



wwPDB EM Validation Summary Report ⓘ

Jul 8, 2025 – 02:53 PM JST

PDB ID : 9IRK / pdb_00009irk
EMDB ID : EMD-60816
Title : Cryo-EM structure of PhyB(Y276H,1-908)-PIF6beta complex
Authors : Jia, H.L.; Guan, Z.Y.; Ding, J.Y.; Wang, X.Y.; Ma, L.; Yin, P.
Deposited on : 2024-07-16
Resolution : 2.80 Å(reported)

This is a wwPDB EM Validation Summary 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/EMValidationReportHelp>

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:

EMDB validation analysis : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

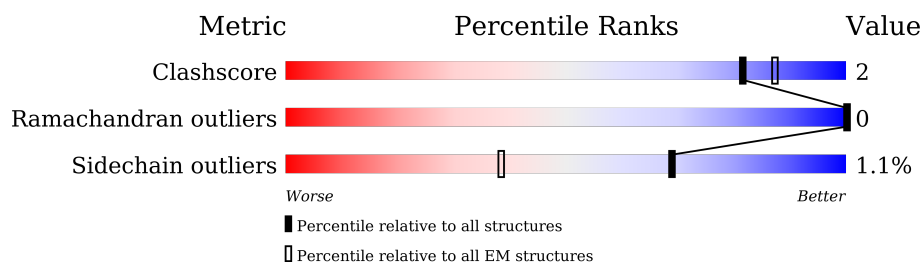
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	907	
1	C	907	
2	B	181	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16504 atoms, of which 8227 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 Phytochrome B.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	C	477	Total	C	H	N	O	S	0	0
			7403	2346	3701	644	682	30		
1	A	533	Total	C	H	N	O	S	0	0
			8261	2616	4122	720	773	30		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	276	HIS	TYR	engineered mutation	UNP P14713
A	276	HIS	TYR	engineered mutation	UNP P14713

- Molecule 2 is a protein called Transcription factor PIF6.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	42	Total	C	H	N	O	S	0	0
			682	219	332	56	72	3		

- Molecule 3 is 3-[5-[[[(3 {R},4 {R})-3-ethyl-4-methyl-5-oxidanylidene-3,4-dihydropyrrol-2-yl]methyl]-2-[[5-[(4-ethyl-3-methyl-5-oxidanylidene-pyrrol-2-yl)methyl]-3-(3-hydroxy-3-oxopropyl)-4-methyl-1 {H}-pyrrol-2-yl]methyl]-4-methyl-1 {H}-pyrrol-3-yl]propanoic acid (CCD ID: O6E) (formula: C₃₃H₃₈N₄O₆).

