



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 28, 2021 – 04:05 am BST

PDB ID : 7AWH
Title : Crystal structure of human butyrylcholinesterase in complex with tert-butyl 3-(((2-((1-(benzenesulfonyl)-1H-indol-4-yl)oxy)ethyl)amino)methyl)piperidine-1-carboxylate
Authors : Brazzolotto, X.; Wichur, T.; Wieckowska, A.
Deposited on : 2020-11-08
Resolution : 2.30 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

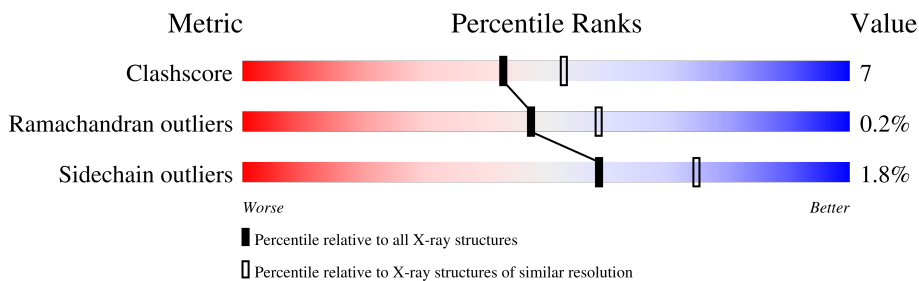
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	529	
2	B	2	
3	C	3	
3	D	3	

2 Entry composition i

There are 10 unique types of molecules in this entry. The entry contains 4590 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 Cholinesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	526	4263	2752	717	778	16	0	10	0

There are 4 discrepancies between the modelled and reference sequences:

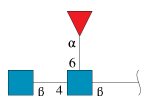
Chain	Residue	Modelled	Actual	Comment	Reference
A	17	GLN	ASN	engineered mutation	UNP P06276
A	455	GLN	ASN	engineered mutation	UNP P06276
A	481	GLN	ASN	engineered mutation	UNP P06276
A	486	GLN	ASN	engineered mutation	UNP P06276

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



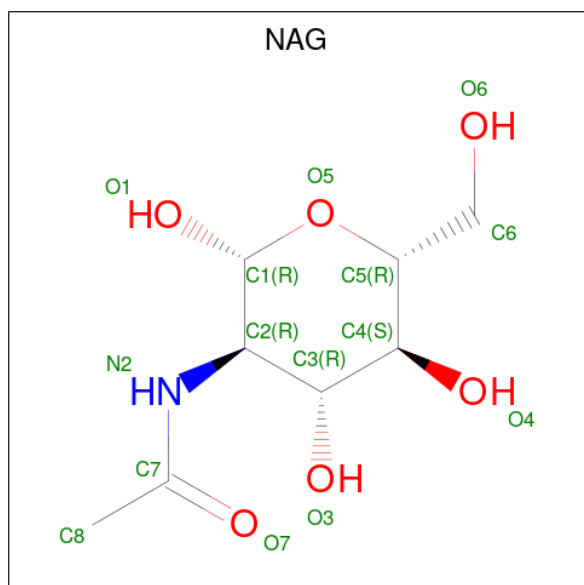
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	2	24	14	1	9	0	0	0

- Molecule 3 is an oligosaccharide called 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
			Total	C	N	O			
3	C	3	38	22	2	14	0	0	0
3	D	3	38	22	2	14	0	0	0

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



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

- Molecule 5 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
5	A	1	12	6	1	4	1	0	0

- Molecule 6 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



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

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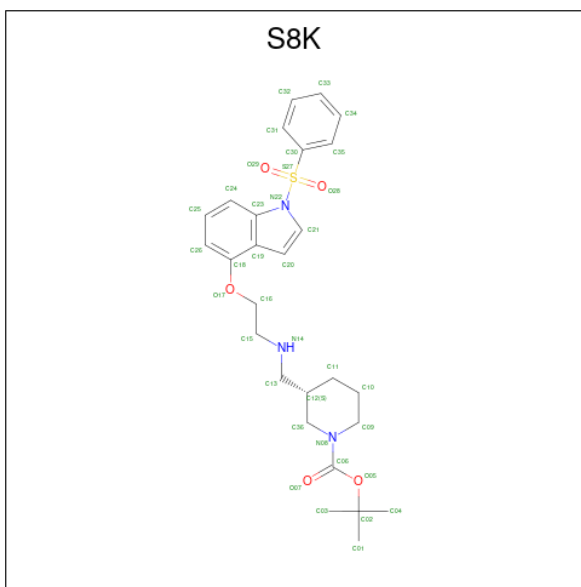
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is {tert}-butyl (3 {S})-3-[[2-[1-(phenylsulfonyl)indol-4-yl]oxyethylamino]methyl]piperidine-1-carboxylate (three-letter code: S8K) (formula: C₂₇H₃₅N₃O₅S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
8	A	1	36	27	3	5	1	0	1

- Molecule 9 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
9	A	1	1	1	0	0

- Molecule 10 is water.

