



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 6, 2023 – 02:14 am GMT

PDB ID : 2VJH
Title : The structure of Phycoerythrin from *Gloeobacter violaceus*
Authors : Murray, J.W.; Benson, S.; Nield, J.; Barber, J.
Deposited on : 2007-12-10
Resolution : 2.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

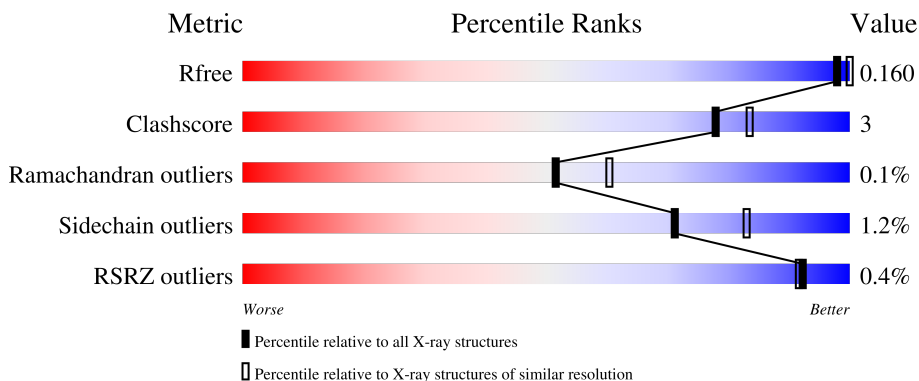
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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

Mol	Chain	Length	Quality of chain
1	A	164	98%
1	C	164	98%
2	B	177	94% 6%
2	D	177	98%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6116 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.

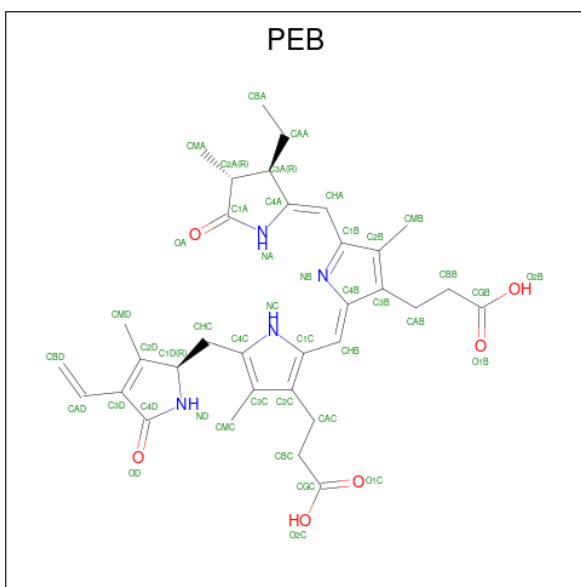
- Molecule 1 is a protein called PHYCOERYTHRIN ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	164	Total	C	N	O	S	0	0	0
			1242	781	218	237	6			
1	C	164	Total	C	N	O	S	0	0	0
			1242	781	218	237	6			

- Molecule 2 is a protein called PHYCOERYTHRIN BETA SUBUNIT.

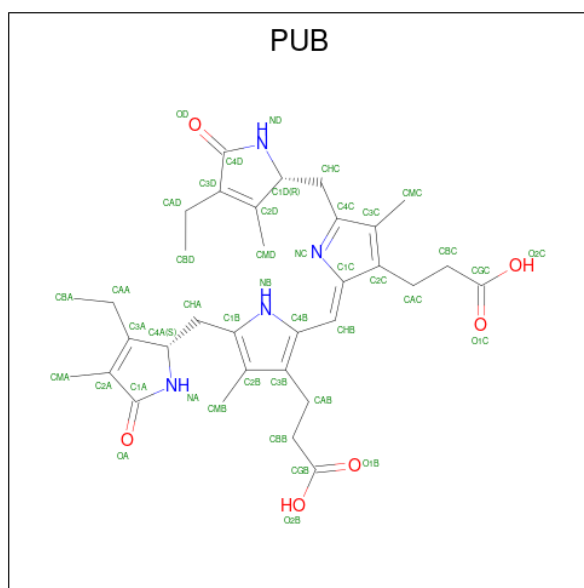
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	177	Total	C	N	O	S	0	0	0
			1285	797	224	252	12			
2	D	177	Total	C	N	O	S	0	0	0
			1285	797	224	252	12			

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



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

- Molecule 4 is PHYCOUROBILIN (three-letter code: PUB) (formula: $C_{33}H_{42}N_4O_6$).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	166	Total 166	O 166	0	0
5	B	166	Total 166	O 166	0	0
5	C	145	Total 145	O 145	0	0
5	D	155	Total 155	O 155	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.

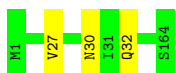
- Molecule 1: PHYCOERYTHRIN ALPHA CHAIN

Chain A:  98%



- Molecule 1: PHYCOERYTHRIN ALPHA CHAIN

Chain C:  98%



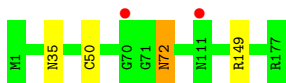
- Molecule 2: PHYCOERYTHRIN BETA SUBUNIT

Chain B:  94% 6%



- Molecule 2: PHYCOERYTHRIN BETA SUBUNIT

Chain D:  98%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	155.83Å 155.83Å 155.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.23 – 2.20 43.22 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (43.23-2.20) 100.0 (43.22-2.20)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.07 (at 2.20Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.153 , 0.186 0.162 , 0.160	Depositor DCC
R_{free} test set	3245 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	25.4	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 37.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.031 for l,-k,h	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6116	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.14% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.65	0/1265	0.67	0/1713
1	C	0.62	0/1265	0.63	0/1713
2	B	0.64	0/1288	0.64	0/1738
2	D	0.61	0/1288	0.63	0/1738
All	All	0.63	0/5106	0.64	0/6902

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	1242	0	1228	5	0
1	C	1242	0	1228	5	0
2	B	1285	0	1300	5	0
2	D	1285	0	1300	2	0
3	A	86	0	73	4	0
3	B	86	0	73	7	0
3	C	86	0	72	5	0
3	D	86	0	72	8	0
4	B	43	0	37	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	43	0	37	0	0
5	A	166	0	0	0	0
5	B	166	0	0	1	0
5	C	145	0	0	1	0
5	D	155	0	0	0	0
All	All	6116	0	5420	32	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 3.

All (32) 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)
3:C:1139:PEB:HNA	3:C:1139:PEB:HMB2	1.41	0.85
3:B:1158:PEB:HMB2	3:B:1158:PEB:HNA	1.45	0.80
3:D:1158:PEB:HMB2	3:D:1158:PEB:HNA	1.48	0.78
1:A:32:GLN:CG	1:C:32:GLN:HG3	2.25	0.66
1:C:27:VAL:O	1:C:30:ASN:HB2	1.98	0.63
1:A:32:GLN:HG3	1:C:32:GLN:CG	2.29	0.63
1:A:32:GLN:HG3	1:C:32:GLN:HG3	1.80	0.62
3:A:1139:PEB:HMB2	3:A:1139:PEB:HNA	1.64	0.61
3:C:1139:PEB:HBD1	3:C:1139:PEB:HMD1	1.88	0.56
3:C:1139:PEB:HMD3	5:C:2114:HOH:O	2.05	0.56
3:C:1139:PEB:HNA	3:C:1139:PEB:CMB	2.17	0.55
3:A:1139:PEB:HMD1	3:A:1139:PEB:HBD1	1.87	0.54
3:D:1082:PEB:HMB2	3:D:1082:PEB:HNA	1.72	0.54
2:B:72:MEN:HE22	3:B:1082:PEB:HBB2	1.89	0.53
3:B:1082:PEB:HNA	3:B:1082:PEB:HMB2	1.74	0.52
3:D:1158:PEB:HMB2	3:D:1158:PEB:NA	2.21	0.52
3:A:1082:PEB:HMB2	3:A:1082:PEB:HNA	1.78	0.48
2:D:72:MEN:HE22	3:D:1082:PEB:HBB2	1.96	0.48
3:B:1158:PEB:HNA	3:B:1158:PEB:CMB	2.23	0.47
1:A:38:LEU:HD22	2:B:24:LEU:HD11	1.96	0.47
2:B:90:LEU:O	2:B:94:THR:HG23	2.14	0.47
3:B:1158:PEB:HBA3	3:B:1158:PEB:HHA1	1.97	0.46
1:A:25:GLU:OE2	1:C:30:ASN:HA	2.17	0.45
3:D:1158:PEB:HBA3	3:D:1158:PEB:HHA1	1.98	0.44
3:D:1158:PEB:HNA	3:D:1158:PEB:CMB	2.25	0.42
3:B:1158:PEB:HMB2	3:B:1158:PEB:NA	2.23	0.42
3:D:1082:PEB:HNA	3:D:1082:PEB:CMB	2.33	0.42
3:A:1082:PEB:HNA	3:A:1082:PEB:CMB	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:35:ASN:HB3	3:D:1158:PEB:C1C	2.51	0.41
2:B:78:ARG:NH1	5:B:2062:HOH:O	2.54	0.41
2:B:82:CYS:HA	3:B:1082:PEB:HAA1	2.03	0.41
3:C:1139:PEB:HMB1	3:C:1139:PEB:HBB1	2.03	0.41

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	162/164 (99%)	161 (99%)	1 (1%)	0	100	100
1	C	162/164 (99%)	161 (99%)	1 (1%)	0	100	100
2	B	174/177 (98%)	171 (98%)	2 (1%)	1 (1%)	25	26
2	D	174/177 (98%)	171 (98%)	3 (2%)	0	100	100
All	All	672/682 (98%)	664 (99%)	7 (1%)	1 (0%)	51	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	21	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	123/123 (100%)	123 (100%)	0	100	100
1	C	123/123 (100%)	123 (100%)	0	100	100
2	B	131/131 (100%)	127 (97%)	4 (3%)	40	51
2	D	131/131 (100%)	129 (98%)	2 (2%)	65	78
All	All	508/508 (100%)	502 (99%)	6 (1%)	71	83

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	38	LEU
2	B	50	CYS
2	B	137	SER
2	B	149	ARG
2	D	50	CYS
2	D	149	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	42	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](#)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	MEN	D	72	2	7,8,9	0.43	0	6,9,11	1.31	1 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MEN	B	72	2	7,8,9	0.43	0	6,9,11	0.49	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MEN	D	72	2	-	3/7/8/10	-
2	MEN	B	72	2	-	3/7/8/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	72	MEN	CB-CG-ND2	2.73	119.16	115.48

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	72	MEN	CA-CB-CG-OD1
2	D	72	MEN	CA-CB-CG-ND2
2	B	72	MEN	CA-CB-CG-ND2
2	D	72	MEN	N-CA-CB-CG
2	B	72	MEN	CA-CB-CG-OD1
2	B	72	MEN	N-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	72	MEN	1	0
2	B	72	MEN	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry

10 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	PEB	B	1158	2	43,46,46	3.57	10 (23%)	45,67,67	1.73	13 (28%)
3	PEB	B	1082	2	43,46,46	3.63	11 (25%)	45,67,67	2.04	12 (26%)
3	PEB	D	1082	2	43,46,46	3.54	8 (18%)	45,67,67	2.20	15 (33%)
3	PEB	A	1082	1	43,46,46	3.35	9 (20%)	45,67,67	2.22	18 (40%)
3	PEB	D	1158	2	43,46,46	3.45	8 (18%)	45,67,67	1.85	12 (26%)
4	PUB	D	1050	2	42,46,46	3.75	8 (19%)	37,67,67	2.70	12 (32%)
3	PEB	A	1139	1	43,46,46	3.38	10 (23%)	45,67,67	1.74	12 (26%)
3	PEB	C	1139	1	43,46,46	3.57	11 (25%)	45,67,67	2.01	17 (37%)
4	PUB	B	1050	2	42,46,46	3.51	9 (21%)	37,67,67	2.96	16 (43%)
3	PEB	C	1082	1	43,46,46	3.60	11 (25%)	45,67,67	2.12	16 (35%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PEB	B	1158	2	-	8/24/74/74	0/4/4/4
3	PEB	B	1082	2	-	6/24/74/74	0/4/4/4
3	PEB	D	1082	2	-	7/24/74/74	0/4/4/4
3	PEB	A	1082	1	-	4/24/74/74	0/4/4/4
3	PEB	D	1158	2	-	8/24/74/74	0/4/4/4
4	PUB	D	1050	2	-	7/24/74/74	0/4/4/4
3	PEB	A	1139	1	-	6/24/74/74	0/4/4/4
3	PEB	C	1139	1	-	8/24/74/74	0/4/4/4
4	PUB	B	1050	2	-	7/24/74/74	0/4/4/4
3	PEB	C	1082	1	-	5/24/74/74	0/4/4/4

