



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 2, 2023 – 10:16 AM EDT

PDB ID : 6MWK
Title : Crystal structure of 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (IspF) Burkholderia pseudomallei in complex with ligand HGN-0883
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2018-10-29
Resolution : 1.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : **FAILED**
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) : 2.35.1

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 1.80 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 4133 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 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	160	Total 1220	C 769	N 225	O 223	S 3	0	5	0
1	B	160	Total 1199	C 757	N 219	O 221	S 2	0	5	0
1	C	160	Total 1182	C 743	N 219	O 218	S 2	0	2	0

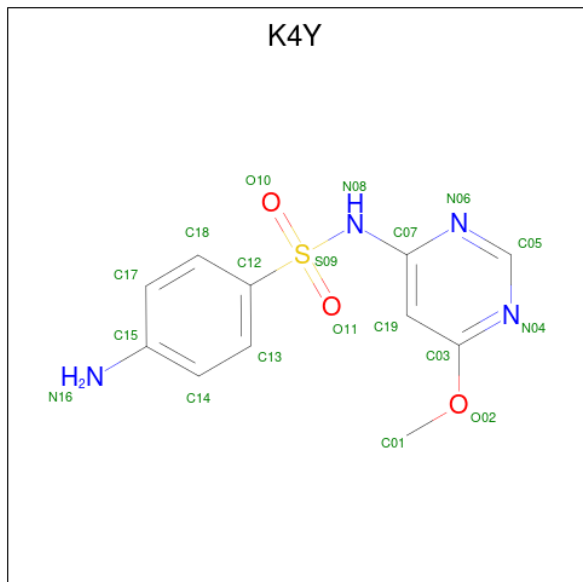
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q3JRA0
A	-2	PRO	-	expression tag	UNP Q3JRA0
A	-1	GLY	-	expression tag	UNP Q3JRA0
A	0	SER	-	expression tag	UNP Q3JRA0
B	-3	GLY	-	expression tag	UNP Q3JRA0
B	-2	PRO	-	expression tag	UNP Q3JRA0
B	-1	GLY	-	expression tag	UNP Q3JRA0
B	0	SER	-	expression tag	UNP Q3JRA0
C	-3	GLY	-	expression tag	UNP Q3JRA0
C	-2	PRO	-	expression tag	UNP Q3JRA0
C	-1	GLY	-	expression tag	UNP Q3JRA0
C	0	SER	-	expression tag	UNP Q3JRA0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

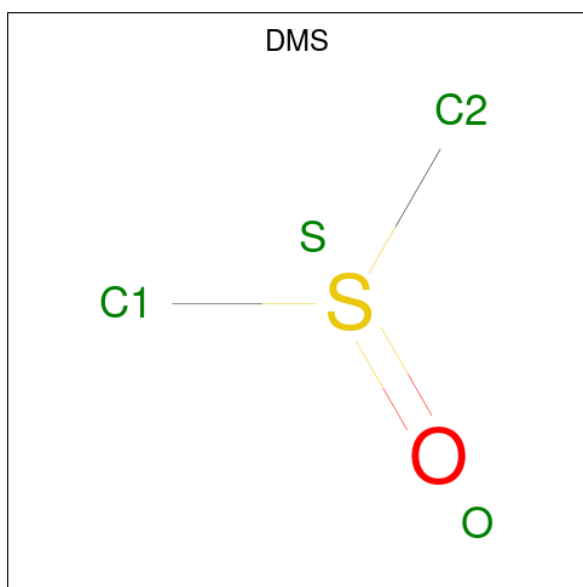
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Zn 1	0	0
2	B	1	Total 1	Zn 1	0	0
2	C	1	Total 1	Zn 1	0	0

- Molecule 3 is 4-amino-N-(6-methoxypyrimidin-4-yl)benzene-1-sulfonamide (three-letter code: K4Y) (formula: $C_{11}H_{12}N_4O_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	A	1	Total	C	N	O	S	0	0
			19	11	4	3	1		
3	B	1	Total	C	N	O	S	0	0
			19	11	4	3	1		
3	C	1	Total	C	N	O	S	0	0
			19	11	4	3	1		

- Molecule 4 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).

