



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 08:12 PM UTC

PDB ID : 7LQ5 / pdb_00007lq5
EMDB ID : EMD-23481
Title : Cryo-EM structure of OmcZ nanowire from *Geobacter sulfurreducens*
Authors : Gu, Y.; Srikanth, V.; Malvankar, N.S.; Samatey, F.A.
Deposited on : 2021-02-13
Resolution : 3.40 Å (reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

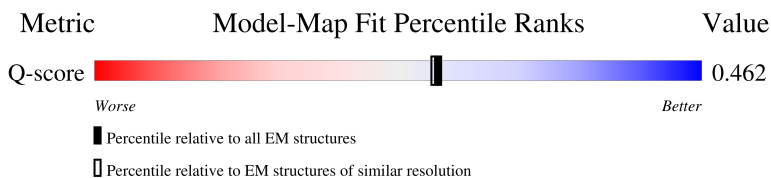
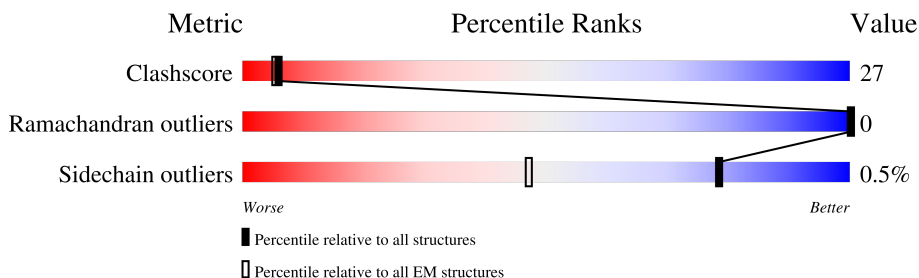
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

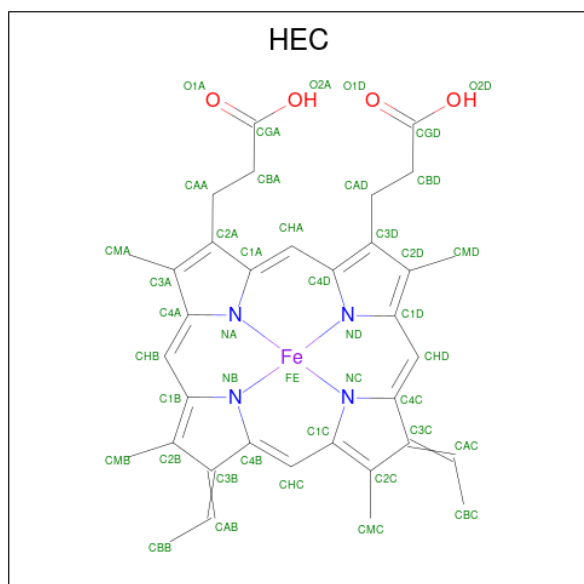
Mol	Chain	Length	Quality of chain
1	A	258	 59% 41%
1	B	258	 60% 40%
1	C	258	 6% 60% 40%

In the tables below, 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 Cytochrome c.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	258	Total 1937	C 1198	N 348	O 373	S 18	0	0
1	B	258	Total 1937	C 1198	N 348	O 373	S 18	0	0
1	C	258	Total 1937	C 1198	N 348	O 373	S 18	0	0

- Molecule 2 is HEME C (CCD ID: HEC) (formula: $\text{C}_{34}\text{H}_{34}\text{FeN}_4\text{O}_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0

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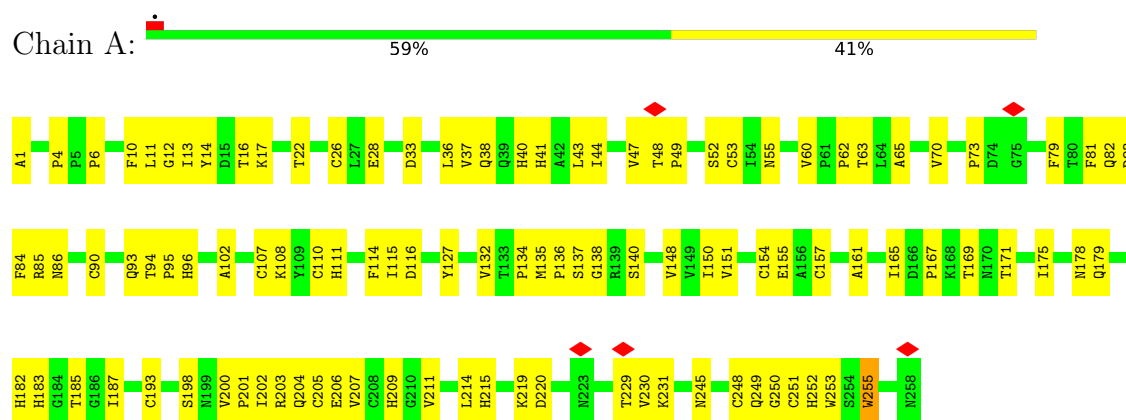
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Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0

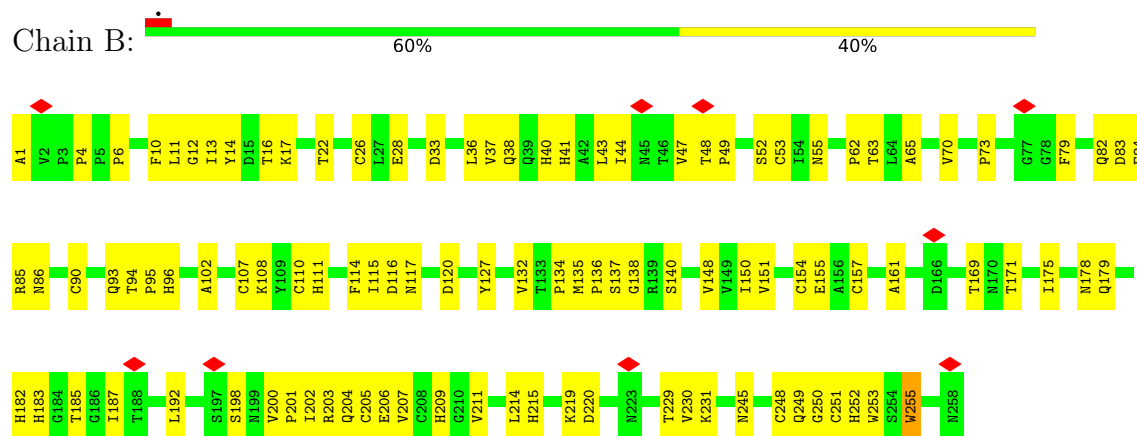
3 Residue-property plots

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

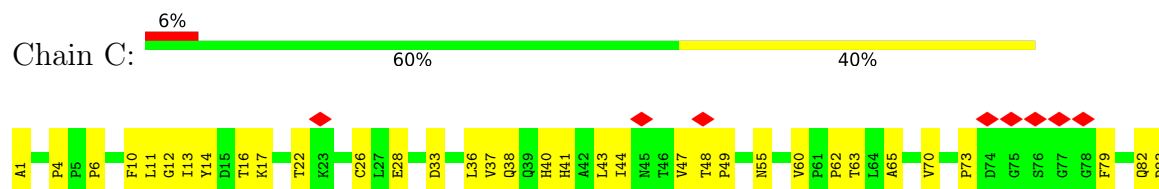
• Molecule 1: Cytochrome c

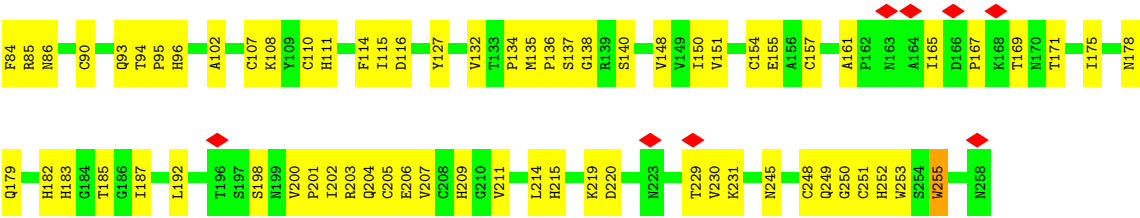


• Molecule 1: Cytochrome c



• Molecule 1: Cytochrome c





4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-159.1°, rise=57.8 Å, axial sym=C1	Depositor
Number of segments used	128409	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.2	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.106	Depositor
Minimum map value	-0.061	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.012	Depositor
Map size (Å)	317.952, 317.952, 317.952	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.828, 0.828, 0.828	Depositor

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: HEC

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	0.59	0/1996	0.68	0/2741
1	B	0.59	0/1996	0.68	0/2741
1	C	0.59	0/1996	0.68	0/2741
All	All	0.59	0/5988	0.68	0/8223

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	1937	0	1796	111	0
1	B	1937	0	1796	117	0
1	C	1937	0	1796	109	0
2	A	344	0	240	37	0
2	B	344	0	240	38	0
2	C	344	0	240	35	0
All	All	6843	0	6108	344	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 27.

All (344) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:204:GLN:O	1:C:207:VAL:HG12	1.79	0.83
1:B:204:GLN:O	1:B:207:VAL:HG12	1.79	0.83
1:A:204:GLN:O	1:A:207:VAL:HG12	1.79	0.82
1:B:11:LEU:HD12	1:B:219:LYS:HG2	1.63	0.81
1:A:11:LEU:HD12	1:A:219:LYS:HG2	1.63	0.80
1:C:11:LEU:HD12	1:C:219:LYS:HG2	1.63	0.79
1:C:179:GLN:HB2	2:C:306:HEC:HAD1	1.64	0.79
1:B:63:THR:HG22	1:B:65:ALA:H	1.48	0.79
1:A:63:THR:HG22	1:A:65:ALA:H	1.48	0.78
1:B:52:SER:HA	1:C:245:ASN:ND2	1.98	0.78
1:B:169:THR:HG22	1:B:171:THR:HG23	1.66	0.78
1:A:179:GLN:HB2	2:A:306:HEC:HAD1	1.64	0.77
1:C:17:LYS:HE3	1:C:22:THR:HA	1.67	0.77
1:A:17:LYS:HE3	1:A:22:THR:HA	1.66	0.77
1:B:179:GLN:HB2	2:B:306:HEC:HAD1	1.64	0.77
1:C:179:GLN:O	1:C:179:GLN:HG2	1.84	0.77
1:C:63:THR:HG22	1:C:65:ALA:H	1.48	0.77
1:C:169:THR:HG22	1:C:171:THR:HG23	1.66	0.77
1:C:17:LYS:CE	1:C:22:THR:HA	2.15	0.77
1:B:17:LYS:CE	1:B:22:THR:HA	2.15	0.77
1:B:179:GLN:HG2	1:B:179:GLN:O	1.84	0.77
1:A:17:LYS:CE	1:A:22:THR:HA	2.15	0.76
2:B:307:HEC:HBD1	2:B:307:HEC:HHA	1.67	0.76
1:B:17:LYS:HE3	1:B:22:THR:HA	1.67	0.76
1:A:179:GLN:O	1:A:179:GLN:HG2	1.84	0.76
1:A:169:THR:HG22	1:A:171:THR:HG23	1.66	0.76
1:B:52:SER:HA	1:C:245:ASN:HD21	1.49	0.76
2:A:307:HEC:HBD1	2:A:307:HEC:HHA	1.67	0.76
1:B:132:VAL:HG23	1:B:253:TRP:HE3	1.49	0.76
1:A:52:SER:HA	1:B:245:ASN:HD21	1.51	0.75
1:C:132:VAL:HG23	1:C:253:TRP:HE3	1.50	0.75
1:A:132:VAL:HG23	1:A:253:TRP:HE3	1.50	0.75
1:B:219:LYS:HG3	1:B:220:ASP:H	1.51	0.74
2:C:307:HEC:HBD1	2:C:307:HEC:HHA	1.67	0.74
1:A:219:LYS:HG3	1:A:220:ASP:H	1.52	0.74
1:A:52:SER:HA	1:B:245:ASN:ND2	2.03	0.74
1:C:219:LYS:HG3	1:C:220:ASP:H	1.52	0.74
1:B:82:GLN:HG3	1:B:83:ASP:H	1.53	0.74
1:C:13:ILE:HD11	2:C:307:HEC:O1D	1.88	0.74
1:A:219:LYS:HG3	1:A:220:ASP:N	2.03	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:ARG:NH2	2:B:302:HEC:O1A	2.21	0.73
1:C:85:ARG:NH2	2:C:302:HEC:O1A	2.21	0.73
1:A:13:ILE:HD11	2:A:307:HEC:O1D	1.88	0.73
1:B:13:ILE:HD11	2:B:307:HEC:O1D	1.88	0.72
1:B:219:LYS:HG3	1:B:220:ASP:N	2.03	0.72
1:A:85:ARG:NH2	2:A:302:HEC:O1A	2.21	0.72
1:C:82:GLN:HG3	1:C:83:ASP:H	1.53	0.72
1:C:219:LYS:HG3	1:C:220:ASP:N	2.03	0.72
1:A:82:GLN:HG3	1:A:83:ASP:H	1.53	0.71
1:B:53:CYS:H	1:C:245:ASN:HD21	1.35	0.71
1:B:255:TRP:O	1:B:255:TRP:CD1	2.44	0.71
1:A:136:PRO:HD2	1:A:201:PRO:HB2	1.73	0.71
1:C:136:PRO:HD2	1:C:201:PRO:HB2	1.73	0.71
1:C:127:TYR:O	1:C:203:ARG:NH2	2.24	0.70
1:C:255:TRP:CD1	1:C:255:TRP:O	2.44	0.70
1:A:255:TRP:O	1:A:255:TRP:CD1	2.44	0.70
1:A:127:TYR:O	1:A:203:ARG:NH2	2.24	0.70
1:A:53:CYS:H	1:B:245:ASN:HD21	1.39	0.70
1:B:1:ALA:N	1:B:155:GLU:O	2.23	0.69
1:B:127:TYR:O	1:B:203:ARG:NH2	2.24	0.69
1:B:136:PRO:HD2	1:B:201:PRO:HB2	1.73	0.69
1:A:1:ALA:N	1:A:155:GLU:O	2.23	0.69
1:C:1:ALA:N	1:C:155:GLU:O	2.23	0.69
1:B:53:CYS:N	1:C:245:ASN:HD21	1.90	0.68
1:A:84:PHE:HE1	1:A:85:ARG:HH21	1.41	0.67
1:B:137:SER:HA	1:B:155:GLU:HB2	1.77	0.67
2:B:306:HEC:HBA2	2:B:306:HEC:HHA	1.77	0.67
1:A:53:CYS:N	1:B:245:ASN:HD21	1.93	0.67
1:B:84:PHE:HE1	1:B:85:ARG:HH21	1.41	0.67
1:A:137:SER:HA	1:A:155:GLU:HB2	1.77	0.66
1:C:137:SER:HA	1:C:155:GLU:HB2	1.77	0.66
2:C:306:HEC:HBA2	2:C:306:HEC:HHA	1.77	0.66
1:B:161:ALA:HB3	1:B:175:ILE:HD12	1.78	0.66
1:C:96:HIS:HB3	2:C:304:HEC:HBC2	1.78	0.66
2:A:306:HEC:HBA2	2:A:306:HEC:HHA	1.77	0.66
1:A:96:HIS:HB3	2:A:304:HEC:HBC2	1.78	0.65
1:C:84:PHE:HE1	1:C:85:ARG:HH21	1.41	0.65
1:C:161:ALA:HB3	1:C:175:ILE:HD12	1.78	0.65
1:A:161:ALA:HB3	1:A:175:ILE:HD12	1.78	0.65
1:B:96:HIS:HB3	2:B:304:HEC:HBC2	1.78	0.65
1:C:11:LEU:HD13	1:C:219:LYS:HE2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:LYS:CG	1:A:220:ASP:H	2.11	0.64
1:C:183:HIS:HE1	2:C:306:HEC:NA	1.96	0.64
1:A:183:HIS:HE1	2:A:306:HEC:NA	1.96	0.64
1:B:11:LEU:HD13	1:B:219:LYS:HE2	1.80	0.63
1:C:219:LYS:CG	1:C:220:ASP:H	2.11	0.63
1:A:11:LEU:HD13	1:A:219:LYS:HE2	1.80	0.63
1:B:52:SER:CA	1:C:245:ASN:ND2	2.61	0.63
1:B:183:HIS:HE1	2:B:306:HEC:NA	1.96	0.62
1:B:219:LYS:CG	1:B:220:ASP:H	2.11	0.62
1:A:214:LEU:HD22	2:A:308:HEC:HBC2	1.83	0.61
1:C:214:LEU:HD22	2:C:308:HEC:HBC2	1.83	0.61
1:B:214:LEU:HD22	2:B:308:HEC:HBC2	1.83	0.60
1:A:132:VAL:O	1:A:132:VAL:HG13	2.02	0.60
1:A:52:SER:CA	1:B:245:ASN:ND2	2.64	0.60
1:B:132:VAL:O	1:B:132:VAL:HG13	2.02	0.59
1:B:154:CYS:HA	2:B:305:HEC:HHC	1.85	0.59
1:C:132:VAL:O	1:C:132:VAL:HG13	2.02	0.59
1:A:52:SER:CA	1:B:245:ASN:HD21	2.15	0.59
1:C:107:CYS:O	1:C:111:HIS:HB2	2.03	0.59
1:B:17:LYS:HE2	1:B:22:THR:HA	1.85	0.59
1:C:73:PRO:HG3	1:C:79:PHE:HE1	1.68	0.58
1:B:73:PRO:HG3	1:B:79:PHE:HE1	1.68	0.58
1:A:107:CYS:O	1:A:111:HIS:HB2	2.03	0.58
1:A:73:PRO:HG3	1:A:79:PHE:HE1	1.68	0.58
1:B:52:SER:CA	1:C:245:ASN:HD21	2.14	0.58
1:B:179:GLN:HB2	2:B:306:HEC:CAD	2.34	0.58
1:A:219:LYS:CG	1:A:220:ASP:N	2.67	0.58
1:C:154:CYS:HA	2:C:305:HEC:HHC	1.84	0.58
1:B:219:LYS:CG	1:B:220:ASP:N	2.67	0.57
1:B:107:CYS:O	1:B:111:HIS:HB2	2.03	0.57
1:C:17:LYS:HE2	1:C:22:THR:HA	1.85	0.57
1:A:154:CYS:HA	2:A:305:HEC:HHC	1.84	0.57
1:A:17:LYS:HE2	1:A:22:THR:HA	1.85	0.56
1:C:179:GLN:HB2	2:C:306:HEC:CAD	2.34	0.56
1:A:132:VAL:HG23	1:A:253:TRP:CE3	2.37	0.56
1:A:179:GLN:HB2	2:A:306:HEC:CAD	2.34	0.56
1:B:185:THR:OG1	1:B:187:ILE:HG13	2.06	0.55
1:B:48:THR:HB	1:B:49:PRO:HD3	1.89	0.55
1:C:248:CYS:O	1:C:252:HIS:HB2	2.07	0.55
1:B:114:PHE:HD2	2:B:305:HEC:HAA1	1.72	0.55
1:A:248:CYS:O	1:A:252:HIS:HB2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:205:CYS:O	1:B:209:HIS:HB2	2.07	0.55
1:A:185:THR:OG1	1:A:187:ILE:HG13	2.06	0.54
1:B:40:HIS:CD2	2:B:302:HEC:HMD1	2.43	0.54
1:C:114:PHE:HD2	2:C:305:HEC:HAA1	1.72	0.54
1:C:219:LYS:CG	1:C:220:ASP:N	2.67	0.54
1:A:48:THR:HB	1:A:49:PRO:HD3	1.89	0.54
1:A:40:HIS:CD2	2:A:302:HEC:HMD1	2.43	0.54
1:A:249:GLN:HB3	1:A:255:TRP:HB2	1.89	0.54
1:C:185:THR:OG1	1:C:187:ILE:HG13	2.07	0.54
1:A:114:PHE:HD2	2:A:305:HEC:HAA1	1.72	0.54
1:C:249:GLN:HB3	1:C:255:TRP:HB2	1.89	0.54
1:A:47:VAL:HG12	1:A:49:PRO:HD2	1.90	0.54
1:B:248:CYS:O	1:B:252:HIS:HB2	2.07	0.54
1:B:249:GLN:HB3	1:B:255:TRP:HB2	1.89	0.53
1:A:151:VAL:HG12	1:A:255:TRP:CZ3	2.44	0.53
1:C:48:THR:HB	1:C:49:PRO:HD3	1.89	0.53
1:C:40:HIS:CD2	2:C:302:HEC:HMD1	2.43	0.53
1:C:93:GLN:O	1:C:95:PRO:HD3	2.09	0.53
1:C:205:CYS:O	1:C:209:HIS:HB2	2.08	0.53
1:C:151:VAL:HG12	1:C:255:TRP:CZ3	2.44	0.53
1:A:205:CYS:O	1:A:209:HIS:HB2	2.08	0.53
1:B:47:VAL:HG12	1:B:49:PRO:HD2	1.90	0.53
1:B:4:PRO:HD3	1:B:157:CYS:HB2	1.91	0.53
1:B:151:VAL:HG12	1:B:255:TRP:CZ3	2.44	0.53
1:B:250:GLY:HA2	1:B:255:TRP:CE3	2.44	0.53
1:B:93:GLN:O	1:B:95:PRO:HD3	2.09	0.52
1:A:198:SER:OG	1:A:200:VAL:HG23	2.10	0.52
1:C:47:VAL:HG12	1:C:49:PRO:HD2	1.90	0.52
1:C:134:PRO:HB3	1:C:251:CYS:O	2.09	0.52
1:C:250:GLY:HA2	1:C:255:TRP:CE3	2.44	0.52
1:A:250:GLY:HA2	1:A:255:TRP:CE3	2.44	0.52
1:A:110:CYS:HB2	2:A:301:HEC:HMD3	1.92	0.52
1:B:110:CYS:HB2	2:B:301:HEC:HMD3	1.92	0.52
1:A:93:GLN:O	1:A:95:PRO:HD3	2.09	0.52
1:C:140:SER:OG	1:C:148:VAL:HG12	2.10	0.52
1:B:132:VAL:HG23	1:B:253:TRP:CE3	2.37	0.51
1:B:134:PRO:HB3	1:B:251:CYS:O	2.10	0.51
1:B:198:SER:OG	1:B:200:VAL:HG23	2.10	0.51
1:A:140:SER:OG	1:A:148:VAL:HG12	2.10	0.51
1:C:17:LYS:HE2	1:C:22:THR:CA	2.40	0.51
1:C:198:SER:OG	1:C:200:VAL:HG23	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:ILE:HG13	2:A:307:HEC:HMD1	1.93	0.51
2:A:307:HEC:HHA	2:A:307:HEC:HBA2	1.93	0.51
1:B:115:ILE:HG13	2:B:307:HEC:HMD1	1.93	0.51
1:B:140:SER:OG	1:B:148:VAL:HG12	2.10	0.51
2:B:307:HEC:HHA	2:B:307:HEC:HBA2	1.93	0.51
1:C:110:CYS:HB2	2:C:301:HEC:HMD3	1.92	0.51
1:C:132:VAL:HG23	1:C:253:TRP:CE3	2.37	0.51
1:A:134:PRO:HB3	1:A:251:CYS:O	2.10	0.51
1:C:115:ILE:HG13	2:C:307:HEC:HMD1	1.93	0.51
2:C:307:HEC:HHA	2:C:307:HEC:HBA2	1.93	0.51
1:A:4:PRO:HD3	1:A:157:CYS:HB2	1.91	0.51
1:B:17:LYS:HE2	1:B:22:THR:CA	2.40	0.51
1:A:17:LYS:HE2	1:A:22:THR:CA	2.40	0.51
1:C:135:MET:HG3	1:C:138:GLY:HA2	1.93	0.51
1:C:4:PRO:HD3	1:C:157:CYS:HB2	1.91	0.51
1:A:135:MET:HG3	1:A:138:GLY:HA2	1.93	0.50
1:C:62:PRO:HG3	1:C:90:CYS:HB3	1.93	0.50
1:B:41:HIS:CE1	2:B:302:HEC:NA	2.79	0.50
1:C:41:HIS:CE1	2:C:302:HEC:NA	2.80	0.50
1:B:62:PRO:HG3	1:B:90:CYS:HB3	1.93	0.50
1:A:41:HIS:CE1	2:A:302:HEC:NA	2.80	0.50
1:B:14:TYR:HE2	1:B:111:HIS:ND1	2.10	0.50
1:B:135:MET:HG3	1:B:138:GLY:HA2	1.93	0.50
1:A:62:PRO:HG3	1:A:90:CYS:HB3	1.93	0.49
1:A:245:ASN:OD1	1:A:249:GLN:NE2	2.45	0.49
1:C:245:ASN:OD1	1:C:249:GLN:NE2	2.45	0.49
1:B:230:VAL:O	1:B:230:VAL:HG23	2.13	0.49
1:B:245:ASN:OD1	1:B:249:GLN:NE2	2.45	0.49
1:B:108:LYS:HE2	1:B:116:ASP:HA	1.95	0.49
1:C:251:CYS:HB3	2:C:308:HEC:HMC2	1.95	0.49
1:A:14:TYR:HE2	1:A:111:HIS:ND1	2.10	0.49
1:C:230:VAL:HG23	1:C:230:VAL:O	2.13	0.49
1:A:82:GLN:HG3	1:A:83:ASP:N	2.26	0.49
1:C:108:LYS:HE2	1:C:116:ASP:HA	1.95	0.49
1:A:108:LYS:HE2	1:A:116:ASP:HA	1.95	0.49
1:A:251:CYS:HB3	2:A:308:HEC:HMC2	1.95	0.49
1:A:37:VAL:HG12	2:A:302:HEC:HBD1	1.96	0.48
1:A:178:ASN:OD1	2:A:307:HEC:HMA2	2.13	0.48
1:C:37:VAL:HG12	2:C:302:HEC:HBD1	1.96	0.48
1:B:251:CYS:HB3	2:B:308:HEC:HMC2	1.95	0.48
1:A:94:THR:HG23	1:A:94:THR:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:179:GLN:HG3	2:B:306:HEC:CHA	2.44	0.48
1:A:230:VAL:HG23	1:A:230:VAL:O	2.13	0.48
1:B:53:CYS:H	1:C:245:ASN:ND2	2.09	0.48
1:B:94:THR:O	1:B:94:THR:HG23	2.14	0.48
1:B:26:CYS:HB3	2:B:301:HEC:CHC	2.44	0.48
1:C:178:ASN:OD1	2:C:307:HEC:HMA2	2.14	0.48
1:A:179:GLN:HG3	2:A:306:HEC:CHA	2.44	0.48
1:B:53:CYS:N	1:C:245:ASN:ND2	2.60	0.48
1:B:82:GLN:HG3	1:B:83:ASP:N	2.26	0.48
1:C:179:GLN:HG3	2:C:306:HEC:CHA	2.44	0.48
2:A:302:HEC:HBB3	2:A:302:HEC:HMB3	1.96	0.47
1:C:26:CYS:HB3	2:C:301:HEC:CHC	2.44	0.47
1:B:178:ASN:OD1	2:B:307:HEC:HMA2	2.13	0.47
1:A:26:CYS:HB3	2:A:301:HEC:CHC	2.44	0.47
1:C:14:TYR:HE2	1:C:111:HIS:ND1	2.10	0.47
2:B:302:HEC:HMB3	2:B:302:HEC:HBB3	1.96	0.47
1:A:178:ASN:O	1:A:179:GLN:HB3	2.15	0.47
2:B:306:HEC:HHA	2:B:306:HEC:CBA	2.44	0.47
1:B:37:VAL:HG12	2:B:302:HEC:HBD1	1.96	0.47
1:C:178:ASN:O	1:C:179:GLN:HB3	2.15	0.47
2:C:306:HEC:HHA	2:C:306:HEC:CBA	2.44	0.47
1:C:137:SER:HA	1:C:155:GLU:HG3	1.97	0.47
1:A:179:GLN:CD	2:A:306:HEC:HBA1	2.40	0.47
1:B:13:ILE:HG13	1:B:14:TYR:N	2.30	0.47
1:C:179:GLN:CD	2:C:306:HEC:HBA1	2.40	0.47
1:A:10:PHE:CZ	1:A:16:THR:HG23	2.50	0.47
1:B:114:PHE:CD2	2:B:305:HEC:HAA1	2.49	0.47
1:C:55:ASN:HB3	1:C:70:VAL:HG23	1.97	0.47
1:C:94:THR:HG23	1:C:94:THR:O	2.14	0.46
1:B:179:GLN:CD	2:B:306:HEC:HBA1	2.40	0.46
1:A:55:ASN:HB3	1:A:70:VAL:HG23	1.97	0.46
1:A:114:PHE:CD2	2:A:305:HEC:HAA1	2.50	0.46
1:C:13:ILE:HG13	1:C:14:TYR:N	2.30	0.46
1:C:114:PHE:CD2	2:C:305:HEC:HAA1	2.49	0.46
1:B:137:SER:HA	1:B:155:GLU:HG3	1.97	0.46
1:C:10:PHE:CZ	1:C:16:THR:HG23	2.50	0.46
1:A:11:LEU:CD1	1:A:219:LYS:HG2	2.41	0.46
1:B:10:PHE:CZ	1:B:16:THR:HG23	2.50	0.46
1:C:102:ALA:HB2	2:C:304:HEC:HHC	1.98	0.46
1:B:55:ASN:HB3	1:B:70:VAL:HG23	1.97	0.46
1:C:82:GLN:HG3	1:C:83:ASP:N	2.26	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:ILE:HG13	1:A:14:TYR:N	2.30	0.46
1:A:28:GLU:H	1:A:28:GLU:CD	2.24	0.46
1:B:43:LEU:HD22	2:B:303:HEC:HAD2	1.98	0.46
1:B:178:ASN:O	1:B:179:GLN:HB3	2.15	0.46
1:C:44:ILE:H	1:C:44:ILE:HG13	1.56	0.46
1:A:137:SER:HA	1:A:155:GLU:HG3	1.97	0.45
1:C:43:LEU:HD22	2:C:303:HEC:HAD2	1.98	0.45
1:A:102:ALA:HB2	2:A:304:HEC:HHC	1.98	0.45
1:A:53:CYS:N	1:B:245:ASN:ND2	2.64	0.45
1:C:28:GLU:CD	1:C:28:GLU:H	2.24	0.45
1:B:86:ASN:OD1	1:B:86:ASN:C	2.59	0.45
1:B:28:GLU:CD	1:B:28:GLU:H	2.24	0.45
1:B:4:PRO:HB2	1:B:6:PRO:HG2	1.99	0.45
1:A:17:LYS:CE	1:A:22:THR:CA	2.93	0.45
1:A:229:THR:O	1:A:229:THR:OG1	2.34	0.45
1:B:132:VAL:O	1:B:132:VAL:CG1	2.65	0.45
1:A:202:ILE:O	1:A:206:GLU:HG2	2.17	0.45
1:B:102:ALA:HB2	2:B:304:HEC:HHC	1.98	0.45
1:A:140:SER:HA	1:A:150:ILE:HA	1.99	0.44
1:B:140:SER:HA	1:B:150:ILE:HA	1.99	0.44
1:C:86:ASN:OD1	1:C:86:ASN:C	2.59	0.44
1:A:43:LEU:HD22	2:A:303:HEC:HAD2	1.98	0.44
1:B:229:THR:O	1:B:229:THR:OG1	2.34	0.44
1:C:229:THR:O	1:C:229:THR:OG1	2.34	0.44
1:B:202:ILE:O	1:B:206:GLU:HG2	2.17	0.44
1:C:37:VAL:HG23	1:C:38:GLN:N	2.33	0.44
1:C:73:PRO:HG3	1:C:79:PHE:CE1	2.49	0.44
1:C:4:PRO:HB2	1:C:6:PRO:HG2	1.98	0.44
1:A:4:PRO:HB2	1:A:6:PRO:HG2	1.98	0.44
1:A:44:ILE:H	1:A:44:ILE:HG13	1.56	0.44
1:C:140:SER:HA	1:C:150:ILE:HA	1.99	0.43
1:C:183:HIS:CD2	2:C:306:HEC:NC	2.85	0.43
1:A:183:HIS:CD2	2:A:306:HEC:NC	2.85	0.43
1:B:73:PRO:HG3	1:B:79:PHE:CE1	2.49	0.43
1:C:132:VAL:O	1:C:132:VAL:CG1	2.65	0.43
1:A:86:ASN:C	1:A:86:ASN:OD1	2.59	0.43
1:C:202:ILE:O	1:C:206:GLU:HG2	2.17	0.43
2:A:307:HEC:HBC3	2:A:307:HEC:HMC3	2.00	0.43
1:B:183:HIS:CD2	2:B:306:HEC:NC	2.85	0.43
1:A:132:VAL:O	1:A:132:VAL:CG1	2.65	0.43
1:A:37:VAL:HG23	1:A:38:GLN:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:306:HEC:HHA	2:A:306:HEC:CBA	2.44	0.43
2:C:307:HEC:HBC3	2:C:307:HEC:HMC3	1.99	0.43
1:C:33:ASP:HA	1:C:36:LEU:HB2	2.01	0.43
2:A:307:HEC:HHA	2:A:307:HEC:CBD	2.45	0.42
1:B:137:SER:HA	1:B:155:GLU:CB	2.48	0.42
1:B:37:VAL:HG23	1:B:38:GLN:N	2.33	0.42
1:B:183:HIS:HE1	2:B:306:HEC:C1A	2.32	0.42
2:B:307:HEC:HBC3	2:B:307:HEC:HMC3	1.99	0.42
1:A:73:PRO:HG3	1:A:79:PHE:CE1	2.49	0.42
1:A:183:HIS:HE1	2:A:306:HEC:C1A	2.32	0.42
1:B:33:ASP:HA	1:B:36:LEU:HB2	2.01	0.42
1:B:203:ARG:NH1	2:B:308:HEC:O1D	2.52	0.42
1:C:203:ARG:NH1	2:C:308:HEC:O1D	2.52	0.42
1:C:14:TYR:HE2	1:C:111:HIS:HD1	1.67	0.42
1:A:203:ARG:NH1	2:A:308:HEC:O1D	2.52	0.42
1:A:14:TYR:HE2	1:A:111:HIS:HD1	1.67	0.42
2:B:307:HEC:HHA	2:B:307:HEC:CBD	2.45	0.42
1:C:183:HIS:HE1	2:C:306:HEC:C1A	2.32	0.42
1:A:33:ASP:HA	1:A:36:LEU:HB2	2.01	0.42
1:C:83:ASP:OD1	1:C:84:PHE:N	2.53	0.41
1:B:231:LYS:HD2	1:B:231:LYS:N	2.36	0.41
2:C:307:HEC:HHA	2:C:307:HEC:CBD	2.45	0.41
1:B:14:TYR:HE2	1:B:111:HIS:HD1	1.67	0.41
1:B:44:ILE:H	1:B:44:ILE:HG13	1.56	0.41
1:C:231:LYS:HD2	1:C:231:LYS:N	2.36	0.41
1:A:83:ASP:OD1	1:A:84:PHE:N	2.53	0.41
1:A:211:VAL:HG13	1:A:215:HIS:CE1	2.56	0.41
1:B:182:HIS:CE1	2:B:307:HEC:NA	2.88	0.41
1:B:211:VAL:HG13	1:B:215:HIS:CE1	2.56	0.41
1:A:12:GLY:HA3	2:A:305:HEC:O2A	2.21	0.41
1:A:182:HIS:CE1	2:A:307:HEC:NA	2.88	0.41
1:B:12:GLY:N	2:B:305:HEC:O2D	2.54	0.41
1:B:83:ASP:OD1	1:B:84:PHE:N	2.53	0.41
1:C:165:ILE:HG22	1:C:167:PRO:HD3	2.03	0.41
1:C:182:HIS:CE1	2:C:307:HEC:NA	2.88	0.41
1:A:137:SER:HA	1:A:155:GLU:CB	2.48	0.41
1:A:231:LYS:HD2	1:A:231:LYS:N	2.36	0.41
2:A:304:HEC:HBD1	2:A:304:HEC:HMD3	2.03	0.41
1:C:211:VAL:HG13	1:C:215:HIS:CE1	2.56	0.41
1:A:12:GLY:N	2:A:305:HEC:O2D	2.54	0.40
1:A:165:ILE:HG22	1:A:167:PRO:HD3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:12:GLY:HA3	2:C:305:HEC:O2A	2.21	0.40
1:C:192:LEU:HD12	1:C:192:LEU:HA	1.91	0.40
1:B:12:GLY:HA3	2:B:305:HEC:O2A	2.21	0.40
1:B:192:LEU:HD12	1:B:192:LEU:HA	1.91	0.40
1:C:12:GLY:N	2:C:305:HEC:O2D	2.54	0.40
1:C:60:VAL:O	1:C:62:PRO:HD3	2.21	0.40
1:C:207:VAL:O	1:C:207:VAL:HG13	2.21	0.40
1:A:81:PHE:CZ	2:B:308:HEC:CHB	3.04	0.40
1:A:207:VAL:O	1:A:207:VAL:HG13	2.21	0.40
1:B:117:ASN:HB2	1:B:120:ASP:HB2	2.04	0.40
1:B:209:HIS:HE1	2:B:305:HEC:HMA1	1.86	0.40
1:A:60:VAL:O	1:A:62:PRO:HD3	2.21	0.40
1:A:193:CYS:HA	2:A:307:HEC:HMC1	2.04	0.40
1:B:102:ALA:HB2	2:B:304:HEC:CHC	2.52	0.40
1:B:207:VAL:O	1:B:207:VAL:HG13	2.21	0.40
1:C:137:SER:HA	1:C:155:GLU:CB	2.48	0.40
2:C:304:HEC:HMD3	2:C:304:HEC:HBD1	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	256/258 (99%)	223 (87%)	33 (13%)	0	100	100
1	B	256/258 (99%)	223 (87%)	33 (13%)	0	100	100
1	C	256/258 (99%)	223 (87%)	33 (13%)	0	100	100
All	All	768/774 (99%)	669 (87%)	99 (13%)	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 PDB entries followed by that with respect to all EM entries.