All (95) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1082	PEB	CHB-C4B	18.27	1.50	1.35
3	C	1082	PEB	CHB-C4B	18.20	1.50	1.35
4	D	1050	PUB	CHB-C1C	18.02	1.50	1.35
3	D	1082	PEB	CHB-C4B	17.93	1.50	1.35
3	B	1158	PEB	CHB-C4B	17.86	1.50	1.35
3	C	1139	PEB	CHB-C4B	17.36	1.49	1.35
3	D	1158	PEB	CHB-C4B	16.67	1.49	1.35
3	A	1139	PEB	CHB-C4B	16.48	1.48	1.35
4	B	1050	PUB	CHB-C1C	16.44	1.48	1.35
3	A	1082	PEB	CHB-C4B	16.12	1.48	1.35
4	D	1050	PUB	C3A-C2A	12.52	1.48	1.34
4	B	1050	PUB	C3A-C2A	11.90	1.47	1.34
3	C	1139	PEB	C2D-C3D	10.96	1.48	1.34
3	A	1082	PEB	C2D-C3D	9.74	1.47	1.34
3	D	1158	PEB	C2D-C3D	9.74	1.47	1.34
3	D	1082	PEB	C2D-C3D	9.66	1.47	1.34
3	B	1158	PEB	C2D-C3D	9.62	1.46	1.34
3	B	1082	PEB	C2D-C3D	9.46	1.46	1.34
3	C	1082	PEB	C2D-C3D	9.43	1.46	1.34
3	A	1139	PEB	C2D-C3D	9.33	1.46	1.34
3	B	1082	PEB	C3C-C4C	5.68	1.50	1.42
3	D	1158	PEB	C3C-C4C	5.58	1.50	1.42
3	D	1082	PEB	C3B-C2B	5.58	1.48	1.36
3	C	1082	PEB	C3C-C4C	5.58	1.50	1.42
3	B	1082	PEB	C3B-C2B	5.45	1.48	1.36
3	C	1139	PEB	C3B-C2B	5.44	1.48	1.36
3	C	1082	PEB	C3B-C2B	5.32	1.48	1.36
4	B	1050	PUB	C2B-C1B	5.26	1.50	1.42
3	A	1139	PEB	C3C-C4C	5.16	1.50	1.42
3	D	1158	PEB	C3B-C2B	5.13	1.47	1.36
4	D	1050	PUB	C2B-C1B	5.04	1.49	1.42
3	D	1082	PEB	C3C-C4C	5.02	1.49	1.42
3	A	1139	PEB	C3B-C2B	5.01	1.47	1.36
3	A	1082	PEB	C3C-C4C	5.00	1.49	1.42
3	C	1139	PEB	C3C-C4C	4.97	1.49	1.42
3	B	1158	PEB	C3B-C2B	4.92	1.47	1.36
3	B	1158	PEB	C3C-C4C	4.88	1.49	1.42
4	D	1050	PUB	C2C-C3C	4.81	1.47	1.36
3	A	1082	PEB	C3B-C2B	4.80	1.46	1.36
4	B	1050	PUB	C2C-C3C	4.69	1.46	1.36
3	B	1158	PEB	CHA-C1B	4.39	1.50	1.40
3	D	1158	PEB	CHA-C1B	4.21	1.50	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1082	PEB	CHA-C1B	4.19	1.50	1.40
3	B	1082	PEB	CHA-C1B	4.11	1.50	1.40
3	A	1139	PEB	CHA-C1B	4.05	1.49	1.40
3	B	1158	PEB	C1A-NA	-4.01	1.32	1.37
3	C	1139	PEB	CHA-C1B	3.93	1.49	1.40
3	A	1139	PEB	C1A-NA	-3.91	1.32	1.37
3	A	1082	PEB	OD-C4D	3.88	1.31	1.23
4	D	1050	PUB	C3B-C2B	3.78	1.48	1.37
3	C	1082	PEB	CHA-C1B	3.76	1.49	1.40
3	D	1082	PEB	C2C-C3C	3.67	1.48	1.37
3	B	1082	PEB	C2C-C3C	3.58	1.48	1.37
3	C	1082	PEB	C2C-C3C	3.57	1.48	1.37
3	A	1082	PEB	CHA-C1B	3.49	1.48	1.40
3	A	1082	PEB	C2C-C3C	3.45	1.47	1.37
3	C	1139	PEB	C2C-C3C	3.33	1.47	1.37
4	B	1050	PUB	C3B-C2B	3.22	1.47	1.37
3	B	1158	PEB	OD-C4D	3.22	1.29	1.23
3	D	1158	PEB	C1A-NA	-3.17	1.33	1.37
3	D	1158	PEB	C2C-C3C	3.06	1.46	1.37
3	A	1139	PEB	C2C-C3C	3.01	1.46	1.37
3	D	1158	PEB	OD-C4D	2.99	1.29	1.23
3	B	1082	PEB	OD-C4D	2.95	1.29	1.23
3	C	1082	PEB	C1A-NA	-2.88	1.33	1.37
3	B	1158	PEB	C2C-C3C	2.88	1.46	1.37
3	A	1082	PEB	C1A-NA	-2.86	1.33	1.37
4	D	1050	PUB	OD-C4D	2.82	1.29	1.23
3	A	1082	PEB	C2A-C1A	-2.77	1.49	1.52
3	C	1082	PEB	C2A-C1A	-2.68	1.49	1.52
3	C	1139	PEB	C1A-NA	-2.59	1.34	1.37
4	D	1050	PUB	OA-C1A	2.59	1.28	1.23
3	A	1139	PEB	OD-C4D	2.47	1.28	1.23
3	C	1082	PEB	OD-C4D	2.40	1.28	1.23
3	C	1139	PEB	OD-C4D	2.40	1.28	1.23
3	D	1082	PEB	OD-C4D	2.37	1.28	1.23
4	B	1050	PUB	OD-C4D	2.33	1.28	1.23
3	B	1082	PEB	C1C-CHB	2.32	1.50	1.41
3	B	1158	PEB	C4A-NA	-2.32	1.32	1.37
3	B	1082	PEB	O2C-CGC	-2.31	1.23	1.30
3	A	1139	PEB	C1D-ND	2.29	1.49	1.45
3	C	1139	PEB	C1C-CHB	2.26	1.49	1.41
3	C	1139	PEB	C4B-C3B	2.26	1.49	1.45
3	B	1082	PEB	C1A-NA	-2.23	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1082	PEB	O2B-CGB	-2.23	1.23	1.30
4	D	1050	PUB	C3C-C4C	2.21	1.50	1.43
4	B	1050	PUB	C3C-C4C	2.20	1.50	1.43
3	A	1139	PEB	C4A-NA	-2.20	1.32	1.37
4	B	1050	PUB	C4B-CHB	2.18	1.49	1.41
4	B	1050	PUB	OA-C1A	2.17	1.27	1.23
3	C	1082	PEB	C1C-CHB	2.16	1.49	1.41
3	D	1082	PEB	C1B-C2B	2.10	1.50	1.45
3	B	1158	PEB	C1B-C2B	2.07	1.50	1.45
3	C	1082	PEB	C1B-C2B	2.02	1.50	1.45
3	C	1139	PEB	C4A-NA	-2.00	1.33	1.37