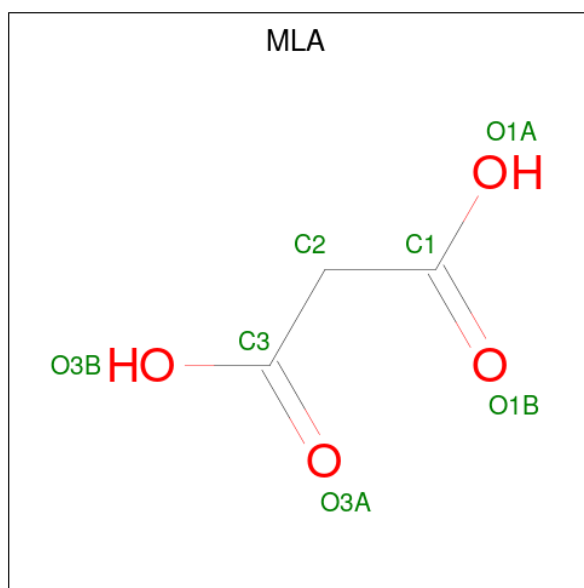


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	S	0	0
			4	2	1	1		
4	A	1	Total	C	O	S	0	0
			4	2	1	1		
4	B	1	Total	C	O	S	0	0
			4	2	1	1		
4	C	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		

- Molecule 6 is MALONIC ACID (three-letter code: MLA) (formula: C₃H₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			7	3	4		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	175	Total	O	0	4
			179	179		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	128	Total 128	O 128	0	0
7	C	138	Total 141	O 141	0	3

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3 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	117.33Å 68.04Å 60.67Å 90.00° 96.46° 90.00°	Depositor
Resolution (Å)	40.94 – 1.80	Depositor
% Data completeness (in resolution range)	99.5 (40.94-1.80)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 1.79Å)	Xtrriage
Refinement program	PHENIX (dev_3297)	Depositor
R, R_{free}	0.142 , 0.178	Depositor
Wilson B-factor (Å ²)	14.3	Xtrriage
Anisotropy	0.290	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	4133	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

4 Model quality [i](#)

4.1 Standard geometry [i](#)

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4.2 Too-close contacts [i](#)

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4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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	MLA	B	204	-	6,6,6	1.13	0	7,7,7	1.02	0
4	DMS	A	203	-	3,3,3	0.58	0	3,3,3	0.51	0
3	K4Y	C	201	2	20,20,20	4.21	3 (15%)	28,28,28	1.54	3 (10%)
3	K4Y	A	202	2	20,20,20	4.19	3 (15%)	28,28,28	1.63	5 (17%)
4	DMS	A	204	-	3,3,3	0.67	0	3,3,3	0.46	0
4	DMS	B	203	-	3,3,3	0.70	0	3,3,3	0.54	0
4	DMS	C	202	-	3,3,3	0.65	0	3,3,3	0.44	0
3	K4Y	B	202	2	20,20,20	4.25	3 (15%)	28,28,28	1.53	3 (10%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	K4Y	C	201	2	-	0/13/13/13	0/2/2/2
6	MLA	B	204	-	-	0/4/4/4	-
3	K4Y	A	202	2	-	4/13/13/13	0/2/2/2
3	K4Y	B	202	2	-	0/13/13/13	0/2/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	202	K4Y	O11-S09	12.76	1.58	1.43
3	B	202	K4Y	O10-S09	12.74	1.58	1.43
3	C	201	K4Y	O11-S09	12.67	1.57	1.43
3	A	202	K4Y	O10-S09	12.66	1.57	1.43
3	C	201	K4Y	O10-S09	12.65	1.57	1.43
3	A	202	K4Y	O11-S09	12.38	1.57	1.43
3	A	202	K4Y	S09-N08	5.47	1.72	1.63
3	B	202	K4Y	S09-N08	5.36	1.72	1.63
3	C	201	K4Y	S09-N08	5.13	1.72	1.63

