



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 26, 2019 – 12:42 PM EDT

PDB ID : 5K5E  
Title : Discovery and Structure-Activity Relationships of a Highly Selective Butyryl cholinesterase Inhibitor by Structure-Based Virtual Screening  
Authors : De la Mora, E.; Dighe, S.N.; Deora, G.S.; Ross, B.P.; Nachon, F.; Brazzolotto, X.  
Deposited on : 2016-05-23  
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](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 : 1.8.0 (224370), CSD as540be (2019)  
Xtriage (Phenix) : 1.13  
EDS : 2.4  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.4

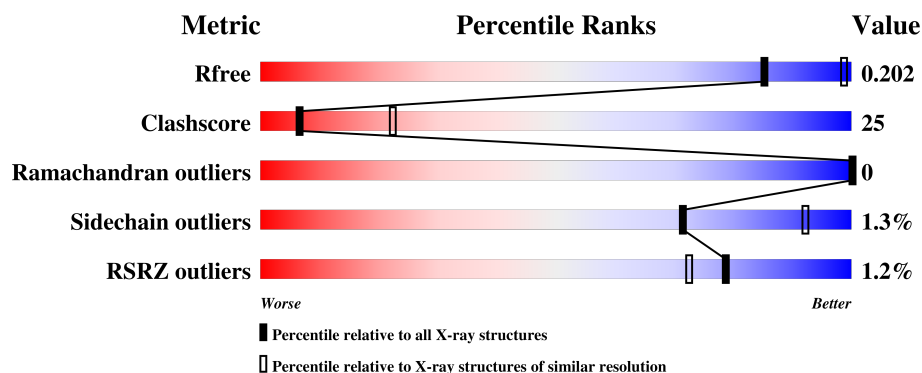
# 1 Overall quality at a glance

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))
$R_{free}$	111664	2792 (2.80-2.80)
Clashscore	122126	3209 (2.80-2.80)
Ramachandran outliers	120053	3158 (2.80-2.80)
Sidechain outliers	120020	3160 (2.80-2.80)
RSRZ outliers	108989	2726 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	529	<div> <div></div> <div>70%28%.</div> </div>
1	B	529	<div> <div>2%</div> <div>66%30%... </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	NAG	A	608	-	-	-	X
2	NAG	B	602	-	-	X	-
2	NAG	B	608	-	-	X	-

## 2 Entry composition [i](#)

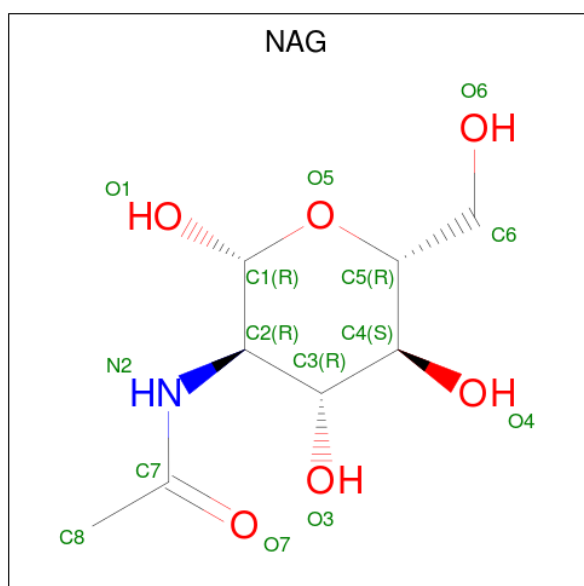
There are 6 unique types of molecules in this entry. The entry contains 8862 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
1	A	527	Total	C	N	O	S	0	2	0
			4215	2718	712	770	15			
1	B	526	Total	C	N	O	S	0	1	0
			4200	2709	706	770	15			

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



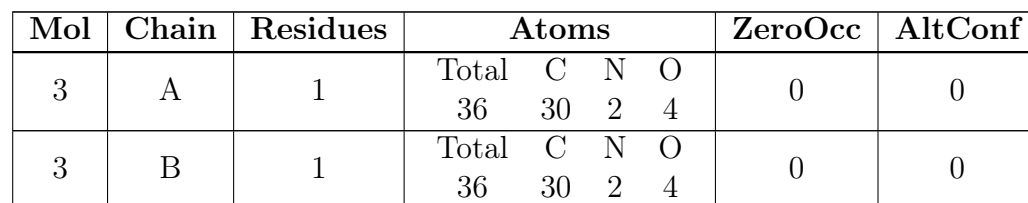
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		


