



## wwPDB EM Validation Summary Report

Nov 6, 2023 – 06:24 pm GMT

PDB ID : 8PBC  
EMDB ID : EMD-17584  
Title : RAD51 filament on ssDNA bound by the BRCA2 c-terminus  
Authors : Appleby, R.; Pellegrini, L.  
Deposited on : 2023-06-09  
Resolution : 2.61 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](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.

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 : 0.0.1.dev70  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

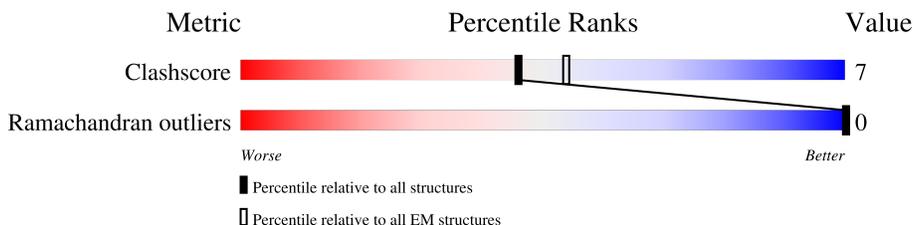
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.61 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	158937	4297
Ramachandran outliers	154571	4023

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  $\geq 3$ , 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	339	<span style="display: inline-block; width: 100%; height: 15px; background: linear-gradient(to right, green 80%, yellow 12%, grey 8%);"></span> 80%                      12%                      8%
1	B	339	<span style="display: inline-block; width: 100%; height: 15px; background: linear-gradient(to right, green 78%, yellow 13%, grey 8%);"></span> 78%                      13%                      8%
1	C	339	<span style="display: inline-block; width: 100%; height: 15px; background: linear-gradient(to right, green 77%, yellow 14%, grey 8%);"></span> 77%                      14%                      8%
1	D	339	<span style="display: inline-block; width: 100%; height: 15px; background: linear-gradient(to right, green 78%, yellow 14%, grey 8%);"></span> 78%                      14%                      8%
1	E	339	<span style="display: inline-block; width: 100%; height: 15px; background: linear-gradient(to right, green 77%, yellow 15%, grey 8%);"></span> 77%                      15%                      8%
1	F	339	<span style="display: inline-block; width: 100%; height: 15px; background: linear-gradient(to right, green 75%, yellow 17%, grey 8%);"></span> 75%                      17%                      8%
1	G	339	<span style="display: inline-block; width: 100%; height: 15px; background: linear-gradient(to right, green 77%, yellow 15%, grey 8%);"></span> 77%                      15%                      8%
1	H	339	<span style="display: inline-block; width: 100%; height: 15px; background: linear-gradient(to right, green 78%, yellow 14%, grey 8%);"></span> 78%                      14%                      8%
1	I	339	<span style="display: inline-block; width: 100%; height: 15px; background: linear-gradient(to right, green 78%, yellow 14%, grey 8%);"></span> 78%                      14%                      8%
1	J	339	<span style="display: inline-block; width: 100%; height: 15px; background: linear-gradient(to right, green 78%, yellow 14%, grey 8%);"></span> 78%                      14%                      8%

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
1	K	339	 78% 14% 8%
2	L	49	 29% 67%
2	M	49	 29% 67%
2	N	49	 31% 67%
2	O	49	 31% 67%
2	P	49	 31% 67%
2	Q	49	 29% 67%
2	R	49	 29% 67%
2	S	49	 29% 67%
2	T	49	 31% 67%
2	U	49	 31% 67%
3	V	30	 30% 63% 7%

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 28447 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 DNA repair protein RAD51 homolog 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	311	2384	1493	421	457	13	0	0
1	B	311	2384	1493	421	457	13	0	0
1	C	311	2384	1493	421	457	13	0	0
1	D	311	2384	1493	421	457	13	0	0
1	E	311	2384	1493	421	457	13	0	0
1	F	311	2384	1493	421	457	13	0	0
1	G	311	2384	1493	421	457	13	0	0
1	H	311	2384	1493	421	457	13	0	0
1	I	311	2384	1493	421	457	13	0	0
1	J	311	2384	1493	421	457	13	0	0
1	K	311	2384	1493	421	457	13	0	0

- Molecule 2 is a protein called Breast cancer type 2 susceptibility protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	L	16	121	78	22	20	1	0	0
2	M	16	121	78	22	20	1	0	0
2	N	16	121	78	22	20	1	0	0
2	O	16	121	78	22	20	1	0	0

*Continued on next page...*

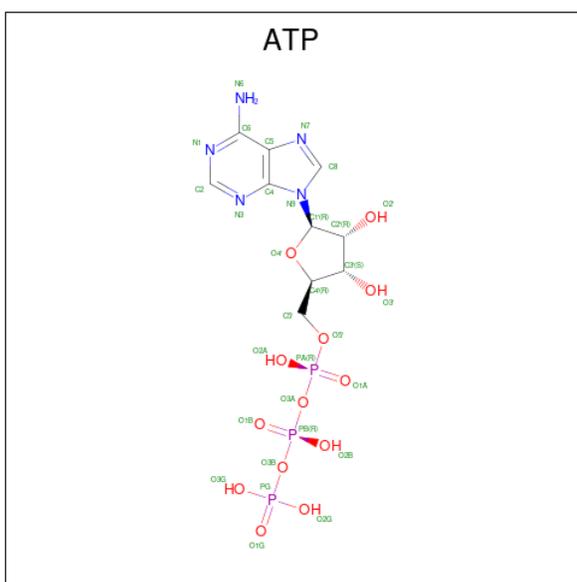
Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	P	16	Total 121	C 78	N 22	O 20	S 1	0	0
2	Q	16	Total 121	C 78	N 22	O 20	S 1	0	0
2	R	16	Total 121	C 78	N 22	O 20	S 1	0	0
2	S	16	Total 121	C 78	N 22	O 20	S 1	0	0
2	T	16	Total 121	C 78	N 22	O 20	S 1	0	0
2	U	16	Total 121	C 78	N 22	O 20	S 1	0	0

- Molecule 3 is a DNA chain called DNA (30-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	V	30	Total 650	C 300	N 150	O 170	P 30	0	0

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula:  $C_{10}H_{16}N_5O_{13}P_3$ ).



*Continued from previous page...*

Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
4	C	1	31	10	5	13	3	0
4	D	1	31	10	5	13	3	0
4	E	1	31	10	5	13	3	0
4	F	1	31	10	5	13	3	0
4	G	1	31	10	5	13	3	0
4	H	1	31	10	5	13	3	0
4	I	1	31	10	5	13	3	0
4	J	1	31	10	5	13	3	0
4	K	1	31	10	5	13	3	0

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
			Total	Ca	
5	A	3	3	3	0
5	B	2	2	2	0
5	C	2	2	2	0
5	D	2	2	2	0
5	E	2	2	2	0
5	F	2	2	2	0
5	G	2	2	2	0
5	H	2	2	2	0
5	I	2	2	2	0
5	J	2	2	2	0

*Continued on next page...*

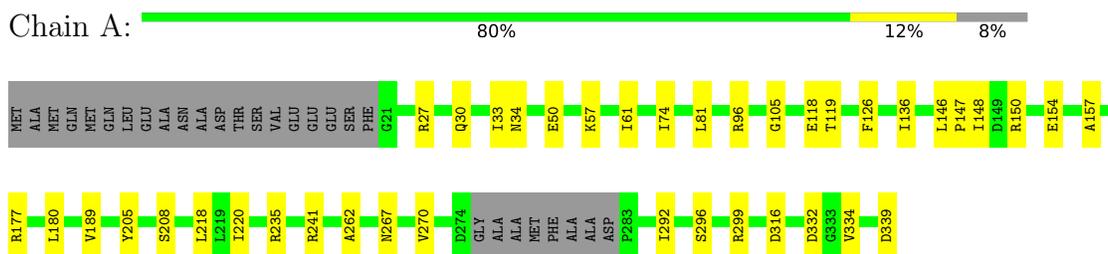
*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>AltConf</b>
5	K	1	Total	Ca	0
			1	1	

