



## Full wwPDB EM Validation Report ⓘ

Apr 9, 2023 – 12:24 AM JST

PDB ID : 7Y1A  
EMDB ID : EMD-33558  
Title : Lateral hexamer  
Authors : You, X.; Zhang, X.; Cheng, J.; Xiao, Y.N.; Sun, S.; Sui, S.F.  
Deposited on : 2022-06-07  
Resolution : 6.30 Å (reported)

This is a Full wwPDB EM 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/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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

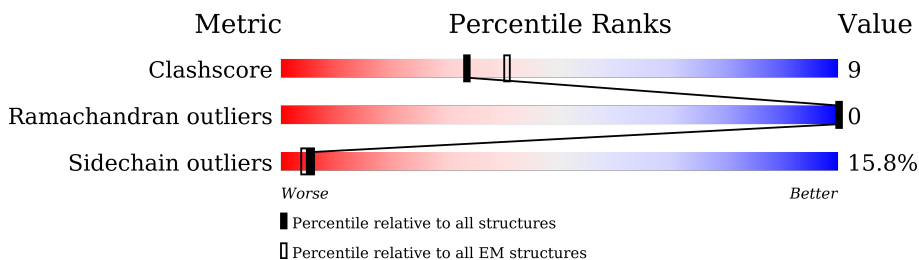
EMDB validation analysis : 0.0.1.dev50  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.32.2

# 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 6.30 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.



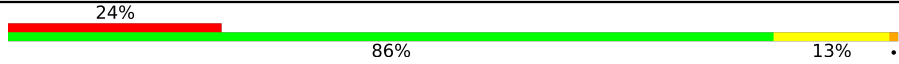
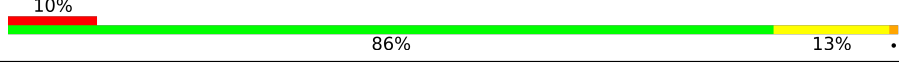


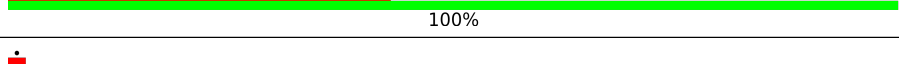
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	l	177	10% (red), 70% (green), 25% (yellow), 5% (orange) •
1	q	177	22% (red), 84% (green), 15% (yellow) •
1	s	177	12% (red), 84% (green), 15% (yellow) •
1	u	177	17% (red), 84% (green), 15% (yellow) •
1	w	177	13% (red), 84% (green), 15% (yellow) •
1	y	177	15% (red), 85% (green), 14% (yellow) •
2	p	164	12% (red), 86% (green), 13% (yellow) •
2	r	164	14% (red), 86% (green), 13% (yellow) •

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Mol	Chain	Length	Quality of chain
2	t	164	
2	v	164	
2	x	164	
2	z	164	
3	a	87	
4	A	150	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 17788 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 B-phycoerythrin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	y	177	1294	800	225	257	12	0	0
1	l	177	1294	800	225	257	12	0	0
1	q	177	1294	800	225	257	12	0	0
1	s	177	1294	800	225	257	12	0	0
1	u	177	1294	800	225	257	12	0	0
1	w	177	1300	804	225	259	12	2	0

- Molecule 2 is a protein called Phycoerythrin alpha subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	z	164	1250	779	219	245	7	0	0
2	p	164	1250	779	219	245	7	0	0
2	r	164	1250	779	219	245	7	0	0
2	t	164	1250	779	219	245	7	0	0
2	v	164	1250	779	219	245	7	0	0
2	x	164	1250	779	219	245	7	0	0

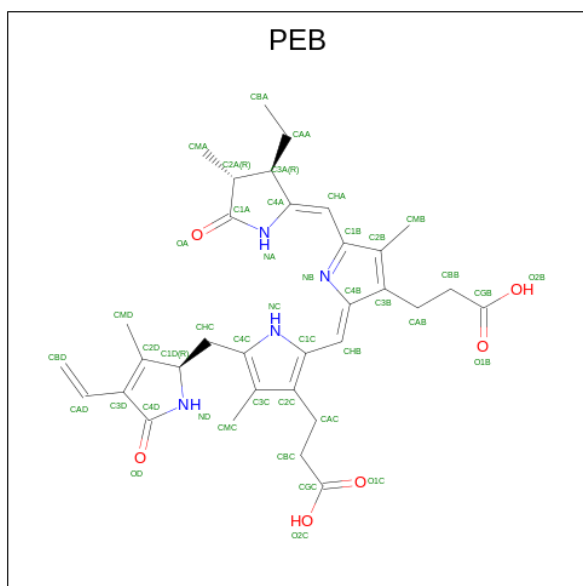
- Molecule 3 is a protein called LRH.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	a	87	435	261	87	87	0	0

- Molecule 4 is a protein called LRH.

Mol	Chain	Residues	Atoms			AltConf	Trace	
			Total	C	N			O
4	A	150	750	450	150	150	0	0

- Molecule 5 is PHYCOERYTHROBILIN (three-letter code: PEB) (formula: C<sub>33</sub>H<sub>40</sub>N<sub>4</sub>O<sub>6</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf	
			Total	C	N		O
5	y	1	43	33	4	6	0
5	y	1	43	33	4	6	0
5	y	1	43	33	4	6	0
5	z	1	43	33	4	6	0
5	z	1	43	33	4	6	0
5	1	1	43	33	4	6	0
5	1	1	43	33	4	6	0
5	1	1	43	33	4	6	0
5	1	1	43	33	4	6	0
5	p	1	43	33	4	6	0

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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
5	p	1	Total 43	C 33	N 4	O 6	0
5	q	1	Total 43	C 33	N 4	O 6	0
5	q	1	Total 43	C 33	N 4	O 6	0
5	q	1	Total 43	C 33	N 4	O 6	0
5	r	1	Total 43	C 33	N 4	O 6	0
5	r	1	Total 43	C 33	N 4	O 6	0
5	s	1	Total 43	C 33	N 4	O 6	0
5	s	1	Total 43	C 33	N 4	O 6	0
5	s	1	Total 43	C 33	N 4	O 6	0
5	t	1	Total 43	C 33	N 4	O 6	0
5	t	1	Total 43	C 33	N 4	O 6	0
5	u	1	Total 43	C 33	N 4	O 6	0
5	u	1	Total 43	C 33	N 4	O 6	0
5	u	1	Total 43	C 33	N 4	O 6	0
5	v	1	Total 43	C 33	N 4	O 6	0
5	v	1	Total 43	C 33	N 4	O 6	0
5	w	1	Total 43	C 33	N 4	O 6	0
5	w	1	Total 43	C 33	N 4	O 6	0
5	w	1	Total 43	C 33	N 4	O 6	0
5	w	1	Total 43	C 33	N 4	O 6	0
5	x	1	Total 43	C 33	N 4	O 6	0

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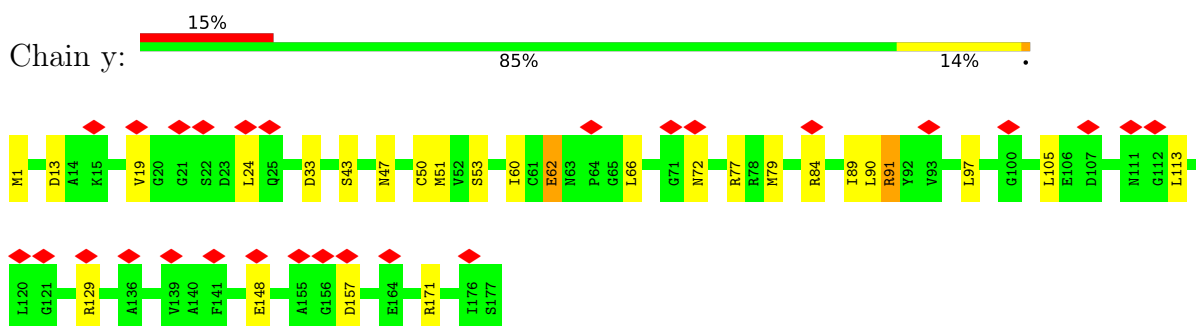
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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
5	x	1	43	33	4	6	0

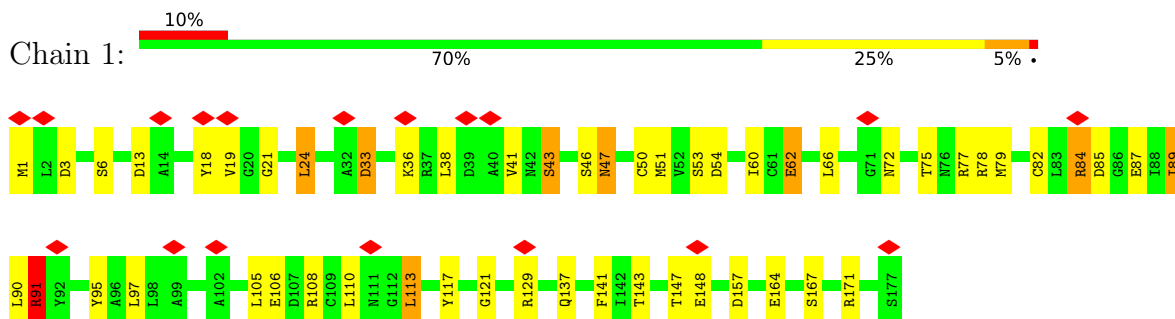
### 3 Residue-property plots [i](#)

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 and atom inclusion in map density. 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. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

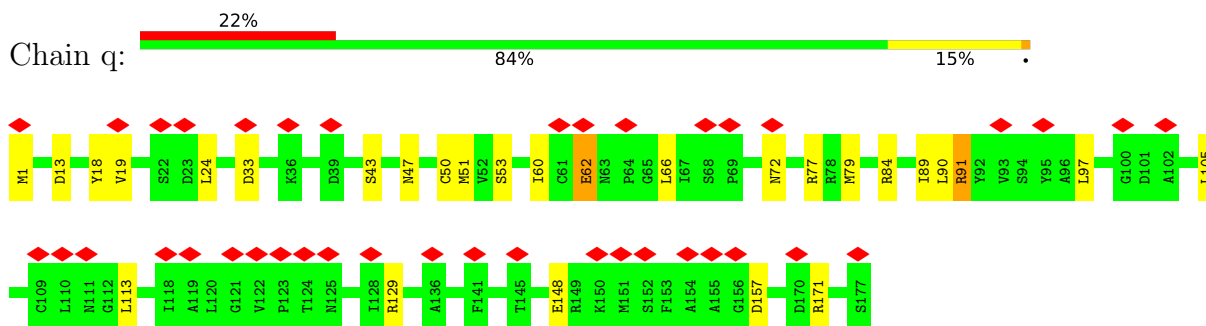
- Molecule 1: B-phycoerythrin beta chain



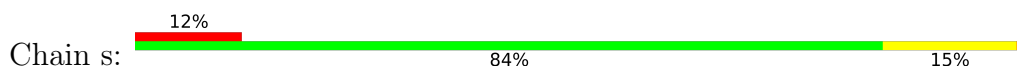
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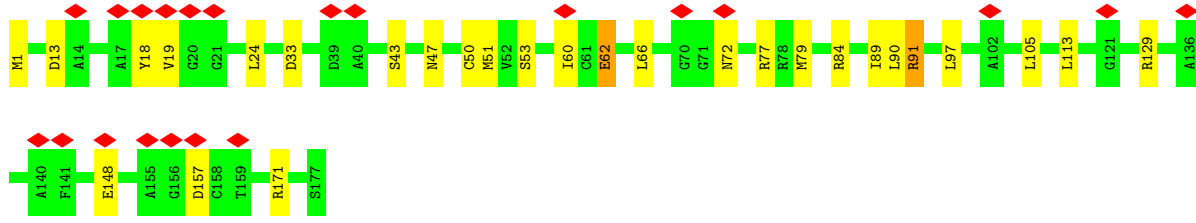
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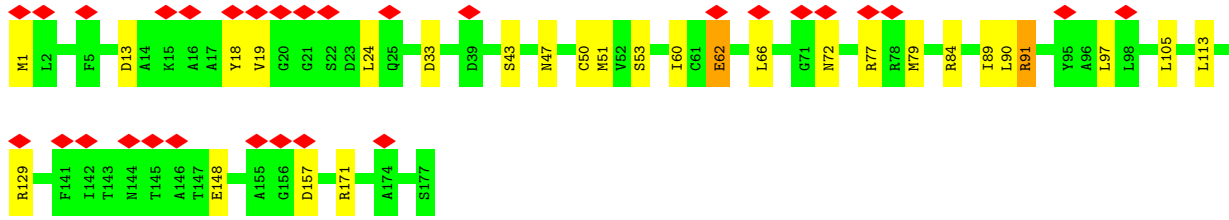
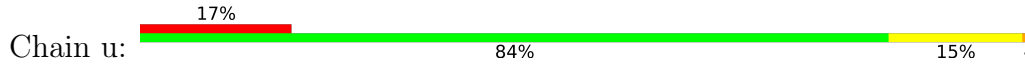
- Molecule 1: B-phycoerythrin beta chain



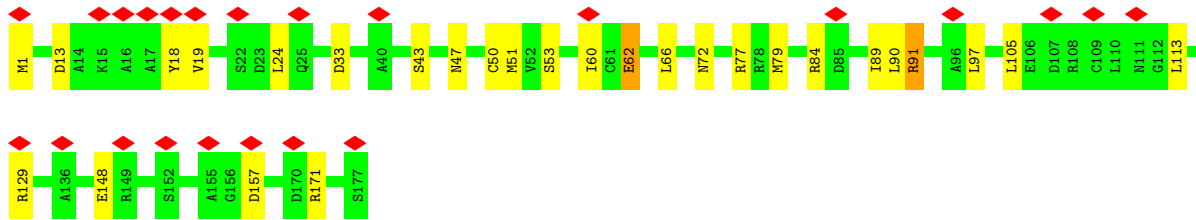
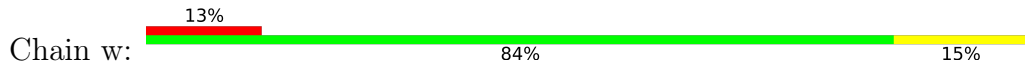




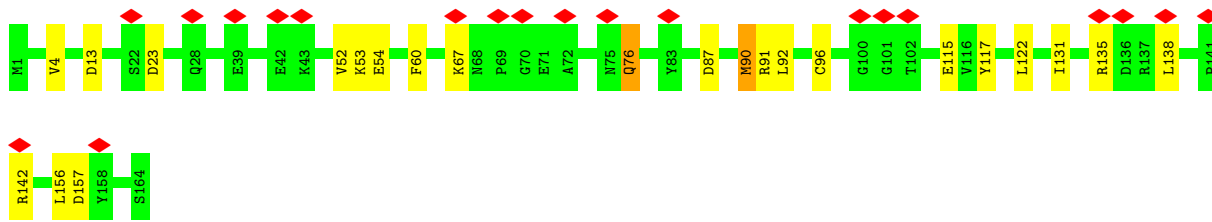
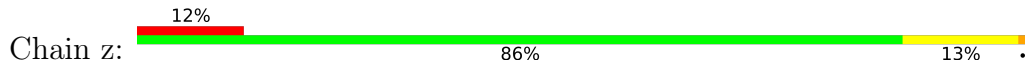
• Molecule 1: B-phycoerythrin beta chain



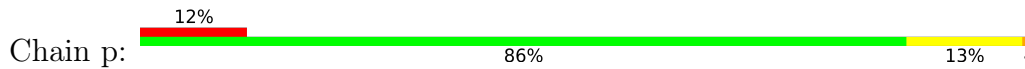
• Molecule 1: B-phycoerythrin beta chain

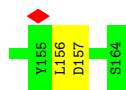


• Molecule 2: Phycoerythrin alpha subunit

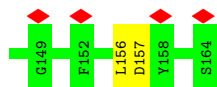
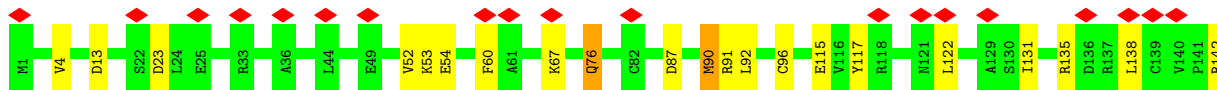
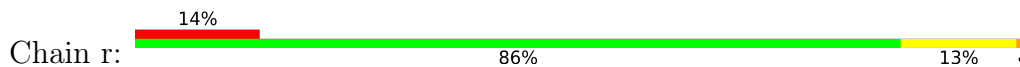


• Molecule 2: Phycoerythrin alpha subunit

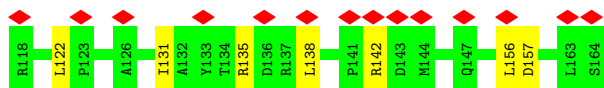
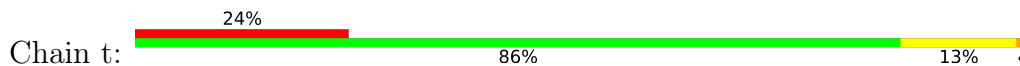




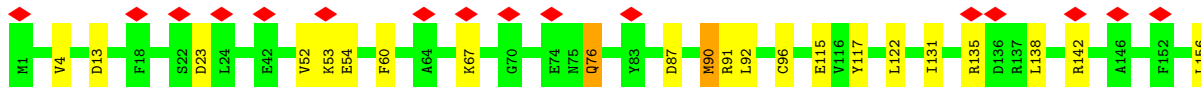
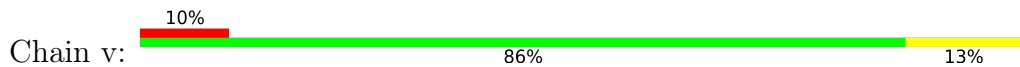
• Molecule 2: Phycoerythrin alpha subunit



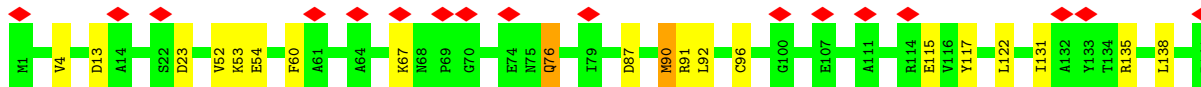
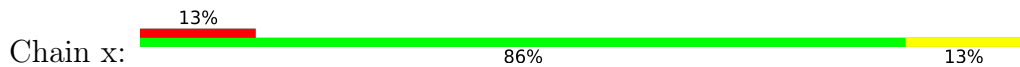
• Molecule 2: Phycoerythrin alpha subunit



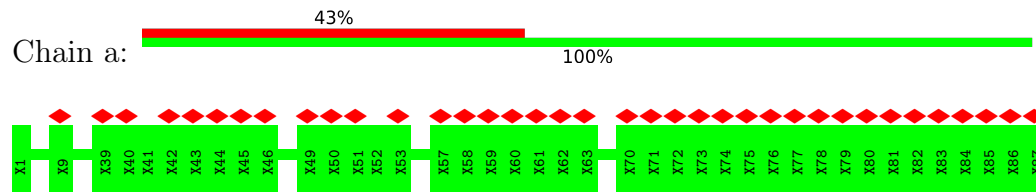
• Molecule 2: Phycoerythrin alpha subunit



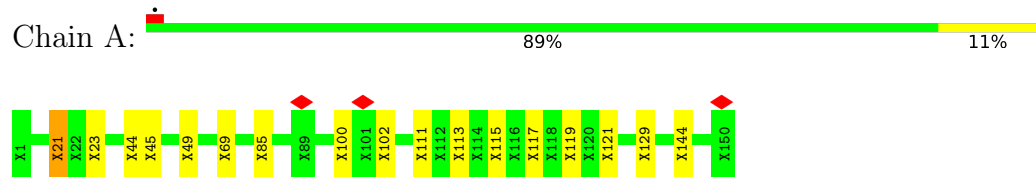
• Molecule 2: Phycoerythrin alpha subunit



• Molecule 3: LRH



● Molecule 4: LRH



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	87000	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 ( $e^-/\text{\AA}^2$ )	35	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	6000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.960	Depositor
Minimum map value	-2.101	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.051	Depositor
Recommended contour level	0.152	Depositor
Map size (Å)	417.792, 417.792, 417.792	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.632, 1.632, 1.632	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: PEB, MEN

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	l	0.43	0/1297	0.85	4/1750 (0.2%)
1	q	0.43	0/1297	0.85	4/1750 (0.2%)
1	s	0.43	0/1297	0.85	4/1750 (0.2%)
1	u	0.43	0/1297	0.85	4/1750 (0.2%)
1	w	0.42	0/1309	0.85	4/1766 (0.2%)
1	y	0.43	0/1297	0.86	4/1750 (0.2%)
2	p	0.48	0/1271	0.97	9/1721 (0.5%)
2	r	0.48	0/1271	0.97	9/1721 (0.5%)
2	t	0.48	0/1271	0.97	9/1721 (0.5%)
2	v	0.48	0/1271	0.97	9/1721 (0.5%)
2	x	0.48	0/1271	0.97	9/1721 (0.5%)
2	z	0.48	0/1271	0.97	9/1721 (0.5%)
All	All	0.45	0/15420	0.91	78/20842 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	p	0	1
2	r	0	1
2	t	0	1
2	v	0	1
2	x	0	1
2	z	0	1
4	A	0	8
All	All	0	14

There are no bond length outliers.

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	x	157	ASP	CB-CG-OD1	10.56	127.81	118.30
2	r	157	ASP	CB-CG-OD1	10.56	127.81	118.30
2	p	157	ASP	CB-CG-OD1	10.55	127.80	118.30
2	z	157	ASP	CB-CG-OD1	10.54	127.79	118.30
2	v	157	ASP	CB-CG-OD1	10.53	127.77	118.30
2	t	157	ASP	CB-CG-OD1	10.49	127.75	118.30
2	z	142	ARG	NE-CZ-NH1	-8.34	116.13	120.30
2	v	142	ARG	NE-CZ-NH1	-8.33	116.14	120.30
2	x	142	ARG	NE-CZ-NH1	-8.32	116.14	120.30
2	t	142	ARG	NE-CZ-NH1	-8.31	116.14	120.30
2	r	142	ARG	NE-CZ-NH1	-8.31	116.15	120.30
2	p	142	ARG	NE-CZ-NH1	-8.24	116.18	120.30
1	l	62	GLU	CA-CB-CG	7.92	130.82	113.40
1	s	62	GLU	CA-CB-CG	7.91	130.79	113.40
1	w	62	GLU	CA-CB-CG	7.91	130.79	113.40
1	y	62	GLU	CA-CB-CG	7.90	130.78	113.40
1	q	62	GLU	CA-CB-CG	7.90	130.78	113.40
1	u	62	GLU	CA-CB-CG	7.90	130.77	113.40
2	x	92	LEU	CA-CB-CG	7.78	133.19	115.30
2	z	92	LEU	CA-CB-CG	7.77	133.18	115.30
2	v	92	LEU	CA-CB-CG	7.77	133.18	115.30
2	p	92	LEU	CA-CB-CG	7.77	133.17	115.30
2	t	92	LEU	CA-CB-CG	7.76	133.15	115.30
2	r	92	LEU	CA-CB-CG	7.76	133.14	115.30
2	z	76	GLN	CA-CB-CG	6.98	128.76	113.40
2	v	76	GLN	CA-CB-CG	6.97	128.74	113.40
2	t	76	GLN	CA-CB-CG	6.97	128.73	113.40
2	r	76	GLN	CA-CB-CG	6.96	128.72	113.40
2	p	76	GLN	CA-CB-CG	6.96	128.72	113.40
2	x	76	GLN	CA-CB-CG	6.96	128.70	113.40
1	u	91	ARG	CG-CD-NE	6.41	125.26	111.80
1	y	91	ARG	CG-CD-NE	6.41	125.25	111.80
1	w	91	ARG	CG-CD-NE	6.41	125.25	111.80
1	q	91	ARG	CG-CD-NE	6.41	125.25	111.80
1	l	91	ARG	CG-CD-NE	6.40	125.25	111.80
1	s	91	ARG	CG-CD-NE	6.39	125.22	111.80
2	p	142	ARG	CA-CB-CG	6.34	127.35	113.40
2	v	142	ARG	CA-CB-CG	6.34	127.35	113.40
2	z	142	ARG	CA-CB-CG	6.34	127.34	113.40
2	t	142	ARG	CA-CB-CG	6.33	127.33	113.40
2	r	142	ARG	CA-CB-CG	6.33	127.31	113.40
2	x	142	ARG	CA-CB-CG	6.31	127.29	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	z	90	MET	CA-CB-CG	6.26	123.94	113.30
2	p	90	MET	CA-CB-CG	6.26	123.94	113.30
2	v	90	MET	CA-CB-CG	6.26	123.94	113.30
2	x	90	MET	CA-CB-CG	6.25	123.93	113.30
2	t	90	MET	CA-CB-CG	6.24	123.91	113.30
2	r	90	MET	CA-CB-CG	6.24	123.91	113.30
1	l	66	LEU	CA-CB-CG	6.14	129.43	115.30
1	w	66	LEU	CA-CB-CG	6.14	129.42	115.30
1	u	66	LEU	CA-CB-CG	6.14	129.42	115.30
1	s	66	LEU	CA-CB-CG	6.13	129.41	115.30
1	q	66	LEU	CA-CB-CG	6.13	129.41	115.30
1	y	66	LEU	CA-CB-CG	6.12	129.37	115.30
2	r	142	ARG	NE-CZ-NH2	5.69	123.14	120.30
2	p	142	ARG	NE-CZ-NH2	5.65	123.13	120.30
2	v	142	ARG	NE-CZ-NH2	5.65	123.12	120.30
2	r	156	LEU	CA-CB-CG	5.64	128.28	115.30
2	p	156	LEU	CA-CB-CG	5.64	128.28	115.30
2	t	156	LEU	CA-CB-CG	5.64	128.28	115.30
2	x	156	LEU	CA-CB-CG	5.64	128.27	115.30
2	x	142	ARG	NE-CZ-NH2	5.63	123.12	120.30
2	v	156	LEU	CA-CB-CG	5.63	128.25	115.30
2	z	156	LEU	CA-CB-CG	5.62	128.23	115.30
2	z	142	ARG	NE-CZ-NH2	5.62	123.11	120.30
2	t	142	ARG	NE-CZ-NH2	5.61	123.11	120.30
1	s	84	ARG	CG-CD-NE	-5.44	100.38	111.80
1	q	84	ARG	CG-CD-NE	-5.43	100.39	111.80
1	u	84	ARG	CG-CD-NE	-5.42	100.42	111.80
1	l	84	ARG	CG-CD-NE	-5.40	100.45	111.80
1	w	84	ARG	CG-CD-NE	-5.40	100.46	111.80
1	y	84	ARG	CG-CD-NE	-5.38	100.50	111.80
2	p	131	ILE	CG1-CB-CG2	-5.21	99.94	111.40
2	r	131	ILE	CG1-CB-CG2	-5.20	99.95	111.40
2	t	131	ILE	CG1-CB-CG2	-5.20	99.95	111.40
2	z	131	ILE	CG1-CB-CG2	-5.20	99.96	111.40
2	x	131	ILE	CG1-CB-CG2	-5.20	99.96	111.40
2	v	131	ILE	CG1-CB-CG2	-5.20	99.97	111.40

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	100	UNK	Peptide

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Mol	Chain	Res	Type	Group
4	A	111	UNK	Peptide
4	A	129	UNK	Peptide
4	A	144	UNK	Peptide
4	A	21	UNK	Peptide
4	A	44	UNK	Peptide
4	A	69	UNK	Peptide
4	A	85	UNK	Peptide
2	p	23	ASP	Peptide
2	r	23	ASP	Peptide
2	t	23	ASP	Peptide
2	v	23	ASP	Peptide
2	x	23	ASP	Peptide
2	z	23	ASP	Peptide

## 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	1	1294	0	1293	21	0
1	q	1294	0	1293	0	0
1	s	1294	0	1293	0	0
1	u	1294	0	1293	0	0
1	w	1300	0	1303	0	0
1	y	1294	0	1293	0	0
2	p	1250	0	1220	0	0
2	r	1250	0	1220	0	0
2	t	1250	0	1220	0	0
2	v	1250	0	1220	0	0
2	x	1250	0	1220	0	0
2	z	1250	0	1220	0	0
3	a	435	0	104	0	0
4	A	750	0	174	6	0
5	1	129	0	105	3	0
5	p	86	0	70	0	0
5	q	129	0	105	0	0
5	r	86	0	70	0	0
5	s	129	0	105	0	0
5	t	86	0	70	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	u	129	0	105	0	0
5	v	86	0	70	0	0
5	w	172	0	142	0	0
5	x	86	0	70	0	0
5	y	129	0	105	0	0
5	z	86	0	70	0	0
All	All	17788	0	16453	26	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 9.

All (26) 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)
1:1:108:ARG:HH12	4:A:23:UNK:HA	1.63	0.63
4:A:21:UNK:HA	4:A:102:UNK:HA	1.81	0.61
1:1:91:ARG:NH1	1:1:95:TYR:OH	2.36	0.58
1:1:47:ASN:OD1	1:1:47:ASN:N	2.35	0.58
1:1:54:ASP:OD2	1:1:137:GLN:NE2	2.39	0.55
1:1:82:CYS:HA	1:1:85:ASP:HB2	1.89	0.53
1:1:33:ASP:HB3	1:1:36:LYS:HD3	1.91	0.52
1:1:75:THR:HB	1:1:78:ARG:HG3	1.92	0.52
1:1:110:LEU:HG	1:1:113:LEU:HD13	1.91	0.51
1:1:106:GLU:HA	1:1:110:LEU:HB2	1.94	0.50
4:A:115:UNK:O	4:A:119:UNK:N	2.44	0.50
1:1:110:LEU:HA	1:1:113:LEU:HB2	1.93	0.49
1:1:141:PHE:HE1	5:1:203:PEB:HMB2	1.78	0.49
1:1:21:GLY:HA2	1:1:24:LEU:HB2	1.96	0.48
4:A:117:UNK:O	4:A:121:UNK:N	2.47	0.47
1:1:43:SER:O	1:1:46:SER:OG	2.33	0.46
1:1:147:THR:HG23	5:1:203:PEB:HMB3	1.98	0.46
1:1:143:THR:HA	5:1:202:PEB:HMA1	1.98	0.45
4:A:113:UNK:O	4:A:117:UNK:N	2.49	0.45
1:1:3:ASP:H	1:1:6:SER:HG	1.62	0.44
1:1:164:GLU:O	1:1:167:SER:OG	2.32	0.44
1:1:117:TYR:O	1:1:121:GLY:N	2.53	0.42
4:A:45:UNK:O	4:A:49:UNK:N	2.52	0.42
1:1:89:ILE:H	1:1:89:ILE:HG13	1.56	0.41
1:1:38:LEU:HA	1:1:41:VAL:HG22	2.03	0.40
1:1:84:ARG:HA	1:1:87:GLU:HG3	2.02	0.40

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	l	174/177 (98%)	163 (94%)	11 (6%)	0	100	100
1	q	174/177 (98%)	163 (94%)	11 (6%)	0	100	100
1	s	174/177 (98%)	163 (94%)	11 (6%)	0	100	100
1	u	174/177 (98%)	163 (94%)	11 (6%)	0	100	100
1	w	176/177 (99%)	165 (94%)	11 (6%)	0	100	100
1	y	174/177 (98%)	163 (94%)	11 (6%)	0	100	100
2	p	162/164 (99%)	143 (88%)	19 (12%)	0	100	100
2	r	162/164 (99%)	143 (88%)	19 (12%)	0	100	100
2	t	162/164 (99%)	143 (88%)	19 (12%)	0	100	100
2	v	162/164 (99%)	143 (88%)	19 (12%)	0	100	100
2	x	162/164 (99%)	143 (88%)	19 (12%)	0	100	100
2	z	162/164 (99%)	143 (88%)	19 (12%)	0	100	100
All	All	2018/2046 (99%)	1838 (91%)	180 (9%)	0	100	100

There are no Ramachandran outliers to report.