All (143) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1050	PUB	C2A-C1A-NA	10.24	116.29	107.21
4	D	1050	PUB	C2A-C1A-NA	9.13	115.31	107.21
3	A	1082	PEB	CHA-C1B-NB	-6.10	112.17	124.93
4	B	1050	PUB	CHC-C1D-ND	-6.04	106.08	113.72
3	C	1082	PEB	CHA-C1B-NB	-5.93	112.54	124.93
4	D	1050	PUB	OD-C4D-C3D	-5.86	121.68	128.04
3	D	1158	PEB	CHC-C1D-ND	-5.59	107.46	113.95
4	B	1050	PUB	CAD-C3D-C4D	5.00	129.28	121.38
3	B	1082	PEB	CMB-C2B-C1B	4.97	132.71	125.06
3	D	1082	PEB	OA-C1A-C2A	-4.89	122.29	126.17
3	C	1082	PEB	CMB-C2B-C1B	4.80	132.46	125.06
3	D	1082	PEB	CMB-C2B-C1B	4.80	132.45	125.06
3	D	1082	PEB	CHA-C4A-NA	4.72	130.82	125.20
3	B	1082	PEB	CHA-C1B-NB	-4.69	115.13	124.93
4	D	1050	PUB	CHC-C1D-ND	-4.52	108.00	113.72
3	A	1082	PEB	CMB-C2B-C1B	4.37	131.79	125.06
4	D	1050	PUB	CMA-C2A-C1A	4.35	131.61	121.39
4	B	1050	PUB	CMA-C2A-C1A	4.34	131.59	121.39
3	B	1082	PEB	CHC-C1D-ND	-4.29	108.96	113.95
4	D	1050	PUB	CAD-C3D-C4D	4.18	127.97	121.38
3	D	1082	PEB	CHA-C1B-NB	-4.16	116.22	124.93
4	D	1050	PUB	CBB-CAB-C3B	-4.15	105.53	112.62
4	B	1050	PUB	CBA-CAA-C3A	-4.08	106.79	112.98
3	C	1139	PEB	CHB-C4B-NB	-4.06	123.20	128.83
3	D	1082	PEB	CHC-C1D-ND	-3.96	109.35	113.95
3	C	1082	PEB	CHA-C1B-C2B	3.94	135.03	124.90
3	C	1139	PEB	CHA-C4A-NA	3.92	129.86	125.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1050	PUB	OD-C4D-C3D	-3.87	123.84	128.04
4	B	1050	PUB	CBB-CAB-C3B	-3.84	106.07	112.62
3	A	1082	PEB	OA-C1A-C2A	-3.78	123.16	126.17
3	A	1139	PEB	CHA-C4A-NA	3.78	129.70	125.20
3	A	1082	PEB	CHA-C4A-NA	3.70	129.61	125.20
3	B	1158	PEB	CHC-C1D-ND	-3.68	109.67	113.95
3	D	1158	PEB	C4B-C3B-C2B	-3.66	102.74	106.78
3	B	1082	PEB	OA-C1A-C2A	-3.65	123.27	126.17
3	D	1158	PEB	CMB-C2B-C1B	3.64	130.67	125.06
3	B	1158	PEB	CMB-C2B-C1B	3.55	130.53	125.06
3	A	1082	PEB	CHA-C1B-C2B	3.54	134.00	124.90
3	A	1139	PEB	CBC-CAC-C2C	-3.52	106.61	112.62
3	C	1139	PEB	OA-C1A-C2A	-3.49	123.40	126.17
3	C	1139	PEB	CMB-C2B-C1B	3.47	130.41	125.06
3	D	1082	PEB	C3D-C4D-ND	3.43	114.00	107.26
3	C	1082	PEB	CHC-C1D-ND	-3.42	109.98	113.95
3	C	1139	PEB	C3D-C4D-ND	3.36	113.85	107.26
3	D	1082	PEB	OD-C4D-ND	-3.35	120.97	125.93
3	C	1082	PEB	CBB-CAB-C3B	-3.31	103.43	112.63
3	B	1082	PEB	CHA-C4A-NA	3.30	129.13	125.20
3	D	1082	PEB	CBA-CAA-C3A	-3.28	106.16	113.47
3	D	1082	PEB	C1B-C2B-C3B	-3.28	102.75	106.51
3	A	1139	PEB	C3D-C4D-ND	3.27	113.68	107.26
3	C	1139	PEB	CHC-C1D-ND	-3.24	110.19	113.95
3	A	1082	PEB	OA-C1A-NA	3.23	128.86	124.94
3	A	1139	PEB	C4B-C3B-C2B	-3.21	103.23	106.78
3	C	1139	PEB	C4B-C3B-C2B	-3.18	103.27	106.78
4	B	1050	PUB	CHA-C4A-NA	-3.17	110.27	113.95
3	B	1082	PEB	CHA-C1B-C2B	3.17	133.05	124.90
3	B	1158	PEB	C4B-C3B-C2B	-3.16	103.28	106.78
3	B	1158	PEB	C1C-CHB-C4B	3.16	132.58	128.81
3	A	1082	PEB	CHC-C1D-ND	-3.12	110.33	113.95
3	B	1082	PEB	C3D-C4D-ND	3.06	113.26	107.26
4	D	1050	PUB	CBA-CAA-C3A	-3.05	108.35	112.98
3	A	1082	PEB	CBA-CAA-C3A	-3.04	106.69	113.47
3	A	1139	PEB	CHB-C4B-NB	-3.04	124.61	128.83
3	C	1139	PEB	CHC-C4C-C3C	-3.03	125.17	130.34
3	A	1139	PEB	CMB-C2B-C1B	3.02	129.71	125.06
3	C	1082	PEB	C3D-C4D-ND	3.02	113.18	107.26
3	D	1158	PEB	C1C-CHB-C4B	3.00	132.39	128.81
3	A	1139	PEB	OD-C4D-C3D	-2.98	122.70	129.46
4	D	1050	PUB	CHA-C4A-NA	-2.97	110.50	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1050	PUB	OD-C4D-ND	-2.96	121.54	125.93
3	D	1158	PEB	C3B-C4B-NB	2.95	114.35	110.05
3	A	1082	PEB	CBB-CAB-C3B	-2.95	104.44	112.63
3	A	1082	PEB	C1B-C2B-C3B	-2.94	103.13	106.51
3	C	1139	PEB	CHA-C1B-NB	-2.93	118.81	124.93
3	B	1082	PEB	C1B-C2B-C3B	-2.91	103.16	106.51
3	C	1082	PEB	CAA-C3A-C4A	2.90	120.12	112.67
3	C	1082	PEB	C1B-C2B-C3B	-2.89	103.18	106.51
3	A	1082	PEB	CAA-C3A-C4A	2.88	120.07	112.67
3	A	1139	PEB	C3B-C4B-NB	2.87	114.22	110.05
3	A	1139	PEB	CHC-C4C-C3C	-2.87	125.45	130.34
3	C	1139	PEB	CAB-CBB-CGB	-2.75	107.68	113.60
3	C	1082	PEB	CHA-C4A-NA	2.73	128.45	125.20
3	B	1082	PEB	CAB-CBB-CGB	-2.71	107.77	113.60
3	D	1158	PEB	OD-C4D-ND	-2.71	121.92	125.93
3	C	1139	PEB	OD-C4D-C3D	-2.71	123.32	129.46
3	D	1158	PEB	CHB-C4B-C3B	-2.70	119.07	125.32
4	B	1050	PUB	C1C-C2C-C3C	-2.70	103.79	106.78
3	B	1158	PEB	C3B-C4B-NB	2.70	113.98	110.05
3	D	1158	PEB	C3D-C4D-ND	2.69	112.54	107.26
4	B	1050	PUB	CHB-C1C-NC	-2.65	125.15	128.83
3	B	1158	PEB	OD-C4D-ND	-2.64	122.02	125.93
3	B	1158	PEB	CHA-C4A-NA	2.59	128.29	125.20
3	A	1082	PEB	OD-C4D-ND	-2.59	122.10	125.93
3	C	1139	PEB	CAB-C3B-C4B	2.57	129.56	125.01
3	D	1158	PEB	CHA-C4A-NA	2.55	128.24	125.20
3	B	1082	PEB	C2A-C1A-NA	2.55	110.47	108.27
3	C	1082	PEB	CMA-C2A-C1A	-2.55	106.91	112.40
3	C	1139	PEB	C1B-C2B-C3B	-2.53	103.60	106.51
3	D	1082	PEB	CAB-CBB-CGB	-2.53	108.16	113.60
3	A	1139	PEB	C1B-C2B-C3B	-2.52	103.61	106.51
3	D	1082	PEB	CHA-C1B-C2B	2.52	131.37	124.90
3	B	1158	PEB	C3D-C4D-ND	2.51	112.19	107.26
3	A	1082	PEB	C1C-CHB-C4B	2.50	131.80	128.81
3	B	1158	PEB	CHC-C4C-C3C	-2.49	126.08	130.34
4	B	1050	PUB	OA-C1A-NA	-2.48	122.26	125.93
3	C	1139	PEB	C2A-C1A-NA	2.43	110.37	108.27
3	D	1158	PEB	CAB-C3B-C4B	2.42	129.30	125.01
3	C	1082	PEB	OD-C4D-ND	-2.41	122.36	125.93
3	A	1082	PEB	CHB-C4B-NB	-2.41	125.49	128.83
3	A	1082	PEB	CMA-C2A-C1A	-2.39	107.24	112.40
4	D	1050	PUB	OA-C1A-NA	-2.39	122.38	125.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1082	PEB	CBA-CAA-C3A	-2.39	108.14	113.47
4	B	1050	PUB	O2B-CGB-CBB	2.38	121.66	114.03
3	D	1082	PEB	OA-C1A-NA	2.38	127.82	124.94
3	B	1082	PEB	OD-C4D-C3D	-2.37	124.10	129.46
4	D	1050	PUB	C1C-C2C-C3C	-2.33	104.20	106.78
3	B	1158	PEB	CHB-C4B-C3B	-2.32	119.95	125.32
4	B	1050	PUB	CBD-CAD-C3D	-2.32	106.04	112.43
3	A	1082	PEB	C3D-C4D-ND	2.30	111.77	107.26
3	D	1158	PEB	CAC-CBC-CGC	-2.29	107.34	113.76
3	C	1139	PEB	C3B-C4B-NB	2.26	113.34	110.05
3	D	1082	PEB	CAA-C3A-C2A	-2.26	108.61	114.26
3	D	1082	PEB	CHB-C4B-C3B	-2.25	120.12	125.32
3	A	1082	PEB	CHC-C4C-C3C	-2.25	126.50	130.34
3	C	1082	PEB	OD-C4D-C3D	-2.23	124.42	129.46
3	D	1158	PEB	CHC-C4C-C3C	-2.22	126.54	130.34
3	B	1082	PEB	OD-C4D-ND	-2.22	122.64	125.93
3	C	1139	PEB	C2A-C3A-C4A	2.21	104.65	101.34
4	D	1050	PUB	CBD-CAD-C3D	-2.20	106.38	112.43
3	C	1082	PEB	OA-C1A-NA	2.17	127.57	124.94
3	C	1082	PEB	CHC-C4C-C3C	-2.15	126.67	130.34
3	B	1158	PEB	C1B-C2B-C3B	-2.14	104.05	106.51
3	A	1139	PEB	CHA-C1B-NB	-2.14	120.46	124.93
3	C	1082	PEB	C1C-CHB-C4B	2.13	131.36	128.81
3	B	1158	PEB	O1C-CGC-CBC	-2.10	116.33	123.08
3	C	1139	PEB	OD-C4D-ND	-2.10	122.82	125.93
4	B	1050	PUB	C2C-C1C-NC	2.09	113.09	110.05
3	B	1158	PEB	CAB-C3B-C4B	2.09	128.70	125.01
3	A	1082	PEB	C3B-C4B-NB	2.06	113.05	110.05
3	D	1082	PEB	C3B-C4B-NB	2.05	113.03	110.05
4	D	1050	PUB	CAC-CBC-CGC	-2.04	109.22	113.60
3	A	1139	PEB	C2A-C1A-NA	2.03	110.03	108.27
4	B	1050	PUB	CAC-C2C-C1C	2.01	128.57	125.01

There are no chirality outliers.

All (66) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1082	PEB	C2B-C1B-CHA-C4A
3	A	1139	PEB	NB-C1B-CHA-C4A
3	A	1139	PEB	C2B-C1B-CHA-C4A
3	B	1082	PEB	NB-C1B-CHA-C4A
3	B	1158	PEB	C2A-C3A-CAA-CBA

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Mol	Chain	Res	Type	Atoms
3	B	1158	PEB	C4A-C3A-CAA-CBA
3	B	1158	PEB	NB-C1B-CHA-C4A
3	B	1158	PEB	C2B-C1B-CHA-C4A
3	C	1082	PEB	C2C-C1C-CHB-C4B
3	C	1082	PEB	C2B-C1B-CHA-C4A
3	C	1139	PEB	NB-C1B-CHA-C4A
3	C	1139	PEB	C2B-C1B-CHA-C4A
3	D	1082	PEB	C2C-C1C-CHB-C4B
3	D	1158	PEB	C2A-C3A-CAA-CBA
3	D	1158	PEB	C4A-C3A-CAA-CBA
3	D	1158	PEB	NB-C1B-CHA-C4A
3	D	1158	PEB	C2B-C1B-CHA-C4A
4	B	1050	PUB	NC-C4C-CHC-C1D
4	B	1050	PUB	C3B-C4B-CHB-C1C
4	D	1050	PUB	NC-C4C-CHC-C1D
4	D	1050	PUB	C3B-C4B-CHB-C1C
3	A	1082	PEB	NB-C1B-CHA-C4A
3	C	1082	PEB	NB-C1B-CHA-C4A
3	D	1082	PEB	NB-C1B-CHA-C4A
3	B	1082	PEB	C2B-C1B-CHA-C4A
3	D	1082	PEB	C2B-C1B-CHA-C4A
3	C	1139	PEB	C4B-C3B-CAB-CBB
4	B	1050	PUB	C3A-C4A-CHA-C1B
4	D	1050	PUB	C3A-C4A-CHA-C1B
3	C	1139	PEB	C2B-C3B-CAB-CBB
3	B	1082	PEB	CAB-CBB-CGB-O2B
3	D	1082	PEB	CAB-CBB-CGB-O1B
4	B	1050	PUB	CAB-CBB-CGB-O2B
3	A	1082	PEB	CAC-CBC-CGC-O1C
3	B	1082	PEB	CAB-CBB-CGB-O1B
4	D	1050	PUB	CAB-CBB-CGB-O1B
3	C	1082	PEB	CAC-CBC-CGC-O1C
3	C	1139	PEB	CAC-CBC-CGC-O1C
4	B	1050	PUB	CAB-CBB-CGB-O1B
3	C	1139	PEB	CAC-CBC-CGC-O2C
3	A	1082	PEB	CAC-CBC-CGC-O2C
3	C	1082	PEB	CAC-CBC-CGC-O2C
3	D	1082	PEB	CAC-CBC-CGC-O2C
3	D	1082	PEB	CAB-CBB-CGB-O2B
3	B	1082	PEB	CAC-CBC-CGC-O2C
4	D	1050	PUB	CAB-CBB-CGB-O2B
3	B	1158	PEB	CAB-CBB-CGB-O2B

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Mol	Chain	Res	Type	Atoms
3	A	1139	PEB	CAC-CBC-CGC-O2C
3	D	1082	PEB	CAC-CBC-CGC-O1C
3	A	1139	PEB	CAC-CBC-CGC-O1C
3	C	1139	PEB	CAB-CBB-CGB-O2B
3	D	1158	PEB	CAB-CBB-CGB-O2B
3	A	1139	PEB	CAB-CBB-CGB-O2B
3	B	1082	PEB	CAC-CBC-CGC-O1C
3	A	1139	PEB	CAB-CBB-CGB-O1B
3	B	1158	PEB	CAB-CBB-CGB-O1B
3	D	1158	PEB	CAB-CBB-CGB-O1B
3	C	1139	PEB	CAB-CBB-CGB-O1B
4	D	1050	PUB	CAC-CBC-CGC-O2C
4	B	1050	PUB	CAC-CBC-CGC-O2C
3	B	1158	PEB	CAC-CBC-CGC-O1C
3	D	1158	PEB	CAC-CBC-CGC-O1C
4	D	1050	PUB	CAC-CBC-CGC-O1C
3	B	1158	PEB	CAC-CBC-CGC-O2C
3	D	1158	PEB	CAC-CBC-CGC-O2C
4	B	1050	PUB	CAC-CBC-CGC-O1C

