



wwPDB X-ray Structure Validation Summary Report ⓘ

May 22, 2020 – 07:25 am BST

PDB ID : 3U8L
Title : Crystal structure of the acetylcholine binding protein (AChBP) from *Lymnaea stagnalis* in complex with NS3570 (1-(5-phenylpyridin-3-yl)-1,4-diazepane)
Authors : Rohde, L.A.H.; Ahring, P.K.; Jensen, M.L.; Nielsen, E.O.; Peters, D.; Helgstrand, C.; Krintel, C.; Harpsoe, K.; Gajhede, M.; Kastrup, J.S.; Balle, T.
Deposited on : 2011-10-17
Resolution : 2.32 Å(reported)

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

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

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

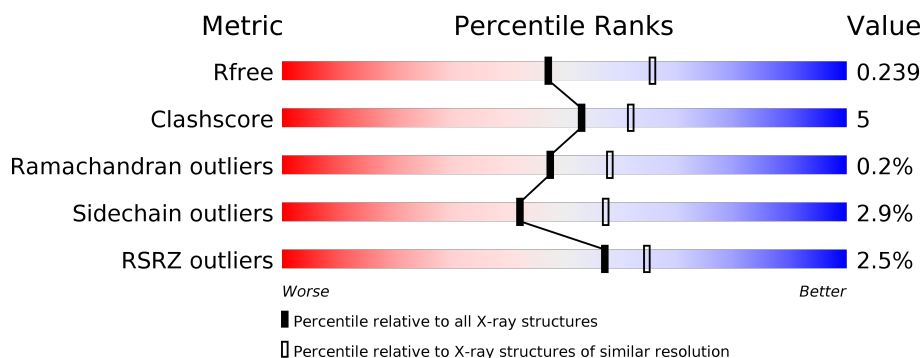
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.32 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	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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	210	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>12%</div> <div>• •</div> </div> </div>
1	B	210	<div> <div>3%</div> <div> <div></div> <div>87%</div> <div>10%</div> <div>•</div> </div> </div>
1	C	210	<div> <div>3%</div> <div> <div></div> <div>86%</div> <div>10%</div> <div>•</div> </div> </div>
1	D	210	<div> <div>%</div> <div> <div></div> <div>88%</div> <div>7%</div> <div>5%</div> </div> </div>
1	E	210	<div> <div>3%</div> <div> <div></div> <div>85%</div> <div>10%</div> <div>• •</div> </div> </div>
1	F	210	<div> <div>3%</div> <div> <div></div> <div>86%</div> <div>10%</div> <div>•</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	210	
1	H	210	
1	I	210	
1	J	210	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	09Q	B	212	-	-	X	-

2 Entry composition

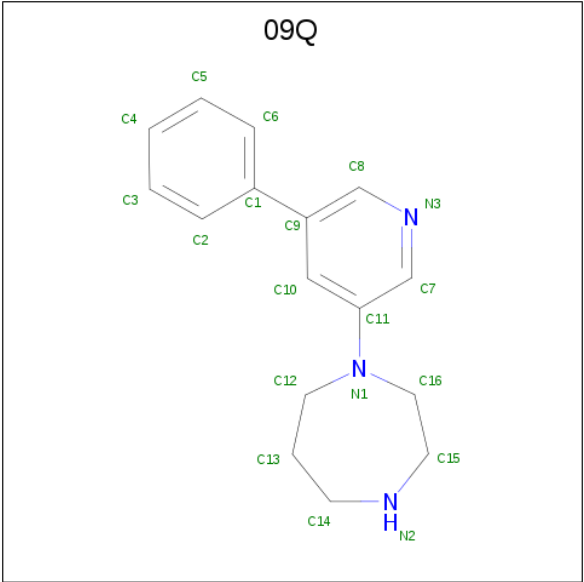
There are 4 unique types of molecules in this entry. The entry contains 17072 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Acetylcholine-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	202	Total	C	N	O	S	0	1	0
			1618	1015	276	321	6			
1	B	205	Total	C	N	O	S	0	0	0
			1636	1023	280	328	5			
1	C	201	Total	C	N	O	S	0	2	0
			1619	1015	279	320	5			
1	D	199	Total	C	N	O	S	0	0	0
			1590	999	273	313	5			
1	E	206	Total	C	N	O	S	0	0	0
			1647	1029	284	329	5			
1	F	202	Total	C	N	O	S	0	1	0
			1618	1015	276	321	6			
1	G	200	Total	C	N	O	S	0	1	0
			1607	1009	274	318	6			
1	H	200	Total	C	N	O	S	0	2	0
			1609	1010	277	316	6			
1	I	204	Total	C	N	O	S	0	1	0
			1635	1023	282	325	5			
1	J	200	Total	C	N	O	S	0	1	0
			1613	1012	280	317	4			

- Molecule 2 is 1-(5-phenylpyridin-3-yl)-1,4-diazepane (three-letter code: 09Q) (formula: C₁₆H₁₉N₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			19	16	3		
2	B	1	Total	C	N	0	0
			19	16	3		
2	B	1	Total	C	N	0	0
			19	16	3		
2	B	1	Total	C	N	0	0
			19	16	3		
2	C	1	Total	C	N	0	0
			19	16	3		
2	D	1	Total	C	N	0	0
			19	16	3		
2	E	1	Total	C	N	0	0
			19	16	3		
2	F	1	Total	C	N	0	0
			19	16	3		
2	G	1	Total	C	N	0	0
			19	16	3		
2	H	1	Total	C	N	0	0
			19	16	3		
2	H	1	Total	C	N	0	0
			19	16	3		
2	H	1	Total	C	N	0	0
			19	16	3		
2	I	1	Total	C	N	0	0
			19	16	3		
2	J	1	Total	C	N	0	0
			19	16	3		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	59	Total	O	0	0
			59	59		
4	B	49	Total	O	0	0
			49	49		
4	C	65	Total	O	0	0
			65	65		
4	D	59	Total	O	0	0
			59	59		
4	E	67	Total	O	0	0
			67	67		
4	F	49	Total	O	0	0
			49	49		
4	G	58	Total	O	0	0
			58	58		
4	H	73	Total	O	0	0
			73	73		

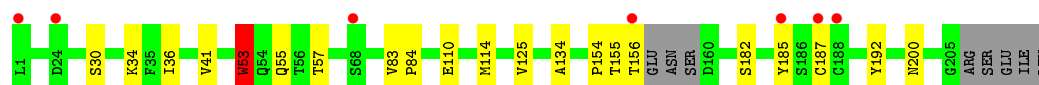
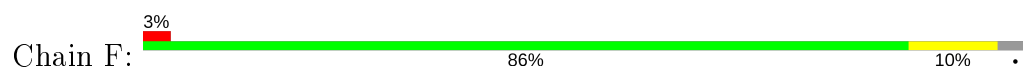
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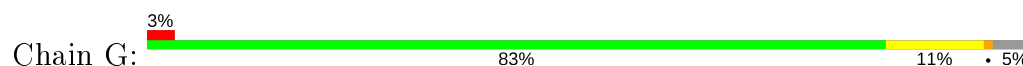
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	I	66	Total 66	O 66	0	0
4	J	54	Total 54	O 54	0	0



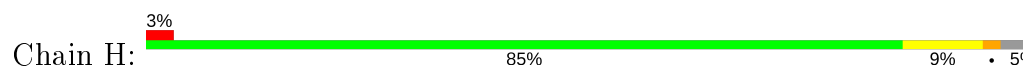
- Molecule 1: Acetylcholine-binding protein



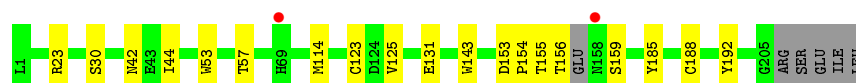
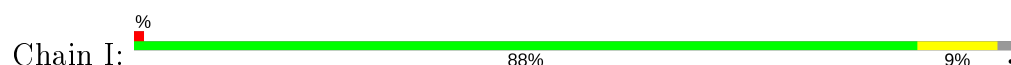
- Molecule 1: Acetylcholine-binding protein



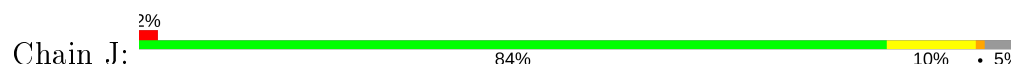
- Molecule 1: Acetylcholine-binding protein



- Molecule 1: Acetylcholine-binding protein



- Molecule 1: Acetylcholine-binding protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.96Å 114.81Å 127.06Å 90.00° 91.08° 90.00°	Depositor
Resolution (Å)	42.35 – 2.32 44.08 – 2.32	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.35-2.32) 99.9 (44.08-2.32)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.11 (at 2.32Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4 _486)	Depositor
R, R_{free}	0.191 , 0.244 0.185 , 0.239	Depositor DCC
R_{free} test set	4597 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	24.2	Xtriage
Anisotropy	0.478	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 48.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.032 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	17072	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 09Q, SO4

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	0.39	0/1656	0.57	1/2259 (0.0%)
1	B	0.39	0/1672	0.54	0/2282
1	C	0.39	0/1660	0.53	0/2264
1	D	0.40	0/1625	0.54	0/2216
1	E	0.40	0/1683	0.56	0/2296
1	F	0.38	0/1656	0.55	1/2259 (0.0%)
1	G	0.39	0/1645	0.57	1/2244 (0.0%)
1	H	0.40	0/1650	0.55	0/2251
1	I	0.40	0/1673	0.54	0/2281
1	J	0.38	0/1650	0.52	0/2247
All	All	0.39	0/16570	0.55	3/22599 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	53	TRP	CA-CB-CG	6.46	125.98	113.70
1	G	53	TRP	CA-CB-CG	5.78	124.69	113.70
1	A	53	TRP	CA-CB-CG	5.74	124.61	113.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1618	0	1574	23	0
1	B	1636	0	1583	24	0
1	C	1619	0	1575	14	0
1	D	1590	0	1548	6	0
1	E	1647	0	1594	21	0
1	F	1618	0	1572	17	0
1	G	1607	0	1562	19	0
1	H	1609	0	1570	12	0
1	I	1635	0	1589	20	0
1	J	1613	0	1573	24	0
2	A	19	0	19	1	0
2	B	57	0	57	12	0
2	C	19	0	19	1	0
2	D	19	0	19	2	0
2	E	19	0	19	1	0
2	F	19	0	19	3	0
2	G	19	0	19	2	0
2	H	57	0	57	6	0
2	I	19	0	19	4	0
2	J	19	0	19	1	0
3	B	10	0	0	0	0
3	G	5	0	0	0	0
4	A	59	0	0	3	0
4	B	49	0	0	0	0
4	C	65	0	0	4	0
4	D	59	0	0	0	0
4	E	67	0	0	4	0
4	F	49	0	0	1	0
4	G	58	0	0	1	0
4	H	73	0	0	0	0
4	I	66	0	0	2	0
4	J	54	0	0	1	0
All	All	17072	0	16006	175	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 175 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:B:154:PRO:HB3	1:B:178:GLN:HE21	1.29	0.98
1:A:89:TYR:HD2	2:B:212:09Q:H4	1.38	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:120[B]:ARG:CG	1:J:120[B]:ARG:HH11	1.87	0.87
1:A:186:SER:HB2	1:B:160:ASP:HB2	1.56	0.85
1:G:55:GLN:HA	1:G:114[B]:MET:HG3	1.59	0.83

