



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 17, 2023 – 10:15 AM EDT

PDB ID : 8EL5
Title : Light harvesting phycobiliprotein HaPE555 from the cryptophyte *Hemiselmis andersenii* CCMP644 in an alternating tight to loose interface filament
Authors : Rathbone, H.W.; Michie, K.A.; Laos, A.L.; Curmi, P.M.G.
Deposited on : 2022-09-23
Resolution : 1.67 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 : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (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

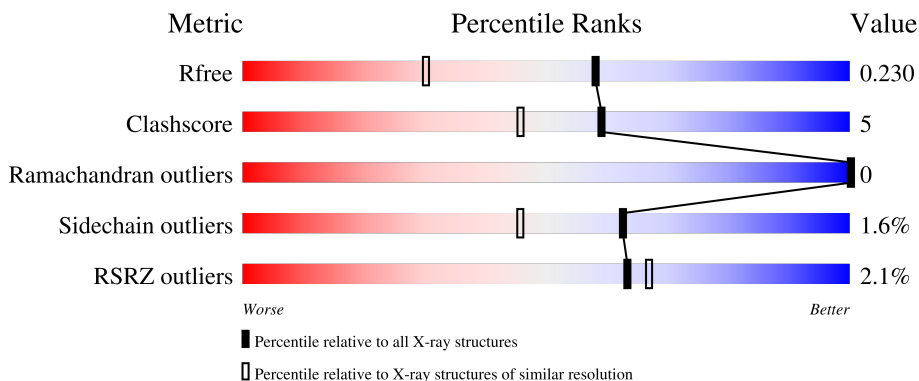
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.67 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.



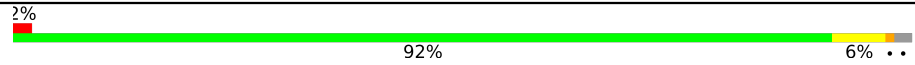
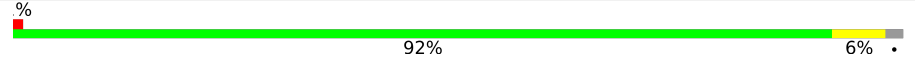
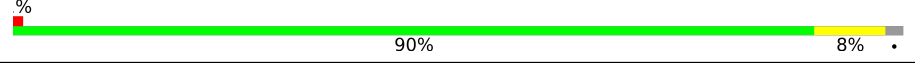
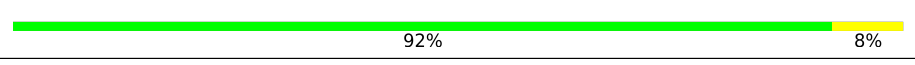
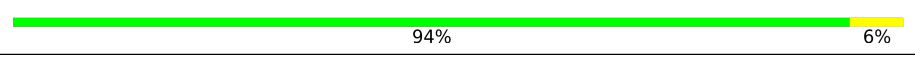
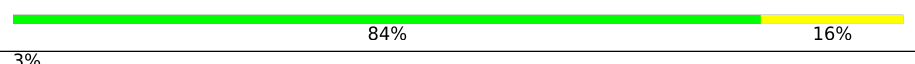
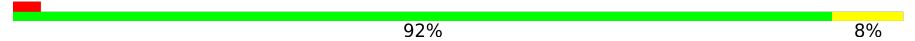
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

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	67	
1	G	67	
1	J	67	
1	K	67	
2	B	177	

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Mol	Chain	Length	Quality of chain
2	D	177	 2% 92% 6% ..
2	F	177	 % 92% 6% .
2	H	177	 % 90% 8% .
3	C	62	 92% 8%
3	E	62	 94% 6%
3	I	62	 84% 16%
3	L	62	 3% 92% 8%

2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 19890 atoms, of which 9718 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-1 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	64	924	287	459	82	91	5	0	64	0
1	G	64	923	287	458	82	91	5	0	64	0
1	J	64	927	287	462	82	91	5	0	64	0
1	K	64	925	287	460	82	91	5	0	64	0

- Molecule 2 is a protein called Phycoerythrin550 beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
2	B	173	2616	804	1309	225	269	9	0	9	0
2	D	174	2636	810	1321	227	269	9	0	8	0
2	F	173	2632	809	1319	225	270	9	0	10	0
2	H	173	2623	807	1314	225	268	9	0	9	0

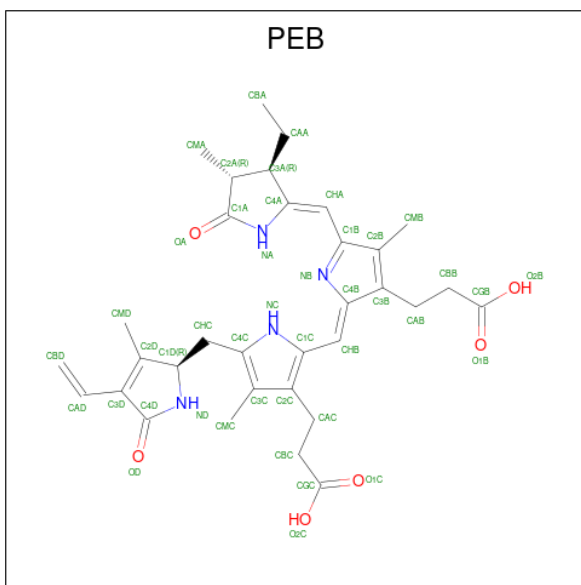
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	172	VAL	GLU	conflict	UNP U5T8W0
D	172	VAL	GLU	conflict	UNP U5T8W0
F	172	VAL	GLU	conflict	UNP U5T8W0
H	172	VAL	GLU	conflict	UNP U5T8W0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
3	C	62	Total 918	C 280	H 460	N 79	O 93	S 6	0	62	0
3	E	62	Total 918	C 280	H 460	N 79	O 93	S 6	0	62	0
3	I	62	Total 917	C 280	H 459	N 79	O 93	S 6	0	62	0
3	L	62	Total 915	C 280	H 457	N 79	O 93	S 6	0	62	0

- Molecule 4 is PHYCOERYTHROBILIN (three-letter code: PEB) (formula: C₃₃H₄₀N₄O₆).



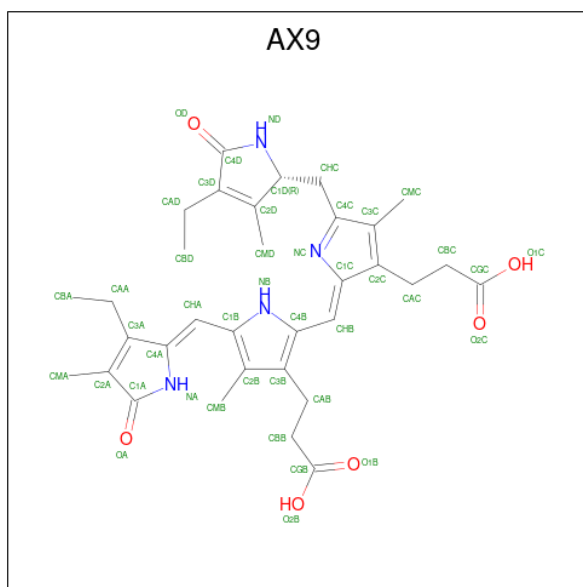
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
4	A	1	Total 80	C 33	H 37	N 4	O 6	0	1
4	B	1	Total 80	C 33	H 37	N 4	O 6	0	0
4	B	1	Total 80	C 33	H 37	N 4	O 6	0	0
4	C	1	Total 80	C 33	H 37	N 4	O 6	0	1
4	D	1	Total 80	C 33	H 37	N 4	O 6	0	0
4	D	1	Total 80	C 33	H 37	N 4	O 6	0	0
4	E	1	Total 80	C 33	H 37	N 4	O 6	0	1
4	F	1	Total 80	C 33	H 37	N 4	O 6	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
4	F	1	Total	C	H	N	O	0	0
			80	33	37	4	6		
4	G	1	Total	C	H	N	O	0	1
			80	33	37	4	6		
4	H	1	Total	C	H	N	O	0	0
			80	33	37	4	6		
4	H	1	Total	C	H	N	O	0	0
			80	33	37	4	6		
4	I	1	Total	C	H	N	O	0	1
			80	33	37	4	6		
4	J	1	Total	C	H	N	O	0	1
			80	33	37	4	6		
4	K	1	Total	C	H	N	O	0	1
			80	33	37	4	6		
4	L	1	Total	C	H	N	O	0	1
			80	33	37	4	6		

- Molecule 5 is DiCys-(15,16)-Dihydrobiliverdin (three-letter code: AX9) (formula: $C_{33}H_{40}N_4O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
5	B	1	Total	C	H	N	O	0	0
			79	33	36	4	6		
5	D	1	Total	C	H	N	O	0	0
			79	33	36	4	6		
5	F	1	Total	C	H	N	O	0	0
			79	33	36	4	6		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
5	H	1	79	33	36	4	6	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
6	C	1	13	3	7	3	0	1
6	E	1	13	3	7	3	0	1
6	G	1	14	3	8	3	0	1
6	J	1	13	3	7	3	0	1
6	K	1	13	3	7	3	0	1
6	L	1	14	3	8	3	0	1

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	23	Total 23 O 23	0	1
7	B	54	Total 54 O 54	0	5

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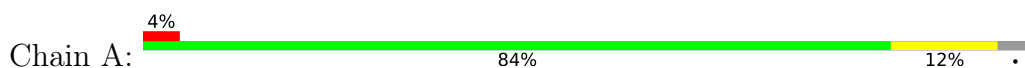
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	26	Total 26	O 26	0	1
7	D	50	Total 51	O 51	0	6
7	E	26	Total 26	O 26	0	0
7	F	46	Total 46	O 46	0	4
7	G	30	Total 30	O 30	0	2
7	H	73	Total 73	O 73	0	3
7	I	4	Total 4	O 4	0	1
7	J	4	Total 4	O 4	0	2
7	K	2	Total 2	O 2	0	0
7	L	1	Total 1	O 1	0	1

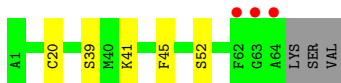
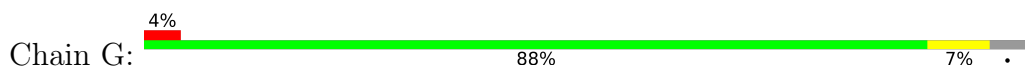
3 Residue-property plots

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.

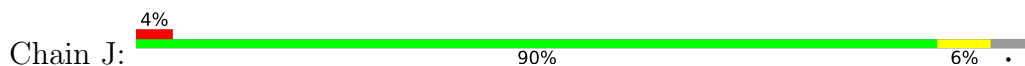
- Molecule 1: Phycoerythrin alpha-1 subunit



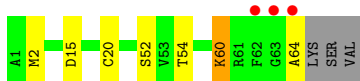
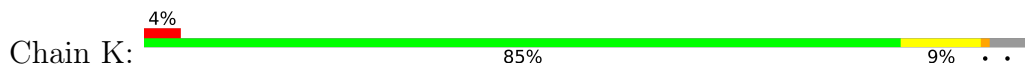
- Molecule 1: Phycoerythrin alpha-1 subunit



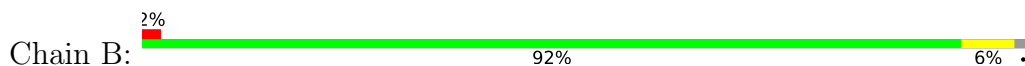
- Molecule 1: Phycoerythrin alpha-1 subunit



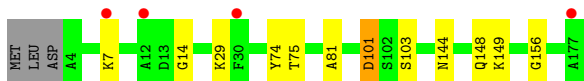
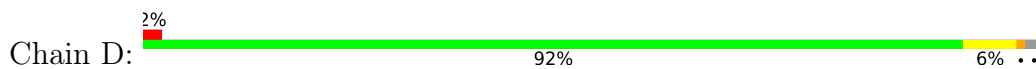
- Molecule 1: Phycoerythrin alpha-1 subunit



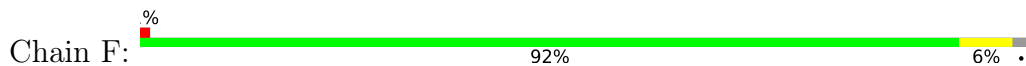
- Molecule 2: Phycoerythrin550 beta subunit



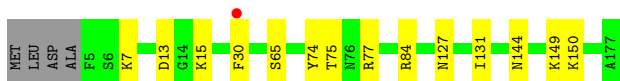
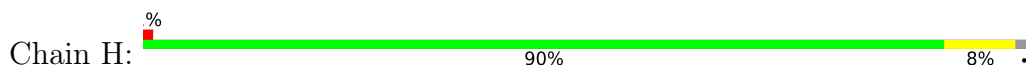
- Molecule 2: Phycoerythrin550 beta subunit



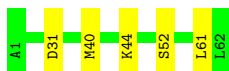
- Molecule 2: Phycoerythrin550 beta subunit



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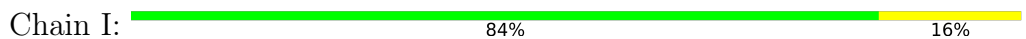
- Molecule 3: Phycoerythrin alpha-2 subunit



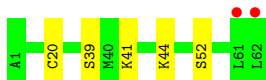
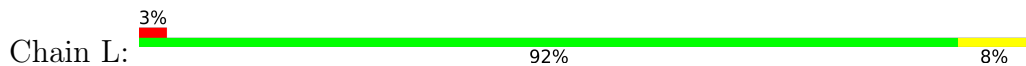
- Molecule 3: Phycoerythrin alpha-2 subunit



- Molecule 3: Phycoerythrin alpha-2 subunit



- Molecule 3: Phycoerythrin alpha-2 subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.86Å 75.60Å 99.36Å 90.00° 110.30° 90.00°	Depositor
Resolution (Å)	61.66 – 1.67 61.66 – 1.67	Depositor EDS
% Data completeness (in resolution range)	99.7 (61.66-1.67) 99.7 (61.66-1.67)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.12 (at 1.67Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.186 , 0.231 0.185 , 0.230	Depositor DCC
R_{free} test set	1998 reflections (1.92%)	wwPDB-VP
Wilson B-factor (Å ²)	28.0	Xtrriage
Anisotropy	0.482	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 44.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.011 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	19890	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.91% 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: LYZ, AX9, GOL, 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	0.51	0/459	0.73	0/609
1	G	0.66	0/459	0.75	0/609
1	J	0.55	0/459	0.71	0/609
1	K	0.61	0/459	0.71	0/609
2	B	0.58	0/1328	0.72	0/1791
2	D	0.56	0/1336	0.69	0/1801
2	F	0.57	0/1334	0.70	0/1799
2	H	0.56	0/1330	0.70	0/1794
3	C	0.55	0/450	0.71	0/597
3	E	0.61	0/450	0.70	0/597
3	I	0.50	0/450	0.68	0/597
3	L	0.66	0/450	0.73	0/597
All	All	0.57	0/8964	0.71	0/12009

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	465	459	451	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	465	458	448	4	0
1	J	465	462	452	4	0
1	K	465	460	450	8	0
2	B	1307	1309	1294	9	2
2	D	1315	1321	1307	11	0
2	F	1313	1319	1304	9	0
2	H	1309	1314	1300	12	0
3	C	458	460	450	3	0
3	E	458	460	451	6	0
3	I	458	459	448	8	2
3	L	458	457	447	8	0
4	A	43	37	37	2	0
4	B	86	74	74	5	0
4	C	43	37	37	1	0
4	D	86	74	74	7	0
4	E	43	37	37	2	0
4	F	86	74	74	9	0
4	G	43	37	37	2	0
4	H	86	74	74	4	0
4	I	43	37	37	2	0
4	J	43	37	37	2	0
4	K	43	37	37	7	0
4	L	43	37	37	1	0
5	B	43	36	0	0	0
5	D	43	36	0	0	0
5	F	43	36	0	0	0
5	H	43	36	0	0	0
6	C	6	7	5	0	0
6	E	6	7	5	2	0
6	G	6	8	5	0	0
6	J	6	7	5	0	0
6	K	6	7	5	2	0
6	L	6	8	5	0	0
7	A	23	0	0	0	0
7	B	54	0	0	0	0
7	C	26	0	0	1	0
7	D	51	0	0	1	0
7	E	26	0	0	0	0
7	F	46	0	0	0	0
7	G	30	0	0	0	0
7	H	73	0	0	0	0
7	I	4	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	J	4	0	0	0	0
7	K	2	0	0	0	0
7	L	1	0	0	0	0
All	All	10172	9718	9424	90	2

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.

All (90) 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)
4:K:101[B]:PEB:O1B	3:L:44[B]:LYS:HD2	1.55	1.06
3:I:44[B]:LYS:HD3	4:J:101[B]:PEB:O2B	1.65	0.96
4:K:101[B]:PEB:CGB	3:L:44[B]:LYS:HD2	2.08	0.84
4:F:202:PEB:HNA	4:F:202:PEB:HMB2	1.51	0.75
3:I:56[B]:ASN:O	3:I:59[B]:THR:HG22	1.89	0.73
2:H:74:TYR:CD1	2:H:75:THR:HG23	2.24	0.72
4:B:202:PEB:HNA	4:B:202:PEB:HMB2	1.54	0.71
4:F:202:PEB:HHC2	1:K:2[B]:MET:HE2	1.72	0.70
3:E:2[A]:MET:HE2	4:F:202:PEB:HHC2	1.72	0.70
2:F:67[A]:ILE:HG22	2:F:73:VAL:HG23	1.74	0.68
2:F:77:ARG:HG3	3:L:20[B]:CYS:SG	2.37	0.65
2:F:77:ARG:HG3	1:G:20[A]:CYS:SG	2.37	0.65
4:H:202:PEB:HMB2	4:H:202:PEB:HNA	1.62	0.64
2:F:67[A]:ILE:CG2	2:F:73:VAL:HG23	2.28	0.63
2:D:81:ALA:HA	1:J:45[B]:PHE:HE1	1.64	0.62
4:D:202:PEB:HMB2	4:D:202:PEB:HNA	1.63	0.62
2:H:144[A]:ASN:ND2	4:H:203:PEB:HMA2	2.17	0.59
4:D:203:PEB:HBA3	4:D:203:PEB:HHA1	1.84	0.58
2:D:148[B]:GLN:O	3:I:59[B]:THR:HG21	2.06	0.56
4:F:203:PEB:HBC1	4:F:203:PEB:HHB1	1.87	0.56
2:D:144[A]:ASN:ND2	4:D:203:PEB:HMA2	2.21	0.55
2:D:81:ALA:HA	1:J:45[B]:PHE:CE1	2.44	0.52
2:D:101:ASP:OD1	2:D:103:SER:OG	2.16	0.52
4:A:101[A]:PEB:HMB2	4:A:101[A]:PEB:NA	2.25	0.51
4:I:101[B]:PEB:HMB2	4:I:101[B]:PEB:NA	2.25	0.51
3:E:15[A]:ASP:O	6:E:102[A]:GOL:H32	2.11	0.51
1:K:15[B]:ASP:O	6:K:102[B]:GOL:H32	2.11	0.51
4:F:202:PEB:HMB2	4:F:202:PEB:NA	2.22	0.50
2:B:149:LYS:HE2	3:C:52[A]:SER:OG	2.13	0.49
2:B:149:LYS:HE2	1:J:52[B]:SER:OG	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:101[B]:PEB:O2B	3:L:44[B]:LYS:HD2	2.12	0.48
4:F:203:PEB:HMB2	4:F:203:PEB:NA	2.29	0.48
1:G:45[A]:PHE:CE1	2:H:84:ARG:HD3	2.48	0.48
2:B:9:ILE:HD11	3:I:9[B]:PRO:HB3	1.96	0.48
3:C:61[A]:LEU:N	7:C:205:HOH:O	2.47	0.47
4:F:203:PEB:HMB2	4:F:203:PEB:HNA	1.78	0.47
1:A:9[A]:PRO:HB3	2:B:9:ILE:HD11	1.96	0.47
4:D:203:PEB:HMB1	4:D:203:PEB:HBC1	1.97	0.47
2:B:121:GLY:HA3	4:F:203:PEB:HAC2	1.96	0.47
3:I:61[B]:LEU:N	7:I:201:HOH:O	2.48	0.46
2:D:156:GLY:HA3	4:D:203:PEB:CMB	2.45	0.46
2:H:13:ASP:OD2	2:H:15:LYS:HD3	2.15	0.46
2:B:74:TYR:O	2:B:75:THR:OG1	2.20	0.46
2:H:77:ARG:HH11	2:H:77:ARG:HG3	1.80	0.46
2:D:74:TYR:O	2:D:75:THR:OG1	2.25	0.45
4:E:101[A]:PEB:NA	4:E:101[A]:PEB:HMB2	2.31	0.45
3:I:59[B]:THR:HG23	3:I:59[B]:THR:O	2.16	0.45
4:K:101[B]:PEB:NA	4:K:101[B]:PEB:HMB2	2.31	0.45
3:C:40[A]:MET:HB2	2:D:14:GLY:HA3	1.98	0.45
2:D:14:GLY:HA3	1:J:40[B]:MET:HB2	1.98	0.45
2:H:77:ARG:HD3	1:K:20[B]:CYS:SG	2.57	0.45
2:F:156:GLY:HA3	4:F:203:PEB:CMB	2.47	0.45
2:H:144[B]:ASN:OD1	2:H:150:LYS:HD2	2.17	0.45
1:G:39[A]:SER:OG	1:G:41[A]:LYS:HE3	2.17	0.44
3:L:39[B]:SER:OG	3:L:41[B]:LYS:HE3	2.17	0.44
3:E:20[A]:CYS:SG	2:H:77:ARG:HD3	2.57	0.44
4:A:101[A]:PEB:HMB2	4:A:101[A]:PEB:HNA	1.83	0.44
4:I:101[B]:PEB:HMB2	4:I:101[B]:PEB:HNA	1.83	0.44
3:E:20[A]:CYS:HB3	4:E:101[A]:PEB:H3A1	1.90	0.44
1:K:20[B]:CYS:HB3	4:K:101[B]:PEB:H3A1	1.90	0.44
4:K:101[B]:PEB:O1B	3:L:44[B]:LYS:CD	2.46	0.44
4:G:101[A]:PEB:HMB2	4:G:101[A]:PEB:NA	2.33	0.43
2:H:144[A]:ASN:ND2	4:H:203:PEB:OA	2.52	0.43
4:L:101[B]:PEB:NA	4:L:101[B]:PEB:HMB2	2.33	0.43
1:A:34[A]:PHE:CZ	4:B:203:PEB:HMC1	2.53	0.43
4:B:203:PEB:HMC1	3:I:34[B]:PHE:CZ	2.53	0.43
1:K:60[B]:LYS:HD3	1:K:64[B]:ALA:O	2.19	0.42
4:H:203:PEB:NA	4:H:203:PEB:HMB2	2.33	0.42
2:F:62:GLU:CD	2:F:129:ARG:HE	2.23	0.42
4:D:203:PEB:HMB2	4:D:203:PEB:NA	2.34	0.42
2:D:144[A]:ASN:CG	4:D:203:PEB:HMA2	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:44[A]:LYS:HD3	4:G:101[A]:PEB:O2B	2.20	0.42
2:H:127:ASN:O	2:H:131[B]:ILE:HG12	2.20	0.42
2:D:149:LYS:HE2	7:D:340:HOH:O	2.19	0.42
2:F:67[B]:ILE:HD11	1:K:54[B]:THR:HG23	2.02	0.41
1:A:61[A]:ARG:N	7:I:201:HOH:O	2.52	0.41
2:H:30:PHE:CD1	2:H:30:PHE:N	2.86	0.41
4:K:101[B]:PEB:O1B	3:L:44[B]:LYS:CB	2.68	0.41
3:E:15[A]:ASP:HB3	6:E:102[A]:GOL:H32	2.02	0.41
2:F:149:LYS:HE3	3:L:52[B]:SER:OG	2.19	0.41
1:K:15[B]:ASP:HB3	6:K:102[B]:GOL:H32	2.02	0.41
2:F:149:LYS:HE3	1:G:52[A]:SER:OG	2.19	0.41
2:B:63:ASN:OD1	2:B:65:SER:OG	2.31	0.41
2:B:156:GLY:HA3	4:B:203:PEB:CMB	2.51	0.41
2:H:149:LYS:HE2	1:K:52[B]:SER:OG	2.21	0.40
2:B:154:PRO:O	4:B:203:PEB:NA	2.50	0.40
1:A:3[A]:LYS:HE2	1:A:5[A]:ASP:OD2	2.21	0.40
4:C:101[A]:PEB:HMB2	4:C:101[A]:PEB:NA	2.37	0.40
3:I:3[B]:LYS:HE2	3:I:5[B]:ASP:OD2	2.21	0.40
4:J:101[B]:PEB:HMB2	4:J:101[B]:PEB:NA	2.37	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:12:ALA:O	3:I:58[B]:ASN:ND2[2_546]	1.90	0.30
2:B:12:ALA:O	3:I:58[B]:ASN:HD22[2_546]	1.46	0.14

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	61/67 (91%)	61 (100%)	0	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	61/67 (91%)	61 (100%)	0	0	100	100
1	J	61/67 (91%)	61 (100%)	0	0	100	100
1	K	61/67 (91%)	61 (100%)	0	0	100	100
2	B	180/177 (102%)	174 (97%)	6 (3%)	0	100	100
2	D	181/177 (102%)	179 (99%)	2 (1%)	0	100	100
2	F	181/177 (102%)	179 (99%)	2 (1%)	0	100	100
2	H	180/177 (102%)	177 (98%)	3 (2%)	0	100	100
3	C	59/62 (95%)	59 (100%)	0	0	100	100
3	E	59/62 (95%)	59 (100%)	0	0	100	100
3	I	59/62 (95%)	59 (100%)	0	0	100	100
3	L	59/62 (95%)	59 (100%)	0	0	100	100
All	All	1202/1224 (98%)	1189 (99%)	13 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	45/48 (94%)	43 (96%)	2 (4%)	28	9
1	G	45/48 (94%)	45 (100%)	0	100	100
1	J	45/48 (94%)	44 (98%)	1 (2%)	52	32
1	K	45/48 (94%)	44 (98%)	1 (2%)	52	32
2	B	146/140 (104%)	145 (99%)	1 (1%)	84	76
2	D	146/140 (104%)	143 (98%)	3 (2%)	53	33
2	F	147/140 (105%)	144 (98%)	3 (2%)	55	36
2	H	146/140 (104%)	144 (99%)	2 (1%)	67	51
3	C	48/48 (100%)	46 (96%)	2 (4%)	30	10
3	E	48/48 (100%)	48 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	I	48/48 (100%)	48 (100%)	0	100	100
3	L	48/48 (100%)	48 (100%)	0	100	100
All	All	957/944 (101%)	942 (98%)	15 (2%)	62	46