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

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	l	137/137 (100%)	112 (82%)	25 (18%)	1	10
1	q	137/137 (100%)	112 (82%)	25 (18%)	1	10
1	s	137/137 (100%)	112 (82%)	25 (18%)	1	10
1	u	137/137 (100%)	112 (82%)	25 (18%)	1	10
1	w	139/137 (102%)	114 (82%)	25 (18%)	1	10
1	y	137/137 (100%)	113 (82%)	24 (18%)	2	11
2	p	128/128 (100%)	111 (87%)	17 (13%)	4	18
2	r	128/128 (100%)	111 (87%)	17 (13%)	4	18
2	t	128/128 (100%)	111 (87%)	17 (13%)	4	18
2	v	128/128 (100%)	111 (87%)	17 (13%)	4	18
2	x	128/128 (100%)	111 (87%)	17 (13%)	4	18
2	z	128/128 (100%)	111 (87%)	17 (13%)	4	18
All	All	1592/1590 (100%)	1341 (84%)	251 (16%)	5	14

All (251) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	y	1	MET
1	y	13	ASP
1	y	19	VAL
1	y	24	LEU
1	y	33	ASP
1	y	43	SER
1	y	47	ASN
1	y	50	CYS
1	y	51	MET
1	y	53	SER
1	y	60	ILE
1	y	62	GLU
1	y	77	ARG
1	y	79	MET
1	y	89	ILE
1	y	90	LEU
1	y	91	ARG
1	y	97	LEU
1	y	105	LEU
1	y	113	LEU
1	y	129	ARG
1	y	148	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	y	157	ASP
1	y	171	ARG
2	z	4	VAL
2	z	13	ASP
2	z	52	VAL
2	z	53	LYS
2	z	54	GLU
2	z	60	PHE
2	z	67	LYS
2	z	76	GLN
2	z	87	ASP
2	z	90	MET
2	z	91	ARG
2	z	96	CYS
2	z	115	GLU
2	z	117	TYR
2	z	122	LEU
2	z	135	ARG
2	z	138	LEU
1	1	1	MET
1	1	13	ASP
1	1	18	TYR
1	1	19	VAL
1	1	24	LEU
1	1	33	ASP
1	1	43	SER
1	1	47	ASN
1	1	50	CYS
1	1	51	MET
1	1	53	SER
1	1	60	ILE
1	1	62	GLU
1	1	77	ARG
1	1	79	MET
1	1	89	ILE
1	1	90	LEU
1	1	91	ARG
1	1	97	LEU
1	1	105	LEU
1	1	113	LEU
1	1	129	ARG
1	1	148	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	1	157	ASP
1	1	171	ARG
2	p	4	VAL
2	p	13	ASP
2	p	52	VAL
2	p	53	LYS
2	p	54	GLU
2	p	60	PHE
2	p	67	LYS
2	p	76	GLN
2	p	87	ASP
2	p	90	MET
2	p	91	ARG
2	p	96	CYS
2	p	115	GLU
2	p	117	TYR
2	p	122	LEU
2	p	135	ARG
2	p	138	LEU
1	q	1	MET
1	q	13	ASP
1	q	18	TYR
1	q	19	VAL
1	q	24	LEU
1	q	33	ASP
1	q	43	SER
1	q	47	ASN
1	q	50	CYS
1	q	51	MET
1	q	53	SER
1	q	60	ILE
1	q	62	GLU
1	q	77	ARG
1	q	79	MET
1	q	89	ILE
1	q	90	LEU
1	q	91	ARG
1	q	97	LEU
1	q	105	LEU
1	q	113	LEU
1	q	129	ARG
1	q	148	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	q	157	ASP
1	q	171	ARG
2	r	4	VAL
2	r	13	ASP
2	r	52	VAL
2	r	53	LYS
2	r	54	GLU
2	r	60	PHE
2	r	67	LYS
2	r	76	GLN
2	r	87	ASP
2	r	90	MET
2	r	91	ARG
2	r	96	CYS
2	r	115	GLU
2	r	117	TYR
2	r	122	LEU
2	r	135	ARG
2	r	138	LEU
1	s	1	MET
1	s	13	ASP
1	s	18	TYR
1	s	19	VAL
1	s	24	LEU
1	s	33	ASP
1	s	43	SER
1	s	47	ASN
1	s	50	CYS
1	s	51	MET
1	s	53	SER
1	s	60	ILE
1	s	62	GLU
1	s	77	ARG
1	s	79	MET
1	s	89	ILE
1	s	90	LEU
1	s	91	ARG
1	s	97	LEU
1	s	105	LEU
1	s	113	LEU
1	s	129	ARG
1	s	148	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	s	157	ASP
1	s	171	ARG
2	t	4	VAL
2	t	13	ASP
2	t	52	VAL
2	t	53	LYS
2	t	54	GLU
2	t	60	PHE
2	t	67	LYS
2	t	76	GLN
2	t	87	ASP
2	t	90	MET
2	t	91	ARG
2	t	96	CYS
2	t	115	GLU
2	t	117	TYR
2	t	122	LEU
2	t	135	ARG
2	t	138	LEU
1	u	1	MET
1	u	13	ASP
1	u	18	TYR
1	u	19	VAL
1	u	24	LEU
1	u	33	ASP
1	u	43	SER
1	u	47	ASN
1	u	50	CYS
1	u	51	MET
1	u	53	SER
1	u	60	ILE
1	u	62	GLU
1	u	77	ARG
1	u	79	MET
1	u	89	ILE
1	u	90	LEU
1	u	91	ARG
1	u	97	LEU
1	u	105	LEU
1	u	113	LEU
1	u	129	ARG
1	u	148	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	u	157	ASP
1	u	171	ARG
2	v	4	VAL
2	v	13	ASP
2	v	52	VAL
2	v	53	LYS
2	v	54	GLU
2	v	60	PHE
2	v	67	LYS
2	v	76	GLN
2	v	87	ASP
2	v	90	MET
2	v	91	ARG
2	v	96	CYS
2	v	115	GLU
2	v	117	TYR
2	v	122	LEU
2	v	135	ARG
2	v	138	LEU
1	w	1	MET
1	w	13	ASP
1	w	18	TYR
1	w	19	VAL
1	w	24	LEU
1	w	33	ASP
1	w	43	SER
1	w	47	ASN
1	w	50	CYS
1	w	51	MET
1	w	53	SER
1	w	60	ILE
1	w	62	GLU
1	w	77	ARG
1	w	79	MET
1	w	89	ILE
1	w	90	LEU
1	w	91	ARG
1	w	97	LEU
1	w	105	LEU
1	w	113	LEU
1	w	129	ARG
1	w	148	GLU

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Mol	Chain	Res	Type
1	w	157	ASP
1	w	171	ARG
2	x	4	VAL
2	x	13	ASP
2	x	52	VAL
2	x	53	LYS
2	x	54	GLU
2	x	60	PHE
2	x	67	LYS
2	x	76	GLN
2	x	87	ASP
2	x	90	MET
2	x	91	ARG
2	x	96	CYS
2	x	115	GLU
2	x	117	TYR
2	x	122	LEU
2	x	135	ARG
2	x	138	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	p	161	ASN
2	r	161	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

6 non-standard protein/DNA/RNA residues 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
1	MEN	s	72	1	7,8,9	0.93	0	6,9,11	1.60	2 (33%)
1	MEN	y	72	1	7,8,9	0.92	0	6,9,11	1.60	2 (33%)
1	MEN	q	72	1	7,8,9	0.93	0	6,9,11	1.60	2 (33%)
1	MEN	1	72	1	7,8,9	0.92	0	6,9,11	1.59	2 (33%)
1	MEN	w	72	1	7,8,9	0.92	0	6,9,11	1.59	2 (33%)
1	MEN	u	72	1	7,8,9	0.91	0	6,9,11	1.59	2 (33%)

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
1	MEN	s	72	1	-	2/7/8/10	-
1	MEN	y	72	1	-	2/7/8/10	-
1	MEN	q	72	1	-	2/7/8/10	-
1	MEN	1	72	1	-	2/7/8/10	-
1	MEN	w	72	1	-	2/7/8/10	-
1	MEN	u	72	1	-	2/7/8/10	-

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	s	72	MEN	CB-CA-C	-3.24	105.40	111.47
1	y	72	MEN	CB-CA-C	-3.22	105.42	111.47
1	q	72	MEN	CB-CA-C	-3.22	105.43	111.47
1	u	72	MEN	CB-CA-C	-3.21	105.46	111.47
1	1	72	MEN	CB-CA-C	-3.20	105.47	111.47
1	w	72	MEN	CB-CA-C	-3.20	105.47	111.47
1	y	72	MEN	CA-CB-CG	-2.19	106.47	112.70
1	s	72	MEN	CA-CB-CG	-2.19	106.48	112.70
1	1	72	MEN	CA-CB-CG	-2.19	106.48	112.70
1	u	72	MEN	CA-CB-CG	-2.18	106.49	112.70
1	q	72	MEN	CA-CB-CG	-2.18	106.49	112.70
1	w	72	MEN	CA-CB-CG	-2.18	106.50	112.70

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	y	72	MEN	CA-CB-CG-OD1
1	l	72	MEN	CA-CB-CG-OD1
1	q	72	MEN	CA-CB-CG-OD1
1	s	72	MEN	CA-CB-CG-OD1
1	u	72	MEN	CA-CB-CG-OD1
1	w	72	MEN	CA-CB-CG-OD1
1	q	72	MEN	CA-CB-CG-ND2
1	s	72	MEN	CA-CB-CG-ND2
1	y	72	MEN	CA-CB-CG-ND2
1	l	72	MEN	CA-CB-CG-ND2
1	u	72	MEN	CA-CB-CG-ND2
1	w	72	MEN	CA-CB-CG-ND2

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

31 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	$\# Z  > 2$
5	PEB	1	203	-	43,46,46	3.29	9 (20%)	45,67,67	2.42	16 (35%)
5	PEB	q	203	-	43,46,46	3.29	9 (20%)	45,67,67	2.42	16 (35%)
5	PEB	y	201	-	43,46,46	3.42	11 (25%)	45,67,67	2.34	18 (40%)
5	PEB	y	202	-	43,46,46	3.30	8 (18%)	45,67,67	2.17	11 (24%)
5	PEB	t	201	-	43,46,46	3.36	10 (23%)	45,67,67	2.25	17 (37%)
5	PEB	z	201	-	43,46,46	3.35	10 (23%)	45,67,67	2.25	17 (37%)
5	PEB	v	202	-	43,46,46	3.58	9 (20%)	45,67,67	2.82	14 (31%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	PEB	p	202	-	43,46,46	3.58	10 (23%)	45,67,67	2.82	14 (31%)
5	PEB	z	202	-	43,46,46	3.58	10 (23%)	45,67,67	2.82	14 (31%)
5	PEB	u	203	-	43,46,46	3.28	9 (20%)	45,67,67	2.42	16 (35%)
5	PEB	s	202	-	43,46,46	3.31	8 (18%)	45,67,67	2.17	11 (24%)
5	PEB	l	202	-	43,46,46	3.29	9 (20%)	45,67,67	2.17	11 (24%)
5	PEB	u	202	-	43,46,46	3.30	8 (18%)	45,67,67	2.17	11 (24%)
5	PEB	q	201	-	43,46,46	3.43	11 (25%)	45,67,67	2.35	18 (40%)
5	PEB	r	202	-	43,46,46	3.59	10 (23%)	45,67,67	2.82	14 (31%)
5	PEB	x	202	-	43,46,46	3.59	11 (25%)	45,67,67	2.82	14 (31%)
5	PEB	v	201	-	43,46,46	3.34	10 (23%)	45,67,67	2.25	17 (37%)
5	PEB	w	203	-	43,46,46	3.27	9 (20%)	45,67,67	2.42	16 (35%)
5	PEB	w	202	-	43,46,46	3.30	8 (18%)	45,67,67	2.17	11 (24%)
5	PEB	y	203	-	43,46,46	3.29	9 (20%)	45,67,67	2.42	16 (35%)
5	PEB	l	201	-	43,46,46	3.42	11 (25%)	45,67,67	2.34	18 (40%)
5	PEB	p	201	-	43,46,46	3.36	10 (23%)	45,67,67	2.25	17 (37%)
5	PEB	w	204	-	43,46,46	3.36	10 (23%)	45,67,67	2.22	18 (40%)
5	PEB	u	201	-	43,46,46	3.43	11 (25%)	45,67,67	2.34	18 (40%)
5	PEB	s	201	-	43,46,46	3.43	11 (25%)	45,67,67	2.34	18 (40%)
5	PEB	r	201	-	43,46,46	3.35	10 (23%)	45,67,67	2.26	18 (40%)
5	PEB	x	201	-	43,46,46	3.34	10 (23%)	45,67,67	2.25	18 (40%)
5	PEB	q	202	-	43,46,46	3.29	9 (20%)	45,67,67	2.17	11 (24%)
5	PEB	w	201	-	43,46,46	3.42	11 (25%)	45,67,67	2.34	18 (40%)
5	PEB	t	202	-	43,46,46	3.59	10 (23%)	45,67,67	2.82	14 (31%)
5	PEB	s	203	-	43,46,46	3.29	9 (20%)	45,67,67	2.42	16 (35%)

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
5	PEB	l	203	-	-	7/24/74/74	0/4/4/4
5	PEB	q	203	-	-	7/24/74/74	0/4/4/4
5	PEB	y	201	-	-	9/24/74/74	0/4/4/4
5	PEB	y	202	-	-	3/24/74/74	0/4/4/4
5	PEB	t	201	-	-	9/24/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PEB	z	201	-	-	9/24/74/74	0/4/4/4
5	PEB	v	202	-	-	11/24/74/74	0/4/4/4
5	PEB	p	202	-	-	11/24/74/74	0/4/4/4
5	PEB	z	202	-	-	11/24/74/74	0/4/4/4
5	PEB	u	203	-	-	7/24/74/74	0/4/4/4
5	PEB	s	202	-	-	3/24/74/74	0/4/4/4
5	PEB	l	202	-	-	3/24/74/74	0/4/4/4
5	PEB	u	202	-	-	3/24/74/74	0/4/4/4
5	PEB	q	201	-	-	9/24/74/74	0/4/4/4
5	PEB	r	202	-	-	11/24/74/74	0/4/4/4
5	PEB	x	202	-	-	11/24/74/74	0/4/4/4
5	PEB	v	201	-	-	9/24/74/74	0/4/4/4
5	PEB	w	203	-	-	7/24/74/74	0/4/4/4
5	PEB	w	202	-	-	3/24/74/74	0/4/4/4
5	PEB	y	203	-	-	7/24/74/74	0/4/4/4
5	PEB	l	201	-	-	9/24/74/74	0/4/4/4
5	PEB	p	201	-	-	9/24/74/74	0/4/4/4
5	PEB	w	204	-	-	12/24/74/74	0/4/4/4
5	PEB	u	201	-	-	9/24/74/74	0/4/4/4
5	PEB	s	201	-	-	9/24/74/74	0/4/4/4
5	PEB	r	201	-	-	9/24/74/74	0/4/4/4
5	PEB	x	201	-	-	9/24/74/74	0/4/4/4
5	PEB	q	202	-	-	3/24/74/74	0/4/4/4
5	PEB	w	201	-	-	9/24/74/74	0/4/4/4
5	PEB	t	202	-	-	11/24/74/74	0/4/4/4
5	PEB	s	203	-	-	7/24/74/74	0/4/4/4

All (300) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	r	202	PEB	CHB-C4B	17.76	1.50	1.35
5	x	202	PEB	CHB-C4B	17.75	1.49	1.35
5	v	202	PEB	CHB-C4B	17.73	1.49	1.35
5	p	202	PEB	CHB-C4B	17.70	1.49	1.35
5	z	202	PEB	CHB-C4B	17.70	1.49	1.35
5	t	202	PEB	CHB-C4B	17.68	1.49	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	q	201	PEB	CHB-C4B	16.68	1.49	1.35
5	s	201	PEB	CHB-C4B	16.66	1.49	1.35
5	u	201	PEB	CHB-C4B	16.64	1.49	1.35
5	y	201	PEB	CHB-C4B	16.59	1.49	1.35
5	l	201	PEB	CHB-C4B	16.59	1.49	1.35
5	w	201	PEB	CHB-C4B	16.57	1.49	1.35
5	s	202	PEB	CHB-C4B	16.16	1.48	1.35
5	y	202	PEB	CHB-C4B	16.14	1.48	1.35
5	w	202	PEB	CHB-C4B	16.12	1.48	1.35
5	u	202	PEB	CHB-C4B	16.11	1.48	1.35
5	q	202	PEB	CHB-C4B	16.06	1.48	1.35
5	l	202	PEB	CHB-C4B	16.01	1.48	1.35
5	w	204	PEB	CHB-C4B	15.97	1.48	1.35
5	p	201	PEB	CHB-C4B	15.73	1.48	1.35
5	t	201	PEB	CHB-C4B	15.71	1.48	1.35
5	z	201	PEB	CHB-C4B	15.66	1.48	1.35
5	r	201	PEB	CHB-C4B	15.64	1.48	1.35
5	v	201	PEB	CHB-C4B	15.57	1.48	1.35
5	x	201	PEB	CHB-C4B	15.52	1.48	1.35
5	q	203	PEB	CHB-C4B	15.23	1.47	1.35
5	l	203	PEB	CHB-C4B	15.21	1.47	1.35
5	y	203	PEB	CHB-C4B	15.21	1.47	1.35
5	s	203	PEB	CHB-C4B	15.20	1.47	1.35
5	u	203	PEB	CHB-C4B	15.15	1.47	1.35
5	w	203	PEB	CHB-C4B	15.08	1.47	1.35
5	y	203	PEB	C2D-C3D	10.01	1.47	1.34
5	u	203	PEB	C2D-C3D	10.00	1.47	1.34
5	q	203	PEB	C2D-C3D	9.99	1.47	1.34
5	s	203	PEB	C2D-C3D	9.98	1.47	1.34
5	w	203	PEB	C2D-C3D	9.98	1.47	1.34
5	l	203	PEB	C2D-C3D	9.97	1.47	1.34
5	p	201	PEB	C2D-C3D	9.84	1.47	1.34
5	r	201	PEB	C2D-C3D	9.82	1.47	1.34
5	z	201	PEB	C2D-C3D	9.82	1.47	1.34
5	t	201	PEB	C2D-C3D	9.81	1.47	1.34
5	w	204	PEB	C2D-C3D	9.81	1.47	1.34
5	x	201	PEB	C2D-C3D	9.80	1.47	1.34
5	v	201	PEB	C2D-C3D	9.76	1.47	1.34
5	l	201	PEB	C2D-C3D	9.52	1.46	1.34
5	y	201	PEB	C2D-C3D	9.51	1.46	1.34
5	w	201	PEB	C2D-C3D	9.51	1.46	1.34
5	u	201	PEB	C2D-C3D	9.50	1.46	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	t	202	PEB	C2D-C3D	9.49	1.46	1.34
5	r	202	PEB	C2D-C3D	9.49	1.46	1.34
5	s	201	PEB	C2D-C3D	9.48	1.46	1.34
5	z	202	PEB	C2D-C3D	9.48	1.46	1.34
5	q	201	PEB	C2D-C3D	9.47	1.46	1.34
5	x	202	PEB	C2D-C3D	9.46	1.46	1.34
5	v	202	PEB	C2D-C3D	9.45	1.46	1.34
5	p	202	PEB	C2D-C3D	9.41	1.46	1.34
5	l	202	PEB	C2D-C3D	9.28	1.46	1.34
5	u	202	PEB	C2D-C3D	9.27	1.46	1.34
5	s	202	PEB	C2D-C3D	9.26	1.46	1.34
5	y	202	PEB	C2D-C3D	9.25	1.46	1.34
5	q	202	PEB	C2D-C3D	9.22	1.46	1.34
5	w	202	PEB	C2D-C3D	9.20	1.46	1.34
5	r	202	PEB	C3B-C2B	5.53	1.48	1.36
5	t	202	PEB	C3B-C2B	5.53	1.48	1.36
5	z	202	PEB	C3B-C2B	5.51	1.48	1.36
5	x	202	PEB	C3B-C2B	5.51	1.48	1.36
5	p	202	PEB	C3B-C2B	5.50	1.48	1.36
5	v	202	PEB	C3B-C2B	5.50	1.48	1.36
5	w	204	PEB	C3C-C4C	5.44	1.50	1.42
5	l	201	PEB	C3B-C2B	5.36	1.48	1.36
5	s	201	PEB	C3B-C2B	5.35	1.48	1.36
5	y	201	PEB	C3B-C2B	5.33	1.48	1.36
5	w	201	PEB	C3B-C2B	5.33	1.48	1.36
5	q	201	PEB	C3B-C2B	5.31	1.48	1.36
5	s	203	PEB	C3C-C4C	5.30	1.50	1.42
5	u	201	PEB	C3B-C2B	5.30	1.48	1.36
5	l	203	PEB	C3C-C4C	5.28	1.50	1.42
5	y	203	PEB	C3C-C4C	5.27	1.50	1.42
5	u	203	PEB	C3C-C4C	5.27	1.50	1.42
5	q	203	PEB	C3C-C4C	5.26	1.50	1.42
5	w	203	PEB	C3C-C4C	5.26	1.50	1.42
5	r	201	PEB	C3C-C4C	5.24	1.50	1.42
5	z	201	PEB	C3C-C4C	5.22	1.50	1.42
5	t	201	PEB	C3C-C4C	5.21	1.50	1.42
5	x	201	PEB	C3C-C4C	5.21	1.50	1.42
5	p	201	PEB	C3C-C4C	5.20	1.50	1.42
5	v	201	PEB	C3C-C4C	5.20	1.50	1.42
5	t	201	PEB	C3B-C2B	5.18	1.47	1.36
5	r	201	PEB	C3B-C2B	5.17	1.47	1.36
5	v	201	PEB	C3B-C2B	5.16	1.47	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	x	201	PEB	C3B-C2B	5.16	1.47	1.36
5	p	201	PEB	C3B-C2B	5.15	1.47	1.36
5	z	201	PEB	C3B-C2B	5.14	1.47	1.36
5	y	203	PEB	C3B-C2B	5.14	1.47	1.36
5	u	203	PEB	C3B-C2B	5.14	1.47	1.36
5	w	203	PEB	C3B-C2B	5.10	1.47	1.36
5	s	203	PEB	C3B-C2B	5.09	1.47	1.36
5	p	202	PEB	C3C-C4C	5.09	1.50	1.42
5	l	203	PEB	C3B-C2B	5.09	1.47	1.36
5	q	203	PEB	C3B-C2B	5.07	1.47	1.36
5	t	202	PEB	C3C-C4C	5.07	1.50	1.42
5	x	202	PEB	C3C-C4C	5.07	1.50	1.42
5	z	202	PEB	C3C-C4C	5.06	1.49	1.42
5	r	202	PEB	C3C-C4C	5.06	1.49	1.42
5	u	202	PEB	C3B-C2B	5.05	1.47	1.36
5	v	202	PEB	C3C-C4C	5.04	1.49	1.42
5	q	202	PEB	C3B-C2B	5.03	1.47	1.36
5	l	202	PEB	C3B-C2B	5.02	1.47	1.36
5	s	202	PEB	C3B-C2B	5.00	1.47	1.36
5	w	202	PEB	C3B-C2B	5.00	1.47	1.36
5	y	202	PEB	C3B-C2B	4.98	1.47	1.36
5	w	204	PEB	C3B-C2B	4.84	1.47	1.36
5	s	202	PEB	C3C-C4C	4.68	1.49	1.42
5	y	202	PEB	C3C-C4C	4.64	1.49	1.42
5	q	202	PEB	C3C-C4C	4.63	1.49	1.42
5	w	202	PEB	C3C-C4C	4.63	1.49	1.42
5	u	202	PEB	C3C-C4C	4.61	1.49	1.42
5	q	201	PEB	C3C-C4C	4.61	1.49	1.42
5	y	201	PEB	C3C-C4C	4.59	1.49	1.42
5	l	202	PEB	C3C-C4C	4.58	1.49	1.42
5	l	201	PEB	C3C-C4C	4.58	1.49	1.42
5	w	201	PEB	C3C-C4C	4.57	1.49	1.42
5	s	201	PEB	C3C-C4C	4.57	1.49	1.42
5	u	201	PEB	C3C-C4C	4.56	1.49	1.42
5	v	202	PEB	CHA-C1B	4.18	1.50	1.40
5	r	202	PEB	CHA-C1B	4.16	1.50	1.40
5	z	202	PEB	CHA-C1B	4.15	1.50	1.40
5	p	202	PEB	CHA-C1B	4.15	1.50	1.40
5	t	202	PEB	CHA-C1B	4.13	1.50	1.40
5	t	202	PEB	C2C-C3C	4.13	1.49	1.37
5	x	202	PEB	CHA-C1B	4.12	1.50	1.40
5	x	202	PEB	C2C-C3C	4.12	1.49	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	r	202	PEB	C2C-C3C	4.11	1.49	1.37
5	p	202	PEB	C2C-C3C	4.10	1.49	1.37
5	v	202	PEB	C2C-C3C	4.09	1.49	1.37
5	z	202	PEB	C2C-C3C	4.08	1.49	1.37
5	w	203	PEB	CHA-C1B	3.78	1.49	1.40
5	l	203	PEB	CHA-C1B	3.77	1.49	1.40
5	y	203	PEB	CHA-C1B	3.76	1.49	1.40
5	q	203	PEB	CHA-C1B	3.75	1.49	1.40
5	s	203	PEB	CHA-C1B	3.74	1.49	1.40
5	u	203	PEB	CHA-C1B	3.74	1.49	1.40
5	v	201	PEB	C2C-C3C	3.65	1.48	1.37
5	p	201	PEB	C2C-C3C	3.65	1.48	1.37
5	t	201	PEB	C2C-C3C	3.65	1.48	1.37
5	z	201	PEB	C2C-C3C	3.65	1.48	1.37
5	x	201	PEB	C2C-C3C	3.63	1.48	1.37
5	r	201	PEB	C2C-C3C	3.62	1.48	1.37
5	t	201	PEB	C2A-C1A	-3.62	1.48	1.52
5	w	204	PEB	CHA-C1B	3.60	1.48	1.40
5	w	201	PEB	C1A-NA	-3.56	1.33	1.37
5	s	201	PEB	C1A-NA	-3.56	1.33	1.37
5	r	201	PEB	C2A-C1A	-3.55	1.48	1.52
5	z	201	PEB	C2A-C1A	-3.54	1.48	1.52
5	q	201	PEB	C1A-NA	-3.54	1.33	1.37
5	v	201	PEB	C2A-C1A	-3.54	1.48	1.52
5	w	201	PEB	C2C-C3C	3.53	1.48	1.37
5	p	201	PEB	C2A-C1A	-3.53	1.48	1.52
5	y	201	PEB	C1A-NA	-3.52	1.33	1.37
5	u	201	PEB	C2C-C3C	3.52	1.48	1.37
5	q	201	PEB	C2C-C3C	3.52	1.48	1.37
5	l	201	PEB	C2C-C3C	3.52	1.48	1.37
5	u	201	PEB	C1A-NA	-3.52	1.33	1.37
5	x	201	PEB	C2A-C1A	-3.51	1.49	1.52
5	s	201	PEB	C2C-C3C	3.51	1.48	1.37
5	w	204	PEB	C2C-C3C	3.51	1.48	1.37
5	y	201	PEB	C2C-C3C	3.51	1.48	1.37
5	w	202	PEB	C1A-NA	-3.50	1.33	1.37
5	q	202	PEB	C1A-NA	-3.49	1.33	1.37
5	l	201	PEB	C1A-NA	-3.48	1.33	1.37
5	s	202	PEB	C1A-NA	-3.48	1.33	1.37
5	l	202	PEB	C1A-NA	-3.47	1.33	1.37
5	z	202	PEB	C4B-C3B	3.47	1.51	1.45
5	r	201	PEB	C1A-NA	-3.47	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	y	202	PEB	C1A-NA	-3.47	1.33	1.37
5	p	202	PEB	C4B-C3B	3.44	1.51	1.45
5	u	202	PEB	C1A-NA	-3.44	1.33	1.37
5	t	202	PEB	C4B-C3B	3.44	1.51	1.45
5	u	203	PEB	C2C-C3C	3.44	1.47	1.37
5	l	203	PEB	C2C-C3C	3.44	1.47	1.37
5	r	202	PEB	C4B-C3B	3.43	1.51	1.45
5	v	202	PEB	C4B-C3B	3.43	1.51	1.45
5	q	203	PEB	C2C-C3C	3.42	1.47	1.37
5	w	203	PEB	C2C-C3C	3.42	1.47	1.37
5	x	202	PEB	C4B-C3B	3.41	1.51	1.45
5	p	201	PEB	C1A-NA	-3.41	1.33	1.37
5	w	204	PEB	C1A-NA	-3.40	1.33	1.37
5	r	201	PEB	CHA-C1B	3.40	1.48	1.40
5	s	203	PEB	C2C-C3C	3.39	1.47	1.37
5	y	203	PEB	C2C-C3C	3.39	1.47	1.37
5	z	201	PEB	C1A-NA	-3.38	1.33	1.37
5	t	201	PEB	CHA-C1B	3.38	1.48	1.40
5	t	201	PEB	C1A-NA	-3.38	1.33	1.37
5	p	201	PEB	CHA-C1B	3.38	1.48	1.40
5	y	201	PEB	C4B-C3B	3.38	1.51	1.45
5	l	201	PEB	C4B-C3B	3.37	1.51	1.45
5	u	201	PEB	C4B-C3B	3.37	1.51	1.45
5	q	201	PEB	C4B-C3B	3.37	1.51	1.45
5	w	201	PEB	C4B-C3B	3.36	1.51	1.45
5	z	201	PEB	CHA-C1B	3.36	1.48	1.40
5	v	201	PEB	C1A-NA	-3.36	1.33	1.37
5	x	201	PEB	C1A-NA	-3.36	1.33	1.37
5	v	201	PEB	CHA-C1B	3.35	1.48	1.40
5	x	201	PEB	CHA-C1B	3.34	1.48	1.40
5	l	203	PEB	C1A-NA	-3.34	1.33	1.37
5	s	203	PEB	C1A-NA	-3.33	1.33	1.37
5	s	201	PEB	C4B-C3B	3.32	1.51	1.45
5	w	203	PEB	C1A-NA	-3.32	1.33	1.37
5	u	203	PEB	C1A-NA	-3.31	1.33	1.37
5	y	203	PEB	C1A-NA	-3.30	1.33	1.37
5	y	202	PEB	CHA-C1B	3.29	1.48	1.40
5	q	203	PEB	C1A-NA	-3.28	1.33	1.37
5	t	202	PEB	C1A-NA	-3.28	1.33	1.37
5	u	202	PEB	CHA-C1B	3.27	1.48	1.40
5	v	202	PEB	C1A-NA	-3.26	1.33	1.37
5	l	202	PEB	CHA-C1B	3.25	1.48	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	q	202	PEB	CHA-C1B	3.24	1.48	1.40
5	w	202	PEB	CHA-C1B	3.24	1.48	1.40
5	s	202	PEB	CHA-C1B	3.24	1.48	1.40
5	q	202	PEB	C2C-C3C	3.24	1.47	1.37
5	r	202	PEB	C1A-NA	-3.22	1.33	1.37
5	l	202	PEB	C2C-C3C	3.22	1.47	1.37
5	y	202	PEB	C2C-C3C	3.22	1.47	1.37
5	u	202	PEB	C2C-C3C	3.22	1.47	1.37
5	w	202	PEB	C2C-C3C	3.21	1.47	1.37
5	s	202	PEB	C2C-C3C	3.20	1.47	1.37
5	z	202	PEB	C1A-NA	-3.18	1.33	1.37
5	x	202	PEB	C1A-NA	-3.16	1.33	1.37
5	p	202	PEB	C1A-NA	-3.16	1.33	1.37
5	l	201	PEB	OD-C4D	3.00	1.29	1.23
5	y	201	PEB	OD-C4D	3.00	1.29	1.23
5	s	201	PEB	OD-C4D	2.99	1.29	1.23
5	q	201	PEB	OD-C4D	2.99	1.29	1.23
5	u	201	PEB	OD-C4D	2.99	1.29	1.23
5	w	201	PEB	OD-C4D	2.97	1.29	1.23
5	s	202	PEB	OD-C4D	2.95	1.29	1.23
5	l	202	PEB	OD-C4D	2.95	1.29	1.23
5	y	202	PEB	OD-C4D	2.94	1.29	1.23
5	z	202	PEB	OD-C4D	2.93	1.29	1.23
5	q	202	PEB	OD-C4D	2.93	1.29	1.23
5	w	202	PEB	OD-C4D	2.92	1.29	1.23
5	u	202	PEB	OD-C4D	2.90	1.29	1.23
5	w	204	PEB	OD-C4D	2.90	1.29	1.23
5	p	202	PEB	OD-C4D	2.89	1.29	1.23
5	v	202	PEB	OD-C4D	2.89	1.29	1.23
5	t	202	PEB	OD-C4D	2.89	1.29	1.23
5	r	202	PEB	OD-C4D	2.87	1.29	1.23
5	l	203	PEB	OD-C4D	2.86	1.29	1.23
5	x	202	PEB	OD-C4D	2.86	1.29	1.23
5	w	203	PEB	OD-C4D	2.86	1.29	1.23
5	v	201	PEB	OD-C4D	2.85	1.29	1.23
5	x	201	PEB	OD-C4D	2.83	1.29	1.23
5	q	203	PEB	OD-C4D	2.83	1.29	1.23
5	t	201	PEB	OD-C4D	2.83	1.29	1.23
5	p	201	PEB	OD-C4D	2.82	1.29	1.23
5	z	201	PEB	OD-C4D	2.82	1.28	1.23
5	s	203	PEB	OD-C4D	2.81	1.28	1.23
5	r	201	PEB	OD-C4D	2.81	1.28	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	y	203	PEB	OD-C4D	2.80	1.28	1.23
5	u	203	PEB	OD-C4D	2.78	1.28	1.23
5	w	201	PEB	CHA-C1B	2.74	1.46	1.40
5	q	201	PEB	CHA-C1B	2.73	1.46	1.40
5	l	201	PEB	CHA-C1B	2.72	1.46	1.40
5	s	201	PEB	CHA-C1B	2.72	1.46	1.40
5	y	201	PEB	CHA-C1B	2.71	1.46	1.40
5	u	201	PEB	CHA-C1B	2.70	1.46	1.40
5	l	203	PEB	C2A-C1A	-2.65	1.49	1.52
5	q	203	PEB	C2A-C1A	-2.62	1.49	1.52
5	u	201	PEB	C2A-C1A	-2.61	1.49	1.52
5	w	203	PEB	C2A-C1A	-2.61	1.49	1.52
5	s	203	PEB	C2A-C1A	-2.58	1.49	1.52
5	y	203	PEB	C2A-C1A	-2.56	1.49	1.52
5	w	201	PEB	C2A-C1A	-2.54	1.49	1.52
5	l	201	PEB	C2A-C1A	-2.54	1.49	1.52
5	u	203	PEB	C2A-C1A	-2.54	1.49	1.52
5	y	201	PEB	C2A-C1A	-2.52	1.49	1.52
5	q	201	PEB	C2A-C1A	-2.46	1.49	1.52
5	s	201	PEB	C2A-C1A	-2.45	1.49	1.52
5	r	201	PEB	C4A-NA	-2.26	1.32	1.37
5	p	201	PEB	C4A-NA	-2.24	1.32	1.37
5	v	201	PEB	C4A-NA	-2.24	1.32	1.37
5	z	201	PEB	C4A-NA	-2.24	1.32	1.37
5	t	201	PEB	C4A-NA	-2.23	1.32	1.37
5	x	201	PEB	C4A-NA	-2.21	1.32	1.37
5	w	204	PEB	C2A-C1A	-2.15	1.50	1.52
5	w	204	PEB	C4A-NA	-2.09	1.33	1.37
5	y	201	PEB	C1C-CHB	2.07	1.49	1.41
5	x	202	PEB	C2A-C1A	-2.06	1.50	1.52
5	r	202	PEB	C2A-C1A	-2.06	1.50	1.52
5	z	202	PEB	C2A-C1A	-2.06	1.50	1.52
5	s	201	PEB	C1C-CHB	2.05	1.49	1.41
5	w	201	PEB	C1C-CHB	2.05	1.49	1.41
5	u	201	PEB	C1C-CHB	2.05	1.49	1.41
5	p	202	PEB	C2A-C1A	-2.04	1.50	1.52
5	l	201	PEB	C1C-CHB	2.04	1.49	1.41
5	q	201	PEB	C1C-CHB	2.03	1.49	1.41
5	t	202	PEB	C2A-C1A	-2.01	1.50	1.52
5	x	202	PEB	C1B-C2B	2.00	1.50	1.45
5	l	202	PEB	C4A-NA	-2.00	1.33	1.37
5	q	202	PEB	C4A-NA	-2.00	1.33	1.37