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	199/210 (95%)	196 (98%)	2 (1%)	1 (0%)	29	35
1	B	203/210 (97%)	201 (99%)	2 (1%)	0	100	100
1	C	199/210 (95%)	197 (99%)	2 (1%)	0	100	100
1	D	195/210 (93%)	192 (98%)	3 (2%)	0	100	100
1	E	204/210 (97%)	199 (98%)	5 (2%)	0	100	100
1	F	199/210 (95%)	195 (98%)	3 (2%)	1 (0%)	29	35
1	G	197/210 (94%)	196 (100%)	1 (0%)	0	100	100
1	H	198/210 (94%)	194 (98%)	4 (2%)	0	100	100
1	I	201/210 (96%)	199 (99%)	2 (1%)	0	100	100
1	J	195/210 (93%)	191 (98%)	3 (2%)	1 (0%)	29	35
All	All	1990/2100 (95%)	1960 (98%)	27 (1%)	3 (0%)	47	58

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	14	SER
1	A	186	SER
1	F	154	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	189/196 (96%)	181 (96%)	8 (4%)	30	41
1	B	191/196 (97%)	186 (97%)	5 (3%)	46	62
1	C	189/196 (96%)	186 (98%)	3 (2%)	62	77
1	D	185/196 (94%)	178 (96%)	7 (4%)	33	46
1	E	192/196 (98%)	185 (96%)	7 (4%)	35	48
1	F	189/196 (96%)	183 (97%)	6 (3%)	39	53
1	G	188/196 (96%)	184 (98%)	4 (2%)	53	70
1	H	188/196 (96%)	177 (94%)	11 (6%)	19	26
1	I	191/196 (97%)	189 (99%)	2 (1%)	76	87
1	J	187/196 (95%)	184 (98%)	3 (2%)	62	77
All	All	1889/1960 (96%)	1833 (97%)	56 (3%)	42	56

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	25	ARG
1	F	110	GLU
1	I	131	GLU
1	E	156	THR
1	E	187	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	146	HIS
1	J	178	GLN
1	I	12	GLN
1	B	178	GLN
1	E	69	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

17 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	09Q	I	211	-	19,21,21	1.21	1 (5%)	23,27,27	1.80	3 (13%)
2	09Q	J	211	-	19,21,21	1.13	0	23,27,27	1.48	2 (8%)
2	09Q	H	211	-	19,21,21	1.14	0	23,27,27	1.10	2 (8%)
2	09Q	H	212	-	19,21,21	1.23	0	23,27,27	1.26	3 (13%)
2	09Q	C	211	-	19,21,21	1.22	1 (5%)	23,27,27	1.47	2 (8%)
3	SO4	B	215	-	4,4,4	0.16	0	6,6,6	0.09	0
2	09Q	A	211	-	19,21,21	1.10	1 (5%)	23,27,27	1.69	4 (17%)
2	09Q	B	211	-	19,21,21	1.08	0	23,27,27	1.20	1 (4%)
2	09Q	G	211	-	19,21,21	1.19	0	23,27,27	1.46	2 (8%)
2	09Q	E	211	-	19,21,21	1.16	0	23,27,27	1.27	2 (8%)
2	09Q	F	211	-	19,21,21	1.13	0	23,27,27	1.30	3 (13%)
2	09Q	B	212	-	19,21,21	1.15	1 (5%)	23,27,27	1.31	2 (8%)
2	09Q	H	213	-	19,21,21	1.24	1 (5%)	23,27,27	1.35	2 (8%)
3	SO4	G	212	-	4,4,4	0.11	0	6,6,6	0.11	0
3	SO4	B	214	-	4,4,4	0.14	0	6,6,6	0.10	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	09Q	B	213	-	19,21,21	1.12	0	23,27,27	1.32	2 (8%)
2	09Q	D	211	-	19,21,21	1.16	1 (5%)	23,27,27	1.40	2 (8%)

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	09Q	I	211	-	-	2/8/17/17	0/3/3/3
2	09Q	J	211	-	-	0/8/17/17	0/3/3/3
2	09Q	H	211	-	-	2/8/17/17	0/3/3/3
2	09Q	H	212	-	-	0/8/17/17	0/3/3/3
2	09Q	C	211	-	-	0/8/17/17	0/3/3/3
2	09Q	A	211	-	-	4/8/17/17	0/3/3/3
2	09Q	B	211	-	-	1/8/17/17	0/3/3/3
2	09Q	G	211	-	-	1/8/17/17	0/3/3/3
2	09Q	E	211	-	-	2/8/17/17	0/3/3/3
2	09Q	F	211	-	-	1/8/17/17	0/3/3/3
2	09Q	B	212	-	-	0/8/17/17	0/3/3/3
2	09Q	H	213	-	-	0/8/17/17	0/3/3/3
2	09Q	B	213	-	-	0/8/17/17	0/3/3/3
2	09Q	D	211	-	-	0/8/17/17	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	211	09Q	C7-C11	2.25	1.43	1.38
2	C	211	09Q	C7-C11	2.11	1.42	1.38
2	B	212	09Q	C7-C11	2.10	1.42	1.38
2	A	211	09Q	C7-C11	2.09	1.42	1.38
2	H	213	09Q	C10-C11	2.08	1.43	1.39

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	211	09Q	C10-C11-C7	-6.60	114.25	119.48
2	A	211	09Q	C10-C11-C7	-5.46	115.15	119.48
2	G	211	09Q	C10-C11-C7	-5.29	115.29	119.48
2	J	211	09Q	C10-C11-C7	-5.27	115.30	119.48
2	C	211	09Q	C10-C11-C7	-5.11	115.43	119.48

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	211	09Q	C2-C1-C9-C8
2	A	211	09Q	C6-C1-C9-C8
2	A	211	09Q	C6-C1-C9-C10
2	A	211	09Q	C2-C1-C9-C10
2	H	211	09Q	C6-C1-C9-C10

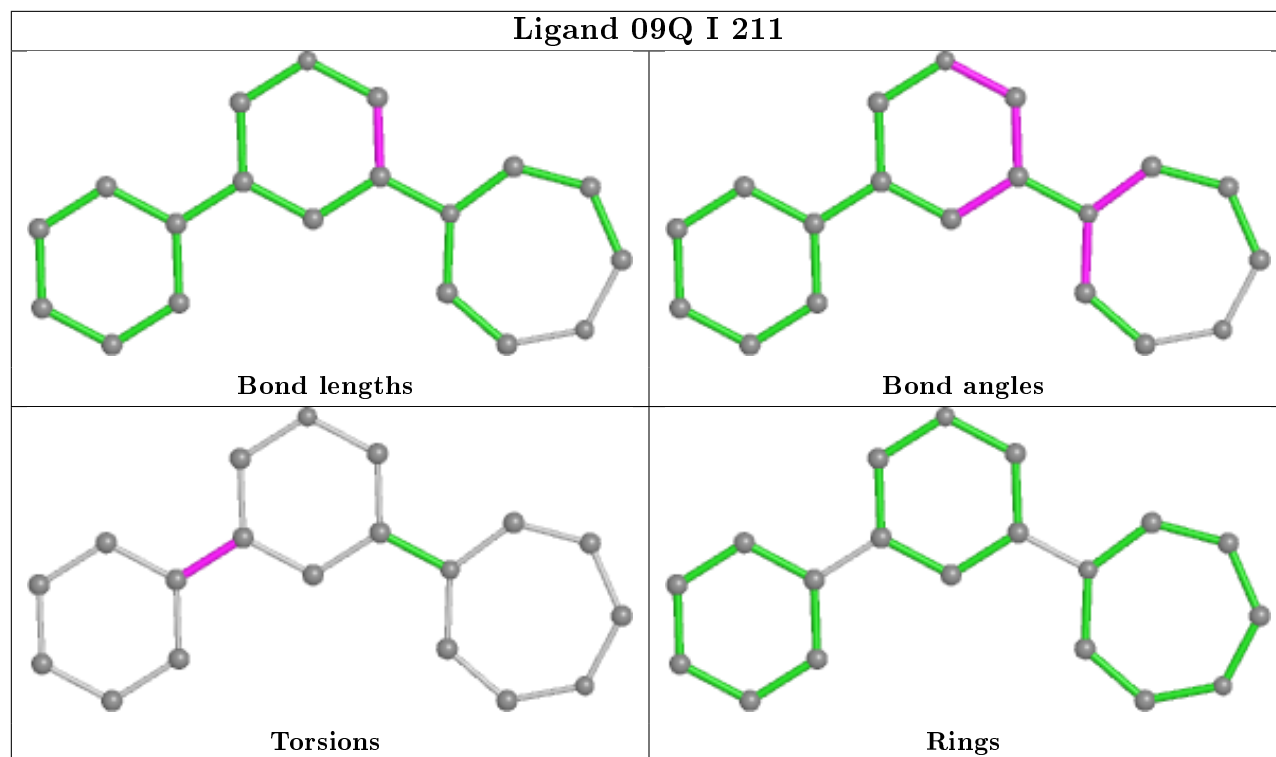
There are no ring outliers.