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60[A]	LYS
1	A	62[A]	PHE
2	B	62	GLU
3	C	31[A]	ASP
3	C	44[A]	LYS
2	D	7	LYS
2	D	29	LYS
2	D	101	ASP
2	F	15	LYS
2	F	76	ASN
2	F	119	SER
2	H	7	LYS
2	H	65	SER
1	J	31[B]	ASP
1	K	60[B]	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26[A]	GLN
3	C	26[A]	GLN
3	E	26[A]	GLN
1	G	46[A]	ASN
3	I	46[B]	ASN
1	J	46[B]	ASN
1	K	46[B]	ASN
3	L	26[B]	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	LYZ	G	4[A]	1	7,9,10	0.68	0	4,10,12	0.96	0
1	LYZ	K	4[B]	1	7,9,10	0.69	0	4,10,12	1.15	0
1	LYZ	J	4[B]	1	7,9,10	0.91	0	4,10,12	1.00	0
3	LYZ	L	4[B]	3	7,9,10	0.68	0	4,10,12	0.96	0
3	LYZ	C	4[A]	3	7,9,10	0.91	0	4,10,12	1.00	0
3	LYZ	I	4[B]	3	7,9,10	1.00	0	4,10,12	1.38	1 (25%)
1	LYZ	A	4[A]	1	7,9,10	1.00	0	4,10,12	1.38	1 (25%)
3	LYZ	E	4[A]	3	7,9,10	0.69	0	4,10,12	1.15	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
1	LYZ	G	4[A]	1	-	0/8/9/11	-
1	LYZ	K	4[B]	1	-	0/8/9/11	-
1	LYZ	J	4[B]	1	-	0/8/9/11	-
3	LYZ	L	4[B]	3	-	0/8/9/11	-
3	LYZ	C	4[A]	3	-	0/8/9/11	-
3	LYZ	I	4[B]	3	-	1/8/9/11	-
1	LYZ	A	4[A]	1	-	1/8/9/11	-
3	LYZ	E	4[A]	3	-	0/8/9/11	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4[A]	LYZ	CG-CD-CE	-2.21	107.10	112.16
3	I	4[B]	LYZ	CG-CD-CE	-2.21	107.10	112.16

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	4[A]	LYZ	O-C-CA-CB
3	I	4[B]	LYZ	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

26 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
4	PEB	G	101[A]	1	43,46,46	4.62	31 (72%)	45,67,67	2.08	14 (31%)
4	PEB	D	202	2	43,46,46	4.52	32 (74%)	45,67,67	2.52	12 (26%)
4	PEB	L	101[B]	3	43,46,46	4.62	31 (72%)	45,67,67	2.08	14 (31%)
4	PEB	E	101[A]	3	43,46,46	4.35	27 (62%)	45,67,67	2.09	10 (22%)
4	PEB	A	101[A]	1	43,46,46	4.55	31 (72%)	45,67,67	2.21	9 (20%)
5	AX9	D	201	2	41,46,46	1.60	10 (24%)	41,67,67	1.36	6 (14%)
6	GOL	G	102[A]	-	5,5,5	0.80	0	5,5,5	0.87	0
6	GOL	C	102[A]	-	5,5,5	0.92	0	5,5,5	0.19	0
4	PEB	B	202	2	43,46,46	4.37	30 (69%)	45,67,67	2.06	14 (31%)
4	PEB	D	203	2	43,46,46	4.32	31 (72%)	45,67,67	1.79	12 (26%)
6	GOL	E	102[A]	-	5,5,5	1.17	0	5,5,5	0.94	0
4	PEB	H	202	2	43,46,46	4.45	30 (69%)	45,67,67	2.14	11 (24%)
4	PEB	C	101[A]	3	43,46,46	4.34	29 (67%)	45,67,67	2.34	13 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	AX9	F	201	2	41,46,46	1.77	12 (29%)	41,67,67	1.47	6 (14%)
5	AX9	H	201	2	41,46,46	1.72	8 (19%)	41,67,67	1.15	5 (12%)
6	GOL	J	102[B]	-	5,5,5	0.92	0	5,5,5	0.19	0
4	PEB	J	101[B]	1	43,46,46	4.34	29 (67%)	45,67,67	2.34	13 (28%)
4	PEB	F	202	2	43,46,46	4.68	33 (76%)	45,67,67	2.17	14 (31%)
4	PEB	F	203	2	43,46,46	4.22	28 (65%)	45,67,67	1.84	13 (28%)
4	PEB	I	101[B]	3	43,46,46	4.55	31 (72%)	45,67,67	2.21	9 (20%)
5	AX9	B	201	2	41,46,46	1.67	9 (21%)	41,67,67	1.41	7 (17%)
6	GOL	K	102[B]	-	5,5,5	1.17	0	5,5,5	0.94	0
6	GOL	L	102[B]	-	5,5,5	0.80	0	5,5,5	0.87	0
4	PEB	B	203	2	43,46,46	4.56	31 (72%)	45,67,67	1.80	9 (20%)
4	PEB	H	203	2	43,46,46	4.42	31 (72%)	45,67,67	1.81	10 (22%)
4	PEB	K	101[B]	1	43,46,46	4.35	27 (62%)	45,67,67	2.09	10 (22%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PEB	G	101[A]	1	-	2/24/74/74	0/4/4/4
4	PEB	D	202	2	-	4/24/74/74	0/4/4/4
4	PEB	L	101[B]	3	-	2/24/74/74	0/4/4/4
4	PEB	E	101[A]	3	-	4/24/74/74	0/4/4/4
4	PEB	A	101[A]	1	-	5/24/74/74	0/4/4/4
5	AX9	D	201	2	-	6/26/74/74	0/4/4/4
6	GOL	G	102[A]	-	-	2/4/4/4	-
6	GOL	C	102[A]	-	-	0/4/4/4	-
4	PEB	B	202	2	-	3/24/74/74	0/4/4/4
4	PEB	D	203	2	-	6/24/74/74	0/4/4/4
6	GOL	E	102[A]	-	-	3/4/4/4	-
4	PEB	H	202	2	-	5/24/74/74	0/4/4/4
4	PEB	C	101[A]	3	-	4/24/74/74	0/4/4/4
5	AX9	F	201	2	-	4/26/74/74	0/4/4/4
5	AX9	H	201	2	-	6/26/74/74	0/4/4/4
6	GOL	J	102[B]	-	-	0/4/4/4	-
4	PEB	J	101[B]	1	-	4/24/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PEB	F	202	2	-	6/24/74/74	0/4/4/4
4	PEB	F	203	2	-	7/24/74/74	0/4/4/4
4	PEB	I	101[B]	3	-	5/24/74/74	0/4/4/4
5	AX9	B	201	2	-	6/26/74/74	0/4/4/4
6	GOL	K	102[B]	-	-	3/4/4/4	-
6	GOL	L	102[B]	-	-	2/4/4/4	-
4	PEB	B	203	2	-	4/24/74/74	0/4/4/4
4	PEB	H	203	2	-	6/24/74/74	0/4/4/4
4	PEB	K	101[B]	1	-	4/24/74/74	0/4/4/4

All (521) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	202	PEB	CHB-C4B	11.93	1.45	1.35
4	G	101[A]	PEB	C2A-C1A	11.60	1.62	1.52
4	L	101[B]	PEB	C2A-C1A	11.60	1.62	1.52
4	G	101[A]	PEB	CHB-C4B	11.49	1.44	1.35
4	L	101[B]	PEB	CHB-C4B	11.49	1.44	1.35
4	D	202	PEB	CHB-C4B	11.21	1.44	1.35
4	H	202	PEB	CHB-C4B	10.71	1.44	1.35
4	B	203	PEB	CHB-C4B	10.42	1.43	1.35
4	H	203	PEB	CHB-C4B	10.34	1.43	1.35
4	F	202	PEB	C1A-NA	10.09	1.50	1.37
4	A	101[A]	PEB	CHB-C4B	10.02	1.43	1.35
4	I	101[B]	PEB	CHB-C4B	10.02	1.43	1.35
4	B	202	PEB	C2A-C1A	9.99	1.61	1.52
4	B	202	PEB	CAC-C2C	9.88	1.66	1.52
4	D	202	PEB	CAC-C2C	9.84	1.66	1.52
4	B	202	PEB	CHB-C4B	9.74	1.43	1.35
4	B	203	PEB	CAC-C2C	9.73	1.66	1.52
4	F	202	PEB	CAC-C2C	9.67	1.66	1.52
4	C	101[A]	PEB	CAC-C2C	9.64	1.66	1.52
4	J	101[B]	PEB	CAC-C2C	9.64	1.66	1.52
4	H	202	PEB	CAC-C2C	9.61	1.66	1.52
4	H	202	PEB	C2A-C1A	9.48	1.60	1.52
4	D	203	PEB	C2A-C1A	9.47	1.60	1.52
4	D	202	PEB	C1A-NA	9.44	1.49	1.37
4	D	203	PEB	CHB-C4B	9.17	1.42	1.35
4	B	203	PEB	C2A-C1A	9.03	1.60	1.52
4	B	203	PEB	CHA-C1B	9.02	1.61	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	203	PEB	C2A-C1A	9.01	1.60	1.52
4	D	203	PEB	CHA-C1B	8.98	1.61	1.40
4	E	101[A]	PEB	C2A-C1A	8.97	1.60	1.52
4	K	101[B]	PEB	C2A-C1A	8.97	1.60	1.52
4	F	202	PEB	C2A-C1A	8.96	1.60	1.52
4	F	203	PEB	C1A-NA	8.87	1.49	1.37
4	B	202	PEB	C1A-NA	8.86	1.49	1.37
4	A	101[A]	PEB	CAC-C2C	8.86	1.65	1.52
4	I	101[B]	PEB	CAC-C2C	8.86	1.65	1.52
4	H	203	PEB	CAC-C2C	8.78	1.64	1.52
4	F	203	PEB	C2A-C1A	8.78	1.59	1.52
4	F	203	PEB	CHB-C4B	8.76	1.42	1.35
4	B	203	PEB	C1A-NA	8.72	1.48	1.37
4	A	101[A]	PEB	C4D-ND	8.71	1.47	1.35
4	I	101[B]	PEB	C4D-ND	8.71	1.47	1.35
4	G	101[A]	PEB	C1A-NA	8.56	1.48	1.37
4	L	101[B]	PEB	C1A-NA	8.56	1.48	1.37
4	E	101[A]	PEB	C1A-NA	8.55	1.48	1.37
4	K	101[B]	PEB	C1A-NA	8.55	1.48	1.37
4	C	101[A]	PEB	CHA-C1B	8.52	1.60	1.40
4	J	101[B]	PEB	CHA-C1B	8.52	1.60	1.40
4	H	203	PEB	CHA-C1B	8.48	1.60	1.40
4	F	203	PEB	CAC-C2C	8.36	1.64	1.52
4	A	101[A]	PEB	C2A-C1A	8.34	1.59	1.52
4	I	101[B]	PEB	C2A-C1A	8.34	1.59	1.52
4	E	101[A]	PEB	CAC-C2C	8.31	1.64	1.52
4	K	101[B]	PEB	CAC-C2C	8.31	1.64	1.52
4	E	101[A]	PEB	CHA-C1B	8.28	1.59	1.40
4	K	101[B]	PEB	CHA-C1B	8.28	1.59	1.40
4	H	203	PEB	C1A-NA	8.27	1.48	1.37
4	A	101[A]	PEB	C1A-NA	8.24	1.48	1.37
4	I	101[B]	PEB	C1A-NA	8.24	1.48	1.37
4	D	203	PEB	C1A-NA	8.21	1.48	1.37
4	H	202	PEB	C4D-ND	8.18	1.46	1.35
4	A	101[A]	PEB	CHA-C1B	8.16	1.59	1.40
4	I	101[B]	PEB	CHA-C1B	8.16	1.59	1.40
4	E	101[A]	PEB	C3A-C4A	8.14	1.62	1.50
4	K	101[B]	PEB	C3A-C4A	8.14	1.62	1.50
4	C	101[A]	PEB	CHB-C4B	8.14	1.41	1.35
4	J	101[B]	PEB	CHB-C4B	8.14	1.41	1.35
4	C	101[A]	PEB	C1A-NA	8.06	1.48	1.37
4	J	101[B]	PEB	C1A-NA	8.06	1.48	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	101[A]	PEB	C3A-C4A	8.02	1.62	1.50
4	J	101[B]	PEB	C3A-C4A	8.02	1.62	1.50
4	D	202	PEB	CHA-C1B	8.00	1.59	1.40
4	D	202	PEB	C4D-ND	7.87	1.45	1.35
4	G	101[A]	PEB	C4D-ND	7.85	1.45	1.35
4	L	101[B]	PEB	C4D-ND	7.85	1.45	1.35
4	D	203	PEB	CAC-C2C	7.81	1.63	1.52
4	F	202	PEB	CHA-C1B	7.76	1.58	1.40
4	G	101[A]	PEB	CHA-C1B	7.71	1.58	1.40
4	L	101[B]	PEB	CHA-C1B	7.71	1.58	1.40
4	C	101[A]	PEB	C4D-ND	7.70	1.45	1.35
4	J	101[B]	PEB	C4D-ND	7.70	1.45	1.35
4	F	203	PEB	CHA-C1B	7.70	1.58	1.40
4	G	101[A]	PEB	C3A-C4A	7.56	1.61	1.50
4	L	101[B]	PEB	C3A-C4A	7.56	1.61	1.50
4	G	101[A]	PEB	CAC-C2C	7.49	1.63	1.52
4	L	101[B]	PEB	CAC-C2C	7.49	1.63	1.52
4	C	101[A]	PEB	C2A-C1A	7.47	1.58	1.52
4	J	101[B]	PEB	C2A-C1A	7.47	1.58	1.52
4	E	101[A]	PEB	CHB-C4B	7.30	1.41	1.35
4	K	101[B]	PEB	CHB-C4B	7.30	1.41	1.35
4	E	101[A]	PEB	C4D-ND	7.28	1.45	1.35
4	K	101[B]	PEB	C4D-ND	7.28	1.45	1.35
4	D	202	PEB	C2A-C1A	7.10	1.58	1.52
4	H	202	PEB	CHA-C1B	7.01	1.56	1.40
4	B	202	PEB	C3A-C4A	6.94	1.61	1.50
4	B	202	PEB	CHA-C1B	6.91	1.56	1.40
4	D	202	PEB	CMD-C2D	6.88	1.61	1.50
4	A	101[A]	PEB	CMD-C2D	6.85	1.61	1.50
4	I	101[B]	PEB	CMD-C2D	6.85	1.61	1.50
4	G	101[A]	PEB	CMD-C2D	6.83	1.61	1.50
4	L	101[B]	PEB	CMD-C2D	6.83	1.61	1.50
4	F	203	PEB	C4D-ND	6.83	1.44	1.35
4	D	203	PEB	CMD-C2D	6.76	1.61	1.50
4	F	202	PEB	C3A-C4A	6.72	1.60	1.50
4	H	202	PEB	C1A-NA	6.61	1.46	1.37
4	D	203	PEB	C4D-ND	6.40	1.43	1.35
4	H	203	PEB	C4D-ND	6.36	1.43	1.35
4	C	101[A]	PEB	CMD-C2D	6.33	1.60	1.50
4	J	101[B]	PEB	CMD-C2D	6.33	1.60	1.50
4	H	203	PEB	CMD-C2D	6.32	1.60	1.50
4	B	203	PEB	CMD-C2D	6.28	1.60	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	203	PEB	C3A-C4A	6.21	1.59	1.50
4	B	202	PEB	C4D-ND	6.19	1.43	1.35
4	E	101[A]	PEB	CMD-C2D	6.19	1.60	1.50
4	K	101[B]	PEB	CMD-C2D	6.19	1.60	1.50
4	A	101[A]	PEB	C3A-C4A	6.16	1.59	1.50
4	I	101[B]	PEB	C3A-C4A	6.16	1.59	1.50
4	H	202	PEB	CMD-C2D	6.16	1.60	1.50
4	F	203	PEB	C3A-C4A	6.09	1.59	1.50
4	D	203	PEB	C3A-C4A	5.86	1.59	1.50
4	A	101[A]	PEB	CBC-CGC	5.83	1.64	1.50
4	I	101[B]	PEB	CBC-CGC	5.83	1.64	1.50
4	H	203	PEB	C3A-C4A	5.83	1.59	1.50
4	F	202	PEB	C4A-NA	5.81	1.49	1.37
4	F	202	PEB	CMD-C2D	5.78	1.59	1.50
4	A	101[A]	PEB	C4A-NA	5.77	1.49	1.37
4	I	101[B]	PEB	C4A-NA	5.77	1.49	1.37
4	F	202	PEB	CBC-CGC	5.62	1.63	1.50
4	B	202	PEB	CMD-C2D	5.57	1.59	1.50
4	F	203	PEB	CMD-C2D	5.54	1.59	1.50
4	D	202	PEB	C3A-C4A	5.54	1.58	1.50
4	B	203	PEB	C4D-ND	5.53	1.42	1.35
4	D	202	PEB	CMB-C2B	5.34	1.62	1.50
4	B	203	PEB	CMB-C2B	5.34	1.62	1.50
4	H	202	PEB	CBC-CGC	5.31	1.62	1.50
4	F	202	PEB	CMB-C2B	5.30	1.62	1.50
4	E	101[A]	PEB	C4A-NA	5.29	1.48	1.37
4	K	101[B]	PEB	C4A-NA	5.29	1.48	1.37
4	H	203	PEB	CMB-C2B	5.29	1.62	1.50
4	D	202	PEB	C1C-CHB	5.27	1.61	1.41
4	H	203	PEB	C4A-NA	5.25	1.48	1.37
4	G	101[A]	PEB	C4A-NA	5.23	1.48	1.37
4	L	101[B]	PEB	C4A-NA	5.23	1.48	1.37
4	B	203	PEB	C2D-C3D	5.22	1.41	1.34
4	E	101[A]	PEB	CBB-CGB	5.21	1.62	1.50
4	K	101[B]	PEB	CBB-CGB	5.21	1.62	1.50
4	A	101[A]	PEB	CBB-CGB	5.15	1.62	1.50
4	I	101[B]	PEB	CBB-CGB	5.15	1.62	1.50
4	A	101[A]	PEB	CMB-C2B	5.15	1.61	1.50
4	I	101[B]	PEB	CMB-C2B	5.15	1.61	1.50
4	H	202	PEB	C3A-C4A	5.15	1.58	1.50
4	C	101[A]	PEB	CBB-CGB	5.14	1.62	1.50
4	J	101[B]	PEB	CBB-CGB	5.14	1.62	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	202	PEB	C1C-CHB	5.11	1.61	1.41
4	F	203	PEB	CBC-CGC	5.11	1.62	1.50
4	H	202	PEB	C1C-CHB	5.09	1.60	1.41
4	D	202	PEB	CBC-CGC	5.08	1.62	1.50
4	D	203	PEB	CBC-CGC	5.08	1.62	1.50
4	B	203	PEB	CBC-CGC	5.06	1.62	1.50
4	G	101[A]	PEB	CMB-C2B	5.04	1.61	1.50
4	L	101[B]	PEB	CMB-C2B	5.04	1.61	1.50
4	C	101[A]	PEB	C2D-C3D	5.03	1.41	1.34
4	J	101[B]	PEB	C2D-C3D	5.03	1.41	1.34
4	D	202	PEB	C4A-NA	5.00	1.47	1.37
4	A	101[A]	PEB	C1C-CHB	4.99	1.60	1.41
4	I	101[B]	PEB	C1C-CHB	4.99	1.60	1.41
4	B	203	PEB	C1C-CHB	4.98	1.60	1.41
5	H	201	AX9	C1C-C2C	-4.98	1.37	1.45
4	H	202	PEB	CMB-C2B	4.97	1.61	1.50
4	B	202	PEB	CBC-CGC	4.96	1.62	1.50
4	E	101[A]	PEB	C1C-CHB	4.95	1.60	1.41
4	K	101[B]	PEB	C1C-CHB	4.95	1.60	1.41
4	B	202	PEB	C4A-NA	4.88	1.47	1.37
4	D	203	PEB	CBB-CGB	4.88	1.61	1.50
4	F	202	PEB	CMA-C2A	4.87	1.63	1.53
4	B	202	PEB	C2D-C3D	4.85	1.40	1.34
4	C	101[A]	PEB	C1C-CHB	4.83	1.59	1.41
4	J	101[B]	PEB	C1C-CHB	4.83	1.59	1.41
4	F	202	PEB	C2D-C3D	4.78	1.40	1.34
4	G	101[A]	PEB	C1C-CHB	4.78	1.59	1.41
4	L	101[B]	PEB	C1C-CHB	4.78	1.59	1.41
4	G	101[A]	PEB	CBC-CGC	4.76	1.61	1.50
4	L	101[B]	PEB	CBC-CGC	4.76	1.61	1.50
4	F	202	PEB	C4D-ND	4.76	1.41	1.35
4	H	202	PEB	C4B-NB	4.75	1.48	1.38
4	E	101[A]	PEB	CMB-C2B	4.73	1.60	1.50
4	K	101[B]	PEB	CMB-C2B	4.73	1.60	1.50
4	F	203	PEB	CMB-C2B	4.73	1.60	1.50
4	B	203	PEB	C4A-NA	4.64	1.47	1.37
4	G	101[A]	PEB	CBB-CGB	4.60	1.61	1.50
4	L	101[B]	PEB	CBB-CGB	4.60	1.61	1.50
4	C	101[A]	PEB	CBC-CGC	4.59	1.61	1.50
4	J	101[B]	PEB	CBC-CGC	4.59	1.61	1.50
4	E	101[A]	PEB	CBC-CGC	4.59	1.61	1.50
4	K	101[B]	PEB	CBC-CGC	4.59	1.61	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	203	PEB	CMB-C2B	4.58	1.60	1.50
4	F	202	PEB	CBB-CGB	4.56	1.61	1.50
4	E	101[A]	PEB	CMA-C2A	4.56	1.63	1.53
4	K	101[B]	PEB	CMA-C2A	4.56	1.63	1.53
4	H	203	PEB	CBC-CGC	4.55	1.61	1.50
4	H	202	PEB	CAD-C3D	4.48	1.59	1.47
4	F	203	PEB	CMA-C2A	4.48	1.62	1.53
4	B	202	PEB	CBB-CGB	4.43	1.60	1.50
4	A	101[A]	PEB	C2D-C3D	4.41	1.40	1.34
4	I	101[B]	PEB	C2D-C3D	4.41	1.40	1.34
4	H	203	PEB	CAB-C3B	4.41	1.62	1.51
5	B	201	AX9	C1C-C2C	-4.41	1.38	1.45
4	H	203	PEB	C1C-CHB	4.39	1.58	1.41
4	F	203	PEB	C1C-CHB	4.39	1.58	1.41
5	F	201	AX9	C1C-C2C	-4.38	1.38	1.45
4	H	202	PEB	C4A-NA	4.36	1.46	1.37
4	B	203	PEB	C1B-NB	4.36	1.46	1.36
4	B	203	PEB	CBB-CGB	4.36	1.60	1.50
4	C	101[A]	PEB	C4A-NA	4.36	1.46	1.37
4	J	101[B]	PEB	C4A-NA	4.36	1.46	1.37
4	H	202	PEB	CHC-C4C	4.33	1.60	1.50
4	D	203	PEB	C1C-CHB	4.31	1.57	1.41
4	H	202	PEB	CBB-CGB	4.30	1.60	1.50
4	F	202	PEB	CHC-C4C	4.27	1.60	1.50
4	B	202	PEB	CMA-C2A	4.25	1.62	1.53
4	G	101[A]	PEB	C2D-C3D	4.25	1.40	1.34
4	L	101[B]	PEB	C2D-C3D	4.25	1.40	1.34
4	D	202	PEB	CBB-CGB	4.23	1.60	1.50
4	H	203	PEB	CBB-CGB	4.23	1.60	1.50
4	F	203	PEB	C4A-NA	4.23	1.46	1.37
4	H	203	PEB	CHC-C4C	4.22	1.60	1.50
4	D	203	PEB	C4A-NA	4.22	1.46	1.37
4	H	203	PEB	CMA-C2A	4.21	1.62	1.53
4	B	202	PEB	C1C-CHB	4.18	1.57	1.41
4	C	101[A]	PEB	CMB-C2B	4.17	1.59	1.50
4	J	101[B]	PEB	CMB-C2B	4.17	1.59	1.50
4	H	203	PEB	C1B-NB	4.16	1.46	1.36
4	E	101[A]	PEB	C2D-C3D	4.16	1.39	1.34
4	K	101[B]	PEB	C2D-C3D	4.16	1.39	1.34
5	D	201	AX9	C1C-C2C	-4.15	1.39	1.45
4	E	101[A]	PEB	CAB-C3B	4.15	1.62	1.51
4	K	101[B]	PEB	CAB-C3B	4.15	1.62	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	101[A]	PEB	C1B-NB	4.14	1.46	1.36
4	I	101[B]	PEB	C1B-NB	4.14	1.46	1.36
4	F	203	PEB	CBB-CGB	4.12	1.60	1.50
4	A	101[A]	PEB	CMA-C2A	4.12	1.62	1.53
4	I	101[B]	PEB	CMA-C2A	4.12	1.62	1.53
4	B	203	PEB	C3C-C4C	4.08	1.48	1.42
4	H	202	PEB	CMA-C2A	4.08	1.62	1.53
4	H	203	PEB	C2D-C3D	4.07	1.39	1.34
4	D	203	PEB	CAB-C3B	4.07	1.61	1.51
5	H	201	AX9	C4A-C3A	-4.04	1.37	1.45
4	B	203	PEB	CHC-C4C	4.03	1.59	1.50
4	H	202	PEB	C2D-C3D	4.00	1.39	1.34
4	D	203	PEB	O1B-CGB	4.00	1.35	1.22
4	E	101[A]	PEB	C1B-NB	3.99	1.45	1.36
4	K	101[B]	PEB	C1B-NB	3.99	1.45	1.36
4	C	101[A]	PEB	O1B-CGB	3.97	1.35	1.22
4	J	101[B]	PEB	O1B-CGB	3.97	1.35	1.22
4	E	101[A]	PEB	CAD-C3D	3.95	1.58	1.47
4	K	101[B]	PEB	CAD-C3D	3.95	1.58	1.47
4	F	203	PEB	C1B-NB	3.95	1.45	1.36
4	F	203	PEB	C3C-C4C	3.94	1.48	1.42
4	B	203	PEB	CAB-C3B	3.93	1.61	1.51
4	A	101[A]	PEB	CAB-C3B	3.89	1.61	1.51
4	I	101[B]	PEB	CAB-C3B	3.89	1.61	1.51
4	D	203	PEB	CHC-C4C	3.87	1.59	1.50
4	D	203	PEB	CMA-C2A	3.87	1.61	1.53
4	G	101[A]	PEB	O1B-CGB	3.87	1.35	1.22
4	L	101[B]	PEB	O1B-CGB	3.87	1.35	1.22
4	F	203	PEB	O1B-CGB	3.82	1.34	1.22
4	A	101[A]	PEB	O1B-CGB	3.80	1.34	1.22
4	I	101[B]	PEB	O1B-CGB	3.80	1.34	1.22
4	F	203	PEB	CAB-C3B	3.80	1.61	1.51
4	F	202	PEB	C1B-NB	3.78	1.45	1.36
4	G	101[A]	PEB	CAB-C3B	3.78	1.61	1.51
4	L	101[B]	PEB	CAB-C3B	3.78	1.61	1.51
4	G	101[A]	PEB	CMA-C2A	3.78	1.61	1.53
4	L	101[B]	PEB	CMA-C2A	3.78	1.61	1.53
4	E	101[A]	PEB	O1B-CGB	3.75	1.34	1.22
4	K	101[B]	PEB	O1B-CGB	3.75	1.34	1.22
4	B	202	PEB	CAD-C3D	3.75	1.57	1.47
5	H	201	AX9	C4D-ND	3.75	1.40	1.35
4	H	202	PEB	O1C-CGC	3.73	1.34	1.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	202	PEB	O1B-CGB	3.73	1.34	1.22
4	A	101[A]	PEB	CAD-C3D	3.68	1.57	1.47
4	I	101[B]	PEB	CAD-C3D	3.68	1.57	1.47
4	D	202	PEB	CAB-C3B	3.66	1.60	1.51
4	F	203	PEB	C2D-C3D	3.66	1.39	1.34
4	C	101[A]	PEB	O1C-CGC	3.65	1.34	1.22
4	J	101[B]	PEB	O1C-CGC	3.65	1.34	1.22
4	B	202	PEB	CMB-C2B	3.65	1.58	1.50
4	B	203	PEB	O1B-CGB	3.65	1.34	1.22
4	H	202	PEB	C3C-C4C	3.63	1.47	1.42
4	B	202	PEB	O1C-CGC	3.60	1.34	1.22
4	F	202	PEB	CAB-C3B	3.60	1.60	1.51
4	D	202	PEB	O1C-CGC	3.57	1.34	1.22
5	B	201	AX9	C4D-ND	3.57	1.39	1.35
4	H	203	PEB	O1B-CGB	3.56	1.33	1.22
4	D	202	PEB	C2D-C3D	3.55	1.39	1.34
4	C	101[A]	PEB	CMA-C2A	3.55	1.60	1.53
4	J	101[B]	PEB	CMA-C2A	3.55	1.60	1.53
4	D	203	PEB	O1C-CGC	3.55	1.33	1.22
4	B	203	PEB	O1C-CGC	3.50	1.33	1.22
5	B	201	AX9	C4A-C3A	-3.47	1.38	1.45
4	C	101[A]	PEB	CAD-C3D	3.47	1.56	1.47
4	J	101[B]	PEB	CAD-C3D	3.47	1.56	1.47
4	H	202	PEB	O1B-CGB	3.47	1.33	1.22
4	H	202	PEB	CAB-C3B	3.47	1.60	1.51
4	D	202	PEB	C3C-C4C	3.44	1.47	1.42
4	B	202	PEB	CAB-C3B	3.43	1.60	1.51
4	D	202	PEB	CMA-C2A	3.42	1.60	1.53
4	C	101[A]	PEB	CAB-C3B	3.42	1.60	1.51
4	J	101[B]	PEB	CAB-C3B	3.42	1.60	1.51
4	C	101[A]	PEB	C3C-C4C	3.40	1.47	1.42
4	J	101[B]	PEB	C3C-C4C	3.40	1.47	1.42
4	F	202	PEB	CAD-C3D	3.40	1.56	1.47
4	A	101[A]	PEB	O1C-CGC	3.39	1.33	1.22
4	I	101[B]	PEB	O1C-CGC	3.39	1.33	1.22
4	F	202	PEB	OD-C4D	3.38	1.30	1.23
4	D	203	PEB	C1B-NB	3.36	1.44	1.36
4	E	101[A]	PEB	CHC-C4C	3.34	1.58	1.50
4	K	101[B]	PEB	CHC-C4C	3.34	1.58	1.50
4	G	101[A]	PEB	CMC-C3C	3.34	1.58	1.51
4	L	101[B]	PEB	CMC-C3C	3.34	1.58	1.51
5	F	201	AX9	CHC-C4C	3.33	1.54	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	201	AX9	C4A-C3A	-3.33	1.38	1.45
4	B	203	PEB	C4B-NB	3.33	1.45	1.38
4	A	101[A]	PEB	CAA-C3A	3.33	1.60	1.54
4	I	101[B]	PEB	CAA-C3A	3.33	1.60	1.54
4	H	203	PEB	C3C-C4C	3.32	1.47	1.42
4	F	203	PEB	CMC-C3C	3.30	1.58	1.51
4	E	101[A]	PEB	O1C-CGC	3.30	1.33	1.22
4	K	101[B]	PEB	O1C-CGC	3.30	1.33	1.22
4	D	203	PEB	C4B-NB	3.30	1.45	1.38
5	B	201	AX9	CHC-C1D	-3.28	1.46	1.53
5	F	201	AX9	CHC-C1D	-3.28	1.46	1.53
4	G	101[A]	PEB	CAA-C3A	3.26	1.60	1.54
4	L	101[B]	PEB	CAA-C3A	3.26	1.60	1.54
4	H	203	PEB	CAD-C3D	3.25	1.56	1.47
4	F	202	PEB	O1C-CGC	3.25	1.32	1.22
5	F	201	AX9	C1A-C2A	-3.25	1.38	1.47
5	H	201	AX9	C1A-C2A	-3.24	1.38	1.47
4	G	101[A]	PEB	CAD-C3D	3.23	1.56	1.47
4	L	101[B]	PEB	CAD-C3D	3.23	1.56	1.47
4	C	101[A]	PEB	C3B-C2B	3.22	1.43	1.36
4	J	101[B]	PEB	C3B-C2B	3.22	1.43	1.36
4	D	202	PEB	CAD-C3D	3.21	1.56	1.47
4	D	202	PEB	CAA-C3A	3.21	1.60	1.54
4	F	203	PEB	CHC-C4C	3.20	1.58	1.50
4	D	202	PEB	C1D-C2D	3.19	1.61	1.50
4	H	203	PEB	O1C-CGC	3.18	1.32	1.22
4	B	203	PEB	CMA-C2A	3.17	1.60	1.53
4	B	203	PEB	CAD-C3D	3.17	1.56	1.47
4	B	202	PEB	O1B-CGB	3.14	1.32	1.22
4	A	101[A]	PEB	CHC-C4C	3.13	1.57	1.50
4	I	101[B]	PEB	CHC-C4C	3.13	1.57	1.50
4	B	202	PEB	CAA-C3A	3.13	1.60	1.54
4	D	202	PEB	CMC-C3C	3.13	1.58	1.51
4	D	202	PEB	O1B-CGB	3.12	1.32	1.22
4	E	101[A]	PEB	CAA-C3A	3.12	1.60	1.54
4	K	101[B]	PEB	CAA-C3A	3.12	1.60	1.54
4	D	202	PEB	CHC-C4C	3.11	1.57	1.50
4	F	202	PEB	CAA-C3A	3.10	1.60	1.54
4	F	202	PEB	C3C-C4C	3.07	1.46	1.42
4	D	203	PEB	C2D-C3D	3.04	1.38	1.34
5	B	201	AX9	C1A-C2A	-3.03	1.39	1.47
5	D	201	AX9	C1A-C2A	-3.03	1.39	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	101[A]	PEB	C2C-C3C	3.02	1.46	1.37
4	I	101[B]	PEB	C2C-C3C	3.02	1.46	1.37
4	F	203	PEB	O1C-CGC	3.02	1.32	1.22
4	B	202	PEB	CHC-C4C	2.98	1.57	1.50
4	D	202	PEB	OD-C4D	2.97	1.29	1.23
4	D	203	PEB	CHA-C4A	2.97	1.42	1.36
4	F	203	PEB	CAD-C3D	2.97	1.55	1.47
5	F	201	AX9	C1D-ND	-2.96	1.41	1.45
4	C	101[A]	PEB	CAA-C3A	2.94	1.59	1.54
4	J	101[B]	PEB	CAA-C3A	2.94	1.59	1.54
4	B	202	PEB	C4B-NB	2.94	1.44	1.38
5	F	201	AX9	C1B-CHA	2.94	1.52	1.41
4	F	202	PEB	CMC-C3C	2.93	1.57	1.51
5	D	201	AX9	CHC-C1D	-2.91	1.47	1.53
4	B	203	PEB	CAA-C3A	2.91	1.59	1.54
4	H	202	PEB	CBB-CAB	2.91	1.61	1.52
4	D	203	PEB	CAD-C3D	2.91	1.55	1.47
5	F	201	AX9	C4D-C3D	-2.87	1.42	1.48
4	H	202	PEB	C1B-NB	2.86	1.43	1.36
5	F	201	AX9	C4D-ND	2.82	1.38	1.35
4	B	203	PEB	C1D-C2D	2.82	1.60	1.50
5	D	201	AX9	C1B-CHA	2.82	1.52	1.41
4	H	203	PEB	CHA-C4A	2.82	1.42	1.36
4	G	101[A]	PEB	O1C-CGC	2.81	1.31	1.22
4	L	101[B]	PEB	O1C-CGC	2.81	1.31	1.22
4	D	203	PEB	CAA-C3A	2.81	1.59	1.54
4	A	101[A]	PEB	OD-C4D	2.80	1.28	1.23
4	I	101[B]	PEB	OD-C4D	2.80	1.28	1.23
4	B	202	PEB	OD-C4D	2.79	1.28	1.23
4	B	203	PEB	CBB-CAB	2.78	1.60	1.52
5	B	201	AX9	C4B-CHB	2.77	1.51	1.41
4	F	202	PEB	CBB-CAB	2.77	1.60	1.52
4	B	202	PEB	C3C-C4C	2.77	1.46	1.42
4	B	203	PEB	CMC-C3C	2.76	1.57	1.51
4	B	202	PEB	C2C-C3C	2.75	1.45	1.37
4	E	101[A]	PEB	C3B-C2B	2.73	1.42	1.36
4	K	101[B]	PEB	C3B-C2B	2.73	1.42	1.36
4	D	202	PEB	C2C-C3C	2.72	1.45	1.37
4	D	202	PEB	CHA-C4A	2.70	1.42	1.36
4	G	101[A]	PEB	C1D-C2D	2.70	1.59	1.50
4	L	101[B]	PEB	C1D-C2D	2.70	1.59	1.50
4	H	203	PEB	C4B-NB	2.68	1.44	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	203	PEB	C3C-C4C	2.68	1.46	1.42
5	H	201	AX9	C4D-C3D	-2.68	1.43	1.48
4	F	202	PEB	C3B-C2B	2.68	1.42	1.36
4	D	203	PEB	C3B-C2B	2.68	1.42	1.36
4	G	101[A]	PEB	C1B-NB	2.68	1.42	1.36
4	L	101[B]	PEB	C1B-NB	2.68	1.42	1.36
5	B	201	AX9	C4C-NC	2.68	1.39	1.35
4	B	202	PEB	CMC-C3C	2.67	1.57	1.51
4	C	101[A]	PEB	C1B-NB	2.67	1.42	1.36
4	J	101[B]	PEB	C1B-NB	2.67	1.42	1.36
4	A	101[A]	PEB	CMC-C3C	2.64	1.57	1.51
4	I	101[B]	PEB	CMC-C3C	2.64	1.57	1.51
5	D	201	AX9	C4B-CHB	2.62	1.51	1.41
4	A	101[A]	PEB	C4B-NB	2.62	1.44	1.38
4	I	101[B]	PEB	C4B-NB	2.62	1.44	1.38
5	D	201	AX9	C4D-ND	2.61	1.38	1.35
4	D	202	PEB	C1B-NB	2.61	1.42	1.36
4	B	202	PEB	CBB-CAB	2.60	1.60	1.52
4	H	202	PEB	C1B-C2B	2.60	1.51	1.45
5	B	201	AX9	C4D-C3D	-2.59	1.43	1.48
4	F	202	PEB	CBD-CAD	2.58	1.43	1.30
5	D	201	AX9	C4C-NC	2.57	1.39	1.35
4	C	101[A]	PEB	C1D-C2D	2.57	1.59	1.50
4	J	101[B]	PEB	C1D-C2D	2.57	1.59	1.50
4	E	101[A]	PEB	CBB-CAB	2.55	1.60	1.52
4	K	101[B]	PEB	CBB-CAB	2.55	1.60	1.52
4	G	101[A]	PEB	CHC-C4C	2.55	1.56	1.50
4	L	101[B]	PEB	CHC-C4C	2.55	1.56	1.50
4	A	101[A]	PEB	CBB-CAB	2.55	1.60	1.52
4	I	101[B]	PEB	CBB-CAB	2.55	1.60	1.52
4	G	101[A]	PEB	CBD-CAD	2.55	1.42	1.30
4	L	101[B]	PEB	CBD-CAD	2.55	1.42	1.30
5	B	201	AX9	C1B-CHA	2.55	1.51	1.41
4	B	203	PEB	CHA-C4A	2.55	1.41	1.36
4	C	101[A]	PEB	CHC-C4C	2.55	1.56	1.50
4	J	101[B]	PEB	CHC-C4C	2.55	1.56	1.50
4	A	101[A]	PEB	C1D-C2D	2.55	1.59	1.50
4	I	101[B]	PEB	C1D-C2D	2.55	1.59	1.50
5	F	201	AX9	C4B-CHB	2.54	1.51	1.41
4	H	203	PEB	CMC-C3C	2.54	1.56	1.51
5	H	201	AX9	CHC-C1D	-2.54	1.48	1.53
4	C	101[A]	PEB	CMC-C3C	2.53	1.56	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	J	101[B]	PEB	CMC-C3C	2.53	1.56	1.51
5	H	201	AX9	C1B-CHA	2.53	1.50	1.41
5	F	201	AX9	C4A-C3A	-2.52	1.40	1.45
4	C	101[A]	PEB	CBB-CAB	2.52	1.60	1.52
4	J	101[B]	PEB	CBB-CAB	2.52	1.60	1.52
4	D	202	PEB	C3B-C2B	2.52	1.42	1.36
4	F	202	PEB	CHA-C4A	2.51	1.41	1.36
4	H	203	PEB	CAA-C3A	2.50	1.58	1.54
5	H	201	AX9	C4B-CHB	2.45	1.50	1.41
4	F	202	PEB	C2C-C3C	2.45	1.44	1.37
4	H	202	PEB	CBD-CAD	2.44	1.42	1.30
4	D	203	PEB	CMC-C3C	2.44	1.56	1.51
4	E	101[A]	PEB	C3C-C4C	2.43	1.45	1.42
4	K	101[B]	PEB	C3C-C4C	2.43	1.45	1.42
4	H	202	PEB	CMC-C3C	2.43	1.56	1.51
4	B	202	PEB	C1D-C2D	2.42	1.58	1.50
4	C	101[A]	PEB	CBD-CAD	2.41	1.42	1.30
4	J	101[B]	PEB	CBD-CAD	2.41	1.42	1.30
4	F	203	PEB	CBB-CAB	2.41	1.59	1.52
4	B	203	PEB	CBD-CAD	2.39	1.42	1.30
4	G	101[A]	PEB	CBB-CAB	2.37	1.59	1.52
4	L	101[B]	PEB	CBB-CAB	2.37	1.59	1.52
4	H	202	PEB	OD-C4D	2.37	1.28	1.23
4	H	202	PEB	C1D-C2D	2.35	1.58	1.50
4	G	101[A]	PEB	C4B-NB	2.34	1.43	1.38
4	L	101[B]	PEB	C4B-NB	2.34	1.43	1.38
4	B	202	PEB	C1B-NB	2.34	1.42	1.36
4	D	202	PEB	CBD-CAD	2.31	1.41	1.30
4	A	101[A]	PEB	C3C-C4C	2.30	1.45	1.42
4	I	101[B]	PEB	C3C-C4C	2.30	1.45	1.42
4	G	101[A]	PEB	C2C-C3C	2.30	1.44	1.37
4	L	101[B]	PEB	C2C-C3C	2.30	1.44	1.37
4	A	101[A]	PEB	CBD-CAD	2.30	1.41	1.30
4	I	101[B]	PEB	CBD-CAD	2.30	1.41	1.30
4	B	203	PEB	C3B-C2B	2.29	1.41	1.36
5	D	201	AX9	CHC-C4C	2.29	1.53	1.50
5	D	201	AX9	C4D-C3D	-2.25	1.44	1.48
4	H	203	PEB	C1D-C2D	2.25	1.58	1.50
4	H	203	PEB	CBB-CAB	2.24	1.59	1.52
4	D	203	PEB	C1D-C2D	2.23	1.58	1.50
4	D	202	PEB	CBB-CAB	2.23	1.59	1.52
4	F	203	PEB	OD-C4D	2.21	1.27	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	203	PEB	CBD-CAD	2.19	1.41	1.30
4	E	101[A]	PEB	CMC-C3C	2.19	1.56	1.51
4	K	101[B]	PEB	CMC-C3C	2.19	1.56	1.51
4	F	203	PEB	C2C-C3C	2.18	1.44	1.37
4	D	203	PEB	C2C-C3C	2.17	1.44	1.37
4	H	203	PEB	CBD-CAD	2.17	1.41	1.30
4	B	202	PEB	CBD-CAD	2.16	1.41	1.30
4	F	202	PEB	C4B-NB	2.16	1.43	1.38
4	D	203	PEB	CBB-CAB	2.15	1.58	1.52
4	F	202	PEB	C1D-C2D	2.12	1.57	1.50
4	B	203	PEB	CAC-CBC	2.12	1.63	1.52
4	F	203	PEB	CAA-C3A	2.12	1.58	1.54
4	F	202	PEB	OA-C1A	2.11	1.27	1.23
4	C	101[A]	PEB	C4B-NB	2.10	1.43	1.38
4	J	101[B]	PEB	C4B-NB	2.10	1.43	1.38
4	G	101[A]	PEB	C3C-C4C	2.10	1.45	1.42
4	L	101[B]	PEB	C3C-C4C	2.10	1.45	1.42
5	F	201	AX9	CHB-C1C	2.10	1.36	1.35
4	E	101[A]	PEB	CBD-CAD	2.09	1.40	1.30
4	K	101[B]	PEB	CBD-CAD	2.09	1.40	1.30
4	H	202	PEB	CHA-C4A	2.07	1.40	1.36
4	H	203	PEB	C1B-C2B	2.07	1.50	1.45
4	A	101[A]	PEB	C3B-C2B	2.06	1.41	1.36
4	I	101[B]	PEB	C3B-C2B	2.06	1.41	1.36
4	G	101[A]	PEB	C3B-C2B	2.05	1.41	1.36
4	L	101[B]	PEB	C3B-C2B	2.05	1.41	1.36
4	F	203	PEB	CHC-C1D	-2.05	1.48	1.54
4	G	101[A]	PEB	OD-C4D	2.03	1.27	1.23
4	L	101[B]	PEB	OD-C4D	2.03	1.27	1.23
4	H	203	PEB	C2C-C3C	2.02	1.43	1.37
4	D	202	PEB	C4B-NB	2.01	1.42	1.38
5	F	201	AX9	O1C-CGC	-2.00	1.24	1.30