All (476) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	x	202	PEB	CHB-C4B-NB	-10.77	113.89	128.83
5	p	202	PEB	CHB-C4B-NB	-10.76	113.91	128.83
5	v	202	PEB	CHB-C4B-NB	-10.75	113.91	128.83
5	r	202	PEB	CHB-C4B-NB	-10.74	113.93	128.83
5	t	202	PEB	CHB-C4B-NB	-10.74	113.93	128.83
5	z	202	PEB	CHB-C4B-NB	-10.73	113.94	128.83
5	s	203	PEB	C1C-CHB-C4B	-7.40	119.97	128.81
5	y	203	PEB	C1C-CHB-C4B	-7.38	119.99	128.81
5	q	203	PEB	C1C-CHB-C4B	-7.38	119.99	128.81
5	l	203	PEB	C1C-CHB-C4B	-7.37	120.00	128.81
5	w	203	PEB	C1C-CHB-C4B	-7.37	120.01	128.81
5	u	203	PEB	C1C-CHB-C4B	-7.36	120.01	128.81
5	y	202	PEB	CHC-C4C-C3C	-6.79	118.75	130.34
5	w	202	PEB	CHC-C4C-C3C	-6.78	118.77	130.34
5	s	202	PEB	CHC-C4C-C3C	-6.78	118.77	130.34
5	q	202	PEB	CHC-C4C-C3C	-6.77	118.78	130.34
5	l	202	PEB	CHC-C4C-C3C	-6.77	118.79	130.34
5	u	202	PEB	CHC-C4C-C3C	-6.76	118.80	130.34
5	t	202	PEB	CHC-C1D-ND	-6.44	106.46	113.95
5	x	202	PEB	CHC-C1D-ND	-6.41	106.50	113.95
5	v	202	PEB	CHC-C1D-ND	-6.41	106.51	113.95
5	p	202	PEB	CHC-C1D-ND	-6.40	106.51	113.95
5	r	202	PEB	CHC-C1D-ND	-6.40	106.52	113.95
5	z	202	PEB	CHC-C1D-ND	-6.38	106.53	113.95
5	r	201	PEB	OA-C1A-C2A	-6.18	121.26	126.17
5	z	201	PEB	OA-C1A-C2A	-6.14	121.29	126.17
5	v	201	PEB	OA-C1A-C2A	-6.11	121.31	126.17
5	x	201	PEB	OA-C1A-C2A	-6.09	121.33	126.17
5	p	201	PEB	OA-C1A-C2A	-6.07	121.34	126.17
5	t	201	PEB	OA-C1A-C2A	-6.07	121.34	126.17
5	q	203	PEB	CHB-C4B-NB	-5.90	120.64	128.83
5	l	203	PEB	CHB-C4B-NB	-5.89	120.66	128.83
5	w	203	PEB	CHB-C4B-NB	-5.89	120.66	128.83
5	y	203	PEB	CHB-C4B-NB	-5.89	120.66	128.83
5	u	203	PEB	CHB-C4B-NB	-5.89	120.66	128.83
5	s	203	PEB	CHB-C4B-NB	-5.87	120.68	128.83
5	s	202	PEB	C1C-CHB-C4B	5.38	135.24	128.81
5	l	202	PEB	C1C-CHB-C4B	5.37	135.23	128.81
5	q	202	PEB	C1C-CHB-C4B	5.36	135.21	128.81
5	u	202	PEB	C1C-CHB-C4B	5.35	135.20	128.81
5	w	202	PEB	C1C-CHB-C4B	5.35	135.20	128.81
5	y	202	PEB	C1C-CHB-C4B	5.34	135.19	128.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	u	201	PEB	C1C-CHB-C4B	5.25	135.08	128.81
5	l	201	PEB	C1C-CHB-C4B	5.23	135.05	128.81
5	q	201	PEB	C1C-CHB-C4B	5.22	135.04	128.81
5	s	201	PEB	C1C-CHB-C4B	5.18	135.00	128.81
5	w	201	PEB	C1C-CHB-C4B	5.18	135.00	128.81
5	y	201	PEB	C1C-CHB-C4B	5.18	134.99	128.81
5	w	204	PEB	C1B-C2B-C3B	-4.82	100.97	106.51
5	q	201	PEB	CHC-C4C-C3C	-4.77	122.21	130.34
5	s	201	PEB	CHC-C4C-C3C	-4.75	122.24	130.34
5	y	201	PEB	CHC-C4C-C3C	-4.74	122.25	130.34
5	u	201	PEB	CHC-C4C-C3C	-4.73	122.27	130.34
5	w	201	PEB	CHC-C4C-C3C	-4.72	122.28	130.34
5	l	201	PEB	CHC-C4C-C3C	-4.72	122.29	130.34
5	l	203	PEB	OA-C1A-C2A	-4.58	122.53	126.17
5	s	203	PEB	OA-C1A-C2A	-4.56	122.55	126.17
5	u	203	PEB	OA-C1A-C2A	-4.55	122.55	126.17
5	y	203	PEB	OA-C1A-C2A	-4.54	122.57	126.17
5	q	203	PEB	OA-C1A-C2A	-4.52	122.58	126.17
5	r	202	PEB	CHA-C4A-NA	-4.50	119.85	125.20
5	w	203	PEB	OA-C1A-C2A	-4.50	122.59	126.17
5	z	202	PEB	CHA-C4A-NA	-4.48	119.88	125.20
5	v	202	PEB	CHA-C4A-NA	-4.47	119.89	125.20
5	x	202	PEB	CHA-C4A-NA	-4.45	119.92	125.20
5	p	202	PEB	CHA-C4A-NA	-4.44	119.92	125.20
5	t	202	PEB	CHA-C4A-NA	-4.44	119.92	125.20
5	r	202	PEB	CAB-C3B-C4B	4.44	132.86	125.01
5	x	202	PEB	CAB-C3B-C4B	4.42	132.84	125.01
5	z	202	PEB	CAB-C3B-C4B	4.42	132.83	125.01
5	t	202	PEB	CAB-C3B-C4B	4.41	132.82	125.01
5	v	202	PEB	CAB-C3B-C4B	4.41	132.81	125.01
5	p	202	PEB	CAB-C3B-C4B	4.40	132.79	125.01
5	w	204	PEB	CHC-C1D-ND	-4.38	108.86	113.95
5	p	202	PEB	C1C-CHB-C4B	-4.32	123.65	128.81
5	t	202	PEB	C1C-CHB-C4B	-4.31	123.66	128.81
5	x	202	PEB	C1C-CHB-C4B	-4.31	123.66	128.81
5	v	202	PEB	C1C-CHB-C4B	-4.29	123.68	128.81
5	z	202	PEB	C1C-CHB-C4B	-4.29	123.68	128.81
5	r	202	PEB	C1C-CHB-C4B	-4.29	123.69	128.81
5	q	203	PEB	CHC-C1D-ND	-4.14	109.14	113.95
5	w	203	PEB	CHC-C1D-ND	-4.13	109.15	113.95
5	y	203	PEB	CHC-C1D-ND	-4.13	109.16	113.95
5	s	203	PEB	CHC-C1D-ND	-4.12	109.16	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	u	203	PEB	CHC-C1D-ND	-4.10	109.19	113.95
5	l	203	PEB	CHC-C1D-ND	-4.09	109.20	113.95
5	y	201	PEB	C3B-C4B-NB	4.06	115.95	110.05
5	s	201	PEB	C3B-C4B-NB	4.05	115.93	110.05
5	u	201	PEB	C3B-C4B-NB	4.04	115.92	110.05
5	l	201	PEB	C3B-C4B-NB	4.03	115.91	110.05
5	w	201	PEB	C3B-C4B-NB	4.03	115.91	110.05
5	q	201	PEB	C3B-C4B-NB	4.02	115.90	110.05
5	r	202	PEB	C4B-C3B-C2B	-3.98	102.37	106.78
5	w	204	PEB	CAB-C3B-C2B	3.97	135.27	127.88
5	x	202	PEB	C4B-C3B-C2B	-3.96	102.39	106.78
5	z	202	PEB	C4B-C3B-C2B	-3.96	102.40	106.78
5	v	202	PEB	C4B-C3B-C2B	-3.95	102.41	106.78
5	t	202	PEB	C4B-C3B-C2B	-3.94	102.42	106.78
5	p	202	PEB	C4B-C3B-C2B	-3.92	102.44	106.78
5	t	201	PEB	C3D-C4D-ND	3.87	114.85	107.26
5	x	201	PEB	C3D-C4D-ND	3.86	114.84	107.26
5	t	201	PEB	C1B-C2B-C3B	-3.86	102.08	106.51
5	v	201	PEB	C3D-C4D-ND	3.86	114.83	107.26
5	r	201	PEB	C1B-C2B-C3B	-3.86	102.08	106.51
5	q	201	PEB	OA-C1A-C2A	-3.85	123.11	126.17
5	r	201	PEB	C3D-C4D-ND	3.85	114.81	107.26
5	y	201	PEB	OA-C1A-C2A	-3.85	123.11	126.17
5	p	201	PEB	C3D-C4D-ND	3.85	114.81	107.26
5	w	203	PEB	C3D-C4D-ND	3.84	114.80	107.26
5	p	201	PEB	C1B-C2B-C3B	-3.84	102.10	106.51
5	x	201	PEB	C1B-C2B-C3B	-3.84	102.10	106.51
5	z	201	PEB	C3D-C4D-ND	3.84	114.79	107.26
5	l	203	PEB	C3D-C4D-ND	3.83	114.78	107.26
5	z	201	PEB	C1B-C2B-C3B	-3.83	102.11	106.51
5	s	201	PEB	OA-C1A-C2A	-3.83	123.13	126.17
5	u	201	PEB	OA-C1A-C2A	-3.83	123.13	126.17
5	w	201	PEB	OA-C1A-C2A	-3.83	123.13	126.17
5	y	203	PEB	C3D-C4D-ND	3.83	114.77	107.26
5	q	203	PEB	C3D-C4D-ND	3.82	114.75	107.26
5	u	203	PEB	C3D-C4D-ND	3.81	114.73	107.26
5	v	201	PEB	C1B-C2B-C3B	-3.80	102.14	106.51
5	s	203	PEB	C3D-C4D-ND	3.80	114.72	107.26
5	t	202	PEB	OA-C1A-C2A	-3.80	123.15	126.17
5	l	201	PEB	OA-C1A-C2A	-3.80	123.15	126.17
5	q	202	PEB	OA-C1A-C2A	-3.79	123.16	126.17
5	t	202	PEB	OD-C4D-ND	-3.79	120.31	125.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	x	202	PEB	OD-C4D-ND	-3.79	120.32	125.93
5	r	202	PEB	OD-C4D-ND	-3.78	120.33	125.93
5	v	202	PEB	OD-C4D-ND	-3.77	120.34	125.93
5	z	202	PEB	OD-C4D-ND	-3.77	120.34	125.93
5	r	202	PEB	OA-C1A-C2A	-3.77	123.17	126.17
5	v	202	PEB	OA-C1A-C2A	-3.77	123.18	126.17
5	p	202	PEB	OD-C4D-ND	-3.76	120.36	125.93
5	w	202	PEB	OA-C1A-C2A	-3.75	123.19	126.17
5	q	201	PEB	C1B-C2B-C3B	-3.75	102.20	106.51
5	s	202	PEB	OA-C1A-C2A	-3.75	123.19	126.17
5	w	204	PEB	C3D-C4D-ND	3.74	114.60	107.26
5	y	203	PEB	C4B-C3B-C2B	-3.74	102.64	106.78
5	w	201	PEB	C1B-C2B-C3B	-3.74	102.22	106.51
5	l	202	PEB	OA-C1A-C2A	-3.73	123.21	126.17
5	s	203	PEB	C4B-C3B-C2B	-3.73	102.65	106.78
5	u	202	PEB	OA-C1A-C2A	-3.73	123.21	126.17
5	p	202	PEB	OA-C1A-C2A	-3.73	123.21	126.17
5	y	201	PEB	C1B-C2B-C3B	-3.72	102.23	106.51
5	s	201	PEB	C1B-C2B-C3B	-3.72	102.24	106.51
5	y	202	PEB	OA-C1A-C2A	-3.71	123.22	126.17
5	l	201	PEB	C1B-C2B-C3B	-3.71	102.25	106.51
5	q	203	PEB	C4B-C3B-C2B	-3.71	102.68	106.78
5	u	203	PEB	C4B-C3B-C2B	-3.70	102.68	106.78
5	u	201	PEB	C1B-C2B-C3B	-3.70	102.26	106.51
5	w	204	PEB	CHB-C4B-C3B	-3.69	116.78	125.32
5	w	203	PEB	C4B-C3B-C2B	-3.69	102.70	106.78
5	z	202	PEB	OA-C1A-C2A	-3.69	123.24	126.17
5	l	203	PEB	C4B-C3B-C2B	-3.68	102.71	106.78
5	u	201	PEB	CHB-C4B-NB	-3.65	123.76	128.83
5	s	201	PEB	C3D-C4D-ND	3.63	114.38	107.26
5	q	201	PEB	C3D-C4D-ND	3.63	114.37	107.26
5	l	201	PEB	C3D-C4D-ND	3.62	114.37	107.26
5	y	201	PEB	C3D-C4D-ND	3.62	114.36	107.26
5	u	201	PEB	C3D-C4D-ND	3.62	114.36	107.26
5	s	201	PEB	CHB-C4B-NB	-3.62	123.81	128.83
5	y	201	PEB	CHB-C4B-NB	-3.61	123.81	128.83
5	w	201	PEB	CHB-C4B-NB	-3.61	123.82	128.83
5	w	201	PEB	C3D-C4D-ND	3.61	114.34	107.26
5	q	201	PEB	CHB-C4B-NB	-3.61	123.82	128.83
5	l	201	PEB	CHB-C4B-NB	-3.61	123.83	128.83
5	x	202	PEB	OA-C1A-C2A	-3.61	123.31	126.17
5	t	201	PEB	CAB-CBB-CGB	-3.57	105.92	113.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	v	201	PEB	CAB-CBB-CGB	-3.56	105.94	113.60
5	x	201	PEB	CAB-CBB-CGB	-3.55	105.96	113.60
5	p	201	PEB	CAB-CBB-CGB	-3.55	105.96	113.60
5	r	201	PEB	CAB-CBB-CGB	-3.55	105.96	113.60
5	z	201	PEB	CAB-CBB-CGB	-3.54	105.99	113.60
5	w	204	PEB	OA-C1A-C2A	-3.52	123.38	126.17
5	y	201	PEB	C4B-C3B-C2B	-3.52	102.89	106.78
5	l	201	PEB	C4B-C3B-C2B	-3.51	102.90	106.78
5	y	201	PEB	CHC-C1D-ND	-3.50	109.88	113.95
5	s	201	PEB	C4B-C3B-C2B	-3.49	102.92	106.78
5	r	202	PEB	C3D-C4D-ND	3.49	114.11	107.26
5	z	202	PEB	C3D-C4D-ND	3.49	114.11	107.26
5	u	201	PEB	C4B-C3B-C2B	-3.49	102.92	106.78
5	x	202	PEB	C3D-C4D-ND	3.49	114.10	107.26
5	t	202	PEB	C3D-C4D-ND	3.49	114.10	107.26
5	v	202	PEB	C3D-C4D-ND	3.49	114.10	107.26
5	s	201	PEB	CHC-C1D-ND	-3.48	109.90	113.95
5	w	201	PEB	C4B-C3B-C2B	-3.48	102.93	106.78
5	p	202	PEB	C3D-C4D-ND	3.48	114.08	107.26
5	q	201	PEB	CHC-C1D-ND	-3.48	109.91	113.95
5	q	201	PEB	C4B-C3B-C2B	-3.47	102.94	106.78
5	w	204	PEB	CAB-C3B-C4B	-3.47	118.86	125.01
5	u	201	PEB	CHC-C1D-ND	-3.47	109.92	113.95
5	w	201	PEB	CHC-C1D-ND	-3.46	109.93	113.95
5	p	202	PEB	C2A-C1A-NA	3.46	111.25	108.27
5	v	202	PEB	C2A-C1A-NA	3.46	111.25	108.27
5	v	201	PEB	CHC-C1D-ND	-3.45	109.94	113.95
5	l	201	PEB	CHC-C1D-ND	-3.45	109.94	113.95
5	z	202	PEB	C2A-C1A-NA	3.45	111.24	108.27
5	r	202	PEB	C2A-C1A-NA	3.43	111.23	108.27
5	y	203	PEB	C3B-C4B-NB	3.42	115.03	110.05
5	t	202	PEB	C2A-C1A-NA	3.42	111.22	108.27
5	s	202	PEB	C2A-C1A-NA	3.42	111.22	108.27
5	y	202	PEB	C2A-C1A-NA	3.42	111.22	108.27
5	q	202	PEB	C2A-C1A-NA	3.42	111.22	108.27
5	u	202	PEB	C2A-C1A-NA	3.41	111.22	108.27
5	w	202	PEB	C2A-C1A-NA	3.41	111.21	108.27
5	l	202	PEB	C2A-C1A-NA	3.41	111.21	108.27
5	r	201	PEB	CHC-C1D-ND	-3.41	109.99	113.95
5	q	203	PEB	C3B-C4B-NB	3.41	115.01	110.05
5	s	203	PEB	C3B-C4B-NB	3.40	115.00	110.05
5	u	203	PEB	C3B-C4B-NB	3.40	115.00	110.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	w	203	PEB	C3B-C4B-NB	3.39	114.98	110.05
5	l	203	PEB	C3B-C4B-NB	3.39	114.98	110.05
5	p	201	PEB	CHC-C1D-ND	-3.39	110.01	113.95
5	t	201	PEB	CHC-C1D-ND	-3.39	110.02	113.95
5	z	201	PEB	CHC-C1D-ND	-3.38	110.02	113.95
5	x	201	PEB	CHC-C1D-ND	-3.38	110.03	113.95
5	r	201	PEB	CAA-C3A-C2A	-3.37	105.83	114.26
5	t	201	PEB	CAA-C3A-C2A	-3.37	105.83	114.26
5	x	201	PEB	OD-C4D-ND	-3.37	120.94	125.93
5	z	201	PEB	CAA-C3A-C2A	-3.37	105.84	114.26
5	v	201	PEB	CAA-C3A-C2A	-3.37	105.85	114.26
5	t	201	PEB	OD-C4D-ND	-3.36	120.94	125.93
5	p	201	PEB	OD-C4D-ND	-3.35	120.96	125.93
5	x	201	PEB	CAA-C3A-C2A	-3.35	105.88	114.26
5	r	201	PEB	OD-C4D-ND	-3.35	120.96	125.93
5	z	201	PEB	OD-C4D-ND	-3.35	120.97	125.93
5	y	202	PEB	C3D-C4D-ND	3.35	113.83	107.26
5	p	201	PEB	CAA-C3A-C2A	-3.35	105.90	114.26
5	l	202	PEB	C3D-C4D-ND	3.35	113.82	107.26
5	x	202	PEB	C2A-C1A-NA	3.35	111.16	108.27
5	v	201	PEB	OD-C4D-ND	-3.34	120.98	125.93
5	s	202	PEB	C3D-C4D-ND	3.33	113.80	107.26
5	q	202	PEB	C3D-C4D-ND	3.33	113.80	107.26
5	u	202	PEB	C3D-C4D-ND	3.32	113.77	107.26
5	u	202	PEB	C1B-C2B-C3B	-3.32	102.70	106.51
5	r	201	PEB	CMB-C2B-C1B	3.31	130.16	125.06
5	t	201	PEB	CMB-C2B-C1B	3.31	130.16	125.06
5	l	202	PEB	C1B-C2B-C3B	-3.31	102.71	106.51
5	l	202	PEB	OD-C4D-ND	-3.31	121.03	125.93
5	q	202	PEB	C1B-C2B-C3B	-3.31	102.71	106.51
5	w	202	PEB	C3D-C4D-ND	3.31	113.75	107.26
5	y	202	PEB	OD-C4D-ND	-3.30	121.04	125.93
5	w	202	PEB	C1B-C2B-C3B	-3.29	102.72	106.51
5	p	201	PEB	CMB-C2B-C1B	3.29	130.13	125.06
5	q	202	PEB	OD-C4D-ND	-3.29	121.06	125.93
5	y	202	PEB	C1B-C2B-C3B	-3.29	102.73	106.51
5	s	202	PEB	C1B-C2B-C3B	-3.29	102.73	106.51
5	s	202	PEB	OD-C4D-ND	-3.29	121.06	125.93
5	w	202	PEB	OD-C4D-ND	-3.29	121.06	125.93
5	v	201	PEB	CMB-C2B-C1B	3.29	130.12	125.06
5	u	202	PEB	OD-C4D-ND	-3.28	121.07	125.93
5	z	201	PEB	CMB-C2B-C1B	3.27	130.10	125.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	s	201	PEB	CMB-C2B-C1B	3.26	130.08	125.06
5	x	201	PEB	CMB-C2B-C1B	3.25	130.07	125.06
5	q	201	PEB	CMB-C2B-C1B	3.24	130.06	125.06
5	w	201	PEB	CMB-C2B-C1B	3.24	130.06	125.06
5	y	201	PEB	CMB-C2B-C1B	3.24	130.05	125.06
5	l	201	PEB	CMB-C2B-C1B	3.23	130.04	125.06
5	w	204	PEB	CMB-C2B-C1B	3.23	130.04	125.06
5	l	203	PEB	C2A-C1A-NA	3.23	111.06	108.27
5	y	203	PEB	C2A-C1A-NA	3.22	111.05	108.27
5	w	203	PEB	OD-C4D-ND	-3.21	121.17	125.93
5	u	201	PEB	CMB-C2B-C1B	3.21	130.00	125.06
5	y	203	PEB	CMB-C2B-C1B	3.20	130.00	125.06
5	q	203	PEB	C2A-C1A-NA	3.20	111.03	108.27
5	l	203	PEB	CMB-C2B-C1B	3.19	129.98	125.06
5	w	203	PEB	C2A-C1A-NA	3.18	111.02	108.27
5	u	203	PEB	CMB-C2B-C1B	3.18	129.96	125.06
5	u	203	PEB	C2A-C1A-NA	3.18	111.01	108.27
5	q	203	PEB	OD-C4D-ND	-3.18	121.23	125.93
5	w	203	PEB	CMB-C2B-C1B	3.17	129.95	125.06
5	l	203	PEB	OD-C4D-ND	-3.17	121.24	125.93
5	x	201	PEB	C1C-CHB-C4B	3.17	132.59	128.81
5	s	203	PEB	C2A-C1A-NA	3.16	111.00	108.27
5	s	203	PEB	CMB-C2B-C1B	3.16	129.93	125.06
5	y	203	PEB	OD-C4D-ND	-3.16	121.25	125.93
5	q	203	PEB	CMB-C2B-C1B	3.15	129.92	125.06
5	p	201	PEB	C1C-CHB-C4B	3.15	132.57	128.81
5	u	203	PEB	OD-C4D-ND	-3.14	121.27	125.93
5	q	201	PEB	C2B-C1B-NB	3.14	117.23	110.53
5	w	201	PEB	C2B-C1B-NB	3.14	117.22	110.53
5	v	201	PEB	C1C-CHB-C4B	3.14	132.55	128.81
5	l	201	PEB	C2B-C1B-NB	3.13	117.22	110.53
5	t	201	PEB	C1C-CHB-C4B	3.13	132.55	128.81
5	u	201	PEB	C2B-C1B-NB	3.13	117.21	110.53
5	s	201	PEB	C2B-C1B-NB	3.13	117.20	110.53
5	s	203	PEB	OD-C4D-ND	-3.13	121.30	125.93
5	s	202	PEB	CHB-C4B-NB	-3.12	124.49	128.83
5	r	201	PEB	C1C-CHB-C4B	3.12	132.54	128.81
5	y	201	PEB	C2B-C1B-NB	3.12	117.19	110.53
5	z	201	PEB	C1C-CHB-C4B	3.11	132.52	128.81
5	l	202	PEB	CHB-C4B-NB	-3.10	124.52	128.83
5	y	202	PEB	CHB-C4B-NB	-3.10	124.53	128.83
5	u	202	PEB	CHB-C4B-NB	-3.10	124.53	128.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	w	202	PEB	CHB-C4B-NB	-3.10	124.53	128.83
5	q	202	PEB	CHB-C4B-NB	-3.09	124.54	128.83
5	s	201	PEB	CAB-C3B-C4B	3.07	130.44	125.01
5	l	201	PEB	CAB-C3B-C4B	3.07	130.43	125.01
5	y	201	PEB	CAB-C3B-C4B	3.07	130.43	125.01
5	q	201	PEB	CAB-C3B-C4B	3.06	130.42	125.01
5	w	201	PEB	CAB-C3B-C4B	3.05	130.40	125.01
5	u	201	PEB	CAB-C3B-C4B	3.04	130.39	125.01
5	p	202	PEB	CHA-C1B-NB	-2.99	118.68	124.93
5	v	202	PEB	CHA-C1B-NB	-2.98	118.71	124.93
5	x	202	PEB	CHA-C1B-NB	-2.98	118.71	124.93
5	r	202	PEB	CHA-C1B-NB	-2.97	118.71	124.93
5	t	202	PEB	CHA-C1B-NB	-2.97	118.72	124.93
5	z	202	PEB	CHA-C1B-NB	-2.97	118.72	124.93
5	z	201	PEB	C2A-C1A-NA	2.97	110.83	108.27
5	r	201	PEB	C2A-C1A-NA	2.96	110.82	108.27
5	v	202	PEB	CMB-C2B-C1B	2.95	129.61	125.06
5	t	201	PEB	C2A-C1A-NA	2.94	110.81	108.27
5	s	201	PEB	OD-C4D-ND	-2.94	121.58	125.93
5	u	202	PEB	C4B-C3B-C2B	-2.94	103.53	106.78
5	p	202	PEB	CHB-C4B-C3B	2.93	132.10	125.32
5	x	201	PEB	C2A-C1A-NA	2.93	110.80	108.27
5	t	202	PEB	CMB-C2B-C1B	2.93	129.58	125.06
5	z	202	PEB	CMB-C2B-C1B	2.93	129.57	125.06
5	p	202	PEB	CMB-C2B-C1B	2.93	129.57	125.06
5	r	202	PEB	CMB-C2B-C1B	2.93	129.57	125.06
5	v	202	PEB	CHB-C4B-C3B	2.93	132.09	125.32
5	t	202	PEB	CHB-C4B-C3B	2.93	132.08	125.32
5	l	201	PEB	OD-C4D-ND	-2.92	121.60	125.93
5	p	201	PEB	C2A-C1A-NA	2.92	110.79	108.27
5	w	201	PEB	OD-C4D-ND	-2.92	121.61	125.93
5	z	202	PEB	CHB-C4B-C3B	2.92	132.06	125.32
5	q	201	PEB	OD-C4D-ND	-2.92	121.61	125.93
5	x	202	PEB	CHB-C4B-C3B	2.91	132.06	125.32
5	s	202	PEB	C4B-C3B-C2B	-2.91	103.56	106.78
5	y	202	PEB	C4B-C3B-C2B	-2.91	103.56	106.78
5	r	202	PEB	CHB-C4B-C3B	2.91	132.04	125.32
5	l	203	PEB	CHC-C4C-C3C	-2.91	125.38	130.34
5	u	203	PEB	CHC-C4C-C3C	-2.90	125.39	130.34
5	x	202	PEB	CMB-C2B-C1B	2.90	129.53	125.06
5	q	202	PEB	C4B-C3B-C2B	-2.90	103.57	106.78
5	w	202	PEB	C4B-C3B-C2B	-2.90	103.57	106.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	z	201	PEB	CHC-C4C-C3C	-2.90	125.39	130.34
5	v	201	PEB	C2A-C1A-NA	2.90	110.77	108.27
5	y	201	PEB	OD-C4D-ND	-2.90	121.64	125.93
5	p	201	PEB	CHB-C4B-NB	-2.90	124.81	128.83
5	r	201	PEB	CHB-C4B-NB	-2.89	124.81	128.83
5	s	203	PEB	CHC-C4C-C3C	-2.89	125.40	130.34
5	z	201	PEB	C3B-C4B-NB	2.89	114.25	110.05
5	z	201	PEB	CHB-C4B-NB	-2.89	124.82	128.83
5	u	201	PEB	OD-C4D-ND	-2.89	121.66	125.93
5	p	201	PEB	CHC-C4C-C3C	-2.89	125.42	130.34
5	l	202	PEB	C4B-C3B-C2B	-2.88	103.59	106.78
5	x	201	PEB	CHC-C4C-C3C	-2.88	125.42	130.34
5	r	201	PEB	CHC-C4C-C3C	-2.88	125.42	130.34
5	y	203	PEB	CHC-C4C-C3C	-2.88	125.42	130.34
5	w	203	PEB	CHC-C4C-C3C	-2.88	125.42	130.34
5	t	201	PEB	CHC-C4C-C3C	-2.88	125.42	130.34
5	t	201	PEB	CHB-C4B-NB	-2.88	124.83	128.83
5	v	201	PEB	CHC-C4C-C3C	-2.87	125.44	130.34
5	p	201	PEB	C3B-C4B-NB	2.87	114.23	110.05
5	q	203	PEB	CHC-C4C-C3C	-2.87	125.44	130.34
5	t	201	PEB	C3B-C4B-NB	2.87	114.23	110.05
5	x	201	PEB	CHB-C4B-NB	-2.87	124.85	128.83
5	v	201	PEB	C3B-C4B-NB	2.87	114.22	110.05
5	v	201	PEB	CHB-C4B-NB	-2.86	124.86	128.83
5	r	201	PEB	C3B-C4B-NB	2.86	114.21	110.05
5	x	201	PEB	C3B-C4B-NB	2.85	114.19	110.05
5	w	204	PEB	CAB-CBB-CGB	-2.85	107.48	113.60
5	u	202	PEB	CMB-C2B-C1B	2.82	129.41	125.06
5	q	202	PEB	CMB-C2B-C1B	2.81	129.39	125.06
5	w	202	PEB	CMB-C2B-C1B	2.79	129.35	125.06
5	l	202	PEB	CMB-C2B-C1B	2.78	129.34	125.06
5	r	201	PEB	CMA-C2A-C1A	-2.77	106.43	112.40
5	v	201	PEB	CMA-C2A-C1A	-2.77	106.43	112.40
5	z	201	PEB	CMA-C2A-C1A	-2.77	106.43	112.40
5	x	201	PEB	CMA-C2A-C1A	-2.77	106.43	112.40
5	y	202	PEB	CMB-C2B-C1B	2.77	129.33	125.06
5	p	201	PEB	CMA-C2A-C1A	-2.76	106.44	112.40
5	s	202	PEB	CMB-C2B-C1B	2.76	129.32	125.06
5	w	204	PEB	OD-C4D-ND	-2.76	121.84	125.93
5	s	202	PEB	C3B-C4B-NB	2.76	114.06	110.05
5	t	201	PEB	CMA-C2A-C1A	-2.75	106.47	112.40
5	x	202	PEB	C3B-C4B-NB	2.75	114.05	110.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	w	204	PEB	C2A-C1A-NA	2.74	110.64	108.27
5	u	202	PEB	C3B-C4B-NB	2.74	114.04	110.05
5	y	202	PEB	C3B-C4B-NB	2.74	114.03	110.05
5	w	204	PEB	CBC-CAC-C2C	-2.74	107.95	112.62
5	r	202	PEB	C3B-C4B-NB	2.74	114.03	110.05
5	w	202	PEB	C3B-C4B-NB	2.72	114.00	110.05
5	l	202	PEB	C3B-C4B-NB	2.72	114.00	110.05
5	v	202	PEB	C3B-C4B-NB	2.72	114.00	110.05
5	w	204	PEB	C3B-C4B-NB	2.71	113.99	110.05
5	z	202	PEB	C3B-C4B-NB	2.71	113.99	110.05
5	p	202	PEB	C3B-C4B-NB	2.71	113.99	110.05
5	q	202	PEB	C3B-C4B-NB	2.71	113.99	110.05
5	t	202	PEB	C3B-C4B-NB	2.70	113.98	110.05
5	w	204	PEB	CHA-C1B-NB	-2.68	119.33	124.93
5	w	204	PEB	CBB-CAB-C3B	2.63	119.93	112.63
5	u	201	PEB	C4B-NB-C1B	-2.63	101.56	106.51
5	s	201	PEB	C4B-NB-C1B	-2.62	101.58	106.51
5	w	201	PEB	C4B-NB-C1B	-2.61	101.59	106.51
5	q	201	PEB	C4B-NB-C1B	-2.61	101.59	106.51
5	l	201	PEB	C4B-NB-C1B	-2.61	101.59	106.51
5	w	204	PEB	OD-C4D-C3D	-2.61	123.56	129.46
5	y	201	PEB	C4B-NB-C1B	-2.60	101.61	106.51
5	w	204	PEB	C1C-CHB-C4B	2.58	131.89	128.81
5	q	201	PEB	C2A-C1A-NA	2.50	110.43	108.27
5	y	201	PEB	C2A-C1A-NA	2.50	110.43	108.27
5	l	201	PEB	C2A-C1A-NA	2.49	110.42	108.27
5	u	201	PEB	C2A-C1A-NA	2.49	110.42	108.27
5	w	204	PEB	CHC-C4C-C3C	-2.48	126.11	130.34
5	w	201	PEB	C2A-C1A-NA	2.46	110.40	108.27
5	r	201	PEB	OA-C1A-NA	2.46	127.92	124.94
5	s	201	PEB	C2A-C1A-NA	2.45	110.39	108.27
5	v	201	PEB	OA-C1A-NA	2.45	127.91	124.94
5	u	201	PEB	OD-C4D-C3D	-2.42	123.97	129.46
5	z	201	PEB	OA-C1A-NA	2.42	127.88	124.94
5	s	203	PEB	OD-C4D-C3D	-2.42	123.97	129.46
5	l	203	PEB	OD-C4D-C3D	-2.42	123.98	129.46
5	x	201	PEB	OA-C1A-NA	2.42	127.87	124.94
5	y	203	PEB	OD-C4D-C3D	-2.42	123.98	129.46
5	u	203	PEB	OD-C4D-C3D	-2.41	123.99	129.46
5	y	201	PEB	OD-C4D-C3D	-2.41	123.99	129.46
5	p	201	PEB	OA-C1A-NA	2.41	127.86	124.94
5	q	201	PEB	OD-C4D-C3D	-2.41	124.01	129.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	l	201	PEB	OD-C4D-C3D	-2.40	124.02	129.46
5	q	203	PEB	OD-C4D-C3D	-2.40	124.02	129.46
5	w	203	PEB	OD-C4D-C3D	-2.40	124.02	129.46
5	s	201	PEB	OD-C4D-C3D	-2.40	124.03	129.46
5	t	201	PEB	OA-C1A-NA	2.40	127.84	124.94
5	w	201	PEB	OD-C4D-C3D	-2.39	124.05	129.46
5	v	201	PEB	OD-C4D-C3D	-2.33	124.18	129.46
5	t	201	PEB	OD-C4D-C3D	-2.33	124.19	129.46
5	x	201	PEB	OD-C4D-C3D	-2.32	124.20	129.46
5	r	201	PEB	OD-C4D-C3D	-2.32	124.21	129.46
5	p	201	PEB	OD-C4D-C3D	-2.32	124.21	129.46
5	z	201	PEB	OD-C4D-C3D	-2.31	124.22	129.46
5	v	201	PEB	C4B-C3B-C2B	-2.31	104.23	106.78
5	z	201	PEB	C4B-C3B-C2B	-2.29	104.25	106.78
5	t	201	PEB	C4B-C3B-C2B	-2.28	104.26	106.78
5	p	201	PEB	C4B-C3B-C2B	-2.28	104.26	106.78
5	u	203	PEB	CBC-CAC-C2C	-2.27	108.74	112.62
5	s	203	PEB	CBC-CAC-C2C	-2.26	108.76	112.62
5	q	203	PEB	CBC-CAC-C2C	-2.26	108.77	112.62
5	w	203	PEB	CBC-CAC-C2C	-2.26	108.77	112.62
5	r	201	PEB	C4B-C3B-C2B	-2.25	104.29	106.78
5	y	203	PEB	CBC-CAC-C2C	-2.25	108.78	112.62
5	x	201	PEB	C4B-C3B-C2B	-2.25	104.29	106.78
5	l	203	PEB	CBC-CAC-C2C	-2.24	108.79	112.62
5	l	201	PEB	O2B-CGB-CBB	2.24	121.22	114.03
5	w	201	PEB	O2B-CGB-CBB	2.23	121.19	114.03
5	y	201	PEB	CHB-C4B-C3B	-2.23	120.17	125.32
5	q	201	PEB	O2B-CGB-CBB	2.22	121.17	114.03
5	s	201	PEB	CHB-C4B-C3B	-2.22	120.20	125.32
5	l	201	PEB	CHB-C4B-C3B	-2.22	120.20	125.32
5	y	201	PEB	O2B-CGB-CBB	2.21	121.15	114.03
5	w	201	PEB	CHB-C4B-C3B	-2.21	120.21	125.32
5	s	201	PEB	O2B-CGB-CBB	2.21	121.14	114.03
5	q	201	PEB	CHB-C4B-C3B	-2.21	120.21	125.32
5	u	201	PEB	O2B-CGB-CBB	2.21	121.12	114.03
5	u	201	PEB	CHB-C4B-C3B	-2.19	120.25	125.32
5	l	203	PEB	C1B-C2B-C3B	-2.19	104.00	106.51
5	y	203	PEB	C1B-C2B-C3B	-2.16	104.02	106.51
5	w	203	PEB	C1B-C2B-C3B	-2.16	104.02	106.51
5	u	203	PEB	C1B-C2B-C3B	-2.16	104.03	106.51
5	y	203	PEB	CMD-C2D-C3D	2.16	133.11	130.06
5	l	203	PEB	CMD-C2D-C3D	2.15	133.10	130.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	q	203	PEB	CMD-C2D-C3D	2.15	133.09	130.06
5	s	203	PEB	CMD-C2D-C3D	2.13	133.07	130.06
5	q	203	PEB	C1B-C2B-C3B	-2.13	104.06	106.51
5	s	203	PEB	C1B-C2B-C3B	-2.13	104.06	106.51
5	w	203	PEB	CMD-C2D-C3D	2.12	133.06	130.06
5	u	203	PEB	CMD-C2D-C3D	2.11	133.04	130.06
5	w	203	PEB	CHA-C1B-NB	-2.10	120.55	124.93
5	l	203	PEB	CHA-C1B-NB	-2.09	120.56	124.93
5	s	203	PEB	CHA-C1B-NB	-2.08	120.58	124.93
5	y	203	PEB	CHA-C1B-NB	-2.07	120.61	124.93
5	u	203	PEB	CHA-C1B-NB	-2.05	120.64	124.93
5	q	203	PEB	CHA-C1B-NB	-2.05	120.64	124.93
5	r	201	PEB	CHA-C1B-NB	-2.01	120.72	124.93
5	x	201	PEB	CHA-C1B-NB	-2.00	120.75	124.93

There are no chirality outliers.

