



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 03:42 am BST

PDB ID : 6S8Y
Title : Crystal structure of cytochrome c in complex with a sulfonated quinoline-derived foldamer
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Deposited on : 2019-07-10
Resolution : 2.09 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

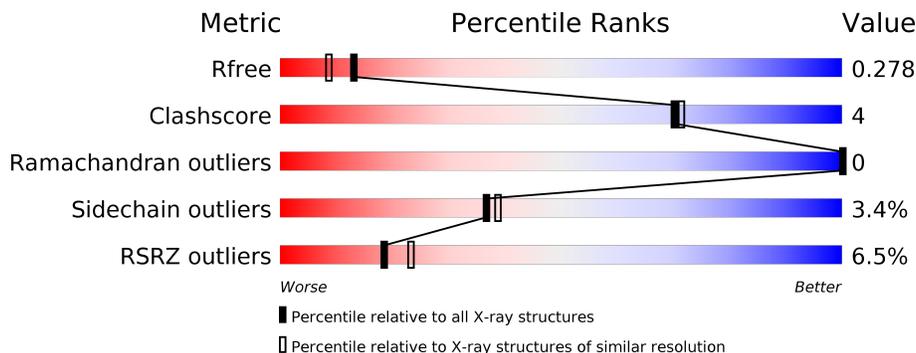
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.09 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 on 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	107	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 1356 atoms, of which 6 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.

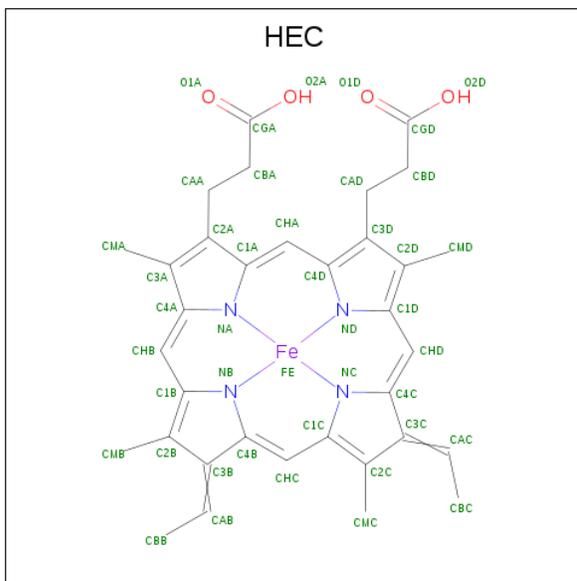
- Molecule 1 is a protein called Cytochrome c iso-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	107	850	537	152	157	4	0	1	0

There is a discrepancy between the modelled and reference sequences:

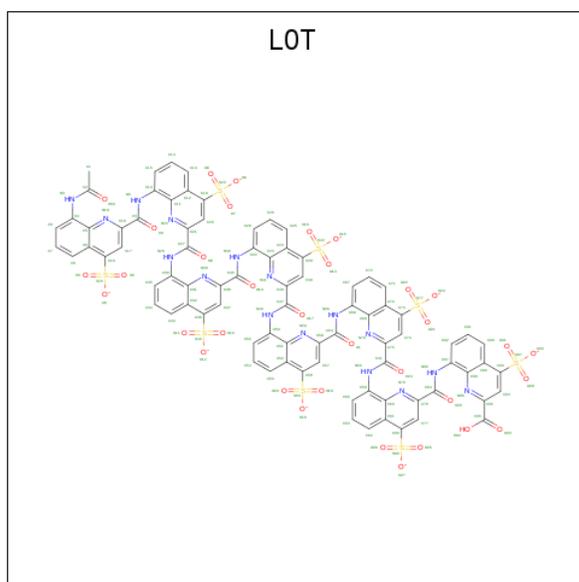
Chain	Residue	Modelled	Actual	Comment	Reference
A	102	THR	CYS	conflict	UNP P00044

- Molecule 2 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



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

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
5	A	1	280	164	32	68	16	0	1
5	A	1	140	82	16	34	8	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	26	Total	O	0	0
			26	26		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Cytochrome c iso-1

Chain A:  7% 95% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	39.14Å 39.14Å 187.37Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.90 – 2.09 62.46 – 2.09	Depositor EDS
% Data completeness (in resolution range)	100.0 (33.90-2.09) 100.0 (62.46-2.09)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.08Å)	Xtrriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.225 , 0.267 0.229 , 0.278	Depositor DCC
R_{free} test set	498 reflections (4.70%)	wwPDB-VP
Wilson B-factor (Å ²)	56.9	Xtrriage
Anisotropy	0.244	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 57.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.040 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	1356	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.94% 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: HEC, ZN, LOT, ACT

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	0.47	0/868	0.67	0/1159

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	850	0	856	2	0
2	A	43	0	31	0	0
3	A	3	0	0	0	0
4	A	8	6	6	1	0
5	A	420	0	0	6	0
6	A	26	0	0	0	0
All	All	1350	6	893	8	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 4.

All (8) 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)
5:A:206[A]:L0T:C35	5:A:206[A]:L0T:C1	2.58	0.81
5:A:206[A]:L0T:O34	5:A:206[A]:L0T:C9	2.36	0.73
5:A:206[A]:L0T:C34	5:A:206[A]:L0T:C1	2.70	0.69
5:A:206[A]:L0T:C28	5:A:206[A]:L0T:C17	2.74	0.64
5:A:206[A]:L0T:C1	5:A:206[A]:L0T:C30	2.79	0.59
1:A:22:LYS:HD3	1:A:33:HIS:CE1	2.40	0.56
5:A:206[A]:L0T:C13	5:A:206[A]:L0T:O6	2.63	0.46
1:A:33:HIS:HE1	4:A:204:ACT:C	2.33	0.42

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	106/107 (99%)	103 (97%)	3 (3%)	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	89/88 (101%)	86 (97%)	3 (3%)	37 39

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

Mol	Chain	Res	Type
1	A	-4	GLU
1	A	61	GLU
1	A	103	GLU

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

Mol	Chain	Res	Type
1	A	33	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 3 are monoatomic - leaving 6 for Mogul analysis.

