



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 01:26 AM UTC

PDB ID : 7BFZ / pdb_00007bfz
Title : X-ray structure of human prostate-specific membrane antigen(PSMA) in complex with a inhibitor Glu-490
Authors : Rakhimbekova, A.; Motlova, L.; Barinka, C.
Deposited on : 2021-01-05
Resolution : 1.73 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

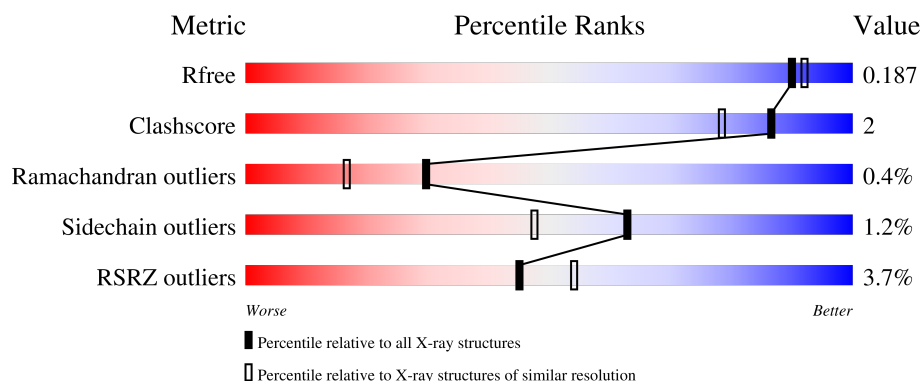
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.73 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.



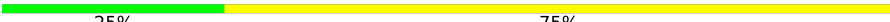
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1187 (1.74-1.74)
Clashscore	190562	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)
RSRZ outliers	180081	1188 (1.74-1.74)

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	707	4% 91% 8%
2	B	3	100%
2	F	3	33% 67%
3	C	5	20% 80%
4	D	2	100%

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Mol	Chain	Length	Quality of chain
5	E	4	 25% 75%

2 Entry composition [i](#)

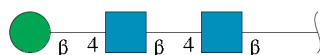
There are 14 unique types of molecules in this entry. The entry contains 6622 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glutamate carboxypeptidase 2.

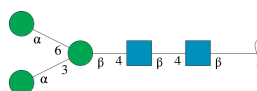
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	694	Total	C	N	O	S	0	63	0
			5836	3753	968	1093	22			

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

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-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.



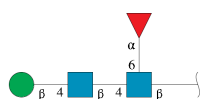
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 4 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
4	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Zn	0	0
			2	2		

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 8 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

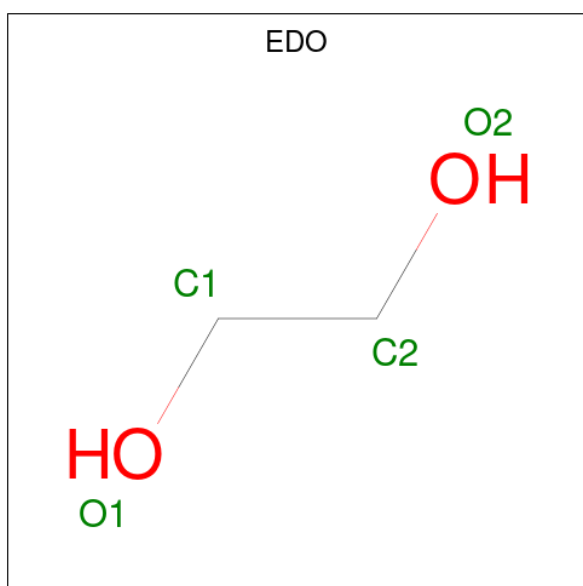
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Cl	0	0
			1	1		

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 10 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



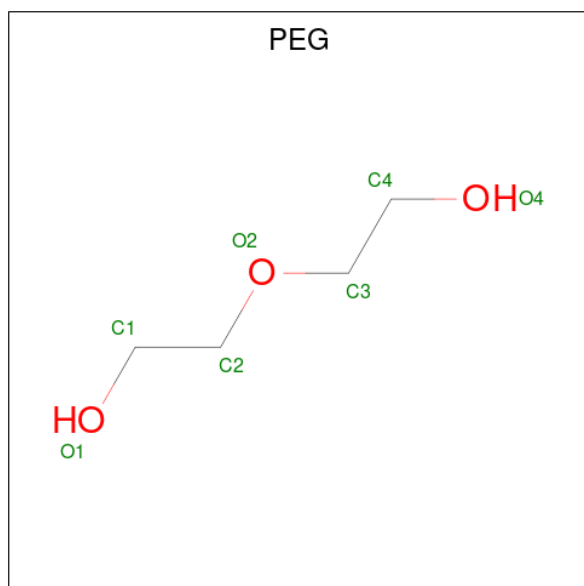
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O		
			4	2	2	0	0
10	A	1	Total	C	O		
			4	2	2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 11 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).

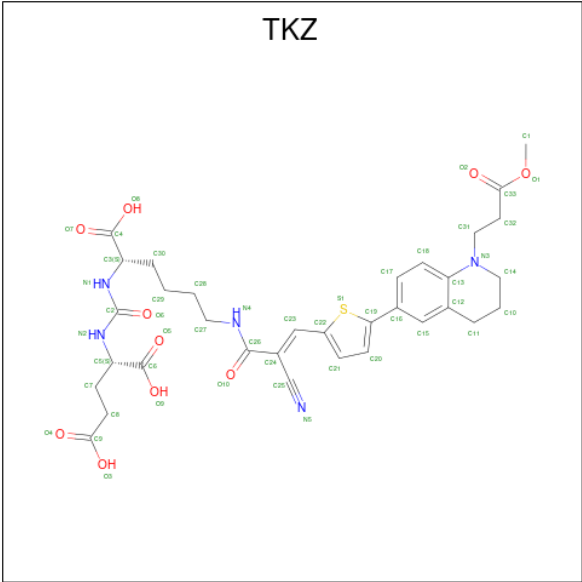


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 12 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	2	Total	Na	0	0
			2	2		

- Molecule 13 is (((S)-1-carboxy-5-((E)-2-cyano-3-(5-(1-(3-methoxy-3-oxopropyl)-1,2,3,4-tetrahydroquinolin-6-yl)thiophen-2-yl)acrylamido)pentyl)carbamoyl)-L-glutamic acid (CCD ID: TKZ) (formula: $C_{33}H_{39}N_5O_{10}S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
13	A	1	Total	C	N	O	S	0	0
			49	33	5	10	1		

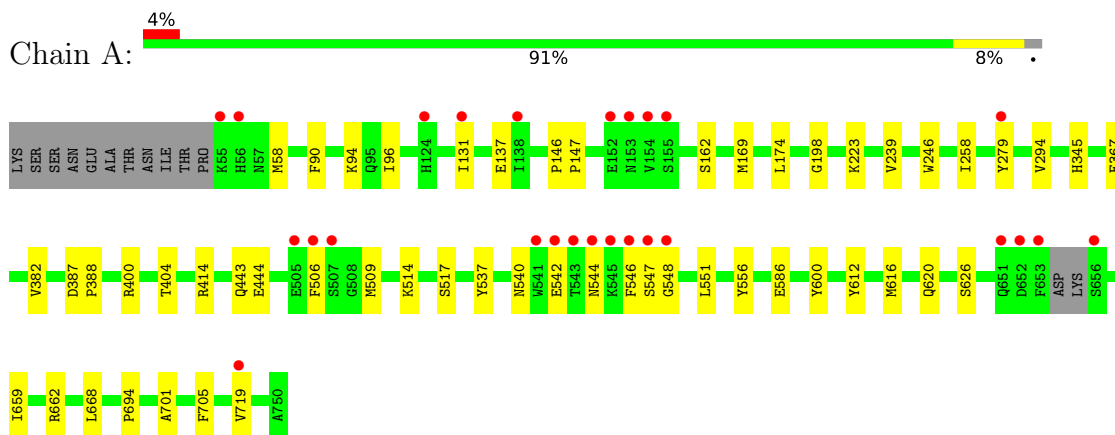
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	467	Total	O	0	1
			468	468		