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	221/221 (100%)	220 (100%)	1 (0%)	81	81
1	B	221/221 (100%)	220 (100%)	1 (0%)	81	81
1	C	221/221 (100%)	220 (100%)	1 (0%)	81	81
All	All	663/663 (100%)	660 (100%)	3 (0%)	78	81

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	255	TRP
1	B	255	TRP
1	C	255	TRP

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

Mol	Chain	Res	Type
1	A	170	ASN
1	B	170	ASN
1	C	39	GLN
1	C	170	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

24 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEC	A	301	1	46,50,50	1.77	7 (15%)	58,82,82	2.04	9 (15%)
2	HEC	B	307	1	46,50,50	1.90	6 (13%)	58,82,82	2.00	14 (24%)
2	HEC	B	304	1	46,50,50	1.80	5 (10%)	58,82,82	2.05	9 (15%)
2	HEC	C	303	1	46,50,50	1.87	6 (13%)	58,82,82	2.11	9 (15%)
2	HEC	A	305	1	46,50,50	1.84	4 (8%)	58,82,82	2.01	8 (13%)
2	HEC	C	308	1	46,50,50	1.87	7 (15%)	58,82,82	2.04	6 (10%)
2	HEC	A	303	1	46,50,50	1.87	6 (13%)	58,82,82	2.11	9 (15%)
2	HEC	B	301	1	46,50,50	1.77	7 (15%)	58,82,82	2.04	8 (13%)
2	HEC	B	308	1	46,50,50	1.87	7 (15%)	58,82,82	2.04	7 (12%)
2	HEC	A	304	1	46,50,50	1.80	5 (10%)	58,82,82	2.05	9 (15%)
2	HEC	C	301	1	46,50,50	1.77	7 (15%)	58,82,82	2.04	9 (15%)
2	HEC	B	303	1	46,50,50	1.87	6 (13%)	58,82,82	2.11	10 (17%)
2	HEC	C	305	1	46,50,50	1.84	4 (8%)	58,82,82	2.01	8 (13%)
2	HEC	C	302	1	46,50,50	1.74	6 (13%)	58,82,82	2.05	13 (22%)
2	HEC	A	307	1	46,50,50	1.90	6 (13%)	58,82,82	2.00	14 (24%)
2	HEC	B	306	1	46,50,50	1.93	7 (15%)	58,82,82	2.19	10 (17%)
2	HEC	B	305	1	46,50,50	1.84	4 (8%)	58,82,82	2.01	8 (13%)
2	HEC	C	307	1	46,50,50	1.89	6 (13%)	58,82,82	2.00	14 (24%)
2	HEC	C	306	1	46,50,50	1.93	7 (15%)	58,82,82	2.19	10 (17%)
2	HEC	A	302	1	46,50,50	1.74	6 (13%)	58,82,82	2.05	13 (22%)
2	HEC	C	304	1	46,50,50	1.80	5 (10%)	58,82,82	2.05	9 (15%)
2	HEC	A	308	1	46,50,50	1.87	7 (15%)	58,82,82	2.04	7 (12%)
2	HEC	B	302	1	46,50,50	1.74	6 (13%)	58,82,82	2.05	13 (22%)
2	HEC	A	306	1	46,50,50	1.93	7 (15%)	58,82,82	2.19	10 (17%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEC	A	301	1	-	4/14/54/54	-
2	HEC	B	307	1	-	9/14/54/54	-
2	HEC	B	304	1	-	9/14/54/54	-
2	HEC	C	303	1	-	8/14/54/54	-
2	HEC	A	305	1	-	6/14/54/54	-
2	HEC	C	308	1	-	5/14/54/54	-
2	HEC	A	303	1	-	8/14/54/54	-
2	HEC	B	301	1	-	4/14/54/54	-
2	HEC	B	308	1	-	5/14/54/54	-
2	HEC	A	304	1	-	9/14/54/54	-
2	HEC	C	301	1	-	4/14/54/54	-
2	HEC	B	303	1	-	8/14/54/54	-
2	HEC	C	305	1	-	6/14/54/54	-
2	HEC	C	302	1	-	5/14/54/54	-
2	HEC	A	307	1	-	9/14/54/54	-
2	HEC	B	306	1	-	7/14/54/54	-
2	HEC	B	305	1	-	6/14/54/54	-
2	HEC	C	307	1	-	9/14/54/54	-
2	HEC	C	306	1	-	7/14/54/54	-
2	HEC	A	302	1	-	5/14/54/54	-
2	HEC	C	304	1	-	9/14/54/54	-
2	HEC	A	308	1	-	5/14/54/54	-
2	HEC	B	302	1	-	5/14/54/54	-
2	HEC	A	306	1	-	7/14/54/54	-

All (144) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	305	HEC	CAC-C3C	6.37	1.55	1.35
2	C	305	HEC	CAC-C3C	6.37	1.55	1.35
2	B	305	HEC	CAC-C3C	6.35	1.55	1.35
2	B	306	HEC	CAC-C3C	6.26	1.55	1.35
2	B	308	HEC	CAB-C3B	6.25	1.55	1.35
2	C	306	HEC	CAC-C3C	6.25	1.55	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	306	HEC	CAC-C3C	6.25	1.55	1.35
2	C	308	HEC	CAB-C3B	6.24	1.55	1.35
2	A	308	HEC	CAB-C3B	6.23	1.55	1.35
2	A	304	HEC	CAB-C3B	6.20	1.55	1.35
2	B	304	HEC	CAB-C3B	6.19	1.55	1.35
2	C	304	HEC	CAB-C3B	6.18	1.55	1.35
2	C	302	HEC	CAB-C3B	6.10	1.54	1.35
2	B	302	HEC	CAB-C3B	6.10	1.54	1.35
2	A	302	HEC	CAB-C3B	6.10	1.54	1.35
2	A	307	HEC	CAB-C3B	6.01	1.54	1.35
2	B	307	HEC	CAB-C3B	6.01	1.54	1.35
2	C	307	HEC	CAB-C3B	5.99	1.54	1.35
2	B	307	HEC	CAC-C3C	5.97	1.54	1.35
2	A	307	HEC	CAC-C3C	5.97	1.54	1.35
2	A	304	HEC	CAC-C3C	5.96	1.54	1.35
2	C	307	HEC	CAC-C3C	5.96	1.54	1.35
2	B	304	HEC	CAC-C3C	5.95	1.54	1.35
2	C	304	HEC	CAC-C3C	5.95	1.54	1.35
2	C	303	HEC	CAC-C3C	5.92	1.54	1.35
2	B	303	HEC	CAC-C3C	5.92	1.54	1.35
2	A	306	HEC	C3D-C2D	5.92	1.54	1.38
2	A	303	HEC	CAC-C3C	5.92	1.54	1.35
2	B	306	HEC	C3D-C2D	5.92	1.54	1.38
2	C	306	HEC	C3D-C2D	5.90	1.54	1.38
2	B	303	HEC	CAB-C3B	5.88	1.54	1.35
2	A	303	HEC	CAB-C3B	5.88	1.54	1.35
2	C	303	HEC	CAB-C3B	5.87	1.54	1.35
2	C	303	HEC	C3D-C2D	5.77	1.54	1.38
2	A	303	HEC	C3D-C2D	5.76	1.53	1.38
2	B	303	HEC	C3D-C2D	5.76	1.53	1.38
2	C	308	HEC	CAC-C3C	5.71	1.53	1.35
2	B	308	HEC	CAC-C3C	5.70	1.53	1.35
2	A	308	HEC	CAC-C3C	5.69	1.53	1.35
2	B	305	HEC	CAB-C3B	5.65	1.53	1.35
2	C	305	HEC	CAB-C3B	5.64	1.53	1.35
2	A	305	HEC	CAB-C3B	5.64	1.53	1.35
2	A	306	HEC	CAB-C3B	5.61	1.53	1.35
2	B	306	HEC	CAB-C3B	5.60	1.53	1.35
2	C	302	HEC	CAC-C3C	5.60	1.53	1.35
2	C	306	HEC	CAB-C3B	5.58	1.53	1.35
2	A	302	HEC	CAC-C3C	5.57	1.53	1.35
2	B	302	HEC	CAC-C3C	5.55	1.53	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	305	HEC	C3D-C2D	5.50	1.53	1.38
2	B	305	HEC	C3D-C2D	5.50	1.53	1.38
2	C	305	HEC	C3D-C2D	5.49	1.53	1.38
2	B	308	HEC	C3D-C2D	5.48	1.53	1.38
2	A	308	HEC	C3D-C2D	5.46	1.53	1.38
2	C	301	HEC	CAB-C3B	5.46	1.52	1.35
2	A	301	HEC	CAB-C3B	5.45	1.52	1.35
2	B	301	HEC	CAB-C3B	5.44	1.52	1.35
2	A	301	HEC	CAC-C3C	5.43	1.52	1.35
2	B	301	HEC	CAC-C3C	5.43	1.52	1.35
2	C	308	HEC	C3D-C2D	5.43	1.53	1.38
2	C	301	HEC	CAC-C3C	5.42	1.52	1.35
2	C	304	HEC	C3D-C2D	5.26	1.52	1.38
2	A	304	HEC	C3D-C2D	5.24	1.52	1.38
2	C	301	HEC	C3D-C2D	5.24	1.52	1.38
2	B	304	HEC	C3D-C2D	5.23	1.52	1.38
2	B	301	HEC	C3D-C2D	5.23	1.52	1.38
2	A	301	HEC	C3D-C2D	5.22	1.52	1.38
2	A	307	HEC	C3D-C2D	4.83	1.51	1.38
2	B	307	HEC	C3D-C2D	4.83	1.51	1.38
2	C	307	HEC	C3D-C2D	4.80	1.51	1.38
2	C	302	HEC	C3D-C2D	4.45	1.50	1.38
2	B	302	HEC	C3D-C2D	4.42	1.50	1.38
2	A	302	HEC	C3D-C2D	4.42	1.50	1.38
2	B	302	HEC	C3B-C2B	-3.24	1.30	1.41
2	C	302	HEC	C3B-C2B	-3.24	1.30	1.41
2	A	302	HEC	C3B-C2B	-3.23	1.30	1.41
2	C	301	HEC	CMA-C3A	3.05	1.57	1.50
2	B	301	HEC	CMA-C3A	3.02	1.57	1.50
2	A	301	HEC	CMA-C3A	3.01	1.56	1.50
2	A	306	HEC	CMA-C3A	2.90	1.56	1.50
2	B	306	HEC	CMA-C3A	2.90	1.56	1.50
2	C	306	HEC	CMA-C3A	2.88	1.56	1.50
2	B	308	HEC	C3B-C2B	-2.74	1.31	1.41
2	A	308	HEC	C3B-C2B	-2.72	1.32	1.41
2	A	301	HEC	C3C-C2C	-2.71	1.32	1.41
2	B	301	HEC	C3C-C2C	-2.71	1.32	1.41
2	C	308	HEC	C3B-C2B	-2.70	1.32	1.41
2	B	307	HEC	C3C-C2C	-2.69	1.32	1.41
2	C	301	HEC	C3C-C2C	-2.69	1.32	1.41
2	C	307	HEC	C3C-C2C	-2.69	1.32	1.41
2	A	307	HEC	C3C-C2C	-2.68	1.32	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	304	HEC	C3B-C2B	-2.56	1.32	1.41
2	A	304	HEC	C3B-C2B	-2.54	1.32	1.41
2	C	304	HEC	C3B-C2B	-2.53	1.32	1.41
2	A	304	HEC	C3C-C2C	-2.48	1.32	1.41
2	B	304	HEC	C3C-C2C	-2.48	1.32	1.41
2	C	304	HEC	C3C-C2C	-2.47	1.32	1.41
2	A	308	HEC	C2A-C3A	-2.47	1.31	1.36
2	C	308	HEC	C2A-C3A	-2.47	1.31	1.36
2	B	308	HEC	C2A-C3A	-2.46	1.31	1.36
2	B	303	HEC	C3B-C2B	-2.45	1.32	1.41
2	A	303	HEC	C3B-C2B	-2.42	1.33	1.41
2	C	303	HEC	C3B-C2B	-2.41	1.33	1.41
2	A	305	HEC	C3C-C2C	-2.34	1.33	1.41
2	C	305	HEC	C3C-C2C	-2.34	1.33	1.41
2	B	305	HEC	C3C-C2C	-2.32	1.33	1.41
2	C	308	HEC	C3C-C2C	-2.31	1.33	1.41
2	A	308	HEC	C3C-C2C	-2.31	1.33	1.41
2	B	308	HEC	C3C-C2C	-2.30	1.33	1.41
2	C	303	HEC	C3C-C2C	-2.29	1.33	1.41
2	A	303	HEC	C3C-C2C	-2.29	1.33	1.41
2	B	306	HEC	C3B-C2B	-2.29	1.33	1.41
2	C	301	HEC	C3B-C2B	-2.29	1.33	1.41
2	C	306	HEC	C3B-C2B	-2.29	1.33	1.41
2	B	303	HEC	C3C-C2C	-2.28	1.33	1.41
2	A	301	HEC	C3B-C2B	-2.28	1.33	1.41
2	A	306	HEC	C3B-C2B	-2.28	1.33	1.41
2	B	301	HEC	C3B-C2B	-2.27	1.33	1.41
2	C	302	HEC	C3C-C2C	-2.24	1.33	1.41
2	A	302	HEC	C3C-C2C	-2.22	1.33	1.41
2	A	307	HEC	C3B-C2B	-2.22	1.33	1.41
2	B	307	HEC	C3B-C2B	-2.21	1.33	1.41
2	B	302	HEC	C3C-C2C	-2.21	1.33	1.41
2	C	307	HEC	C3B-C2B	-2.20	1.33	1.41
2	C	306	HEC	CMC-C2C	2.19	1.55	1.50
2	C	308	HEC	CMD-C2D	2.18	1.55	1.50
2	B	306	HEC	CMC-C2C	2.18	1.55	1.50
2	B	308	HEC	CMD-C2D	2.18	1.55	1.50
2	A	308	HEC	CMD-C2D	2.17	1.55	1.50
2	A	306	HEC	CMC-C2C	2.17	1.55	1.50
2	B	307	HEC	CMB-C2B	2.13	1.55	1.50
2	A	307	HEC	CMB-C2B	2.12	1.55	1.50
2	C	307	HEC	CMB-C2B	2.12	1.55	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	HEC	CMC-C2C	2.11	1.55	1.50
2	A	301	HEC	CMC-C2C	2.11	1.55	1.50
2	C	301	HEC	CMC-C2C	2.08	1.55	1.50
2	B	306	HEC	C2A-C3A	-2.07	1.32	1.36
2	A	306	HEC	C2A-C3A	-2.06	1.32	1.36
2	A	302	HEC	CMA-C3A	2.04	1.55	1.50
2	C	306	HEC	C2A-C3A	-2.04	1.32	1.36
2	B	303	HEC	C1A-NA	-2.02	1.35	1.39
2	C	303	HEC	C1A-NA	-2.02	1.35	1.39
2	C	302	HEC	CMA-C3A	2.02	1.54	1.50
2	A	303	HEC	C1A-NA	-2.02	1.35	1.39
2	B	302	HEC	CMA-C3A	2.01	1.54	1.50