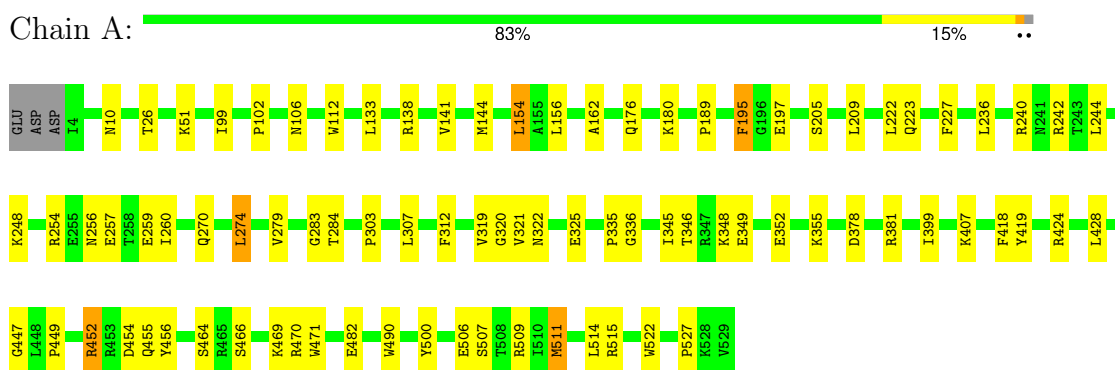
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
10	A	98	98	98	0	0

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. 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. 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.

Note EDS was not executed.

- Molecule 1: Cholinesterase



- Molecule 2: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	154.47Å 154.47Å 127.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.85 – 2.30	Depositor
% Data completeness (in resolution range)	99.9 (48.85-2.30)	Depositor
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PHENIX 1.19rc4_4035	Depositor
R, R_{free}	0.192 , 0.222	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	4590	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

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: MES, FUC, SO4, GOL, NA, NAG, S8K

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	0.45	0/4391	0.62	0/5961

There are no bond length outliers.

There are no bond angle outliers.

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	4263	0	4165	59	0
2	B	24	0	22	0	0
3	C	38	0	34	2	0
3	D	38	0	34	1	0
4	A	42	0	39	1	0
5	A	12	0	12	5	0
6	A	20	0	0	0	0
7	A	18	0	24	1	0
8	A	36	0	0	0	0
9	A	1	0	0	0	0
10	A	98	0	0	1	0
All	All	4590	0	4330	60	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 7.