### 3 Residue-property plots [i](#)

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: DNA repair protein RAD51 homolog 1



- Molecule 1: DNA repair protein RAD51 homolog 1



- Molecule 1: DNA repair protein RAD51 homolog 1



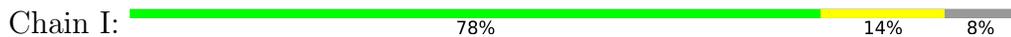
- Molecule 1: DNA repair protein RAD51 homolog 1







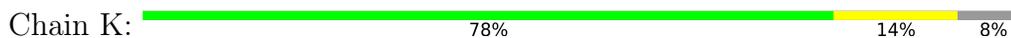
• Molecule 1: DNA repair protein RAD51 homolog 1



• Molecule 1: DNA repair protein RAD51 homolog 1



• Molecule 1: DNA repair protein RAD51 homolog 1



• Molecule 2: Breast cancer type 2 susceptibility protein

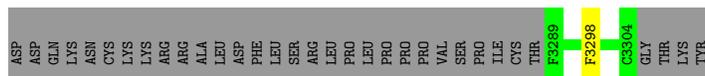


• Molecule 2: Breast cancer type 2 susceptibility protein





- Molecule 2: Breast cancer type 2 susceptibility protein



- Molecule 2: Breast cancer type 2 susceptibility protein



- Molecule 2: Breast cancer type 2 susceptibility protein



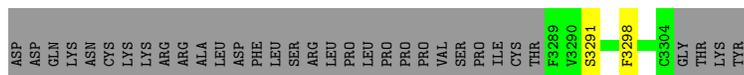
- Molecule 2: Breast cancer type 2 susceptibility protein



- Molecule 2: Breast cancer type 2 susceptibility protein



- Molecule 2: Breast cancer type 2 susceptibility protein

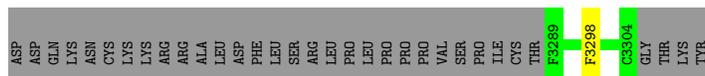


- Molecule 2: Breast cancer type 2 susceptibility protein





- Molecule 2: Breast cancer type 2 susceptibility protein



- Molecule 3: DNA (30-MER)



## 4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=56.2, 56.2°, rise=16.1, 16.1 Å, axial sym=C1, C1	Depositor
Number of segments used	1	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 ( $e^-/\text{Å}^2$ )	52.6	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 (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: CA, ATP

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	0.39	0/2418	0.50	0/3258
1	B	0.39	0/2418	0.50	0/3258
1	C	0.39	0/2418	0.50	0/3258
1	D	0.39	0/2418	0.50	0/3258
1	E	0.39	0/2418	0.50	0/3258
1	F	0.39	0/2418	0.50	0/3258
1	G	0.39	0/2418	0.50	0/3258
1	H	0.39	0/2418	0.50	0/3258
1	I	0.39	0/2418	0.50	0/3258
1	J	0.39	0/2418	0.50	0/3258
1	K	0.39	0/2418	0.50	0/3258
2	L	0.28	0/125	0.42	0/169
2	M	0.27	0/125	0.42	0/169
2	N	0.28	0/125	0.42	0/169
2	O	0.28	0/125	0.42	0/169
2	P	0.28	0/125	0.42	0/169
2	Q	0.28	0/125	0.41	0/169
2	R	0.28	0/125	0.42	0/169
2	S	0.28	0/125	0.42	0/169
2	T	0.28	0/125	0.42	0/169
2	U	0.28	0/125	0.41	0/169
3	V	1.19	1/739 (0.1%)	0.72	1/1146 (0.1%)
All	All	0.42	1/28587 (0.0%)	0.50	1/38674 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	V	14	DG	C3'-O3'	-5.31	1.37	1.44

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	V	9	DA	O4'-C4'-C3'	-5.08	102.47	104.50

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	2384	0	2405	27	0
1	B	2384	0	2405	32	0
1	C	2384	0	2405	35	0
1	D	2384	0	2405	34	0
1	E	2384	0	2405	40	0
1	F	2384	0	2405	52	0
1	G	2384	0	2405	43	0
1	H	2384	0	2405	34	0
1	I	2384	0	2405	34	0
1	J	2384	0	2405	33	0
1	K	2384	0	2405	32	0
2	L	121	0	119	2	0
2	M	121	0	119	2	0
2	N	121	0	119	1	0
2	O	121	0	119	1	0
2	P	121	0	119	1	0
2	Q	121	0	119	2	0
2	R	121	0	119	2	0
2	S	121	0	119	2	0
2	T	121	0	119	1	0
2	U	121	0	119	1	0
3	V	650	0	331	23	0
4	A	31	0	12	0	0
4	B	31	0	12	0	0
4	C	31	0	12	0	0
4	D	31	0	12	0	0
4	E	31	0	12	0	0
4	F	31	0	12	0	0
4	G	31	0	12	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	31	0	12	0	0
4	I	31	0	12	0	0
4	J	31	0	12	0	0
4	K	31	0	12	1	0
5	A	3	0	0	0	0
5	B	2	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	0	0
5	E	2	0	0	0	0
5	F	2	0	0	0	0
5	G	2	0	0	0	0
5	H	2	0	0	0	0
5	I	2	0	0	0	0
5	J	2	0	0	0	0
5	K	1	0	0	0	0
All	All	28447	0	28108	373	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 7.

The worst 5 of 373 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:E:235:ARG:HH21	1:F:273:VAL:HG23	1.31	0.94
1:E:229:ARG:NH1	3:V:18:DA:OP2	2.14	0.81
1:J:229:ARG:NH1	3:V:3:DA:OP2	2.18	0.75
1:F:229:ARG:NH1	3:V:15:DA:OP2	2.21	0.74
1:B:235:ARG:HH21	1:C:273:VAL:HG23	1.54	0.73

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	307/339 (91%)	299 (97%)	8 (3%)	0	100	100
1	B	307/339 (91%)	299 (97%)	8 (3%)	0	100	100
1	C	307/339 (91%)	299 (97%)	8 (3%)	0	100	100
1	D	307/339 (91%)	299 (97%)	8 (3%)	0	100	100
1	E	307/339 (91%)	299 (97%)	8 (3%)	0	100	100
1	F	307/339 (91%)	299 (97%)	8 (3%)	0	100	100
1	G	307/339 (91%)	299 (97%)	8 (3%)	0	100	100
1	H	307/339 (91%)	299 (97%)	8 (3%)	0	100	100
1	I	307/339 (91%)	299 (97%)	8 (3%)	0	100	100
1	J	307/339 (91%)	299 (97%)	8 (3%)	0	100	100
1	K	307/339 (91%)	299 (97%)	8 (3%)	0	100	100
2	L	14/49 (29%)	14 (100%)	0	0	100	100
2	M	14/49 (29%)	14 (100%)	0	0	100	100
2	N	14/49 (29%)	14 (100%)	0	0	100	100
2	O	14/49 (29%)	14 (100%)	0	0	100	100
2	P	14/49 (29%)	14 (100%)	0	0	100	100
2	Q	14/49 (29%)	14 (100%)	0	0	100	100
2	R	14/49 (29%)	14 (100%)	0	0	100	100
2	S	14/49 (29%)	14 (100%)	0	0	100	100
2	T	14/49 (29%)	14 (100%)	0	0	100	100
2	U	14/49 (29%)	14 (100%)	0	0	100	100
All	All	3517/4219 (83%)	3429 (98%)	88 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 33 ligands modelled in this entry, 22 are monoatomic - leaving 11 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
4	ATP	E	400	5	26,33,33	0.71	0	31,52,52	0.75	1 (3%)
4	ATP	F	400	5	26,33,33	0.71	0	31,52,52	0.76	1 (3%)
4	ATP	A	401	5	26,33,33	0.72	0	31,52,52	0.76	1 (3%)
4	ATP	J	400	5	26,33,33	0.72	0	31,52,52	0.76	1 (3%)
4	ATP	I	400	5	26,33,33	0.71	0	31,52,52	0.76	1 (3%)
4	ATP	C	400	5	26,33,33	0.72	0	31,52,52	0.76	1 (3%)
4	ATP	G	400	5	26,33,33	0.72	0	31,52,52	0.76	1 (3%)
4	ATP	K	400	5	26,33,33	0.72	0	31,52,52	0.76	1 (3%)
4	ATP	H	400	5	26,33,33	0.72	0	31,52,52	0.76	1 (3%)
4	ATP	D	400	5	26,33,33	0.71	0	31,52,52	0.76	1 (3%)
4	ATP	B	400	5	26,33,33	0.72	0	31,52,52	0.76	1 (3%)

