



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 3, 2024 – 05:55 am GMT

PDB ID : 5AQD
Title : Crystal structure of Phormidium Phycoerythrin at pH 8.5
Authors : Kumar, V.; Sharma, M.; Sonani, R.R.; Gupta, G.D.; Madamwar, D.
Deposited on : 2015-09-22
Resolution : 2.12 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

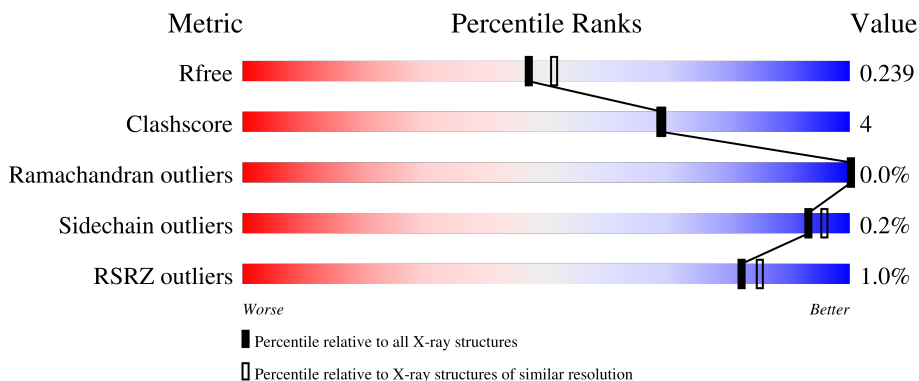
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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.



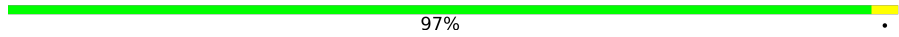
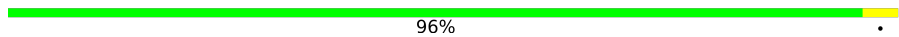
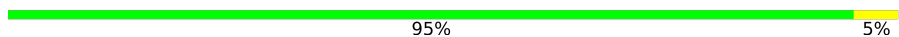
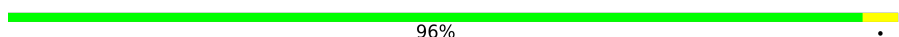

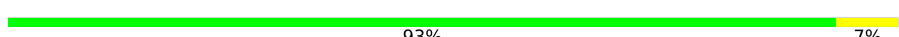




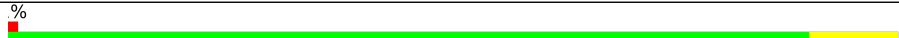


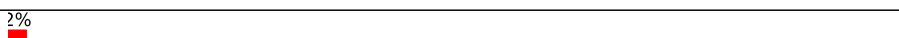
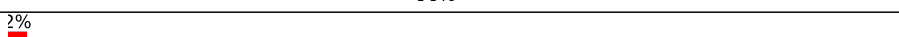
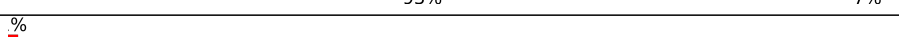

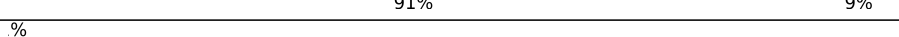
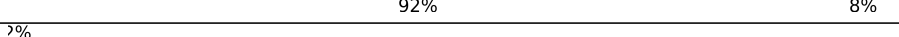
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705 (2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	164	96% (0% poor fit)
1	B	164	93% (7% poor fit)
1	C	164	91% (9% poor fit)
1	D	164	98% (0% poor fit)
1	E	164	95% (5% poor fit)

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Mol	Chain	Length	Quality of chain
1	F	164	 97% .
1	G	164	 96% .
1	H	164	 95% 5%
1	I	164	 96% .
1	J	164	 95% 5%
1	K	164	 93% 7%
1	L	164	 93% 7%
2	M	184	 2% 92% 8%
2	N	184	 2% 96% .
2	O	184	 2% 95% 5%
2	P	184	 % 90% 10%
2	Q	184	 3% 91% 9%
2	R	184	 2% 92% 8%
2	S	184	 2% 96% .
2	T	184	 2% 93% 7%
2	U	184	 % 90% 10%
2	V	184	 3% 91% 9%
2	W	184	 % 92% 8%
2	X	184	 2% 93% 7%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 37483 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PHYCOERYTHRIN ALPHA SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	164	1239	771	218	244	6	0	0	0
1	B	164	1239	771	218	244	6	0	0	0
1	C	164	1239	771	218	244	6	0	0	0
1	D	164	1239	771	218	244	6	0	0	0
1	E	164	1239	771	218	244	6	0	0	0
1	F	164	1239	771	218	244	6	0	0	0
1	G	164	1239	771	218	244	6	0	0	0
1	H	164	1239	771	218	244	6	0	0	0
1	I	164	1239	771	218	244	6	0	0	0
1	J	164	1239	771	218	244	6	0	0	0
1	K	164	1239	771	218	244	6	0	0	0
1	L	164	1239	771	218	244	6	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	161	ASN	-	SEE REMARK 999	UNP A0A0E3W01
A	162	SER	-	SEE REMARK 999	UNP A0A0E3W01
A	163	LEU	-	SEE REMARK 999	UNP A0A0E3W01
A	164	SER	-	SEE REMARK 999	UNP A0A0E3W01
B	161	ASN	-	SEE REMARK 999	UNP A0A0E3W01

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Chain	Residue	Modelled	Actual	Comment	Reference
B	162	SER	-	SEE REMARK 999	UNP A0A0E3W01
B	163	LEU	-	SEE REMARK 999	UNP A0A0E3W01
B	164	SER	-	SEE REMARK 999	UNP A0A0E3W01
C	161	ASN	-	SEE REMARK 999	UNP A0A0E3W01
C	162	SER	-	SEE REMARK 999	UNP A0A0E3W01
C	163	LEU	-	SEE REMARK 999	UNP A0A0E3W01
C	164	SER	-	SEE REMARK 999	UNP A0A0E3W01
D	161	ASN	-	SEE REMARK 999	UNP A0A0E3W01
D	162	SER	-	SEE REMARK 999	UNP A0A0E3W01
D	163	LEU	-	SEE REMARK 999	UNP A0A0E3W01
D	164	SER	-	SEE REMARK 999	UNP A0A0E3W01
E	161	ASN	-	SEE REMARK 999	UNP A0A0E3W01
E	162	SER	-	SEE REMARK 999	UNP A0A0E3W01
E	163	LEU	-	SEE REMARK 999	UNP A0A0E3W01
E	164	SER	-	SEE REMARK 999	UNP A0A0E3W01
F	161	ASN	-	SEE REMARK 999	UNP A0A0E3W01
F	162	SER	-	SEE REMARK 999	UNP A0A0E3W01
F	163	LEU	-	SEE REMARK 999	UNP A0A0E3W01
F	164	SER	-	SEE REMARK 999	UNP A0A0E3W01
G	161	ASN	-	SEE REMARK 999	UNP A0A0E3W01
G	162	SER	-	SEE REMARK 999	UNP A0A0E3W01
G	163	LEU	-	SEE REMARK 999	UNP A0A0E3W01
G	164	SER	-	SEE REMARK 999	UNP A0A0E3W01
H	161	ASN	-	SEE REMARK 999	UNP A0A0E3W01
H	162	SER	-	SEE REMARK 999	UNP A0A0E3W01
H	163	LEU	-	SEE REMARK 999	UNP A0A0E3W01
H	164	SER	-	SEE REMARK 999	UNP A0A0E3W01
I	161	ASN	-	SEE REMARK 999	UNP A0A0E3W01
I	162	SER	-	SEE REMARK 999	UNP A0A0E3W01
I	163	LEU	-	SEE REMARK 999	UNP A0A0E3W01
I	164	SER	-	SEE REMARK 999	UNP A0A0E3W01
J	161	ASN	-	SEE REMARK 999	UNP A0A0E3W01
J	162	SER	-	SEE REMARK 999	UNP A0A0E3W01
J	163	LEU	-	SEE REMARK 999	UNP A0A0E3W01
J	164	SER	-	SEE REMARK 999	UNP A0A0E3W01
K	161	ASN	-	SEE REMARK 999	UNP A0A0E3W01
K	162	SER	-	SEE REMARK 999	UNP A0A0E3W01
K	163	LEU	-	SEE REMARK 999	UNP A0A0E3W01
K	164	SER	-	SEE REMARK 999	UNP A0A0E3W01
L	161	ASN	-	SEE REMARK 999	UNP A0A0E3W01
L	162	SER	-	SEE REMARK 999	UNP A0A0E3W01
L	163	LEU	-	SEE REMARK 999	UNP A0A0E3W01

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Chain	Residue	Modelled	Actual	Comment	Reference
L	164	SER	-	SEE REMARK 999	UNP A0A0E3W01

- Molecule 2 is a protein called PHYCOERYTHRIN BETA SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	M	184	1347	827	244	263	13	0	0	0
2	N	184	1347	827	244	263	13	0	0	0
2	O	184	1347	827	244	263	13	0	0	0
2	P	184	1347	827	244	263	13	0	0	0
2	Q	184	1347	827	244	263	13	0	0	0
2	R	184	1347	827	244	263	13	0	0	0
2	S	184	1347	827	244	263	13	0	0	0
2	T	184	1347	827	244	263	13	0	0	0
2	U	184	1347	827	244	263	13	0	0	0
2	V	184	1347	827	244	263	13	0	0	0
2	W	184	1347	827	244	263	13	0	0	0
2	X	184	1347	827	244	263	13	0	0	0

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	1	MET	-	SEE REMARK 999	UNP A0A0E4G45
M	2	LEU	-	SEE REMARK 999	UNP A0A0E4G45
M	3	ASP	-	SEE REMARK 999	UNP A0A0E4G45
M	4	ALA	-	SEE REMARK 999	UNP A0A0E4G45
M	5	PHE	-	SEE REMARK 999	UNP A0A0E4G45
M	6	SER	-	SEE REMARK 999	UNP A0A0E4G45
M	7	ARG	-	SEE REMARK 999	UNP A0A0E4G45
N	1	MET	-	SEE REMARK 999	UNP A0A0E4G45
N	2	LEU	-	SEE REMARK 999	UNP A0A0E4G45

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Chain	Residue	Modelled	Actual	Comment	Reference
N	3	ASP	-	SEE REMARK 999	UNP A0A0E4G45
N	4	ALA	-	SEE REMARK 999	UNP A0A0E4G45
N	5	PHE	-	SEE REMARK 999	UNP A0A0E4G45
N	6	SER	-	SEE REMARK 999	UNP A0A0E4G45
N	7	ARG	-	SEE REMARK 999	UNP A0A0E4G45
O	1	MET	-	SEE REMARK 999	UNP A0A0E4G45
O	2	LEU	-	SEE REMARK 999	UNP A0A0E4G45
O	3	ASP	-	SEE REMARK 999	UNP A0A0E4G45
O	4	ALA	-	SEE REMARK 999	UNP A0A0E4G45
O	5	PHE	-	SEE REMARK 999	UNP A0A0E4G45
O	6	SER	-	SEE REMARK 999	UNP A0A0E4G45
O	7	ARG	-	SEE REMARK 999	UNP A0A0E4G45
P	1	MET	-	SEE REMARK 999	UNP A0A0E4G45
P	2	LEU	-	SEE REMARK 999	UNP A0A0E4G45
P	3	ASP	-	SEE REMARK 999	UNP A0A0E4G45
P	4	ALA	-	SEE REMARK 999	UNP A0A0E4G45
P	5	PHE	-	SEE REMARK 999	UNP A0A0E4G45
P	6	SER	-	SEE REMARK 999	UNP A0A0E4G45
P	7	ARG	-	SEE REMARK 999	UNP A0A0E4G45
Q	1	MET	-	SEE REMARK 999	UNP A0A0E4G45
Q	2	LEU	-	SEE REMARK 999	UNP A0A0E4G45
Q	3	ASP	-	SEE REMARK 999	UNP A0A0E4G45
Q	4	ALA	-	SEE REMARK 999	UNP A0A0E4G45
Q	5	PHE	-	SEE REMARK 999	UNP A0A0E4G45
Q	6	SER	-	SEE REMARK 999	UNP A0A0E4G45
Q	7	ARG	-	SEE REMARK 999	UNP A0A0E4G45
R	1	MET	-	SEE REMARK 999	UNP A0A0E4G45
R	2	LEU	-	SEE REMARK 999	UNP A0A0E4G45
R	3	ASP	-	SEE REMARK 999	UNP A0A0E4G45
R	4	ALA	-	SEE REMARK 999	UNP A0A0E4G45
R	5	PHE	-	SEE REMARK 999	UNP A0A0E4G45
R	6	SER	-	SEE REMARK 999	UNP A0A0E4G45
R	7	ARG	-	SEE REMARK 999	UNP A0A0E4G45
S	1	MET	-	SEE REMARK 999	UNP A0A0E4G45
S	2	LEU	-	SEE REMARK 999	UNP A0A0E4G45
S	3	ASP	-	SEE REMARK 999	UNP A0A0E4G45
S	4	ALA	-	SEE REMARK 999	UNP A0A0E4G45
S	5	PHE	-	SEE REMARK 999	UNP A0A0E4G45
S	6	SER	-	SEE REMARK 999	UNP A0A0E4G45
S	7	ARG	-	SEE REMARK 999	UNP A0A0E4G45
T	1	MET	-	SEE REMARK 999	UNP A0A0E4G45
T	2	LEU	-	SEE REMARK 999	UNP A0A0E4G45

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Chain	Residue	Modelled	Actual	Comment	Reference
T	3	ASP	-	SEE REMARK 999	UNP A0A0E4G45
T	4	ALA	-	SEE REMARK 999	UNP A0A0E4G45
T	5	PHE	-	SEE REMARK 999	UNP A0A0E4G45
T	6	SER	-	SEE REMARK 999	UNP A0A0E4G45
T	7	ARG	-	SEE REMARK 999	UNP A0A0E4G45
U	1	MET	-	SEE REMARK 999	UNP A0A0E4G45
U	2	LEU	-	SEE REMARK 999	UNP A0A0E4G45
U	3	ASP	-	SEE REMARK 999	UNP A0A0E4G45
U	4	ALA	-	SEE REMARK 999	UNP A0A0E4G45
U	5	PHE	-	SEE REMARK 999	UNP A0A0E4G45
U	6	SER	-	SEE REMARK 999	UNP A0A0E4G45
U	7	ARG	-	SEE REMARK 999	UNP A0A0E4G45
V	1	MET	-	SEE REMARK 999	UNP A0A0E4G45
V	2	LEU	-	SEE REMARK 999	UNP A0A0E4G45
V	3	ASP	-	SEE REMARK 999	UNP A0A0E4G45
V	4	ALA	-	SEE REMARK 999	UNP A0A0E4G45
V	5	PHE	-	SEE REMARK 999	UNP A0A0E4G45
V	6	SER	-	SEE REMARK 999	UNP A0A0E4G45
V	7	ARG	-	SEE REMARK 999	UNP A0A0E4G45
W	1	MET	-	SEE REMARK 999	UNP A0A0E4G45
W	2	LEU	-	SEE REMARK 999	UNP A0A0E4G45
W	3	ASP	-	SEE REMARK 999	UNP A0A0E4G45
W	4	ALA	-	SEE REMARK 999	UNP A0A0E4G45
W	5	PHE	-	SEE REMARK 999	UNP A0A0E4G45
W	6	SER	-	SEE REMARK 999	UNP A0A0E4G45
W	7	ARG	-	SEE REMARK 999	UNP A0A0E4G45
X	1	MET	-	SEE REMARK 999	UNP A0A0E4G45
X	2	LEU	-	SEE REMARK 999	UNP A0A0E4G45
X	3	ASP	-	SEE REMARK 999	UNP A0A0E4G45
X	4	ALA	-	SEE REMARK 999	UNP A0A0E4G45
X	5	PHE	-	SEE REMARK 999	UNP A0A0E4G45
X	6	SER	-	SEE REMARK 999	UNP A0A0E4G45
X	7	ARG	-	SEE REMARK 999	UNP A0A0E4G45

- Molecule 3 is PHYCOERYTHROBILIN (three-letter code: PEB) (formula: C₃₃H₄₀N₄O₆).

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	H	1	Total 43	C 33	N 4	O 6	0	0
3	H	1	Total 43	C 33	N 4	O 6	0	0
3	I	1	Total 43	C 33	N 4	O 6	0	0
3	I	1	Total 43	C 33	N 4	O 6	0	0
3	J	1	Total 43	C 33	N 4	O 6	0	0
3	J	1	Total 43	C 33	N 4	O 6	0	0
3	K	1	Total 43	C 33	N 4	O 6	0	0
3	K	1	Total 43	C 33	N 4	O 6	0	0
3	L	1	Total 43	C 33	N 4	O 6	0	0
3	L	1	Total 43	C 33	N 4	O 6	0	0
3	M	1	Total 43	C 33	N 4	O 6	0	0
3	M	1	Total 43	C 33	N 4	O 6	0	0
3	M	1	Total 43	C 33	N 4	O 6	0	0
3	N	1	Total 43	C 33	N 4	O 6	0	0
3	N	1	Total 43	C 33	N 4	O 6	0	0
3	N	1	Total 43	C 33	N 4	O 6	0	0
3	O	1	Total 43	C 33	N 4	O 6	0	0
3	O	1	Total 43	C 33	N 4	O 6	0	0
3	O	1	Total 43	C 33	N 4	O 6	0	0
3	P	1	Total 43	C 33	N 4	O 6	0	0
3	P	1	Total 43	C 33	N 4	O 6	0	0

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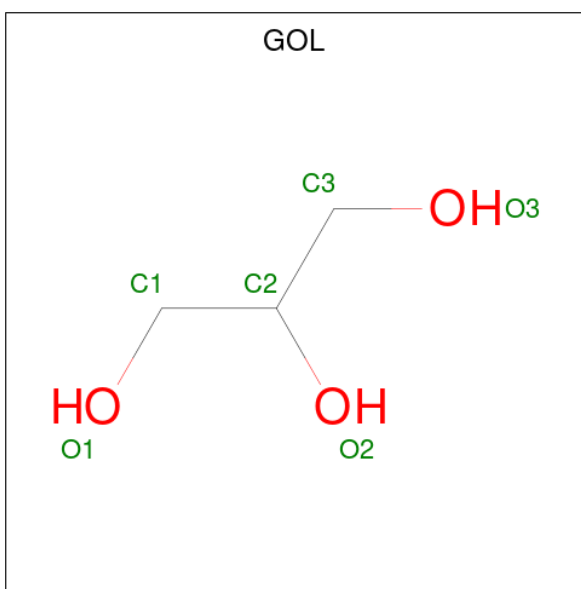
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	P	1	43	33	4	6	0	0
3	Q	1	43	33	4	6	0	0
3	Q	1	43	33	4	6	0	0
3	Q	1	43	33	4	6	0	0
3	R	1	43	33	4	6	0	0
3	R	1	43	33	4	6	0	0
3	R	1	43	33	4	6	0	0
3	S	1	43	33	4	6	0	0
3	S	1	43	33	4	6	0	0
3	S	1	43	33	4	6	0	0
3	T	1	43	33	4	6	0	0
3	T	1	43	33	4	6	0	0
3	T	1	43	33	4	6	0	0
3	U	1	43	33	4	6	0	0
3	U	1	43	33	4	6	0	0
3	U	1	43	33	4	6	0	0
3	V	1	43	33	4	6	0	0
3	V	1	43	33	4	6	0	0
3	V	1	43	33	4	6	0	0
3	W	1	43	33	4	6	0	0
3	W	1	43	33	4	6	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	W	1	Total	C	N	O	0	0
			43	33	4	6		
3	X	1	Total	C	N	O	0	0
			43	33	4	6		
3	X	1	Total	C	N	O	0	0
			43	33	4	6		
3	X	1	Total	C	N	O	0	0
			43	33	4	6		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



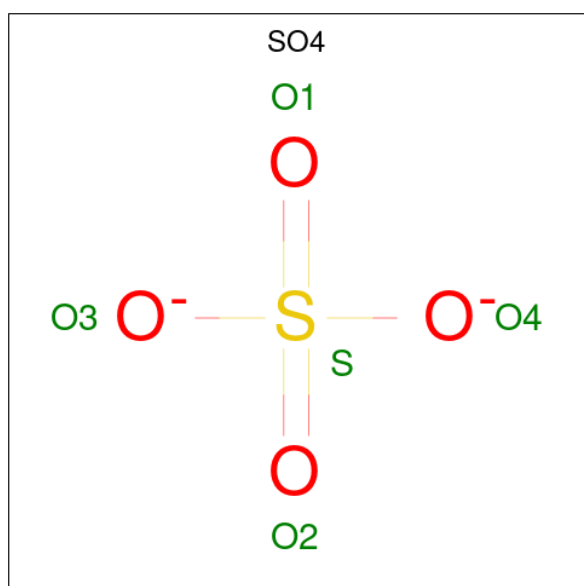
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	C	O	0	0
			6	3	3		
4	I	1	Total	C	O	0	0
			6	3	3		
4	J	1	Total	C	O	0	0
			6	3	3		
4	K	1	Total	C	O	0	0
			6	3	3		
4	L	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	H	1	Total	O	S	0	0
			5	4	1		
5	I	1	Total	O	S	0	0
			5	4	1		
5	L	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	M	1	Total	O	S	0	0
			5	4	1		
5	N	1	Total	O	S	0	0
			5	4	1		
5	O	1	Total	O	S	0	0
			5	4	1		
5	P	1	Total	O	S	0	0
			5	4	1		
5	Q	1	Total	O	S	0	0
			5	4	1		
5	R	1	Total	O	S	0	0
			5	4	1		
5	S	1	Total	O	S	0	0
			5	4	1		
5	T	1	Total	O	S	0	0
			5	4	1		
5	U	1	Total	O	S	0	0
			5	4	1		
5	V	1	Total	O	S	0	0
			5	4	1		
5	W	1	Total	O	S	0	0
			5	4	1		
5	X	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	212	Total	O	0	0
			212	212		
6	B	194	Total	O	0	0
			194	194		
6	C	178	Total	O	0	0
			178	178		
6	D	168	Total	O	0	0
			168	168		
6	E	167	Total	O	0	0
			167	167		
6	F	161	Total	O	0	0
			161	161		
6	G	206	Total	O	0	0
			206	206		

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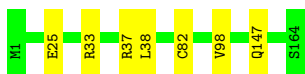
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	208	Total 208	O 208	0	0
6	I	188	Total 188	O 188	0	0
6	J	163	Total 163	O 163	0	0
6	K	133	Total 133	O 133	0	0
6	L	148	Total 148	O 148	0	0
6	M	149	Total 149	O 149	0	0
6	N	140	Total 140	O 140	0	0
6	O	121	Total 121	O 121	0	0
6	P	144	Total 144	O 144	0	0
6	Q	134	Total 134	O 134	0	0
6	R	118	Total 118	O 118	0	0
6	S	134	Total 134	O 134	0	0
6	T	107	Total 107	O 107	0	0
6	U	123	Total 123	O 123	0	0
6	V	153	Total 153	O 153	0	0
6	W	134	Total 134	O 134	0	0
6	X	126	Total 126	O 126	0	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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: PHYCOERYTHRIN ALPHA SUBUNIT

Chain A:  96%



- Molecule 1: PHYCOERYTHRIN ALPHA SUBUNIT

Chain B:  93%



- Molecule 1: PHYCOERYTHRIN ALPHA SUBUNIT

Chain C:  91%



- Molecule 1: PHYCOERYTHRIN ALPHA SUBUNIT

Chain D:  98%



- Molecule 1: PHYCOERYTHRIN ALPHA SUBUNIT

Chain E:  95%



- Molecule 1: PHYCOERYTHRIN ALPHA SUBUNIT

Chain F:  97%



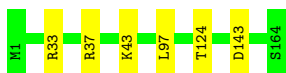
- Molecule 1: PHYCOERYTHRIN ALPHA SUBUNIT



- Molecule 1: PHYCOERYTHRIN ALPHA SUBUNIT



- Molecule 1: PHYCOERYTHRIN ALPHA SUBUNIT



- Molecule 1: PHYCOERYTHRIN ALPHA SUBUNIT



- Molecule 1: PHYCOERYTHRIN ALPHA SUBUNIT



- Molecule 1: PHYCOERYTHRIN ALPHA SUBUNIT



- Molecule 2: PHYCOERYTHRIN BETA SUBUNIT





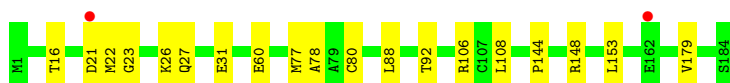
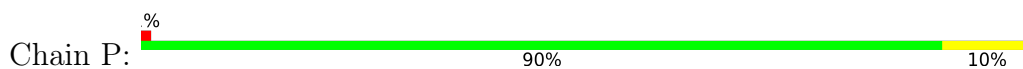
- Molecule 2: PHYCOERYTHRIN BETA SUBUNIT



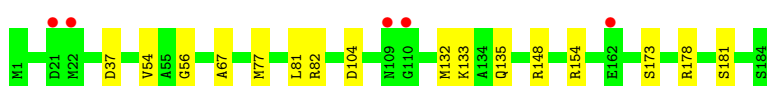
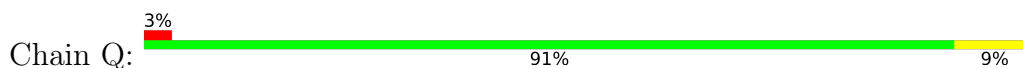
- Molecule 2: PHYCOERYTHRIN BETA SUBUNIT



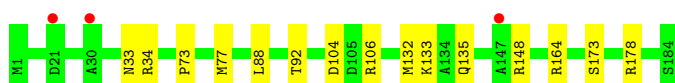
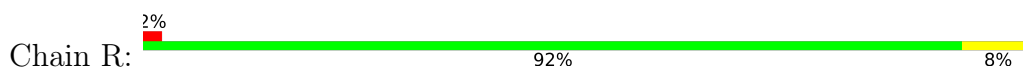
- Molecule 2: PHYCOERYTHRIN BETA SUBUNIT



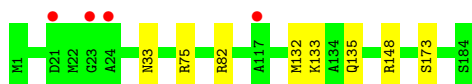
- Molecule 2: PHYCOERYTHRIN BETA SUBUNIT



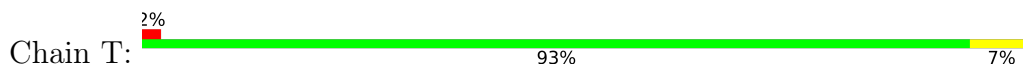
- Molecule 2: PHYCOERYTHRIN BETA SUBUNIT

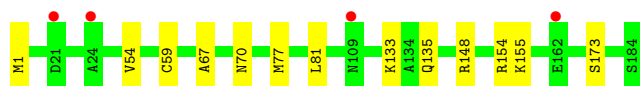


- Molecule 2: PHYCOERYTHRIN BETA SUBUNIT

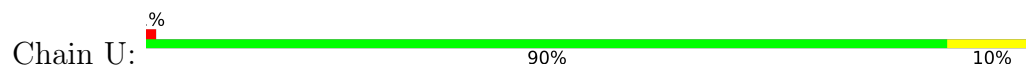


- Molecule 2: PHYCOERYTHRIN BETA SUBUNIT

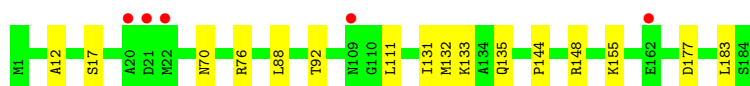
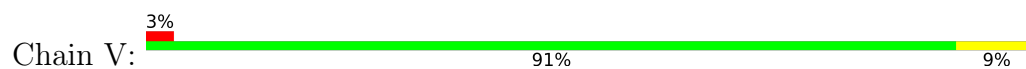




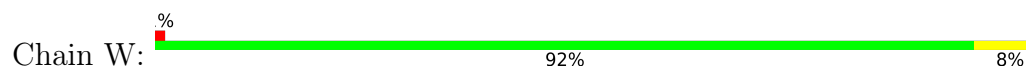
- Molecule 2: PHYCOERYTHRIN BETA SUBUNIT



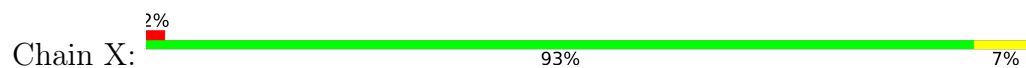
- Molecule 2: PHYCOERYTHRIN BETA SUBUNIT



- Molecule 2: PHYCOERYTHRIN BETA SUBUNIT



- Molecule 2: PHYCOERYTHRIN BETA SUBUNIT



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	108.30Å 108.36Å 116.59Å 78.94° 82.50° 60.34°	Depositor
Resolution (Å)	29.29 – 2.12 29.29 – 2.12	Depositor EDS
% Data completeness (in resolution range)	96.0 (29.29-2.12) 96.0 (29.29-2.12)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.51 (at 2.12Å)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.175 , 0.239 0.177 , 0.239	Depositor DCC
R_{free} test set	12523 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	15.7	Xtrriage
Anisotropy	0.578	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 57.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.004 for h-k,-k,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	37483	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PEB, SO4, GOL, 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	A	0.40	0/1259	0.54	0/1706
1	B	0.41	0/1259	0.54	0/1706
1	C	0.39	0/1259	0.52	0/1706
1	D	0.40	0/1259	0.52	0/1706
1	E	0.39	0/1259	0.51	0/1706
1	F	0.41	0/1259	0.51	0/1706
1	G	0.42	0/1259	0.53	0/1706
1	H	0.40	0/1259	0.52	0/1706
1	I	0.38	0/1259	0.52	0/1706
1	J	0.38	0/1259	0.51	0/1706
1	K	0.38	0/1259	0.52	0/1706
1	L	0.39	0/1259	0.53	0/1706
2	M	0.38	0/1349	0.50	0/1820
2	N	0.38	0/1349	0.50	0/1820
2	O	0.37	0/1349	0.50	0/1820
2	P	0.40	0/1349	0.52	0/1820
2	Q	0.36	0/1349	0.51	0/1820
2	R	0.35	0/1349	0.50	0/1820
2	S	0.36	0/1349	0.50	0/1820
2	T	0.33	0/1349	0.49	0/1820
2	U	0.39	0/1349	0.51	0/1820
2	V	0.38	0/1349	0.50	0/1820
2	W	0.36	0/1349	0.48	0/1820
2	X	0.37	0/1349	0.51	0/1820
All	All	0.38	0/31296	0.51	0/42312

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1239	0	1221	7	0
1	B	1239	0	1221	10	0
1	C	1239	0	1221	10	0
1	D	1239	0	1221	3	0
1	E	1239	0	1221	10	0
1	F	1239	0	1221	5	0
1	G	1239	0	1221	6	0
1	H	1239	0	1221	6	0
1	I	1239	0	1221	5	0
1	J	1239	0	1221	7	0
1	K	1239	0	1221	10	0
1	L	1239	0	1221	8	0
2	M	1347	0	1359	10	0
2	N	1347	0	1359	6	0
2	O	1347	0	1359	7	0
2	P	1347	0	1359	15	0
2	Q	1347	0	1359	12	0
2	R	1347	0	1359	11	0
2	S	1347	0	1359	7	0
2	T	1347	0	1359	12	0
2	U	1347	0	1359	14	0
2	V	1347	0	1359	10	0
2	W	1347	0	1359	9	0
2	X	1347	0	1359	8	0
3	A	86	0	74	2	0
3	B	86	0	74	2	0
3	C	86	0	74	4	0
3	D	86	0	73	2	0
3	E	86	0	74	7	0
3	F	86	0	74	1	0
3	G	86	0	74	3	0
3	H	86	0	74	3	0
3	I	86	0	74	3	0
3	J	86	0	74	4	0
3	K	86	0	74	3	0
3	L	86	0	74	2	0
3	M	129	0	110	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	N	129	0	110	6	0
3	O	129	0	110	6	0
3	P	129	0	110	8	0
3	Q	129	0	110	12	0
3	R	129	0	110	6	0
3	S	129	0	110	7	0
3	T	129	0	110	8	0
3	U	129	0	110	9	0
3	V	129	0	109	6	0
3	W	129	0	110	6	0
3	X	129	0	110	4	0
4	A	6	0	8	0	0
4	B	6	0	8	0	0
4	C	6	0	8	0	0
4	D	6	0	8	0	0
4	E	6	0	8	1	0
4	F	6	0	8	0	0
4	G	6	0	8	0	0
4	H	6	0	8	1	0
4	I	6	0	8	0	0
4	J	6	0	8	0	0
4	K	6	0	8	0	0
4	L	6	0	8	0	0
5	A	5	0	0	0	0
5	D	5	0	0	0	0
5	E	5	0	0	0	0
5	H	5	0	0	0	0
5	I	5	0	0	1	0
5	L	5	0	0	0	0
5	M	5	0	0	0	0
5	N	5	0	0	0	0
5	O	5	0	0	0	0
5	P	5	0	0	1	0
5	Q	5	0	0	0	0
5	R	5	0	0	1	0
5	S	5	0	0	0	0
5	T	5	0	0	0	0
5	U	5	0	0	0	0
5	V	5	0	0	0	0
5	W	5	0	0	0	0
5	X	5	0	0	0	0
6	A	212	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	194	0	0	1	0
6	C	178	0	0	0	0
6	D	168	0	0	0	0
6	E	167	0	0	1	0
6	F	161	0	0	0	0
6	G	206	0	0	0	0
6	H	208	0	0	1	0
6	I	188	0	0	0	0
6	J	163	0	0	0	0
6	K	133	0	0	2	0
6	L	148	0	0	0	0
6	M	149	0	0	1	0
6	N	140	0	0	0	0
6	O	121	0	0	0	0
6	P	144	0	0	0	0
6	Q	134	0	0	0	0
6	R	118	0	0	1	0
6	S	134	0	0	1	0
6	T	107	0	0	0	0
6	U	123	0	0	0	0
6	V	153	0	0	0	0
6	W	134	0	0	0	0
6	X	126	0	0	0	0
All	All	37483	0	33262	247	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 4.

All (247) 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)
2:P:16:THR:HG23	2:Q:67:ALA:HB2	1.66	0.77
2:T:54:VAL:HG21	2:T:81:LEU:HD23	1.72	0.72
2:X:22:MET:HG2	2:X:25:LEU:HD12	1.72	0.71
2:M:88:LEU:O	2:M:92:THR:HG23	1.98	0.64
3:Q:186:PEB:HNA	3:Q:186:PEB:HMB2	1.63	0.63
2:Q:82:ARG:NH1	3:Q:186:PEB:O2C	2.32	0.62
1:L:37:ARG:NH1	1:L:98:VAL:O	2.34	0.61
2:P:22:MET:HB2	2:P:26:LYS:NZ	2.16	0.60
2:N:104:ASP:OD2	2:N:178:ARG:NH2	2.34	0.60
2:T:133:LYS:HE3	2:T:173:SER:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:37:ARG:NE	1:F:25:GLU:OE2	2.36	0.59
3:U:186:PEB:HMB2	3:U:186:PEB:HNA	1.68	0.58
3:W:187:PEB:HMB2	3:W:187:PEB:HNA	1.68	0.58
1:A:37:ARG:NH1	1:A:98:VAL:O	2.36	0.58
2:X:88:LEU:O	2:X:92:THR:HG23	2.03	0.58
1:H:25:GLU:OE2	1:K:37:ARG:NE	2.35	0.58
3:K:166:PEB:HBD1	2:X:72:TYR:CE1	2.39	0.57
3:P:186:PEB:HNA	3:P:186:PEB:HMB2	1.69	0.57
2:N:148:ARG:NH1	3:N:188:PEB:HND	2.02	0.57
3:V:186:PEB:HMB2	3:V:186:PEB:HNA	1.70	0.57
2:M:148:ARG:NE	3:M:188:PEB:O2C	2.30	0.57
3:O:186:PEB:HNA	3:O:186:PEB:HMB2	1.70	0.56
3:R:186:PEB:HNA	3:R:186:PEB:HMB2	1.70	0.56
3:S:187:PEB:HNA	3:S:187:PEB:HMB2	1.71	0.56
2:X:82:ARG:NH1	3:X:186:PEB:O2C	2.38	0.56
2:S:148:ARG:NH1	3:S:188:PEB:HND	2.03	0.56
1:G:25:GLU:OE2	1:J:37:ARG:NE	2.36	0.56
3:T:186:PEB:HNA	3:T:186:PEB:HMB2	1.69	0.56
1:H:37:ARG:NE	1:K:25:GLU:OE2	2.30	0.56
1:E:37:ARG:HD2	1:E:97:LEU:O	2.05	0.56
2:R:148:ARG:NH1	3:R:188:PEB:HND	2.03	0.56
1:K:115:GLU:HG3	6:K:2086:HOH:O	2.06	0.55
1:K:37:ARG:HD2	1:K:97:LEU:O	2.07	0.55
2:O:174:SER:O	2:O:178:ARG:HG3	2.07	0.55
2:X:148:ARG:NE	3:X:188:PEB:O2C	2.27	0.54
2:R:88:LEU:O	2:R:92:THR:HG23	2.07	0.54
3:D:166:PEB:HMC2	2:Q:77:MET:HG2	1.90	0.54
2:T:148:ARG:NH1	3:T:188:PEB:HND	2.05	0.54
2:W:148:ARG:NH1	3:W:188:PEB:HND	2.06	0.54
1:E:118:ARG:NH1	6:E:2120:HOH:O	2.41	0.53
2:S:135:GLN:HG2	3:S:188:PEB:C1B	2.38	0.53
3:N:186:PEB:HMB2	3:N:186:PEB:HNA	1.73	0.53
1:B:37:ARG:HD2	1:B:97:LEU:O	2.10	0.52
3:J:166:PEB:HNA	3:J:166:PEB:HMB2	1.73	0.52
3:F:166:PEB:HMC2	2:P:77:MET:HG2	1.92	0.52
3:N:187:PEB:HMB2	3:N:187:PEB:HNA	1.74	0.52
1:I:37:ARG:HD2	1:I:97:LEU:O	2.08	0.52
3:S:186:PEB:HNA	3:S:186:PEB:HMB2	1.75	0.52
2:U:5:PHE:HE1	2:U:28:PHE:CD1	2.28	0.52
2:V:88:LEU:O	2:V:92:THR:HG23	2.10	0.52
3:I:166:PEB:HMC2	2:T:77:MET:HG2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:105:LEU:HD21	1:L:159:ALA:HB2	1.93	0.51
3:Q:188:PEB:HNA	3:Q:188:PEB:HMB3	1.75	0.51
3:T:188:PEB:HNA	3:T:188:PEB:HMB3	1.75	0.51
1:I:43:LYS:NZ	1:I:143:ASP:O	2.40	0.51
3:M:187:PEB:HNA	3:M:187:PEB:HMB2	1.75	0.51
3:T:188:PEB:HBB1	3:T:188:PEB:HBB1	1.93	0.51
2:V:70:MEN:HB2	3:V:186:PEB:OA	2.11	0.51
2:P:88:LEU:O	2:P:92:THR:HG23	2.11	0.50
2:P:148:ARG:NH2	2:U:184:SER:OXT	2.44	0.50
2:Q:104:ASP:OD2	2:Q:178:ARG:NH2	2.38	0.50
1:H:114:ARG:NH2	6:H:2143:HOH:O	2.43	0.50
2:R:132:MET:HA	2:R:135:GLN:OE1	2.12	0.50
3:O:188:PEB:HNA	3:O:188:PEB:HMB3	1.76	0.50
3:A:166:PEB:HMC2	2:O:77:MET:HG2	1.94	0.50
1:G:37:ARG:HD2	1:G:97:LEU:O	2.12	0.50
2:P:106:ARG:NE	5:P:189:SO4:O3	2.43	0.50
1:I:124:THR:OG1	5:I:1200:SO4:O1	2.27	0.49
2:Q:135:GLN:HG2	3:Q:188:PEB:C1B	2.43	0.49
2:P:60:GLU:OE1	2:U:130:GLN:NE2	2.46	0.49
2:U:48:CYS:SG	2:U:152:LYS:HD3	2.52	0.49
4:H:1165:GOL:H12	2:T:1:MET:HG2	1.94	0.49
3:C:166:PEB:HMB2	3:C:166:PEB:HNA	1.77	0.49
3:W:186:PEB:HNA	3:W:186:PEB:HMB2	1.77	0.49
2:P:22:MET:HB2	2:P:26:LYS:HZ2	1.77	0.49
3:Q:187:PEB:HBA3	3:Q:187:PEB:HHA1	1.95	0.49
2:S:132:MET:HA	2:S:135:GLN:OE1	2.12	0.49
2:O:131:ILE:O	2:O:135:GLN:HG3	2.12	0.48
3:O:188:PEB:HBB1	3:O:188:PEB:HBB1	1.95	0.48
1:G:25:GLU:OE1	1:J:30:SER:HA	2.13	0.48
1:K:1:MET:N	2:W:1:MET:O	2.46	0.48
2:N:133:LYS:HE3	2:N:173:SER:HB3	1.95	0.48
2:U:26:LYS:HD2	2:U:26:LYS:HA	1.66	0.48
3:M:186:PEB:HMB2	3:M:186:PEB:HNA	1.78	0.48
3:Q:187:PEB:HNA	3:Q:187:PEB:HMB2	1.78	0.48
2:U:148:ARG:NH1	3:U:188:PEB:HND	2.11	0.47
3:U:186:PEB:HNA	3:U:186:PEB:CMB	2.26	0.47
1:C:25:GLU:HG2	1:F:33:ARG:HG2	1.97	0.47
3:C:166:PEB:HMC2	2:N:77:MET:HG2	1.96	0.47
3:U:188:PEB:HNA	3:U:188:PEB:HMB3	1.79	0.47
2:W:125:THR:HG21	2:W:183:LEU:HD13	1.95	0.47
1:E:43:LYS:HG3	3:E:167:PEB:HBD1	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:148:ARG:NH1	3:P:188:PEB:HND	2.12	0.47
1:C:68:ASN:O	1:C:74:SER:HB3	2.15	0.47
1:I:33:ARG:HG2	1:L:25:GLU:HG2	1.96	0.47
3:P:188:PEB:HBB1	3:P:188:PEB:HBB1	1.97	0.47
2:U:83:ASP:OD1	3:U:186:PEB:H1D1	2.15	0.47
1:A:33:ARG:HH12	3:P:187:PEB:HMC1	1.80	0.47
3:E:166:PEB:HMB2	3:E:166:PEB:HNA	1.80	0.47
1:L:72:ALA:O	1:L:78:PHE:HB3	2.15	0.47
3:W:188:PEB:HMB3	3:W:188:PEB:HNA	1.79	0.47
1:B:37:ARG:NE	1:E:25:GLU:OE2	2.44	0.47
3:N:188:PEB:HNA	3:N:188:PEB:HMB3	1.80	0.47
2:R:104:ASP:OD2	2:R:178:ARG:NH2	2.47	0.47
3:V:188:PEB:HNA	3:V:188:PEB:HMB3	1.80	0.46
3:X:186:PEB:HNA	3:X:186:PEB:HMB2	1.80	0.46
2:R:133:LYS:HE3	2:R:173:SER:HB3	1.97	0.46
1:H:33:ARG:NH1	1:H:147:GLN:OE1	2.40	0.46
2:M:132:MET:HA	2:M:135:GLN:OE1	2.14	0.46
2:Q:132:MET:HA	2:Q:135:GLN:OE1	2.15	0.46
2:T:135:GLN:HG2	3:T:188:PEB:C1B	2.44	0.46
2:U:82:ARG:NH1	3:U:186:PEB:O2C	2.48	0.46
1:G:1:MET:HG3	1:G:103:GLY:HA3	1.96	0.46
1:B:25:GLU:OE2	1:E:37:ARG:NE	2.42	0.46
3:Q:187:PEB:HMB2	3:Q:187:PEB:NA	2.31	0.46
3:C:166:PEB:HNA	3:C:166:PEB:CMB	2.29	0.46
2:W:88:LEU:O	2:W:92:THR:HG23	2.16	0.46
1:H:72:ALA:O	1:H:78:PHE:HB3	2.16	0.46
3:E:166:PEB:HNA	3:E:166:PEB:CMB	2.29	0.46
3:X:187:PEB:HNA	3:X:187:PEB:HMB2	1.80	0.46
2:O:33:ASN:HB3	3:O:187:PEB:C1C	2.46	0.46
1:E:43:LYS:HG3	3:E:167:PEB:CBD	2.45	0.45
3:G:166:PEB:HNA	3:G:166:PEB:HMB2	1.81	0.45
1:C:33:ARG:NH1	1:C:147:GLN:OE1	2.45	0.45
2:S:82:ARG:NH1	3:S:186:PEB:O2C	2.49	0.45
3:B:166:PEB:HMC2	2:M:77:MET:HG2	1.97	0.45
1:J:33:ARG:NH1	1:J:147:GLN:OE1	2.40	0.45
3:P:187:PEB:HNA	3:P:187:PEB:HMB2	1.80	0.45
2:V:12:ALA:HB1	2:V:17:SER:O	2.16	0.45
1:B:21:SER:HB2	6:B:2036:HOH:O	2.17	0.45
1:A:33:ARG:NH2	1:A:147:GLN:OE1	2.40	0.45
1:F:115:GLU:OE1	2:P:78:ALA:HB1	2.17	0.45
3:O:187:PEB:HBA3	3:O:187:PEB:HHA1	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:166:PEB:HMB2	3:H:166:PEB:HNA	1.82	0.45
2:T:67:ALA:HB2	2:U:16:THR:HG23	1.99	0.45
2:U:88:LEU:O	2:U:92:THR:HG23	2.16	0.45
1:J:37:ARG:HD2	1:J:97:LEU:O	2.17	0.45
3:V:188:PEB:HBB1	3:V:188:PEB:HBB1	1.99	0.45
3:J:166:PEB:HNA	3:J:166:PEB:CMB	2.30	0.44
1:A:25:GLU:HG2	1:D:33:ARG:HG2	1.99	0.44
1:B:72:ALA:O	1:B:78:PHE:HB3	2.16	0.44
1:C:139:CYS:SG	3:C:167:PEB:HHA1	2.58	0.44
2:S:33:ASN:HB3	3:S:187:PEB:C1C	2.47	0.44
3:E:166:PEB:HMC2	2:R:77:MET:HG2	2.00	0.44
3:O:187:PEB:HMB2	3:O:187:PEB:NA	2.33	0.44
3:I:166:PEB:HNA	3:I:166:PEB:HMB2	1.82	0.44
2:S:133:LYS:HE3	2:S:173:SER:HB3	1.98	0.44
2:V:133:LYS:NZ	2:V:177:ASP:OD1	2.50	0.44
6:A:2155:HOH:O	1:F:114:ARG:NH1	2.50	0.44
2:N:135:GLN:HG2	3:N:188:PEB:C1B	2.48	0.44
1:C:19:PRO:HG2	2:O:92:THR:HG22	1.98	0.44
1:B:139:CYS:SG	3:B:167:PEB:HHA1	2.58	0.44
2:U:108:LEU:HD21	2:U:179:VAL:HG22	1.99	0.44
3:R:188:PEB:HBB1	3:R:188:PEB:HBB1	2.00	0.43
2:T:59:CYS:HB2	3:T:188:PEB:HBD2	1.78	0.43
2:M:72:TYR:O	2:M:76:ARG:HD2	2.19	0.43
2:R:33:ASN:HB3	3:R:187:PEB:C1C	2.48	0.43
2:R:34:ARG:HE	3:R:187:PEB:CGB	2.31	0.43
2:W:104:ASP:O	2:W:109:ASN:HB2	2.18	0.43
1:C:123:PRO:O	1:C:126:PRO:HD2	2.18	0.43
2:V:144:PRO:HD2	2:V:155:LYS:NZ	2.33	0.43
3:U:187:PEB:HBA3	3:U:187:PEB:HHA1	1.99	0.43
2:Q:133:LYS:HE3	2:Q:173:SER:HB3	2.00	0.43
3:W:187:PEB:HMB2	3:W:187:PEB:NA	2.34	0.43
1:B:25:GLU:HG2	1:E:33:ARG:HG2	2.01	0.43
2:M:148:ARG:HD3	6:M:2114:HOH:O	2.18	0.43
2:N:104:ASP:CG	2:N:178:ARG:HH21	2.22	0.43
1:A:82:CYS:HA	3:A:166:PEB:HAA1	1.85	0.43
2:M:33:ASN:HB3	3:M:187:PEB:C1C	2.49	0.43
3:T:187:PEB:HMB2	3:T:187:PEB:HNA	1.83	0.43
1:H:25:GLU:HG2	1:K:33:ARG:HG2	2.01	0.43
1:B:34:SER:HA	1:B:37:ARG:HG2	2.00	0.43
1:J:139:CYS:SG	3:J:167:PEB:HHA1	2.59	0.43
1:L:37:ARG:HD2	1:L:97:LEU:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:70:MEN:HE22	2:V:76:ARG:HD3	2.01	0.43
3:J:167:PEB:HNA	3:J:167:PEB:HMB2	1.84	0.42
2:P:80:CYS:HA	3:P:186:PEB:HAA1	1.84	0.42
1:E:1:MET:N	4:E:1165:GOL:H31	2.34	0.42
2:M:34:ARG:HE	3:M:187:PEB:CGB	2.32	0.42
2:P:22:MET:HE3	2:P:26:LYS:HE3	2.02	0.42
2:S:75:ARG:NH2	6:S:2063:HOH:O	2.51	0.42
3:S:188:PEB:HBB1	3:S:188:PEB:HBB1	2.01	0.42
1:D:37:ARG:HD2	1:D:97:LEU:O	2.19	0.42
1:G:33:ARG:HG2	1:J:25:GLU:HG2	2.00	0.42
3:H:167:PEB:HNA	3:H:167:PEB:HMB2	1.83	0.42
1:C:97:LEU:HG	1:C:155:LEU:HD12	2.01	0.42
3:P:187:PEB:HBA3	3:P:187:PEB:HHA1	2.00	0.42
2:W:133:LYS:HE3	2:W:173:SER:HB3	2.00	0.42
1:I:43:LYS:HG3	3:I:167:PEB:HBD1	2.01	0.42
2:T:70:MEN:HB2	3:T:186:PEB:OA	2.20	0.42
1:L:1:MET:HG3	1:L:103:GLY:HA3	2.01	0.42
2:Q:54:VAL:HG21	2:Q:81:LEU:HD23	2.01	0.42
3:Q:187:PEB:OD	3:Q:187:PEB:HBD1	2.19	0.42
2:V:148:ARG:NH1	3:V:188:PEB:HND	2.17	0.42
1:C:33:ARG:NH2	1:C:147:GLN:OE1	2.52	0.42
1:L:139:CYS:SG	3:L:167:PEB:HHA1	2.59	0.42
2:P:27:GLN:OE1	2:P:31:GLU:HG3	2.19	0.42
2:Q:56:GLY:HA3	3:Q:188:PEB:HHC2	2.02	0.42
2:U:135:GLN:HG2	3:U:188:PEB:C1B	2.50	0.42
2:V:131:ILE:O	2:V:135:GLN:HG3	2.19	0.42
2:W:111:LEU:HG	2:W:183:LEU:HD21	2.02	0.42
2:X:112:LYS:NZ	2:X:184:SER:O	2.40	0.42
2:X:127:ARG:HA	2:X:127:ARG:HD2	1.83	0.42
2:M:5:PHE:HE1	2:M:28:PHE:CD1	2.37	0.42
2:O:96:LEU:HD12	2:O:96:LEU:HA	1.87	0.42
2:W:31:GLU:O	2:W:34:ARG:HB2	2.19	0.42
3:Q:186:PEB:HNA	3:Q:186:PEB:CMB	2.30	0.41
2:W:33:ASN:HB3	3:W:187:PEB:C1C	2.50	0.41
1:B:58:ALA:O	1:B:61:GLN:HG2	2.19	0.41
3:H:166:PEB:HNA	3:H:166:PEB:CMB	2.33	0.41
2:U:22:MET:HA	2:U:25:LEU:HD12	2.02	0.41
1:L:82:CYS:HA	3:L:166:PEB:HAA1	1.80	0.41
2:P:144:PRO:HG2	2:P:153:LEU:HD11	2.03	0.41
2:T:81:LEU:HD23	2:T:81:LEU:HA	1.93	0.41
1:F:38:LEU:HD23	1:F:38:LEU:HA	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:187:PEB:HMB2	3:N:187:PEB:NA	2.36	0.41
1:K:136:ASN:OD1	2:T:154:ARG:NH1	2.53	0.41
1:K:137:ARG:HG3	3:K:167:PEB:HHC1	2.03	0.41
3:P:188:PEB:HMB3	3:P:188:PEB:HNA	1.86	0.41
2:P:108:LEU:HD21	2:P:179:VAL:HG22	2.02	0.41
2:R:106:ARG:NH2	5:R:189:SO4:O3	2.46	0.41
2:V:111:LEU:HG	2:V:183:LEU:HD21	2.01	0.41
1:G:139:CYS:SG	3:G:167:PEB:HHA1	2.61	0.41
1:B:132:SER:OG	2:Q:154:ARG:NH2	2.54	0.41
3:E:167:PEB:NA	3:E:167:PEB:HMB2	2.36	0.41
2:R:164:ARG:NH2	6:R:2089:HOH:O	2.44	0.41
3:R:188:PEB:HNA	3:R:188:PEB:HMB3	1.85	0.41
1:A:38:LEU:HA	1:A:38:LEU:HD23	1.77	0.41
2:X:132:MET:HA	2:X:135:GLN:OE1	2.21	0.41
3:E:167:PEB:HMB2	3:E:167:PEB:HNA	1.86	0.40
3:G:166:PEB:HNA	3:G:166:PEB:CMB	2.34	0.40
2:Q:37:ASP:OD1	3:Q:187:PEB:HHC1	2.21	0.40
1:A:25:GLU:O	1:D:29:GLY:HA3	2.21	0.40
1:C:114:ARG:HD2	1:E:118:ARG:NH1	2.37	0.40
1:J:155:LEU:HD23	1:J:155:LEU:HA	1.94	0.40
2:V:132:MET:HA	2:V:135:GLN:OE1	2.21	0.40
3:V:187:PEB:NA	3:V:187:PEB:HMB2	2.35	0.40
2:T:155:LYS:HA	2:T:155:LYS:HD3	1.72	0.40
3:D:166:PEB:HNA	3:D:166:PEB:HMB2	1.86	0.40
2:M:29:ILE:HD13	2:M:29:ILE:HA	1.92	0.40
2:O:155:LYS:HD3	2:O:155:LYS:HA	1.90	0.40
2:Q:148:ARG:NH1	3:Q:188:PEB:HND	2.18	0.40
3:U:187:PEB:HNA	3:U:187:PEB:HMB2	1.86	0.40
1:E:108:TRP:O	2:R:73:PRO:HB2	2.21	0.40
1:K:64:PRO:HG3	6:K:2059:HOH:O	2.22	0.40
1:K:127:TYR:CE1	3:K:166:PEB:H3A1	2.57	0.40
2:U:126:VAL:O	2:U:130:GLN:HG3	2.21	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 X-ray entries followed by that with respect to entries

of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	162/164 (99%)	159 (98%)	3 (2%)	0	100	100
1	B	162/164 (99%)	158 (98%)	4 (2%)	0	100	100
1	C	162/164 (99%)	158 (98%)	4 (2%)	0	100	100
1	D	162/164 (99%)	160 (99%)	2 (1%)	0	100	100
1	E	162/164 (99%)	158 (98%)	4 (2%)	0	100	100
1	F	162/164 (99%)	159 (98%)	3 (2%)	0	100	100
1	G	162/164 (99%)	158 (98%)	4 (2%)	0	100	100
1	H	162/164 (99%)	158 (98%)	4 (2%)	0	100	100
1	I	162/164 (99%)	160 (99%)	2 (1%)	0	100	100
1	J	162/164 (99%)	158 (98%)	4 (2%)	0	100	100
1	K	162/164 (99%)	158 (98%)	4 (2%)	0	100	100
1	L	162/164 (99%)	160 (99%)	2 (1%)	0	100	100
2	M	181/184 (98%)	177 (98%)	3 (2%)	1 (1%)	25	20
2	N	181/184 (98%)	180 (99%)	1 (1%)	0	100	100
2	O	181/184 (98%)	178 (98%)	3 (2%)	0	100	100
2	P	181/184 (98%)	175 (97%)	5 (3%)	1 (1%)	25	20
2	Q	181/184 (98%)	175 (97%)	6 (3%)	0	100	100
2	R	181/184 (98%)	173 (96%)	8 (4%)	0	100	100
2	S	181/184 (98%)	176 (97%)	5 (3%)	0	100	100
2	T	181/184 (98%)	176 (97%)	5 (3%)	0	100	100
2	U	181/184 (98%)	174 (96%)	7 (4%)	0	100	100
2	V	181/184 (98%)	177 (98%)	4 (2%)	0	100	100
2	W	181/184 (98%)	177 (98%)	4 (2%)	0	100	100
2	X	181/184 (98%)	176 (97%)	5 (3%)	0	100	100
All	All	4116/4176 (99%)	4018 (98%)	96 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	P	23	GLY

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Mol	Chain	Res	Type
2	M	73	PRO

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 X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	127/127 (100%)	127 (100%)	0	100	100
1	B	127/127 (100%)	127 (100%)	0	100	100
1	C	127/127 (100%)	126 (99%)	1 (1%)	81	86
1	D	127/127 (100%)	127 (100%)	0	100	100
1	E	127/127 (100%)	127 (100%)	0	100	100
1	F	127/127 (100%)	127 (100%)	0	100	100
1	G	127/127 (100%)	127 (100%)	0	100	100
1	H	127/127 (100%)	126 (99%)	1 (1%)	81	86
1	I	127/127 (100%)	127 (100%)	0	100	100
1	J	127/127 (100%)	127 (100%)	0	100	100
1	K	127/127 (100%)	126 (99%)	1 (1%)	81	86
1	L	127/127 (100%)	127 (100%)	0	100	100
2	M	138/138 (100%)	137 (99%)	1 (1%)	84	88
2	N	138/138 (100%)	138 (100%)	0	100	100
2	O	138/138 (100%)	138 (100%)	0	100	100
2	P	138/138 (100%)	137 (99%)	1 (1%)	84	88
2	Q	138/138 (100%)	137 (99%)	1 (1%)	84	88
2	R	138/138 (100%)	138 (100%)	0	100	100
2	S	138/138 (100%)	138 (100%)	0	100	100
2	T	138/138 (100%)	138 (100%)	0	100	100
2	U	138/138 (100%)	138 (100%)	0	100	100
2	V	138/138 (100%)	138 (100%)	0	100	100
2	W	138/138 (100%)	137 (99%)	1 (1%)	84	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	X	138/138 (100%)	138 (100%)	0	100	100
All	All	3180/3180 (100%)	3173 (100%)	7 (0%)	93	96

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	30	SER
1	H	30	SER
1	K	61	GLN
2	M	17	SER
2	P	21	ASP
2	Q	181	SER
2	W	26	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

12 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	$\# Z > 2$
2	MEN	P	70	2	7,8,9	0.51	0	6,9,11	0.69	0
2	MEN	X	70	2	7,8,9	0.52	0	6,9,11	0.46	0
2	MEN	N	70	2	7,8,9	0.53	0	6,9,11	0.75	0
2	MEN	Q	70	2	7,8,9	0.62	0	6,9,11	0.43	0
2	MEN	S	70	2	7,8,9	0.61	0	6,9,11	0.53	0
2	MEN	O	70	2	7,8,9	0.61	0	6,9,11	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MEN	R	70	2	7,8,9	0.51	0	6,9,11	0.34	0
2	MEN	V	70	2	7,8,9	0.68	0	6,9,11	0.76	0
2	MEN	U	70	2	7,8,9	0.62	0	6,9,11	0.98	0
2	MEN	W	70	2	7,8,9	0.46	0	6,9,11	0.68	0
2	MEN	T	70	2	7,8,9	0.56	0	6,9,11	0.55	0
2	MEN	M	70	2	7,8,9	0.57	0	6,9,11	0.37	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MEN	P	70	2	-	4/7/8/10	-
2	MEN	X	70	2	-	4/7/8/10	-
2	MEN	N	70	2	-	4/7/8/10	-
2	MEN	Q	70	2	-	4/7/8/10	-
2	MEN	S	70	2	-	4/7/8/10	-
2	MEN	O	70	2	-	3/7/8/10	-
2	MEN	R	70	2	-	4/7/8/10	-
2	MEN	V	70	2	-	6/7/8/10	-
2	MEN	U	70	2	-	3/7/8/10	-
2	MEN	W	70	2	-	4/7/8/10	-
2	MEN	T	70	2	-	4/7/8/10	-
2	MEN	M	70	2	-	4/7/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (48) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	M	70	MEN	C-CA-CB-CG
2	N	70	MEN	C-CA-CB-CG
2	Q	70	MEN	C-CA-CB-CG
2	T	70	MEN	C-CA-CB-CG
2	V	70	MEN	C-CA-CB-CG
2	V	70	MEN	CB-CG-ND2-CE2

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Mol	Chain	Res	Type	Atoms
2	W	70	MEN	C-CA-CB-CG
2	X	70	MEN	C-CA-CB-CG
2	M	70	MEN	N-CA-CB-CG
2	N	70	MEN	N-CA-CB-CG
2	P	70	MEN	N-CA-CB-CG
2	Q	70	MEN	N-CA-CB-CG
2	T	70	MEN	N-CA-CB-CG
2	V	70	MEN	N-CA-CB-CG
2	W	70	MEN	N-CA-CB-CG
2	X	70	MEN	N-CA-CB-CG
2	O	70	MEN	CA-CB-CG-OD1
2	V	70	MEN	OD1-CG-ND2-CE2
2	N	70	MEN	CA-CB-CG-OD1
2	Q	70	MEN	CA-CB-CG-OD1
2	R	70	MEN	CA-CB-CG-OD1
2	S	70	MEN	CA-CB-CG-OD1
2	V	70	MEN	CA-CB-CG-OD1
2	W	70	MEN	CA-CB-CG-ND2
2	M	70	MEN	CA-CB-CG-OD1
2	T	70	MEN	CA-CB-CG-OD1
2	U	70	MEN	CA-CB-CG-OD1
2	W	70	MEN	CA-CB-CG-OD1
2	X	70	MEN	CA-CB-CG-OD1
2	R	70	MEN	CA-CB-CG-ND2
2	P	70	MEN	C-CA-CB-CG
2	R	70	MEN	C-CA-CB-CG
2	S	70	MEN	C-CA-CB-CG
2	M	70	MEN	CA-CB-CG-ND2
2	N	70	MEN	CA-CB-CG-ND2
2	O	70	MEN	CA-CB-CG-ND2
2	P	70	MEN	CA-CB-CG-ND2
2	Q	70	MEN	CA-CB-CG-ND2
2	S	70	MEN	CA-CB-CG-ND2
2	T	70	MEN	CA-CB-CG-ND2
2	U	70	MEN	CA-CB-CG-ND2
2	V	70	MEN	CA-CB-CG-ND2
2	X	70	MEN	CA-CB-CG-ND2
2	R	70	MEN	N-CA-CB-CG
2	S	70	MEN	N-CA-CB-CG
2	P	70	MEN	CA-CB-CG-OD1
2	O	70	MEN	N-CA-CB-CG
2	U	70	MEN	N-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	V	70	MEN	2	0
2	T	70	MEN	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

90 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PEB	U	186	2	43,46,46	3.56	10 (23%)	45,67,67	2.33	15 (33%)
3	PEB	N	188	2	43,46,46	3.35	8 (18%)	45,67,67	2.12	14 (31%)
3	PEB	M	188	2	43,46,46	3.49	12 (27%)	45,67,67	2.03	15 (33%)
5	SO4	I	1200	-	4,4,4	0.14	0	6,6,6	0.20	0
3	PEB	C	166	1	43,46,46	3.33	10 (23%)	45,67,67	2.46	20 (44%)
3	PEB	O	186	2	43,46,46	3.38	11 (25%)	45,67,67	2.27	17 (37%)
5	SO4	S	189	-	4,4,4	0.12	0	6,6,6	0.11	0
5	SO4	W	189	-	4,4,4	0.14	0	6,6,6	0.15	0
3	PEB	Q	187	2	43,46,46	3.55	12 (27%)	45,67,67	2.05	15 (33%)
3	PEB	N	186	2	43,46,46	3.43	10 (23%)	45,67,67	2.10	15 (33%)
3	PEB	L	167	1	43,46,46	3.19	8 (18%)	45,67,67	2.04	15 (33%)
3	PEB	I	166	1	43,46,46	3.42	11 (25%)	45,67,67	2.44	18 (40%)
4	GOL	F	1165	-	5,5,5	0.33	0	5,5,5	0.33	0
3	PEB	W	186	2	43,46,46	3.44	8 (18%)	45,67,67	2.05	17 (37%)
3	PEB	X	187	2	43,46,46	3.29	11 (25%)	45,67,67	2.10	15 (33%)
3	PEB	H	167	1	43,46,46	3.32	11 (25%)	45,67,67	2.04	14 (31%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PEB	W	187	2	43,46,46	3.24	10 (23%)	45,67,67	2.03	17 (37%)
3	PEB	R	186	2	43,46,46	3.49	10 (23%)	45,67,67	2.00	15 (33%)
3	PEB	I	167	1	43,46,46	3.28	10 (23%)	45,67,67	2.28	16 (35%)
3	PEB	S	187	2	43,46,46	3.37	10 (23%)	45,67,67	2.02	15 (33%)
3	PEB	V	188	2	43,46,46	3.44	11 (25%)	45,67,67	2.04	16 (35%)
4	GOL	B	1165	-	5,5,5	0.35	0	5,5,5	0.45	0
3	PEB	T	188	2	43,46,46	3.52	12 (27%)	45,67,67	2.09	15 (33%)
3	PEB	U	188	2	43,46,46	3.42	9 (20%)	45,67,67	1.95	17 (37%)
4	GOL	I	1165	-	5,5,5	0.34	0	5,5,5	0.34	0
4	GOL	J	1165	-	5,5,5	0.34	0	5,5,5	0.47	0
5	SO4	T	189	-	4,4,4	0.16	0	6,6,6	0.07	0
3	PEB	P	187	2	43,46,46	3.40	8 (18%)	45,67,67	1.91	15 (33%)
3	PEB	V	187	2	43,46,46	3.35	11 (25%)	45,67,67	2.00	17 (37%)
5	SO4	L	1200	-	4,4,4	0.17	0	6,6,6	0.27	0
3	PEB	D	166	1	43,46,46	3.41	10 (23%)	45,67,67	2.40	19 (42%)
3	PEB	Q	186	2	43,46,46	3.37	9 (20%)	45,67,67	2.15	15 (33%)
3	PEB	J	166	1	43,46,46	3.50	10 (23%)	45,67,67	2.46	18 (40%)
3	PEB	D	167	1	43,46,46	3.34	10 (23%)	45,67,67	2.33	16 (35%)
3	PEB	W	188	2	43,46,46	3.43	9 (20%)	45,67,67	1.96	16 (35%)
3	PEB	G	166	1	43,46,46	3.20	10 (23%)	45,67,67	2.36	16 (35%)
3	PEB	G	167	1	43,46,46	3.43	13 (30%)	45,67,67	1.94	14 (31%)
5	SO4	M	189	-	4,4,4	0.19	0	6,6,6	0.15	0
3	PEB	R	187	2	43,46,46	3.28	10 (23%)	45,67,67	1.99	16 (35%)
5	SO4	N	189	-	4,4,4	0.19	0	6,6,6	0.15	0
3	PEB	Q	188	2	43,46,46	3.47	10 (23%)	45,67,67	2.09	14 (31%)
5	SO4	Q	189	-	4,4,4	0.12	0	6,6,6	0.16	0
3	PEB	A	167	1	43,46,46	3.30	9 (20%)	45,67,67	1.92	13 (28%)
3	PEB	N	187	2	43,46,46	3.41	11 (25%)	45,67,67	1.99	15 (33%)
3	PEB	X	186	2	43,46,46	3.39	9 (20%)	45,67,67	2.21	17 (37%)
3	PEB	O	187	2	43,46,46	3.30	10 (23%)	45,67,67	1.86	13 (28%)
4	GOL	D	1165	-	5,5,5	0.30	0	5,5,5	0.48	0
3	PEB	L	166	1	43,46,46	3.31	9 (20%)	45,67,67	2.46	17 (37%)
4	GOL	E	1165	-	5,5,5	0.27	0	5,5,5	0.48	0
3	PEB	K	166	1	43,46,46	3.29	10 (23%)	45,67,67	2.41	16 (35%)
3	PEB	E	167	1	43,46,46	3.39	11 (25%)	45,67,67	1.97	14 (31%)
4	GOL	H	1165	-	5,5,5	0.40	0	5,5,5	0.47	0
5	SO4	X	189	-	4,4,4	0.13	0	6,6,6	0.14	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	SO4	V	189	-	4,4,4	0.10	0	6,6,6	0.24	0
3	PEB	S	186	2	43,46,46	3.51	11 (25%)	45,67,67	2.12	15 (33%)
3	PEB	T	186	2	43,46,46	3.33	9 (20%)	45,67,67	2.40	15 (33%)
3	PEB	M	187	2	43,46,46	3.25	8 (18%)	45,67,67	2.11	14 (31%)
3	PEB	U	187	2	43,46,46	3.41	9 (20%)	45,67,67	2.08	16 (35%)
4	GOL	L	1165	-	5,5,5	0.35	0	5,5,5	0.33	0
5	SO4	O	189	-	4,4,4	0.18	0	6,6,6	0.20	0
3	PEB	E	166	1	43,46,46	3.38	10 (23%)	45,67,67	2.36	17 (37%)
5	SO4	A	1200	-	4,4,4	0.11	0	6,6,6	0.18	0
5	SO4	U	189	-	4,4,4	0.16	0	6,6,6	0.12	0
3	PEB	B	166	1	43,46,46	3.38	10 (23%)	45,67,67	2.41	18 (40%)
4	GOL	G	1165	-	5,5,5	0.29	0	5,5,5	0.35	0
3	PEB	V	186	2	43,46,46	3.34	10 (23%)	45,67,67	2.46	17 (37%)
3	PEB	B	167	1	43,46,46	3.31	11 (25%)	45,67,67	2.06	16 (35%)
3	PEB	F	166	1	43,46,46	3.17	9 (20%)	45,67,67	2.62	18 (40%)
3	PEB	C	167	1	43,46,46	3.28	11 (25%)	45,67,67	1.90	12 (26%)
3	PEB	P	188	2	43,46,46	3.41	11 (25%)	45,67,67	2.07	16 (35%)
3	PEB	K	167	1	43,46,46	3.30	12 (27%)	45,67,67	2.02	14 (31%)
5	SO4	E	1200	-	4,4,4	0.12	0	6,6,6	0.22	0
3	PEB	T	187	2	43,46,46	3.34	10 (23%)	45,67,67	2.05	16 (35%)
4	GOL	K	1165	-	5,5,5	0.34	0	5,5,5	0.38	0
3	PEB	R	188	2	43,46,46	3.43	10 (23%)	45,67,67	2.02	17 (37%)
3	PEB	X	188	2	43,46,46	3.51	10 (23%)	45,67,67	1.98	17 (37%)
3	PEB	M	186	2	43,46,46	3.43	8 (18%)	45,67,67	2.07	16 (35%)
5	SO4	R	189	-	4,4,4	0.12	0	6,6,6	0.15	0
5	SO4	D	1200	-	4,4,4	0.19	0	6,6,6	0.12	0
3	PEB	S	188	2	43,46,46	3.49	11 (25%)	45,67,67	2.09	14 (31%)
3	PEB	F	167	1	43,46,46	3.51	10 (23%)	45,67,67	1.85	13 (28%)
3	PEB	A	166	1	43,46,46	3.41	9 (20%)	45,67,67	2.57	20 (44%)
4	GOL	C	1165	-	5,5,5	0.34	0	5,5,5	0.30	0
5	SO4	P	189	-	4,4,4	0.13	0	6,6,6	0.18	0
5	SO4	H	1200	-	4,4,4	0.22	0	6,6,6	0.17	0
3	PEB	P	186	2	43,46,46	3.45	9 (20%)	45,67,67	2.27	19 (42%)
3	PEB	H	166	1	43,46,46	3.38	11 (25%)	45,67,67	2.32	18 (40%)
3	PEB	O	188	2	43,46,46	3.38	11 (25%)	45,67,67	2.18	16 (35%)
3	PEB	J	167	1	43,46,46	3.30	9 (20%)	45,67,67	1.97	14 (31%)
4	GOL	A	1165	-	5,5,5	0.28	0	5,5,5	0.56	0