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	202	K4Y	C12-S09-N08	-5.20	100.29	106.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	202	K4Y	C05-N04-C03	5.01	118.25	114.48
3	C	201	K4Y	C05-N04-C03	4.80	118.09	114.48
3	C	201	K4Y	C12-S09-N08	-4.62	101.02	106.83
3	B	202	K4Y	C05-N04-C03	4.27	117.69	114.48
3	A	202	K4Y	C12-S09-N08	-4.00	101.80	106.83
3	A	202	K4Y	N06-C05-N04	-2.79	124.23	128.60
3	C	201	K4Y	N06-C05-N04	-2.77	124.26	128.60
3	B	202	K4Y	N06-C05-N04	-2.71	124.37	128.60
3	A	202	K4Y	O11-S09-C12	-2.24	105.21	107.97
3	A	202	K4Y	C13-C12-S09	-2.15	117.44	119.77

There are no chirality outliers.

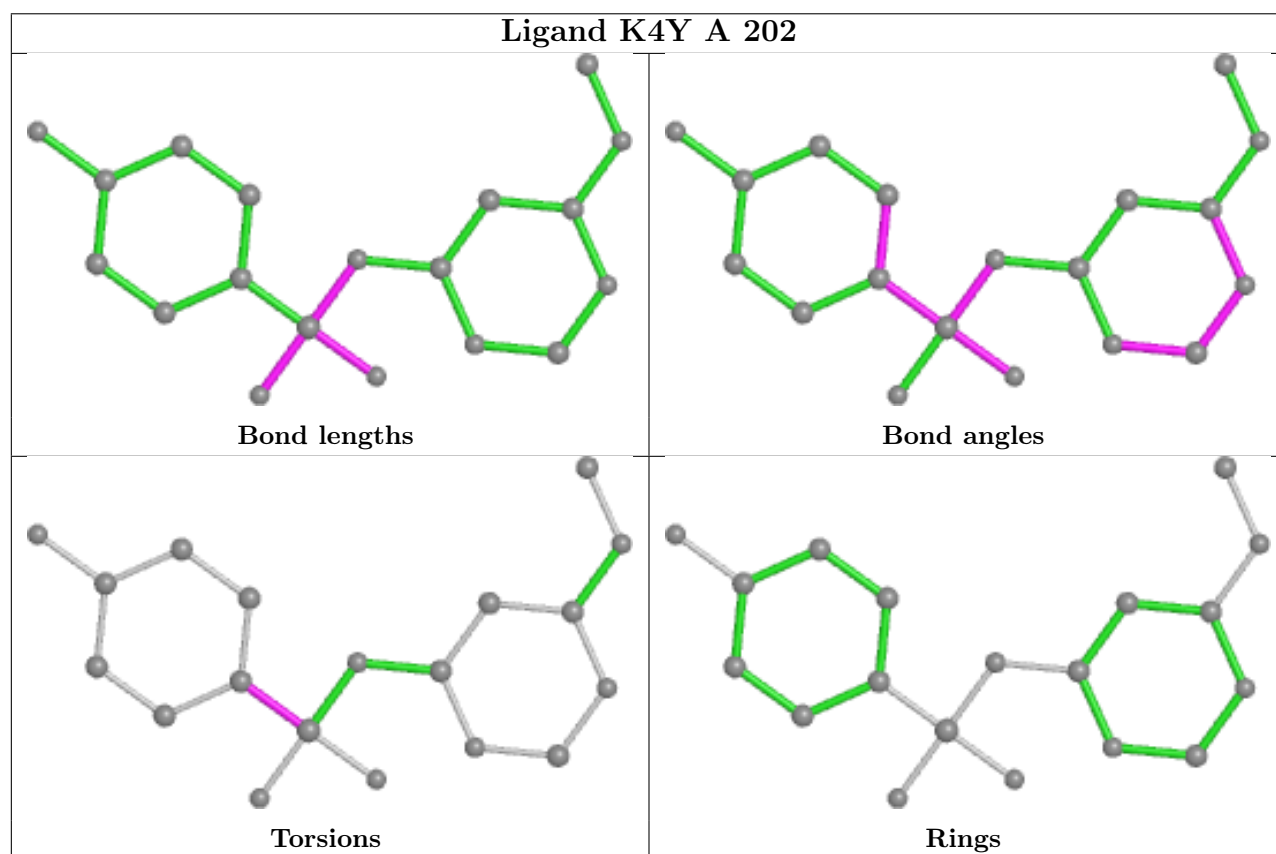
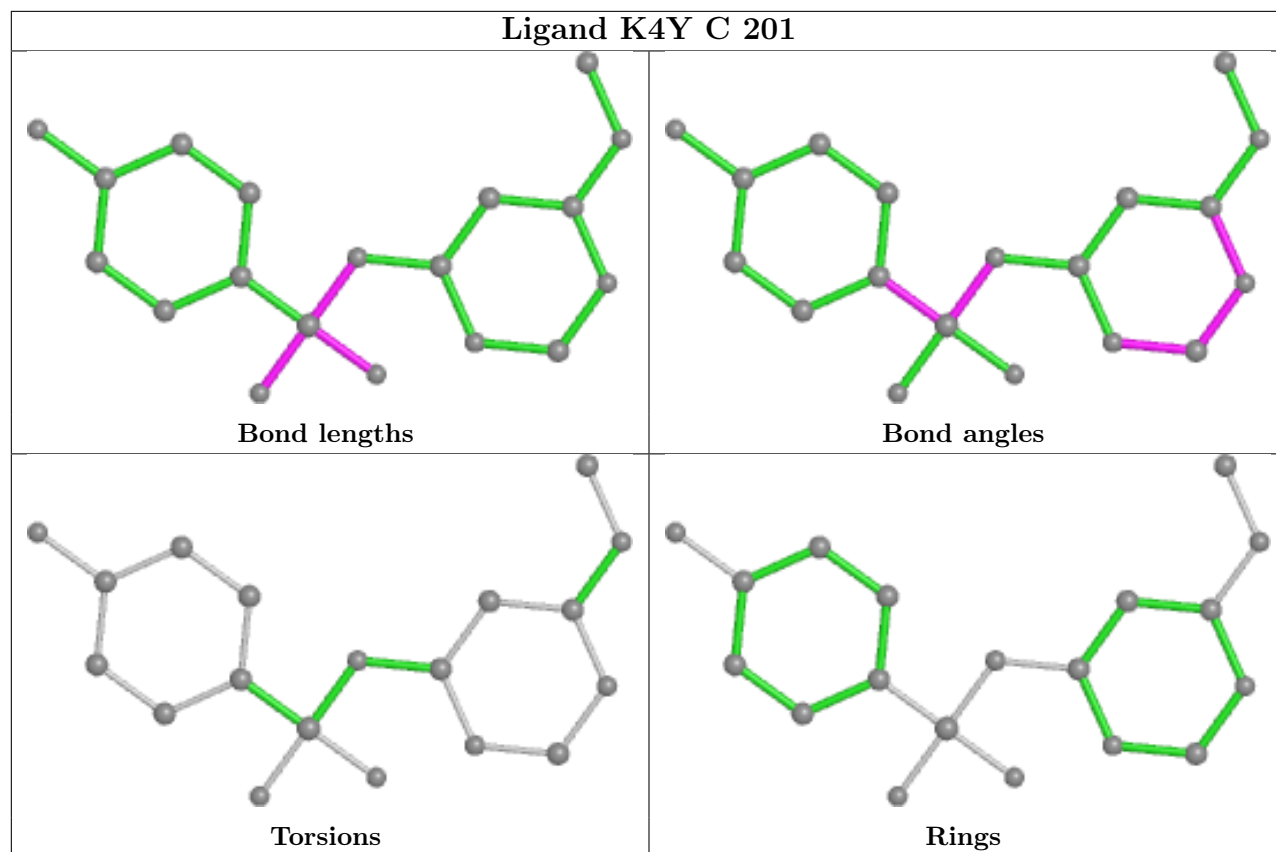
All (4) torsion outliers are listed below:

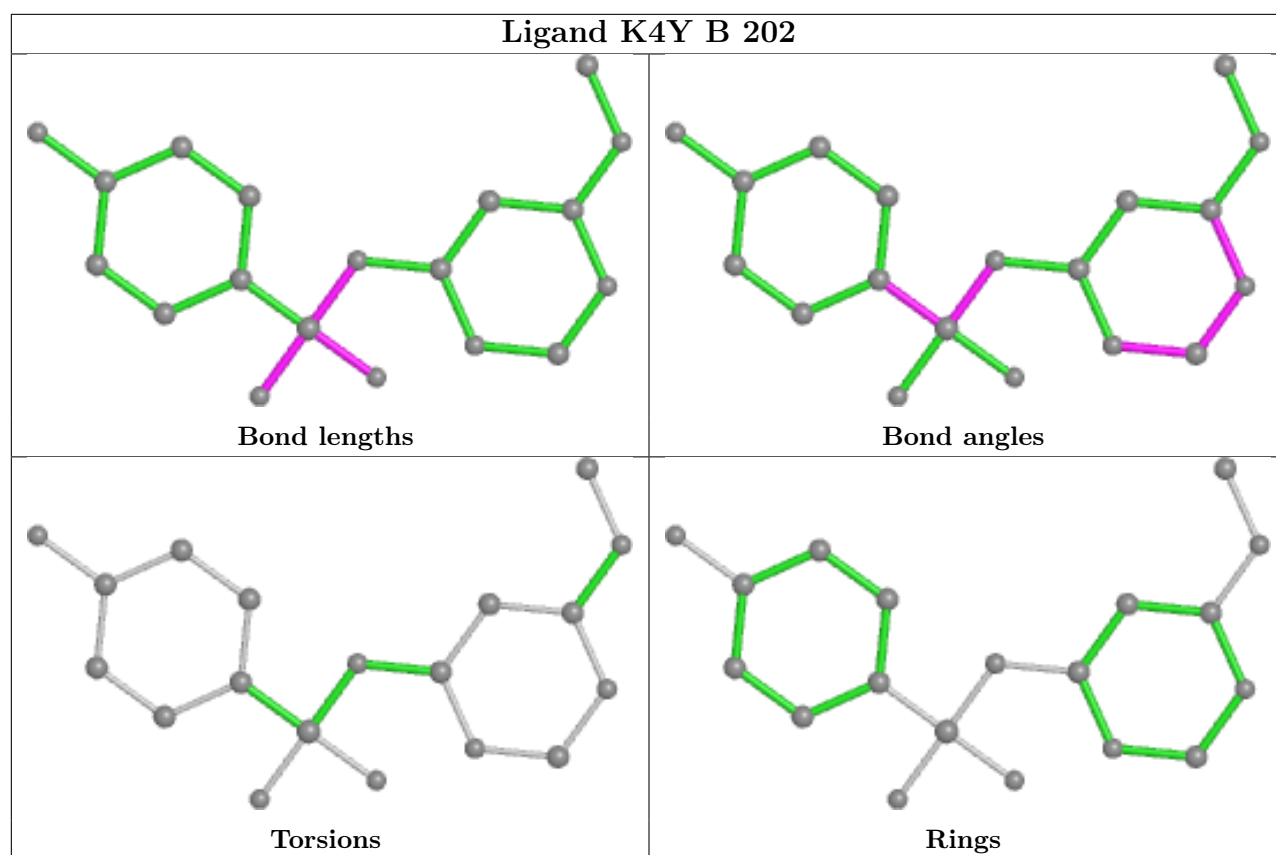
Mol	Chain	Res	Type	Atoms
3	A	202	K4Y	C13-C12-S09-N08
3	A	202	K4Y	C13-C12-S09-O11
3	A	202	K4Y	C18-C12-S09-O11
3	A	202	K4Y	C18-C12-S09-N08

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 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.





4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates [i](#)

EDS failed to run properly - this section is therefore empty.

5.4 Ligands [i](#)

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers [i](#)

EDS failed to run properly - this section is therefore empty.