All (211) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	101[A]	PEB	C1C-CHB-C4B	-10.98	115.70	128.81
4	J	101[B]	PEB	C1C-CHB-C4B	-10.98	115.70	128.81
4	A	101[A]	PEB	C1C-CHB-C4B	-8.78	118.32	128.81
4	I	101[B]	PEB	C1C-CHB-C4B	-8.78	118.32	128.81
4	F	202	PEB	C1C-CHB-C4B	-8.54	118.61	128.81
4	D	202	PEB	C1C-CHB-C4B	-8.13	119.10	128.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	202	PEB	C1C-CHB-C4B	-7.81	119.48	128.81
4	D	202	PEB	OA-C1A-C2A	-7.23	120.43	126.17
4	B	202	PEB	C1C-CHB-C4B	-7.04	120.41	128.81
4	G	101[A]	PEB	C1C-CHB-C4B	-6.98	120.47	128.81
4	L	101[B]	PEB	C1C-CHB-C4B	-6.98	120.47	128.81
4	E	101[A]	PEB	C1C-CHB-C4B	-6.74	120.76	128.81
4	K	101[B]	PEB	C1C-CHB-C4B	-6.74	120.76	128.81
4	D	202	PEB	CBB-CAB-C3B	-6.26	95.22	112.63
4	F	203	PEB	C1C-CHB-C4B	-5.94	121.72	128.81
4	H	202	PEB	CHA-C4A-NA	5.93	132.26	125.20
4	D	203	PEB	CHC-C1D-ND	-5.07	108.06	113.95
4	B	203	PEB	CBC-CAC-C2C	-4.96	104.15	112.62
4	D	202	PEB	CMB-C2B-C1B	4.84	132.51	125.06
4	A	101[A]	PEB	OA-C1A-C2A	-4.83	122.33	126.17
4	I	101[B]	PEB	OA-C1A-C2A	-4.83	122.33	126.17
4	F	202	PEB	CHC-C1D-ND	-4.74	108.44	113.95
4	E	101[A]	PEB	CHC-C1D-ND	-4.60	108.61	113.95
4	K	101[B]	PEB	CHC-C1D-ND	-4.60	108.61	113.95
4	E	101[A]	PEB	CAC-CBC-CGC	-4.38	101.49	113.76
4	K	101[B]	PEB	CAC-CBC-CGC	-4.38	101.49	113.76
4	G	101[A]	PEB	CAC-CBC-CGC	-4.32	101.65	113.76
4	L	101[B]	PEB	CAC-CBC-CGC	-4.32	101.65	113.76
4	A	101[A]	PEB	CAB-CBB-CGB	-4.30	104.35	113.60
4	I	101[B]	PEB	CAB-CBB-CGB	-4.30	104.35	113.60
4	G	101[A]	PEB	CAB-CBB-CGB	-4.27	104.41	113.60
4	L	101[B]	PEB	CAB-CBB-CGB	-4.27	104.41	113.60
4	E	101[A]	PEB	CBC-CAC-C2C	-4.25	105.37	112.62
4	K	101[B]	PEB	CBC-CAC-C2C	-4.25	105.37	112.62
4	B	203	PEB	C1C-CHB-C4B	-4.13	123.88	128.81
4	A	101[A]	PEB	OD-C4D-ND	-3.98	120.03	125.93
4	I	101[B]	PEB	OD-C4D-ND	-3.98	120.03	125.93
4	D	203	PEB	CBC-CAC-C2C	-3.96	105.86	112.62
5	F	201	AX9	CMD-C2D-C3D	-3.90	121.91	127.77
4	H	203	PEB	C4B-C3B-C2B	3.86	111.05	106.78
4	B	202	PEB	CHB-C4B-C3B	-3.86	116.41	125.32
4	B	202	PEB	CBB-CAB-C3B	-3.81	102.04	112.63
4	H	202	PEB	CMB-C2B-C1B	3.80	130.91	125.06
4	D	202	PEB	OA-C1A-NA	3.69	129.41	124.94
4	B	203	PEB	CAC-CBC-CGC	-3.68	103.44	113.76
4	H	203	PEB	C1C-CHB-C4B	-3.68	124.42	128.81
4	B	202	PEB	CHA-C1B-NB	-3.66	117.28	124.93
4	F	202	PEB	CBB-CAB-C3B	-3.64	102.51	112.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	202	PEB	CHA-C4A-NA	3.61	129.50	125.20
4	E	101[A]	PEB	OD-C4D-ND	-3.59	120.61	125.93
4	K	101[B]	PEB	OD-C4D-ND	-3.59	120.61	125.93
4	H	203	PEB	CBC-CAC-C2C	-3.58	106.52	112.62
4	E	101[A]	PEB	CAB-CBB-CGB	-3.57	105.91	113.60
4	K	101[B]	PEB	CAB-CBB-CGB	-3.57	105.91	113.60
5	F	201	AX9	C4B-CHB-C1C	-3.57	124.55	128.81
4	F	203	PEB	CHC-C4C-C3C	-3.52	124.34	130.34
4	G	101[A]	PEB	C2A-C1A-NA	3.52	111.30	108.27
4	L	101[B]	PEB	C2A-C1A-NA	3.52	111.30	108.27
4	C	101[A]	PEB	CAA-C3A-C2A	3.51	123.04	114.26
4	J	101[B]	PEB	CAA-C3A-C2A	3.51	123.04	114.26
4	D	202	PEB	CBA-CAA-C3A	-3.50	105.67	113.47
4	C	101[A]	PEB	OA-C1A-C2A	-3.32	123.53	126.17
4	J	101[B]	PEB	OA-C1A-C2A	-3.32	123.53	126.17
4	H	202	PEB	CBC-CAC-C2C	-3.31	106.97	112.62
4	C	101[A]	PEB	CBC-CAC-C2C	-3.30	106.98	112.62
4	J	101[B]	PEB	CBC-CAC-C2C	-3.30	106.98	112.62
4	A	101[A]	PEB	CAC-CBC-CGC	-3.27	104.58	113.76
4	I	101[B]	PEB	CAC-CBC-CGC	-3.27	104.58	113.76
4	H	202	PEB	C2A-C3A-C4A	3.25	106.21	101.34
4	H	203	PEB	OA-C1A-C2A	-3.24	123.59	126.17
4	G	101[A]	PEB	CBC-CAC-C2C	-3.23	107.11	112.62
4	L	101[B]	PEB	CBC-CAC-C2C	-3.23	107.11	112.62
4	C	101[A]	PEB	CAC-CBC-CGC	-3.22	104.72	113.76
4	J	101[B]	PEB	CAC-CBC-CGC	-3.22	104.72	113.76
4	A	101[A]	PEB	CBA-CAA-C3A	-3.21	106.32	113.47
4	I	101[B]	PEB	CBA-CAA-C3A	-3.21	106.32	113.47
4	B	202	PEB	OD-C4D-ND	-3.20	121.19	125.93
4	H	203	PEB	CAC-CBC-CGC	-3.20	104.80	113.76
4	F	202	PEB	OA-C1A-C2A	-3.18	123.64	126.17
4	D	203	PEB	CHC-C4C-C3C	-3.17	124.93	130.34
4	A	101[A]	PEB	CAA-C3A-C4A	-3.17	104.53	112.67
4	I	101[B]	PEB	CAA-C3A-C4A	-3.17	104.53	112.67
5	D	201	AX9	C4A-NA-C1A	-3.15	106.65	110.67
4	B	202	PEB	C2A-C1A-NA	3.10	110.94	108.27
4	D	203	PEB	CBB-CAB-C3B	-3.09	104.03	112.63
4	F	203	PEB	CMB-C2B-C1B	3.04	129.74	125.06
4	E	101[A]	PEB	OA-C1A-C2A	-2.99	123.80	126.17
4	K	101[B]	PEB	OA-C1A-C2A	-2.99	123.80	126.17
4	C	101[A]	PEB	CAA-C3A-C4A	-2.97	105.04	112.67
4	J	101[B]	PEB	CAA-C3A-C4A	-2.97	105.04	112.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	202	PEB	CMB-C2B-C1B	2.96	129.63	125.06
5	B	201	AX9	C4B-CHB-C1C	-2.94	125.30	128.81
4	A	101[A]	PEB	C2A-C1A-NA	2.93	110.80	108.27
4	I	101[B]	PEB	C2A-C1A-NA	2.93	110.80	108.27
4	B	202	PEB	CHB-C4B-NB	2.91	132.86	128.83
4	D	203	PEB	C1C-CHB-C4B	-2.90	125.34	128.81
4	H	203	PEB	CMB-C2B-C1B	2.90	129.52	125.06
4	H	202	PEB	OA-C1A-C2A	-2.89	123.88	126.17
4	C	101[A]	PEB	CMA-C2A-C1A	-2.88	106.19	112.40
4	J	101[B]	PEB	CMA-C2A-C1A	-2.88	106.19	112.40
5	B	201	AX9	CAC-CBC-CGC	-2.87	107.44	113.60
4	E	101[A]	PEB	CAA-C3A-C4A	-2.86	105.33	112.67
4	K	101[B]	PEB	CAA-C3A-C4A	-2.86	105.33	112.67
4	G	101[A]	PEB	CHA-C4A-NA	2.82	128.56	125.20
4	L	101[B]	PEB	CHA-C4A-NA	2.82	128.56	125.20
4	F	202	PEB	OD-C4D-ND	-2.81	121.77	125.93
4	F	202	PEB	C2A-C1A-NA	2.80	110.69	108.27
4	F	202	PEB	CMA-C2A-C1A	-2.80	106.38	112.40
4	G	101[A]	PEB	CHC-C1D-ND	-2.79	110.71	113.95
4	L	101[B]	PEB	CHC-C1D-ND	-2.79	110.71	113.95
4	D	202	PEB	CAB-CBB-CGB	-2.79	107.61	113.60
4	H	203	PEB	CBB-CAB-C3B	-2.78	104.89	112.63
4	F	203	PEB	OD-C4D-C3D	-2.78	123.17	129.46
4	H	202	PEB	CBB-CAB-C3B	-2.77	104.92	112.63
4	F	202	PEB	CAB-CBB-CGB	-2.77	107.63	113.60
4	B	203	PEB	CHC-C4C-C3C	-2.75	125.64	130.34
4	B	203	PEB	CMB-C2B-C1B	2.74	129.29	125.06
4	G	101[A]	PEB	CHB-C4B-C3B	-2.74	119.00	125.32
4	L	101[B]	PEB	CHB-C4B-C3B	-2.74	119.00	125.32
4	G	101[A]	PEB	OA-C1A-C2A	-2.72	124.01	126.17
4	L	101[B]	PEB	OA-C1A-C2A	-2.72	124.01	126.17
4	B	202	PEB	CBC-CAC-C2C	-2.69	108.03	112.62
4	B	202	PEB	CHC-C1D-ND	-2.66	110.86	113.95
4	H	203	PEB	C1B-C2B-C3B	-2.65	103.46	106.51
4	B	203	PEB	O2C-CGC-CBC	2.64	122.50	114.03
5	D	201	AX9	C4B-CHB-C1C	-2.63	125.66	128.81
5	H	201	AX9	CHC-C1D-ND	-2.63	110.39	113.72
4	H	202	PEB	CHB-C4B-C3B	-2.62	119.27	125.32
4	H	203	PEB	O2B-CGB-CBB	2.58	122.31	114.03
4	F	203	PEB	CHA-C1B-NB	-2.56	119.57	124.93
4	B	202	PEB	CMB-C2B-C1B	2.56	129.01	125.06
5	F	201	AX9	OD-C4D-C3D	-2.54	125.29	128.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	202	PEB	C2A-C3A-C4A	2.54	105.14	101.34
4	C	101[A]	PEB	CMD-C2D-C3D	-2.53	126.50	130.06
4	J	101[B]	PEB	CMD-C2D-C3D	-2.53	126.50	130.06
5	B	201	AX9	CBD-CAD-C3D	-2.52	105.49	112.43
4	G	101[A]	PEB	C2A-C3A-C4A	2.51	105.09	101.34
4	L	101[B]	PEB	C2A-C3A-C4A	2.51	105.09	101.34
4	D	203	PEB	CMB-C2B-C1B	2.50	128.92	125.06
4	B	202	PEB	CHA-C1B-C2B	2.48	131.28	124.90
4	C	101[A]	PEB	CBB-CAB-C3B	-2.47	105.76	112.63
4	J	101[B]	PEB	CBB-CAB-C3B	-2.47	105.76	112.63
5	D	201	AX9	CAA-C3A-C4A	2.47	127.71	124.38
4	C	101[A]	PEB	OA-C1A-NA	2.47	127.93	124.94
4	J	101[B]	PEB	OA-C1A-NA	2.47	127.93	124.94
4	G	101[A]	PEB	OD-C4D-ND	-2.46	122.28	125.93
4	L	101[B]	PEB	OD-C4D-ND	-2.46	122.28	125.93
5	B	201	AX9	CAD-C3D-C4D	2.46	125.26	121.38
4	B	203	PEB	O2B-CGB-CBB	2.45	121.92	114.03
5	H	201	AX9	O1C-CGC-CBC	2.45	121.92	114.03
5	B	201	AX9	O1C-CGC-CBC	2.45	121.90	114.03
4	D	202	PEB	CAC-CBC-CGC	-2.41	107.01	113.76
4	B	202	PEB	CBD-CAD-C3D	-2.40	115.66	127.62
4	G	101[A]	PEB	CAA-C3A-C4A	-2.40	106.50	112.67
4	L	101[B]	PEB	CAA-C3A-C4A	-2.40	106.50	112.67
4	G	101[A]	PEB	O2C-CGC-CBC	2.40	121.73	114.03
4	L	101[B]	PEB	O2C-CGC-CBC	2.40	121.73	114.03
5	F	201	AX9	O1C-CGC-O2C	-2.39	117.34	123.30
4	E	101[A]	PEB	CAA-C3A-C2A	2.39	120.23	114.26
4	K	101[B]	PEB	CAA-C3A-C2A	2.39	120.23	114.26
4	C	101[A]	PEB	CMB-C2B-C1B	2.39	128.74	125.06
4	J	101[B]	PEB	CMB-C2B-C1B	2.39	128.74	125.06
5	F	201	AX9	CHC-C1D-ND	-2.33	110.77	113.72
5	B	201	AX9	C4A-NA-C1A	-2.33	107.70	110.67
5	H	201	AX9	CAA-C3A-C4A	2.30	127.48	124.38
4	F	203	PEB	CHB-C4B-NB	-2.30	125.64	128.83
4	H	202	PEB	CAB-CBB-CGB	-2.29	108.67	113.60
5	F	201	AX9	CMA-C2A-C1A	2.27	126.73	121.39
4	F	203	PEB	CHA-C4A-NA	2.27	127.90	125.20
4	F	202	PEB	C2A-C3A-C4A	2.26	104.72	101.34
4	F	203	PEB	C4B-NB-C1B	-2.25	102.27	106.51
4	E	101[A]	PEB	CBD-CAD-C3D	-2.25	116.45	127.62
4	K	101[B]	PEB	CBD-CAD-C3D	-2.25	116.45	127.62
4	F	202	PEB	CHB-C4B-C3B	-2.24	120.14	125.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	203	PEB	CMD-C2D-C3D	-2.24	126.90	130.06
4	H	203	PEB	OA-C1A-NA	2.23	127.64	124.94
4	D	203	PEB	OD-C4D-C3D	-2.23	124.42	129.46
4	B	203	PEB	CBB-CAB-C3B	-2.22	106.47	112.63
4	D	203	PEB	O2B-CGB-CBB	2.21	121.12	114.03
4	H	202	PEB	C2A-C1A-NA	2.21	110.17	108.27
5	H	201	AX9	OD-C4D-C3D	-2.20	125.65	128.04
4	F	203	PEB	OA-C1A-C2A	2.19	127.92	126.17
4	B	202	PEB	CAB-CBB-CGB	-2.19	108.89	113.60
4	F	202	PEB	CBA-CAA-C3A	-2.19	108.59	113.47
4	D	202	PEB	C2A-C1A-NA	2.19	110.16	108.27
4	C	101[A]	PEB	CAB-CBB-CGB	-2.17	108.92	113.60
4	J	101[B]	PEB	CAB-CBB-CGB	-2.17	108.92	113.60
4	A	101[A]	PEB	C2A-C3A-C4A	2.16	104.57	101.34
4	I	101[B]	PEB	C2A-C3A-C4A	2.16	104.57	101.34
4	F	203	PEB	C3B-C4B-NB	2.15	113.18	110.05
4	D	203	PEB	CHB-C4B-C3B	-2.15	120.35	125.32
4	G	101[A]	PEB	O1C-CGC-CBC	-2.14	116.19	123.08
4	L	101[B]	PEB	O1C-CGC-CBC	-2.14	116.19	123.08
4	B	202	PEB	CMA-C2A-C1A	-2.14	107.80	112.40
4	D	203	PEB	O2C-CGC-CBC	2.12	120.84	114.03
5	D	201	AX9	CAC-C2C-C3C	-2.12	123.94	127.88
4	F	202	PEB	C4B-C3B-C2B	2.11	109.12	106.78
4	B	203	PEB	CAA-C3A-C2A	-2.10	109.00	114.26
4	F	203	PEB	O2C-CGC-CBC	2.10	120.78	114.03
4	F	203	PEB	O2B-CGB-CBB	2.10	120.77	114.03
4	H	202	PEB	CAC-CBC-CGC	-2.09	107.90	113.76
4	C	101[A]	PEB	CHC-C4C-C3C	-2.09	126.78	130.34
4	J	101[B]	PEB	CHC-C4C-C3C	-2.09	126.78	130.34
4	F	202	PEB	CHA-C4A-NA	2.08	127.68	125.20
5	B	201	AX9	CBB-CAB-C3B	-2.08	109.06	112.62
4	D	203	PEB	CHA-C1B-NB	-2.08	120.59	124.93
5	D	201	AX9	CBB-CAB-C3B	-2.07	109.08	112.62
5	H	201	AX9	C4A-NA-C1A	-2.06	108.04	110.67
4	D	202	PEB	O1B-CGB-CBB	-2.06	116.46	123.08
4	D	203	PEB	CMA-C2A-C1A	-2.03	108.02	112.40
5	D	201	AX9	CMA-C2A-C1A	2.02	126.14	121.39