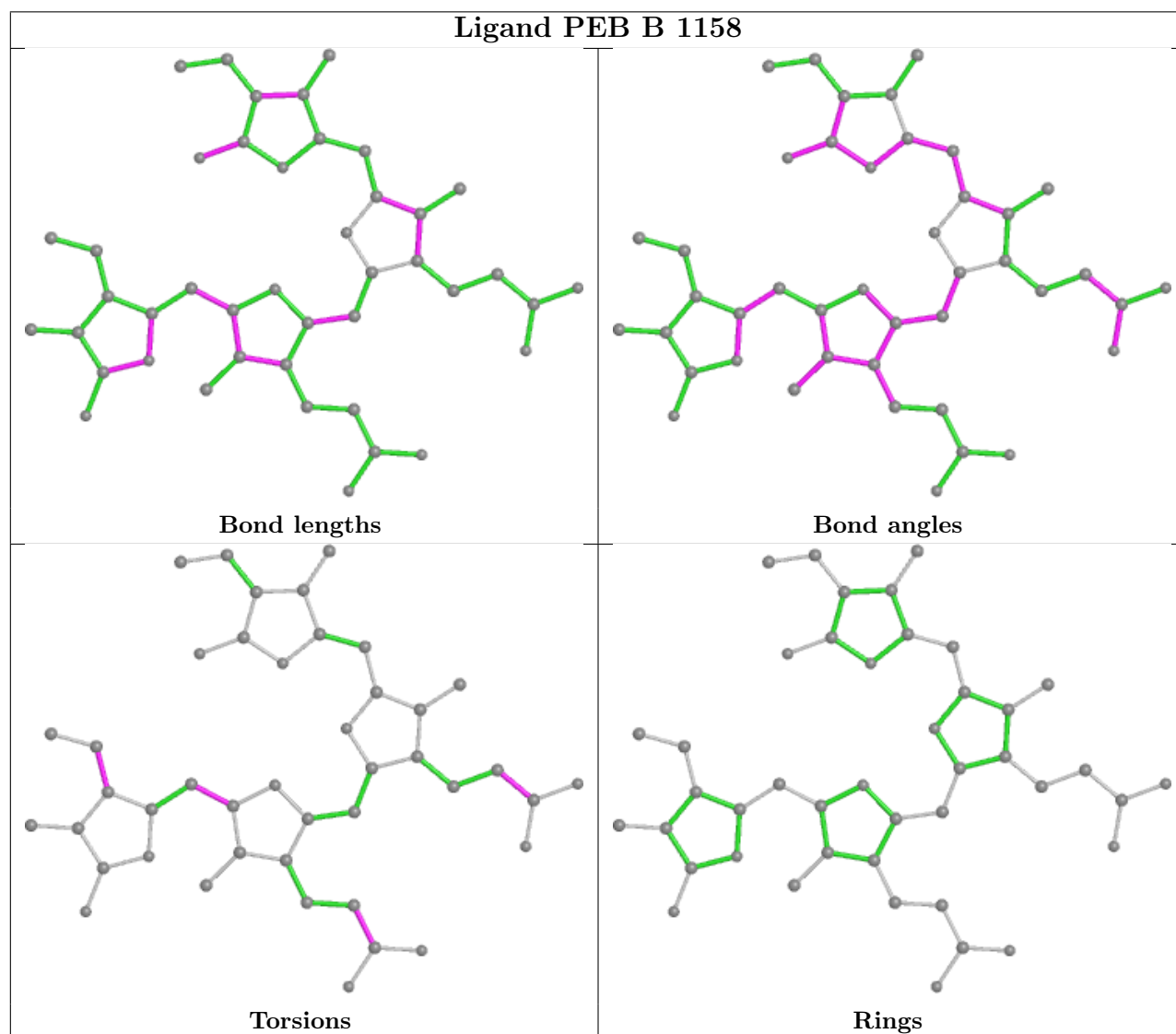
There are no ring outliers.

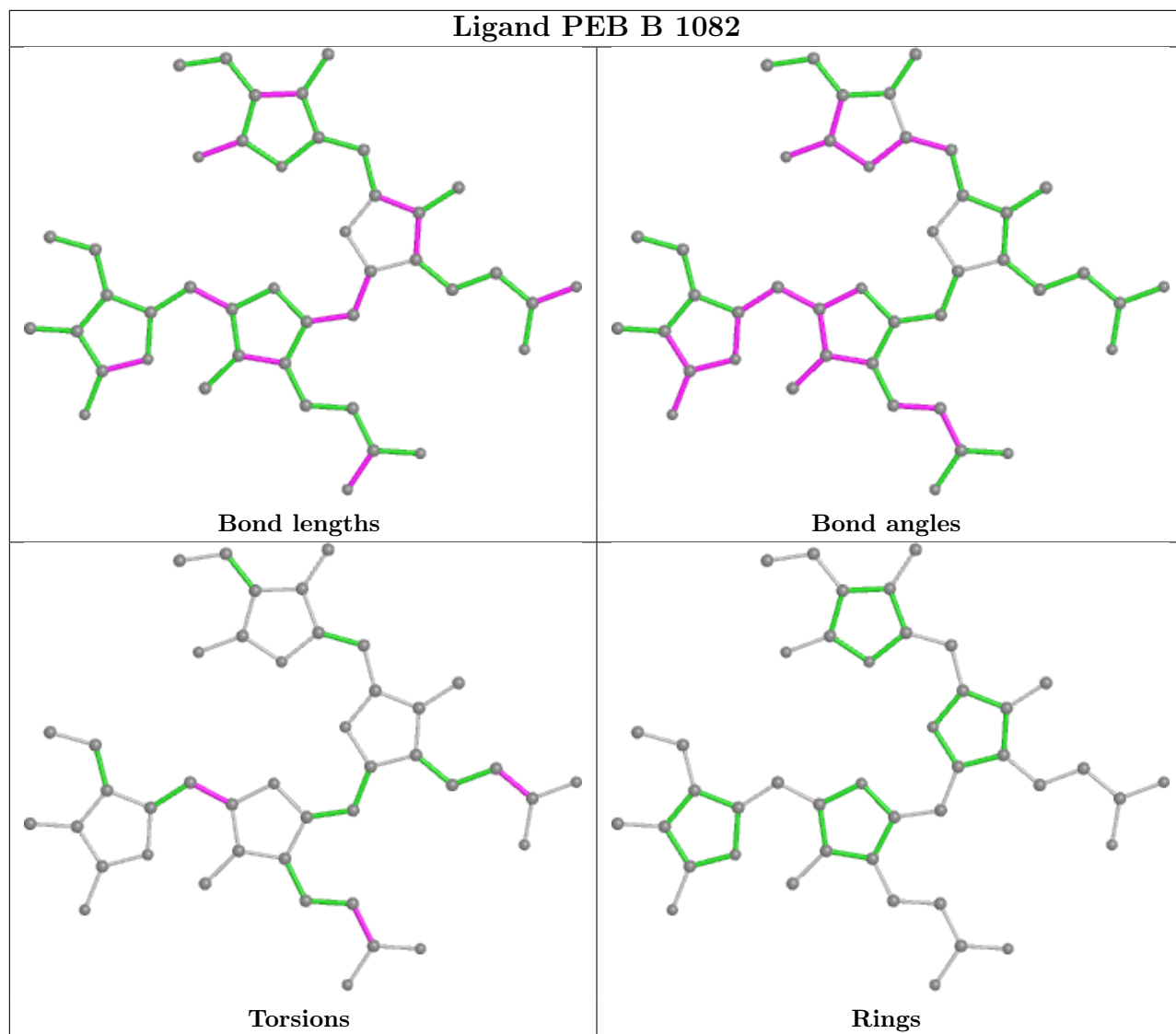
7 monomers are involved in 24 short contacts:

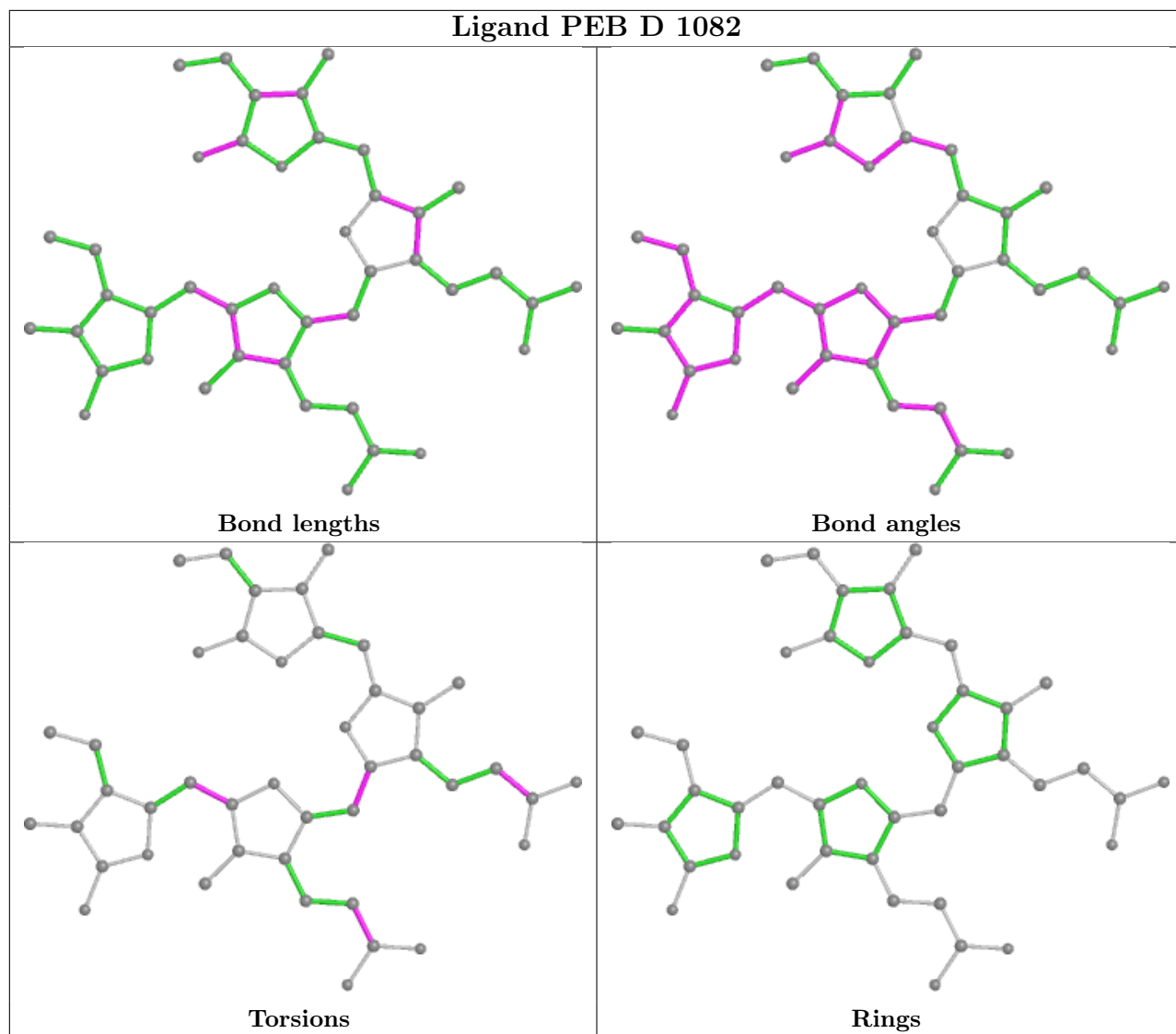
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1158	PEB	4	0
3	B	1082	PEB	3	0
3	D	1082	PEB	3	0
3	A	1082	PEB	2	0
3	D	1158	PEB	5	0
3	A	1139	PEB	2	0
3	C	1139	PEB	5	0

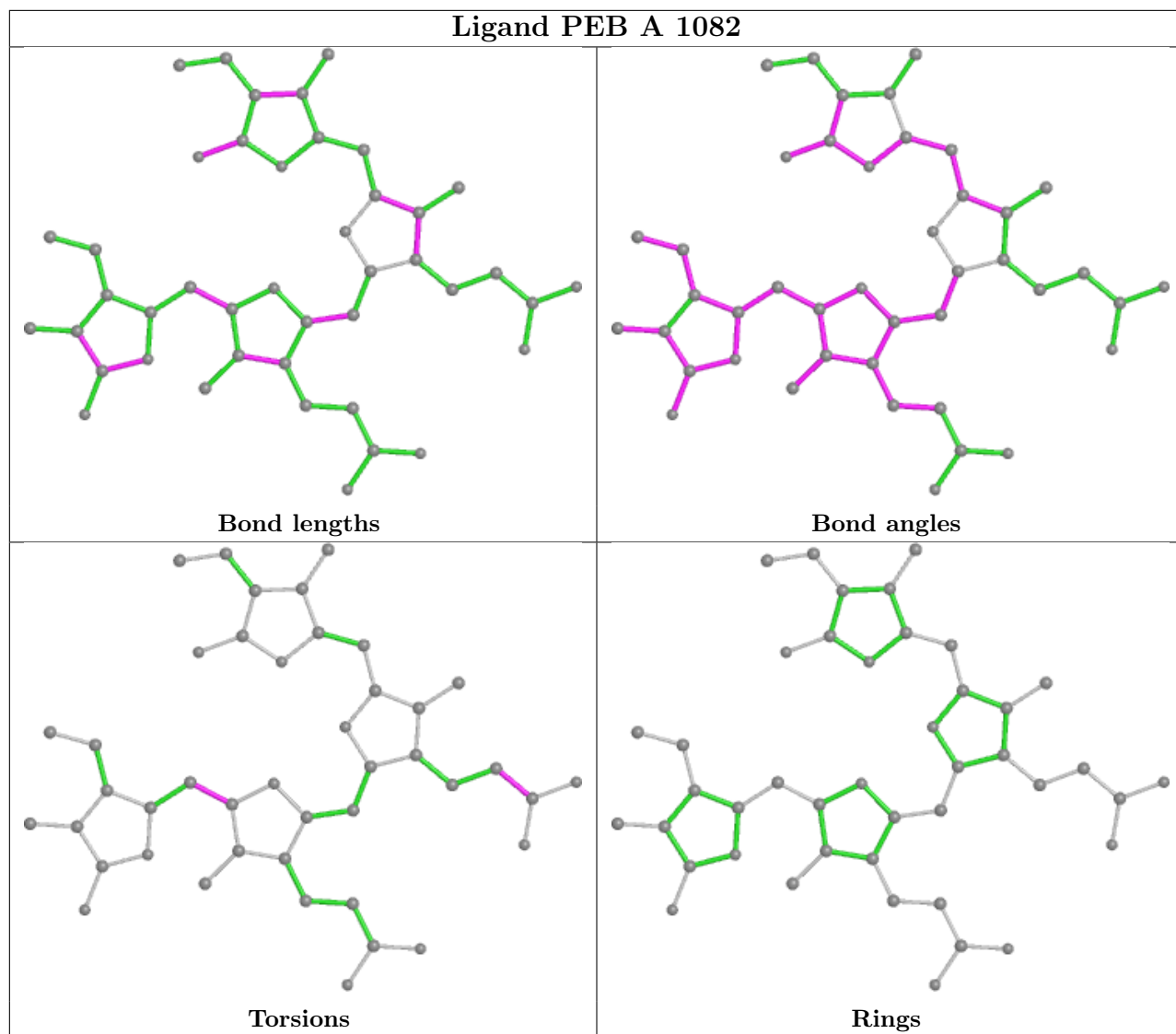
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