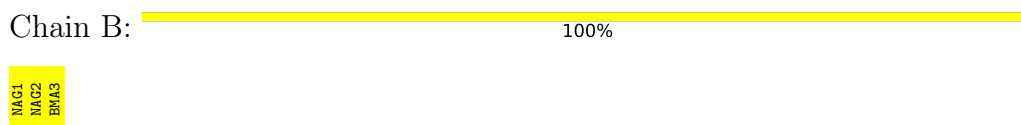
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Glutamate carboxypeptidase 2



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



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



- Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-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



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

Chain D:  100%

MAG1
MAG2

- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  25% 75%

MAG1
MAG2
BMA3
FUC4

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	101.54Å 130.10Å 158.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.96 – 1.73 46.96 – 1.73	Depositor EDS
% Data completeness (in resolution range)	99.5 (46.96-1.73) 99.6 (46.96-1.73)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 1.73Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.163 , 0.183 0.171 , 0.187	Depositor DCC
R_{free} test set	2101 reflections (1.93%)	wwPDB-VP
Wilson B-factor (Å ²)	23.9	Xtriage
Anisotropy	0.576	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 41.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6622	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% 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: PEG, TKZ, ZN, MAN, FUC, NAG, NA, EDO, BMA, CL, CA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.04	2/6177 (0.0%)	0.97	7/8361 (0.1%)

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	705	PHE	N-CA	7.04	1.51	1.46
1	A	414	ARG	N-CA	5.49	1.52	1.45

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	146	PRO	CA-C-N	-6.67	114.86	119.66
1	A	146	PRO	C-N-CA	-6.67	114.86	119.66
1	A	701	ALA	CA-C-N	-5.76	115.35	121.45
1	A	701	ALA	C-N-CA	-5.76	115.35	121.45
1	A	540	ASN	N-CA-C	-5.33	101.10	109.25
1	A	547	SER	N-CA-C	-5.32	101.09	109.50
1	A	147	PRO	O-C-N	5.17	123.58	121.15

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	546	PHE	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	5836	0	5757	26	0
2	B	39	0	34	0	0
2	F	39	0	34	0	0
3	C	61	0	52	0	0
4	D	28	0	25	0	0
5	E	49	0	43	0	0
6	A	2	0	0	0	0
7	A	1	0	0	0	0
8	A	1	0	0	0	0
9	A	28	0	26	1	0
10	A	12	0	18	0	0
11	A	7	0	10	0	0
12	A	2	0	0	0	0
13	A	49	0	0	1	0
14	A	468	0	0	3	0
All	All	6622	0	5999	26	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 2.

All (26) 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:620[A]:GLN:NE2	14:A:901:HOH:O	2.21	0.72
1:A:58:MET:CE	1:A:586:GLU:HG2	2.32	0.59
1:A:400:ARG:O	1:A:404[B]:THR:HG23	2.02	0.58
1:A:162:SER:HB3	1:A:258[B]:ILE:HD13	1.86	0.58
1:A:612:TYR:CZ	1:A:616:MET:HG3	2.39	0.57
1:A:131[B]:ILE:O	1:A:131[B]:ILE:HG23	2.07	0.55
1:A:90:PHE:CE2	1:A:94:LYS:HE2	2.46	0.50
1:A:58:MET:HE1	1:A:586:GLU:HG2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96[B]:ILE:HD13	14:A:942:HOH:O	2.12	0.48
1:A:367:GLU:OE1	1:A:662[A]:ARG:NH1	2.42	0.48
1:A:131[B]:ILE:O	1:A:131[B]:ILE:CG2	2.63	0.47
1:A:169:MET:HE3	1:A:345:HIS:HD2	1.80	0.46
1:A:58:MET:HE2	1:A:586:GLU:HG2	1.97	0.45
1:A:626[A]:SER:HA	14:A:1082:HOH:O	2.16	0.45
1:A:258[A]:ILE:HD13	1:A:294:VAL:HB	1.99	0.45
1:A:246:TRP:CD1	9:A:806:NAG:H83	2.52	0.44
1:A:131[A]:ILE:HG22	1:A:137:GLU:HG2	1.99	0.44
1:A:659[B]:ILE:HD13	1:A:659[B]:ILE:HA	1.67	0.44
1:A:506:PHE:HB2	1:A:509[A]:MET:HG3	2.00	0.43
1:A:198:GLY:O	1:A:223:LYS:HE2	2.18	0.43
1:A:551:LEU:HD22	1:A:556:TYR:HB2	2.00	0.42
1:A:514[A]:LYS:HG3	13:A:813:TKZ:C1	2.49	0.42
1:A:387:ASP:HA	1:A:388:PRO:HA	1.89	0.41
1:A:443[B]:GLN:HG3	1:A:444:GLU:CD	2.46	0.41
1:A:517[A]:SER:HB2	1:A:694:PRO:HG3	2.02	0.41

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	754/707 (107%)	735 (98%)	16 (2%)	3 (0%)	30 16

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	544	ASN
1	A	382	VAL
1	A	548	GLY

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	656/603 (109%)	647 (99%)	9 (1%)	59 41

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	174	LEU
1	A	239[A]	VAL
1	A	239[B]	VAL
1	A	537	TYR
1	A	542	GLU
1	A	600	TYR
1	A	668[A]	LEU
1	A	668[B]	LEU
1	A	719	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	95	GLN
1	A	136	ASN
1	A	544	ASN

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 ⓘ

17 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	B	1	1,2	14,14,15	0.34	0	17,19,21	1.08	1 (5%)
2	NAG	B	2	2	14,14,15	0.57	0	17,19,21	1.53	3 (17%)
2	BMA	B	3	2	11,11,12	0.68	0	15,15,17	0.99	1 (6%)
3	NAG	C	1	1,3	14,14,15	0.66	0	17,19,21	1.32	2 (11%)
3	NAG	C	2	3	14,14,15	0.48	0	17,19,21	0.92	1 (5%)
3	BMA	C	3	3	11,11,12	0.51	0	15,15,17	0.96	1 (6%)
3	MAN	C	4	3	11,11,12	0.53	0	15,15,17	0.97	1 (6%)
3	MAN	C	5	3	11,11,12	0.73	0	15,15,17	0.73	0
4	NAG	D	1	1,4	14,14,15	0.70	0	17,19,21	1.43	2 (11%)
4	NAG	D	2	4	14,14,15	0.74	0	17,19,21	1.32	2 (11%)
5	NAG	E	1	1,5	14,14,15	0.71	0	17,19,21	1.42	2 (11%)
5	NAG	E	2	5	14,14,15	0.58	0	17,19,21	1.08	2 (11%)
5	BMA	E	3	5	11,11,12	0.57	0	15,15,17	1.31	3 (20%)
5	FUC	E	4	5	10,10,11	0.79	0	14,14,16	0.66	0
2	NAG	F	1	1,2	14,14,15	0.53	0	17,19,21	0.96	1 (5%)
2	NAG	F	2	2	14,14,15	0.45	0	17,19,21	0.64	0
2	BMA	F	3	2	11,11,12	0.59	0	15,15,17	1.22	2 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	2/6/23/26	0/1/1/1
2	BMA	B	3	2	-	0/2/19/22	0/1/1/1
3	NAG	C	1	1,3	-	1/6/23/26	0/1/1/1