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
4	GOL	I	1165	-	-	0/4/4/4	-
4	GOL	J	1165	-	-	2/4/4/4	-
3	PEB	U	186	2	-	7/24/74/74	0/4/4/4
3	PEB	P	187	2	-	8/24/74/74	0/4/4/4
4	GOL	E	1165	-	-	3/4/4/4	-
3	PEB	N	188	2	-	6/24/74/74	0/4/4/4
3	PEB	P	188	2	-	9/24/74/74	0/4/4/4
3	PEB	K	166	1	-	4/24/74/74	0/4/4/4
3	PEB	M	188	2	-	4/24/74/74	0/4/4/4
3	PEB	V	187	2	-	8/24/74/74	0/4/4/4
3	PEB	E	167	1	-	6/24/74/74	0/4/4/4
3	PEB	K	167	1	-	6/24/74/74	0/4/4/4
4	GOL	H	1165	-	-	3/4/4/4	-
3	PEB	D	166	1	-	4/24/74/74	0/4/4/4
3	PEB	T	187	2	-	6/24/74/74	0/4/4/4
3	PEB	C	166	1	-	4/24/74/74	0/4/4/4
3	PEB	S	186	2	-	6/24/74/74	0/4/4/4
3	PEB	Q	186	2	-	6/24/74/74	0/4/4/4
3	PEB	R	188	2	-	9/24/74/74	0/4/4/4
4	GOL	D	1165	-	-	2/4/4/4	-
4	GOL	K	1165	-	-	0/4/4/4	-
3	PEB	J	166	1	-	4/24/74/74	0/4/4/4
3	PEB	D	167	1	-	6/24/74/74	0/4/4/4
3	PEB	O	186	2	-	4/24/74/74	0/4/4/4
3	PEB	T	186	2	-	4/24/74/74	0/4/4/4
3	PEB	W	188	2	-	6/24/74/74	0/4/4/4
3	PEB	X	188	2	-	7/24/74/74	0/4/4/4
3	PEB	M	186	2	-	4/24/74/74	0/4/4/4
3	PEB	G	166	1	-	4/24/74/74	0/4/4/4
3	PEB	M	187	2	-	8/24/74/74	0/4/4/4
3	PEB	U	187	2	-	8/24/74/74	0/4/4/4
4	GOL	L	1165	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PEB	Q	187	2	-	8/24/74/74	0/4/4/4
3	PEB	N	186	2	-	6/24/74/74	0/4/4/4
3	PEB	S	188	2	-	8/24/74/74	0/4/4/4
3	PEB	E	166	1	-	4/24/74/74	0/4/4/4
3	PEB	G	167	1	-	6/24/74/74	0/4/4/4
3	PEB	L	167	1	-	6/24/74/74	0/4/4/4
3	PEB	I	166	1	-	4/24/74/74	0/4/4/4
3	PEB	F	167	1	-	7/24/74/74	0/4/4/4
3	PEB	R	187	2	-	5/24/74/74	0/4/4/4
3	PEB	B	166	1	-	4/24/74/74	0/4/4/4
4	GOL	F	1165	-	-	2/4/4/4	-
3	PEB	A	166	1	-	4/24/74/74	0/4/4/4
3	PEB	J	167	1	-	7/24/74/74	0/4/4/4
3	PEB	Q	188	2	-	6/24/74/74	0/4/4/4
4	GOL	C	1165	-	-	2/4/4/4	-
3	PEB	W	186	2	-	6/24/74/74	0/4/4/4
4	GOL	G	1165	-	-	1/4/4/4	-
3	PEB	X	187	2	-	8/24/74/74	0/4/4/4
3	PEB	H	167	1	-	6/24/74/74	0/4/4/4
3	PEB	W	187	2	-	6/24/74/74	0/4/4/4
3	PEB	R	186	2	-	6/24/74/74	0/4/4/4
3	PEB	V	186	2	-	4/24/74/74	0/4/4/4
3	PEB	B	167	1	-	6/24/74/74	0/4/4/4
3	PEB	S	187	2	-	8/24/74/74	0/4/4/4
3	PEB	A	167	1	-	6/24/74/74	0/4/4/4
3	PEB	V	188	2	-	8/24/74/74	0/4/4/4
3	PEB	F	166	1	-	4/24/74/74	0/4/4/4
3	PEB	C	167	1	-	6/24/74/74	0/4/4/4
3	PEB	N	187	2	-	8/24/74/74	0/4/4/4
3	PEB	X	186	2	-	6/24/74/74	0/4/4/4
3	PEB	P	186	2	-	4/24/74/74	0/4/4/4
3	PEB	O	187	2	-	8/24/74/74	0/4/4/4
4	GOL	B	1165	-	-	4/4/4/4	-
3	PEB	H	166	1	-	4/24/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PEB	O	188	2	-	8/24/74/74	0/4/4/4
3	PEB	I	167	1	-	4/24/74/74	0/4/4/4
3	PEB	T	188	2	-	6/24/74/74	0/4/4/4
4	GOL	A	1165	-	-	2/4/4/4	-
3	PEB	L	166	1	-	4/24/74/74	0/4/4/4
3	PEB	U	188	2	-	7/24/74/74	0/4/4/4

All (602) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	U	186	PEB	CHB-C4B	17.73	1.49	1.35
3	X	188	PEB	CHB-C4B	17.70	1.49	1.35
3	M	188	PEB	CHB-C4B	17.43	1.49	1.35
3	P	186	PEB	CHB-C4B	17.33	1.49	1.35
3	F	167	PEB	CHB-C4B	17.29	1.49	1.35
3	J	166	PEB	CHB-C4B	17.28	1.49	1.35
3	T	188	PEB	CHB-C4B	17.20	1.49	1.35
3	Q	187	PEB	CHB-C4B	17.19	1.49	1.35
3	Q	188	PEB	CHB-C4B	17.19	1.49	1.35
3	S	188	PEB	CHB-C4B	17.15	1.49	1.35
3	S	186	PEB	CHB-C4B	17.10	1.49	1.35
3	R	186	PEB	CHB-C4B	17.00	1.49	1.35
3	W	186	PEB	CHB-C4B	16.90	1.49	1.35
3	M	186	PEB	CHB-C4B	16.74	1.49	1.35
3	X	186	PEB	CHB-C4B	16.70	1.49	1.35
3	P	188	PEB	CHB-C4B	16.65	1.49	1.35
3	U	188	PEB	CHB-C4B	16.64	1.49	1.35
3	G	167	PEB	CHB-C4B	16.60	1.49	1.35
3	U	187	PEB	CHB-C4B	16.55	1.49	1.35
3	V	188	PEB	CHB-C4B	16.55	1.49	1.35
3	O	188	PEB	CHB-C4B	16.50	1.48	1.35
3	N	186	PEB	CHB-C4B	16.49	1.48	1.35
3	N	187	PEB	CHB-C4B	16.47	1.48	1.35
3	S	187	PEB	CHB-C4B	16.45	1.48	1.35
3	E	166	PEB	CHB-C4B	16.45	1.48	1.35
3	D	166	PEB	CHB-C4B	16.42	1.48	1.35
3	W	188	PEB	CHB-C4B	16.42	1.48	1.35
3	P	187	PEB	CHB-C4B	16.38	1.48	1.35
3	R	188	PEB	CHB-C4B	16.38	1.48	1.35
3	D	167	PEB	CHB-C4B	16.36	1.48	1.35
3	I	166	PEB	CHB-C4B	16.34	1.48	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	167	PEB	CHB-C4B	16.33	1.48	1.35
3	O	186	PEB	CHB-C4B	16.30	1.48	1.35
3	H	166	PEB	CHB-C4B	16.25	1.48	1.35
3	B	166	PEB	CHB-C4B	16.24	1.48	1.35
3	H	167	PEB	CHB-C4B	16.14	1.48	1.35
3	A	166	PEB	CHB-C4B	16.08	1.48	1.35
3	T	186	PEB	CHB-C4B	16.08	1.48	1.35
3	V	187	PEB	CHB-C4B	16.05	1.48	1.35
3	T	187	PEB	CHB-C4B	16.02	1.48	1.35
3	Q	186	PEB	CHB-C4B	15.95	1.48	1.35
3	C	166	PEB	CHB-C4B	15.93	1.48	1.35
3	J	167	PEB	CHB-C4B	15.87	1.48	1.35
3	V	186	PEB	CHB-C4B	15.85	1.48	1.35
3	A	167	PEB	CHB-C4B	15.81	1.48	1.35
3	X	187	PEB	CHB-C4B	15.67	1.48	1.35
3	N	188	PEB	CHB-C4B	15.61	1.48	1.35
3	L	166	PEB	CHB-C4B	15.55	1.48	1.35
3	M	187	PEB	CHB-C4B	15.54	1.48	1.35
3	B	167	PEB	CHB-C4B	15.48	1.48	1.35
3	O	187	PEB	CHB-C4B	15.41	1.48	1.35
3	K	167	PEB	CHB-C4B	15.40	1.48	1.35
3	I	167	PEB	CHB-C4B	15.36	1.48	1.35
3	L	167	PEB	CHB-C4B	15.31	1.47	1.35
3	K	166	PEB	CHB-C4B	15.24	1.47	1.35
3	R	187	PEB	CHB-C4B	15.22	1.47	1.35
3	G	166	PEB	CHB-C4B	15.20	1.47	1.35
3	C	167	PEB	CHB-C4B	15.15	1.47	1.35
3	W	187	PEB	CHB-C4B	14.83	1.47	1.35
3	F	166	PEB	CHB-C4B	14.67	1.47	1.35
3	Q	187	PEB	C2D-C3D	10.47	1.48	1.34
3	U	186	PEB	C2D-C3D	10.14	1.47	1.34
3	A	166	PEB	C2D-C3D	10.01	1.47	1.34
3	B	167	PEB	C2D-C3D	9.95	1.47	1.34
3	L	166	PEB	C2D-C3D	9.88	1.47	1.34
3	S	186	PEB	C2D-C3D	9.87	1.47	1.34
3	W	188	PEB	C2D-C3D	9.82	1.47	1.34
3	M	186	PEB	C2D-C3D	9.81	1.47	1.34
3	Q	186	PEB	C2D-C3D	9.79	1.47	1.34
3	R	188	PEB	C2D-C3D	9.78	1.47	1.34
3	R	186	PEB	C2D-C3D	9.72	1.47	1.34
3	U	187	PEB	C2D-C3D	9.72	1.47	1.34
3	N	186	PEB	C2D-C3D	9.67	1.47	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	N	188	PEB	C2D-C3D	9.65	1.46	1.34
3	D	166	PEB	C2D-C3D	9.61	1.46	1.34
3	O	186	PEB	C2D-C3D	9.61	1.46	1.34
3	T	187	PEB	C2D-C3D	9.56	1.46	1.34
3	W	186	PEB	C2D-C3D	9.54	1.46	1.34
3	V	186	PEB	C2D-C3D	9.54	1.46	1.34
3	T	186	PEB	C2D-C3D	9.53	1.46	1.34
3	P	187	PEB	C2D-C3D	9.53	1.46	1.34
3	I	166	PEB	C2D-C3D	9.52	1.46	1.34
3	T	188	PEB	C2D-C3D	9.51	1.46	1.34
3	R	187	PEB	C2D-C3D	9.49	1.46	1.34
3	C	166	PEB	C2D-C3D	9.47	1.46	1.34
3	E	167	PEB	C2D-C3D	9.45	1.46	1.34
3	K	167	PEB	C2D-C3D	9.44	1.46	1.34
3	A	167	PEB	C2D-C3D	9.43	1.46	1.34
3	O	187	PEB	C2D-C3D	9.42	1.46	1.34
3	G	167	PEB	C2D-C3D	9.42	1.46	1.34
3	P	188	PEB	C2D-C3D	9.41	1.46	1.34
3	I	167	PEB	C2D-C3D	9.41	1.46	1.34
3	W	187	PEB	C2D-C3D	9.40	1.46	1.34
3	V	187	PEB	C2D-C3D	9.35	1.46	1.34
3	X	187	PEB	C2D-C3D	9.35	1.46	1.34
3	P	186	PEB	C2D-C3D	9.34	1.46	1.34
3	V	188	PEB	C2D-C3D	9.34	1.46	1.34
3	U	188	PEB	C2D-C3D	9.32	1.46	1.34
3	B	166	PEB	C2D-C3D	9.32	1.46	1.34
3	Q	188	PEB	C2D-C3D	9.31	1.46	1.34
3	F	167	PEB	C2D-C3D	9.30	1.46	1.34
3	O	188	PEB	C2D-C3D	9.30	1.46	1.34
3	F	166	PEB	C2D-C3D	9.28	1.46	1.34
3	K	166	PEB	C2D-C3D	9.27	1.46	1.34
3	C	167	PEB	C2D-C3D	9.25	1.46	1.34
3	S	188	PEB	C2D-C3D	9.23	1.46	1.34
3	H	167	PEB	C2D-C3D	9.18	1.46	1.34
3	N	187	PEB	C2D-C3D	9.17	1.46	1.34
3	E	166	PEB	C2D-C3D	9.15	1.46	1.34
3	X	188	PEB	C2D-C3D	9.13	1.46	1.34
3	X	186	PEB	C2D-C3D	9.13	1.46	1.34
3	J	166	PEB	C2D-C3D	9.11	1.46	1.34
3	J	167	PEB	C2D-C3D	9.09	1.46	1.34
3	G	166	PEB	C2D-C3D	9.02	1.46	1.34
3	M	187	PEB	C2D-C3D	9.00	1.46	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	167	PEB	C2D-C3D	8.98	1.46	1.34
3	H	166	PEB	C2D-C3D	8.90	1.46	1.34
3	S	187	PEB	C2D-C3D	8.90	1.46	1.34
3	M	188	PEB	C2D-C3D	8.78	1.45	1.34
3	L	167	PEB	C2D-C3D	8.53	1.45	1.34
3	N	188	PEB	C3C-C4C	6.15	1.51	1.42
3	F	166	PEB	C3C-C4C	5.94	1.51	1.42
3	O	187	PEB	C3C-C4C	5.84	1.51	1.42
3	C	167	PEB	C3C-C4C	5.77	1.51	1.42
3	F	167	PEB	C3B-C2B	5.73	1.48	1.36
3	S	188	PEB	C3C-C4C	5.73	1.51	1.42
3	R	188	PEB	C3B-C2B	5.71	1.48	1.36
3	H	166	PEB	C3C-C4C	5.71	1.51	1.42
3	K	166	PEB	C3C-C4C	5.70	1.51	1.42
3	P	187	PEB	C3C-C4C	5.69	1.50	1.42
3	C	166	PEB	C3C-C4C	5.69	1.50	1.42
3	N	188	PEB	C3B-C2B	5.68	1.48	1.36
3	G	167	PEB	C3B-C2B	5.67	1.48	1.36
3	E	166	PEB	C3C-C4C	5.67	1.50	1.42
3	T	186	PEB	C3C-C4C	5.62	1.50	1.42
3	P	187	PEB	C3B-C2B	5.61	1.48	1.36
3	P	188	PEB	C3B-C2B	5.61	1.48	1.36
3	B	166	PEB	C3C-C4C	5.59	1.50	1.42
3	N	187	PEB	C3B-C2B	5.58	1.48	1.36
3	H	166	PEB	C3B-C2B	5.57	1.48	1.36
3	X	186	PEB	C3C-C4C	5.56	1.50	1.42
3	T	187	PEB	C3C-C4C	5.54	1.50	1.42
3	W	188	PEB	C3B-C2B	5.53	1.48	1.36
3	W	187	PEB	C3B-C2B	5.53	1.48	1.36
3	V	186	PEB	C3C-C4C	5.51	1.50	1.42
3	Q	186	PEB	C3C-C4C	5.50	1.50	1.42
3	V	188	PEB	C3C-C4C	5.49	1.50	1.42
3	R	186	PEB	C3C-C4C	5.49	1.50	1.42
3	F	167	PEB	C3C-C4C	5.49	1.50	1.42
3	Q	188	PEB	C3B-C2B	5.48	1.48	1.36
3	M	188	PEB	C3C-C4C	5.48	1.50	1.42
3	B	166	PEB	C3B-C2B	5.47	1.48	1.36
3	U	187	PEB	C3C-C4C	5.46	1.50	1.42
3	S	188	PEB	C3B-C2B	5.46	1.48	1.36
3	L	167	PEB	C3B-C2B	5.46	1.48	1.36
3	I	166	PEB	C3C-C4C	5.46	1.50	1.42
3	U	188	PEB	C3B-C2B	5.45	1.48	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	167	PEB	C3B-C2B	5.45	1.48	1.36
3	T	188	PEB	C3B-C2B	5.44	1.48	1.36
3	I	167	PEB	C3B-C2B	5.44	1.48	1.36
3	J	167	PEB	C3B-C2B	5.43	1.48	1.36
3	W	188	PEB	C3C-C4C	5.43	1.50	1.42
3	V	187	PEB	C3C-C4C	5.42	1.50	1.42
3	C	167	PEB	C3B-C2B	5.42	1.48	1.36
3	S	187	PEB	C3C-C4C	5.42	1.50	1.42
3	R	187	PEB	C3B-C2B	5.42	1.48	1.36
3	U	187	PEB	C3B-C2B	5.41	1.48	1.36
3	J	166	PEB	C3B-C2B	5.40	1.48	1.36
3	O	186	PEB	C3C-C4C	5.39	1.50	1.42
3	G	166	PEB	C3B-C2B	5.39	1.48	1.36
3	M	187	PEB	C3B-C2B	5.38	1.48	1.36
3	A	166	PEB	C3B-C2B	5.36	1.48	1.36
3	A	166	PEB	C3C-C4C	5.35	1.50	1.42
3	S	186	PEB	C3B-C2B	5.34	1.48	1.36
3	E	166	PEB	C3B-C2B	5.34	1.48	1.36
3	X	188	PEB	C3C-C4C	5.34	1.50	1.42
3	O	188	PEB	C3C-C4C	5.33	1.50	1.42
3	K	167	PEB	C3B-C2B	5.32	1.48	1.36
3	V	188	PEB	C3B-C2B	5.32	1.48	1.36
3	G	166	PEB	C3C-C4C	5.31	1.50	1.42
3	M	188	PEB	C3B-C2B	5.31	1.48	1.36
3	B	167	PEB	C3B-C2B	5.31	1.48	1.36
3	I	166	PEB	C3B-C2B	5.30	1.48	1.36
3	U	188	PEB	C3C-C4C	5.29	1.50	1.42
3	L	166	PEB	C3B-C2B	5.29	1.48	1.36
3	W	186	PEB	C3B-C2B	5.28	1.47	1.36
3	N	186	PEB	C3C-C4C	5.28	1.50	1.42
3	N	187	PEB	C3C-C4C	5.27	1.50	1.42
3	X	187	PEB	C3C-C4C	5.27	1.50	1.42
3	Q	187	PEB	C3B-C2B	5.26	1.47	1.36
3	R	188	PEB	C3C-C4C	5.26	1.50	1.42
3	D	166	PEB	C3B-C2B	5.26	1.47	1.36
3	E	167	PEB	C3B-C2B	5.25	1.47	1.36
3	L	166	PEB	C3C-C4C	5.25	1.50	1.42
3	L	167	PEB	C3C-C4C	5.23	1.50	1.42
3	F	166	PEB	C3B-C2B	5.21	1.47	1.36
3	J	167	PEB	C3C-C4C	5.21	1.50	1.42
3	T	188	PEB	C3C-C4C	5.20	1.50	1.42
3	R	187	PEB	C3C-C4C	5.19	1.50	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	Q	188	PEB	C3C-C4C	5.19	1.50	1.42
3	K	166	PEB	C3B-C2B	5.18	1.47	1.36
3	V	187	PEB	C3B-C2B	5.16	1.47	1.36
3	X	186	PEB	C3B-C2B	5.16	1.47	1.36
3	D	167	PEB	C3B-C2B	5.16	1.47	1.36
3	S	187	PEB	C3B-C2B	5.16	1.47	1.36
3	U	186	PEB	C3C-C4C	5.15	1.50	1.42
3	N	186	PEB	C3B-C2B	5.15	1.47	1.36
3	B	167	PEB	C3C-C4C	5.15	1.50	1.42
3	P	188	PEB	C3C-C4C	5.15	1.50	1.42
3	V	186	PEB	C3B-C2B	5.14	1.47	1.36
3	D	166	PEB	C3C-C4C	5.14	1.50	1.42
3	E	167	PEB	C3C-C4C	5.14	1.50	1.42
3	X	187	PEB	C3B-C2B	5.14	1.47	1.36
3	S	186	PEB	C3C-C4C	5.13	1.50	1.42
3	J	166	PEB	C3C-C4C	5.13	1.50	1.42
3	M	186	PEB	C3B-C2B	5.13	1.47	1.36
3	X	188	PEB	C3B-C2B	5.11	1.47	1.36
3	G	167	PEB	C3C-C4C	5.11	1.50	1.42
3	U	186	PEB	C3B-C2B	5.11	1.47	1.36
3	O	187	PEB	C3B-C2B	5.09	1.47	1.36
3	Q	187	PEB	C3C-C4C	5.08	1.50	1.42
3	K	167	PEB	C3C-C4C	5.07	1.50	1.42
3	P	186	PEB	C3B-C2B	5.06	1.47	1.36
3	Q	186	PEB	C3B-C2B	5.05	1.47	1.36
3	T	187	PEB	C3B-C2B	5.03	1.47	1.36
3	H	167	PEB	C3C-C4C	5.02	1.49	1.42
3	C	166	PEB	C3B-C2B	5.01	1.47	1.36
3	H	167	PEB	C3B-C2B	4.99	1.47	1.36
3	W	186	PEB	C3C-C4C	4.99	1.49	1.42
3	A	167	PEB	C3C-C4C	4.98	1.49	1.42
3	R	186	PEB	C3B-C2B	4.97	1.47	1.36
3	M	187	PEB	C3C-C4C	4.93	1.49	1.42
3	M	186	PEB	C3C-C4C	4.93	1.49	1.42
3	W	187	PEB	C3C-C4C	4.91	1.49	1.42
3	P	186	PEB	C3C-C4C	4.90	1.49	1.42
3	I	167	PEB	C3C-C4C	4.89	1.49	1.42
3	D	167	PEB	C3C-C4C	4.84	1.49	1.42
3	O	188	PEB	C3B-C2B	4.81	1.47	1.36
3	T	186	PEB	C3B-C2B	4.78	1.46	1.36
3	O	186	PEB	C3B-C2B	4.77	1.46	1.36
3	S	186	PEB	CHA-C1B	4.73	1.51	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	166	PEB	C2A-C1A	-4.69	1.47	1.52
3	R	186	PEB	CHA-C1B	4.32	1.50	1.40
3	W	186	PEB	CHA-C1B	4.32	1.50	1.40
3	N	186	PEB	CHA-C1B	4.29	1.50	1.40
3	O	186	PEB	CHA-C1B	4.27	1.50	1.40
3	W	188	PEB	CHA-C1B	4.23	1.50	1.40
3	B	166	PEB	CHA-C1B	4.22	1.50	1.40
3	S	188	PEB	CHA-C1B	4.21	1.50	1.40
3	W	187	PEB	CHA-C1B	4.18	1.50	1.40
3	I	166	PEB	CHA-C1B	4.16	1.50	1.40
3	H	166	PEB	CHA-C1B	4.15	1.50	1.40
3	Q	188	PEB	CHA-C1B	4.13	1.50	1.40
3	U	186	PEB	CHA-C1B	4.12	1.50	1.40
3	V	186	PEB	CHA-C1B	4.11	1.50	1.40
3	M	188	PEB	CHA-C1B	4.10	1.50	1.40
3	X	188	PEB	CHA-C1B	4.10	1.50	1.40
3	V	188	PEB	CHA-C1B	4.09	1.50	1.40
3	O	187	PEB	CHA-C1B	4.09	1.50	1.40
3	K	166	PEB	CHA-C1B	4.08	1.50	1.40
3	N	187	PEB	CHA-C1B	4.08	1.50	1.40
3	T	188	PEB	CHA-C1B	4.07	1.49	1.40
3	M	186	PEB	CHA-C1B	4.06	1.49	1.40
3	P	188	PEB	CHA-C1B	4.05	1.49	1.40
3	R	188	PEB	CHA-C1B	4.02	1.49	1.40
3	S	187	PEB	CHA-C1B	4.01	1.49	1.40
3	M	187	PEB	CHA-C1B	3.98	1.49	1.40
3	O	188	PEB	CHA-C1B	3.98	1.49	1.40
3	P	186	PEB	CHA-C1B	3.98	1.49	1.40
3	U	187	PEB	CHA-C1B	3.98	1.49	1.40
3	T	187	PEB	CHA-C1B	3.97	1.49	1.40
3	U	188	PEB	CHA-C1B	3.96	1.49	1.40
3	P	187	PEB	CHA-C1B	3.95	1.49	1.40
3	R	187	PEB	CHA-C1B	3.92	1.49	1.40
3	E	166	PEB	CHA-C1B	3.91	1.49	1.40
3	B	167	PEB	CHA-C1B	3.89	1.49	1.40
3	X	187	PEB	CHA-C1B	3.87	1.49	1.40
3	E	167	PEB	CHA-C1B	3.87	1.49	1.40
3	W	187	PEB	C1A-NA	-3.80	1.32	1.37
3	Q	186	PEB	CHA-C1B	3.78	1.49	1.40
3	K	167	PEB	CHA-C1B	3.78	1.49	1.40
3	Q	186	PEB	C2C-C3C	3.76	1.48	1.37
3	H	167	PEB	CHA-C1B	3.74	1.49	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	V	187	PEB	CHA-C1B	3.73	1.49	1.40
3	Q	187	PEB	CHA-C1B	3.72	1.49	1.40
3	J	166	PEB	C2C-C3C	3.72	1.48	1.37
3	X	186	PEB	CHA-C1B	3.71	1.49	1.40
3	G	167	PEB	CHA-C1B	3.70	1.49	1.40
3	F	167	PEB	CHA-C1B	3.69	1.49	1.40
3	D	166	PEB	CHA-C1B	3.69	1.49	1.40
3	D	167	PEB	CHA-C1B	3.69	1.49	1.40
3	T	186	PEB	CHA-C1B	3.67	1.49	1.40
3	N	187	PEB	C2C-C3C	3.67	1.48	1.37
3	W	186	PEB	C2C-C3C	3.66	1.48	1.37
3	C	167	PEB	CHA-C1B	3.66	1.49	1.40
3	V	188	PEB	C2C-C3C	3.64	1.48	1.37
3	I	167	PEB	CHA-C1B	3.62	1.48	1.40
3	H	166	PEB	C2C-C3C	3.62	1.48	1.37
3	U	186	PEB	C2C-C3C	3.61	1.48	1.37
3	N	186	PEB	C2C-C3C	3.61	1.48	1.37
3	N	188	PEB	CHA-C1B	3.61	1.48	1.40
3	T	186	PEB	C2C-C3C	3.60	1.48	1.37
3	X	186	PEB	C2C-C3C	3.59	1.48	1.37
3	T	188	PEB	C2C-C3C	3.58	1.48	1.37
3	M	186	PEB	C2C-C3C	3.56	1.48	1.37
3	A	167	PEB	C2C-C3C	3.55	1.48	1.37
3	B	166	PEB	C2C-C3C	3.55	1.48	1.37
3	T	188	PEB	C1A-NA	-3.55	1.33	1.37
3	K	167	PEB	C1A-NA	-3.55	1.33	1.37
3	I	166	PEB	C2C-C3C	3.54	1.48	1.37
3	W	187	PEB	C2C-C3C	3.54	1.48	1.37
3	K	166	PEB	C2C-C3C	3.54	1.48	1.37
3	W	188	PEB	C2C-C3C	3.54	1.48	1.37
3	O	187	PEB	C2C-C3C	3.54	1.48	1.37
3	M	187	PEB	C1A-NA	-3.53	1.33	1.37
3	L	167	PEB	CHA-C1B	3.53	1.48	1.40
3	V	187	PEB	C2C-C3C	3.51	1.48	1.37
3	V	188	PEB	C1A-NA	-3.51	1.33	1.37
3	J	167	PEB	CHA-C1B	3.50	1.48	1.40
3	M	188	PEB	C1A-NA	-3.50	1.33	1.37
3	R	187	PEB	C1A-NA	-3.50	1.33	1.37
3	A	166	PEB	CHA-C1B	3.50	1.48	1.40
3	C	166	PEB	C2C-C3C	3.49	1.48	1.37
3	L	166	PEB	CHA-C1B	3.49	1.48	1.40
3	S	187	PEB	C1A-NA	-3.49	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	Q	188	PEB	C2C-C3C	3.48	1.48	1.37
3	J	166	PEB	CHA-C1B	3.46	1.48	1.40
3	M	187	PEB	C2C-C3C	3.46	1.47	1.37
3	O	186	PEB	C2C-C3C	3.46	1.47	1.37
3	E	166	PEB	C2C-C3C	3.45	1.47	1.37
3	F	167	PEB	C1A-NA	-3.45	1.33	1.37
3	E	167	PEB	C2C-C3C	3.45	1.47	1.37
3	P	188	PEB	C2C-C3C	3.45	1.47	1.37
3	G	166	PEB	C2C-C3C	3.45	1.47	1.37
3	F	166	PEB	C2C-C3C	3.44	1.47	1.37
3	F	167	PEB	C2C-C3C	3.44	1.47	1.37
3	G	167	PEB	C2C-C3C	3.44	1.47	1.37
3	A	166	PEB	C2C-C3C	3.43	1.47	1.37
3	P	187	PEB	C2C-C3C	3.43	1.47	1.37
3	I	167	PEB	C2C-C3C	3.43	1.47	1.37
3	R	187	PEB	C2C-C3C	3.43	1.47	1.37
3	D	166	PEB	C2C-C3C	3.42	1.47	1.37
3	N	187	PEB	C1A-NA	-3.42	1.33	1.37
3	K	167	PEB	C2C-C3C	3.41	1.47	1.37
3	O	187	PEB	C1A-NA	-3.40	1.33	1.37
3	C	166	PEB	C2A-C1A	-3.40	1.49	1.52
3	F	166	PEB	CHA-C1B	3.40	1.48	1.40
3	X	188	PEB	C2C-C3C	3.39	1.47	1.37
3	H	167	PEB	C2C-C3C	3.39	1.47	1.37
3	P	186	PEB	C2C-C3C	3.39	1.47	1.37
3	R	188	PEB	C2C-C3C	3.39	1.47	1.37
3	R	186	PEB	C2C-C3C	3.37	1.47	1.37
3	T	187	PEB	C2C-C3C	3.37	1.47	1.37
3	S	186	PEB	C2C-C3C	3.36	1.47	1.37
3	Q	187	PEB	C2C-C3C	3.36	1.47	1.37
3	J	167	PEB	C2C-C3C	3.35	1.47	1.37
3	M	188	PEB	C2C-C3C	3.35	1.47	1.37
3	C	167	PEB	C2C-C3C	3.34	1.47	1.37
3	W	186	PEB	C1A-NA	-3.34	1.33	1.37
3	A	167	PEB	CHA-C1B	3.33	1.48	1.40
3	L	166	PEB	C2C-C3C	3.32	1.47	1.37
3	V	186	PEB	C2C-C3C	3.31	1.47	1.37
3	O	188	PEB	C2C-C3C	3.31	1.47	1.37
3	L	167	PEB	C2C-C3C	3.30	1.47	1.37
3	N	188	PEB	C2C-C3C	3.28	1.47	1.37
3	I	167	PEB	C1A-NA	-3.27	1.33	1.37
3	I	167	PEB	OD-C4D	3.27	1.29	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	167	PEB	C2C-C3C	3.27	1.47	1.37
3	R	186	PEB	OD-C4D	3.26	1.29	1.23
3	A	166	PEB	OD-C4D	3.26	1.29	1.23
3	S	188	PEB	C2C-C3C	3.25	1.47	1.37
3	X	187	PEB	C2C-C3C	3.24	1.47	1.37
3	D	166	PEB	C2A-C1A	-3.24	1.49	1.52
3	S	187	PEB	C2C-C3C	3.23	1.47	1.37
3	U	188	PEB	C2C-C3C	3.22	1.47	1.37
3	G	166	PEB	CHA-C1B	3.21	1.47	1.40
3	X	187	PEB	C1A-NA	-3.21	1.33	1.37
3	C	167	PEB	C1A-NA	-3.20	1.33	1.37
3	L	167	PEB	C1A-NA	-3.19	1.33	1.37
3	D	167	PEB	C2C-C3C	3.19	1.47	1.37
3	Q	186	PEB	C1A-NA	-3.18	1.33	1.37
3	Q	188	PEB	OD-C4D	3.18	1.29	1.23
3	C	167	PEB	OD-C4D	3.17	1.29	1.23
3	W	188	PEB	C1A-NA	-3.16	1.33	1.37
3	R	188	PEB	C1A-NA	-3.16	1.33	1.37
3	P	187	PEB	OD-C4D	3.13	1.29	1.23
3	I	166	PEB	C2A-C1A	-3.13	1.49	1.52
3	B	167	PEB	C1A-NA	-3.13	1.33	1.37
3	U	187	PEB	C2C-C3C	3.13	1.46	1.37
3	N	188	PEB	C1A-NA	-3.13	1.33	1.37
3	L	166	PEB	OD-C4D	3.13	1.29	1.23
3	K	167	PEB	OD-C4D	3.13	1.29	1.23
3	J	167	PEB	C1A-NA	-3.11	1.33	1.37
3	B	166	PEB	OD-C4D	3.11	1.29	1.23
3	A	167	PEB	OD-C4D	3.10	1.29	1.23
3	K	166	PEB	OD-C4D	3.09	1.29	1.23
3	R	187	PEB	OD-C4D	3.08	1.29	1.23
3	Q	187	PEB	C1A-NA	-3.08	1.33	1.37
3	R	186	PEB	C1A-NA	-3.08	1.33	1.37
3	D	166	PEB	OD-C4D	3.08	1.29	1.23
3	E	167	PEB	C1A-NA	-3.07	1.33	1.37
3	V	187	PEB	C1A-NA	-3.06	1.33	1.37
3	V	187	PEB	OD-C4D	3.06	1.29	1.23
3	G	167	PEB	C1A-NA	-3.05	1.33	1.37
3	S	186	PEB	OD-C4D	3.04	1.29	1.23
3	C	166	PEB	CHA-C1B	3.04	1.47	1.40
3	Q	186	PEB	OD-C4D	3.02	1.29	1.23
3	B	166	PEB	C2A-C1A	-3.01	1.49	1.52
3	U	187	PEB	OD-C4D	3.01	1.29	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	187	PEB	C1A-NA	-3.01	1.33	1.37
3	E	167	PEB	OD-C4D	3.00	1.29	1.23
3	X	188	PEB	OD-C4D	3.00	1.29	1.23
3	V	188	PEB	OD-C4D	2.98	1.29	1.23
3	Q	187	PEB	OD-C4D	2.97	1.29	1.23
3	G	166	PEB	C1A-NA	-2.96	1.33	1.37
3	D	167	PEB	OD-C4D	2.95	1.29	1.23
3	O	187	PEB	OD-C4D	2.95	1.29	1.23
3	H	167	PEB	C1A-NA	-2.94	1.33	1.37
3	O	188	PEB	OD-C4D	2.93	1.29	1.23
3	O	188	PEB	C1A-NA	-2.93	1.33	1.37
3	U	188	PEB	OD-C4D	2.93	1.29	1.23
3	T	188	PEB	OD-C4D	2.92	1.29	1.23
3	X	188	PEB	C1A-NA	-2.92	1.33	1.37
3	X	186	PEB	C1A-NA	-2.92	1.33	1.37
3	U	188	PEB	C1A-NA	-2.92	1.33	1.37
3	P	188	PEB	C1A-NA	-2.91	1.33	1.37
3	C	166	PEB	OD-C4D	2.91	1.29	1.23
3	W	187	PEB	C2A-C1A	-2.91	1.49	1.52
3	P	188	PEB	OD-C4D	2.90	1.29	1.23
3	S	186	PEB	C1A-NA	-2.89	1.33	1.37
3	V	186	PEB	C2A-C1A	-2.87	1.49	1.52
3	S	188	PEB	C1A-NA	-2.87	1.33	1.37
3	E	166	PEB	OD-C4D	2.87	1.29	1.23
3	G	167	PEB	OD-C4D	2.87	1.29	1.23
3	H	166	PEB	OD-C4D	2.87	1.29	1.23
3	I	166	PEB	OD-C4D	2.84	1.29	1.23
3	W	188	PEB	OD-C4D	2.83	1.29	1.23
3	I	166	PEB	C1A-NA	-2.82	1.33	1.37
3	P	186	PEB	C1A-NA	-2.82	1.34	1.37
3	T	187	PEB	OD-C4D	2.80	1.28	1.23
3	U	187	PEB	C1A-NA	-2.79	1.34	1.37
3	P	186	PEB	OD-C4D	2.78	1.28	1.23
3	D	167	PEB	C1A-NA	-2.78	1.34	1.37
3	N	188	PEB	OD-C4D	2.78	1.28	1.23
3	N	187	PEB	OD-C4D	2.78	1.28	1.23
3	J	167	PEB	OD-C4D	2.77	1.28	1.23
3	O	186	PEB	C2A-C1A	-2.77	1.49	1.52
3	M	186	PEB	C1A-NA	-2.76	1.34	1.37
3	M	186	PEB	OD-C4D	2.76	1.28	1.23
3	R	188	PEB	OD-C4D	2.76	1.28	1.23
3	H	167	PEB	OD-C4D	2.76	1.28	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	S	187	PEB	OD-C4D	2.75	1.28	1.23
3	N	186	PEB	C1A-NA	-2.74	1.34	1.37
3	X	186	PEB	OD-C4D	2.72	1.28	1.23
3	N	186	PEB	OD-C4D	2.72	1.28	1.23
3	A	167	PEB	C1A-NA	-2.72	1.34	1.37
3	S	188	PEB	OD-C4D	2.71	1.28	1.23
3	T	186	PEB	OD-C4D	2.69	1.28	1.23
3	M	188	PEB	OD-C4D	2.69	1.28	1.23
3	A	166	PEB	C2A-C1A	-2.69	1.49	1.52
3	J	166	PEB	OD-C4D	2.69	1.28	1.23
3	D	166	PEB	C1A-NA	-2.69	1.34	1.37
3	V	186	PEB	C1A-NA	-2.68	1.34	1.37
3	H	166	PEB	C1A-NA	-2.68	1.34	1.37
3	Q	188	PEB	C1A-NA	-2.67	1.34	1.37
3	K	166	PEB	C2A-C1A	-2.66	1.49	1.52
3	V	187	PEB	C2A-C1A	-2.64	1.49	1.52
3	A	166	PEB	C1A-NA	-2.64	1.34	1.37
3	D	167	PEB	C2A-C1A	-2.64	1.49	1.52
3	B	167	PEB	OD-C4D	2.63	1.28	1.23
3	T	186	PEB	C1A-NA	-2.61	1.34	1.37
3	J	166	PEB	C1A-NA	-2.60	1.34	1.37
3	F	167	PEB	OD-C4D	2.60	1.28	1.23
3	K	166	PEB	C1A-NA	-2.58	1.34	1.37
3	D	167	PEB	C4B-C3B	2.57	1.49	1.45
3	V	186	PEB	OD-C4D	2.55	1.28	1.23
3	U	188	PEB	C4B-C3B	2.53	1.49	1.45
3	E	166	PEB	C1A-NA	-2.52	1.34	1.37
3	K	166	PEB	C1B-C2B	2.52	1.51	1.45
3	O	186	PEB	C1A-NA	-2.52	1.34	1.37
3	E	166	PEB	C2A-C1A	-2.51	1.49	1.52
3	U	186	PEB	OD-C4D	2.51	1.28	1.23
3	T	187	PEB	C1A-NA	-2.51	1.34	1.37
3	L	166	PEB	C1A-NA	-2.51	1.34	1.37
3	W	186	PEB	OD-C4D	2.50	1.28	1.23
3	T	188	PEB	C4B-C3B	2.49	1.49	1.45
3	C	166	PEB	C1A-NA	-2.49	1.34	1.37
3	C	167	PEB	C1D-ND	2.48	1.49	1.45
3	O	188	PEB	C4B-C3B	2.47	1.49	1.45
3	H	167	PEB	C2A-C1A	-2.45	1.49	1.52
3	G	166	PEB	C2A-C1A	-2.44	1.49	1.52
3	L	167	PEB	OD-C4D	2.43	1.28	1.23
3	F	166	PEB	C1A-NA	-2.43	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	U	186	PEB	C1A-NA	-2.43	1.34	1.37
3	H	166	PEB	C1B-C2B	2.42	1.51	1.45
3	N	186	PEB	C2A-C1A	-2.41	1.49	1.52
3	W	187	PEB	OD-C4D	2.41	1.28	1.23
3	O	186	PEB	OD-C4D	2.41	1.28	1.23
3	X	187	PEB	OD-C4D	2.41	1.28	1.23
3	I	167	PEB	C4B-C3B	2.38	1.49	1.45
3	M	187	PEB	C1D-ND	2.37	1.49	1.45
3	H	166	PEB	C2A-C1A	-2.36	1.50	1.52
3	R	187	PEB	C1D-ND	2.34	1.49	1.45
3	P	188	PEB	C4B-C3B	2.34	1.49	1.45
3	E	167	PEB	C4B-C3B	2.34	1.49	1.45
3	K	167	PEB	C1D-ND	2.33	1.49	1.45
3	X	187	PEB	C2A-C1A	-2.31	1.50	1.52
3	T	187	PEB	C1D-ND	2.30	1.49	1.45
3	S	188	PEB	C2A-C1A	-2.29	1.50	1.52
3	M	188	PEB	C4B-C3B	2.29	1.49	1.45
3	I	166	PEB	C1B-C2B	2.29	1.50	1.45
3	V	188	PEB	C1D-ND	2.28	1.49	1.45
3	A	167	PEB	C1D-ND	2.28	1.49	1.45
3	G	167	PEB	C1D-ND	2.27	1.49	1.45
3	F	166	PEB	C2A-C1A	-2.27	1.50	1.52
3	G	166	PEB	OD-C4D	2.26	1.27	1.23
3	T	186	PEB	C2A-C1A	-2.25	1.50	1.52
3	G	167	PEB	C4B-C3B	2.25	1.49	1.45
3	H	167	PEB	C1D-ND	2.25	1.49	1.45
3	V	188	PEB	C4B-C3B	2.25	1.49	1.45
3	V	186	PEB	C1B-C2B	2.24	1.50	1.45
3	R	188	PEB	C4B-C3B	2.24	1.49	1.45
3	X	188	PEB	C4B-C3B	2.23	1.49	1.45
3	I	167	PEB	C1D-ND	2.23	1.49	1.45
3	Q	187	PEB	C1D-ND	2.23	1.49	1.45
3	N	187	PEB	C4B-C3B	2.22	1.49	1.45
3	O	186	PEB	C1B-C2B	2.22	1.50	1.45
3	B	167	PEB	C1D-ND	2.22	1.49	1.45
3	K	167	PEB	C4B-C3B	2.21	1.49	1.45
3	V	188	PEB	C4A-NA	-2.21	1.32	1.37
3	Q	187	PEB	C1C-CHB	2.21	1.49	1.41
3	M	188	PEB	C1B-C2B	2.21	1.50	1.45
3	E	166	PEB	C1C-CHB	2.21	1.49	1.41
3	E	167	PEB	C1D-ND	2.20	1.49	1.45
3	O	188	PEB	C1C-CHB	2.18	1.49	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	X	187	PEB	C1D-ND	2.18	1.49	1.45
3	N	186	PEB	C1D-ND	2.17	1.49	1.45
3	Q	187	PEB	C4B-C3B	2.17	1.49	1.45
3	Q	186	PEB	C1B-C2B	2.16	1.50	1.45
3	O	187	PEB	C2A-C1A	-2.16	1.50	1.52
3	P	186	PEB	C1C-CHB	2.16	1.49	1.41
3	N	187	PEB	C1C-CHB	2.16	1.49	1.41
3	U	186	PEB	C1B-C2B	2.15	1.50	1.45
3	V	187	PEB	C1D-ND	2.15	1.49	1.45
3	T	188	PEB	C1C-CHB	2.15	1.49	1.41
3	M	188	PEB	C2A-C1A	-2.14	1.50	1.52
3	S	188	PEB	C1C-CHB	2.14	1.49	1.41
3	B	166	PEB	C1A-NA	-2.14	1.34	1.37
3	Q	188	PEB	C1B-C2B	2.14	1.50	1.45
3	W	187	PEB	C4A-NA	-2.14	1.32	1.37
3	S	188	PEB	C4B-C3B	2.13	1.49	1.45
3	F	166	PEB	C1B-C2B	2.13	1.50	1.45
3	U	186	PEB	C2A-C1A	-2.13	1.50	1.52
3	J	167	PEB	C4B-C3B	2.13	1.49	1.45
3	J	166	PEB	C1C-CHB	2.13	1.49	1.41
3	S	186	PEB	C1C-CHB	2.13	1.49	1.41
3	I	166	PEB	C1C-CHB	2.12	1.49	1.41
3	G	167	PEB	C1C-CHB	2.11	1.49	1.41
3	B	167	PEB	C1B-C2B	2.11	1.50	1.45
3	E	167	PEB	C1C-CHB	2.11	1.49	1.41
3	K	167	PEB	C1B-C2B	2.11	1.50	1.45
3	Q	187	PEB	C4A-NA	-2.09	1.32	1.37
3	R	186	PEB	C1D-ND	2.09	1.48	1.45
3	P	188	PEB	C1C-CHB	2.08	1.49	1.41
3	X	188	PEB	C1C-CHB	2.08	1.49	1.41
3	H	166	PEB	C1C-CHB	2.08	1.49	1.41
3	C	167	PEB	C4A-NA	-2.08	1.33	1.37
3	N	187	PEB	C2A-C1A	-2.07	1.50	1.52
3	R	186	PEB	C1C-CHB	2.07	1.49	1.41
3	X	186	PEB	C4A-NA	-2.06	1.33	1.37
3	O	186	PEB	C1C-CHB	2.06	1.49	1.41
3	Q	188	PEB	C1C-CHB	2.06	1.49	1.41
3	B	166	PEB	C1B-C2B	2.06	1.50	1.45
3	U	187	PEB	C1C-CHB	2.06	1.49	1.41
3	R	188	PEB	C1C-CHB	2.06	1.49	1.41
3	T	188	PEB	C1B-C2B	2.05	1.50	1.45
3	S	186	PEB	C1B-C2B	2.05	1.50	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	S	187	PEB	C1D-ND	2.05	1.48	1.45
3	K	167	PEB	C2A-C1A	-2.05	1.50	1.52
3	F	167	PEB	C1C-CHB	2.04	1.49	1.41
3	O	187	PEB	C1D-ND	2.04	1.48	1.45
3	C	167	PEB	C4B-C3B	2.04	1.49	1.45
3	S	186	PEB	C2A-C1A	-2.04	1.50	1.52
3	M	188	PEB	C1C-CHB	2.04	1.49	1.41
3	D	166	PEB	C1B-C2B	2.04	1.50	1.45
3	G	166	PEB	C4B-NB	-2.03	1.34	1.38
3	V	187	PEB	C1C-CHB	2.03	1.49	1.41
3	H	167	PEB	C1C-CHB	2.03	1.49	1.41
3	O	188	PEB	C1B-C2B	2.03	1.50	1.45
3	X	187	PEB	C4A-NA	-2.03	1.33	1.37
3	L	166	PEB	C1B-C2B	2.02	1.50	1.45
3	S	187	PEB	C1B-C2B	2.02	1.50	1.45
3	R	187	PEB	C2A-C1A	-2.02	1.50	1.52
3	C	166	PEB	C4A-NA	-2.02	1.33	1.37
3	T	187	PEB	C1C-CHB	2.01	1.48	1.41
3	W	188	PEB	C4B-C3B	2.01	1.48	1.45
3	B	167	PEB	C4B-C3B	2.01	1.48	1.45
3	F	167	PEB	C2A-C1A	-2.01	1.50	1.52
3	G	167	PEB	C1B-C2B	2.01	1.50	1.45
3	P	188	PEB	C1B-C2B	2.01	1.50	1.45
3	T	188	PEB	C4A-NA	-2.00	1.33	1.37
3	G	167	PEB	C2A-C1A	-2.00	1.50	1.52