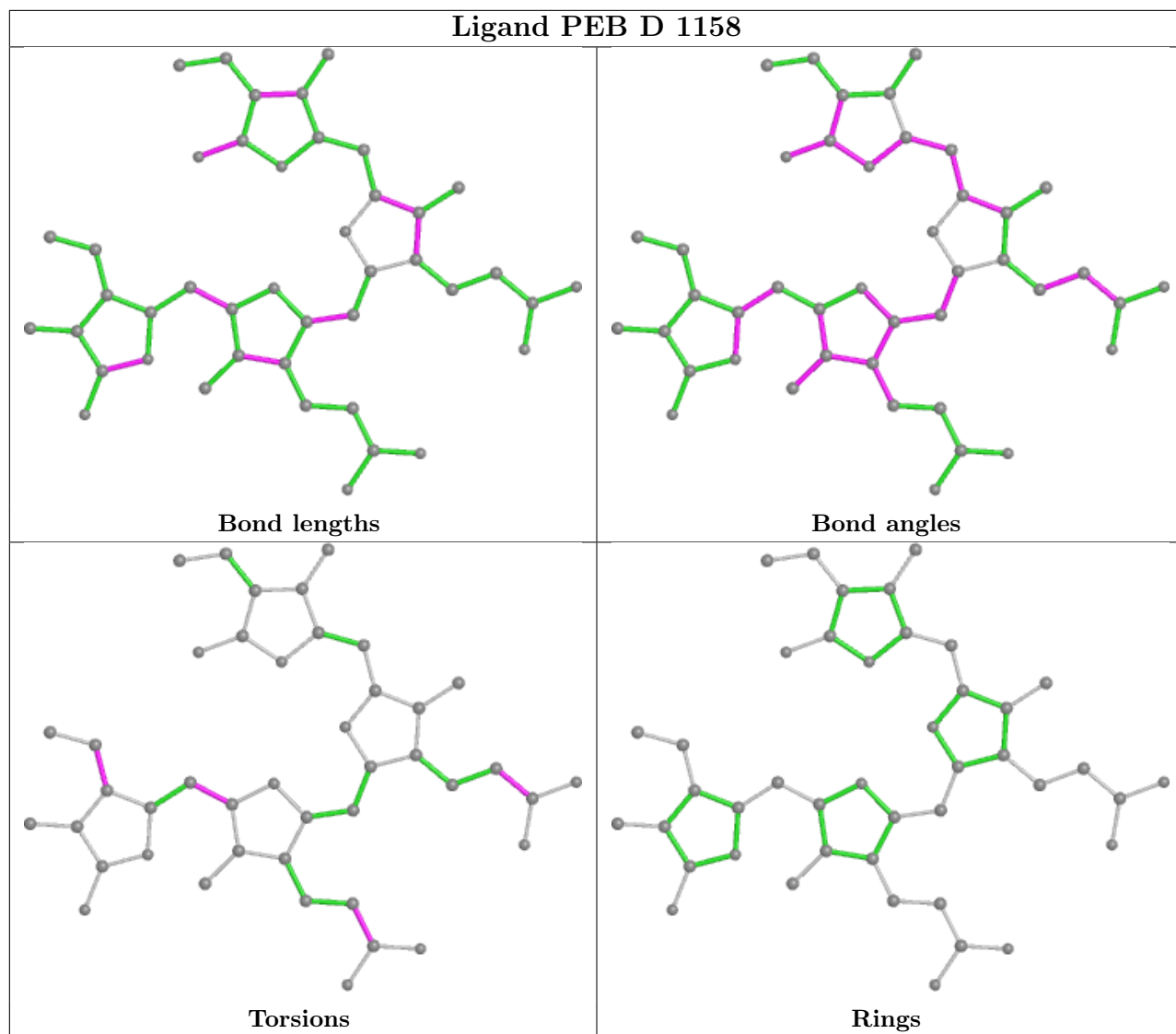
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

