



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2020 – 08:28 AM BST

PDB ID : 5EIE  
Title : mAChE-TZ2 complex  
Authors : Bourne, Y.; Marchot, P.  
Deposited on : 2015-10-29  
Resolution : 2.10 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

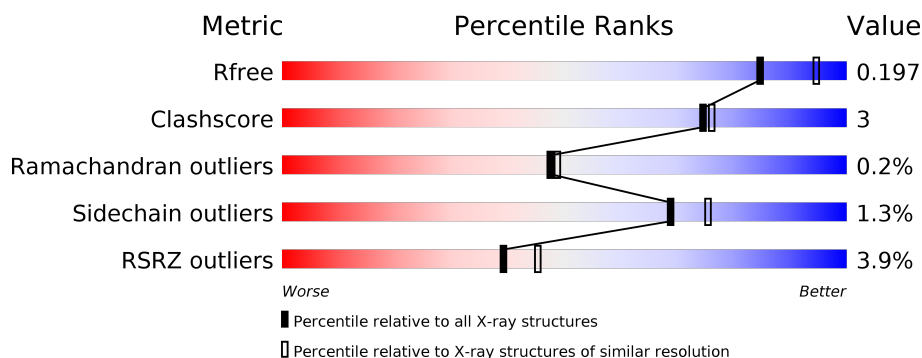
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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))
$R_{free}$	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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

Mol	Chain	Length	Quality of chain
1	A	543	<div> <div>3%</div> <div> <div></div> <div>89%</div> <div>10%</div> <div></div> </div> </div>
1	B	543	<div> <div>5%</div> <div> <div></div> <div>90%</div> <div>8%</div> <div></div> </div> </div>
2	C	3	<div> <div></div> <div> <div>33%</div> <div>67%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FUC	C	3	-	-	-	X
3	NAG	B	602	-	-	-	X

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 9330 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 Acetylcholinesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	538	Total	C	N	O	S	0	8	0
			4239	2721	735	768	15			
1	B	536	Total	C	N	O	S	0	13	0
			4245	2728	729	772	16			

- Molecule 2 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.



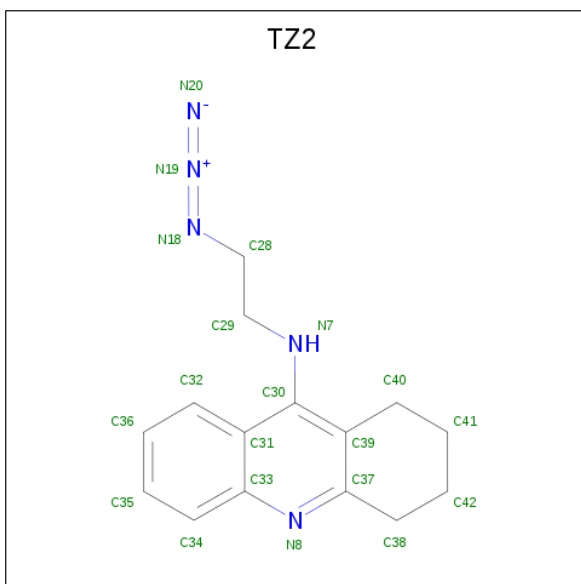
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



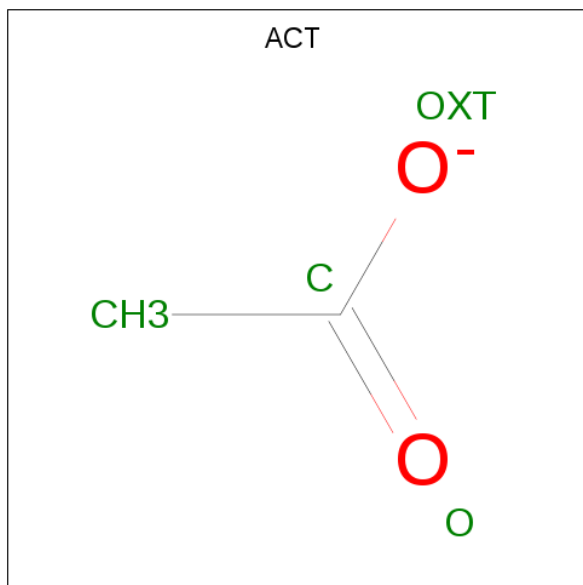
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is {N}-(2-azidoethyl)-1,2,3,4-tetrahydroacridin-9-amine (three-letter code: TZ2) (formula: C<sub>15</sub>H<sub>17</sub>N<sub>5</sub>).



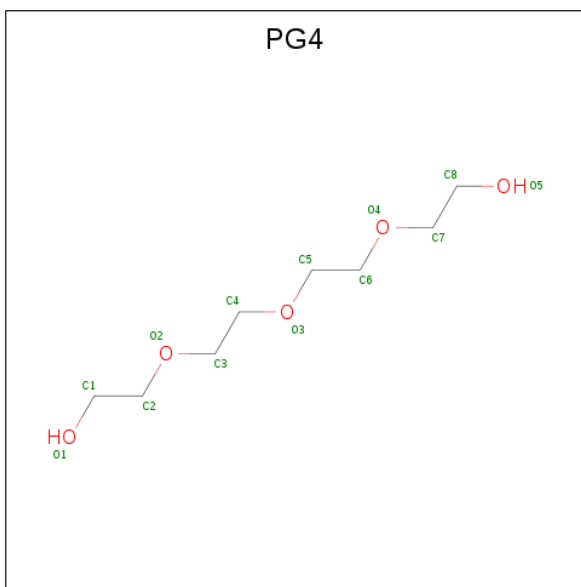
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			20	15	5		
4	B	1	Total	C	N	0	0
			20	15	5		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



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

- Molecule 6 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula:  $C_8H_{18}O_5$ ).

