



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 2, 2023 – 03:00 PM EDT

PDB ID : 6NPF  
Title : Structure of E.coli enolase in complex with an analog of the natural product SF-2312 metabolite.  
Authors : Erlandsen, H.; Krucinska, J.; Lombardo, M.; Wright, D.  
Deposited on : 2019-01-17  
Resolution : 2.57 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.

The types of validation reports are described at

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

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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)  
Xtrriage (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 2.57 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 19725 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 Enolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	438	3249	2033	558	643	15	0	0	0
1	B	436	3234	2024	554	641	15	0	0	0
1	C	438	3249	2033	558	643	15	0	0	0
1	D	432	3206	2008	549	634	15	0	0	0
1	F	434	3219	2015	551	638	15	0	0	0
1	E	426	3168	1988	542	623	15	0	0	0

There are 102 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	GLY	-	expression tag	UNP B7MLA0
A	-16	SER	-	expression tag	UNP B7MLA0
A	-15	HIS	-	expression tag	UNP B7MLA0
A	-14	MET	-	expression tag	UNP B7MLA0
A	-13	ALA	-	expression tag	UNP B7MLA0
A	-12	SER	-	expression tag	UNP B7MLA0
A	-11	MET	-	expression tag	UNP B7MLA0
A	-10	THR	-	expression tag	UNP B7MLA0
A	-9	GLY	-	expression tag	UNP B7MLA0
A	-8	GLY	-	expression tag	UNP B7MLA0
A	-7	GLN	-	expression tag	UNP B7MLA0
A	-6	GLN	-	expression tag	UNP B7MLA0
A	-5	MET	-	expression tag	UNP B7MLA0
A	-4	GLY	-	expression tag	UNP B7MLA0
A	-3	ARG	-	expression tag	UNP B7MLA0
A	-2	GLY	-	expression tag	UNP B7MLA0
A	-1	SER	-	expression tag	UNP B7MLA0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-17	GLY	-	expression tag	UNP B7MLA0
B	-16	SER	-	expression tag	UNP B7MLA0
B	-15	HIS	-	expression tag	UNP B7MLA0
B	-14	MET	-	expression tag	UNP B7MLA0
B	-13	ALA	-	expression tag	UNP B7MLA0
B	-12	SER	-	expression tag	UNP B7MLA0
B	-11	MET	-	expression tag	UNP B7MLA0
B	-10	THR	-	expression tag	UNP B7MLA0
B	-9	GLY	-	expression tag	UNP B7MLA0
B	-8	GLY	-	expression tag	UNP B7MLA0
B	-7	GLN	-	expression tag	UNP B7MLA0
B	-6	GLN	-	expression tag	UNP B7MLA0
B	-5	MET	-	expression tag	UNP B7MLA0
B	-4	GLY	-	expression tag	UNP B7MLA0
B	-3	ARG	-	expression tag	UNP B7MLA0
B	-2	GLY	-	expression tag	UNP B7MLA0
B	-1	SER	-	expression tag	UNP B7MLA0
C	-17	GLY	-	expression tag	UNP B7MLA0
C	-16	SER	-	expression tag	UNP B7MLA0
C	-15	HIS	-	expression tag	UNP B7MLA0
C	-14	MET	-	expression tag	UNP B7MLA0
C	-13	ALA	-	expression tag	UNP B7MLA0
C	-12	SER	-	expression tag	UNP B7MLA0
C	-11	MET	-	expression tag	UNP B7MLA0
C	-10	THR	-	expression tag	UNP B7MLA0
C	-9	GLY	-	expression tag	UNP B7MLA0
C	-8	GLY	-	expression tag	UNP B7MLA0
C	-7	GLN	-	expression tag	UNP B7MLA0
C	-6	GLN	-	expression tag	UNP B7MLA0
C	-5	MET	-	expression tag	UNP B7MLA0
C	-4	GLY	-	expression tag	UNP B7MLA0
C	-3	ARG	-	expression tag	UNP B7MLA0
C	-2	GLY	-	expression tag	UNP B7MLA0
C	-1	SER	-	expression tag	UNP B7MLA0
D	-17	GLY	-	expression tag	UNP B7MLA0
D	-16	SER	-	expression tag	UNP B7MLA0
D	-15	HIS	-	expression tag	UNP B7MLA0
D	-14	MET	-	expression tag	UNP B7MLA0
D	-13	ALA	-	expression tag	UNP B7MLA0
D	-12	SER	-	expression tag	UNP B7MLA0
D	-11	MET	-	expression tag	UNP B7MLA0
D	-10	THR	-	expression tag	UNP B7MLA0