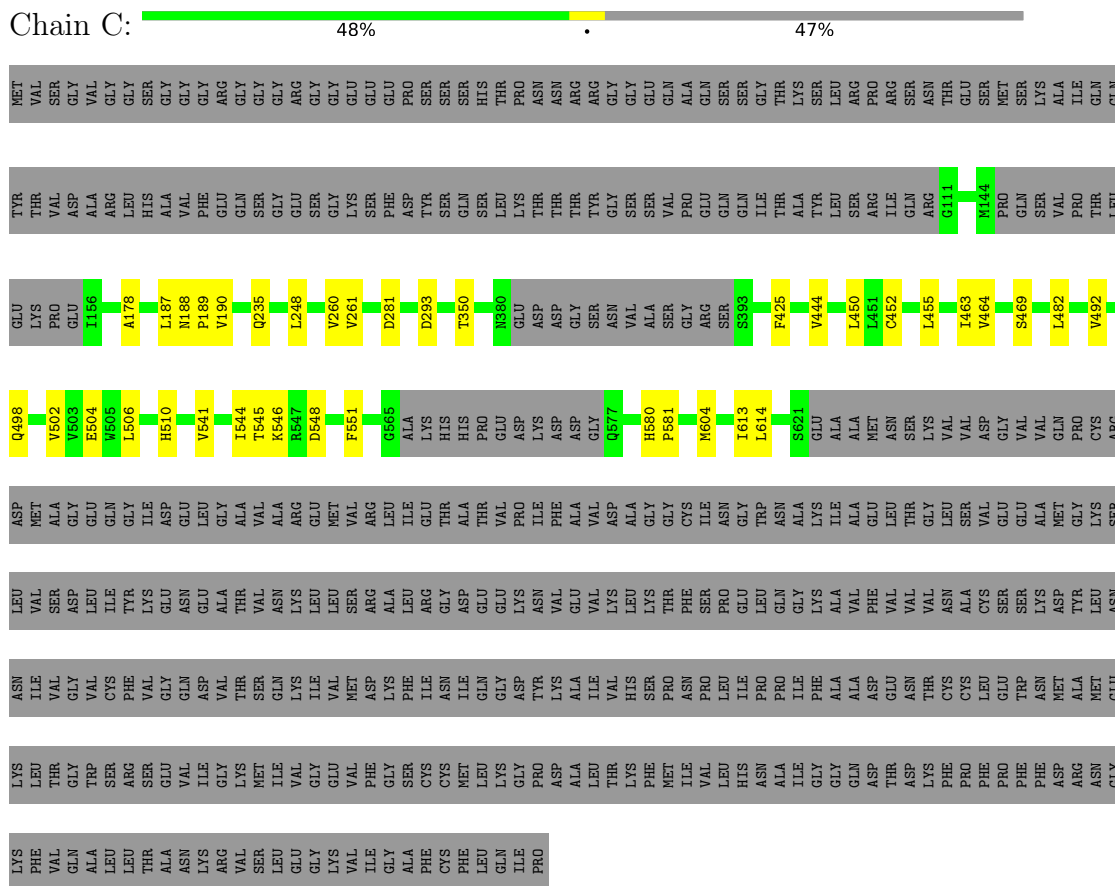


Mol	Chain	Residues	Atoms					AltConf
3	C	1	Total 79	C 33	H 36	N 4	O 6	0
3	A	1	Total 79	C 33	H 36	N 4	O 6	0

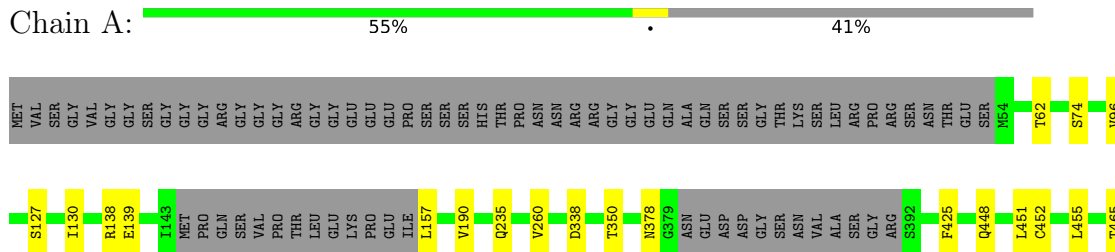
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Phytochrome B



• Molecule 1: Phytochrome B



Q466	S467	P468	Q498	I499	K500	D501	V502	V503	E504	W505	L506	H510	V541	T545	K546	R547	D548	F551	G565	ALA	LYS	HIS	HIS	PRO	GLU	ASP	LYS	ASP	ASP	G576	S609	I613	S621	GLU	ALA	ALA	MET	ASN	LYS	VAL	VAL	ASP	GLY	VAL	VAL	GLN	PRO	CYS	ARG					
ASN	MET	ALA	GLY	GLN	GLY	ILE	ASP	GLU	LEU	GLY	ALA	VAL	ASN	LEU	ARG	LEU	ILE	GLU	THR	ALA	THR	VAL	ILE	PHE	ALA	VAL	LYS	ASP	ALA	GLY	CYS	ILE	ASN	ASN	GLY	LYS	ILE	ALA	ALA	GLU	LEU	VAL	ASN	ALA	VAL	GLU	VAL	GLY	ASN	SER				
LEU	VAL	SER	ASP	ILE	TYR	LYS	GLY	ASN	GLU	ALA	THR	VAL	ASN	LYS	ARG	ALA	LEU	ARG	ASP	ALA	GLY	GLU	LYS	ASN	GLY	VAL	LYS	LEU	LYS	PHE	SER	PRO	GLU	LEU	GLN	GLY	LYS	ALA	VAL	PHE	GLU	VAL	VAL	ASN	CYS	VAL	SER	LEU	ASN					
ASN	ILE	VAL	GLY	VAL	CYS	PHE	VAL	GLY	GLN	ASP	VAL	THR	SER	GLN	ILE	LYS	ILE	ARG	ASN	CYS	ILE	GLN	GLY	TYR	LYS	ALA	ILE	VAL	VAL	HIS	SER	PRO	ASN	PRO	ILE	PHE	ALA	ALA	ASP	GLU	THR	ASN	THR	CYS	LEU	GLU	SER	TRP	PHE	ASN	MET	ALA	MET	GLY
LYS	LEU	THR	TRP	SER	ARG	SER	VAL	GLU	GLN	ASP	VAL	THR	MET	ILE	VAL	GLY	VAL	PHE	CYS	MET	LEU	LYS	PRO	ASP	ALA	LEU	THR	LYS	PHE	MET	ILE	VAL	LEU	HIS	ASN	ALA	ILE	GLY	GLN	ASP	THR	ASP	LYS	PHE	PRO	PHE	PRO	PHE	ASP	ARG	ASN	GLY		
LYS	PHE	VAL	GLN	ALA	LEU	LEU	THR	ALA	LYS	ARG	VAL	SER	LEU	GLU	GLY	LYS	ILE	ALA	PHE	CYS	PHE	GLN	ILE	GLY	LYS	ILE	GLY	GLY	VAL	ALA	THR	ASN	VAL	GLY	LYS	GLN	ASP	THR	ASP	LYS	PHE	PRO	PHE	PRO	PHE	ASP	ARG	ASN	GLY					