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	$\# Z >$
5	L0T	A	207	3	144,155,155	1.74	31 (21%)	206,243,243	1.15	17 (8%)
5	L0T	A	206[B]	-	144,155,155	1.54	29 (20%)	206,243,243	1.05	17 (8%)
5	L0T	A	206[A]	3	144,155,155	1.54	32 (22%)	206,243,243	1.12	17 (8%)
4	ACT	A	204	3	1,3,3	3.67	1 (100%)	0,3,3	0.00	-
2	HEC	A	201	1	26,50,50	1.76	7 (26%)	18,82,82	1.89	3 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >
4	ACT	A	205	3	1,3,3	3.69	1 (100%)	0,3,3	0.00	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	L0T	A	206[B]	-	-	31/108/112/112	0/16/16/16
5	L0T	A	206[A]	3	-	14/108/112/112	0/16/16/16
5	L0T	A	207	3	-	9/108/112/112	0/16/16/16
2	HEC	A	201	1	-	0/6/54/54	-

All (101) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	207	L0T	C36-C32	5.16	1.51	1.43
5	A	207	L0T	C16-C6	4.63	1.50	1.43
5	A	207	L0T	C73-C70	4.60	1.50	1.43
5	A	207	L0T	C56-C52	4.57	1.50	1.43
5	A	207	L0T	C19-C12	4.46	1.50	1.43
5	A	206[B]	L0T	C56-C52	4.39	1.50	1.43
5	A	207	L0T	C66-C61	4.23	1.50	1.43
2	A	201	HEC	CBB-CAB	-4.21	1.33	1.49
5	A	206[A]	L0T	C73-C70	4.10	1.50	1.43
5	A	206[B]	L0T	C19-C12	4.05	1.49	1.43
5	A	206[A]	L0T	C29-C24	4.00	1.49	1.43
5	A	206[A]	L0T	C36-C32	3.99	1.49	1.43
5	A	207	L0T	C29-C24	3.88	1.49	1.43
5	A	206[B]	L0T	C29-C24	3.88	1.49	1.43
5	A	206[B]	L0T	C36-C32	3.74	1.49	1.43
5	A	206[A]	L0T	C66-C61	3.74	1.49	1.43
4	A	205	ACT	CH3-C	3.69	1.53	1.48
5	A	206[A]	L0T	C56-C52	3.68	1.49	1.43
4	A	204	ACT	CH3-C	3.67	1.53	1.48
5	A	207	L0T	C93-C89	3.66	1.49	1.43
5	A	206[B]	L0T	C73-C70	3.65	1.49	1.43
5	A	206[A]	L0T	C93-C89	3.65	1.49	1.43
5	A	206[B]	L0T	C16-C6	3.53	1.49	1.43
5	A	206[B]	L0T	C93-C89	3.49	1.49	1.43
5	A	206[B]	L0T	C66-C61	3.47	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	206[A]	L0T	C16-C6	3.46	1.49	1.43
5	A	207	L0T	C70-C69	3.45	1.50	1.42
5	A	206[A]	L0T	C19-C12	3.25	1.48	1.43
5	A	207	L0T	C12-C11	3.22	1.50	1.42
5	A	207	L0T	C32-C31	3.17	1.49	1.42
2	A	201	HEC	C3B-C4B	3.11	1.48	1.43
5	A	207	L0T	C52-C51	3.11	1.49	1.42
5	A	207	L0T	C89-C88	3.08	1.49	1.42
5	A	207	L0T	C30-C31	3.03	1.50	1.43
5	A	207	L0T	C6-C5	3.02	1.49	1.42
2	A	201	HEC	C1C-NC	2.98	1.42	1.36
5	A	207	L0T	C68-C69	2.96	1.50	1.43
5	A	207	L0T	C87-C88	2.91	1.49	1.43
5	A	207	L0T	C59-N50	-2.85	1.33	1.41
5	A	206[B]	L0T	C59-C60	2.84	1.49	1.43
2	A	201	HEC	CAA-C2A	2.80	1.57	1.52
5	A	207	L0T	C4-C5	2.76	1.49	1.43
5	A	207	L0T	C24-C23	2.76	1.48	1.42
5	A	206[B]	L0T	C10-C11	2.75	1.49	1.43
2	A	201	HEC	C3B-C2B	-2.75	1.37	1.40
5	A	206[A]	L0T	C4-C5	2.74	1.49	1.43
5	A	206[A]	L0T	C30-C31	2.69	1.49	1.43
5	A	207	L0T	C59-C60	2.65	1.49	1.43
5	A	206[B]	L0T	C12-C11	2.62	1.48	1.42
5	A	206[B]	L0T	C50-C51	2.60	1.49	1.43
5	A	206[A]	L0T	C24-C23	2.57	1.48	1.42
5	A	206[A]	L0T	C52-C51	2.57	1.48	1.42
5	A	206[B]	L0T	C52-C51	2.57	1.48	1.42
5	A	207	L0T	C10-C11	2.53	1.49	1.43
5	A	206[A]	L0T	C6-C5	2.51	1.48	1.42
5	A	206[A]	L0T	C87-C88	2.48	1.48	1.43
5	A	206[A]	L0T	C32-C31	2.48	1.48	1.42
5	A	206[A]	L0T	C61-C60	2.47	1.48	1.42
5	A	207	L0T	C22-C23	2.46	1.48	1.43
5	A	206[A]	L0T	C89-C88	2.46	1.48	1.42
5	A	206[A]	L0T	C68-C69	2.45	1.48	1.43
5	A	206[B]	L0T	C68-C69	2.45	1.48	1.43
2	A	201	HEC	C3C-C2C	-2.45	1.38	1.40
5	A	206[A]	L0T	C50-C51	2.43	1.48	1.43
5	A	206[B]	L0T	C22-C23	2.43	1.48	1.43
5	A	206[B]	L0T	C6-C5	2.42	1.48	1.42
5	A	206[A]	L0T	C70-C69	2.42	1.48	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	206[B]	L0T	C32-C31	2.41	1.48	1.42
5	A	206[B]	L0T	C70-C69	2.41	1.48	1.42
5	A	206[B]	L0T	C87-N86	-2.39	1.35	1.41
5	A	206[A]	L0T	C22-C23	2.36	1.48	1.43
5	A	207	L0T	C95-N96	2.34	1.36	1.33
5	A	207	L0T	C50-C51	2.34	1.48	1.43
2	A	201	HEC	C4D-ND	2.33	1.41	1.36
5	A	206[A]	L0T	C59-C60	2.32	1.48	1.43
5	A	206[B]	L0T	C22-N46	-2.32	1.35	1.41
5	A	206[B]	L0T	C4-C5	2.31	1.48	1.43
5	A	206[B]	L0T	C89-C88	2.28	1.47	1.42
5	A	206[B]	L0T	C61-C60	2.28	1.47	1.42
5	A	206[B]	L0T	C24-C23	2.27	1.47	1.42
5	A	207	L0T	C61-C60	2.27	1.47	1.42
5	A	206[B]	L0T	C68-N66	-2.26	1.35	1.41
5	A	206[A]	L0T	C87-N86	-2.26	1.35	1.41
5	A	207	L0T	C87-N86	-2.22	1.35	1.41
5	A	206[A]	L0T	C30-N28	-2.20	1.35	1.41
5	A	206[A]	L0T	C95-N96	2.20	1.36	1.33
5	A	206[A]	L0T	C10-N5	-2.19	1.35	1.41
5	A	206[B]	L0T	C30-C31	2.13	1.48	1.43
5	A	206[A]	L0T	C12-C11	2.12	1.47	1.42
5	A	206[A]	L0T	C50-N49	-2.12	1.35	1.41
5	A	207	L0T	C10-N5	-2.11	1.35	1.41
5	A	206[A]	L0T	C59-N50	-2.09	1.35	1.41
5	A	206[A]	L0T	C68-N66	-2.09	1.35	1.41
5	A	206[A]	L0T	C4-N3	-2.08	1.35	1.41
5	A	207	L0T	C54-C53	2.06	1.41	1.36
5	A	207	L0T	C34-C33	2.06	1.41	1.36
5	A	206[A]	L0T	C10-C11	2.05	1.47	1.43
5	A	206[B]	L0T	C4-N3	-2.03	1.36	1.41
5	A	206[B]	L0T	C59-N50	-2.01	1.36	1.41
5	A	206[B]	L0T	C10-N5	-2.01	1.36	1.41
5	A	207	L0T	C72-C71	2.00	1.41	1.36

