



wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 28, 2021 – 12:14 PM JST

PDB ID : 7E1I
Title : Crystal structure of Pr55Gag-matrix domain in complex with IP6 at ambient temperature in space group P1
Authors : DeMirici, H.; Destan, E.
Deposited on : 2021-02-01
Resolution : 3.30 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.22
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) : 2.22

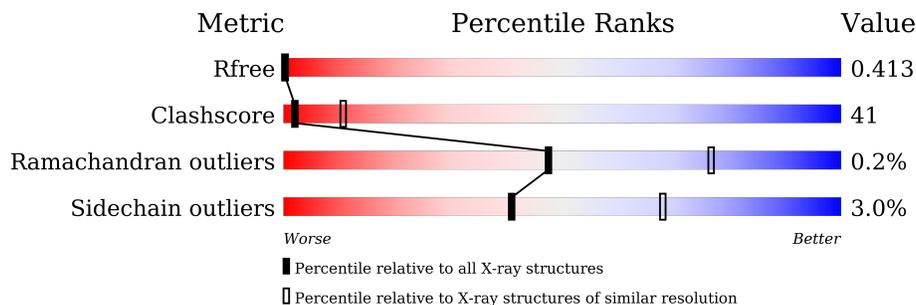
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	121	38% 60% ..
1	B	121	43% 56% .
1	C	121	30% 68% .
1	D	121	43% 55% .
1	E	121	30% 65% ..
1	F	121	45% 55%
1	G	121	36% 61% .

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Mol	Chain	Length	Quality of chain
1	H	121	 37% 59%
1	I	121	 39% 60%
1	J	121	 34% 64%
1	K	121	 31% 66%
1	L	121	 40% 58%

2 Entry composition [i](#)

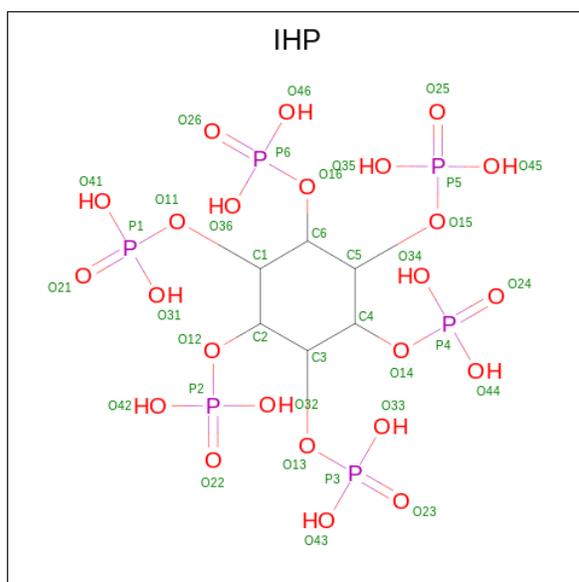
There are 2 unique types of molecules in this entry. The entry contains 11919 atoms, of which 72 are hydrogens and 0 are deuteriums.

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 Capsid protein p24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	121	952	593	173	184	2	0	1	1
1	B	121	952	593	173	184	2	0	1	1
1	C	121	952	593	173	184	2	0	1	1
1	D	121	952	593	173	184	2	0	1	1
1	E	119	943	588	171	182	2	0	1	0
1	F	121	952	593	173	184	2	0	1	1
1	G	121	952	593	173	184	2	0	1	1
1	H	121	952	593	173	184	2	0	1	1
1	I	121	952	593	173	184	2	0	1	1
1	J	121	952	593	173	184	2	0	1	1
1	K	121	952	593	173	184	2	0	1	1
1	L	121	952	593	173	184	2	0	1	1

- Molecule 2 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: $C_6H_{18}O_{24}P_6$) (labeled as "Ligand of Interest" by depositor).



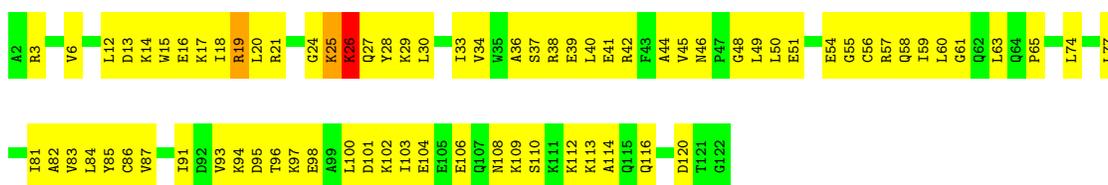
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	H	O			P
2	A	1	42	6	6	24	6	0	0
2	B	1	42	6	6	24	6	0	0
2	C	1	42	6	6	24	6	0	0
2	D	1	42	6	6	24	6	0	0
2	E	1	42	6	6	24	6	0	0
2	E	1	42	6	6	24	6	0	0
2	F	1	42	6	6	24	6	0	0
2	G	1	42	6	6	24	6	0	0
2	I	1	42	6	6	24	6	0	0
2	J	1	42	6	6	24	6	0	0
2	K	1	42	6	6	24	6	0	0
2	L	1	42	6	6	24	6	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. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

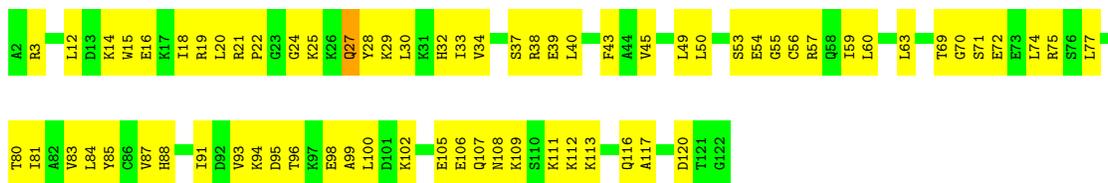
- Molecule 1: Capsid protein p24

Chain A: 



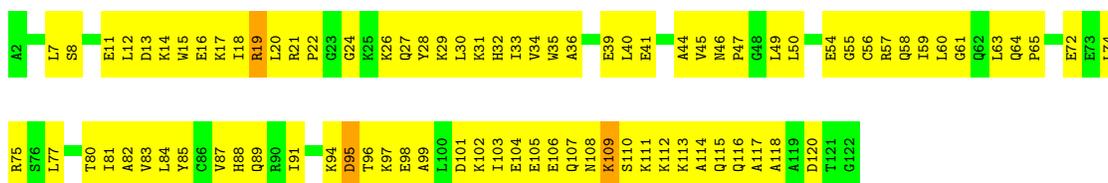
- Molecule 1: Capsid protein p24

Chain B: 



- Molecule 1: Capsid protein p24

Chain C: 



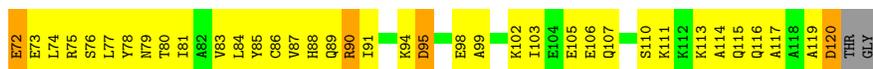
- Molecule 1: Capsid protein p24

Chain D: 





- Molecule 1: Capsid protein p24



- Molecule 1: Capsid protein p24



- Molecule 1: Capsid protein p24



- Molecule 1: Capsid protein p24



- Molecule 1: Capsid protein p24





• Molecule 1: Capsid protein p24



• Molecule 1: Capsid protein p24



• Molecule 1: Capsid protein p24



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	96.60Å 96.60Å 91.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.57 – 3.30 40.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	83.4 (24.57-3.30) 61.9 (40.00-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.80 (at 2.51Å)	Xtriage
Refinement program	PHENIX DEV-3318	Depositor
R, R_{free}	0.351 , 0.408 0.354 , 0.413	Depositor DCC
R_{free} test set	1993 reflections (3.26%)	wwPDB-VP
Wilson B-factor (Å ²)	25.9	Xtriage
Anisotropy	0.257	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 184.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.388 for h+k,-h,l 0.388 for -k,h+k,l 0.388 for k,-h-k,l 0.388 for -h-k,h,l 0.407 for -h,-k,l 0.388 for h,-h-k,-l 0.397 for -h-k,k,-l 0.398 for k,h,-l 0.397 for -k,-h,-l 0.387 for -h,h+k,-l 0.398 for h+k,-k,-l	Xtriage
F_o, F_c correlation	0.77	EDS
Total number of atoms	11919	wwPDB-VP
Average B, all atoms (Å ²)	170.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% 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: IHP

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	0.22	0/964	0.38	0/1295
1	B	0.23	0/964	0.37	0/1295
1	C	0.22	0/964	0.38	0/1295
1	D	0.23	0/964	0.37	0/1295
1	E	0.22	0/955	0.37	0/1282
1	F	0.22	0/964	0.37	0/1295
1	G	0.22	0/964	0.38	0/1295
1	H	0.22	0/964	0.38	0/1295
1	I	0.22	0/964	0.37	0/1295
1	J	0.22	0/964	0.37	0/1295
1	K	0.22	0/964	0.37	0/1295
1	L	0.22	0/964	0.37	0/1295
All	All	0.22	0/11559	0.37	0/15527

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	47	PRO	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	952	0	960	86	2
1	B	952	0	960	70	0
1	C	952	0	960	99	2
1	D	952	0	960	77	3
1	E	943	0	952	92	4
1	F	952	0	960	72	2
1	G	952	0	958	83	3
1	H	952	0	960	80	2
1	I	952	0	960	81	2
1	J	952	0	960	76	2
1	K	952	0	960	96	0
1	L	952	0	960	72	1
2	A	36	6	6	0	1
2	B	36	6	6	0	2
2	C	36	6	6	1	1
2	D	36	6	6	0	2
2	E	72	12	12	0	1
2	F	36	6	6	0	1
2	G	36	6	6	0	2
2	I	36	6	6	0	1
2	J	36	6	6	0	1
2	K	36	6	6	0	0
2	L	36	6	6	0	3
All	All	11847	72	11582	952	19

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 41.

The worst 5 of 952 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:19:ARG:HA	1:C:27:GLN:HA	1.20	1.18
1:K:106:GLU:HA	1:K:109:LYS:HB3	1.31	1.11
1:H:49:LEU:HB3	1:H:55:GLY:HA3	1.34	1.09
1:D:19:ARG:HA	1:D:27:GLN:HA	1.26	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:19:ARG:HA	1:A:27:GLN:HA	1.28	1.08

The worst 5 of 19 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:LYS:NZ	2:J:201:IHP:O26[1_545]	1.30	0.90
1:J:26:LYS:NZ	2:A:201:IHP:O26[1_565]	1.30	0.90
1:D:26:LYS:NZ	2:B:201:IHP:O26[1_554]	1.30	0.90
1:D:31:LYS:NZ	2:B:201:IHP:O45[1_554]	1.30	0.90
1:C:26:LYS:NZ	2:L:201:IHP:O26[1_445]	1.30	0.90

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	120/121 (99%)	113 (94%)	6 (5%)	1 (1%)	19	51
1	B	120/121 (99%)	117 (98%)	3 (2%)	0	100	100
1	C	120/121 (99%)	119 (99%)	1 (1%)	0	100	100
1	D	120/121 (99%)	118 (98%)	1 (1%)	1 (1%)	19	51
1	E	118/121 (98%)	113 (96%)	5 (4%)	0	100	100
1	F	120/121 (99%)	118 (98%)	2 (2%)	0	100	100
1	G	120/121 (99%)	116 (97%)	4 (3%)	0	100	100
1	H	120/121 (99%)	112 (93%)	7 (6%)	1 (1%)	19	51
1	I	120/121 (99%)	115 (96%)	5 (4%)	0	100	100
1	J	120/121 (99%)	116 (97%)	4 (3%)	0	100	100
1	K	120/121 (99%)	117 (98%)	3 (2%)	0	100	100
1	L	120/121 (99%)	119 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1438/1452 (99%)	1393 (97%)	42 (3%)	3 (0%)	47 77

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	26	LYS
1	D	121	THR
1	H	48	GLY