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

- Molecule 3 is [(2 {R})-oxolan-2-yl]methyl 4-(9-ethylcarbazol-3-yl)-2-methyl-5-oxidanylidene-4,6,7,8-tetrahydro-1 {H}-quinoline-3-carboxylate (three-letter code: 6QS) (formula: C<sub>30</sub>H<sub>32</sub>N<sub>2</sub>O<sub>4</sub>).



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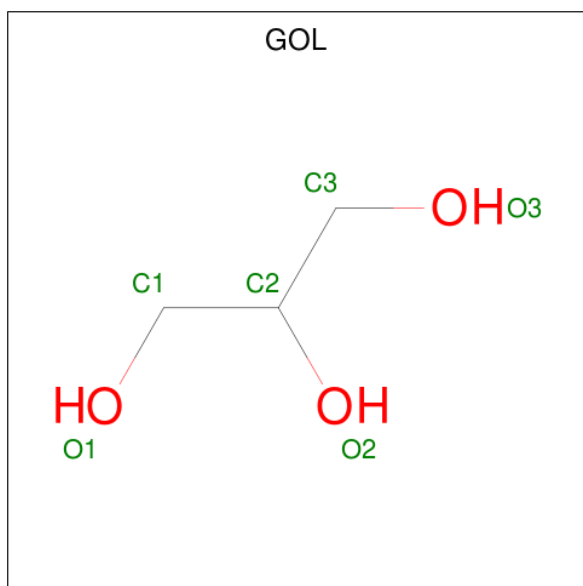
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0



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

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		

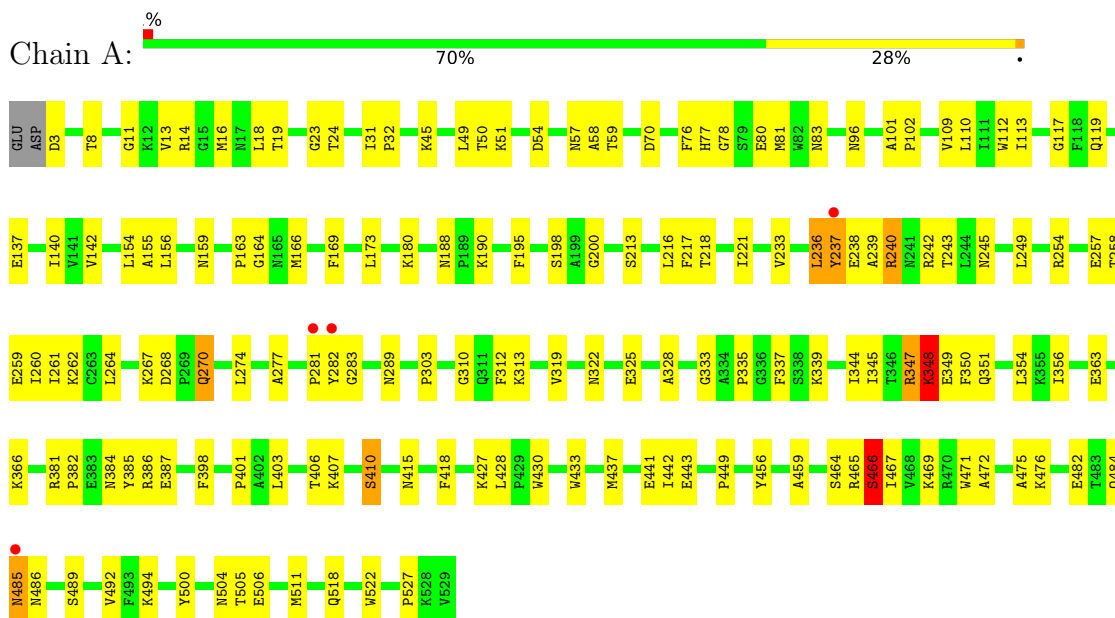
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	67	Total	O	0	0
			67	67		
6	B	60	Total	O	0	0
			60	60		