All (950) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	166	PEB	OA-C1A-C2A	-6.96	120.64	126.17
3	J	166	PEB	OA-C1A-C2A	-6.81	120.76	126.17
3	P	186	PEB	CHC-C1D-ND	-6.62	106.26	113.95
3	T	186	PEB	OA-C1A-C2A	-6.51	120.99	126.17
3	A	166	PEB	OA-C1A-C2A	-6.33	121.14	126.17
3	V	186	PEB	OA-C1A-C2A	-6.31	121.16	126.17
3	F	166	PEB	CHA-C1B-NB	-6.10	112.17	124.93
3	C	166	PEB	OA-C1A-C2A	-6.09	121.33	126.17
3	K	166	PEB	CHA-C1B-NB	-6.06	112.25	124.93
3	U	186	PEB	CHC-C1D-ND	-6.04	106.93	113.95
3	I	166	PEB	OA-C1A-C2A	-6.04	121.37	126.17
3	U	186	PEB	CMB-C2B-C1B	6.00	134.31	125.06
3	K	166	PEB	OA-C1A-C2A	-5.88	121.50	126.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	166	PEB	CHC-C1D-ND	-5.85	107.15	113.95
3	V	186	PEB	CHC-C1D-ND	-5.83	107.18	113.95
3	G	166	PEB	CHA-C1B-NB	-5.77	112.85	124.93
3	T	186	PEB	CHC-C1D-ND	-5.76	107.25	113.95
3	L	166	PEB	CHA-C1B-NB	-5.75	112.90	124.93
3	I	167	PEB	CHB-C4B-NB	-5.72	120.89	128.83
3	D	167	PEB	OA-C1A-C2A	-5.65	121.68	126.17
3	F	166	PEB	OA-C1A-C2A	-5.62	121.71	126.17
3	D	166	PEB	OA-C1A-C2A	-5.60	121.72	126.17
3	A	166	PEB	CHA-C1B-NB	-5.54	113.35	124.93
3	Q	188	PEB	CHC-C1D-ND	-5.53	107.53	113.95
3	T	188	PEB	CHC-C1D-ND	-5.52	107.53	113.95
3	O	186	PEB	OA-C1A-C2A	-5.49	121.81	126.17
3	E	166	PEB	OA-C1A-C2A	-5.48	121.82	126.17
3	O	188	PEB	CHC-C1D-ND	-5.42	107.66	113.95
3	B	166	PEB	CHA-C1B-NB	-5.40	113.65	124.93
3	L	166	PEB	CHB-C4B-NB	-5.38	121.37	128.83
3	W	188	PEB	CHC-C1D-ND	-5.35	107.73	113.95
3	H	166	PEB	OA-C1A-C2A	-5.35	121.92	126.17
3	V	186	PEB	CMB-C2B-C1B	5.34	133.29	125.06
3	H	166	PEB	CHA-C1B-NB	-5.33	113.79	124.93
3	C	166	PEB	CHA-C1B-NB	-5.32	113.81	124.93
3	I	166	PEB	CHC-C1D-ND	-5.28	107.82	113.95
3	O	186	PEB	CMB-C2B-C1B	5.23	133.12	125.06
3	D	166	PEB	CHA-C1B-NB	-5.21	114.04	124.93
3	X	186	PEB	CMB-C2B-C1B	5.20	133.08	125.06
3	L	166	PEB	OA-C1A-C2A	-5.19	122.04	126.17
3	T	186	PEB	CMB-C2B-C1B	5.19	133.06	125.06
3	X	186	PEB	CHC-C1D-ND	-5.17	107.94	113.95
3	A	166	PEB	CHA-C4A-NA	5.14	131.32	125.20
3	H	166	PEB	CHB-C4B-NB	-5.10	121.76	128.83
3	K	166	PEB	CMB-C2B-C1B	5.08	132.89	125.06
3	V	188	PEB	CHC-C1D-ND	-5.08	108.04	113.95
3	A	166	PEB	CHB-C4B-NB	-5.07	121.80	128.83
3	I	166	PEB	CHA-C1B-NB	-5.06	114.34	124.93
3	E	166	PEB	CHA-C1B-NB	-5.03	114.40	124.93
3	D	167	PEB	CHC-C4C-C3C	-4.90	121.99	130.34
3	D	167	PEB	CHB-C4B-NB	-4.89	122.04	128.83
3	V	187	PEB	OA-C1A-C2A	-4.87	122.30	126.17
3	N	188	PEB	CHC-C1D-ND	-4.87	108.30	113.95
3	B	166	PEB	CHC-C1D-ND	-4.85	108.31	113.95
3	U	187	PEB	CHC-C1D-ND	-4.84	108.33	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	U	186	PEB	OA-C1A-C2A	-4.81	122.35	126.17
3	E	166	PEB	CHB-C4B-NB	-4.80	122.16	128.83
3	G	166	PEB	CMB-C2B-C1B	4.80	132.46	125.06
3	Q	186	PEB	CMB-C2B-C1B	4.76	132.40	125.06
3	S	186	PEB	OA-C1A-C2A	-4.75	122.39	126.17
3	P	186	PEB	CMB-C2B-C1B	4.68	132.28	125.06
3	S	188	PEB	CHC-C1D-ND	-4.68	108.51	113.95
3	M	188	PEB	OA-C1A-C2A	-4.66	122.47	126.17
3	I	167	PEB	CHC-C4C-C3C	-4.66	122.39	130.34
3	I	166	PEB	CHB-C4B-NB	-4.64	122.38	128.83
3	O	188	PEB	OA-C1A-C2A	-4.64	122.48	126.17
3	X	187	PEB	OA-C1A-C2A	-4.63	122.49	126.17
3	J	166	PEB	CHA-C4A-NA	4.62	130.70	125.20
3	D	166	PEB	CHC-C1D-ND	-4.62	108.59	113.95
3	T	187	PEB	OA-C1A-C2A	-4.58	122.53	126.17
3	J	166	PEB	CHA-C1B-NB	-4.58	115.36	124.93
3	K	167	PEB	CHB-C4B-NB	-4.56	122.50	128.83
3	E	167	PEB	CHB-C4B-NB	-4.55	122.52	128.83
3	J	166	PEB	CHB-C4B-NB	-4.55	122.52	128.83
3	X	188	PEB	OA-C1A-C2A	-4.54	122.56	126.17
3	R	186	PEB	CMB-C2B-C1B	4.54	132.06	125.06
3	G	166	PEB	CHC-C4C-C3C	-4.53	122.62	130.34
3	I	166	PEB	CMB-C2B-C1B	4.52	132.03	125.06
3	P	188	PEB	C1C-CHB-C4B	4.52	134.20	128.81
3	N	188	PEB	OA-C1A-C2A	-4.50	122.59	126.17
3	F	166	PEB	CMB-C2B-C1B	4.50	131.99	125.06
3	P	188	PEB	CHC-C1D-ND	-4.47	108.76	113.95
3	N	186	PEB	OA-C1A-C2A	-4.46	122.62	126.17
3	U	188	PEB	OA-C1A-C2A	-4.46	122.62	126.17
3	S	188	PEB	OA-C1A-C2A	-4.46	122.63	126.17
3	X	186	PEB	CHA-C1B-NB	-4.44	115.65	124.93
3	E	167	PEB	OA-C1A-C2A	-4.44	122.65	126.17
3	Q	186	PEB	CHA-C1B-NB	-4.43	115.67	124.93
3	M	187	PEB	C3D-C4D-ND	4.42	115.93	107.26
3	D	166	PEB	CMB-C2B-C1B	4.40	131.84	125.06
3	R	186	PEB	OA-C1A-C2A	-4.39	122.68	126.17
3	L	166	PEB	CHC-C1D-ND	-4.39	108.86	113.95
3	M	186	PEB	CMB-C2B-C1B	4.39	131.82	125.06
3	E	166	PEB	CHC-C1D-ND	-4.38	108.86	113.95
3	C	166	PEB	CMB-C2B-C1B	4.38	131.81	125.06
3	D	167	PEB	C2A-C1A-NA	4.37	112.04	108.27
3	U	186	PEB	CHA-C1B-NB	-4.35	115.83	124.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	X	187	PEB	CHC-C1D-ND	-4.35	108.89	113.95
3	H	166	PEB	CMB-C2B-C1B	4.35	131.76	125.06
3	T	186	PEB	CHA-C1B-NB	-4.34	115.86	124.93
3	I	167	PEB	OA-C1A-C2A	-4.33	122.73	126.17
3	M	186	PEB	CHA-C1B-NB	-4.33	115.88	124.93
3	Q	186	PEB	OA-C1A-C2A	-4.32	122.74	126.17
3	J	167	PEB	CHC-C1D-ND	-4.31	108.94	113.95
3	G	166	PEB	CHB-C4B-NB	-4.31	122.85	128.83
3	C	166	PEB	CHC-C1D-ND	-4.30	108.96	113.95
3	F	166	PEB	CHA-C4A-NA	4.29	130.31	125.20
3	N	188	PEB	C2A-C1A-NA	4.27	111.95	108.27
3	N	186	PEB	CHA-C1B-NB	-4.25	116.05	124.93
3	A	167	PEB	OA-C1A-C2A	-4.22	122.81	126.17
3	U	188	PEB	CHB-C4B-NB	-4.21	122.99	128.83
3	D	166	PEB	CHB-C4B-NB	-4.20	123.00	128.83
3	W	186	PEB	CMB-C2B-C1B	4.19	131.51	125.06
3	I	167	PEB	C2A-C1A-NA	4.19	111.88	108.27
3	U	187	PEB	CAC-CBC-CGC	-4.19	102.03	113.76
3	B	167	PEB	CHB-C4B-NB	-4.18	123.03	128.83
3	V	186	PEB	CHA-C1B-NB	-4.18	116.19	124.93
3	S	186	PEB	CMB-C2B-C1B	4.18	131.50	125.06
3	Q	187	PEB	CHB-C4B-NB	-4.17	123.04	128.83
3	A	166	PEB	CHC-C1D-ND	-4.17	109.11	113.95
3	T	186	PEB	C2A-C1A-NA	4.15	111.85	108.27
3	L	166	PEB	CMB-C2B-C1B	4.14	131.43	125.06
3	X	187	PEB	C3D-C4D-ND	4.13	115.35	107.26
3	S	187	PEB	CMB-C2B-C1B	4.12	131.41	125.06
3	N	186	PEB	CMB-C2B-C1B	4.12	131.41	125.06
3	O	186	PEB	C3D-C4D-ND	4.12	115.34	107.26
3	M	186	PEB	OA-C1A-C2A	-4.11	122.90	126.17
3	V	186	PEB	C2A-C1A-NA	4.11	111.82	108.27
3	X	186	PEB	OA-C1A-C2A	-4.11	122.91	126.17
3	L	166	PEB	CHC-C4C-C3C	-4.10	123.34	130.34
3	H	167	PEB	CMB-C2B-C1B	4.10	131.38	125.06
3	Q	187	PEB	CBC-CAC-C2C	-4.09	105.64	112.62
3	G	166	PEB	OA-C1A-C2A	-4.08	122.92	126.17
3	U	186	PEB	C3D-C4D-ND	4.08	115.27	107.26
3	X	186	PEB	C3D-C4D-ND	4.08	115.26	107.26
3	L	167	PEB	C3D-C4D-ND	4.08	115.26	107.26
3	F	166	PEB	C3D-C4D-ND	4.07	115.25	107.26
3	U	187	PEB	C3D-C4D-ND	4.07	115.24	107.26
3	S	187	PEB	C3D-C4D-ND	4.06	115.23	107.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	166	PEB	C3D-C4D-ND	4.06	115.23	107.26
3	O	188	PEB	CHB-C4B-NB	-4.06	123.20	128.83
3	N	187	PEB	C1C-CHB-C4B	4.05	133.65	128.81
3	K	166	PEB	CHA-C1B-C2B	4.04	135.29	124.90
3	W	186	PEB	CHA-C1B-NB	-4.04	116.48	124.93
3	D	166	PEB	CBB-CAB-C3B	-4.04	101.41	112.63
3	M	186	PEB	C3D-C4D-ND	4.03	115.17	107.26
3	T	187	PEB	C3D-C4D-ND	4.02	115.15	107.26
3	R	188	PEB	CHB-C4B-NB	-4.02	123.25	128.83
3	R	186	PEB	CHA-C1B-NB	-4.01	116.54	124.93
3	T	188	PEB	CHB-C4B-NB	-4.01	123.27	128.83
3	N	186	PEB	CHC-C4C-C3C	-4.01	123.51	130.34
3	S	186	PEB	C2A-C1A-NA	4.00	111.72	108.27
3	J	166	PEB	C3D-C4D-ND	4.00	115.11	107.26
3	M	188	PEB	CHC-C1D-ND	-4.00	109.30	113.95
3	S	186	PEB	CHA-C1B-NB	-4.00	116.57	124.93
3	P	188	PEB	CHC-C4C-C3C	-3.99	123.52	130.34
3	E	167	PEB	CHC-C4C-C3C	-3.99	123.53	130.34
3	K	166	PEB	CHB-C4B-NB	-3.98	123.30	128.83
3	G	167	PEB	OA-C1A-C2A	-3.98	123.01	126.17
3	R	188	PEB	OA-C1A-C2A	-3.98	123.01	126.17
3	W	186	PEB	C3D-C4D-ND	3.97	115.05	107.26
3	E	166	PEB	CMB-C2B-C1B	3.96	131.16	125.06
3	P	186	PEB	CHA-C1B-NB	-3.96	116.65	124.93
3	B	167	PEB	OA-C1A-C2A	-3.96	123.03	126.17
3	N	188	PEB	C3D-C4D-ND	3.95	115.01	107.26
3	W	187	PEB	C3D-C4D-ND	3.95	115.01	107.26
3	O	186	PEB	CHA-C1B-NB	-3.95	116.67	124.93
3	B	166	PEB	CMB-C2B-C1B	3.95	131.14	125.06
3	Q	188	PEB	C1C-CHB-C4B	3.94	133.52	128.81
3	H	166	PEB	C3D-C4D-ND	3.93	114.98	107.26
3	C	167	PEB	OA-C1A-C2A	-3.93	123.05	126.17
3	Q	186	PEB	CHB-C4B-NB	-3.93	123.37	128.83
3	V	188	PEB	CHB-C4B-NB	-3.93	123.38	128.83
3	C	166	PEB	CHA-C4A-NA	3.93	129.87	125.20
3	F	167	PEB	C2A-C1A-NA	3.92	111.65	108.27
3	J	167	PEB	C3D-C4D-ND	3.91	114.93	107.26
3	J	167	PEB	CHB-C4B-NB	-3.91	123.40	128.83
3	R	186	PEB	C2A-C1A-NA	3.91	111.64	108.27
3	V	186	PEB	C3D-C4D-ND	3.90	114.92	107.26
3	H	167	PEB	OA-C1A-C2A	-3.90	123.07	126.17
3	F	167	PEB	C3D-C4D-ND	3.90	114.92	107.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	167	PEB	OA-C1A-C2A	-3.90	123.07	126.17
3	G	167	PEB	C3D-C4D-ND	3.90	114.91	107.26
3	S	188	PEB	C2A-C1A-NA	3.89	111.63	108.27
3	M	187	PEB	OA-C1A-C2A	-3.89	123.08	126.17
3	M	188	PEB	CHC-C4C-C3C	-3.89	123.70	130.34
3	M	186	PEB	CHC-C4C-C3C	-3.89	123.70	130.34
3	A	166	PEB	CHC-C4C-C3C	-3.89	123.71	130.34
3	Q	187	PEB	C3D-C4D-ND	3.89	114.89	107.26
3	L	167	PEB	CHB-C4B-NB	-3.88	123.45	128.83
3	W	188	PEB	C3D-C4D-ND	3.88	114.87	107.26
3	D	167	PEB	C3D-C4D-ND	3.88	114.86	107.26
3	B	167	PEB	C3D-C4D-ND	3.87	114.86	107.26
3	F	166	PEB	CHB-C4B-NB	-3.87	123.46	128.83
3	A	167	PEB	C2A-C1A-NA	3.86	111.60	108.27
3	R	188	PEB	C3D-C4D-ND	3.85	114.82	107.26
3	S	186	PEB	C3D-C4D-ND	3.85	114.82	107.26
3	T	188	PEB	CHC-C4C-C3C	-3.84	123.79	130.34
3	K	166	PEB	C3D-C4D-ND	3.83	114.78	107.26
3	S	188	PEB	C3D-C4D-ND	3.83	114.78	107.26
3	N	187	PEB	CHC-C4C-C3C	-3.83	123.81	130.34
3	N	187	PEB	OA-C1A-C2A	-3.83	123.13	126.17
3	X	188	PEB	C2A-C1A-NA	3.82	111.57	108.27
3	R	188	PEB	CBC-CAC-C2C	-3.81	106.11	112.62
3	P	187	PEB	CHC-C1D-ND	-3.81	109.53	113.95
3	I	166	PEB	C3D-C4D-ND	3.81	114.73	107.26
3	H	167	PEB	CHB-C4B-NB	-3.81	123.55	128.83
3	N	186	PEB	C3D-C4D-ND	3.80	114.72	107.26
3	C	167	PEB	CHB-C4B-NB	-3.80	123.56	128.83
3	A	167	PEB	C3D-C4D-ND	3.80	114.71	107.26
3	M	188	PEB	C3D-C4D-ND	3.80	114.70	107.26
3	E	167	PEB	C2A-C1A-NA	3.79	111.54	108.27
3	O	188	PEB	OD-C4D-C3D	-3.79	120.87	129.46
3	R	187	PEB	CHC-C4C-C3C	-3.79	123.87	130.34
3	N	186	PEB	CHB-C4B-NB	-3.79	123.57	128.83
3	P	188	PEB	CHB-C4B-NB	-3.79	123.58	128.83
3	H	167	PEB	CHC-C1D-ND	-3.78	109.56	113.95
3	T	186	PEB	C3D-C4D-ND	3.77	114.67	107.26
3	M	187	PEB	C4B-C3B-C2B	-3.77	102.61	106.78
3	T	187	PEB	CMB-C2B-C1B	3.77	130.87	125.06
3	O	188	PEB	C2A-C1A-NA	3.77	111.52	108.27
3	P	186	PEB	OA-C1A-C2A	-3.76	123.18	126.17
3	R	187	PEB	OA-C1A-C2A	-3.76	123.18	126.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	188	PEB	C4B-C3B-C2B	-3.76	102.62	106.78
3	A	167	PEB	CHC-C4C-C3C	-3.76	123.92	130.34
3	N	187	PEB	C3D-C4D-ND	3.76	114.64	107.26
3	K	167	PEB	OA-C1A-C2A	-3.76	123.18	126.17
3	G	166	PEB	C1B-C2B-C3B	-3.75	102.20	106.51
3	M	188	PEB	CMB-C2B-C1B	3.75	130.84	125.06
3	H	167	PEB	C3D-C4D-ND	3.75	114.61	107.26
3	W	186	PEB	CHC-C4C-C3C	-3.74	123.95	130.34
3	D	166	PEB	CHA-C4A-NA	3.74	129.66	125.20
3	Q	186	PEB	C3D-C4D-ND	3.74	114.60	107.26
3	N	188	PEB	CHB-C4B-NB	-3.74	123.64	128.83
3	U	188	PEB	C3D-C4D-ND	3.73	114.57	107.26
3	O	188	PEB	C3D-C4D-ND	3.72	114.56	107.26
3	Q	188	PEB	OA-C1A-C2A	-3.72	123.22	126.17
3	W	187	PEB	OA-C1A-C2A	-3.72	123.22	126.17
3	S	188	PEB	CHB-C4B-NB	-3.71	123.67	128.83
3	L	167	PEB	OA-C1A-C2A	-3.70	123.23	126.17
3	T	188	PEB	C3D-C4D-ND	3.70	114.52	107.26
3	E	166	PEB	OD-C4D-ND	-3.68	120.48	125.93
3	P	186	PEB	C3D-C4D-ND	3.67	114.46	107.26
3	V	187	PEB	C3D-C4D-ND	3.67	114.45	107.26
3	P	188	PEB	C3D-C4D-ND	3.67	114.45	107.26
3	O	188	PEB	CMB-C2B-C1B	3.67	130.71	125.06
3	R	188	PEB	C2A-C1A-NA	3.67	111.43	108.27
3	C	166	PEB	C3D-C4D-ND	3.66	114.45	107.26
3	J	167	PEB	C1B-C2B-C3B	-3.65	102.31	106.51
3	L	167	PEB	CHC-C4C-C3C	-3.65	124.11	130.34
3	W	187	PEB	CHC-C4C-C3C	-3.65	124.12	130.34
3	R	188	PEB	CHC-C4C-C3C	-3.64	124.13	130.34
3	I	167	PEB	C3D-C4D-ND	3.64	114.40	107.26
3	O	187	PEB	C3D-C4D-ND	3.64	114.39	107.26
3	B	166	PEB	C3D-C4D-ND	3.63	114.39	107.26
3	C	167	PEB	C3D-C4D-ND	3.63	114.39	107.26
3	X	187	PEB	CHB-C4B-NB	-3.63	123.79	128.83
3	U	186	PEB	CAB-CBB-CGB	-3.63	105.79	113.60
3	V	188	PEB	C3D-C4D-ND	3.62	114.36	107.26
3	G	167	PEB	CHB-C4B-NB	-3.62	123.81	128.83
3	A	167	PEB	CHB-C4B-NB	-3.61	123.82	128.83
3	J	166	PEB	CHC-C1D-ND	-3.61	109.76	113.95
3	R	187	PEB	C3D-C4D-ND	3.61	114.33	107.26
3	M	187	PEB	CHC-C4C-C3C	-3.61	124.19	130.34
3	S	186	PEB	CHC-C4C-C3C	-3.60	124.19	130.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Q	188	PEB	C3D-C4D-ND	3.60	114.32	107.26
3	E	166	PEB	C3D-C4D-ND	3.60	114.32	107.26
3	C	166	PEB	CBB-CAB-C3B	-3.60	102.64	112.63
3	V	188	PEB	OD-C4D-C3D	-3.59	121.31	129.46
3	U	186	PEB	C2A-C1A-NA	3.59	111.37	108.27
3	J	166	PEB	CMA-C2A-C1A	-3.59	104.66	112.40
3	K	167	PEB	C3D-C4D-ND	3.58	114.28	107.26
3	S	187	PEB	CHB-C4B-NB	-3.58	123.86	128.83
3	O	186	PEB	CHC-C1D-ND	-3.58	109.80	113.95
3	P	188	PEB	C2A-C1A-NA	3.57	111.35	108.27
3	L	166	PEB	C3D-C4D-ND	3.57	114.25	107.26
3	R	187	PEB	CHB-C4B-NB	-3.56	123.88	128.83
3	B	166	PEB	CHA-C1B-C2B	3.56	134.06	124.90
3	X	187	PEB	C2A-C1A-NA	3.56	111.34	108.27
3	H	167	PEB	CHC-C4C-C3C	-3.55	124.28	130.34
3	X	186	PEB	C2A-C1A-NA	3.55	111.34	108.27
3	A	166	PEB	C3D-C4D-ND	3.55	114.23	107.26
3	J	166	PEB	CHC-C4C-C3C	-3.55	124.28	130.34
3	D	166	PEB	C3D-C4D-ND	3.55	114.22	107.26
3	S	186	PEB	CHC-C1D-ND	-3.55	109.83	113.95
3	I	167	PEB	CAB-CBB-CGB	-3.55	105.97	113.60
3	Q	187	PEB	OD-C4D-C3D	-3.54	121.43	129.46
3	U	187	PEB	CHC-C4C-C3C	-3.54	124.30	130.34
3	S	188	PEB	C1C-CHB-C4B	3.54	133.03	128.81
3	N	187	PEB	C4B-C3B-C2B	-3.54	102.87	106.78
3	P	187	PEB	C3D-C4D-ND	3.53	114.19	107.26
3	E	167	PEB	C3D-C4D-ND	3.53	114.18	107.26
3	K	166	PEB	C2A-C1A-NA	3.53	111.31	108.27
3	X	188	PEB	C3D-C4D-ND	3.53	114.18	107.26
3	P	187	PEB	OA-C1A-C2A	-3.52	123.37	126.17
3	C	166	PEB	CHB-C4B-NB	-3.52	123.94	128.83
3	V	188	PEB	OA-C1A-C2A	-3.52	123.38	126.17
3	B	167	PEB	C2A-C1A-NA	3.51	111.30	108.27
3	L	167	PEB	C4B-C3B-C2B	-3.50	102.90	106.78
3	B	166	PEB	CHA-C4A-NA	3.49	129.35	125.20
3	S	187	PEB	OA-C1A-C2A	-3.49	123.40	126.17
3	M	188	PEB	C2A-C1A-NA	3.48	111.27	108.27
3	Q	187	PEB	OA-C1A-C2A	-3.48	123.41	126.17
3	O	186	PEB	CHC-C4C-C3C	-3.47	124.41	130.34
3	R	186	PEB	C3D-C4D-ND	3.47	114.07	107.26
3	O	187	PEB	CHC-C1D-ND	-3.47	109.92	113.95
3	L	167	PEB	CHC-C1D-ND	-3.47	109.92	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Q	188	PEB	CHC-C4C-C3C	-3.46	124.43	130.34
3	C	167	PEB	C4B-C3B-C2B	-3.45	102.96	106.78
3	C	167	PEB	C2A-C1A-NA	3.45	111.25	108.27
3	M	187	PEB	C2A-C1A-NA	3.45	111.24	108.27
3	W	187	PEB	C4B-C3B-C2B	-3.44	102.97	106.78
3	M	187	PEB	CHC-C1D-ND	-3.44	109.95	113.95
3	X	188	PEB	CHC-C1D-ND	-3.44	109.95	113.95
3	U	188	PEB	C2A-C1A-NA	3.44	111.24	108.27
3	L	167	PEB	OD-C4D-ND	-3.44	120.84	125.93
3	V	188	PEB	C4B-C3B-C2B	-3.43	102.99	106.78
3	P	187	PEB	CHB-C4B-NB	-3.42	124.08	128.83
3	V	186	PEB	CHC-C4C-C3C	-3.42	124.50	130.34
3	H	166	PEB	CHC-C1D-ND	-3.42	109.97	113.95
3	K	167	PEB	CHC-C4C-C3C	-3.42	124.51	130.34
3	I	166	PEB	CBB-CAB-C3B	-3.41	103.14	112.63
3	D	167	PEB	CAB-CBB-CGB	-3.41	106.26	113.60
3	S	188	PEB	C4B-C3B-C2B	-3.41	103.01	106.78
3	O	186	PEB	CAB-CBB-CGB	-3.41	106.27	113.60
3	A	166	PEB	CMB-C2B-C1B	3.41	130.31	125.06
3	W	186	PEB	OA-C1A-C2A	-3.40	123.47	126.17
3	U	187	PEB	OA-C1A-C2A	-3.39	123.47	126.17
3	L	166	PEB	C1B-C2B-C3B	-3.39	102.62	106.51
3	J	166	PEB	CMB-C2B-C1B	3.39	130.28	125.06
3	F	166	PEB	CHA-C1B-C2B	3.39	133.60	124.90
3	R	187	PEB	CMB-C2B-C1B	3.38	130.27	125.06
3	A	166	PEB	OD-C4D-ND	-3.38	120.92	125.93
3	P	187	PEB	C4B-C3B-C2B	-3.38	103.04	106.78
3	V	187	PEB	OD-C4D-ND	-3.38	120.92	125.93
3	F	166	PEB	C3B-C4B-NB	3.38	114.96	110.05
3	M	187	PEB	CHB-C4B-NB	-3.38	124.14	128.83
3	G	167	PEB	CHC-C4C-C3C	-3.38	124.58	130.34
3	M	187	PEB	CMB-C2B-C1B	3.38	130.26	125.06
3	W	188	PEB	CHB-C4B-NB	-3.38	124.14	128.83
3	T	186	PEB	CHB-C4B-NB	-3.37	124.15	128.83
3	X	188	PEB	C1C-CHB-C4B	3.37	132.83	128.81
3	S	187	PEB	CHC-C1D-ND	-3.37	110.04	113.95
3	O	188	PEB	C1C-CHB-C4B	3.36	132.82	128.81
3	T	188	PEB	C1C-CHB-C4B	3.36	132.82	128.81
3	U	188	PEB	CHC-C4C-C3C	-3.36	124.60	130.34
3	V	187	PEB	CHB-C4B-NB	-3.36	124.17	128.83
3	L	166	PEB	CHA-C4A-NA	3.36	129.20	125.20
3	L	166	PEB	CHA-C1B-C2B	3.36	133.53	124.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	X	188	PEB	CHC-C4C-C3C	-3.36	124.61	130.34
3	T	187	PEB	CHB-C4B-NB	-3.35	124.18	128.83
3	R	187	PEB	CHA-C1B-NB	-3.35	117.93	124.93
3	J	167	PEB	C2A-C1A-NA	3.35	111.16	108.27
3	S	188	PEB	OD-C4D-C3D	-3.35	121.88	129.46
3	S	187	PEB	CHA-C1B-NB	-3.34	117.94	124.93
3	P	186	PEB	C2A-C1A-NA	3.34	111.16	108.27
3	H	166	PEB	CHA-C1B-C2B	3.34	133.49	124.90
3	K	167	PEB	CMB-C2B-C1B	3.34	130.21	125.06
3	U	187	PEB	CHB-C4B-NB	-3.34	124.20	128.83
3	X	188	PEB	CMB-C2B-C1B	3.34	130.20	125.06
3	V	187	PEB	CHC-C4C-C3C	-3.33	124.65	130.34
3	X	187	PEB	C4B-C3B-C2B	-3.33	103.09	106.78
3	V	188	PEB	C2A-C1A-NA	3.33	111.14	108.27
3	J	167	PEB	CMB-C2B-C1B	3.33	130.19	125.06
3	X	187	PEB	CHC-C4C-C3C	-3.32	124.67	130.34
3	I	167	PEB	C4B-C3B-C2B	-3.32	103.11	106.78
3	P	186	PEB	OD-C4D-C3D	-3.31	121.95	129.46
3	G	167	PEB	CMB-C2B-C1B	3.30	130.15	125.06
3	K	166	PEB	CBB-CAB-C3B	-3.30	103.46	112.63
3	O	186	PEB	C2A-C1A-NA	3.30	111.11	108.27
3	O	187	PEB	CMB-C2B-C1B	3.29	130.14	125.06
3	W	187	PEB	C2A-C1A-NA	3.29	111.11	108.27
3	P	188	PEB	OA-C1A-C2A	-3.29	123.56	126.17
3	T	187	PEB	CHC-C4C-C3C	-3.29	124.72	130.34
3	I	166	PEB	CHA-C1B-C2B	3.29	133.36	124.90
3	I	167	PEB	CBC-CAC-C2C	-3.29	107.01	112.62
3	F	166	PEB	C1B-C2B-C3B	-3.29	102.73	106.51
3	F	166	PEB	CBB-CAB-C3B	-3.28	103.50	112.63
3	B	167	PEB	CHC-C4C-C3C	-3.28	124.74	130.34
3	Q	187	PEB	CHC-C4C-C3C	-3.28	124.74	130.34
3	F	167	PEB	CHC-C4C-C3C	-3.28	124.74	130.34
3	W	187	PEB	CAB-CBB-CGB	-3.28	106.54	113.60
3	M	187	PEB	CHA-C1B-NB	-3.28	118.08	124.93
3	L	166	PEB	CBB-CAB-C3B	-3.27	103.53	112.63
3	C	167	PEB	CMB-C2B-C1B	3.27	130.11	125.06
3	X	188	PEB	CHB-C4B-NB	-3.27	124.29	128.83
3	A	166	PEB	C2A-C1A-NA	3.27	111.09	108.27
3	C	167	PEB	OD-C4D-C3D	-3.27	122.05	129.46
3	L	167	PEB	C2A-C1A-NA	3.27	111.09	108.27
3	M	188	PEB	CHB-C4B-NB	-3.26	124.30	128.83
3	N	187	PEB	CHC-C1D-ND	-3.26	110.17	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	187	PEB	OD-C4D-C3D	-3.26	122.08	129.46
3	D	167	PEB	CMB-C2B-C1B	3.25	130.07	125.06
3	D	167	PEB	CBC-CAC-C2C	-3.24	107.09	112.62
3	M	187	PEB	C3B-C4B-NB	3.24	114.76	110.05
3	M	186	PEB	C2A-C1A-NA	3.24	111.06	108.27
3	B	167	PEB	OD-C4D-C3D	-3.23	122.13	129.46
3	Q	186	PEB	CHC-C1D-ND	-3.23	110.20	113.95
3	W	186	PEB	C2A-C1A-NA	3.22	111.05	108.27
3	O	187	PEB	C4B-C3B-C2B	-3.22	103.21	106.78
3	H	166	PEB	CHC-C4C-C3C	-3.22	124.84	130.34
3	N	188	PEB	C3B-C4B-NB	3.22	114.73	110.05
3	S	186	PEB	CHB-C4B-NB	-3.22	124.36	128.83
3	U	187	PEB	C1C-CHB-C4B	3.21	132.64	128.81
3	X	187	PEB	OD-C4D-C3D	-3.21	122.19	129.46
3	B	167	PEB	C4B-C3B-C2B	-3.21	103.23	106.78
3	W	188	PEB	C1C-CHB-C4B	3.21	132.64	128.81
3	V	188	PEB	CMB-C2B-C1B	3.21	130.00	125.06
3	J	166	PEB	CBB-CAB-C3B	-3.21	103.72	112.63
3	T	187	PEB	CHC-C1D-ND	-3.21	110.22	113.95
3	Q	188	PEB	C4B-C3B-C2B	-3.20	103.24	106.78
3	N	187	PEB	CHB-C4B-NB	-3.20	124.38	128.83
3	J	167	PEB	OA-C1A-C2A	-3.20	123.63	126.17
3	R	188	PEB	C4B-C3B-C2B	-3.20	103.24	106.78
3	Q	186	PEB	C2A-C1A-NA	3.20	111.03	108.27
3	I	167	PEB	C3B-C4B-NB	3.20	114.70	110.05
3	P	188	PEB	CMB-C2B-C1B	3.19	129.98	125.06
3	W	187	PEB	C3B-C4B-NB	3.19	114.69	110.05
3	Q	188	PEB	C2A-C1A-NA	3.19	111.02	108.27
3	B	166	PEB	CHB-C4B-NB	-3.19	124.40	128.83
3	K	166	PEB	OD-C4D-C3D	-3.19	122.23	129.46
3	O	188	PEB	CHC-C4C-C3C	-3.19	124.90	130.34
3	Q	188	PEB	CHB-C4B-NB	-3.18	124.41	128.83
3	W	188	PEB	C2A-C1A-NA	3.18	111.02	108.27
3	V	186	PEB	C1B-C2B-C3B	-3.18	102.86	106.51
3	G	167	PEB	C2A-C1A-NA	3.18	111.01	108.27
3	U	187	PEB	OD-C4D-C3D	-3.17	122.27	129.46
3	N	188	PEB	OD-C4D-C3D	-3.17	122.28	129.46
3	L	167	PEB	CMB-C2B-C1B	3.17	129.94	125.06
3	X	186	PEB	OD-C4D-C3D	-3.16	122.29	129.46
3	P	186	PEB	CHC-C4C-C3C	-3.16	124.94	130.34
3	A	166	PEB	C4B-C3B-C2B	-3.16	103.29	106.78
3	I	166	PEB	OD-C4D-ND	-3.15	121.26	125.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	188	PEB	CBC-CAC-C2C	-3.15	107.25	112.62
3	G	167	PEB	OD-C4D-C3D	-3.14	122.33	129.46
3	K	167	PEB	C3B-C4B-NB	3.14	114.62	110.05
3	S	186	PEB	OD-C4D-C3D	-3.14	122.34	129.46
3	O	187	PEB	C3B-C4B-NB	3.14	114.62	110.05
3	K	167	PEB	C4B-C3B-C2B	-3.14	103.31	106.78
3	T	187	PEB	OD-C4D-C3D	-3.14	122.35	129.46
3	N	186	PEB	C2A-C1A-NA	3.14	110.98	108.27
3	B	167	PEB	C3B-C4B-NB	3.14	114.61	110.05
3	C	167	PEB	C3B-C4B-NB	3.14	114.61	110.05
3	W	187	PEB	C1C-CHB-C4B	3.14	132.56	128.81
3	W	187	PEB	OD-C4D-C3D	-3.13	122.36	129.46
3	K	167	PEB	C2A-C1A-NA	3.13	110.97	108.27
3	U	187	PEB	C4B-C3B-C2B	-3.13	103.31	106.78
3	T	188	PEB	CMB-C2B-C1B	3.13	129.89	125.06
3	O	187	PEB	CHB-C4B-NB	-3.13	124.48	128.83
3	G	166	PEB	CHA-C1B-C2B	3.13	132.95	124.90
3	R	186	PEB	CHB-C4B-NB	-3.13	124.48	128.83
3	H	166	PEB	C4B-C3B-C2B	-3.13	103.32	106.78
3	D	166	PEB	CHA-C1B-C2B	3.13	132.94	124.90
3	W	187	PEB	CHC-C1D-ND	-3.12	110.32	113.95
3	Q	188	PEB	CMB-C2B-C1B	3.11	129.86	125.06
3	E	166	PEB	CHA-C4A-NA	3.11	128.90	125.20
3	B	167	PEB	CMB-C2B-C1B	3.11	129.85	125.06
3	A	167	PEB	CMB-C2B-C1B	3.11	129.85	125.06
3	G	166	PEB	C3B-C4B-NB	3.11	114.57	110.05
3	I	167	PEB	CMB-C2B-C1B	3.10	129.84	125.06
3	A	166	PEB	CHA-C1B-C2B	3.09	132.85	124.90
3	N	186	PEB	OD-C4D-C3D	-3.09	122.46	129.46
3	Q	187	PEB	C1C-CHB-C4B	3.08	132.49	128.81
3	W	188	PEB	C4B-C3B-C2B	-3.08	103.38	106.78
3	R	187	PEB	C4B-C3B-C2B	-3.07	103.38	106.78
3	K	167	PEB	CAB-CBB-CGB	-3.07	107.00	113.60
3	B	167	PEB	CHC-C1D-ND	-3.07	110.39	113.95
3	J	167	PEB	CHC-C4C-C3C	-3.07	125.11	130.34
3	C	166	PEB	C4B-C3B-C2B	-3.07	103.39	106.78
3	W	187	PEB	CMB-C2B-C1B	3.07	129.78	125.06
3	J	166	PEB	C2A-C1A-NA	3.06	110.91	108.27
3	U	186	PEB	OD-C4D-C3D	-3.06	122.53	129.46
3	U	188	PEB	OD-C4D-C3D	-3.06	122.53	129.46
3	D	166	PEB	C1B-C2B-C3B	-3.05	103.00	106.51
3	M	186	PEB	OD-C4D-C3D	-3.05	122.54	129.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P	186	PEB	CHB-C4B-NB	-3.05	124.59	128.83
3	G	166	PEB	CHA-C4A-NA	3.05	128.83	125.20
3	L	167	PEB	C3B-C4B-NB	3.04	114.48	110.05
3	I	167	PEB	C1B-C2B-C3B	-3.04	103.01	106.51
3	T	186	PEB	C1B-C2B-C3B	-3.04	103.01	106.51
3	A	166	PEB	CBB-CAB-C3B	-3.04	104.18	112.63
3	A	166	PEB	C1B-C2B-C3B	-3.04	103.02	106.51
3	G	166	PEB	CBB-CAB-C3B	-3.04	104.19	112.63
3	M	186	PEB	CHB-C4B-NB	-3.04	124.61	128.83
3	B	166	PEB	CHC-C4C-C3C	-3.03	125.16	130.34
3	D	167	PEB	C4B-C3B-C2B	-3.03	103.42	106.78
3	T	188	PEB	CHA-C1B-NB	-3.03	118.59	124.93
3	F	166	PEB	C4B-C3B-C2B	-3.03	103.43	106.78
3	I	166	PEB	CMA-C2A-C1A	-3.03	105.88	112.40
3	T	186	PEB	CAB-CBB-CGB	-3.03	107.09	113.60
3	S	187	PEB	OD-C4D-C3D	-3.02	122.61	129.46
3	F	166	PEB	CHC-C4C-C3C	-3.02	125.19	130.34
3	B	166	PEB	C2A-C1A-NA	3.02	110.88	108.27
3	X	186	PEB	C1B-C2B-C3B	-3.02	103.04	106.51
3	O	186	PEB	OD-C4D-C3D	-3.02	122.62	129.46
3	V	187	PEB	C4B-C3B-C2B	-3.01	103.45	106.78
3	U	188	PEB	CMB-C2B-C1B	3.01	129.70	125.06
3	F	166	PEB	CBA-CAA-C3A	-3.01	106.77	113.47
3	U	186	PEB	C1B-C2B-C3B	-3.01	103.06	106.51
3	C	166	PEB	CBA-CAA-C3A	-3.00	106.79	113.47
3	V	186	PEB	CHB-C4B-NB	-3.00	124.67	128.83
3	N	187	PEB	C2A-C1A-NA	3.00	110.86	108.27
3	C	166	PEB	C3B-C4B-NB	2.99	114.39	110.05
3	I	166	PEB	CHC-C4C-C3C	-2.99	125.25	130.34
3	T	188	PEB	OA-C1A-C2A	-2.98	123.80	126.17
3	A	166	PEB	C3B-C4B-NB	2.98	114.38	110.05
3	N	187	PEB	OD-C4D-C3D	-2.97	122.72	129.46
3	R	187	PEB	C2A-C1A-NA	2.97	110.84	108.27
3	E	166	PEB	CHA-C1B-C2B	2.97	132.53	124.90
3	T	187	PEB	C1C-CHB-C4B	2.97	132.35	128.81
3	B	167	PEB	CAB-CBB-CGB	-2.97	107.22	113.60
3	G	167	PEB	C4B-C3B-C2B	-2.96	103.50	106.78
3	G	167	PEB	C1B-C2B-C3B	-2.96	103.11	106.51
3	X	187	PEB	C3B-C4B-NB	2.96	114.36	110.05
3	I	167	PEB	CHA-C1B-NB	-2.96	118.75	124.93
3	W	188	PEB	OD-C4D-C3D	-2.95	122.77	129.46
3	J	166	PEB	OD-C4D-C3D	-2.95	122.77	129.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	167	PEB	OD-C4D-C3D	-2.95	122.77	129.46
3	R	188	PEB	C1C-CHB-C4B	2.95	132.33	128.81
3	R	186	PEB	CHC-C1D-ND	-2.95	110.53	113.95
3	K	166	PEB	C3B-C4B-NB	2.95	114.33	110.05
3	Q	187	PEB	C4B-C3B-C2B	-2.94	103.52	106.78
3	V	188	PEB	CBC-CAC-C2C	-2.94	107.60	112.62
3	G	166	PEB	OD-C4D-ND	-2.94	121.57	125.93
3	E	167	PEB	C1B-C2B-C3B	-2.94	103.13	106.51
3	O	187	PEB	CHC-C4C-C3C	-2.94	125.33	130.34
3	K	167	PEB	C1B-C2B-C3B	-2.93	103.14	106.51
3	K	166	PEB	C1B-C2B-C3B	-2.93	103.14	106.51
3	K	167	PEB	OD-C4D-C3D	-2.93	122.82	129.46
3	X	187	PEB	C1C-CHB-C4B	2.93	132.31	128.81
3	K	167	PEB	CBC-CAC-C2C	-2.92	107.63	112.62
3	E	166	PEB	CHC-C4C-C3C	-2.92	125.35	130.34
3	L	166	PEB	C2A-C1A-NA	2.92	110.79	108.27
3	Q	187	PEB	CAB-CBB-CGB	-2.92	107.31	113.60
3	C	167	PEB	CHC-C4C-C3C	-2.92	125.36	130.34
3	A	167	PEB	OD-C4D-ND	-2.92	121.61	125.93
3	T	187	PEB	C4B-C3B-C2B	-2.92	103.56	106.78
3	B	166	PEB	OA-C1A-NA	2.92	128.47	124.94
3	O	186	PEB	CHB-C4B-NB	-2.91	124.78	128.83
3	O	187	PEB	OD-C4D-C3D	-2.91	122.86	129.46
3	H	166	PEB	OD-C4D-C3D	-2.91	122.87	129.46
3	Q	188	PEB	OD-C4D-C3D	-2.91	122.87	129.46
3	T	188	PEB	C2A-C1A-NA	2.91	110.78	108.27
3	F	167	PEB	C1B-C2B-C3B	-2.90	103.17	106.51
3	L	167	PEB	CHA-C1B-NB	-2.90	118.87	124.93
3	R	187	PEB	C3B-C4B-NB	2.90	114.26	110.05
3	S	186	PEB	CAB-CBB-CGB	-2.89	107.37	113.60
3	D	167	PEB	C1B-C2B-C3B	-2.89	103.19	106.51
3	F	166	PEB	OD-C4D-ND	-2.89	121.64	125.93
3	N	188	PEB	C1C-CHB-C4B	2.89	132.26	128.81
3	Q	186	PEB	C3B-C4B-NB	2.89	114.25	110.05
3	Q	186	PEB	C1B-C2B-C3B	-2.89	103.19	106.51
3	M	188	PEB	OD-C4D-C3D	-2.89	122.92	129.46
3	E	167	PEB	C4B-C3B-C2B	-2.89	103.59	106.78
3	W	188	PEB	OA-C1A-C2A	-2.88	123.88	126.17
3	R	186	PEB	C1B-C2B-C3B	-2.88	103.20	106.51
3	O	187	PEB	OA-C1A-C2A	-2.88	123.88	126.17
3	A	167	PEB	C1B-C2B-C3B	-2.88	103.20	106.51
3	V	188	PEB	C3B-C4B-NB	2.88	114.23	110.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	167	PEB	OD-C4D-C3D	-2.87	122.95	129.46
3	H	166	PEB	C3B-C4B-NB	2.87	114.23	110.05
3	X	187	PEB	CMB-C2B-C1B	2.87	129.48	125.06
3	C	166	PEB	CHA-C1B-C2B	2.87	132.27	124.90
3	H	167	PEB	C4B-C3B-C2B	-2.87	103.61	106.78
3	N	187	PEB	C3B-C4B-NB	2.87	114.22	110.05
3	T	187	PEB	CHA-C1B-NB	-2.86	118.94	124.93
3	I	166	PEB	C1B-C2B-C3B	-2.86	103.22	106.51
3	M	188	PEB	C1B-C2B-C3B	-2.86	103.22	106.51
3	R	187	PEB	OD-C4D-C3D	-2.86	122.97	129.46
3	Q	187	PEB	CMB-C2B-C1B	2.86	129.47	125.06
3	S	187	PEB	CHC-C4C-C3C	-2.86	125.45	130.34
3	O	188	PEB	C4B-C3B-C2B	-2.86	103.62	106.78
3	Q	187	PEB	CHA-C1B-NB	-2.86	118.95	124.93
3	V	186	PEB	OD-C4D-C3D	-2.86	122.98	129.46
3	Q	188	PEB	C3B-C4B-NB	2.86	114.21	110.05
3	D	166	PEB	CHC-C4C-C3C	-2.85	125.47	130.34
3	H	167	PEB	OD-C4D-ND	-2.85	121.71	125.93
3	H	167	PEB	C2A-C1A-NA	2.85	110.73	108.27
3	P	187	PEB	C1C-CHB-C4B	2.84	132.21	128.81
3	O	186	PEB	C1B-C2B-C3B	-2.84	103.25	106.51
3	R	188	PEB	CHC-C1D-ND	-2.84	110.65	113.95
3	L	166	PEB	OD-C4D-ND	-2.83	121.73	125.93
3	P	188	PEB	OD-C4D-ND	-2.83	121.74	125.93
3	V	187	PEB	CMB-C2B-C1B	2.83	129.42	125.06
3	Q	186	PEB	CHC-C4C-C3C	-2.83	125.51	130.34
3	Q	188	PEB	CHA-C1B-NB	-2.83	119.02	124.93
3	Q	186	PEB	OD-C4D-C3D	-2.82	123.06	129.46
3	R	186	PEB	CHC-C4C-C3C	-2.82	125.53	130.34
3	R	186	PEB	CBB-CAB-C3B	-2.82	104.80	112.63
3	W	187	PEB	CHA-C1B-NB	-2.82	119.04	124.93
3	B	167	PEB	CBC-CAC-C2C	-2.82	107.81	112.62
3	D	167	PEB	C3B-C4B-NB	2.81	114.14	110.05
3	N	186	PEB	C4B-C3B-C2B	-2.81	103.67	106.78
3	S	187	PEB	C1B-C2B-C3B	-2.81	103.28	106.51
3	F	166	PEB	OD-C4D-C3D	-2.81	123.10	129.46
3	S	188	PEB	CBC-CAC-C2C	-2.80	107.84	112.62
3	V	187	PEB	CHC-C1D-ND	-2.80	110.69	113.95
3	J	166	PEB	OA-C1A-NA	2.80	128.33	124.94
3	C	166	PEB	OD-C4D-C3D	-2.80	123.12	129.46
3	E	166	PEB	C1B-C2B-C3B	-2.80	103.30	106.51
3	T	188	PEB	OD-C4D-C3D	-2.80	123.12	129.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	166	PEB	CHC-C4C-C3C	-2.80	125.57	130.34
3	W	186	PEB	OD-C4D-ND	-2.79	121.79	125.93
3	V	187	PEB	C2A-C1A-NA	2.79	110.68	108.27
3	X	187	PEB	CHA-C1B-NB	-2.79	119.10	124.93
3	T	188	PEB	C4B-C3B-C2B	-2.79	103.69	106.78
3	V	186	PEB	CBA-CAA-C3A	-2.79	107.26	113.47
3	Q	186	PEB	C4B-C3B-C2B	-2.79	103.70	106.78
3	U	188	PEB	C1B-C2B-C3B	-2.78	103.31	106.51
3	W	186	PEB	OD-C4D-C3D	-2.78	123.15	129.46
3	I	166	PEB	OA-C1A-NA	2.78	128.31	124.94
3	E	167	PEB	CMB-C2B-C1B	2.78	129.34	125.06
3	D	167	PEB	CAB-C3B-C4B	2.78	129.93	125.01
3	T	186	PEB	CHC-C4C-C3C	-2.78	125.60	130.34
3	W	186	PEB	C4B-C3B-C2B	-2.78	103.71	106.78
3	T	188	PEB	C1B-C2B-C3B	-2.77	103.32	106.51
3	P	188	PEB	C1B-C2B-C3B	-2.77	103.33	106.51
3	S	187	PEB	C4B-C3B-C2B	-2.77	103.72	106.78
3	X	188	PEB	C1B-C2B-C3B	-2.77	103.33	106.51
3	D	167	PEB	OD-C4D-C3D	-2.76	123.20	129.46
3	M	187	PEB	C1C-CHB-C4B	2.76	132.11	128.81
3	G	166	PEB	OD-C4D-C3D	-2.76	123.20	129.46
3	H	167	PEB	C1B-C2B-C3B	-2.76	103.33	106.51
3	W	186	PEB	C3B-C4B-NB	2.76	114.06	110.05
3	P	187	PEB	C3B-C4B-NB	2.76	114.06	110.05
3	R	187	PEB	C1B-C2B-C3B	-2.75	103.35	106.51
3	M	186	PEB	CHA-C1B-C2B	2.75	131.96	124.90
3	T	186	PEB	OD-C4D-C3D	-2.75	123.24	129.46
3	J	166	PEB	C1B-C2B-C3B	-2.75	103.36	106.51
3	G	167	PEB	C1C-CHB-C4B	2.74	132.09	128.81
3	C	166	PEB	C1B-C2B-C3B	-2.74	103.36	106.51
3	P	188	PEB	C4B-C3B-C2B	-2.74	103.75	106.78
3	R	188	PEB	OD-C4D-C3D	-2.74	123.26	129.46
3	O	187	PEB	CAB-CBB-CGB	-2.73	107.72	113.60
3	R	187	PEB	CAA-C3A-C2A	-2.73	107.44	114.26
3	X	188	PEB	OD-C4D-C3D	-2.73	123.28	129.46
3	U	186	PEB	CHA-C1B-C2B	2.73	131.92	124.90
3	V	187	PEB	C1C-CHB-C4B	2.73	132.07	128.81
3	H	166	PEB	CHA-C4A-NA	2.73	128.45	125.20
3	T	187	PEB	C3B-C4B-NB	2.73	114.02	110.05
3	M	188	PEB	C1C-CHB-C4B	2.72	132.06	128.81
3	S	187	PEB	C2A-C1A-NA	2.72	110.62	108.27
3	B	167	PEB	C1B-C2B-C3B	-2.72	103.38	106.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P	187	PEB	CMB-C2B-C1B	2.72	129.26	125.06
3	Q	187	PEB	C2A-C1A-NA	2.72	110.62	108.27
3	I	167	PEB	OD-C4D-C3D	-2.72	123.30	129.46
3	G	167	PEB	CHA-C1B-NB	-2.71	119.25	124.93
3	W	188	PEB	C3B-C4B-NB	2.71	114.00	110.05
3	S	187	PEB	C3B-C4B-NB	2.71	113.99	110.05
3	L	166	PEB	C3B-C4B-NB	2.71	113.99	110.05
3	R	188	PEB	OD-C4D-ND	-2.71	121.92	125.93
3	U	187	PEB	CAB-CBB-CGB	-2.71	107.78	113.60
3	U	188	PEB	C1C-CHB-C4B	2.70	132.04	128.81
3	P	187	PEB	OD-C4D-C3D	-2.70	123.34	129.46
3	K	166	PEB	C4B-C3B-C2B	-2.70	103.80	106.78
3	D	167	PEB	OD-C4D-ND	-2.70	121.94	125.93
3	D	166	PEB	CMA-C2A-C1A	-2.69	106.60	112.40
3	J	167	PEB	C3B-C4B-NB	2.69	113.96	110.05
3	H	167	PEB	C3B-C4B-NB	2.69	113.96	110.05
3	A	167	PEB	C4B-C3B-C2B	-2.69	103.81	106.78
3	V	187	PEB	CAB-CBB-CGB	-2.68	107.83	113.60
3	S	188	PEB	CHC-C4C-C3C	-2.68	125.77	130.34
3	I	166	PEB	CHA-C4A-NA	2.68	128.39	125.20
3	F	167	PEB	C4B-C3B-C2B	-2.68	103.82	106.78
3	D	166	PEB	OA-C1A-NA	2.68	128.18	124.94
3	C	167	PEB	C1B-C2B-C3B	-2.67	103.44	106.51
3	D	166	PEB	OD-C4D-ND	-2.67	121.97	125.93
3	C	167	PEB	CHA-C1B-NB	-2.67	119.35	124.93
3	M	187	PEB	OD-C4D-ND	-2.67	121.98	125.93
3	S	188	PEB	CMB-C2B-C1B	2.66	129.17	125.06
3	R	188	PEB	C1B-C2B-C3B	-2.66	103.45	106.51
3	J	167	PEB	CHA-C1B-NB	-2.66	119.37	124.93
3	O	188	PEB	CAB-C3B-C4B	2.66	129.71	125.01
3	V	187	PEB	C3B-C4B-NB	2.65	113.91	110.05
3	B	166	PEB	CBB-CAB-C3B	-2.65	105.26	112.63
3	N	187	PEB	CHA-C1B-NB	-2.65	119.39	124.93
3	N	186	PEB	C3B-C4B-NB	2.65	113.90	110.05
3	Q	187	PEB	C1B-C2B-C3B	-2.64	103.47	106.51
3	P	186	PEB	C1B-C2B-C3B	-2.64	103.47	106.51
3	E	167	PEB	OD-C4D-ND	-2.64	122.02	125.93
3	B	166	PEB	OD-C4D-ND	-2.64	122.02	125.93
3	K	166	PEB	CHC-C4C-C3C	-2.63	125.84	130.34
3	H	166	PEB	CMA-C2A-C1A	-2.63	106.73	112.40
3	C	166	PEB	C2A-C1A-NA	2.63	110.54	108.27
3	C	166	PEB	OA-C1A-NA	2.63	128.13	124.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	S	186	PEB	CHA-C1B-C2B	2.63	131.66	124.90
3	O	186	PEB	OD-C4D-ND	-2.63	122.04	125.93
3	J	166	PEB	CHA-C1B-C2B	2.62	131.63	124.90
3	L	167	PEB	C1B-C2B-C3B	-2.62	103.50	106.51
3	S	188	PEB	C3B-C4B-NB	2.61	113.85	110.05
3	E	167	PEB	C3B-C4B-NB	2.61	113.85	110.05
3	N	186	PEB	C1B-C2B-C3B	-2.61	103.51	106.51
3	G	167	PEB	C3B-C4B-NB	2.61	113.85	110.05
3	L	166	PEB	C4B-C3B-C2B	-2.61	103.89	106.78
3	F	166	PEB	OA-C1A-NA	2.61	128.10	124.94
3	U	188	PEB	C4B-C3B-C2B	-2.61	103.89	106.78
3	W	186	PEB	CHB-C4B-NB	-2.61	125.21	128.83
3	B	166	PEB	C1B-C2B-C3B	-2.61	103.51	106.51
3	R	186	PEB	OD-C4D-C3D	-2.60	123.56	129.46
3	W	187	PEB	CHB-C4B-NB	-2.60	125.22	128.83
3	U	187	PEB	C3B-C4B-NB	2.60	113.83	110.05
3	N	186	PEB	CBB-CAB-C3B	-2.60	105.41	112.63
3	B	166	PEB	OD-C4D-C3D	-2.59	123.59	129.46
3	V	186	PEB	OD-C4D-ND	-2.59	122.09	125.93
3	D	166	PEB	CBA-CAA-C3A	-2.59	107.70	113.47
3	E	166	PEB	C4B-C3B-C2B	-2.59	103.92	106.78
3	T	186	PEB	OD-C4D-ND	-2.59	122.10	125.93
3	T	187	PEB	C1B-C2B-C3B	-2.59	103.54	106.51
3	W	188	PEB	CBC-CAC-C2C	-2.59	108.21	112.62
3	B	166	PEB	C4B-C3B-C2B	-2.58	103.93	106.78
3	J	166	PEB	OD-C4D-ND	-2.58	122.11	125.93
3	W	188	PEB	CMB-C2B-C1B	2.57	129.03	125.06
3	U	187	PEB	CHA-C1B-NB	-2.57	119.55	124.93
3	F	167	PEB	OD-C4D-ND	-2.57	122.13	125.93
3	F	167	PEB	CMB-C2B-C1B	2.57	129.01	125.06
3	F	167	PEB	CHB-C4B-NB	-2.56	125.27	128.83
3	V	188	PEB	CAB-C3B-C4B	2.56	129.54	125.01
3	S	187	PEB	C1C-CHB-C4B	2.56	131.87	128.81
3	W	188	PEB	C1B-C2B-C3B	-2.56	103.57	106.51
3	X	186	PEB	C1C-CHB-C4B	2.56	131.87	128.81
3	A	167	PEB	C3B-C4B-NB	2.56	113.78	110.05
3	V	188	PEB	C1C-CHB-C4B	2.56	131.87	128.81
3	R	188	PEB	C3B-C4B-NB	2.56	113.77	110.05
3	U	187	PEB	CMB-C2B-C1B	2.56	129.00	125.06
3	M	186	PEB	C1B-C2B-C3B	-2.56	103.57	106.51
3	O	186	PEB	CBA-CAA-C3A	-2.55	107.78	113.47
3	S	187	PEB	OD-C4D-ND	-2.55	122.15	125.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	167	PEB	OD-C4D-C3D	-2.55	123.68	129.46
3	H	166	PEB	OD-C4D-ND	-2.55	122.15	125.93
3	X	188	PEB	C4B-C3B-C2B	-2.55	103.96	106.78
3	A	167	PEB	OD-C4D-C3D	-2.55	123.68	129.46
3	H	166	PEB	C1B-C2B-C3B	-2.54	103.59	106.51
3	N	188	PEB	CHC-C4C-C3C	-2.54	126.01	130.34
3	A	167	PEB	CBC-CAC-C2C	-2.53	108.30	112.62
3	P	188	PEB	CHA-C1B-NB	-2.53	119.63	124.93
3	N	188	PEB	C1B-C2B-C3B	-2.53	103.60	106.51
3	P	187	PEB	CHA-C1B-NB	-2.53	119.65	124.93
3	M	188	PEB	C4B-C3B-C2B	-2.53	103.99	106.78
3	O	188	PEB	C1B-C2B-C3B	-2.52	103.62	106.51
3	U	186	PEB	OD-C4D-ND	-2.52	122.20	125.93
3	V	186	PEB	C3B-C4B-NB	2.52	113.71	110.05
3	J	167	PEB	CBB-CAB-C3B	-2.52	105.64	112.63
3	W	186	PEB	C1B-C2B-C3B	-2.51	103.62	106.51
3	R	188	PEB	CMB-C2B-C1B	2.51	128.93	125.06
3	V	187	PEB	C1B-C2B-C3B	-2.51	103.63	106.51
3	W	188	PEB	CHC-C4C-C3C	-2.51	126.06	130.34
3	D	167	PEB	CHA-C1B-NB	-2.50	119.70	124.93
3	U	188	PEB	CHC-C1D-ND	-2.50	111.04	113.95
3	E	167	PEB	OD-C4D-C3D	-2.50	123.80	129.46
3	D	166	PEB	OD-C4D-C3D	-2.50	123.80	129.46
3	P	188	PEB	OD-C4D-C3D	-2.50	123.80	129.46
3	N	188	PEB	CBD-CAD-C3D	-2.50	115.20	127.62
3	I	167	PEB	O1B-CGB-CBB	-2.50	115.06	123.08
3	W	186	PEB	CHA-C4A-NA	2.49	128.17	125.20
3	X	186	PEB	CHB-C4B-NB	-2.49	125.37	128.83
3	X	186	PEB	CHA-C1B-C2B	2.49	131.30	124.90
3	P	186	PEB	C1C-CHB-C4B	2.48	131.77	128.81
3	P	187	PEB	CAA-C3A-C2A	-2.48	108.06	114.26
3	I	167	PEB	CAB-C3B-C4B	2.48	129.39	125.01
3	C	167	PEB	CAB-CBB-CGB	-2.48	108.28	113.60
3	E	166	PEB	C2A-C1A-NA	2.47	110.41	108.27
3	M	186	PEB	CAB-CBB-CGB	-2.47	108.28	113.60
3	X	186	PEB	C3B-C4B-NB	2.47	113.64	110.05
3	K	166	PEB	CAC-CBC-CGC	-2.47	106.84	113.76
3	M	186	PEB	OD-C4D-ND	-2.46	122.28	125.93
3	W	186	PEB	CBB-CAB-C3B	-2.46	105.78	112.63
3	X	186	PEB	CAB-CBB-CGB	-2.46	108.31	113.60
3	L	166	PEB	CBA-CAA-C3A	-2.46	108.00	113.47
3	Q	188	PEB	C1B-C2B-C3B	-2.46	103.69	106.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	167	PEB	OD-C4D-C3D	-2.45	123.90	129.46
3	J	167	PEB	OD-C4D-ND	-2.45	122.30	125.93
3	U	186	PEB	CHC-C4C-C3C	-2.45	126.16	130.34
3	I	167	PEB	OD-C4D-ND	-2.45	122.30	125.93
3	E	166	PEB	CBB-CAB-C3B	-2.45	105.83	112.63
3	O	188	PEB	C3B-C4B-NB	2.44	113.60	110.05
3	O	187	PEB	C1B-C2B-C3B	-2.44	103.70	106.51
3	F	167	PEB	C1C-CHB-C4B	2.44	131.72	128.81
3	J	166	PEB	C4B-C3B-C2B	-2.44	104.09	106.78
3	A	166	PEB	CAC-CBC-CGC	-2.44	106.93	113.76
3	S	186	PEB	C1B-C2B-C3B	-2.44	103.71	106.51
3	E	166	PEB	CMA-C2A-C1A	-2.43	107.16	112.40
3	P	186	PEB	C4B-C3B-C2B	-2.43	104.09	106.78
3	P	188	PEB	C3B-C4B-NB	2.43	113.58	110.05
3	H	167	PEB	CAB-C3B-C4B	2.43	129.30	125.01
3	Q	186	PEB	OD-C4D-ND	-2.43	122.33	125.93
3	L	166	PEB	OD-C4D-C3D	-2.43	123.96	129.46
3	E	167	PEB	CAB-CBB-CGB	-2.43	108.38	113.60
3	P	187	PEB	CHC-C4C-C3C	-2.42	126.20	130.34
3	T	186	PEB	C3B-C4B-NB	2.42	113.57	110.05
3	H	166	PEB	CBB-CAB-C3B	-2.42	105.91	112.63
3	H	167	PEB	CHA-C1B-NB	-2.42	119.88	124.93
3	N	186	PEB	CHA-C1B-C2B	2.41	131.11	124.90
3	R	187	PEB	CHC-C1D-ND	-2.41	111.14	113.95
3	G	166	PEB	C4B-C3B-C2B	-2.41	104.12	106.78
3	T	188	PEB	OD-C4D-ND	-2.41	122.36	125.93
3	V	188	PEB	CHC-C4C-C3C	-2.41	126.23	130.34
3	M	186	PEB	CBB-CAB-C3B	-2.41	105.94	112.63
3	K	167	PEB	CHA-C1B-NB	-2.41	119.90	124.93
3	B	166	PEB	C3B-C4B-NB	2.41	113.55	110.05
3	W	188	PEB	OD-C4D-ND	-2.41	122.36	125.93
3	I	166	PEB	OD-C4D-C3D	-2.41	124.01	129.46
3	S	186	PEB	C4B-C3B-C2B	-2.40	104.12	106.78
3	R	186	PEB	OD-C4D-ND	-2.40	122.37	125.93
3	M	188	PEB	OD-C4D-ND	-2.40	122.37	125.93
3	M	186	PEB	CHC-C1D-ND	-2.39	111.18	113.95
3	Q	186	PEB	CHA-C4A-NA	2.39	128.04	125.20
3	U	187	PEB	C1B-C2B-C3B	-2.39	103.77	106.51
3	J	167	PEB	C4B-C3B-C2B	-2.39	104.14	106.78
3	P	186	PEB	CBC-CAC-C2C	-2.38	108.56	112.62
3	V	186	PEB	CAB-CBB-CGB	-2.38	108.49	113.60
3	O	186	PEB	CHA-C1B-C2B	2.38	131.01	124.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	V	186	PEB	CHA-C1B-C2B	2.37	131.01	124.90
3	I	166	PEB	C2A-C1A-NA	2.37	110.32	108.27
3	U	186	PEB	CBB-CAB-C3B	-2.37	106.04	112.63
3	Q	186	PEB	CHA-C1B-C2B	2.37	131.00	124.90
3	C	166	PEB	OD-C4D-ND	-2.37	122.42	125.93
3	M	188	PEB	C3B-C4B-NB	2.37	113.50	110.05
3	U	188	PEB	CAB-C3B-C4B	2.37	129.19	125.01
3	V	188	PEB	CBD-CAD-C3D	-2.37	115.85	127.62
3	U	188	PEB	C3B-C4B-NB	2.37	113.49	110.05
3	X	187	PEB	C1B-C2B-C3B	-2.36	103.79	106.51
3	U	188	PEB	CHA-C1B-NB	-2.36	120.00	124.93
3	O	188	PEB	CBC-CAC-C2C	-2.36	108.59	112.62
3	K	166	PEB	CHC-C1D-ND	-2.36	111.21	113.95
3	X	186	PEB	OD-C4D-ND	-2.36	122.44	125.93
3	X	187	PEB	OD-C4D-ND	-2.35	122.44	125.93
3	Q	187	PEB	CHC-C1D-ND	-2.35	111.22	113.95
3	H	166	PEB	C2A-C1A-NA	2.35	110.30	108.27
3	O	188	PEB	CHA-C1B-NB	-2.35	120.03	124.93
3	T	186	PEB	CHA-C1B-C2B	2.35	130.93	124.90
3	P	188	PEB	CAC-CBC-CGC	-2.34	107.19	113.76
3	E	166	PEB	OA-C1A-NA	2.34	127.78	124.94
3	H	166	PEB	OA-C1A-NA	2.34	127.78	124.94
3	O	188	PEB	CBD-CAD-C3D	-2.34	115.98	127.62
3	E	166	PEB	C3B-C4B-NB	2.34	113.45	110.05
3	P	187	PEB	OD-C4D-ND	-2.33	122.47	125.93
3	V	187	PEB	CHA-C1B-NB	-2.33	120.06	124.93
3	A	166	PEB	OA-C1A-NA	2.33	127.76	124.94
3	P	187	PEB	C1B-C2B-C3B	-2.33	103.84	106.51
3	M	186	PEB	C4B-C3B-C2B	-2.32	104.21	106.78
3	U	187	PEB	OD-C4D-ND	-2.32	122.49	125.93
3	T	188	PEB	C3B-C4B-NB	2.32	113.42	110.05
3	X	188	PEB	CAC-CBC-CGC	-2.32	107.26	113.76
3	T	187	PEB	OD-C4D-ND	-2.31	122.50	125.93
3	Q	187	PEB	C3B-C4B-NB	2.31	113.41	110.05
3	P	186	PEB	C3B-C4B-NB	2.31	113.41	110.05
3	O	187	PEB	CHA-C1B-NB	-2.31	120.11	124.93
3	L	167	PEB	CBC-CAC-C2C	-2.31	108.68	112.62
3	X	186	PEB	C4B-C3B-C2B	-2.30	104.23	106.78
3	G	167	PEB	CAB-CBB-CGB	-2.30	108.65	113.60
3	F	167	PEB	CHA-C1B-NB	-2.30	120.12	124.93
3	S	188	PEB	CAB-C3B-C4B	2.30	129.07	125.01
3	P	186	PEB	CBB-CAB-C3B	-2.29	106.26	112.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	166	PEB	CBA-CAA-C3A	-2.29	108.37	113.47
3	A	167	PEB	CHA-C1B-NB	-2.29	120.15	124.93
3	R	186	PEB	CHA-C1B-C2B	2.28	130.77	124.90
3	X	188	PEB	OD-C4D-ND	-2.28	122.55	125.93
3	X	186	PEB	CHC-C4C-C3C	-2.27	126.46	130.34
3	T	187	PEB	CAB-CBB-CGB	-2.27	108.72	113.60
3	S	188	PEB	CBD-CAD-C3D	-2.27	116.33	127.62
3	W	186	PEB	CHA-C1B-C2B	2.27	130.73	124.90
3	W	187	PEB	CHB-C4B-C3B	-2.27	120.09	125.32
3	D	166	PEB	C4B-C3B-C2B	-2.26	104.28	106.78
3	V	188	PEB	C1B-C2B-C3B	-2.26	103.91	106.51
3	W	187	PEB	CAA-C3A-C2A	-2.26	108.61	114.26
3	M	188	PEB	CBD-CAD-C3D	-2.25	116.40	127.62
3	M	188	PEB	CHA-C1B-NB	-2.25	120.22	124.93
3	F	167	PEB	C3B-C4B-NB	2.25	113.32	110.05
3	A	166	PEB	CBA-CAA-C3A	-2.25	108.47	113.47
3	B	167	PEB	CHA-C1B-NB	-2.24	120.24	124.93
3	W	187	PEB	OD-C4D-ND	-2.23	122.63	125.93
3	N	186	PEB	CBA-CAA-C3A	-2.23	108.51	113.47
3	M	186	PEB	C3B-C4B-NB	2.23	113.29	110.05
3	D	166	PEB	C3B-C4B-NB	2.22	113.28	110.05
3	X	188	PEB	C3B-C4B-NB	2.22	113.28	110.05
3	N	187	PEB	OD-C4D-ND	-2.22	122.64	125.93
3	R	187	PEB	C1C-CHB-C4B	2.22	131.46	128.81
3	W	186	PEB	CMD-C2D-C3D	2.20	133.17	130.06
3	A	166	PEB	CMA-C2A-C1A	-2.20	107.67	112.40
3	W	188	PEB	CHA-C1B-NB	-2.20	120.34	124.93
3	J	166	PEB	CBA-CAA-C3A	-2.20	108.58	113.47
3	R	187	PEB	OD-C4D-ND	-2.19	122.68	125.93
3	W	187	PEB	C1B-C2B-C3B	-2.19	103.99	106.51
3	E	167	PEB	CAB-C3B-C4B	2.19	128.88	125.01
3	T	186	PEB	C4B-C3B-C2B	-2.19	104.36	106.78
3	N	187	PEB	CMB-C2B-C1B	2.19	128.43	125.06
3	R	187	PEB	CAB-CBB-CGB	-2.18	108.90	113.60
3	X	188	PEB	CBD-CAD-C3D	-2.18	116.76	127.62
3	N	188	PEB	OD-C4D-ND	-2.18	122.70	125.93
3	O	186	PEB	C3B-C4B-NB	2.18	113.21	110.05
3	D	167	PEB	O1B-CGB-CBB	-2.17	116.10	123.08
3	I	166	PEB	C4B-C3B-C2B	-2.17	104.38	106.78
3	F	166	PEB	C2A-C1A-NA	2.17	110.14	108.27
3	N	187	PEB	C1B-C2B-C3B	-2.17	104.02	106.51
3	P	187	PEB	CAB-CBB-CGB	-2.17	108.94	113.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	167	PEB	CHA-C1B-NB	-2.16	120.41	124.93
3	O	186	PEB	CHA-C4A-NA	2.16	127.77	125.20
3	O	187	PEB	OD-C4D-ND	-2.16	122.73	125.93
3	T	187	PEB	CAB-C3B-C4B	2.16	128.82	125.01
3	G	167	PEB	OD-C4D-ND	-2.15	122.75	125.93
3	V	188	PEB	CHA-C1B-NB	-2.15	120.44	124.93
3	V	187	PEB	OD-C4D-C3D	-2.15	124.60	129.46
3	U	188	PEB	CBD-CAD-C3D	-2.14	116.98	127.62
3	R	188	PEB	CHA-C1B-NB	-2.14	120.46	124.93
3	X	186	PEB	CBB-CAB-C3B	-2.13	106.70	112.63
3	G	166	PEB	CHC-C1D-ND	-2.13	111.47	113.95
3	S	186	PEB	C3B-C4B-NB	2.13	113.14	110.05
3	P	186	PEB	CHA-C1B-C2B	2.13	130.37	124.90
3	T	187	PEB	C2A-C1A-NA	2.13	110.11	108.27
3	D	166	PEB	C2A-C1A-NA	2.12	110.10	108.27
3	Q	188	PEB	OD-C4D-ND	-2.11	122.80	125.93
3	U	188	PEB	CAC-CBC-CGC	-2.11	107.84	113.76
3	R	186	PEB	C3B-C4B-NB	2.10	113.11	110.05
3	V	186	PEB	CBB-CAB-C3B	-2.10	106.79	112.63
3	N	186	PEB	OD-C4D-ND	-2.10	122.82	125.93
3	S	187	PEB	CAA-C3A-C2A	-2.10	109.02	114.26
3	P	188	PEB	CBD-CAD-C3D	-2.09	117.21	127.62
3	V	187	PEB	CMA-C2A-C1A	-2.09	107.89	112.40
3	M	187	PEB	CAB-CBB-CGB	-2.09	109.10	113.60
3	S	186	PEB	OD-C4D-ND	-2.09	122.84	125.93
3	N	187	PEB	CAA-C3A-C2A	-2.08	109.07	114.26
3	X	187	PEB	CAA-C3A-C2A	-2.08	109.07	114.26
3	R	186	PEB	C4B-C3B-C2B	-2.07	104.49	106.78
3	R	188	PEB	CAB-C3B-C4B	2.07	128.66	125.01
3	B	167	PEB	O1B-CGB-CBB	-2.07	116.45	123.08
3	B	167	PEB	CAB-C3B-C4B	2.06	128.66	125.01
3	U	186	PEB	CHB-C4B-NB	-2.06	125.97	128.83
3	C	166	PEB	CMA-C2A-C1A	-2.06	107.96	112.40
3	W	186	PEB	CHC-C1D-ND	-2.06	111.56	113.95
3	C	166	PEB	CAC-CBC-CGC	-2.05	108.00	113.76
3	X	188	PEB	CAB-C3B-C4B	2.05	128.64	125.01
3	K	166	PEB	CMA-C2A-C1A	-2.05	107.99	112.40
3	K	167	PEB	OD-C4D-ND	-2.05	122.89	125.93
3	U	188	PEB	OD-C4D-ND	-2.05	122.90	125.93
3	T	188	PEB	CAB-C3B-C4B	2.04	128.62	125.01
3	P	186	PEB	CHA-C4A-NA	2.04	127.63	125.20
3	P	186	PEB	CAB-C3B-C4B	2.03	128.61	125.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	166	PEB	OD-C4D-C3D	-2.03	124.85	129.46
3	W	188	PEB	CBD-CAD-C3D	-2.03	117.54	127.62
3	U	186	PEB	C3B-C4B-NB	2.02	112.99	110.05
3	X	188	PEB	CHA-C1B-NB	-2.02	120.71	124.93
3	U	187	PEB	C2A-C1A-NA	2.02	110.01	108.27
3	B	166	PEB	CBA-CAA-C3A	-2.02	108.98	113.47
3	V	187	PEB	O2C-CGC-CBC	2.01	120.50	114.03
3	P	186	PEB	CAC-CBC-CGC	-2.01	108.12	113.76
3	G	166	PEB	OA-C1A-NA	2.01	127.37	124.94
3	O	186	PEB	CBB-CAB-C3B	-2.00	107.06	112.63
3	V	186	PEB	C4B-C3B-C2B	-2.00	104.57	106.78
3	L	167	PEB	C1C-CHB-C4B	2.00	131.20	128.81
3	R	188	PEB	CBD-CAD-C3D	-2.00	117.67	127.62

There are no chirality outliers.

All (377) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	166	PEB	C2B-C1B-CHA-C4A
3	A	167	PEB	NB-C1B-CHA-C4A
3	A	167	PEB	C2B-C1B-CHA-C4A
3	B	167	PEB	NB-C1B-CHA-C4A
3	B	167	PEB	C2B-C1B-CHA-C4A
3	C	167	PEB	NB-C1B-CHA-C4A
3	C	167	PEB	C2B-C1B-CHA-C4A
3	D	167	PEB	NB-C1B-CHA-C4A
3	D	167	PEB	C2B-C1B-CHA-C4A
3	E	167	PEB	NB-C1B-CHA-C4A
3	E	167	PEB	C2B-C1B-CHA-C4A
3	F	167	PEB	NB-C1B-CHA-C4A
3	F	167	PEB	C2B-C1B-CHA-C4A
3	G	167	PEB	NB-C1B-CHA-C4A
3	G	167	PEB	C2B-C1B-CHA-C4A
3	H	167	PEB	NB-C1B-CHA-C4A
3	H	167	PEB	C2B-C1B-CHA-C4A
3	I	167	PEB	NB-C1B-CHA-C4A
3	I	167	PEB	C2B-C1B-CHA-C4A
3	J	167	PEB	NB-C1B-CHA-C4A
3	J	167	PEB	C2B-C1B-CHA-C4A
3	K	167	PEB	NB-C1B-CHA-C4A
3	K	167	PEB	C2B-C1B-CHA-C4A
3	L	166	PEB	C2B-C1B-CHA-C4A

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Mol	Chain	Res	Type	Atoms
3	L	167	PEB	NB-C1B-CHA-C4A
3	L	167	PEB	C2B-C1B-CHA-C4A
3	M	186	PEB	NB-C1B-CHA-C4A
3	M	186	PEB	C2B-C1B-CHA-C4A
3	M	187	PEB	C4A-C3A-CAA-CBA
3	M	187	PEB	NB-C1B-CHA-C4A
3	M	187	PEB	C2B-C1B-CHA-C4A
3	M	188	PEB	NB-C1B-CHA-C4A
3	M	188	PEB	C2B-C1B-CHA-C4A
3	N	186	PEB	NB-C1B-CHA-C4A
3	N	186	PEB	C2B-C1B-CHA-C4A
3	N	187	PEB	C2A-C3A-CAA-CBA
3	N	187	PEB	C4A-C3A-CAA-CBA
3	N	187	PEB	NB-C1B-CHA-C4A
3	N	187	PEB	C2B-C1B-CHA-C4A
3	N	188	PEB	NB-C1B-CHA-C4A
3	N	188	PEB	C2B-C1B-CHA-C4A
3	O	187	PEB	C4A-C3A-CAA-CBA
3	O	187	PEB	NB-C1B-CHA-C4A
3	O	187	PEB	C2B-C1B-CHA-C4A
3	O	188	PEB	NB-C1B-CHA-C4A
3	O	188	PEB	C2B-C1B-CHA-C4A
3	P	186	PEB	NB-C1B-CHA-C4A
3	P	187	PEB	NB-C1B-CHA-C4A
3	P	187	PEB	C2B-C1B-CHA-C4A
3	P	188	PEB	NB-C1B-CHA-C4A
3	P	188	PEB	C2B-C1B-CHA-C4A
3	Q	186	PEB	NB-C1B-CHA-C4A
3	Q	187	PEB	C4A-C3A-CAA-CBA
3	Q	187	PEB	NB-C1B-CHA-C4A
3	Q	187	PEB	C2B-C1B-CHA-C4A
3	Q	188	PEB	C2D-C3D-CAD-CBD
3	Q	188	PEB	C4D-C3D-CAD-CBD
3	Q	188	PEB	NB-C1B-CHA-C4A
3	Q	188	PEB	C2B-C1B-CHA-C4A
3	R	186	PEB	NB-C1B-CHA-C4A
3	R	186	PEB	C2B-C1B-CHA-C4A
3	R	187	PEB	C2A-C3A-CAA-CBA
3	R	187	PEB	C4A-C3A-CAA-CBA
3	R	187	PEB	NB-C1B-CHA-C4A
3	R	187	PEB	C2B-C1B-CHA-C4A
3	R	188	PEB	C2D-C3D-CAD-CBD

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Mol	Chain	Res	Type	Atoms
3	R	188	PEB	C4D-C3D-CAD-CBD
3	R	188	PEB	NB-C1B-CHA-C4A
3	R	188	PEB	C2B-C1B-CHA-C4A
3	S	187	PEB	C2A-C3A-CAA-CBA
3	S	187	PEB	C4A-C3A-CAA-CBA
3	S	187	PEB	NB-C1B-CHA-C4A
3	S	187	PEB	C2B-C1B-CHA-C4A
3	S	188	PEB	C2D-C3D-CAD-CBD
3	S	188	PEB	C4D-C3D-CAD-CBD
3	S	188	PEB	NB-C1B-CHA-C4A
3	S	188	PEB	C2B-C1B-CHA-C4A
3	T	186	PEB	NB-C1B-CHA-C4A
3	T	186	PEB	C2B-C1B-CHA-C4A
3	T	187	PEB	C2A-C3A-CAA-CBA
3	T	187	PEB	C4A-C3A-CAA-CBA
3	T	187	PEB	NB-C1B-CHA-C4A
3	T	187	PEB	C2B-C1B-CHA-C4A
3	T	188	PEB	NB-C1B-CHA-C4A
3	T	188	PEB	C2B-C1B-CHA-C4A
3	U	187	PEB	C4A-C3A-CAA-CBA
3	U	187	PEB	NB-C1B-CHA-C4A
3	U	187	PEB	C2B-C1B-CHA-C4A
3	U	188	PEB	NB-C1B-CHA-C4A
3	U	188	PEB	C2B-C1B-CHA-C4A
3	V	186	PEB	NB-C1B-CHA-C4A
3	V	187	PEB	C2A-C3A-CAA-CBA
3	V	187	PEB	C4A-C3A-CAA-CBA
3	V	187	PEB	NB-C1B-CHA-C4A
3	V	187	PEB	C2B-C1B-CHA-C4A
3	V	188	PEB	NB-C1B-CHA-C4A
3	V	188	PEB	C2B-C1B-CHA-C4A
3	W	186	PEB	NB-C1B-CHA-C4A
3	W	187	PEB	C4A-C3A-CAA-CBA
3	W	187	PEB	NB-C1B-CHA-C4A
3	W	187	PEB	C2B-C1B-CHA-C4A
3	W	188	PEB	NB-C1B-CHA-C4A
3	W	188	PEB	C2B-C1B-CHA-C4A
3	X	186	PEB	NB-C1B-CHA-C4A
3	X	186	PEB	C2B-C1B-CHA-C4A
3	X	187	PEB	C2A-C3A-CAA-CBA
3	X	187	PEB	C4A-C3A-CAA-CBA
3	X	187	PEB	NB-C1B-CHA-C4A

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Mol	Chain	Res	Type	Atoms
3	X	187	PEB	C2B-C1B-CHA-C4A
3	X	188	PEB	C2D-C3D-CAD-CBD
3	X	188	PEB	C4D-C3D-CAD-CBD
3	X	188	PEB	NB-C1B-CHA-C4A
3	X	188	PEB	C2B-C1B-CHA-C4A
4	A	1165	GOL	C1-C2-C3-O3
4	B	1165	GOL	O1-C1-C2-C3
4	B	1165	GOL	C1-C2-C3-O3
4	C	1165	GOL	C1-C2-C3-O3
4	D	1165	GOL	C1-C2-C3-O3
4	E	1165	GOL	C1-C2-C3-O3
4	F	1165	GOL	C1-C2-C3-O3
4	H	1165	GOL	C1-C2-C3-O3
4	J	1165	GOL	C1-C2-C3-O3
3	O	186	PEB	NB-C1B-CHA-C4A
3	P	186	PEB	C2B-C1B-CHA-C4A
3	V	186	PEB	C2B-C1B-CHA-C4A
3	W	186	PEB	C2B-C1B-CHA-C4A
3	P	187	PEB	C2C-CAC-CBC-CGC
4	C	1165	GOL	O2-C2-C3-O3
3	E	166	PEB	C2B-C1B-CHA-C4A
3	F	166	PEB	C2B-C1B-CHA-C4A
3	A	166	PEB	NB-C1B-CHA-C4A
3	B	166	PEB	NB-C1B-CHA-C4A
3	C	166	PEB	NB-C1B-CHA-C4A
3	D	166	PEB	NB-C1B-CHA-C4A
3	E	166	PEB	NB-C1B-CHA-C4A
3	F	166	PEB	NB-C1B-CHA-C4A
3	G	166	PEB	NB-C1B-CHA-C4A
3	H	166	PEB	NB-C1B-CHA-C4A
3	I	166	PEB	NB-C1B-CHA-C4A
3	J	166	PEB	NB-C1B-CHA-C4A
3	K	166	PEB	NB-C1B-CHA-C4A
3	L	166	PEB	NB-C1B-CHA-C4A
3	S	186	PEB	NB-C1B-CHA-C4A
3	U	186	PEB	NB-C1B-CHA-C4A
3	B	166	PEB	C2B-C1B-CHA-C4A
3	C	166	PEB	C2B-C1B-CHA-C4A
3	D	166	PEB	C2B-C1B-CHA-C4A
3	G	166	PEB	C2B-C1B-CHA-C4A
3	H	166	PEB	C2B-C1B-CHA-C4A
3	I	166	PEB	C2B-C1B-CHA-C4A

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Mol	Chain	Res	Type	Atoms
3	J	166	PEB	C2B-C1B-CHA-C4A
3	K	166	PEB	C2B-C1B-CHA-C4A
3	O	186	PEB	C2B-C1B-CHA-C4A
3	Q	186	PEB	C2B-C1B-CHA-C4A
3	S	186	PEB	C2B-C1B-CHA-C4A
3	U	186	PEB	C2B-C1B-CHA-C4A
4	E	1165	GOL	O2-C2-C3-O3
4	F	1165	GOL	O2-C2-C3-O3
4	H	1165	GOL	O2-C2-C3-O3
3	N	188	PEB	C4D-C3D-CAD-CBD
3	O	188	PEB	C4D-C3D-CAD-CBD
3	U	188	PEB	C4D-C3D-CAD-CBD
3	V	188	PEB	C4D-C3D-CAD-CBD
3	W	188	PEB	C4D-C3D-CAD-CBD
3	N	188	PEB	C2D-C3D-CAD-CBD
3	O	188	PEB	C2D-C3D-CAD-CBD
3	P	188	PEB	C2D-C3D-CAD-CBD
3	U	188	PEB	C2D-C3D-CAD-CBD
3	V	188	PEB	C2D-C3D-CAD-CBD
3	W	188	PEB	C2D-C3D-CAD-CBD
3	O	187	PEB	C2A-C3A-CAA-CBA
3	Q	187	PEB	C2A-C3A-CAA-CBA
3	W	187	PEB	C2A-C3A-CAA-CBA
3	O	188	PEB	C4B-C3B-CAB-CBB
4	A	1165	GOL	O2-C2-C3-O3
4	B	1165	GOL	O1-C1-C2-O2
4	B	1165	GOL	O2-C2-C3-O3
4	D	1165	GOL	O2-C2-C3-O3
3	T	188	PEB	C2B-C3B-CAB-CBB
4	G	1165	GOL	O2-C2-C3-O3
4	J	1165	GOL	O2-C2-C3-O3
3	T	188	PEB	C4B-C3B-CAB-CBB
3	P	188	PEB	C4A-C3A-CAA-CBA
3	R	188	PEB	C4A-C3A-CAA-CBA
3	U	188	PEB	C4A-C3A-CAA-CBA
3	X	188	PEB	C4A-C3A-CAA-CBA
3	O	188	PEB	C2B-C3B-CAB-CBB
3	R	188	PEB	C2B-C3B-CAB-CBB
3	R	188	PEB	C4B-C3B-CAB-CBB
3	M	187	PEB	C2A-C3A-CAA-CBA
3	U	187	PEB	C2A-C3A-CAA-CBA
3	P	188	PEB	C4D-C3D-CAD-CBD

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Mol	Chain	Res	Type	Atoms
3	V	188	PEB	C4B-C3B-CAB-CBB
3	W	186	PEB	CAC-CBC-CGC-O1C
4	E	1165	GOL	O1-C1-C2-O2
3	S	186	PEB	CAB-CBB-CGB-O2B
3	V	187	PEB	CAB-CBB-CGB-O1B
3	O	188	PEB	CAC-CBC-CGC-O1C
3	P	187	PEB	CAB-CBB-CGB-O1B
3	N	187	PEB	CAB-CBB-CGB-O1B
3	U	186	PEB	CAB-CBB-CGB-O1B
3	R	186	PEB	CAB-CBB-CGB-O2B
3	R	188	PEB	CAC-CBC-CGC-O2C
3	S	187	PEB	CAB-CBB-CGB-O1B
3	M	186	PEB	CAB-CBB-CGB-O1B
3	N	186	PEB	CAB-CBB-CGB-O1B
3	P	188	PEB	CAC-CBC-CGC-O1C
3	Q	186	PEB	CAB-CBB-CGB-O1B
3	R	186	PEB	CAB-CBB-CGB-O1B
3	T	187	PEB	CAB-CBB-CGB-O1B
3	X	187	PEB	CAB-CBB-CGB-O1B
3	Q	187	PEB	CAB-CBB-CGB-O1B
3	R	188	PEB	CAC-CBC-CGC-O1C
3	U	188	PEB	CAC-CBC-CGC-O2C
3	W	188	PEB	CAC-CBC-CGC-O1C
3	B	167	PEB	CAC-CBC-CGC-O1C
3	N	188	PEB	CAC-CBC-CGC-O1C
3	Q	187	PEB	CAB-CBB-CGB-O2B
3	U	188	PEB	CAC-CBC-CGC-O1C
3	V	187	PEB	CAC-CBC-CGC-O1C
3	V	188	PEB	CAC-CBC-CGC-O1C
3	D	166	PEB	CAC-CBC-CGC-O1C
3	K	167	PEB	CAC-CBC-CGC-O1C
3	M	187	PEB	CAB-CBB-CGB-O1B
3	O	186	PEB	CAB-CBB-CGB-O1B
3	Q	188	PEB	CAC-CBC-CGC-O1C
3	S	186	PEB	CAB-CBB-CGB-O1B
3	S	188	PEB	CAC-CBC-CGC-O1C
3	W	186	PEB	CAB-CBB-CGB-O2B
3	S	188	PEB	C4B-C3B-CAB-CBB
3	E	167	PEB	CAC-CBC-CGC-O1C
3	H	166	PEB	CAC-CBC-CGC-O1C
3	K	166	PEB	CAC-CBC-CGC-O1C
3	U	187	PEB	CAB-CBB-CGB-O1B

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Mol	Chain	Res	Type	Atoms
3	W	187	PEB	CAB-CBB-CGB-01B
3	S	188	PEB	C2B-C3B-CAB-CBB
3	V	188	PEB	C2B-C3B-CAB-CBB
3	K	166	PEB	CAC-CBC-CGC-O2C
3	Q	186	PEB	CAC-CBC-CGC-O2C
3	T	186	PEB	CAB-CBB-CGB-01B
3	T	187	PEB	CAB-CBB-CGB-02B
3	T	188	PEB	CAC-CBC-CGC-O1C
3	X	186	PEB	CAB-CBB-CGB-01B
3	P	187	PEB	CAC-CBC-CGC-O2C
3	Q	186	PEB	CAC-CBC-CGC-O1C
3	V	186	PEB	CAB-CBB-CGB-01B
3	V	188	PEB	CAC-CBC-CGC-O2C
3	W	187	PEB	CAB-CBB-CGB-02B
3	H	167	PEB	CAC-CBC-CGC-O2C
3	O	186	PEB	CAB-CBB-CGB-02B
3	P	187	PEB	CAC-CBC-CGC-O1C
3	R	186	PEB	CAC-CBC-CGC-O2C
3	S	187	PEB	CAB-CBB-CGB-02B
3	V	186	PEB	CAB-CBB-CGB-02B
3	X	188	PEB	CAC-CBC-CGC-O2C
3	A	167	PEB	CAC-CBC-CGC-O1C
3	L	167	PEB	CAC-CBC-CGC-O2C
3	N	187	PEB	CAB-CBB-CGB-02B
3	X	187	PEB	CAB-CBB-CGB-02B
3	P	188	PEB	C4B-C3B-CAB-CBB
3	M	186	PEB	CAB-CBB-CGB-02B
3	N	186	PEB	CAB-CBB-CGB-02B
3	N	188	PEB	CAC-CBC-CGC-O2C
3	Q	186	PEB	CAB-CBB-CGB-02B
3	S	188	PEB	CAC-CBC-CGC-O2C
3	U	186	PEB	CAB-CBB-CGB-02B
3	W	186	PEB	CAC-CBC-CGC-O2C
3	W	186	PEB	CAB-CBB-CGB-01B
3	L	167	PEB	CAC-CBC-CGC-O1C
3	R	186	PEB	CAC-CBC-CGC-O1C
3	X	188	PEB	CAC-CBC-CGC-O1C
3	G	167	PEB	CAC-CBC-CGC-O1C
3	I	166	PEB	CAC-CBC-CGC-O1C
3	O	188	PEB	CAC-CBC-CGC-O2C
3	V	187	PEB	CAB-CBB-CGB-02B
3	W	188	PEB	CAC-CBC-CGC-O2C

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Mol	Chain	Res	Type	Atoms
3	B	167	PEB	CAC-CBC-CGC-O2C
3	F	166	PEB	CAC-CBC-CGC-O1C
3	F	166	PEB	CAC-CBC-CGC-O2C
3	P	188	PEB	CAC-CBC-CGC-O2C
3	T	188	PEB	CAC-CBC-CGC-O2C
3	G	166	PEB	CAC-CBC-CGC-O1C
3	H	167	PEB	CAC-CBC-CGC-O1C
3	J	166	PEB	CAC-CBC-CGC-O1C
3	P	187	PEB	CAB-CBB-CGB-O2B
3	U	186	PEB	C2A-C3A-CAA-CBA
3	M	187	PEB	CAB-CBB-CGB-O2B
3	T	186	PEB	CAB-CBB-CGB-O2B
3	D	166	PEB	CAC-CBC-CGC-O2C
3	E	167	PEB	CAC-CBC-CGC-O2C
3	G	166	PEB	CAC-CBC-CGC-O2C
3	H	166	PEB	CAC-CBC-CGC-O2C
3	K	167	PEB	CAC-CBC-CGC-O2C
3	A	167	PEB	CAC-CBC-CGC-O2C
3	Q	187	PEB	CAC-CBC-CGC-O2C
3	I	166	PEB	CAC-CBC-CGC-O2C
3	P	187	PEB	C4A-C3A-CAA-CBA
3	G	167	PEB	CAC-CBC-CGC-O2C
3	J	166	PEB	CAC-CBC-CGC-O2C
3	J	167	PEB	CAB-CBB-CGB-O2B
3	A	166	PEB	CAC-CBC-CGC-O2C
3	C	167	PEB	CAC-CBC-CGC-O2C
3	L	167	PEB	CAB-CBB-CGB-O2B
3	U	186	PEB	CAC-CBC-CGC-O2C
3	X	186	PEB	CAB-CBB-CGB-O2B
3	P	188	PEB	C2B-C3B-CAB-CBB
3	C	167	PEB	CAB-CBB-CGB-O2B
3	D	167	PEB	CAC-CBC-CGC-O2C
3	F	167	PEB	CAB-CBB-CGB-O1B
3	L	166	PEB	CAC-CBC-CGC-O2C
3	C	166	PEB	CAC-CBC-CGC-O2C
3	F	167	PEB	CAB-CBB-CGB-O2B
3	Q	187	PEB	CAC-CBC-CGC-O1C
3	F	167	PEB	CAC-CBC-CGC-O2C
3	U	187	PEB	CAC-CBC-CGC-O2C
3	B	166	PEB	CAC-CBC-CGC-O2C
3	I	167	PEB	CAC-CBC-CGC-O2C
3	U	187	PEB	CAC-CBC-CGC-O1C

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Mol	Chain	Res	Type	Atoms
3	S	187	PEB	CAC-CBC-CGC-01C
3	A	166	PEB	CAC-CBC-CGC-01C
3	C	166	PEB	CAC-CBC-CGC-01C
3	D	167	PEB	CAC-CBC-CGC-01C
3	E	167	PEB	CAB-CBB-CGB-02B
3	F	167	PEB	CAC-CBC-CGC-01C
3	Q	188	PEB	CAC-CBC-CGC-02C
3	V	187	PEB	CAC-CBC-CGC-02C
3	G	167	PEB	CAB-CBB-CGB-02B
3	J	167	PEB	CAC-CBC-CGC-02C
3	K	167	PEB	CAB-CBB-CGB-02B
3	O	187	PEB	CAC-CBC-CGC-01C
3	O	187	PEB	CAB-CBB-CGB-02B
3	S	186	PEB	CAC-CBC-CGC-02C
3	U	187	PEB	CAB-CBB-CGB-02B
3	X	186	PEB	CAC-CBC-CGC-02C
3	C	167	PEB	CAB-CBB-CGB-01B
3	D	167	PEB	CAB-CBB-CGB-02B
3	N	186	PEB	CAC-CBC-CGC-02C
3	A	167	PEB	CAB-CBB-CGB-02B
3	B	167	PEB	CAB-CBB-CGB-02B
3	H	167	PEB	CAB-CBB-CGB-02B
3	I	167	PEB	CAC-CBC-CGC-01C
3	J	167	PEB	CAB-CBB-CGB-01B
3	X	187	PEB	CAC-CBC-CGC-01C
3	C	167	PEB	CAC-CBC-CGC-01C
3	G	167	PEB	CAB-CBB-CGB-01B
3	L	167	PEB	CAB-CBB-CGB-01B
3	N	187	PEB	CAC-CBC-CGC-01C
3	S	186	PEB	CAC-CBC-CGC-01C
3	E	167	PEB	CAB-CBB-CGB-01B
3	L	166	PEB	CAC-CBC-CGC-01C
3	O	187	PEB	CAB-CBB-CGB-01B
3	X	186	PEB	CAC-CBC-CGC-01C
3	B	166	PEB	CAC-CBC-CGC-01C
3	E	166	PEB	CAC-CBC-CGC-01C
3	E	166	PEB	CAC-CBC-CGC-02C
3	H	167	PEB	CAB-CBB-CGB-01B
3	J	167	PEB	CAC-CBC-CGC-01C
3	M	188	PEB	CAC-CBC-CGC-01C
3	M	188	PEB	CAC-CBC-CGC-02C
3	U	186	PEB	CAC-CBC-CGC-01C

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Mol	Chain	Res	Type	Atoms
3	A	167	PEB	CAB-CBB-CGB-O1B
3	B	167	PEB	CAB-CBB-CGB-O1B
3	M	187	PEB	CAC-CBC-CGC-O1C
4	H	1165	GOL	O1-C1-C2-O2
3	N	187	PEB	CAC-CBC-CGC-O2C
3	O	187	PEB	CAC-CBC-CGC-O2C
3	X	187	PEB	CAC-CBC-CGC-O2C
3	K	167	PEB	CAB-CBB-CGB-O1B
3	S	187	PEB	CAC-CBC-CGC-O2C
3	F	167	PEB	C2C-CAC-CBC-CGC
3	J	167	PEB	C2C-CAC-CBC-CGC
3	N	186	PEB	CAC-CBC-CGC-O1C
3	D	167	PEB	CAB-CBB-CGB-O1B
3	M	187	PEB	CAC-CBC-CGC-O2C
3	P	186	PEB	CAB-CBB-CGB-O1B
3	R	187	PEB	CAB-CBB-CGB-O2B
3	P	186	PEB	CAB-CBB-CGB-O2B

There are no ring outliers.