All (236) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	303	HEC	CBB-CAB-C3B	-9.90	107.64	127.43
2	A	303	HEC	CBB-CAB-C3B	-9.89	107.67	127.43
2	C	303	HEC	CBB-CAB-C3B	-9.88	107.69	127.43
2	C	305	HEC	CBC-CAC-C3C	-9.56	108.32	127.43
2	A	305	HEC	CBC-CAC-C3C	-9.56	108.33	127.43
2	B	305	HEC	CBC-CAC-C3C	-9.54	108.36	127.43
2	A	308	HEC	CBC-CAC-C3C	-9.14	109.17	127.43
2	C	308	HEC	CBC-CAC-C3C	-9.13	109.19	127.43
2	B	308	HEC	CBC-CAC-C3C	-9.11	109.22	127.43
2	A	301	HEC	CBB-CAB-C3B	-8.99	109.46	127.43
2	C	301	HEC	CBB-CAB-C3B	-8.98	109.48	127.43
2	B	301	HEC	CBB-CAB-C3B	-8.98	109.48	127.43
2	A	306	HEC	CBB-CAB-C3B	-8.88	109.68	127.43
2	B	306	HEC	CBB-CAB-C3B	-8.87	109.70	127.43
2	C	306	HEC	CBB-CAB-C3B	-8.87	109.72	127.43
2	B	308	HEC	CBB-CAB-C3B	-8.79	109.86	127.43
2	C	308	HEC	CBB-CAB-C3B	-8.79	109.86	127.43
2	A	308	HEC	CBB-CAB-C3B	-8.77	109.91	127.43
2	C	304	HEC	CBC-CAC-C3C	-8.39	110.66	127.43
2	A	304	HEC	CBC-CAC-C3C	-8.38	110.68	127.43
2	B	304	HEC	CBC-CAC-C3C	-8.37	110.70	127.43
2	C	302	HEC	CBC-CAC-C3C	-8.24	110.96	127.43
2	A	302	HEC	CBC-CAC-C3C	-8.23	110.98	127.43
2	B	302	HEC	CBC-CAC-C3C	-8.22	111.01	127.43
2	A	307	HEC	CBB-CAB-C3B	-8.09	111.25	127.43
2	B	307	HEC	CBB-CAB-C3B	-8.09	111.26	127.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	307	HEC	CBB-CAB-C3B	-8.08	111.29	127.43
2	A	301	HEC	CBC-CAC-C3C	-7.89	111.67	127.43
2	C	301	HEC	CBC-CAC-C3C	-7.88	111.68	127.43
2	B	301	HEC	CBC-CAC-C3C	-7.88	111.69	127.43
2	C	302	HEC	CBB-CAB-C3B	-7.87	111.69	127.43
2	A	302	HEC	CBB-CAB-C3B	-7.87	111.70	127.43
2	B	302	HEC	CBB-CAB-C3B	-7.86	111.73	127.43
2	A	306	HEC	CBC-CAC-C3C	-7.75	111.94	127.43
2	B	306	HEC	CBC-CAC-C3C	-7.75	111.95	127.43
2	C	306	HEC	CBC-CAC-C3C	-7.73	111.97	127.43
2	A	307	HEC	CBC-CAC-C3C	-7.69	112.06	127.43
2	C	307	HEC	CBC-CAC-C3C	-7.69	112.06	127.43
2	B	307	HEC	CBC-CAC-C3C	-7.68	112.09	127.43
2	C	303	HEC	CBC-CAC-C3C	-7.65	112.14	127.43
2	A	303	HEC	CBC-CAC-C3C	-7.64	112.17	127.43
2	B	303	HEC	CBC-CAC-C3C	-7.62	112.20	127.43
2	C	305	HEC	CBB-CAB-C3B	-7.51	112.41	127.43
2	A	305	HEC	CBB-CAB-C3B	-7.50	112.44	127.43
2	B	305	HEC	CBB-CAB-C3B	-7.49	112.47	127.43
2	B	304	HEC	CBB-CAB-C3B	-7.32	112.80	127.43
2	A	304	HEC	CBB-CAB-C3B	-7.31	112.83	127.43
2	C	304	HEC	CBB-CAB-C3B	-7.30	112.84	127.43
2	C	306	HEC	CAA-C2A-C3A	-4.54	119.36	127.87
2	A	306	HEC	CAA-C2A-C3A	-4.53	119.38	127.87
2	B	306	HEC	CAA-C2A-C3A	-4.53	119.38	127.87
2	B	304	HEC	C2A-C1A-NA	-4.50	105.98	110.32
2	A	304	HEC	C2A-C1A-NA	-4.47	106.01	110.32
2	C	304	HEC	C2A-C1A-NA	-4.46	106.02	110.32
2	A	304	HEC	CHB-C4A-NA	3.90	128.70	124.45
2	B	304	HEC	CHB-C4A-NA	3.89	128.69	124.45
2	B	302	HEC	CAD-CBD-CGD	-3.88	103.39	113.67
2	C	302	HEC	CAD-CBD-CGD	-3.86	103.43	113.67
2	A	302	HEC	CAD-CBD-CGD	-3.86	103.43	113.67
2	C	304	HEC	CHB-C4A-NA	3.86	128.65	124.45
2	B	302	HEC	CAD-C3D-C4D	3.85	132.46	124.94
2	C	302	HEC	CAD-C3D-C4D	3.84	132.44	124.94
2	A	302	HEC	CAD-C3D-C4D	3.84	132.44	124.94
2	C	301	HEC	CAA-CBA-CGA	-3.70	103.84	113.67
2	A	301	HEC	CAA-CBA-CGA	-3.70	103.85	113.67
2	B	301	HEC	CAA-CBA-CGA	-3.69	103.88	113.67
2	B	305	HEC	CBD-CAD-C3D	-3.65	102.45	112.53
2	C	305	HEC	CBD-CAD-C3D	-3.64	102.47	112.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	305	HEC	CBD-CAD-C3D	-3.64	102.47	112.53
2	A	306	HEC	C2A-C1A-NA	-3.63	106.82	110.32
2	B	306	HEC	C2A-C1A-NA	-3.63	106.82	110.32
2	C	306	HEC	C2A-C1A-NA	-3.61	106.84	110.32
2	C	306	HEC	CAA-C2A-C1A	3.49	131.95	124.85
2	A	306	HEC	CAA-C2A-C1A	3.47	131.92	124.85
2	B	306	HEC	CAA-C2A-C1A	3.46	131.89	124.85
2	C	303	HEC	CHC-C4B-NB	3.40	128.16	124.45
2	B	302	HEC	CHD-C4C-NC	3.40	128.15	124.45
2	A	302	HEC	CHD-C4C-NC	3.39	128.14	124.45
2	C	302	HEC	CHD-C4C-NC	3.38	128.13	124.45
2	A	303	HEC	CHC-C4B-NB	3.36	128.11	124.45
2	B	303	HEC	CHC-C4B-NB	3.35	128.10	124.45
2	C	306	HEC	C4D-ND-C1D	3.31	111.22	105.82
2	A	306	HEC	C4D-ND-C1D	3.28	111.17	105.82
2	B	306	HEC	C4D-ND-C1D	3.28	111.17	105.82
2	B	308	HEC	C4D-ND-C1D	3.25	111.11	105.82
2	A	308	HEC	C4D-ND-C1D	3.22	111.07	105.82
2	C	308	HEC	C4D-ND-C1D	3.21	111.06	105.82
2	B	303	HEC	C4D-ND-C1D	3.19	111.02	105.82
2	C	303	HEC	C4D-ND-C1D	3.18	111.01	105.82
2	A	303	HEC	C4D-ND-C1D	3.18	111.00	105.82
2	B	305	HEC	C4D-ND-C1D	3.15	110.95	105.82
2	C	305	HEC	C4D-ND-C1D	3.14	110.94	105.82
2	A	305	HEC	C4D-ND-C1D	3.13	110.93	105.82
2	B	303	HEC	CHA-C1A-NA	3.04	127.77	124.45
2	A	303	HEC	CHA-C1A-NA	3.04	127.76	124.45
2	C	303	HEC	CHA-C1A-NA	3.00	127.72	124.45
2	C	307	HEC	C2A-C1A-NA	-3.00	107.43	110.32
2	B	302	HEC	C4D-ND-C1D	2.99	110.70	105.82
2	A	307	HEC	C2A-C1A-NA	-2.98	107.45	110.32
2	B	307	HEC	C2A-C1A-NA	-2.97	107.45	110.32
2	A	302	HEC	C4D-ND-C1D	2.97	110.66	105.82
2	C	301	HEC	CAD-CBD-CGD	-2.96	105.82	113.67
2	B	301	HEC	CAD-CBD-CGD	-2.96	105.82	113.67
2	A	301	HEC	CAD-CBD-CGD	-2.95	105.85	113.67
2	C	302	HEC	C4D-ND-C1D	2.94	110.62	105.82
2	A	308	HEC	C2A-C1A-NA	-2.78	107.64	110.32
2	C	308	HEC	C2A-C1A-NA	-2.78	107.64	110.32
2	B	308	HEC	C2A-C1A-NA	-2.75	107.67	110.32
2	C	303	HEC	C2A-C1A-NA	-2.73	107.69	110.32
2	A	303	HEC	C2A-C1A-NA	-2.71	107.70	110.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	303	HEC	C2A-C1A-NA	-2.71	107.71	110.32
2	B	306	HEC	CHD-C4C-NC	2.71	127.40	124.45
2	A	306	HEC	CHC-C4B-NB	2.71	127.40	124.45
2	C	306	HEC	CHC-C4B-NB	2.70	127.40	124.45
2	A	306	HEC	CHD-C4C-NC	2.70	127.39	124.45
2	C	304	HEC	C4D-ND-C1D	2.69	110.21	105.82
2	B	306	HEC	CHC-C4B-NB	2.68	127.37	124.45
2	B	304	HEC	C4D-ND-C1D	2.67	110.18	105.82
2	C	306	HEC	CHD-C4C-NC	2.67	127.36	124.45
2	A	304	HEC	C4D-ND-C1D	2.67	110.18	105.82
2	A	307	HEC	CAD-CBD-CGD	-2.62	106.72	113.67
2	C	307	HEC	CAD-CBD-CGD	-2.62	106.72	113.67
2	B	307	HEC	CAD-CBD-CGD	-2.61	106.74	113.67
2	C	307	HEC	CHC-C1C-NC	2.55	128.49	123.86
2	C	302	HEC	CMD-C2D-C1D	2.55	129.30	125.42
2	A	307	HEC	CHC-C1C-NC	2.54	128.46	123.86
2	B	307	HEC	CHC-C1C-NC	2.53	128.45	123.86
2	A	302	HEC	CMD-C2D-C1D	2.52	129.25	125.42
2	B	302	HEC	CMD-C2D-C1D	2.50	129.23	125.42
2	C	301	HEC	C2A-C1A-NA	-2.47	107.94	110.32
2	C	307	HEC	O1D-CGD-CBD	-2.46	115.28	123.09
2	A	307	HEC	O1D-CGD-CBD	-2.45	115.31	123.09
2	B	307	HEC	O1D-CGD-CBD	-2.45	115.31	123.09
2	A	301	HEC	C2A-C1A-NA	-2.43	107.98	110.32
2	C	305	HEC	CHC-C4B-NB	2.41	127.08	124.45
2	B	302	HEC	CBD-CAD-C3D	-2.41	105.87	112.53
2	A	302	HEC	CBD-CAD-C3D	-2.41	105.88	112.53
2	B	301	HEC	C2A-C1A-NA	-2.41	108.00	110.32
2	C	302	HEC	CBD-CAD-C3D	-2.41	105.88	112.53
2	A	305	HEC	CHC-C4B-NB	2.39	127.06	124.45
2	C	307	HEC	CHC-C4B-NB	2.39	127.05	124.45
2	A	307	HEC	CHC-C4B-NB	2.38	127.05	124.45
2	C	304	HEC	CAA-C2A-C3A	-2.35	123.46	127.87
2	B	305	HEC	CHC-C4B-NB	2.35	127.01	124.45
2	B	307	HEC	CHC-C4B-NB	2.35	127.01	124.45
2	A	304	HEC	CAA-C2A-C3A	-2.34	123.48	127.87
2	B	302	HEC	C2B-C1B-NB	-2.34	106.39	110.14
2	A	302	HEC	C2B-C1B-NB	-2.32	106.42	110.14
2	C	302	HEC	C2B-C1B-NB	-2.32	106.42	110.14
2	B	304	HEC	CAA-C2A-C3A	-2.32	123.51	127.87
2	A	301	HEC	CHB-C4A-NA	-2.26	121.99	124.45
2	B	301	HEC	CHB-C4A-NA	-2.25	122.00	124.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	HEC	CHC-C4B-NB	2.25	126.90	124.45
2	C	301	HEC	CHC-C4B-NB	2.24	126.89	124.45
2	B	301	HEC	CHC-C4B-NB	2.23	126.89	124.45
2	C	301	HEC	CHB-C4A-NA	-2.22	122.03	124.45
2	A	307	HEC	CAD-C3D-C4D	2.22	129.27	124.94
2	B	307	HEC	CAD-C3D-C4D	2.21	129.26	124.94
2	A	307	HEC	C4D-ND-C1D	2.21	109.42	105.82
2	B	304	HEC	CHA-C1A-C2A	2.21	128.35	124.86
2	C	307	HEC	C2C-C1C-NC	-2.21	106.60	110.14
2	B	307	HEC	C4D-ND-C1D	2.21	109.42	105.82
2	C	307	HEC	CAD-C3D-C4D	2.20	129.25	124.94
2	A	304	HEC	CHA-C1A-C2A	2.20	128.34	124.86
2	C	307	HEC	C4D-ND-C1D	2.20	109.41	105.82
2	A	307	HEC	C2C-C1C-NC	-2.20	106.61	110.14
2	C	304	HEC	CHA-C1A-C2A	2.20	128.34	124.86
2	C	303	HEC	CHD-C1D-ND	2.19	127.83	123.86
2	B	307	HEC	C2C-C1C-NC	-2.19	106.64	110.14
2	B	303	HEC	CHD-C1D-ND	2.17	127.80	123.86
2	C	302	HEC	CBA-CAA-C2A	-2.17	106.53	112.53
2	B	303	HEC	CAD-CBD-CGD	-2.17	107.90	113.67
2	A	303	HEC	CHD-C1D-ND	2.17	127.79	123.86
2	A	303	HEC	CAD-CBD-CGD	-2.17	107.92	113.67
2	B	302	HEC	CBA-CAA-C2A	-2.17	106.54	112.53
2	C	306	HEC	CHA-C4D-ND	2.17	127.79	123.86
2	C	303	HEC	CAD-CBD-CGD	-2.17	107.92	113.67
2	A	302	HEC	CBA-CAA-C2A	-2.16	106.55	112.53
2	C	304	HEC	O1A-CGA-CBA	-2.15	116.28	123.09
2	C	302	HEC	CAD-C3D-C2D	-2.15	122.25	127.07
2	B	302	HEC	CAD-C3D-C2D	-2.15	122.25	127.07
2	A	302	HEC	CAD-C3D-C2D	-2.15	122.26	127.07
2	A	307	HEC	CHD-C1D-C2D	-2.14	121.20	127.43
2	A	306	HEC	CHA-C4D-ND	2.14	127.74	123.86
2	C	307	HEC	CHD-C1D-C2D	-2.14	121.22	127.43
2	B	307	HEC	O2D-CGD-CBD	2.14	120.75	114.00
2	A	307	HEC	O2D-CGD-CBD	2.14	120.75	114.00
2	B	307	HEC	CHD-C1D-C2D	-2.14	121.23	127.43
2	A	304	HEC	O2A-CGA-CBA	2.13	120.73	114.00
2	C	304	HEC	O2A-CGA-CBA	2.13	120.73	114.00
2	A	306	HEC	CHB-C4A-NA	2.13	126.77	124.45
2	C	307	HEC	O2D-CGD-CBD	2.13	120.73	114.00
2	B	304	HEC	O2A-CGA-CBA	2.12	120.71	114.00
2	A	304	HEC	O1A-CGA-CBA	-2.12	116.36	123.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	302	HEC	CHB-C1B-NB	2.12	127.71	123.86
2	C	302	HEC	CHB-C1B-NB	2.12	127.70	123.86
2	C	308	HEC	CAD-CBD-CGD	-2.12	108.05	113.67
2	B	308	HEC	CAD-CBD-CGD	-2.12	108.05	113.67
2	A	305	HEC	C4B-NB-C1B	2.11	109.27	105.82
2	C	306	HEC	CHB-C4A-NA	2.11	126.75	124.45
2	B	306	HEC	CHA-C4D-ND	2.11	127.69	123.86
2	B	305	HEC	C4B-NB-C1B	2.11	109.26	105.82
2	B	304	HEC	O1A-CGA-CBA	-2.11	116.40	123.09
2	A	308	HEC	CAD-CBD-CGD	-2.11	108.07	113.67
2	C	305	HEC	C4B-NB-C1B	2.11	109.26	105.82
2	A	305	HEC	C4D-C3D-C2D	-2.10	103.61	106.87
2	B	305	HEC	C4D-C3D-C2D	-2.10	103.62	106.87
2	B	302	HEC	CHB-C1B-NB	2.10	127.67	123.86
2	B	308	HEC	CBD-CAD-C3D	-2.09	106.75	112.53
2	A	308	HEC	CBD-CAD-C3D	-2.09	106.75	112.53
2	C	305	HEC	C4D-C3D-C2D	-2.09	103.63	106.87
2	B	307	HEC	CHD-C1D-ND	2.09	127.65	123.86
2	C	308	HEC	CBD-CAD-C3D	-2.09	106.76	112.53
2	A	307	HEC	CHD-C1D-ND	2.08	127.64	123.86
2	B	306	HEC	CHB-C4A-NA	2.08	126.72	124.45
2	C	307	HEC	CHD-C1D-ND	2.08	127.64	123.86
2	C	301	HEC	C4D-ND-C1D	2.08	109.21	105.82
2	A	301	HEC	C4D-ND-C1D	2.07	109.20	105.82
2	A	305	HEC	CHD-C1D-ND	2.07	127.61	123.86
2	B	303	HEC	CAA-CBA-CGA	-2.06	108.19	113.67
2	C	305	HEC	CHD-C1D-ND	2.06	127.60	123.86
2	A	303	HEC	CAA-CBA-CGA	-2.06	108.20	113.67
2	C	303	HEC	CAA-CBA-CGA	-2.06	108.20	113.67
2	B	305	HEC	CHD-C1D-ND	2.06	127.59	123.86
2	B	301	HEC	C4D-ND-C1D	2.05	109.17	105.82
2	C	302	HEC	C2A-C1A-NA	-2.03	108.36	110.32
2	C	307	HEC	CMD-C2D-C3D	2.03	129.93	125.62
2	B	308	HEC	CHA-C1A-NA	2.03	126.66	124.45
2	C	301	HEC	C1A-C2A-C3A	2.03	109.78	107.11
2	A	308	HEC	CHA-C1A-NA	2.03	126.66	124.45
2	A	301	HEC	C1A-C2A-C3A	2.02	109.77	107.11
2	B	307	HEC	CMD-C2D-C3D	2.02	129.91	125.62
2	A	302	HEC	C2A-C1A-NA	-2.02	108.37	110.32
2	A	307	HEC	CMD-C2D-C3D	2.02	129.91	125.62
2	B	302	HEC	C2A-C1A-NA	-2.02	108.38	110.32
2	B	303	HEC	CHA-C4D-ND	2.00	127.49	123.86

There are no chirality outliers.

All (159) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	HEC	C2B-C3B-CAB-CBB
2	A	301	HEC	C2C-C3C-CAC-CBC
2	A	301	HEC	C4C-C3C-CAC-CBC
2	A	302	HEC	C2B-C3B-CAB-CBB
2	A	302	HEC	C4B-C3B-CAB-CBB
2	A	302	HEC	C2C-C3C-CAC-CBC
2	A	303	HEC	C2B-C3B-CAB-CBB
2	A	303	HEC	C4B-C3B-CAB-CBB
2	A	303	HEC	C2C-C3C-CAC-CBC
2	A	303	HEC	C2D-C3D-CAD-CBD
2	A	304	HEC	C2B-C3B-CAB-CBB
2	A	304	HEC	C4B-C3B-CAB-CBB
2	A	305	HEC	C2B-C3B-CAB-CBB
2	A	305	HEC	C4B-C3B-CAB-CBB
2	A	305	HEC	C2C-C3C-CAC-CBC
2	A	306	HEC	C1A-C2A-CAA-CBA
2	A	306	HEC	C3A-C2A-CAA-CBA
2	A	306	HEC	C2C-C3C-CAC-CBC
2	A	306	HEC	C4C-C3C-CAC-CBC
2	A	307	HEC	C2B-C3B-CAB-CBB
2	A	307	HEC	C2C-C3C-CAC-CBC
2	A	307	HEC	C4C-C3C-CAC-CBC
2	A	308	HEC	C2B-C3B-CAB-CBB
2	A	308	HEC	C4B-C3B-CAB-CBB
2	B	301	HEC	C2B-C3B-CAB-CBB
2	B	301	HEC	C2C-C3C-CAC-CBC
2	B	301	HEC	C4C-C3C-CAC-CBC
2	B	302	HEC	C2B-C3B-CAB-CBB
2	B	302	HEC	C4B-C3B-CAB-CBB
2	B	302	HEC	C2C-C3C-CAC-CBC
2	B	303	HEC	C2B-C3B-CAB-CBB
2	B	303	HEC	C4B-C3B-CAB-CBB
2	B	303	HEC	C2C-C3C-CAC-CBC
2	B	303	HEC	C2D-C3D-CAD-CBD
2	B	304	HEC	C2B-C3B-CAB-CBB
2	B	304	HEC	C4B-C3B-CAB-CBB
2	B	305	HEC	C2B-C3B-CAB-CBB
2	B	305	HEC	C4B-C3B-CAB-CBB
2	B	305	HEC	C2C-C3C-CAC-CBC
2	B	306	HEC	C1A-C2A-CAA-CBA

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Mol	Chain	Res	Type	Atoms
2	B	306	HEC	C3A-C2A-CAA-CBA
2	B	306	HEC	C2C-C3C-CAC-CBC
2	B	306	HEC	C4C-C3C-CAC-CBC
2	B	307	HEC	C2B-C3B-CAB-CBB
2	B	307	HEC	C2C-C3C-CAC-CBC
2	B	307	HEC	C4C-C3C-CAC-CBC
2	B	308	HEC	C2B-C3B-CAB-CBB
2	B	308	HEC	C4B-C3B-CAB-CBB
2	C	301	HEC	C2B-C3B-CAB-CBB
2	C	301	HEC	C2C-C3C-CAC-CBC
2	C	301	HEC	C4C-C3C-CAC-CBC
2	C	302	HEC	C2B-C3B-CAB-CBB
2	C	302	HEC	C4B-C3B-CAB-CBB
2	C	302	HEC	C2C-C3C-CAC-CBC
2	C	303	HEC	C2B-C3B-CAB-CBB
2	C	303	HEC	C4B-C3B-CAB-CBB
2	C	303	HEC	C2C-C3C-CAC-CBC
2	C	303	HEC	C2D-C3D-CAD-CBD
2	C	304	HEC	C2B-C3B-CAB-CBB
2	C	304	HEC	C4B-C3B-CAB-CBB
2	C	305	HEC	C2B-C3B-CAB-CBB
2	C	305	HEC	C4B-C3B-CAB-CBB
2	C	305	HEC	C2C-C3C-CAC-CBC
2	C	306	HEC	C1A-C2A-CAA-CBA
2	C	306	HEC	C3A-C2A-CAA-CBA
2	C	306	HEC	C2C-C3C-CAC-CBC
2	C	306	HEC	C4C-C3C-CAC-CBC
2	C	307	HEC	C2B-C3B-CAB-CBB
2	C	307	HEC	C2C-C3C-CAC-CBC
2	C	307	HEC	C4C-C3C-CAC-CBC
2	C	308	HEC	C2B-C3B-CAB-CBB
2	C	308	HEC	C4B-C3B-CAB-CBB
2	A	303	HEC	C4D-C3D-CAD-CBD
2	A	307	HEC	C4D-C3D-CAD-CBD
2	B	303	HEC	C4D-C3D-CAD-CBD
2	B	307	HEC	C4D-C3D-CAD-CBD
2	C	303	HEC	C4D-C3D-CAD-CBD
2	C	307	HEC	C4D-C3D-CAD-CBD
2	A	304	HEC	C2A-CAA-CBA-CGA
2	B	304	HEC	C2A-CAA-CBA-CGA
2	C	304	HEC	C2A-CAA-CBA-CGA
2	A	307	HEC	C2D-C3D-CAD-CBD

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Mol	Chain	Res	Type	Atoms
2	B	307	HEC	C2D-C3D-CAD-CBD
2	C	307	HEC	C2D-C3D-CAD-CBD
2	A	304	HEC	C1A-C2A-CAA-CBA
2	B	304	HEC	C1A-C2A-CAA-CBA
2	C	304	HEC	C1A-C2A-CAA-CBA
2	A	304	HEC	C3A-C2A-CAA-CBA
2	B	304	HEC	C3A-C2A-CAA-CBA
2	C	304	HEC	C3A-C2A-CAA-CBA
2	A	305	HEC	C2A-CAA-CBA-CGA
2	B	305	HEC	C2A-CAA-CBA-CGA
2	C	305	HEC	C2A-CAA-CBA-CGA
2	A	302	HEC	C2A-CAA-CBA-CGA
2	B	302	HEC	C2A-CAA-CBA-CGA
2	C	302	HEC	C2A-CAA-CBA-CGA
2	A	307	HEC	C1A-C2A-CAA-CBA
2	B	307	HEC	C1A-C2A-CAA-CBA
2	C	307	HEC	C1A-C2A-CAA-CBA
2	A	308	HEC	C3D-CAD-CBD-CGD
2	B	308	HEC	C3D-CAD-CBD-CGD
2	C	308	HEC	C3D-CAD-CBD-CGD
2	A	301	HEC	C4B-C3B-CAB-CBB
2	A	302	HEC	C4C-C3C-CAC-CBC
2	A	303	HEC	C4C-C3C-CAC-CBC
2	A	304	HEC	C4C-C3C-CAC-CBC
2	A	305	HEC	C4C-C3C-CAC-CBC
2	A	306	HEC	C4B-C3B-CAB-CBB
2	A	307	HEC	C4B-C3B-CAB-CBB
2	A	308	HEC	C4C-C3C-CAC-CBC
2	B	301	HEC	C4B-C3B-CAB-CBB
2	B	302	HEC	C4C-C3C-CAC-CBC
2	B	303	HEC	C4C-C3C-CAC-CBC
2	B	304	HEC	C4C-C3C-CAC-CBC
2	B	305	HEC	C4C-C3C-CAC-CBC
2	B	306	HEC	C4B-C3B-CAB-CBB
2	B	307	HEC	C4B-C3B-CAB-CBB
2	B	308	HEC	C4C-C3C-CAC-CBC
2	C	301	HEC	C4B-C3B-CAB-CBB
2	C	302	HEC	C4C-C3C-CAC-CBC
2	C	303	HEC	C4C-C3C-CAC-CBC
2	C	304	HEC	C4C-C3C-CAC-CBC
2	C	305	HEC	C4C-C3C-CAC-CBC
2	C	306	HEC	C4B-C3B-CAB-CBB

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	C	307	HEC	C4B-C3B-CAB-CBB
2	C	308	HEC	C4C-C3C-CAC-CBC
2	A	304	HEC	C2C-C3C-CAC-CBC
2	A	306	HEC	C2B-C3B-CAB-CBB
2	A	308	HEC	C2C-C3C-CAC-CBC
2	B	304	HEC	C2C-C3C-CAC-CBC
2	B	306	HEC	C2B-C3B-CAB-CBB
2	B	308	HEC	C2C-C3C-CAC-CBC
2	C	304	HEC	C2C-C3C-CAC-CBC
2	C	306	HEC	C2B-C3B-CAB-CBB
2	C	308	HEC	C2C-C3C-CAC-CBC
2	A	303	HEC	CAA-CBA-CGA-O2A
2	B	303	HEC	CAA-CBA-CGA-O2A
2	C	303	HEC	CAA-CBA-CGA-O2A
2	A	307	HEC	CAA-CBA-CGA-O1A
2	B	307	HEC	CAA-CBA-CGA-O1A
2	C	307	HEC	CAA-CBA-CGA-O1A
2	A	303	HEC	CAA-CBA-CGA-O1A
2	C	303	HEC	CAA-CBA-CGA-O1A
2	B	303	HEC	CAA-CBA-CGA-O1A
2	A	304	HEC	CAD-CBD-CGD-O2D
2	B	304	HEC	CAD-CBD-CGD-O2D
2	C	304	HEC	CAD-CBD-CGD-O2D
2	A	307	HEC	CAA-CBA-CGA-O2A
2	B	307	HEC	CAA-CBA-CGA-O2A
2	C	307	HEC	CAA-CBA-CGA-O2A
2	A	304	HEC	CAD-CBD-CGD-O1D
2	B	304	HEC	CAD-CBD-CGD-O1D
2	C	304	HEC	CAD-CBD-CGD-O1D
2	A	305	HEC	C3D-CAD-CBD-CGD
2	B	305	HEC	C3D-CAD-CBD-CGD
2	C	305	HEC	C3D-CAD-CBD-CGD
2	A	306	HEC	CAA-CBA-CGA-O2A
2	B	306	HEC	CAA-CBA-CGA-O2A
2	C	306	HEC	CAA-CBA-CGA-O2A

There are no ring outliers.