There are no chirality outliers.

All (103) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	101[A]	PEB	NB-C1B-CHA-C4A
4	A	101[A]	PEB	C2B-C1B-CHA-C4A
4	B	203	PEB	NA-C4A-CHA-C1B
4	C	101[A]	PEB	NA-C4A-CHA-C1B
4	C	101[A]	PEB	NB-C1B-CHA-C4A
4	C	101[A]	PEB	C2B-C1B-CHA-C4A
4	D	202	PEB	C1C-C2C-CAC-CBC
4	D	202	PEB	C3C-C2C-CAC-CBC
4	D	202	PEB	NB-C1B-CHA-C4A
4	D	202	PEB	C2B-C1B-CHA-C4A
4	D	203	PEB	NA-C4A-CHA-C1B
4	D	203	PEB	NB-C1B-CHA-C4A
4	D	203	PEB	C2B-C1B-CHA-C4A
4	E	101[A]	PEB	NB-C1B-CHA-C4A
4	E	101[A]	PEB	C2B-C1B-CHA-C4A
4	F	202	PEB	C1C-C2C-CAC-CBC
4	F	203	PEB	C4A-C3A-CAA-CBA
4	F	203	PEB	NB-C1B-CHA-C4A
4	F	203	PEB	C2B-C1B-CHA-C4A
4	G	101[A]	PEB	NB-C1B-CHA-C4A
4	G	101[A]	PEB	C2B-C1B-CHA-C4A
4	H	202	PEB	NB-C1B-CHA-C4A
4	H	202	PEB	C2B-C1B-CHA-C4A
4	H	203	PEB	NA-C4A-CHA-C1B
4	I	101[B]	PEB	NB-C1B-CHA-C4A
4	I	101[B]	PEB	C2B-C1B-CHA-C4A
4	J	101[B]	PEB	NA-C4A-CHA-C1B
4	J	101[B]	PEB	NB-C1B-CHA-C4A
4	J	101[B]	PEB	C2B-C1B-CHA-C4A
4	K	101[B]	PEB	NB-C1B-CHA-C4A
4	K	101[B]	PEB	C2B-C1B-CHA-C4A
4	L	101[B]	PEB	NB-C1B-CHA-C4A
4	L	101[B]	PEB	C2B-C1B-CHA-C4A
5	B	201	AX9	NB-C1B-CHA-C4A
5	B	201	AX9	NC-C4C-CHC-C1D
5	D	201	AX9	NB-C1B-CHA-C4A
5	D	201	AX9	C2B-C1B-CHA-C4A
5	D	201	AX9	NC-C4C-CHC-C1D
5	F	201	AX9	NB-C1B-CHA-C4A
5	F	201	AX9	NC-C4C-CHC-C1D
5	H	201	AX9	NB-C1B-CHA-C4A
5	H	201	AX9	NC-C4C-CHC-C1D
6	E	102[A]	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
6	K	102[B]	GOL	C1-C2-C3-O3
4	B	202	PEB	NB-C1B-CHA-C4A
4	B	203	PEB	NB-C1B-CHA-C4A
4	F	202	PEB	NB-C1B-CHA-C4A
4	H	203	PEB	NB-C1B-CHA-C4A
4	B	202	PEB	C2B-C1B-CHA-C4A
4	B	203	PEB	C2B-C1B-CHA-C4A
4	F	202	PEB	C2B-C1B-CHA-C4A
4	H	203	PEB	C2B-C1B-CHA-C4A
6	G	102[A]	GOL	C1-C2-C3-O3
6	L	102[B]	GOL	C1-C2-C3-O3
4	C	101[A]	PEB	C2C-CAC-CBC-CGC
4	F	203	PEB	C2A-C3A-CAA-CBA
4	J	101[B]	PEB	C2C-CAC-CBC-CGC
4	A	101[A]	PEB	C4B-C3B-CAB-CBB
4	I	101[B]	PEB	C4B-C3B-CAB-CBB
4	A	101[A]	PEB	C2C-CAC-CBC-CGC
4	I	101[B]	PEB	C2C-CAC-CBC-CGC
5	D	201	AX9	C4D-C3D-CAD-CBD
6	E	102[A]	GOL	O2-C2-C3-O3
6	G	102[A]	GOL	O2-C2-C3-O3
6	K	102[B]	GOL	O2-C2-C3-O3
6	L	102[B]	GOL	O2-C2-C3-O3
4	A	101[A]	PEB	C2B-C3B-CAB-CBB
4	I	101[B]	PEB	C2B-C3B-CAB-CBB
4	F	202	PEB	C3C-C2C-CAC-CBC
4	H	202	PEB	C3B-CAB-CBB-CGB
4	B	202	PEB	NA-C4A-CHA-C1B
5	B	201	AX9	CAB-CBB-CGB-O1B
5	H	201	AX9	CAC-CBC-CGC-O2C
5	B	201	AX9	CAB-CBB-CGB-O2B
5	H	201	AX9	CAC-CBC-CGC-O1C
5	D	201	AX9	CAB-CBB-CGB-O1B
5	F	201	AX9	CAB-CBB-CGB-O1B
4	F	202	PEB	CAB-CBB-CGB-O2B
4	F	203	PEB	NA-C4A-CHA-C1B
6	E	102[A]	GOL	O1-C1-C2-C3
6	K	102[B]	GOL	O1-C1-C2-C3
5	B	201	AX9	CAC-CBC-CGC-O2C
5	H	201	AX9	CAB-CBB-CGB-O2B
4	F	202	PEB	CAB-CBB-CGB-O1B
4	H	203	PEB	CAC-CBC-CGC-O2C

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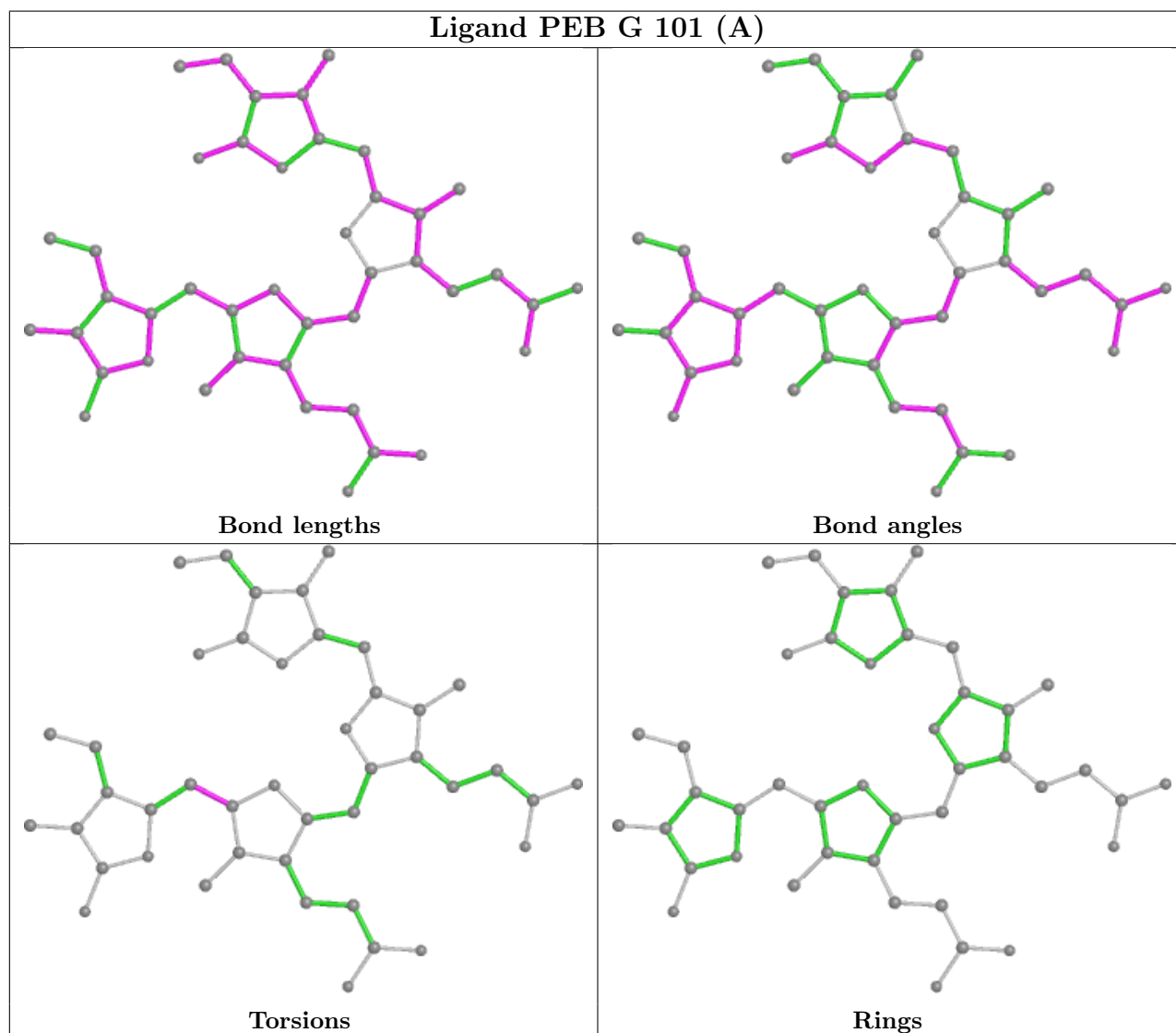
Mol	Chain	Res	Type	Atoms
4	H	203	PEB	CAC-CBC-CGC-O1C
4	H	202	PEB	CAC-CBC-CGC-O1C
5	H	201	AX9	CAB-CBB-CGB-O1B
4	H	202	PEB	CAC-CBC-CGC-O2C
5	D	201	AX9	CAB-CBB-CGB-O2B
4	F	203	PEB	CAB-CBB-CGB-O1B
4	E	101[A]	PEB	CAB-CBB-CGB-O1B
4	K	101[B]	PEB	CAB-CBB-CGB-O1B
5	B	201	AX9	CAC-CBC-CGC-O1C
4	D	203	PEB	CAB-CBB-CGB-O1B
5	F	201	AX9	CAB-CBB-CGB-O2B
4	F	203	PEB	CAB-CBB-CGB-O2B
4	B	203	PEB	CAB-CBB-CGB-O1B
4	E	101[A]	PEB	CAB-CBB-CGB-O2B
4	K	101[B]	PEB	CAB-CBB-CGB-O2B
4	H	203	PEB	CAB-CBB-CGB-O1B
4	D	203	PEB	CAC-CBC-CGC-O2C
4	D	203	PEB	CAB-CBB-CGB-O2B

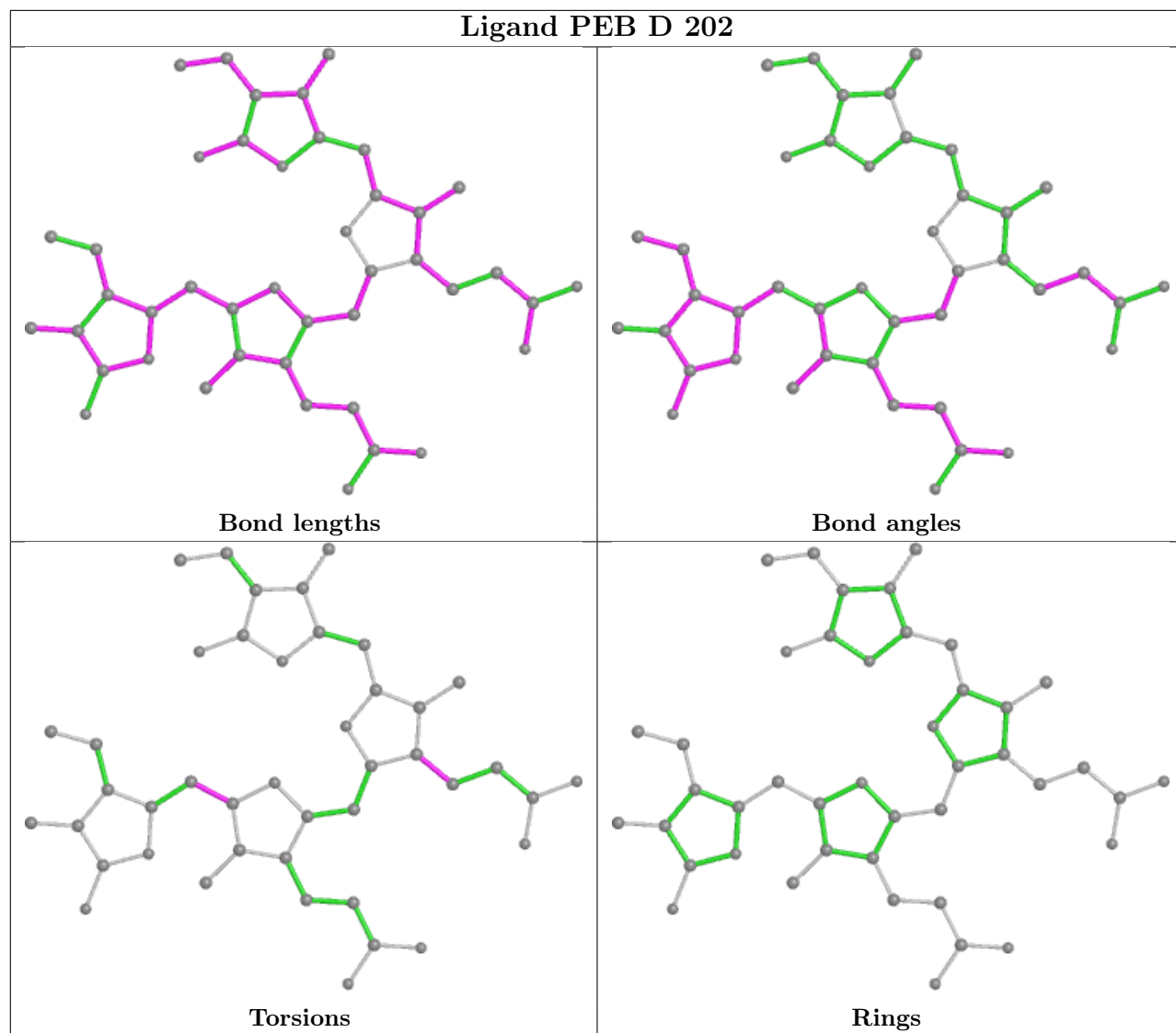
There are no ring outliers.

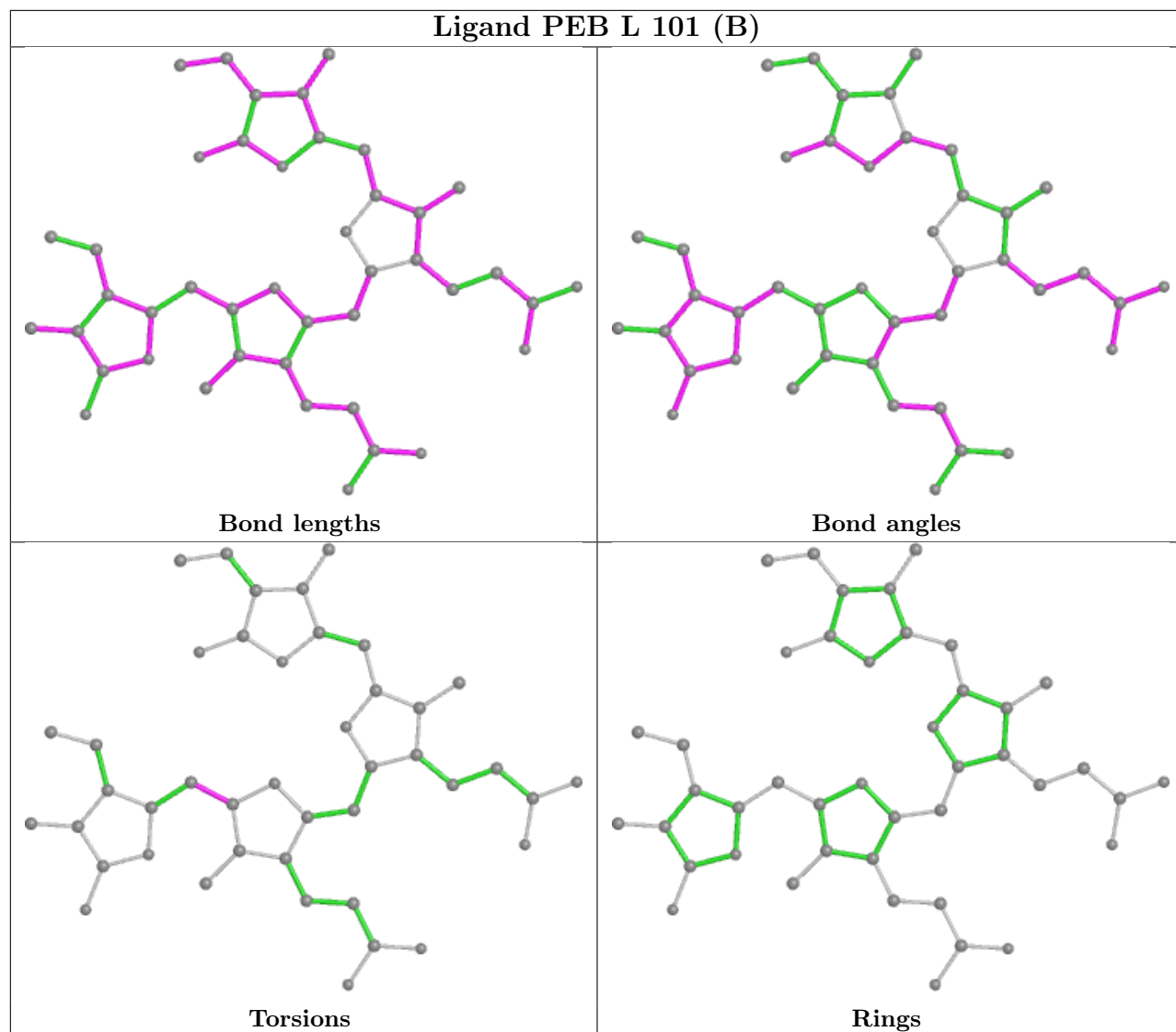
18 monomers are involved in 48 short contacts:

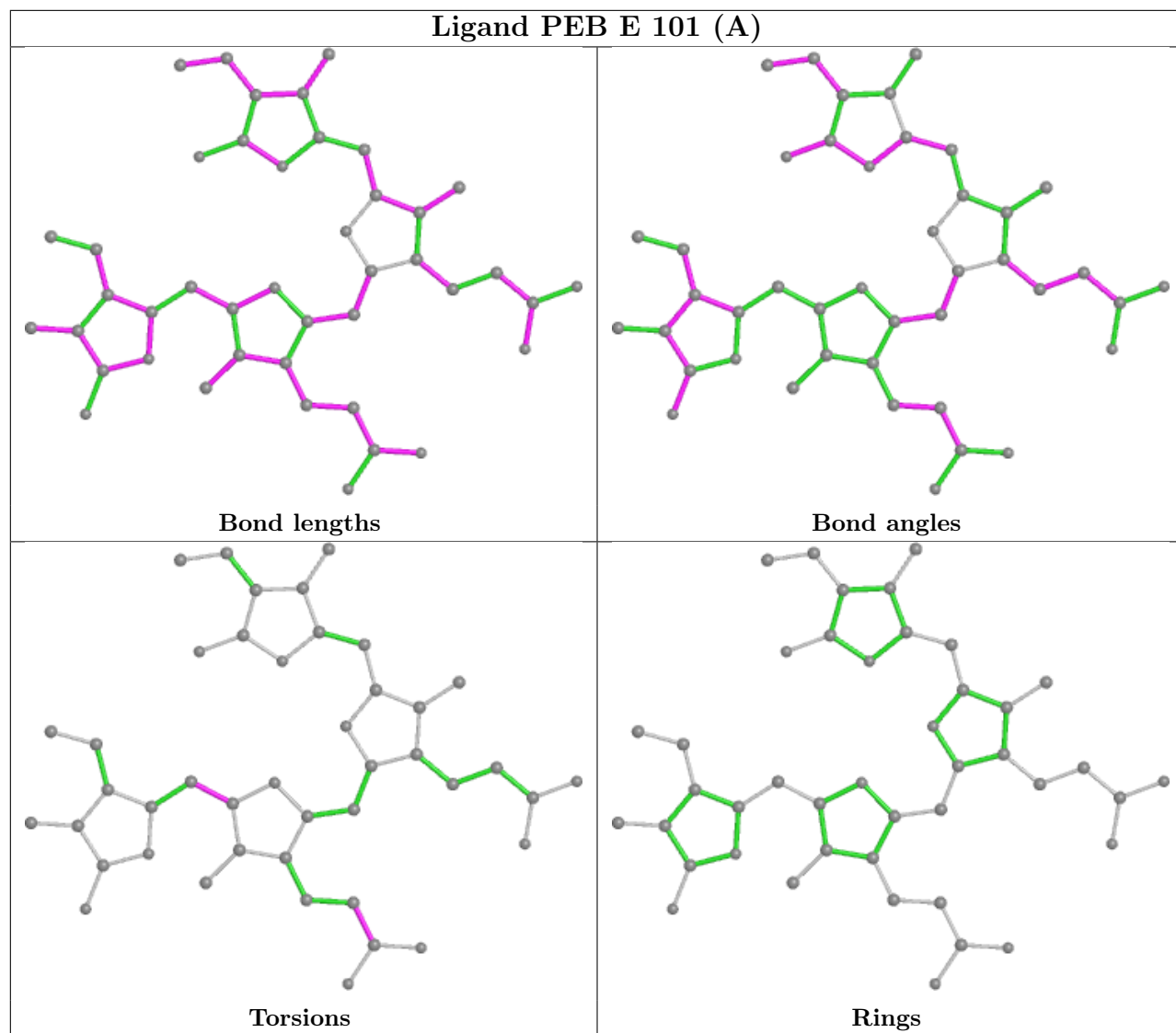
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	101[A]	PEB	2	0
4	D	202	PEB	1	0
4	L	101[B]	PEB	1	0
4	E	101[A]	PEB	2	0
4	A	101[A]	PEB	2	0
4	B	202	PEB	1	0
4	D	203	PEB	6	0
6	E	102[A]	GOL	2	0
4	H	202	PEB	1	0
4	C	101[A]	PEB	1	0
4	J	101[B]	PEB	2	0
4	F	202	PEB	4	0
4	F	203	PEB	5	0
4	I	101[B]	PEB	2	0
6	K	102[B]	GOL	2	0
4	B	203	PEB	4	0
4	H	203	PEB	3	0
4	K	101[B]	PEB	7	0

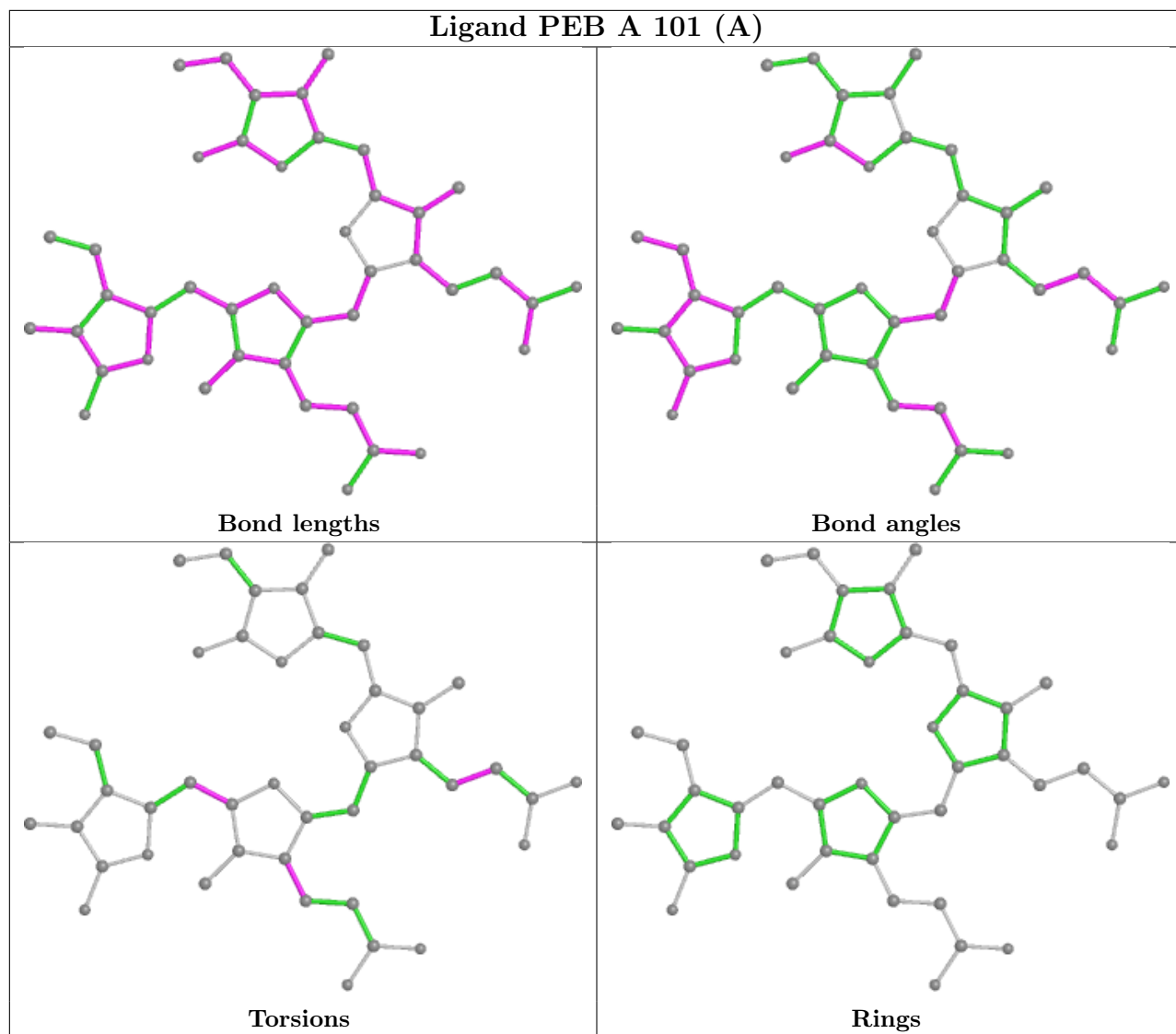
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

