



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2022 – 12:55 PM EST

PDB ID : 7TLF  
Title : Structure of the photoacclimated Light Harvesting Complex PE545 from *Proteomonas sulcata*  
Authors : Jeffrey, P.D.; Spangler, L.C.; Scholes, G.D.  
Deposited on : 2022-01-18  
Resolution : 2.80 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](mailto: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.

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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 : 2.26  
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) : 2.26

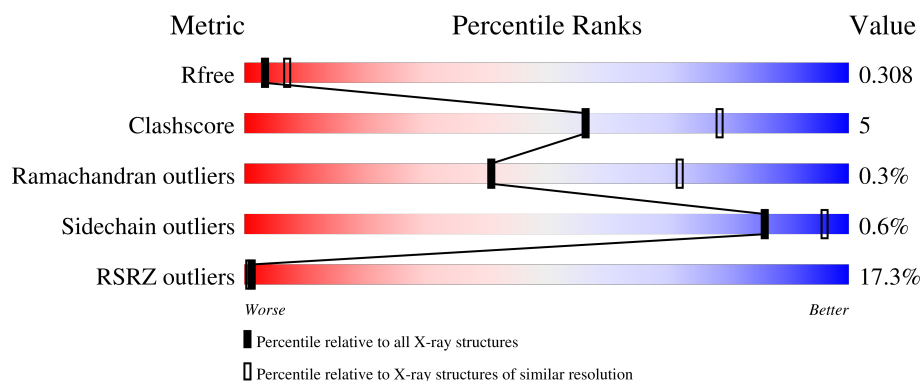
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	76	<div> <div>25%</div> <div>79%</div> <div>16%</div> <div>5%</div> </div>
1	E	76	<div> <div>11%</div> <div>91%</div> <div>7%</div> <div>.</div> </div>
1	I	76	<div> <div>21%</div> <div>93%</div> <div>5%</div> <div>.</div> </div>
1	M	76	<div> <div>14%</div> <div>93%</div> <div>.</div> <div>.</div> </div>
2	B	177	<div> <div>25%</div> <div>76%</div> <div>16%</div> <div>8%</div> </div>

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Mol	Chain	Length	Quality of chain
2	D	177	
2	F	177	
2	H	177	
2	J	177	
2	L	177	
2	N	177	
2	P	177	
3	C	67	
3	G	67	
3	K	67	
3	O	67	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 15397 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 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	72	Total	C	N	O	S	0	0	0
			528	326	91	108	3			
1	E	74	Total	C	N	O	S	0	0	0
			544	337	94	110	3			
1	I	75	Total	C	N	O	S	0	0	0
			553	343	96	111	3			
1	M	74	Total	C	N	O	S	0	0	0
			544	337	94	110	3			

- Molecule 2 is a protein called Phycoerythrin beta-subunit.

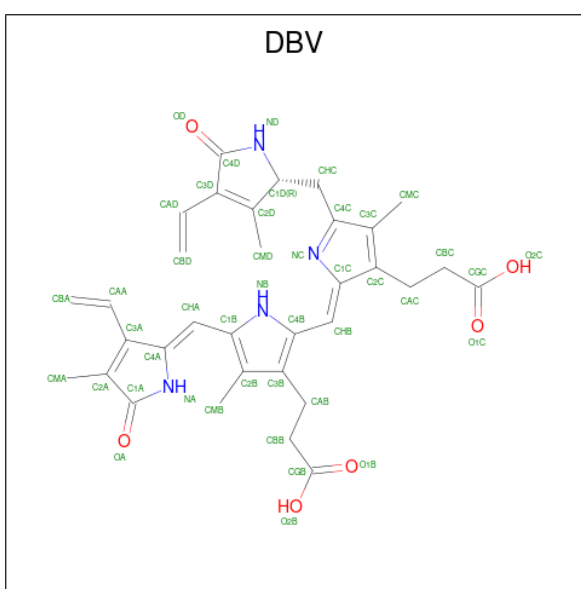
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	162	Total	C	N	O	S	0	1	0
			1180	728	206	236	10			
2	D	173	Total	C	N	O	S	0	0	0
			1262	776	220	256	10			
2	F	166	Total	C	N	O	S	0	1	0
			1207	743	209	245	10			
2	H	170	Total	C	N	O	S	0	0	0
			1231	759	211	251	10			
2	J	170	Total	C	N	O	S	0	0	0
			1241	765	217	249	10			
2	L	172	Total	C	N	O	S	0	0	0
			1253	771	219	253	10			
2	N	170	Total	C	N	O	S	0	0	0
			1239	765	217	247	10			
2	P	173	Total	C	N	O	S	0	1	0
			1261	777	220	254	10			

- Molecule 3 is a protein called Phycoerythrin alpha-subunit 2.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	60	Total 445	C 274	N 78	O 89	S 4	0	0	0
3	G	67	Total 496	C 304	N 87	O 100	S 5	0	0	0
3	K	67	Total 496	C 304	N 87	O 100	S 5	0	0	0
3	O	67	Total 496	C 304	N 87	O 100	S 5	0	0	0

- Molecule 4 is 15,16-DIHYDROBILIVERDIN (three-letter code: DBV) (formula:  $C_{33}H_{36}N_4O_6$ ) (labeled as "Ligand of Interest" by depositor).



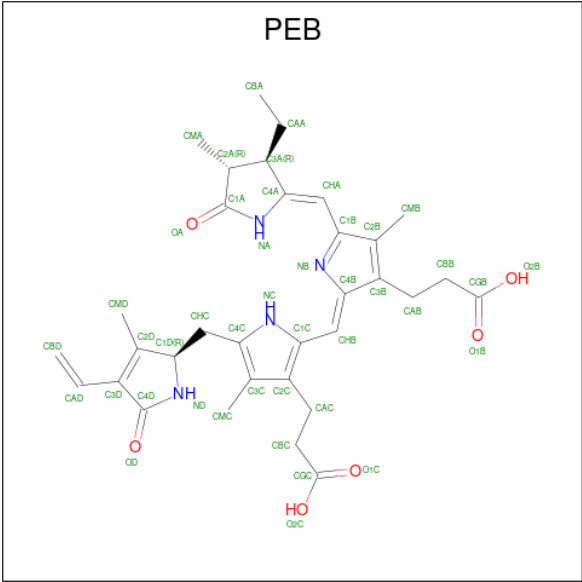
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 43	C 33	N 4	O 6	0	0
4	C	1	Total 43	C 33	N 4	O 6	0	0
4	E	1	Total 43	C 33	N 4	O 6	0	0
4	G	1	Total 43	C 33	N 4	O 6	0	0
4	I	1	Total 43	C 33	N 4	O 6	0	0
4	K	1	Total 43	C 33	N 4	O 6	0	0
4	M	1	Total 43	C 33	N 4	O 6	0	0

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

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			43	33	4	6		
5	B	1	Total	C	N	O	0	0
			43	33	4	6		
5	B	1	Total	C	N	O	0	0
			43	33	4	6		
5	D	1	Total	C	N	O	0	0
			43	33	4	6		
5	D	1	Total	C	N	O	0	0
			43	33	4	6		
5	D	1	Total	C	N	O	0	0
			43	33	4	6		
5	F	1	Total	C	N	O	0	0
			43	33	4	6		
5	F	1	Total	C	N	O	0	0
			43	33	4	6		
5	F	1	Total	C	N	O	0	0
			43	33	4	6		
5	H	1	Total	C	N	O	0	0
			43	33	4	6		

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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	2	Total	O	0	0
			2	2		
6	C	2	Total	O	0	0
			2	2		
6	D	4	Total	O	0	0
			4	4		
6	E	4	Total	O	0	0
			4	4		
6	G	2	Total	O	0	0
			2	2		

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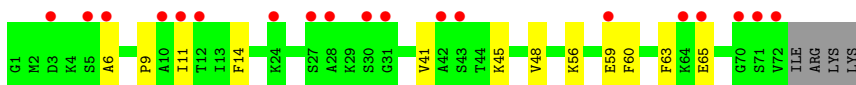
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	5	Total 5	O 5	0	0
6	H	8	Total 8	O 8	0	0
6	I	4	Total 4	O 4	0	0
6	K	2	Total 2	O 2	0	0
6	J	3	Total 3	O 3	0	0
6	L	2	Total 2	O 2	0	0
6	M	2	Total 2	O 2	0	0
6	O	1	Total 1	O 1	0	0
6	N	1	Total 1	O 1	0	0
6	P	3	Total 3	O 3	0	0

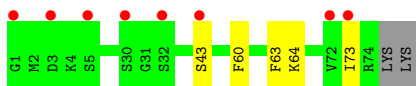
### 3 Residue-property plots [i](#)

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 1



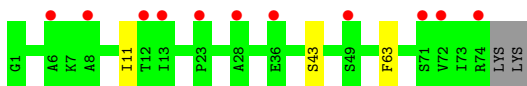
- Molecule 1: Phycoerythrin alpha-subunit 1



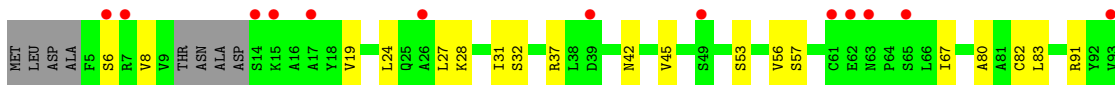
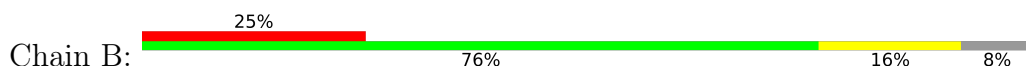
- Molecule 1: Phycoerythrin alpha-subunit 1

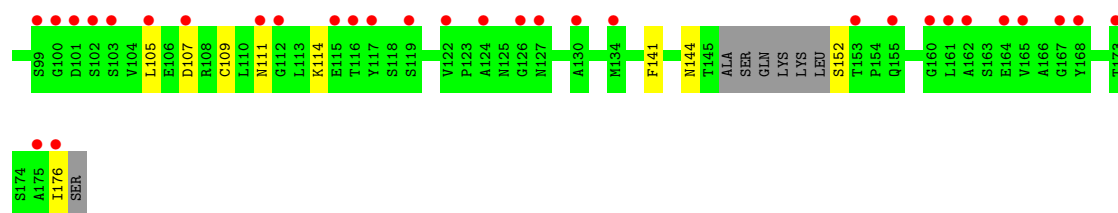


- Molecule 1: Phycoerythrin alpha-subunit 1

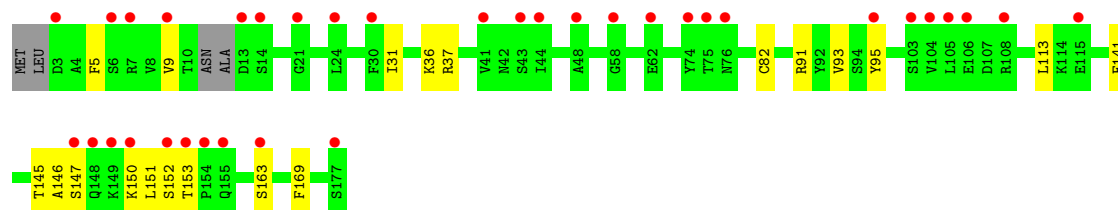
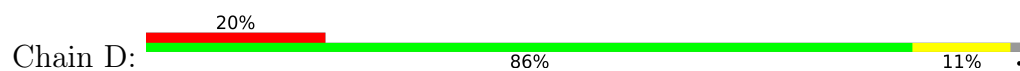


- Molecule 2: Phycoerythrin beta-subunit

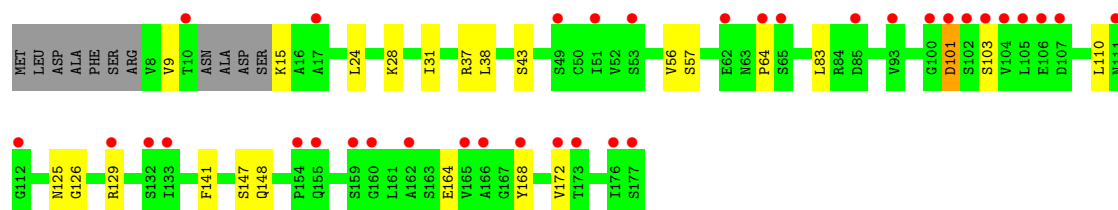
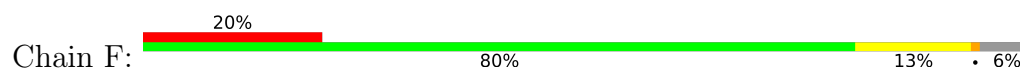




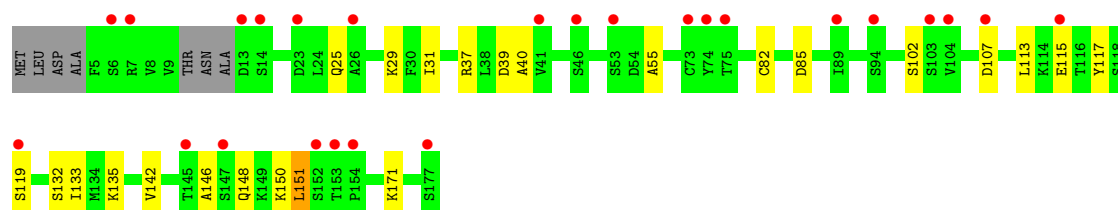
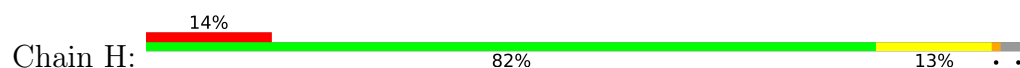
• Molecule 2: Phycoerythrin beta-subunit



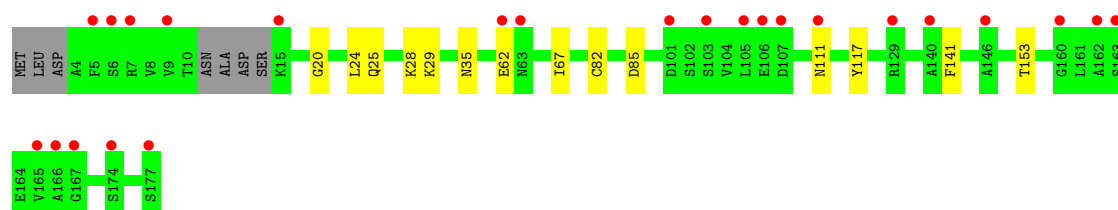
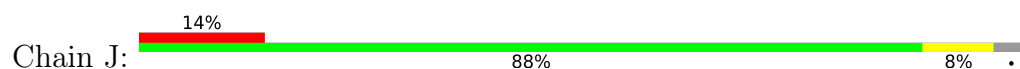
• Molecule 2: Phycoerythrin beta-subunit



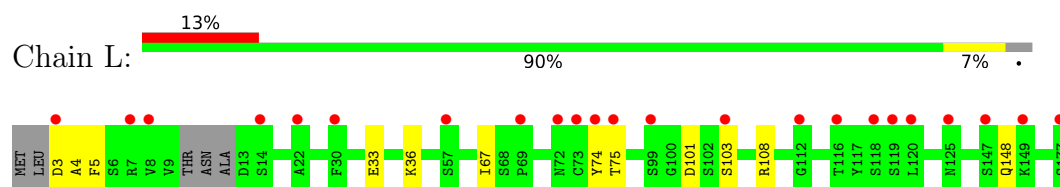
• Molecule 2: Phycoerythrin beta-subunit



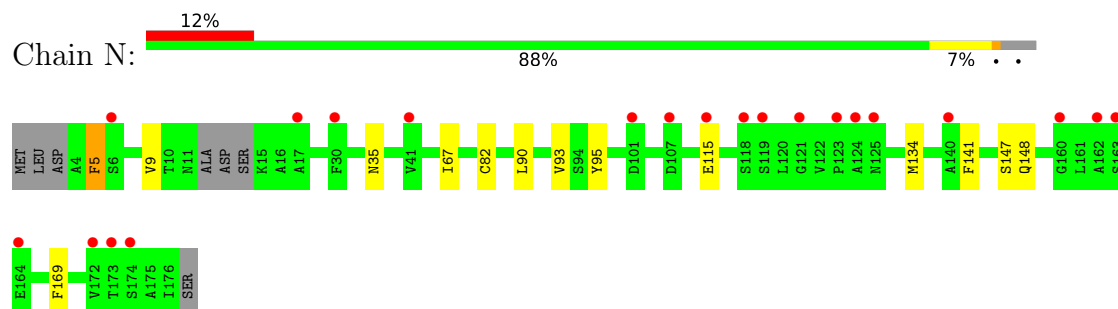
• Molecule 2: Phycoerythrin beta-subunit



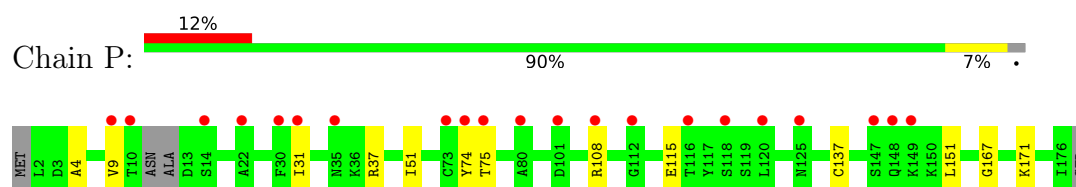
- Molecule 2: Phycoerythrin beta-subunit



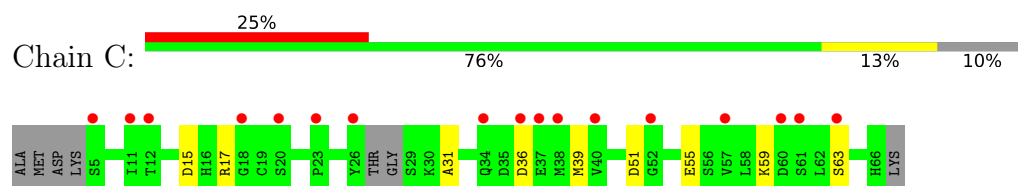
- Molecule 2: Phycoerythrin beta-subunit



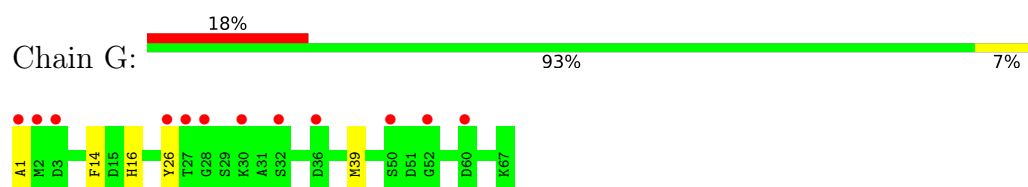
- Molecule 2: Phycoerythrin beta-subunit



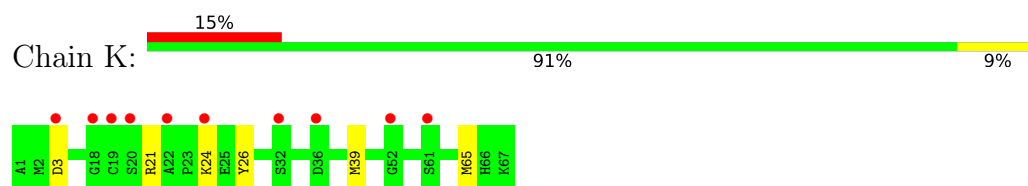
- Molecule 3: Phycoerythrin alpha-subunit 2



- Molecule 3: Phycoerythrin alpha-subunit 2



- Molecule 3: Phycoerythrin alpha-subunit 2



- Molecule 3: Phycoerythrin alpha-subunit 2





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	88.25Å 132.24Å 93.41Å 90.00° 116.92° 90.00°	Depositor
Resolution (Å)	29.35 – 2.80 29.35 – 2.78	Depositor EDS
% Data completeness (in resolution range)	99.0 (29.35-2.80) 97.3 (29.35-2.78)	Depositor EDS
$R_{merge}$	0.24	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.96 (at 2.76Å)	Xtriage
Refinement program	PHENIX 1.17_3644	Depositor
R, $R_{free}$	0.245 , 0.306 0.246 , 0.308	Depositor DCC
$R_{free}$ test set	2457 reflections (5.24%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.6	Xtriage
Anisotropy	0.620	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 61.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	15397	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.06 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2086e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PEB, DBV

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	0.33	0/533	0.62	0/711
1	E	0.31	0/549	0.59	0/732
1	I	0.29	0/558	0.54	0/743
1	M	0.32	0/549	0.52	0/732
2	B	0.31	0/1191	0.48	0/1607
2	D	0.31	0/1274	0.47	0/1720
2	F	0.30	0/1221	0.51	0/1649
2	H	0.34	0/1243	0.53	0/1678
2	J	0.31	0/1253	0.48	0/1690
2	L	0.29	0/1265	0.44	0/1706
2	N	0.31	0/1251	0.47	0/1689
2	P	0.30	0/1276	0.45	0/1723
3	C	0.29	0/449	0.53	0/600
3	G	0.28	0/501	0.53	0/668
3	K	0.28	0/501	0.53	0/668
3	O	0.29	0/501	0.49	0/668
All	All	0.30	0/14115	0.50	0/18984

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	528	0	533	13	0
1	E	544	0	555	6	0
1	I	553	0	568	4	0
1	M	544	0	555	3	0
2	B	1180	0	1171	18	0
2	D	1262	0	1257	16	0
2	F	1207	0	1206	19	0
2	H	1231	0	1219	15	0
2	J	1241	0	1244	13	0
2	L	1253	0	1248	7	0
2	N	1239	0	1241	12	0
2	P	1261	0	1257	7	0
3	C	445	0	447	5	0
3	G	496	0	505	3	0
3	K	496	0	505	5	0
3	O	496	0	505	3	0
4	A	43	0	33	3	0
4	C	43	0	32	2	0
4	E	43	0	33	2	0
4	G	43	0	32	2	0
4	I	43	0	32	2	0
4	K	43	0	32	2	0
4	M	43	0	32	2	0
4	O	43	0	32	2	0
5	B	129	0	110	3	0
5	D	129	0	109	5	0
5	F	129	0	110	3	0
5	H	129	0	110	4	0
5	J	129	0	110	7	0
5	L	129	0	110	2	0
5	N	129	0	109	5	0
5	P	129	0	110	2	0
6	B	2	0	0	0	0
6	C	2	0	0	0	0
6	D	4	0	0	1	0
6	E	4	0	0	0	0
6	F	5	0	0	1	0
6	G	2	0	0	0	0
6	H	8	0	0	0	0
6	I	4	0	0	0	0
6	J	3	0	0	0	0
6	K	2	0	0	0	0
6	L	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	M	2	0	0	0	0
6	N	1	0	0	0	0
6	O	1	0	0	0	0
6	P	3	0	0	0	0
All	All	15397	0	15152	151	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 5.

The worst 5 of 151 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:D:31:ILE:HD12	2:D:37:ARG:HD2	1.68	0.76
3:G:1:ALA:N	2:H:107:ASP:O	2.21	0.73
2:B:31:ILE:HD12	2:B:37:ARG:HD2	1.72	0.71
4:G:101:DBV:HNA	4:G:101:DBV:HMB3	1.56	0.70
2:H:146:ALA:HB1	2:H:150:LYS:HG3	1.74	0.70

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	70/76 (92%)	65 (93%)	5 (7%)	0	100	100
1	E	72/76 (95%)	69 (96%)	3 (4%)	0	100	100
1	I	73/76 (96%)	69 (94%)	4 (6%)	0	100	100
1	M	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
2	B	156/177 (88%)	152 (97%)	2 (1%)	2 (1%)	12	36
2	D	169/177 (96%)	163 (96%)	5 (3%)	1 (1%)	25	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F	163/177 (92%)	161 (99%)	2 (1%)	0	100	100
2	H	166/177 (94%)	164 (99%)	2 (1%)	0	100	100
2	J	166/177 (94%)	163 (98%)	3 (2%)	0	100	100
2	L	168/177 (95%)	163 (97%)	4 (2%)	1 (1%)	25	56
2	N	166/177 (94%)	163 (98%)	3 (2%)	0	100	100
2	P	170/177 (96%)	165 (97%)	4 (2%)	1 (1%)	25	56
3	C	56/67 (84%)	54 (96%)	2 (4%)	0	100	100
3	G	65/67 (97%)	63 (97%)	2 (3%)	0	100	100
3	K	65/67 (97%)	63 (97%)	2 (3%)	0	100	100
3	O	65/67 (97%)	63 (97%)	1 (2%)	1 (2%)	10	33
All	All	1862/1988 (94%)	1810 (97%)	46 (2%)	6 (0%)	41	72

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	4	ALA
2	B	6	SER
2	B	144	ASN
2	D	9	VAL
3	O	24	LYS

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	57/62 (92%)	57 (100%)	0	100	100
1	E	59/62 (95%)	59 (100%)	0	100	100
1	I	60/62 (97%)	60 (100%)	0	100	100
1	M	59/62 (95%)	59 (100%)	0	100	100
2	B	130/143 (91%)	129 (99%)	1 (1%)	81	94
2	D	140/143 (98%)	138 (99%)	2 (1%)	67	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	F	134/143 (94%)	132 (98%)	2 (2%)	65	89
2	H	136/143 (95%)	134 (98%)	2 (2%)	65	89
2	J	137/143 (96%)	137 (100%)	0	100	100
2	L	138/143 (96%)	138 (100%)	0	100	100
2	N	136/143 (95%)	135 (99%)	1 (1%)	84	95
2	P	139/143 (97%)	139 (100%)	0	100	100
3	C	50/55 (91%)	49 (98%)	1 (2%)	55	84
3	G	55/55 (100%)	55 (100%)	0	100	100
3	K	55/55 (100%)	55 (100%)	0	100	100
3	O	55/55 (100%)	55 (100%)	0	100	100
All	All	1540/1612 (96%)	1531 (99%)	9 (1%)	86	96

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	151	LEU
2	N	5	PHE
2	D	163	SER
2	F	43	SER
2	F	101	ASP

