



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Nov 27, 2019 – 12:48 PM EST

PDB ID : 6UIW
EMDB ID: : EMD-20789
Title : Cryo-EM structure of human CALHM2 in a ruthenium red-bound inhibited state
Authors : Lu, W.; Du, J.; Choi, W.
Deposited on : 2019-10-01
Resolution : 2.70 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report for a publicly released PDB/EMDB 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.

MolProbity : 4.02b-467
Mogul : 1.8.0 (224370), CSD as540be (2019)
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

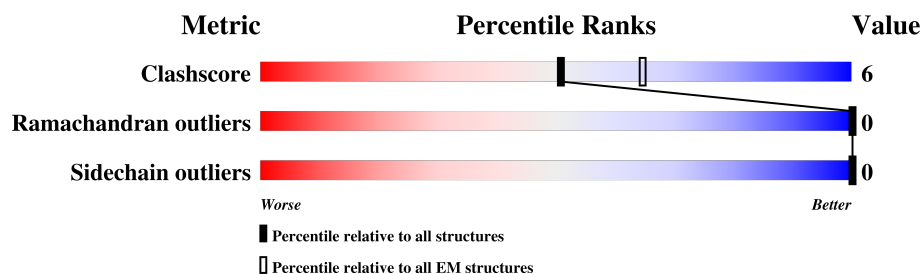
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	331	77% 12% 11%
1	B	331	76% 13% 11%
1	C	331	77% 11% 11%
1	D	331	78% 11% 11%
1	E	331	77% 11% 11%
1	F	331	77% 12% 11%
1	G	331	77% 12% 11%
1	H	331	77% 11% 11%
1	I	331	78% 11% 11%

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Mol	Chain	Length	Quality of chain
1	J	331	 78% 11% 11%
1	K	331	 77% 12% 11%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 23617 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 Calcium homeostasis modulator protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	294	Total	C	N	O	S	0	0
			2128	1381	388	352	7		
1	B	294	Total	C	N	O	S	0	0
			2128	1381	388	352	7		
1	C	294	Total	C	N	O	S	0	0
			2128	1381	388	352	7		
1	D	294	Total	C	N	O	S	0	0
			2128	1381	388	352	7		
1	E	294	Total	C	N	O	S	0	0
			2128	1381	388	352	7		
1	F	294	Total	C	N	O	S	0	0
			2128	1381	388	352	7		
1	G	294	Total	C	N	O	S	0	0
			2128	1381	388	352	7		
1	H	294	Total	C	N	O	S	0	0
			2128	1381	388	352	7		
1	I	294	Total	C	N	O	S	0	0
			2128	1381	388	352	7		
1	J	294	Total	C	N	O	S	0	0
			2128	1381	388	352	7		
1	K	294	Total	C	N	O	S	0	0
			2128	1381	388	352	7		

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	324	PHE	-	expression tag	UNP Q9HA72
A	325	GLU	-	expression tag	UNP Q9HA72
A	326	SER	-	expression tag	UNP Q9HA72
A	327	ARG	-	expression tag	UNP Q9HA72
A	328	LEU	-	expression tag	UNP Q9HA72
A	329	VAL	-	expression tag	UNP Q9HA72
A	330	PRO	-	expression tag	UNP Q9HA72
A	331	ARG	-	expression tag	UNP Q9HA72

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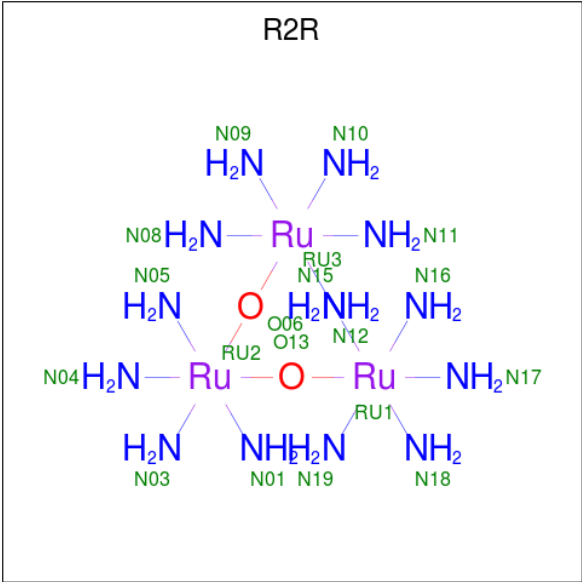
Chain	Residue	Modelled	Actual	Comment	Reference
B	324	PHE	-	expression tag	UNP Q9HA72
B	325	GLU	-	expression tag	UNP Q9HA72
B	326	SER	-	expression tag	UNP Q9HA72
B	327	ARG	-	expression tag	UNP Q9HA72
B	328	LEU	-	expression tag	UNP Q9HA72
B	329	VAL	-	expression tag	UNP Q9HA72
B	330	PRO	-	expression tag	UNP Q9HA72
B	331	ARG	-	expression tag	UNP Q9HA72
C	324	PHE	-	expression tag	UNP Q9HA72
C	325	GLU	-	expression tag	UNP Q9HA72
C	326	SER	-	expression tag	UNP Q9HA72
C	327	ARG	-	expression tag	UNP Q9HA72
C	328	LEU	-	expression tag	UNP Q9HA72
C	329	VAL	-	expression tag	UNP Q9HA72
C	330	PRO	-	expression tag	UNP Q9HA72
C	331	ARG	-	expression tag	UNP Q9HA72
D	324	PHE	-	expression tag	UNP Q9HA72
D	325	GLU	-	expression tag	UNP Q9HA72
D	326	SER	-	expression tag	UNP Q9HA72
D	327	ARG	-	expression tag	UNP Q9HA72
D	328	LEU	-	expression tag	UNP Q9HA72
D	329	VAL	-	expression tag	UNP Q9HA72
D	330	PRO	-	expression tag	UNP Q9HA72
D	331	ARG	-	expression tag	UNP Q9HA72
E	324	PHE	-	expression tag	UNP Q9HA72
E	325	GLU	-	expression tag	UNP Q9HA72
E	326	SER	-	expression tag	UNP Q9HA72
E	327	ARG	-	expression tag	UNP Q9HA72
E	328	LEU	-	expression tag	UNP Q9HA72
E	329	VAL	-	expression tag	UNP Q9HA72
E	330	PRO	-	expression tag	UNP Q9HA72
E	331	ARG	-	expression tag	UNP Q9HA72
F	324	PHE	-	expression tag	UNP Q9HA72
F	325	GLU	-	expression tag	UNP Q9HA72
F	326	SER	-	expression tag	UNP Q9HA72
F	327	ARG	-	expression tag	UNP Q9HA72
F	328	LEU	-	expression tag	UNP Q9HA72
F	329	VAL	-	expression tag	UNP Q9HA72
F	330	PRO	-	expression tag	UNP Q9HA72
F	331	ARG	-	expression tag	UNP Q9HA72
G	324	PHE	-	expression tag	UNP Q9HA72
G	325	GLU	-	expression tag	UNP Q9HA72

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Chain	Residue	Modelled	Actual	Comment	Reference
G	326	SER	-	expression tag	UNP Q9HA72
G	327	ARG	-	expression tag	UNP Q9HA72
G	328	LEU	-	expression tag	UNP Q9HA72
G	329	VAL	-	expression tag	UNP Q9HA72
G	330	PRO	-	expression tag	UNP Q9HA72
G	331	ARG	-	expression tag	UNP Q9HA72
H	324	PHE	-	expression tag	UNP Q9HA72
H	325	GLU	-	expression tag	UNP Q9HA72
H	326	SER	-	expression tag	UNP Q9HA72
H	327	ARG	-	expression tag	UNP Q9HA72
H	328	LEU	-	expression tag	UNP Q9HA72
H	329	VAL	-	expression tag	UNP Q9HA72
H	330	PRO	-	expression tag	UNP Q9HA72
H	331	ARG	-	expression tag	UNP Q9HA72
I	324	PHE	-	expression tag	UNP Q9HA72
I	325	GLU	-	expression tag	UNP Q9HA72
I	326	SER	-	expression tag	UNP Q9HA72
I	327	ARG	-	expression tag	UNP Q9HA72
I	328	LEU	-	expression tag	UNP Q9HA72
I	329	VAL	-	expression tag	UNP Q9HA72
I	330	PRO	-	expression tag	UNP Q9HA72
I	331	ARG	-	expression tag	UNP Q9HA72
J	324	PHE	-	expression tag	UNP Q9HA72
J	325	GLU	-	expression tag	UNP Q9HA72
J	326	SER	-	expression tag	UNP Q9HA72
J	327	ARG	-	expression tag	UNP Q9HA72
J	328	LEU	-	expression tag	UNP Q9HA72
J	329	VAL	-	expression tag	UNP Q9HA72
J	330	PRO	-	expression tag	UNP Q9HA72
J	331	ARG	-	expression tag	UNP Q9HA72
K	324	PHE	-	expression tag	UNP Q9HA72
K	325	GLU	-	expression tag	UNP Q9HA72
K	326	SER	-	expression tag	UNP Q9HA72
K	327	ARG	-	expression tag	UNP Q9HA72
K	328	LEU	-	expression tag	UNP Q9HA72
K	329	VAL	-	expression tag	UNP Q9HA72
K	330	PRO	-	expression tag	UNP Q9HA72
K	331	ARG	-	expression tag	UNP Q9HA72

