WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 2, 2023 – 09:18 AM EDT

PDB ID	:	6N0Z
Title	:	Crystal structure of Anaerolinea thermophila mevalonate 5-phosphate decarboxylase N20K H194M mutant complexed with (R)-MVAPP
Authors	:	Noel, J.P.; Thomas, S.T.; Louie, G.V.
Deposited on	:	2018-11-07
Resolution	:	1.95 Å(reported)

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 1.95 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 ⓘ

There are 3 unique types of molecules in this entry. The entry contains 16769 atoms, of which 60 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 Diphosphomevalonate decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	323	Total	C	N	O	S	0	0	0
			2459	1557	431	459	12			
1	B	327	Total	C	N	O	S	0	0	0
			2488	1573	437	466	12			
1	C	327	Total	C	N	O	S	0	0	0
			2487	1573	435	467	12			
1	D	325	Total	C	N	O	S	0	0	0
			2475	1566	435	462	12			
1	E	321	Total	C	N	O	S	0	0	0
			2447	1550	429	457	11			
1	F	327	Total	C	N	O	S	0	0	0
			2491	1576	436	467	12			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP E8N6F3
A	-2	SER	-	expression tag	UNP E8N6F3
A	-1	HIS	-	expression tag	UNP E8N6F3
A	0	GLY	-	expression tag	UNP E8N6F3
A	20	LYS	ASN	engineered mutation	UNP E8N6F3
A	194	MET	HIS	engineered mutation	UNP E8N6F3
B	-3	GLY	-	expression tag	UNP E8N6F3
B	-2	SER	-	expression tag	UNP E8N6F3
B	-1	HIS	-	expression tag	UNP E8N6F3
B	0	GLY	-	expression tag	UNP E8N6F3
B	20	LYS	ASN	engineered mutation	UNP E8N6F3
B	194	MET	HIS	engineered mutation	UNP E8N6F3
C	-3	GLY	-	expression tag	UNP E8N6F3
C	-2	SER	-	expression tag	UNP E8N6F3
C	-1	HIS	-	expression tag	UNP E8N6F3
C	0	GLY	-	expression tag	UNP E8N6F3
C	20	LYS	ASN	engineered mutation	UNP E8N6F3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	194	MET	HIS	engineered mutation	UNP E8N6F3
D	-3	GLY	-	expression tag	UNP E8N6F3
D	-2	SER	-	expression tag	UNP E8N6F3
D	-1	HIS	-	expression tag	UNP E8N6F3
D	0	GLY	-	expression tag	UNP E8N6F3
D	20	LYS	ASN	engineered mutation	UNP E8N6F3
D	194	MET	HIS	engineered mutation	UNP E8N6F3
E	-3	GLY	-	expression tag	UNP E8N6F3
E	-2	SER	-	expression tag	UNP E8N6F3
E	-1	HIS	-	expression tag	UNP E8N6F3
E	0	GLY	-	expression tag	UNP E8N6F3
E	20	LYS	ASN	engineered mutation	UNP E8N6F3
E	194	MET	HIS	engineered mutation	UNP E8N6F3
F	-3	GLY	-	expression tag	UNP E8N6F3
F	-2	SER	-	expression tag	UNP E8N6F3
F	-1	HIS	-	expression tag	UNP E8N6F3
F	0	GLY	-	expression tag	UNP E8N6F3
F	20	LYS	ASN	engineered mutation	UNP E8N6F3
F	194	MET	HIS	engineered mutation	UNP E8N6F3

- Molecule 2 is (3R)-3-HYDROXY-5-{[(R)-HYDROXY(PHOSPHONOOXY)PHOSPHORYL]OXY}-3-METHYLPENTANOIC ACID (three-letter code: DP6) (formula: $C_6H_{14}O_{10}P_2$).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	O	P		
2	A	1	28	6	10	10	2	0	0