24 monomers are involved in 110 short contacts:

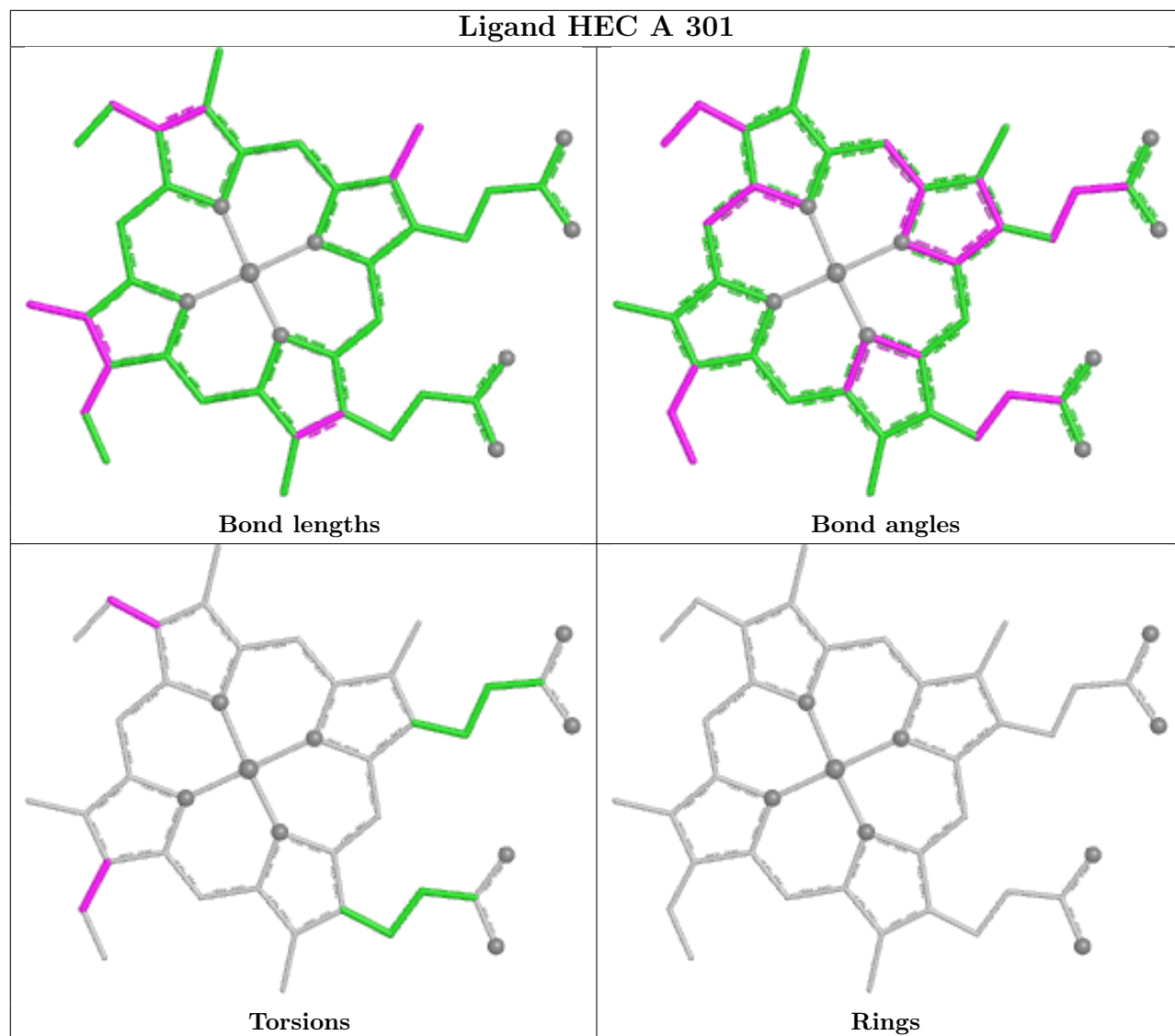
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	HEC	2	0
2	B	307	HEC	8	0

Continued on next page...

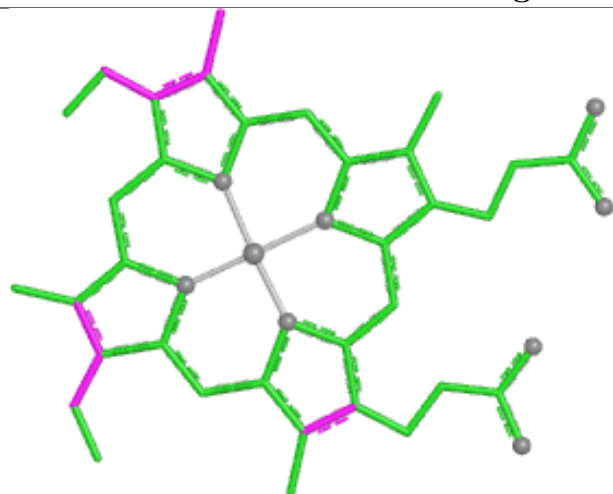
Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	304	HEC	3	0
2	C	303	HEC	1	0
2	A	305	HEC	5	0
2	C	308	HEC	3	0
2	A	303	HEC	1	0
2	B	301	HEC	2	0
2	B	308	HEC	4	0
2	A	304	HEC	3	0
2	C	301	HEC	2	0
2	B	303	HEC	1	0
2	C	305	HEC	5	0
2	C	302	HEC	4	0
2	A	307	HEC	9	0
2	B	306	HEC	9	0
2	B	305	HEC	6	0
2	C	307	HEC	8	0
2	C	306	HEC	9	0
2	A	302	HEC	5	0
2	C	304	HEC	3	0
2	A	308	HEC	3	0
2	B	302	HEC	5	0
2	A	306	HEC	9	0

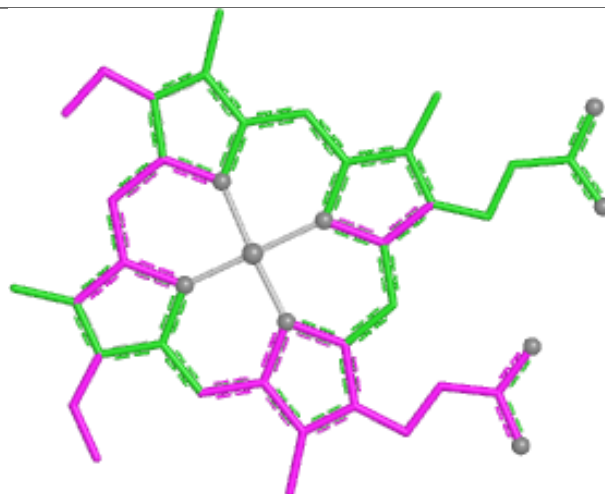
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