- Molecule 2 is ruthenium(6+) azanide pentaamino(oxido)ruthenium (1/4/2) (three-letter code: R2R) (formula: $\text{H}_{28}\text{N}_{14}\text{O}_2\text{Ru}_3$) (labeled as "Ligand of Interest" by author).




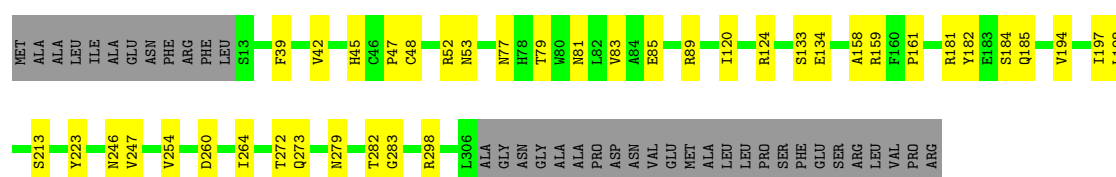
Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	N	O	Ru	0
			19	14	2	3	
2	B	1	Total	N	O	Ru	0
			19	14	2	3	
2	C	1	Total	N	O	Ru	0
			19	14	2	3	
2	D	1	Total	N	O	Ru	0
			19	14	2	3	
2	E	1	Total	N	O	Ru	0
			19	14	2	3	
2	F	1	Total	N	O	Ru	0
			19	14	2	3	
2	G	1	Total	N	O	Ru	0
			19	14	2	3	
2	H	1	Total	N	O	Ru	0
			19	14	2	3	
2	I	1	Total	N	O	Ru	0
			19	14	2	3	
2	J	1	Total	N	O	Ru	0
			19	14	2	3	
2	K	1	Total	N	O	Ru	0
			19	14	2	3	

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

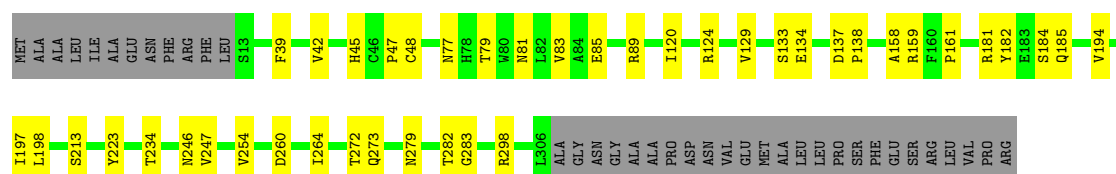
- Molecule 1: Calcium homeostasis modulator protein 2

Chain A: 



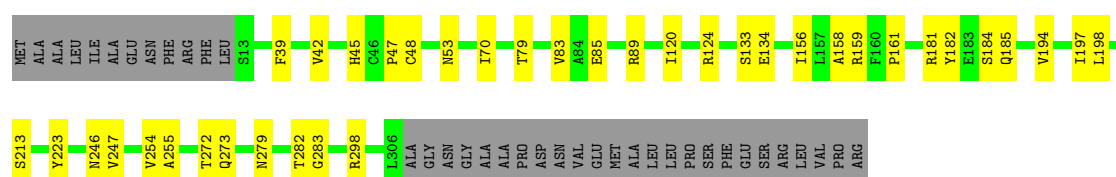
- Molecule 1: Calcium homeostasis modulator protein 2

Chain B: 




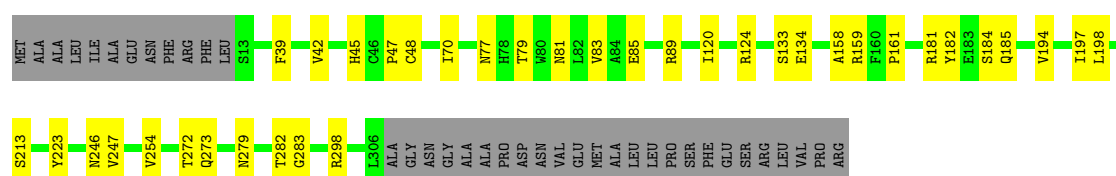
- Molecule 1: Calcium homeostasis modulator protein 2

Chain C: 




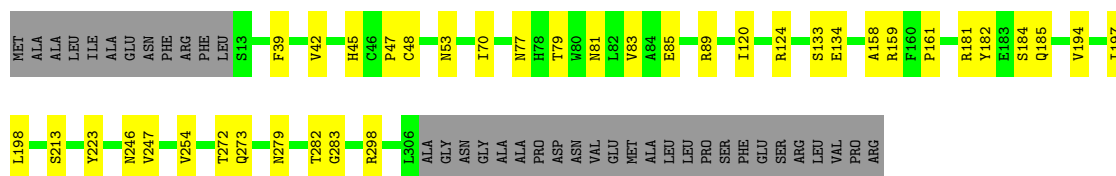
- Molecule 1: Calcium homeostasis modulator protein 2

Chain D: 




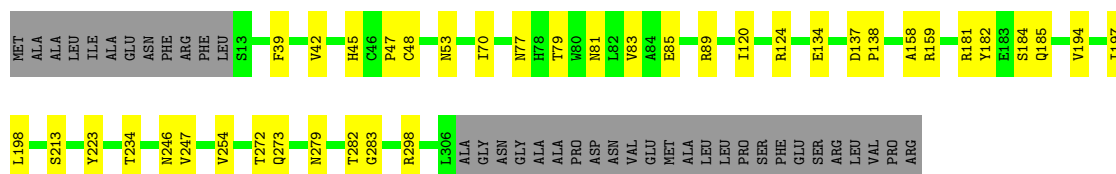
- Molecule 1: Calcium homeostasis modulator protein 2

Chain E: 




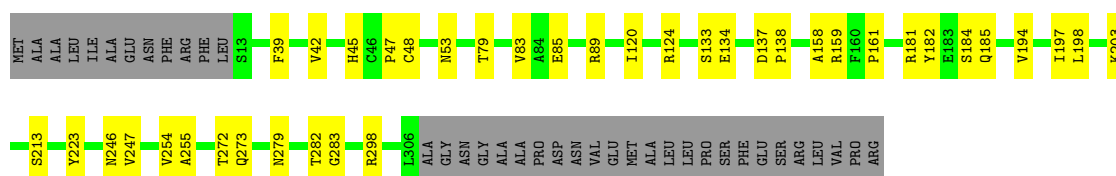
- Molecule 1: Calcium homeostasis modulator protein 2

Chain F: 




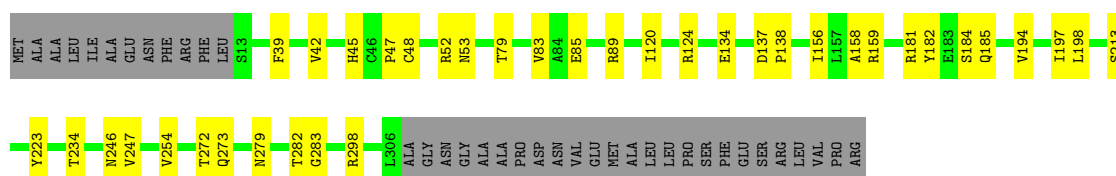
- Molecule 1: Calcium homeostasis modulator protein 2