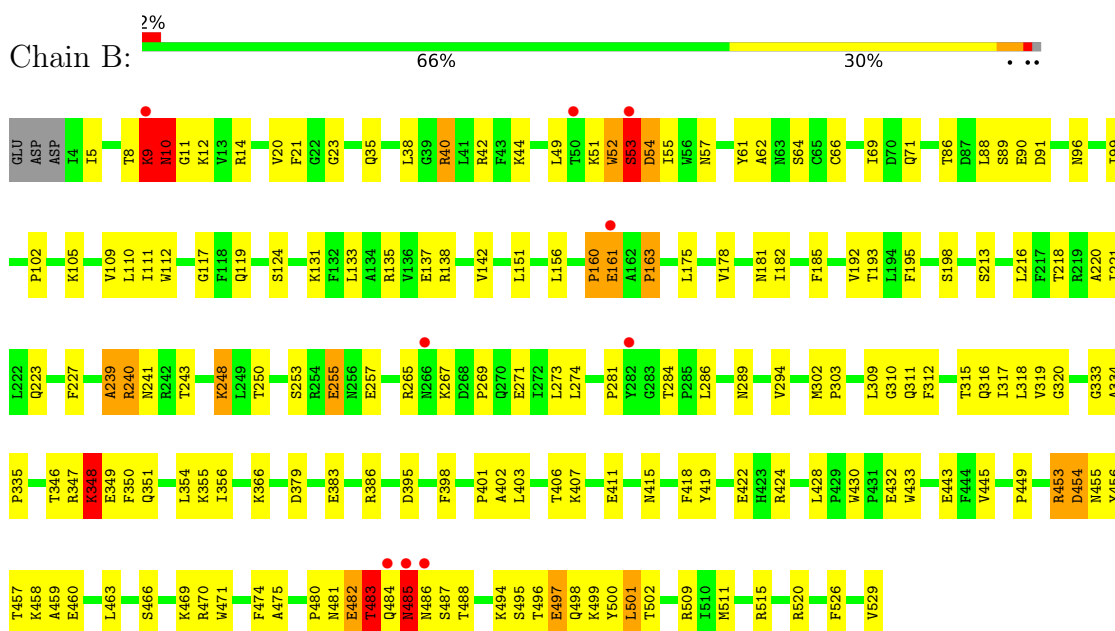
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: Cholinesterase



#### • Molecule 1: Cholinesterase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.81Å 80.07Å 230.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.98 – 2.80 19.98 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.2 (19.98-2.80) 99.1 (19.98-2.80)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.55 (at 2.79Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, $R_{free}$	0.173 , 0.202 0.173 , 0.202	Depositor DCC
$R_{free}$ test set	1707 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	69.3	Xtriage
Anisotropy	0.258	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 50.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8862	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.64% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, EDO, 6QS, NAG

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	0.54	1/4340 (0.0%)	0.81	8/5891 (0.1%)
1	B	0.57	3/4319 (0.1%)	0.89	19/5864 (0.3%)
All	All	0.55	4/8659 (0.0%)	0.85	27/11755 (0.2%)

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	5
1	B	0	9
All	All	0	14

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	497[A]	GLU	CD-OE1	-6.33	1.18	1.25
1	B	497[B]	GLU	CD-OE1	-6.33	1.18	1.25
1	A	348	LYS	CB-CG	5.36	1.67	1.52
1	B	163	PRO	N-CD	5.05	1.54	1.47

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	485	ASN	O-C-N	-18.96	92.37	122.70
1	B	483	THR	O-C-N	-15.10	98.55	122.70
1	A	348	LYS	O-C-N	-14.33	99.78	122.70
1	B	53	SER	CA-C-N	-14.20	85.97	117.20
1	B	485	ASN	O-C-N	-12.51	102.68	122.70

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	237	TYR	Mainchain
1	A	348	LYS	Mainchain,Peptide
1	A	466	SER	Mainchain
1	A	485	ASN	Mainchain
1	B	9	LYS	Peptide

## 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	4215	0	4118	174	3
1	B	4200	0	4092	259	3
2	A	112	0	102	6	0
2	B	112	0	103	19	0
3	A	36	0	0	1	0
3	B	36	0	0	3	0
4	A	4	0	6	1	0
4	B	8	0	12	0	0
5	B	12	0	16	1	0
6	A	67	0	0	6	0
6	B	60	0	0	5	0
All	All	8862	0	8449	433	3

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 25.