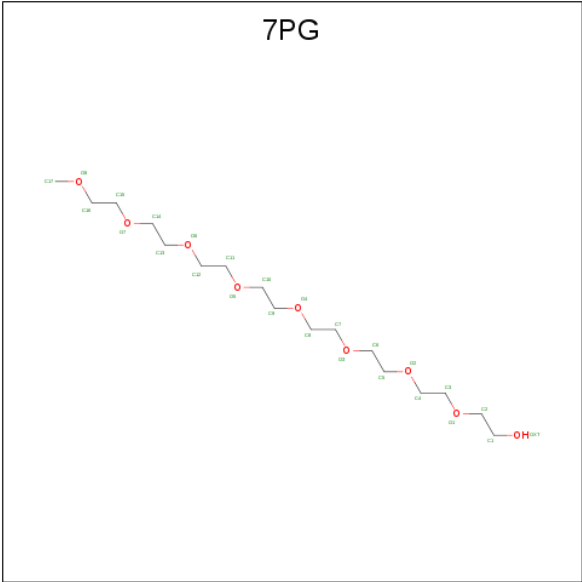


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			13	8	5		
6	B	1	Total	C	O	0	0
			13	8	5		

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Cl	0	0
			1	1		

- Molecule 8 is 2,5,8,11,14,17,20,23-OCTAOXAPENTACOSAN-25-OL (three-letter code: 7PG) (formula: C<sub>17</sub>H<sub>36</sub>O<sub>9</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			22	14	8		

- Molecule 9 is water.

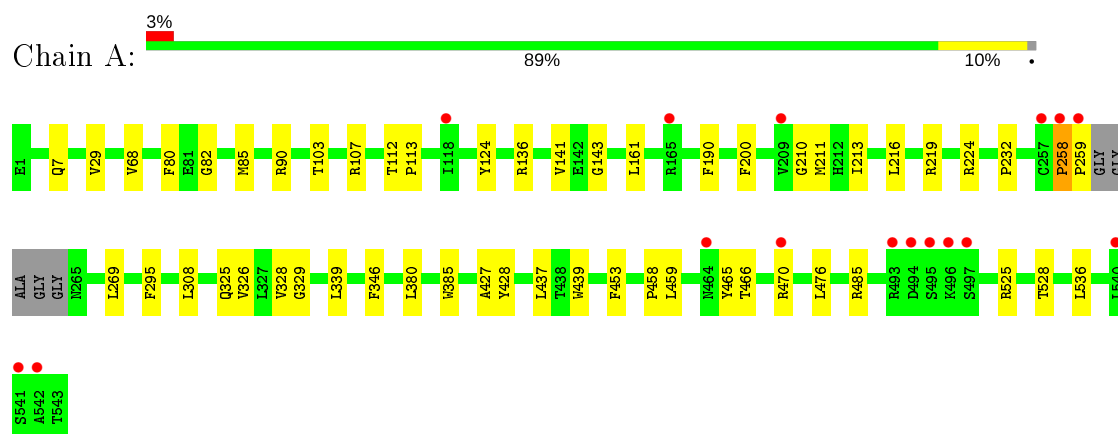
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	362	Total	O	0	0
			362	362		
9	B	307	Total	O	0	0
			307	307		



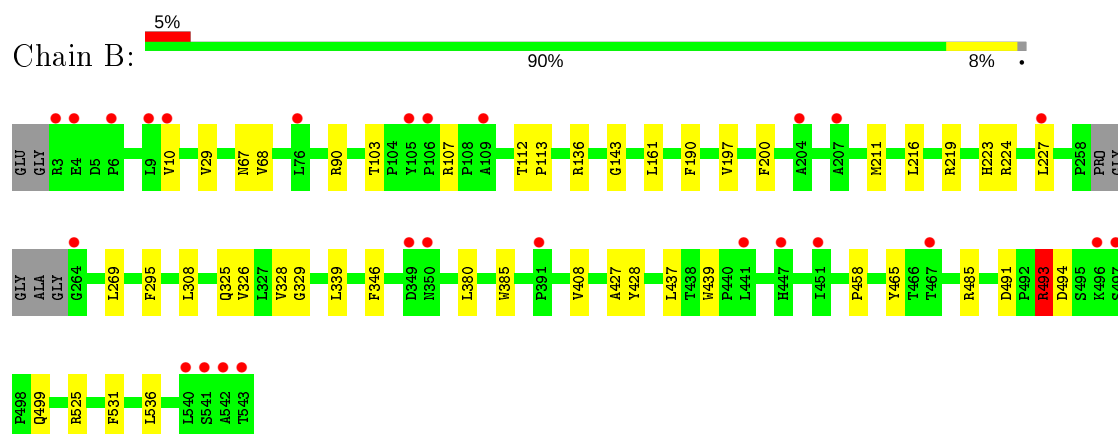
### 3 Residue-property plots [i](#)

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: Acetylcholinesterase



#### • Molecule 1: Acetylcholinesterase



#### • Molecule 2: 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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.66Å 113.12Å 226.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.00 – 2.10 46.12 – 2.10	Depositor EDS
% Data completeness (in resolution range)	96.4 (46.00-2.10) 96.4 (46.12-2.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.16 (at 2.10Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, $R_{free}$	0.176 , 0.193 0.178 , 0.197	Depositor DCC
$R_{free}$ test set	2294 reflections (1.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.8	Xtriage
Anisotropy	0.750	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 51.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	9330	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.55% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: TZ2, NAG, CL, PG4, FUC, ACT, 7PG

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	0.52	0/4387	0.65	0/5993
1	B	0.50	0/4407	0.71	3/6021 (0.0%)
All	All	0.51	0/8794	0.68	3/12014 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	493	ARG	N-CA-C	14.66	150.58	111.00
1	B	493	ARG	CB-CA-C	-12.73	84.95	110.40
1	B	493	ARG	C-N-CA	10.43	147.78	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	493	ARG	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	4239	0	4144	27	0
1	B	4245	0	4145	26	0
2	C	38	0	34	0	0
3	A	14	0	13	0	0
3	B	28	0	26	0	0
4	A	20	0	17	2	0
4	B	20	0	17	1	0
5	A	4	0	3	0	0
5	B	4	0	3	0	0
6	A	13	0	18	0	0
6	B	13	0	18	1	0
7	B	1	0	0	0	0
8	B	22	0	29	3	0
9	A	362	0	0	1	0
9	B	307	0	0	1	0
All	All	9330	0	8467	55	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 3.

