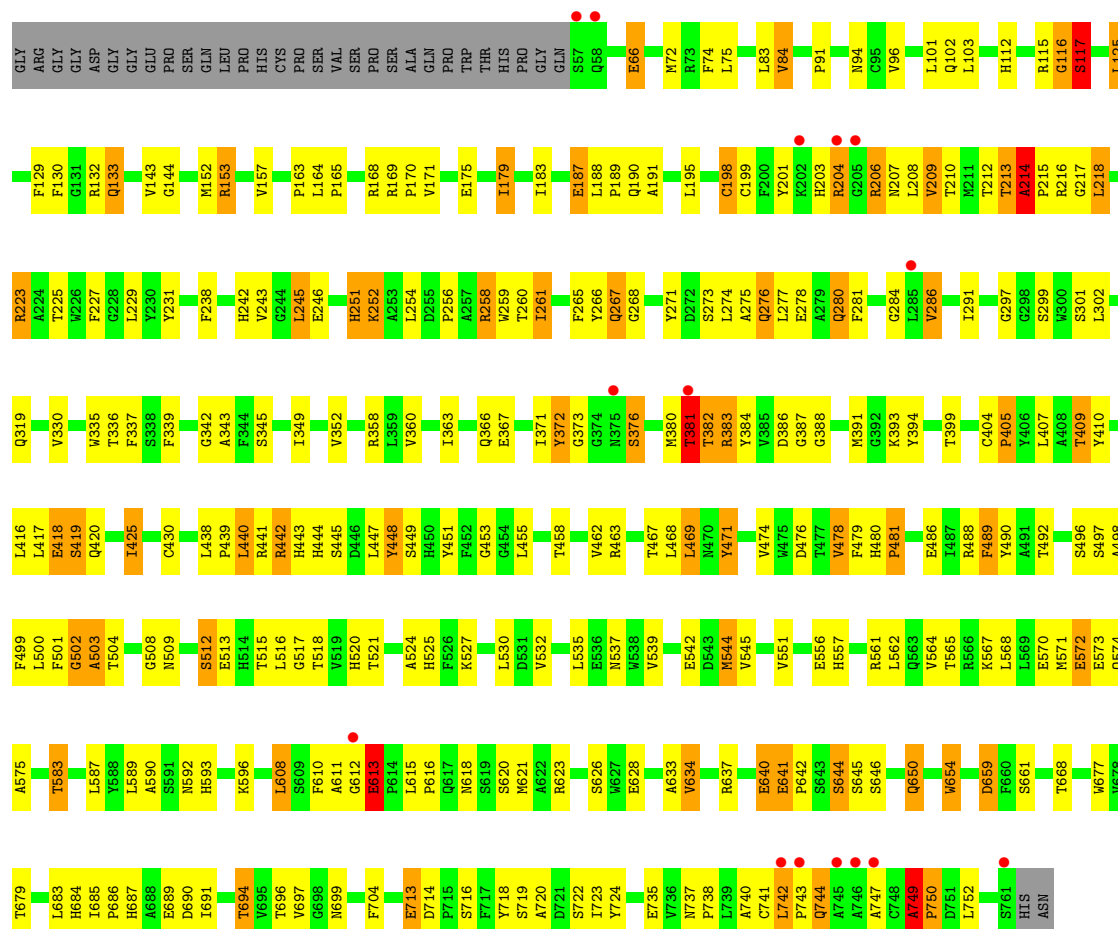
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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



• Molecule 1: MEMBRANE PRIMARY AMINE OXIDASE





- Molecule 2: beta-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: 100%

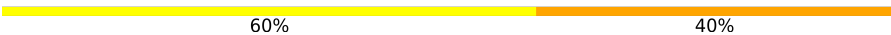


- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F: 100%



- Molecule 4: α -D-mannopyranose-(1-3)-[β -D-mannopyranose-(1-6)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain E: 

MAG1
MAG2
BMJ3
MAM4
BMJ5

4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	226.47Å 226.47Å 219.25Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.39 – 2.80 49.39 – 2.80	Depositor EDS
% Data completeness (in resolution range)	77.9 (49.39-2.80) 77.9 (49.39-2.80)	Depositor EDS
R_{merge}	0.32	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.205 , 0.260 0.199 , 0.251	Depositor DCC
R_{free} test set	3176 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	53.3	Xtriage
Anisotropy	0.531	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 49.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11573	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CU, JW7, BMA, MAN, NAG, CA, TPQ

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	0.98	2/5774 (0.0%)	1.20	35/7874 (0.4%)
1	B	0.95	5/5724 (0.1%)	1.18	26/7805 (0.3%)
All	All	0.96	7/11498 (0.1%)	1.19	61/15679 (0.4%)

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	3
1	B	0	4
All	All	0	7

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	641	GLU	CA-C	7.57	1.62	1.52
1	B	214	ALA	CA-C	-6.46	1.44	1.52
1	B	613	GLU	CA-C	5.75	1.59	1.53
1	A	169	ARG	CA-C	-5.70	1.47	1.53
1	B	373	GLY	N-CA	5.56	1.49	1.44

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	214	ALA	CA-C-N	-9.60	111.01	120.52
1	B	214	ALA	C-N-CA	-9.60	111.01	120.52
1	B	613	GLU	N-CA-C	8.84	120.44	109.57
1	B	685	ILE	CA-C-N	-8.33	111.20	119.78

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	685	ILE	C-N-CA	-8.33	111.20	119.78

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	198	CYS	Peptide
1	A	205	GLY	Peptide
1	A	437	GLY	Peptide
1	B	213	THR	Peptide
1	B	214	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	5609	0	5351	194	1
1	B	5562	0	5313	222	0
2	C	39	0	34	1	0
3	D	28	0	25	0	0
3	F	28	0	25	0	0
4	E	61	0	52	3	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	2	0	0	0	0
6	B	2	0	0	0	0
7	A	28	0	26	0	0
7	B	56	0	52	2	0
8	A	25	0	20	4	0
8	B	25	0	20	6	0
9	A	64	0	0	1	0
9	B	42	0	0	8	0
All	All	11573	0	10918	394	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 18.