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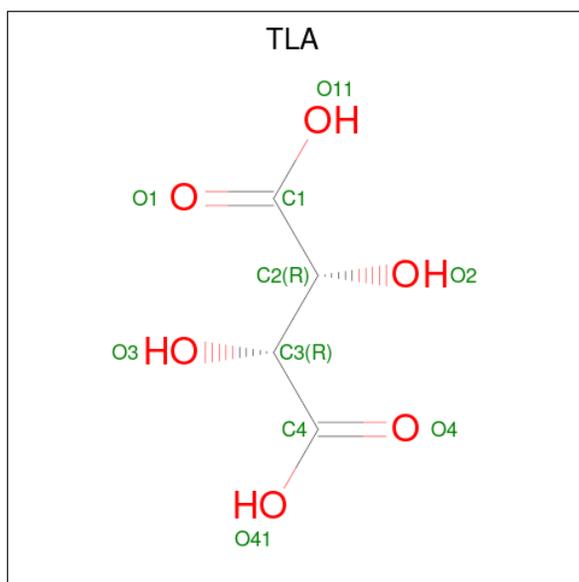
Chain	Residue	Modelled	Actual	Comment	Reference
D	-9	GLY	-	expression tag	UNP B7MLA0
D	-8	GLY	-	expression tag	UNP B7MLA0
D	-7	GLN	-	expression tag	UNP B7MLA0
D	-6	GLN	-	expression tag	UNP B7MLA0
D	-5	MET	-	expression tag	UNP B7MLA0
D	-4	GLY	-	expression tag	UNP B7MLA0
D	-3	ARG	-	expression tag	UNP B7MLA0
D	-2	GLY	-	expression tag	UNP B7MLA0
D	-1	SER	-	expression tag	UNP B7MLA0
F	-17	GLY	-	expression tag	UNP B7MLA0
F	-16	SER	-	expression tag	UNP B7MLA0
F	-15	HIS	-	expression tag	UNP B7MLA0
F	-14	MET	-	expression tag	UNP B7MLA0
F	-13	ALA	-	expression tag	UNP B7MLA0
F	-12	SER	-	expression tag	UNP B7MLA0
F	-11	MET	-	expression tag	UNP B7MLA0
F	-10	THR	-	expression tag	UNP B7MLA0
F	-9	GLY	-	expression tag	UNP B7MLA0
F	-8	GLY	-	expression tag	UNP B7MLA0
F	-7	GLN	-	expression tag	UNP B7MLA0
F	-6	GLN	-	expression tag	UNP B7MLA0
F	-5	MET	-	expression tag	UNP B7MLA0
F	-4	GLY	-	expression tag	UNP B7MLA0
F	-3	ARG	-	expression tag	UNP B7MLA0
F	-2	GLY	-	expression tag	UNP B7MLA0
F	-1	SER	-	expression tag	UNP B7MLA0
E	-17	GLY	-	expression tag	UNP B7MLA0
E	-16	SER	-	expression tag	UNP B7MLA0
E	-15	HIS	-	expression tag	UNP B7MLA0
E	-14	MET	-	expression tag	UNP B7MLA0
E	-13	ALA	-	expression tag	UNP B7MLA0
E	-12	SER	-	expression tag	UNP B7MLA0
E	-11	MET	-	expression tag	UNP B7MLA0
E	-10	THR	-	expression tag	UNP B7MLA0
E	-9	GLY	-	expression tag	UNP B7MLA0
E	-8	GLY	-	expression tag	UNP B7MLA0
E	-7	GLN	-	expression tag	UNP B7MLA0
E	-6	GLN	-	expression tag	UNP B7MLA0
E	-5	MET	-	expression tag	UNP B7MLA0
E	-4	GLY	-	expression tag	UNP B7MLA0
E	-3	ARG	-	expression tag	UNP B7MLA0
E	-2	GLY	-	expression tag	UNP B7MLA0