All (246) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	y	201	PEB	C2A-C3A-CAA-CBA
5	y	201	PEB	C4A-C3A-CAA-CBA
5	y	201	PEB	NB-C1B-CHA-C4A
5	y	201	PEB	C2B-C1B-CHA-C4A
5	y	202	PEB	NB-C1B-CHA-C4A
5	y	202	PEB	C2B-C1B-CHA-C4A
5	y	203	PEB	ND-C1D-CHC-C4C
5	y	203	PEB	C2D-C1D-CHC-C4C
5	y	203	PEB	NC-C1C-CHB-C4B
5	y	203	PEB	C2C-C1C-CHB-C4B
5	y	203	PEB	NB-C1B-CHA-C4A
5	y	203	PEB	C2B-C1B-CHA-C4A
5	z	201	PEB	ND-C1D-CHC-C4C
5	z	201	PEB	C2A-C3A-CAA-CBA
5	z	201	PEB	C4A-C3A-CAA-CBA
5	z	201	PEB	NB-C1B-CHA-C4A
5	z	201	PEB	C2B-C1B-CHA-C4A
5	z	202	PEB	NC-C1C-CHB-C4B
5	z	202	PEB	C2C-C1C-CHB-C4B
5	z	202	PEB	NB-C1B-CHA-C4A
5	z	202	PEB	C2B-C1B-CHA-C4A
5	1	201	PEB	C2A-C3A-CAA-CBA
5	1	201	PEB	C4A-C3A-CAA-CBA

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Mol	Chain	Res	Type	Atoms
5	1	201	PEB	NB-C1B-CHA-C4A
5	1	201	PEB	C2B-C1B-CHA-C4A
5	1	202	PEB	NB-C1B-CHA-C4A
5	1	202	PEB	C2B-C1B-CHA-C4A
5	1	203	PEB	ND-C1D-CHC-C4C
5	1	203	PEB	C2D-C1D-CHC-C4C
5	1	203	PEB	NC-C1C-CHB-C4B
5	1	203	PEB	C2C-C1C-CHB-C4B
5	1	203	PEB	NB-C1B-CHA-C4A
5	1	203	PEB	C2B-C1B-CHA-C4A
5	p	201	PEB	ND-C1D-CHC-C4C
5	p	201	PEB	C2A-C3A-CAA-CBA
5	p	201	PEB	C4A-C3A-CAA-CBA
5	p	201	PEB	NB-C1B-CHA-C4A
5	p	201	PEB	C2B-C1B-CHA-C4A
5	p	202	PEB	NC-C1C-CHB-C4B
5	p	202	PEB	C2C-C1C-CHB-C4B
5	p	202	PEB	NB-C1B-CHA-C4A
5	p	202	PEB	C2B-C1B-CHA-C4A
5	q	201	PEB	C2A-C3A-CAA-CBA
5	q	201	PEB	C4A-C3A-CAA-CBA
5	q	201	PEB	NB-C1B-CHA-C4A
5	q	201	PEB	C2B-C1B-CHA-C4A
5	q	202	PEB	NB-C1B-CHA-C4A
5	q	202	PEB	C2B-C1B-CHA-C4A
5	q	203	PEB	ND-C1D-CHC-C4C
5	q	203	PEB	C2D-C1D-CHC-C4C
5	q	203	PEB	NC-C1C-CHB-C4B
5	q	203	PEB	C2C-C1C-CHB-C4B
5	q	203	PEB	NB-C1B-CHA-C4A
5	q	203	PEB	C2B-C1B-CHA-C4A
5	r	201	PEB	ND-C1D-CHC-C4C
5	r	201	PEB	C2A-C3A-CAA-CBA
5	r	201	PEB	C4A-C3A-CAA-CBA
5	r	201	PEB	NB-C1B-CHA-C4A
5	r	201	PEB	C2B-C1B-CHA-C4A
5	r	202	PEB	NC-C1C-CHB-C4B
5	r	202	PEB	C2C-C1C-CHB-C4B
5	r	202	PEB	NB-C1B-CHA-C4A
5	r	202	PEB	C2B-C1B-CHA-C4A
5	s	201	PEB	C2A-C3A-CAA-CBA
5	s	201	PEB	C4A-C3A-CAA-CBA

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Mol	Chain	Res	Type	Atoms
5	s	201	PEB	NB-C1B-CHA-C4A
5	s	201	PEB	C2B-C1B-CHA-C4A
5	s	202	PEB	NB-C1B-CHA-C4A
5	s	202	PEB	C2B-C1B-CHA-C4A
5	s	203	PEB	ND-C1D-CHC-C4C
5	s	203	PEB	C2D-C1D-CHC-C4C
5	s	203	PEB	NC-C1C-CHB-C4B
5	s	203	PEB	C2C-C1C-CHB-C4B
5	s	203	PEB	NB-C1B-CHA-C4A
5	s	203	PEB	C2B-C1B-CHA-C4A
5	t	201	PEB	ND-C1D-CHC-C4C
5	t	201	PEB	C2A-C3A-CAA-CBA
5	t	201	PEB	C4A-C3A-CAA-CBA
5	t	201	PEB	NB-C1B-CHA-C4A
5	t	201	PEB	C2B-C1B-CHA-C4A
5	t	202	PEB	NC-C1C-CHB-C4B
5	t	202	PEB	C2C-C1C-CHB-C4B
5	t	202	PEB	NB-C1B-CHA-C4A
5	t	202	PEB	C2B-C1B-CHA-C4A
5	u	201	PEB	C2A-C3A-CAA-CBA
5	u	201	PEB	C4A-C3A-CAA-CBA
5	u	201	PEB	NB-C1B-CHA-C4A
5	u	201	PEB	C2B-C1B-CHA-C4A
5	u	202	PEB	NB-C1B-CHA-C4A
5	u	202	PEB	C2B-C1B-CHA-C4A
5	u	203	PEB	ND-C1D-CHC-C4C
5	u	203	PEB	C2D-C1D-CHC-C4C
5	u	203	PEB	NC-C1C-CHB-C4B
5	u	203	PEB	C2C-C1C-CHB-C4B
5	u	203	PEB	NB-C1B-CHA-C4A
5	u	203	PEB	C2B-C1B-CHA-C4A
5	v	201	PEB	ND-C1D-CHC-C4C
5	v	201	PEB	C2A-C3A-CAA-CBA
5	v	201	PEB	C4A-C3A-CAA-CBA
5	v	201	PEB	NB-C1B-CHA-C4A
5	v	201	PEB	C2B-C1B-CHA-C4A
5	v	202	PEB	NC-C1C-CHB-C4B
5	v	202	PEB	C2C-C1C-CHB-C4B
5	v	202	PEB	NB-C1B-CHA-C4A
5	v	202	PEB	C2B-C1B-CHA-C4A
5	w	201	PEB	C2A-C3A-CAA-CBA
5	w	201	PEB	C4A-C3A-CAA-CBA

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Mol	Chain	Res	Type	Atoms
5	w	201	PEB	NB-C1B-CHA-C4A
5	w	201	PEB	C2B-C1B-CHA-C4A
5	w	202	PEB	NB-C1B-CHA-C4A
5	w	202	PEB	C2B-C1B-CHA-C4A
5	w	203	PEB	ND-C1D-CHC-C4C
5	w	203	PEB	C2D-C1D-CHC-C4C
5	w	203	PEB	NC-C1C-CHB-C4B
5	w	203	PEB	C2C-C1C-CHB-C4B
5	w	203	PEB	NB-C1B-CHA-C4A
5	w	203	PEB	C2B-C1B-CHA-C4A
5	w	204	PEB	ND-C1D-CHC-C4C
5	w	204	PEB	NC-C1C-CHB-C4B
5	w	204	PEB	C2C-C1C-CHB-C4B
5	w	204	PEB	C4A-C3A-CAA-CBA
5	w	204	PEB	NB-C1B-CHA-C4A
5	w	204	PEB	C2B-C1B-CHA-C4A
5	x	201	PEB	ND-C1D-CHC-C4C
5	x	201	PEB	C2A-C3A-CAA-CBA
5	x	201	PEB	C4A-C3A-CAA-CBA
5	x	201	PEB	NB-C1B-CHA-C4A
5	x	201	PEB	C2B-C1B-CHA-C4A
5	x	202	PEB	NC-C1C-CHB-C4B
5	x	202	PEB	C2C-C1C-CHB-C4B
5	x	202	PEB	NB-C1B-CHA-C4A
5	x	202	PEB	C2B-C1B-CHA-C4A
5	z	201	PEB	C2C-CAC-CBC-CGC
5	p	201	PEB	C2C-CAC-CBC-CGC
5	r	201	PEB	C2C-CAC-CBC-CGC
5	t	201	PEB	C2C-CAC-CBC-CGC
5	v	201	PEB	C2C-CAC-CBC-CGC
5	x	201	PEB	C2C-CAC-CBC-CGC
5	z	202	PEB	C3B-C4B-CHB-C1C
5	p	202	PEB	C3B-C4B-CHB-C1C
5	r	202	PEB	C3B-C4B-CHB-C1C
5	t	202	PEB	C3B-C4B-CHB-C1C
5	v	202	PEB	C3B-C4B-CHB-C1C
5	x	202	PEB	C3B-C4B-CHB-C1C
5	y	203	PEB	C3B-CAB-CBB-CGB
5	l	203	PEB	C3B-CAB-CBB-CGB
5	q	203	PEB	C3B-CAB-CBB-CGB
5	s	203	PEB	C3B-CAB-CBB-CGB
5	u	203	PEB	C3B-CAB-CBB-CGB

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Mol	Chain	Res	Type	Atoms
5	w	203	PEB	C3B-CAB-CBB-CGB
5	w	204	PEB	C4B-C3B-CAB-CBB
5	y	201	PEB	C3B-CAB-CBB-CGB
5	l	201	PEB	C3B-CAB-CBB-CGB
5	q	201	PEB	C3B-CAB-CBB-CGB
5	s	201	PEB	C3B-CAB-CBB-CGB
5	u	201	PEB	C3B-CAB-CBB-CGB
5	w	201	PEB	C3B-CAB-CBB-CGB
5	w	204	PEB	C2A-C3A-CAA-CBA
5	z	202	PEB	NA-C4A-CHA-C1B
5	p	202	PEB	NA-C4A-CHA-C1B
5	r	202	PEB	NA-C4A-CHA-C1B
5	t	202	PEB	NA-C4A-CHA-C1B
5	v	202	PEB	NA-C4A-CHA-C1B
5	x	202	PEB	NA-C4A-CHA-C1B
5	z	201	PEB	C2D-C1D-CHC-C4C
5	p	201	PEB	C2D-C1D-CHC-C4C
5	r	201	PEB	C2D-C1D-CHC-C4C
5	t	201	PEB	C2D-C1D-CHC-C4C
5	v	201	PEB	C2D-C1D-CHC-C4C
5	w	204	PEB	C2D-C1D-CHC-C4C
5	x	201	PEB	C2D-C1D-CHC-C4C
5	w	204	PEB	C3B-CAB-CBB-CGB
5	z	202	PEB	NB-C4B-CHB-C1C
5	p	202	PEB	NB-C4B-CHB-C1C
5	r	202	PEB	NB-C4B-CHB-C1C
5	t	202	PEB	NB-C4B-CHB-C1C
5	v	202	PEB	NB-C4B-CHB-C1C
5	x	202	PEB	NB-C4B-CHB-C1C
5	w	204	PEB	C2B-C3B-CAB-CBB
5	z	201	PEB	CAB-CBB-CGB-O1B
5	p	201	PEB	CAB-CBB-CGB-O1B
5	r	201	PEB	CAB-CBB-CGB-O1B
5	t	201	PEB	CAB-CBB-CGB-O1B
5	v	201	PEB	CAB-CBB-CGB-O1B
5	x	201	PEB	CAB-CBB-CGB-O1B
5	z	202	PEB	CAC-CBC-CGC-O1C
5	p	202	PEB	CAC-CBC-CGC-O1C
5	r	202	PEB	CAC-CBC-CGC-O1C
5	t	202	PEB	CAC-CBC-CGC-O1C
5	v	202	PEB	CAC-CBC-CGC-O1C
5	x	202	PEB	CAC-CBC-CGC-O1C

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Mol	Chain	Res	Type	Atoms
5	z	201	PEB	CAB-CBB-CGB-O2B
5	p	201	PEB	CAB-CBB-CGB-O2B
5	r	201	PEB	CAB-CBB-CGB-O2B
5	t	201	PEB	CAB-CBB-CGB-O2B
5	v	201	PEB	CAB-CBB-CGB-O2B
5	x	201	PEB	CAB-CBB-CGB-O2B
5	z	202	PEB	CAC-CBC-CGC-O2C
5	p	202	PEB	CAC-CBC-CGC-O2C
5	r	202	PEB	CAC-CBC-CGC-O2C
5	t	202	PEB	CAC-CBC-CGC-O2C
5	v	202	PEB	CAC-CBC-CGC-O2C
5	x	202	PEB	CAC-CBC-CGC-O2C
5	s	201	PEB	CAB-CBB-CGB-O1B
5	y	201	PEB	CAB-CBB-CGB-O1B
5	y	201	PEB	CAB-CBB-CGB-O2B
5	l	201	PEB	CAB-CBB-CGB-O1B
5	l	201	PEB	CAB-CBB-CGB-O2B
5	q	201	PEB	CAB-CBB-CGB-O1B
5	u	201	PEB	CAB-CBB-CGB-O1B
5	u	201	PEB	CAB-CBB-CGB-O2B
5	w	201	PEB	CAB-CBB-CGB-O1B
5	q	201	PEB	CAB-CBB-CGB-O2B
5	s	201	PEB	CAB-CBB-CGB-O2B
5	w	201	PEB	CAB-CBB-CGB-O2B
5	w	204	PEB	C2C-CAC-CBC-CGC
5	l	201	PEB	CAC-CBC-CGC-O1C
5	s	201	PEB	CAC-CBC-CGC-O1C
5	u	201	PEB	CAC-CBC-CGC-O1C
5	w	201	PEB	CAC-CBC-CGC-O1C
5	y	201	PEB	CAC-CBC-CGC-O1C
5	z	202	PEB	CAB-CBB-CGB-O1B
5	z	202	PEB	CAB-CBB-CGB-O2B
5	p	202	PEB	CAB-CBB-CGB-O2B
5	q	201	PEB	CAC-CBC-CGC-O1C
5	r	202	PEB	CAB-CBB-CGB-O1B
5	t	202	PEB	CAB-CBB-CGB-O1B
5	t	202	PEB	CAB-CBB-CGB-O2B
5	x	202	PEB	CAB-CBB-CGB-O1B
5	p	202	PEB	CAB-CBB-CGB-O1B
5	r	202	PEB	CAB-CBB-CGB-O2B
5	v	202	PEB	CAB-CBB-CGB-O1B
5	v	202	PEB	CAB-CBB-CGB-O2B

*Continued on next page...*

*Continued from previous page...*

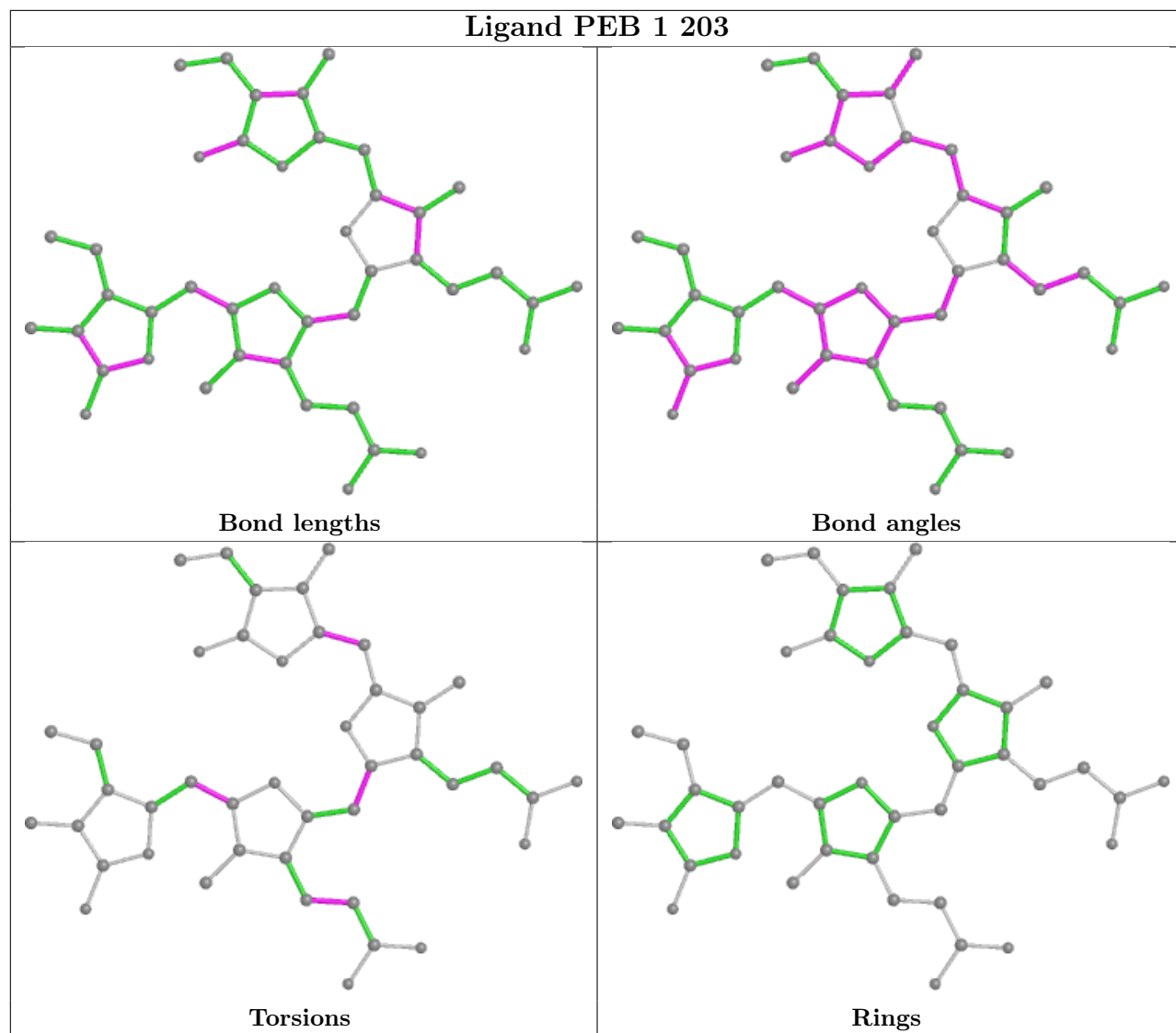
Mol	Chain	Res	Type	Atoms
5	x	202	PEB	CAB-CBB-CGB-O2B
5	l	201	PEB	CAC-CBC-CGC-O2C
5	q	201	PEB	CAC-CBC-CGC-O2C
5	u	201	PEB	CAC-CBC-CGC-O2C
5	w	201	PEB	CAC-CBC-CGC-O2C
5	s	201	PEB	CAC-CBC-CGC-O2C
5	y	201	PEB	CAC-CBC-CGC-O2C
5	y	202	PEB	CAC-CBC-CGC-O2C
5	l	202	PEB	CAC-CBC-CGC-O2C
5	q	202	PEB	CAC-CBC-CGC-O2C
5	s	202	PEB	CAC-CBC-CGC-O2C
5	u	202	PEB	CAC-CBC-CGC-O2C
5	w	202	PEB	CAC-CBC-CGC-O2C

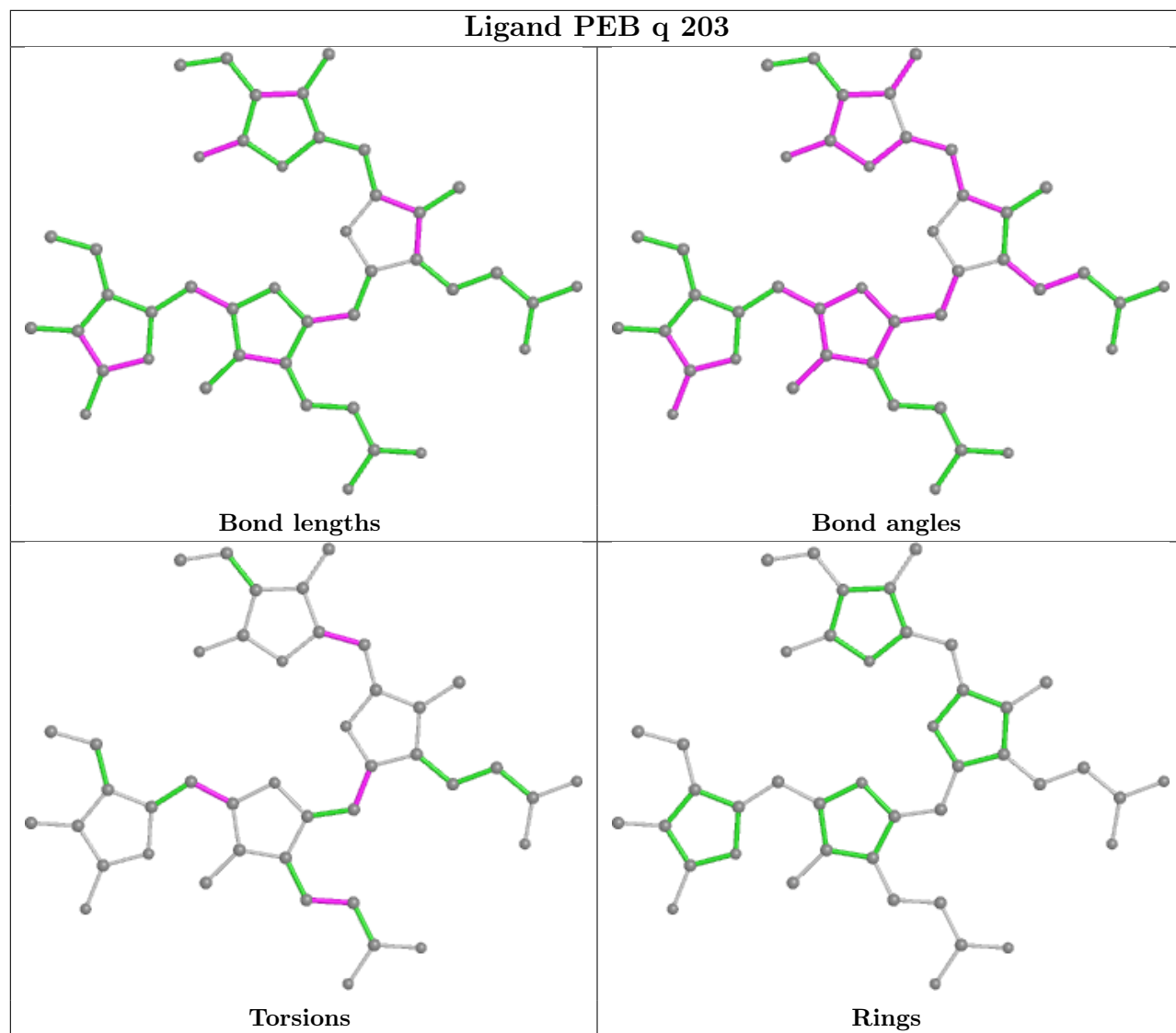
There are no ring outliers.

2 monomers are involved in 3 short contacts:

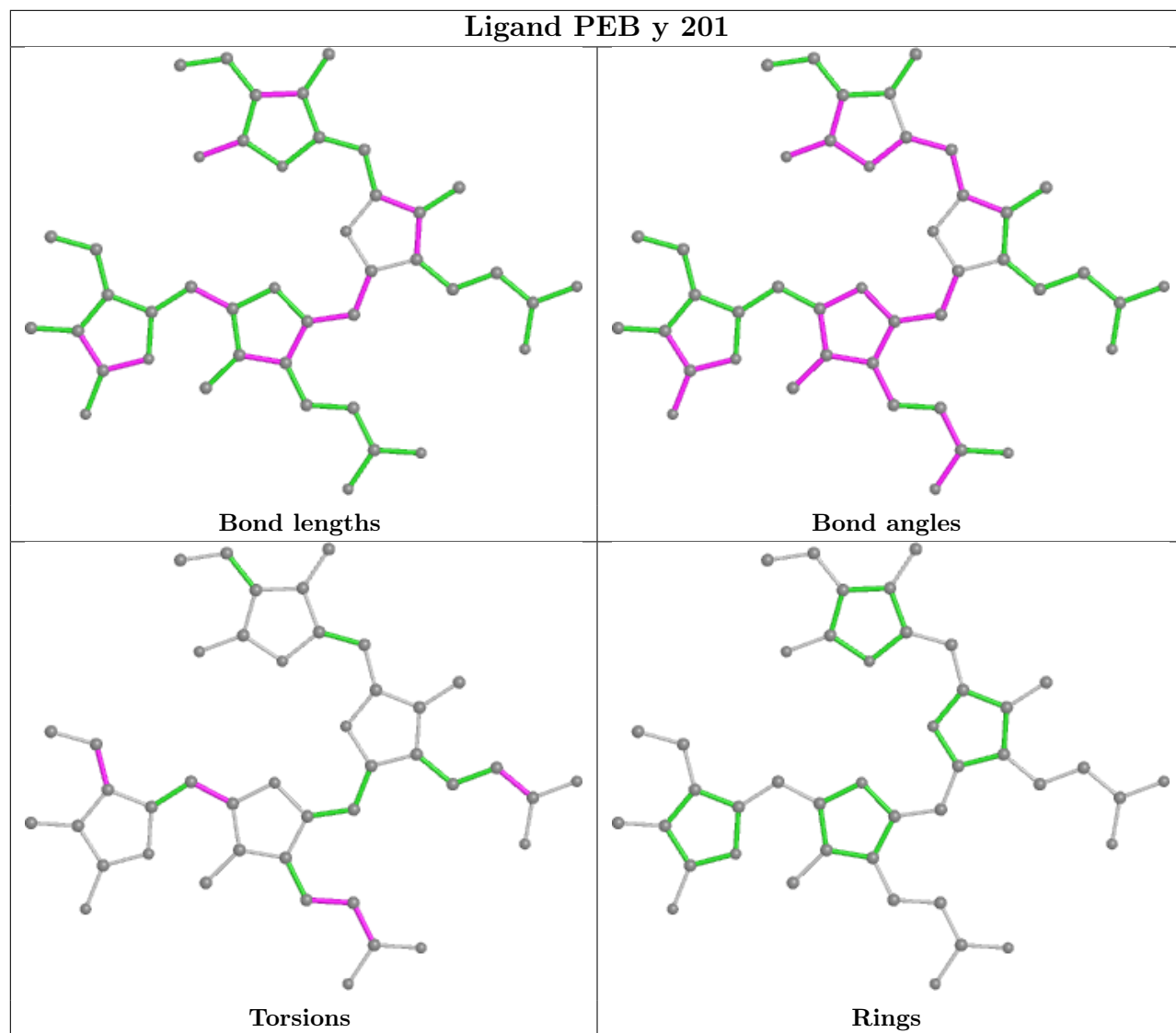
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	l	203	PEB	2	0
5	l	202	PEB	1	0

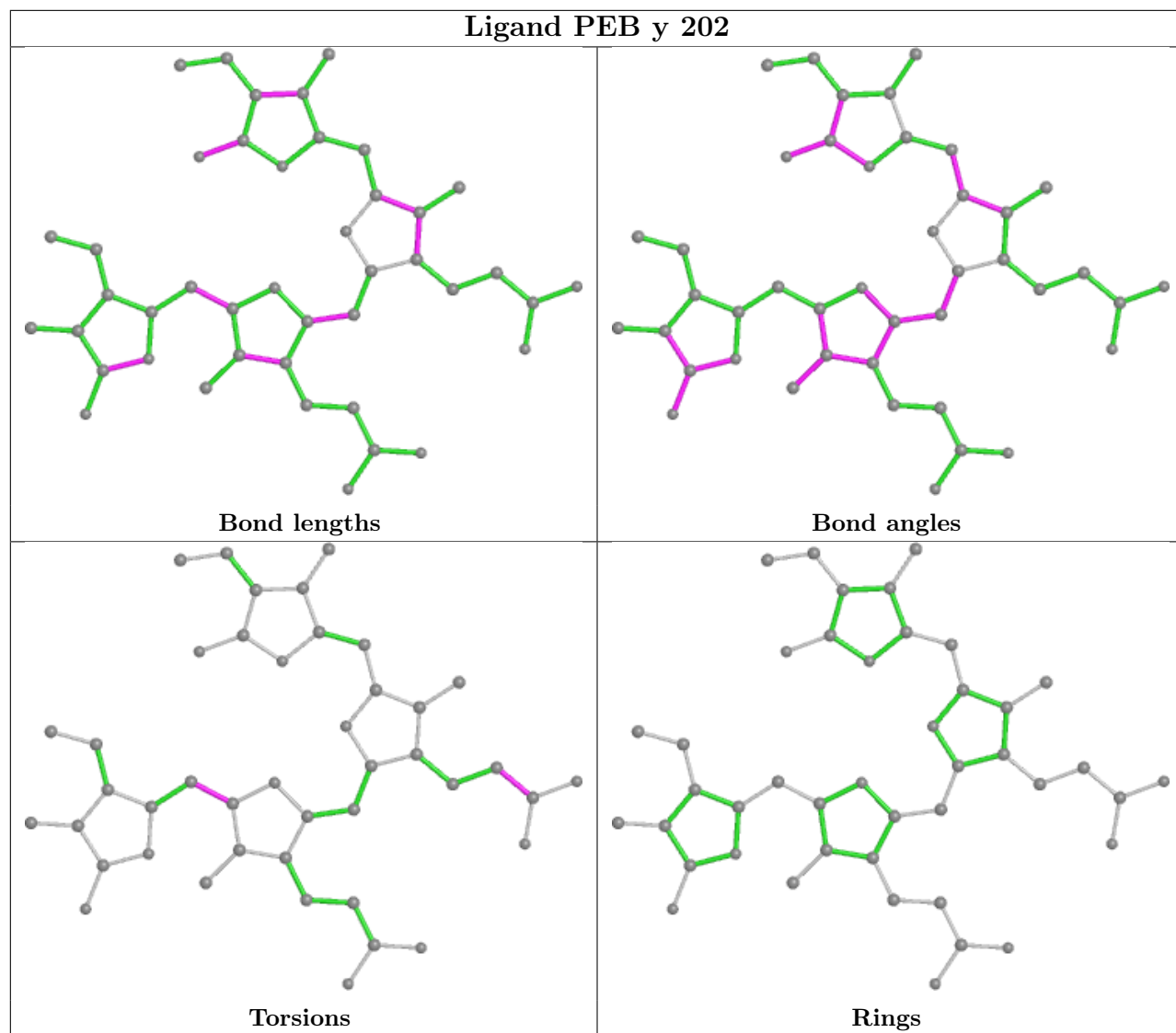
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