62 monomers are involved in 124 short contacts:

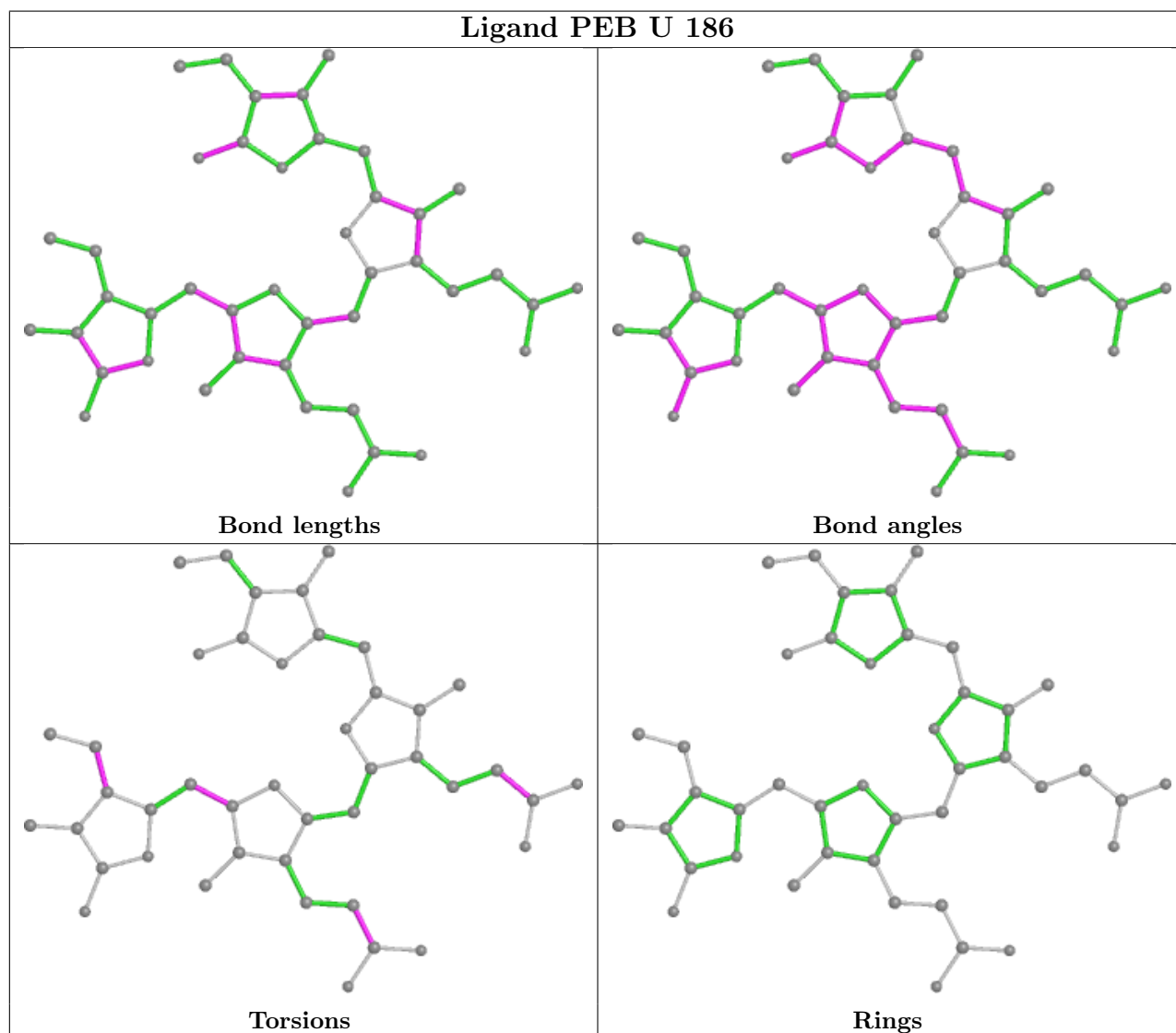
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	U	186	PEB	4	0
3	N	188	PEB	3	0
3	M	188	PEB	1	0
5	I	1200	SO4	1	0
3	C	166	PEB	3	0
3	O	186	PEB	1	0
3	Q	187	PEB	5	0
3	N	186	PEB	1	0
3	L	167	PEB	1	0
3	I	166	PEB	2	0
3	W	186	PEB	1	0
3	X	187	PEB	1	0
3	H	167	PEB	1	0
3	W	187	PEB	3	0
3	R	186	PEB	1	0
3	I	167	PEB	1	0
3	S	187	PEB	2	0
3	V	188	PEB	3	0
3	T	188	PEB	5	0
3	U	188	PEB	3	0

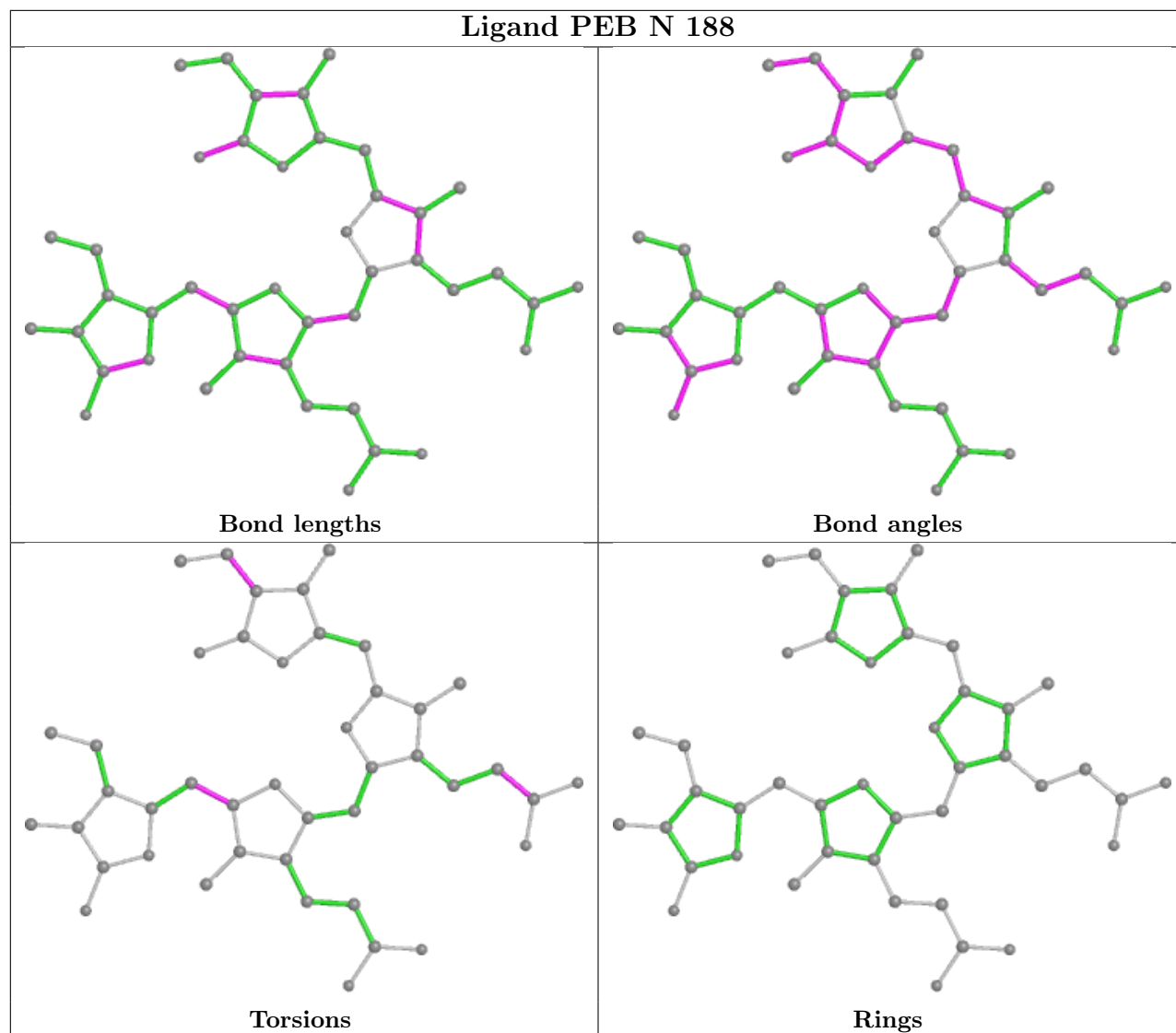
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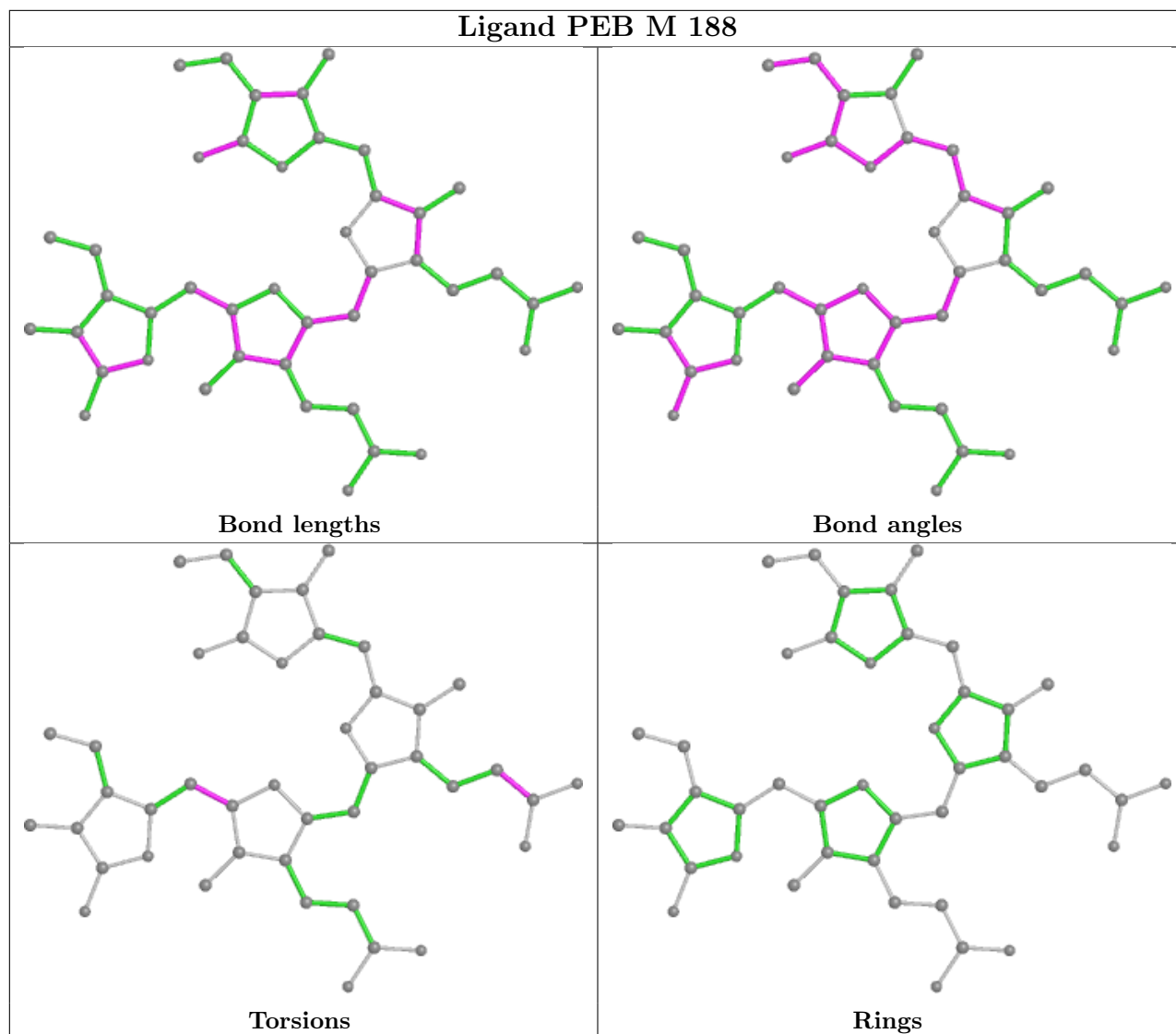
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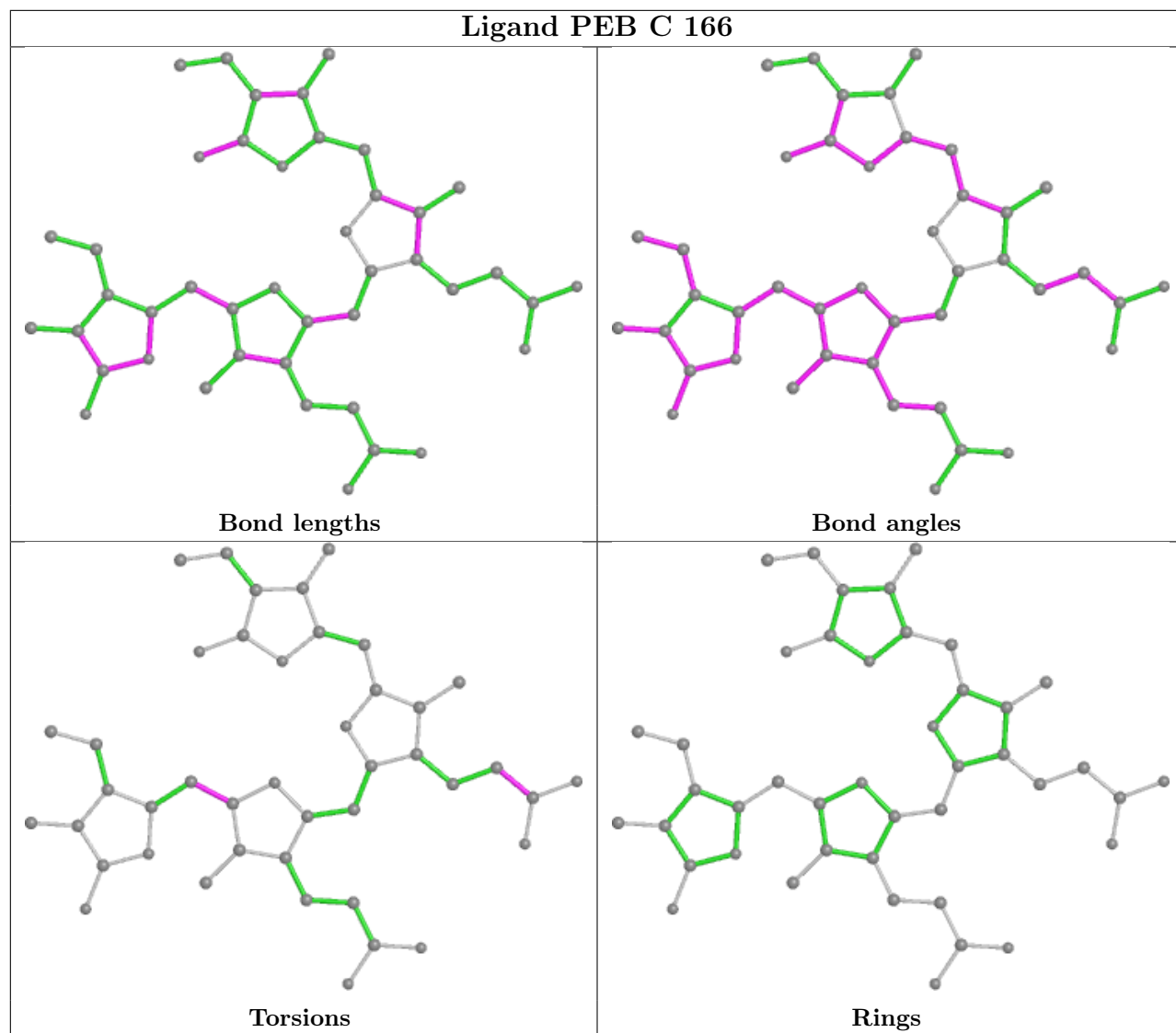
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	P	187	PEB	3	0
3	V	187	PEB	1	0
3	D	166	PEB	2	0
3	Q	186	PEB	3	0
3	J	166	PEB	2	0
3	W	188	PEB	2	0
3	G	166	PEB	2	0
3	G	167	PEB	1	0
3	R	187	PEB	2	0
3	Q	188	PEB	4	0
3	N	187	PEB	2	0
3	X	186	PEB	2	0
3	O	187	PEB	3	0
3	L	166	PEB	1	0
4	E	1165	GOL	1	0
3	K	166	PEB	2	0
3	E	167	PEB	4	0
4	H	1165	GOL	1	0
3	S	186	PEB	2	0
3	T	186	PEB	2	0
3	M	187	PEB	3	0
3	U	187	PEB	2	0
3	E	166	PEB	3	0
3	B	166	PEB	1	0
3	V	186	PEB	2	0
3	B	167	PEB	1	0
3	F	166	PEB	1	0
3	C	167	PEB	1	0
3	P	188	PEB	3	0
3	K	167	PEB	1	0
3	T	187	PEB	1	0
3	R	188	PEB	3	0
3	X	188	PEB	1	0
3	M	186	PEB	1	0
5	R	189	SO4	1	0
3	S	188	PEB	3	0
3	A	166	PEB	2	0
5	P	189	SO4	1	0
3	P	186	PEB	2	0
3	H	166	PEB	2	0
3	O	188	PEB	2	0
3	J	167	PEB	2	0

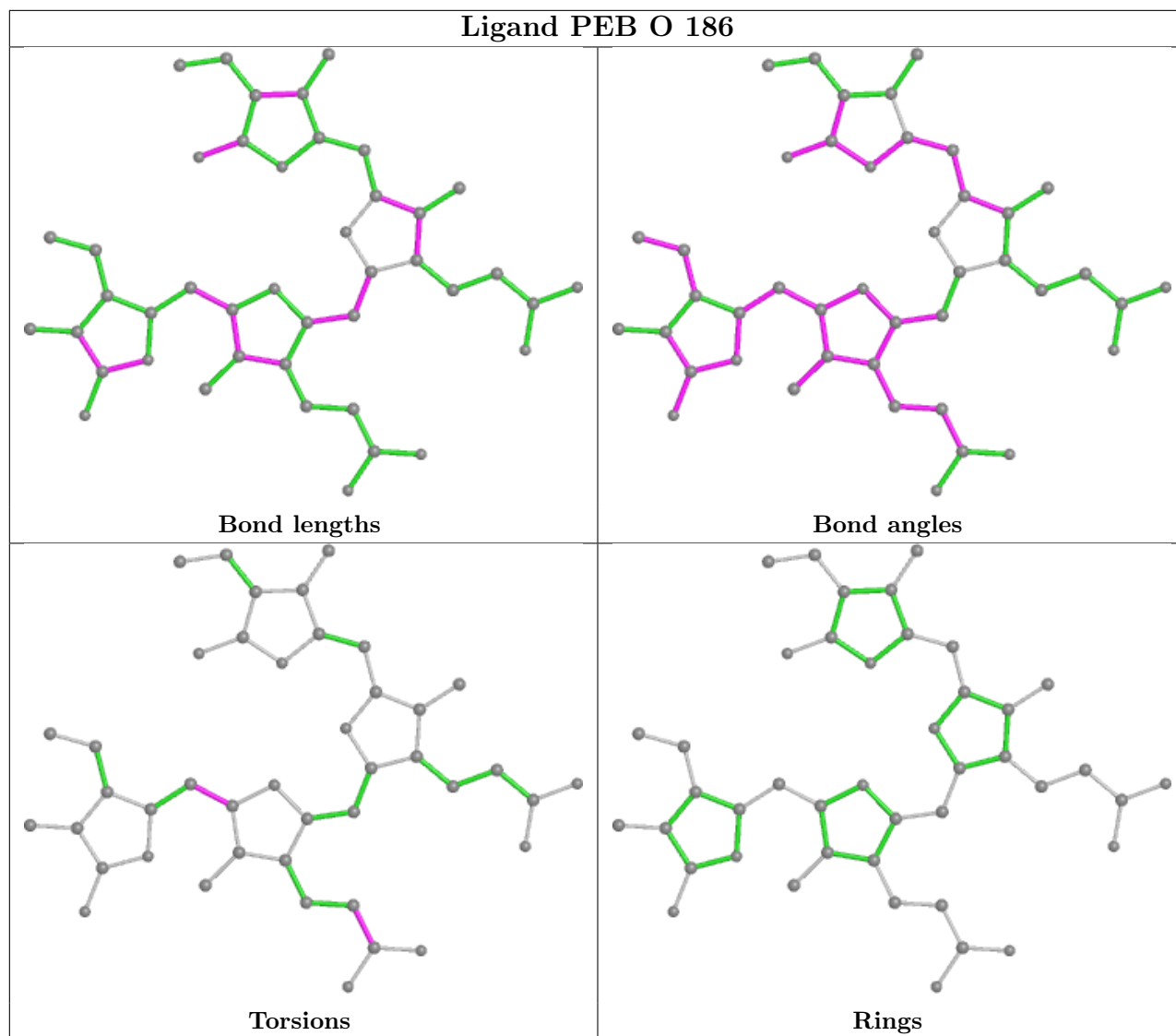
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