All (55) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:197:VAL:H	1:B:223:HIS:HD2	1.37	0.71
1:B:161[A]:LEU:HD11	1:B:269:LEU:HD22	1.73	0.71
1:A:113:PRO:HG2	1:A:485:ARG:HG2	1.74	0.70
1:A:85[B]:MET:HE1	9:A:821:HOH:O	1.91	0.69
1:B:113:PRO:HG2	1:B:485:ARG:HG2	1.73	0.69
1:A:7:GLN:NE2	1:A:107:ARG:H	1.93	0.65
1:B:197:VAL:H	1:B:223:HIS:CD2	2.17	0.61
1:A:326:VAL:HG12	1:A:328:VAL:HG13	1.84	0.59
1:A:258:PRO:HB2	1:A:259:PRO:CD	2.34	0.58
1:B:326:VAL:HG12	1:B:328:VAL:HG13	1.85	0.57
8:B:606:7PG:H141	6:B:607:PG4:H41	1.87	0.55
1:A:161[B]:LEU:HD21	1:A:269:LEU:HD22	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:TYR:OH	4:A:605:TZ2:H3	2.11	0.51
1:B:408:VAL:HG11	1:B:525:ARG:HG3	1.91	0.51
8:B:606:7PG:H131	8:B:606:7PG:H12	1.95	0.49
1:B:112:THR:HG21	1:B:143:GLY:O	2.13	0.49
1:B:161[B]:LEU:HD21	1:B:269:LEU:HD22	1.94	0.48
1:A:211:MET:HG2	1:A:308:LEU:HD21	1.95	0.48
1:B:211:MET:HG2	1:B:308:LEU:HD21	1.94	0.48
1:B:531:PHE:HB2	8:B:606:7PG:H32	1.95	0.47
1:B:328:VAL:O	1:B:427:ALA:HA	2.14	0.47
1:B:10[B]:VAL:HG11	1:B:190:PHE:CE2	2.50	0.47
1:B:458:PRO:HA	1:B:465:TYR:CD1	2.52	0.45
1:B:491:ASP:C	1:B:493:ARG:H	2.20	0.45
1:A:213:ILE:O	1:A:219[A]:ARG:HD3	2.15	0.45
1:A:112:THR:HG21	1:A:143:GLY:O	2.17	0.45
1:A:439:TRP:CZ2	4:A:605:TZ2:H18	2.52	0.45
1:A:458:PRO:HA	1:A:465:TYR:CD1	2.52	0.45
1:A:466:THR:O	1:A:470:ARG:HG3	2.17	0.45
1:B:224:ARG:HG2	1:B:325:GLN:HB2	1.99	0.45
1:A:339:LEU:HD13	1:A:346:PHE:CE2	2.53	0.44
1:B:339:LEU:HD13	1:B:346:PHE:CE2	2.53	0.44
1:A:141:VAL:HG21	1:A:459:LEU:HD23	2.00	0.44
1:A:29:VAL:HG21	1:A:136:ARG:HB2	2.00	0.44
1:B:439:TRP:CZ2	4:B:604:TZ2:H18	2.53	0.44
1:A:328:VAL:O	1:A:427:ALA:HA	2.17	0.43
1:A:525:ARG:HG2	1:A:528:THR:HB	2.00	0.43
1:A:224:ARG:HG2	1:A:325:GLN:HB2	2.00	0.43
1:B:380:LEU:HD23	1:B:385:TRP:HZ2	1.84	0.42
1:B:219[B]:ARG:HA	1:B:219[B]:ARG:NE	2.35	0.42
1:A:380:LEU:HD23	1:A:385:TRP:HZ2	1.85	0.42
1:B:107:ARG:HD3	1:B:190:PHE:HA	2.00	0.42
1:A:80:PHE:CE2	1:A:82:GLY:HA3	2.54	0.42
1:B:103:THR:HG21	1:B:190:PHE:HB3	2.01	0.42
1:B:67:ASN:ND2	9:B:702:HOH:O	2.52	0.41
1:B:29:VAL:HG21	1:B:136:ARG:HB2	2.01	0.41
1:A:103:THR:HG21	1:A:190:PHE:HB3	2.02	0.41
1:A:453:PHE:HB3	1:A:476:LEU:HD12	2.03	0.41
1:B:329:GLY:HA3	1:B:428:TYR:CZ	2.56	0.41
1:A:210:GLY:HA3	1:A:232:PRO:HD3	2.03	0.40
1:B:227:LEU:HB2	1:B:328:VAL:HG12	2.02	0.40
1:A:329:GLY:HA3	1:A:428:TYR:CZ	2.56	0.40
1:A:141:VAL:HG21	1:A:459:LEU:CD2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:68:VAL:HG23	1:B:90:ARG:HB2	2.03	0.40
1:A:68:VAL:HG23	1:A:90:ARG:HB2	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	542/543 (100%)	528 (97%)	13 (2%)	1 (0%)	47	49
1	B	545/543 (100%)	529 (97%)	15 (3%)	1 (0%)	47	49
All	All	1087/1086 (100%)	1057 (97%)	28 (3%)	2 (0%)	47	49

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	494	ASP
1	A	258	PRO

### 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	448/443 (101%)	443 (99%)	5 (1%)	73	79
1	B	451/443 (102%)	444 (98%)	7 (2%)	62	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	899/886 (102%)	887 (99%)	12 (1%)	69	75

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	200	PHE
1	A	216	LEU
1	A	295	PHE
1	A	437	LEU
1	A	536	LEU
1	B	200	PHE
1	B	216	LEU
1	B	295	PHE
1	B	437	LEU
1	B	499[A]	GLN
1	B	499[B]	GLN
1	B	536	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	A	287	HIS
1	A	447	HIS
1	B	223	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

3 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	0.30	0	17,19,21	0.84	1 (5%)
2	NAG	C	2	2	14,14,15	0.35	0	17,19,21	0.78	1 (5%)
2	FUC	C	3	2	10,10,11	0.46	0	14,14,16	0.70	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
2	NAG	C	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	FUC	C	3	2	-	-	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	NAG	C1-O5-C5	2.54	115.64	112.19
2	C	1	NAG	C1-C2-N2	-2.09	106.92	110.49

There are no chirality outliers.