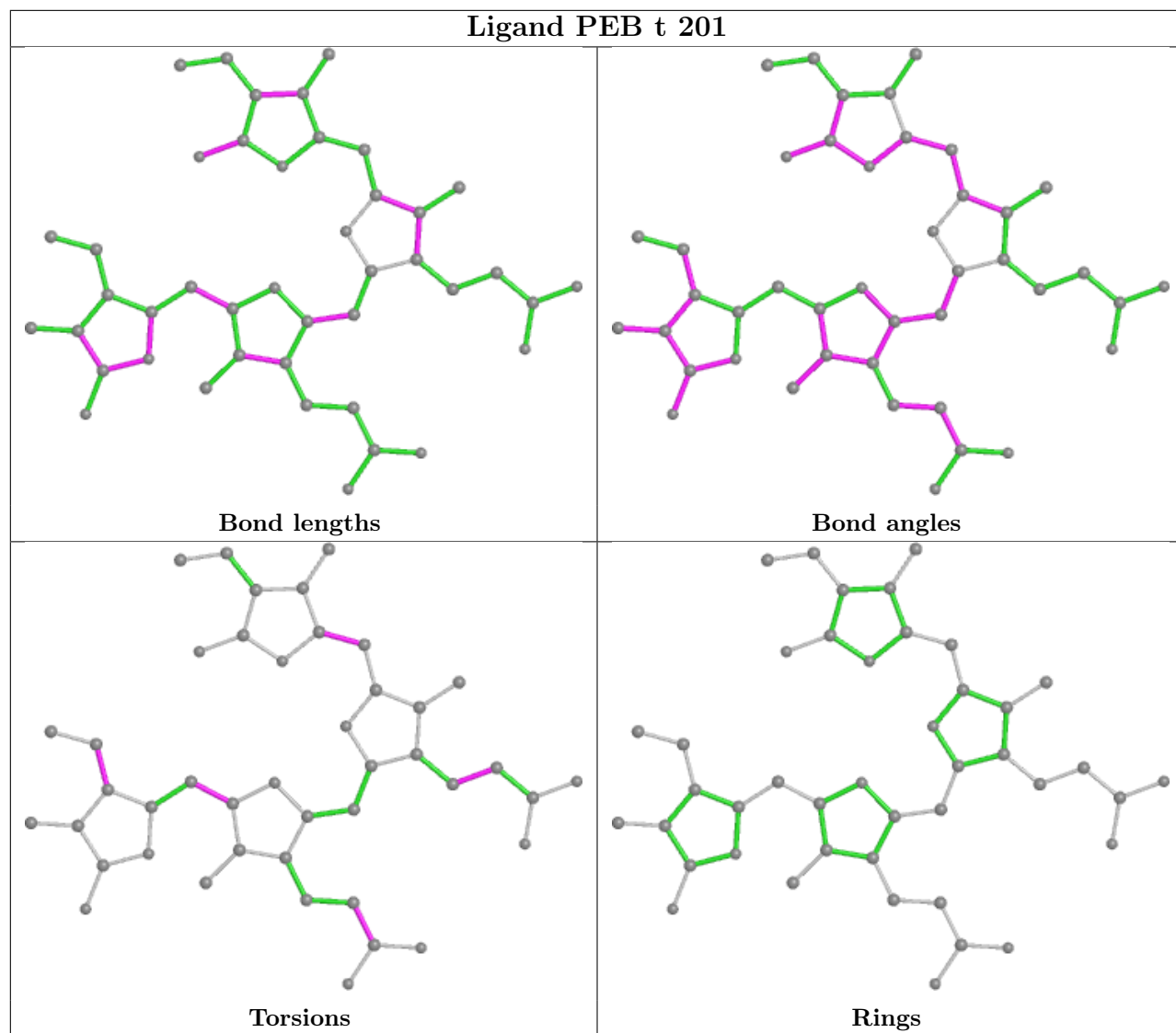


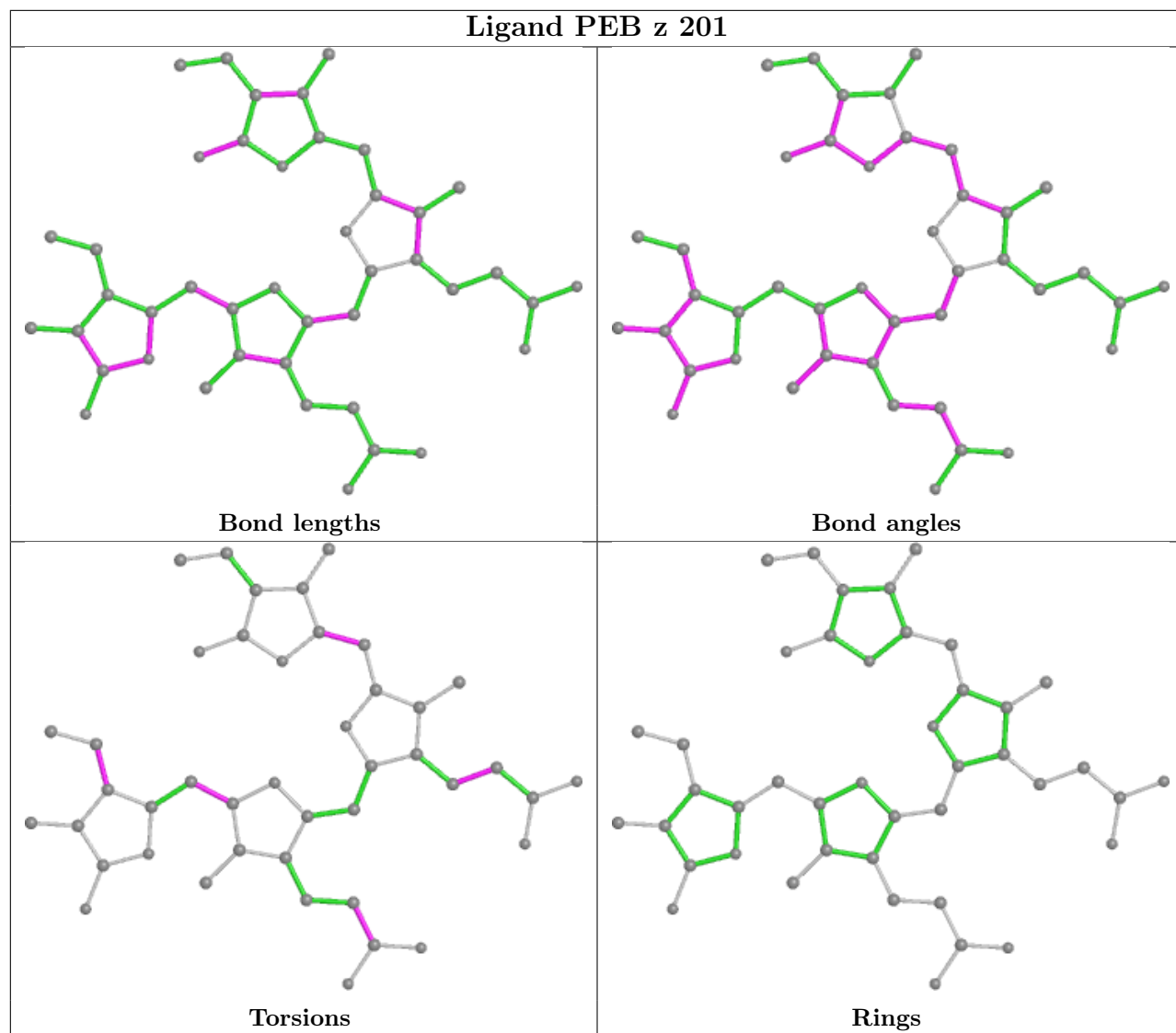


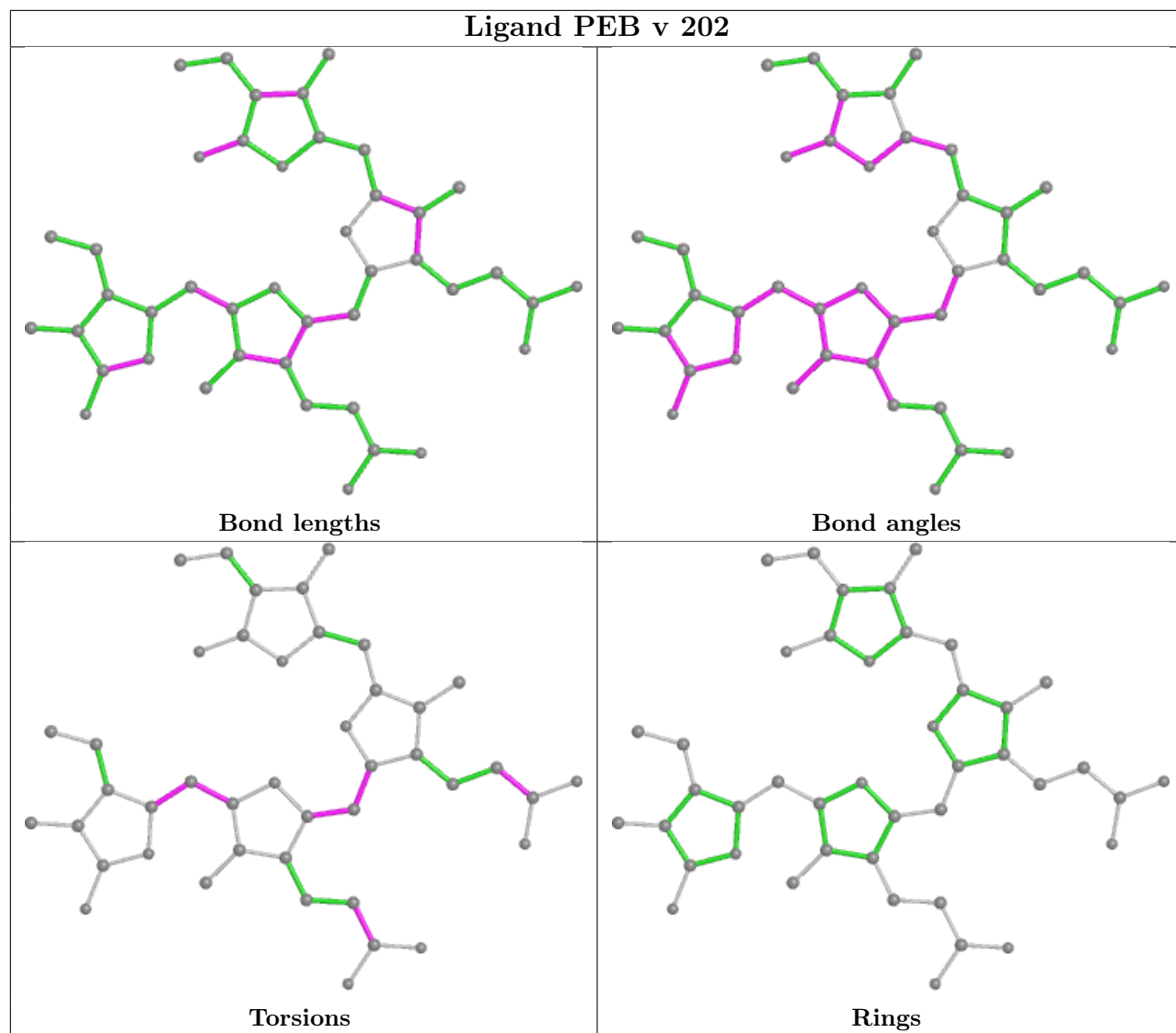


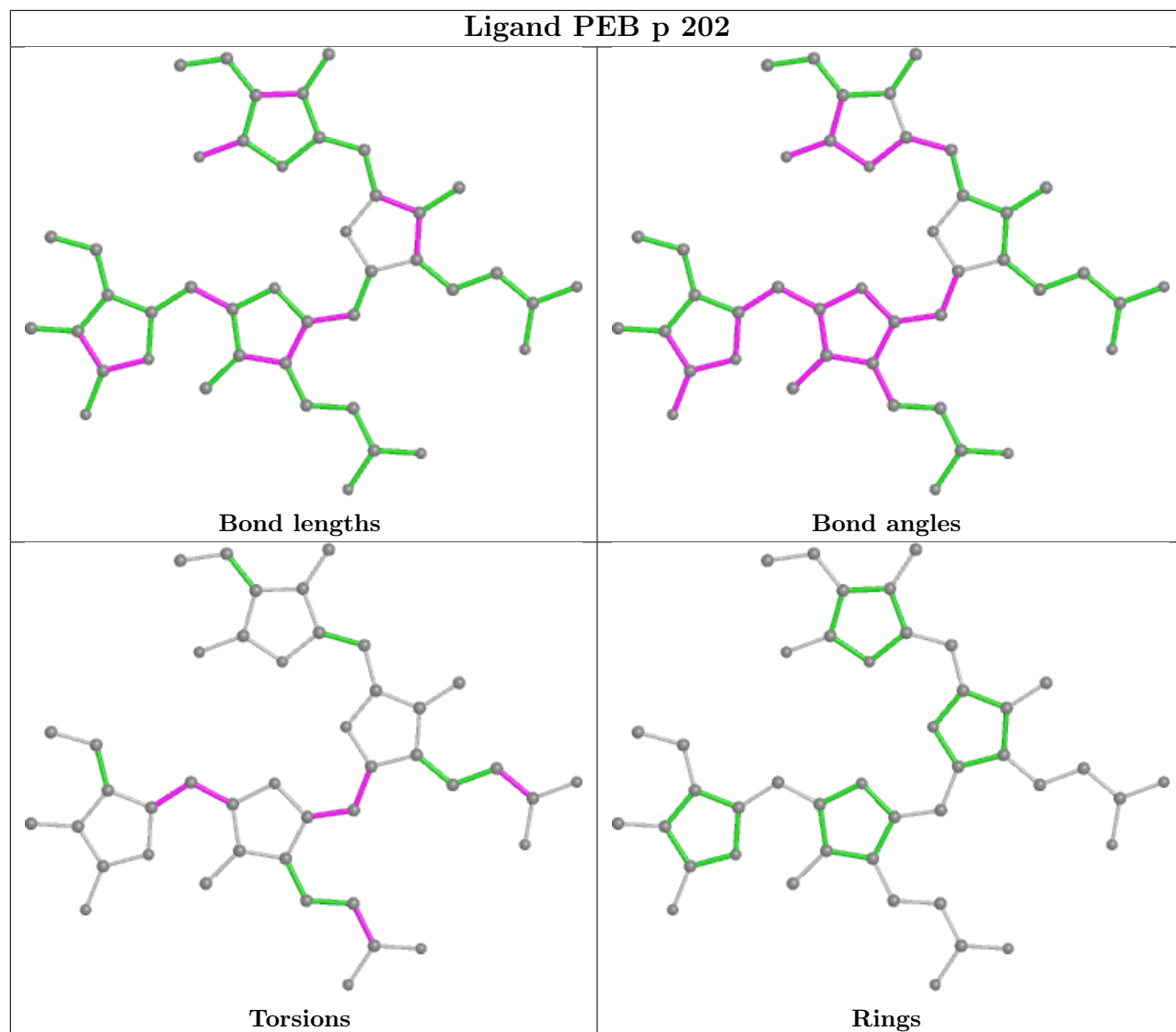


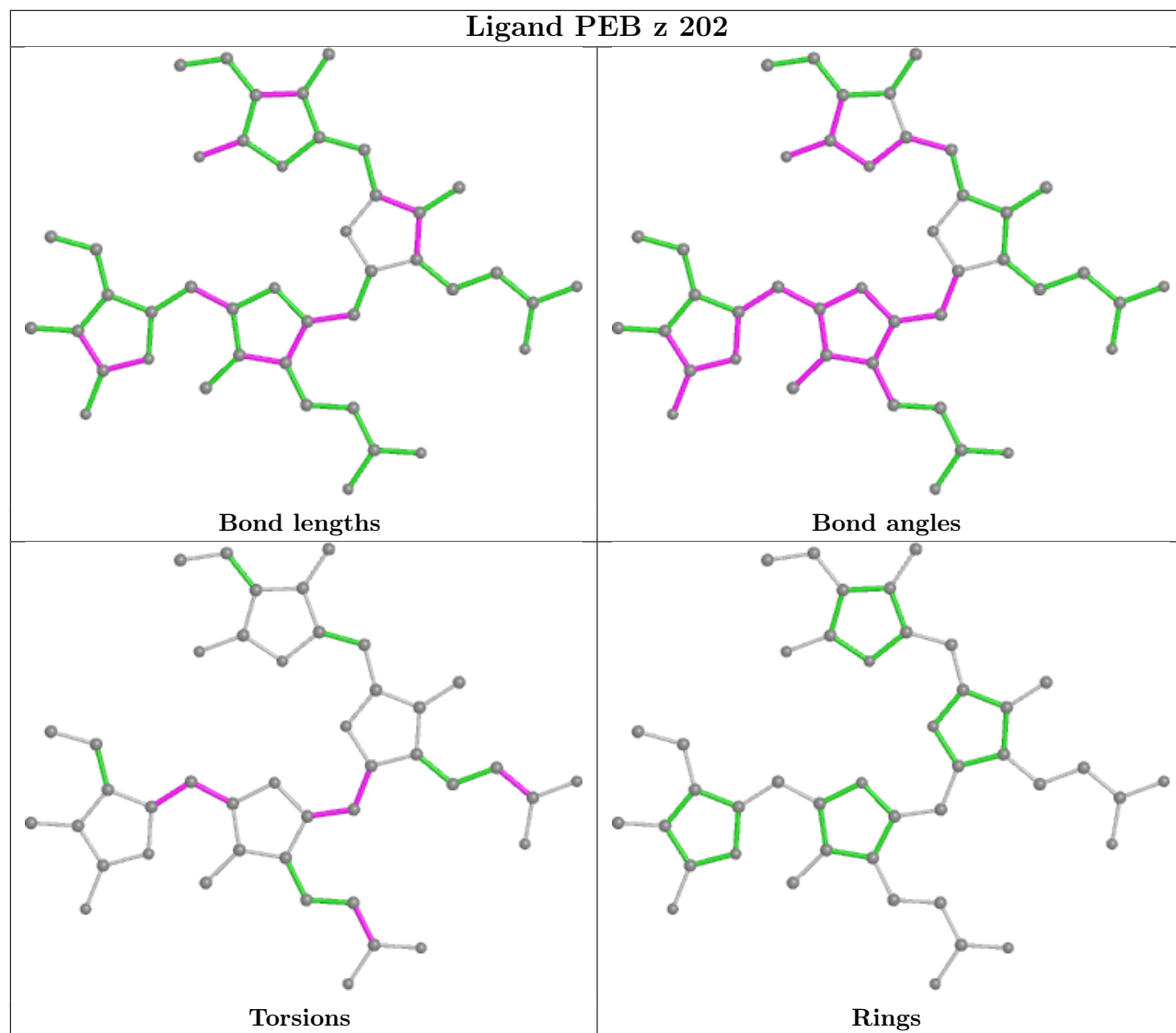


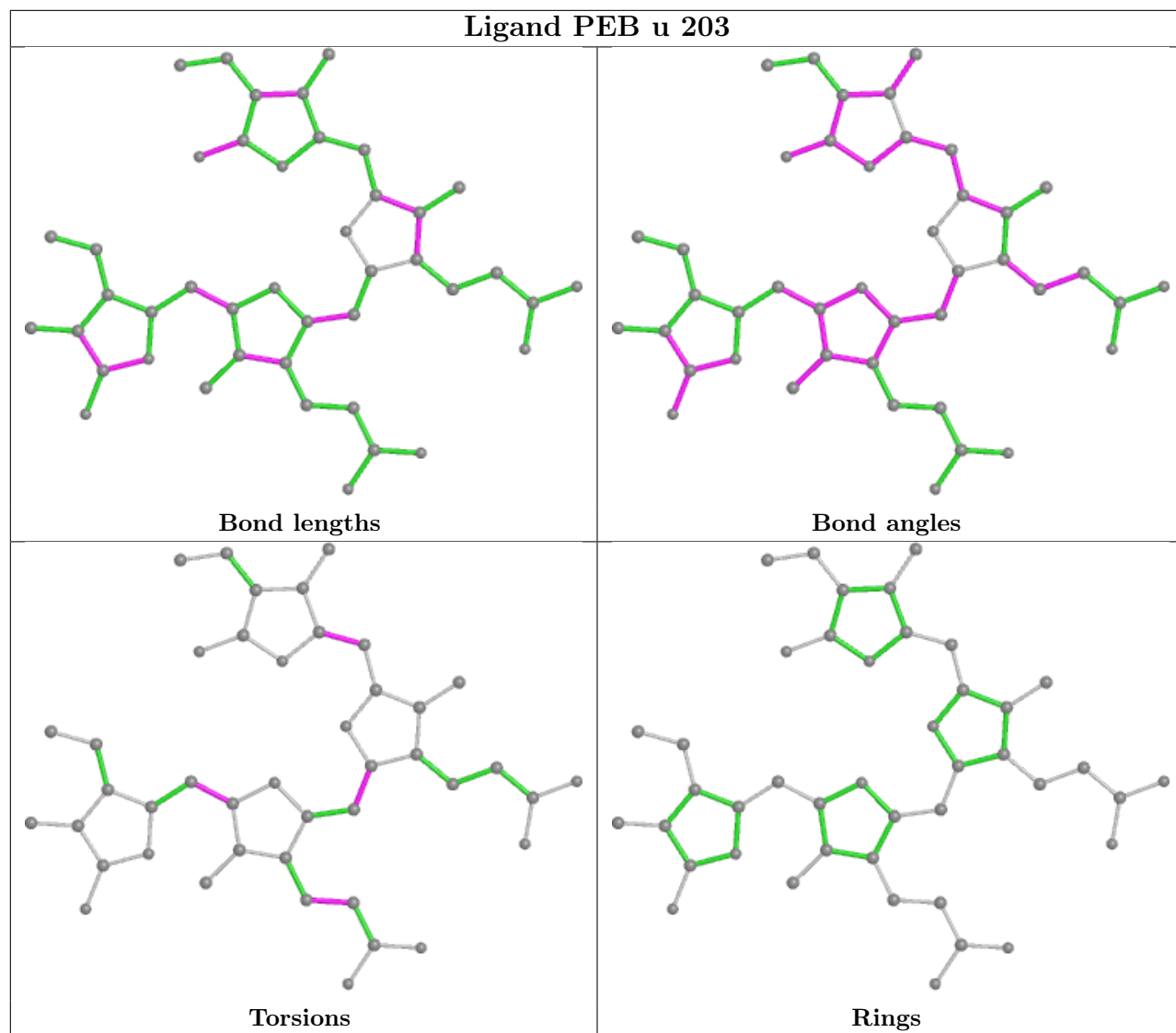




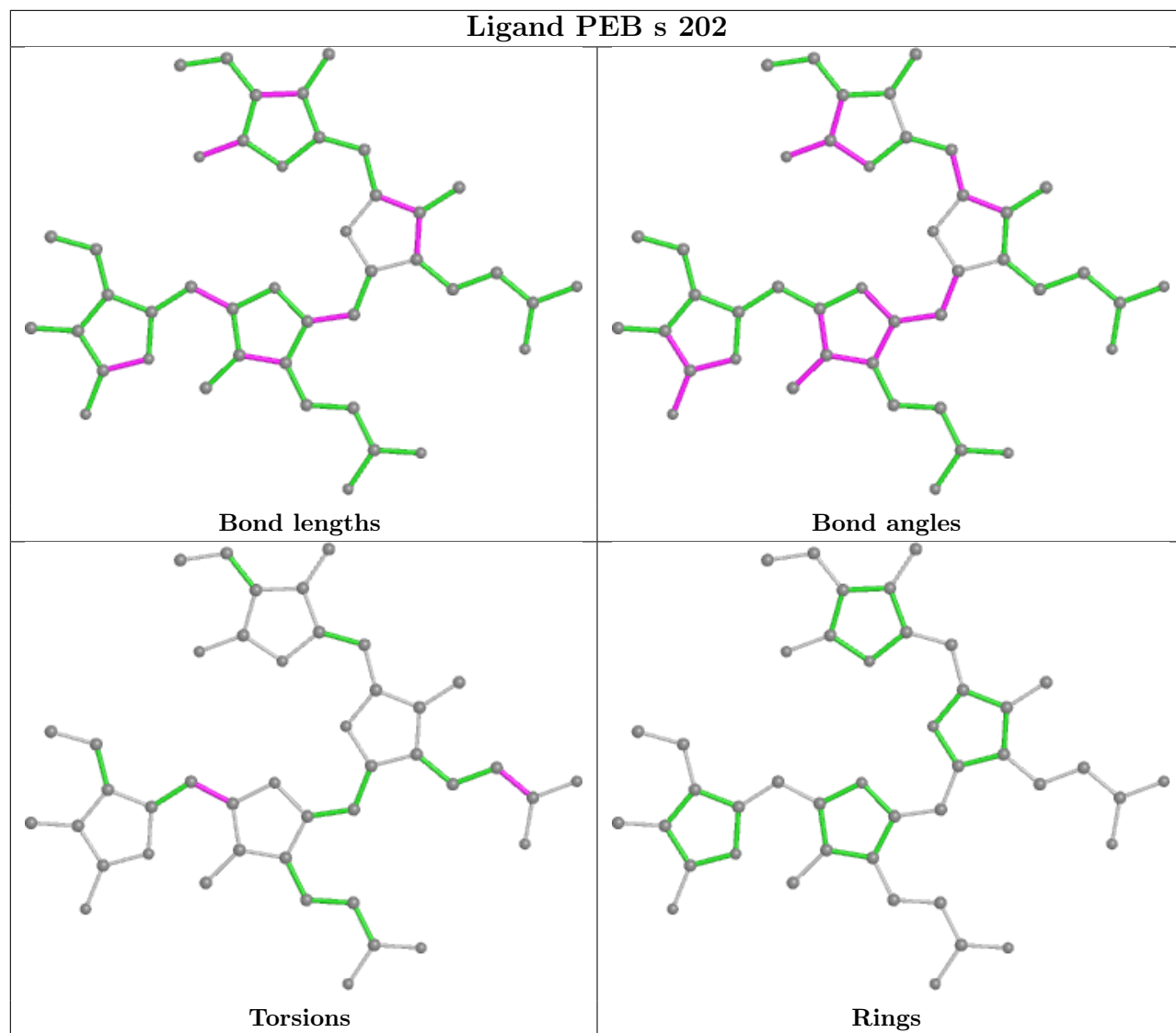


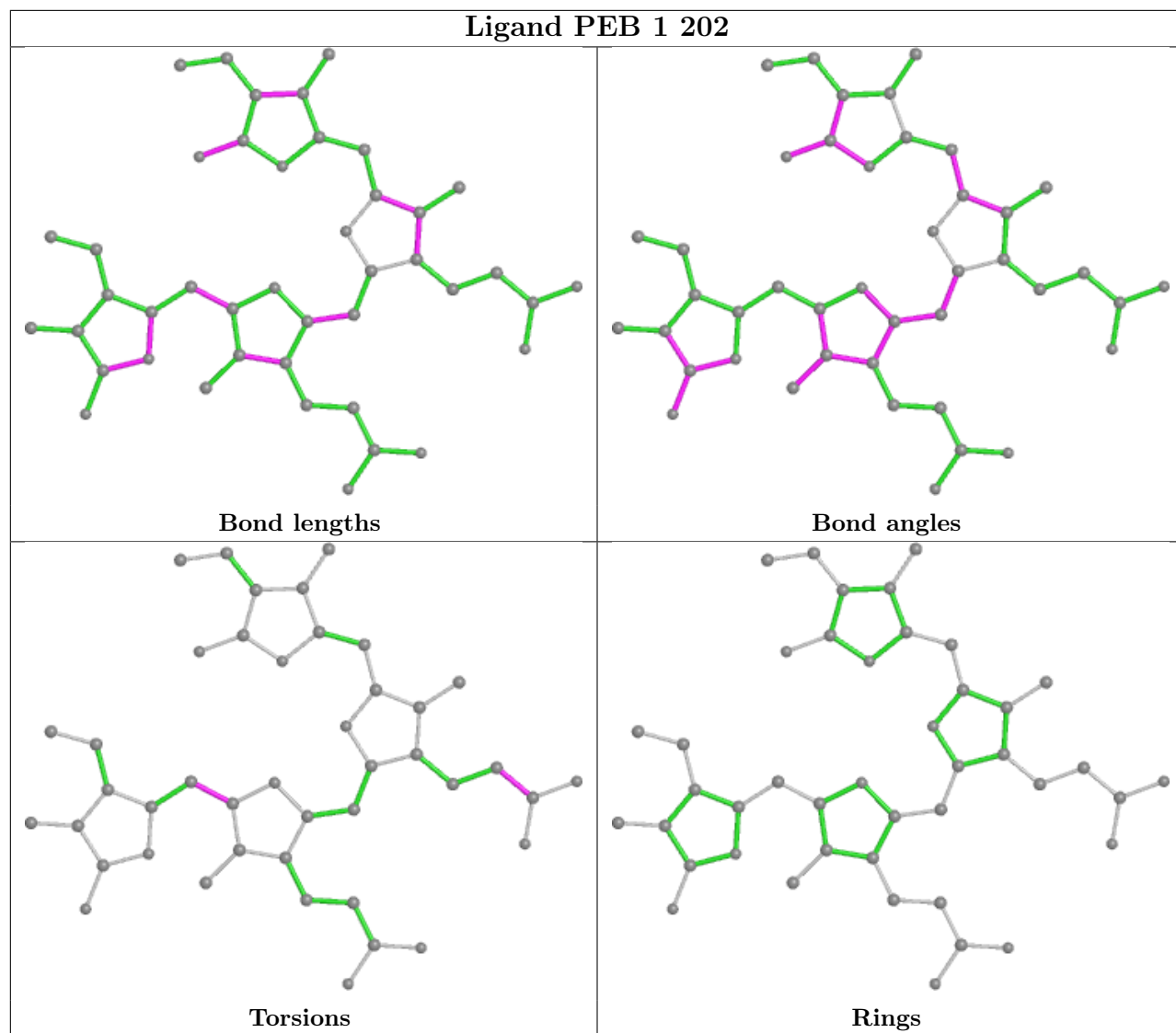


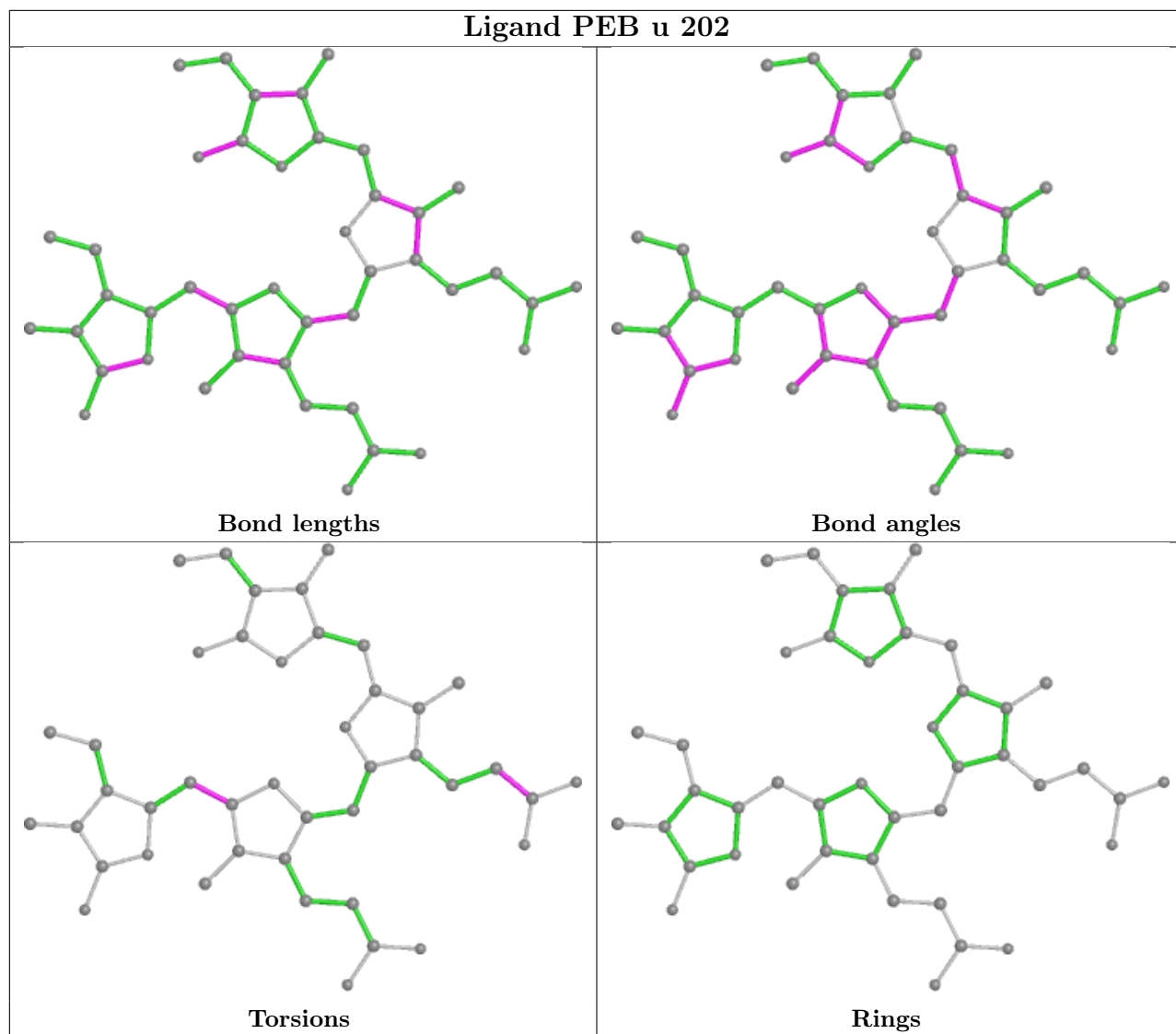


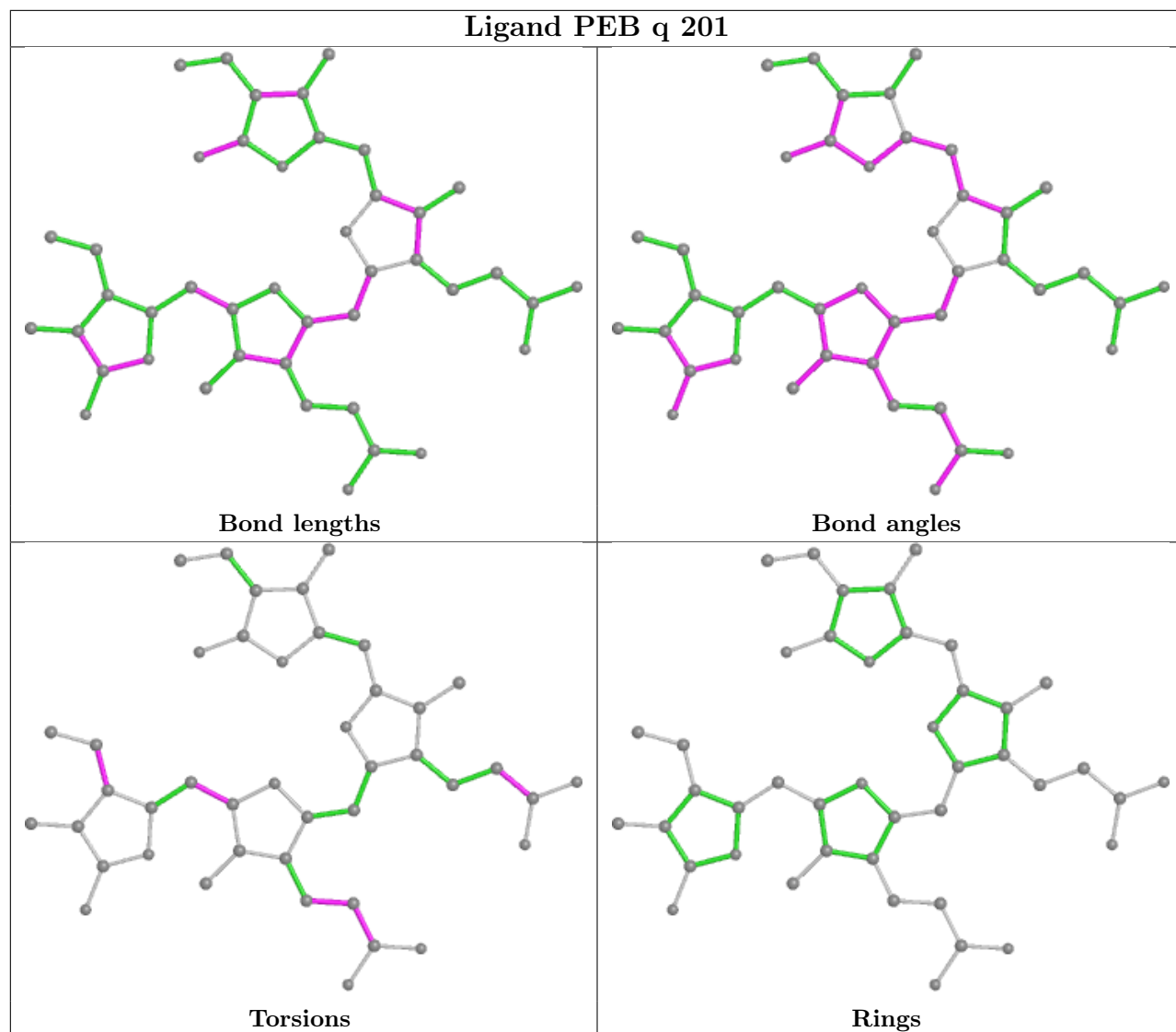


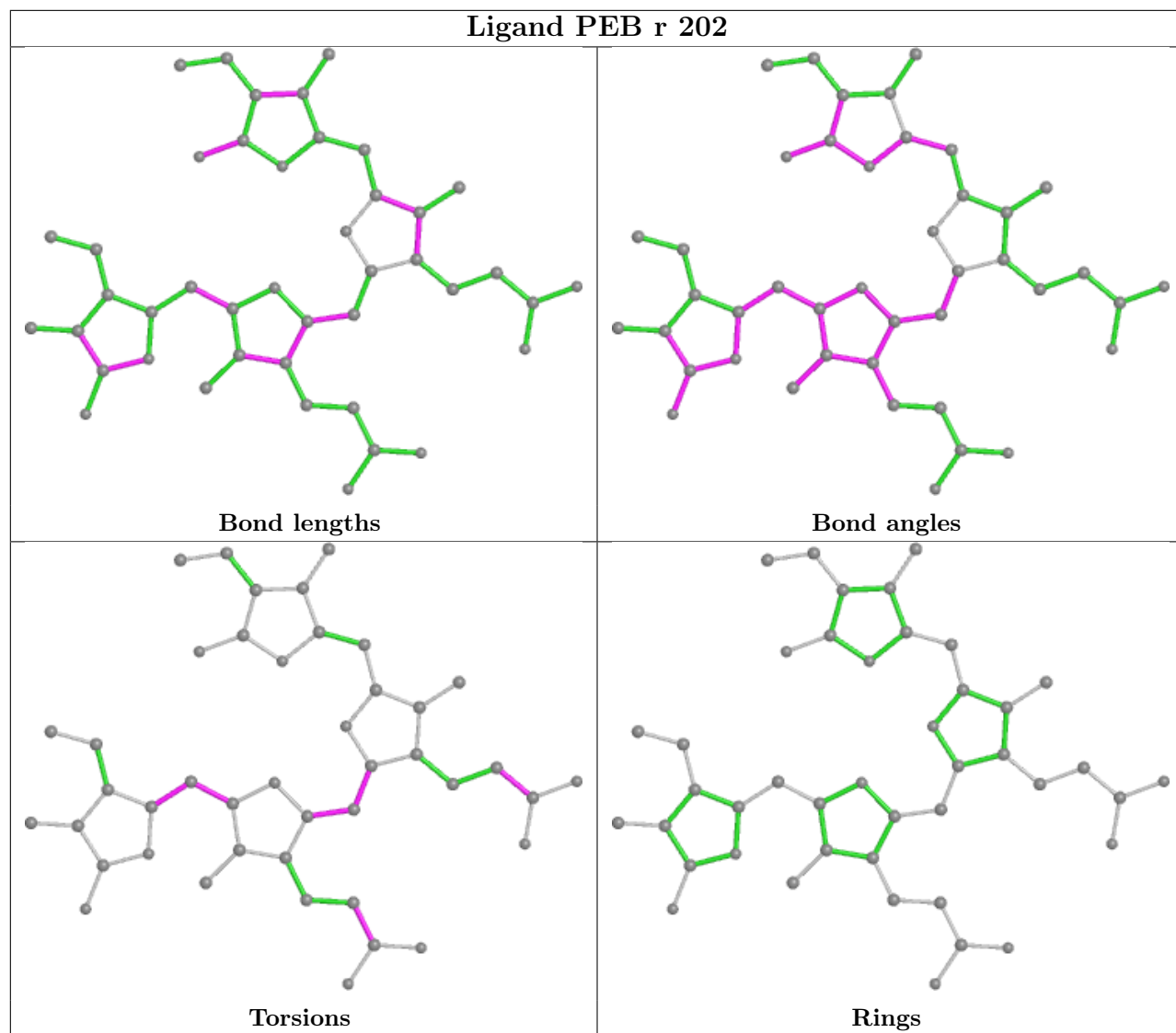


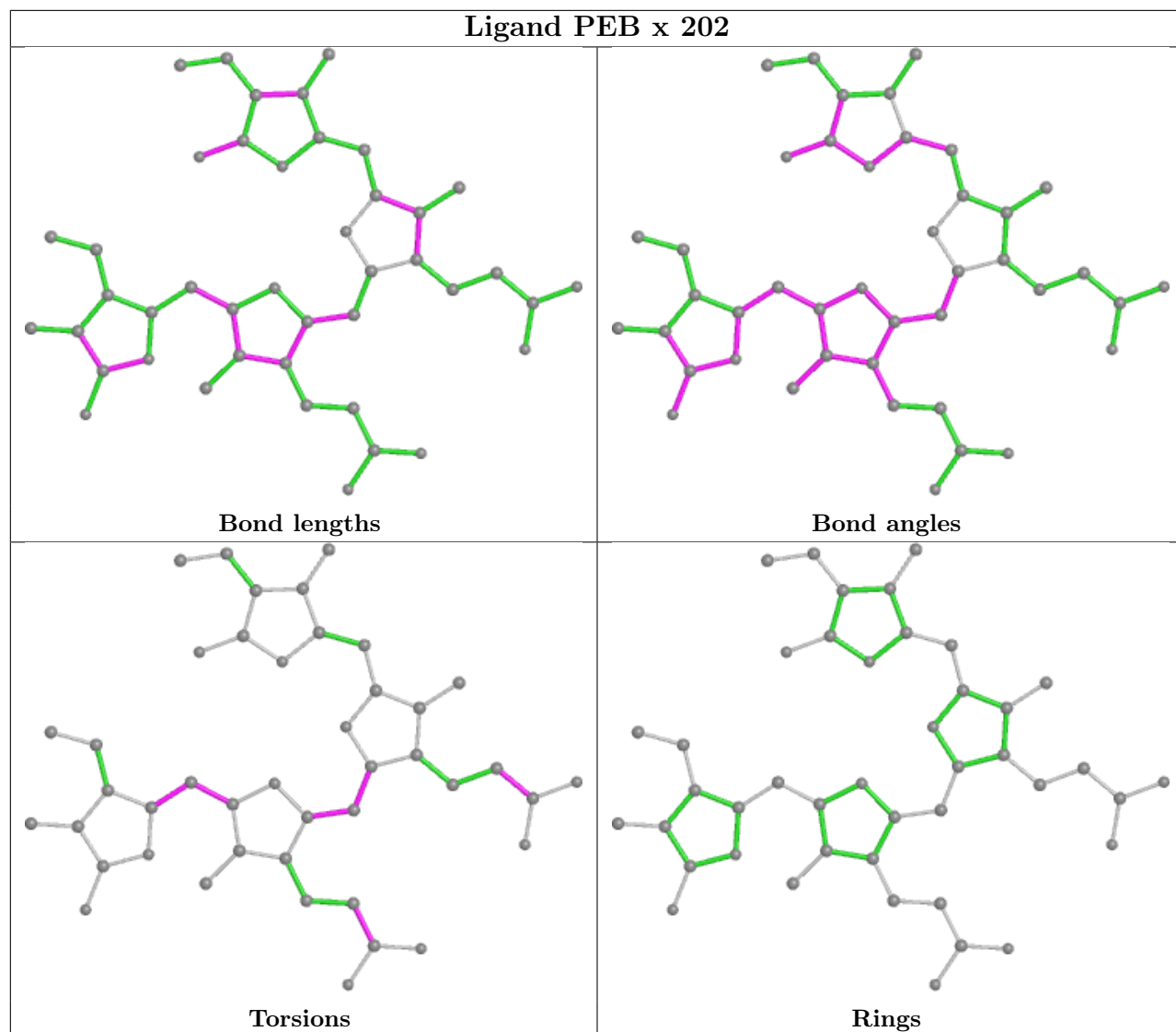


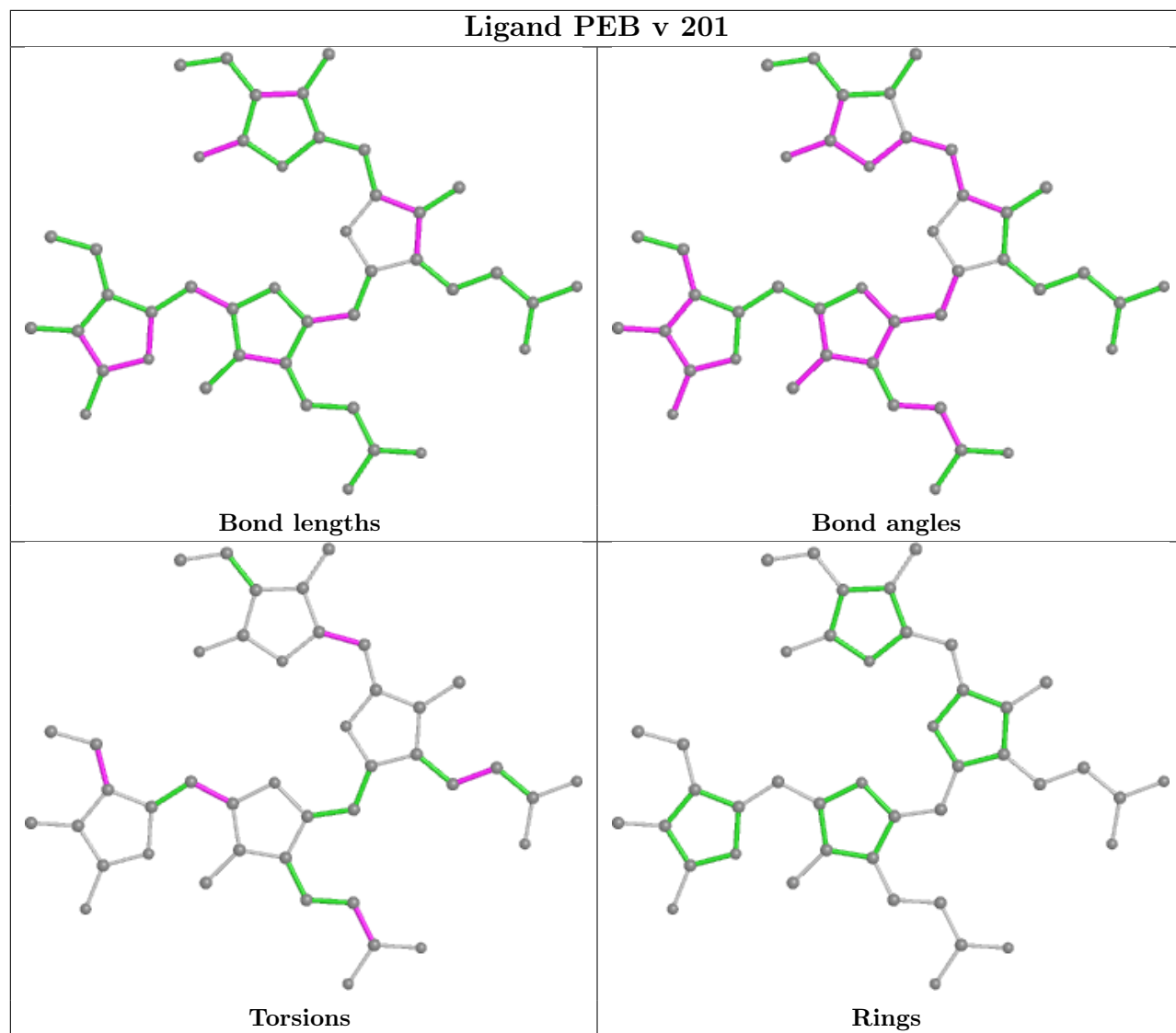


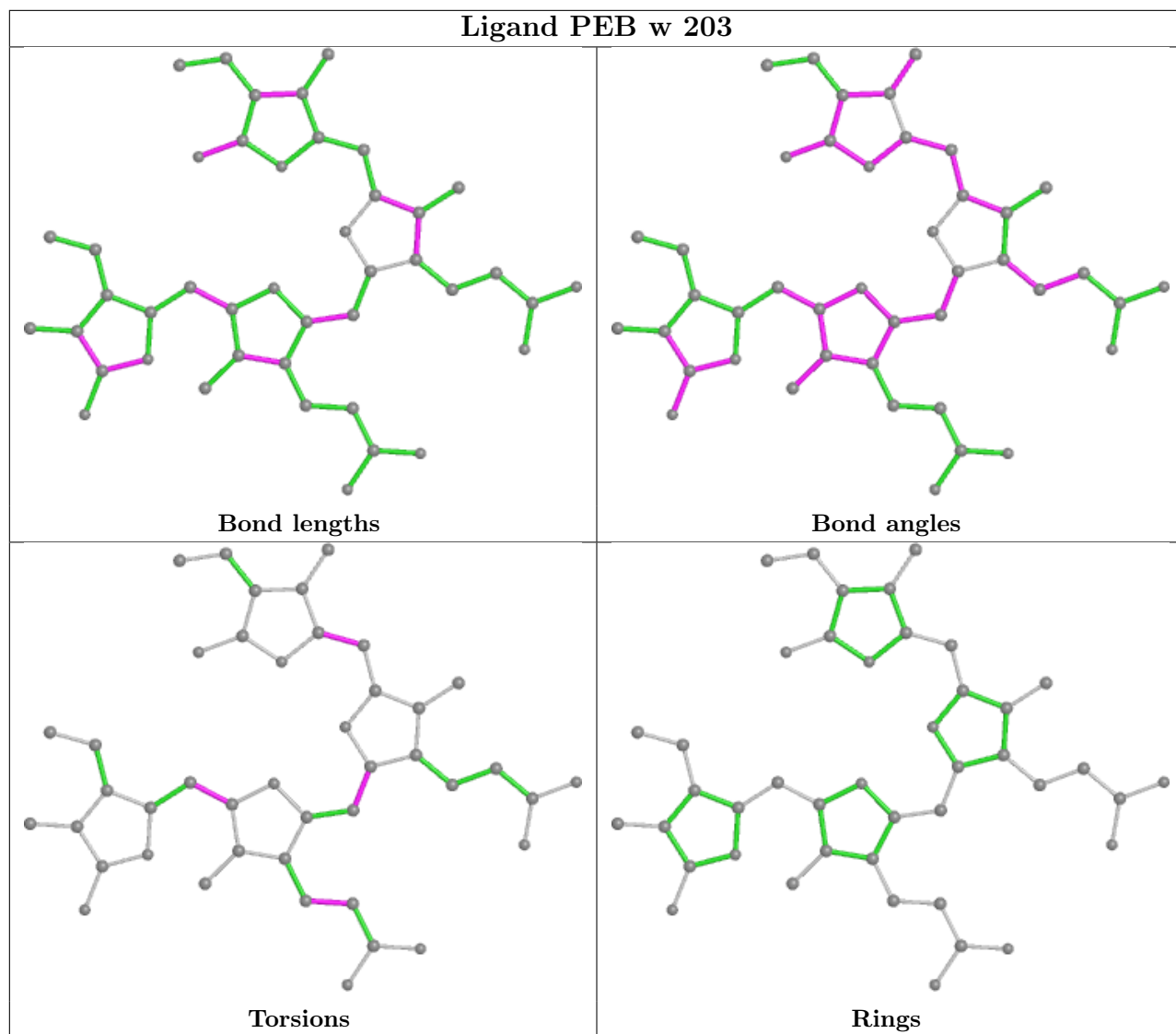




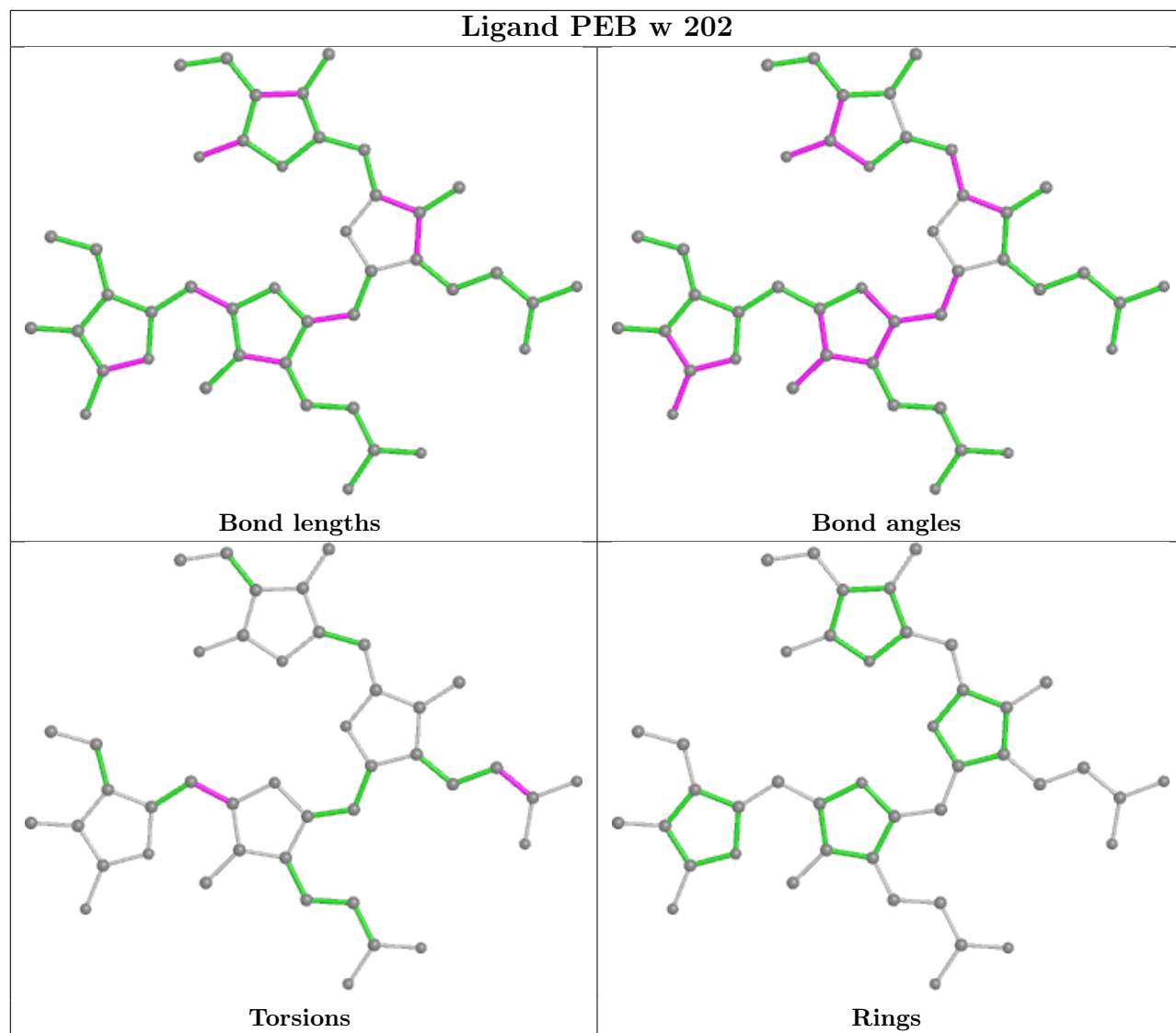


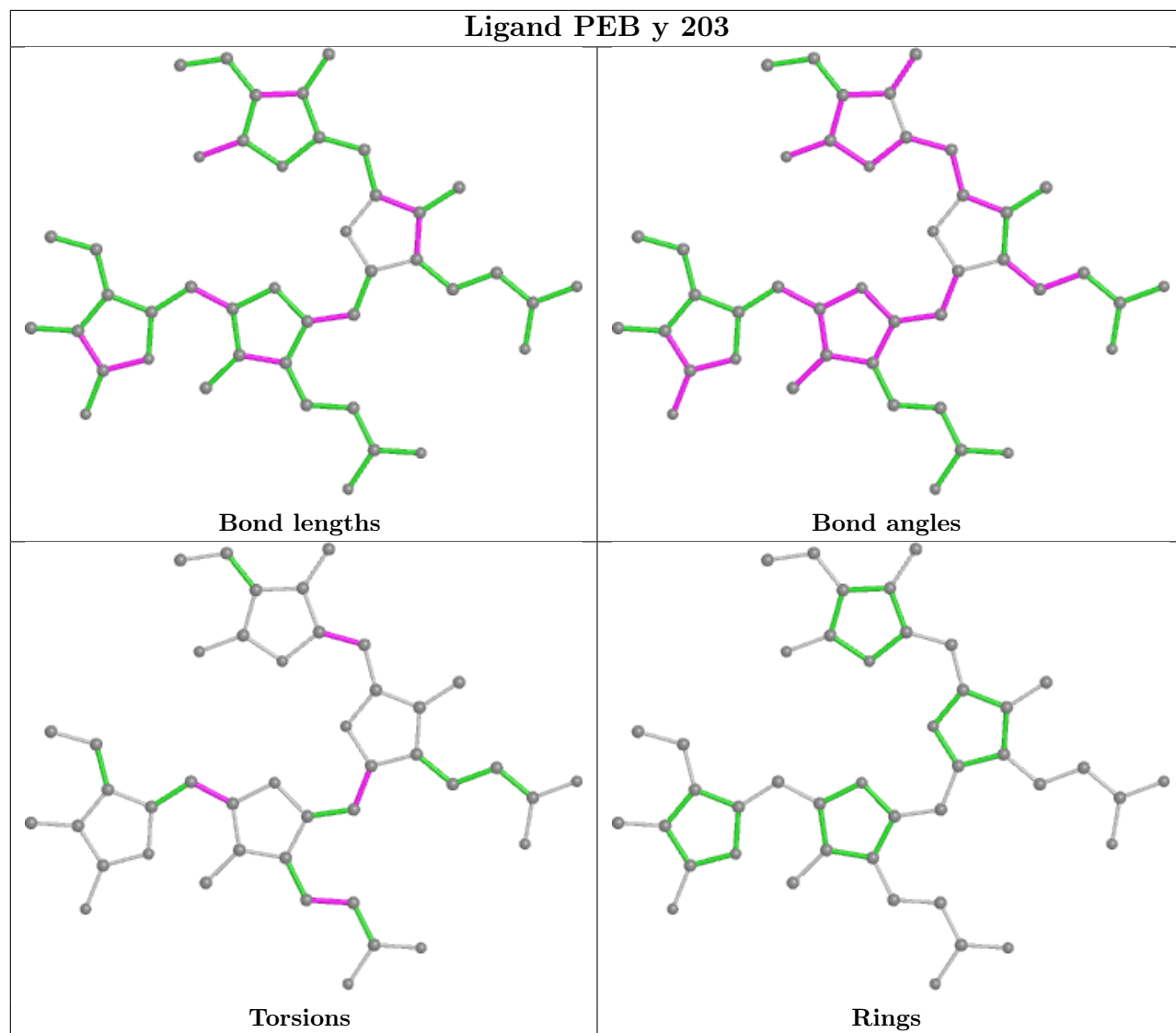


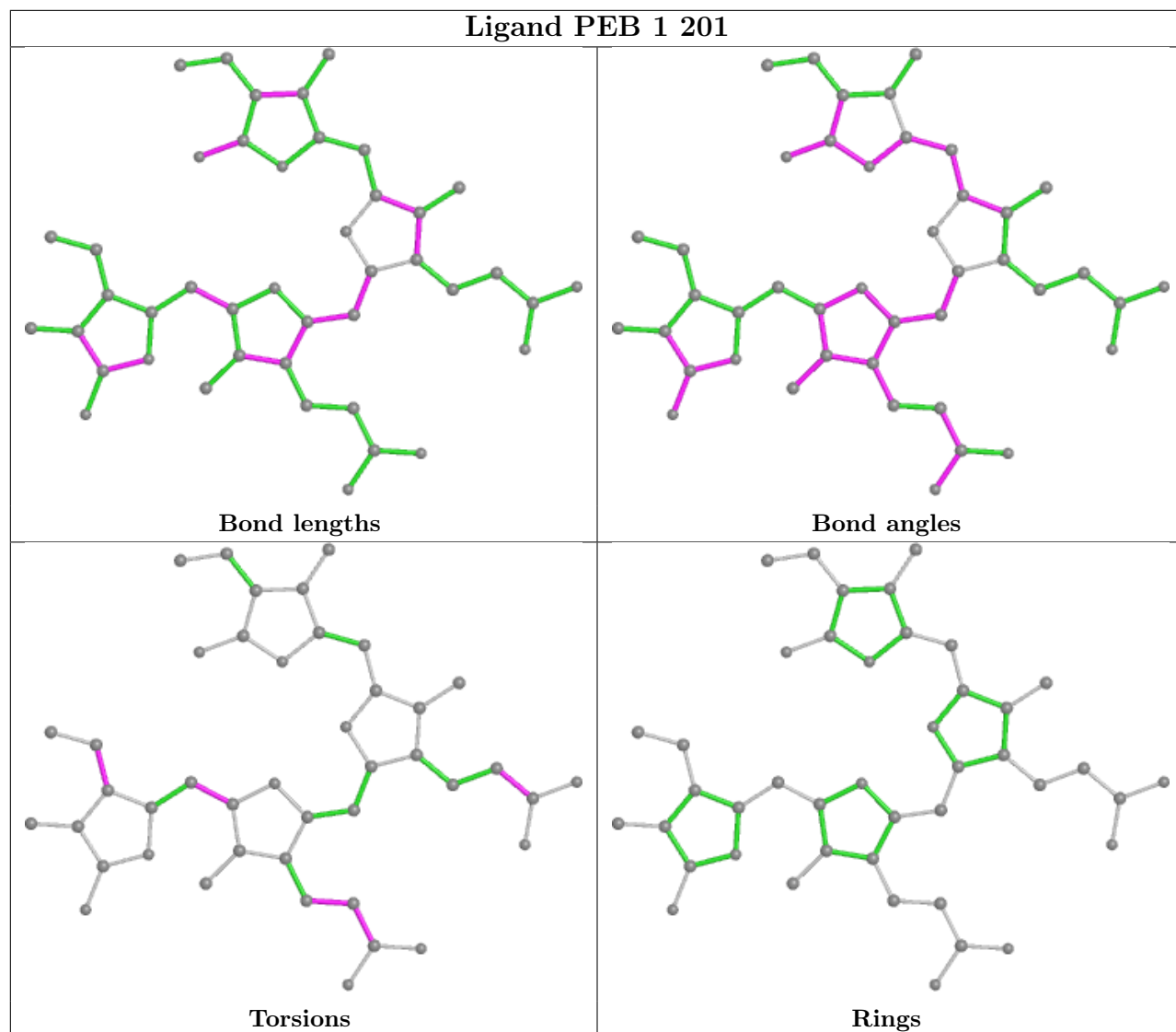


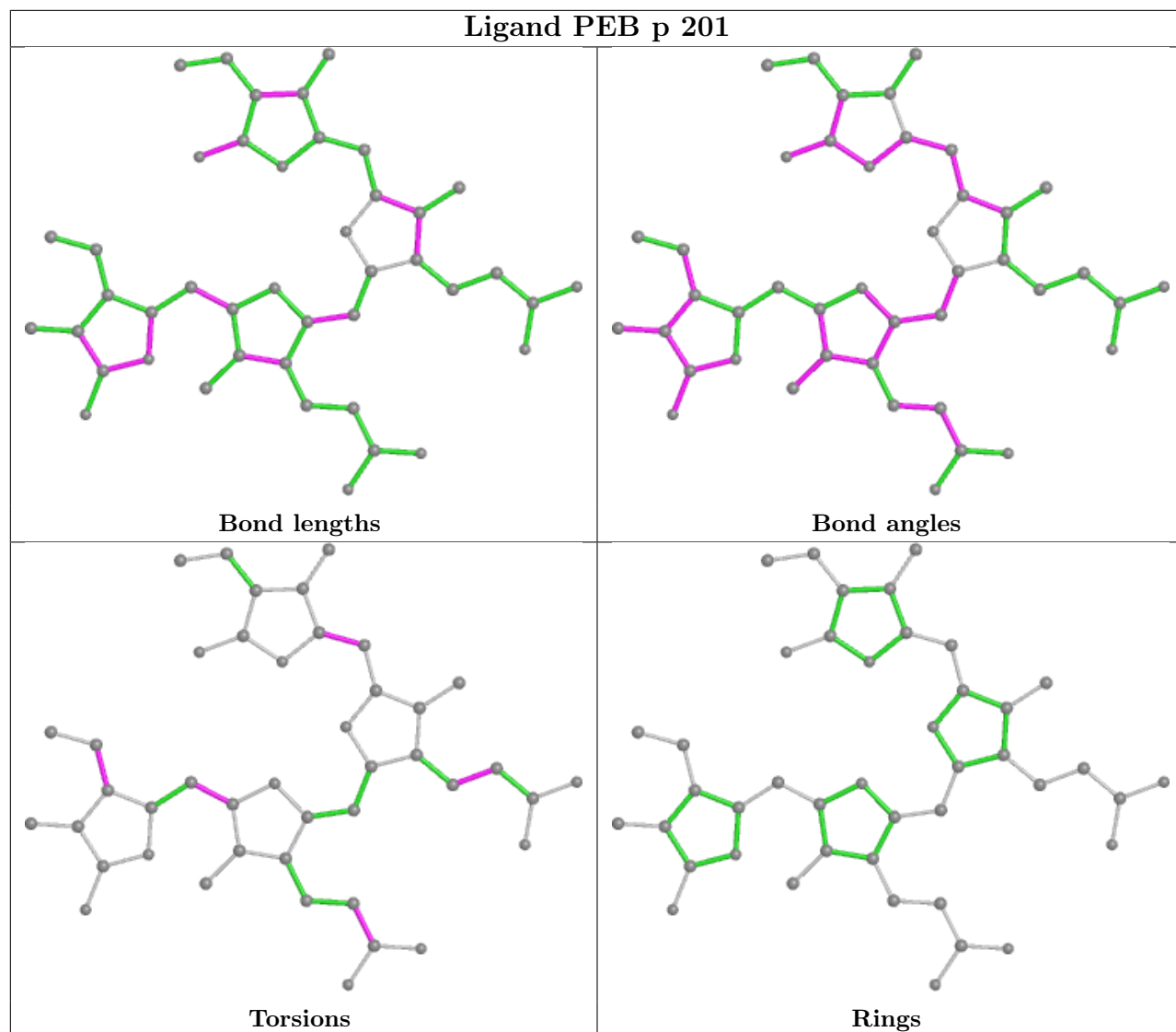


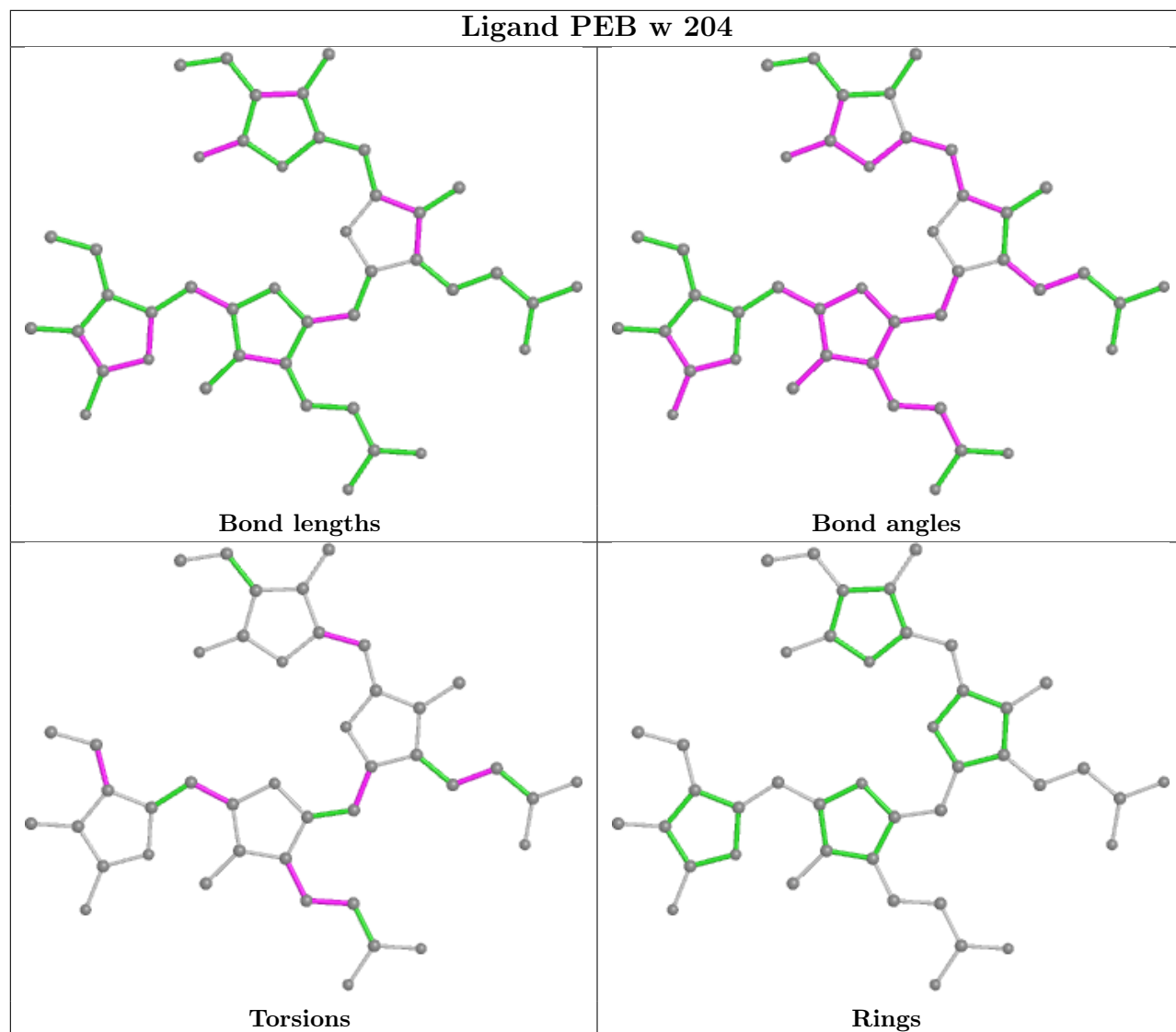


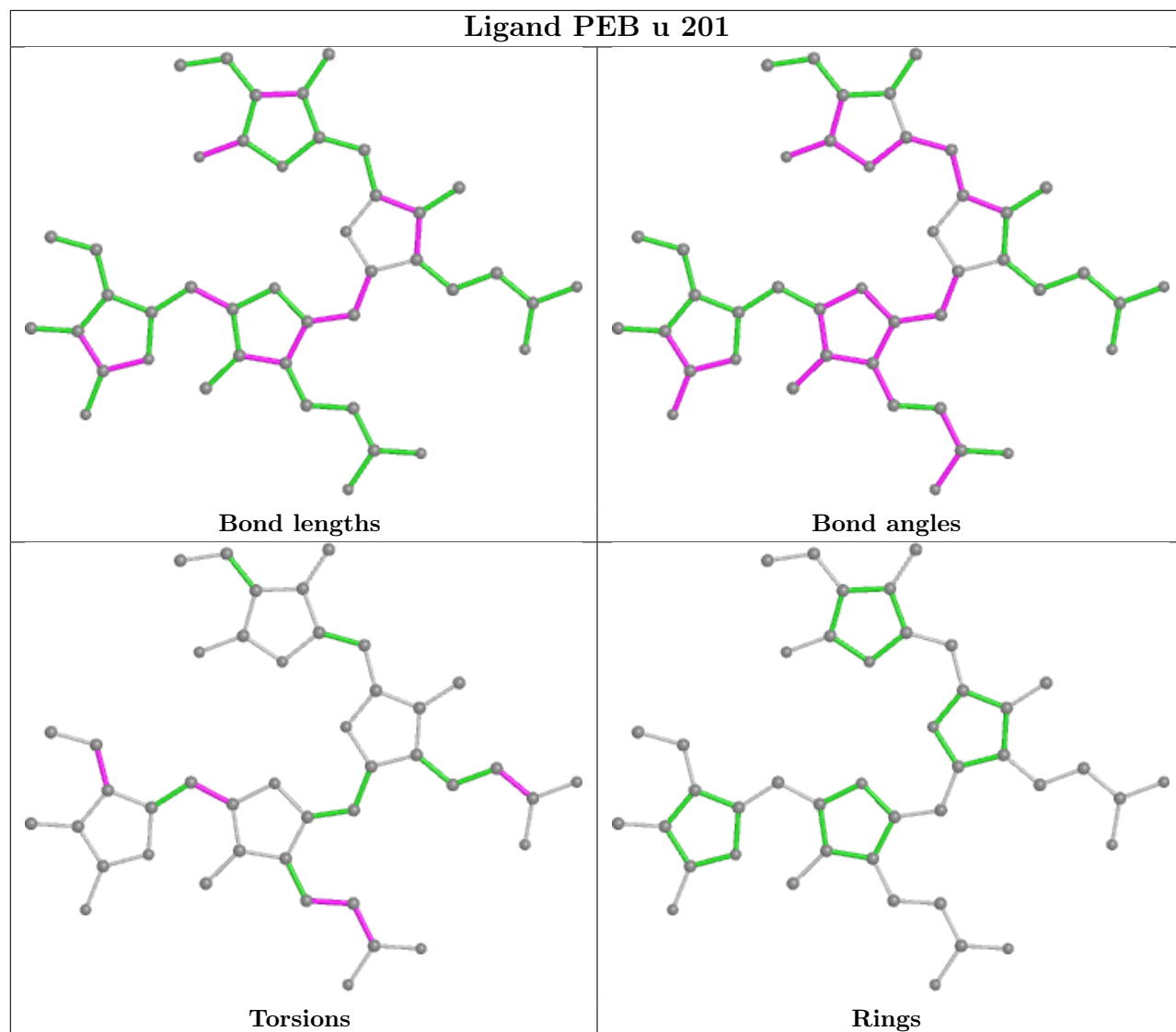


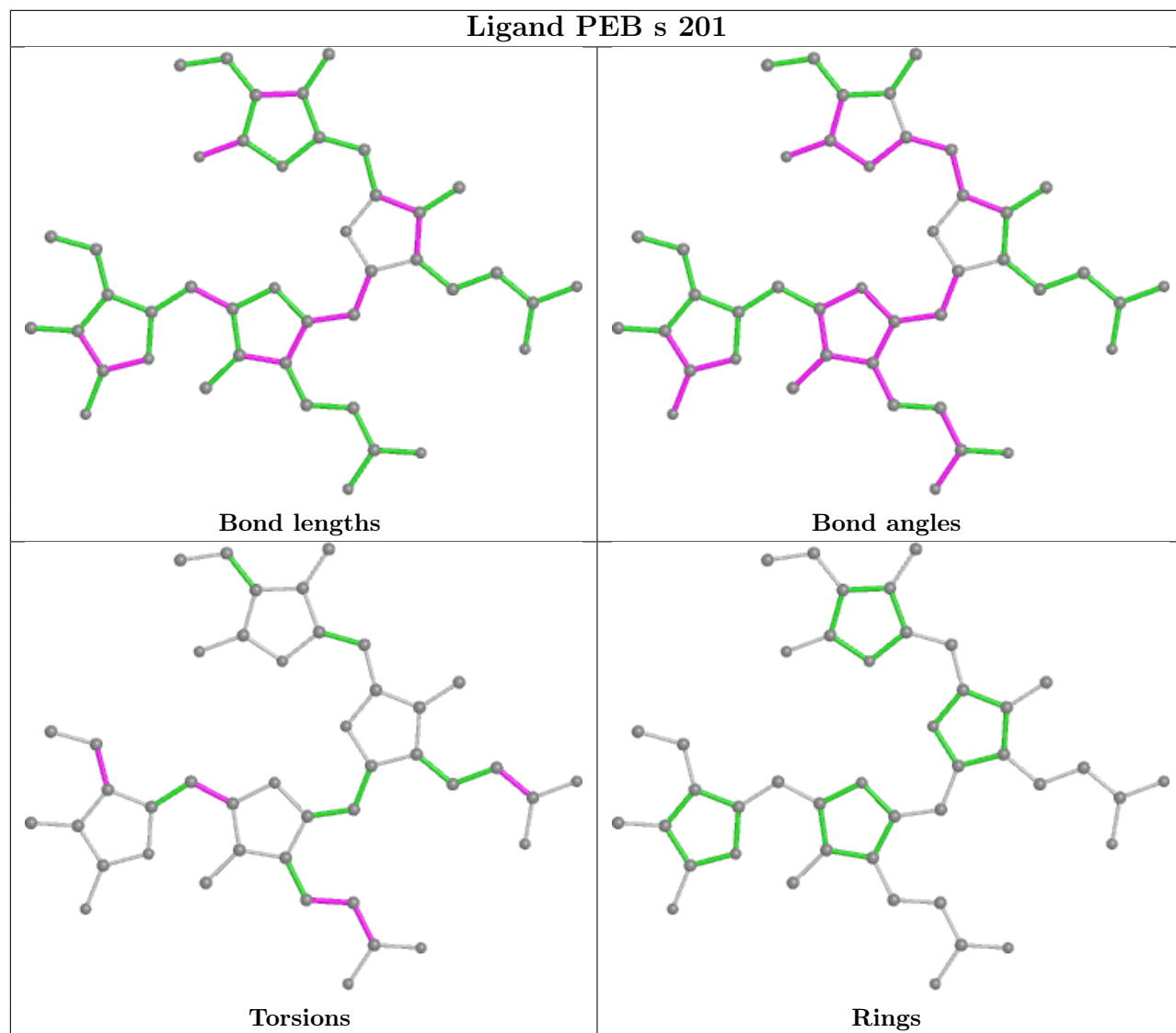