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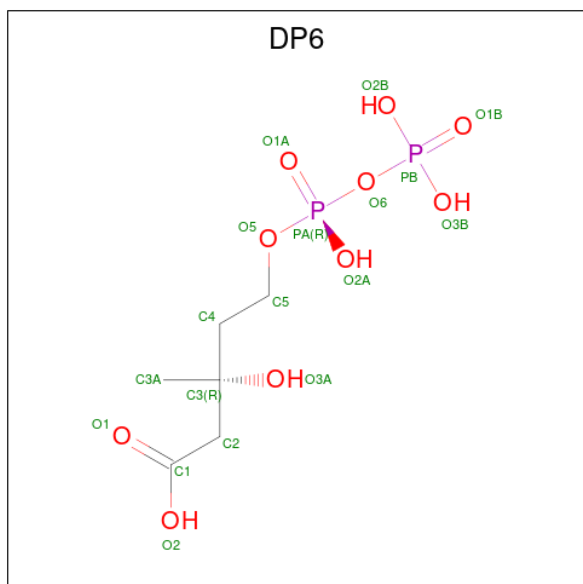
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	H	O	P	0	0
			28	6	10	10	2		
2	C	1	Total	C	H	O	P	0	0
			28	6	10	10	2		
2	D	1	Total	C	H	O	P	0	0
			28	6	10	10	2		
2	E	1	Total	C	H	O	P	0	0
			28	6	10	10	2		
2	F	1	Total	C	H	O	P	0	0
			28	6	10	10	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	310	Total	O	0	0
			310	310		
3	B	312	Total	O	0	0
			312	312		
3	C	324	Total	O	0	0
			324	324		
3	D	293	Total	O	0	0
			293	293		
3	E	256	Total	O	0	0
			256	256		
3	F	259	Total	O	0	0
			259	259		

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

3 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	80.80Å 138.09Å 105.13Å 90.00° 96.12° 90.00°	Depositor
Resolution (Å)	45.57 – 1.95	Depositor
% Data completeness (in resolution range)	78.9 (45.57-1.95)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	1.72 (at 1.95Å)	Xtriage
Refinement program	PHENIX (1.14_3260)	Depositor
R, R_{free}	0.167 , 0.202	Depositor
Wilson B-factor (Å^2)	19.5	Xtriage
Anisotropy	0.322	Xtriage
L-test for twinning[2]	$<|L|> = 0.49$, $<L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	16769	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.91% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $<|L|>$, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

4 Model quality ⓘ

4.1 Standard geometry ⓘ

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

4.2 Too-close contacts ⓘ

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

4.3 Torsion angles ⓘ

4.3.1 Protein backbone ⓘ

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

4.3.2 Protein sidechains ⓘ

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

4.3.3 RNA ⓘ

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

4.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

4.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

4.6 Ligand geometry ⓘ

6 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	DP6	D	401	-	14,17,17	1.23	2 (14%)	17,26,26	0.87	0
2	DP6	F	401	-	14,17,17	1.28	1 (7%)	17,26,26	1.06	1 (5%)
2	DP6	A	401	-	14,17,17	1.14	1 (7%)	17,26,26	0.81	0
2	DP6	E	401	-	14,17,17	1.01	1 (7%)	17,26,26	1.05	0
2	DP6	C	401	-	14,17,17	1.26	1 (7%)	17,26,26	0.97	0
2	DP6	B	401	-	14,17,17	1.46	2 (14%)	17,26,26	0.81	1 (5%)

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	DP6	D	401	-	-	4/19/19/19	-
2	DP6	F	401	-	-	5/19/19/19	-
2	DP6	A	401	-	-	4/19/19/19	-
2	DP6	E	401	-	-	7/19/19/19	-
2	DP6	C	401	-	-	5/19/19/19	-
2	DP6	B	401	-	-	5/19/19/19	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	401	DP6	C2-C3	-3.60	1.51	1.54
2	C	401	DP6	C2-C3	-3.24	1.51	1.54
2	B	401	DP6	O3A-C3	-3.10	1.40	1.44
2	B	401	DP6	C2-C3	-3.09	1.51	1.54
2	D	401	DP6	O3A-C3	-2.82	1.40	1.44

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	F	401	DP6	O2-C1-C2	2.11	121.13	114.35
2	B	401	DP6	O2B-PB-O6	2.08	111.62	104.64