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

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

32 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	PEB	F	203	2	37,46,46	1.11	3 (8%)	39,67,67	1.64	10 (25%)
4	DBV	M	101	1	36,46,46	1.38	4 (11%)	36,67,67	1.81	12 (33%)
5	PEB	D	202	2	37,46,46	1.21	5 (13%)	39,67,67	1.44	7 (17%)
5	PEB	J	203	2	37,46,46	1.29	4 (10%)	39,67,67	1.64	8 (20%)
4	DBV	C	101	3	36,46,46	1.40	6 (16%)	36,67,67	1.87	11 (30%)
4	DBV	I	101	1	36,46,46	1.45	6 (16%)	36,67,67	1.89	13 (36%)
5	PEB	B	202	2	37,46,46	1.13	3 (8%)	39,67,67	1.45	8 (20%)
5	PEB	H	202	2	37,46,46	1.27	3 (8%)	39,67,67	1.66	7 (17%)
5	PEB	B	203	2	37,46,46	1.17	3 (8%)	39,67,67	1.59	9 (23%)
5	PEB	F	202	2	37,46,46	1.20	3 (8%)	39,67,67	1.51	7 (17%)
4	DBV	K	101	3	36,46,46	1.35	6 (16%)	36,67,67	1.88	12 (33%)
5	PEB	J	202	2	37,46,46	1.17	4 (10%)	39,67,67	1.41	5 (12%)
5	PEB	N	201	2	37,46,46	1.14	3 (8%)	39,67,67	1.39	6 (15%)
5	PEB	P	203	2	37,46,46	1.13	2 (5%)	39,67,67	1.65	10 (25%)
5	PEB	D	203	2	37,46,46	1.18	3 (8%)	39,67,67	1.58	9 (23%)
5	PEB	L	201	2	37,46,46	1.15	1 (2%)	39,67,67	1.74	10 (25%)
4	DBV	G	101	3	36,46,46	1.45	5 (13%)	36,67,67	1.82	11 (30%)
5	PEB	H	201	2	37,46,46	1.07	3 (8%)	39,67,67	1.47	6 (15%)
5	PEB	J	201	2	37,46,46	1.18	3 (8%)	39,67,67	1.53	8 (20%)
5	PEB	L	202	2	37,46,46	1.25	4 (10%)	39,67,67	1.47	6 (15%)
5	PEB	P	202	2	37,46,46	1.32	7 (18%)	39,67,67	1.54	7 (17%)
5	PEB	B	201	2	37,46,46	1.15	3 (8%)	39,67,67	1.38	7 (17%)
4	DBV	O	101	3	36,46,46	1.37	5 (13%)	36,67,67	1.94	13 (36%)
5	PEB	H	203	2	37,46,46	1.14	4 (10%)	39,67,67	1.60	9 (23%)
5	PEB	L	203	2	37,46,46	1.22	4 (10%)	39,67,67	1.51	9 (23%)
5	PEB	P	201	2	37,46,46	1.07	2 (5%)	39,67,67	1.72	10 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	PEB	N	202	2	37,46,46	1.30	5 (13%)	39,67,67	1.40	7 (17%)
5	PEB	D	201	2	37,46,46	1.12	2 (5%)	39,67,67	1.77	11 (28%)
5	PEB	N	203	2	37,46,46	1.14	2 (5%)	39,67,67	1.53	8 (20%)
4	DBV	A	101	1	36,46,46	1.51	7 (19%)	36,67,67	1.90	10 (27%)
5	PEB	F	201	2	37,46,46	1.24	4 (10%)	39,67,67	1.57	10 (25%)
4	DBV	E	101	1	36,46,46	1.39	6 (16%)	36,67,67	1.91	11 (30%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PEB	F	203	2	-	2/20/74/74	0/4/4/4
4	DBV	M	101	1	-	7/22/74/74	0/4/4/4
5	PEB	D	202	2	-	6/20/74/74	0/4/4/4
5	PEB	J	203	2	-	2/20/74/74	0/4/4/4
4	DBV	C	101	3	-	11/22/74/74	0/4/4/4
4	DBV	I	101	1	-	6/22/74/74	0/4/4/4
5	PEB	B	202	2	-	6/20/74/74	0/4/4/4
5	PEB	H	202	2	-	5/20/74/74	0/4/4/4
5	PEB	B	203	2	-	2/20/74/74	0/4/4/4
5	PEB	F	202	2	-	4/20/74/74	0/4/4/4
4	DBV	K	101	3	-	5/22/74/74	0/4/4/4
5	PEB	J	202	2	-	4/20/74/74	0/4/4/4
5	PEB	N	201	2	-	4/20/74/74	0/4/4/4
5	PEB	P	203	2	-	2/20/74/74	0/4/4/4
5	PEB	D	203	2	-	2/20/74/74	0/4/4/4
5	PEB	L	201	2	-	4/20/74/74	0/4/4/4
4	DBV	G	101	3	-	5/22/74/74	0/4/4/4
5	PEB	H	201	2	-	5/20/74/74	0/4/4/4
5	PEB	J	201	2	-	4/20/74/74	0/4/4/4
5	PEB	L	202	2	-	7/20/74/74	0/4/4/4
5	PEB	P	202	2	-	5/20/74/74	0/4/4/4
5	PEB	B	201	2	-	6/20/74/74	0/4/4/4
4	DBV	O	101	3	-	4/22/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PEB	H	203	2	-	3/20/74/74	0/4/4/4
5	PEB	L	203	2	-	2/20/74/74	0/4/4/4
5	PEB	P	201	2	-	4/20/74/74	0/4/4/4
5	PEB	N	202	2	-	4/20/74/74	0/4/4/4
5	PEB	D	201	2	-	5/20/74/74	0/4/4/4
5	PEB	N	203	2	-	2/20/74/74	0/4/4/4
4	DBV	A	101	1	-	5/22/74/74	0/4/4/4
5	PEB	F	201	2	-	4/20/74/74	0/4/4/4
4	DBV	E	101	1	-	5/22/74/74	0/4/4/4

The worst 5 of 125 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	101	DBV	C1B-CHA	3.50	1.54	1.41
4	G	101	DBV	CAB-C3B	-3.43	1.47	1.52
4	A	101	DBV	CHB-C1C	3.34	1.37	1.35
4	I	101	DBV	C1B-CHA	3.30	1.54	1.41
4	O	101	DBV	C1B-CHA	3.30	1.53	1.41

The worst 5 of 287 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	O	101	DBV	C1D-CHC-C4C	4.93	124.09	113.37
5	P	202	PEB	C1C-CHB-C4B	4.86	134.61	128.81
5	H	202	PEB	C1C-CHB-C4B	4.70	134.42	128.81
5	F	202	PEB	C1C-CHB-C4B	4.54	134.23	128.81
4	A	101	DBV	C1D-CHC-C4C	4.24	122.59	113.37

There are no chirality outliers.

5 of 142 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	101	DBV	C2A-C3A-CAA-CBA
4	A	101	DBV	C4A-C3A-CAA-CBA
4	A	101	DBV	NB-C1B-CHA-C4A
4	A	101	DBV	C2B-C1B-CHA-C4A
4	C	101	DBV	C2A-C3A-CAA-CBA

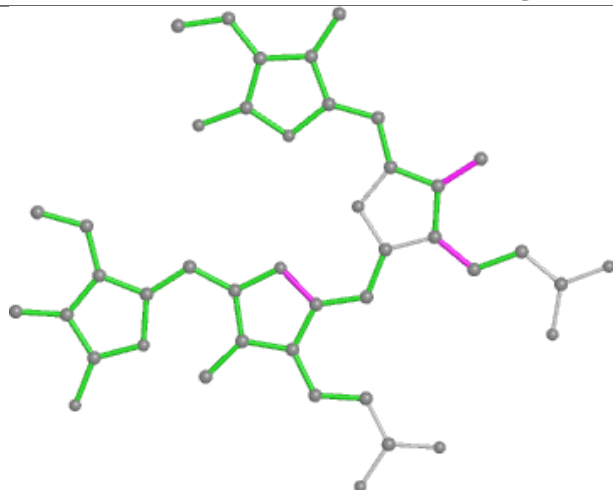
There are no ring outliers.

28 monomers are involved in 48 short contacts:

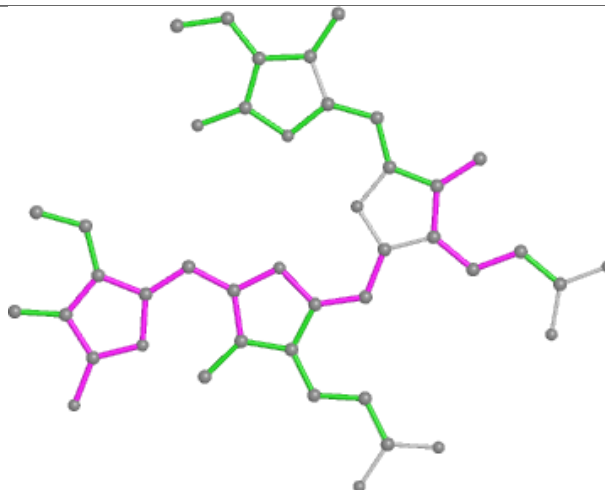
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	F	203	PEB	1	0
4	M	101	DBV	2	0
5	D	202	PEB	2	0
5	J	203	PEB	2	0
4	C	101	DBV	2	0
4	I	101	DBV	2	0
5	H	202	PEB	1	0
5	B	203	PEB	2	0
5	F	202	PEB	1	0
4	K	101	DBV	2	0
5	J	202	PEB	3	0
5	N	201	PEB	2	0
5	P	203	PEB	1	0
5	D	203	PEB	2	0
5	L	201	PEB	1	0
4	G	101	DBV	2	0
5	J	201	PEB	2	0
5	B	201	PEB	1	0
4	O	101	DBV	2	0
5	H	203	PEB	3	0
5	L	203	PEB	1	0
5	P	201	PEB	1	0
5	N	202	PEB	1	0
5	D	201	PEB	1	0
5	N	203	PEB	2	0
4	A	101	DBV	3	0
5	F	201	PEB	1	0
4	E	101	DBV	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.