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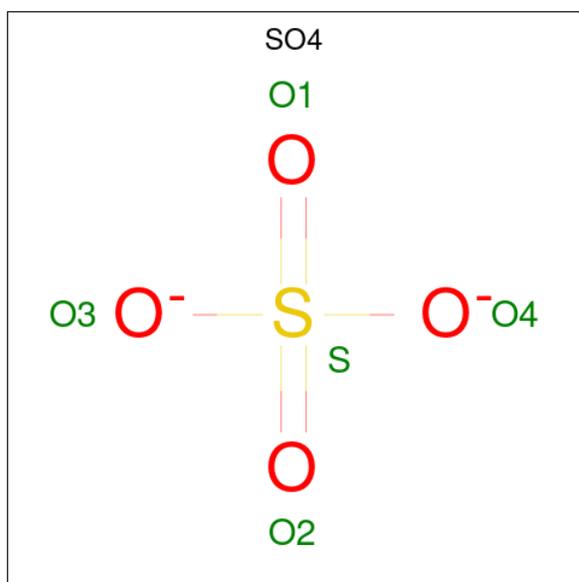
Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	SER	-	expression tag	UNP B7MLA0

- Molecule 2 is L(+)-TARTARIC ACID (three-letter code: TLA) (formula: C<sub>4</sub>H<sub>6</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	10	4	6	0	0
2	B	1	10	4	6	0	0
2	C	1	10	4	6	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

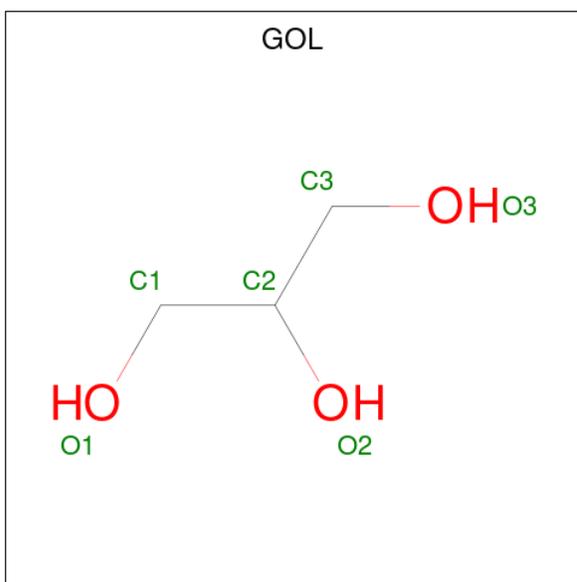
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Mg 1 1	0	0

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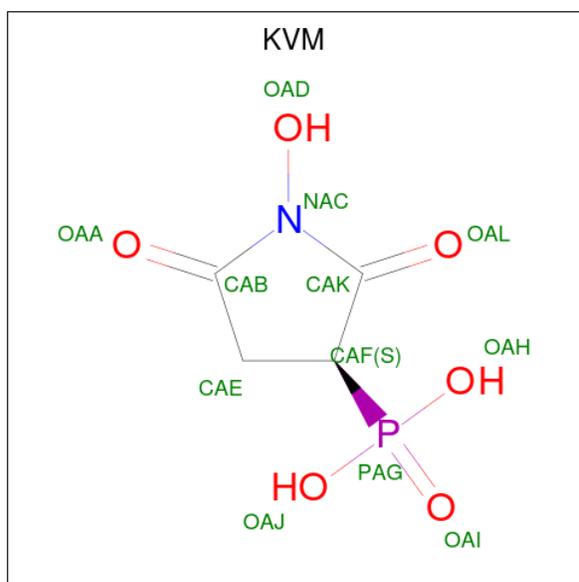
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Mg 1 1	0	0
4	C	1	Total Mg 1 1	0	0
4	D	1	Total Mg 1 1	0	0
4	F	1	Total Mg 1 1	0	0
4	E	1	Total Mg 1 1	0	0

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



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

- Molecule 6 is [(3S)-1-hydroxy-2,5-dioxopyrrolidin-3-yl]phosphonic acid (three-letter code: KVM) (formula:  $C_4H_6NO_6P$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
6	D	1	12	4	1	6	1	0	0
6	F	1	12	4	1	6	1	0	0
6	E	1	12	4	1	6	1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	53	Total	O	0	0
			53	53		
7	B	36	Total	O	0	0
			36	36		
7	C	49	Total	O	0	0
			49	49		
7	D	46	Total	O	0	0
			46	46		
7	F	39	Total	O	0	0
			39	39		
7	E	26	Total	O	0	0
			26	26		

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

### 3 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	104.18Å 143.11Å 206.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	93.03 – 2.57	Depositor
% Data completeness (in resolution range)	99.1 (93.03-2.57)	Depositor
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.53 (at 2.58Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, $R_{free}$	0.191 , 0.256	Depositor
Wilson B-factor (Å <sup>2</sup> )	43.1	Xtriage
Anisotropy	0.063	Xtriage
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
Total number of atoms	19725	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 2.80% 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.