All (2) torsion outliers are listed below:

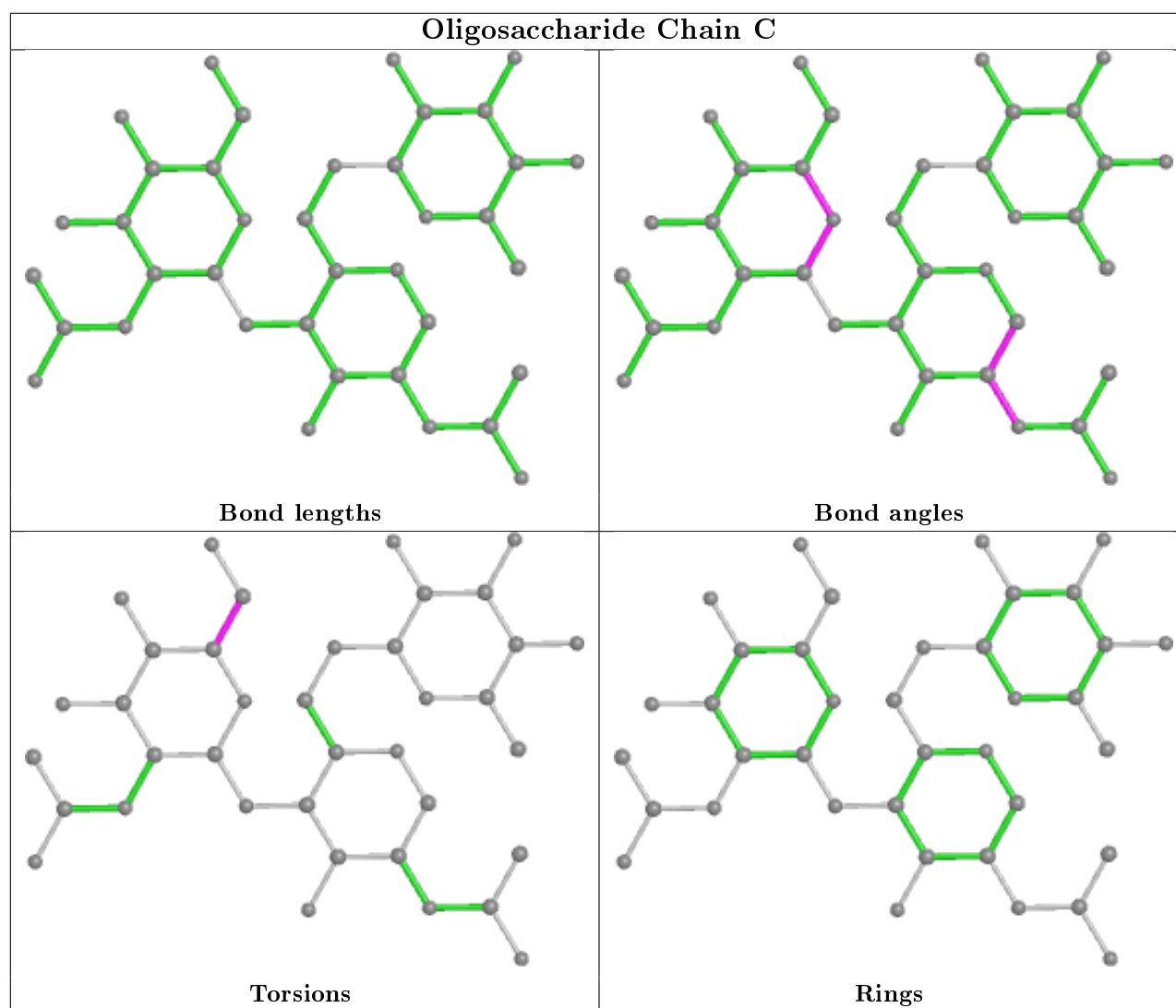
Mol	Chain	Res	Type	Atoms
2	C	2	NAG	C4-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6

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 ⓘ

Of 11 ligands modelled in this entry, 1 is monoatomic - leaving 10 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	$\# Z  > 2$
4	TZ2	B	604	-	21,22,22	2.60	5 (23%)	25,29,29	1.66	2 (8%)
8	7PG	B	606	-	21,21,25	0.60	0	20,20,24	0.48	0
3	NAG	B	601	1	14,14,15	0.32	0	17,19,21	1.17	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	ACT	A	606	-	1,3,3	2.76	1 (100%)	0,3,3	0.00	-
6	PG4	B	607	-	12,12,12	0.50	0	11,11,11	0.25	0
6	PG4	A	607	-	12,12,12	0.52	0	11,11,11	0.27	0
4	TZ2	A	605	-	21,22,22	2.51	5 (23%)	25,29,29	1.63	2 (8%)
3	NAG	A	604	1	14,14,15	0.33	0	17,19,21	0.71	1 (5%)
3	NAG	B	602	1	14,14,15	0.33	0	17,19,21	0.50	0
5	ACT	B	605	-	1,3,3	2.28	1 (100%)	0,3,3	0.00	-