14 monomers are involved in 33 short contacts:

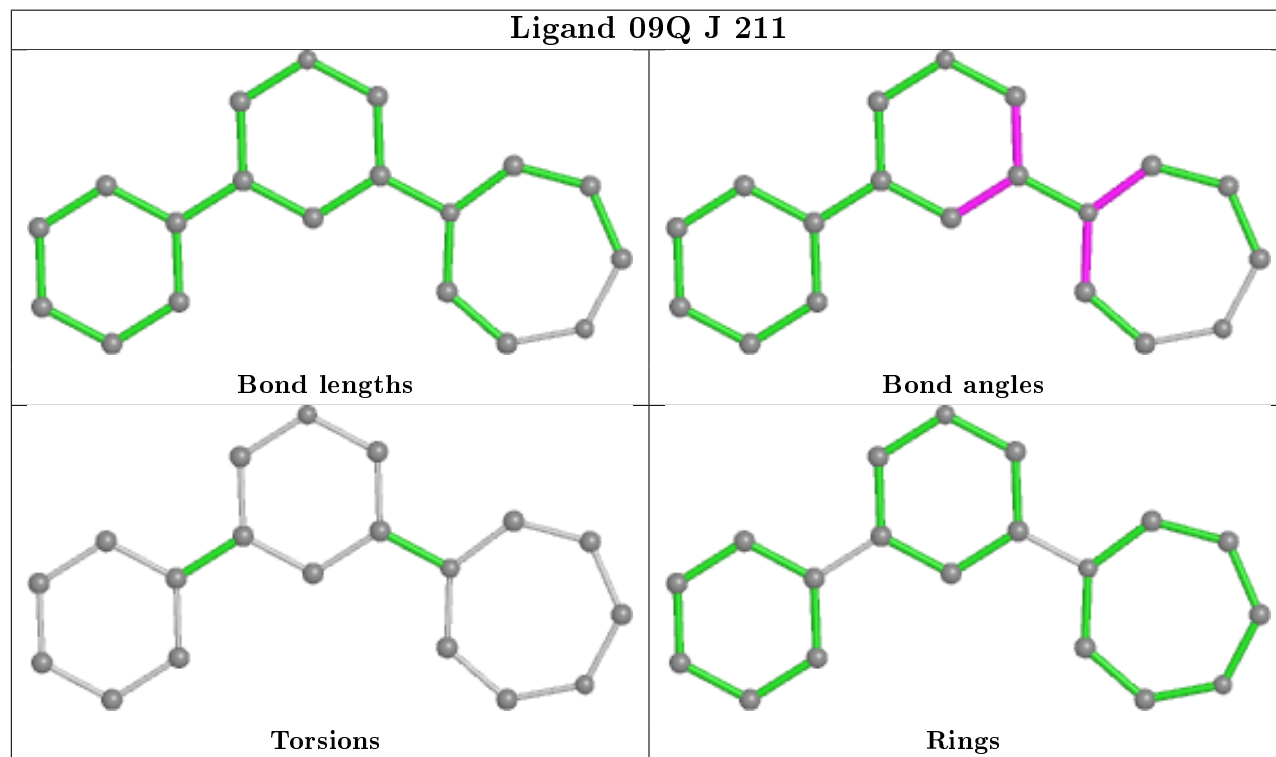
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	I	211	09Q	4	0
2	J	211	09Q	1	0
2	H	211	09Q	2	0
2	H	212	09Q	3	0
2	C	211	09Q	1	0
2	A	211	09Q	1	0
2	B	211	09Q	3	0
2	G	211	09Q	2	0
2	E	211	09Q	1	0
2	F	211	09Q	3	0
2	B	212	09Q	7	0
2	H	213	09Q	3	0
2	B	213	09Q	2	0
2	D	211	09Q	2	0

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

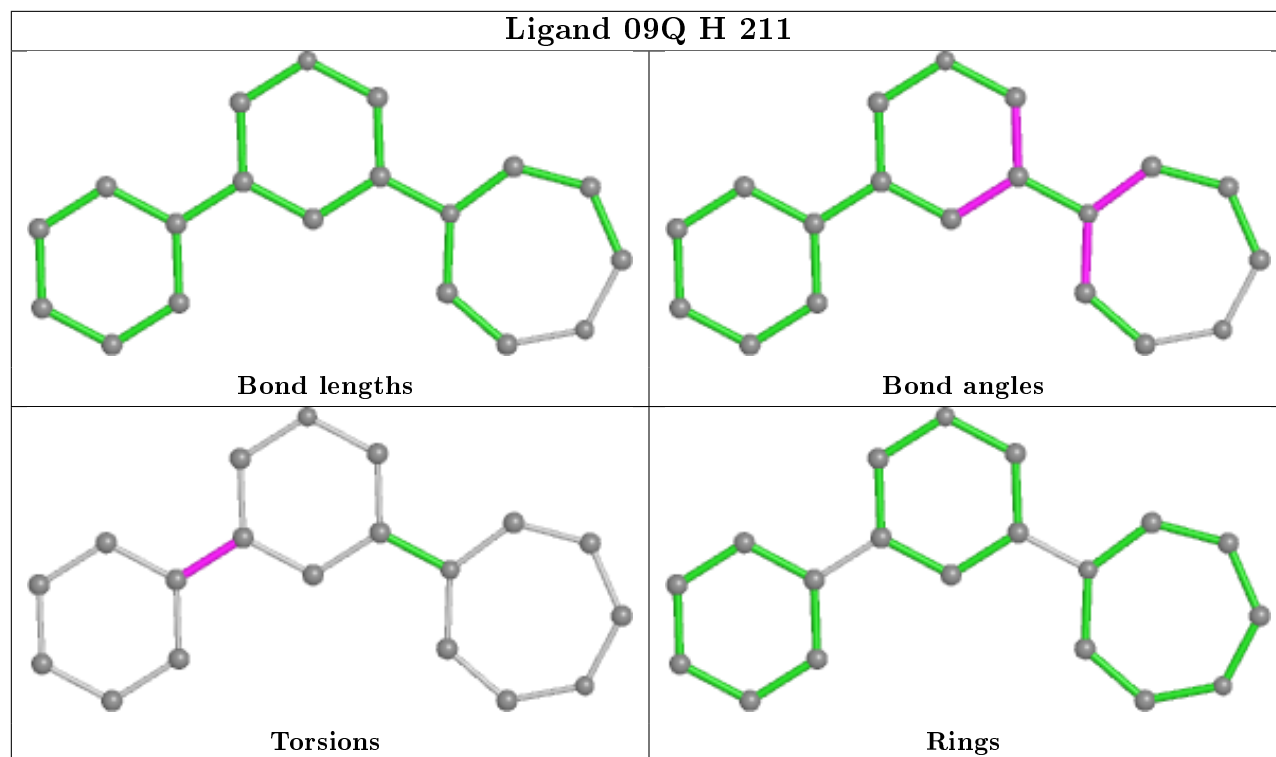
Ligand 09Q I 211



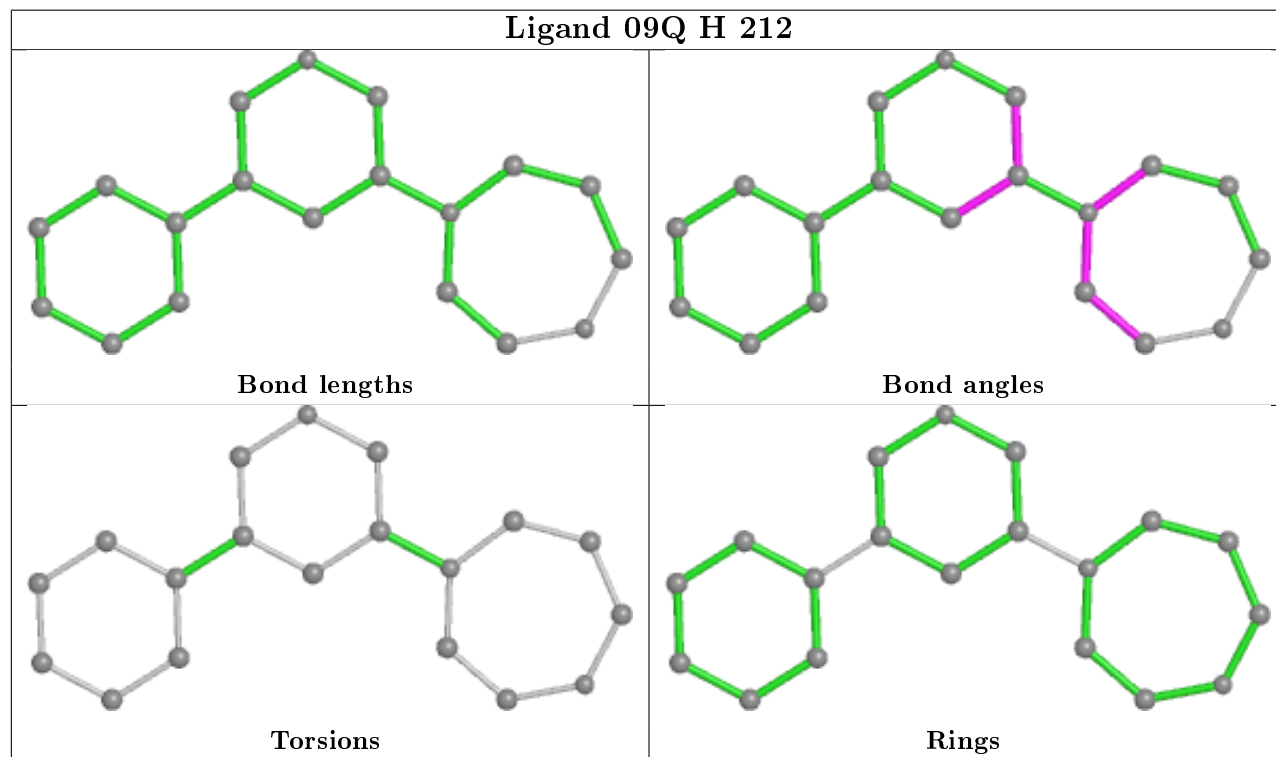
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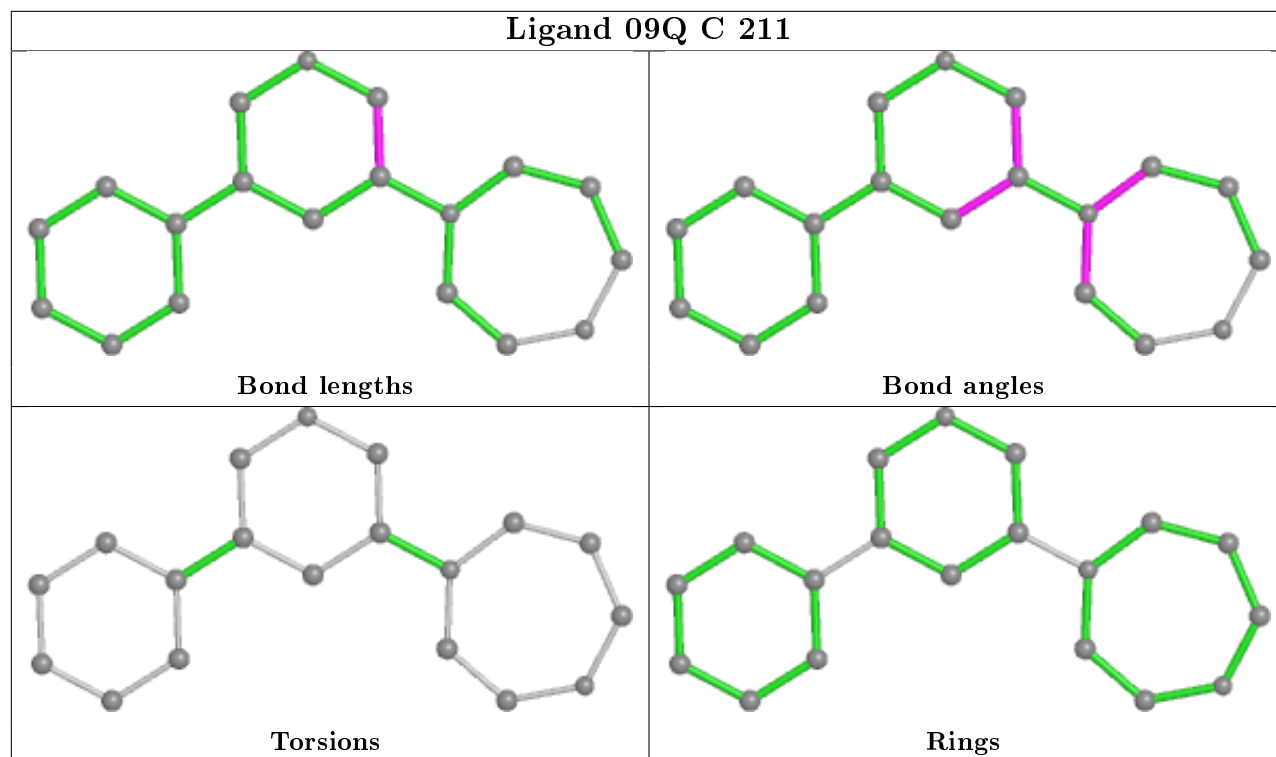
Ligand 09Q H 211