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

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	NAG	C2-N2-C7	4.17	128.49	122.90
4	D	1	NAG	C1-O5-C5	3.65	117.08	112.19
5	E	1	NAG	C2-N2-C7	3.63	127.76	122.90
3	C	1	NAG	C1-O5-C5	3.56	116.96	112.19
2	F	3	BMA	C1-O5-C5	3.52	116.90	112.19
4	D	2	NAG	C2-N2-C7	2.93	126.83	122.90
5	E	3	BMA	C1-O5-C5	2.90	116.07	112.19
5	E	3	BMA	C3-C4-C5	2.87	115.43	110.23
5	E	2	NAG	C2-N2-C7	2.84	126.70	122.90
4	D	1	NAG	C4-C3-C2	2.77	115.07	111.02
3	C	1	NAG	O5-C1-C2	-2.63	107.22	111.29
4	D	2	NAG	C4-C3-C2	2.56	114.77	111.02
5	E	1	NAG	C8-C7-N2	2.52	120.30	116.12
3	C	3	BMA	C1-O5-C5	2.48	115.51	112.19
2	B	2	NAG	C4-C3-C2	2.39	114.51	111.02
3	C	2	NAG	C1-O5-C5	2.37	115.36	112.19
2	B	2	NAG	C8-C7-N2	2.32	119.97	116.12
2	F	3	BMA	C3-C4-C5	2.17	114.17	110.23
5	E	2	NAG	C4-C3-C2	2.14	114.16	111.02
3	C	4	MAN	C1-O5-C5	2.12	115.03	112.19
2	B	1	NAG	C4-C3-C2	2.08	114.06	111.02
5	E	3	BMA	C2-C3-C4	2.07	114.49	110.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3	BMA	C3-C4-C5	2.03	113.91	110.23
2	F	1	NAG	C2-N2-C7	-2.03	120.18	122.90

There are no chirality outliers.

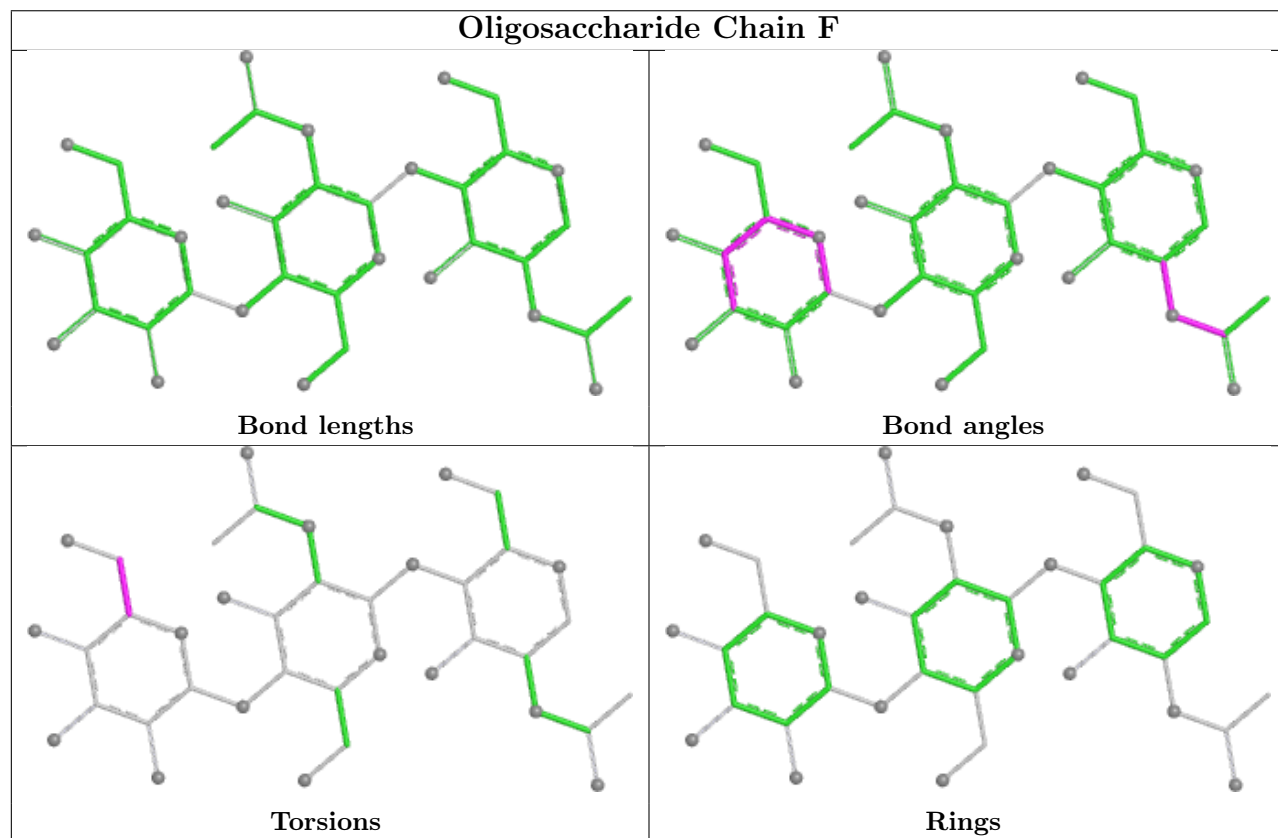
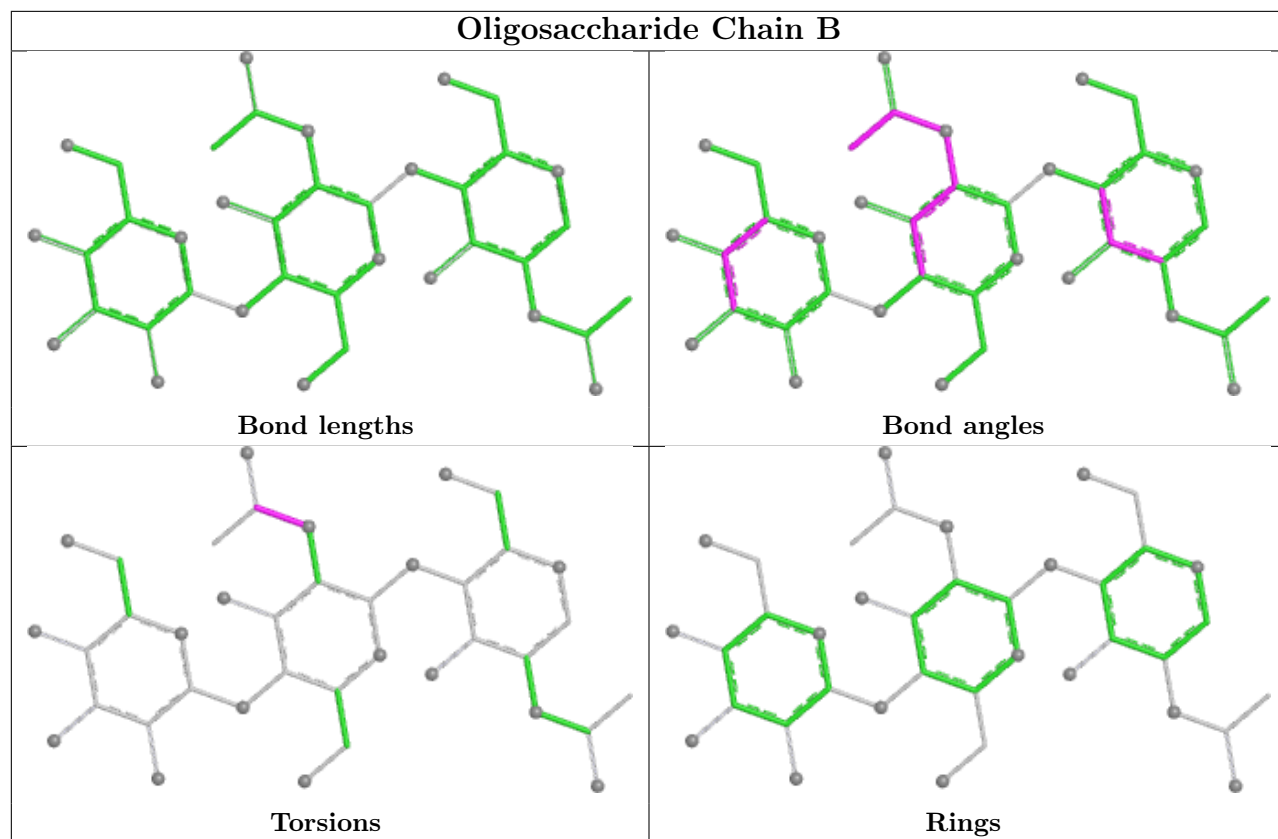
All (15) torsion outliers are listed below:

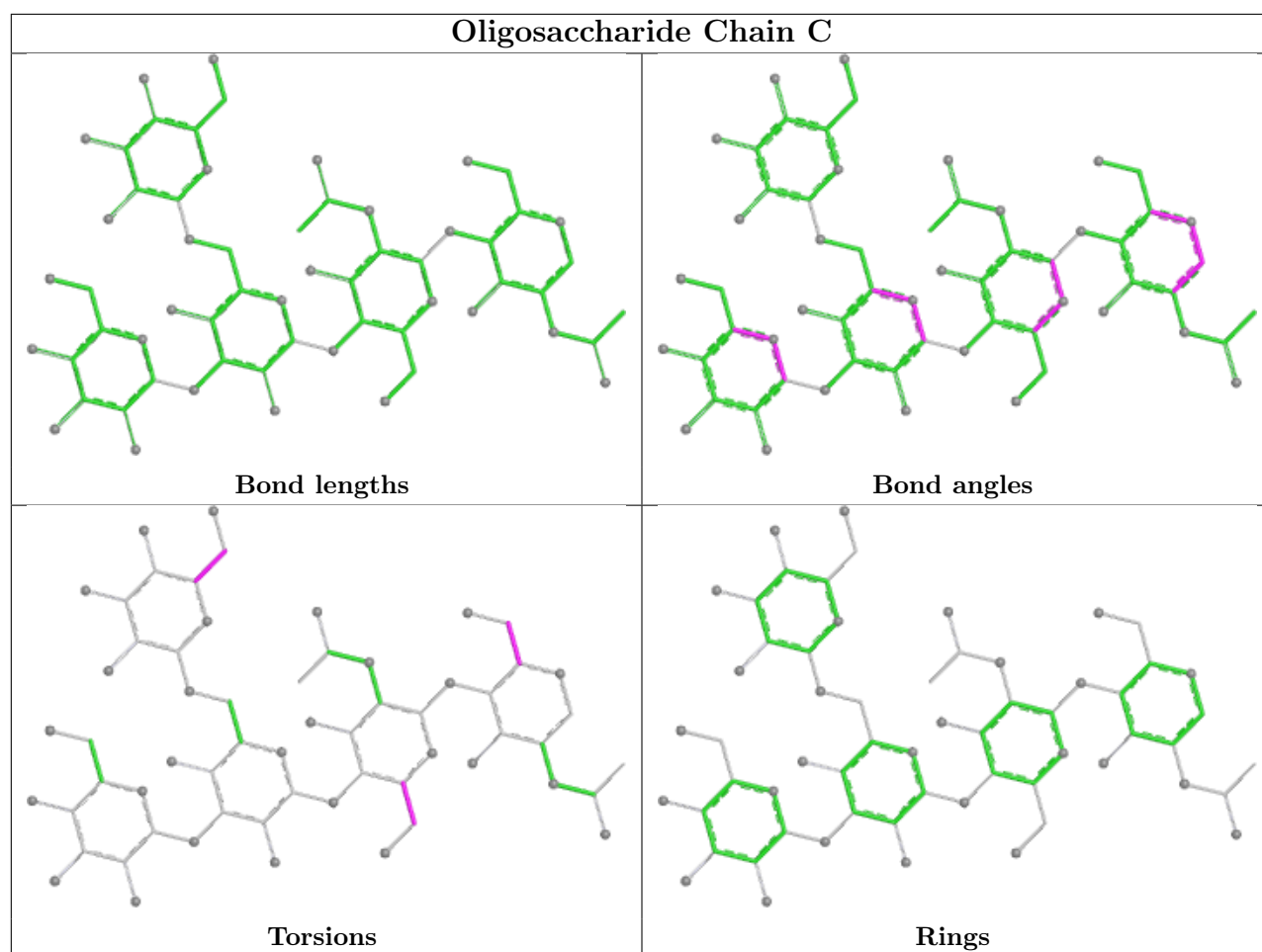
Mol	Chain	Res	Type	Atoms
3	C	5	MAN	O5-C5-C6-O6
5	E	3	BMA	O5-C5-C6-O6
3	C	5	MAN	C4-C5-C6-O6
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2
5	E	1	NAG	C8-C7-N2-C2
5	E	1	NAG	O7-C7-N2-C2
5	E	3	BMA	C4-C5-C6-O6
3	C	2	NAG	C4-C5-C6-O6
2	F	3	BMA	C4-C5-C6-O6
5	E	2	NAG	C4-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6
5	E	2	NAG	O5-C5-C6-O6
3	C	1	NAG	C4-C5-C6-O6
2	F	3	BMA	O5-C5-C6-O6

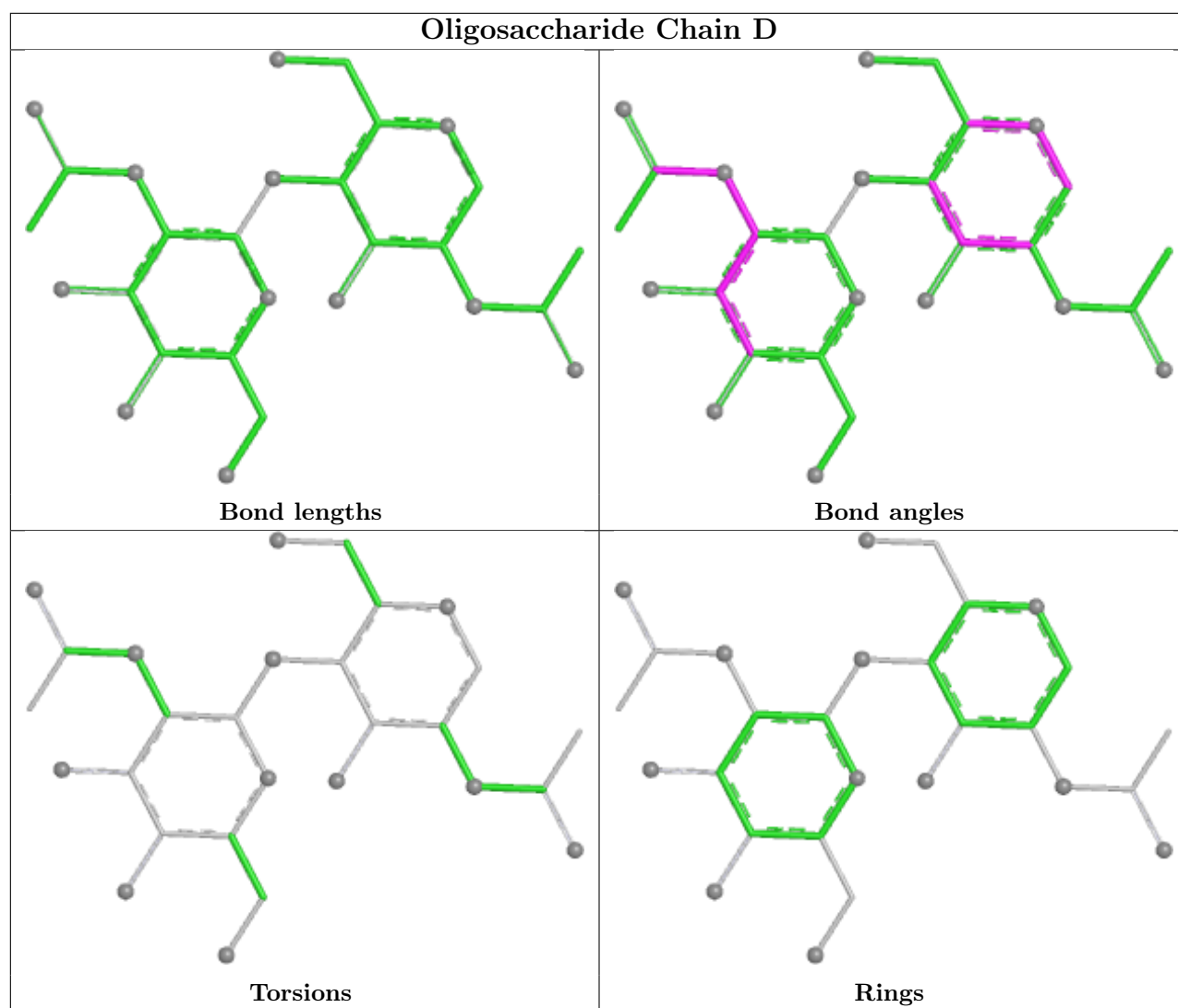
There are no ring outliers.