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	100/102 (98%)	96 (96%)	4 (4%)	31 61
1	B	100/102 (98%)	98 (98%)	2 (2%)	55 76
1	C	100/102 (98%)	95 (95%)	5 (5%)	24 55
1	D	100/102 (98%)	96 (96%)	4 (4%)	31 61
1	E	99/102 (97%)	95 (96%)	4 (4%)	31 61
1	F	100/102 (98%)	100 (100%)	0	100 100
1	G	100/102 (98%)	96 (96%)	4 (4%)	31 61
1	H	100/102 (98%)	93 (93%)	7 (7%)	15 43
1	I	100/102 (98%)	99 (99%)	1 (1%)	76 86
1	J	100/102 (98%)	98 (98%)	2 (2%)	55 76
1	K	100/102 (98%)	97 (97%)	3 (3%)	41 68
1	L	100/102 (98%)	97 (97%)	3 (3%)	41 68
All	All	1199/1224 (98%)	1160 (97%)	39 (3%)	41 66

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	102	LYS

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Mol	Chain	Res	Type
1	K	106	GLU
1	H	105	GLU
1	J	106	GLU
1	L	31	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	88	HIS
1	E	64	GLN
1	F	88	HIS
1	K	79	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

12 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	IHP	E	202	-	36,36,36	1.49	6 (16%)	54,60,60	0.64	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	IHP	D	201	-	36,36,36	1.49	6 (16%)	54,60,60	0.76	2 (3%)
2	IHP	J	201	-	36,36,36	1.49	6 (16%)	54,60,60	0.87	2 (3%)
2	IHP	I	201	-	36,36,36	1.42	6 (16%)	54,60,60	1.01	3 (5%)
2	IHP	C	201	-	36,36,36	1.52	6 (16%)	54,60,60	0.73	1 (1%)
2	IHP	E	201	-	36,36,36	1.44	6 (16%)	54,60,60	0.97	2 (3%)
2	IHP	F	201	-	36,36,36	1.51	6 (16%)	54,60,60	0.65	0
2	IHP	G	201	-	36,36,36	1.52	6 (16%)	54,60,60	0.63	0
2	IHP	L	201	-	36,36,36	1.46	6 (16%)	54,60,60	0.81	3 (5%)
2	IHP	K	201	-	36,36,36	1.45	6 (16%)	54,60,60	0.97	3 (5%)
2	IHP	A	201	-	36,36,36	1.50	6 (16%)	54,60,60	0.63	0
2	IHP	B	201	-	36,36,36	1.49	6 (16%)	54,60,60	0.77	1 (1%)

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
2	IHP	E	202	-	-	7/30/54/54	0/1/1/1
2	IHP	D	201	-	-	6/30/54/54	0/1/1/1
2	IHP	J	201	-	-	11/30/54/54	0/1/1/1
2	IHP	I	201	-	-	3/30/54/54	0/1/1/1
2	IHP	C	201	-	-	8/30/54/54	0/1/1/1
2	IHP	E	201	-	-	7/30/54/54	0/1/1/1
2	IHP	F	201	-	-	7/30/54/54	0/1/1/1
2	IHP	G	201	-	-	9/30/54/54	0/1/1/1
2	IHP	L	201	-	-	7/30/54/54	0/1/1/1
2	IHP	K	201	-	-	9/30/54/54	0/1/1/1
2	IHP	A	201	-	-	5/30/54/54	0/1/1/1
2	IHP	B	201	-	-	4/30/54/54	0/1/1/1

The worst 5 of 72 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	201	IHP	P3-O13	3.53	1.66	1.59
2	J	201	IHP	P3-O13	3.51	1.65	1.59
2	D	201	IHP	P3-O13	3.49	1.65	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	202	IHP	P3-O13	3.48	1.65	1.59
2	F	201	IHP	P6-O16	3.48	1.65	1.59

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	201	IHP	C3-C2-C1	4.41	120.07	110.41
2	I	201	IHP	C3-C2-C1	4.35	119.94	110.41
2	E	201	IHP	C3-C2-C1	4.19	119.57	110.41
2	E	201	IHP	C6-C1-C2	3.82	118.78	110.41
2	I	201	IHP	C6-C1-C2	3.54	118.16	110.41

There are no chirality outliers.

5 of 83 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	201	IHP	C4-C3-O13-P3
2	A	201	IHP	C3-C4-O14-P4
2	A	201	IHP	C1-O11-P1-O21
2	A	201	IHP	C2-O12-P2-O32
2	A	201	IHP	C3-O13-P3-O43

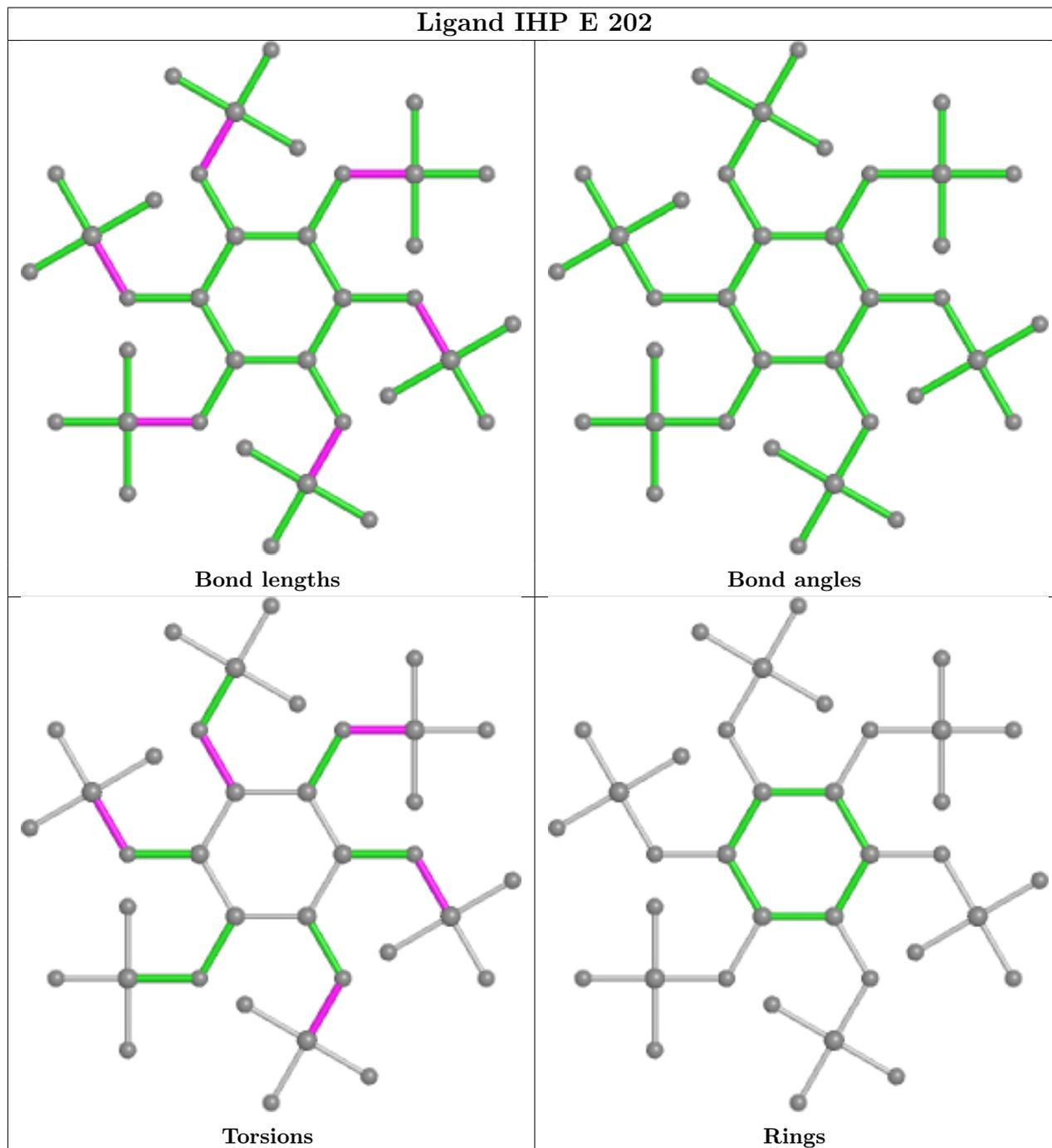
There are no ring outliers.

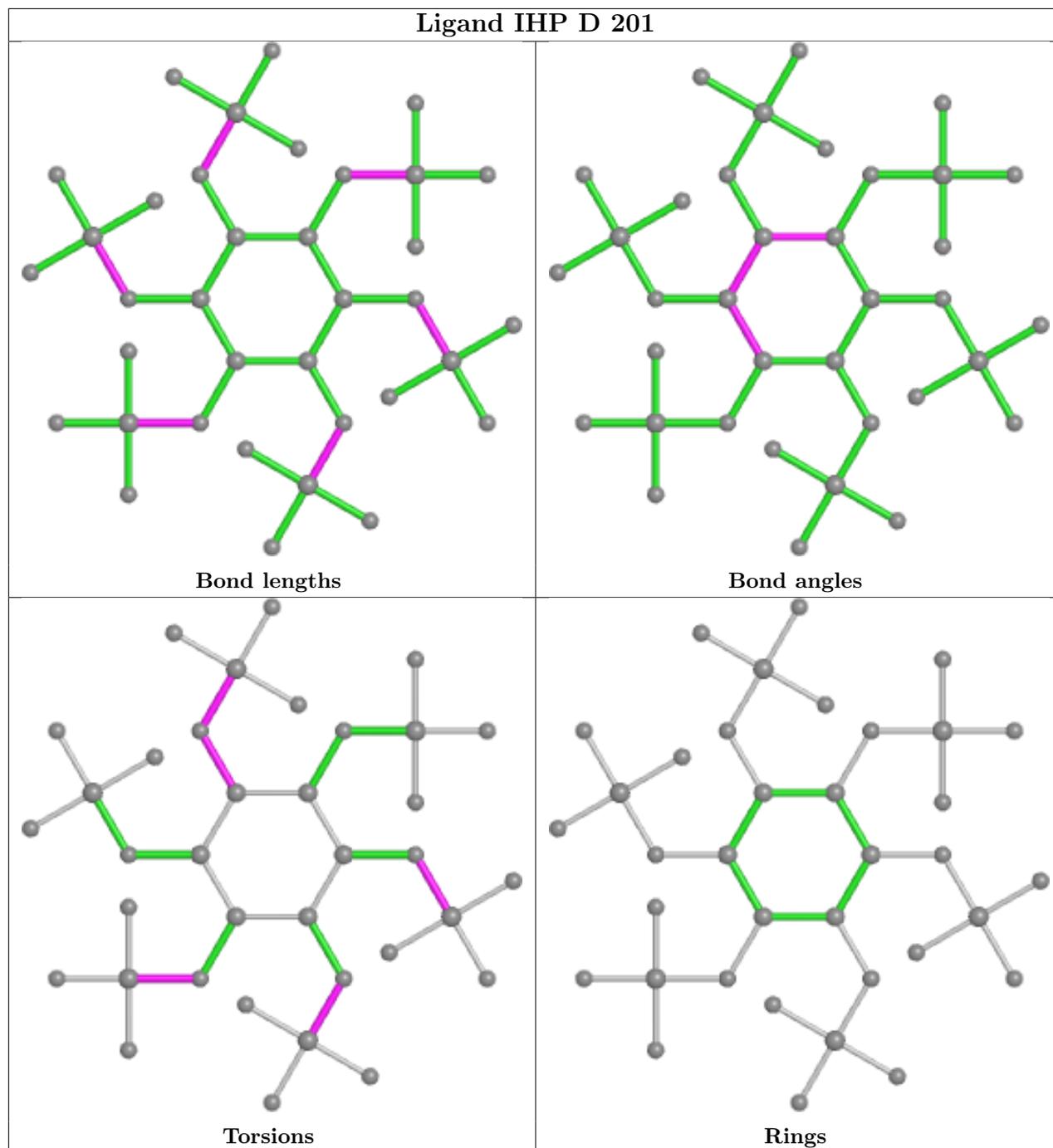
10 monomers are involved in 16 short contacts:

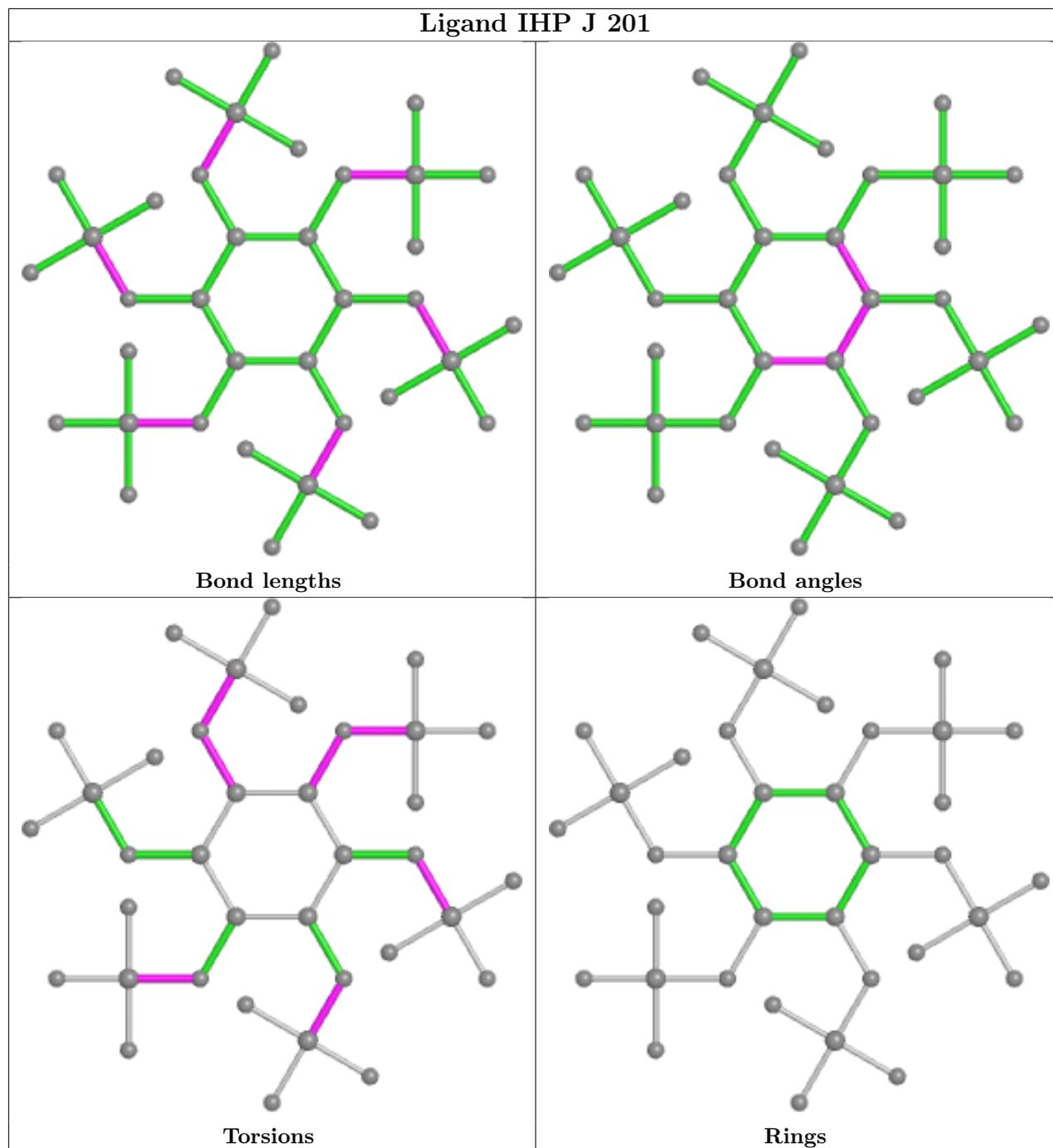
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	201	IHP	0	2
2	J	201	IHP	0	1
2	I	201	IHP	0	1
2	C	201	IHP	1	1
2	E	201	IHP	0	1
2	F	201	IHP	0	1
2	G	201	IHP	0	2
2	L	201	IHP	0	3
2	A	201	IHP	0	1
2	B	201	IHP	0	2

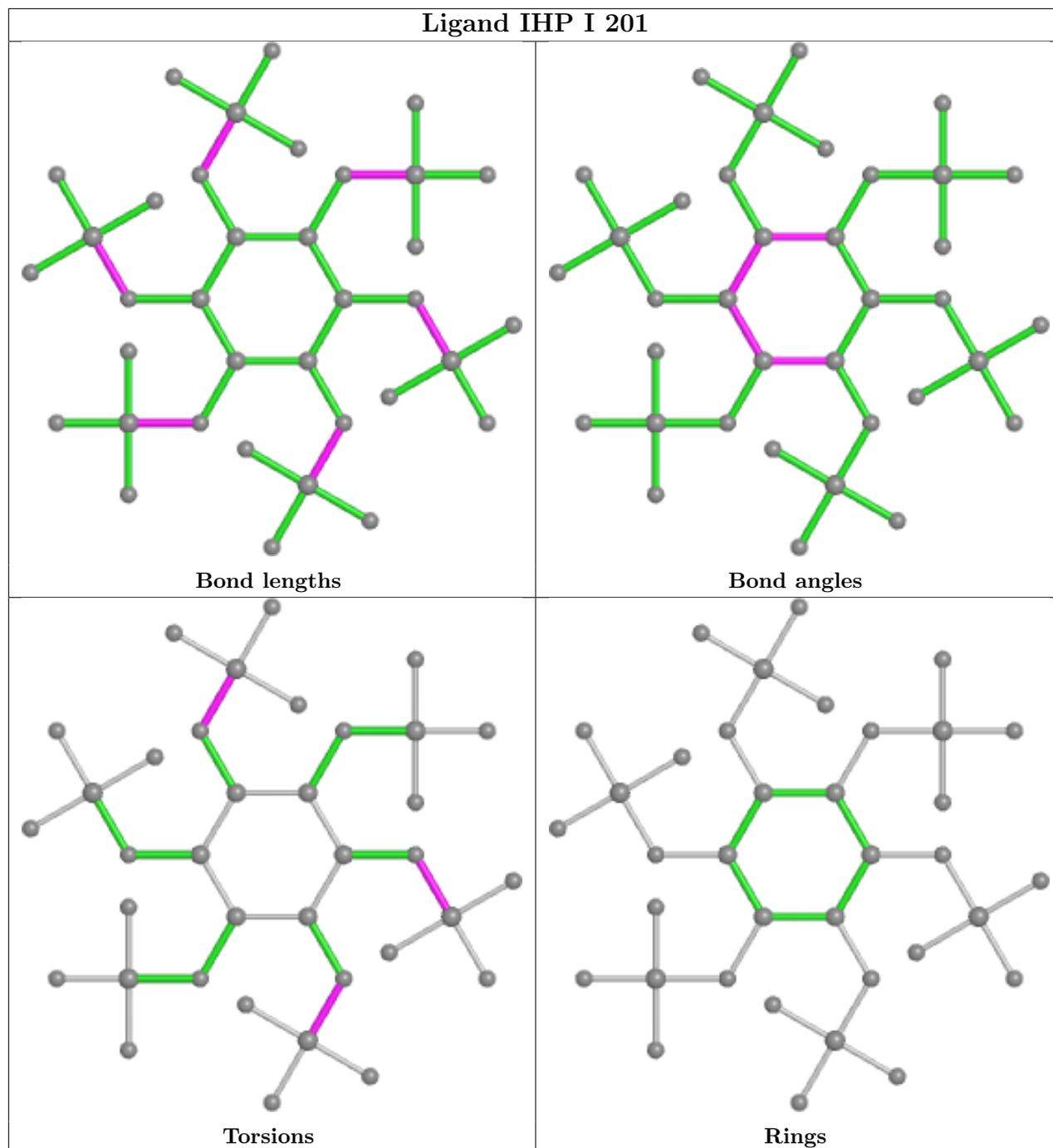
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

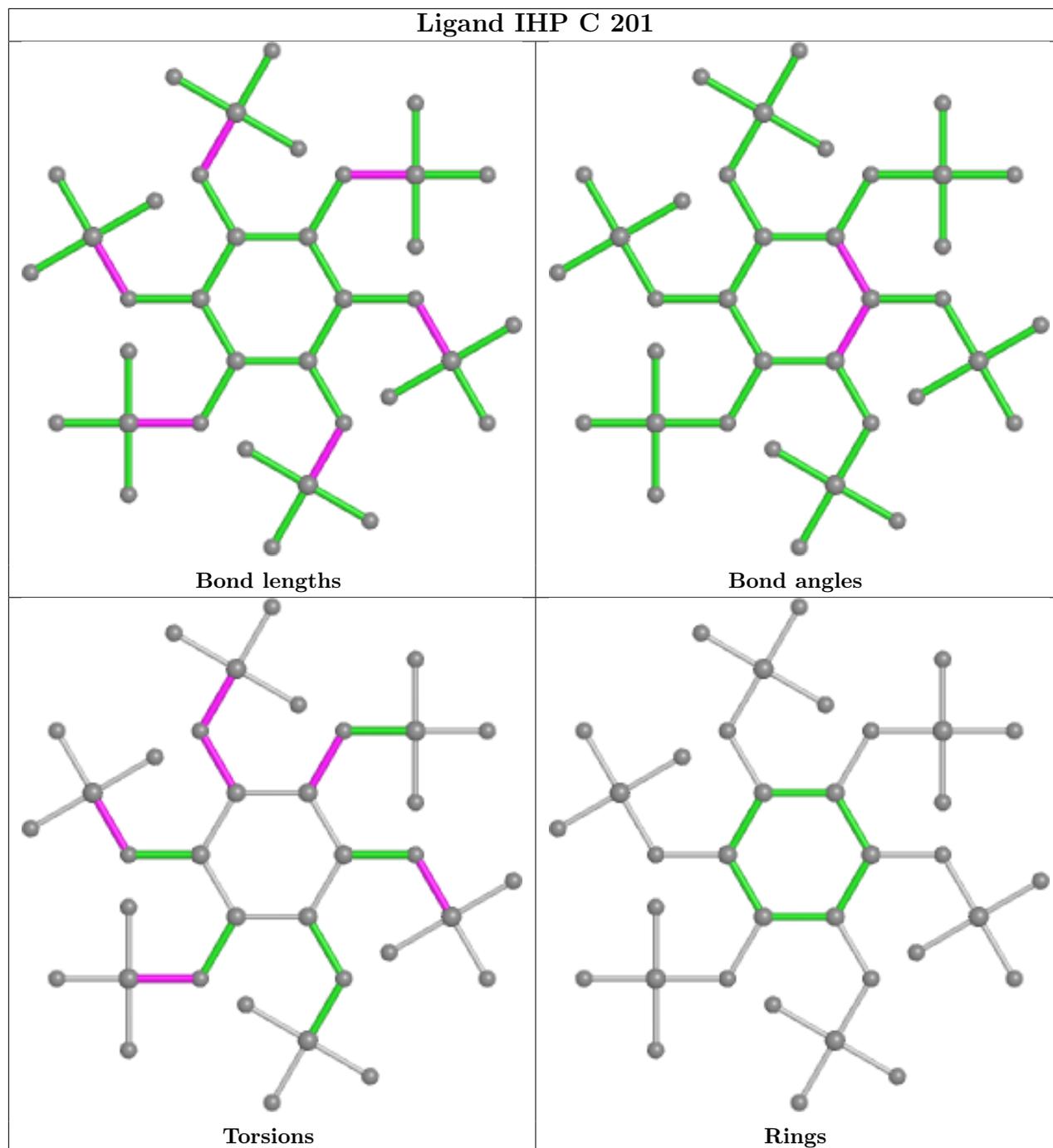
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question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