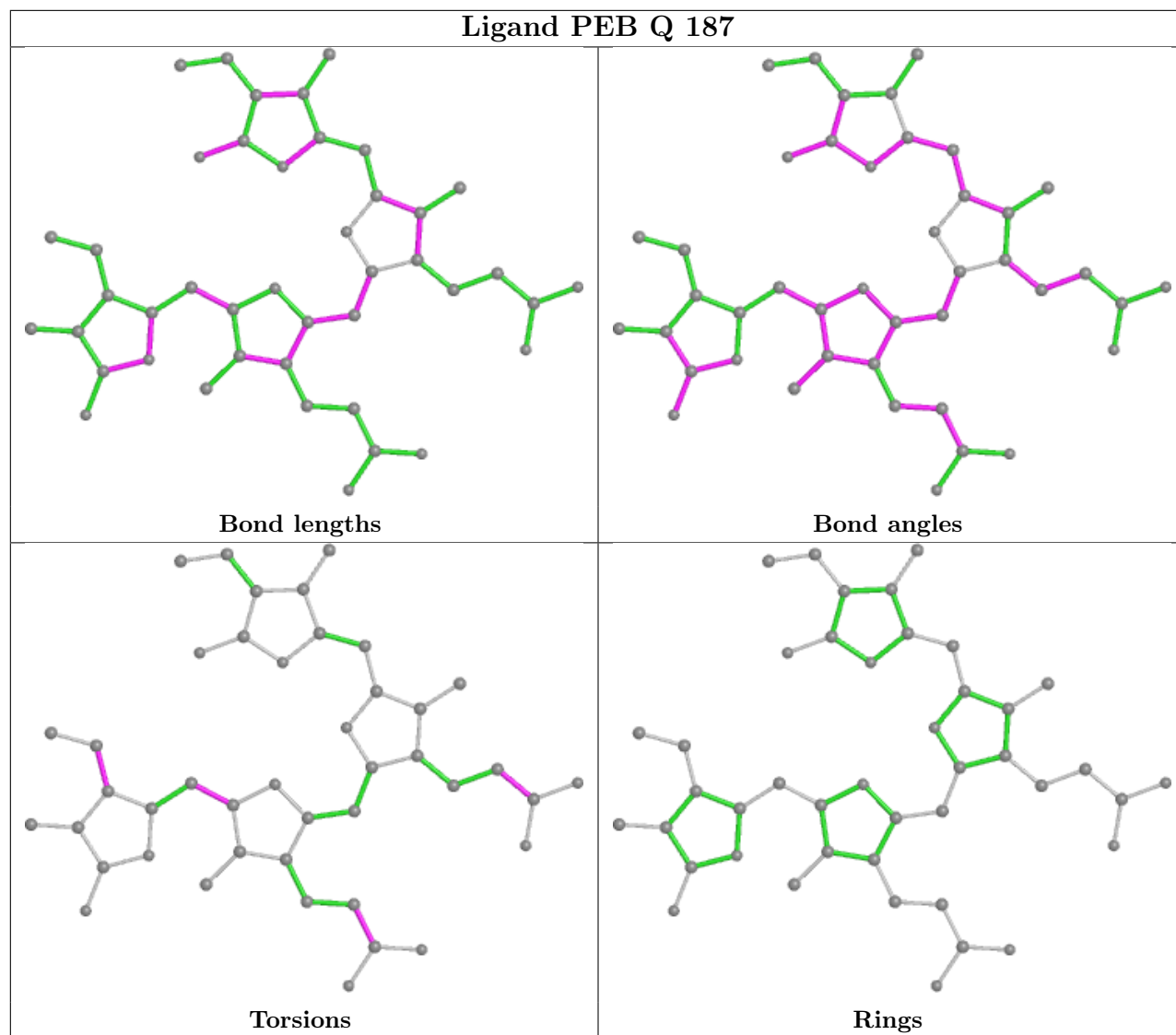


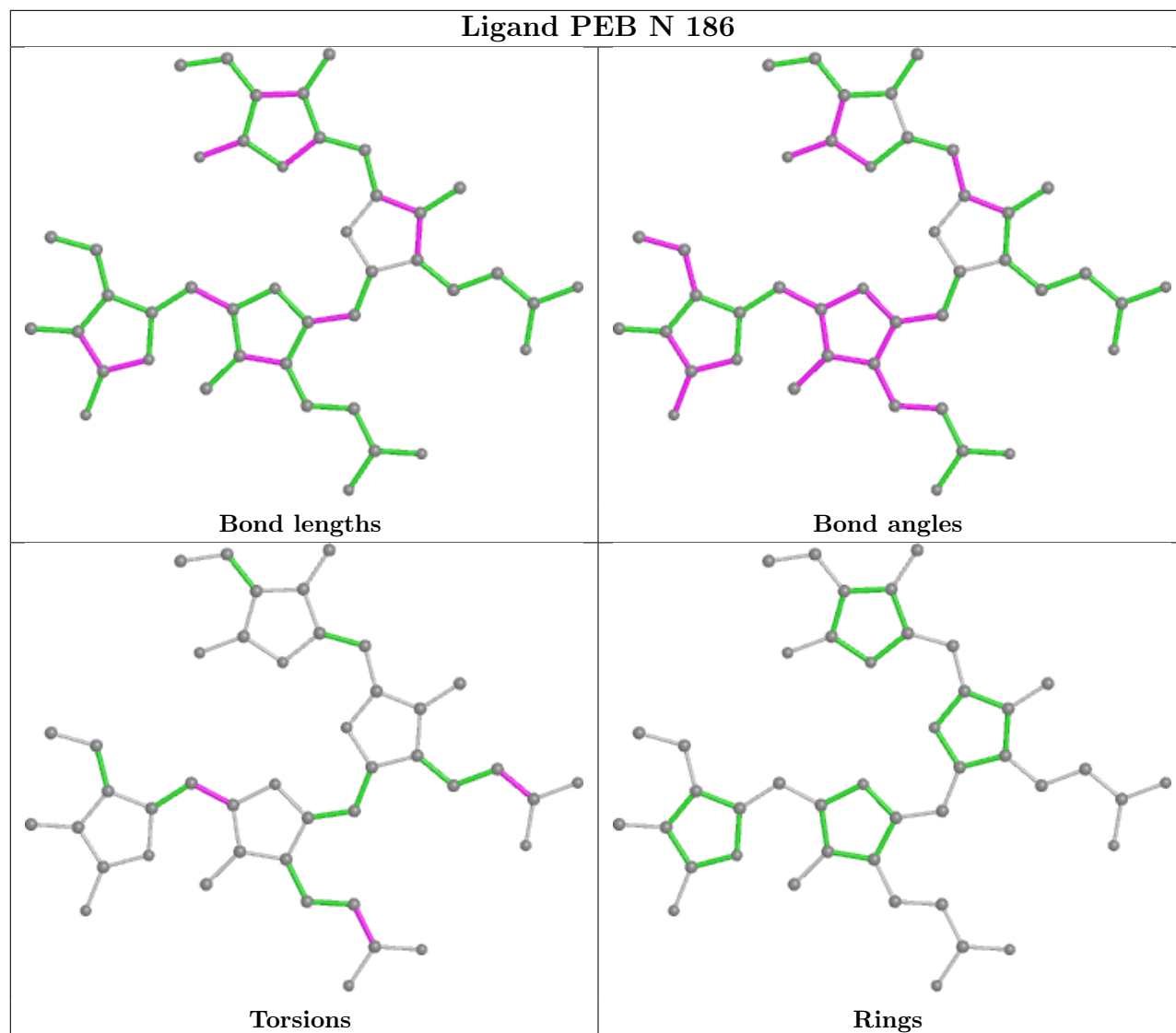


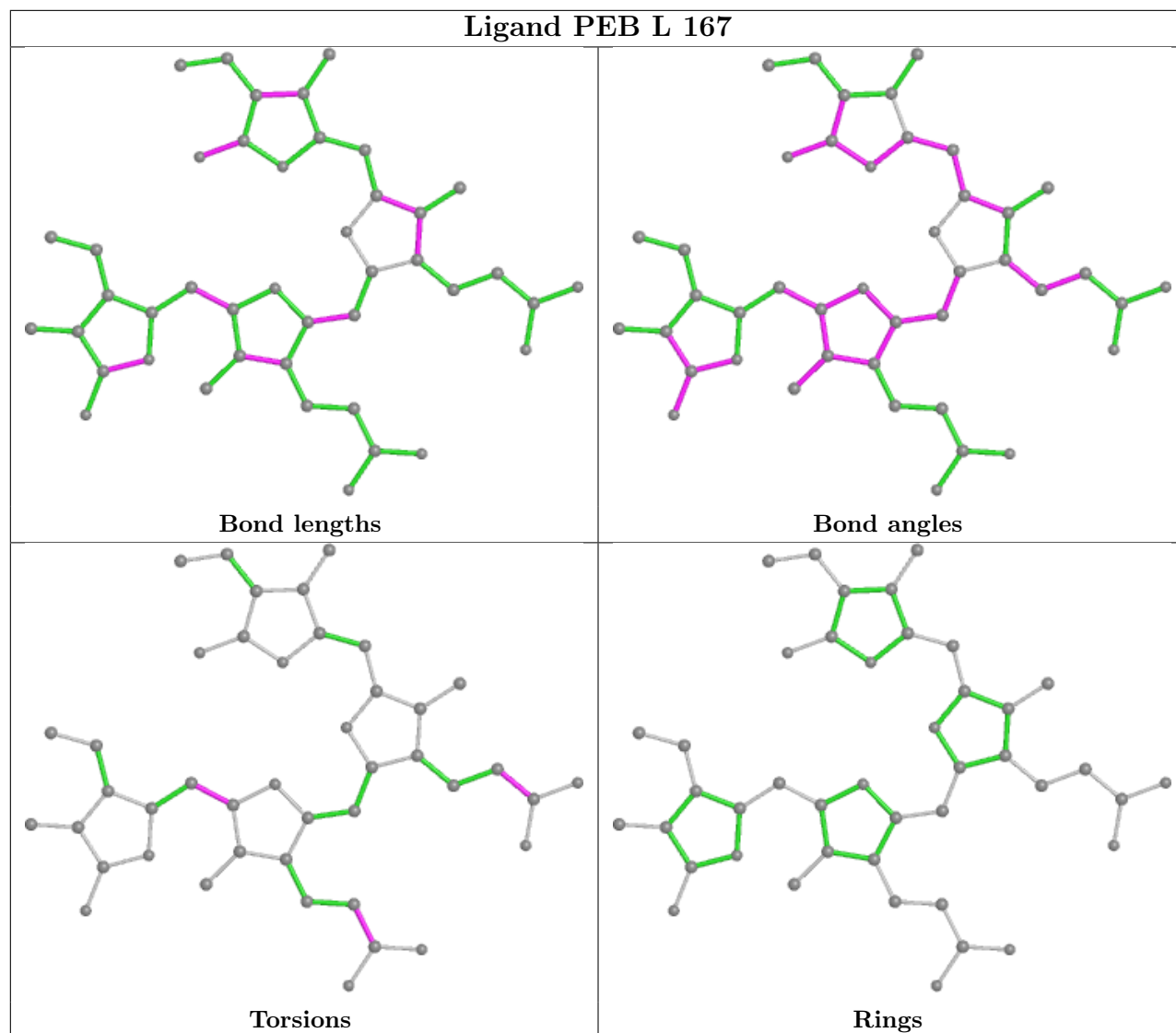


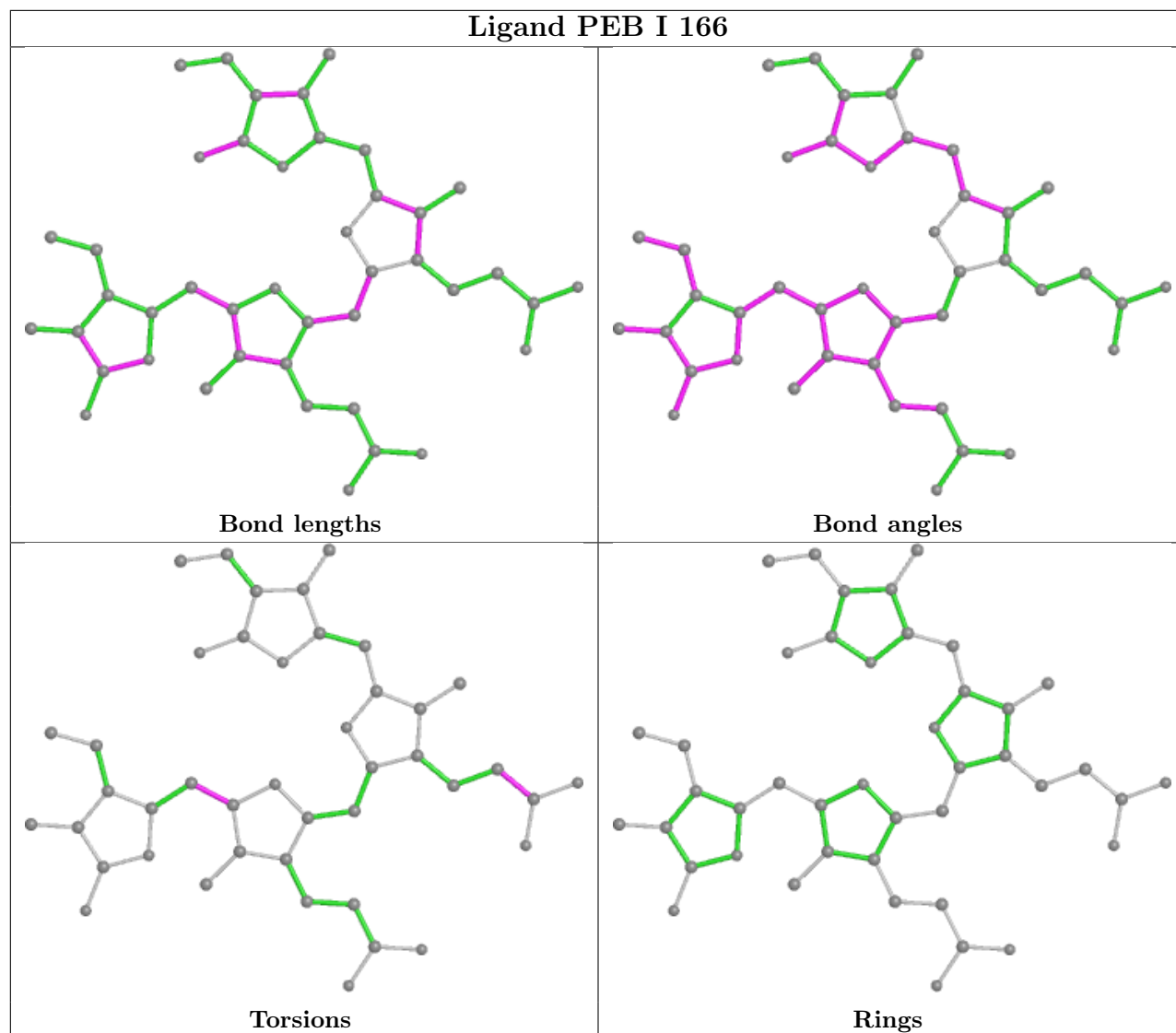


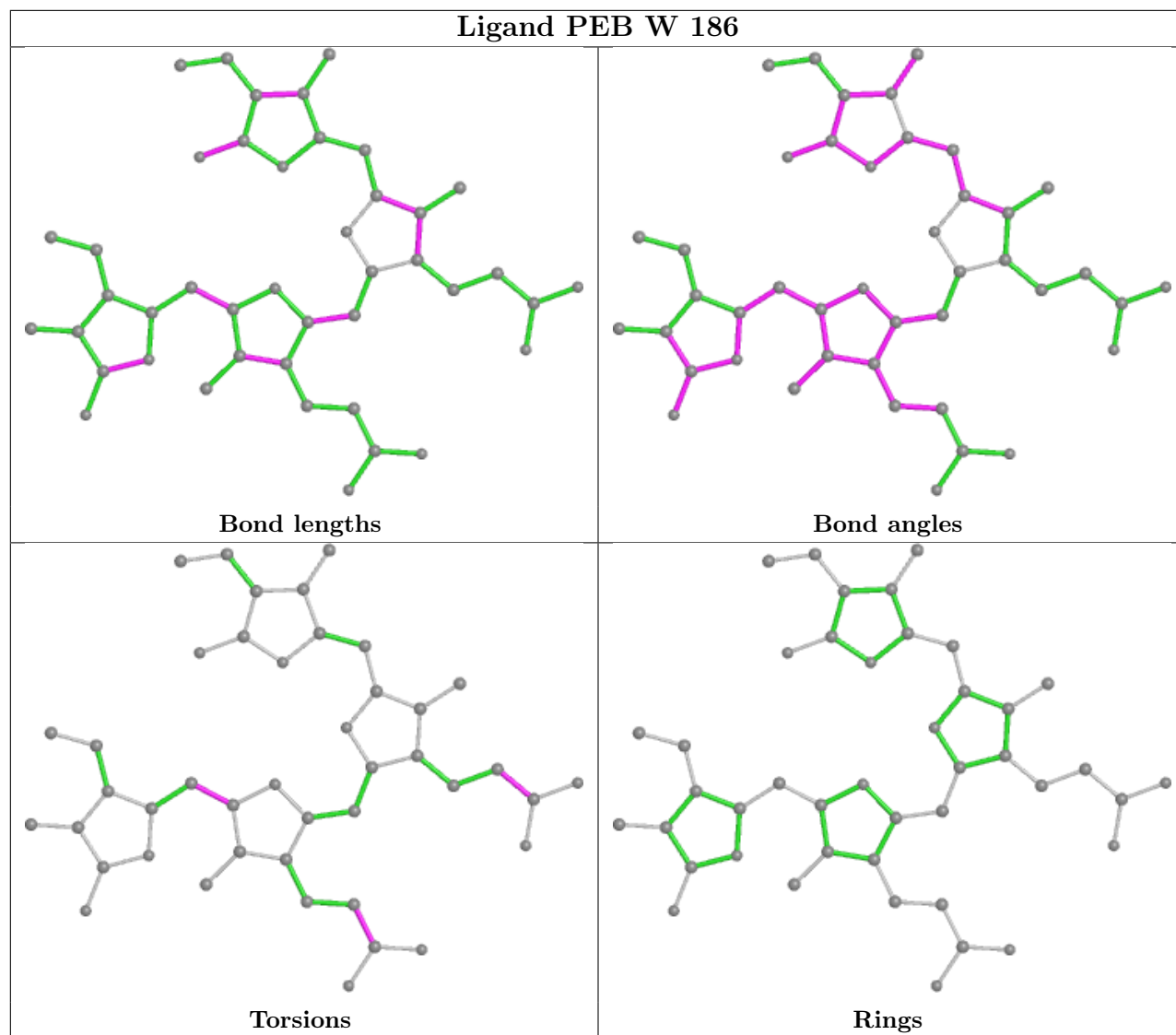


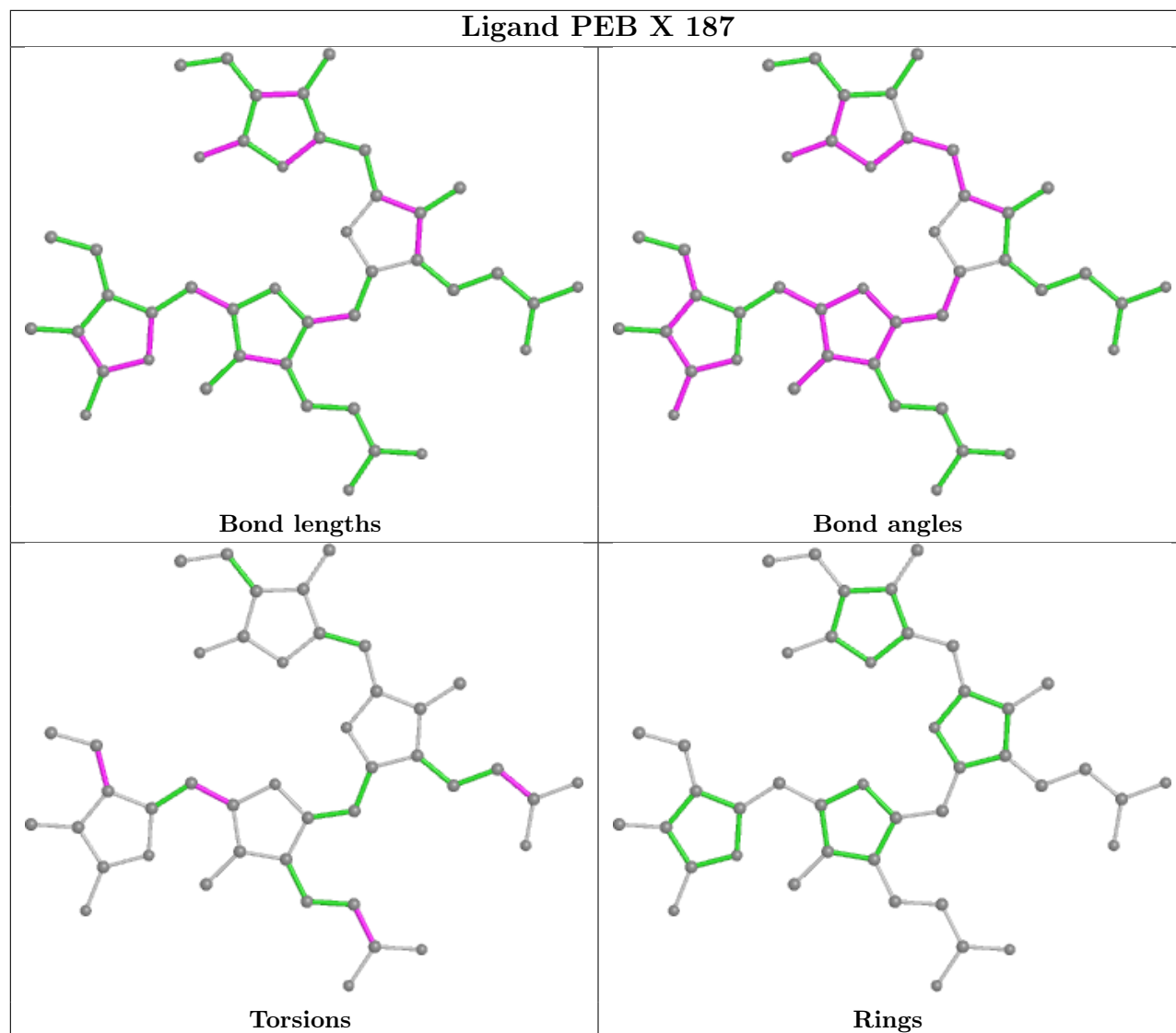


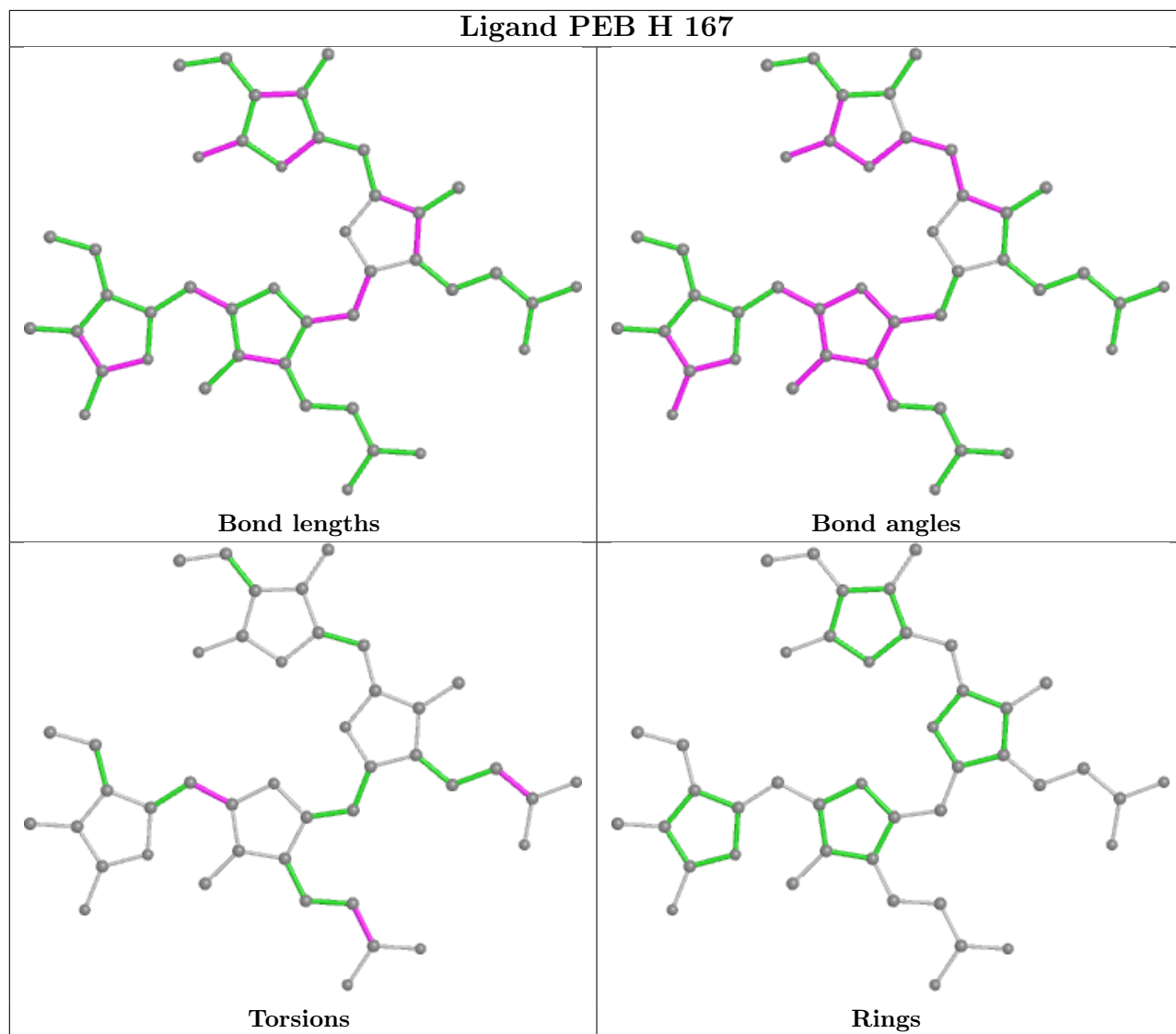


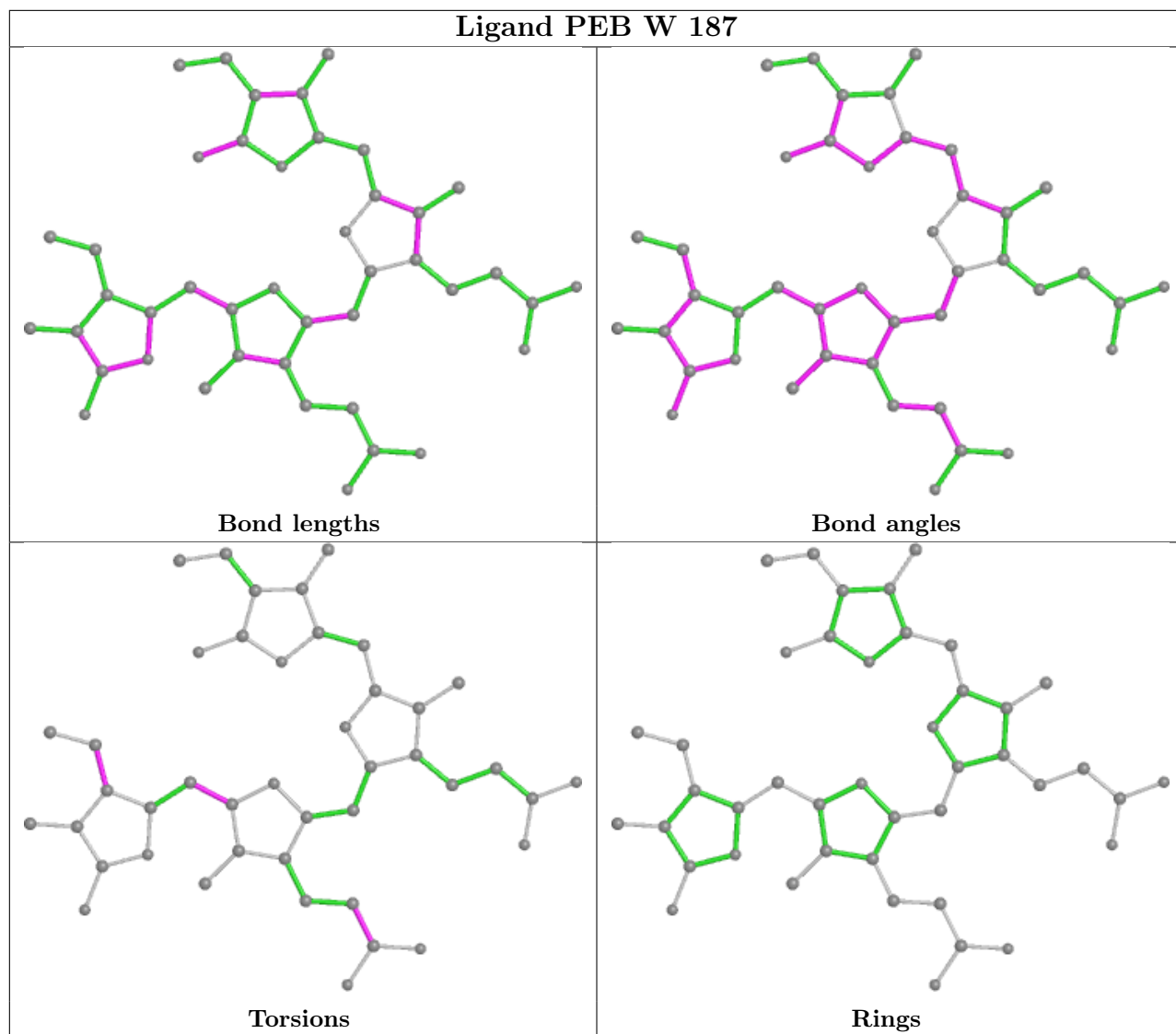


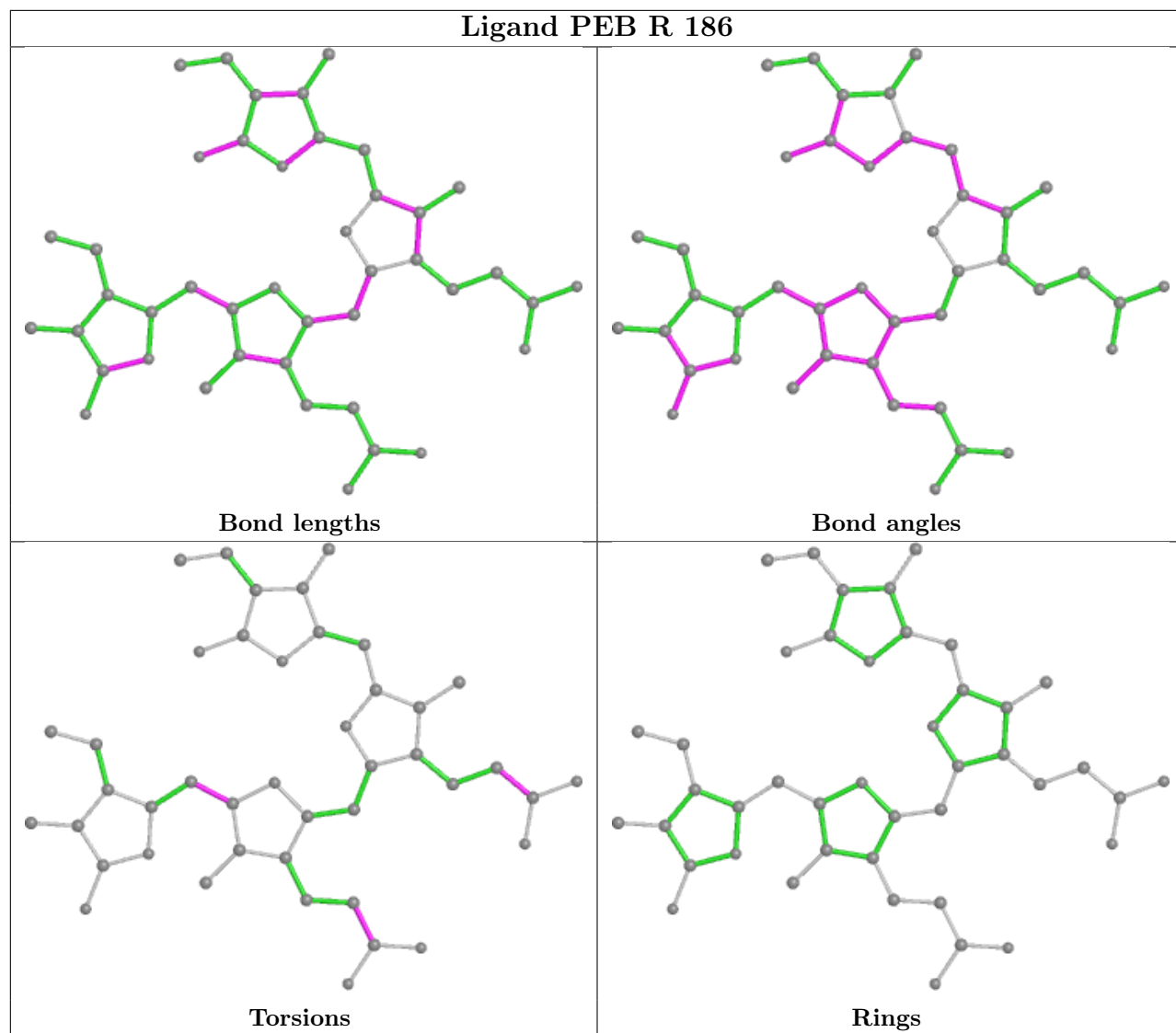


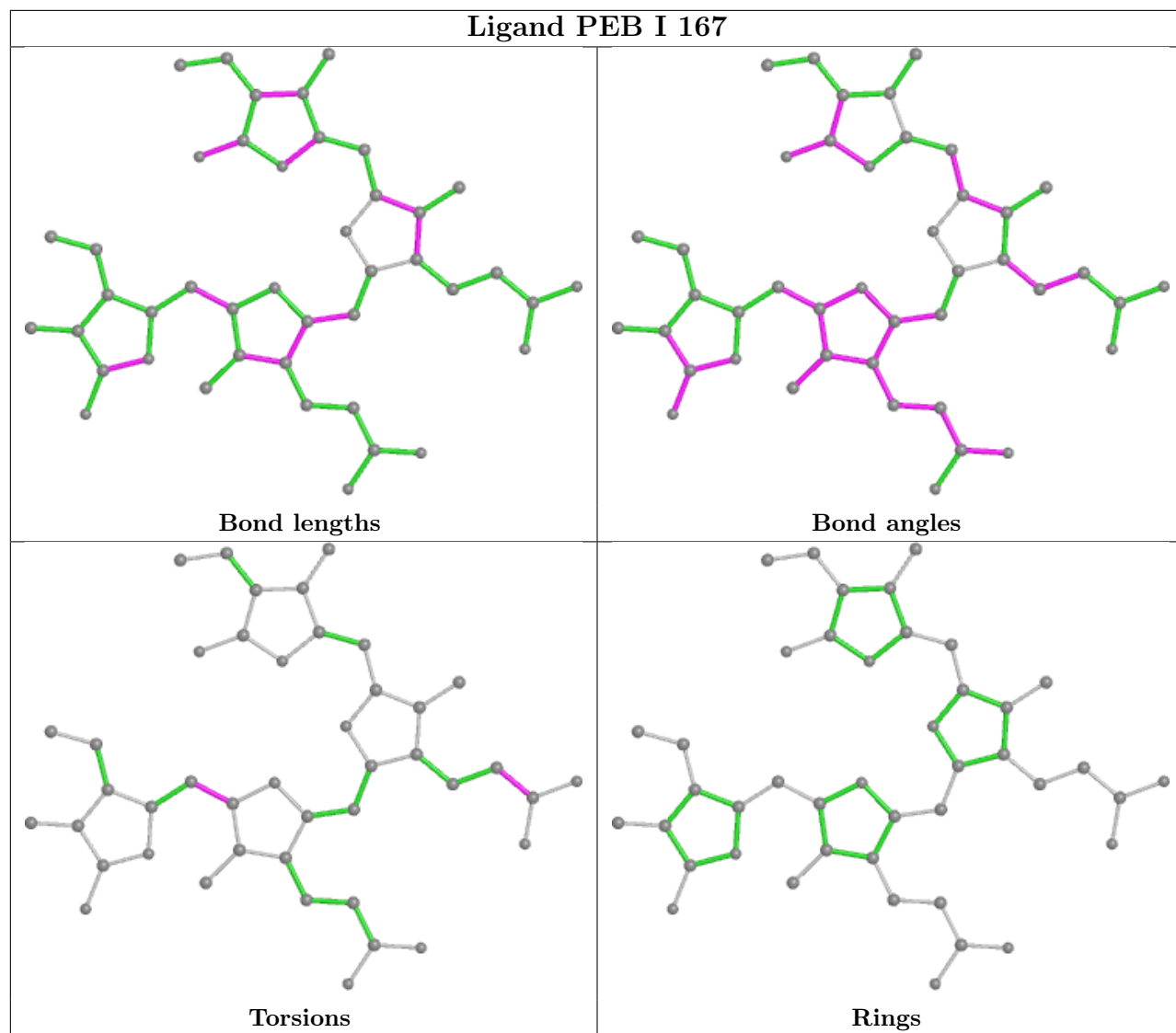


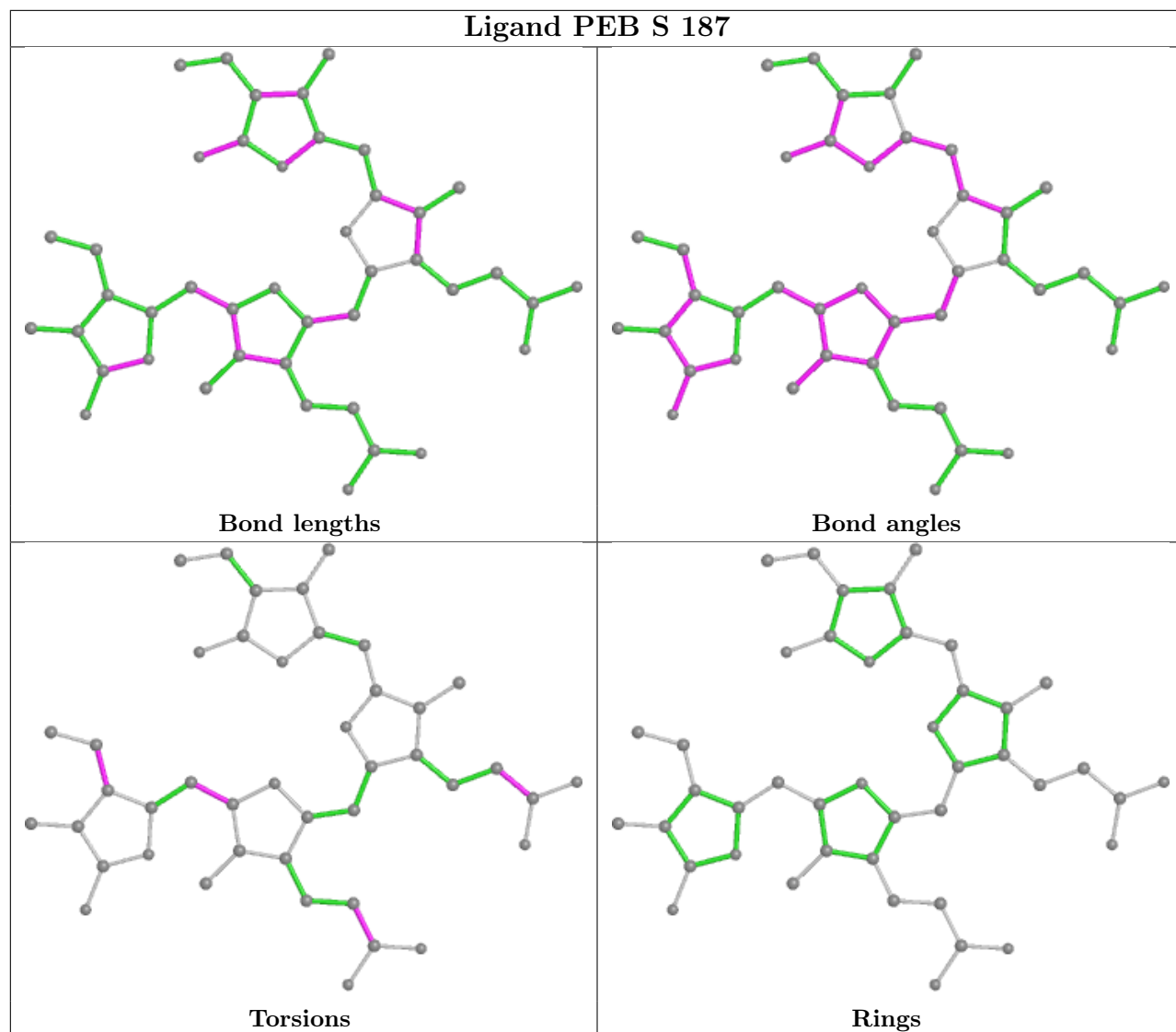


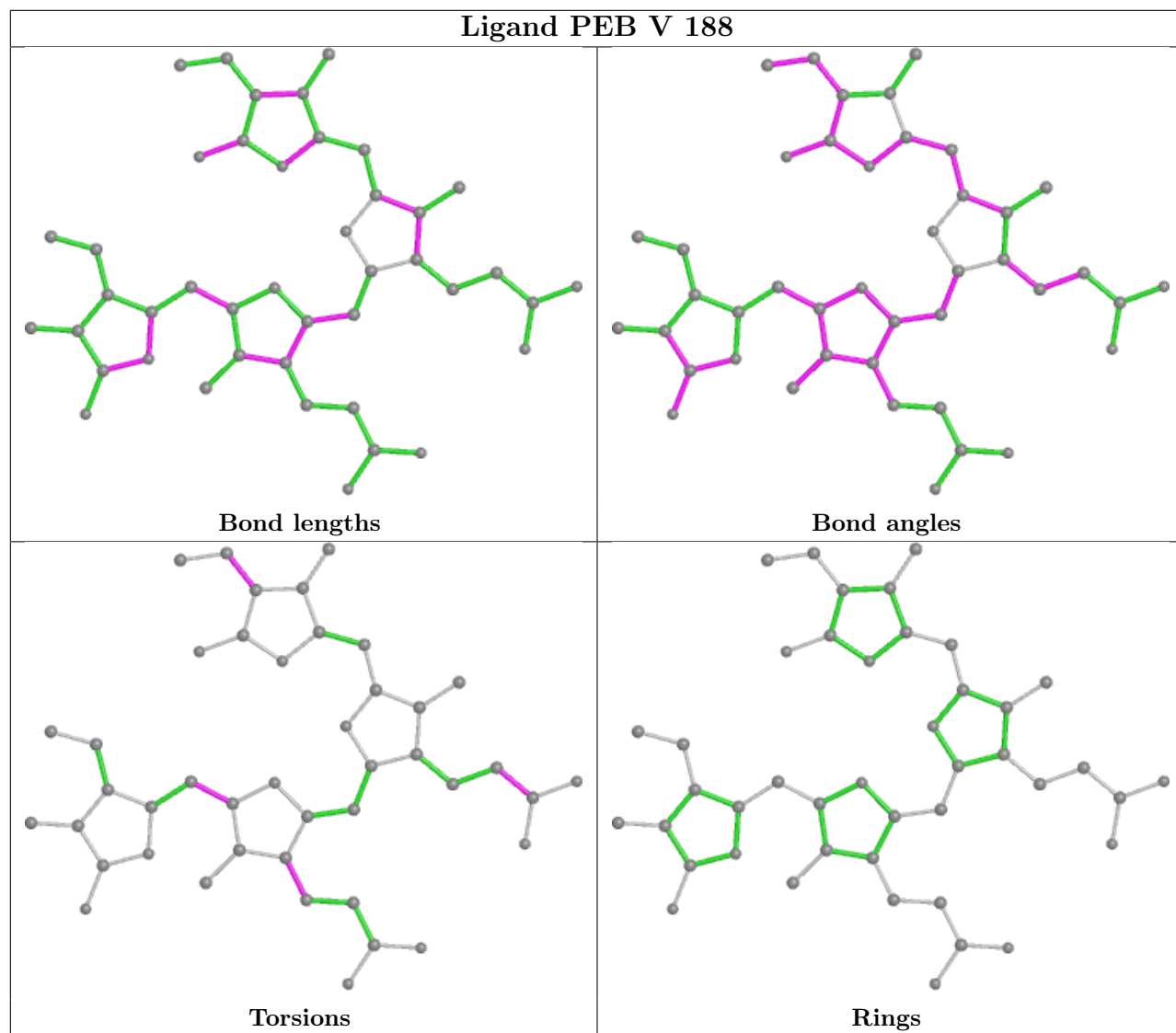


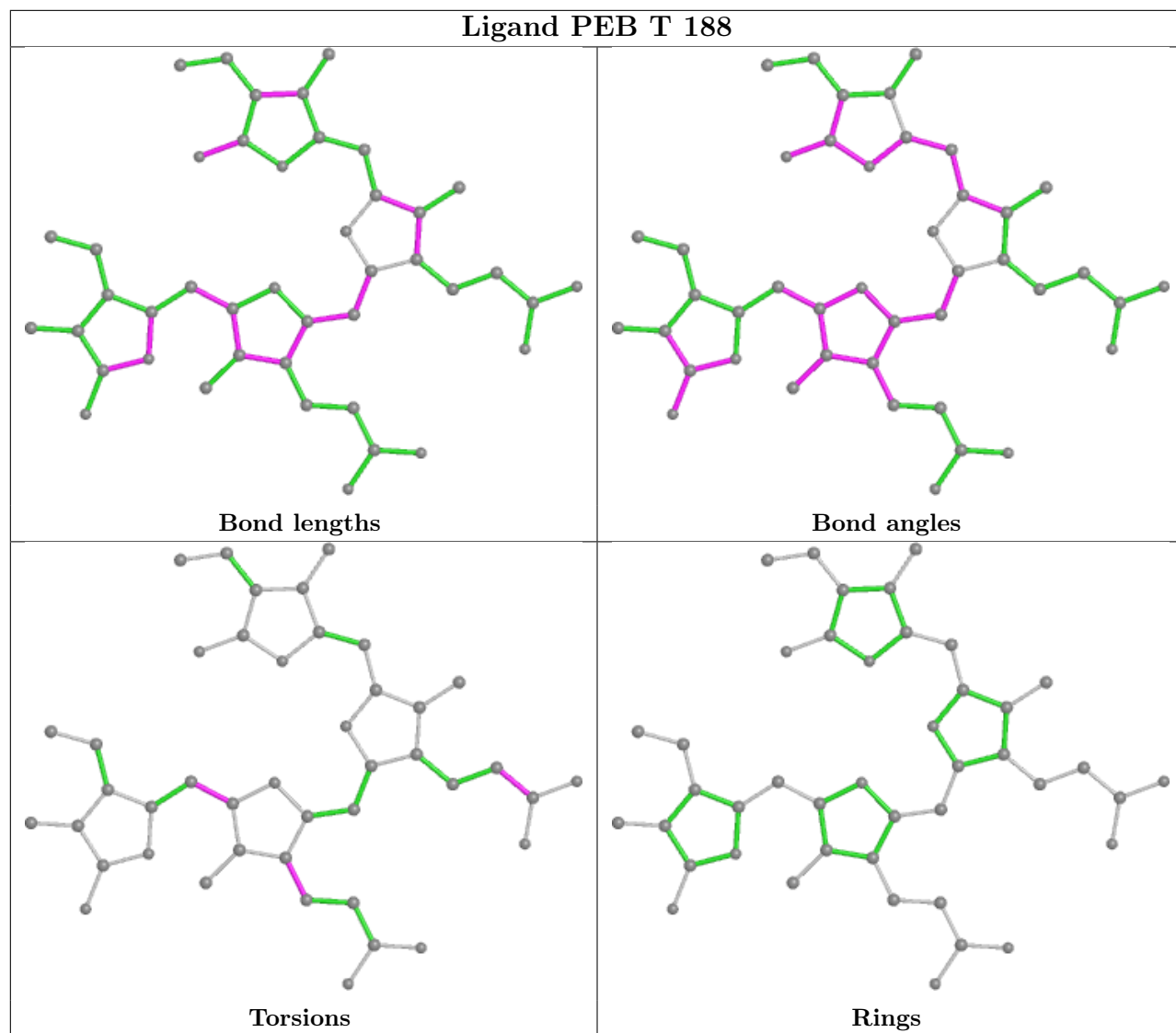


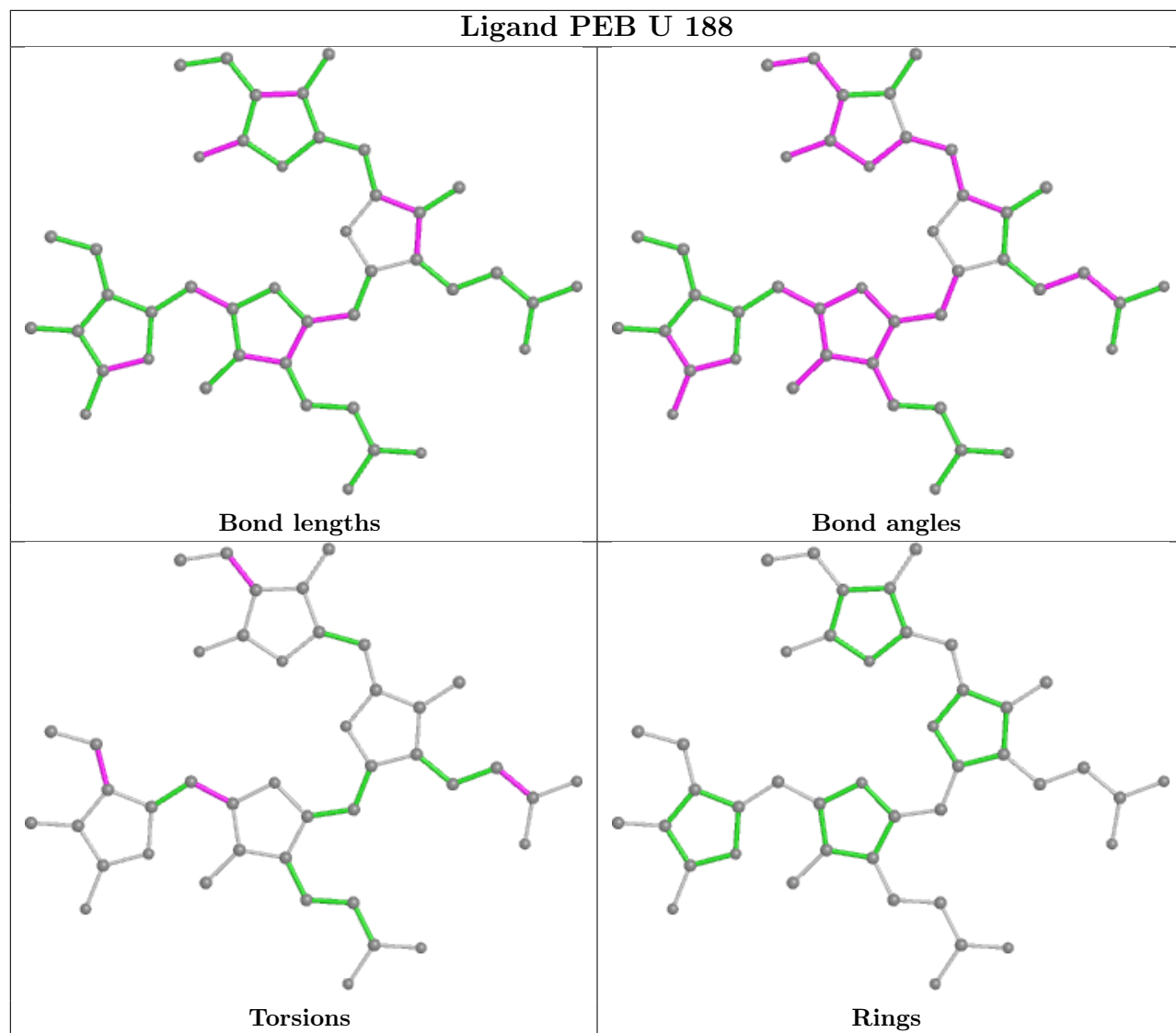


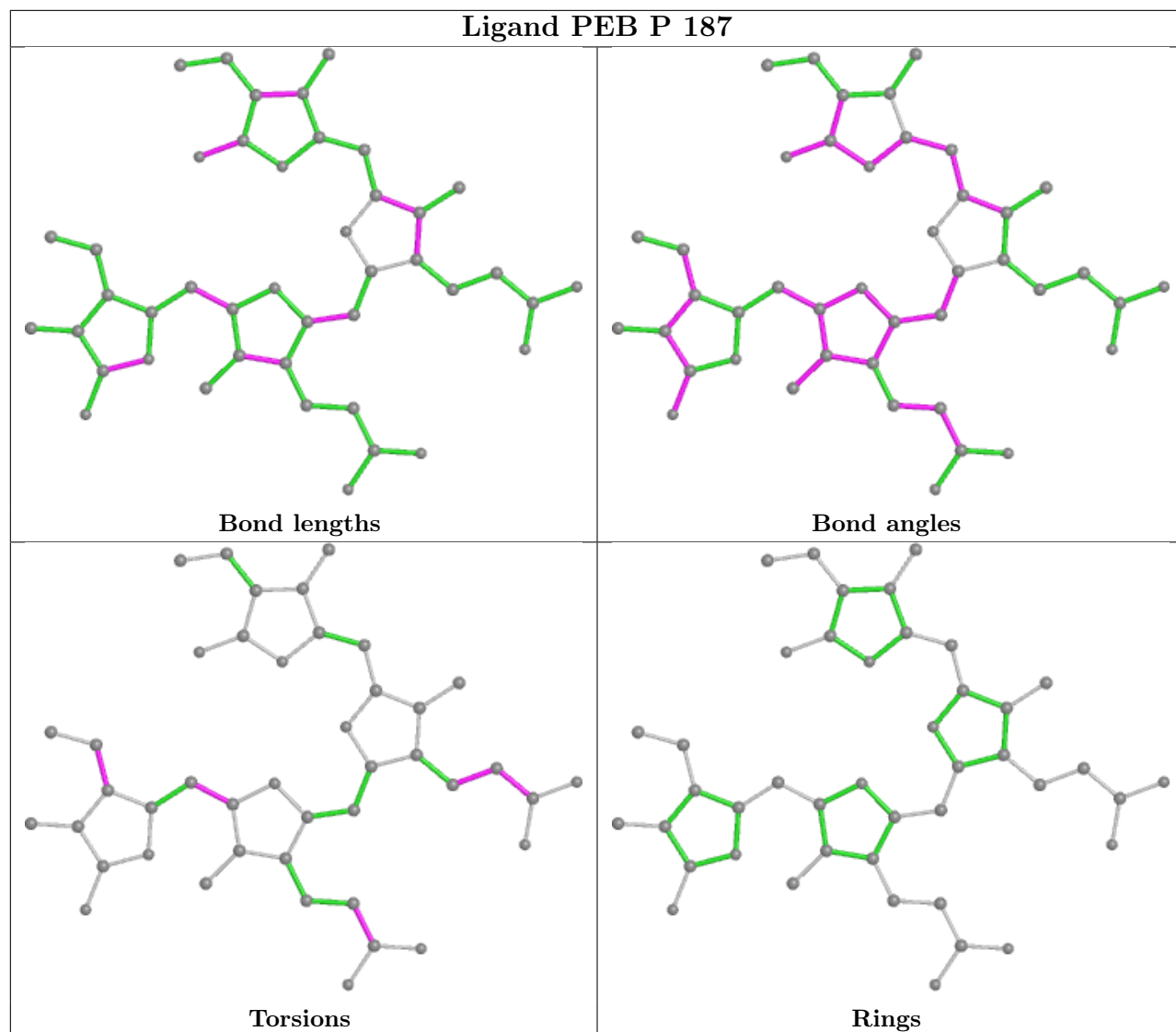


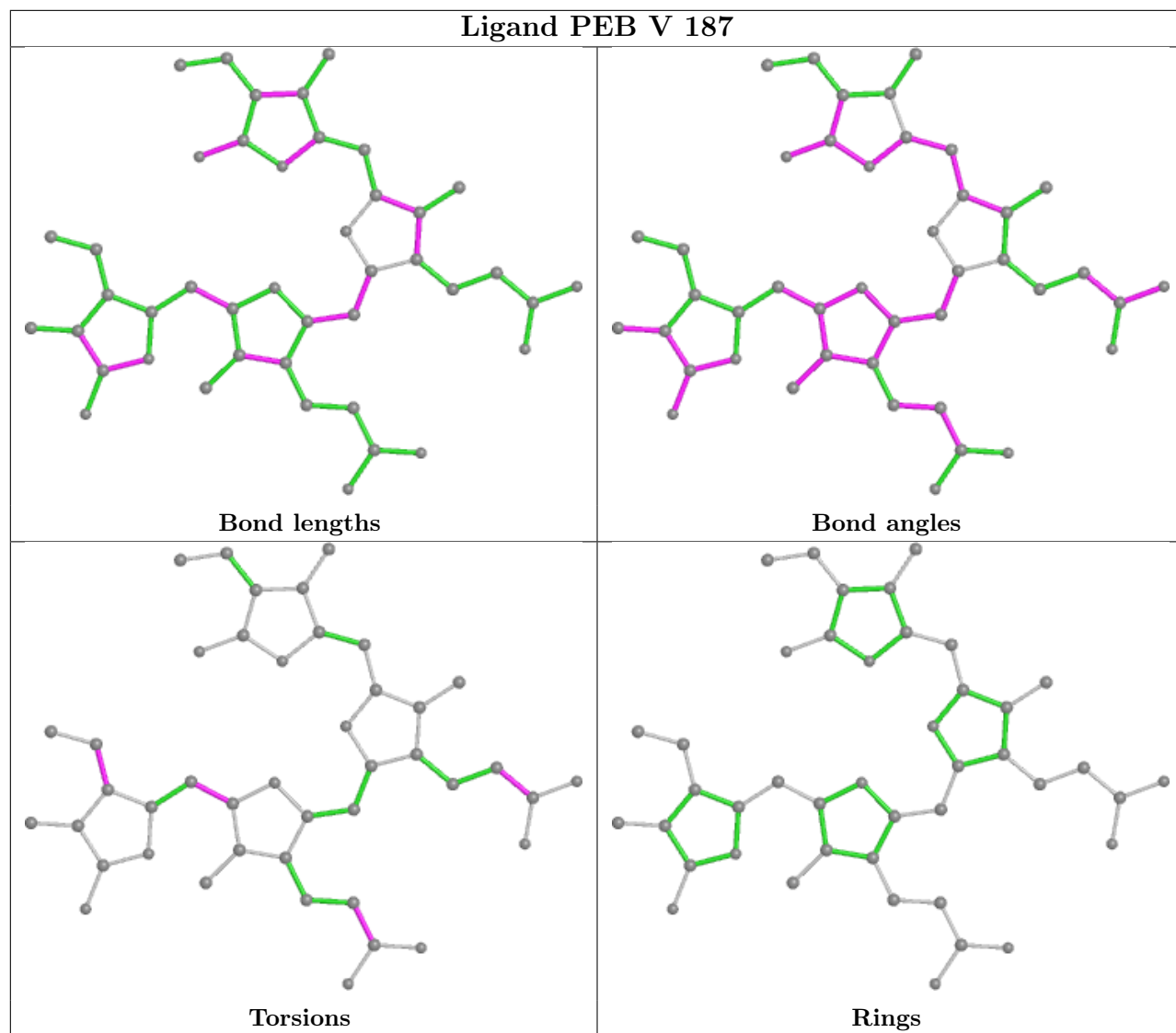


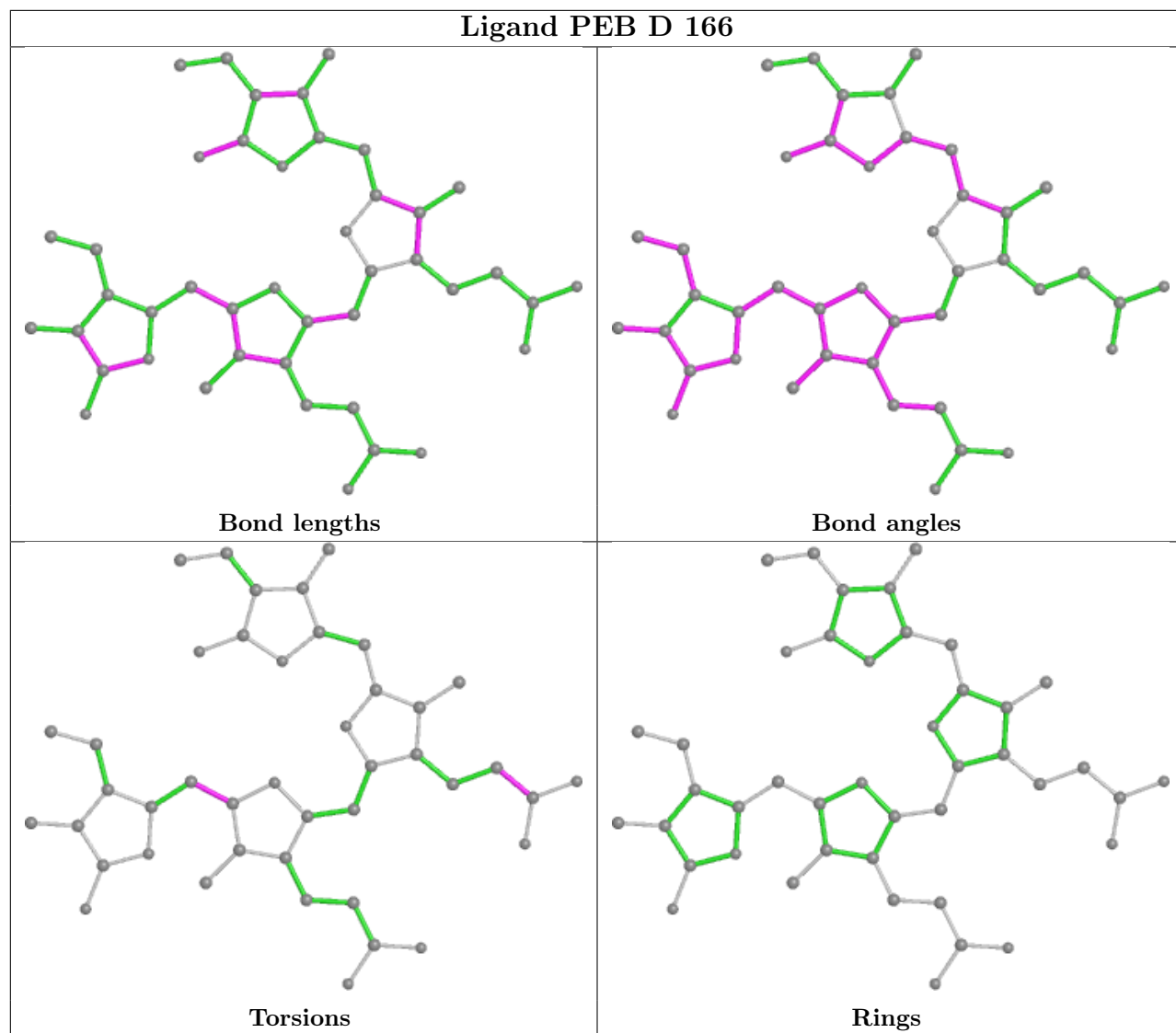


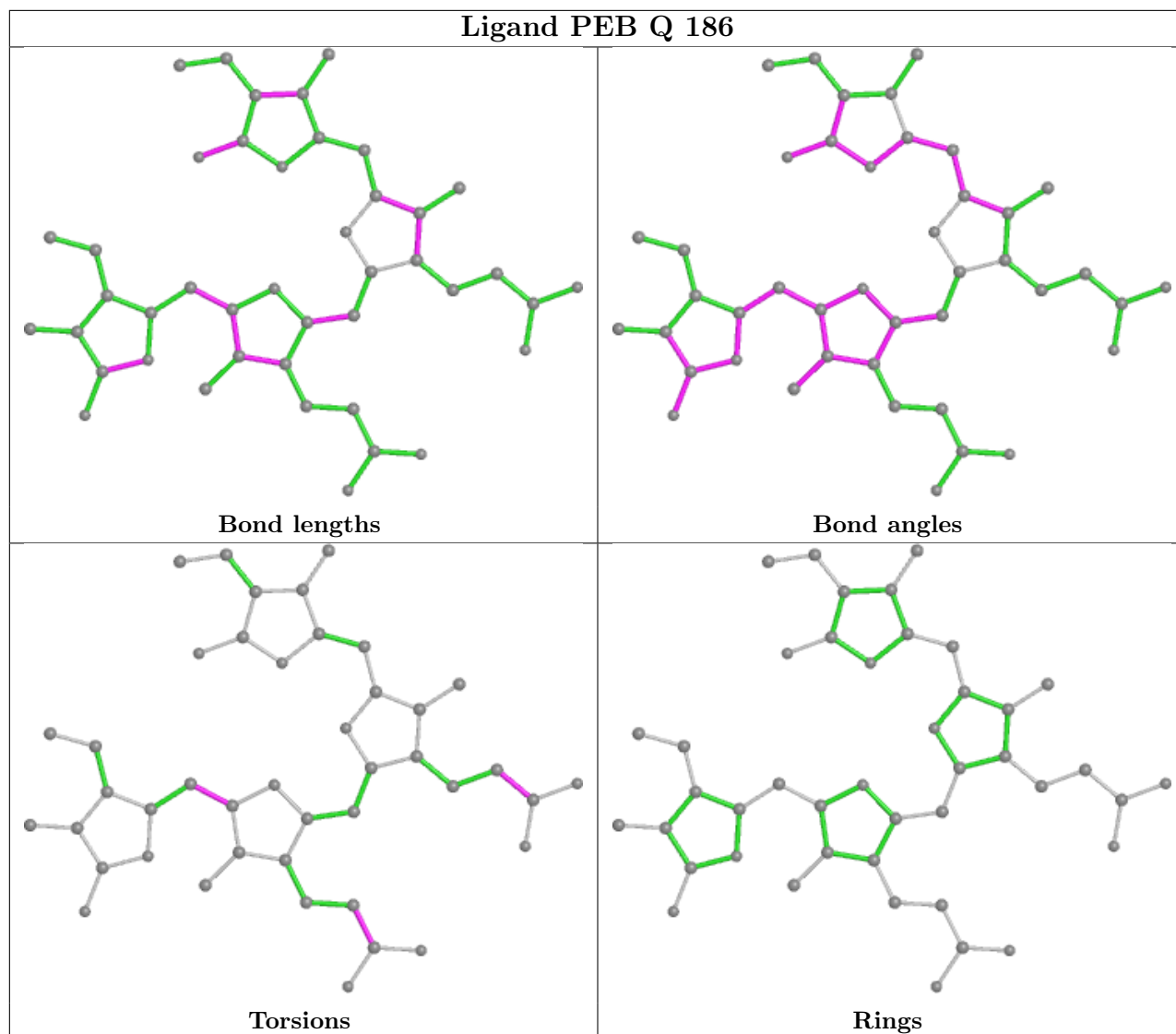


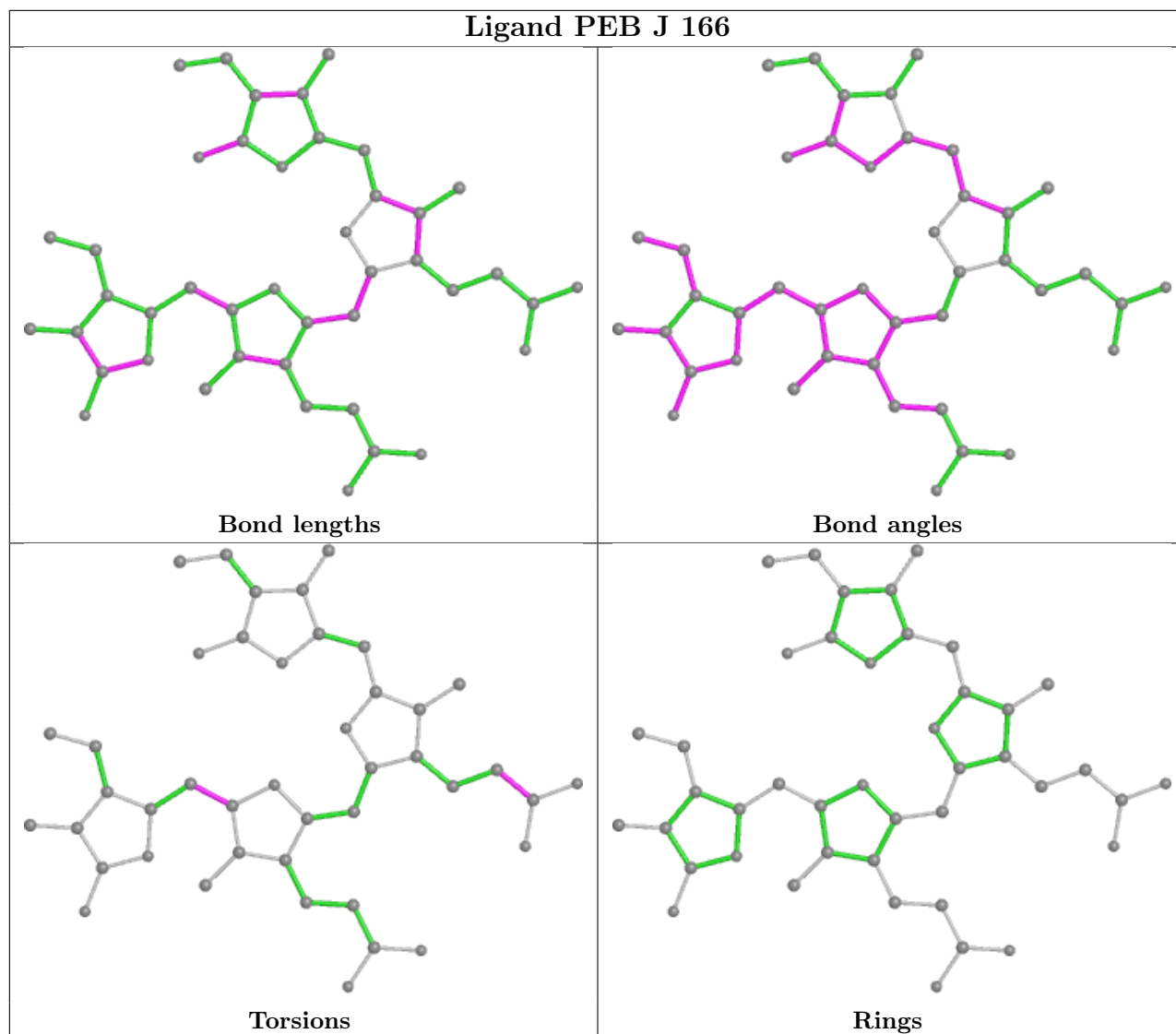


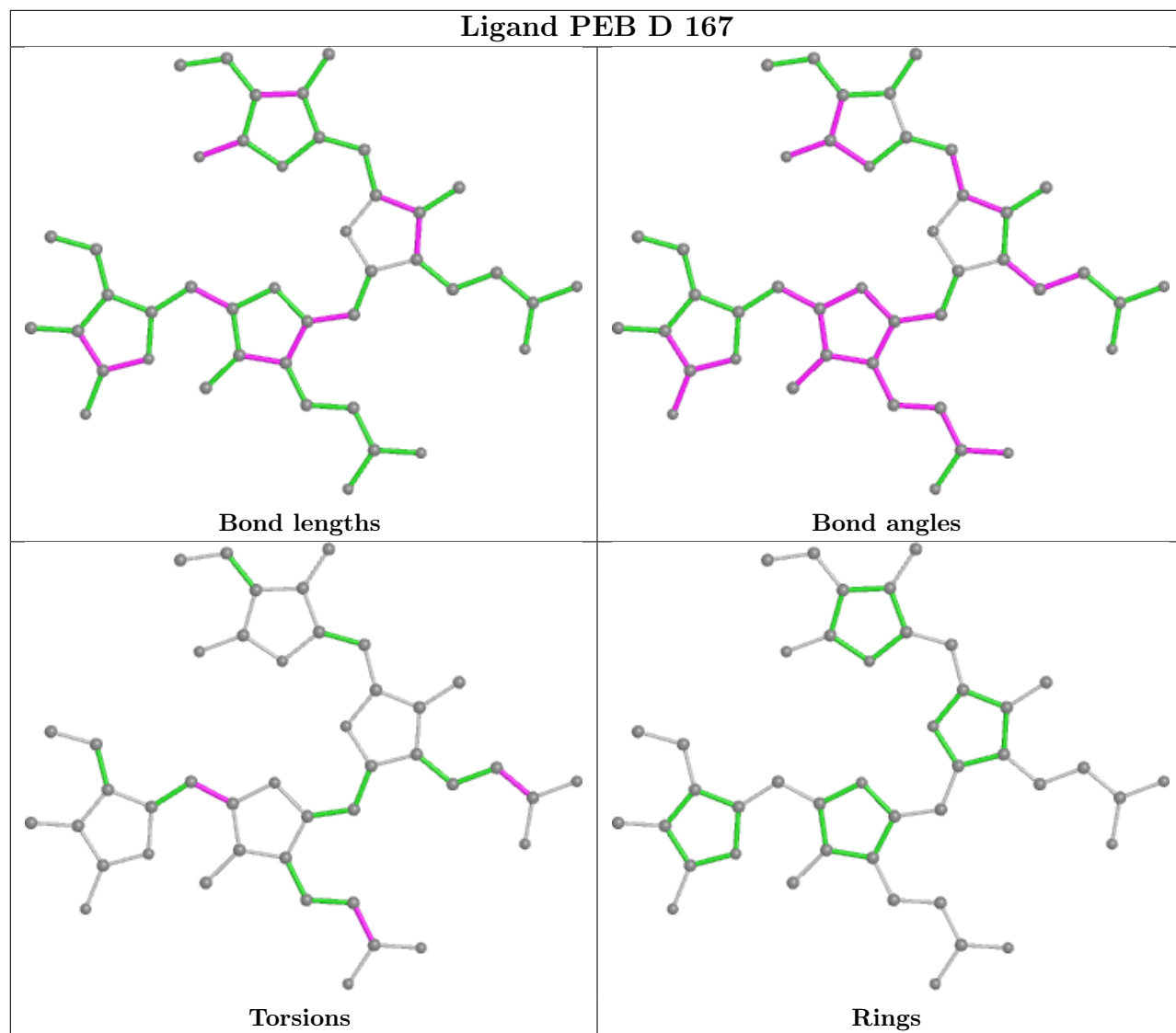


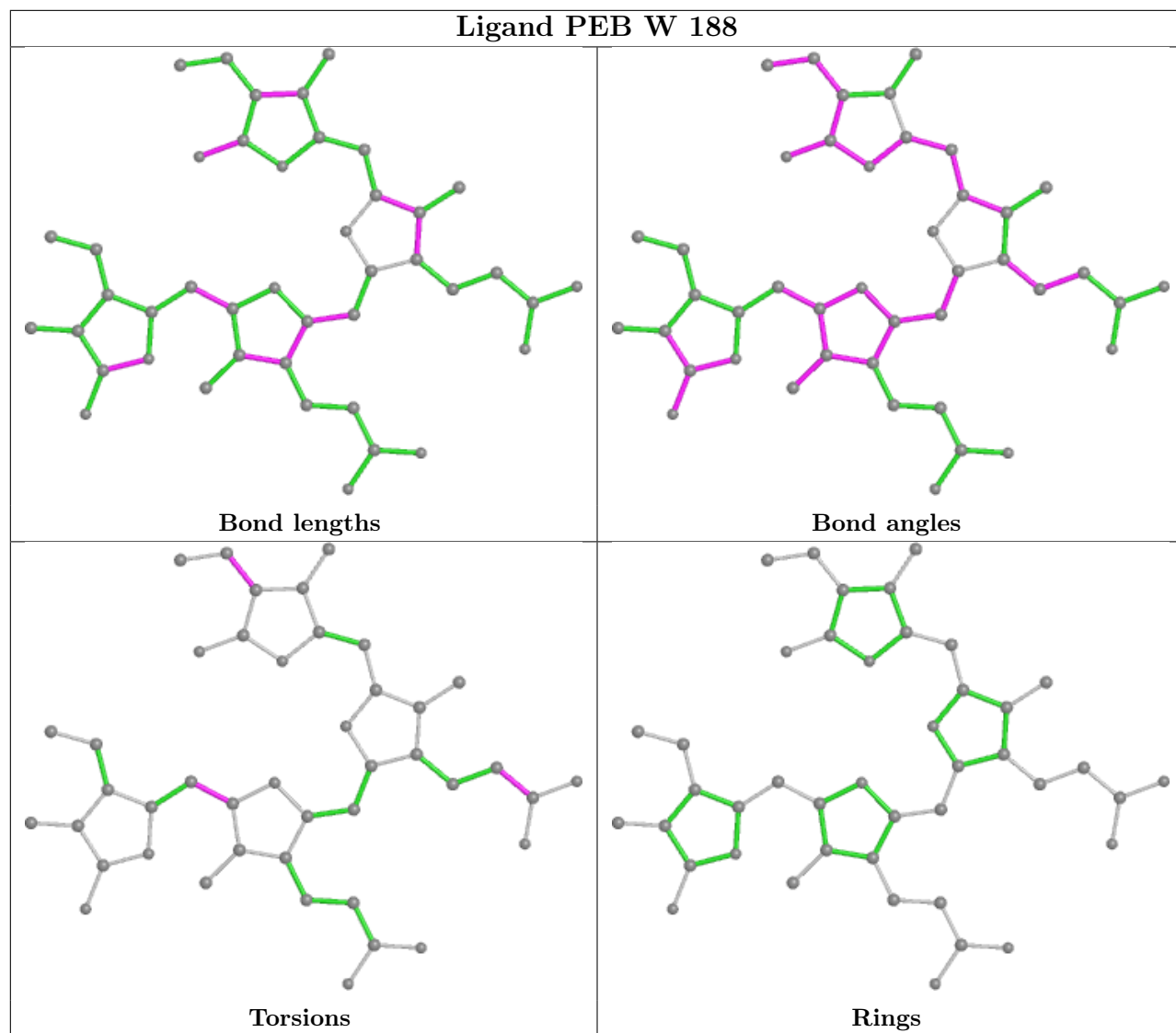


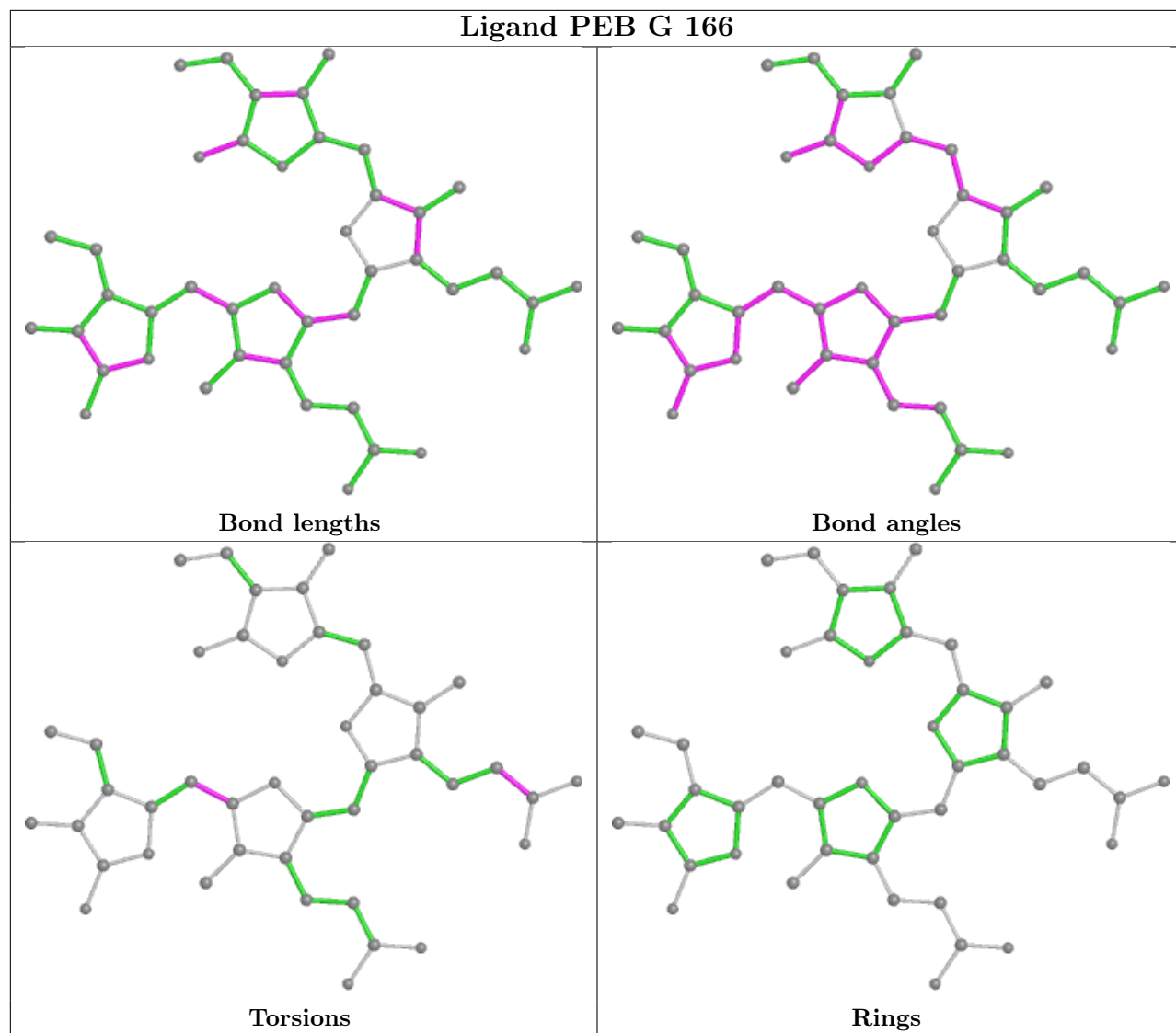


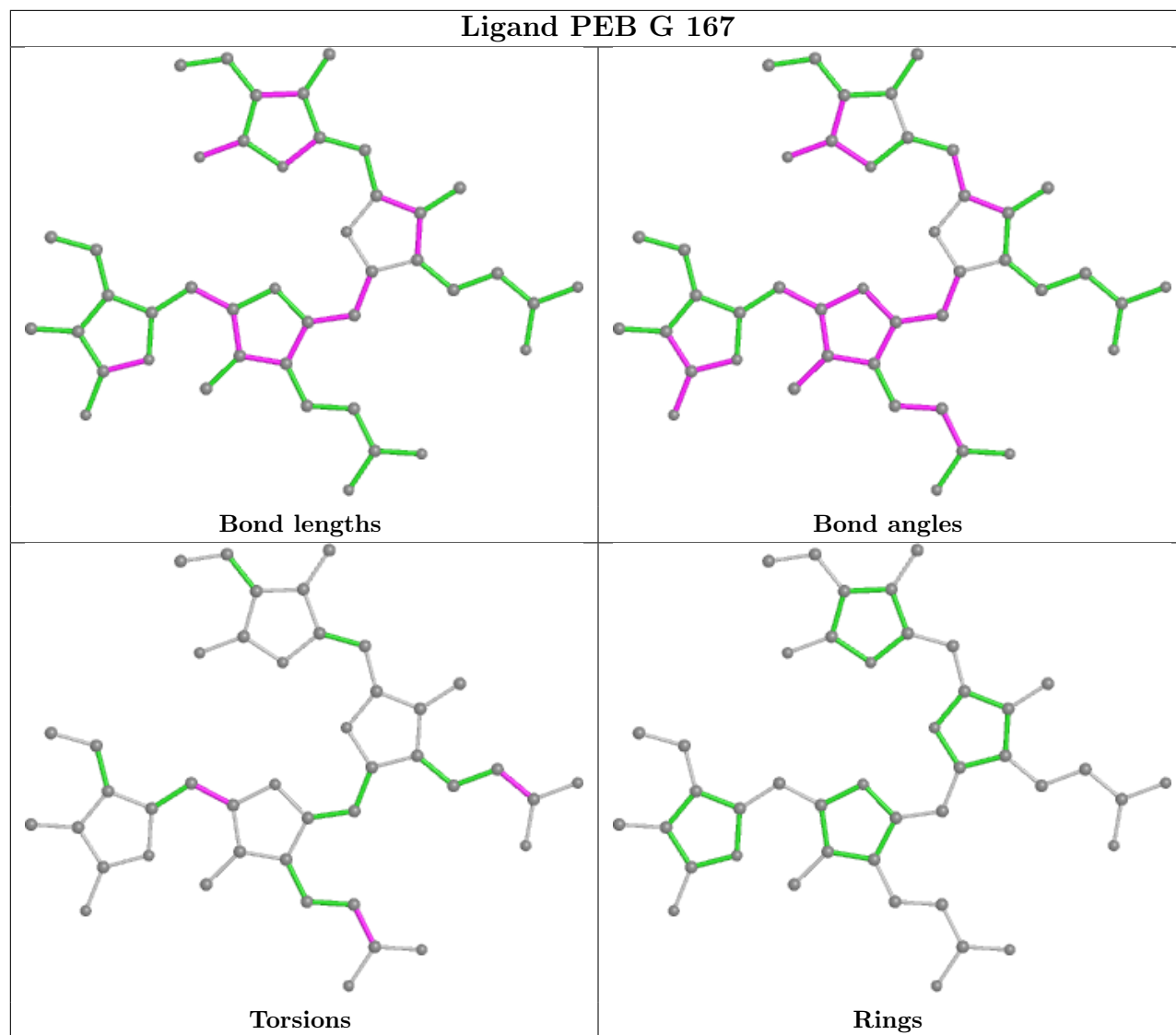


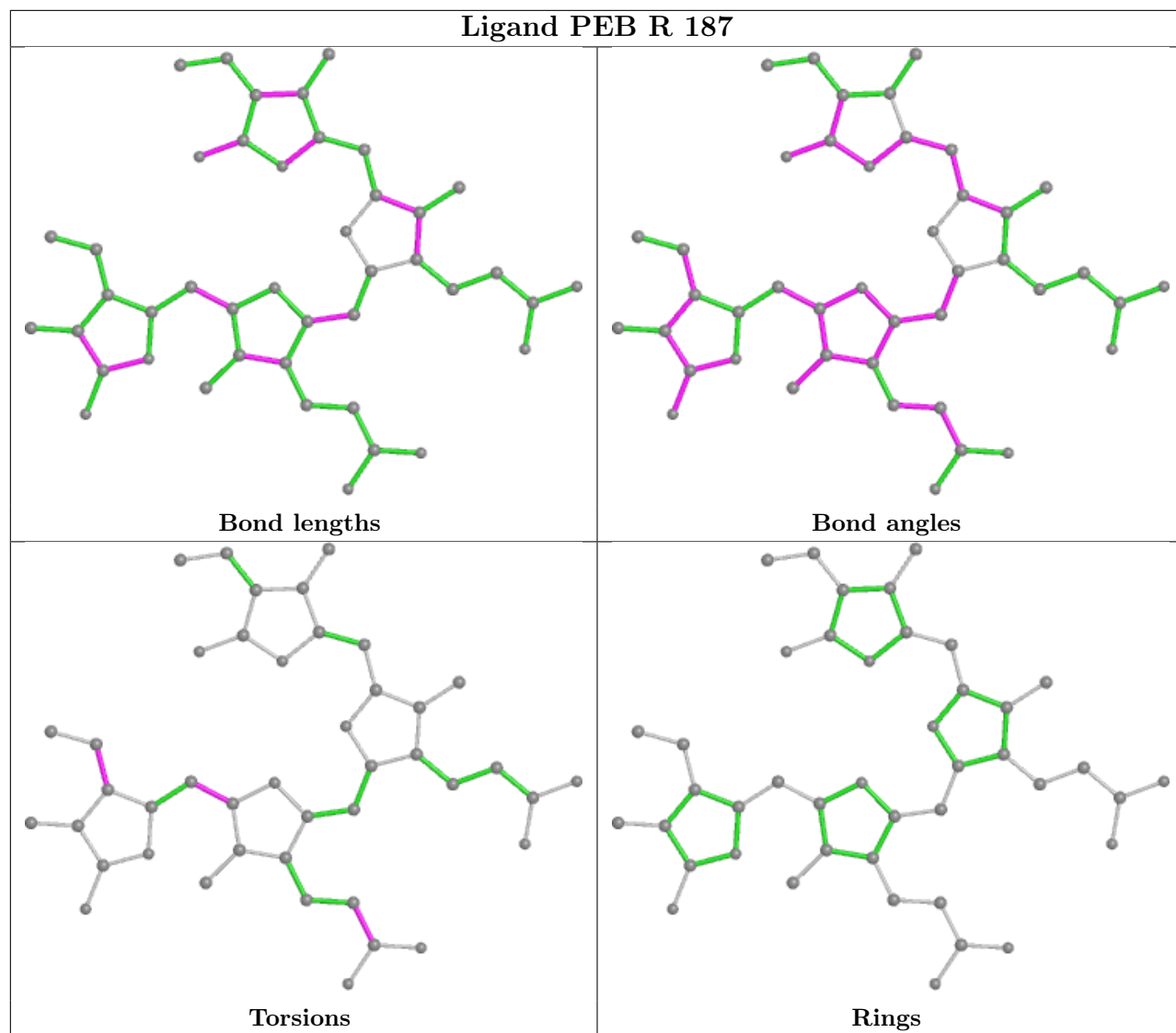


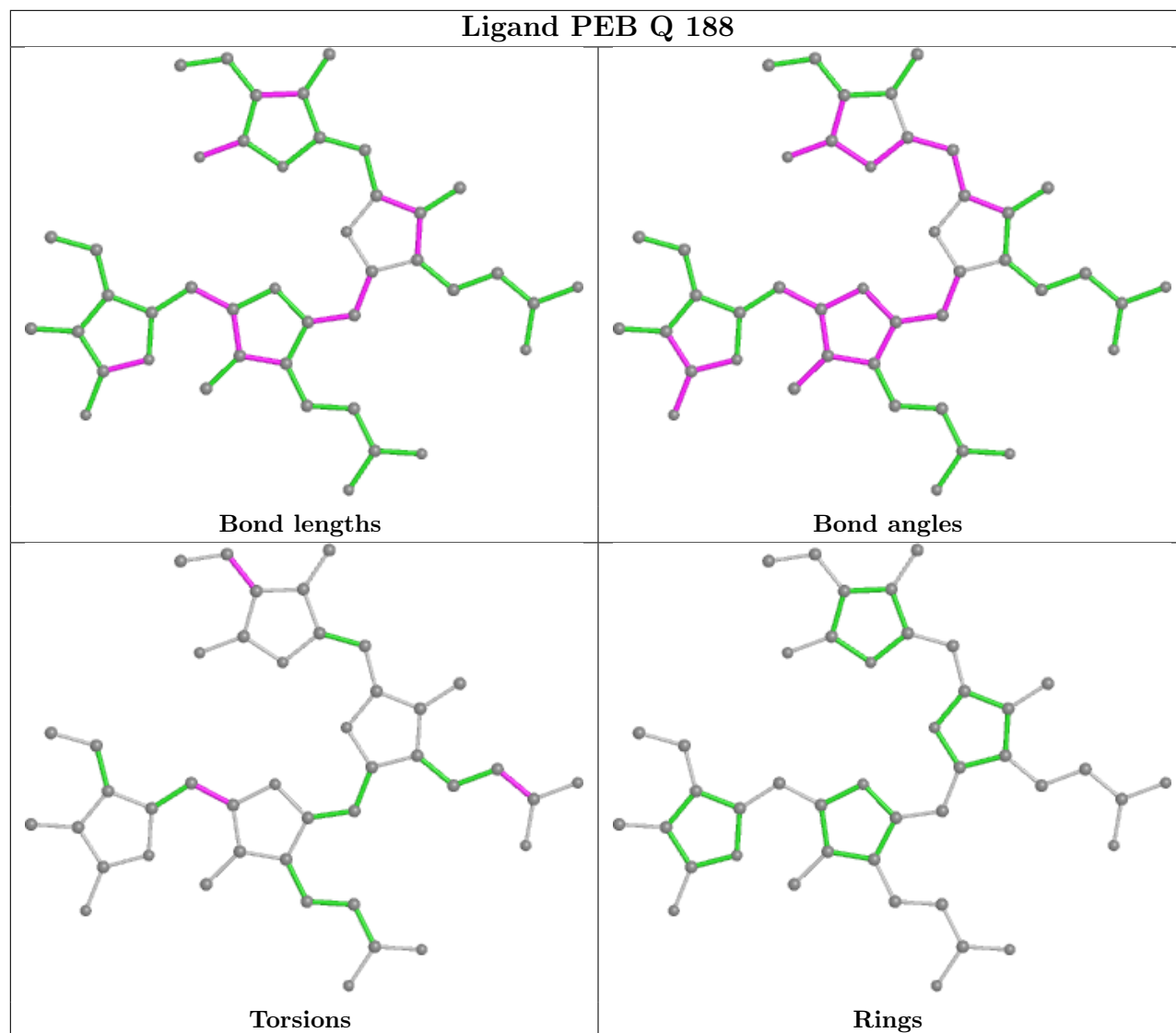


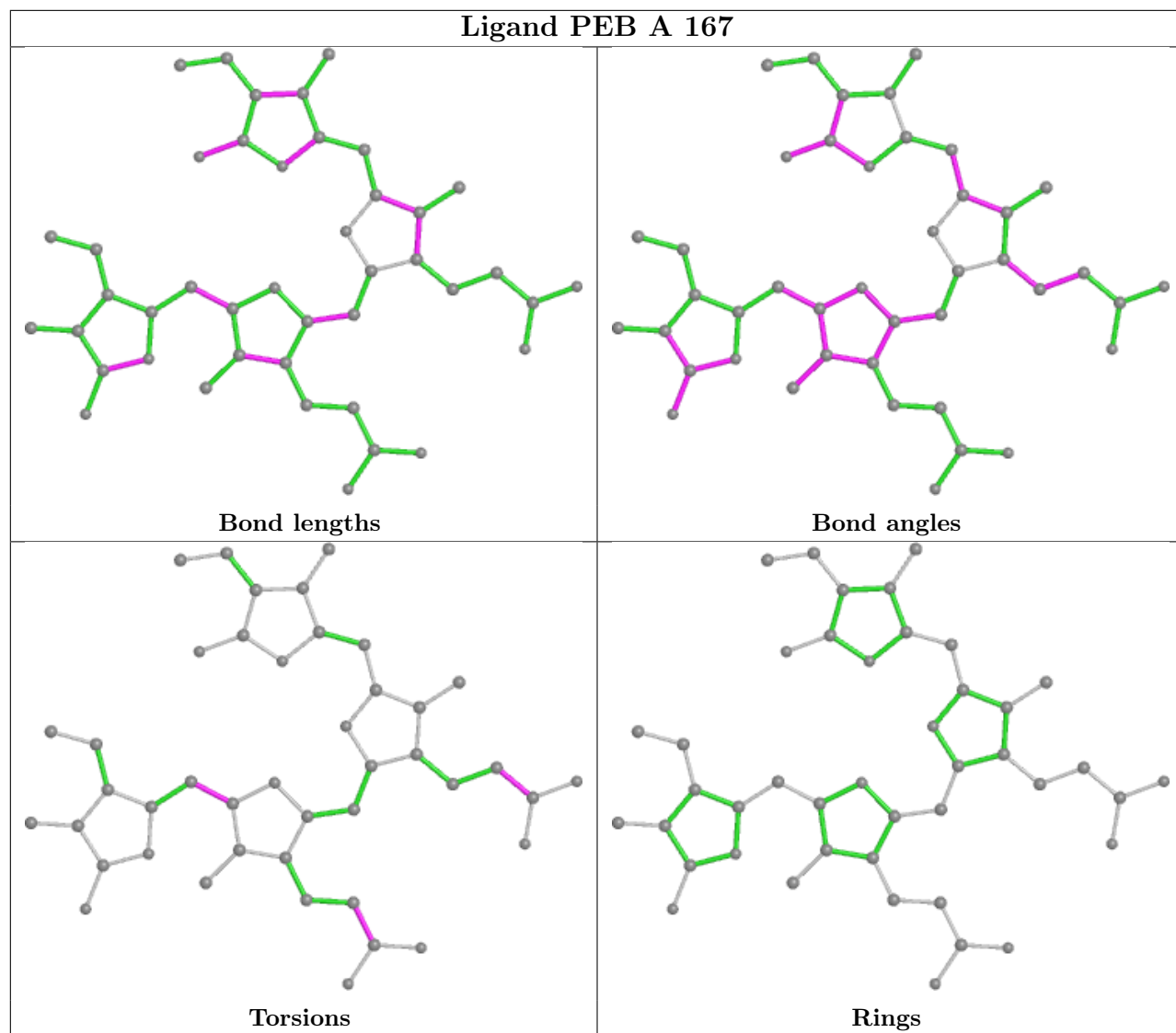


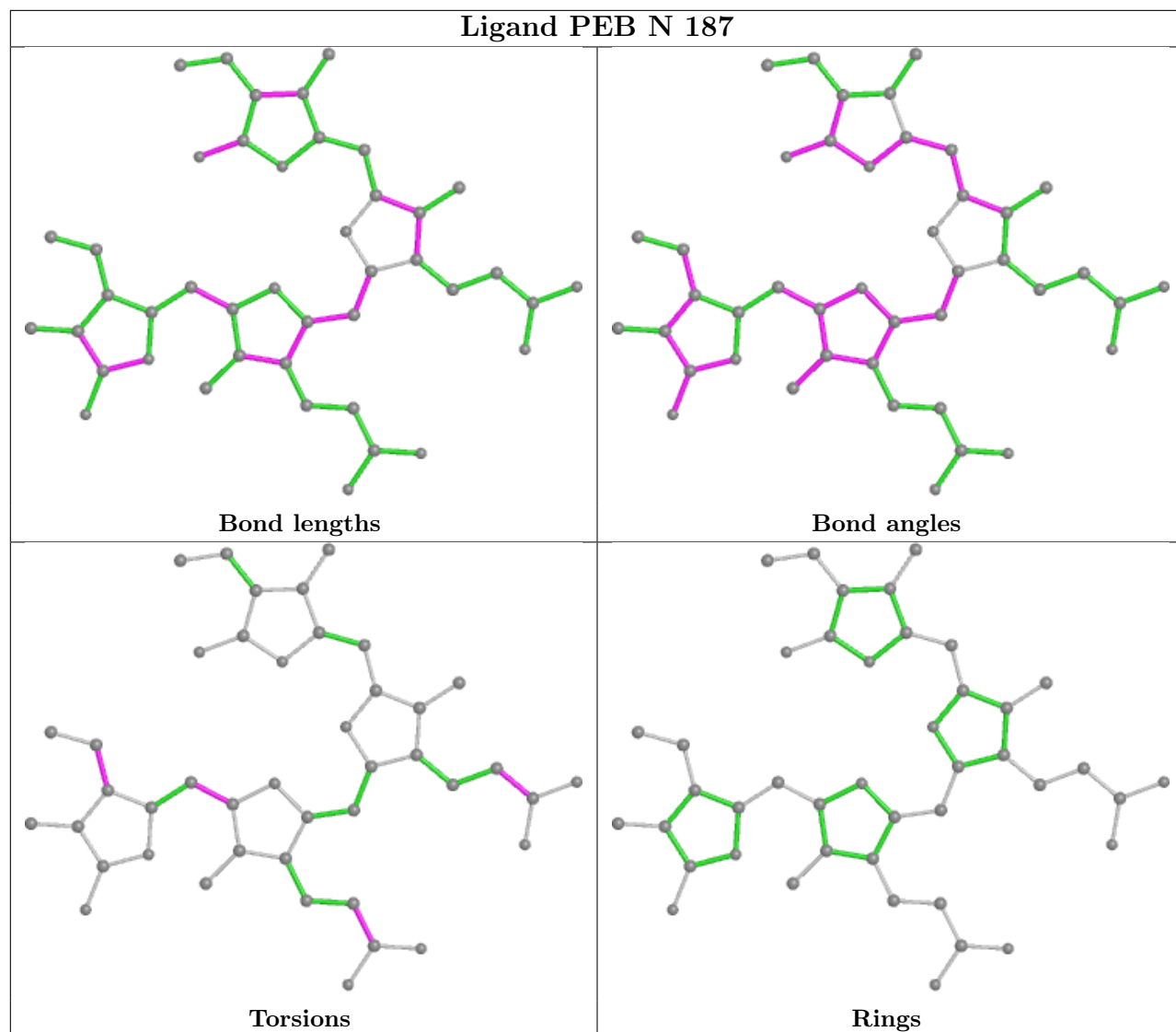


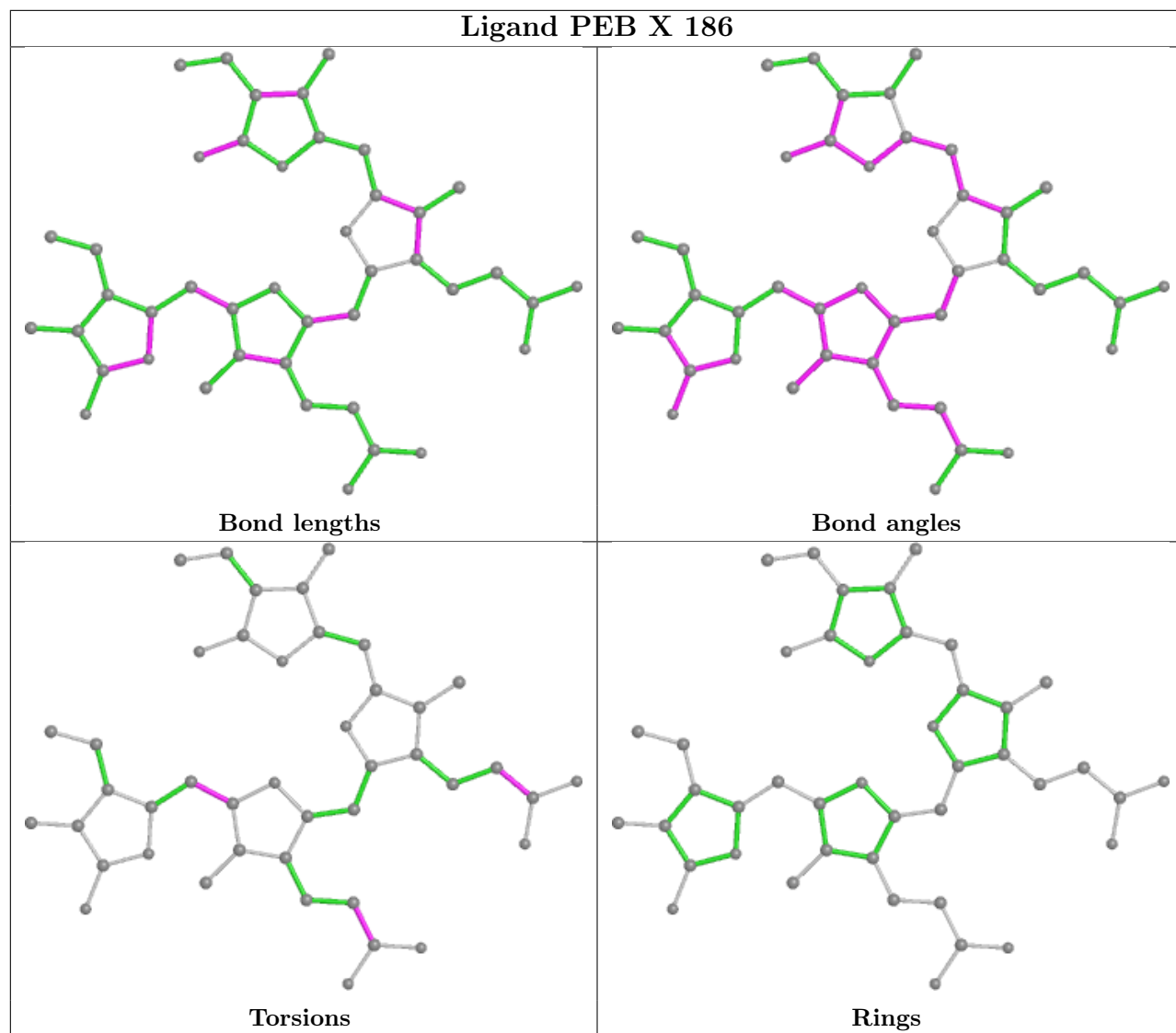


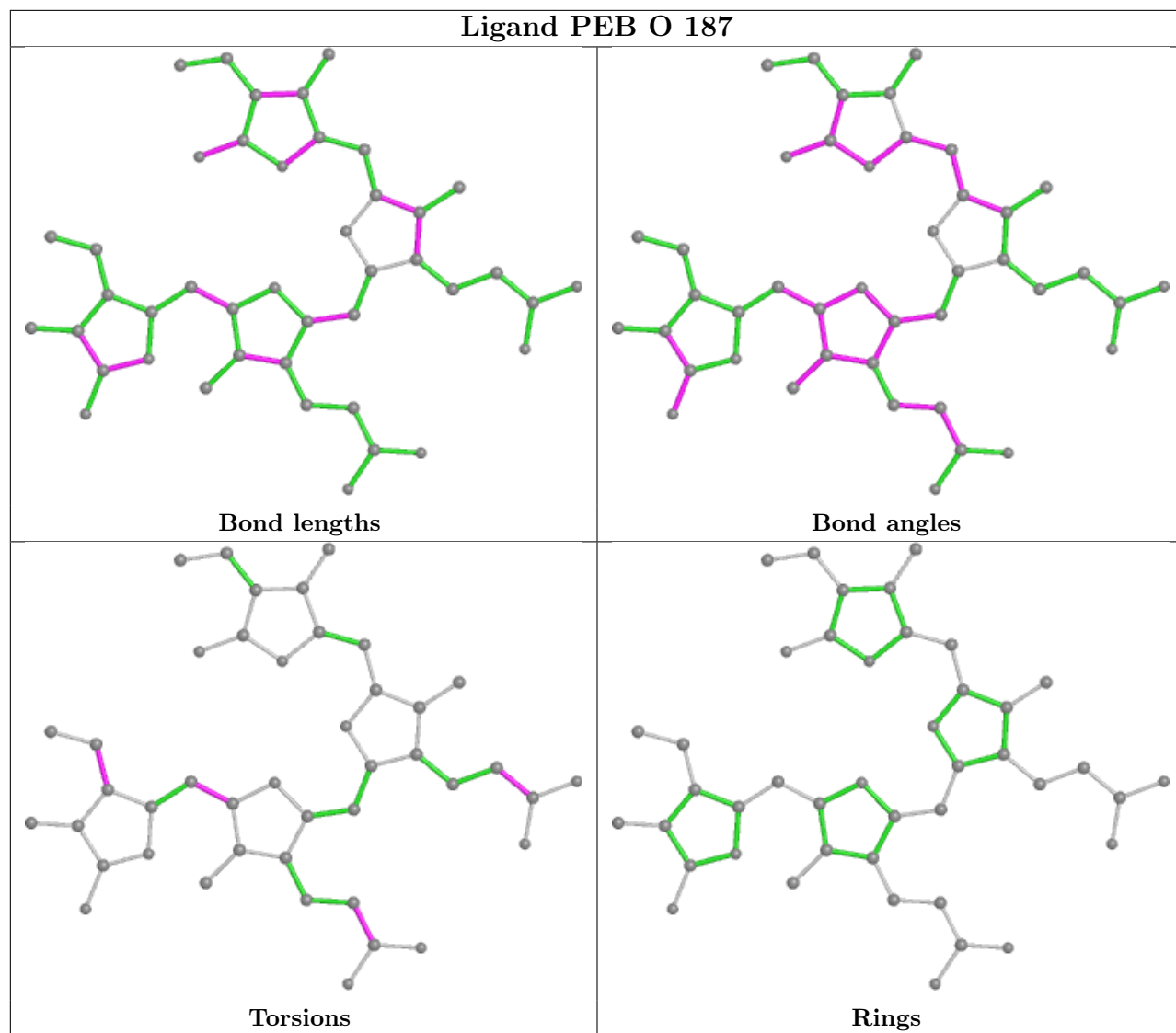


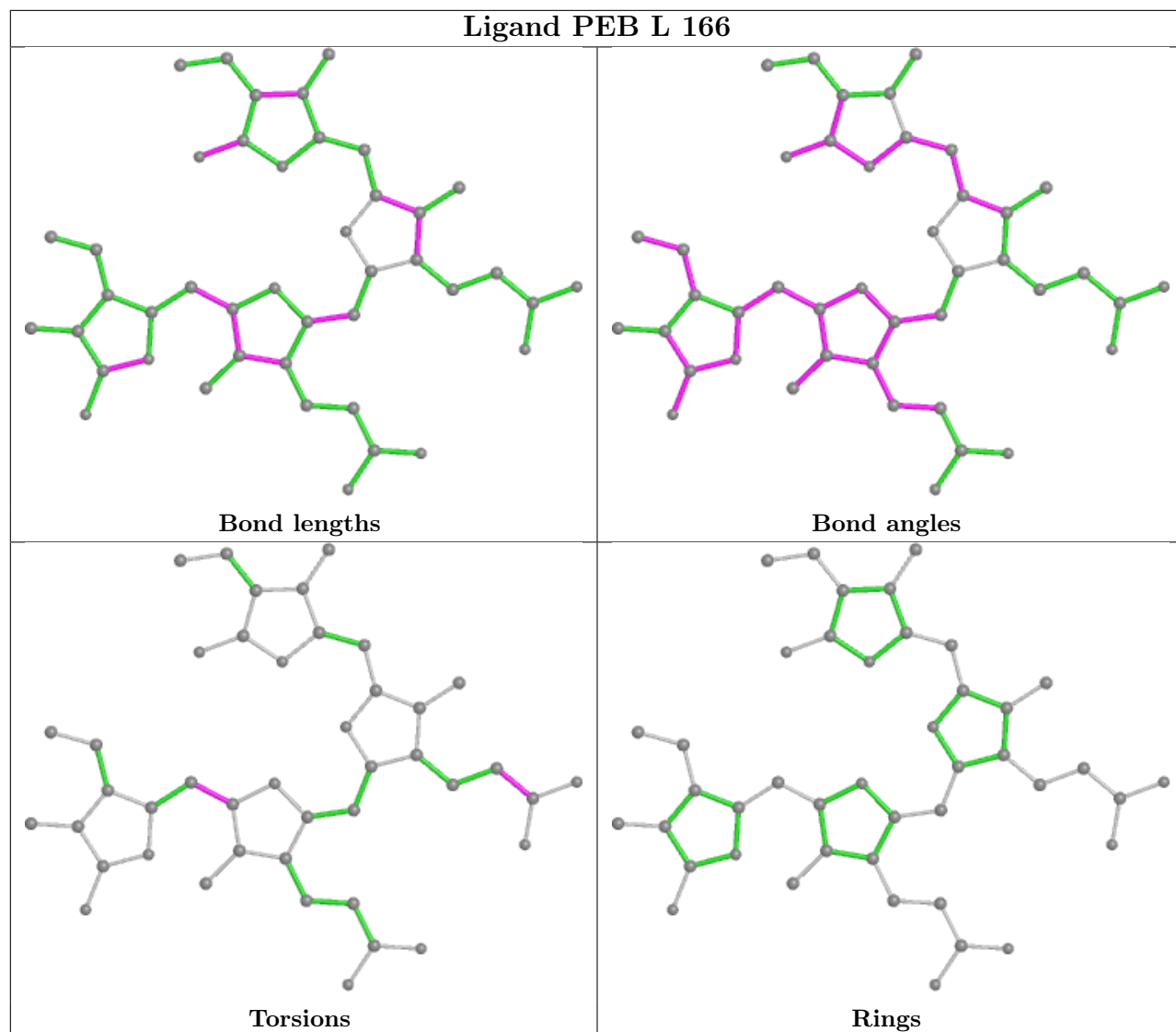


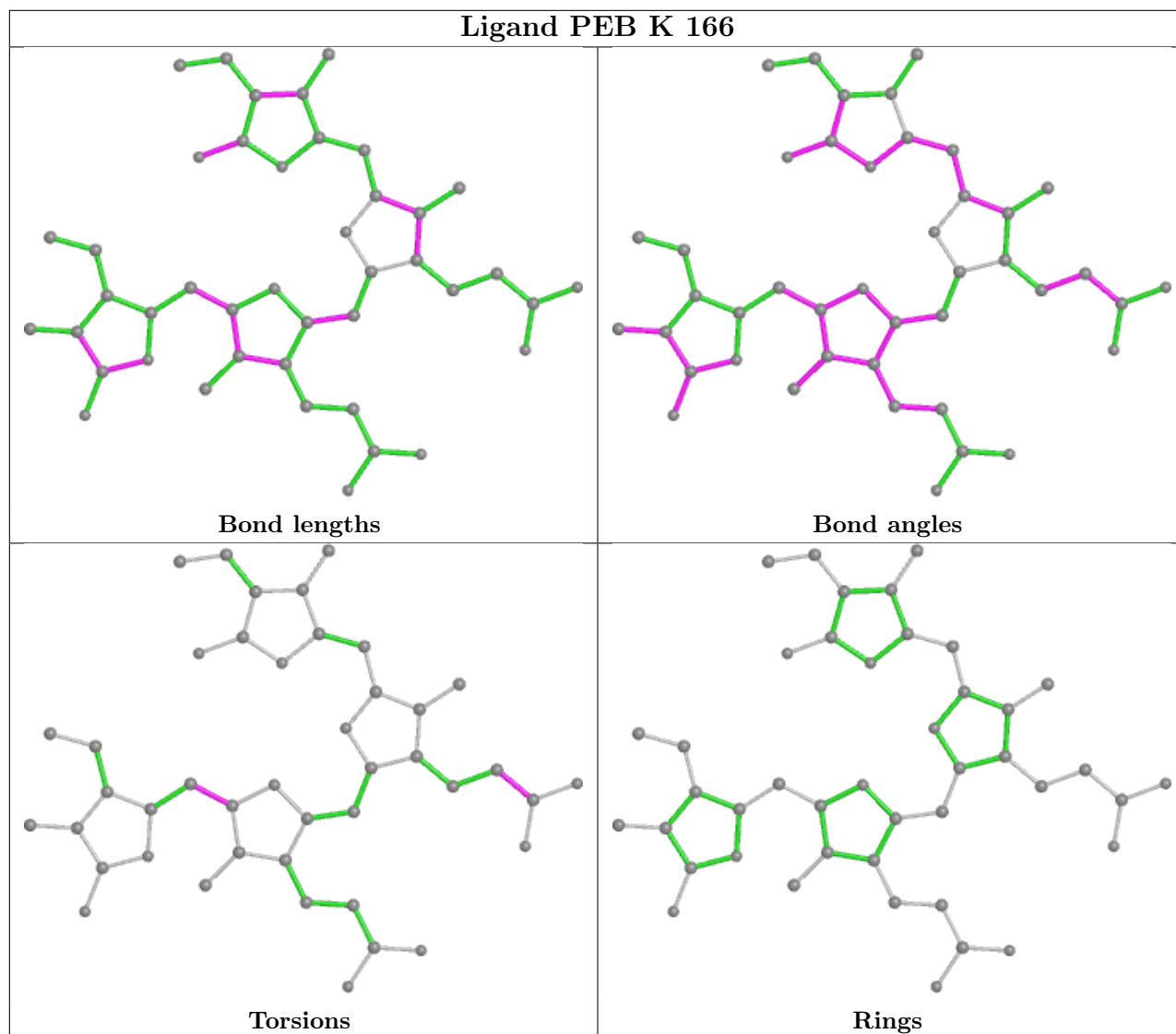


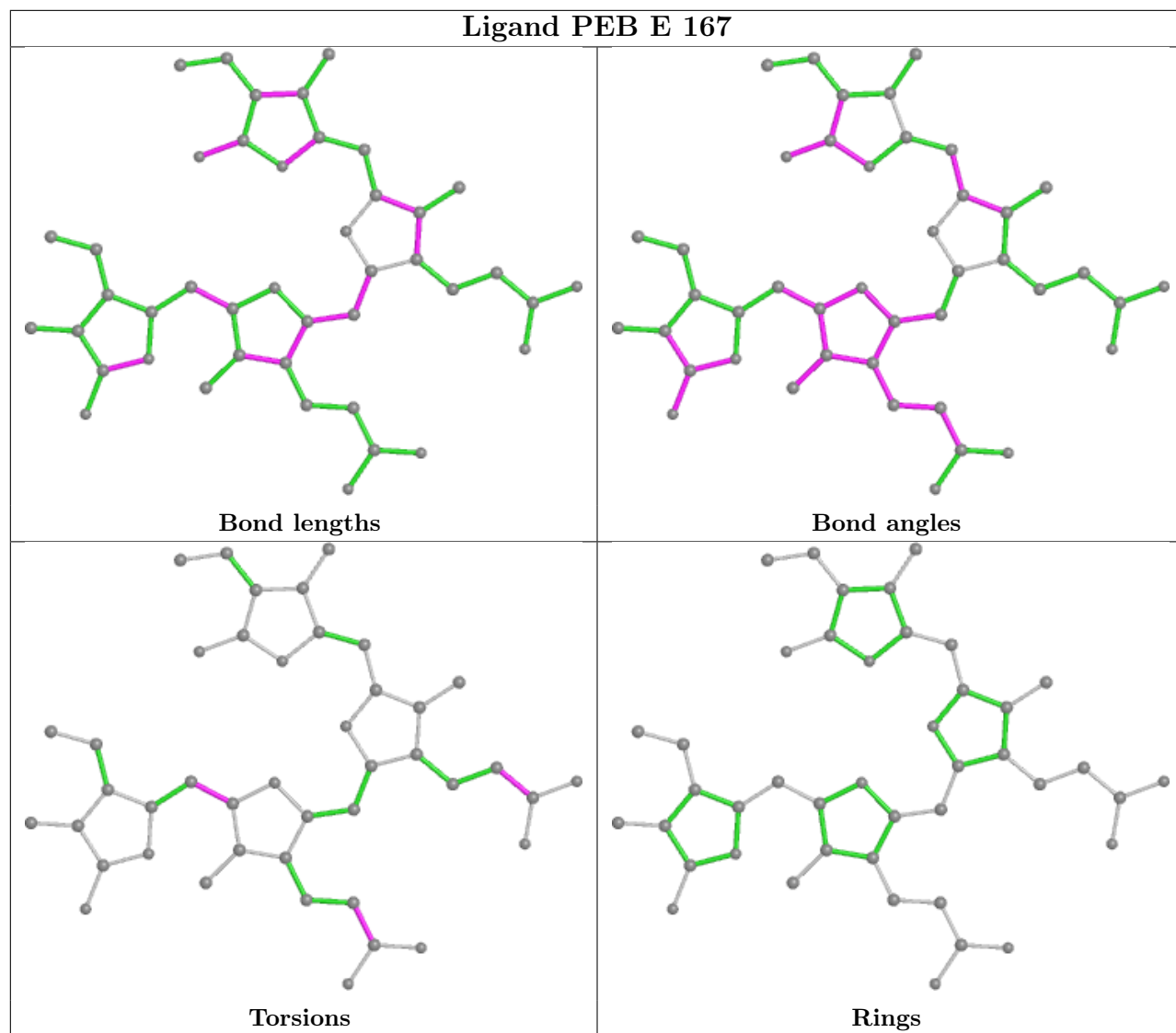


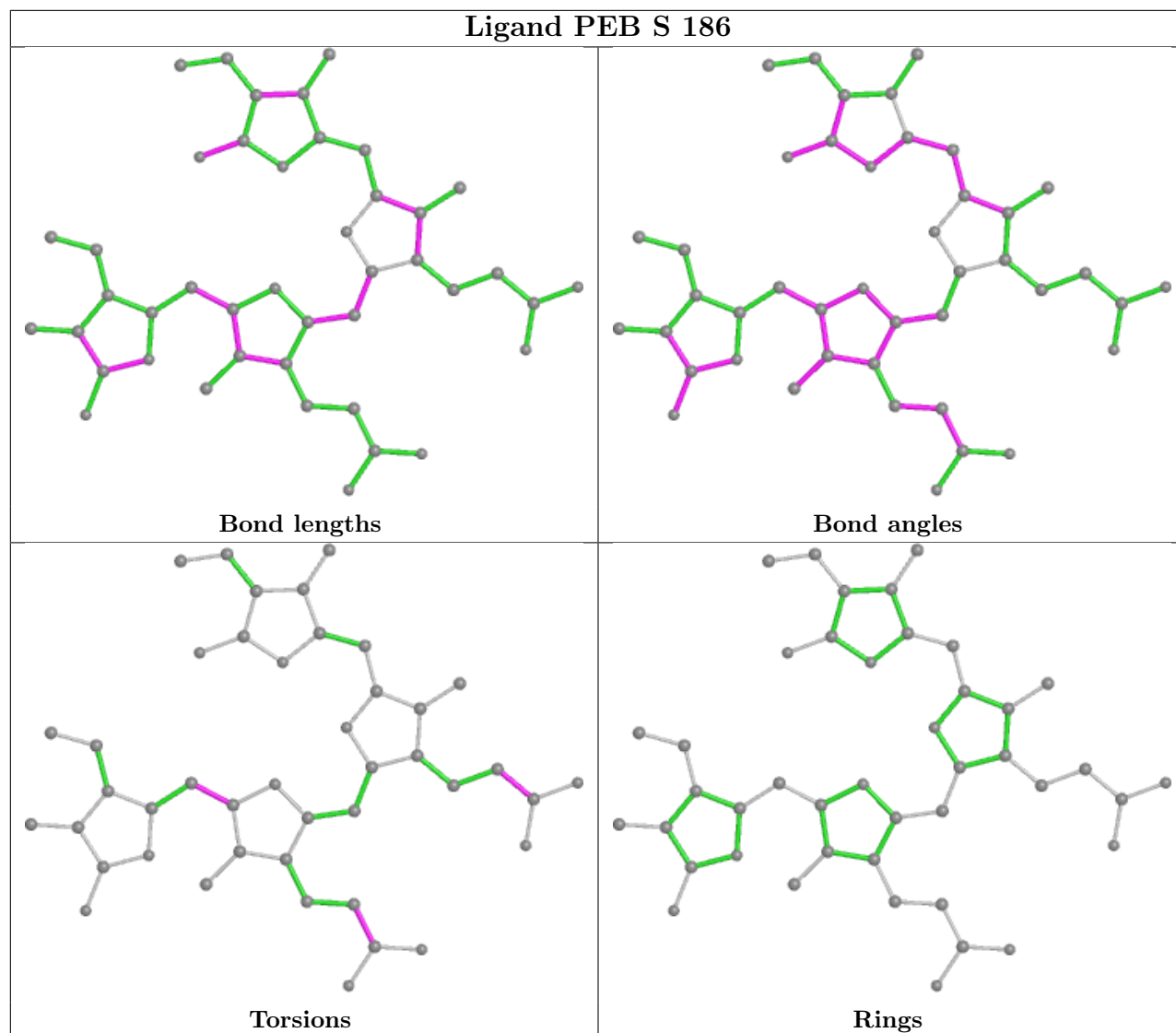


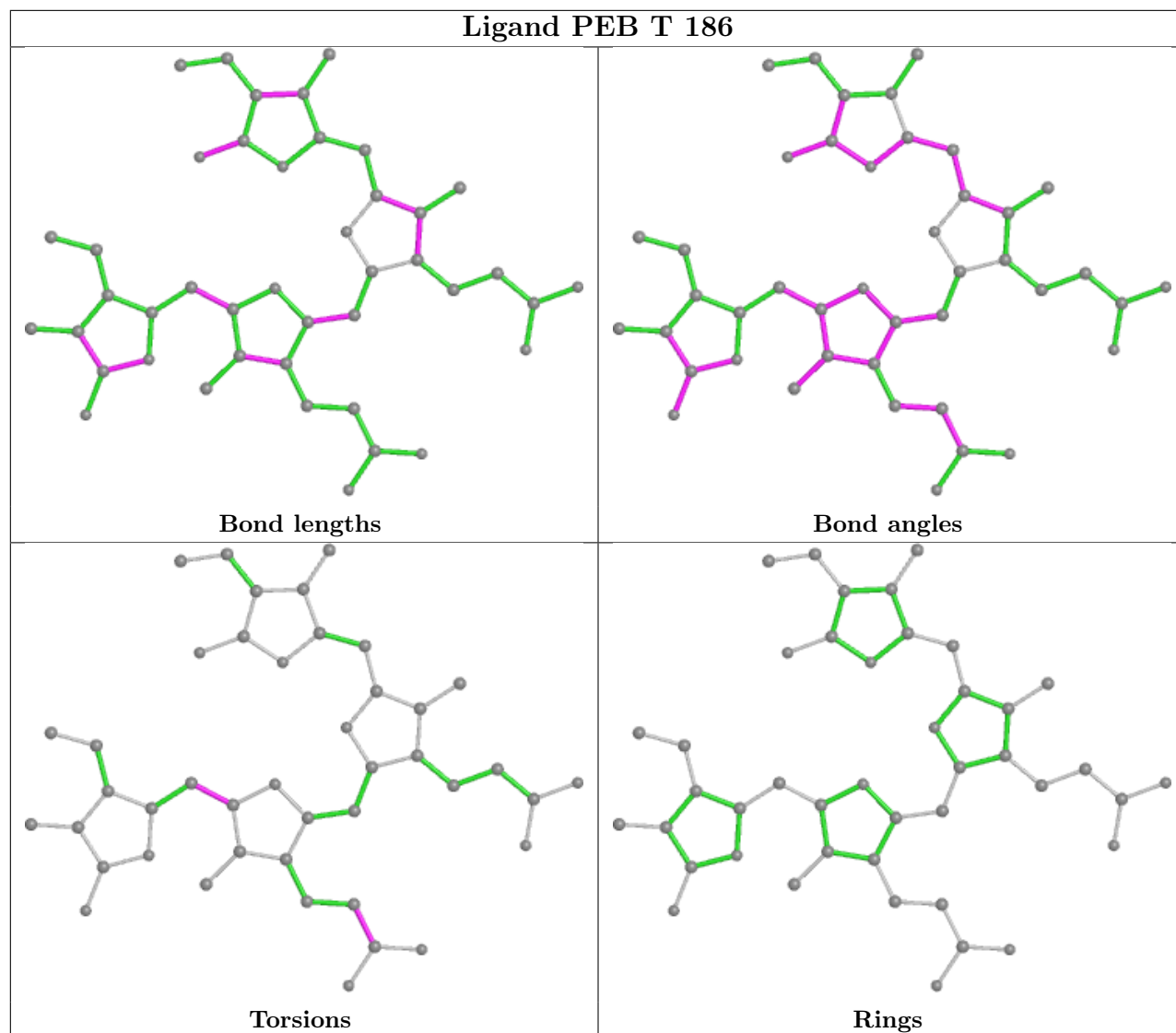


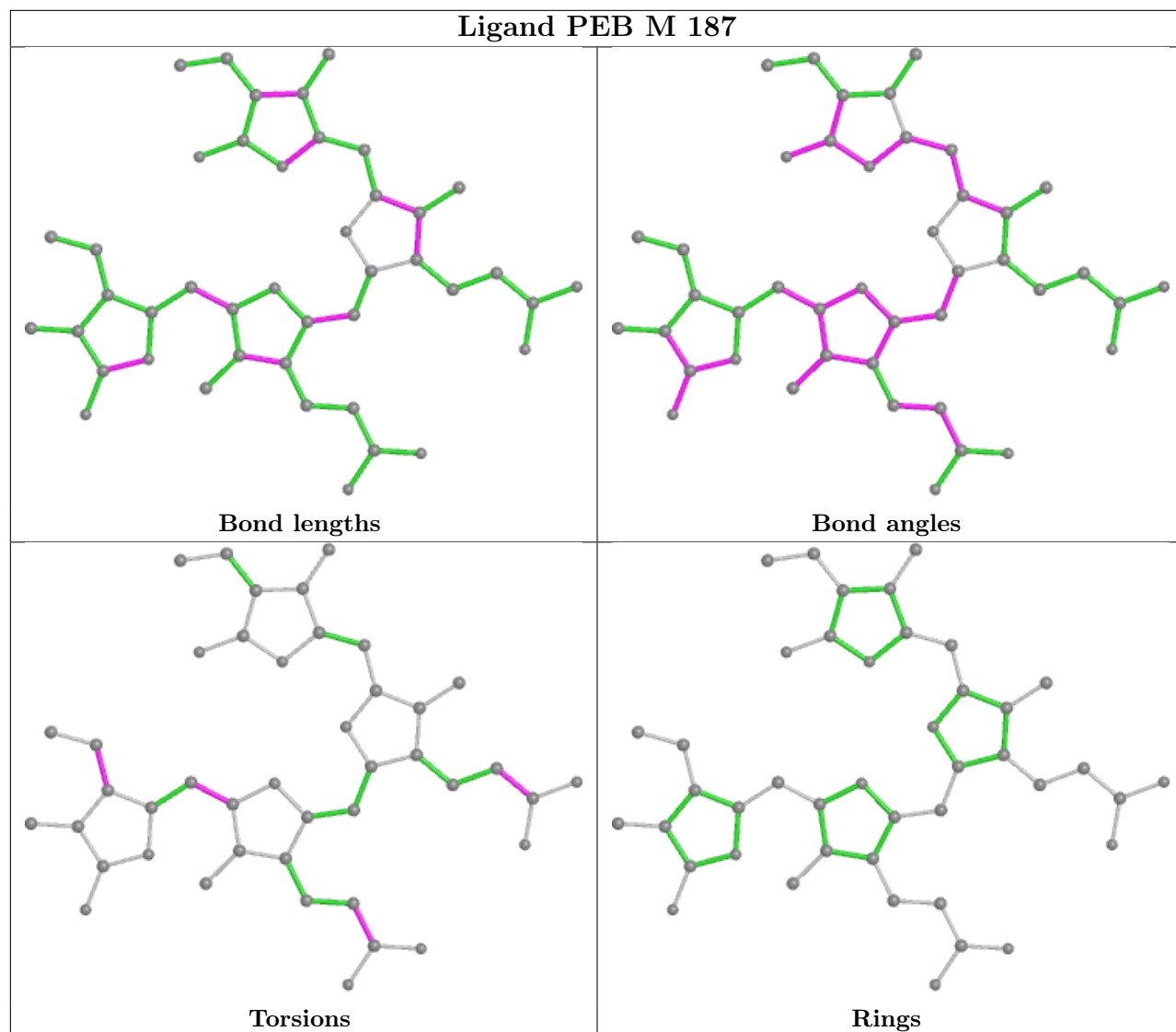


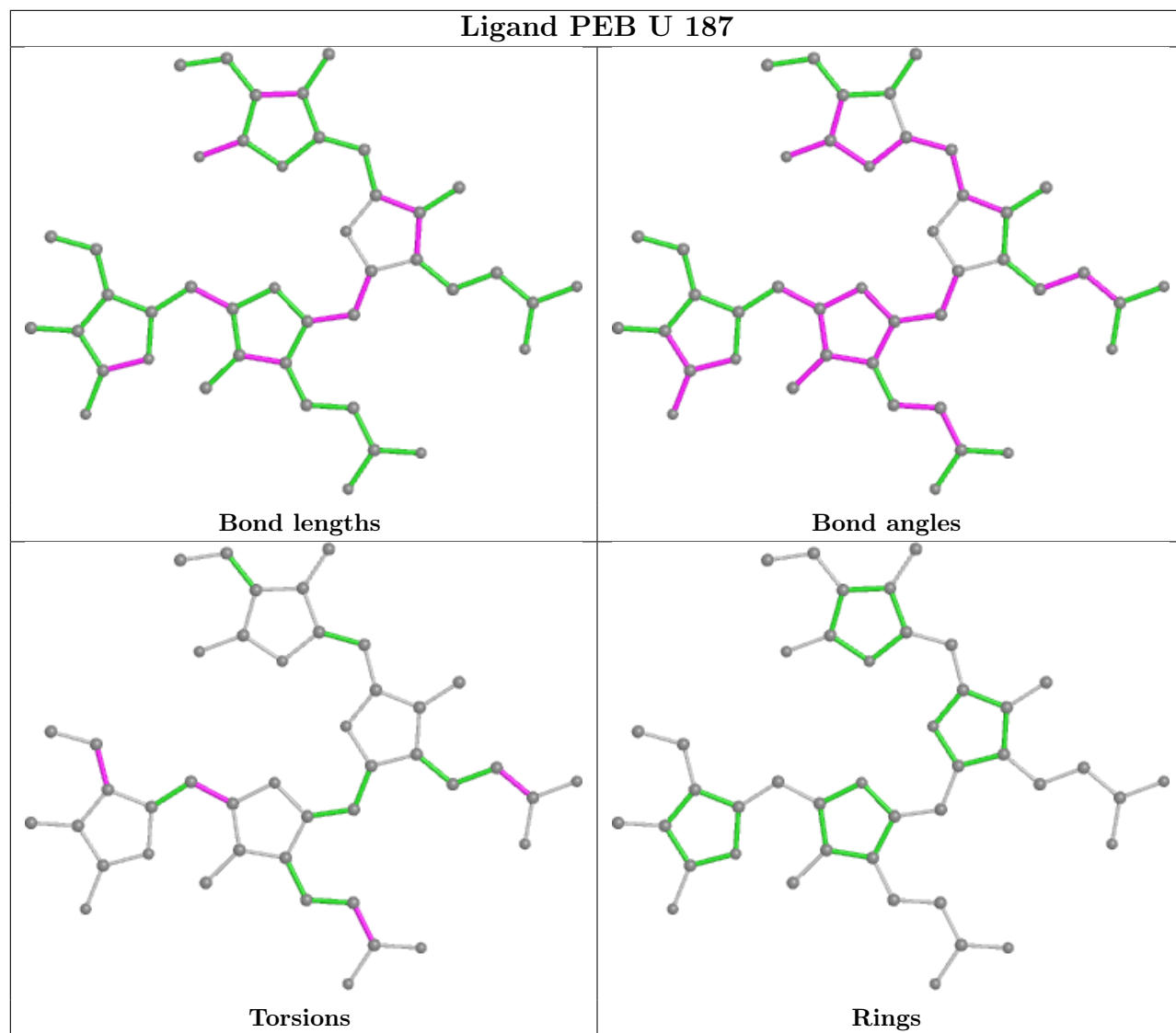


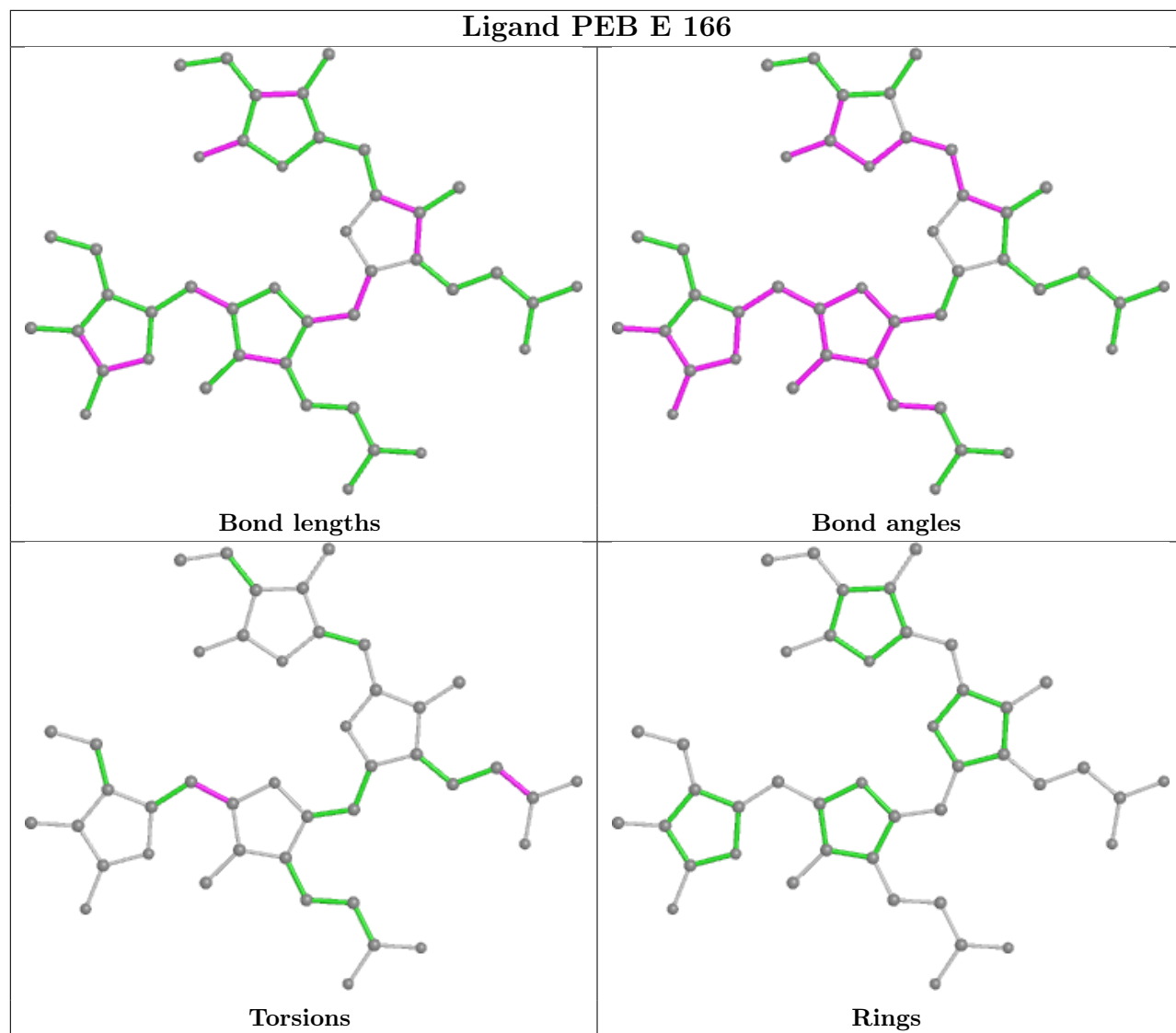


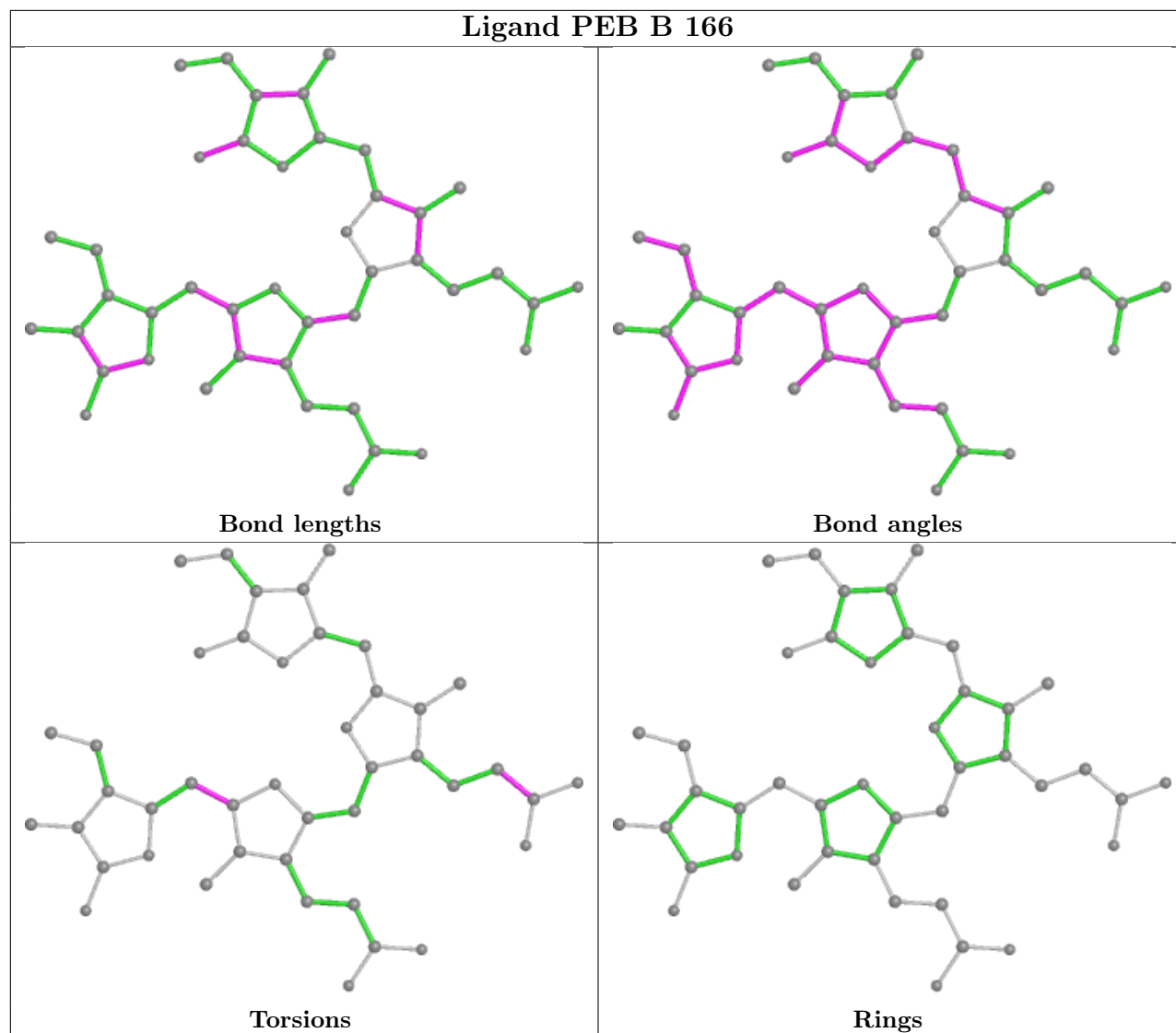


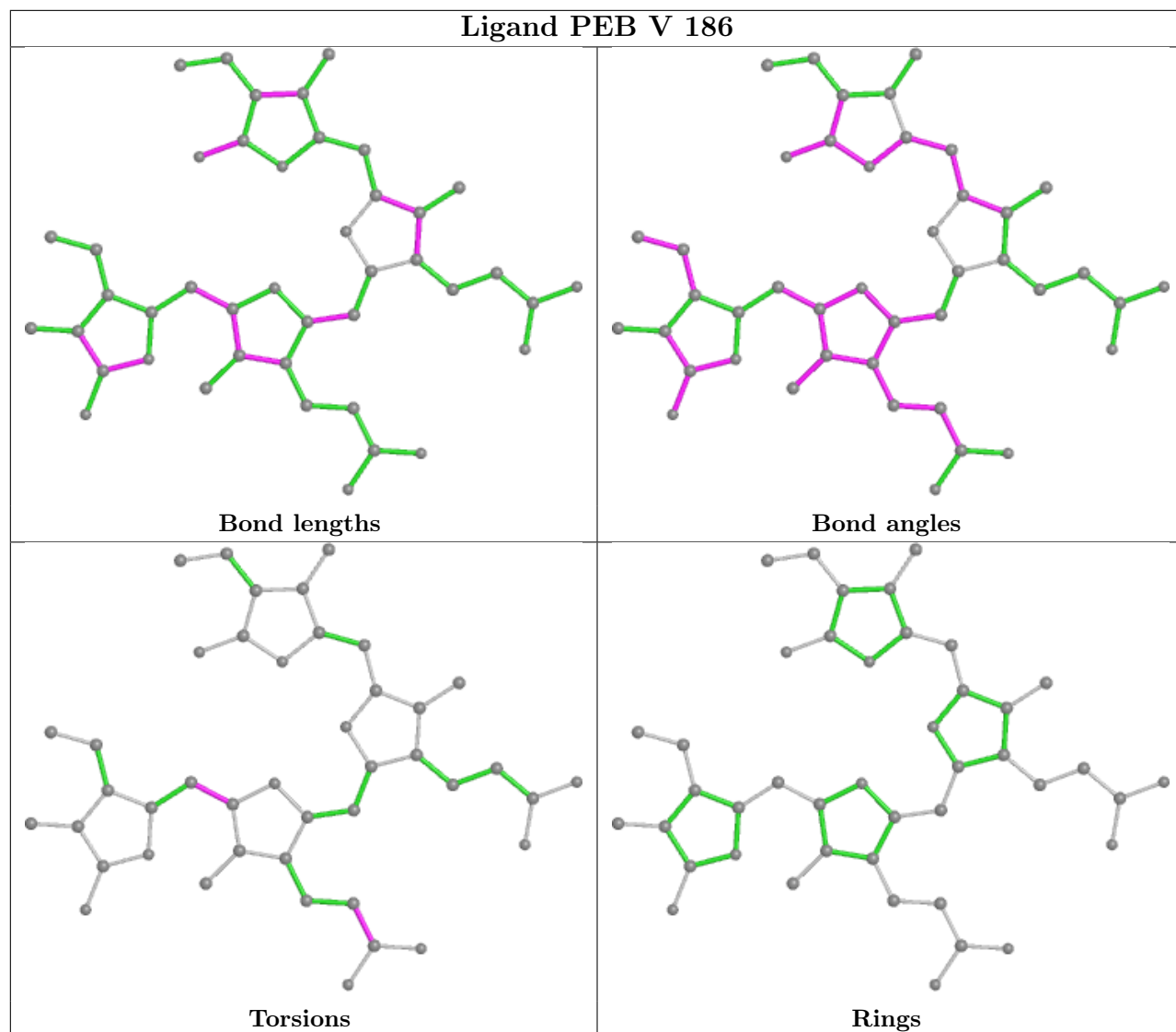


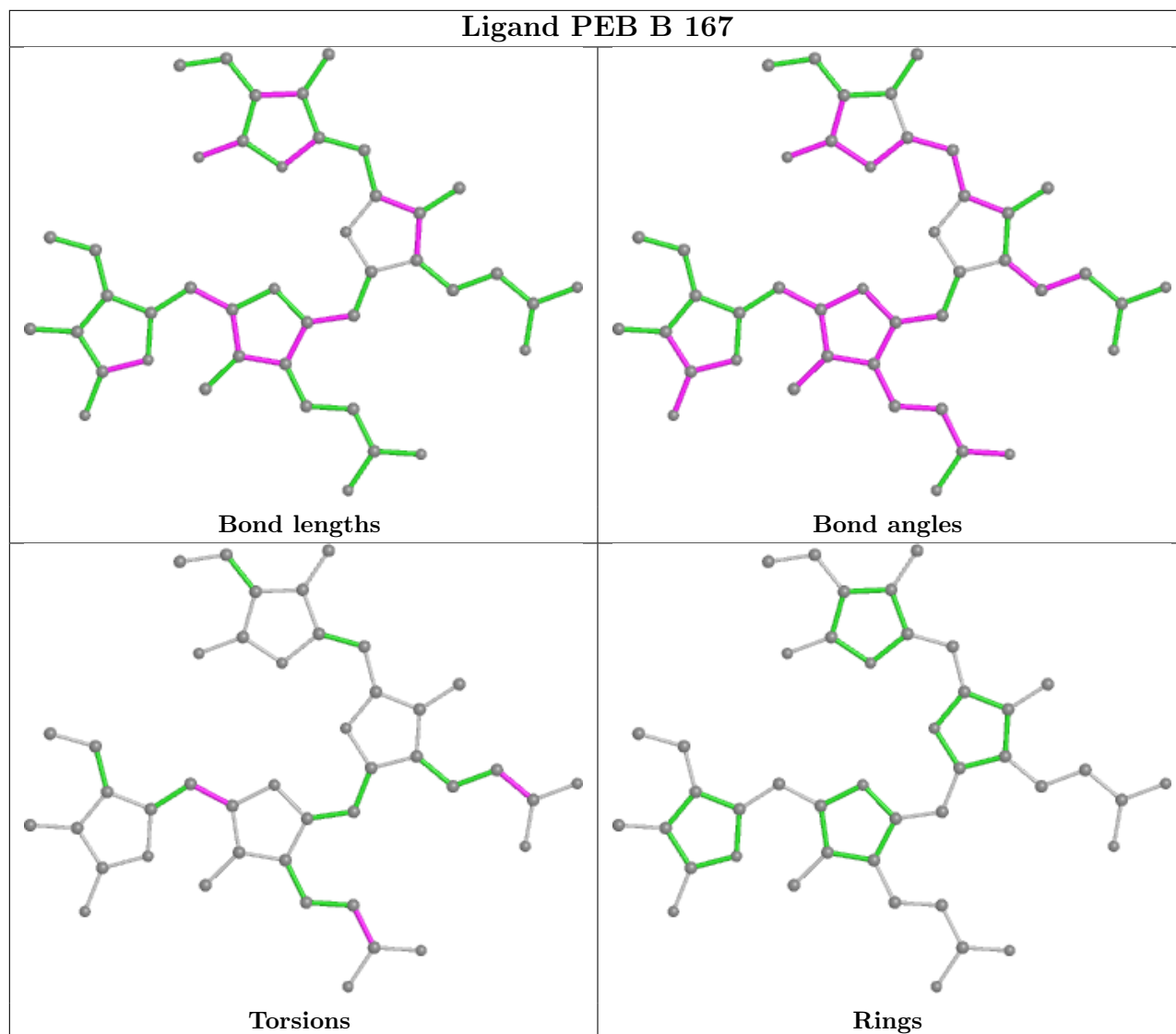


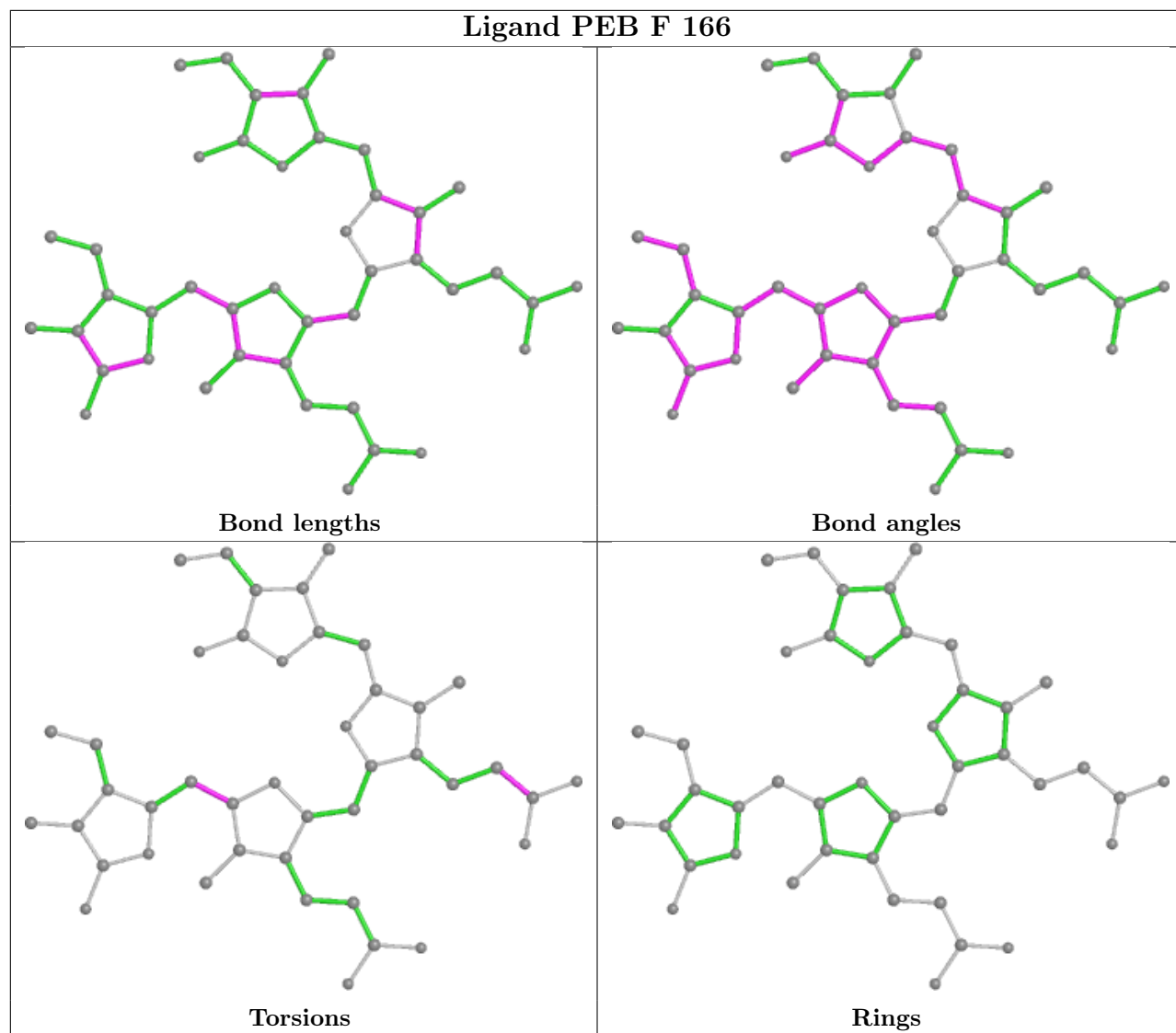


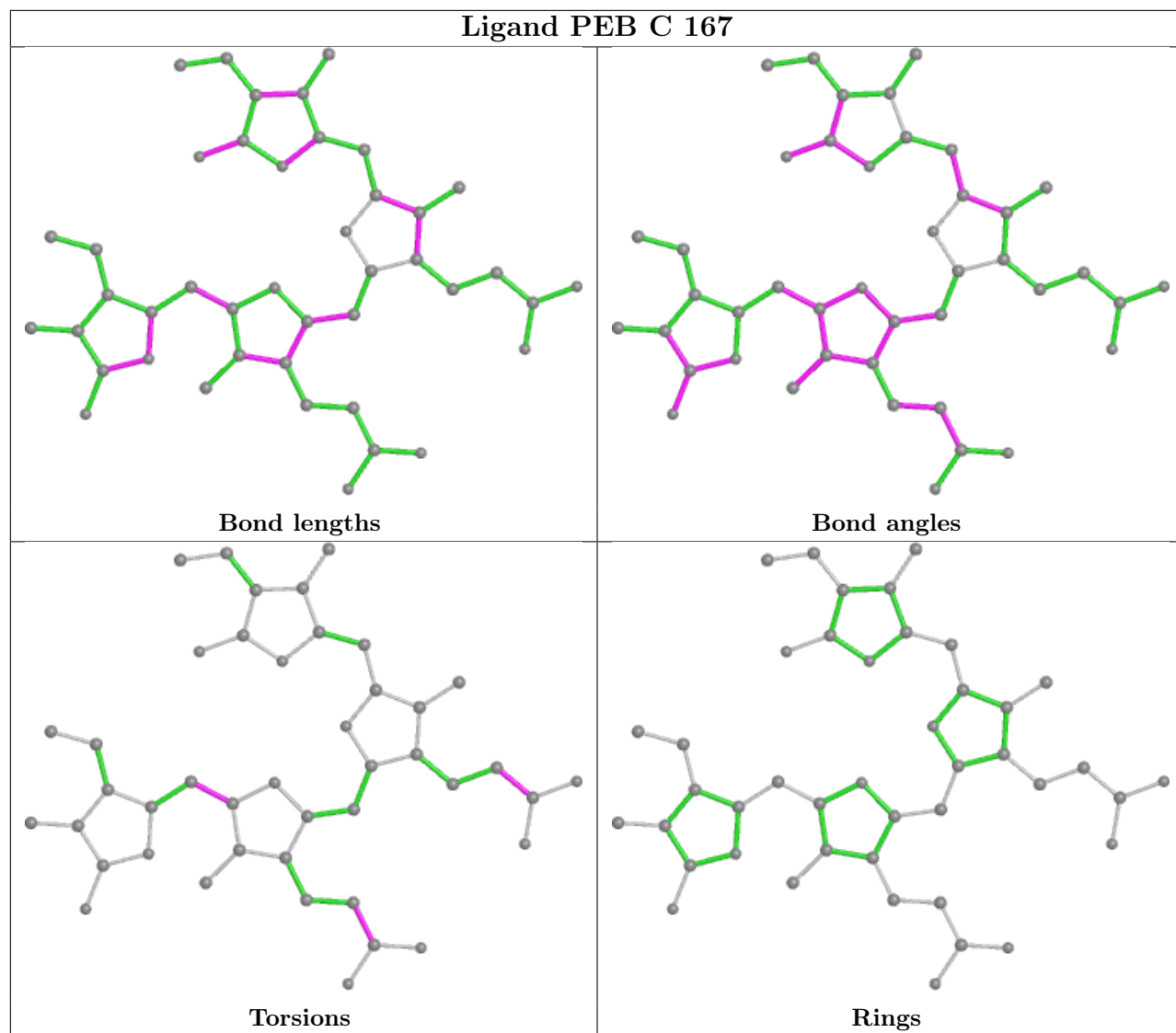


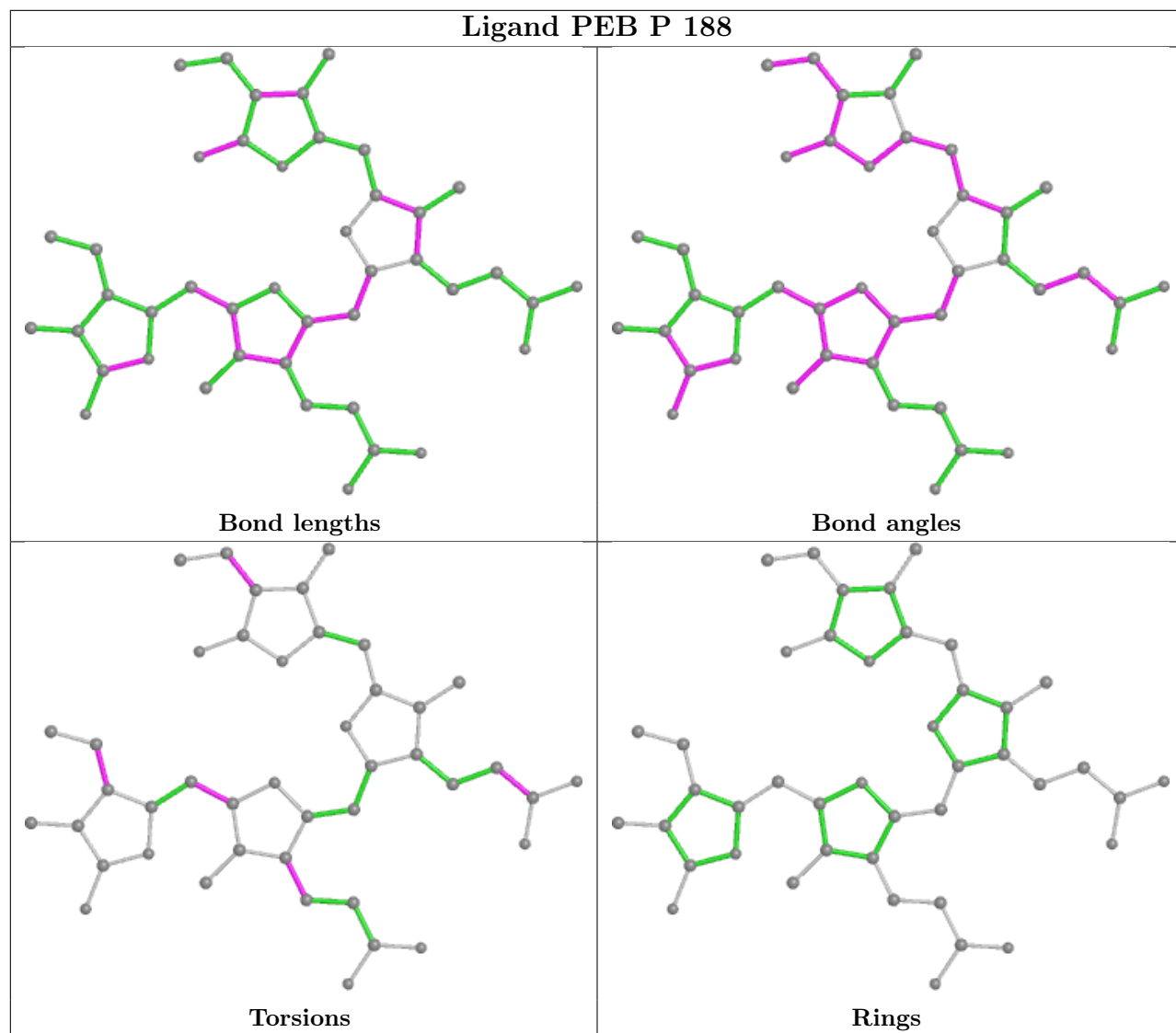


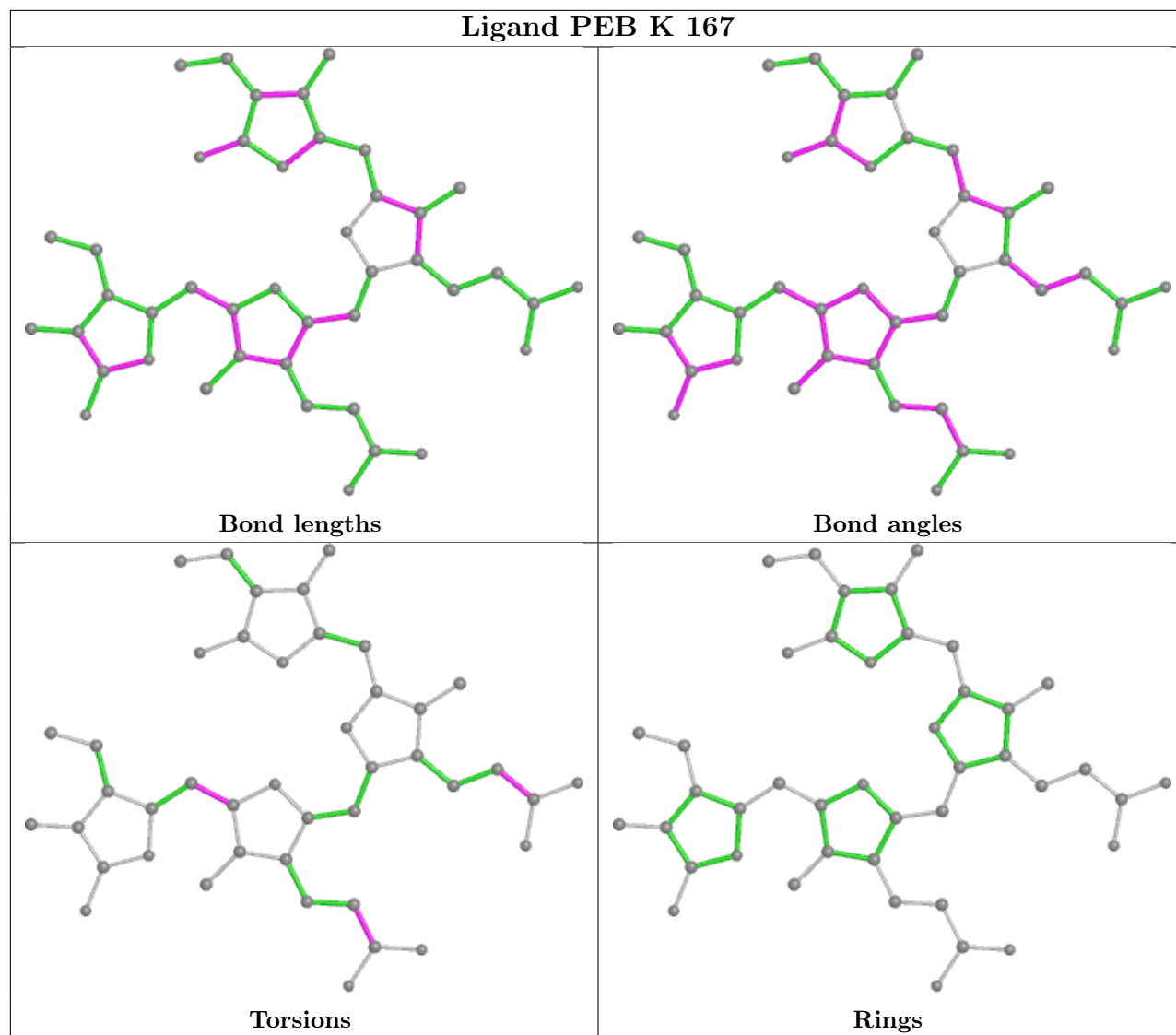


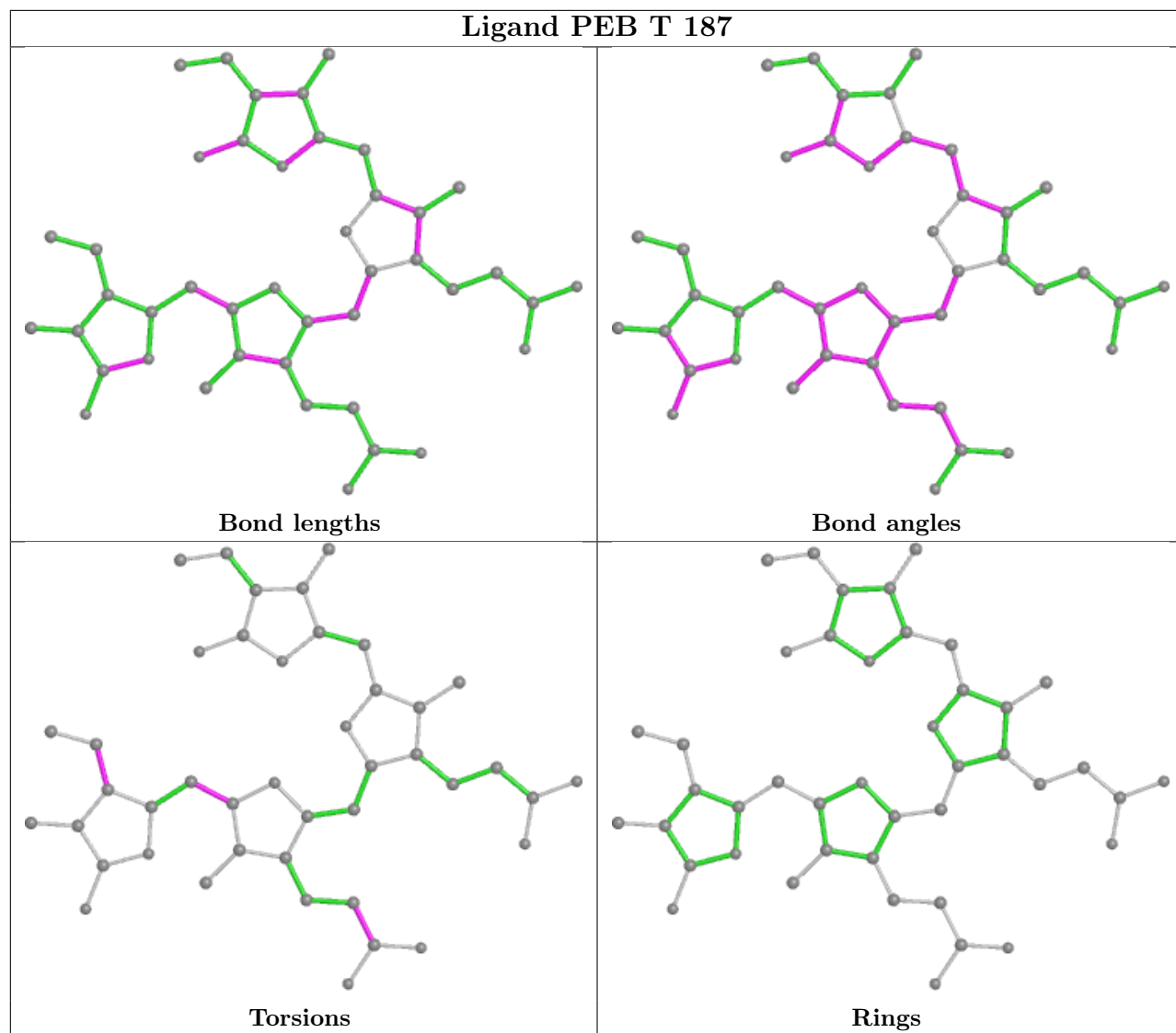


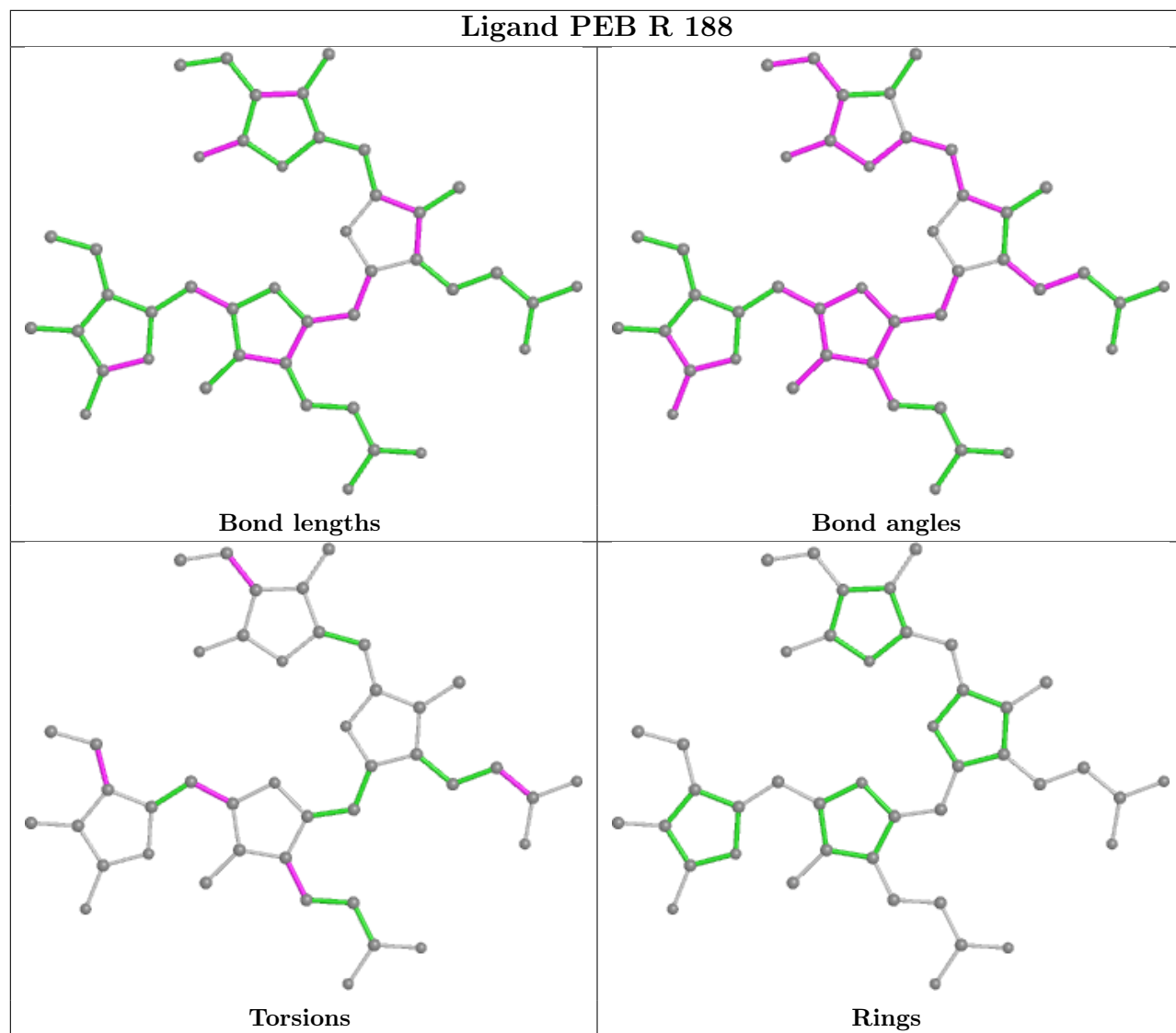


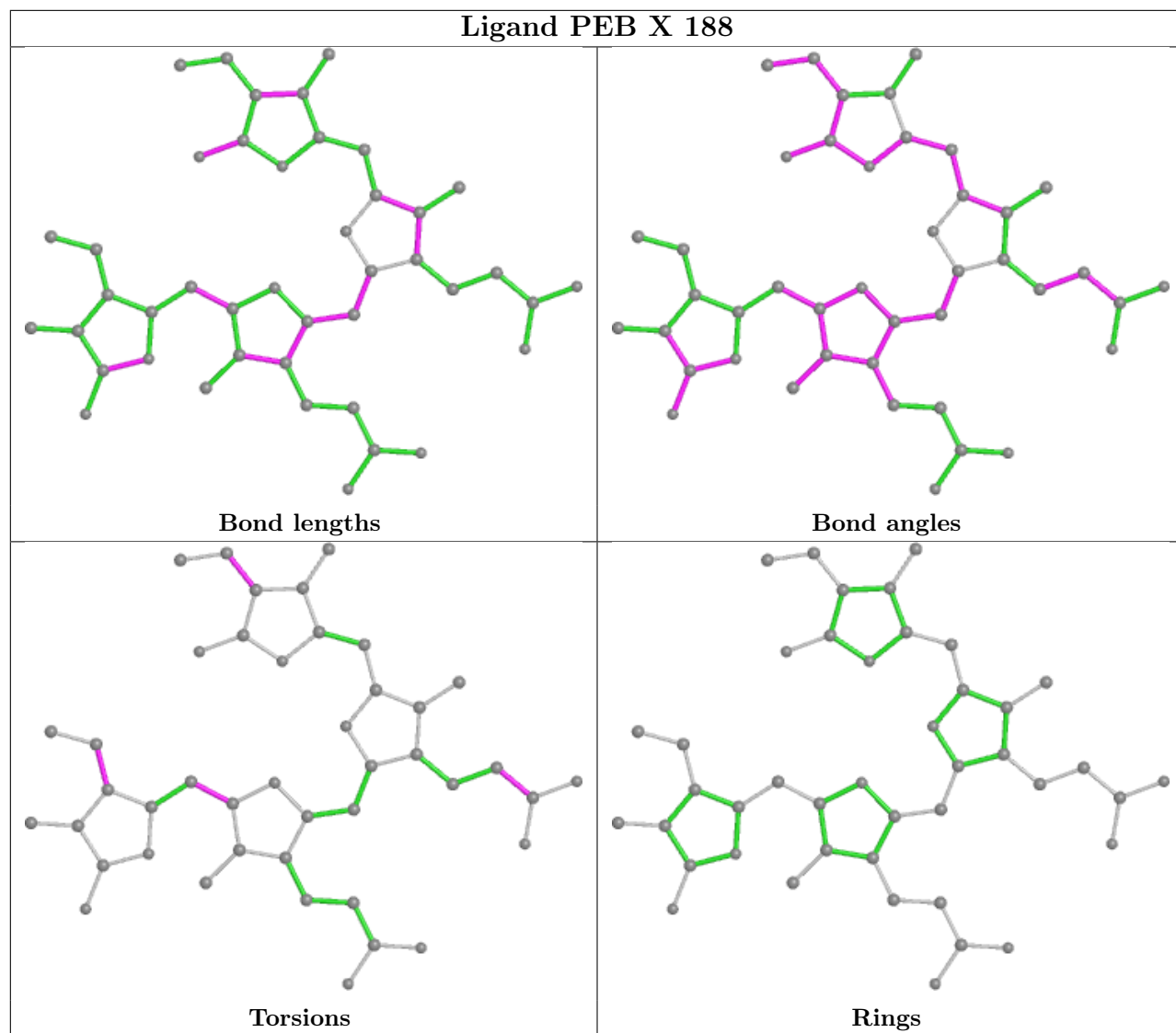


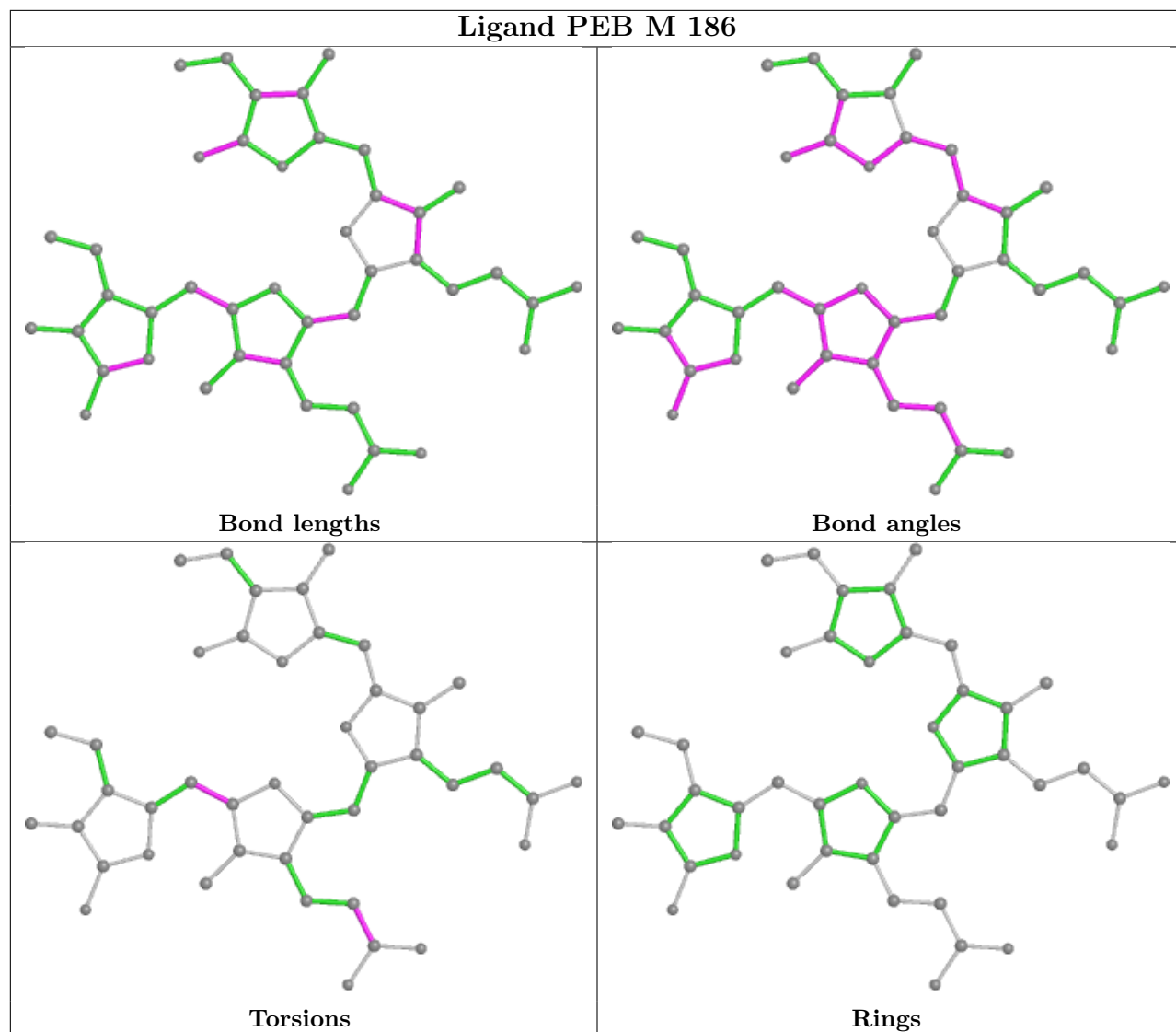


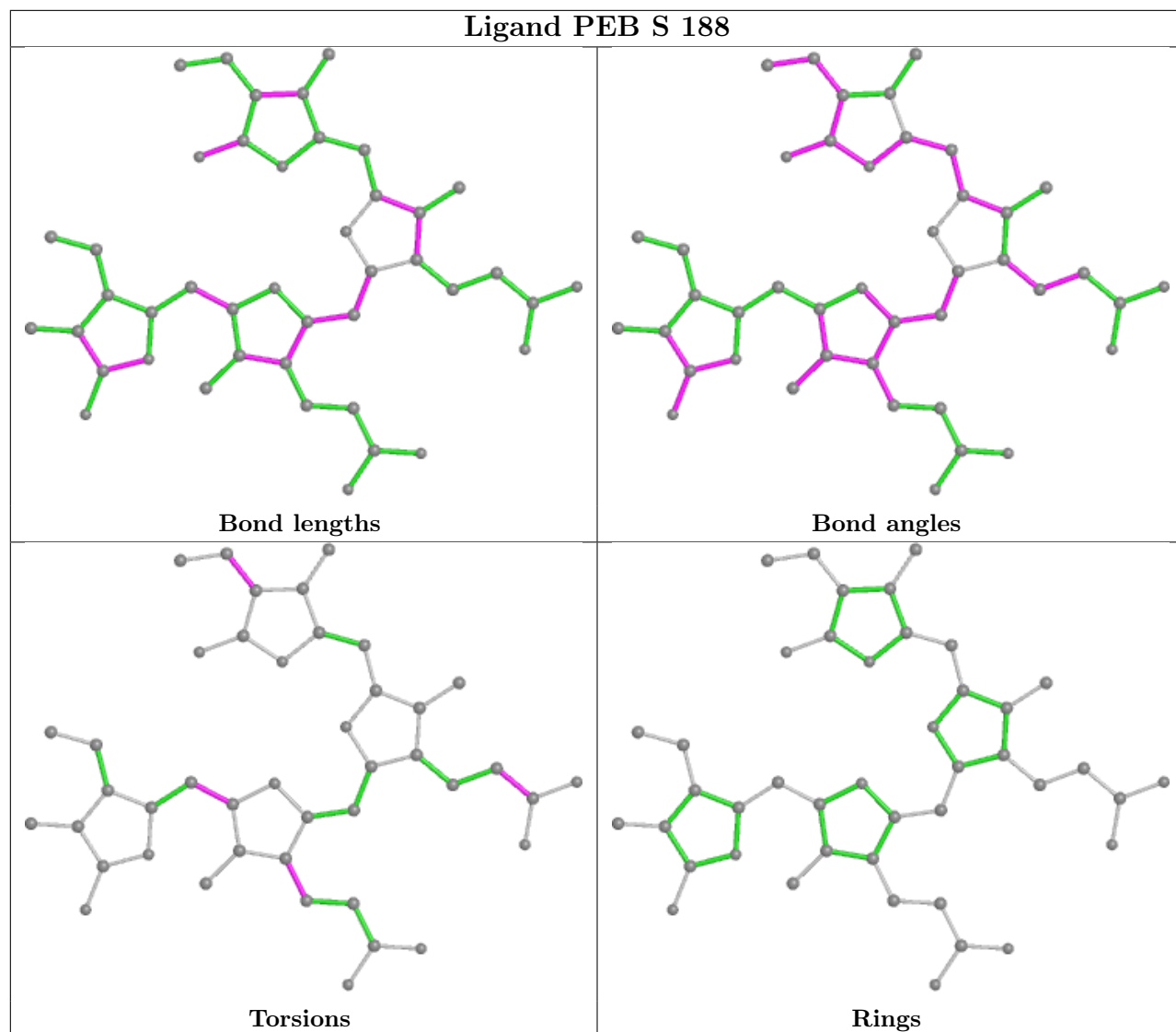


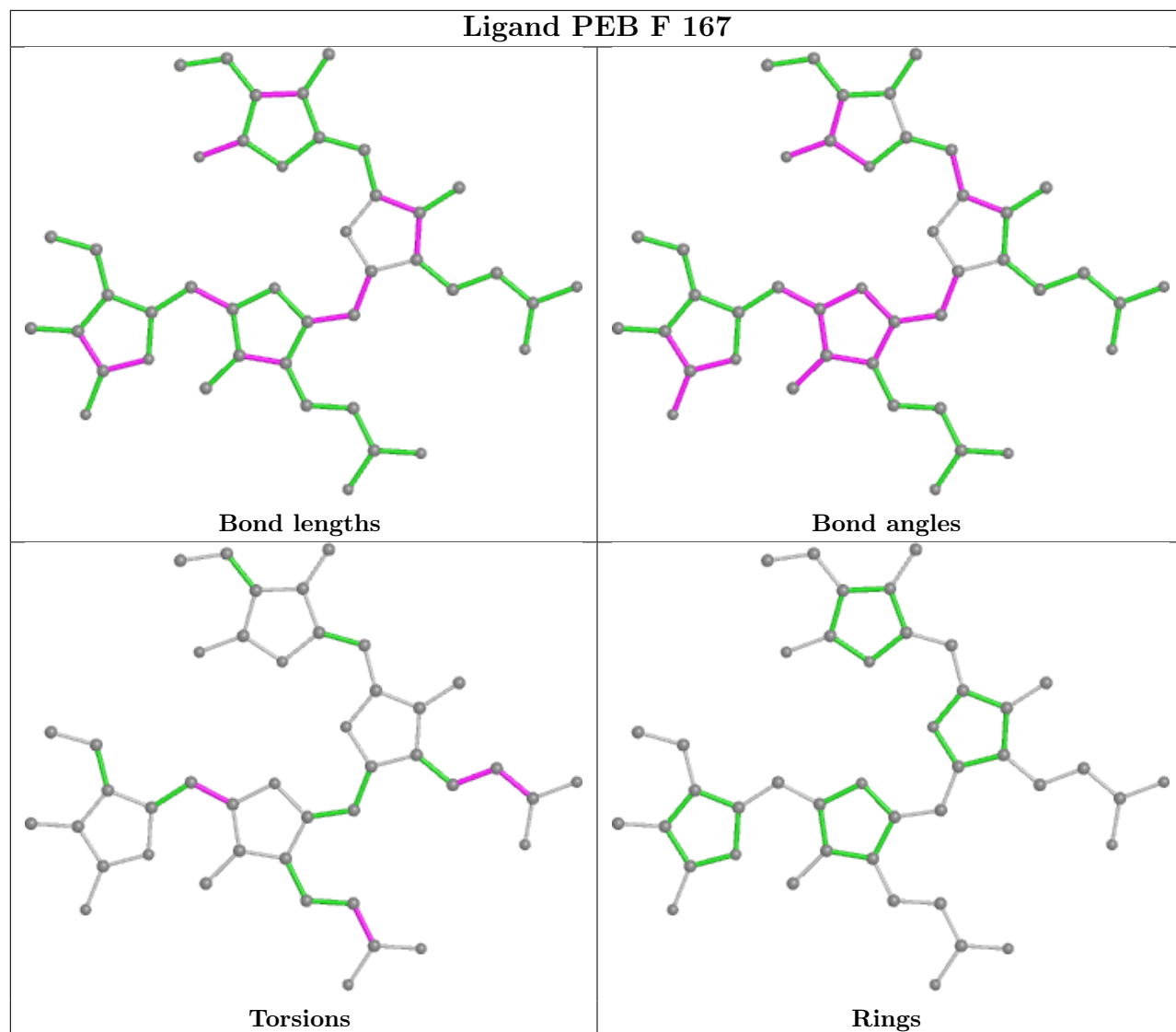


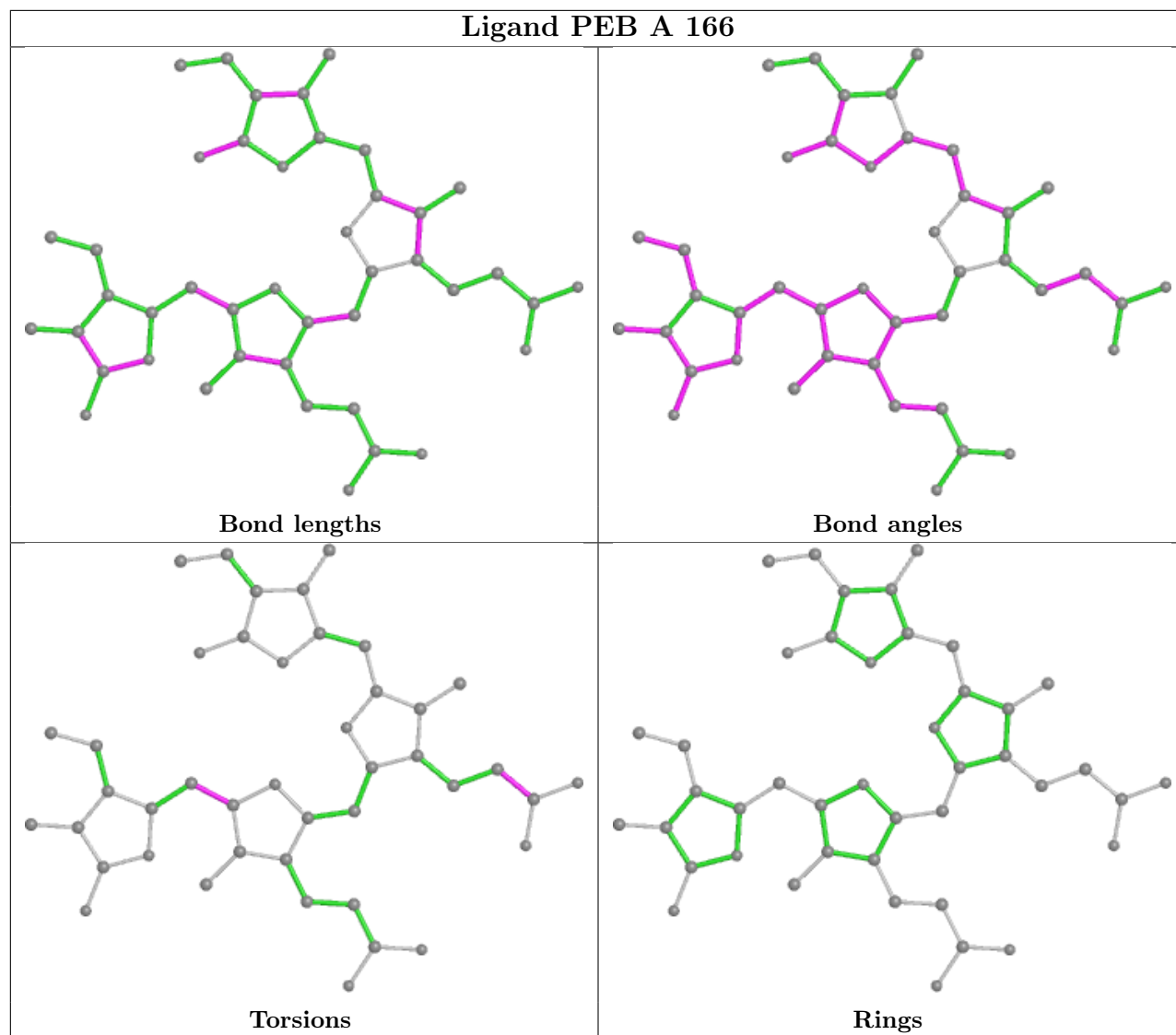


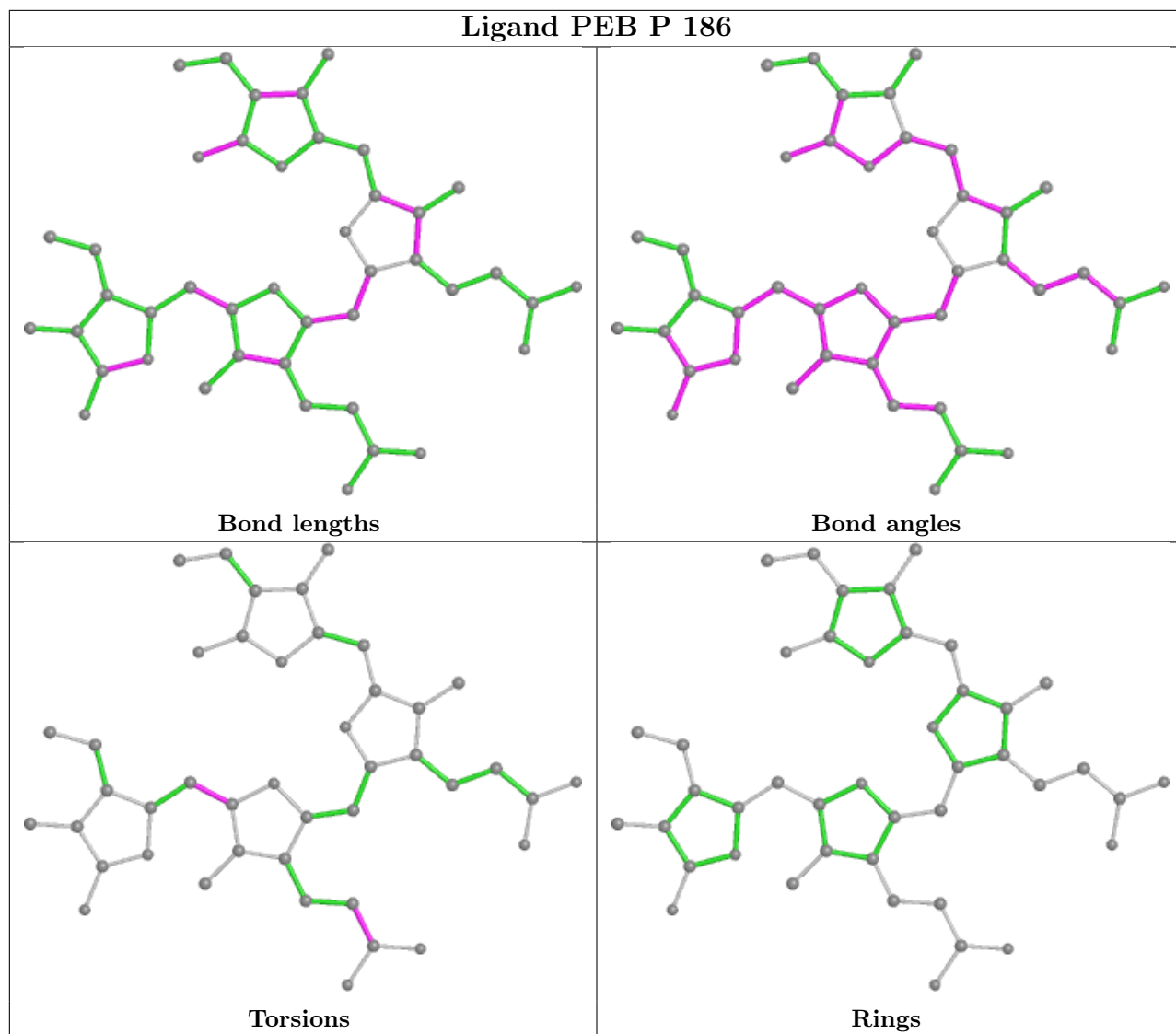


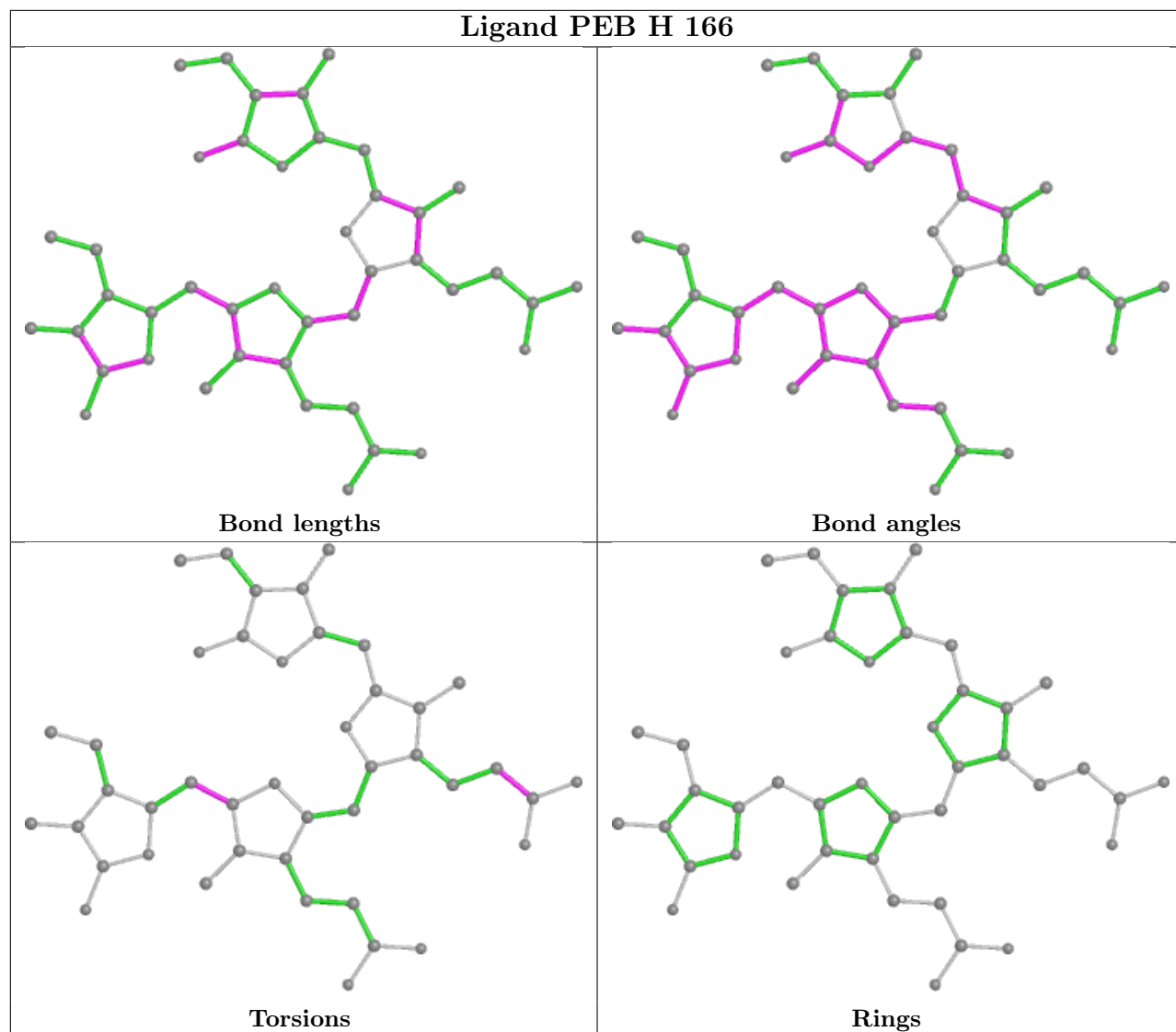


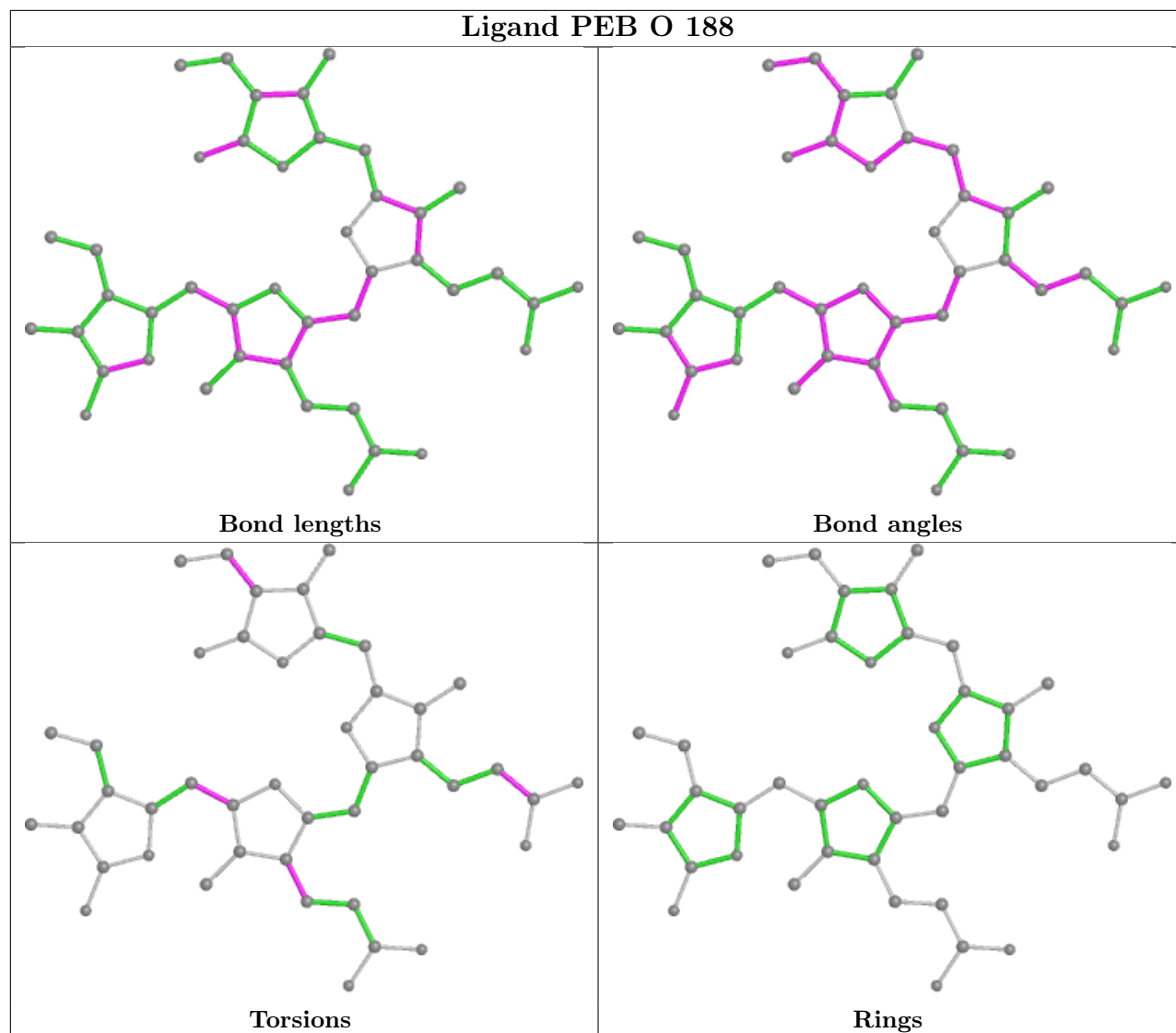


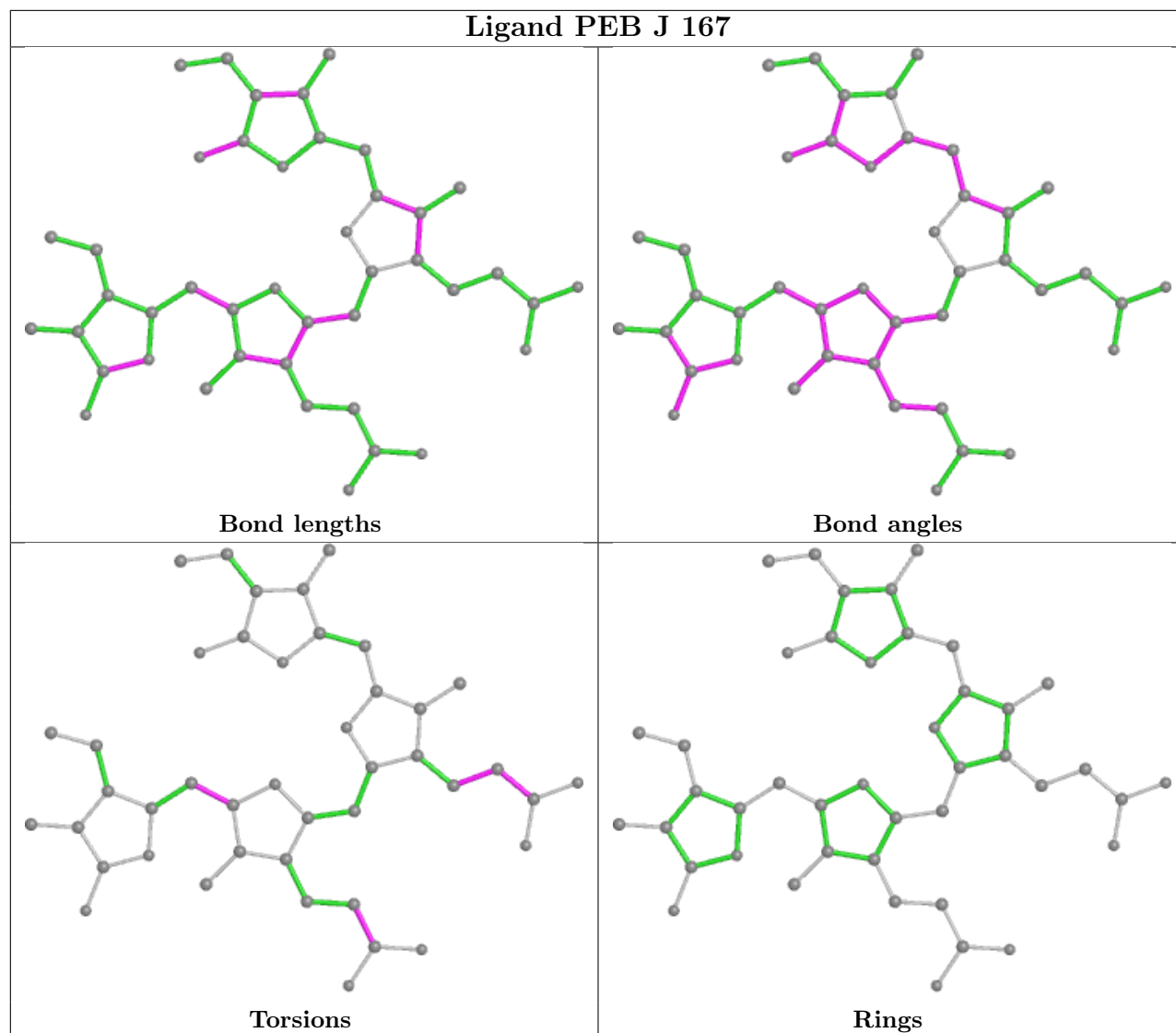












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	164/164 (100%)	-0.43	0 100 100	8, 13, 20, 27	0
1	B	164/164 (100%)	-0.46	0 100 100	8, 14, 22, 27	0
1	C	164/164 (100%)	-0.46	0 100 100	10, 16, 23, 31	0
1	D	164/164 (100%)	-0.40	0 100 100	8, 14, 24, 30	0
1	E	164/164 (100%)	-0.45	0 100 100	9, 14, 23, 29	0
1	F	164/164 (100%)	-0.41	0 100 100	10, 15, 22, 33	0
1	G	164/164 (100%)	-0.46	0 100 100	9, 14, 21, 29	0
1	H	164/164 (100%)	-0.50	0 100 100	9, 14, 21, 28	0
1	I	164/164 (100%)	-0.39	0 100 100	9, 15, 26, 33	0
1	J	164/164 (100%)	-0.47	0 100 100	11, 15, 23, 29	0
1	K	164/164 (100%)	-0.42	0 100 100	10, 16, 25, 30	0
1	L	164/164 (100%)	-0.38	0 100 100	9, 14, 23, 28	0
2	M	183/184 (99%)	-0.40	4 (2%) 62 66	8, 14, 29, 53	0
2	N	183/184 (99%)	-0.32	3 (1%) 72 76	9, 16, 29, 41	0
2	O	183/184 (99%)	-0.26	3 (1%) 72 76	10, 18, 30, 42	0
2	P	183/184 (99%)	-0.32	2 (1%) 80 84	6, 14, 29, 52	0
2	Q	183/184 (99%)	-0.23	5 (2%) 54 60	9, 17, 30, 47	0
2	R	183/184 (99%)	-0.24	3 (1%) 72 76	12, 19, 34, 54	0
2	S	183/184 (99%)	-0.25	4 (2%) 62 66	10, 16, 30, 55	0
2	T	183/184 (99%)	-0.10	4 (2%) 62 66	13, 21, 36, 49	0
2	U	183/184 (99%)	-0.34	2 (1%) 80 84	8, 14, 28, 42	0
2	V	183/184 (99%)	-0.35	5 (2%) 54 60	9, 15, 29, 48	0
2	W	183/184 (99%)	-0.31	2 (1%) 80 84	10, 17, 31, 50	0
2	X	183/184 (99%)	-0.36	3 (1%) 72 76	9, 15, 28, 47	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	4164/4176 (99%)	-0.36	40 (0%) 82 85	6, 15, 27, 55	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	W	23	GLY	3.7
2	S	21	ASP	3.5
2	M	21	ASP	3.4
2	P	21	ASP	3.4
2	O	162	GLU	3.1
2	M	23	GLY	3.1
2	N	23	GLY	3.1
2	X	22	MET	3.1
2	X	24	ALA	3.0
2	M	22	MET	3.0
2	T	21	ASP	3.0
2	R	21	ASP	2.9
2	Q	109	ASN	2.9
2	X	23	GLY	2.9
2	S	23	GLY	2.8
2	Q	21	ASP	2.8
2	V	162	GLU	2.8
2	S	24	ALA	2.6
2	T	162	GLU	2.6
2	O	20	ALA	2.6
2	V	22	MET	2.5
2	U	23	GLY	2.4
2	N	162	GLU	2.3
2	V	109	ASN	2.3
2	T	24	ALA	2.3
2	U	24	ALA	2.3
2	V	20	ALA	2.3
2	R	30	ALA	2.2
2	O	22	MET	2.2
2	N	22	MET	2.2
2	V	21	ASP	2.1
2	S	117	ALA	2.1
2	M	27	GLN	2.1
2	P	162	GLU	2.1
2	Q	110	GLY	2.1
2	R	147	ALA	2.1
2	Q	22	MET	2.1

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Mol	Chain	Res	Type	RSRZ
2	T	109	ASN	2.0
2	Q	162	GLU	2.0
2	W	22	MET	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MEN	S	70	9/10	0.95	0.09	9,14,17,17	0