The worst 5 of 394 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:367:GLU:OE2	1:A:645:SER:OG	1.75	1.04
1:A:492:THR:HG21	1:B:441:ARG:HA	1.42	1.01
1:B:620:SER:HG	1:B:654:TRP:HD1	1.10	0.91
1:B:620:SER:HG	1:B:654:TRP:CD1	1.87	0.91
1:A:80:GLY:O	1:A:81:PRO:O	1.90	0.90

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)
1:A:326:GLN:OE1	1:A:326:GLN:OE1[10_665]	1.91	0.29

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	708/737 (96%)	599 (85%)	82 (12%)	27 (4%)	2	9
1	B	702/737 (95%)	607 (86%)	71 (10%)	24 (3%)	3	11
All	All	1410/1474 (96%)	1206 (86%)	153 (11%)	51 (4%)	2	10

5 of 51 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	81	PRO
1	A	116	GLY
1	A	206	ARG
1	A	214	ALA
1	A	267	GLN

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	590/610 (97%)	519 (88%)	71 (12%)	5	17
1	B	585/610 (96%)	513 (88%)	72 (12%)	4	16
All	All	1175/1220 (96%)	1032 (88%)	143 (12%)	5	16

5 of 143 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	478	VAL
1	B	545	VAL
1	B	640	GLU
1	A	585	ARG
1	A	573	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	294	ASN
1	B	375	ASN
1	B	744	GLN
1	B	563	GLN
1	B	593	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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
1	TPQ	A	471	1	13,14,15	1.49	2 (15%)	13,19,21	1.59	2 (15%)
1	TPQ	B	471	1	13,14,15	1.44	2 (15%)	13,19,21	1.53	2 (15%)

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
1	TPQ	A	471	1	-	0/5/22/24	0/1/1/1
1	TPQ	B	471	1	-	2/5/22/24	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	471	TPQ	C3-C4	3.00	1.41	1.36
1	A	471	TPQ	C6-C1	2.81	1.41	1.34
1	B	471	TPQ	C6-C1	2.69	1.41	1.34
1	B	471	TPQ	C3-C4	2.31	1.40	1.36

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	471	TPQ	C6-C1-C2	3.82	121.38	118.66
1	A	471	TPQ	O5-C5-C4	3.67	125.22	119.43
1	A	471	TPQ	C6-C1-C2	2.97	120.77	118.66
1	B	471	TPQ	O5-C5-C4	2.43	123.27	119.43

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	471	TPQ	N-CA-CB-C1
1	B	471	TPQ	C-CA-CB-C1

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	471	TPQ	1	0

5.5 Carbohydrates

12 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	NAG	C	1	1,2	14,14,15	0.74	0	17,19,21	1.58	4 (23%)
2	NAG	C	2	2	14,14,15	0.80	1 (7%)	17,19,21	1.63	4 (23%)
2	BMA	C	3	2	11,11,12	0.63	0	15,15,17	1.28	2 (13%)
3	NAG	D	1	3,1	14,14,15	0.61	0	17,19,21	1.54	3 (17%)
3	NAG	D	2	3	14,14,15	0.82	1 (7%)	17,19,21	1.36	2 (11%)
4	NAG	E	1	1,4	14,14,15	0.58	0	17,19,21	1.14	0
4	NAG	E	2	4	14,14,15	0.47	0	17,19,21	1.79	4 (23%)
4	BMA	E	3	4	11,11,12	0.77	0	15,15,17	2.04	2 (13%)
4	MAN	E	4	4	11,11,12	0.53	0	15,15,17	2.51	3 (20%)
4	BMA	E	5	4	11,11,12	0.67	0	15,15,17	2.13	6 (40%)
3	NAG	F	1	3,1	14,14,15	0.84	0	17,19,21	2.17	5 (29%)
3	NAG	F	2	3	14,14,15	0.67	0	17,19,21	1.54	3 (17%)

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	1,2	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	BMA	C	3	2	-	2/2/19/22	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	D	1	3,1	-	3/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
4	NAG	E	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	E	2	4	-	0/6/23/26	0/1/1/1
4	BMA	E	3	4	-	1/2/19/22	0/1/1/1
4	MAN	E	4	4	-	0/2/19/22	0/1/1/1
4	BMA	E	5	4	-	0/2/19/22	0/1/1/1
3	NAG	F	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	F	2	3	-	1/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	2	NAG	C1-C2	2.16	1.55	1.52
2	C	2	NAG	O5-C1	-2.01	1.40	1.43

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	4	MAN	C1-O5-C5	8.45	123.50	112.19
3	F	1	NAG	C2-N2-C7	5.73	130.58	122.90
4	E	3	BMA	C3-C4-C5	5.21	119.68	110.23
4	E	5	BMA	C1-O5-C5	4.67	118.44	112.19
4	E	3	BMA	O4-C4-C3	-4.63	99.46	110.38

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	1	NAG	C3-C2-N2-C7
3	F	1	NAG	C3-C2-N2-C7
2	C	3	BMA	O5-C5-C6-O6
2	C	3	BMA	C4-C5-C6-O6
3	D	1	NAG	O5-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 4 short contacts:

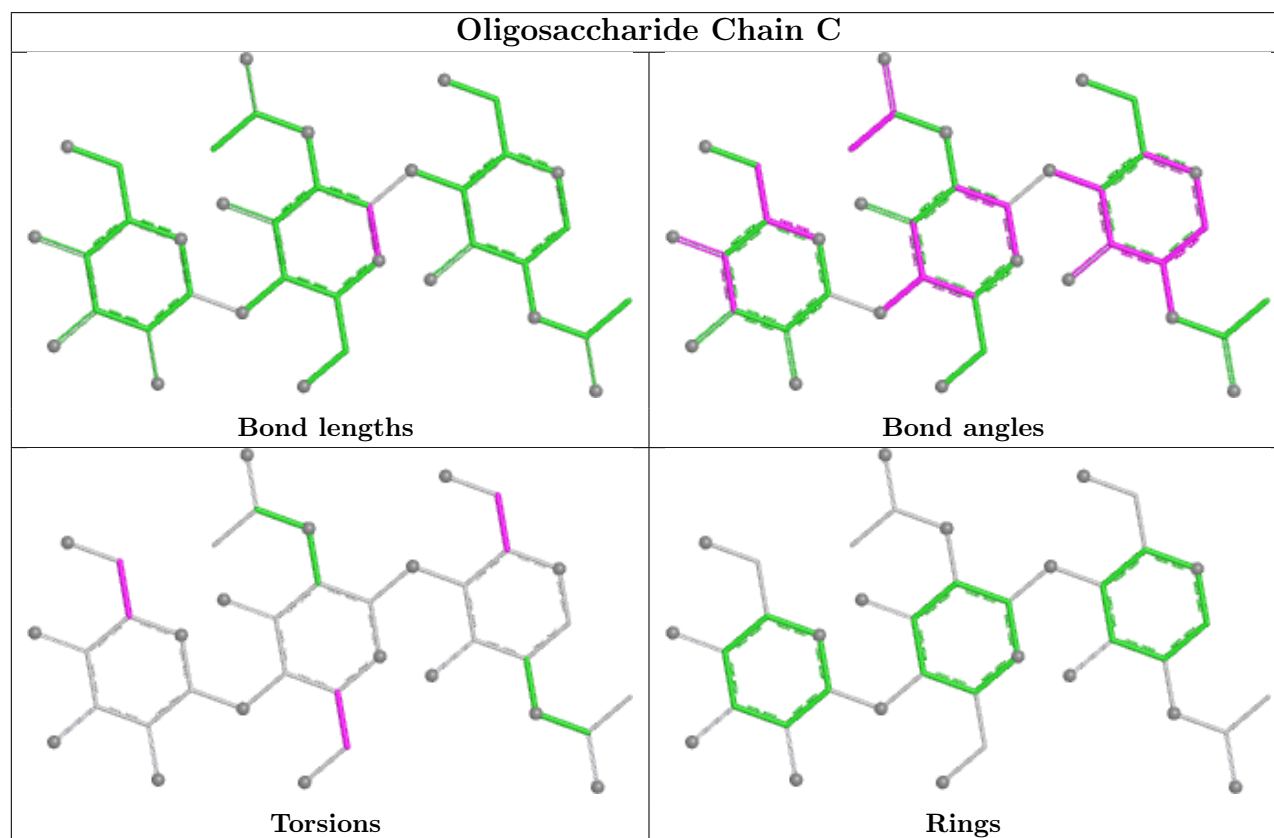
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	NAG	1	0