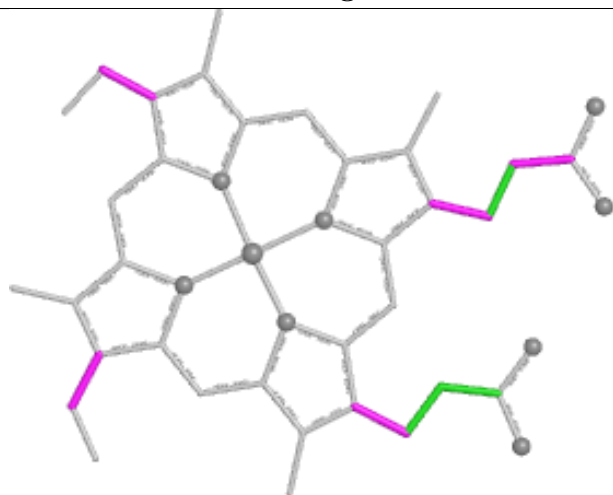
Ligand HEC B 307



Bond lengths



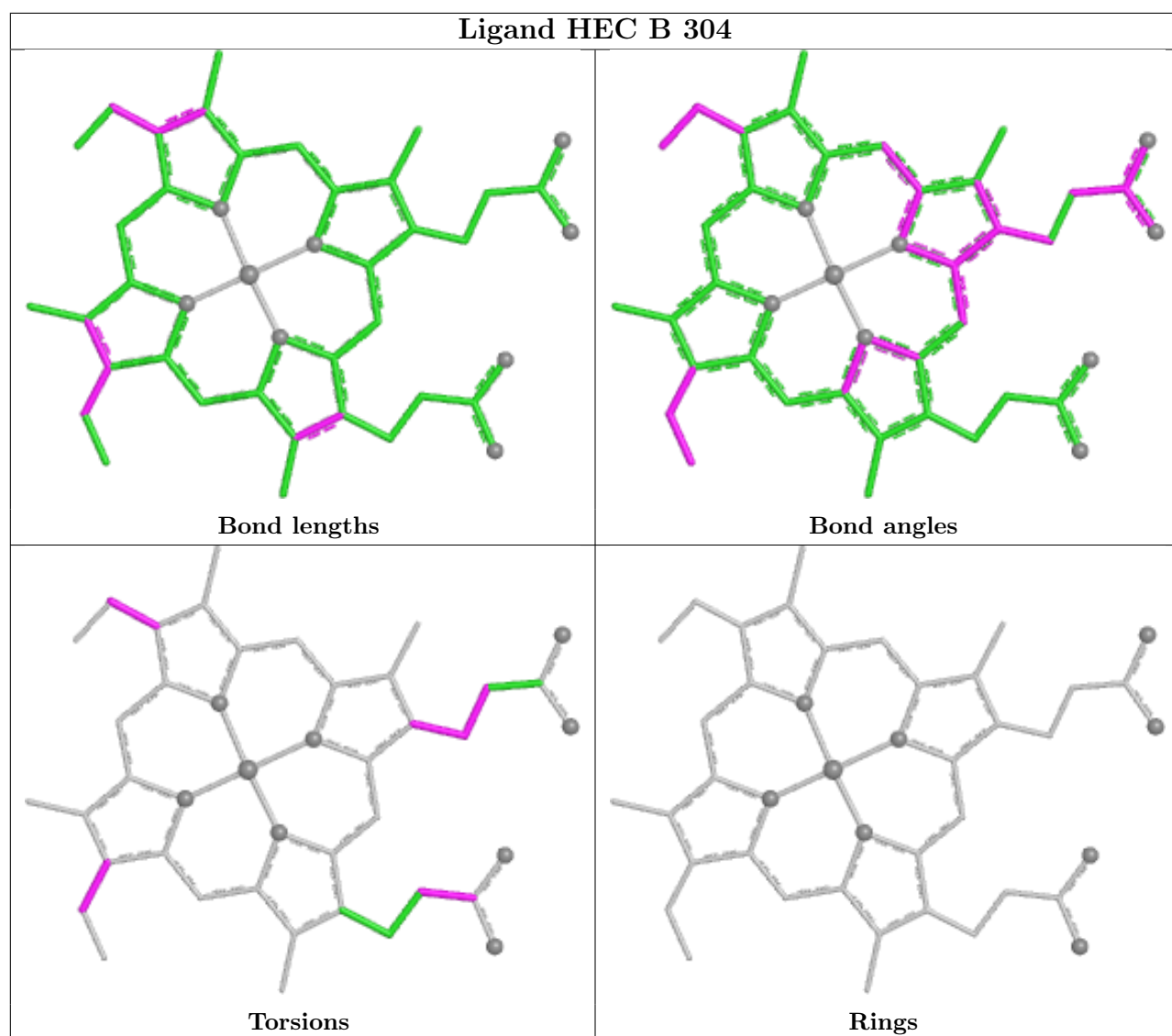
Bond angles



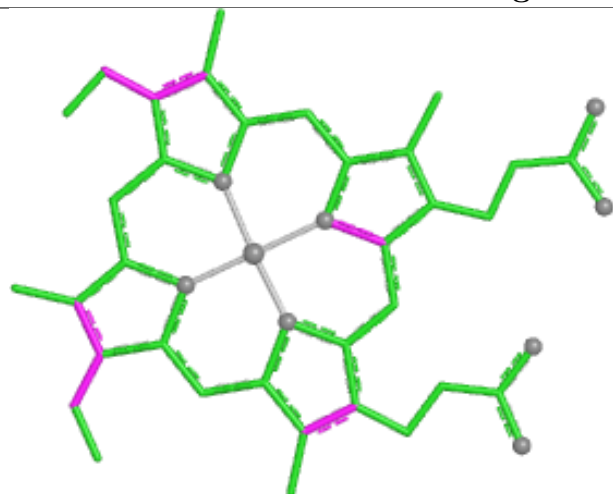
Torsions



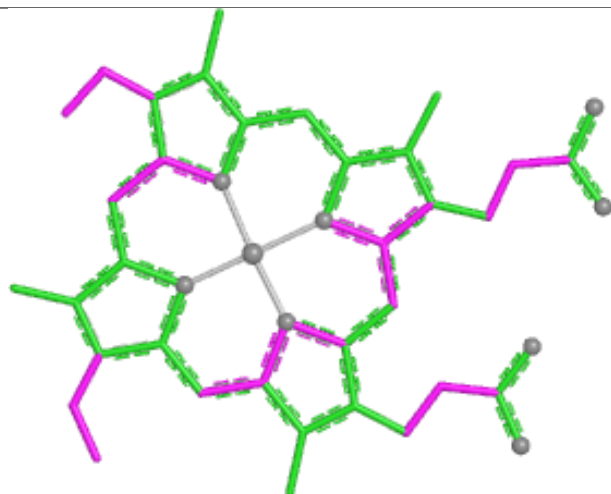
Rings



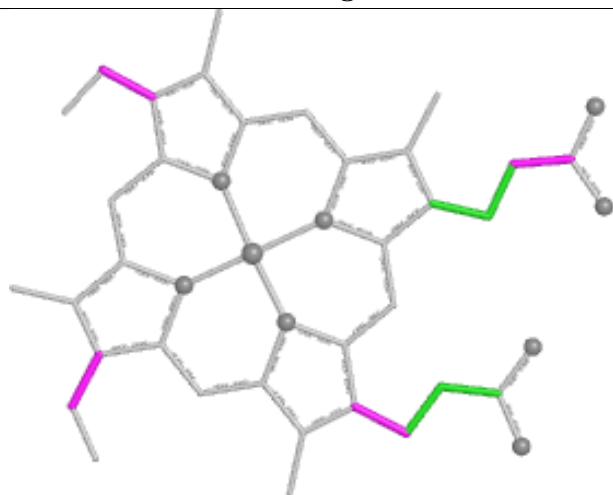
Ligand HEC C 303



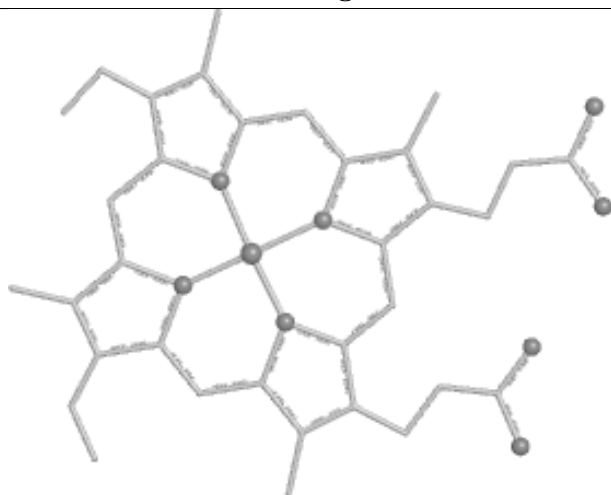
Bond lengths



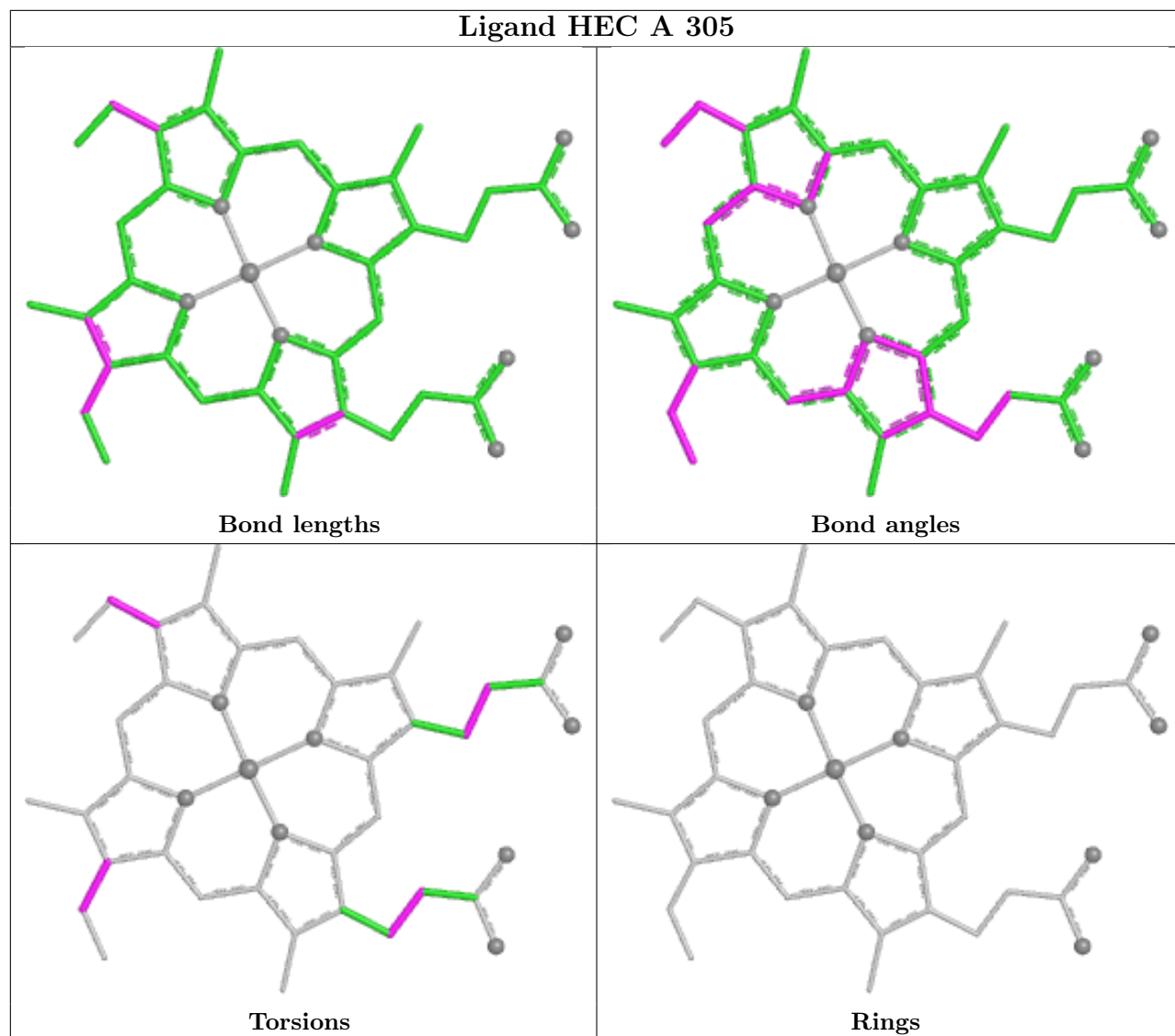
Bond angles

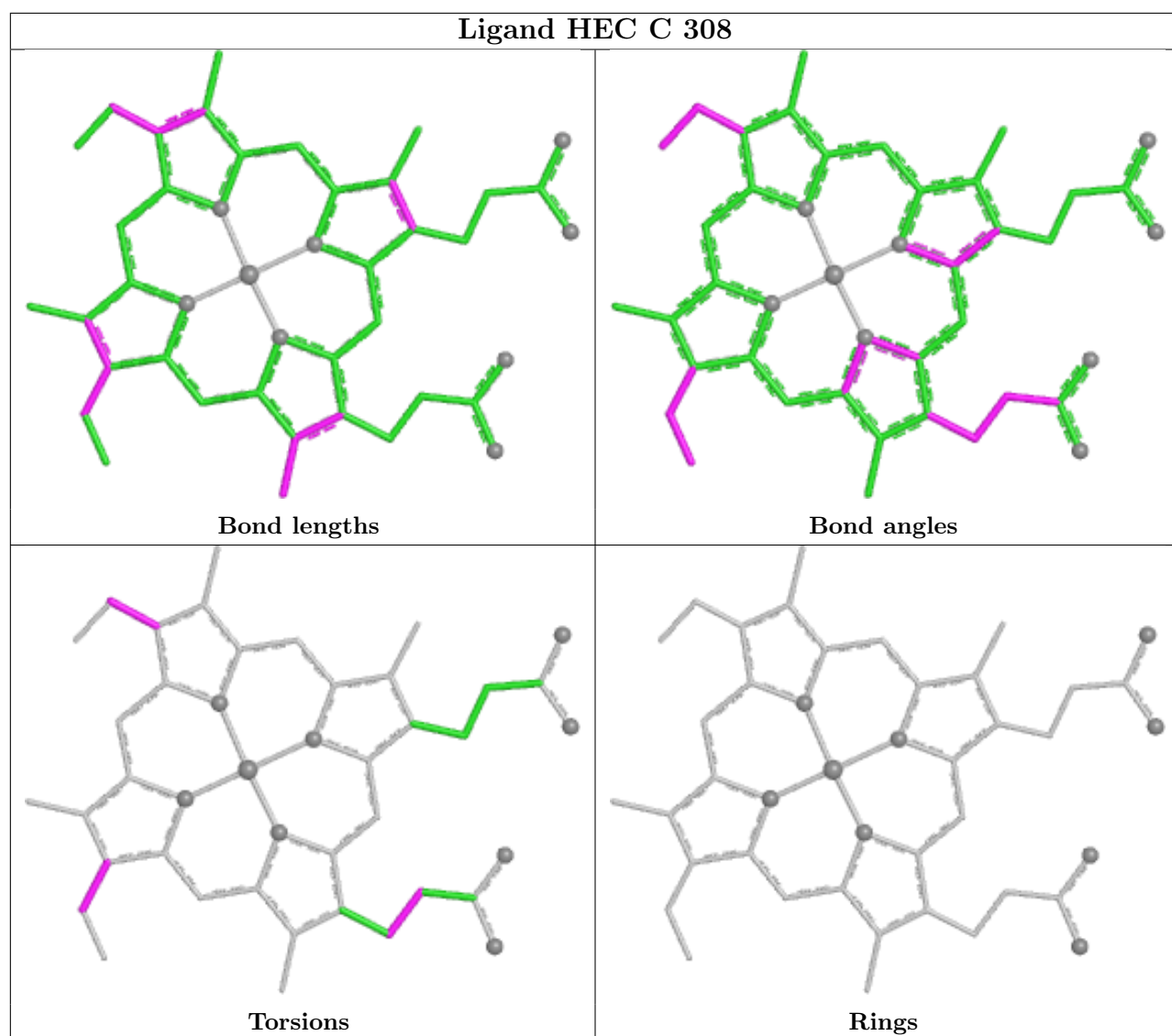


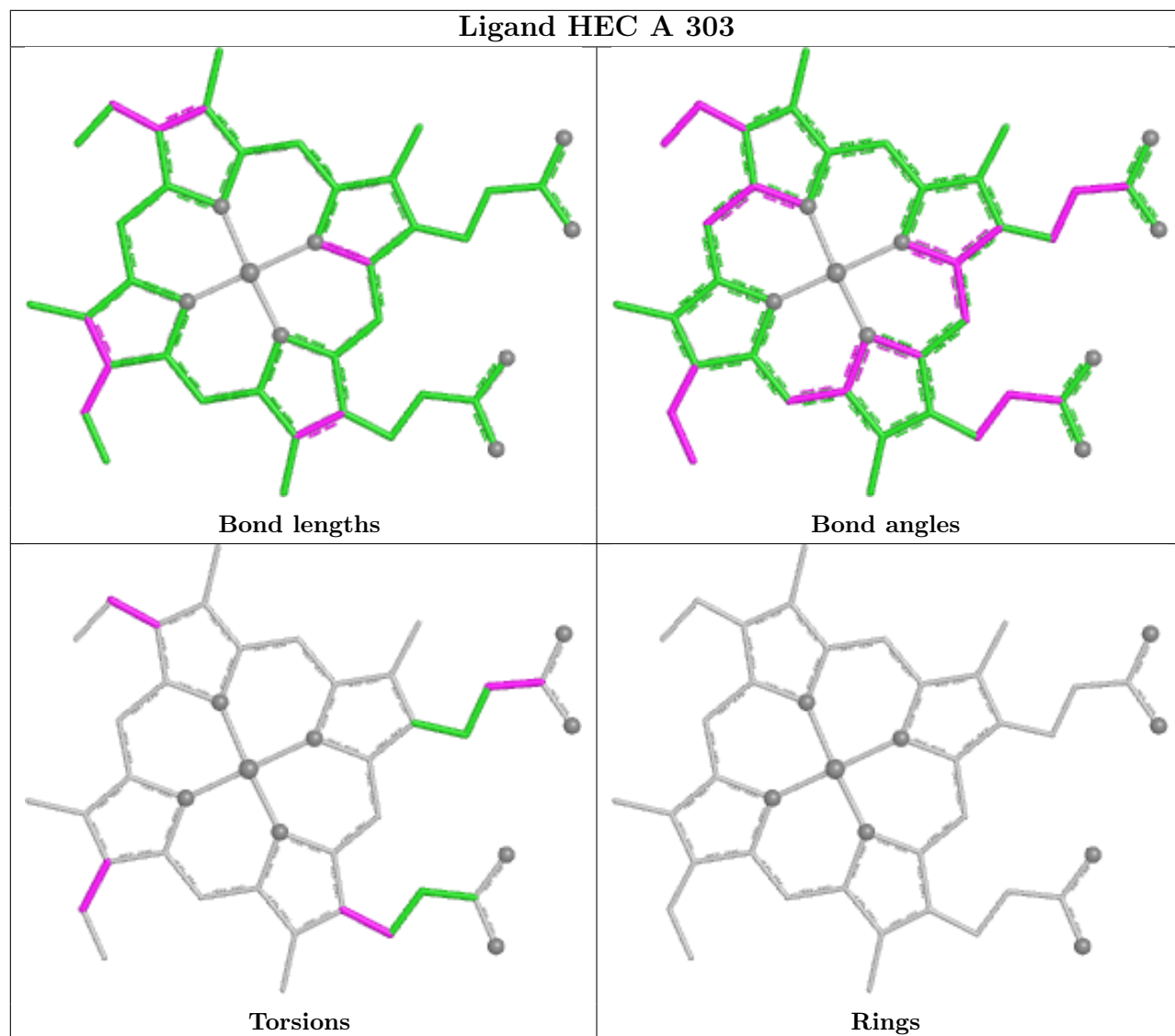
Torsions



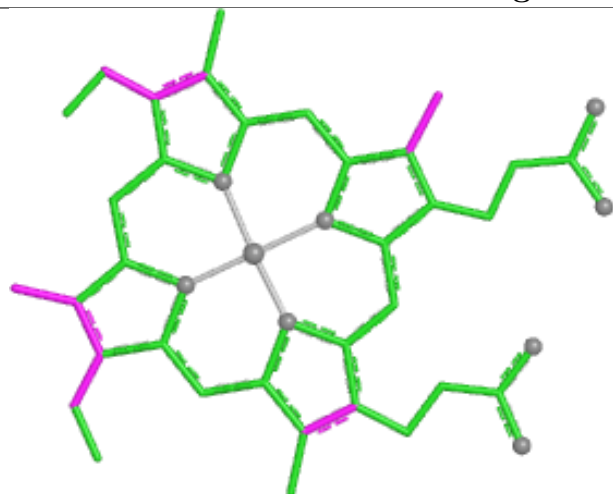
Rings



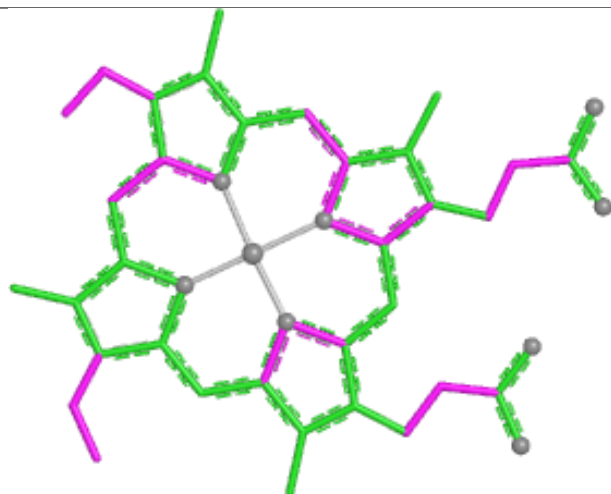




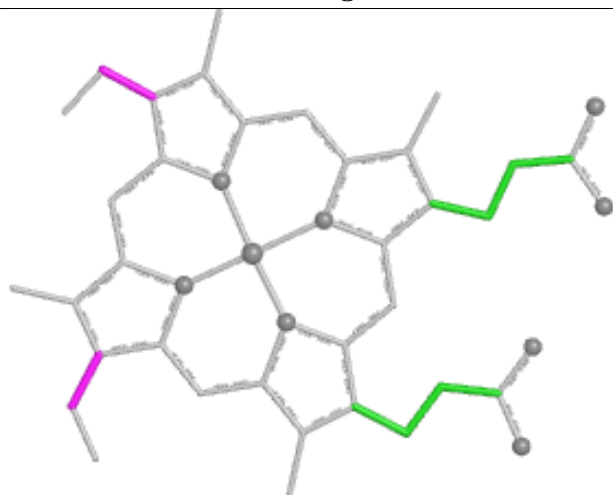
Ligand HEC B 301



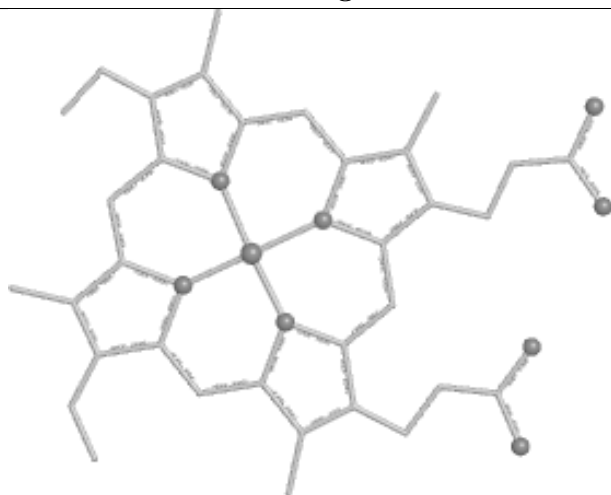
Bond lengths



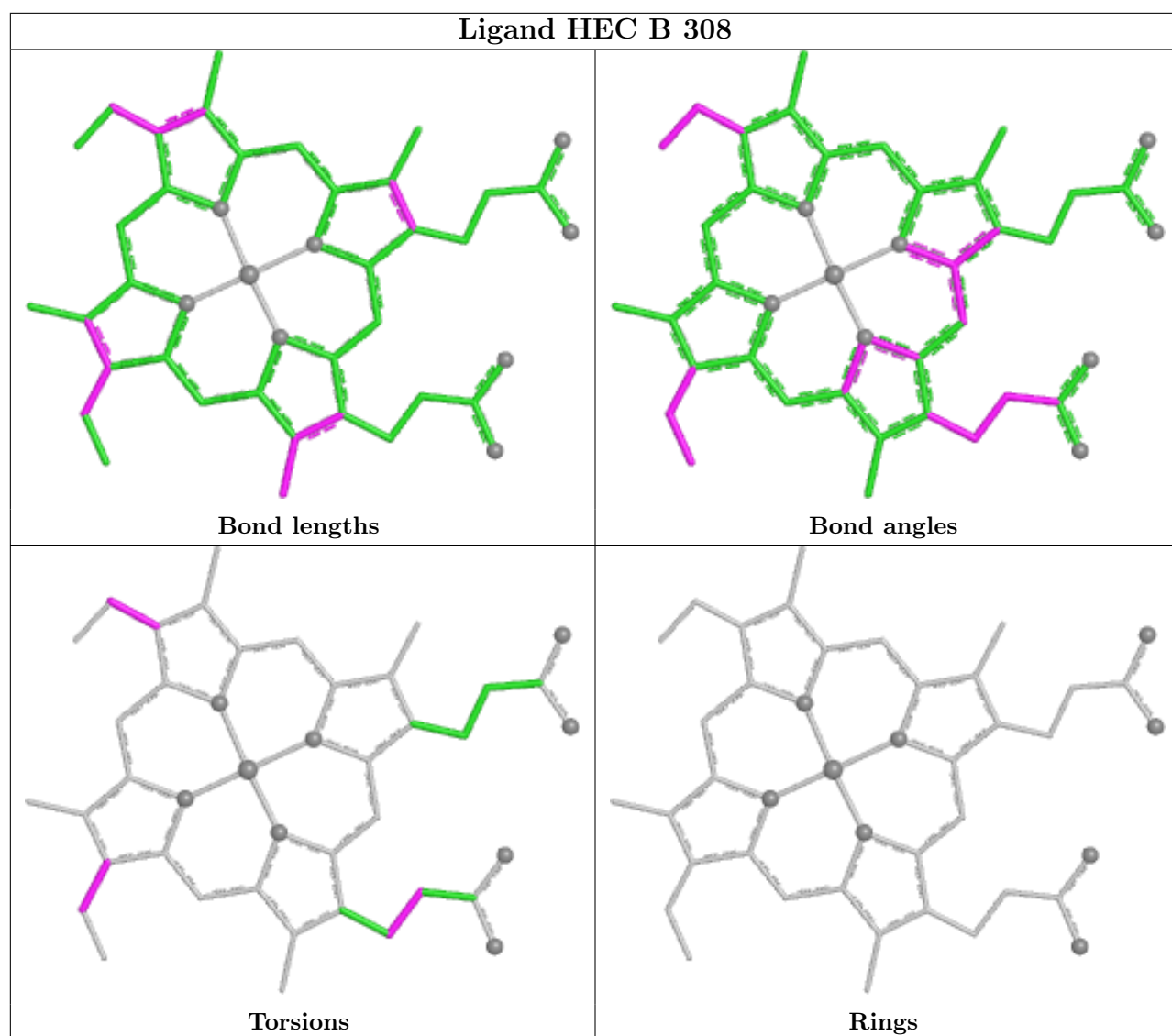
Bond angles

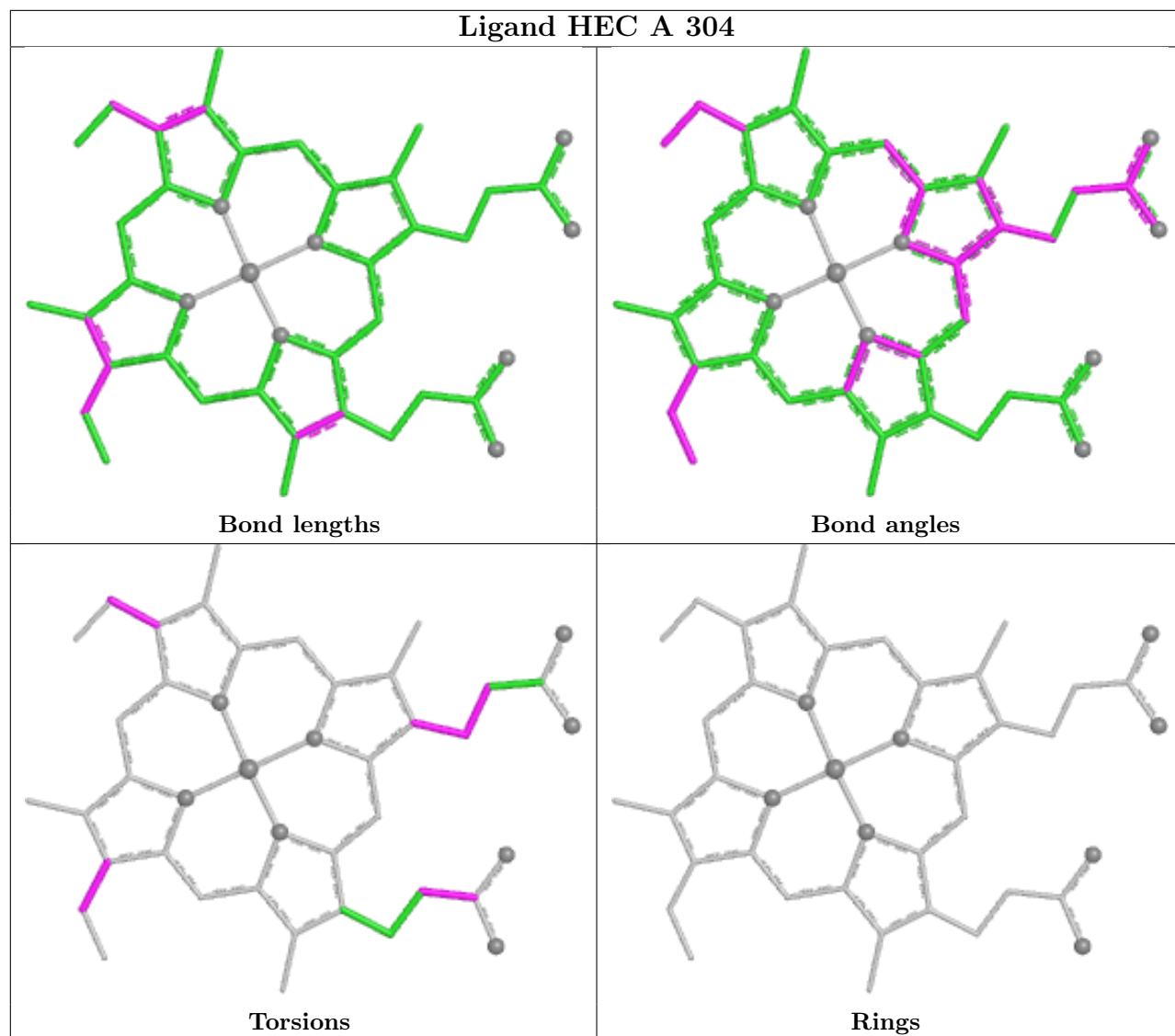


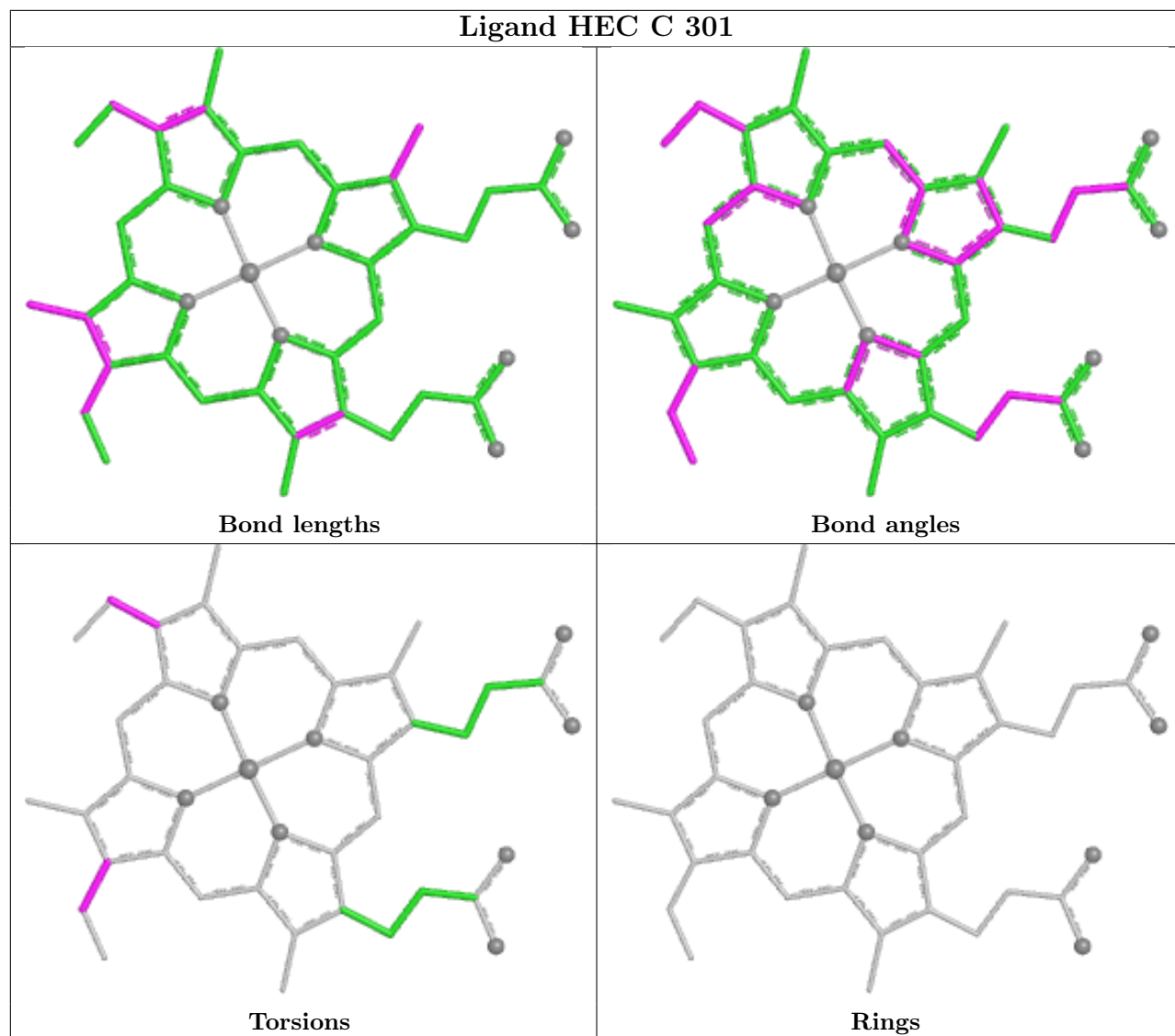
Torsions



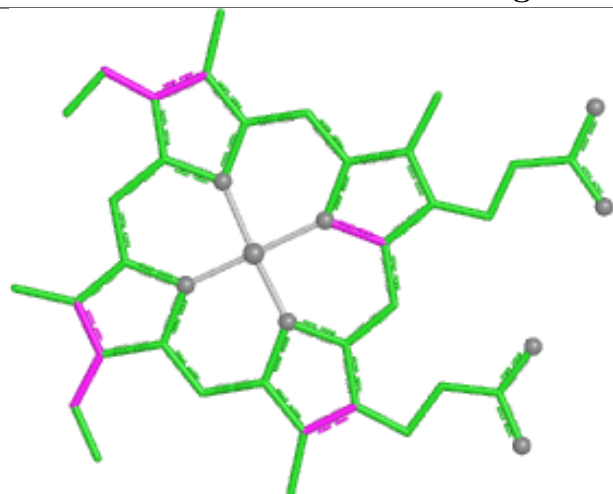
Rings



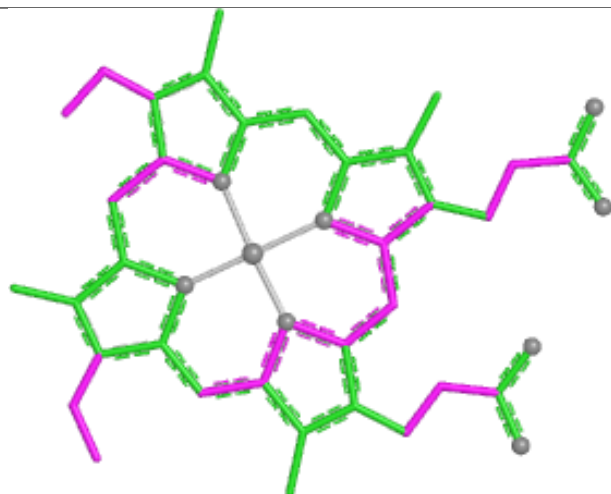




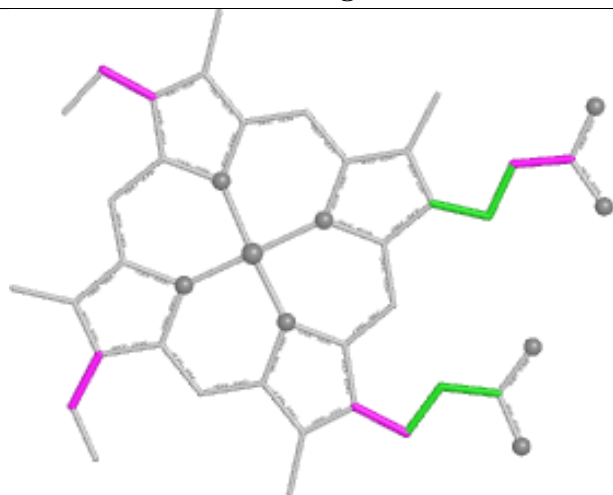
Ligand HEC B 303



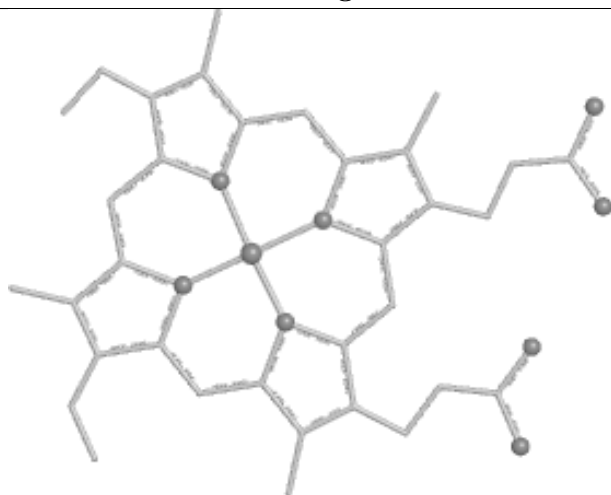
Bond lengths



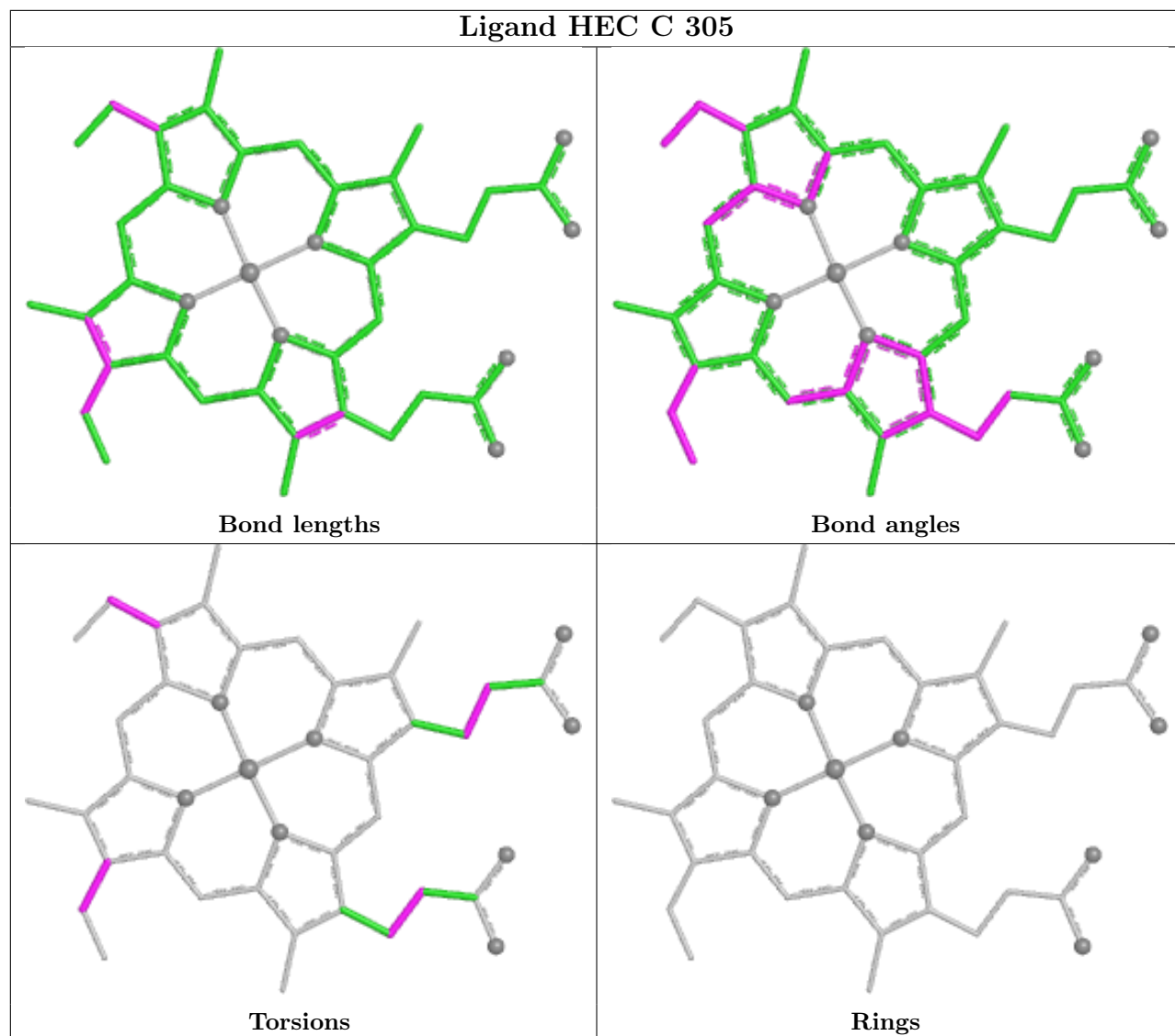
Bond angles

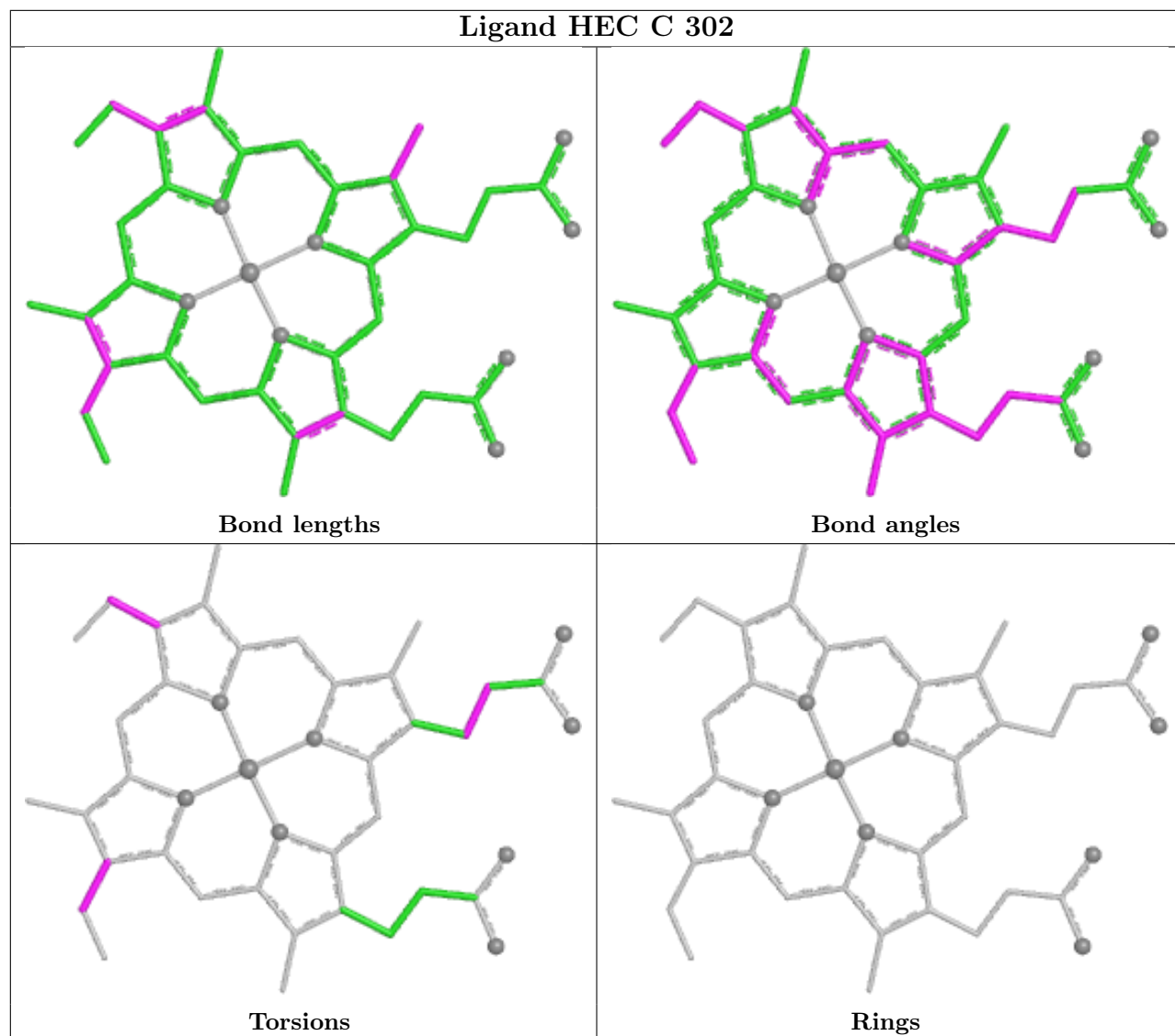