2	MEN	N	70	9/10	0.96	0.09	10,13,17,18	0
2	MEN	P	70	9/10	0.97	0.07	8,11,17,17	0
2	MEN	Q	70	9/10	0.97	0.08	14,17,20,21	0
2	MEN	R	70	9/10	0.97	0.06	16,17,19,23	0
2	MEN	O	70	9/10	0.97	0.07	12,16,17,20	0
2	MEN	U	70	9/10	0.97	0.07	9,11,13,15	0
2	MEN	W	70	9/10	0.97	0.09	8,11,14,16	0
2	MEN	M	70	9/10	0.98	0.09	10,12,13,16	0
2	MEN	V	70	9/10	0.98	0.07	13,14,17,18	0
2	MEN	T	70	9/10	0.98	0.07	18,21,23,24	0
2	MEN	X	70	9/10	0.98	0.09	8,13,16,16	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	SO4	U	189	5/5	0.80	0.22	40,41,51,63	0
4	GOL	G	1165	6/6	0.83	0.13	27,30,31,37	0
4	GOL	I	1165	6/6	0.85	0.20	24,28,28,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	GOL	D	1165	6/6	0.85	0.17	23,28,31,35	0
4	GOL	C	1165	6/6	0.87	0.15	25,27,32,34	0
5	SO4	Q	189	5/5	0.87	0.23	32,46,54,57	0
4	GOL	H	1165	6/6	0.87	0.18	25,28,33,36	0
3	PEB	R	187	43/43	0.88	0.15	12,20,31,40	0
5	SO4	W	189	5/5	0.88	0.22	25,37,52,54	0
4	GOL	B	1165	6/6	0.89	0.13	16,23,31,33	0
3	PEB	P	187	43/43	0.89	0.13	9,15,27,31	0
3	PEB	I	167	43/43	0.89	0.14	12,18,23,26	0
5	SO4	R	189	5/5	0.89	0.23	35,51,58,64	0
4	GOL	E	1165	6/6	0.89	0.21	25,30,33,37	0
3	PEB	V	186	43/43	0.89	0.12	8,17,28,36	0
3	PEB	T	187	43/43	0.90	0.13	11,20,31,35	0
3	PEB	O	186	43/43	0.90	0.11	7,17,27,37	0
3	PEB	O	187	43/43	0.90	0.12	12,20,26,31	0
3	PEB	D	167	43/43	0.90	0.13	12,18,26,35	0
3	PEB	Q	186	43/43	0.90	0.13	12,17,25,38	0
3	PEB	K	167	43/43	0.90	0.15	15,24,29,32	0
5	SO4	V	189	5/5	0.90	0.27	27,31,51,54	0
4	GOL	F	1165	6/6	0.90	0.14	27,29,31,37	0
3	PEB	X	187	43/43	0.91	0.12	8,16,23,34	0
3	PEB	S	186	43/43	0.91	0.12	10,16,27,38	0
4	GOL	L	1165	6/6	0.91	0.14	22,28,33,34	0
5	SO4	N	189	5/5	0.91	0.21	28,34,47,52	0
5	SO4	O	189	5/5	0.91	0.25	30,41,48,58	0
3	PEB	S	187	43/43	0.91	0.14	11,17,26,30	0
3	PEB	T	186	43/43	0.91	0.13	14,22,29,37	0
3	PEB	P	186	43/43	0.91	0.13	9,14,24,34	0
3	PEB	U	187	43/43	0.91	0.12	7,15,25,38	0
3	PEB	J	167	43/43	0.91	0.13	10,21,29,32	0
4	GOL	J	1165	6/6	0.92	0.10	18,24,27,27	0
3	PEB	Q	187	43/43	0.92	0.12	7,16,34,39	0
5	SO4	M	189	5/5	0.92	0.18	26,31,38,46	0
3	PEB	R	186	43/43	0.92	0.11	9,17,25,32	0
3	PEB	U	186	43/43	0.92	0.13	9,13,24,33	0
3	PEB	M	187	43/43	0.92	0.10	9,14,20,36	0
3	PEB	L	167	43/43	0.92	0.12	10,16,25,32	0
5	SO4	S	189	5/5	0.92	0.28	32,38,53,56	0
3	PEB	V	187	43/43	0.92	0.11	13,17,23,25	0
3	PEB	X	186	43/43	0.92	0.13	8,14,24,41	0
3	PEB	M	186	43/43	0.92	0.11	8,14,23,45	0
3	PEB	C	167	43/43	0.93	0.13	11,19,26,27	0

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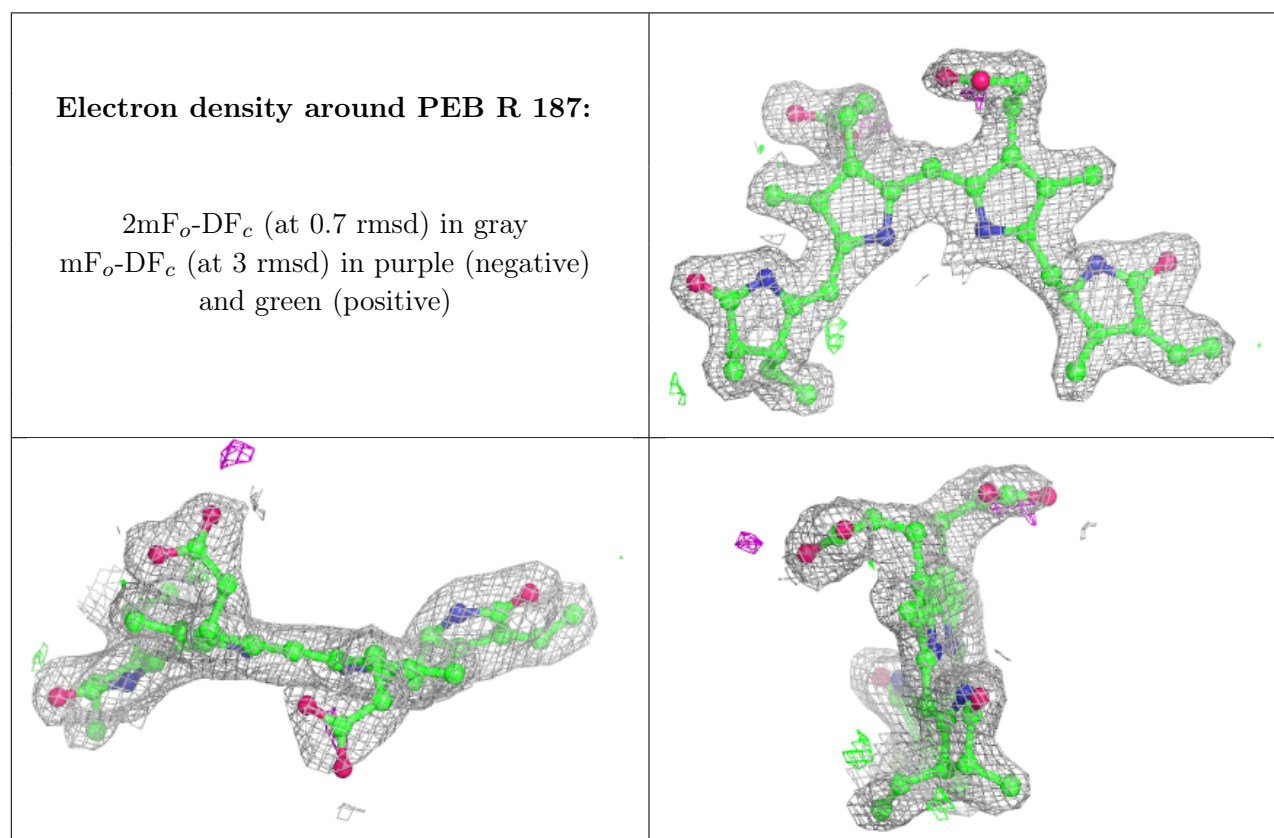
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	PEB	A	167	43/43	0.93	0.11	8,15,21,28	0
3	PEB	W	186	43/43	0.93	0.12	8,15,23,39	0
5	SO4	P	189	5/5	0.93	0.21	28,35,56,56	0
3	PEB	W	187	43/43	0.93	0.12	8,16,25,38	0
3	PEB	N	186	43/43	0.93	0.13	7,15,23,35	0
3	PEB	T	188	43/43	0.93	0.11	13,22,30,40	0
3	PEB	N	187	43/43	0.93	0.11	10,15,22,24	0
4	GOL	K	1165	6/6	0.93	0.14	15,25,26,29	0
3	PEB	P	188	43/43	0.93	0.10	6,12,16,19	0
3	PEB	K	166	43/43	0.94	0.10	8,12,17,21	0
3	PEB	C	166	43/43	0.94	0.10	7,13,17,28	0
3	PEB	E	166	43/43	0.94	0.10	8,15,19,30	0
3	PEB	U	188	43/43	0.94	0.10	8,11,16,28	0
3	PEB	F	166	43/43	0.94	0.10	6,12,15,18	0
3	PEB	G	166	43/43	0.94	0.10	7,10,15,19	0
3	PEB	V	188	43/43	0.94	0.09	8,14,19,23	0
3	PEB	Q	188	43/43	0.94	0.10	9,16,25,31	0
3	PEB	H	166	43/43	0.94	0.11	9,14,20,25	0
3	PEB	W	188	43/43	0.94	0.10	9,16,23,24	0
3	PEB	I	166	43/43	0.94	0.10	11,17,25,28	0
3	PEB	R	188	43/43	0.94	0.10	11,17,21,35	0
3	PEB	X	188	43/43	0.94	0.10	10,13,22,24	0
3	PEB	N	188	43/43	0.94	0.10	9,15,22,25	0
3	PEB	B	167	43/43	0.94	0.13	10,18,28,31	0
3	PEB	D	166	43/43	0.94	0.09	9,15,22,31	0
3	PEB	O	188	43/43	0.94	0.11	10,16,24,31	0
3	PEB	F	167	43/43	0.95	0.10	10,15,19,25	0
3	PEB	J	166	43/43	0.95	0.09	9,13,19,24	0
3	PEB	B	166	43/43	0.95	0.09	6,10,14,18	0
3	PEB	G	167	43/43	0.95	0.09	8,15,20,27	0
3	PEB	E	167	43/43	0.95	0.09	11,15,20,24	0
4	GOL	A	1165	6/6	0.95	0.15	21,23,25,30	0
3	PEB	S	188	43/43	0.95	0.10	9,14,20,25	0
3	PEB	L	166	43/43	0.95	0.09	7,12,17,18	0
3	PEB	A	166	43/43	0.95	0.10	8,12,16,20	0
5	SO4	T	189	5/5	0.96	0.32	42,46,49,60	0
3	PEB	H	167	43/43	0.96	0.08	8,14,17,21	0
5	SO4	L	1200	5/5	0.96	0.10	20,24,32,35	0
3	PEB	M	188	43/43	0.96	0.08	10,13,19,20	0
5	SO4	X	189	5/5	0.96	0.15	30,33,43,52	0
5	SO4	E	1200	5/5	0.97	0.13	18,18,30,38	0
5	SO4	H	1200	5/5	0.97	0.14	21,26,33,36	0

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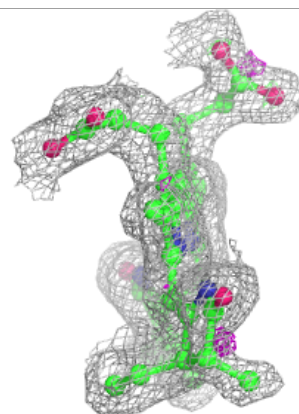
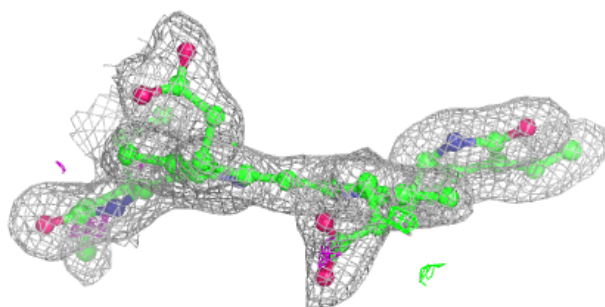
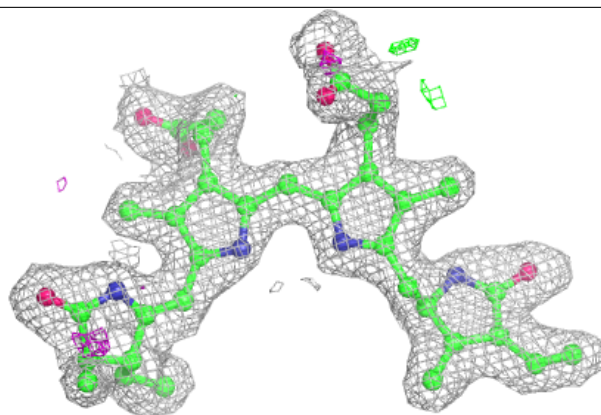
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	SO4	I	1200	5/5	0.97	0.12	24,31,37,38	0
5	SO4	A	1200	5/5	0.97	0.08	23,24,34,40	0