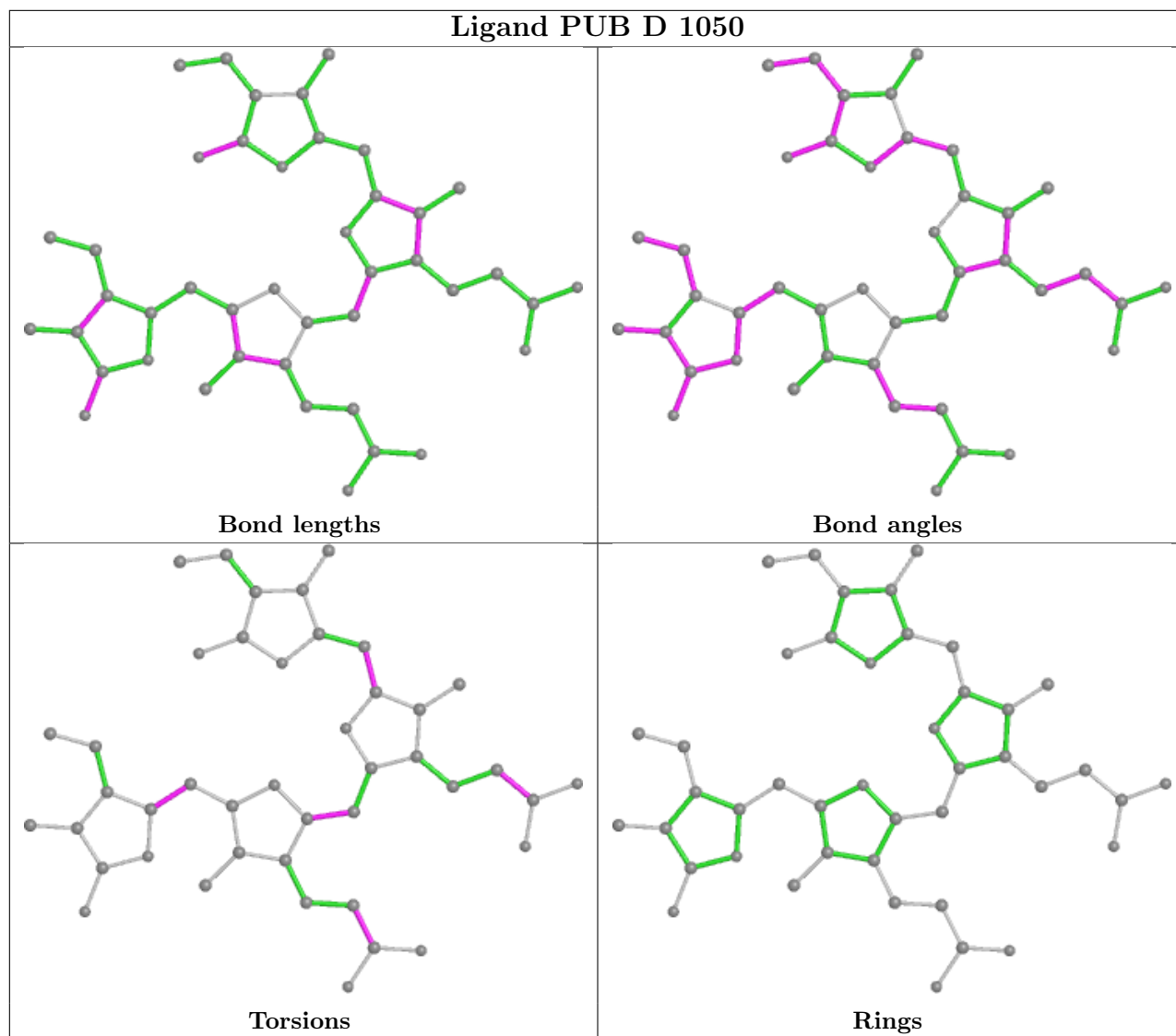


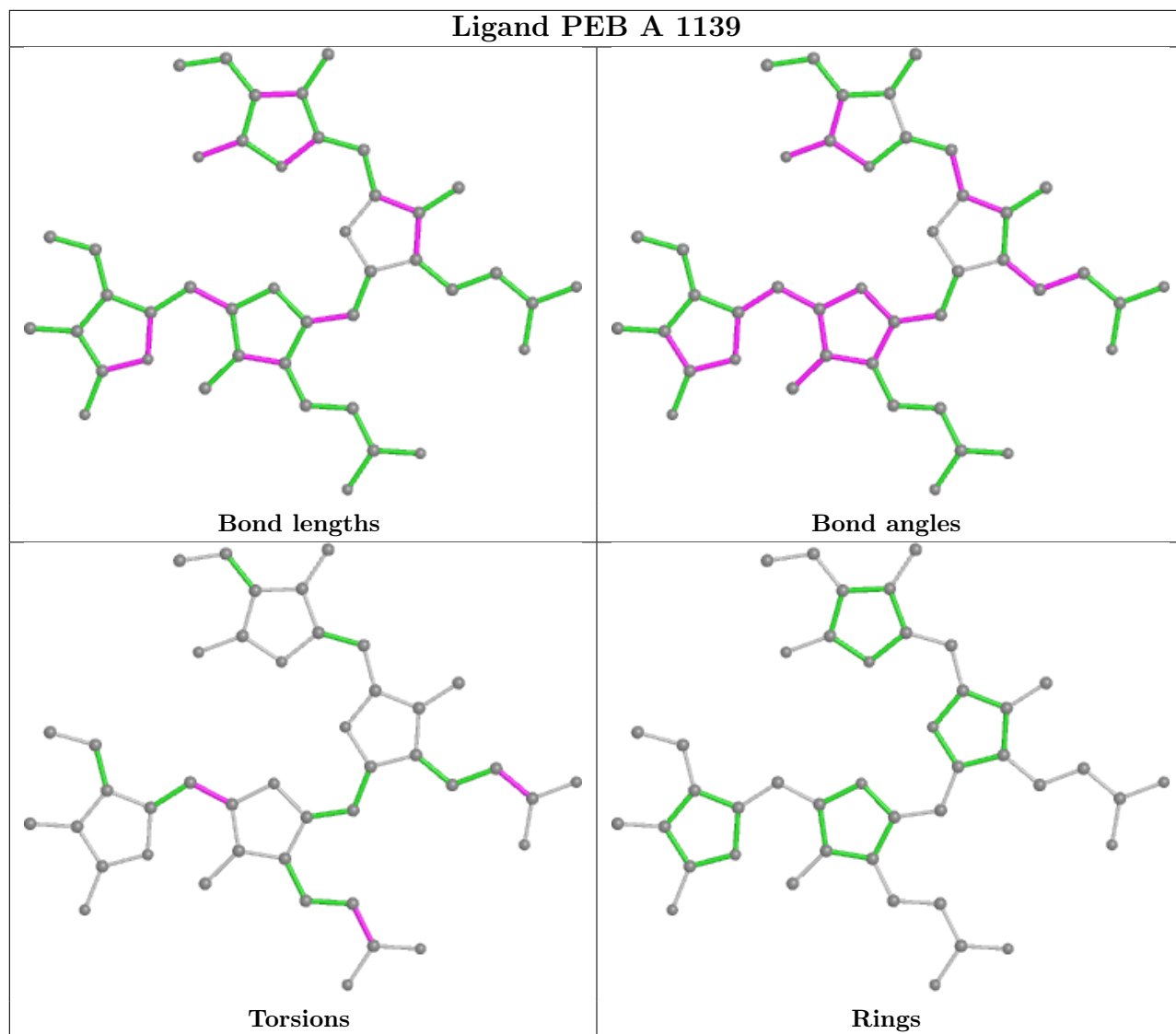


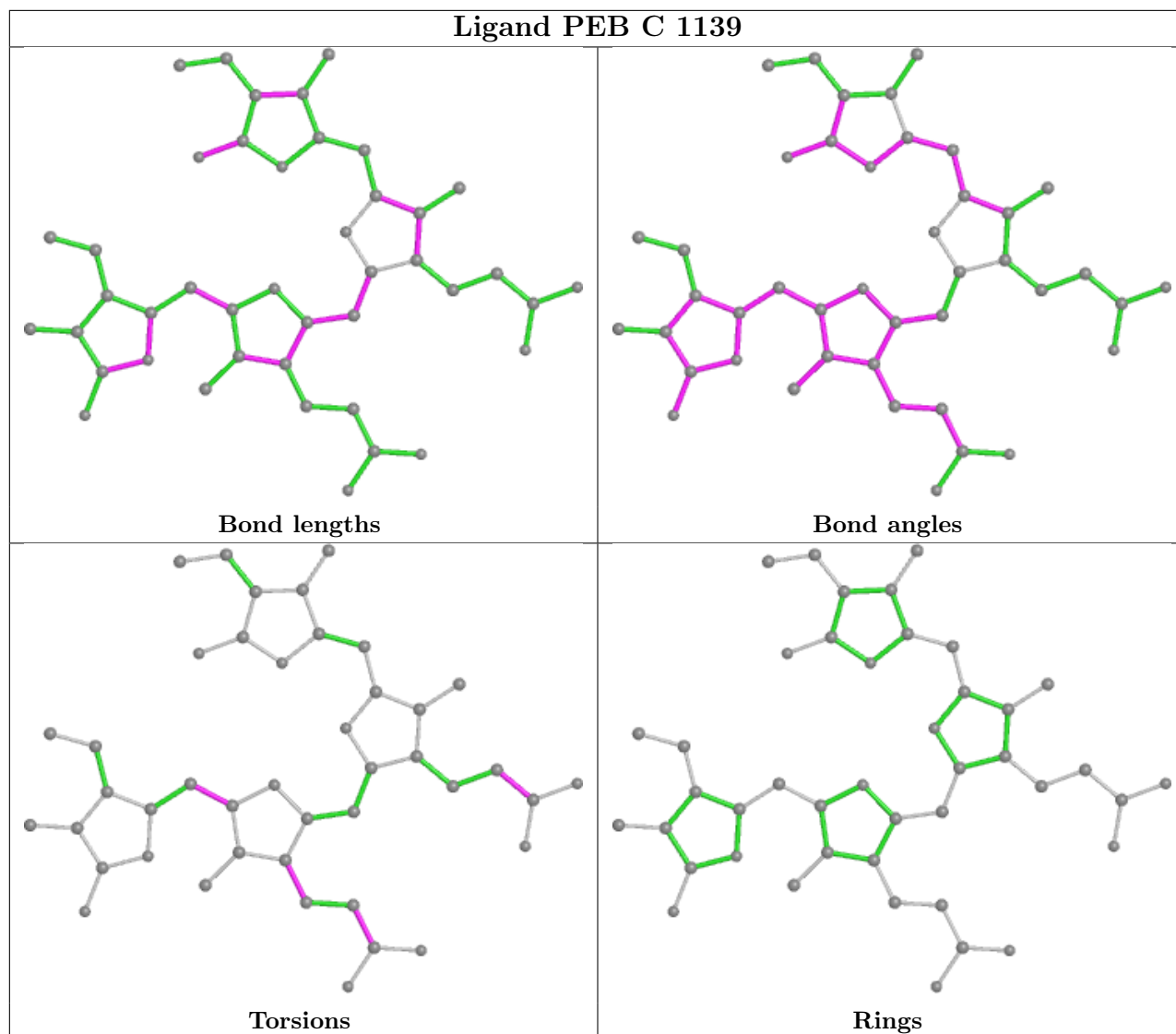


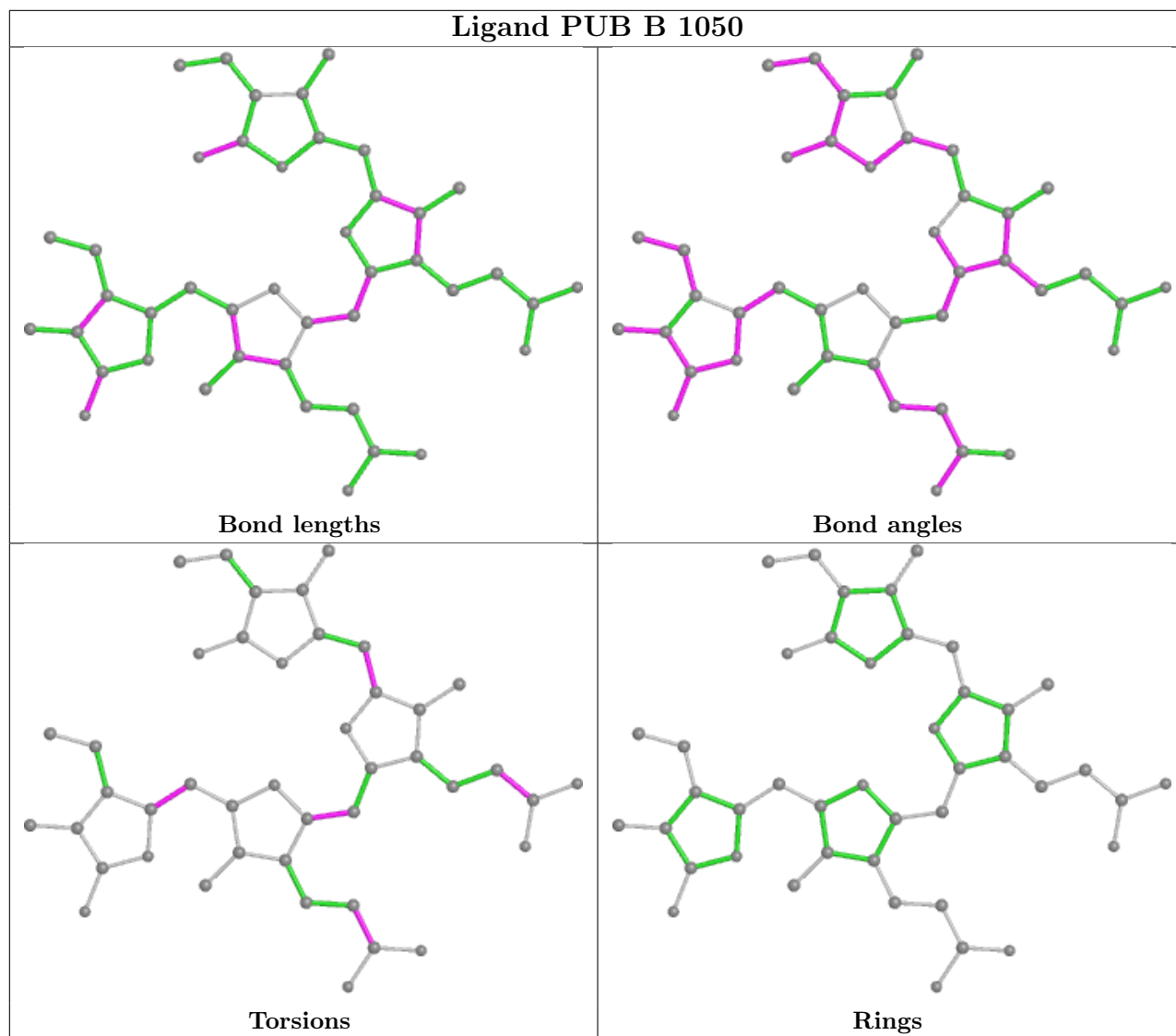


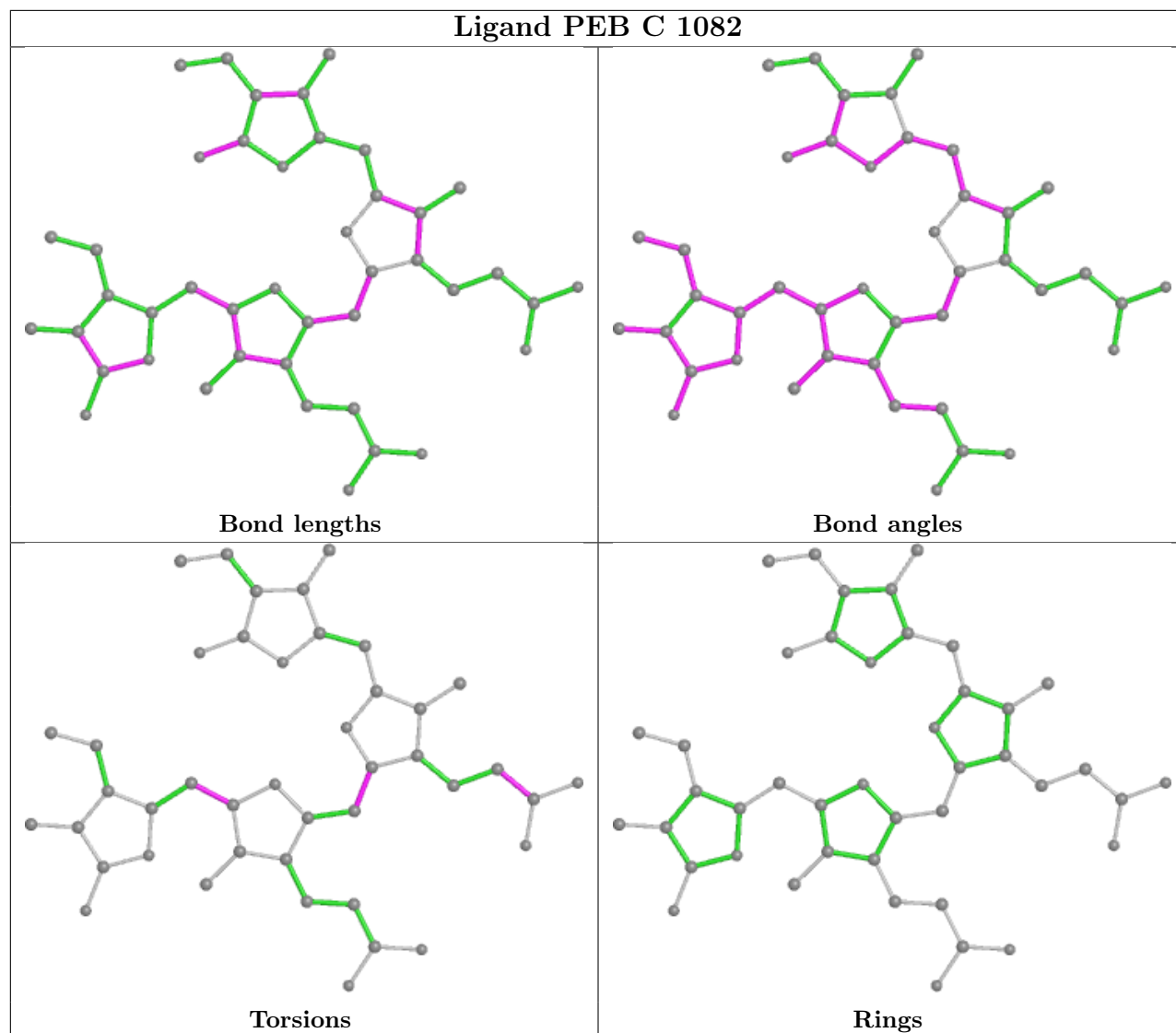












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	164/164 (100%)	-0.36	0 100 100	23, 29, 37, 48	0
1	C	164/164 (100%)	-0.42	0 100 100	25, 29, 35, 48	0
2	B	176/177 (99%)	-0.55	1 (0%) 89 88	22, 28, 38, 48	0
2	D	176/177 (99%)	-0.55	2 (1%) 80 79	23, 28, 38, 47	0
All	All	680/682 (99%)	-0.47	3 (0%) 92 91	22, 28, 38, 48	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	111	ASN	2.7
2	D	70	GLY	2.3
2	B	155	GLN	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MEN	B	72	9/10	0.97	0.07	26,28,29,29	0
2	MEN	D	72	9/10	0.98	0.07	26,27,27,29	0