## 4 Model quality [i](#)

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

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

### 4.2 Too-close contacts [i](#)

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

### 4.3 Torsion angles [i](#)

#### 4.3.1 Protein backbone [i](#)

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

#### 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 27 ligands modelled in this entry, 6 are monoatomic - leaving 21 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
3	SO4	C	701	-	4,4,4	0.32	0	6,6,6	0.19	0
6	KVM	F	703	4	9,12,12	4.97	6 (66%)	11,19,19	3.18	5 (45%)
2	TLA	B	501	4	9,9,9	2.53	3 (33%)	12,12,12	2.98	5 (41%)
6	KVM	E	602	4	9,12,12	7.08	6 (66%)	11,19,19	2.74	6 (54%)
3	SO4	F	704	-	4,4,4	0.34	0	6,6,6	0.16	0
3	SO4	A	604	-	4,4,4	0.30	0	6,6,6	0.15	0
3	SO4	B	504	-	4,4,4	0.33	0	6,6,6	0.19	0
3	SO4	A	602	-	4,4,4	0.30	0	6,6,6	0.15	0
2	TLA	C	703	4	9,9,9	1.90	2 (22%)	12,12,12	1.78	3 (25%)
5	GOL	B	503	-	5,5,5	0.16	0	5,5,5	0.36	0
5	GOL	C	705	-	5,5,5	0.17	0	5,5,5	0.38	0
3	SO4	F	701	-	4,4,4	0.39	0	6,6,6	0.11	0
3	SO4	D	603	-	4,4,4	0.36	0	6,6,6	0.14	0
3	SO4	D	606	-	4,4,4	0.35	0	6,6,6	0.12	0
3	SO4	F	705	-	4,4,4	0.31	0	6,6,6	0.14	0
3	SO4	C	704	-	4,4,4	0.34	0	6,6,6	0.15	0
5	GOL	A	605	-	5,5,5	0.20	0	5,5,5	0.44	0
3	SO4	D	602	-	4,4,4	0.24	0	6,6,6	0.12	0
5	GOL	D	605	-	5,5,5	0.16	0	5,5,5	0.36	0
2	TLA	A	601	4	9,9,9	2.44	2 (22%)	12,12,12	1.94	3 (25%)
6	KVM	D	601	4	9,12,12	5.75	6 (66%)	11,19,19	4.68	6 (54%)

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	TLA	C	703	4	-	8/12/12/12	-
5	GOL	D	605	-	-	2/4/4/4	-
6	KVM	F	703	4	-	6/6/22/22	0/1/1/1
5	GOL	B	503	-	-	0/4/4/4	-
2	TLA	B	501	4	-	4/12/12/12	-
6	KVM	E	602	4	-	0/6/22/22	0/1/1/1
5	GOL	C	705	-	-	4/4/4/4	-
2	TLA	A	601	4	-	2/12/12/12	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	KVM	D	601	4	-	6/6/22/22	0/1/1/1
5	GOL	A	605	-	-	4/4/4/4	-