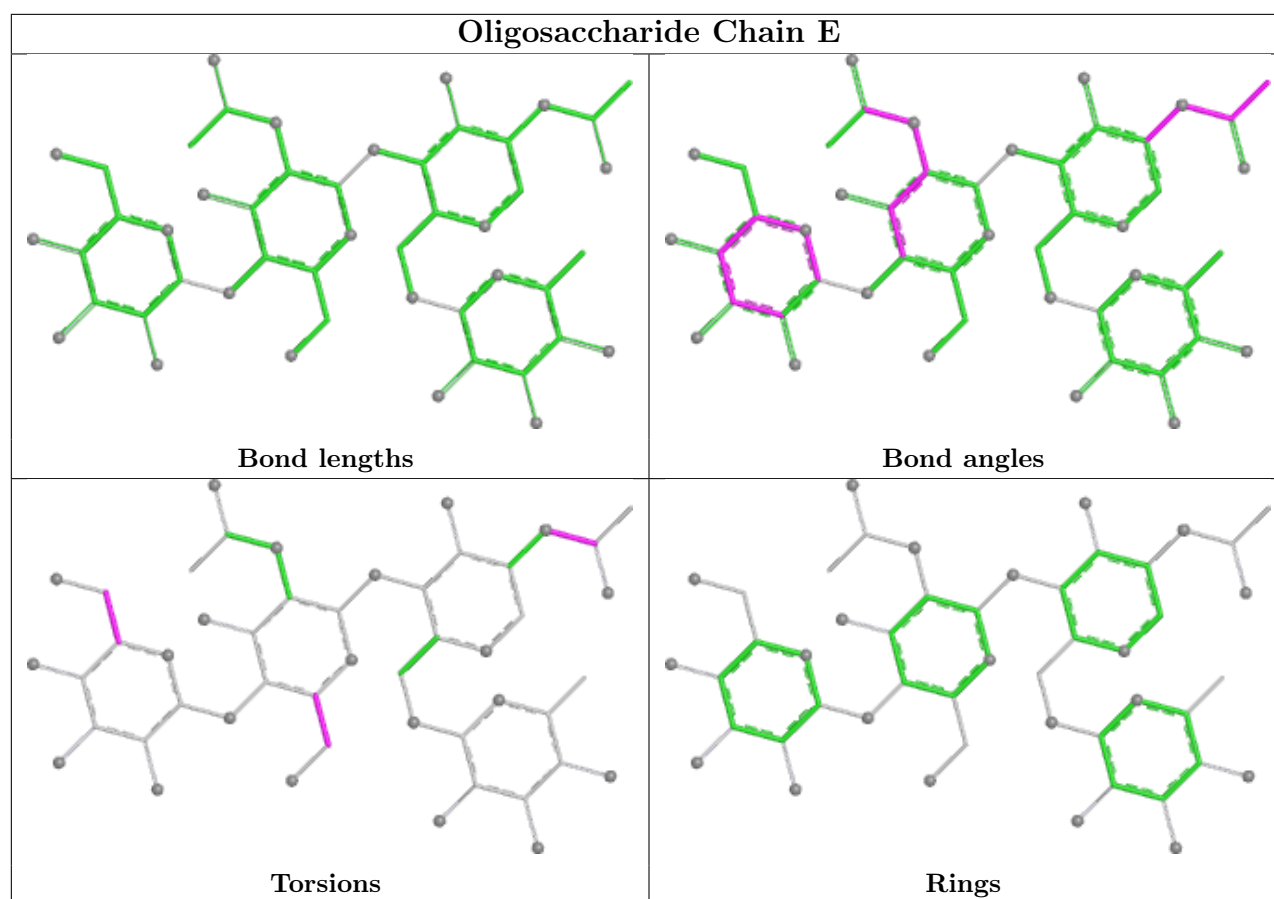
No monomer is involved in short contacts.

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









5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 6 are monoatomic - leaving 7 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
13	TKZ	A	813	6	51,51,51	0.99	1 (1%)	68,68,68	1.12	4 (5%)
9	NAG	A	806	1	14,14,15	0.91	1 (7%)	17,19,21	1.40	3 (17%)
9	NAG	A	805	1	14,14,15	0.68	0	17,19,21	1.39	2 (11%)
10	EDO	A	808	-	3,3,3	0.39	0	2,2,2	0.60	0
10	EDO	A	807	-	3,3,3	0.40	0	2,2,2	0.50	0
11	PEG	A	809	-	6,6,6	0.46	0	5,5,5	0.29	0
10	EDO	A	810	-	3,3,3	0.44	0	2,2,2	0.43	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	TKZ	A	813	6	-	13/49/60/60	0/3/3/3
9	NAG	A	806	1	-	0/6/23/26	0/1/1/1
9	NAG	A	805	1	-	0/6/23/26	0/1/1/1
10	EDO	A	808	-	-	0/1/1/1	-
10	EDO	A	807	-	-	1/1/1/1	-
11	PEG	A	809	-	-	1/4/4/4	-
10	EDO	A	810	-	-	0/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	813	TKZ	C24-C26	-4.78	1.41	1.50
9	A	806	NAG	C1-C2	2.04	1.55	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	A	813	TKZ	C12-C13-N3	-5.03	117.73	121.60
9	A	806	NAG	C1-O5-C5	3.98	117.52	112.19
9	A	805	NAG	C1-O5-C5	3.89	117.40	112.19
13	A	813	TKZ	C24-C26-N4	3.04	119.89	116.86
9	A	805	NAG	O5-C5-C6	2.50	112.53	107.66
9	A	806	NAG	O3-C3-C4	-2.43	104.64	110.38
13	A	813	TKZ	C24-C23-C22	-2.18	127.21	130.28
13	A	813	TKZ	C18-C13-N3	2.12	122.50	119.11
9	A	806	NAG	O5-C1-C2	-2.07	108.09	111.29

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	A	813	TKZ	C22-C23-C24-C25
13	A	813	TKZ	C22-C23-C24-C26
13	A	813	TKZ	C23-C24-C26-O10
13	A	813	TKZ	C32-C33-O1-C1
13	A	813	TKZ	S1-C22-C23-C24
13	A	813	TKZ	O2-C33-O1-C1