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	206[A]	L0T	C95-N96-C88	5.06	122.14	118.26
5	A	207	L0T	C95-N96-C88	4.68	121.85	118.26
5	A	206[B]	L0T	C95-N96-C88	4.62	121.81	118.26
2	A	201	HEC	CBD-CAD-C3D	-4.35	104.47	112.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	206[A]	L0T	C5-C4-N3	3.60	122.45	115.42
2	A	201	HEC	CMB-C2B-C3B	3.40	129.82	125.82
2	A	201	HEC	CMB-C2B-C1B	-3.15	123.62	128.46
5	A	206[B]	L0T	C78-N79-C60	2.97	123.49	117.24
5	A	206[A]	L0T	C4-C5-N19	2.85	123.20	117.74
5	A	207	L0T	C74-C73-C70	-2.84	116.36	120.82
5	A	207	L0T	C38-N39-C31	2.78	123.10	117.24
5	A	207	L0T	O31-S97-C93	2.78	114.72	106.43
5	A	207	L0T	C87-C88-N96	2.71	122.94	117.74
5	A	206[A]	L0T	C38-N39-C31	2.69	122.92	117.24
5	A	207	L0T	C58-N59-C51	2.67	122.88	117.24
5	A	207	L0T	C18-N19-C5	2.65	122.83	117.24
5	A	206[A]	L0T	C4-N3-C2	-2.65	118.76	126.84
5	A	207	L0T	C37-C36-C32	-2.52	116.86	120.82
5	A	206[A]	L0T	C75-N76-C69	2.52	122.55	117.24
5	A	206[A]	L0T	C18-N19-C5	2.47	122.44	117.24
5	A	206[A]	L0T	C78-N79-C60	2.45	122.40	117.24
5	A	207	L0T	C57-C56-C52	-2.44	117.00	120.82
5	A	207	L0T	C59-C60-N79	2.41	122.36	117.74
5	A	206[B]	L0T	C21-N22-C11	2.39	122.28	117.24
5	A	207	L0T	C78-N79-C60	2.39	122.27	117.24
5	A	206[B]	L0T	C94-C93-C89	-2.37	117.10	120.82
5	A	206[B]	L0T	C18-N19-C5	2.35	122.19	117.24
5	A	207	L0T	C40-N41-C23	2.34	122.18	117.24
5	A	206[B]	L0T	C40-N41-C23	2.32	122.14	117.24
5	A	207	L0T	C21-N22-C11	2.32	122.13	117.24
5	A	206[A]	L0T	C57-C56-C52	-2.30	117.21	120.82
5	A	206[A]	L0T	C40-N41-C23	2.29	122.07	117.24
5	A	206[B]	L0T	C75-N76-C69	2.29	122.07	117.24
5	A	206[B]	L0T	C20-C19-C12	-2.28	117.24	120.82
5	A	206[A]	L0T	C21-N22-C11	2.27	122.03	117.24
5	A	206[A]	L0T	C37-C36-C32	-2.27	117.25	120.82
5	A	206[B]	L0T	C74-C73-C70	-2.27	117.25	120.82
5	A	207	L0T	C39-C29-C24	-2.26	117.27	120.82
5	A	207	L0T	C94-C95-N96	-2.23	120.19	122.23
5	A	206[B]	L0T	C39-C29-C24	-2.23	117.31	120.82
5	A	207	L0T	C17-C16-C6	-2.22	117.33	120.82
5	A	206[B]	L0T	C11-C10-N5	2.22	119.75	115.42
5	A	206[B]	L0T	C58-N59-C51	2.21	121.90	117.24
5	A	206[B]	L0T	C17-C16-C6	-2.20	117.36	120.82
5	A	206[B]	L0T	C59-C60-N79	2.20	121.95	117.74
5	A	206[B]	L0T	C37-C36-C32	-2.14	117.45	120.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	206[A]	L0T	C39-C29-C24	-2.13	117.47	120.82
5	A	206[A]	L0T	C74-C73-C70	-2.13	117.48	120.82
5	A	206[B]	L0T	C38-N39-C31	2.13	121.72	117.24
5	A	207	L0T	C20-C19-C12	-2.10	117.53	120.82
5	A	206[A]	L0T	C58-N59-C51	2.08	121.63	117.24
5	A	206[B]	L0T	C57-C56-C52	-2.08	117.56	120.82
5	A	206[A]	L0T	C94-C93-C89	-2.03	117.63	120.82
5	A	206[A]	L0T	C30-C31-N39	2.03	121.64	117.74

There are no chirality outliers.