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
4	ATP	E	400	5	-	4/18/38/38	0/3/3/3

*Continued on next page...*

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ATP	F	400	5	-	4/18/38/38	0/3/3/3
4	ATP	A	401	5	-	4/18/38/38	0/3/3/3
4	ATP	J	400	5	-	4/18/38/38	0/3/3/3
4	ATP	I	400	5	-	4/18/38/38	0/3/3/3
4	ATP	C	400	5	-	4/18/38/38	0/3/3/3
4	ATP	G	400	5	-	4/18/38/38	0/3/3/3
4	ATP	K	400	5	-	4/18/38/38	0/3/3/3
4	ATP	H	400	5	-	4/18/38/38	0/3/3/3
4	ATP	D	400	5	-	4/18/38/38	0/3/3/3
4	ATP	B	400	5	-	4/18/38/38	0/3/3/3

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	400	ATP	C5-C6-N6	2.27	123.81	120.35
4	D	400	ATP	C5-C6-N6	2.27	123.81	120.35
4	C	400	ATP	C5-C6-N6	2.27	123.80	120.35
4	A	401	ATP	C5-C6-N6	2.26	123.79	120.35
4	B	400	ATP	C5-C6-N6	2.26	123.78	120.35

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	401	ATP	C3'-C4'-C5'-O5'
4	B	400	ATP	C3'-C4'-C5'-O5'
4	C	400	ATP	C3'-C4'-C5'-O5'
4	D	400	ATP	C3'-C4'-C5'-O5'
4	E	400	ATP	C3'-C4'-C5'-O5'

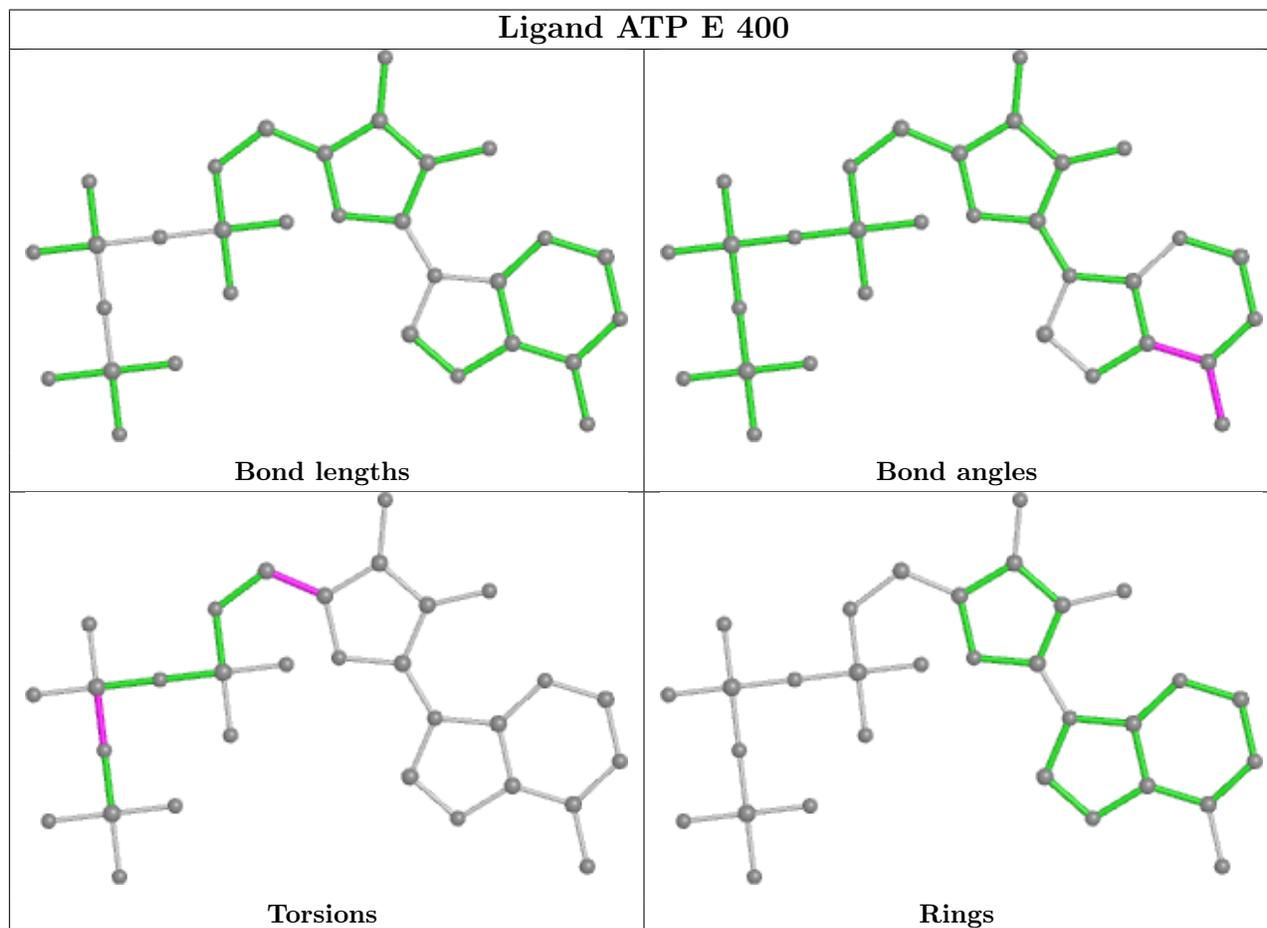
There are no ring outliers.