The worst 5 of 433 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:483:THR:CG2	2:B:608:NAG:HN2	1.12	1.58
1:B:12:LYS:CG	1:B:55:ILE:CD1	1.83	1.54
1:B:12:LYS:HG3	1:B:55:ILE:CD1	1.06	1.54
1:B:12:LYS:CG	1:B:55:ILE:HD13	1.36	1.47
1:A:110:LEU:HB3	1:A:195:PHE:CE2	1.51	1.44

All (3) 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:237:TYR:OH	1:B:455:ASN:ND2[1_565]	1.11	1.09
1:A:237:TYR:CZ	1:B:455:ASN:ND2[1_565]	1.57	0.63
1:A:237:TYR:OH	1:B:455:ASN:CG[1_565]	2.02	0.18

## 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	527/529 (100%)	498 (94%)	29 (6%)	0	100	100
1	B	525/529 (99%)	491 (94%)	34 (6%)	0	100	100
All	All	1052/1058 (99%)	989 (94%)	63 (6%)	0	100	100

There are no Ramachandran outliers to report.

### 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	454/454 (100%)	449 (99%)	5 (1%)	76	93
1	B	452/454 (100%)	445 (98%)	7 (2%)	67	91
All	All	906/908 (100%)	894 (99%)	12 (1%)	71	92

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	40	ARG
1	B	248	LYS
1	B	494	LYS
1	A	471	TRP
1	B	485	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	486	ASN
1	B	311	GLN
1	B	57	ASN
1	A	188	ASN
1	B	181	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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

23 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	A	601	1	14,14,15	0.63	1 (7%)	17,19,21	0.82	1 (5%)
2	NAG	A	602	-	14,14,15	1.61	2 (14%)	17,19,21	1.16	1 (5%)
2	NAG	A	603	1,2	14,14,15	0.99	1 (7%)	17,19,21	1.77	2 (11%)
2	NAG	A	604	2	14,14,15	0.68	0	17,19,21	0.72	1 (5%)
2	NAG	A	605	1	14,14,15	0.35	0	17,19,21	0.71	1 (5%)
2	NAG	A	606	1	14,14,15	0.53	0	17,19,21	0.87	1 (5%)
2	NAG	A	607	1,2	14,14,15	0.72	0	17,19,21	1.09	1 (5%)
2	NAG	A	608	2	14,14,15	1.62	2 (14%)	17,19,21	1.33	1 (5%)
3	6QS	A	609	-	39,41,41	2.82	12 (30%)	52,60,60	2.18	17 (32%)
4	EDO	A	610	-	3,3,3	0.67	0	2,2,2	0.46	0
2	NAG	B	601	1	14,14,15	0.42	0	17,19,21	0.92	1 (5%)
2	NAG	B	602	-	14,14,15	2.12	2 (14%)	17,19,21	1.93	1 (5%)
2	NAG	B	603	1	14,14,15	0.27	0	17,19,21	0.47	0
2	NAG	B	604	1	14,14,15	0.64	1 (7%)	17,19,21	1.03	1 (5%)
2	NAG	B	605	1	14,14,15	0.64	1 (7%)	17,19,21	0.71	1 (5%)
2	NAG	B	606	1,2	14,14,15	0.60	1 (7%)	17,19,21	0.73	0
2	NAG	B	607	2	14,14,15	0.52	0	17,19,21	0.59	0
2	NAG	B	608	1	14,14,15	0.27	0	17,19,21	0.56	0
3	6QS	B	609	-	39,41,41	2.75	13 (33%)	52,60,60	2.06	13 (25%)
4	EDO	B	610	-	3,3,3	0.79	0	2,2,2	0.16	0
4	EDO	B	611	-	3,3,3	0.66	0	2,2,2	0.08	0
5	GOL	B	612	-	5,5,5	0.36	0	5,5,5	0.30	0
5	GOL	B	613	-	5,5,5	0.47	0	5,5,5	0.28	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	A	601	1	-	0/6/23/26	0/1/1/1
2	NAG	A	602	-	-	2/6/23/26	0/1/1/1
2	NAG	A	603	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	604	2	-	2/6/23/26	0/1/1/1
2	NAG	A	605	1	-	2/6/23/26	0/1/1/1
2	NAG	A	606	1	-	0/6/23/26	0/1/1/1
2	NAG	A	607	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	608	2	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	6QS	A	609	-	-	6/15/52/52	0/6/6/6
4	EDO	A	610	-	-	1/1/1/1	-
2	NAG	B	601	1	-	2/6/23/26	0/1/1/1
2	NAG	B	602	-	-	2/6/23/26	0/1/1/1
2	NAG	B	603	1	-	2/6/23/26	0/1/1/1
2	NAG	B	604	1	-	1/6/23/26	0/1/1/1
2	NAG	B	605	1	-	4/6/23/26	0/1/1/1
2	NAG	B	606	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	607	2	-	2/6/23/26	0/1/1/1
2	NAG	B	608	1	-	4/6/23/26	0/1/1/1
3	6QS	B	609	-	-	4/15/52/52	0/6/6/6
4	EDO	B	610	-	-	0/1/1/1	-
4	EDO	B	611	-	-	0/1/1/1	-
5	GOL	B	612	-	-	0/4/4/4	-
5	GOL	B	613	-	-	2/4/4/4	-