● Molecule 2: Transcription factor PIF6



ASP	SER	GLU	GLY	SER	MET	TYR	LEU	SER	SER	SER	ASP	GLU	ASP	SER	ASP	ALA	ARG	PRO	GLN	VAL	PRO	ALA	ARG	THR	ARG	LYS																												
MET	MET	PHE	LEU	ASN	PRO	THR	ASP	TYR	CYS	R11	K30	G31	Q32	ARG	SER	ASN	VAL	SER	LEU	HIS	ASN	R42	E51	S61	ILE	ILE	LYS	HIS	GLY	GLY	GLY	ALA	ILE	THR	ASN	LEU	GLY	ASP	THR	GLN	VAL	VAL	PRO	GLN	SER	HIS	VAL	ALA	ALA	HIS	GLU	THR	ASN	MET

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	565463	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: O6E

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	0.17	0/4221	0.35	0/5711
1	C	0.23	2/3776 (0.1%)	0.40	2/5111 (0.0%)
2	B	0.15	0/353	0.30	0/468
All	All	0.20	2/8350 (0.0%)	0.37	2/11290 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	190	VAL	C-O	-5.77	1.16	1.24
1	C	188	ASN	C-O	-5.41	1.18	1.25

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	189	PRO	N-CA-CB	-5.66	96.38	102.60
1	C	190	VAL	CA-C-O	-5.03	115.41	121.54

There are no chirality outliers.

There are no planarity outliers.

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	4139	4122	4121	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3702	3701	3700	21	0
2	B	350	332	332	1	0
3	A	43	36	0	0	0
3	C	43	36	0	0	0
All	All	8277	8227	8153	40	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 2.

The worst 5 of 40 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:C:498:GLN:O	1:C:502:VAL:HG23	1.86	0.76
1:C:248:LEU:O	1:A:378:ASN:ND2	2.31	0.64
1:A:448:GLN:OE1	1:A:609:SER:OG	2.16	0.64
1:C:544:ILE:HG22	1:C:545:THR:HG23	1.84	0.59
1:A:500:LYS:O	1:A:504:GLU:HG3	2.03	0.59

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	525/907 (58%)	507 (97%)	18 (3%)	0	100	100
1	C	469/907 (52%)	449 (96%)	20 (4%)	0	100	100
2	B	38/181 (21%)	38 (100%)	0	0	100	100
All	All	1032/1995 (52%)	994 (96%)	38 (4%)	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	451/758 (60%)	446 (99%)	5 (1%)	70	90
1	C	403/758 (53%)	399 (99%)	4 (1%)	73	91
2	B	38/161 (24%)	37 (97%)	1 (3%)	41	75
All	All	892/1677 (53%)	882 (99%)	10 (1%)	69	90

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	451	LEU
1	A	465	THR
2	B	30	LYS
1	C	469	SER
1	A	74	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	403	HIS
1	A	404	HIS
1	A	608	HIS
1	A	428	GLN
1	C	358	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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
3	O6E	A	1001	1	42,46,46	1.24	4 (9%)	50,67,67	1.53	7 (14%)
3	O6E	C	1001	1	42,46,46	1.20	5 (11%)	50,67,67	1.62	7 (14%)

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
3	O6E	A	1001	1	-	7/25/74/74	0/4/4/4
3	O6E	C	1001	1	-	8/25/74/74	0/4/4/4