There are no chirality outliers.
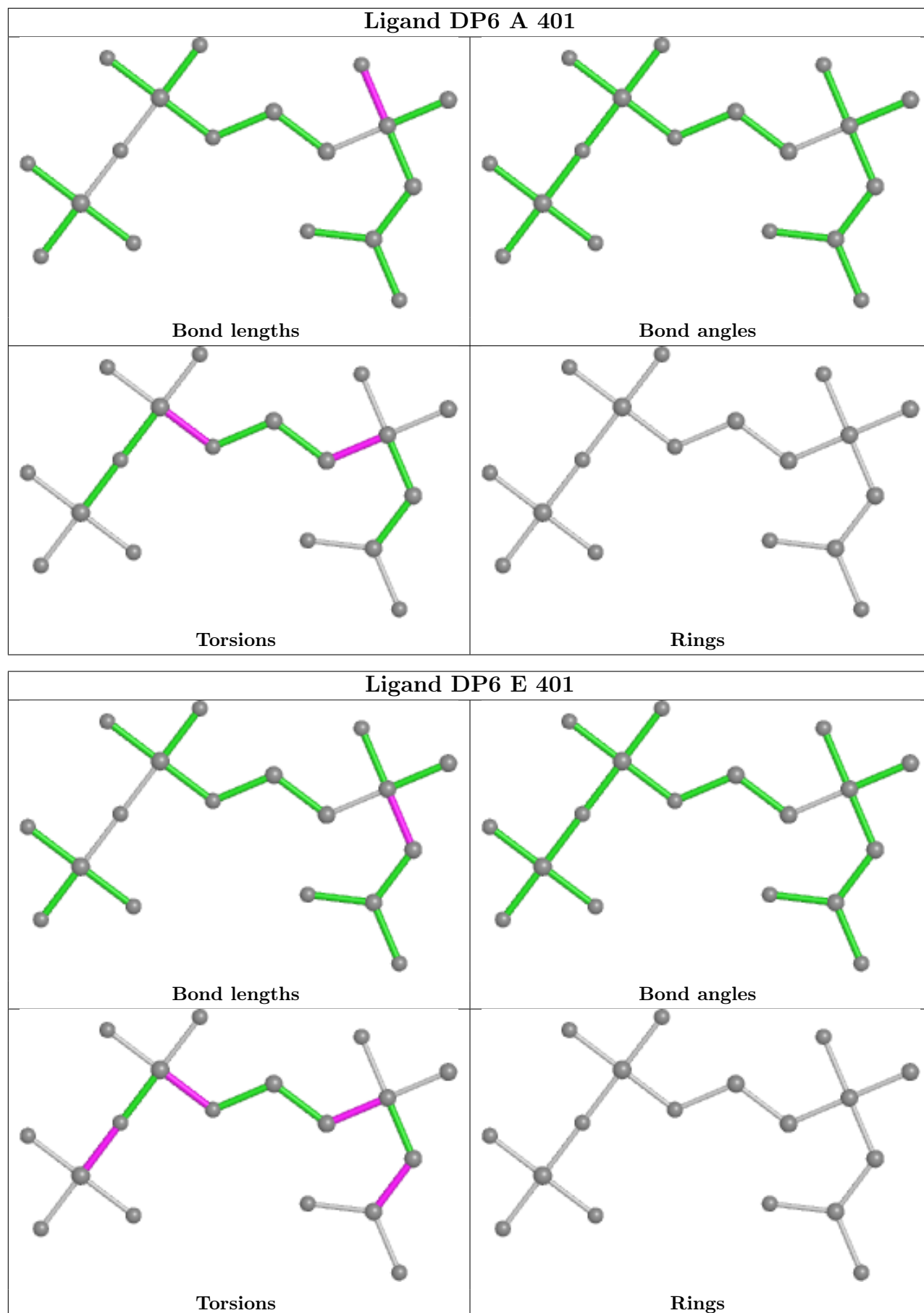
5 of 30 torsion outliers are listed below:

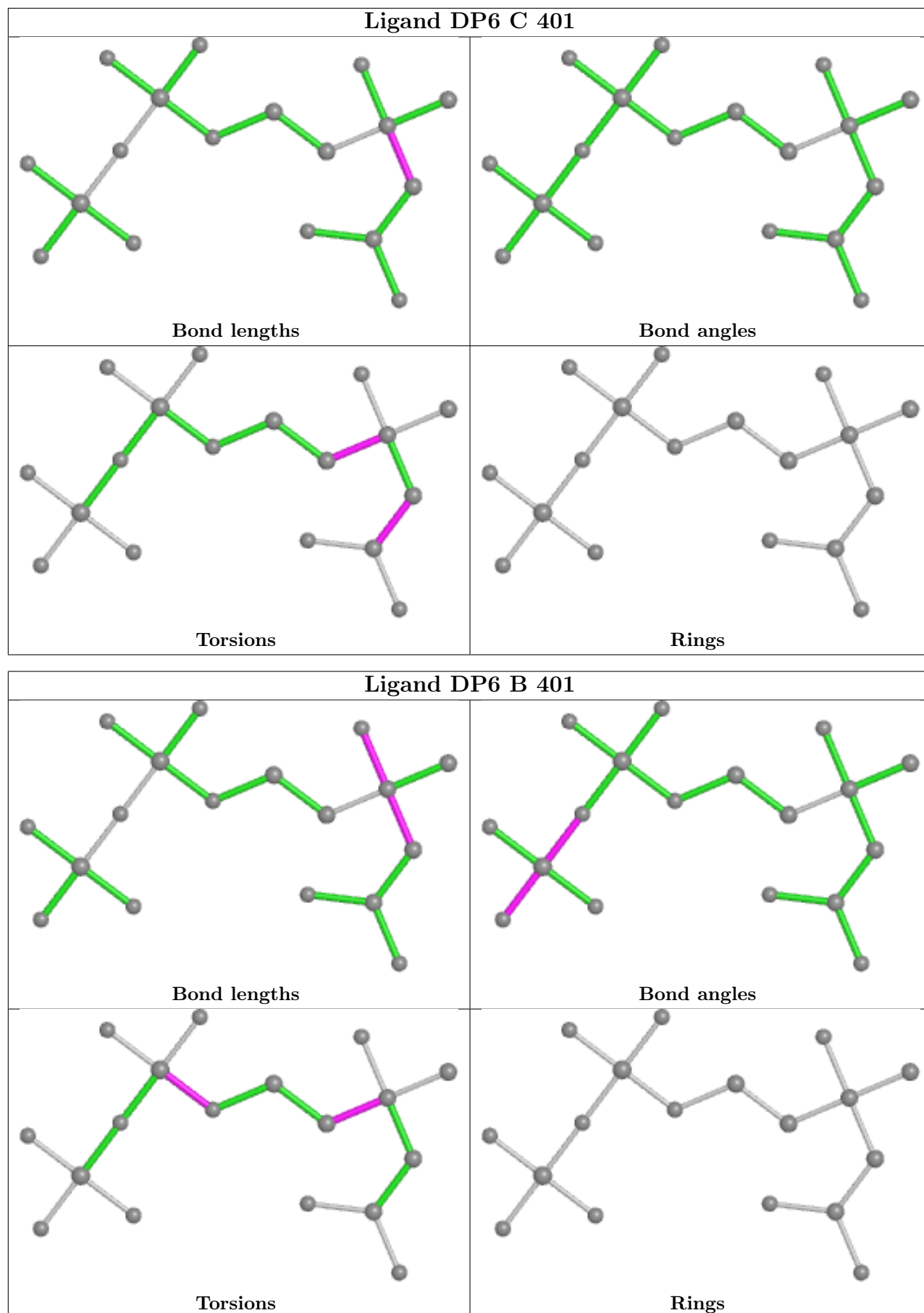| Mol	Chain	Res	Type	Atoms
2	A	401	DP6	C5-O5-PA-O1A
2	A	401	DP6	C3A-C3-C4-C5
2	A	401	DP6	C2-C3-C4-C5
2	B	401	DP6	C5-O5-PA-O1A
2	B	401	DP6	C3A-C3-C4-C5

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 then 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 DP6 D 401