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	609	6QS	C19-C09	9.31	1.47	1.35
3	A	609	6QS	C19-C09	9.24	1.47	1.35
3	A	609	6QS	C06-C07	7.45	1.46	1.36
3	B	609	6QS	C06-C07	7.32	1.45	1.36
2	B	602	NAG	O5-C1	7.25	1.55	1.43

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	602	NAG	C1-O5-C5	7.70	122.66	112.20
3	B	609	6QS	C20-C19-C09	-7.47	120.10	127.61
3	A	609	6QS	C20-C19-C09	-7.00	120.57	127.61
2	A	603	NAG	C1-O5-C5	5.19	119.26	112.20
3	A	609	6QS	C04-C03-C02	-4.94	104.63	113.57

There are no chirality outliers.

5 of 37 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	609	6QS	O11-C12-C13-O14

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Mol	Chain	Res	Type	Atoms
3	A	609	6QS	O11-C12-C13-C17
3	A	609	6QS	C30-C29-N28-C27
3	A	609	6QS	C30-C29-N28-C31
5	B	613	GOL	O1-C1-C2-C3

There are no ring outliers.

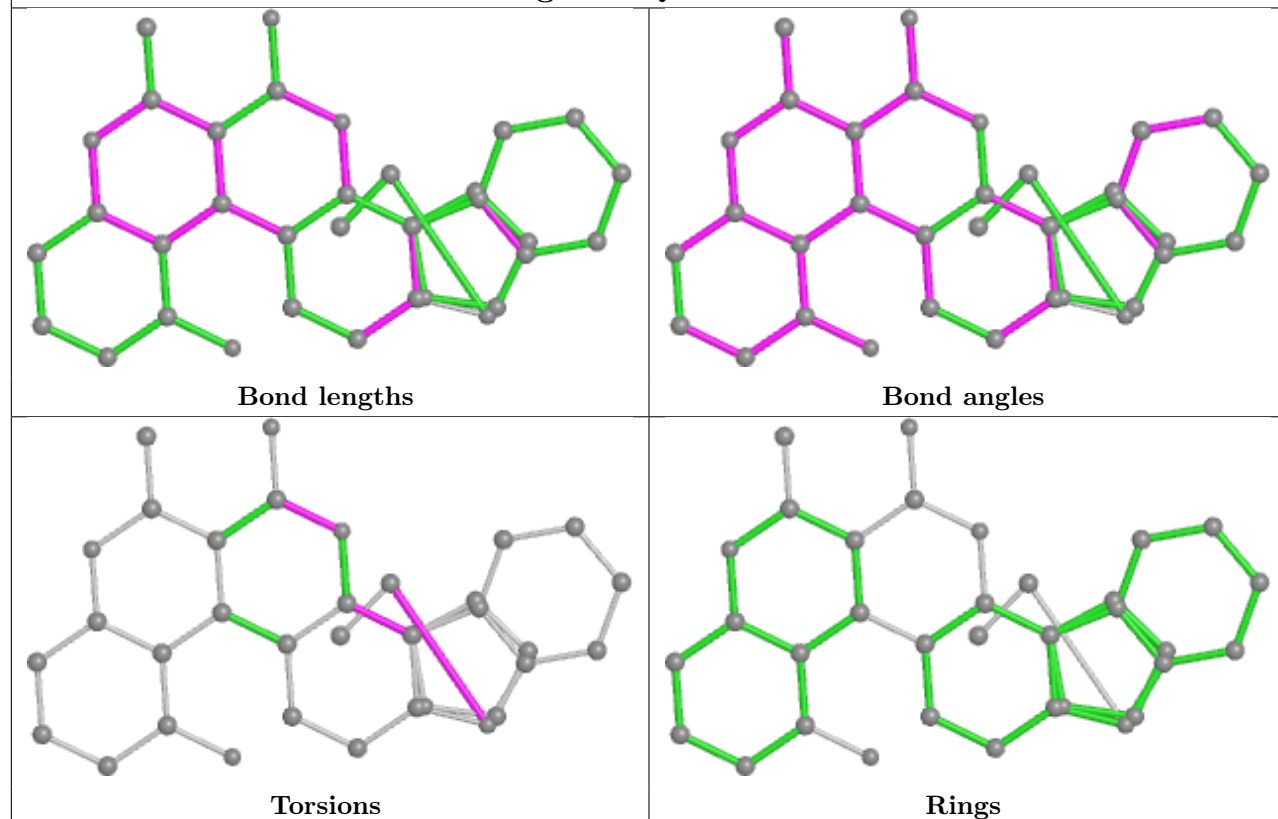
9 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	602	NAG	5	0
2	A	603	NAG	1	0
3	A	609	6QS	1	0
4	A	610	EDO	1	0
2	B	602	NAG	9	0
2	B	604	NAG	2	0
2	B	608	NAG	8	0
3	B	609	6QS	3	0
5	B	612	GOL	1	0