Chain G: 



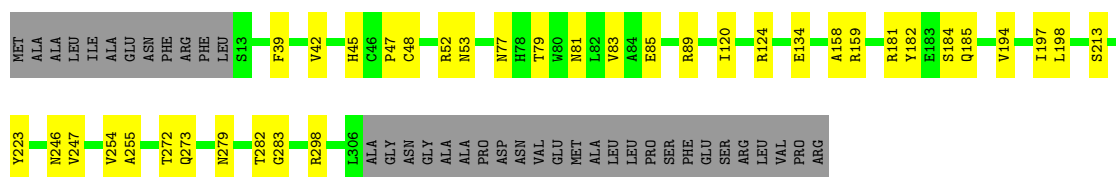
- Molecule 1: Calcium homeostasis modulator protein 2

Chain H: 




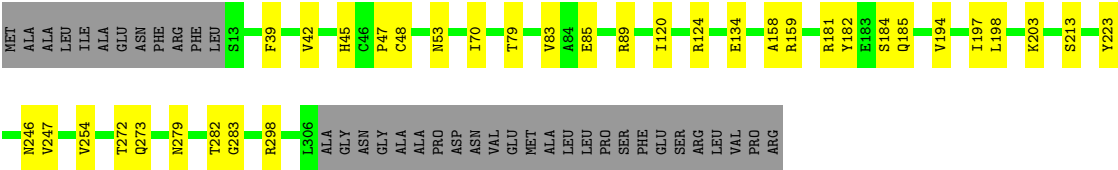
- Molecule 1: Calcium homeostasis modulator protein 2

Chain I: 



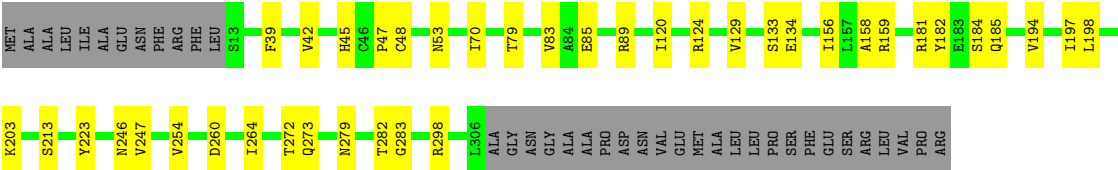
- Molecule 1: Calcium homeostasis modulator protein 2

Chain J: 



● Molecule 1: Calcium homeostasis modulator protein 2

Chain K: 77% 12% 11%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C11	Depositor
Number of particles used	83728	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 ($e^-/\text{\AA}^2$)	54.4	Depositor
Minimum defocus (nm)	1000.0	Depositor
Maximum defocus (nm)	2500.0	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k 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: R2R

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 >2	RMSZ	# Z >2
1	A	0.49	0/2185	0.53	0/2999
1	B	0.49	0/2185	0.53	0/2999
1	C	0.49	0/2185	0.53	0/2999
1	D	0.49	0/2185	0.53	0/2999
1	E	0.49	0/2185	0.53	0/2999
1	F	0.49	0/2185	0.53	0/2999
1	G	0.49	0/2185	0.53	0/2999
1	H	0.49	0/2185	0.53	0/2999
1	I	0.49	0/2185	0.53	0/2999
1	J	0.49	0/2185	0.53	0/2999
1	K	0.49	0/2185	0.53	0/2999
All	All	0.49	0/24035	0.53	0/32989

There are no bond length outliers.

There are no bond angle outliers.

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	2128	0	1939	31	0
1	B	2128	0	1939	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2128	0	1939	30	0
1	D	2128	0	1939	28	0
1	E	2128	0	1939	29	0
1	F	2128	0	1939	31	0
1	G	2128	0	1939	31	0
1	H	2128	0	1939	32	0
1	I	2128	0	1939	31	0
1	J	2128	0	1939	29	0
1	K	2128	0	1939	32	0
2	A	19	0	0	0	0
2	B	19	0	0	0	0
2	C	19	0	0	0	0
2	D	19	0	0	0	0
2	E	19	0	0	0	0
2	F	19	0	0	0	0
2	G	19	0	0	0	0
2	H	19	0	0	0	0
2	I	19	0	0	0	0
2	J	19	0	0	0	0
2	K	19	0	0	0	0
All	All	23617	0	21329	289	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 6.

The worst 5 of 289 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:J:120:ILE:O	1:J:124:ARG:HG2	1.44	1.18
1:C:120:ILE:O	1:C:124:ARG:HG2	1.44	1.18
1:I:120:ILE:O	1:I:124:ARG:HG2	1.44	1.18
1:K:120:ILE:O	1:K:124:ARG:HG2	1.44	1.18
1:H:120:ILE:O	1:H:124:ARG:HG2	1.44	1.18

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	292/331 (88%)	283 (97%)	9 (3%)	0	100	100
1	B	292/331 (88%)	283 (97%)	9 (3%)	0	100	100
1	C	292/331 (88%)	283 (97%)	9 (3%)	0	100	100
1	D	292/331 (88%)	283 (97%)	9 (3%)	0	100	100
1	E	292/331 (88%)	283 (97%)	9 (3%)	0	100	100
1	F	292/331 (88%)	283 (97%)	9 (3%)	0	100	100
1	G	292/331 (88%)	283 (97%)	9 (3%)	0	100	100
1	H	292/331 (88%)	283 (97%)	9 (3%)	0	100	100
1	I	292/331 (88%)	283 (97%)	9 (3%)	0	100	100
1	J	292/331 (88%)	283 (97%)	9 (3%)	0	100	100
1	K	292/331 (88%)	283 (97%)	9 (3%)	0	100	100
All	All	3212/3641 (88%)	3113 (97%)	99 (3%)	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	181/278 (65%)	181 (100%)	0	100	100
1	B	181/278 (65%)	181 (100%)	0	100	100
1	C	181/278 (65%)	181 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	181/278 (65%)	181 (100%)	0	100	100
1	E	181/278 (65%)	181 (100%)	0	100	100
1	F	181/278 (65%)	181 (100%)	0	100	100
1	G	181/278 (65%)	181 (100%)	0	100	100
1	H	181/278 (65%)	181 (100%)	0	100	100
1	I	181/278 (65%)	181 (100%)	0	100	100
1	J	181/278 (65%)	181 (100%)	0	100	100
1	K	181/278 (65%)	181 (100%)	0	100	100
All	All	1991/3058 (65%)	1991 (100%)	0	100	100

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

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	81	ASN
1	G	185	GLN
1	K	185	GLN
1	F	185	GLN
1	F	246	ASN

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

11 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	R2R	A	501	-	14,18,18	3.89	14 (100%)	-		
2	R2R	B	501	-	14,18,18	3.89	14 (100%)	-		
2	R2R	C	501	-	14,18,18	3.88	14 (100%)	-		
2	R2R	D	501	-	14,18,18	3.89	14 (100%)	-		
2	R2R	E	501	-	14,18,18	3.88	14 (100%)	-		
2	R2R	F	501	-	14,18,18	3.88	14 (100%)	-		
2	R2R	G	501	-	14,18,18	3.88	14 (100%)	-		
2	R2R	H	501	-	14,18,18	3.88	14 (100%)	-		
2	R2R	I	501	-	14,18,18	3.89	14 (100%)	-		
2	R2R	J	501	-	14,18,18	3.89	14 (100%)	-		
2	R2R	K	501	-	14,18,18	3.90	14 (100%)	-		

The worst 5 of 154 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	501	R2R	RU2-N01	-4.15	2.04	2.11
2	E	501	R2R	RU2-N01	-4.13	2.04	2.11
2	I	501	R2R	RU2-N05	-4.12	2.04	2.11
2	K	501	R2R	RU2-N05	-4.12	2.04	2.11
2	J	501	R2R	RU2-N05	-4.12	2.04	2.11

There are no bond angle outliers.

There are no chirality outliers.