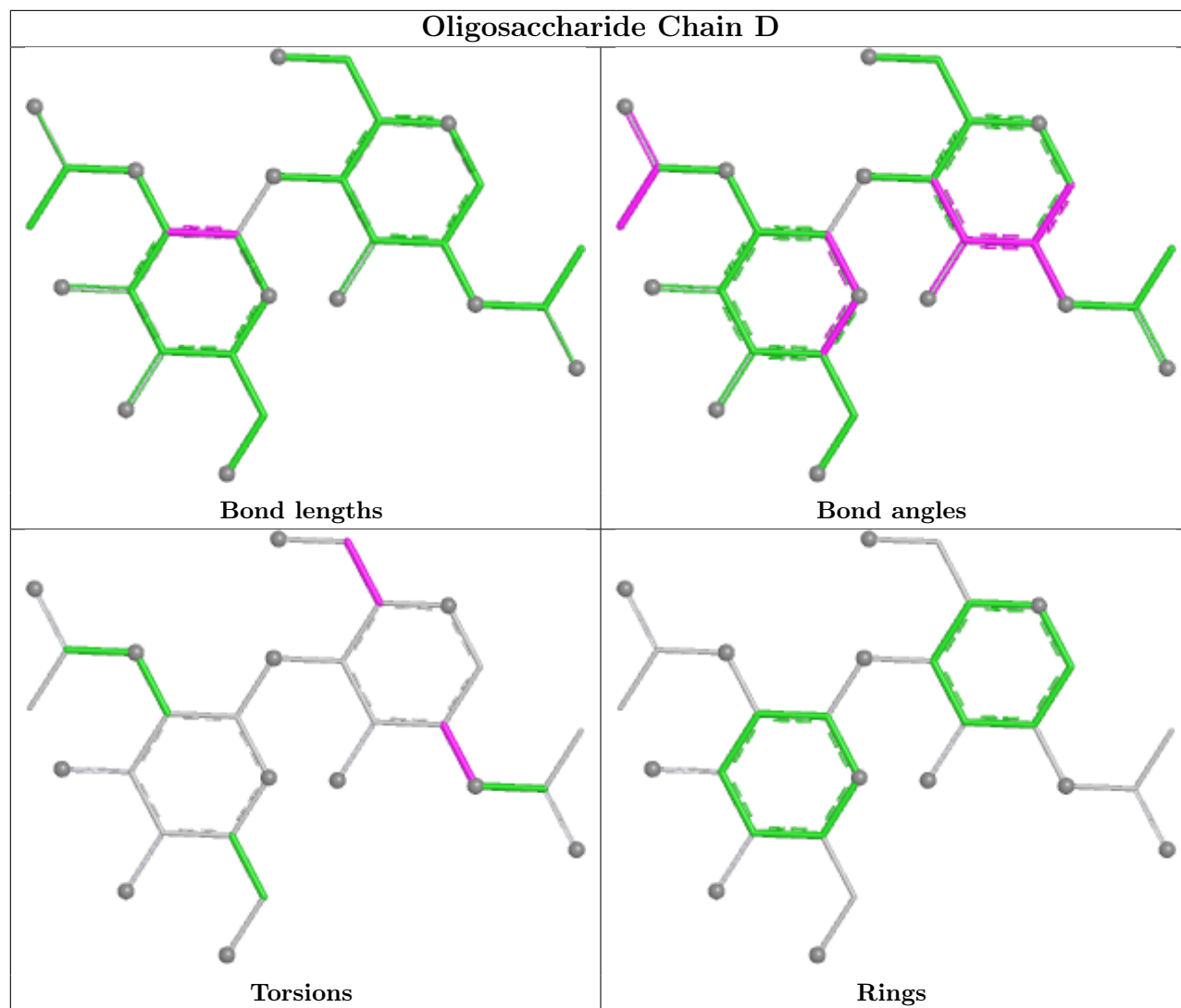
Continued on next page...

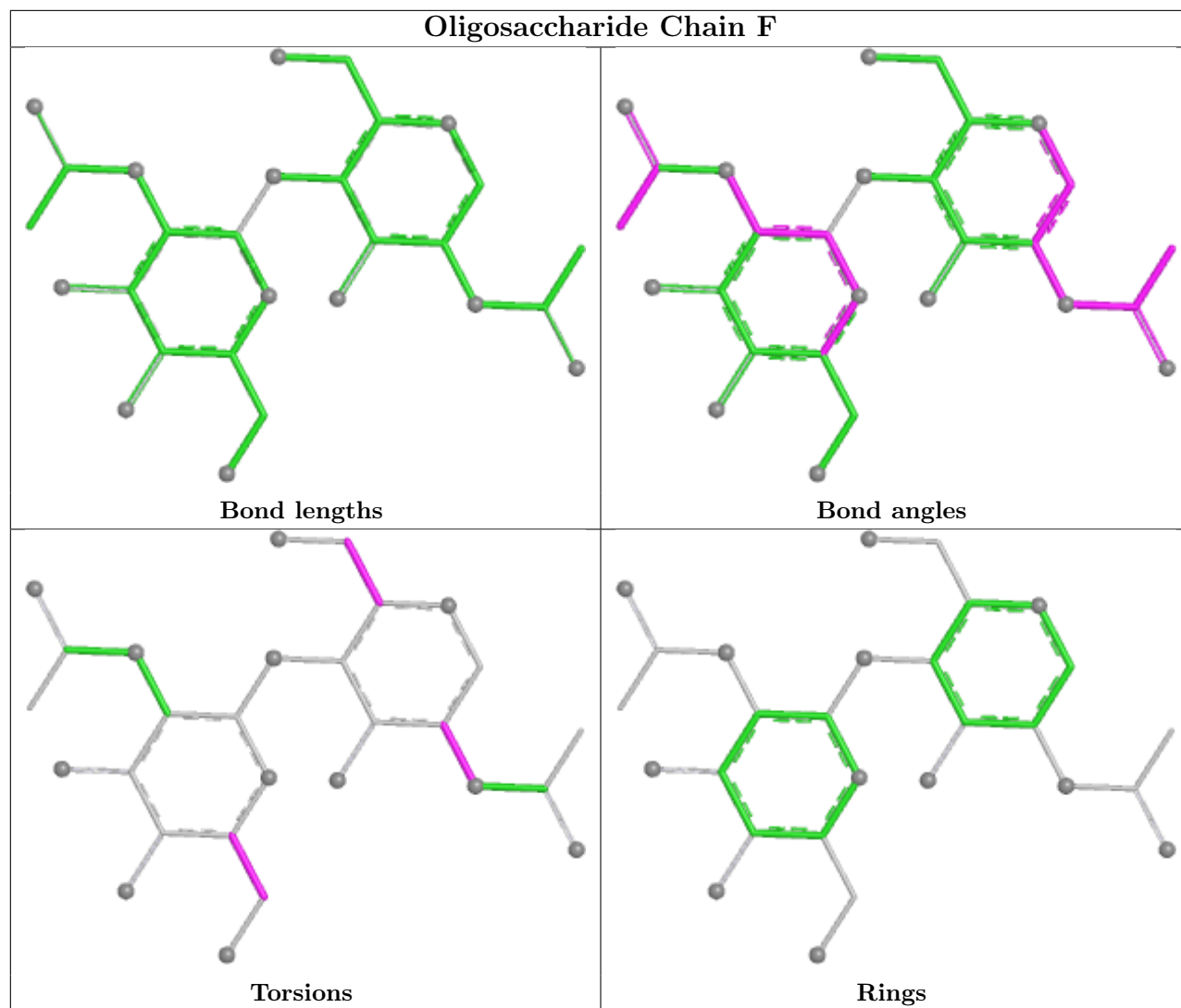
Continued from previous page...