All (60) 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:176:GLN:HE21	1:A:180:LYS:HD2	1.34	0.92
1:A:176:GLN:NE2	1:A:180:LYS:HD2	2.00	0.76
1:A:452:ARG:H	1:A:452:ARG:HD2	1.59	0.67
1:A:500:TYR:CZ	1:A:511[B]:MET:HB2	2.36	0.61
1:A:515:ARG:NH1	5:A:604:MES:H71	2.16	0.61
1:A:256:ASN:HB3	1:A:259:GLU:HB2	1.85	0.58
1:A:522:TRP:O	1:A:527:PRO:HD3	2.04	0.58
1:A:346:THR:OG1	1:A:349:GLU:HG3	2.04	0.57
1:A:378:ASP:HB3	1:A:381:ARG:HG3	1.86	0.57
1:A:227:PHE:HZ	1:A:307:LEU:HB2	1.71	0.56
1:A:102:PRO:O	1:A:138:ARG:NH2	2.39	0.56
1:A:514:LEU:HD12	5:A:604:MES:H52	1.89	0.54
1:A:209:LEU:HD12	1:A:312:PHE:HB3	1.90	0.54
1:A:454:ASP:O	1:A:455:GLN:HG2	2.07	0.54
1:A:469:LYS:HG2	1:A:482:GLU:HG2	1.89	0.54
1:A:319:VAL:O	1:A:418:PHE:HA	2.08	0.54
1:A:320:GLY:HA3	1:A:419:TYR:CE2	2.43	0.53
1:A:345:ILE:HB	1:A:349:GLU:HB2	1.92	0.50
1:A:515:ARG:HH12	5:A:604:MES:H71	1.75	0.49
1:A:336:GLY:H	3:C:2:NAG:C8	2.25	0.49
1:A:236:LEU:H	1:A:236:LEU:HD22	1.78	0.49
1:A:156:LEU:HD13	1:A:257:GLU:HB3	1.95	0.48
1:A:424:ARG:CZ	1:A:428:LEU:HD23	2.43	0.48
1:A:509:ARG:NH2	10:A:706:HOH:O	2.46	0.48
1:A:254:ARG:HB2	1:A:260:ILE:HG12	1.96	0.47
1:A:227:PHE:CD1	1:A:303:PRO:HB2	2.50	0.46
1:A:248:LYS:HE3	3:D:3:FUC:H61	1.97	0.46
1:A:189:PRO:O	7:A:611:GOL:H12	2.16	0.46
1:A:352:GLU:OE2	1:A:355:LYS:HE3	2.16	0.46
1:A:500:TYR:CZ	1:A:511[A]:MET:HB2	2.50	0.46
1:A:227:PHE:CE1	1:A:303:PRO:HB2	2.51	0.46
1:A:10:ASN:HA	1:A:51:LYS:HG2	1.97	0.45
1:A:205:SER:HB3	1:A:222:LEU:HD21	1.97	0.45
1:A:240:ARG:O	1:A:244:LEU:HG	2.17	0.45
1:A:348:LYS:HE3	1:A:348:LYS:HB3	1.79	0.45
1:A:466[B]:SER:O	1:A:470:ARG:HG3	2.17	0.45
1:A:454:ASP:C	1:A:455:GLN:HG2	2.38	0.44
1:A:506:GLU:HG3	1:A:507:SER:H	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:LEU:HD23	1:A:162:ALA:HB1	2.00	0.44
1:A:197:GLU:HA	1:A:223:GLN:O	2.18	0.44
1:A:336:GLY:H	3:C:2:NAG:H83	1.83	0.43
1:A:447:GLY:HA2	1:A:464:SER:OG	2.19	0.43
1:A:322:ASN:O	1:A:325:GLU:HG2	2.19	0.43
1:A:133:LEU:HB2	1:A:141:VAL:HG21	2.00	0.43
1:A:112:TRP:HA	1:A:195:PHE:O	2.18	0.43
1:A:106:ASN:ND2	4:A:601:NAG:H83	2.34	0.43
1:A:242:ARG:HG2	1:A:279:VAL:HG23	2.00	0.43
1:A:320:GLY:HA3	1:A:419:TYR:CZ	2.54	0.42
1:A:399:ILE:HG21	1:A:515:ARG:HG3	2.01	0.42
1:A:515:ARG:HD3	5:A:604:MES:H22	2.01	0.42
5:A:604:MES:H32	5:A:604:MES:H82	1.66	0.42
1:A:419:TYR:HB3	1:A:490:TRP:CZ2	2.56	0.41
1:A:270:GLN:O	1:A:274:LEU:HD23	2.20	0.41
1:A:407:LYS:HE2	1:A:407:LYS:HB3	1.61	0.41
1:A:320:GLY:HA3	1:A:419:TYR:CD2	2.56	0.41
1:A:335:PRO:HG2	1:A:352:GLU:HB3	2.03	0.41
1:A:156:LEU:HD23	1:A:156:LEU:HA	1.88	0.40
1:A:449:PRO:HA	1:A:456:TYR:CD2	2.57	0.40
1:A:26:THR:HB	1:A:99:ILE:HG12	2.03	0.40
1:A:321:VAL:HG21	1:A:399:ILE:HG12	2.03	0.40

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	534/529 (101%)	508 (95%)	24 (4%)	2 (0%)	34 42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	283[A]	GLY
1	A	283[B]	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	460/454 (101%)	450 (98%)	10 (2%)	52 69