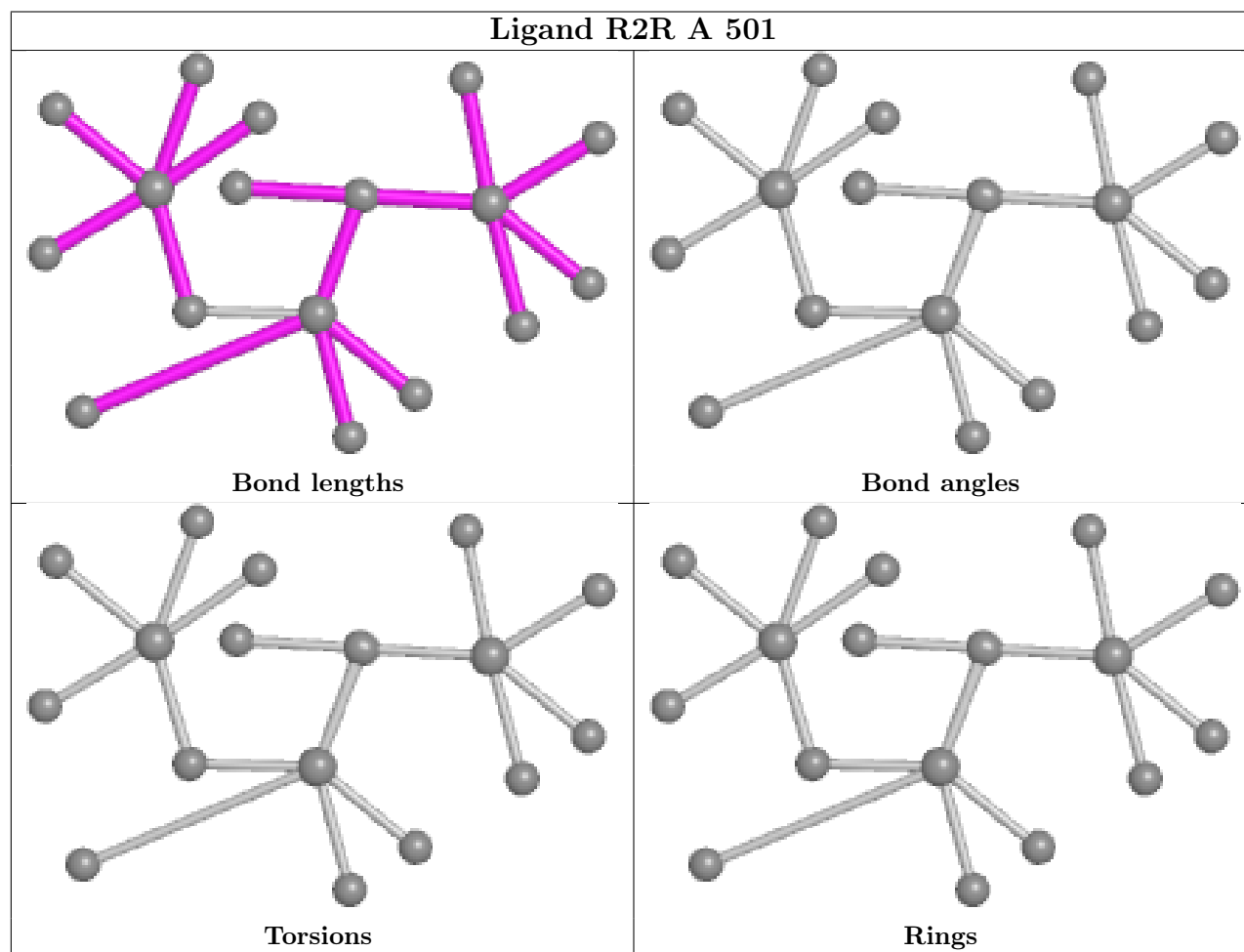
There are no torsion outliers.

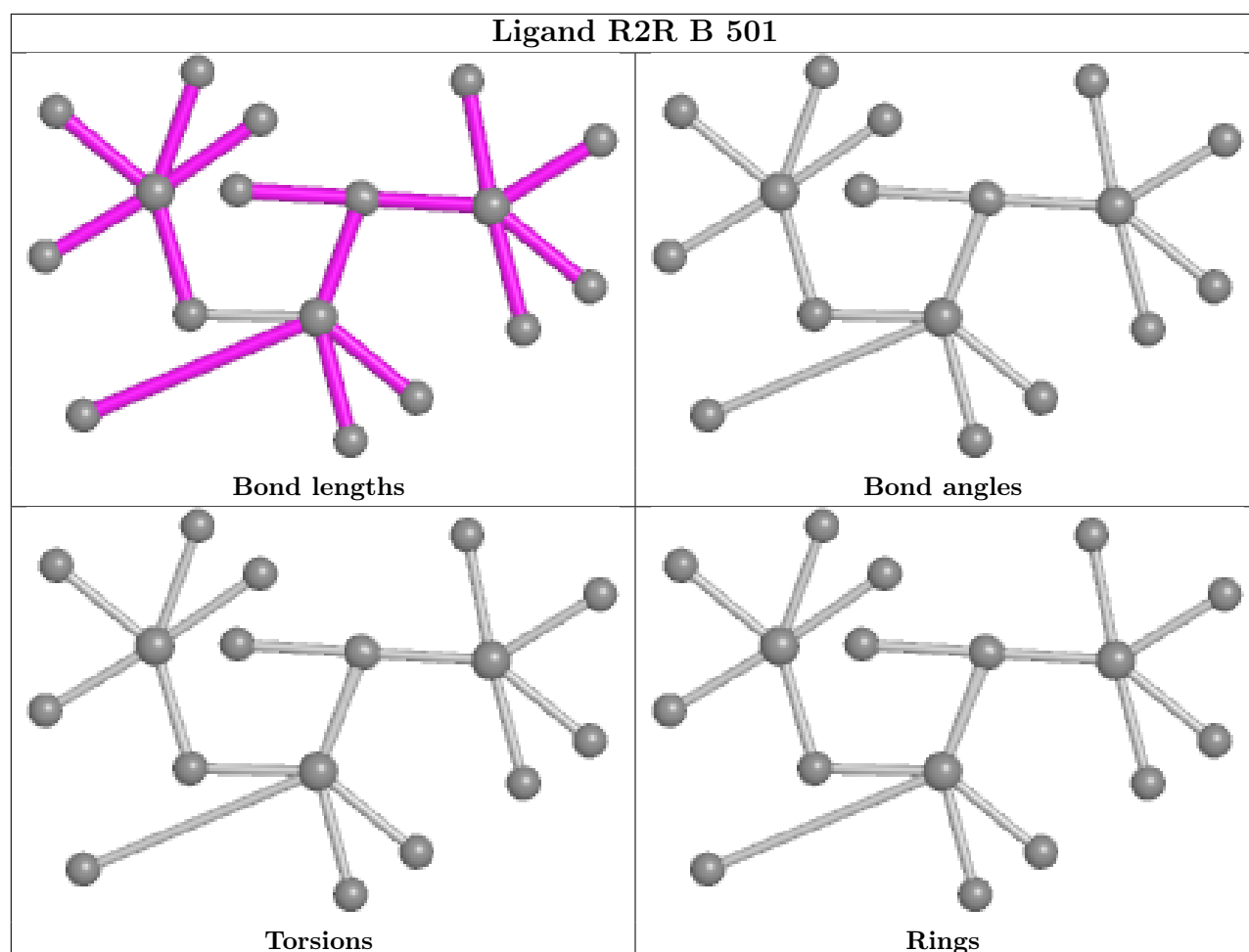
There are no ring outliers.