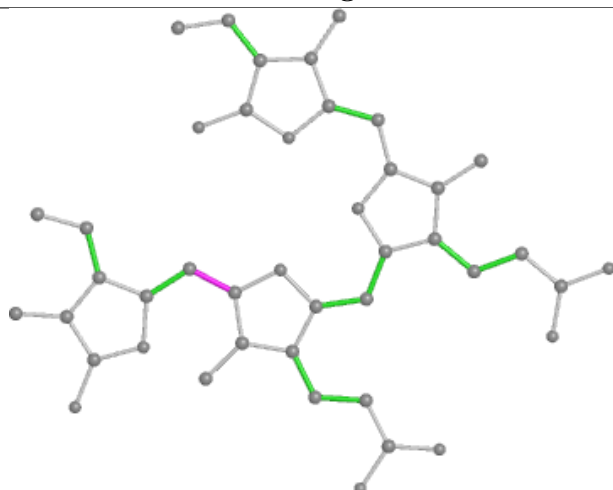
## Ligand PEB F 203



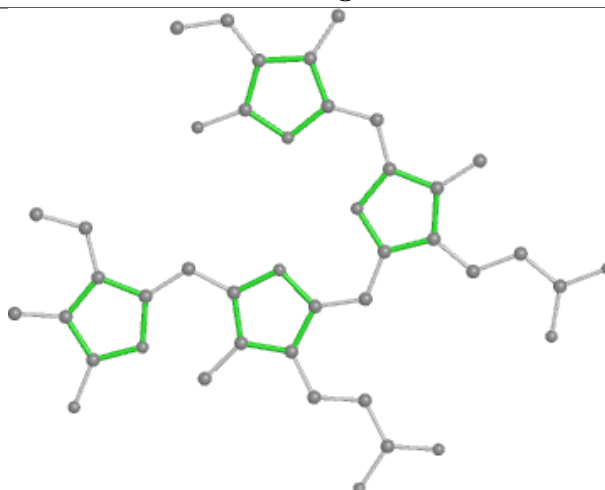
Bond lengths



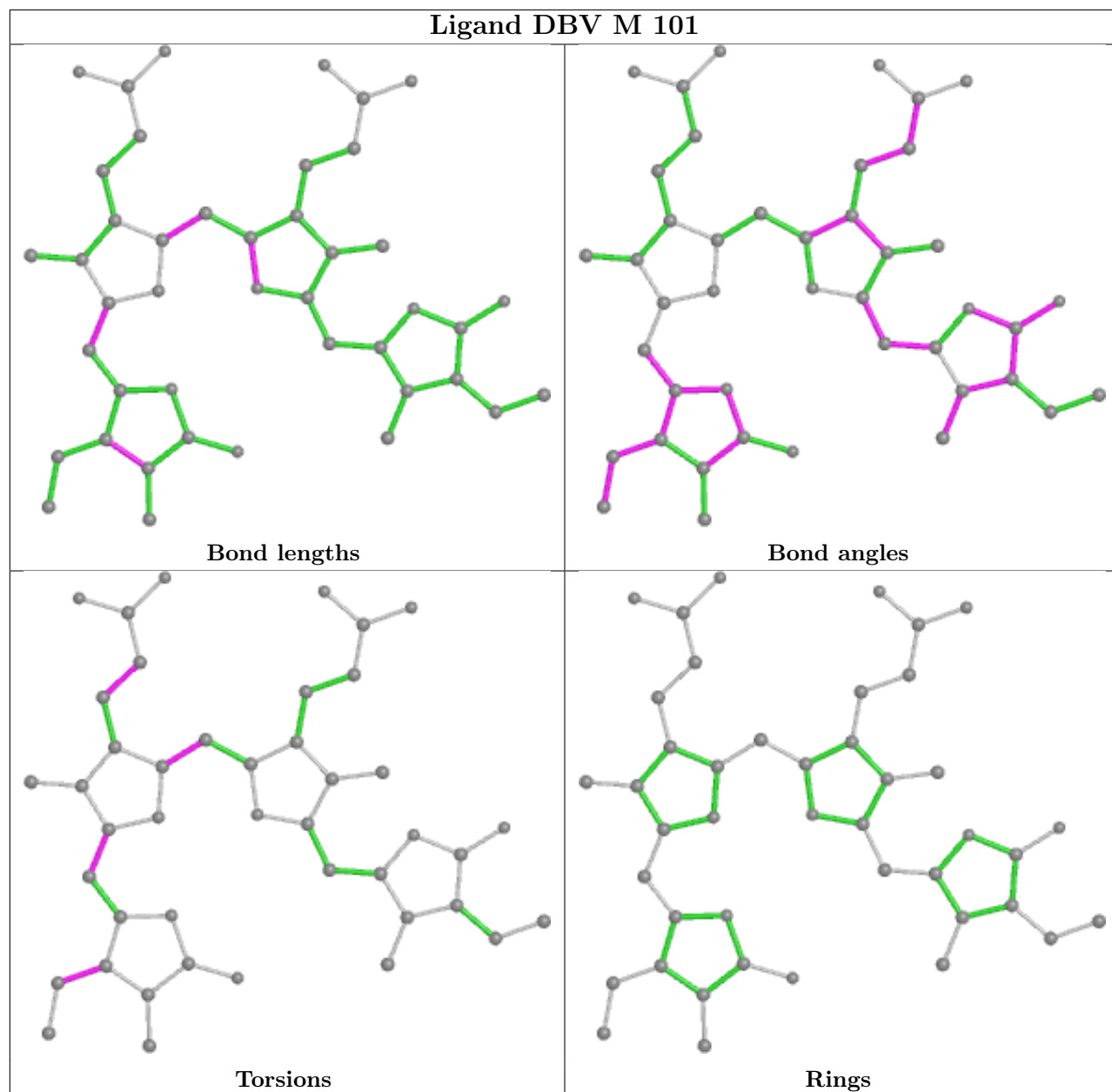
Bond angles

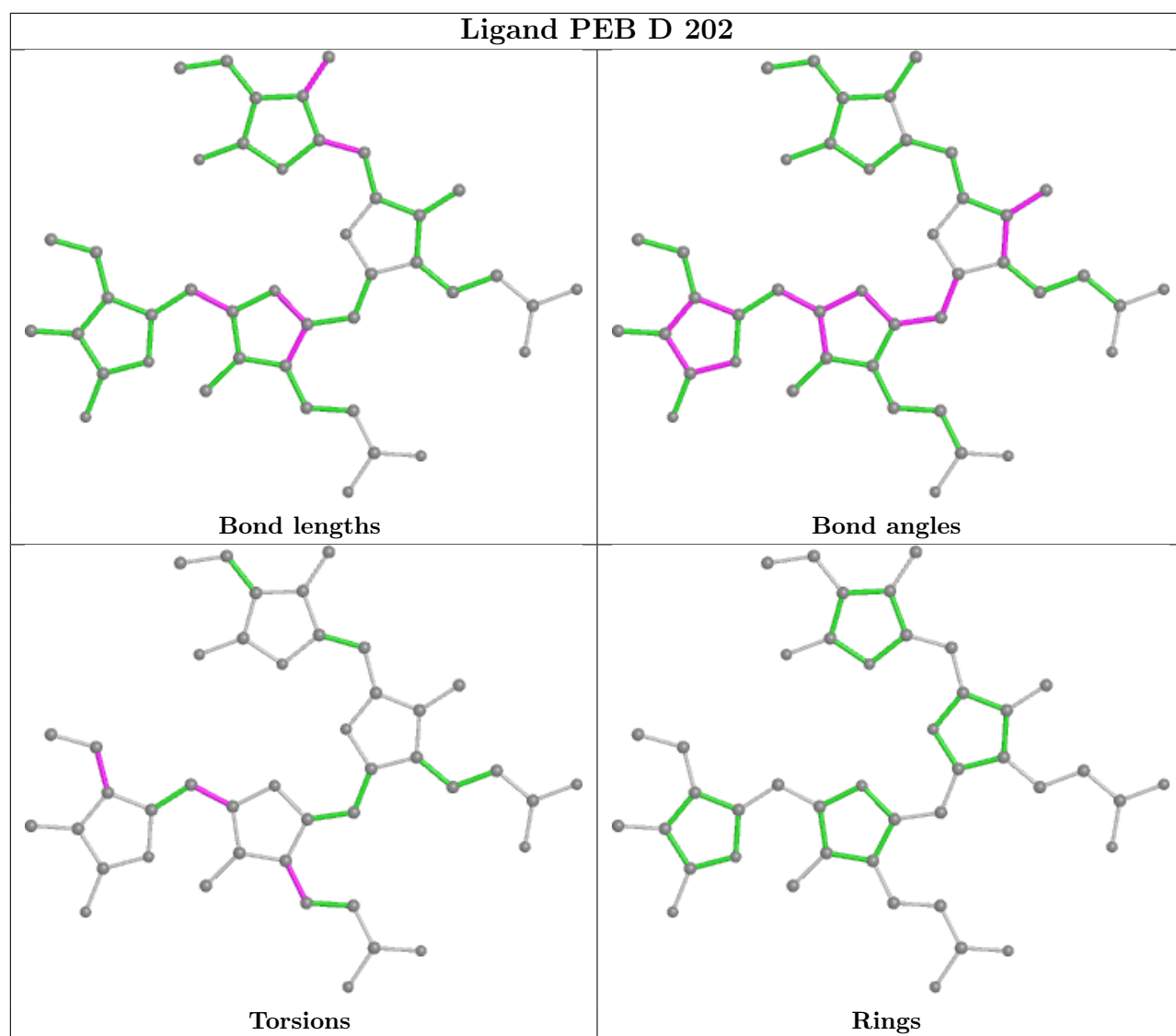


Torsions

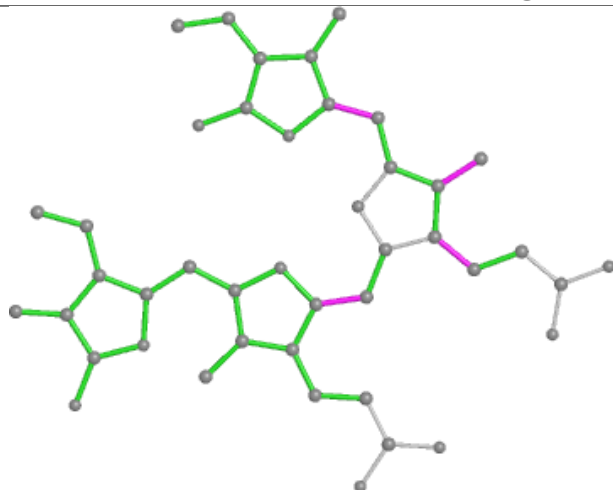


Rings

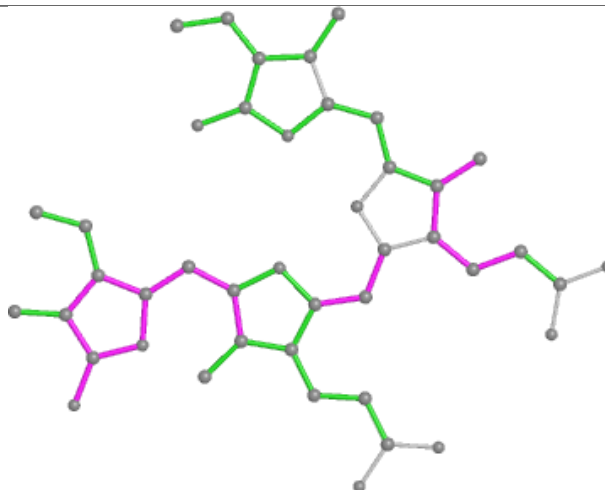




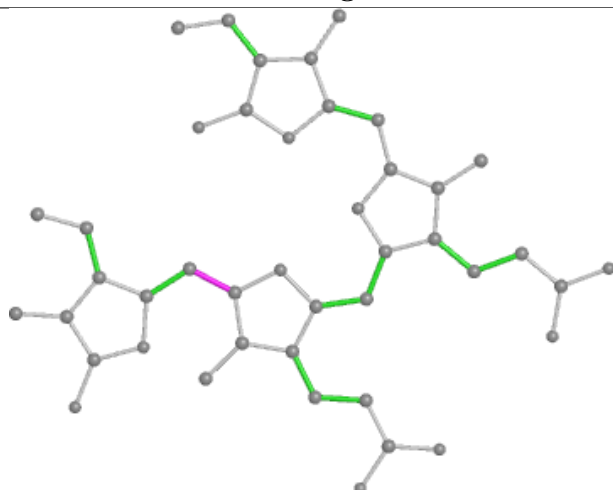
## Ligand PEB J 203



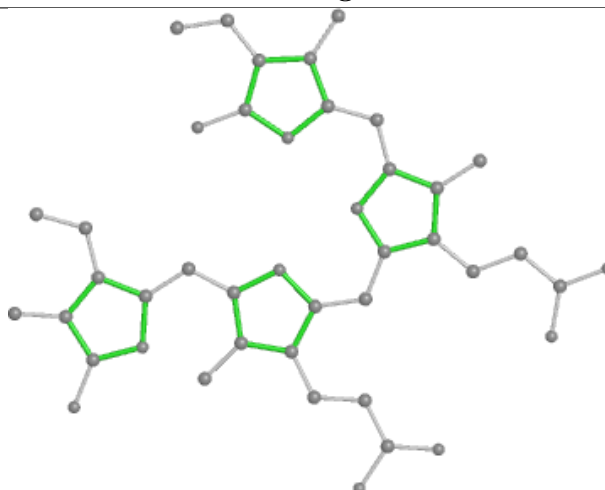
Bond lengths



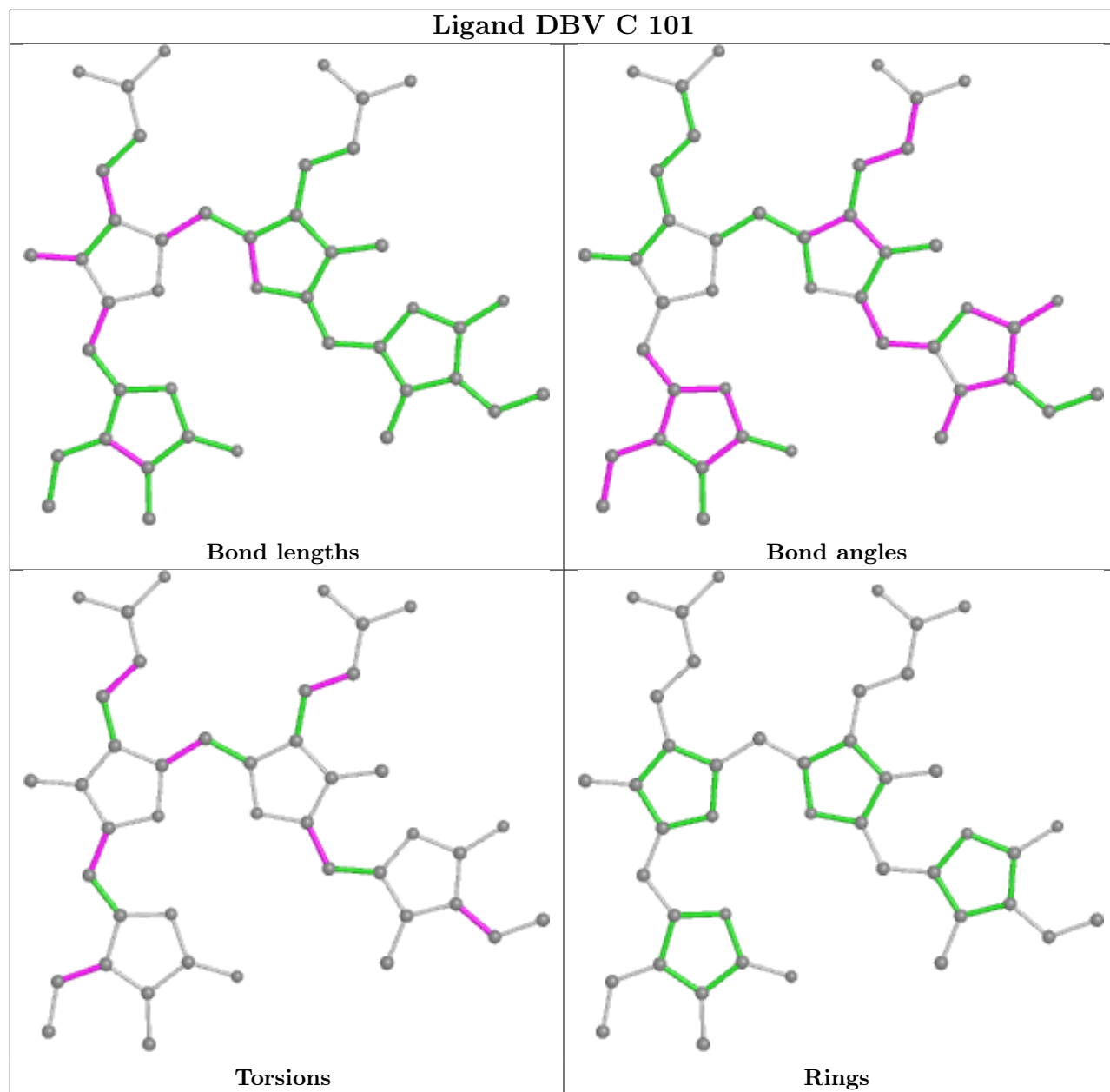
Bond angles



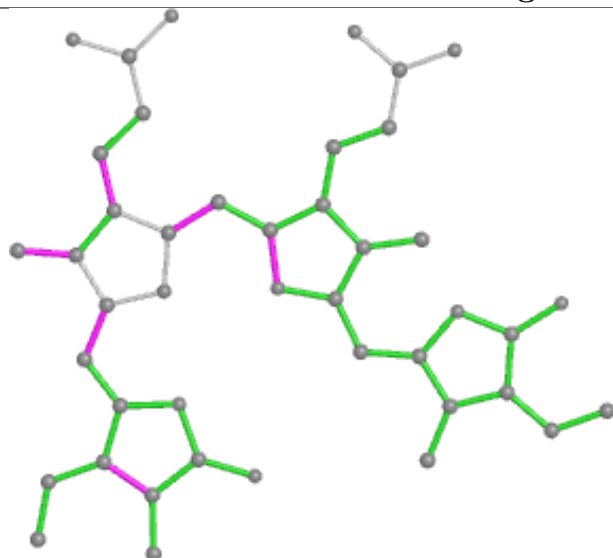
Torsions



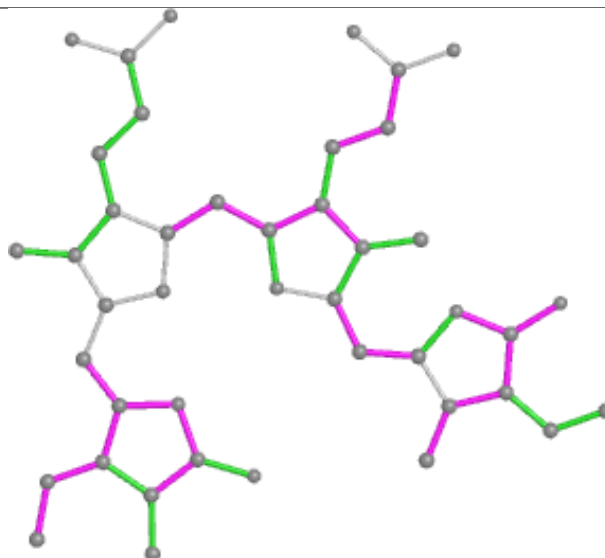
Rings



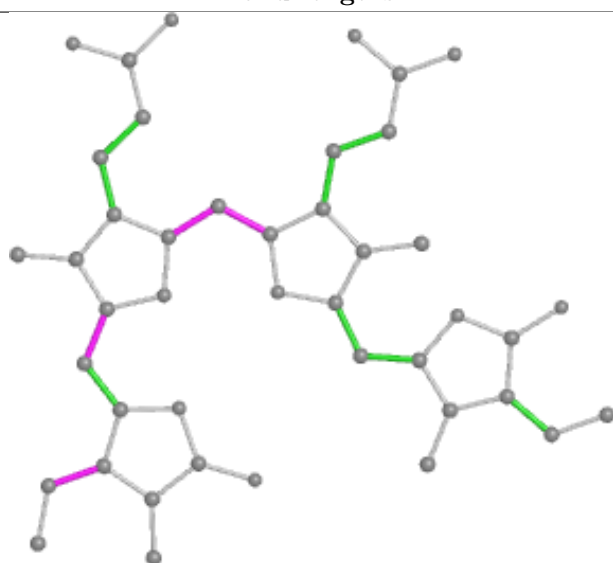
## Ligand DBV I 101



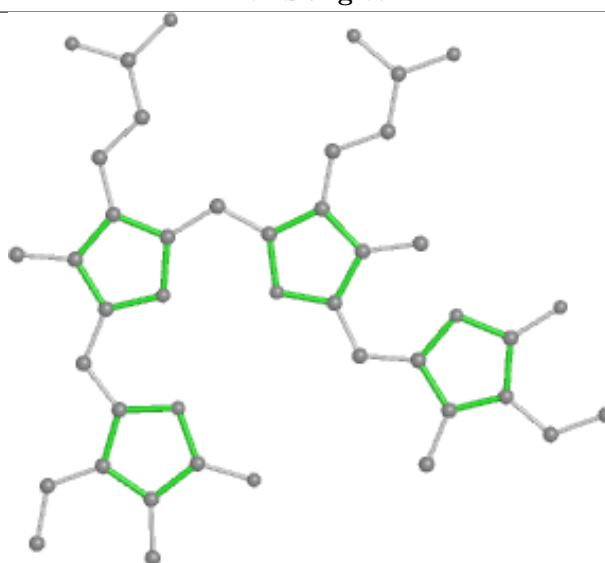
Bond lengths



Bond angles



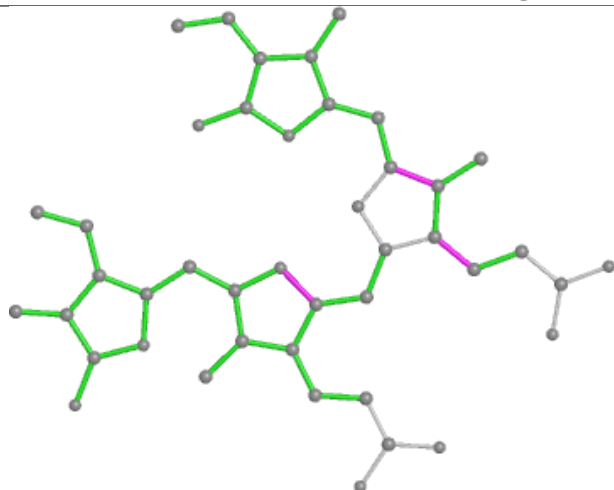
Torsions



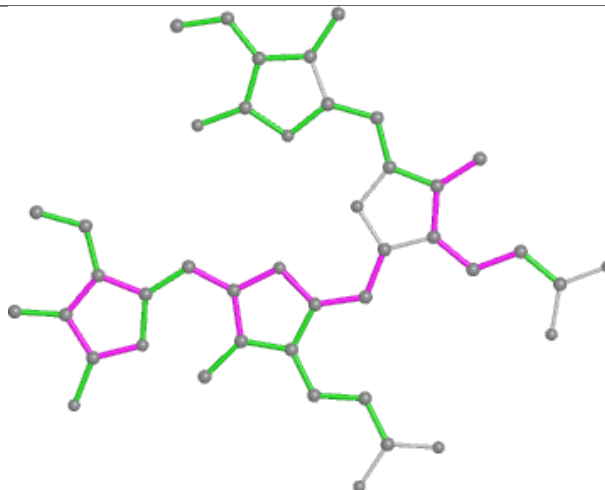
Rings



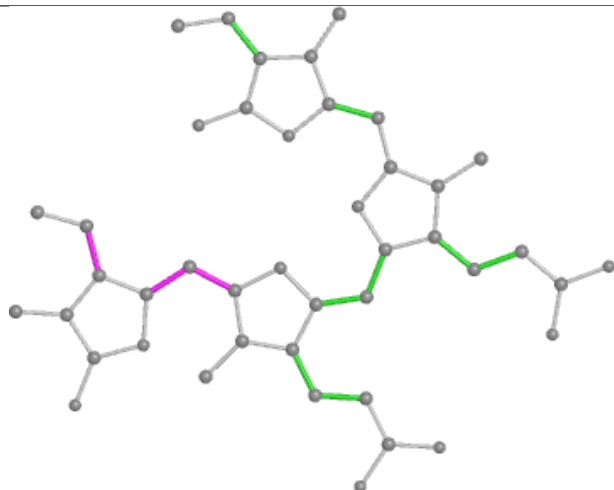
## Ligand PEB B 202



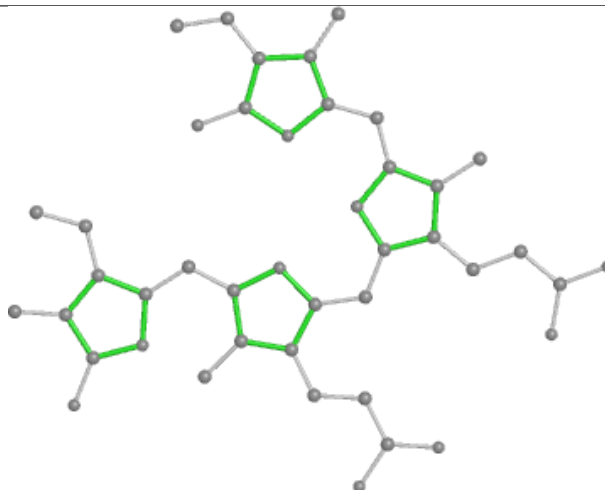
Bond lengths



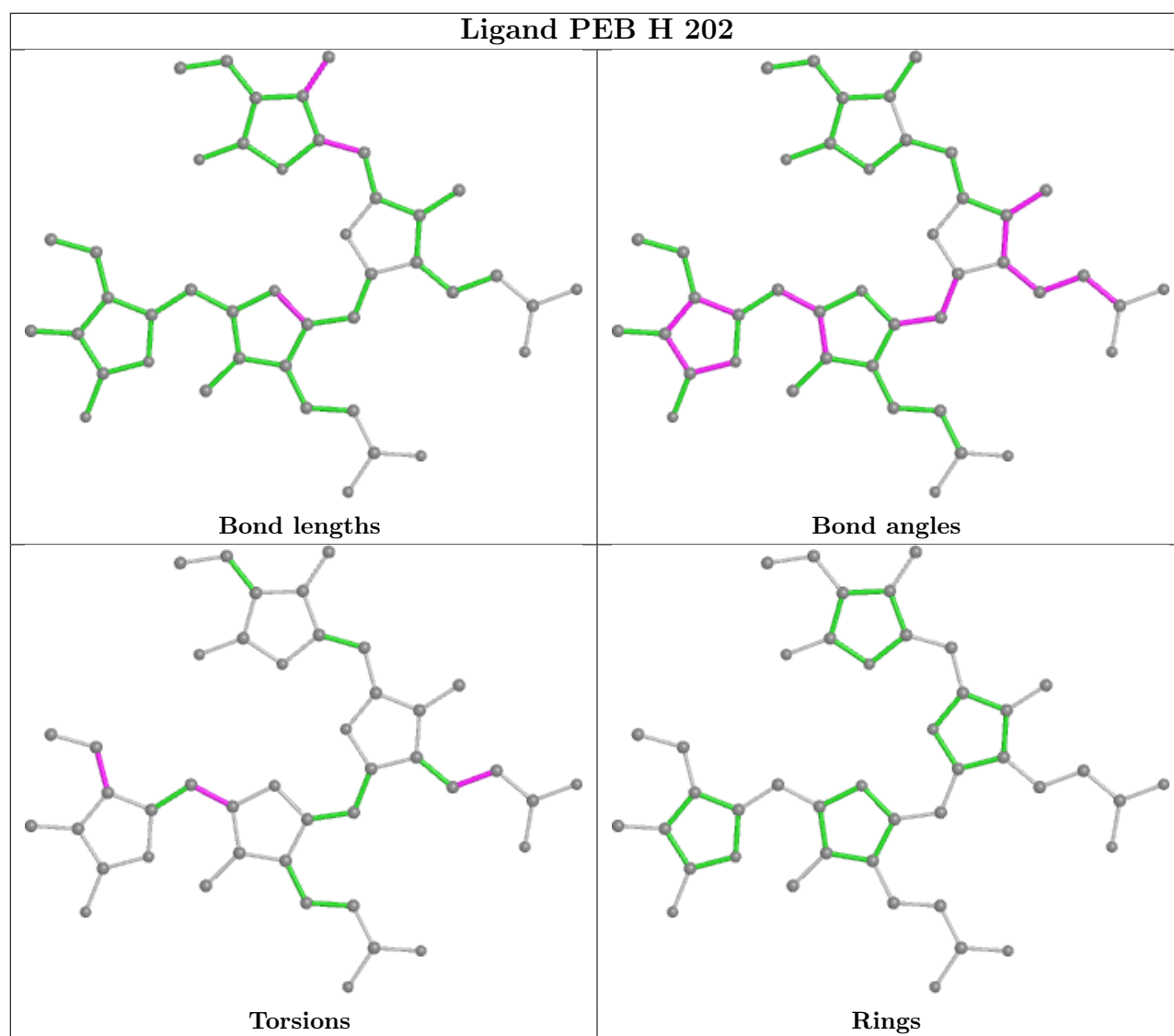
Bond angles



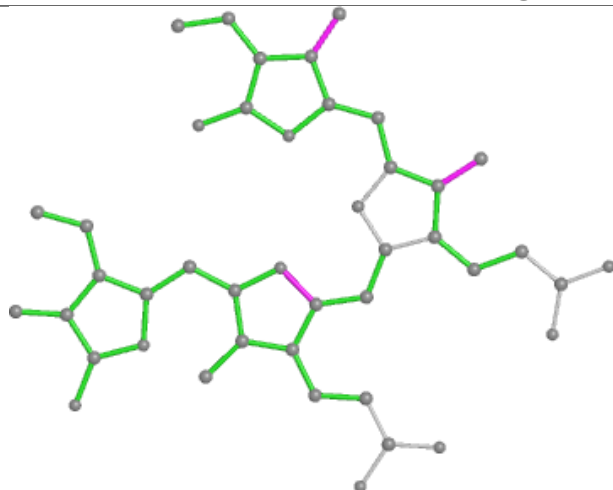
Torsions



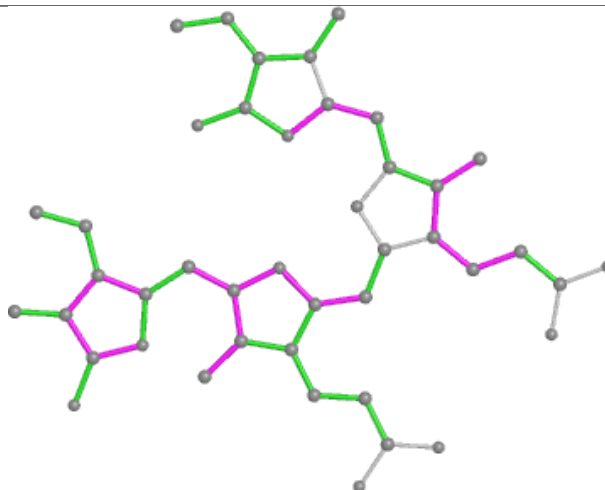
Rings



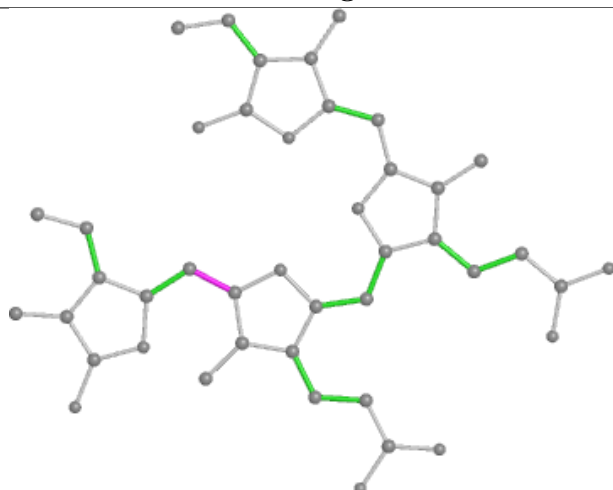
## Ligand PEB B 203



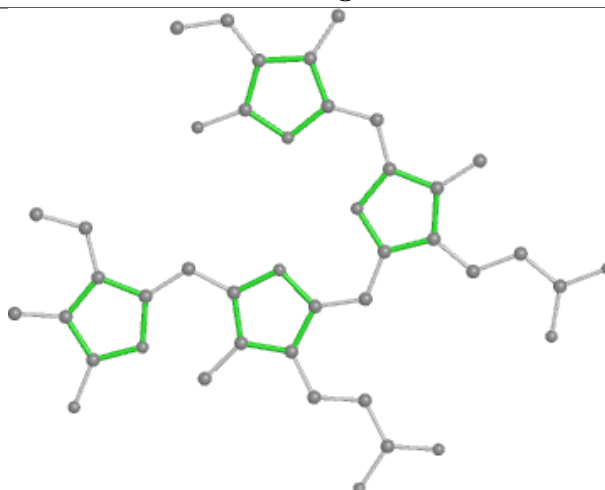
Bond lengths



Bond angles

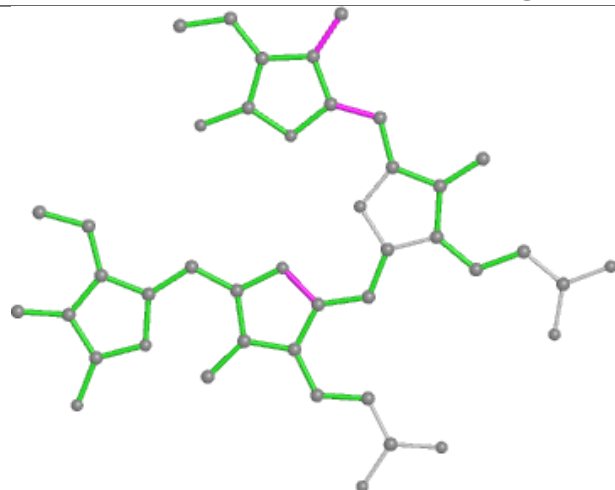


Torsions

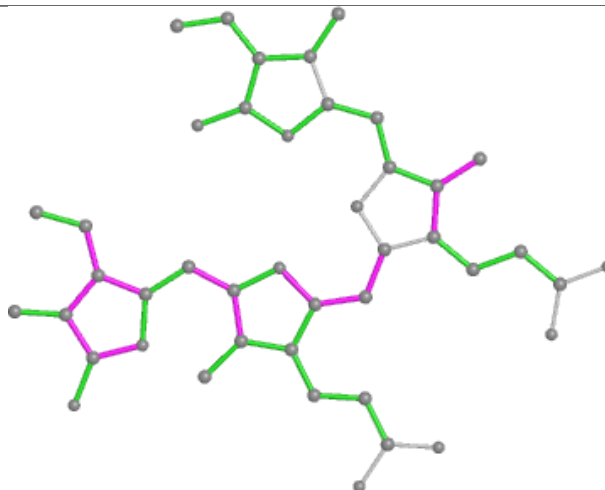


Rings

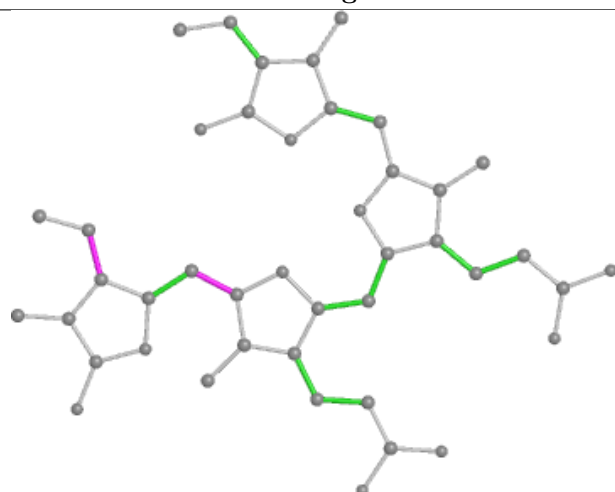
## Ligand PEB F 202



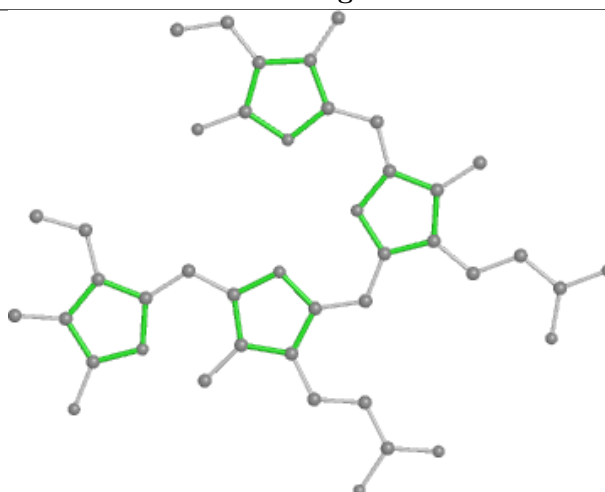
Bond lengths



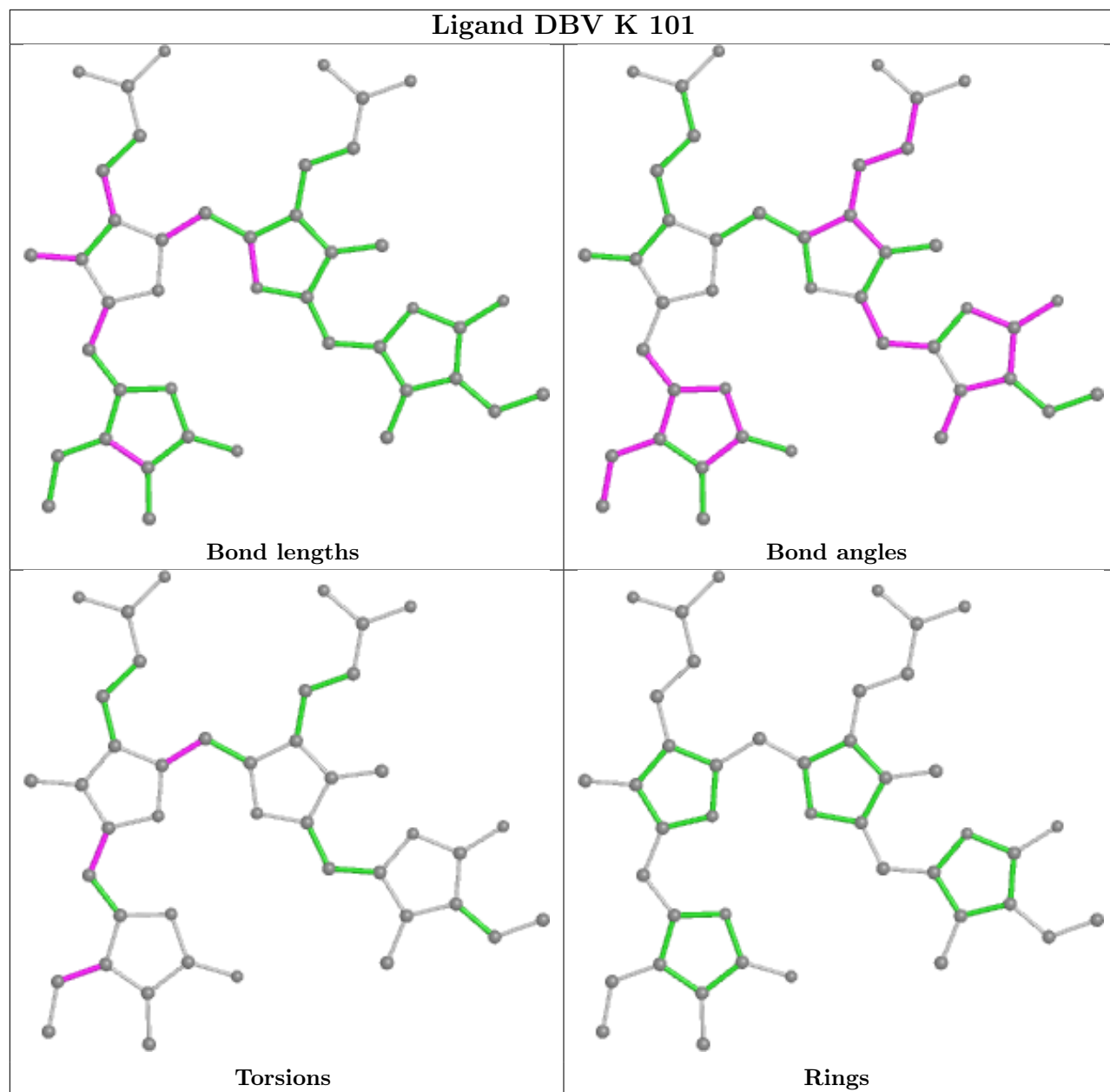
Bond angles

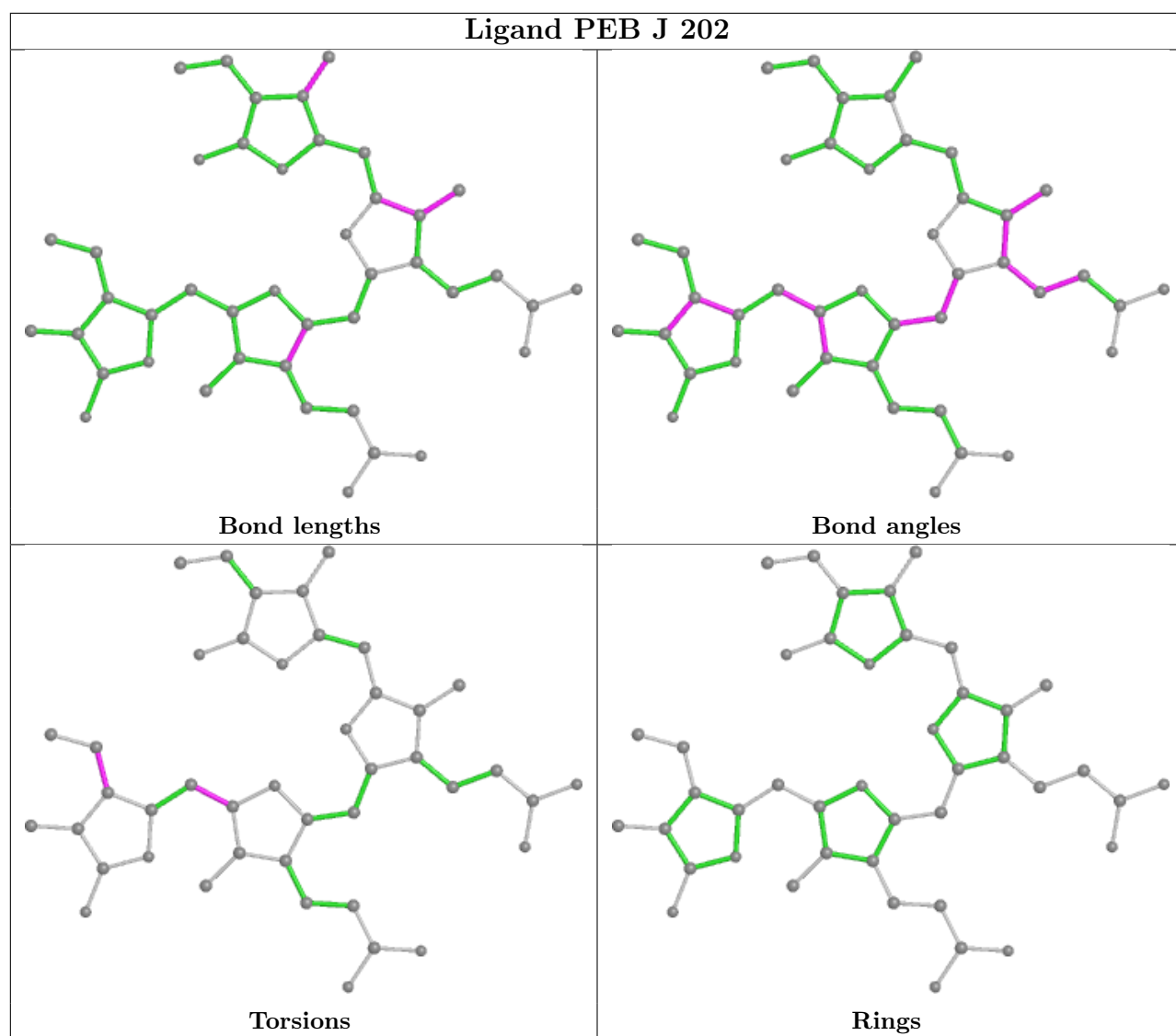


Torsions

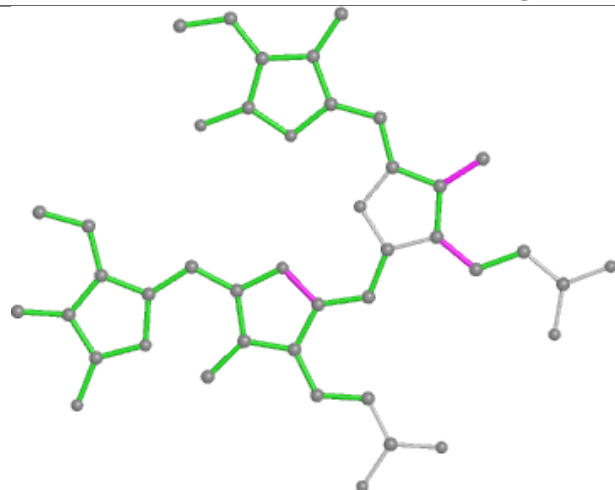


Rings

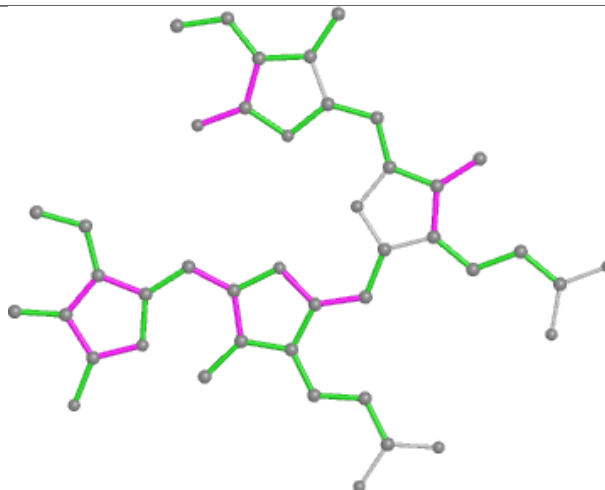




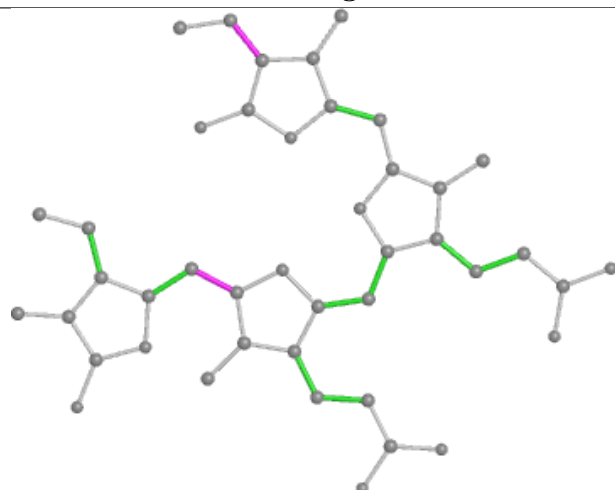
## Ligand PEB N 201



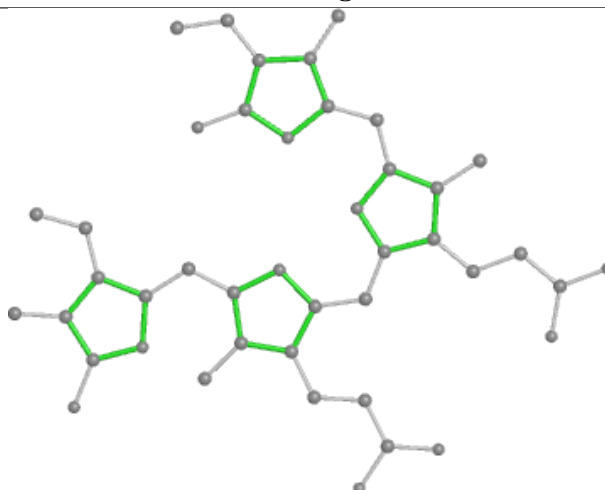
Bond lengths



Bond angles

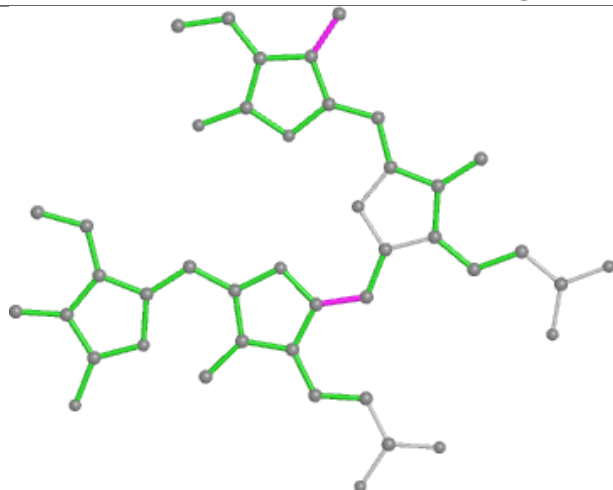