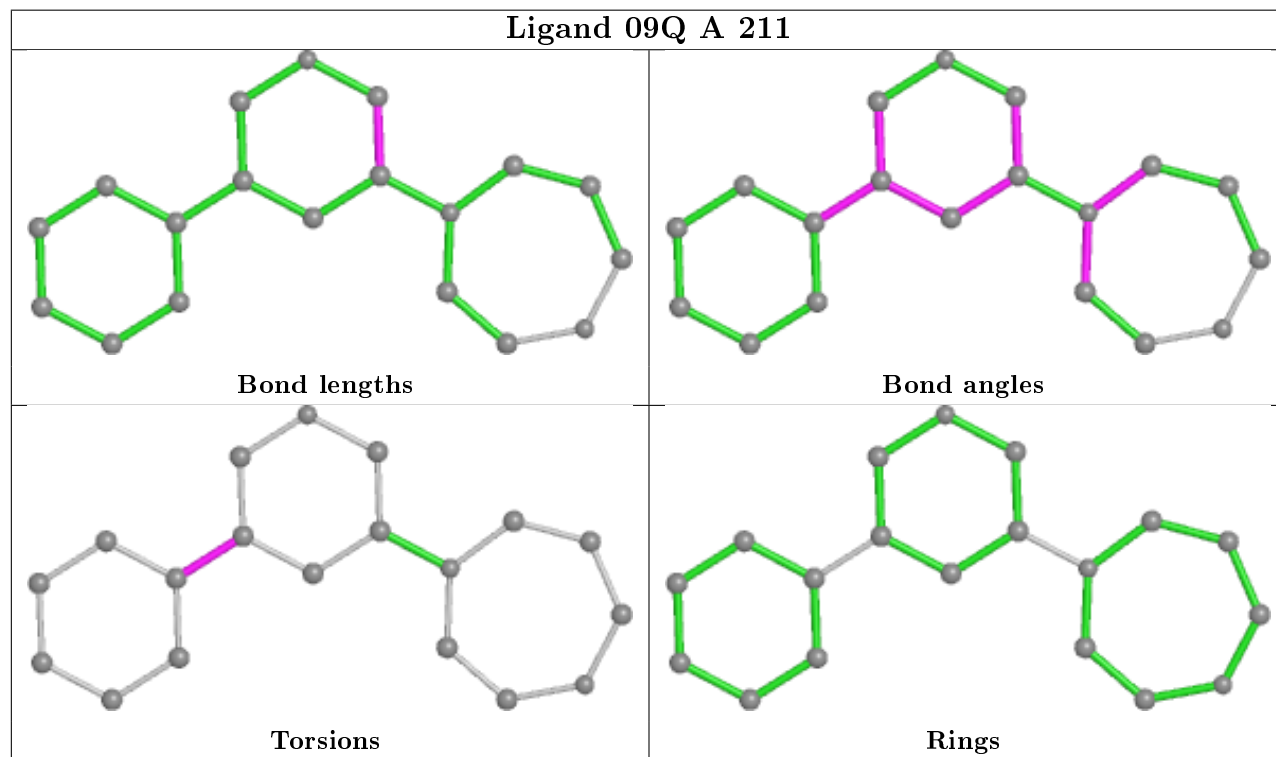
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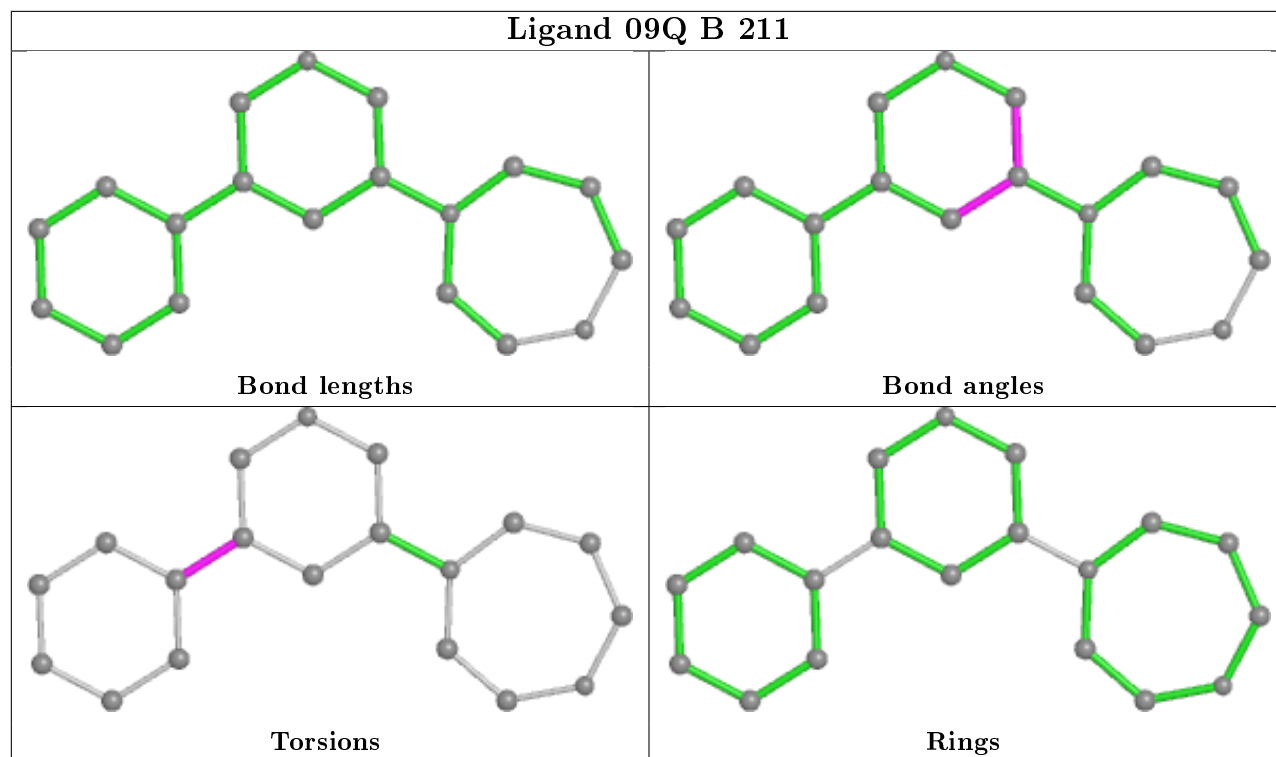
Ligand 09Q C 211