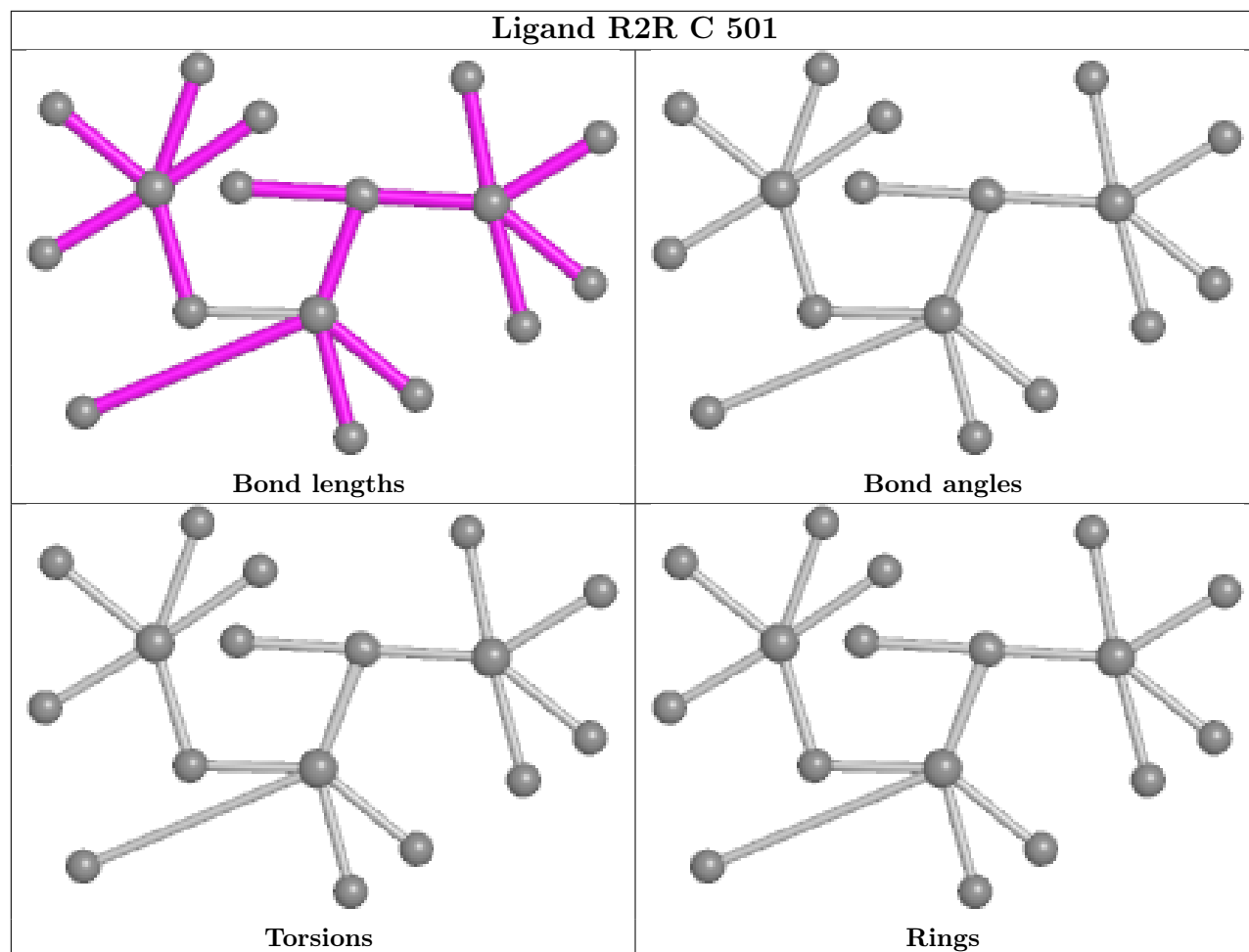
No monomer is involved in short contacts.

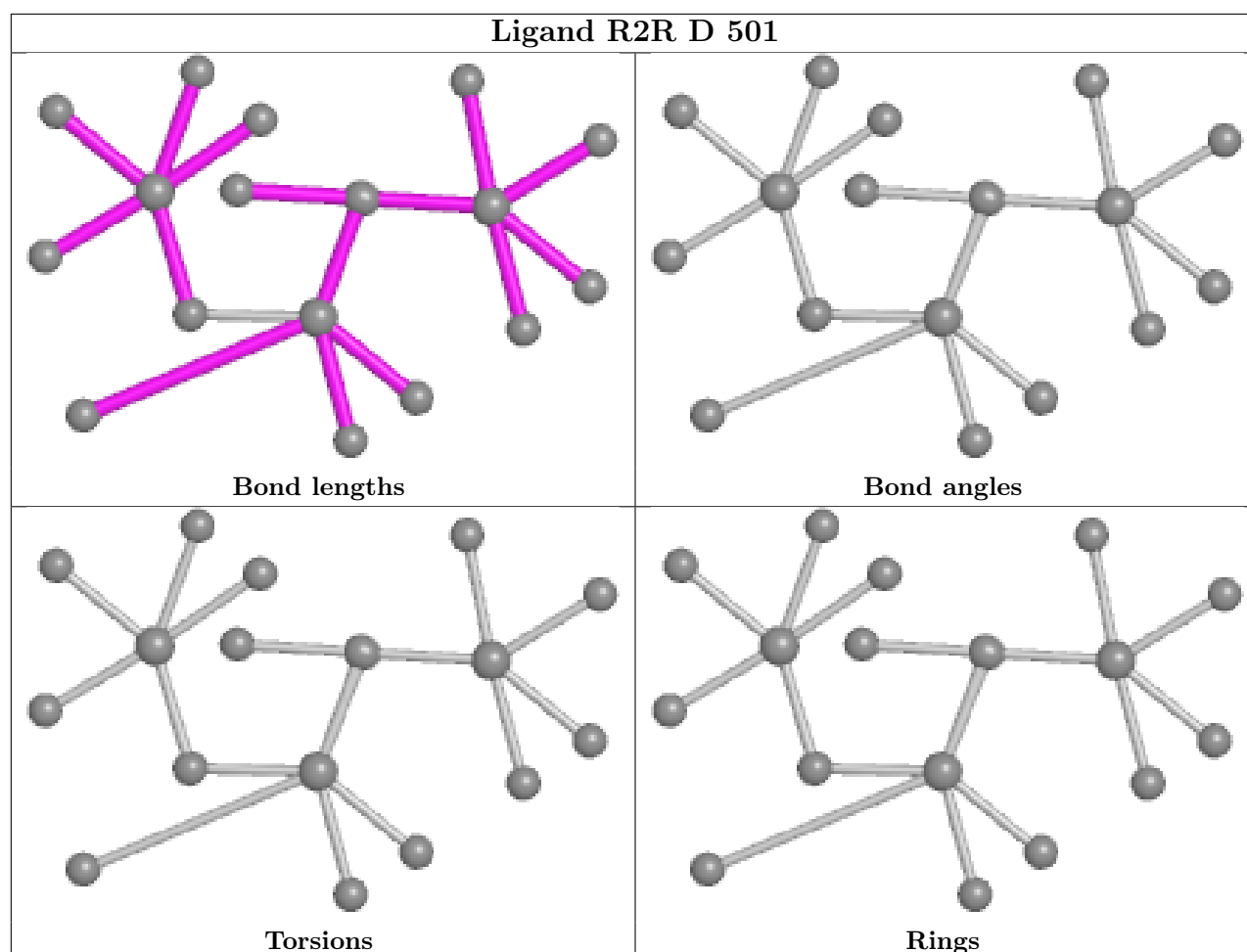
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