5	SO4	D	1200	5/5	0.98	0.11	20,26,34,34	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

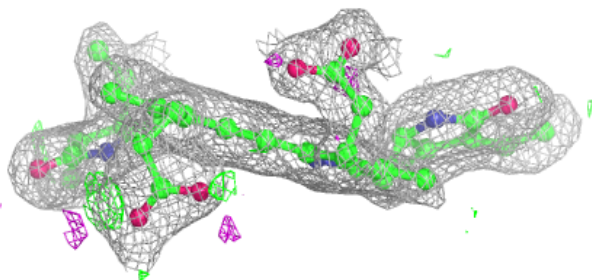
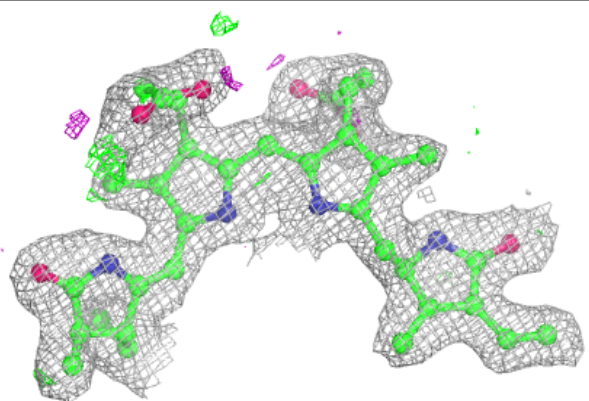


Electron density around PEB P 187:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

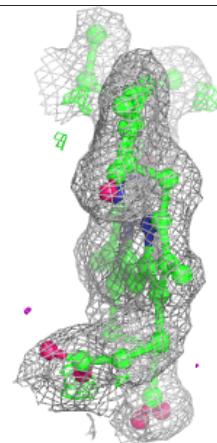
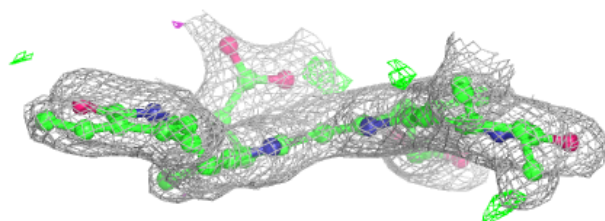
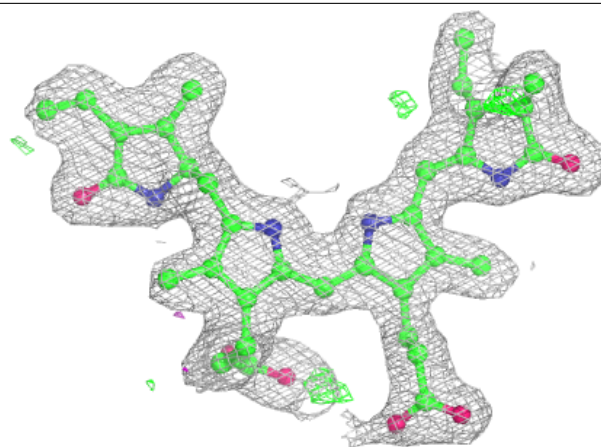
**Electron density around PEB I 167:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



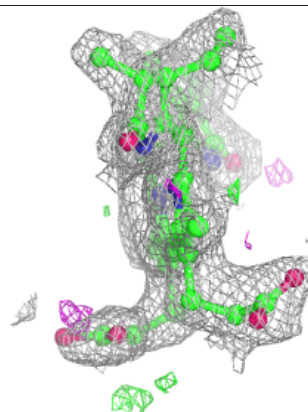
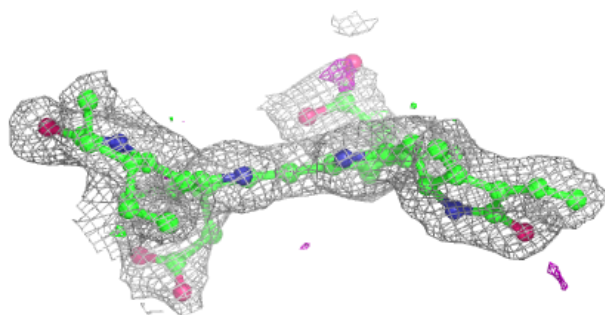
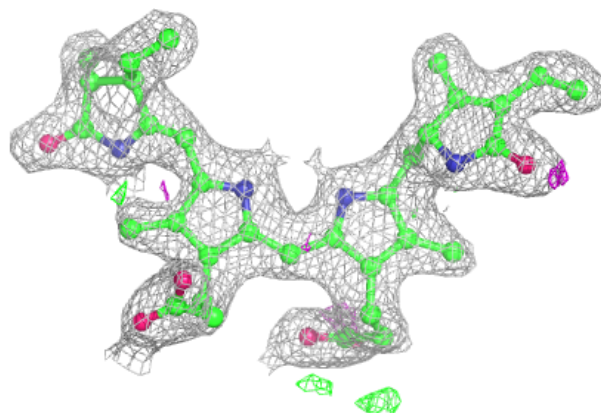
Electron density around PEB V 186:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



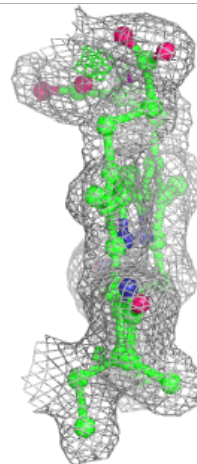
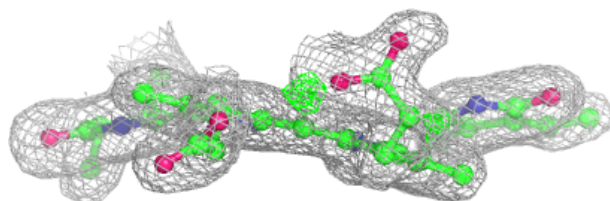
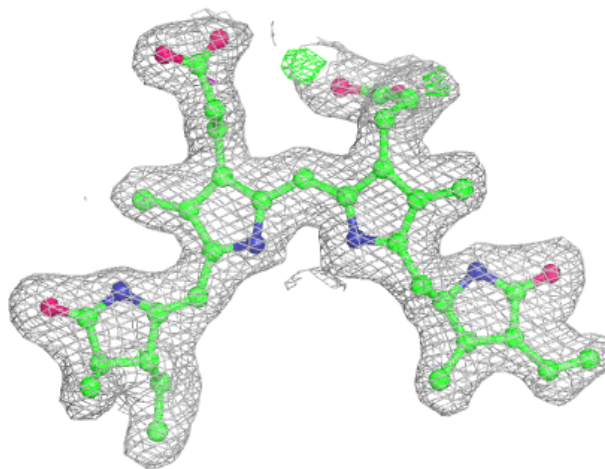
Electron density around PEB T 187:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



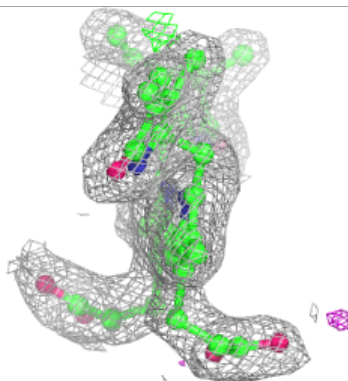
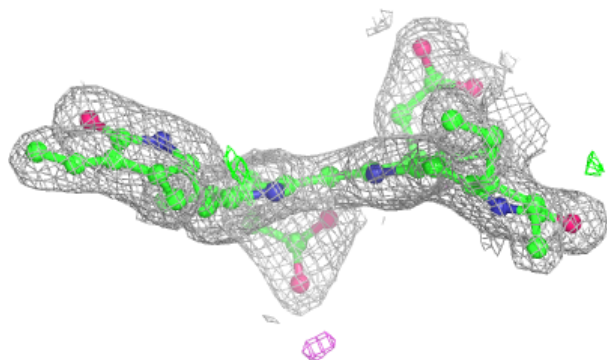
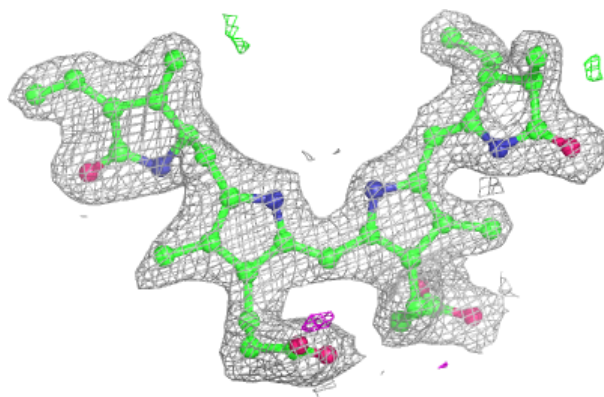
Electron density around PEB O 186:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

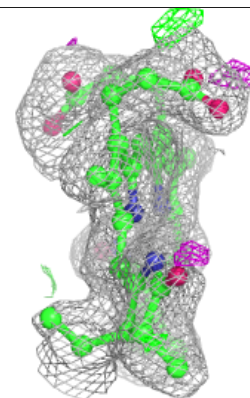
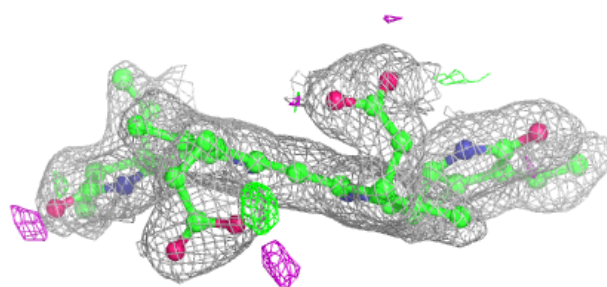
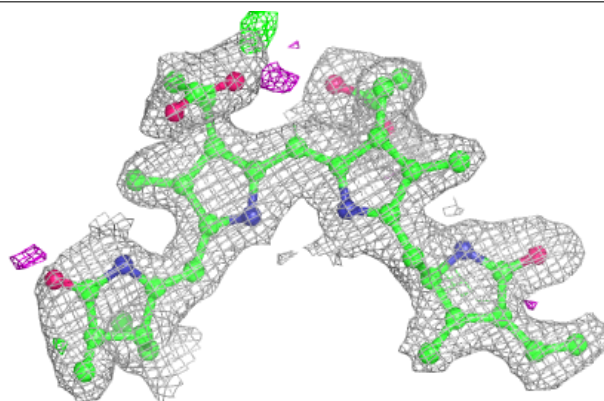


Electron density around PEB O 187:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

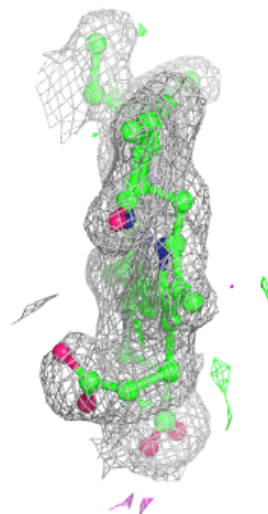
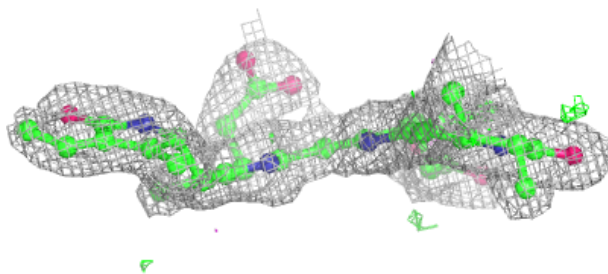
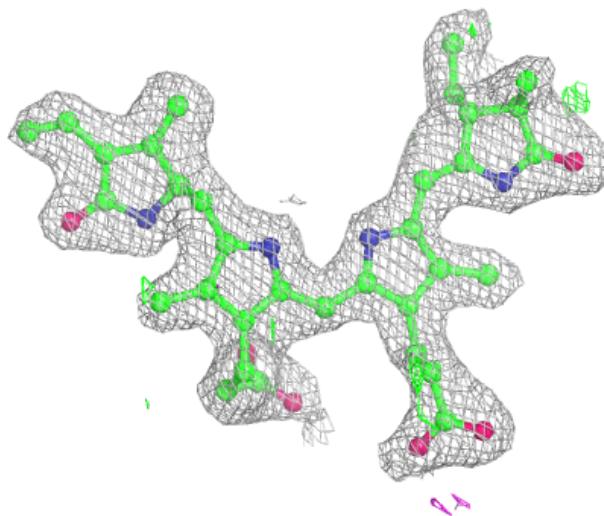
**Electron density around PEB D 167:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



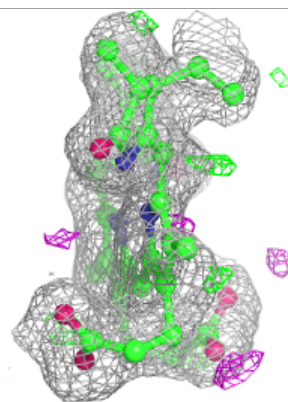
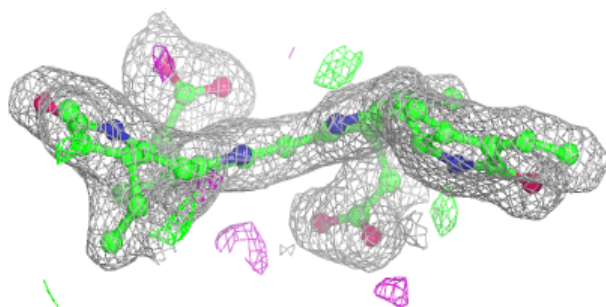
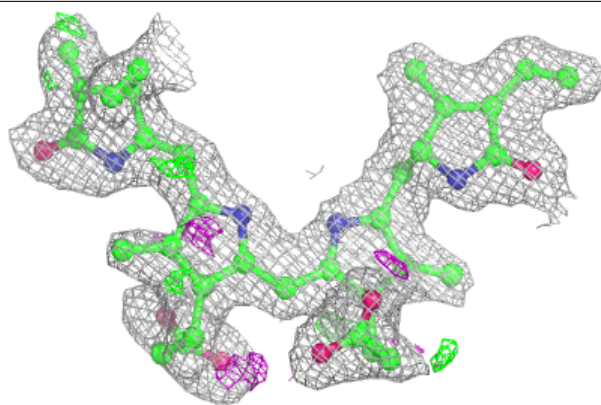
Electron density around PEB Q 186:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

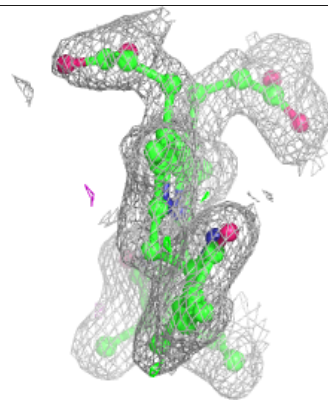
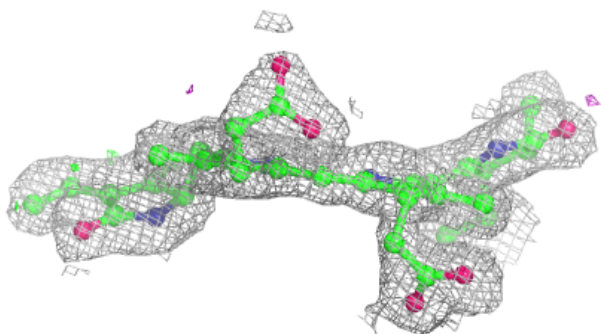
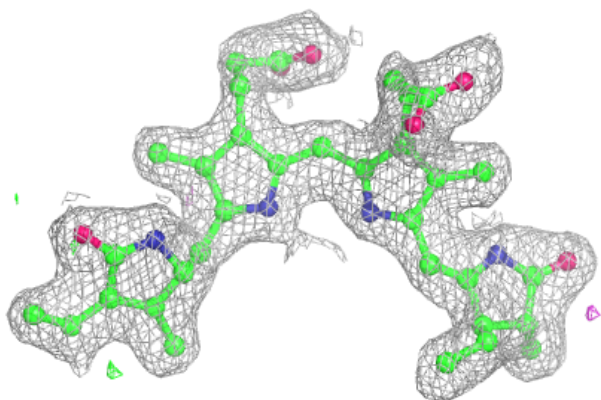


Electron density around PEB K 167:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

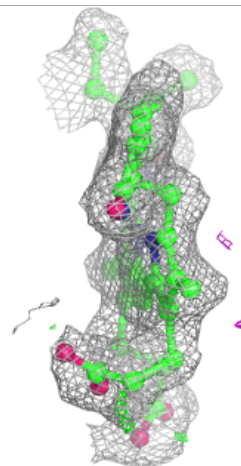
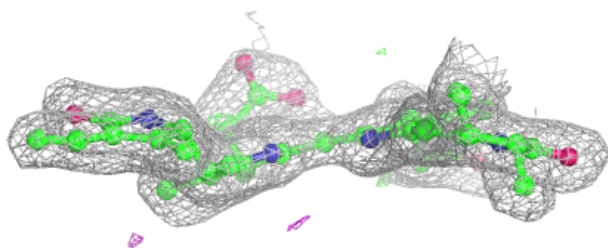
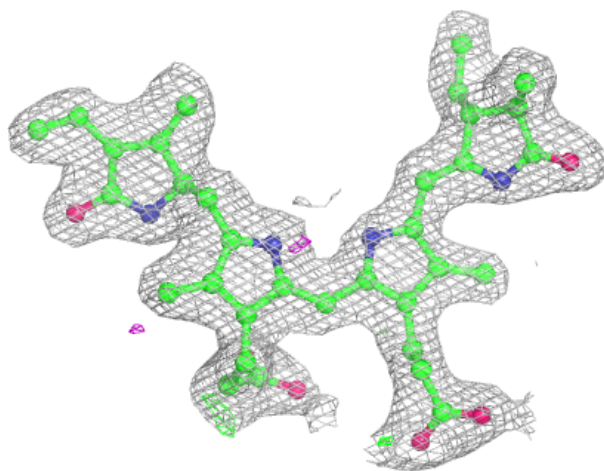
**Electron density around PEB X 187:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



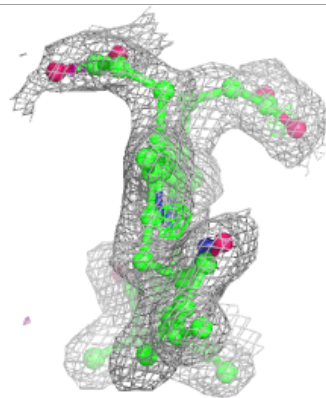
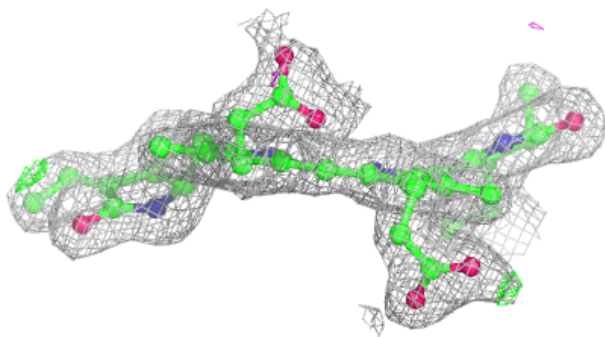
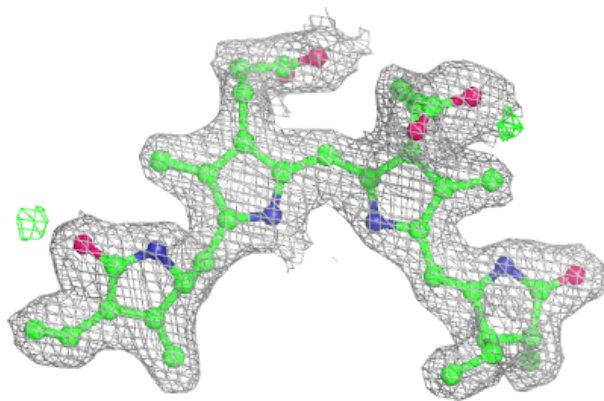
Electron density around PEB S 186:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



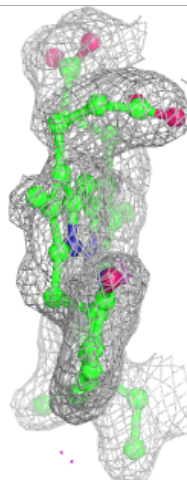
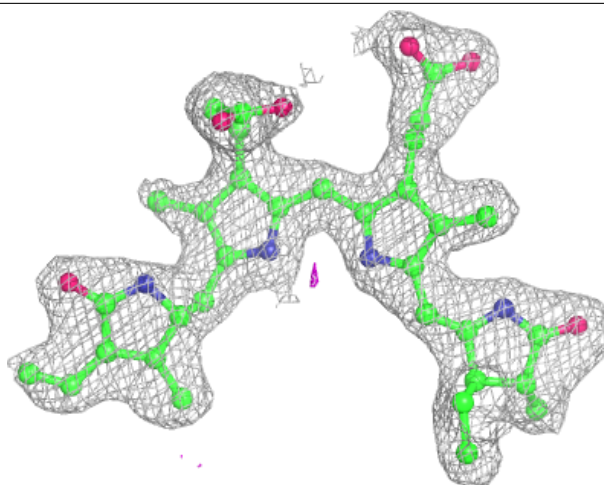
Electron density around PEB S 187:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



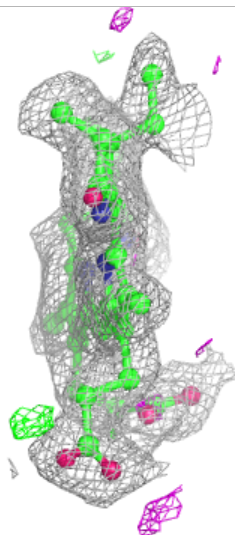
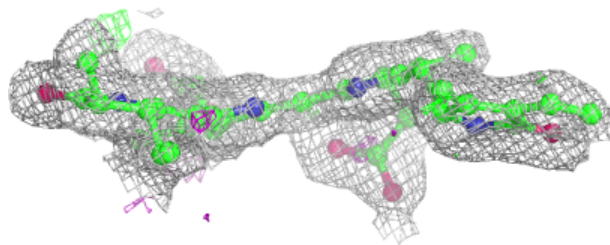
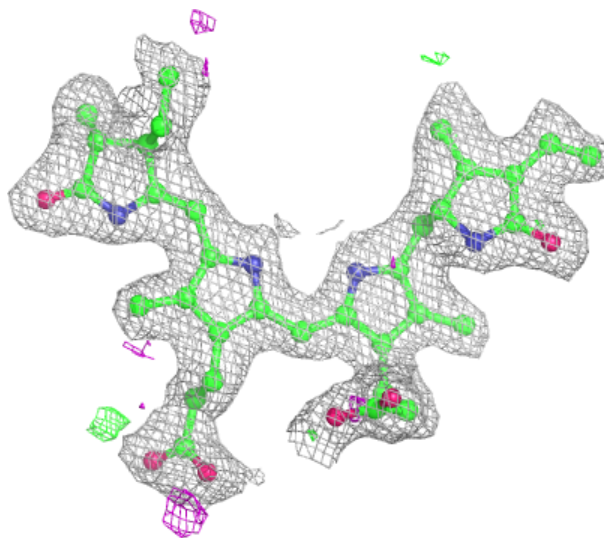
Electron density around PEB T 186:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



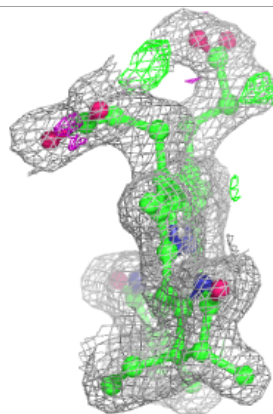
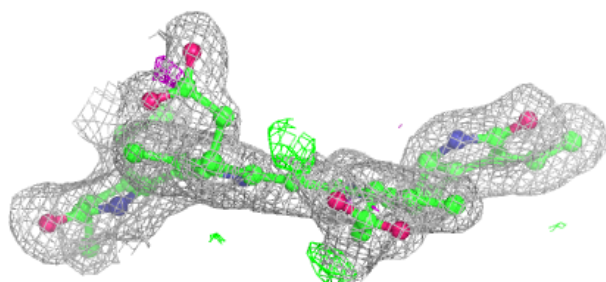
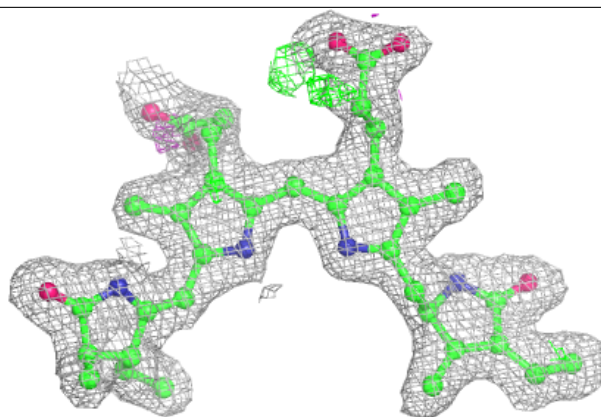
Electron density around PEB P 186:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

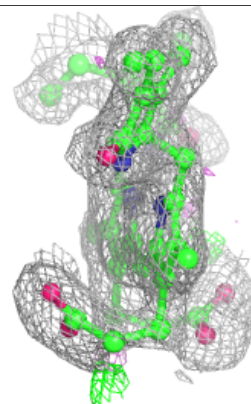
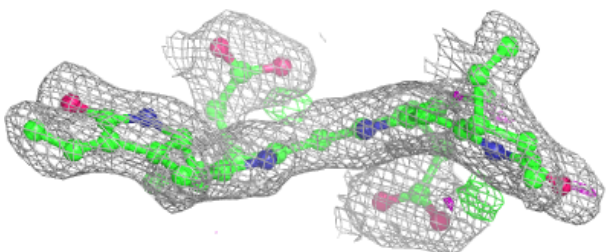
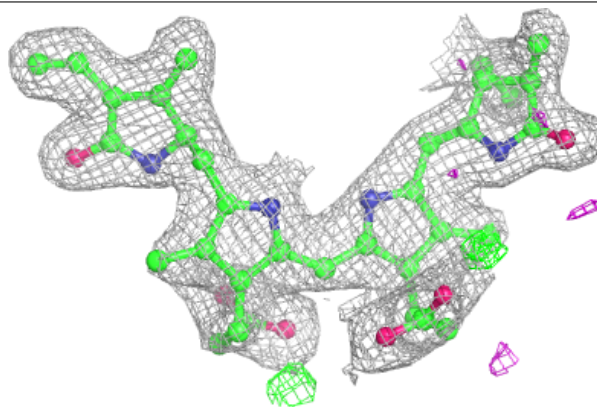


Electron density around PEB U 187:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

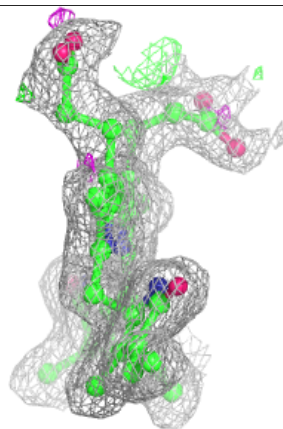
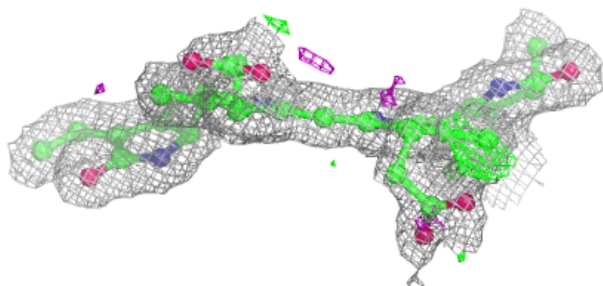
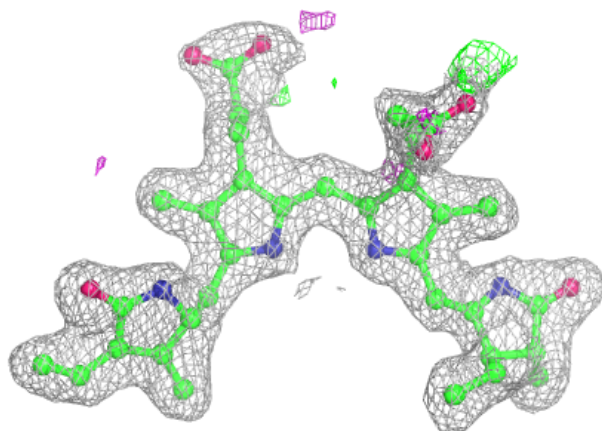
**Electron density around PEB J 167:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



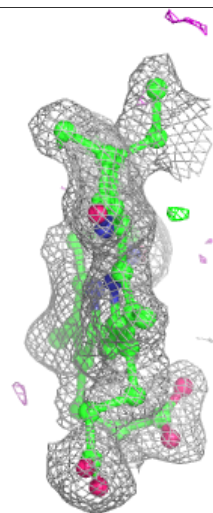
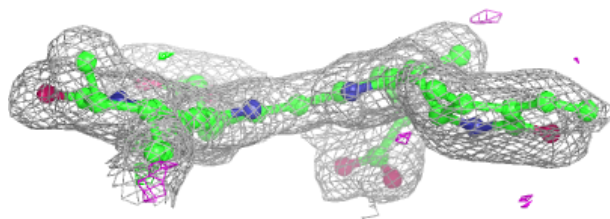
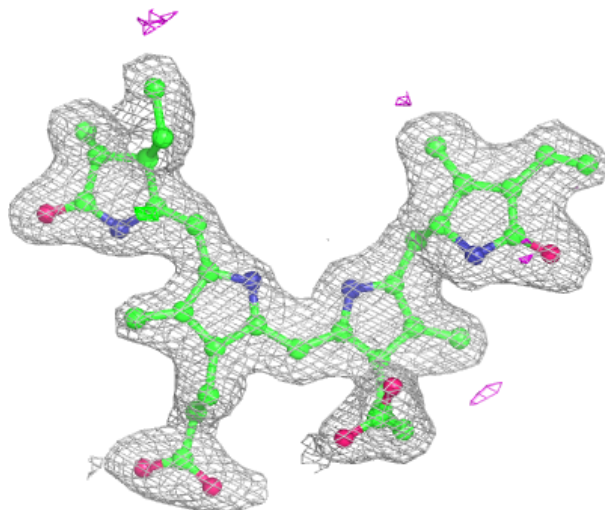
Electron density around PEB Q 187:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



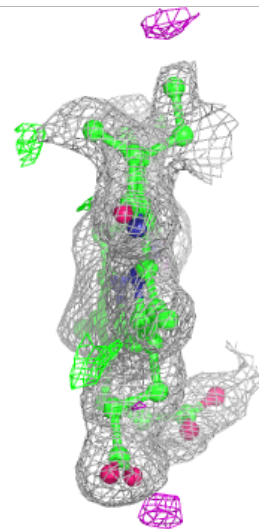
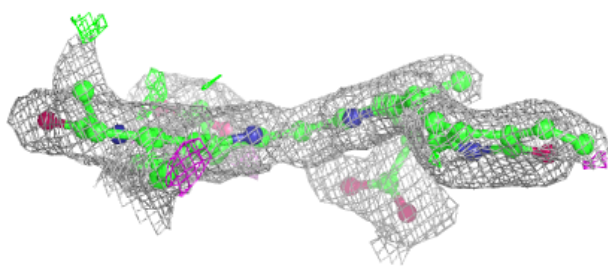
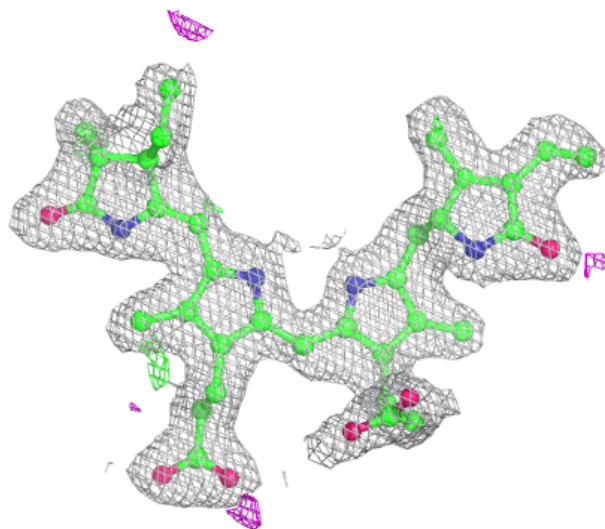
Electron density around PEB R 186:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



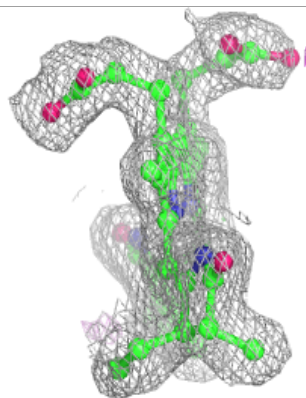
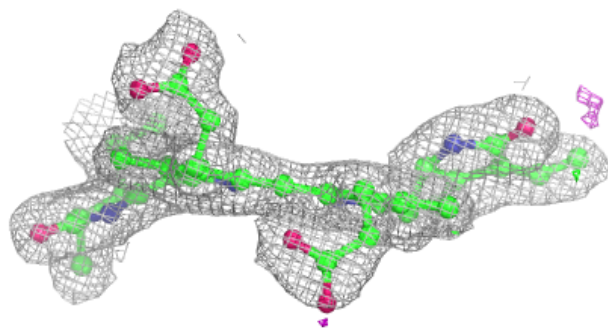
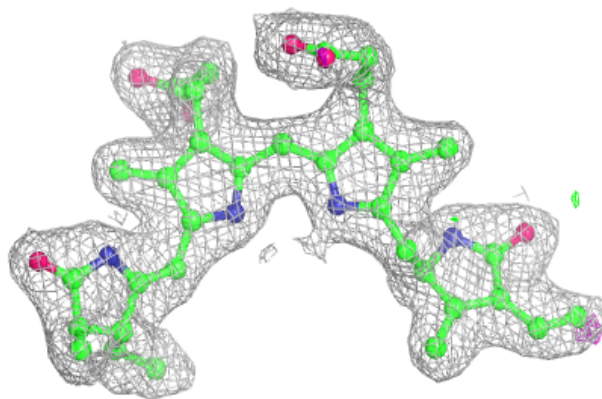
Electron density around PEB U 186:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

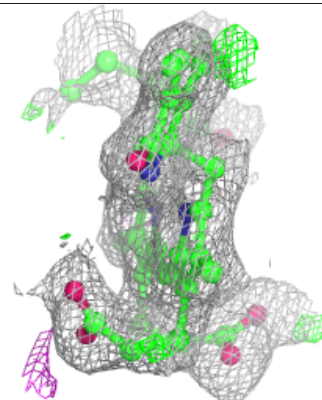
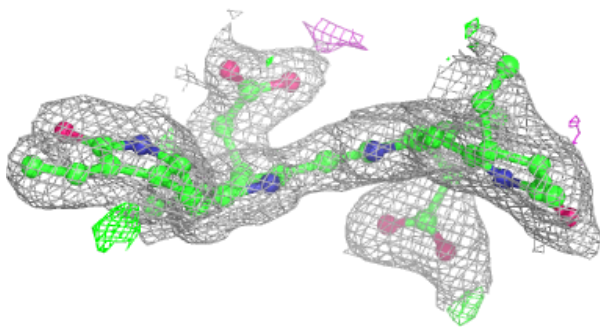
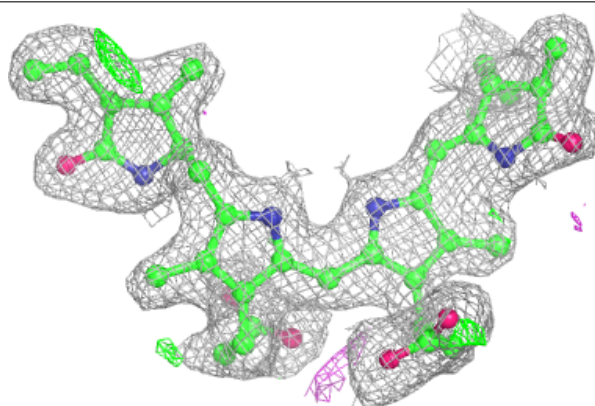


Electron density around PEB M 187:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

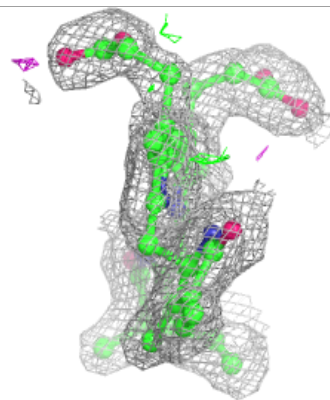
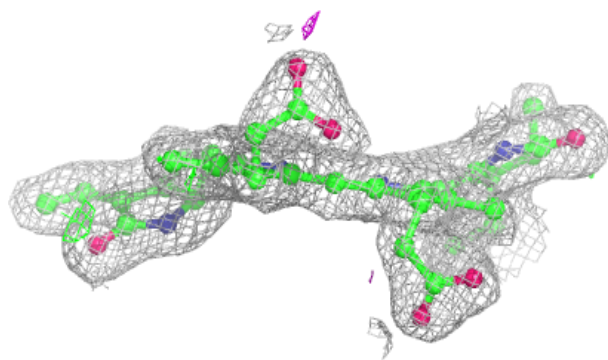
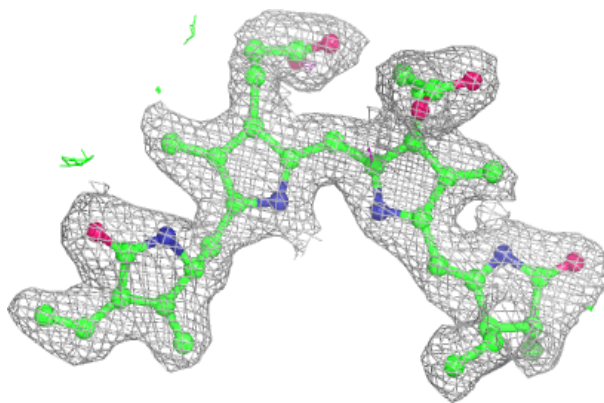
**Electron density around PEB L 167:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

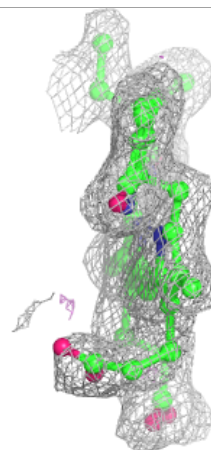
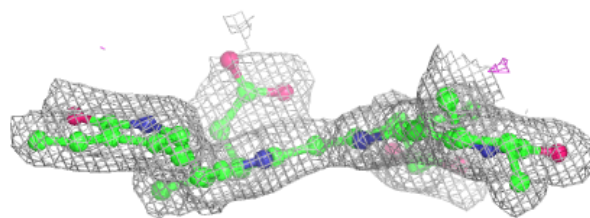
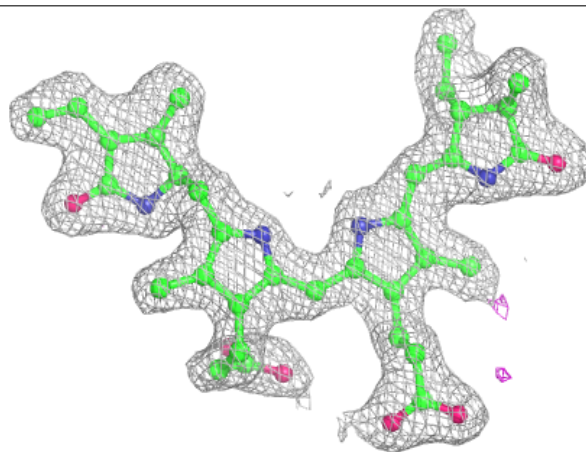