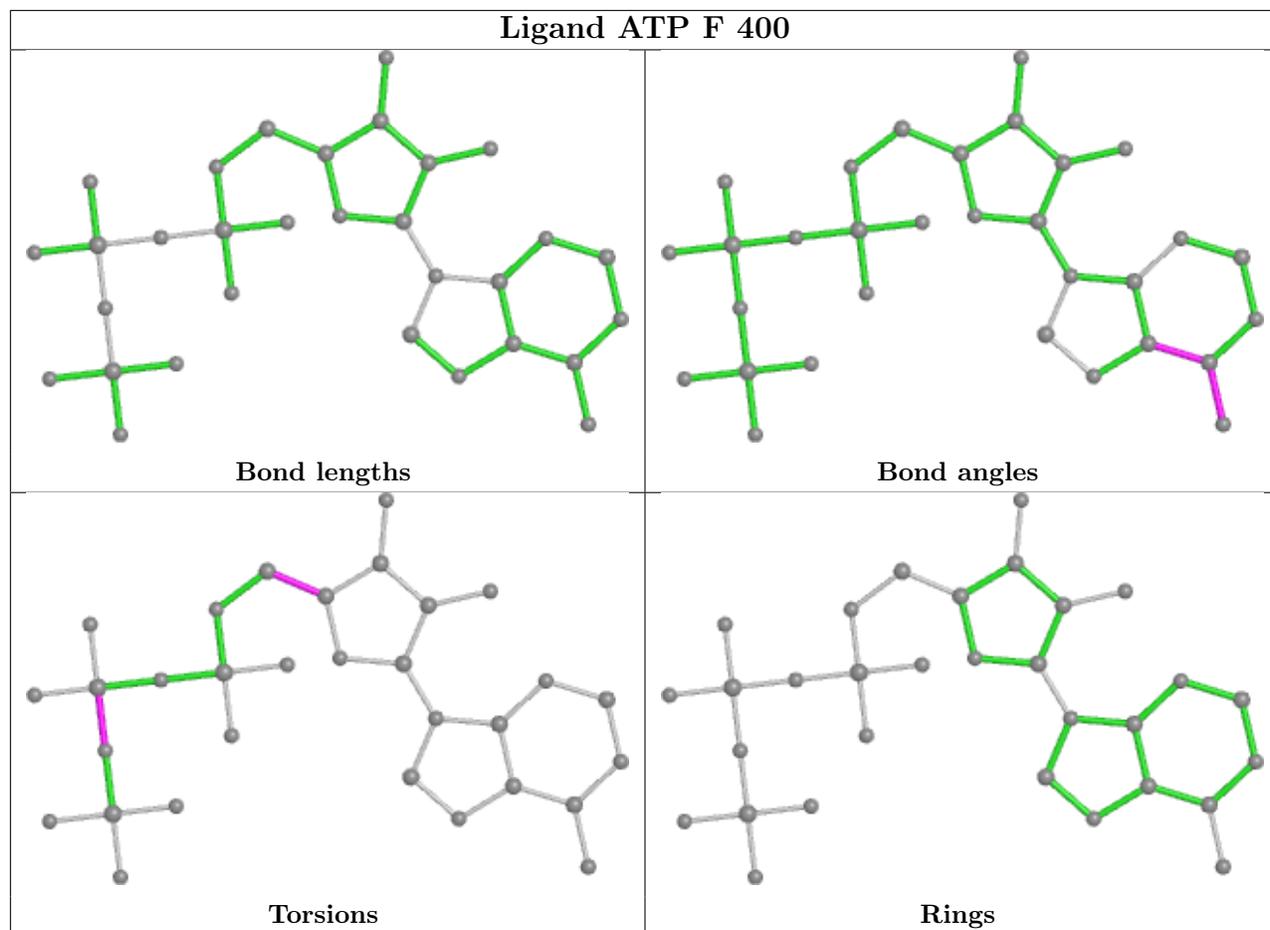
1 monomer is involved in 1 short contact:

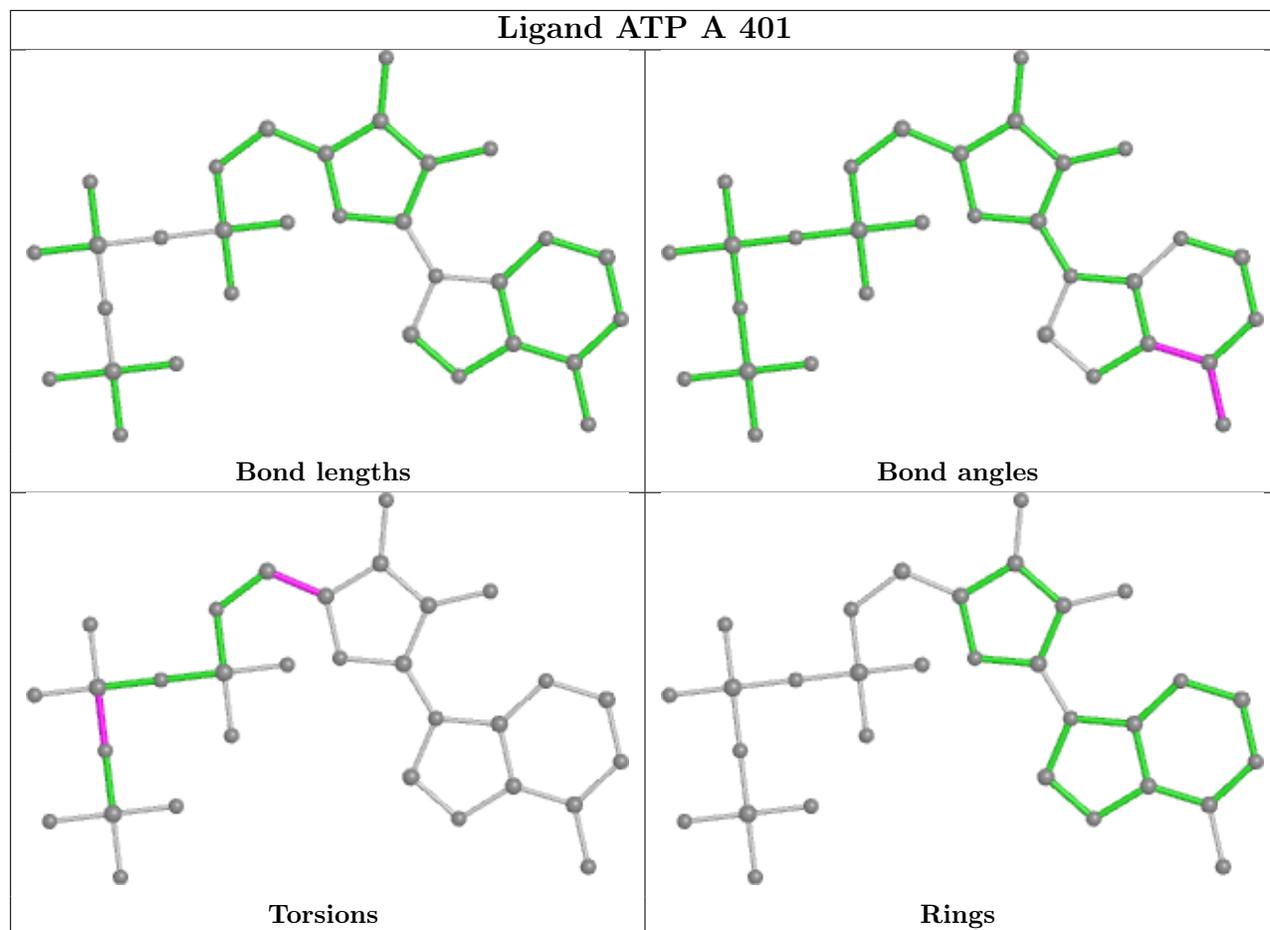
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	K	400	ATP	1	0