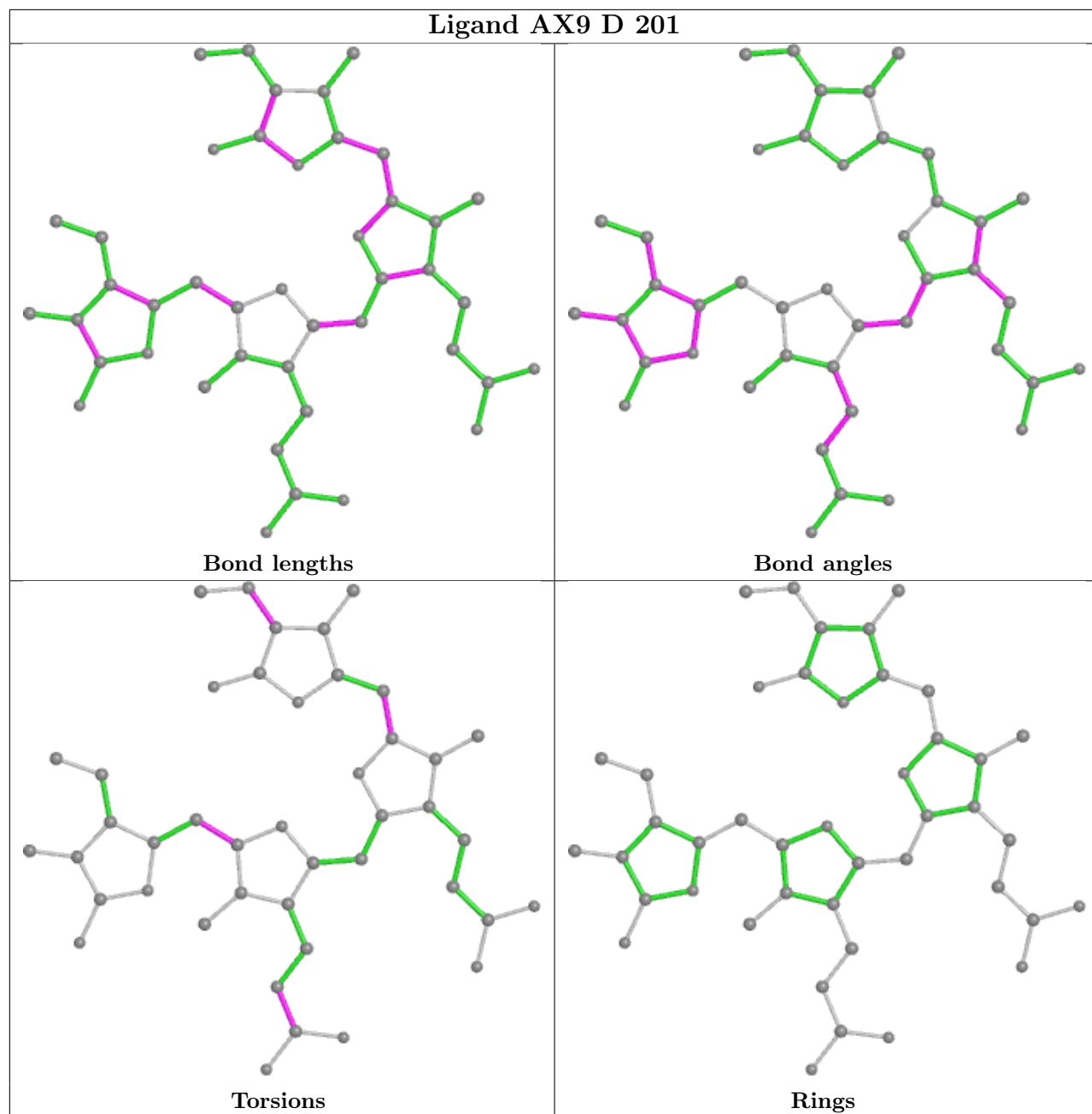


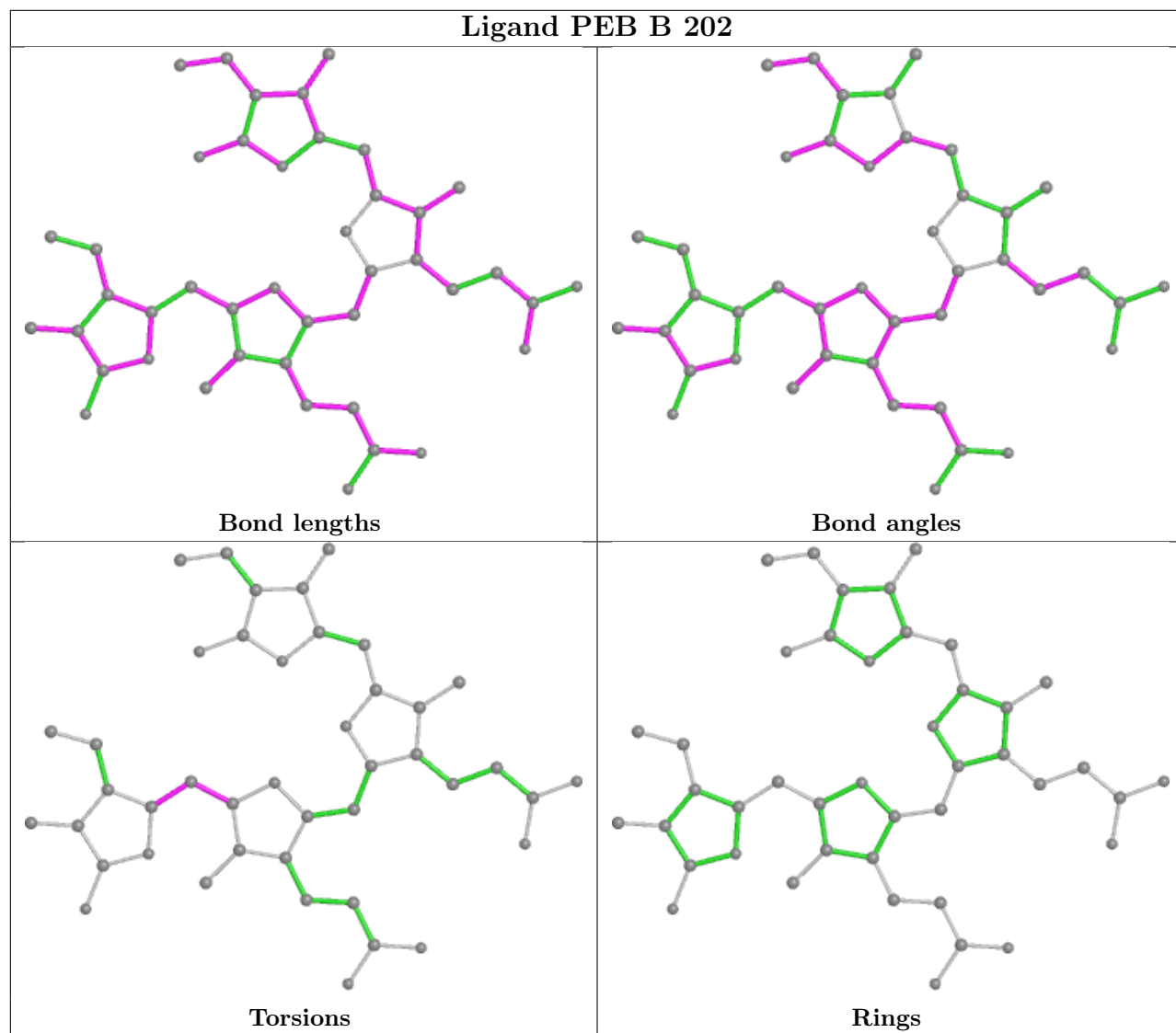


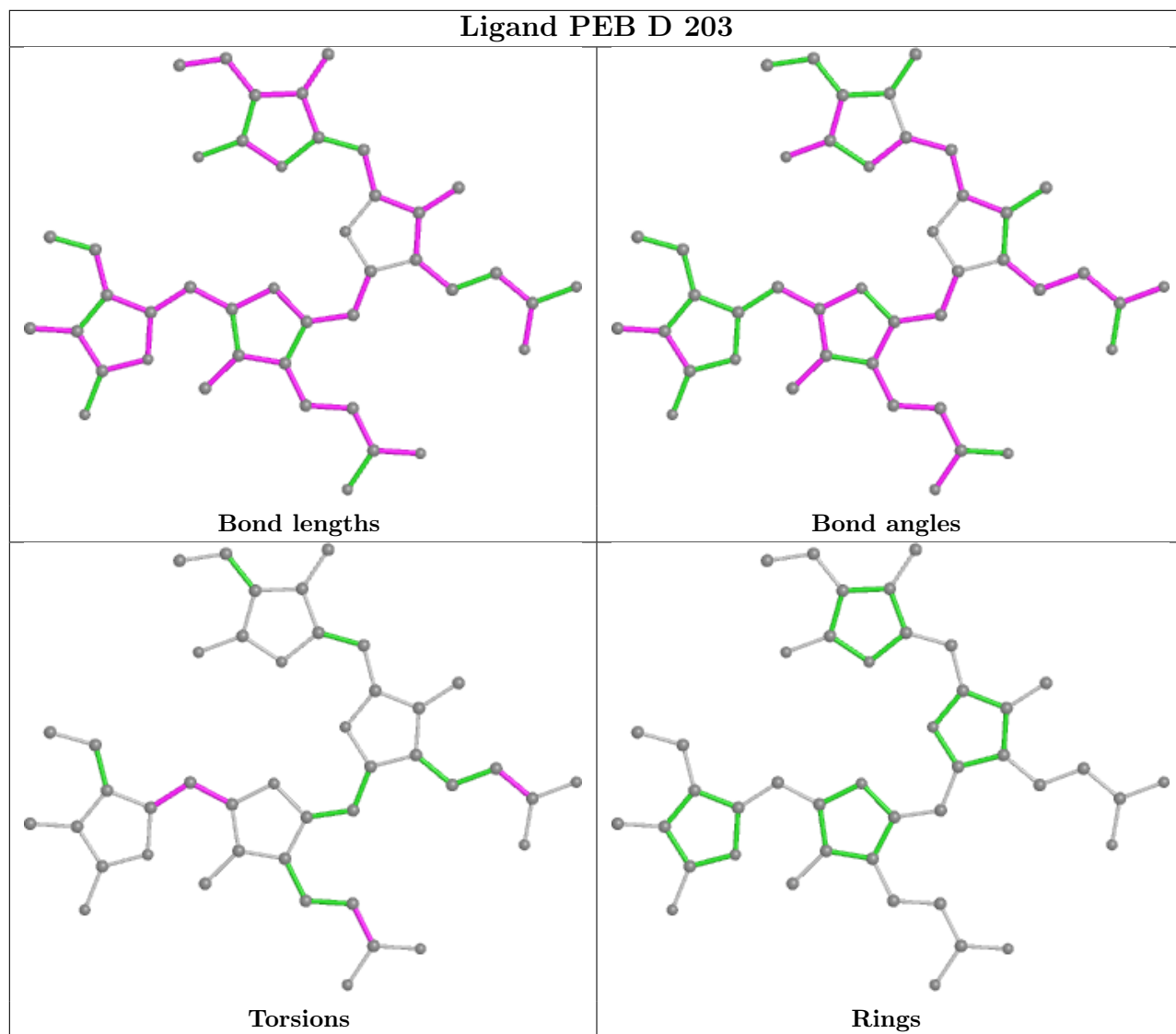


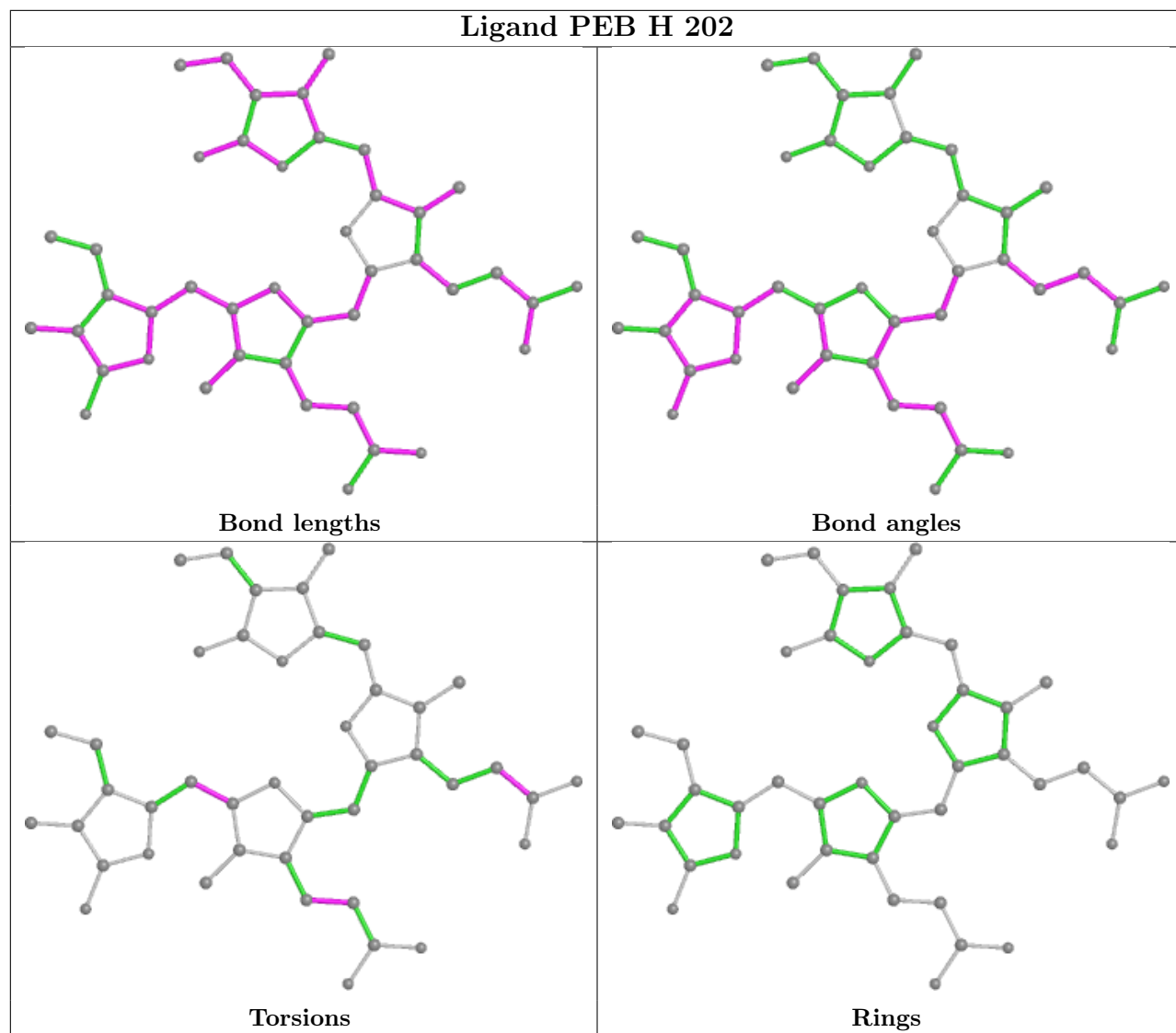


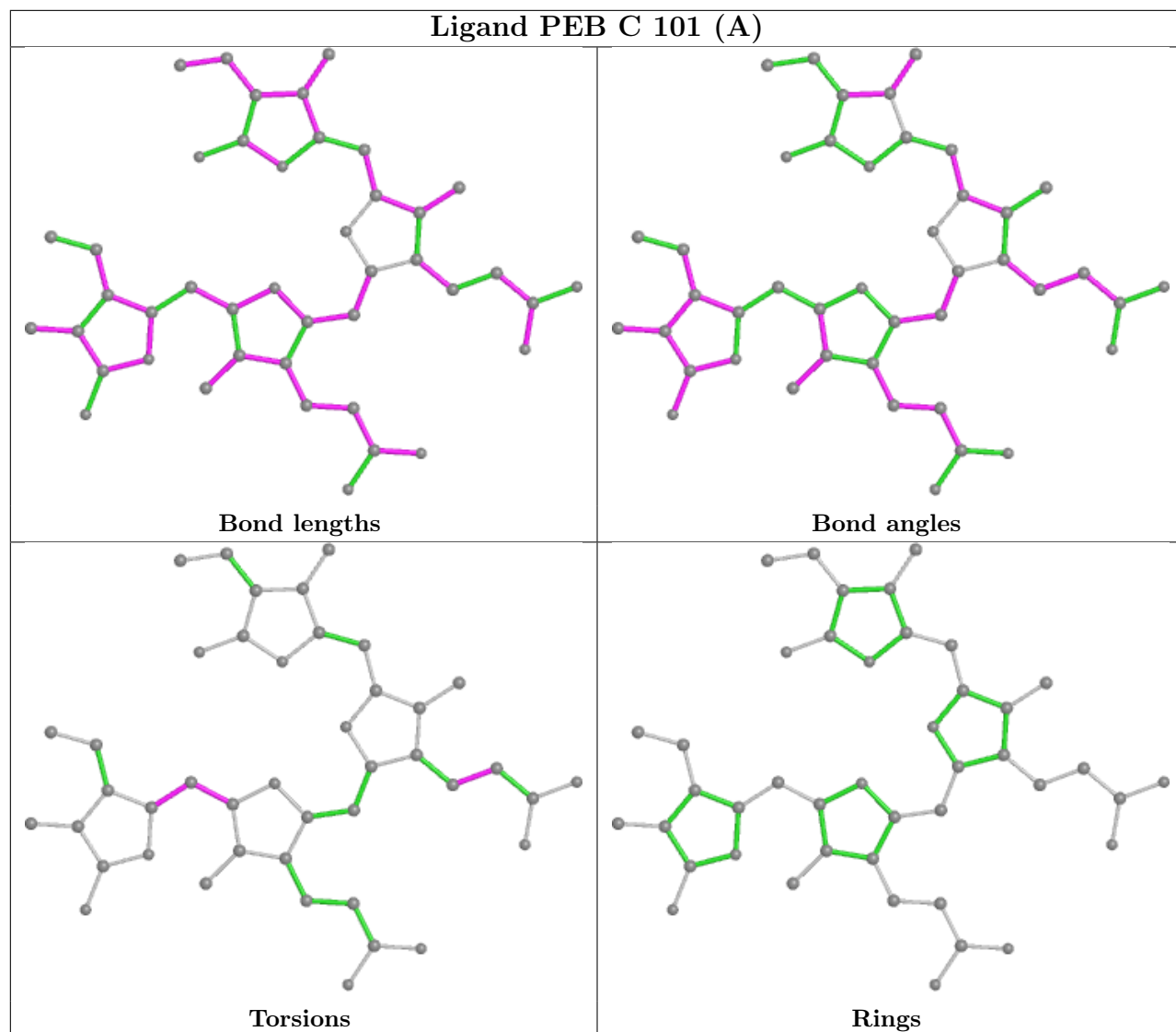


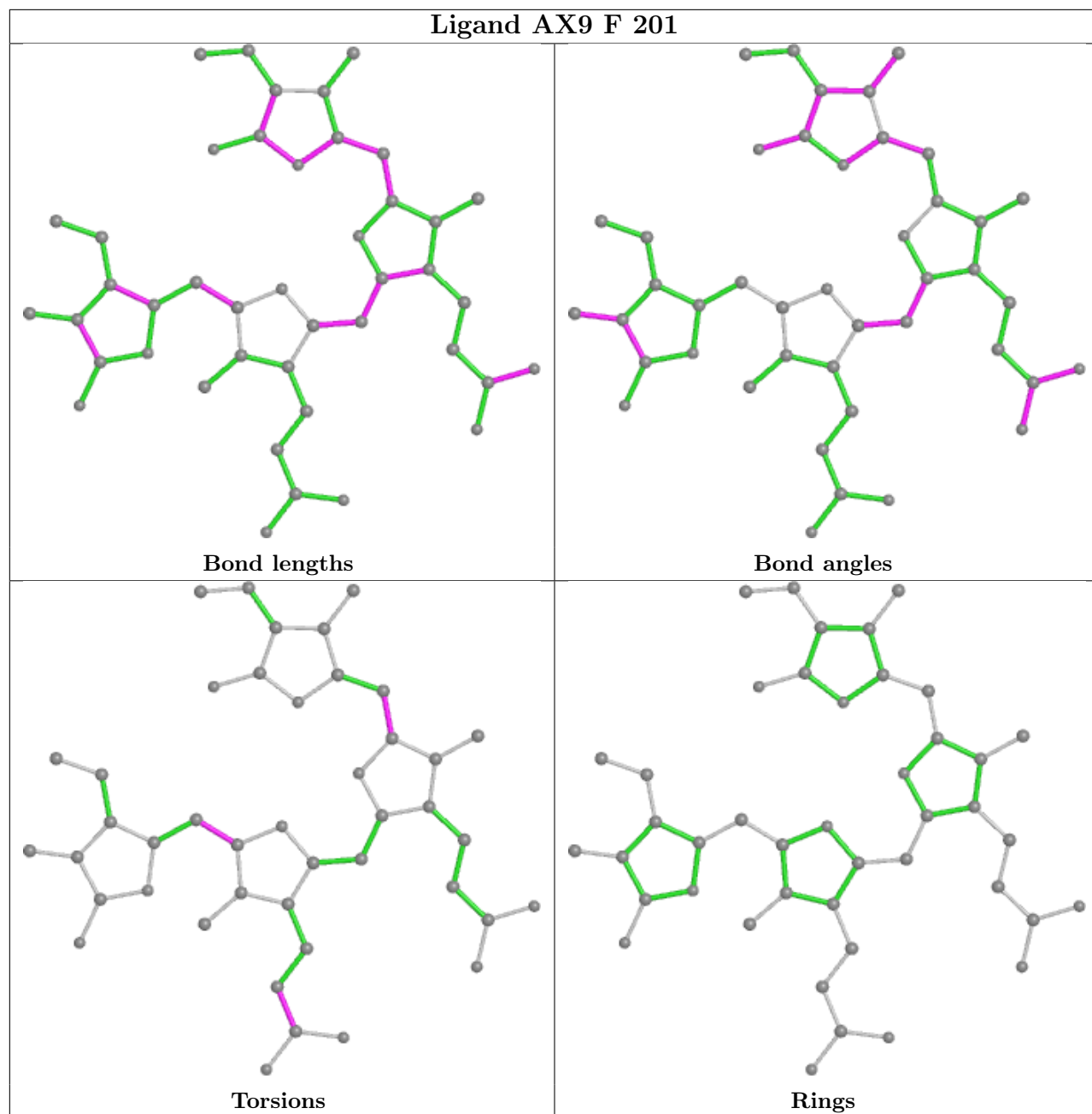


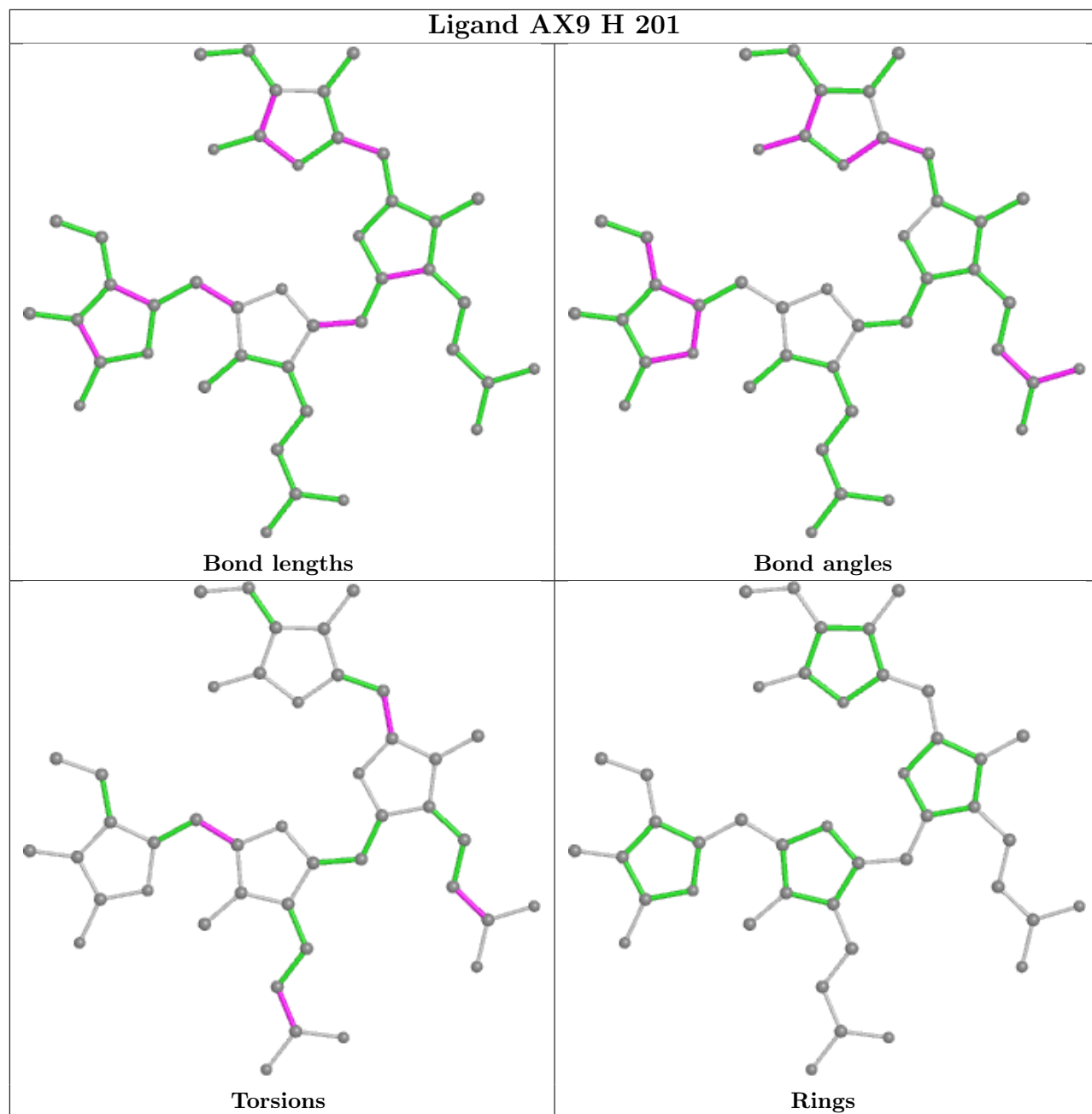


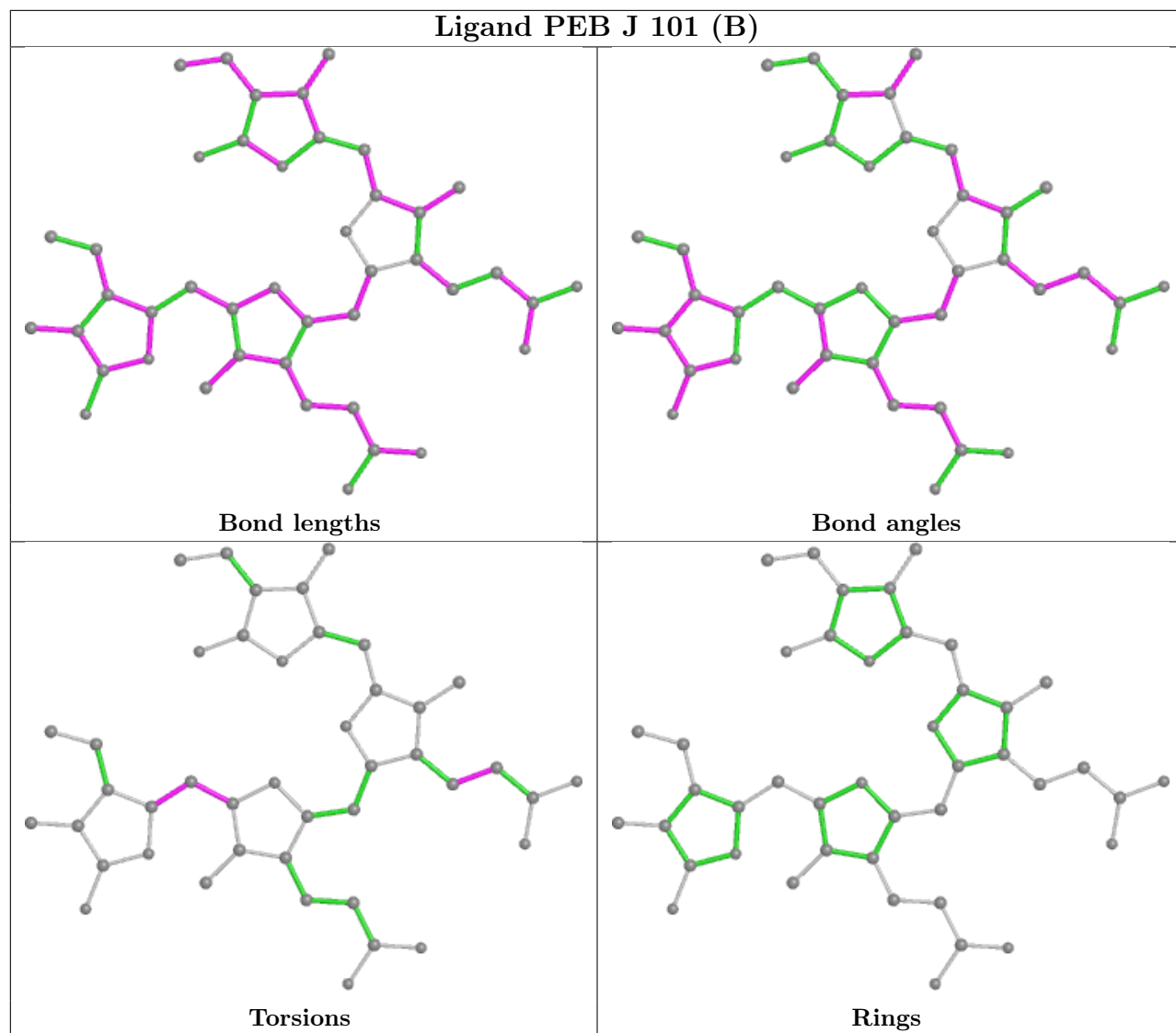


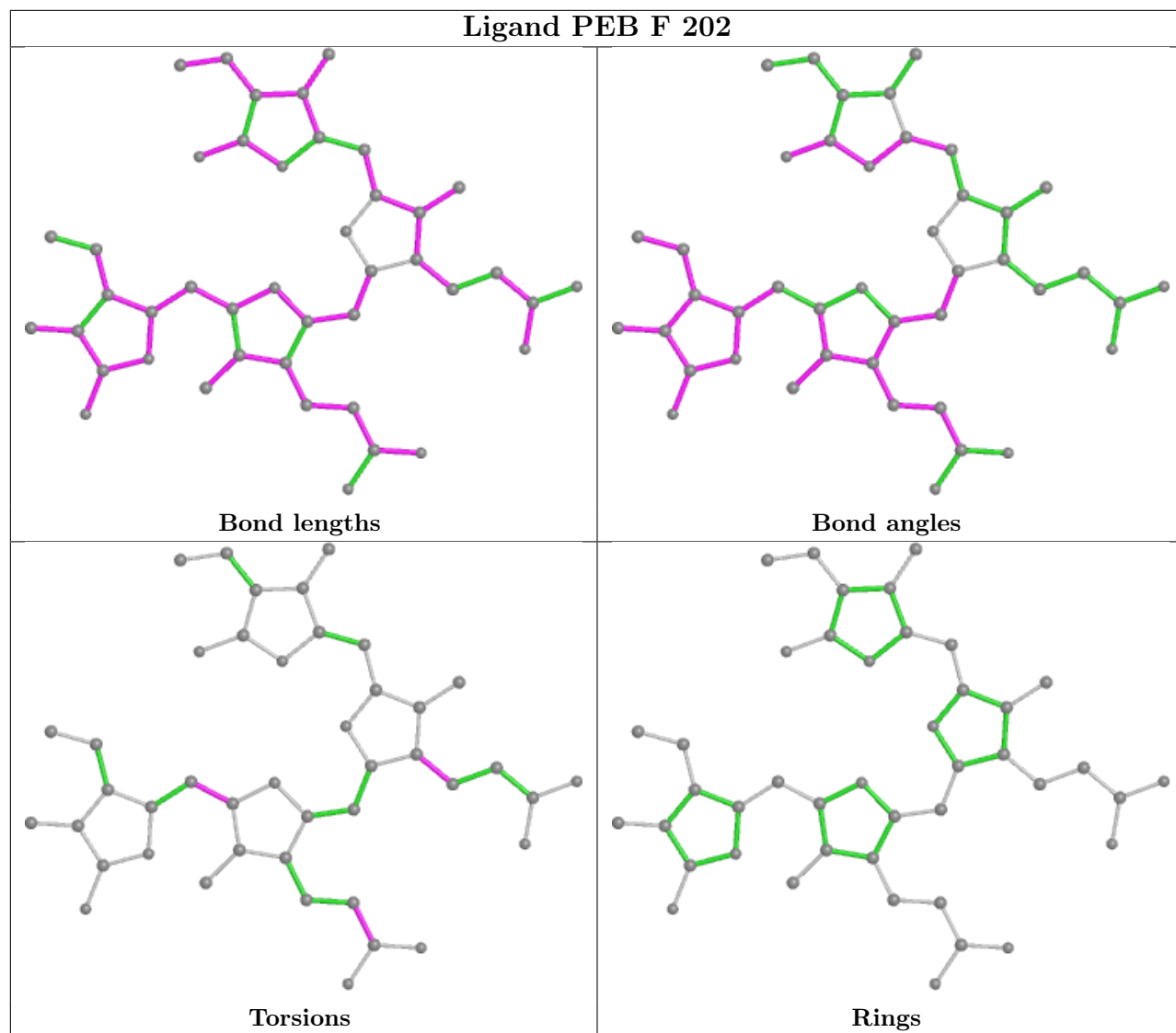


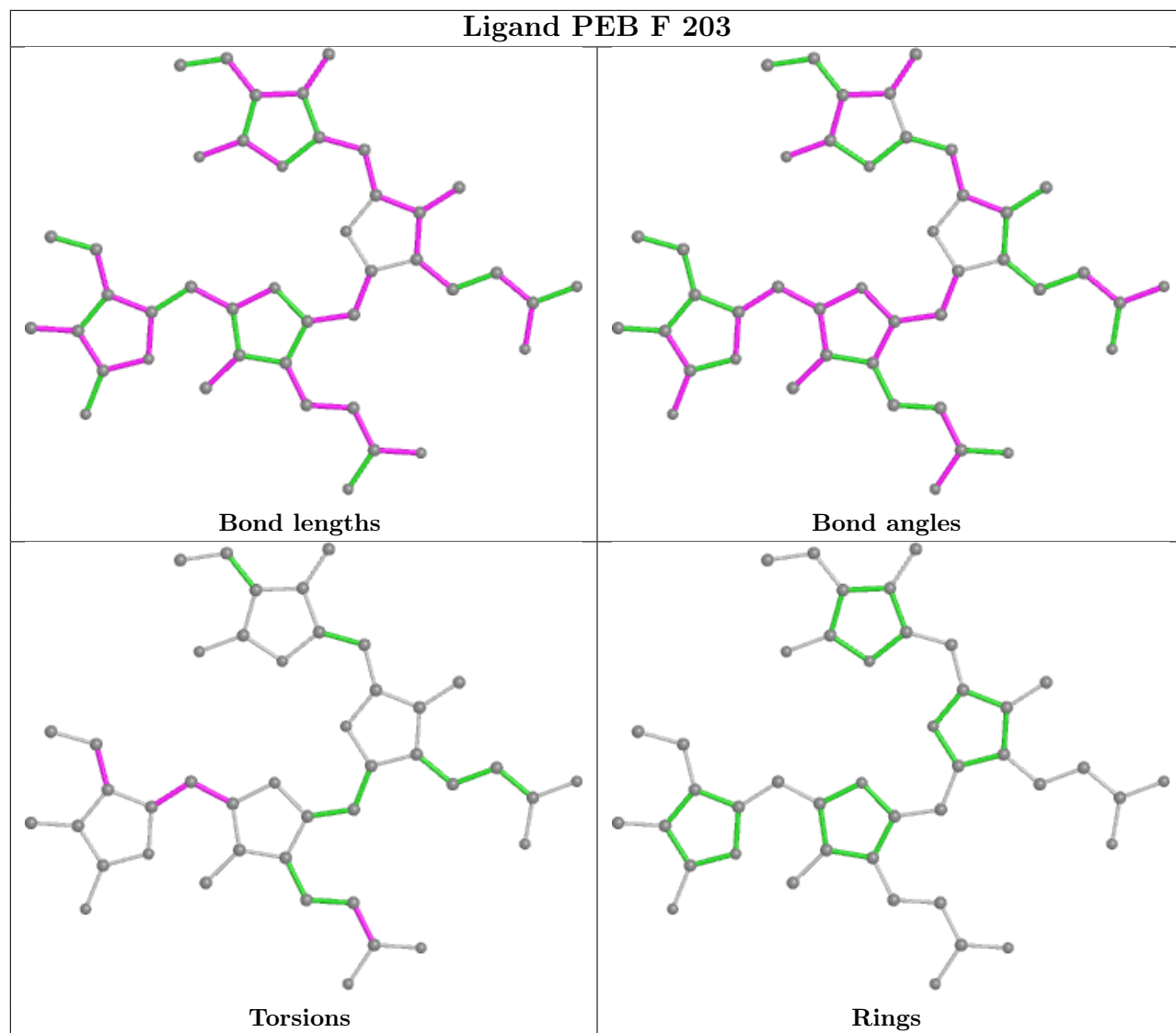


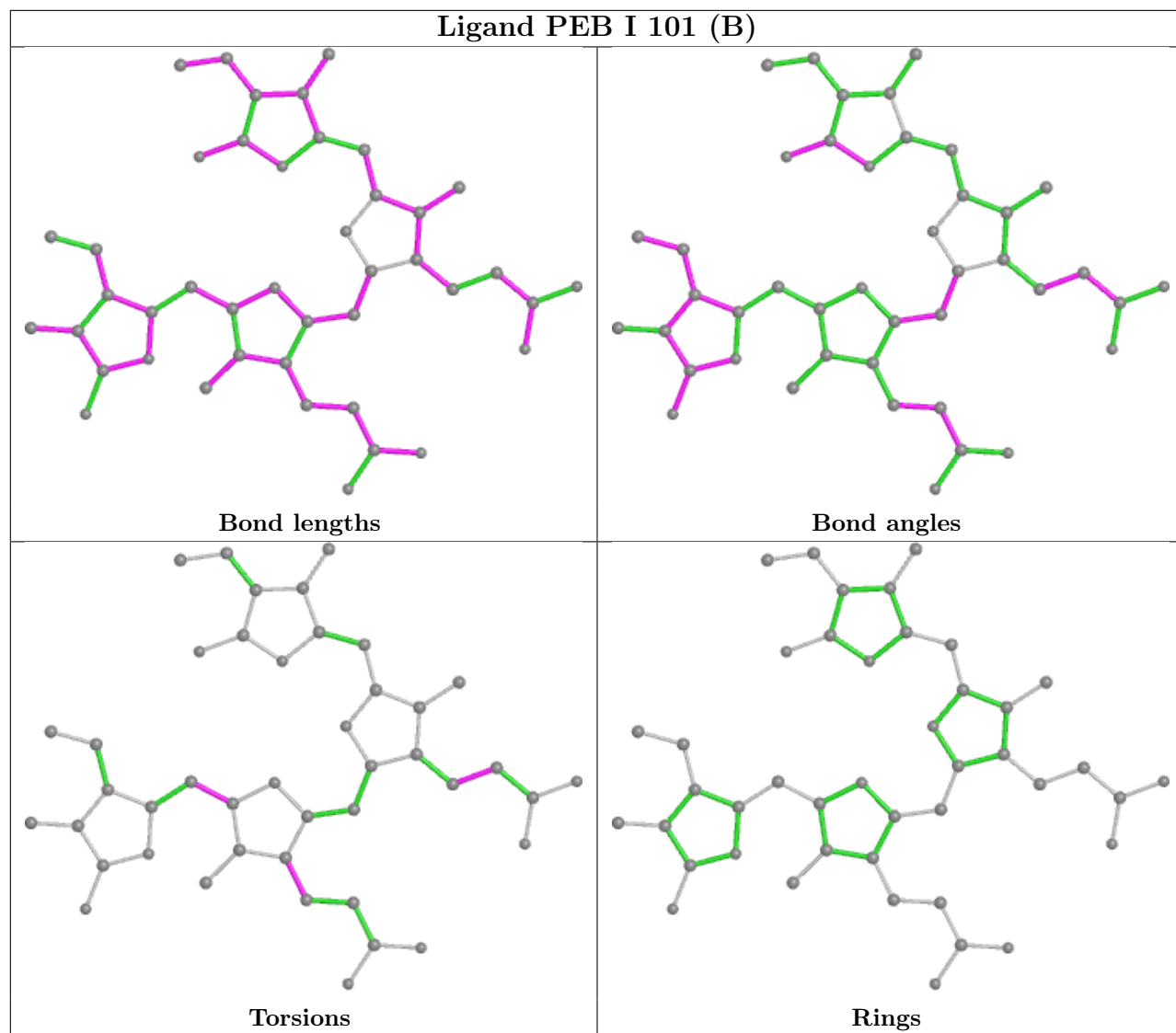


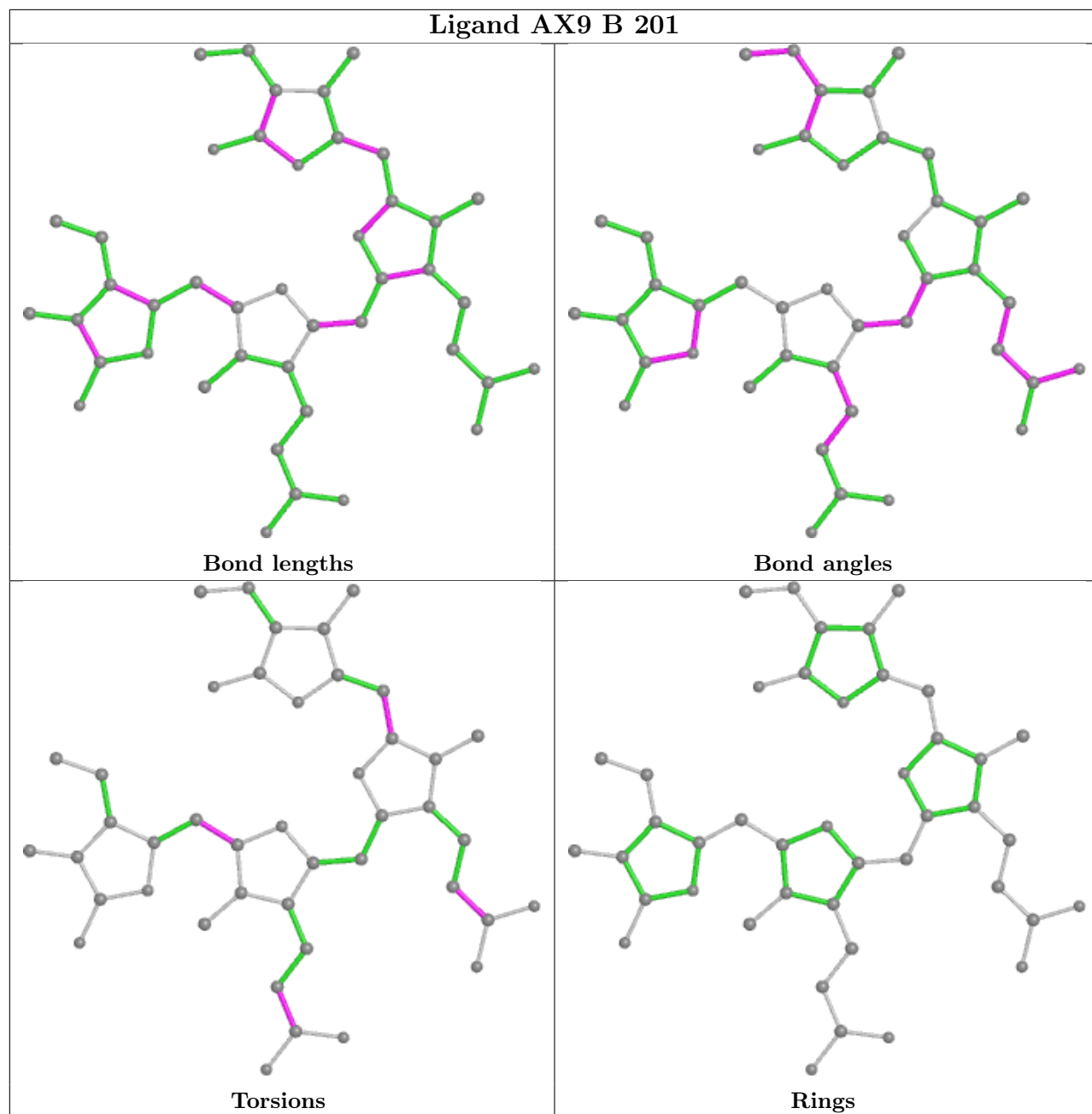


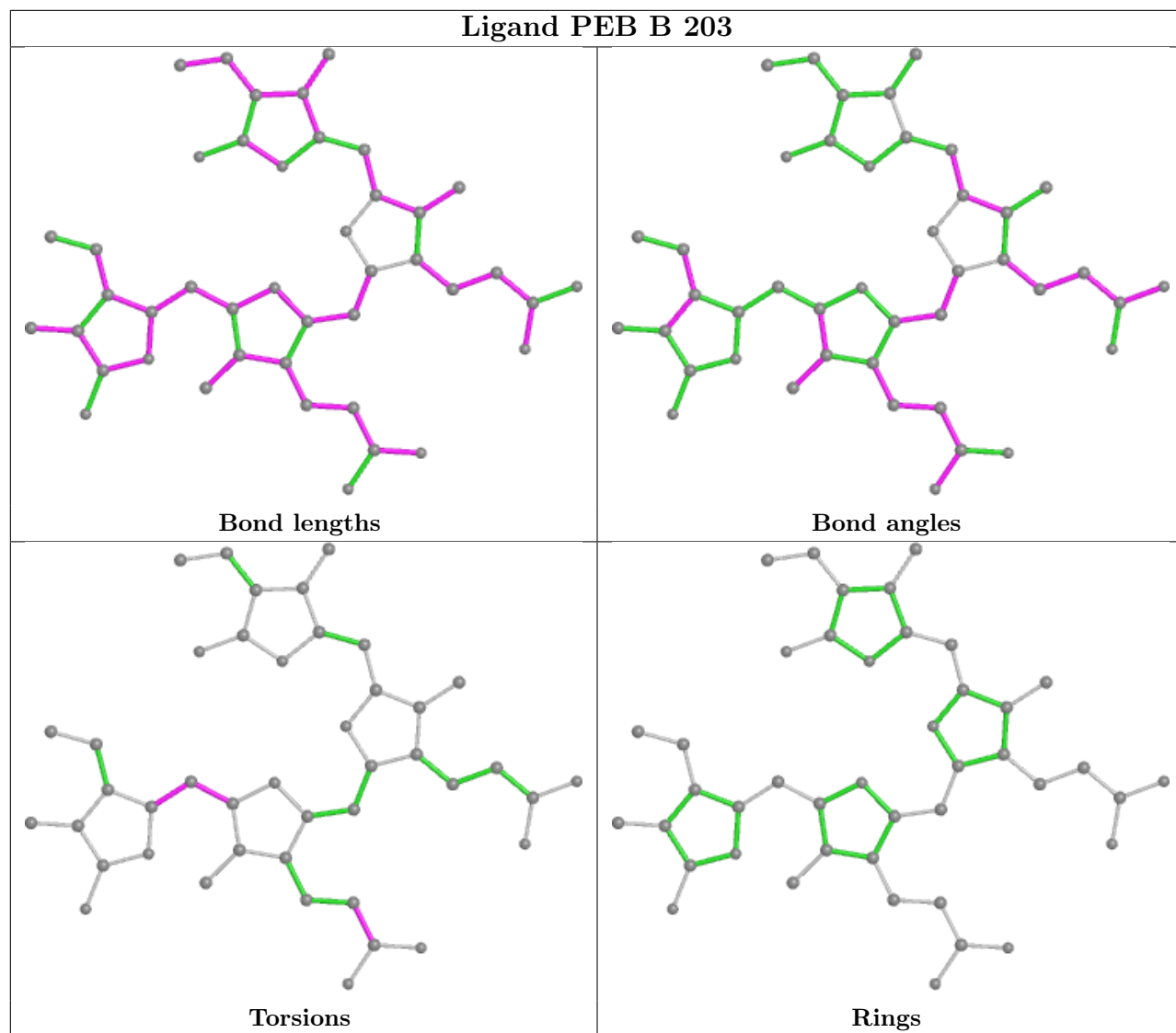


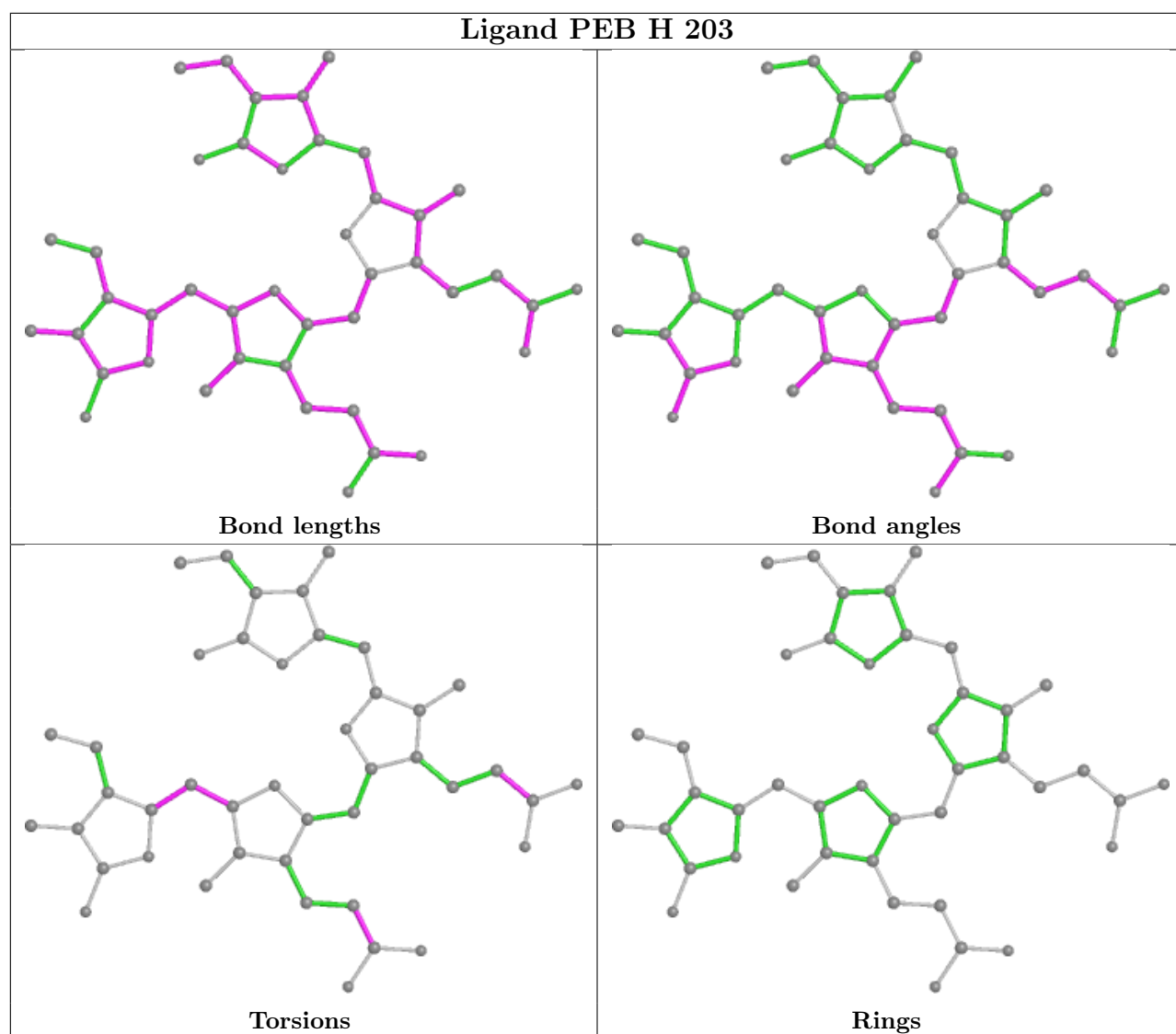


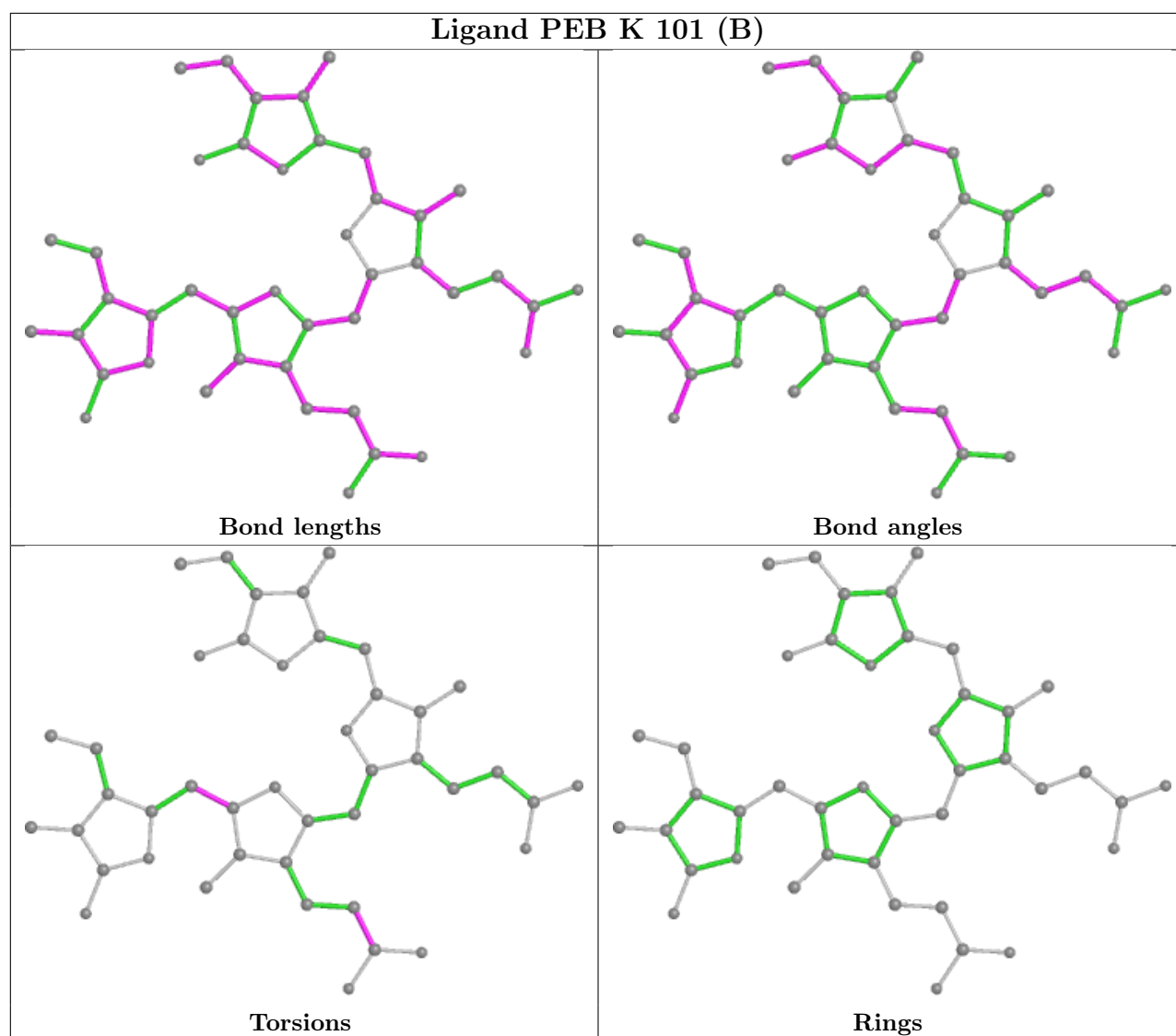












5.7 Other polymers [i](#)

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	63/67 (94%)	-0.09	3 (4%) 30 32	27, 37, 56, 87	63 (100%)
1	G	63/67 (94%)	-0.10	3 (4%) 30 32	24, 34, 54, 75	63 (100%)
1	J	63/67 (94%)	-0.22	3 (4%) 30 32	27, 36, 50, 70	63 (100%)
1	K	63/67 (94%)	-0.09	3 (4%) 30 32	27, 40, 55, 68	63 (100%)
2	B	173/177 (97%)	-0.14	4 (2%) 60 64	23, 36, 63, 118	0
2	D	174/177 (98%)	-0.22	4 (2%) 60 64	25, 38, 62, 80	0
2	F	173/177 (97%)	-0.11	2 (1%) 79 82	26, 40, 68, 98	0
2	H	173/177 (97%)	-0.35	1 (0%) 89 91	23, 34, 55, 68	0
3	C	61/62 (98%)	-0.31	0 100 100	27, 36, 52, 70	61 (100%)
3	E	61/62 (98%)	-0.26	0 100 100	27, 39, 54, 68	61 (100%)
3	I	61/62 (98%)	-0.22	0 100 100	27, 37, 56, 87	61 (100%)
3	L	61/62 (98%)	-0.26	2 (3%) 46 49	24, 34, 52, 75	61 (100%)
All	All	1189/1224 (97%)	-0.20	25 (2%) 63 67	23, 37, 60, 118	496 (41%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	12	ALA	11.0
1	G	62[A]	PHE	5.1
2	F	12	ALA	5.0
1	A	64[A]	ALA	4.4
1	K	64[B]	ALA	4.3
2	D	30	PHE	4.2
1	G	64[A]	ALA	4.2
2	B	177	ALA	3.6
2	B	11	SER	3.5
1	J	63[B]	GLY	3.4
1	J	62[B]	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
1	K	62[B]	PHE	3.2
1	G	63[A]	GLY	2.8
1	K	63[B]	GLY	2.7
2	B	10	THR	2.5
2	D	177	ALA	2.5
3	L	62[B]	LEU	2.5
1	A	63[A]	GLY	2.4
1	J	64[B]	ALA	2.4
3	L	61[B]	LEU	2.3
1	A	62[A]	PHE	2.2
2	D	7	LYS	2.2
2	H	30	PHE	2.1
2	D	12	ALA	2.1
2	F	177	ALA	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
3	LYZ	C	4[A]	10/11	0.90	0.09	40,52,73,87	21
1	LYZ	J	4[B]	10/11	0.90	0.09	40,52,73,87	21
3	LYZ	E	4[A]	10/11	0.93	0.12	47,62,82,88	21
3	LYZ	I	4[B]	10/11	0.93	0.08	34,44,59,63	21
1	LYZ	A	4[A]	10/11	0.93	0.08	34,44,59,63	21
1	LYZ	K	4[B]	10/11	0.93	0.12	47,62,82,88	21
1	LYZ	G	4[A]	10/11	0.95	0.10	32,47,63,75	21
3	LYZ	L	4[B]	10/11	0.95	0.10	32,47,63,75	21

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

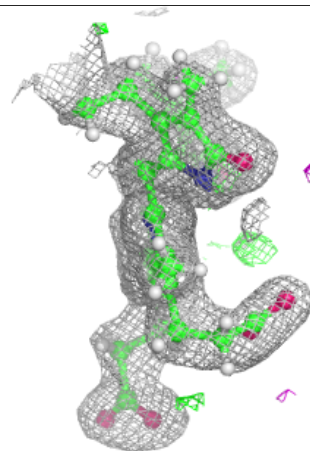
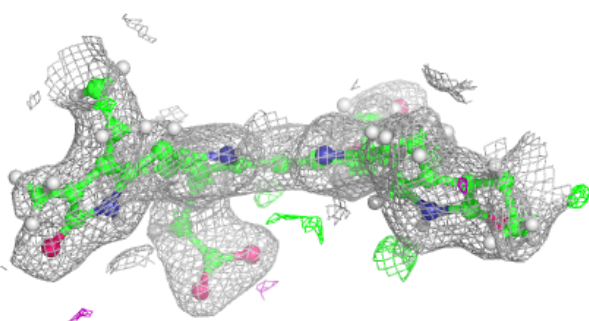