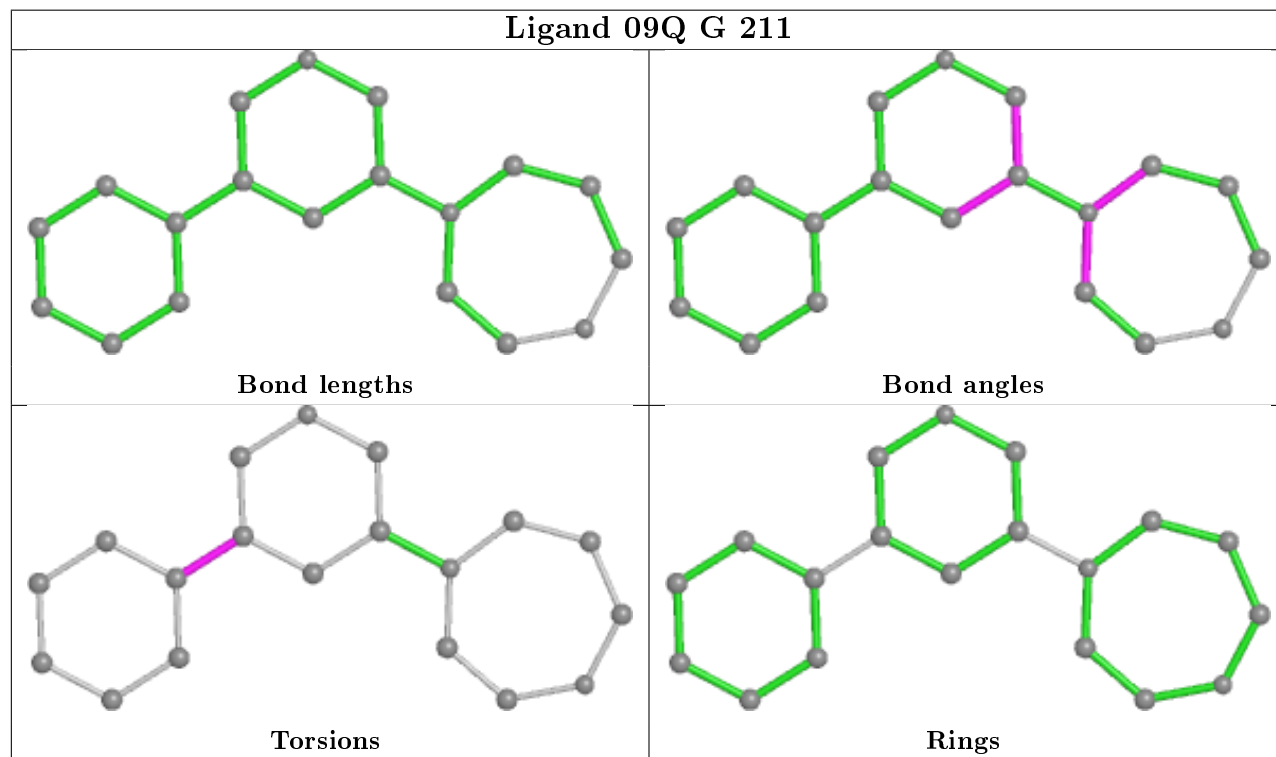
Ligand 09Q A 211



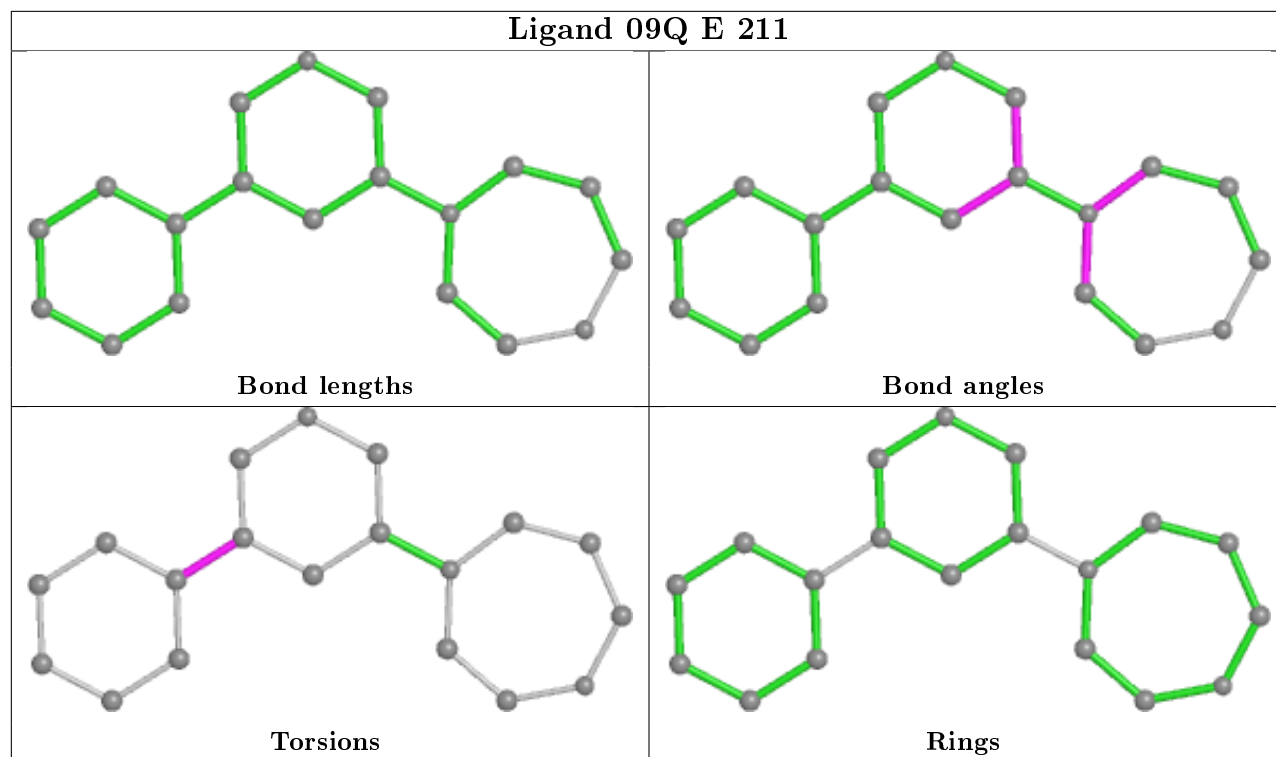
Ligand 09Q B 211



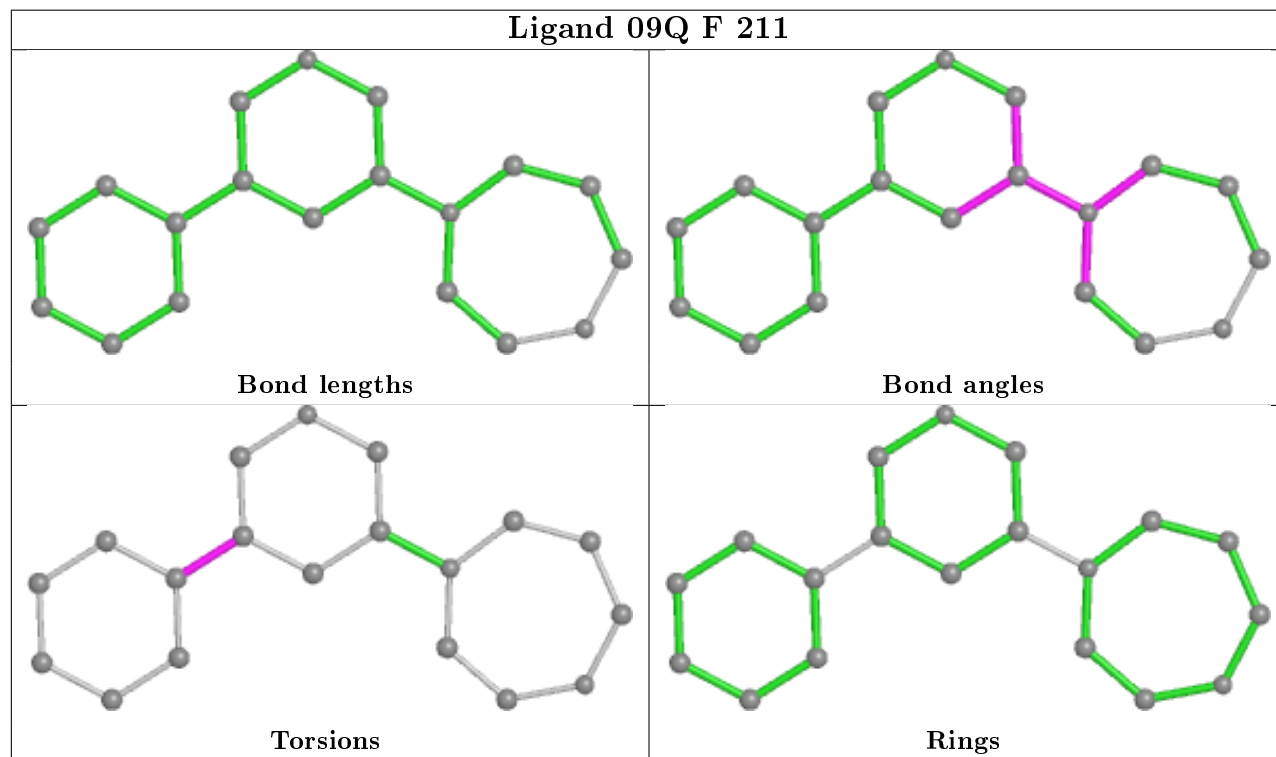
Ligand 09Q G 211



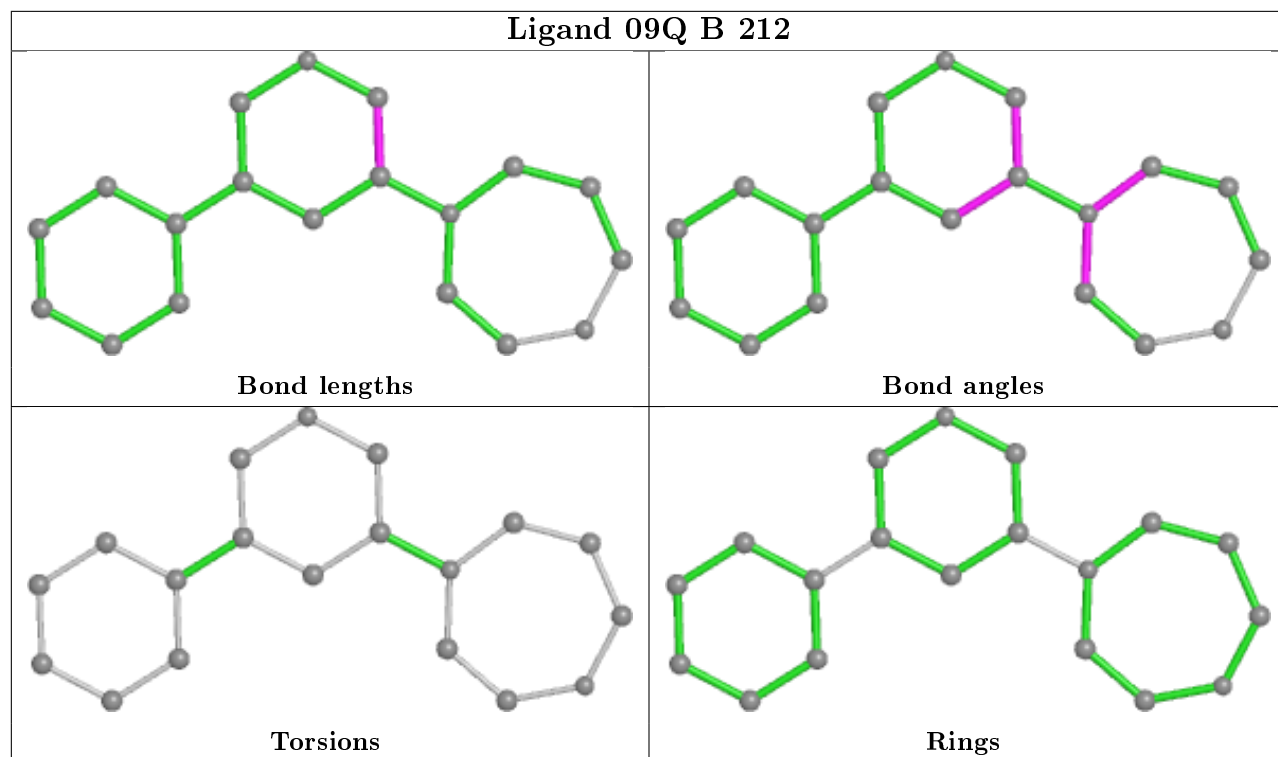
Ligand 09Q E 211



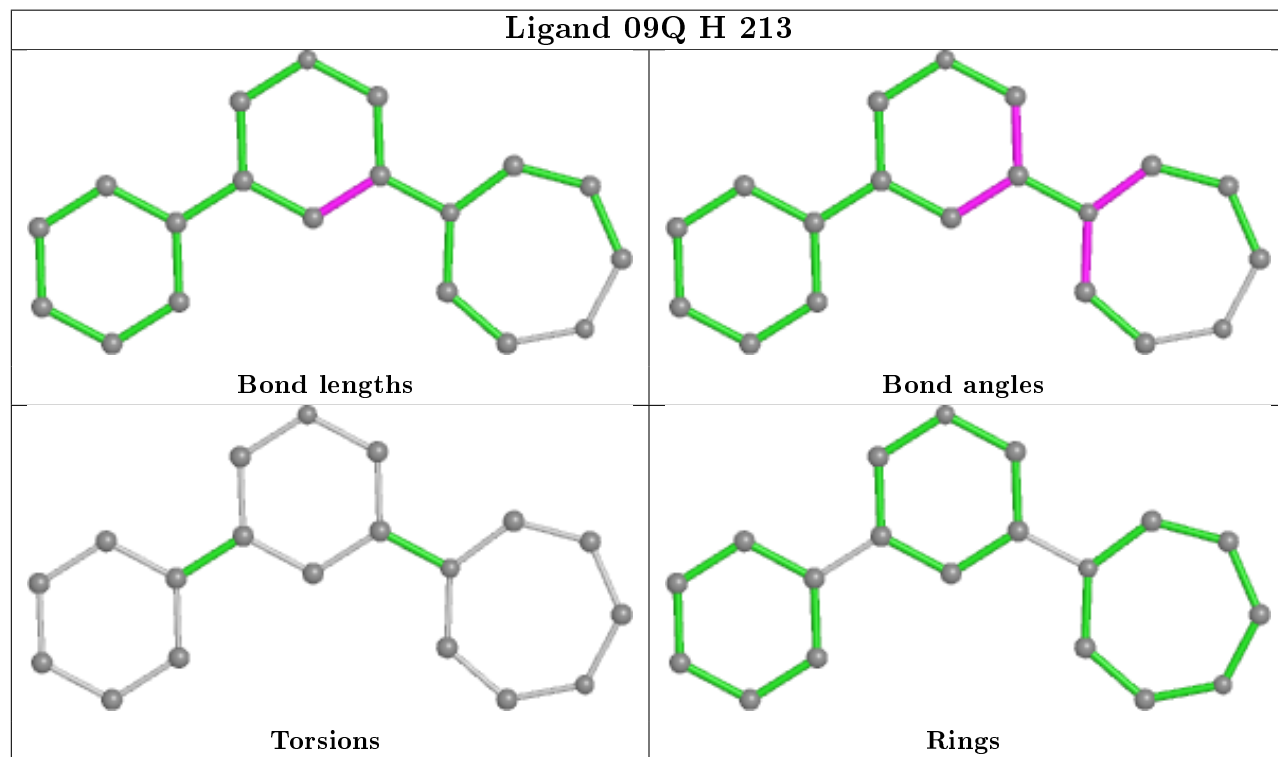
Ligand 09Q F 211

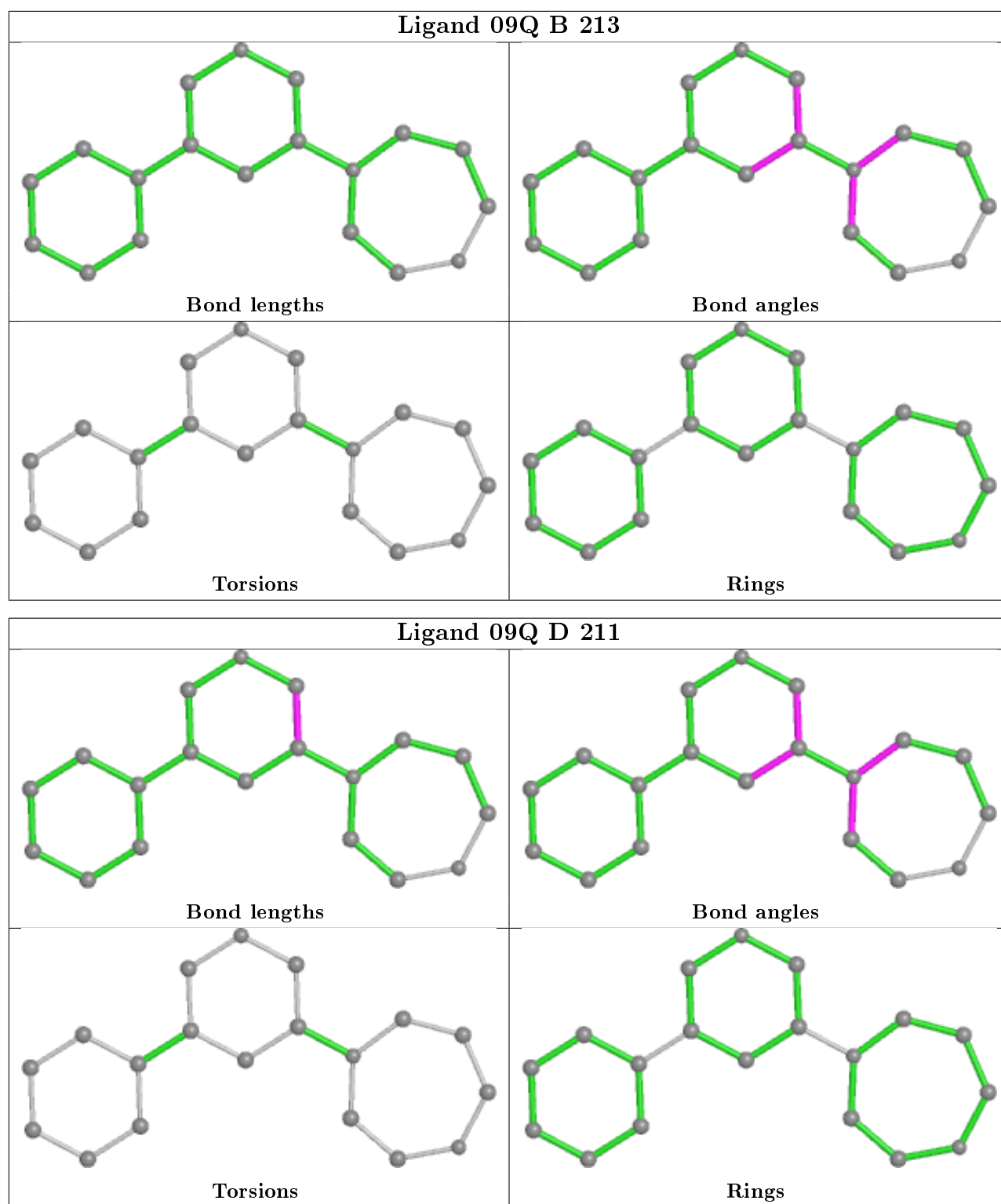


Ligand 09Q B 212



Ligand 09Q H 213





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	202/210 (96%)	-0.12	5 (2%)	57	64	14, 26, 59, 78	0
1	B	205/210 (97%)	-0.04	6 (2%)	51	59	12, 26, 58, 85	0
1	C	201/210 (95%)	-0.12	6 (2%)	50	57	12, 24, 55, 84	0
1	D	199/210 (94%)	-0.18	2 (1%)	82	86	12, 24, 50, 74	0
1	E	206/210 (98%)	-0.07	6 (2%)	51	59	12, 23, 61, 93	0
1	F	202/210 (96%)	-0.02	7 (3%)	44	51	13, 26, 63, 86	0
1	G	200/210 (95%)	-0.10	6 (3%)	50	57	12, 25, 61, 85	0
1	H	200/210 (95%)	-0.15	6 (3%)	50	57	12, 24, 54, 81	0
1	I	204/210 (97%)	-0.16	2 (0%)	82	86	12, 24, 58, 84	0
1	J	200/210 (95%)	-0.07	4 (2%)	65	72	13, 24, 60, 92	0
All	All	2019/2100 (96%)	-0.10	50 (2%)	57	64	12, 25, 61, 93	0

The worst 5 of 50 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	187	CYS	5.2