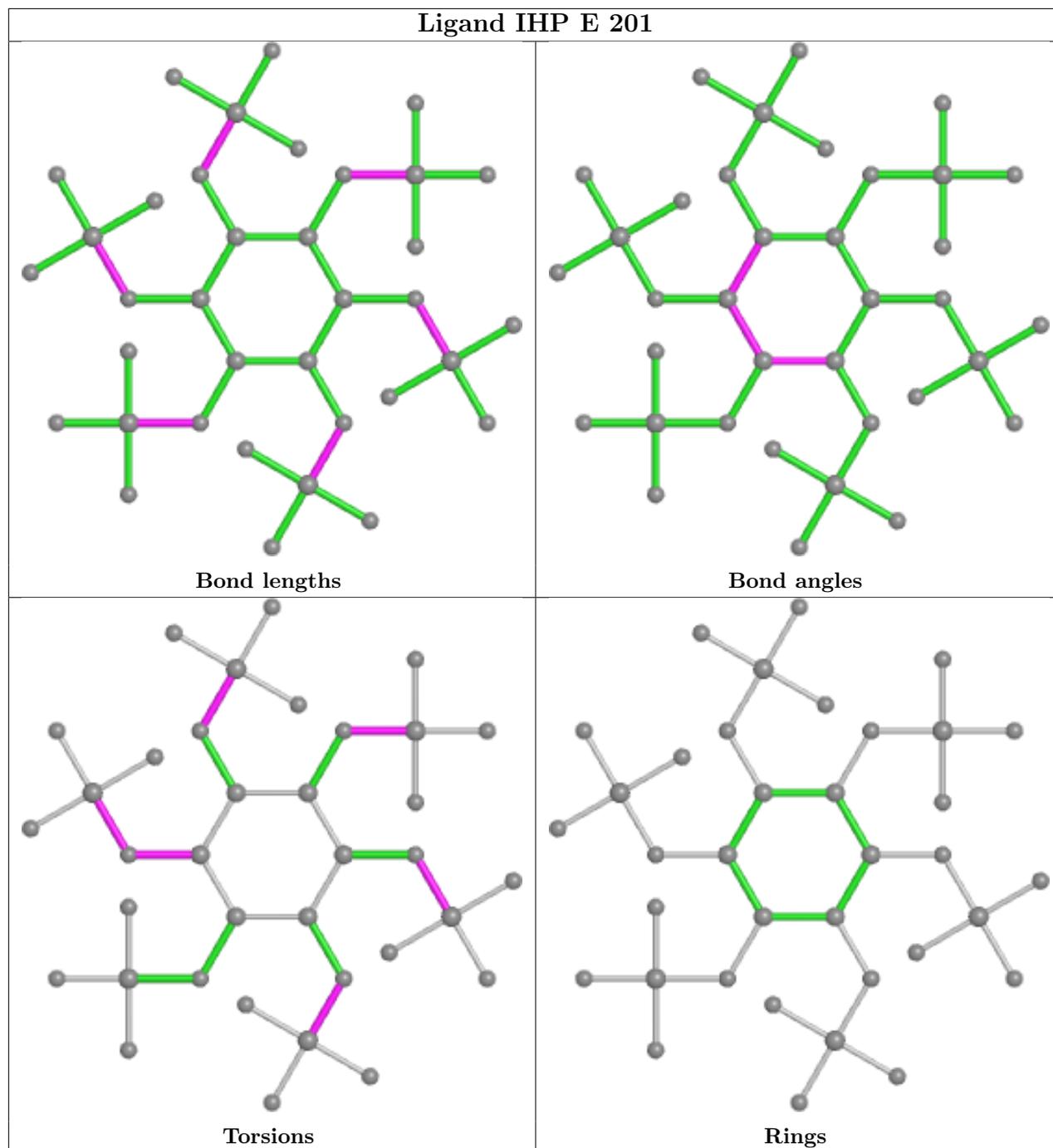


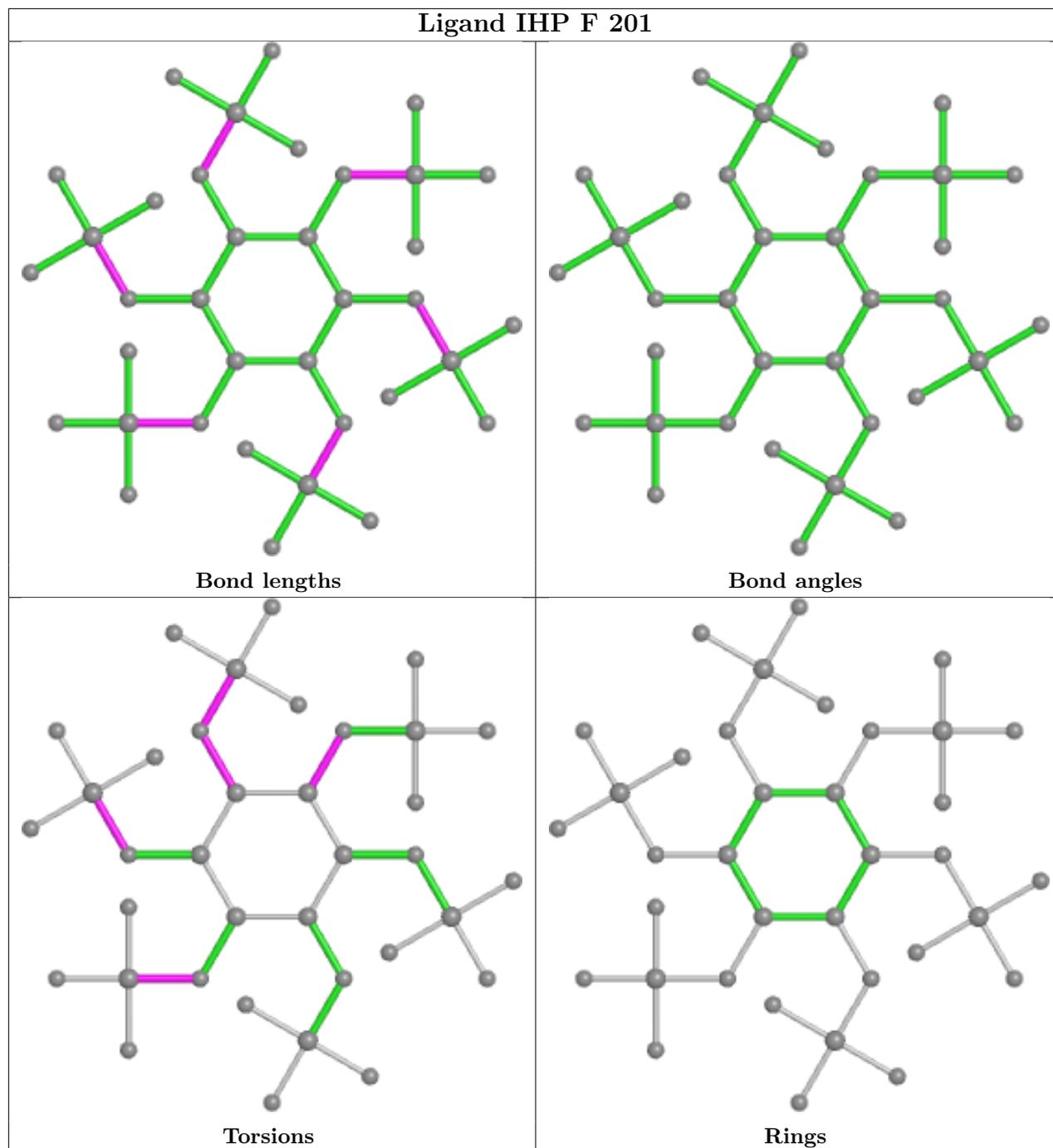


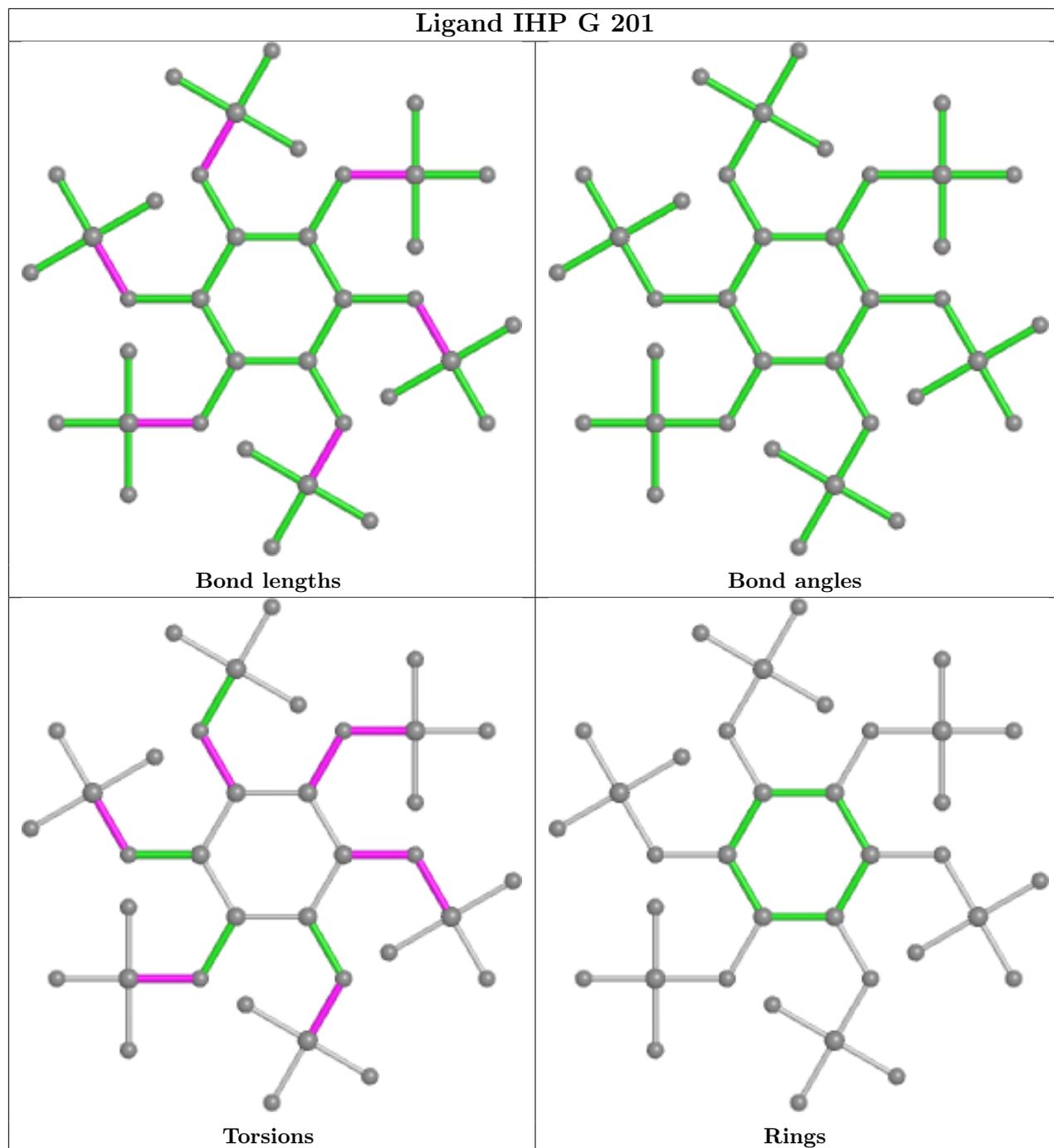


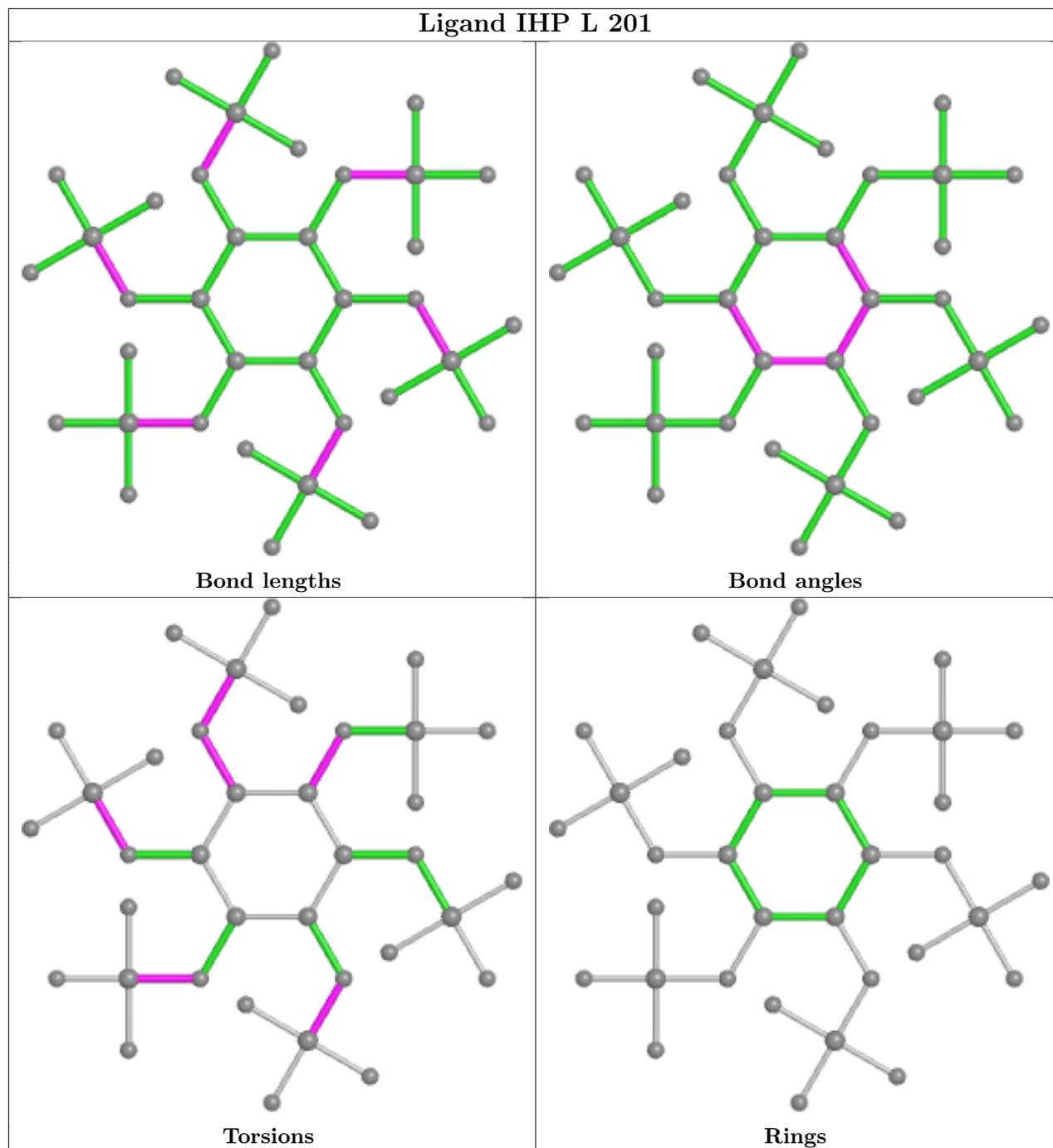


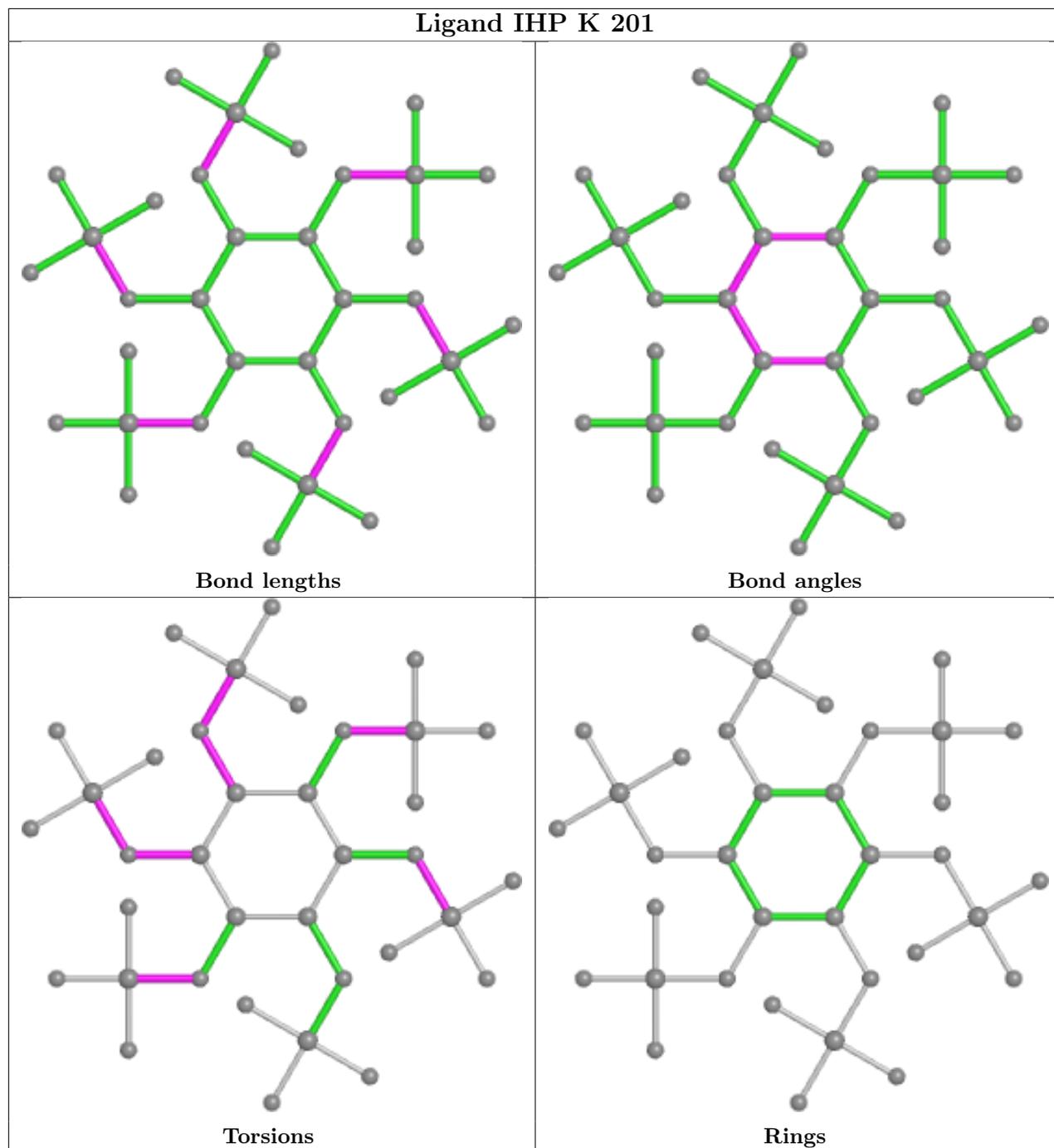


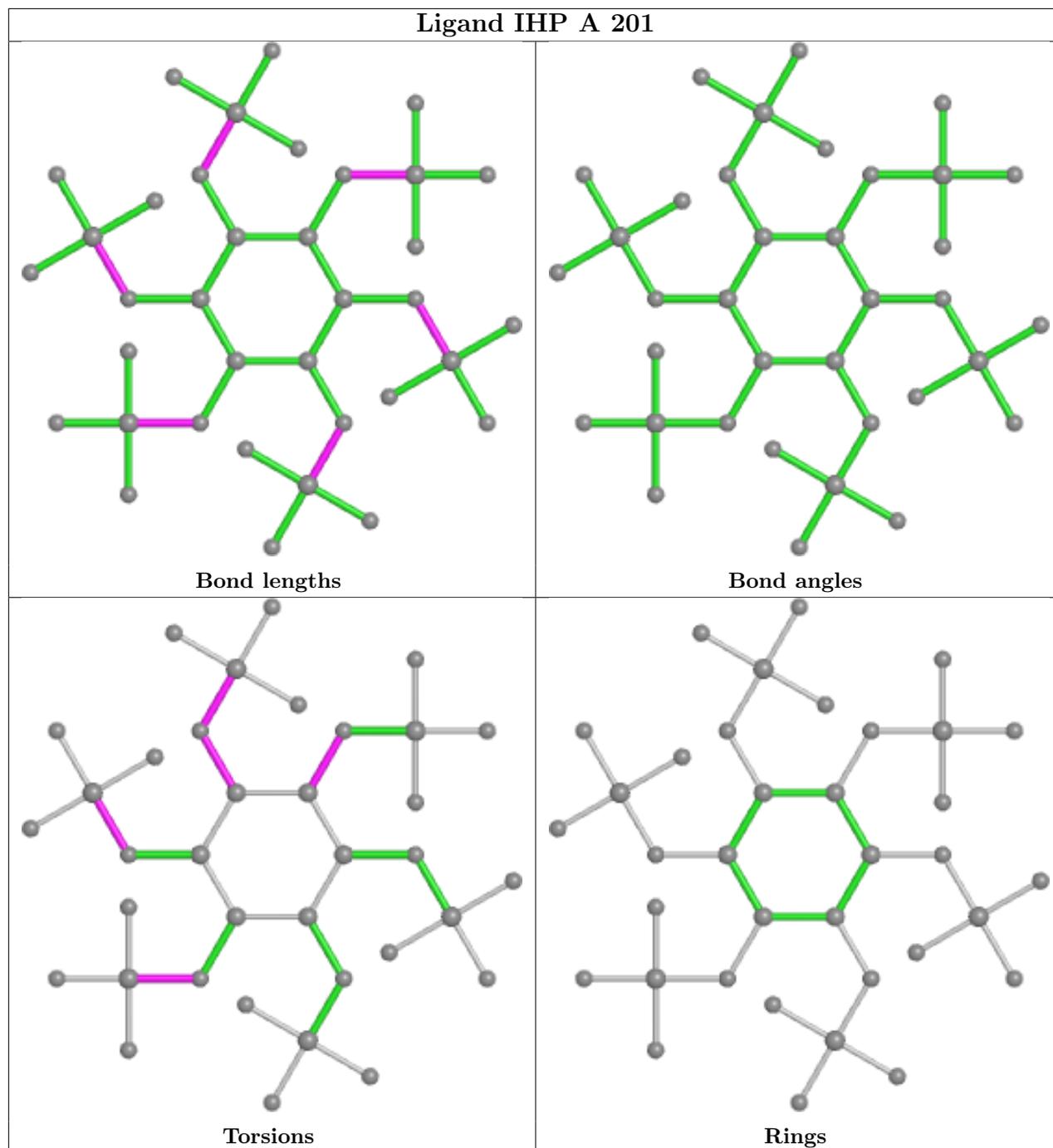


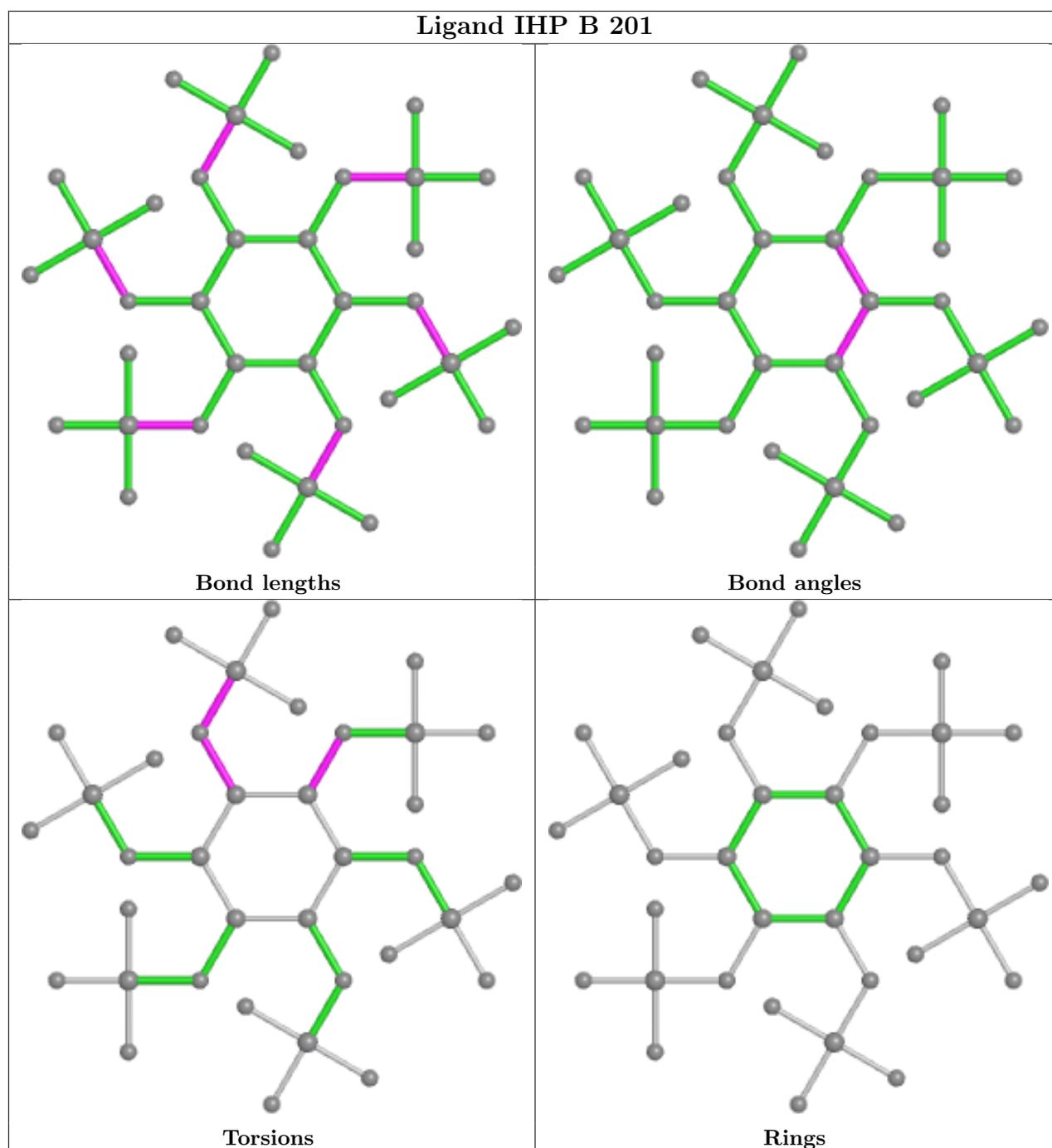












5.7 Other polymers [i](#)

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

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