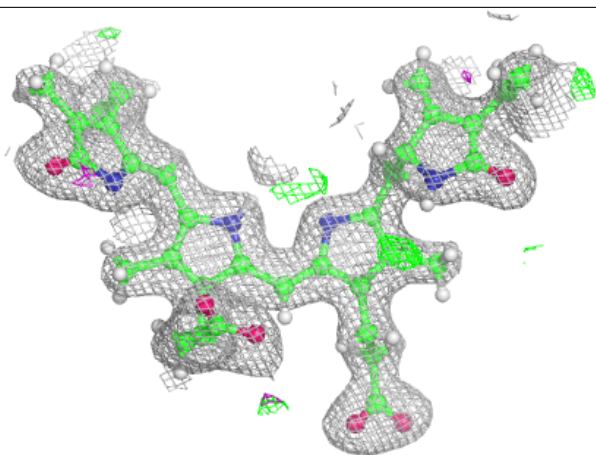
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	GOL	E	102[A]	6/6	0.90	0.11	30,46,55,56	13
6	GOL	K	102[B]	6/6	0.90	0.11	30,46,55,56	13
6	GOL	G	102[A]	6/6	0.92	0.12	31,51,65,65	14
5	AX9	F	201	43/43	0.92	0.09	28,41,57,62	0
6	GOL	L	102[B]	6/6	0.92	0.12	31,51,65,65	14
6	GOL	C	102[A]	6/6	0.93	0.16	33,42,50,54	13
6	GOL	J	102[B]	6/6	0.93	0.16	33,42,50,54	13
4	PEB	J	101[B]	43/43	0.94	0.09	25,33,53,80	80
4	PEB	L	101[B]	43/43	0.94	0.10	25,36,66,86	80
5	AX9	B	201	43/43	0.94	0.08	26,38,54,54	0
5	AX9	D	201	43/43	0.94	0.08	29,38,50,52	0
4	PEB	A	101[A]	43/43	0.94	0.10	25,37,78,94	80
5	AX9	H	201	43/43	0.94	0.08	24,38,52,59	0
4	PEB	B	203	43/43	0.94	0.10	27,38,54,56	0
4	PEB	C	101[A]	43/43	0.94	0.09	25,33,53,80	80
4	PEB	F	202	43/43	0.94	0.10	24,39,57,58	0
4	PEB	G	101[A]	43/43	0.94	0.10	25,36,66,86	80
4	PEB	H	202	43/43	0.94	0.11	21,31,44,50	0
4	PEB	I	101[B]	43/43	0.94	0.10	25,37,78,94	80
4	PEB	K	101[B]	43/43	0.95	0.10	25,33,54,80	80
4	PEB	D	202	43/43	0.95	0.08	24,34,47,50	0
4	PEB	D	203	43/43	0.95	0.09	23,32,43,48	0
4	PEB	H	203	43/43	0.95	0.08	20,32,42,42	0
4	PEB	E	101[A]	43/43	0.95	0.10	25,33,54,80	80
4	PEB	B	202	43/43	0.95	0.09	21,31,42,65	0
4	PEB	F	203	43/43	0.96	0.08	20,32,42,44	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.

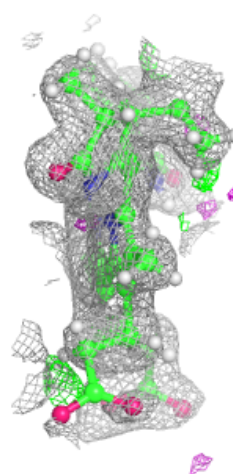
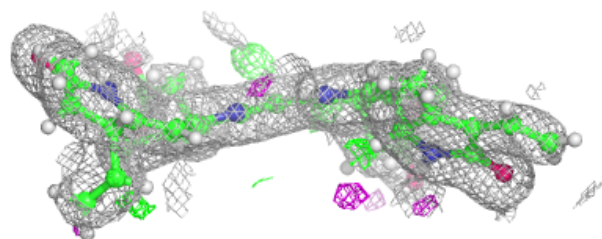
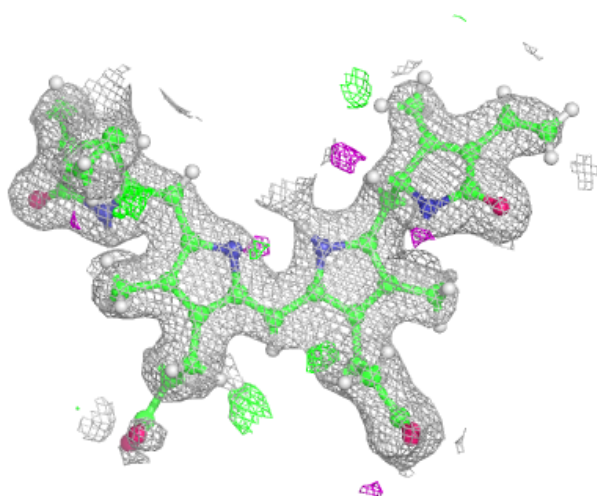
Electron density around AX9 F 201:

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



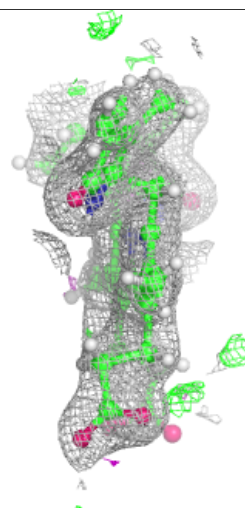
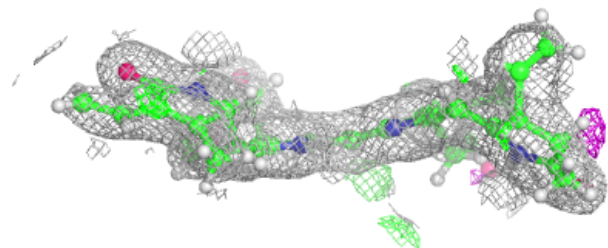
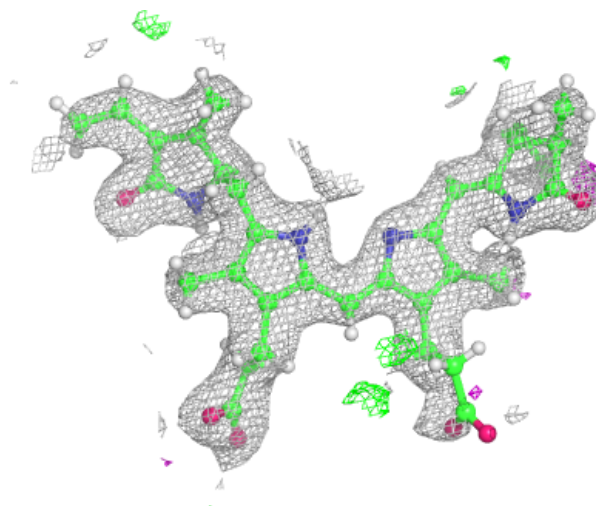
Electron density around PEB J 101 (B):

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



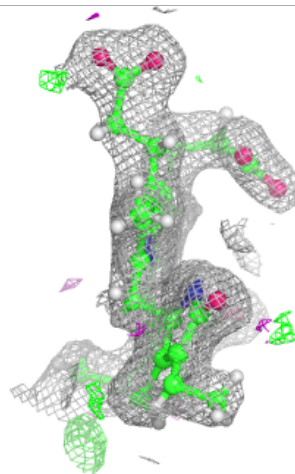
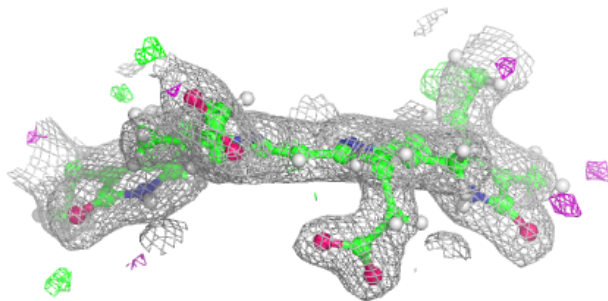
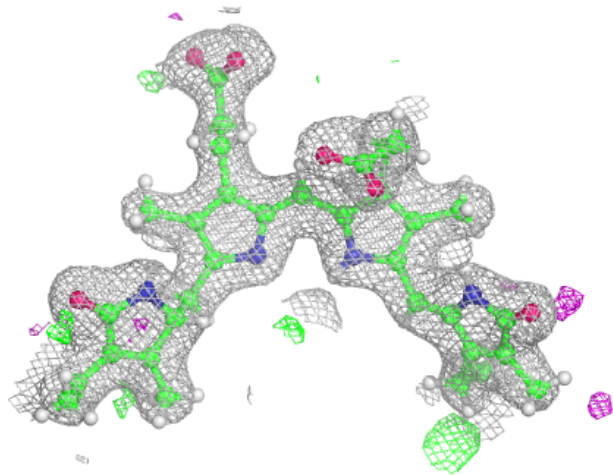
Electron density around PEB L 101 (B):

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



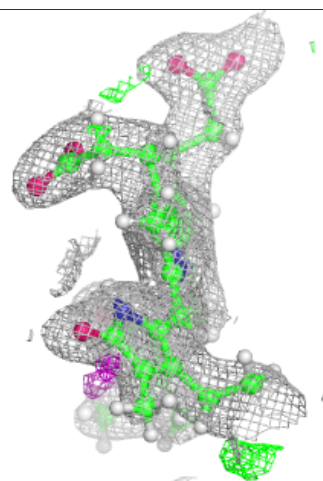
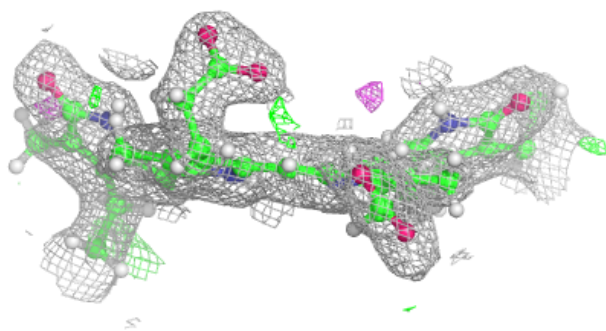
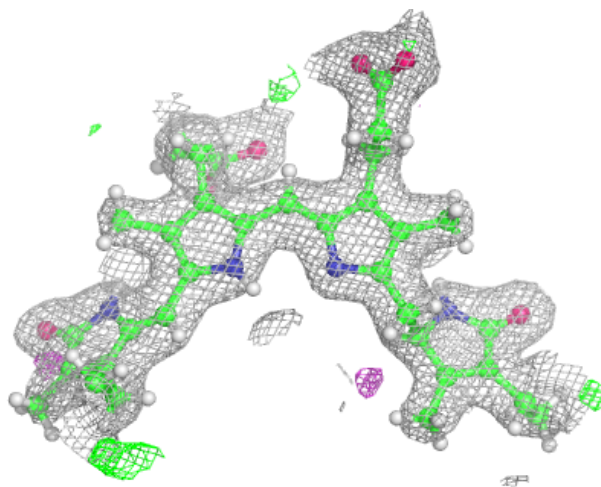
Electron density around AX9 B 201:

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and green (positive)



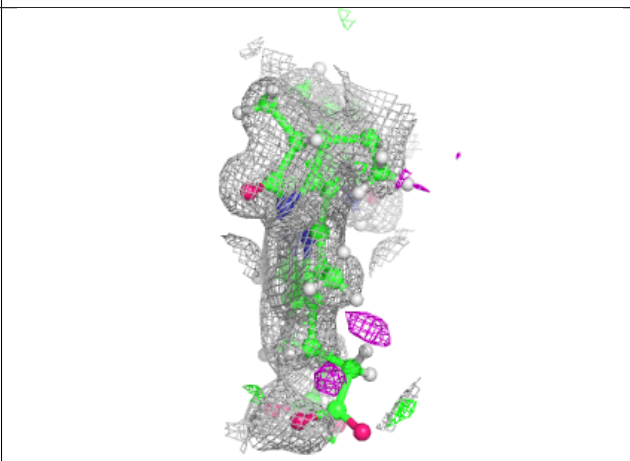
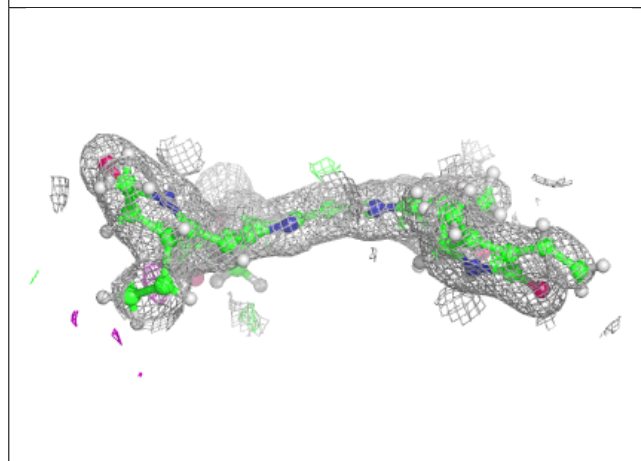
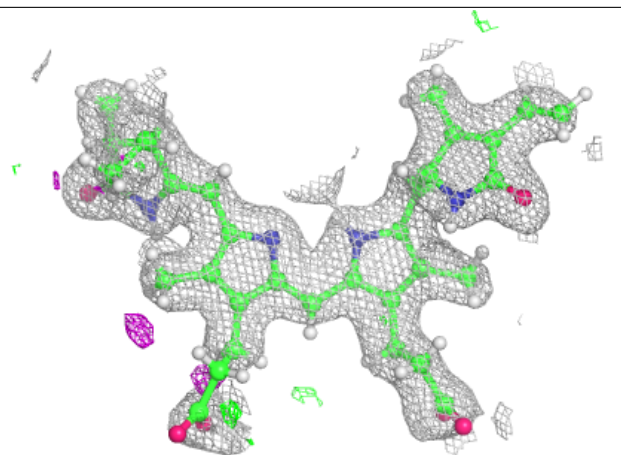
Electron density around AX9 D 201:

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



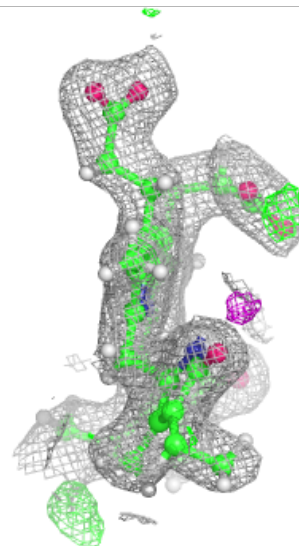
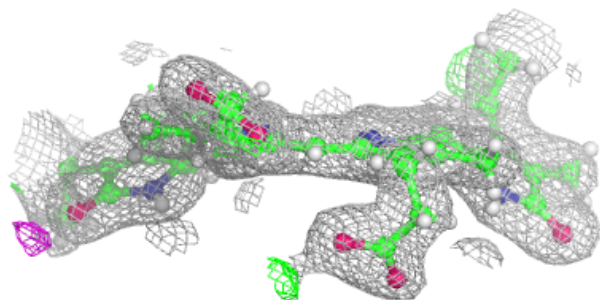
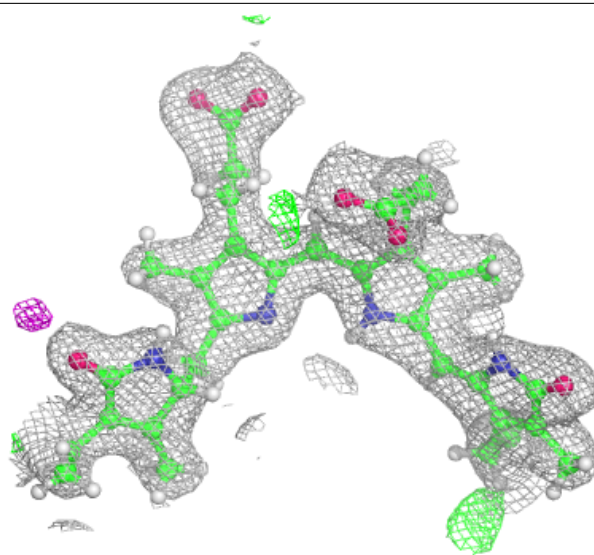
Electron density around PEB A 101 (A):