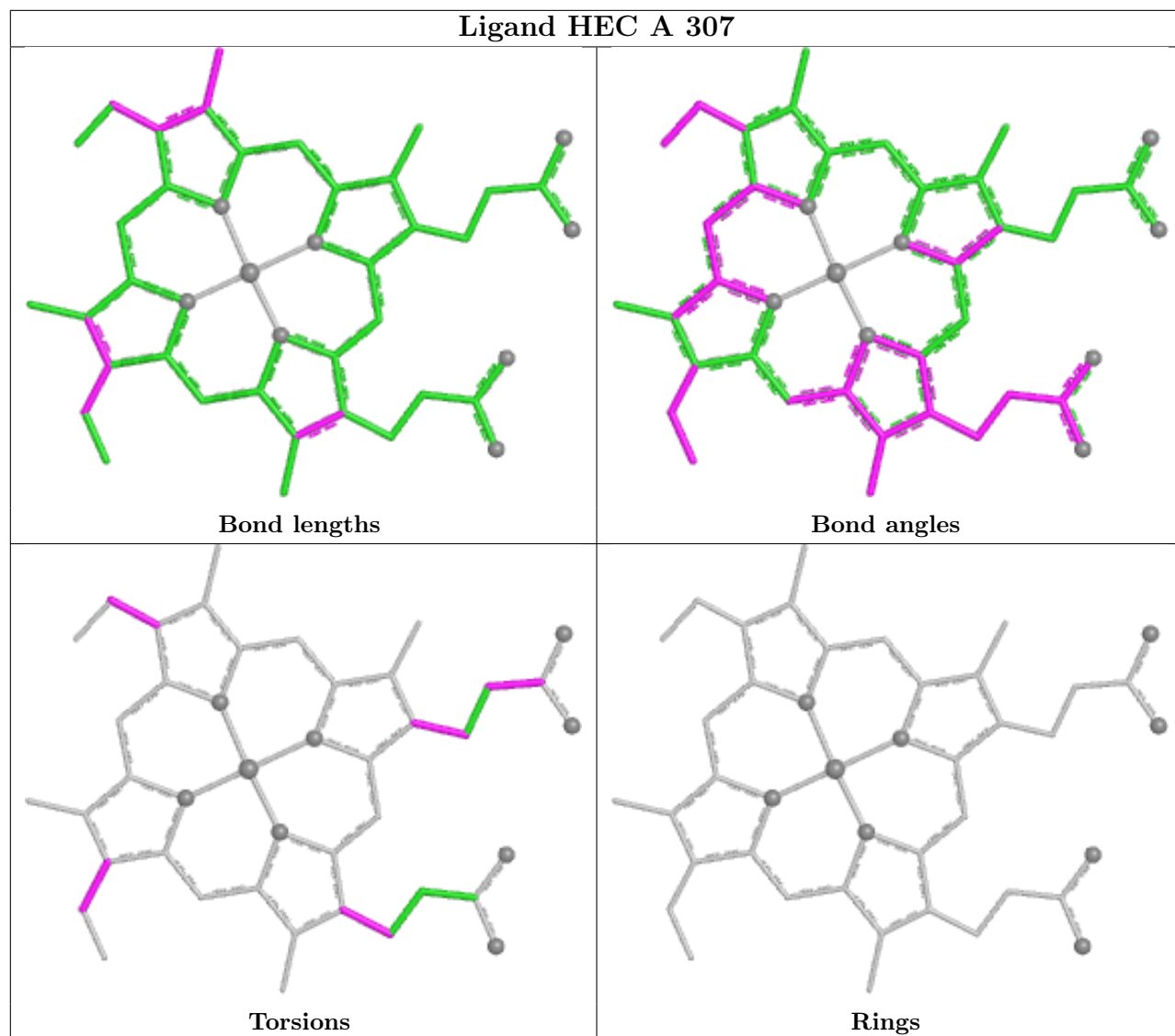
Torsions



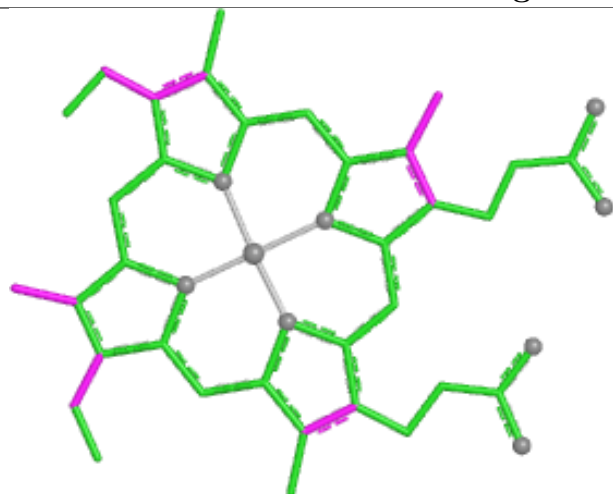
Rings



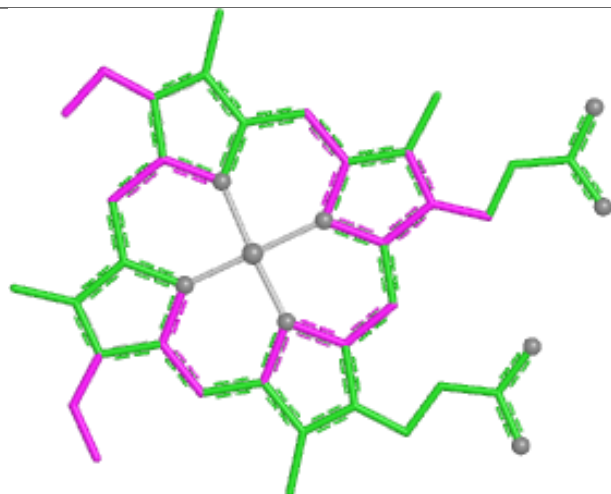




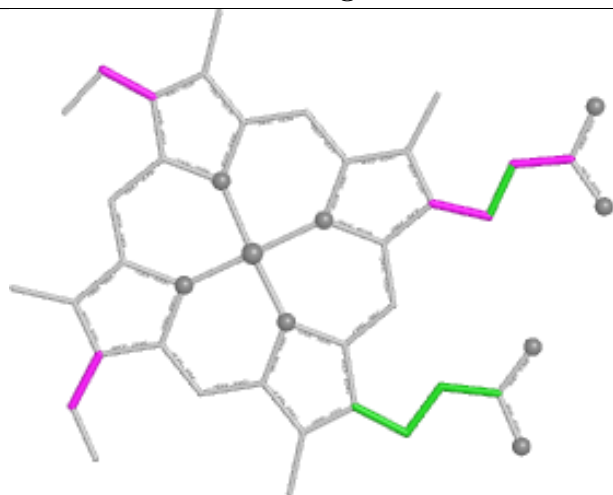
Ligand HEC B 306



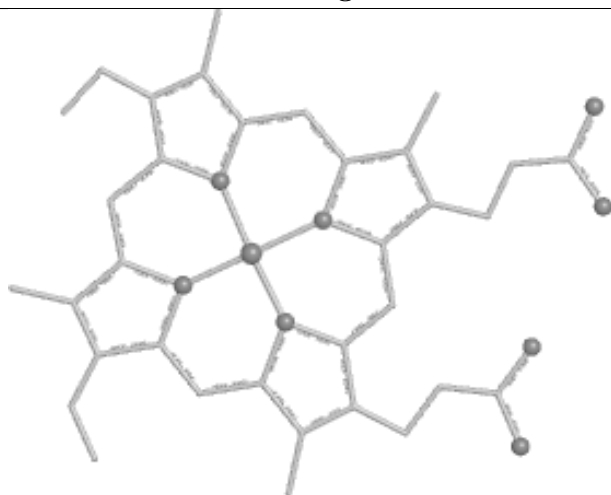
Bond lengths



Bond angles

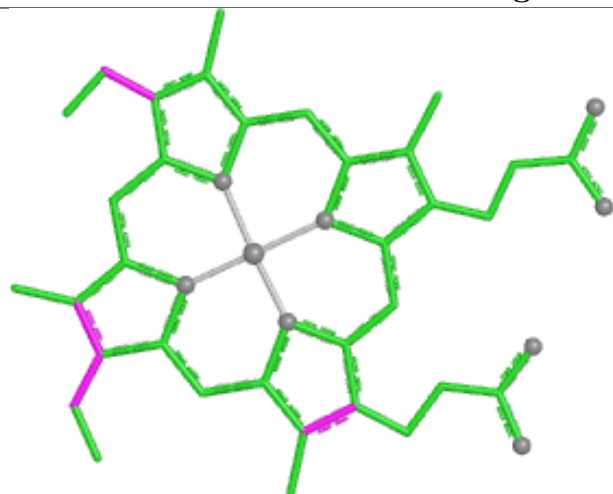


Torsions

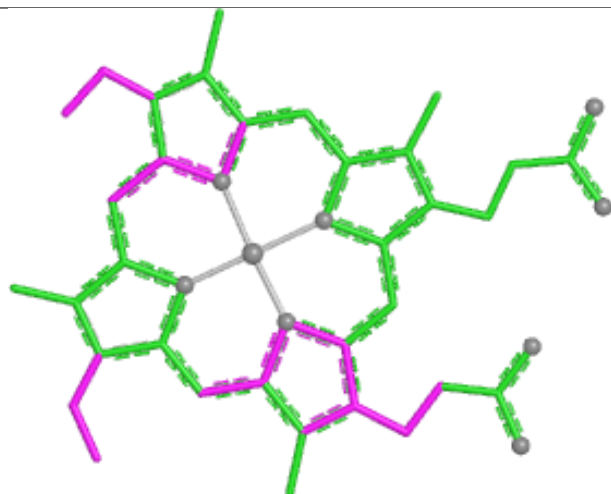


Rings

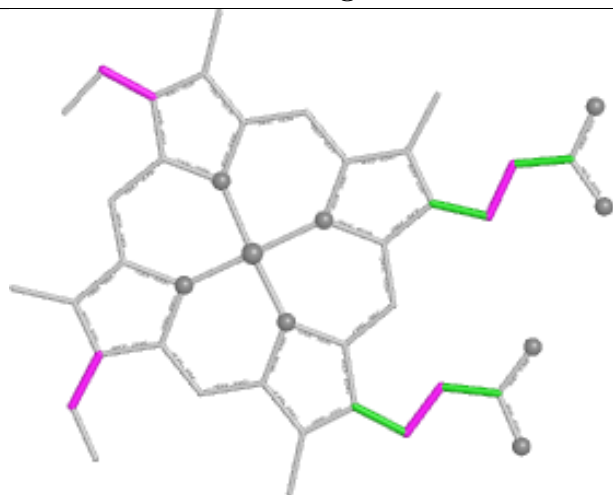
Ligand HEC B 305



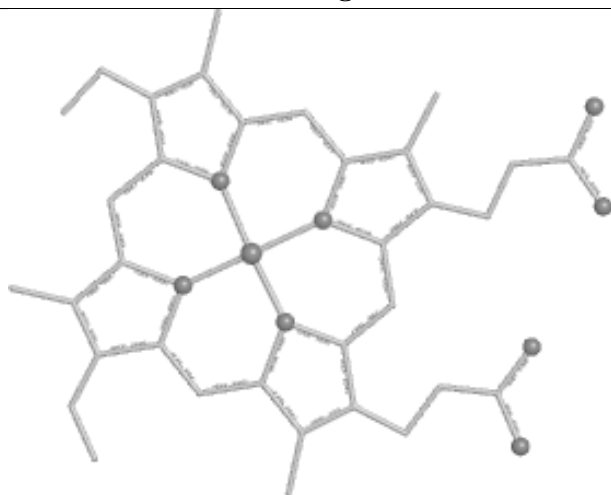
Bond lengths



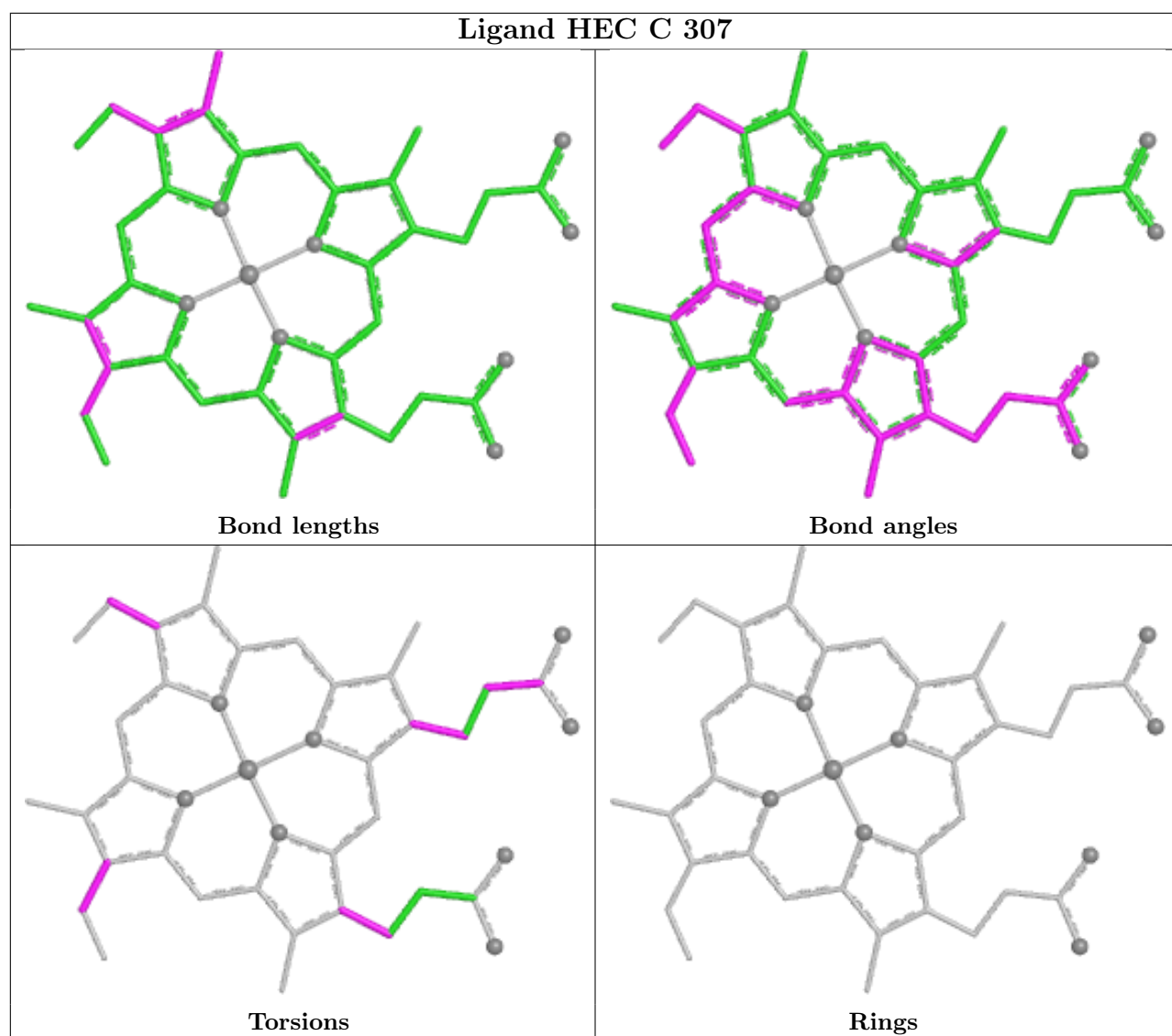
Bond angles

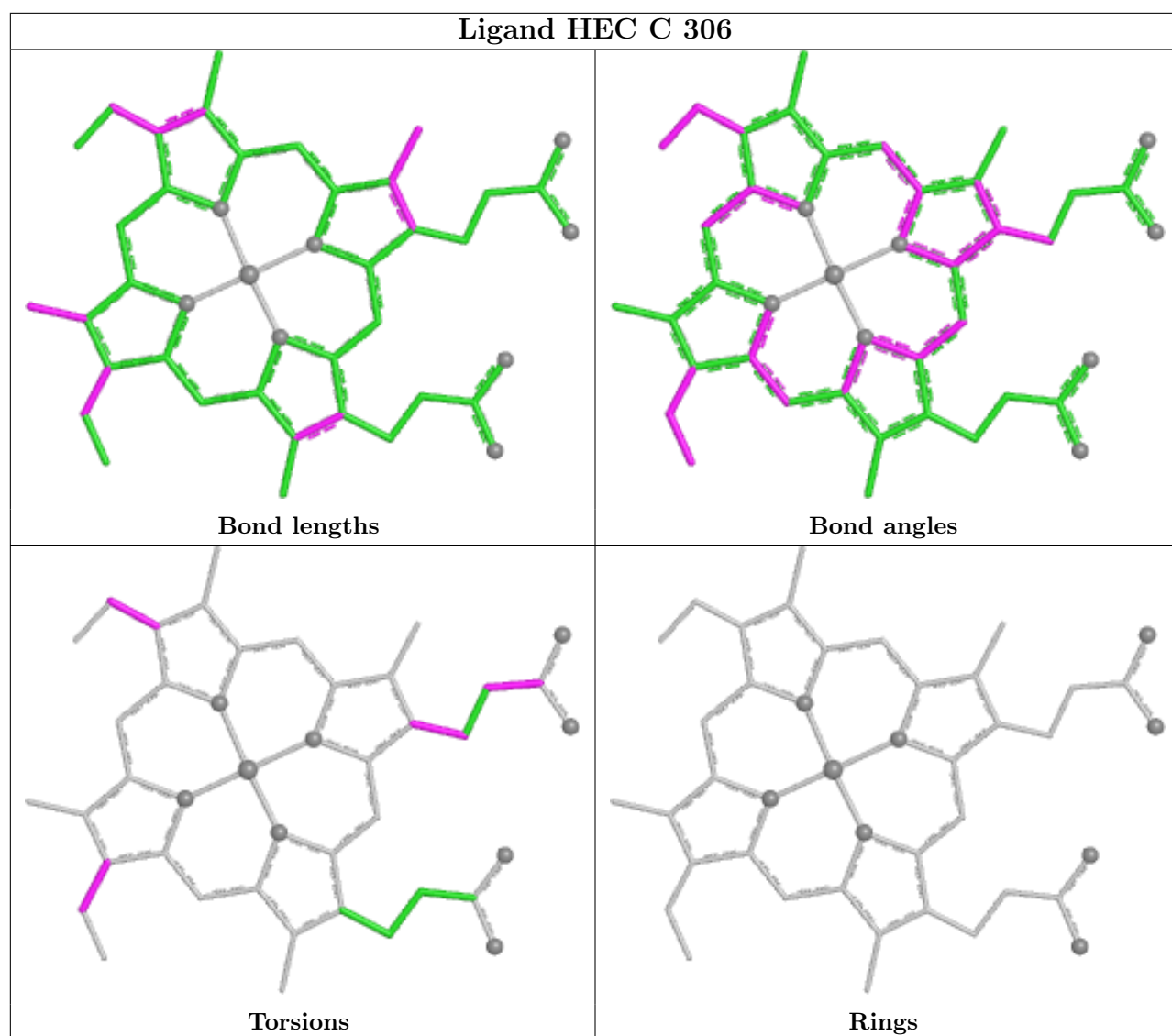


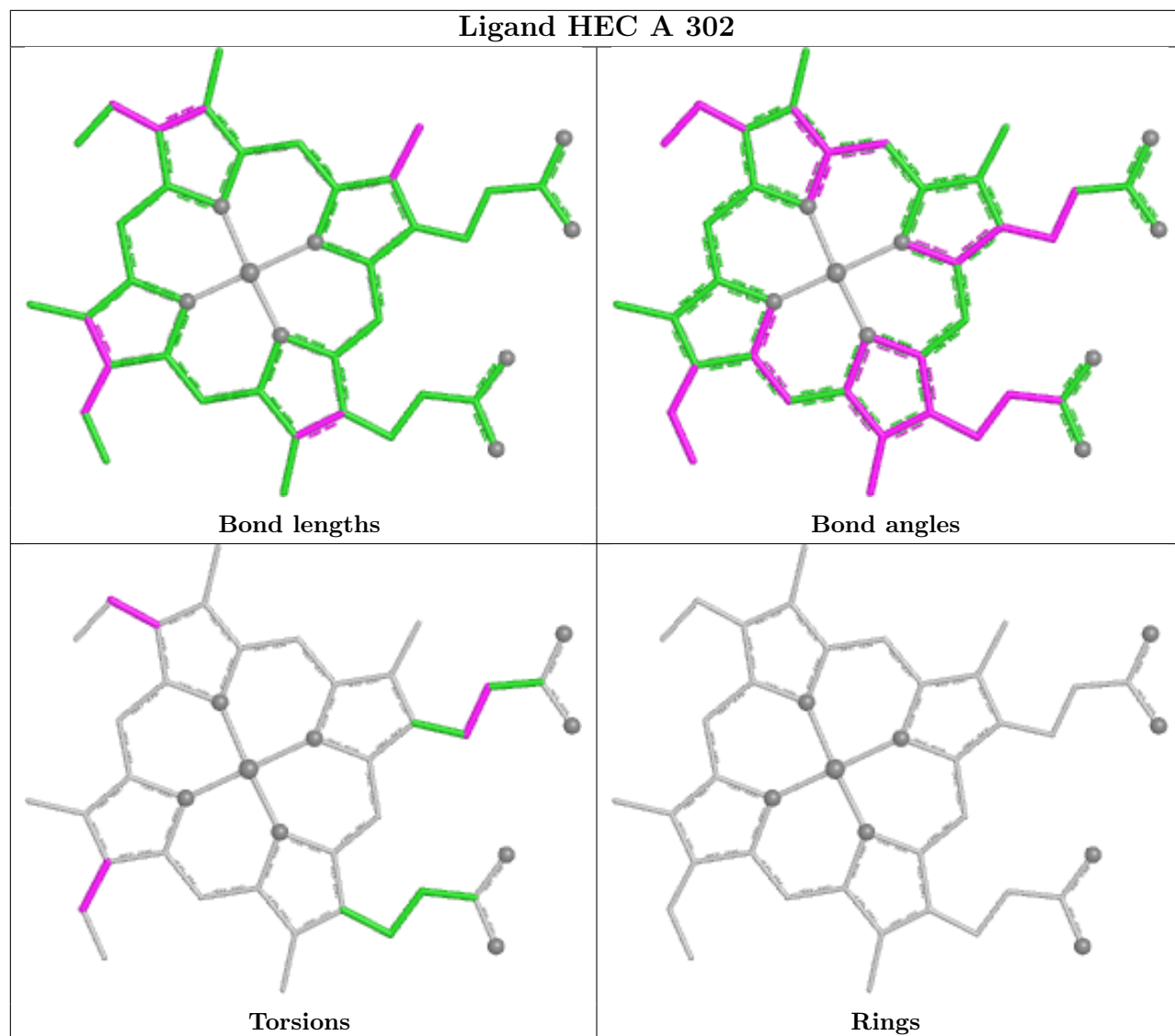
Torsions

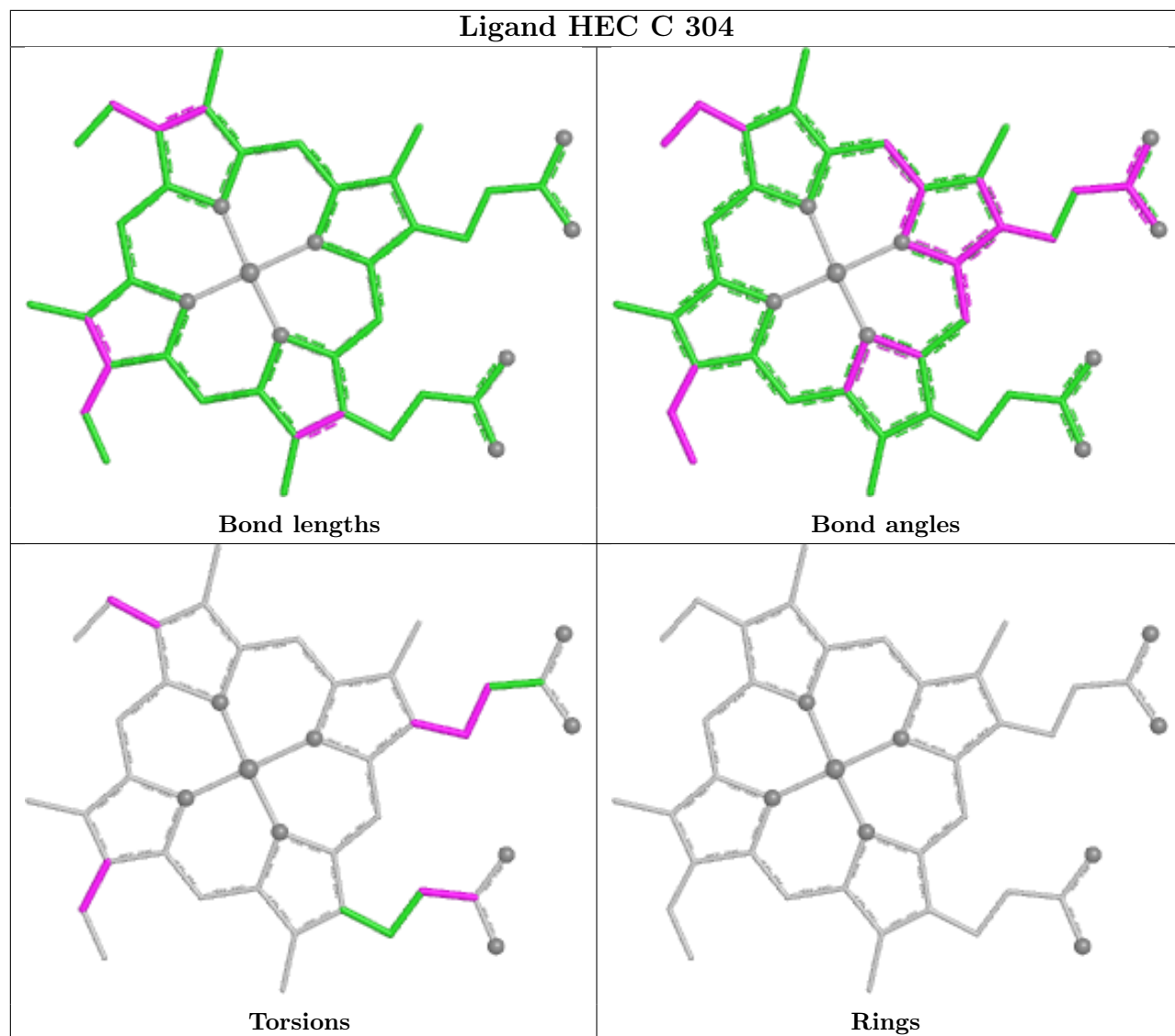


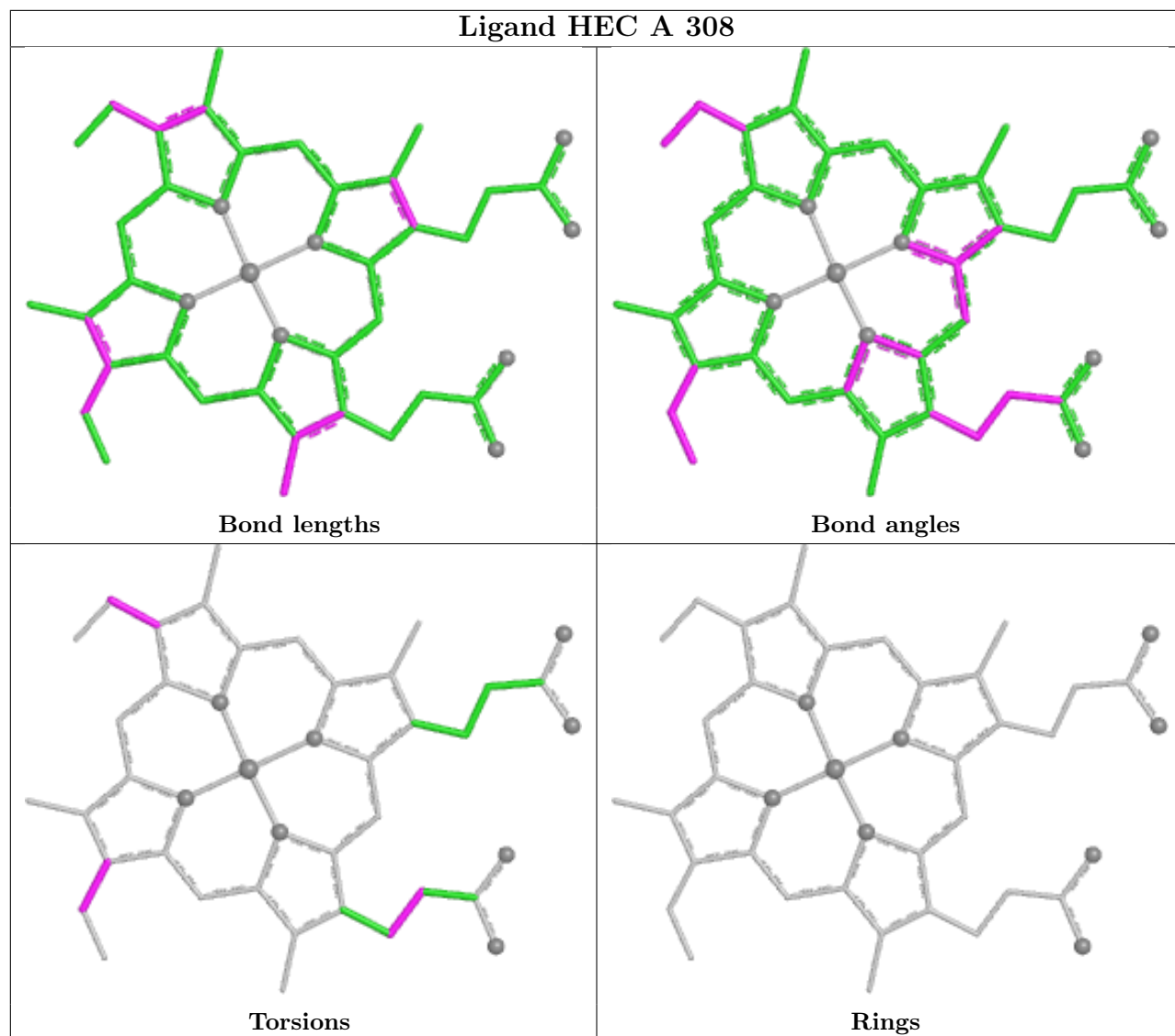
Rings

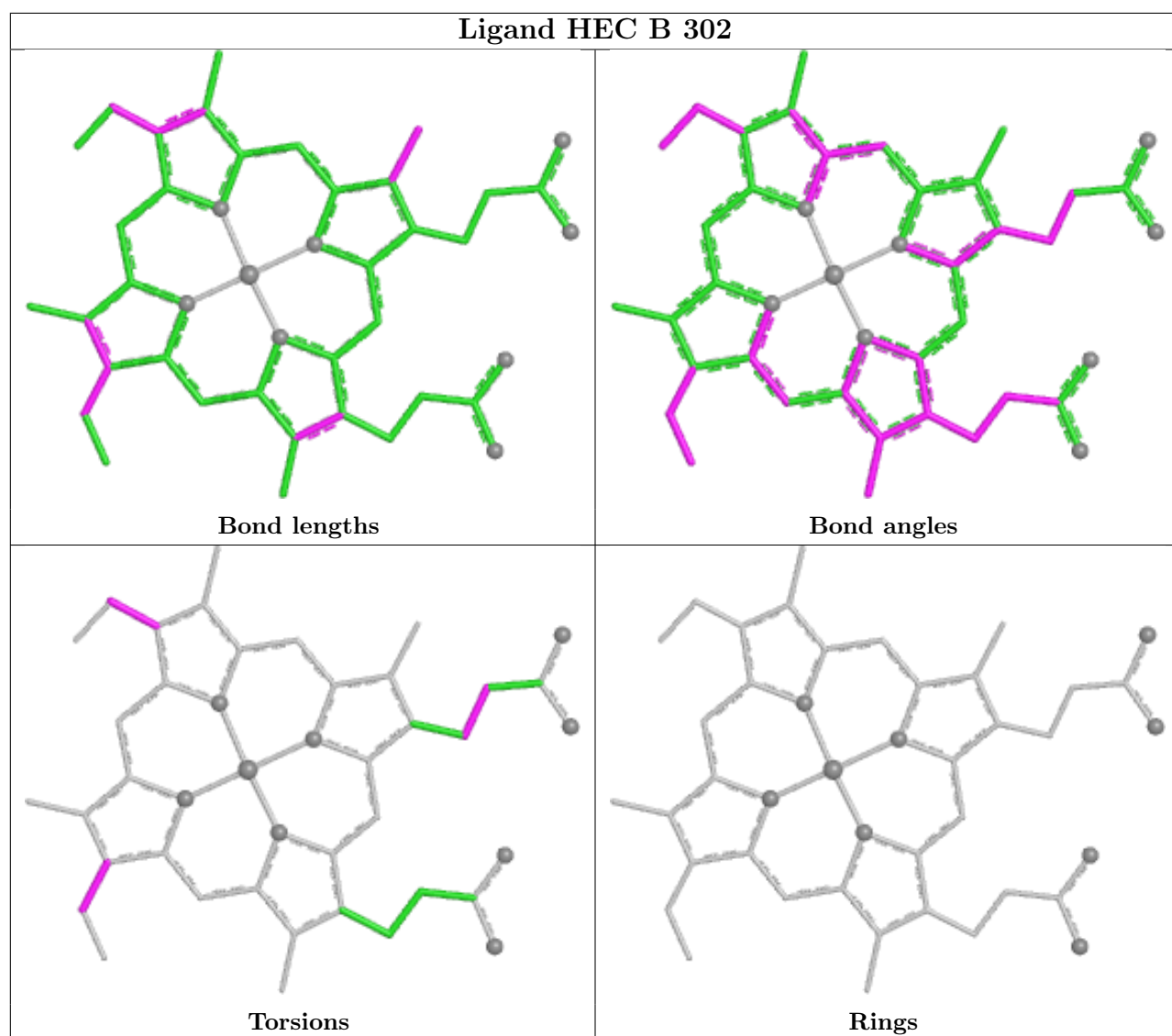


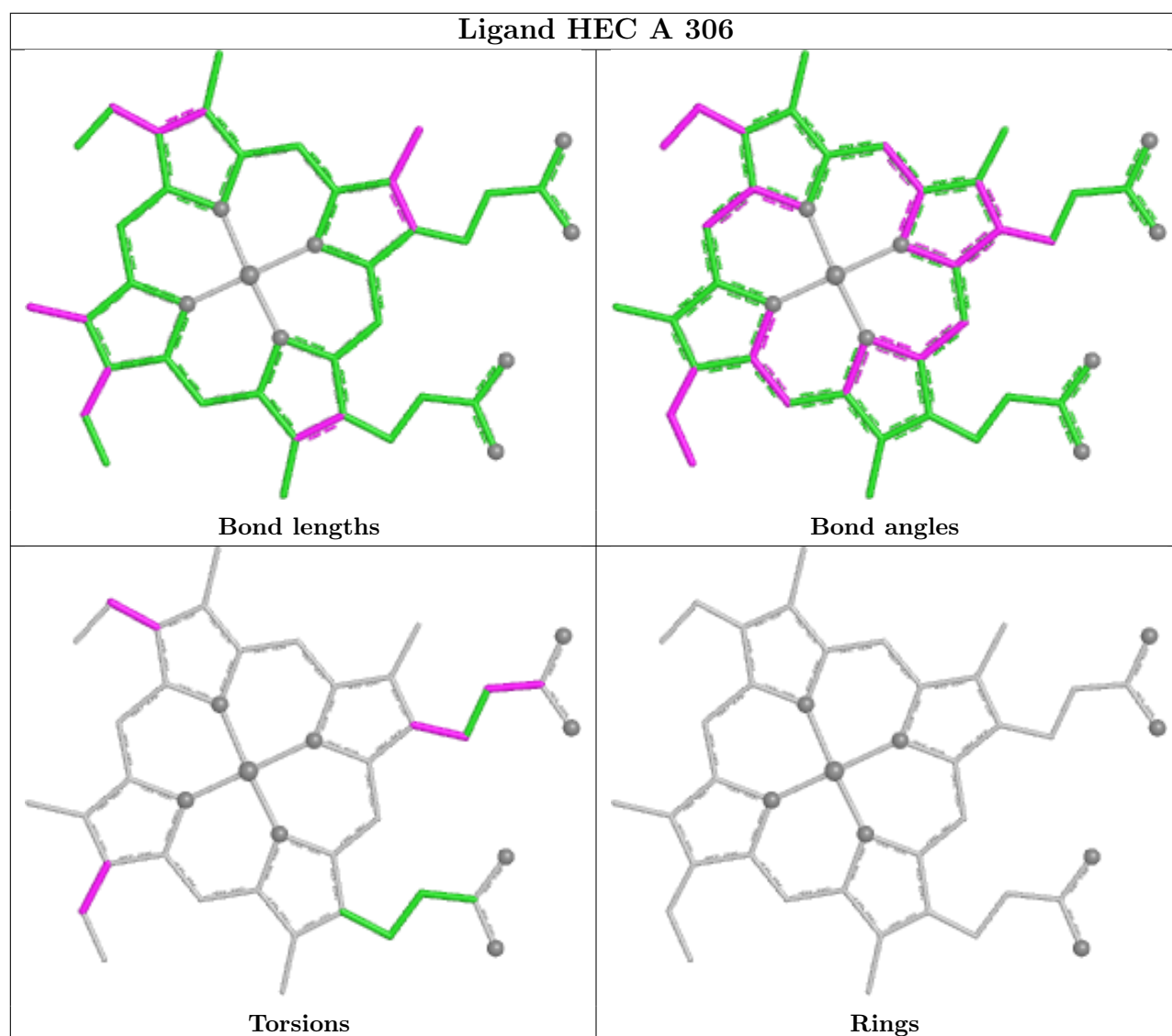












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

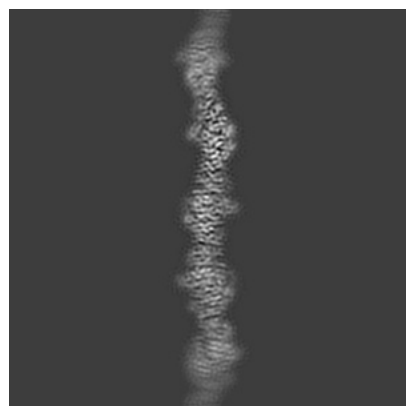
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23481. These allow visual inspection of the internal detail of the map and identification of artifacts.

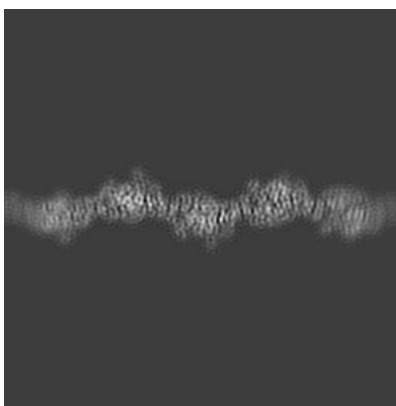
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