Torsions

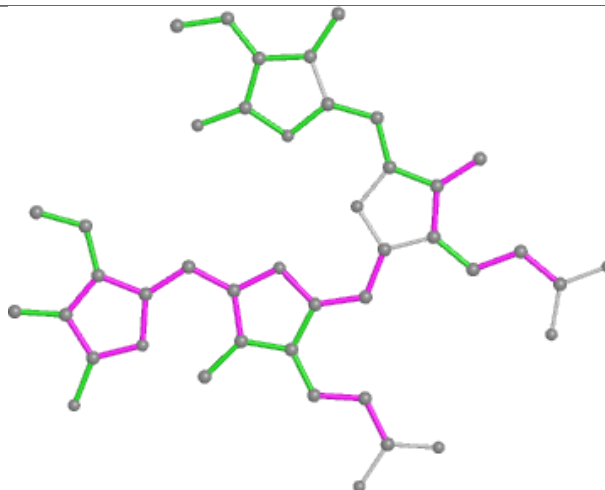


Rings

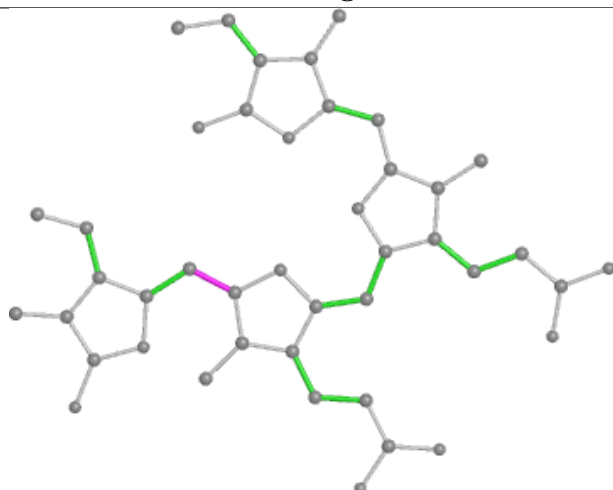
## Ligand PEB P 203



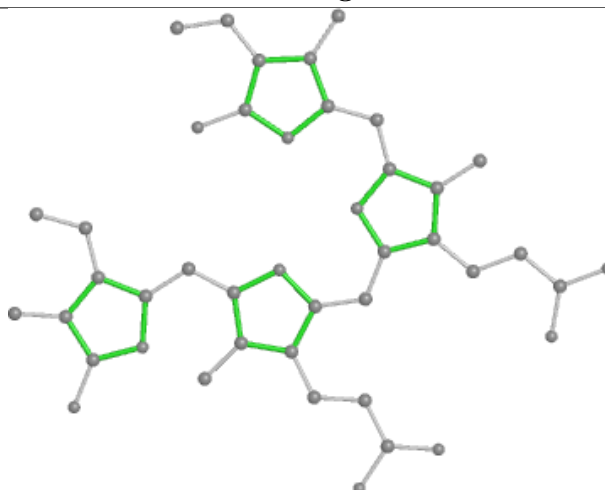
Bond lengths



Bond angles



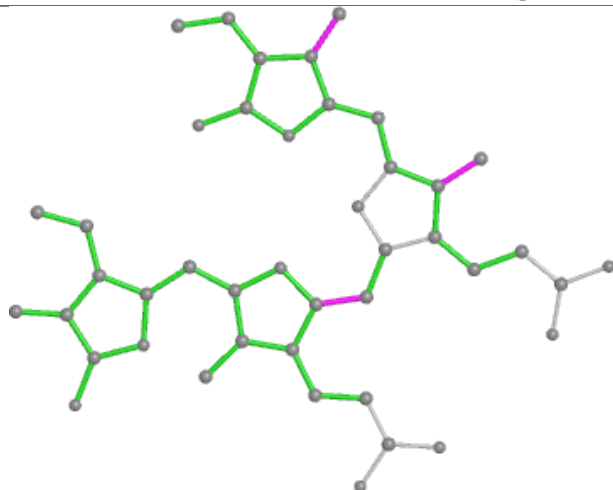
Torsions



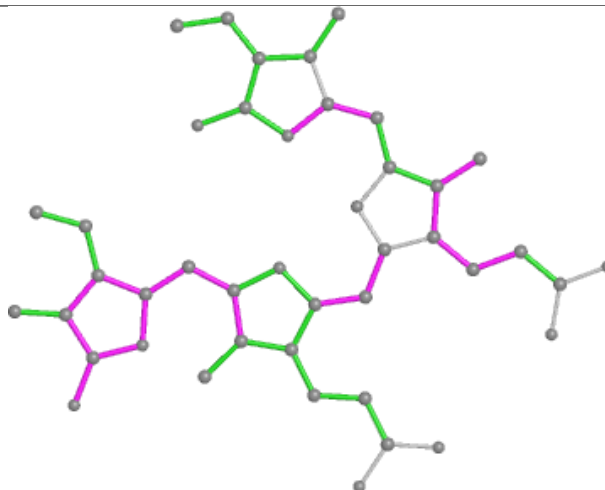
Rings



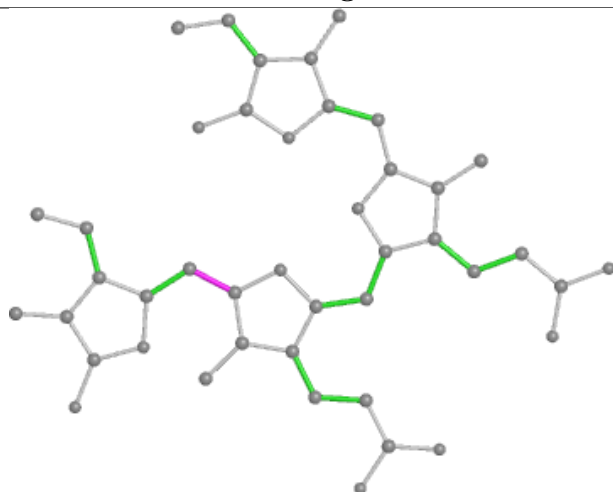
## Ligand PEB D 203



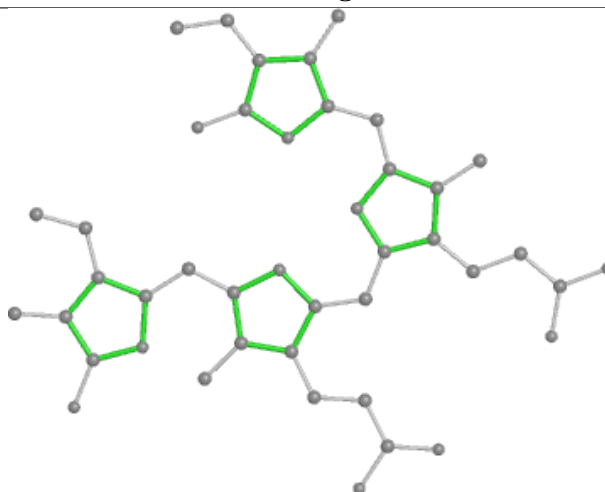
Bond lengths



Bond angles

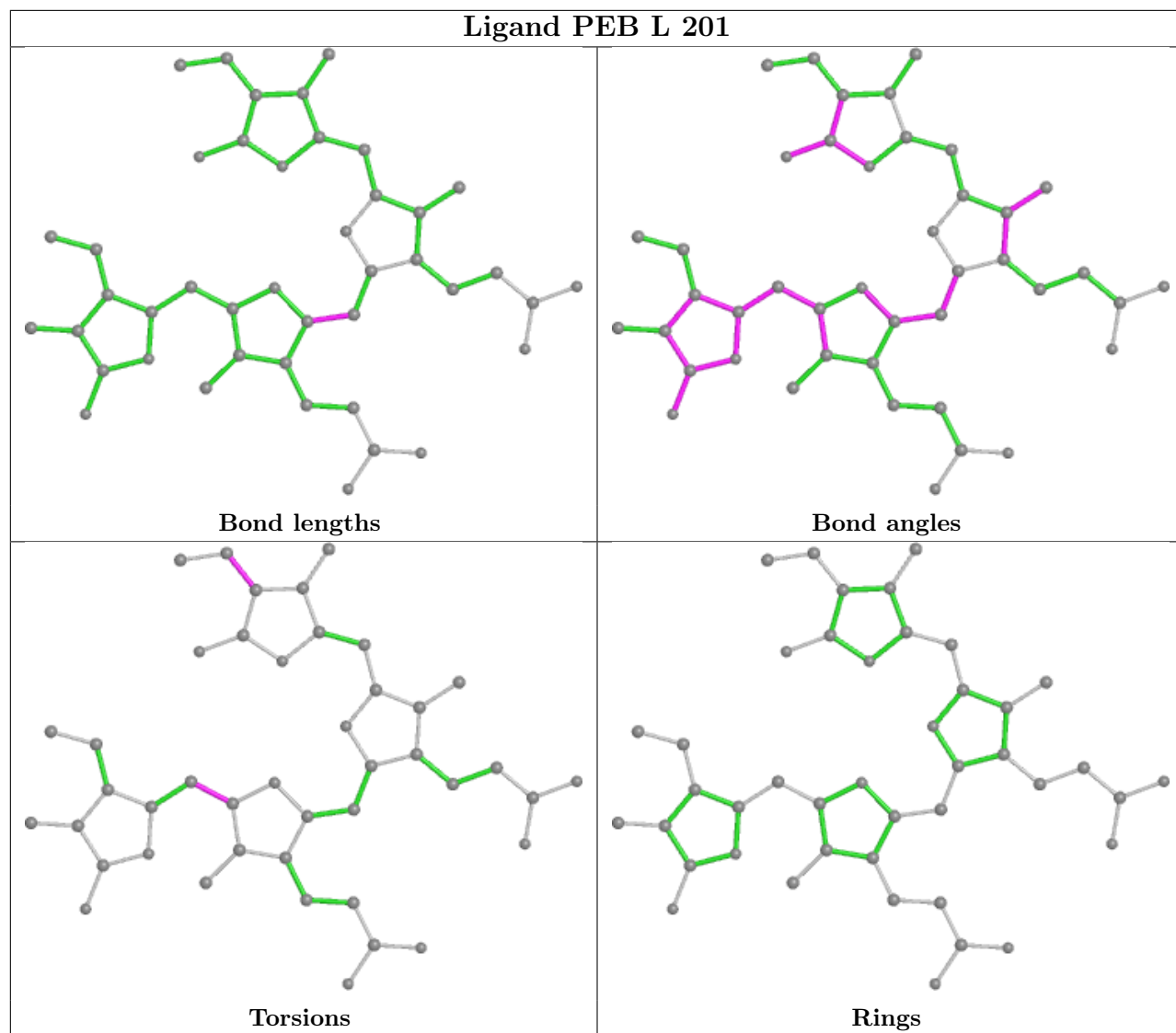


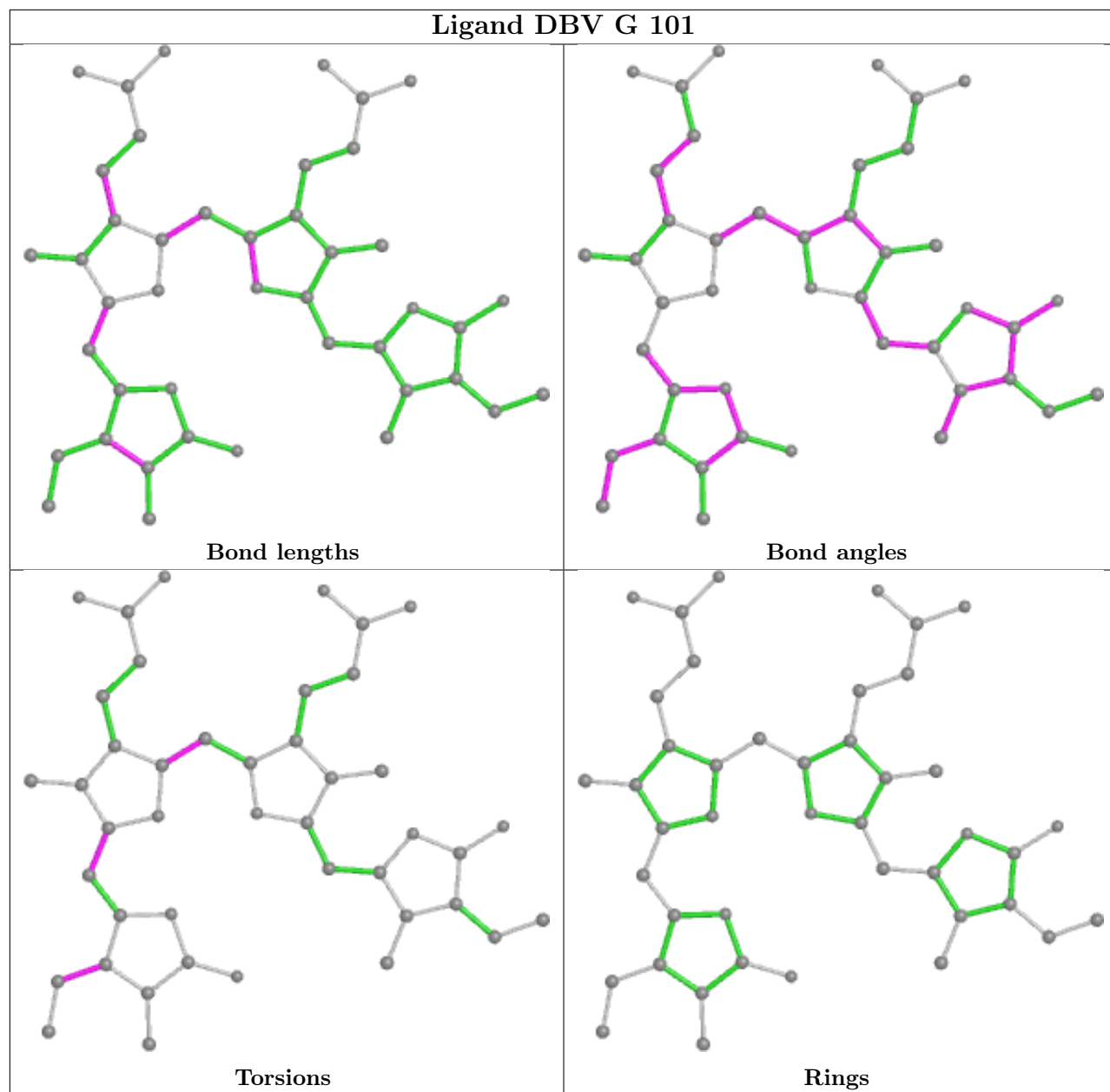
Torsions



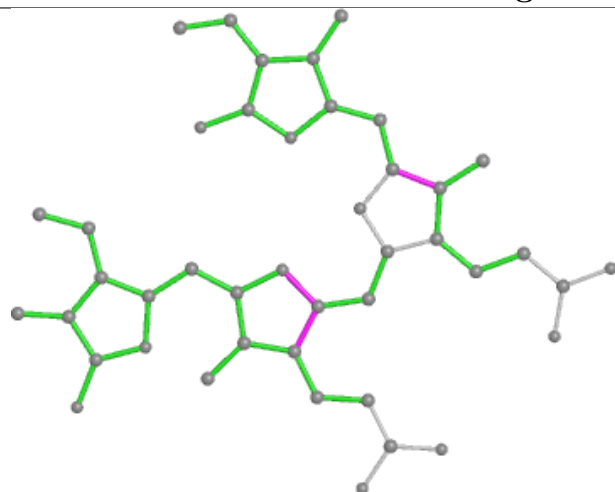
Rings

## Ligand PEB L 201

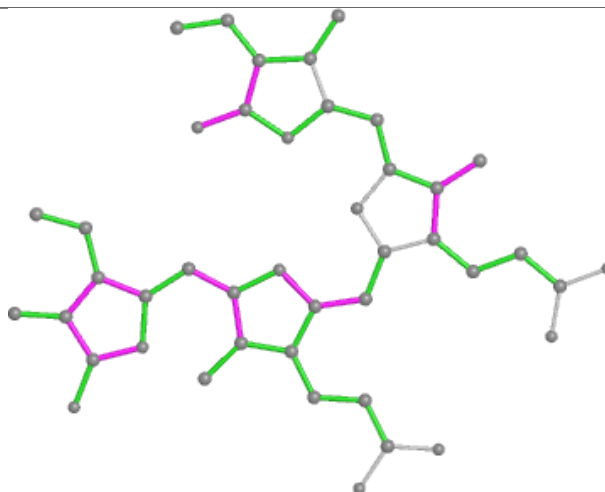




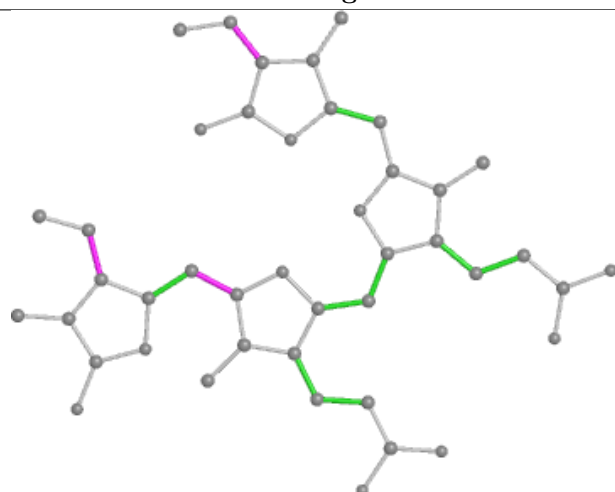
## Ligand PEB H 201



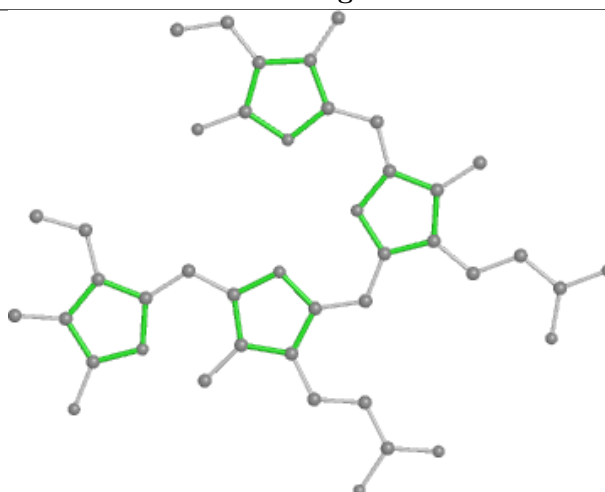
Bond lengths



Bond angles

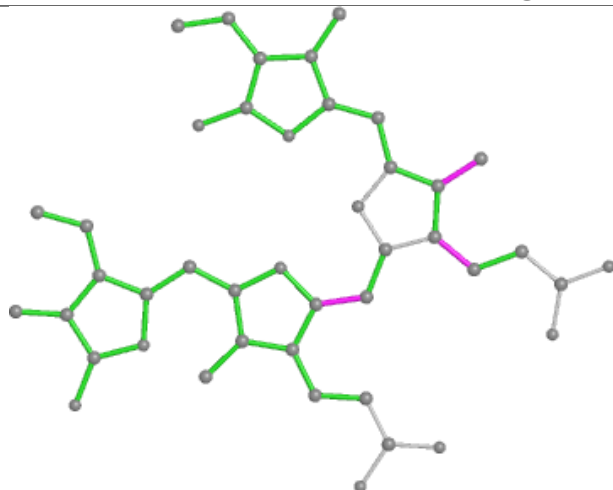


Torsions

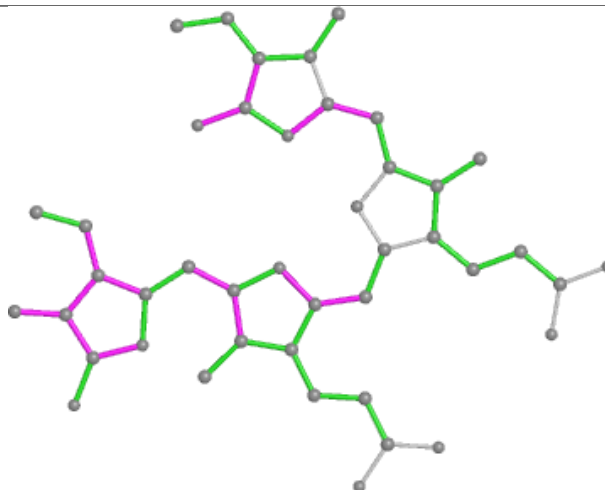


Rings

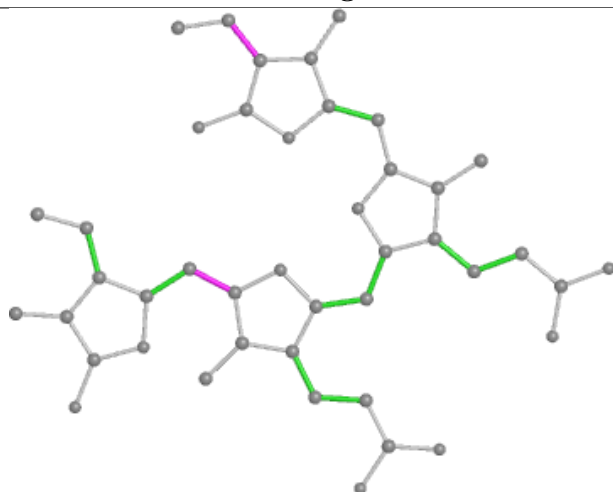
## Ligand PEB J 201



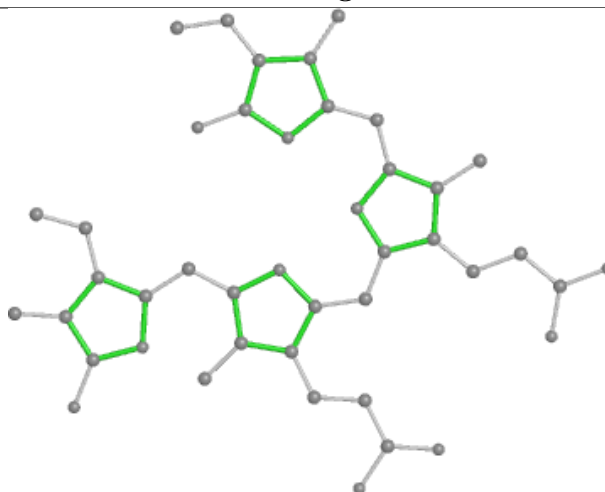
Bond lengths



Bond angles

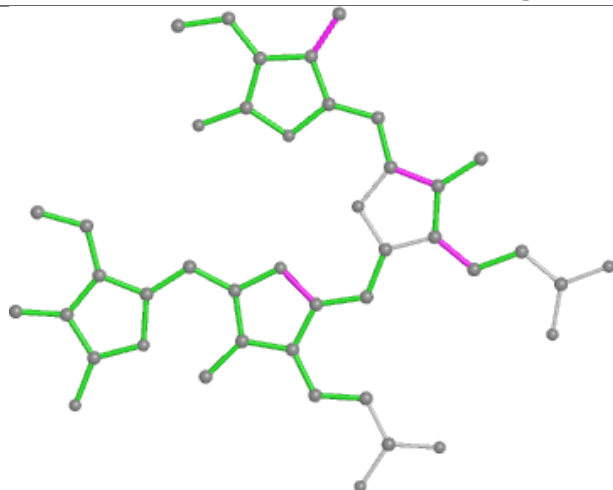


Torsions

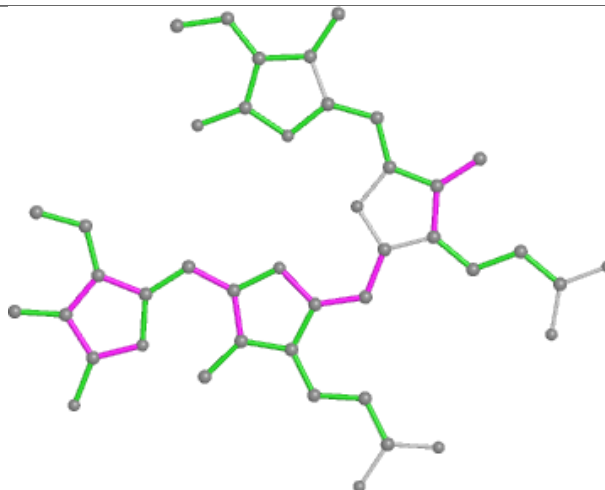


Rings

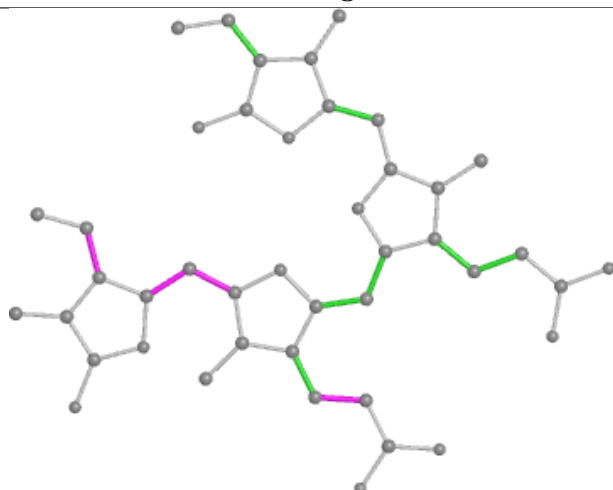
## Ligand PEB L 202



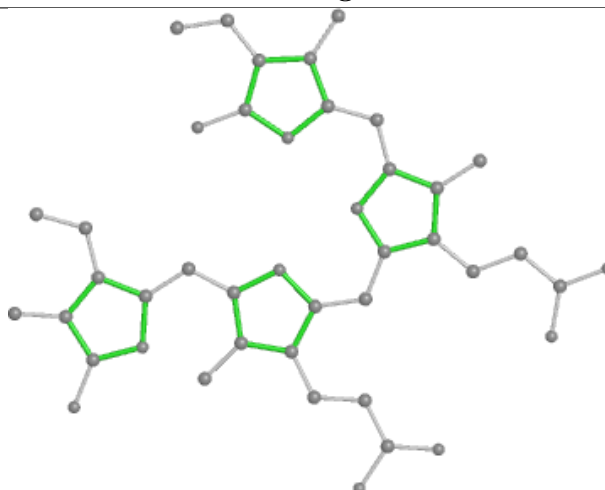
Bond lengths



Bond angles

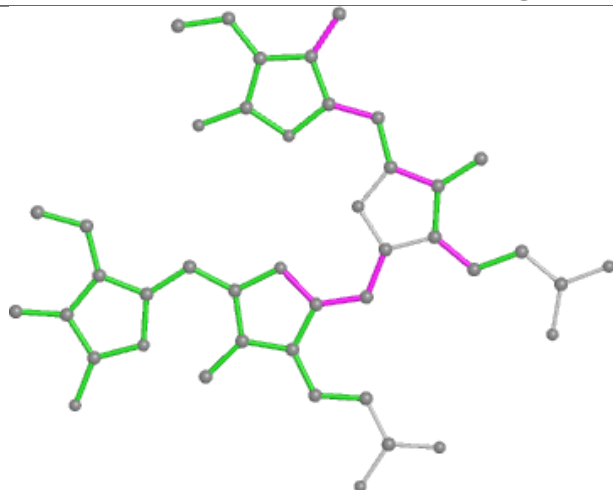


Torsions

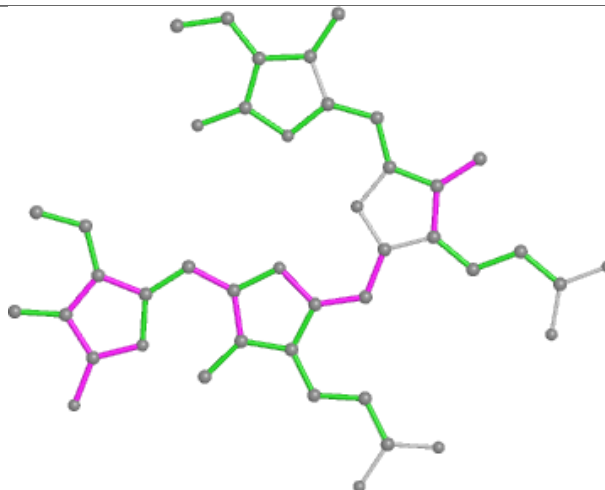


Rings

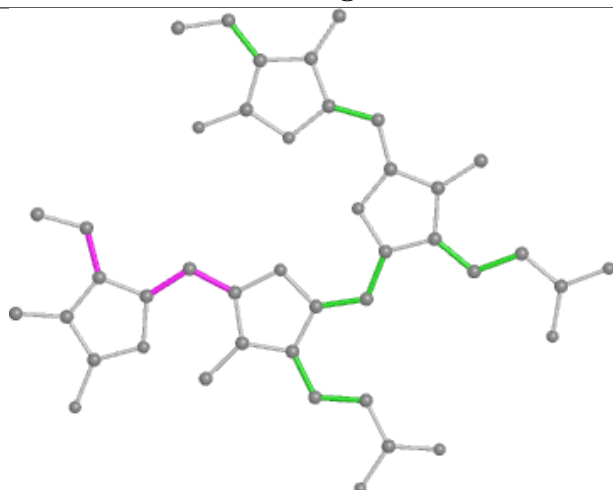
## Ligand PEB P 202



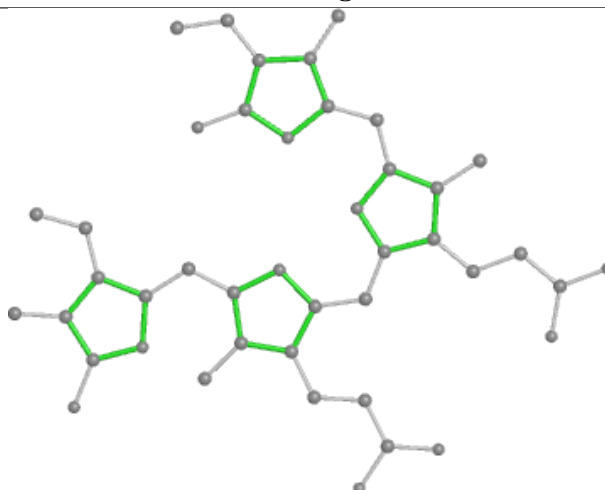
Bond lengths



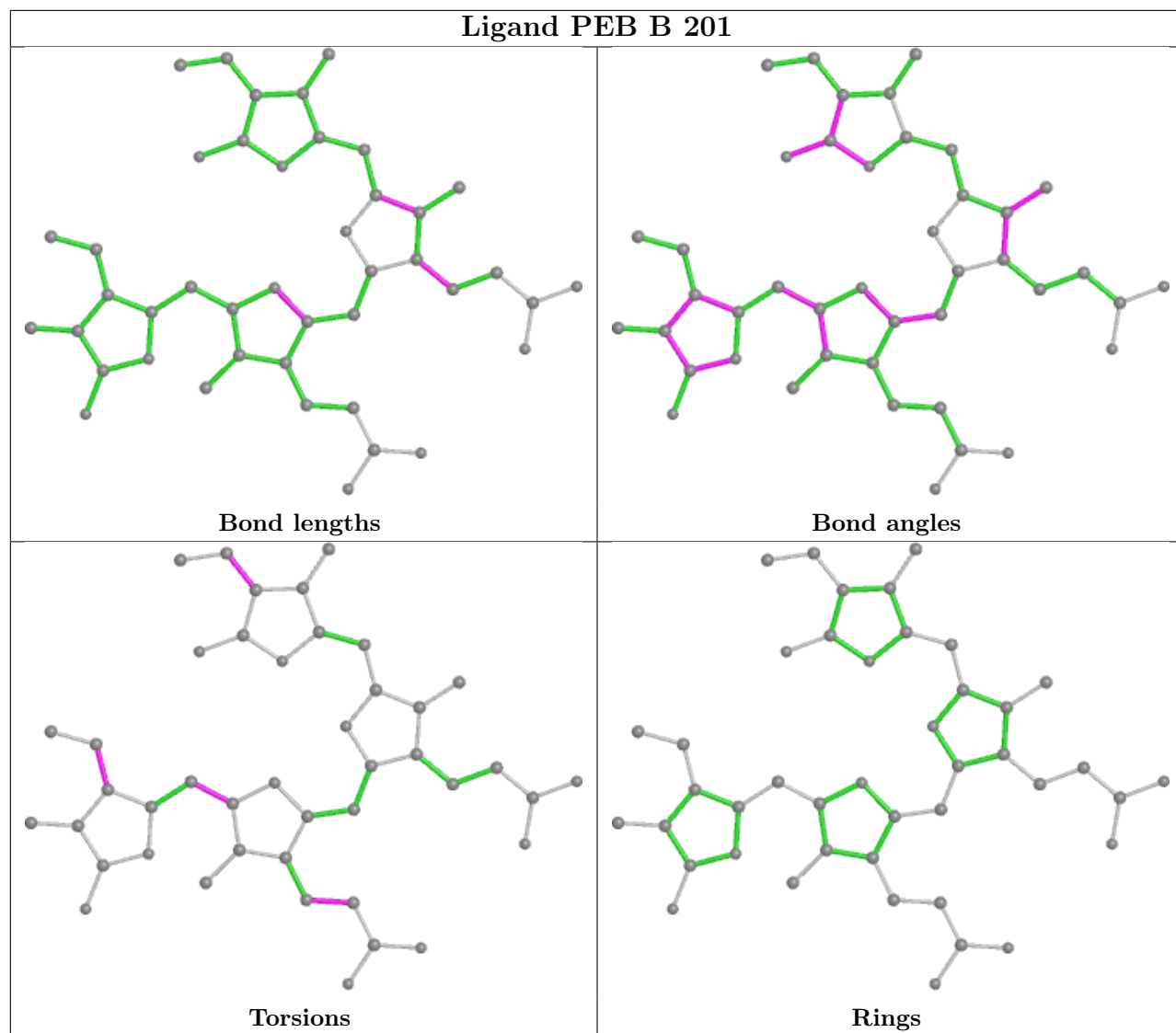
Bond angles



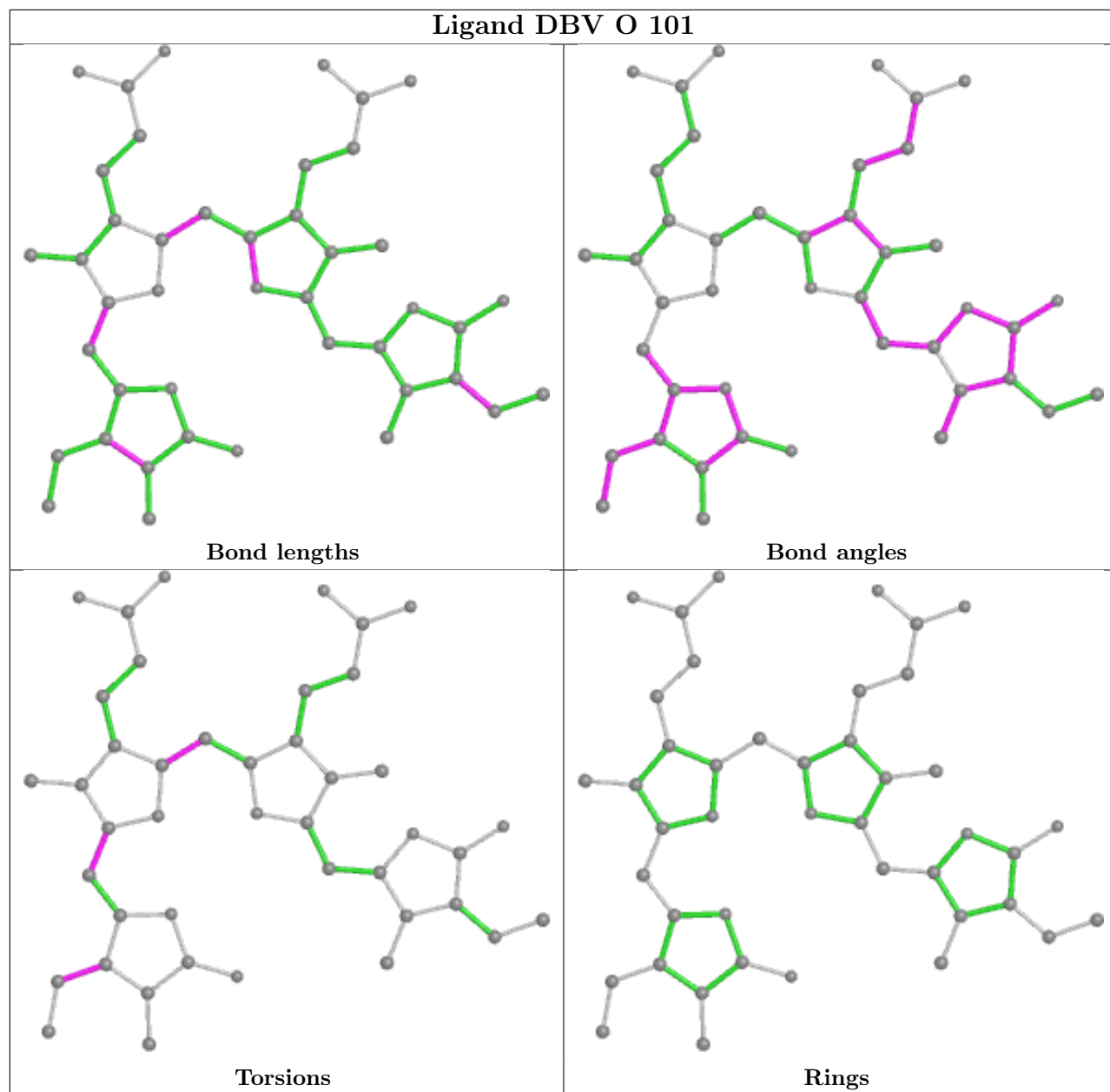
Torsions



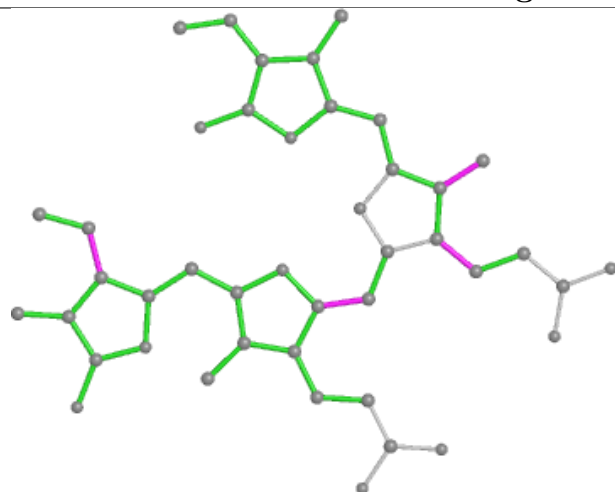
Rings



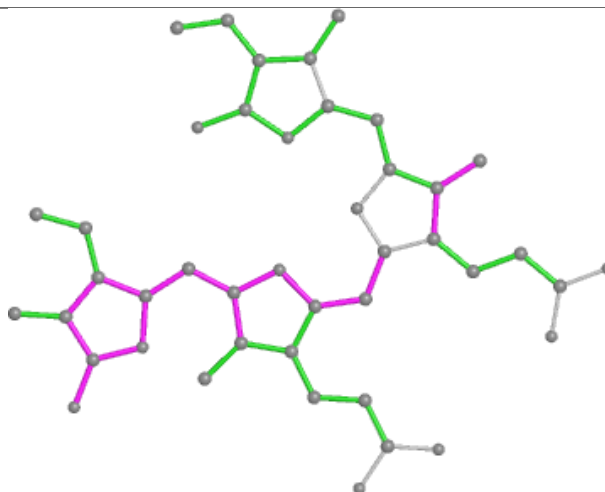




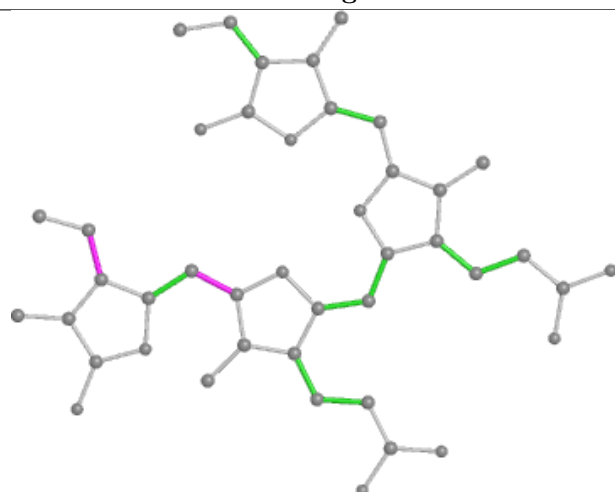
## Ligand PEB H 203



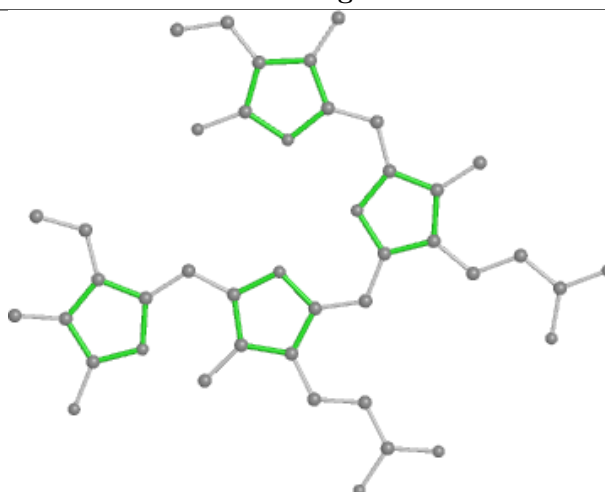
Bond lengths



Bond angles