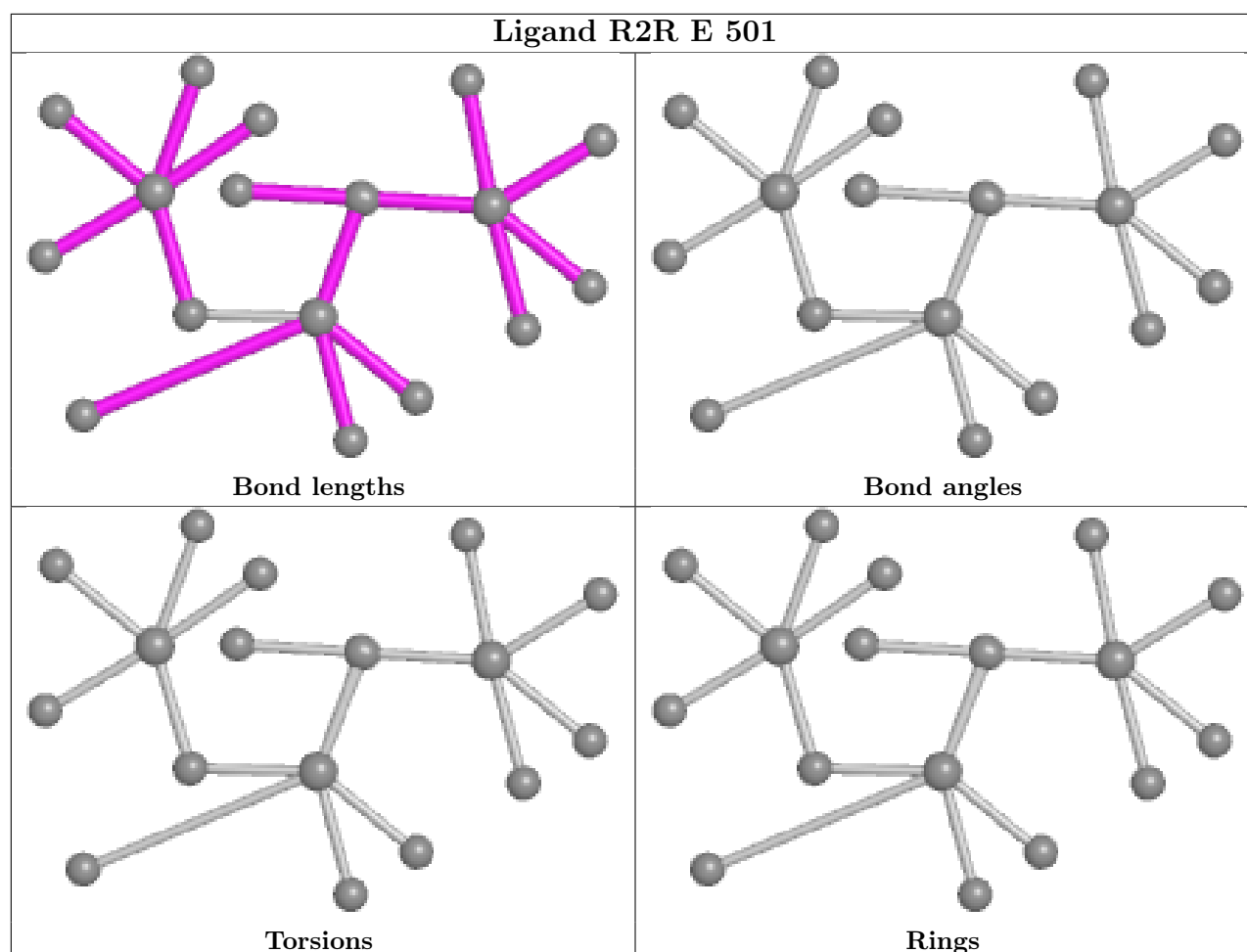
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question 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.