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
4	TZ2	B	604	-	-	1/6/13/13	0/3/3/3
8	7PG	B	606	-	-	9/19/19/23	-
3	NAG	B	601	1	-	1/6/23/26	0/1/1/1
6	PG4	B	607	-	-	7/10/10/10	-
6	PG4	A	607	-	-	5/10/10/10	-
4	TZ2	A	605	-	-	1/6/13/13	0/3/3/3
3	NAG	A	604	1	-	0/6/23/26	0/1/1/1
3	NAG	B	602	1	-	0/6/23/26	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	604	TZ2	C39-C37	6.94	1.50	1.40
4	B	604	TZ2	C30-C39	6.80	1.50	1.38
4	A	605	TZ2	C39-C37	6.18	1.49	1.40
4	A	605	TZ2	C30-C39	6.14	1.49	1.38
4	B	604	TZ2	C31-C33	4.44	1.49	1.42
4	A	605	TZ2	C30-C31	4.05	1.50	1.43
4	A	605	TZ2	C31-C33	3.82	1.48	1.42
4	A	605	TZ2	C37-N8	3.51	1.36	1.32
4	B	604	TZ2	C30-C31	3.28	1.49	1.43
5	A	606	ACT	CH3-C	2.76	1.52	1.48
4	B	604	TZ2	C37-N8	2.61	1.35	1.32
5	B	605	ACT	CH3-C	2.28	1.51	1.48

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	605	TZ2	C37-N8-C33	5.92	124.98	117.67
4	B	604	TZ2	C37-N8-C33	5.68	124.67	117.67
3	B	601	NAG	C1-O5-C5	4.31	118.04	112.19
4	A	605	TZ2	C39-C37-N8	-4.13	120.16	123.68
4	B	604	TZ2	C39-C37-N8	-3.89	120.36	123.68
3	A	604	NAG	C1-O5-C5	2.69	115.84	112.19

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	604	TZ2	N18-C28-C29-N7
4	A	605	TZ2	N18-C28-C29-N7
6	B	607	PG4	O4-C7-C8-O5
8	B	606	7PG	O1-C3-C4-O2
8	B	606	7PG	O2-C5-C6-O3
8	B	606	7PG	O5-C11-C12-O6
8	B	606	7PG	O5-C10-C9-O4
6	A	607	PG4	O4-C7-C8-O5
3	B	601	NAG	O5-C5-C6-O6
6	A	607	PG4	O2-C3-C4-O3
6	A	607	PG4	C8-C7-O4-C6
6	B	607	PG4	O1-C1-C2-O2
6	A	607	PG4	C3-C4-O3-C5
8	B	606	7PG	C5-C6-O3-C7
8	B	606	7PG	C3-C4-O2-C5
6	B	607	PG4	C3-C4-O3-C5
6	B	607	PG4	C6-C5-O3-C4
6	A	607	PG4	C1-C2-O2-C3
6	B	607	PG4	O2-C3-C4-O3
8	B	606	7PG	C14-C13-O6-C12
6	B	607	PG4	C4-C3-O2-C2
6	B	607	PG4	O3-C5-C6-O4
8	B	606	7PG	C11-C12-O6-C13
8	B	606	7PG	C4-C3-O1-C2

There are no ring outliers.

4 monomers are involved in 6 short contacts:

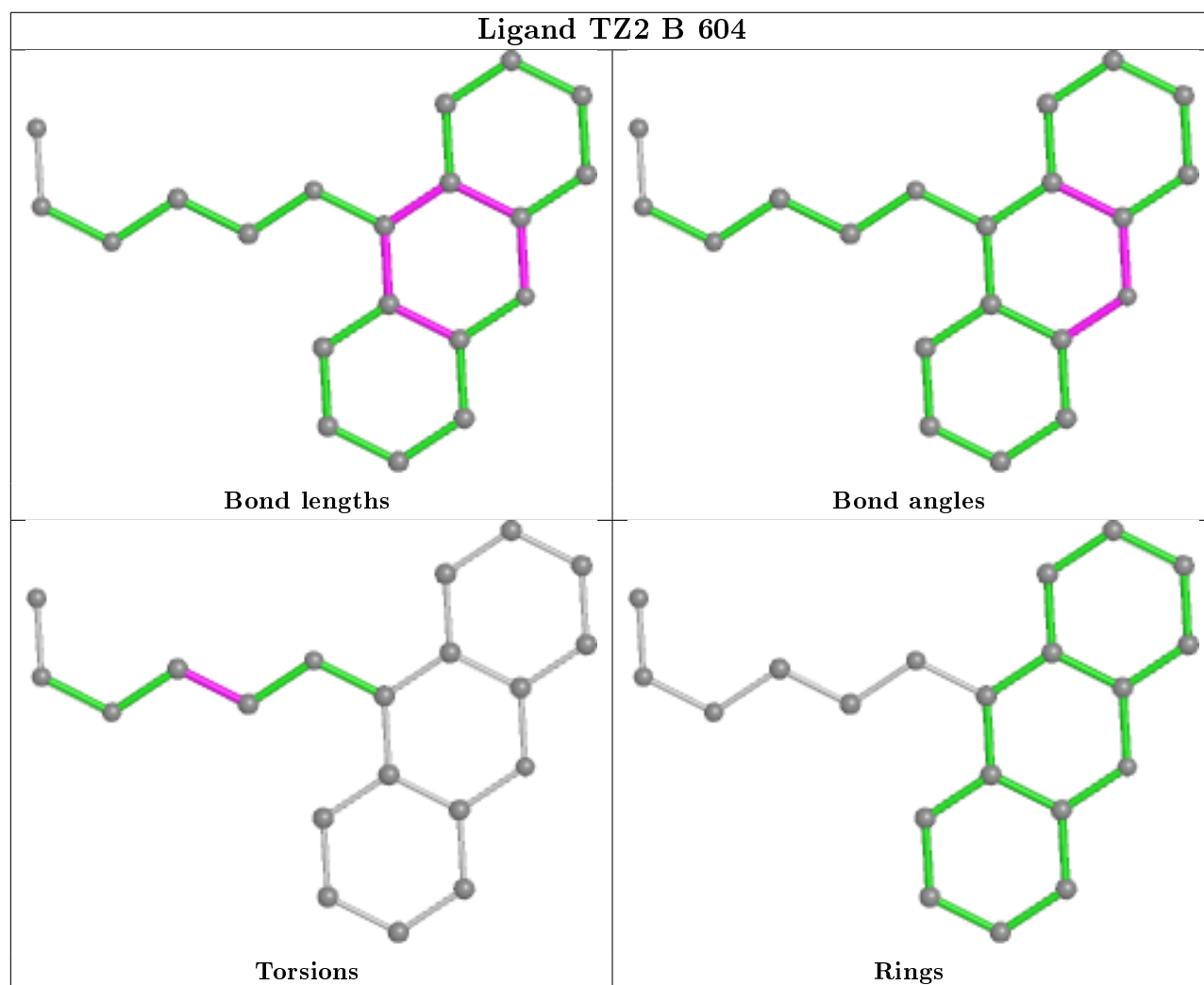
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	604	TZ2	1	0
8	B	606	7PG	3	0

