



## wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Dec 3, 2019 – 09:07 PM EST

PDB ID : 6FEQ  
EMDB ID: : EMD-4246  
Title : Structure of inhibitor-bound ABCG2  
Authors : Jackson, S.M.; Manolaridis, I.; Kowal, J.; Zechner, M.; Altmann, K.H.; Locher, K.P.  
Deposited on : 2018-01-03  
Resolution : 3.60 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report  
for a publicly released PDB/EMDB 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/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Mogul : 1.8.0 (224370), CSD as540be (2019)  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.4

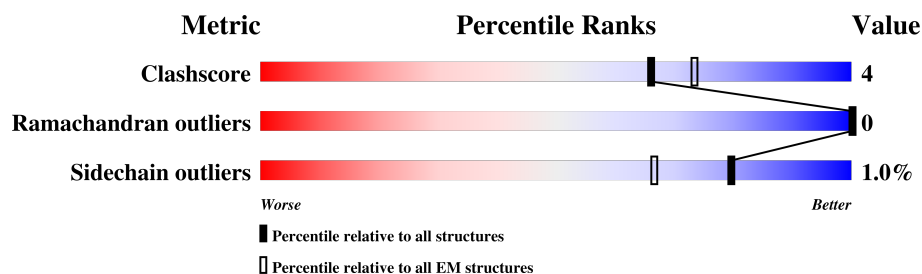
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.60 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)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	655	73% 13% 14%
1	B	655	76% 10% 14%
2	C	214	47% . 50%
2	E	214	47% . 50%
3	D	221	44% 9% 47%
3	F	221	44% 9% 47%

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12397 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 ATP-binding cassette sub-family G member 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	566	Total	C	N	O	S	0	0
			4405	2859	726	791	29		
1	B	566	Total	C	N	O	S	0	0
			4405	2859	726	791	29		

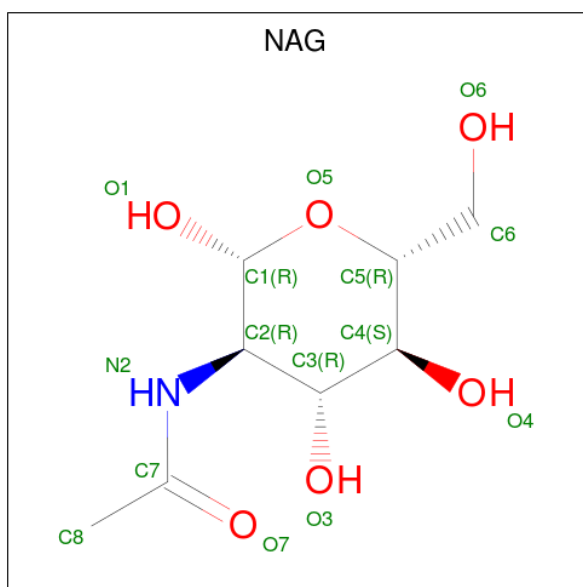
- Molecule 2 is a protein called 5D3(Fab) light chain variable domain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	107	Total	C	N	O	S	0	0
			822	521	137	162	2		
2	E	107	Total	C	N	O	S	0	0
			822	521	137	162	2		

- Molecule 3 is a protein called 5D3(Fab) heavy chain variable domain.

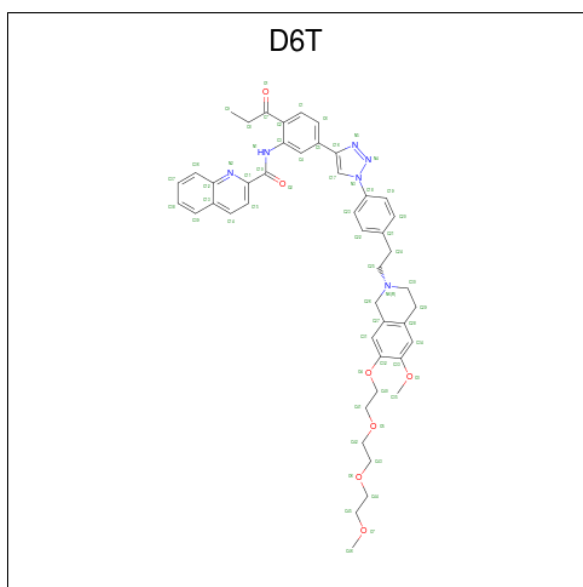
Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	118	Total	C	N	O	S	0	0
			928	592	153	180	3		
3	F	118	Total	C	N	O	S	0	0
			928	592	153	180	3		