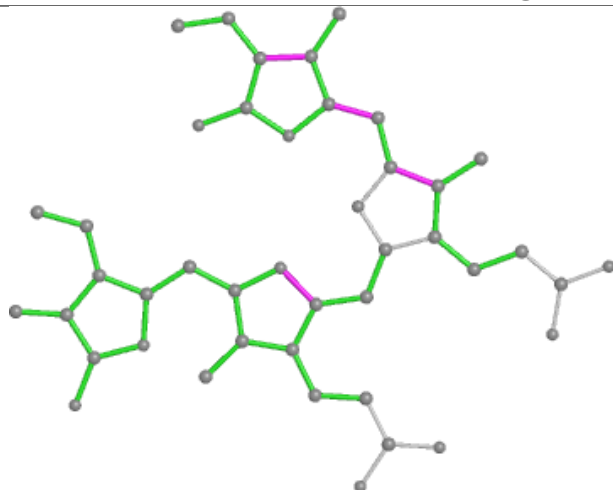


Torsions

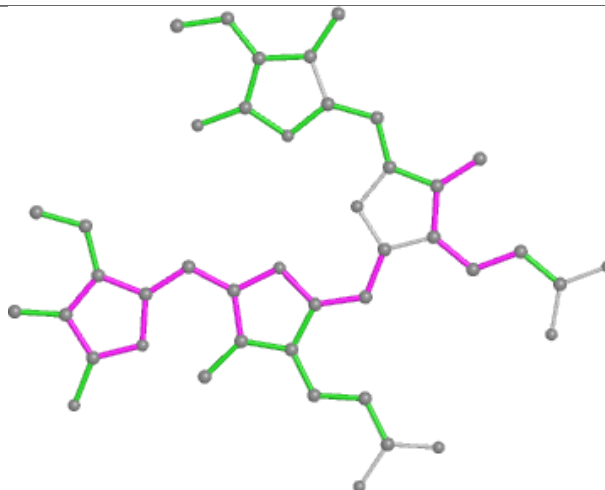


Rings

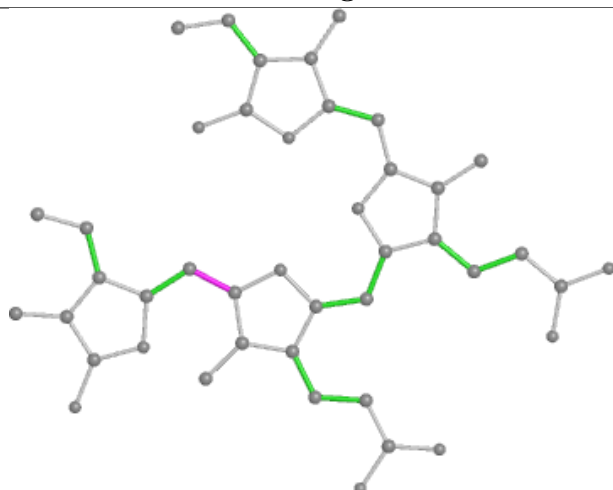
## Ligand PEB L 203



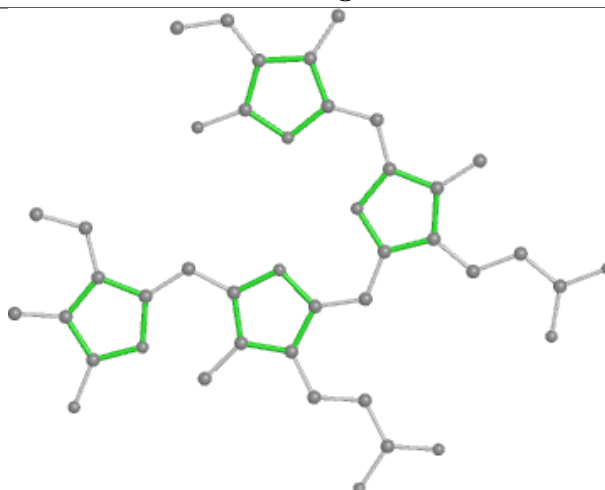
Bond lengths



Bond angles

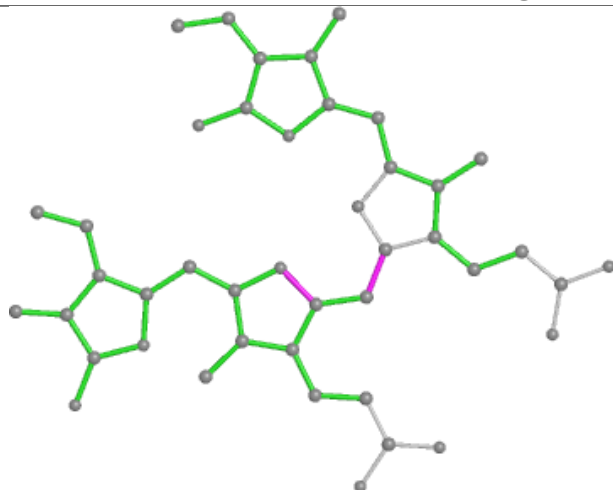


Torsions

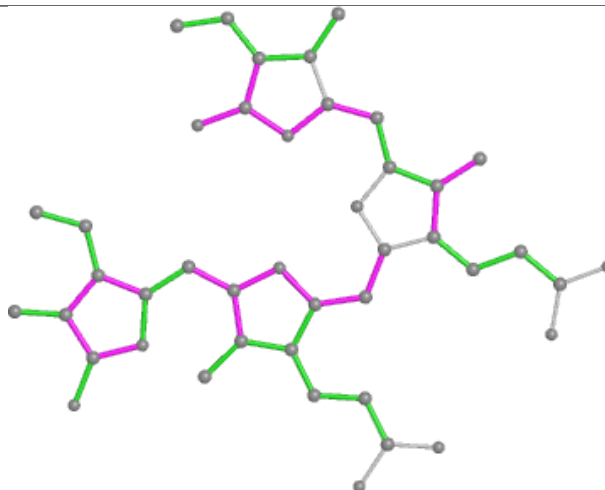


Rings

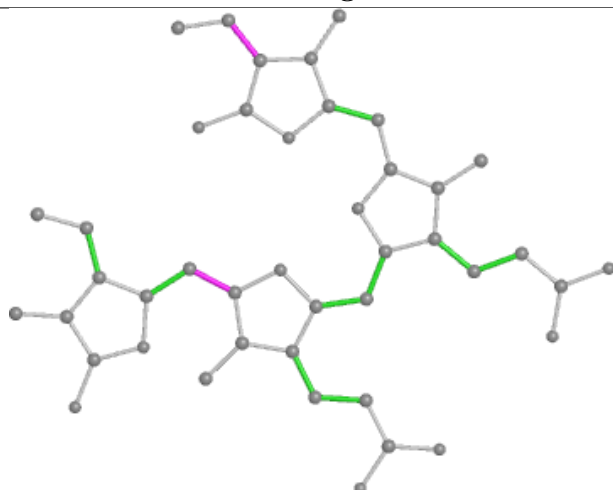
## Ligand PEB P 201



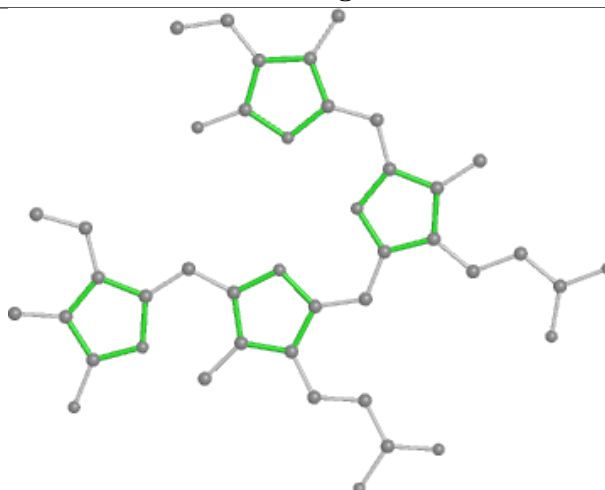
Bond lengths



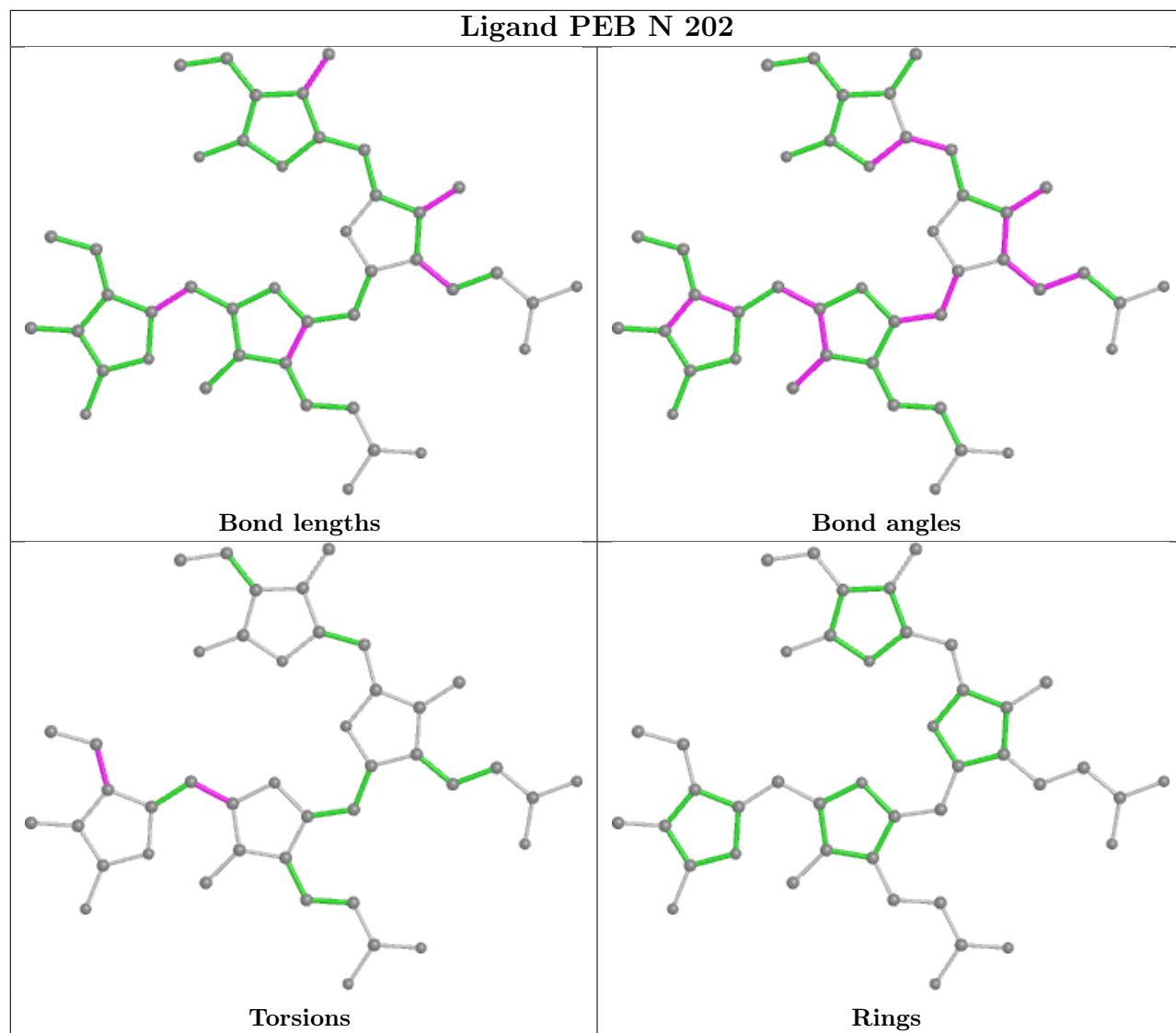
Bond angles

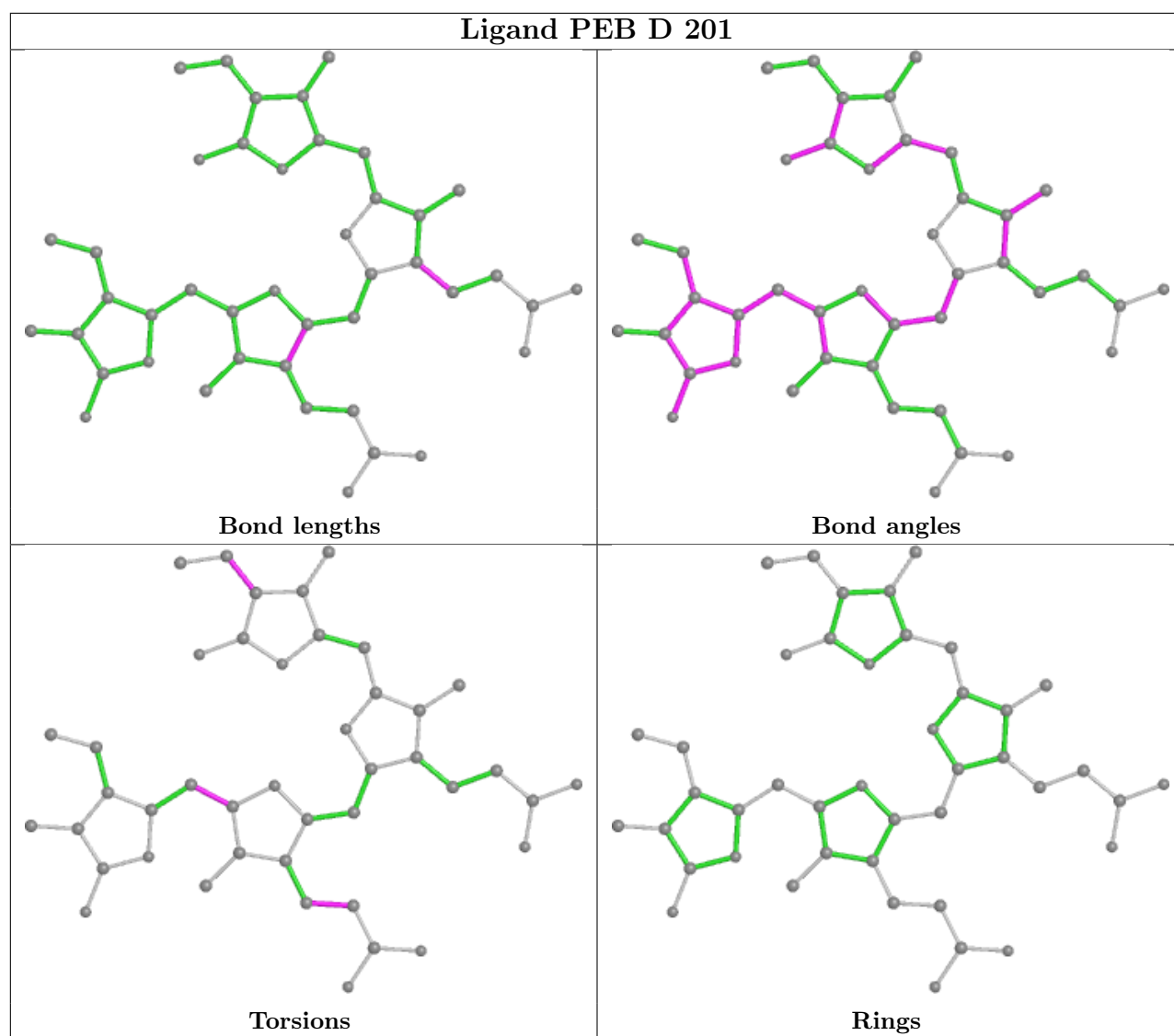


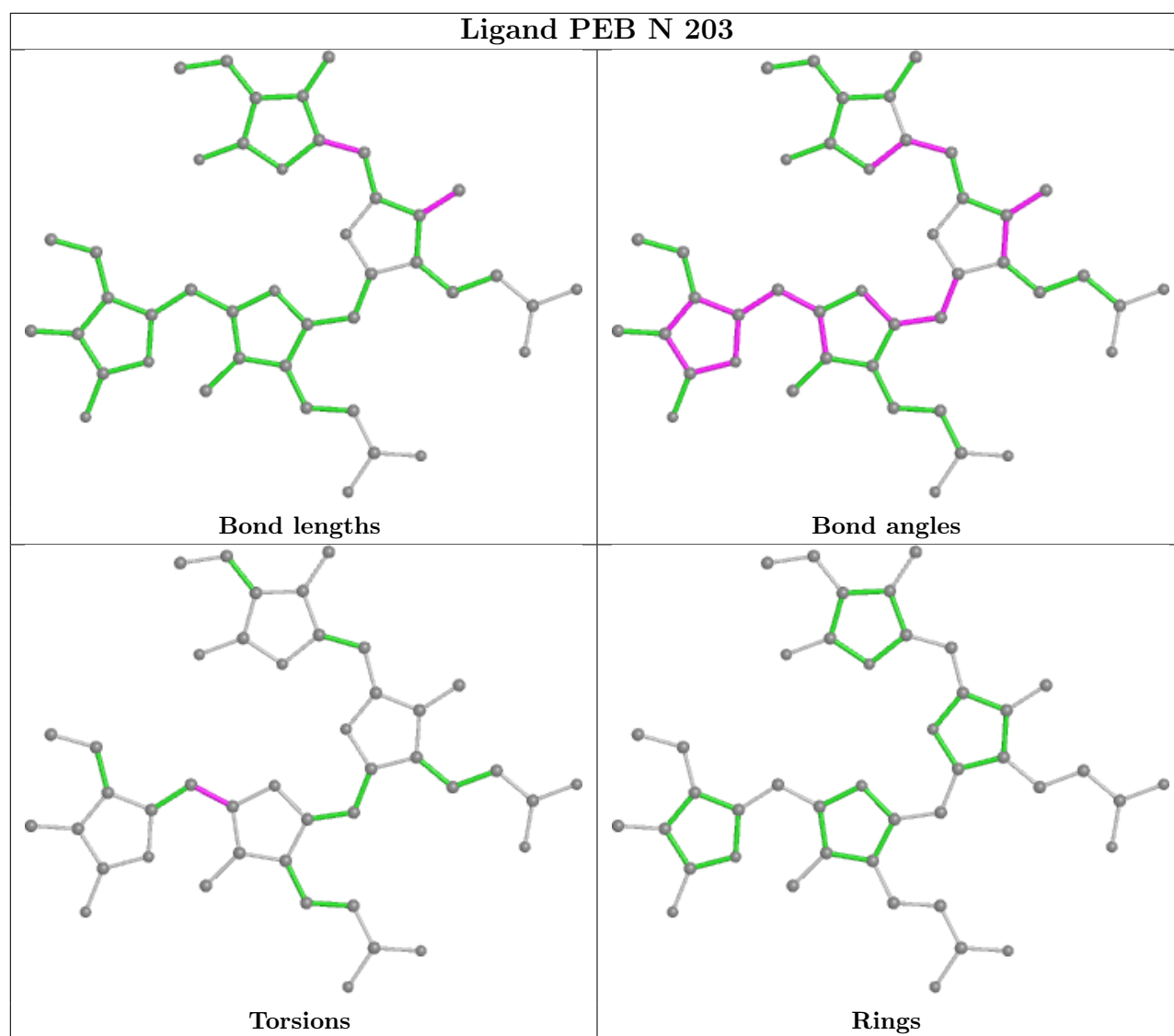
Torsions

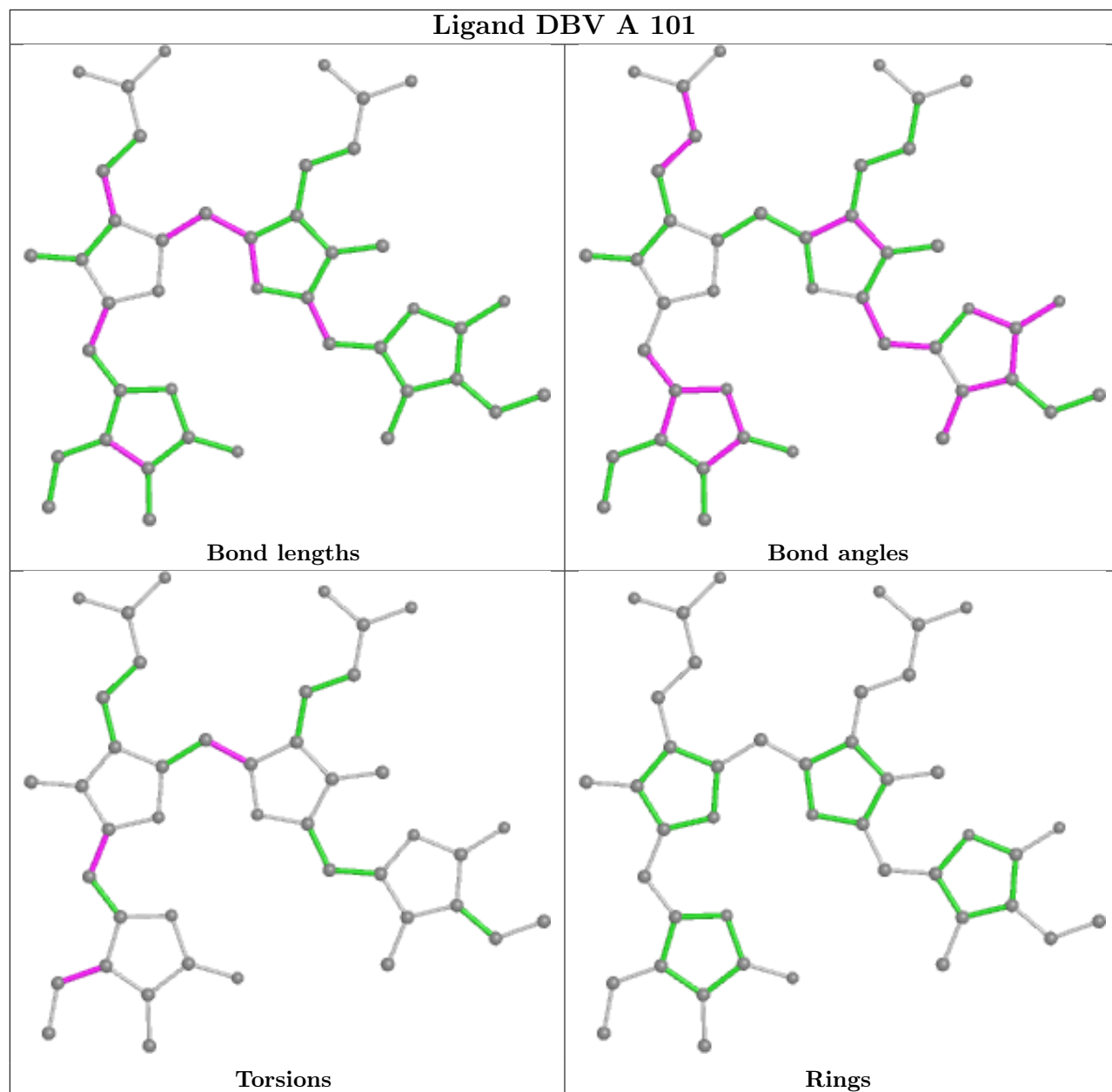


Rings



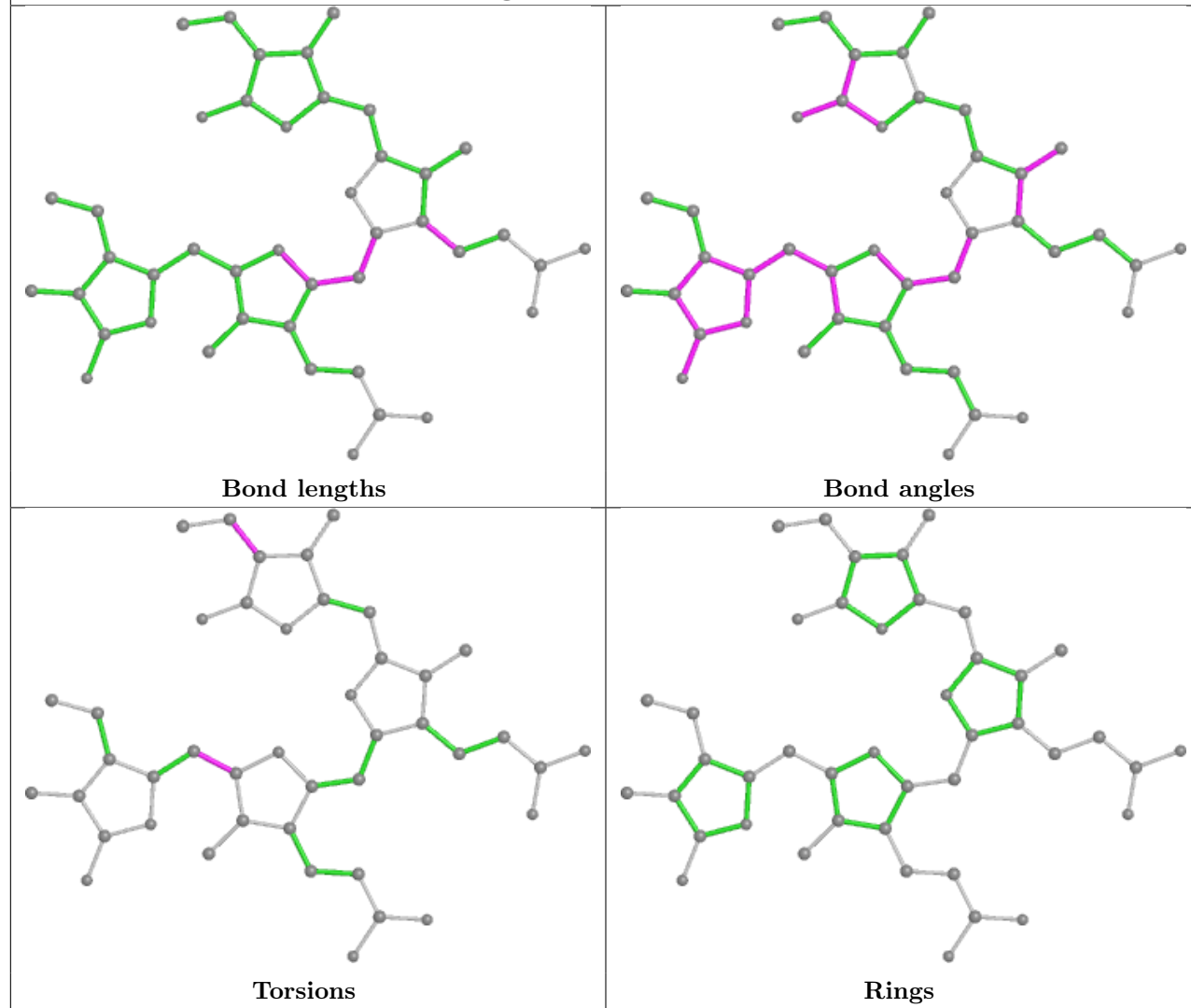


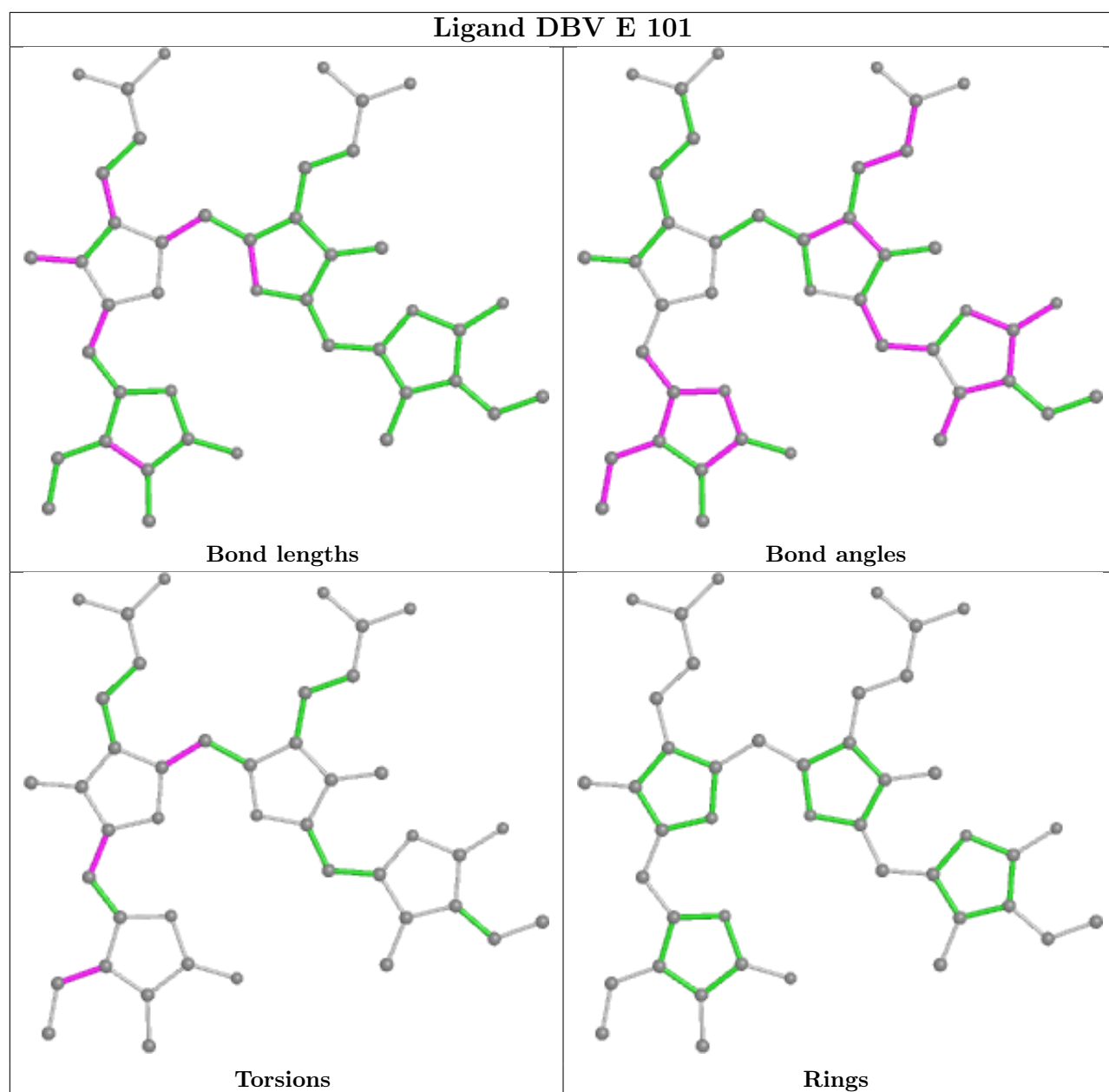






## Ligand PEB F 201





## 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

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	72/76 (94%)	1.37	19 (26%) 0 0	50, 68, 100, 141	0
1	E	74/76 (97%)	0.84	8 (10%) 5 3	28, 45, 64, 68	0
1	I	75/76 (98%)	1.04	16 (21%) 0 0	32, 54, 75, 113	0
1	M	74/76 (97%)	1.04	11 (14%) 2 1	38, 58, 74, 93	0
2	B	162/177 (91%)	1.44	44 (27%) 0 0	32, 59, 89, 116	0
2	D	173/177 (97%)	1.11	35 (20%) 1 0	32, 56, 107, 143	0
2	F	166/177 (93%)	1.08	35 (21%) 1 0	30, 47, 82, 98	0
2	H	170/177 (96%)	0.89	25 (14%) 2 1	27, 45, 78, 150	0
2	J	170/177 (96%)	1.00	24 (14%) 2 1	33, 47, 76, 124	0
2	L	172/177 (97%)	0.91	23 (13%) 3 1	33, 52, 87, 106	0
2	N	170/177 (96%)	0.90	21 (12%) 4 2	36, 55, 79, 105	0
2	P	173/177 (97%)	0.83	21 (12%) 4 2	27, 53, 89, 112	0
3	C	60/67 (89%)	1.61	17 (28%) 0 0	57, 75, 106, 145	0
3	G	67/67 (100%)	0.93	12 (17%) 1 1	32, 47, 74, 114	0
3	K	67/67 (100%)	1.02	10 (14%) 2 1	38, 53, 74, 90	0
3	O	67/67 (100%)	1.11	9 (13%) 3 1	40, 59, 78, 91	0
All	All	1912/1988 (96%)	1.05	330 (17%) 1 1	27, 53, 89, 150	0

The worst 5 of 330 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	167	GLY	9.9