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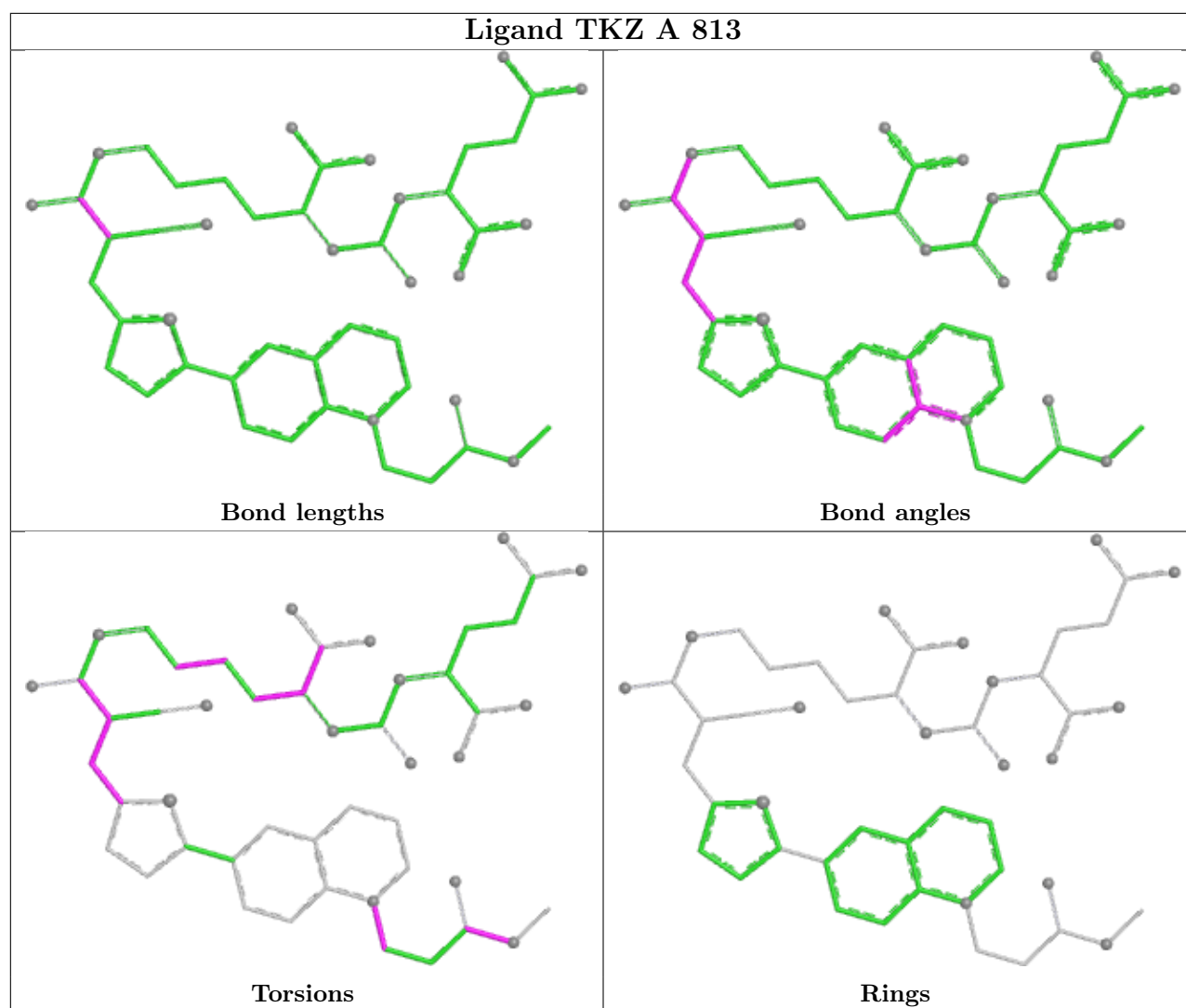
Mol	Chain	Res	Type	Atoms
13	A	813	TKZ	C21-C22-C23-C24
10	A	807	EDO	O1-C1-C2-O2
13	A	813	TKZ	C25-C24-C26-O10
13	A	813	TKZ	C32-C31-N3-C13
13	A	813	TKZ	C27-C28-C29-C30
13	A	813	TKZ	C4-C3-C30-C29
13	A	813	TKZ	C23-C24-C26-N4
11	A	809	PEG	O2-C3-C4-O4
13	A	813	TKZ	N1-C3-C4-O8

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	A	813	TKZ	1	0
9	A	806	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	694/707 (98%)	0.02	26 (3%)	45 54	11, 31, 53, 97	63 (9%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	546	PHE	11.2
1	A	656[A]	SER	6.2
1	A	543	THR	5.0
1	A	653	PHE	4.4
1	A	541	TRP	4.2
1	A	545	LYS	4.2
1	A	544	ASN	3.6
1	A	506	PHE	3.4
1	A	548	GLY	3.0
1	A	547	SER	3.0
1	A	542	GLU	2.6
1	A	154	VAL	2.6
1	A	153	ASN	2.6
1	A	155	SER	2.5
1	A	55	LYS	2.5
1	A	131[A]	ILE	2.3
1	A	138	ILE	2.3
1	A	651	GLN	2.3
1	A	124	HIS	2.3
1	A	279[A]	TYR	2.2
1	A	152	GLU	2.2
1	A	719	VAL	2.1
1	A	56	HIS	2.1
1	A	507	SER	2.1
1	A	652	ASP	2.1
1	A	505	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

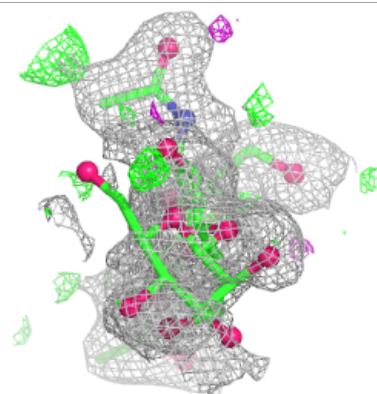
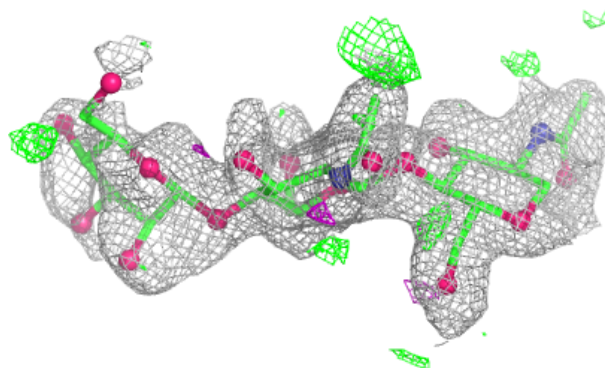
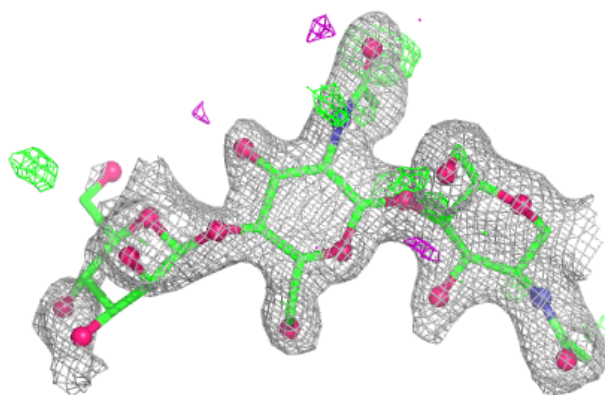
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	BMA	B	3	11/12	0.52	0.17	93,100,105,105	0
5	BMA	E	3	11/12	0.52	0.14	109,116,121,124	0
4	NAG	D	2	14/15	0.62	0.20	88,92,96,104	0
2	BMA	F	3	11/12	0.63	0.17	69,74,82,89	0
4	NAG	D	1	14/15	0.71	0.20	57,65,82,89	0
5	FUC	E	4	10/11	0.75	0.20	74,81,84,86	0
3	MAN	C	5	11/12	0.80	0.17	67,74,84,91	0
2	NAG	B	2	14/15	0.82	0.16	46,61,72,83	0
5	NAG	E	2	14/15	0.85	0.13	59,69,81,98	0
3	NAG	C	2	14/15	0.87	0.15	44,47,54,64	0
3	MAN	C	4	11/12	0.88	0.12	49,53,56,56	0
5	NAG	E	1	14/15	0.89	0.13	46,51,57,62	0
2	NAG	F	2	14/15	0.92	0.10	42,51,59,64	0
3	BMA	C	3	11/12	0.92	0.11	45,47,53,54	0
2	NAG	B	1	14/15	0.93	0.10	38,45,51,56	0
3	NAG	C	1	14/15	0.93	0.10	27,35,44,57	0
2	NAG	F	1	14/15	0.94	0.10	34,37,40,48	0