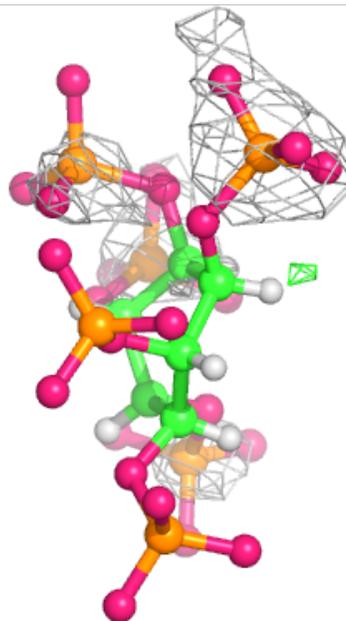
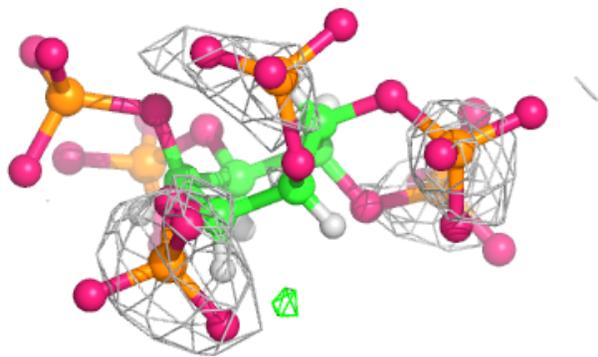
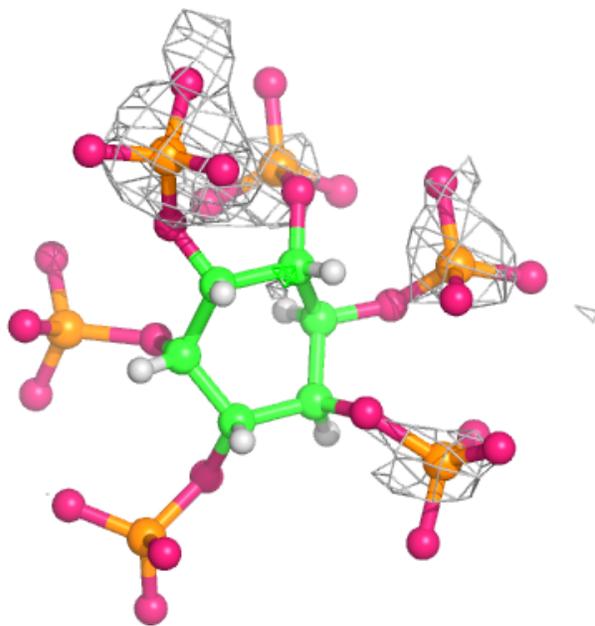
6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

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.

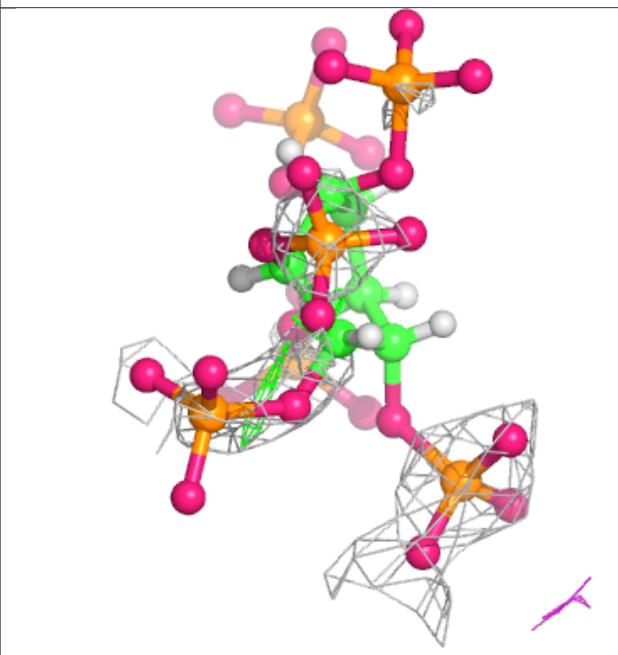
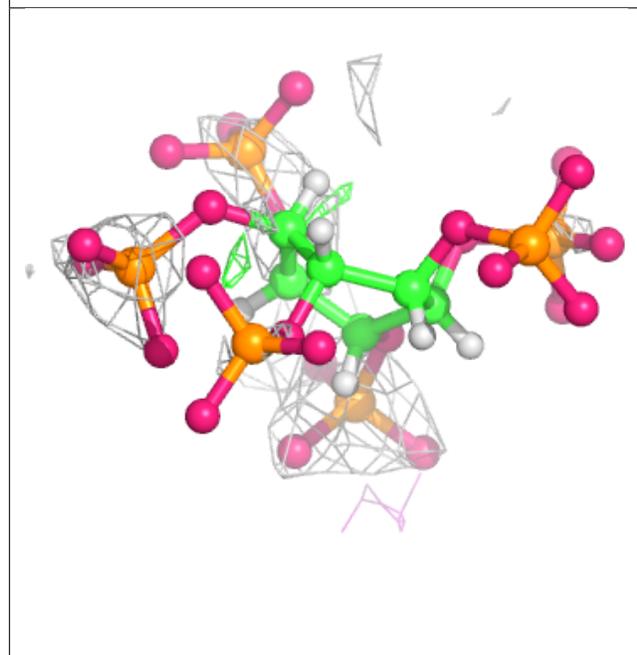
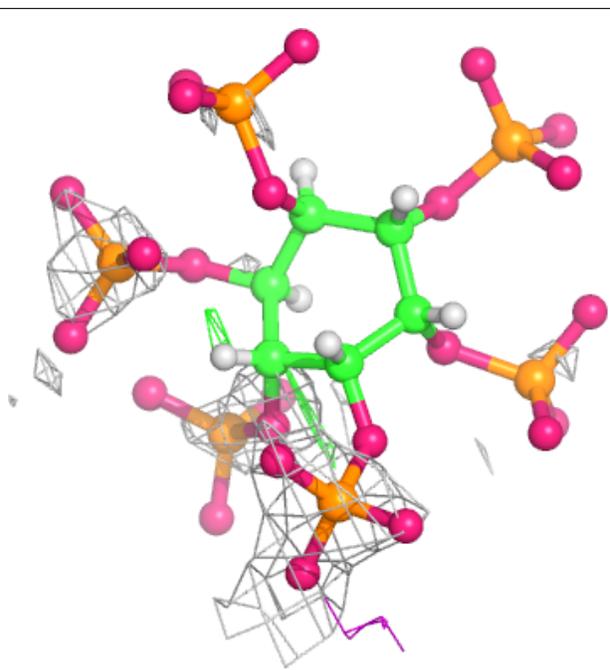
Electron density around IHP A 201:

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



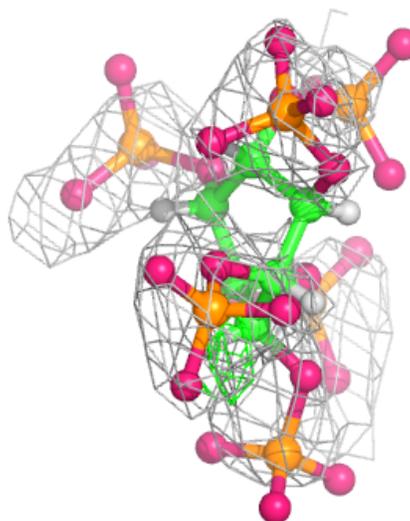
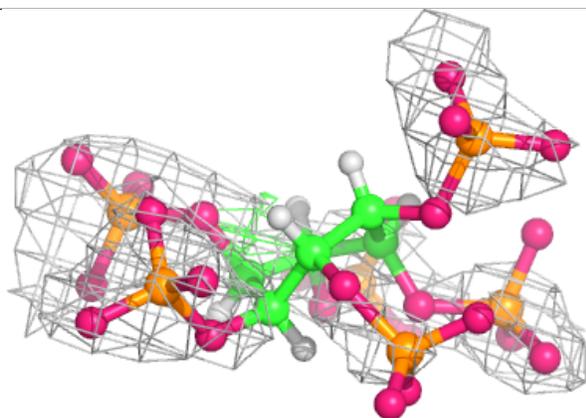
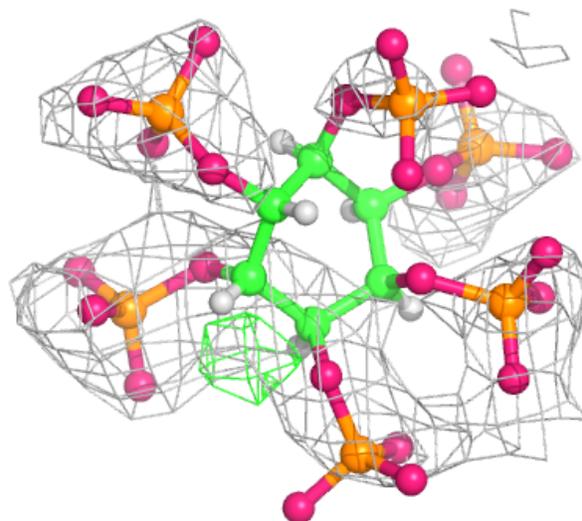
Electron density around IHP B 201:

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



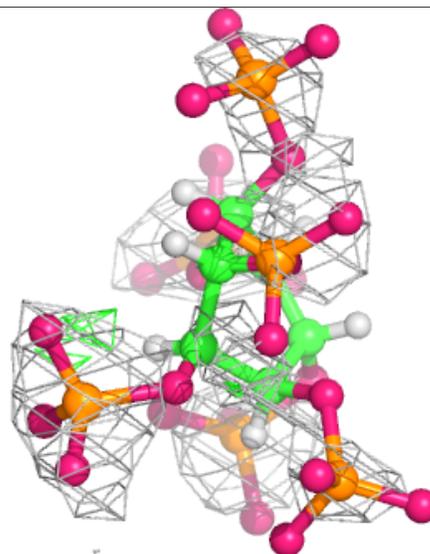
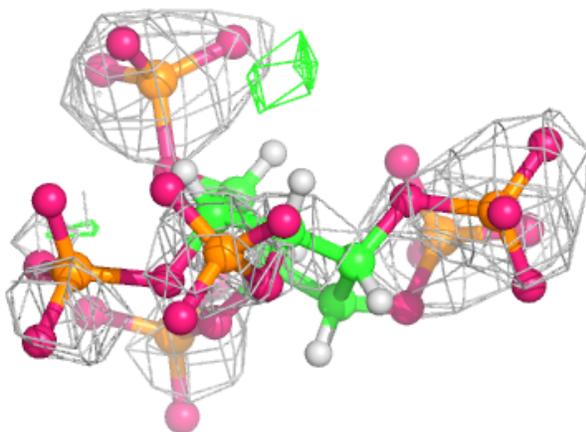
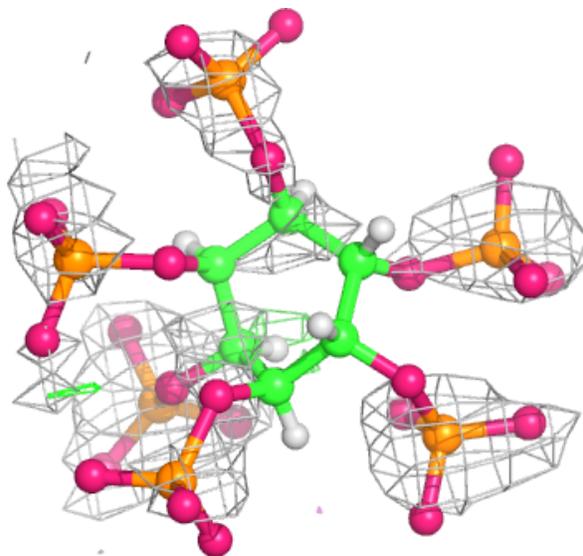
Electron density around IHP C 201:

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



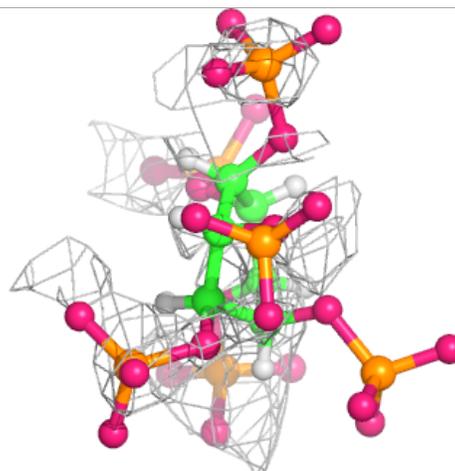
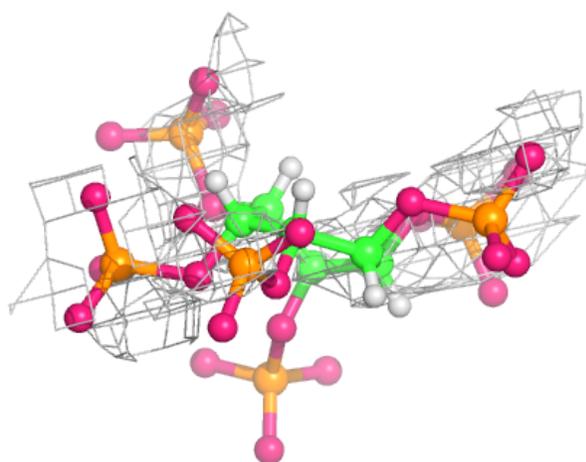
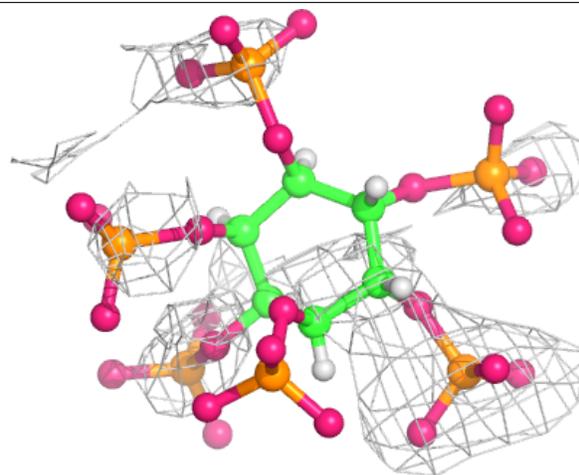
Electron density around IHP D 201:

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



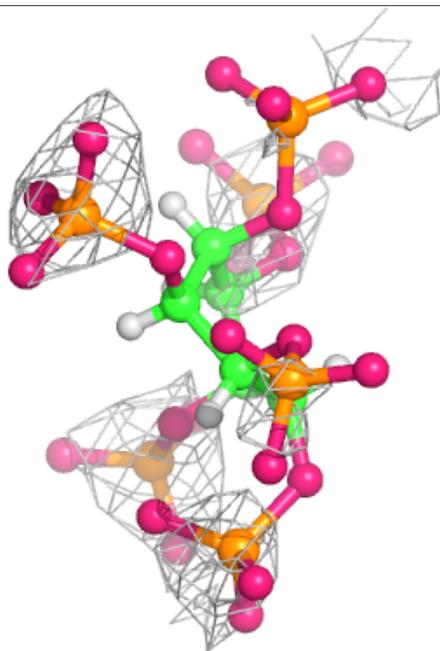
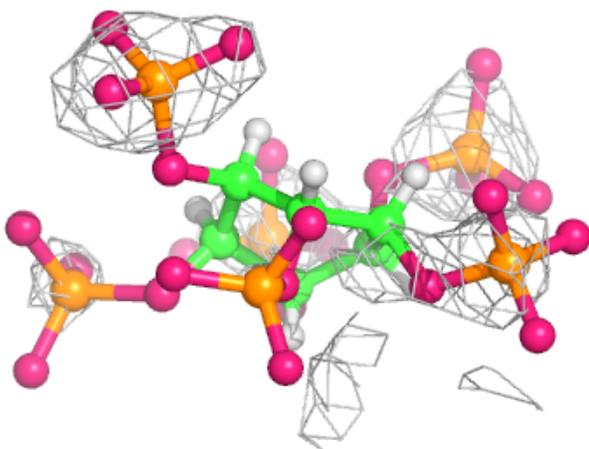
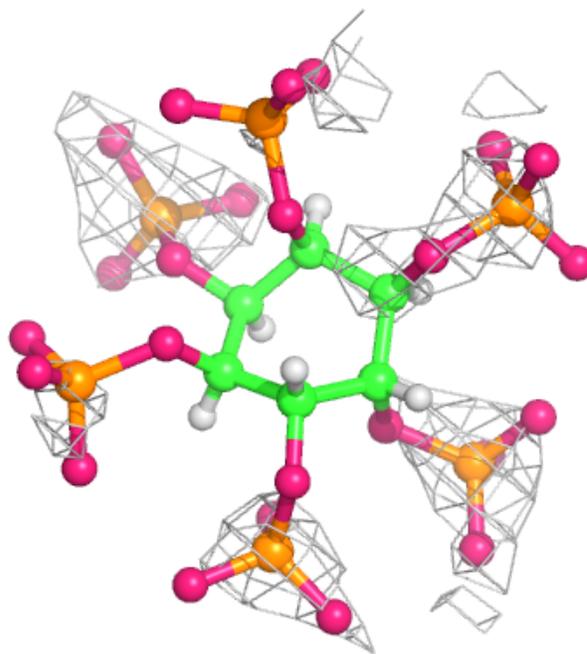
Electron density around IHP E 201:

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



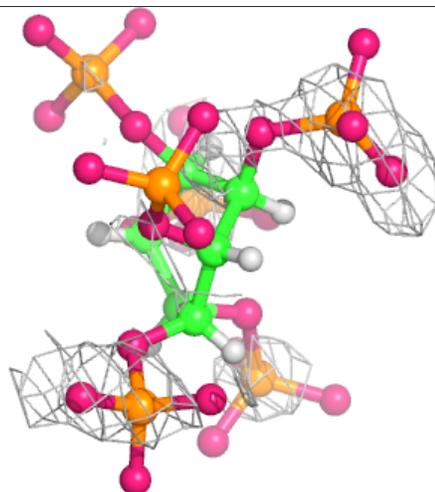
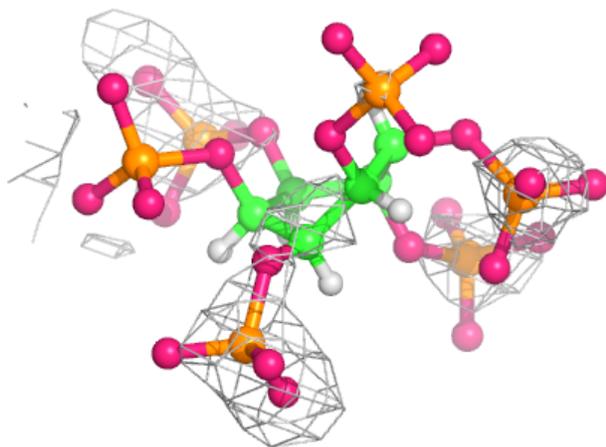
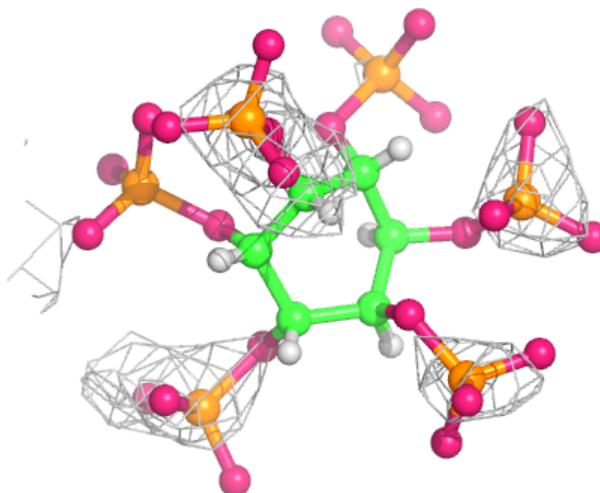
Electron density around IHP E 202:

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



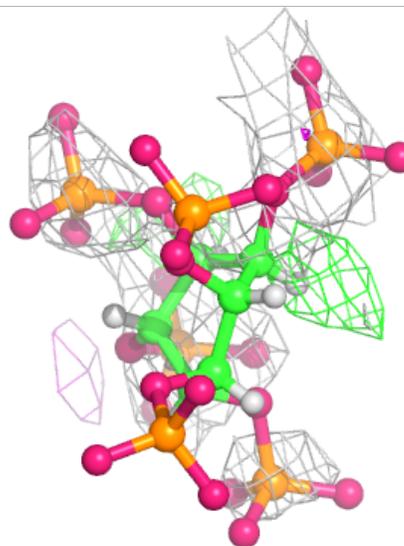
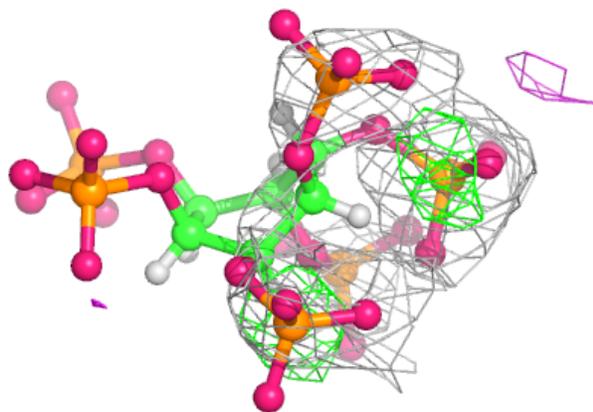
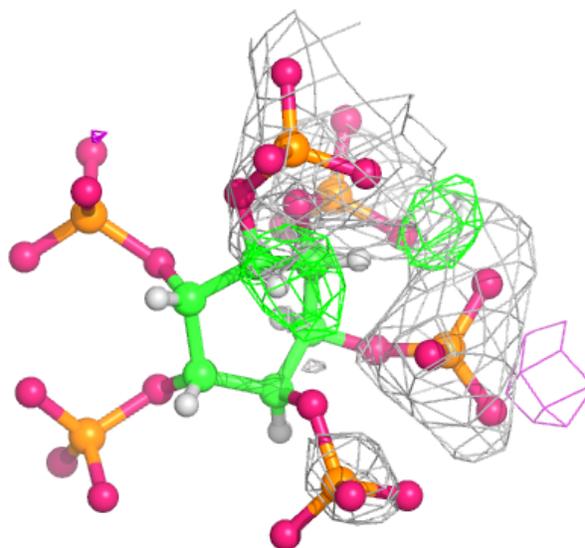
Electron density around IHP F 201:

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



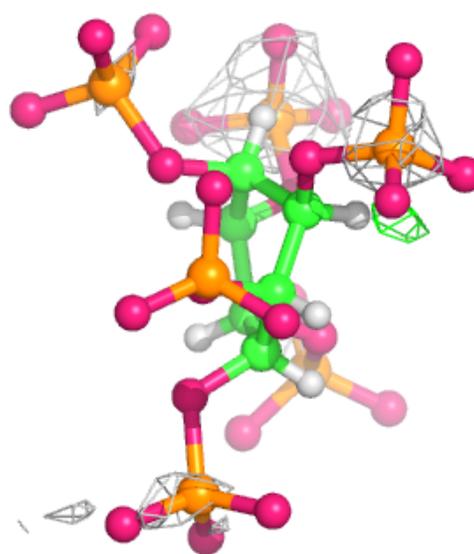
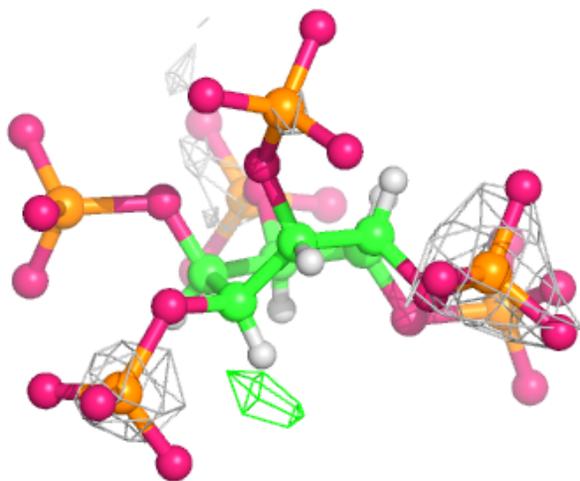
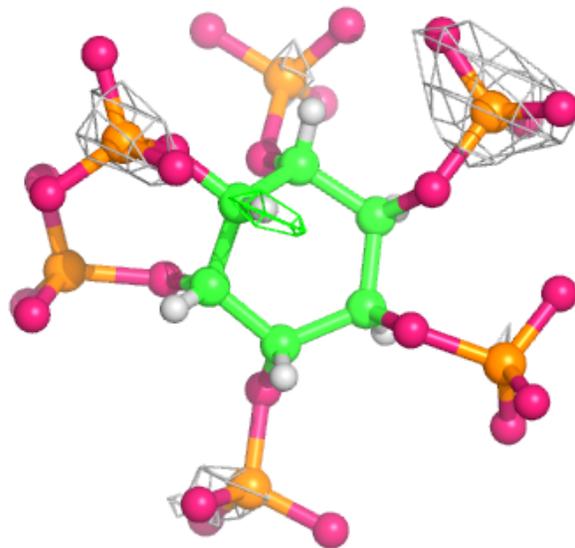
Electron density around IHP G 201:

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



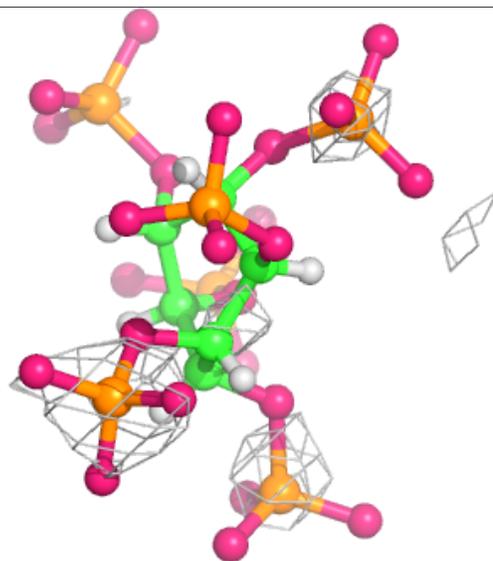
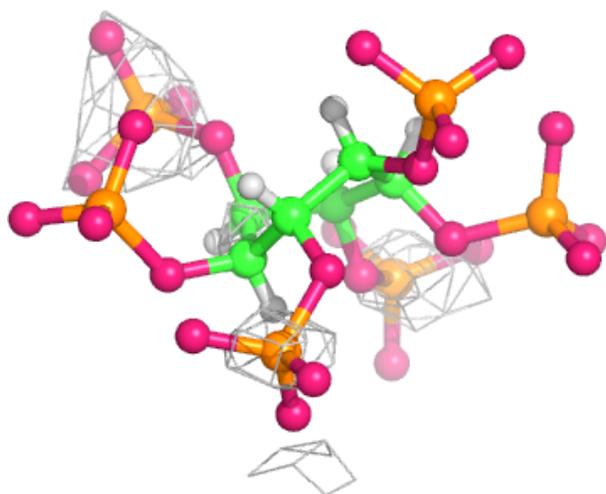
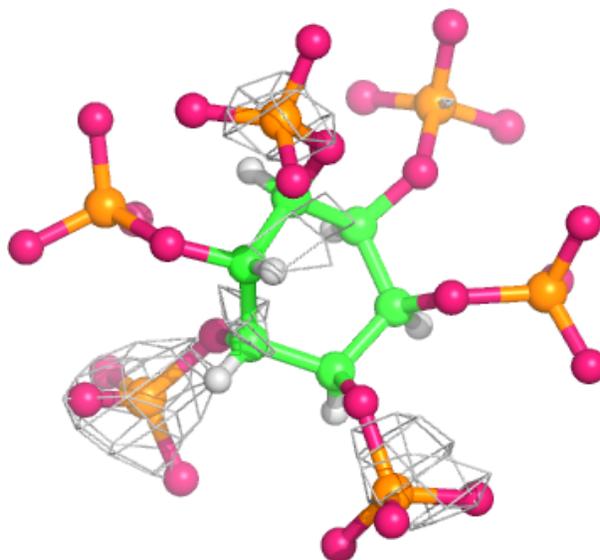
Electron density around IHP I 201:

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



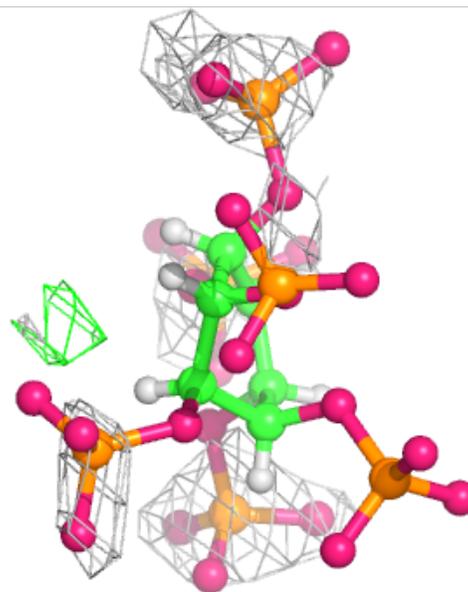
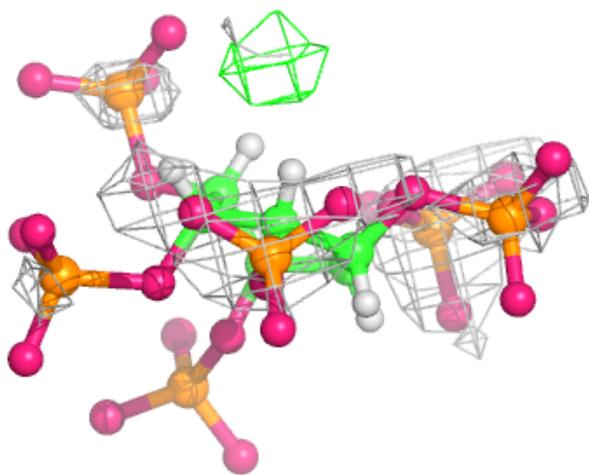
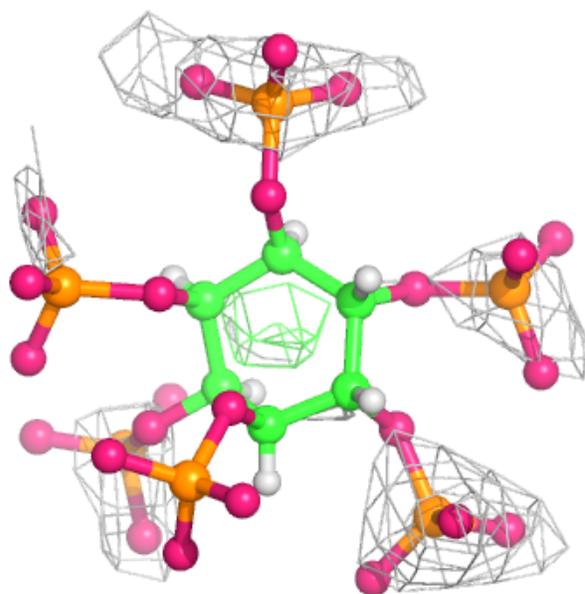
Electron density around IHP J 201:

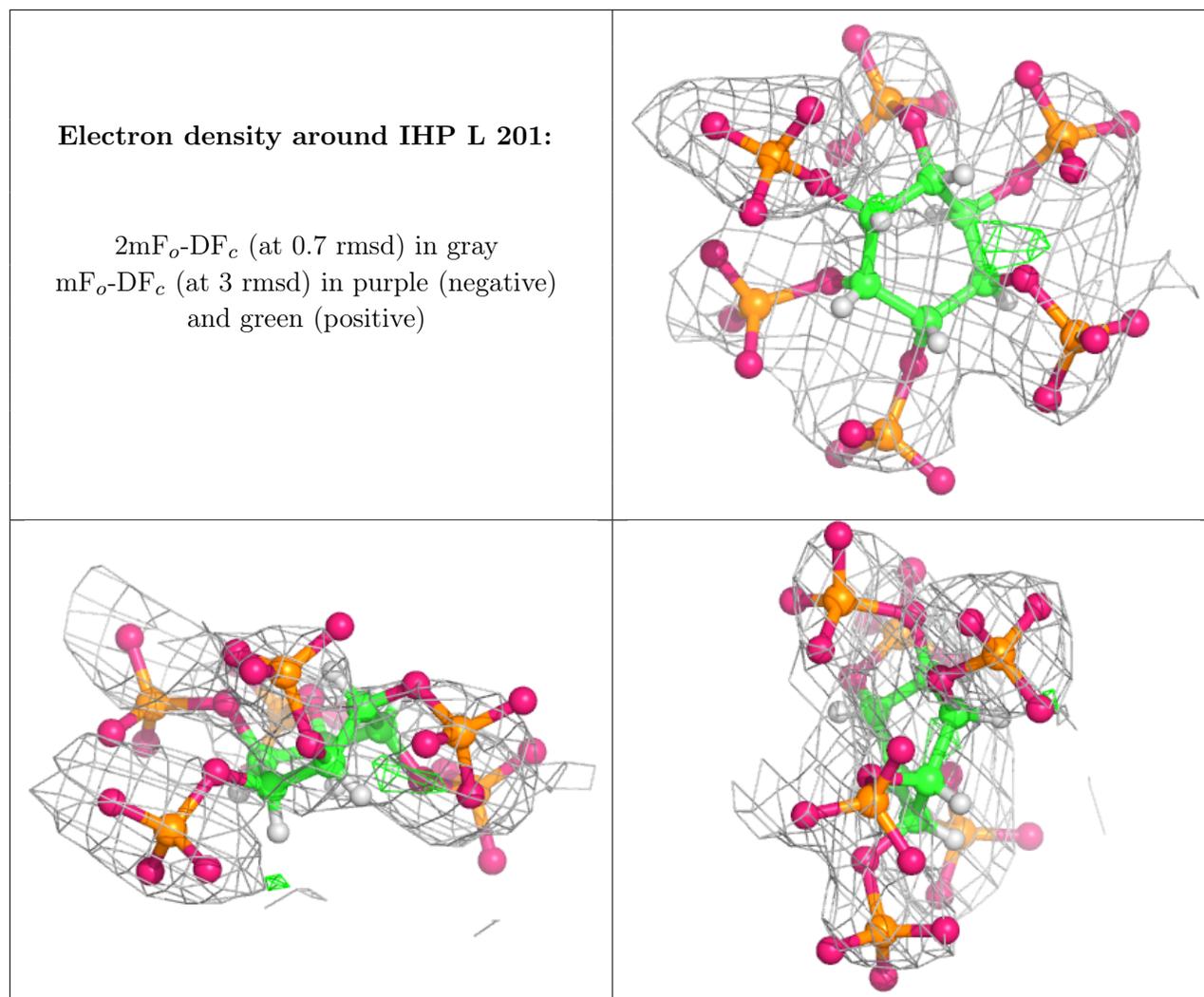
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around IHP K 201:

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





6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.