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



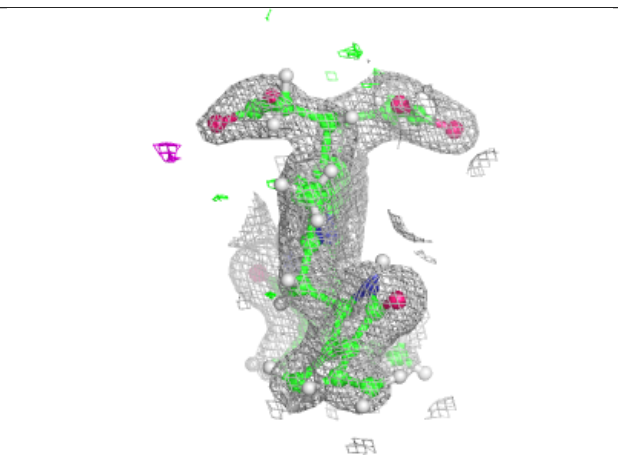
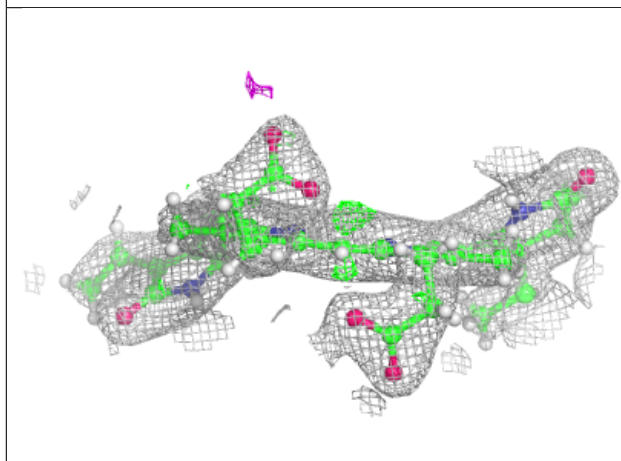
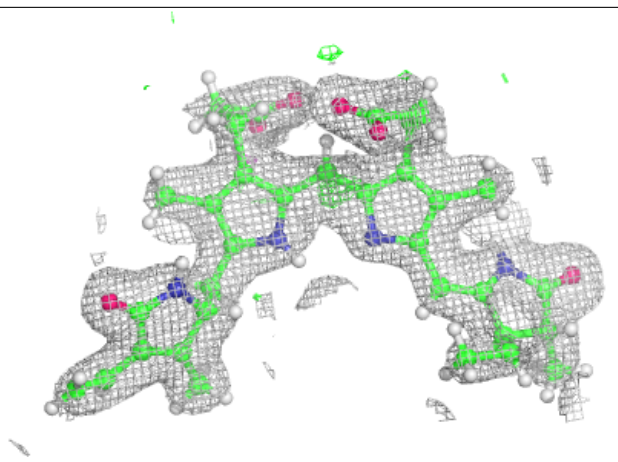
Electron density around AX9 H 201:

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



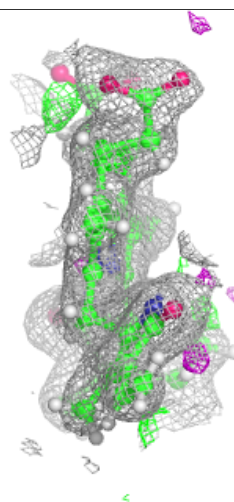
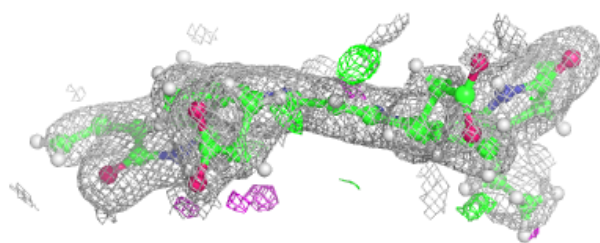
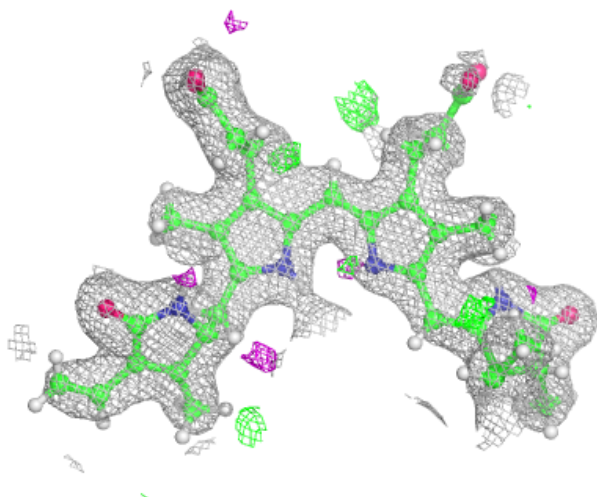
Electron density around PEB B 203:

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



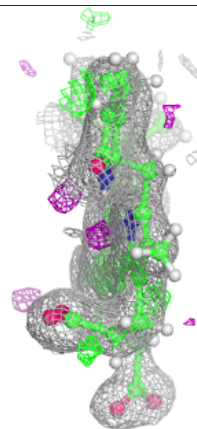
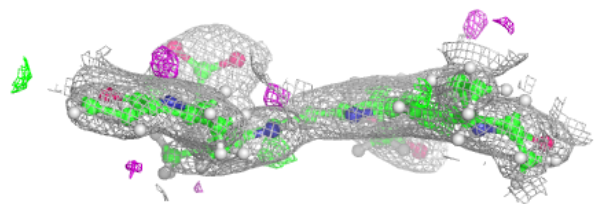
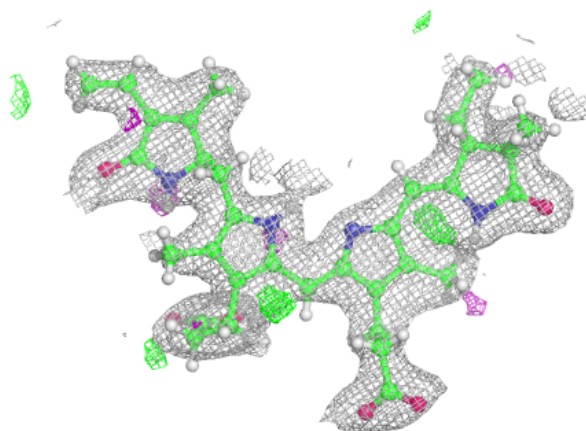
Electron density around PEB C 101 (A):

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



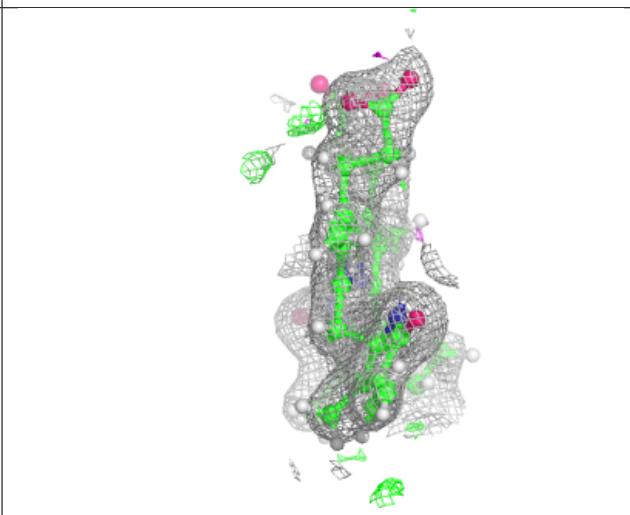
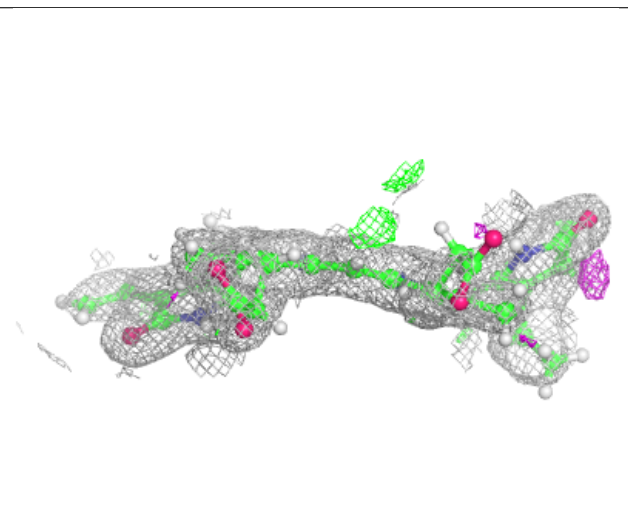
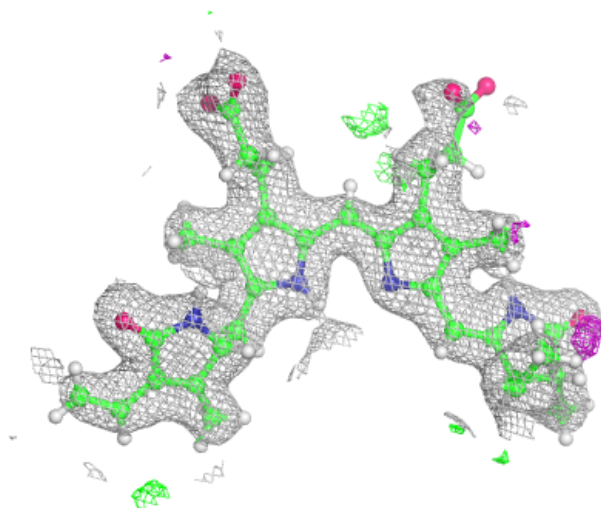
Electron density around PEB F 202:

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



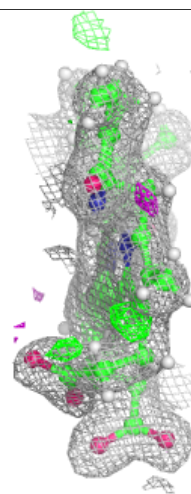
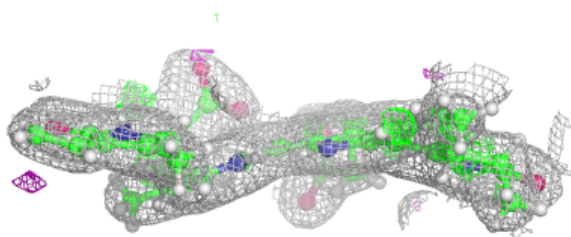
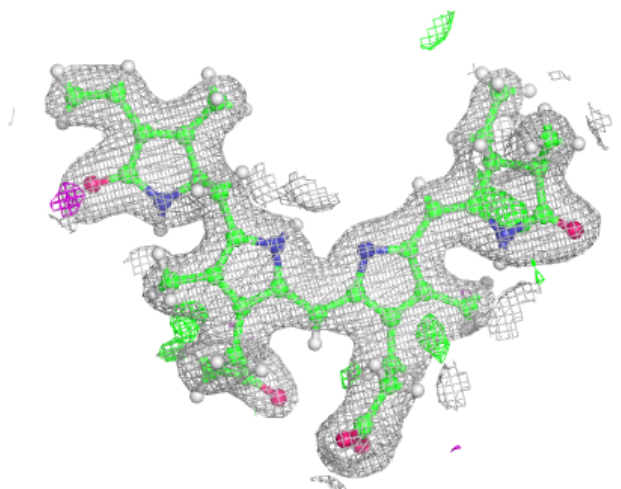
Electron density around PEB G 101 (A):

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



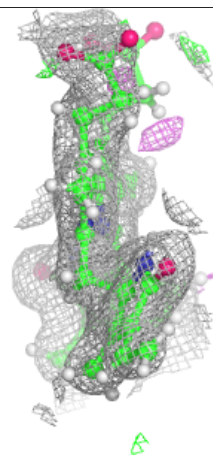
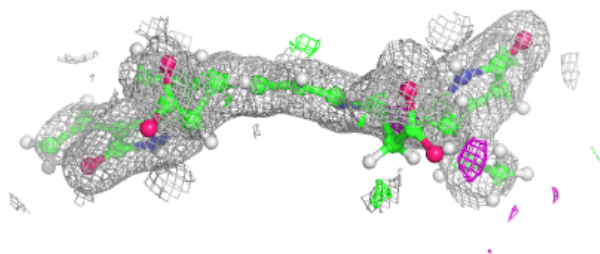
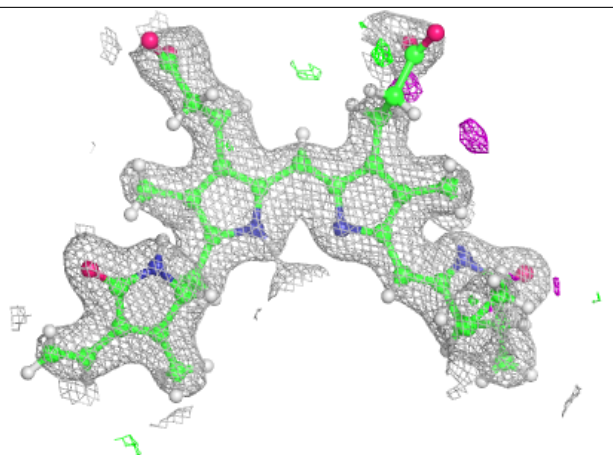
Electron density around PEB H 202:

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



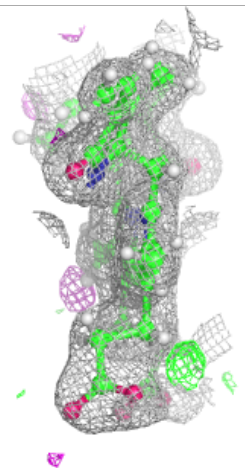
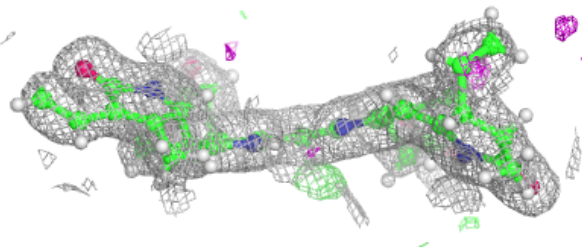
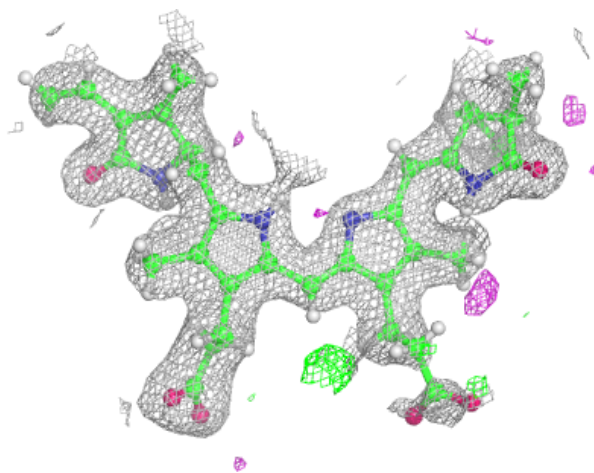
Electron density around PEB I 101 (B):

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



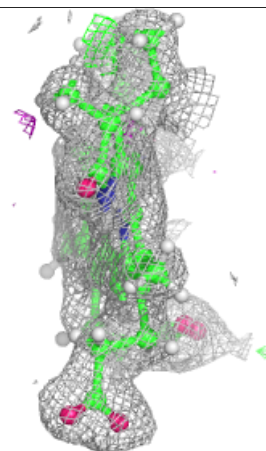
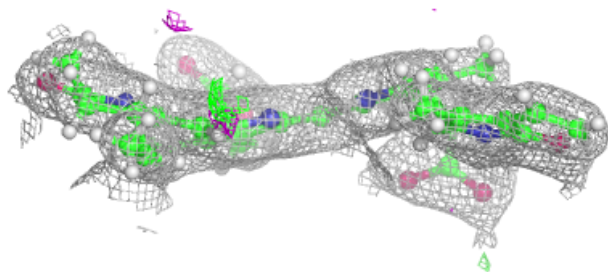
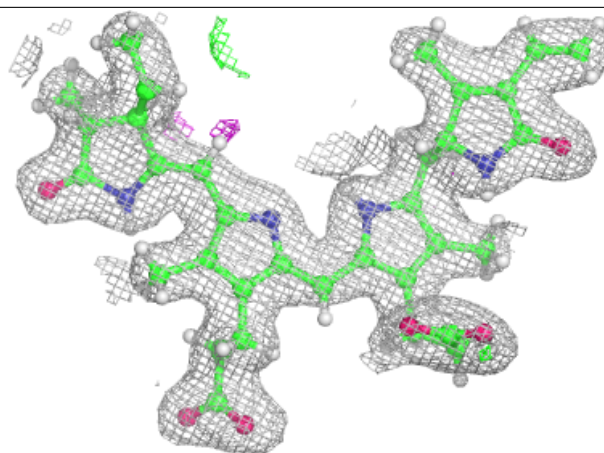
Electron density around PEB K 101 (B):

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



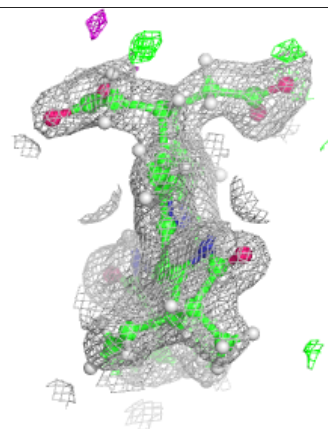
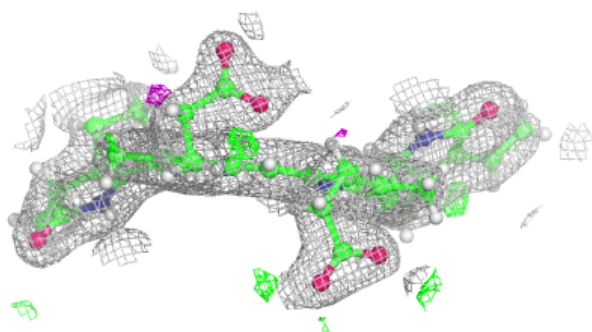
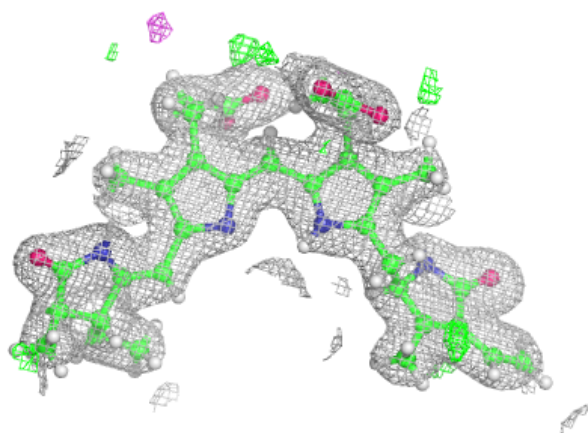
Electron density around PEB D 202:

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

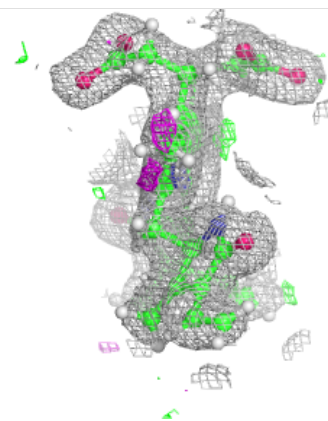
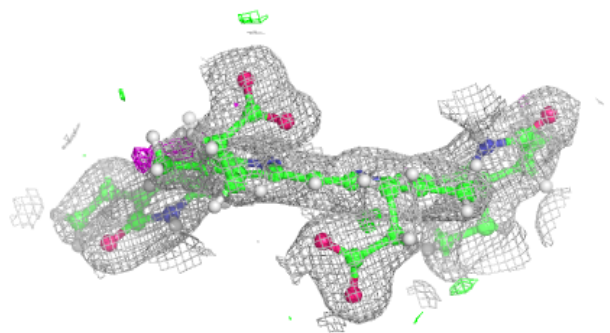
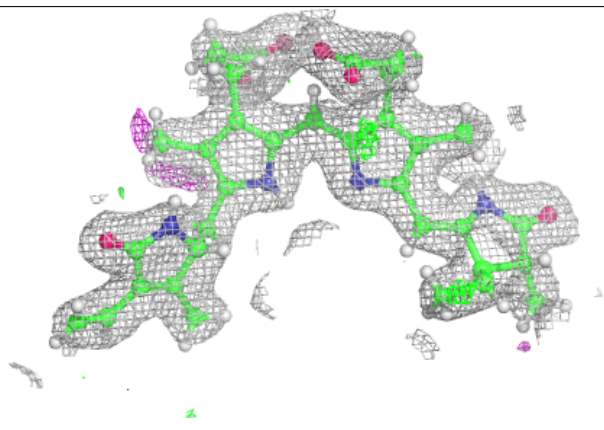


Electron density around PEB D 203:

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

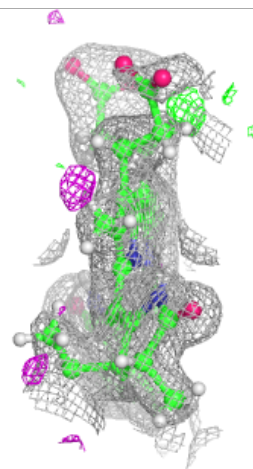
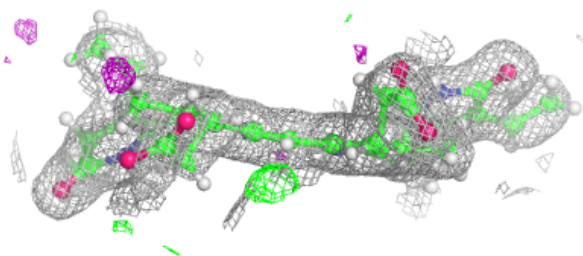
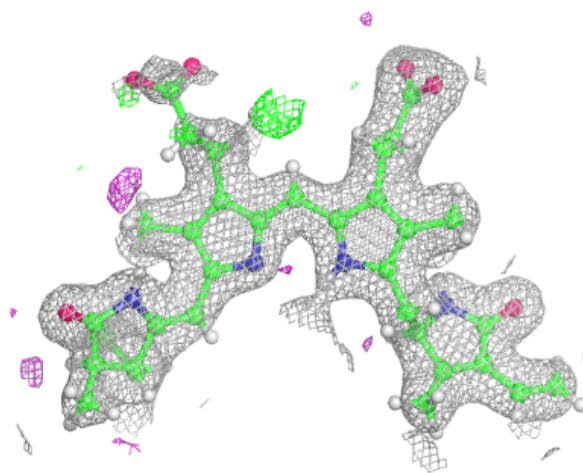
**Electron density around PEB H 203:**

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



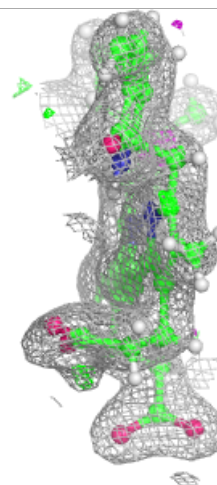
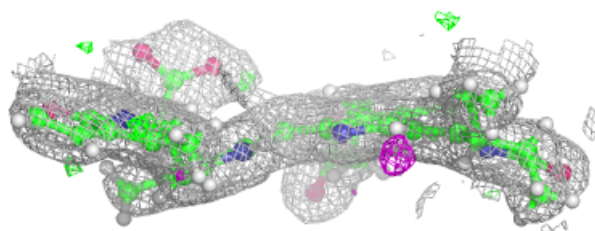
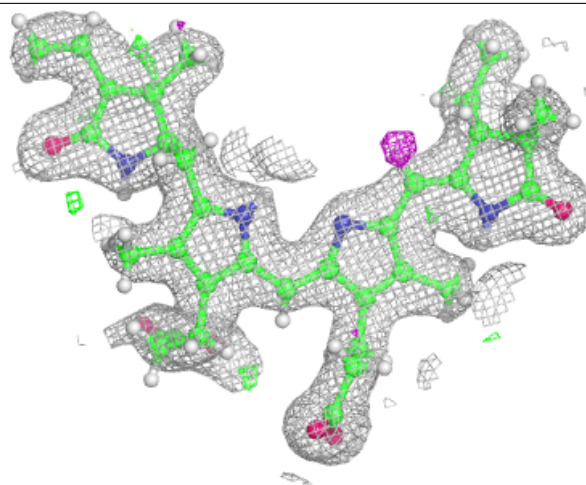
Electron density around PEB E 101 (A):

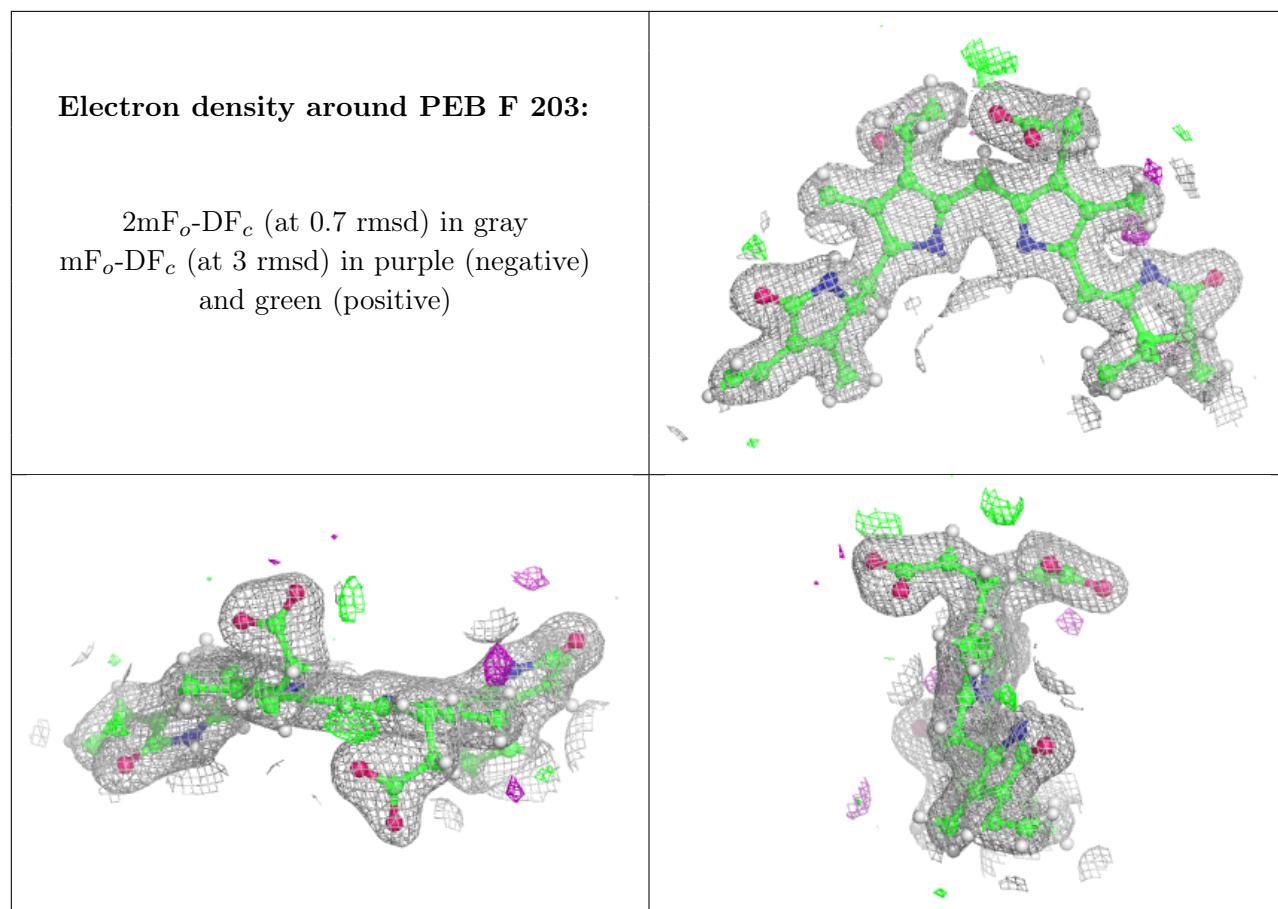
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around PEB B 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.