1	E	188	CYS	4.7
1	F	187	CYS	4.7
1	J	24	ASP	4.5
1	B	68	SER	4.2

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

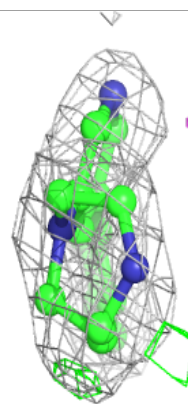
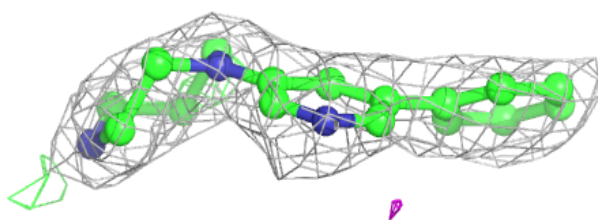
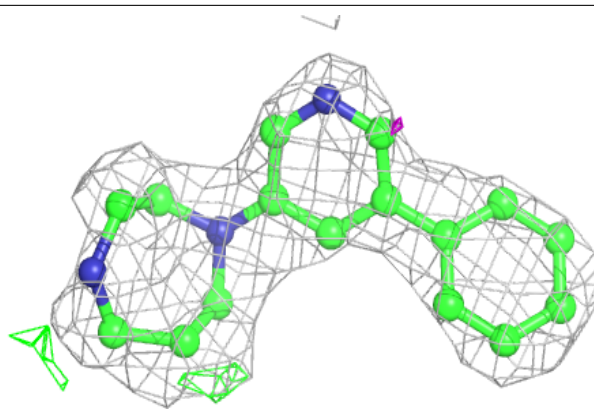
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	SO4	G	212	5/5	0.74	0.18	119,127,137,139	0
2	09Q	B	213	19/19	0.84	0.23	39,47,65,71	0
2	09Q	A	211	19/19	0.91	0.22	29,38,76,76	0
2	09Q	B	212	19/19	0.91	0.16	33,53,73,75	0
2	09Q	H	212	19/19	0.93	0.15	20,34,48,53	0
2	09Q	H	213	19/19	0.93	0.16	16,44,66,67	0
2	09Q	C	211	19/19	0.95	0.14	17,26,47,50	0
2	09Q	F	211	19/19	0.95	0.16	16,26,47,47	0
2	09Q	J	211	19/19	0.96	0.14	17,33,42,45	0
2	09Q	H	211	19/19	0.96	0.14	13,23,28,31	0
2	09Q	G	211	19/19	0.96	0.13	9,24,39,40	0
2	09Q	I	211	19/19	0.96	0.12	16,27,47,48	0
3	SO4	B	215	5/5	0.97	0.13	62,65,83,88	0
3	SO4	B	214	5/5	0.97	0.15	36,86,102,106	0
2	09Q	B	211	19/19	0.97	0.14	20,29,35,40	0
2	09Q	D	211	19/19	0.97	0.14	11,21,40,44	0
2	09Q	E	211	19/19	0.98	0.13	14,23,33,37	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.