- Molecule 4 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



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

- Molecule 5 is {N}-[5-[1-[4-[2-[6-methoxy-7-[2-[2-(2-methoxyethoxy)ethoxy]ethoxy]-3,4-dihydro-1 {H}-isoquinolin-2-yl]ethyl]phenyl]-1,2,3-triazol-4-yl]-2-propanoyl-phenyl]quinoline-2-carboxamide (three-letter code: D6T) (formula: C<sub>46</sub>H<sub>50</sub>N<sub>6</sub>O<sub>7</sub>).

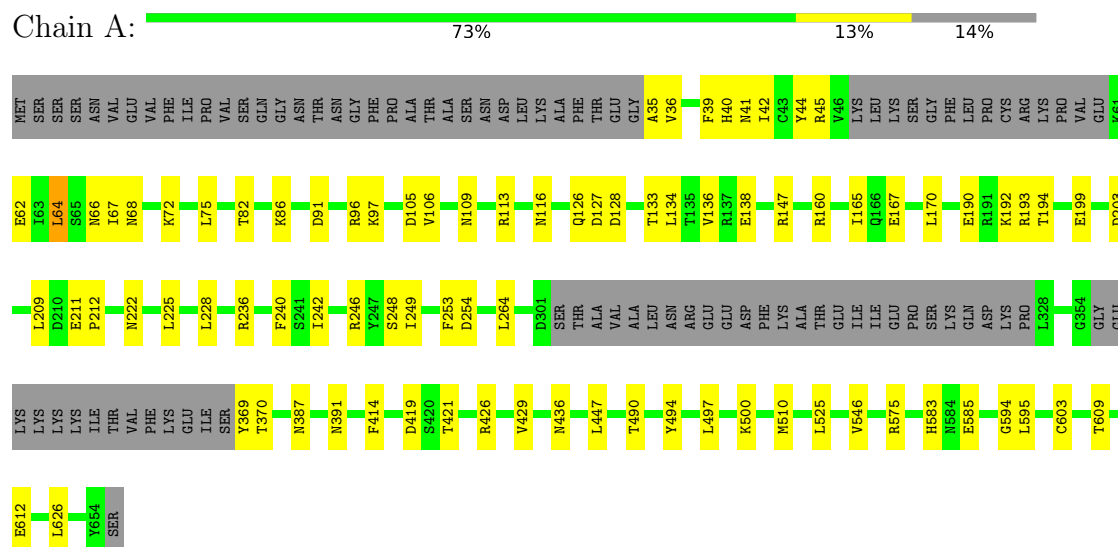


Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total	C	N	O	0
			59	46	6	7	

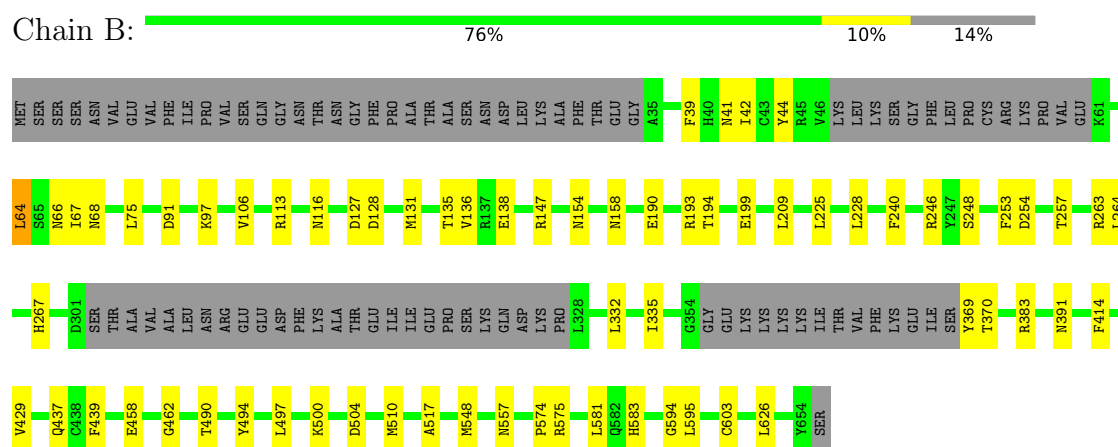
### 3 Residue-property plots

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. 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.