Electron density around PEB V 187:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

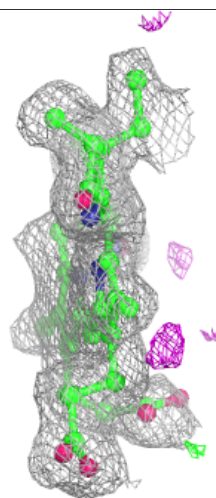
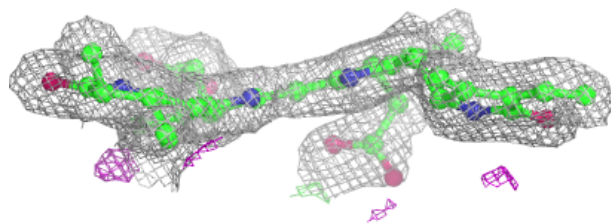
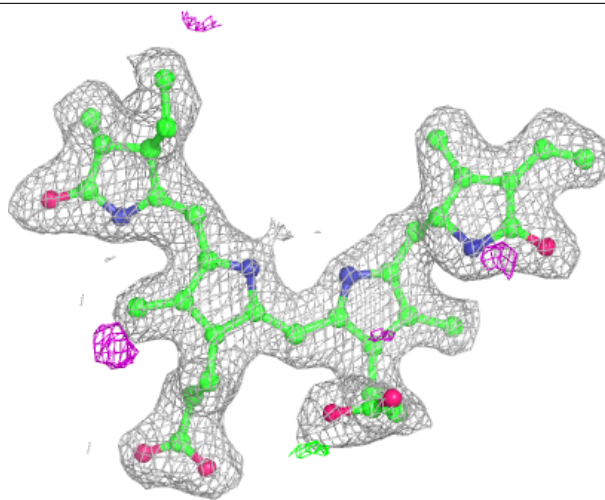
**Electron density around PEB X 186:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



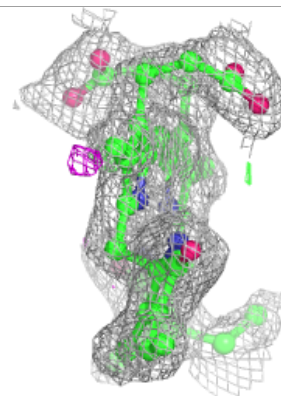
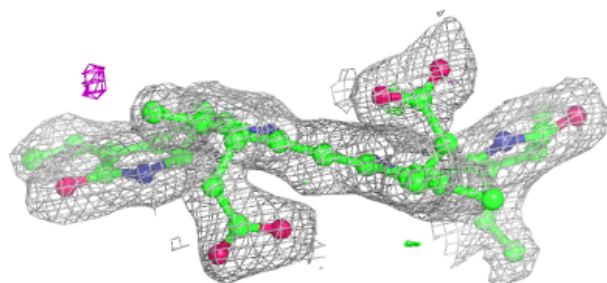
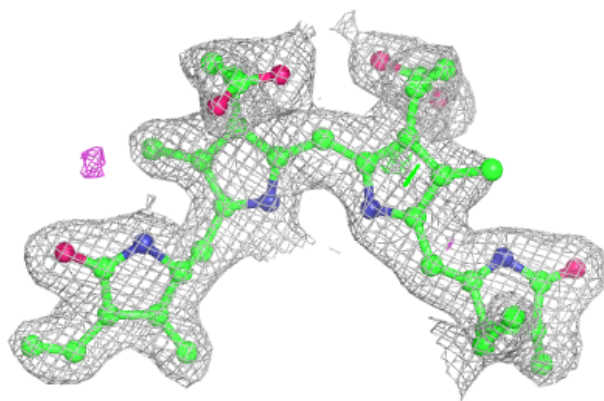
Electron density around PEB M 186:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

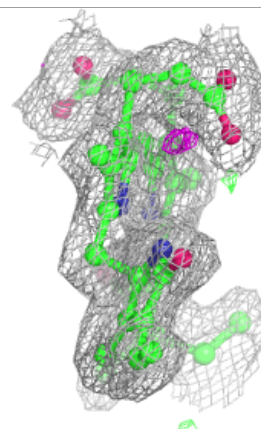
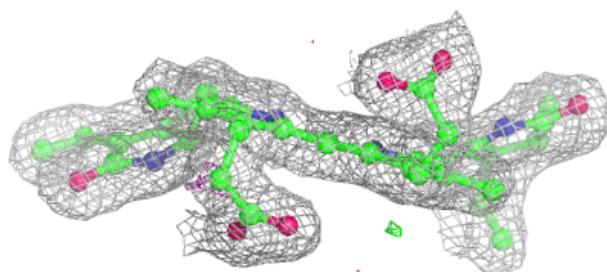
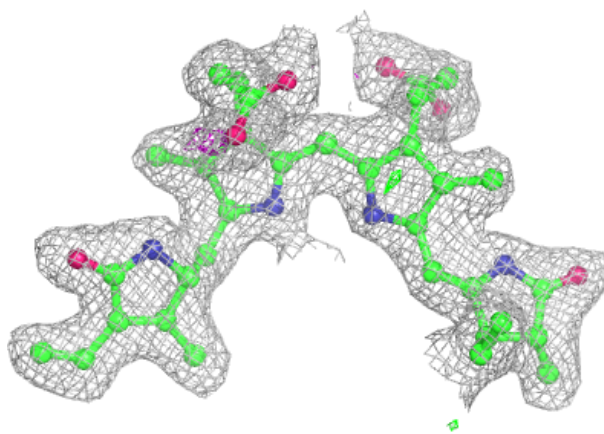


Electron density around PEB C 167:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

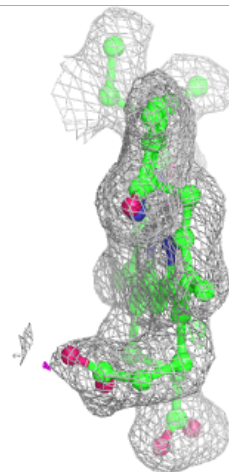
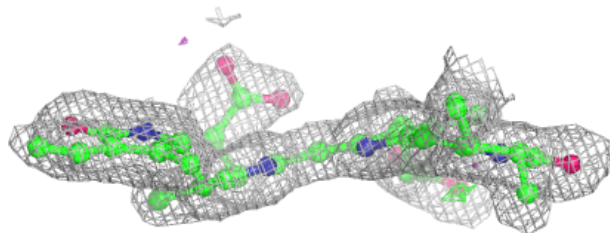
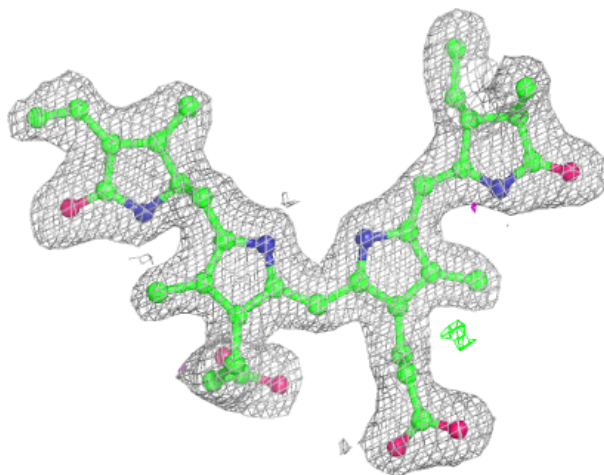
**Electron density around PEB A 167:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



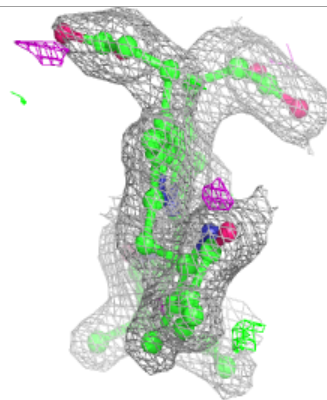
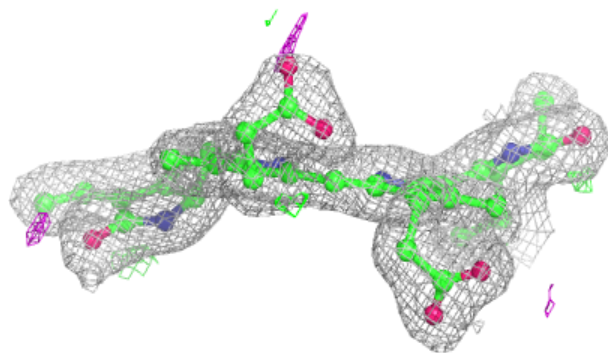
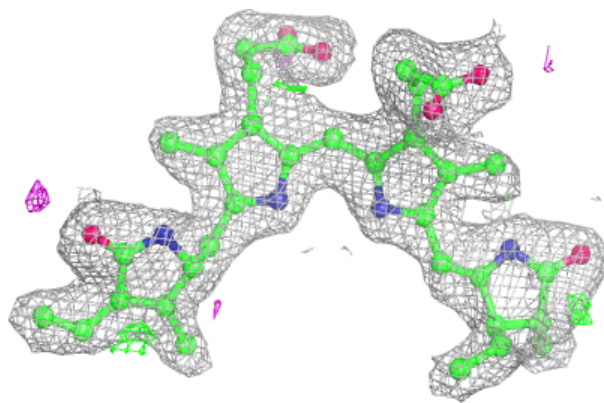
Electron density around PEB W 186:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



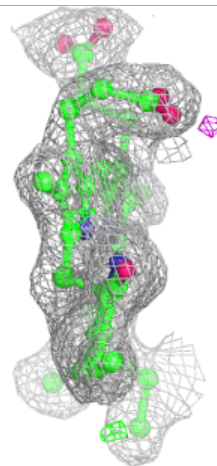
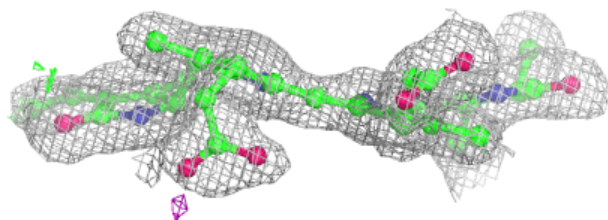
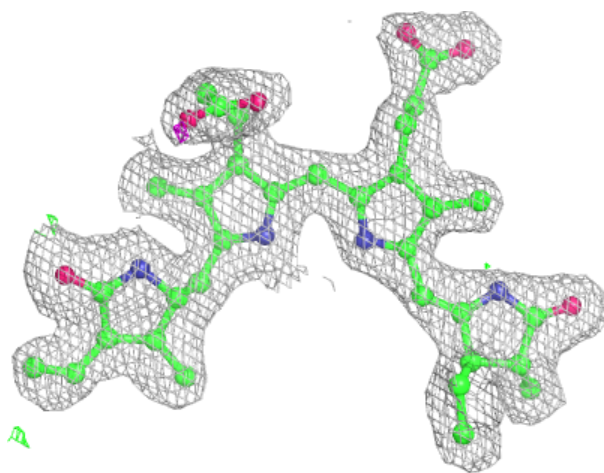
Electron density around PEB W 187:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



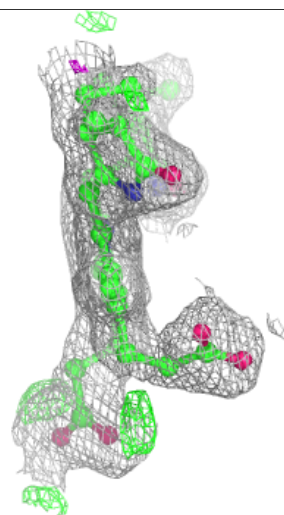
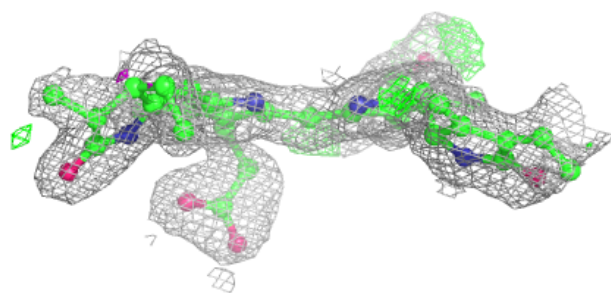
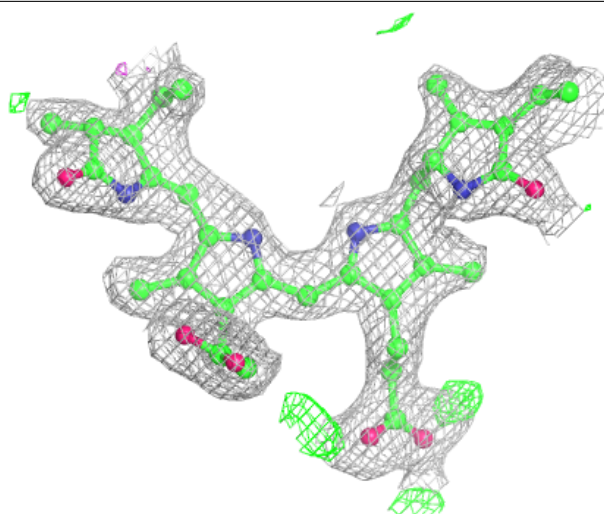
Electron density around PEB N 186:

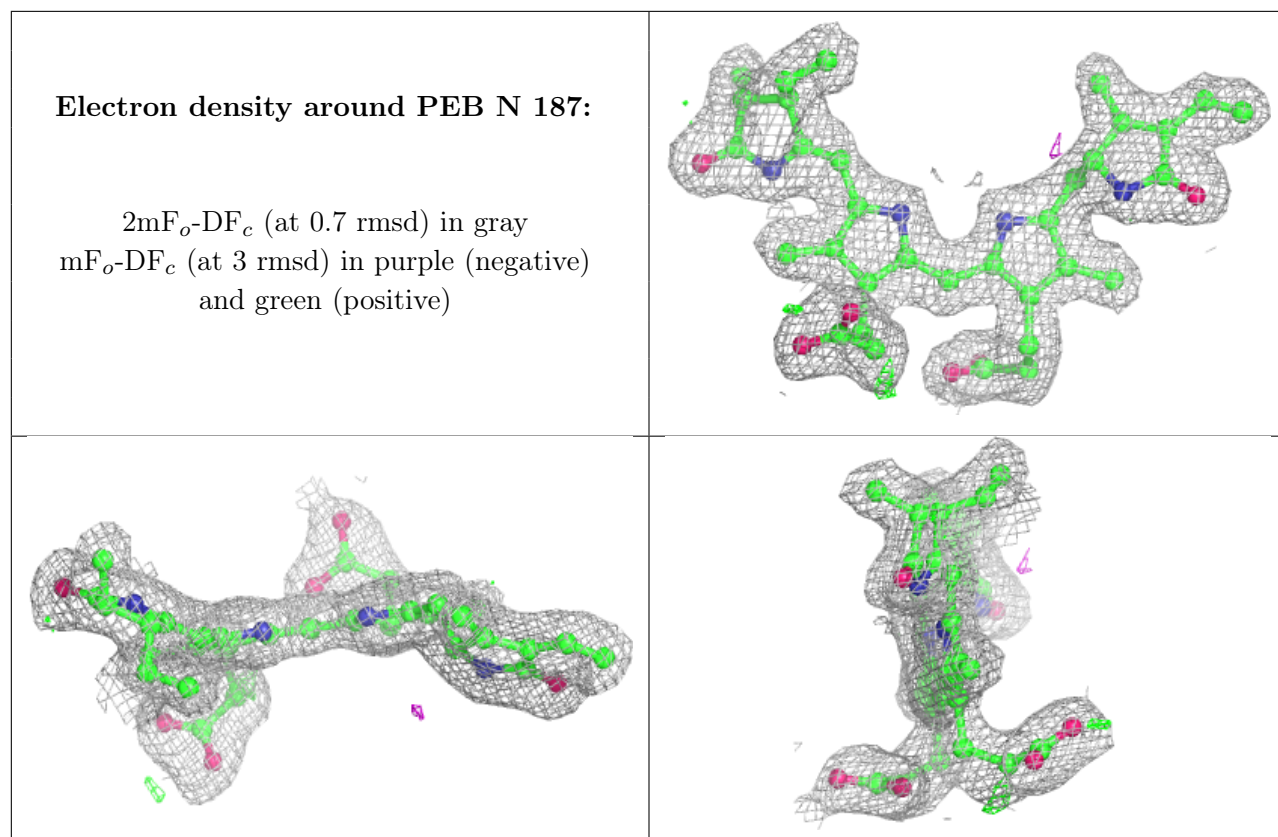
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around PEB T 188:

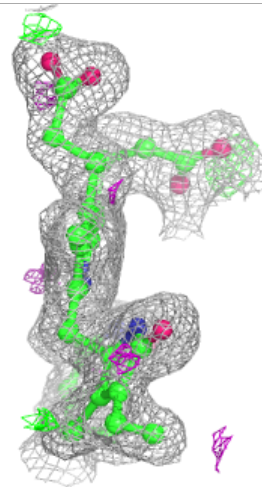
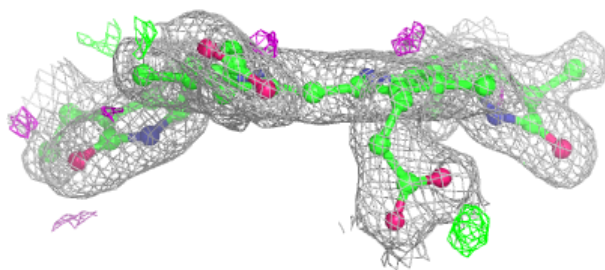
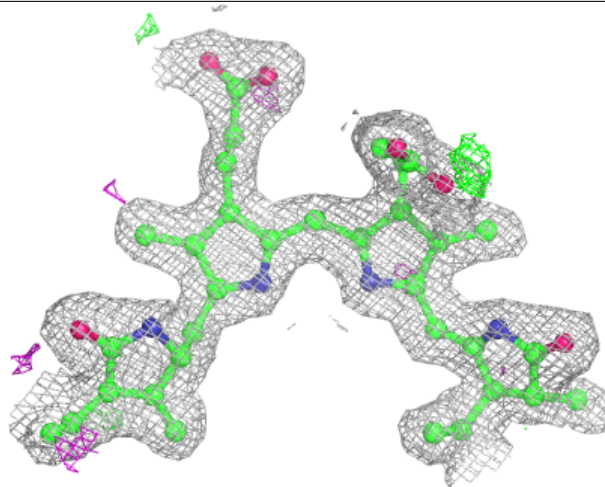
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





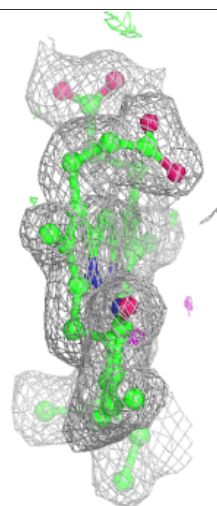
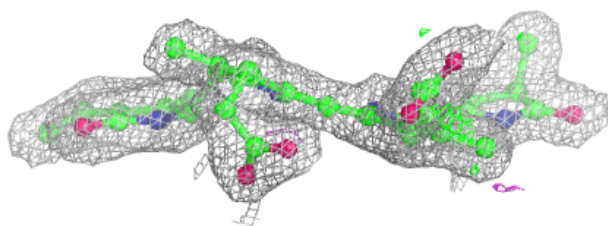
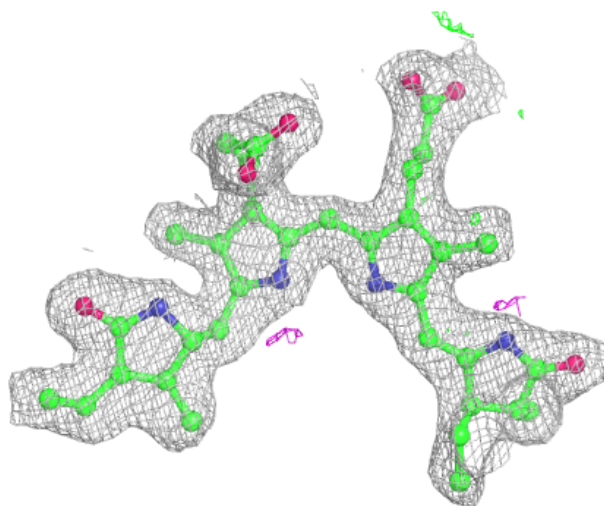
Electron density around PEB P 188:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



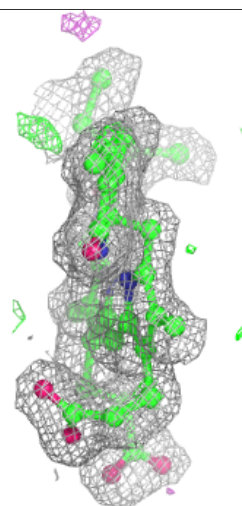
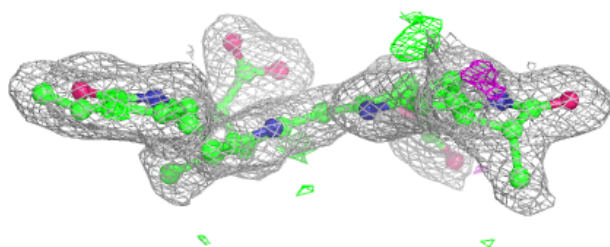
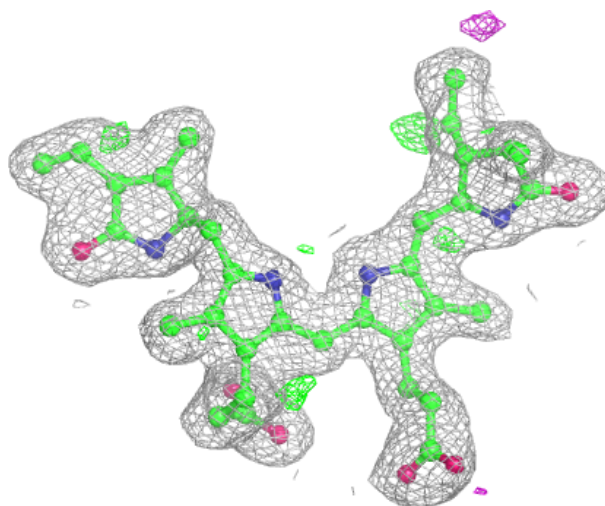
Electron density around PEB K 166:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



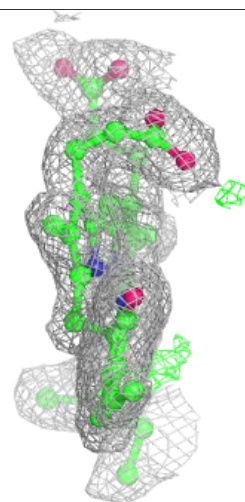
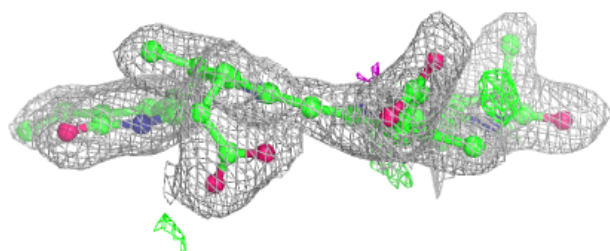
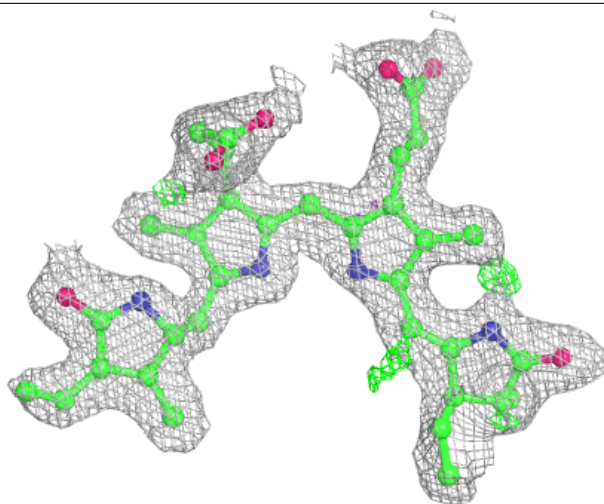
Electron density around PEB C 166:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



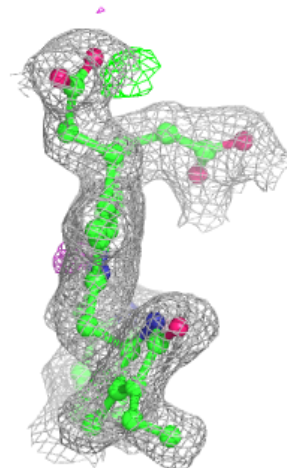
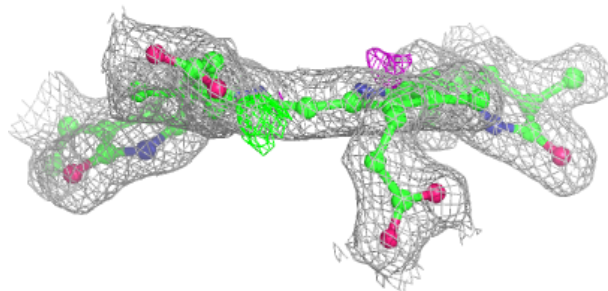
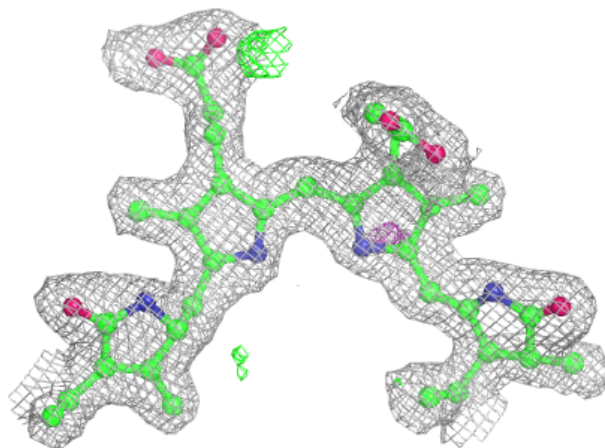
Electron density around PEB E 166:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



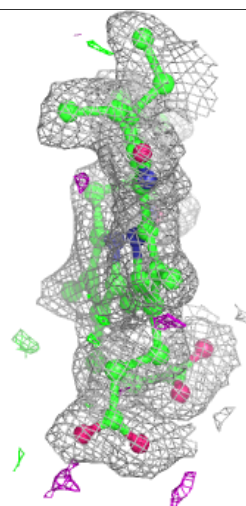
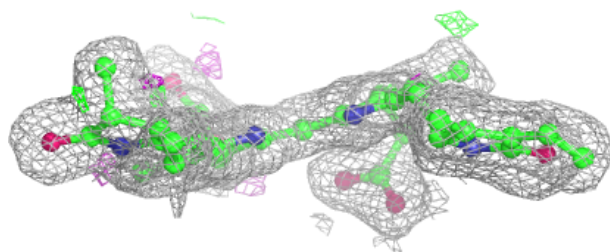
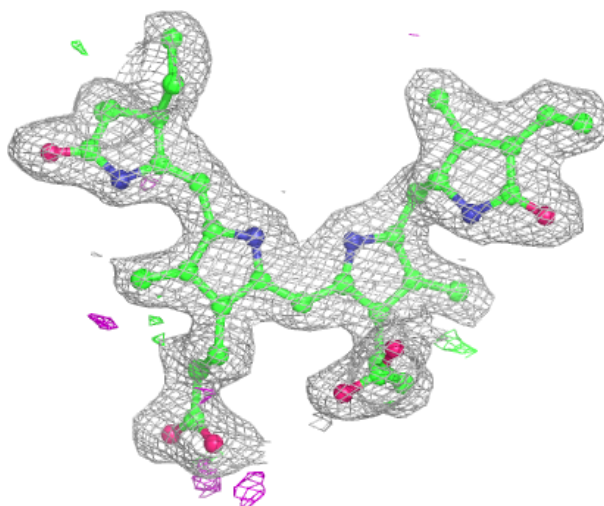
Electron density around PEB U 188:

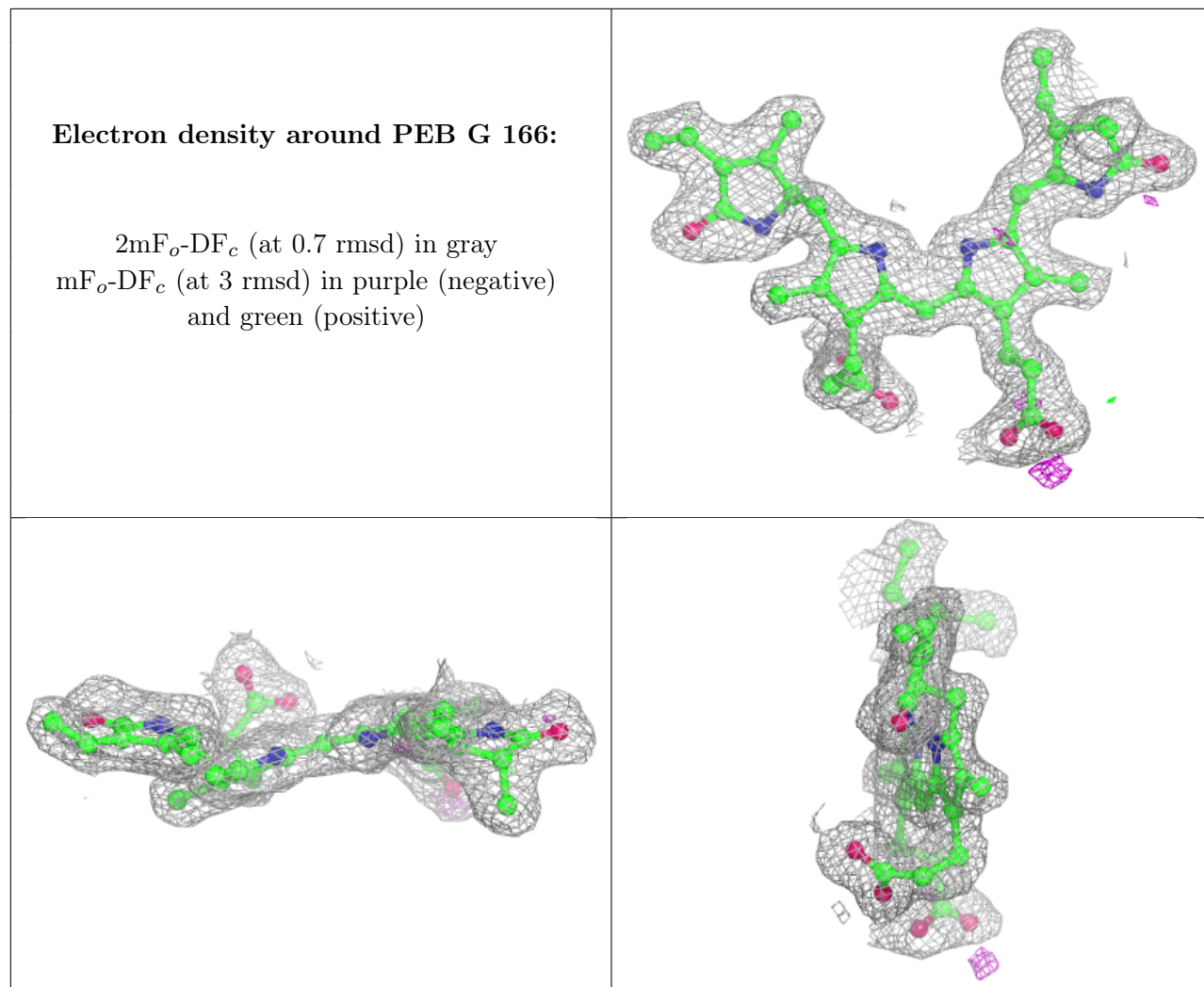
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around PEB F 166:

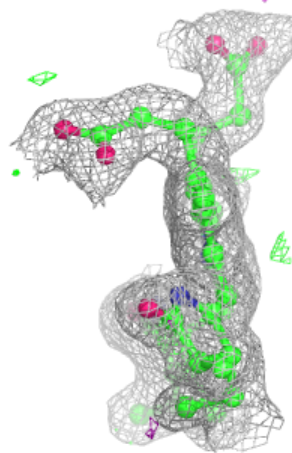
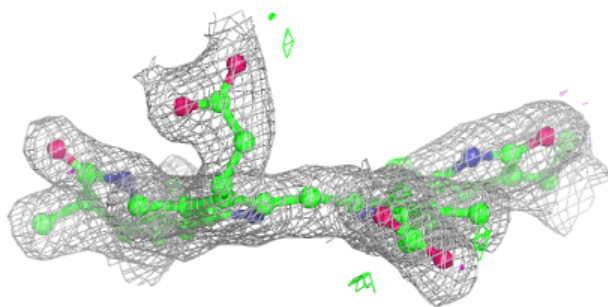
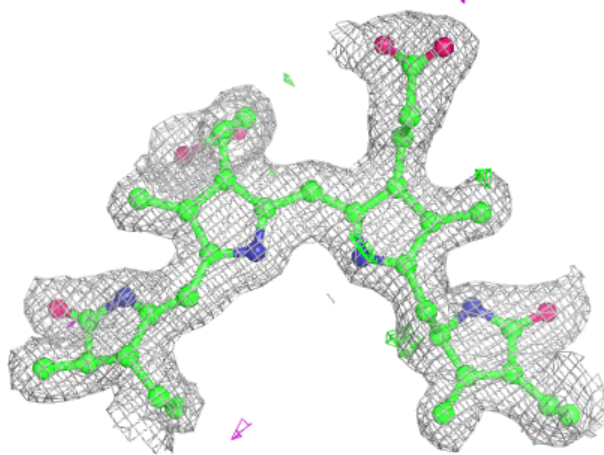
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





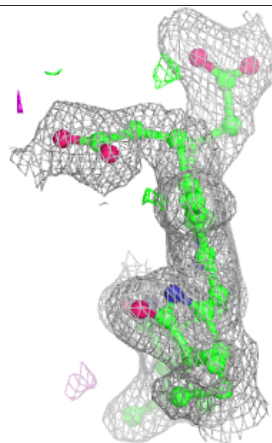
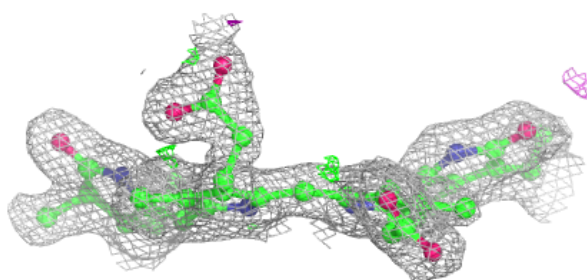
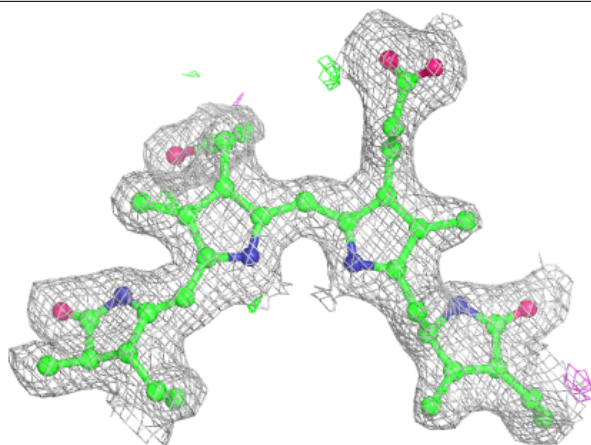
Electron density around PEB V 188:

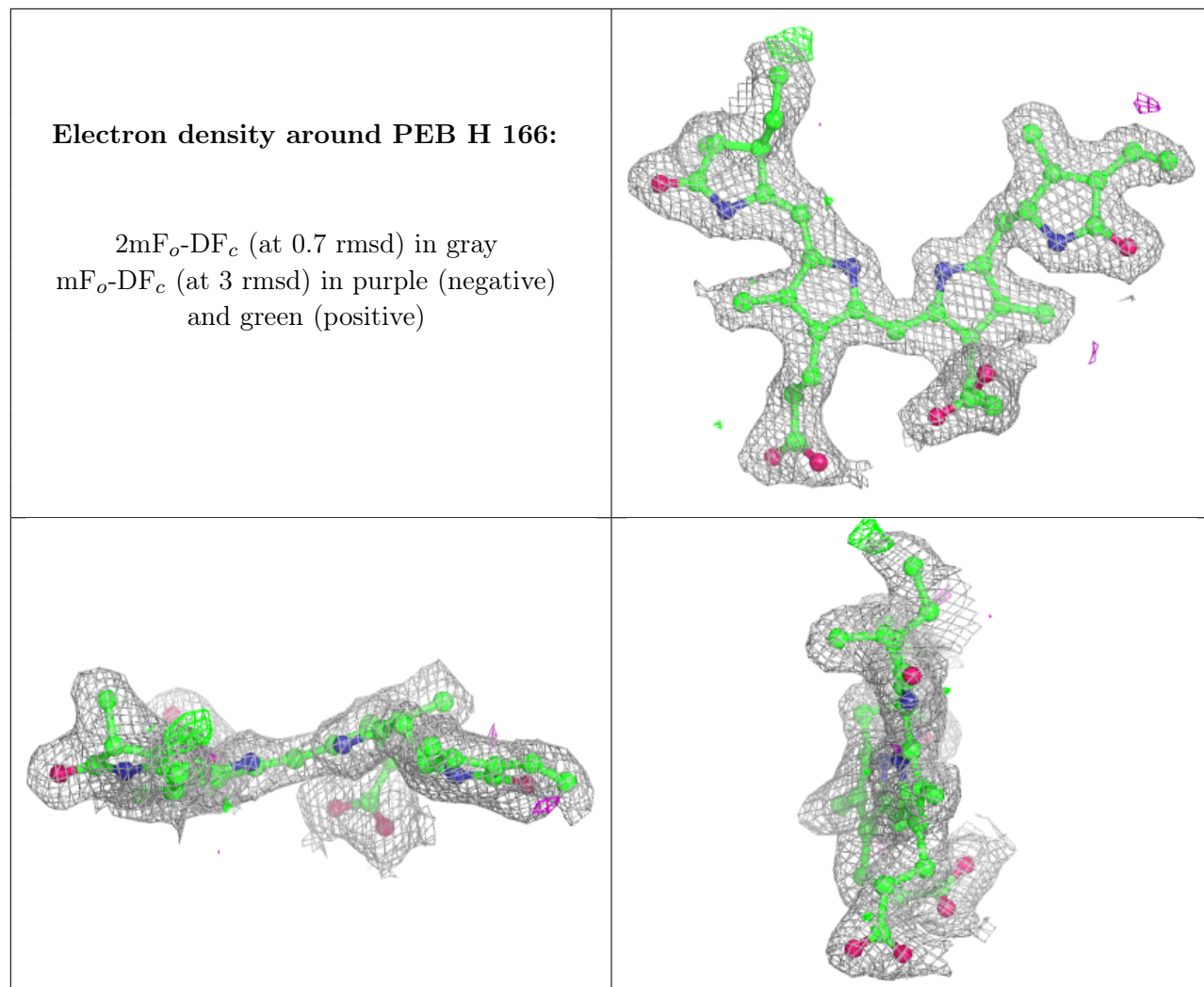
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around PEB Q 188:

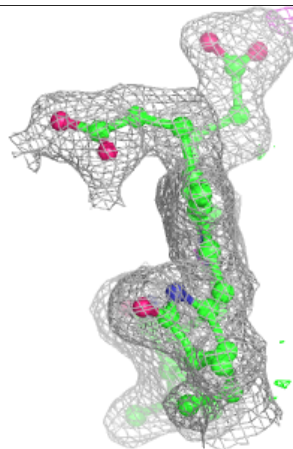
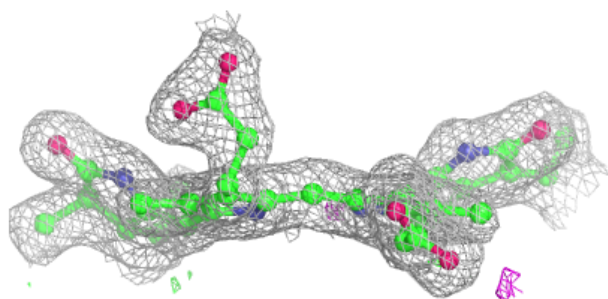
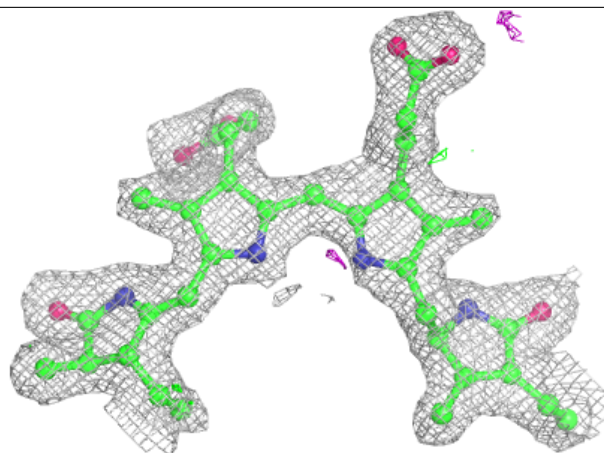
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





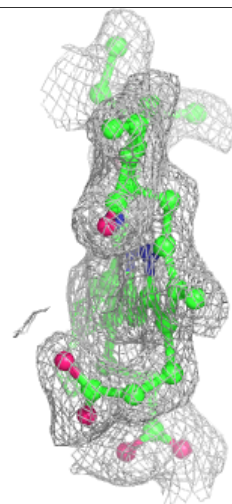
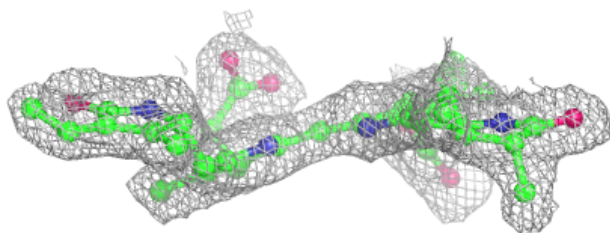
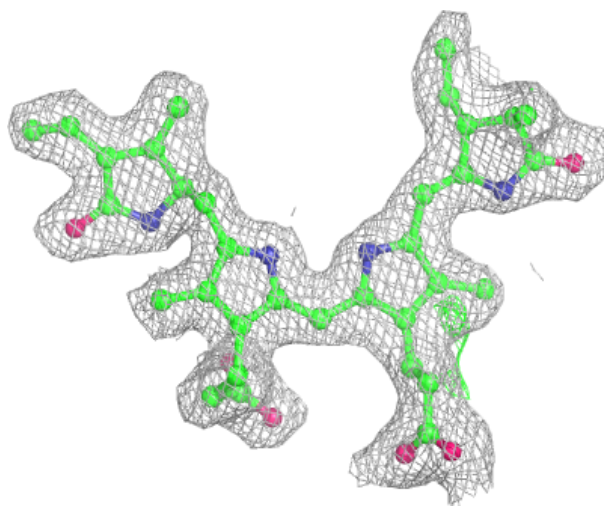
Electron density around PEB W 188:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



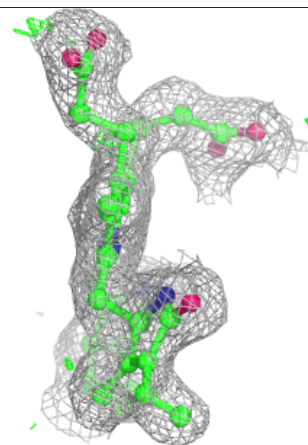
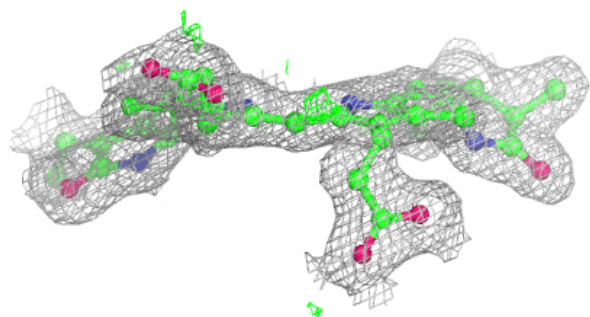
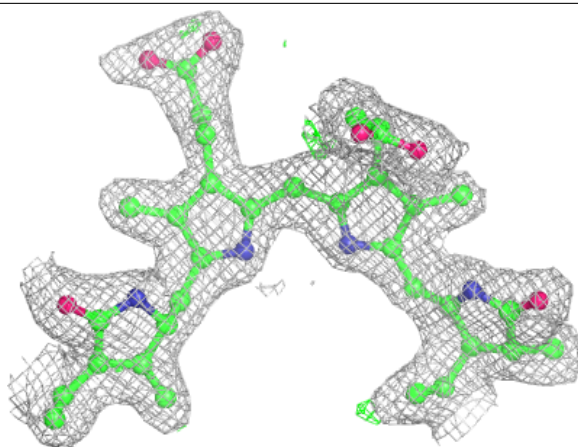
Electron density around PEB I 166:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



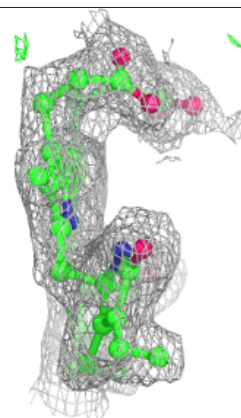
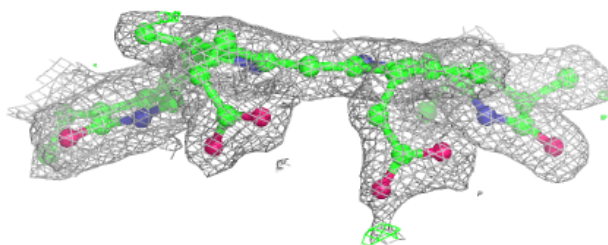
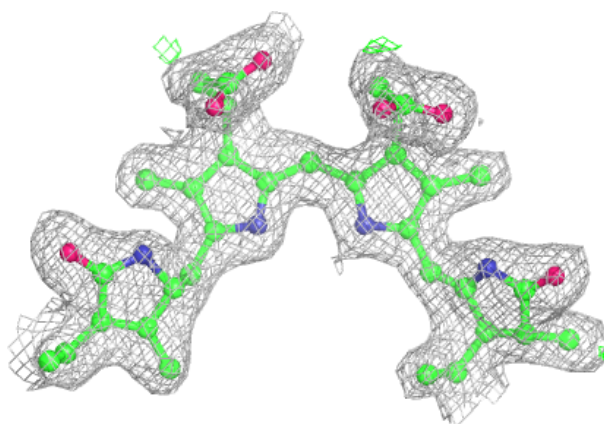
Electron density around PEB R 188:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

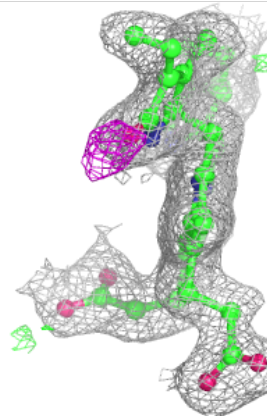
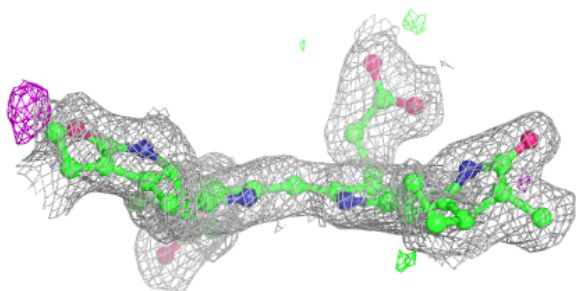
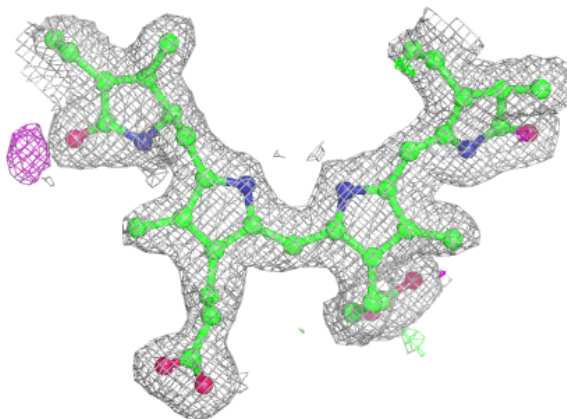


Electron density around PEB X 188:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

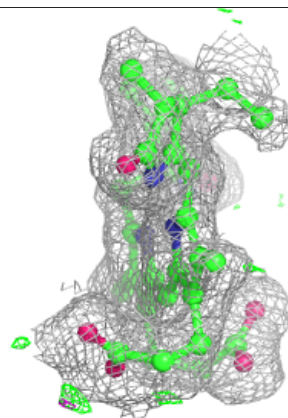
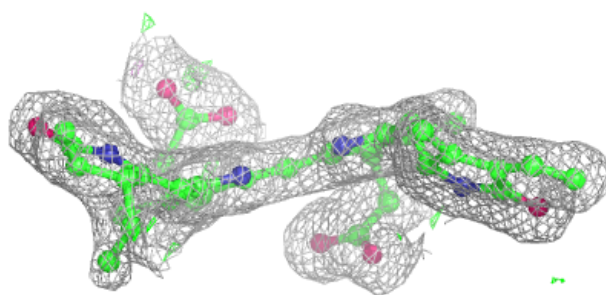
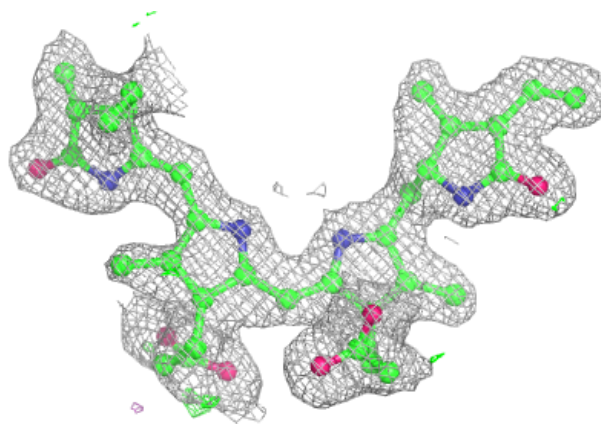
**Electron density around PEB N 188:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



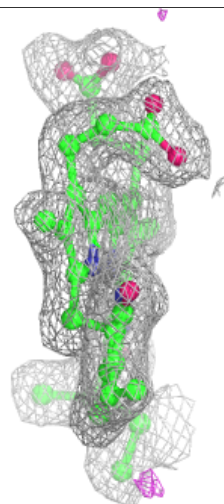
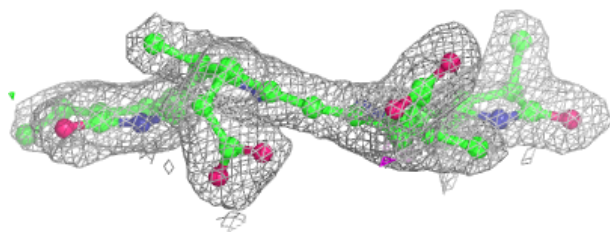
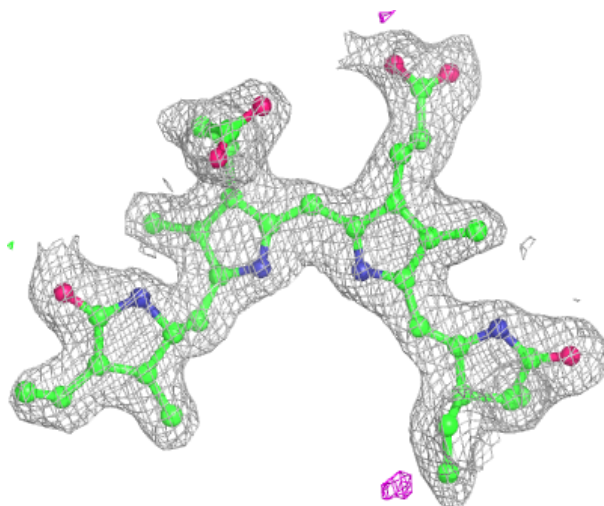
Electron density around PEB B 167:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



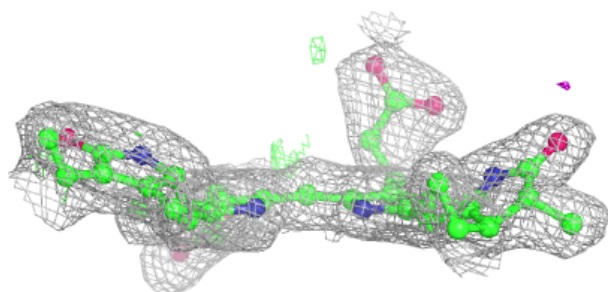
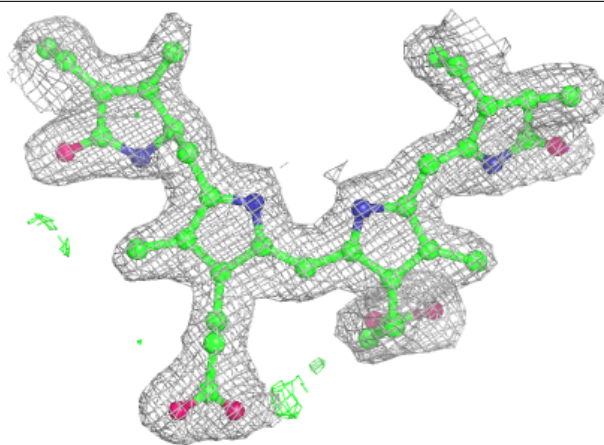
Electron density around PEB D 166:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

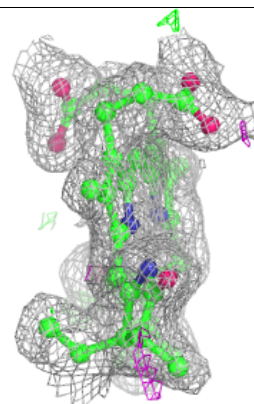
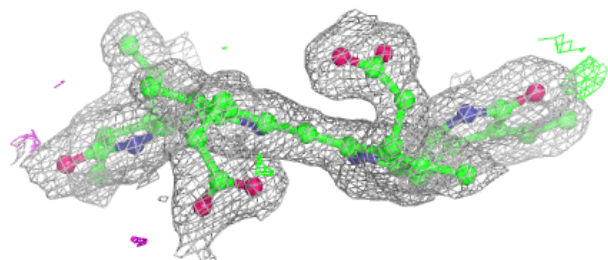
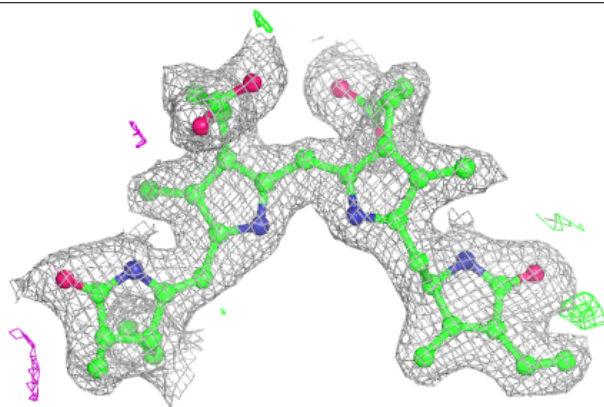


Electron density around PEB O 188:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

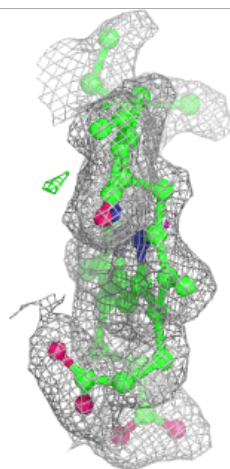
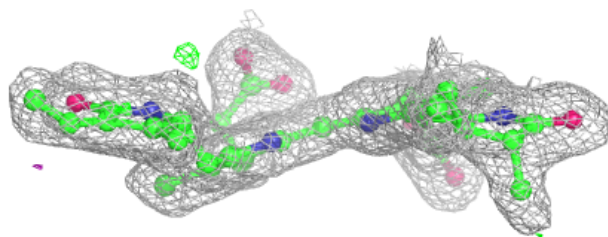
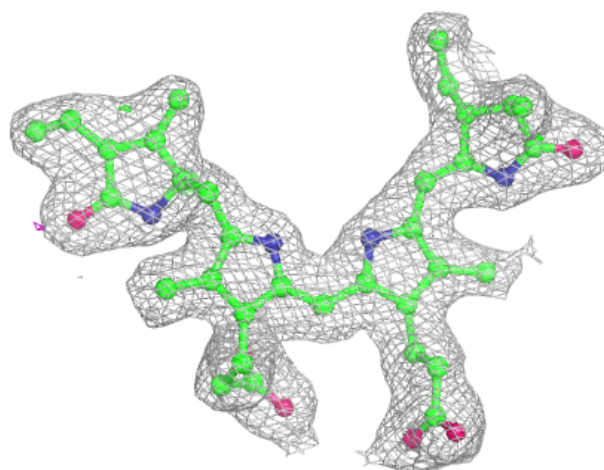
**Electron density around PEB F 167:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



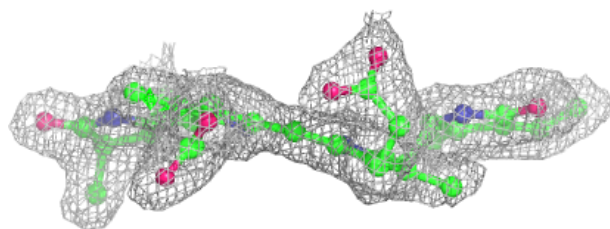
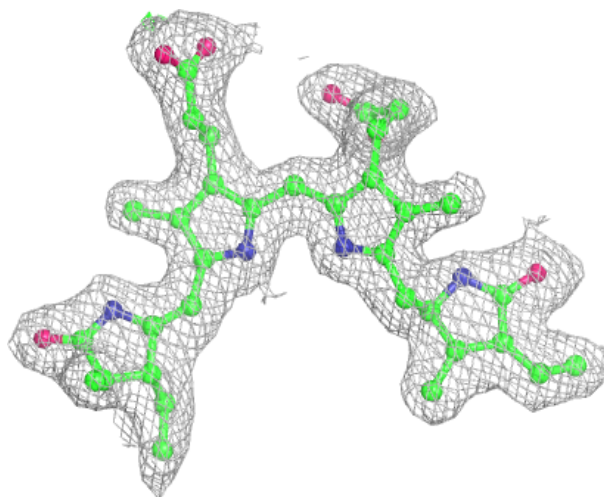
Electron density around PEB J 166:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



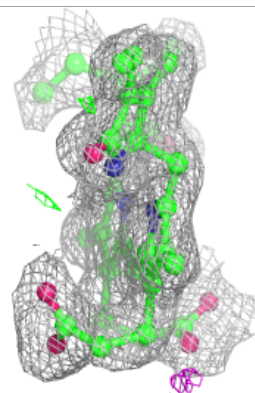
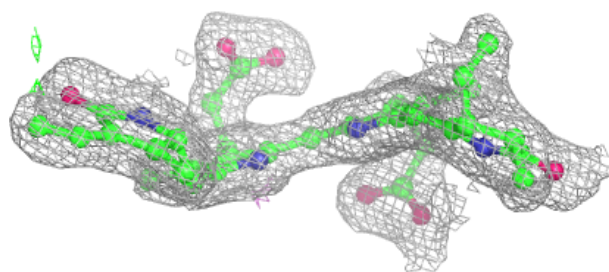
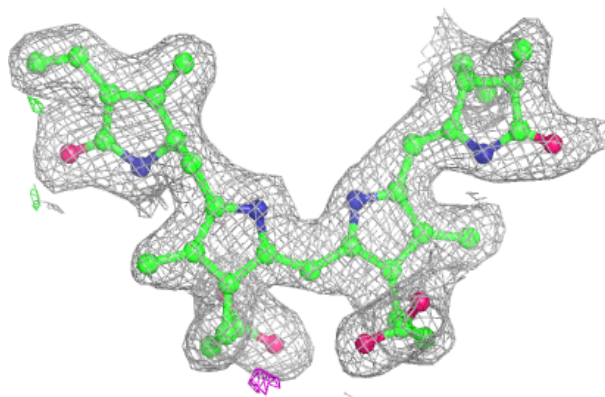
Electron density around PEB B 166:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

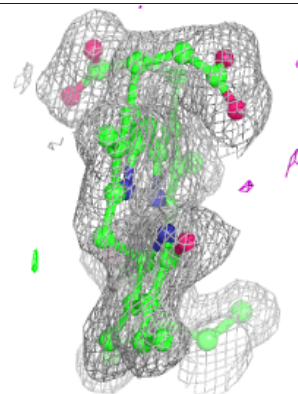
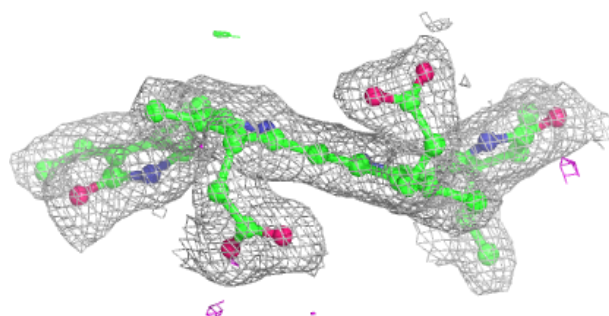
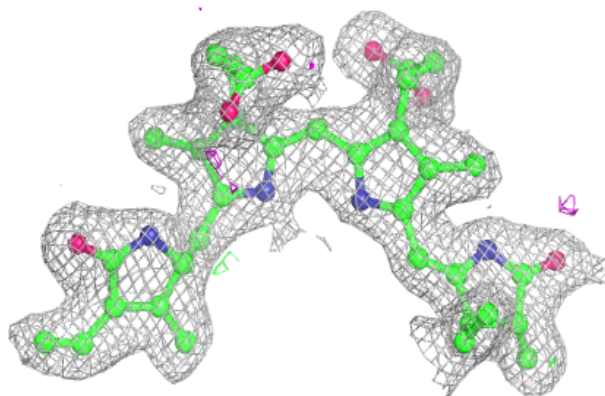


Electron density around PEB G 167:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

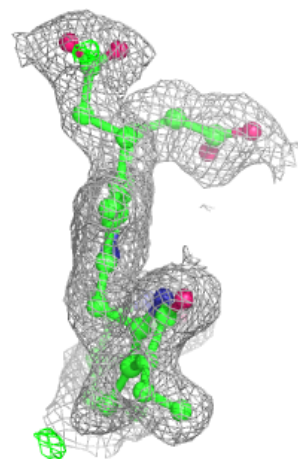
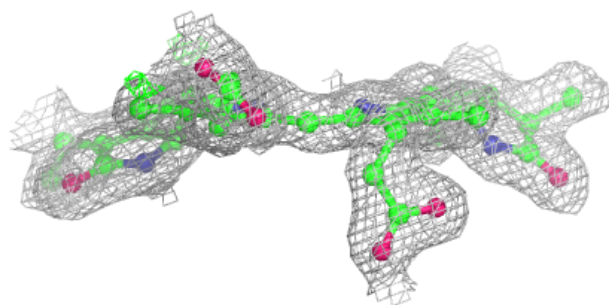
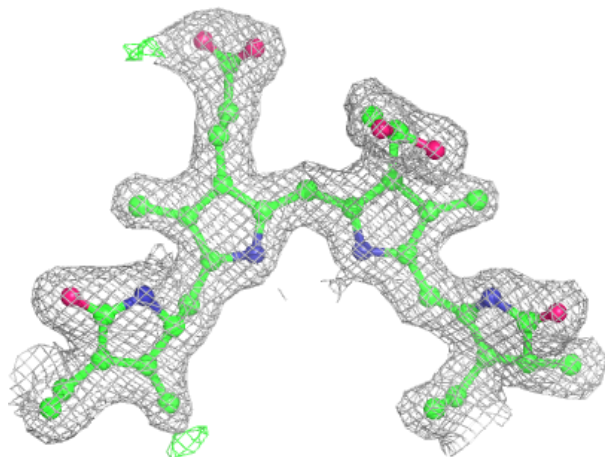
**Electron density around PEB E 167:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



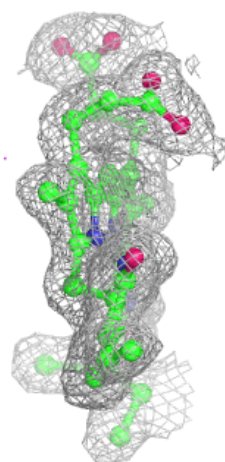
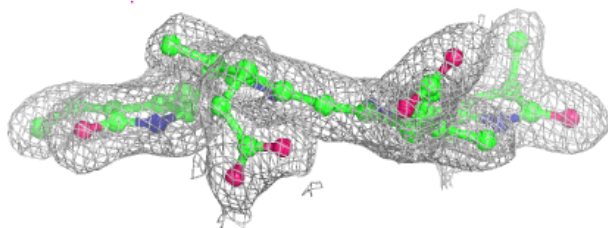
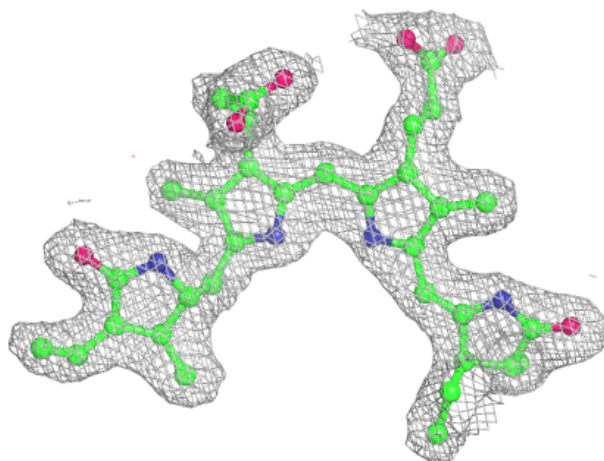
Electron density around PEB S 188:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



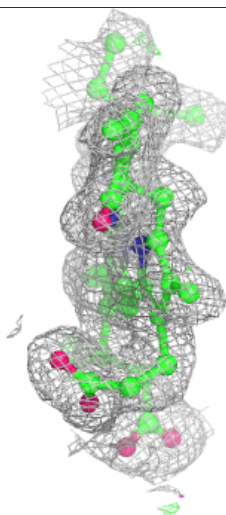
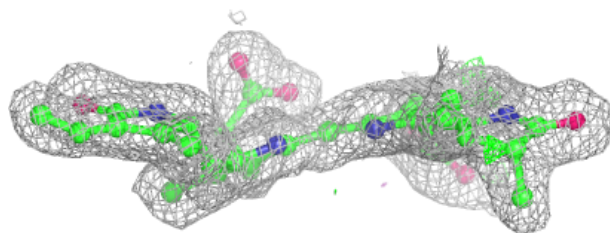
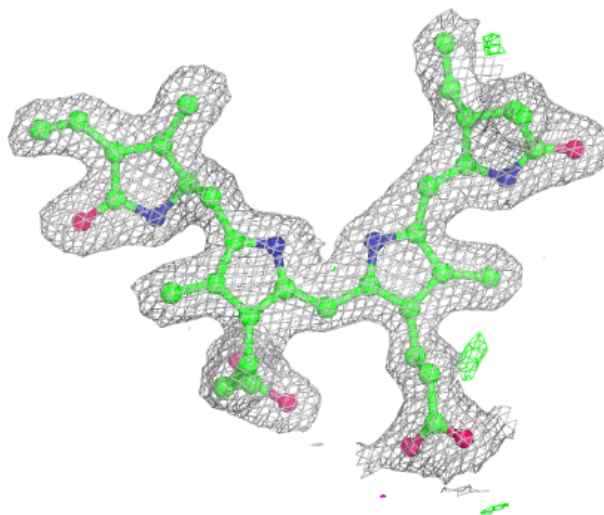
Electron density around PEB L 166:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



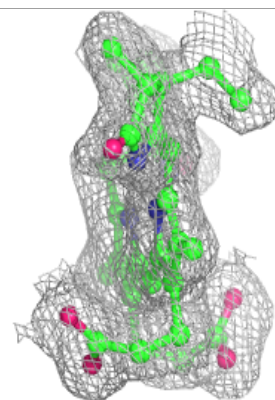
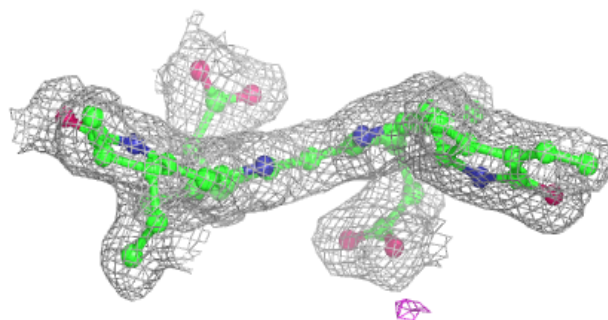
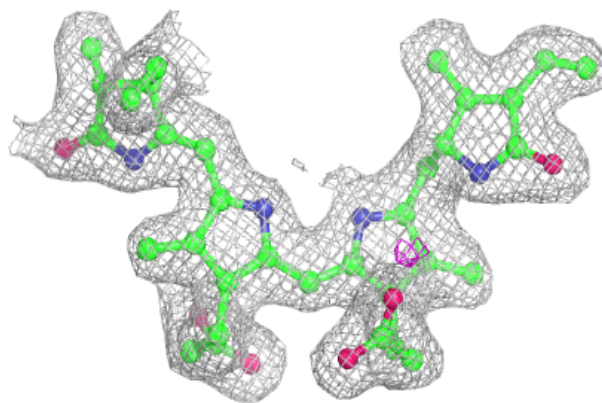
Electron density around PEB A 166:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

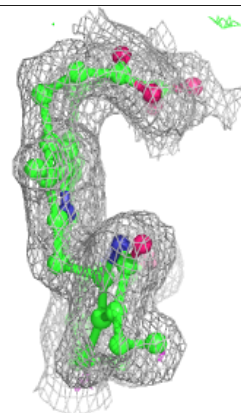
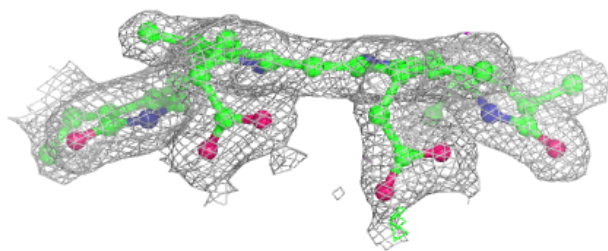
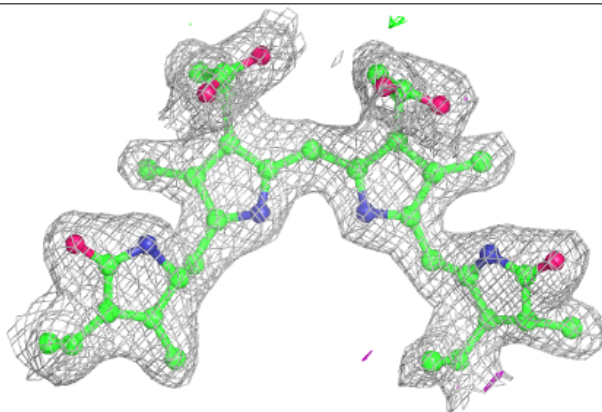


Electron density around PEB H 167:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around PEB M 188:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.