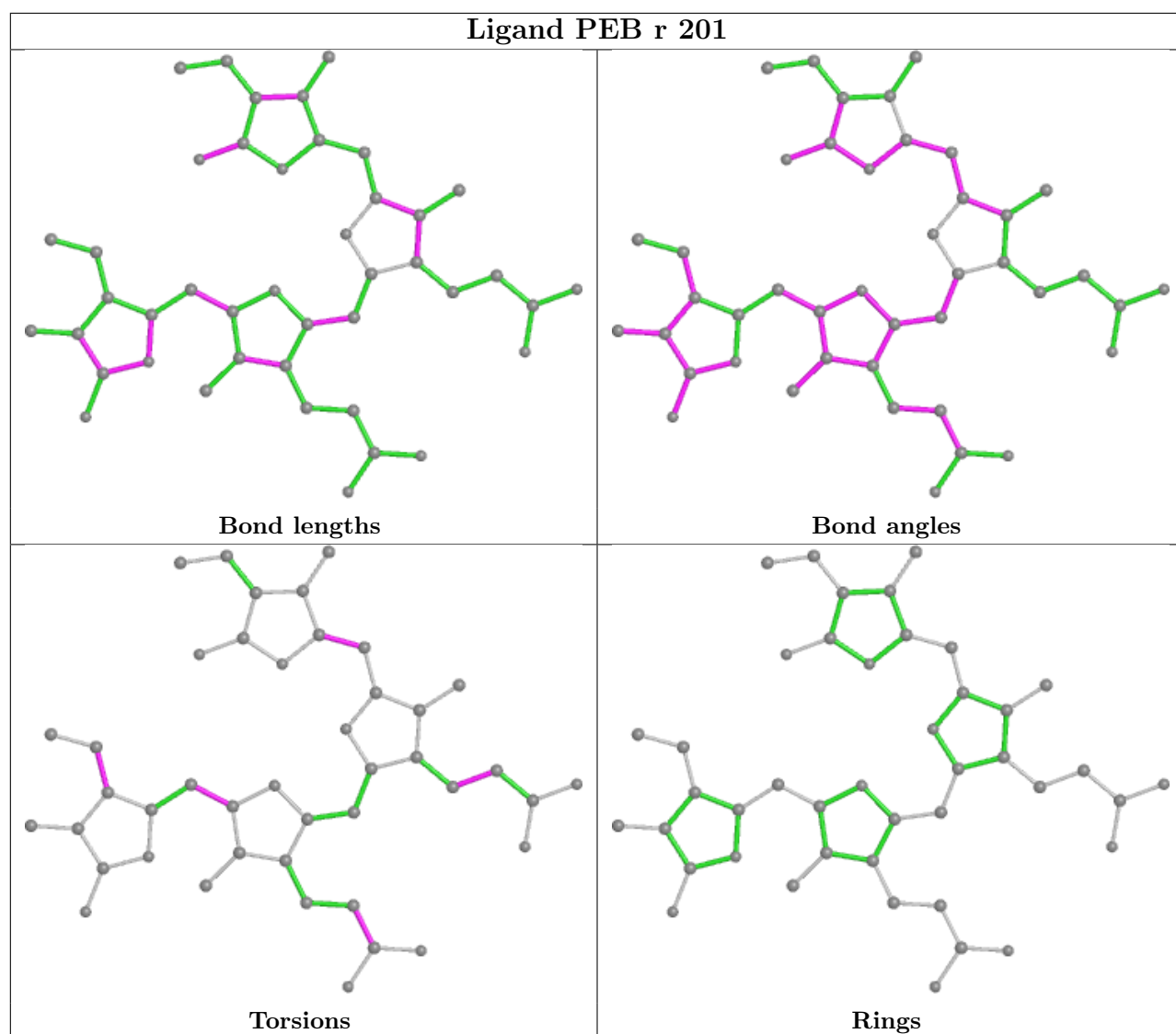




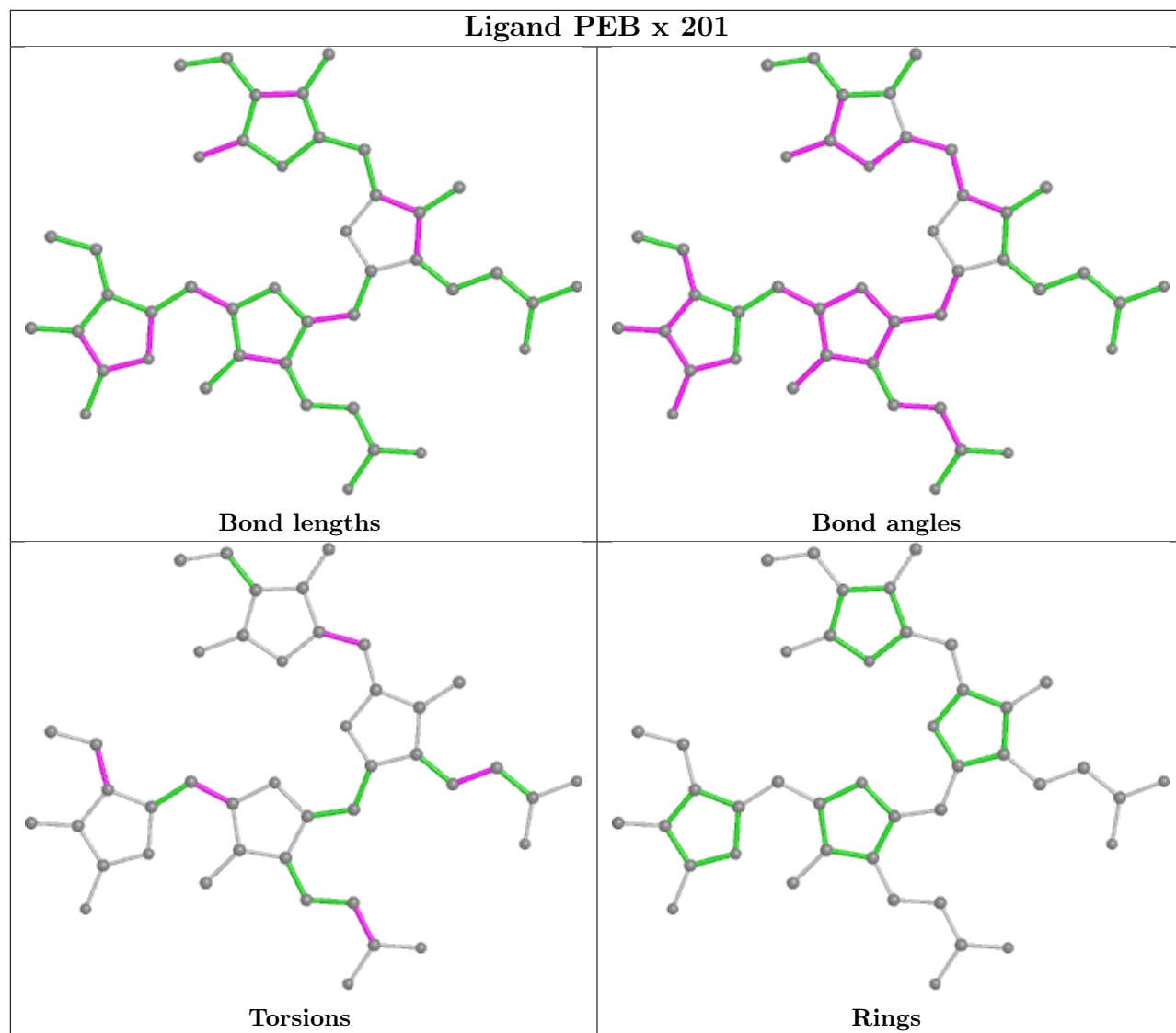


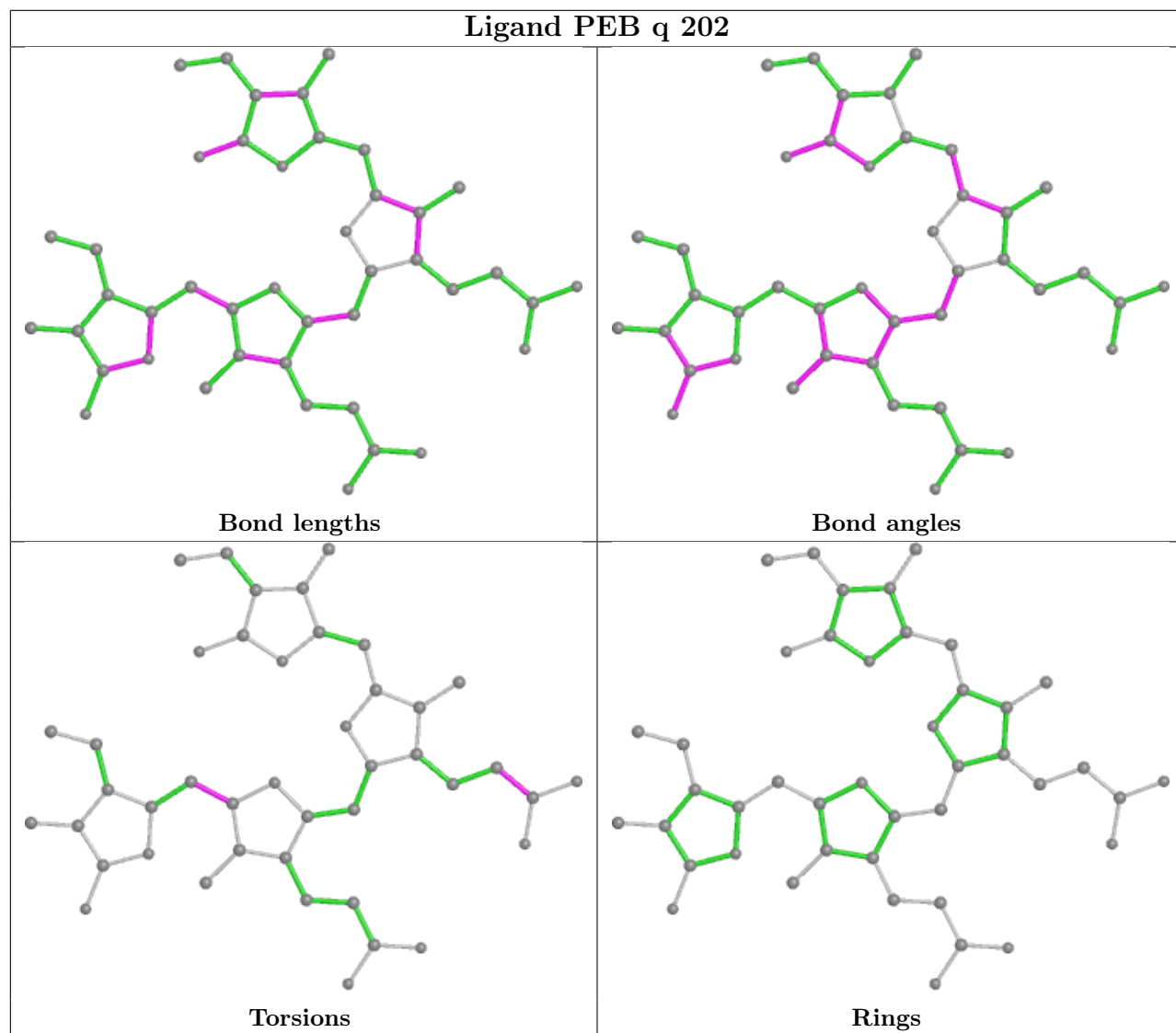


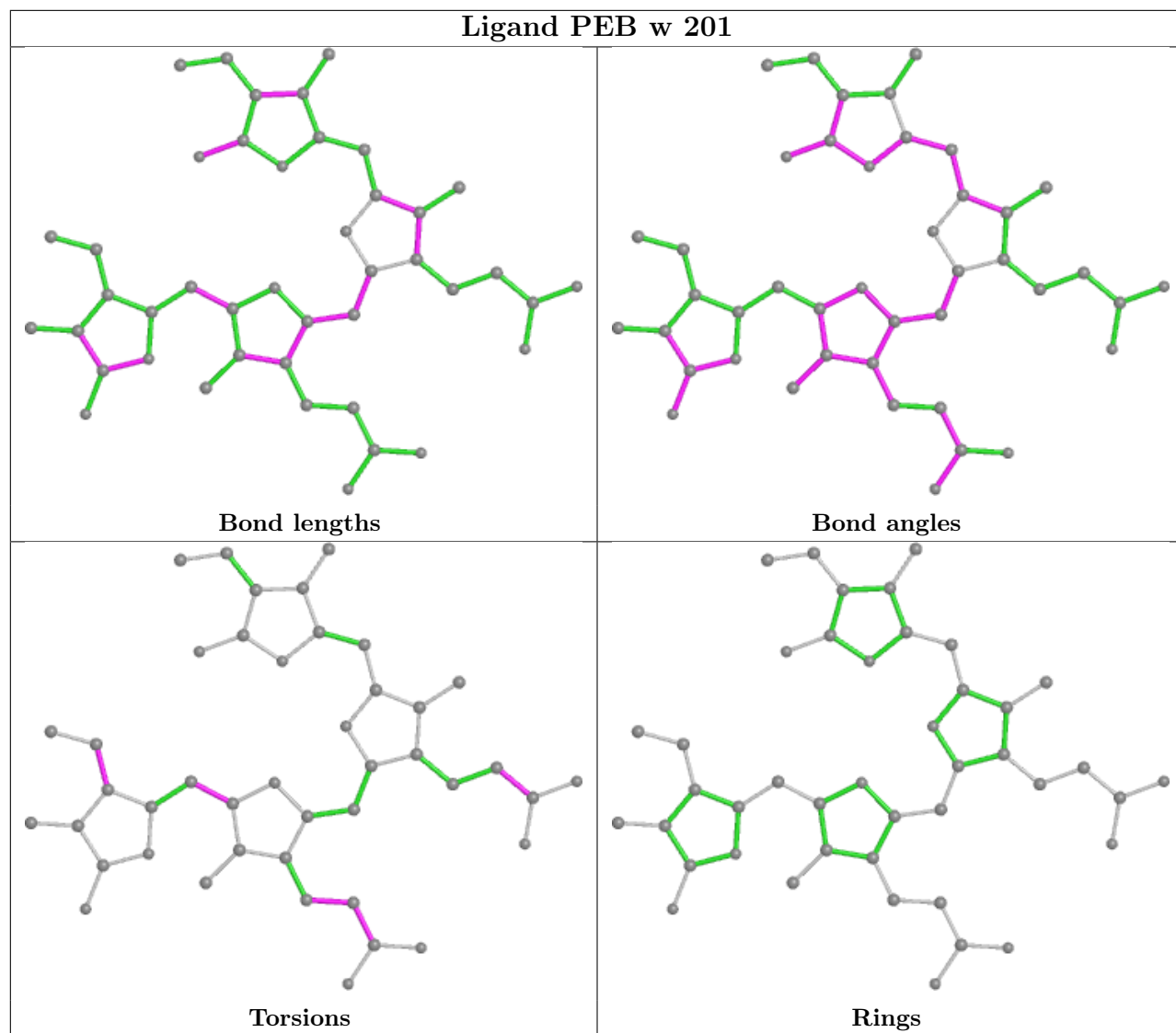


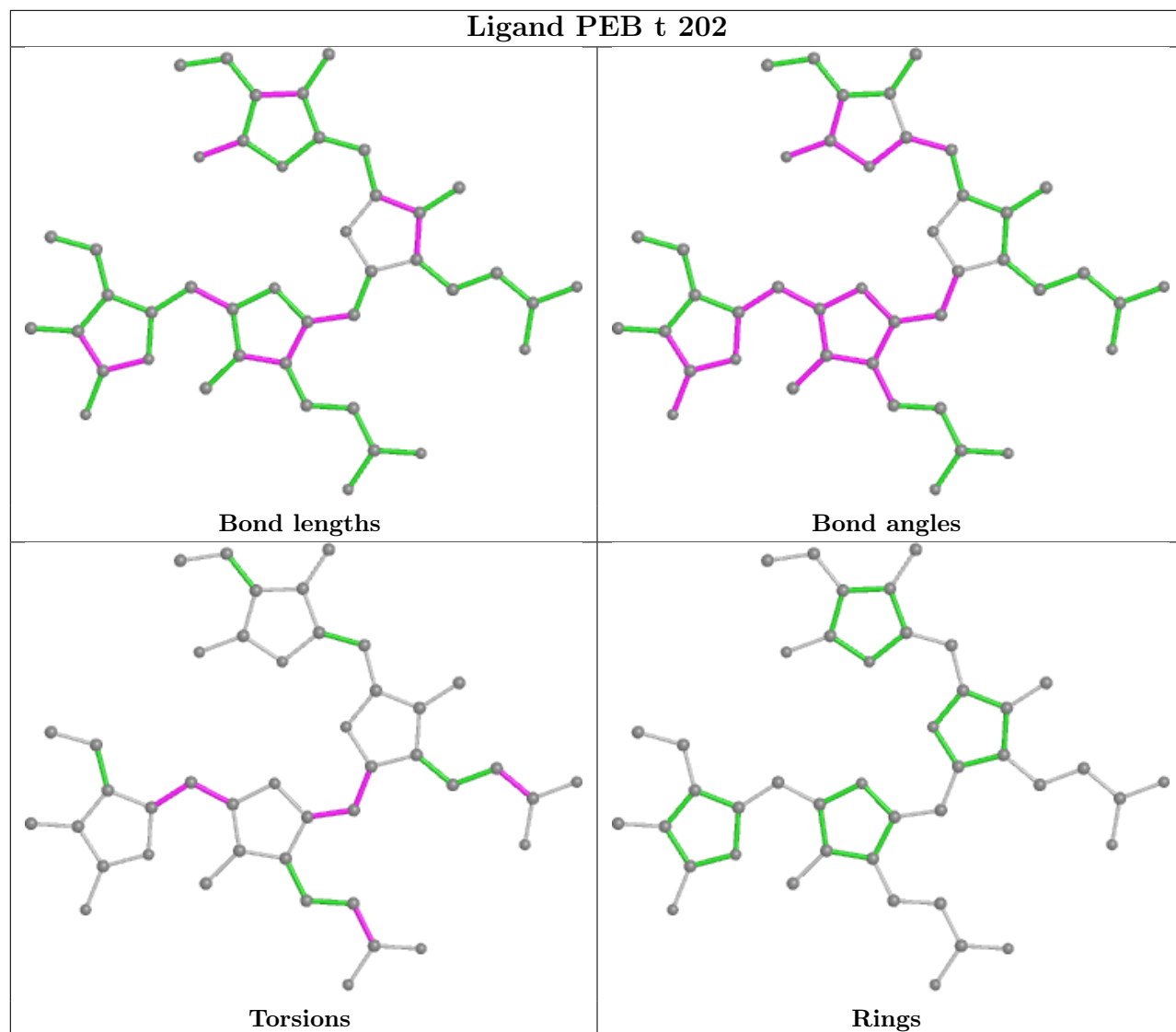


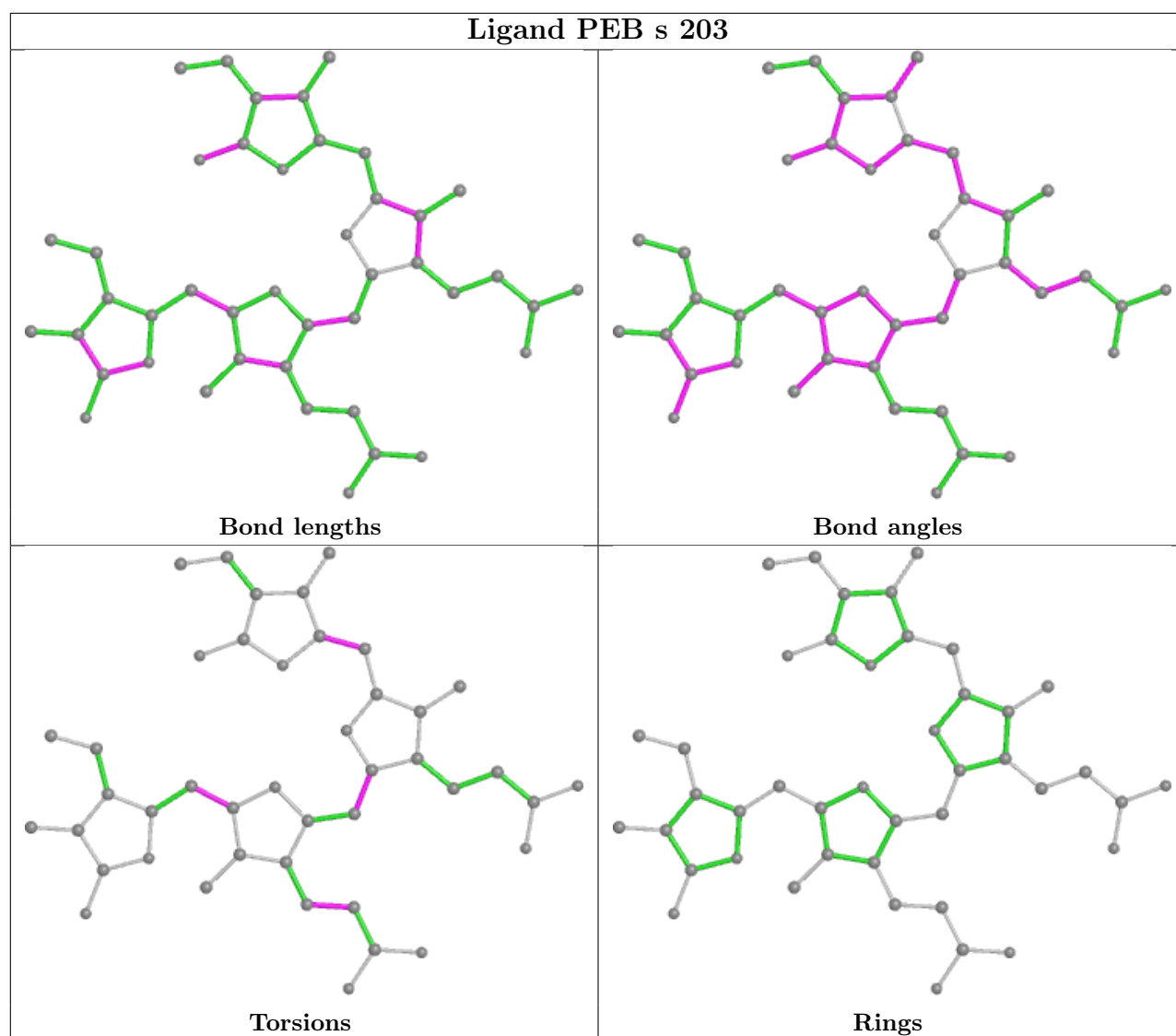












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

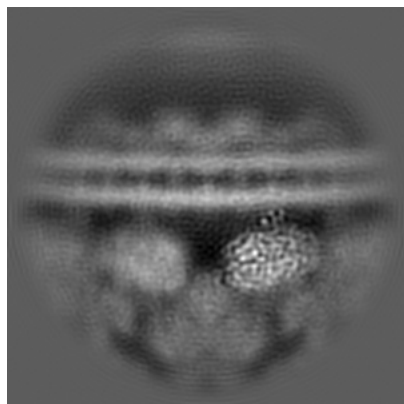
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33558. These allow visual inspection of the internal detail of the map and identification of artifacts.

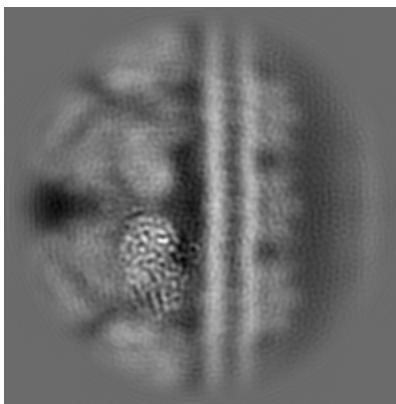
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

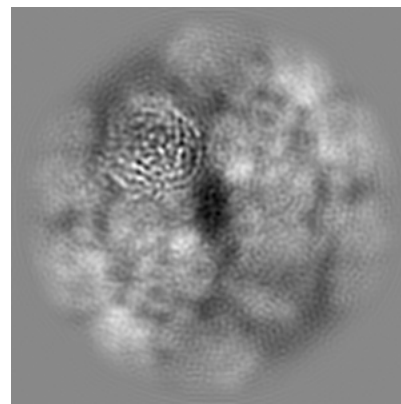
#### 6.1.1 Primary map



X

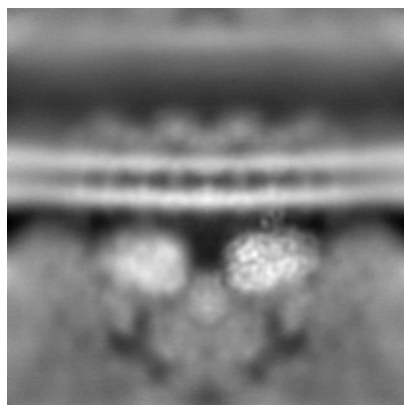


Y

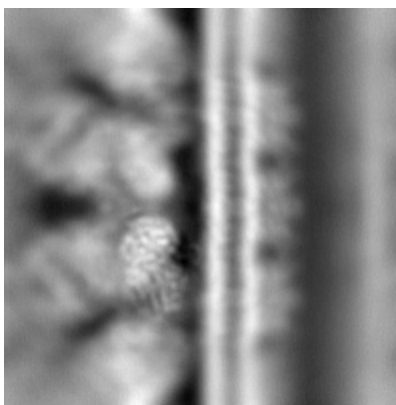


Z

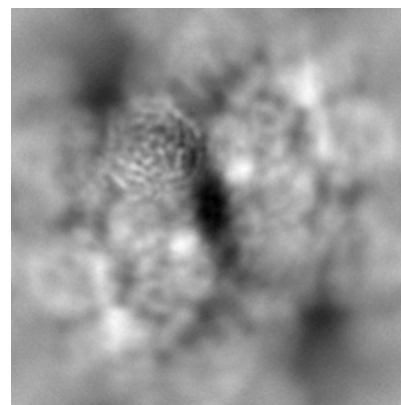
#### 6.1.2 Raw map



X



Y

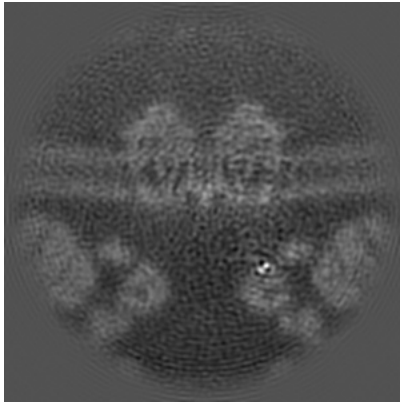


Z

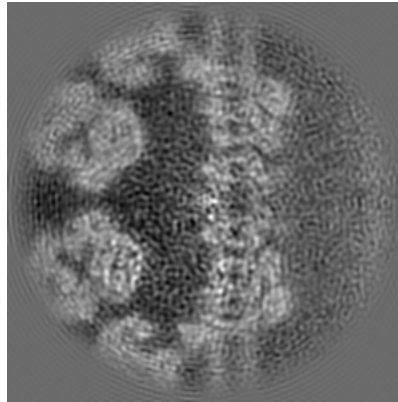