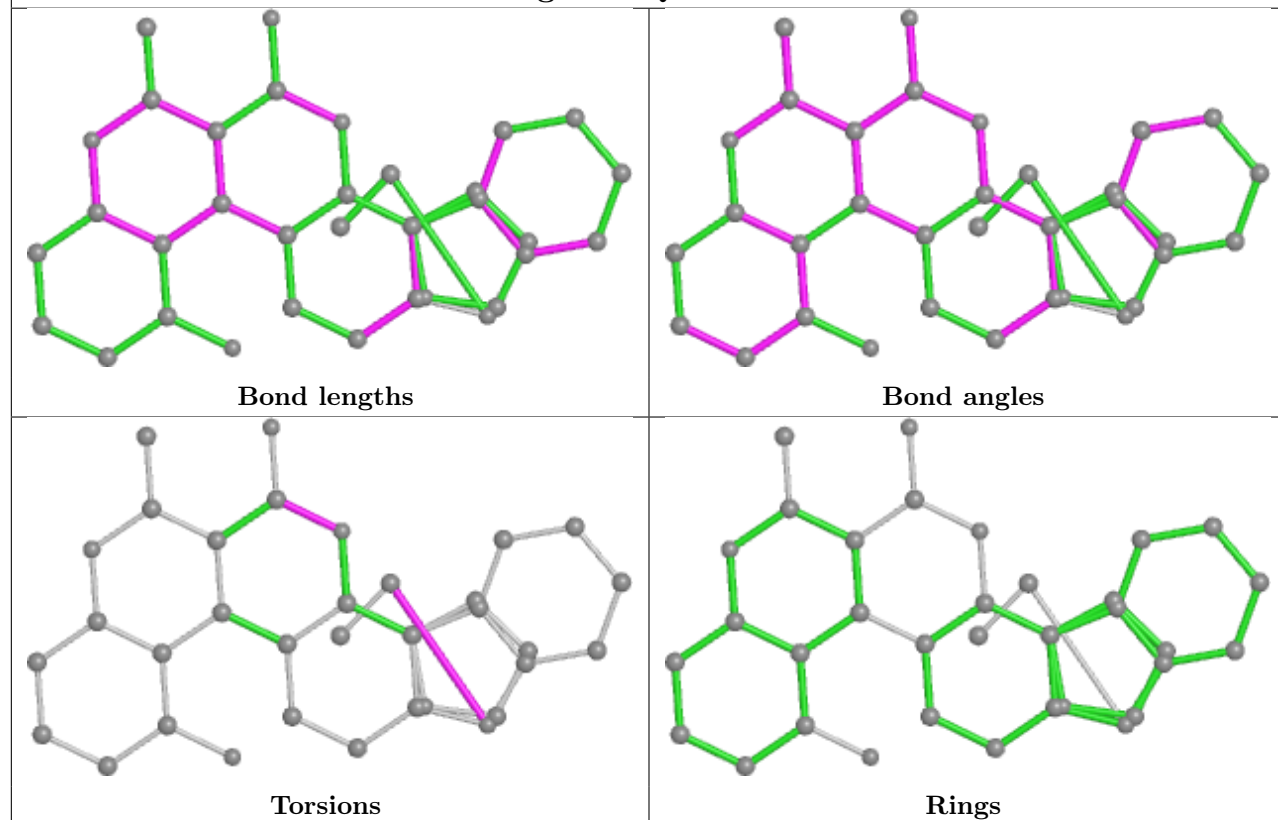
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