All (54) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	206[B]	L0T	C89-C93-S97-O30
5	A	206[A]	L0T	C12-C19-S23-O6
5	A	206[A]	L0T	C12-C19-S23-O7
5	A	206[A]	L0T	C20-C19-S23-O6
5	A	206[A]	L0T	C20-C19-S23-O7
5	A	206[B]	L0T	C75-C41-N50-C59
5	A	207	L0T	O34-C2-N3-C4
5	A	206[B]	L0T	C1-C2-N3-C4
5	A	206[B]	L0T	O34-C2-N3-C4
5	A	206[B]	L0T	O24-C41-N50-C59
5	A	207	L0T	C1-C2-N3-C4
5	A	206[B]	L0T	C17-C18-C3-N5
5	A	206[B]	L0T	C17-C18-C3-O4
5	A	206[B]	L0T	N50-C41-C75-C74
5	A	206[B]	L0T	C6-C16-S20-O2
5	A	206[B]	L0T	C70-C73-S77-O21
5	A	206[B]	L0T	C89-C93-S97-O29
5	A	206[B]	L0T	C89-C93-S97-O31
5	A	206[A]	L0T	C6-C16-S20-O2
5	A	206[A]	L0T	C12-C19-S23-O8
5	A	207	L0T	C94-C93-S97-O31
5	A	206[B]	L0T	C74-C73-S77-O21
5	A	206[B]	L0T	C74-C73-S77-O22
5	A	206[B]	L0T	O17-C47-N49-C50
5	A	206[B]	L0T	O1-C64-N66-C68
5	A	206[B]	L0T	N19-C18-C3-O4
5	A	206[B]	L0T	N19-C18-C3-N5
5	A	207	L0T	C89-C93-S97-O31
5	A	206[B]	L0T	C6-C16-S20-O3

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Mol	Chain	Res	Type	Atoms
5	A	206[B]	L0T	C70-C73-S77-O22
5	A	207	L0T	O9-C27-N28-C30
5	A	206[B]	L0T	C74-C73-S77-O23
5	A	207	L0T	O24-C41-N50-C59
5	A	207	L0T	O28-C84-N86-C87
5	A	206[B]	L0T	C17-C16-S20-O2
5	A	206[B]	L0T	C17-C16-S20-O3
5	A	206[A]	L0T	C20-C19-S23-O8
5	A	206[A]	L0T	C17-C18-C3-N5
5	A	206[A]	L0T	O13-C45-N46-C22
5	A	206[B]	L0T	O24-C41-C75-C74
5	A	206[B]	L0T	C24-C29-S42-O14
5	A	206[A]	L0T	C61-C66-S80-O25
5	A	206[A]	L0T	C6-C16-S20-O3
5	A	206[B]	L0T	C18-C3-N5-C10
5	A	206[B]	L0T	O4-C3-N5-C10
5	A	206[A]	L0T	O24-C41-N50-C59
5	A	206[B]	L0T	C37-C38-C45-N46
5	A	206[B]	L0T	N50-C41-C75-N76
5	A	206[A]	L0T	N19-C18-C3-N5
5	A	207	L0T	C94-C93-S97-O29
5	A	206[A]	L0T	C61-C66-S80-O26
5	A	206[B]	L0T	C40-C47-N49-C50
5	A	206[B]	L0T	C58-C64-N66-C68
5	A	207	L0T	O4-C3-N5-C10

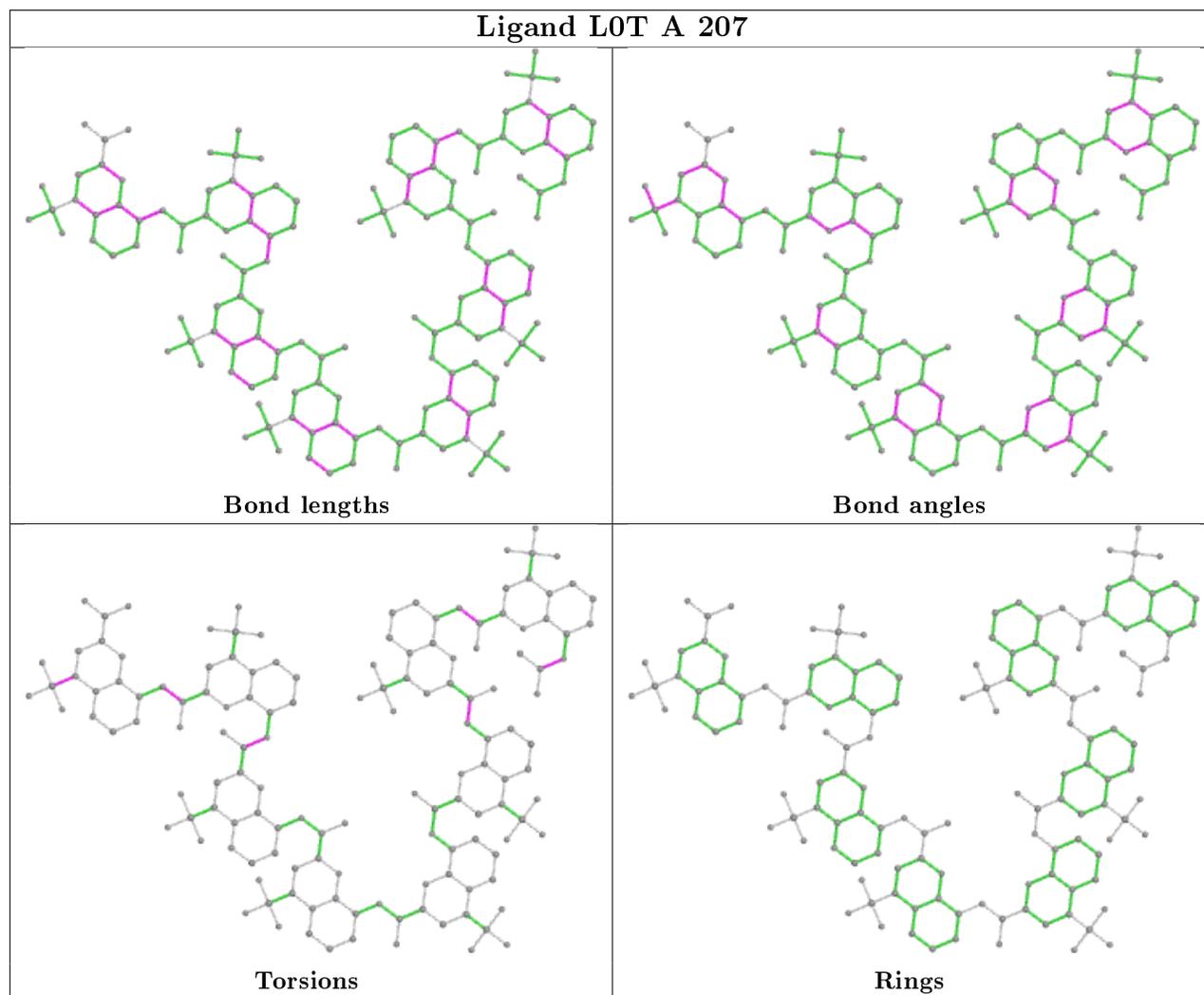
There are no ring outliers.