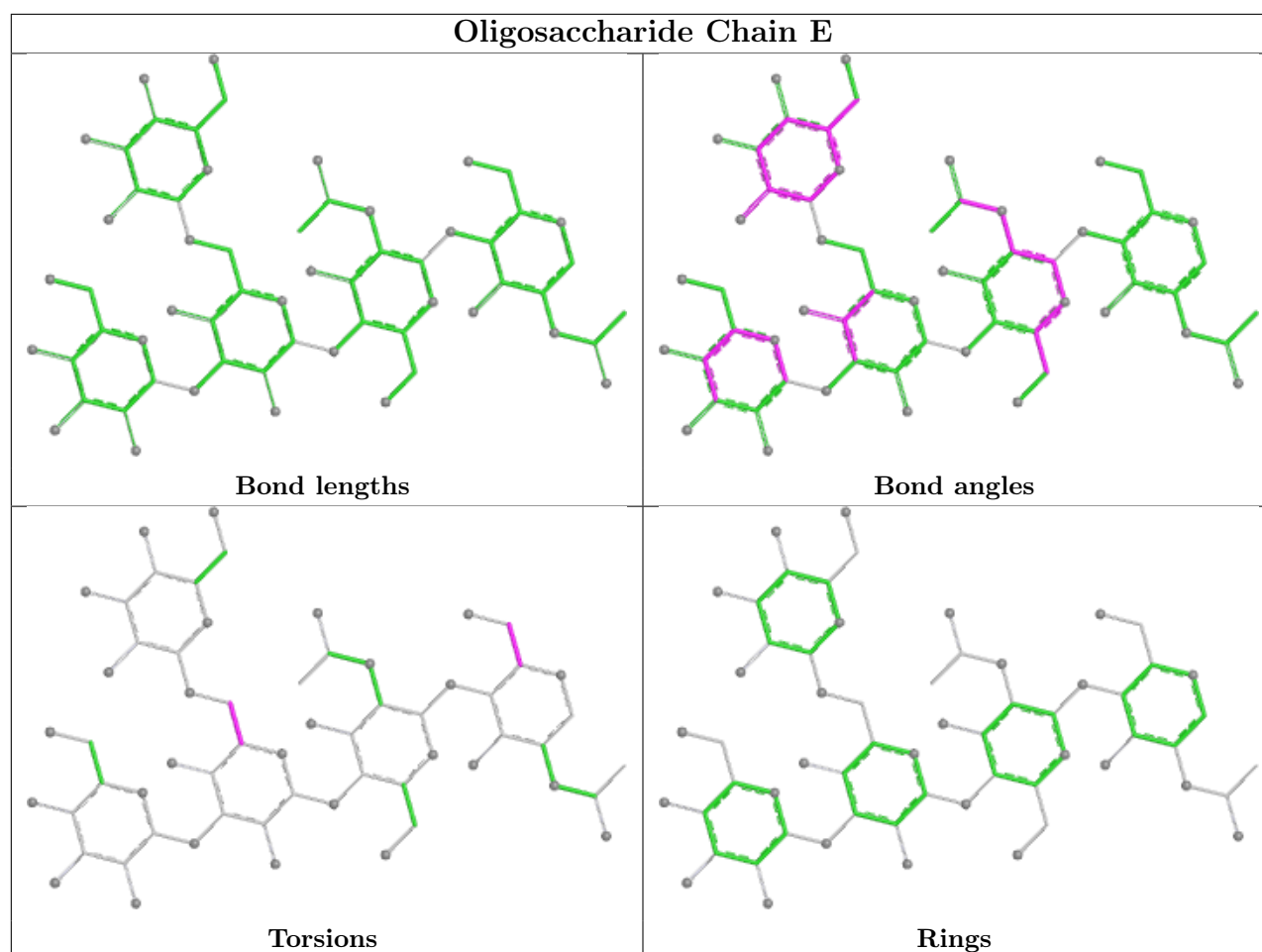
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	3	BMA	2	0
4	E	1	NAG	1	0
4	E	5	BMA	2	0

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









5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 6 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
7	NAG	B	1774	1	14,14,15	1.55	1 (7%)	17,19,21	2.67	6 (35%)
8	JW7	B	2000	-	28,28,28	2.12	4 (14%)	34,38,38	2.08	13 (38%)
7	NAG	A	1770	1	14,14,15	1.22	2 (14%)	17,19,21	2.15	5 (29%)
7	NAG	A	1771	1	14,14,15	1.89	3 (21%)	17,19,21	3.44	8 (47%)
8	JW7	A	2000	-	28,28,28	1.94	6 (21%)	34,38,38	2.17	10 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	NAG	B	1775	1	14,14,15	0.73	0	17,19,21	1.43	2 (11%)
7	NAG	B	1772	-	14,14,15	0.79	1 (7%)	17,19,21	1.49	2 (11%)
7	NAG	B	1773	1	14,14,15	1.06	1 (7%)	17,19,21	2.85	5 (29%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	B	1774	1	1/1/5/7	4/6/23/26	0/1/1/1
8	JW7	B	2000	-	-	5/8/20/20	0/4/4/4
7	NAG	A	1770	1	1/1/5/7	2/6/23/26	0/1/1/1
7	NAG	A	1771	1	1/1/5/7	1/6/23/26	0/1/1/1
8	JW7	A	2000	-	-	4/8/20/20	0/4/4/4
7	NAG	B	1775	1	-	2/6/23/26	0/1/1/1
7	NAG	B	1772	-	-	1/6/23/26	0/1/1/1
7	NAG	B	1773	1	-	2/6/23/26	0/1/1/1