## Ligand 6QS A 609



## Ligand 6QS B 609



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	527/529 (99%)	-0.45	4 (0%) 86 81	39, 68, 107, 164	0
1	B	526/529 (99%)	-0.39	9 (1%) 70 63	43, 74, 118, 167	0
All	All	1053/1058 (99%)	-0.42	13 (1%) 79 72	39, 71, 113, 167	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	237	TYR	5.3
1	A	282	TYR	4.7
1	B	53	SER	4.3
1	B	282	TYR	4.2
1	A	281	PRO	3.6

### 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](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

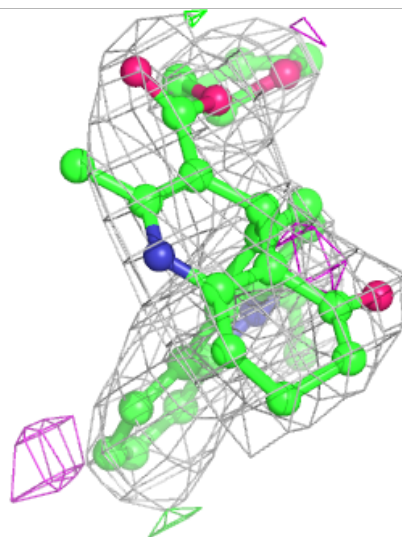
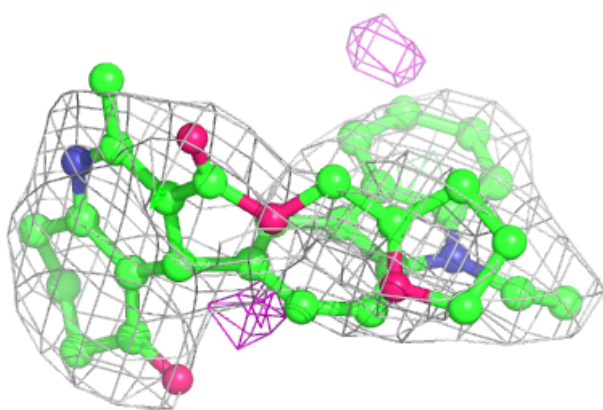
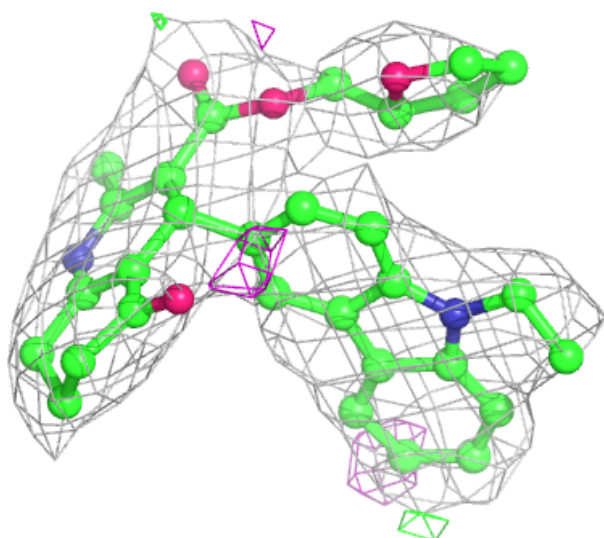
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	A	601	14/15	0.71	0.39	81,110,127,132	0
2	NAG	A	602	14/15	0.72	0.31	83,114,120,124	0
2	NAG	A	608	14/15	0.72	0.46	104,118,122,124	0
2	NAG	B	604	14/15	0.76	0.31	98,133,145,154	0
2	NAG	B	601	14/15	0.76	0.39	102,117,136,140	0
2	NAG	B	602	14/15	0.78	0.31	103,116,128,128	0
4	EDO	B	610	4/4	0.79	0.28	80,87,95,96	0
2	NAG	B	607	14/15	0.80	0.49	110,128,140,141	0
2	NAG	B	608	14/15	0.81	0.27	109,131,153,161	0
2	NAG	A	604	14/15	0.82	0.46	134,141,149,150	0
2	NAG	A	605	14/15	0.83	0.31	105,124,131,131	0
2	NAG	B	603	14/15	0.84	0.30	104,121,127,127	0
2	NAG	A	606	14/15	0.84	0.24	83,93,111,115	0
5	GOL	B	613	6/6	0.85	0.20	79,92,100,108	0
4	EDO	B	611	4/4	0.87	0.18	78,87,91,95	0
2	NAG	A	607	14/15	0.87	0.26	92,111,120,121	0
2	NAG	B	606	14/15	0.90	0.22	81,91,113,118	0
2	NAG	B	605	14/15	0.90	0.23	100,107,117,120	0
3	6QS	B	609	36/36	0.92	0.19	48,73,116,118	0
5	GOL	B	612	6/6	0.92	0.28	77,80,90,91	0
2	NAG	A	603	14/15	0.93	0.24	76,92,110,124	0
4	EDO	A	610	4/4	0.93	0.21	80,80,81,83	0
3	6QS	A	609	36/36	0.94	0.17	62,77,93,98	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.