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	144	MET
1	A	154	LEU
1	A	195	PHE
1	A	274	LEU
1	A	284[A]	THR
1	A	284[B]	THR
1	A	452	ARG
1	A	471	TRP
1	A	511[A]	MET
1	A	511[B]	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	176	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	B	1	1,2	14,14,15	0.64	0	17,19,21	0.50	0
2	FUC	B	2	2	10,10,11	1.31	1 (10%)	14,14,16	0.73	0
3	NAG	C	1	1,3	14,14,15	0.45	0	17,19,21	0.45	0
3	NAG	C	2	3	14,14,15	0.24	0	17,19,21	0.53	0
3	FUC	C	3	3	10,10,11	1.67	2 (20%)	14,14,16	1.45	1 (7%)
3	NAG	D	1	1,3	14,14,15	0.28	0	17,19,21	0.69	0
3	NAG	D	2	3	14,14,15	0.66	1 (7%)	17,19,21	0.80	1 (5%)
3	FUC	D	3	3	10,10,11	1.34	2 (20%)	14,14,16	1.20	1 (7%)

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	FUC	B	2	2	-	-	0/1/1/1
3	NAG	C	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	C	2	3	-	4/6/23/26	0/1/1/1
3	FUC	C	3	3	-	-	0/1/1/1
3	NAG	D	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
3	FUC	D	3	3	-	-	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	3	FUC	C2-C3	3.40	1.57	1.52
3	C	3	FUC	C1-C2	3.08	1.59	1.52
3	D	3	FUC	C2-C3	2.63	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	FUC	C2-C3	2.17	1.55	1.52
3	D	2	NAG	C1-C2	2.12	1.55	1.52
3	D	3	FUC	C1-C2	2.08	1.56	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	3	FUC	C1-C2-C3	3.96	114.54	109.67
3	D	2	NAG	C1-O5-C5	2.69	115.83	112.19
3	D	3	FUC	O5-C5-C4	2.50	114.01	109.52

There are no chirality outliers.

All (8) torsion outliers are listed below:

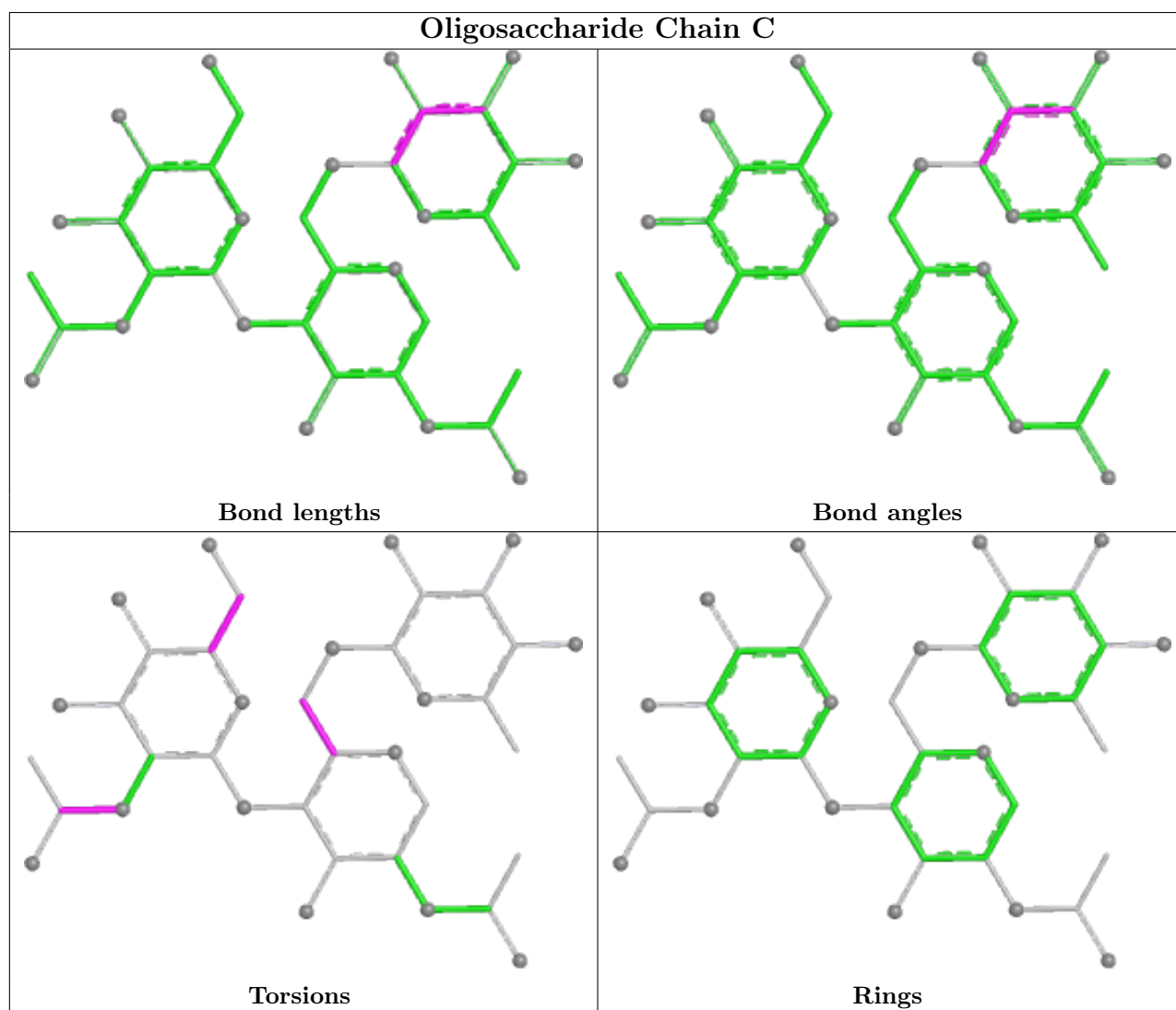
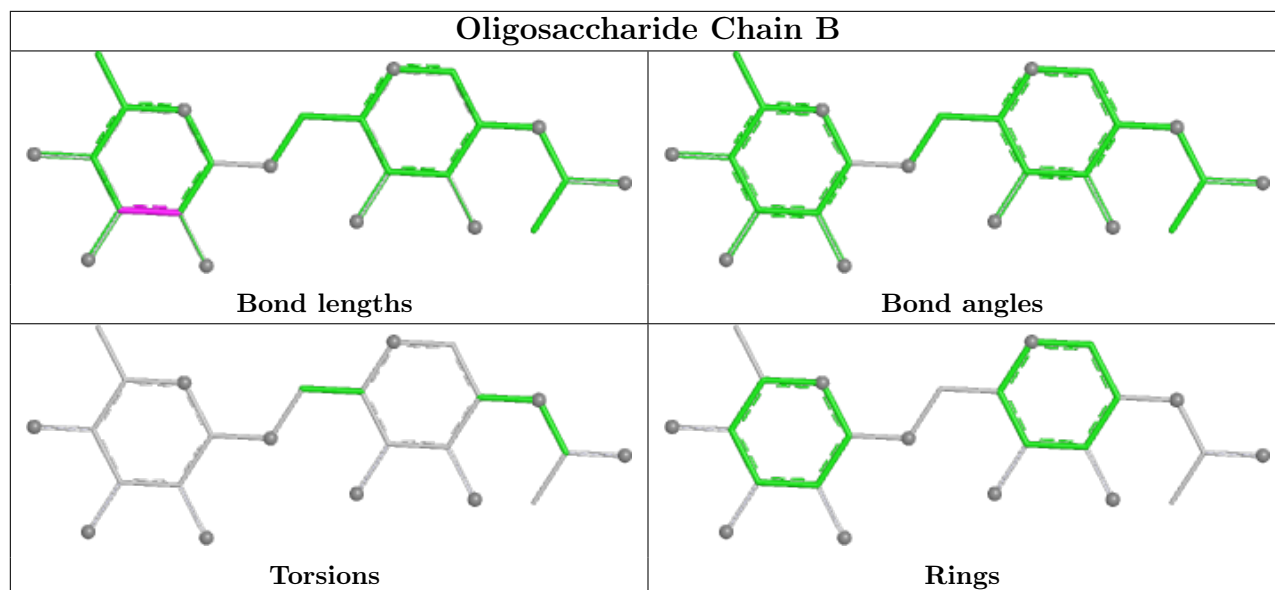
Mol	Chain	Res	Type	Atoms
3	D	2	NAG	O5-C5-C6-O6
3	C	2	NAG	C8-C7-N2-C2
3	C	2	NAG	O7-C7-N2-C2
3	D	2	NAG	C4-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6
3	C	2	NAG	C4-C5-C6-O6
3	D	1	NAG	C3-C2-N2-C7
3	C	1	NAG	C4-C5-C6-O6