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	B	2000	JW7	OAA-CAW	6.43	1.37	1.23
8	A	2000	JW7	OAA-CAW	6.21	1.36	1.23
8	B	2000	JW7	CAS-NAY	-5.42	1.33	1.43
8	B	2000	JW7	CAV-CAU	-5.27	1.39	1.46
7	A	1771	NAG	C1-C2	5.26	1.59	1.52

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	1773	NAG	C1-O5-C5	8.55	123.64	112.19
7	A	1771	NAG	C2-N2-C7	6.83	132.06	122.90
7	B	1774	NAG	C1-O5-C5	6.51	120.91	112.19
7	A	1771	NAG	O5-C1-C2	-6.24	101.64	111.29
8	A	2000	JW7	CAH-CAT-NAQ	-6.09	120.95	125.78

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	A	1770	NAG	C1
7	A	1771	NAG	C1
7	B	1774	NAG	C1

5 of 21 torsion outliers are listed below:

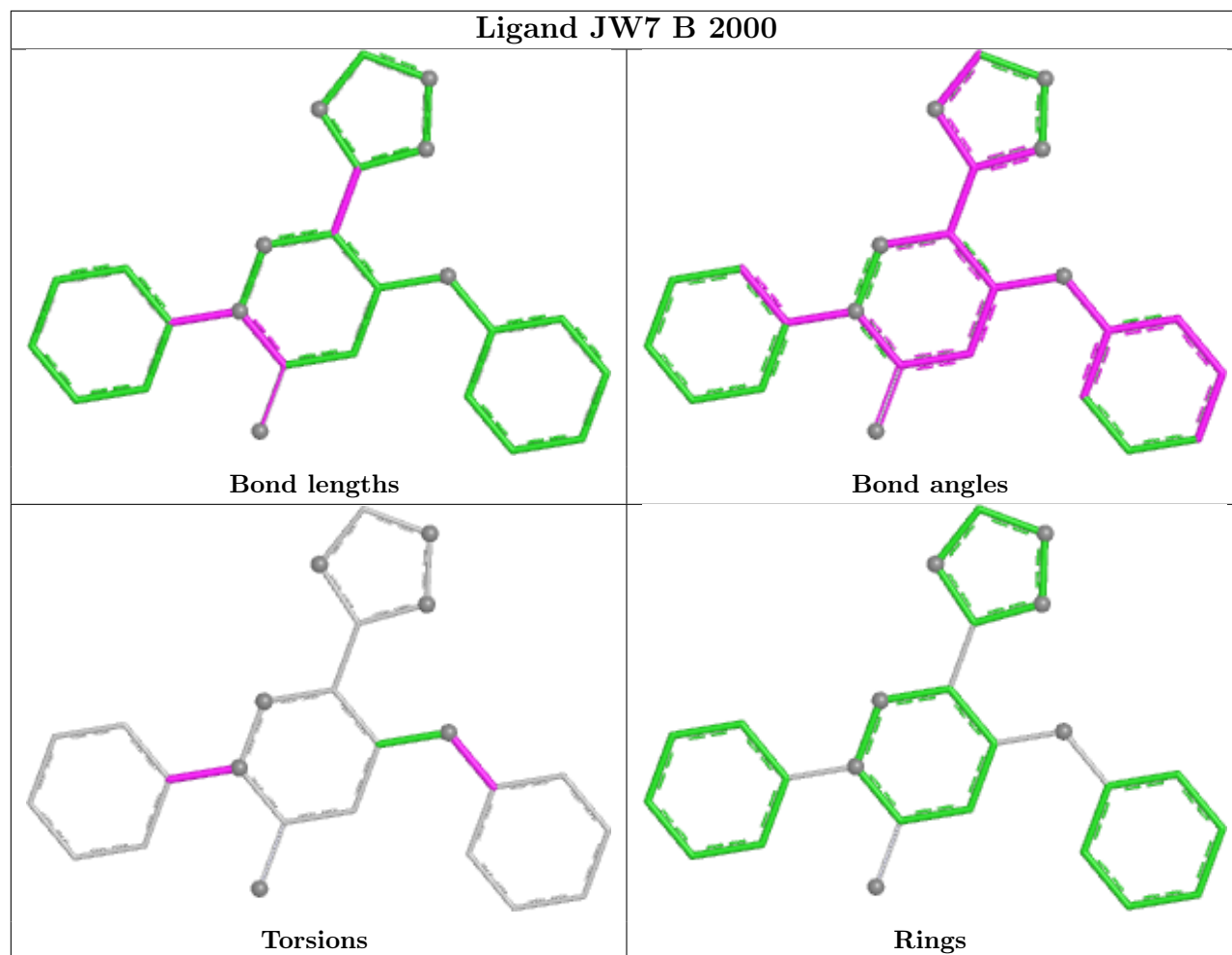
Mol	Chain	Res	Type	Atoms
7	A	1770	NAG	C4-C5-C6-O6
8	A	2000	JW7	CAE-CAS-NAY-CAW
8	A	2000	JW7	CAF-CAS-NAY-CAW
8	B	2000	JW7	CAE-CAS-NAY-CAW
8	B	2000	JW7	CAF-CAS-NAY-CAW