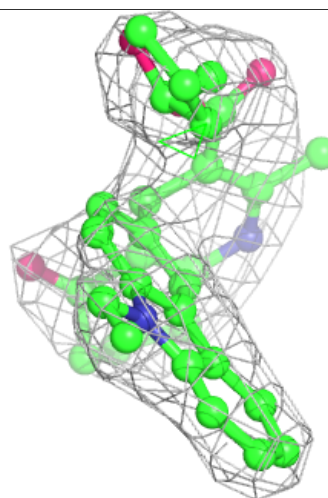
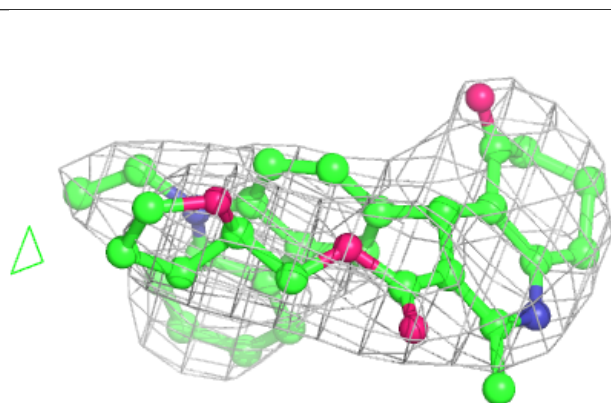
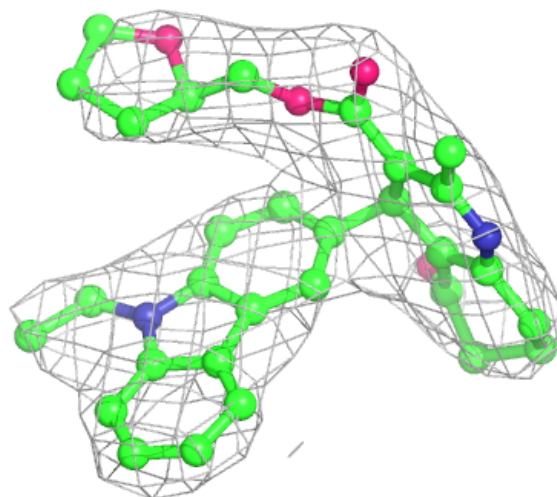
**Electron density around 6QS B 609:**

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



**Electron density around 6QS A 609:**

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.