2	D	147	SER	6.9
2	H	13	ASP	6.7
3	C	18	GLY	6.6
3	G	27	THR	6.5

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

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

## 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
5	PEB	B	202	43/43	0.76	0.33	31,51,65,80	0
5	PEB	P	203	43/43	0.77	0.29	21,59,80,85	0
5	PEB	D	202	43/43	0.80	0.35	35,61,102,108	0
4	DBV	C	101	43/43	0.80	0.27	32,53,67,78	0
5	PEB	J	203	43/43	0.81	0.29	26,41,59,66	0
5	PEB	F	202	43/43	0.82	0.30	14,41,60,63	0
5	PEB	D	201	43/43	0.83	0.28	21,45,64,66	0
5	PEB	L	203	43/43	0.83	0.26	5,53,69,84	0
5	PEB	F	203	43/43	0.83	0.30	20,38,48,61	0
5	PEB	H	201	43/43	0.84	0.25	2,36,49,80	0
5	PEB	B	201	43/43	0.84	0.32	16,44,71,73	0
4	DBV	E	101	43/43	0.84	0.30	17,42,67,86	0
4	DBV	I	101	43/43	0.84	0.29	28,51,70,76	0
5	PEB	B	203	43/43	0.85	0.32	19,48,62,66	0
5	PEB	L	202	43/43	0.85	0.27	24,56,78,84	0
4	DBV	K	101	43/43	0.85	0.28	17,46,63,77	0
5	PEB	N	203	43/43	0.85	0.29	21,48,65,67	0
5	PEB	P	202	43/43	0.85	0.29	19,49,73,102	0
5	PEB	H	202	43/43	0.85	0.29	15,54,71,80	0
4	DBV	M	101	43/43	0.86	0.27	21,52,71,82	0
5	PEB	H	203	43/43	0.87	0.29	21,45,59,75	0
5	PEB	J	201	43/43	0.87	0.24	15,36,51,69	0
5	PEB	F	201	43/43	0.88	0.22	2,28,44,64	0
5	PEB	N	202	43/43	0.88	0.23	10,39,50,71	0
4	DBV	O	101	43/43	0.88	0.23	16,40,55,59	0
5	PEB	L	201	43/43	0.88	0.22	9,32,63,69	0
4	DBV	A	101	43/43	0.88	0.26	23,39,60,74	0

*Continued on next page...*

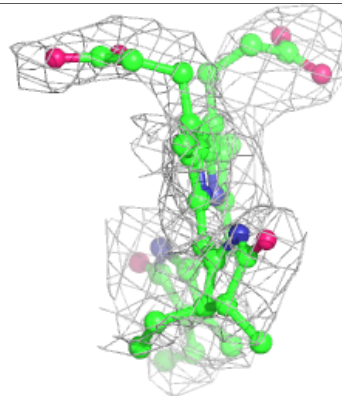
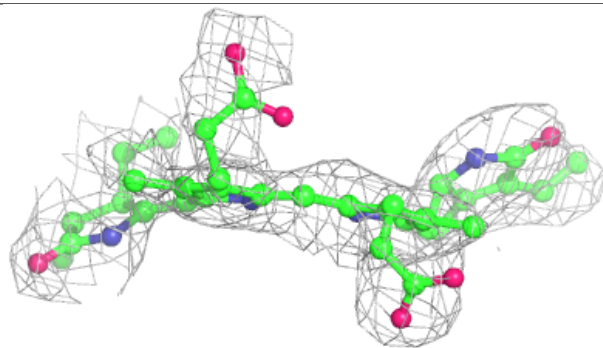
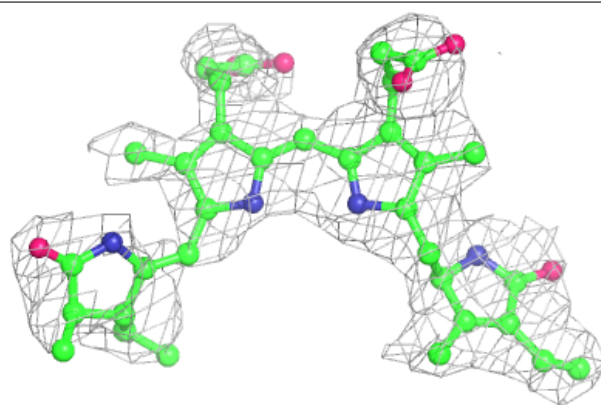
*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	PEB	N	201	43/43	0.89	0.22	14,34,63,68	0
5	PEB	P	201	43/43	0.90	0.23	2,30,62,92	0
4	DBV	G	101	43/43	0.90	0.21	2,32,51,72	0
5	PEB	D	203	43/43	0.90	0.25	14,40,60,70	0
5	PEB	J	202	43/43	0.91	0.20	14,36,55,58	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.