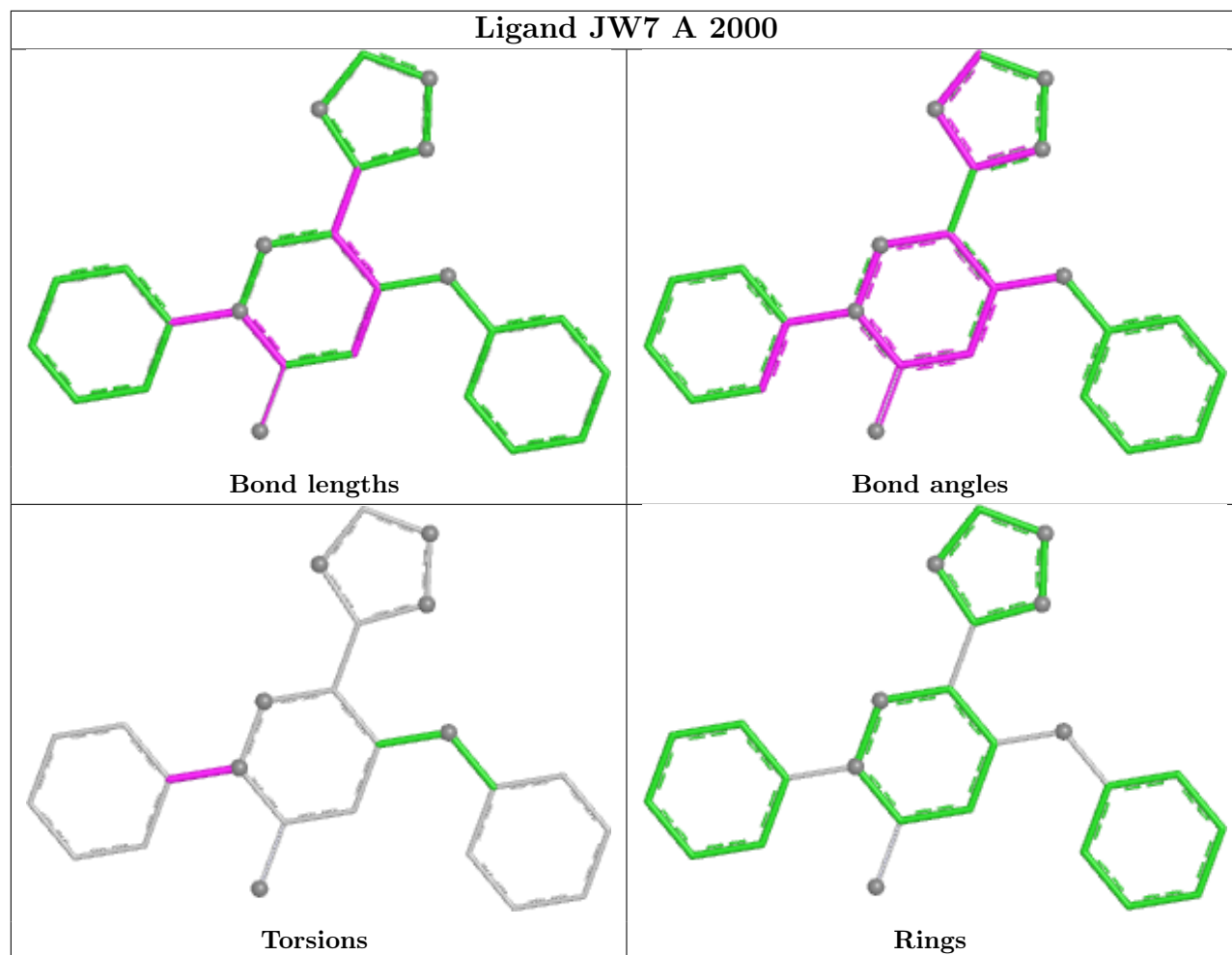
There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	1774	NAG	1	0
8	B	2000	JW7	6	0
8	A	2000	JW7	4	0
7	B	1773	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 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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	710/737 (96%)	-0.32	13 (1%) 67 58	39, 58, 82, 138	0
1	B	704/737 (95%)	-0.22	15 (2%) 63 54	38, 59, 91, 153	0
All	All	1414/1474 (95%)	-0.27	28 (1%) 65 56	38, 59, 86, 153	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	747	ALA	5.3
1	B	57	SER	5.0
1	B	746	ALA	4.2
1	B	747	ALA	3.8
1	A	54	PRO	3.5

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

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

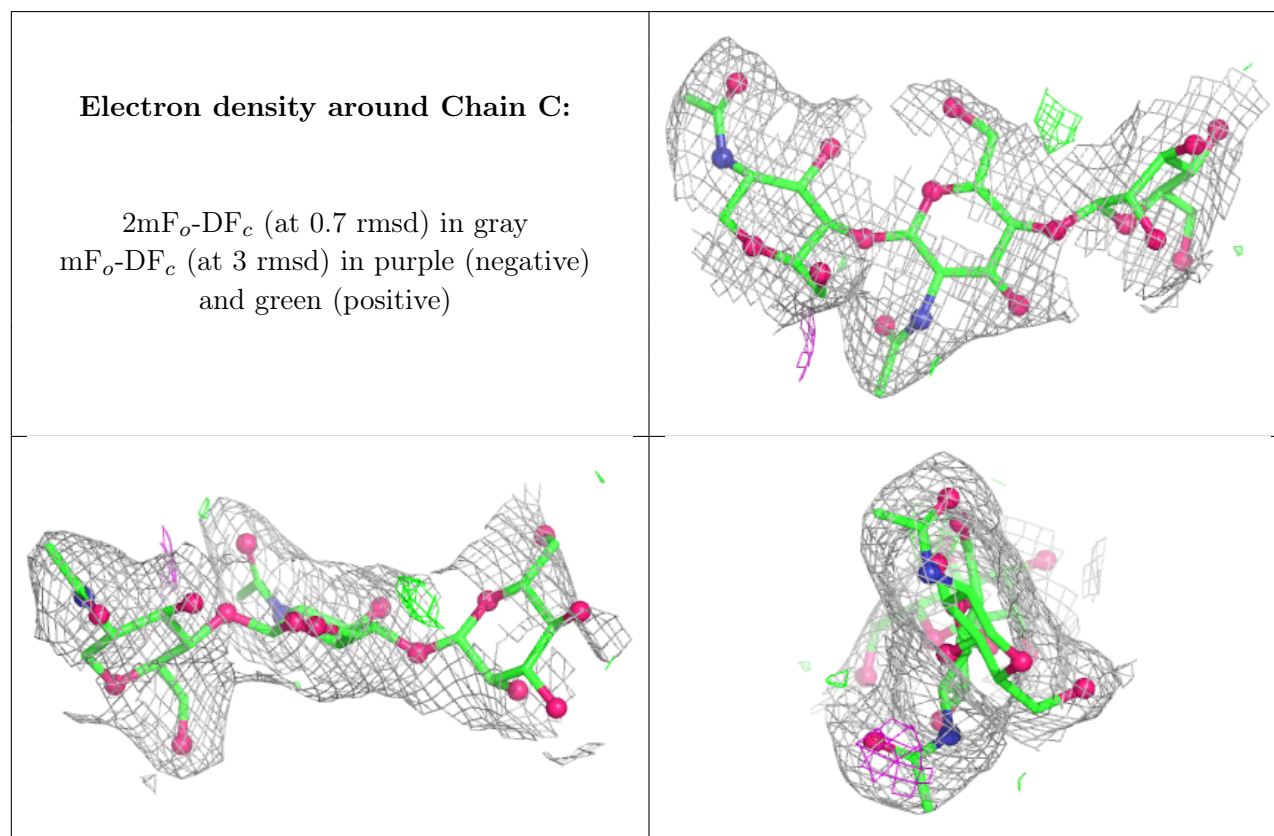
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	TPQ	A	471	14/15	0.96	0.07	43,48,52,54	0
1	TPQ	B	471	14/15	0.96	0.07	44,53,56,59	0