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

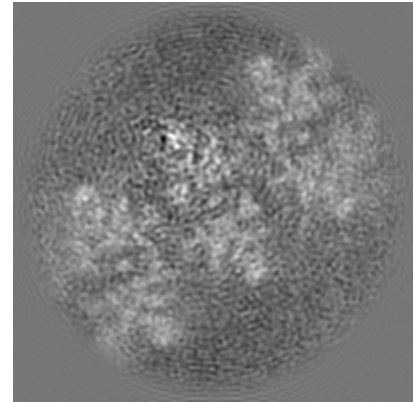
### 6.2.1 Primary map



X Index: 128

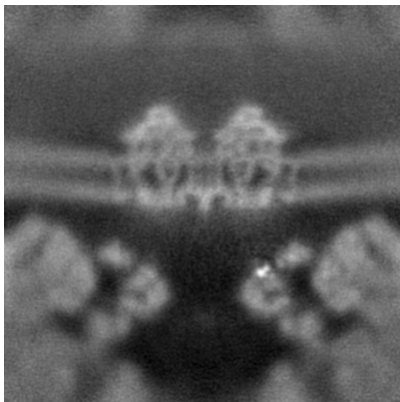


Y Index: 128

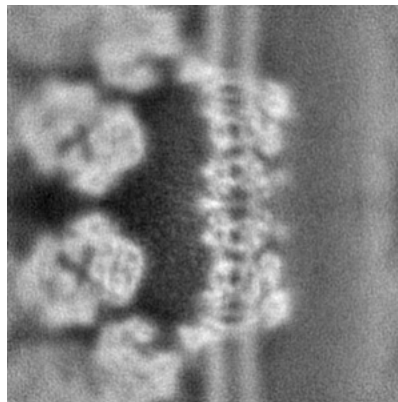


Z Index: 128

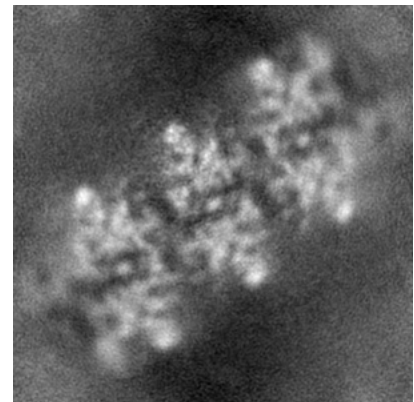
### 6.2.2 Raw map



X Index: 128



Y Index: 128

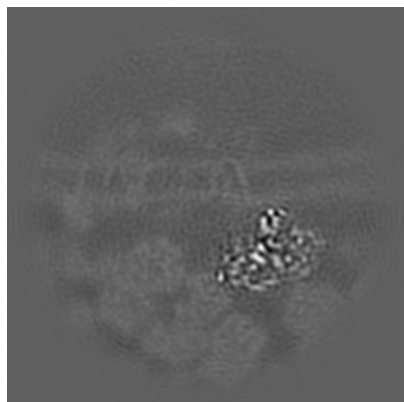


Z Index: 128

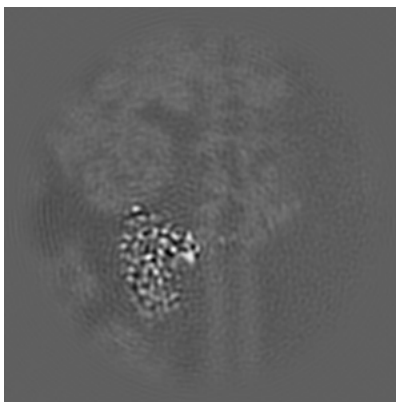
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

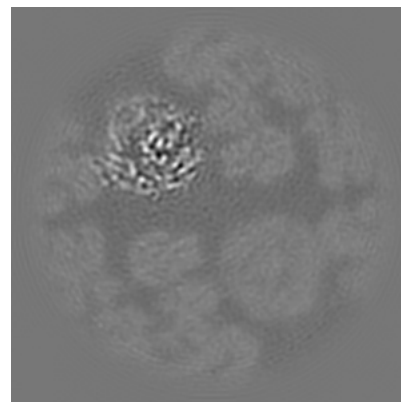
### 6.3.1 Primary map



X Index: 97

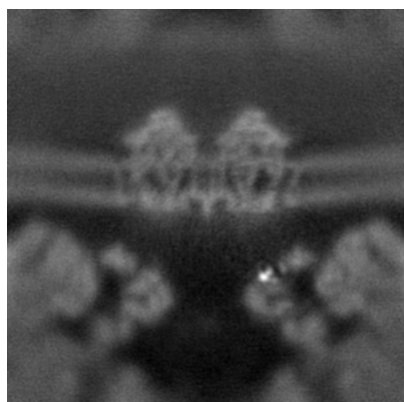


Y Index: 164

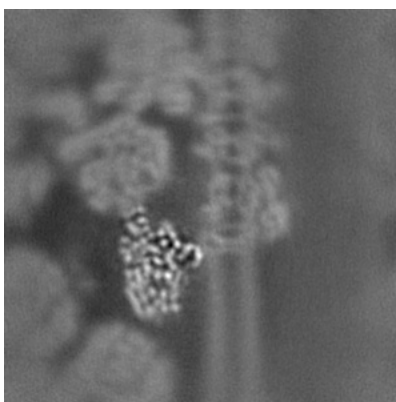


Z Index: 97

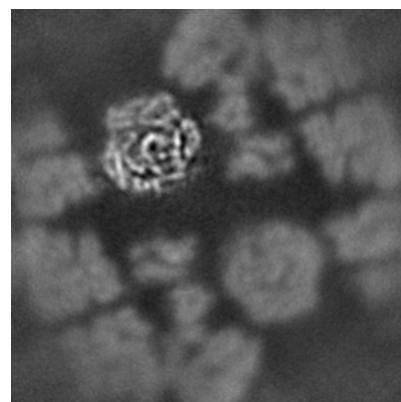
### 6.3.2 Raw map



X Index: 127



Y Index: 168



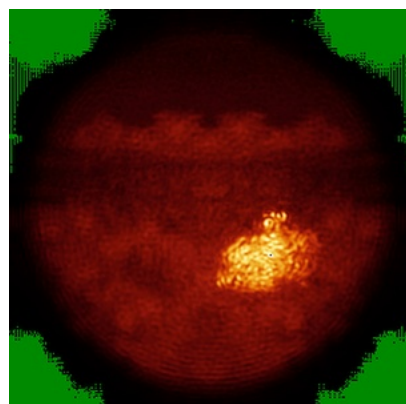
Z Index: 103

The images above show the largest variance slices of the map in three orthogonal directions.