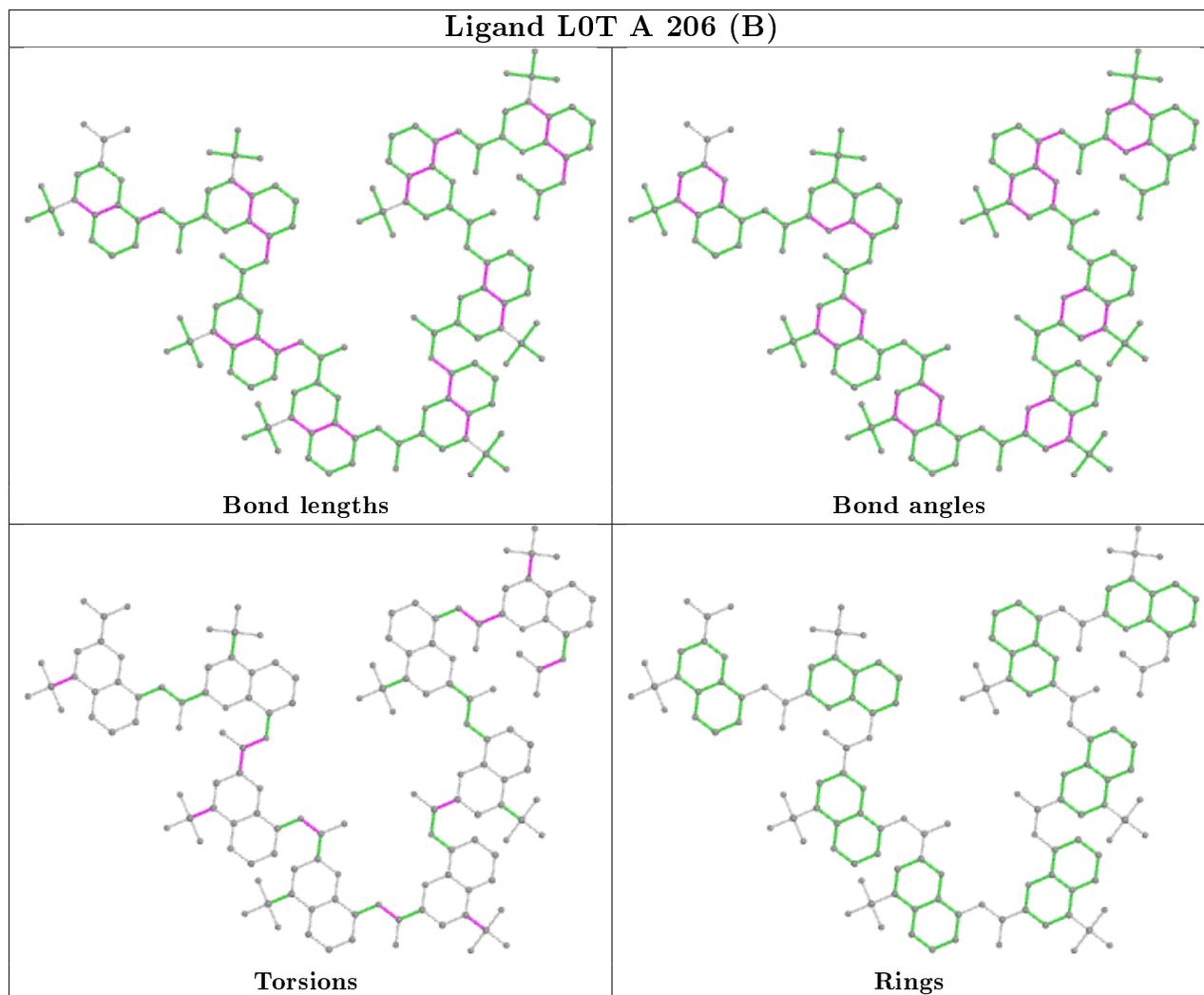
2 monomers are involved in 7 short contacts:

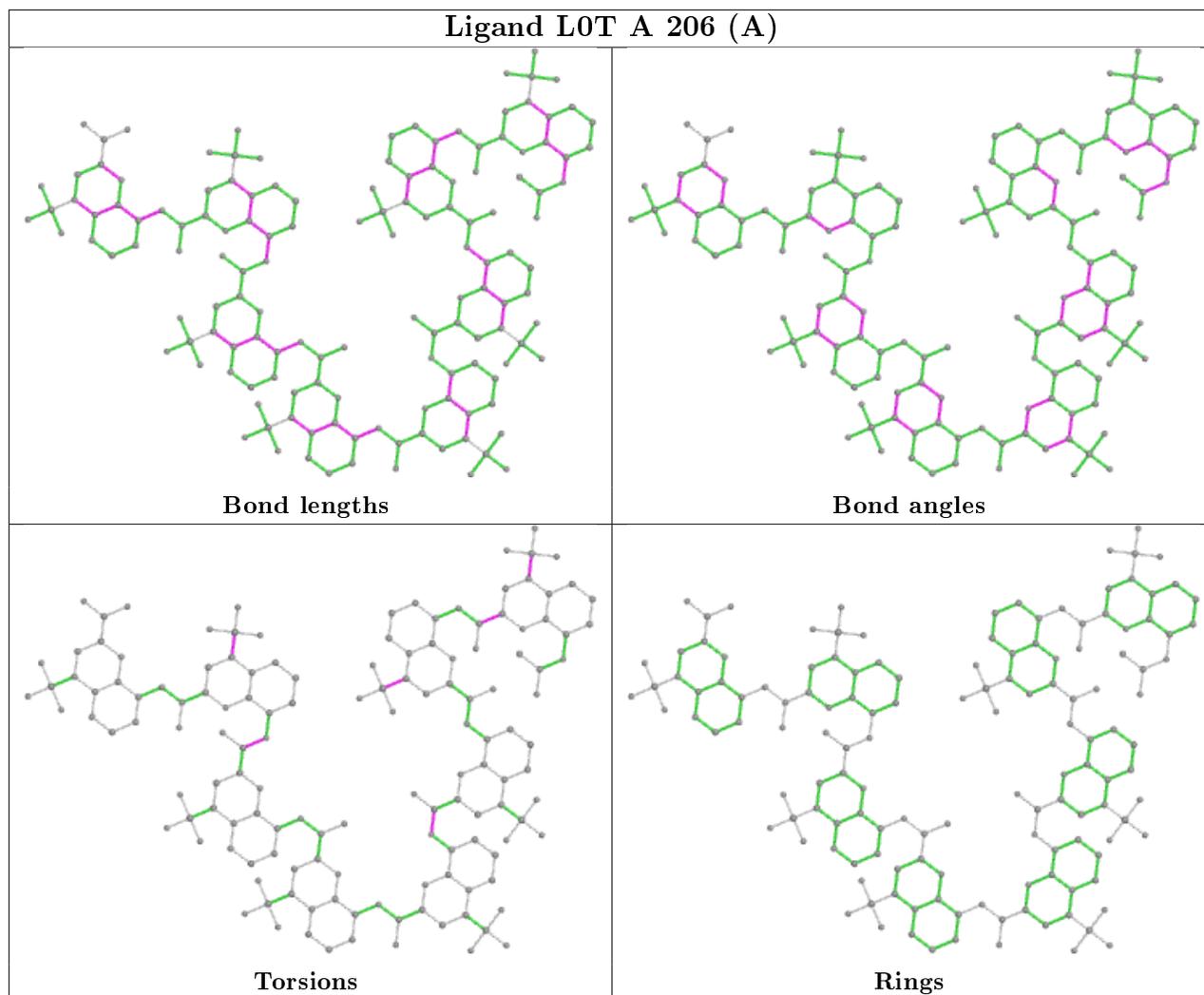
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	206[A]	L0T	6	0
4	A	204	ACT	1	0