6.3 Carbohydrates [i](#)

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

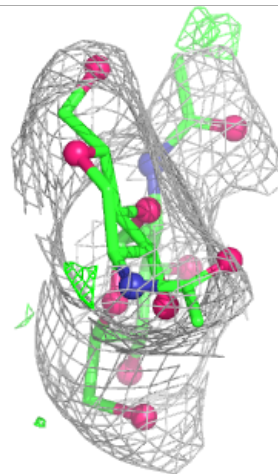
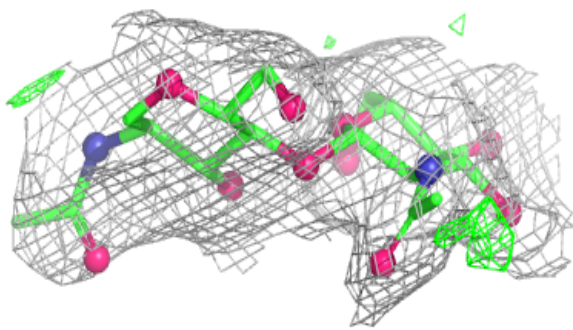
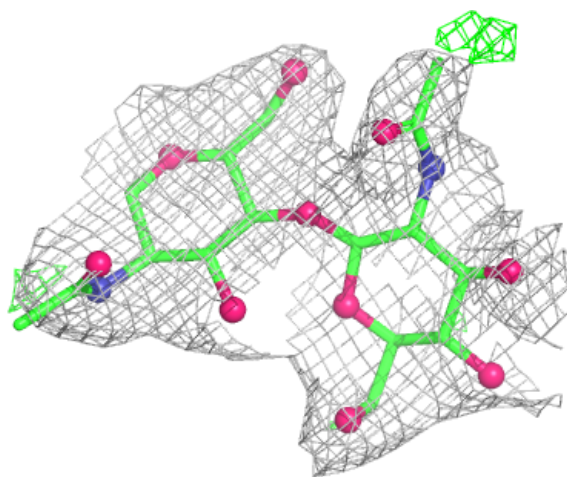
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	BMA	E	5	11/12	0.57	0.16	116,140,161,163	0
4	BMA	E	3	11/12	0.73	0.13	116,126,135,160	0
3	NAG	F	2	14/15	0.74	0.17	105,119,128,130	0
2	BMA	C	3	11/12	0.76	0.11	110,116,124,128	0
4	MAN	E	4	11/12	0.78	0.09	112,126,141,142	0
4	NAG	E	2	14/15	0.81	0.14	67,101,115,119	0
3	NAG	D	2	14/15	0.90	0.13	91,112,124,126	0
3	NAG	F	1	14/15	0.94	0.10	70,86,93,104	0
2	NAG	C	2	14/15	0.94	0.07	63,76,95,112	0
2	NAG	C	1	14/15	0.96	0.06	65,71,75,77	0
4	NAG	E	1	14/15	0.96	0.07	49,56,59,66	0
3	NAG	D	1	14/15	0.96	0.08	72,83,99,101	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.



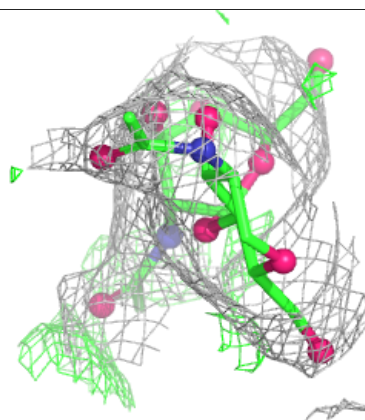
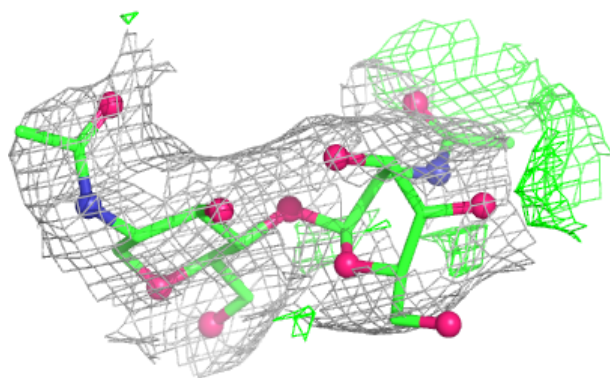
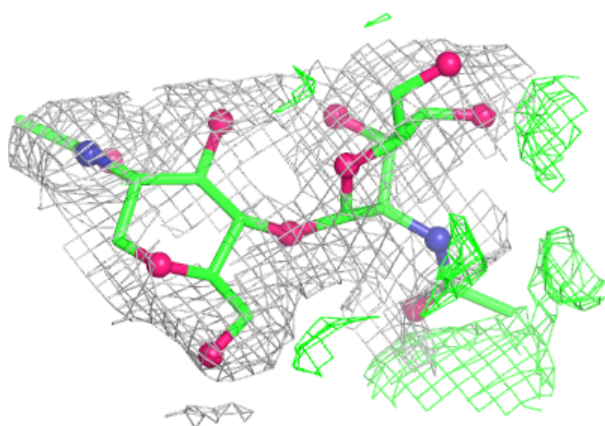
Electron density around Chain D:

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

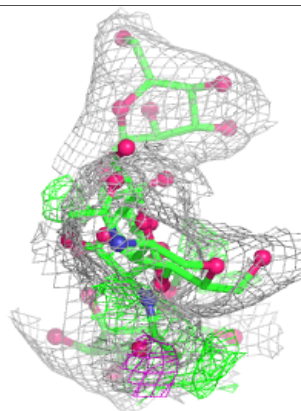
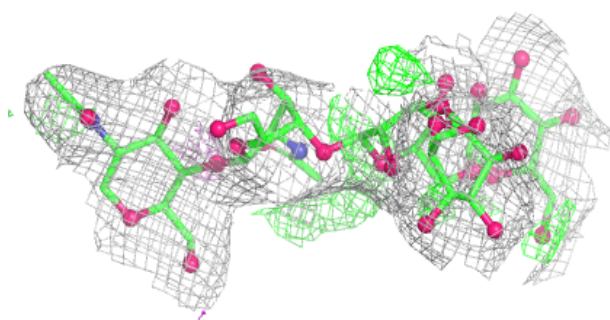
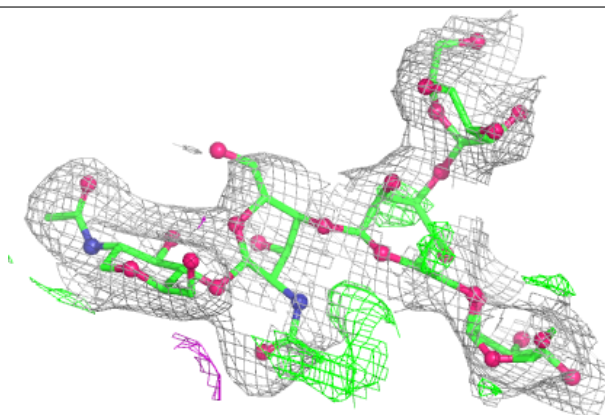