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	602	KVM	OAD-NAC	-15.32	1.18	1.38
6	D	601	KVM	OAD-NAC	10.53	1.52	1.38
6	D	601	KVM	CAE-CAB	-10.08	1.35	1.50
6	F	703	KVM	OAD-NAC	10.06	1.51	1.38
6	E	602	KVM	CAE-CAB	-9.34	1.36	1.50
6	F	703	KVM	CAE-CAB	-8.43	1.38	1.50
6	E	602	KVM	PAG-CAF	-7.45	1.71	1.81
6	E	602	KVM	PAG-OAI	7.03	1.61	1.49
2	B	501	TLA	C2-C1	-6.44	1.43	1.52
2	A	601	TLA	C2-C1	-5.60	1.45	1.52
6	D	601	KVM	PAG-OAI	5.55	1.58	1.49
6	D	601	KVM	PAG-OAJ	-4.59	1.47	1.54
2	C	703	TLA	C3-C4	-4.29	1.46	1.52
6	D	601	KVM	PAG-OAH	4.18	1.61	1.54
6	F	703	KVM	PAG-OAH	3.92	1.61	1.54
6	F	703	KVM	PAG-OAJ	3.85	1.61	1.54
6	E	602	KVM	CAK-NAC	-3.77	1.32	1.37
2	A	601	TLA	O11-C1	-3.69	1.18	1.30
6	F	703	KVM	PAG-CAF	3.41	1.86	1.81
6	D	601	KVM	CAK-NAC	-3.35	1.33	1.37
6	E	602	KVM	PAG-OAJ	-2.73	1.50	1.54
6	F	703	KVM	CAK-NAC	-2.62	1.34	1.37
2	B	501	TLA	O11-C1	-2.23	1.23	1.30
2	B	501	TLA	O3-C3	2.20	1.46	1.42
2	C	703	TLA	O41-C4	-2.04	1.23	1.30

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	601	KVM	OAD-NAC-CAB	10.56	134.06	121.99
6	F	703	KVM	OAD-NAC-CAB	7.86	130.97	121.99
6	D	601	KVM	OAD-NAC-CAK	-7.71	116.00	122.14
2	B	501	TLA	O2-C2-C1	-7.55	94.85	110.66
6	D	601	KVM	OAA-CAB-CAE	-5.58	119.12	127.24
6	E	602	KVM	OAD-NAC-CAB	4.95	127.65	121.99
2	B	501	TLA	O2-C2-C3	4.62	119.40	110.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	703	KVM	OAA-CAB-CAE	-4.45	120.76	127.24
2	A	601	TLA	O2-C2-C1	-4.07	102.13	110.66
2	A	601	TLA	O2-C2-C3	3.77	117.73	110.23
6	E	602	KVM	PAG-CAF-CAK	3.55	121.88	114.55
6	D	601	KVM	OAJ-PAG-OAI	-3.52	104.61	113.45
6	F	703	KVM	OAD-NAC-CAK	-3.51	119.34	122.14
6	D	601	KVM	OAL-CAK-NAC	-3.41	121.26	124.48
6	E	602	KVM	OAJ-PAG-OAH	3.14	116.07	107.64
2	B	501	TLA	O3-C3-C2	3.08	116.36	110.23
6	E	602	KVM	CAE-CAF-CAK	3.03	105.23	103.68
2	C	703	TLA	C2-C3-C4	-3.01	103.15	109.87
6	E	602	KVM	OAA-CAB-CAE	-2.92	122.98	127.24
2	C	703	TLA	O2-C2-C3	-2.67	104.93	110.23
6	F	703	KVM	OAL-CAK-NAC	-2.58	122.04	124.48
6	E	602	KVM	OAH-PAG-OAI	-2.56	107.02	113.45
2	A	601	TLA	O41-C4-C3	2.53	120.10	113.27
2	B	501	TLA	O1-C1-C2	-2.35	115.45	121.63
2	C	703	TLA	O3-C3-C4	-2.31	105.82	110.66
2	B	501	TLA	O11-C1-O1	2.24	129.17	124.09
6	F	703	KVM	CAE-CAF-CAK	-2.23	102.54	103.68
6	D	601	KVM	OAH-PAG-OAI	-2.13	108.10	113.45

There are no chirality outliers.

All (36) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	605	GOL	O1-C1-C2-C3
5	C	705	GOL	O1-C1-C2-C3
5	C	705	GOL	C1-C2-C3-O3
5	C	705	GOL	O2-C2-C3-O3
5	D	605	GOL	C1-C2-C3-O3
6	D	601	KVM	CAE-CAF-PAG-OAH
6	D	601	KVM	CAK-CAF-PAG-OAH
6	D	601	KVM	CAE-CAF-PAG-OAI
6	D	601	KVM	CAK-CAF-PAG-OAI
6	D	601	KVM	CAE-CAF-PAG-OAJ
6	D	601	KVM	CAK-CAF-PAG-OAJ
6	F	703	KVM	CAE-CAF-PAG-OAH
6	F	703	KVM	CAK-CAF-PAG-OAH
6	F	703	KVM	CAE-CAF-PAG-OAI
6	F	703	KVM	CAK-CAF-PAG-OAI
6	F	703	KVM	CAE-CAF-PAG-OAJ