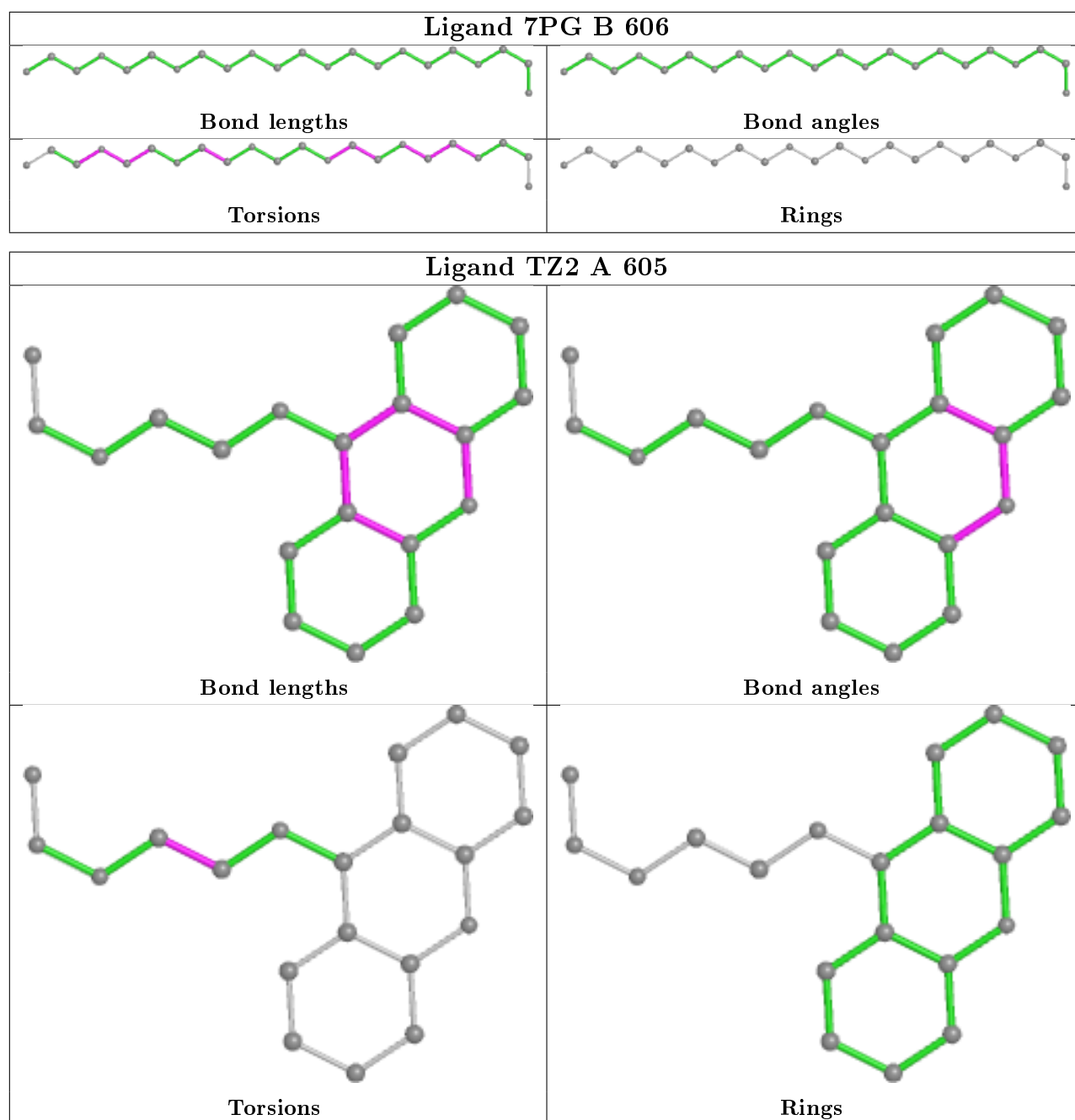
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	607	PG4	1	0
4	A	605	TZ2	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 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, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	538/543 (99%)	-0.22	16 (2%) 50 56	31, 44, 70, 141	0
1	B	536/543 (98%)	0.14	26 (4%) 29 35	33, 49, 81, 143	0
All	All	1074/1086 (98%)	-0.04	42 (3%) 39 45	31, 45, 78, 143	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	259	PRO	8.5
1	A	542	ALA	6.2
1	B	3	ARG	5.8
1	B	543	THR	5.8
1	A	541	SER	5.4
1	B	542	ALA	5.3
1	A	495	SER	5.2
1	A	540	LEU	4.9
1	B	264	GLY	4.7
1	A	496	LYS	4.4
1	B	540	LEU	3.9
1	A	493	ARG	3.5
1	B	497	SER	3.3
1	B	105	TYR	3.2
1	B	109	ALA	3.1
1	B	496	LYS	3.0
1	A	497	SER	3.0
1	B	76	LEU	3.0
1	A	165	ARG	2.9
1	B	541	SER	2.9
1	A	258	PRO	2.9
1	B	391	PRO	2.8
1	B	4	GLU	2.8
1	B	349	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	207	ALA	2.6
1	B	447[A]	HIS	2.5
1	B	441	LEU	2.5
1	A	118	ILE	2.5
1	B	204	ALA	2.5
1	A	464	ASN	2.4
1	B	350	ASN	2.4
1	A	494	ASP	2.4
1	B	451	ILE	2.3
1	B	227	LEU	2.3
1	B	10[A]	VAL	2.3
1	B	9	LEU	2.2
1	B	6	PRO	2.2
1	A	257	CYS	2.1
1	A	209	VAL	2.1
1	B	106	PRO	2.1
1	A	470	ARG	2.0
1	B	467	THR	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