Electron density around Chain F:

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

**Electron density around Chain E:**

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



6.4 Ligands

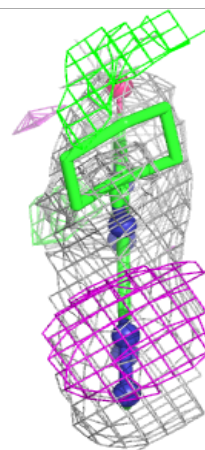
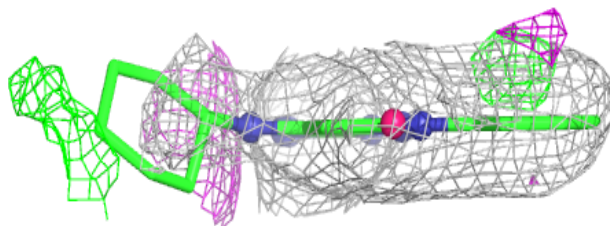
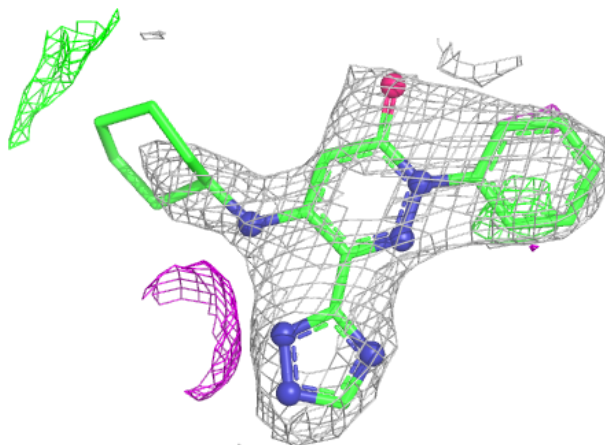
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

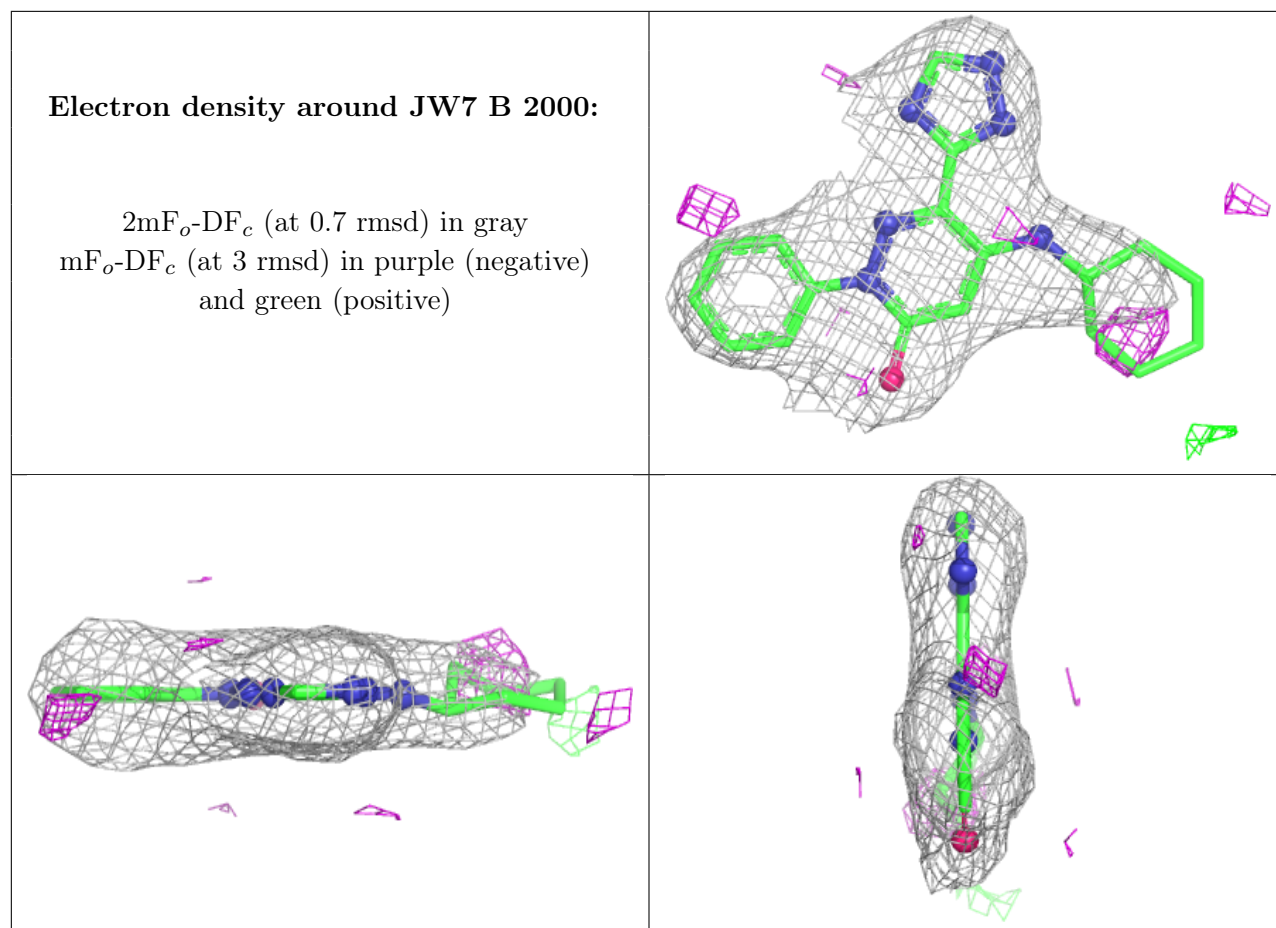
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	NAG	B	1774	14/15	0.45	0.17	94,121,135,136	0
7	NAG	A	1771	14/15	0.66	0.14	77,97,104,105	0
7	NAG	B	1772	14/15	0.67	0.16	103,132,140,141	0
7	NAG	B	1775	14/15	0.74	0.13	72,97,107,109	0
7	NAG	A	1770	14/15	0.75	0.15	74,93,115,115	0
7	NAG	B	1773	14/15	0.84	0.13	87,129,136,136	0
8	JW7	A	2000	25/25	0.92	0.19	65,90,143,148	0
6	CA	A	1764	1/1	0.94	0.07	59,59,59,59	0
8	JW7	B	2000	25/25	0.95	0.11	46,54,97,99	0
6	CA	A	1763	1/1	0.98	0.04	51,51,51,51	0
6	CA	B	1764	1/1	0.98	0.07	60,60,60,60	0
6	CA	B	1763	1/1	0.99	0.02	51,51,51,51	0
5	CU	A	1762	1/1	1.00	0.07	54,54,54,54	0
5	CU	B	1762	1/1	1.00	0.02	54,54,54,54	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 JW7 A 2000:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.