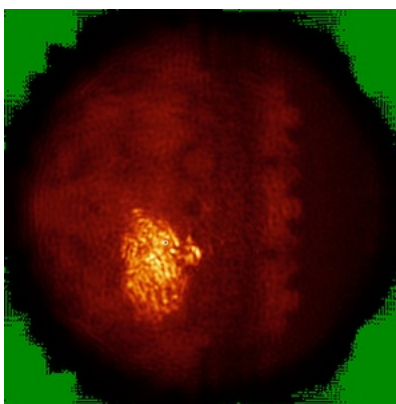


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

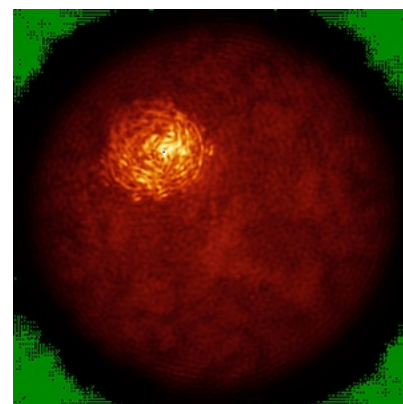
### 6.4.1 Primary map



X

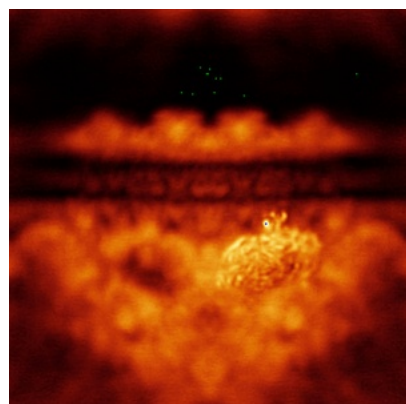


Y

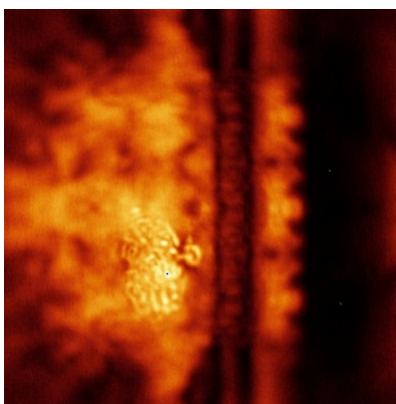


Z

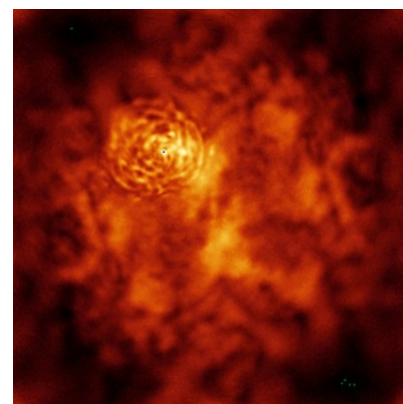
### 6.4.2 Raw map



X



Y

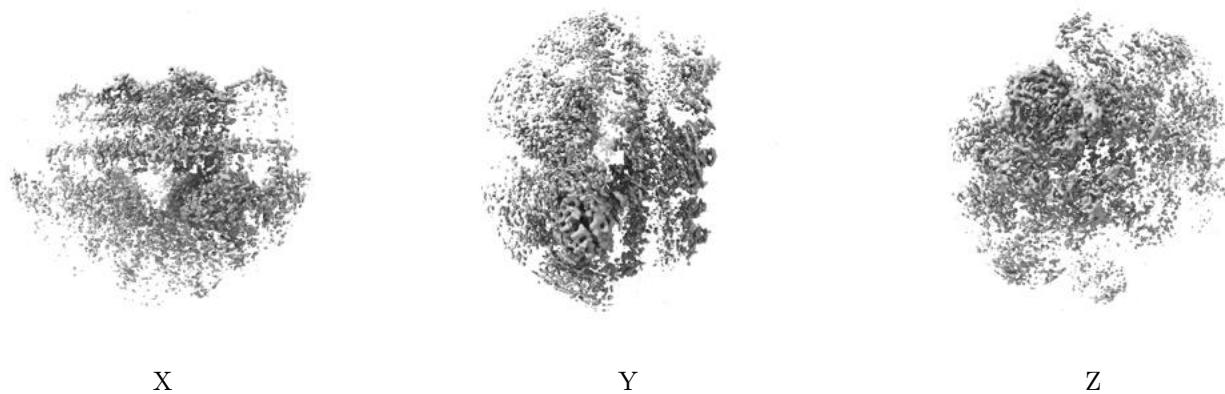


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

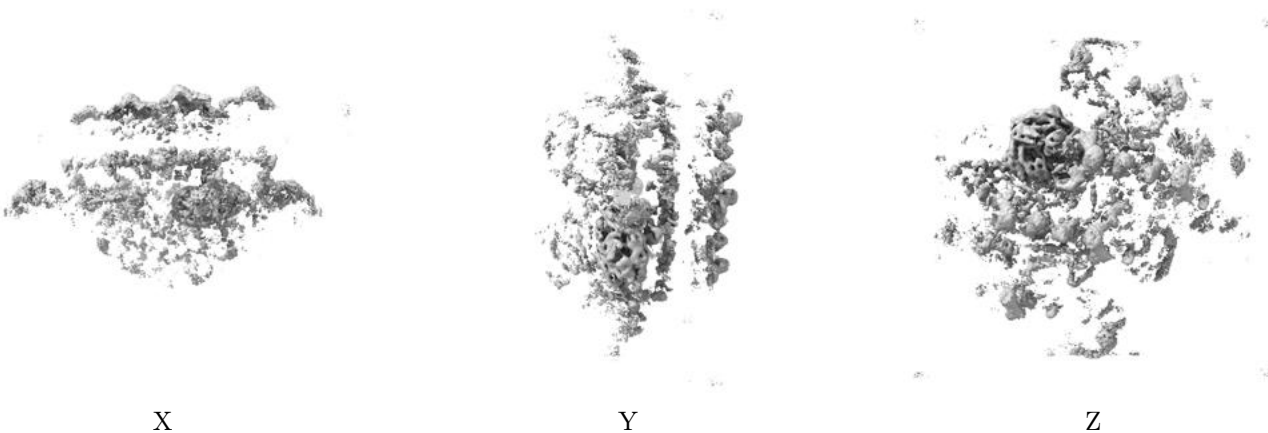
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.152. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

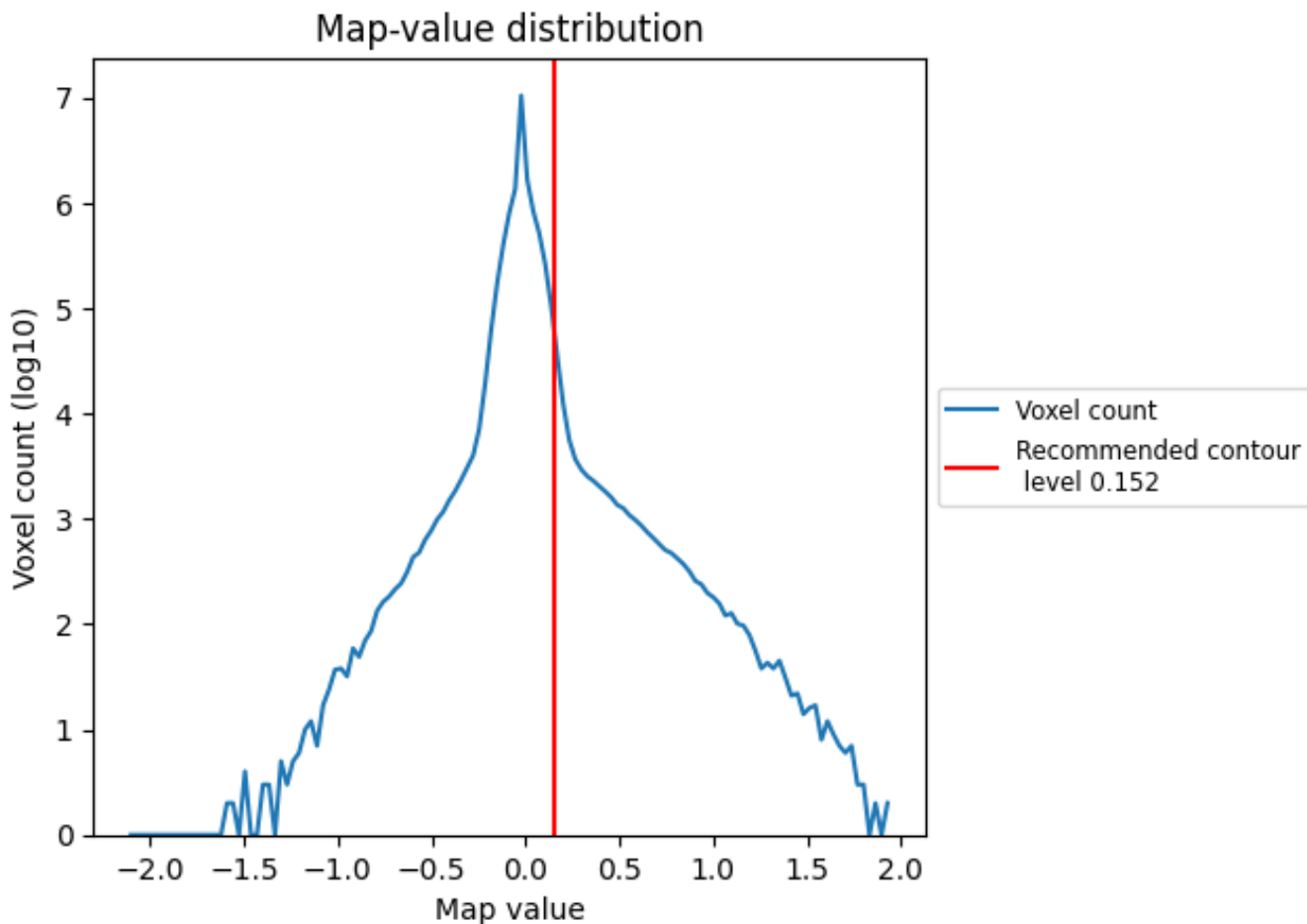
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

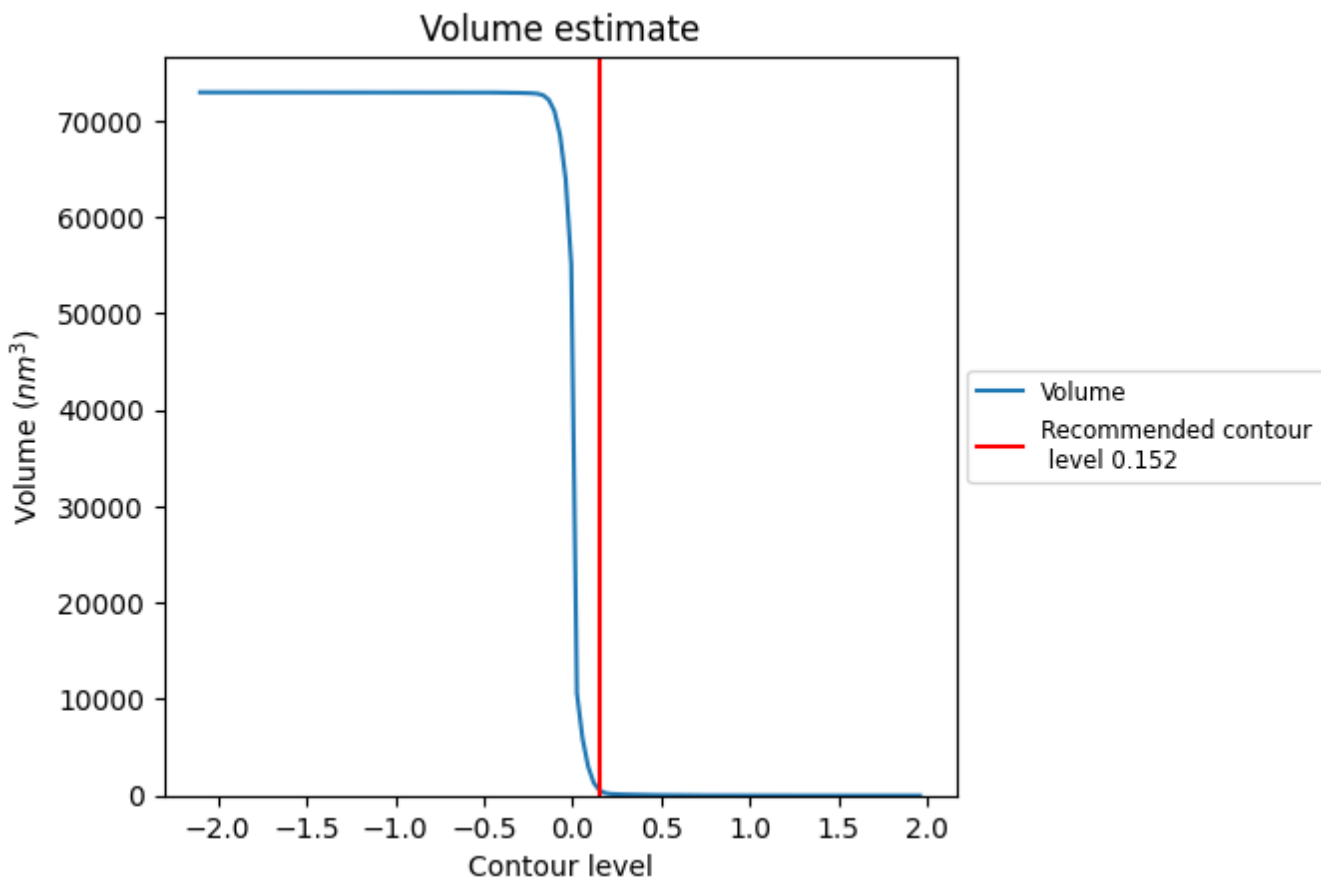
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

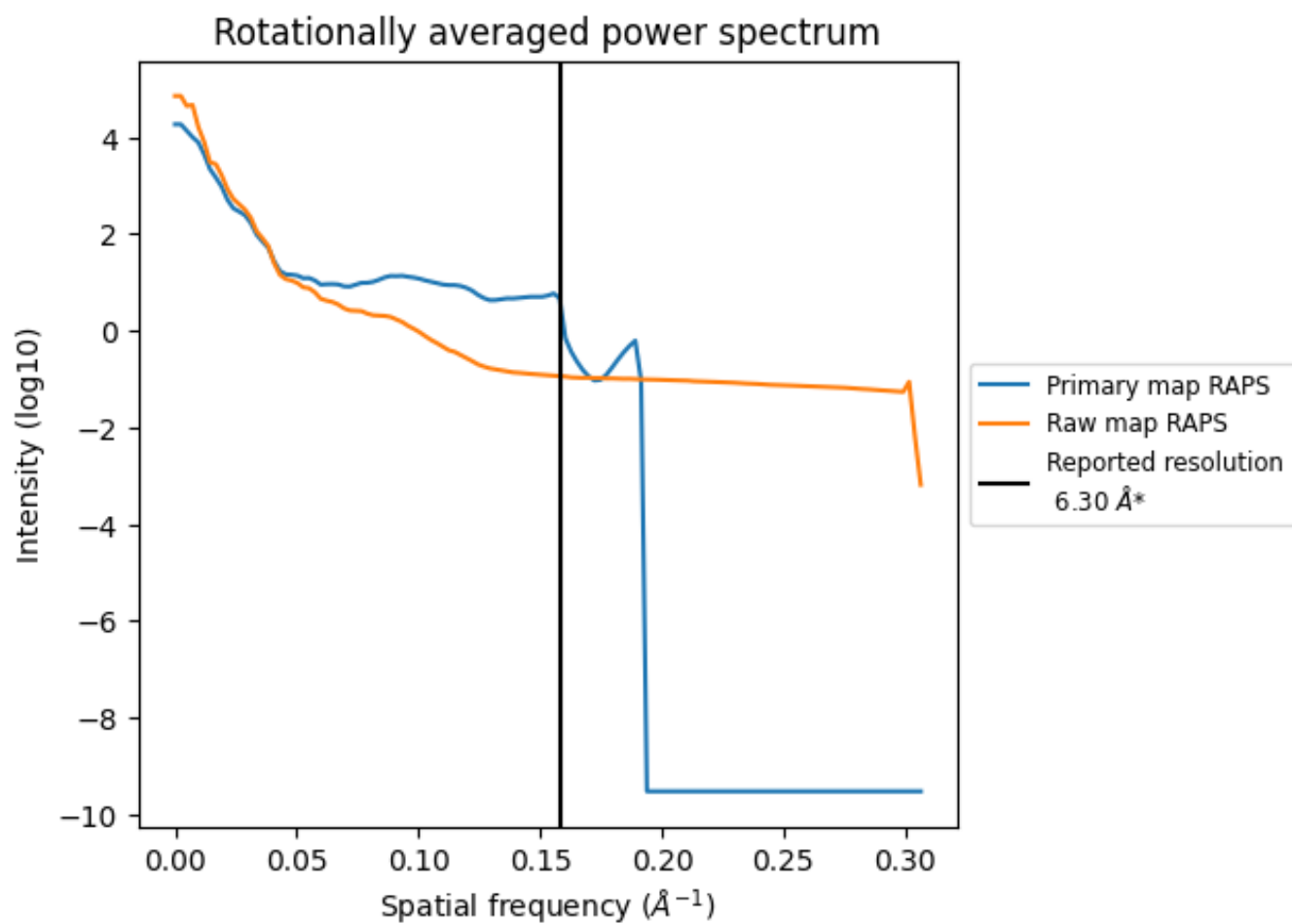
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 542 nm<sup>3</sup>; this corresponds to an approximate mass of 490 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [\(i\)](#)

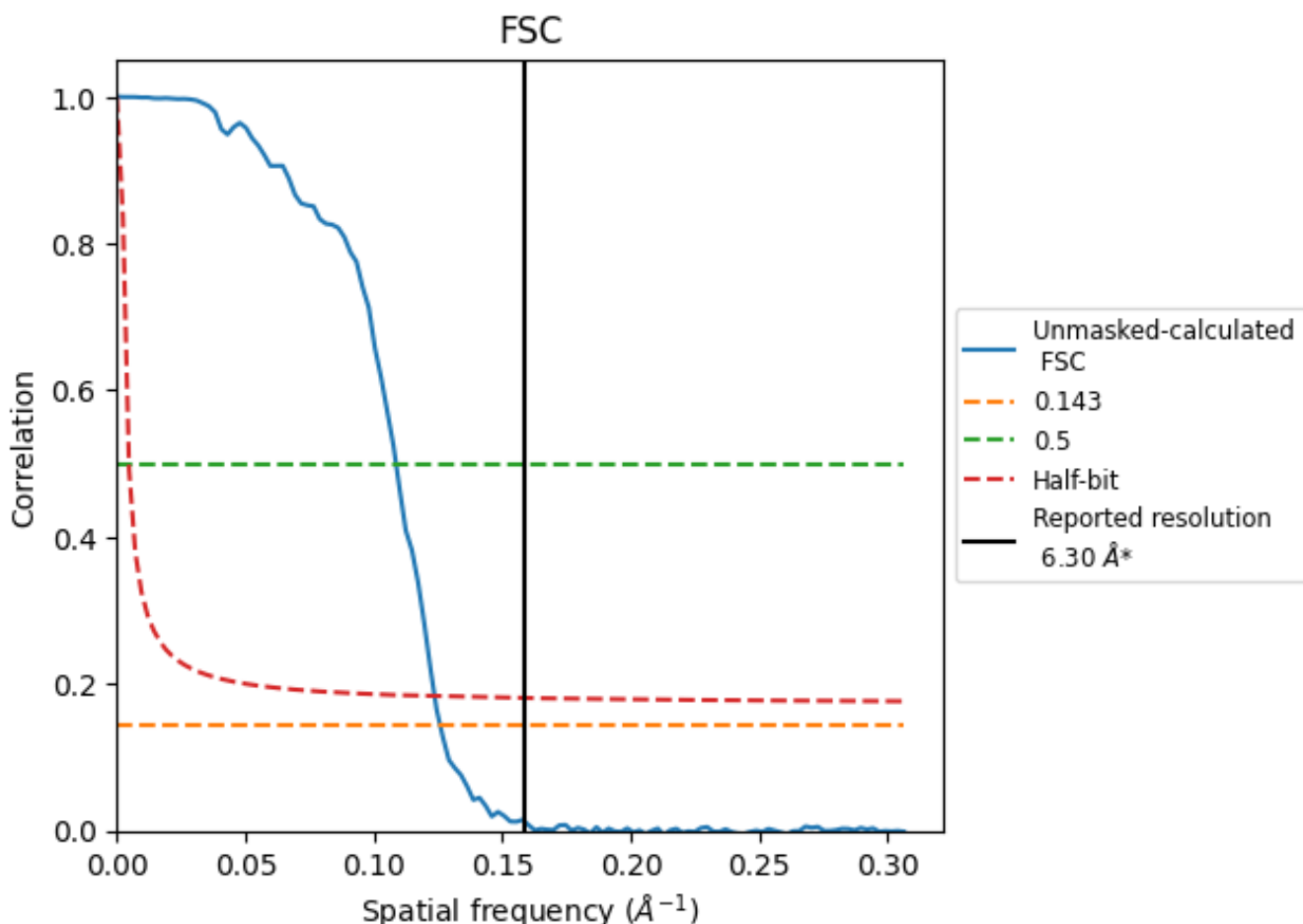


\*Reported resolution corresponds to spatial frequency of 0.159 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.159 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

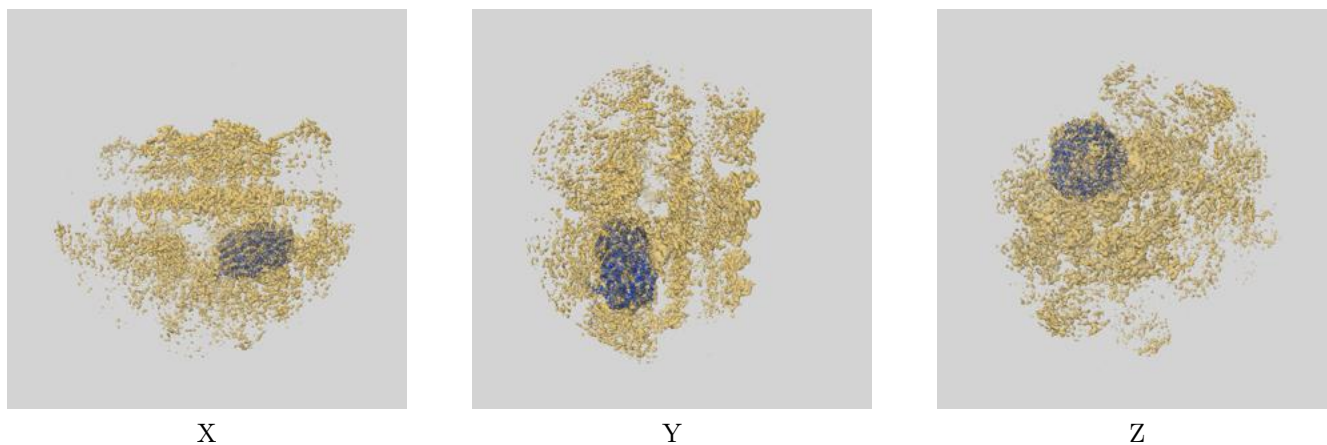
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.94	9.20	8.08

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.94 differs from the reported value 6.3 by more than 10 %

## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-33558 and PDB model 7Y1A. Per-residue inclusion information can be found in section 3 on page 8.

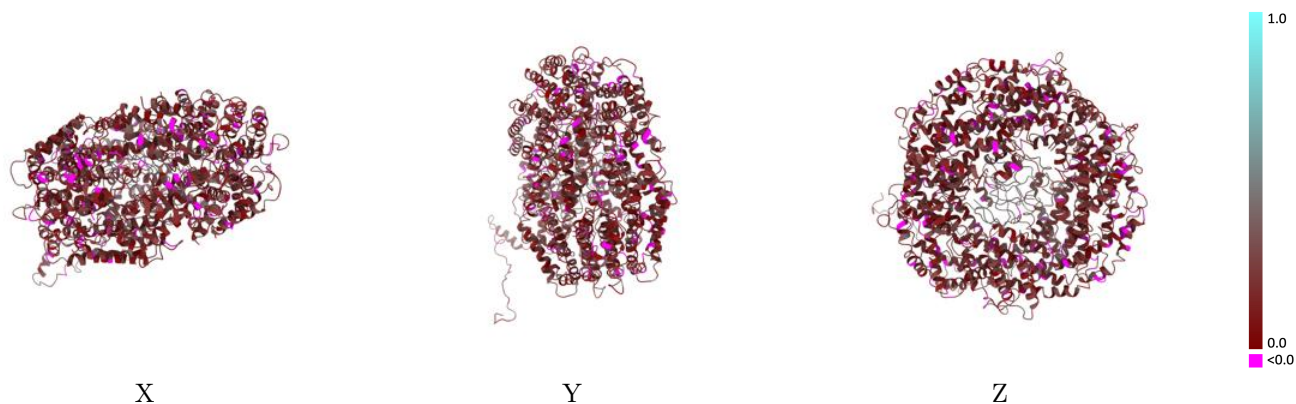
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.152 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

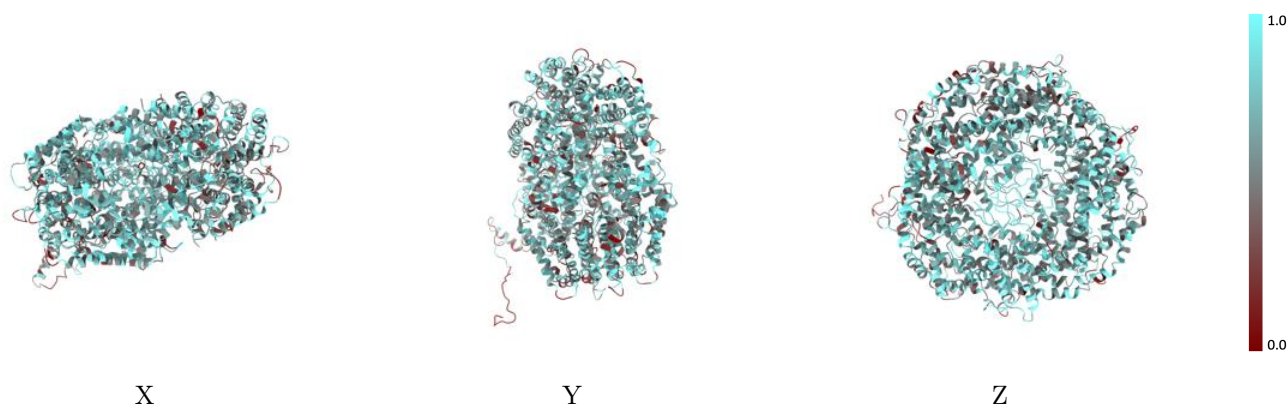


## 9.2 Q-score mapped to coordinate model [i](#)



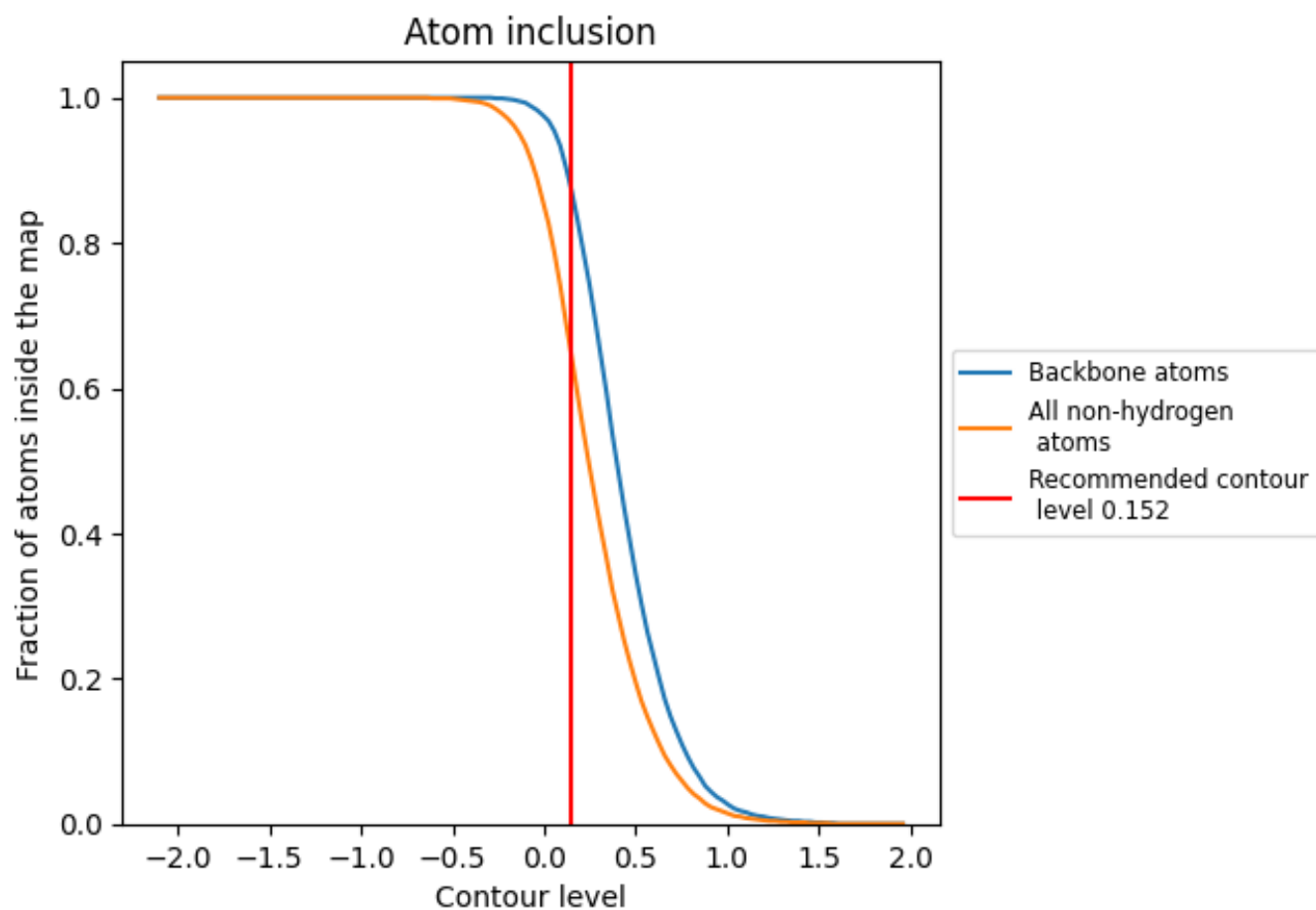
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.152).































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 64% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.152) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6410	 0.1690
1	 0.6900	 0.1630
A	 0.9610	 0.3780
a	 0.5610	 0.2960
p	 0.6240	 0.1610
q	 0.5880	 0.1590
r	 0.6230	 0.1470
s	 0.6690	 0.1700
t	 0.5640	 0.1510
u	 0.6100	 0.1650
v	 0.6520	 0.1410
w	 0.6160	 0.1470
x	 0.6390	 0.1490
y	 0.6250	 0.1630
z	 0.6430	 0.1510