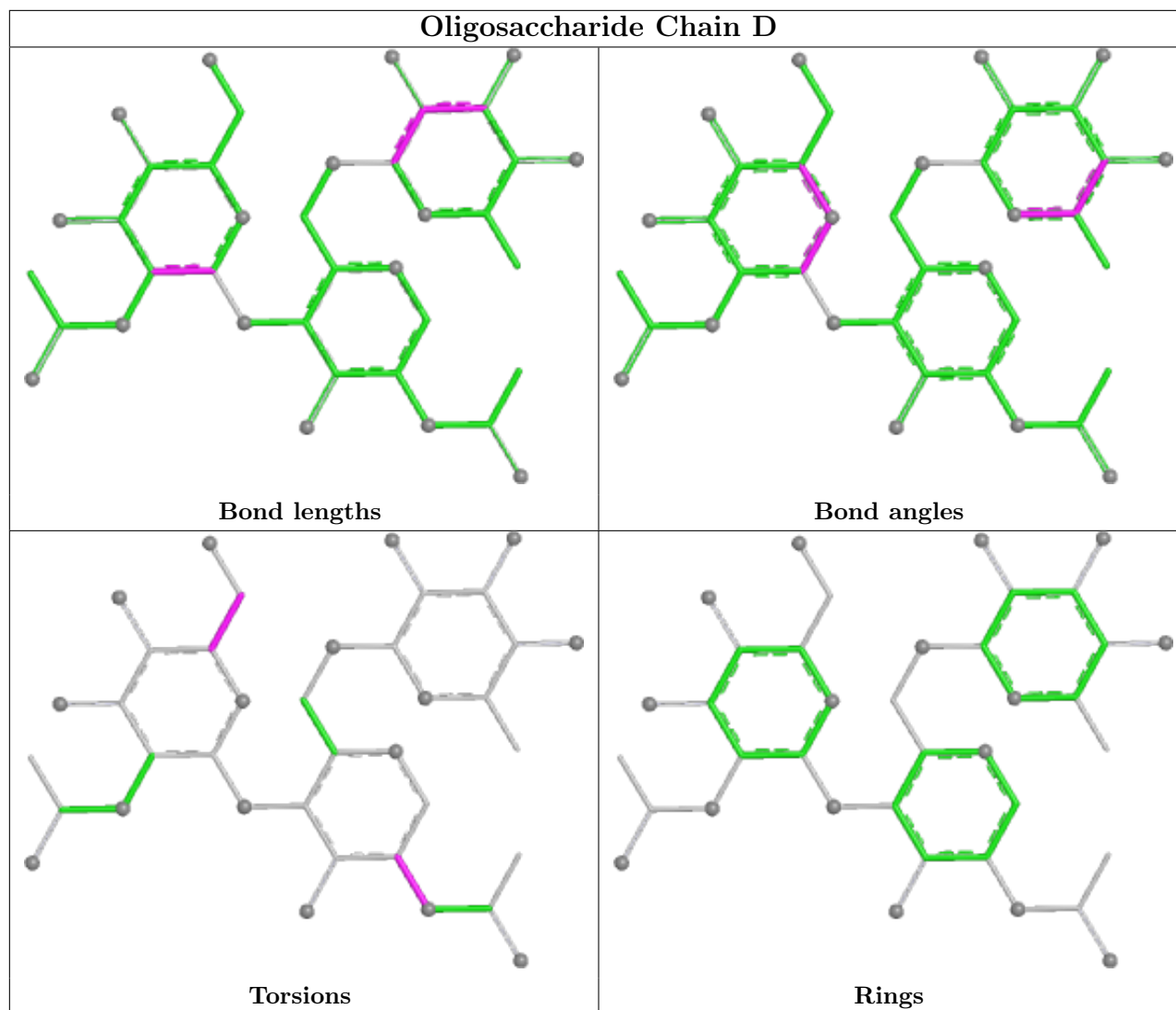
There are no ring outliers.

2 monomers are involved in 3 short contacts:

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

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





5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 1 is monoatomic - leaving 12 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	SO4	A	607	-	4,4,4	0.17	0	6,6,6	0.15	0
7	GOL	A	610	-	5,5,5	0.86	0	5,5,5	1.04	0
4	NAG	A	601	1	14,14,15	0.92	1 (7%)	17,19,21	0.79	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	SO4	A	612	-	4,4,4	0.22	0	6,6,6	0.10	0
4	NAG	A	602	1	14,14,15	0.52	0	17,19,21	0.48	0
6	SO4	A	605	-	4,4,4	0.21	0	6,6,6	0.26	0
7	GOL	A	611	-	5,5,5	0.75	0	5,5,5	1.14	1 (20%)
4	NAG	A	603	1	14,14,15	0.58	0	17,19,21	0.76	1 (5%)
8	S8K	A	609[A]	-	35,39,39	2.73	18 (51%)	46,56,56	2.58	18 (39%)
7	GOL	A	608	-	5,5,5	1.04	0	5,5,5	0.89	0
6	SO4	A	606	-	4,4,4	0.20	0	6,6,6	0.11	0
5	MES	A	604	-	12,12,12	1.99	1 (8%)	14,16,16	2.48	7 (50%)