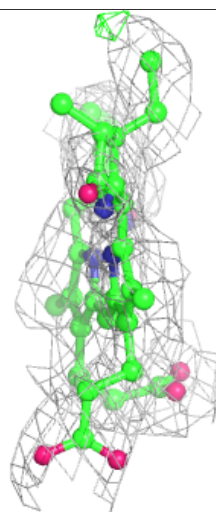
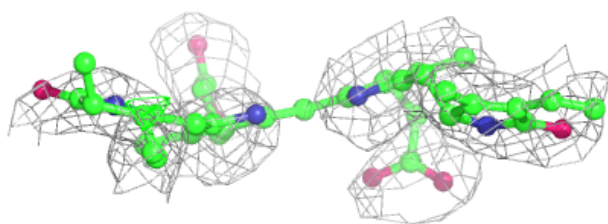
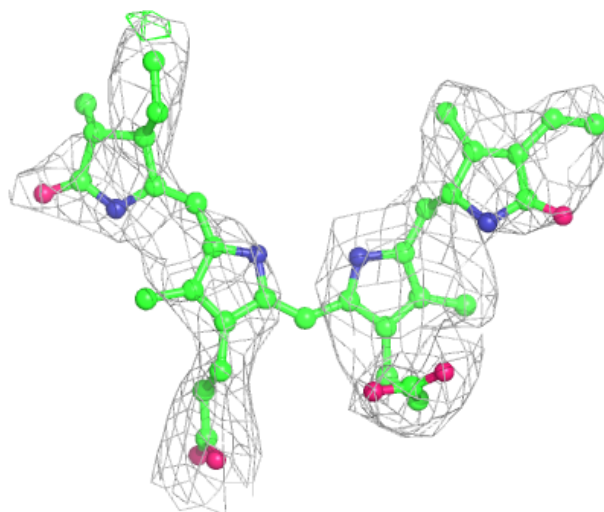
**Electron density around PEB B 202:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



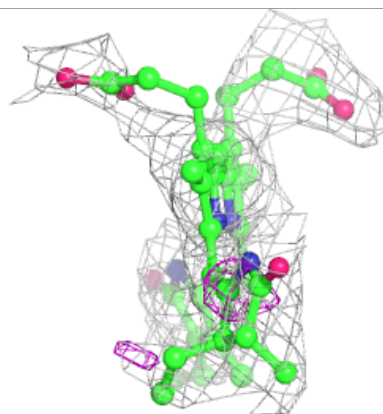
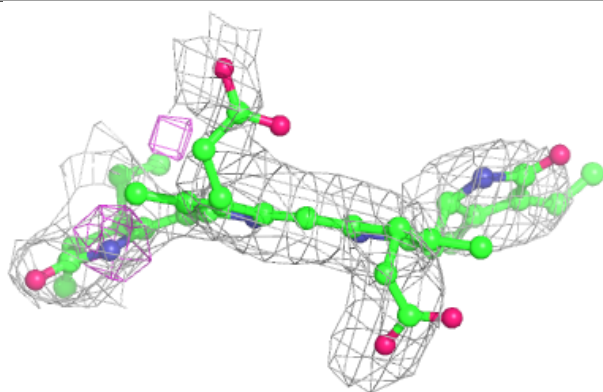
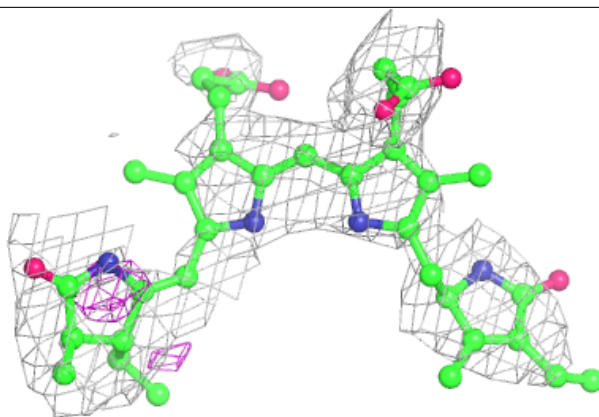
**Electron density around PEB P 203:**

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

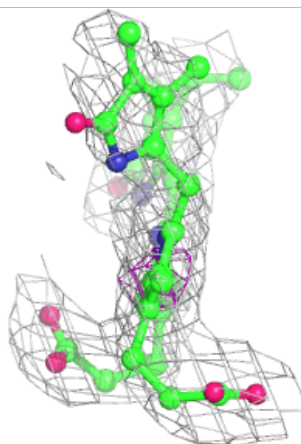
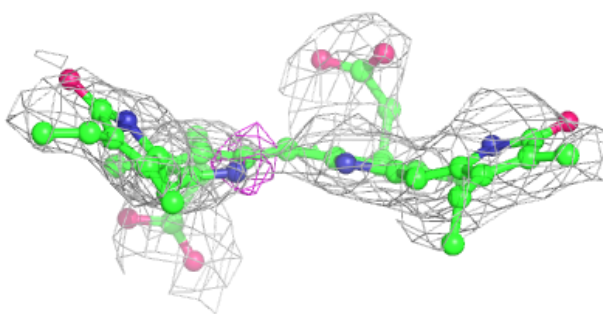
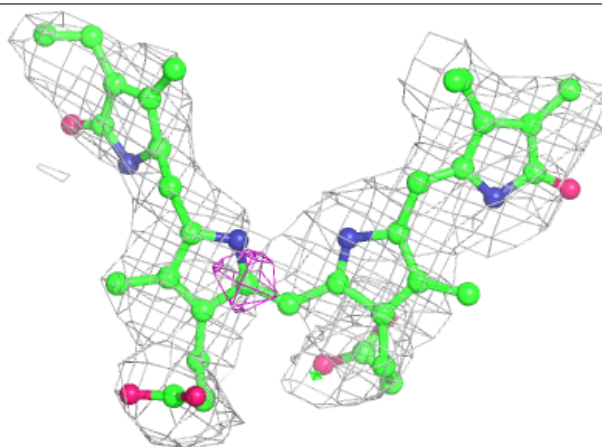


**Electron density around PEB D 202:**

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

**Electron density around DBV C 101:**

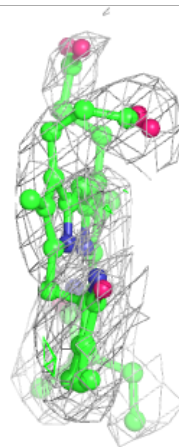
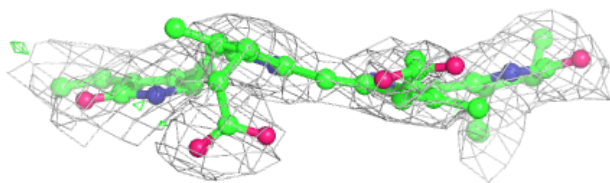
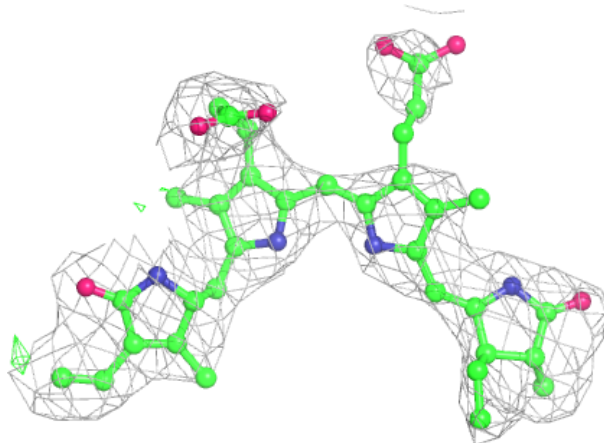
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around PEB J 203:**

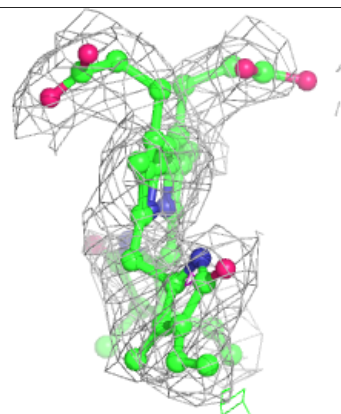
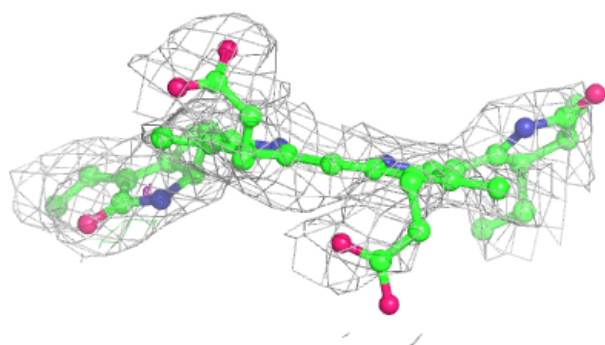
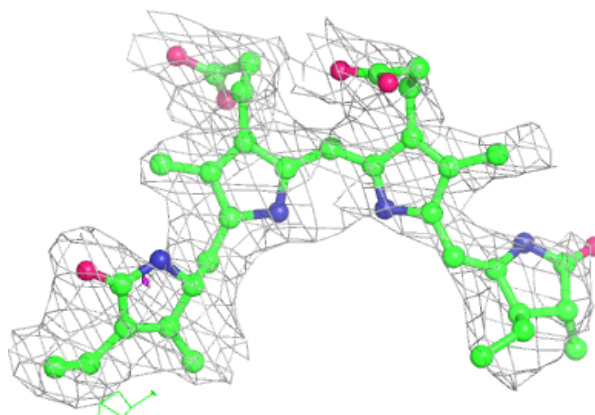
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





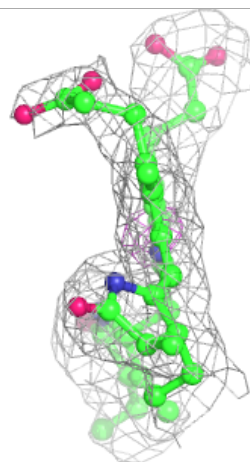
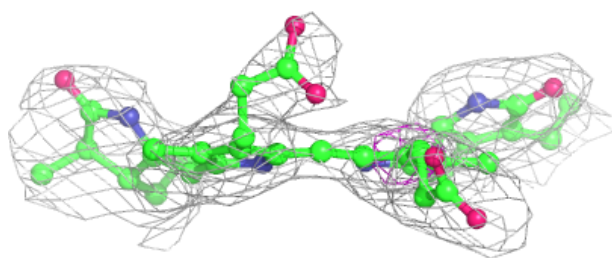
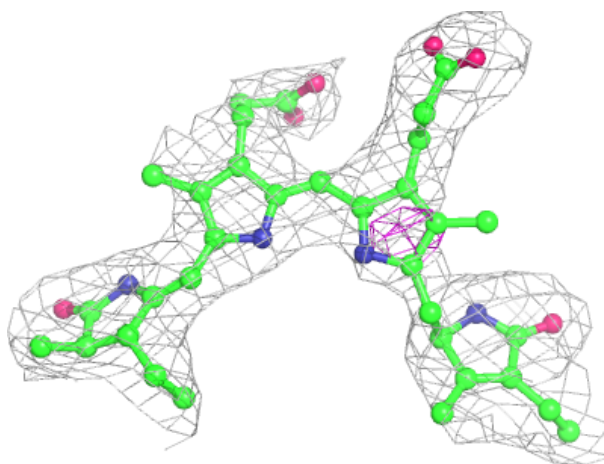
**Electron density around PEB F 202:**

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



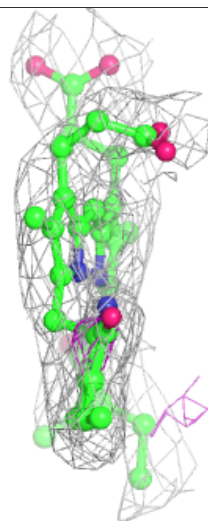
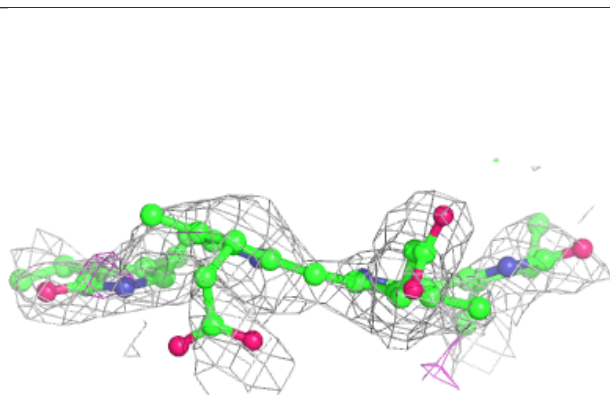
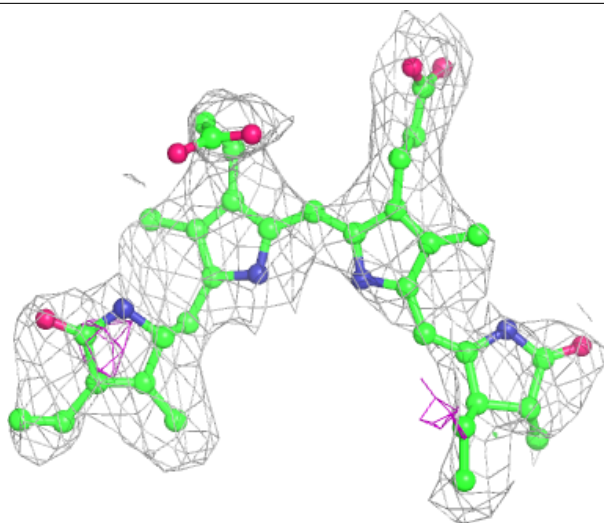
**Electron density around PEB D 201:**

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



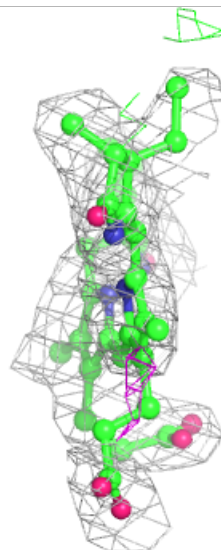
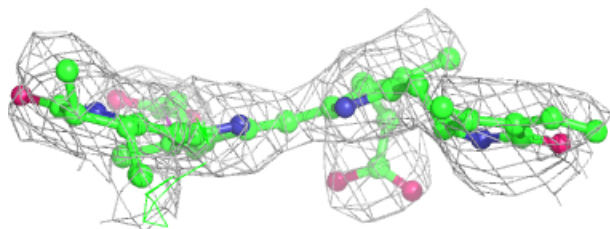
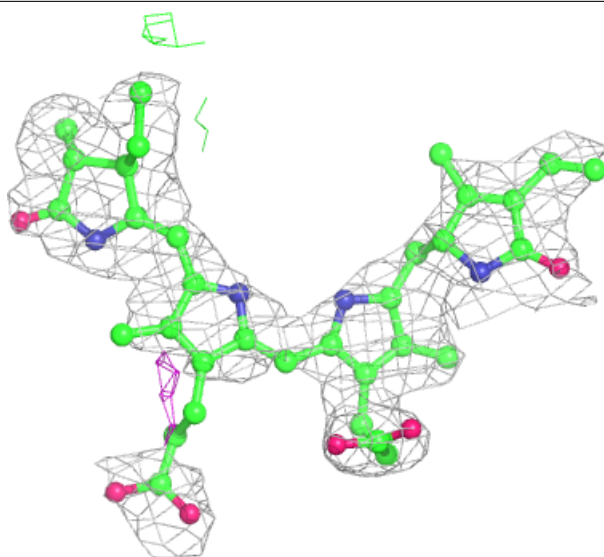
**Electron density around PEB L 203:**

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



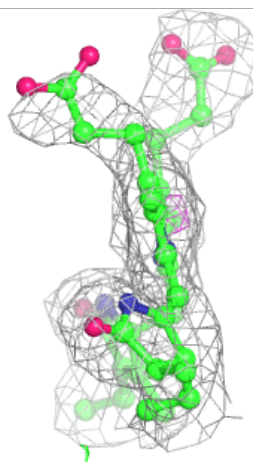
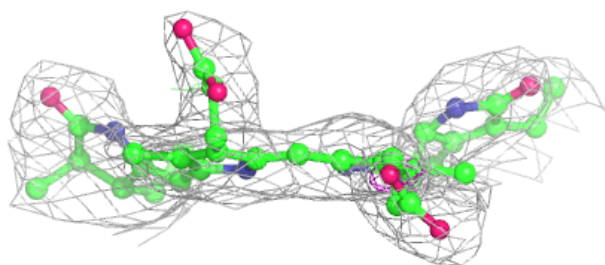
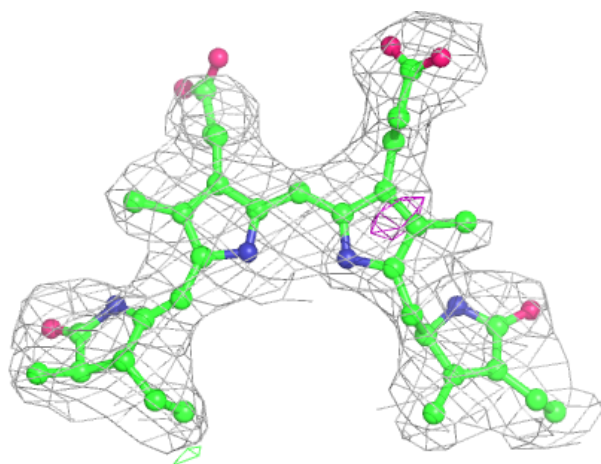
**Electron density around PEB F 203:**

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



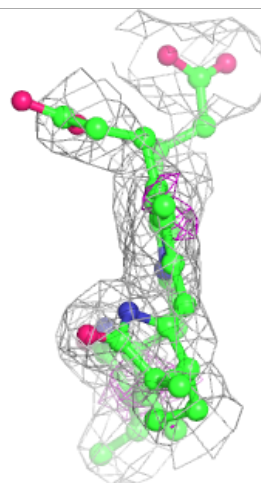
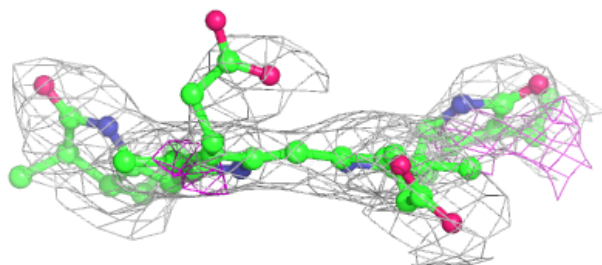
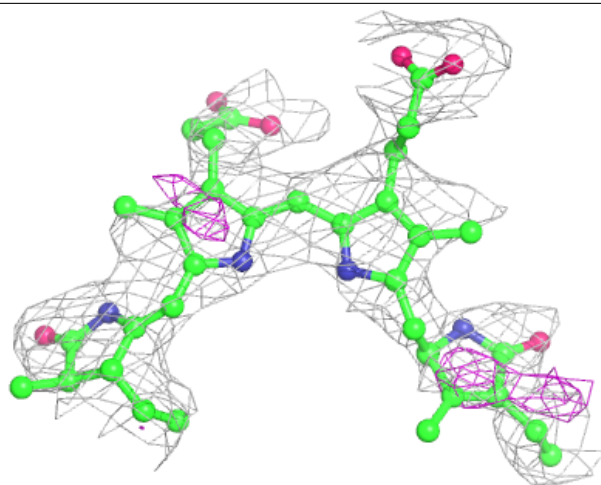
**Electron density around PEB H 201:**

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



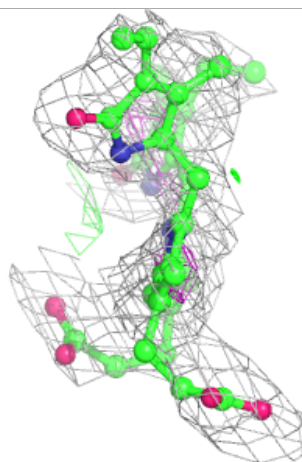
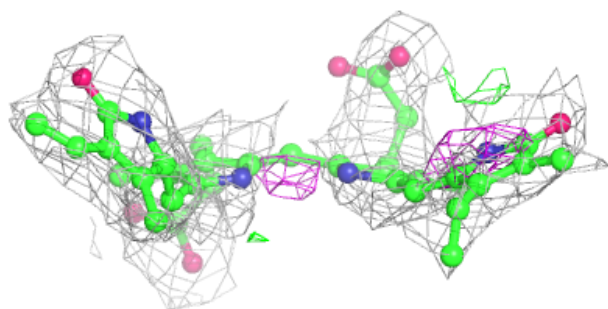
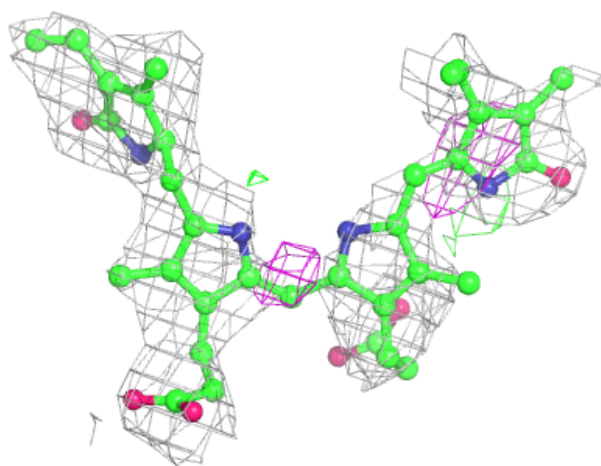
**Electron density around PEB B 201:**

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



**Electron density around DBV E 101:**

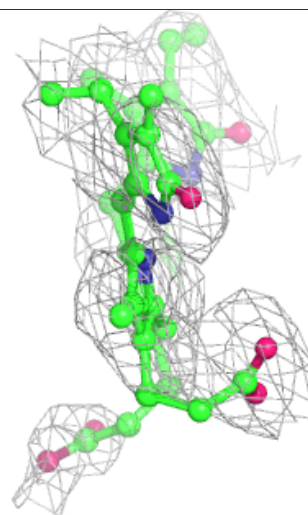
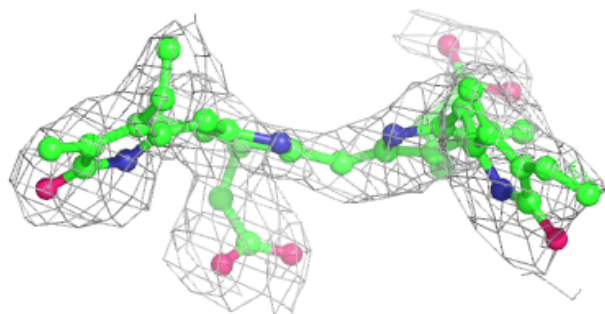
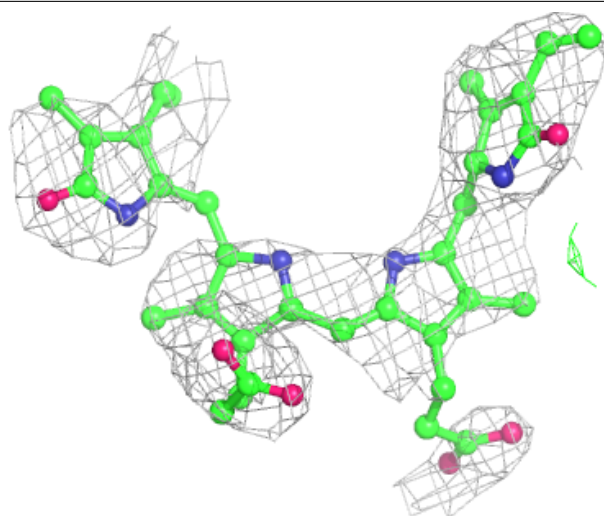
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around DBV I 101:**

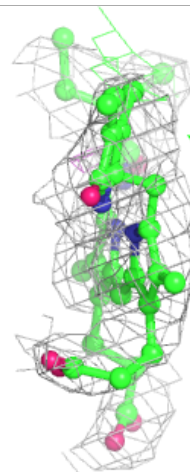
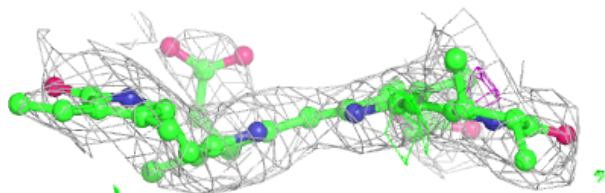
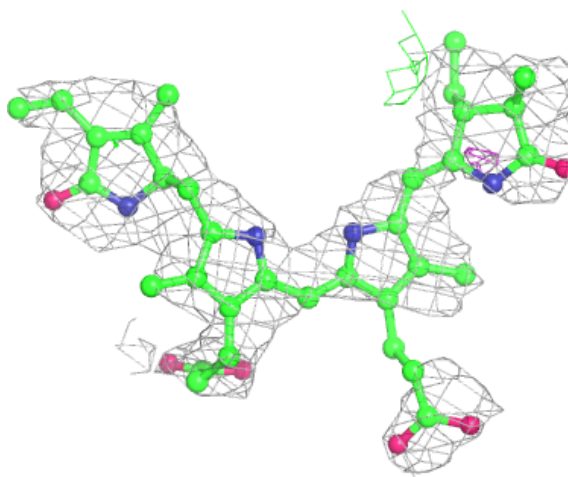
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





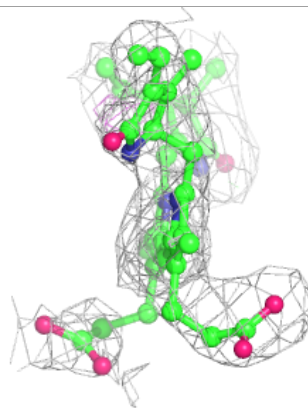
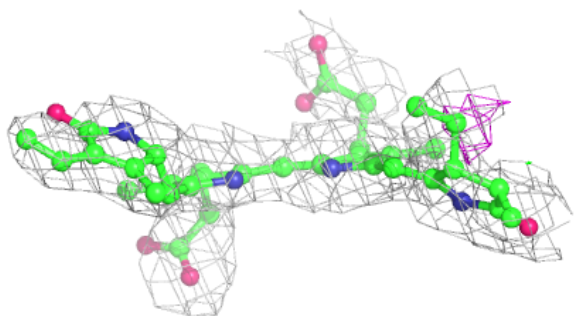
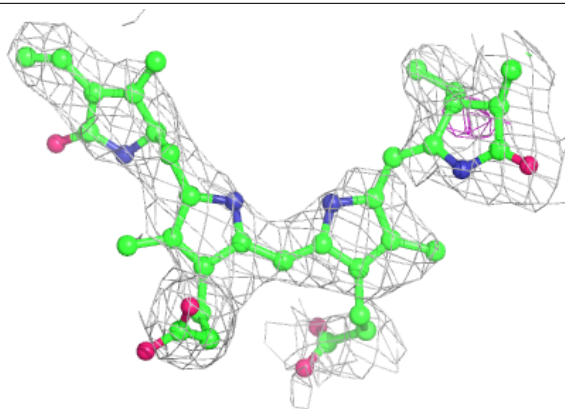
**Electron density around PEB B 203:**

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



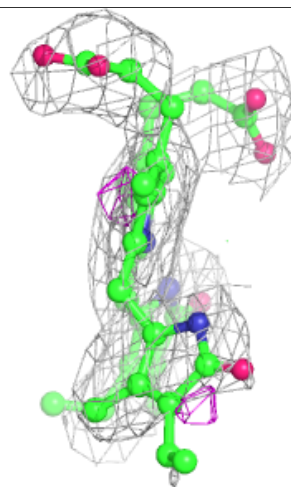
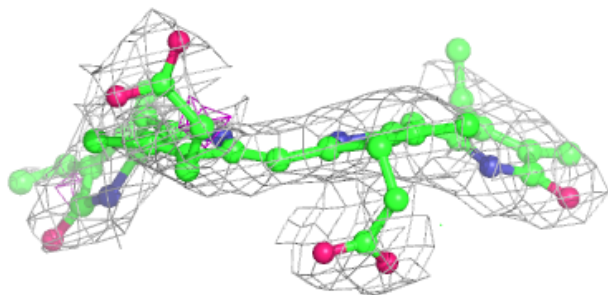
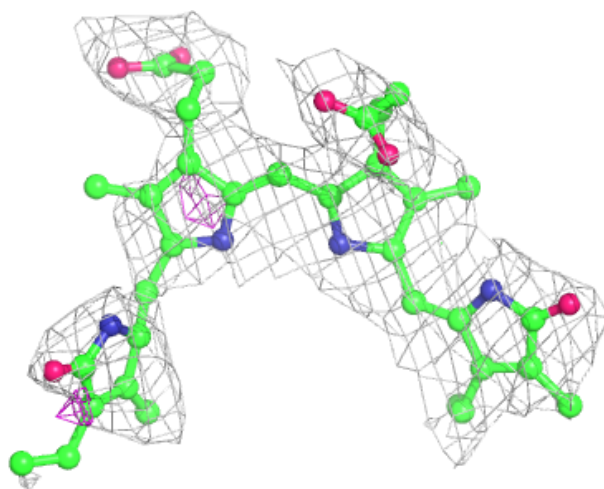
**Electron density around PEB L 202:**

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



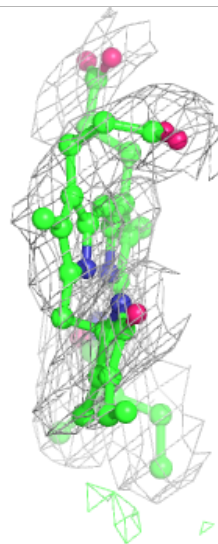
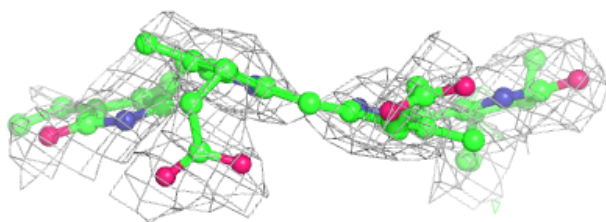
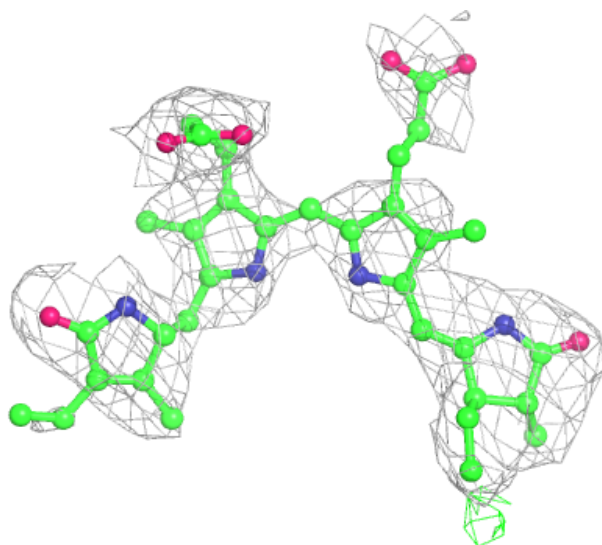
**Electron density around DBV K 101:**