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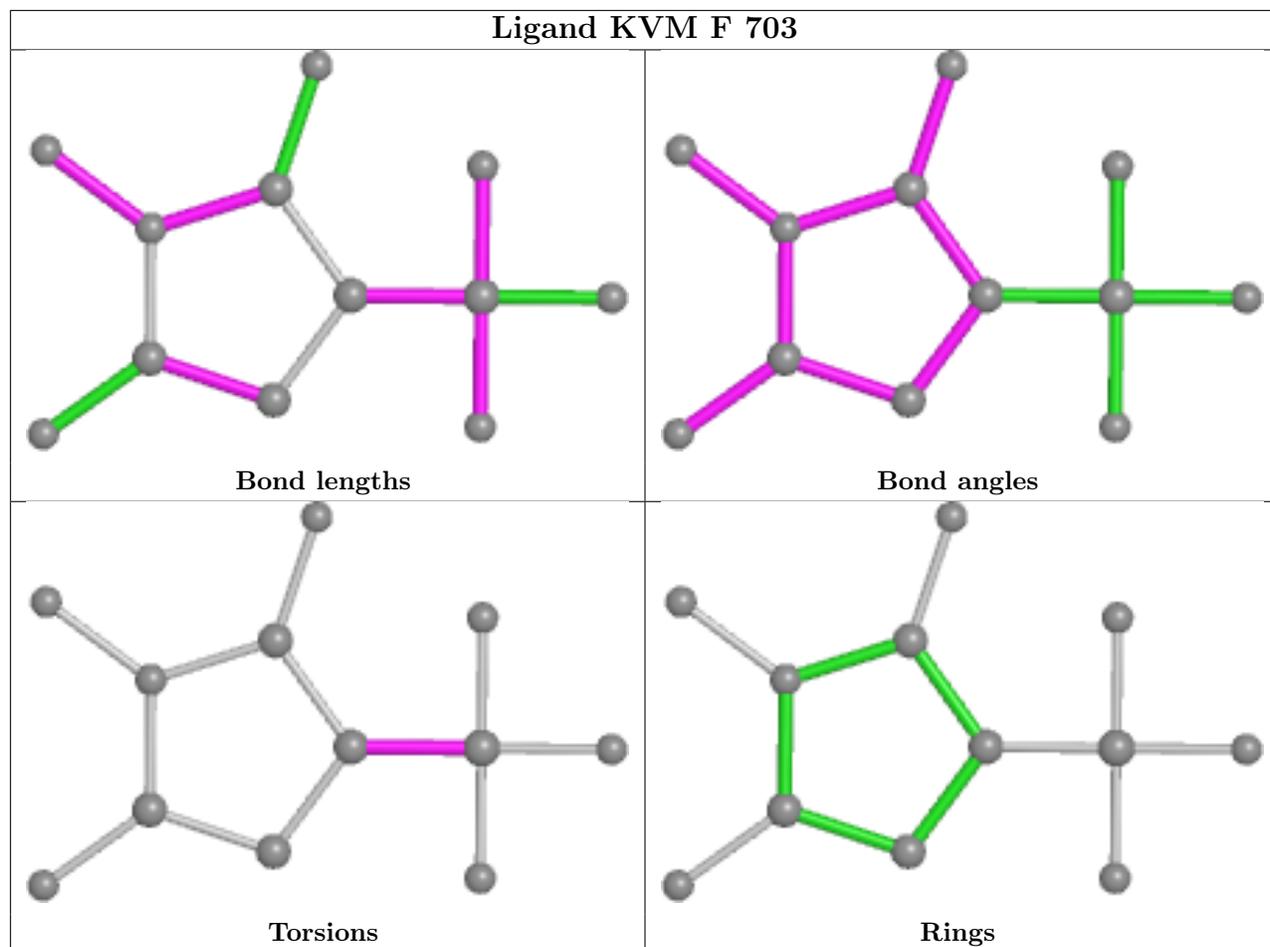
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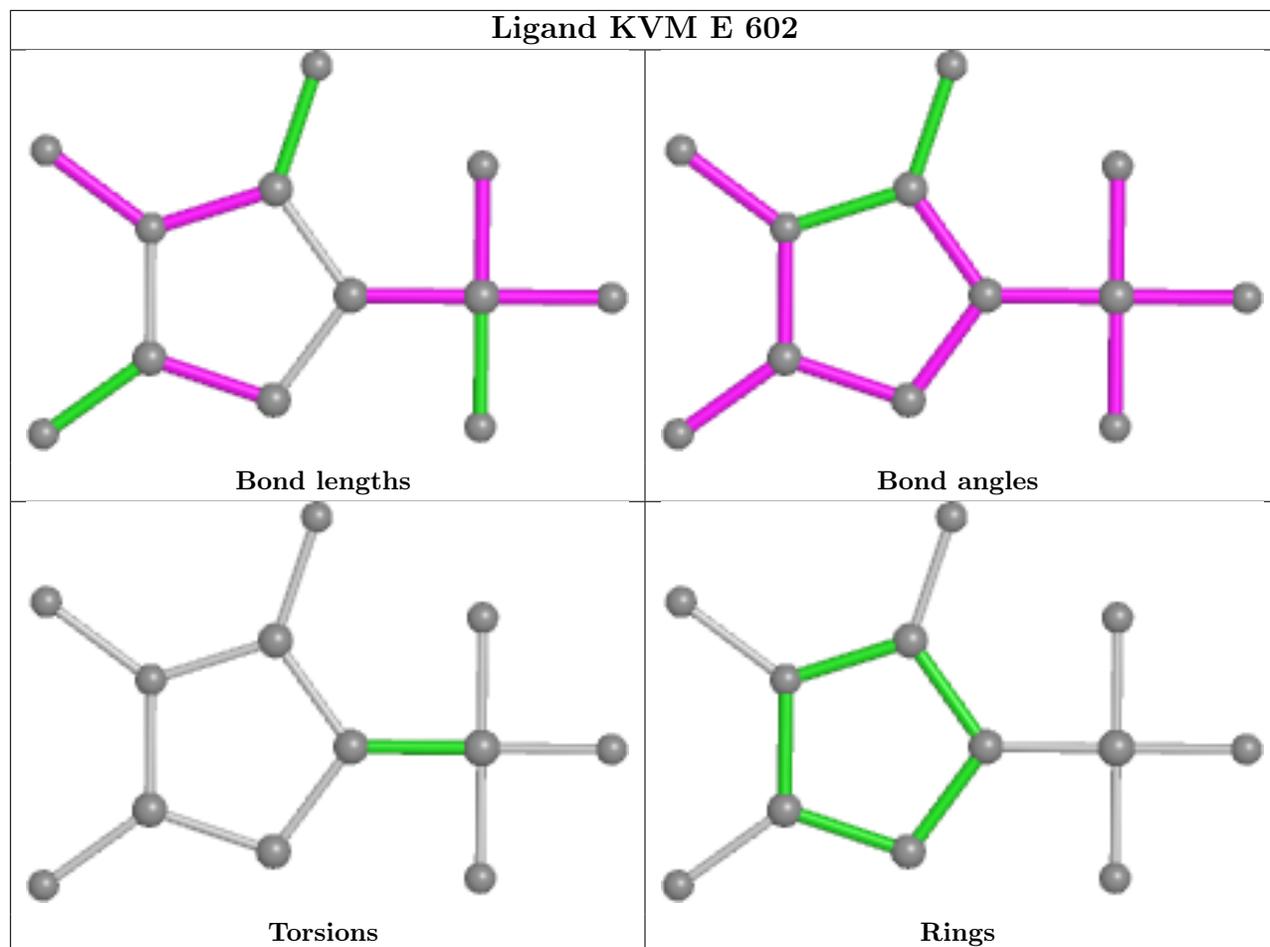
Mol	Chain	Res	Type	Atoms
6	F	703	KVM	CAK-CAF-PAG-OAJ
2	A	601	TLA	O1-C1-C2-O2
2	A	601	TLA	O11-C1-C2-O2
2	C	703	TLA	O2-C2-C3-C4
2	B	501	TLA	O11-C1-C2-O2
2	C	703	TLA	C1-C2-C3-C4
2	B	501	TLA	O1-C1-C2-O2
2	C	703	TLA	O2-C2-C3-O3
5	A	605	GOL	O1-C1-C2-O2
2	C	703	TLA	C1-C2-C3-O3
5	A	605	GOL	O2-C2-C3-O3
5	C	705	GOL	O1-C1-C2-O2
5	D	605	GOL	O2-C2-C3-O3
2	C	703	TLA	O11-C1-C2-O2
2	B	501	TLA	O1-C1-C2-C3
2	C	703	TLA	O11-C1-C2-C3
5	A	605	GOL	C1-C2-C3-O3
2	C	703	TLA	O1-C1-C2-C3
2	B	501	TLA	O11-C1-C2-C3
2	C	703	TLA	O1-C1-C2-O2