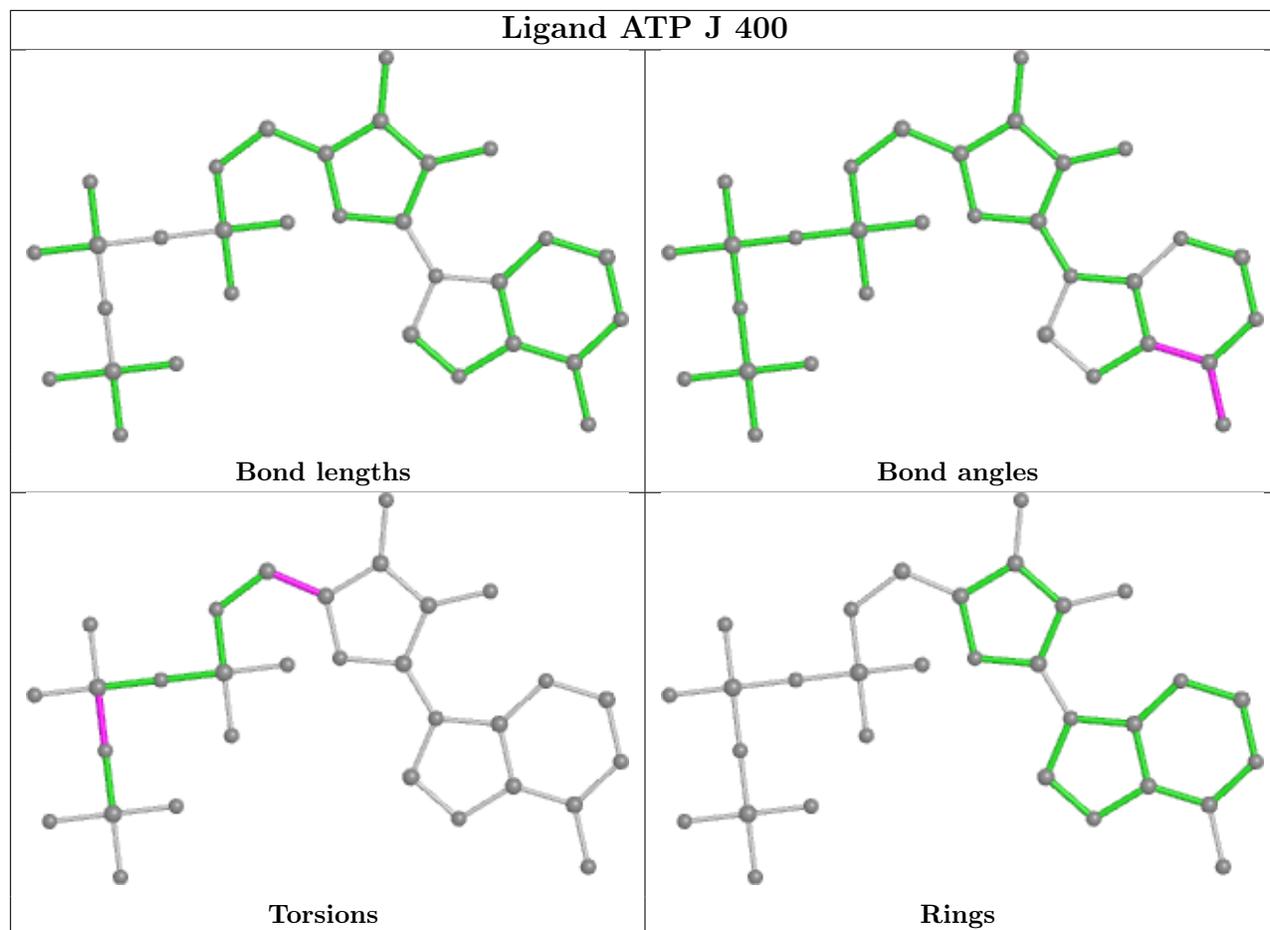
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

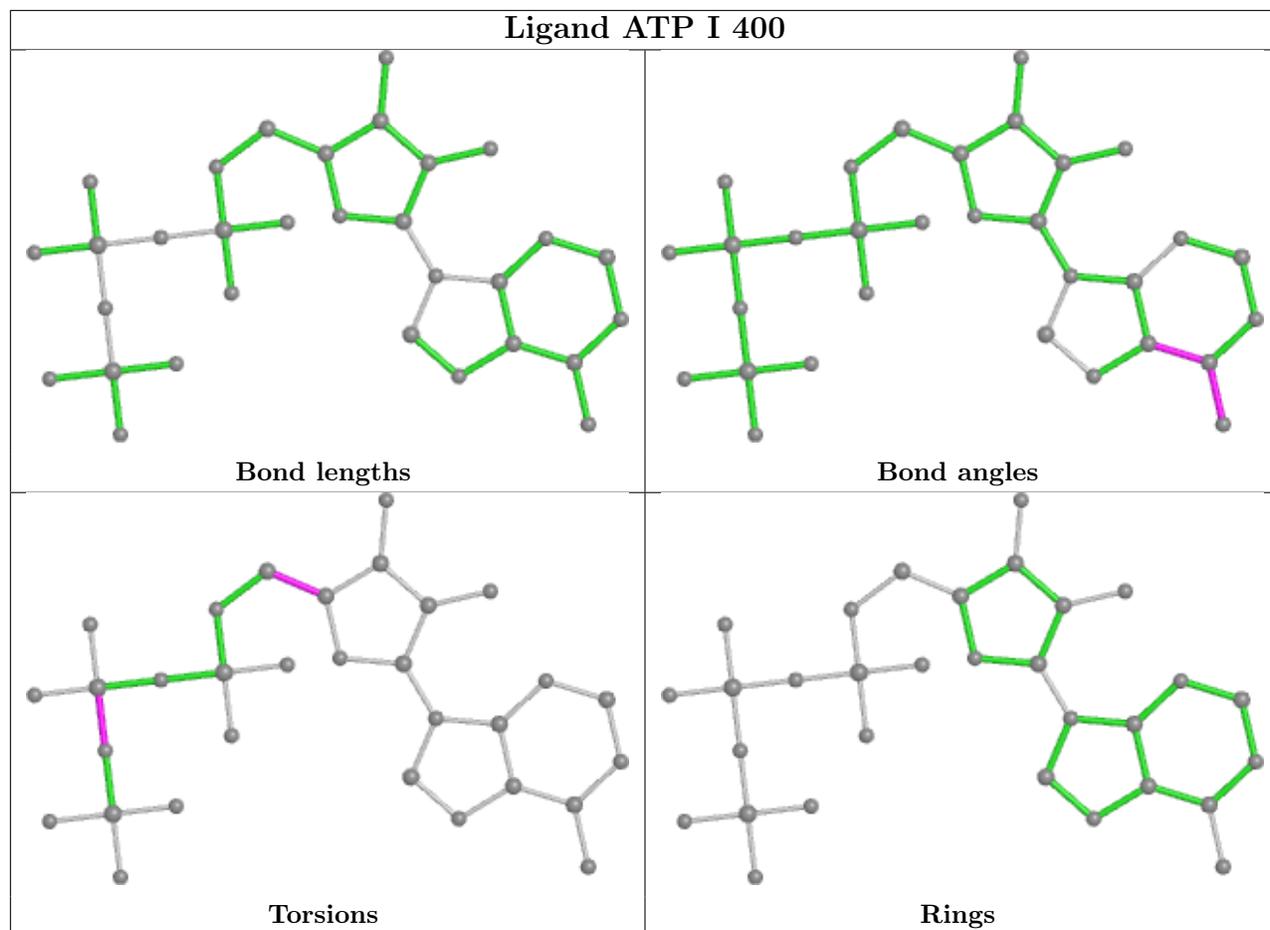
addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. 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.