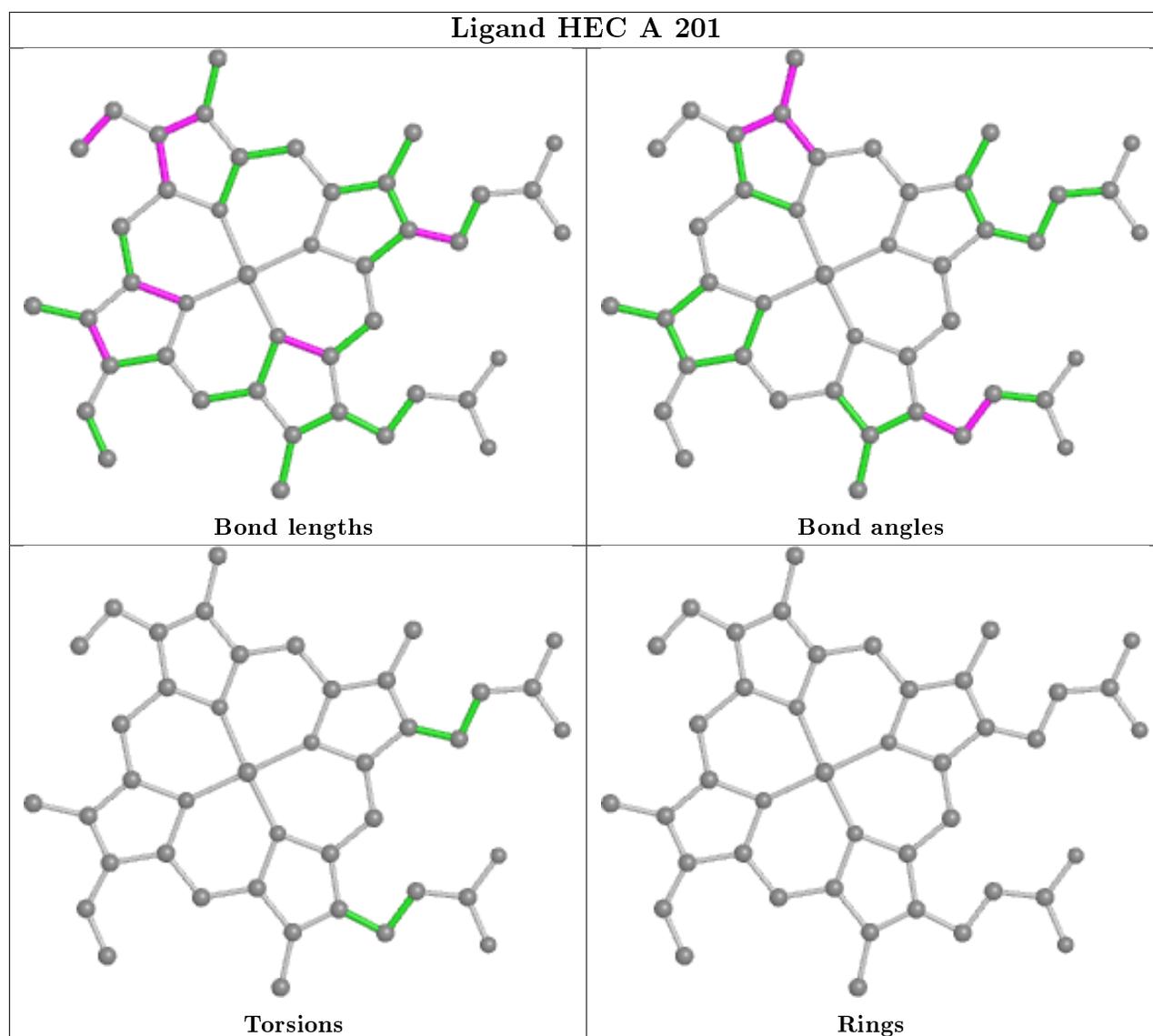
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	107/107 (100%)	0.55	7 (6%) 18 23	49, 68, 94, 112	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	73[A]	LYS	5.8
1	A	57	VAL	2.6
1	A	-3	PHE	2.4
1	A	-4	GLU	2.2
1	A	-2	LYS	2.2
1	A	-1	ALA	2.1
1	A	81	ALA	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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
3	ZN	A	208	1/1	0.83	0.06	98,98,98,98	0