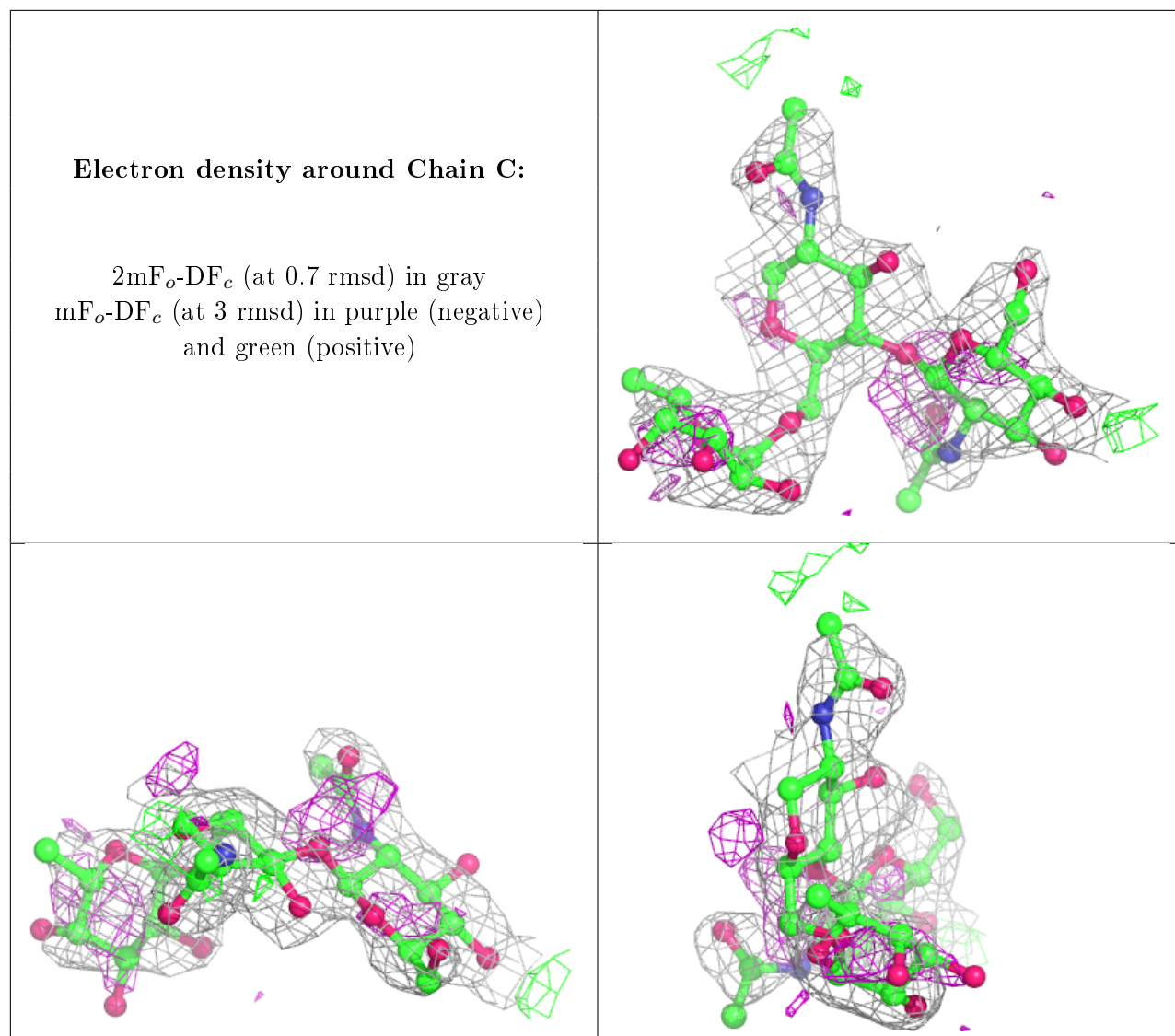
There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	NAG	C	2	14/15	0.77	0.39	98,101,102,104	0
2	FUC	C	3	10/11	0.79	0.49	101,104,109,109	0
2	NAG	C	1	14/15	0.88	0.31	76,83,94,97	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.



## 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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	PG4	A	607	13/13	0.75	0.18	74,82,88,89	0
3	NAG	A	604	14/15	0.76	0.35	109,112,115,116	0
3	NAG	B	602	14/15	0.77	0.42	113,118,119,120	0
3	NAG	B	601	14/15	0.83	0.44	98,103,106,107	0
6	PG4	B	607	13/13	0.84	0.15	76,83,94,95	0
8	7PG	B	606	22/26	0.87	0.16	55,63,79,80	0
7	CL	B	603	1/1	0.92	0.13	76,76,76,76	0