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	GOL	A	610	-	-	4/4/4/4	-
4	NAG	A	601	1	-	2/6/23/26	0/1/1/1
4	NAG	A	602	1	-	2/6/23/26	0/1/1/1
7	GOL	A	611	-	-	4/4/4/4	-
4	NAG	A	603	1	-	0/6/23/26	0/1/1/1
8	S8K	A	609[A]	-	-	6/23/39/39	0/4/4/4
7	GOL	A	608	-	-	2/4/4/4	-
5	MES	A	604	-	-	3/6/14/14	0/1/1/1

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	609[A]	S8K	C06-N08	7.74	1.48	1.35
5	A	604	MES	C8-S	-6.53	1.68	1.77
8	A	609[A]	S8K	C36-N08	6.37	1.54	1.46
8	A	609[A]	S8K	C13-N14	5.05	1.55	1.47
8	A	609[A]	S8K	C36-C12	5.00	1.59	1.52
8	A	609[A]	S8K	O05-C06	3.17	1.39	1.33
8	A	609[A]	S8K	C09-N08	2.98	1.52	1.47
4	A	601	NAG	O5-C1	2.87	1.48	1.43
8	A	609[A]	S8K	C30-S27	2.62	1.90	1.77
8	A	609[A]	S8K	C35-C30	2.54	1.42	1.38
8	A	609[A]	S8K	C31-C30	2.52	1.42	1.38
8	A	609[A]	S8K	C15-N14	2.47	1.55	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	609[A]	S8K	C25-C24	2.46	1.42	1.36
8	A	609[A]	S8K	C13-C12	2.41	1.56	1.51
8	A	609[A]	S8K	C15-C16	2.37	1.58	1.50
8	A	609[A]	S8K	C25-C26	2.23	1.43	1.38
8	A	609[A]	S8K	C21-N22	2.17	1.43	1.38
8	A	609[A]	S8K	C34-C35	2.16	1.43	1.38
8	A	609[A]	S8K	C32-C31	2.14	1.43	1.38
8	A	609[A]	S8K	C10-C09	2.06	1.58	1.51

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	609[A]	S8K	O05-C06-N08	9.98	124.12	111.01
8	A	609[A]	S8K	O05-C06-O07	-5.08	118.06	126.40
8	A	609[A]	S8K	C30-S27-N22	4.87	110.03	104.95
5	A	604	MES	C5-N4-C3	4.55	119.06	108.83
8	A	609[A]	S8K	C34-C35-C30	4.41	123.54	118.95
8	A	609[A]	S8K	C35-C30-C31	-3.99	114.88	120.44
8	A	609[A]	S8K	C32-C31-C30	3.91	123.02	118.95
8	A	609[A]	S8K	O07-C06-N08	-3.89	117.82	124.32
8	A	609[A]	S8K	C11-C12-C36	3.55	112.69	108.68
5	A	604	MES	O2S-S-C8	3.34	110.93	106.92
5	A	604	MES	C7-N4-C3	3.17	119.34	111.23
8	A	609[A]	S8K	O29-S27-O28	-3.12	107.09	117.71
5	A	604	MES	O3S-S-C8	2.94	110.52	105.77
8	A	609[A]	S8K	C35-C30-S27	2.93	123.02	119.77
5	A	604	MES	C2-C3-N4	-2.91	105.69	110.10
8	A	609[A]	S8K	C02-O05-C06	2.70	123.89	120.92
8	A	609[A]	S8K	O28-S27-C30	2.64	113.59	107.62
8	A	609[A]	S8K	C11-C12-C13	-2.46	106.25	111.47
5	A	604	MES	O1-C6-C5	-2.45	106.41	111.80
5	A	604	MES	C7-N4-C5	2.36	117.26	111.23
8	A	609[A]	S8K	O17-C18-C19	2.31	121.48	115.01
4	A	601	NAG	C1-O5-C5	2.25	115.25	112.19
4	A	603	NAG	C1-O5-C5	2.25	115.24	112.19
8	A	609[A]	S8K	C11-C10-C09	2.12	113.82	110.85
8	A	609[A]	S8K	C31-C30-S27	2.10	122.09	119.77
8	A	609[A]	S8K	O17-C18-C26	-2.09	119.86	124.46
7	A	611	GOL	C3-C2-C1	-2.02	103.85	111.70
8	A	609[A]	S8K	O29-S27-C30	2.02	112.18	107.62