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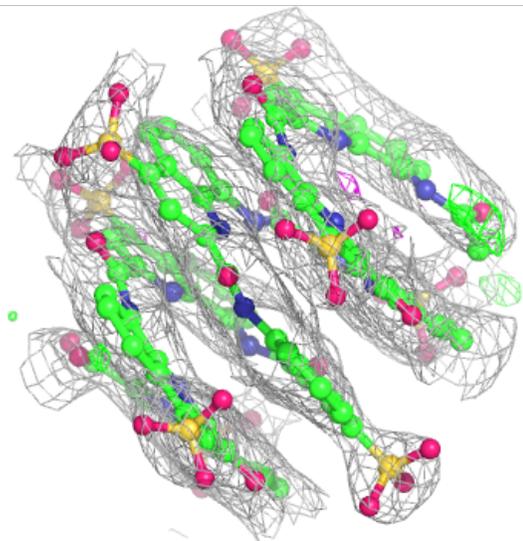
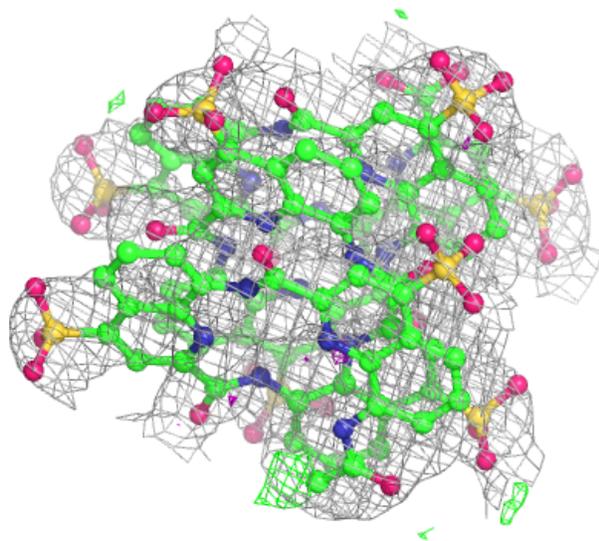
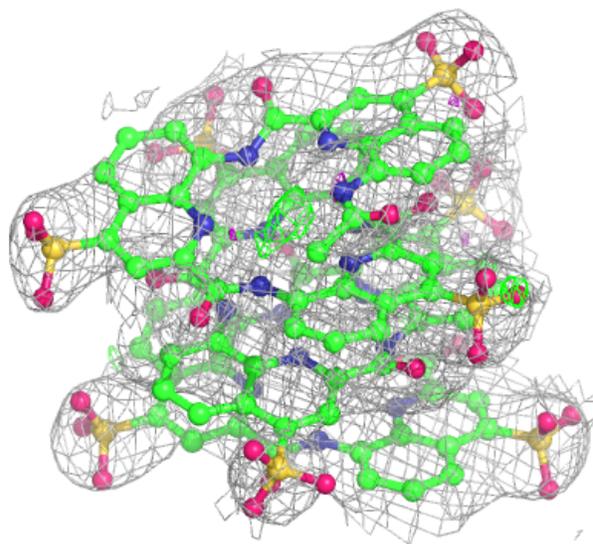
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	L0T	A	206[A]	140/140	0.89	0.20	45,64,70,77	140
5	L0T	A	206[B]	140/140	0.89	0.20	44,56,69,72	140
5	L0T	A	207	140/140	0.91	0.13	53,63,75,79	0
3	ZN	A	203	1/1	0.92	0.03	77,77,77,77	1
4	ACT	A	204	4/4	0.93	0.07	42,45,72,73	0
3	ZN	A	202	1/1	0.94	0.05	102,102,102,102	0
4	ACT	A	205	4/4	0.97	0.15	56,58,67,70	7
2	HEC	A	201	43/43	0.98	0.15	52,54,58,60	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.

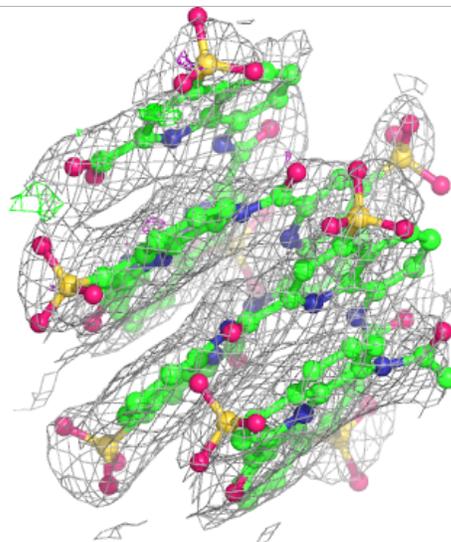
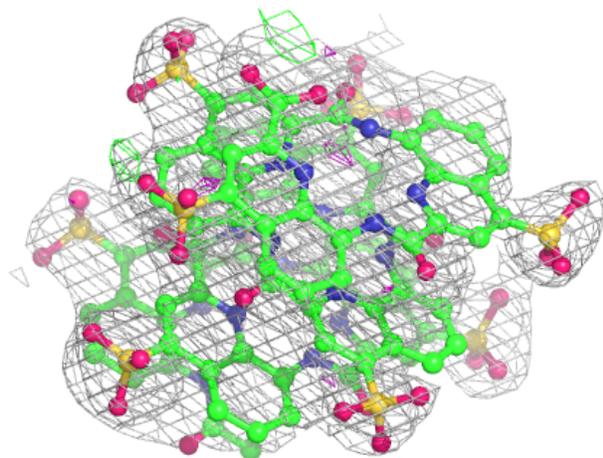
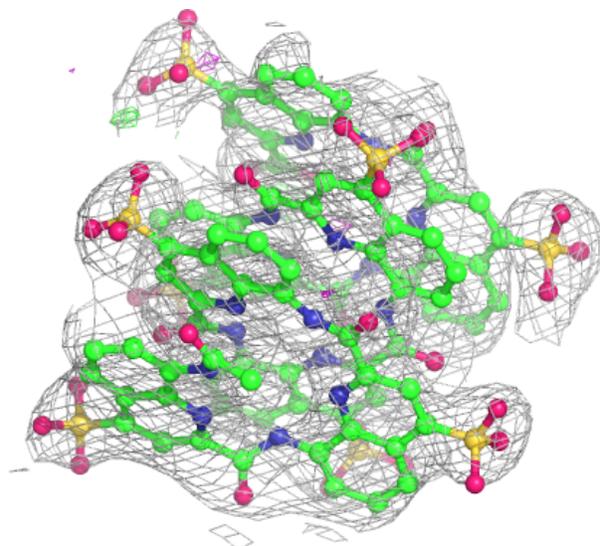
Electron density around L0T A 206 (A):