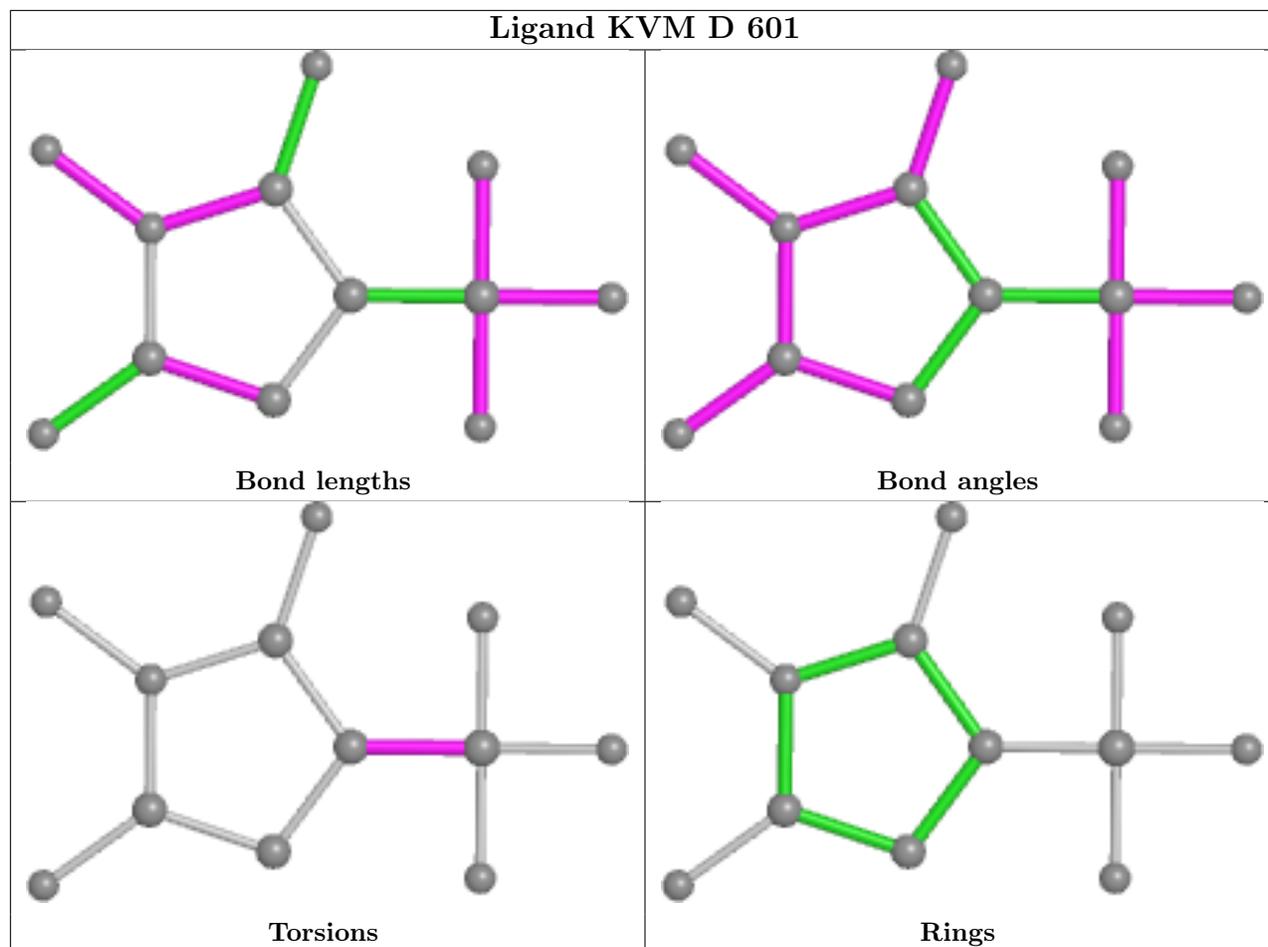
There are no ring outliers.

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.