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1001	O6E	CAB-CBI	-3.42	1.38	1.47
3	A	1001	O6E	CAB-CBI	-3.32	1.38	1.47
3	A	1001	O6E	CAO-CAV	2.66	1.37	1.35
3	C	1001	O6E	OAZ-CAL	-2.13	1.23	1.30
3	C	1001	O6E	CAC-CBJ	-2.11	1.49	1.54

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1001	O6E	CAH-CAC-CBJ	-5.17	101.95	113.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1001	O6E	CAC-CBJ-CBN	-4.96	99.94	112.67
3	A	1001	O6E	CAH-CAC-CBJ	-4.93	102.48	113.47
3	A	1001	O6E	CAC-CBJ-CBN	-4.70	100.59	112.67
3	C	1001	O6E	CAO-CAV-NAE	-3.67	123.74	128.83

There are no chirality outliers.

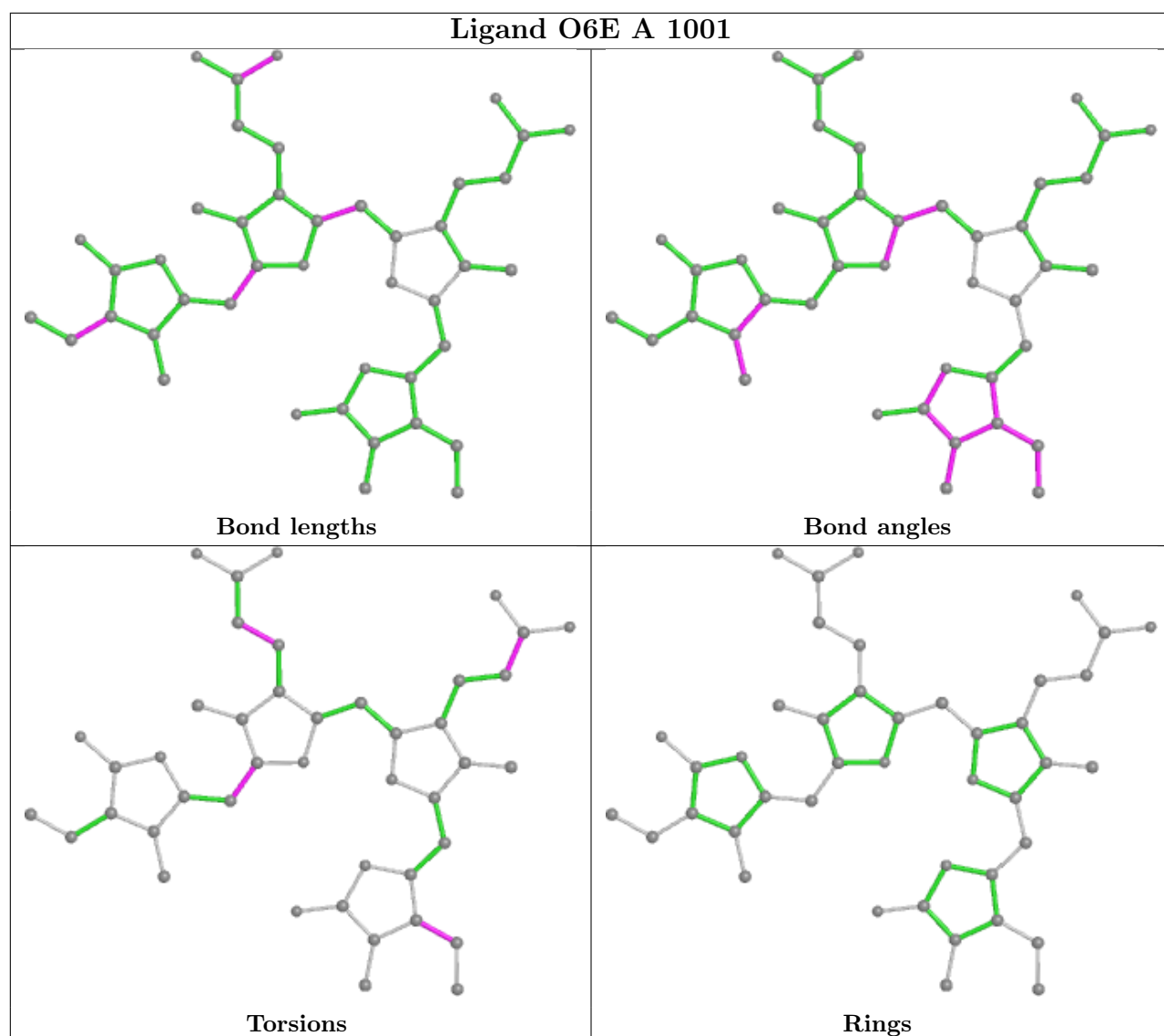
5 of 15 torsion outliers are listed below:

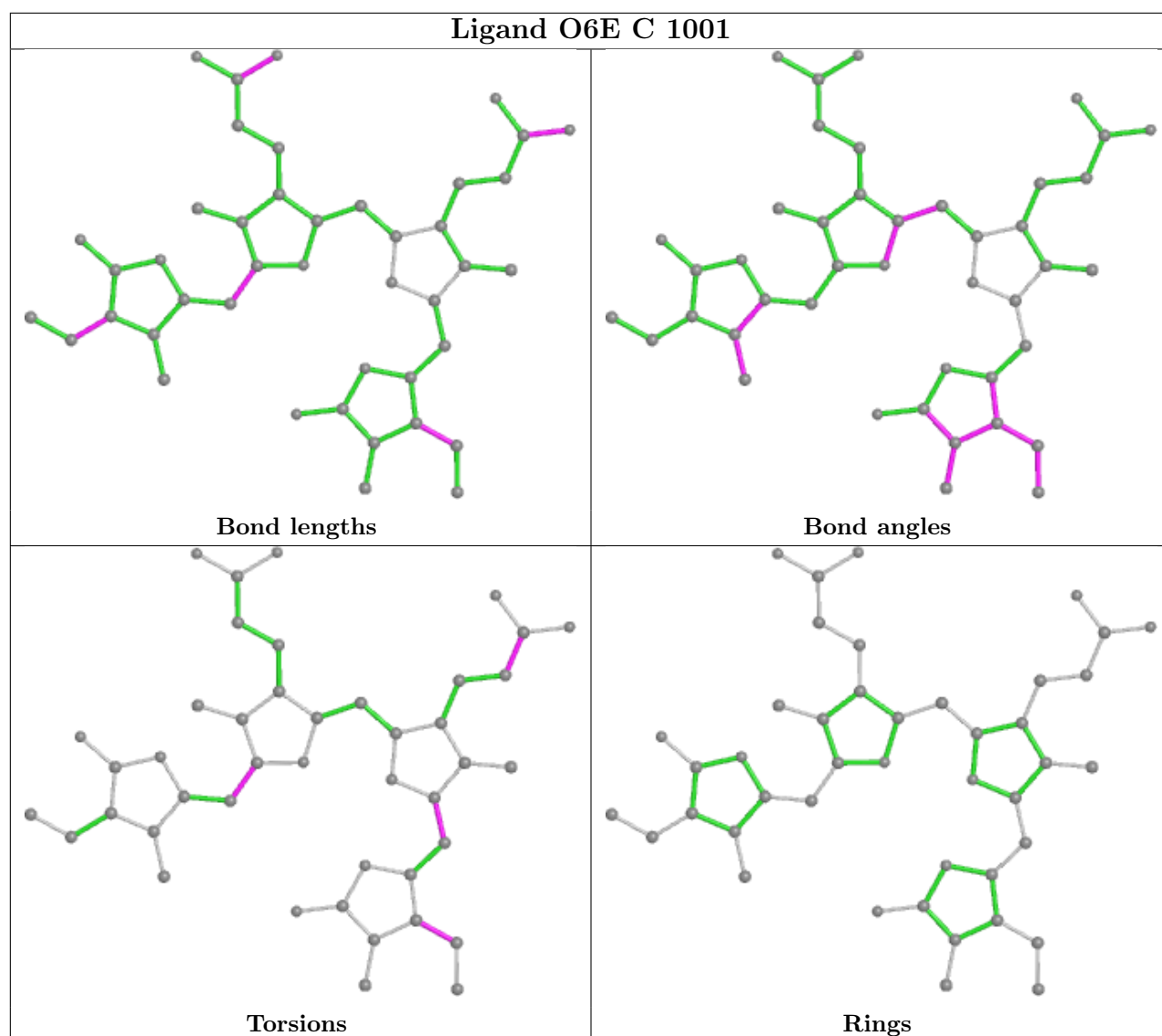
Mol	Chain	Res	Type	Atoms
3	C	1001	O6E	CAH-CAC-CBJ-CBN
3	C	1001	O6E	CBN-CAQ-CAY-NAN
3	C	1001	O6E	CBN-CAQ-CAY-CBE
3	C	1001	O6E	CAW-CAP-CBL-NAE
3	C	1001	O6E	CAW-CAP-CBL-CBH

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.





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.