- Molecule 1: ATP-binding cassette sub-family G member 2



- Molecule 1: ATP-binding cassette sub-family G member 2



- Molecule 2: 5D3(Fab) light chain variable domain





## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	306913	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	1.55	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: D6T, 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  >2	RMSZ	# Z  >2
1	A	0.44	0/4497	0.56	1/6085 (0.0%)
1	B	0.44	0/4497	0.55	1/6085 (0.0%)
2	C	0.54	0/842	0.64	1/1144 (0.1%)
2	E	0.54	0/842	0.64	1/1144 (0.1%)
3	D	0.54	0/953	0.62	0/1297
3	F	0.54	0/953	0.62	0/1297
All	All	0.47	0/12584	0.58	4/17052 (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	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	64	LEU	CA-CB-CG	7.22	131.90	115.30
1	B	64	LEU	CA-CB-CG	6.90	131.17	115.30
2	C	33	LEU	CA-CB-CG	5.02	126.84	115.30
2	E	33	LEU	CA-CB-CG	5.00	126.80	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	A	414	PHE	Peptide
1	B	414	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	4405	0	4481	48	0
1	B	4405	0	4481	38	0
2	C	822	0	801	4	0
2	E	822	0	801	4	0
3	D	928	0	890	12	0
3	F	928	0	890	12	0
4	A	14	0	13	1	0
4	B	14	0	13	1	0
5	A	59	0	0	2	0
All	All	12397	0	12370	110	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 4.

The worst 5 of 110 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:39:PHE:HB2	1:B:42:ILE:HD11	1.81	0.61
1:B:594:GLY:H	3:F:53:ASN:HD21	1.48	0.61
1:A:75:LEU:H	1:A:254:ASP:HB2	1.65	0.61
1:B:44:TYR:HB3	1:B:64:LEU:HD13	1.83	0.59
3:F:18:LEU:HB3	3:F:83:LEU:HB3	1.84	0.59

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 PDB entries followed by that with respect to all EM entries.

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	558/655 (85%)	537 (96%)	21 (4%)	0	100	100
1	B	558/655 (85%)	534 (96%)	24 (4%)	0	100	100
2	C	105/214 (49%)	94 (90%)	11 (10%)	0	100	100
2	E	105/214 (49%)	94 (90%)	11 (10%)	0	100	100
3	D	116/221 (52%)	104 (90%)	12 (10%)	0	100	100
3	F	116/221 (52%)	105 (90%)	11 (10%)	0	100	100
All	All	1558/2180 (72%)	1468 (94%)	90 (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 PDB entries followed by that with respect to all EM entries.

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	482/560 (86%)	477 (99%)	5 (1%)	78	90
1	B	482/560 (86%)	478 (99%)	4 (1%)	83	93
2	C	91/189 (48%)	91 (100%)	0	100	100
2	E	91/189 (48%)	91 (100%)	0	100	100
3	D	102/193 (53%)	100 (98%)	2 (2%)	58	83
3	F	102/193 (53%)	100 (98%)	2 (2%)	58	83
All	All	1350/1884 (72%)	1337 (99%)	13 (1%)	80	90

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	41	ASN
1	B	116	ASN
3	D	65	ARG
1	A	575	ARG
3	D	53	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	68	ASN
1	B	375	HIS
3	F	53	ASN
1	B	116	ASN
1	B	243	HIS

### 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](#)

3 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
4	NAG	A	1001	1	14,14,15	0.73	1 (7%)	17,19,21	0.71	0
5	D6T	A	1002	-	64,65,65	4.17	32 (50%)	80,88,88	2.93	21 (26%)
4	NAG	B	1001	1	14,14,15	0.63	1 (7%)	17,19,21	0.66	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
4	NAG	A	1001	1	-	2/6/23/26	0/1/1/1
5	D6T	A	1002	-	-	20/40/49/49	0/7/7/7
4	NAG	B	1001	1	-	2/6/23/26	0/1/1/1