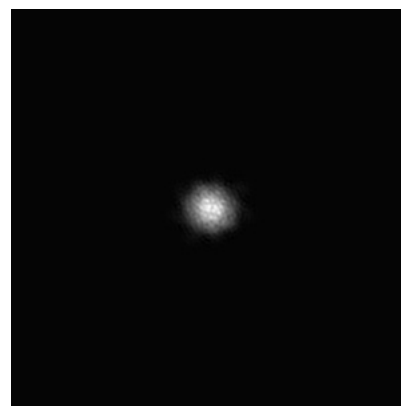
6.1.1 Primary map



X

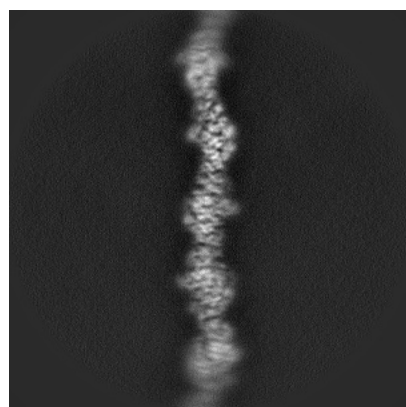


Y

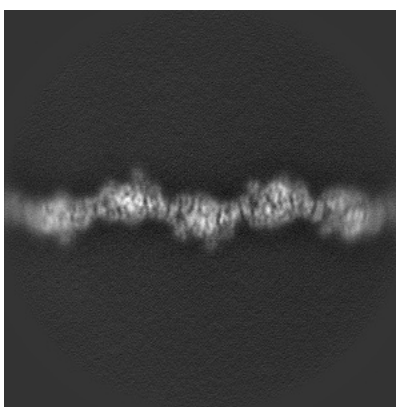


Z

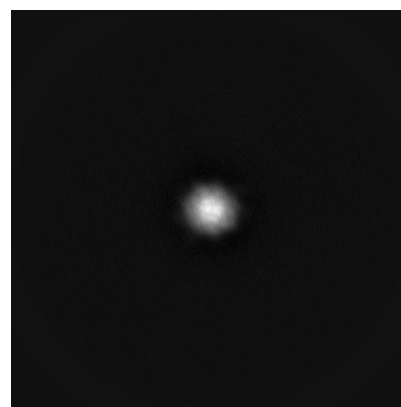
6.1.2 Raw map



X



Y

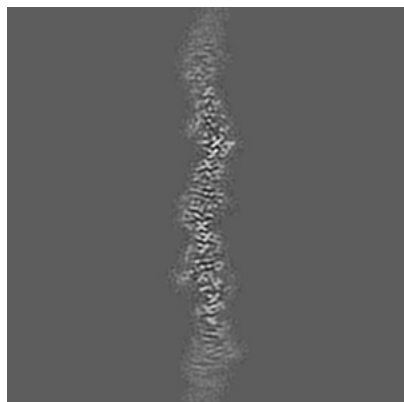


Z

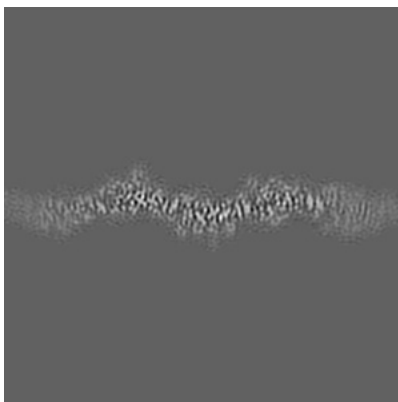
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 192

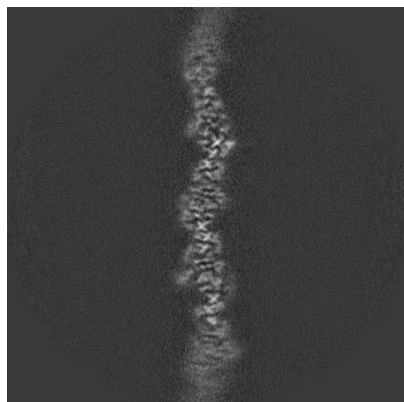


Y Index: 192

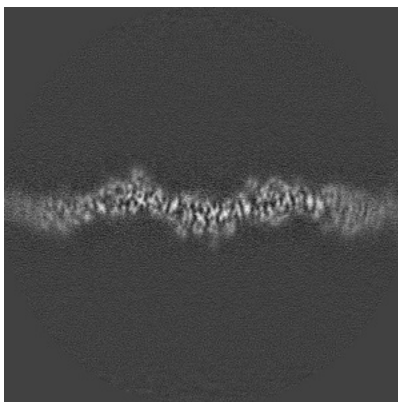


Z Index: 192

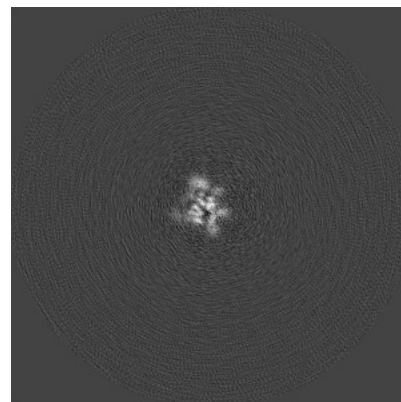
6.2.2 Raw map



X Index: 192



Y Index: 192

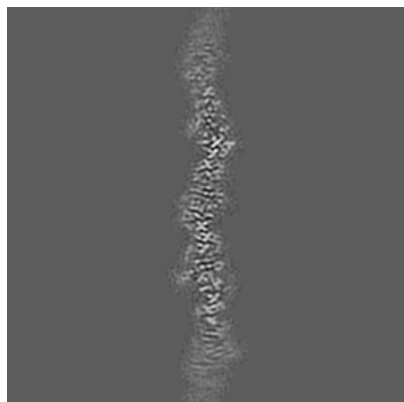


Z Index: 192

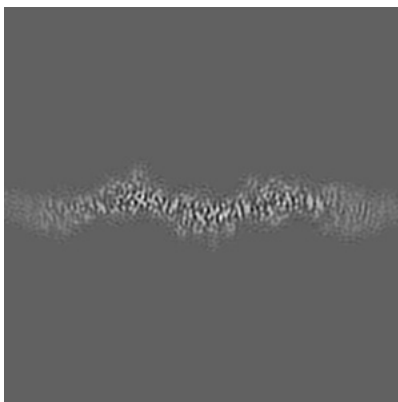
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

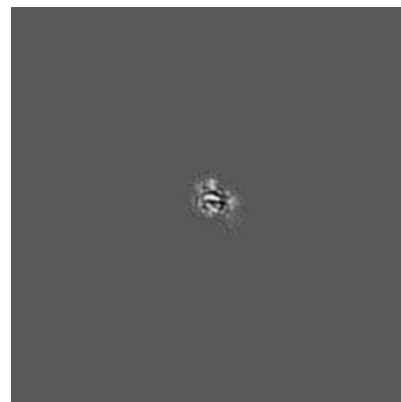
6.3.1 Primary map



X Index: 192

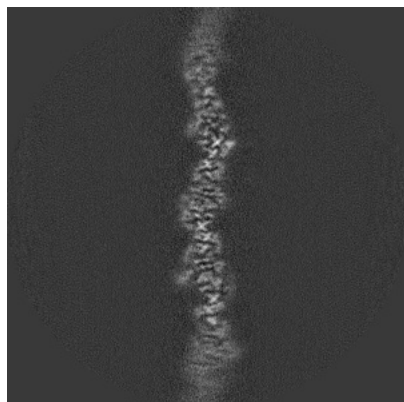


Y Index: 192

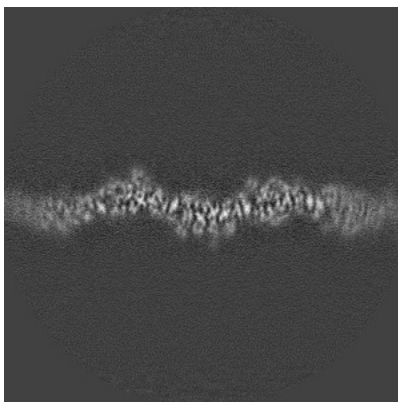


Z Index: 253

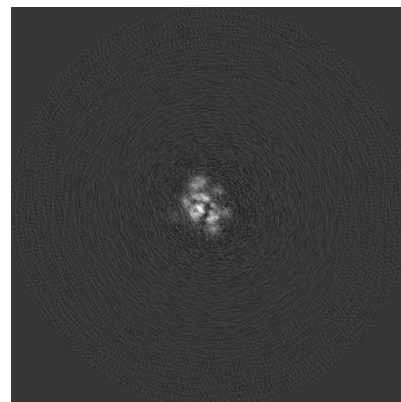
6.3.2 Raw map



X Index: 192



Y Index: 192

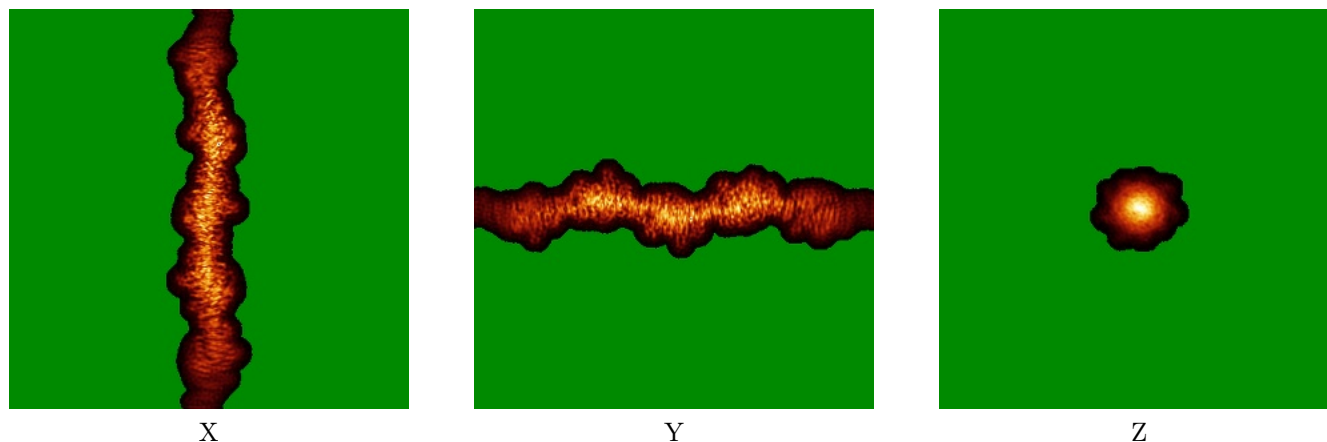


Z Index: 190

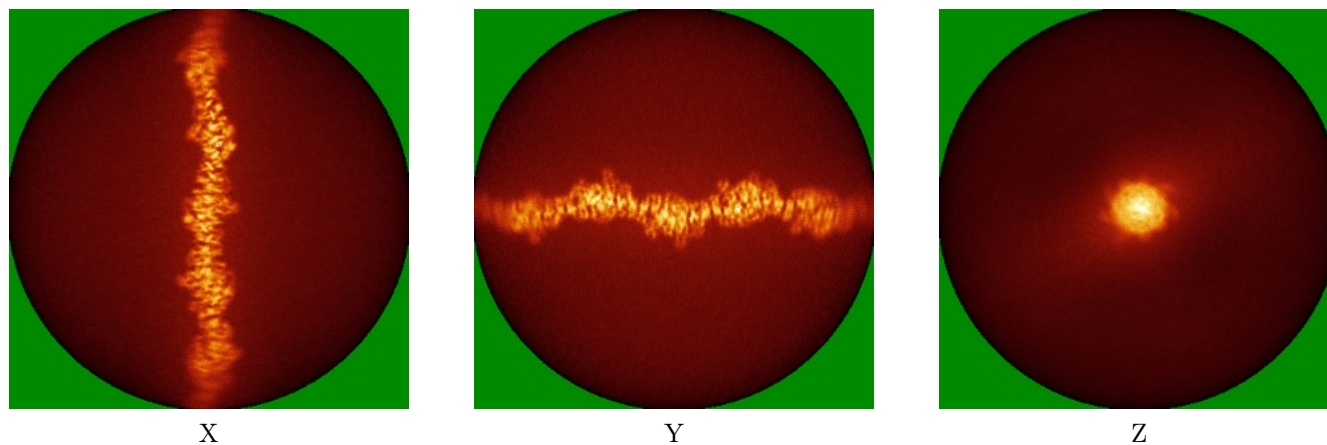
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