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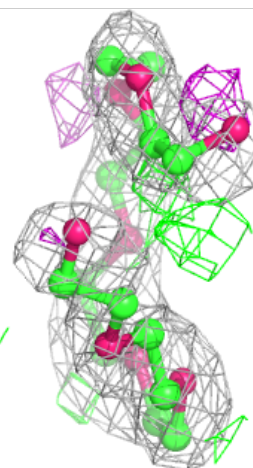
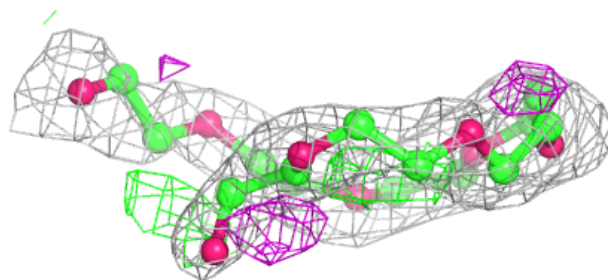
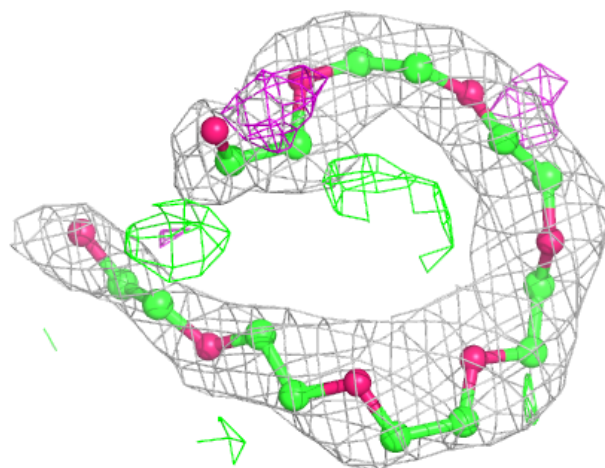
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	TZ2	B	604	20/20	0.94	0.19	40,48,74,75	0
4	TZ2	A	605	20/20	0.95	0.13	35,38,67,68	0
5	ACT	A	606	4/4	0.95	0.14	48,51,52,54	0
5	ACT	B	605	4/4	0.96	0.19	57,61,61,62	0

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.

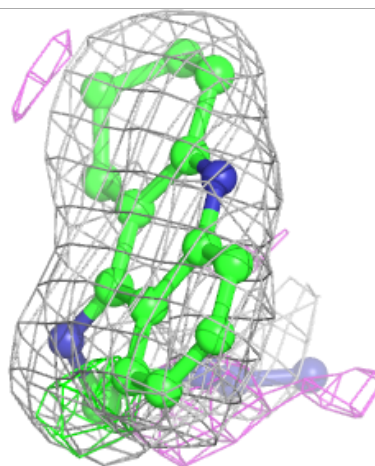
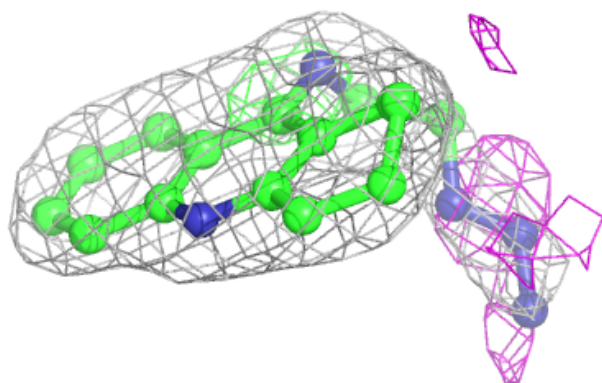
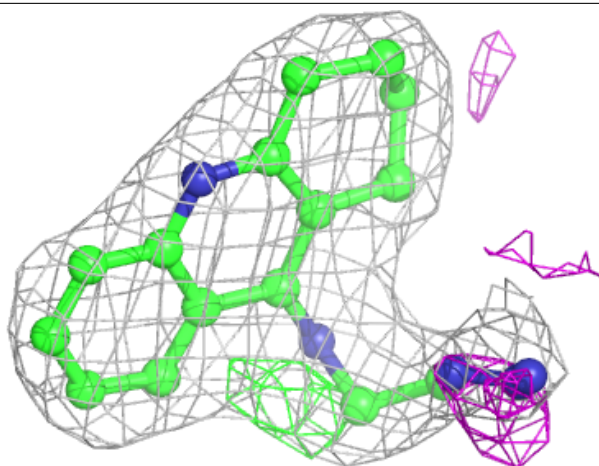
**Electron density around 7PG B 606:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



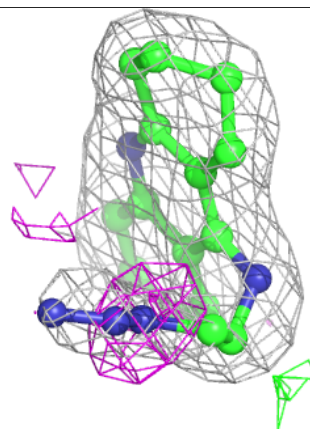
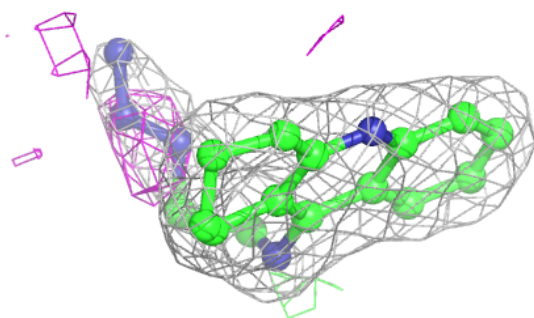
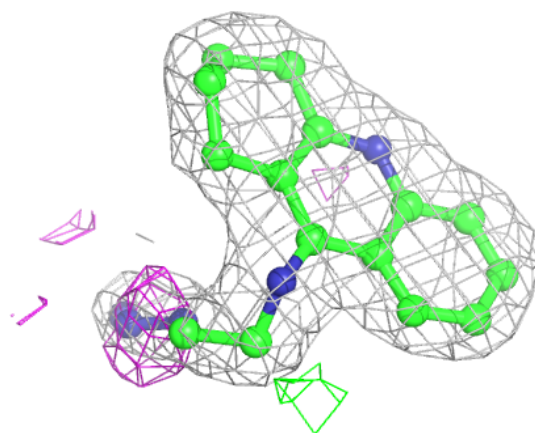
**Electron density around TZ2 B 604:**

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



**Electron density around TZ2 A 605:**

$2mF_o-DF_c$  (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.