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1002	D6T	C31-C27	13.16	1.62	1.39
5	A	1002	D6T	C34-C28	13.00	1.61	1.39
5	A	1002	D6T	C4-C3	9.76	1.54	1.39
5	A	1002	D6T	C20-C19	9.13	1.55	1.38
5	A	1002	D6T	C1-C2	8.79	1.54	1.39

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1002	D6T	C29-C30-N6	16.31	129.48	111.06
5	A	1002	D6T	C27-C26-N6	13.43	129.64	112.05
5	A	1002	D6T	O3-C33-C34	-4.55	116.38	124.14
5	A	1002	D6T	C18-N3-N4	4.32	126.08	117.28
5	A	1002	D6T	C31-C27-C28	-4.23	113.26	118.84

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1002	D6T	C2-C7-C8-C9
5	A	1002	D6T	O1-C7-C8-C9
4	B	1001	NAG	O5-C5-C6-O6
5	A	1002	D6T	N1-C10-C11-C15

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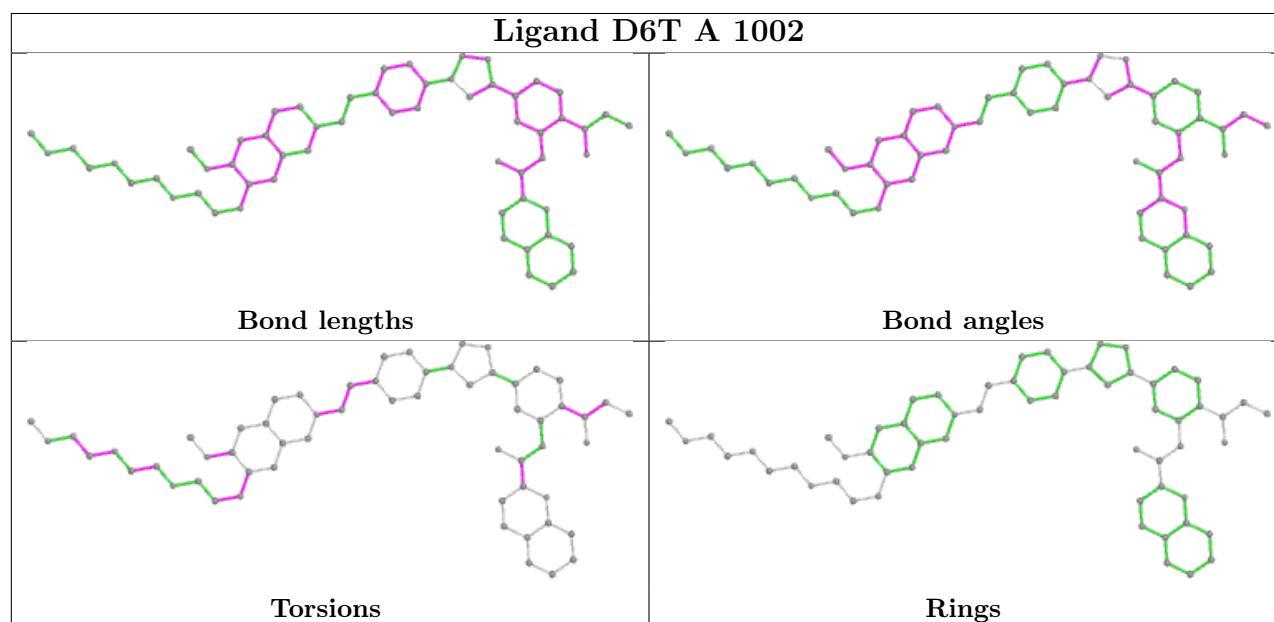
Mol	Chain	Res	Type	Atoms
5	A	1002	D6T	O2-C10-C11-N2

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1001	NAG	1	0
5	A	1002	D6T	2	0
4	B	1001	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 ⓘ

There are no chain breaks in this entry.