6.4.1 Primary map



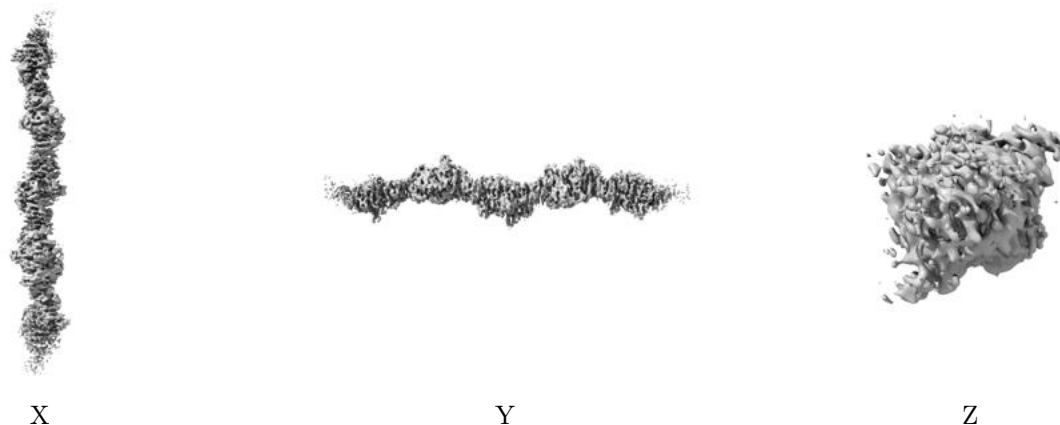
6.4.2 Raw map



The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.012. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

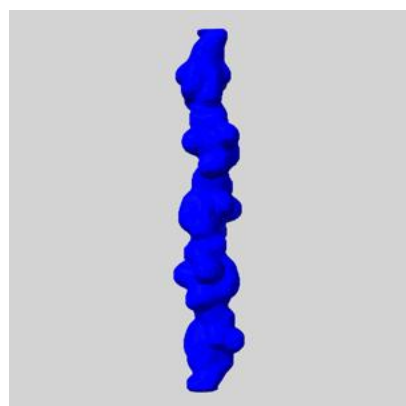
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

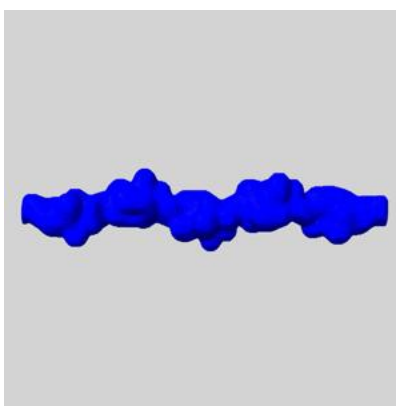
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

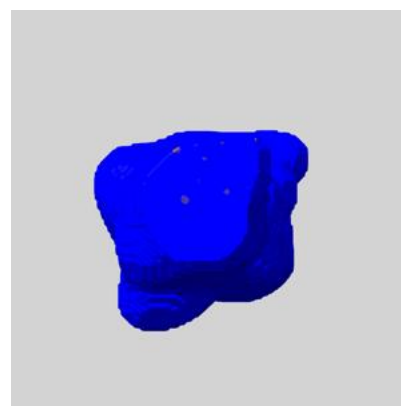
6.6.1 emd_23481_msk_1.map [i](#)



X



Y

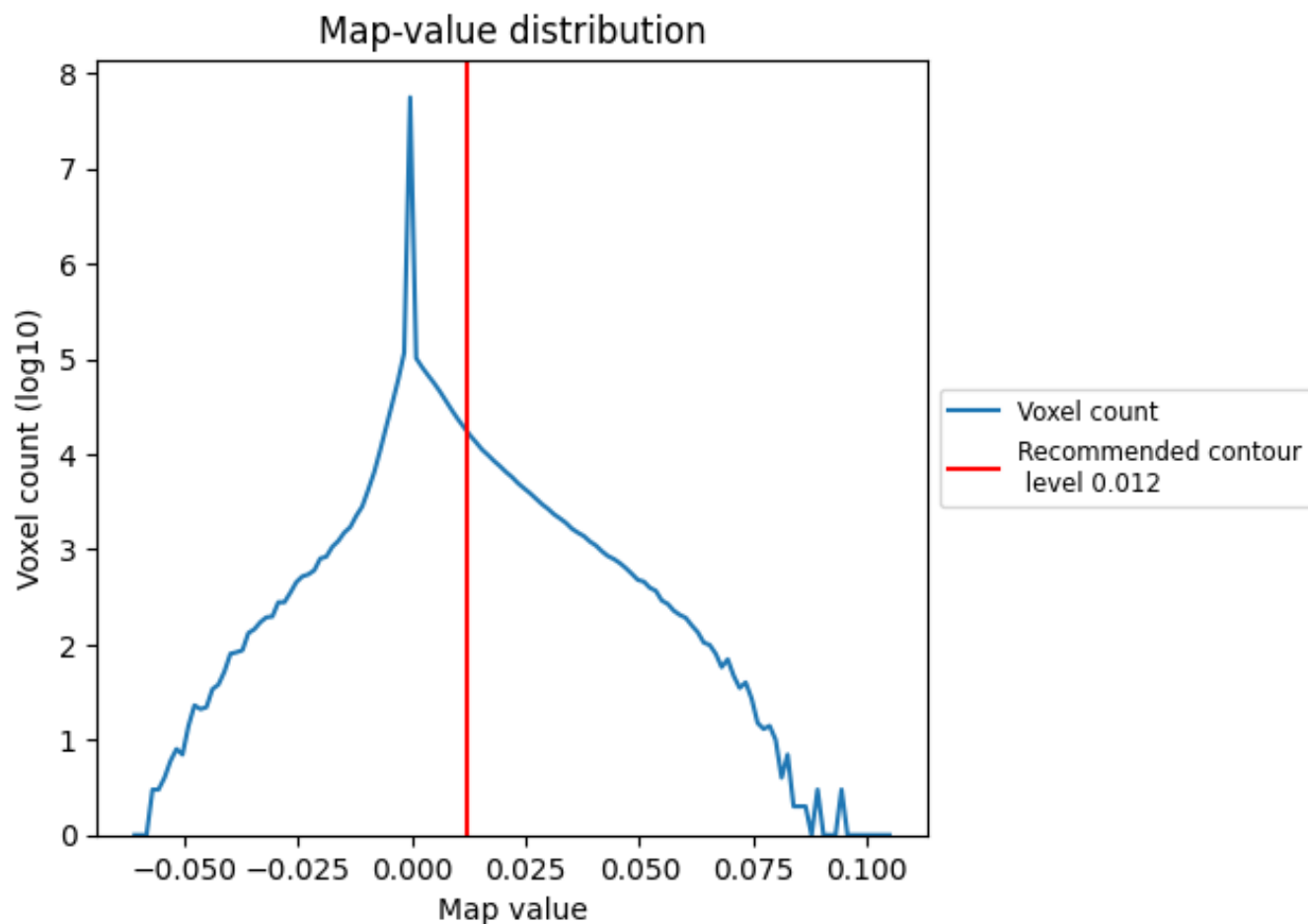


Z

7 Map analysis [i](#)

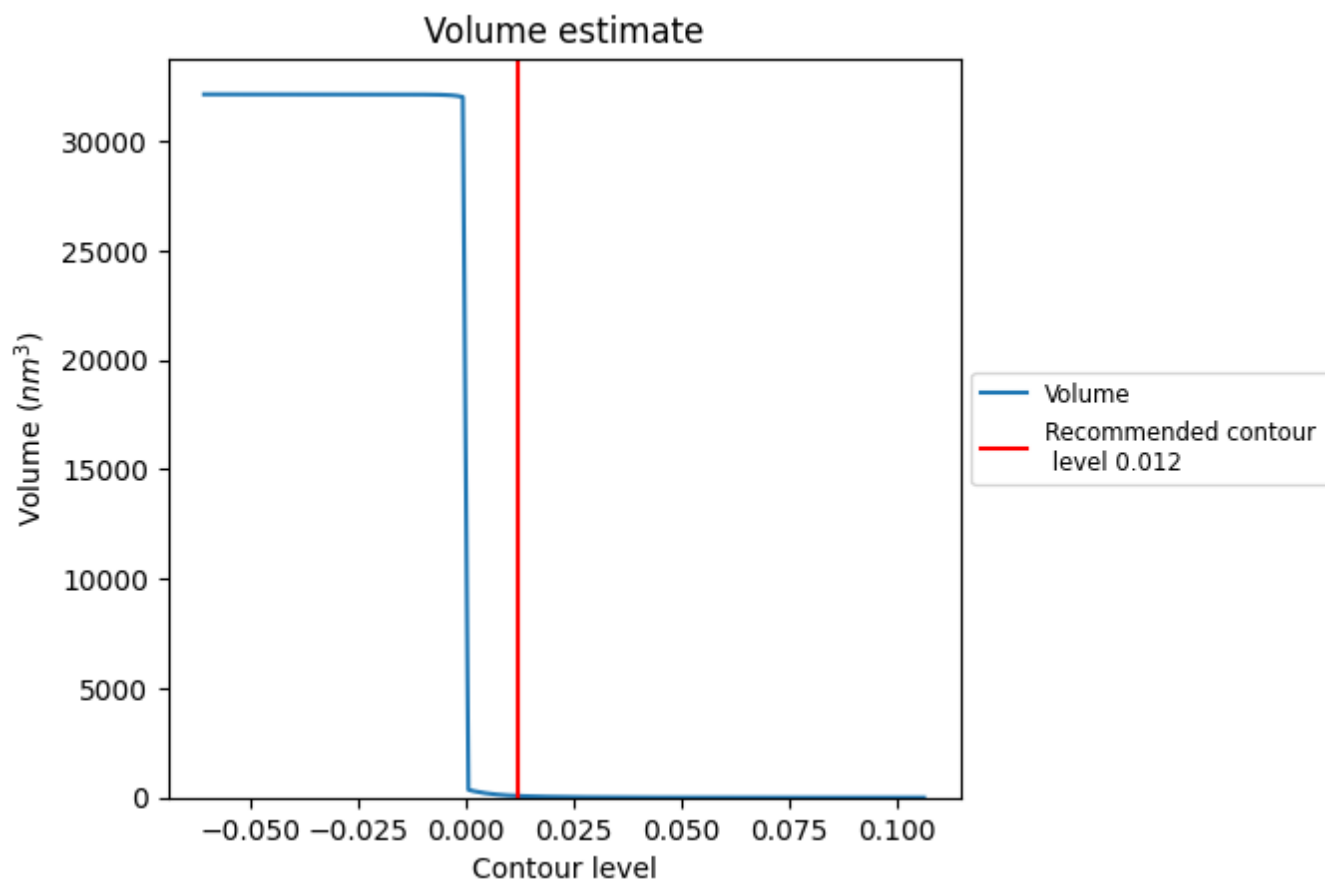
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

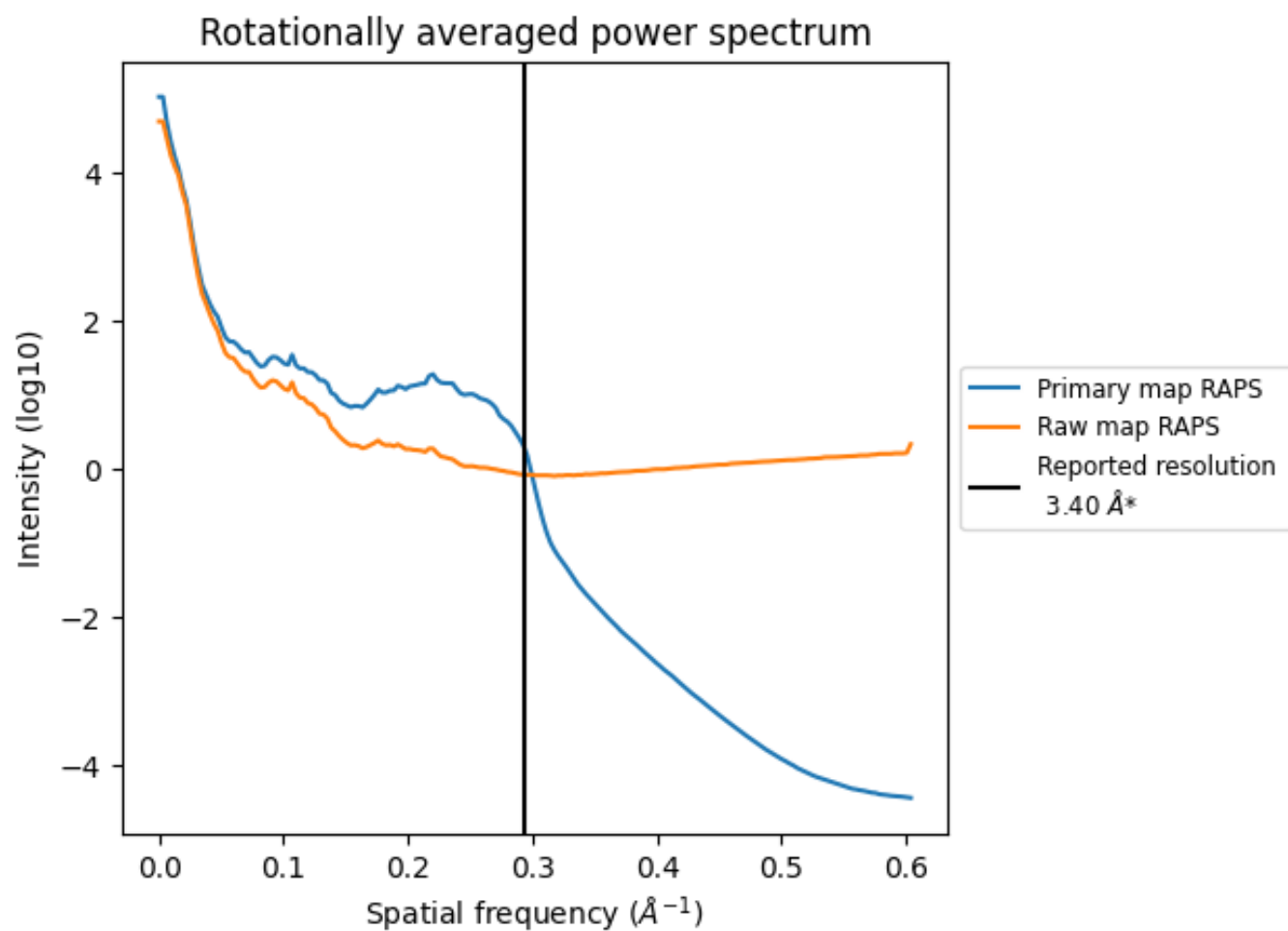
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 76 nm^3 ; this corresponds to an approximate mass of 69 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

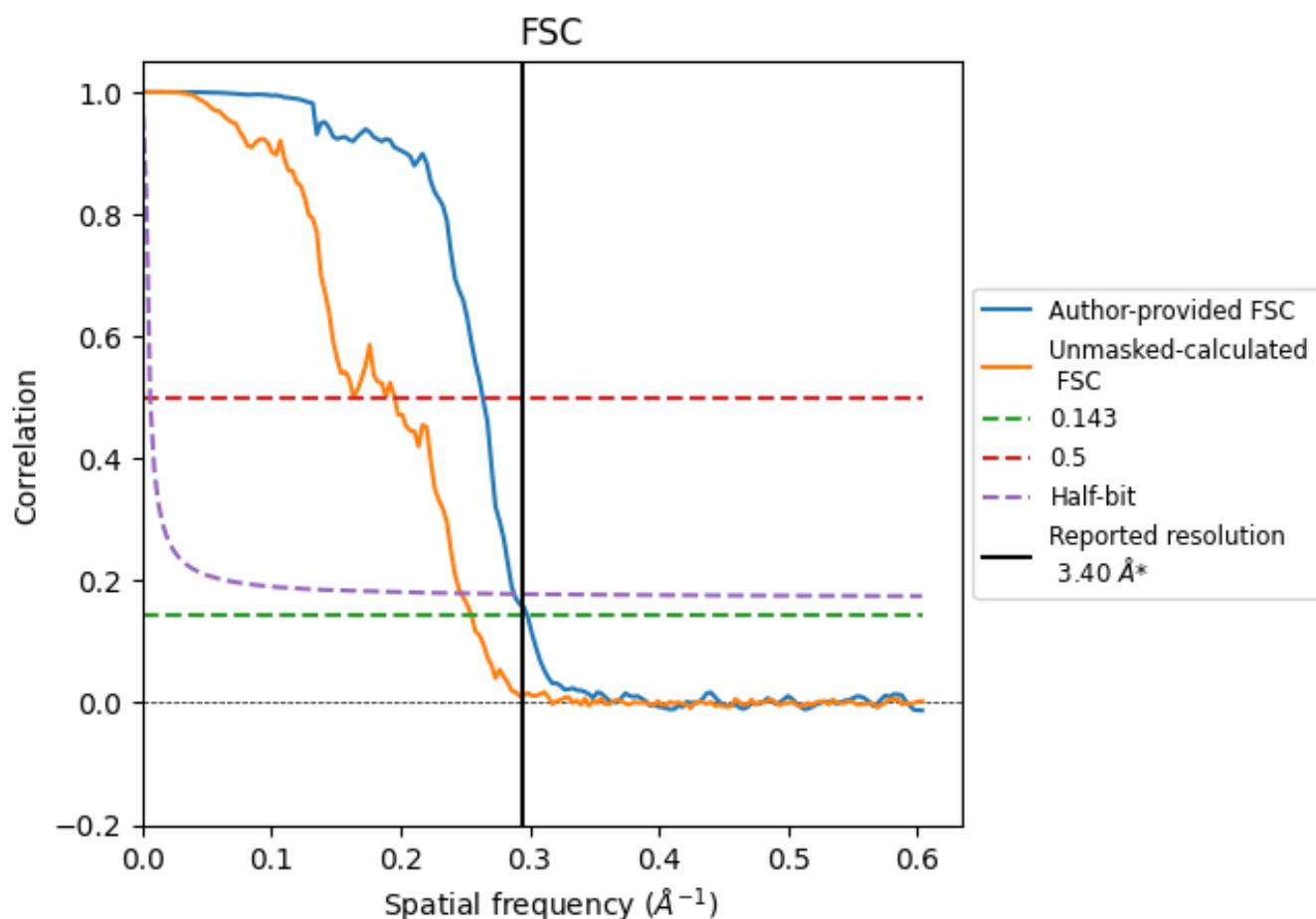


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.36	3.79	3.47
Unmasked-calculated*	3.92	6.12	4.05

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.92 differs from the reported value 3.4 by more than 10 %

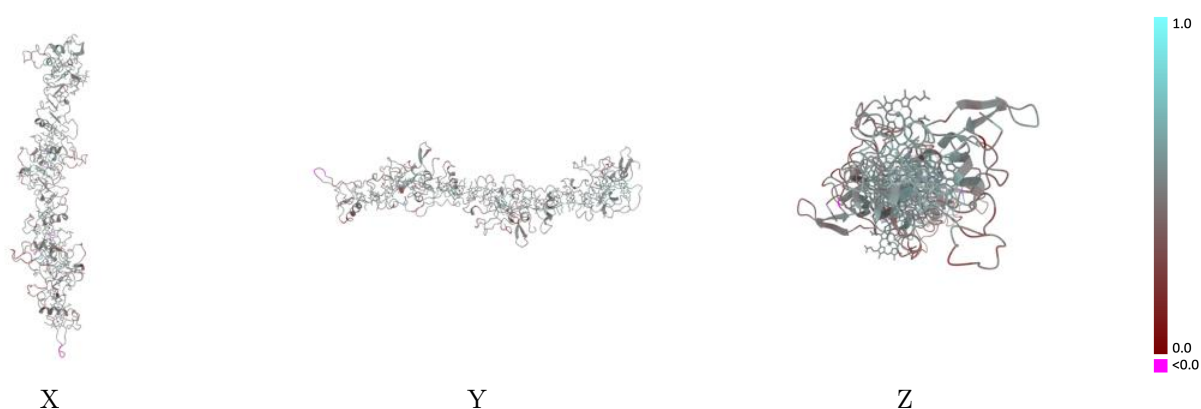
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23481 and PDB model 7LQ5. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)

This section was not generated.

9.2 Q-score mapped to coordinate model [i](#)

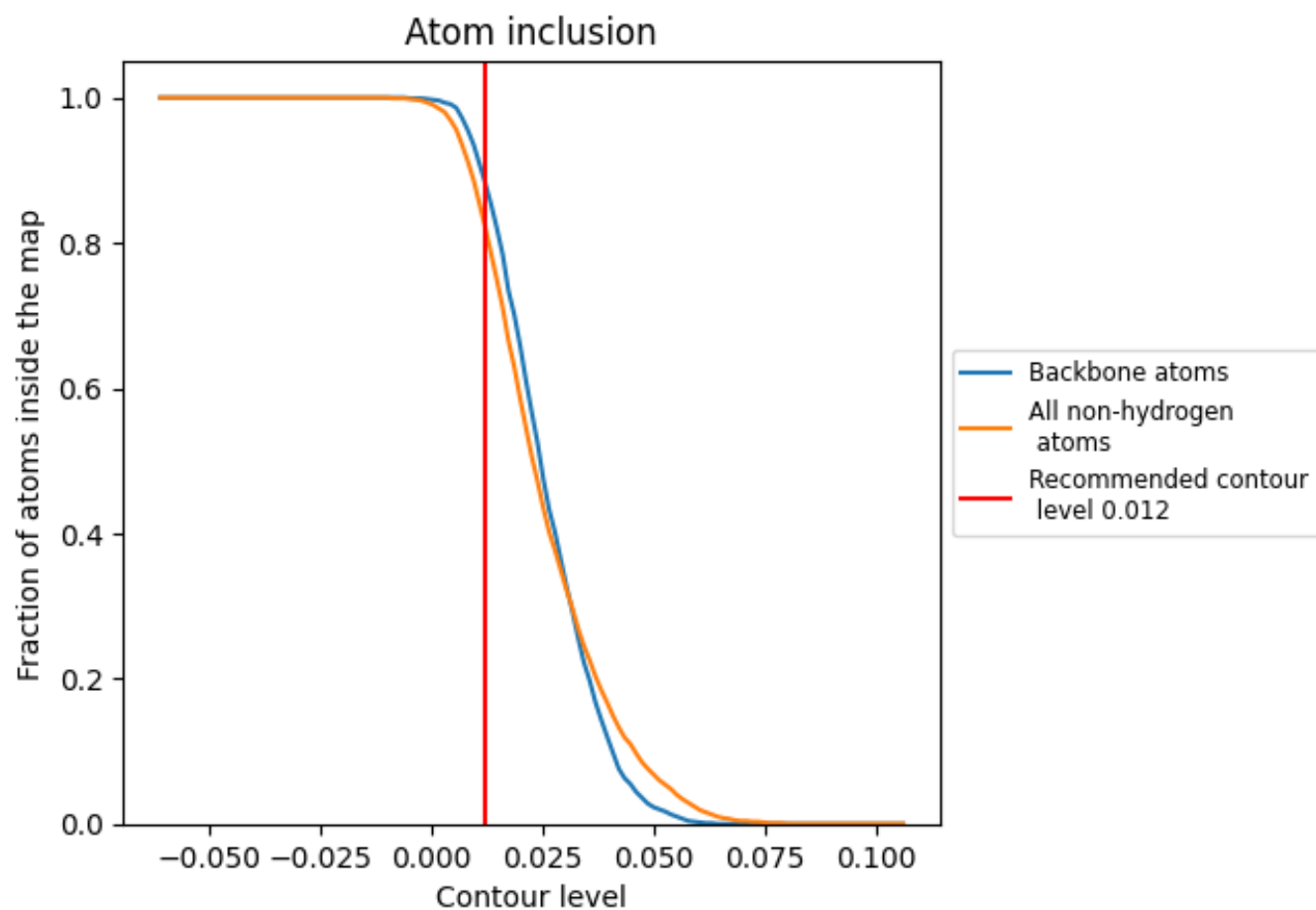


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 83% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8270	0.4620
A	0.8590	0.4900
B	0.8320	0.4580
C	0.7910	0.4400