Bond lengths

Bond angles

Torsions

Rings

Ligand DP6 F 401

Bond lengths

Bond angles

Torsions

Rings

Ligand DP6 A 401

Bond lengths

Bond angles

Torsions

Rings

Ligand DP6 E 401

Bond lengths

Bond angles

Torsions

Rings

Ligand DP6 C 401

Bond lengths

Bond angles

Torsions

Rings

Ligand DP6 B 401

Bond lengths

Bond angles

Torsions

Rings
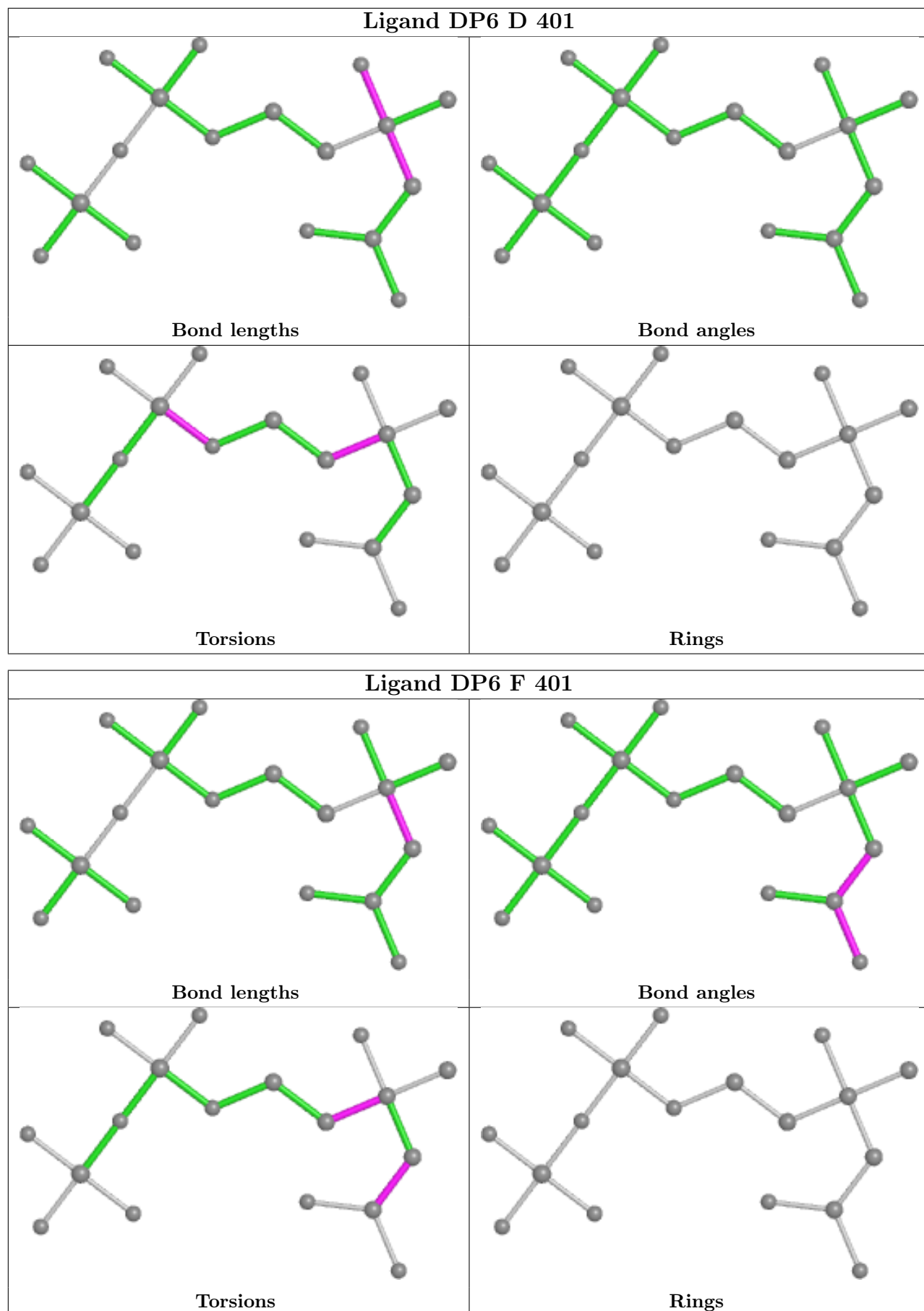
4.7 Other polymers ⓘ

There are no such residues in this entry.

4.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

5 Fit of model and data ⓘ

5.1 Protein, DNA and RNA chains ⓘ

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

5.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.3 Carbohydrates ⓘ

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

5.4 Ligands ⓘ

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

5.5 Other polymers ⓘ

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