6.3 Carbohydrates [i](#)

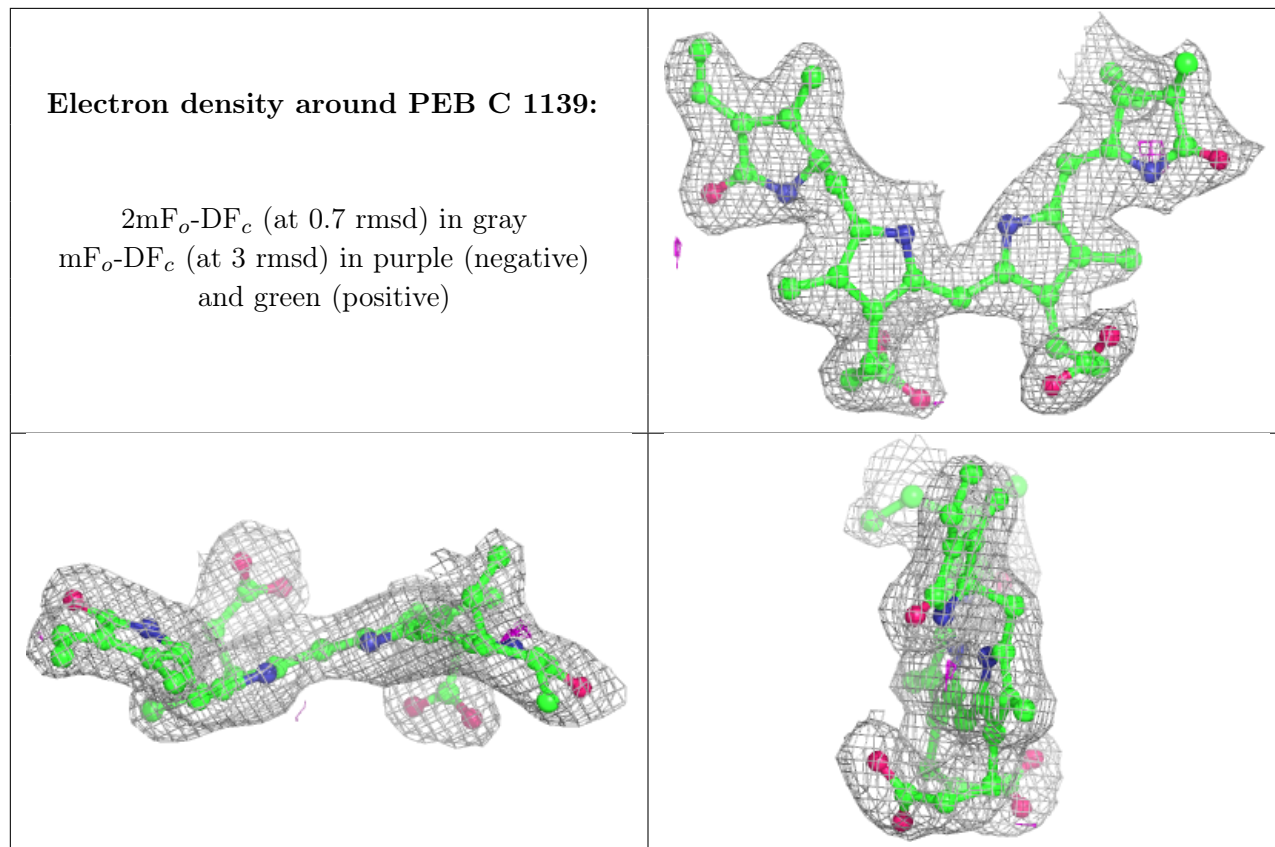
There are no monosaccharides in this entry.

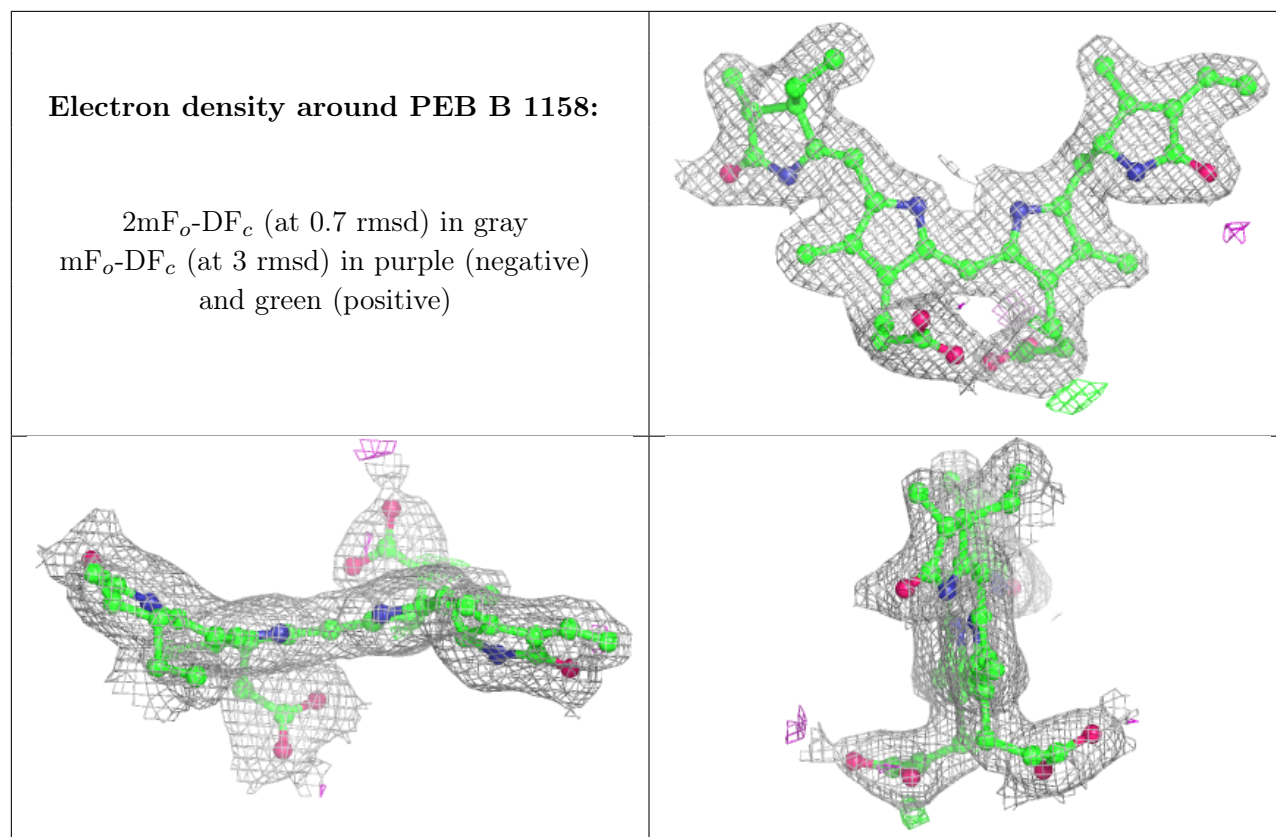
6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	PEB	C	1139	43/43	0.91	0.20	29,32,38,40	0
3	PEB	B	1158	43/43	0.93	0.11	25,27,36,47	0
3	PEB	D	1082	43/43	0.93	0.13	26,28,37,46	0
3	PEB	D	1158	43/43	0.93	0.12	23,26,39,51	0
3	PEB	B	1082	43/43	0.94	0.11	25,28,39,47	0
4	PUB	B	1050	43/43	0.94	0.10	27,29,36,38	0
4	PUB	D	1050	43/43	0.94	0.11	27,31,35,36	0
3	PEB	C	1082	43/43	0.95	0.09	25,27,30,34	0
3	PEB	A	1082	43/43	0.97	0.12	23,25,30,36	0
3	PEB	A	1139	43/43	0.97	0.10	22,25,29,30	0

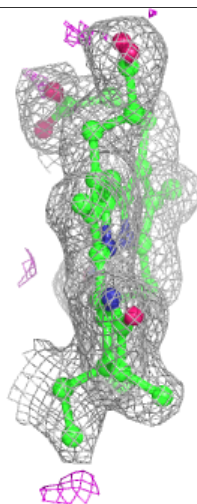
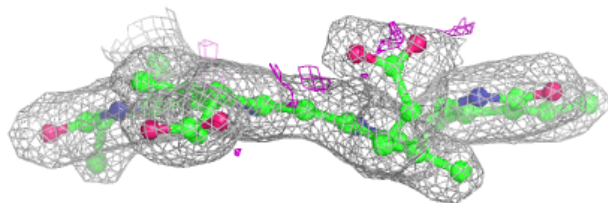
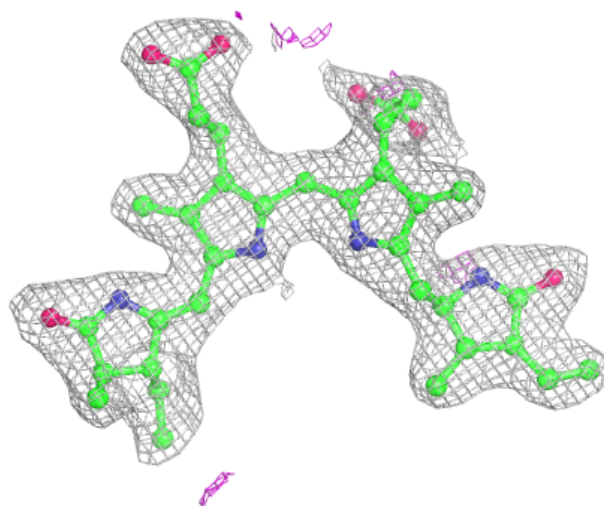
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

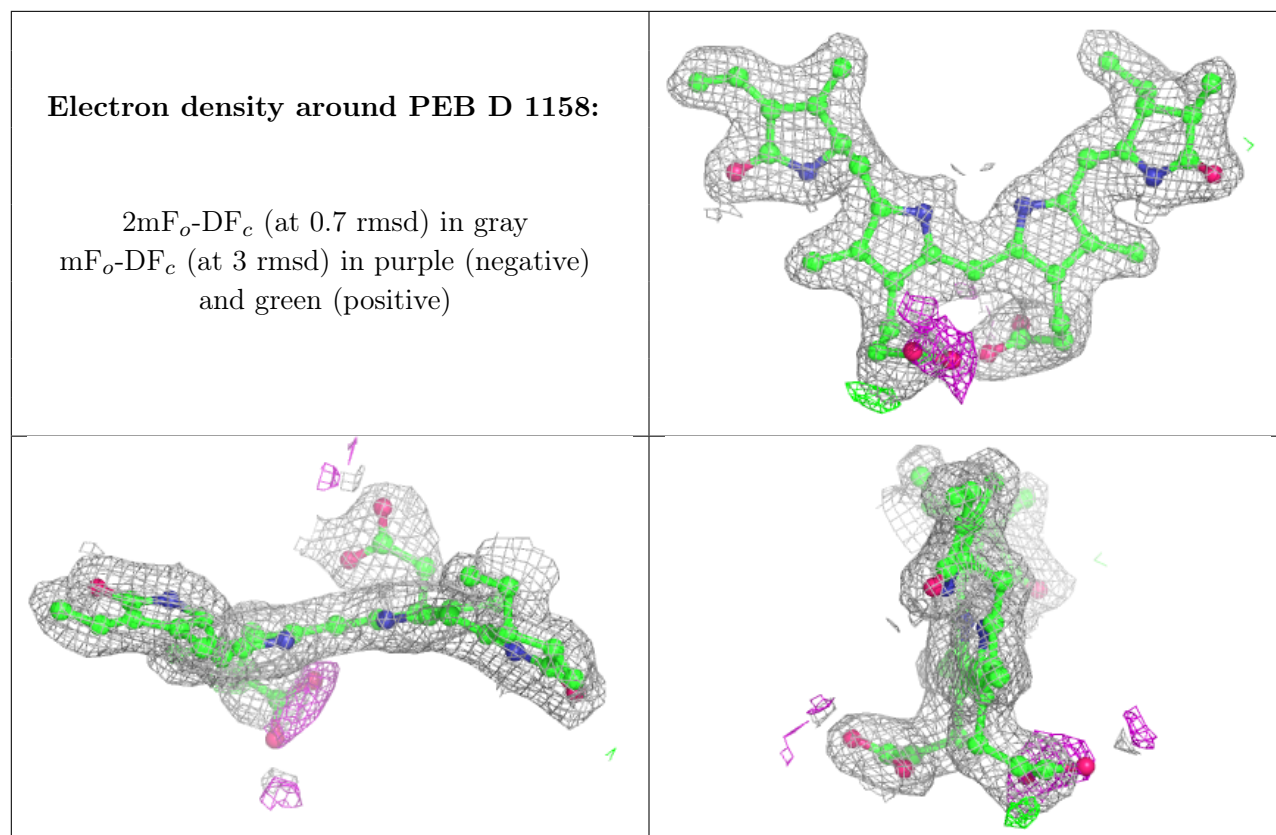




Electron density around PEB D 1082:

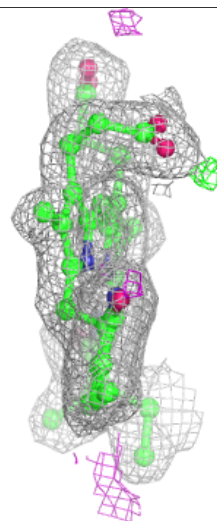
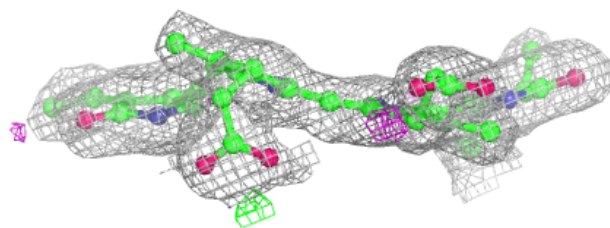
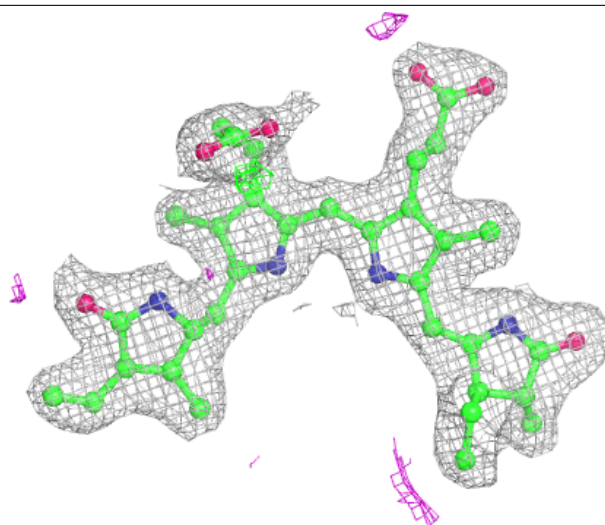
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





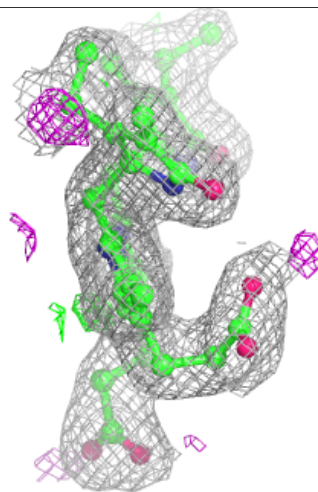
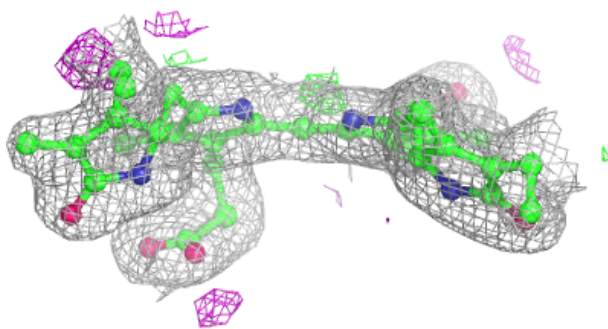
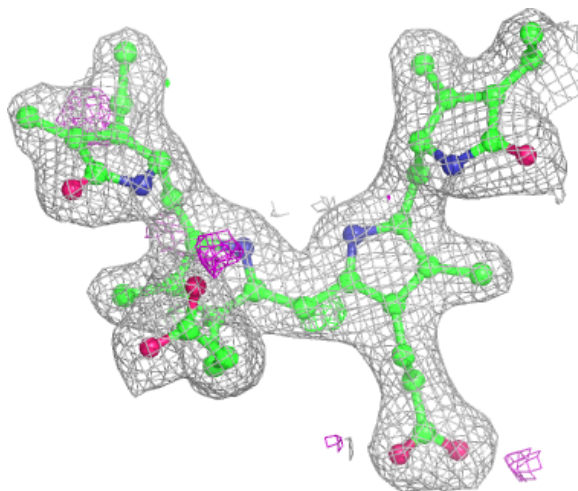
Electron density around PEB B 1082:

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



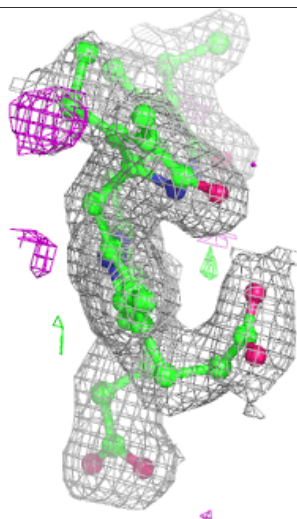
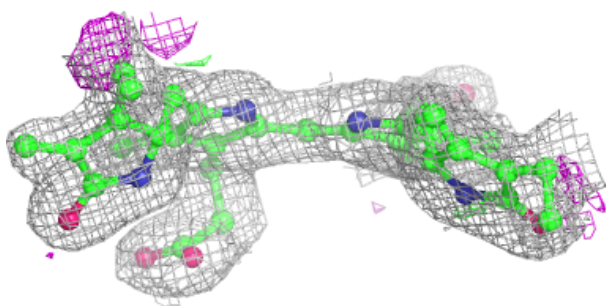
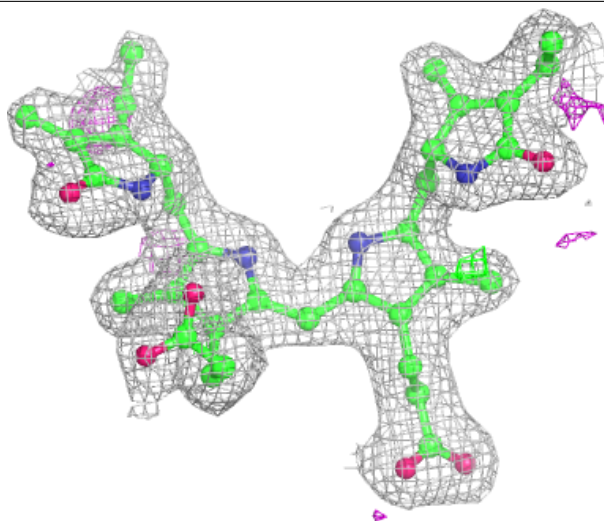
Electron density around PUB B 1050:

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



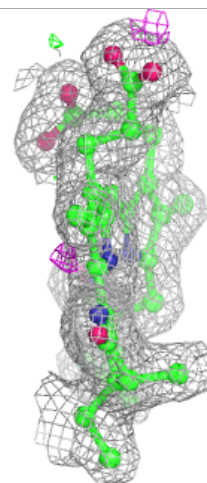
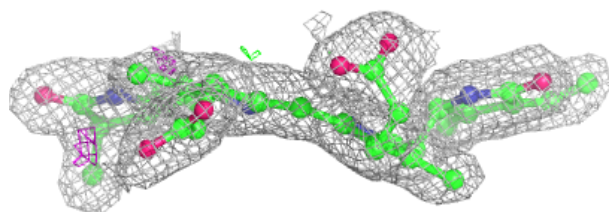
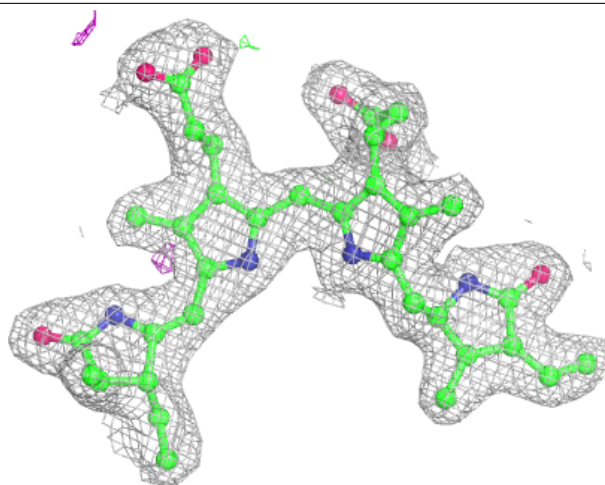
Electron density around PUB D 1050:

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



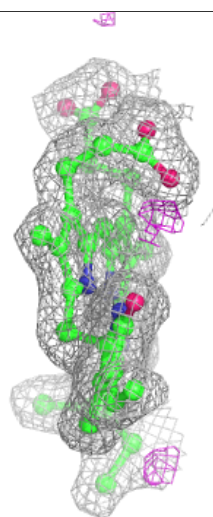
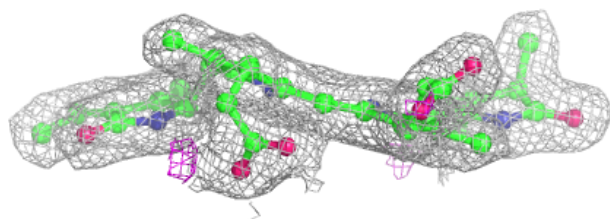
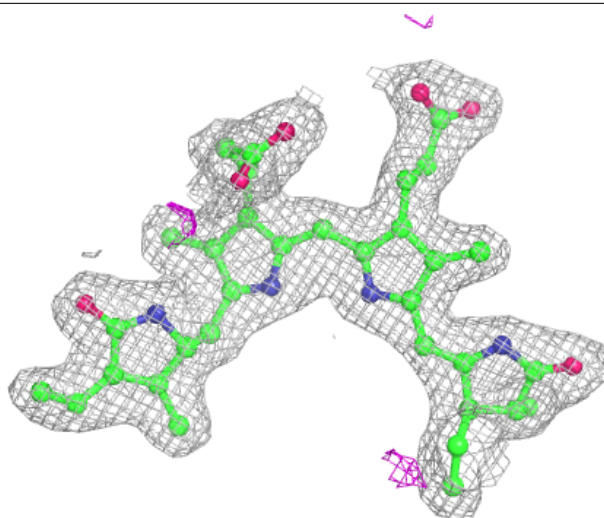
Electron density around PEB C 1082:

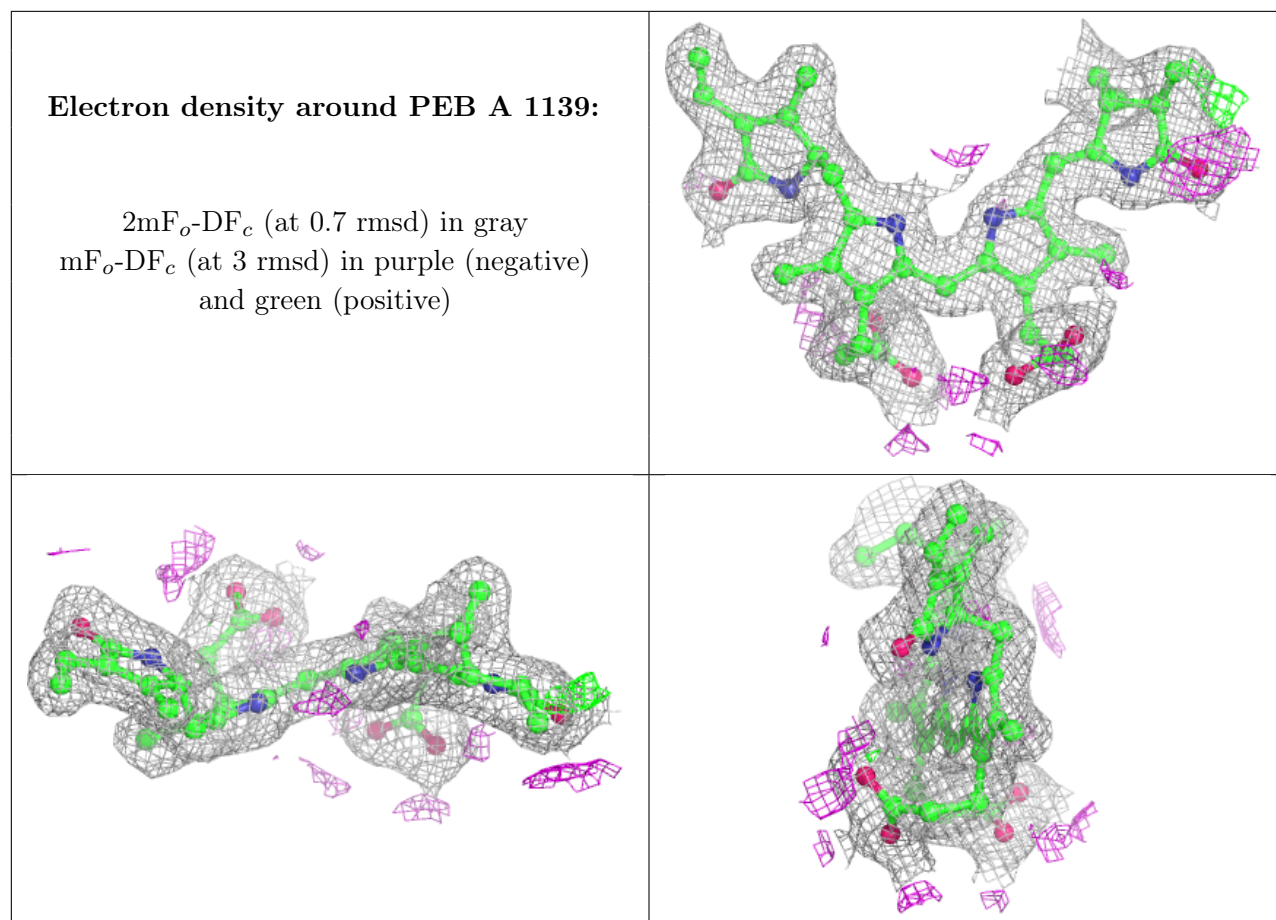
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around PEB A 1082:

$2mF_o-DF_c$ (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.