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	604	MES	C8-C7-N4-C3
5	A	604	MES	N4-C7-C8-S
7	A	608	GOL	C1-C2-C3-O3
7	A	610	GOL	C1-C2-C3-O3
7	A	611	GOL	O1-C1-C2-O2
7	A	611	GOL	O1-C1-C2-C3
7	A	611	GOL	C1-C2-C3-O3
7	A	611	GOL	O2-C2-C3-O3
4	A	602	NAG	O5-C5-C6-O6
4	A	602	NAG	C4-C5-C6-O6
4	A	601	NAG	C8-C7-N2-C2
4	A	601	NAG	O7-C7-N2-C2
8	A	609[A]	S8K	C19-C18-O17-C16
7	A	610	GOL	O1-C1-C2-C3
8	A	609[A]	S8K	C26-C18-O17-C16
7	A	610	GOL	O1-C1-C2-O2
7	A	610	GOL	O2-C2-C3-O3
7	A	608	GOL	O2-C2-C3-O3
5	A	604	MES	C8-C7-N4-C5
8	A	609[A]	S8K	C15-C16-O17-C18
8	A	609[A]	S8K	O07-C06-N08-C09
8	A	609[A]	S8K	C12-C13-N14-C15
8	A	609[A]	S8K	O05-C06-N08-C09

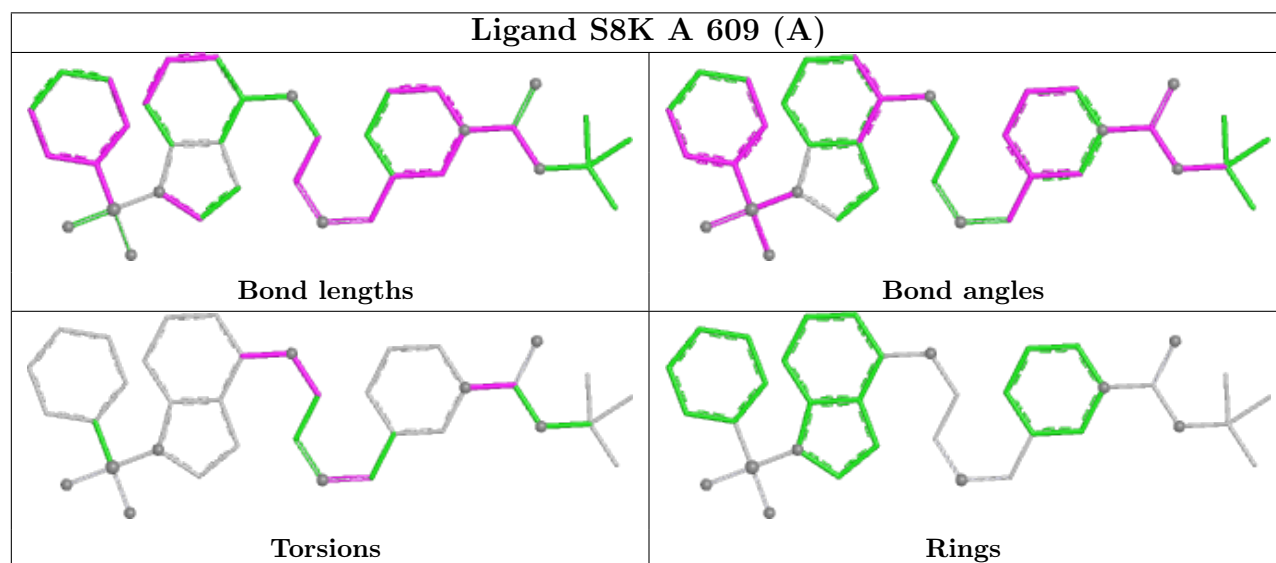
There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	601	NAG	1	0
7	A	611	GOL	1	0
5	A	604	MES	5	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](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.