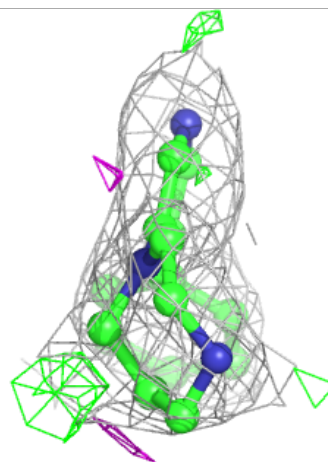
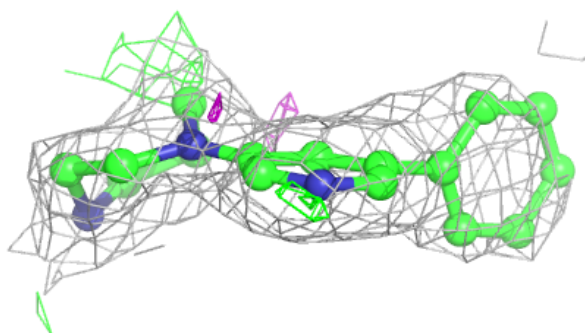
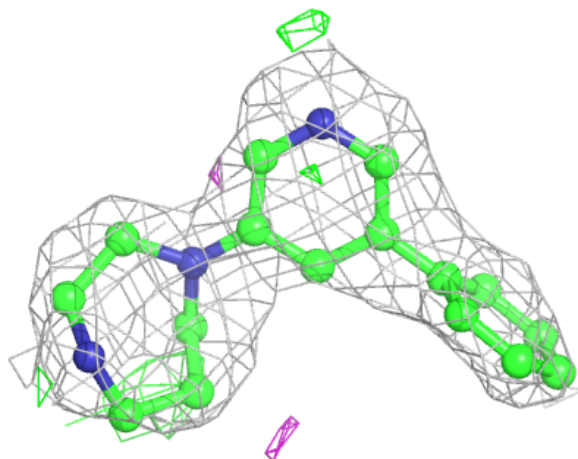
Electron density around 09Q B 213:

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



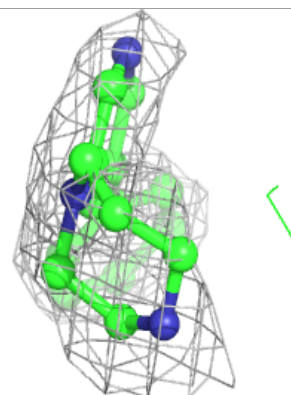
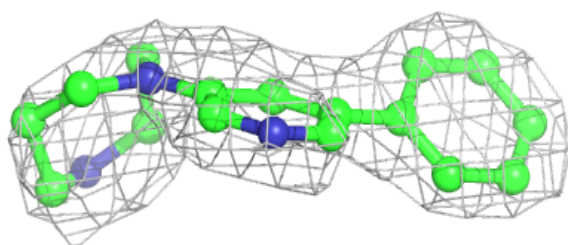
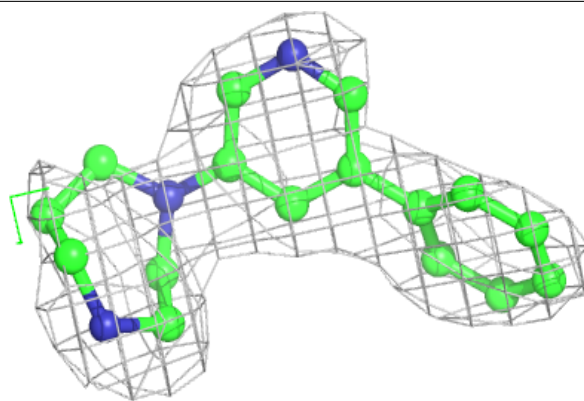
Electron density around 09Q A 211:

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

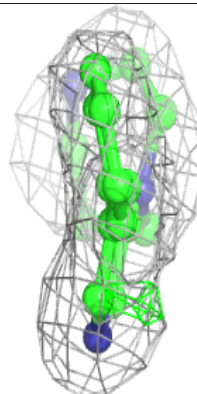
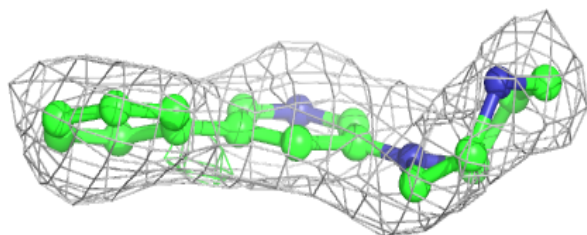
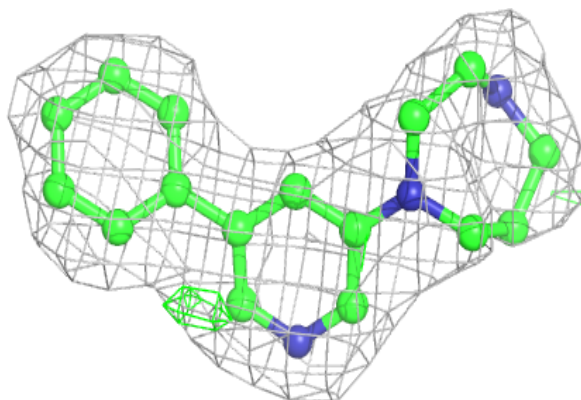


Electron density around 09Q B 212:

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

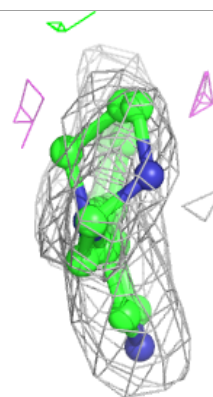
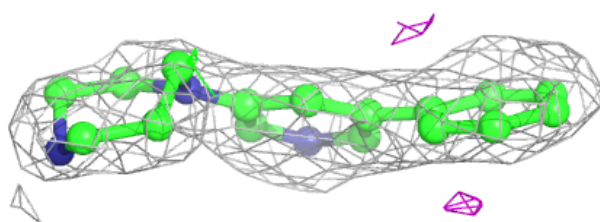
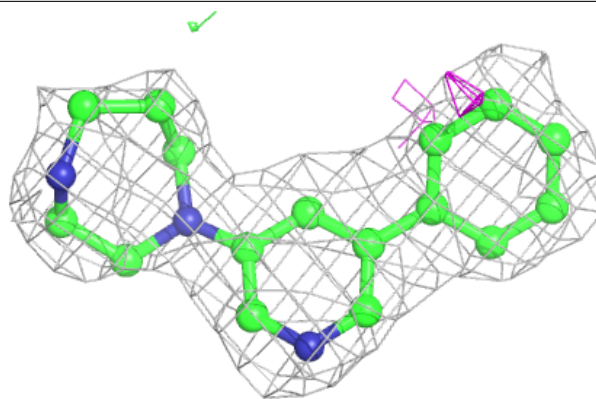
**Electron density around 09Q H 212:**

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

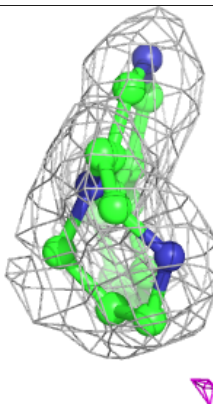
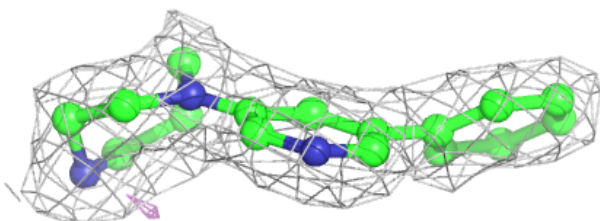
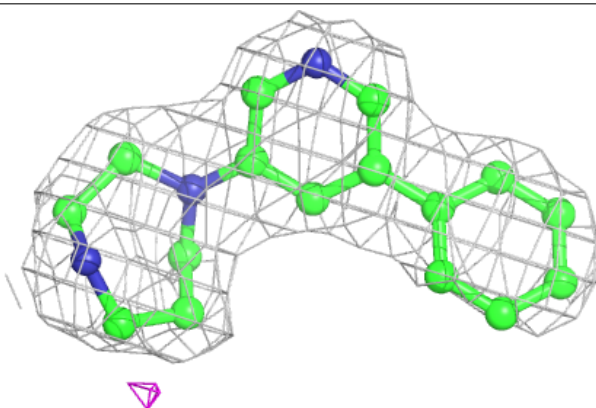


Electron density around 09Q H 213:

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

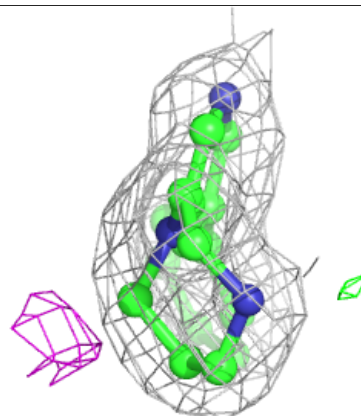
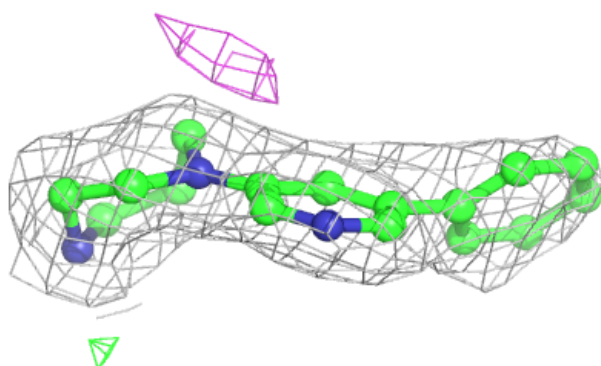
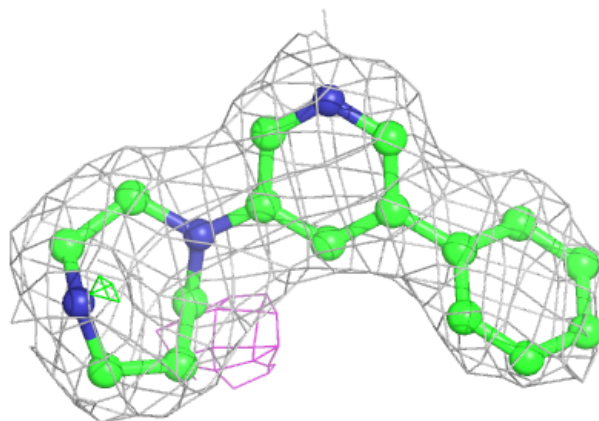
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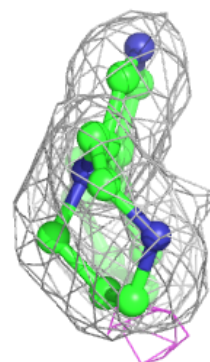
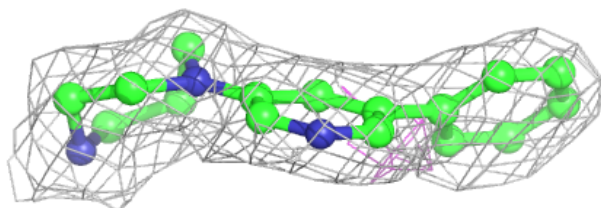
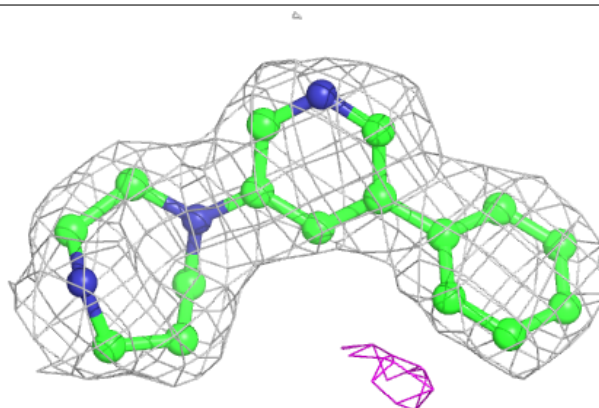