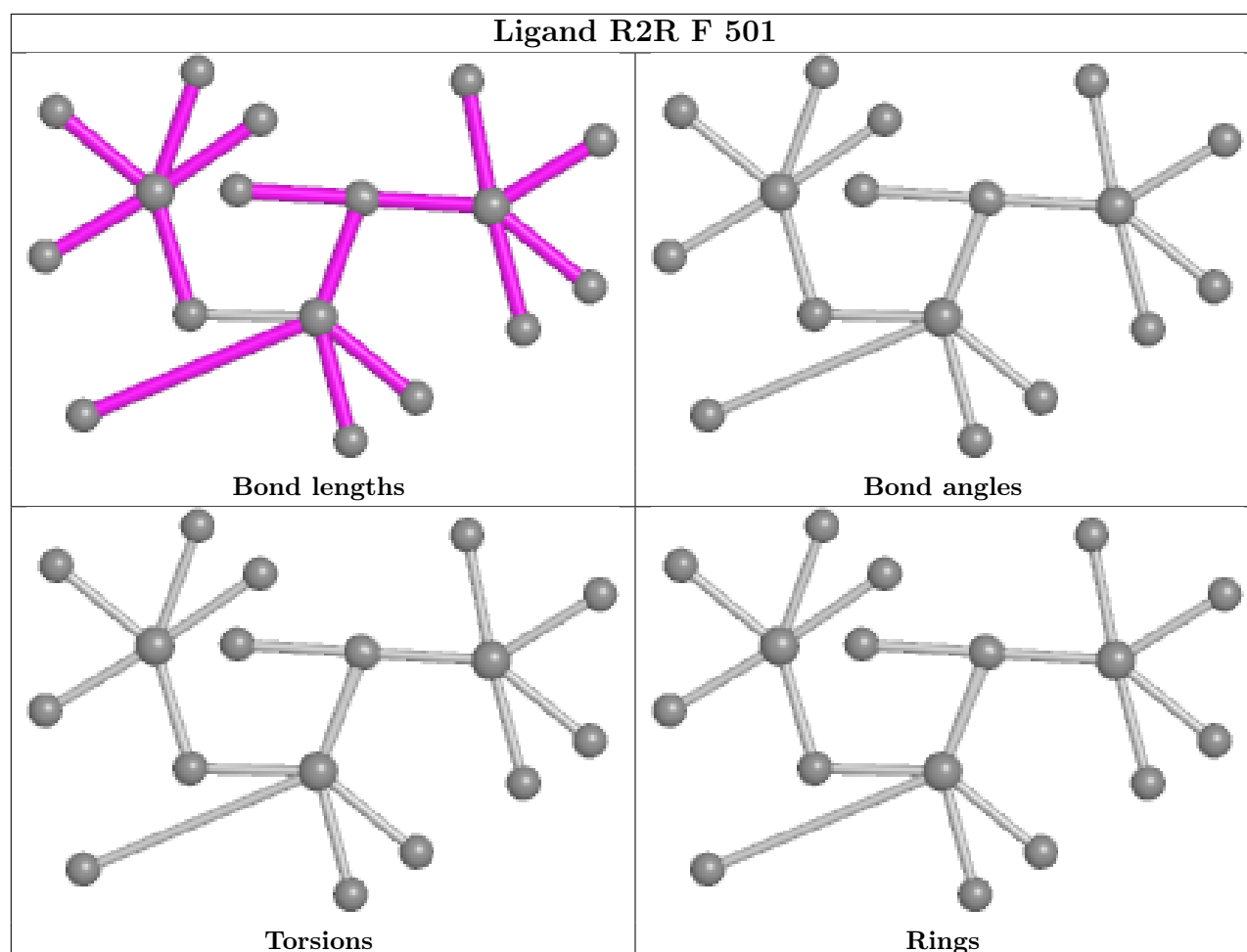


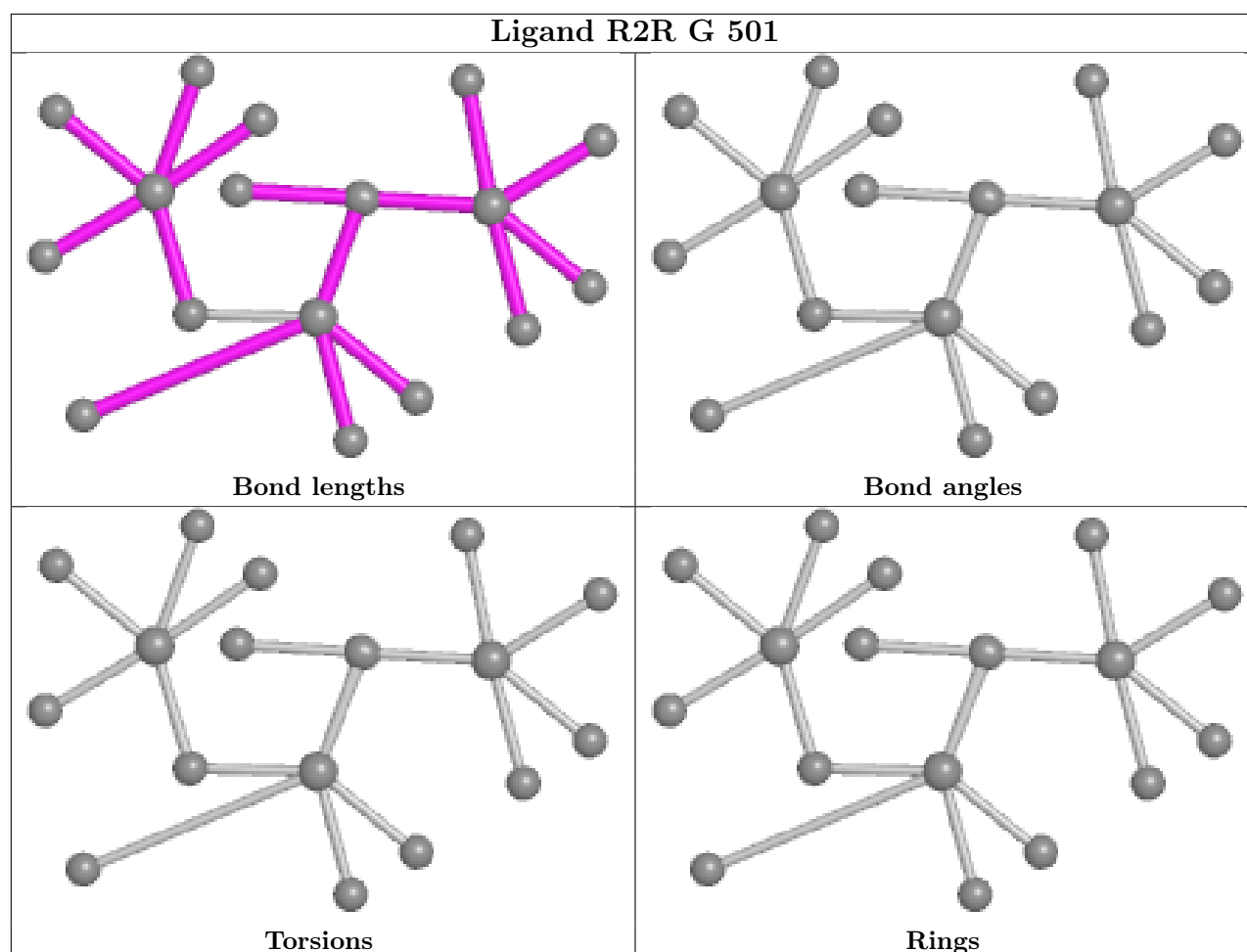


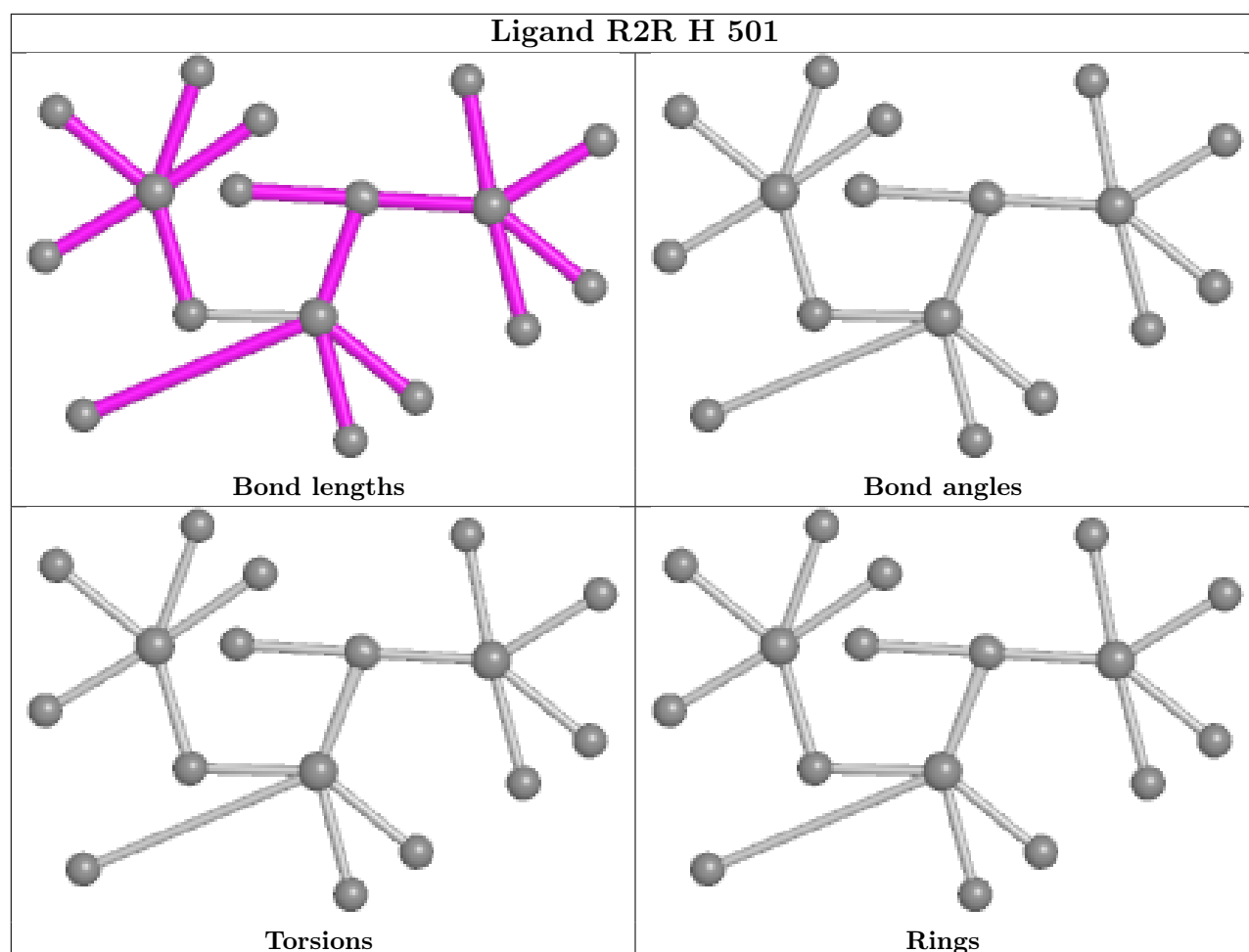


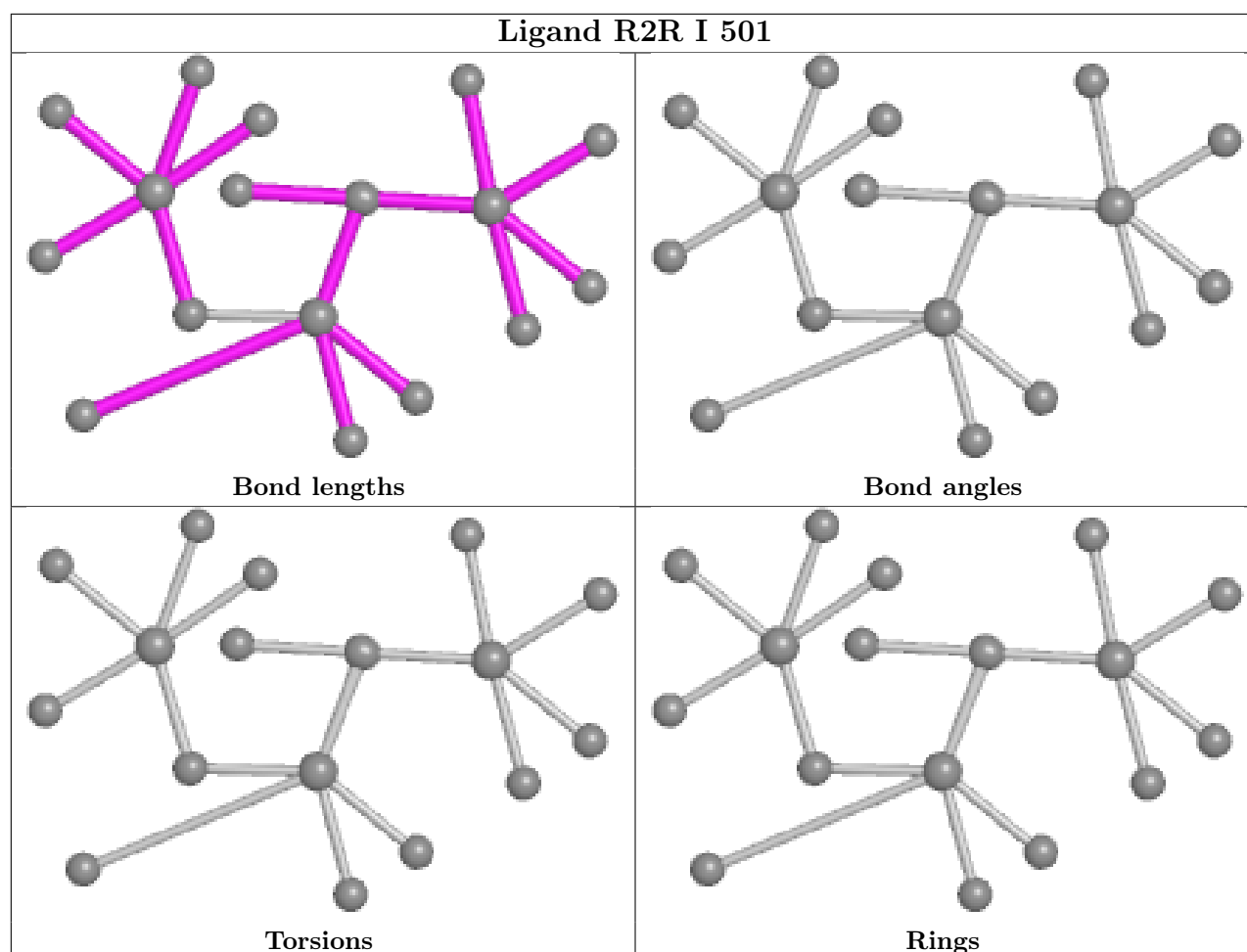