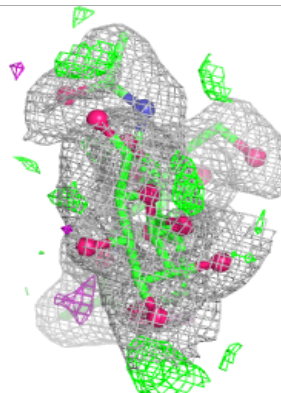
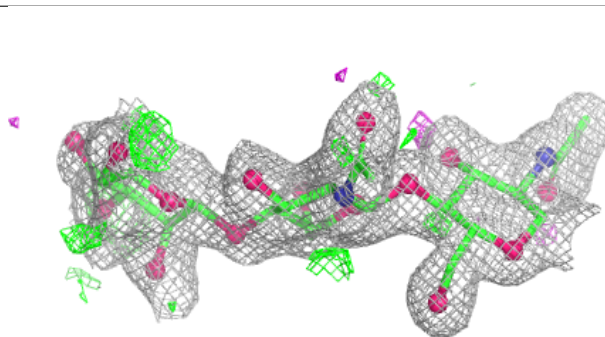
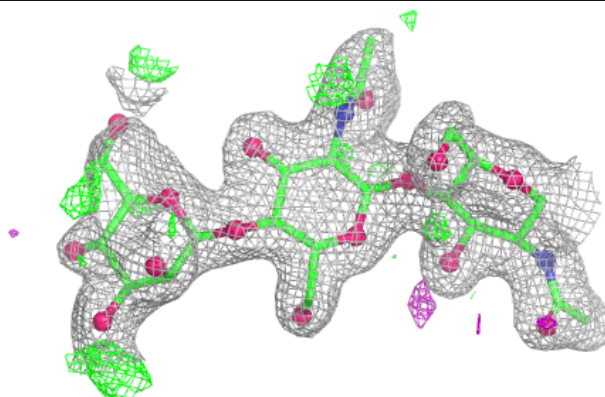
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain B:

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

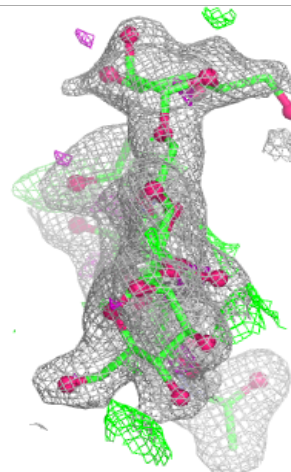
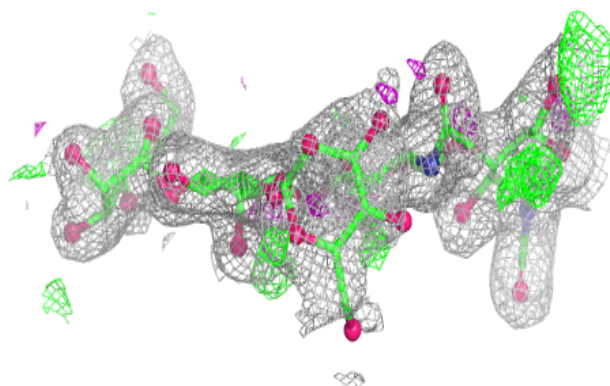
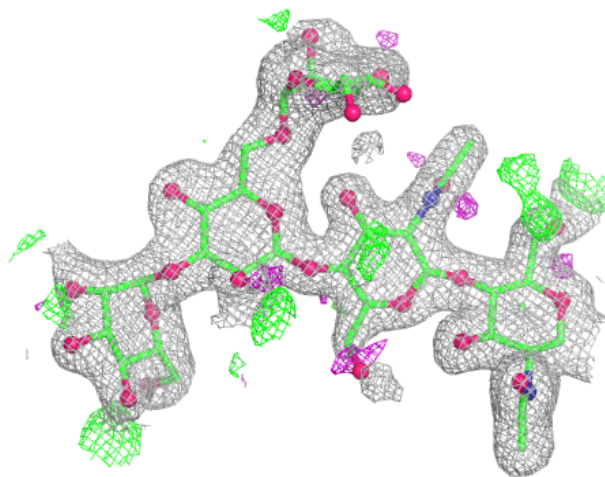
**Electron density around Chain F:**

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



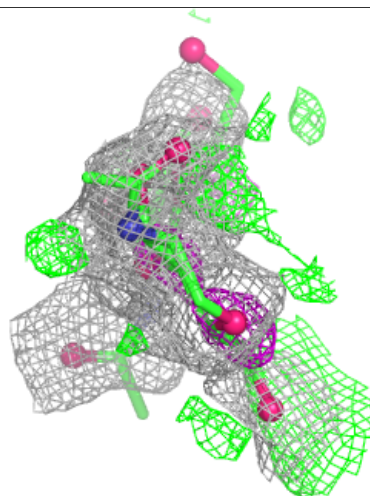
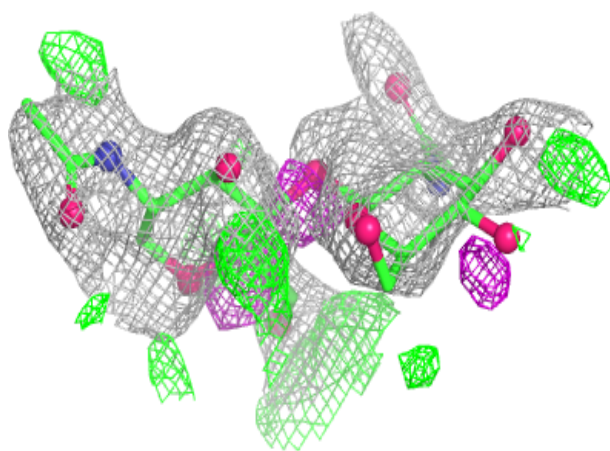
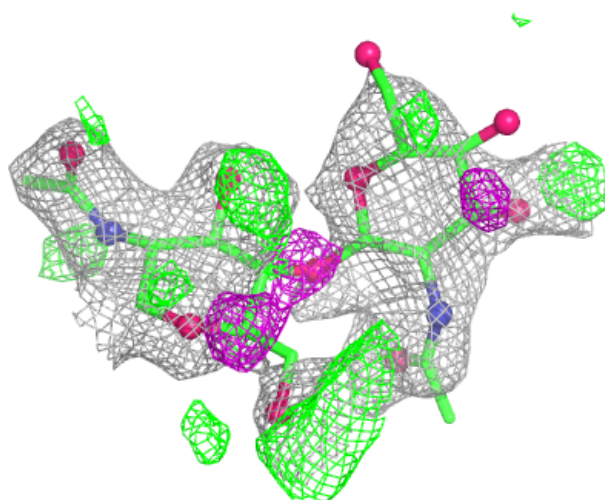
Electron density around Chain C:

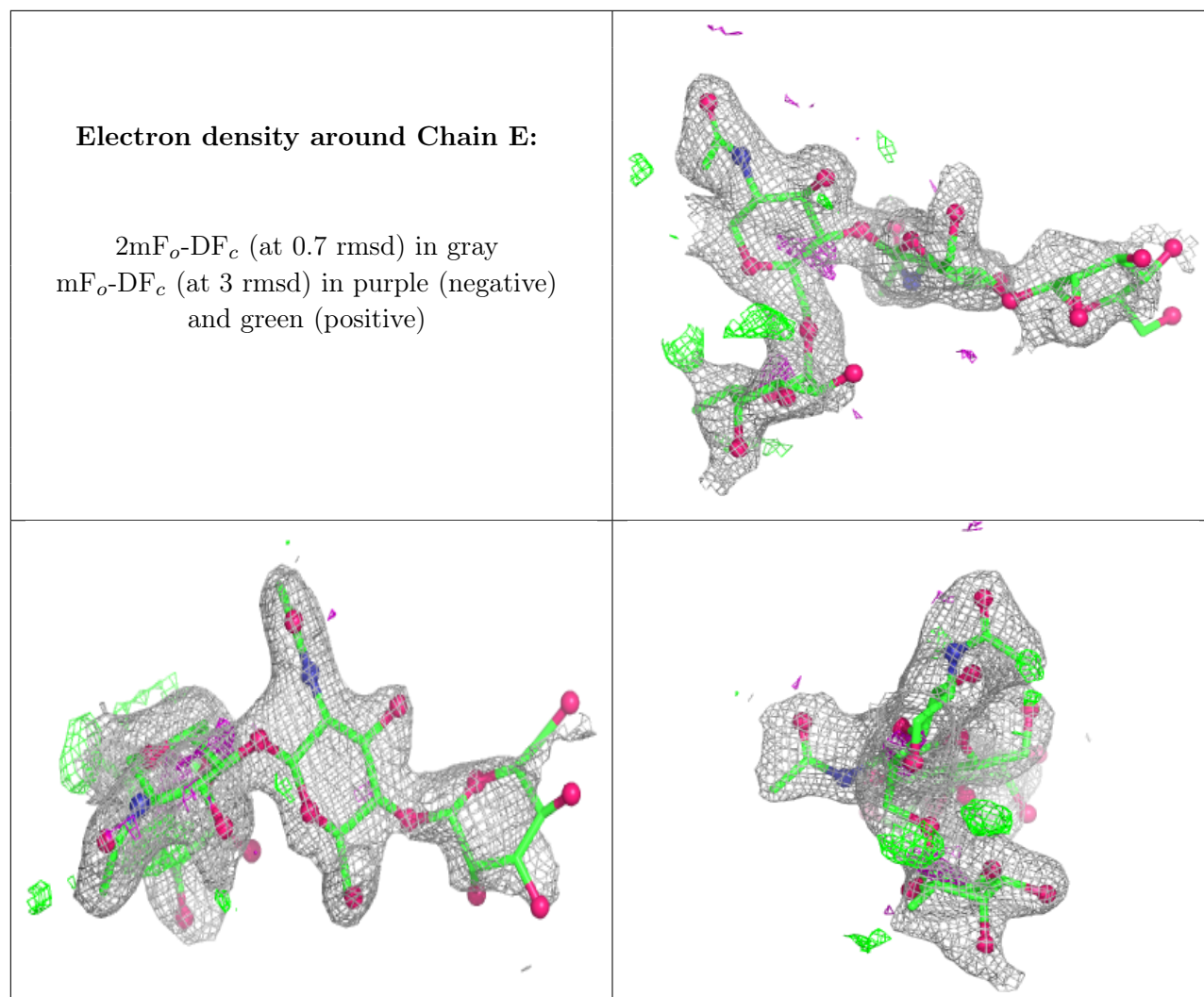
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain D:

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





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.

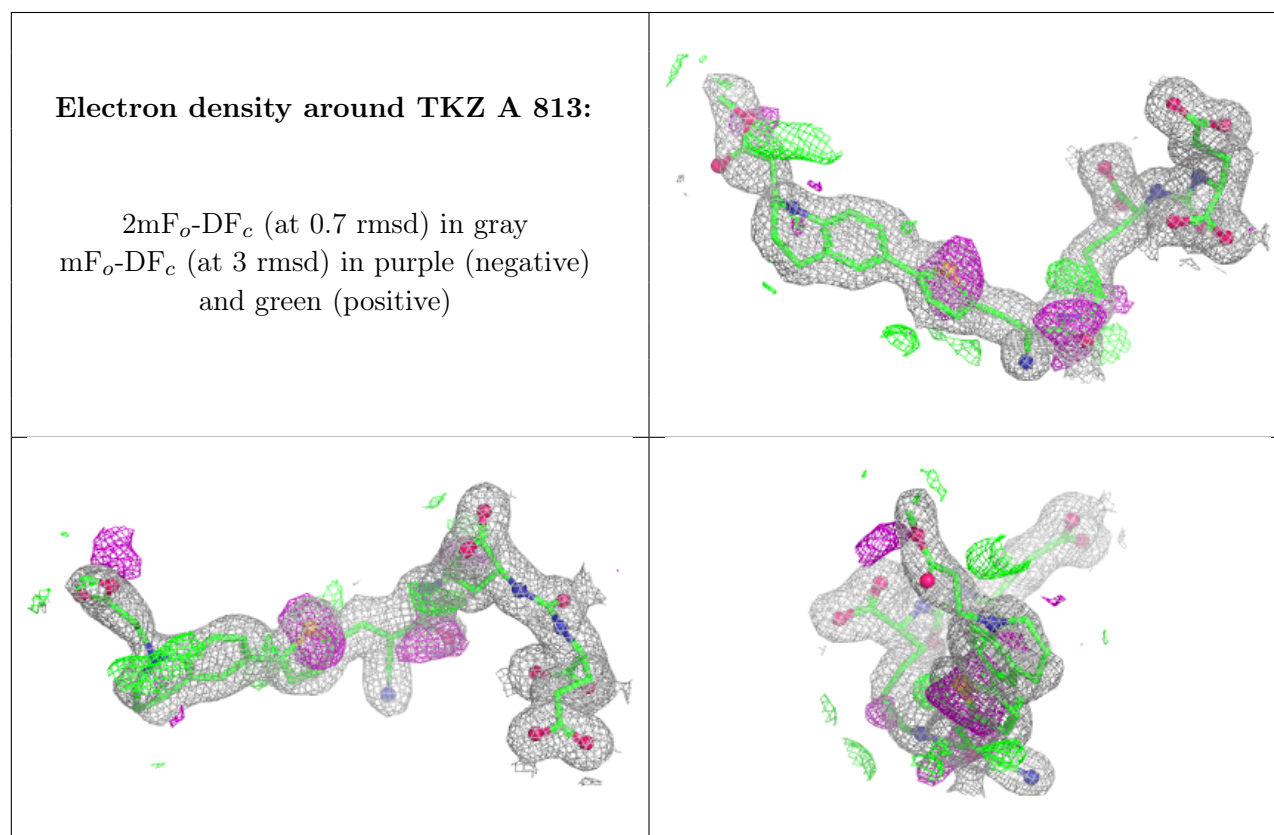
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
9	NAG	A	805	14/15	0.77	0.17	67,77,84,84	0
10	EDO	A	808	4/4	0.81	0.18	50,57,59,62	0
12	NA	A	811	1/1	0.85	0.35	55,55,55,55	0
12	NA	A	812	1/1	0.85	0.19	57,57,57,57	0
10	EDO	A	807	4/4	0.86	0.15	49,57,60,62	0
11	PEG	A	809	7/7	0.87	0.18	61,62,68,69	0
9	NAG	A	806	14/15	0.90	0.12	37,52,57,60	0
10	EDO	A	810	4/4	0.92	0.13	44,55,58,64	0
13	TKZ	A	813	49/49	0.95	0.12	23,45,69,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	ZN	A	802	1/1	1.00	0.02	25,25,25,25	0
7	CA	A	803	1/1	1.00	0.01	24,24,24,24	0
8	CL	A	804	1/1	1.00	0.03	26,26,26,26	0
6	ZN	A	801	1/1	1.00	0.02	25,25,25,25	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.