Electron density around 09Q F 211:

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and green (positive)

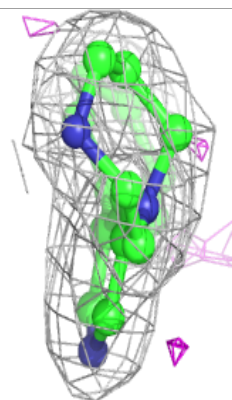
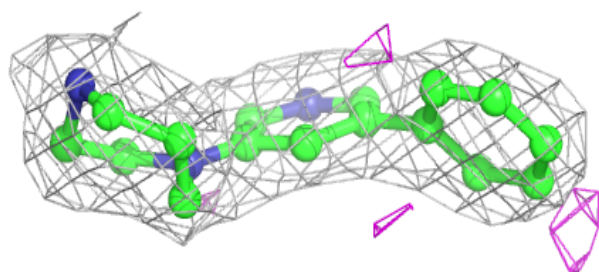
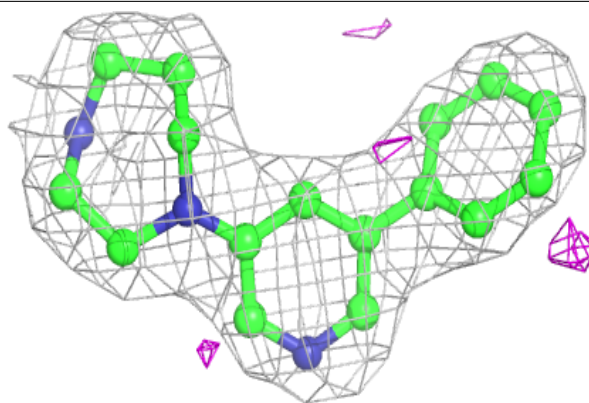
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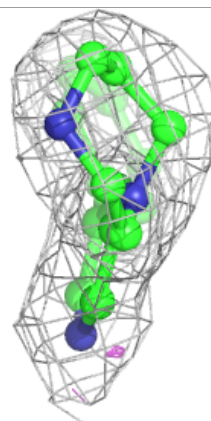
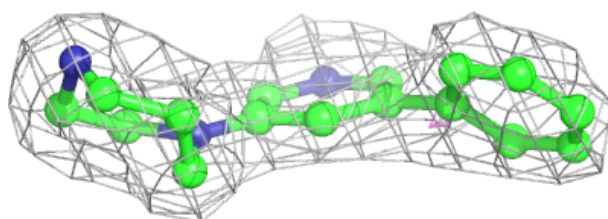
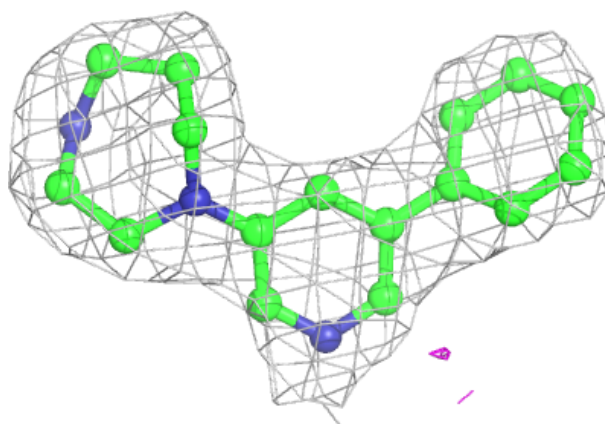


Electron density around 09Q H 211:

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and green (positive)

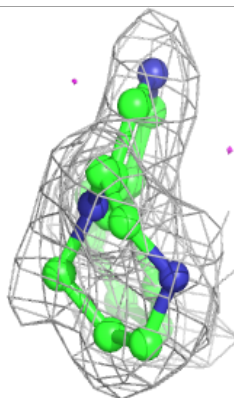
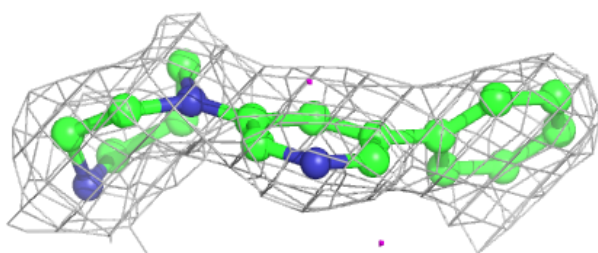
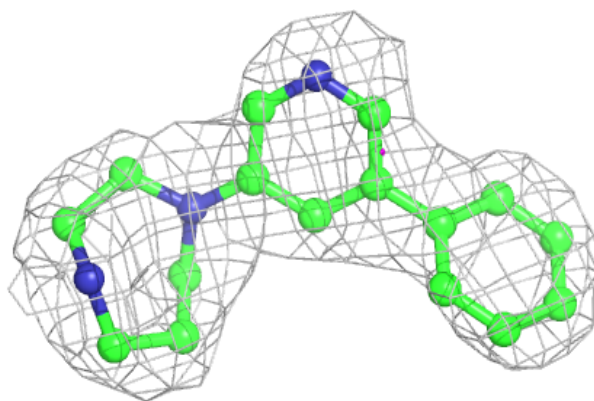
**Electron density around 09Q G 211:**

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and green (positive)

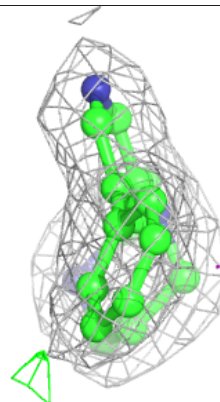
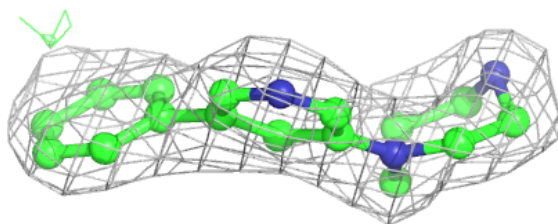
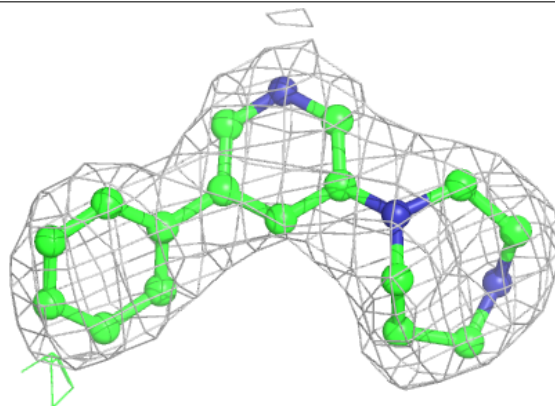


Electron density around 09Q I 211:

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and green (positive)

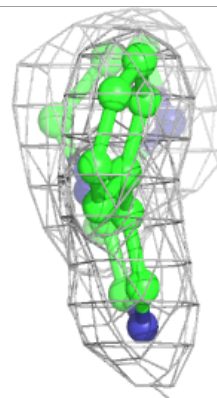
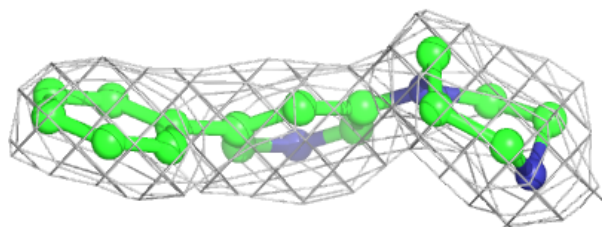
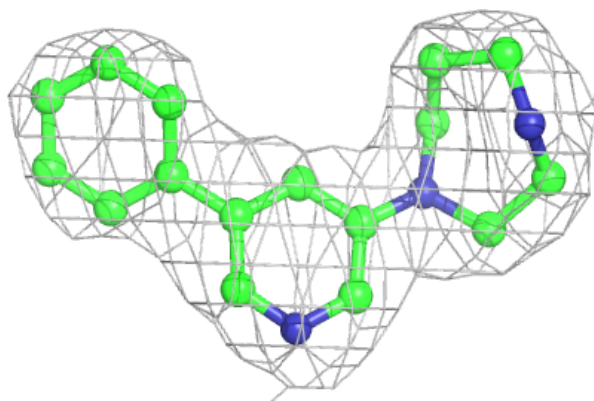
**Electron density around 09Q B 211:**

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

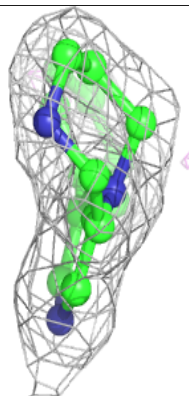
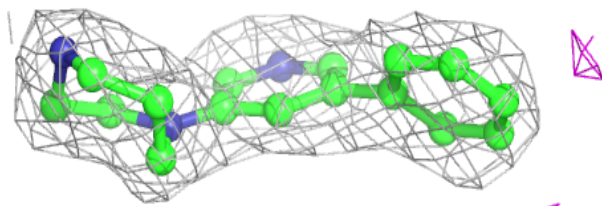
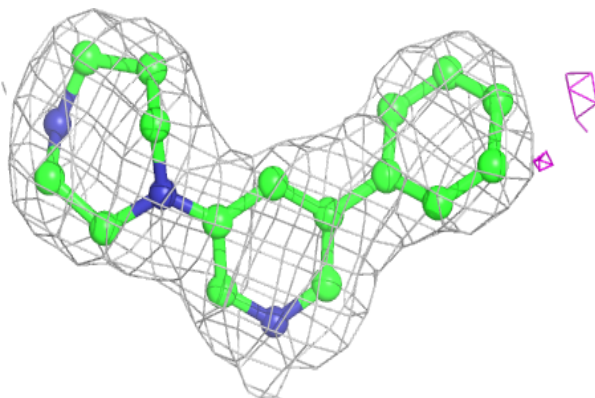


Electron density around 09Q D 211:

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and green (positive)

**Electron density around 09Q E 211:**

$2mF_o-DF_c$ (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.