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



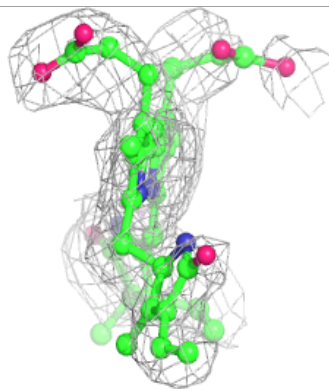
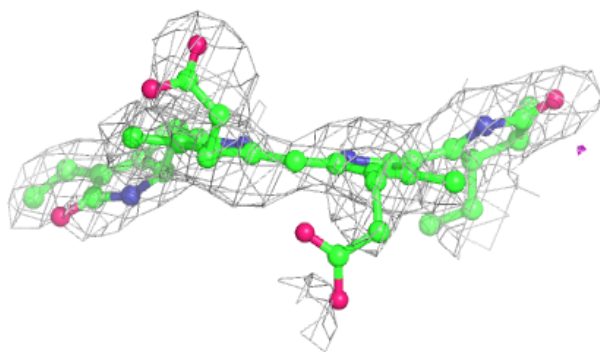
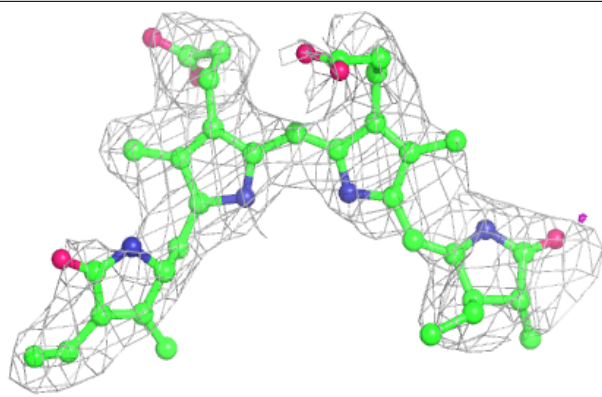
**Electron density around PEB N 203:**

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



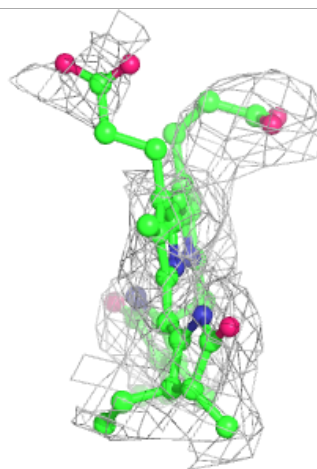
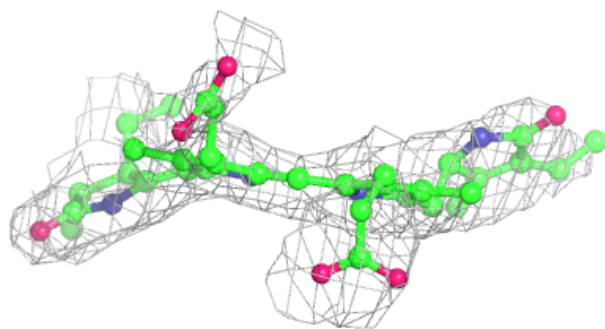
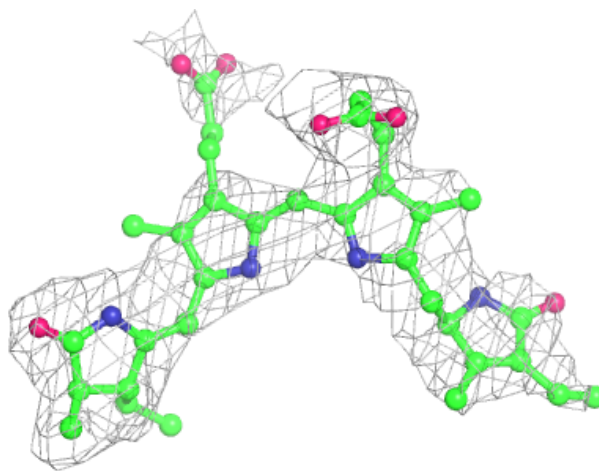
**Electron density around PEB P 202:**

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



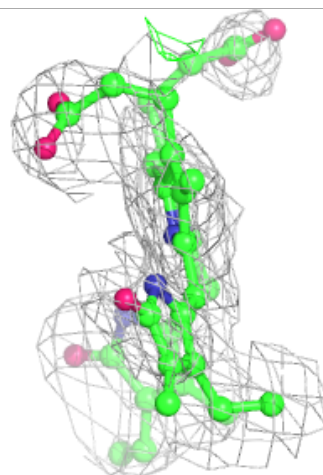
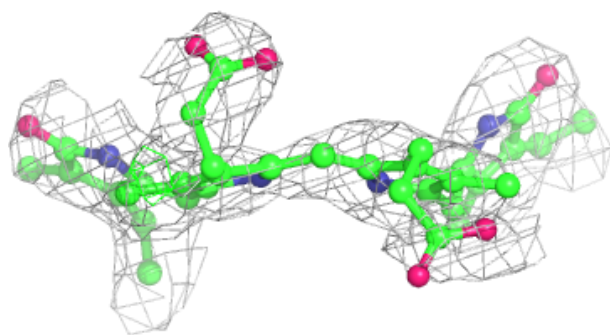
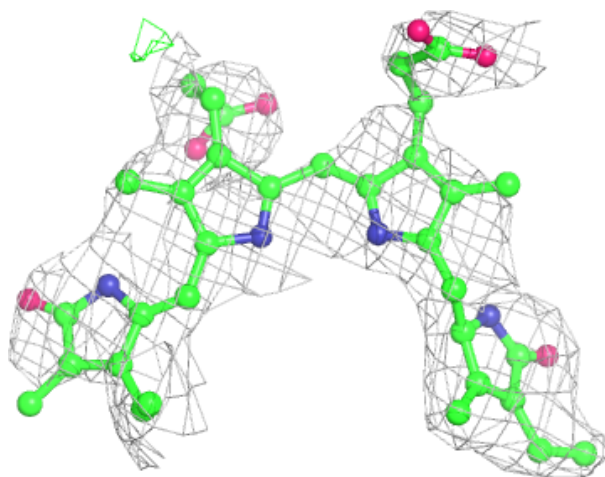
**Electron density around PEB H 202:**

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



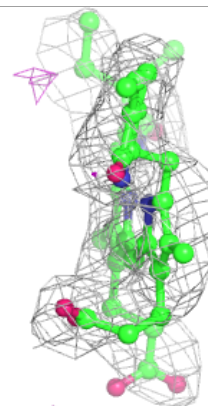
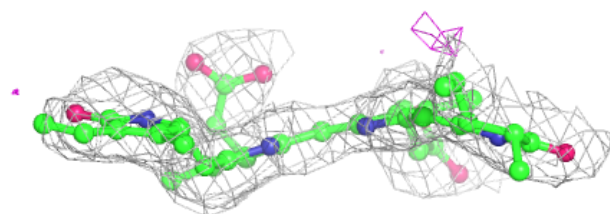
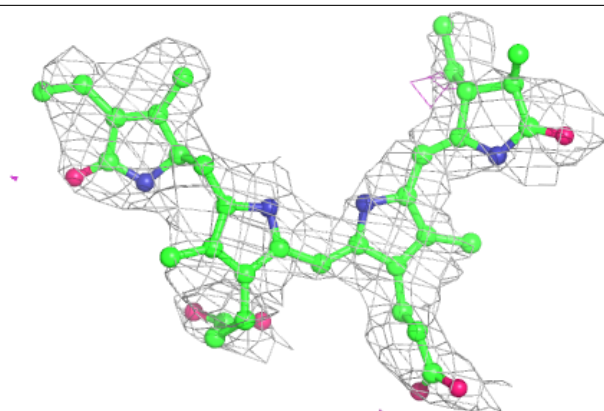
**Electron density around DBV M 101:**

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



**Electron density around PEB H 203:**

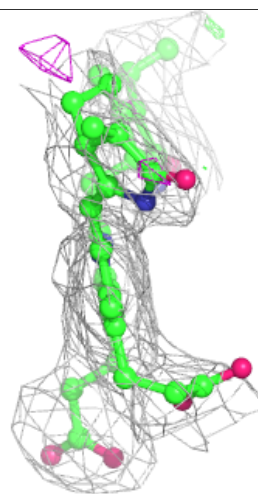
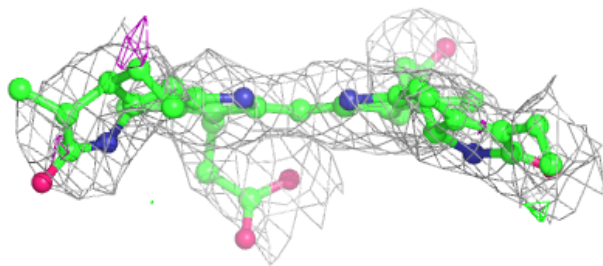
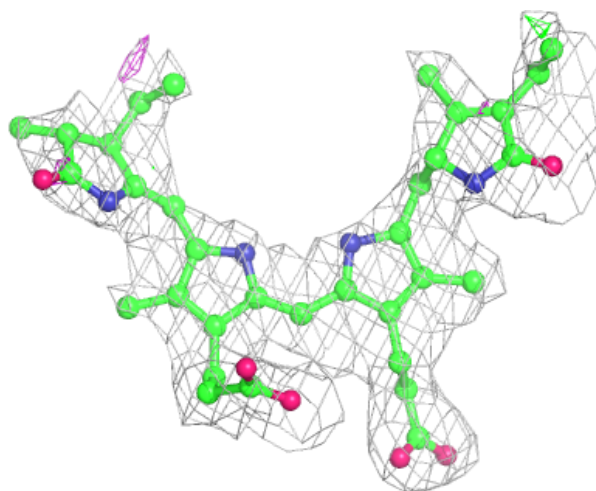
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





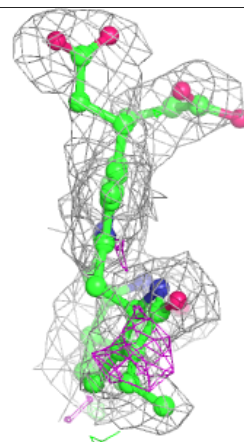
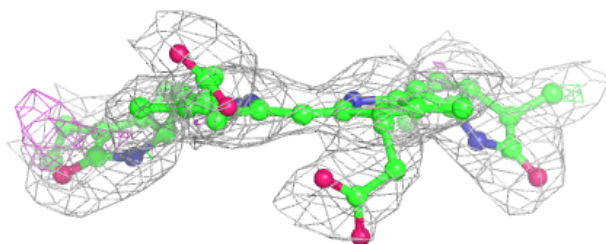
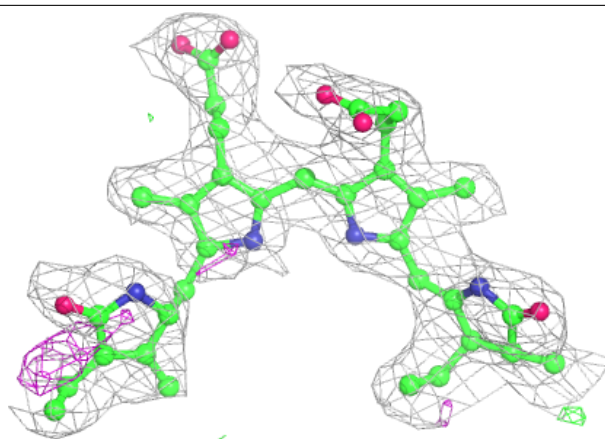
**Electron density around PEB J 201:**

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

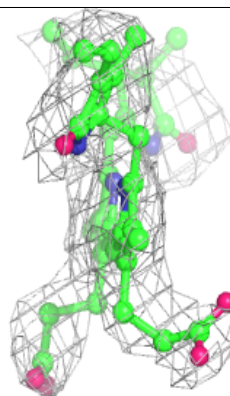
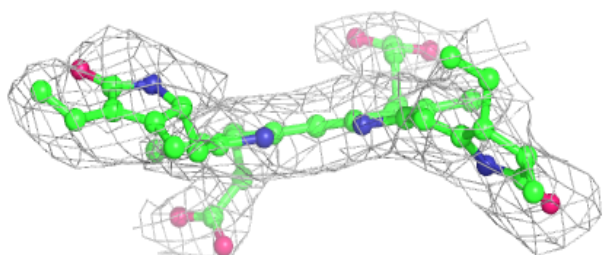
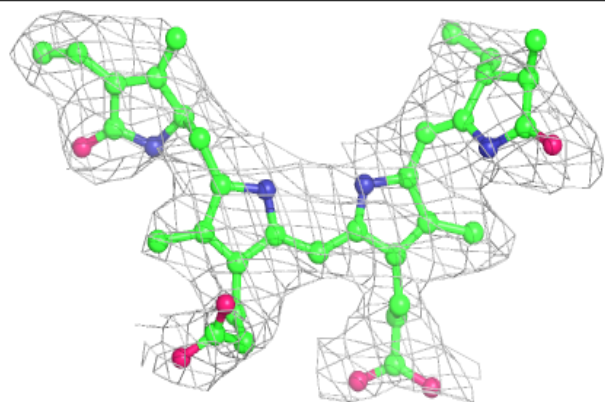


**Electron density around PEB F 201:**

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

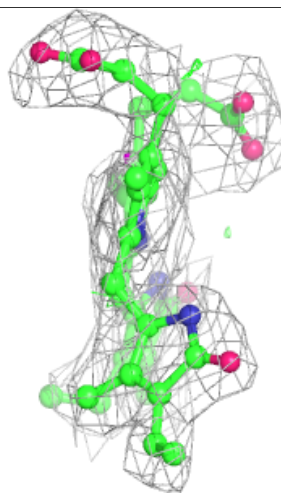
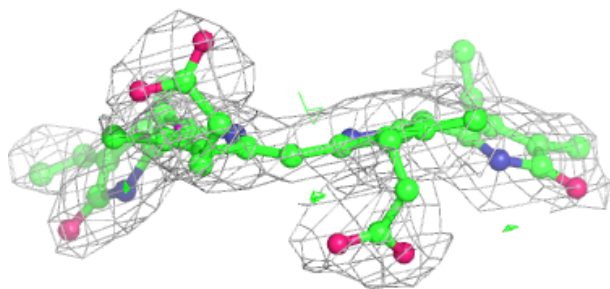
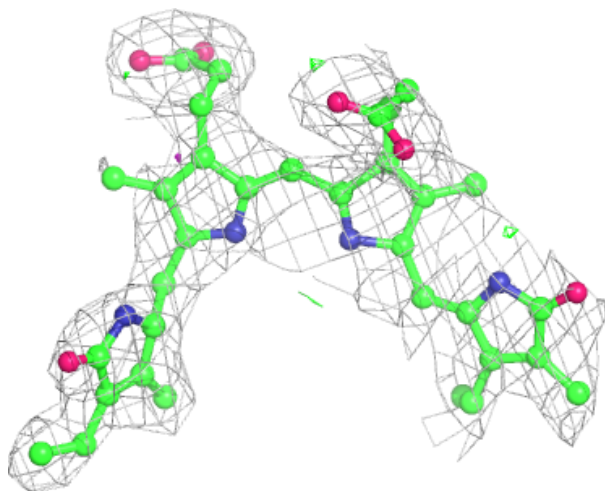
**Electron density around PEB N 202:**

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



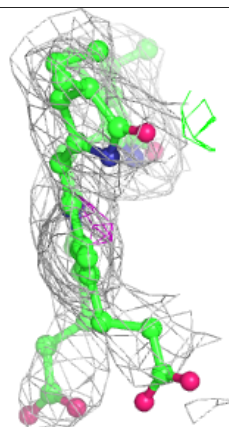
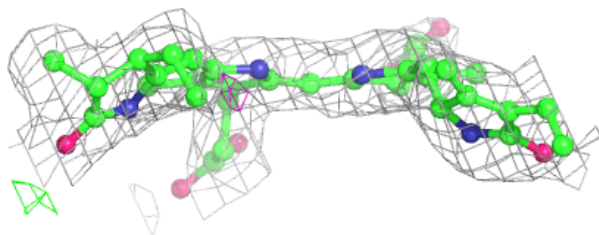
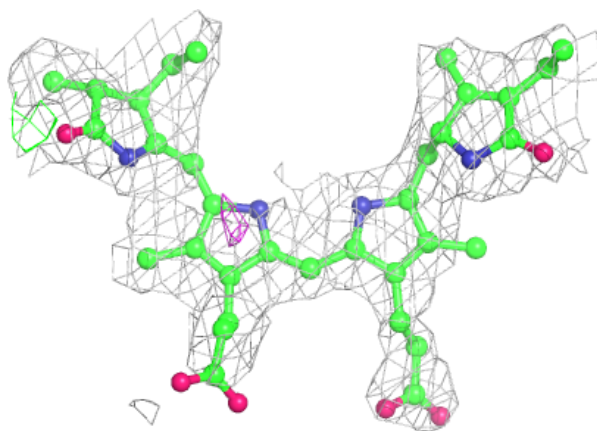
**Electron density around DBV O 101:**

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



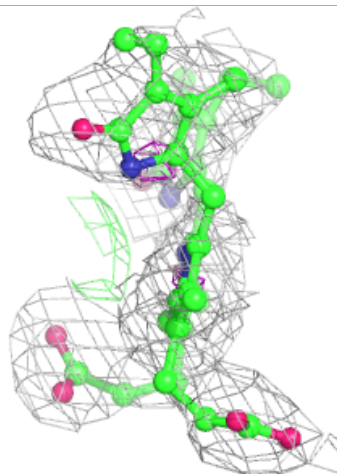
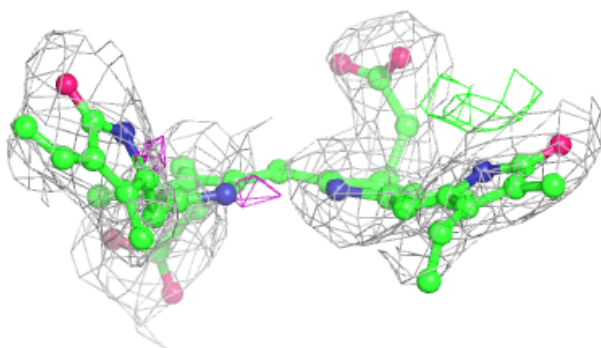
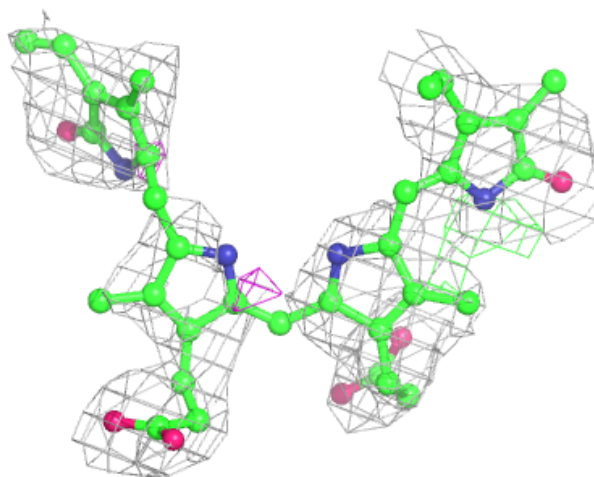
**Electron density around PEB L 201:**

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



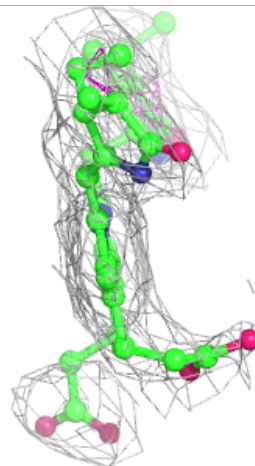
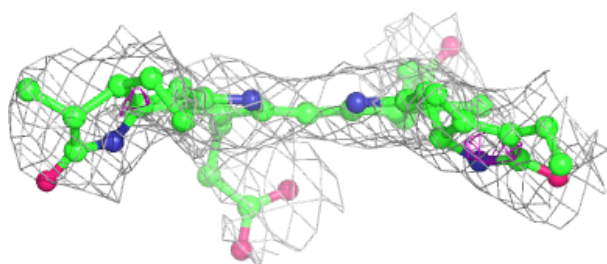
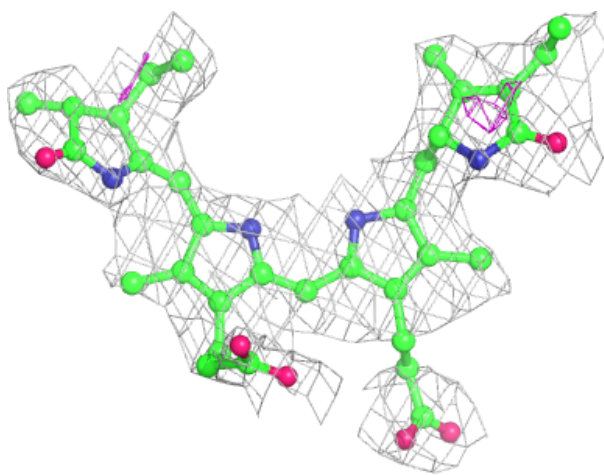
**Electron density around DBV A 101:**

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



**Electron density around PEB N 201:**

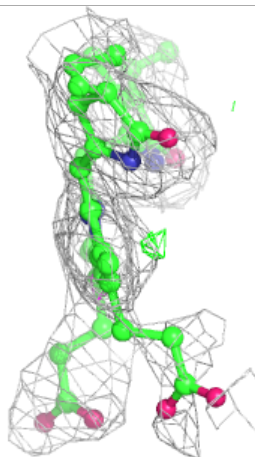
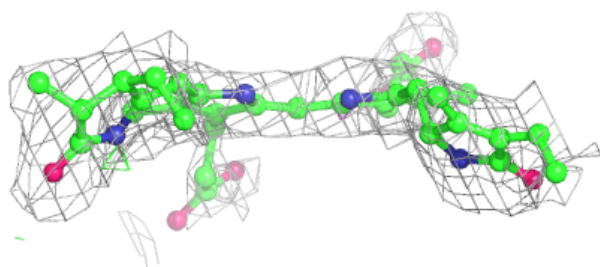
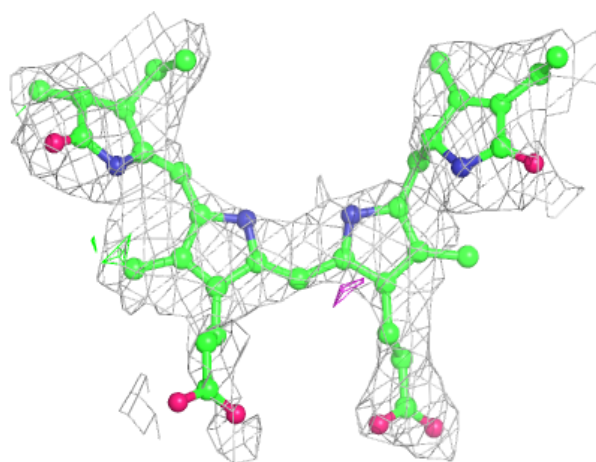
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





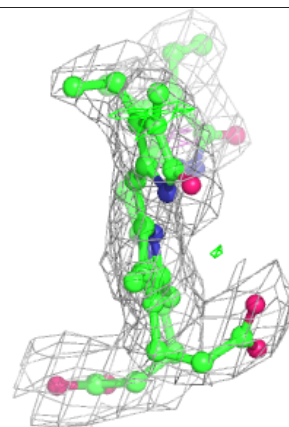
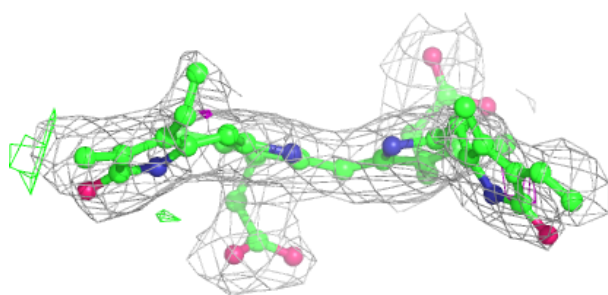
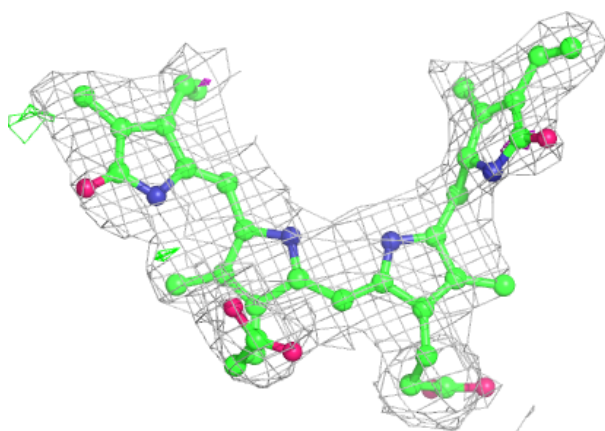
**Electron density around PEB P 201:**

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

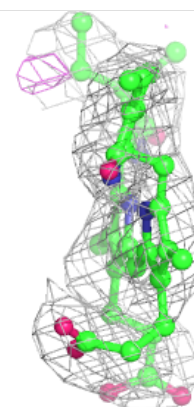
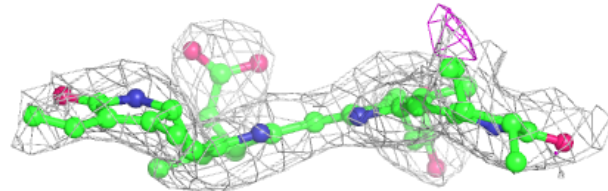
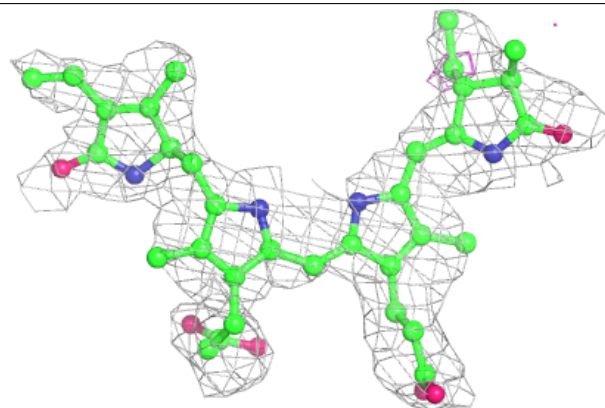


**Electron density around DBV G 101:**

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

**Electron density around PEB D 203:**

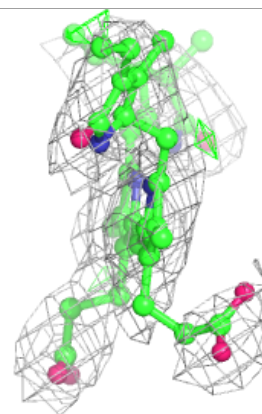
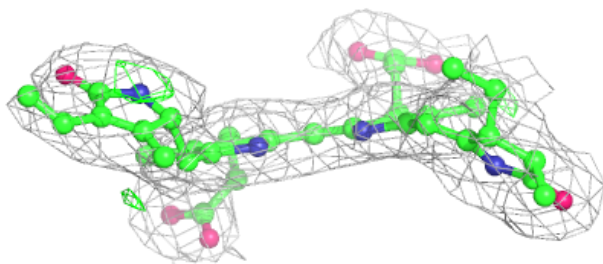
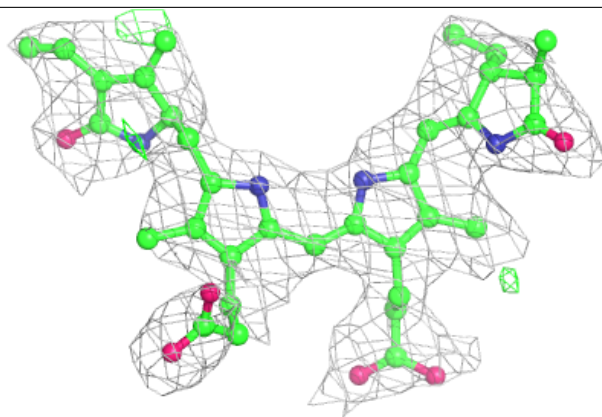
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around PEB J 202:**

$2mF_o - DF_c$  (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.