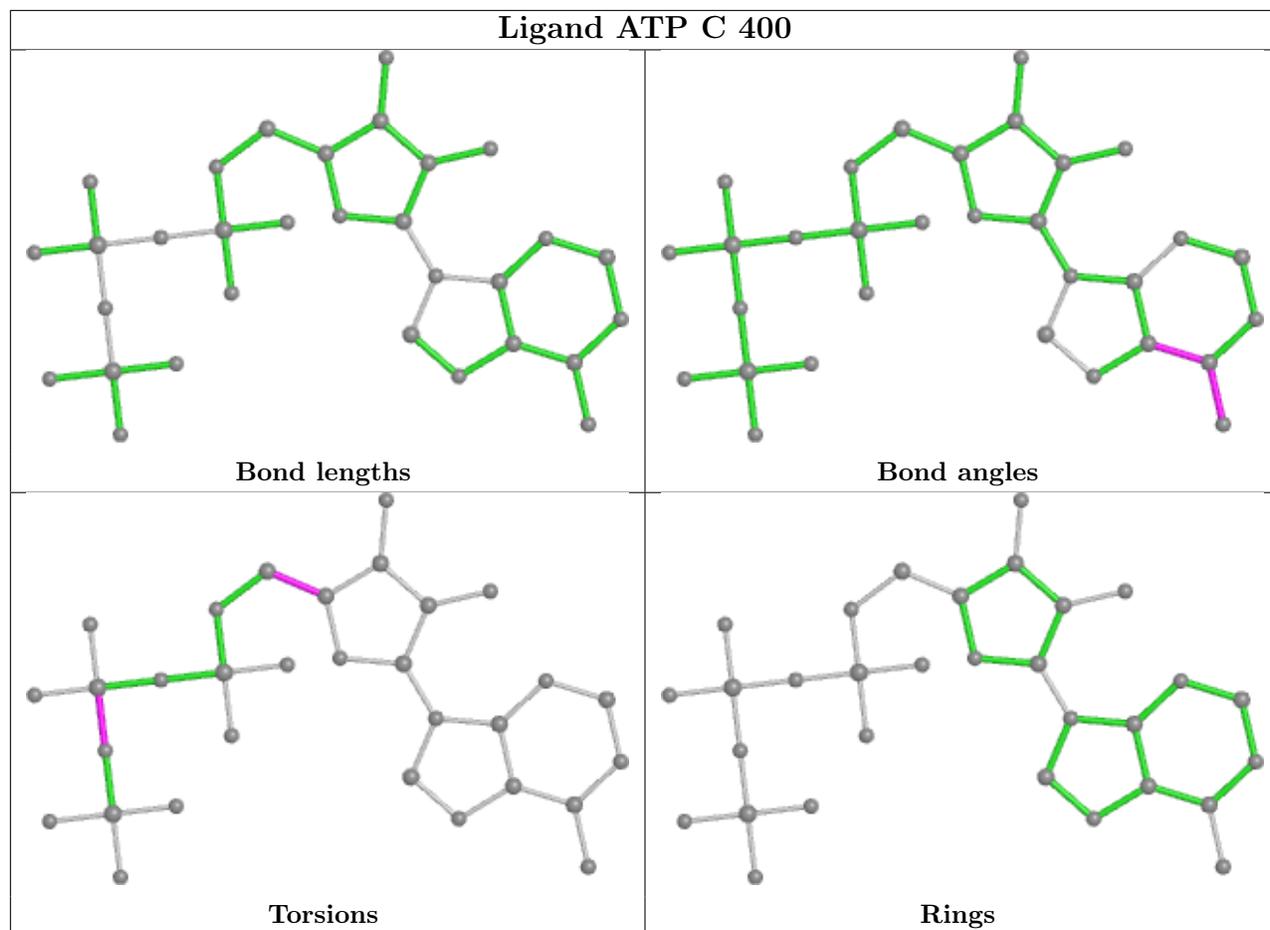


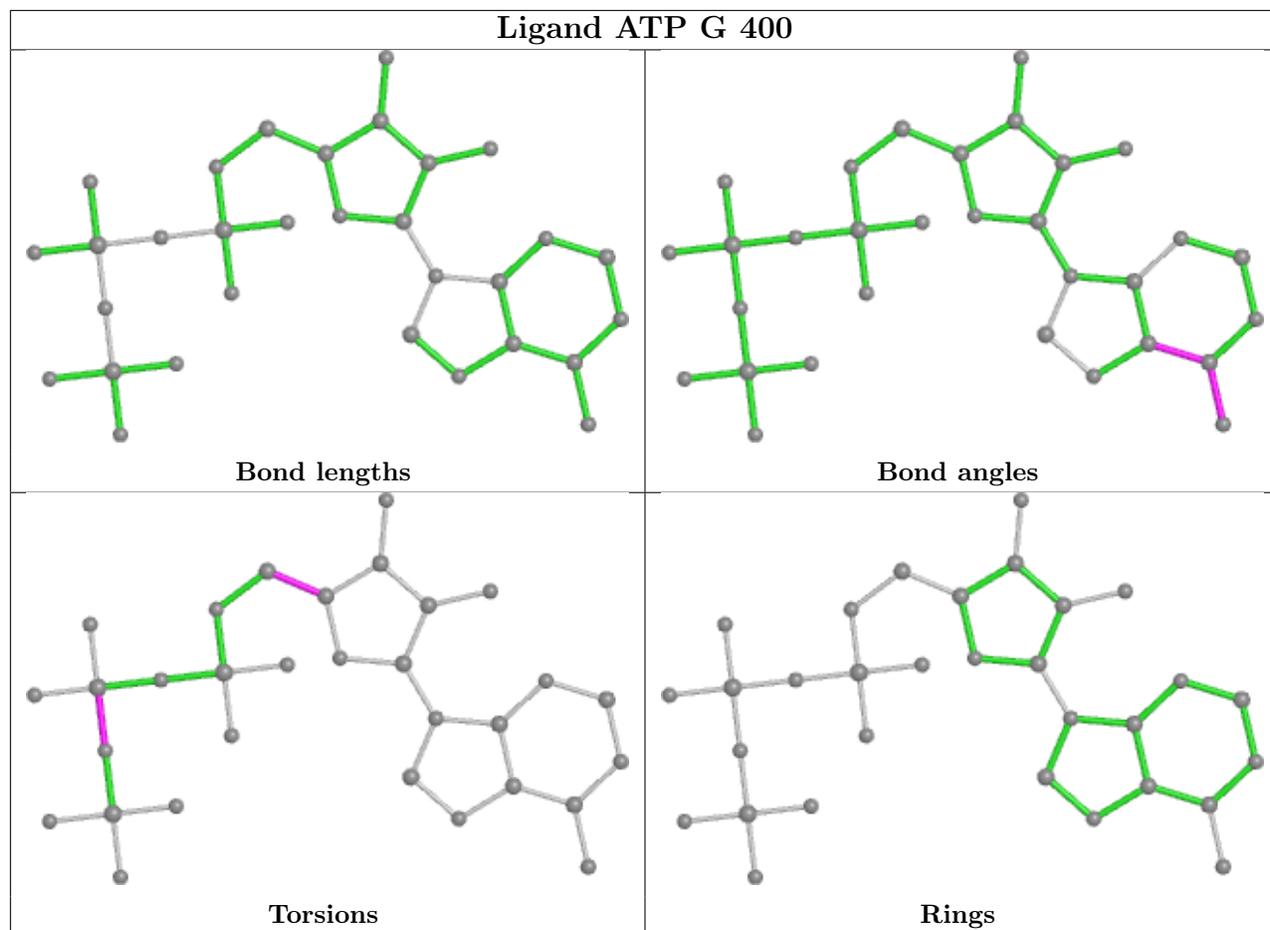


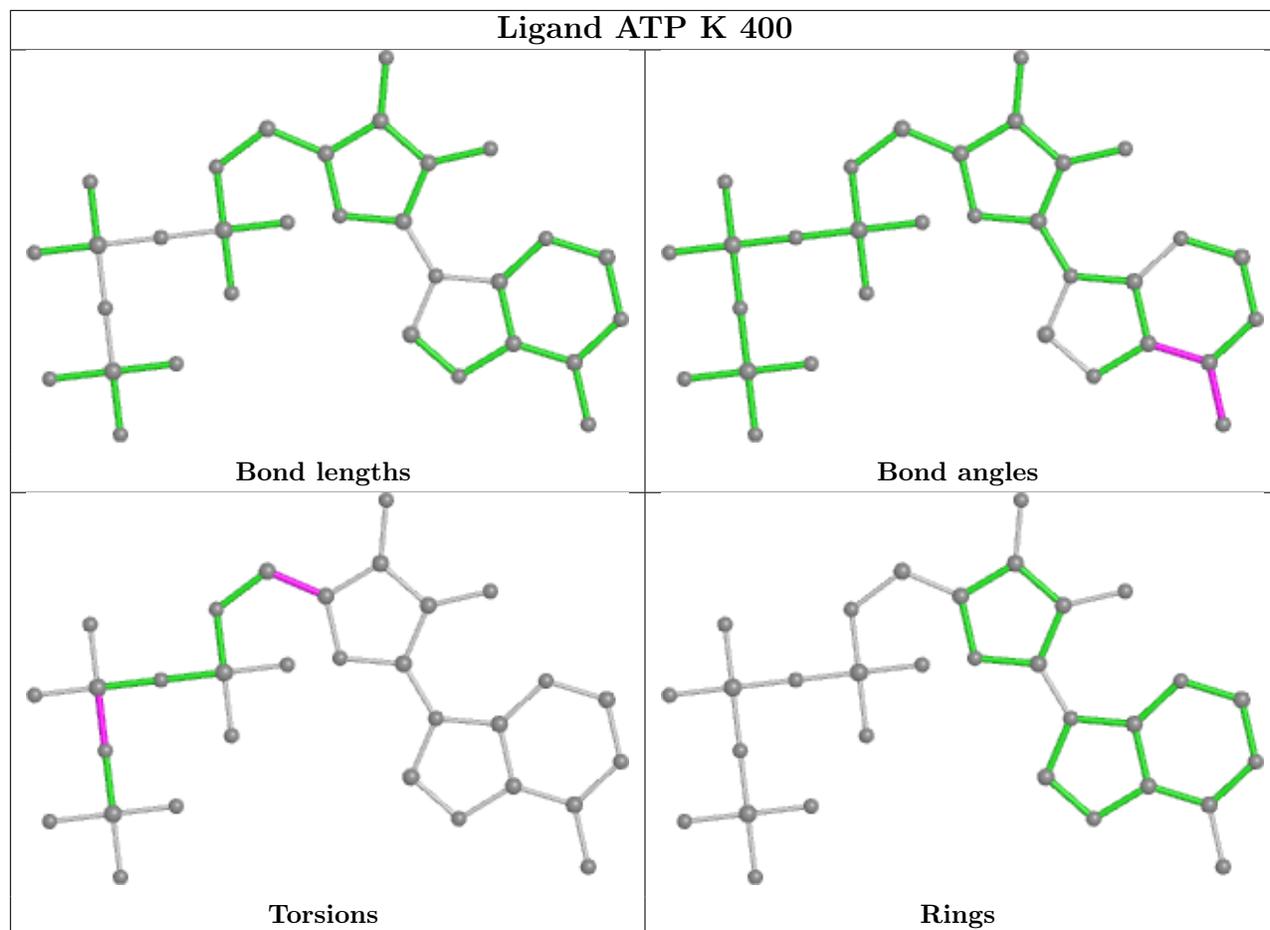


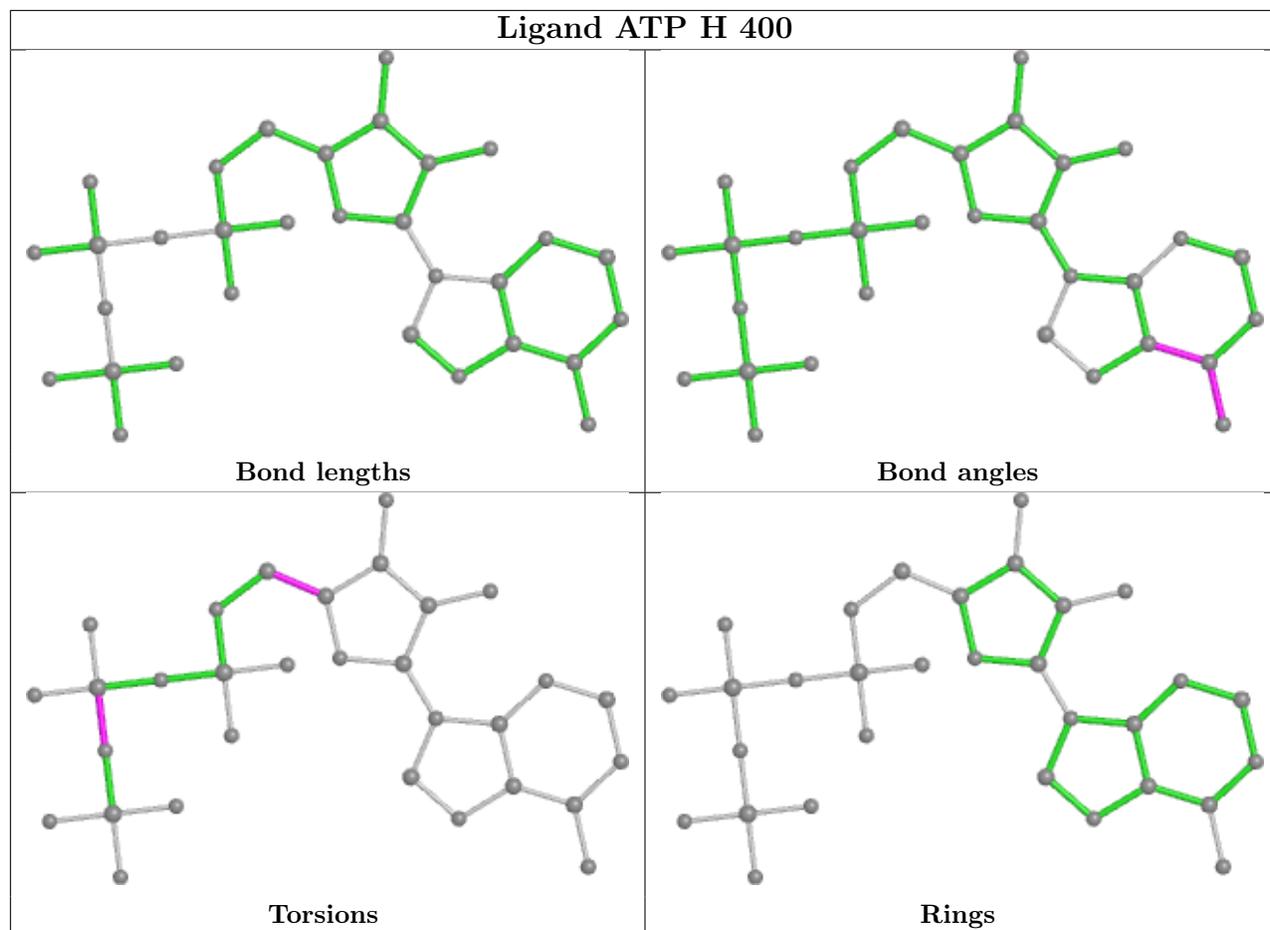


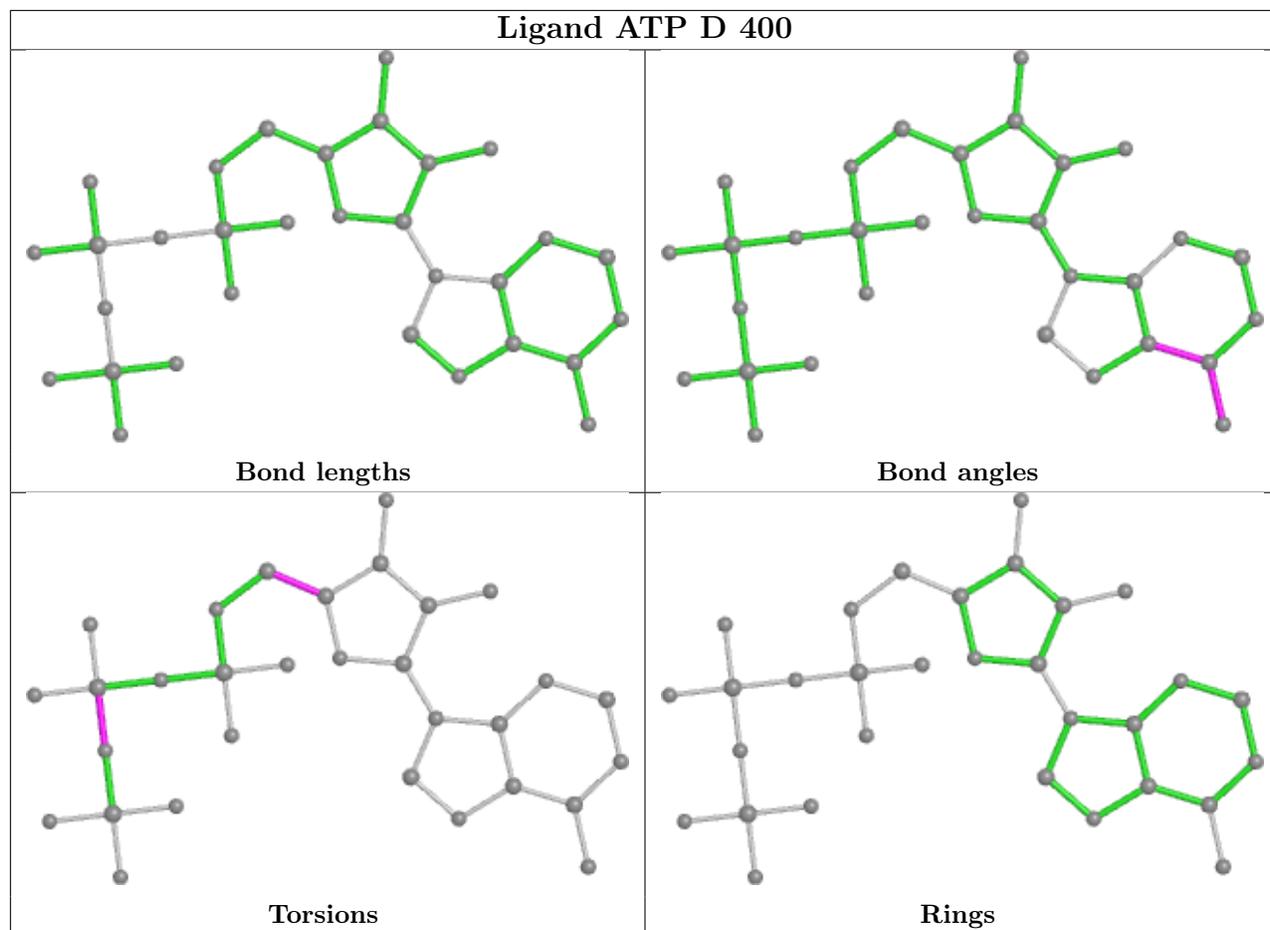


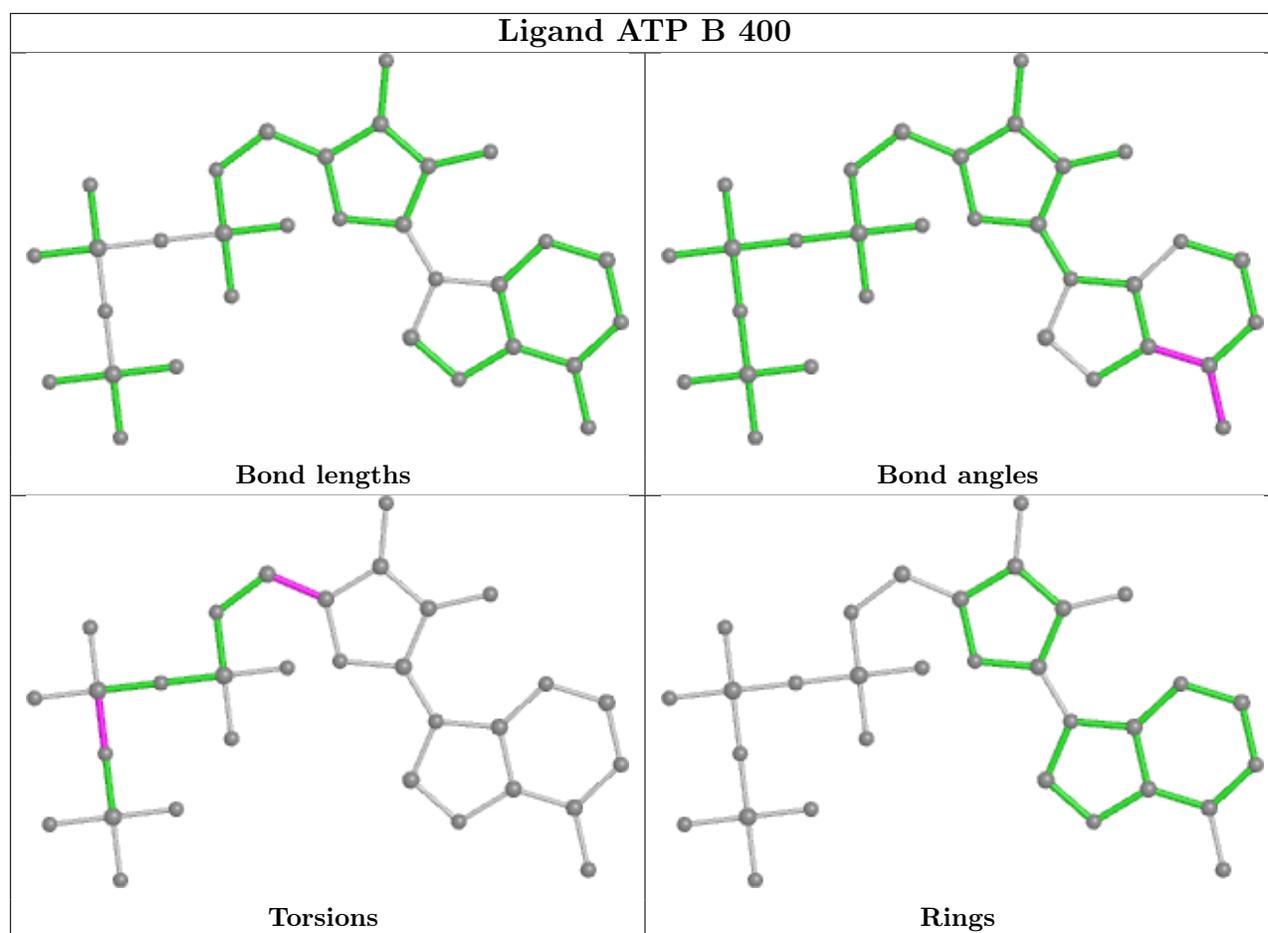












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-17584. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections

This section was not generated.

### 6.2 Central slices

This section was not generated.

### 6.3 Largest variance slices

This section was not generated.

### 6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

### 6.5 Orthogonal surface views

This section was not generated.

### 6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis

This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution

This section was not generated.

### 7.2 Volume estimate versus contour level

This section was not generated.

### 7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit

This section was not generated.