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



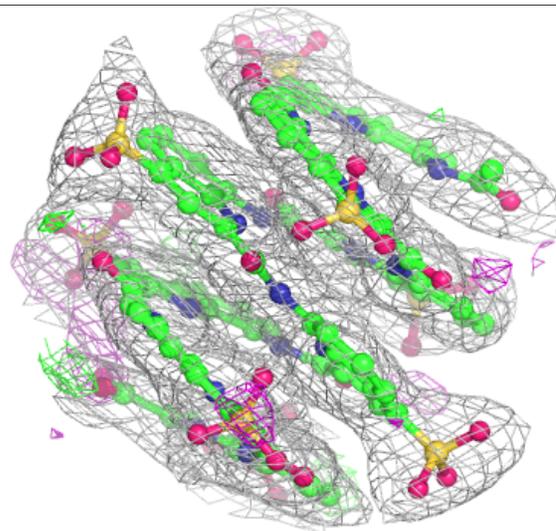
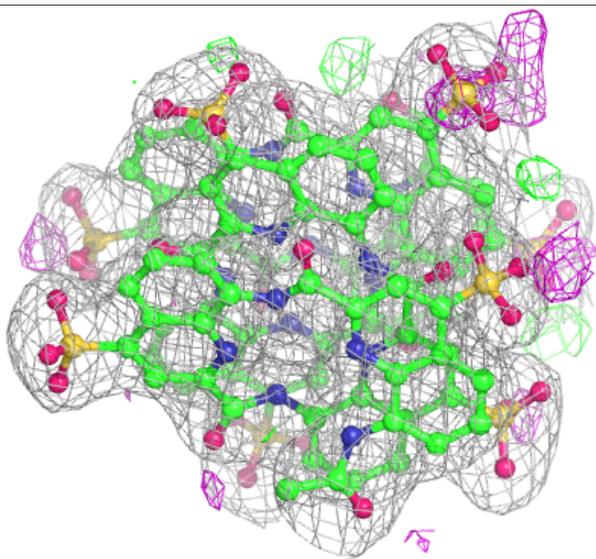
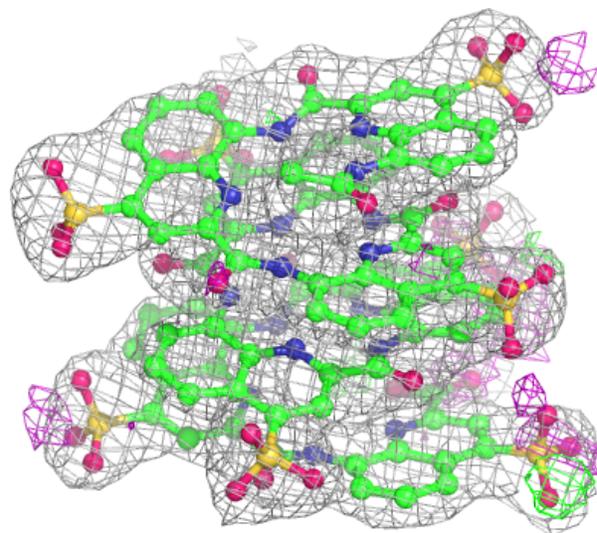
Electron density around LOT A 206 (B):

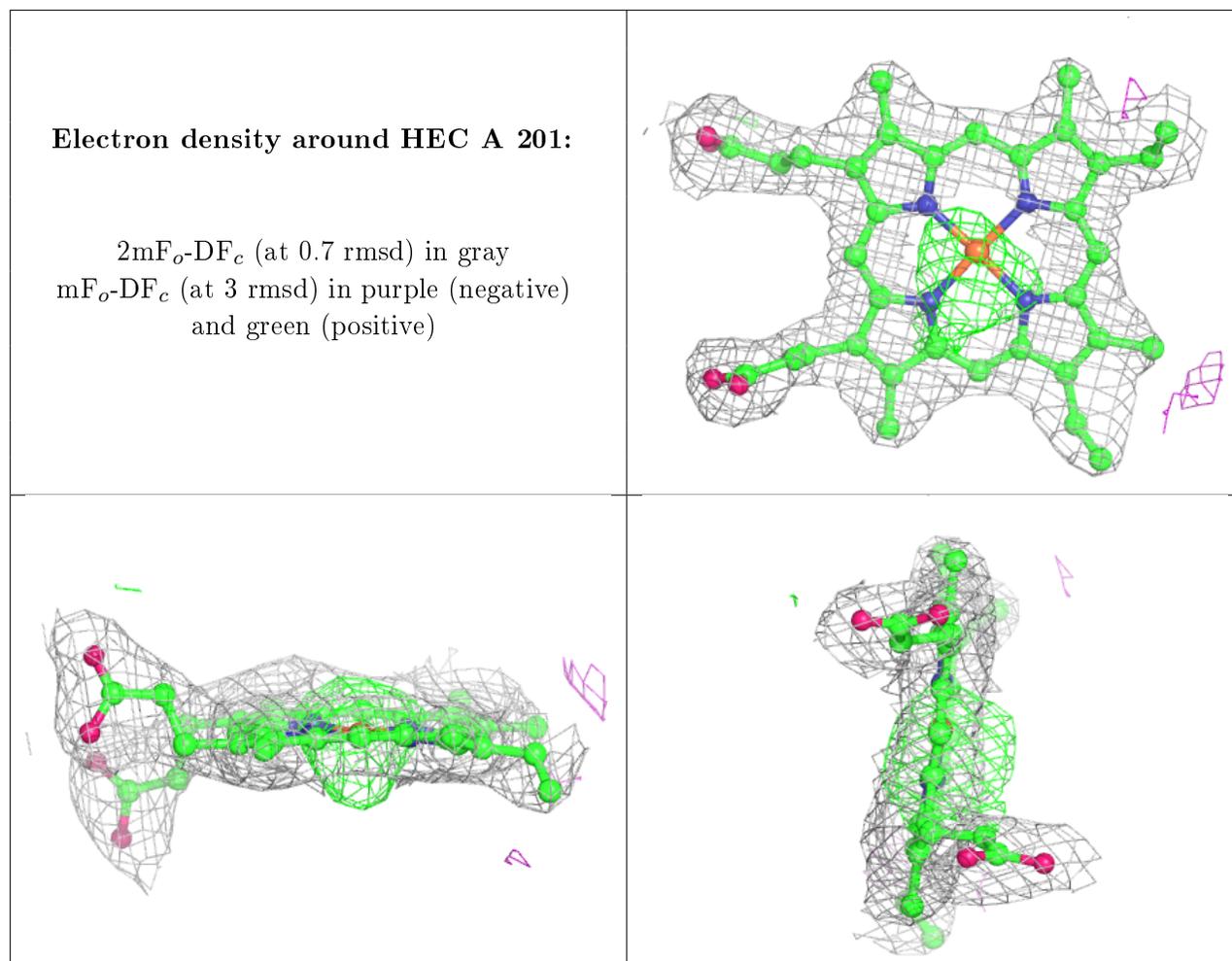
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around LOT A 207:

$2mF_o-DF_c$ (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.