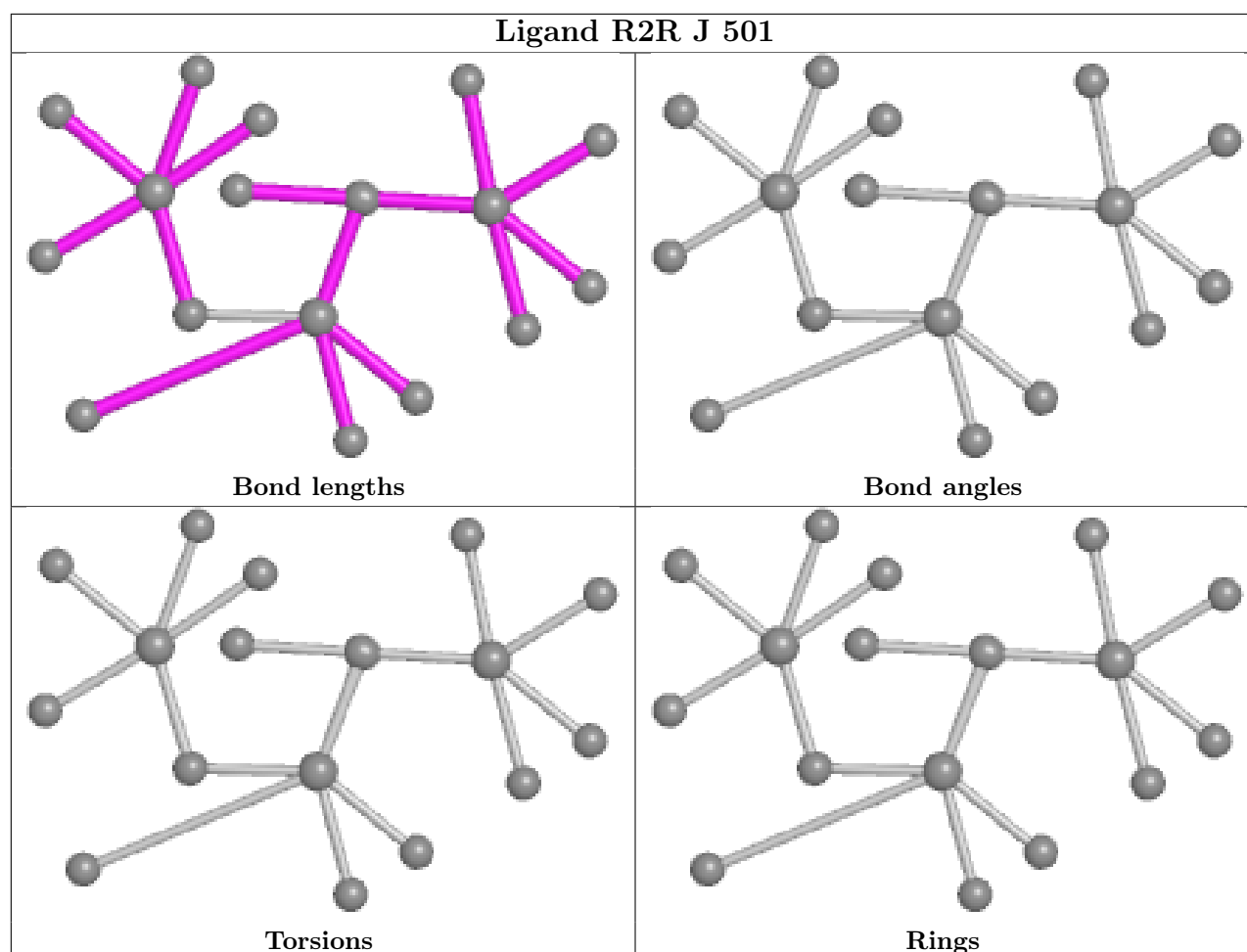


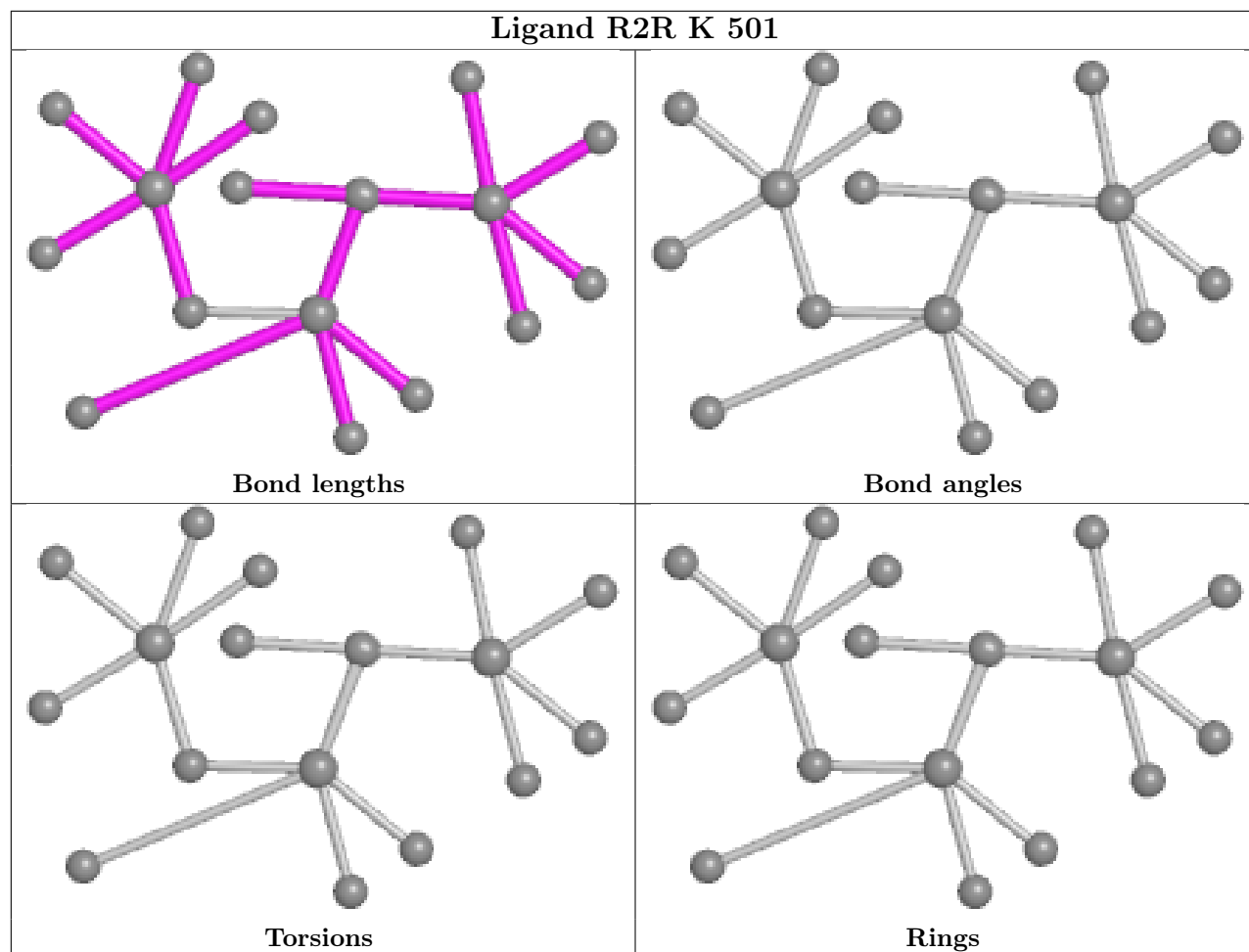












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.